

Supplementary Table 1. Clinical characteristics at diagnosis of the PT-DLBCL study cohort

Variable	Number of patients (%)
Age	median, 65 years old
≤60	77 (40.1)
>60	115 (59.9)
Stage	
I/II	135 (73)
III/IV	50 (27)
LDH	
Normal	115 (63.5)
Elevated	66 (36.5)
ECOG performance score	
<2	162 (93.6)
≥2	11 (6.4)
Extranodal involvement in addition to testis	
No	148 (80.4)
Yes	36 (19.6)
Nodal involvement at diagnosis	
No	116 (67.4)
Yes	56 (32.6)
IPI score	
0-2	143 (83.1)
3 to 5	29 (16.9)
B symptoms	
Absence	166 (91.7)
Presence	15 (8.3)
Tumor size	
<7 cm	110 (65.9)
≥7 cm	57 (34.1)
Tumor size	
<5 cm	65 (38.9)
≥5 cm	102 (61.1)
Tumor laterality	
Left	66 (44.3)
Right	70 (47)
Bilatera	13 (8.7)
Immunohistochemical subtype	
GCB	40 (22.3)
Non-GCB	139 (77.7)

Suppl. Table 2.

Suppl. Table 2.1 Significantly differentially expressed 533 genes between PT-DLBCL and systemic DLBCL (corresponding to Figure 2A)

Gene ID	Gene ID	Gene Name	Score(d)	Fold Change	q-value(%)	Local fdr(%)
WT1	WT1	WT1 transcription factor(WT1)	13.4079	3.689568	0	0
GAB1	GAB1	GRB2 associated binding protein 1(GAB1)	11.14957	2.201391	0	0.097666
RASAL1	RASAL1	RAS protein activator like 1(RASAL1)	9.81972	2.872343	0	0.090371
PLA2G5	PLA2G5	phospholipase A2 group V(PLA2G5)	9.808556	2.173042	0	0.089413
PAK6	PAK6	p21 (RAC1) activated kinase 6(PAK6)	9.274048	2.09253	0	0.01281
PEG3	PEG3	paternally expressed 3(PEG3)	9.262277	2.840433	0	0.01034
ZNF444	ZNF444	zinc finger protein 444(ZNF444)	8.922662	1.809619	0	0
AMH	AMH	anti-Mullerian hormone(AMH)	8.896133	1.788231	0	0
ERBB4	ERBB4	erb-b2 receptor tyrosine kinase 4(ERBB4)	8.774481	2.068742	0	0
DMRT1	DMRT1	doublesex and mab-3 related transcription factor 1(DMRT1)	8.528131	1.956402	0	0
EPHB1	EPHB1	EPH receptor B1(EPHB1)	8.356464	2.725126	0	0
FSTL3	FSTL3	folliculin like 3(FSTL3)	8.304536	1.781074	0	0
LAMA1	LAMA1	laminin subunit alpha 1(LAMA1)	8.30349	1.949333	0	0
EPCAM	EPCAM	epithelial cell adhesion molecule(EPCAM)	8.036773	3.455655	0	0
AR	AR	androgen receptor(AR)	7.812203	1.658092	0	0
LEFTY2	LEFTY2	left-right determination factor 2(LEFTY2)	7.756401	1.777408	0	0
TCL1A	TCL1A	TCL1 family AKT coactivator A(TCL1A)	7.607283	3.358009	0	0
FOXP1	FOXP1	forkhead box P1(FOXP1)	7.453495	1.586365	0	0
BCL2L2	BCL2L2	BCL2 like 2(BCL2L2)	7.38817	1.584418	0	0
WNT6	WNT6	Wnt family member 6(WNT6)	7.363937	1.475891	0	0
ACSBG1	ACSBG1	acyl-CoA synthetase bubblegum family member 1(ACSBG1)	7.311733	1.822768	0	0
ATP8A2	ATP8A2	ATPase phospholipid transporting 8A2(ATP8A2)	7.267225	1.954322	0	0
NEURL1	NEURL1	neuralized E3 ubiquitin protein ligase 1(NEURL1)	6.886525	1.566828	0	0
GLI1	GLI1	GLI family zinc finger 1(GLI1)	6.691176	1.652739	0	0
COL9A3	COL9A3	collagen type IX alpha 3 chain(COL9A3)	6.520066	1.712384	0	0
MDC1	MDC1	mediator of DNA damage checkpoint 1(MDC1)	6.458594	1.256966	0	0
MYH11	MYH11	myosin heavy chain 11(MYH11)	6.369736	2.262366	0	0
RASGRF1	RASGRF1	Ras protein specific guanine nucleotide releasing factor 1(RASGRF1)	6.366034	1.868653	0	0
FBXW7	FBXW7	F-box and WD repeat domain containing 7(FBXW7)	6.197275	1.338916	0	0
USP6	USP6	ubiquitin specific peptidase 6(USP6)	6.129284	1.736066	0	0
PRICKLE1	PRICKLE1	prickle planar cell polarity protein 1(PRICKLE1)	6.02755	1.625731	0	0
RUNX1T1	RUNX1T1	RUNX1 partner transcriptional co-repressor 1(RUNX1T1)	5.875501	1.697718	0	0
PHOX2B	PHOX2B	paired like homeobox 2B(PHOX2B)	5.775431	1.47931	0	0
DMRTA2	DMRTA2	DMRT like family A2(DMRTA2)	5.772268	1.322655	0	0
CARD11	CARD11	caspase recruitment domain family member 11(CARD11)	5.747666	1.447848	0	0
EGR4	EGR4	early growth response 4(EGR4)	5.746704	1.443523	0	0
SUV39H2	SUV39H2	SUV39H2 histone lysine methyltransferase(SUV39H2)	5.676705	1.380588	0	0
WDR90	WDR90	WD repeat domain 90(WDR90)	5.642067	1.421415	0	0
RERG	RERG	RAS like estrogen regulated growth inhibitor(RERG)	5.640519	1.682549	0	0
OLIG1	OLIG1	oligodendrocyte transcription factor 1(OLIG1)	5.575717	1.193596	0	0
CENPF	CENPF	centromere protein F(CENPF)	5.544379	1.364029	0	0

CHEK1	CHEK1	checkpoint kinase 1(CHEK1)	5.543981	1.396491	0	0
SMARCA1	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1(SMARCA1)	5.529357	1.600971	0	0
DUSP9	DUSP9	dual specificity phosphatase 9(DUSP9)	5.52012	1.325312	0	0
MALAT1	MALAT1	metastasis associated lung adenocarcinoma transcript 1(MALAT1)	5.495807	7.104867	0	0
FOXL2	FOXL2	forkhead box L2(FOXL2)	5.488088	1.395043	0	0
BCL9	BCL9	BCL9 transcription coactivator(BCL9)	5.482572	1.265048	0	0
BRCA1	BRCA1	BRCA1 DNA repair associated(BRCA1)	5.47907	1.319167	0	0
CCT6B	CCT6B	chaperonin containing TCP1 subunit 6B(CCT6B)	5.447162	1.570563	0	0
CREB3L2	CREB3L2	cAMP responsive element binding protein 3 like 2(CREB3L2)	5.433269	1.401236	0	0
BRCA2	BRCA2	BRCA2 DNA repair associated(BRCA2)	5.400316	1.30479	0	0
CEBPD	CEBPD	CCAAT enhancer binding protein delta(CEBPD)	5.393212	1.529567	0	0
KIAA1549	KIAA1549	KIAA1549	5.255351	1.476754	0	0
WNT3	WNT3	Wnt family member 3(WNT3)	5.21112	1.534012	0	0
HOXD9	HOXD9	homeobox D9(HOXD9)	5.206607	1.484233	0	0
WNT10B	WNT10B	Wnt family member 10B(WNT10B)	5.194366	1.481691	0	0
BAZ2A	BAZ2A	bromodomain adjacent to zinc finger domain 2A(BAZ2A)	5.124135	1.144671	0	0
CDK4	CDK4	cyclin dependent kinase 4(CDK4)	5.103921	1.268306	0	0
PRKCG	PRKCG	protein kinase C gamma(PRKCG)	5.097023	1.375862	0	0
FANCF	FANCF	FA complementation group F(FANCF)	5.080526	1.324754	0	0
BAP1	BAP1	BRCA1 associated protein 1(BAP1)	5.079329	1.197043	0	0
DIRAS3	DIRAS3	DIRAS family GTPase 3(DIRAS3)	5.059647	1.684777	0	0
PDCD11	PDCD11	programmed cell death 11(PDCD11)	5.051232	1.217568	0	0
CCND2	CCND2	cyclin D2(CCND2)	5.039559	1.565053	0	0
TLX3	TLX3	T cell leukemia homeobox 3(TLX3)	5.023708	1.297986	0	0
SH2D5	SH2D5	SH2 domain containing 5(SH2D5)	5.016853	1.218057	0	0
HLF	HLF	HLF transcription factor, PAR bZIP family member(HLF)	4.915785	1.564397	0	0
FZD3	FZD3	frizzled class receptor 3(FZD3)	4.889125	1.431513	0	0
CXXC4	CXXC4	CXXC finger protein 4(CXXC4)	4.878559	1.432233	0	0
WNT4	WNT4	Wnt family member 4(WNT4)	4.877962	1.357028	0	0
CDK8	CDK8	cyclin dependent kinase 8(CDK8)	4.877334	1.217312	0	0
TGFBR3	TGFBR3	transforming growth factor beta receptor 3(TGFBR3)	4.825242	1.454045	0	0
NCAM1	NCAM1	neural cell adhesion molecule 1(NCAM1)	4.816127	1.513984	0	0
MIB1	MIB1	MIB E3 ubiquitin protein ligase 1(MIB1)	4.809697	1.186171	0	0
PPP3R2	PPP3R2	protein phosphatase 3 regulatory subunit B, beta(PPP3R2)	4.759569	1.503578	0	0
SRRM3	SRRM3	serine/arginine repetitive matrix 3(SRRM3)	4.751301	1.219335	0	0
DCLK2	DCLK2	doublecortin like kinase 2(DCLK2)	4.721746	1.538948	0	0
SOX10	SOX10	SRY-box transcription factor 10(SOX10)	4.695177	1.220194	0	0
CKB	CKB	creatine kinase B(CKB)	4.677684	1.66572	0	0
KTN1	KTN1	kinectin 1(KTN1)	4.631864	1.232806	0	0
CNTN1	CNTN1	contactin 1(CNTN1)	4.626353	1.588691	0	0
DLL3	DLL3	delta like canonical Notch ligand 3(DLL3)	4.624723	1.530573	0	0
ABI1	ABI1	abl interactor 1(ABI1)	4.616897	1.186457	0	0
RYR3	RYR3	ryanodine receptor 3(RYR3)	4.607899	1.531619	0	0
FHL2	FHL2	four and a half LIM domains 2(FHL2)	4.59493	1.511428	0	0

WIF1	WIF1	WNT inhibitory factor 1(WIF1)	4.572745	1.415063	0	0
FRK	FRK	fyn related Src family tyrosine kinase(FRK)	4.530607	1.508592	0	0
ID4	ID4	inhibitor of DNA binding 4(ID4)	4.481841	1.480165	0	0
EPHA10	EPHA10	EPH receptor A10(EPHA10)	4.462884	1.572071	0	0
CAD	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase(CAD)	4.45177	1.208563	0	0
MLLT4	AFDN	AFDN (Afadin, Adherens Junction Formation Factor)	4.445064	1.24324	0	0
PAX8	PAX8	paired box 8(PAX8)	4.443077	1.344075	0	0
BCL2	BCL2	BCL2 apoptosis regulator(BCL2)	4.430267	1.507281	0	0
HNF1A	HNF1A	HNF1 homeobox A(HNF1A)	4.428539	1.284995	0	0
TLX1	TLX1	T cell leukemia homeobox 1(TLX1)	4.375319	1.352988	0	0
FEV	FEV	FEV transcription factor, ETS family member(FEV)	4.362901	1.182595	0	0
LRRC7	LRRC7	leucine rich repeat containing 7(LRRC7)	4.330506	1.468103	0	0.068082
FANCM	FANCM	FA complementation group M(FANCM)	4.295807	1.21452	0	0.251768
MN1	MN1	MN1 proto-oncogene, transcriptional regulator(MN1)	4.279777	1.333908	0	0.339371
TERT	TERT	telomerase reverse transcriptase(TERT)	4.268286	1.382554	0	0.403246
RNF43	RNF43	ring finger protein 43(RNF43)	4.261064	1.377974	0	0.44386
HOXC13	HOXC13	homeobox C13(HOXC13)	4.204312	1.408629	0	0.775696
FZD6	FZD6	frizzled class receptor 6(FZD6)	4.202428	1.348321	0	0.787106
IRS2	IRS2	insulin receptor substrate 2(IRS2)	4.199383	1.309727	0	0.805594
NUTM1	NUTM1	NUT midline carcinoma family member 1(NUTM1)	4.195306	1.598825	0	0.830454
GDF6	GDF6	growth differentiation factor 6(GDF6)	4.188316	1.263298	0	0.87336
KIAA1524	CIP2A	CIP2A (Cellular Inhibitor Of PP2A)	4.176383	1.241956	0	0.947427
DUX4L4	DUX4L4	DUX4L4 (Double Homeobox 4 Like 4 (Pseudogene))	4.172016	1.065508	0	0.974785
NAV3	NAV3	neuron navigator 3(NAV3)	4.16889	1.381747	0	0.994458
DUX2	DUX4L8	DUX4L8 (Double Homeobox 4 Like 8 (Pseudogene))	4.166087	1.097724	0	1.012159
PRMT8	PRMT8	protein arginine methyltransferase 8(PRMT8)	4.122929	1.328727	0	1.292018
BUB1B	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B(BUB1B)	4.121297	1.305377	0	1.30287
TRHDE	TRHDE	thyrotropin releasing hormone degrading enzyme(TRHDE)	4.100741	1.399767	0	1.441307
DLEC1	DLEC1	DLEC1 cilia and flagella associated protein(DLEC1)	4.057117	1.431416	0	1.74573
NGFR	NGFR	nerve growth factor receptor(NGFR)	4.027668	1.305821	0	1.959537
PIM1	PIM1	Pim-1 proto-oncogene, serine/threonine kinase(PIM1)	4.024249	1.33605	0	1.984797
IKZF1	IKZF1	IKAROS family zinc finger 1(IKZF1)	4.019558	1.219199	0	2.019607
AKAP9	AKAP9	A-kinase anchoring protein 9(AKAP9)	3.999488	1.140959	0	2.170495
RECQL4	RECQL4	RecQ like helicase 4(RECQL4)	3.994513	1.314573	0	2.20839
LINGO2	LINGO2	leucine rich repeat and Ig domain containing 2(LINGO2)	3.991021	1.485745	0	2.235104
GRHPR	GRHPR	glyoxylate and hydroxypyruvate reductase(GRHPR)	3.9858	1.405218	0	2.275232
DAB2IP	DAB2IP	DAB2 interacting protein(DAB2IP)	3.983234	1.347815	0	2.295036
SOX2	SOX2	SRY-box transcription factor 2(SOX2)	3.96446	1.286762	0	2.441519
EPO	EPO	erythropoietin(EPO)	3.95561	1.260871	0	2.51156
MAPK8IP2	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2(MAPK8IP2)	3.93804	1.272299	0	2.652486
ANKRD28	ANKRD28	ankyrin repeat domain 28(ANKRD28)	3.934712	1.154651	0	2.679469
GFAP	GFAP	glial fibrillary acidic protein(GFAP)	3.921495	1.401359	0	2.787506
ARHGAP20	ARHGAP20	Rho GTPase activating protein 20(ARHGAP20)	3.910248	1.412938	0	2.880568

IGFBP2	IGFBP2	insulin like growth factor binding protein 2(IGFBP2)	3.908406	1.459945	0	2.895916
HOXA11	HOXA11	homeobox A11(HOXA11)	3.90542	1.386092	0	2.920848
DACH1	DACH1	dachshund family transcription factor 1(DACH1)	3.900413	1.322581	0	2.962817
DEK	DEK	DEK proto-oncogene(DEK)	3.896496	1.219003	0	2.995794
DDX20	DDX20	DEAD-box helicase 20(DDX20)	3.857799	1.176031	0	3.328483
BCL11A	BCL11A	BCL11 transcription factor A(BCL11A)	3.852107	1.323167	0	3.378487
CIRH1A	UTP4	UTP4 (UTP4 Small Subunit Processome Component)	3.822538	1.169702	0	3.64268
NKX2-5	NKX2-5	NK2 homeobox 5(NKX2-5)	3.818874	1.39759	0	3.67594
IRF4	IRF4	interferon regulatory factor 4(IRF4)	3.783172	1.478962	0	4.006081
C10orf55	C10orf55	chromosome 10 putative open reading frame 55(C10orf55)	3.772033	1.182469	0	4.111364
TP63	TP63	tumor protein p63(TP63)	3.770095	1.472939	0	4.129792
PRKACG	PRKACG	protein kinase cAMP-activated catalytic subunit gamma(PRKACG)	3.76415	1.331325	0	4.186526
WNT7B	WNT7B	Wnt family member 7B(WNT7B)	3.761432	1.217567	0	4.212568
ZIC2	ZIC2	Zic family member 2(ZIC2)	3.757963	1.247721	0	4.245909
SMC3	SMC3	structural maintenance of chromosomes 3(SMC3)	3.757443	1.165256	0	4.250912
NTRK1	NTRK1	neurotrophic receptor tyrosine kinase 1(NTRK1)	3.748111	1.291971	0	4.34115
PTCRA	PTCRA	pre T cell antigen receptor alpha(PTCRA)	3.741074	1.409412	0	4.409715
ITPKA	ITPKA	inositol-trisphosphate 3-kinase A(ITPKA)	3.734852	1.239429	0	4.470696
FAM19A5	TAF A5	TAF A5 (TAF A Chemokine Like Family Member 5)	3.71663	1.185582	0	4.651301
KMT2D	KMT2D	lysine methyltransferase 2D(KMT2D)	3.688723	1.138068	0	4.933673
TBL1XR1	TBL1XR1	TBL1X/Y related 1(TBL1XR1)	3.683361	1.229598	0	4.988741
PAK7	PAK5	PAK5 (P21 (RAC1) Activated Kinase 5)	3.682669	1.379861	0	4.995868
TNC	TNC	tenascin C(TNC)	-14.3253	0.383572	0	0
KDM6A	KDM6A	lysine demethylase 6A(KDM6A)	-12.5291	0.620371	0	0.030677
TMEM30A	TMEM30A	transmembrane protein 30A(TMEM30A)	-12.4776	0.595126	0	0.032667
PTK2B	PTK2B	protein tyrosine kinase 2 beta(PTK2B)	-12.4476	0.497058	0	0.033842
MMP9	MMP9	matrix metalloproteinase 9(MMP9)	-11.773	0.275911	0	0.062845
ABCC3	ABCC3	ATP binding cassette subfamily C member 3(ABCC3)	-11.7118	0.41381	0	0.065666
ITGAV	ITGAV	integrin subunit alpha V(ITGAV)	-11.5309	0.535185	0	0.074044
IL7R	IL7R	interleukin 7 receptor(IL7R)	-11.1731	0.403581	0	0.09008
MSN	MSN	moesin(MSN)	-10.5457	0.607818	0	0.110526
NDE1	NDE1	nudE neurodevelopment protein 1(NDE1)	-10.5042	0.608593	0	0.111187
GPHN	GPHN	gephyrin(GPHN)	-10.4939	0.423268	0	0.111332
NDRG1	NDRG1	N-myc downstream regulated 1(NDRG1)	-10.4289	0.453193	0	0.112073
LMO2	LMO2	LIM domain only 2(LMO2)	-10.3961	0.33667	0	0.112326
CD74	CD74	CD74 molecule(CD74)	-10.1728	0.478904	0	0.111517
TGFB1	TGFB1	transforming growth factor beta induced(TGFB1)	-10.1632	0.459355	0	0.111369
ITGA5	ITGA5	integrin subunit alpha 5(ITGA5)	-10.0653	0.484548	0	0.109268
SNX9	SNX9	sorting nexin 9(SNX9)	-9.95052	0.549269	0	0.105282
PLAU	PLAU	plasminogen activator, urokinase(PLAU)	-9.87714	0.454444	0	0.101784
VTI1A	VTI1A	vesicle transport through interaction with t-SNAREs 1A(VTI1A)	-9.82568	0.640011	0	0.098855
MAPK3	MAPK3	mitogen-activated protein kinase 3(MAPK3)	-9.81829	0.583755	0	0.098401
SGK1	SGK1	serum/glucocorticoid regulated kinase 1(SGK1)	-9.73866	0.514758	0	0.092948

ENPP2	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2(ENPP2)	-9.70672	0.453012	0	0.090461
MYH9	MYH9	myosin heavy chain 9(MYH9)	-9.69887	0.632152	0	0.089823
TNFAIP3	TNFAIP3	TNF alpha induced protein 3(TNFAIP3)	-9.64944	0.596105	0	0.08555
LASP1	LASP1	LIM and SH3 protein 1(LASP1)	-9.58647	0.654577	0	0.079449
PRKCD	PRKCD	protein kinase C delta(PRKCD) hypoxia inducible factor 1 subunit alpha(HIF1A)	-9.56618	0.598565	0	0.077322
HIF1A	HIF1A		-9.49973	0.650132	0	0.069771
SNX29	SNX29	sorting nexin 29(SNX29) Fli-1 proto-oncogene, ETS transcription factor(FLI1)	-9.37308	0.591637	0	0.052764
FLI1	FLI1		-9.33089	0.659675	0	0.046285
HDAC1	HDAC1	histone deacetylase 1(HDAC1)	-9.32569	0.613072	0	0.045458
LPAR1	LPAR1	lysophosphatidic acid receptor 1(LPAR1)	-9.32482	0.49734	0	0.045319
ROBO1	ROBO1	roundabout guidance receptor 1(ROBO1)	-9.29388	0.525416	0	0.040249
S1PR2	S1PR2	sphingosine-1-phosphate receptor 2(S1PR2)	-9.21394	0.465547	0	0.02604
CALR	CALR	calreticulin(CALR)	-9.14656	0.690137	0	0.012765
VCAM1	VCAM1	vascular cell adhesion molecule 1(VCAM1) zinc finger CCCH-type, RNA binding motif and serine/arginine rich 2(ZRSR2)	-9.10712	0.560738	0	0.00442
ZRSR2	ZRSR2		-9.08438	0.690368	0	0
HAS2	HAS2	hyaluronan synthase 2(HAS2) lysosomal associated membrane protein 2(LAMP2)	-9.05806	0.431224	0	0
LAMP2	LAMP2		-9.01285	0.630772	0	0
VEGFA	VEGFA	vascular endothelial growth factor A(VEGFA)	-9.00955	0.517089	0	0
DNM1	DNM1	dynamain 1(DNM1) LCK proto-oncogene, Src family tyrosine kinase(LCK)	-8.98358	0.494685	0	0
LCK	LCK		-8.98216	0.492493	0	0
LCP1	LCP1	lymphocyte cytosolic protein 1(LCP1) OFD1 centriole and centriolar satellite protein(OFD1)	-8.95714	0.601489	0	0
OFD1	OFD1		-8.9114	0.672435	0	0
CSNK1G2	CSNK1G2	casein kinase 1 gamma 2(CSNK1G2)	-8.9111	0.664391	0	0
DPYD	DPYD	dihydropyrimidine dehydrogenase(DPYD)	-8.88169	0.604931	0	0
RPN2	RPN2	ribophorin II(RPN2)	-8.87861	0.659053	0	0
PRRX1	PRRX1	paired related homeobox 1(PRRX1)	-8.83618	0.51536	0	0
ICAM1	ICAM1	intercellular adhesion molecule 1(ICAM1)	-8.80463	0.60025	0	0
BIRC3	BIRC3	baculoviral IAP repeat containing 3(BIRC3)	-8.74776	0.569793	0	0
CHN1	CHN1	chimerin 1(CHN1) TATA-box binding protein associated factor 1(TAF1)	-8.6785	0.506993	0	0
TAF1	TAF1		-8.67813	0.750601	0	0
TNF	TNF	tumor necrosis factor(TNF)	-8.64405	0.445537	0	0
JAK1	JAK1	Janus kinase 1(JAK1)	-8.55619	0.688472	0	0
P2RY8	P2RY8	P2Y receptor family member 8(P2RY8)	-8.50911	0.528841	0	0
KDM5C	KDM5C	lysine demethylase 5C(KDM5C)	-8.49641	0.698075	0	0
SDC4	SDC4	syndecan 4(SDC4) ral guanine nucleotide dissociation stimulator(RALGDS)	-8.20324	0.514583	0	0
RALGDS	RALGDS		-8.17344	0.640674	0	0
CDH11	CDH11	cadherin 11(CDH11)	-8.17136	0.574322	0	0
FAS	FAS	Fas cell surface death receptor(FAS)	-8.13141	0.60248	0	0
ARRDC4	ARRDC4	arrestin domain containing 4(ARRDC4)	-8.10041	0.561984	0	0
PLCG1	PLCG1	phospholipase C gamma 1(PLCG1)	-8.09014	0.689382	0	0
VEGFC	VEGFC	vascular endothelial growth factor C(VEGFC) signal transducer and activator of transcription 5B(STAT5B)	-8.08585	0.581862	0	0
STAT5B	STAT5B		-8.07398	0.715257	0	0
LYL1	LYL1	LYL1 basic helix-loop-helix family member(LYL1)	-8.05617	0.581971	0	0
CDH1	CDH1	cadherin 1(CDH1)	-8.0023	0.413278	0	0

SOD2	SOD2	superoxide dismutase 2(SOD2)	-7.98187	0.547529	0	0
PSEN1	PSEN1	presenilin 1(PSEN1)	-7.90869	0.7714	0	0
SSBP2	SSBP2	single stranded DNA binding protein 2(SSBP2)	-7.90305	0.487113	0	0
SPTAN1	SPTAN1	spectrin alpha, non-erythrocytic 1(SPTAN1)	-7.89911	0.745662	0	0
NCOA3	NCOA3	nuclear receptor coactivator 3(NCOA3)	-7.85056	0.701462	0	0
CD58	CD58	CD58 molecule(CD58)	-7.84971	0.556081	0	0
WHSC1L1	NSD3	NSD3 (Nuclear Receptor Binding SET Domain Protein 3)	-7.78301	0.754943	0	0
MAP2K1	MAP2K1	mitogen-activated protein kinase kinase 1(MAP2K1)	-7.77867	0.691544	0	0
LPXN	LPXN	leupaxin(LPXN)	-7.71335	0.667891	0	0
POSTN	POSTN	periostin(POSTN)	-7.70971	0.388049	0	0
EML1	EML1	EMAP like 1(EML1)	-7.70686	0.575879	0	0
CTSA	CTSA	cathepsin A(CTSA)	-7.70596	0.658781	0	0
PAG1	PAG1	phosphoprotein membrane anchor with glycosphingolipid microdomains 1(PAG1)	-7.64998	0.641439	0	0
NFKB2	NFKB2	nuclear factor kappa B subunit 2(NFKB2)	-7.63036	0.677257	0	0
RUNX2	RUNX2	RUNX family transcription factor 2(RUNX2)	-7.62745	0.558536	0	0
HTRA1	HTRA1	HtrA serine peptidase 1(HTRA1)	-7.61362	0.526163	0	0
ELF4	ELF4	E74 like ETS transcription factor 4(ELF4)	-7.58637	0.695896	0	0
GNA13	GNA13	G protein subunit alpha 13(GNA13)	-7.55919	0.734045	0	0
RPN1	RPN1	ribophorin I(RPN1)	-7.5502	0.75349	0	0
CLTC	CLTC	clathrin heavy chain(CLTC)	-7.54233	0.813214	0	0
SQSTM1	SQSTM1	sequestosome 1(SQSTM1)	-7.48818	0.695869	0	0
CCND3	CCND3	cyclin D3(CCND3)	-7.3578	0.59735	0	0
PDGFRB	PDGFRB	platelet derived growth factor receptor beta(PDGFRB)	-7.32223	0.623407	0	0
KLHL6	KLHL6	kelch like family member 6(KLHL6)	-7.28529	0.586047	0	0
RICTOR	RICTOR	RPTOR independent companion of MTOR complex 2(RICTOR)	-7.25909	0.768161	0	0
PTK2	PTK2	protein tyrosine kinase 2(PTK2)	-7.19829	0.635847	0	0
KDM4C	KDM4C	lysine demethylase 4C(KDM4C)	-7.19148	0.771203	0	0
DNM2	DNM2	dynamain 2(DNM2)	-7.18412	0.73382	0	0
LPP	LPP	LIM domain containing preferred translocation partner in lipoma(LPP)	-7.18292	0.659244	0	0
IKBKB	IKBKB	inhibitor of nuclear factor kappa B kinase subunit beta(IKBKB)	-7.17812	0.727721	0	0
DLL1	DLL1	delta like canonical Notch ligand 1(DLL1)	-7.14952	0.617941	0	0
ZNF217	ZNF217	zinc finger protein 217(ZNF217)	-7.14527	0.770531	0	0
POLD4	POLD4	DNA polymerase delta 4, accessory subunit(POLD4)	-7.0872	0.616746	0	0
TEAD1	TEAD1	TEA domain transcription factor 1(TEAD1)	-7.05997	0.624806	0	0
SFRP2	SFRP2	secreted frizzled related protein 2(SFRP2)	-7.05515	0.361574	0	0
IL1B	IL1B	interleukin 1 beta(IL1B)	-7.03568	0.456984	0	0
WDR70	WDR70	WD repeat domain 70(WDR70)	-6.96915	0.730582	0	0
CIITA	CIITA	class II major histocompatibility complex transactivator(CIITA)	-6.95885	0.64343	0	0
REEP3	REEP3	receptor accessory protein 3(REEP3)	-6.9554	0.749252	0	0
MEF2C	MEF2C	myocyte enhancer factor 2C(MEF2C)	-6.92976	0.67621	0	0
PI4KA	PI4KA	phosphatidylinositol 4-kinase alpha(PI4KA)	-6.87536	0.768933	0	0
BCL6	BCL6	BCL6 transcription repressor(BCL6)	-6.87367	0.64567	0	0
MBNL1	MBNL1	muscleblind like splicing regulator 1(MBNL1)	-6.84701	0.741578	0	0
TFE3	TFE3	transcription factor binding to IGHM enhancer 3(TFE3)	-6.84378	0.715206	0	0

CHL1	CHL1	cell adhesion molecule L1 like(CHL1)	-6.82359	0.512092	0	0
BCAS3	BCAS3	BCAS3 microtubule associated cell migration factor(BCAS3)	-6.81648	0.754154	0	0
NFKBIA	NFKBIA	NFKB inhibitor alpha(NFKBIA)	-6.72729	0.721767	0	0
FAF1	FAF1	Fas associated factor 1(FAF1)	-6.72296	0.769292	0	0
AFF4	AFF4	ALF transcription elongation factor 4(AFF4)	-6.6987	0.852098	0	0
HSPA1A	HSPA1A	heat shock protein family A (Hsp70) member 1A(HSPA1A)	-6.6644	0.568135	0	0
PPAP2B	PLPP3	PLPP3 (Phospholipid Phosphatase 3)	-6.64821	0.657142	0	0
APLP2	APLP2	amyloid beta precursor like protein 2(APLP2)	-6.64621	0.752026	0	0
LGALS3	LGALS3	galectin 3(LGALS3)	-6.64522	0.663617	0	0
EBF1	EBF1	EBF transcription factor 1(EBF1)	-6.6218	0.670495	0	0
PICALM	PICALM	phosphatidylinositol binding clathrin assembly protein(PICALM)	-6.61106	0.739189	0	0
DDX6	DDX6	DEAD-box helicase 6(DDX6)	-6.59739	0.808422	0	0
HSPA5	HSPA5	heat shock protein family A (Hsp70) member 5(HSPA5)	-6.59514	0.754023	0	0
AUTS2	AUTS2	activator of transcription and developmental regulator AUTS2(AUTS2)	-6.59044	0.498263	0	0
SDHB	SDHB	succinate dehydrogenase complex iron sulfur subunit B(SDHB)	-6.58955	0.674222	0	0
BAIAP2L1	BAIAP2L1	BAR/IMD domain containing adaptor protein 2 like 1(BAIAP2L1)	-6.5815	0.485926	0	0
CDC42	CDC42	cell division cycle 42(CDC42)	-6.58061	0.761307	0	0
TRAF5	TRAF5	TNF receptor associated factor 5(TRAF5)	-6.51725	0.707943	0	0
CSF1R	CSF1R	colony stimulating factor 1 receptor(CSF1R)	-6.50665	0.666008	0	0
XPC	XPC	XPC complex subunit, DNA damage recognition and repair factor(XPC)	-6.48521	0.779137	0	0
COL6A3	COL6A3	collagen type VI alpha 3 chain(COL6A3)	-6.46545	0.623078	0	0
SULF1	SULF1	sulfatase 1(SULF1)	-6.46512	0.531068	0	0
RASGRP1	RASGRP1	RAS guanyl releasing protein 1(RASGRP1)	-6.43034	0.653449	0	0
DDX39B	DDX39B	DEd-box helicase 39B(DDX39B)	-6.4145	0.763215	0	0
SERPINF1	SERPINF1	serpin family F member 1(SERPINF1)	-6.39888	0.637825	0	0
CD22	CD22	CD22 molecule(CD22)	-6.38528	0.570207	0	0
SMARCA4	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4(SMARCA4)	-6.38122	0.73678	0	0
ITK	ITK	IL2 inducible T cell kinase(ITK)	-6.36293	0.572945	0	0
LRMP	IRAG2	IRAG2 (Inositol 1,4,5-Triphosphate Receptor Associated 2)	-6.36223	0.588793	0	0
MGMT	MGMT	O-6-methylguanine-DNA methyltransferase(MGMT)	-6.36054	0.603167	0	0
PDK1	PDK1	pyruvate dehydrogenase kinase 1(PDK1)	-6.29903	0.680169	0	0
LFNG	LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase(LFNG)	-6.29665	0.634691	0	0
ALDH2	ALDH2	aldehyde dehydrogenase 2 family member(ALDH2)	-6.2901	0.608437	0	0
IGFBP3	IGFBP3	insulin like growth factor binding protein 3(IGFBP3)	-6.28772	0.619968	0	0
GANAB	GANAB	glucosidase II alpha subunit(GANAB)	-6.26339	0.77017	0	0
CCND1	CCND1	cyclin D1(CCND1)	-6.26123	0.638481	0	0
NUP98	NUP98	nucleoporin 98 and 96 precursor(NUP98)	-6.25836	0.822375	0	0
EZR	EZR	ezrin(EZR)	-6.25699	0.703157	0	0
PTPRK	PTPRK	protein tyrosine phosphatase receptor type K(PTPRK)	-6.2183	0.646173	0	0
MYBL1	MYBL1	MYB proto-oncogene like 1(MYBL1)	-6.21762	0.469699	0	0
GIT2	GIT2	GIT ArfGAP 2(GIT2)	-6.20335	0.807031	0	0
CYFIP2	CYFIP2	cytoplasmic FMR1 interacting protein 2(CYFIP2)	-6.20054	0.741303	0	0

DDB2	DDB2	damage specific DNA binding protein 2(DDB2)	-6.19878	0.730646	0	0
TNFRSF10D	TNFRSF10D	TNF receptor superfamily member 10d(TNFRSF10D)	-6.19371	0.687522	0	0
ARHGAP26	ARHGAP26	Rho GTPase activating protein 26(ARHGAP26)	-6.16507	0.740568	0	0
TNFRSF10B	TNFRSF10B	TNF receptor superfamily member 10b(TNFRSF10B)	-6.13824	0.751036	0	0
HEY1	HEY1	hes related family bHLH transcription factor with YRPW motif 1(HEY1)	-6.13793	0.571756	0	0
RBM6	RBM6	RNA binding motif protein 6(RBM6)	-6.09548	0.778515	0	0
RTEL1-TNFRSF6B	RTEL1-TNFRSF6B	RTEL1-TNFRSF6B readthrough (NMD candidate)(RTEL1-TNFRSF6B)	-6.06504	0.666445	0	0
PTGS2	PTGS2	prostaglandin-endoperoxide synthase 2(PTGS2)	-6.04904	0.548174	0	0
SHC1	SHC1	SHC adaptor protein 1(SHC1)	-6.04585	0.766512	0	0
FOS	FOS	Fos proto-oncogene, AP-1 transcription factor subunit(FOS)	-6.03921	0.517477	0	0
MYO1F	MYO1F	myosin IF(MYO1F)	-6.0371	0.661907	0	0
CDKN2A	CDKN2A	cyclin dependent kinase inhibitor 2A(CDKN2A)	-6.03295	0.515131	0	0
TLR4	TLR4	toll like receptor 4(TLR4)	-5.99516	0.700653	0	0
CHST11	CHST11	carbohydrate sulfotransferase 11(CHST11)	-5.97647	0.71811	0	0
TFEB	TFEB	transcription factor EB(TFEB)	-5.97643	0.705312	0	0
CHMP2B	CHMP2B	charged multivesicular body protein 2B(CHMP2B)	-5.95837	0.750471	0	0
IL21R	IL21R	interleukin 21 receptor(IL21R)	-5.95142	0.657916	0	0
DDX3X	DDX3X	DEAD-box helicase 3 X-linked(DDX3X)	-5.91961	0.821788	0	0
GSTT1	GSTT1	glutathione S-transferase theta 1(GSTT1)	-5.83685	0.502362	0	0
BIN1	BIN1	bridging integrator 1(BIN1)	-5.82067	0.658961	0	0
ZNF207	ZNF207	zinc finger protein 207(ZNF207)	-5.8043	0.790908	0	0
ARAF	ARAF	A-Raf proto-oncogene, serine/threonine kinase(ARAF)	-5.78279	0.778683	0	0
OLR1	OLR1	oxidized low density lipoprotein receptor 1(OLR1)	-5.77929	0.540974	0	0
ADD3	ADD3	adducin 3(ADD3)	-5.76904	0.791214	0	0
FGFR1	FGFR1	fibroblast growth factor receptor 1(FGFR1)	-5.74762	0.678555	0	0
LOX	LOX	lysyl oxidase(LOX)	-5.74756	0.632888	0	0
PDCD1LG2	PDCD1LG2	programmed cell death 1 ligand 2(PDCD1LG2)	-5.7381	0.611933	0	0
SOCS3	SOCS3	suppressor of cytokine signaling 3(SOCS3)	-5.73659	0.64169	0	0
SMAD3	SMAD3	SMAD family member 3(SMAD3)	-5.72912	0.731639	0	0
TFRC	TFRC	transferrin receptor(TFRC)	-5.71961	0.696677	0	0
TOP1	TOP1	DNA topoisomerase I(TOP1)	-5.71848	0.759975	0	0
FLNA	FLNA	filamin A(FLNA)	-5.70695	0.708706	0	0
FGFR1OP2	FGFR1OP2	FGFR1 oncogene partner 2(FGFR1OP2)	-5.68391	0.790345	0	0
TGFBR2	TGFBR2	transforming growth factor beta receptor 2(TGFBR2)	-5.66799	0.753621	0	0
MGEA5	OGA	OGA (O-GlcNAcase)	-5.66214	0.811092	0	0
GOSR1	GOSR1	golgi SNAP receptor complex member 1(GOSR1)	-5.64941	0.776246	0	0
SMAD6	SMAD6	SMAD family member 6(SMAD6)	-5.62776	0.6259	0	0
KDR	KDR	kinase insert domain receptor(KDR)	-5.6193	0.729424	0	0
MAPK1	MAPK1	mitogen-activated protein kinase 1(MAPK1)	-5.60155	0.768434	0	0
PTPRA	PTPRA	protein tyrosine phosphatase receptor type A(PTPRA)	-5.57948	0.791238	0	0
SP1	SP1	Sp1 transcription factor(SP1)	-5.57807	0.811972	0	0
GOPC	GOPC	golgi associated PDZ and coiled-coil motif containing(GOPC)	-5.5712	0.813394	0	0
IKBKE	IKBKE	inhibitor of nuclear factor kappa B kinase subunit epsilon(IKBKE)	-5.56488	0.714902	0	0

CAMK2G	CAMK2G	calcium/calmodulin dependent protein kinase II gamma(CAMK2G)	-5.54919	0.739667	0	0
RCOR1	RCOR1	REST corepressor 1(RCOR1)	-5.52888	0.784158	0	0
INPP5D	INPP5D	inositol polyphosphate-5-phosphatase D(INPP5D)	-5.52206	0.747676	0	0
RPS6KA1	RPS6KA1	ribosomal protein S6 kinase A1(RPS6KA1)	-5.48925	0.761314	0	0
CTLA4	CTLA4	cytotoxic T-lymphocyte associated protein 4(CTLA4)	-5.47815	0.590295	0	0
COL3A1	COL3A1	collagen type III alpha 1 chain(COL3A1)	-5.47468	0.555027	0	0
GRB2	GRB2	growth factor receptor bound protein 2(GRB2)	-5.45406	0.774051	0	0
STAT4	STAT4	signal transducer and activator of transcription 4(STAT4)	-5.44009	0.659642	0	0
WDR1	WDR1	WD repeat domain 1(WDR1)	-5.43166	0.760968	0	0
RHOH	RHOH	ras homolog family member H(RHOH)	-5.40682	0.724945	0	0
PDE4DIP	PDE4DIP	phosphodiesterase 4D interacting protein(PDE4DIP)	-5.4008	0.726187	0	0
TBX15	TBX15	T-box transcription factor 15(TBX15)	-5.37152	0.605709	0	0
SEPTIN5	SEPTIN5	SEPTIN5 (Septin 5)	-5.35012	0.688755	0	0
INPP5A	INPP5A	inositol polyphosphate-5-phosphatase A(INPP5A)	-5.34225	0.666746	0	0
ARFRP1	ARFRP1	ADP ribosylation factor related protein 1(ARFRP1)	-5.28773	0.777352	0	0
ABLIM1	ABLIM1	actin binding LIM protein 1(ABLIM1)	-5.28241	0.689049	0	0
PLCG2	PLCG2	phospholipase C gamma 2(PLCG2)	-5.27817	0.728656	0	0
NCOR2	NCOR2	nuclear receptor corepressor 2(NCOR2)	-5.27793	0.816196	0	0
SEPTIN6	SEPTIN6	SEPTIN6 (Septin 6)	-5.26354	0.767286	0	0
FRYL	FRYL	FRY like transcription coactivator(FRYL)	-5.26041	0.876929	0	0
MDH1	MDH1	malate dehydrogenase 1(MDH1)	-5.24904	0.753334	0	0
NBR1	NBR1	NBR1 autophagy cargo receptor(NBR1)	-5.24114	0.839203	0	0
SH3GL1	SH3GL1	SH3 domain containing GRB2 like 1, endophilin A2(SH3GL1)	-5.2327	0.739254	0	0
DDX5	DDX5	DEAD-box helicase 5(DDX5)	-5.22126	0.817449	0	0
TEC	TEC	tec protein tyrosine kinase(TEC)	-5.21195	0.696135	0	0
CSF1	CSF1	colony stimulating factor 1(CSF1)	-5.20463	0.700452	0	0
ST6GAL1	ST6GAL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1(ST6GAL1)	-5.18934	0.748722	0	0
EPHA3	EPHA3	EPH receptor A3(EPHA3)	-5.18199	0.605637	0	0
TPM4	TPM4	tropomyosin 4(TPM4)	-5.17158	0.752417	0	0
MED12	MED12	mediator complex subunit 12(MED12)	-5.15666	0.834283	0	0
FOXO1	FOXO1	forkhead box O1(FOXO1)	-5.14253	0.800445	0	0
PIK3CG	PIK3CG	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma(PIK3CG)	-5.13047	0.740348	0	0
GADD45B	GADD45B	growth arrest and DNA damage inducible beta(GADD45B)	-5.1296	0.703574	0	0
MMP7	MMP7	matrix metalloproteinase 7(MMP7)	-5.11378	0.459219	0	0
PRRX2	PRRX2	paired related homeobox 2(PRRX2)	-5.09897	0.739446	0	0
IL6	IL6	interleukin 6(IL6)	-5.07775	0.568846	0	0
PKM	PKM	pyruvate kinase M1/2(PKM)	-5.07325	0.742168	0	0
PCBP1	PCBP1	poly(rC) binding protein 1(PCBP1)	-5.06944	0.818108	0	0
PLAG1	PLAG1	PLAG1 zinc finger(PLAG1)	-5.03732	0.658499	0	0
PDGFD	PDGFD	platelet derived growth factor D(PDGFD)	-5.03335	0.635746	0	0
LRRC37B	LRRC37B	leucine rich repeat containing 37B(LRRC37B)	-5.02999	0.760392	0	0
FHIT	FHIT	fragile histidine triad diadenosine triphosphatase(FHIT)	-5.02767	0.642462	0	0
HIP1	HIP1	huntingtin interacting protein 1(HIP1)	-5.02049	0.732078	0	0

SMAP1	SMAP1	small ArfGAP 1(SMAP1)	-5.01959	0.807642	0	0
LRIG3	LRIG3	leucine rich repeats and immunoglobulin like domains 3(LRIG3)	-5.01833	0.677054	0	0
CXCL8	CXCL8	C-X-C motif chemokine ligand 8(CXCL8)	-5.00236	0.470313	0	0
CRKL	CRKL	CRK like proto-oncogene, adaptor protein(CRKL)	-4.99752	0.846512	0	0
GNA12	GNA12	G protein subunit alpha 12(GNA12)	-4.99722	0.760732	0	0
JAK3	JAK3	Janus kinase 3(JAK3)	-4.98276	0.744661	0	0
FNBP1	FNBP1	formin binding protein 1(FNBP1)	-4.97653	0.762634	0	0
CCDC28A	CCDC28A	coiled-coil domain containing 28A(CCDC28A)	-4.95317	0.767781	0	0
BICC1	BICC1	BicC family RNA binding protein 1(BICC1)	-4.93434	0.675265	0	0
LMBRD1	LMBRD1	LMBR1 domain containing 1(LMBRD1)	-4.93405	0.796443	0	0
MADD	MADD	MAP kinase activating death domain(MADD)	-4.88922	0.828366	0	0
IL2RA	IL2RA	interleukin 2 receptor subunit alpha(IL2RA)	-4.87775	0.656051	0	0
DST	DST	dystonin(DST)	-4.8606	0.745022	0	0
CD44	CD44	CD44 molecule (IN blood group)(CD44)	-4.85994	0.711661	0	0
EPHA2	EPHA2	EPH receptor A2(EPHA2)	-4.79376	0.676954	0	0
CSF3R	CSF3R	colony stimulating factor 3 receptor(CSF3R)	-4.7903	0.690273	0	0
HSPA1B	HSPA1B	heat shock protein family A (Hsp70) member 1B(HSPA1B)	-4.78962	0.62906	0	0
PPARG	PPARG	peroxisome proliferator activated receptor gamma(PPARG)	-4.77858	0.658195	0	0
EXT2	EXT2	exostosin glycosyltransferase 2(EXT2)	-4.77758	0.824067	0	0
LIFR	LIFR	LIF receptor subunit alpha(LIFR)	-4.7594	0.699823	0	0
CD19	CD19	CD19 molecule(CD19)	-4.74467	0.641385	0	0
SMC1A	SMC1A	structural maintenance of chromosomes 1A(SMC1A)	-4.7435	0.800113	0	0
WSB1	WSB1	WD repeat and SOCS box containing 1(WSB1)	-4.74257	0.800236	0	0
TCF12	TCF12	transcription factor 12(TCF12)	-4.74085	0.835765	0	0
MAP2K2	MAP2K2	mitogen-activated protein kinase kinase 2(MAP2K2)	-4.73195	0.793323	0	0
PIK3R1	PIK3R1	phosphoinositide-3-kinase regulatory subunit 1(PIK3R1)	-4.71493	0.840151	0	0
SF3B1	SF3B1	splicing factor 3b subunit 1(SF3B1)	-4.70948	0.836054	0	0
CRTC1	CRTC1	CREB regulated transcription coactivator 1(CRTC1)	-4.6934	0.785064	0	0
STAT5A	STAT5A	signal transducer and activator of transcription 5A(STAT5A)	-4.68343	0.765107	0	0
IRF8	IRF8	interferon regulatory factor 8(IRF8)	-4.66407	0.736188	0	0
CACNA2D3	CACNA2D3	calcium voltage-gated channel auxiliary subunit alpha2delta 3(CACNA2D3)	-4.65915	0.550059	0	0
TERF2	TERF2	telomeric repeat binding factor 2(TERF2)	-4.64683	0.82446	0	0
EGR1	EGR1	early growth response 1(EGR1)	-4.64469	0.697255	0	0
RAC1	RAC1	Rac family small GTPase 1(RAC1)	-4.63632	0.824482	0	0
CEP85L	CEP85L	centrosomal protein 85 like(CEP85L)	-4.6304	0.772378	0	0
CD79A	CD79A	CD79a molecule(CD79A)	-4.62797	0.647524	0	0
DNAJB1	DNAJB1	DnaJ heat shock protein family (Hsp40) member B1(DNAJB1)	-4.62605	0.778509	0	0
MEF2BNB-MEF2B	MEF2BNB-MEF2B		-4.62137	0.867386	0	0
INHBA	INHBA	inhibin subunit beta A(INHBA)	-4.60487	0.611824	0	0
SBDS	SBDS	SBDS ribosome maturation factor(SBDS)	-4.59936	0.818048	0	0
CD274	CD274	CD274 molecule(CD274)	-4.59685	0.659036	0	0
RAC2	RAC2	Rac family small GTPase 2(RAC2)	-4.55913	0.693075	0	0
CHD6	CHD6	chromodomain helicase DNA binding protein 6(CHD6)	-4.54906	0.864698	0	0

BTK	BTK	Bruton tyrosine kinase(BTK)	-4.54371	0.761789	0	0
STX5	STX5	syntaxin 5(STX5)	-4.54213	0.81106	0	0
MYO18A	MYO18A	myosin XVIIIa(MYO18A)	-4.53325	0.828021	0	0
PRKACA	PRKACA	protein kinase cAMP-activated catalytic subunit alpha(PRKACA)	-4.52574	0.817245	0	0
JUN	JUN	Jun proto-oncogene, AP-1 transcription factor subunit(JUN)	-4.52154	0.731531	0	0
EPS15	EPS15	epidermal growth factor receptor pathway substrate 15(EPS15)	-4.52103	0.835096	0	0
FOXO3	FOXO3	forkhead box O3(FOXO3)	-4.51166	0.782715	0	0
GOT1	GOT1	glutamic-oxaloacetic transaminase 1(GOT1)	-4.47666	0.782505	0	0
MAX	MAX	MYC associated factor X(MAX)	-4.47608	0.82311	0	0
PSIP1	PSIP1	PC4 and SRSF1 interacting protein 1(PSIP1)	-4.47301	0.780384	0	0
PCNA	PCNA	proliferating cell nuclear antigen(PCNA)	-4.45673	0.758512	0	0
ZFYVE19	ZFYVE19	zinc finger FYVE-type containing 19(ZFYVE19)	-4.44643	0.799766	0	0
AHCYL1	AHCYL1	adenosylhomocysteinase like 1(AHCYL1)	-4.43422	0.887326	0	0
MALT1	MALT1	MALT1 paracaspase(MALT1)	-4.39951	0.821422	0	0
KSR1	KSR1	kinase suppressor of ras 1(KSR1)	-4.38947	0.759244	0	0
FLT3LG	FLT3LG	fms related receptor tyrosine kinase 3 ligand(FLT3LG)	-4.37211	0.715937	0	0
GSN	GSN	gelsolin(GSN)	-4.36441	0.742548	0	0
MAPRE1	MAPRE1	microtubule associated protein RP/EB family member 1(MAPRE1)	-4.34649	0.832149	0	0
RELA	RELA	RELA proto-oncogene, NF-kB subunit(RELA)	-4.32984	0.835918	0	0
ETS2	ETS2	ETS proto-oncogene 2, transcription factor(ETS2)	-4.31182	0.767807	0	0
CRLF2	CRLF2	cytokine receptor like factor 2(CRLF2)	-4.29859	0.702246	0	0
CHEK2	CHEK2	checkpoint kinase 2(CHEK2)	-4.27077	0.771162	0	0
HDAC7	HDAC7	histone deacetylase 7(HDAC7)	-4.26719	0.796151	0	0
SRC	SRC	SRC proto-oncogene, non-receptor tyrosine kinase(SRC)	-4.25122	0.74559	0	0
GTF2I	GTF2I	general transcription factor Iii(GTF2I)	-4.20011	0.827299	0	0.043423
SS18L1	SS18L1	SS18L1 subunit of BAF chromatin remodeling complex(SS18L1)	-4.19883	0.806814	0	0.050061
NCOA4	NCOA4	nuclear receptor coactivator 4(NCOA4)	-4.19344	0.85933	0	0.0781
CD28	CD28	CD28 molecule(CD28)	-4.19275	0.701465	0	0.081689
ALDOC	ALDOC	aldolase, fructose-bisphosphate C(ALDOC)	-4.18864	0.73215	0	0.103182
RHOA	RHOA	ras homolog family member A(RHOA)	-4.17822	0.847969	0	0.158282
SERPINE1	SERPINE1	serpin family E member 1(SERPINE1)	-4.17807	0.687002	0	0.159031
ATM	ATM	ATM serine/threonine kinase(ATM)	-4.17765	0.850897	0	0.161312
PTBP1	PTBP1	polypyrimidine tract binding protein 1(PTBP1)	-4.15927	0.814625	0	0.260284
ZNF331	ZNF331	zinc finger protein 331(ZNF331)	-4.14096	0.766886	0	0.36113
TCF7L2	TCF7L2	transcription factor 7 like 2(TCF7L2)	-4.13434	0.766575	0	0.398203
GLI3	GLI3	GLI family zinc finger 3(GLI3)	-4.13033	0.730142	0	0.420798
RPS6KA3	RPS6KA3	ribosomal protein S6 kinase A3(RPS6KA3)	-4.11298	0.826421	0	0.519764
ID3	ID3	inhibitor of DNA binding 3(ID3)	-4.0982	0.727117	0	0.605727
NFIB	NFIB	nuclear factor I B(NFIB)	-4.06039	0.779906	0	0.832761
MKL1	MKL1	MRTFA (Myocardin Related Transcription Factor A)	-4.05231	0.8411	0	0.882611
PRDM1	PRDM1	PR/SET domain 1(PRDM1)	-4.03632	0.733122	0	0.982652
COMMD1	COMMD1	copper metabolism domain containing 1(COMMD1)	-4.02153	0.800599	0	1.076822
DNMT1	DNMT1	DNA methyltransferase 1(DNMT1)	-4.00293	0.820692	0	1.197553
IL15	IL15	interleukin 15(IL15)	-3.98327	0.749011	0	1.327986

CTNNA1	CTNNA1	catenin alpha 1(CTNNA1)	-3.97226	0.856594	0	1.40233
RPS6KA2	RPS6KA2	ribosomal protein S6 kinase A2(RPS6KA2)	-3.96089	0.786485	0	1.480051
SMARCB1	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1(SMARCB1)	-3.94524	0.796686	0	1.588565
COG5	COG5	component of oligomeric golgi complex 5(COG5)	-3.93941	0.872189	0	1.629492
PPP3CC	PPP3CC	protein phosphatase 3 catalytic subunit gamma(PPP3CC)	-3.93848	0.819932	0	1.636104
HUWE1	HUWE1	HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1(HUWE1)	-3.93716	0.850586	0	1.645385
YAP1	YAP1	Yes1 associated transcriptional regulator(YAP1)	-3.91831	0.749098	0	1.779842
SPP1	SPP1	secreted phosphoprotein 1(SPP1)	-3.90531	0.590822	0	1.87421
NFATC2	NFATC2	nuclear factor of activated T cells 2(NFATC2)	-3.9037	0.820775	0	1.885929
FOSB	FOSB	FosB proto-oncogene, AP-1 transcription factor subunit(FOSB)	-3.90316	0.642237	0	1.889923
NEDD4	NEDD4	NEDD4 E3 ubiquitin protein ligase(NEDD4)	-3.90293	0.791363	0	1.89163
HHEX	HHEX	hematopoietically expressed homeobox(HHEX)	-3.89835	0.759852	0	1.925259
KMT2A	KMT2A	lysine methyltransferase 2A(KMT2A)	-3.86131	0.88293	0	2.203421
CNOT2	CNOT2	CCR4-NOT transcription complex subunit 2(CNOT2)	-3.85814	0.85535	0	2.227669
SDHD	SDHD	succinate dehydrogenase complex subunit D(SDHD)	-3.84444	0.806396	0	2.333711
NOTCH1	NOTCH1	notch receptor 1(NOTCH1)	-3.84393	0.825715	0	2.337685
ACKR3	ACKR3	atypical chemokine receptor 3(ACKR3)	-3.84241	0.734679	0	2.349546
MNAT1	MNAT1	MNAT1 component of CDK activating kinase(MNAT1)	-3.8254	0.811303	0	2.483551
DDR2	DDR2	discoidin domain receptor tyrosine kinase 2(DDR2)	-3.82518	0.782697	0	2.485289
HMGN2P46	HMGN2P46	high mobility group nucleosomal binding domain 2 pseudogene 46(HMGN2P46)	-3.8191	0.639287	0	2.533781
SOCS1	SOCS1	suppressor of cytokine signaling 1(SOCS1)	-3.81341	0.769721	0	2.579482
TFG	TFG	trafficking from ER to golgi regulator(TFG)	-3.81125	0.861105	0	2.596879
XPO1	XPO1	exportin 1(XPO1)	-3.80835	0.845218	0	2.62028
EGR2	EGR2	early growth response 2(EGR2)	-3.79502	0.762787	0	2.72882
CDC14B	CDC14B	cell division cycle 14B(CDC14B)	-3.78429	0.766624	0	2.817296
ID1	ID1	inhibitor of DNA binding 1(ID1)	-3.77071	0.716617	0	2.930633
CTNNB1	CTNNB1	catenin beta 1(CTNNB1)	-3.76159	0.904836	0	3.007552
ETS1	ETS1	ETS proto-oncogene 1, transcription factor(ETS1)	-3.74597	0.862405	0	3.141021
FUS	FUS	FUS RNA binding protein(FUS)	-3.74323	0.850721	0	3.16466
MDS2	MDS2	myelodysplastic syndrome 2 translocation associated(MDS2)	-3.74301	0.692584	0	3.166548
STAG2	STAG2	STAG2 cohesin complex component(STAG2)	-3.73247	0.877239	0	3.258122
MAP3K6	MAP3K6	mitogen-activated protein kinase kinase kinase 6(MAP3K6)	-3.73024	0.787949	0	3.27753
LTBP1	LTBP1	latent transforming growth factor beta binding protein 1(LTBP1)	-3.72557	0.749258	0	3.318476
FLT4	FLT4	fms related receptor tyrosine kinase 4(FLT4)	-3.7214	0.777174	0	3.355222
GSK3B	GSK3B	glycogen synthase kinase 3 beta(GSK3B)	-3.68642	0.893152	0	3.669026
RAF1	RAF1	Raf-1 proto-oncogene, serine/threonine kinase(RAF1)	-3.68621	0.878739	0	3.670963
GPC3	GPC3	glypican 3(GPC3)	-3.67867	0.695826	0	3.740081
IRF1	IRF1	interferon regulatory factor 1(IRF1)	-3.66909	0.785737	0	3.828501
SEPTIN9	SEPTIN9	SEPTIN9 (Septin 9)	-3.6602	0.843147	0	3.91128
EP300	EP300	E1A binding protein p300(EP300)	-3.64764	0.924886	0	4.029481
MAGEE1	MAGEE1	MAGE family member E1(MAGEE1)	-3.6389	0.750627	0	4.1126

PPP1R13B	PPP1R13B	protein phosphatase 1 regulatory subunit 13B(PPP1R13B)	-3.63033	0.830552	0	4.194668
DLL4	DLL4	delta like canonical Notch ligand 4(DLL4)	-3.62401	0.783156	0	4.255653
COL1A1	COL1A1	collagen type I alpha 1 chain(COL1A1)	-3.62183	0.651461	0	4.276835
SUGP2	SUGP2	SURP and G-patch domain containing 2(SUGP2)	-3.61077	0.867805	0	4.384611
PPFIBP1	PPFIBP1	PPFIA binding protein 1(PPFIBP1)	-3.61045	0.79593	0	4.387725
JAK2	JAK2	Janus kinase 2(JAK2)	-3.60775	0.83377	0	4.41421
TNFRSF14	TNFRSF14	TNF receptor superfamily member 14(TNFRSF14)	-3.60018	0.80001	0	4.488835
COL1A2	COL1A2	collagen type I alpha 2 chain(COL1A2)	-3.59873	0.691552	0	4.503174
TACC1	TACC1	transforming acidic coiled-coil containing protein 1(TACC1)	-3.58092	0.868255	0	4.680936
HSPA4	HSPA4	heat shock protein family A (Hsp70) member 4(HSPA4)	-3.57614	0.833927	0	4.729166
HERPUD1	HERPUD1	homocysteine inducible ER protein with ubiquitin like domain 1(HERPUD1)	-3.57477	0.837242	0	4.742992
THBS1	THBS1	thrombospondin 1(THBS1)	-3.56547	0.734429	0	4.837583
DOCK1	DOCK1	dedicator of cytokinesis 1(DOCK1)	-3.56512	0.817289	0	4.841109
FBXO11	FBXO11	F-box protein 11(FBXO11)	-3.56498	0.85295	0	4.842496
SS18	SS18	SS18 subunit of BAF chromatin remodeling complex(SS18)	-3.52044	0.8291	0	5.30629
RHOD	RHOD	ras homolog family member D(RHOD)	-3.51533	0.738098	0	5.360722
BTG2	BTG2	BTG anti-proliferation factor 2(BTG2)	-3.51182	0.811674	0	5.398196
HIPK1	HIPK1	homeodomain interacting protein kinase 1(HIPK1)	-3.50781	0.89052	0	5.44114

Suppl. Table S2.2 &2.3 Significantly enriched terms with FDR≤0.05 by DAVID functional annotation tool for genes upregulated in PTL compared with systemic DLBCL

Category	Term	Count	P Value	Genes	Fold Enrichment	Bonferroni	FDR
GOTERM_B P_DIRECT	GO:0006974~DNA damage response	8	4.82E-06	MDC1, FBXW7, CHEK1, BCL2, BRCA1, CIP2A, TP63, FOXF1	11.42757872	0.002805	0.00279
GOTERM_B P_DIRECT	GO:0006338~chromatin remodeling	8	9.94E-06	SUV39H2, IRF4, CHEK1, BAZ2A, DEK, BRCA2, TP63, BAP1	10.2281827	0.005777	0.002877
GOTERM_B P_DIRECT	GO:0006281~DNA repair	7	2.66E-05	RECQL4, MDC1, FBXW7, CHEK1, BRCA1, BRCA2, SMC3	11.49712859	0.015385	0.005133
GOTERM_B P_DIRECT	GO:0007049~cell cycle	7	7.80E-05	MDC1, SUV39H2, CHEK1, PIM1, IKZF1, BRCA1, TP63	9.474485597	0.044481	0.011297
GOTERM_B P_DIRECT	GO:0006325~chromatin organization	6	1.10E-04	MDC1, SUV39H2, TBL1XR1, IKZF1, DEK, BAP1 KMT2D, SUV39H2, MDC1, IKZF1, BRCA1, BRCA2, SMC3, RECQL4, TCL1A, CCND2, PDCD11, TERT, CHEK1, CREB3L2, PIM1, TP63, ANKRD28, FANCM, UTP4, BCL11A, FBXW7, DEK, FOXF1, CDK8, AFDN, CENPF, IRF4, TBL1XR1, CDK4, BAP1	12.2953271	0.062211	0.012757
GOTERM_C C_DIRECT	GO:0005654~nucleoplasm	30	1.86E-11	RASGRF1, BUB1B, BAZ2A, RASAL1, IKZF1, BRCA2, SMC3, TCL1A, CCND2, PDCD11, TERT, CHEK1, PIM1, ANKRD28, FANCM, BCL11A, FBXW7, CAD, GAB1, CIP2A, MIB1, AFDN, GRHPR, CENPF, IRF4, CDK4, ABI1, AKAP9, BCL2, CARD11, BAP1	3.455252275	2.57E-09	2.36E-09
GOTERM_C C_DIRECT	GO:0005829~cytosol	31	1.47E-08	KMT2D, SUV39H2, MDC1, BUB1B, BAZ2A, IKZF1, BRCA1, BRCA2, SMC3, RECQL4, CCND2, PDCD11, TERT, CHEK1, CREB3L2, PIM1, TP63, BCL11A, FBXW7, CAD, DEK, FOXF1, CDK8, CENPF, IRF4, TBL1XR1, CDK4, ABI1, BCL2, BAP1	2.547145021	2.03E-06	9.33E-07
GOTERM_C C_DIRECT	GO:0005634~nucleus	30	6.57E-07	RECQL4, MDC1, UTP4, FBXW7, BRCA1, CIP2A, SMC3	2.255006748	9.07E-05	2.78E-05
GOTERM_C C_DIRECT	GO:0005694~chromosome	7	1.46E-05	RECQL4, MDC1, UTP4, FBXW7, BRCA1, CIP2A, SMC3	12.79168854	0.002014	4.64E-04
GOTERM_C C_DIRECT	GO:0032991~protein-containing complex	9	7.92E-05	CDK8, FBXW7, CAD, CHEK1, BCL2, IKZF1, BRCA1, BRCA2, TP63	6.107309942	0.010877	0.002013
GOTERM_C C_DIRECT	GO:0000785~chromatin	11	1.15E-04	SUV39H2, CENPF, CCND2, FANCM, CDK4, IRF4, CHEK1, CREB3L2, SMC3, TP63, FOXF1	4.416705113	0.015689	0.002425
GOTERM_C C_DIRECT	GO:0005813~centrosome	8	4.66E-04	CENPF, CCND2, WDR90, CHEK1, AKAP9, BUB1B, BRCA2, MIB1	5.53389634	0.062291	0.008108
GOTERM_C C_DIRECT	GO:0000800~lateral element	3	5.11E-04	BRCA1, BRCA2, SMC3	87.02916667	0.068076	0.008108
GOTERM_C C_DIRECT	GO:0005730~nucleolus	10	0.002227	CDK8, CCND2, UTP4, TERT, PDCD11, CDK4, FBXW7, PIM1, BAZ2A, DEK	3.315396825	0.264798	0.031419
GOTERM_C C_DIRECT	GO:0016363~nuclear matrix	4	0.00259	CENPF, BCL11A, CAD, SMC3	14.2817094	0.300813	0.032889
GOTERM_C C_DIRECT	GO:0005737~cytoplasm	22	0.003386	BCL11A, FBXW7, RASGRF1, CAD, GAB1, BUB1B, BRCA1, CIP2A, MIB1, RECQL4, GRHPR, CENPF, CCND2, TERT, CDK4, WDR90, CHEK1, PIM1, BCL2, CARD11, TP63, BAP1	1.774664967	0.373805	0.039096
GOTERM_C C_DIRECT	GO:000307~cyclin-dependent protein kinase holoenzyme complex	3	0.003879	CDK8, CCND2, CDK4	31.6469697	0.415086	0.041049

GOTERM_MF_DIRECT	GO:0005515~protein binding	41	1.36E-04	KMT2D, SUV39H2, MDC1, BUB1B, BAZ2A, IKZF1, BRCA1, BRCA2, SMC3, RECQL4, TCL1A, CCND2, PDCD11, TERT, WDR90, CHEK1, PIM1, TP63, ANKRD28, FANCM, UTP4, FBXW7, CAD, GAB1, DEK, CIP2A, FOXF1, KTN1, MIB1, CDK8, AFDN, GRHRP, CENPF, IRF4, TBL1XR1, CDK4, ABI1, AKAP9, BCL2, CARD11, BAP1	1.379025317	0.022272	0.021703
UP_KW_BIOLOGICAL_PROCESS	KW-0131~Cell cycle	14	3.35E-08	SUV39H2, MDC1, BUB1B, BRCA1, IKZF1, BRCA2, SMC3, CDK8, CENPF, CCND2, CDK4, CHEK1, PIM1, TP63	6.666666667	1.00E-06	9.71E-07
UP_KW_BIOLOGICAL_PROCESS	KW-0227~DNA damage	8	2.54E-04	MDC1, FANCM, FBXW7, CHEK1, BRCA1, CIP2A, BRCA2, SMC3	5.961601041	0.007594	0.003684
UP_KW_BIOLOGICAL_PROCESS	KW-0234~DNA repair	7	6.26E-04	MDC1, FANCM, FBXW7, CHEK1, BRCA1, BRCA2, SMC3	6.291208791	0.018625	0.006056
UP_KW_CELLULAR_COMPONENT	KW-0539~Nucleus	34	1.12E-10	KMT2D, SUV39H2, MDC1, BUB1B, BAZ2A, IKZF1, BRCA1, BRCA2, SMC3, RECQL4, TCL1A, CCND2, PDCD11, TERT, CHEK1, CREB3L2, PIM1, TP63, ANKRD28, FANCM, UTP4, BCL11A, FBXW7, CAD, DEK, FOXF1, CDK8, CENPF, IRF4, TBL1XR1, CDK4, ABI1, BCL2, BAP1	2.539899574	1.91E-09	1.80E-09
UP_KW_CELLULAR_COMPONENT	KW-0158~Chromosome	12	7.99E-08	MDC1, SUV39H2, CENPF, UTP4, TERT, BCL11A, FBXW7, CHEK1, BUB1B, BRCA1, CIP2A, SMC3	8.375306337	1.36E-06	6.39E-07
UP_KW_CELLULAR_COMPONENT	KW-0963~Cytoplasm	24	9.02E-04	BCL11A, FBXW7, CAD, BUB1B, BRCA1, IKZF1, CIP2A, BRCA2, MIB1, RECQL4, CENPF, TCL1A, CCND2, TERT, CDK4, WDR90, ABI1, CHEK1, AKAP9, PIM1, BCL2, CARD11, TP63, BAP1	1.809239302	0.015232	0.004813
UP_KW_CELLULAR_COMPONENT	KW-0137~Centromere	4	0.004346	SUV39H2, CENPF, BUB1B, SMC3	11.82729071	0.071369	0.017384
UP_KW_MOLECULAR_FUNCTION	KW-0156~Chromatin regulator	7	1.18E-04	KMT2D, SUV39H2, TBL1XR1, BAZ2A, IKZF1, DEK, BAP1	8.46881042	0.003194	0.003199
UP_KW_MOLECULAR_FUNCTION	KW-0678~Repressor	7	0.004515	CDK8, SUV39H2, BCL11A, TBL1XR1, BAZ2A, IKZF1, FOXF1	4.22108947	0.11501	0.048411
UP_KW_MOLECULAR_FUNCTION	KW-0436~Ligase	4	0.007313	MDC1, CAD, BRCA1, MIB1	9.648204504	0.179769	0.048411
UP_KW_MOLECULAR_FUNCTION	KW-0010~Activator	7	0.008488	CDK8, TBL1XR1, IRF4, CREB3L2, IKZF1, BRCA1, TP63	3.702914349	0.205593	0.048411
UP_KW_MOLECULAR_FUNCTION	KW-0808~Transferase	12	0.009387	CDK8, KMT2D, SUV39H2, TERT, CDK4, CAD, CHEK1, AKAP9, PIM1, BUB1B, BRCA1, MIB1	2.221135882	0.224808	0.048411
UP_KW_MOLECULAR_FUNCTION	KW-0238~DNA-binding	12	0.010758	RECQL4, FANCM, TERT, IRF4, CREB3L2, BAZ2A, IKZF1, BRCA1, DEK, BRCA2, TP63, FOXF1	2.181134383	0.253259	0.048411

Suppl. Tabl S2.3. Significant DAVID functional terms with FDR ≤0.05 for 105 genes associated with the right PTL cluster on the heatmap (relatively better OS)

Category	Term	Count	P Value	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription by RNA polymerase II	26	1.17E-09	HLF, CEBPD, HOXC13, GLI1, FSTL3, SOX2, EPCAM, NKX2-5, DMRT1, EGR4, PEG3, DAB2IP, FOXL2, OLIG1, HNF1A, SMARCA1, SOX10, PHOX2B, BCL9, AR, PAX8, WT1, FEV, TLX1, ID4, HOXD9	4.168432	1.22E-06	1.22E-06	1.19E-06
GOTERM_BP_DIRECT	GO:0045893~positive regulation of DNA-templated transcription	18	6.40E-08	EPO, FOXL2, HNF1A, HOXC13, SMARCA1, GLI1, GDF6, SOX10, HOXA11, SOX2, AR, WNT6, PAX8, ZIC2, WT1, ERBB4, NKX2-5, WNT4	5.083608	6.67E-05	3.34E-05	3.24E-05
GOTERM_BP_DIRECT	GO:0006357~regulation of transcription by RNA polymerase II	26	1.56E-07	HLF, CEBPD, EPO, HOXC13, GLI1, HOXA11, FSTL3, DACH1, ZIC2, NKX2-5, ZNF444, DMRT1, EGR4, PEG3, FOXL2, HNF1A, SMARCA1, SOX10, PHOX2B, DMRTA2, PAX8, TLX3, WT1, FEV, TLX1, HOXD9	3.259994	1.63E-04	5.42E-05	5.26E-05
GOTERM_BP_DIRECT	GO:0045165~cell fate commitment	7	3.58E-07	SOX2, WNT6, WNT10B, ERBB4, WNT7B, WNT3, WNT4	24.72932	3.73E-04	9.32E-05	9.05E-05
GOTERM_BP_DIRECT	GO:0060070~canonical Wnt signaling pathway	8	1.32E-06	WNT6, WNT10B, BCL9, FZD3, WNT7B, FZD6, WNT3, WNT4	14.38338	0.00138	2.76E-04	2.68E-04
GOTERM_BP_DIRECT	GO:000122~negative regulation of transcription by RNA polymerase II	18	4.15E-06	WNT10B, DMRT1, PEG3, EPO, DAB2IP, FHL2, DDX20, FOXL2, HNF1A, SOX10, SOX2, AR, DACH1, WT1, ID4, NKX2-5, HOXD9, FRK	3.763876	0.004321	7.22E-04	7.01E-04
GOTERM_BP_DIRECT	GO:0090090~negative regulation of canonical Wnt signaling pathway	8	1.19E-05	SOX2, FZD6, IGFBP2, DAB2IP, PRICKLE1, NKX2-5, GLI1, SOX10	10.32653	0.012373	0.001779	0.001727
GOTERM_BP_DIRECT	GO:0030182~neuron differentiation	8	1.65E-05	SOX2, WNT6, WNT10B, FZD3, WNT7B, SMARCA1, WNT3, WNT4	9.822797	0.017083	0.002154	0.002092
GOTERM_BP_DIRECT	GO:0001658~branching involved in ureteric bud morphogenesis	5	6.40E-05	WNT6, PAX8, WT1, HOXA11, WNT4	22.88265	0.064611	0.007421	0.007208
GOTERM_BP_DIRECT	GO:0050680~negative regulation of epithelial cell proliferation	5	1.54E-04	SOX2, TGFBF3, WNT10B, AR, DAB2IP	18.30612	0.148724	0.016101	0.015638
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	11	2.02E-04	TGFBF3, WNT6, AR, WT1, FEV, ID4, CNTN1, NKX2-5, AMH, SOX10, WNT3	4.35175	0.18959	0.019109	0.018559
GOTERM_BP_DIRECT	GO:0072207~metanephric epithelium development	3	2.37E-04	PAX8, WT1, WNT7B	120.8204	0.218898	0.020585	0.019993
GOTERM_BP_DIRECT	GO:0016310~phosphorylation	12	2.77E-04	NTRK1, PRKCG, EPHA10, ERBB4, PRKACG, ITPKA, DCLK2, PAK6, CKB, MAPK8IP2, PAK5, FRK	3.81739	0.250849	0.021357	0.020743
GOTERM_BP_DIRECT	GO:008285~negative regulation of cell population proliferation	10	2.87E-04	NTRK1, AR, ATP8A2, ERBB4, WT1, NEURL1, DAB2IP, DDX20, DLEC1, RERG	4.639801	0.258472	0.021357	0.020743

GOTERM_BP_DIRECT	GO:0010976~positive regulation of neuron projection development	6	3.67E-04	NTRK1, ATP8A2, LRRC7, EPO, DAB2IP, CNTN1	9.743581	0.318065	0.025517	0.024783
GOTERM_BP_DIRECT	GO:0051602~response to electrical stimulus	4	4.68E-04	NTRK1, FZD3, EPO, PRICKLE1	25.98288	0.386474	0.028731	0.027904
GOTERM_BP_DIRECT	GO:0060071~Wnt signaling pathway, planar cell polarity pathway	4	4.68E-04	FZD3, WNT7B, FZD6, PRICKLE1	25.98288	0.386474	0.028731	0.027904
GOTERM_BP_DIRECT	GO:0045892~negative regulation of DNA-templated transcription	11	5.14E-04	DACH1, ZIC2, CEBPD, WT1, DAB2IP, ID4, FOXL2, PRICKLE1, NKX2-5, WNT4, RUNX1T1	3.865691	0.415107	0.029788	0.028931
GOTERM_BP_DIRECT	GO:0007411~axon guidance	7	5.68E-04	NTRK1, NGFR, EPHA10, CNTN1, NCAM1, EPHB1, WNT3	6.776786	0.447329	0.031201	0.030304
GOTERM_BP_DIRECT	GO:0045669~positive regulation of osteoblast differentiation	5	6.22E-04	WNT10B, CEBPD, WNT7B, WNT3, WNT4	12.74477	0.477152	0.032413	0.031481
GOTERM_BP_DIRECT	GO:0061180~mammary gland epithelium development	3	6.57E-04	WNT7B, WNT3, WNT4	75.51276	0.496037	0.03262	0.031682
GOTERM_BP_DIRECT	GO:0009653~anatomical structure morphogenesis	6	7.97E-04	SOX2, PAX8, FOXL2, HOXC13, SOX10, HOXA11	8.219075	0.564438	0.037763	0.036677
GOTERM_BP_DIRECT	GO:0002052~positive regulation of neuroblast proliferation	4	8.57E-04	DMRTA2, FZD3, ID4, SOX10	21.19656	0.591181	0.038874	0.037756
GOTERM_CC_DIRECT	GO:0000785~chromatin	21	5.67E-07	HLF, DMRT1, EGR4, CEBPD, OLIG1, FOXL2, HNF1A, HOXC13, SMARCA1, SOX10, PHOX2B, FANCF, SOX2, DMRTA2, AR, PAX8, TLX3, FEV, TLX1, NKX2-5, HOXD9	3.719952	9.24E-05	9.24E-05	9.01E-05
GOTERM_M_F_DIRECT	GO:0001228~DNA-binding transcription activator activity, RNA polymerase II-specific	17	4.81E-09	HLF, CEBPD, HOXC13, GLI1, HOXA11, SOX2, DACH1, ZIC2, NKX2-5, ZNF444, DMRT1, EGR4, PEG3, FOXL2, OLIG1, HNF1A, SOX10, PHOX2B, DMRTA2, AR, PAX8, TLX3, WT1, FEV, TLX1, HOXD9	6.590645	1.11E-06	1.11E-06	1.08E-06
GOTERM_M_F_DIRECT	GO:0000981~DNA-binding transcription factor activity, RNA polymerase II-specific	26	1.77E-08	HLF, CEBPD, HOXC13, GLI1, HOXA11, SOX2, DACH1, ZIC2, NKX2-5, ZNF444, DMRT1, EGR4, PEG3, FOXL2, HNF1A, SOX10, PHOX2B, DMRTA2, AR, PAX8, TLX3, WT1, FEV, TLX1, HOXD9	3.65662	4.07E-06	1.92E-06	1.87E-06
GOTERM_M_F_DIRECT	GO:0000978~RNA polymerase II cis-regulatory region sequence-specific DNA binding	25	2.51E-08	HLF, CEBPD, HOXC13, GLI1, HOXA11, SOX2, DACH1, ZIC2, NKX2-5, ZNF444, DMRT1, EGR4, PEG3, FOXL2, HNF1A, SOX10, PHOX2B, DMRTA2, AR, PAX8, TLX3, WT1, FEV, TLX1, HOXD9	3.735901	5.77E-06	1.92E-06	1.87E-06
GOTERM_M_F_DIRECT	GO:1990837~sequence-specific double-stranded DNA binding	16	1.88E-07	HLF, DMRT1, EGR4, CEBPD, FOXL2, HOXC13, SOX10, PHOX2B, HOXA11, DMRTA2, PAX8, TLX3, FEV, NKX2-5, HOXD9, ZNF444	5.46082	4.32E-05	1.08E-05	1.05E-05
GOTERM_M_F_DIRECT	GO:0005109~frizzled binding	6	1.69E-06	WNT6, WNT10B, RNF43, WNT7B, WNT3, WNT4	29.40442	3.88E-04	7.77E-05	7.56E-05
GOTERM_M_F_DIRECT	GO:0000976~transcription cis-regulatory region binding	10	4.97E-06	SOX2, AR, PAX8, ERBB4, WT1, HOXC13, HNF1A, NKX2-5, GLI1, SOX10	7.833144	0.001143	1.91E-04	1.86E-04
GOTERM_M_F_DIRECT	GO:0005125~cytokine activity	9	7.90E-06	WNT6, WNT10B, TAF45, EPO, WNT7B, GDF6, LEFTY2, WNT3, WNT4	8.821325	0.001815	2.60E-04	2.53E-04
GOTERM_M_F_DIRECT	GO:0003700~DNA-binding transcription factor activity	12	1.04E-04	SOX2, AR, EGR4, PAX8, ZIC2, WT1, FOXL2, HOXC13, HNF1A, NKX2-5, HOXD9, SOX10	4.279001	0.023605	0.002986	0.002908
GOTERM_M_F_DIRECT	GO:0048018~receptor ligand activity	5	5.05E-04	WNT10B, TAF45, WNT7B, WNT3, WNT4	13.45977	0.109651	0.012901	0.012565
GOTERM_M_F_DIRECT	GO:0005524~ATP binding	19	8.78E-04	PRKCG, NTRK1, ATP8A2, EPHA10, DDX20, DCLK2, SMARCA1, CCT6B, NAV3, ERBB4, PRKACG, ITPKA, PAK6, ACSBG1, MYH11, CKB, EPHB1, FRK, PAK5	2.356551	0.182874	0.020187	0.019661
KEGG_PATH_WAY	hsa04310:Wnt signaling pathway	14	4.90E-11	PRKCG, RNF43, WNT10B, FZD3, WNT7B, FZD6, PRICKLE1, CXCC4, WNT6, PPP3R2, WIF1, PRKACG, WNT3, WNT4	12.26318	8.37E-09	8.37E-09	7.54E-09
KEGG_PATH_WAY	hsa04550:Signaling pathways regulating pluripotency of stem cells	11	2.16E-08	SOX2, WNT6, WNT10B, FZD3, WNT7B, FZD6, ID4, LEFTY2, DUSP9, WNT3, WNT4	11.64272	3.69E-06	1.85E-06	1.66E-06
KEGG_PATH_WAY	hsa05217:Basal cell carcinoma	8	1.33E-07	WNT6, WNT10B, FZD3, WNT7B, FZD6, GLI1, WNT3, WNT4	19.35413	2.27E-05	5.99E-06	5.40E-06
KEGG_PATH_WAY	hsa05200:Pathways in cancer	17	1.40E-07	PRKCG, NTRK1, WNT10B, FZD3, EPO, LAMA1, WNT7B, FZD6, GLI1, DLL3, AR, WNT6, PAX8, PRKACG, WNT3, WNT4, RUNX1T1	4.861228	2.40E-05	5.99E-06	5.40E-06
KEGG_PATH_WAY	hsa04916:Melanogenesis	9	2.29E-07	PRKCG, WNT6, WNT10B, FZD3, PRKACG, WNT7B, FZD6, WNT3, WNT4	13.58143	3.91E-05	7.82E-06	7.04E-06
KEGG_PATH_WAY	hsa04390:Hippo signaling pathway	10	6.07E-07	SOX2, WNT6, WNT10B, FZD3, WNT7B, FZD6, GDF6, AMH, WNT3, WNT4	9.707885	1.04E-04	1.73E-05	1.56E-05
KEGG_PATH_WAY	hsa05202:Transcriptional misregulation in cancer	10	3.40E-06	NTRK1, PTCRA, NGFR, PAX8, TLX3, WT1, FEV, TLX1, HOXA11, RUNX1T1	7.897088	5.82E-04	8.31E-05	7.49E-05
KEGG_PATH_WAY	hsa05205:Proteoglycans in cancer	10	5.36E-06	PRKCG, WNT6, WNT10B, FZD3, ERBB4, PRKACG, WNT7B, FZD6, WNT3, WNT4	7.471264	9.17E-04	1.15E-04	1.03E-04
KEGG_PATH_WAY	hsa05224:Breast cancer	8	4.20E-05	WNT6, WNT10B, FZD3, WNT7B, FZD6, WNT3, WNT4, DLL3	8.238583	0.007152	7.97E-04	7.18E-04
KEGG_PATH_WAY	hsa04934:Cushing syndrome	8	5.64E-05	WNT6, WNT10B, FZD3, PRKACG, WNT7B, FZD6, WNT3, WNT4	7.866518	0.009597	9.64E-04	8.68E-04
KEGG_PATH_WAY	hsa04150:mTOR signaling pathway	8	6.37E-05	PRKCG, WNT6, WNT10B, FZD3, WNT7B, FZD6, WNT3, WNT4	7.717154	0.010834	9.90E-04	8.92E-04
KEGG_PATH_WAY	hsa05225:Hepatocellular carcinoma	8	1.01E-04	PRKCG, WNT6, WNT10B, FZD3, WNT7B, FZD6, WNT3, WNT4	7.172414	0.017148	0.001441	0.001298
KEGG_PATH_WAY	hsa05165:Human papillomavirus infection	10	2.49E-04	WNT6, WNT10B, FZD3, LAMA1, PRKACG, WNT7B, FZD6, COL9A3, WNT3, WNT4	4.576991	0.041769	0.003282	0.002955
KEGG_PATH_WAY	hsa05226:Gastric cancer	7	3.84E-04	WNT6, WNT10B, FZD3, WNT7B, FZD6, WNT3, WNT4	7.112644	0.063573	0.004691	0.00424
KEGG_PATH_WAY	hsa05010:Alzheimer disease	10	8.06E-04	WNT6, WNT10B, FZD3, PPP3R2, WNT7B, FZD6, IRS2, WNT3, RYR3, WNT4	3.898051	0.128779	0.009187	0.00824
KEGG_PATH_WAY	hsa04010:MAPK signaling pathway	8	0.002981	NTRK1, PRKCG, NGFR, PPP3R2, ERBB4, PRKACG, MAPK8IP2, DUSP9	4.064368	0.39985	0.031863	0.028696
KEGG_PATH_WAY	hsa05022:Pathways of neurodegeneration - multiple diseases	10	0.003472	PRKCG, WNT6, WNT10B, FZD3, PPP3R2, WNT7B, FZD6, WNT3, RYR3, WNT4	3.155565	0.44825	0.034919	0.03148
KEGG_PATH_WAY	hsa04014:Ras signaling pathway	7	0.004119	NTRK1, PRKCG, NGFR, PRKACG, PAK6, PLA2G5, PAK5	4.482759	0.50625	0.039126	0.035236
KEGG_PATH_WAY	hsa04020:Calcium signaling pathway	7	0.005646	NTRK1, PRKCG, PPP3R2, ERBB4, PRKACG, ITPKA, RYR3	4.20038	0.62024	0.050815	0.045763

KEGG_PATHWAY	hsa04360:Axon guidance	6	0.006458	FZD3, PPP3R2, PAK6, EPHB1, PAK5, WNT4	4.970015	0.669763	0.055218	0.049729
UP_KW_BIOLOGICAL_PROCESS	KW-0879~Wnt signaling pathway	11	1.10E-07	WNT6, WNT10B, RNF43, BCL9, FZD3, WIF1, WNT7B, FZD6, CXXC4, WNT3, WNT4 HLF, CEBPD, FHL2, HOXC13, GLI1, HOXA11, FSTL3, SOX2, DACH1, ZIC2, ERBB4, ZNF444, RUNX1T1, DMRT1, EGR4, FOXL2, OLIG1, HNF1A, SMARCA1, SOX10, PHOX2B, MN1, AR, PAX8, WT1, FEV, ID4, HOXD9	9.939236	4.39E-06	4.39E-06	4.06E-06
UP_KW_BIOLOGICAL_PROCESS	KW-0805~Transcription regulation	28	7.75E-05	HLF, CEBPD, FHL2, HOXC13, GLI1, HOXA11, FSTL3, SOX2, DACH1, ZIC2, ERBB4, ZNF444, RUNX1T1, DMRT1, EGR4, FOXL2, OLIG1, HNF1A, SMARCA1, SOX10, PHOX2B, MN1, AR, PAX8, WT1, FEV, ID4, HOXD9	2.075135	0.003095	0.00155	0.001434
UP_KW_BIOLOGICAL_PROCESS	KW-0804~Transcription	28	1.29E-04	HLF, CEBPD, FHL2, HOXC13, GLI1, HOXA11, FSTL3, SOX2, DACH1, ZIC2, ERBB4, ZNF444, RUNX1T1, DMRT1, EGR4, FOXL2, OLIG1, HNF1A, SMARCA1, SOX10, PHOX2B, MN1, AR, PAX8, WT1, FEV, ID4, HOXD9	2.017469	0.005129	0.001714	0.001585
UP_KW_CELLULAR_COMPONENT	KW-0272~Extracellular matrix	8	7.95E-04	TGFBF3, WNT6, WNT10B, LAMA1, WNT7B, COL9A3, WNT3, WNT4	5.249653	0.018133	0.018293	0.018293
UP_KW_DISEASE	KW-0656~Proto-oncogene	10	3.03E-04	NTRK1, BCL9, USP6, HLF, TLX1, MYH11, GLI1, WNT3, FSTL3, RUNX1T1	4.361249	0.009659	0.009705	0.009705
UP_KW_DOMAIN	KW-0371~Homeobox	8	2.35E-04	TLX3, TLX1, HOXC13, HNF1A, NKX2-5, HOXD9, PHOX2B, HOXA11	6.360349	0.003981	0.003989	0.003989
UP_KW_DOMAIN	KW-0732~Signal	33	0.0057	EPHA10, EPO, LAMA1, PLA2G5, FSTL3, DLL3, WNT6, ERBB4, EPCAM, WIF1, NCAM1, AMH, LEFTY2, EPHB1, WNT3, WNT4, LINGO2, PTCRA, NTRK1, NGFR, RNF43, WNT10B, FZD3, WNT7B, FZD6, IGFBP2, DAB2IP, GDF6, TGFBF3, TAFAS, WT1, CNTN1, COL9A3	1.517073	0.092608	0.048452	0.048452
UP_KW_LIGAND	KW-0067~ATP-binding	18	0.00106	PRKCG, NTRK1, ATP8A2, EPHA10, DDX20, DCLK2, SMARCA1, CCT6B, ERBB4, PRKACG, ITPKA, PAK6, ACSBG1, MYH11, CKB, EPHB1, FRK, PAK5	2.166424	0.011604	0.011665	0.011665
UP_KW_LIGAND	KW-0547~Nucleotide-binding	20	0.003076	PRKCG, NTRK1, DIRAS3, ATP8A2, EPHA10, DDX20, DCLK2, SMARCA1, RERG, CCT6B, ERBB4, PRKACG, ITPKA, PAK6, ACSBG1, MYH11, CKB, EPHB1, FRK, PAK5	1.84859	0.033315	0.016915	0.016915
UP_KW_MOLECULAR_FUNCTION	KW-9996~Developmental protein	32	2.01E-13	HOXC13, GLI1, HOXA11, DLL3, SOX2, WNT6, DACH1, ZIC2, ERBB4, WIF1, NKX2-5, LEFTY2, WNT3, WNT4, NTRK1, NGFR, RNF43, WNT10B, FZD3, DMRT1, WNT7B, FZD6, DAB2IP, OLIG1, GDF6, PHOX2B, MN1, PAX8, TLX3, FEV, TLX1, HOXD9	4.520532	8.05E-12	4.03E-12	3.82E-12
UP_KW_MOLECULAR_FUNCTION	KW-0217~Developmental protein	32	2.01E-13	HOXC13, GLI1, HOXA11, DLL3, SOX2, WNT6, DACH1, ZIC2, ERBB4, WIF1, NKX2-5, LEFTY2, WNT3, WNT4, NTRK1, NGFR, RNF43, WNT10B, FZD3, DMRT1, WNT7B, FZD6, DAB2IP, OLIG1, GDF6, PHOX2B, MN1, PAX8, TLX3, FEV, TLX1, HOXD9	4.520532	8.05E-12	4.03E-12	3.82E-12
UP_KW_MOLECULAR_FUNCTION	KW-0238~DNA-binding	28	3.27E-04	HLF, CEBPD, DDX20, HOXC13, GLI1, CXXC4, HOXA11, SOX2, DACH1, ZIC2, NKX2-5, ZNF444, RUNX1T1, DMRT1, EGR4, FOXL2, OLIG1, HNF1A, SOX10, PHOX2B, DMRTA2, AR, PAX8, TLX3, WT1, FEV, TLX1, HOXD9	1.972109	0.013013	0.004365	0.004147
UP_KW_MOLECULAR_FUNCTION	KW-0418~Kinase	13	0.00396	PRKCG, NTRK1, EPHA10, DCLK2, MAPK8IP2, ERBB4, PRKACG, ITPKA, PAK6, CKB, EPHB1, FRK, PAK5	2.558891	0.146749	0.039597	0.037617

Supplemental Table 3.1 Significant DEGs between the TLT and ME clusters of primary testicular DLBCL

Gene ID	Gene Name	Score(d)	Fold Change	q-value(%)	local fdr(%)
GAS5	GAS5 (Growth Arrest Specific 5)	-8.16142	0.229896	0	0.017705
TCL1A	TCL1 family AKT coactivator A(TCL1A)	-6.02715	0.250049	0	0
RPS21	ribosomal protein S21(RPS21)	-5.49659	0.30617	0	0
BTK	Bruton tyrosine kinase(BTK)	-9.79975	0.332097	0	0.220697
NACA	nascent polypeptide associated complex subunit alpha(NACA)	-8.24663	0.340907	0	0.039299
IRF4	interferon regulatory factor 4(IRF4)	-6.70971	0.358688	0	0
NPM1	nucleophosmin 1(NPM1)	-9.12335	0.361332	0	0.170002
H2BC4	H2B clustered histone 4(H2BC4)	-5.40133	0.368138	0	0
POU2AF1	POU class 2 homeobox associating factor 1(POU2AF1)	-7.84905	0.370191	0	0
RPL22	ribosomal protein L22(RPL22)	-7.27356	0.381056	0	0
TBL1XR1	TBL1X/Y related 1(TBL1XR1)	-9.06883	0.384566	0	0.165018
TFRC	transferrin receptor(TFRC)	-7.66602	0.400686	0	0
RB1	RB transcriptional corepressor 1(RB1)	-7.09328	0.403163	0	0
TYMS	thymidylate synthetase(TYMS)	-6.7717	0.416547	0	0
H3C2	H3 clustered histone 2(H3C2)	-4.85963	0.417977	0	0
PLCG2	phospholipase C gamma 2(PLCG2)	-7.44463	0.419964	0	0
HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1(HNRNPA2B1)	-6.54582	0.423193	0	0
SNHG5	Small Nucleolar RNA Host Gene 5	-3.84952	0.427873	0	0
HMGA1	high mobility group AT-hook 1(HMGA1)	-5.30229	0.431372	0	0
RAC2	Rac family small GTPase 2(RAC2)	-4.85228	0.431729	0	0
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B(BUB1B)	-7.09105	0.437909	0	0
DEK	DEK proto-oncogene(DEK)	-8.71104	0.438198	0	0.124702
MAD2L1	mitotic arrest deficient 2 like 1(MAD2L1)	-6.00044	0.439599	0	0
PFDN5	prefoldin subunit 5(PFDN5)	-5.39263	0.447034	0	0
CD79B	CD79b molecule(CD79B)	-5.66071	0.447733	0	0
CCNA2	cyclin A2(CCNA2)	-7.34307	0.448602	0	0
SET	SET nuclear proto-oncogene(SET)	-7.67044	0.450024	0	0
MELK	maternal embryonic leucine zipper kinase(MELK)	-7.1999	0.455132	0	0
LYN	LYN proto-oncogene, Src family tyrosine kinase(LYN)	-8.29085	0.46051	0	0.049672
HSPA4	heat shock protein family A (Hsp70) member 4(HSPA4)	-6.52557	0.460686	0	0
TOP2A	DNA topoisomerase II alpha(TOP2A)	-7.52513	0.461591	0	0
PAX5	paired box 5(PAX5)	-6.51388	0.462194	0	0
CDK1	cyclin dependent kinase 1(CDK1)	-7.4733	0.464612	0	0
PTPN2	protein tyrosine phosphatase non-receptor type 2(PTPN2)	-7.21917	0.464921	0	0
PRKCB	protein kinase C beta(PRKCB)	-6.15999	0.466489	0	0
U2AF1	U2 small nuclear RNA auxiliary factor 1(U2AF1)	-5.22215	0.467193	0	0
IRAG2	inositol 1,4,5-triphosphate receptor associated 2(IRAG2)	-5.17564	0.467327	0	0
SYK	spleen associated tyrosine kinase(SYK)	-7.68146	0.469034	0	0
PTEN	phosphatase and tensin homolog(PTEN)	-7.94082	0.470286	0	0
CD79A	CD79a molecule(CD79A)	-4.7914	0.470805	0	0
MKI67	marker of proliferation Ki-67(MKI67)	-6.56756	0.480298	0	0
PCNA	proliferating cell nuclear antigen(PCNA)	-5.64578	0.483701	0	0
NONO	non-POU domain containing octamer binding(NONO)	-5.97219	0.488131	0	0
AFF3	ALF transcription elongation factor 3(AFF3)	-5.94804	0.490817	0	0
NUP107	nucleoporin 107(NUP107)	-7.06136	0.491408	0	0

PRKDC	protein kinase, DNA-activated, catalytic subunit(PRKDC)	-8.29222	0.495157	0	0.049984
TOP1	DNA topoisomerase I(TOP1)	-6.61873	0.495462	0	0
SS18	SS18 subunit of BAF chromatin remodeling complex(SS18)	-5.73806	0.503837	0	0
H2BC12	H2B clustered histone 12(H2BC12)	-4.65538	0.50532	0	0
NFKB1	nuclear factor kappa B subunit 1(NFKB1)	-7.33284	0.506808	0	0
KTN1	kinectin 1(KTN1)	-6.3606	0.507429	0	0
MSI2	musashi RNA binding protein 2(MSI2)	-5.45784	0.510298	0	0
PRMT1	protein arginine methyltransferase 1(PRMT1)	-5.56919	0.512594	0	0
FOXP1	forkhead box P1(FOXP1)	-8.47781	0.513078	0	0.087866
EZH2	enhancer of zeste 2 polycomb repressive complex 2 subunit(EZH2)	-7.66862	0.515979	0	0
MDM2	MDM2 proto-oncogene(MDM2)	-6.92465	0.520742	0	0
CENPU	centromere protein U(CENPU)	-4.76339	0.52174	0	0
GMPS	guanine monophosphate synthase(GMPS)	-6.29099	0.524475	0	0
BIRC3	baculoviral IAP repeat containing 3(BIRC3)	-5.2502	0.52882	0	0
XPO1	exportin 1(XPO1)	-6.65665	0.530203	0	0
CYFIP2	cytoplasmic FMR1 interacting protein 2(CYFIP2)	-7.39359	0.531752	0	0
SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5(SMARCA5)	-6.75839	0.532225	0	0
TOP2B	DNA topoisomerase II beta(TOP2B)	-6.92889	0.532517	0	0
INPP5D	inositol polyphosphate-5-phosphatase D(INPP5D)	-5.57217	0.533993	0	0
USP7	ubiquitin specific peptidase 7(USP7)	-6.54094	0.534006	0	0
H2AC11	H2A clustered histone 11(H2AC11)	-4.01978	0.535459	0	0
STAG2	STAG2 cohesin complex component(STAG2)	-8.77445	0.537104	0	0.133044
SH3BP1	SH3 domain binding protein 1(SH3BP1)	-3.9452	0.537306	0	0
GTF2I	general transcription factor Iii(GTF2I)	-6.24425	0.537483	0	0
ST6GAL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1(ST6GAL1)	-6.56414	0.538581	0	0
LCP1	lymphocyte cytosolic protein 1(LCP1)	-4.9395	0.539395	0	0
SMC1A	structural maintenance of chromosomes 1A(SMC1A)	-6.72404	0.539982	0	0
LRPPRC	leucine rich pentatricopeptide repeat containing(LRPPRC)	-7.54948	0.541283	0	0
H2AC17	H2A clustered histone 17(H2AC17)	-4.1938	0.542192	0	0
PHF6	PHD finger protein 6(PHF6)	-6.24764	0.54405	0	0
RAD21	RAD21 cohesin complex component(RAD21)	-6.55457	0.546755	0	0
PKM	pyruvate kinase M1/2(PKM)	-4.39869	0.54784	0	0
HSP90AB1	heat shock protein 90 alpha family class B member 1(HSP90AB1)	-5.7208	0.548115	0	0
SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1(SMARCB1)	-4.9053	0.548467	0	0
SARNP	SAP domain containing ribonucleoprotein(SARNP)	-3.79462	0.552132	0	0
BCL2A1	BCL2 related protein A1(BCL2A1)	-3.70222	0.554085	0	0.476895
SEPTIN2	septin 2(SEPTIN2)	-4.67478	0.554155	0	0
ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase(ATIC)	-7.77055	0.555487	0	0
RASAL1	RAS protein activator like 1(RASAL1)	-3.59874	0.556849	0.018157	1.204524
PTPN11	protein tyrosine phosphatase non-receptor type 11(PTPN11)	-5.79429	0.557639	0	0
RPS6KA3	ribosomal protein S6 kinase A3(RPS6KA3)	-5.57065	0.559105	0	0
ZNF207	zinc finger protein 207(ZNF207)	-5.91591	0.560078	0	0
POLD1	DNA polymerase delta 1, catalytic subunit(POLD1)	-4.65699	0.560726	0	0
TFDP1	transcription factor Dp-1(TFDP1)	-6.68656	0.561206	0	0
KIF5B	kinesin family member 5B(KIF5B)	-5.35399	0.565587	0	0

SUZ12	SUZ12 polycomb repressive complex 2 subunit(SUZ12)	-7.3201	0.565648	0	0
CAPRIN1	cell cycle associated protein 1(CAPRIN1)	-6.06219	0.567744	0	0
AURKB	aurora kinase B(AURKB)	-4.02274	0.569252	0	0
NDC80	NDC80 kinetochore complex component(NDC80)	-4.16728	0.570893	0	0
HERPUD1	homocysteine inducible ER protein with ubiquitin like domain 1(HERPUD1)	-5.36068	0.571704	0	0
YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon(YWHAE)	-5.15921	0.57208	0	0
XRCC6	X-ray repair cross complementing 6(XRCC6)	-5.81393	0.572984	0	0
TCEA1	transcription elongation factor A1(TCEA1)	-6.56653	0.574694	0	0
KRAS	KRAS proto-oncogene, GTPase(KRAS)	-5.75437	0.574951	0	0
TTK	TTK protein kinase(TTK)	-4.58719	0.576131	0	0
STAT1	signal transducer and activator of transcription 1(STAT1)	-3.86265	0.5784	0	0
LRRK2	leucine rich repeat kinase 2(LRRK2)	-4.30107	0.579214	0	0
CARD11	caspase recruitment domain family member 11(CARD11)	-5.19838	0.57937	0	0
NRAS	NRAS proto-oncogene, GTPase(NRAS)	-6.29765	0.583156	0	0
SEPTIN6	septin 6(SEPTIN6)	-5.33275	0.584503	0	0
NCOA3	nuclear receptor coactivator 3(NCOA3)	-6.37523	0.58502	0	0
IKZF3	IKAROS family zinc finger 3(IKZF3)	-6.72609	0.585088	0	0
KPNB1	karyopherin subunit beta 1(KPNB1)	-5.7585	0.585623	0	0
PPP3R1	protein phosphatase 3 regulatory subunit B, alpha(PPP3R1)	-5.85343	0.586457	0	0
FANCA	FA complementation group A(FANCA)	-4.98392	0.58668	0	0
WEE1	WEE1 G2 checkpoint kinase(WEE1)	-5.81727	0.589172	0	0
RAP1GDS1	Rap1 GTPase-GDP dissociation stimulator 1(RAP1GDS1)	-5.77213	0.589617	0	0
PICALM	phosphatidylinositol binding clathrin assembly protein(PICALM)	-4.60767	0.590726	0	0
RPS6KA1	ribosomal protein S6 kinase A1(RPS6KA1)	-4.62011	0.591879	0	0
SMC3	structural maintenance of chromosomes 3(SMC3)	-5.9264	0.592358	0	0
HOOK3	hook microtubule tethering protein 3(HOOK3)	-6.09795	0.592937	0	0
BLM	BLM RecQ like helicase(BLM)	-6.28868	0.594205	0	0
LPXN	leupaxin(LPXN)	-5.59389	0.595998	0	0
SFPQ	splicing factor proline and glutamine rich(SFPQ)	-5.58104	0.596816	0	0
FBXO11	F-box protein 11(FBXO11)	-5.05302	0.597052	0	0
RASGRF1	Ras protein specific guanine nucleotide releasing factor 1(RASGRF1)	-3.38567	0.597749	0.018157	3.035428
COX6C	cytochrome c oxidase subunit 6C(COX6C)	-4.59641	0.601354	0	0
HDAC2	histone deacetylase 2(HDAC2)	-5.37866	0.602674	0	0
EIF4A2	eukaryotic translation initiation factor 4A2(EIF4A2)	-6.84118	0.602754	0	0
FANCI	FA complementation group I(FANCI)	-7.20983	0.604909	0	0
FUS	FUS RNA binding protein(FUS)	-5.5982	0.605158	0	0
BCL11A	BCL11 transcription factor A(BCL11A)	-5.04236	0.60607	0	0
RAD50	RAD50 double strand break repair protein(RAD50)	-5.75313	0.60732	0	0
CHEK1	checkpoint kinase 1(CHEK1)	-4.81864	0.608386	0	0
IRF8	interferon regulatory factor 8(IRF8)	-3.61177	0.608674	0.018157	1.107367
CIP2A	cellular inhibitor of PP2A(CIP2A)	-5.35297	0.609148	0	0
ATM	ATM serine/threonine kinase(ATM)	-7.27918	0.61235	0	0
MRE11	MRE11 homolog, double strand break repair nuclease(MRE11)	-6.1796	0.612804	0	0
CXCR4	C-X-C motif chemokine receptor 4(CXCR4)	-4.77516	0.613717	0	0
IKZF1	IKAROS family zinc finger 1(IKZF1)	-5.08033	0.614127	0	0
MAPK1	mitogen-activated protein kinase 1(MAPK1)	-4.17079	0.616019	0	0

NBN	nibrin(NBN)	-5.29752	0.61689	0	0
PTBP1	polypyrimidine tract binding protein 1(PTBP1)	-4.40412	0.617546	0	0
VHL	von Hippel-Lindau tumor suppressor(VHL)	-5.30247	0.618791	0	0
GIT2	GIT ArfGAP 2(GIT2)	-7.20378	0.619173	0	0
FANCL	FA complementation group L(FANCL)	-3.79013	0.620127	0	0
HUWE1	HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1(HUWE1)	-4.89675	0.6224	0	0
IDH2	isocitrate dehydrogenase (NADP(+)) 2(IDH2)	-3.59779	0.623019	0.018157	1.211723
MBNL1	muscleblind like splicing regulator 1(MBNL1)	-4.64585	0.624428	0	0
PRKAR1A	protein kinase cAMP-dependent type I regulatory subunit alpha(PRKAR1A)	-4.35243	0.624879	0	0
DNMT1	DNA methyltransferase 1(DNMT1)	-4.76894	0.626988	0	0
MNAT1	MNAT1 component of CDK activating kinase(MNAT1)	-3.6273	0.629269	0.018157	0.993688
CARMIL2	capping protein regulator and myosin 1 linker 2(CARMIL2)	-4.00425	0.629855	0	0
UBE2C	ubiquitin conjugating enzyme E2 C(UBE2C)	-3.64638	0.630024	0.018157	0.857122
FNBP1	formin binding protein 1(FNBP1)	-4.23059	0.630112	0	0
TMEM230	transmembrane protein 230(TMEM230)	-4.44414	0.6302	0	0
PHB1	prohibitin 1(PHB1)	-3.91647	0.630759	0	0
SRSF3	serine and arginine rich splicing factor 3(SRSF3)	-5.17435	0.633723	0	0
FANCD2	FA complementation group D2(FANCD2)	-5.89642	0.63561	0	0
DDX3X	DEAD-box helicase 3 X-linked(DDX3X)	-6.18859	0.636896	0	0
WDR1	WD repeat domain 1(WDR1)	-3.60357	0.638437	0.018157	1.168368
EZR	ezrin(EZR)	-3.65983	0.639265	0.018157	0.762911
DPM1	dolichyl-phosphate mannosyltransferase subunit 1, catalytic(DPM1)	-4.48539	0.639392	0	0
CEP57	centrosomal protein 57(CEP57)	-6.31914	0.640931	0	0
RRM1	ribonucleotide reductase catalytic subunit M1(RRM1)	-4.30187	0.642842	0	0
MAPRE1	microtubule associated protein RP/EB family member 1(MAPRE1)	-4.03684	0.644696	0	0
CENPF	centromere protein F(CENPF)	-4.28384	0.645602	0	0
U2AF2	U2 small nuclear RNA auxiliary factor 2(U2AF2)	-4.17122	0.646562	0	0
PIM1	Pim-1 proto-oncogene, serine/threonine kinase(PIM1)	-3.35198	0.64839	0.034444	3.368729
GRB2	growth factor receptor bound protein 2(GRB2)	-4.03594	0.649686	0	0
SF3B1	splicing factor 3b subunit 1(SF3B1)	-4.64427	0.653736	0	0
GOSR1	golgi SNAP receptor complex member 1(GOSR1)	-4.65347	0.655913	0	0
CDC42	cell division cycle 42(CDC42)	-4.19445	0.657802	0	0
RABEP1	rabaptin, RAB GTPase binding effector protein 1(RABEP1)	-4.14504	0.658778	0	0
BRCA1	BRCA1 DNA repair associated(BRCA1)	-4.82963	0.659788	0	0
SRSF2	serine and arginine rich splicing factor 2(SRSF2)	-4.81011	0.66006	0	0
EED	embryonic ectoderm development(EED)	-6.39119	0.660524	0	0
NIN	ninein(NIN)	-4.42806	0.661377	0	0
PTPN6	protein tyrosine phosphatase non-receptor type 6(PTPN6)	-3.50066	0.661611	0.018157	1.989526
MSH2	mutS homolog 2(MSH2)	-4.90907	0.662096	0	0
GNAS	GNAS complex locus(GNAS)	-3.5378	0.662254	0.018157	1.681034
CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase(CAD)	-5.514	0.664516	0	0
ARHGEF7	Rho guanine nucleotide exchange factor 7(ARHGEF7)	-5.25708	0.666687	0	0
ABI1	abl interactor 1(ABI1)	-6.97271	0.668612	0	0
MDM4	MDM4 regulator of p53(MDM4)	-5.21516	0.669597	0	0
CD44	CD44 molecule (IN blood group)(CD44)	-3.20781	0.670988	0.034444	4.939348

OFD1	OFD1 centriole and centriolar satellite protein(OFD1)	-3.9829	0.671047	0	0
FLI1	Fli-1 proto-oncogene, ETS transcription factor(FLI1)	-4.06695	0.671748	0	0
EML4	EMAP like 4(EML4)	-5.46604	0.673103	0	0
TPM3	tropomyosin 3(TPM3)	-3.36416	0.673339	0.034444	3.246813
FGFR1OP2	FGFR1 oncogene partner 2(FGFR1OP2)	-4.82312	0.673635	0	0
LASP1	LIM and SH3 protein 1(LASP1)	-3.95848	0.675151	0	0
CNOT2	CCR4-NOT transcription complex subunit 2(CNOT2)	-4.76416	0.675281	0	0
XBP1	X-box binding protein 1(XBP1)	-3.58037	0.67728	0.018157	1.344305
RHOA	ras homolog family member A(RHOA)	-3.87395	0.678629	0	0
ETS1	ETS proto-oncogene 1, transcription factor(ETS1)	-5.17886	0.678658	0	0
DDX39B	DExD-box helicase 39B(DDX39B)	-3.85536	0.67993	0	0
CPSF6	cleavage and polyadenylation specific factor 6(CPSF6)	-7.38607	0.684088	0	0
PVT1	Pvt1 Oncogene	-3.44198	0.686504	0.018157	2.505825
BTG1	BTG anti-proliferation factor 1(BTG1)	-4.55436	0.687431	0	0
DDX5	DEAD-box helicase 5(DDX5)	-3.92985	0.687974	0	0
AKT2	AKT serine/threonine kinase 2(AKT2)	-3.34724	0.688537	0.034444	3.416658
GAB1	GRB2 associated binding protein 1(GAB1)	-3.67035	0.688679	0	0.690403
UTP4	UTP4 small subunit processome component(UTP4)	-5.17664	0.690091	0	0
HSP90AA1	heat shock protein 90 alpha family class A member 1(HSP90AA1)	-3.36506	0.691576	0.034444	3.237849
NFKB2	nuclear factor kappa B subunit 2(NFKB2)	-3.27166	0.69215	0.034444	4.214375
TACC3	transforming acidic coiled-coil containing protein 3(TACC3)	-3.69348	0.694599	0	0.534512
STAT6	signal transducer and activator of transcription 6(STAT6)	-3.69513	0.695499	0	0.523619
EIF4E	eukaryotic translation initiation factor 4E(EIF4E)	-4.46613	0.698955	0	0
TPR	translocated promoter region, nuclear basket protein(TPR)	-4.24051	0.699709	0	0
KDM1A	lysine demethylase 1A(KDM1A)	-4.16968	0.703911	0	0
AURKA	aurora kinase A(AURKA)	-3.98754	0.704382	0	0
MLH1	mutL homolog 1(MLH1)	-4.37731	0.704702	0	0
COG5	component of oligomeric golgi complex 5(COG5)	-4.84499	0.706691	0	0
CNTRL	centriolin(CNTRL)	-4.98503	0.707472	0	0
EPS15	epidermal growth factor receptor pathway substrate 15(EPS15)	-3.80103	0.708709	0	0
CCNG1	cyclin G1(CCNG1)	-4.91657	0.710367	0	0
POT1	protection of telomeres 1(POT1)	-4.17087	0.711235	0	0
PCBP1	poly(rC) binding protein 1(PCBP1)	-3.43963	0.711321	0.018157	2.527305
PDCD11	programmed cell death 11(PDCD11)	-4.2366	0.7125	0	0
DDX6	DEAD-box helicase 6(DDX6)	-5.17653	0.713163	0	0
HMGB1	high mobility group box 1(HMGB1)	-3.53463	0.715012	0.018157	1.706827
ELK4	ETS transcription factor ELK4(ELK4)	-4.77096	0.716487	0	0
TCF3	transcription factor 3(TCF3)	-3.37631	0.716695	0.018157	3.12681
CCDC6	coiled-coil domain containing 6(CCDC6)	-4.45916	0.719357	0	0
BIRC6	baculoviral IAP repeat containing 6(BIRC6)	-6.48567	0.719887	0	0
CLTA	clathrin light chain A(CLTA)	-3.63363	0.720346	0.018157	0.948008
CDK4	cyclin dependent kinase 4(CDK4)	-4.14699	0.720828	0	0
NSD2	nuclear receptor binding SET domain protein 2(NSD2)	-3.99059	0.721553	0	0
CUX1	cut like homeobox 1(CUX1)	-3.62319	0.723505	0.018157	1.023583
FAF1	Fas associated factor 1(FAF1)	-3.83657	0.72377	0	0
FH	fumarate hydratase(FH)	-3.22412	0.723882	0.034444	4.749546
HIF1A	hypoxia inducible factor 1 subunit alpha(HIF1A)	-3.2183	0.725121	0.034444	4.816984

CALR	calreticulin(CALR)	-3.64104	0.729037	0.018157	0.895026
ZC3H7A	zinc finger CCCH-type containing 7A(ZC3H7A)	-3.94784	0.733154	0	0
TYK2	tyrosine kinase 2(TYK2)	-3.38324	0.735369	0.018157	3.059081
MALT1	MALT1 paracaspase(MALT1)	-3.75821	0.735815	0	0.123823
WASF2	WASP family member 2(WASF2)	-3.62587	0.740169	0.018157	1.004062
STIL	STIL centriolar assembly protein(STIL)	-3.30642	0.741936	0.034444	3.839428
RAF1	Raf-1 proto-oncogene, serine/threonine kinase(RAF1)	-3.6026	0.744591	0.018157	1.17559
MSH3	mutS homolog 3(MSH3)	-4.11923	0.747618	0	0
XIAP	X-linked inhibitor of apoptosis(XIAP)	-3.23077	0.750117	0.034444	4.673102
KAT2B	lysine acetyltransferase 2B(KAT2B)	-3.55511	0.75057	0.018157	1.541946
SOS1	SOS Ras/Rac guanine nucleotide exchange factor 1(SOS1)	-3.83076	0.753407	0	0
FIP1L1	factor interacting with PAPOLA and CPSF1(FIP1L1)	-4.98763	0.754763	0	0
YTHDF2	YTH N6-methyladenosine RNA binding protein F2(YTHDF2)	-3.51264	0.759313	0.018157	1.888534
TERF2	telomeric repeat binding factor 2(TERF2)	-3.26682	0.761278	0.034444	4.267671
CHD2	chromodomain helicase DNA binding protein 2(CHD2)	-4.55105	0.762166	0	0
CCDC88C	coiled-coil domain containing 88C(CCDC88C)	-3.55947	0.762656	0.018157	1.507427
NSD3	nuclear receptor binding SET domain protein 3(NSD3)	-3.48091	0.762713	0.018157	2.159363
STRN	striatin(STRN)	-3.93491	0.76762	0	0
FRYL	FRY like transcription coactivator(FRYL)	-5.25183	0.773859	0	0
PMS2	PMS1 homolog 2, mismatch repair system component(PMS2)	-3.27058	0.774119	0.034444	4.226206
CBFB	core-binding factor subunit beta(CBFB)	-3.54065	0.776945	0.018157	1.657946
NUP98	nucleoporin 98 and 96 precursor(NUP98)	-3.33726	0.777236	0.034444	3.518247
SP3	Sp3 transcription factor(SP3)	-3.36866	0.778098	0.018157	3.202227
EWSR1	EWS RNA binding protein 1(EWSR1)	-4.09657	0.778121	0	0
DDX10	DEAD-box helicase 10(DDX10)	-3.81761	0.779694	0	0
MAP3K1	mitogen-activated protein kinase kinase kinase 1(MAP3K1)	-3.2651	0.783319	0.034444	4.2866
MAP3K7	mitogen-activated protein kinase kinase kinase 7(MAP3K7)	-3.27003	0.787219	0.034444	4.232208
EP400	E1A binding protein p400(EP400)	-3.41949	0.789105	0.018157	2.713295
CLTC	clathrin heavy chain(CLTC)	-3.77724	0.790458	0	0.010055
ATR	ATR serine/threonine kinase(ATR)	-3.31486	0.79181	0.034444	3.750499
ARID1A	AT-rich interaction domain 1A(ARID1A)	-3.33087	0.791868	0.034444	3.583984
ATRX	ATRX chromatin remodeler(ATRX)	-4.79549	0.803745	0	0
CDC73	cell division cycle 73(CDC73)	-3.76556	0.820459	0	0.079535
CDK12	cyclin dependent kinase 12(CDK12)	-3.87555	0.834349	0	0
CDK5RAP2	CDK5 regulatory subunit associated protein 2(CDK5RAP2)	-3.35497	0.845454	0.034444	3.338695
BAZ2A	bromodomain adjacent to zinc finger domain 2A(BAZ2A)	-3.31745	0.848717	0.034444	3.723364
GHR	growth hormone receptor(GHR)	14.79563	8.322049	0	0
DUX4L4	DUX4L4 (Double Homeobox 4 Like 4 (Pseudogene))	4.129928	1.189785	0	0
DUX4L8	DUX4L8 (Double Homeobox 4 Like 8 (Pseudogene))	4.496398	1.322424	0	0
DDX20	DEAD-box helicase 20(DDX20)	3.478378	1.33468	0	4.548721
PPM1D	protein phosphatase, Mg2+/Mn2+ dependent 1D(PPM1D)	3.86695	1.349331	0	0.846106
MYO18A	myosin XVIIIa(MYO18A)	3.499874	1.354069	0	4.29854
APLP2	amyloid beta precursor like protein 2(APLP2)	4.329199	1.356228	0	0
KAT6B	lysine acetyltransferase 6B(KAT6B)	3.469279	1.367505	0	4.656339
HES5	hes family bHLH transcription factor 5(HES5)	3.939853	1.372818	0	0.329371
AHI1	Abelson helper integration site 1(AHI1)	3.919163	1.381542	0	0.470817

FRS2	fibroblast growth factor receptor substrate 2(FRS2)	3.960223	1.38936	0	0.194063
CTRB1	chymotrypsinogen B1(CTRB1)	4.416958	1.391114	0	0
JARID2	jumonji and AT-rich interaction domain containing 2(JARID2)	3.719828	1.3997	0	2.05196
CTNNA1	catenin alpha 1(CTNNA1)	5.336484	1.426348	0	0
AXIN1	axin 1(AXIN1)	4.20788	1.449582	0	0
DNAJB1	DnaJ heat shock protein family (Hsp40) member B1(DNAJB1)	3.964503	1.463005	0	0.166129
OLIG2	oligodendrocyte transcription factor 2(OLIG2)	4.385126	1.470119	0	0
ZNF687	zinc finger protein 687(ZNF687)	4.081901	1.471584	0	0
KIAA0232	KIAA0232(KIAA0232)	4.7331	1.48036	0	0
FANCC	FA complementation group C(FANCC)	3.658865	1.482114	0	2.619254
ZMYND11	zinc finger MYND-type containing 11(ZMYND11)	4.24874	1.484302	0	0
FANCF	FA complementation group F(FANCF)	3.454045	1.491172	0	4.838804
BMPR1A	bone morphogenetic protein receptor type 1A(BMPR1A)	3.896372	1.503515	0	0.631365
NOTCH2	notch receptor 2(NOTCH2)	4.62814	1.509114	0	0
ERCC6	ERCC excision repair 6, chromatin remodeling factor(ERCC6)	5.046649	1.509189	0	0
MAML2	mastermind like transcriptional coactivator 2(MAML2)	3.98356	1.511982	0	0.043784
TRPS1	transcriptional repressor GATA binding 1(TRPS1)	4.559944	1.521868	0	0
MAGED1	MAGE family member D1(MAGED1)	3.752676	1.525763	0	1.763088
LPP	LIM domain containing preferred translocation partner in lipoma(LPP)	4.165417	1.52859	0	0
DPYD	dihydropyrimidine dehydrogenase(DPYD)	4.212976	1.536308	0	0
MRTFB	MRTFB (Myocardin Related Transcription Factor B)	5.531659	1.539261	0	0
SNX9	sorting nexin 9(SNX9)	3.675175	1.54242	0	2.463458
BRD3	bromodomain containing 3(BRD3)	6.167707	1.554365	0	0
CCDC28A	coiled-coil domain containing 28A(CCDC28A)	3.545792	1.560517	0	3.782943
RPS6KA2	ribosomal protein S6 kinase A2(RPS6KA2)	3.906243	1.568216	0	0.561213
ZFYVE19	zinc finger FYVE-type containing 19(ZFYVE19)	3.765695	1.575303	0	1.65178
NCKIPSD	NCK interacting protein with SH3 domain(NCKIPSD)	3.632755	1.578367	0	2.874899
BRD1	bromodomain containing 1(BRD1)	5.03313	1.580462	0	0
SLX4	SLX4 structure-specific endonuclease subunit(SLX4)	4.022507	1.584478	0	0
HIP1	huntingtin interacting protein 1(HIP1)	3.949831	1.589274	0	0.262609
CHD6	chromodomain helicase DNA binding protein 6(CHD6)	7.713621	1.590681	0	0
CRTC3	CREB regulated transcription coactivator 3(CRTC3)	4.022611	1.594894	0	0
OLIG1	oligodendrocyte transcription factor 1(OLIG1)	5.384315	1.596055	0	0
SYP	synaptophysin(SYP)	5.211242	1.598966	0	0
SMAD3	SMAD family member 3(SMAD3)	4.612574	1.608546	0	0
NOD1	nucleotide binding oligomerization domain containing 1(NOD1)	4.827444	1.612422	0	0
SHTN1	SHTN1 (Shootin 1)	4.157198	1.621906	0	0
ABL2	ABL proto-oncogene 2, non-receptor tyrosine kinase(ABL2)	5.784122	1.640858	0	0
FEV	FEV transcription factor, ETS family member(FEV)	5.005915	1.651379	0	0
GADD45B	growth arrest and DNA damage inducible beta(GADD45B)	3.488373	1.653111	0	4.431682
BCORL1	BCL6 corepressor like 1(BCORL1)	5.664171	1.653203	0	0
RARA	retinoic acid receptor alpha(RARA)	4.802782	1.666536	0	0
ZIC2	Zic family member 2(ZIC2)	3.977119	1.668503	0	0.08476
HDAC4	histone deacetylase 4(HDAC4)	5.189768	1.669738	0	0
PRKCA	protein kinase C alpha(PRKCA)	4.649713	1.676951	0	0
CSF3R	colony stimulating factor 3 receptor(CSF3R)	3.7495	1.677944	0	1.790512

HDAC5	histone deacetylase 5(HDAC5)	5.493504	1.684181	0	0
SOCS3	suppressor of cytokine signaling 3(SOCS3)	4.014891	1.686	0	0
TLL2	tolloid like 2(TLL2)	5.028875	1.700031	0	0
TNFRSF6B	TNF receptor superfamily member 6b(TNFRSF6B)	4.19745	1.700604	0	0
ITGAV	integrin subunit alpha V(ITGAV)	4.902727	1.707522	0	0
EXT2	exostosin glycosyltransferase 2(EXT2)	6.909134	1.714343	0	0
CRLF2	cytokine receptor like factor 2(CRLF2)	3.781216	1.725254	0	1.52142
TNFRSF10D	TNF receptor superfamily member 10d(TNFRSF10D)	4.009763	1.725348	0	0
TNC	tenascin C(TNC)	4.23517	1.726933	0	0
P2RY8	P2Y receptor family member 8(P2RY8)	3.842409	1.733092	0	1.031792
SOX11	SRY-box transcription factor 11(SOX11)	5.410027	1.733678	0	0
PIK3R2	phosphoinositide-3-kinase regulatory subunit 2(PIK3R2)	6.041315	1.734096	0	0
DLL4	delta like canonical Notch ligand 4(DLL4)	3.785688	1.735318	0	1.484325
ABLIM1	actin binding LIM protein 1(ABLIM1)	4.747185	1.737471	0	0
CEP85L	centrosomal protein 85 like(CEP85L)	5.305226	1.74095	0	0
CDC14A	cell division cycle 14A(CDC14A)	5.150878	1.741606	0	0
VEGFC	vascular endothelial growth factor C(VEGFC)	3.919026	1.743623	0	0.471765
CSF1R	colony stimulating factor 1 receptor(CSF1R)	4.642867	1.744533	0	0
LRRC37B	leucine rich repeat containing 37B(LRRC37B)	4.688377	1.745144	0	0
CILK1	CILK1 (Ciliogenesis Associated Kinase 1)	5.388088	1.749342	0	0
PHF1	PHD finger protein 1(PHF1)	4.839036	1.75548	0	0
CRTC1	CREB regulated transcription coactivator 1(CRTC1)	5.066229	1.756061	0	0
CEBPB	CCAAT enhancer binding protein beta(CEBPB)	3.744146	1.757886	0	1.836985
SULF1	sulfatase 1(SULF1)	3.947054	1.777388	0	0.281096
ETS2	ETS proto-oncogene 2, transcription factor(ETS2)	5.444679	1.777836	0	0
NR4A3	nuclear receptor subfamily 4 group A member 3(NR4A3)	3.539167	1.788872	0	3.855765
AMER1	APC membrane recruitment protein 1(AMER1)	4.957359	1.788901	0	0
BIN1	bridging integrator 1(BIN1)	4.15218	1.79011	0	0
CLP1	cleavage factor polyribonucleotide kinase subunit 1(CLP1)	4.071484	1.792262	0	0
CHST11	carbohydrate sulfotransferase 11(CHST11)	5.772906	1.79572	0	0
TCTA	T cell leukemia translocation altered(TCTA)	4.284855	1.811825	0	0
ITK	IL2 inducible T cell kinase(ITK)	4.000562	1.81355	0	0
GNG4	G protein subunit gamma 4(GNG4)	4.958144	1.814997	0	0
ALDOC	aldolase, fructose-bisphosphate C(ALDOC)	3.884517	1.815706	0	0.71687
SH2D5	SH2 domain containing 5(SH2D5)	5.857424	1.817895	0	0
EGR3	early growth response 3(EGR3)	4.540972	1.824342	0	0
PRF1	perforin 1(PRF1)	3.885989	1.826638	0	0.706178
CANT1	calcium activated nucleotidase 1(CANT1)	6.988797	1.830216	0	0
SETBP1	SET binding protein 1(SETBP1)	5.004993	1.84487	0	0
GNAQ	G protein subunit alpha q(GNAQ)	6.038852	1.848273	0	0
PLAU	plasminogen activator, urokinase(PLAU)	3.983216	1.856949	0	0.045966
FLYWCH1	FLYWCH-type zinc finger 1(FLYWCH1)	5.277178	1.857221	0	0
BCL9	BCL9 transcription coactivator(BCL9)	8.32263	1.883438	0	0.000834
CD36	CD36 molecule (CD36 blood group)(CD36)	3.559535	1.893422	0	3.633556
ETV5	ETS variant transcription factor 5(ETV5)	5.56361	1.896305	0	0
BCR	BCR activator of RhoGEF and GTPase(BCR)	6.030242	1.918901	0	0
WNT6	Wnt family member 6(WNT6)	4.800669	1.919599	0	0

ERCC4	ERCC excision repair 4, endonuclease catalytic subunit(ERCC4)	5.990062	1.920347	0	0
IRS1	insulin receptor substrate 1(IRS1)	6.637791	1.923666	0	0
PHOX2B	paired like homeobox 2B(PHOX2B)	4.128029	1.929131	0	0
TIRAP	TIR domain containing adaptor protein(TIRAP)	4.132881	1.945213	0	0
GSN	gelsoin(GSN)	5.049895	1.947331	0	0
DUSP9	dual specificity phosphatase 9(DUSP9)	5.738546	1.949355	0	0
MAFB	MAF bZIP transcription factor B(MAFB)	5.24202	1.953922	0	0
KSR1	kinase suppressor of ras 1(KSR1)	5.912132	1.95482	0	0
ZNF444	zinc finger protein 444(ZNF444)	4.482204	1.954906	0	0
SOX10	SRY-box transcription factor 10(SOX10)	7.462533	1.962231	0	0
TAFA2	TAFA2 (TAFA Chemokine Like Family Member 2) Chemokine Like Family Member 2)	6.291193	1.963466	0	0
C10orf55	chromosome 10 putative open reading frame 55(C10orf55)	6.503524	1.964616	0	0
SERPINF1	serpin family F member 1(SERPINF1)	4.410896	1.967178	0	0
INPP4B	inositol polyphosphate-4-phosphatase type II B(INPP4B)	5.217482	1.981538	0	0
CTLA4	cytotoxic T-lymphocyte associated protein 4(CTLA4)	4.060925	1.993162	0	0
EXT1	exostosin glycosyltransferase 1(EXT1)	7.852564	1.995911	0	0
SRC	SRC proto-oncogene, non-receptor tyrosine kinase(SRC)	5.610545	2.000467	0	0
PDGFB	platelet derived growth factor subunit B(PDGFB)	5.514994	2.001316	0	0
NDRG1	N-myc downstream regulated 1(NDRG1)	4.779059	2.005474	0	0
STAT4	signal transducer and activator of transcription 4(STAT4)	4.969537	2.005724	0	0
PTCH1	patched 1(PTCH1)	5.707059	2.012668	0	0
CDX2	caudal type homeobox 2(CDX2)	5.928895	2.015635	0	0
KDR	kinase insert domain receptor(KDR)	6.765798	2.027435	0	0
CDKN2B	cyclin dependent kinase inhibitor 2B(CDKN2B)	7.139052	2.029501	0	0
AMH	anti-Mullerian hormone(AMH)	5.04979	2.034336	0	0
MNX1	motor neuron and pancreas homeobox 1(MNX1)	5.407353	2.047163	0	0
WNT7B	Wnt family member 7B(WNT7B)	5.594353	2.05128	0	0
COL3A1	collagen type III alpha 1 chain(COL3A1)	4.274946	2.055238	0	0
FGF3	fibroblast growth factor 3(FGF3)	5.308702	2.055708	0	0
DNMT3A	DNA methyltransferase 3 alpha(DNMT3A)	6.940494	2.05619	0	0
NOTCH4	notch receptor 4(NOTCH4)	6.501828	2.059783	0	0
LAMA5	laminin subunit alpha 5(LAMA5)	6.957768	2.060045	0	0
SLC1A2	solute carrier family 1 member 2(SLC1A2)	6.803971	2.062831	0	0
ASPH	aspartate beta-hydroxylase(ASPH)	7.569709	2.064112	0	0
ZFTA	ZFTA (Zinc Finger Translocation Associated)	7.133244	2.064576	0	0
RASGEF1A	RasGEF domain family member 1A(RASGEF1A)	5.213251	2.067101	0	0
GNA12	G protein subunit alpha 12(GNA12)	6.349639	2.072052	0	0
FZD3	frizzled class receptor 3(FZD3)	5.064886	2.074011	0	0
BHLHE22	basic helix-loop-helix family member e22(BHLHE22)	5.262439	2.076528	0	0
BCL2L2	BCL2 like 2(BCL2L2)	5.613572	2.076586	0	0
FZD6	frizzled class receptor 6(FZD6)	5.202745	2.078156	0	0
DDIT3	DNA damage inducible transcript 3(DDIT3)	5.130575	2.07858	0	0
IL15	interleukin 15(IL15)	5.082716	2.079664	0	0
CACNA1F	calcium voltage-gated channel subunit alpha1 F(CACNA1F)	5.649501	2.094461	0	0
PPP1R13L	protein phosphatase 1 regulatory subunit 13 like(PPP1R13L)	6.584414	2.095317	0	0
STYK1	serine/threonine/tyrosine kinase 1(STYK1)	5.721617	2.09552	0	0

LRP5	LDL receptor related protein 5(LRP5)	5.459217	2.097857	0	0
CRADD	CASP2 and RIPK1 domain containing adaptor with death domain(CRADD)	5.271676	2.102922	0	0
SRRM3	serine/arginine repetitive matrix 3(SRRM3)	7.981429	2.108368	0	0
FGF2	fibroblast growth factor 2(FGF2)	6.649114	2.11025	0	0
FANCE	FA complementation group E(FANCE)	5.03704	2.113095	0	0
PPP1R13B	protein phosphatase 1 regulatory subunit 13B(PPP1R13B)	6.846165	2.117321	0	0
CDX1	caudal type homeobox 1(CDX1)	6.742536	2.118989	0	0
WNT3	Wnt family member 3(WNT3)	4.525431	2.123256	0	0
ETV4	ETS variant transcription factor 4(ETV4)	4.449367	2.135498	0	0
IL7R	interleukin 7 receptor(IL7R)	5.568968	2.136496	0	0
NEDD4	NEDD4 E3 ubiquitin protein ligase(NEDD4)	6.130607	2.137812	0	0
CSF3	colony stimulating factor 3(CSF3)	5.365338	2.13836	0	0
CAMK2A	calcium/calmodulin dependent protein kinase II alpha(CAMK2A)	6.690269	2.147807	0	0
DMRTA2	DMRT like family A2(DMRTA2)	5.969216	2.148352	0	0
FGF23	fibroblast growth factor 23(FGF23)	5.954796	2.15222	0	0
TCF7L2	transcription factor 7 like 2(TCF7L2)	6.471214	2.153998	0	0
TAFAS	TAFAS (TAFAS Chemokine Like Family Member 5)	7.286852	2.160556	0	0
DLL1	delta like canonical Notch ligand 1(DLL1)	5.465924	2.161257	0	0
COL1A1	collagen type I alpha 1 chain(COL1A1)	4.010244	2.163885	0	0
ACE	angiotensin I converting enzyme(ACE)	6.301159	2.170109	0	0
NUTM2B	NUT family member 2B(NUTM2B)	6.121221	2.177605	0	0
PDGFD	platelet derived growth factor D(PDGFD)	5.026925	2.177659	0	0
COL1A2	collagen type I alpha 2 chain(COL1A2)	4.536251	2.186688	0	0
RTL8B	RTL8B (Retrotransposon Gag Like 8B)	7.860215	2.189001	0	0
TLX3	T cell leukemia homeobox 3(TLX3)	5.77798	2.189432	0	0
COL6A3	collagen type VI alpha 3 chain(COL6A3)	7.658923	2.193092	0	0
ACVR2A	activin A receptor type 2A(ACVR2A)	5.478121	2.196152	0	0
TET1	tet methylcytosine dioxygenase 1(TET1)	6.116676	2.19906	0	0
FLT3LG	fms related receptor tyrosine kinase 3 ligand(FLT3LG)	4.715383	2.20399	0	0
ITPKA	inositol-trisphosphate 3-kinase A(ITPKA)	6.241901	2.208142	0	0
FLCN	folliculin(FLCN)	8.347527	2.215691	0	0.007426
WDFY3	WD repeat and FYVE domain containing 3(WDFY3)	8.565429	2.223089	0	0.055427
RASGRF2	Ras protein specific guanine nucleotide releasing factor 2(RASGRF2)	5.281363	2.225345	0	0
TAL1	TAL bHLH transcription factor 1, erythroid differentiation factor(TAL1)	7.588581	2.228291	0	0
PRICKLE1	prickle planar cell polarity protein 1(PRICKLE1)	5.396549	2.233173	0	0
ZNF331	zinc finger protein 331(ZNF331)	6.028781	2.235404	0	0
PER1	period circadian regulator 1(PER1)	7.718813	2.235995	0	0
FASLG	Fas ligand(FASLG)	4.13455	2.236433	0	0
ALDH2	aldehyde dehydrogenase 2 family member(ALDH2)	5.9962	2.23652	0	0
MYBL1	MYB proto-oncogene like 1(MYBL1)	4.005283	2.24665	0	0
LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase(LFNG)	5.629878	2.264752	0	0
IL2	interleukin 2(IL2)	4.975486	2.269604	0	0
COL9A3	collagen type IX alpha 3 chain(COL9A3)	4.824172	2.274962	0	0
FGF6	fibroblast growth factor 6(FGF6)	5.741636	2.276748	0	0
WNT8B	Wnt family member 8B(WNT8B)	4.955214	2.279231	0	0

PRRX2	paired related homeobox 2(PRRX2)	7.760668	2.281131	0	0
IL1R1	interleukin 1 receptor type 1(IL1R1)	7.920651	2.288865	0	0
MLLT11	MLLT11 transcription factor 7 cofactor(MLLT11)	4.883881	2.300162	0	0
NOS3	nitric oxide synthase 3(NOS3)	6.380957	2.301254	0	0
PDGFA	platelet derived growth factor subunit A(PDGFA)	4.994012	2.302371	0	0
SPECC1	sperm antigen with calponin homology and coiled-coil domains 1(SPECC1)	7.577689	2.319786	0	0
TMPRSS2	transmembrane serine protease 2(TMPRSS2)	7.666994	2.322506	0	0
TIAM1	TIAM Rac1 associated GEF 1(TIAM1)	7.162885	2.327637	0	0
FGF19	fibroblast growth factor 19(FGF19)	6.115152	2.328253	0	0
PLAG1	PLAG1 zinc finger(PLAG1)	4.777779	2.328963	0	0
CDH11	cadherin 11(CDH11)	7.230888	2.330208	0	0
NFIB	nuclear factor I B(NFIB)	7.631868	2.341997	0	0
MGMT	O-6-methylguanine-DNA methyltransferase(MGMT)	5.393534	2.345891	0	0
TGFB2	transforming growth factor beta 2(TGFB2)	9.684782	2.352377	0	0.115985
MATK	megakaryocyte-associated tyrosine kinase(MATK)	5.444354	2.355539	0	0
PDE4DIP	phosphodiesterase 4D interacting protein(PDE4DIP)	6.970515	2.35963	0	0
TFAP2A	transcription factor AP-2 alpha(TFAP2A)	7.33054	2.371239	0	0
AHRR	aryl hydrocarbon receptor repressor(AHRR)	7.480548	2.371701	0	0
POU5F1	POU class 5 homeobox 1(POU5F1)	3.595615	2.388062	0	3.251936
JUN	Jun proto-oncogene, AP-1 transcription factor subunit(JUN)	6.669584	2.391486	0	0
PIMREG	PIMREG (PICALM Interacting Mitotic Regulator)	5.935124	2.395907	0	0
HNF1A	HNF1 homeobox A(HNF1A)	7.109971	2.406032	0	0
LOX	lysyl oxidase(LOX)	6.768958	2.406092	0	0
CAV1	caveolin 1(CAV1)	6.96031	2.413254	0	0
INPP5A	inositol polyphosphate-5-phosphatase A(INPP5A)	5.808232	2.422725	0	0
LMO2	LIM domain only 2(LMO2)	4.728785	2.42305	0	0
GDF6	growth differentiation factor 6(GDF6)	6.475373	2.430134	0	0
CDKN1A	cyclin dependent kinase inhibitor 1A(CDKN1A)	6.751227	2.430228	0	0
PLCB1	phospholipase C beta 1(PLCB1)	6.959786	2.43322	0	0
CD28	CD28 molecule(CD28)	6.561004	2.435456	0	0
NAB2	NGFI-A binding protein 2(NAB2)	6.439171	2.448958	0	0
EPO	erythropoietin(EPO)	6.684202	2.458509	0	0
RUNX2	RUNX family transcription factor 2(RUNX2)	6.163341	2.461359	0	0
AGR3	anterior gradient 3, protein disulphide isomerase family member(AGR3)	5.824754	2.46463	0	0
IL3	interleukin 3(IL3)	5.647752	2.47436	0	0
MDS2	myelodysplastic syndrome 2 translocation associated(MDS2)	5.028916	2.486177	0	0
WNT5B	Wnt family member 5B(WNT5B)	4.78638	2.492252	0	0
GAS7	growth arrest specific 7(GAS7)	9.253438	2.496393	0	0.118855
FGFR1	fibroblast growth factor receptor 1(FGFR1)	7.434258	2.505174	0	0
TBX15	T-box transcription factor 15(TBX15)	4.719523	2.50525	0	0
DOCK1	dedicator of cytokinesis 1(DOCK1)	10.83845	2.505368	0	0.058167
PLPP3	PLPP3 (Phospholipid Phosphatase 3)	7.399348	2.512268	0	0
CSF1	colony stimulating factor 1(CSF1)	7.502156	2.512522	0	0
WNT4	Wnt family member 4(WNT4)	7.524917	2.519318	0	0
EGR1	early growth response 1(EGR1)	6.852871	2.520246	0	0
IL1B	interleukin 1 beta(IL1B)	4.864171	2.5219	0	0

PPFIBP1	PPFIA binding protein 1(PPFIBP1)	7.650592	2.53002	0	0
HMGA2	high mobility group AT-hook 2(HMGA2)	6.195115	2.532555	0	0
SRGAP3	SLIT-ROBO Rho GTPase activating protein 3(SRGAP3)	10.60105	2.537728	0	0.071131
MAP3K6	mitogen-activated protein kinase kinase kinase 6(MAP3K6)	8.250834	2.539816	0	0
CYP1B1	cytochrome P450 family 1 subfamily B member 1(CYP1B1)	7.23426	2.542346	0	0
FOXO3	forkhead box O3(FOXO3)	9.330091	2.54572	0	0.120026
ACER1	alkaline ceramidase 1(ACER1)	6.555484	2.551417	0	0
FGF8	fibroblast growth factor 8(FGF8)	5.525352	2.561536	0	0
NUTM2A	NUT family member 2A(NUTM2A)	7.401547	2.579717	0	0
VEGFD	VEGFD (Vascular Endothelial Growth Factor D)	6.205128	2.582934	0	0
EGR2	early growth response 2(EGR2)	7.659307	2.582961	0	0
SORT1	sortilin 1(SORT1)	6.280267	2.58976	0	0
CEBPD	CCAAT enhancer binding protein delta(CEBPD)	6.697402	2.600815	0	0
SOX2	SRY-box transcription factor 2(SOX2)	6.669876	2.606446	0	0
PDGFRB	platelet derived growth factor receptor beta(PDGFRB)	8.451733	2.611138	0	0.032479
HOXA13	homeobox A13(HOXA13)	5.35406	2.631678	0	0
S1PR2	sphingosine-1-phosphate receptor 2(S1PR2)	7.043035	2.635564	0	0
ASTN2	astrotactin 2(ASTN2)	6.563845	2.641582	0	0
KLK7	kallikrein related peptidase 7(KLK7)	6.3062	2.643141	0	0
LINC01565	LINC01565 (Long Intergenic Non-Protein Coding RNA 1565)	6.601476	2.644742	0	0
CCND1	cyclin D1(CCND1)	7.26625	2.658175	0	0
MPL	MPL proto-oncogene, thrombopoietin receptor(MPL)	7.285526	2.666668	0	0
ATP1B4	ATPase Na ⁺ /K ⁺ transporting family member beta 4(ATP1B4)	6.048613	2.666792	0	0
PTPRK	protein tyrosine phosphatase receptor type K(PTPRK)	8.047847	2.669044	0	0
FOXL2	forkhead box L2(FOXL2)	6.372779	2.669566	0	0
ACVR1B	activin A receptor type 1B(ACVR1B)	8.934688	2.671313	0	0.103156
ALDH1A1	aldehyde dehydrogenase 1 family member A1(ALDH1A1)	6.241787	2.67512	0	0
FOXO4	forkhead box O4(FOXO4)	8.658221	2.679015	0	0.071046
WNT11	Wnt family member 11(WNT11)	5.775043	2.682254	0	0
LNP1	leukemia NUP98 fusion partner 1(LNP1)	5.989541	2.685948	0	0
ATF3	activating transcription factor 3(ATF3)	5.763465	2.727445	0	0
TLX1	T cell leukemia homeobox 1(TLX1)	6.152216	2.737066	0	0
APOD	apolipoprotein D(APOD)	4.990945	2.742162	0	0
CEBPA	CCAAT enhancer binding protein alpha(CEBPA)	5.753131	2.748047	0	0
FGF9	fibroblast growth factor 9(FGF9)	7.313946	2.750547	0	0
FLT3	fms related receptor tyrosine kinase 3(FLT3)	6.245023	2.750667	0	0
NOTCH3	notch receptor 3(NOTCH3)	9.492809	2.759768	0	0.119896
WNT10B	Wnt family member 10B(WNT10B)	6.589646	2.760301	0	0
NR6A1	nuclear receptor subfamily 6 group A member 1(NR6A1)	6.415212	2.78315	0	0
DST	dystonin(DST)	11.3376	2.786615	0	0.034166
SSX1	SSX family member 1(SSX1)	7.204865	2.792988	0	0
FOSL1	FOS like 1, AP-1 transcription factor subunit(FOSL1)	5.810294	2.802117	0	0
FLT4	fms related receptor tyrosine kinase 4(FLT4)	9.114094	2.803848	0	0.114335
MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2(MAPK8IP2)	8.250577	2.809986	0	0
LHX2	LIM homeobox 2(LHX2)	6.185403	2.815969	0	0
GRIN2B	glutamate ionotropic receptor NMDA type subunit 2B(GRIN2B)	5.034868	2.817626	0	0

TGFB3	transforming growth factor beta 3(TGFB3)	9.303754	2.819822	0	0.11972
FGF4	fibroblast growth factor 4(FGF4)	6.867181	2.820889	0	0
CBLC	Cbl proto-oncogene C(CBLC)	6.970806	2.834973	0	0
SOCS2	suppressor of cytokine signaling 2(SOCS2)	7.567499	2.835992	0	0
SPRY4	sprouty RTK signaling antagonist 4(SPRY4)	8.613145	2.839909	0	0.063792
NKX2-1	NK2 homeobox 1(NKX2-1)	6.274792	2.849283	0	0
IGF1R	insulin like growth factor 1 receptor(IGF1R)	9.234451	2.857663	0	0.118429
GPHN	gephyrin(GPHN)	6.698842	2.877797	0	0
GATA1	GATA binding protein 1(GATA1)	6.645643	2.88339	0	0
ERG	ETS transcription factor ERG(ERG)	8.582385	2.885009	0	0.058482
WWTR1	WW domain containing transcription regulator 1(WWTR1)	8.866438	2.888708	0	0.097056
ID1	inhibitor of DNA binding 1(ID1)	6.766525	2.898009	0	0
DKK2	dickkopf WNT signaling pathway inhibitor 2(DKK2)	6.512098	2.899692	0	0
NEURL1	neuralized E3 ubiquitin protein ligase 1(NEURL1)	7.756408	2.900846	0	0
GRB10	growth factor receptor bound protein 10(GRB10)	9.278299	2.906613	0	0.11933
LHFPL6	LHFPL6 (LHFPL Tetraspan Subfamily Member 6)	8.519844	2.907952	0	0.04675
DLL3	delta like canonical Notch ligand 3(DLL3)	5.392407	2.919372	0	0
CXXC4	CXXC finger protein 4(CXXC4)	7.070795	2.941286	0	0
KANK1	KN motif and ankyrin repeat domains 1(KANK1)	6.527358	2.957777	0	0
TGFBR3	transforming growth factor beta receptor 3(TGFBR3)	7.922402	2.96585	0	0
IL1RAP	interleukin 1 receptor accessory protein(IL1RAP)	7.056773	2.969074	0	0
KIAA1549	KIAA1549(KIAA1549)	7.425258	2.978627	0	0
HOXA3	homeobox A3(HOXA3)		3.003865	0	0.110739
MECOM	MDS1 and EVI1 complex locus(MECOM)	7.552758	3.008871	0	0
MAF	MAF bZIP transcription factor(MAF)	8.328138	3.028871	0	0.002313
SMO	smoothened, frizzled class receptor(SMO)	8.349426	3.041092	0	0.007919
BCL11B	BCL11 transcription factor B(BCL11B)	8.703546	3.042688	0	0.077729
PTCRA	pre T cell antigen receptor alpha(PTCRA)	5.317307	3.042936	0	0
SDC4	syndecan 4(SDC4)	7.275648	3.046776	0	0
EGR4	early growth response 4(EGR4)	7.542865	3.050621	0	0
LMO1	LIM domain only 1(LMO1)	7.146829	3.055068	0	0
IRS2	insulin receptor substrate 2(IRS2)	8.992557	3.06753	0	0.107493
PRMT8	protein arginine methyltransferase 8(PRMT8)	7.335135	3.075462	0	0
FSTL3	folliculin like 3(FSTL3)	9.049532	3.090462	0	0.111065
NTRK1	neurotrophic receptor tyrosine kinase 1(NTRK1)	8.072775	3.091165	0	0
TEAD1	TEA domain transcription factor 1(TEAD1)	10.16821	3.093379	0	0.095122
CDC14B	cell division cycle 14B(CDC14B)	8.290884	3.095295	0	0
IL12RB2	interleukin 12 receptor subunit beta 2(IL12RB2)	7.13727	3.097878	0	0
CDKL5	cyclin dependent kinase like 5(CDKL5)	7.231457	3.104088	0	0
ELOVL2	ELOVL fatty acid elongase 2(ELOVL2)	7.95511	3.110453	0	0
GFAP	glial fibrillary acidic protein(GFAP)	6.112629	3.118904	0	0
SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1(SMARCA1)	6.386931	3.124851	0	0
ECT2L	epithelial cell transforming 2 like(ECT2L)	8.194887	3.131564	0	0
HOXA9	homeobox A9(HOXA9)	7.202862	3.141032	0	0
DACH2	dachshund family transcription factor 2(DACH2)	6.837433	3.142387	0	0
SEPTIN5	SEPTIN5 (Septin 5)	6.771114	3.153926	0	0

PLA2G2A	phospholipase A2 group IIA(PLA2G2A)	5.106943	3.154834	0	0
DDR2	discoidin domain receptor tyrosine kinase 2(DDR2)	11.19947	3.156527	0	0.040235
TSHR	thyroid stimulating hormone receptor(TSHR)	5.181947	3.162255	0	0
FZD2	frizzled class receptor 2(FZD2)	8.819454	3.167774	0	0.092198
RNF43	ring finger protein 43(RNF43)	8.183359	3.169924	0	0
ROBO1	roundabout guidance receptor 1(ROBO1)	9.877464	3.19061	0	0.109071
ROBO2	roundabout guidance receptor 2(ROBO2)	6.107276	3.201952	0	0
MYCL	MYCL proto-oncogene, bHLH transcription factor(MYCL)	6.861783	3.211811	0	0
NODAL	nodal growth differentiation factor(NODAL)	6.640145	3.220799	0	0
TMT1B	TMT1B (Thiol Methyltransferase 1B)	6.130799	3.233565	0	0
PRRX1	paired related homeobox 1(PRRX1)	9.187352	3.241569	0	0.117121
AXL	AXL receptor tyrosine kinase(AXL)	8.84344	3.246852	0	0.094747
CTNND2	catenin delta 2(CTNND2) activator of transcription and developmental regulator	6.64889	3.274639	0	0
AUTS2	AUTS2(AUTS2)	6.144875	3.278806	0	0
TEAD4	TEA domain transcription factor 4(TEAD4)	6.513401	3.278971	0	0
ZNF703	zinc finger protein 703(ZNF703)	11.98682	3.282152	0	0.01219
LIFR	LIF receptor subunit alpha(LIFR)	12.05203	3.282708	0	0.010571
ERBB2	erb-b2 receptor tyrosine kinase 2(ERBB2)	10.48564	3.285345	0	0.077598
EPOR	erythropoietin receptor(EPOR)	9.10672	3.286975	0	0.114002
SPRY2	sprouty RTK signaling antagonist 2(SPRY2)	9.574911	3.288324	0	0.118661
DNM3	dynamitin 3(DNM3)	8.860312	3.289566	0	0.096454
MITF	melanocyte inducing transcription factor(MITF)	8.172624	3.290782	0	0
HOXD13	homeobox D13(HOXD13)	6.676377	3.291756	0	0
SLC45A3	solute carrier family 45 member 3(SLC45A3)	8.378971	3.296956	0	0.015411
LTBP1	latent transforming growth factor beta binding protein 1(LTBP1)	9.278643	3.297757	0	0.119336
FZD10	frizzled class receptor 10(FZD10)	6.956235	3.306778	0	0
ABCC3	ATP binding cassette subfamily C member 3(ABCC3)	8.428753	3.308579	0	0.027297
PTPRR	protein tyrosine phosphatase receptor type R(PTPRR)	6.141495	3.318368	0	0
OLR1	oxidized low density lipoprotein receptor 1(OLR1)	7.431158	3.326121	0	0
RET	ret proto-oncogene(RET)	9.547548	3.331424	0	0.119151
KLK2	kallikrein related peptidase 2(KLK2)	8.623123	3.334623	0	0.065451
PRKCG	protein kinase C gamma(PRKCG)	9.375595	3.343705	0	0.120329
HOXC11	homeobox C11(HOXC11)	6.69669	3.360171	0	0
ACKR3	atypical chemokine receptor 3(ACKR3)	7.900973	3.364725	0	0
HOXC13	homeobox C13(HOXC13)	6.751105	3.378389	0	0
KIT	KIT proto-oncogene, receptor tyrosine kinase(KIT)	8.98004	3.409269	0	0.106617
CAMK2B	calcium/calmodulin dependent protein kinase II beta(CAMK2B)	8.116996	3.414135	0	0
ITGB3	integrin subunit beta 3(ITGB3)	9.459517	3.415074	0	0.120187
WIF1	WNT inhibitory factor 1(WIF1)	8.158407	3.433915	0	0
TUSC3	tumor suppressor candidate 3(TUSC3) ENSG00000271779 (G Protein-Coupled Receptor 128	8.692922	3.437094	0	0.076216
ENSG00000271779	(GPR128) Pseudogene)	6.90802	3.440202	0	0
SCN8A	sodium voltage-gated channel alpha subunit 8(SCN8A)	7.71492	3.445128	0	0
JAG2	jagged canonical Notch ligand 2(JAG2)	11.00293	3.446636	0	0.049658
BRSK1	BR serine/threonine kinase 1(BRSK1)	9.348495	3.452959	0	0.120182
CKB	creatine kinase B(CKB)	6.096322	3.453079	0	0
RUNX1T1	RUNX1 partner transcriptional co-repressor 1(RUNX1T1)	6.425886	3.455772	0	0

PAX8	paired box 8(PAX8)	9.076886	3.462458	0	0.112548
FGFR4	fibroblast growth factor receptor 4(FGFR4)	8.870866	3.465592	0	0.097485
ADGRA2	ADGRA2 (Adhesion G Protein-Coupled Receptor A2)	11.48912	3.469652	0	0.028058
GATA3	GATA binding protein 3(GATA3)	7.954256	3.470536	0	0
HOXA11	homeobox A11(HOXA11)	7.051099	3.470682	0	0
LPAR1	lysophosphatidic acid receptor 1(LPAR1)	8.640729	3.482608	0	0.068304
DNM1	dynamin 1(DNM1)	8.844399	3.483033	0	0.094846
FUT1	fucosyltransferase 1 (H blood group)(FUT1)	8.071499	3.48964	0	0
CCT6B	chaperonin containing TCP1 subunit 6B(CCT6B)	6.911699	3.48978	0	0
LINC00598	LINC00598 (Long Intergenic Non-Protein Coding RNA 598)	6.459037	3.490041	0	0
GNA11	G protein subunit alpha 11(GNA11)	10.60572	3.491076	0	0.07087
FGF14	fibroblast growth factor 14(FGF14)	8.154482	3.502443	0	0
NKX2-5	NK2 homeobox 5(NKX2-5)	6.173856	3.511173	0	0
MYCN	MYCN proto-oncogene, bHLH transcription factor(MYCN)	8.357631	3.513849	0	0.010033
ALK	ALK receptor tyrosine kinase(ALK)	7.855242	3.529819	0	0
PTGS2	prostaglandin-endoperoxide synthase 2(PTGS2)	8.162889	3.533043	0	0
PAK6	p21 (RAC1) activated kinase 6(PAK6)	8.268843	3.53619	0	0
NPM2	nucleophosmin/nucleoplasmin 2(NPM2)	6.836298	3.539034	0	0
RAC3	Rac family small GTPase 3(RAC3)	7.248936	3.550341	0	0
IGFBP2	insulin like growth factor binding protein 2(IGFBP2)	8.447511	3.559875	0	0.031541
MAGEE1	MAGE family member E1(MAGEE1)	8.238488	3.560034	0	0
IL13	interleukin 13(IL13)	8.104867	3.563626	0	0
FCGBP	Fc gamma binding protein(FCGBP)	7.639967	3.579634	0	0
PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta(PPP2R2B)	8.347944	3.587577	0	0.007534
HLF	HLF transcription factor, PAR bZIP family member(HLF)	7.598852	3.595153	0	0
HEPH	hephaestin(HEPH)	9.882717	3.597455	0	0.108851
DCN	decorin(DCN)	7.976555	3.600311	0	0
VGLL3	vestigial like family member 3(VGLL3)	11.04128	3.612445	0	0.04775
TEAD3	TEA domain transcription factor 3(TEAD3)	9.15319	3.613243	0	0.115939
TAL2	TAL bHLH transcription factor 2(TAL2)	6.165718	3.636389	0	0
FGFR3	fibroblast growth factor receptor 3(FGFR3)	10.15102	3.645667	0	0.096027
TNFRSF11A	TNF receptor superfamily member 11a(TNFRSF11A)	8.958261	3.661781	0	0.105012
GRID1	glutamate ionotropic receptor delta type subunit 1(GRID1)	10.31116	3.668794	0	0.08736
PCNA-AS1	PCNA-AS1 (PCNA Antisense RNA 1)	5.458794	3.671557	0	0
GABRG2	gamma-aminobutyric acid type A receptor subunit gamma2(GABRG2)	7.610099	3.672997	0	0
CHL1	cell adhesion molecule L1 like(CHL1)	7.501803	3.698772	0	0
PRDM16	PR/SET domain 16(PRDM16)	10.62608	3.710534	0	0.069738
PRSS8	serine protease 8(PRSS8)	8.343626	3.730484	0	0.006409
CEBPE	CCAAT enhancer binding protein epsilon(CEBPE)	6.873133	3.732005	0	0
WNT16	Wnt family member 16(WNT16)	6.471186	3.746193	0	0
GAS1	growth arrest specific 1(GAS1)	10.96923	3.763824	0	0.051361
RHOD	ras homolog family member D(RHOD)	9.512418	3.769976	0	0.119666
PRKG2	protein kinase cGMP-dependent 2(PRKG2)	8.444869	3.783601	0	0.030951
COL11A1	collagen type XI alpha 1 chain(COL11A1)	6.593684	3.785859	0	0
HES1	hes family bHLH transcription factor 1(HES1)	7.813414	3.797598	0	0
TPO	thyroid peroxidase(TPO)	8.555754	3.799446	0	0.053642

HOXD9	homeobox D9(HOXD9)	9.009423	3.805479	0	0.10862
DKK1	dickkopf WNT signaling pathway inhibitor 1(DKK1)	6.813029	3.814411	0	0
PDGFRA	platelet derived growth factor receptor alpha(PDGFR)	11.48353	3.816482	0	0.028273
PLA2G5	phospholipase A2 group V(PLA2G5)	8.500663	3.834013	0	0.042893
ARRDC4	arrestin domain containing 4(ARRDC4)	10.8596	3.847827	0	0.057047
CHN1	chimerin 1(CHN1)	8.889036	3.857477	0	0.099198
PRKACG	protein kinase cAMP-activated catalytic subunit gamma(PRKACG)	9.006517	3.858893	0	0.10843
EPHA2	EPH receptor A2(EPHA2)	10.52613	3.86932	0	0.075324
EML1	EMAP like 1(EML1)	11.34131	3.893324	0	0.034009
RNF217-AS1	RNF217-AS1 (RNF217 Antisense RNA 1 (Head To Head))	9.023308	3.894563	0	0.109504
DAB2IP	DAB2 interacting protein(DAB2IP)	10.63575	3.906203	0	0.069201
IBSP	integrin binding sialoprotein(IBSP)	6.113519	3.912351	0	0
GRM1	glutamate metabotropic receptor 1(GRM1)	7.887063	3.914406	0	0
PRG2	proteoglycan 2, pro eosinophil major basic protein(PRG2)	5.926432	3.916173	0	0
SLC34A2	solute carrier family 34 member 2(SLC34A2)	9.866937	3.9203	0	0.109507
SMAD6	SMAD family member 6(SMAD6)	9.29432	3.954976	0	0.119587
PBX1	PBX homeobox 1(PBX1)	11.00705	3.956133	0	0.049452
EGF	epidermal growth factor(EGF)	7.974134	3.964207	0	0
PAK5	PAK5 (P21 (RAC1) Activated Kinase 5)	7.719968	3.972488	0	0
LRP1B	LDL receptor related protein 1B(LRP1B)	8.393952	3.980095	0	0.019084
CDH1	cadherin 1(CDH1)	7.786044	3.993127	0	0
DACH1	dachshund family transcription factor 1(DACH1)	11.44928	3.993694	0	0.029607
CYP2C19	cytochrome P450 family 2 subfamily C member 19(CYP2C19)	6.888668	3.994415	0	0
MB21D2	Mab-21 domain containing 2(MB21D2)	8.358709	3.999228	0	0.010309
FRMPD4	FERM and PDZ domain containing 4(FRMPD4)	9.549426	4.018145	0	0.11912
HECW1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1(HECW1)	8.225036	4.026576	0	0
ACSL6	acyl-CoA synthetase long chain family member 6(ACSL6)	11.94784	4.026884	0	0.013206
PSD3	pleckstrin and Sec7 domain containing 3(PSD3)	10.41677	4.031352	0	0.081468
SH3GL2	SH3 domain containing GRB2 like 2, endophilin A1(SH3GL2)	9.534701	4.045408	0	0.119354
FZD7	frizzled class receptor 7(FZD7)	10.47677	4.059457	0	0.078097
CCK	cholecystokinin(CCK)	7.126057	4.06221	0	0
MMP7	matrix metalloproteinase 7(MMP7)	5.899764	4.074175	0	0
PPARG	peroxisome proliferator activated receptor gamma(PPARG)	8.282056	4.08094	0	0
IL13RA2	interleukin 13 receptor subunit alpha 2(IL13RA2)	9.081641	4.09223	0	0.112791
SNCG	synuclein gamma(SNCG)	7.971104	4.092781	0	0
GRM3	glutamate metabotropic receptor 3(GRM3)	6.928162	4.099464	0	0
PAX7	paired box 7(PAX7)	6.778921	4.131855	0	0
MUC1	mucin 1, cell surface associated(MUC1)	8.295721	4.141765	0	0
PLCB4	phospholipase C beta 4(PLCB4)	10.50426	4.154809	0	0.076552
MN1	MN1 proto-oncogene, transcriptional regulator(MN1)	12.08889	4.173805	0	0.009699
CREB3L1	cAMP responsive element binding protein 3 like 1(CREB3L1)	9.277681	4.176319	0	0.119319
CACNA1G	calcium voltage-gated channel subunit alpha1 G(CACNA1G)	9.896236	4.178741	0	0.108279
GLI1	GLI family zinc finger 1(GLI1)	10.00668	4.182223	0	0.103278
HEY1	hes related family bHLH transcription factor with YRPW motif 1(HEY1)	8.195531	4.189453	0	0
GATA2	GATA binding protein 2(GATA2)	10.71948	4.192632	0	0.064586
CPS1	carbamoyl-phosphate synthase 1(CPS1)	10.64825	4.226	0	0.068508

HOXD11	homeobox D11(HOXD11)	8.282553	4.234973	0	0
ETV1	ETS variant transcription factor 1(ETV1)	10.58511	4.25209	0	0.07202
ACVR1C	activin A receptor type 1C(ACVR1C)	8.790125	4.257845	0	0.088879
MIPOL1	mirror-image polydactyly 1(MIPOL1)	11.335	4.263549	0	0.034276
YAP1	Yes1 associated transcriptional regulator(YAP1)	11.15776	4.284803	0	0.042159
EDNRB	endothelin receptor type B(EDNRB)	9.554244	4.293992	0	0.119038
NGFR	nerve growth factor receptor(NGFR)	13.30876	4.303058	0	0
SLCO1B3	solute carrier organic anion transporter family member 1B3(SLCO1B3)	9.0744	4.307998	0	0.112419
LEFTY2	left-right determination factor 2(LEFTY2)	10.14262	4.316494	0	0.096467
ITGA7	integrin subunit alpha 7(ITGA7)	12.43803	4.32374	0	0.002922
HTRA1	HtrA serine peptidase 1(HTRA1)	9.956149	4.32745	0	0.105634
SFRP4	secreted frizzled related protein 4(SFRP4)	7.896492	4.329125	0	0
IRS4	insulin receptor substrate 4(IRS4)	7.682498	4.335632	0	0
CDKN1C	cyclin dependent kinase inhibitor 1C(CDKN1C)	10.21668	4.350288	0	0.092532
CLTCL1	clathrin heavy chain like 1(CLTCL1)	10.76364	4.359196	0	0.062182
FOS	Fos proto-oncogene, AP-1 transcription factor subunit(FOS)	8.152503	4.361267	0	0
NAV3	neuron navigator 3(NAV3)	11.09636	4.388004	0	0.045067
PLAT	plasminogen activator, tissue type(PLAT)	10.39462	4.402625	0	0.082709
NTF4	neurotrophin 4(NTF4)	7.074559	4.407358	0	0
ACSBG1	acyl-CoA synthetase bubblegum family member 1(ACSBG1)	9.222632	4.410216	0	0.118134
LHX4	LIM homeobox 4(LHX4)	8.816462	4.412155	0	0.091869
HGF	hepatocyte growth factor(HGF)	9.409378	4.451961	0	0.120377
LRIG3	leucine rich repeats and immunoglobulin like domains 3(LRIG3)	11.8854	4.464093	0	0.014912
PRDM7	PR/SET domain 7(PRDM7)	8.402903	4.467068	0	0.021239
ATL1	atlastin GTPase 1(ATL1)	9.270849	4.503302	0	0.119198
GLI3	GLI family zinc finger 3(GLI3)	11.55336	4.508074	0	0.025648
ATP8A2	ATPase phospholipid transporting 8A2(ATP8A2)	7.86956	4.512801	0	0
ZNF521	zinc finger protein 521(ZNF521)	11.35265	4.524173	0	0.033533
DUSP26	dual specificity phosphatase 26(DUSP26)	8.563962	4.532275	0	0.055158
GRIN2A	glutamate ionotropic receptor NMDA type subunit 2A(GRIN2A)	10.74132	4.552701	0	0.063395
RGS7	regulator of G protein signaling 7(RGS7)	8.499199	4.552813	0	0.042593
FGF1	fibroblast growth factor 1(FGF1)	10.27142	4.561459	0	0.089551
PC	pyruvate carboxylase(PC)	11.61437	4.562813	0	0.02346
CEP170B	centrosomal protein 170B(CEP170B)	13.0157	4.563758	0	0
FHL2	four and a half LIM domains 2(FHL2)	9.768817	4.573279	0	0.113269
AR	androgen receptor(AR)	13.93741	4.58157	0	0
DKK4	dickkopf WNT signaling pathway inhibitor 4(DKK4)	7.796543	4.587793	0	0
FBN2	fibrillin 2(FBN2)	11.67048	4.588841	0	0.021534
USP6	ubiquitin specific peptidase 6(USP6)	8.635393	4.603686	0	0.067449
PROM1	prominin 1(PROM1)	9.825811	4.615787	0	0.111153
GATA6	GATA binding protein 6(GATA6)	11.55867	4.617352	0	0.025454
NTRK3	neurotrophic receptor tyrosine kinase 3(NTRK3)	9.693829	4.618552	0	0.115718
ITGA8	integrin subunit alpha 8(ITGA8)	10.15882	4.62457	0	0.095617
SHC2	SHC adaptor protein 2(SHC2)	11.48586	4.664826	0	0.028183
EPHA10	EPH receptor A10(EPHA10)	7.840761	4.697684	0	0
SH3D19	SH3 domain containing 19(SH3D19)	11.89865	4.706739	0	0.014542

KALRN	kalirin RhoGEF kinase(KALRN)	12.86299	4.713225	0	0
DGKB	diacylglycerol kinase beta(DGKB)	9.586705	4.714276	0	0.118427
PAPPA	pappalysin 1(PAPPA)	13.13838	4.75696	0	0
LGR5	leucine rich repeat containing G protein-coupled receptor 5(LGR5)	8.166079	4.776896	0	0
TRHDE	thyrotropin releasing hormone degrading enzyme(TRHDE)	10.30876	4.789372	0	0.087493
ESR1	estrogen receptor 1(ESR1)	10.23972	4.801505	0	0.091283
BICC1	BicC family RNA binding protein 1(BICC1)	12.65011	4.817382	0	0
HMGN2P46	high mobility group nucleosomal binding domain 2 pseudogene 46(HMGN2P46)	7.454227	4.820444	0	0
EDIL3	EGF like repeats and discoidin domains 3(EDIL3)	11.70986	4.887656	0	0.020231
DMRT1	doublesex and mab-3 related transcription factor 1(DMRT1)	9.620284	4.890481	0	0.117687
KLF4	KLF transcription factor 4(KLF4)	11.88813	4.905601	0	0.014835
AKAP6	A-kinase anchoring protein 6(AKAP6)	9.964059	4.920618	0	0.105273
FZD8	frizzled class receptor 8(FZD8)	12.16188	4.925234	0	0.008065
SORBS2	sorbin and SH3 domain containing 2(SORBS2)	10.77949	4.928678	0	0.061325
PTK7	protein tyrosine kinase 7 (inactive)(PTK7)	11.83194	5.019504	0	0.016449
INHBA	inhibin subunit beta A(INHBA)	9.960847	5.059267	0	0.10542
AK5	adenylate kinase 5(AK5)	10.46172	5.062056	0	0.078943
RANBP17	RAN binding protein 17(RANBP17)	12.32019	5.063057	0	0.004923
EYA1	EYA transcriptional coactivator and phosphatase 1(EYA1)	10.7263	5.067816	0	0.064214
HAS2	hyaluronan synthase 2(HAS2)	8.979627	5.098133	0	0.106588
EPHA3	EPH receptor A3(EPHA3)	9.850536	5.101245	0	0.110175
EPHA5	EPH receptor A5(EPHA5)	8.859577	5.119473	0	0.096381
PPP3R2	protein phosphatase 3 regulatory subunit B, beta(PPP3R2)	9.802211	5.162363	0	0.112054
TACC2	transforming acidic coiled-coil containing protein 2(TACC2)	11.56699	5.183508	0	0.025151
RELN	reelin(RELN)	11.95794	5.24036	0	0.012939
NCAM1	neural cell adhesion molecule 1(NCAM1)	12.2863	5.260727	0	0.00555
LRRC7	leucine rich repeat containing 7(LRRC7)	10.22241	5.265087	0	0.092222
SERP2	stress associated endoplasmic reticulum protein family member 2(SERP2)	10.09214	5.267867	0	0.099067
CCNB3	cyclin B3(CCNB3)	9.723022	5.282252	0	0.114814
GNAI1	G protein subunit alpha i1(GNAI1)	11.61967	5.306946	0	0.023274
CCN6	CCN6 (Cellular Communication Network Factor 6)	6.972234	5.316279	0	0
EPHB6	EPH receptor B6(EPHB6)	12.64197	5.324555	0	7.62E-05
CACNA2D3	calcium voltage-gated channel auxiliary subunit alpha2delta 3(CACNA2D3)	9.069121	5.426866	0	0.112142
GPC3	glypican 3(GPC3)	10.44916	5.492767	0	0.079649
BAIAP2L1	BAR/IMD domain containing adaptor protein 2 like 1(BAIAP2L1)	11.03866	5.526881	0	0.047879
ERBB4	erb-b2 receptor tyrosine kinase 4(ERBB4)	10.8498	5.528663	0	0.057565
RERG	RAS like estrogen regulated growth inhibitor(RERG)	10.92367	5.556091	0	0.053697
BTBD18	BTB domain containing 18(BTBD18)	8.043071	5.561089	0	0
PPARGC1A	PPARG coactivator 1 alpha(PPARGC1A)	12.09095	5.5741	0	0.009651
EYA2	EYA transcriptional coactivator and phosphatase 2(EYA2)	7.337358	5.589893	0	0
ANGPT1	angiopoietin 1(ANGPT1)	11.41814	5.614186	0	0.030846
BDNF	brain derived neurotrophic factor(BDNF)	8.649245	5.634504	0	0.06965
NBEAP1	neurobeachin pseudogene 1(NBEAP1)	7.874275	5.641538	0	0
AKAP12	A-kinase anchoring protein 12(AKAP12)	13.95249	5.643636	0	0
FGF13	fibroblast growth factor 13(FGF13)	12.5827	5.746209	0	0.000828

BMP4	bone morphogenetic protein 4(BMP4)	10.16062	5.772504	0	0.095522
MTUS2	microtubule associated scaffold protein 2(MTUS2)	8.507613	5.866566	0	0.044305
LINGO2	leucine rich repeat and Ig domain containing 2(LINGO2)	9.753639	5.914792	0	0.113797
ROS1	ROS proto-oncogene 1, receptor tyrosine kinase(ROS1)	9.801893	5.966141	0	0.112065
ELN	elastin(ELN)	10.32313	6.08393	0	0.086697
EGFR	epidermal growth factor receptor(EGFR)	14.26231	6.086231	0	0
NGF	nerve growth factor(NGF)	10.06229	6.102157	0	0.100567
RYR3	ryanodine receptor 3(RYR3)	11.69348	6.134619	0	0.020768
NTRK2	neurotrophic receptor tyrosine kinase 2(NTRK2)	12.21567	6.149078	0	0.006937
PRDM16-DT	PRDM16-DT (PRDM16 Divergent Transcript)	10.37071	6.157592	0	0.084046
AKR1C3	aldo-keto reductase family 1 member C3(AKR1C3)	11.14673	6.209329	0	0.042675
XKR3	XK related 3(XKR3)	8.333294	6.222105	0	0.003687
ZBTB16	zinc finger and BTB domain containing 16(ZBTB16)	11.18993	6.345327	0	0.040672
MAP2	microtubule associated protein 2(MAP2)	10.72133	6.359601	0	0.064485
ATRNL1	attractin like 1(ATRNL1)	8.009239	6.377284	0	0
PAX3	paired box 3(PAX3)	7.790554	6.412734	0	0
PAK3	p21 (RAC1) activated kinase 3(PAK3)	11.48797	6.485449	0	0.028102
EPHA7	EPH receptor A7(EPHA7)	9.540564	6.553014	0	0.119264
FLNC	filamin C(FLNC)	14.30667	6.636655	0	0
ARHGAP20	Rho GTPase activating protein 20(ARHGAP20)	13.78307	6.671752	0	0
OMD	osteomodulin(OMD)	11.83415	6.706535	0	0.016384
PPFIA2	PTPRF interacting protein alpha 2(PPFIA2)	13.13276	6.737995	0	0
LAMA1	laminin subunit alpha 1(LAMA1)	14.35358	6.739522	0	0
TENM1	teneurin transmembrane protein 1(TENM1)	13.36199	6.796623	0	0
ID4	inhibitor of DNA binding 4(ID4)	13.43572	6.852426	0	0
FGFR2	fibroblast growth factor receptor 2(FGFR2)	12.62742	6.878625	0	0.000255
WNT2B	Wnt family member 2B(WNT2B)	12.68086	6.945762	0	0
NTF3	neurotrophin 3(NTF3)	8.171146	7.016388	0	0
WT1	WT1 transcription factor(WT1)	12.08032	7.070595	0	0.009899
FOSB	FosB proto-oncogene, AP-1 transcription factor subunit(FOSB)	11.53409	7.085912	0	0.026359
FGF10	fibroblast growth factor 10(FGF10)	9.271534	7.138911	0	0.11921
ZFPM2	zinc finger protein, FOG family member 2(ZFPM2)	13.05228	7.147371	0	0
NUTM1	NUT midline carcinoma family member 1(NUTM1)	10.10405	7.474924	0	0.09846
ERBB3	erb-b2 receptor tyrosine kinase 3(ERBB3)	10.96615	7.612785	0	0.051517
MYH11	myosin heavy chain 11(MYH11)	10.42548	7.773862	0	0.080979
KCNB1	potassium voltage-gated channel subfamily B member 1(KCNB1)	12.01167	7.91958	0	0.011561
HSPA2	heat shock protein family A (Hsp70) member 2(HSPA2)	11.98074	8.355465	0	0.012346
DLEC1	DLEC1 cilia and flagella associated protein(DLEC1)	13.46048	8.662548	0	0
CNTN1	contactin 1(CNTN1)	13.81549	8.691502	0	0
MLF1	myeloid leukemia factor 1(MLF1)	11.6109	8.804576	0	0.023581
IGF1	insulin like growth factor 1(IGF1)	11.55049	8.808863	0	0.025753
SFRP2	secreted frizzled related protein 2(SFRP2)	10.57596	9.197523	0	0.072532
DIRAS3	DIRAS family GTPase 3(DIRAS3)	11.91992	9.343766	0	0.013957
PCLO	piccolo presynaptic cytomatrix protein(PCLO)	12.20889	10.87115	0	0.007075
PEG3	paternally expressed 3(PEG3)	12.23794	11.16497	0	0.006488

Suppl. Table S3.2 Significantly enriched terms with FDR ≤ 0.05 by DAVID functional annotation for 264 genes upregulated in the TLT vs. ME subtypes of PT-DLBCL

Category	Term	Count	P Value	Genes	Fold Enrichment	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0006338~chromatin remodeling	30	1.82E-15	RB1, HDAC2, SMARCB1, KDM1A, PRKDC, BAZ2A, AURKA, NSD3, CHEK1, NSD2, EP400, SF3B1, MAP3K7, SS18, NPM1, PRKCB, PRMT1, NCOA3, ATRX, SMARCA5, HUWE1, DEK, ARID1A, KAT2B, SFPQ, IRF4, CDK1, ATM, TOP1, ATR	6.613049	4.25E-12	4.05E-12
GOTERM_BP_DIRECT	GO:0006281~DNA repair	25	1.45E-13	BLM, FH, MRE11, HMGB1, BRCA1, SMC3, POLD1, CHEK1, EP400, FANCI, NPM1, RRM1, FANCL, NONO, ATRX, SMARCA5, FANCA, MLH1, SMC1A, RAD50, MSH2, MSH3, CDK1, MNAT1, ATR	7.079513	1.69E-10	1.61E-10
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription by RNA polymerase II	52	4.28E-13	RB1, TOP2A, SMARCB1, DDX3X, KDM1A, BRCA1, HMGB1, IKZF3, ETS1, CDC73, ELK4, RPS6KA3, RPS6KA1, GTF2I, SS18, NCOA3, ATRX, PAX5, KAT2B, SFPQ, PKM, TFDP1, IRF4, TBL1XR1, IRF8, RAF1, HDAC2, CBFB, PRKDC, HIF1A, PPP3R1, PCBP1, STAT6, SF3B1, NPM1, XBP1, XRCC6, BCL11A, STAT1, SMARCA5, HMGA1, DEK, FLI1, NFKB1, NFKB2, NACA, POU2AF1, SP3, TCEA1, ATM, TCF3, CDK12	3.130317	3.32E-10	3.16E-10
GOTERM_BP_DIRECT	GO:0051301~cell division	27	9.94E-12	RB1, CLTC, CLTA, BUB1B, SMC3, CDC73, AURKB, AURKA, RAD21, TPR, CNTRL, ZNF207, UBE2C, SMC1A, NDC80, EML4, CCNA2, CENPF, WEE1, STAG2, CDK4, CCNG1, CDK1, TACC3, BIRC6, MAPRE1, MAD2L1	5.302463	5.79E-09	5.51E-09
GOTERM_BP_DIRECT	GO:000122~negative regulation of transcription by RNA polymerase II	42	2.83E-11	RB1, DDX5, DNMT1, HDAC2, PHB1, PCNA, CBFB, KDM1A, HMGB1, PHF6, CDC73, AURKB, ELK4, CUX1, TPR, NSD2, STAT6, VHL, SUZ12, XBP1, EED, BCL11A, STAT1, PAX5, NFKB1, FOXF1, KAT2B, SFPQ, TBL1XR1, NACA, SARNP, CNOT2, SP3, HNRNPA2B1, MDM2, IRF8, MDM4, TCF3, CALR, EZR, PTPN2, EZH2	3.297597	1.32E-08	1.26E-08
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	29	1.72E-10	HDAC2, MRE11, DDX3X, HSP90AB1, BCL2A1, TFRF, PRKDC, XIAP, MALT1, CDC73, AURKA, RPS6KA3, RPS6KA1, PIM1, VHL, NPM1, XBP1, STIL, NFKB1, CCNG1, CDK1, MDM2, MDM4, BIRC6, RAF1, MNAT1, CD44, BIRC3, MAD2L1	4.324786	6.67E-08	6.36E-08
GOTERM_BP_DIRECT	GO:0050853~B cell receptor signaling pathway	12	3.93E-10	LYN, CD79B, CD79A, SYK, PRKCB, BTK, PLCG2, MAPK1, PTPN6, GRB2, SOS1, NFKB1	14.87394	1.31E-07	1.25E-07
GOTERM_BP_DIRECT	GO:0030183~B cell differentiation	13	2.34E-09	TOP2B, SYK, PAX5, IKZF3, CD79B, CD79A, MSH2, SP3, PLCG2, TCF3, PTPN2, CARD11, EZH2	10.92133	6.81E-07	6.49E-07
GOTERM_BP_DIRECT	GO:0007094~mitotic spindle assembly checkpoint signaling	9	4.95E-09	CENPF, TPR, ZNF207, BUB1B, TTK, ATM, MNAT1, NDC80, MAD2L1, RB1, FANCI, SMARCB1, YTHDF2, CLTA, BRCA1, IKZF1, MKI67, TERF2, CDC73, KAT2B, RPS6KA3, TFDP1, RPS6KA1, CHEK1, CNTRL, MDM2, PIM1, MAPK1, MDM4, BIRC6	21.95106	1.28E-06	1.22E-06
GOTERM_BP_DIRECT	GO:0007049~cell cycle	21	1.24E-08	YWHAE, SS18, DDX3X, SYK, TFRF, PRKCB, LRRK2, RASGRF1, PTPN11, RASAL1, TYK2, RPS6KA3, TCL1A, MELK, PRKAR1A, AKT2, INPP5D, RPS6KA1, CHEK1, BTK, PLCG2, MAPK1, PTPN6, ARHGEF7	4.900596	2.89E-06	2.76E-06
GOTERM_BP_DIRECT	GO:0035556~intracellular signal transduction	24	1.59E-08	LYN, TOP2A, BLM, FH, MRE11, PRMT1, FANCL, PRKDC, SMARCA5, XIAP, BRCA1, CIP2A, CHD2, FOXF1, RAD50, CHEK1, CDK1, MAPK1, ATM, ATR	4.200511	3.35E-06	3.20E-06
GOTERM_BP_DIRECT	GO:0006974~DNA damage response	20	2.78E-08	LYN, MAP3K1, SYK, PRKCB, PRKDC, LRRK2, TYK2, AURKB, AURKA, WEE1, MELK, CDK4, RPS6KA1, CHEK1, PIM1, BTK, CDK1, MAPK1, BIRC6, ATM, CDK12, RAF1	4.92568	5.40E-06	5.15E-06
GOTERM_BP_DIRECT	GO:0006468~protein phosphorylation	22	3.04E-08	PRKDC, LRRK2, BUB1B, TTK, AURKB, AURKA, RPS6KA3, AKT2, CHEK1, RPS6KA1, MAPK1, MAP3K7, LYN, GIT2, SYK, PRKCB, TYK2, WEE1, PKM, MELK, PRKAR1A, CDK4, CDK1, BTK, CDK12, TOP1, RAF1, ATR	4.423942	5.44E-06	5.18E-06
GOTERM_BP_DIRECT	GO:0016310~phosphorylation	28	8.91E-08	BLM, HDAC2, PHB1, BRCA1, ETS1, HIF1A, NSD3, RPS6KA1, EP400, PIM1, VHL, CDK5RAP2, NPM1, XRCC6, PRKCB, FUS, STAT1, HMGA1, ARID1A, FLI1, NFKB1, CCNA2, KAT2B, IRF4, TBL1XR1, SP3, NUP98, TCF3, PICALM	3.344483	1.48E-05	1.41E-05
GOTERM_BP_DIRECT	GO:0045893~positive regulation of DNA-templated transcription	29	2.72E-07	HSP90AA1, PHB1, STAT1, XIAP, ETS1, FBXO11, IKZF3, MALT1, EP400, BIRC6, PTPN6, ATM, CALR, RAF1, CARD11, BIRC3	3.075269	4.22E-05	4.02E-05
GOTERM_BP_DIRECT	GO:0042981~regulation of apoptotic process	16	3.43E-07	LYN, MAP3K1, SYK, BTK, PLCG2, SOS1, MAP3K7	5.352863	4.99E-05	4.76E-05
GOTERM_BP_DIRECT	GO:0038095~Fc-epsilon receptor signaling pathway	7	5.45E-07	LYN, MAP3K1, SYK, BTK, PLCG2, SOS1, MAP3K7	22.05268	7.32E-05	6.98E-05
GOTERM_BP_DIRECT	GO:0007095~mitotic G2 DNA damage checkpoint signaling	8	5.66E-07	BLM, MRE11, CCNG1, CHEK1, CDK1, ATM, BRCA1, NBN	15.91773	7.32E-05	6.98E-05
GOTERM_BP_DIRECT	GO:0006302~double-strand break repair	10	7.70E-07	RAD50, MRE11, MSH2, PRKDC, RAD21, NSD2, ATM, BRCA1, NBN, ATR	9.819376	9.43E-05	8.99E-05
GOTERM_BP_DIRECT	GO:0048511~rhythmic process	10	9.59E-07	TOP2A, KAT2B, USP7, SFPQ, DDX5, PRKDC, CDK1, TOP1, EZH2, NFKB2	9.570784	1.12E-04	1.06E-04
GOTERM_BP_DIRECT	GO:0000723~telomere maintenance	9	1.15E-06	BLM, XRCC6, RAD50, MRE11, PRKDC, ATM, NBN, TERF2, ATR	11.34138	1.21E-04	1.15E-04
GOTERM_BP_DIRECT	GO:0007059~chromosome segregation	11	1.17E-06	TOP2A, CENPU, CENPF, DDX3X, STAG2, RAD21, TTK, BRCA1, TOP1, NDC80, CDK5RAP2	7.997126	1.21E-04	1.15E-04
GOTERM_BP_DIRECT	GO:0018105~peptidyl-serine phosphorylation	13	1.19E-06	PRKCB, PRKDC, LRRK2, TTK, AURKA, RPS6KA3, AKT2, RPS6KA1, CDK1, MAPK1, ATM, TOP1, ATR	6.260634	1.21E-04	1.15E-04
GOTERM_BP_DIRECT	GO:0031507~heterochromatin formation	9	1.49E-06	RB1, H2AC11, HDAC2, EED, SMARCA5, BAZ2A, HMGB1, H2AC17, EZH2	10.97553	1.45E-04	1.38E-04
GOTERM_BP_DIRECT	GO:0032206~positive regulation of telomere maintenance	6	2.08E-06	RAD50, MRE11, ATRX, POT1, NBN, TERF2	26.6856	1.93E-04	1.84E-04
GOTERM_BP_DIRECT	GO:0090307~mitotic spindle assembly	8	2.95E-06	STAG2, CLTC, ZNF207, SMC1A, SMC3, RHOA, AURKB, KPNB1	12.60153	2.64E-04	2.52E-04
GOTERM_BP_DIRECT	GO:0051726~regulation of cell cycle	15	3.71E-06	RB1, HSP90AB1, XIAP, BRCA1, KAT2B, TFDP1, CDK4, AKT2, MDM2, EP400, MDM4, ATM, CDK12, NBN, BIRC3	4.745347	3.20E-04	3.05E-04
GOTERM_BP_DIRECT	GO:0009410~response to xenobiotic stimulus	15	7.47E-06	LYN, SS18, HSP90AA1, HDAC2, PRKCB, STAT1, TYMS, CENPF, CDK4, MDM2, CDK1, PMS2, CALR, TOP1, ATR	4.46511	6.21E-04	5.92E-04
GOTERM_BP_DIRECT	GO:0044818~mitotic G2/M transition checkpoint	6	8.37E-06	RAD50, MRE11, CHEK1, BRCA1, NBN, ATR	20.62069	6.72E-04	6.41E-04
GOTERM_BP_DIRECT	GO:0000729~DNA double-strand break processing	5	1.34E-05	BLM, RAD50, MRE11, ATM, NBN	31.50383	0.001041	9.92E-04

GOTERM_BP_DIRECT	GO:0006357~regulation of transcription by RNA polymerase II	43	1.42E-05	RB1, DDX5, SMARCB1, CBFB, KDM1A, HMGB1, IKZF1, BRCA1, CHD2, ETS1, HIF1A, IKZF3, ELK4, CUX1, RAD21, MAPK1, STAT6, SS18, XBP1, PRKCB, BCL11A, FUS, STAT1, SMARCA5, PAX5, DEK, ARID1A, RHOA, FLI1, NFKB1, FOXP1, KAT2B, TFDP1, PRKAR1A, IRF4, TBL1XR1, CNOT2, SP3, CDK1, IRF8, TCF3, MNAT1, SOS1	2.024406	0.001068	0.001018
GOTERM_BP_DIRECT	GO:0006406~mRNA export from nucleus	8	1.69E-05	NUP107, XPO1, DDX39B, SARNP, TPR, HNRNPA2B1, SRSF3, EIF4E	9.756025	0.001226	0.001169
GOTERM_BP_DIRECT	GO:1904354~negative regulation of telomere capping	4	2.22E-05	RAD50, ATM, NBN, TERF2	60.48736	0.001564	0.001491
GOTERM_BP_DIRECT	GO:0006355~regulation of DNA-templated transcription	28	2.70E-05	RB1, PHB1, BTG1, BAZ2A, AFF3, HIF1A, NSD3, NSD2, ZNF207, STAT6, VHL, UTP4, FUS, NONO, ATRX, SMARCA5, HMGA1, NFKB2, KAT2B, SFPQ, TFDP1, EWSR1, CNOT2, SP3, TCF3, CALR, PFDN5, EZH2	2.467433	0.001826	0.001741
GOTERM_BP_DIRECT	GO:0000278~mitotic cell cycle	11	2.75E-05	EML4, CENPF, WEE1, KIF5B, CLTC, PTPN6, PTPN11, SMC3, NDC80, AURKB, AURKA	5.619602	0.001826	0.001741
GOTERM_BP_DIRECT	GO:0006310~DNA recombination	8	3.76E-05	BLM, XRCC6, RAD50, MRE11, NONO, RAD21, BRCA1, HMGB1, CYFIP2, XBP1, PRKCB, FAF1, PTEN, CXCR4, BUB1B, NFKB1, AURKA, MELK, RABEP1, INPP5D, RAD21, CHEK1, MDM2, PIM1, CDK1, MAPK1, BIRC6, RAF1, MAP3K7, BIRC3	8.641051	0.002429	0.002315
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	22	4.25E-05	RAF1, MAP3K7, BIRC3	2.805063	0.002673	0.002548
GOTERM_BP_DIRECT	GO:0045740~positive regulation of DNA replication	6	4.90E-05	CDC42, WEE1, PCNA, FAF1, SMARCA5, CDK1	14.63404	0.003004	0.002864
GOTERM_BP_DIRECT	GO:0034087~establishment of mitotic sister chromatid cohesion	4	7.61E-05	STAG2, RAD21, SMC1A, SMC3	43.20525	0.004241	0.004043
GOTERM_BP_DIRECT	GO:0008380~RNA splicing	12	7.61E-05	PTBP1, SFPQ, MBNL1, DDX39B, FUS, U2AF2, PRMT1, NONO, SRSF2, U2AF1, CDK12, SF3B1	4.513982	0.004241	0.004043
GOTERM_BP_DIRECT	GO:0002218~activation of innate immune response	6	7.78E-05	XRCC6, SFPQ, HSP90AA1, PRKDC, NONO, HMGB1	13.3428	0.004241	0.004043
GOTERM_BP_DIRECT	GO:0045648~positive regulation of erythrocyte differentiation	6	7.78E-05	STAT1, PRKDC, PRMT1, INPP5D, ETS1, HIF1A	13.3428	0.004241	0.004043
GOTERM_BP_DIRECT	GO:0045892~negative regulation of DNA-templated transcription	21	7.83E-05	RB1, XRCC6, HDAC2, PHB1, SET, KDM1A, EED, NONO, HMGA1, BRCA1, IKZF1, FOXP1, CENPF, SFPQ, SP3, MDM2, SRSF2, MDM4, CALR, PFDN5, EZH2	2.771018	0.004241	0.004043
GOTERM_BP_DIRECT	GO:0007165~signal transduction	34	9.40E-05	YWHAE, PHB1, LRRK2, RASGRF1, RASAL1, HMGB1, HIF1A, CD79B, RPS6KA3, SH3BP1, AKT2, INPP5D, RPS6KA1, RAC2, MAPK1, LPXN, STAT6, LYN, NPM1, SYK, FNBP1, PRKCB, GAB1, DEK, RHOA, NFKB1, NFKB2, RABEP1, CDK4, GRB2, ATM, RAF1, ARHGGEF7, SOS1	2.073155	0.004976	0.004743
GOTERM_BP_DIRECT	GO:0006303~double-strand break repair via nonhomologous end joining	6	1.03E-04	XRCC6, MRE11, PRKDC, ATM, HMGB1, MLH1	12.60153	0.005335	0.005085
GOTERM_BP_DIRECT	GO:0048298~positive regulation of isotype switching to IgA isotypes	4	1.21E-04	MSH2, NSD2, PMS2, MLH1	37.8046	0.005972	0.005692
GOTERM_BP_DIRECT	GO:0110025~DNA strand resection involved in replication fork processing	4	1.21E-04	RAD50, MRE11, BRCA1, NBN	37.8046	0.005972	0.005692
GOTERM_BP_DIRECT	GO:0032508~DNA duplex unwinding	7	1.24E-04	BLM, XRCC6, RAD50, DDX3X, MRE11, POT1, NBN	8.970583	0.006012	0.005731
GOTERM_BP_DIRECT	GO:0046777~protein autophosphorylation	10	1.63E-04	LYN, MELK, LRRK2, CAD, PIM1, ATM, CDK12, AURKB, ATR, AURKA	5.074443	0.007766	0.007403
GOTERM_BP_DIRECT	GO:0000077~DNA damage checkpoint signaling	6	1.72E-04	LYN, CHEK1, PTPN11, ATM, NBN, ATR	11.34138	0.007971	0.007598
GOTERM_BP_DIRECT	GO:0007265~Ras protein signal transduction	8	1.75E-04	RB1, CCNA2, NRAS, RASGRF1, KRAS, GRB2, RAF1, SOS1	6.796332	0.007971	0.007598
GOTERM_BP_DIRECT	GO:0007004~telomere maintenance via telomerase	5	1.79E-04	HSP90AA1, RAD50, MRE11, HSP90AB1, POT1	17.18391	0.007998	0.007624
GOTERM_BP_DIRECT	GO:0035855~megakaryocyte development	5	2.14E-04	ABI1, PTPN6, PTPN11, WASF2, FLI1	16.43678	0.009397	0.008957
GOTERM_BP_DIRECT	GO:0043154~negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	6	2.18E-04	RPS6KA3, DDX3X, RPS6KA1, XIAP, RAF1, CD44	10.80131	0.009397	0.008957
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell population proliferation	17	2.22E-04	LYN, NPM1, PHB1, SMARCB1, BTG1, PTEN, HMGA1, ETS1, CDC73, KAT2B, ABI1, MDM4, STRN, PTPN6, VHL, RAF1, PTPN2	2.961651	0.009397	0.008957
GOTERM_BP_DIRECT	GO:0042752~regulation of circadian rhythm	7	2.51E-04	TOP2A, USP7, SFPQ, PRKDC, NONO, CDK1, EZH2	7.899468	0.01003	0.009561
GOTERM_BP_DIRECT	GO:0006265~DNA topological change	4	2.53E-04	TOP2A, TOP2B, HMGB1, TOP1	30.24368	0.01003	0.009561
GOTERM_BP_DIRECT	GO:0035825~homologous recombination	4	2.53E-04	RAD50, MRE11, BRCA1, NBN	30.24368	0.01003	0.009561
GOTERM_BP_DIRECT	GO:0007062~sister chromatid cohesion	5	2.54E-04	MRE11, STAG2, RAD21, SMC1A, SMC3	15.75192	0.01003	0.009561
GOTERM_BP_DIRECT	GO:0070301~cellular response to hydrogen peroxide	7	2.73E-04	TOP2B, HDAC2, PCNA, MDM2, CDK1, STAT6, EZH2	7.7833	0.010586	0.01009
GOTERM_BP_DIRECT	GO:0006366~transcription by RNA polymerase II	12	2.99E-04	RB1, XBP1, TFDP1, CBFB, ATRX, TCEA1, PAX5, DEK, CDK12, ETS1, NFKB1, GTF2I	3.860895	0.011417	0.010882
GOTERM_BP_DIRECT	GO:0006260~DNA replication	8	3.17E-04	RRM1, BLM, SET, POLD1, CHEK1, CDK1, TOP1, ATR	6.172179	0.011815	0.011262
GOTERM_BP_DIRECT	GO:0000082~G1/S transition of mitotic cell cycle	7	3.20E-04	RB1, CCNA2, CDK4, CDK1, MNAT1, EIF4E, EZH2	7.56092	0.011815	0.011262

GOTERM_BP_DIRECT	GO:0008286~insulin receptor signaling pathway	7	3.45E-04	AKT2, GAB1, MAPK1, GRB2, RAF1, SOS1, PTPN2	7.454428	0.012566	0.011978
GOTERM_BP_DIRECT	GO:0071480~cellular response to gamma radiation	5	4.07E-04	XRCC6, KDM1A, MDM2, ATM, ATR	14.0017	0.014577	0.013895
GOTERM_BP_DIRECT	GO:0090267~positive regulation of mitotic cell cycle spindle assembly checkpoint	4	4.55E-04	TPR, NDC80, AURKB, MAD2L1	25.20307	0.016066	0.015313
GOTERM_BP_DIRECT	GO:0031398~positive regulation of protein ubiquitination	7	5.36E-04	FANCI, KDM1A, LRRK2, HUWE1, XIAP, MALT1, BIRC3	6.873563	0.018461	0.017597
GOTERM_BP_DIRECT	GO:0000724~double-strand break repair via homologous recombination	8	5.41E-04	BLM, SFPQ, RAD50, MRE11, CNTRL, ATM, BRCA1, NBN	5.653024	0.018461	0.017597
GOTERM_BP_DIRECT	GO:0000086~G2/M transition of mitotic cell cycle	6	5.47E-04	CCNA2, WEE1, MELK, CHEK1, CDK1, AURKA	8.895199	0.018461	0.017597
GOTERM_BP_DIRECT	GO:0031623~receptor internalization	6	5.99E-04	SYK, TFRC, CLTC, GRB2, EZR, PICALM	8.724138	0.019919	0.018987
GOTERM_BP_DIRECT	GO:0010592~positive regulation of lamellipodium assembly	5	6.16E-04	CDC42, HSP90AA1, CARMIL2, RAC2, WASF2	12.60153	0.020204	0.019258
GOTERM_BP_DIRECT	GO:0006298~mismatch repair	5	7.00E-04	PCNA, MSH2, MSH3, PMS2, MLH1	12.19503	0.02264	0.02158
GOTERM_BP_DIRECT	GO:0042127~regulation of cell population proliferation	9	7.52E-04	FANCL, STAT1, CHEK1, XIAP, BIRC6, STAT6, SOS1, EPS15, EZH2	4.629134	0.023984	0.022861
GOTERM_BP_DIRECT	GO:0018107~peptidyl-threonine phosphorylation	6	7.76E-04	PRKDC, LRRK2, CAD, CHEK1, CDK1, MAPK1	8.248276	0.024426	0.023282
GOTERM_BP_DIRECT	GO:0010629~negative regulation of gene expression	13	8.84E-04	RB1, DNMT1, DDX3X, TERF2, HIF1A, NFKB1, AURKA, FOXP1, PRKAR1A, CDK1, VHL, MAP3K7, PICALM	3.170708	0.027304	0.026026
GOTERM_BP_DIRECT	GO:0051973~positive regulation of telomerase activity	5	8.92E-04	HSP90AA1, HSP90AB1, POT1, MAPK1, AURKB	11.45594	0.027304	0.026026
GOTERM_BP_DIRECT	GO:0034644~cellular response to UV	6	9.15E-04	NPM1, PCNA, KDM1A, POLD1, AURKB, ATR	7.958863	0.027304	0.026026
GOTERM_BP_DIRECT	GO:0014044~Schwann cell development	4	9.15E-04	MAPK1, GRB2, RAF1, SOS1	20.16245	0.027304	0.026026
GOTERM_BP_DIRECT	GO:0016447~somatic recombination of immunoglobulin gene segments	3	0.00102	MSH2, MSH3, PMS2	56.7069	0.029303	0.027931
GOTERM_BP_DIRECT	GO:0031860~telomeric 3' overhang formation	3	0.00102	RAD50, MRE11, NBN	56.7069	0.029303	0.027931
GOTERM_BP_DIRECT	GO:0034089~establishment of meiotic sister chromatid cohesion	3	0.00102	RAD21, SMC1A, SMC3	56.7069	0.029303	0.027931
GOTERM_BP_DIRECT	GO:0032743~positive regulation of interleukin-2 production	5	0.001118	IRF4, PLCG2, MAP3K7, CARD11, MALT1	10.80131	0.031283	0.029818
GOTERM_BP_DIRECT	GO:0032212~positive regulation of telomere maintenance via telomerase	5	0.001118	POT1, MAPK1, ATM, AURKB, ATR	10.80131	0.031283	0.029818
GOTERM_BP_DIRECT	GO:0031647~regulation of protein stability	7	0.001151	USP7, XBP1, LRRK2, PTEN, MAPK1, NDC80, AURKA	5.946791	0.031283	0.029818
GOTERM_BP_DIRECT	GO:0034605~cellular response to heat	6	0.001156	LYN, YWHAE, HSP90AA1, HDAC2, HSP90AB1, TPR	7.56092	0.031283	0.029818
GOTERM_BP_DIRECT	GO:0045597~positive regulation of cell differentiation	6	0.001156	RPS6KA3, SMARCB1, HSP90AB1, RPS6KA1, VHL, ARID1A	7.56092	0.031283	0.029818
GOTERM_BP_DIRECT	GO:0042113~B cell activation	5	0.001245	CD79A, PHB1, PRKCB, BTK, MALT1	10.50128	0.033313	0.031754
GOTERM_BP_DIRECT	GO:0048268~clathrin coat assembly	4	0.001341	CLTC, CLTA, EPS15, PICALM	17.7904	0.035471	0.033811
GOTERM_BP_DIRECT	GO:0031100~animal organ regeneration	5	0.001382	CCNA2, ATIC, CAD, CDK1, LCP1	10.21746	0.036138	0.034446
GOTERM_BP_DIRECT	GO:0006397~mRNA processing	11	0.001401	PTBP1, SFPQ, MBNL1, CPSF6, FIP1L1, U2AF2, NONO, HNRNPA2B1, SRSF2, U2AF1, CDK12	3.451042	0.036231	0.034535
GOTERM_BP_DIRECT	GO:0000165~MAPK cascade	8	0.001419	YWHAE, NRAS, MAP3K1, LRRK2, PTPN6, KRAS, RAF1, MAP3K7	4.800584	0.036294	0.034595
GOTERM_BP_DIRECT	GO:0098586~cellular response to virus	7	0.001528	HSP90AA1, DDX3X, POU2AF1, TYK2, CALR, HIF1A, NFKB1	5.630472	0.03785	0.036077
GOTERM_BP_DIRECT	GO:0032869~cellular response to insulin stimulus	7	0.001528	RB1, KAT2B, XBP1, PKM, STAT1, PRKDC, AKT2	5.630472	0.03785	0.036077
GOTERM_BP_DIRECT	GO:0036297~interstrand cross-link repair	5	0.001528	FANCI, FANCL, FANCD2, FANCA, ATR	9.948578	0.03785	0.036077
GOTERM_BP_DIRECT	GO:0008608~attachment of spindle microtubules to kinetochore	4	0.001593	EML4, ZNF207, NDC80, AURKB	16.80204	0.038242	0.036452
GOTERM_BP_DIRECT	GO:0030889~negative regulation of B cell proliferation	4	0.001593	LYN, INPP5D, BTK, ATM	16.80204	0.038242	0.036452
GOTERM_BP_DIRECT	GO:0045579~positive regulation of B cell differentiation	4	0.001593	XBP1, SYK, INPP5D, BTK	16.80204	0.038242	0.036452

	GO:2001032~regulation of double-strand break repair via nonhomologous end joining							
GOTERM_BP_DIRECT	GO:0007052~mitotic spindle organization	3	0.001684	NSD2, POT1, DEK	45.36552	0.040015	0.038142	
GOTERM_BP_DIRECT	GO:0034504~protein localization to nucleus	6	0.002026	STIL, TACC3, TTK, NDC80, AURKB, AURKA	6.6714	0.047329	0.045113	
GOTERM_BP_DIRECT	GO:0120162~positive regulation of cold-induced thermogenesis	5	0.002033	YWHAЕ, XPO1, RAP1GDS1, MDM2, CALR	9.220634	0.047329	0.045113	
GOTERM_BP_DIRECT	GO:0032733~positive regulation of interleukin-10 production	7	0.002204	FH, SYK, KDM1A, IRF4, GNAS, CXCR4, STAT6	5.240241	0.050761	0.048385	
GOTERM_BP_DIRECT	GO:1901796~regulation of signal transduction by p53 class mediator	5	0.002224	SYK, IRF4, RAD21, PLCG2, HMGB1	9.001095	0.050761	0.048385	
GOTERM_BP_DIRECT	GO:0032755~positive regulation of interleukin-6 production	5	0.002427	USP7, CHEK1, ATM, AURKB, AURKA	8.791767	0.054374	0.051828	
GOTERM_BP_DIRECT	GO:0051096~positive regulation of helicase activity	7	0.002433	XBP1, SYK, POU2AF1, BTK, PLCG2, PTPN11, HMGB1	5.138489	0.054374	0.051828	
GOTERM_BP_DIRECT	GO:0032210~regulation of telomere maintenance via telomerase	3	0.002505	MSH2, MSH3, POT1	37.8046	0.054374	0.051828	
GOTERM_BP_DIRECT	GO:0006337~nucleosome disassembly	3	0.002505	POT1, ATM, TERF2	37.8046	0.054374	0.051828	
GOTERM_BP_DIRECT	GO:0007276~gamete generation	4	0.002523	SET, SMARCB1, HMGA1, ARID1A	14.40175	0.054374	0.051828	
		4	0.002523	YTHDF2, DDX3X, FANCL, FANCD2 RB1, PHB1, MRE11, SMARCB1, KDM1A, IKZF1, SMC3, MKI67, IKZF3, ETS1, ELK4, RPS6KA3, TCL1A, AKT2, RPS6KA1, CHEK1, ZNF207, PIM1, NBN, GTF2I, MBNL1, USP7, PRKCB, COG5, FBXO11, FOXP1, MSH2, DDX39B, EWSR1, MSH3, TBL1XR1, FANCD2, SARNP, SRSF2, SRSF3, NUP98, KPNB1, DDX5, BLM, DNMT1, SET, CBFB, PRKDC, HIF1A, PPP3R1, PDCCD11, PCBP1, RAD21, TPR, EP400, H3C2, FANCI, LYN, XBP1, STIL, XRCC6, CPSF6, UBE2C, FANCL, BCL11A, FUS, NONO, SMARCA5, HMGA1, FANCA, FLI1, NDC80, NFKB1, NFKB2, STAG2, CDK4, CNOT2, SP3, MDM2, CDK1, GRB2, MDM4, ATM, TCF3, CDK12, MNAT1, RPS21, ATR, EZH2, TOP2A, TOP2B, DDX3X, BTG1, HSP90AB1, FAF1, PTEN, HMGB1, BRCA1, AFF3, PHF6, CDC73, PTBP1, XPO1, HSP90AA1, EED, PRMT1, NCOA3, ATRX, PAX5, SMC1A, ARID1A, TERF2, CCNA2, H2BC12, KAT2B, SFPQ, TFDP1, IRF4, POT1, IRF8, TOP1, BIRC3, HDAC2, PCNA, XIAP, U2AF1, AURKB, AURKA, NSD3, FIP1L1, CUX1, U2AF2, POLD1, NSD2, PMS2, MAPK1, STAT6, VHL, SF3B1, SUZ12, CENPU, GIT2, NPM1, UTP4, STAT1, SEPTIN2, H2BC4, HUWE1, PTPN11, DEK, MLH1, LRRPRC, CENPF, WEE1, RAD50, NIN, HNRNPA2B1, CCNG1, TCEA1, PTPN6, PTPN2, MAD2L1	14.40175	0.054374	0.051828	
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	157	6.12E-48	RB1, PHB1, MRE11, SMARCB1, KDM1A, BUB1B, IKZF1, SMC3, MKI67, IKZF3, ETS1, H2AC17, H2AC11, ELK4, RPS6KA3, AKT2, RPS6KA1, CHEK1, ZNF207, PIM1, NBN, MAP3K7, GTF2I, MBNL1, USP7, PRKCB, RPL22, DDX10, FBXO11, FOXP1, DPM1, MSH2, DDX39B, EWSR1, MSH3, TBL1XR1, FANCD2, SARNP, SRSF2, BTK, NUP98, RAF1, KPNB1, DDX6, DDX5, BLM, DNMT1, SET, PRKDC, BAZ2A, HIF1A, PDCCD11, PCBP1, RAD21, TPR, LPXN, H3C2, LYN, XBP1, XRCC6, CPSF6, UBE2C, FANCL, BCL11A, FUS, HSPA4, NONO, SMARCA5, HMGA1, FANCA, FLI1, NDC80, NFKB1, NFKB2, STAG2, NACA, CDK4, CNOT2, SP3, MDM2, CDK1, GNAS, GRB2, MDM4, ATM, TCF3, CDK12, CALR, ATR, EZH2, PICALM, YWHAЕ, CEP57, TOP2A, TOP2B, DDX3X, BTG1, HSP90AB1, FAF1, PTEN, HMGB1, BRCA1, AFF3, CHD2, PHF6, CDC73, PTBP1, XPO1, ZC3H7A, CNTRL, OFD1, SS18, HSP90AA1, SYK, EED, PRMT1, NCOA3, CAD, ATRX, TYK2, PAX5, SMC1A, ARID1A, TERF2, RHOA, CCNA2, H2BC12, KAT2B, SFPQ, TFDP1, PKM, IRF4, IRF8, BIRC6, TOP1, PFDNS, BIRC3, FH, HDAC2, PCNA, RAP1GDS1, XIAP, TTK, TYMS, MALT1, AURKB, AURKA, NSD3, SH3BP1, CUX1, U2AF2, POLD1, NSD2, PMS2, MAPK1, STAT6, VHL, EPS15, SF3B1, EIF4E, SUZ12, CENPU, NPM1, YTHDF2, STAT1, SEPTIN2, H2BC4, HUWE1, PTPN11, DEK, MLH1, LRRPRC, CENPF, WEE1, RAD50, ABI1, HNRNPA2B1, CCNG1, TCEA1, PTPN6, PTPN2, MAD2L1	3.11767	3.00E-45	2.58E-45	
GOTERM_CC_DIRECT	GO:0005634~nucleus	183	9.11E-42	RB1, CYFIP2, EIF4A2, MRE11, NUP107, BUB1B, IKZF1, MSI2, SMC3, IKZF3, ELK4, RPS6KA3, TCL1A, AKT2, KIF5B, FGFR1OP2, RPS6KA1, CHEK1, PIM1, NBN, MAP3K7, CDK5RAP2, MBNL1, USP7, TPM3, FNBP1, PRKCB, COG5, RPL22, FBXO11, EML4, DDX39B, FANCD2, PRKAR1A, SRSF2, BTK, NUP98, EZR, RAF1, CARD11, KPNB1, DDX6, DDX5, BLM, SET, PRKDC, GMPS, BAZ2A, RASAL1, HIF1A, PPP3R1, PDCCD11, INPP5D, PCBP1, RAD21, PLCG2, LPXN, FANCI, LYN, XBP1, STIL, XRCC6, UBE2C, FANCL, BCL11A, HSPA4, IDH2, HMGA1, FANCA, HOOK3, FLI1, NDC80, NFKB1, NFKB2, STAG2, CDK4, CAPRIN1, CNOT2, SP3, MDM2, CDK1, GNAS, GRB2, STRN, ATM, CALR, RPS21, PICALM, YWHAЕ, CEP57, TOP2B, DDX3X, HSP90AB1, WDR1, LRRK2, FAF1, RASGRF1, CLTC, PTEN, CLTA, AFF3, CDC73, XPO1, ATIC, CNTRL, RAC2, OFD1, HSP90AA1, SYK, EED, PRMT1, NCOA3, CAD, GAB1, CIP2A, TYK2, SMC1A, RHOA, CCNA2, H2BC12, KAT2B, SFPQ, TFDP1, PKM, IRF4, IRF8, BIRC6, LCP1, MAPRE1, ARHGEF7, SOS1, PFDNS, CD44, BIRC3, FH, BCL2A1, RAP1GDS1, GOSR1, XIAP, TYMS, MALT1, AURKB, AURKA, CDC42, NRAS, SH3BP1, FIP1L1, CUX1, POLD1, PMS2, MAPK1, STAT6, VHL, EPS15, WASF2, EIF4E, CENPU, NPM1, RRM1, MAP3K1, YTHDF2, STAT1, H2BC4, HUWE1, PTPN11, CENPF, ABI1, CCDC6, TACC3, KRAS, PTPN6, PTPN2, MAD2L1	2.371645	2.24E-39	1.92E-39	
GOTERM_CC_DIRECT	GO:0005829~cytosol	173	5.08E-40	TOP2A, BLM, HDAC2, SMARCB1, SET, HSP90AB1, KDM1A, PRKDC, CLTC, CXCR4, IKZF1, BRCA1, HIF1A, MALT1, CDC42, XPO1, CHEK1, H3C2, WASF2, USP7, NPM1, XRCC6, HSP90AA1, SYK, STAT1, NCOA3, CAD, PTPN11, KAT2B, RABEP1, PRKAR1A, MDM2, STRN, PTPN6, TCF3, EZR, ARHGEF7, BIRC3	2.450813	8.32E-38	7.13E-38	
GOTERM_CC_DIRECT	GO:0032991~protein-containing complex	38	5.14E-14		4.445934	5.23E-12	4.48E-12	

GOTERM_CC_ DIRECT	GO:0000781~chromosome, telomeric region	21	5.33E-14	BLM, XRCC6, HDAC2, MRE11, PCNA, KDM1A, PRKDC, ATRX, TERF2, CDC73, RAD50, MSH2, POLD1, HNRNPA2B1, CHEK1, CDK1, POT1, ATM, NBN, ATR, EZH2	9.714238	5.23E-12	4.48E-12
GOTERM_CC_ DIRECT	GO:0005737~cytoplasm	129	7.09E-14	CYFIP2, PHB1, MRE11, BUB1B, MSI2, IKZF3, ETS1, RPS6KA3, AKT2, KIF5B, RPS6KA1, CHEK1, ZNF207, PIM1, MAP3K7, GTF2I, CDK5RAP2, MBNL1, PRKCB, RPL22, IRAG2, FBXO11, EML4, MELK, DDX39B, EWSR1, PRKAR1A, BTK, SRSF3, EZR, RAF1, CARD11, KPNB1, DDX6, DDX5, BLM, SET, HIF1A, PCBP1, TPR, PLCG2, LPXN, FANCI, LYN, CARMIL2, XBP1, STIL, CPSF6, BCL11A, FUS, FANCA, HOOK3, NDC80, NFKB1, NFKB2, NACA, CDK4, CAPRIN1, CNOT2, CDC88C, MDM2, CDK1, GNAS, GRB2, ATM, TCF3, CALR, MNAT1, RPS21, YWHAE, CEP57, TOP2A, DDX3X, BTG1, HSP90AB1, LRRK2, RASGRF1, PTEN, BRCA1, LASP1, XPO1, HSP90AA1, SYK, PRMT1, NCOA3, CAD, GAB1, CIP2A, TYK2, CCNA2, TFDP1, PKM, IRF8, LCP1, ARHGEF7, SOS1, PFDN5, BIRC3, FH, HDAC2, BCL2A1, XIAP, CXCR4, TTK, TYMS, MALT1, AURKA, CDC42, NSD2, MAPK1, STAT6, EPS15, EIF4E, NPM1, MAP3K1, YTHDF2, STAT1, SEPTIN2, HUWE1, PTPN11, CENPF, WEE1, HNRNPA2B1, CCNG1, TACC3, KRAS, PTPN6, PTPN2, MAD2L1, NUP107, SMARCB1, SEPTIN2, SEPTINE6, BUB1B, TTK, SMC1A, PHF6, NDC80, AURKB, AURKA, KAT2B, CENPF, XPO1, TPR, ZNF207, NUP98, MNAT1, MAD2L1	1.794136	5.81E-12	4.98E-12
GOTERM_CC_ DIRECT	GO:0000776~kinetochore	19	3.37E-12	CENPU, BLM, USP7, FH, UTP4, EED, NONO, IRAG2, BRCA1, HMGB1, CIP2A, MKI67, MLH1, SMC3, SMC1A, FBXO11, STAG2, MSH2, RAD21, TOP1, ATR, EZH2	9.104848	2.37E-10	2.03E-10
GOTERM_CC_ DIRECT	GO:0005694~chromosome	22	8.91E-12	RB1, HDAC2, SMARCB1, SET, PCNA, KDM1A, PRKDC, CHD2, SMC3, ETS1, HIF1A, ELK4, NSD3, CUX1, RAD21, CHEK1, NSD2, STAT6, FANCI, SS18, FANCL, STAT1, NCOA3, SMARCA5, HMGA1, FANCA, PAX5, ARID1A, FLI1, NFKB1, FOXP1, NFKB2, SFPQ, CENPF, STAG2, TFDP1, FANCD2, IRF4	6.931457	5.47E-10	4.69E-10
GOTERM_CC_ DIRECT	GO:0000785~chromatin	43	3.76E-10	CDK4, SP3, IRF8, TCF3, EZH2	2.976776	2.05E-08	1.76E-08
GOTERM_CC_ DIRECT	GO:0097431~mitotic spindle pole	10	5.64E-09	NIN, STAG2, CNTRL, SMC1A, SMC3, MAPRE1, ARHGEF7, AURKB, AURKA, CDK5RAP2	17.02698	2.77E-07	2.37E-07
GOTERM_CC_ DIRECT	GO:0005819~spindle	14	6.51E-08	RB1, SEPTIN2, CLTC, SEPTINE6, CLTA, BUB1B, TTK, AURKB, AURKA, CENPF, ZNF207, MAPK1, ATM, MAPRE1	7.322716	2.91E-06	2.49E-06
GOTERM_CC_ DIRECT	GO:0005813~centrosome	28	9.21E-08	CEP57, DDX3X, PCNA, BUB1B, AURKA, CDC42, CHEK1, CNTRL, MAPK1, CDK5RAP2, OFD1, NPM1, STIL, PRKCB, IRAG2, HOOK3, NDC80, CCNA2, KAT2B, CENPF, NIN, PRKAR1A, CCDC88C, CDK1, ATM, BIRC6, MAPRE1, ARHGEF7	3.33942	3.77E-06	3.23E-06
GOTERM_CC_ DIRECT	GO:0016363~nuclear matrix	12	7.09E-07	BLM, SFPQ, CENPF, SMARCB1, STAG2, BCL11A, NONO, RAD21, CAD, HNRNPA2B1, SMC1A, SMC3	7.387091	2.68E-05	2.30E-05
GOTERM_CC_ DIRECT	GO:0070062~extracellular exosome	56	7.79E-07	YWHAE, CYFIP2, PHB1, DDX3X, HSP90AB1, WDR1, TFRC, LRRK2, CLTC, H2AC17, H2AC11, PTBP1, ATIC, RAC2, CDK5RAP2, HSP90AA1, TPM3, PRKCB, NCOA3, RPL22, CAD, TYK2, RHOA, PKM, LCP1, EZR, CD44, CARD11, KPNB1, FH, DDX5, PCNA, RAP1GDS1, CXCR4, CD79B, CDC42, NRAS, PCBP1, PLCG2, H3C2, WASF2, EIF4E, LYN, HSPA4, SEPTIN2, H2BC4, IDH2, HUWE1, NACA, AB1, HNRNPA2B1, CDK1, GNAS, PTPN6, GRB2, CALR	1.984722	2.73E-05	2.34E-05
GOTERM_CC_ DIRECT	GO:0048471~perinuclear region of cytoplasm	28	1.09E-06	EIF4A2, CYFIP2, SET, HSP90AB1, TFRC, FAF1, BUB1B, MALT1, AURKA, KIF5B, CNTRL, PLCG2, LPXN, EIF4E, CDK5RAP2, LYN, HSP90AA1, STAT1, LRPPRC, CENPF, CCNG1, GNAS, BTK, LCP1, CALR, EZR, PICALM, MAD2L1	2.944482	3.56E-05	3.06E-05
GOTERM_CC_ DIRECT	GO:1990904~ribonucleo protein complex	14	2.46E-06	TOP2A, SUZ12, TOP2B, NPM1, DDX5, CPSF6, LRRK2, RPL22, BRCA1, LRPPRC, XPO1, PCBP1, HNRNPA2B1, NUP98	5.335121	7.39E-05	6.34E-05
GOTERM_CC_ DIRECT	GO:0072686~mitotic spindle	12	2.56E-06	CDC42, EML4, KAT2B, NIN, TBL1XR1, TPR, CLTC, CDK1, TACC3, MAPK1, MAD2L1, AURKA	6.488661	7.39E-05	6.34E-05
GOTERM_CC_ DIRECT	GO:0005925~focal adhesion	19	9.57E-06	YWHAE, GIT2, NPM1, RPL22, CLTC, HMGA1, RHOA, CDC42, LASP1, RAC2, MAPK1, LPXN, KRAS, LCP1, CALR, EZR, MAPRE1, ARHGEF7, CD44	3.495424	2.61E-04	2.24E-04
GOTERM_CC_ DIRECT	GO:0005730~nucleolus	38	1.17E-05	TOP2A, TOP2B, BLM, DDX5, SMARCB1, PRKDC, BAZ2A, MKI67, PHF6, PTBP1, RPS6KA3, XPO1, PDCD11, NSD2, ZNF207, PIM1, NBN, SF3B1, SUZ12, NPM1, XRCC6, UTP4, STAT1, SMARCA5, DEK, FBXO11, WEE1, NIN, STAG2, FANCD2, EWSR1, CDK4, MDM2, TCEA1, GRB2, PTPN6, ATM, TOP1	2.172157	3.01E-04	2.58E-04
GOTERM_CC_ DIRECT	GO:0005635~nuclear envelope	13	1.49E-05	RRM1, NUP107, FANCL, FAF1, IRAG2, CENPF, XPO1, TPR, RAC2, NUP98, CALR, KPNB1, ATR	4.907305	3.59E-04	3.08E-04
GOTERM_CC_ DIRECT	GO:1990391~DNA repair complex	5	1.54E-05	FANCI, KDM1A, FANCD2, ATM, BRCA1	30.77955	3.59E-04	3.08E-04
GOTERM_CC_ DIRECT	GO:1904813~ficolin-1-rich granule lumen	10	2.72E-05	XRCC6, HSP90AA1, PKM, DDX3X, HSP90AB1, HUWE1, MAPK1, HOOK3, HMGB1, KPNB1	6.402146	6.07E-04	5.20E-04
GOTERM_CC_ DIRECT	GO:0090575~RNA polymerase II transcription regulator complex	10	3.09E-05	SFPQ, XBP1, TFDP1, STAT1, NONO, POU2AF1, HMGA1, STAT6, TCF3, HIF1A	6.301324	6.54E-04	5.61E-04
GOTERM_CC_ DIRECT	GO:0016607~nuclear speck	18	3.20E-05	DDX5, CPSF6, NONO, BAZ2A, U2AF1, HIF1A, SFPQ, DDX39B, U2AF2, SARNP, PCBP1, EP400, SRSF2, LPXN, SRSF3, CDK12, EIF4E, SF3B1	3.334451	6.54E-04	5.61E-04
GOTERM_CC_ DIRECT	GO:0070533~BRCA1-C complex	4	3.71E-05	RAD50, MRE11, BRCA1, NBN	53.35121	7.00E-04	6.01E-04
GOTERM_CC_ DIRECT	GO:0030892~mitotic cohesin complex	4	3.71E-05	STAG2, RAD21, SMC1A, SMC3	53.35121	7.00E-04	6.01E-04
GOTERM_CC_ DIRECT	GO:0005938~cell cortex	11	4.80E-05	LASP1, STIL, MELK, FNBP1, SEPTIN2, AKT2, GRB2, EZR, ARHGEF7, FRYL, RHOA	5.271228	8.72E-04	7.48E-04
GOTERM_CC_ DIRECT	GO:0005657~replication fork	6	5.13E-05	BLM, DNMT1, PCNA, MRE11, CHEK1, NBN	14.55033	9.00E-04	7.72E-04
GOTERM_CC_ DIRECT	GO:0016605~PML body	9	7.57E-05	RB1, BLM, USP7, MRE11, ATRX, SP3, PTEN, NBN, ATR	6.488661	0.001282	0.001099
GOTERM_CC_ DIRECT	GO:0034774~secretory granule lumen	9	1.03E-04	XRCC6, HSP90AA1, PKM, DDX3X, HSP90AB1, HUWE1, HOOK3, HMGB1, NFKB1	6.208977	0.00169	0.001449
GOTERM_CC_ DIRECT	GO:0000775~chromosome, centromeric region	7	1.10E-04	TOP2A, CENPF, STAG2, RAD21, SMC1A, SMC3, NDC80	9.183406	0.001741	0.001493
GOTERM_CC_ DIRECT	GO:0016604~nuclear body	15	1.28E-04	SUZ12, USP7, PCNA, FANCL, ATRX, BRCA1, MKI67, AFF3, TERF2, HIF1A, FLI1, FANCD2, MDM2, NUP98, EIF4E	3.449432	0.001967	0.001686
GOTERM_CC_ DIRECT	GO:0030496~midbody	11	1.53E-04	CDC42, EML4, CENPF, SEPTIN2, RAD21, CDK1, SEPTIN6, BIRC6, RHOA, AURKB, AURKA	4.58487	0.002278	0.001953
GOTERM_CC_ DIRECT	GO:0000307~cyclin-dependent protein kinase holoenzyme complex	6	2.10E-04	CCNA2, PCNA, CDK4, CCNG1, CDK1, MNAT1	10.91275	0.003009	0.00258

GOTERM_CC_	GO:0005677~chromatin							
DIRECT	silencing complex	4	2.14E-04	SUZ12, SMARCA5, BAZ2A, EZH2	32.01073	0.003009	0.00258	
GOTERM_CC_	GO:0042382~paraspeckl							
DIRECT	es	4	2.92E-04	SFPQ, CPSF6, BCL11A, NONO	29.10066	0.003985	0.003417	
GOTERM_CC_	GO:0000228~nuclear							
DIRECT	chromosome	5	3.29E-04	TOP2A, BLM, SMARCB1, ATRX, TOP1	14.81978	0.004361	0.003739	
GOTERM_CC_	GO:0030132~clathrin							
DIRECT	coat of coated pit	4	3.86E-04	CLTC, CLTA, EPS15, PICALM	26.67561	0.00486	0.004167	
GOTERM_CC_	GO:0008278~cohesin							
DIRECT	complex	4	3.86E-04	STAG2, RAD21, SMC1A, SMC3	26.67561	0.00486	0.004167	
GOTERM_CC_	GO:0000793~condensed							
DIRECT	chromosome	5	4.36E-04	TOP2A, FANCD2, SMARCA5, HMGB1, MKI67	13.79773	0.005353	0.00459	
GOTERM_CC_	GO:0098687~chromoso							
DIRECT	mal region	3	4.59E-04	RAD50, MRE11, NBN	80.02682	0.0055	0.004716	
GOTERM_CC_	GO:0016514~SWI/SNF							
DIRECT	complex	5	6.41E-04	RB1, SS18, SMARCB1, BCL11A, ARID1A	12.50419	0.007303	0.006262	
GOTERM_CC_	GO:0005721~pericentric							
DIRECT	heterochromatin	5	6.41E-04	DNMT1, ATRX, SMARCA5, IKZF1, EZH2	12.50419	0.007303	0.006262	
GOTERM_CC_	GO:0001673~male germ							
DIRECT	cell nucleus	6	6.54E-04	TOP2A, PCNA, BRCA1, TOP1, MLH1, TERF2	8.574302	0.007303	0.006262	
GOTERM_CC_	GO:0035098~ESC/E(Z)							
DIRECT	complex	4	9.47E-04	SUZ12, HDAC2, EED, EZH2	20.0067	0.010333	0.00886	
GOTERM_CC_	GO:0034451~centriolar							
DIRECT	satellite	8	0.001125	OFD1, CEP57, CENPU, YTHDF2, KIF5B, CNTRL, TACC3, HOOK3	5.001676	0.012003	0.010292	
GOTERM_CC_	GO:0043232~intracellula							
DIRECT	r non-membrane-	4	0.001355	FUS, CAPRIN1, BRCA1, VHL	17.78374	0.014015	0.012017	
GOTERM_CC_	GO:0032993~protein-							
DIRECT	DNA complex	5	0.00137	XRCC6, NPM1, PRKDC, SP3, TOP1	10.25985	0.014015	0.012017	
GOTERM_CC_	GO:0010494~cytoplasmic							
DIRECT	stress granule	7	0.001422	DDX6, MBNL1, YTHDF2, DDX3X, CAPRIN1, EIF4E, KPNB1	5.716201	0.014247	0.012216	
GOTERM_CC_	GO:0030870~Mre11							
DIRECT	complex	3	0.001506	RAD50, MRE11, NBN	48.01609	0.014497	0.012431	
GOTERM_CC_	GO:0045120~pronucleus							
DIRECT		3	0.001506	CENPF, EZH2, AURKA	48.01609	0.014497	0.012431	
GOTERM_CC_	GO:0000794~condensed							
DIRECT	nuclear chromosome	5	0.001654	RAD50, RAD21, CHEK1, SMC1A, LRPPRC	9.759368	0.015622	0.013395	
GOTERM_CC_	GO:0035861~site of							
DIRECT	double-strand break	7	0.001746	FH, RAD50, MRE11, CNTRL, SMARCA5, ATM, NBN	5.492037	0.016171	0.013866	
GOTERM_CC_	GO:0000786~nucleosom							
DIRECT	e	8	0.002211	H2BC12, H2AC11, IRF4, H2BC4, EP400, H3C2, SOS1, H2AC17	4.445934	0.020105	0.017239	
GOTERM_CC_	GO:0000922~spindle							
DIRECT	pole	8	0.00239	CENPF, NIN, RAD21, TACC3, IRAG2, BIRC6, MAD2L1, CDK5RAP2	4.385031	0.021335	0.018294	
GOTERM_CC_	GO:0001650~fibrillar							
DIRECT	center	8	0.002994	SMARCB1, STAG2, UTP4, NONO, SMARCA5, TOP1, EZR, MALT1	4.211938	0.026247	0.022505	
GOTERM_CC_	GO:0030893~meiotic							
DIRECT	cohesin complex	3	0.003111	RAD21, SMC1A, SMC3	34.29721	0.026249	0.022507	
GOTERM_CC_	GO:0019815~B cell							
DIRECT	receptor complex	3	0.003111	CD79B, CD79A, SYK	34.29721	0.026249	0.022507	
GOTERM_CC_	GO:0030027~lamellipodi							
DIRECT	um	9	0.003154	CARMIL2, DDX3X, SH3BP1, CAPRIN1, ABI1, RAC2, ARHGEF7, WASF2, RHOA	3.693546	0.026249	0.022507	
GOTERM_CC_	GO:0036464~cytoplasmic							
DIRECT	ribonucleoprotein granule	6	0.003793	CDC42, DDX6, YTHDF2, SARNP, PCBP1, EIF4E YWHA, CYFIP2, PHB1, NUP107, DDX3X, HSP90AB1, TFRC, FAF1, CLTC, CLTA, MKI67, HERPUD1, PTBP1, ATIC, XPO1, KIF5B, CNTRL, GTF2I, CDK5RAP2, OFD1, HSP90AA1, EED, COG5, CAD, IRAG2, TYK2, RHOA, EML4, DPM1, MELK, MSH2, PRKAR1A, IRF4, MSH3, TBL1XR1, BIRC6, NUP98, EZR, KPNB1, DDX6, DDX5, HDAC2, CBF, PRKDC, GOSR1, CXCR4, TTK, CDC42, NRAS, POLD1, PCBP1, RAD21, LPXN, H3C2, EPS15, FANCI, NPM1, CARMIL2, RRM1, XRCC6, CPSF6, FANCL, FUS, NONO, HUWE1, MLH1, TMEM230, LRPPRC, NDC80, KTN1, RAD50, STAG2, CAPRIN1, CNOT2, HNRNPA2B1, CDK1, GNAS, KRAS, STRN, PTPN6, CALR, PTPN2, PICALM	5.785071	0.031037	0.026612	
GOTERM_CC_	GO:0016020~membrane	83	0.003986		1.315813	0.032087	0.027513	
DIRECT								
GOTERM_CC_	GO:0110016~B-WICH							
DIRECT	complex	3	0.004113	SMARCA5, DEK, SF3B1	30.01006	0.032576	0.027932	
GOTERM_CC_	GO:0051233~spindle							
DIRECT	midzone	4	0.004963	CDC42, MAPRE1, AURKB, AURKA	11.4324	0.038677	0.033163	
GOTERM_CC_	GO:0031252~cell leading							
DIRECT	edge	5	0.005189	CARMIL2, DDX3X, SH3BP1, CAPRIN1, CXCR4	7.145252	0.039623	0.033974	
GOTERM_CC_	GO:0000783~nuclear							
DIRECT	telomere cap complex	3	0.005245	XRCC6, POT1, TERF2	26.67561	0.039623	0.033974	
GOTERM_CC_	GO:0005856~cytoskeleto							
DIRECT	n	15	0.005619	TPM3, FNBP1, LRRK2, TYK2, RHOA, LRPPRC, LASP1, INPP5D, ABI1, RAC2, CCDC6, MAPK1, EZR, WASF2, CDK5RAP2	2.317379	0.041799	0.03584	
GOTERM_CC_	GO:0017053~transcriptio							
DIRECT	n repressor complex	5	0.007439	TBL1XR1, SP3, MDM2, MDM4, HMGB1	6.453776	0.054513	0.046741	
GOTERM_CC_	GO:0000940~outer							
DIRECT	kinetochore	3	0.007883	CENPF, BUB1B, NDC80	21.8255	0.056671	0.048591	
GOTERM_CC_	GO:0001726~ruffle							
DIRECT		6	0.007964	CARMIL2, GNAS, LCP1, EZR, ARHGEF7, WASF2 RB1, CYFIP2, EIF4A2, PHB1, NUP107, SMARCB1, TFRC, IKZF1, MKI67, SMC3, IKZF3, H2AC17, H2AC11, ELK4, RPS6KA3, TCL1A, AKT2, FGFR1OP2, RPS6KA1, CHEK1, CDK5RAP2, MBNL1, ST6GAL1, FNBP1, COG5, PRKCB, RPL22, EML4, DDX39B, EWSR1, PRKAR1A, SARNP, BTK, NUP98, EZR, SET, PRKDC, BAZ2A, HIF1A, CD79B, CD79A, PPP3R1, PDCCD11, INPP5D, RAD21, PCBP1, PLCG2, H3C2, LYN, XBP1, XRCC6, SMARCA5, FLI1, STAG2, CCDC88C, STRN, GRB2, ATM, CDK12, CALR, RPS21, ATR, EZH2, CEP57, TOP2A, TOP2B, BTG1, FAF1, CLTC, CLTA, BRCA1, PHF6, HERPUD1, XPO1, CNTRL, RAC2, OFD1, SS18, SYK, PRMT1, NCOA3, GAB1, TYK2, PAX5, TERF2, RHOA, KAT2B, POT1, ARHGEF7, MAPRE1, CD44, FH, PCNA, CXCR4, XIAP, NSD3, NRAS, NSD2, PMS2, STAT6, EPS15, SF3B1, SUZ12, GIT2, CENPU, NPM1, MAP3K1, YTHDF2, UTP4, STAT1, SEPTIN2, H2BC4, HUWE1, SEPTIN6, MLH1, COX6C, LRPPRC, KTN1, CENPF, HNRNPA2B1,	4.85011	0.056671	0.048591	
GOTERM_MF_	GO:0005515~protein							
DIRECT	binding	243	5.37E-27		1.420062	3.06E-24	2.68E-24	

					ABI1, CCNG1, TACC3, CDC6, TCEA1, MAD2L1, MRE11, KDM1A, BUB1B, MSI2, ETS1, KIF5B, ZNF207, PIM1, NBN, MAP3K7, GTF2I, USP7, TPM3, FBXO11, FOXF1, DPM1, MELK, MSH2, FANCD2, MSH3, TBL1XR1, SRSF2, SRSF3, RAF1, KPNB1, CARD11, DDX6, DDX5, BLM, DNMT1, CBFB, TPR, EP400, LPXN, FANCI, STIL, CPSF6, HSPA4, UBE2C, FANCL, FUS, NONO, HMGA1, FANCA, HOOK3, NDC80, NFKB1, NFKB2, NACA, CDK4, CNOT2, CAPRIN1, SP3, MDM2, GNAS, CDK1, MDM4, TCF3, MNAT1, PICALM, YWHAE, DDX3X, HSP90AB1, LRRK2, PTEN, HMGB1, CHD2, CDC73, PTBP1, LASP1, HSP90AA1, EED, ATRX, CAD, CIP2A, SMC1A, ARID1A, H2BC12, CCNA2, SFPQ, PKM, TFDP1, RABEP1, IRF4, IRF8, BIRC6, TOP1, SOS1, PFDN5, BIRC3, HDAC2, BCL2A1, RAP1GDS1, TTK, U2AF1, MALT1, AURKB, AURKA, CDC42, SH3BP1, FIP1L1, U2AF2, POLD1, MAPK1, VHL, WASF2, EIF4E, RRM1, PTPN11, DEK, WEE1, RAD50, NIN, POU2AF1, PTPN6, KRAS, PTPN2 EIF4A2, YWHAE, TOP2A, DDX3X, HSP90AB1, TFRC, CLTC, BRCA1, HMGB1, MSI2, MKI67, CHD2, PHF6, PTBP1, XPO1, ZC3H7A, ZNF207, MBNL1, HSP90AA1, PRMT1, RPL22, DDX10, SMC1A, SFPQ, PKM, DDX39B, EWSR1, SARNP, SRSF2, SRSF3, NUP98, TOP1, EZR, MAPRE1, KPNB1, DDX6, DDX5, DNMT1, HDAC2, PRKDC, U2AF1, BAZ2A, PDCD11, FIP1L1, U2AF2, PCBP1, TPR, SF3B1, EIF4E, NPM1, XRCC6, CPSF6, YTHDF2, UTPA, FUS, NONO, HMGA1, HUWE1, DEK, LRPPRC, KTN1, CAPRIN1, HNRNPA2B1, GRB2, CALR, RPS21 TOP2A, TOP2B, MRE11, SMARCB1, DDX3X, BRCA1, IKZF1, MKI67, CHD2, ETS1, PHF6, H2AC17, H2AC11, ELK4, ZNF207, GTF2I, SMC1A, ARID1A, H2BC12, SFPQ, MSH2, SARNP, TOP1, SOS1, BLM, DNMT1, SET, PCNA, BAZ2A, POLD1, RAD21, NSD2, EP400, PMS2, MAPK1, H3C2, FANCI, XBP1, XRCC6, FUS, NONO, H2BC4, SMARCA5, HMGA1, HUWE1, DEK, FLI1, RAD50, NACA, POU2AF1, TCEA1, ATM, TCF3, CALR, ATR EIF4A2, TOP2A, TOP2B, DDX3X, HSP90AB1, LRRK2, BUB1B, SMC3, MKI67, CHD2, RPS6KA3, AKT2, KIF5B, RPS6KA1, CNTRL, CHEK1, PIM1, MAP3K7, GTF2I, HSP90AA1, SYK, PRKCB, CAD, ATRX, DDX10, TYK2, SMC1A, PKM, MELK, MSH2, DDX39B, MSH3, BTK, TOP1, RAF1, DDX6, BLM, DDX5, PRKDC, GMP5, TTK, AURKB, AURKA, EP400, PMS2, MAPK1, LYN, RRM1, XRCC6, MAP3K1, UBE2C, HSPA4, SMARCA5, HOOK3, MLH1, WEE1, RAD50, CDK4, CAPRIN1, CDK1, KRAS, ATM, CDK12, ATR TOP2A, TOP2B, DNMT1, HDAC2, SET, PCNA, KDM1A, CHD2, SMC3, ELK4, POLD1, RAD21, TPR, NSD2, EP400, NPM1, PRKCB, FUS, NONO, ATRX, SMARCA5, HMGA1, MLH1, SMC1A, FLI1, NFKB1, KAT2B, SFPQ, CENPF, STAG2, MSH2, SARNP, SP3, CDK1, TOP1, EZH2 YWHAE, DDX5, HDAC2, PHB1, BTG1, PCNA, KDM1A, PRKDC, PTEN, BRCA1, PHF6, HIF1A, H2AC17, H2AC11, U2AF2, POLD1, VHL, EIF4E, LYN, PRMT1, STAT1, CAD, HMGA1, MLH1, TERF2, MSH3, MDM2, MDM4, RAF1, KPNB1 RB1, CEP57, YWHAE, MRE11, SMARCB1, HSP90AB1, KDM1A, TFRC, LRRK2, PTEN, BRCA1, IKZF1, MSI2, IKZF3, ETS1, TCL1A, KIF5B, FGFR1OP2, MAP3K7, OFD1, HSP90AA1, FBNP1, EED, PRMT1, RPL22, CAD, FOXF1, DDX39B, EWSR1, BTK, EZR, RAF1, MAPRE1, BLM, PCNA, XIAP, TTK, MALT1, CD79B, CDC42, CD79A, MAPK1, STAT6, XBP1, STIL, RRM1, FUS, STAT1, SEPTIN2, NONO, H2BC4, HOOK3, NDC80, NFKB1, RAD50, CCD88C, HNRNPA2B1, CDC6, MDM2, KRAS, GRB2, ATM, MAD2L1 MAP3K1, SYK, PRKCB, PRKDC, LRRK2, BUB1B, TTK, AURKB, AURKA, RPS6KA3, MELK, AKT2, RPS6KA1, CHEK1, PIM1, CDK1, MAPK1, ATM, CDK12, TOP1, RAF1, MAP3K7, ATR, GTF2I HSP90AB1, TFRC, FAF1, CLTC, HIF1A, AURKA, CDC42, RPS6KA3, TCL1A, PLCG2, RAC2, CDK5RAP2, NPM1, XBP1, MAP3K1, SYK, BCL11A, PTPN11, RHOA, CCNA2, KAT2B, GRB2, PTPN6, CDK12, MAPRE1, ARHGEF7, PTPN2 YWHAE, DDX6, MRE11, DDX3X, HSP90AB1, STAT1, SEPTIN2, PTPN11, CIP2A, KTN1, LASP1, PKM, ATIC, PCBP1, KIF5B, ABI1, H3C2, EZR, MAPRE1, EPS15, WASF2, PICALM MAP3K1, PRKCB, PRKDC, LRRK2, BUB1B, TTK, AURKB, AURKA, RPS6KA3, MELK, CDK4, AKT2, RPS6KA1, CHEK1, PIM1, CDK1, MAPK1, ATM, CDK12, RAF1, MAP3K7, ATR YWHAE, DDX6, PRKDC, FAF1, IKZF1, HIF1A, CCNA2, PPP3R1, RABEP1, TFDP1, PRKAR1A, CHEK1, MDM2, GRB2, TOP1, EZR, KPNB1 RB1, NPM1, KDM1A, BCL11A, HMGB1, KAT2B, CENPF, TFDP1, RAD21, VHL, NBN, TCF3, MAP3K7, EIF4E RB1, RRM1, HSP90AA1, HSP90AB1, NCOA3, CLTC, MDM2, EZR DDX6, HSP90AA1, CPSF6, YTHDF2, DDX3X, NONO, MSI2, TYMS, PTBP1, PKM, DDX39B, PCBP1, CAPRIN1, TPR, NUP98, CALR, SF3B1 SS18, NPM1, SMARCB1, CBFB, KDM1A, FUS, NCOA3, HMGA1, BRCA1, HMGB1, ARID1A, KAT2B, PKM, IRF4, NACA, POU2AF1, NUP98 SUZ12, DDX5, DNMT1, HDAC2, KDM1A, STAT1, NUP98, IKZF3, EZH2 LYN, RB1, YWHAE, XBP1, HSP90AA1, HSP90AB1, FANCL, FAF1, CXCR4, BRCA1, HIF1A, LRPPRC, AURKA, PRKAR1A, MDM2, CALR, MAP3K7 EIF4A2, DDX6, BLM, XRCC6, DDX5, HSP90AA1, DDX3X, HSP90AB1, ATRX, SMARCA5, DDX10, MLH1, SMC3, CHD2, SMC1A, RAD50, DDX39B, MSH2, KIF5B, PMS2 FANCI, HSP90AA1, PCNA, HSP90AB1, FANCD2, HMGB1 XRCC6, MRE11, MSH2, STAT1, MSH3, PRKDC, HMGB1, TOP1, SMC3, AFF3 YWHAE, TOP2A, XBP1, PHB1, BCL2A1, BCL11A, H2BC4, SMC3, SMC1A, HIF1A, IKZF3, H2AC17, AURKA, H2AC11, H2BC12, H3C2, TCF3, SOS1 NPM1, HDAC2, FH, SET, PRKCB, STAT1, ATRX, SMARCA5, BAZ2A, DEK, CHD2, PHF6, TBL1XR1, NBN BLM, MSH2, MSH3, PCBP1, CNTRL, PMS2, HMGB1, TOP1, MLH1, LRPPRC			
GOTERM_MF_	GO:0003723~RNA							
DIRECT	binding	66	1.32E-18			3.38087	3.76E-16	3.29E-16
GOTERM_MF_	GO:0003677~DNA							
DIRECT	binding	55	4.23E-16			3.543047	6.77E-14	5.93E-14
GOTERM_MF_	GO:0005524~ATP							
DIRECT	binding	64	4.75E-16			3.095458	6.77E-14	5.93E-14
GOTERM_MF_	GO:0003682~chromatin							
DIRECT	binding	36	3.84E-15			5.130366	4.38E-13	3.84E-13
GOTERM_MF_	GO:0019899~enzyme							
DIRECT	binding	30	2.16E-14			6.010711	2.05E-12	1.79E-12
GOTERM_MF_	GO:0042802~identical							
DIRECT	protein binding	63	4.29E-13			2.703263	3.49E-11	3.06E-11
GOTERM_MF_	GO:0004674~protein							
DIRECT	serine/threonine kinase activity	24	2.02E-09			4.68269	1.44E-07	1.26E-07
GOTERM_MF_	GO:0019901~protein							
DIRECT	kinase binding	27	4.15E-09			4.008737	2.63E-07	2.30E-07
GOTERM_MF_	GO:0045296~cadherin							
DIRECT	binding	22	5.14E-09			4.894693	2.93E-07	2.56E-07
GOTERM_MF_	GO:0106310~protein							
DIRECT	serine kinase activity	22	2.41E-08			4.480115	1.25E-06	1.10E-06
GOTERM_MF_	GO:0019904~protein							
DIRECT	domain specific binding	17	3.90E-08			5.838977	1.85E-06	1.62E-06
GOTERM_MF_	GO:0140297~DNA-							
DIRECT	binding transcription	14	5.67E-07			6.066625	2.49E-05	2.18E-05
GOTERM_MF_	GO:0097718~disordered							
DIRECT	domain specific binding	8	6.22E-07			15.69112	2.53E-05	2.22E-05
GOTERM_MF_	GO:0003729~mRNA							
DIRECT	binding	17	7.32E-07			4.710252	2.78E-05	2.43E-05
GOTERM_MF_	GO:0003713~transcriptio							
DIRECT	n coactivator activity	17	1.07E-06			4.574216	3.81E-05	3.34E-05
GOTERM_MF_	GO:1990841~promoter-							
DIRECT	specific chromatin	9	3.38E-06			9.846438	1.13E-04	9.92E-05
GOTERM_MF_	GO:0031625~ubiquitin							
DIRECT	protein ligase binding	17	4.82E-06			4.074141	1.53E-04	1.34E-04
GOTERM_MF_	GO:0016887~ATP							
DIRECT	hydrolysis activity	20	6.54E-06			3.434692	1.96E-04	1.72E-04
GOTERM_MF_	GO:0070182~DNA							
DIRECT	polymerase binding	6	8.97E-06			20.32713	2.56E-04	2.24E-04
GOTERM_MF_	GO:0003690~double-							
DIRECT	stranded DNA binding	10	1.26E-05			7.031398	3.41E-04	2.99E-04
GOTERM_MF_	GO:0046982~protein							
DIRECT	heterodimerization activity	18	1.43E-05			3.549182	3.71E-04	3.25E-04
GOTERM_MF_	GO:0042393~histone							
DIRECT	binding	14	1.69E-05			4.459228	4.19E-04	3.67E-04
GOTERM_MF_	GO:0003697~single-							
DIRECT	stranded DNA binding	10	1.96E-05			6.654716	4.66E-04	4.08E-04

GOTERM_MF_ DIRECT	GO:0097110~scaffold protein binding	8	4.11E-05	LYN, YWHAE, XRCC6, HSP90AA1, SYK, PLCG2, MAP3K7, PHF6	8.518036	9.37E-04	8.20E-04
GOTERM_MF_ DIRECT	GO:0003684~damaged DNA binding	8	4.51E-05	XRCC6, PCNA, MSH2, POLD1, CNTRL, BRCA1, HMGB1, NBN	8.398064	9.51E-04	8.33E-04
GOTERM_MF_ DIRECT	GO:0002039~p53 binding	8	4.51E-05	BLM, USP7, SMARCB1, KDM1A, MDM2, MDM4, BRCA1, HIF1A	8.398064	9.51E-04	8.33E-04
GOTERM_MF_ DIRECT	GO:0003712~transcriptio n coregulator activity	10	4.70E-05	KAT2B, BTG1, EWSR1, BCL11A, FUS, CNOT2, POU2AF1, HMGA1, LPXN, NFKB1	5.962625	9.56E-04	8.37E-04
GOTERM_MF_ DIRECT	GO:0017124~SH3 domain binding	10	5.00E-05	LYN, SH3BP1, INPP5D, ABI1, CCDC6, PTPN6, GRB2, SOS1, WASF2, EPS15	5.915303	9.83E-04	8.61E-04
GOTERM_MF_ DIRECT	GO:0042826~histone deacetylase binding	10	7.19E-05	YWHAE, KAT2B, SFPQ, HSP90AA1, HDAC2, PHB1, HSP90AB1, HIF1A, IKZF3, PHF6	5.646426	0.001357	0.001188
GOTERM_MF_ DIRECT	GO:0042803~protein homodimerization activity	25	7.38E-05	CEP57, TOP2A, BLM, HSP90AB1, BCL2A1, TFRC, LRRK2, TYMS, IKZF3, ATIC, TPR, NPM1, ST6GAL1, HSP90AA1, BCL11A, STAT1, CIP2A, TERF2, SFPQ, CENPF, PKM, RABEP1, MSH2, TCF3, MAD2L1	2.484427	0.001357	0.001188
GOTERM_MF_ DIRECT	GO:0001784~phosphoty rosine residue binding	7	8.11E-05	LYN, SYK, PLCG2, MAPK1, PTPN6, PTPN11, GRB2	9.661662	0.001445	0.001265
GOTERM_MF_ DIRECT	GO:0004386~helicase activity	8	9.72E-05	EIF4A2, DDX6, BLM, DDX39B, ATRX, EP400, SMARCA5, CHD2	7.453282	0.001679	0.00147
GOTERM_MF_ DIRECT	GO:0140031~phosphoryl ation-dependent protein binding	4	1.26E-04	LYN, PLCG2, PTPN6, NBN	37.26641	0.002108	0.001846
GOTERM_MF_ DIRECT	GO:0043015~gamma- tubulin binding	6	2.07E-04	OFD1, LYN, CEP57, DDX3X, ARHGEF7, CDK5RAP2	10.90724	0.003379	0.002958
GOTERM_MF_ DIRECT	GO:0004842~ubiquitin- protein transferase activity	12	2.51E-04	FANCL, UBE2C, MDM2, HUWE1, XIAP, MDM4, BIRC6, BRCA1, VHL, FBXO11, MALT1, BIRC3	3.940061	0.003971	0.003477
GOTERM_MF_ DIRECT	GO:0004715~non- membrane spanning protein tyrosine kinase activity	6	3.59E-04	LYN, WEE1, MELK, SYK, BTK, TYK2	9.721672	0.005268	0.004612
GOTERM_MF_ DIRECT	GO:0008017~microtubul e binding	13	3.67E-04	CEP57, LRRK2, IRAG2, HOOK3, NDC80, LRPPRC, EML4, CENPF, KIF5B, CCDC88C, ZNF207, EZR, CDK5RAP2	3.49793	0.005268	0.004612
GOTERM_MF_ DIRECT	GO:0004672~protein kinase activity	13	3.67E-04	MAP3K1, SYK, PRKDC, LRRK2, CAD, BUB1B, AURKA, RPS6KA3, CHEK1, CDK1, CDK12, RAF1, ATR	3.49793	0.005268	0.004612
GOTERM_MF_ DIRECT	GO:0050681~nuclear androgen receptor binding	5	3.70E-04	DDX5, KDM1A, PRKCB, CALR, FOXP1	14.33323	0.005268	0.004612
GOTERM_MF_ DIRECT	GO:0016301~kinase activity	11	4.70E-04	LYN, RPS6KA3, GIT2, PKM, SYK, PRKAR1A, CDK4, LRRK2, BTK, CDK1, CDK12	3.979908	0.00628	0.005498
GOTERM_MF_ DIRECT	GO:0030983~mismatche d DNA binding	4	4.75E-04	MSH2, MSH3, PMS2, MLH1	24.84427	0.00628	0.005498
GOTERM_MF_ DIRECT	GO:0001222~transcriptio n corepressor binding	6	4.84E-04	SUZ12, STAT1, EED, CNOT2, ETS1, EZH2	9.126468	0.00628	0.005498
GOTERM_MF_ DIRECT	GO:0004713~protein tyrosine kinase activity	8	4.96E-04	LYN, WEE1, PKM, SYK, BTK, TTK, TYK2, MAP3K7	5.733294	0.00628	0.005498
GOTERM_MF_ DIRECT	GO:0140677~molecular function activator activity	5	4.96E-04	BLM, AKT2, CAPRIN1, HMGA1, AURKA	13.30943	0.00628	0.005498
GOTERM_MF_ DIRECT	GO:0035979~histone H2AXS139 kinase activity	3	5.29E-04	PRKDC, ATM, ATR	74.53282	0.006417	0.005618
GOTERM_MF_ DIRECT	GO:0032139~dinucleotid e insertion or deletion binding	3	5.29E-04	PCNA, MSH2, MSH3	74.53282	0.006417	0.005618
GOTERM_MF_ DIRECT	GO:0008094~ATP- dependent activity, acting on DNA	5	5.69E-04	TOP2A, BLM, XRCC6, MSH2, SMARCA5	12.85049	0.006758	0.005917
GOTERM_MF_ DIRECT	GO:0061629~RNA polymerase II-specific DNA-binding transcription factor binding	10	8.50E-04	RB1, HDAC2, KDM1A, PRKDC, SP3, TCF3, HMGB1, ETS1, HIF1A, GTF2I	4.050697	0.009885	0.008654
GOTERM_MF_ DIRECT	GO:0030374~nuclear receptor coactivator activity	6	0.001055	SS18, KDM1A, PRKCB, NCOA3, HMGA1, ETS1	7.710292	0.012027	0.010529
GOTERM_MF_ DIRECT	GO:0030332~cyclin binding	5	0.001178	XRCC6, CDK4, CDK1, CDK12, NDC80	10.64755	0.013169	0.011529
GOTERM_MF_ DIRECT	GO:0043021~ribonucleo protein complex binding	5	0.001312	TOP2B, DDX5, MDM2, PHF6, EZH2	10.35178	0.01438	0.012589
GOTERM_MF_ DIRECT	GO:0044877~protein- containing complex binding	13	0.001575	XRCC6, CARMIL2, PCNA, TFRC, CLTA, TERF2, NRAS, KIF5B, KRAS, STRN, ATM, BIRC3, CDK5RAP2	2.963078	0.01694	0.01483
GOTERM_MF_ DIRECT	GO:0043047~single- stranded telomeric DNA binding	3	0.001733	RAD50, HNRNPA2B1, POT1	44.71969	0.01829	0.016011
GOTERM_MF_ DIRECT	GO:0003678~DNA helicase activity	5	0.001775	BLM, XRCC6, RAD50, DDX3X, MRE11	9.55549	0.018398	0.016107
GOTERM_MF_ DIRECT	GO:0008301~DNA binding, bending	4	0.001952	TOP2A, HMGA1, HMGB1, TOP1	15.69112	0.019864	0.01739
GOTERM_MF_ DIRECT	GO:0035591~signaling adaptor activity	6	0.002298	YWHAE, DDX3X, SYK, CAPRIN1, ABI1, GAB1	6.481115	0.022979	0.020117
GOTERM_MF_ DIRECT	GO:0003700~DNA- binding transcription factor activity	17	0.002418	XBP1, STAT1, BCL11A, IKZF1, AFF3, ETS1, HIF1A, IKZF3, FLI1, NFKB1, NFKB2, ELK4, TFDP1, IRF4, STAT6, TCF3, GTF2I	2.363914	0.023765	0.020805
GOTERM_MF_ DIRECT	GO:0032405~MutLalpha complex binding	3	0.002576	PCNA, MSH2, ATR	37.26641	0.024541	0.021484
GOTERM_MF_ DIRECT	GO:0043027~cysteine- type endopeptidase inhibitor activity involved in apoptotic process	4	0.002626	RPS6KA3, RPS6KA1, XIAP, BIRC3	14.19673	0.024541	0.021484
GOTERM_MF_ DIRECT	GO:0004709~MAP kinase kinase activity	4	0.002626	MAP3K1, LRRK2, RAF1, MAP3K7	14.19673	0.024541	0.021484

GOTERM_MF_DIRECT	GO:0140693~molecular condensate scaffold activity	5	0.002781	FUS, CAPRIN1, HNRNPA2B1, NUP98, SOS1	8.469638	0.025164	0.02203
GOTERM_MF_DIRECT	GO:0016922~nuclear receptor binding	5	0.002781	STAT1, NCOA3, BAZ2A, ARID1A, HIF1A	8.469638	0.025164	0.02203
GOTERM_MF_DIRECT	GO:0030527~structural constituent of chromatin	7	0.003157	H2BC12, H2AC11, H2BC4, HMG1, H3C2, SOS1, H2AC17	4.875979	0.028114	0.024612
GOTERM_MF_DIRECT	GO:0003724~RNA helicase activity	6	0.003503	EIF4A2, DDX6, DDX5, DDX3X, DDX39B, DDX10	5.88417	0.030721	0.026894
GOTERM_MF_DIRECT	GO:0032407~MutSalp complex binding	3	0.003575	PMS2, MLH1, ATR	31.94264	0.030874	0.027028
GOTERM_MF_DIRECT	GO:0140664~ATP-dependent DNA damage sensor activity	4	0.003881	MSH2, MSH3, PMS2, MLH1	12.42214	0.033013	0.028901
GOTERM_MF_DIRECT	GO:0023026~MHC class II protein complex binding	4	0.005445	YWHA, HSP90AA1, PKM, HSP90AB1	11.0419	0.045644	0.039958
GOTERM_MF_DIRECT	GO:000976~transcription cis-regulatory region binding	10	0.005696	XRCC6, SFPQ, XBP1, TBL1XR1, BRCA1, HMGB1, ETS1, NFKB1, FLI1, CDK5RAP2	3.054624	0.047057	0.041196
GOTERM_MF_DIRECT	GO:003691~double-stranded telomeric DNA binding	3	0.006021	XRCC6, RAD50, TERF2	24.84427	0.048338	0.042317
GOTERM_MF_DIRECT	GO:0070878~primary miRNA binding	3	0.006021	DDX5, SRSF3, EZH2	24.84427	0.048338	0.042317
GOTERM_MF_DIRECT	GO:0043539~protein serine/threonine kinase activator activity	5	0.007072	TCL1A, RAD50, DDX3X, PIM1, NBN, LYN, SYK, PRKCB, MALT1, NFKB1, CD79B, CD79A, NRAS, PPP3R1, AKT2, INPP5D, BTK, PLCG2, RAC2, MAPK1, KRAS, GRB2, PTPN6, RAF1, SOS1, CARD11	6.537967	0.055985	0.049012
KEGG_PATHWAY	hsa04662:B cell receptor signaling pathway	21	5.13E-15	RB1, YWHA, HDAC2, PCNA, PRKDC, ATRX, BUB1B, TTK, SMC3, SMC1A, NDC80, AURKB, CCNA2, WEE1, STAG2, TFDP1, CDK4, RAD21, CHEK1, MDM2, CDK1, ATM, ATR, MAD2L1	10.35533	1.26E-12	7.49E-13
KEGG_PATHWAY	hsa04110:Cell cycle	24	4.89E-13	RB1, FH, HDAC2, HSP90AB1, PTEN, XIAP, CXCR4, ETS1, HIF1A, CDC42, NRAS, AKT2, TPR, PLCG2, PIM1, RAC2, MAPK1, STAT6, VHL, HSP90AA1, TPM3, PRKCB, STAT1, NCOA3, MLH1, RHOA, NFKB1, NFKB2, EML4, CCNA2, MSH2, MSH3, CDK4, GNAS, CCDC6, MDM2, KRAS, GRB2, RAF1, SOS1, BIRC3	6.816167	6.00E-11	3.57E-11
KEGG_PATHWAY	hsa05200:Pathways in cancer	41	4.89E-12	LYN, RB1, YWHA, USP7, HDAC2, DDX3X, SYK, H2BC4, RHOA, NFKB1, NFKB2, CDC42, H2BC12, CCNA2, KAT2B, NRAS, PKM, CDK4, CHEK1, MDM2, CDK1, MAPK1, KRAS, GRB2	3.451777	3.99E-10	2.38E-10
KEGG_PATHWAY	hsa05203:Viral carcinogenesis	24	1.18E-10	RB1, MAP3K1, PTEN, XIAP, BUB1B, ETS1, NFKB1, NFKB2, ELK4, CCNA2, KAT2B, NRAS, PPP3R1, XPO1, CDK4, AKT2, CHEK1, MAPK1, KRAS, ATM, CALR, TCF3, ATR, MAD2L1	4.829392	3.16E-08	1.89E-08
KEGG_PATHWAY	hsa05166:Human T-cell leukemia virus 1 infection	24	6.46E-10	RB1, MRE11, PTEN, ETS1, NFKB1, CCNA2, NRAS, PPP3R1, RAD50, CDK4, AKT2, CHEK1, MDM2, CDK1, MAPK1, KRAS, ATM, NBN, RAF1, ATR	5.716318	6.09E-08	3.63E-08
KEGG_PATHWAY	hsa04218:Cellular senescence	20	1.49E-09	FH, GAB1, PTPN11, ETS1, HIF1A, CDC42, NRAS, AKT2, MAPK1, KRAS, GRB2, VHL, RAF1, SOS1	8.974619	1.15E-07	6.87E-08
KEGG_PATHWAY	hsa05211:Renal cell carcinoma	14	3.29E-09	YWHA, MAP3K1, GAB1, PTPN11, RHOA, NFKB1, CDC42, RPS6KA3, NRAS, AKT2, RPS6KA1, PLCG2, MAPK1, KRAS, GRB2, RAF1, SOS1	6.357022	2.33E-07	1.39E-07
KEGG_PATHWAY	hsa04660:T cell receptor signaling pathway	17	7.59E-09	PTPN11, RHOA, MALT1, NFKB1, CDC42, NRAS, PPP3R1, CDK4, AKT2, MAPK1, KRAS, GRB2, PTPN6, RAF1, SOS1, MAP3K7, CARD11	6.252809	2.64E-07	1.57E-07
KEGG_PATHWAY	hsa04664:Fc epsilon RI signaling pathway	13	2.94E-08	LYN, SYK, NRAS, AKT2, INPP5D, BTK, PLCG2, RAC2, MAPK1, KRAS, GRB2, RAF1, SOS1	8.454352	7.20E-07	4.29E-07
KEGG_PATHWAY	hsa05223:Non-small cell lung cancer	13	5.67E-08	RB1, PRKCB, EML4, NRAS, CDK4, AKT2, KIF5B, PLCG2, MAPK1, KRAS, GRB2, RAF1, SOS1	7.991099	1.26E-06	7.53E-07
KEGG_PATHWAY	hsa04625:C-type lectin receptor signaling pathway	15	6.81E-08	SYK, STAT1, PTPN11, RHOA, MALT1, NFKB1, NFKB2, NRAS, PPP3R1, AKT2, MDM2, PLCG2, MAPK1, KRAS, RAF1	6.410442	1.39E-06	8.29E-07
KEGG_PATHWAY	hsa05214:Glioma	13	9.03E-08	RB1, PRKCB, PTEN, NRAS, CDK4, AKT2, MDM2, PLCG2, MAPK1, KRAS, GRB2, RAF1, SOS1	7.675661	1.70E-06	1.01E-06
KEGG_PATHWAY	hsa05220:Chronic myeloid leukemia	13	1.05E-07	RB1, HDAC2, PTPN11, NFKB1, NRAS, CDK4, AKT2, MDM2, MAPK1, KRAS, GRB2, RAF1, SOS1	7.575977	1.73E-06	1.03E-06
KEGG_PATHWAY	hsa05161:Hepatitis B	18	1.06E-07	RB1, DDX3X, MAP3K1, PCNA, PRKCB, STAT1, TYK2, NFKB1, CCNA2, NRAS, AKT2, MAPK1, KRAS, GRB2, STAT6, RAF1, SOS1, MAP3K7	4.955311	1.73E-06	1.03E-06
KEGG_PATHWAY	hsa04064:NF-kappa B signaling pathway	14	4.91E-07	LYN, SYK, BCL2A1, PRKCB, XIAP, MALT1, NFKB1, NFKB2, BTK, PLCG2, ATM, MAP3K7, CARD11, BIRC3	5.98308	7.52E-06	4.48E-06
KEGG_PATHWAY	hsa05205:Proteoglycans in cancer	19	5.63E-07	DDX5, PRKCB, GAB1, PTPN11, HIF1A, RHOA, CDC42, NRAS, AKT2, MDM2, PLCG2, MAPK1, KRAS, GRB2, PTPN6, EZR, RAF1, SOS1, CD44	4.179357	8.11E-06	4.83E-06
KEGG_PATHWAY	hsa05235:PD-L1 expression and PD-1 checkpoint pathway in cancer	13	6.08E-07	STAT1, PTEN, PTPN11, HIF1A, NFKB1, EML4, NRAS, PPP3R1, AKT2, MAPK1, KRAS, PTPN6, RAF1	6.481669	8.27E-06	4.93E-06
KEGG_PATHWAY	hsa01524:Platinum drug resistance	12	6.83E-07	TOP2A, TOP2B, MSH2, MSH3, AKT2, MDM2, MAPK1, XIAP, ATM, BRCA1, MLH1, BIRC3	7.179695	8.80E-06	5.24E-06
KEGG_PATHWAY	hsa01521:EGFR tyrosine kinase inhibitor resistance	12	1.33E-06	NRAS, PRKCB, AKT2, PTEN, GAB1, PLCG2, MAPK1, KRAS, GRB2, RAF1, SOS1, EIF4E	6.730964	1.62E-05	9.68E-06
KEGG_PATHWAY	hsa05206:MicroRNAs in cancer	23	1.43E-06	DNMT1, HDAC2, PRKCB, PTEN, BRCA1, RHOA, NFKB1, FOXF1, NRAS, CCNG1, MDM2, PIM1, PLCG2, MAPK1, MDM4, KRAS, GRB2, ATM, EZR, RAF1, SOS1, CD44, EZH2	3.307953	1.67E-05	9.96E-06
KEGG_PATHWAY	hsa05215:Prostate cancer	13	1.54E-06	RB1, HSP90AA1, HSP90AB1, PTEN, NFKB1, NRAS, AKT2, MDM2, MAPK1, KRAS, GRB2, RAF1, SOS1	5.952554	1.72E-05	1.02E-05
KEGG_PATHWAY	hsa05221:Acute myeloid leukemia	11	2.17E-06	CCNA2, NRAS, BCL2A1, AKT2, PIM1, MAPK1, KRAS, GRB2, RAF1, SOS1, NFKB1	7.258883	2.31E-05	1.38E-05
KEGG_PATHWAY	hsa05169:Epstein-Barr virus infection	18	2.42E-06	LYN, RB1, USP7, HDAC2, SYK, STAT1, TYK2, NFKB1, NFKB2, CCNA2, CDK4, AKT2, MDM2, BTK, PLCG2, CALR, MAP3K7, CD44	3.978895	2.47E-05	1.47E-05
KEGG_PATHWAY	hsa05210:Colorectal cancer	12	3.09E-06	NRAS, MSH2, MSH3, AKT2, RAC2, MAPK1, KRAS, GRB2, MLH1, RAF1, SOS1, RHOA	6.189393	3.03E-05	1.81E-05
KEGG_PATHWAY	hsa05170:Human immunodeficiency virus 1 infection	18	4.68E-06	PRKCB, CXCR4, NFKB1, WEE1, NRAS, PPP3R1, AKT2, CHEK1, CDK1, PLCG2, RAC2, MAPK1, KRAS, ATM, CALR, RAF1, MAP3K7, ATR	3.792093	4.41E-05	2.63E-05

KEGG_PATHWAY	hsa05202:Transcriptional misregulation in cancer	17	5.53E-06	SS18, DDX5, HDAC2, BCL2A1, FUS, PAX5, FLI1, NFKB1, ELK4, CCNA2, EWSR1, NSD2, MDM2, ATM, H3C2, TCF3, BIRC3	3.952553	5.02E-05	2.99E-05
KEGG_PATHWAY	hsa04370:VEGF signaling pathway	10	5.99E-06	CDC42, NRAS, PPP3R1, PRKCB, AKT2, PLCG2, RAC2, MAPK1, KRAS, RAF1	7.478849	5.25E-05	3.13E-05
KEGG_PATHWAY	hsa05163:Human cytomegalovirus infection	18	1.03E-05	RB1, PRKCB, CXCR4, RHOA, NFKB1, NRAS, PPP3R1, CDK4, AKT2, MDM2, RAC2, GNAS, MAPK1, KRAS, GRB2, CALR, RAF1, SOS1	3.573963	8.71E-05	5.19E-05
KEGG_PATHWAY	hsa01522:Endocrine resistance	12	1.10E-05	RB1, NRAS, CDK4, AKT2, NCOA3, MDM2, GNAS, MAPK1, KRAS, GRB2, RAF1, SOS1	5.439163	9.02E-05	5.38E-05
KEGG_PATHWAY	hsa04919:Thyroid hormone signaling pathway	13	1.55E-05	HDAC2, PRKCB, STAT1, NCOA3, HIF1A, KAT2B, NRAS, AKT2, MDM2, PLCG2, MAPK1, KRAS, RAF1	4.781559	1.22E-04	7.30E-05
KEGG_PATHWAY	hsa04014:Ras signaling pathway	18	2.02E-05	PRKCB, RASGRF1, GAB1, PTPN11, RASAL1, ETS1, RHOA, NFKB1, CDC42, NRAS, AKT2, PLCG2, RAC2, MAPK1, KRAS, GRB2, RAF1, SOS1	3.393764	1.55E-04	9.22E-05
KEGG_PATHWAY	hsa05207:Chemical carcinogenesis - receptor activation	17	2.17E-05	RB1, HSP90AA1, HSP90AB1, PRKCB, XIAP, NFKB1, RPS6KA3, NRAS, AKT2, RPS6KA1, GNAS, MAPK1, KRAS, GRB2, RAF1, SOS1, KPNB1	3.548105	1.61E-04	9.58E-05
KEGG_PATHWAY	hsa04613:Neutrophil extracellular trap formation	16	2.23E-05	HDAC2, SYK, PRKCB, H2BC4, HMGB1, H2AC17, NFKB1, H2AC11, H2BC12, AKT2, PLCG2, RAC2, MAPK1, H3C2, RAF1, MAP3K7	3.739425	1.61E-04	9.58E-05
KEGG_PATHWAY	hsa05225:Hepatocellular carcinoma	15	2.35E-05	RB1, SMARCB1, PRKCB, PTEN, GAB1, ARID1A, NRAS, CDK4, AKT2, PLCG2, MAPK1, KRAS, GRB2, RAF1, SOS1	3.959391	1.61E-04	9.62E-05
KEGG_PATHWAY	hsa04062:Chemokine signaling pathway	16	2.37E-05	LYN, PRKCB, STAT1, CXCR4, RHOA, NFKB1, CDC42, NRAS, AKT2, PLCG2, RAC2, MAPK1, KRAS, GRB2, RAF1, SOS1	3.720049	1.61E-04	9.62E-05
KEGG_PATHWAY	hsa03460:Fanconi anemia pathway	9	2.52E-05	FANCI, BLM, FANCL, FANCD2, FANCA, PMS2, BRCA1, MLH1, ATR	7.34287	1.67E-04	9.96E-05
KEGG_PATHWAY	hsa04650:Natural killer cell mediated cytotoxicity	13	2.95E-05	SYK, PRKCB, PTPN11, NRAS, PPP3R1, PLCG2, RAC2, MAPK1, KRAS, GRB2, PTPN6, RAF1, SOS1	4.48731	1.90E-04	1.13E-04
KEGG_PATHWAY	hsa04914:Progesterone-mediated oocyte maturation	12	3.29E-05	CCNA2, RPS6KA3, HSP90AA1, HSP90AB1, AKT2, RPS6KA1, CDK1, MAPK1, KRAS, RAF1, MAD2L1, AURKA	4.851146	2.07E-04	1.23E-04
KEGG_PATHWAY	hsa05213:Endometrial cancer	9	4.26E-05	NRAS, AKT2, PTEN, MAPK1, KRAS, GRB2, MLH1, RAF1, SOS1	6.845049	2.61E-04	1.55E-04
KEGG_PATHWAY	hsa05165:Human papillomavirus infection	21	4.67E-05	RB1, HDAC2, STAT1, PTEN, TYK2, NFKB1, CDC42, CCNA2, NRAS, PKM, CDK4, AKT2, MDM2, GNAS, MAPK1, KRAS, GRB2, ATM, RAF1, SOS1, ATR	2.829835	2.76E-04	1.64E-04
KEGG_PATHWAY	hsa05212:Pancreatic cancer	10	4.73E-05	RB1, CDC42, STAT1, CDK4, AKT2, RAC2, MAPK1, KRAS, RAF1, NFKB1	5.827675	2.76E-04	1.64E-04
KEGG_PATHWAY	hsa04666:Fc gamma R-mediated phagocytosis	11	5.87E-05	LYN, CDC42, SYK, PRKCB, AKT2, INPP5D, PLCG2, RAC2, MAPK1, RAF1, WASF2	5.036776	3.34E-04	1.99E-04
KEGG_PATHWAY	hsa05231:Choline metabolism in cancer	11	6.41E-05	NRAS, PRKCB, AKT2, RAC2, MAPK1, KRAS, GRB2, RAF1, SOS1, HIF1A, WASF2	4.9859	3.57E-04	2.13E-04
KEGG_PATHWAY	hsa04933:AGE-RAGE signaling pathway in diabetic complications	11	7.60E-05	CDC42, NRAS, STAT1, PRKCB, CDK4, AKT2, PLCG2, PIM1, MAPK1, KRAS, NFKB1	4.887169	4.14E-04	2.47E-04
KEGG_PATHWAY	hsa04935:Growth hormone synthesis, secretion and action	12	7.89E-05	NRAS, MAP3K1, STAT1, PRKCB, AKT2, PLCG2, GNAS, MAPK1, KRAS, GRB2, RAF1, SOS1	4.413747	4.20E-04	2.50E-04
KEGG_PATHWAY	hsa05224:Breast cancer	13	1.05E-04	RB1, NCOA3, PTEN, BRCA1, NFKB2, NRAS, CDK4, AKT2, MAPK1, KRAS, GRB2, RAF1, SOS1	3.941556	5.49E-04	3.27E-04
KEGG_PATHWAY	hsa05167:Kaposi sarcoma-associated herpesvirus infection	15	1.12E-04	LYN, RB1, SYK, STAT1, TYK2, HIF1A, NFKB1, NRAS, PPP3R1, CDK4, AKT2, PLCG2, MAPK1, KRAS, RAF1	3.434166	5.56E-04	3.31E-04
KEGG_PATHWAY	hsa04072:Phospholipase D signaling pathway	13	1.12E-04	SYK, GAB1, PTPN11, RHOA, NRAS, AKT2, PLCG2, GNAS, MAPK1, KRAS, GRB2, RAF1, SOS1	3.915102	5.56E-04	3.31E-04
KEGG_PATHWAY	hsa04012:ErbB signaling pathway	10	1.13E-04	NRAS, PRKCB, AKT2, GAB1, PLCG2, MAPK1, KRAS, GRB2, RAF1, SOS1, MAP3K1, PRKCB, RASGRF1, NFKB1, NFKB2, CDC42, ELK4, RPS6KA3, NRAS, PPP3R1, AKT2, RPS6KA1, RAC2, MAPK1, KRAS, GRB2, RAF1, SOS1, MAP3K7	5.217802	5.56E-04	3.31E-04
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	19	1.16E-04	PCNA, MSH2, MSH3, POLD1, PMS2, MLH1	2.841963	5.57E-04	3.32E-04
KEGG_PATHWAY	hsa03430:Mismatch repair	6	1.24E-04	FNBP1, SEPTIN2, SEPTIN6, U2AF1, RHOA, MALT1, NFKB1, CDC42, AKT2, MDM2, PLCG2, MAPK1, ATM, H3C2, MAP3K7, WASF2, CD44	11.70603	5.83E-04	3.47E-04
KEGG_PATHWAY	hsa05131:Shigellosis	17	1.27E-04	USP7, NRAS, PRMT1, AKT2, PTEN, MDM2, MAPK1, KRAS, GRB2, ATM, RAF1, SOS1	3.063625	5.85E-04	3.49E-04
KEGG_PATHWAY	hsa04068:FoxO signaling pathway	12	1.61E-04	RAF1, SOS1	4.079372	7.12E-04	4.25E-04
KEGG_PATHWAY	hsa04917:Prolactin signaling pathway	9	1.63E-04	NRAS, STAT1, AKT2, MAPK1, KRAS, GRB2, RAF1, SOS1, NFKB1	5.688139	7.12E-04	4.25E-04
KEGG_PATHWAY	hsa05230:Central carbon metabolism in cancer	9	1.63E-04	NRAS, PKM, AKT2, IDH2, PTEN, MAPK1, KRAS, RAF1, HIF1A	5.688139	7.12E-04	4.25E-04
KEGG_PATHWAY	hsa04150:mTOR signaling pathway	13	1.96E-04	PRKCB, PTEN, RHOA, RPS6KA3, NRAS, AKT2, RPS6KA1, MAPK1, KRAS, GRB2, RAF1, SOS1, EIF4E	3.69209	8.37E-04	4.99E-04
KEGG_PATHWAY	hsa05218:Melanoma	9	1.98E-04	RB1, NRAS, CDK4, AKT2, PTEN, MDM2, MAPK1, KRAS, RAF1	5.5323	8.37E-04	4.99E-04
KEGG_PATHWAY	hsa04912:GnRH signaling pathway	10	2.08E-04	CDC42, NRAS, MAP3K1, PRKCB, GNAS, MAPK1, KRAS, GRB2, RAF1, SOS1	4.825064	8.49E-04	5.06E-04
KEGG_PATHWAY	hsa05160:Hepatitis C	13	2.08E-04	RB1, YWHA, STAT1, TYK2, NFKB1, NRAS, CDK4, AKT2, MAPK1, KRAS, GRB2, RAF1, SOS1	3.66887	8.49E-04	5.06E-04
KEGG_PATHWAY	hsa05135:Yersinia infection	12	2.38E-04	CDC42, RPS6KA3, GIT2, AKT2, RPS6KA1, RAC2, MAPK1, ARHGEF7, WASF2, MAP3K7, RHOA, NFKB1	3.902008	9.46E-04	5.64E-04
KEGG_PATHWAY	hsa04115:p53 signaling pathway	9	2.39E-04	CDK4, CCNG1, CHEK1, PTEN, MDM2, CDK1, MDM4, ATM, ATR	5.384772	9.46E-04	5.64E-04
KEGG_PATHWAY	hsa03440:Homologous recombination	7	2.59E-04	BLM, RAD50, MRE11, POLD1, ATM, BRCA1, NBN	7.66126	9.92E-04	5.91E-04
KEGG_PATHWAY	hsa05219:Bladder cancer	7	2.59E-04	RB1, NRAS, CDK4, MDM2, MAPK1, KRAS, RAF1	7.66126	9.92E-04	5.91E-04
KEGG_PATHWAY	hsa04380:Osteoclast differentiation	12	3.05E-04	PPP3R1, SYK, STAT1, AKT2, BTK, PLCG2, MAPK1, GRB2, TYK2, MAP3K7, NFKB1, NFKB2	3.792093	0.00115	6.85E-04
KEGG_PATHWAY	hsa04659:Th17 cell differentiation	10	6.35E-04	HSP90AA1, PPP3R1, HSP90AB1, STAT1, IRF4, MAPK1, STAT6, TYK2, HIF1A, NFKB1	4.154916	0.002358	0.001405
KEGG_PATHWAY	hsa04720:Long-term potentiation	8	6.68E-04	RPS6KA3, NRAS, PPP3R1, PRKCB, RPS6KA1, MAPK1, KRAS, RAF1	5.357982	0.002443	0.001456

KEGG_PATHWAY				HDAC2, H2BC4, H2AC17, H2AC11, H2BC12, NRAS, GNAS, MAPK1, KRAS, GRB2, H3C2, RAF1, SOS1	3.102927	0.003405	0.002029
AY	hsa05034:Alcoholism	13	9.49E-04				
KEGG_PATHWAY				NRAS, PRKCB, CDK1, GNAS, MAPK1, KRAS, GRB2, RAF1, SOS1	4.389759	0.003405	0.002029
AY	hsa04540:Gap junction	9	9.59E-04				
KEGG_PATHWAY				LYN, XBP1, HSP90AA1, HSP90AB1, HSPA4, RHOA, NFKB1, CDC42, NRAS, PPP3R1, AKT2, MAPK1, KRAS, MAP3K7	2.908441	0.003515	0.002094
AY	hsa05417:Lipid and atherosclerosis	14	0.001013				
KEGG_PATHWAY				HSP90AA1, NRAS, HSP90AB1, AKT2, NCOA3, GNAS, MAPK1, KRAS, GRB2, RAF1, SOS1	3.551108	0.003515	0.002094
AY	hsa04915:Estrogen signaling pathway	11	0.001019				
KEGG_PATHWAY				H2AC11, SS18, HDAC2, SMARCB1, EP400, SMARCA5, BAZ2A, ARID1A, PHF6, H2AC17	3.835307	0.003847	0.002292
AY	hsa03082:ATP-dependent chromatin remodeling	10	0.001131				
KEGG_PATHWAY				NRAS, TPM3, TPR, CCD6, MAPK1, KRAS	7.276718	0.004183	0.002493
AY	hsa05216:Thyroid cancer	6	0.001246				
KEGG_PATHWAY				NRAS, PRKCB, AKT2, PTEN, RAC2, MAPK1, KRAS, RAF1, RHOA, NFKB1	3.678123	0.005028	0.002996
AY	hsa04071:Sphingolipid signaling pathway	10	0.001519				
KEGG_PATHWAY							
AY	hsa05100:Bacterial invasion of epithelial cells	8	0.001654				
KEGG_PATHWAY				CDC42, SEPTIN2, CLTC, GAB1, SEPTIN6, CLTA, WASF2, RHOA, CYFIP2, CXCR4, RHOA, CDC42, NRAS, AKT2, RAC2, MAPK1, KRAS, EZR, RAF1, ARHGEF7, SOS1, WASF2	4.602369	0.005402	0.003219
AY	hsa04810:Regulation of actin cytoskeleton	14	0.001789				
KEGG_PATHWAY				PRKCB, RASGRF1, PTEN, XIAP, RHOA, CDC42, AKT2, RAC2, MAPK1, GRB2, RAF1, SOS1, BIRC3	2.731406	0.005766	0.003436
AY	hsa04510:Focal adhesion	13	0.001834				
KEGG_PATHWAY							
AY	hsa04730:Long-term depression	7	0.002037				
KEGG_PATHWAY				LYN, NRAS, PRKCB, GNAS, MAPK1, KRAS, RAF1	2.873647	0.005837	0.003478
AY	hsa03450:Non-homologous end-joining	4	0.002605				
KEGG_PATHWAY				XRCC6, RAD50, MRE11, PRKDC	5.235195	0.006397	0.003812
AY	hsa04151:PI3K-Akt signaling pathway	18	0.00278				
KEGG_PATHWAY				YWHAE, HSP90AA1, HSP90AB1, SYK, PTEN, BRCA1, NFKB1, TCL1A, NRAS, CDK4, AKT2, MDM2, MAPK1, KRAS, GRB2, RAF1, SOS1, EIF4E	13.80711	0.00808	0.004815
AY	hsa04066:ILF-1 signaling pathway	9	0.002844				
KEGG_PATHWAY				TFRC, PRKCB, AKT2, PLCG2, MAPK1, VHL, HIF1A, EIF4E, NFKB1	2.231259	0.008513	0.005073
AY	hsa04210:Apoptosis	10	0.003198				
KEGG_PATHWAY				NRAS, BCL2A1, AKT2, MAPK1, XIAP, KRAS, ATM, RAF1, NFKB1, BIRC3	3.705118	0.008602	0.005126
AY	hsa04114:Oocyte meiosis	10	0.003699				
KEGG_PATHWAY				YWHAE, RPS6KA3, PPP3R1, RPS6KA1, CDK1, MAPK1, SMC1A, SMC3, MAD2L1, AURKA	3.299492	0.009554	0.005693
AY	hsa04630:JAK-STAT signaling pathway	11	0.004139				
KEGG_PATHWAY				STAT1, AKT2, PIM1, PTPN6, PTPN11, GRB2, STAT6, TYK2, RAF1, SOS1, PTPN2	3.22828	0.010919	0.006507
AY	hsa04120:Ubiquitin mediated proteolysis	10	0.00426				
KEGG_PATHWAY				MAP3K1, FANCL, UBE2C, MDM2, HUWE1, XIAP, BIRC6, BRCA1, VHL, BIRC3	2.938119	0.012073	0.007194
AY	hsa05226:Gastric cancer	10	0.006085				
KEGG_PATHWAY				RB1, NRAS, AKT2, GAB1, MAPK1, KRAS, GRB2, MLH1, RAF1, SOS1	3.160077	0.012279	0.007317
AY	hsa04360:Axon guidance	11	0.007749				
KEGG_PATHWAY				CDC42, NRAS, PPP3R1, PLCG2, RAC2, MAPK1, CXCR4, PTPN11, KRAS, RAF1, RHOA	2.99154	0.017335	0.01033
AY	hsa04926:Relaxin signaling pathway	9	0.008212				
KEGG_PATHWAY				NRAS, AKT2, GNAS, MAPK1, KRAS, GRB2, RAF1, SOS1, NFKB1	2.682631	0.021822	0.013004
AY	hsa04217:Necroptosis	10	0.008802				
KEGG_PATHWAY				H2AC11, HSP90AA1, HSP90AB1, STAT1, XIAP, STAT6, TYK2, HMGB1, H2AC17, BIRC3	3.106599	0.022864	0.013625
AY	hsa04621:NOD-like receptor signaling pathway	11	0.009303				
KEGG_PATHWAY				YWHAE, HSP90AA1, HSP90AB1, STAT1, MAPK1, XIAP, TYK2, MAP3K7, RHOA, NFKB1, BIRC3	2.822207	0.02423	0.014439
AY	hsa05132:Salmonella infection	13	0.009949				
KEGG_PATHWAY				CYFIP2, HSP90AA1, HSP90AB1, RHOA, NFKB1, CDC42, AKT2, KIF5B, ABI1, MAPK1, RAF1, MAP3K7, BIRC3	2.611662	0.025325	0.015091
AY	hsa03083:Polycomb repressive complex	7	0.010106				
KEGG_PATHWAY				SUZ12, USP7, HDAC2, TFDP1, EED, AURKB, EZH2	2.324105	0.026786	0.015962
AY	hsa05145:Toxoplasmosis	8	0.011557				
KEGG_PATHWAY				STAT1, AKT2, MAPK1, XIAP, TYK2, MAP3K7, NFKB1, BIRC3	3.784478	0.026913	0.016038
AY	hsa04910:Insulin signaling pathway	9	0.011559				
KEGG_PATHWAY				NRAS, PRKAR1A, AKT2, MAPK1, KRAS, GRB2, RAF1, SOS1, EIF4E	3.234097	0.030126	0.017953
AY	hsa05208:Chemical carcinogenesis - reactive oxygen species	12	0.011791				
KEGG_PATHWAY				NRAS, AKT2, PTEN, MAPK1, PTPN11, KRAS, GRB2, COX6C, RAF1, SOS1, HIF1A, NFKB1	2.926506	0.030126	0.017953
AY	hsa04140:Autophagy - animal	10	0.012817				
KEGG_PATHWAY				NRAS, AKT2, PTEN, MAPK1, KRAS, BIRC6, HMGB1, RAF1, HIF1A, MAP3K7	2.382642	0.030408	0.018121
AY	hsa05164:Influenza A	10	0.01425				
KEGG_PATHWAY				XPO1, STAT1, PRKCB, CDK4, AKT2, MAPK1, NUP98, TYK2, RAF1, NFKB1	2.655213	0.03271	0.019492
AY	hsa04929:GnRH secretion	6	0.014358				
KEGG_PATHWAY				NRAS, PRKCB, AKT2, MAPK1, KRAS, RAF1	2.608901	0.035822	0.021347
AY	hsa04670:Leukocyte transendothelial migration	8	0.014475				
KEGG_PATHWAY				CDC42, PRKCB, PLCG2, RAC2, CXCR4, PTPN11, EZR, RHOA	4.142132	0.035822	0.021347
AY	hsa05130:Pathogenic Escherichia coli infection	11	0.014827				
KEGG_PATHWAY				CDC42, CYFIP2, ABI1, MAPK1, PTPN6, PTPN11, EZR, WASF2, MAP3K7, RHOA, NFKB1	3.094696	0.035822	0.021347
AY	hsa04520:Adherens junction	7	0.017038				
KEGG_PATHWAY				CDC42, RAC2, MAPK1, PTPN6, WASF2, MAP3K7, RHOA	2.431547	0.036326	0.021647
AY	hsa05222:Small cell lung cancer	7	0.017038				
KEGG_PATHWAY				RB1, CDK4, AKT2, PTEN, XIAP, NFKB1, BIRC3	3.377545	0.040925	0.024388
AY	hsa04611:Platelet activation	8	0.020995				
KEGG_PATHWAY				LYN, SYK, AKT2, BTK, PLCG2, GNAS, MAPK1, RHOA	3.377545	0.040925	0.024388
AY	hsa05140:Leishmaniasis	6	0.027813				
KEGG_PATHWAY				STAT1, PRKCB, MAPK1, PTPN6, MAP3K7, NFKB1	2.871878	0.049939	0.02976
AY	hsa04931:Insulin resistance	7	0.033968				
KEGG_PATHWAY				RPS6KA3, PRKCB, AKT2, RPS6KA1, PTEN, PTPN11, NFKB1	3.496605	0.065521	0.039045
AY	hsa04714:Thermogenesis	11	0.036098				
UP_KW_BIOLOGICAL_PROCESSES	KW-0131~Cell cycle	51	1.75E-18				
UP_KW_BIOLOGICAL_PROCESSES	KW-0945~Host-virus interaction	47	1.85E-15				

UP_KW_BIOLOGICAL_PROCESS	KW-0234~DNA repair	29	4.40E-11	RAD50, ABI1, HNRNPA2B1, CDK1, MDM2, GRB2, NUP98, CDK12, TOP1, KPNB1	4.493721	1.07E-09	8.94E-10
				BLM, FH, MRE11, PCNA, PRKDC, HMGB1, BRCA1, SMC3, POLD1, RAD21, CHEK1, PMS2, NBN, FANCI, USP7, XRCC6, FANCL, NONO, ATRX, HUWE1, FANCA, MLH1, SMC1A, SFPQ, RAD50, MSH2, FANCD2, MSH3, ATR			
				BLM, FH, MRE11, PCNA, PRKDC, HMGB1, BRCA1, SMC3, POLD1, RAD21, CHEK1, PMS2, NBN, FANCI, USP7, XRCC6, FANCL, NONO, ATRX, HUWE1, FANCA, CIP2A, MLH1, SMC1A, SFPQ, RAD50, MSH2, FANCD2, MSH3, ATM, ATR			
				CLTC, CLTA, BUB1B, SMC3, CDC73, AURKB, AURKA, RAD21, TPR, CNTRL, ZNF207, YTHDF2, UBE2C, SEPTIN2, SEPTIN6, SMC1A, RHOA, NDC80, EML4, CCNA2, CENPF, WEE1, STAG2, CDK4, CCNG1, CDK1, TACC3, BIRC6, MAPRE1, MAD2L1			
				CLTC, CLTA, BUB1B, SMC3, AURKB, AURKA, RAD21, TPR, ZNF207, YTHDF2, UBE2C, SEPTIN2, SMC1A, NDC80, EML4, CCNA2, CENPF, WEE1, STAG2, CCNG1, CDK1, TACC3, BIRC6, MAPRE1, MAD2L1			
UP_KW_BIOLOGICAL_PROCESS	KW-0132~Cell division	30	2.29E-10	CLTC, CLTA, BUB1B, SMC3, AURKB, AURKA, RAD21, TPR, ZNF207, YTHDF2, UBE2C, SEPTIN2, SMC1A, NDC80, EML4, CCNA2, CENPF, WEE1, STAG2, CCNG1, CDK1, TACC3, BIRC6, MAPRE1, MAD2L1	4.04813	3.34E-09	2.79E-09
UP_KW_BIOLOGICAL_PROCESS	KW-0498~Mitosis	25	3.12E-10	CLTC, CLTA, BUB1B, SMC3, AURKB, AURKA, RAD21, TPR, ZNF207, YTHDF2, UBE2C, SEPTIN2, SMC1A, NDC80, EML4, CCNA2, CENPF, WEE1, STAG2, CCNG1, CDK1, TACC3, BIRC6, MAPRE1, MAD2L1	4.829105	3.80E-09	3.17E-09
UP_KW_BIOLOGICAL_PROCESS	KW-0090~Biological rhythms	13	1.34E-05	TOP2A, USP7, DDX5, HDAC2, PRKDC, NONO, HUWE1, NFKB2, KAT2B, SFPQ, CDK1, TOP1, EZH2	4.888342	1.40E-04	1.17E-04
UP_KW_BIOLOGICAL_PROCESS	KW-0805~Transcription regulation	66	1.37E-04	RB1, SMARCB1, DDX3X, KDM1A, BRCA1, IKZF1, AFF3, CHD2, IKZF3, ETS1, PHF6, CDC73, ELK4, MAP3K7, GTF2I, SS18, EED, PRKCB, NCOA3, ATRX, PAX5, ARID1A, FOXF1, KAT2B, SFPQ, TFDPI, IRF4, EWSR1, TBL1XR1, SARNP, BTK, IRF8, DDX5, DNMT1, HDAC2, BAZ2A, HIF1A, NSD3, CUX1, RAD21, NSD2, LPXN, MAPK1, STAT6, SUZ12, CENPU, XBP1, XRCC6, UTP4, BCL11A, STAT1, NONO, HMGA1, FLI1, LRPPRC, NFKB1, NFKB2, NACA, POU2AF1, CNOT2, SP3, TCEA1, TCF3, MNAT1, FRYL, EZH2	1.542113	0.001249	0.001043
				NUP107, XPO1, DDX39B, SARNP, TPR, HNRNPA2B1, SRSF3, NUP98, EIF4E, LRPPRC			
				CYFIP2, XBP1, DDX3X, BCL2A1, PRKCB, FAF1, PTEN, XIAP, BUB1B, NFKB1, MELK, RABEP1, AKT2, INPP5D, RAD21, MDM2, PIM1, BTK, CDK1, MAPK1, BIRC6, MAP3K7, BIRC3			
				RB1, SMARCB1, DDX3X, KDM1A, BRCA1, IKZF1, AFF3, CHD2, IKZF3, ETS1, PHF6, CDC73, ELK4, MAP3K7, GTF2I, SS18, EED, PRKCB, NCOA3, ATRX, PAX5, ARID1A, FOXF1, KAT2B, SFPQ, TFDPI, IRF4, EWSR1, TBL1XR1, SARNP, BTK, IRF8, DDX5, DNMT1, HDAC2, BAZ2A, HIF1A, NSD3, CUX1, RAD21, NSD2, LPXN, MAPK1, STAT6, SUZ12, CENPU, XBP1, XRCC6, UTP4, BCL11A, STAT1, NONO, HMGA1, FLI1, LRPPRC, NFKB1, NFKB2, NACA, POU2AF1, CNOT2, SP3, TCEA1, TCF3, MNAT1, FRYL, EZH2			
				DDX5, MBNL1, NONO, U2AF1, PTBP1, SFPQ, DDX39B, U2AF2, HNRNPA2B1, SRSF2, SRSF3, CDK12, SF3B1			
UP_KW_BIOLOGICAL_PROCESS	KW-0509~mRNA transport	10	2.51E-04	RB1, CYFIP2, PHB1, MRE11, NUP107, SMARCB1, KDM1A, BUB1B, IKZF1, SMC3, MKI67, IKZF3, ETS1, H2AC17, H2AC11, ELK4, RPS6KA3, TCL1A, AKT2, RPS6KA1, CHEK1, ZNF207, PIM1, NBN, GTF2I, MBNL1, USP7, PRKCB, IRAG2, FBXO11, FOXF1, MSH2, DDX39B, EWSR1, TBL1XR1, FANCD2, SARNP, SRSF2, BTK, SRSF3, NUP98, RAF1, KPNB1, DDX6, DDX5, BLM, DNMT1, SET, CBF8, PRKDC, BAZ2A, HIF1A, PDCD11, PCBP1, RAD21, TPR, EP400, LPXN, H3C2, FANCI, LYN, XBP1, XRCC6, CPSF6, FANCL, BCL11A, FUS, NONO, SMARCA5, HMGA1, FANCA, FLI1, NDC80, NFKB1, NFKB2, STAG2, NACA, CDK4, CNOT2, SP3, MDM2, CDK1, GRB2, MDM4, ATM, TCF3, CDK12, MNAT1, ATR, EZH2, PICALM, YWHAE, CEP57, TOP2A, TOP2B, DDX3X, HSP90AB1, FAF1, PTEN, HMGB1, BRCA1, AFF3, CHD2, PHF6, CDC73, PTBP1, XPO1, ZC3H7A, CNTRL, OFD1, SS18, HSP90AA1, EED, PRMT1, NCOA3, CAD, ATRX, PAX5, SMC1A, ARID1A, TERF2, RHOA, CCNA2, H2BC12, KAT2B, SFPQ, TFDPI, PKM, IRF4, POT1, IRF8, TOP1, PFDN5, BIRC3, FH, HDAC2, PCNA, RAP1GDS1, XIAP, U2AF1, TYMS, MALT1, AURKB, NSD3, SH3BP1, FIP1L1, CUX1, U2AF2, POLD1, NSD2, PMS2, MAPK1, STAT6, VHL, SF3B1, EIF4E, SUZ12, CENPU, NPM1, YTHDF2, UTP4, STAT1, H2BC4, HUWE1, PTPN11, DEK, MLH1, LRPPRC, CENPF, WEE1, RAD50, POU2AF1, ABI1, HNRNPA2B1, CCNG1, TCEA1, PTPN6, PTPN2, MAD2L1	4.739827	0.001988	0.001661
				MRE11, NUP107, KDM1A, BUB1B, BRCA1, HMGB1, SMC3, MKI67, PHF6, H2AC17, H2AC11, CNTRL, CHEK1, ZNF207, NBN, USP7, EED, ATRX, IRAG2, CIP2A, SMC1A, FBXO11, TERF2, H2BC12, MSH2, POT1, FH, AURKB, NSD3, RAD21, TPR, NSD2, H3C2, CENPU, XRCC6, UTP4, BCL11A, SEPTIN2, NONO, H2BC4, SMARCA5, HMGA1, SEPTIN6, MLH1, NDC80, CENPF, RAD50, STAG2, ATR, MAD2L1			
				CYFIP2, PHB1, BUB1B, IKZF1, MSI2, IKZF3, ETS1, RPS6KA3, TCL1A, AKT2, KIF5B, FGFR1OP2, RPS6KA1, CHEK1, ZNF207, PIM1, MAP3K7, GTF2I, CDK5RAP2, MBNL1, USP7, TPM3, FNBP1, PRKCB, COG5, RPL22, IRAG2, EML4, DDX39B, EWSR1, BTK, SRSF3, EZR, RAF1, CARD11, KPNB1, DDX6, DDX5, SET, GMPS, HIF1A, PPP3R1, INPP5D, PCBP1, RAD21, TPR, LPXN, FANCI, LYN, CARMIL2, XBP1, STIL, CPSF6, FANCL, BCL11A, HSPA4, FANCA, HOOK3, NFKB1, NFKB2, NACA, CDK4, CAPRIN1, CNOT2, CCDC88C, MDM2, CDK1, GRB2, STRN, ATM, CALR, RPS21, YWHAE, CEP57, TOP2A, DDX3X, HSP90AB1, WDR1, LRRK2, CLTC, PTEN, CLTA, HMGB1, BRCA1, LASP1, XPO1, ATIC, CNTRL, RAC2, OFD1, HSP90AA1, SYK, PRMT1, NCOA3, CAD, CIP2A, RHOA, CCNA2, KAT2B, SFPQ, TFDPI, RABEP1, PKM, IRF8, BIRC6, LCP1, MAPRE1, ARHGEF7, PFDN5, BIRC3, FH, HDAC2, BCL2A1, RAP1GDS1, XIAP, TYMS, MALT1, AURKB, AURKA, CDC42, SH3BP1, NSD2, MAPK1, STAT6, VHL, EPS15, WASF2, EIF4E, CENPU, NPM1, RRM1, YTHDF2, STAT1, SEPTIN2, HUWE1, SEPTIN6, PTPN11, CENPF, NIN, ABI1, HNRNPA2B1, CCDC6, TACC3, KRAS, PTPN6, PTPN2, MAD2L1			
				CENPU, NUP107, SEPTIN2, SEPTIN6, BUB1B, SMC3, SMC1A, PHF6, NDC80, AURKB, CENPF, STAG2, RAD21, TPR, ZNF207, MAD2L1			
				CENPU, NUP107, SEPTIN2, SEPTIN6, BUB1B, SMC1A, PHF6, NDC80, AURKB, CENPF, TPR, ZNF207, MAD2L1			
UP_KW_BIOLOGICAL_PROCESS	KW-0804~Transcription	66	3.17E-04	DDX5, MBNL1, NONO, U2AF1, PTBP1, SFPQ, DDX39B, U2AF2, HNRNPA2B1, SRSF2, SRSF3, CDK12, SF3B1	1.499259	0.002103	0.001757
UP_KW_BIOLOGICAL_PROCESS	KW-0508~mRNA splicing	13	0.009577	RB1, CYFIP2, PHB1, MRE11, NUP107, SMARCB1, KDM1A, BUB1B, IKZF1, SMC3, MKI67, IKZF3, ETS1, H2AC17, H2AC11, ELK4, RPS6KA3, TCL1A, AKT2, RPS6KA1, CHEK1, ZNF207, PIM1, NBN, GTF2I, MBNL1, USP7, PRKCB, IRAG2, FBXO11, FOXF1, MSH2, DDX39B, EWSR1, TBL1XR1, FANCD2, SARNP, SRSF2, BTK, SRSF3, NUP98, RAF1, KPNB1, DDX6, DDX5, BLM, DNMT1, SET, CBF8, PRKDC, BAZ2A, HIF1A, PDCD11, PCBP1, RAD21, TPR, EP400, LPXN, H3C2, FANCI, LYN, XBP1, XRCC6, CPSF6, FANCL, BCL11A, FUS, NONO, SMARCA5, HMGA1, FANCA, FLI1, NDC80, NFKB1, NFKB2, STAG2, NACA, CDK4, CNOT2, SP3, MDM2, CDK1, GRB2, MDM4, ATM, TCF3, CDK12, MNAT1, ATR, EZH2, PICALM, YWHAE, CEP57, TOP2A, TOP2B, DDX3X, HSP90AB1, FAF1, PTEN, HMGB1, BRCA1, AFF3, CHD2, PHF6, CDC73, PTBP1, XPO1, ZC3H7A, CNTRL, OFD1, SS18, HSP90AA1, EED, PRMT1, NCOA3, CAD, ATRX, PAX5, SMC1A, ARID1A, TERF2, RHOA, CCNA2, H2BC12, KAT2B, SFPQ, TFDPI, PKM, IRF4, POT1, IRF8, TOP1, PFDN5, BIRC3, FH, HDAC2, PCNA, RAP1GDS1, XIAP, U2AF1, TYMS, MALT1, AURKB, NSD3, SH3BP1, FIP1L1, CUX1, U2AF2, POLD1, NSD2, PMS2, MAPK1, STAT6, VHL, SF3B1, EIF4E, SUZ12, CENPU, NPM1, YTHDF2, UTP4, STAT1, H2BC4, HUWE1, PTPN11, DEK, MLH1, LRPPRC, CENPF, WEE1, RAD50, POU2AF1, ABI1, HNRNPA2B1, CCNG1, TCEA1, PTPN6, PTPN2, MAD2L1	2.342656	0.05826	0.048683
UP_KW_CELLULAR_COMPONENT	KW-0539~Nucleus	179	1.02E-37	MRE11, NUP107, KDM1A, BUB1B, BRCA1, HMGB1, SMC3, MKI67, PHF6, H2AC17, H2AC11, CNTRL, CHEK1, ZNF207, NBN, USP7, EED, ATRX, IRAG2, CIP2A, SMC1A, FBXO11, TERF2, H2BC12, MSH2, POT1, FH, AURKB, NSD3, RAD21, TPR, NSD2, H3C2, CENPU, XRCC6, UTP4, BCL11A, SEPTIN2, NONO, H2BC4, SMARCA5, HMGA1, SEPTIN6, MLH1, NDC80, CENPF, RAD50, STAG2, ATR, MAD2L1	2.219615	3.56E-36	2.95E-36
UP_KW_CELLULAR_COMPONENT	KW-0158~Chromosome	50	1.37E-23	CYFIP2, PHB1, BUB1B, IKZF1, MSI2, IKZF3, ETS1, RPS6KA3, TCL1A, AKT2, KIF5B, FGFR1OP2, RPS6KA1, CHEK1, ZNF207, PIM1, MAP3K7, GTF2I, CDK5RAP2, MBNL1, USP7, TPM3, FNBP1, PRKCB, COG5, RPL22, IRAG2, EML4, DDX39B, EWSR1, BTK, SRSF3, EZR, RAF1, CARD11, KPNB1, DDX6, DDX5, SET, GMPS, HIF1A, PPP3R1, INPP5D, PCBP1, RAD21, TPR, LPXN, FANCI, LYN, CARMIL2, XBP1, STIL, CPSF6, FANCL, BCL11A, HSPA4, FANCA, HOOK3, NFKB1, NFKB2, NACA, CDK4, CAPRIN1, CNOT2, CCDC88C, MDM2, CDK1, GRB2, STRN, ATM, CALR, RPS21, YWHAE, CEP57, TOP2A, DDX3X, HSP90AB1, WDR1, LRRK2, CLTC, PTEN, CLTA, HMGB1, BRCA1, LASP1, XPO1, ATIC, CNTRL, RAC2, OFD1, HSP90AA1, SYK, PRMT1, NCOA3, CAD, CIP2A, RHOA, CCNA2, KAT2B, SFPQ, TFDPI, RABEP1, PKM, IRF8, BIRC6, LCP1, MAPRE1, ARHGEF7, PFDN5, BIRC3, FH, HDAC2, BCL2A1, RAP1GDS1, XIAP, TYMS, MALT1, AURKB, AURKA, CDC42, SH3BP1, NSD2, MAPK1, STAT6, VHL, EPS15, WASF2, EIF4E, CENPU, NPM1, RRM1, YTHDF2, STAT1, SEPTIN2, HUWE1, SEPTIN6, PTPN11, CENPF, NIN, ABI1, HNRNPA2B1, CCDC6, TACC3, KRAS, PTPN6, PTPN2, MAD2L1	5.792638	2.40E-22	1.99E-22
UP_KW_CELLULAR_COMPONENT	KW-0963~Cytoplasm	147	1.31E-18	CENPU, NUP107, SEPTIN2, SEPTIN6, BUB1B, SMC3, SMC1A, PHF6, NDC80, AURKB, CENPF, STAG2, RAD21, TPR, ZNF207, MAD2L1	1.839454	1.53E-17	1.27E-17
UP_KW_CELLULAR_COMPONENT	KW-0137~Centromere	16	1.93E-09	CENPU, NUP107, SEPTIN2, SEPTIN6, BUB1B, SMC1A, PHF6, NDC80, AURKB, CENPF, TPR, ZNF207, MAD2L1	7.852938	1.69E-08	1.40E-08
UP_KW_CELLULAR_COMPONENT	KW-0995~Kinetochore	13	2.14E-08	CENPU, NUP107, SEPTIN2, SEPTIN6, BUB1B, SMC1A, PHF6, NDC80, AURKB, CENPF, TPR, ZNF207, MAD2L1	8.993484	1.49E-07	1.24E-07
UP_KW_CELLULAR_COMPONENT	KW-0206~Cytoskeleton	46	9.80E-08	CEP57, DDX3X, WDR1, LRRK2, CLTC, CLTA, BUB1B, AURKB, AURKA, CDC42, LASP1, KIF5B, INPP5D, RAD21, TPR, CHEK1, CNTRL, ZNF207, MAPK1, WASF2, CDK5RAP2, OFD1, NPM1, STIL, CARMIL2, TPM3, FNBP1,	2.349807	5.72E-07	4.74E-07

				SEPTIN2, IRAG2, SEPTIN6, HOOK3, RHOA, EML4, KAT2B, CENPF, NIN, ABI1, CDK1, TACC3, CCDC6, ATM, BIRC6, LCP1, EZR, MAPRE1, MAD2L1				
UP_KW_CELLULAR_COMPONENT	KW-0779~Telomere	6	5.96E-04	RAD50, MRE11, ATRX, POT1, NBN, TERF2				
UP_KW_CELLULAR_COMPONENT	KW-0168~Coated pit	5	0.006805	FNBP1, CLTC, CLTA, EPS15, PICALM				
UP_KW_DISEASE	KW-0656~Proto-oncogene	38	4.42E-18	DDX6, PHB1, SET, BTG1, CBF8, GMPS, ETS1, AURKA, NSD3, NRAS, TCL1A, AKT2, TPR, NSD2, PIM1, EPS15, SUZ12, LYN, SS18, NPM1, STIL, TPM3, FUS, PAX5, DEK, RHOA, FLI1, NFKB2, EWSR1, POU2AF1, GNAS, CCDC6, MDM2, KRAS, TCF3, TOP1, RAF1, PICALM				
UP_KW_DOMA IN	KW-0175~Coiled coil	67	7.65E-11	CEP57, PHB1, KDM1A, LRRK2, FAF1, RASGRF1, CLTC, CLTA, BRCA1, SMC3, ZC3H7A, KIF5B, FGFR1OP2, CNTRL, MAP3K7, CDK5RAP2, OFD1, TPM3, FNBP1, ATRX, IRAG2, CIP2A, SMC1A, EML4, SFPQ, RABEP1, BIRC6, TOP1, EZR, ARHGEF7, CARD11, BIRC3, SET, GOSR1, BAZ2A, NSD3, CUX1, TPR, EP400, EPS15, SF3B1, CENPU, GIT2, XBP1, STAT1, NONO, SMARCA5, SEPTIN6, HOOK3, NDC80, KTN1, CENPF, WEE1, RAD50, NIN, STAG2, CAPRIN1, CCDC88C, ABI1, GNAS, TACC3, CCDC6, STRN, MNAT1, PTPN2, FRYL, PICALM				
UP_KW_DOMA IN	KW-0727~SH2 domain	11	4.11E-07	LYN, SYK, STAT1, INPP5D, BTK, PLCG2, PTPN6, PTPN11, GRB2, STAT6, TYK2				
UP_KW_DOMA IN	KW-0677~Repeat	87	1.51E-06	SMARCB1, WDR1, LRRK2, RASGRF1, CLTC, BRCA1, HMGB1, IKZF1, MSI2, MKI67, CHD2, IKZF3, PHF6, RPS6KA3, PTBP1, LASP1, XPO1, ZC3H7A, RPS6KA1, CNTRL, ZNF207, GTF2I, SS18, MBNL1, SYK, EED, PRKCB, NCOA3, CAD, TYK2, FBXO11, EML4, SFPQ, PRKAR1A, EWSR1, TBL1XR1, SRSF3, NUP98, LCP1, KPNB1, BIRC3, DNMT1, PRKDC, RAP1GDS1, XIAP, U2AF1, BAZ2A, RASAL1, HIF1A, MALT1, NSD3, PPP3R1, PDCD11, CUX1, U2AF2, INPP5D, PCBP1, NSD2, PLCG2, LPXN, VHL, EPS15, SF3B1, GIT2, CARMIL2, UTP4, BCL11A, FUS, NONO, SMARCA5, HMGA1, PTPN11, HOOK3, LRPPRC, NFKB1, NFKB2, CENPF, NIN, NACA, SP3, HNRNPA2B1, CCDC6, STRN, PTPN6, GRB2, CALR, ATR				
UP_KW_DOMA IN	KW-0863~Zinc-finger	34	0.00406	DNMT1, XIAP, U2AF1, BAZ2A, RASAL1, IKZF1, BRCA1, PHF6, IKZF3, NSD3, ZC3H7A, POLD1, NSD2, ZNF207, SUZ12, GIT2, MBNL1, MAP3K1, PRKCB, FANCL, BCL11A, FUS, ATRX, FBXO11, FOXF1, EWSR1, SP3, MDM2, BTK, TCEA1, MDM4, RAF1, MNAT1, BIRC3				
UP_KW_DOMA IN	KW-0728~SH3 domain	8	0.014146	LYN, LASP1, FNBP1, ABI1, BTK, PLCG2, GRB2, ARHGEF7				
UP_KW_LIGAND	KW-0067~ATP-binding	62	6.64E-14	EIF4A2, TOP2A, TOP2B, DDX3X, HSP90AB1, LRRK2, BUB1B, SMC3, MKI67, CHD2, RPS6KA3, AKT2, KIF5B, RPS6KA1, CNTRL, CHEK1, PIM1, MAP3K7, HSP90AA1, SYK, PRKCB, CAD, ATRX, DDX10, TYK2, SMC1A, PKM, MELK, MSH2, DDX39B, MSH3, BTK, RAF1, DDX6, BLM, DDX5, PRKDC, GMPS, TTK, AURKB, AURKA, EP400, PMS2, MAPK1, LYN, RRM1, XRCC6, MAP3K1, UBE2C, HSPA4, SMARCA5, HOOK3, MLH1, WEE1, RAD50, CDK4, CAPRIN1, CDK1, KRAS, ATM, CDK12, ATR				
UP_KW_LIGAND	KW-0547~Nucleotide-binding	71	1.16E-13	EIF4A2, TOP2A, TOP2B, DDX3X, HSP90AB1, LRRK2, BUB1B, SMC3, MKI67, CHD2, RPS6KA3, AKT2, KIF5B, RPS6KA1, CNTRL, CHEK1, PIM1, RAC2, MAP3K7, HSP90AA1, SYK, PRKCB, CAD, ATRX, DDX10, TYK2, SMC1A, RHOA, PKM, MELK, MSH2, DDX39B, PRKAR1A, MSH3, BTK, RAF1, DDX6, BLM, DDX5, PRKDC, GMPS, TTK, AURKB, AURKA, CDC42, NRAS, EP400, PMS2, MAPK1, LYN, RRM1, XRCC6, MAP3K1, UBE2C, HSPA4, SEPTIN2, SMARCA5, SEPTIN6, HOOK3, MLH1, WEE1, RAD50, NIN, CDK4, CAPRIN1, CDK1, GNAS, KRAS, ATM, CDK12, ATR				
UP_KW_MOLECULAR_FUNCTION	KW-0238~DNA-binding	71	3.02E-09	RB1, TOP2A, TOP2B, SMARCB1, DDX3X, BRCA1, HMGB1, IKZF1, AFF3, MKI67, CHD2, IKZF3, ETS1, PHF6, H2AC17, H2AC11, ELK4, ZNF207, GTF2I, ATRX, PAX5, ARID1A, TERF2, FOXF1, H2BC12, SFPQ, TFDP1, MSH2, IRF4, MSH3, SARNP, POT1, IRF8, TOP1, BLM, DNMT1, SET, PCNA, PRKDC, BAZ2A, HIF1A, CUX1, POLD1, PCBP1, RAD21, NSD2, EP400, PMS2, MAPK1, STAT6, H3C2, FANCI, XBP1, XRCC6, FUS, STAT1, NONO, H2BC4, HMGA1, HUWE1, DEK, FLI1, LRPPRC, NFKB1, NFKB2, NACA, SP3, TCEA1, ATM, TCF3, ATR				
UP_KW_MOLECULAR_FUNCTION	KW-0156~Chromatin regulator	21	3.79E-07	RB1, SUZ12, DNMT1, HDAC2, SMARCB1, KDM1A, PRKCB, EED, ATRX, SMARCA5, BAZ2A, DEK, IKZF1, ARID1A, CHD2, NSD3, TBL1XR1, NSD2, EP400, NUP98, EZH2				
UP_KW_MOLECULAR_FUNCTION	KW-0723~Serine/threonine-protein kinase	23	9.64E-07	MAP3K1, PRKCB, PRKDC, LRRK2, BUB1B, TTK, AURKB, AURKA, RPS6KA3, MELK, CDK4, AKT2, RPS6KA1, CHEK1, PIM1, CDK1, MAPK1, ATM, CDK12, RAF1, MAP3K7, ATR, GTF2I				
UP_KW_MOLECULAR_FUNCTION	KW-0694~RNA-binding	32	2.89E-06	EIF4A2, DDX6, DDX5, DDX3X, U2AF1, BAZ2A, MSI2, PTBP1, XPO1, FIP1L1, ZC3H7A, U2AF2, PCBP1, SF3B1, EIF4E, NPM1, MBNL1, CPSF6, YTHDF2, FUS, NONO, RPL22, DDX10, LRPPRC, SFPQ, DDX39B, EWSR1, SARNP, CAPRIN1, HNRNPA2B1, SRSF2, SRSF3				
UP_KW_MOLECULAR_FUNCTION	KW-0418~Kinase	32	3.22E-06	PRKDC, LRRK2, BUB1B, TTK, AURKB, AURKA, RPS6KA3, AKT2, CHEK1, RPS6KA1, PIM1, MAPK1, MAP3K7, GTF2I, LYN, GIT2, MAP3K1, SYK, PRKCB, TYK2, HOOK3, WEE1, PKM, MELK, PRKAR1A, CDK4, CDK1, BTK, ATM, CDK12, RAF1, ATR				
UP_KW_MOLECULAR_FUNCTION	KW-0010~Activator	29	3.12E-05	DNMT1, SMARCB1, IKZF1, BRCA1, AFF3, HIF1A, ELK4, PTBP1, RAD21, LPXN, STAT6, SS18, XBP1, XRCC6, STAT1, NCOA3, NONO, FLI1, NFKB1, NFKB2, KAT2B, SFPQ, TFDP1, IRF4, TBL1XR1, NACA, POU2AF1, SP3, IRF8				
UP_KW_MOLECULAR_FUNCTION	KW-0347~Helicase	12	3.74E-05	EIF4A2, DDX6, BLM, XRCC6, DDX5, DDX3X, DDX39B, ATRX, EP400, SMARCA5, DDX10, CHD2				
UP_KW_MOLECULAR_FUNCTION	KW-0678~Repressor	26	6.50E-05	RB1, DNMT1, HDAC2, KDM1A, BAZ2A, IKZF1, ELK4, PTBP1, CUX1, U2AF2, RAD21, MAPK1, SUZ12, CENPU, EED, BCL11A, NONO, FOXF1, NFKB2, SFPQ, EWSR1, TBL1XR1, CNOT2, SP3, IRF8, EZH2				
UP_KW_MOLECULAR_FUNCTION	KW-0808~Transferase	55	4.39E-04	LRRK2, BUB1B, BRCA1, RPS6KA3, ATIC, AKT2, RPS6KA1, CHEK1, PIM1, MAP3K7, GTF2I, STG6GAL1, SYK, PRKCB, PRMT1, NCOA3, CAD, TYK2, DPM1, KAT2B, PKM, MELK, PRKAR1A, BTK, BIRC6, NUP98, RAF1, BIRC3, DNMT1, PRKDC, XIAP, TTK, TYMS, AURKB, AURKA, NSD3, POLD1, NSD2, MAPK1, LYN, GIT2, MAP3K1, UBE2C, FANCL, HUWE1, HOOK3, WEE1, CDK4, CDK1, MDM2, KRAS, ATM, CDK12, ATR, EZH2				
UP_KW_MOLECULAR_FUNCTION	KW-0799~Topoisomerase	3	0.005593	TOP2A, TOP2B, TOP1				

Suppl. Table S3.3 Significantly enriched terms with FDR ≤ 0.05 by DAVID functional annotation tool for 606 genes upregulated in the ME vs. TLT subtypes of PT-DLBCL

Category	Term	Count	P Value	Genes	Fold Enrichment	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription by RNA polymerase II	147	8.99E-50	CSF3, CRT3, MAML2, CRT1, FGF1, HOXA13, FGF2, ETS2, FGF4, SOX2, HOXA9, CREB3L1, LMO1, HGF, LMO2, MRTF8, SOX11, MITF, HNF1A, SOX10, RUNX2, AR, MYCN, SFRP2, MAF, SMO, KAT6B, DDIT3, ERG, ZFPM2, ATF3, NOTCH2, NOTCH3, NOTCH4, GATA6, PIK3R2, GATA3, BHLHE22, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, NKX2-5, PPARGC1A, TFAP2A, WWTR1, EGR1, JUN, EGR2, EGR3, SMAD3, BCL11B, EGR4, AUTS2, TGFB3, ZBTB16, HMGA2, INHBA, IGF1, SMARCA1, ESR1, PBX1, PHOX2B, IL2, FOSL1, BMP4, AHI1, BCL9, NR4A3, MAFB, LHX2, TLX1, FEV, ID4, CD28, LHX4, HOXD9, FGFR2, NODAL, BMPR1A, FGF10, CHD6, HOXC13, GLI1, HOXC11, GLI3, MECOM, HEY1, ZNF521, TEAD1, MYBL1, TEAD3, BRD3, TEAD4, PEG3, TET1, PAX3, ETV1, FOXL2, OLIG1, FOS, OLIG2, ETV4, ETV5, POU5F1, DCN, PAX8, TAL1, IL1B, RARA, ITGA8, PPARG, HDAC4, YAP1, CEBPA, HDAC5, CEBPB, HLF, CEBPD, CEBPE, PLAG1, LRP5, HOXD13, DLL1, EGFR, FSTL3, MUC1, STAT4, HES1, HES5, TCF7L2, PRRX1, CDX2, EYA1, DMRT1, CDX1, DAB2IP, KLF4, ACVR2A, PER1, NR6A1, WT1, NFIB, FOSB, ERCC6	4.002829	3.52E-46	3.20E-46
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell population proliferation	80	2.91E-35	CSF3, CSF1, EPO, FLT3, IRS1, FLT4, TNC, IRS2, FASLG, GLI1, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, FGF8, EDNRB, FGF9, KDR, ITGAV, PDGFRB, PDGFRA, IL15, MATK, FLT3LG, LIFR, TIAM1, AR, SFRP2, IL1B, RARA, ATF3, HDAC4, CSF1R, PDGFB, LRP5, PDGFA, TNFRSF11A, DLL1, EGFR, ERBB3, ERBB4, PDGFD, ZNF703, ERBB2, NTF3, HAS2, HES1, S1PR2, NKX2-5, FGF23, HES5, IL12RB2, NTRK2, WWTR1, TGFB2, CDX2, EGR4, TGFB3, EGF, NTRK3, AKR1C3, VEGFC, VEGFD, IGF1, EPOR, TSHR, IL2, BMP4, FOSL1, IL3, FGF19, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1, CRLF2	5.407279	5.70E-32	5.18E-32
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	78	2.09E-33	RET, CSF1, ITGB3, TNC, FGF1, FGF2, FGF3, FGF4, ROBO1, FGF6, FGF8, FGF9, CD36, AMH, IL13, SOX11, MITF, WNT16, NGF, SOX10, DKK1, POU5F1, RUNX2, TGFB3, SFRP4, AR, MYCN, MAF, SMO, IL1B, RARA, PPARG, ATF3, YAP1, CEBPA, CEBPE, PLAG1, PDGFB, GATA2, ACVR1B, DLL1, DLL4, WNT6, ERBB3, ERBB2, NKX2-1, HES1, NKX2-5, FGF23, PPARGC1A, WNT3, TFAP2A, EGR1, NTRK2, GSN, SMAD3, ANGPT1, EGF, NOS3, NTRK3, CAV1, HMGA2, IGF1, INHBA, KLF4, BMP4, WT1, FEV, FGF19, CD28, ID4, CNTN1, SPRY2, ERCC6, FGFR4, IL7R, BMPR1A, FGF10	5.241024	2.72E-30	2.48E-30
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription by RNA polymerase II	101	2.15E-29	EPO, ETS2, SOX2, DACH1, EDNRB, CCND1, FGF9, CREB3L1, MNX1, SSX1, LMO1, SOX11, MITF, HNF1A, SOX10, DKK1, AR, MAF, SMO, BIN1, DDIT3, FLYWCH1, BCORL1, ZFPM2, ATF3, NOTCH2, NOTCH3, MAGED1, NOTCH4, GATA6, GATA3, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, NKX2-5, TFAP2A, WNT10B, WWTR1, EGR1, JUN, SMAD3, MAGEE1, ZBTB16, CAV1, PTCH1, HMGA2, ESR1, BMP4, NR4A3, MAFB, ID1, ID4, HOXD9, FGFR2, NODAL, FGFR1, FHL2, FASLG, GLI3, FLCN, HEY1, PPP1R13L, TRPS1, CD36, JARID2, PEG3, DNMT3A, TET1, FOXL2, OLIG2, DUSP26, ETV5, POU5F1, TAL1, RARA, PPARG, HDAC4, YAP1, CEBPA, HDAC5, CEBPB, DDX20, DLL4, DNAJB1, HES1, HES5, TCF7L2, PRRX1, CDX2, DMRT1, DAB2IP, KLF4, TBX15, PER1, NR6A1, WT1, NFIB, NEDD4, FOSB	3.587025	2.10E-26	1.91E-26
GOTERM_BP_DIRECT	GO:0060070~canonical Wnt signaling pathway	36	1.06E-26	YAP1, WNT2B, LRP5, WNT8B, GATA3, FZD10, FOXO3, FGF2, WNT6, EDNRB, WNT11, FGF9, ADGRA2, GPC3, WNT3, WNT4, TCF7L2, WNT10B, FZD3, FZD2, WNT5B, EGF, FZD7, CAV1, WNT7B, FZD6, AXIN1, FZD8, KLF4, WNT16, DKK1, LRP1B, EXT1, SFRP4, BCL9, SFRP2	10.99319	8.28E-24	7.52E-24
GOTERM_BP_DIRECT	GO:0045893~positive regulation of DNA-templated transcription	81	1.08E-25	CDKN1C, RET, EPO, HOXC13, GLI1, FGF2, GLI3, HOXA11, SOX2, MECOM, ZIC2, CDH1, TEAD1, MYBL1, PAX3, FOXL2, MITF, HNF1A, FOS, SOX10, RUNX2, AR, MYCN, PAX8, ASPH, KAT6B, TAL1, IL1B, DDIT3, RARA, PPARG, PLCB1, HDAC4, YAP1, CEBPB, MAGED1, NOTCH4, PDGFB, GATA6, LRP5, GATA3, FOXO3, GATA1, EGFR, WNT6, WNT11, ERBB4, PRDM16, NKX2-1, NKX2-5, FGF23, PPARGC1A, HES5, WNT4, TFAP2A, EGR1, JUN, EGR2, FZD2, SMAD3, TGFB3, EGF, FZD7, ZBTB16, PTCH1, HMGA2, PDE4DIP, IGF1, INHBA, GDF6, SMARCA1, KLF4, ESR1, BMP4, MLLT11, COL1A1, TBX15, MAFB, LHX2, NFIB, WT1	3.885392	7.06E-23	6.41E-23
GOTERM_BP_DIRECT	GO:0051897~positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	42	5.43E-24	RET, CSF1R, CSF3, HIP1, FLT3, IRS1, SRC, PDGFB, PDGFA, IRS2, GATA3, FGF2, EGFR, IGF1R, RELN, ERBB3, ERBB4, PDGFD, KDR, PDGFRB, NTRK1, TCF7L2, PDGFRA, NTRK2, TGFB2, ANGPT1, EGF, HGF, NTRK3, AKR1C3, HNF1A, IGF1, WNT16, DCN, AXL, NEDD4, KIT, CD28, SPRY2, FGFR3, FGFR1, DDR2	7.481477	3.04E-21	2.76E-21
GOTERM_BP_DIRECT	GO:0007169~cell surface receptor protein tyrosine kinase signaling pathway	33	2.68E-23	RET, ALK, CSF1R, SHC2, CSF1, FLT3, SRC, FLT4, EGFR, NTF4, ERBB3, ERBB4, ERBB2, NTF3, KDR, ROS1, PDGFRB, NTRK1, PDGFRA, NTRK2, BDNF, NTRK3, STYK1, NGF, AHI1, AXL, PTK7, FGFR4, FGFR3, FGFR2, FGFR1, EPHA2, DDR2	10.16788	1.31E-20	1.19E-20
GOTERM_BP_DIRECT	GO:0045165~cell fate commitment	25	2.69E-22	WNT2B, GATA6, WNT8B, GATA3, GATA2, GATA1, SOX2, WNT6, FGF8, WNT11, ERBB4, KDR, WNT3, WNT4, WNT10B, WNT5B, WNT7B, MITF, WNT16, EXT1, TAL1, SPRY2, GAS1, PPARG, FGFR2	15.00046	1.17E-19	1.06E-19
GOTERM_BP_DIRECT	GO:0007275~multicellular organism development	28	9.98E-22	RET, ALK, CSF1R, FLT3, FLT4, EGFR, IGF1R, FSTL3, ERBB3, ERBB4, CDH1, ERBB2, KDR, ROS1, PDGFRB, NTRK1, PDGFRA, NTRK2, NTRK3, AXL, KIT, CDH11, FGFR4, FGFR3, FGF2, FGFR1, EPHA2, DDR2	11.82258	3.91E-19	3.55E-19
GOTERM_BP_DIRECT	GO:1902895~positive regulation of miRNA transcription	25	1.18E-21	NOTCH2, NOTCH3, PDGFB, GATA3, GATA2, FOXO3, FGF2, EGFR, TEAD1, NGFR, EGR1, TGFB2, JUN, SMAD3, MRTF8, FOS, KLF4, SMAD6, BMP4, FOSL1, AR, MYCN, WT1, PPARG, BMPR1A	14.25043	4.21E-19	3.82E-19
GOTERM_BP_DIRECT	GO:0033674~positive regulation of kinase activity	24	2.44E-21	PDGFRB, ALK, NTRK1, RET, PDGFRA, NTRK2, CSF1R, FLT3, FLT4, NTRK3, EGFR, IGF1R, ERBB3, AXL, ERBB4, ERBB2, KDR, FGFR4, ROS1, FGFR3, FGFR2, EPHA2, FGFR1, DDR2	14.92409	7.96E-19	7.23E-19
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	40	2.88E-19	NOTCH2, CSF1R, EPO, SRC, FLT4, ITGB3, PDGFB, PDGFA, NOD1, PLA2G5, TNFRSF11A, FGF1, FGF2, EGFR, FGF4, AKAP12, FGF8, ERBB4, PDGFD, KDR, CD36, FGF23, PDGFRB, NTRK1, PDGFRA, ANGPT1, PLA2G2A, PRKCA, IGF1, INHBA, TIRAP, BMP4, FGF19, SPRY2, ACKR3, FGFR4, FGFR3, FGFR2, NODAL, FGF10	6.000182	8.68E-17	7.88E-17
GOTERM_BP_DIRECT	GO:0001934~positive regulation of protein phosphorylation	37	3.40E-18	CSF1R, CDKN1A, FLT4, ITGB3, FGF1, FGF2, FGF3, EGFR, FGF4, FGF6, FGF8, RELN, EDNRB, FGF9, CCND1, ERBB4, ERBB2, KDR, FGF23, NTRK1, NTRK2, EPHA7, ANGPT1, HGF, NTRK3, AXIN1, VEGFC, FZD8, VEGFD, HNF1A, INHBA, HSPA2, ACVR2A, BMP4, IL1B, FGF19, FGF10	6.142905	9.52E-16	8.65E-16

GOTERM_BP_DIRECT	GO:0043410~positive regulation of MAPK cascade	35	9.89E-18	RET, FLT3, FLT4, PDGFB, LPAR1, PDGFA, FGF2, FGF3, GRM1, FGF4, IGF1R, SOX2, FGF6, FGF8, FGF9, ERBB2, KDR, FGF23, WNT4, NTRK2, KSR1, TGFβ3, EGF, FZD7, HGF, DAB2IP, FRS2, IGF1, AR, FGF19, KIT, FGFR3, FGFR2, FGF10, FGFR1	6.367215	2.58E-15	2.35E-15
GOTERM_BP_DIRECT	GO:0007165~signal transduction	91	6.88E-16	RET, ALK, TENM1, ITK, PTPRR, CSF3R, EPO, IRS1, CTNND2, IRS4, CBL, IRS2, FASLG, PTPRK, FGF1, FGF2, FGF3, IGF1R, FGF4, AKAP12, FGF9, CHL1, PLAU, RPS6KA2, CCN6, PRKG2, RAC3, MAP3K6, SH3GL2, PDGFRB, IL15, IL13, MATK, FLT3LG, RHOD, GABRG2, BCR, AR, INPP4B, IL1B, KIT, ITPKA, PPARG, ERG, PLPP3, PLCB1, DOCK1, CILK1, DDR2, FBN2, CAMK2B, CSF1R, SRC, WNT8B, NOD1, PIK3R2, GATA3, TNFRSF11A, ACVR1B, TRHD, NDRG1, KALRN, EGFR, DLL4, ARHGAP20, WNT11, ERBB3, ERBB4, WIF1, GNA11, ERBB2, NTF3, GNA12, CHN1, ABL2, SRGAP3, LEFTY2, PAK5, VEGFC, CCK, IGF1, ESR1, EPOR, TNFRSF10D, NR4A3, FGF14, TAF2, AXL, PTK7, FGF13, IL7R	2.509915	1.66E-13	1.51E-13
GOTERM_BP_DIRECT	GO:0030182~neuron differentiation	31	7.20E-16	HDAC5, BRSK1, CEBPB, WNT2B, WNT8B, FZD10, SOX2, WNT6, FGF8, WNT11, CCND1, ERBB2, WNT3, WNT4, NTRK2, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, DNMT3A, FZD8, SOX11, SMARCA1, WNT16, RUNX2, LHX2, ERCC6, LHX4, EPHA2	6.464831	1.66E-13	1.51E-13
GOTERM_BP_DIRECT	GO:0018108~peptidyl-tyrosine phosphorylation	19	1.42E-15	PDGFRB, NTRK1, PDGFRA, CSF1R, FLT3, SRC, FLT4, PDGFB, EGFR, RELN, ERBB4, ERBB2, KDR, ABL2, FGFR4, FGFR2, EPHA3, FGFR1, DDR2	12.9964	3.10E-13	2.81E-13
GOTERM_BP_DIRECT	GO:0071300~cellular response to retinoic acid	21	6.08E-15	YAP1, RET, WNT10B, WNT5B, FZD7, WNT7B, SERPINF1, TNC, WNT8B, FZD10, KLF4, COL1A1, WNT6, WNT11, PTK7, RARA, ABL2, PPARG, WNT3, FGFR2, EPHA3	10.26031	1.23E-12	1.12E-12
GOTERM_BP_DIRECT	GO:0045669~positive regulation of osteoblast differentiation	22	6.27E-15	YAP1, FBN2, WWTR1, WNT10B, CEBPA, CEBPB, CEBPD, HGF, WNT7B, LRP5, SOX11, IGF1, FGF2, GLI3, ACVR2A, RUNX2, BMP4, SFRP2, WNT3, BMPR1A, WNT4, DDR2	9.52434	1.23E-12	1.12E-12
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell population proliferation	48	9.13E-15	HDAC4, TENM1, CEBPA, CSF1R, CDKN1A, ATP8A2, DD20, GATA3, FOXO4, PTPRK, PPM1D, PTGS2, NDRG1, DLL1, GATA1, RERG, DLL4, ERBB4, RPS6KA2, CCN6, CYP1B1, TFAP2A, NTRK1, TGFβ2, CDKN2B, SMAD3, BCL11B, TGFβ3, NOS3, ZBTB16, DAB2IP, DLEC1, INHBA, NGF, KLF4, SMAD6, BMP4, FOSL1, SFRP4, AR, SFRP2, ASPH, WT1, IL1B, NEUR1, RARA, SPRY2, ACKR3	3.782603	1.70E-12	1.55E-12
GOTERM_BP_DIRECT	GO:0006357~regulation of transcription by RNA polymerase II	104	1.58E-14	ZNF331, EPO, DACH2, HOXA13, ETS2, HOXA11, HOXA9, DACH1, CREB3L1, HOXA3, ZNF444, MITF, HNF1A, SOX10, RUNX2, MYCL, MYCN, MAF, KAT6B, DDIT3, ERG, ATF3, FOXO4, FOXO3, PRDM16, NKX2-1, NKX2-5, TFAP2A, EGR1, JUN, EGR2, EGR3, SMAD3, EGR4, ZBTB16, INHBA, SMARCA1, SMAD6, ESR1, PBX1, PHOX2B, FOSL1, NR4A3, MAFB, TLX3, LHX2, TLX1, FEV, LHX4, HOXD9, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, PPP1R13L, TRPS1, ZNF521, TEAD1, TEAD3, BRD3, TEAD4, BRD1, PEG3, PAX3, ETV1, FOXL2, FOS, ETV4, ETV5, POU5F1, DMRTA2, PAX8, TAL2, PAX7, TAL1, AHRR, PPARG, VGLL3, CEBPA, CEBPB, HLF, CEBPD, CEBPE, HOXD13, HOXD11, FSTL3, STAT4, HES1, HES5, TCF7L2, PRRX1, CDX2, DMRT1, CDX1, PRRX2, KLF4, TBX15, NR6A1, WT1, NFIB, FOSB	2.214762	2.82E-12	2.56E-12
GOTERM_BP_DIRECT	GO:0072089~stem cell proliferation	18	1.75E-14	RNF43, PRRX1, WNT7B, PTCH1, FGF2, GLI3, RUNX2, PBX1, FGF4, FGF8, WNT11, FGF9, NFIB, HOXA3, KDR, WNT3, FGF10, FGFR1	12.56365	2.98E-12	2.71E-12
GOTERM_BP_DIRECT	GO:0008543~fibroblast growth factor receptor signaling pathway	19	2.76E-14	NGFR, FRS2, FGF1, FGF2, FGF3, FGF4, EXT1, FGF6, FGF8, FGF9, FGF19, SPRY2, FGFR4, FGF23, FGFR3, FGFR2, FGF10, FGFR1, WNT4	11.20379	4.51E-12	4.10E-12
GOTERM_BP_DIRECT	GO:0042060~wound healing	21	5.95E-14	YAP1, NOTCH2, PDGFRA, CDKN1A, TGFβ2, SMAD3, SDC4, DST, ITGB3, NOTCH4, PDGFA, IGF1, FGF1, FGF2, EXT1, COL3A1, ERBB3, PTK7, ERBB2, PLPP3, FGF10	9.207972	9.33E-12	8.48E-12
GOTERM_BP_DIRECT	GO:0043406~positive regulation of MAP kinase activity	18	1.57E-13	PDGFRB, TENM1, FLT3, EGF, NTRK3, PDGFB, PDGFA, FGF1, FGF2, EGFR, ROBO1, GHR, IL1B, PDGFD, KIT, NTF3, ERBB2, FGFR1	11.19307	2.36E-11	2.14E-11
GOTERM_BP_DIRECT	GO:0051781~positive regulation of cell division	17	3.10E-13	TGFβ2, TGFβ3, PDGFB, VEGFC, PDGFA, VEGFD, FGF1, FGF2, FGF3, FGF4, FGF6, FGF8, FGF9, TAL1, IL1B, PDGFD, FGFR2	11.86567	4.50E-11	4.09E-11
GOTERM_BP_DIRECT	GO:0050673~epithelial cell proliferation	17	4.44E-13	YAP1, EYA1, EGF, HGF, FGF1, EGFR, RUNX2, BMP4, FLCN, AR, SMO, KIT, KDR, GPC3, NKX2-5, FGF10, BMPR1A	11.62835	6.21E-11	5.64E-11
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	49	7.47E-13	CDKN1A, TNFRSF6B, FLT4, FHL2, GLI3, IGF1R, FGF4, EDNRB, MYO18A, KDR, HGF, MITF, HNF1A, SOX10, DKK1, SMO, PAX7, DDR2, NOTCH2, CSF1R, SRC, GATA6, GATA1, EGFR, SOCS2, SOCS3, ERBB3, CHST11, ERBB4, ERBB2, NKX2-5, NTRK1, TFAP2A, EGR3, SMAD3, ANGPT1, MGMT, HMGA2, IGF1, SMAD6, IL2, TNFRSF10D, AH11, AXL, WT1, CD28, SPRY2, LHX4, BCL2L2	3.305426	1.01E-10	9.16E-11
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	36	8.73E-13	RET, CSF1R, CSF1, FLT4, PDGFB, PDGFA, FGF1, GLI1, EGFR, IGF1R, PLAU, PDGFD, ZNF703, NTF3, KDR, HAS2, ITGAV, PDGFRB, PDGFRA, MMP7, SMAD3, WNT5B, EGF, HGF, CAV1, NTRK3, PRKCA, IGF1, RHOD, COL1A1, TIAM1, SMO, IL1B, KIT, SPRY2, EPHA2	4.290026	1.14E-10	1.04E-10
GOTERM_BP_DIRECT	GO:0009887~animal organ morphogenesis	25	9.20E-13	NOTCH2, LAMAS, ELN, PDGFA, FGF1, FGF2, FGF3, FGF4, LFNG, FGF6, ABLIM1, FGF8, FGF9, FGF23, CDX2, CDX1, PTCH1, VEGFC, PAX3, PBX1, DCN, FGF19, LHX4, FGFR2, FGF10	6.380791	1.16E-10	1.06E-10
GOTERM_BP_DIRECT	GO:0010629~negative regulation of gene expression	37	1.77E-12	YAP1, NOTCH2, CDKN1A, PLAG1, SRC, PDGFB, GATA2, ACVR1B, FGF2, ROBO1, DLL4, CREB3L1, KDR, HES1, CD36, ROS1, SH3GL2, WNT4, TGFβ2, ACE, SMAD3, SERPINF1, AXIN1, SOX11, IGF1, KLF4, ESR1, POU5F1, BMP4, MYCN, SFRP2, PC, SMO, FGF19, CD28, PPARG, BMPR1A	4.08206	2.16E-10	1.96E-10
GOTERM_BP_DIRECT	GO:0030154~cell differentiation	57	2.37E-12	HIP1, FGF1, FGF2, ETS2, FGF3, FGF4, FGF6, FGF9, ZIC2, ROS1, MYBL1, FOXL2, ETV1, DLEC1, ETV4, ETV5, SFRP4, SFRP2, RARA, PPARG, ERG, ZFPM2, CAMK2B, SRC, NOTCH4, DLL1, FSTL3, DLL3, SOCS3, ACVR1C, GNA12, NKX2-1, NKX2-5, FGF23, JAG2, NTRK1, NTRK2, SMAD3, GADD45B, CDX2, ANGPT1, EYA1, CDX1, BTBD18, EYA2, NTRK3, CAV1, INHBA, SMAD6, ACER1, FEV, FGF19, ID1, ID4, TLL2, FGF10, FGFR1	2.875309	2.81E-10	2.56E-10
GOTERM_BP_DIRECT	GO:0007411~axon guidance	30	2.88E-12	EPHB6, ROBO2, RET, NOTCH2, CSF1R, NOTCH3, EPHA10, GATA3, KALRN, GLI3, RELN, CHL1, NKX2-1, NCAM1, WNT3, NTRK1, EPHA5, NGFR, EPHA7, BDNF, NTRK3, ETV1, EXT1, LHX2, PTK7, KIT, CNTN1, FGFR2, EPHA3, EPHA2	4.932842	3.31E-10	3.01E-10
GOTERM_BP_DIRECT	GO:0090090~negative regulation of canonical Wnt signaling pathway	26	4.09E-12	AMER1, PRICKLE1, FOXO3, GLI1, GLI3, SOX2, WNT11, GPC3, NKX2-5, WWTR1, TCF7L2, EGR1, CAV1, FZD6, IGFBP2, DAB2IP, AXIN1, SOX10, DKK1, BICC1, DKK2, DKK4, SFRP4, SFRP2, DDIT3, HECW1	5.700173	4.58E-10	4.16E-10
GOTERM_BP_DIRECT	GO:0042475~odontogenesis of dentin-containing tooth	17	7.75E-12	JAG2, PDGFRA, NGFR, LAMAS, BCL11B, GATA6, TNC, GLI3, ACVR2A, RUNX2, FGF4, BMP4, WNT6, SMO, CTNNA1, FGF10, BMPR1A	9.854537	8.44E-10	7.67E-10
GOTERM_BP_DIRECT	GO:0050679~positive regulation of epithelial cell proliferation	18	9.36E-12	YAP1, TCF7L2, EYA1, IGF1, FGF1, FGF2, EGFR, RUNX2, BMP4, NR4A3, FGF9, SMO, ERBB2, NKX2-5, NODAL, FGFR2, FGF10, BMPR1A	8.92201	9.91E-10	9.00E-10
GOTERM_BP_DIRECT	GO:0001701~in utero embryonic development	30	1.33E-11	NOTCH2, CDKN1A, PTPRR, GATA6, GATA3, ACVR1B, GATA1, GLI3, FLCN, CHST11, GNA12, JAG2, SLC34A2, PDGFRA, SMAD3, ANGPT1, TGFβ3, NOS3,	4.642675	1.37E-09	1.24E-09

				PTCH1, WNT7B, AXIN1, SOX10, FOSL1, AR, COL3A1, SMO, ZFPM2, FGFR2, BMPR1A, FGFR1			
GOTERM_BP_DIRECT	GO:0001658~branching involved in ureteric bud morphogenesis	15	1.43E-11	LAMA5, EYA1, PTCH1, HOXD11, FGF2, GLI3, PBX1, HOXA11, BMP4, WNT6, FGF8, PAX8, WT1, GPC3, WNT4 RET, ALK, ITK, CDKN1A, FLT3, FLT4, IGF1R, PLAU, CLP1, RPS6KA2, PRKACG, KDR, PRKG2, PDGFRB, PRKCG, EPHA5, EPHA7, CDKL5, KSR1, MATK, PRKCA, MAPK8IP2, KIT, ITPKA, CILK1, EPHA2, CAMK2B, BRSK1, EPHA10, SRC, CAMK2A, AKAP6, AK5, KALRN, EGFR, ERBB3, ERBB4, ERBB2, PAK6, CKB, PAK3, PAK5, NTRK1, NTRK2, NTRK3, STYK1, ACVR2A, AXL, FGFR4, FGFR3, FGFR2, BMPR1A, FGFR1	11.65945	1.44E-09	1.31E-09
GOTERM_BP_DIRECT	GO:0016310~phosphorylation	53	1.87E-11	PDGFRA, LAMA5, CEBPA, NOS3, WNT7B, FGF1, GLI1, FGF2, EGFR, GLI3, COL3A1, FGF9, LOX, NKX2-1, GPC3, HES1, ZFPM2, FGFR2, BMPR1A	2.863594	1.79E-09	1.63E-09
GOTERM_BP_DIRECT	GO:0030324~lung development	19	1.88E-11	TFAP2A, FZD3, ATP8A2, PRRX1, COL11A1, FZD6, GATA3, GATA2, BCR, MAFB, PAX8, FGF9, ITGA8, SPRY2, FGFR2, FGFR1	7.924631	1.79E-09	1.63E-09
GOTERM_BP_DIRECT	GO:0042472~inner ear morphogenesis	16	4.27E-11	RET, HDACS, CDKN1A, SRC, GATA6, SLC1A2, PRICKLE1, FOXO3, PTGS2, GRIN2A, FGF8, CCND1, CDH1, GNA12, AMH, NTRK1, FZD3, MMP7, ACE, PTCH1, IGFBP2, DNMT3A, VEGFC, FOS, COL1A1, FOSL1, SFRP2, CPS1, LOX, FOSB, PPARG	9.771726	3.99E-09	3.62E-09
GOTERM_BP_DIRECT	GO:0009410~response to xenobiotic stimulus	31	8.49E-11	EGR2, PDGFB, GATA6, LRP5, PRICKLE1, RUNX2, GFAP, GRM3, EXT1, FOSL1, EXT2, EDNRB, SMO, NFIB, DDIT3, HOXA3, GRB10, NKX2-1, CNTN1, IL7R, ROS1, WNT3, FGFR1	4.174143	7.74E-09	7.03E-09
GOTERM_BP_DIRECT	GO:0010467~gene expression	23	1.37E-10	BMP4, FGF8, FRS2, FGF1, FGF2, HOXC11, FGFR1, HOXA11, FGF10	5.578893	1.22E-08	1.11E-08
GOTERM_BP_DIRECT	GO:0001759~organ induction	9	2.24E-10	FBN2, SMAD3, EYA1, GATA6, SOX11, FOXL2, GATA3, HOXC13, GATA2, FGF1, SMAD6, SOX10, GATA1, FGF3, POU5F1, HOXA11, SOX2, FGF8, PAX8, PAX7, CLTC1, GPC3, ZFPM2	25.65078	1.95E-08	1.77E-08
GOTERM_BP_DIRECT	GO:0009653~anatomical structure morphogenesis	23	3.14E-10	NOTCH2, SRC, DDX20, HTRA1, LPAR1, NOD1, FASLG, FOXO3, PTGS2, FLCN, GRIN2A, ACVR1C, RPS6KA2, CYP1B1, CTLA4, WNT10B, JUN, ACE, GADD45B, CRADD, TGFBR3, ZBTB16, DAB2IP, FOXL2, TNFRSF10D, BMP4, MLLT11, FOSL1, SFRP4, SFRP2, WT1, BIN1, NEURL1, PPARG	5.351183	2.67E-08	2.43E-08
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	34	4.23E-10	YAP1, AMER1, KANK1, WNT10B, SMAD3, SRC, EGF, FGF2, EGFR, DKK2, POU5F1, COL1A1, SFRP4, SFRP2, FGF9, ADGRA2, PTK7, GPC3, LGR5, FGFR2, FGF10	3.61129	3.53E-08	3.20E-08
GOTERM_BP_DIRECT	GO:0090263~positive regulation of canonical Wnt signaling pathway	21	4.46E-10	EPHB6, RET, CAMK2B, BRSK1, ITK, EPHA10, SRC, CAMK2A, PDGFB, ACVR1B, KALRN, ACVR1C, WNT11, ERBB2, PRKG2, ABL2, PAK6, PAK3, MAP3K6, ROS1, PAK5, PRKCG, NTRK1, EPHA5, EPHA7, CDKL5, STYK1, MATK, PRKCA, ACVR2A, BCR, RARA, ERG, CILK1, EPHA3, BMPR1A, FGFR1	5.839202	3.58E-08	3.25E-08
GOTERM_BP_DIRECT	GO:0006468~protein phosphorylation	37	4.48E-10	TGFB2, ACE, WNT2B, GATA6, AKR1C3, GATA3, INHBA, ESR1, GATA1, HOXA11, AR, HOXA9, SFRP2, FGF9, WT1, PRKACG, KIT, CTNNA1, CYP1B1, WNT4	3.365528	3.58E-08	3.25E-08
GOTERM_BP_DIRECT	GO:0008584~male gonad development	20	5.78E-10	CDKN1C, CEBPA, HDACS, CEBPD, GATA6, PDGFB, GATA3, PTPRK, PRICKLE1, GLI3, DACH1, WNT11, MECOM, HEY1, ZIC2, CREB3L1, ZNF703, PRDM16, NKX2-1, HES1, NKX2-5, WNT4, RUNX1T1, TFAP2A, TCF7L2, JUN, ZBTB16, DNMT3A, DAB2IP, HMGA2, FOXL2, KLF4, RUNX2, BMP4, ZFTA, PER1, SFRP2, WT1, KAT6B, DDIT3, ID1, ID4, RARA, PPARG, PLCB1, ZMYND11, ZFPM2	6.107329	4.53E-08	4.11E-08
GOTERM_BP_DIRECT	GO:0045892~negative regulation of DNA-templated transcription	47	6.01E-10	BMP4, ROBO2, TGFBR2, FGF8, GATA6, ZFPM2, NKX2-5, SMAD6, FGFR2, BMPR1A, ROBO1	2.805321	4.62E-08	4.20E-08
GOTERM_BP_DIRECT	GO:0003148~outflow tract septum morphogenesis	11	9.15E-10	JAG2, ROBO2, YAP1, TGFBR2, NOS3, SRC, DLL1, ROBO1, DLL4, LFNG, KIT, HES1, HES5, FGF10	15.04846	6.89E-08	6.26E-08
GOTERM_BP_DIRECT	GO:0045747~positive regulation of Notch signaling pathway	14	1.68E-09	PRRX1, HMGA2, SOX11, FGF2, RUNX2, PBX1, FGF4, FGF8, FGF9, HOXA3, KDR, FGF10, FGFR1	9.388521	1.23E-07	1.12E-07
GOTERM_BP_DIRECT	GO:2000648~positive regulation of stem cell proliferation	13	1.70E-09	TCF7L2, WNT10B, CEBPA, EGR2, WNT5B, CEBPD, HMGA2, GATA2, KLF4, GDF6, SMAD6, NR4A3, MAFB, CCND1, ID4, PLCB1, ZFPM2	10.58604	1.23E-07	1.12E-07
GOTERM_BP_DIRECT	GO:0045444~fat cell differentiation	17	2.30E-09	PDGFRB, ALK, CAMK2B, NTRK1, PDGFRA, NTRK2, CSF1R, CDKL5, FLT3, SRC, FLT4, CAMK2A, ACVR1B, EGFR, IGF1R, ERBB4, KIT, KDR, FGFR4, FGFR2, FGFR1, DDR2	6.921639	1.64E-07	1.49E-07
GOTERM_BP_DIRECT	GO:0046777~protein autophosphorylation	22	2.44E-09	NOTCH2, CSF1R, TGFBR2, ANGPT1, FLT3, NOTCH4, ZBTB16, DLL1, EPOR, RUNX2, FLCN, TAL1, KIT, NKX2-5, IL7R	5.049818	1.71E-07	1.55E-07
GOTERM_BP_DIRECT	GO:0030097~hemopoiesis	15	3.48E-09	PDGFRB, NOTCH3, ITGB3, IL13, PDGFB, IGF1, PTGS2, FGF2, EGFR, IGF1R, BMP4, NR4A3, PDGFD, HES5	8.015869	2.39E-07	2.17E-07
GOTERM_BP_DIRECT	GO:0048661~positive regulation of smooth muscle cell proliferation	14	3.61E-09	YAP1, CDX2, LRP5, GATA2, KLF4, POU5F1, FGF4, SOX2, BCL9, KIT, HES1, NODAL, FGF10, BMPR1A	8.866936	2.44E-07	2.21E-07
GOTERM_BP_DIRECT	GO:0035019~somatic stem cell population maintenance	14	4.60E-09	CEBPB, CEBPD, HOXD13, GATA3, GATA2, FGF2, HOXA13, GATA1, NKX2-5, WNT10B, PRRX1, BCL11B, ETV1, HNF1A, INHBA, FOS, KLF4, ESR1, IL2, BMP4, BCL9, AR, MAF, TAL1, CD28, FOSB, ERCC6	8.705719	3.06E-07	2.78E-07
GOTERM_BP_DIRECT	GO:0006366~transcription by RNA polymerase II	27	6.27E-09	TGFB3, ROBO2, TGFBR2, WNT11, HEY1, NOS3, HES1, SOX11, ZFPM2, NKX2-5, BMPR1A, ROBO1	3.929481	4.10E-07	3.72E-07
GOTERM_BP_DIRECT	GO:0060412~ventricular septum morphogenesis	12	7.01E-09	WWTR1, WNT10B, FHL2, TNC, GLI1, FGF2, GLI3, RUNX2, SOX2, BMP4, COL1A1, WNT11, FGF9, LOX, SMO, IBSP, CREB3L1, ID4, BMPR1A, EPHA2	10.80033	4.50E-07	4.09E-07
GOTERM_BP_DIRECT	GO:0001649~osteoblast differentiation	20	7.62E-09	WNT10B, WNT2B, WNT5B, HMGA2, GLI3, RUNX2, BMP4, EXT2, COL3A1, FGF9, NFIB, FGFR3, BMPR1A, FGFR1	5.261698	4.82E-07	4.38E-07
GOTERM_BP_DIRECT	GO:0002062~chondrocyte differentiation	14	9.23E-09	FLT4, PDGFA, FGF1, PTGS2, DLL4, FGF6, FGF9, HEY1, HOXA3, KDR, CYP1B1, APOD, ITGAV, PDGFRB, ANGPT1, EGF, NOS3, CAV1, DAB2IP, FZD8, PRKCA, TAL1, ID1, ACKR3, FGFR2, FGF10, BMPR1A, FGFR1	8.255423	5.74E-07	5.22E-07
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	28	9.84E-09	FOSL1, CEBPA, CEBPB, JUN, MAF, MAFB, CEBPD, CEBPE, DDIT3, FOS	3.726183	6.03E-07	5.47E-07
GOTERM_BP_DIRECT	GO:0140467~integrated stress response signaling	10	1.28E-08	CSF3, ANGPT1, IL15, SRC, EGF, ITGB3, IGF1, GATA1, GHR, IL3, FGF8, RELN, NTF3, CD36, PLPP3, FGF10	14.25043	7.70E-07	6.99E-07
GOTERM_BP_DIRECT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	16	1.83E-08		6.514484	1.09E-06	9.88E-07
GOTERM_BP_DIRECT	GO:0002053~positive regulation of mesenchymal cell proliferation	10	1.94E-08	SMO, PRRX1, FGF9, LRP5, KDR, PDGFA, IRS2, FGFR2, BMPR1A, FGFR1	13.68042	1.14E-06	1.03E-06
GOTERM_BP_DIRECT	GO:0060045~positive regulation of cardiac muscle cell proliferation	11	2.10E-08	TGFB3, YAP1, FGF9, ERBB4, GATA6, ZFPM2, GLI1, FGF2, FGFR2, BMPR1A, FGFR1	11.40035	1.20E-06	1.09E-06

GOTERM_ BP_DIRECT	GO:0010976~positive regulation of neuron projection development	19	2.11E-08	CAMK2B, NTRK1, RET, NTRK2, ATP8A2, EPO, BDNF, NTRK3, SERPINF1, DAB2IP, NCKIPSD, RELN, LRRC7, PTK7, CNTN1, ABL2, EPHA3, FGFR1, DDR2	5.240482	1.20E-06	1.09E-06
GOTERM_ BP_DIRECT	GO:0009952~anterior/posterior pattern specification	17	2.34E-08	ZBTB16, LRP5, HOXD13, HOXC13, HOXC11, GLI3, ACVR2A, PBX1, HOXA11, HOXA9, HEY1, SMO, WIF1, HOXA3, HES1, HOXD9, HES5	5.932833	1.31E-06	1.19E-06
GOTERM_ BP_DIRECT	GO:0001942~hair follicle development	12	2.94E-08	LAMAS, TGF2, FZD3, LHX2, FZD6, PDGFA, INHBA, HOXC13, ACVR1B, LGR5, DKK1, EGFR	9.544476	1.62E-06	1.47E-06
GOTERM_ BP_DIRECT	GO:0007179~transforming growth factor beta receptor signaling pathway	17	3.14E-08	TGF2, JUN, SMAD3, TGF2, SRC, PTPRK, FOS, SMAD6, TGF2, FLCN, COL3A1, COL1A2, CHST11, ID1, ITGA8, NODAL, BMPR1A	5.814177	1.71E-06	1.55E-06
GOTERM_ BP_DIRECT	GO:0007422~peripheral nervous system development	10	4.23E-08	NTF4, EGR2, EDNRB, EGR3, ERBB3, BDNF, SCN8A, NTF3, NGF, SOX10	12.66705	2.27E-06	2.06E-06
GOTERM_ BP_DIRECT	GO:0050680~negative regulation of epithelial cell proliferation	13	4.76E-08	CDKN1C, WNT10B, TGF2, CDKN2B, MAGED1, DAB2IP, SOX2, TGF2, BMP4, FLCN, AR, SFRP2, GPC3	8.083882	2.52E-06	2.29E-06
GOTERM_ BP_DIRECT	GO:0007420~brain development	24	5.69E-08	ROBO2, EGR2, EPHA7, PTCH1, SOX11, IRS2, SMARCA1, GRIN2B, EML1, EPOR, PBX1, SOX2, BCR, GRIN2A, RELN, ZIC2, CHL1, NFIB, NKX2-1, CNTN1, NCAM1, APOD, NODAL, HES5	3.90869	2.97E-06	2.70E-06
GOTERM_ BP_DIRECT	GO:0001764~neuron migration	18	5.83E-08	NTRK2, CDKL5, AUTS2, CEP85L, CCK, GATA3, GATA2, PHOX2B, COL3A1, RELN, TLX3, CHL1, AXL, KIT, ASTN2, FGF13, FGFR2, FGFR1	5.217108	2.97E-06	2.70E-06
GOTERM_ BP_DIRECT	GO:0042531~positive regulation of tyrosine phosphorylation of STAT protein	14	5.84E-08	CSF1R, EPO, IL15, FLT3, IL13, IGF1, IL2, GHR, IL3, ERBB4, KIT, HES1, FGFR3, HES5	7.146486	2.97E-06	2.70E-06
GOTERM_ BP_DIRECT	GO:1902894~negative regulation of miRNA transcription	10	6.08E-08	BMP4, HDAC4, SMAD3, NFIB, PDGFB, GATA6, RARA, PPARG, ESR1, POU5F1	12.21466	3.05E-06	2.77E-06
GOTERM_ BP_DIRECT	GO:0045665~negative regulation of neuron differentiation	13	1.09E-07	NOTCH3, OLIG2, FOXO3, DLL1, PHOX2B, GLI3, PBX1, SOX2, HEY1, TLX3, ID4, HES1, HES5	7.535822	5.42E-06	4.92E-06
GOTERM_ BP_DIRECT	GO:0001656~metanephros development	10	1.20E-07	BMP4, ROBO2, FGF8, EYA1, ITGA8, GDF6, HOXC11, GLI3, HOXA11, FGF10	11.40035	5.85E-06	5.32E-06
GOTERM_ BP_DIRECT	GO:0030326~embryonic limb morphogenesis	11	1.60E-07	NOTCH2, FBN2, TGF2, PRRX1, FGF9, PTCH1, HNF1A, DKK1, PBX1, FGFR1, HOXA11	9.405286	7.73E-06	7.02E-06
GOTERM_ BP_DIRECT	GO:0045840~positive regulation of mitotic nuclear division	10	1.64E-07	PDGFRB, FGF8, DMRT1, EGF, IL1B, PDGFB, LRP5, CD28, IGF1, HOXA13	11.03259	7.84E-06	7.12E-06
GOTERM_ BP_DIRECT	GO:0046579~positive regulation of Ras protein signal transduction	9	1.67E-07	NTRK1, NOTCH2, RASGEF1A, CSF1, EPO, SRC, IGF1, NGF, FGF10	13.38302	7.89E-06	7.16E-06
GOTERM_ BP_DIRECT	GO:0033138~positive regulation of peptidylserine phosphorylation	14	1.69E-07	TENM1, NTRK2, ANGPT1, BDNF, NTRK3, CAV1, AXIN1, NGF, PTGS2, EGFR, NTF4, SFRP2, NTF3, SPRY2	6.559104	7.89E-06	7.16E-06
GOTERM_ BP_DIRECT	GO:0030509~BMP signaling pathway	15	1.83E-07	NOTCH2, EGR1, GDF6, SMAD6, POU5F1, ACVR2A, RUNX2, TGF2, BMP4, EXT1, SFRP2, HES1, PPARG, HES5, BMPR1A	5.965298	8.43E-06	7.66E-06
GOTERM_ BP_DIRECT	GO:0048013~ephrin receptor signaling pathway	12	1.97E-07	NTRK1, EPHB6, EPHA5, TIAM1, EPHA7, EPHA10, SRC, CHN1, PAK3, KALRN, EPHA3, EPHA2	8.047303	8.96E-06	8.14E-06
GOTERM_ BP_DIRECT	GO:0016477~cell migration	27	2.39E-07	LAMAS, SDC4, ITGB3, PTPRK, RASGEF1A, ERBB4, CDH1, MYO18A, KDR, CTNNA1, GPC3, HES1, ITGAV, PAK5, TGF2, MATK, RHOD, TGF2, TIAM1, AXL, PTK7, CDH11, FGFR4, DOCK1, EPHA3, FGFR1, EPHA2	3.286221	1.08E-05	9.77E-06
GOTERM_ BP_DIRECT	GO:0001501~skeletal system development	18	2.46E-07	JAG2, TEAD4, HDAC4, TGF2, HOXD13, IGF1, HOXA13, ETS2, HOXA11, DLL3, COL1A1, COL1A2, GNA11, TRPS1, CDH11, FGFR3, EPHA2, FGFR1	4.735529	1.09E-05	9.94E-06
GOTERM_ BP_DIRECT	GO:0035162~embryonic hemopoiesis	8	2.62E-07	IL3, TPO, TAL1, KIT, KDR, FLT3LG, GATA3, PBX1	16.09461	1.15E-05	1.04E-05
GOTERM_ BP_DIRECT	GO:0007405~neuroblast proliferation	11	2.63E-07	DMRTA2, SMO, CTNNA1, ID4, ACSL6, FRS2, GATA2, FGF2, SOX10, EML1, GLI3	8.957415	1.15E-05	1.04E-05
GOTERM_ BP_DIRECT	GO:0001570~vasculogenesis	13	3.35E-07	YAP1, NTRK2, CAV1, HOXA13, SMO, WT1, KDR, ACKR3, HAS2, ITGAV, NKX2-5, ZFPM2, EPHA2	6.840208	1.44E-05	1.31E-05
GOTERM_ BP_DIRECT	GO:0048589~developmental growth	9	3.50E-07	SMAD3, CHST11, NOTCH4, GAS1, GATA3, SOX10, GLI3, BMPR1A, HOXA11	12.31237	1.49E-05	1.35E-05
GOTERM_ BP_DIRECT	GO:0048146~positive regulation of fibroblast proliferation	12	3.65E-07	PDGFRB, NGFR, CDKN1A, PDGFR, ITGB3, PDGFB, PDGFA, IGF1, ESR1, EGFR, DDR2, FGF10	7.600231	1.54E-05	1.40E-05
GOTERM_ BP_DIRECT	GO:0048568~embryonic organ development	10	3.95E-07	TEAD4, WNT7B, PTCH1, GATA3, ZFPM2, TEAD1, FGFR2, PBX1, BMPR1A, TEAD3	10.05913	1.64E-05	1.49E-05
GOTERM_ BP_DIRECT	GO:0009611~response to wounding	13	3.99E-07	TGF2, DST, PDGFB, SLC1A2, TNC, PDGFA, GLI1, POU5F1, SOX2, FOSL1, GRIN2A, NFIB, DDIT3	6.736568	1.64E-05	1.49E-05
GOTERM_ BP_DIRECT	GO:0007267~cell-cell signaling	24	4.06E-07	FZD2, IL15, PDGFA, FASLG, INHBA, TNFRSF11A, TRHDE, GATA1, IL2, FGF3, TSHR, FGF4, IL3, AR, FGF14, SFRP2, FGF9, IL1B, CCN6, NTF3, AMH, FGF13, FGFR3, FGFR2	3.507799	1.66E-05	1.51E-05
GOTERM_ BP_DIRECT	GO:0045937~positive regulation of phosphate metabolic process	6	4.17E-07	PDGFRB, CSF1R, FLT3, FLT4, KIT, KDR	29.31518	1.68E-05	1.53E-05
GOTERM_ BP_DIRECT	GO:0043627~response to estrogen	12	5.39E-07	SLC34A2, TGF2, EPO, CAV1, IGF2, GATA6, CTNNA1, PPARG, GATA3, SMAD6, ESR1, HOXA11	7.328794	2.15E-05	1.96E-05
GOTERM_ BP_DIRECT	GO:0051091~positive regulation of DNA-binding transcription factor activity	15	5.67E-07	HDAC4, HDAC5, FZD2, SMAD3, TNFRSF11A, ESR1, ZIC2, IL1B, DDIT3, KIT, PPARG, PLPP3, PPARGC1A, NODAL, DDR2	5.457613	2.24E-05	2.04E-05
GOTERM_ BP_DIRECT	GO:0019221~cytokine-mediated signaling pathway	19	6.63E-07	CEBPA, CSF1R, CSF3, CSF3R, FLT3, IRS1, CAV1, LIFR, INHBA, EPOR, GHR, FOSL1, IL1B, KIT, STAT4, IL13RA2, IL7R, IL12RB2, CRLF2	4.192386	2.60E-05	2.36E-05
GOTERM_ BP_DIRECT	GO:0097192~extrinsic apoptotic signaling pathway in absence of ligand	10	6.73E-07	ERBB3, EYA1, EYA2, IL1B, CTNNA1, ITGAV, FOXO3, IL2, BCL2L2, FGF10	9.500289	2.61E-05	2.37E-05
GOTERM_ BP_DIRECT	GO:0001657~ureteric bud development	10	8.66E-07	RET, BMP4, ROBO2, SMAD3, SDC4, WT1, RARA, SMAD6, FGFR2, FGFR1	9.243524	3.29E-05	2.99E-05

GOTERM_ BP_DIRECT	GO:0003180~aortic valve morphogenesis	10	8.66E-07	DLL4, BMP4, ROBO2, HEY1, NOS3, ELN, GATA3, NKX2-5, SMAD6, ROBO1	9.243524	3.29E-05	2.99E-05
GOTERM_ BP_DIRECT	GO:0050804~modulation of chemical synaptic transmission	14	9.15E-07	EPHA7, CDKL5, DGKB, GRID1, BDNF, NGF, DNM1, BCR, NTF4, AKAP12, RELN, PLCB4, NTF3, CDH11	5.700173	3.45E-05	3.13E-05
GOTERM_ BP_DIRECT	GO:0035567~non-canonical Wnt signaling pathway	9	9.31E-07	SFRP4, FZD3, SFRP2, FZD2, FZD7, FZD6, FZD8, FZD10, WNT4	10.99319	3.47E-05	3.16E-05
GOTERM_ BP_DIRECT	GO:0007613~memory	14	1.38E-06	CRTC1, BDNF, NGF, PTGS2, KALRN, NTF4, GRIN2A, TAF4, NTF3, ITGA8, PAK6, PLCB1, FGF13, PAK5	5.503616	5.09E-05	4.63E-05
GOTERM_ BP_DIRECT	GO:0060391~positive regulation of SMAD protein signal transduction	10	1.40E-06	TGFBR3, BMP4, TGF2, TGF3, INHBA, GDF6, AMH, NODAL, ACVR2A, BMPR1A	8.769497	5.09E-05	4.63E-05
GOTERM_ BP_DIRECT	GO:0003184~pulmonary valve morphogenesis	8	1.42E-06	NOTCH2, BMP4, ROBO2, TGF2, HEY1, NOS3, SMAD6, ROBO1	13.02897	5.09E-05	4.63E-05
GOTERM_ BP_DIRECT	GO:0014911~positive regulation of smooth muscle cell migration	8	1.42E-06	PDGFRB, SRC, ITGB3, PDGFB, CYP1B1, HAS2, IGF1, FOXO4	13.02897	5.09E-05	4.63E-05
GOTERM_ BP_DIRECT	GO:0007399~nervous system development	32	1.80E-06	HDAC4, CAMK2B, NOTCH2, TENM1, LRP5, WNT8B, ACVR1B, FGF2, KALRN, ROBO1, ACVR1C, EDNRB, ERBB4, NTF3, HES1, NTRK1, NTRK2, BDNF, NTRK3, PAX3, SOX11, INHBA, FOS, IL3, FGF14, NAV3, AXL, FGF19, SCN8A, NEURL1, ITGA8, FGF13	2.643559	6.40E-05	5.81E-05
GOTERM_ BP_DIRECT	GO:0043524~negative regulation of neuron apoptotic process	18	2.08E-06	PRKCG, NTRK1, NTRK2, CEBPB, ANGPT1, TGF3, BDNF, CBL, NGF, NTF4, FGF8, ERBB3, CCND1, CHL1, AXL, NTF3, KDR, PPARGC1A	4.076945	7.36E-05	6.68E-05
GOTERM_ BP_DIRECT	GO:0048701~embryonic cranial skeleton morphogenesis	9	2.19E-06	BMP4, TFAP2A, TBX15, PDGFRA, SMAD3, PRRX1, NODAL, FGFR2, RUNX2	9.929334	7.42E-05	6.74E-05
GOTERM_ BP_DIRECT	GO:0048010~vascular endothelial growth factor receptor signaling pathway	9	2.19E-06	FGF9, SRC, AXL, FLT4, KDR, VEGFC, VEGFD, SULF1, FGF10	9.929334	7.42E-05	6.74E-05
GOTERM_ BP_DIRECT	GO:0045664~regulation of neuron differentiation	9	2.19E-06	NTF4, ALK, RELN, BCL11B, EYA1, BIN1, BDNF, NTF3, NGF	9.929334	7.42E-05	6.74E-05
GOTERM_ BP_DIRECT	GO:0060071~Wnt signaling pathway, planar cell polarity pathway	9	2.19E-06	TIAM1, FZD3, FZD2, WNT11, FZD7, WNT7B, FZD6, GPC3, PRICKLE1	9.929334	7.42E-05	6.74E-05
GOTERM_ BP_DIRECT	GO:0030217~T cell differentiation	10	2.20E-06	JAG2, LFNG, DLL4, EGR1, WNT10B, KIT, PIK3R2, GATA3, IL2, RUNX2	8.341717	7.42E-05	6.74E-05
GOTERM_ BP_DIRECT	GO:0003151~outflow tract morphogenesis	11	2.61E-06	TGFBR3, SFRP2, FZD2, WNT11, EYA1, ELN, HES1, SOX11, PRICKLE1, NKX2-5, BMPR1A	7.098329	8.68E-05	7.88E-05
GOTERM_ BP_DIRECT	GO:1904707~positive regulation of vascular associated smooth muscle cell proliferation	11	2.61E-06	JUN, NR4A3, FGF9, SRC, PDGFB, FRS2, IGF1, FGF2, FGFR2, BMPR1A, DDR2	7.098329	8.68E-05	7.88E-05
GOTERM_ BP_DIRECT	GO:0010595~positive regulation of endothelial cell migration	12	2.98E-06	ANGPT1, ADGRA2, EGF, FLT4, ITGB3, KDR, PRKCA, GATA3, PLPP3, FGF1, FGF2, FUT1	6.218371	9.83E-05	8.93E-05
GOTERM_ BP_DIRECT	GO:0032496~response to lipopolysaccharide	17	3.10E-06	CEBPB, ACE, EPO, NOS3, IL13, FASLG, FOS, TNFRSF11A, PTGS2, SMAD6, TIRAP, AKAP12, CPS1, IL1B, FGFR2, IL12RB2, FGF10	4.182861	1.00E-04	9.12E-05
GOTERM_ BP_DIRECT	GO:0001837~epithelial to mesenchymal transition	11	3.13E-06	TGFBR3, TGF2, WNT11, NOTCH4, HGF, HMG2A, NCAM1, IGF1, FGFR2, FGFR1, WNT4	6.966878	1.00E-04	9.12E-05
GOTERM_ BP_DIRECT	GO:0042733~embryonic digit morphogenesis	11	3.13E-06	BMP4, SFRP2, CHST11, ZBTB16, GNA12, LRP5, HOXD13, HOXC11, GLI3, BMPR1A, HOXA11	6.966878	1.00E-04	9.12E-05
GOTERM_ BP_DIRECT	GO:0048008~platelet-derived growth factor receptor signaling pathway	9	3.66E-06	PDGFRB, PDGFRA, NR4A3, SRC, PDGFD, ITGB3, PDGFB, PDGFA, PLAT	9.327556	1.16E-04	1.05E-04
GOTERM_ BP_DIRECT	GO:0048469~cell maturation	9	3.66E-06	IL15, AXL, HES1, PPARG, GATA3, SOX10, HES5, RUNX2, FGFR1	9.327556	1.16E-04	1.05E-04
GOTERM_ BP_DIRECT	GO:0007155~cell adhesion	36	3.87E-06	ROBO2, CSF3R, SRC, LAMA1, CTNND2, ITGB3, TNC, PTPRK, ROBO1, RELN, IBSP, CHL1, CCN6, CTNNA1, CYP1B1, ABL2, NCAM1, HES1, ITGAV, CD36, EDIL3, HES5, DST, OMD, PRKCA, IL2, COL1A1, PPFIBP1, PTK7, CDH11, CNTN1, COL6A3, ACKR3, EPHA3, EPHA2, DDR2	2.381504	1.21E-04	1.10E-04
GOTERM_ BP_DIRECT	GO:0030282~bone mineralization	11	6.14E-06	WNT11, COL1A2, IBSP, LOX, GPC3, PRICKLE1, PTGS2, FGFR3, GATA1, FGFR2, RUNX2	6.486404	1.91E-04	1.73E-04
GOTERM_ BP_DIRECT	GO:0042127~regulation of cell population proliferation	17	6.43E-06	JAG2, TFAP2A, ALK, TGF2, JUN, MMP7, KSR1, TGF3, HOXD13, MITF, ERBB3, CHST11, TAL1, PLAU, KIT, STAT4, LGR5	3.955222	1.98E-04	1.80E-04
GOTERM_ BP_DIRECT	GO:0060395~SMAD protein signal transduction	8	7.06E-06	WWTR1, JUN, SMAD3, FOS, INHBA, GDF6, SMAD6, RUNX2	10.5234	2.16E-04	1.96E-04
GOTERM_ BP_DIRECT	GO:0001938~positive regulation of endothelial cell proliferation	12	7.17E-06	BMP4, EGR3, EGF, FLT4, ITGB3, PDGFB, KDR, VEGFC, VEGFD, PRKCA, FGF2, FGF10	5.700173	2.18E-04	1.98E-04
GOTERM_ BP_DIRECT	GO:0030334~regulation of cell migration	15	7.32E-06	LAMA5, LAMA1, TNC, FGF1, FGF2, FGF3, FGF4, FGF6, FGF8, FGF9, ERBB4, FGF19, RAC3, FGF23, FGF10	4.422548	2.20E-04	2.00E-04
GOTERM_ BP_DIRECT	GO:0070372~regulation of ERK1 and ERK2 cascade	9	7.38E-06	TIAM1, EPHA7, IL1B, ERBB2, FRS2, ROS1, EGFR, FGFR2, EPHA2	8.55026	2.21E-04	2.00E-04
GOTERM_ BP_DIRECT	GO:0060749~mammary gland alveolus development	7	8.29E-06	SOC2, AR, CCND1, ERBB4, EGF, TNFRSF11A, ESR1	13.3004	2.43E-04	2.21E-04
GOTERM_ BP_DIRECT	GO:0060065~uterus development	7	8.29E-06	TGF2, HOXA9, SRC, FOXL2, GATA3, ESR1, HOXA11	13.3004	2.43E-04	2.21E-04
GOTERM_ BP_DIRECT	GO:0001823~mesonephros development	6	8.31E-06	BMP4, FGF8, PAX8, ZBTB16, GATA3, FGF10	18.65511	2.43E-04	2.21E-04
GOTERM_ BP_DIRECT	GO:0009954~proximal/distal pattern formation	8	9.29E-06	HOXA9, GLI1, DLL1, HOXD9, HOXC11, GLI3, PBX1, HOXA11	10.13364	2.70E-04	2.45E-04

GOTERM_ BP_DIRECT	GO:0046330~positive regulation of JNK cascade	14	9.43E-06	GADD45B, FZD7, FLT4, WNT7B, DAB2IP, AXIN1, NOD1, FZD10, WNT16, DKK1, TIRAP, IL1B, FGF19, PLCB1	4.648685	2.72E-04	2.47E-04
GOTERM_ BP_DIRECT	GO:0030336~negative regulation of cell migration	19	9.83E-06	NGFR, KANK1, TET1, MITF, PTPRK, FOXO3, SULF1, ROBO1, TGFB3, DACH1, SFRP2, WNT11, NAV3, CDH1, CDH11, NKX2-1, CYP1B1, SRGAP3, WNT4	3.474972	2.81E-04	2.55E-04
GOTERM_ BP_DIRECT	GO:0001822~kidney development	15	1.09E-05	TFAP2A, TGFB2, ACE, SERPINF1, SOX11, GATA3, SULF1, BICC1, BMP4, PAX8, WT1, PTK7, ITGA8, HAS2, WNT4	4.27513	3.09E-04	2.80E-04
GOTERM_ BP_DIRECT	GO:0032332~positive regulation of chondrocyte differentiation	7	1.18E-05	SMAD3, ZBTB16, PRKG2, GDF6, GLI3, RUNX2, HOXA11	12.60038	3.33E-04	3.03E-04
GOTERM_ BP_DIRECT	GO:0050918~positive chemotaxis	10	1.24E-05	BMP4, FGF8, ANGPT1, HGF, NTF3, PDGFB, VEGFC, VEGFD, FGF2, FGF10	6.840208	3.48E-04	3.16E-04
GOTERM_ BP_DIRECT	GO:2001237~negative regulation of extrinsic apoptotic signaling pathway	9	1.39E-05	BMP4, YAP1, TCF7L2, AR, SRC, ITGAV, IGF1, ZMYND11, PAK5	7.892548	3.83E-04	3.48E-04
GOTERM_ BP_DIRECT	GO:0008217~regulation of blood pressure	12	1.39E-05	EXT1, EXT2, ACE, EDNRB, COL1A2, NOS3, GNA11, GNA12, LRP5, PPARG, PTGS2, DLL1	5.330032	3.83E-04	3.48E-04
GOTERM_ BP_DIRECT	GO:0007219~Notch signaling pathway	15	1.45E-05	JAG2, NOTCH2, NOTCH3, CECPA, MAML2, NOTCH4, SORBS2, DLL1, DLL3, DLL4, HEY1, NEURL1, CNTN1, HES1, HES5	4.170859	3.96E-04	3.60E-04
GOTERM_ BP_DIRECT	GO:0070371~ERK1 and ERK2 cascade	10	1.73E-05	FLCN, EGF, GRB10, SPRY2, ITGAV, NOD1, FGF2, FGF23, DUSP9, FGF10	6.577123	4.72E-04	4.29E-04
GOTERM_ BP_DIRECT	GO:0030199~collagen fibril organization	11	1.75E-05	EXT1, COL1A1, COL3A1, TGFB2, SFRP2, COL1A2, LOX, COL11A1, TLL2, CYP1B1, DDR2	5.787868	4.74E-04	4.30E-04
GOTERM_ BP_DIRECT	GO:0098609~cell-cell adhesion	20	1.91E-05	ROBO2, LAMAS, SRC, CTNND2, LRP5, PRICKLE1, LPP, EGFR, ROBO1, BAIAP2L1, CDH1, LRRC7, KIT, ITGA8, CTNNA1, CNTN1, ITGA7, ITGAV, PLPP3, FGFR2	3.181492	5.12E-04	4.65E-04
GOTERM_ BP_DIRECT	GO:0042476~odontogenesis	8	1.97E-05	BMP4, TGFB2, FGF8, COL1A2, TGFB3, SRC, INHBA, FGFR2	9.120277	5.26E-04	4.78E-04
GOTERM_ BP_DIRECT	GO:0031401~positive regulation of protein modification process	6	2.21E-05	PDGFRB, CSF1R, FLT3, FLT4, KIT, KDR	15.7851	5.80E-04	5.27E-04
GOTERM_ BP_DIRECT	GO:0060644~mammary gland epithelial cell differentiation	6	2.21E-05	CEBPB, SMO, ERBB4, PTCH1, ZNF703, FGF2	15.7851	5.80E-04	5.27E-04
GOTERM_ BP_DIRECT	GO:0009948~anterior/posterior axis specification	7	2.25E-05	BMP4, CDX2, CDX1, DDIT3, GPC3, LEFTY2, WNT3	11.40035	5.80E-04	5.27E-04
GOTERM_ BP_DIRECT	GO:0032924~activin receptor signaling pathway	7	2.25E-05	SMAD3, ACVR1C, FGF9, INHBA, GDF6, ACVR1B, ACVR2A	11.40035	5.80E-04	5.27E-04
GOTERM_ BP_DIRECT	GO:0001709~cell fate determination	7	2.25E-05	NOTCH2, NOTCH4, PTCH1, HES1, GATA3, GATA2, DLL1	11.40035	5.80E-04	5.27E-04
GOTERM_ BP_DIRECT	GO:0032956~regulation of actin cytoskeleton organization	13	2.29E-05	PDGFRB, EPHA5, PDGFRA, CSF1R, ITGB3, PDGFA, FZD10, RHOD, BAIAP2L1, RAC3, ABL2, PAK3, EPHA3	4.631391	5.85E-04	5.32E-04
GOTERM_ BP_DIRECT	GO:0060449~bud elongation involved in lung branching	5	2.34E-05	BMP4, YAP1, SPRY2, FGFR2, FGF10	24.42931	5.92E-04	5.38E-04
GOTERM_ BP_DIRECT	GO:0002067~glandular epithelial cell differentiation	5	2.34E-05	EXT1, YAP1, NFIB, CAV1, KLF4	24.42931	5.92E-04	5.38E-04
GOTERM_ BP_DIRECT	GO:0035264~multicellular organism growth	13	2.82E-05	NOTCH2, WWTR1, PLAG1, SLC1A2, PRICKLE1, EXT1, AR, COL3A1, TAL2, SMO, PPP1R13L, RARA, ERCC6	4.536873	7.08E-04	6.43E-04
GOTERM_ BP_DIRECT	GO:0048856~anatomical structure development	9	2.95E-05	TFAP2A, PAX8, EYA1, PAX7, EYA2, PAX3, HOXD11, HOXC11, HOXA11	7.158357	7.37E-04	6.70E-04
GOTERM_ BP_DIRECT	GO:0040037~negative regulation of fibroblast growth factor receptor signaling pathway	7	3.02E-05	NGFR, CREB3L1, SPRY4, SPRY2, SULF1, FGF2, WNT4	10.88215	7.48E-04	6.79E-04
GOTERM_ BP_DIRECT	GO:0001889~liver development	12	3.21E-05	TGFB3, CECPA, CDKN2B, SMAD3, HGF, GATA6, RARA, HES1, HNF1A, JARID2, NODAL, WNT4	4.885863	7.88E-04	7.16E-04
GOTERM_ BP_DIRECT	GO:0010718~positive regulation of epithelial to mesenchymal transition	10	3.22E-05	BMP4, COL1A1, WWTR1, TIAM1, TCF7L2, TGFB2, SMAD3, TGFB3, IL1B, ZNF703	6.107329	7.88E-04	7.16E-04
GOTERM_ BP_DIRECT	GO:0010463~mesenchymal cell proliferation	6	3.35E-05	WNT11, PRRX1, FGF9, KDR, FGFR1, FGF4	14.65759	8.10E-04	7.36E-04
GOTERM_ BP_DIRECT	GO:0038180~nerve growth factor signaling pathway	6	3.35E-05	NTRK1, NTF4, SORT1, BDNF, NTF3, NGF	14.65759	8.10E-04	7.36E-04
GOTERM_ BP_DIRECT	GO:0007224~smooth end signaling pathway	12	3.60E-05	WNT10B, SMO, PRRX1, FGF9, PTCH1, CTNNA1, GPC3, HES1, GLI1, GLI3, HES5, RUNX2	4.828382	8.64E-04	7.85E-04
GOTERM_ BP_DIRECT	GO:0032355~response to estradiol	12	4.02E-05	GHR, SOCS2, COL1A1, PTCH1, DNMT3A, IGF2BP2, RARA, WNT8B, CYP1B1, PTGS2, ESR1, FGF10	4.772238	9.59E-04	8.71E-04
GOTERM_ BP_DIRECT	GO:0030513~positive regulation of BMP signaling pathway	9	4.17E-05	NOTCH2, BMP4, GATA6, GPC3, KDR, HES1, SOX11, SULF1, HES5	6.840208	9.90E-04	9.00E-04
GOTERM_ BP_DIRECT	GO:0045599~negative regulation of fat cell differentiation	10	4.30E-05	YAP1, WWTR1, WNT10B, SMAD3, SORT1, DDIT3, AXIN1, ID4, ZFPM2, RUNX1T1	5.896731	0.001014	9.21E-04
GOTERM_ BP_DIRECT	GO:0045666~positive regulation of neuron differentiation	12	4.48E-05	SOCS2, BMP4, EPO, RARA, SOX11, GATA2, NGF, GDF6, NKX2-5, PHOX2B, ETV5, FGFR1	4.717385	0.001051	9.54E-04
GOTERM_ BP_DIRECT	GO:0003129~heart induction	5	4.58E-05	BMP4, ROBO2, DKK1, POU5F1, ROBO1	21.37565	0.001068	9.70E-04
GOTERM_ BP_DIRECT	GO:0045648~positive regulation of erythrocyte differentiation	8	4.72E-05	BRD1, TAL1, INHBA, GATA2, FOXO3, ACVR1B, GATA1, ACVR2A	8.047303	0.001093	9.93E-04
GOTERM_ BP_DIRECT	GO:0048863~stem cell differentiation	9	4.92E-05	CDX2, KIT, GATA6, HMGA2, FOXO4, JARID2, ESR1, RUNX2, FGFR1	6.691508	0.001134	0.00103

GOTERM_BP_DIRECT	GO:0030325~adrenal gland development	7	5.18E-05	PDGFRA, SMAD3, WNT11, WT1, CYP1B1, PBX1, WNT4	9.975303	0.001186	0.001077
GOTERM_BP_DIRECT	GO:0097150~neuronal stem cell population maintenance	7	6.64E-05	SOX2, PRRX1, FANCC, HES1, FOXO3, DLL1, HES5	9.576291	0.001496	0.001359
GOTERM_BP_DIRECT	GO:0021983~pituitary gland development	7	6.64E-05	SOX2, BMP4, CDH1, NKX2-1, GLI1, BMPR1A, FGF10	9.576291	0.001496	0.001359
GOTERM_BP_DIRECT	GO:0060038~cardiac muscle cell proliferation	7	6.64E-05	TGFBF3, TGFB2, FGF9, GATA6, JARID2, NKX2-5, FGFR1	9.576291	0.001496	0.001359
GOTERM_BP_DIRECT	GO:0007417~central nervous system development	15	6.71E-05	ROBO2, NGFR, GSN, APLP2, ZBTB16, AHI1, RELN, PAX8, SMO, ZIC2, TLX3, ADGRA2, JARID2, MNX1, SH3GL2	3.638408	0.001497	0.00136
GOTERM_BP_DIRECT	GO:0035914~skeletal muscle cell differentiation	9	6.76E-05	EGR1, DMRTA2, BCL9, EGR2, HLF, SOX11, FOS, PHOX2B, ATF3	6.412695	0.001497	0.00136
GOTERM_BP_DIRECT	GO:0048839~inner ear development	9	6.76E-05	SOX2, CEBPA, TGFB2, MAF, CEBPD, TGFB3, LGR5, HOXA13, PHOX2B	6.412695	0.001497	0.00136
GOTERM_BP_DIRECT	GO:0045471~response to ethanol	13	7.43E-05	CSF3, IL13, TNC, FOS, TNFRSF11A, GRIN2B, IL2, IGF1R, GRIN2A, RARA, FOSB, FGFR2, RGS7	4.116792	0.001636	0.001486
GOTERM_BP_DIRECT	GO:0035556~intracellular signal transduction	29	7.65E-05	NOTCH2, BRSK1, ITK, SHC2, DGKB, SRC, NOD1, KALRN, SOCS2, FLCN, SOCS3, EDNRB, RPS6KA2, ERBB2, PAK6, RAC3, PAK3, PAK5, RGS7, PRKCG, DMRT1, DAB2IP, HMGA2, PRKCA, TGFBF3, BCR, NR4A3, KIT, CILK1	2.295903	0.001674	0.00152
GOTERM_BP_DIRECT	GO:0030178~negative regulation of Wnt signaling pathway	9	7.88E-05	DKK4, SFRP4, RNF43, SFRP2, FGF9, WIF1, GRB10, CXXC4, DKK1	6.281824	0.001715	0.001558
GOTERM_BP_DIRECT	GO:0060484~lung-associated mesenchyme development	5	8.05E-05	WNT11, FGF9, PTK7, FGFR2, FGFR1	19.00058	0.001743	0.001583
GOTERM_BP_DIRECT	GO:0000165~MAPK cascade	14	8.17E-05	RET, KSR1, CAV1, MAPK8IP2, DUSP9, EGFR, AR, FGF8, CD36, PAK3, MAP3K6, FGF13, FGFR3, FGFR1	3.800116	0.001759	0.001598
GOTERM_BP_DIRECT	GO:0031100~animal organ regeneration	8	8.37E-05	TGFBF3, CDKN1A, ACE, NR4A3, FLT3, AXL, PPARG, GATA1	7.394819	0.001781	0.001618
GOTERM_BP_DIRECT	GO:0070555~response to interleukin-1	8	8.37E-05	GHR, HDAC4, IL1R1, EPO, SRC, IL1B, PRKCA, TNFRSF11A	7.394819	0.001781	0.001618
GOTERM_BP_DIRECT	GO:0043491~phosphatidylinositol 3-kinase/protein kinase B signal transduction	11	8.78E-05	FLCN, ERBB3, IRS1, ERBB2, CD28, COL6A3, PIK3R2, GATA3, FGF2, EPHA2, IGF1R	4.823224	0.001859	0.001688
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	16	8.93E-05	NTRK1, NOS3, ITGB3, GATA6, VEGFC, HMGA2, VEGFD, PRKCA, GATA2, FGF1, FGF2, SFRP2, IL1B, KDR, CYP1B1, NODAL	3.357157	0.001882	0.001709
GOTERM_BP_DIRECT	GO:0043536~positive regulation of blood vessel endothelial cell migration	9	9.14E-05	ANGPT1, NOS3, PDGFB, KDR, VEGFC, PRKCA, GATA2, FGF2, FGFR1	6.156187	0.001915	0.00174
GOTERM_BP_DIRECT	GO:0071230~cellular response to amino acid stimulus	10	9.52E-05	COL1A1, NTRK2, PDGFRA, COL3A1, CEBPB, COL1A2, PDGFD, DNMT3A, NEURL1, EGFR	5.343912	0.001983	0.001801
GOTERM_BP_DIRECT	GO:2000573~positive regulation of DNA biosynthetic process	6	9.63E-05	PDGFRB, HGF, PDGFB, CYP1B1, FGFR4, FGF2	12.07096	0.001996	0.001813
GOTERM_BP_DIRECT	GO:0002052~positive regulation of neuroblast proliferation	8	1.00E-04	DMRTA2, FZD3, SMO, ID4, VEGFC, FGF2, SOX10, GLI3	7.200219	0.002062	0.001873
GOTERM_BP_DIRECT	GO:0009953~dorsal/ventral pattern formation	8	1.19E-04	FGF8, LHX2, PTCH1, TLL2, HOXD11, GLI1, BMPR1A, HOXA11	7.015598	0.002412	0.002191
GOTERM_BP_DIRECT	GO:0001541~ovarian follicle development	8	1.19E-04	LFNG, CEBPB, KIT, CTNNA1, KDR, FOXL2, INHBA, AMH	7.015598	0.002412	0.002191
GOTERM_BP_DIRECT	GO:0048144~fibroblast proliferation	8	1.19E-04	NGFR, COL3A1, CDKN1A, WNT7B, CAV1, VEGFD, ESR1, FGF10	7.015598	0.002412	0.002191
GOTERM_BP_DIRECT	GO:0097009~energy homeostasis	9	1.22E-04	ALK, FLCN, CEBPA, CRT3, NR4A3, CRT1, CD36, DLL1, PPARGC1A	5.919411	0.002459	0.002233
GOTERM_BP_DIRECT	GO:0050678~regulation of epithelial cell proliferation	6	1.30E-04	LAMA5, EDNRB, SMAD3, HES1, FRS2, HES5	11.40035	0.002562	0.002327
GOTERM_BP_DIRECT	GO:0030857~negative regulation of epithelial cell differentiation	6	1.30E-04	YAP1, SMO, CCND1, CAV1, DLL1, FGF10	11.40035	0.002562	0.002327
GOTERM_BP_DIRECT	GO:0051145~smooth muscle cell differentiation	6	1.30E-04	BMP4, GATA6, ITGA8, MRTFB, WNT4, FGF10	11.40035	0.002562	0.002327
GOTERM_BP_DIRECT	GO:0071548~response to dexamethasone	6	1.30E-04	ACE, CPS1, EPO, PAPP, CYP1B1, FOXO3	11.40035	0.002562	0.002327
GOTERM_BP_DIRECT	GO:0002063~chondrocyte development	6	1.30E-04	SFRP2, CHST11, COL11A1, SULF1, RUNX2, HOXA11	11.40035	0.002562	0.002327
GOTERM_BP_DIRECT	GO:0016055~Wnt signaling pathway	16	1.34E-04	AMER1, RNF43, FZD2, WNT7B, CTNND2, AXIN1, MITF, WNT16, CXXC4, DKK2, DKK4, CCND1, WIF1, DIT3, RAC3, FGF10	3.237968	0.002628	0.002387
GOTERM_BP_DIRECT	GO:0001974~blood vessel remodeling	8	1.40E-04	EXT1, DLL4, ACE, FGF8, AXL, NOS3, HOXA3, FGF10	6.840208	0.002724	0.002474
GOTERM_BP_DIRECT	GO:0050767~regulation of neurogenesis	8	1.40E-04	DLL4, YAP1, HEY1, IL1B, HES1, DLL1, WNT3, HES5	6.840208	0.002724	0.002474
GOTERM_BP_DIRECT	GO:0060349~bone morphogenesis	7	1.61E-04	TFAP2A, SFRP4, CDX1, LRPS, HAS2, FGFR3, FGFR2	8.255423	0.003115	0.002829
GOTERM_BP_DIRECT	GO:0007507~heart development	18	1.70E-04	CDKN1A, TGFB2, NTRK3, PDGFB, EPOR, GLI3, BICC1, COL3A1, LOX, ERBB3, WT1, ERBB4, WIF1, GNA11, ERBB2, PPARG, NKX2-5, ZFPM2	2.903862	0.003274	0.002974
GOTERM_BP_DIRECT	GO:0071560~cellular response to transforming growth factor beta stimulus	10	1.72E-04	COL1A1, CDKN2B, SMAD3, PDGFD, CAV1, FOS, FGFR2, IGF1R, WNT4, DDR2	4.956672	0.003278	0.002978
GOTERM_BP_DIRECT	GO:0030949~positive regulation of vascular endothelial growth	6	1.72E-04	FGF9, IL1B, ITGB3, GRB10, ROBO1, FGF10	10.80033	0.003278	0.002978

	factor receptor signaling pathway							
GOTERM_	GO:0030501~positive regulation of bone mineralization	8	1.93E-04	FBN2, BMP4, TFAP2A, WNT10B, SMAD3, ACVR2A, BMPR1A, WNT4	6.514484	0.003657	0.003322	
BP_DIRECT				EXT1, COL1A1, EXT2, SORT1, COL11A1, CDH11, TNFRSF11A, EGFR, RUNX2, FSTL3, DDR2	4.374552	0.003773	0.003428	
GOTERM_	GO:0001503~ossification	11	2.01E-04					
BP_DIRECT	GO:0060445~branching involved in salivary gland morphogenesis	5	2.01E-04	LAMA5, FGF8, LAMA1, FGFR2, FGFR1	15.54593	0.003773	0.003428	
GOTERM_	GO:0001892~embryonic placenta development	6	2.24E-04	CEBPA, CEBPB, PDGFB, GATA2, EGFR, NODAL	10.26031	0.004121	0.003743	
BP_DIRECT	GO:0036342~post-anal tail morphogenesis	6	2.24E-04	FZD3, SFRP2, CHST11, AXIN1, PRICKLE1, EPHA2	10.26031	0.004121	0.003743	
GOTERM_	GO:0007215~glutamate receptor signaling pathway	6	2.24E-04	GRIN2A, KCNB1, GRID1, GNAQ, PLCB1, GRIN2B	10.26031	0.004121	0.003743	
BP_DIRECT	GO:2000647~negative regulation of stem cell proliferation	6	2.24E-04	WNT11, NFIB, PTCH1, FGF2, GLI3, FGF10	10.26031	0.004121	0.003743	
GOTERM_	GO:0046427~positive regulation of receptor signaling pathway via JAK-STAT	8	2.25E-04	GHR, ERBB4, KIT, CAMK2A, CYP1B1, HES1, IL7R, HES5	6.362984	0.004121	0.003743	
BP_DIRECT	GO:0009612~response to mechanical stimulus	9	2.35E-04	COL1A1, FOSL1, SRC, PTCH1, IGFBP2, TNC, FOSB, PPARG, TNFRSF11A	5.400164	0.004287	0.003894	
GOTERM_	GO:0030878~thyroid gland development	7	2.38E-04	SMAD3, FGF8, PAX8, HOXA3, NKX2-1, NKX2-5, FGF10	7.722815	0.004298	0.003904	
BP_DIRECT	GO:0051602~response to electrical stimulus	7	2.38E-04	NTRK1, AKAP12, FZD3, BRD1, EPO, SRC, PRICKLE1	7.722815	0.004298	0.003904	
GOTERM_	GO:0048009~insulin-like growth factor receptor signaling pathway	7	2.86E-04	GHR, AR, IRS1, GRB10, IGF1, PLCB1, IGF1R	7.481477	0.005137	0.004666	
BP_DIRECT	GO:0030850~prostate gland development	5	2.95E-04	HOXA9, PTCH1, RARA, GLI1, HOXA11	14.25043	0.005207	0.00473	
GOTERM_	GO:0048333~mesoderm al cell differentiation	5	2.95E-04	ITGB3, ITGA8, HMGA2, INHBA, FGFR2	14.25043	0.005207	0.00473	
BP_DIRECT	GO:0043433~negative regulation of DNA-binding transcription factor activity	10	2.95E-04	HDAC4, TCF7L2, SFRP4, DDIT3, PTCH1, FZD6, ID1, HES1, ESR1, PBX1	4.621762	0.005207	0.00473	
GOTERM_	GO:0050808~synapse organization	10	2.95E-04	NTRK2, PTK7, WNT7B, CTNND2, SNCG, NCAM1, PAK3, FGFR4, PPFIA2, ROBO1	4.621762	0.005207	0.00473	
BP_DIRECT	GO:0045597~positive regulation of cell differentiation	9	3.37E-04	SOX2, GHR, SOCS3, AR, FGF8, CDX2, PPP1R13L, CCN6, FGFR1	5.130156	0.005856	0.00532	
GOTERM_	GO:0045785~positive regulation of cell adhesion	9	3.37E-04	IBSP, ANGPT1, LAMA1, ERBB2, PIK3R2, ITGAV, PRKCA, DUSP26, RHOD	5.130156	0.005856	0.00532	
BP_DIRECT	GO:0030225~macrophage differentiation	7	3.41E-04	BMP4, CEBPA, CSF1R, CSF1, IL15, CEBPE, GATA3	7.254766	0.005856	0.00532	
GOTERM_	GO:0003281~ventricular septum development	7	3.41E-04	PAX8, PTK7, HES1, FR52, GATA3, SMAD6, HOXA13	7.254766	0.005856	0.00532	
BP_DIRECT	GO:0035115~embryonic forelimb morphogenesis	7	3.41E-04	TFAP2A, HOXA9, HOXD9, HOXA13, WNT3, RUNX2, HOXA11	7.254766	0.005856	0.00532	
GOTERM_	GO:0035924~cellular response to vascular endothelial growth factor stimulus	7	3.41E-04	DLL4, EGR3, FLT4, DAB2IP, KDR, GAS1, SPRY2	7.254766	0.005856	0.00532	
BP_DIRECT	GO:0032868~response to insulin	10	3.61E-04	COL1A1, EGR1, EGR2, ACVR1C, SORT1, IRS1, IGFBP2, GRB10, FOS, TNFRSF11A	4.500137	0.006158	0.005593	
GOTERM_	GO:0030879~mammary gland development	6	3.63E-04	HOXA9, TGF83, NOTCH4, CAV1, IRS2, HOXD9	9.327556	0.006158	0.005593	
BP_DIRECT	GO:0048665~neuron fate specification	6	3.63E-04	DMRTA2, EYA1, TLX3, NFIB, FEV, DLL1	9.327556	0.006158	0.005593	
GOTERM_	GO:0048812~neuron projection morphogenesis	9	3.79E-04	NTF4, SHTN1, BDNF, NTF3, DAB2IP, NGF, EGFR, MNX1, GAS7	5.046055	0.006394	0.005808	
BP_DIRECT	GO:0048286~lung alveolus development	8	3.97E-04	BMP4, ACE, TGF83, FLT4, KDR, PDGFA, FGFR2, FGF10	5.821454	0.006674	0.006063	
GOTERM_	GO:0071260~cellular response to mechanical stimulus	10	3.99E-04	COL1A1, WNT11, CRADD, IL1B, ITGB3, IL13, PTGS2, FGF2, EGFR, IGF1R	4.441693	0.006674	0.006063	
BP_DIRECT	GO:0035987~endoderm al cell differentiation	7	4.04E-04	BRD3, COL11A1, HMGA2, ITGA7, ITGAV, INHBA, NODAL	7.041391	0.006731	0.006114	
GOTERM_	GO:0071679~commissural neuron axon guidance	5	4.16E-04	FZD3, SMO, NFIB, PTCH1, NCAM1	13.15425	0.006824	0.006199	
BP_DIRECT	GO:0061029~eyelid development in camera-type eye	5	4.16E-04	TFAP2A, SOX11, PRICKLE1, INHBA, EGFR	13.15425	0.006824	0.006199	
GOTERM_	GO:0048584~positive regulation of response to stimulus	5	4.16E-04	PDGFRB, CSF1R, FLT3, FLT4, KDR	13.15425	0.006824	0.006199	
BP_DIRECT	GO:0033690~positive regulation of osteoblast proliferation	5	4.16E-04	ITGB3, LRP5, ITGAV, GATA1, IGF1R	13.15425	0.006824	0.006199	
GOTERM_	GO:0048663~neuron fate commitment	6	4.53E-04	BMP4, NOTCH3, OLIG1, BHLHE22, OLIG2, ZNF521	8.92201	0.007341	0.006669	
BP_DIRECT	GO:0036120~cellular response to platelet-derived growth factor stimulus	6	4.53E-04	PDGFRB, SRC, PDGFD, ITGB3, PDGFB, HAS2	8.92201	0.007341	0.006669	

GOTERM_BP_DIRECT	GO:0048538~thymus development	8	4.53E-04	MAFB, BCL11B, HOXA3, HES1, GATA3, JARID2, PBX1, FGF10	5.700173	0.007341	0.006669
GOTERM_BP_DIRECT	GO:0014807~regulation of somitogenesis	4	4.63E-04	LFNG, CDX2, CDX1, DLL1	22.80069	0.007378	0.006702
GOTERM_BP_DIRECT	GO:0060527~prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis	4	4.63E-04	FRS2, HOXD13, ESR1, FGFR2	22.80069	0.007378	0.006702
GOTERM_BP_DIRECT	GO:0060129~thyroid-stimulating hormone-secreting cell differentiation	4	4.63E-04	FGF8, GATA2, FGF2, WNT4	22.80069	0.007378	0.006702
GOTERM_BP_DIRECT	GO:0060510~type II pneumocyte differentiation	4	4.63E-04	NFIB, GATA6, NKX2-1, FGF10	22.80069	0.007378	0.006702
GOTERM_BP_DIRECT	GO:0060828~regulation of canonical Wnt signaling pathway	7	4.75E-04	AMER1, PTK7, FZD7, GNAQ, CTNND2, ZNF703, GPC3	6.840208	0.00754	0.00685
GOTERM_BP_DIRECT	GO:0006919~activation of cysteine-type endopeptidase activity involved in apoptotic process	10	4.83E-04	RET, NGFR, HIP1, SMAD3, CRADD, FASLG, NOD1, PPARG, BCL2L2, ROBO1	4.329246	0.007631	0.006932
GOTERM_BP_DIRECT	GO:0038083~peptidyl-tyrosine autophosphorylation	5	5.69E-04	NTRK1, ALK, KDR, EGFR, IGF1R	12.21466	0.008923	0.008106
GOTERM_BP_DIRECT	GO:0042491~inner ear auditory receptor cell differentiation	5	5.69E-04	BMP4, HES1, DLL1, FGF2, HES5	12.21466	0.008923	0.008106
GOTERM_BP_DIRECT	GO:0016525~negative regulation of angiogenesis	13	6.06E-04	TGFB2, SERPINF1, DAB2IP, FASLG, FOXO4, KLF4, SULF1, DCN, CCN6, SPRY2, PPARG, CD36, EPHA2	3.293433	0.009455	0.008589
GOTERM_BP_DIRECT	GO:0046326~positive regulation of glucose import	7	6.48E-04	IRS1, FGF19, CLTC1, SLC1A2, GPC3, IRS2, IGF1	6.470467	0.010036	0.009116
GOTERM_BP_DIRECT	GO:0032570~response to progesterone	7	6.48E-04	YAP1, FOSL1, TGFB2, TGFB3, CAV1, FOSB, FOS	6.470467	0.010036	0.009116
GOTERM_BP_DIRECT	GO:0048546~digestive tract morphogenesis	5	7.59E-04	SFRP2, GLI1, SOX10, EGFR, NODAL	11.40035	0.011701	0.010629
GOTERM_BP_DIRECT	GO:0010518~positive regulation of phospholipase activity	4	7.93E-04	PLA2G5, FGFR3, FGFR2, FGFR1	19.54345	0.011997	0.010898
GOTERM_BP_DIRECT	GO:0007501~mesodermal cell fate specification	4	7.93E-04	SFRP2, EYA1, EYA2, HOXA11	19.54345	0.011997	0.010898
GOTERM_BP_DIRECT	GO:2000144~positive regulation of DNA-templated transcription initiation	4	7.93E-04	FOSL1, CEBPA, JUN, MITF	19.54345	0.011997	0.010898
GOTERM_BP_DIRECT	GO:0032927~positive regulation of activin receptor signaling pathway	4	7.93E-04	FGF9, ACVR1B, NODAL, ACVR2A	19.54345	0.011997	0.010898
GOTERM_BP_DIRECT	GO:0071393~cellular response to progesterone stimulus	4	7.93E-04	SRC, CYP1B1, SOX10, IGF1R	19.54345	0.011997	0.010898
GOTERM_BP_DIRECT	GO:0008045~motor neuron axon guidance	6	8.24E-04	EGR2, FGF8, ERBB2, CHN1, RAC3, LHX4	7.892548	0.012315	0.011187
GOTERM_BP_DIRECT	GO:0001894~tissue homeostasis	6	8.24E-04	YAP1, WWTR1, COL3A1, NFIB, PRICKLE1, HOXA13	7.892548	0.012315	0.011187
GOTERM_BP_DIRECT	GO:0071542~dopaminergic neuron differentiation	6	8.24E-04	DMRTA2, FGF8, SMO, VEGFD, PHOX2B, TSHR	7.892548	0.012315	0.011187
GOTERM_BP_DIRECT	GO:0065003~protein-containing complex assembly	13	8.37E-04	YAP1, AXIN1, PDE4DIP, FANCC, MITF, IL1RAP, EXT1, TIAM1, SNX9, HES1, PPARGC1A, TEAD1, HES5	3.175811	0.012474	0.011331
GOTERM_BP_DIRECT	GO:0045595~regulation of cell differentiation	7	8.66E-04	TFAP2A, CEBPB, CEBPD, KLF4, HES5, RUNX2, FGFR1	6.138648	0.012848	0.011671
GOTERM_BP_DIRECT	GO:0032753~positive regulation of interleukin-4 production	6	9.87E-04	CEBPB, PRG2, RARA, CD28, GATA3, IL1RAP	7.600231	0.014447	0.013124
GOTERM_BP_DIRECT	GO:0032967~positive regulation of collagen biosynthetic process	6	9.87E-04	BMP4, TGFB3, CREB3L1, INHBA, WNT4, DDR2	7.600231	0.014447	0.013124
GOTERM_BP_DIRECT	GO:0038092~nodal signaling pathway	5	9.88E-04	SMAD3, ACVR1C, WIF1, ACVR1B, NODAL	10.68782	0.014447	0.013124
GOTERM_BP_DIRECT	GO:0033630~positive regulation of cell adhesion mediated by integrin	5	9.88E-04	RET, TGFB2, SFRP2, ITGB3, RAC3	10.68782	0.014447	0.013124
GOTERM_BP_DIRECT	GO:0021766~hippocampus development	9	0.001163	EPHA5, ALK, RELN, ID4, NKX2-1, RARA, FGF13, GLI3, IGF1R	4.27513	0.016944	0.015391
GOTERM_BP_DIRECT	GO:0045600~positive regulation of fat cell differentiation	8	0.001169	LMO1, CEBPA, CEBPB, SFRP2, WIF1, ZBTB16, LRP5, PPARG	4.885863	0.016954	0.0154
GOTERM_BP_DIRECT	GO:0035116~embryonic hindlimb morphogenesis	6	0.001173	BMP4, FGF8, ZBTB16, GPC3, WNT3, FGF4	7.328794	0.016954	0.0154
GOTERM_BP_DIRECT	GO:0003149~membrane septum morphogenesis	4	0.001241	BMP4, TGFB2, FZD2, FGFR2	17.10052	0.017817	0.016184
GOTERM_BP_DIRECT	GO:0010544~negative regulation of platelet activation	4	0.001241	PDGFRA, NOS3, PDGFB, PDGFA	17.10052	0.017817	0.016184

GOTERM_ BP_DIRECT	GO:0060326~cell chemotaxis	10	0.00125	PDGFRB, PDGFRA, LOX, HGF, KIT, PDGFB, LPAR1, RAC3, ACKR3, EPHA2	3.800116	0.017869	0.016232
GOTERM_ BP_DIRECT	GO:0060216~definitive hemopoiesis	5	0.001263	BCR, TGFBR3, HOXA9, TAL1, GATA2	10.05913	0.017925	0.016282
GOTERM_ BP_DIRECT	GO:0048557~embryonic digestive tract morphogenesis	5	0.001263	PDGFRA, SOX11, GLI3, FGFR2, FGF10	10.05913	0.017925	0.016282
GOTERM_ BP_DIRECT	GO:0002244~hematopoietic progenitor cell differentiation	9	0.001274	BMP4, PDGFRA, CEBPD, KIT, INHBA, GATA2, DOCK1, EML1, FSTL3	4.216567	0.018017	0.016366
GOTERM_ BP_DIRECT	GO:0009880~embryonic pattern specification	6	0.001383	SMAD3, ERBB4, ZBTB16, NODAL, FGFR2, FGF10 NOTCH2, ZNF331, CEBPA, PRDM7, CEBPB, PLAG1, MAGED1, PHF1, NOTCH4, NAB2, HOXD13, FOXO4, ACVR1B, GLI1, GLI3, SOX2, ZNF703, NKX2-1, PAK6, NKX2-5, ZNF687, PPARGC1A, BRD3, WWTR1, JUN, BRD1, SMAD3, FZD7, PRRX2, ATP1B4, HMG2, MITF, SMARCA1, ESR1, MLF1, POU5F1, MN1, MAFB, SETBP1, WT1, KAT6B, DDIT3	7.076077	0.019496	0.017771
GOTERM_ BP_DIRECT	GO:0006355~regulation of DNA-templated transcription	42	0.001401		1.674177	0.01968	0.017877
GOTERM_ BP_DIRECT	GO:0007229~integrin- mediated signaling pathway	11	0.001426	LAMA5, COL3A1, DST, SRC, ITGB3, ITGA8, CTNNA1, ITGA7, ITGAV, PLPP3, DOCK1	3.420104	0.019955	0.018126
GOTERM_ BP_DIRECT	GO:0071363~cellular response to growth factor stimulus	8	0.001441	ACVR1C, IBSP, ERBB2, PDGFB, KLF4, ACVR1B, ACVR2A, BMPR1A	4.717385	0.020092	0.018251
GOTERM_ BP_DIRECT	GO:0048704~embryonic skeletal system morphogenesis	7	0.001466	PDGFRA, HOXA9, EYA1, COL11A1, HOXA3, SOX11, HOXD9	5.567611	0.020368	0.018502
GOTERM_ BP_DIRECT	GO:0042326~negative regulation of phosphorylation	5	0.001586	CDKN1C, CDKN1A, CDKN2B, GRB10, INHBA	9.500289	0.021884	0.019879
GOTERM_ BP_DIRECT	GO:0043388~positive regulation of DNA binding	5	0.001586	EGF, HES1, PPARC, IGF1, NGF	9.500289	0.021884	0.019879
GOTERM_ BP_DIRECT	GO:0030155~regulation of cell adhesion	8	0.001595	JAG2, RET, LAMA5, PLAU, TNC, ABL2, DLL1, FUT1	4.637429	0.021921	0.019913
GOTERM_ BP_DIRECT	GO:0071773~cellular response to BMP stimulus	6	0.001621	BMP4, GATA6, GATA3, PHOX2B, ACVR2A, BMPR1A	6.840208	0.022201	0.020167
GOTERM_ BP_DIRECT	GO:0034446~substrate adhesion-dependent cell spreading	8	0.001761	LAMA5, SRC, LAMA1, AXL, FZD7, ITGB3, ITGA8, ITGAV	4.560139	0.024035	0.021833
GOTERM_ BP_DIRECT	GO:1904383~response to sodium phosphate	4	0.001822	EDNRB, FGF23, RUNX2, FGF1	15.20046	0.024363	0.022131
GOTERM_ BP_DIRECT	GO:0061626~pharyngeal arch artery morphogenesis	4	0.001822	BMP4, TGFBR2, HES1, BMPR1A	15.20046	0.024363	0.022131
GOTERM_ BP_DIRECT	GO:0003416~endochondral bone growth	4	0.001822	EXT1, FGFR3, FGFR2, DDR2	15.20046	0.024363	0.022131
GOTERM_ BP_DIRECT	GO:0060231~mesenchymal to epithelial transition	4	0.001822	WT1, FZD7, GATA3, WNT4	15.20046	0.024363	0.022131
GOTERM_ BP_DIRECT	GO:0010907~positive regulation of glucose metabolic process	4	0.001822	SLC45A3, IRS1, SRC, IRS2	15.20046	0.024363	0.022131
GOTERM_ BP_DIRECT	GO:0090129~positive regulation of synapse maturation	4	0.001822	CAMK2B, RELN, NEURL1, DAB2IP	15.20046	0.024363	0.022131
GOTERM_ BP_DIRECT	GO:0007281~germ cell development	7	0.001865	BMP4, DMRTA2, DMRT1, WT1, RARA, FANCC, NODAL	5.320162	0.024682	0.022421
GOTERM_ BP_DIRECT	GO:0043408~regulation of MAPK cascade	7	0.001865	ITK, CSF1R, FLT4, KDR, PAK6, PAK3, PAK5	5.320162	0.024682	0.022421
GOTERM_ BP_DIRECT	GO:0030316~osteoclast differentiation	7	0.001865	CSF1R, CSF1, GPC3, MITF, FOS, TNFRSF11A, EPHA2	5.320162	0.024682	0.022421
GOTERM_ BP_DIRECT	GO:0038084~vascular endothelial growth factor signaling pathway	5	0.001963	FLT3, FLT4, KDR, VEGFC, VEGFD	9.000274	0.025813	0.023448
GOTERM_ BP_DIRECT	GO:0046849~bone remodeling	5	0.001963	NOTCH2, LRP5, MITF, WNT16, EPHA2	9.000274	0.025813	0.023448
GOTERM_ BP_DIRECT	GO:0071333~cellular response to glucose stimulus	9	0.002124	COL1A1, ACE, SMAD3, KCNB1, SERPINF1, IRS2, HNF1A, FOXO3, IGF1R	3.896321	0.027734	0.025193
GOTERM_ BP_DIRECT	GO:0001843~neural tube closure	9	0.002124	BMP4, TGFBR2, FZD3, SDC4, LH2, PTCH1, FZD6, RARA, PRICKLE1	3.896321	0.027734	0.025193
GOTERM_ BP_DIRECT	GO:0010575~positive regulation of vascular endothelial growth factor production	6	0.002183	IL1B, FLT4, CYP1B1, SULF1, PTGS2, NODAL	6.412695	0.028227	0.02564
GOTERM_ BP_DIRECT	GO:0060325~face morphogenesis	6	0.002183	COL1A1, PDGFRA, ASPH, TGFBR3, PRICKLE1, DKK1	6.412695	0.028227	0.02564
GOTERM_ BP_DIRECT	GO:0048706~embryonic skeletal system development	6	0.002183	COL1A1, WNT11, FGF9, SULF1, ACVR2A, PBX1	6.412695	0.028227	0.02564
GOTERM_ BP_DIRECT	GO:0007565~female pregnancy	9	0.002301	FOSL1, ACE, TGFBR3, PAPP, IGFBP2, RARA, FOSB, FOS, TEAD3	3.847617	0.02965	0.026934
GOTERM_ BP_DIRECT	GO:0030539~male genitalia development	5	0.002398	PDGFRA, FGF8, WT1, HOXD13, HOXA13	8.55026	0.030605	0.027801
GOTERM_ BP_DIRECT	GO:0021675~nerve development	5	0.002398	NTF4, NGFR, BDNF, NTF3, NGF	8.55026	0.030605	0.027801
GOTERM_ BP_DIRECT	GO:0045780~positive regulation of bone resorption	5	0.002398	SRC, ITGB3, PRKCA, TNFRSF11A, EGFR	8.55026	0.030605	0.027801
GOTERM_ BP_DIRECT	GO:0007409~axonogenesis	10	0.002433	SHTN1, BRSK1, ATP8A2, ATL1, APLP2, CCK, PRICKLE1, PAK3, FGFR2, IGF1R	3.45465	0.030848	0.028022

GOTERM_BP_DIRECT	GO:0007517~muscle organ development GO:0035793~positive regulation of metanephric mesenchymal cell migration by platelet-derived growth factor receptor-beta signaling pathway	10	0.002433	TEAD4, LAMA5, EGR3, MRTFB, PAX3, COL6A3, ITGA7, ETV1, IGF1, FOXO4	3.45465	0.030848	0.028022
GOTERM_BP_DIRECT	GO:0010966~regulation of phosphate transport GO:2000544~regulation of endothelial cell chemotaxis to fibroblast growth factor	3	0.002502	PDGFRB, PDGFB, PDGFA	34.20104	0.031144	0.02829
GOTERM_BP_DIRECT	GO:0051799~negative regulation of hair follicle development GO:0051968~positive regulation of synaptic transmission, glutamatergic	3	0.002502	ROS1, FGF23, FGFR1	34.20104	0.031144	0.02829
GOTERM_BP_DIRECT	GO:0044344~cellular response to fibroblast growth factor stimulus GO:0001958~endochondral ossification GO:2000726~negative regulation of cardiac muscle cell differentiation	3	0.002502	FGF1, FGF2, FGF4	34.20104	0.031144	0.02829
GOTERM_BP_DIRECT	GO:0060351~cartilage development involved in endochondral bone morphogenesis GO:0042552~myelination	3	0.002502	NGFR, SMO, INHBA	34.20104	0.031144	0.02829
GOTERM_BP_DIRECT	GO:0051402~neuron apoptotic process GO:0030308~negative regulation of cell growth	6	0.002512	NTRK1, GRIN2A, RELN, PTGS2, GRIN2B, EGFR	6.218371	0.031144	0.02829
GOTERM_BP_DIRECT	GO:0006338~chromatin remodeling GO:0120162~positive regulation of cold-induced thermogenesis GO:0048873~homeostasis of number of cells within a tissue GO:0030511~positive regulation of transforming growth factor beta receptor signaling pathway	6	0.002512	DLL4, COL1A1, EXT2, EGR3, CPS1, FGFR1	6.218371	0.031144	0.02829
GOTERM_BP_DIRECT	GO:0001958~endochondral ossification GO:2000726~negative regulation of cardiac muscle cell differentiation	6	0.002512	EXT1, BMP4, COL1A1, NAB2, FGFR3, RUNX2	6.218371	0.031144	0.02829
GOTERM_BP_DIRECT	GO:0060351~cartilage development involved in endochondral bone morphogenesis GO:0042552~myelination	4	0.002547	FZD7, FRS2, DLL1, DKK1	13.68042	0.031376	0.028501
GOTERM_BP_DIRECT	GO:0051402~neuron apoptotic process GO:0030308~negative regulation of cell growth	4	0.002547	GHR, EXT1, COL1A1, HOXA11	13.68042	0.031376	0.028501
GOTERM_BP_DIRECT	GO:0006338~chromatin remodeling GO:0120162~positive regulation of cold-induced thermogenesis GO:0048873~homeostasis of number of cells within a tissue GO:0030511~positive regulation of transforming growth factor beta receptor signaling pathway	8	0.002563	EGR2, ERBB3, SCN8A, ERBB2, NAB2, LPAR1, ACSBG1, OLIG2	4.27513	0.031477	0.028593
GOTERM_BP_DIRECT	GO:0031069~hair follicle morphogenesis GO:0060037~pharyngeal system development GO:0060252~positive regulation of glial cell proliferation	9	0.002689	NTRK1, NGFR, EPHA7, FGF8, ERBB3, ANGPT1, AXL, COL6A3, PPARGC1A, CDKN1A, TGF2, SFRP2, SMAD3, WNT11, WT1, GNG4, PPARG, INHBA, ACVR1B, RERG	3.753773	0.032926	0.029909
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	11	0.002727	BRD3, HDAC4, PRDM7, PRMT8, BRD1, NPM2, EYA1, EYA2, CHD6, TET1, PRKCA, GATA3, HNF1A, SMARCA1, ESR1, PER1, MECOM, SETBP1, PRDM16, ERCC6, JARID2	3.135095	0.033286	0.030236
GOTERM_BP_DIRECT	GO:0006338~chromatin remodeling GO:0120162~positive regulation of cold-induced thermogenesis GO:0048873~homeostasis of number of cells within a tissue GO:0030511~positive regulation of transforming growth factor beta receptor signaling pathway	21	0.002752	CEBPB, CAV1, PRDM16, IL13, GRB10, CD36, PPARGC1A, PHOX2B, TSHR, IGF1R	2.093941	0.03348	0.030412
GOTERM_BP_DIRECT	GO:0031069~hair follicle morphogenesis GO:0060037~pharyngeal system development GO:0060252~positive regulation of glial cell proliferation	10	0.002789	CEBPB, CAV1, PRDM16, IL13, GRB10, CD36, PPARGC1A, PHOX2B, TSHR, IGF1R	3.386242	0.03383	0.03073
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	6	0.002875	SMO, CSF1, NOS3, RAC3, GATA2, GATA1	6.035478	0.034557	0.031391
GOTERM_BP_DIRECT	GO:0031069~hair follicle morphogenesis GO:0060037~pharyngeal system development GO:0060252~positive regulation of glial cell proliferation	6	0.002875	CDKN1C, TGFB3, FLCN, CDKN2B, ITGA8, AXIN1	6.035478	0.034557	0.031391
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	6	0.002875	EXT1, NGFR, TGF2, SMO, FGFR2, FGF10	6.035478	0.034557	0.031391
GOTERM_BP_DIRECT	GO:0031069~hair follicle morphogenesis GO:0060037~pharyngeal system development GO:0060252~positive regulation of glial cell proliferation	5	0.002895	FGF8, EYA1, PTCH1, GATA3, NKX2-5	8.143105	0.034578	0.031409
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	5	0.002895	PLAG1, IL1B, VEGFC, EGFR, ETV5	8.143105	0.034578	0.031409
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	12	0.003034	SRC, DNMT3A, MPL, GATA6, PPARG, FOS, INHBA, FOXO3, PTGS2, NDRG1, FGFR2, DDR2	2.890229	0.036128	0.032818
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	8	0.003057	GRIN2A, ERBB3, NAV3, ERBB4, ERBB2, LPAR1, ERCC6, EGFR	4.145581	0.03629	0.032965
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	7	0.003218	SOX2, NOTCH3, DNAJB1, SRC, NKX2-1, FRS2, DKK1	4.788146	0.038095	0.034604
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	6	0.003275	CEBPA, CEBPB, PRDM16, GATA2, PTGS2, PPARGC1A	5.863035	0.038537	0.035006
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	6	0.003275	NTRK1, KCNB1, EPO, AXL, APOD, FGF2	5.863035	0.038537	0.035006
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	8	0.003329	BCR, YAP1, ACER1, CDKN1A, MAFB, AKR1C3, WNT16, EPHA2	4.083706	0.039054	0.035475
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	10	0.003399	YAP1, TGF2, RELN, DMRT1, CDH1, HGF, CDH11, IL7R, DKK1, WNT3	3.288562	0.03948	0.035863
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	4	0.003426	JAG2, LAMA5, VEGFC, FGFR2	12.43674	0.03948	0.035863
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	4	0.003426	WNT6, WNT2B, SOX11, PRICKLE1	12.43674	0.03948	0.035863
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	4	0.003426	CDKN2B, MAF, TAL1, GATA1	12.43674	0.03948	0.035863
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	4	0.003426	BMP4, TCF7L2, NR4A3, ELN	12.43674	0.03948	0.035863
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	4	0.003426	PDGFRA, AR, NKX2-1, AMH	12.43674	0.03948	0.035863
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia GO:0022008~neurogenesis GO:0030900~forebrain development GO:0050873~brown fat cell differentiation GO:0048678~response to axon injury GO:0030216~keratinocyte differentiation GO:0000902~cell morphogenesis GO:0016331~morphogenesis of embryonic epithelium	5	0.003457	EDNRB, KIT, MITF, SOX10, GLI3	7.772964	0.039607	0.035978

GOTERM_ BP_DIRECT	GO:0061003~positive regulation of dendritic spine morphogenesis	5	0.003457	CAMK2B, TIAM1, RELN, ITPKA, KALRN	7.772964	0.039607	0.035978
GOTERM_ BP_DIRECT	GO:0007611~learning or memory	8	0.00362	NTRK1, PRKCG, GRIN2A, EGR2, SRC, GRIN2B, DKK1, EGFR	4.023652	0.041351	0.037562
GOTERM_ BP_DIRECT	GO:0006351~DNA-templated transcription	9	0.003886	TEAD4, CEBPA, HOXA9, CEBPB, PAX8, CEBPE, HOXD9, MLF1, RUNX1T1	3.538039	0.044262	0.040206
GOTERM_ BP_DIRECT	GO:0031623~receptor internalization	7	0.003926	GHR, DNM3, CAV1, NEDD4, ACKR3, CD36, DNM1	4.603986	0.044371	0.040305
GOTERM_ BP_DIRECT	GO:0097190~apoptotic signaling pathway	8	0.00393	MLLT11, HIP1, CRADD, CAV1, CD28, FASLG, PRKCA, WNT4	3.965338	0.044371	0.040305
GOTERM_ BP_DIRECT	GO:0045668~negative regulation of osteoblast differentiation	8	0.00393	HDAC4, SMAD3, PTCH1, LRP5, VEGFC, PPARG, SMAD6, FGF23	3.965338	0.044371	0.040305
GOTERM_ BP_DIRECT	GO:0007492~endoderm development	5	0.00409	EXT1, BMP4, SMAD3, NKX2-1, HOXC11	7.435009	0.045652	0.041469
GOTERM_ BP_DIRECT	GO:0070498~interleukin-1-mediated signaling pathway	5	0.00409	EGR1, IL1R1, IL1B, IL1RAP, PLCB1	7.435009	0.045652	0.041469
GOTERM_ BP_DIRECT	GO:0008589~regulation of smoothened signaling pathway	5	0.00409	PTCH1, GAS1, GLI1, FGFR2, FGF10	7.435009	0.045652	0.041469
GOTERM_ BP_DIRECT	GO:0048168~regulation of neuronal synaptic plasticity	5	0.00409	GRIN2A, EGR2, CAMK2A, SYP, GRIN2B	7.435009	0.045652	0.041469
GOTERM_ BP_DIRECT	GO:2001240~negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	6	0.004193	EYA1, EYA2, IL1B, CTNNA1, GATA1, FGF10	5.546115	0.046538	0.042274
GOTERM_ BP_DIRECT	GO:0043407~negative regulation of MAP kinase activity	6	0.004193	IL1B, SPRY4, DAB2IP, CBLC, SPRY2, PPARG	5.546115	0.046538	0.042274
GOTERM_ BP_DIRECT	GO:0048666~neuron development	7	0.004321	NTRK1, EPHA5, ALK, TENM1, TGFB2, ATP8A2, PBX1	4.517118	0.047685	0.043316
GOTERM_ BP_DIRECT	GO:0097191~extrinsic apoptotic signaling pathway	7	0.004321	MLLT11, YAP1, TGFB2, SMAD3, FASLG, INHBA, ACVR1B	4.517118	0.047685	0.043316
GOTERM_ BP_DIRECT	GO:0060444~branching involved in mammary gland duct morphogenesis	4	0.00447	CSF1, SRC, LRP5, EPHA2	11.40035	0.048646	0.044188
GOTERM_ BP_DIRECT	GO:0048484~enteric nervous system development	4	0.00447	RET, EDNRB, SOX10, PHOX2B	11.40035	0.048646	0.044188
GOTERM_ BP_DIRECT	GO:0032754~positive regulation of interleukin-5 production	4	0.00447	RARA, GATA3, IL1RAP, CRLF2	11.40035	0.048646	0.044188
GOTERM_ BP_DIRECT	GO:0072112~podocyte differentiation	4	0.00447	EXT1, EDNRB, WT1, PROM1	11.40035	0.048646	0.044188
GOTERM_ BP_DIRECT	GO:0010936~negative regulation of macrophage cytokine production	4	0.00447	TGFB2, TGFB3, AXL, PRG2	11.40035	0.048646	0.044188
GOTERM_ BP_DIRECT	GO:0001947~heart looping	8	0.004609	NOTCH2, AHI1, SMAD3, FGF8, SMO, NKX2-5, DLL1, NODAL	3.853638	0.050022	0.045438
GOTERM_ BP_DIRECT	GO:0045880~positive regulation of smoothened signaling pathway	6	0.004714	SMO, PRRX1, FGF9, CTNNA1, GPC3, GLI1	5.400164	0.050745	0.046095
GOTERM_ BP_DIRECT	GO:0051591~response to cAMP	6	0.004714	COL1A1, FOSL1, PER1, GATA6, FOSB, FOS	5.400164	0.050745	0.046095
GOTERM_ BP_DIRECT	GO:2000352~negative regulation of endothelial cell apoptotic process	6	0.004714	ANGPT1, ITGB3, IL13, KDR, GATA3, GATA2	5.400164	0.050745	0.046095
GOTERM_ BP_DIRECT	GO:0030099~myeloid cell differentiation	5	0.004796	CEBPA, CEBPE, ZBTB16, DLL1, TIRAP	7.125217	0.050865	0.046204
GOTERM_ BP_DIRECT	GO:0017015~regulation of transforming growth factor beta receptor signaling pathway	5	0.004796	TGFBR3, SMAD3, LOX, ZNF703, SOX11	7.125217	0.050865	0.046204
GOTERM_ BP_DIRECT	GO:0071425~hematopoietic stem cell proliferation	5	0.004796	WNT10B, CEBPA, SFRP2, WNT2B, MECOM	7.125217	0.050865	0.046204
GOTERM_ BP_DIRECT	GO:0060571~morphogenesis of an epithelial fold	3	0.004907	AR, HOXD13, EGFR	25.65078	0.050865	0.046204
GOTERM_ BP_DIRECT	GO:0045608~negative regulation of inner ear auditory receptor cell differentiation	3	0.004907	HES1, DLL1, HES5	25.65078	0.050865	0.046204
GOTERM_ BP_DIRECT	GO:0072050~S-shaped body morphogenesis	3	0.004907	PAX8, HES1, HES5	25.65078	0.050865	0.046204
GOTERM_ BP_DIRECT	GO:0060684~epithelial-mesenchymal cell signaling	3	0.004907	BMP4, WNT6, SMO	25.65078	0.050865	0.046204
GOTERM_ BP_DIRECT	GO:1900127~positive regulation of hyaluronan biosynthetic process	3	0.004907	EGF, PDGFB, HAS2	25.65078	0.050865	0.046204
GOTERM_ BP_DIRECT	GO:0060486~club cell differentiation	3	0.004907	NFIB, GATA6, NKX2-1	25.65078	0.050865	0.046204
GOTERM_ BP_DIRECT	GO:0038162~erythropoietin-mediated signaling pathway	3	0.004907	EPO, KIT, EPOR	25.65078	0.050865	0.046204

GOTERM_BP_DIRECT	GO:0042490~mechanoreceptor differentiation	3	0.004907	NTRK1, NTF4, NTRK2	25.65078	0.050865	0.046204
GOTERM_BP_DIRECT	GO:0007386~compartment pattern specification	3	0.004907	LFNG, DLL1, DLL3	25.65078	0.050865	0.046204
GOTERM_BP_DIRECT	GO:1904238~pericyte cell differentiation	3	0.004907	BMP4, EPHA2, WNT4	25.65078	0.050865	0.046204
GOTERM_BP_DIRECT	GO:0060665~regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling	3	0.004907	HGF, FGFR1, FGF10	25.65078	0.050865	0.046204
GOTERM_BP_DIRECT	GO:0045786~negative regulation of cell cycle	7	0.005196	BMP4, CEBPA, PPP1R13B, RPS6KA2, GATA3, PTPRK, PTGS2, HOXA13, ETS2, SOX2, HOXA9, CREB3L1, HOXA3, MNX1, SOX11, MITF, HNF1A, SOX10, RUNX2, MYCL, AR, MYCN, MAF, KAT6B, DDIT3, ERG, ZFPM2, ATF3, MAGED1, GATA6, GATA3, BHLHE22, FOXO4, FOXO3, GATA1, NKX2-1, NKX2-5, PPARGC1A, TFAP2A, EGR1, JUN, EGR2, EGR3, SMAD3, EGR4, HMGA2, FANCC, FANCE, SMARCA1, SMAD6, ESR1, PBX1, PHOX2B, FANCF, FOSL1, NR4A3, MAFB, TLX3, LHX2, TLX1, FEV, LHX4, HOXD9, CHD6, HOXC13, HOXC11, HEY1, TRPS1, JARID2, TEAD1, TEAD3, BRD3, TEAD4, PAX3, ETV1, FOXL2, OLIG1, FOS, OLIG2, ETV4, ETV5, POU5F1, DMRTA2, PAX8, TAL2, PAX7, TAL1, RARA, AHRR, PPARG, PLCB1, HDAC4, CEBPA, CEBPB, HLF, CEBPD, CEBPE, HOXD13, HOXD11, MUC1, SLX4, STAT4, HES1, HES5, TCF7L2, NPM2, PRRX1, CDX2, DMRT1, CDX1, PRRX2, KLF4, TBX15, NR6A1, NFIB, NEDD4, FOSB	4.35286	0.053714	0.048792
GOTERM_CC_DIRECT	GO:0000785~chromatin	110	8.79E-30	RET, ALK, CSF3R, FLT3, FLT4, ITGB3, PTPRK, IGF1R, GHR, KDR, OLR1, CD36, IL13RA2, ROS1, PDGFRB, PDGFRA, LIFR, TGFB3, KIT, PPARG, EPHA2, DDR2, NOTCH2, CSF1R, NOTCH3, SRC, LRP5, ACVR1B, EGFR, ERBB3, ERBB4, ERBB2, IL12RB2, NTRK1, NTRK2, SMAD3, NTRK3, STYK1, TSHR, ACVR2A, LRP1B, AXL, PTK7, FGFR4, FGFR3, FGFR2, BMPR1A, FGFR1, CRLF2	3.380131	4.37E-27	4.02E-27
GOTERM_CC_DIRECT	GO:0043235~receptor complex	49	1.40E-28	EPHB6, ROBO2, EPO, ITGB3, MPL, PLAT, PTPRK, FZD10, ROBO1, GHR, PLAU, ADGRA2, MYO18A, ITGAV, CD36, ROS1, PPIA2, FLT3LG, TIRAP, TGFB3, SFRP4, KIT, ITGA8, ITGA7, EPHA2, NOTCH2, CSF1R, NOTCH3, SDC4, NOTCH4, PDGFB, SLC1A2, LPAR1, PDGFA, ACVR1B, EGFR, WNT6, TPO, GRIN2A, WIF1, GPC3, NCAM1, PROM1, WNT4, NTRK1, NGFR, FZD3, SORT1, TGFB3, KCNB1, FZD6, HSPA2, SULF1, GRIN2B, TSHR, ACVR2A, TNFRSF10D, AXL, CD28, ACKR3, FGFR3, FGFR2, FGF10	7.735926	3.47E-26	3.20E-26
GOTERM_CC_DIRECT	GO:0009986~cell surface	63	4.14E-17	EPHB6, CSF3, TNFRSF6B, CSF3R, CSF1, EPO, TNC, PRF1, PLAT, IL1RAP, FGF1, FGF2, FGF3, FGF4, FGF6, FGF8, IBSP, FGF9, PLAU, CDH1, CCN6, KDR, PRSS8, IL13RA2, WNT5B, IL1R1, HGF, SERPINF1, OMD, IGFBP2, CTRB1, FLT3LG, DKK1, SFRP4, LOX, PAPPA, EPHA3, FBN2, NOTCH2, NOTCH3, EPHA10, NOTCH4, HTRA1, PDGFB, PDGFA, PLA2G5, KLK2, LTBP1, KLK7, WNT6, PDGFD, APOD, FGF23, WNT3, WNT4, WNT10B, NGFR, TGFB2, ACE, BDNF, TGFB3, PRG2, INHBA, IGF1, IL2, BMP4, COL1A1, IL3, COL1A2, FGF19, COL9A3, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1, TENM1, WNT2B, FLT4, ELN, FASLG, LFNG, GHR, OLR1, AMH, MMP7, IL15, IL13, WNT16, NGF, DCN, LRRC7, IL1B, CDH11, COL6A3, ALDOC, LAMA5, CANT1, LAMA1, COL11A1, WNT8B, TMPPSS2, DLL1, FSTL3, NTF4, RELN, WNT11, ERBB4, WIF1, NTF3, GPC3, NCAM1, LEFTY2, GSN, ANGPT1, EGF, WNT7B, PLA2G2A, VEGFC, CCK, VEGFD, EPOR, COL3A1, TLL2, CRLF2	3.40623	6.86E-15	6.32E-15
GOTERM_CC_DIRECT	GO:0005576~extracellular region	126	2.55E-16	EPHB6, PRF1, CBLC, FZD10, BAIAP2L1, EDNRB, ADGRA2, KDR, PRSS8, ARRD4, PRKCG, EPHA5, SLC34A2, EPHA7, IL1R1, ACSL6, FLT3LG, SOX11, FRS2, PRKCA, DKK1, GABRG2, BCR, AR, TIAM1, BIN1, BCORL1, PLPP3, EPHA3, EPHA2, SLC45A3, SDC4, EPHA10, MAGED1, LPAR1, PLA2G5, KALRN, GRIN2A, INPP5A, SNX9, PROM1, JAG2, NGFR, WWTR1, FZD3, ACE, FZD2, MAGEE1, FZD7, FZD6, FZD8, GRIN2B, PPIBP1, PTK7, CD28, XKR3, RET, DIRAS3, ROBO2, ITK, TENM1, PTPRR, PTPRK, ROBO1, AKAP12, CHL1, RAC3, OLR1, CTLA4, CD36, PRMT8, RHOD, PLCB4, LRRC7, KIT, RARA, GAS1, ACSBG1, DDR2, GAS7, AMER1, KANK1, TMPPSS2, GNAI1, EGFR, RELN, GPC3, CTNNA1, HAS2, CKB, FLNC, PAK3, PAK5, IL12RB2, GSN, SORT1, KCNB1, WNT7B, DAB2IP, SEPTIN5, SORBS2, SULF1, AXL, NEDD4, TACC2, LGR5, CRLF2, ATP8A2, CSF3R, CSF1, DGKB, IRS1, TUSC3, CRT1, CTNND2, MPL, IRS4, IRS2, IL1RAP, ETS2, IGF1R, PLAU, CDH1, GRB10, ROS1, SH3GL2, RGS7, PDGFRB, PDGFRA, RNF43, USP6, WNT5B, APLP2, MATK, ATP1B4, LIFR, SMO, SCN8A, WDFY3, NOTCH2, NOTCH3, CSF1R, SHC2, NOTCH4, HTRA1, SLC1A2, TNFRSF11A, CYP2C19, NDRG1, TRHDE, LPP, FUT1, CACNA1G, WNT6, TPO, SLC01B3, ABL2, WNT3, WNT4, SMAD3, TGFB3, PTCH1, CAV1, HSPA2, ESR1, LRP1B, TNFRSF10D, CPS1, GNAQ, CNTN1, FGF13, FGFR4, IL7R, FGFR3, FGFR2, BMPR1A, FGF10, FGFR1, ALK, PPP1R13B, FLT3, ITGB3, FLT4, RASGRF2, FASLG, GPHN, RERG, GRM1, GHR, GRM3, FLCN, KIAA1549, HEPH, RASGEF1A, ITGAV, SH3D19, ABCC3, DST, GRID1, AXIN1, DNMT1, TIRAP, TGFB3, DNMT3, ASPH, CDH11, ITGA8, ITGA7, DOCK1, CANT1, CEBPE, SRC, LRP5, NOD1, ACVR1B, DLL1, DLL3, DLL4, P2RY8, MUC1, ACVR1C, ERBB3, ERBB4, GNG4, GNA11, ERBB2, GNA12, NCAM1, LRIG3, S1PR2, NTRK1, NTRK2, ANGPT1, NOS3, EGF, NTRK3, STYK1, PLA2G2A, EPOR, TSHR, ACVR2A, NEURL1, SPRY2, ACKR3	2.130312	3.16E-14	2.91E-14
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	244	5.28E-15	CRTC3, ATP8A2, MAML2, CRT1, IRS1, NAB2, FZD10, FGF1, HOXA13, ETS2, CDC14A, CDC14B, HOXA11, SOX2, HOXA9, DACH1, BAIAP2L1, CCND1, CLP1, RPS6KA2, CREB3L1, PRKACG, HOXA3, ZNF687, MNX1, LMO1, PDGFRA, CDKL5, LMO2, SOX11, MITF, PRKCA, PIMREG, SOX10, RUNX2, MYCL, AR, MYCN, KAT6B, WDFY3, ERG, FLYWCH1, BCORL1, ZFPM2, ATF3, EPHA3, NOTCH2, CSF1R, BRK1, NOTCH3, NOTCH4, GATA6, GATA3, AK5, FOXO4, FOXO3, GATA2, KALRN, GATA1, PRDM16, NKX2-1, NKX2-5, PPARGC1A, SPECC1, TFAP2A, WWTR1, EGR1, NGFR, JUN, EGR2, EGR3, SMAD3, EGR4, HMGA2, FANCC, FANCE, SMARCA1, SMAD6, ESR1, PBX1, PHOX2B, FANCF, FOSL1, MLLT11, BCL9, NR4A3, TLX3, ID1, ID4, IL7R, HOXD9, ITK, CDKN1A, PPP1R13B, FLT4, ITGB3, PHF1, CHD6, FHL2, GLI1, HOXC11, RERG, GLI3, MECOM, ZIC2, HEY1, PPP1R13L, TRPS1, OLR1, JARID2, ZNF521, TEAD1, MYBL1, TEAD3, SH3D19, TEAD4, DST, IL15, DNMT3A, PAX3, FOXL2, FOS, DUSP26, ETV4, ETV5, POU5F1, PAX8, SETBP1, LRRC7, TAL1, RARA, AHRR, PPARG, ZMYND11, DOCK1, HDAC4, CAMK2B, YAP1, CEBPA, HDAC5, CEBPB, HLF, CEBPD, CEBPE, SRC, PLAG1, CAMK2A, DDX20, TMPPSS2, HOXD13, PPM1D, HOXD11, GNAI1, FSTL3, DNAJB1, SLX4, ERBB4, ERBB2, STAT4, PAK6,	1.549963	5.25E-13	4.84E-13
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	182	8.28E-12		1.604224	6.86E-10	6.32E-10

					LRIG3, HES1, PAK5, HES5, RUNX1T1, TCF7L2, NPM2, PRRX1, CDX2, EYA1, EYA2, MGMT, KLF4, PER1, NR6A1, ERCC4, WT1, NFIB, FOSB, ERCC6, TACC2, LGR5 FCGBP, CSF3, TNFRSF6B, CSF1, EPO, TNC, PLAT, FGF1, FGF2, FGF3, FGF4, FGF6, FGF8, IBSF, FGF9, PLAU, CCN6, PRSS8, IL13RA2, WNT5B, HGF, SERPINF1, OMD, IGFBP2, FLT3LG, DKK1, DKK2, DKK4, SFRP4, MDS2, SFRP2, LOX, PAPP, HTRA1, PDGFB, PDGFA, KLK2, TRHDE, KLK7, WNT6, TPO, PDGFD, APOD, PROM1, FGF23, WNT3, WNT4, WNT10B, TGFb2, ACE, BDNF, TGFb3, INHBA, IGF1, GDF6, IL2, BMP4, COL1A1, IL3, COL1A2, FGF19, COL9A3, NODAL, FGF10, PTPRR, WNT2B, FASLG, GHR, CD36, AMH, MMP7, IL15, IL13, WNT16, NGF, DCN, TGFbR3, IL18, KIT, COL6A3, LAMA5, LAMA1, COL11A1, WNT8B, EGFR, FSTL3, NTF4, MUC1, RELN, WNT11, ERBB3, NTF3, LRIG3, CKB, LEFTY2, LINGO2, GSN, ANGPT1, EGF, WNT7B, PLA2G2A, VEGFC, CCK, VEGFD, SULF1, TSHR, COL3A1, TAF5, TAF2, AXL, TLL2	1.939476	7.60E-10	7.01E-10
GOTERM_	GO:0005615~extracellular space	111	1.07E-11		CEBPA, GATA6, GATA2, DACH2, GATA1, HOXA11, SOX2, HOXA9, DACH1, NKX2-1, NKX2-5, TEAD1, TEAD3, TEAD4, WWTR1, JUN, SMAD3, LMO2, HNF1A, KLF4, ESR1, POU5F1, RUNX2, NR4A3, NR6A1, TAL1, DDIT3, RARA, FLYWCH1	4.187566	2.32E-08	2.14E-08
GOTERM_	GO:0005667~transcription regulator complex	29	3.74E-10		RET, ATL1, ROBO1, IGF1R, GRM3, NTF4, PCLO, CHL1, NTF3, NCAM1, PPFA2, NTRK1, EPHA5, NTRK2, TGFb2, FZD3, DST, KCNB1, BDNF, NTRK3, DAB2IP, CCK, NGF, GABRG2, DNMT3, BCR, SHTN1, BIN1, PTK7, SCN8A, ALDH1A1, CNTN1, WDFY3, FGF13, FGFR4	3.271773	1.69E-07	1.56E-07
GOTERM_	GO:0030424~axon	35	3.11E-09		MAML2, SOX2, HOXA9, HMGN2P46, CLP1, RPS6KA2, CREB3L1, PRKACG, HOXA3, KDR, MNX1, PRKCG, SRRM3, MTRFB, MTUS2, SOX11, PRKCA, HNF1A, SOX10, RUNX2, SFRP4, AR, BIN1, DDIT3, BCORL1, ZFPM2, ATF3, MAGED1, GATA6, PIK3R2, GATA3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, NKX2-5, PPARGC1A, WWTR1, EGR1, JUN, EGR2, EGR3, GADD45B, CRADD, MAGEE1, BCL11B, BTBD18, SMARCA1, PBX1, FOSL1, ID1, ID4, HOXD9, CDKN1C, ITK, TENM1, CDKN1A, HIP1, PHF1, HOXC13, GLI1, HOXC11, GLI3, MECOM, HEY1, JARID2, TEAD1, TEAD3, BRD3, TEAD4, BRD1, TET1, PAX3, FOS, DUSP9, MLF1, POU5F1, ZFTA, MN1, PLCB4, PAX8, TAL1, PAX7, ITPKA, RARA, AHRH, PPARG, PLCB1, VGLL3, YAP1, KANK1, PRICKLE1, HOXD11, GNAI1, EGFR, FSTL3, MIPOL1, STAT4, CTNNA1, RUNX1T1, CDKN2B, NPM2, GSN, CDX2, DMRT1, CDX1, MGMT, AKR1C3, SORBS2, PER1, NR6A1, NFIB, WT1, NEDD4, FOSB, ZNF331, PRDM7, CRTC3, IRS1, CRTC1, CTNND2, NAB2, FGF1, DACH2, HOXA13, FGF2, ETS2, HOXA11, CDC14B, DACH1, CCND1, ZNF444, SSX1, PDGFRB, LMO1, PDGFRA, CDKL5, APLP2, LMO2, MTF, MYCN, MAF, KAT6B, ERG, NOTCH2, BRSK1, NOTCH4, AK5, BHLHE22, FOXO4, FOXO3, NDRG1, LPP, NCKIPSD, CCNB3, TFAP2A, SMAD3, AUTS2, ZBTB16, HMGA2, FANCC, HSPA2, FANCE, SMAD6, ESR1, PHOX2B, MAFB, FGF14, NR4A3, TLX3, LHX2, TLX1, FEV, LHX4, FGF13, FGFR2, FGF10, FGF1, PPP1R13B, ITGB3, CHD6, FHL2, FASLG, RERG, GRM1, FLCN, ZIC2, PPP1R13L, TRPS1, MYO18A, ZNF521, MYBL1, PEG3, DST, DNMT3A, AXIN1, ETV1, FOXL2, OLIG1, OLIG2, DUSP26, ETV4, ETV5, DMRTA2, ZMYND11, CILK1, HDAC4, CEBPA, HDAC5, LAMA5, CEBPB, NUTM1, HLF, CEBPD, CEBPE, PLAG1, CAMK2A, DDX20, PPM1D, CXXC4, DNAJB1, MUC1, ERBB4, ERBB2, HES1, LRIG3, HES5, TCF7L2, EYA1, PRRX1, EYA2, NOS3, PRRX2, PDE4DIP, TBX15, TAF2, ERCC4, SPRY2, ERCC6			
GOTERM_	GO:0005634~nucleus	240	3.40E-09		LAMA5, HIP1, DGKB, FRMPD4, SRC, ITGB3, SLC1A2, LPAR1, PLAT, IL1RAP, GRM1, GRM3, DNAJB1, GRIN2A, PCLO, ERBB4, CDH1, RAC3, SH3GL2, PPFA2, EPHA7, CDKL5, USP6, GRD1, DNMT1, DNMT3, BCR, TIAM1, PLCB4, BIN1, SCN8A, CDH11, ITPKA, ITGA8, PLCB1, DOCK1	1.380616	1.69E-07	1.56E-07
GOTERM_	GO:0098978~glutamatergic synapse	37	7.06E-09			3.042403	3.19E-07	2.94E-07
GOTERM_	GO:0090575~RNA polymerase II transcription regulator complex	17	5.64E-07		CEBPA, JUN, CEBPB, HLF, CEBPD, CEBPE, FOS, PBX1, FOSL1, MAFB, MAF, DDIT3, STAT4, RARA, PPARG, NKX2-5, ATF3	4.754928	2.33E-05	2.14E-05
GOTERM_	GO:0062023~collagen-containing extracellular matrix	32	6.08E-07		FBN2, LAMA5, WNT2B, LAMA1, COL11A1, ELN, HTRA1, PDGFB, TNC, LTBP1, RELN, GPC3, NCAM1, LEFTY2, EDIL3, TGFb2, WNT5B, ANGPT1, TGFb3, SERPINF1, PRG2, SULF1, DCN, COL1A1, COL3A1, SFRP2, COL1A2, LOX, COL6A3, COL9A3, FGFR2, FGF10	2.786048	2.33E-05	2.14E-05
GOTERM_	GO:0030425~dendrite	34	9.60E-07		EPHB6, RET, EPHA10, CTNND2, GPHN, GRM1, NTF4, RELN, INPP5A, CHL1, MAP2, NTF3, APOD, PRKCG, NTRK1, EPHA5, NTRK2, BRD1, FZD3, EPHA7, MAGEE1, KCNB1, BDNF, DAB2IP, SORBS2, NGF, PLCB4, SMO, BIN1, RARA, FGF13, EPHA3, BMPR1A, EPHA2	2.625547	3.22E-05	2.97E-05
GOTERM_	GO:0030666~endocytic vesicle membrane	13	9.72E-07		CAMK2B, CSF3R, WNT5B, NOS3, WNT7B, CAV1, PTCH1, CAMK2A, WNT6, SMO, CD36, WNT3, WNT4	6.24037	3.22E-05	2.97E-05
GOTERM_	GO:0014069~postsynaptic density	23	1.69E-06		PRKCG, NGFR, NTRK2, FRMPD4, CTNND2, CAMK2A, MAPK8IP2, KALRN, GRIN2B, GPHN, GRM3, DNMT3, BCR, DNAJB1, GRIN2A, PLCB4, PCLO, LRRC7, PSD3, NEURL1, PAK6, PAK3, SH2D5	3.348396	5.24E-05	4.83E-05
GOTERM_	GO:0009897~external side of plasma membrane	31	4.95E-06		CSF3R, ITGB3, MPL, FASLG, TNFRSF11A, GHR, FGF8, PLAU, KDR, CTLA4, NCAM1, ITGAV, CD36, IL13RA2, IL12RB2, EPHA5, PDGFRA, ACE, IL1R1, IL13, LIFR, EPOR, TGFbR3, KIT, ITGA8, CD28, ITGA7, ACKR3, IL7R, BMPR1A, CRLF2	2.566866	1.45E-04	1.33E-04
GOTERM_	GO:0048471~perinuclear region of cytoplasm	45	5.40E-06		TENM1, CDKN1A, PTPRR, PPP1R13B, CSF1, SRC, AKAP6, FASLG, NDRG1, EGFR, HEPH, CDH1, ERBB2, CTLA4, SNCG, RAC3, APOD, ROS1, SH3GL2, PRKCG, EPHA5, NTRK2, CDKL5, MAGEE1, SORT1, KCNB1, BDNF, CAV1, PTCH1, SERPINF1, PLA2G2A, AXIN1, PDE4DIP, PRKCA, SORBS2, SYP, INHBA, EML1, MLF1, DNMT3, SHTN1, NEDD4, NEURL1, RARA, PPARG	2.100519	1.48E-04	1.37E-04
GOTERM_	GO:0032587~ruffle membrane	14	5.67E-06		KANK1, CDKL5, KSR1, SRC, ITGB3, SPRY4, EGFR, TIRAP, TIAM1, PSD3, ERBB2, SPRY2, ITGAV, EPHA2	4.875584	1.48E-04	1.37E-04
GOTERM_	GO:0005901~caveola	12	7.55E-06		SMO, IRS1, SRC, NOS3, CAV1, PTCH1, AKAP6, FASLG, CD36, PTGS2, BMPR1A, IGF1R	5.683537	1.88E-04	1.73E-04
GOTERM_	GO:0005788~endoplasmic reticulum lumen	25	8.71E-06		CSF1, FLT3, COL11A1, PDGFB, TNC, PDGFA, PTGS2, LTBP1, FSTL3, WNT6, PDGFD, GPC3, FGF23, WNT3, WNT4, WNT5B, BDNF, APLP2, WNT7B, BMP4, COL1A1, COL3A1, COL1A2, COL6A3, COL9A3	2.855475	2.06E-04	1.90E-04
GOTERM_	GO:0005796~Golgi lumen	14	9.65E-06		WNT5B, SDC4, WNT7B, OMD, PDGFB, PDGFA, NGF, DCN, WNT6, MUC1, GPC3, FGF23, WNT3, WNT4	4.647753	2.17E-04	2.00E-04
GOTERM_	GO:0043025~neuronal cell body	28	1.00E-05		RET, SRC, MPL, LPAR1, ROBO1, IGF1R, GHR, AKAP12, DNAJB1, MAP2, GNA12, SNCG, RAC3, NCAM1, APOD, NTRK1, EPHA5, NTRK2, TGFb2, FZD3, TGFb3, DAB2IP, SORBS2, MAPK8IP2, TIAM1, PTK7, FGFR4, BMPR1A	2.631267	2.17E-04	2.00E-04
GOTERM_	GO:0032993~protein-DNA complex	9	1.06E-05		TEAD4, TCF7L2, EYA1, DDIT3, HMGA2, FOS, NKX2-5, GATA1, HOXA11	8.19741	2.19E-04	2.02E-04
GOTERM_	GO:0035867~alpha-beta3 integrin-IGF-1-IGF1R complex	4	8.65E-05		ITGB3, ITGAV, IGF1, IGF1R	35.52211	0.001719	0.001585

GOTERM_	GO:0005925~focal	28	1.14E-04	SDC4, SRC, ITGB3, FHL2, TNC, PIK3R2, LPP, EGFR, AKAP12, PLAU, GNA12, CTNNA1, RAC3, ITGAV, FLNC, PDGFRB, FZD2, GSN, DST, CAV1, SPRY4, SORBS2, PPFIBP1, PTK7, ITGA8, FGFR3, EPHA2, DDR2	2.286481	0.00213	0.001963
CC_DIRECT	adhesion						
GOTERM_	GO:0031093~platelet	10	1.16E-04	TGFB2, TGFB3, EGF, HGF, PDGFB, VEGFC, PDGFA, VEGFD, IGF1, LEFTY2 FZD10, SOX2, HOXA9, RPS6KA2, ARRDCA, PRKCG, MTUS2, FRS2, DLEC1, PRKCA, HNF1A, MAPK8IP2, RUNX2, INPP4B, SFRP4, SHTN1, AR, BIN1, DDTIT3, ZFYVE19, HECW1, ZFPM2, CEP8SL, PDGFB, LPAR1, GATA2, KALRN, MAP2, ZNF703, SNX9, APOD, NKX2-5, VVWTR1, EGR1, FZD3, EGR2, ACE, FZD2, GADD45B, CRADD, RANBP17, GRIN2B, PBX1, COL1A1, ID1, ID4, CDKN1C, TENM1, HIP1, GLI1, GLI3, ROBO1, AKAP12, HEY1, CD36, TEAD4, IL15, IL13, DUSP9, MLF1, POU5F1, ITPKA, DPYD, RARA, AHRR, ACSBG1, PPARG, PLCB1, GAS7, YAP1, KANK1, AKAP6, PTGS2, GNAI1, EGFR, RELN, STAT4, CTNNA1, PAK6, FLNC, PAK3, PAK5, CDKN2B, NPM2, GSN, DMRT1, DAB2IP, AKR1C3, PER1, WT1, NEDD4, TACC2, CRTCS, DGKB, IRS1, CRTC1, CTNND2, PLAT, FGF1, FGF2, FGF3, CDC14A, FGF4, CDC14B, FGF6, FGF8, CCND1, FGF9, CDH1, GRB10, SH3GL2, SSX1, PPIA2, RGS7, PDGFRB, LMO1, PDGFRA, USP6, MATK, MITF, MAF, WDFY3, BRSK1, AK5, FOXO4, CYP2C19, FOXO3, NDRG1, TRHDE, CACNA1G, SOCS2, CCNB3, MYH11, SRGAP3, FGF23, WNT4, SMAD3, AUTS2, BDNF, FANCC, HSPA2, SMAD6, ESR1, GFAP, FGF14, CPS1, GNAQ, FGF19, FGF13, FGFR4, FGFR2, FGF10, PPP1R13B, RASGRF2, GPHN, FLCN, ZIC2, MYO18A, CEP170B, KSR1, DST, DNMT3A, AXIN1, OLIG2, DUSP26, WNT16, DNMT1, TIRAP, DNMT3, ALDH1A1, CDH11, DOCK1, CLK1, HDAC4, CAMK2B, HDAC5, CEBPB, NUTM1, SRC, CAMK2A, DDX20, NOD1, CXXC4, DNAJB1, ABLIM1, MUC1, WNT11, GNA11, ERBB2, GNA12, SLCG, HES1, S1PR2, NTRK2, EYA1, NOS3, SPRY4, PDE4DIP, ACVR2A, BICC1, TAFAS, PC, TAFAS2 LINGO2, FBN2, FCGBP, MMP7, LAMA1, ELN, OMD, FGF1, LTBP1, TSHR, COL1A1, WNT6, RELN, WNT11, CCN6, COL6A3, LRIG3, WNT3, WNT4 NGFR, NTRK2, FRMPD4, CAMK2A, LPAR1, GRM3, DNMT3, BCR, TIAM1, DNAJB1, GRIN2A, NEDD4, ITPKA, NEURL1, PPIA2	5.22384	0.00213	0.001963
CC_DIRECT	alpha granule lumen						
GOTERM_	GO:0005737~cytoplasm	203	1.28E-04	ABLIM1, MUC1, WNT11, GNA11, ERBB2, GNA12, SLCG, HES1, S1PR2, NTRK2, EYA1, NOS3, SPRY4, PDE4DIP, ACVR2A, BICC1, TAFAS, PC, TAFAS2 LINGO2, FBN2, FCGBP, MMP7, LAMA1, ELN, OMD, FGF1, LTBP1, TSHR, COL1A1, WNT6, RELN, WNT11, CCN6, COL6A3, LRIG3, WNT3, WNT4 NGFR, NTRK2, FRMPD4, CAMK2A, LPAR1, GRM3, DNMT3, BCR, TIAM1, DNAJB1, GRIN2A, NEDD4, ITPKA, NEURL1, PPIA2	1.253213	0.002274	0.002095
CC_DIRECT	GO:0031012~extracellular matrix	19	1.62E-04	COL1A1, WNT6, RELN, WNT11, CCN6, COL6A3, LRIG3, WNT3, WNT4 NGFR, NTRK2, FRMPD4, CAMK2A, LPAR1, GRM3, DNMT3, BCR, TIAM1, DNAJB1, GRIN2A, NEDD4, ITPKA, NEURL1, PPIA2	2.812167	0.002776	0.002559
GOTERM_	GO:0043197~dendritic spine	15	2.00E-04	YAP1, PDGFRA, BRSK1, PTPRR, DST, SRC, PTPRK, EGFR, SLX4, PPP1R13L, CDH1, SCN8A, KDR, CTNNA1, PAK6	3.289084	0.003319	0.003058
CC_DIRECT	GO:0030054~cell junction	15	8.55E-04	CDH1, SCN8A, KDR, CTNNA1, PAK6	2.849367	0.013704	0.012629
GOTERM_	GO:0090571~RNA polymerase II transcription repressor complex	4	0.001113	TBX15, BIN1, DDX20, FOXO3	17.76105	0.017283	0.015927
CC_DIRECT	GO:0044294~dendritic growth cone	4	0.001634	CDKL5, MAP2, SRC, PTCH1	15.7876	0.024616	0.022684
GOTERM_	GO:0036488~CHOP-C/EBP complex	3	0.002321	CEBPA, CEBPB, DDIT3	35.52211	0.032963	0.030376
CC_DIRECT	GO:0035866~alpha-beta3 integrin-PKAlpha complex	3	0.002321	ITGB3, ITGAV, PRKCA	35.52211	0.032963	0.030376
GOTERM_	GO:0005911~cell-cell junction	14	0.003282	YAP1, PRKCG, NGFR, ITK, LAMA1, ITGB3, FRS2, PTPRK, TIAM1, AH11, PTK7, KIT, CTNNA1, FGF4	2.576733	0.045306	0.041751
CC_DIRECT	GO:0009925~basal plasma membrane	8	0.004061	ABCC3, ACE, ERBB3, DST, ERBB4, ERBB2, SLC01B3, EGFR HOXC13, GLI1, HOXA13, HOXC11, SOX2, HOXA9, MECOM, CREB3L1, ZNF521, MYBL1, TEAD4, SOX11, FOXL2, MITF, ETV1, HNF1A, FOS, SOX10, ETV4, ETV5, RUNX2, AR, MYCN, MAF, PAX8, DDIT3, PPARG, ERG, ATF3, NOTCH2, CEBPA, CEBPB, HLF, CEBPD, CEBPE, PLAG1, NOTCH4, HOXD13, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-5, TFAP2A, EGR1, JUN, EGR2, EGR3, SMAD3, PRRX2, BCL11B, EGR4, DMRT1, CDX1, ZBTB16, KLF4, ESR1, PBX1, PHOX2B, FOSL1, NR4A3, MAFB, NR6A1, LHX2, NFIB, WT1, FEV, TLX1, FOSB, LHX4	3.946901	0.054551	0.050271
GOTERM_	GO:0001228~DNA-binding transcription activator activity, RNA polymerase II-specific	72	1.32E-28	ALK, NTRK1, RET, PDGFRA, NTRK2, CSF1R, FLT3, SRC, FLT4, NTRK3, STYK1, EGFR, IGF1R, ERBB3, AXL, ERBB4, PTK7, KIT, ERBB2, KDR, ROS1, EPHA2, DDR2 HOXC13, HOXA13, HOXC11, GLI3, ETS2, HOXA11, HOXA9, HEY1, CREB3L1, ZNF444, TEAD1, MNX1, PAX3, FOXL2, ETV1, FOS, OLIG2, SOX10, ETV4, ETV5, POU5F1, RUNX2, DMRTA2, MYCN, MAF, PAX8, PAX7, RARA, ERG, ATF3, CEBPB, HLF, CEBPD, CEBPE, GATA6, HOXD13, BHLHE22, GATA3, FOXO4, FOXO3, HOXD11, GATA2, GATA1, HES1, NKX2-5, HES5, TFAP2A, EGR1, JUN, EGR2, EGR3, CDX2, BCL11B, EGR4, DMRT1, CDX1, PRRX2, KLF4, ESR1, PBX1, PHOX2B, FOSL1, TBX15, NR6A1, TLX3, NFIB, FEV, FOSB, LHX4, HOXD9 CSF3, CSF1, PDGFB, PDGFA, FGF1, FGF2, FGF3, FGF4, NTF4, FGF6, FGF8, FGF9, PDGFD, CCN6, NTF3, AMH, LEFTY2, FGF23, JAG2, TGFB2, TGFB3, EGF, BDNF, HGF, VEGFC, VEGFD, IGF1, INHBA, NGF, GDF6, DKK1, IL2, BMP4, IL3, FGF14, FGF19, FGF13, NODAL, FGF10	4.835755	1.09E-25	9.86E-26
MF_DIRECT	GO:0004714~transmembrane receptor protein tyrosine kinase activity	23	7.32E-24	HOXC13, GLI1, HOXA13, HOXC11, SOX2, HOXA9, MECOM, CREB3L1, ZNF521, MYBL1, TEAD4, SOX11, FOXL2, MITF, ETV1, HNF1A, FOS, SOX10, ETV4, ETV5, RUNX2, AR, MYCN, MAF, PAX8, DDIT3, PPARG, ERG, ATF3, NOTCH2, CEBPA, CEBPB, HLF, CEBPD, CEBPE, PLAG1, NOTCH4, HOXD13, GATA3, FOXO4, FOXO3, HOXD11, GATA2, GATA1, HES1, NKX2-5, HES5, TFAP2A, EGR1, JUN, EGR2, EGR3, CDX2, BCL11B, EGR4, DMRT1, CDX1, PRRX2, KLF4, ESR1, PBX1, PHOX2B, FOSL1, TBX15, NR6A1, TLX3, NFIB, FEV, FOSB, LHX4, HOXD9 CSF3, CSF1, PDGFB, PDGFA, FGF1, FGF2, FGF3, FGF4, NTF4, FGF6, FGF8, FGF9, PDGFD, CCN6, NTF3, AMH, LEFTY2, FGF23, JAG2, TGFB2, TGFB3, EGF, BDNF, HGF, VEGFC, VEGFD, IGF1, INHBA, NGF, GDF6, DKK1, IL2, BMP4, IL3, FGF14, FGF19, FGF13, NODAL, FGF10	19.52729	2.47E-21	2.23E-21
GOTERM_	GO:1990837~sequence-specific double-stranded DNA binding	70	8.96E-24	HOXC13, GLI1, HOXA13, HOXC11, SOX2, HOXA9, MECOM, CREB3L1, ZNF521, MYBL1, TEAD4, SOX11, FOXL2, MITF, ETV1, HNF1A, FOS, SOX10, ETV4, ETV5, RUNX2, AR, MYCN, MAF, PAX8, DDIT3, PPARG, ERG, ATF3, NOTCH2, CEBPA, CEBPB, HLF, CEBPD, CEBPE, PLAG1, NOTCH4, HOXD13, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-5, TFAP2A, EGR1, JUN, EGR2, EGR3, SMAD3, CDX2, BCL11B, EGR4, CDX1, ZBTB16, PRRX2, KLF4, ESR1, PBX1, FOSL1, WT1, HOXD9 ZNF331, DACH2, HOXA13, ETS2, HOXA11, SOX2, HOXA9, DACH1, HOXA3, ZNF444, SOX11, MITF, HNF1A, SOX10, RUNX2, MYCL, AR, MYCN, MAF, DDIT3, ERG, ATF3, GATA6, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, NKX2-5, TFAP2A, EGR1, JUN, EGR2, EGR3, SMAD3, BCL11B, EGR4, ZBTB16, ESR1, PBX1, PHOX2B, FOSL1, NR4A3, MAFB, TLX3, LHX2, TLX1, FEV, HOXD9, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, PEG3, DNMT3A, TET1, PAX3, ETV1, FOXL2, FOS, ETV4, POU5F1, DMRTA2, PAX8, TAL2, PAX7, TAL1, RARA, PPARG, HDAC4, YAP1, CEBPA, HDAC5, CEBPB, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, MUC1, STAT4, HES5, TCF7L2, PRRX1, CDX2, DMRT1, CDX1, PRRX2, KLF4, TBX15, PER1, NR6A1, WT1, NFIB, FOSB	4.138937	2.47E-21	2.23E-21
MF_DIRECT	GO:0008083~growth factor activity	39	4.40E-23	HOXC13, GLI1, ETS2, SOX2, HOXA9, HEY1, MECOM, ZIC2, TRPS1, ZNF687, TEAD1, TEAD3, TEAD4, PAX3, SOX11, FOXL2, ETV1, HNF1A, FOS, SOX10, ETV4, ETV5, POU5F1, RUNX2, AR, MYCN, PAX8, PAX7, TAL1, DDIT3, RARA, PPARG, ATF3, CEBPA, CEBPB, PLAG1, GATA6, HOXD13, BHLHE22, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, STAT4, NKX2-5, TFAP2A, TCF7L2, EGR1, JUN, EGR2, EGR3, SMAD3, CDX2, BCL11B, EGR4, CDX1, ZBTB16, PRRX2, KLF4, ESR1, PBX1, FOSL1, WT1, HOXD9 ZNF331, DACH2, HOXA13, ETS2, HOXA11, SOX2, HOXA9, DACH1, HOXA3, ZNF444, SOX11, MITF, HNF1A, SOX10, RUNX2, MYCL, AR, MYCN, MAF, DDIT3, ERG, ATF3, GATA6, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, NKX2-5, TFAP2A, EGR1, JUN, EGR2, EGR3, SMAD3, BCL11B, EGR4, ZBTB16, ESR1, PBX1, PHOX2B, FOSL1, NR4A3, MAFB, TLX3, LHX2, TLX1, FEV, HOXD9, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, PEG3, DNMT3A, TET1, PAX3, ETV1, FOXL2, FOS, ETV4, POU5F1, DMRTA2, PAX8, TAL2, PAX7, TAL1, RARA, PPARG, HDAC4, YAP1, CEBPA, HDAC5, CEBPB, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, MUC1, STAT4, HES5, TCF7L2, PRRX1, CDX2, DMRT1, CDX1, PRRX2, KLF4, TBX15, PER1, NR6A1, WT1, NFIB, FOSB	7.826353	9.09E-21	8.22E-21
GOTERM_	GO:0003700~DNA-binding transcription factor activity	67	9.38E-23	HOXC13, GLI1, ETS2, SOX2, HOXA9, HEY1, MECOM, ZIC2, TRPS1, ZNF687, TEAD1, TEAD3, TEAD4, PAX3, SOX11, FOXL2, ETV1, HNF1A, FOS, SOX10, ETV4, ETV5, POU5F1, RUNX2, AR, MYCN, PAX8, PAX7, TAL1, DDIT3, RARA, PPARG, ATF3, CEBPA, CEBPB, PLAG1, GATA6, HOXD13, BHLHE22, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, STAT4, NKX2-5, TFAP2A, TCF7L2, EGR1, JUN, EGR2, EGR3, SMAD3, CDX2, BCL11B, EGR4, CDX1, ZBTB16, PRRX2, KLF4, ESR1, PBX1, FOSL1, WT1, HOXD9 ZNF331, DACH2, HOXA13, ETS2, HOXA11, SOX2, HOXA9, DACH1, HOXA3, ZNF444, SOX11, MITF, HNF1A, SOX10, RUNX2, MYCL, AR, MYCN, MAF, DDIT3, ERG, ATF3, GATA6, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, NKX2-5, TFAP2A, EGR1, JUN, EGR2, EGR3, SMAD3, BCL11B, EGR4, ZBTB16, ESR1, PBX1, PHOX2B, FOSL1, NR4A3, MAFB, TLX3, LHX2, TLX1, FEV, HOXD9, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, PEG3, DNMT3A, TET1, PAX3, ETV1, FOXL2, FOS, ETV4, POU5F1, DMRTA2, PAX8, TAL2, PAX7, TAL1, RARA, PPARG, HDAC4, YAP1, CEBPA, HDAC5, CEBPB, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, MUC1, STAT4, HES5, TCF7L2, PRRX1, CDX2, DMRT1, CDX1, PRRX2, KLF4, TBX15, PER1, NR6A1, WT1, NFIB, FOSB	4.138937	1.55E-20	1.40E-20
MF_DIRECT	GO:0000978~RNA polymerase II cis-regulatory region sequence-specific DNA binding	106	1.39E-21	HOXC13, GLI1, ETS2, SOX2, HOXA9, HEY1, MECOM, ZIC2, TRPS1, ZNF687, TEAD1, TEAD3, TEAD4, PAX3, SOX11, FOXL2, ETV1, HNF1A, FOS, SOX10, ETV4, ETV5, POU5F1, RUNX2, AR, MYCN, PAX8, PAX7, TAL1, DDIT3, RARA, PPARG, ATF3, CEBPA, CEBPB, PLAG1, GATA6, HOXD13, BHLHE22, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, STAT4, NKX2-5, TFAP2A, TCF7L2, EGR1, JUN, EGR2, EGR3, SMAD3, CDX2, BCL11B, EGR4, CDX1, ZBTB16, PRRX2, KLF4, ESR1, PBX1, FOSL1, WT1, HOXD9 ZNF331, DACH2, HOXA13, ETS2, HOXA11, SOX2, HOXA9, DACH1, HOXA3, ZNF444, SOX11, MITF, HNF1A, SOX10, RUNX2, MYCL, AR, MYCN, MAF, DDIT3, ERG, ATF3, GATA6, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, NKX2-5, TFAP2A, EGR1, JUN, EGR2, EGR3, SMAD3, BCL11B, EGR4, ZBTB16, ESR1, PBX1, PHOX2B, FOSL1, NR4A3, MAFB, TLX3, LHX2, TLX1, FEV, HOXD9, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, PEG3, DNMT3A, TET1, PAX3, ETV1, FOXL2, FOS, ETV4, POU5F1, DMRTA2, PAX8, TAL2, PAX7, TAL1, RARA, PPARG, HDAC4, YAP1, CEBPA, HDAC5, CEBPB, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, MUC1, STAT4, HES5, TCF7L2, PRRX1, CDX2, DMRT1, CDX1, PRRX2, KLF4, TBX15, PER1, NR6A1, WT1, NFIB, FOSB	2.744189	1.92E-19	1.73E-19
GOTERM_	GO:0000976~transcription cis-regulatory region binding	44	4.12E-21	HOXC13, GLI1, ETS2, SOX2, HOXA9, HEY1, MECOM, ZIC2, TRPS1, ZNF687, TEAD1, TEAD3, TEAD4, PAX3, SOX11, FOXL2, ETV1, HNF1A, FOS, SOX10, ETV4, ETV5, POU5F1, RUNX2, AR, MYCN, PAX8, PAX7, TAL1, DDIT3, RARA, PPARG, ATF3, CEBPA, HDAC5, CEBPB, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, MUC1, STAT4, HES5, TCF7L2, PRRX1, CDX2, DMRT1, CDX1, PRRX2, KLF4, TBX15, PER1, NR6A1, WT1, NFIB, FOSB	5.970925	4.86E-19	4.39E-19

GOTERM_MF_DIRECT	GO:0000981~DNA-binding transcription factor activity, RNA polymerase II-specific	106	1.23E-19	ZNF331, DACH2, HOXA13, ETS2, HOXA11, SOX2, HOXA9, DACH1, CREB3L1, HOXA3, ZNF444, MNX1, SOX11, MITF, HNF1A, SOX10, RUNX2, MYCL, AR, MYCN, MAF, DDIT3, ERG, ATF3, GATA6, GATA3, BHLHE22, FOXO4, FOXO3, GATA2, GATA1, NKX2-1, NKX2-5, TFAP2A, EGR1, JUN, EGR2, EGR3, SMAD3, EGR4, ZBTB16, ESR1, PBX1, PHOX2B, FOSL1, NR4A3, MAFB, TLX3, LHX2, TLX1, FEV, LHX4, HOXD9, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, PEG3, PAX3, ETV1, FOXL2, OLIG1, FOS, OLIG2, ETV4, ETV5, POU5F1, DMRTA2, PAX8, TAL2, PAX7, TAL1, RARA, AHRR, PPARG, CEBPA, CEBPB, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, STAT4, HES1, HES5, TCF7L2, PRRX1, CDX2, DMRT1, CDX1, PRRX2, KLF4, TBX15, NR6A1, WT1, NFIB, FOSB	2.582648	1.27E-17	1.15E-17
GOTERM_MF_DIRECT	GO:0061629~RNA polymerase II-specific DNA-binding transcription factor binding	31	4.07E-14	HDAC4, CEBPA, HDAC5, GATA3, GATA2, GATA1, ETS2, HEY1, NKX2-1, HES1, NKX2-5, PPARGC1A, TEAD3, TCF7L2, JUN, EGR2, SMAD3, PRRX1, LMO2, DNMT3A, HMGA2, FOS, SMARCA1, DUSP26, KLF4, POU5F1, AR, TAL1, DDIT3, ID4, ZFPM2	5.578567	3.74E-12	3.38E-12
GOTERM_MF_DIRECT	GO:0004713~protein tyrosine kinase activity	24	4.83E-14	PDGFRB, ALK, NTRK1, RET, CSF1R, EPHA7, FLT3, SRC, STYK1, MATK, EGFR, IGF1R, BCR, ERBB3, AXL, ERBB4, KIT, ERBB2, KDR, ABL2, ROS1, FGFR3, FGFR2, FGFR1	7.641114	3.99E-12	3.61E-12
GOTERM_MF_DIRECT	GO:0019838~growth factor binding	16	1.67E-13	CSF1R, EPHA7, FLT3, SRC, FLT4, HTRA1, LIFR, ACVR1B, ACVR2A, GHR, ACVR1G, ERBB3, KIT, ERBB2, KDR, EPHA2	13.5842	1.25E-11	1.13E-11
GOTERM_MF_DIRECT	GO:0005515~protein binding	463	5.36E-13	MAML2, FRMPD4, FZD10, HOXA9, CLP1, PRKACG, CREB3L1, HOXA3, CYP1B1, PRSS8, PRKCG, SERPINF1, MRTFB, PRKCA, FRS2, DKK1, SOX10, EML1, DKK2, GABRG2, DKK4, BCR, AR, BIN1, DDIT3, ZFYVE19, HECW1, ATF3, PDGFB, GATA6, PDGFA, GATA3, GATA2, GATA1, GRIN2A, PPP3R2, PRDM16, NKX2-1, NKX2-5, PROM1, PPARGC1A, JAG2, WNT10B, NGFR, JUN, FZD3, FZD2, BTBD18, FZD7, FZD6, FZD8, GRIN2B, PBX1, COL1A1, MLLT11, FOSL1, PPF1BP1, COL1A2, CDKN1C, RET, ITK, CDKN1A, PHF1, ELN, HOXC13, GLI1, HOXC11, GLI3, MECOM, HEY1, CTLA4, OLR1, TEAD1, TEAD3, BRD3, TEAD4, BRD1, ELOVL2, TET1, PAX3, FOS, DUSP9, POU5F1, PLCB4, PAX8, TAL2, LRRC7, TAL1, DPYD, RARA, AHRR, GAS1, PPARG, PLCB1, GAS7, KANK1, ATL1, PTGS2, EGFR, FSTL3, MIPOL1, NTF4, CHN1, NTF3, STAT4, AGR3, HAS2, CKB, FLNC, RUNX1T1, CDKN2B, GSN, KCNB1, WNT7B, SEPTIN5, DAB2IP, COL3A1, WT1, NFIB, FOSB, LGR5, CSF3R, ATP8A2, CSF1, EPO, IRS1, CTNND2, NAB2, IRS4, TNC, IRS2, FGF1, FGF2, FGF3, CDC14A, CDC14B, FGF6, DACH1, IBSP, CDH1, GRB10, ZNF687, MB21D2, IL13RA2, MAP3K6, ROS1, SSX1, RNF43, CDKL5, USP6, IGFBP2, MITF, MAF, SMO, KAT6B, ERG, TCTA, NOTCH2, CSF1R, NOTCH3, SHC2, NOTCH4, FOXO4, TNFRSF11A, FOXO3, SOCS2, SOCS3, CLTCL1, ABL2, SRGAP3, BDNF, ZBTB16, FANCC, FANCF, TNFRSF10D, GFAP, BCL9, MAFB, LHX2, LHX4, BCL2L2, ALK, PPP1R13B, FLT3, FLT4, ITGB3, FHL2, FASLG, KIAA1549, PPP1R13L, ITGAV, AMH, ZNF521, SH3D19, PTCRA, KSR1, DST, DNMT3A, FOXL2, DUSP26, NGF, TIRAP, ASPH, ITGA7, HDAC4, CEBPA, HDAC5, CEBPB, NUTM1, CANT1, CEBPD, CEBPE, SRC, LRP5, NOD1, PPM1D, DNAJB1, ABLIM1, NTRK1, NTRK2, PRRX1, ANGPT1, NTRK3, STYK1, KLF4, PC, EPHB6, TNFRSF6B, PRF1, CBLC, SOX2, BAIAP2L1, EDNRB, ADGRA2, RP56KA2, KDR, ARRDCA, EPHA5, EPHA7, IL1R1, FLT3LG, C10ORF55, MTUS2, DLEC1, HNF1A, PIMREG, MAPK8IP2, RUNX2, SFRP4, SHTN1, INPP4B, TIAM1, PAPPA, FLYWCH1, PLPP3, ZFPM2, EPHA3, EPHA2, SDC4, EPHA10, MAGED1, LPAR1, PIK3R2, KALRN, INPP5A, MAP2, ZNF703, SNX9, APOD, WWTR1, EGR1, EGR2, MAGEE1, BCL11B, GADD45B, CRADD, EGR4, PRG2, IGF1, SMARCA1, EXT1, ACER1, EXT2, PTK7, ID1, ID4, CD28, RTL8B, NODAL, DIRAS3, ROBO2, PTPRR, HIP1, PTPRK, ROBO1, AKAP12, SERP2, RAC3, CD36, PRMT8, IL15, IL13, SYP, MLF1, MN1, IL1B, KIT, ALDOC, DDR2, AMER1, YAP1, TMPPRS2, AKAP6, PRICKLE1, GNAI1, SLX4, WIF1, CTNNA1, GPC3, PAK6, PAK3, PAK5, NPM2, CDX2, CDX1, SORT1, VEGFC, VEGFD, SORBS2, PER1, AXL, NEDD4, FCGBP, PRDM7, CRTC3, CRTC1, MPL, PLAT, ETS2, CCDC28A, IGF1R, CCND1, PLAUI, SH3GL2, PPP1A2, PDGFRB, LMO1, PDGFRA, HGF, APLP2, LMO2, MATK, ATP1B4, LIFR, MYCN, LOX, SCN8A, WDFY3, FBN2, SLC1A2, HTRA1, NDRG1, LPP, LTBP1, NCKIPSD, CCNB3, MYH11, FGF23, WNT3, TFAP2A, TGFBI, SMAD3, AUTS2, TGFBI, PTH1, CAV1, HMGA2, HSPA2, INHBA, SMAD6, ESR1, LRP1B, IL2, BMP4, IL3, AHI1, FGF14, NR4A3, TLX3, CPS1, TLX1, GNAQ, FGF19, CNTN1, FGF13, FGF4, IL7R, FGF3, FGF2, FGF10, FGF1, BMP1A, GPHN, GRM1, GHR, FLCN, TRPS1, MYO18A, MMP7, AXIN1, ETV1, OLIG1, OLIG2, ETV4, ETV5, DCN, DNMT1, DNMT3, TGFBR3, SETBP1, ALDH1A1, ZMYND11, DOCK1, CILK1, CAMK2B, HLF, LAMA1, CAMK2A, DDX20, ACVR1B, DLL1, DLL4, MUC1, WNT11, ERBB3, ERBB4, GNG4, GNAI1, ERBB2, GNA12, SNCG, HES1, LRIG3, NCAM1, S1PR2, TCF7L2, EYA1, EYA2, NOS3, EGF, SPRY4, PDE4DIP, CCK, EPOR, TSHR, ACVR2A, TBX15, ERCC4, PPP2R2B, NEURL1, SPRY2, ACKR3, ERCC6	1.202025	3.69E-11	3.34E-11
GOTERM_MF_DIRECT	GO:0005125~cytokine activity	29	7.09E-12	CSF3, WNT2B, CSF1, EPO, WNT8B, FASLG, FGF2, WNT6, WNT11, LEFTY2, WNT3, WNT4, WNT10B, TGFBI, WNT5B, TGFBI, IL15, WNT7B, IL13, FLT3LG, INHBA, WNT16, GDF6, IL2, BMP4, IL3, TAFI5, IL1B, NODAL	4.924273	4.51E-10	4.08E-10
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	102	7.67E-11	CSF1, NAB2, PRF1, FGF2, IGF1R, CDH1, GRB10, KDR, SH3GL2, HGF, APLP2, LMO2, C10ORF55, HNF1A, SOX10, SHTN1, MAF, BIN1, DDIT3, ATF3, NOTCH3, SDC4, MAGED1, HTRA1, PDGFB, PDGFA, GATA3, FOXO4, SNX9, TFAP2A, JUN, SMAD3, TGFBI, ZBTB16, CAV1, INHBA, GDF6, SMAD6, ESR1, GFAP, COL1A1, AHI1, MAFB, COL1A2, CD28, FGF3, BCL2L2, FGF2, FGF1, ROBO2, ALK, ITGB3, PHF1, FHL2, GPHN, ROBO1, GHR, PPP1R13L, OLR1, PRKG2, PRMT8, GRID1, DNMT3A, AXIN1, FOS, SYP, OLIG2, TIRAP, DNMT1, DNMT3, DMRTA2, PPARG, PLCB1, GAS7, HDAC4, CAMK2B, CEBPA, HDAC5, CEBPD, CEBPE, ATL1, CAMK2A, NOD1, EGFR, MIPOL1, ERBB3, ERBB2, STAT4, CTNNA1, HAS2, FLNC, NTRK1, NPM2, ANGPT1, DMRT1, DAB2IP, SEPTIN5, SORBS2, VEGFD, EPOR, PC, ERCC4	1.944371	4.53E-09	4.09E-09
GOTERM_MF_DIRECT	GO:0043565~sequence-specific DNA binding	31	2.98E-09	HLF, PLAG1, FOXO4, FOXO3, GLI1, HOXA13, GATA1, ETS2, SOX2, PRDM16, HES1, NKX2-5, PPARGC1A, TFAP2A, TCF7L2, EGR1, EGR2, SMAD3, EGR4, PAX3, ETV1, ETV4, ESR1, POU5F1, MAFB, NR6A1, WT1, PPARG, ERCC6, LHX4, ERG	3.601601	1.64E-07	1.48E-07
GOTERM_MF_DIRECT	GO:0005178~integrin binding	23	3.74E-09	LAMAS, DST, SRC, ITGB3, TNC, PRKCA, IGF1, FGF1, FGF2, EGFR, GFAP, COL3A1, SFRP2, IBSP, IL1B, CCN6, ITGA8, KDR, ITGA7, ITGAV, S1PR2, PLPP3, EDIL3	4.701014	1.93E-07	1.75E-07

GOTERM_ MF_DIRECT T	GO:0005104~fibroblast growth factor receptor binding	10	6.78E-09	FGF6, FGF8, FGF9, FGF19, FRS2, FGF1, FGF2, FGF3, FGF4, FGF10 ZNF331, PHF1, CHD6, GLI1, HOXA13, ETS2, SOX2, MECOM, ZIC2, MYO18A, JARID2, ZNF687, TEAD1, APLP2, DNMT3A, TET1, PAX3, FOXL2, HNF1A, SOX10, MLF1, ETV5, POU5F1, MYCL, AR, MYCN, PAX8, SETBP1, TAL2, KAT6B, DDIT3, PPARG, ERG, FLYWCH1, ZMYND11, ZFPM2, HDAC4, CEBPA, CEBPB, HLF, DDX20, HOXD13, GATA3, FOXO4, FOXO3, GATA1, SLX4, PRDM16, NKX2- 1, LRIG3, HES1, NKX2-5, PPARGC1A, RUNX1T1, TFAP2A, EGR1, JUN, EGR2, SMAD3, MGMT, ZBTB16, HMGGA2, SMARCA1, ESR1, PBX1, NR4A3, NR6A1, ERCC4, NFIB, FOSB, ERCC6, LHX4	15.05068	3.29E-07	2.98E-07
GOTERM_ MF_DIRECT T	GO:0003677~DNA binding	72	8.56E-09		2.060525	3.93E-07	3.55E-07
GOTERM_ MF_DIRECT T	GO:0017147~Wnt- protein binding	12	9.78E-09	SFRP4, FZD3, SFRP2, FZD2, WIF1, EGF, FZD7, FZD6, LRP5, FZD8, FZD10, LRP1B	10.45626	4.25E-07	3.85E-07
GOTERM_ MF_DIRECT T	GO:0005109~frizzled binding	12	1.33E-08	WNT6, WNT10B, RNF43, WNT11, WNT2B, WNT5B, FZD7, WNT7B, WNT8B, WNT16, WNT3, WNT4	10.18815	5.48E-07	4.95E-07
GOTERM_ MF_DIRECT T	GO:0005161~platelet- derived growth factor receptor binding	8	6.24E-08	PDGFRB, PDGFRA, IL1R1, PDGFD, ITGB3, PDGFB, PDGFA, VEGFD	18.92085	2.45E-06	2.22E-06
GOTERM_ MF_DIRECT T	GO:0042813~Wnt receptor activity	9	1.43E-07	FZD3, FZD2, EGF, FZD7, FZD6, LRP5, FZD8, FZD10, LRP1B	13.54561	5.38E-06	4.86E-06
GOTERM_ MF_DIRECT T	GO:0015026~coreceptor activity	13	1.55E-07	NGFR, ITGB3, LRP5, IL1RAP, ACVR2A, TGFBR3, PTK7, ERBB2, CD28, KDR, ACKR3, ITGAV, IL12RB2	7.295753	5.56E-06	5.02E-06
GOTERM_ MF_DIRECT T	GO:0008013~beta- catenin binding	17	1.93E-07	AMER1, KANK1, TCF7L2, SMAD3, CTNND2, AXIN1, PTPRK, FOXO4, KLF4, FOXO3, ESR1, GLI3, AR, BCL9, CDH1, CDH11, CTNNA1 EPHB6, RET, ALK, ITK, ATP8A2, FLT3, DGKB, FLT4, CHD6, GPHN, IGF1R, CCT6B, CLP1, RPS6KA2, PRKACG, MYO18A, KDR, PRKG2, MAP3K6, ROS1, ABCC3, PDGFRB, PRKCG, EPHA5, PDGFRA, EPHA7, CDKL5, KSR1, ACSL6, MATK, PRKCA, RUNX2, BCR, NAV3, SCN8A, KIT, ITPKA, ACSBG1, CILK1, EPHA3, EPHA2, DDR2, CAMK2B, CSF1R, BRSK1, EPHA10, SRC, CAMK2A, DDX20, NOD1, AK5, ACVR1B, KALRN, EGFR, ACVR1C, ERBB3, ERBB4, ERBB2, ABL2, PAK6, LRIG3, MYH11, CKB, PAK3, PAK5, NTRK1, NTRK2, NTRK3, STYK1, KIAA0232, HSPA2, SMARCA1, ACVR2A, PC, CPS1, AXL, PTK7, ERCC6, FGFR4, FGFR3, FGFR2, BMPR1A, FGFR1	5.117231	6.63E-06	5.99E-06
GOTERM_ MF_DIRECT T	GO:0005524~ATP binding	83	2.94E-07	NOTCH2, NOTCH3, CSF3, SRC, ITGB3, FOXO4, CYP2C19, PTGS2, EGFR, FLCN, HOXA9, CCND1, NKX2-1, PDGFRB, EGR1, JUN, PRMT8, NPM2, SORT1, CAV1, ACSL6, AXIN1, PDE4DIP, PRKCA, HSPA2, ESR1, AR, TAL1, NEDD4, RARA, PPARG, PLCB1	1.783422	9.70E-06	8.77E-06
GOTERM_ MF_DIRECT T	GO:0019899~enzyme binding	32	3.61E-07		2.8483	1.15E-05	1.04E-05
GOTERM_ MF_DIRECT T	GO:0048407~platelet- derived growth factor binding	7	5.79E-07	PDGFRB, COL1A1, PDGFRA, COL3A1, COL1A2, PDGFB, PDGFA	19.31504	1.77E-05	1.60E-05
GOTERM_ MF_DIRECT T	GO:0001223~transcriptio n coactivator binding	11	1.34E-06	AR, SMAD3, GATA6, RARA, PPARG, FLYWCH1, GATA3, HNF1A, GATA2, ESR1, GATA1	7.58805	3.95E-05	3.57E-05
GOTERM_ MF_DIRECT T	GO:0001221~transcriptio n coregulator binding	10	1.44E-06	LMO2, CHD6, PPARG, FOS, GATA2, KLF4, FOXO3, ESR1, GATA1, PBX1 HDAC4, YAP1, HDAC5, PHF1, GATA6, CHD6, HOXD13, HOXC13, GATA2, GLI1, EGFR, GLI3, HMGN2P46, CREB3L1, HES1, JARID2, NKX2-5, HES5, BRD3, TFAP2A, EGR2, NPM2, AUTS2, DMRT1, DNMT3A, MITF, HNF1A, FOS, SMAD6, ESR1, AR, LHX2, KAT6B, TAL1, RARA, PPARG, ERCC6, ERG CAMK2B, TENM1, CEBPA, CSF1R, CEBPB, HIP1, CANT1, CSF1, FLT4, CAMK2A, PDGFB, PDGFA, NOD1, PTGS2, GHR, MECOM, ERBB4, HES1, SNX9, NKX2-5, NTRK1, WWTR1, PDGFRA, NTRK2, TGFBR2, PRMT8, SMAD3, DST, ZBTB16, DAB2IP, ACSL6, AXIN1, MTUS2, HNF1A, DNMT1, EXT1, TBX15, NR4A3, NR6A1, DDIT3, DPYD, KIT, COL9A3, ATF3, FGFR2, BCL2L2, BMPR1A, FGFR1	8.713551	4.11E-05	3.72E-05
GOTERM_ MF_DIRECT T	GO:0003682~chromatin binding	38	1.55E-06		2.405806	4.27E-05	3.87E-05
GOTERM_ MF_DIRECT T	GO:0042803~protein homodimerization activity	48	1.86E-06		2.119136	4.96E-05	4.49E-05
GOTERM_ MF_DIRECT T	GO:0019955~cytokine binding	10	7.87E-06	GHR, CSF1R, CSF3R, KIT, LIFR, TNFRSF11A, IL13RA2, POU5F1, IL12RB2, CRLF2	7.19815	2.03E-04	1.84E-04
GOTERM_ MF_DIRECT T	GO:0048018~receptor ligand activity	12	8.45E-06	DLL4, WNT10B, RELN, SFRP2, TAFAS, TAFAS, EGF, WNT7B, WNT8B, DLL1, WNT3, WNT4	5.596309	2.12E-04	1.91E-04
GOTERM_ MF_DIRECT T	GO:0008201~heparin binding	19	1.63E-05	ALK, TENM1, APLP2, COL11A1, PTCH1, PRG2, FGF1, FGF2, FGF4, TGFBR3, BMP4, COL1A1, FGF14, FGF9, CCN6, FGFR4, FGFR2, FGF10, FGFR1 LMO1, YAP1, HDAC4, HDAC5, SMAD3, LMO2, GATA6, DDX20, FOXO4, HOXC13, SOX10, PBX1, PER1, PRDM16, ZNF703, PPARG, PPARGC1A, RUNX1T1	3.346374	3.96E-04	3.58E-04
GOTERM_ MF_DIRECT T	GO:0140297~DNA- binding transcription factor binding	18	1.84E-05		3.465156	4.35E-04	3.93E-04
GOTERM_ MF_DIRECT T	GO:0071837~HMG box domain binding	6	2.58E-05	EGR2, PRRX1, HOXA3, PAX3, GATA3, OLIG2	15.28223	5.91E-04	5.35E-04
GOTERM_ MF_DIRECT T	GO:0005158~insulin receptor binding	7	3.62E-05	IRS1, SRC, IRS4, GRB10, IRS2, IGF1, IGF1R	10.53547	8.07E-04	7.30E-04
GOTERM_ MF_DIRECT T	GO:0042056~chemoattr actant activity	9	4.42E-05	BMP4, FGF8, HGF, NTF3, PDGFB, VEGFC, VEGFD, FGF2, FGF10	6.772805	9.61E-04	8.69E-04
GOTERM_ MF_DIRECT T	GO:0005112~Notch binding	8	4.72E-05	JAG2, NOTCH2, DLL4, NOTCH3, ATRNL1, NOTCH4, DLL1, DLL3	8.027028	9.61E-04	8.69E-04
GOTERM_ MF_DIRECT T	GO:0008046~axon guidance receptor activity	7	4.77E-05	ROBO2, NTRK2, EPHA7, PTK7, NCAM1, FGFR4, ROBO1	10.07741	9.61E-04	8.69E-04
GOTERM_ MF_DIRECT T	GO:0017134~fibroblast growth factor binding	7	4.77E-05	TGFBR3, ITGB3, ITGAV, FGFR4, FGFR3, FGFR2, FGFR1	10.07741	9.61E-04	8.69E-04
GOTERM_ MF_DIRECT T	GO:0043548~phosphatid ylinositol 3-kinase binding	6	8.12E-05	IRS1, AXL, DAB2IP, IRS4, IRS2, IGF1R	12.41681	0.001596	0.001443

GOTERM_MF_DIRECT	GO:0043121~neurotrophin binding	4	1.07E-04	NTRK1, NTRK2, NGFR, NTRK3	33.11149	0.002048	0.001852
GOTERM_MF_DIRECT	GO:0005005~transmembrane-ephrin receptor activity	6	1.12E-04	EPHB6, EPHA5, EPHA7, EPHA10, EPHA3, EPHA2	11.68641	0.002105	0.001904
GOTERM_MF_DIRECT	GO:0003714~transcription corepressor activity	18	1.67E-04	YAP1, HDAC4, WWTR1, NAB2, DNMT3A, FHL2, HMGA2, DNAJB1, CCND1, PPP1R13L, DDI1, FLYWCH1, ZMYND11, ZFPM2, BCORL1, SSK1, WNT4, RUNX1T1	2.907351	0.003065	0.002772
GOTERM_MF_DIRECT	GO:0070064~proline-rich region binding	6	2.00E-04	GHR, YAP1, BAIAP2L1, CCND1, NEDD4, SH3D19	10.45626	0.003599	0.003255
GOTERM_MF_DIRECT	GO:0031490~chromatin DNA binding	11	2.60E-04	PER1, CEBPA, CEBPB, SMAD3, ZIC2, RARA, KLF4, FOXO3, PPARGC1A, GATA1, RUNX2	4.235191	0.004392	0.003972
GOTERM_MF_DIRECT	GO:0005163~nerve growth factor receptor binding	4	2.61E-04	NTF4, BDNF, NTF3, NGF	26.48919	0.004392	0.003972
GOTERM_MF_DIRECT	GO:0005007~fibroblast growth factor receptor activity	4	2.61E-04	FGFR4, FGFR3, FGFR2, FGFR1	26.48919	0.004392	0.003972
GOTERM_MF_DIRECT	GO:0004896~cytokine receptor activity	8	3.66E-04	GHR, CSF3R, FLT3, LIFR, IL7R, IL13RA2, IL12RB2, CRLF2	5.886488	0.006051	0.005473
GOTERM_MF_DIRECT	GO:0070888~E-box binding	9	4.18E-04	PER1, TAL1, HES1, OLIG1, PPARG, MITF, GATA3, BHLHE22, OLIG2	4.966724	0.006778	0.00613
GOTERM_MF_DIRECT	GO:0005004~GPI-linked ephrin receptor activity	4	5.09E-04	NTRK1, EPHA5, EPHA7, EPHA3	22.07433	0.008092	0.007318
GOTERM_MF_DIRECT	GO:0046332~SMAD binding	8	5.50E-04	TGFBR3, COL3A1, COL1A2, CREB3L1, AXIN1, HMGA2, ACVR1B, BMPR1A	5.518582	0.008568	0.007749
GOTERM_MF_DIRECT	GO:0001222~transcription corepressor binding	8	6.25E-04	PER1, HDAC5, SMAD3, PHF1, ZBTB16, HES1, ESR1, PBX1	5.405958	0.00956	0.008646
GOTERM_MF_DIRECT	GO:0001227~DNA-binding transcription repressor activity, RNA polymerase II-specific	24	6.50E-04	TFAP2A, JUN, CEBPB, PRRX1, CDX2, PEG3, ZBTB16, MITF, GATA3, FOXO3, ETS2, POU5F1, TBX15, DACH1, HEY1, CREB3L1, TRPS1, PRDM16, HES1, PPARG, HOXD9, MNX1, HES5, ATF3	2.201318	0.009767	0.008833
GOTERM_MF_DIRECT	GO:0070412~R-SMAD binding	6	7.89E-04	JUN, SMAD3, AXIN1, PPARG, FOS, SMAD6	7.946758	0.011631	0.010518
GOTERM_MF_DIRECT	GO:0005516~calmodulin binding	17	8.46E-04	CAMK2B, NGFR, ACE, USP6, NOS3, RASGRF2, CAMK2A, PDE4DIP, ESR1, EGFR, RYR3, AKAP12, MAP2, RPS6KA2, ITPKA, MYH11, PLCB1	2.618118	0.012181	0.011016
GOTERM_MF_DIRECT	GO:0005160~transforming growth factor beta receptor binding	5	8.56E-04	TGFBR3, TGFBR2, SMAD3, TGFBR3, LEFTY2	11.03716	0.012181	0.011016
GOTERM_MF_DIRECT	GO:0005003~ephrin receptor activity	4	8.72E-04	EPHB6, EPHA5, EPHA3, EPHA2	18.92085	0.012181	0.011016
GOTERM_MF_DIRECT	GO:0002020~protease binding	12	8.85E-04	COL1A1, NTRK2, COL3A1, COL1A2, CRADD, CHL1, BIN1, IL1R1, ITGB3, KIT, CD28, ITGAV	3.36727	0.012181	0.011016
GOTERM_MF_DIRECT	GO:0005021~vascular endothelial growth factor receptor activity	4	0.001363	PDGFRA, FLT3, FLT4, KDR	16.55575	0.01846	0.016694
GOTERM_MF_DIRECT	GO:0019901~protein kinase binding	29	0.001407	HDAC4, BRSK1, CDKN1A, PTPRR, GATA6, PTPRK, FOXO3, EGFR, GHR, CCND1, RAC3, IL12RB2, PDGFRB, TCF7L2, CDKN2B, SMAD3, CAV1, DAB2IP, AXIN1, PDE4DIP, MAPK8IP2, NBEAP1, RHOD, ESR1, DNMT1, NR4A3, LRRK7, CD28, SPRY2	1.912815	0.018659	0.016874
GOTERM_MF_DIRECT	GO:0035259~nuclear glucocorticoid receptor binding	5	0.001423	SMAD3, NR4A3, FLT3, RARA, ETS2	9.738674	0.018659	0.016874
GOTERM_MF_DIRECT	GO:0046983~protein dimerization activity	15	0.001492	OLIG1, MITF, OLIG2, HNF1A, BHLHE22, MYCL, MYCN, HEY1, TAL2, TAL1, ID1, ID4, AHR, HES1, HES5	2.684716	0.01926	0.017418
GOTERM_MF_DIRECT	GO:0044877~protein-containing complex binding	21	0.002307	CDKN1C, PDGFRA, CDKN1A, TGFBR3, FLT3, CEBPE, CAV1, PTCH1, DAB2IP, NOD1, PRICKLE1, INHBA, MAPK8IP2, TSHR, IGF1R, FLCN, MAFB, CPS1, CD36, MB21D2, BCL2L2	2.126426	0.029312	0.026509
GOTERM_MF_DIRECT	GO:0140416~transcription regulator inhibitor activity	6	0.002512	DNAJB1, NFIB, DDIT3, ID1, ID4, SMAD6	6.208405	0.031442	0.028435
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	11	0.002856	FBN2, COL1A1, LAMA5, COL3A1, COL1A2, LAMA1, COL11A1, ELN, TNC, LTBP1, EDIL3	3.113046	0.035214	0.031846
GOTERM_MF_DIRECT	GO:000977~RNA polymerase II transcription regulatory region sequence-specific DNA binding	22	0.003397	TFAP2A, EGR1, CEBPB, CDX2, PEG3, CDX1, PAX3, GLI1, GATA1, PHOX2B, ETV5, GLI3, PBX1, DACH1, MECOM, LHX2, TRPS1, NKX2-1, RARA, LHX4, HOXD9, ATF3	2.012301	0.041262	0.037315
GOTERM_MF_DIRECT	GO:0005114~type II transforming growth factor beta receptor binding	4	0.003754	TGFBR3, TGFBR2, TGFBR3, AMH	12.04054	0.044298	0.040061
GOTERM_MF_DIRECT	GO:0048185~activin binding	4	0.003754	TGFBR3, ACVR1B, ACVR2A, FSTL3	12.04054	0.044298	0.040061
GOTERM_MF_DIRECT	GO:0016301~kinase activity	15	0.004001	ALK, RET, NTRK2, CDKN1A, CDKL5, CAMK2A, AKAP6, PRKCA, MAPK8IP2, EGFR, PLAU, RPS6KA2, ERBB2, CKB, EPHA2	2.411031	0.046549	0.042097

GOTERM_MF_DIRECT	GO:1990841~promoter-specific chromatin binding	8	0.004318	FOSL1, TCF7L2, EGR1, SMAD3, ERCC4, FOXO4, KLF4, SOX10	3.89547	0.049539	0.044801
GOTERM_MF_DIRECT	GO:0004672~protein kinase activity	18	0.004585	PDGFRB, PRKCG, CAMK2B, PDGFRA, CDKL5, KSR1, SRC, FLT4, CAMK2A, STYK1, PRKCA, ERBB3, CCND1, PTK7, ERBB2, PRKG2, ABL2, CILK1	2.151649	0.051278	0.046374
GOTERM_MF_DIRECT	GO:0005080~protein kinase C binding	7	0.004594	HDAC5, SDC4, IRS1, SRC, ITGB3, ITGAV, TIRAP, CSF3R, EPO, FZD10, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, EDNRB, FGF8, CCND1, FGF9, CDH1, PRKACG, PDGFRB, PRKCG, PDGFRA, WNT5B, HGF, FLT3LG, MITF, PRKCA, BCR, AR, SMO, NOTCH2, CSF1R, NOTCH3, NOTCH4, PDGFB, LPAR1, PDGFA, PIK3R2, WNT6, FGF23, WNT3, WNT4, JAG2, WNT10B, FZD3, TGFb2, JUN, FZD2, SMAD3, GADD45B, TGFb3, ZBTB16, PTCH1, FZD7, FZD6, FZD8, IGF1, ESR1, IL2, BMP4, IL3, GNAQ, FGF19, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1, RET, ALK, CDKN1A, WNT2B, FLT3, FLT4, FASLG, GLI1, GLI3, MECOM, HEY1, RAC3, ITGAV, IL15, IL13, AXIN1, FOS, WNT16, PLCB4, PAX8, KIT, RARA, PPARG, PLCB1, CAMK2B, CEBPA, LAMA5, LAMA1, CAMK2A, LRP5, WNT8B, PTGS2, DLL1, EGFR, GNAI1, DLL3, DLL4, WNT11, GNG4, GNA11, ERBB2, GNA12, STAT4, CTNNA1, HES1, HES5, IL12RB2, RUNX1T1, NTRK1, TCF7L2, CDKN2B, EGF, WNT7B, VEGFC, VEGFD, EPOR	4.457316	0.051278	0.046374
KEGG_PATHWAY	hsa05200:Pathways in cancer	121	5.49E-53	CDKN1A, WNT2B, FLT4, FZD10, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, FGF8, HEY1, FGF9, CCND1, WNT5B, AXIN1, FOS, WNT16, KIT, NOTCH2, NOTCH3, SHC2, NOTCH4, LRP5, WNT8B, PIK3R2, DLL1, EGFR, DLL3, DLL4, WNT6, WNT11, ERBB2, HES1, FGF23, WNT3, HES5, WNT4, JAG2, TCF7L2, WNT10B, JUN, FZD3, FZD2, GADD45B, EGF, FZD7, WNT7B, FZD6, FZD8, IGF1, ESR1, FGF19, FGF10, FGFR1	4.882796	1.60E-50	1.02E-50
KEGG_PATHWAY	hsa05224:Breast cancer	55	5.97E-35	RET, CDKN1A, CSF3, CSF3R, CSF1, EPO, FLT3, IRS1, FLT4, ITGB3, TNC, FASLG, FGF1, FGF2, FGF3, IGF1R, FGF4, GHR, FGF6, FGF8, IBSF, FGF9, CCND1, CREB3L1, KDR, ITGAV, PDGFRB, PDGFRA, HGF, FLT3LG, PRKCA, NGF, KIT, ITGA8, COL6A3, ITGA7, EPHA2, CSF1R, LAMA5, LAMA1, PDGFB, LPAR1, PDGFA, PIK3R2, FOXO3, EGFR, NTF4, RELN, ERBB3, ERBB4, GNG4, PDGFD, ERBB2, NTF3, FGF23, NTRK1, NTRK2, NGFR, ANGPT1, EGF, NOS3, BDNF, VEGFC, VEGFD, IGF1, EPOR, IL2, COL1A1, IL3, COL1A2, PPP2R2B, FGF19, COL9A3, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1	7.99303	8.72E-33	5.55E-33
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	79	3.22E-32	RET, PTPRR, CSF1, FLT3, FLT4, RASGRF2, FASLG, IL1RAP, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, FGF8, MECOM, FGF9, RPS6KA2, PRKACG, KDR, RAC3, MAP3K6, PDGFRB, PRKCG, PDGFRA, IL1R1, HGF, CACNA2D3, FLT3LG, PRKCA, FOS, NGF, MAPK8IP2, DUSP9, IL1B, DDIT3, KIT, EPHA2, CSF1R, PDGFB, PDGFA, CACNA1F, EGFR, CACNA1G, NTF4, PPP3R2, ERBB3, ERBB4, PDGFD, ERBB2, NTF3, GNA12, FGF23, NTRK1, NTRK2, NGFR, TGFb2, JUN, GADD45B, ANGPT1, TGFb3, EGF, BDNF, VEGFC, VEGFD, IGF1, FGF19, FGFR4, FGFR3, FGFR2, FGF10, FGFR1	4.693847	3.14E-30	2.00E-30
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	72	4.88E-32	CSF1, FLT3, FLT4, RASGRF2, FASLG, FGF1, FGF2, ETS2, FGF3, IGF1R, FGF4, FGF6, FGF8, FGF9, PRKACG, KDR, RAC3, PDGFRB, PRKCG, PDGFRA, KSR1, HGF, FLT3LG, PRKCA, NGF, TIAM1, KIT, EPHA2, CSF1R, SHC2, PDGFB, PDGFA, PIK3R2, PLA2G5, FOXO4, EGFR, NTF4, GRIN2A, GNG4, PDGFD, NTF3, ABL2, PAK6, PAK3, FGF23, PAK5, NTRK1, NTRK2, NGFR, ANGPT1, EGF, BDNF, PLA2G2A, VEGFC, VEGFD, IGF1, GRIN2B, FGF19, FGFR4, FGFR3, FGF2, FGF10, FGFR1	5.162044	3.56E-30	2.27E-30
KEGG_PATHWAY	hsa04014:Ras signaling pathway	63	1.69E-30	CDKN1A, SHC2, WNT2B, LRP5, WNT8B, PIK3R2, FZD10, FGF1, FGF2, FGF3, EGFR, FGF4, FGF6, WNT6, FGF8, WNT11, FGF9, CCND1, CDH1, ERBB2, CTNNA1, FGF23, WNT3, WNT4, TCF7L2, WNT10B, TGFb2, CDKN2B, FZD3, FZD2, SMAD3, WNT5B, GADD45B, CDX2, TGFb3, EGF, FZD7, HGF, WNT7B, FZD6, AXIN1, FZD8, WNT16, FGF19, FGFR2, FGF10	5.693431	9.84E-29	6.27E-29
KEGG_PATHWAY	hsa05226:Gastric cancer	46	4.42E-25	CDKN1A, FLT3, PLAT, HOXA11, IGF1R, HOXA9, PLAU, SSX1, PTCRA, LMO2, PAX3, MITF, ETV1, WNT16, ETV4, MLF1, ETV5, RUNX2, MYCN, MAF, PAX8, PAX7, DDIT3, RARA, PPARG, ERG, CEBPA, CSF1R, CEBPB, SLC45A3, CEBPE, PDGFA, TMPSR52, PROM1, RUNX1T1, NTRK1, NGFR, GADD45B, BCL11B, EYA1, ZBTB16, HMGA2, IGF1, PBX1, IL3, NR4A3, TLX3, WT1, FEV, TLX1	6.595945	2.15E-23	1.37E-23
KEGG_PATHWAY	hsa05202:Transcriptional misregulation in cancer	50	1.18E-23	CDKN1A, WNT2B, ITGB3, FASLG, FZD10, FGF2, IGF1R, CCND1, PLAU, PRKACG, KDR, ITGAV, PRKCG, WNT5B, HGF, FRS2, PRKCA, WNT16, DCN, TIAM1, SMO, CAMK2B, SDC4, SRC, CAMK2A, WNT8B, PIK3R2, EGFR, WNT6, WNT11, ERBB3, ERBB4, ERBB2, GPC3, WNT3, WNT4, WNT10B, TGFb2, FZD3, FZD2, FZD7, WNT7B, CAV1, PTCH1, FZD6, FZD8, IGF1, ESR1, COL1A1, COL1A2, FGFR1	5.572154	4.94E-22	3.14E-22
KEGG_PATHWAY	hsa05205:Proteoglycans in cancer	51	2.25E-23	CSF1, FLT4, ITGB3, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, FGF8, FGF9, CDH1, KDR, RAC3, PDGFRB, PRKCG, PDGFRA, HGF, PRKCA, NGF, TIAM1, PLCB4, KIT, PLCB1, EPHA2, CSF1R, SRC, PDGFB, LPAR1, PDGFA, PIK3R2, EGFR, GNAI1, GRIN2A, PDGFD, FGF23, NGFR, ANGPT1, EGF, VEGFC, VEGFD, IGF1, GRIN2B, GNAQ, FGF19, ID1, FGFR4, FGFR3, FGFR2, FGF10, FGFR1	5.377129	8.19E-22	5.22E-22
KEGG_PATHWAY	hsa04015:Rap1 signaling pathway	51	1.43E-22	WNT2B, WNT8B, PIK3R2, FZD10, ACVR1B, FGF2, IGF1R, SOX2, WNT6, ACVR1C, WNT11, JARID2, LEFTY2, WNT3, WNT4, WNT10B, FZD3, FZD2, SMAD3, WNT5B, FZD7, WNT7B, FZD6, AXIN1, FZD8, LIFR, IGF1, INHBA, KLF4, WNT16, DUSP9, POU5F1, ACVR2A, BMP4, ID1, ID4, FGFR4, FGFR3, FGFR2, NODAL, BMPR1A, FGFR1	5.174218	4.65E-21	2.96E-21
KEGG_PATHWAY	hsa04550:Signaling pathways regulating pluripotency of stem cells	42	5.72E-22	CAMK2B, WNT2B, CTNND2, CAMK2A, LRP5, WNT8B, FZD10, PRICKLE1, CXCC4, WNT6, PPP3R2, WNT11, CCND1, WIF1, PRKACG, RAC3, WNT3, WNT4, PRKCG, TCF7L2, RNF43, WNT10B, JUN, FZD3, MMP7, FZD2, SMAD3, WNT5B, FZD7, WNT7B, SERPINF1, FZD6, AXIN1, FZD8, PRKCA, WNT16, DKK1, DKK2, DKK4, FOSL1, SFRP4, PLCB4, SFRP2, PLCB1, LGR5	6.273317	1.67E-20	1.06E-20
KEGG_PATHWAY	hsa04310:Wnt signaling pathway	45	3.02E-21	RET, FLT4, FGF1, FGF2, FGF3, GRM1, RYR3, FGF4, FGF6, FGF8, EDNRB, FGF9, PRKACG, KDR, PDGFRB, PRKCG, PDGFRA, HGF, PRKCA, NGF, PLCB4, ASPH, ITPKA, PLCB1, CAMK2B, CAMK2A, PDGFB, PDGFA, CACNA1F, EGFR, CACNA1G, GRIN2A, PPP3R2, ERBB3, ERBB4, PDGFD, GNA11, ERBB2, FGF23, NTRK1, NTRK2, EGF, NOS3, NTRK3, VEGFC, VEGFD, GRIN2B, GNAQ, FGF19, FGFR4, FGFR3, FGFR2, FGF10, FGFR1	5.562547	7.37E-20	4.70E-20
KEGG_PATHWAY	hsa04020:Calcium signaling pathway	54	3.03E-21	CDKN1A, PDGFB, PDGFA, PIK3R2, FGF1, FGF2, FGF3, EGFR, FGF4, IGF1R, FGF6, FGF8, FGF9, CCND1, CDH1, PDGFD, FGF23, PDGFRB, PDGFRA, GADD45B, EGF, HGF, MITF, IGF1, FGF19, FGF10, FGFR1	4.572677	7.37E-20	4.70E-20
KEGG_PATHWAY	hsa05218:Melanoma	27	5.12E-17	CDKN1A, WNT2B, WNT8B, FZD10, GLI1, GLI3, WNT6, WNT11, WNT3, WNT4, TCF7L2, WNT10B, FZD3, FZD2, WNT5B, GADD45B, FZD7, PTCH1, WNT7B, FZD6, AXIN1, FZD8, WNT16, BMP4, SMO	7.955204	1.15E-15	7.33E-16
KEGG_PATHWAY	hsa05217:Basal cell carcinoma	25	1.39E-16		8.535125	2.89E-15	1.84E-15

KEGG_PATHWAY	hsa04390:Hippo signaling pathway	37	5.33E-16	YAP1, WNT2B, WNT8B, FZD10, FGF1, SOX2, WNT6, WNT11, CCND1, CDH1, CTNNA1, AMH, TEAD1, WNT3, WNT4, TEAD3, TEAD4, WWTR1, TCF7L2, WNT10B, TGFβ2, FZD3, FZD2, SMAD3, WNT5B, TGFβ3, FZD7, WNT7B, FZD6, AXIN1, FZD8, WNT16, GDF6, BMP4, PPP2R2B, ID1, BMPR1A CAMK2B, WNT2B, CAMK2A, WNT8B, FZD10, GNAI1, WNT6, EDNRB, WNT11, PRKACG, CREB3L1, WNT3, WNT4, PRKCG, TCF7L2, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, MITF, WNT16, PLCB4, GNAQ, KIT, PLCB1	5.068886	1.04E-14	6.60E-15
KEGG_PATHWAY	hsa04916:Melanogenesis	30	6.81E-16	LAMA5, SHC2, SRC, LAMA1, FLT4, ITGB3, PDGFB, TNC, PDGFA, PIK3R2, EGFR, IGF1R, RELN, CCND1, IBSP, PDGFG, ERBB2, KDR, PAK6, RAC3, ITGAV, PAK3, PAK5, PRKCG, PDGFRB, PDGFRA, JUN, EGF, HGF, CAV1, VEGFC, PRKCA, VEGFD, IGF1, COL1A1, COL1A2, ITGA8, COL6A3, ITGA7, COL9A3, DOCK1 CAMK2B, CDKN1A, WNT2B, CAMK2A, WNT8B, FZD10, CACNA1F, GNAI1, EGFR, CACNA1G, WNT6, WNT11, CCND1, PRKACG, GNA11, CREB3L1, WNT3, WNT4, TCF7L2, WNT10B, CDKN2B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, AXIN1, FZD8, WNT16, PBX1, PLCB4, GNAQ, PLCB1	6.388668	1.24E-14	7.92E-15
KEGG_PATHWAY	hsa04510:Focal adhesion	41	2.88E-15	CDKN1A, WNT2B, MAML2, ITGB3, TNC, FASLG, FZD10, LFNG, HEY1, IBSP, CCND1, PRKACG, CREB3L1, ITGAV, PDGFRB, WNT5B, AXIN1, WNT16, ITGA8, COL6A3, ITGA7, NOTCH2, LAMA5, NOTCH3, LAMA1, NOTCH4, WNT8B, PIK3R2, PTGS2, EGFR, WNT6, RELN, WNT11, HES1, WNT3, HES5, WNT4, TCF7L2, WNT10B, FZD3, FZD2, EGF, FZD7, WNT7B, FZD6, FZD8, COL1A1, COL1A2, PPP2R2B, COL9A3	4.344084	4.95E-14	3.16E-14
KEGG_PATHWAY	hsa04934:Cushing syndrome	34	8.50E-14	PDGFRB, PRKCG, PDGFRA, SHC2, SRC, EGF, HGF, PDGFB, PDGFA, PRKCA, PIK3R2, IGF1, FOXO3, FGF2, EGFR, IGF1R, ERBB3, AXL, PDGFD, ERBB2, KDR, FGFR3, FGFR2	4.717997	1.38E-12	8.79E-13
KEGG_PATHWAY	hsa05165:Human papillomavirus infection	50	3.00E-13	CDKN1A, SHC2, WNT2B, LRP5, WNT8B, PIK3R2, FZD10, EGFR, IGF1R, WNT6, WNT11, CCND1, WNT3, WNT4, PRKCG, TCF7L2, WNT10B, TGFβ2, FZD3, FZD2, SMAD3, WNT5B, GADD45B, TGFβ3, FZD7, HGF, WNT7B, FZD6, AXIN1, FZD8, PRKCA, WNT16	3.229507	4.62E-12	2.94E-12
KEGG_PATHWAY	hsa01521:EGFR tyrosine kinase inhibitor resistance	23	5.90E-12	SRC, ITGB3, PDGFB, LPAR1, PDGFA, PIK3R2, FGF1, FGF2, FGF3, EGFR, FGF4, FGF6, FGF8, FGF9, PDGFD, GNA12, PAK6, RAC3, MYH11, ITGAV, PAK3, FGF23, PAK5, PDGFRB, PDGFRA, GSN, EGF, TIAM1, FGF19, ITGA8, ITGA7, FGFR4, DOCK1, FGFR3, FGFR2, FGF10, FGFR1	6.183698	8.61E-11	5.48E-11
KEGG_PATHWAY	hsa05225:Hepatocellular carcinoma	32	3.59E-11	PDGFRB, PDGFRA, TCF7L2, CDKN1A, EGF, PDGFB, PDGFA, TMPPRS2, PLAT, PIK3R2, IGF1, EGFR, ETV5, IGF1R, AR, CCND1, PLAU, CREB3L1, PDGFD, ERBB2, ERG, FGFR2, FGFR1	4.048662	5.00E-10	3.18E-10
KEGG_PATHWAY	hsa04810:Regulation of actin cytoskeleton	37	8.81E-11	CDKN1A, CSF3, CSF3R, EPO, MPL, PDGFB, PDGFA, PIK3R2, EGFR, GHR, SOCS2, SOCS3, CCND1, STAT4, IL13RA2, IL12RB2, PDGFRB, PDGFRA, IL15, EGF, IL13, LIFR, EPOR, IL2, FGAP, IL3, IL7R, CRLF2	3.460066	1.17E-09	7.45E-10
KEGG_PATHWAY	hsa05215:Prostate cancer	23	4.46E-10	CSF1R, CSF3, TNFRSF6B, CSF3R, CSF1, EPO, MPL, FASLG, TNFRSF11A, IL1RAP, ACVR1B, GHR, ACVR1C, AMH, IL13RA2, IL12RB2, NGFR, TGFβ2, TGFβ3, IL15, IL1R1, IL13, LIFR, INHBA, NGF, GDF6, EPOR, ACVR2A, IL2, TNFRSF10D, BMP4, IL3, IL1B, ACKR3, IL7R, NODAL, BMPR1A, CRLF2	5.047917	5.67E-09	3.61E-09
KEGG_PATHWAY	hsa04630:JAK-STAT signaling pathway	28	1.22E-08	WNT2B, IRS1, LRP5, WNT8B, PIK3R2, FZD10, IGF1R, FLCN, WNT6, WNT11, RPS6KA2, GRB10, WNT3, WNT4, PRKCG, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, IGF1, WNT16	3.584753	1.48E-07	9.44E-08
KEGG_PATHWAY	hsa04060:Cytokine-cytokine receptor interaction	38	3.39E-08	JAG2, NOTCH2, NOTCH3, CDKN1A, JUN, SHC2, SRC, NOTCH4, PIK3R2, FOS, IGF1, DLL1, ESR1, EGFR, IGF1R, DLL3, DLL4, CCND1, PRKACG, ERBB2	2.742697	3.96E-07	2.52E-07
KEGG_PATHWAY	hsa04150:mTOR signaling pathway	26	5.89E-08	PDGFRB, PRKCG, PDGFRA, SRC, EGF, PDGFB, LPAR1, PDGFA, PRKCA, EGFR, GNAI1, GRM1, PLCB4, PRKACG, GNA11, PDGFD, GNAQ, PRKG2, PLCB1	3.539376	6.61E-07	4.21E-07
KEGG_PATHWAY	hsa01522:Endocrine resistance	20	1.05E-07	PRKCG, EGR1, SLC34A2, CDKN1A, LRP5, PRKCA, GATA3, FOS, EGFR, GNAI1, RUNX2, MAFB, PLCB4, PRKACG, GNA11, CREB3L1, GNAQ, GNA12, PLCB1, FGF23, FGFR1	4.345155	1.14E-06	7.23E-07
KEGG_PATHWAY	hsa04540:Gap junction	19	1.68E-07	PDGFRB, PRKCG, CAMK2B, PDGFRA, CDKN1A, SHC2, GADD45B, EGF, CAMK2A, PDGFB, PDGFA, PRKCA, PIK3R2, IGF1, EGFR, IGF1R, CCND1	4.441976	1.75E-06	1.12E-06
KEGG_PATHWAY	hsa04928:Parathyroid hormone synthesis, secretion and action	21	2.65E-07	PRKCG, CAMK2B, CDKN1A, JUN, SHC2, SRC, EGF, CAMK2A, PRKCA, PIK3R2, EGFR, ERBB3, ERBB4, ERBB2, ABL2, PAK6, PAK3, PAK5	3.927642	2.67E-06	1.70E-06
KEGG_PATHWAY	hsa05214:Glioma	17	2.86E-07	CAMK2B, NTRK1, NGFR, NTRK2, JUN, SHC2, SORT1, IRS1, BDNF, MAGED1, NTRK3, CAMK2A, MATK, FR52, FASLG, PIK3R2, NGF, FOXO3, NTF4, RPS6KA2, NTF3	4.811115	2.78E-06	1.77E-06
KEGG_PATHWAY	hsa04012:ErbB signaling pathway	18	3.18E-07	NOTCH2, SRC, PIK3R2, CACNA1F, FGF2, DLL1, FGF3, GNAI1, EGFR, FGF4, DLL3, DLL4, FGF6, FGF8, FGF9, CCND1, PRKACG, CREB3L1, RPS6KA2, CYP1B1, PRKCG, JUN, EGF, PRKCA, FOS, KLF4, ESR1, AR, FGF10	4.501782	2.99E-06	1.91E-06
KEGG_PATHWAY	hsa04722:Neurotrophin signaling pathway	21	5.41E-07	EPH86, ROBO2, CAMK2B, SRC, CAMK2A, PIK3R2, GNAI1, ROBO1, ABLIM1, PPP3R2, PAK6, RAC3, SRGAP3, PAK3, PAK5, WNT4, EPHA5, FZD3, EPHA7, WNT5B, PTCH1, PRKCA, RHOD, SMO, EPHA3, EPHA2	3.76399	4.93E-06	3.14E-06
KEGG_PATHWAY	hsa05207:Chemical carcinogenesis - receptor activation	29	6.38E-07	TGFβ2, CDKN2B, SMAD3, TGFβ3, INHBA, GDF6, ACVR1B, SMAD6, LTBP1, DCN, ACVR2A, BMP4, ACVR1C, ID1, ID4, AMH, LEFTY2, NODAL, BMPR1A	2.901149	5.64E-06	3.59E-06
KEGG_PATHWAY	hsa04360:Axon guidance	26	1.17E-06	CDKN1A, TGFβ2, CDKN2B, SMAD3, GADD45B, TGFβ3, IRS1, EGF, IRS4, FASLG, PIK3R2, IRS2, FOXO4, IGF1, FOXO3, EGFR, GRM1, IGF1R, CCNB3, CCND1, IL7R	3.039247	1.00E-05	6.38E-06
KEGG_PATHWAY	hsa04350:TGF-beta signaling pathway	19	2.01E-06	PRKCG, SHC2, IRS1, IRS4, PRKCA, PIK3R2, IRS2, FOS, IGF1, CACNA1F, GNAI1, GHR, SOCS2, SOCS3, PLCB4, PRKACG, GNA11, CREB3L1, GNAQ, PLCB1	3.783906	1.67E-05	1.07E-05
KEGG_PATHWAY	hsa04068:FoxO signaling pathway	21	2.55E-06	HDAC4, NOTCH2, HDAC5, NOTCH3, CDKN1A, SLC45A3, IRS1, ITGB3, NOTCH4, PDGFB, TNC, PDGFA, IRS2, PIK3R2, PTGS2, EGFR, ERBB3, CCND1, PLAU, ERBB2, CYP1B1, WNT3, PRKCG, PDGFRB, PDGFRA, TGFβ2, FZD3, DNMT3A, HMGA2, PRKCA, SPRY2, ZFPM2, FGFR3, BCL2L2	3.421809	2.07E-05	1.32E-05
KEGG_PATHWAY	hsa04935:Growth hormone synthesis, secretion and action	20	2.99E-06	JUN, SHC2, NOS3, SRC, VEGFC, VEGFD, PRKCA, PIK3R2, FOS, EGFR, GNAI1, COL1A1, COL3A1, PLCB4, EDNRB, COL1A2, GNG4, PRKACG, CREB3L1, PLCB1	3.525986	2.36E-05	1.50E-05
KEGG_PATHWAY	hsa05206:MicroRNAs in cancer	34	7.25E-06	PRKCG, CAMK2B, CAMK2A, PRKCA, FOS, GRIN2B, GNAI1, RYR3, CACNA1G, PER1, GRIN2A, PLCB4, GNG4, PRKACG, GNAQ, PRKG2, PLCB1	2.343877	5.57E-05	3.55E-05
KEGG_PATHWAY	hsa04926:Relaxin signaling pathway	20	7.81E-06	EGR1, TGFβ2, JUN, SMAD3, TGFβ3, NOS3, VEGFC, VEGFD, PRKCA, PIK3R2, COL1A1, COL3A1, PLCB4, COL1A2, CCND1, IL1B, PLCB1	3.309002	5.85E-05	3.73E-05
KEGG_PATHWAY	hsa04713:Circadian entrainment	17	8.54E-06	PDGFRB, PDGFRA, SHC2, DGKB, EGF, PDGFB, LPAR1, PDGFA, PRKCA, PIK3R2, EGFR, DNMT1, GRM1, GRM3, DNMT3, PLCB4, PDGFD, KIT, GNA12, PLCB1, PLPPP	3.769534	6.24E-05	3.97E-05
KEGG_PATHWAY	hsa04933:AGE-RAGE signaling pathway in diabetic complications	17	1.45E-05	PRKCG, LAMA5, TGFβ2, IL1R1, TGFβ3, LAMA1, PRKCA, PIK3R2, COL1A1, COL3A1, PLCB4, COL1A2, PRKACG, IL1B, GNA11, GNAQ, PLCB1	3.620245	1.03E-04	6.59E-05
KEGG_PATHWAY	hsa04072:Phospholipase D signaling pathway	21	1.66E-05	JAG2, NOTCH2, NOTCH3, JUN, MAML2, IL13, GATA3, FOS, DLL1, IL2, DLL3, DLL4, MAF, PPP3R2, STAT4, IL12RB2	3.031402	1.16E-04	7.37E-05
KEGG_PATHWAY	hsa05146:Amoebiasis	17	1.87E-05	JAG2, PTCRA, NOTCH2, NOTCH3, MAML2, NOTCH4, DLL1, DLL3, DLL4, LFNG, HEY1, HES1, HES5	3.549949	1.25E-04	7.97E-05
KEGG_PATHWAY	hsa04658:Th1 and Th2 cell differentiation	16	1.89E-05		3.740611	1.25E-04	7.97E-05
KEGG_PATHWAY	hsa04330:Notch signaling pathway	13	2.21E-05		4.50985	1.43E-04	9.13E-05

KEGG_PAT HWAY	hsa04961:Endocrine and other factor-regulated calcium reabsorption	12	2.44E-05	DNM3, PRKCG, PLCB4, PRKACG, GNAQ, CLTCL1, ATP1B4, PRKCA, KLK2, PLCB1, ESR1, DNM1	4.869853	1.55E-04	9.87E-05
KEGG_PAT HWAY	hsa04921:Oxytocin signaling pathway	21	2.72E-05	PRKCG, CAMK2B, CDKN1A, JUN, NOS3, SRC, CAMK2A, CACNA2D3, PRKCA, FOS, CACNA1F, PTGS2, EGFR, GNAI1, RYR3, PLCB4, PPP3R2, CCND1, PRKACG, GNAQ, PLCB1	2.932979	1.69E-04	1.08E-04
KEGG_PAT HWAY	hsa04750:Inflammatory mediator regulation of TRP channels	16	4.60E-05	PRKCG, CAMK2B, NTRK1, IL1R1, SRC, CAMK2A, PRKCA, PIK3R2, IL1RAP, IGF1, NGF, PLCB4, PRKACG, IL1B, GNAQ, PLCB1	3.476124	2.80E-04	1.78E-04
KEGG_PAT HWAY	hsa04720:Long-term potentiation	13	4.97E-05	PRKCG, CAMK2B, CAMK2A, PRKCA, GRIN2B, GRM1, GRIN2A, PLCB4, PPP3R2, PRKACG, RPS6KA2, GNAQ, PLCB1	4.173294	2.96E-04	1.89E-04
KEGG_PAT HWAY	hsa04512:ECM-receptor interaction	15	5.38E-05	LAMA5, SDC4, LAMA1, ITGB3, TNC, COL1A1, RELN, COL1A2, IBSP, ITGA8, COL6A3, ITGA7, ITGAV, COL9A3, CD36	3.625031	3.14E-04	2.00E-04
KEGG_PAT HWAY	hsa05010:Alzheimer disease	37	5.95E-05	WNT2B, CSF1, IRS1, LRP5, IRS4, WNT8B, IRS2, PIK3R2, FZD10, CACNA1F, PTGS2, RYR3, WNT6, GRIN2A, PPP3R2, WNT11, WNT3, WNT4, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, AXIN1, FZD8, WNT16, GRIN2B, DKK1, DKK2, DKK4, PLCB4, GNAQ, IL1B, DDIT3, PLCB1	2.035333	3.41E-04	2.17E-04
KEGG_PAT HWAY	hsa05213:Endometrial cancer	12	6.97E-05	TCF7L2, CDKN1A, CCND1, GADD45B, CDH1, EGF, ERBB2, CTNNA1, AXIN1, PIK3R2, FOXO3, EGFR	4.374613	3.92E-04	2.49E-04
KEGG_PAT HWAY	hsa04730:Long-term depression	12	8.19E-05	PRKCG, PLCB4, GNAQ, GNA11, GNA12, PRKG2, PRKCA, IGF1, PLCB1, GNAI1, GRM1, IGF1R	4.301703	4.51E-04	2.87E-04
KEGG_PAT HWAY	hsa05418:Fluid shear stress and atherosclerosis	19	8.57E-05	JUN, SDC4, IL1R1, NOS3, SRC, ITGB3, CAV1, PDGFB, PDGFA, PLAT, PIK3R2, FOS, ACVR2A, BMP4, IL1B, KDR, RAC3, ITGAV, BMPR1A	2.898311	4.64E-04	2.95E-04
KEGG_PAT HWAY	hsa05230:Central carbon metabolism in cancer	13	8.97E-05	PDGFRB, NTRK1, RET, PDGFRA, FLT3, NTRK3, PIK3R2, EGFR, KIT, ERBB2, FGFR3, FGFR2, FGFR1	3.938179	4.76E-04	3.03E-04
KEGG_PAT HWAY	hsa05022:Pathways of neurodegeneration - multiple diseases	42	1.15E-04	CAMK2B, HIP1, WNT2B, CSF1, CAMK2A, LRP5, WNT8B, FASLG, FZD10, CACNA1F, PTGS2, GRM1, RYR3, WNT6, GRIN2A, PPP3R2, WNT11, WNT3, WNT4, PRKCG, WNT10B, FZD3, FZD2, WNT5B, BDNF, FZD7, WNT7B, FZD6, SEPTIN5, AXIN1, FZD8, PRKCA, WNT16, GRIN2B, DKK1, DKK2, DKK4, PLCB4, GNAQ, IL1B, DDIT3, PLCB1	1.870306	6.00E-04	3.82E-04
KEGG_PAT HWAY	hsa05223:Non-small cell lung cancer	13	1.18E-04	ALK, PRKCG, RET, CDKN1A, GADD45B, EGF, HGF, PRKCA, PIK3R2, FOXO3, EGFR, CCND1, ERBB2	3.830284	6.07E-04	3.86E-04
KEGG_PAT HWAY	hsa05163:Human cytomegalovirus infection	25	1.23E-04	CDKN1A, SRC, ITGB3, FASLG, PIK3R2, PTGS2, GNAI1, EGFR, PPP3R2, CCND1, GNG4, PRKACG, GNA11, CREB3L1, GNA12, RAC3, ITGAV, PRKCG, PDGFRA, IL1R1, PRKCA, PLCB4, GNAQ, IL1B, PLCB1	2.379261	6.19E-04	3.94E-04
KEGG_PAT HWAY	hsa04911:Insulin secretion	14	1.50E-04	PRKCG, CAMK2B, CAMK2A, ATP1B4, PRKCA, CCK, CACNA1F, PLCB4, PCLO, PRKACG, GNA11, CREB3L1, GNAQ, PLCB1	3.501386	7.45E-04	4.74E-04
KEGG_PAT HWAY	hsa04919:Thyroid hormone signaling pathway	17	1.53E-04	PRKCG, NOTCH2, NOTCH3, SRC, ITGB3, NOTCH4, ATP1B4, PRKCA, PIK3R2, ESR1, BMP4, PLCB4, CCND1, PRKACG, ITGAV, PLCB1, WNT4	2.997088	7.45E-04	4.74E-04
KEGG_PAT HWAY	hsa05210:Colorectal cancer	14	1.70E-04	TCF7L2, CDKN1A, TGFB2, JUN, SMAD3, GADD45B, TGFB3, EGF, AXIN1, PIK3R2, FOS, EGFR, CCND1, RAC3	3.461114	8.12E-04	5.17E-04
KEGG_PAT HWAY	hsa04640:Hematopoietic cell lineage	15	1.76E-04	CSF1R, CSF3, CSF3R, CSF1, IL1R1, EPO, FLT3, ITGB3, FLT3LG, EPOR, IL3, IL1B, KIT, CD36, IL7R	3.258866	8.14E-04	5.18E-04
KEGG_PAT HWAY	hsa05231:Choline metabolism in cancer	15	1.76E-04	PDGFRB, PRKCG, PDGFRA, JUN, DGKB, EGF, PDGFB, PDGFA, PRKCA, PIK3R2, FOS, EGFR, PDGFD, RAC3, PLPP3	3.258866	8.14E-04	5.18E-04
KEGG_PAT HWAY	hsa05216:Thyroid cancer	9	2.36E-04	NTRK1, RET, TCF7L2, CDKN1A, CCND1, GADD45B, PAX8, CDH1, PPARG	5.231801	0.001075	6.85E-04
KEGG_PAT HWAY	hsa05221:Acute myeloid leukemia	12	2.62E-04	TCF7L2, CDKN1A, IL3, CSF1R, CCND1, FLT3, CEBPE, ZBTB16, KIT, RARA, PIK3R2, RUNX1T1	3.79562	0.001179	7.51E-04
KEGG_PAT HWAY	hsa05142:Chagas disease	15	2.69E-04	TGFB2, JUN, ACE, TGFB3, FASLG, PIK3R2, FOS, IL2, GNAI1, PLCB4, PPP2R2B, IL1B, GNA11, GNAQ, PLCB1	3.132308	0.001188	7.57E-04
KEGG_PAT HWAY	hsa05031:Amphetamine addiction	12	2.99E-04	CAMK2B, PRKCG, GRIN2A, JUN, PPP3R2, PRKACG, CREB3L1, CAMK2A, FOSB, PRKCA, FOS, GRIN2B	3.740611	0.001305	8.31E-04
KEGG_PAT HWAY	hsa04066:HIF-1 signaling pathway	15	4.86E-04	PRKCG, CAMK2B, CDKN1A, ANGPT1, EPO, NOS3, EGF, CAMK2A, PRKCA, PIK3R2, IGF1, EGFR, IGF1R, ERBB2, ALDOC	2.959887	0.002086	0.001329
KEGG_PAT HWAY	hsa04371:Apelin signaling pathway	17	7.39E-04	HDAC4, EGR1, NOTCH3, HDACS, SMAD3, NOS3, PLAT, GNAI1, RYR3, PLCB4, CCND1, GNG4, CDH1, PRKACG, GNAQ, PLCB1, PPARGCIA	2.611748	0.003122	0.001989
KEGG_PAT HWAY	hsa05321:Inflammatory bowel disease	11	7.48E-04	TGFB2, JUN, SMAD3, MAF, TGFB3, IL1B, IL13, STAT4, GATA3, IL2, IL12RB2	3.639903	0.003122	0.001989
KEGG_PAT HWAY	hsa04725:Cholinergic synapse	15	8.38E-04	PRKCG, CAMK2B, CAMK2A, PRKCA, PIK3R2, FOS, CACNA1F, GNAI1, PLCB4, GNG4, PRKACG, GNA11, CREB3L1, GNAQ, PLCB1	2.805459	0.003445	0.002194
KEGG_PAT HWAY	hsa04380:Osteoclast differentiation	17	8.64E-04	CSF1R, TGFB2, JUN, CSF1, IL1R1, ITGB3, FHL2, PIK3R2, MITF, FOS, TNFRSF11A, FOSL1, SOCS3, PPP3R2, IL1B, FOSB, PPARG	2.574963	0.003503	0.002231
KEGG_PAT HWAY	hsa04912:GnRH signaling pathway	13	0.001162	CAMK2B, EGR1, JUN, SRC, CAMK2A, PRKCA, CACNA1F, EGFR, PLCB4, PRKACG, GNA11, GNAQ, PLCB1	3.006567	0.004648	0.002961
KEGG_PAT HWAY	hsa05211:Renal cell carcinoma	11	0.00135	FLCN, CDKN1A, TGFB2, JUN, TGFB3, HGF, PDGFB, PAK6, PIK3R2, PAK3, PAK5	3.37991	0.005325	0.003392
KEGG_PAT HWAY	hsa05166:Human T-cell leukemia virus 1 infection	22	0.001558	EGR1, CDKN1A, TGFB2, CDKN2B, EGR2, JUN, CRTC3, SMAD3, MMP7, IL1R1, TGFB3, CRTC1, IL15, PIK3R2, FOS, ETS2, IL2, FOSL1, PPP3R2, CCND1, PRKACG, CREB3L1	2.121916	0.006068	0.003865
KEGG_PAT HWAY	hsa04370:VEGF signaling pathway	10	0.00164	PRKCG, SHC2, PPP3R2, SRC, NOS3, KDR, RAC3, PIK3R2, PRKCA, PTGS2	3.584753	0.006302	0.004014
KEGG_PAT HWAY	hsa05030:Cocaine addiction	9	0.001691	GRM3, GRIN2A, JUN, BDNF, PRKACG, CREB3L1, FOSB, GRIN2B, GNAI1	3.950544	0.006413	0.004085
KEGG_PAT HWAY	hsa04925:Aldosterone synthesis and secretion	13	0.00184	PRKCG, CAMK2B, CAMK2A, ATP1B4, PRKCA, CACNA1F, CACNA1G, PLCB4, PRKACG, GNA11, CREB3L1, GNAQ, PLCB1	2.85317	0.006887	0.004387
KEGG_PAT HWAY	hsa04915:Estrogen signaling pathway	16	0.001921	JUN, SHC2, NOS3, SRC, PIK3R2, FOS, ESR1, EGFR, GNAI1, GRM1, PLCB4, PRKACG, CREB3L1, GNAQ, RARA, PLCB1	2.4758	0.007099	0.004522
KEGG_PAT HWAY	hsa04918:Thyroid hormone synthesis	11	0.002295	PRKCG, TPO, PLCB4, PAX8, PRKACG, CREB3L1, GNAQ, ATP1B4, PRKCA, PLCB1, TSHR	3.154582	0.008378	0.005337
KEGG_PAT HWAY	hsa04724:Glutamatergic synapse	14	0.002501	PRKCG, SLC1A2, PRKCA, GRIN2B, GNAI1, GRM1, GRM3, GRIN2A, PLCB4, PPP3R2, GNG4, PRKACG, GNAQ, PLCB1	2.618428	0.008935	0.005691
KEGG_PAT HWAY	hsa05219:Bladder cancer	8	0.002509	CDKN1A, CCND1, CDH1, SRC, EGF, ERBB2, FGFR3, EGFR	4.196784	0.008935	0.005691
KEGG_PAT HWAY	hsa05212:Pancreatic cancer	11	0.002798	CDKN1A, TGFB2, SMAD3, CCND1, GADD45B, TGFB3, EGF, ERBB2, RAC3, PIK3R2, EGFR	3.072645	0.009844	0.00627
KEGG_PAT HWAY	hsa04728:Dopaminergic synapse	15	0.003154	PRKCG, CAMK2B, CAMK2A, PRKCA, FOS, GRIN2B, GNAI1, GRIN2A, PLCB4, GNG4, PPP2R2B, PRKACG, CREB3L1, GNAQ, PLCB1	2.44415	0.010965	0.006985
KEGG_PAT HWAY	hsa04917:Prolactin signaling pathway	10	0.00528	SOC2, SOC3, SHC2, CCND1, SRC, PIK3R2, FOS, TNFRSF11A, FOXO3, ESR1	3.029368	0.018137	0.011553

KEGG_PATHWAY	hsa04923:Regulation of lipolysis in adipocytes	9	0.005557	IRS1, PRKACG, IRS4, PRKG2, PIK3R2, IRS2, PTGS2, GNAI1, TSHR	3.28096	0.018867	0.012018
KEGG_PATHWAY	hsa05143:African trypanosomiasis	7	0.00657	PRKCG, PLCB4, IL1B, GNAQ, FASLG, PRKCA, PLCB1	4.069179	0.02205	0.014046
KEGG_PATHWAY	hsa04971:Gastric acid secretion	10	0.008247	CAMK2B, PRKCG, PLCB4, PRKACG, GNAQ, CAMK2A, ATP1B4, PRKCA, PLCB1, GNAI1	2.830068	0.027365	0.017431
KEGG_PATHWAY	hsa04211:Longevity regulating pathway	11	0.008569	IRS1, PRKACG, CREB3L1, IRS4, PIK3R2, IRS2, PPARG, IGF1, FOXO3, PPARGC1A, IGF1R	2.628819	0.027923	0.017787
KEGG_PATHWAY	hsa05161:Hepatitis B	16	0.008606	PRKCG, CDKN1A, TGFβ2, EGR2, JUN, EGR3, SMAD3, TGFβ3, SRC, FASLG, PRKCA, PIK3R2, FOS, TIRAP, CREB3L1, STAT4	2.111265	0.027923	0.017787
KEGG_PATHWAY	hsa04024:cAMP signaling pathway	20	0.008729	CAMK2B, JUN, BDNF, PTCH1, CAMK2A, ATP1B4, PIK3R2, FOS, CACNA1F, GLI1, GRIN2B, GLI3, GNAI1, TSHR, TIAM1, GRIN2A, PRKACG, CREB3L1, RAC3, AMH	1.903408	0.028011	0.017842
KEGG_PATHWAY	hsa05220:Chronic myeloid leukemia	10	0.008968	BCR, CDKN1A, TGFβ2, SHC2, SMAD3, CCND1, GADD45B, MECOM, TGFβ3, PIK3R2	2.793314	0.028232	0.017983
KEGG_PATHWAY	hsa04668:TNF signaling pathway	13	0.008992	JUN, CEBPB, CSF1, IL15, DAB2IP, VEGFC, VEGFD, PIK3R2, FOS, PTGS2, SOCS3, IL1B, CREB3L1	2.34967	0.028232	0.017983
KEGG_PATHWAY	hsa05100:Bacterial invasion of epithelial cells	10	0.009736	DNM3, SHC2, CDH1, SRC, CAV1, CLTCL1, CTNNA1, PIK3R2, DOCK1, DNM1	2.757502	0.030244	0.019265
KEGG_PATHWAY	hsa04929:GnRH secretion	9	0.009944	PRKCG, PLCB4, GNAQ, GNAI1, PIK3R2, PRKCA, PLCB1, CACNA1F, CACNA1G	2.978102	0.030247	0.019267
KEGG_PATHWAY	hsa04927:Cortisol synthesis and secretion	9	0.009944	PLCB4, PRKACG, CREB3L1, GNAQ, GNAI1, PLCB1, CACNA1F, PBX1, CACNA1G	2.978102	0.030247	0.019267
KEGG_PATHWAY	hsa04022:cGMP-PKG signaling pathway	16	0.010104	NOS3, IRS1, IRS4, ATP1B4, IRS2, CACNA1F, GNAI1, PLCB4, EDNRB, PPP3R2, GNAI1, CREB3L1, GNAQ, GNAI2, PRKG2, PLCB1	2.07311	0.030415	0.019374
KEGG_PATHWAY	hsa04152:AMPK signaling pathway	13	0.010867	IRS1, IRS4, PIK3R2, IRS2, IGF1, FOXO3, IGF1R, CCND1, PPP2R2B, CREB3L1, PPARG, CD36, PPARGC1A	2.291891	0.032053	0.020417
KEGG_PATHWAY	hsa04071:Sphingolipid signaling pathway	13	0.010867	PRKCG, NOS3, PRKCA, PIK3R2, GNAI1, ACER1, PLCB4, PPP2R2B, GNAQ, GNAI2, RAC3, S1PR2, PLCB1	2.291891	0.032053	0.020417
KEGG_PATHWAY	hsa05417:Lipid and atherosclerosis	19	0.011476	CAMK2B, JUN, NOS3, SRC, CAMK2A, FASLG, PRKCA, PIK3R2, HSPA2, FOS, TIRAP, PLCB4, PPP3R2, IL1B, DDIT3, OLR1, PPARG, CD36, PLCB1	1.891953	0.033263	0.021188
KEGG_PATHWAY	hsa05323:Rheumatoid arthritis	11	0.011505	TGFβ2, JUN, CSF1, ANGPT1, IL15, TGFβ3, IL1B, CD28, CTLA4, FOS, TNFRSF11A	2.516954	0.033263	0.021188
KEGG_PATHWAY	hsa04611:Platelet activation	13	0.013032	NOS3, SRC, ITGB3, PIK3R2, GNAI1, COL1A1, COL3A1, PLCB4, COL1A2, PRKACG, GNAQ, PRKG2, PLCB1	2.236886	0.037306	0.023764
KEGG_PATHWAY	hsa04148:Efferocytosis	15	0.013443	CAMK2B, CEBPB, ATP8A2, EPO, ITGB3, CAMK2A, DNMT3A, PTGS2, EPOR, PBX1, AXL, ITGAV, PPARG, CD36, DOCK1	2.068127	0.03811	0.024276
KEGG_PATHWAY	hsa04924:Renin secretion	9	0.014041	PLCB4, ACE, PPP3R2, PRKACG, GNAQ, PRKG2, PLCB1, CACNA1F, GNAI1	2.805459	0.039424	0.025112
KEGG_PATHWAY	hsa05410:Hypertrophic cardiomyopathy	11	0.016178	TGFβ2, ACE, TGFβ3, LAMA1, ITGB3, ITGA8, CACNA2D3, ITGA7, ITGAV, IGF1, CACNA1F	2.389835	0.04499	0.028658
KEGG_PATHWAY	hsa04930:Type II diabetes mellitus	7	0.020603	SOC3, SOCS3, IRS1, IRS4, PIK3R2, IRS2, CACNA1G	3.203396	0.056756	0.036153
KEGG_PATHWAY	hsa04820:Cytoskeleton in muscle cells	19	0.022295	FBN2, SDC4, LAMA1, ITGB3, COL11A1, ELN, FHL2, ATP1B4, DCN, COL1A1, COL3A1, COL1A2, ITGA8, COL6A3, ITGA7, ITGAV, COL9A3, MYH11, FLNC	1.761473	0.060842	0.038755
KEGG_PATHWAY	hsa05414:Dilated cardiomyopathy	11	0.023489	TGFβ2, TGFβ3, LAMA1, PRKACG, ITGB3, ITGA8, CACNA2D3, ITGA7, ITGAV, IGF1, CACNA1F	2.253273	0.063508	0.040453
KEGG_PATHWAY	hsa04213:Longevity regulating pathway - multiple species	8	0.023949	IRS1, PRKACG, IRS4, PIK3R2, IRS2, IGF1, FOXO3, IGF1R	2.775292	0.064157	0.040867
KEGG_PATHWAY	hsa04660:T cell receptor signaling pathway	12	0.025901	ITK, JUN, PPP3R2, PPP2R2B, CD28, CTLA4, PAK6, PIK3R2, FOS, PAK3, IL2, PAK5	2.115592	0.068756	0.043797
KEGG_PATHWAY	hsa04520:Adherens junction	10	0.028084	TCF7L2, SMAD3, CDH1, SRC, ERBB2, CTNNA1, RAC3, EGFR, FGFR1, IGF1R	2.312744	0.073879	0.04706
KEGG_PATHWAY	hsa05415:Diabetic cardiomyopathy	17	0.028688	PRKCG, CAMK2B, TGFβ2, ACE, SMAD3, TGFβ3, NOS3, IRS1, CAMK2A, PRKCA, PIK3R2, COL1A1, COL3A1, PLCB4, COL1A2, CD36, PLCB1	1.783633	0.074793	0.047642
KEGG_PATHWAY	hsa04960:Aldosterone-regulated sodium reabsorption	6	0.029809	PRKCG, IRS1, ATP1B4, PIK3R2, PRKCA, IGF1	3.396081	0.07703	0.049067
PIR_SUPERFAMILY	PIRSF000615:TyrPK_CSF1-R	14	1.14E-11	PDGFRB, NTRK1, PDGFRA, NTRK2, CSF1R, FLT3, FLT4, NTRK3, AXL, PTK7, KIT, KDR, FGFR3, FGFR2	11.43579	7.65E-10	7.19E-10
PIR_SUPERFAMILY	PIRSF000666:TyrPK_ephrin_receptor	6	3.40E-04	EPHB6, EPHA5, EPHA7, EPHA10, EPHA3, EPHA2	8.75188	0.004754	0.00447
PIR_SUPERFAMILY	PIRSF001789:NGF	4	4.26E-04	NTF4, BDNF, NTF3, NGF	20.42105	0.004754	0.00447
PIR_SUPERFAMILY	PIRSF000619:TyrPK_EGFR	4	4.26E-04	ERBB3, ERBB4, ERBB2, EGFR	20.42105	0.004754	0.00447
PIR_SUPERFAMILY	PIRSF005879:CCAAT/enhancer-binding	4	4.26E-04	CEBPA, CEBPB, CEBPD, CEBPE	20.42105	0.004754	0.00447
PIR_SUPERFAMILY	PIRSF000628:FGFR	4	4.26E-04	FGFR4, FGFR3, FGFR2, FGFR1	20.42105	0.004754	0.00447
UP_KW_BIOLOGICAL_PROCESS	KW-0805~Transcription regulation	151	3.02E-16	ZNF331, CRT3, MAML2, CRT1, CTNND2, NAB2, DACH2, HOXA13, ETS2, HOXA11, SOX2, HOXA9, DACH1, CCND1, CREB3L1, HOXA3, ZNF687, ZNF444, MNX1, SSX1, LMO1, MRTFB, ATP1B4, SOX11, MITF, HNF1A, SOX10, RUNX2, AR, MYCN, MAF, KAT6B, DDIT3, ERG, FLYWCH1, BCORL1, ZFPM2, ATF3, NOTCH2, NOTCH3, NOTCH4, GATA6, GATA3, BHLHE22, FOXO4, FOXO3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, PPARGC1A, TFAP2A, WWTR1, EGR1, JUN, EGR2, EGR3, SMAD3, BCL11B, EGR4, AUTS2, BTBD18, ZBTB16, HMG2A, SMARCA1, SMAD6, ESR1, PBX1, PHOX2B, NR4A3, MAFB, LHX2, FEV, ID1, ID4, LHX4, HOXD9, FGFR1, TENM1, HIP1, PHF1, CHD6, FHL2, FASLG, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, PPP1R13L, TRPS1, JARID2, ZNF521, TEAD1, MYBL1, TEAD3, BRD3, TEAD4, TET1, PAX3, ETV1, FOXL2, OLIG1, OLIG2, ETV4, POU5F1, MN1, PAX8, TAL2, PAX7, TAL1, RARA, AHRH, PPARG, ZMYND11, VGLL3, HDAC4, YAP1, CEBPA, HDACS, KANK1, CEBPB, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, FSTL3, ERBB4, ERBB2, STAT4, HES1, HES5, RUNX1T1, TCF7L2, CDX2, EYA1, DMRT1, CDX1, EYA2, KLF4, TBX15, PER1, NR6A1, WT1, NFIB, ERCC6	1.855487	2.84E-14	2.66E-14
UP_KW_BIOLOGICAL_PROCESS	KW-0804~Transcription	151	4.08E-15	ZNF331, CRT3, MAML2, CRT1, CTNND2, NAB2, DACH2, HOXA13, ETS2, HOXA11, SOX2, HOXA9, DACH1, CCND1, CREB3L1, HOXA3, ZNF687, ZNF444, MNX1, SSX1, LMO1, MRTFB, ATP1B4, SOX11, MITF, HNF1A, SOX10, RUNX2, AR, MYCN, MAF, KAT6B, DDIT3, ERG, FLYWCH1, BCORL1, ZFPM2, ATF3,	1.803925	1.92E-13	1.80E-13

UP_KW_BI OLOGICAL_ PROCESS	KW-0879~Wnt signaling pathway	33	1.03E-13	NOTCH2, NOTCH3, NOTCH4, GATA6, GATA3, BHLHE22, FOXO4, FOXO3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, PPARGC1A, TFAP2A, WWTR1, EGR1, JUN, EGR2, EGR3, SMAD3, BCL11B, EGR4, AUTS2, BTBD18, ZBTB16, HMGA2, SMARCA1, SMAD6, ESR1, PBX1, PHOX2B, NR4A3, MAFB, LHX2, FEV, ID1, ID4, LHX4, HOXD9, FGFR1, TENM1, HIP1, PHF1, CHD6, FHL2, FASLG, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, PPP1R13L, TRPS1, JARID2, ZNF521, TEAD1, MYBL1, TEAD3, BRD3, TEAD4, TET1, PAX3, ETV1, FOXL2, OLIG1, OLIG2, ETV4, POU5F1, MN1, PAX8, TAL2, PAX7, TAL1, RARA, AHRR, PPARG, ZMYND11, VGLL3, HDAC4, YAP1, CEBPA, HDAC5, KANK1, CEBPB, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, FSTL3, ERBB4, ERBB2, STAT4, HES1, HES5, RUNX1T1, TCF7L2, CDX2, EYA1, DMRT1, CDX1, EYA2, KLF4, TBX15, PER1, NR6A1, WT1, NFIB, ERCC6, AMER1, WNT2B, CTNND2, LRP5, WNT8B, FZD10, CXXC4, WNT6, WNT11, ADGRA2, WIF1, WNT3, WNT4, TCF7L2, RNF43, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, AXIN1, FZD8, WNT16, DKK1, DKK2, DKK4, SFRP4, BCL9, SFRP2, PTK7, DDIT3	4.943869	3.24E-12	3.03E-12
				ROBO2, HIP1, GLI1, FGF1, FGF2, FGF3, FGF4, ROBO1, FGF6, FGF8, MECOM, FGF9, ZIC2, CHL1, KDR, JARID2, AMH, ZNF521, MYBL1, MRTFB, SOX11, FOXL2, DLEC1, MLF1, RUNX2, SFRP4, SFRP2, PAX8, BIN1, TAL1, ITGA8, ZFPM2, EPHA2, GAS7, CAMK2B, NOTCH2, NOTCH3, CEBPB, NOTCH4, FOXO4, DLL1, DLL3, DLL4, PRDM16, FGF23, HES5, NTRK1, NTRK2, NGFR, GADD45B, ANGPT1, DMRT1, SORT1, BTBD18, NTRK3, VEGFC, VEGFD, HSPA2, PBX1, BMP4, AH1, AXL, FEV, TLL2			
				JAG2, NOTCH2, DLL4, NOTCH3, HEY1, MAML2, NOTCH4, NEURL1, CNTN1, DLL1, DLL3			
				ROBO2, CAMK2B, BRSK1, BHLHE22, ROBO1, DLL4, ZIC2, CHL1, CHN1, HES5, NTRK1, EPHA5, NGFR, NTRK2, FZD3, EPHA7, NTRK3, PAX3, SOX11, FEV, NEDD4, ITGA8, ERCC6, FGF13, GAS7			
				RET, LAMA5, CSF3R, SRC, LAMA1, CTNND2, ITGB3, TNC, LPP, RELN, IBSP, CHL1, CDH1, CTNNA1, ABL2, OLR1, NCAM1, ITGAV, CD36, EDIL3, DST, OMD, PRKCA, PTK7, KIT, CDH11, ITGA8, CNTN1, COL6A3, ITGA7, ACKR3, EPHA3, EPHA2			
UP_KW_BI OLOGICAL_ PROCESS	KW-0221~Differentiation	64	4.50E-10	ANGPT1, FLT4, DAB2IP, VEGFC, VEGFD, PRKCA, FGF1, FGF2, DLL4, FGF6, ADGRA2, KDR, EPHA2	2.303939	1.06E-08	9.90E-09
				EPHB6, FCGBP, CSF3, TNFRSF6B, CSF3R, CSF1, EPO, TNC, PRF1, PLAT, IL1RAP, FGF1, FGF2, FGF3, FGF4, FGF6, FGF8, IBSP, FGF9, PLAU, CCN6, KDR, PRSS8, WNT5B, IL1R1, SERPINF1, OMD, IGF8P2, CTRB1, FLT3LG, LIFR, DKK1, DKK2, DKK4, SFRP4, SFRP2, LOX, PAPP, EPHA3, FBN2, SDC4, EPHA10, HTRA1, PDGFB, PDGFA, PLA2G5, LTBP1, KLK7, WNT6, PDGFD, APOD, FGF23, WNT3, WNT4, WNT10B, TGF82, ACE, BDNF, TGF83, PRG2, INHBA, IGF1, GDF6, IL2, BMP4, COL1A1, EXT2, IL3, COL1A2, FGF19, COL9A3, FGFR4, IL7R, FGFR3, FGFR2, NODAL, FGF10, PTPRR, WNT2B, FLT4, ELN, FASLG, GHR, CHL1, OLR1, AMH, EDIL3, MMP7, IL15, IL13, WNT16, NGF, DCN, TGFBR3, IL1B, COL6A3, LAMA5, LAMA1, COL11A1, WNT8B, TMPPRS2, EGFR, FSTL3, NTF4, MUC1, RELN, WNT11, ERBB3, WIF1, NTF3, NCAM1, LEFTY2, GSN, ANGPT1, WNT7B, PLA2G2A, VEGFC, CCK, VEGFD, SULF1, EPOR, COL3A1, TAFAS, TLL2, CRLF2, FBN2, LAMA5, WNT2B, LAMA1, COL11A1, ELN, TNC, WNT8B, LTBP1, WNT6, RELN, WNT11, CHL1, WNT3, WNT4, WNT10B, TGF82, MMP7, WNT5B, TGF83, WNT7B, OMD, WNT16, DCN, TGFBR3, BMP4, COL1A1, COL3A1, COL1A2, COL6A3, COL9A3			
				MAML2, SOX2, HOXA9, CLP1, RPS6KA2, CREB3L1, HOXA3, KDR, MNX1, MRTFB, SOX11, PRKCA, HNF1A, PIMREG, SOX10, RUNX2, AR, BIN1, DDIT3, FLYWCH1, BCORL1, ZFPM2, ATF3, MAGED1, GATA6, GATA3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, NKX2-5, PPARGC1A, WWTR1, EGR1, JUN, EGR2, EGR3, CRADD, MAGEE1, BCL11B, EGR4, BTBD18, RANBP17, SMARCA1, PBX1, MLLT11, FOSL1, ID1, ID4, HOXD9, CDKN1C, ITK, TENM1, CDKN1A, HIP1, PHF1, HOXC13, GLI1, HOXC11, GLI3, MECOM, HEY1, JARID2, TEAD1, TEAD3, BRD3, TEAD4, BRD1, IL15, TET1, PAX3, FOS, MLF1, POU5F1, MN1, PAX8, TAL1, PAX7, RARA, AHRR, PPARG, PLCB1, VGLL3, AMER1, YAP1, KANK1, HOXD13, AKAP6, PRICKLE1, PTGS2, HOXD11, GNAI1, EGFR, FSTL3, SLX4, STAT4, CTNNA1, PAK6, PAK5, RUNX1T1, NPM2, CDX2, DMRT1, CDX1, SORT1, MGMT, PER1, NR6A1, NFIB, WT1, NEDD4, FOSB, TACC2, ZNF331, PRDM7, CRTC3, CRTC1, CTNND2, NAB2, FGF1, DACH2, HOXA13, FGF2, ETS2, CDC14A, HOXA11, CDC14B, DACH1, CCND1, ZNF687, ZNF444, LMO1, RNF43, CDKL5, APLP2, LMO2, ATP1B4, MITF, MYCL, MYCN, MAF, KAT6B, WDFY3, ERG, NOTCH2, NOTCH3, BRSK1, NOTCH4, AK5, BHLHE22, FOXO4, FOXO3, NDRG1, LPP, NCKIPSD, CCNB3, SPECC1, TFAP2A, SMAD3, AUTS2, ZBTB16, HMGA2, FANCC, FANCE, SMAD6, ESR1, PHOX2B, FANCF, BCL9, MAFB, FGF14, NR4A3, TLX3, CPS1, LHX2, TLX1, GNAQ, FEV, LHX4, FGF13, FGFR1, PPP1R13B, FLT4, CHD6, FHL2, FASLG, FLCN, ZIC2, PPP1R13L, TRPS1, MYO18A, ZNF521, MYBL1, SH3D19, PEG3, DST, DNMT3A, AXIN1, ETV1, FOXL2, OLIG1, OLIG2, DUSP26, ETV4, ETV5, DMRTA2, NAV3, SETBP1, ZMYND11, CLK1, HDAC4, CEBPA, HDAC5, CEBPB, NUTM1, HLF, CEBPD, CEBPE, SRC, PLAG1, DDX20, PPM1D, DNAJB1, MUC1, ERBB4, ERBB2, HES1, LRIG3, HES5, TCF7L2, EYA1, PRRX1, EYA2, PRRX2, KLF4, TBX15, TAF42, ERCC4, ERCC6			
				ATP8A2, CSF3R, CSF1, DGKB, MPL, IRS4, PRF1, FZD10, IL1RAP, IGF1R, EDNRB, ADGRA2, CDH1, KDR, PRSS8, ROS1, RGS7, PDGFRB, ARDC4, PRKCG, EPHA5, PDGFRA, SLC34A2, RNF43, EPHA7, USP6, IL1R1, APLP2, FLT3LG, LIFR, PRKCA, GABRG2, TIAM1, SMO, BIN1, SCN8A, PLPP3, EPHA3, EPHA2, NOTCH2, CSF1R, NOTCH3, EPHA10, MAGED1, NOTCH4, HTRA1, SLC1A2, LPAR1, TNFRSF11A, PLA2G5, NDRG1, LPP, CACNA1G, GRIN2A, INPP5A, SLC01B3, SNX9, PROM1, WWTR1, NGFR, FZD3, ACE, FZD2, MAGEE1, CAV1, PTCH1, FZD7, FZD6, FZD8, ESR1, GRIN2B, CPS1, GNAQ, CNTN1, FGF13, FGFR4, IL7R, XKR3, FGFR3, FGFR2, BMPR1A, FGFR1, RET, DIRAS3, ALK, TENM1, PTPRR, FLT4, RASGRF2, ITGB3, FASLG, PTPRK, GPHN, GRM1, ROBO1, GRM3, GHR, CHL1, PSD3, OLR1, CTLA4, PRKG2, RAC3, ITGAV, CD36, ABCC3, PRMT8, KSR1, DST, GRID1, AXIN1, RHOD, TIRAP, DNMI1, TGFBR3, PLCB4, KIT, CDH11, ITGA8, GAS1, ACSBG1, DDR2, AMER1, KANK1, CANT1, SRC, TMPPRS2, NOD1, ACVR1B, DLL1, EGFR, GNAI1, DLL4, P2RY8, MUC1, ERBB3, ERBB4, GNG4, GNA11, ERBB2, GNA12, GPC3, CTNNA1, HAS2, NCAM1, LRIG3, S1PR2, CKB, NTRK1,			
UP_KW_BI OLOGICAL_ PROCESS	KW-0914~Notch signaling pathway	11	8.80E-06		6.156516	1.65E-04	1.55E-04
UP_KW_BI OLOGICAL_ PROCESS	KW-0524~Neurogenesis	25	4.66E-05		2.548386	7.30E-04	6.83E-04
UP_KW_BI OLOGICAL_ PROCESS	KW-0130~Cell adhesion	33	2.67E-04		1.989606	0.003587	0.003358
UP_KW_BI OLOGICAL_ PROCESS	KW-0037~Angiogenesis	13	0.003001		2.715646	0.035262	0.033011
UP_KW_CE LLULAR_C OMPONEN T	KW-0964~Secreted	125	1.92E-11		1.820857	6.90E-10	6.52E-10
UP_KW_CE LLULAR_C OMPONEN T	KW-0272~Extracellular matrix	31	4.58E-09		3.528417	8.25E-08	7.79E-08
UP_KW_CE LLULAR_C OMPONEN T	KW-0539~Nucleus	240	5.75E-07		1.301021	6.90E-06	6.52E-06
UP_KW_CE LLULAR_C OMPONEN T	KW-1003~Cell membrane	167	7.32E-05		1.309758	6.59E-04	6.23E-04

UP_KW_DI SEASE	KW-0656~Proto- oncogene	70	2.54E-30	NTRK2, SORT1, KCNB1, NOS3, SPRY4, PLA2G2A, DAB2IP, SORBS2, EPOR, TSHR, ACVR2A, AXL, NEDD4, NEUR1, SPRY2, ACKR3, LGR5, CRLF2 RET, ALK, FLT3, GLI1, ETS2, FGF3, FGF4, FGF6, HOXA9, MECOM, CCND1, ZNF521, ROS1, SSI1, LMO1, PDGFRB, PDGFRA, USP6, LMO2, PAX3, ETV1, PRKCA, FOS, OLIG2, BCR, MDS2, MYCN, MAF, TAL2, PAX7, TAL1, ZFYVE19, DDIT3, KIT, RARA, ERG, TCTA, GAS7, YAP1, CSF1R, HLF, SRC, PLAG1, PDGFB, FOXO4, FOXO3, EGFR, FSTL3, NCKIPSD, PDGFD, MYH11, WNT3, RUNX1T1, NTRK1, SPEC1, VVVTR1, JUN, ZBTB16, STYK1, HMGA2, PBX1, IL2, MLLT11, BCL9, NR4A3, MAFB, AXL, TLX1, LHX4, FGF2 EPHB6, TNFRSF6B, PRF1, FZD10, EDNRB, ADGRA2, CCN6, KDR, PRSS8, EPHA5, EPHA7, IL1R1, SERPINF1, OMD, CTRB1, CACNA2D3, FLT3LG, SOX11, DKK1, GABRG2, LRRC37B, DKK2, DKK4, SFRP4, SFRP2, PAPP, ASTN2, EPHA3, EPHA2, SDC4, EPHA10, PDGFB, PDGFA, PLA2G5, KLK2, KLK7, GRIN2A, PDGFD, APOD, PROM1, JAG2, NGFR, WNT10B, FZD3, ACE, FZD2, FZD7, FZD6, PRG2, FZD8, IGF1, GDF6, GRIN2B, COL1A1, COL1A2, PTK7, CD28, COL9A3, NODAL, RET, ROBO2, PTPRR, ELN, PTPRK, ROBO1, CHL1, CTAA4, IL15, IL13, TMT1B, KIT, GAS1, DDR2, COL11A1, WNT8B, PTGS2, EGFR, FSTL3, NTF4, RELN, WIF1, CHN1, NTF3, GPC3, CTNNA1, AGR3, LEFTY2, IL12RB2, GSN, SORT1, ATRNL1, WNT7B, DAB2IP, VEGFC, VEGFD, SULF1, COL3A1, AXL, WT1, LHFPL6, LGR5, CRLF2, FCGBP, CSF3, CSF3R, CSF1, EPO, TUSC3, MPL, TNC, PLAT, IL1RAP, FGF3, FGF4, IGF1R, FGF6, FGF8, IBSF, PLAU, CDH1, IL13RA2, ROS1, PDGFRB, PDGFRA, RNF43, WNT5B, HGF, APLP2, IGFBP2, LIFR, LOX, SMO, FBN2, NOTCH2, NOTCH3, CSF1R, NOTCH4, HTRA1, TNFRSF11A, CYP2C19, NDRG1, LTBP1, FUT1, WNT6, TPO, FGF23, WNT3, WNT4, TGFβ2, BDNF, TGFβ3, INHBA, LRP1B, IL2, TNFRSF10D, BMP4, IL3, FGF19, CNTN1, FGFR4, IL7R, FGFR3, FGFR2, BMPRI1A, FGF10, FGFR1, ALK, WNT2B, FLT3, ITGB3, FLT4, GRM1, GHR, GRM3, HEPH, ITGAV, AMH, EDIL3, PTCRA, MMP7, GRID1, WNT16, NGF, DCN, TGFβR3, CDH11, ITGA8, ITGA7, COL6A3, LAMA5, LAMA1, CAMK2A, LRP5, ACVR1B, DLL1, DLL3, DLL4, MUC1, WNT11, ACVR1C, ERBB3, ERBB4, ERBB2, NCAM1, LRIG3, NTRK1, LINGO2, NTRK2, ANGPT1, EGF, NTRK3, PLA2G2A, CCK, EPOR, TSHR, ACVR2A, TAF5, TAF2, TLL2 HOXD13, HOXC13, HOXD11, HOXA13, HOXC11, HOXA11, HOXA9, HOXA3, NKX2-1, NKX2-5, MNX1, PRRX1, CDX2, CDX1, PRRX2, PAX3, HNF1A, POU5F1, PBX1, PHOX2B, TLX3, LHX2, PAX7, TLX1, LHX4, HOXD9 FBN2, NOTCH2, TENM1, NOTCH3, ITGB3, NOTCH4, LRP5, TNC, PRF1, PLAT, PTGS2, LTBP1, DLL1, DLL3, DLL4, TPO, RELN, PLAU, WIF1, EDIL3, JAG2, EGF, ATRNL1, LRP1B, TLL2, ASTN2 EPHB6, TNFRSF6B, CBL, ADGRA2, RPS6KA2, KDR, ARRC4, PRKCG, EPHA5, EPHA7, IL1R1, OMD, MRTFB, PRKCA, PIMREG, EML1, LRRC37B, TIAM1, PAPP, HECW1, FLYWCH1, BCORL1, ASTN2, ZFPM2, EPHA3, EPHA2, EPHA10, MAGED1, GATA6, PIK3R2, GATA3, GATA2, GATA1, KALRN, PPP3R2, MAP2, PRDM16, JAG2, NGFR, EGR1, EGR2, ACE, EGR3, MAGEE1, BCL11B, EGR4, SMARCA1, COL1A1, PPFIBP1, COL1A2, PTK7, COL9A3, CDKN1C, ROBO2, TENM1, PHF1, ELN, PTPRK, GLI1, RYR3, GLI3, ROBO1, AKAP12, PCLO, MECOM, CHL1, BRD3, PRMT8, BRD1, SYP, LRRC7, KIT, DPYD, YAP1, KANK1, COL11A1, AKAP6, PRICKLE1, EGFR, FSTL3, RELN, SLX4, WIF1, FLNC, IL12RB2, CDKN2B, GSN, SORT1, ATRNL1, VEGFC, VEGFD, SORBS2, PER1, COL3A1, AXL, WT1, NEDD4, LGR5, ZNF331, FCGBP, CSF3R, DGKB, IRS1, CTNND2, MPL, IRS4, TNC, PLAT, IL1RAP, IGF1R, CDH1, IL13RA2, ZNF687, ZNF444, ROS1, PPFIA2, PDGFRB, LMO1, PDGFRA, HGF, LMO2, LIFR, KAT6B, SCN8A, WDFY3, FBN2, NOTCH2, NOTCH3, CSF1R, NOTCH4, TNFRSF11A, CACNA1F, NDRG1, LPP, LTBP1, CACNA1G, CLTCL1, ZBTB16, HMGA2, LRP1B, TNFRSF10D, AH1, CPS1, LHX2, CNTN1, LHX4, FGFR4, FGFR3, FGFR2, FGFR1, ALK, PPP1R13B, ITGB3, FLT4, RASGRF2, CHD6, FHL2, HEPH, ZIC2, PPP1R13L, TRPS1, ITGAV, ZNF521, EDIL3, MYBL1, SH3D19, ABCC3, PEG3, DST, DCN, SETBP1, ASPH, CDH11, ITGA8, ITGA7, COL6A3, LAMA5, LAMA1, PLAG1, LRP5, NOD1, DLL1, DLL3, DLL4, ABLIM1, MUC1, ERBB4, SNCG, NCAM1, LRIG3, NTRK1, LINGO2, NTRK2, EGF, NTRK3, KLF4, TSHR, BICC1, ERCC4, PPP2R2B, NEUR1, TLL2 ITK, PPP1R13B, DST, SRC, MATK, PIK3R2, SORBS2, MAPK8IP2, KALRN, NCKIPSD, AH1, BAIAP2L1, PPP1R13L, BIN1, ABL2, SNX9, SRGAP3, DOCK1, SH3GL2, GAS7, SH3D19 SOC52, ITK, SOC53, SHC2, SRC, CHN1, MATK, STAT4, GRB10, ABL2, PIK3R2, SH2D5	4.735482	2.00E-28	1.93E-28
UP_KW_D OMAIN	KW-0732~Signal	219	9.33E-16	EPHB6, TNFRSF6B, CBL, ADGRA2, RPS6KA2, KDR, ARRC4, PRKCG, EPHA5, EPHA7, IL1R1, OMD, MRTFB, PRKCA, PIMREG, EML1, LRRC37B, TIAM1, PAPP, HECW1, FLYWCH1, BCORL1, ASTN2, ZFPM2, EPHA3, EPHA2, EPHA10, MAGED1, GATA6, PIK3R2, GATA3, GATA2, GATA1, KALRN, PPP3R2, MAP2, PRDM16, JAG2, NGFR, EGR1, EGR2, ACE, EGR3, MAGEE1, BCL11B, EGR4, SMARCA1, COL1A1, PPFIBP1, COL1A2, PTK7, COL9A3, CDKN1C, ROBO2, TENM1, PHF1, ELN, PTPRK, GLI1, RYR3, GLI3, ROBO1, AKAP12, PCLO, MECOM, CHL1, BRD3, PRMT8, BRD1, SYP, LRRC7, KIT, DPYD, YAP1, KANK1, COL11A1, AKAP6, PRICKLE1, EGFR, FSTL3, RELN, SLX4, WIF1, FLNC, IL12RB2, CDKN2B, GSN, SORT1, ATRNL1, VEGFC, VEGFD, SORBS2, PER1, COL3A1, AXL, WT1, NEDD4, LGR5, ZNF331, FCGBP, CSF3R, DGKB, IRS1, CTNND2, MPL, IRS4, TNC, PLAT, IL1RAP, IGF1R, CDH1, IL13RA2, ZNF687, ZNF444, ROS1, PPFIA2, PDGFRB, LMO1, PDGFRA, HGF, LMO2, LIFR, KAT6B, SCN8A, WDFY3, FBN2, NOTCH2, NOTCH3, CSF1R, NOTCH4, TNFRSF11A, CACNA1F, NDRG1, LPP, LTBP1, CACNA1G, CLTCL1, ZBTB16, HMGA2, LRP1B, TNFRSF10D, AH1, CPS1, LHX2, CNTN1, LHX4, FGFR4, FGFR3, FGFR2, FGFR1, ALK, PPP1R13B, ITGB3, FLT4, RASGRF2, CHD6, FHL2, HEPH, ZIC2, PPP1R13L, TRPS1, ITGAV, ZNF521, EDIL3, MYBL1, SH3D19, ABCC3, PEG3, DST, DCN, SETBP1, ASPH, CDH11, ITGA8, ITGA7, COL6A3, LAMA5, LAMA1, PLAG1, LRP5, NOD1, DLL1, DLL3, DLL4, ABLIM1, MUC1, ERBB4, SNCG, NCAM1, LRIG3, NTRK1, LINGO2, NTRK2, EGF, NTRK3, KLF4, TSHR, BICC1, ERCC4, PPP2R2B, NEUR1, TLL2 ITK, PPP1R13B, DST, SRC, MATK, PIK3R2, SORBS2, MAPK8IP2, KALRN, NCKIPSD, AH1, BAIAP2L1, PPP1R13L, BIN1, ABL2, SNX9, SRGAP3, DOCK1, SH3GL2, GAS7, SH3D19 SOC52, ITK, SOC53, SHC2, SRC, CHN1, MATK, STAT4, GRB10, ABL2, PIK3R2, SH2D5	1.586182	2.52E-14	1.96E-14
UP_KW_D OMAIN	KW-0371~Homeobox	26	4.40E-07	EPHB6, TNFRSF6B, CBL, ADGRA2, RPS6KA2, KDR, ARRC4, PRKCG, EPHA5, EPHA7, IL1R1, OMD, MRTFB, PRKCA, PIMREG, EML1, LRRC37B, TIAM1, PAPP, HECW1, FLYWCH1, BCORL1, ASTN2, ZFPM2, EPHA3, EPHA2, EPHA10, MAGED1, GATA6, PIK3R2, GATA3, GATA2, GATA1, KALRN, PPP3R2, MAP2, PRDM16, JAG2, NGFR, EGR1, EGR2, ACE, EGR3, MAGEE1, BCL11B, EGR4, SMARCA1, COL1A1, PPFIBP1, COL1A2, PTK7, COL9A3, CDKN1C, ROBO2, TENM1, PHF1, ELN, PTPRK, GLI1, RYR3, GLI3, ROBO1, AKAP12, PCLO, MECOM, CHL1, BRD3, PRMT8, BRD1, SYP, LRRC7, KIT, DPYD, YAP1, KANK1, COL11A1, AKAP6, PRICKLE1, EGFR, FSTL3, RELN, SLX4, WIF1, FLNC, IL12RB2, CDKN2B, GSN, SORT1, ATRNL1, VEGFC, VEGFD, SORBS2, PER1, COL3A1, AXL, WT1, NEDD4, LGR5, ZNF331, FCGBP, CSF3R, DGKB, IRS1, CTNND2, MPL, IRS4, TNC, PLAT, IL1RAP, IGF1R, CDH1, IL13RA2, ZNF687, ZNF444, ROS1, PPFIA2, PDGFRB, LMO1, PDGFRA, HGF, LMO2, LIFR, KAT6B, SCN8A, WDFY3, FBN2, NOTCH2, NOTCH3, CSF1R, NOTCH4, TNFRSF11A, CACNA1F, NDRG1, LPP, LTBP1, CACNA1G, CLTCL1, ZBTB16, HMGA2, LRP1B, TNFRSF10D, AH1, CPS1, LHX2, CNTN1, LHX4, FGFR4, FGFR3, FGFR2, FGFR1, ALK, PPP1R13B, ITGB3, FLT4, RASGRF2, CHD6, FHL2, HEPH, ZIC2, PPP1R13L, TRPS1, ITGAV, ZNF521, EDIL3, MYBL1, SH3D19, ABCC3, PEG3, DST, DCN, SETBP1, ASPH, CDH11, ITGA8, ITGA7, COL6A3, LAMA5, LAMA1, PLAG1, LRP5, NOD1, DLL1, DLL3, DLL4, ABLIM1, MUC1, ERBB4, SNCG, NCAM1, LRIG3, NTRK1, LINGO2, NTRK2, EGF, NTRK3, KLF4, TSHR, BICC1, ERCC4, PPP2R2B, NEUR1, TLL2 ITK, PPP1R13B, DST, SRC, MATK, PIK3R2, SORBS2, MAPK8IP2, KALRN, NCKIPSD, AH1, BAIAP2L1, PPP1R13L, BIN1, ABL2, SNX9, SRGAP3, DOCK1, SH3GL2, GAS7, SH3D19 SOC52, ITK, SOC53, SHC2, SRC, CHN1, MATK, STAT4, GRB10, ABL2, PIK3R2, SH2D5	3.256721	4.58E-06	3.56E-06
UP_KW_D OMAIN	KW-0245~EGF-like domain	26	5.09E-07	EPHB6, TNFRSF6B, CBL, ADGRA2, RPS6KA2, KDR, ARRC4, PRKCG, EPHA5, EPHA7, IL1R1, OMD, MRTFB, PRKCA, PIMREG, EML1, LRRC37B, TIAM1, PAPP, HECW1, FLYWCH1, BCORL1, ASTN2, ZFPM2, EPHA3, EPHA2, EPHA10, MAGED1, GATA6, PIK3R2, GATA3, GATA2, GATA1, KALRN, PPP3R2, MAP2, PRDM16, JAG2, NGFR, EGR1, EGR2, ACE, EGR3, MAGEE1, BCL11B, EGR4, SMARCA1, COL1A1, PPFIBP1, COL1A2, PTK7, COL9A3, CDKN1C, ROBO2, TENM1, PHF1, ELN, PTPRK, GLI1, RYR3, GLI3, ROBO1, AKAP12, PCLO, MECOM, CHL1, BRD3, PRMT8, BRD1, SYP, LRRC7, KIT, DPYD, YAP1, KANK1, COL11A1, AKAP6, PRICKLE1, EGFR, FSTL3, RELN, SLX4, WIF1, FLNC, IL12RB2, CDKN2B, GSN, SORT1, ATRNL1, VEGFC, VEGFD, SORBS2, PER1, COL3A1, AXL, WT1, NEDD4, LGR5, ZNF331, FCGBP, CSF3R, DGKB, IRS1, CTNND2, MPL, IRS4, TNC, PLAT, IL1RAP, IGF1R, CDH1, IL13RA2, ZNF687, ZNF444, ROS1, PPFIA2, PDGFRB, LMO1, PDGFRA, HGF, LMO2, LIFR, KAT6B, SCN8A, WDFY3, FBN2, NOTCH2, NOTCH3, CSF1R, NOTCH4, TNFRSF11A, CACNA1F, NDRG1, LPP, LTBP1, CACNA1G, CLTCL1, ZBTB16, HMGA2, LRP1B, TNFRSF10D, AH1, CPS1, LHX2, CNTN1, LHX4, FGFR4, FGFR3, FGFR2, FGFR1, ALK, PPP1R13B, ITGB3, FLT4, RASGRF2, CHD6, FHL2, HEPH, ZIC2, PPP1R13L, TRPS1, ITGAV, ZNF521, EDIL3, MYBL1, SH3D19, ABCC3, PEG3, DST, DCN, SETBP1, ASPH, CDH11, ITGA8, ITGA7, COL6A3, LAMA5, LAMA1, PLAG1, LRP5, NOD1, DLL1, DLL3, DLL4, ABLIM1, MUC1, ERBB4, SNCG, NCAM1, LRIG3, NTRK1, LINGO2, NTRK2, EGF, NTRK3, KLF4, TSHR, BICC1, ERCC4, PPP2R2B, NEUR1, TLL2 ITK, PPP1R13B, DST, SRC, MATK, PIK3R2, SORBS2, MAPK8IP2, KALRN, NCKIPSD, AH1, BAIAP2L1, PPP1R13L, BIN1, ABL2, SNX9, SRGAP3, DOCK1, SH3GL2, GAS7, SH3D19 SOC52, ITK, SOC53, SHC2, SRC, CHN1, MATK, STAT4, GRB10, ABL2, PIK3R2, SH2D5	3.231377	4.58E-06	3.56E-06
UP_KW_D OMAIN	KW-0677~Repeat	202	1.57E-05	LMO1, ABLIM1, LHX2, LMO2, FHL2, PRICKLE1, LHX4, LPP EPHB6, RET, ALK, ITK, ATP8A2, FLT3, DGKB, FLT4, CHD6, GPHN, IGF1R, CCT6B, CLP1, RPS6KA2, PRKACG, MYO18A, KDR, PRKG2, MAP3K6, ROS1, ABCC3, PDGFRB, PRKCG, EPHA5, PDGFRA, EPHA7, CDKL5, KSR1, ACSL6, MATK, PRKCA, BCR, SCN8A, KIT, ITPKA, ACSBG1, CILK1, EPHA3, EPHA2, DDR2, CAMK2B, CSF1R, BRSK1, EPHA10, SRC, CAMK2A, DDX20, NOD1, AK5, ACVR1B, KALRN, EGFR, ACVR1C, ERBB3, ERBB4, ERBB2, ABL2, PAK6, LRIG3, MYH11, CKB, PAK3, PAK5, NTRK1, NTRK2, NTRK3, STYK1, KIAA0232, HSPA2, SMARCA1, ACVR2A, PC, CPS1, AXL, ERCC6, FGFR4, FGFR3, FGFR2, BMPRI1A, FGFR1	1.274105	1.06E-04	8.25E-05
UP_KW_D OMAIN	KW-0728~SH3 domain	21	3.23E-05	EPHB6, RET, ALK, DIRAS3, ITK, ATP8A2, FLT3, DGKB, FLT4, CHD6, GPHN, IGF1R, RERG, IGF1R, CCT6B, CLP1, RPS6KA2, PRKACG, MYO18A, KDR, PRKG2, RAC3, MAP3K6, ROS1, ABCC3, PDGFRB, PRKCG, EPHA5, PDGFRA, EPHA7, CDKL5, KSR1, ACSL6, MATK, PRKCA, RHOD, DNM1, DNM3, BCR, SCN8A, DPYD, ALDH1A1, KIT, ITPKA, ACSBG1, CILK1, EPHA3, EPHA2, DDR2, CAMK2B, CSF1R, BRSK1, EPHA10, SRC, ATL1, CAMK2A, DDX20, NOD1, AK5, ACVR1B, KALRN, EGFR, GNAI1, ACVR1C, ERBB3, ERBB4, GNA11, ERBB2, GNA12, ABL2, PAK6, LRIG3, MYH11, CKB, PAK3, PAK5, NTRK1, NTRK2, NTRK3, STYK1, SEPTIN5, KIAA0232, HSPA2, SMARCA1, ACVR2A, PC, CPS1, AXL, GNAQ, ERCC6, FGFR4, FGFR3, FGFR2, BMPRI1A, FGFR1	2.941927	1.75E-04	1.36E-04
UP_KW_D OMAIN	KW-0727~SH2 domain	12	6.47E-04	EPHB6, RET, ALK, DIRAS3, ITK, ATP8A2, FLT3, DGKB, FLT4, CHD6, GPHN, IGF1R, RERG, IGF1R, CCT6B, CLP1, RPS6KA2, PRKACG, MYO18A, KDR, PRKG2, RAC3, MAP3K6, ROS1, ABCC3, PDGFRB, PRKCG, EPHA5, PDGFRA, EPHA7, CDKL5, KSR1, ACSL6, MATK, PRKCA, RHOD, DNM1, DNM3, BCR, SCN8A, DPYD, ALDH1A1, KIT, ITPKA, ACSBG1, CILK1, EPHA3, EPHA2, DDR2, CAMK2B, CSF1R, BRSK1, EPHA10, SRC, ATL1, CAMK2A, DDX20, NOD1, AK5, ACVR1B, KALRN, EGFR, GNAI1, ACVR1C, ERBB3, ERBB4, GNA11, ERBB2, GNA12, ABL2, PAK6, LRIG3, MYH11, CKB, PAK3, PAK5, NTRK1, NTRK2, NTRK3, STYK1, SEPTIN5, KIAA0232, HSPA2, SMARCA1, ACVR2A, PC, CPS1, AXL, GNAQ, ERCC6, FGFR4, FGFR3, FGFR2, BMPRI1A, FGFR1	3.484464	0.002912	0.002265
UP_KW_D OMAIN	KW-0440~LIM domain	8	0.008237	LMO1, ABLIM1, LHX2, LMO2, FHL2, PRICKLE1, LHX4, LPP EPHB6, RET, ALK, ITK, ATP8A2, FLT3, DGKB, FLT4, CHD6, GPHN, IGF1R, CCT6B, CLP1, RPS6KA2, PRKACG, MYO18A, KDR, PRKG2, MAP3K6, ROS1, ABCC3, PDGFRB, PRKCG, EPHA5, PDGFRA, EPHA7, CDKL5, KSR1, ACSL6, MATK, PRKCA, BCR, SCN8A, KIT, ITPKA, ACSBG1, CILK1, EPHA3, EPHA2, DDR2, CAMK2B, CSF1R, BRSK1, EPHA10, SRC, CAMK2A, DDX20, NOD1, AK5, ACVR1B, KALRN, EGFR, ACVR1C, ERBB3, ERBB4, ABL2, PAK6, LRIG3, MYH11, CKB, PAK3, PAK5, NTRK1, NTRK2, NTRK3, STYK1, KIAA0232, HSPA2, SMARCA1, ACVR2A, PC, CPS1, AXL, ERCC6, FGFR4, FGFR3, FGFR2, BMPRI1A, FGFR1	3.453072	0.031771	0.024711
UP_KW_LI GAND	KW-0067~ATP-binding	80	7.54E-06	EPHB6, RET, ALK, DIRAS3, ITK, ATP8A2, FLT3, DGKB, FLT4, CHD6, GPHN, RERG, IGF1R, CCT6B, CLP1, RPS6KA2, PRKACG, MYO18A, KDR, PRKG2, RAC3, MAP3K6, ROS1, ABCC3, PDGFRB, PRKCG, EPHA5, PDGFRA, EPHA7, CDKL5, KSR1, ACSL6, MATK, PRKCA, RHOD, DNM1, DNM3, BCR, SCN8A, DPYD, ALDH1A1, KIT, ITPKA, ACSBG1, CILK1, EPHA3, EPHA2, DDR2, CAMK2B, CSF1R, BRSK1, EPHA10, SRC, ATL1, CAMK2A, DDX20, NOD1, AK5, ACVR1B, KALRN, EGFR, GNAI1, ACVR1C, ERBB3, ERBB4, GNA11, ERBB2, GNA12, ABL2, PAK6, LRIG3, MYH11, CKB, PAK3, PAK5, NTRK1, NTRK2, NTRK3, STYK1, SEPTIN5, KIAA0232, HSPA2, SMARCA1, ACVR2A, PC, CPS1, AXL, GNAQ, ERCC6, FGFR4, FGFR3, FGFR2, BMPRI1A, FGFR1	1.584947	2.64E-04	2.64E-04
UP_KW_LI GAND	KW-0547~Nucleotide- binding	94	5.71E-05	EPHB6, RET, ALK, DIRAS3, ITK, ATP8A2, FLT3, DGKB, FLT4, CHD6, GPHN, RERG, IGF1R, CCT6B, CLP1, RPS6KA2, PRKACG, MYO18A, KDR, PRKG2, RAC3, MAP3K6, ROS1, ABCC3, PDGFRB, PRKCG, EPHA5, PDGFRA, EPHA7, CDKL5, KSR1, ACSL6, MATK, PRKCA, RHOD, DNM1, DNM3, BCR, SCN8A, DPYD, ALDH1A1, KIT, ITPKA, ACSBG1, CILK1, EPHA3, EPHA2, DDR2, CAMK2B, CSF1R, BRSK1, EPHA10, SRC, ATL1, CAMK2A, DDX20, NOD1, AK5, ACVR1B, KALRN, EGFR, GNAI1, ACVR1C, ERBB3, ERBB4, GNA11, ERBB2, GNA12, ABL2, PAK6, LRIG3, MYH11, CKB, PAK3, PAK5, NTRK1, NTRK2, NTRK3, STYK1, SEPTIN5, KIAA0232, HSPA2, SMARCA1, ACVR2A, PC, CPS1, AXL, GNAQ, ERCC6, FGFR4, FGFR3, FGFR2, BMPRI1A, FGFR1	1.430185	9.99E-04	9.99E-04
UP_KW_LI GAND	KW-0460~Magnesium	40	0.001569	CSF1R, BRSK1, ATP8A2, TUSC3, FLT4, ITGB3, CAMK2A, ACVR1B, PPM1D, KALRN, GPHN, GNAI1, GRIN2A, ACVR1C, CLP1, GNA11, RPS6KA2, GNA12, KDR, ABL2, LRIG3, PAK3, MAP3K6, PDGFRB, NTRK1, NTRK2, EYA1, EYA2, NTRK3, ACSL6, GRIN2B, ACVR2A, ERCC4, PTK7, GNAQ, KIT, FGFR3, CILK1, FGFR2, BMPRI1A	1.652513	0.018305	0.018305
UP_KW_M OLECULAR _FUNCTIO N	KW-0217~Developmental protein	135	6.21E-36	CTNND2, FZD10, DACH2, FGF1, HOXA13, FGF2, FGF3, HOXA11, FGF4, SOX2, FGF6, HOXA9, DACH1, FGF8, FGF9, CREB3L1, HOXA3, KDR, PDGFRB, PDGFRA, RNF43, EPHA7, WNT5B, MRTFB, SOX11, MITF, DKK1, DKK2, DKK4, SFRP4, SHTN1, SFRP2, SMO, BIN1, WDFY3, NOTCH2, NOTCH3, NOTCH4, PDGFB,	3.185135	2.45E-34	2.27E-34

UP_KW_M OLECULAR _FUNCTIO N	KW- 9996~Developmental protein	135	6.21E-36	PDGFA, FOXO4, WNT6, PDGFD, NKX2-5, WNT3, WNT4, JAG2, WNT10B, NGFR, FZD3, FZD2, GADD45B, FZD7, FZD6, FZD8, GDF6, PBX1, PHOX2B, BMP4, AHI1, TLX3, TLX1, FEV, ID1, HOXD9, NODAL, ROBO2, WNT2B, HOXC13, GLI1, HOXC11, ROBO1, LFNG, MECOM, ZIC2, HEY1, CHL1, JARID2, ZNF521, EDIL3, AXIN1, TET1, PAX3, OLIG1, OLIG2, WNT16, POU5F1, MLF1, MN1, PAX8, PAX7, TAL1, ITGA8, CILK1, GAS7, CAMK2B, CEBPA, LRP5, WNT8B, HOXD13, HOXD11, DLL1, EGFR, DLL3, DLL4, RELN, WNT11, ERBB4, WIF1, LRIG3, PAK3, LEFTY2, HES5, NTRK1, NTRK2, NPM2, PRRX1, CDX2, ANGPT1, EYA1, DMRT1, CDX1, EYA2, SORT1, NTRK3, WNT7B, SPRY4, PRRX2, DAB2IP, VEGFC, VEGFD, BICC1, SPRY2, ACKR3, TLL2	3.185135	2.45E-34	2.27E-34
				CTNND2, FZD10, DACH2, FGF1, HOXA13, FGF2, FGF3, HOXA11, FGF4, SOX2, FGF6, HOXA9, DACH1, FGF8, FGF9, CREB3L1, HOXA3, KDR, PDGFRB, PDGFRA, RNF43, EPHA7, WNT5B, MRTFB, SOX11, MITF, DKK1, DKK2, DKK4, SFRP4, SHTN1, SFRP2, SMO, BIN1, WDFY3, NOTCH2, NOTCH3, NOTCH4, PDGFB, PDGFA, FOXO4, WNT6, PDGFD, NKX2-5, WNT3, WNT4, JAG2, WNT10B, NGFR, FZD3, FZD2, GADD45B, FZD7, FZD6, FZD8, GDF6, PBX1, PHOX2B, BMP4, AHI1, TLX3, TLX1, FEV, ID1, HOXD9, NODAL, ROBO2, WNT2B, HOXC13, GLI1, HOXC11, ROBO1, LFNG, MECOM, ZIC2, HEY1, CHL1, JARID2, ZNF521, EDIL3, AXIN1, TET1, PAX3, OLIG1, OLIG2, WNT16, POU5F1, MLF1, MN1, PAX8, PAX7, TAL1, ITGA8, CILK1, GAS7, CAMK2B, CEBPA, LRP5, WNT8B, HOXD13, HOXD11, DLL1, EGFR, DLL3, DLL4, RELN, WNT11, ERBB4, WIF1, LRIG3, PAK3, LEFTY2, HES5, NTRK1, NTRK2, NPM2, PRRX1, CDX2, ANGPT1, EYA1, DMRT1, CDX1, EYA2, SORT1, NTRK3, WNT7B, SPRY4, PRRX2, DAB2IP, VEGFC, VEGFD, BICC1, SPRY2, ACKR3, TLL2			
				CSF3, CSF1, PDGFB, PDGFA, FGF1, FGF2, FGF3, FGF4, NTF4, FGF6, FGF8, FGF9, PDGFD, CCN6, NTF3, AMH, LEFTY2, FGF23, TGFB2, TGFB3, EGF, BDNF, HGF, VEGFC, VEGFD, IGF1, INHBA, NGF, GDF6, IL2, BMP4, IL3, FGF14, FGF19, NODAL, FGF10			
UP_KW_M OLECULAR _FUNCTIO N	KW-0339~Growth factor	36	1.14E-19	RET, ALK, CSF1R, ITK, EPHA10, FLT3, SRC, FLT4, EGFR, IGF1R, ERBB3, ERBB4, ERBB2, KDR, ABL2, ROS1, PDGFRB, NTRK1, EPHA5, PDGFRA, NTRK2, EPHA7, NTRK3, STYK1, MATK, AXL, KIT, FGFR4, FGFR3, FGFR2, EPHA3, FGFR1, EPHA2, DDR2	6.769216	2.38E-18	2.20E-18
UP_KW_M OLECULAR _FUNCTIO N	KW-0829~Tyrosine- protein kinase	34	1.21E-19	CRTC3, HIP1, MAML2, CRTC1, GLI1, GLI3, SOX2, DACH1, ZIC2, CREB3L1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, MRTFB, TET1, SOX11, MITF, ETV1, HNF1A, SOX10, ETV4, MN1, AR, MYCN, MAF, KAT6B, DDIT3, PPARG, ZFPM2, YAP1, NOTCH2, CEBPA, NOTCH3, CEBPB, CEBPD, CEBPE, PLAG1, NOTCH4, GATA6, GATA3, FOXO4, FOXO3, GATA2, LPP, GATA1, ERBB4, ERBB2, PRDM16, NKX2-1, STAT4, PPARGC1A, TFAP2A, TCF7L2, EGR1, WWTR1, JUN, EGR2, CDX2, EYA1, CDX1, EYA2, SMARCA1, KLF4, ESR1, PBX1, PHOX2B, MAFB, LHX2, NFIB	7.274962	2.38E-18	2.20E-18
UP_KW_M OLECULAR _FUNCTIO N	KW-0010~Activator	71	4.21E-12	TGFB2, TGFB3, PDGFB, VEGFC, PDGFA, VEGFD, FGF1, FGF2, FGF3, FGF4, FGF6, FGF8, FGF9, IL1B, PDGFD	2.430693	6.65E-11	6.14E-11
UP_KW_M OLECULAR _FUNCTIO N	KW-0497~Mitogen	15	3.10E-10	RET, ALK, ITK, CDKN1A, FLT3, DGKB, FLT4, IGF1R, PLAU, CLP1, RPS6KA2, PRKACG, KDR, PRKG2, MAP3K6, ROS1, PDGFRB, PRKCG, EPHA5, PDGFRA, EPHA7, CDKL5, KSR1, MATK, PRKCA, MAPK8IP2, BCR, KIT, ITPKA, CILK1, EPHA3, EPHA2, DDR2, CAMK2B, CSF1R, BRSK1, EPHA10, SRC, CAMK2A, AKAP6, AK5, ACVR1B, KALRN, EGFR, ACVR1C, ERBB3, ERBB4, ERBB2, ABL2, PAK6, CKB, PAK3, PAK5, NTRK1, NTRK2, NTRK3, STYK1, ACVR2A, AXL, FGFR4, FGFR3, FGFR2, BMPR1A, FGFR1	9.080656	4.09E-09	3.78E-09
UP_KW_M OLECULAR _FUNCTIO N	KW-0418~Kinase	64	2.02E-08	ZNF331, DACH2, HOXA13, ETS2, HOXA11, SOX2, HOXA9, DACH1, CREB3L1, HOXA3, ZNF687, ZNF444, MNX1, APLP2, SOX11, MITF, HNF1A, SOX10, RUNX2, MYCL, AR, MYCN, MAF, DDIT3, ERG, FLYWCH1, ZFPM2, ATF3, GATA6, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, NKX2-5, TFAP2A, EGR1, JUN, EGR2, EGR3, SMAD3, EGR4, ZBTB16, HMGA2, ESR1, PBX1, PHOX2B, FOSL1, NR4A3, MAFB, TLX3, LHX2, TLX1, FEV, LHX4, HOXD9, CHD6, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, TRPS1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, DNMT3A, TET1, PAX3, ETV1, FOXL2, OLIG1, FOS, OLIG2, ETV4, ETV5, POU5F1, MLF1, DMRTA2, PAX8, SETBP1, TAL2, PAX7, TAL1, RARA, AHRR, PPARG, ZMYND11, CEBPA, CEBPB, HLF, CEBPD, CEBPE, PLAG1, DDX20, HOXD13, HOXD11, CXCC4, STAT4, HES1, HES5, RUNX1T1, TCF7L2, PRRX1, CDX2, DMRT1, CDX1, MGMT, PRRX2, KLF4, TBX15, NR6A1, ERCC4, WT1, NFIB, FOSB, ERCC6	2.103986	2.28E-07	2.10E-07
UP_KW_M OLECULAR _FUNCTIO N	KW-0238~DNA-binding	123	9.00E-06	EPHB6, TNFRSF6B, CSF3R, IRS1, MPL, IRS2, FZD10, IL1RAP, CCDC28A, IGF1R, EDNRB, ADGRA2, KDR, IL13RA2, ROS1, PDGFRB, EPHA5, PDGFRA, EPHA7, IL1R1, FR52, LIFR, GABRG2, AR, SMO, EPHA3, EPHA2, NOTCH2, CSF1R, NOTCH3, EPHA10, NOTCH4, LPAR1, TNFRSF11A, GRIN2A, NGFR, FZD3, FZD2, PTCH1, FZD7, FZD6, FZD8, ESR1, GRIN2B, LRP1B, TNFRSF10D, NR4A3, PTK7, FGFR4, IL7R, FGFR3, FGFR2, BMPR1A, FGFR1, RET, ROBO2, ALK, PTPRR, FLT3, FLT4, ITGB3, PTPRK, GRM1, RYR3, ROBO1, GRM3, GHR, OLR1, ITGAV, CD36, PTCRA, GRID1, TGFB3, KIT, RARA, ITGA8, ITGA7, PPARG, DDR2, LRP5, ACVR1B, EGFR, P2RY8, ACVR1C, ERBB3, ERBB4, ERBB2, NCAM1, S1PR2, IL12RB2, NTRK1, NTRK2, SORT1, NTRK3, EPOR, TSHR, ACVR2A, NR6A1, AXL, ACKR3, LGR5, CRLF2	1.44688	8.89E-05	8.21E-05
UP_KW_M OLECULAR _FUNCTIO N	KW-0675~Receptor	102	6.96E-04	HDAC4, YAP1, TENM1, HDACS, PHF1, NAB2, FASLG, BHLHE22, DACH2, GATA1, GLI3, DACH1, CCND1, HEY1, ZIC2, PPP1R13L, TRPS1, ZNF703, PRDM16, NKX2-1, HES1, JARID2, ZNF521, HES5, RUNX1T1, TCF7L2, BCL11B, ZBTB16, DNMT3A, TET1, PBX1, MAFB, MAF, KAT6B, DDIT3, ID1, ID4, ZMYND11, ZFPM2, BCORL1, ATF3	1.361854	0.006109	0.005645
UP_KW_M OLECULAR _FUNCTIO N	KW-0678~Repressor	41	0.003268		1.600061	0.025817	0.023856

Suppl. Table S4. significantly differentially expressed 198 genes between patients over 60 years old and patients ≤60 years old (corresponding to Supplementary Figure 1C top heatmap)

Gene ID	Gene Name	Score(d)	Fold Change	q-value(%)	Local fdr(%)
BCL2A1	BCL2 related protein A1(BCL2A1)	4.001408	1.84407	0	0.040211
BAZ2A	bromodomain adjacent to zinc finger domain 2A(BAZ2A)	2.642889	1.140408	4.288321	3.921346
CPSF6	cleavage and polyadenylation specific factor 6(CPSF6)	2.938434	1.18163	1.360741	1.733889
SNW1	SNW domain containing 1(SNW1)	2.660654	1.242948	2.929613	3.746671
ABI1	abl interactor 1(ABI1)	3.540921	1.25344	0	0.31096
MCL1	MCL1 apoptosis regulator, BCL2 family member(MCL1)	2.810699	1.258046	2.136364	2.509171
TRAF3	TNF receptor associated factor 3(TRAF3)	2.854469	1.260291	2.136364	2.217742
KDM2B	lysine demethylase 2B(KDM2B)	2.568512	1.265129	4.288321	4.727753
CBFB	core-binding factor subunit beta(CBFB)	3.302361	1.267033	0	0.561009
CDK4	cyclin dependent kinase 4(CDK4)	2.8544	1.269873	2.136364	2.218179
BTG1	BTG anti-proliferation factor 1(BTG1)	3.224958	1.278731	0.613898	0.709067
EZH2	enhancer of zeste 2 polycomb repressive complex 2 subunit(EZH2)	2.613878	1.279176	4.288321	4.221042
SRSF2	serine and arginine rich splicing factor 2(SRSF2)	2.747245	1.289027	2.929613	2.984011
NRAS	NRAS proto-oncogene, GTPase(NRAS)	2.743811	1.28978	2.929613	3.01162
NOTCH1	notch receptor 1(NOTCH1)	2.598087	1.295133	4.288321	4.391996
CASP3	caspase 3(CASP3)	2.76049	1.303502	2.929613	2.879421
CHEK1	checkpoint kinase 1(CHEK1)	3.143434	1.323171	0.613898	0.916394
RUNX1	RUNX family transcription factor 1(RUNX1)	3.040102	1.330364	0.613898	1.269699
ZNF207	zinc finger protein 207(ZNF207)	2.635771	1.330942	4.288321	3.993197
BAX	BCL2 associated X, apoptosis regulator(BAX)	2.572235	1.336306	4.288321	4.684339
NIN	ninein(NIN)	2.999937	1.341226	0.613898	1.438199
FOXP1	forkhead box P1(FOXP1)	3.280268	1.344829	0.613898	0.598914
SKP2	S-phase kinase associated protein 2(SKP2)	3.144524	1.359876	0.613898	0.913233
TRAF2	TNF receptor associated factor 2(TRAF2)	2.584171	1.376462	4.288321	4.547404
THBS1	thrombospondin 1(THBS1)	2.564671	1.38045	4.288321	4.772881
AHR	aryl hydrocarbon receptor(AHR)	2.819366	1.382507	2.136364	2.449247
SYK	spleen associated tyrosine kinase(SYK)	2.915788	1.382574	1.360741	1.854959
TNFRSF10B	TNF receptor superfamily member 10b(TNFRSF10B)	3.341321	1.387186	0	0.501831
NFKB1	nuclear factor kappa B subunit 1(NFKB1)	3.133029	1.388062	0.613898	0.947124
NDC80	NDC80 kinetochore complex component(NDC80)	2.58137	1.391598	4.288321	4.579234
ST6GAL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1(ST6GAL1)	3.4783	1.395978	0	0.356218
PIM1	Pim-1 proto-oncogene, serine/threonine kinase(PIM1)	2.573564	1.398728	4.288321	4.668923
LCP1	lymphocyte cytosolic protein 1(LCP1)	2.548372	1.40139	4.288321	4.968459
IKZF1	IKAROS family zinc finger 1(IKZF1)	3.525293	1.417144	0	0.321524
MELK	maternal embryonic leucine zipper kinase(MELK)	3.050746	1.418445	0.613898	1.22812
CDK1	cyclin dependent kinase 1(CDK1)	3.182407	1.420212	0.613898	0.810117
NPM1	nucleophosmin 1(NPM1)	2.651641	1.422866	2.929613	3.834474
BTK	Bruton tyrosine kinase(BTK)	2.644774	1.433702	2.929613	3.902496
ICAM1	intercellular adhesion molecule 1(ICAM1)	3.417965	1.439146	0	0.410279
CARD11	caspase recruitment domain family member 11(CARD11)	3.579712	1.464876	0	0.286068
DUSP2	dual specificity phosphatase 2(DUSP2)	2.792604	1.467568	2.136364	2.637975
PTPN6	protein tyrosine phosphatase non-receptor type 6(PTPN6)	3.369964	1.46995	0	0.464055
POLD1	DNA polymerase delta 1, catalytic subunit(POLD1)	3.069125	1.471163	0.613898	1.159247
PAX5	paired box 5(PAX5)	3.180276	1.476077	0.613898	0.815579
LYN	LYN proto-oncogene, Src family tyrosine kinase(LYN)	3.663111	1.480051	0	0.236397
IL21R	interleukin 21 receptor(IL21R)	3.129173	1.486802	0.613898	0.958775

AURKB	aurora kinase B(AURKB)	3.346102	1.498251	0	0.495204
RB1	RB transcriptional corepressor 1(RB1)	2.835938	1.502589	2.136364	2.337737
TYMS	thymidylate synthetase(TYMS)	2.935636	1.51621	1.360741	1.748484
RASGRF1	Ras protein specific guanine nucleotide releasing factor 1(RASGRF1)	3.058603	1.555206	0.613898	1.198227
IRF8	interferon regulatory factor 8(IRF8)	3.280126	1.571828	0.613898	0.599168
H2AC17	H2A clustered histone 17(H2AC17)	3.072085	1.592701	0.613898	1.148496
PRMT1	protein arginine methyltransferase 1(PRMT1)	3.632105	1.59477	0	0.254479
IRF4	interferon regulatory factor 4(IRF4)	3.696112	1.789882	0	0.217415
IL6	interleukin 6(IL6)	3.259806	1.798985	0.613898	0.637035
CD70	CD70 molecule(CD70)	2.905068	1.857192	1.360741	1.914662
WNT10A	Wnt family member 10A(WNT10A)	3.901779	1.96013	0	0.099026
ATRNL1	atractin like 1(ATRNL1)	-4.93612	0.293512	0	0.04778
EPCAM	epithelial cell adhesion molecule(EPCAM)	-3.68199	0.387679	0	0
MLF1	myeloid leukemia factor 1(MLF1)	-4.0055	0.390996	0	0
PCLO	piccolo presynaptic cytomatrix protein(PCLO)	-3.44198	0.424433	0	0
NBEAP1	neurobeachin pseudogene 1(NBEAP1)	-3.36544	0.427338	0	0
ERBB4	erb-b2 receptor tyrosine kinase 4(ERBB4)	-4.31946	0.439834	0	0
DLEC1	DLEC1 cilia and flagella associated protein(DLEC1)	-3.61933	0.457	0	0
AKR1C3	aldo-keto reductase family 1 member C3(AKR1C3)	-3.82092	0.457879	0	0
CACNA2D3	calcium voltage-gated channel auxiliary subunit alpha2delta 3(CACNA2D3)	-3.58196	0.462759	0	0
PEG3	paternally expressed 3(PEG3)	-2.93064	0.469365	0	0
CNTN1	contactin 1(CNTN1)	-3.44226	0.477787	0	0
DIRAS3	DIRAS family GTPase 3(DIRAS3)	-2.96303	0.489782	0	0
SSBP2	single stranded DNA binding protein 2(SSBP2)	-3.97309	0.493352	0	0
CCT6B	chaperonin containing TCP1 subunit 6B(CCT6B)	-3.6012	0.496415	0	0
RGS7	regulator of G protein signaling 7(RGS7)	-3.18261	0.522819	0	0
RANBP17	RAN binding protein 17(RANBP17)	-3.71979	0.531414	0	0
AUTS2	activator of transcription and developmental regulator AUTS2(AUTS2)	-3.08014	0.532894	0	0
TUSC3	tumor suppressor candidate 3(TUSC3)	-3.90275	0.533605	0	0
BICC1	BicC family RNA binding protein 1(BICC1)	-3.95717	0.535748	0	0
FGFR2	fibroblast growth factor receptor 2(FGFR2)	-3.05517	0.538507	0	0
TENM1	teneurin transmembrane protein 1(TENM1)	-3.18025	0.539701	0	0
HSPA2	heat shock protein family A (Hsp70) member 2(HSPA2)	-2.63721	0.544641	0.613898	1.265275
TAL2	TAL bHLH transcription factor 2(TAL2)	-2.63044	0.553344	0.613898	1.319392
LAMA1	laminin subunit alpha 1(LAMA1)	-3.22383	0.555886	0	0
DMRT1	doublesex and mab-3 related transcription factor 1(DMRT1)	-2.94745	0.55602	0	0
GHR	growth hormone receptor(GHR)	-2.89747	0.556455	0	0
ATP8A2	ATPase phospholipid transporting 8A2(ATP8A2)	-2.62694	0.556719	0.613898	1.347887
EPHB6	EPH receptor B6(EPHB6)	-3.3515	0.561678	0	0
ESR1	estrogen receptor 1(ESR1)	-3.08867	0.563894	0	0
AR	androgen receptor(AR)	-3.77667	0.565804	0	0
CCNB3	cyclin B3(CCNB3)	-2.75691	0.567344	0.613898	0.497
GATA6	GATA binding protein 6(GATA6)	-3.38796	0.568214	0	0
WT1	WT1 transcription factor(WT1)	-2.72026	0.568355	0.613898	0.696871
MYBL1	MYB proto-oncogene like 1(MYBL1)	-2.7229	0.568628	0.613898	0.681504
PPP3R2	protein phosphatase 3 regulatory subunit B, beta(PPP3R2)	-2.7662	0.569937	0.613898	0.450742
ELOVL2	ELOVL fatty acid elongase 2(ELOVL2)	-3.5106	0.570591	0	0
EGFR	epidermal growth factor receptor(EGFR)	-3.23935	0.57064	0	0
GLI1	GLI family zinc finger 1(GLI1)	-3.24107	0.57326	0	0

SHC2	SHC adaptor protein 2(SHC2)	-3.12349	0.584191	0	0
CDC14B	cell division cycle 14B(CDC14B)	-3.49481	0.584435	0	0
ID4	inhibitor of DNA binding 4(ID4)	-2.79431	0.58485	0.613898	0.320889
ANGPT1	angiopoietin 1(ANGPT1)	-2.82659	0.58581	0.613898	0.189537
WNT2B	Wnt family member 2B(WNT2B)	-2.67367	0.586089	0.613898	0.994626
RYR3	ryanodine receptor 3(RYR3)	-2.66316	0.587993	0.613898	1.069158
CDH1	cadherin 1(CDH1)	-2.72095	0.589583	0.613898	0.692855
AKAP12	A-kinase anchoring protein 12(AKAP12)	-3.03378	0.591452	0	0
ZFPM2	zinc finger protein, FOG family member 2(ZFPM2)	-2.52614	0.596267	1.360741	2.322893
DNM1	dynamain 1(DNM1)	-3.19907	0.598531	0	0
ROBO1	roundabout guidance receptor 1(ROBO1)	-3.76555	0.598624	0	0
PROM1	prominin 1(PROM1)	-2.66557	0.599076	0.613898	1.051827
INPP5A	inositol polyphosphate-5-phosphatase A(INPP5A)	-3.26117	0.599314	0	0
EPHA3	EPH receptor A3(EPHA3)	-2.54888	0.600239	1.360741	2.075505
ARHGAP20	Rho GTPase activating protein 20(ARHGAP20)	-2.69123	0.601043	0.613898	0.876374
LIFR	LIF receptor subunit alpha(LIFR)	-4.00585	0.602942	0	0
ACSL6	acyl-CoA synthetase long chain family member 6(ACSL6)	-3.30686	0.60348	0	0
NTRK2	neurotrophic receptor tyrosine kinase 2(NTRK2)	-2.56786	0.603516	1.360741	1.881621
AK5	adenylate kinase 5(AK5)	-2.65969	0.607218	0.613898	1.094358
CXXC4	CXXC finger protein 4(CXXC4)	-2.93048	0.613276	0	0
SOCS2	suppressor of cytokine signaling 2(SOCS2)	-3.19422	0.614186	0	0
PSD3	pleckstrin and Sec7 domain containing 3(PSD3)	-3.03198	0.615552	0	0
ACSBG1	acyl-CoA synthetase bubblegum family member 1(ACSBG1)	-2.51818	0.617882	1.360741	2.413492
AKAP6	A-kinase anchoring protein 6(AKAP6)	-2.4422	0.620009	1.360741	3.389273
NTRK3	neurotrophic receptor tyrosine kinase 3(NTRK3)	-2.46663	0.62342	1.360741	3.053076
EYA1	EYA transcriptional coactivator and phosphatase 1(EYA1)	-2.53361	0.624907	1.360741	2.239712
NR6A1	nuclear receptor subfamily 6 group A member 1(NR6A1)	-2.78098	0.62533	0.613898	0.380578
PRKG2	protein kinase cGMP-dependent 2(PRKG2)	-2.57624	0.625442	1.360741	1.799607
SORT1	sortilin 1(SORT1)	-2.84625	0.625887	0.613898	0.118202
FGF13	fibroblast growth factor 13(FGF13)	-2.48445	0.626763	1.360741	2.821399
EDNRB	endothelin receptor type B(EDNRB)	-2.58565	0.627258	1.360741	1.710126
TACC2	transforming acidic coiled-coil containing protein 2(TACC2)	-2.63997	0.627396	0.613898	1.243581
PPARGC1A	PPARG coactivator 1 alpha(PPARGC1A)	-2.50174	0.627983	1.360741	2.607421
NAV3	neuron navigator 3(NAV3)	-2.76833	0.62906	0.613898	0.440337
GABRG2	gamma-aminobutyric acid type A receptor subunit gamma2(GABRG2)	-2.38828	0.629529	1.360741	4.210539
TRHDE	thyrotropin releasing hormone degrading enzyme(TRHDE)	-2.44951	0.634552	1.360741	3.286502
EML1	EMAP like 1(EML1)	-2.97919	0.636043	0	0
GNAI1	G protein subunit alpha i1(GNAI1)	-2.46457	0.637305	1.360741	3.080691
SH3GL2	SH3 domain containing GRB2 like 2, endophilin A1(SH3GL2)	-2.48775	0.639249	1.360741	2.779739
BRSK1	BR serine/threonine kinase 1(BRSK1)	-2.83388	0.644157	0.613898	0.162351
EDIL3	EGF like repeats and discoidin domains 3(EDIL3)	-2.51877	0.644463	1.360741	2.406711
PLCB4	phospholipase C beta 4(PLCB4)	-2.56126	0.644546	1.360741	1.947735
FBN2	fibrillin 2(FBN2)	-2.58743	0.644885	1.360741	1.693413
DCN	decorin(DCN)	-2.44856	0.645972	1.360741	3.299643
LTBP1	latent transforming growth factor beta binding protein 1(LTBP1)	-2.86643	0.647157	0.613898	0.051335
FGFR4	fibroblast growth factor receptor 4(FGFR4)	-2.72641	0.647397	0.613898	0.661314
NGFR	nerve growth factor receptor(NGFR)	-2.85386	0.647723	0.613898	0.092241
BIN1	bridging integrator 1(BIN1)	-2.9613	0.649087	0	0

CAMK2B	calcium/calmodulin dependent protein kinase II beta(CAMK2B)	-2.4893	0.64941	1.360741	2.760392
NCAM1	neural cell adhesion molecule 1(NCAM1)	-2.41695	0.650592	1.360741	3.760085
LNP1	leukemia NUP98 fusion partner 1(LNP1)	-2.42875	0.652653	1.360741	3.583876
GAS1	growth arrest specific 1(GAS1)	-2.73401	0.654149	0.613898	0.618527
CLTCL1	clathrin heavy chain like 1(CLTCL1)	-2.4537	0.655323	1.360741	3.228415
CPS1	carbamoyl-phosphate synthase 1(CPS1)	-2.48272	0.656653	1.360741	2.843426
TEAD1	TEA domain transcription factor 1(TEAD1)	-3.08119	0.656675	0	0
PDGFRA	platelet derived growth factor receptor alpha(PDGFR)	-2.84112	0.658632	0.613898	0.136197
CHN1	chimerin 1(CHN1)	-2.35724	0.661941	1.360741	4.734477
FGFR3	fibroblast growth factor receptor 3(FGFR3)	-2.59109	0.66468	1.360741	1.659588
LPAR1	lysophosphatidic acid receptor 1(LPAR1)	-2.46677	0.665338	1.360741	3.051231
GLI3	GLI family zinc finger 3(GLI3)	-2.47861	0.668637	1.360741	2.896087
LHFP L6	LHFP L6 (LHFP L Tetraspan Subfamily Member 6)	-2.65069	0.67009	0.613898	1.161204
ABCC3	ATP binding cassette subfamily C member 3(ABCC3)	-2.39313	0.673188	1.360741	4.132048
CD28	CD28 molecule(CD28)	-2.68997	0.673342	0.613898	0.884617
SLC34A2	solute carrier family 34 member 2(SLC34A2)	-2.36239	0.674307	1.360741	4.644856
DST	dystonin(DST)	-3.41562	0.675283	0	0
KLK2	kallikrein related peptidase 2(KLK2)	-2.40105	0.676158	1.360741	4.005981
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2(ENPP2)	-2.66548	0.678087	0.613898	1.052436
DACH1	dachshund family transcription factor 1(DACH1)	-2.43431	0.682392	1.360741	3.502559
CEP170B	centrosomal protein 170B(CEP170B)	-2.44209	0.685861	1.360741	3.390904
CYP1B1	cytochrome P450 family 1 subfamily B member 1(CYP1B1)	-2.75111	0.686317	0.613898	0.526752
ACVR1B	activin A receptor type 1B(ACVR1B)	-2.96671	0.688529	0	0
GAS7	growth arrest specific 7(GAS7)	-3.26468	0.688795	0	0
PLCB1	phospholipase C beta 1(PLCB1)	-2.68063	0.688888	0.613898	0.94686
FSTL3	folliculin like 3(FSTL3)	-2.53557	0.689202	1.360741	2.218169
DNM3	dynamitin 3(DNM3)	-2.35841	0.691887	1.360741	4.714082
DOCK1	dedicator of cytokinesis 1(DOCK1)	-3.46708	0.694193	0	0
SMO	smoothened, frizzled class receptor(SMO)	-2.42665	0.694536	1.360741	3.614779
PRKCG	protein kinase C gamma(PRKCG)	-2.35752	0.697465	1.360741	4.729509
S1PR2	sphingosine-1-phosphate receptor 2(S1PR2)	-2.34648	0.697791	1.360741	4.925073
AHRR	aryl hydrocarbon receptor repressor(AHRR)	-2.65735	0.701798	0.613898	1.111538
ABLIM1	actin binding LIM protein 1(ABLIM1)	-3.01716	0.7024	0	0
RET	ret proto-oncogene(RET)	-2.37796	0.702904	1.360741	4.38046
GNA11	G protein subunit alpha 11(GNA11)	-2.47355	0.703327	1.360741	2.961781
FGFR1	fibroblast growth factor receptor 1(FGFR1)	-2.52558	0.713868	1.360741	2.329126
NFIB	nuclear factor I B(NFIB)	-2.62137	0.716761	1.360741	1.393912
ZNF703	zinc finger protein 703(ZNF703)	-2.50194	0.717136	1.360741	2.605019
TCF7L2	transcription factor 7 like 2(TCF7L2)	-2.50686	0.717617	1.360741	2.546053
PPFIBP1	PPFIA binding protein 1(PPFIBP1)	-2.56621	0.717678	1.360741	1.897996
PTPRK	protein tyrosine phosphatase receptor type K(PTPRK)	-2.35862	0.72137	1.360741	4.710386
HDAC4	histone deacetylase 4(HDAC4)	-3.11414	0.734681	0	0
PRKCA	protein kinase C alpha(PRKCA)	-2.60391	0.736051	1.360741	1.543863
IL1R1	interleukin 1 receptor type 1(IL1R1)	-2.54608	0.736357	1.360741	2.104978
DDR2	discoidin domain receptor tyrosine kinase 2(DDR2)	-2.41336	0.739332	1.360741	3.814773
FOXO3	forkhead box O3(FOXO3)	-2.42851	0.750286	1.360741	3.587426
PPP1R13B	protein phosphatase 1 regulatory subunit 13B(PPP1R13B)	-2.40988	0.753845	1.360741	3.868152
HIP1	huntingtin interacting protein 1(HIP1)	-2.51059	0.755046	1.360741	2.501829
SRGAP3	SLIT-ROBO Rho GTPase activating protein 3(SRGAP3)	-2.53415	0.756672	1.360741	2.233736

TMPRSS2	transmembrane serine protease 2(TMPRSS2)	-2.3481	0.760781	1.360741	4.89608
CRTC1	CREB regulated transcription coactivator 1(CRTC1)	-2.37478	0.76153	1.360741	4.433695
EXT1	exostosin glycosyltransferase 1(EXT1)	-2.47309	0.793805	1.360741	2.967839
DDX20	DEAD-box helicase 20(DDX20)	-2.46526	0.808473	1.360741	3.07137
EXT2	exostosin glycosyltransferase 2(EXT2)	-2.41756	0.814573	1.360741	3.750793
AFF4	ALF transcription elongation factor 4(AFF4)	-2.87293	0.877584	0.613898	0.031128

Table S5.1. 384 up and 63 down-regulated genes in PT-DLBCL with mutated (vs. wild-type) *MYD88* RNA (corresponding to the 3rd heatmap in Figure 2)

Gene ID	Gene Name	Score(d)	Fold Change	q-value(%)	Local fdr(%)
IRF4	interferon regulatory factor 4(IRF4)	6.421221	2.51742	0	0
SH3BP1	SH3 domain binding protein 1(SH3BP1)	5.862425	2.312197	0	0.014367
H2AC16	H2AC16 (H2A Clustered Histone 16)	5.725936	2.269515	0	0.022266
FOXP1	forkhead box P1(FOXP1)	5.603739	1.58825	0	0.029842
PRMT1	protein arginine methyltransferase 1(PRMT1)	5.351419	1.833661	0	0.045819
TYMS	thymidylate synthetase(TYMS)	5.303638	1.897318	0	0.048625
H2AC17	H2AC17 (H2A Clustered Histone 17)	5.240674	2.077372	0	0.052021
FAF1	Fas associated factor 1(FAF1)	5.215595	1.519168	0	0.053246
PKM	pyruvate kinase M1/2(PKM)	5.205288	1.800911	0	0.053724
ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase(ATIC)	5.101342	1.488015	0	0.057559
FUS	FUS RNA binding protein(FUS)	5.039496	1.406466	0	0.058756
CCNE1	cyclin E1(CCNE1)	5.034245	1.710902	0	0.058811
H3C2	H3C2 (H3 Clustered Histone 2)	5.031476	2.108958	0	0.058837
H2BC12	H2BC12 (H2B Clustered Histone 12)	5.029009	1.901679	0	0.058859
H2BC17	H2BC17 (H2B Clustered Histone 17)	4.932977	2.30919	0	0.058147
PCNA	proliferating cell nuclear antigen(PCNA)	4.927273	1.753471	0	0.057998
RAC2	Rac family small GTPase 2(RAC2)	4.886249	2.194502	0	0.056517
CDC42	cell division cycle 42(CDC42)	4.873823	1.535624	0	0.055918
H2BC11	H2BC11 (H2B Clustered Histone 11)	4.871385	1.999421	0	0.055792
ELF4	E74 like ETS transcription factor 4(ELF4)	4.862823	1.483896	0	0.055327
PHB1	PHB1 (Prohibitin 1)	4.815627	1.546062	0	0.052099
SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1(SMARCB1)	4.810833	1.641341	0	0.051705
H2BC4	H2BC4 (H2B Clustered Histone 4)	4.80038	2.015157	0	0.050802
CDK2	cyclin dependent kinase 2(CDK2)	4.799397	1.469639	0	0.050713
SYK	spleen associated tyrosine kinase(SYK)	4.79671	1.644143	0	0.05047
SARNP	SAP domain containing ribonucleoprotein(SARNP)	4.786964	1.7199	0	0.04955
MELK	maternal embryonic leucine zipper kinase(MELK)	4.780631	1.637869	0	0.048923
H1-4	H1-4 (H1.4 Linker Histone, Cluster Member)	4.780058	1.795329	0	0.048865
LYN	LYN proto-oncogene, Src family tyrosine kinase(LYN)	4.774878	1.620929	0	0.048332
PTBP1	polypyrimidine tract binding protein 1(PTBP1)	4.746319	1.651243	0	0.045095
NAPA	NSF attachment protein alpha(NAPA)	4.731406	1.793661	0	0.043194
CBFB	core-binding factor subunit beta(CBFB)	4.715142	1.338832	0	0.040948
U2AF2	U2 small nuclear RNA auxiliary factor 2(U2AF2)	4.701057	1.588154	0	0.038853
FANCI	FA complementation group I(FANCI)	4.672991	1.394877	0	0.034243
POU2AF1	POU class 2 homeobox associating factor 1(POU2AF1)	4.669279	1.791055	0	0.033589

TFDP1	transcription factor Dp-1(TFDP1)	4.660911	1.512999	0	0.032074
UTP4	UTP4 (UTP4 Small Subunit Processome Component)	4.655371	1.386868	0	0.03104
EED	embryonic ectoderm development(EED)	4.649475	1.306007	0	0.029914
NFKB1	nuclear factor kappa B subunit 1(NFKB1)	4.647332	1.511529	0	0.029497
RPA3	replication protein A3(RPA3)	4.62661	1.730539	0	0.025275
LASP1	LIM and SH3 protein 1(LASP1)	4.615709	1.556813	0	0.022909
RPS6KA1	ribosomal protein S6 kinase A1(RPS6KA1)	4.603259	1.579191	0	0.020082
H2AC11	H2AC11 (H2A Clustered Histone 11)	4.600238	1.848588	0	0.019375
PAX5	paired box 5(PAX5)	4.587701	1.730685	0	0.016356
H1-2	H1-2 (H1.2 Linker Histone, Cluster Member)	4.556948	1.713069	0	0.008337
IKZF3	IKAROS family zinc finger 3(IKZF3)	4.520373	1.451069	0	0
RB1	RB transcriptional corepressor 1(RB1)	4.518799	1.69201	0	0
LCP1	lymphocyte cytosolic protein 1(LCP1)	4.515865	1.753478	0	0
ZNF207	zinc finger protein 207(ZNF207)	4.451865	1.536961	0	0
CD79B	CD79b molecule(CD79B)	4.432352	1.83008	0	0
SEPTIN6	septin 6(SEPTIN6)	4.40477	1.553153	0	0
SDHB	succinate dehydrogenase complex iron sulfur subunit B(SDHB)	4.401502	1.758565	0	0
INPP5D	inositol polyphosphate-5-phosphatase D(INPP5D)	4.395319	1.62604	0	0
CCNA2	cyclin A2(CCNA2)	4.379414	1.527794	0	0
HDAC3	histone deacetylase 3(HDAC3)	4.375803	1.564601	0	0
AURKB	aurora kinase B(AURKB)	4.367717	1.719932	0	0
WDR1	WD repeat domain 1(WDR1)	4.365786	1.589005	0	0
PPP4C	protein phosphatase 4 catalytic subunit(PPP4C)	4.347265	1.593686	0	0
GRHPR	glyoxylate and hydroxypyruvate reductase(GRHPR)	4.344701	2.016503	0	0
ABI1	abl interactor 1(ABI1)	4.333184	1.287096	0	0
ZNF384	zinc finger protein 384(ZNF384)	4.330504	1.429444	0	0
HMGA1	high mobility group AT-hook 1(HMGA1)	4.32225	1.869702	0	0
GRB2	growth factor receptor bound protein 2(GRB2)	4.282441	1.487313	0	0
TFRC	transferrin receptor(TFRC)	4.26952	1.631366	0	0
CD79A	CD79a molecule(CD79A)	4.256747	1.842879	0	0
POLD1	DNA polymerase delta 1, catalytic subunit(POLD1)	4.253818	1.615715	0	0
RPN2	ribophorin II(RPN2)	4.244089	1.486808	0	0
BAX	BCL2 associated X, apoptosis regulator(BAX)	4.209503	1.520061	0	0
FNBP1	formin binding protein 1(FNBP1)	4.173238	1.441452	0	0
SS18	SS18 subunit of BAF chromatin remodeling complex(SS18)	4.152506	1.567202	0	0
DNM2	dynammin 2(DNM2)	4.151897	1.348847	0	0
RELA	RELA proto-oncogene, NF-kB subunit(RELA)	4.138258	1.399172	0	0
PLCG2	phospholipase C gamma 2(PLCG2)	4.136993	1.629421	0	0
CALR	calreticulin(CALR)	4.121406	1.411732	0	0
PPP2R1A	protein phosphatase 2 scaffold subunit Aalpha(PPP2R1A)	4.115581	1.512047	0	0
MAD2L1	mitotic arrest deficient 2 like 1(MAD2L1)	4.102562	1.638	0	0
IDH2	isocitrate dehydrogenase (NADP(+)) 2(IDH2)	4.097564	1.579785	0	0
CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase(CAD)	4.090535	1.306388	0	0
CTDSP2	CTD small phosphatase 2(CTDSP2)	4.078711	1.274441	0	0
NFKBIA	NFKB inhibitor alpha(NFKBIA)	4.044654	1.434904	0	0
FH	fumarate hydratase(FH)	4.042524	1.381291	0	0

XRCC6	X-ray repair cross complementing 6(XRCC6)	4.034502	1.459302	0	0
PTTG1	PTTG1 regulator of sister chromatid separation, securin(PTTG1)	4.027134	1.731852	0	0
JAK1	Janus kinase 1(JAK1)	4.017373	1.433875	0	0
NRAS	NRAS proto-oncogene, GTPase(NRAS)	4.016472	1.423382	0	0
ETS1	ETS proto-oncogene 1, transcription factor(ETS1)	4.001986	1.324446	0	0
CDK4	cyclin dependent kinase 4(CDK4)	3.995981	1.350227	0	0
GIT2	GIT ArfGAP 2(GIT2)	3.991529	1.314285	0	0
TOP2A	DNA topoisomerase II alpha(TOP2A)	3.985931	1.543744	0	0
MRTFA	MRTFA (Myocardin Related Transcription Factor A)	3.972699	1.39131	0	0
PRKCD	protein kinase C delta(PRKCD)	3.970466	1.512785	0	0
MUTYH	mutY DNA glycosylase(MUTYH)	3.964021	1.477371	0	0
H4C9	H4C9 (H4 Clustered Histone 9)	3.957287	1.865528	0	0
IL21R	interleukin 21 receptor(IL21R)	3.956766	1.671842	0	0
STAT3	signal transducer and activator of transcription 3(STAT3)	3.953895	1.634479	0	0
RAD51	RAD51 recombinase(RAD51)	3.939376	1.648863	0	0
AK2	adenylate kinase 2(AK2)	3.93741	1.31363	0	0
CREB1	cAMP responsive element binding protein 1(CREB1)	3.920548	1.225415	0	0
NDC80	NDC80 kinetochore complex component(NDC80)	3.915417	1.619916	0	0
CARD11	caspase recruitment domain family member 11(CARD11)	3.91426	1.514291	0	0
CD44	CD44 molecule (IN blood group)(CD44)	3.90876	1.582906	0	0
PTPA	PTPA (Protein Phosphatase 2 Phosphatase Activator)	3.908141	1.522296	0	0
MSH2	mutS homolog 2(MSH2)	3.907883	1.382311	0	0
RASGRF1	Ras protein specific guanine nucleotide releasing factor 1(RASGRF1)	3.900322	1.768571	0	0
LPXN	leupaxin(LPXN)	3.897113	1.444217	0	0
PIK3CD	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta(PIK3CD)	3.882527	1.397775	0	0
BRD4	bromodomain containing 4(BRD4)	3.877835	1.187224	0	0
CYFIP2	cytoplasmic FMR1 interacting protein 2(CYFIP2)	3.876471	1.420829	0	0
FANCG	FA complementation group G(FANCG)	3.87104	1.450542	0	0
TBL1XR1	TBL1X/Y related 1(TBL1XR1)	3.845033	1.567146	0	0
CKS1B	CDC28 protein kinase regulatory subunit 1B(CKS1B)	3.832188	1.907804	0	0
MAPK1	mitogen-activated protein kinase 1(MAPK1)	3.832136	1.456362	0	0
RAF1	Raf-1 proto-oncogene, serine/threonine kinase(RAF1)	3.823771	1.352892	0	0
FLI1	Fli-1 proto-oncogene, ETS transcription factor(FLI1)	3.810442	1.29261	0	0
PDK1	pyruvate dehydrogenase kinase 1(PDK1)	3.806041	1.507306	0	0
EP300	E1A binding protein p300(EP300)	3.802509	1.153458	0	0
PIM1	Pim-1 proto-oncogene, serine/threonine kinase(PIM1)	3.791529	1.549256	0	0
TACC3	transforming acidic coiled-coil containing protein 3(TACC3)	3.783949	1.440969	0	0
TFG	trafficking from ER to golgi regulator(TFG)	3.755962	1.339465	0	0
STAT6	signal transducer and activator of transcription 6(STAT6)	3.738534	1.382849	0	0
HDAC1	histone deacetylase 1(HDAC1)	3.733273	1.474168	0	0
PHF6	PHD finger protein 6(PHF6)	3.728031	1.449756	0	0
CTSA	cathepsin A(CTSA)	3.723705	1.436918	0	0
AHR	aryl hydrocarbon receptor(AHR)	3.710731	1.518981	0	0
AURKA	aurora kinase A(AURKA)	3.703276	1.374479	0	0
SEPTIN2	septin 2(SEPTIN2)	3.699587	1.519991	0	0
CBL	Cbl proto-oncogene(CBL)	3.688542	1.251482	0	0

SLC7A5	solute carrier family 7 member 5(SLC7A5)	3.668661	1.595822	0	0
MYD88	MYD88 innate immune signal transduction adaptor(MYD88)	3.668601	1.402219	0	0
CLTC	clathrin heavy chain(CLTC)	3.667722	1.222799	0	0
CAPZB	capping actin protein of muscle Z-line subunit beta(CAPZB)	3.666904	1.347802	0	0
NSD2	NSD2 (Nuclear Receptor Binding SET Domain Protein 2)	3.665849	1.340419	0	0
EWSR1	EWS RNA binding protein 1(EWSR1)	3.661509	1.234874	0	0
CDK6	cyclin dependent kinase 6(CDK6)	3.632745	1.331531	0	0
EZH2	enhancer of zeste 2 polycomb repressive complex 2 subunit(EZH2)	3.63073	1.390958	0	0
HMGB1	high mobility group box 1(HMGB1)	3.627752	1.400423	0	0
PSMD2	proteasome 26S subunit ubiquitin receptor, non-ATPase 2(PSMD2)	3.621893	1.356828	0	0
FANCL	FA complementation group L(FANCL)	3.575895	1.404599	0	0
BCL3	BCL3 transcription coactivator(BCL3)	3.575245	1.423449	0	0
PAK1	p21 (RAC1) activated kinase 1(PAK1)	3.572923	1.370134	0	0
AHCYL1	adenosylhomocysteinase like 1(AHCYL1)	3.564871	1.20286	0	0
KPNB1	karyopherin subunit beta 1(KPNB1)	3.555508	1.400482	0	0
DNMT1	DNA methyltransferase 1(DNMT1)	3.548549	1.404035	0	0
CPSF6	cleavage and polyadenylation specific factor 6(CPSF6)	3.541528	1.216773	0	0
E2F1	E2F transcription factor 1(E2F1)	3.532518	1.560176	0	0
POM121	POM121 transmembrane nucleoporin(POM121)	3.528914	1.312813	0	0
RUNX1	RUNX family transcription factor 1(RUNX1)	3.528244	1.37374	0	0
NUP93	nucleoporin 93(NUP93)	3.515064	1.345743	0	0
CDC25A	cell division cycle 25A(CDC25A)	3.508583	1.507819	0	0
CDK1	cyclin dependent kinase 1(CDK1)	3.499798	1.404192	0	0
CHEK1	checkpoint kinase 1(CHEK1)	3.48605	1.361532	0	0
GTSE1	G2 and S-phase expressed 1(GTSE1)	3.481692	1.477711	0	0
SEPTIN9	septin 9(SEPTIN9)	3.469206	1.448179	0	0
AKT1	AKT serine/threonine kinase 1(AKT1)	3.465468	1.32129	0	0
PRKCB	protein kinase C beta(PRKCB)	3.454635	1.471725	0	0
NUP214	nucleoporin 214(NUP214)	3.448084	1.279388	0	0
MLH1	mutL homolog 1(MLH1)	3.445995	1.309083	0	0
PTPN6	protein tyrosine phosphatase non-receptor type 6(PTPN6)	3.445069	1.489498	0	0
TCL1A	TCL1 family AKT coactivator A(TCL1A)	3.436933	2.18633	0	0
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B(BUB1B)	3.416997	1.47456	0	0
RCOR1	REST corepressor 1(RCOR1)	3.398863	1.338661	0	0
CNBP	CCHC-type zinc finger nucleic acid binding protein(CNBP)	3.397637	1.262626	0	0
ARAF	A-Raf proto-oncogene, serine/threonine kinase(ARAF)	3.389018	1.338831	0	0
PPP3CA	protein phosphatase 3 catalytic subunit alpha(PPP3CA)	3.380983	1.283018	0	0
RRM1	ribonucleotide reductase catalytic subunit M1(RRM1)	3.380206	1.338676	0	0
TP63	tumor protein p63(TP63)	3.379652	1.70669	0	0
SUZ12	SUZ12 polycomb repressive complex 2 subunit(SUZ12)	3.367904	1.32519	0	0
TP53	tumor protein p53(TP53)	3.363326	1.414645	0	0
H2AX	H2AX (H2A.X Variant Histone)	3.344144	1.558276	0	0
PRKDC	protein kinase, DNA-activated, catalytic subunit(PRKDC)	3.342308	1.369302	0	0
ST6GAL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1(ST6GAL1)	3.339429	1.387024	0	0
VHL	von Hippel-Lindau tumor suppressor(VHL)	3.331069	1.323061	0	0
ICAM1	intercellular adhesion molecule 1(ICAM1)	3.324426	1.415626	0	0

SOD2	superoxide dismutase 2(SOD2)	3.322007	1.525029	0	0
SRSF3	serine and arginine rich splicing factor 3(SRSF3)	3.318836	1.327529	0	0
SIN3A	SIN3 transcription regulator family member A(SIN3A)	3.314145	1.232523	0	0
NR1I3	(Nuclear Receptor Subfamily 1 Group I Member 3)	3.304337	1.246667	0	0
EPS15	epidermal growth factor receptor pathway substrate 15(EPS15)	3.303851	1.343845	0	0
NUP107	nucleoporin 107(NUP107)	3.301538	1.345622	0	0
SMC1A	structural maintenance of chromosomes 1A(SMC1A)	3.301497	1.358515	0	0
CARMIL2	CARMIL2 (Capping Protein Regulator And Myosin 1 Linker 2)	3.295555	1.448107	0	0
TFE3	transcription factor binding to IGHM enhancer 3(TFE3)	3.292467	1.398658	0	0
ETV6	ETS variant transcription factor 6(ETV6)	3.290762	1.327615	0	0
NCSTN	nicastrin(NCSTN)	3.290644	1.321951	0	0
CCAR2	cell cycle and apoptosis regulator 2(CCAR2)	3.287692	1.287039	0	0
HUWE1	HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1(HUWE1)	3.285169	1.342982	0	0
TPM3	tropomyosin 3(TPM3)	3.266098	1.404288	0	0
PRKAR1A	protein kinase cAMP-dependent type I regulatory subunit alpha(PRKAR1A)	3.259618	1.417245	0	0
NDE1	nudE neurodevelopment protein 1(NDE1)	3.253685	1.289881	0	0
CDC73	cell division cycle 73(CDC73)	3.242094	1.182755	0	0
SRF	serum response factor(SRF)	3.241003	1.316945	0	0
DDB2	damage specific DNA binding protein 2(DDB2)	3.236475	1.367654	0	0
CMKLR1	chemerin chemokine-like receptor 1(CMKLR1)	3.234515	1.445255	0	0
MEF2B	myocyte enhancer factor 2B(MEF2B)	3.211928	1.795117	0	0
BTK	Bruton tyrosine kinase(BTK)	3.200632	1.464235	0	0
GNAS	GNAS complex locus(GNAS)	3.197163	1.427605	0	0
U2AF1	U2 small nuclear RNA auxiliary factor 1(U2AF1)	3.185249	1.436265	0	0
YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon(YWHAE)	3.185172	1.41505	0	0
MAPK3	mitogen-activated protein kinase 3(MAPK3)	3.184276	1.481096	0	0
CENPU	centromere protein U(CENPU)	3.183862	1.436271	0	0
BTG2	BTG anti-proliferation factor 2(BTG2)	3.176514	1.335554	0	0
AKT2	AKT serine/threonine kinase 2(AKT2)	3.172234	1.298441	0	0
CCDC6	coiled-coil domain containing 6(CCDC6)	3.163768	1.238479	0	0
APH1A	aph-1 homolog A, gamma-secretase subunit(APH1A)	3.161217	1.280672	0	0
NFKB2	nuclear factor kappa B subunit 2(NFKB2)	3.155828	1.363089	0	0
NUP98	nucleoporin 98 and 96 precursor(NUP98)	3.14605	1.258527	0	0
SET	SET nuclear proto-oncogene(SET)	3.138862	1.376148	0	0
GSK3B	glycogen synthase kinase 3 beta(GSK3B)	3.116217	1.229416	0	0
RHOA	ras homolog family member A(RHOA)	3.115695	1.336116	0	0
TRIM33	tripartite motif containing 33(TRIM33)	3.102021	1.213771	0	0
FANCD2	FA complementation group D2(FANCD2)	3.088446	1.258682	0	0
NONO	non-POU domain containing octamer binding(NONO)	3.079235	1.390176	0	0
DPM1	dolichyl-phosphate mannosyltransferase subunit 1, catalytic(DPM1)	3.079036	1.341422	0	0
MLLT1	MLLT1 super elongation complex subunit(MLLT1)	3.072796	1.330879	0	0
IRF2BP2	interferon regulatory factor 2 binding protein 2(IRF2BP2)	3.068912	1.255585	0	0
ARID1A	AT-rich interaction domain 1A(ARID1A)	3.06818	1.231699	0	0
ELL	elongation factor for RNA polymerase II(ELL)	3.068053	1.359149	0	0
UFM1	ubiquitin fold modifier 1(UFM1)	3.06079	1.404644	0	0

H2AC6	H2AC6 (H2A Clustered Histone 6)	3.052867	1.464583	0	0
POMGNT1	protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-)(POMGNT1)	3.047513	1.3282	0	0
KDM1A	lysine demethylase 1A(KDM1A)	3.047221	1.270078	0	0
AFF3	ALF transcription elongation factor 3(AFF3)	3.029601	1.462875	0	0
FCGR2B	Fc gamma receptor IIb(FCGR2B)	3.02438	1.732066	0	0
RPN1	ribophorin I(RPN1)	3.023885	1.286331	0	0
RASAL1	RAS protein activator like 1(RASAL1)	3.018727	1.616826	0	0
MAPRE1	microtubule associated protein RP/EB family member 1(MAPRE1)	3.016223	1.327977	0	0
TYK2	tyrosine kinase 2(TYK2)	3.013427	1.308675	0	0
SDHAF2	succinate dehydrogenase complex assembly factor 2(SDHAF2)	3.013002	1.290372	0	0
PRCC	proline rich mitotic checkpoint control factor(PRCC)	3.010107	1.272405	0	0
IKZF1	IKAROS family zinc finger 1(IKZF1)	3.005912	1.341537	0	0
SKP2	S-phase kinase associated protein 2(SKP2)	2.982741	1.276117	0	0
FIP1L1	factor interacting with PAPOLA and CPSF1(FIP1L1)	2.979031	1.17939	0	0
PLEKHM2	pleckstrin homology and RUN domain containing M2(PLEKHM2)	2.975427	1.27464	0	0
MNAT1	MNAT1 component of CDK activating kinase(MNAT1)	2.967309	1.368865	0	0
SF3B1	splicing factor 3b subunit 1(SF3B1)	2.95877	1.314533	0	0
BCL2A1	BCL2 related protein A1(BCL2A1)	2.958308	1.575128	0	0
PRKACA	protein kinase cAMP-activated catalytic subunit alpha(PRKACA)	2.95092	1.38086	0	0
RPS6KA3	ribosomal protein S6 kinase A3(RPS6KA3)	2.935861	1.320402	0	0
SERPINE1	serpin family E member 1(SERPINE1)	2.925829	1.521152	0	0
MDH1	malate dehydrogenase 1(MDH1)	2.925161	1.296796	0	0
JAK3	Janus kinase 3(JAK3)	2.921544	1.356089	0	0
HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1(HNRNPA2B1)	2.918775	1.426793	0	0
GTF2I	general transcription factor Iii(GTF2I)	2.91355	1.351854	0	0
BAZ2A	bromodomain adjacent to zinc finger domain 2A(BAZ2A)	2.9119	1.146618	0	0
ARHGEF7	Rho guanine nucleotide exchange factor 7(ARHGEF7)	2.901702	1.252031	0	0
USP5	ubiquitin specific peptidase 5(USP5)	2.890712	1.295298	0	0
GMPS	guanine monophosphate synthase(GMPS)	2.883221	1.32132	0	0
FEN1	flap structure-specific endonuclease 1(FEN1)	2.863418	1.369166	0	0
POLD4	DNA polymerase delta 4, accessory subunit(POLD4)	2.862487	1.393285	0	0
TCEA1	transcription elongation factor A1(TCEA1)	2.862246	1.271725	0	0
DDX3X	DEAD-box helicase 3 X-linked(DDX3X)	2.861477	1.224442	0	0
DUSP22	dual specificity phosphatase 22(DUSP22)	2.861318	1.245178	0	0
SP1	Sp1 transcription factor(SP1)	2.853533	1.222654	0	0
GOSR1	golgi SNAP receptor complex member 1(GOSR1)	2.829805	1.224259	0	0
KDM5C	lysine demethylase 5C(KDM5C)	2.822531	1.244466	0	0
BIRC3	baculoviral IAP repeat containing 3(BIRC3)	2.820314	1.40795	0	0
RASGRP1	RAS guanyl releasing protein 1(RASGRP1)	2.813817	1.393256	0	0
ERCC1	ERCC excision repair 1, endonuclease non-catalytic subunit(ERCC1)	2.809316	1.302918	0	0
CD74	CD74 molecule(CD74)	2.803165	1.531057	0	0
IRF8	interferon regulatory factor 8(IRF8)	2.802287	1.458573	0	0
IGFBP3	insulin like growth factor binding protein 3(IGFBP3)	2.799633	1.496861	0	0
TNF	tumor necrosis factor(TNF)	2.799462	1.597928	0	0
PDCD11	programmed cell death 11(PDCD11)	2.796643	1.243276	0	0
HERPUD1	homocysteine inducible ER protein with ubiquitin like domain 1(HERPUD1)	2.794533	1.33807	0	0

ZC3H7B	zinc finger CCCH-type containing 7B(ZC3H7B)	2.789158	1.267502	0.12749	0
PI4KA	phosphatidylinositol 4-kinase alpha(PI4KA)	2.788397	1.242939	0.12749	0
TOP1	DNA topoisomerase I(TOP1)	2.779227	1.308578	0.12749	0
RAP1GDS1	Rap1 GTPase-GDP dissociation stimulator 1(RAP1GDS1)	2.774804	1.244076	0.12749	0
LRPPRC	leucine rich pentatricopeptide repeat containing(LRPPRC)	2.772323	1.281126	0.12749	0
STAT1	signal transducer and activator of transcription 1(STAT1)	2.769912	1.45757	0.12749	0
CSF3R	colony stimulating factor 3 receptor(CSF3R)	2.764411	1.4238	0.12749	0
BCL11A	BCL11 transcription factor A(BCL11A)	2.759006	1.32143	0.12749	0
WEE1	WEE1 G2 checkpoint kinase(WEE1)	2.752421	1.286464	0.12749	0
CDK12	cyclin dependent kinase 12(CDK12)	2.749299	1.133987	0.12749	0
TRIM24	tripartite motif containing 24(TRIM24)	2.743224	1.238041	0.12749	0
IKBKE	inhibitor of nuclear factor kappa B kinase subunit epsilon(IKBKE)	2.742578	1.378205	0.12749	0
CSNK2A1	casein kinase 2 alpha 1(CSNK2A1)	2.742374	1.183359	0.12749	0
CAPRIN1	cell cycle associated protein 1(CAPRIN1)	2.742347	1.270953	0.12749	0
CDK5RAP2	CDK5 regulatory subunit associated protein 2(CDK5RAP2)	2.741752	1.141766	0.12749	0
NCOA4	nuclear receptor coactivator 4(NCOA4)	2.717353	1.242408	0.12749	0
CCND2	cyclin D2(CCND2)	2.710582	1.565066	0.12749	0
NF2	NF2, moesin-ezrin-radixin like (MERLIN) tumor suppressor(NF2)	2.699647	1.203913	0.12749	0
ERCC2	ERCC excision repair 2, TFIIH core complex helicase subunit(ERCC2)	2.698014	1.240302	0.12749	0
TFEB	transcription factor EB(TFEB)	2.687879	1.352286	0.12749	0
CCDC88C	coiled-coil domain containing 88C(CCDC88C)	2.683546	1.217001	0.12749	0
CNOT2	CCR4-NOT transcription complex subunit 2(CNOT2)	2.674134	1.250423	0.12749	0
MAP2K7	mitogen-activated protein kinase kinase 7(MAP2K7)	2.672061	1.286364	0.12749	0
RAC1	Rac family small GTPase 1(RAC1)	2.662777	1.232201	0.12749	0
HSPA5	heat shock protein family A (Hsp70) member 5(HSPA5)	2.654835	1.269164	0.12749	0.048578
COG5	component of oligomeric golgi complex 5(COG5)	2.651945	1.198709	0.12749	0.069513
BCL6	BCL6 transcription repressor(BCL6)	2.649126	1.36	0.12749	0.090133
LRRC59	leucine rich repeat containing 59(LRRC59)	2.645365	1.243945	0.12749	0.117949
CHEK2	checkpoint kinase 2(CHEK2)	2.643869	1.386879	0.12749	0.129115
THRAP3	thyroid hormone receptor associated protein 3(THRAP3)	2.636805	1.216746	0.12749	0.182586
MTOR	mechanistic target of rapamycin kinase(MTOR)	2.636275	1.218674	0.12749	0.18665
PFDN5	prefoldin subunit 5(PFDN5)	2.634546	1.425665	0.12749	0.199955
SPP1	secreted phosphoprotein 1(SPP1)	2.632304	1.729751	0.12749	0.217326
MSN	moesin(MSN)	2.629644	1.342022	0.12749	0.238096
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2(ENPP2)	2.620831	1.411134	0.12749	0.308235
STRN	striatin(STRN)	2.618395	1.192015	0.12749	0.327984
MAP2K2	mitogen-activated protein kinase kinase 2(MAP2K2)	2.617736	1.305562	0.12749	0.333349
ACSL3	acyl-CoA synthetase long chain family member 3(ACSL3)	2.616045	1.197256	0.12749	0.347182
HDAC6	histone deacetylase 6(HDAC6)	2.614692	1.221292	0.12749	0.358298
MMP9	matrix metalloproteinase 9(MMP9)	2.612916	1.79193	0.12749	0.372967
CD70	CD70 molecule(CD70)	2.606319	1.714112	0.12749	0.4282
MRE11	MRE11 (MRE11 Homolog, Double Strand Break Repair Nuclease)	2.604586	1.211936	0.12749	0.4429
MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase(MFNG)	2.604068	1.380163	0.12749	0.447308
PTPN11	protein tyrosine phosphatase non-receptor type 11(PTPN11)	2.597497	1.251703	0.12749	0.503891
HIF1A	hypoxia inducible factor 1 subunit alpha(HIF1A)	2.596826	1.279392	0.12749	0.509741
GANAB	glucosidase II alpha subunit(GANAB)	2.593057	1.230289	0.12749	0.542796

CIP2A	CIP2A (Cellular Inhibitor Of PP2A)	2.590776	1.2751	0.12749	0.562994
BCL10	BCL10 immune signaling adaptor(BCL10)	2.585177	1.231406	0.322139	0.613182
SFPQ	splicing factor proline and glutamine rich(SFPQ)	2.566398	1.279316	0.322139	0.787999
MYO1F	myosin IF(MYO1F)	2.561213	1.375742	0.322139	0.838045
CD19	CD19 molecule(CD19)	2.556676	1.483992	0.322139	0.882493
TCF12	transcription factor 12(TCF12)	2.553535	1.237822	0.322139	0.913614
RPTOR	regulatory associated protein of MTOR complex 1(RPTOR)	2.547383	1.192722	0.322139	0.975412
ZC3H7A	zinc finger CCCH-type containing 7A(ZC3H7A)	2.544706	1.217006	0.322139	1.002659
MAP2K3	mitogen-activated protein kinase kinase 3(MAP2K3)	2.542719	1.280761	0.322139	1.023018
RECQL4	RecQ like helicase 4(RECQL4)	2.541765	1.372377	0.322139	1.032836
SRSF2	serine and arginine rich splicing factor 2(SRSF2)	2.541612	1.187244	0.322139	1.034413
PSEN1	presenilin 1(PSEN1)	2.531711	1.20966	0.322139	1.137986
NFATC2	nuclear factor of activated T cells 2(NFATC2)	2.531642	1.239717	0.322139	1.138719
TNFAIP3	TNF alpha induced protein 3(TNFAIP3)	2.52741	1.257959	0.322139	1.183909
GID4	GID complex subunit 4 homolog(GID4)	2.523772	1.27741	0.322139	1.223206
XBP1	X-box binding protein 1(XBP1)	2.520325	1.312343	0.322139	1.260806
EP400	E1A binding protein p400(EP400)	2.519472	1.182913	0.322139	1.270167
HSP90AB1	heat shock protein 90 alpha family class B member 1(HSP90AB1)	2.514485	1.314814	0.322139	1.325364
MAX	MYC associated factor X(MAX)	2.513761	1.24366	0.322139	1.333442
STK11	serine/threonine kinase 11(STK11)	2.505468	1.238672	0.322139	1.427151
SDHC	succinate dehydrogenase complex subunit C(SDHC)	2.49839	1.248611	0.322139	1.508867
NDRG1	N-myc downstream regulated 1(NDRG1)	2.496634	1.424935	0.322139	1.529384
NPM1	nucleophosmin 1(NPM1)	2.496246	1.375531	0.322139	1.533932
CLTA	clathrin light chain A(CLTA)	2.491119	1.148464	0.322139	1.594488
VTI1A	vesicle transport through interaction with t-SNAREs 1A(VTI1A)	2.47973	1.278446	0.322139	1.73206
RHBDF2	rhomboid 5 homolog 2(RHBDF2)	2.476668	1.273798	0.322139	1.769766
RPL22	ribosomal protein L22(RPL22)	2.469934	1.402664	0.322139	1.853814
CCND3	cyclin D3(CCND3)	2.468124	1.357032	0.322139	1.876657
CAMTA1	calmodulin binding transcription activator 1(CAMTA1)	2.463914	1.236374	0.322139	1.930232
POT1	protection of telomeres 1(POT1)	2.462561	1.204128	0.322139	1.947577
PLAU	plasminogen activator, urokinase(PLAU)	2.454513	1.441775	0.322139	2.052018
CARM1	coactivator associated arginine methyltransferase 1(CARM1)	2.447618	1.249355	0.322139	2.143271
IDH1	isocitrate dehydrogenase (NADP(+)) 1(IDH1)	2.447459	1.252743	0.322139	2.145391
IRF1	interferon regulatory factor 1(IRF1)	2.445275	1.319064	0.322139	2.174646
MKI67	marker of proliferation Ki-67(MKI67)	2.443736	1.338191	0.322139	2.195359
CUX1	cut like homeobox 1(CUX1)	2.43915	1.24299	0.322139	2.25758
TACC1	transforming acidic coiled-coil containing protein 1(TACC1)	2.438776	1.22192	0.322139	2.262695
SDHA	succinate dehydrogenase complex flavoprotein subunit A(SDHA)	2.437062	1.205867	0.322139	2.286155
WASF2	WASP family member 2(WASF2)	2.434575	1.214106	0.322139	2.32038
NCOR2	nuclear receptor corepressor 2(NCOR2)	2.432961	1.217153	0.322139	2.342712
H1-3	H1-3 (H1.3 Linker Histone, Cluster Member)	2.432502	1.308582	0.322139	2.349079
MEF2D	myocyte enhancer factor 2D(MEF2D)	2.421361	1.224732	0.322139	2.505929
PCBP1	poly(rC) binding protein 1(PCBP1)	2.414765	1.26214	0.322139	2.600888
MCL1	MCL1 apoptosis regulator, BCL2 family member(MCL1)	2.407352	1.209035	0.322139	2.709465
MAP2K1	mitogen-activated protein kinase kinase 1(MAP2K1)	2.405998	1.235493	0.322139	2.729517
RAD51C	RAD51 paralog C(RAD51C)	2.399099	1.253297	0.322139	2.83272

TPD52L2	TPD52 like 2(TPD52L2)	2.396877	1.261356	0.322139	2.866331
AIP	aryl hydrocarbon receptor interacting protein(AIP)	2.395396	1.21892	0.322139	2.888829
WDR70	WD repeat domain 70(WDR70)	2.384414	1.226502	0.322139	3.058253
DDX6	DEAD-box helicase 6(DDX6)	2.380832	1.175088	0.322139	3.114489
KIF5B	kinesin family member 5B(KIF5B)	2.38063	1.248767	0.322139	3.11767
MBNL1	muscleblind like splicing regulator 1(MBNL1)	2.37899	1.23615	0.471012	3.143598
TTK	TTK protein kinase(TTK)	2.374009	1.277719	0.471012	3.222938
SLC66A3	SLC66A3 (Solute Carrier Family 66 Member 3)	2.370247	1.399914	0.471012	3.283504
LGALS3	galectin 3(LGALS3)	2.367851	1.305301	0.471012	3.32236
CREBBP	CREB binding protein(CREBBP)	2.364295	1.114749	0.471012	3.380423
EML4	EMAP like 4(EML4)	2.358367	1.189544	0.471012	3.47829
HSP90AA1	heat shock protein 90 alpha family class A member 1(HSP90AA1)	2.348889	1.274272	0.471012	3.637628
WDR18	WD repeat domain 18(WDR18)	2.337589	1.356706	0.471012	3.832192
FRK	fyn related Src family tyrosine kinase(FRK)	2.337312	1.376847	0.471012	3.837037
SNW1	SNW domain containing 1(SNW1)	2.333458	1.189529	0.471012	3.904582
PICALM	phosphatidylinositol binding clathrin assembly protein(PICALM)	2.326582	1.293748	0.471012	4.026598
EZR	ezrin(EZR)	2.326165	1.280141	0.471012	4.034047
TPR	translocated promoter region, nuclear basket protein(TPR)	2.324858	1.220109	0.471012	4.057483
STAG2	STAG2 cohesin complex component(STAG2)	2.319199	1.206832	0.471012	4.159701
UFC1	ubiquitin-fold modifier conjugating enzyme 1(UFC1)	2.315106	1.229207	0.471012	4.23444
PPP2R1B	protein phosphatase 2 scaffold subunit Abeta(PPP2R1B)	2.309086	1.18613	0.471012	4.345616
CREB3L2	cAMP responsive element binding protein 3 like 2(CREB3L2)	2.306991	1.250445	0.471012	4.384653
DOT1L	DOT1 like histone lysine methyltransferase(DOT1L)	2.303622	1.219533	0.471012	4.447788
SEC31A	SEC31 homolog A, COPII coat complex component(SEC31A)	2.297046	1.202928	0.471012	4.572401
REEP3	receptor accessory protein 3(REEP3)	2.294988	1.213793	0.471012	4.611751
CPNE1	copine 1(CPNE1)	2.294509	1.162838	0.471012	4.620938
CSNK1G2	casein kinase 1 gamma 2(CSNK1G2)	2.284304	1.243211	0.471012	4.818917
ZMIZ1	zinc finger MIZ-type containing 1(ZMIZ1)	2.276242	1.30078	0.471012	4.97838
BCL2L2	BCL2 like 2(BCL2L2)	-4.20093	0.590699	2.95965	1.272802
FRS2	fibroblast growth factor receptor substrate 2(FRS2)	-3.588	0.758863	8.609892	1.324519
MN1	MN1 proto-oncogene, transcriptional regulator(MN1)	-3.44358	0.599971	8.609892	1.241289
TENM1	teneurin transmembrane protein 1(TENM1)	-3.44281	0.538449	8.609892	1.240769
EPHA3	EPH receptor A3(EPHA3)	-3.17444	0.549703	12.58463	1.060235
LRP1B	LDL receptor related protein 1B(LRP1B)	-3.11457	0.585751	12.58463	1.035996
KALRN	kalirin RhoGEF kinase(KALRN)	-3.09245	0.62743	12.58463	1.030642
GHR	growth hormone receptor(GHR)	-3.05209	0.550926	12.58463	1.027055
PCLO	piccolo presynaptic cytomatrix protein(PCLO)	-3.03007	0.481763	12.58463	1.028904
PSD3	pleckstrin and Sec7 domain containing 3(PSD3)	-3.01253	0.623461	12.58463	1.032513
CEP85L	centrosomal protein 85 like(CEP85L)	-2.89409	0.742287	12.58463	1.119013
PRKG2	protein kinase cGMP-dependent 2(PRKG2)	-2.87487	0.614283	12.58463	1.145461
CPS1	carbamoyl-phosphate synthase 1(CPS1)	-2.83362	0.642798	12.58463	1.216554
DIRAS3	DIRAS family GTPase 3(DIRAS3)	-2.82822	0.513463	12.58463	1.227403
CYP2C19	cytochrome P450 family 2 subfamily C member 19(CYP2C19)	-2.82297	0.558933	12.58463	1.238322
AKAP6	A-kinase anchoring protein 6(AKAP6)	-2.81811	0.597498	12.58463	1.248753
CD28	CD28 molecule(CD28)	-2.81278	0.674816	12.58463	1.260564
GAS1	growth arrest specific 1(GAS1)	-2.80429	0.663227	12.58463	1.280149
CXXC4	CXXC finger protein 4(CXXC4)	-2.7403	0.644357	12.58463	1.461557

TNFRSF6B	TNF receptor superfamily member 6b(TNFRSF6B)	-2.72389	0.707589	12.58463	1.518381
DST	dystonin(DST)	-2.70518	0.740299	12.58463	1.58875
GATA2	GATA binding protein 2(GATA2)	-2.69222	0.65989	12.58463	1.641073
EGF	epidermal growth factor(EGF)	-2.68801	0.61568	12.58463	1.658695
APC	APC regulator of WNT signaling pathway(APC)	-2.67771	0.857616	12.58463	1.703235
AK5	adenylate kinase 5(AK5)	-2.67748	0.608442	12.58463	1.704254
NGF	nerve growth factor(NGF)	-2.66663	0.570758	12.58463	1.753343
RYR3	ryanodine receptor 3(RYR3)	-2.66565	0.609378	12.58463	1.75789
NAV3	neuron navigator 3(NAV3)	-2.63912	0.653511	12.58463	1.888166
CEBPE	CCAAT enhancer binding protein epsilon(CEBPE)	-2.60589	0.591887	12.58463	2.071678
LHFPL6	(LHFPL Tetraspan Subfamily Member 6)	-2.59756	0.70585	12.58463	2.121458
EYA2	EYA transcriptional coactivator and phosphatase 2(EYA2)	-2.59678	0.520978	12.58463	2.126206
FGF13	fibroblast growth factor 13(FGF13)	-2.59633	0.636337	12.58463	2.128928
AKAP12	A-kinase anchoring protein 12(AKAP12)	-2.57225	0.648332	12.58463	2.282142
ACVR1C	activin A receptor type 1C(ACVR1C)	-2.56978	0.64261	12.58463	2.298622
ANGPT1	angiopoietin 1(ANGPT1)	-2.56653	0.62152	12.58463	2.320546
NF217-AS1	(RN217 Antisense RNA 1 (Head To Head))	-2.56471	0.650292	12.58463	2.332931
NTRK2	neurotrophic receptor tyrosine kinase 2(NTRK2)	-2.53319	0.627983	12.58463	2.559963
LIFR	LIF receptor subunit alpha(LIFR)	-2.5242	0.733447	13.49002	2.629169
TSHR	thyroid stimulating hormone receptor(TSHR)	-2.50676	0.570755	13.49002	2.769494
AR	androgen receptor(AR)	-2.49897	0.694167	13.49002	2.83471
OLIG1	oligodendrocyte transcription factor 1(OLIG1)	-2.4967	0.797935	13.49002	2.854028
IGF1	insulin like growth factor 1(IGF1)	-2.47757	0.565687	13.49002	3.022318
DACH2	dachshund family transcription factor 2(DACH2)	-2.47524	0.639862	13.49002	3.043503
MIPOL1	mirror-image polydactyly 1(MIPOL1)	-2.47313	0.675801	13.49002	3.062875
DLEC1	DLEC1 cilia and flagella associated protein(DLEC1)	-2.46997	0.596392	13.49002	3.092057
ARHGAP20	Rho GTPase activating protein 20(ARHGAP20)	-2.44219	0.637628	13.49002	3.360578
PBX1	PBX homeobox 1(PBX1)	-2.43945	0.69123	13.49002	3.388241
CDH1	cadherin 1(CDH1)	-2.43492	0.622069	13.49002	3.43451
PRSS8	serine protease 8(PRSS8)	-2.43105	0.65786	13.49002	3.474555
ERCC6	ERCC excision repair 6, chromatin remodeling factor(ERCC6)	-2.42417	0.830221	13.49002	3.546831
PLCB1	phospholipase C beta 1(PLCB1)	-2.39966	0.725392	13.49002	3.815793
ELOVL2	ELOVL fatty acid elongase 2(ELOVL2)	-2.39545	0.68298	13.49002	3.863922
ATRNL1	attractin like 1(ATRNL1)	-2.39475	0.543071	13.49002	3.871938
FGF9	fibroblast growth factor 9(FGF9)	-2.39013	0.702062	13.49002	3.92555
CDKN2B	cyclin dependent kinase inhibitor 2B(CDKN2B)	-2.37869	0.774213	13.49002	4.060955
TGFB2	transforming growth factor beta 2(TGFB2)	-2.37162	0.780934	13.49002	4.146806
CCK	cholecystokinin(CCK)	-2.35973	0.605703	13.49002	4.294787
CHD6	chromodomain helicase DNA binding protein 6(CHD6)	-2.3523	0.863517	13.49002	4.389622
BCL9	BCL9 transcription coactivator(BCL9)	-2.3516	0.817822	13.49002	4.398624
ID4	inhibitor of DNA binding 4(ID4)	-2.32669	0.641668	13.49002	4.730832
RGS7	regulator of G protein signaling 7(RGS7)	-2.31812	0.647271	13.49002	4.850112
OMD	osteomodulin(OMD)	-2.31551	0.6327	13.49002	4.886913
SOX11	SRY-box transcription factor 11(SOX11)	-2.31068	0.804543	13.49002	4.955625

Suppl. Table S5.2. Significantly enriched functional terms with FDR ≤0.05 for 384 genes upregulated in PT-DLBCL with mutated (vs. wild-type) *MYD88* RNA

Category	Terms associated with upregulated 384 genes	Count	P Value	Genes	Fold Enrichment	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0045893~positive regulation of DNA-templated transcription	63	9.55E-24	PHB1, AHR, ETS1, TNF, CHEK2, RPS6KA1, CREB3L2, PIM1, TRIM24, AKT1, EP300, TP63, CDK5RAP2, MAP2K3, MAP2K1, MAP2K2, PRKCB, NCOA4, TFE3, TFE3, AIP, ARID1A, RUNX1, DNMT2, CCNA2, CREB1, IRF4, ELF4, TBL1XR1, THRAP3, IRF1, NUP98, TP53, MAX, HDAC1, MLLT1, PSEN1, BCL10, HIF1A, RELA, EP400, SPP1, E2F1, VHL, MAP2K7, BRD4, CD74, NPM1, CREBBP, XRCC6, FUS, STAT1, CNBP, STAT3, HMGA1, NFATC2, FLI1, NFKB1, SP1, BCL3, CDK2, TACC1, PICALM	4.564601	2.91E-20	2.72E-20
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription by RNA polymerase II	82	1.75E-22	RB1, TOP2A, SMARCB1, DDX3X, KDM1A, AHR, HMGB1, IKZF3, ETS1, TNF, CDC73, PPP3CA, RPS6KA3, ZMIZ1, RPS6KA1, CREB3L2, AKT1, EP300, TP63, GTF2I, SS18, MEF2B, TCF12, TFE3, TFE3, MRTFA, PAX5, ETV6, RUNX1, SFPO, PKM, CREB1, TFDPI, IRF4, ELF4, TBL1XR1, THRAP3, IRF1, IRF8, RAF1, TP53, HDAC3, CBFB, MAX, PRKDC, HDAC1, SRF, NR1I3, DOT1L, HIF1A, RELA, PCBP1, E2F1, CAMTA1, STAT6, SF3B1, MEF2D, BRD4, MAPK3, NPM1, ZNF384, XBP1, CREBBP, XRCC6, HSPA5, BCL11A, STAT1, CNBP, STAT3, HMGA1, NFATC2, FLI1, NFKB1, NFKB2, NFKBIA, SNW1, SP1, POU2AF1, BCL3, TCEA1, CDK12, MYD88	3.372686	2.67E-19	2.49E-19
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription by RNA polymerase II	67	1.15E-19	RB1, BTG2, KDM5C, PHB1, KDM1A, HMGB1, PHF6, TNF, CDC73, CCND3, SIN3A, EP300, TP63, EED, PAX5, ETV6, FOXF1, RUNX1, NCOR2, DUSP22, SFPO, CCNE1, TBL1XR1, SARNP, IRF8, EZR, TP53, DNMT1, HDAC3, PCNA, CBFB, MAX, HDAC1, NR1I3, PSEN1, HDAC6, RELA, AURKB, CUX1, TPR, NSD2, E2F1, STAT6, VHL, SUZ12, XBP1, CREBBP, BCL11A, STAT1, CNBP, STAT3, IRF2BP2, NFATC2, NFKB1, H1-3, H1-2, H1-4, SNW1, CDK6, BCL6, CNOT2, HNRNPAB21, CDK2, CALR, TRIM33, FRK, EZH2	3.594184	1.17E-16	1.09E-16
GOTERM_BP_DIRECT	GO:0016310~phosphorylation	53	6.52E-19	GSK3B, ARAF, PIK3CD, BUB1B, CKS1B, RPS6KA3, STK11, PLAU, CHEK2, AKT2, RPS6KA1, CHEK1, AKT1, PRKACA, SKP2, JAK3, IKBKE, JAK1, PDK1, MAP2K3, MAP2K1, MAP2K2, CSNK2A1, SYK, PRKCB, PRKCD, TYK2, PKM, MELK, PRKAR1A, BTK, TOP1, RAF1, PRKDC, AK2, TTK, AURKB, AURKA, PAK1, MAPK1, MAP2K7, MAPK3, LYN, GIT2, STAT3, MTOR, WEE1, CDK4, CDK2, PI4KA, CDK1, CDK12, FRK	4.325377	4.97E-16	4.65E-16
GOTERM_BP_DIRECT	GO:0006468~protein phosphorylation	40	8.60E-18	GSK3B, PRKDC, PIK3CD, AURKB, AURKA, PAK1, STK11, CHEK2, CHEK1, RPS6KA1, PIM1, AKT1, MAPK1, PRKACA, JAK3, JAK1, MAPK3, PDK1, LYN, MAP2K1, SYK, CSNK2A1, PRKCB, IGF1BP3, PRKCD, TYK2, MTOR, WEE1, CREB1, MELK, CDK6, CCNE1, CDK4, CDK2, CDK1, BTK, CDK12, RAF1, FRK, CSNK1G2, H2AX, TOP2A, BTG2, FH, MRE11, PRKDC, PSEN1, CBL, CCAR2, RPTOR, PAK1, STK11, CHEK2, CHEK1, MAPK1, TP63, MCL1, MAPK3, BRD4, LYN, CSNK2A1, PRMT1, FANCL, PRKCD, NFATC2, CIP2A, FANGC, MTOR, FOXF1, DDB2, RAD51, BCL6, ERCC2, BCL3, CDK1, TP53	5.495711	5.24E-15	4.90E-15
GOTERM_BP_DIRECT	GO:0006974~DNA damage response	36	2.32E-17	GSK3B, MRE11, HDAC3, DDX3X, HSP90AB1, BCL2A1, TFRC, PRKDC, HDAC1, ARAF, PSEN1, CBL, TNF, RELA, CDC73, AURKA, RPS6KA3, CCND2, SIN3A, RPS6KA1, PIM1, AKT1, VHL, MCL1, CD74, NPM1, XBP1, HSPA5, SOD2, MMP9, MTOR, NFKB1, UFM1, CREB1, BCL3, CDK1, RAF1, MNAT1, TP53, CD44, BIRC3, MAD2L1	6.057813	1.18E-14	1.10E-14
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	42	8.92E-15	BTG2, FH, FEN1, MRE11, DOT1L, HMGB1, RECQL4, PTTG1, POLD1, CHEK1, EP400, MUTHY, FANCL, NPM1, RRM1, FANCL, NONO, MLH1, SMC1A, FANGC, DDB2, RAD51, RAD51C, MSH2, ERCC1, RPA3, CDK2, CDK1, MNAT1	4.279501	3.89E-12	3.63E-12
GOTERM_BP_DIRECT	GO:0006281~DNA repair	29	3.72E-13	TOP2A, CREBBP, KDM5C, CSNK2A1, PRKDC, AHR, MTOR, CCAR2, NFKB2, SFPO, SP1, SIN3A, CDK1, EP300, TOP1, TP53, EZH2	5.610977	1.42E-10	1.32E-10
GOTERM_BP_DIRECT	GO:0048511~rhythmic process	17	1.94E-12		11.11664	6.58E-10	6.15E-10
GOTERM_BP_DIRECT	GO:0050853~B cell receptor signaling pathway	15	7.80E-12	LYN, SYK, PRKCB, NFATC2, PIK3CD, NFKB1, CD79B, NFKBIA, CD79A, CD19, BTK, PLCG2, MAPK1, GRB2, PTPN6	12.7032	2.38E-09	2.22E-09
GOTERM_BP_DIRECT	GO:0035556~intracellular signal transduction	34	1.95E-11	YWHAE, GSK3B, DDX3X, TFRC, RASGRF1, RASAL1, PSEN1, RELA, RPS6KA3, PAK1, TCL1A, PPP2R1A, AKT2, INPP5D, CHEK1, RPS6KA1, PLCG2, AKT1, MAPK1, RAC1, JAK3, JAK1, MAPK3, SS18, SYK, PRKCB, PRKCD, PTPN11, TYK2, MELK, PRKAR1A, BTK, PTPN6, ARHGEF7	4.065809	5.42E-09	5.06E-09
GOTERM_BP_DIRECT	GO:0051301~cell division	32	2.16E-11	RB1, CLTC, CLTA, BUB1B, CDC73, AURKB, AURKA, CKS1B, CCND3, CCND2, PTTG1, CHEK2, TPR, ZNF207, NDE1, SMC1A, CDC25A, NDC80, EML4, CCNA2, WEE1, STAG2, CDK6, CCNE1, CDK4, REEP3, CDK2, CDK1, TACC3, TACC1, MAPRE1, MAD2L1	4.293792	5.48E-09	5.12E-09
GOTERM_BP_DIRECT	GO:0000082~G1/S transition of mitotic cell cycle	15	5.72E-11	RB1, CDC25A, CCNA2, PPP3CA, CCND3, CDK6, CCND2, CCNE1, CDK4, CDK2, E2F1, CDK1, SKP2, MNAT1, EZH2	11.06993	1.34E-08	1.25E-08
GOTERM_BP_DIRECT	GO:0031507~heterochromatin formation	14	1.49E-10	RB1, H2AX, H2AC6, EED, HDAC1, DOT1L, BAZ2A, HMGB1, H2AC16, H2AC17, H2AC11, BCL6, SIN3A, EZH2	11.66509	3.10E-08	2.90E-08
GOTERM_BP_DIRECT	GO:0006338~chromatin remodeling	29	1.52E-10	RB1, KDM5C, SMARCB1, KDM1A, PRKDC, HDAC1, BAZ2A, AURKA, PAK1, CHEK1, NSD2, EP400, SF3B1, TP63, BRD4, SS18, NPM1, CREBBP, PRKCB, PRMT1, HUWE1, ARID1A, SFPO, IRF4, CARM1, CDK2, CDK1, TOP1, MYD88	4.367729	3.10E-08	2.90E-08
GOTERM_BP_DIRECT	GO:0007165~signal transduction	59	3.18E-10	YWHAE, PHB1, CSF3R, RASGRF1, ARAF, PIK3CD, HMGB1, RPS6KA3, CCND3, STK11, PLAU, AKT2, RPS6KA1, RAC2, AKT1, RAC1, MAP2K3, MAP2K1, CSNK2A1, SYK, FNBP1, PRKCB, PRKCD, RHOA, DNMT2, DUSP22, CREB1, RAF1, ARHGEF7, CSNK1G2, LRRC59, NR1I3, RASAL1, CBL, RASGRP1, HIF1A, NDRG1, CD79B, SH3BP1, INPP5D, SPP1, LPXN, MAPK1, STAT6, MAP2K7, LYN, NPM1, CREBBP, CD70, STAT3, NFKB1, NFKB2, CDK6, SP1, CDK4, CDK2, PI4KA, GRB2, MYD88	2.458001	6.06E-08	5.66E-08
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	35	3.53E-10	GSK3B, DNMT1, PHB1, DDX3X, TFRC, HDAC1, PIK3CD, PSEN1, ETS1, HIF1A, TNF, RELA, PPP3CA, E2F1, PLCG2, TRIM24, AKT1, IKBKE, CD74, MAP2K1, MAP2K2, BCL11A, TCF12, STAT3, NFATC2, MSN, MTOR, CDK6, BCL6, SP1, CDK1, CALR, EZR, TP53, MYD88	3.552238	6.33E-08	5.91E-08
GOTERM_BP_DIRECT	GO:0018105~peptidyl-serine phosphorylation	19	1.54E-09	GSK3B, CSNK2A1, PRKCB, PRKDC, TTK, MTOR, AURKA, RPS6KA3, AKT2, RPS6KA1, CDK2, CDK1, AKT1, MAPK1, TOP1, PRKACA, IKBKE, CSNK1G2, CYFIP2, AHYCYL1, FAF1, TNFAIP3, BUB1B, AHR, BCL10, PSEN1, AURKA, PAK1, INPP5D, CHEK1, PIM1, MAPK1, EP300, MAP2K7, MEF2D, TP63, MAPK3, XBP1, CSNK2A1, PRKCB, IGF1BP3, PRKCD, MMP9, NFKB1, NFKBIA, MELK, IRF1, ERCC2, CDK1, BAX, RAF1, TP53, MYD88, BIRC3	6.251809	2.61E-07	2.44E-07
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	36	5.03E-09	RB1, KDM5C, PHB1, HDAC3, SET, KDM1A, HDAC1, AHR, IKZF1, TNF, CCAR2, RELA, HDAC6, SIN3A, E2F1, TRIM24, TP63, XRCC6, EED, NONO, HMGA1, FOXF1, NCOR2, SFPO, SNW1, BCL6, IRF1, BCL3, SRSF2, CALR, PFDN5, TP53, TRIM33, RCOR1, EZH2	3.13617	8.08E-07	7.55E-07
GOTERM_BP_DIRECT	GO:0045892~negative regulation of DNA-templated transcription	35	7.39E-09		3.155478	1.13E-06	1.05E-06

GOTERM_BP_DIRECT	GO:0034644~cellular response to UV	12	1.00E-08	NPM1, CREBBP, PCNA, KDM1A, POLD1, PRKCD, EP300, BAX, TP53, CDC25A, AURKB, DDB2	10.87572	1.39E-06	1.30E-06
GOTERM_BP_DIRECT	GO:0090398~cellular senescence	12	1.00E-08	MAP2K3, H2AX, MAP2K1, NPM1, ZMIZ1, SRF, CDK2, PRKCD, CALR, MAP2K7, TP53, TP63	10.87572	1.39E-06	1.30E-06
GOTERM_BP_DIRECT	GO:000086~G2/M transition of mitotic cell cycle	11	4.04E-08	CCNA2, WEE1, MELK, CHEK2, CHEK1, CDK2, CDK1, SKP2, CDC25A, AURKA, DNM2	11.14229	5.36E-06	5.01E-06
GOTERM_BP_DIRECT	GO:0007249~canonical NF-kappaB signal transduction	11	5.96E-08	NFKBIA, CREBBP, BCL3, EP300, AKT1, BCL10, CARD11, RELA, NFKB1, NFKB2, BIRC3	10.72182	7.57E-06	7.07E-06
GOTERM_BP_DIRECT	GO:0042981~regulation of apoptotic process	20	9.07E-08	HSP90AA1, PHB1, STAT1, ETS1, IKZF3, BCL3, EP400, TRIM24, BAX, AKT1, PTPN6, NF2, CALR, SKP2, RAF1, JAK3, TP53, CARD11, MCL1, BIRC3	4.571654	1.08E-05	1.01E-05
GOTERM_BP_DIRECT	GO:0007049~cell cycle	24	9.24E-08	RB1, FANCI, SMARCB1, CSNK2A1, PRCC, PRKCD, CLTA, AHR, IKZF1, MKI67, CCAR2, CDC73, CKS1B, RPS6KA3, STK11, TFDP1, RPS6KA1, CHEK1, PIM1, EP300, MAPK1, TP53, TP63, MAPK3	3.826643	1.08E-05	1.01E-05
GOTERM_BP_DIRECT	GO:0048009~insulin-like growth factor receptor signaling pathway	9	1.26E-07	MAP2K1, MAP2K2, ERCC1, ERCC2, MAPK1, AKT1, GRB2, RAF1, MAPK3	14.52929	1.42E-05	1.33E-05
GOTERM_BP_DIRECT	GO:0006606~protein import into nucleus	14	1.49E-07	NUP214, POM121, NUP107, SYK, STAT3, NUP93, NFKBIA, PPP3CA, TPR, BCL3, AKT1, NUP98, TP53, KPNB1	6.759211	1.62E-05	1.51E-05
GOTERM_BP_DIRECT	GO:0038061~non-canonical NF-kappaB signal transduction	8	1.78E-07	NFKBIA, CREBBP, AKT1, BCL10, RELA, NFKB1, NFKB2, BIRC3	17.96859	1.87E-05	1.75E-05
GOTERM_BP_DIRECT	GO:0051726~regulation of cell cycle	20	2.18E-07	RB1, NUP214, HSP90AB1, CSNK2A1, PRCC, STAT3, STK11, TFDP1, CDK6, CDK4, IRF1, AKT2, EP400, BAX, NF2, CDK12, SKP2, PRKACA, TP53, BIRC3	4.322986	2.22E-05	2.07E-05
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	23	3.41E-07	TOP2A, DDX3X, BCL2A1, PRKDC, FAF1, IGFBP3, HMGB1, BCL10, PSEN1, TNF, MMP9, CCAR2, DNM2, PTPA, MELK, BCL6, INPP5D, E2F1, IRF8, BAX, ARHGEF7, TP53, MCL1	3.689978	3.35E-05	3.13E-05
GOTERM_BP_DIRECT	GO:0008630~intrinsic apoptotic signaling pathway in response to DNA damage	10	5.04E-07	BCL2A1, PRKDC, CHEK2, E2F1, BAX, MLH1, SOD2, TNF, IKBKE, MCL1	10.12935	4.80E-05	4.49E-05
GOTERM_BP_DIRECT	GO:0006357~regulation of transcription by RNA polymerase II	61	5.51E-07	RB1, SMARCB1, KDM1A, AHR, HMGB1, IKZF1, IKZF3, ETS1, ZMIZ1, CREB3L2, TP63, SS18, PRKCB, TCF12, TFE3, TFEB, PAX5, ARID1A, RHOA, ETV6, FOXP1, RUNX1, CREB1, TFDP1, PRKAR1A, IRF4, ELF4, TBL1XR1, IRF1, CTDSP2, IRF8, TP53, CBFB, MAX, HDAC1, HIF1A, RELA, CUX1, E2F1, MAPK1, CAMTA1, STAT6, BRD4, ZNF384, XBP1, BCL11A, FUS, STAT1, IRF2BP2, NFATC2, SOD2, FLI1, NFKB1, SNW1, SP1, CNOT2, ERCC2, CDK1, MNAT1, RCOR1	1.962167	5.06E-05	4.73E-05
GOTERM_BP_DIRECT	GO:0001934~positive regulation of protein phosphorylation	18	5.64E-07	LYN, MAP2K3, CD74, XBP1, HSP90AA1, HDAC3, TFRC, ARAF, PSEN1, RASGRP1, TNF, MMP9, CCND3, PAK1, CCND2, AKT1, RAC1, RAF1	4.513953	5.06E-05	4.73E-05
GOTERM_BP_DIRECT	GO:0060397~growth hormone receptor signaling pathway via JAK-STAT	6	6.08E-07	LYN, STAT3, STAT6, TYK2, JAK3, JAK1	30.99581	5.30E-05	4.95E-05
GOTERM_BP_DIRECT	GO:0032755~positive regulation of interleukin-6 production	13	7.11E-07	CD74, XBP1, SYK, STAT3, PTPN11, HMGB1, BCL10, TNF, RELA, POU2AF1, BTK, PLCG2, MYD88	6.520155	6.02E-05	5.63E-05
GOTERM_BP_DIRECT	GO:0018107~peptidyl-threonine phosphorylation	10	9.85E-07	GSK3B, STK11, CSNK2A1, PRKDC, CAD, CHEK1, PRKCD, CDK1, MAPK1, AKT1	9.39267	7.98E-05	7.46E-05
GOTERM_BP_DIRECT	GO:0071222~cellular response to lipopolysaccharide	17	9.94E-07	MAP2K3, XBP1, SERPINE1, TNFAIP3, HMGB1, BCL10, TNF, MMP9, RHOA, RELA, NFKB1, CDC73, SLC7A5, CDK4, IRF8, MAP2K7, MYD88	4.597983	7.98E-05	7.46E-05
GOTERM_BP_DIRECT	GO:0030183~B cell differentiation	12	1.28E-06	CD79B, CD79A, SYK, MSH2, PLCG2, EP300, PIK3CD, PAX5, IKZF3, JAK3, CARD11, EZH2	6.887958	1.00E-04	9.34E-05
GOTERM_BP_DIRECT	GO:1901796~regulation of signal transduction by p53 class mediator	9	1.44E-06	STK11, CHEK2, CHEK1, TRIM24, EP300, AKT1, MTOR, AURKB, AURKA	10.81249	1.10E-04	1.03E-04
GOTERM_BP_DIRECT	GO:0010629~negative regulation of gene expression	21	2.83E-06	RB1, GSK3B, DNMT1, DDX3X, HDAC1, STAT3, PSEN1, HIF1A, TNF, NFKB1, AURKA, FOXP1, SLC7A5, PPP3CA, PRKAR1A, CPNE1, CDK1, AKT1, VHL, RCOR1, PICALM	3.499527	2.10E-04	1.96E-04
GOTERM_BP_DIRECT	GO:0060333~type II interferon-mediated signaling pathway	6	2.96E-06	STAT1, IRF1, TYK2, RAF1, TP53, JAK1	23.84293	2.15E-04	2.01E-04
GOTERM_BP_DIRECT	GO:0031663~lipopolysaccharide-mediated signaling pathway	8	3.25E-06	LYN, NFKBIA, PLCG2, MAPK1, AKT1, BCL10, MYD88, MAPK3	12.15522	2.30E-04	2.15E-04
GOTERM_BP_DIRECT	GO:0006366~transcription by RNA polymerase II	18	3.47E-06	RB1, XBP1, HDAC3, CBFB, SRF, NFATC2, PAX5, ETS1, NFKB1, TFDP1, BCL6, IRF1, ERCC2, TRIM24, TCEA1, CDK12, TP63, GTF2I	3.956912	2.40E-04	2.25E-04
GOTERM_BP_DIRECT	GO:0035855~megakaryocyte development	7	3.81E-06	SRF, ABI1, EP300, PTPN6, PTPN11, WASF2, FLI1	15.72251	2.58E-04	2.41E-04
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell population proliferation	25	4.34E-06	BTG2, PHB1, SMARCB1, SRF, ETS1, NDRG1, CDC73, STK11, VHL, LYN, NPM1, MAP2K1, H2AC6, IGFBP3, STAT3, HMGA1, SOD2, CDK6, IRF1, ABI1, STRN, PTPN6, NF2, RAF1, TP53	2.975788	2.87E-04	2.69E-04
GOTERM_BP_DIRECT	GO:0006355~regulation of DNA-templated transcription	38	4.56E-06	RB1, KDM5C, PHB1, BAZ2A, AHR, AFF3, HIF1A, CCAR2, RELA, CKS1B, CHEK2, NSD2, ZNF207, E2F1, STAT6, VHL, BRD4, CREBBP, UTP4, FUS, CNBP, NONO, STAT3, TFEB, HMGA1, NFATC2, NFKB2, DNM2, SFPO, TFDP1, SP1, EWSR1, CARM1, CNOT2, CALR, PFDN5, TP53, EZH2	2.287958	2.96E-04	2.77E-04
GOTERM_BP_DIRECT	GO:0007059~chromosome segregation	12	5.39E-06	TOP2A, CENPU, DDX3X, STAG2, PPP2R1B, PPP2R1A, NDE1, ERCC2, TTK, TOP1, NDC80, CDK5RAP2	5.960733	3.36E-04	3.14E-04
GOTERM_BP_DIRECT	GO:0042752~regulation of circadian rhythm	10	5.40E-06	TOP2A, GSK3B, SFPO, HDAC3, PRKDC, NONO, CDK1, MTOR, CCAR2, EZH2	7.710401	3.36E-04	3.14E-04
GOTERM_BP_DIRECT	GO:0042127~regulation of cell population proliferation	14	5.70E-06	FANCL, STAT1, STAT3, TPD52L2, DUSP22, NFKBIA, CCND3, BCL6, PLAU, RPA3, CHEK1, STAT6, EPS15, EZH2	4.91997	3.48E-04	3.25E-04

GOTERM_BP_DIRECT	GO:0014044~Schwann cell development	6	6.69E-06	MAP2K1, MAP2K2, MAPK1, GRB2, RAF1, MAPK3	20.66387	4.00E-04	3.74E-04
GOTERM_BP_DIRECT	GO:0006099~tricarboxylic acid cycle	8	7.13E-06	FH, SDHAF2, MDH1, IDH1, IDH2, SDHC, SDHA, SDHB	10.87572	4.18E-04	3.91E-04
GOTERM_BP_DIRECT	GO:0009410~response to xenobiotic stimulus	18	9.76E-06	LYN, SS18, HSP90AA1, PRKCB, STAT1, NFATC2, AHR, TYMS, SOD2, TNF, RELA, RPTOR, CREB1, CDK4, CDK1, CALR, TOP1, TP53	3.660923	5.61E-04	5.25E-04
GOTERM_BP_DIRECT	GO:0019221~cytokine-mediated signaling pathway	14	1.02E-05	CSF3R, STAT3, PTPN11, TYK2, CBL, RELA, IL21R, AKT1, PTPN6, STAT6, PRKACA, JAK3, CD44, JAK1	4.666036	5.75E-04	5.37E-04
GOTERM_BP_DIRECT	GO:0033138~positive regulation of peptidyl-serine phosphorylation	10	1.11E-05	RPTOR, PAK1, TCL1A, TFRC, ARAF, AKT1, RAF1, TNF, CD44, HDAC6	7.076669	6.14E-04	5.74E-04
GOTERM_BP_DIRECT	GO:0010971~positive regulation of G2/M transition of mitotic cell cycle	7	1.31E-05	RRM1, RAD51C, SIN3A, CDK4, CDK1, CDC25A, BRD4	12.91492	7.13E-04	6.66E-04
GOTERM_BP_DIRECT	GO:0043154~negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	8	1.43E-05	RPS6KA3, DDX3X, CSNK2A1, RPS6KA1, AKT1, RAF1, TNF, CD44	9.83994	7.50E-04	7.01E-04
GOTERM_BP_DIRECT	GO:0042307~positive regulation of protein import into nucleus	8	1.43E-05	XBP1, HSP90AA1, HDAC3, TPR, PRKCD, CDK1, EP300, PSEN1	9.83994	7.50E-04	7.01E-04
GOTERM_BP_DIRECT	GO:0038133~ERBB2-ERBB3 signaling pathway	5	1.60E-05	MAP2K1, MAP2K2, MAPK1, RAF1, MAPK3	28.69983	8.25E-04	7.71E-04
GOTERM_BP_DIRECT	GO:0006302~double-strand break repair	10	1.72E-05	H2AX, FEN1, MRE11, CSNK2A1, MSH2, PRKDC, CHEK2, ERCC1, NSD2, TP53	6.70905	8.74E-04	8.17E-04
GOTERM_BP_DIRECT	GO:0045597~positive regulation of cell differentiation	9	1.91E-05	GSK3B, RPS6KA3, SMARCB1, HSP90AB1, SRF, RPS6KA1, NF2, VHL, ARID1A	7.748953	9.40E-04	8.78E-04
GOTERM_BP_DIRECT	GO:0021987~cerebral cortex development	10	1.91E-05	H2AX, YWHAE, ATIC, KDM1A, NDE1, TACC3, BAX, TACC1, PAX5, HIF1A	6.623037	9.40E-04	8.78E-04
GOTERM_BP_DIRECT	GO:0006260~DNA replication	11	1.98E-05	RECQL4, RRM1, FEN1, SET, SIN3A, POLD1, RPA3, CHEK1, CDK2, CDK1, TOP1	5.798536	9.51E-04	8.89E-04
GOTERM_BP_DIRECT	GO:0010592~positive regulation of lamellipodium assembly	7	2.00E-05	CDC42, HSP90AA1, CARMIL2, RAC2, RAC1, WASF2, MTOR	12.05393	9.51E-04	8.89E-04
GOTERM_BP_DIRECT	GO:0007094~mitotic spindle assembly checkpoint signaling	7	2.44E-05	TPR, ZNF207, BUB1B, TTK, MNAT1, NDC80, MAD2L1	11.66509	0.001126	0.001052
GOTERM_BP_DIRECT	GO:0045740~positive regulation of DNA replication	7	2.44E-05	CDC42, WEE1, PCNA, FAF1, CDK2, CDK1, CDC25A	11.66509	0.001126	0.001052
GOTERM_BP_DIRECT	GO:0090170~regulation of Golgi inheritance	4	2.82E-05	MAP2K1, MAP2K2, MAPK1, MAPK3	51.65969	0.001281	0.001198
GOTERM_BP_DIRECT	GO:0032757~positive regulation of interleukin-8 production	9	3.09E-05	CD74, SYK, STAT3, SERPINE1, BCL10, HMGB1, TNF, RELA, MYD88	7.264643	0.001386	0.001295
GOTERM_BP_DIRECT	GO:0046777~protein autophosphorylation	13	3.33E-05	LYN, GSK3B, CAD, MTOR, AURKB, AURKA, PAK1, STK11, MELK, CHEK2, PIM1, AKT1, CDK12	4.507221	0.001473	0.001376
GOTERM_BP_DIRECT	GO:0090307~mitotic spindle assembly	8	3.52E-05	STAG2, CHEK2, CLTC, ZNF207, SMC1A, RHOA, AURKB, KPNB1	8.609948	0.001502	0.001404
GOTERM_BP_DIRECT	GO:0051973~positive regulation of telomerase activity	7	3.55E-05	HSP90AA1, HSP90AB1, POT1, MAPK1, MAP2K7, AURKB, MAPK3	10.95812	0.001502	0.001404
GOTERM_BP_DIRECT	GO:0042771~intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	7	3.55E-05	SNW1, MSH2, CHEK2, BCL3, EP300, TP53, TP63	10.95812	0.001502	0.001404
GOTERM_BP_DIRECT	GO:0002218~activation of innate immune response	7	4.24E-05	XRCC6, SFPQ, HSP90AA1, SIN3A, PRKDC, NONO, HMGB1	10.63582	0.001746	0.001632
GOTERM_BP_DIRECT	GO:0045648~positive regulation of erythrocyte differentiation	7	4.24E-05	STAT1, PRKDC, PRMT1, INPP5D, STAT3, ETS1, HIF1A	10.63582	0.001746	0.001632
GOTERM_BP_DIRECT	GO:0060324~face development	6	5.25E-05	MAP2K1, MAP2K2, SRF, MAPK1, RAF1, MAPK3	14.08901	0.002134	0.001995
GOTERM_BP_DIRECT	GO:0031647~regulation of protein stability	10	5.53E-05	CTSA, XBP1, HDAC3, TRIM24, MAPK1, NF2, NDC80, CCAR2, HDAC6, AURKA	5.804459	0.002189	0.002046
GOTERM_BP_DIRECT	GO:0007265~Ras protein signal transduction	10	5.53E-05	RB1, CCNA2, NRAS, RASGRF1, CDK2, ARAF, GRB2, RAF1, TP53, RASGRP1	5.804459	0.002189	0.002046
GOTERM_BP_DIRECT	GO:0043276~anoikis	5	5.99E-05	STK11, TFDP1, E2F1, AKT1, MTOR	21.52487	0.002284	0.002135
GOTERM_BP_DIRECT	GO:0031334~positive regulation of protein-containing complex assembly	8	5.99E-05	GSK3B, LGALS3, SYK, TFRC, FAF1, BAX, TNF, RHOA	7.947644	0.002284	0.002135
GOTERM_BP_DIRECT	GO:0031648~protein destabilization	8	5.99E-05	XBP1, CREBBP, PRKDC, CCDC88C, EP300, CDC73, MTOR, HDAC6	7.947644	0.002284	0.002135
GOTERM_BP_DIRECT	GO:0002223~stimulatory C-type lectin receptor signaling pathway	6	6.60E-05	LYN, PAK1, CREBBP, SYK, PLCG2, EP300	13.47644	0.002485	0.002323
GOTERM_BP_DIRECT	GO:1900087~positive regulation of G1/S	8	6.79E-05	RPTOR, RRM1, CCND3, TFDP1, DDX3X, CCND2, CCNE1, AKT1	7.797688	0.002525	0.00236

GOTERM_BP_DIRECT	transition of mitotic cell cycle GO:0031333~negative regulation of protein-containing complex assembly GO:0048661~positive regulation of smooth muscle cell proliferation	7	6.98E-05	CDC42, GSK3B, DDX3X, HSPA5, EP300, RAF1, HDAC6	9.773454	0.002563	0.002396
GOTERM_BP_DIRECT	GO:0098586~cellular response to virus	8	7.67E-05	PHB1, STAT1, HDAC1, AKT1, MNAT1, TNF, MYD88, FOXP1	7.653287	0.002785	0.002604
GOTERM_BP_DIRECT	GO:1900182~positive regulation of protein localization to nucleus	10	8.50E-05	HSP90AA1, DDX3X, POU2AF1, BAX, TYK2, CALR, HIF1A, IKBKE, NFKB1, JAK1	5.495711	0.00305	0.002851
GOTERM_BP_DIRECT	GO:0000077~DNA damage checkpoint signaling	7	1.10E-04	STK11, CREBBP, TFRC, CDK1, AKT1, TYK2, JAK1	9.040445	0.003845	0.003594
GOTERM_BP_DIRECT	GO:0010332~response to gamma radiation	7	1.10E-04	LYN, H2AX, CHEK2, CHEK1, DOT1L, E2F1, PTPN11	9.040445	0.003845	0.003594
GOTERM_BP_DIRECT	GO:1902895~positive regulation of miRNA transcription	6	1.49E-04	FANCD2, PRKDC, BAX, CBL, SOD2, TP53	11.47993	0.005149	0.004813
GOTERM_BP_DIRECT	GO:0008380~RNA splicing	8	1.52E-04	SRF, STAT3, MRTFA, ETS1, HIF1A, TNF, TP53, RELA	6.887958	0.005149	0.004813
GOTERM_BP_DIRECT	GO:0010507~negative regulation of autophagy	14	1.52E-04	MBNL1, PRMT1, FUS, NONO, U2AF1, CCAR2, LGALS3, PTBP1, SFPQ, U2AF2, THRAP3, SRSF2, CDK12, SF3B1	3.598187	0.005149	0.004813
GOTERM_BP_DIRECT	GO:0000165~MAPK cascade	8	1.68E-04	RPTOR, SLC7A5, STAT3, EP300, AKT1, VHL, MTOR, MCL1	6.775041	0.005603	0.005237
GOTERM_BP_DIRECT	GO:0090399~replicative senescence	11	1.69E-04	MAP2K3, YWHAE, MAP2K1, NRAS, MAP2K2, IGFBP3, ARAF, PTPN6, NF2, RAF1, MAPK3	4.509973	0.005603	0.005237
GOTERM_BP_DIRECT	GO:0038113~interleukin-9-mediated signaling pathway	5	2.07E-04	CHEK2, ERCC1, CHEK1, SERPINE1, TP53	16.14365	0.00679	0.006347
GOTERM_BP_DIRECT	GO:0060440~trachea formation	4	2.36E-04	STAT1, STAT3, JAK3, JAK1	29.51982	0.007571	0.007077
GOTERM_BP_DIRECT	GO:0034097~response to cytokine	4	2.36E-04	MAP2K1, MAP2K2, MAPK1, MAPK3	29.51982	0.007571	0.007077
GOTERM_BP_DIRECT	GO:0071902~positive regulation of protein kinase activity	7	2.43E-04	STAT1, SRF, TYMS, RELA, NFKB1, NFKB2, MCL1	7.861257	0.007714	0.007211
GOTERM_BP_DIRECT	GO:1902042~negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	6	2.50E-04	MAP2K1, MAP2K2, DDX3X, PIM1, RHOA, EZH2	10.33194	0.007784	0.007275
GOTERM_BP_DIRECT	GO:0006914~autophagy	6	2.50E-04	GSK3B, DDX3X, SERPINE1, TNFAIP3, RAF1, ICAM1	10.33194	0.007784	0.007275
GOTERM_BP_DIRECT	GO:0006397~mRNA processing	12	2.57E-04	XBP1, STK11, CHEK2, CLTC, VTI1A, TFE8, HMGB1, TP53, LRPPRC, HDAC6, DNMT2	3.92352	0.007922	0.007405
GOTERM_BP_DIRECT	GO:0030878~thyroid gland development	15	2.63E-04	MBNL1, CPSF6, NONO, U2AF1, CCAR2, LGALS3, PTBP1, SFPQ, FIP1L1, U2AF2, THRAP3, HNRNPA2B1, SRSF2, CDK12, PRKACA	3.215333	0.008011	0.007488
GOTERM_BP_DIRECT	GO:0097421~liver regeneration	6	2.94E-04	MAP2K1, MAP2K2, SRF, MAPK1, RAF1, MAPK3	9.998649	0.008776	0.008204
GOTERM_BP_DIRECT	GO:0048538~thymus development	6	2.94E-04	SLC7A5, PCNA, TYMS, TNF, EZH2, AURKA	9.998649	0.008776	0.008204
GOTERM_BP_DIRECT	GO:0006913~nucleocytoplasmic transport	7	3.08E-04	MAP2K1, MAP2K2, SRF, MAPK1, PSEN1, RAF1, MAPK3	7.533704	0.009031	0.008442
GOTERM_BP_DIRECT	GO:0032760~positive regulation of tumor necrosis factor production	7	3.08E-04	NUP214, NUP93, NPM1, POM121, NUP107, TPR, NUP98	7.533704	0.009031	0.008442
GOTERM_BP_DIRECT	GO:0030154~cell differentiation	10	3.24E-04	SYK, STAT3, BTK, PLCG2, PTPN11, HMGB1, PSEN1, FCGR2B, RASGRP1, MYD88	4.612472	0.009412	0.008797
GOTERM_BP_DIRECT	GO:0007623~circadian rhythm	28	3.29E-04	RB1, GSK3B, DDX3X, NR1I3, RASAL1, ETS1, RASGRP1, AKT1, JAK3, MEF2D, JAK1, MCL1, MEF2B, SYK, SEPTIN2, NDE1, TCF12, STAT3, HUWE1, SEPTIN6, PTPN11, TYK2, FLI1, ETV6, ELF4, CAPRIN1, PTPN6, FRK	2.133438	0.009412	0.008797
GOTERM_BP_DIRECT	GO:0070301~cellular response to hydrogen peroxide	8	3.33E-04	GSK3B, CREB1, THRAP3, NONO, EP300, TOP1, TYMS, TNF	6.07761	0.009412	0.008797
GOTERM_BP_DIRECT	GO:2000641~regulation of early endosome to late endosome transport	8	3.33E-04	PCNA, PRKCD, CDK1, TNFAIP3, STAT6, RELA, HDAC6, EZH2	6.07761	0.009412	0.008797
GOTERM_BP_DIRECT	GO:0032869~cellular response to insulin stimulus	4	3.72E-04	MAP2K1, MAP2K2, MAPK1, MAPK3	25.82984	0.010407	0.009728
GOTERM_BP_DIRECT	GO:0031623~receptor internalization	9	4.71E-04	RB1, XBP1, PKM, STAT1, PRKDC, SP1, AKT2, AKT1, MTOR	4.94614	0.013045	0.012194
GOTERM_BP_DIRECT	GO:0006121~mitochondrial electron transport, succinate to ubiquinone	7	4.79E-04	SYK, TFRC, CLTC, GRB2, EZR, DNMT2, PICALM	6.954188	0.013158	0.012299
GOTERM_BP_DIRECT	GO:0009651~response to salt stress	4	5.50E-04	SDHAF2, SDHC, SDHA, SDHB	22.95986	0.014842	0.013874
GOTERM_BP_DIRECT	GO:0006303~double-strand break repair via nonhomologous end joining	4	5.50E-04	HSP90AA1, BAX, TNF, TP53	22.95986	0.014842	0.013874
GOTERM_BP_DIRECT		6	6.02E-04	XRCC6, MRE11, PRKDC, ERCC1, HMGB1, MLH1	8.609948	0.015959	0.014917

GOTERM_BP_DIRECT	GO:0042113~B cell activation	6	6.02E-04	CD79A, PHB1, PRKCB, BTK, PIK3CD, RASGRP1	8.609948	0.015959	0.014917
GOTERM_BP_DIRECT	GO:0032481~positive regulation of type I interferon production	6	6.85E-04	DDX3X, SYK, IRF1, PLCG2, IKBKE, MYD88	8.377246	0.017853	0.016687
GOTERM_BP_DIRECT	GO:0008340~determination of adult lifespan	6	6.85E-04	MSH2, ERCC1, INPP5D, ERCC2, TP53, TP63	8.377246	0.017853	0.016687
GOTERM_BP_DIRECT	GO:0031398~positive regulation of protein ubiquitination	8	7.13E-04	FANCI, GSK3B, HDAC3, KDM1A, HSPA5, HUWE1, BCL10, BIRC3	5.36724	0.018427	0.017225
GOTERM_BP_DIRECT	GO:0008283~cell population proliferation	11	7.57E-04	SUZ12, MRE11, MELK, ERCC1, STAT3, TACC3, AKT1, TACC1, MKI67, CDC25A, PDK1	3.73853	0.019249	0.017992
GOTERM_BP_DIRECT	GO:0033554~cellular response to stress	5	7.60E-04	MAPK1, RELA, NFKB1, NFKB2, MAPK3	11.74084	0.019249	0.017992
GOTERM_BP_DIRECT	GO:0071803~positive regulation of podosome assembly	4	7.75E-04	MSN, LCP1, TNF, RHOA	20.66387	0.019249	0.017992
GOTERM_BP_DIRECT	GO:0032872~regulation of stress-activated MAPK cascade	4	7.75E-04	MAP2K1, MAP2K2, MAPK1, MAPK3	20.66387	0.019249	0.017992
GOTERM_BP_DIRECT	GO:0036297~interstrand cross-link repair	6	7.77E-04	FANCI, RAD51, FANCL, FANCD2, ERCC1, FANCG	8.156793	0.019249	0.017992
GOTERM_BP_DIRECT	GO:0050821~protein stabilization	14	8.00E-04	CD74, HSP90AA1, PHB1, HSP90AB1, CSNK2A1, PRKCD, CREB1, CHEK2, PIM1, ZNF207, EP300, VHL, CALR, TP53	3.02609	0.019665	0.018382
GOTERM_BP_DIRECT	GO:0046330~positive regulation of JNK cascade	9	8.65E-04	CDC42, DUSP22, CCDC88C, HMGB1, FCGR2B, MAP2K7, TNF, RASGRP1, MYD88	4.513953	0.021109	0.019731
GOTERM_BP_DIRECT	GO:0007507~heart development	13	8.92E-04	MAP2K3, MAP2K1, MAP2K2, MEF2B, PCNA, PRKDC, SRF, CAD, PTPN11, SOD2, EP300, LPXN, MEF2D	3.167811	0.021588	0.020179
GOTERM_BP_DIRECT	GO:0030220~platelet formation	5	9.06E-04	WDR1, SRF, EP300, PTPN6, PTPN11	11.23037	0.02174	0.020321
GOTERM_BP_DIRECT	GO:0006325~chromatin organization	13	9.67E-04	RB1, H4C9, HDAC3, HDAC1, IKZF1, RELA, TBL1XR1, H2BC11, NSD2, H3C2, RCOR1, EZH2, BRD4	3.138205	0.023043	0.021539
GOTERM_BP_DIRECT	GO:0034605~cellular response to heat	7	0.001035	LYN, YWHAE, HSP90AA1, HSP90AB1, TPR, PRKACA, HDAC6	6.026963	0.024466	0.022869
GOTERM_BP_DIRECT	GO:0060020~Bergmann glial cell differentiation	4	0.00105	MAP2K1, MAPK1, PTPN11, MAPK3	18.78534	0.024624	0.023016
GOTERM_BP_DIRECT	GO:0038095~Fc-epsilon receptor signaling pathway	5	0.00107	LYN, SYK, BTK, PLCG2, MAP2K7	10.76243	0.024909	0.023283
GOTERM_BP_DIRECT	GO:0002316~follicular B cell differentiation	3	0.001101	PLCG2, IRF8, FCGR2B	51.65969	0.025434	0.023774
GOTERM_BP_DIRECT	GO:0000724~double-strand break repair via homologous recombination	9	0.00111	H2AX, RECQL4, SFPQ, FEN1, RAD51, RAD51C, MRE11, PPP4C, RPA3	4.345207	0.025449	0.023788
GOTERM_BP_DIRECT	GO:0033209~tumor necrosis factor-mediated signaling pathway	7	0.00113	NFKBIA, STAT1, CD70, TNF, TP53, RELA, BIRC3	5.928161	0.025704	0.024027
GOTERM_BP_DIRECT	GO:0006334~nucleosome assembly	11	0.001175	H2AX, H1-4, NPM1, SET, H4C9, H2BC11, H2BC4, H3C2, H2BC17, H1-3, H1-2	3.529544	0.026548	0.024815
GOTERM_BP_DIRECT	GO:0016477~cell migration	15	0.001195	CARMIL2, SYK, NDE1, NFATC2, PIK3CD, TNFAIP3, MMP9, RHOA, PAK1, SH3BP1, CDK1, LCP1, RAC1, MAPRE1, CD44	2.757634	0.026649	0.02491
GOTERM_BP_DIRECT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	8	0.001197	CD74, SYK, ENPP2, PLCG2, PTPN11, TP53, CD44, MTOR	4.91997	0.026649	0.02491
GOTERM_BP_DIRECT	GO:0032733~positive regulation of interleukin-10 production	6	0.001236	SYK, IRF4, STAT3, BCL3, PLCG2, HMGB1	7.379955	0.027299	0.025517
GOTERM_BP_DIRECT	GO:0001836~release of cytochrome c from mitochondria	5	0.001255	BCL2A1, BAX, SOD2, TP53, MCL1	10.33194	0.027329	0.025545
GOTERM_BP_DIRECT	GO:0008361~regulation of cell size	5	0.001255	RPTOR, CREB1, MSN, RAC1, MTOR	10.33194	0.027329	0.025545
GOTERM_BP_DIRECT	GO:0006289~nucleotide excision repair	6	0.001376	ERCC1, RPA3, ERCC2, MNAT1, TP53, DDB2	7.208328	0.029198	0.027292
GOTERM_BP_DIRECT	GO:0031295~T cell costimulation	6	0.001376	LYN, AKT1, PTPN6, PTPN11, CARD11, MTOR	7.208328	0.029198	0.027292
GOTERM_BP_DIRECT	GO:0010469~regulation of signaling receptor activity	4	0.00138	PLAU, PRKCD, SERPINE1, FCGR2B	17.2199	0.029198	0.027292
GOTERM_BP_DIRECT	GO:0090267~positive regulation of mitotic cell cycle spindle assembly checkpoint	4	0.00138	TPR, NDC80, AURKB, MAD2L1	17.2199	0.029198	0.027292
GOTERM_BP_DIRECT	GO:0051092~positive regulation of NF-kappaB transcription factor activity	10	0.001389	NPM1, TFRC, STAT3, BTK, PLCG2, BCL10, TNF, CARD11, RELA, MYD88	3.77078	0.029198	0.027292
GOTERM_BP_DIRECT	GO:0042552~myelination	7	0.001453	MAP2K1, MAP2K2, MAPK1, GRB2, RAF1, POMGNT1, MAPK3	5.650278	0.030095	0.02813
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	15	0.001458	LYN, XBP1, CARMIL2, HSPA5, STAT3, PIK3CD, SOD2, RHOA, CDC42, PPP3CA, PAK1, PLAU, AKT2, AKT1, EZH2	2.699984	0.030095	0.02813
GOTERM_BP_DIRECT	GO:0045732~positive regulation of protein catabolic process	8	0.001471	GSK3B, HSP90AA1, CSNK2A1, FAF1, TNFAIP3, MSN, EZR, TNF	4.750316	0.030095	0.02813

GOTERM_BP_DIRECT	GO:0006351~DNA-templated transcription	8	0.001471	CCNA2, DNMT1, CDK2, E2F1, TCEA1, BAZ2A, RELA, MAPK3	4.750316	0.030095	0.02813
GOTERM_BP_DIRECT	GO:000132~establishment of mitotic spindle orientation	6	0.001529	HDAC3, NDE1, MAPRE1, NDC80, MAD2L1, CDK5RAP2	7.044503	0.030864	0.02885
GOTERM_BP_DIRECT	GO:0032735~positive regulation of interleukin-12 production	6	0.001529	SYK, IRF1, PLCG2, IRF8, HMGB1, RELA	7.044503	0.030864	0.02885
GOTERM_BP_DIRECT	GO:0030036~actin cytoskeleton organization	13	0.001543	SRF, MRTFA, RHOA, CDC42, PAK1, CAPZB, BCL6, LPXN, GRB2, NF2, RAC1, EZR, WASF2	2.971575	0.030952	0.02893 2
GOTERM_BP_DIRECT	GO:0030307~positive regulation of cell growth	8	0.001572	RPTOR, CDC42, RPS6KA3, DDX3X, CSNK2A1, RPS6KA1, AKT1, MTOR	4.696335	0.031323	0.02927 9
GOTERM_BP_DIRECT	GO:0043123~positive regulation of canonical NF-kappaB signal transduction	13	0.001602	CD74, TRFC, PRKCB, BCL10, TNF, RHOA, RELA, TFG, IKBKE, MYD88, CARD11, BIRC3, BRD4	2.958484	0.031718	0.02964 8
GOTERM_BP_DIRECT	GO:0071480~cellular response to gamma radiation	5	0.001689	H2AX, XRCC6, KDM1A, CHEK2, TP53	9.566608	0.032797	0.03065 6
GOTERM_BP_DIRECT	GO:2001243~negative regulation of intrinsic apoptotic signaling pathway	5	0.001689	DDX3X, HDAC1, AKT1, MMP9, HERPUD1	9.566608	0.032797	0.03065 6
GOTERM_BP_DIRECT	GO:0072332~intrinsic apoptotic signaling pathway by p53 class mediator	5	0.001689	STK11, ERCC2, E2F1, BAX, TP53	9.566608	0.032797	0.03065 6
GOTERM_BP_DIRECT	GO:0010389~regulation of G2/M transition of mitotic cell cycle	4	0.001768	CDK6, CDK4, CDK2, AURKA	15.89529	0.033909	0.03169 5
GOTERM_BP_DIRECT	GO:0033628~regulation of cell adhesion	4	0.001768	LYN, PLAU, LPXN, PTPN11	15.89529	0.033909	0.03169 5
GOTERM_BP_DIRECT	GO:0030890~positive regulation of B cell proliferation	6	0.00187	CD74, BCL6, TRFC, BTK, NFATC2, CARD11	6.73822	0.035627	0.03330 2
GOTERM_BP_DIRECT	GO:1902894~negative regulation of miRNA transcription	5	0.001941	NCOR2, SRF, HIF1A, TNF, RELA	9.224944	0.03675	0.03435 2
GOTERM_BP_DIRECT	GO:0006470~protein dephosphorylation	9	0.001967	LRRC59, PPP3CA, STK11, SDHAF2, PPP2R1B, PPP2R1A, CTDSP2, PTPN6, PTPN11	3.973822	0.037029	0.03461 2
GOTERM_BP_DIRECT	GO:0007052~mitotic spindle organization	7	0.001989	PTPA, TACC3, TACC1, TTK, NDC80, AURKB, AURKA	5.317909	0.037213	0.03478 4
GOTERM_BP_DIRECT	GO:0007259~cell surface receptor signaling pathway via JAK-STAT	6	0.00206	STAT1, STAT3, STAT6, TYK2, JAK3, JAK1	6.594854	0.038058	0.03557 4
GOTERM_BP_DIRECT	GO:0042100~B cell proliferation	6	0.00206	CD79A, BCL6, CD70, PRKCD, RASGRP1, CARD11	6.594854	0.038058	0.03557 4
GOTERM_BP_DIRECT	GO:0001764~neuron migration	9	0.002076	YWHAE, HSP90AA1, SRF, NDE1, ABI1, BAX, RAC1, PSEN1, RHOA	3.940146	0.038128	0.03563 9
GOTERM_BP_DIRECT	GO:0043371~negative regulation of CD4-positive, alpha-beta T cell differentiation	3	0.002174	CBFB, HMGB1, RUNX1	38.74476	0.039223	0.03666 3
GOTERM_BP_DIRECT	GO:1902622~regulation of neutrophil migration	3	0.002174	RAC2, RAC1, MYD88	38.74476	0.039223	0.03666 3
GOTERM_BP_DIRECT	GO:0070849~response to epidermal growth factor	3	0.002174	TPR, MAPK1, MAPK3	38.74476	0.039223	0.03666 3
GOTERM_BP_DIRECT	GO:0045737~positive regulation of cyclin-dependent protein serine/threonine kinase activity	4	0.002218	CCND3, CCND2, PIM1, AKT1	14.75991	0.039557	0.03697 5
GOTERM_BP_DIRECT	GO:1904996~positive regulation of leukocyte adhesion to vascular endothelial cell	4	0.002218	ETS1, TNF, RELA, RHOA	14.75991	0.039557	0.03697 5
GOTERM_BP_DIRECT	GO:0021549~cerebellum development	6	0.002263	NCOR2, NCSTN, ATIC, PSEN1, FCGR2B, TP53	6.457461	0.039887	0.03728 4
GOTERM_BP_DIRECT	GO:0060337~type I interferon-mediated signaling pathway	6	0.002263	STAT1, SIN3A, TYK2, IKBKE, MYD88, JAK1	6.457461	0.039887	0.03728 4
GOTERM_BP_DIRECT	GO:0051091~positive regulation of DNA-binding transcription factor activity	8	0.002297	TFDP1, SMARCB1, SRF, PLCG2, EP300, AKT1, TNF, IKBKE	4.396569	0.040208	0.03758 3
GOTERM_BP_DIRECT	GO:0006310~DNA recombination	7	0.002308	XRCC6, RAD51, RAD51C, MRE11, ERCC1, NONO, HMGB1	5.165969	0.040208	0.03758 3
GOTERM_BP_DIRECT	GO:0008286~insulin receptor signaling pathway	7	0.002481	GSK3B, AKT2, MAPK1, AKT1, GRB2, RAF1, MAPK3	5.093208	0.042974	0.04016 9
GOTERM_BP_DIRECT	GO:0050852~T cell receptor signaling pathway	9	0.002557	STK11, INPP5D, BTK, PLCG2, MAPK1, PIK3CD, PTPN6, BCL10, PSEN1	3.81096	0.044052	0.04117 7

GOTERM_BP_DIRECT	GO:0032956~regulation of actin cytoskeleton organization	8	0.002589	CDC42, PAK1, SH3BP1, PRKCD, RAC2, RAC1, RHOA, MTOR	4.304974	0.04435	0.041456
GOTERM_BP_DIRECT	GO:0043536~positive regulation of blood vessel endothelial cell migration	6	0.002714	MAP2K3, SP1, AKT1, HMG81, ETS1, HIF1A	6.199162	0.045797	0.042808
GOTERM_BP_DIRECT	GO:0044319~wound healing, spreading of cells	4	0.002734	CARMIL2, MRTFA, CD44, RHOA	13.77592	0.045797	0.042808
GOTERM_BP_DIRECT	GO:1900034~regulation of cellular response to heat	4	0.002734	GSK3B, CREBBP, EP300, MTOR	13.77592	0.045797	0.042808
GOTERM_BP_DIRECT	GO:0060766~negative regulation of androgen receptor signaling pathway	4	0.002734	NCOR2, PHB1, HDAC1, FOXF1	13.77592	0.045797	0.042808
GOTERM_BP_DIRECT	GO:0006298~mismatch repair	5	0.00285	PCNA, MSH2, RPA3, MLH1, MUTYH	8.332207	0.047313	0.044225
GOTERM_BP_DIRECT	GO:0002244~hematopoietic progenitor cell differentiation	7	0.002855	TOP2A, LYN, SIN3A, PTPN6, PSEN1, ARHGEF7, TP53	4.953669	0.047313	0.044225
GOTERM_BP_DIRECT	GO:0008104~protein localization	10	0.002954	CDC42, YWHAE, NPM1, BCL6, SIN3A, SEPTIN2, SEPTIN6, SEPTIN9, MAPRE1, TP53	3.37645	0.048556	0.045387
GOTERM_BP_DIRECT	GO:0048013~ephrin receptor signaling pathway	6	0.002962	LYN, SS18, PAK1, PTPN11, ARHGEF7, MMP9	6.07761	0.048556	0.045387
GOTERM_BP_DIRECT	GO:2001234~negative regulation of apoptotic signaling pathway	5	0.003208	RB1, CSNK2A1, BAX, PSEN1, TNF	8.071826	0.052302	0.048888
GOTERM_BP_DIRECT	GO:0051496~positive regulation of stress fiber assembly	6	0.003226	CDC42, PAK1, NF2, RAC1, RHOA, MTOR	5.960733	0.052323	0.048908
GOTERM_BP_DIRECT	GO:0012501~programmed cell death	4	0.003317	PKM, PLCG2, BCL10, TOP1	12.91492	0.052947	0.049491
GOTERM_BP_DIRECT	GO:0042129~regulation of T cell proliferation	4	0.003317	LGALS3, BCL6, RAC2, RAC1	12.91492	0.052947	0.049491
GOTERM_BP_DIRECT	GO:0045198~establishment of epithelial cell apical/basal polarity	4	0.003317	CDC42, SH3BP1, MSN, RHOA	12.91492	0.052947	0.049491
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	216	1.05E-58	RB1, PHB1, SMARCB1, IKZF1, MKI67, IKZF3, CCAR2, RPS6KA3, LGALS3, TCL1A, ZMIZ1, PSMD2, AKT2, CHEK2, RPS6KA1, CHEK1, CREB3L2, TRIM24, CPNE1, AKT1, SKP2, PRKACA, GTSE1, TP63, NUP214, MBNL1, MEF2B, CSNK2A1, COG5, PRKCB, PRKCD, MRTFA, RUNX1, EWSR1, SARNP, NUP98, TP53, POM121, SET, PRKDC, HIF1A, PPP4C, WDR70, PDCD11, PCBP1, H3C2, LYN, XBP1, CREBBP, XRCC6, H4C9, BCL11A, IRF2BP2, NFATC2, FLI1, SNW1, STAG2, GRB2, CDK12, RCOR1, EZH2, H2AX, TOP2A, FEN1, ELL, FAF1, PHF6, RPTOR, PPP3CA, IKBKE, PRMT1, TCF12, TFE3, PAX5, DDB2, NCOR2, RAD51C, POT1, PCNA, NR1I3, DOT1L, RELA, RECQL4, PTPA, PAK1, CUX1, NSD2, STAT6, MEF2D, SF3B1, BRD4, SUZ12, GIT2, CENPU, NPM1, UTP4, STAT1, SEPTIN2, WDR18, STAT3, H2BC4, HUWE1, MLH1, LRP1, RPA3, HNRNPA2B1, TCEA1, FRK, MAD2L1, MRE11, KDM1A, AHR, ETS1, STK11, CCND3, CCND2, ZNF207, PIM1, EP300, GTF2I, MAP2K3, H2AC6, AIP, SDHB, CDC25A, FOXF1, MSH2, FANCD2, TBL1XR1, CCNE1, SRSF2, SRSF3, KPNB1, DNMT1, CBFB, MAX, PSEN1, TPR, EP400, MCL1, FANCI, CPSF6, FANCL, FUS, NONO, HMGA1, FANCG, NDC80, NFKB1, NFKB2, NFKBIA, CDK6, BCL6, SP1, CDK4, CNOT2, BCL3, CDK2, CDK1, MNAT1, GSK3B, KDM5C, DDX3X, HSP90AB1, HMG81, AFF3, CDC73, CKS1B, PTBP1, SIN3A, HSP90AA1, EED, SMC1A, ARID1A, H2BC17, H2BC12, CCNA2, SFPQ, CREB1, TFDP1, IRF4, THRAP3, ELF4, IRF1, CTDS2, H2BC11, IRF8, TOP1, BIRC3, HDAC3, HDAC1, SRF, PRCC, U2AF1, MLLT1, HDAC6, AURKB, AURKA, POLD4, FIP1L1, U2AF2, POLD1, E2F1, MAPK1, VHL, MAPK3, MUTYH, PTPN11, MTOR, WEE1, RAD51, ERCC1, CARM1, ERCC2, PTPN6, TRIM33	2.915369	5.93E-56	5.33E-56
GOTERM_CC_DIRECT	GO:0005634~nucleus	252	7.42E-49	RB1, CYFIP2, PHB1, SMARCB1, IKZF1, MKI67, H2AC16, IKZF3, H2AC17, CCAR2, H2AC11, RPS6KA3, LGALS3, PPP2R1B, ZMIZ1, PPP2R1A, PSMD2, AKT2, CHEK2, RPS6KA1, CHEK1, CREB3L2, TRIM24, CPNE1, AKT1, SKP2, PRKACA, TP63, MBNL1, MEF2B, CSNK2A1, PRKCB, RPL22, PRKCD, MRTFA, RUNX1, EWSR1, SARNP, BTK, NUP98, TP53, SET, PRKDC, BAZ2A, BCL10, HIF1A, PPP4C, WDR70, PDCD11, PCBP1, H3C2, LYN, ZNF384, XBP1, CREBBP, XRCC6, H4C9, BCL11A, IRF2BP2, NFATC2, FLI1, H1-3, H1-2, H1-4, SNW1, STAG2, GRB2, CDK12, CALR, RCOR1, EZH2, H2AX, TOP2A, BTG2, FEN1, FAF1, PHF6, PPP3CA, RAC1, IKBKE, JAK1, SS18, SYK, PRMT1, TCF12, NCOA4, TFE3, TFE8, TYK2, PAX5, RHOA, DDB2, NCOR2, RAD51C, FH, PCNA, NR1I3, DOT1L, TYMS, RELA, RECQL4, PTPA, CUX1, NSD2, STAT6, EPS15, MEF2D, SF3B1, BRD4, SUZ12, CENPU, CD74, NPM1, STAT1, SEPTIN2, STAT3, H2BC4, HUWE1, MLH1, LRP1, RPA3, HNRNPA2B1, ABI1, TCEA1, TACC1, FRK, MAD2L1, MRE11, KDM1A, BUB1B, AHR, ETS1, STK11, CCND3, CCND2, PTTG1, ZNF207, PIM1, EP300, GTF2I, MAP2K1, MAP2K2, H2AC6, USP5, IGF1BP3, CDC25A, FOXF1, DPM1, MSH2, FANCD2, TBL1XR1, CCNE1, SRSF2, RAF1, KPNB1, CSNK1G2, DDX6, DNMT1, MAX, PSEN1, NDRG1, TPR, LPXN, CAMTA1, MAP2K7, MCL1, CPSF6, HSPA5, FANCL, FUS, NONO, HMGA1, MSN, NDC80, NFKB1, NFKB2, NFKBIA, CDK6, BCL6, SP1, CDK4, CNOT2, BCL3, CDK2, GNAS, CDK1, NF2, MYD88, PICALM, YWHAE, GSK3B, KDM5C, DDX3X, HSP90AB1, TNFAIP3, HMG81, AFF3, CDC73, PTBP1, ZC3H7A, ZC3H7B, SIN3A, HSP90AA1, EED, CAD, SMC1A, ARID1A, H2BC17, ETV6, H2BC12, CCNA2, SFPQ, PKM, CREB1, TFDP1, IRF4, THRAP3, ELF4, IRF1, H2BC11, IRF8, TOP1, PFDN5, BIRC3, HDAC3, HDAC1, SRF, RAP1GDS1, PRCC, TTK, HDAC6, AURKB, AURKA, SH3BP1, U2AF2, POLD1, E2F1, MAPK1, VHL, MAPK3, MUTYH, CNBP, PTPN11, MTOR, WEE1, UFM1, RAD51, ERCC1, CARM1, ERCC2, BAX, PTPN6, TRIM33	2.219772	2.09E-46	1.88E-46
GOTERM_CC_DIRECT	GO:0005829~cytosol	234	1.65E-44	RB1, CYFIP2, AHYCL1, NUP107, ARAF, IKZF1, IKZF3, RPS6KA3, LGALS3, TCL1A, TFG, PPP2R1B, ZMIZ1, PPP2R1A, PSMD2, AKT2, RPS6KA1, CHEK1, TRIM24, CPNE1, AKT1, SKP2, PRKACA, GTSE1, CDK5RAP2, NUP214, MBNL1, MEF2B, CSNK2A1, FBNP1, COG5, PRKCB, RPL22, PRKCD, MRTFA, EML4, NUP93, PRKAR1A, BTK, NUP98, EZR, TP53, SET, PRKDC, RPN1, BAZ2A, BCL10, HIF1A,	2.253145	3.10E-42	2.79E-42

				PPP4C, PDCD11, INPP5D, PCBP1, PLCG2, VTI1A, SEC31A, LYN, XBP1, CREBBP, XRCC6, BCL11A, NFATC2, FLI1, STAG2, STRN, GRB2, CALR, BTG2, ELL, FAF1, CLTC, CLTA, RPTOR, PPP3CA, ATIC, RAC2, RAC1, JAK3, IKBKE, JAK1, SYK, PRMT1, TFE3, TFE8, TYK2, RHOA, SLC7A5, RAD51C, SDHAF2, ARHGEF7, MAPRE1, CD44, NAPA, FH, NR1I3, TYMS, RELA, NRAS, PAK1, CUX1, STAT6, EPS15, CENPU, NPM1, MDH1, STAT1, NDE1, STAT3, H2BC4, HUWE1, AB1, TACC3, CCDC6, TACC1, FRK, MAD2L1, MRE11, BUB1B, AHR, STK11, CCND3, CCND2, PTTG1, KIF5B, PIM1, EP300, MAP2K3, MAP2K1, MAP2K2, USP5, TPM3, AIP, CDC25A, FANCD2, CCNE1, SRSF2, RAF1, KPNB1, CSNK1G2, CARD11, DDX6, GMPS, RASAL1, NDRG1, RASGRP1, LPXN, CAMTA1, MAP2K7, MCL1, FANCI, HSPA5, FANCL, IDH1, IDH2, HMGA1, MSN, FANCG, NDC80, NFKB1, NFKB2, NFKBIA, GRHPR, CDK6, CDK4, CNOT2, CAPRIN1, BCL3, CDK2, PI4KA, GNAS, CDK1, NF2, MYD88, PICALM, YWHAE, GSK3B, KDM5C, DDX3X, HSP90AB1, WDR1, RASGRF1, PIK3CD, TNFAIP3, AFF3, CDC73, CAPZB, HSP90AA1, EED, CAD, CIP2A, SMC1A, H2BC17, ETV6, DNM2, DUSP22, H2BC12, CCNA2, SFPQ, PKM, TFDPI, IRF4, IRF1, H2BC11, IRF8, LCP1, PFDN5, BIRC3, HDAC3, BCL2A1, HDAC1, RAP1GDS1, GOSR1, MLLT1, CBL, HDAC6, AURKB, AURKA, CDC42, SH3BP1, FIP1L1, POLD1, MAPK1, VHL, WASF2, MAPK3, RRM1, CNBP, PTPN11, MTOR, RAD51, CARM1, ERCC2, BAX, PTPN6, MYO1F CYFIP2, PHB1, MRE11, AHCYL1, ARAF, BUB1B, AHR, IKZF3, ETS1, CCAR2, RPS6KA3, LGALS3, CCND3, STK11, CCND2, PTTG1, TFG, PPP2R1B, ZMIZ1, PPP2R1A, CHEK2, AKT2, KIF5B, RPS6KA1, CHEK1, ZNF207, PIM1, CPNE1, AKT1, EP300, PRKACA, TP63, GTF2I, CDK5RAP2, MAP2K3, MBNL1, PRKCB, RPL22, PRKCD, AIP, MRTFA, CDC25A, EML4, MELK, EWSR1, CCNE1, PRKAR1A, BTK, SRSF3, EZR, RAF1, TP53, CSNK1G2, CARD11, KPNB1, LRRC59, DDX6, SET, AK2, BCL10, HIF1A, NDRG1, PPP4C, PCBP1, TPR, PLCG2, LPXN, MAP2K7, MCL1, SEC31A, FANCI, LYN, CARMIL2, XBP1, CREBBP, CPSF6, HSPA5, BCL11A, FUS, IDH1, IRF2BP2, MSN, NFATC2, NDC80, NFKB1, NFKB2, NFKBIA, GRHPR, CDK6, SP1, CDK4, CAPRIN1, CNOT2, BCL3, CCDC88C, CDK2, PI4KA, CDK1, GNAS, GRB2, CALR, NF2, MNAT1, MYD88, YWHAE, TOP2A, GSK3B, KDM5C, BTG2, FEN1, DDX3X, HSP90AB1, RASGRF1, PIK3CD, TNFAIP3, RPTOR, PPP3CA, LASP1, RAC1, IKBKE, JAK1, HSP90AA1, SYK, PRMT1, CAD, TCF12, TFE3, TFE8, CIP2A, TYK2, DNM2, DUSP22, CCNA2, RAD51C, TFDPI, PKM, IRF1, UFC1, IRF8, LCP1, ARHGEF7, PFDN5, BIRC3, FH, HDAC3, BCL2A1, HDAC1, SRF, NR1I3, DOT1L, TTK, TYMS, HDAC6, RELA, AURKA, PTPA, RECQL4, CDC42, PAK1, NSD2, E2F1, MAPK1, STAT6, EPS15, MEF2D, MAPK3, CD74, NPM1, MDH1, STAT1, SEPTIN2, NDE1, CNBP, STAT3, HUWE1, PTPN11, SEPTIN9, TPDS2L2, MTOR, WEE1, UFM1, RAD51, CARM1, ERCC1, ERCC2, HNRNPA2B1, TACC3, BAX, PTPN6, TACC1, MYO1F, MAD2L1 RB1, KDM5C, SMARCB1, KDM1A, AHR, ETS1, CCAR2, CCND2, SIN3A, ZMIZ1, CHEK1, CREB3L2, TRIM24, EP300, TP63, SS18, MEF2B, TCF12, TFE3, TFE8, PAX5, ARID1A, ETV6, FOXF1, RUNX1, DDB2, NCOR2, SFPQ, CREB1, TFDPI, FANCD2, IRF4, ELF4, IRF1, IRF8, TP53, SET, PCNA, MAX, PRKDC, HDAC1, SRF, NR1I3, HIF1A, RELA, PPP4C, CUX1, NSD2, E2F1, STAT6, MEF2D, BRD4, FANCI, CREBBP, FANCL, STAT1, STAT3, HMGA1, NFATC2, FLI1, FANCG, NFKB1, H1-3, NFKB2, RAD51, STAG2, SP1, CDK4, TRIM33, EZH2 H2AX, YWHAE, CYFIP2, BTG2, PHB1, AHCYL1, DDX3X, HSP90AB1, WDR1, TFRG, CLTC, SERPINE1, TNFAIP3, H2AC16, H2AC17, ICAM1, H2AC11, PTBP1, LGALS3, STK11, ATIC, PPP2R1B, CAPZB, PPP2R1A, PLAU, PSMD2, CPNE1, RAC2, RAC1, PRKACA, CDK5RAP2, HSP90AA1, H2AC6, TPM3, PRKCB, RPL22, CAD, PRKCD, TYK2, MMP9, RHOA, DNM2, SLC7A5, PKM, THRAP3, UFC1, LCP1, EZR, CD44, CARD11, KPNB1, NAPA, FH, PCNA, RAP1GDS1, AK2, NDRG1, PTPA, CD79B, CDC42, GANAB, NRAS, NCSTN, CD19, PCBP1, SPP1, PLCG2, H3C2, WASF2, LYN, CTSA, CD74, H4C9, MDH1, HSPA5, CD70, SEPTIN2, IDH1, H2BC4, IDH2, HUWE1, MSN, SOD2, GRHPR, AB1, HNRNPA2B1, PI4KA, CDK1, GNAS, BAX, PTPN6, GRB2, CALR, FRK TOP2A, FEN1, SMARCB1, SET, HSP90AB1, KDM1A, PRKDC, HDAC1, DOT1L, CLTC, AHR, IKZF1, BCL10, PSEN1, HIF1A, CDC42, PAK1, STK11, CD19, CHEK1, E2F1, AKT1, H3C2, WASF2, TP63, CD74, NPM1, XRCC6, HSP90AA1, H4C9, SYK, HSPA5, STAT1, CAD, PTPN11, DDB2, RAD51, PRKAR1A, BCL3, STRN, PTPN6, EZR, ARHGEF7, TP53, MYD88, BIRC3 H2AX, XRCC6, FEN1, H4C9, MRE11, PCNA, KDM1A, PRKDC, CDC73, RECQL4, RAD51, MSH2, CHEK2, POLD1, ERCC1, HNRNPA2B1, CHEK1, CDK2, CDK1, POT1, EZH2 YWHAE, CLTC, CBL, ICAM1, CDC42, PAK1, LASP1, NCSTN, PLAU, RAC2, MAPK1, LPXN, RAC1, JAK1, MAPK3, GIT2, NPM1, MAP2K1, MAP2K2, HSPA5, RPL22, HMGA1, MSN, RHOA, DNM2, PI4KA, LCP1, CALR, EZR, MAPRE1, ARHGEF7, CD44 H2AX, GSK3B, DDX3X, PCNA, BUB1B, PSEN1, NDRG1, HDAC6, AURKA, CDC42, CCND3, PAK1, PPP4C, CCND2, CHEK1, E2F1, MAPK1, PRKACA, CDK5RAP2, NPM1, MAP2K1, MDH1, PRKCB, NDE1, NDC80, DNM2, NUP93, CCNA2, RAD51, CDK6, CCNE1, PRKAR1A, CCDC88C, CDK2, CDK1, TACC1, MAPRE1, ARHGEF7, TP53 NUP107, SMARCB1, SEPTIN2, NDE1, SEPTIN6, BUB1B, TTK, PSEN1, SMC1A, PHF6, NDC80, AURKB, AURKA, SIN3A, TPR, ZNF207, NUP98, MNAT1, MAD2L1 CYFIP2, SET, HSP90AB1, TFRG, FAF1, BUB1B, BCL10, CBL, NDRG1, HDAC6, AURKA, KIF5B, VTI1A, PLCG2, SPP1, LPXN, PRKACA, CDK5RAP2, SEC31A, LYN, HSP90AA1, MAP2K2, STAT1, PRKCD, MSN, ACSL3, SEPTIN9, TPDS2L2, LRPPRC, RAD51, RAD51C, BCL3, GNAS, BTK, LCP1, NF2, CALR, EZR, PICALM, MAD2L1 H2AX, H4C9, H2AC6, H2BC4, H2AC16, H2BC17, H2AC17, H1-3, H1-2, H2AC11, H2BC12, H1-4, IRF4, H2BC11, EP400, H3C2				
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	192	5.11E-21			1.814998	7.19E-19	6.46E-19
GOTERM_CC_DIRECT	GO:0000785~chromatin	70	1.68E-18			3.293708	1.89E-16	1.70E-16
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	94	3.35E-14			2.264377	3.14E-12	2.82E-12
GOTERM_CC_DIRECT	GO:0032991~protein-containing complex	46	1.16E-13			3.658024	9.30E-12	8.36E-12
GOTERM_CC_DIRECT	GO:0000781~chromosome, telomeric region	21	6.60E-11			6.602646	4.65E-09	4.18E-09
GOTERM_CC_DIRECT	GO:0005925~focal adhesion	32	1.34E-10			4.001341	8.37E-09	7.53E-09
GOTERM_CC_DIRECT	GO:0005813~centrosome	39	8.18E-10			3.161454	4.61E-08	4.14E-08
GOTERM_CC_DIRECT	GO:0000776~kinetochore	19	1.89E-09			6.188451	9.66E-08	8.69E-08
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytoplasm	40	7.97E-09			2.85904	3.74E-07	3.36E-07
GOTERM_CC_DIRECT	GO:0000786~nucleosome	16	6.77E-08			6.043692	2.93E-06	2.63E-06
GOTERM_CC_DIRECT	GO:0000307~cyclin-dependent protein kinase holoenzyme complex	10	8.58E-08			12.3621	3.45E-06	3.10E-06
GOTERM_CC_DIRECT	GO:0005819~spindle	16	1.51E-07			5.688181	5.69E-06	5.11E-06
GOTERM_CC_DIRECT	GO:0005635~nuclear envelope	18	4.18E-07			4.618293	1.47E-05	1.32E-05
GOTERM_CC_DIRECT	GO:0090575~RNA polymerase II transcription regulator complex	14	6.24E-07			5.996104	2.07E-05	1.86E-05

GOTERM_CC_DIRECT	GO:0005657~replication fork	8	1.87E-06	H2AX, DNMT1, RAD51C, PCNA, MRE11, BCL6, CHEK1, TP53	13.18624	5.84E-05	5.25E-05
GOTERM_CC_DIRECT	GO:0005667~transcription regulator complex	18	3.27E-06	CREBBP, XRCC6, MEF2B, KDM1A, PRKDC, STAT3, TCF12, HMGA1, NFATC2, AHR, RELA, NFKB1, TFDPI, CDK4, CDK2, EP300, TP53, RCOR1	3.979992	9.69E-05	8.71E-05
GOTERM_CC_DIRECT	GO:0005694~chromosome	18	5.02E-06	CENPU, FH, UTP4, EED, NONO, HMGB1, CIP2A, MKI67, MLH1, SMC1A, RECQL4, PAK1, STAG2, MSH2, CARM1, TOP1, EZH2, BRD4	3.854638	1.41E-04	1.27E-04
GOTERM_CC_DIRECT	GO:0017053~transcription repressor complex	9	1.69E-05	NCOR2, HDAC3, SIN3A, TBL1XR1, HDAC1, SP1, HMGB1, TP53, RCOR1	7.895791	4.54E-04	4.08E-04
GOTERM_CC_DIRECT	GO:1904813~ficolin-1-rich granule lumen	12	1.96E-05	XRCC6, HSP90AA1, PKM, DDX3X, HSP90AB1, IDH1, PSMD2, HUWE1, MAPK1, HMGB1, MMP9, KPNB1	5.22175	5.01E-04	4.50E-04
GOTERM_CC_DIRECT	GO:0016363~nuclear matrix	12	2.83E-05	NCOR2, SFPQ, SMARCB1, SNW1, STAG2, BCL11A, NONO, CAD, PRKCD, HNRNPA2B1, SMC1A, TP53	5.020913	6.92E-04	6.22E-04
GOTERM_CC_DIRECT	GO:0042382~paraspeckles	5	3.32E-05	SFPQ, CPSF6, BCL6, BCL11A, NONO	24.7242	7.78E-04	6.99E-04
GOTERM_CC_DIRECT	GO:0031234~extrinsic component of cytoplasmic side of plasma membrane	7	3.78E-05	LYN, CARMIL2, TYK2, JAK3, MYD88, FRK, JAK1	10.87865	8.52E-04	7.66E-04
GOTERM_CC_DIRECT	GO:0016607~nuclear speck	22	5.38E-05	H2AX, CPSF6, ELL, NONO, PRC, TCF12, BAZ2A, U2AF1, HIF1A, SFPQ, SNW1, U2AF2, THRAP3, SARNP, PCBP1, EP400, SRSF2, LPXN, SRSF3, CDK12, PRKACA, SF3B1	2.770026	0.001166	0.001048
GOTERM_CC_DIRECT	GO:0005938~cell cortex	13	6.23E-05	FNBP1, SEPTIN2, PSEN1, RHOA, LASP1, MELK, AKT2, AKT1, GRB2, RAC1, EZR, ARHGEF7, CSNK1G2	4.234203	0.001299	0.001168
GOTERM_CC_DIRECT	GO:0030027~lamellipodium	14	6.75E-05	CARMIL2, DDX3X, RHOA, PAK1, SH3BP1, CAPZB, CAPRIN1, ABI1, RAC2, AKT1, NF2, RAC1, ARHGEF7, WASF2	3.905155	0.001342	0.001206
GOTERM_CC_DIRECT	GO:0001673~male germ cell nucleus	8	7.06E-05	TOP2A, H2AX, RAD51, PCNA, CDK2, TRIM24, TOP1, MLH1	7.770461	0.001342	0.001206
GOTERM_CC_DIRECT	GO:0032993~protein-DNA complex	7	7.15E-05	XRCC6, NPM1, MAX, PRKDC, SP1, EP300, TOP1	9.762887	0.001342	0.001206
GOTERM_CC_DIRECT	GO:0042470~melanosome	10	1.27E-04	YWHA, HSP90AA1, GANAB, NCSTN, HSP90AB1, HSPA5, TFRC, RPN1, CLTC, RAC1	5.230118	0.002298	0.002065
GOTERM_CC_DIRECT	GO:0000791~euchromatin	8	1.67E-04	H1-4, CREB1, ELL, SP1, TRIM24, HIF1A, H1-3, H1-2	6.799154	0.002847	0.002559
GOTERM_CC_DIRECT	GO:0000793~condensed chromosome	6	1.67E-04	TOP2A, RAD51, FANCD2, CDK2, HMGB1, MKI67	11.25377	0.002847	0.002559
GOTERM_CC_DIRECT	GO:0005739~mitochondrion	48	1.79E-04	GSK3B, FH, PHB1, FEN1, HSP90AB1, RAP1GDS1, AK2, ARAF, PSEN1, TYMS, PPP3CA, STK11, PPP2R1A, KIF5B, TRIM24, AKT1, MAPK1, VHL, PRKACA, MCL1, MAPK3, PDK1, MUTYH, RRM1, MAP2K1, HSP90AA1, MAP2K2, MDH1, HSPA5, IDH1, PRKCD, IDH2, HUWE1, SDHC, SDHA, SOD2, SDHB, FANCG, LRPPRC, NFKB1, RAD51, RAD51C, PKM, SDHAF2, CDK1, BAX, RAF1, TP53	1.758165	0.002957	0.002658
GOTERM_CC_DIRECT	GO:0097431~mitotic spindle pole	7	2.08E-04	STAG2, SMC1A, MAPRE1, ARHGEF7, AURKB, AURKA, CDK5RAP2	8.101119	0.003346	0.003007
GOTERM_CC_DIRECT	GO:0005856~cytoskeleton	23	2.51E-04	TPM3, FNBP1, NR1I3, MSN, TYK2, RHOA, LRPPRC, LASP1, CAPZB, INPP5D, ABI1, RAC2, CDC6, MAPK1, TACC1, NF2, RAC1, EZR, JAK3, WASF2, JAK1, CDK5RAP2, MAPK3	2.415143	0.003926	0.003528
GOTERM_CC_DIRECT	GO:0034774~secretory granule lumen	10	2.90E-04	XRCC6, HSP90AA1, PKM, DDX3X, HSP90AB1, IDH1, PSMD2, HUWE1, HMGB1, NFKB1	4.689071	0.004408	0.003962
GOTERM_CC_DIRECT	GO:0072686~mitotic spindle	11	4.14E-04	CDC42, EML4, HDAC3, TBL1XR1, TPR, CLTC, CDK1, TACC3, MAPK1, MAD2L1, AURKA	4.04274	0.006129	0.005509
GOTERM_CC_DIRECT	GO:0016020~membrane	122	5.25E-04	CYFIP2, PHB1, NUP107, TFRC, MKI67, ICAM1, LGALS3, STK11, PPP2R1A, PSMD2, KIF5B, CREB3L2, ENPP2, CPNE1, AKT1, PRKACA, GTSE1, GTF2I, CDK5RAP2, CMKLR1, MAP2K3, COG5, AIP, SDHC, ACSL3, EML4, DPM1, NUP93, MELK, MSH2, TBL1XR1, PRKAR1A, MFNG, NUP98, EZR, TP53, CSNK1G2, KPNB1, LRRC59, DDX6, RPN2, CBF, PRKDC, RPN1, PSEN1, RASGRP1, APH1A, NCSTN, PCBP1, LPXN, H3C2, MCL1, CTSA, FANCI, CARMIL2, XRCC6, CPSF6, H4C9, HSPA5, FANCL, FUS, NONO, NDC80, STAG2, CAPRIN1, CNOT2, PI4KA, CDK1, GNAS, STRN, CALR, NF2, PICALM, YWHA, FEN1, DDX3X, HSP90AB1, FAF1, CLTC, CLTA, HERPUD1, PTBP1, ATIC, CAPZB, RAC1, JAK3, JAK1, HSP90AA1, EED, CAD, TYK2, POMGNT1, RHOA, ETV6, DNM2, NCOR2, SLC7A5, IRF4, NAPA, SLC6A3, GOSR1, TTK, RECQL4, CDC42, NRAS, GANAB, POLD1, IL21R, EPS15, CD74, NPM1, RRM1, NDE1, HUWE1, MLH1, LRPPRC, MTOR, HNRNPA2B1, BAX, PTPN6, TACC1, FCGR2B	1.314575	0.007583	0.006815
GOTERM_CC_DIRECT	GO:0045121~membrane raft	13	5.48E-04	LYN, BCL10, PSEN1, CBL, TNF, ICAM1, CD79A, PPP2R1B, CD19, INPP5D, BTK, PLCG2, CARD11	3.351242	0.007717	0.006935
GOTERM_CC_DIRECT	GO:0030496~midbody	12	8.69E-04	CDC42, EML4, HSPA5, SEPTIN2, BCL3, CDK1, SEPTIN6, TACC1, RHOA, AURKB, AURKA, DNMT2	3.399577	0.011179	0.010596
GOTERM_CC_DIRECT	GO:0000794~condensed nuclear chromosome	6	8.80E-04	H2AX, RAD51, CHEK1, SMC1A, LRPPRC, BRD4	7.959985	0.011179	0.010596
GOTERM_CC_DIRECT	GO:0016605~PML body	9	0.001016	RB1, RAD51, MRE11, CSNK2A1, ELF4, CHEK2, TP53, IKBKE, MTOR	4.410262	0.013303	0.011957
GOTERM_CC_DIRECT	GO:0030132~clathrin coat of coated pit	4	0.00119	CLTC, CLTA, EPS15, PICALM	18.13108	0.014888	0.01338
GOTERM_CC_DIRECT	GO:0019897~extrinsic component of plasma membrane	4	0.00119	PPP3CA, TYK2, JAK3, MYD88	18.13108	0.014888	0.01338
GOTERM_CC_DIRECT	GO:0000118~histone deacetylase complex	6	0.001351	HDAC3, SIN3A, TBL1XR1, HDAC1, RCOR1, HDAC6	7.252431	0.01653	0.014857
GOTERM_CC_DIRECT	GO:0001772~immunological synapse	6	0.001493	LGALS3, PRKAR1A, BCL10, EZR, CARD11, ICAM1	7.094769	0.017882	0.016072
GOTERM_CC_DIRECT	GO:1990391~DNA repair complex	4	0.001526	FANCI, KDM1A, FANCD2, RCOR1	16.73638	0.017899	0.016087
GOTERM_CC_DIRECT	GO:0035189~Rb-E2F complex	3	0.001964	RB1, TFDPI, E2F1	40.79492	0.022562	0.020278
GOTERM_CC_DIRECT	GO:0016604~nuclear body	16	0.00204	SUZ12, CREBBP, PCNA, RPN2, ELL, FANCL, MKI67, AFF3, HIF1A, FLI1, NCOR2, SNW1, FANCD2, ELF4, NUP98, TP53	2.500838	0.022971	0.020646
GOTERM_CC_DIRECT	GO:0001726~ruffle	8	0.002317	PAK1, CARMIL2, CDK6, GNAS, LCP1, EZR, ARHGEF7, WASF2	4.395412	0.025573	0.022984
GOTERM_CC_DIRECT	GO:0031616~spindle pole centrosome	4	0.002363	NPM1, NDE1, AURKB, AURKA	14.50486	0.025579	0.022989
GOTERM_CC_DIRECT	GO:0016514~SWI/SNF complex	5	0.002667	RB1, SS18, SMARCB1, BCL11A, ARID1A	8.498942	0.028329	0.025461

GOTERM_CC_DIRECT	GO:0032587~ruffle membrane	8	0.002743	PAK1, AKT2, PLCG2, LCP1, NF2, RAC1, EZR, RHOA	4.266136	0.028598	0.025703
GOTERM_CC_DIRECT	GO:0034399~nuclear periphery	4	0.003436	NUP93, NUP107, TPR, NUP98 TOP2A, FEN1, SMARCB1, PRKDC, BAZ2A, MKI67, PHF6, PTBP1, RPS6KA3, CCND2, PDCD11, SIN3A, NSD2, ZNF207, PIM1, CAMTA1, SKP2, SF3B1, SUZ12, NPM1, XRCC6, UTP4, STAT1, WDR18, SDHA, FANCG, ETV6, WEE1, RAD51, STAG2, BCL6, SDHAF2, FANCD2, EWSR1, CDK4, TCEA1, GRB2, PTPN6, NF2, TOP1, TP53	12.79841	0.035174	0.031613
GOTERM_CC_DIRECT	GO:0005730~nucleolus	41	0.003591	MAPK1, MSN, RAF1, MAPK3 EML4, SS18, PPP2R1A, SEPTIN2, SEPTIN6, AKT1, SEPTIN9, GTSE1, NDRG1, AURKB, AURKA	1.592945	0.0361	0.032445
GOTERM_CC_DIRECT	GO:0031143~pseudopodium	4	0.004068	CPSF6, TRIM24, SRSF2	12.08738	0.040179	0.036111
GOTERM_CC_DIRECT	GO:0015630~microtubule cytoskeleton	11	0.00425	GSK3B, PPP3CA, BCL11A, AKT1, RAC1, PSEN1, ARHGEF7, EPS15, RHOA RB1, CYFIP2, PHB1, AHCYL1, NUP107, SMARCB1, TFRC, SERPINE1, ARAF, IKZF1, MKI67, H2AC16, IKZF3, H2AC17, CCAR2, ICAM1, H2AC11, RPS6KA3, LGALS3, TCL1A, TFG, PPP2R1B, PPP2R1A, PSMD2, AKT2, CHEK2, RPS6KA1, CHEK1, TRIM24, CPNE1, AKT1, SKP2, PRKACA, GTSE1, TP63, PDK1, CMKLR1, CDK5RAP2, NUP214, MBNL1, ST6GAL1, MEF2B, CSNK2A1, FNBP1, COG5, PRKCB, RPL22, PRKCD, MRTFA, ACSL3, RUNX1, EML4, NUP93, EWSR1, PRKAR1A, SARNP, BTK, NUP98, EZR, TP53, POM121, SET, RPN2, PRKDC, RPN1, BAZ2A, BCL10, HIF1A, APH1A, CD79B, CD79A, NCSTN, PPP4C, PDCD11, INPP5D, PCBP1, PLCG2, VTI1A, H3C2, SEC31A, LYN, XBP1, CREBBP, XRCC6, H4C9, NFATC2, FLI1, H1-2, H1-4, SNW1, STAG2, CCDC88C, STRN, GRB2, CDK12, CALR, RCOR1, EZH2, H2AX, TOP2A, BTG2, FEN1, ELL, FAF1, CLTC, CLTA, PHF6, HERPUD1, RPTOR, PPP3CA, RAC2, RAC1, JAK3, IKBKE, JAK1, SS18, SYK, PRMT1, TCF12, TFE3, TFEB, TYK2, PAX5, RHOA, DDB2, NCOR2, SLC7A5, RAD51C, SDHAF2, UFC1, POT1, ARHGEF7, MAPRE1, CD44, NAPA, FH, PCNA, NR1I3, DOT1L, RELA, RECQL4, PTPA, NRAS, PAK1, NSD2, SPP1, STAT6, EPS15, MEF2D, SF3B1, BRD4, SUZ12, GIT2, CENPU, CD74, NPM1, MDH1, UTP4, STAT1, SEPTIN2, CD70, NDE1, WDR18, STAT3, H2BCA, HUWE1, SEPTIN6, SEPTIN9, MLH1, LRPPRC, RPA3, HNRNPA2B1, ABI1, TACC3, CCDC6, TCEA1, TACC1, FRK, MAD2L1, MRE11, CSF3R, KDM1A, BUB1B, AHR, ETS1, TNF, STK11, CCND3, CCND2, PTTG1, PLAU, KIF5B, ZNF207, PIM1, EP300, GTF2I, MAP2K3, MAP2K1, MAP2K2, H2AC6, USP5, TPM3, IGF1BP3, AIP, SDHC, SDHA, SDHB, CDC25A, FOXPI1, DPM1, MELK, MSH2, FANCD2, TBL1XR1, CCNE1, SRSF2, SRSF3, RAF1, KPNB1, CSNK1G2, CARD11, LRRC59, DDHG, DNMT1, CBFB, MAX, AK2, PSEN1, NDRG1, TPR, EP400, LPXN, MAP2K7, MCL1, FANCI, CPSF6, HSPA5, FANCL, FUS, NONO, IDH1, HMGA1, MSN, FANCG, NDC80, NFKB1, NFKB2, NFKBIA, GRHRP, CDK6, BCL6, SP1, CDK4, CNOT2, REEP3, CAPRIN1, BCL3, CDK2, PI4KA, GNAS, CDK1, PLEKHM2, NF2, MNAT1, MYD88, PICALM, YWHAE, GSK3B, KDM5C, DDX3X, HSP90AB1, PIK3CD, TNFAIP3, HMGB1, CDC73, CKS1B, PTBP1, LASP1, CAPZB, ZC3H7B, SIN3A, HSP90AA1, EED, CAD, RHBDF2, CIP2A, SMC1A, ARID1A, H2BC17, MMP9, POMGNT1, ETV6, DNMT2, H2BC12, CCNA2, SFPO, PKM, CREB1, TFDPI1, IRF4, THRAP3, ELF4, IRF1, CTDSP2, H2BC11, IRF8, TOP1, PFDN5, BIRC3, HDAC3, BCL2A1, HDAC1, SRF, RAP1GDS1, PRCC, TTK, U2AF1, MLLT1, CBL, HDAC6, AURKB, AURKA, CDC42, POLD4, GANAB, SH3BP1, FIP1L1, U2AF2, POLD1, E2F1, IL21R, MAPK1, VHL, WASF2, MAPK3, MUTYH, RRM1, CNBP, PTPN11, SOD2, TPDS2L2, MTOR, WEE1, UFM1, RAD51, ERCC1, CARM1, POU2AF1, ERCC2, BAX, PTPN6, FCGR2B, TRIM33, MYO1F	2.962008	0.041254	0.041087
GOTERM_CC_DIRECT	GO:0005726~perichromatin fibrils	3	0.004791	GSK3B, PRKDC, ARAF, BUB1B, TTK, AURKB, AURKA, RPS6KA3, PAK1, STK11, CHEK2, AKT2, CHEK1, RPS6KA1, PIM1, AKT1, MAPK1, MAP2K7, PRKACA, IKBKE, GTF2I, MAPK3, MAP2K3, MAP2K1, MAP2K2, SYK, CSNK2A1, PRKCB, PRKCD, MTOR, MELK, CDK2, CDK1, CDK12, TOP1, RAF1, CSNK1G2	27.19661	0.045716	0.041708
GOTERM_CC_DIRECT	GO:0098794~postsynapse	9	0.004945	GSK3B, PRKDC, ARAF, BUB1B, TTK, AURKB, AURKA, RPS6KA3, PAK1, STK11, CHEK2, AKT2, CHEK1, RPS6KA1, PIM1, AKT1, MAPK1, MAP2K7, PRKACA, IKBKE, GTF2I, MAPK3, MAP2K3, MAP2K1, MAP2K2, SYK, CSNK2A1, PRKCB, PRKCD, MTOR, MELK, CDK2, CDK1, CDK12, TOP1, RAF1, CSNK1G2	3.42335	0.046403	0.041705
GOTERM_MF_DIRECT	GO:0005515~protein binding	354	1.37E-35	TOP2A, DNMT1, HDAC3, SET, PCNA, KDM1A, MLLT1, RELA, SIN3A, POLD1, TPR, NSD2, EP400, TRIM24, EP300, TP63, BRD4, NPM1, CREBBP, PRKCB, FUS, NONO, HMGA1, NFATC2, MLH1, SMC1A, FLI1, NFKB1, NCOR2, SFPO, RAD51, STAG2, MSH2, BCL6, SARNP, CDK1, TOP1, TP53, RCOR1, EZH2	1.402622	9.67E-33	8.65E-33
GOTERM_MF_DIRECT	GO:0019899~enzyme binding	46	1.01E-22	H2AX, YWHAE, PHB1, HDAC3, PCNA, KDM1A, PRKDC, HDAC1, PHF6, H2AC16, HIF1A, CCAR2, H2AC17, RELA, HDAC6, H2AC11, APH1A, PPP3CA, WDR70, U2AF2, POLD1, AKT1, VHL, RAC1, MAP2K7, BRD4, LYN, HSPA5, PRMT1, STAT1, PRKCD, CAD, TFEB, HMGA1, MSN, MLH1, SOD2, DNMT2, NFKBIA, RAD51, SNW1, CREB1, RAF1, TP53, RCOR1, KPNB1	6.248832	3.58E-20	3.20E-20
GOTERM_MF_DIRECT	GO:0003677~DNA binding	72	5.24E-18	H2AX, TOP2A, KDM5C, FEN1, MRE11, SMARCB1, DDX3X, TNFAIP3, AHR, IKZF1, MKI67, H2AC16, ETS1, PHF6, H2AC17, H2AC11, SIN3A, ZNF207, EP300, TP63, GTF2I, H2AC6, SMC1A, ARID1A, H2BC17, RUNX1, DDB2, NCOR2, H2BC12, SFPO, RAD51C, MSH2, THRAP3, IRF1, SARNP, H2BC11, TOP1, TP53, DNMT1, SET, PCNA, MAX, DOT1L, BAZ2A, RELA, POLD1, NSD2, EP400, E2F1, MAPK1, H3C2, FANCI, XBP1, XRCC6, H4C9, FUS, NONO, H2BC4, STAT3, HMGA1, HUWE1, NFATC2, SOD2, FLI1, H1-4, BCL6, SP1, ERCC1, POU2AF1, TCEA1, CALR, TRIM33	3.144728	1.24E-15	1.11E-15
GOTERM_MF_DIRECT	GO:0004674~protein serine/threonine kinase activity	37	7.75E-15	GSK3B, PRKDC, ARAF, BUB1B, TTK, AURKB, AURKA, RPS6KA3, PAK1, STK11, CHEK2, AKT2, CHEK1, RPS6KA1, PIM1, AKT1, MAPK1, MAP2K7, PRKACA, IKBKE, GTF2I, MAPK3, MAP2K3, MAP2K1, MAP2K2, SYK, CSNK2A1, PRKCB, PRKCD, MTOR, MELK, CDK2, CDK1, CDK12, TOP1, RAF1, CSNK1G2	4.894657	1.37E-12	1.23E-12
GOTERM_MF_DIRECT	GO:0019901~protein kinase binding	42	1.33E-14	GSK3B, HSP90AB1, TFRC, FAF1, CLTC, HIF1A, RELA, AURKA, CKS1B, CDC42, RPTOR, RPS6KA3, CCND3, TCL1A, CCND2, CHEK2, PLCG2, RAC2, AKT1, RAC1, MAP2K7, PRKACA, CDK5RAP2, MAP2K3, NPM1, XBP1, SYK, BCL11A, PRKCD, STAT3, MSN, PTPN11, ACSL3, RHOA, CDC25A, CCNA2, CCNE1, GRB2, PTPN6, CDK12, MAPRE1, ARHGEF7	4.227947	1.88E-12	1.68E-12
GOTERM_MF_DIRECT	GO:0005524~ATP binding	77	6.15E-14	TOP2A, GSK3B, DDX3X, HSP90AB1, ARAF, PIK3CD, BUB1B, MKI67, RPS6KA3, STK11, CHEK2, AKT2, KIF5B, RPS6KA1, CHEK1, PIM1, AKT1, PRKACA, JAK3, IKBKE, JAK1, GTF2I, PDK1, MAP2K3, MAP2K1, HSP90AA1, MAP2K2, CSNK2A1, SYK, PRKCB, CAD, PRKCD, TYK2, ACSL3, SMC1A, RUNX1, RAD51C, PKM, MELK, MSH2, THRAP3, BTK, TOP1, RAF1, CSNK1G2, DDX6, PRKDC, GMPS, AK2, TTK, AURKB, AURKA, PTPA, RECQL4, PAK1, EP400, MAPK1, MAP2K7, MAPK3, LYN, RRM1, XRCC6, HSPA5, MLH1, MTOR, WEE1, RAD51, CDK6, CDK4, CAPRIN1, ERCC2, CDK2, PI4KA, CDK1, CDK12, FRK, MYO1F	2.525062	6.95E-12	6.21E-12
GOTERM_MF_DIRECT	GO:0106310~protein serine kinase activity	35	6.87E-14	GSK3B, PRKDC, ARAF, BUB1B, TTK, AURKB, AURKA, RPS6KA3, PAK1, STK11, CHEK2, AKT2, CHEK1, RPS6KA1, PIM1, AKT1, MAPK1, MAP2K7, PRKACA, MAPK3, MAP2K3, MAP2K1, MAP2K2, CSNK2A1, PRKCB, PRKCD, MTOR, MELK, CDK6, CDK4, CDK2, CDK1, CDK12, RAF1, CSNK1G2	4.832489	6.95E-12	6.21E-12
GOTERM_MF_DIRECT	GO:0003682~chromatin binding	40	1.07E-12	TOP2A, DNMT1, HDAC3, SET, PCNA, KDM1A, MLLT1, RELA, SIN3A, POLD1, TPR, NSD2, EP400, TRIM24, EP300, TP63, BRD4, NPM1, CREBBP, PRKCB, FUS, NONO, HMGA1, NFATC2, MLH1, SMC1A, FLI1, NFKB1, NCOR2, SFPO, RAD51, STAG2, MSH2, BCL6, SARNP, CDK1, TOP1, TP53, RCOR1, EZH2	3.864935	9.50E-11	8.49E-11

GOTERM_MF_DIRECT	GO:0140297~DNA-binding transcription factor binding	23	3.83E-12	RB1, NPM1, CREBBP, HDAC3, KDM1A, MAX, BCL11A, HDAC1, SRF, STAT3, TCF12, HMGB1, RELA, RUNX1, TFDP1, BCL6, CARM1, BCL3, E2F1, EP300, VHL, MEF2D, MAPK3	6.757458	3.01E-10	2.69E-10
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	78	9.06E-12	RB1, YWHAE, KDM5C, MRE11, AHCYL1, SMARCB1, HSP90AB1, KDM1A, TFRC, TNFAIP3, IKZF1, IKZF3, ETS1, TNF, TCF1A, TFG, CHEK2, KIF5B, CPNE1, AKT1, SKP2, IKBKE, TP63, HSP90AA1, CSNK2A1, FNBP1, EED, PRMT1, RPL22, CAD, MMP9, FOXF1, CREB1, EWSR1, BTK, EZR, RAF1, MAPRE1, TP53, PCNA, MAX, TTK, BCL10, RASGRP1, RELA, CD79B, CDC42, CD79A, PAK1, MAPK1, STAT6, MAPK3, CD74, XBP1, RRM1, FUS, STAT1, SEPTIN2, NDE1, IDH1, NONO, H2BC4, STAT3, SOD2, NDC80, MTOR, NFKB1, NFKBIA, RAD51, BCL6, SP1, CCDC88C, HNRNPA2B1, CCDC6, BAX, GRB2, MYD88, MAD2L1	2.269231	6.41E-10	5.74E-10
GOTERM_MF_DIRECT	GO:0042826~histone deacetylase binding	20	1.41E-11	YWHAE, HSP90AA1, PHB1, HDAC3, MEF2B, HSP90AB1, HDAC1, SRF, PHF6, HIF1A, IKZF3, RELA, HDAC6, NCOR2, H1-4, SFPQ, SP1, BCL3, MEF2D, TP53	7.656671	9.05E-10	8.09E-10
GOTERM_MF_DIRECT	GO:0045296~cadherin binding	30	2.88E-11	YWHAE, LRRC59, DDX6, MRE11, DDX3X, HSP90AB1, PSEN1, CBL, NDRG1, LASP1, ATIC, CAPZB, KIF5B, PCBP1, H3C2, EPS15, WASF2, HSPA5, STAT1, SEPTIN2, IDH1, PTPN11, CIP2A, SEPTIN9, PKM, ABI1, PI4KA, EZR, MAPRE1, PICALM	4.525436	1.70E-09	1.52E-09
GOTERM_MF_DIRECT	GO:0003713~transcription coactivator activity	27	5.28E-11	SMARCB1, CBFb, KDM1A, DOT1L, HMGB1, BCL10, ZMIZ1, TRIM24, EP300, BRD4, SS18, NPM1, CREBBP, FUS, NCOA4, HMGA1, AIP, MRTFA, ARID1A, PKM, SNW1, IRF4, THRAP3, CARM1, POU2AF1, BCL3, NUP98	4.9257	2.70E-09	2.41E-09
GOTERM_MF_DIRECT	GO:0003723~RNA binding	68	5.33E-11	YWHAE, TOP2A, AHCYL1, DDX3X, HSP90AB1, TFRC, CLTC, HMGB1, MKI67, PHF6, CCAR2, PTBP1, LGALS3, ZC3H7A, SIN3A, ZC3H7B, ZNF207, MBNL1, HSP90AA1, PRMT1, RPL22, SMC1A, SFPQ, PKM, EWSR1, THRAP3, SARNP, SRSF2, SRSF3, NUP98, TOP1, EZR, MAPRE1, KPNB1, LRRC59, DDX6, DNMT1, PRKDC, RPN1, U2AF1, BAZ2A, GANAB, PDCD11, FIP1L1, U2AF2, PCBP1, TPR, SF3B1, NPM1, XRCC6, CPSF6, H4C9, UTP4, FUS, CENP, NONO, HMGA1, HUWE1, TPD52L2, LRPPRC, H1-3, H1-2, H1-4, SNW1, CAPRIN1, HNRNPA2B1, GRB2, CALR	2.361728	2.70E-09	2.41E-09
GOTERM_MF_DIRECT	GO:0003684~damaged DNA binding	15	9.32E-11	H2AX, CREBBP, XRCC6, FEN1, PCNA, HMGB1, FANCG, DDB2, MSH2, RPA3, POLD1, ERCC1, ERCC2, EP300, TP63	10.6762	4.40E-09	3.93E-09
GOTERM_MF_DIRECT	GO:0061629~RNA polymerase II-specific DNA-binding transcription factor binding	21	7.12E-10	RB1, GSK3B, CREBBP, KDM5C, KDM1A, PRKDC, HDAC1, SRF, STAT3, DOT1L, AHR, HMGB1, ETS1, HIF1A, CREB1, SP1, SIN3A, EP300, MEF2D, TP53, GTF2I, LYN, GSK3B, GIT2, SYK, CSNK2A1, PIK3CD, MTOR, CKS1B, RPS6KA3, STK11, PKM, CCNE1, PRKAR1A, PLAU, CDK4, CHEK2, PI4KA, BTK, CDK1, AKT1, CDK12, SKP2	5.767471	3.15E-08	2.82E-08
GOTERM_MF_DIRECT	GO:0016301~kinase activity	22	8.74E-10	H2AX, YWHAE, TOP2A, PHB1, BCL2A1, AHR, H2AC16, HIF1A, IKZF3, H2AC17, AURKA, H2AC11, PPP2R1A, H3C2, MEF2D, MCL1, XBP1, H4C9, H2AC6, BCL11A, TCF12, H2BC4, SMC1A, H2BC17, RUNX1, H2BC12, H2BC11, BAX, TP53	5.396838	3.64E-08	3.25E-08
GOTERM_MF_DIRECT	GO:0046982~protein heterodimerization activity	29	2.27E-09	MAX, SRF, NR1I3, AHR, IKZF1, AFF3, ETS1, HIF1A, IKZF3, RELA, E2F1, STAT6, MEF2D, TP63, GTF2I, XBP1, MEF2B, BCL11A, STAT1, TCF12, STAT3, TFE3, TFEB, NFATC2, FLI1, NFKB1, ETV6, RUNX1, NFKB2, CREB1, TFDP1, BCL6, SP1, IRF4, TP53	3.876949	8.75E-08	7.82E-08
GOTERM_MF_DIRECT	GO:0003700~DNA-binding transcription factor activity	35	2.35E-09	MEF2D, TP63, GTF2I, XBP1, MEF2B, BCL11A, STAT1, TCF12, STAT3, TFE3, TFEB, NFATC2, FLI1, NFKB1, ETV6, RUNX1, NFKB2, CREB1, TFDP1, BCL6, SP1, IRF4, TP53	3.299797	8.75E-08	7.82E-08
GOTERM_MF_DIRECT	GO:0000976~transcription cis-regulatory region binding	23	3.52E-09	XBP1, XRCC6, STAT3, TFE3, TCF12, TFEB, AHR, HMGB1, ETS1, TNF, FLI1, RELA, NFKB1, RUNX1, SFPQ, TBL1XR1, SP1, CARM1, IRF1, CREB3L2, TP53, CDK5RAP2, BRD4	4.763454	1.25E-07	1.11E-07
GOTERM_MF_DIRECT	GO:0051059~NF-kappaB binding	11	3.99E-09	NFKBIA, GSK3B, NPM1, HDAC3, PDCD11, HDAC1, FAF1, CPNE1, EP300, BCL10, RELA	13.89686	1.34E-07	1.20E-07
GOTERM_MF_DIRECT	GO:0003690~double-stranded DNA binding	15	2.19E-08	XRCC6, FEN1, MRE11, STAT1, PRKDC, HMGB1, AFF3, H1-3, H1-2, H1-4, RAD51, MSH2, SP1, CAMTA1, TOP1	7.151042	7.05E-07	6.30E-07
GOTERM_MF_DIRECT	GO:0030527~structural constituent of chromatin	15	2.48E-08	H2AX, H4C9, H2AC6, H2BC4, HMGA1, H2AC16, H2BC17, H2AC17, H1-3, H1-2, H2AC11, H2BC12, H1-4, H2BC11, H3C2	7.08421	7.62E-07	6.81E-07
GOTERM_MF_DIRECT	GO:0001222~transcription corepressor binding	11	3.30E-08	SUZ12, HDAC3, BCL6, STAT1, EED, HDAC1, CNOT2, ETS1, HDAC6, EZH2, RUNX1, GSK3B, MAP2K1, MAP2K2, SYK, PRKDC, PRKCD, CAD, ARAF, BUB1B, MTOR, AURKA, RPS6KA3, PAK1, CHEK1, CDK2, TRIM24, CDK1, AKT1, CDK12, RAF1, PRKACA, CSNK1G2, PDK1	11.34437	9.74E-07	8.71E-07
GOTERM_MF_DIRECT	GO:0004672~protein kinase activity	23	3.56E-08	LYN, RB1, YWHAE, GSK3B, XBP1, HSP90AA1, HSP90AB1, HSPA5, FANCL, FAF1, BCL10, HIF1A, LRPPRC, RELA, HDAC6, AURKA, NFKBIA, PRKAR1A, CHEK2, CALR, PRKACA, IKBKE, TP53, JAK1	4.195967	1.01E-06	9.02E-07
GOTERM_MF_DIRECT	GO:0031625~ubiquitin protein ligase binding	24	6.48E-08	LYN, RB1, YWHAE, GSK3B, XBP1, HSP90AA1, HSP90AB1, HSPA5, FANCL, FAF1, BCL10, HIF1A, LRPPRC, RELA, HDAC6, AURKA, NFKBIA, PRKAR1A, CHEK2, CALR, PRKACA, IKBKE, TP53, JAK1	3.899732	1.75E-06	1.56E-06
GOTERM_MF_DIRECT	GO:0019904~protein domain specific binding	20	6.67E-08	YWHAE, DDX6, HSPA5, PRKDC, FAF1, ACSL3, IKZF1, HIF1A, ETV6, CCNA2, TFDP1, PRKAR1A, CHEK1, CDK2, GRB2, TOP1, EZR, PRKACA, TP63, KPNB1	4.657514	1.75E-06	1.56E-06
GOTERM_MF_DIRECT	GO:0031490~chromatin DNA binding	13	1.21E-07	SUZ12, XBP1, CREBBP, HDAC3, SRF, STAT3, RELA, H1-3, H1-2, H1-4, BCL6, EP300, EZH2	7.638865	3.05E-06	2.73E-06
GOTERM_MF_DIRECT	GO:0004713~protein tyrosine kinase activity	14	1.36E-07	LYN, MAP2K3, MAP2K1, MAP2K2, SYK, TTK, TYK2, WEE1, PKM, BTK, MAP2K7, JAK3, FRK, JAK1	6.802658	3.21E-06	2.87E-06
GOTERM_MF_DIRECT	GO:0002039~p53 binding	12	1.36E-07	GSK3B, STK11, CREBBP, SMARCB1, KDM1A, HDAC1, TRIM24, EP300, HIF1A, TP53, TP63, BRD4	8.540963	3.21E-06	2.87E-06
GOTERM_MF_DIRECT	GO:0003714~transcription corepressor activity	19	1.42E-07	RB1, CREBBP, BTG2, PHB1, HDAC3, HDAC1, IRF2BP2, HMGB1, RUNX1, NCOR2, SNW1, TBL1XR1, SIN3A, BCL3, SRSF2, VHL, PFDN5, RCOR1, EZH2	4.683642	3.24E-06	2.90E-06
GOTERM_MF_DIRECT	GO:0004712~protein serine/threonine/tyrosine kinase activity	9	1.49E-07	GSK3B, MAP2K1, MAP2K2, RPS6KA1, AKT1, TTK, PRKACA, AURKB, AURKA	14.2127	3.29E-06	2.94E-06
GOTERM_MF_DIRECT	GO:0001228~DNA-binding transcription activator activity, RNA polymerase II-specific	30	1.85E-07	SRF, NR1I3, ETS1, HIF1A, IKZF3, RELA, CREB3L2, STAT6, MEF2D, TP63, GTF2I, ZNF384, MEF2B, TCF12, STAT3, TFE3, NFATC2, PAX5, FLI1, NFKB1, ETV6, RUNX1, NFKB2, CREB1, TFDP1, SP1, IRF4, ELF4, IRF1, TP53	3.075093	3.97E-06	3.55E-06
GOTERM_MF_DIRECT	GO:0004715~non-membrane spanning protein tyrosine kinase activity	10	2.39E-07	LYN, WEE1, MELK, SYK, PRKDC, BTK, TYK2, JAK3, FRK, JAK1	10.98566	4.98E-06	4.45E-06
GOTERM_MF_DIRECT	GO:1990841~promoter-specific chromatin binding	11	8.37E-07	SUZ12, DNMT1, KDM1A, STAT1, HDAC1, ERCC1, NUP98, TP53, IKZF3, TP63, EZH2	8.174623	1.69E-05	1.51E-05
GOTERM_MF_DIRECT	GO:0070182~DNA polymerase binding	7	3.24E-06	FANCI, HSP90AA1, RAD51, PCNA, HSP90AB1, FANCD2, HMGB1	16.07901	6.38E-05	5.71E-05

GOTERM_MF_DIRECT	GO:0030332~cyclin binding	8	4.61E-06	XRCC6, HDAC3, CDK6, CDK4, CDK2, CDK1, CDK12, NDC80	11.55064	8.82E-05	7.89E-05
GOTERM_MF_DIRECT	GO:0031492~nucleosomal DNA binding	10	7.29E-06	H2AX, H2AC11, H1-4, SMARCB1, H2AC6, HDAC1, H2AC16, H2AC17, H1-3, H1-2	7.431475	1.36E-04	1.22E-04
GOTERM_MF_DIRECT	GO:0001784~phosphotyrosine residue binding	9	1.01E-05	LYN, SYK, PLCG2, MAPK1, PTPN6, PTPN11, GRB2, CBL, MAPK3	8.422339	1.83E-04	1.63E-04
GOTERM_MF_DIRECT	GO:0140677~molecular function activator activity	7	1.48E-05	PTTG1, AKT2, CAPRIN1, HMGA1, MAP2K7, TP53, AURKA	12.63351	2.62E-04	2.35E-04
GOTERM_MF_DIRECT	GO:0030374~nuclear receptor coactivator activity	9	1.73E-05	SS18, KDM1A, ZMIZ1, PRKCB, THRAP3, CARM1, HMGA1, TACC1, ETS1	7.841488	2.99E-04	2.67E-04
GOTERM_MF_DIRECT	GO:0000987~cis-regulatory region sequence-specific DNA binding	9	1.97E-05	XBP1, TFDP1, ELL, TCF12, HMGA1, E2F1, AHR, HIF1A, TP53	7.708581	3.32E-04	2.97E-04
GOTERM_MF_DIRECT	GO:0016922~nuclear receptor binding	8	2.25E-05	SNW1, STAT1, TRIM24, EP300, TACC1, BAZ2A, ARID1A, HIF1A	9.188006	3.71E-04	3.32E-04
GOTERM_MF_DIRECT	GO:0003712~transcription coregulator activity	12	3.81E-05	CREBBP, EWSR1, BCL11A, FUS, THRAP3, CNOT2, POU2AF1, HMGA1, LPXN, CAMTA1, NFKB1, BRD4	4.851267	6.10E-04	5.45E-04
GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	33	3.88E-05	TOP2A, HSP90AB1, BCL2A1, TFRC, SRF, AHR, TYMS, IKZF3, RELA, PTPA, ATIC, CHEK2, TPR, AKT1, MEF2D, MCL1, NPM1, ST6GAL1, HSP90AA1, BCL11A, STAT1, IDH1, STAT3, CIP2A, TPD52L2, RUNX1, GRHPR, SFPO, PKM, MSH2, SP1, BAX, MAD2L1	2.223497	6.10E-04	5.45E-04
GOTERM_MF_DIRECT	GO:0001223~transcription coactivator binding	8	4.05E-05	CREBBP, STAT1, EP300, STAT6, AHR, HIF1A, RELA, RUNX1	8.422339	6.17E-04	5.52E-04
GOTERM_MF_DIRECT	GO:0017124~SH3 domain binding	12	4.10E-05	LYN, PTTG1, SH3BP1, INPP5D, ABI1, CCDC6, PTPN6, GRB2, CBL, WASF2, EPS15, DNM2	4.812765	6.17E-04	5.52E-04
GOTERM_MF_DIRECT	GO:0019903~protein phosphatase binding	10	6.54E-05	YWHAЕ, LGALS3, HSP90AA1, STAT3, GRB2, STAT6, MAP2K7, JAK3, IKBKE, JAK1	5.677981	9.65E-04	8.62E-04
GOTERM_MF_DIRECT	GO:0097110~scaffold protein binding	9	6.95E-05	LYN, YWHAЕ, XRCC6, MAP2K1, HSP90AA1, MAP2K2, SYK, PLCG2, PHF6	6.497233	0.001004	8.97E-04
GOTERM_MF_DIRECT	GO:0097718~disordered domain specific binding	7	9.20E-05	RB1, RRM1, HSP90AA1, HSP90AB1, CLTC, EZR, TP53	9.308901	0.001302	0.001164
GOTERM_MF_DIRECT	GO:0044877~protein-containing complex binding	19	9.61E-05	NAPA, XRCC6, CARMIL2, PCNA, TFRC, CLTA, BCL10, MTOR, DDB2, RPTOR, PPP3CA, STK11, NRAS, KIF5B, STRN, RAC1, FCGR2B, BIRC3, CDK5RAP2	2.936228	0.001334	0.001192
GOTERM_MF_DIRECT	GO:0017056~structural constituent of nuclear pore	6	1.36E-04	NUP214, NUP93, POM121, NUP107, TPR, NUP98	11.6617	0.001821	0.001628
GOTERM_MF_DIRECT	GO:0050681~nuclear androgen receptor binding	6	1.36E-04	SNW1, KDM1A, PRKCB, EP300, CALR, FOXP1	11.6617	0.001821	0.001628
GOTERM_MF_DIRECT	GO:0004693~cyclin-dependent protein serine/threonine kinase activity	6	2.34E-04	CCND3, CDK6, CDK4, CDK2, CDK1, CDK12	10.45532	0.003074	0.002748
GOTERM_MF_DIRECT	GO:0042054~histone methyltransferase activity	6	3.25E-04	SUZ12, EED, PRMT1, CARM1, DOT1L, EZH2	9.78078	0.004181	0.003738
GOTERM_MF_DIRECT	GO:0070878~primary miRNA binding	4	5.87E-04	SRF, STAT3, SRSF3, EZH2	22.45957	0.007415	0.006633
GOTERM_MF_DIRECT	GO:0051219~phosphoprotein binding	6	7.56E-04	LYN, RB1, YWHAЕ, THRAP3, PHF6, MTOR	8.194708	0.009393	0.008398
GOTERM_MF_DIRECT	GO:1990837~sequence-specific double-stranded DNA binding	24	8.08E-04	XBP1, ZNF384, MEF2B, MAX, SRF, NR113, TFE3, TCF12, TFEB, NFATC2, AHR, ETS1, FLI1, FOXP1, NFKB2, CREB1, CUX1, BCL6, SP1, IRF4, ELF4, E2F1, IRF8, MEF2D	2.165744	0.009824	0.008783
GOTERM_MF_DIRECT	GO:0008353~RNA polymerase II CTD heptapeptide repeat kinase activity	4	8.26E-04	CDK1, MAPK1, CDK12, BRD4	20.21361	0.009824	0.008783
GOTERM_MF_DIRECT	GO:0000978~RNA polymerase II cis-regulatory region sequence-specific DNA binding	43	8.33E-04	HDAC1, SRF, NR113, IKZF1, ETS1, HIF1A, IKZF3, RELA, HDAC6, E2F1, STAT6, MEF2D, TP63, SUZ12, XBP1, ZNF384, MEF2B, BCL11A, STAT1, TCF12, STAT3, TFE3, TFEB, HMGA1, NFATC2, PAX5, FLI1, NFKB1, ETV6, FOXP1, RUNX1, NFKB2, CREB1, BCL6, SP1, IRF4, ELF4, THRAP3, IRF1, IRF8, TOP1, TP53, EZH2	1.698955	0.009824	0.008783
GOTERM_MF_DIRECT	GO:0000977~RNA polymerase II transcription regulatory region sequence-specific DNA binding	18	9.21E-04	RB1, XBP1, STAT1, MAX, NR113, IKZF1, HIF1A, RELA, NFKB1, ETV6, RUNX1, TFDP1, CUX1, SP1, IRF1, STAT6, MEF2D, TP63	2.512742	0.010693	0.00956
GOTERM_MF_DIRECT	GO:0003729~mRNA dimerization activity	15	9.70E-04	DDX6, HSP90AA1, CPSF6, DDX3X, CNBP, NONO, TYMS, PTBP1, PKM, PCBP1, CAPRIN1, TPR, NUP98, CALR, SF3B1	2.817883	0.011073	0.0099
GOTERM_MF_DIRECT	GO:0046983~protein dimerization activity	12	0.001157	PPP3CA, MEF2B, HSP90AB1, MAX, STAT3, TFE3, TCF12, TFEB, E2F1, AHR, MEF2D, HIF1A	3.277883	0.013001	0.011623
GOTERM_MF_DIRECT	GO:0043015~gamma-tubulin binding	6	0.001219	LYN, PAK1, DDX3X, ARHGEF7, NDRG1, CDK5RAP2	7.395224	0.013484	0.012056
GOTERM_MF_DIRECT	GO:0008139~nuclear localization sequence binding	5	0.001361	NUP214, NFKBIA, POM121, NUP98, KPNB1	10.10681	0.014821	0.013251
GOTERM_MF_DIRECT	GO:0048156~tau protein binding	6	0.001516	GSK3B, HSP90AA1, HSP90AB1, EP300, HDAC6, PICALM	7.05126	0.016264	0.014541
GOTERM_MF_DIRECT	GO:0003697~single-stranded DNA binding	9	0.00171	RAD51, MSH2, ERCC1, PCBP1, RPA3, HMGB1, TOP1, MLH1, LRPPRC	4.06077	0.018071	0.016157
GOTERM_MF_DIRECT	GO:0070577~lysine-acetylated histone binding	5	0.00183	CARM1, TRIM24, BAZ2A, MLLT1, BRD4	9.358154	0.018777	0.016788

GOTERM_MF_DIRECT	GO:0023026~MHC class II protein complex binding	5	0.00183	YWHAЕ, CD74, HSP90AA1, PKM, HSP90AB1	9.358154	0.018777	0.016788
GOTERM_MF_DIRECT	GO:0035591~signaling adaptor activity	7	0.002392	YWHAЕ, DDX3X, SYK, CAPRIN1, STAT3, ABI1, MYD88	5.126641	0.023942	0.021405
GOTERM_MF_DIRECT	GO:0016538~cyclin-dependent protein serine/threonine kinase regulator activity	5	0.002401	CCNA2, CCND3, CCND2, CCNE1, CDK4	8.712764	0.023942	0.021405
GOTERM_MF_DIRECT	GO:0000287~magnesium ion binding	13	0.002932	TOP2A, FEN1, IDH1, IDH2, RPS6KA3, WEE1, STK11, PKM, MSH2, RPS6KA1, CDK2, MAP2K7, PRKACA	2.748713	0.028828	0.025774
GOTERM_MF_DIRECT	GO:0004708~MAP kinase activity	4	0.003529	MAP2K3, MAP2K1, MAP2K2, MAP2K7	12.63351	0.033709	0.030138
GOTERM_MF_DIRECT	GO:0001046~core promoter sequence-specific DNA binding	4	0.003529	NPM1, HDAC1, TP53, FOXF1	12.63351	0.033709	0.030138
GOTERM_MF_DIRECT	GO:0008017~microtubule binding	14	0.003571	NDE1, NDRG1, NDC80, LRPPRC, HDAC6, DNMT2, EML4, REEP3, KIF5B, CCDC88C, ZNF207, EZR, GTSЕ1, CDK5RAP2	2.554067	0.033709	0.030138
GOTERM_MF_DIRECT	GO:0030235~nitric oxide synthase regulator activity	3	0.003735	HSP90AA1, HSP90AB1, AKT1	30.32042	0.034795	0.031109
GOTERM_MF_DIRECT	GO:0060090~molecular adaptor activity	11	0.004431	RB1, SP1, SEPTIN2, HMGA1, E2F1, SEPTIN6, NFATC2, PTPN11, VHL, SEPTIN9, MYD88	2.941134	0.04074	0.036425
GOTERM_MF_DIRECT	GO:0008301~DNA binding, bending	4	0.005844	TOP2A, HMGA1, HMGB1, TOP1	10.63874	0.051721	0.046242
GOTERM_MF_DIRECT	GO:0061575~cyclin-dependent protein serine/threonine kinase activator activity	4	0.005844	CCND3, CCND2, MNAT1, CKS1B	10.63874	0.051721	0.046242
GOTERM_MF_DIRECT	GO:0019887~protein kinase regulator activity	4	0.005844	HSP90AB1, FAF1, RAC2, RAC1	10.63874	0.051721	0.046242
UP_KW_BIOLOGICAL_PROCESS	KW-0945~Host-virus interaction	65	2.95E-20	RB1, H2AX, YWHAЕ, PHB1, MRE11, SMARCB1, DDX3X, TFRC, HMGB1, ICAM1, RPTOR, PPP2R1A, ZC3H7B, CHEK2, RPS6KA1, PIM1, EP300, SKP2, IKBKE, NUP214, HSP90AA1, SYK, EED, SDHB, RHOA, CCNA2, CREB1, NUP98, TOP1, TP53, KPNB1, HDAC3, SET, PCNA, HIF1A, RELA, E2F1, MAPK1, EP515, WASF2, BRD4, MAPK3, LYN, CENPU, NPM1, CREBBP, XRCC6, HSPA5, STAT1, STAT3, SEPTIN6, MSN, NFKB1A, SNW1, SP1, CARM1, ERCC2, ABI1, HNRNPA2B1, CDK1, BAX, GRB2, CDK12, FCGR2B, RCOR1	3.681308	2.63E-18	2.30E-18
UP_KW_BIOLOGICAL_PROCESS	KW-0131~Cell cycle	62	2.31E-18	RB1, H2AX, SMARCB1, CLTC, CLTA, BUB1B, AHR, IKZF1, MKI67, CCAR2, CDC73, CKS1B, RPS6KA3, CCND3, STK11, CCND2, PTTG1, CHEK2, RPS6KA1, CHEK1, PIM1, ZNF207, EP300, TP63, CSNK2A1, PRKDC, SMC1A, RHOA, CDC25A, EML4, CCNA2, MELK, TFDP1, FANCD2, CCNE1, MAPRE1, TP53, PRCC, AURKB, AURKA, TPR, E2F1, MAPK1, MAPK3, FANCI, SEPTIN2, NDE1, SEPTIN6, SEPTIN9, MLH1, NDC80, WEE1, STAG2, CDK6, CDK4, REEP3, CDK2, CDK1, TACC3, TACC1, MNAT1, MAD2L1	3.526735	1.03E-16	9.01E-17
UP_KW_BIOLOGICAL_PROCESS	KW-0090~Biological rhythms	24	3.79E-12	TOP2A, GSK3B, CREBBP, KDM5C, HDAC3, CSNK2A1, PRKDC, HDAC1, NONO, HUWE1, AHR, MTOR, CCAR2, NFKB2, SFPQ, CREB1, SP1, THRAP3, SIN3A, CDK1, EP300, TOP1, TP53, EZH2	6.25256	1.12E-10	9.84E-11
UP_KW_BIOLOGICAL_PROCESS	KW-0227~DNA damage	36	1.84E-09	H2AX, FH, FEN1, MRE11, PCNA, PRKDC, HMGB1, CCAR2, POLD4, STK11, PTTG1, CHEK2, POLD1, CHEK1, IKBKE, MUTHYH, BRD4, FANCI, XRCC6, FANCL, NONO, HUWE1, CIP2A, MLH1, SMC1A, FANCG, DDB2, SFPQ, RAD51, RAD51C, MSH2, FANCD2, ERCC1, RPA3, ERCC2, CDK2	3.204615	3.35E-08	2.93E-08
UP_KW_BIOLOGICAL_PROCESS	KW-0132~Cell division	35	1.90E-09	CLTC, CLTA, BUB1B, CDC73, AURKB, AURKA, CKS1B, CCND3, CCND2, PTTG1, CHEK2, TPR, ZNF207, SEPTIN2, NDE1, SEPTIN6, SEPTIN9, SMC1A, RHOA, CDC25A, NDC80, EML4, CCNA2, WEE1, STAG2, CDK6, CCNE1, CDK4, REEP3, CDK2, CDK1, TACC3, TACC1, MAPRE1, MAD2L1	3.272123	3.35E-08	2.93E-08
UP_KW_BIOLOGICAL_PROCESS	KW-0805~Transcription regulation	106	2.26E-09	RB1, SMARCB1, KDM1A, IKZF1, AHR, IKZF3, ETS1, CCAR2, CCND3, ZMIZ1, CHEK2, CREB3L2, TRIM24, CPNE1, EP300, TP63, GTF2I, MEF2B, CSNK2A1, PRKCB, MRTFA, RUNX1, FOXF1, EWSR1, TBL1XR1, SARNP, BTK, TP53, DNMT1, MAX, BAZ2A, HIF1A, LPXN, CAMTA1, ZNF384, XBP1, CREBBP, XRCC6, BCL11A, NONO, HMGA1, IRF2BP2, NFATC2, FLI1, NFKB1, NFKB2, SNW1, BCL6, SP1, CNOT2, BCL3, MNAT1, RCOR1, EZH2, KDM5C, BTG2, DDX3X, ELL, AFF3, PHF6, CDC73, SIN3A, SS18, EED, TCF12, NCOA4, TFE3, TFEB, PAX5, ARID1A, ETV6, NCOR2, SFPQ, CREB1, TFDP1, IRF4, ELF4, THRAP3, IRF1, IRF8, HDAC3, HDAC1, SRF, NR113, MLLT1, HDAC6, RELA, CUX1, NSD2, E2F1, MAPK1, STAT6, MEF2D, BRD4, SUZ12, CENPU, UTP4, STAT1, CNBP, STAT3, LRPPRC, CARM1, POU2AF1, ERCC2, TCEA1, TRIM33	1.715957	3.35E-08	2.93E-08
UP_KW_BIOLOGICAL_PROCESS	KW-0804~Transcription	106	1.12E-08	RB1, SMARCB1, KDM1A, IKZF1, AHR, IKZF3, ETS1, CCAR2, CCND3, ZMIZ1, CHEK2, CREB3L2, TRIM24, CPNE1, EP300, TP63, GTF2I, MEF2B, CSNK2A1, PRKCB, MRTFA, RUNX1, FOXF1, EWSR1, TBL1XR1, SARNP, BTK, TP53, DNMT1, MAX, BAZ2A, HIF1A, LPXN, CAMTA1, ZNF384, XBP1, CREBBP, XRCC6, BCL11A, NONO, HMGA1, IRF2BP2, NFATC2, FLI1, NFKB1, NFKB2, SNW1, BCL6, SP1, CNOT2, BCL3, MNAT1, RCOR1, EZH2, KDM5C, BTG2, DDX3X, ELL, AFF3, PHF6, CDC73, SIN3A, SS18, EED, TCF12, NCOA4, TFE3, TFEB, PAX5, ARID1A, ETV6, NCOR2, SFPQ, CREB1, TFDP1, IRF4, ELF4, THRAP3, IRF1, IRF8, HDAC3, HDAC1, SRF, NR113, MLLT1, HDAC6, RELA, CUX1, NSD2, E2F1, MAPK1, STAT6, MEF2D, BRD4, SUZ12, CENPU, UTP4, STAT1, CNBP, STAT3, LRPPRC, CARM1, POU2AF1, ERCC2, TCEA1, TRIM33	1.668273	1.43E-07	1.25E-07
UP_KW_BIOLOGICAL_PROCESS	KW-0234~DNA repair	31	1.35E-08	H2AX, FH, FEN1, MRE11, PCNA, PRKDC, HMGB1, POLD4, PTTG1, CHEK2, POLD1, CHEK1, MUTHYH, FANCI, XRCC6, FANCL, NONO, HUWE1, MLH1, SMC1A, FANCG, DDB2, SFPQ, RAD51, RAD51C, MSH2, FANCD2, ERCC1, RPA3, ERCC2, CDK2	3.328114	1.51E-07	1.32E-07
UP_KW_BIOLOGICAL_PROCESS	KW-0053~Apoptosis	35	1.42E-06	CYFIP2, DDX3X, BCL2A1, FAF1, TNFAIP3, BUB1B, BCL10, PSEN1, CCAR2, PAK1, STK11, CHEK2, AKT2, INPP5D, E2F1, PIM1, AKT1, MAPK1, MAP2K7, MEF2D, TP63, MCL1, MAPK3, XBP1, CSNK2A1, PRKCB, IGF1BP3, PRKDC, NFKB1, MELK, CDK1, BTK, BAX, TP53, BIRC3	2.491343	1.41E-05	1.23E-05
UP_KW_BIOLOGICAL_PROCESS	KW-0498~Mitosis	24	1.59E-06	SEPTIN2, NDE1, CLTC, CLTA, BUB1B, SMC1A, CDC25A, NDC80, AURKB, AURKA, EML4, CCNA2, WEE1, STAG2, PTTG1, CHEK2, REEP3, TPR, CDK2, ZNF207, CDK1, TACC3, MAPRE1, MAD2L1	3.211931	1.41E-05	1.24E-05

UP_KW_BIOLOGICAL_PROCESS	KW-0816~Tricarboxylic acid cycle	7	4.92E-05	FH, MDH1, IDH1, IDH2, SDHC, SDHA, SDHB	10.13146	3.98E-04	3.49E-04
UP_KW_BIOLOGICAL_PROCESS	KW-0233~DNA recombination	9	0.00237	H2AX, XRCC6, SFPQ, RAD51, RAD51C, PRKCD, RPA3, NONO, HMGB1	3.822897	0.017577	0.015405
UP_KW_BIOLOGICAL_PROCESS	KW-0509~mRNA transport	10	0.003369	NUP214, NUP93, POM121, NUP107, SARNP, TPR, HNRNPA2B1, SRSF3, NUP98, LRPPRC	3.283907	0.023065	0.020214
UP_KW_BIOLOGICAL_PROCESS	KW-0159~Chromosome partition	6	0.00666	DDX3X, STAG2, PTTG1, PPP2R1A, ERCC2, ZNF207 RB1, CYFIP2, PHB1, NUP107, SMARCB1, IKZF1, MKI67, H2AC16, IKZF3, H2AC17, CCAR2, H2AC11, RPS6KA3, LGALS3, TCL1A, ZMIZ1, PPP2R1A, AKT2, CHEK2, RPS6KA1, CHEK1, CREB3L2, TRIM24, CPNE1, AKT1, SKP2, PRKACA, TP63, NUP214, MBNL1, MEF2B, CSNK2A1, PRKCB, PRKCD, MRTFA, RUNX1, NUP93, EWSR1, SARNP, BTK, NUP98, TP53, POM121, SET, PRKDC, BAZ2A, HIF1A, PPP4C, PDCD11, PCBP1, H3C2, LYN, ZNF384, XBP1, CREBBP, XRCC6, H4C9, BCL11A, IRF2BP2, NFATC2, FLI1, H1-3, H1-2, H1-4, SNW1, STAG2, GRB2, CDK12, RCOR1, EZH2, H2AX, TOP2A, FEN1, ELL, FAF1, PHF6, RAC1, IKBKE, SS18, PRMT1, TCF12, TFE3, TFEB, PAX5, RHOA, DDB2, NCOR2, RAD51C, POT1, FH, PCNA, NR1I3, DOT1L, TYMS, RELA, RECQL4, PTPA, PAK1, CUX1, NSD2, STAT6, MEF2D, SF3B1, BRD4, SUZ12, CENPU, NPM1, UTP4, STAT1, WDR18, STAT3, H2BC4, HUWE1, MLH1, LRPPRC, RPA3, HNRNPA2B1, ABI1, TCEA1, TACC1, FRK, MAD2L1, MRE11, KDM1A, BUB1B, AHR, ETS1, STK11, CCND3, CCND2, PTTG1, ZNF207, PIM1, EP300, GTF2I, MAP2K1, H2AC6, FOXF1, MSH2, FANCD2, TBL1XR1, CCNE1, SRSF2, SRSF3, RAF1, KPNB1, LRRC59, DDX6, DNMT1, CBF, MAX, NDRG1, TPR, EP400, LPXN, CAMTA1, MAP2K7, MCL1, FANCI, CPSF6, FANCL, FUS, NONO, HMGA1, FANCG, NDC80, NFKB1, NFKB2, NFKBIA, CDK6, BCL6, SP1, CDK4, CNOT2, BCL3, CDK2, CDK1, NF2, MNAT1, MYD88, PICALM, YWHAE, GSK3B, KDM5C, DDX3X, HSP90A1, TNFAIP3, HMGB1, AFF3, CDC73, PTBP1, ZC3H7A, ZC3H7B, IN3A, HSP90AA1, EED, CAD, SMC1A, ARID1A, H2BC17, ETV6, H2BC12, CCNA2, SFPQ, PKM, CREB1, TFDP1, IRF4, THRAP3, ELF4, IRF1, CTDSBP2, H2BC11, IRF8, TOP1, PFDN5, BIRC3, HDAC3, HDAC1, SRF, RAP1GDS1, PRCC, U2AF1, MLLT1, HDAC6, AURKB, POLD4, SH3BP1, FIP1L1, U2AF2, POLD1, E2F1, MAPK1, VHL, MAPK3, MUTYH, CNBP, PTPN11, MTOR, WEE1, UFM1, RAD51, ERCC1, CARM1, POU2AF1, ERCC2, BAX, PTPN6, TRIM33	4.988744	0.042341	0.037108
UP_KW_CELLULAR_COMPONENT	KW-0539~Nucleus	249	1.54E-44	CYFIP2, PHB1, AHYCL1, IKZF1, IKZF3, CCAR2, RPS6KA3, LGALS3, TCL1A, ZMIZ1, PPP2R1A, AKT2, RPS6KA1, CHEK1, TRIM24, CPNE1, AKT1, SKP2, PRKACA, GTSE1, TP63, CDK5RAP2, MBNL1, FNB1P, COG5, PRKCB, RPL22, PRKCD, MRTFA, EML4, EWSR1, BTK, EZR, TP53, SET, BCL10, HIF1A, PPP4C, INPP5D, PCBP1, SEC31A, LYN, CARMIL2, XBP1, CREBBP, BCL11A, IRF2BP2, NFATC2, CCDC88C, STRN, GRB2, CALR, TOP2A, CLTC, CLTA, RPTOR, PPP3CA, ATIC, RAC2, RAC1, JAK3, IKBKE, SYK, PRMT1, TFE3, TFEB, RHOA, RAD51C, ARHGEF7, MAPRE1, FH, NR1I3, TYMS, RELA, RECQL4, PTPA, PAK1, NSD2, STAT6, EPS15, CENPU, NPM1, MDH1, STAT1, SEPTIN2, NDE1, WDR18, STAT3, HUWE1, SEPTIN6, SEPTIN9, HNRNPA2B1, ABI1, TACC3, CCDC6, TACC1, FRK, MAD2L1, BUB1B, AHR, ETS1, STK11, CCND3, CCND2, PTTG1, KIF5B, ZNF207, PIM1, EP300, GTF2I, MAP2K1, MAP2K2, TPM3, AIP, SRSF3, RAF1, KPNB1, CSNK1G2, CARD11, DDX6, GMPS, NDRG1, RASGRP1, TPR, LPXN, CAMTA1, MAP2K7, MCL1, FANCI, CPSF6, HSPA5, FANCL, IDH1, MSN, FANCG, NFKB1, NFKB2, NFKBIA, CDK6, SP1, CDK4, CNOT2, CAPRIN1, BCL3, CDK2, PI4KA, CDK1, PLEKHM2, NF2, MYD88, YWHAE, GSK3B, DDX3X, HSP90A1, WDR1, PIK3CD, TNFAIP3, HMGB1, LASP1, CAPZB, HSP90AA1, CAD, CIP2A, DNMT2, DUSP22, CCNA2, SFPQ, PKM, TFDP1, IRF1, IRF8, LCP1, PFDN5, BIRC3, HDAC3, BCL2A1, RAP1GDS1, CBL, HDAC6, AURKB, AURKA, CDC42, SH3BP1, MAPK1, VHL, WASF2, MAPK3, RRM1, CNBP, PTPN11, MTOR, UFM1, RAD51, ERCC1, CARM1, ERCC2, BAX, PTPN6	2.089431	5.54E-43	4.61E-43
UP_KW_CELLULAR_COMPONENT	KW-0963~Cytoplasm	198	2.62E-18	H2AX, MRE11, NUP107, KDM1A, BUB1B, HMGB1, MKI67, H2AC16, PHF6, H2AC17, H2AC11, PPP2R1A, CHEK1, ZNF207, EP300, H2AC6, EED, CIP2A, SMC1A, H2BC17, DDB2, H2BC12, MSH2, H2BC11, POT1, FH, AURKB, PAK1, TPR, NSD2, H3C2, BRD4, CENPU, XRCC6, H4C9, UTP4, BCL11A, SEPTIN2, NDE1, NONO, H2BC4, HMGA1, SEPTIN6, MLH1, NDC80, H1-3, H1-2, H1-4, RAD51, STAG2, CARM1, MAD2L1	1.676644	4.71E-17	3.92E-17
UP_KW_CELLULAR_COMPONENT	KW-0158~Chromosome	52	1.50E-17	CENPU, NUP107, SEPTIN2, NDE1, SEPTIN6, BUB1B, SMC1A, PHF6, NDC80, AURKB, TPR, ZNF207, MAD2L1	4.076747	1.80E-16	1.50E-16
UP_KW_CELLULAR_COMPONENT	KW-0995~Kinetochore	13	1.45E-06	CENPU, NUP107, SEPTIN2, NDE1, SEPTIN6, BUB1B, SMC1A, PHF6, NDC80, AURKB, STAG2, PPP2R1A, TPR, ZNF207, MAD2L1	6.086001	1.31E-05	1.09E-05
UP_KW_CELLULAR_COMPONENT	KW-0137~Centromere	15	1.97E-06	H2BC12, H2AX, H2AC11, H4C9, H2AC6, H2BC11, H2BC4, H3C2, H2AC16, H2BC17, H2AC17	4.982044	1.42E-05	1.18E-05
UP_KW_CELLULAR_COMPONENT	KW-0544~Nucleosome core	11	1.72E-05	DDX3X, WDR1, CLTC, CLTA, BUB1B, CCAR2, LASP1, CAPZB, KIF5B, CHEK1, ZNF207, GTSE1, CDK5RAP2, MAP2K1, TPM3, FNB1P, RHOA, DNMT2, EML4, LCP1, EZR, MAPRE1, TP53, NR1I3, NDRG1, HDAC6, AURKB, AURKA, CDC42, PAK1, PPP4C, INPP5D, TPR, MAPK1, WASF2, NPM1, CARMIL2, SEPTIN2, NDE1, SEPTIN6, MSN, SEPTIN9, RAD51, CDK6, ERCC2, ABI1, CDK2, CDK1, TACC3, CCDC6, TACC1, NF2, MAD2L1	5.877367	1.03E-04	8.59E-05
UP_KW_CELLULAR_COMPONENT	KW-0206~Cytoskeleton	53	2.37E-05	NUP214, NUP93, POM121, NUP107, TPR, NUP98	1.832121	1.22E-04	1.02E-04
UP_KW_CELLULAR_COMPONENT	KW-0906~Nuclear pore complex	6	0.003351	FNB1P, CLTC, CLTA, EPS15, DNMT2, PICALM	5.362491	0.020271	0.012566
UP_KW_CELLULAR_COMPONENT	KW-0168~Coated pit	6	0.005068	PHB1, ELL, ARAF, ETS1, TCL1A, PTTG1, TFG, AKT2, CREB3L2, PIM1, AKT1, NUP214, SS18, TPM3, NCOA4, TFE3, MRTFA, PAX5, RHOA, ETV6, RUNX1, ELF4, EWSR1, TOP1, RAF1, DDX6, SET, CBF, GMPS, MLLT1, CBL, AURKA, NRAS, TPR, NSD2, EPS15, SEC31A, SUZ12, LYN, NPM1, FUS, FLI1, NFKB2, BCL6, POU2AF1, BCL3, GNAS, CCDC6, FCGR2B, PICALM	5.001873	5.19E-21	5.10E-21
UP_KW_DISEASE	KW-0043~Tumor suppressor	21	1.34E-04	RB1, FH, SMARCB1, PRKCD, BUB1B, BCL10, MLH1, SDHA, CCAR2, CDC73, STK11, MSH2, CHEK2, IRF1, TRIM24, BAX, NF2, VHL, TP53, FRK, MUTYH	2.588261	0.003884	0.003817
UP_KW_DISEASE	KW-0923~Fanconi anemia	6	0.001652	FANCI, RAD51, RAD51C, FANCL, FANCD2, FANCG	6.585099	0.031929	0.031379
UP_KW_DOMAIN	KW-0727~SH2 domain	15	2.63E-09	LYN, SYK, STAT1, STAT3, PTPN11, TYK2, INPP5D, BTK, PLCG2, GRB2, PTPN6, STAT6, JAK3, FRK, JAK1	8.398734	6.06E-08	4.74E-08
UP_KW_DOMAIN	KW-0677~Repeat	124	2.36E-08	CSF3R, SMARCB1, IKZF1, AHR, MKI67, IKZF3, ICAM1, RPS6KA3, LGALS3, PTTG1, PPP2R1B, PPP2R1A, PSMD2, RPS6KA1, ENPP2, ZNF207, TRIM24, CPNE1, EP300, SKP2, GTF2I, NUP214, MBNL1, USP5, PRKCB, PRKCD, AIP, MRTFA, EML4, EWSR1, TBL1XR1, PRKAR1A, SRSF3, NUP98, KPNB1, LRRC59, POM121,	1.508146	2.72E-07	2.13E-07

				DNMT1, PRKDC, BAZ2A, RASAL1, HIF1A, RASGRP1, NDRG1, WDR70, PDCD11, INPP5D, CD19, PCBP1, PLCG2, LPXN, CAMTA1, SEC31A, ZNF384, CARMIL2, CREBBP, BCL11A, FUS, NONO, HMGA1, NFATC2, FANCG, NFKB1, NFKB2, NFKBIA, BCL6, SP1, BCL3, GRB2, STRN, CALR, RCOR1, KDM5C, WDR1, RASGRF1, CLTC, TNFAIP3, HMGB1, PHF6, RPTOR, PTBP1, LASP1, ZC3H7A, SIN3A, ZC3H7B, JAK3, JAK1, SS18, SYK, EED, CAD, TYK2, MMP9, DDB2, NCOR2, SFPQ, LCP1, BIRC3, RAP1GDS1, DOT1L, U2AF1, CBL, HDAC6, CUX1, U2AF2, NSD2, IL21R, VHL, EPS15, SF3B1, BRD4, GIT2, UTP4, WDR18, CNBP, PTPN11, LRPPRC, MTOR, HNRNPA2B1, CCDC6, PTPN6, TACC1, FCGR2B, TRIM33 FEN1, PHB1, KDM1A, FAF1, RASGRF1, CLTC, CLTA, CCAR2, ZC3H7A, TFG, SIN3A, KIF5B, CREB3L2, TRIM24, IKBKE, CDKSRAP2, NUP214, MAP2K1, TPM3, FNBP1, TFE3, MRTFA, CIP2A, SMC1A, RUNX1, NCOR2, EML4, SFPQ, CREB1, TOP1, EZR, ARHGEF7, CARD11, BIRC3, LRRC59, SET, MAX, RPN1, GOSR1, DOT1L, BAZ2A, RASGRP1, CUX1, TPR, EP400, VTI1A, MAP2K7, EPS15, SF3B1, CENPU, GIT2, XBP1, HSPA5, STAT1, NDE1, NONO, STAT3, SEPTIN6, TPDS2L2, NDC80, WEE1, STAG2, CAPRIN1, CCDC88C, ABI1, GNAS, TACC3, CCDC6, STRN, TACC1, NF2, MNAT1, TRIM33, RCOR1, PICALM	1.689577	1.43E-05	1.12E-05		
UP_KW_DOMAIN	KW-0175~Coiled coil	75	1.86E-06						0.00222
UP_KW_DOMAIN	KW-0103~Bromodomain	6	4.94E-04	CREBBP, TRIM24, EP300, BAZ2A, TRIM33, BRD4	9.013276	0.002838			1
				KDM5C, DNMT1, NR1I3, ARAF, TNFAIP3, U2AF1, BAZ2A, RASAL1, IKZF1, CBL, PHF6, RASGRP1, IKZF3, HDAC6, ZC3H7A, ZMIZ1, ZC3H7B, POLD1, NSD2, ZNF207, TRIM24, EP300, SUZ12, GIT2, ZNF384, CREBBP, MBNL1, USP5, PRKCB, FANCL, BCL11A, FUS, CNBP, PRKCD, IRF2BP2, FOXF1, BCL6, SP1, EWSR1, BTK, TCEA1, RAF1, MNAT1, TRIM33, BIRC3	1.498153	0.024115	0.01887		
UP_KW_DOMAIN	KW-0863~Zinc-finger	45	0.005242						3
UP_KW_DOMAIN	KW-0728~SH3 domain	10	0.011991	LYN, LASP1, FNBP1, ABI1, BTK, PLCG2, GRB2, ARHGEF7, FRK, MYO1F	2.701347	0.045967			4
UP_KW_DOMAIN	KW-0853~WD repeat	11	0.016964	RPTOR, EML4, UTP4, WDR1, WDR70, EED, TBL1XR1, WDR18, STRN, SEC31A, DDB2	2.393985	0.055739			2
UP_KW_DOMAIN	KW-0729~SH3-binding	5	0.019872	PTTG1, SH3BP1, INPP5D, CCDC6, EPS15	4.811775	0.057132			2
				TOP2A, GSK3B, DDX3X, HSP90A1, ARAF, PIK3CD, BUB1B, MKI67, RPS6KA3, STK11, CHEK2, AKT2, KIF5B, RPS6KA1, CHEK1, PIM1, AKT1, PRKACA, JAK3, IKBKE, JAK1, PDK1, MAP2K3, MAP2K1, HSP90AA1, MAP2K2, CSNK2A1, SYK, PRKCB, CAD, PRKCD, TYK2, ACSL3, SMC1A, RAD51C, PKM, MELK, MSH2, THRAP3, BTK, RAF1, CSNK1G2, DDX6, PRKDC, GMPS, AK2, TTK, AURKB, AURKA, PTPA, RECQL4, PAK1, EP400, MAPK1, MAP2K7, MAPK3, LYN, RRM1, XRCC6, HSPA5, MLH1, MTOR, WEE1, RAD51, CDK6, CDK4, CAPRIN1, ERCC2, CDK2, PI4KA, CDK1, CDK12, FRK, MYO1F	2.133272	2.20E-10	2.20E-10		
UP_KW_LIGAND	KW-0067~ATP-binding	74	7.85E-12						
				TOP2A, GSK3B, DDX3X, HSP90A1, ARAF, PIK3CD, BUB1B, MKI67, RPS6KA3, STK11, CHEK2, AKT2, KIF5B, RPS6KA1, CHEK1, PIM1, RAC2, AKT1, RAC1, PRKACA, JAK3, IKBKE, JAK1, PDK1, MAP2K3, MAP2K1, HSP90AA1, MAP2K2, CSNK2A1, SYK, PRKCB, CAD, PRKCD, TYK2, ACSL3, SMC1A, RHOA, DNM2, RAD51C, PKM, MELK, MSH2, PRKARIA, THRAP3, BTK, RAF1, CSNK1G2, DDX6, PRKDC, GMPS, AK2, TTK, AURKB, AURKA, PTPA, RECQL4, CDC42, NRAS, PAK1, EP400, MAPK1, MAP2K7, MAPK3, LYN, RRM1, XRCC6, HSPA5, SEPTIN2, SEPTIN6, SEPTIN9, MLH1, MTOR, WEE1, RAD51, CDK6, CDK4, CAPRIN1, ERCC2, CDK2, PI4KA, CDK1, GNAS, CDK12, FRK, MYO1F	1.881798	8.18E-10	8.18E-10		
UP_KW_LIGAND	KW-0547~Nucleotide-binding	85	5.84E-11						
				GSK3B, ARAF, PIK3CD, BUB1B, CKS1B, RPS6KA3, STK11, PLAU, CHEK2, AKT2, RPS6KA1, CHEK1, PIM1, AKT1, PRKACA, SKP2, JAK3, IKBKE, JAK1, GTF2I, PDK1, MAP2K3, MAP2K1, MAP2K2, CSNK2A1, SYK, PRKCB, PRKCD, TYK2, PKM, MELK, PRKARIA, BTK, RAF1, CSNK1G2, PRKDC, AK2, TTK, AURKB, AURKA, PAK1, MAPK1, MAP2K7, MAPK3, LYN, GIT2, MTOR, WEE1, CDK6, CDK4, CDK2, PI4KA, CDK1, CDK12, FRK	2.867835	1.56E-10	1.49E-10		
UP_KW_MOLECULA R_FUNCTION	KW-0418~Kinase	55	2.32E-12	SMARCB1, AHR, IKZF1, AFF3, CCAR2, PTBP1, ZMIZ1, CREB3L2, TP63, SS18, MEF2B, NCOA4, TFE3, TFEB, RUNX1, SFPQ, CREB1, TFDP1, IRF4, ELF4, TBL1XR1, THRAP3, IRF1, IRF8, TP53, DNMT1, MAX, SRF, NR1I3, MLLT1, HIF1A, RELA, E2F1, LPXN, CAMTA1, STAT6, MEF2D, XBP1, CREBBP, XRCC6, STAT1, NONO, STAT3, IRF2BP2, NFATC2, FLI1, NFKB1, NFKB2, BCL6, SP1, POU2AF1, BCL3, TACC1	2.877904	1.93E-10	1.84E-10		
UP_KW_MOLECULA R_FUNCTION	KW-0010~Activator	53	5.76E-12	GSK3B, PRKDC, ARAF, BUB1B, TTK, AURKB, AURKA, RPS6KA3, PAK1, STK11, CHEK2, AKT2, CHEK1, RPS6KA1, PIM1, AKT1, MAPK1, MAP2K7, PRKACA, IKBKE, GTF2I, MAPK3, MAP2K3, MAP2K1, MAP2K2, CSNK2A1, PRKCB, PRKCD, MTOR, MELK, CDK6, CDK4, CDK2, CDK1, CDK12, RAF1, CSNK1G2	3.650625	6.27E-10	5.99E-10		
UP_KW_MOLECULA R_FUNCTION	KW-0723~Serine/threonine e-protein kinase	37	2.81E-11	RB1, SMARCB1, IKZF1, AHR, MKI67, IKZF3, ETS1, H2AC16, H2AC17, H2AC11, CREB3L2, ZNF207, TRIM24, TP63, GTF2I, MEF2B, H2AC6, RUNX1, FOXF1, MSH2, SARNP, TP53, DNMT1, SET, MAX, PRKDC, BAZ2A, HIF1A, PCBP1, EP400, H3C2, FANCI, ZNF384, XBP1, XRCC6, H4C9, FUS, NONO, HMGA1, NFATC2, FLI1, NFKB1, H1-3, NFKB2, H1-2, H1-4, BCL6, SP1, H2AX, TOP2A, DDX3X, TNFAIP3, HMGB1, AFF3, PHF6, TCF12, TFE3, TFEB, PAX5, ARID1A, H2BC17, ETV6, DDB2, NCOR2, H2BC12, SFPQ, RAD51C, CREB1, TFDP1, IRF4, ELF4, IRF1, H2BC11, POT1, IRF8, TOP1, PCNA, SRF, NR1I3, DOT1L, RELA, RECQL4, CUX1, POLD1, NSD2, E2F1, MAPK1, STAT6, MEF2D, STAT1, CNBP, STAT3, H2BC4, HUWE1, LRPPRC, RAD51, ERCC1, ERCC2, TCEA1, TRIM33	1.865761	1.64E-09	1.57E-09		
UP_KW_MOLECULA R_FUNCTION	KW-0238~DNA-binding	100	9.79E-11	RB1, KDM5C, DNMT1, HDAC3, KDM1A, MAX, HDAC1, BAZ2A, AHR, IKZF1, CCAR2, HDAC6, PTBP1, CUX1, U2AF2, SIN3A, CPNE1, TRIM24, MAPK1, SUZ12, CENPU, EED, BCL11A, CNBP, NONO, IRF2BP2, ETV6, FOXF1, RUNX1, NFKB2, NCOR2, SFPQ, BCL6, SP1, EWSR1, TBL1XR1, IRF1, CNOT2, IRF8, TP53, TRIM33, RCOR1, EZH2	2.661643	1.29E-07	1.23E-07		
UP_KW_MOLECULA R_FUNCTION	KW-0678~Repressor	43	9.64E-09	RB1, SUZ12, KDM5C, DNMT1, SMARCB1, HDAC3, KDM1A, PRKCB, EED, HDAC1, DOT1L, BAZ2A, IKZF1, ARID1A, HDAC6, TBL1XR1, CARM1, NSD2, EP400, NUP98, RCOR1, EZH2, BRD4	2.856321	2.06E-04	1.97E-04		
UP_KW_MOLECULA R_FUNCTION	KW-0156~Chromatin regulator	23	1.84E-05	LYN, MAP2K3, MAP2K1, MAP2K2, SYK, TTK, TYK2, WEE1, BTK, MAP2K7, JAK3, FRK, JAK1	4.411881	3.23E-04	3.09E-04		
UP_KW_MOLECULA R_FUNCTION	KW-0829~Tyrosine-protein kinase	13	3.65E-05	GSK3B, KDM5C, ARAF, PIK3CD, BUB1B, TNFAIP3, CKS1B, RPS6KA3, STK11, ATIC, PLAU, CHEK2, AKT2, RPS6KA1, CHEK1, PIM1, TRIM24, AKT1, EP300, PRKACA, SKP2, JAK3, IKBKE, JAK1, GTF2I, PDK1, MAP2K3, ST6GAL1, MAP2K1, MAP2K2, CSNK2A1, SYK, PRKCB, PRMT1, CAD, PRKCD, TYK2, POMGNT1, DPM1, PKM, MELK, PRKARIA, MFNG, BTK, NUP98, RAF1, CSNK1G2, BIRC3, DNMT1, PRKDC, RPN1, DOT1L, AK2, TTK, TYMS, CBL, AURKB, AURKA, PAK1, POLD1, NSD2, MAPK1, MAP2K7, MAPK3, LYN, GIT2, CREBBP, FANCL, HUWE1, MTOR, WEE1, CDK6, CDK4, CARM1, CDK2, PI4KA, CDK1, CDK12, TRIM33, FRK, EZH2	1.538982	3.23E-04	3.09E-04		
UP_KW_MOLECULA R_FUNCTION	KW-0808~Transferase	81	3.86E-05						

KEGG_PATHWAY	hsa05203:Viral carcinogenesis	48	1.19E-26	RB1, YWHAE, HDAC3, DDX3X, HDAC1, SRF, PIK3CD, RELA, HDAC6, CDC42, CCND3, NRAS, CCND2, CHEK1, CREB3L2, MAPK1, EP300, RAC1, SKP2, PRKACA, JAK3, JAK1, MAPK3, LYN, CREBBP, H4C9, SYK, H2BC4, STAT3, H2BC17, RHOA, NFKB1, NFKB2, H2BC12, NFKBIA, CCNA2, PKM, SNW1, CREB1, CDK6, CCNE1, CDK4, H2BC11, CDK2, CDK1, BAX, GRB2, TP53	6.87659	3.25E-24	1.41E-24
KEGG_PATHWAY	hsa05161:Hepatitis B	42	5.52E-25	RB1, DDX3X, PCNA, ARAF, PIK3CD, TNF, RELA, NRAS, AKT2, CREB3L2, E2F1, AKT1, MAPK1, EP300, STAT6, MAP2K7, JAK3, IKBE, JAK1, MAPK3, MAP2K3, MAP2K1, CREBBP, MAP2K2, PRKCB, STAT1, STAT3, NFATC2, TYK2, MMP9, NFKB1, DDB2, NFKBIA, CCNA2, CREB1, CCNE1, CDK2, BAX, GRB2, RAF1, TP53, MYD88	7.567413	7.57E-23	3.29E-23
KEGG_PATHWAY	hsa05200:Pathways in cancer	71	5.07E-24	RB1, GSK3B, CSF3R, HSP90AB1, ARAF, PIK3CD, ETS1, CKS1B, CCND3, CCND2, TFG, AKT2, PIM1, RAC2, AKT1, EP300, RAC1, PRKACA, SKP2, JAK3, JAK1, MAP2K1, HSP90AA1, MAP2K2, TPM3, PRKCB, NCOA4, MMP9, RHOA, RUNX1, DDB2, EML4, CCNA2, MSH2, CCNE1, RAF1, TP53, BIRC3, FH, MAX, HDAC1, CBL, RASGRP1, HIF1A, RELA, CDC42, NRAS, TPR, E2F1, PLCG2, MAPK1, STAT6, VHL, MAPK3, CREBBP, STAT1, STAT3, MLH1, MTOR, NFKB1, NFKB2, NFKBIA, RAD51, CDK6, SP1, CDK4, CDK2, GNAS, CCDC6, BAX, GRB2	3.912163	4.48E-22	1.95E-22
KEGG_PATHWAY	hsa05169:Epstein-Barr virus infection	45	6.54E-24	RB1, HDAC1, TNFAIP3, PIK3CD, TNF, RELA, ICAM1, CCND3, CCND2, SIN3A, PSMD2, AKT2, CD19, E2F1, PLCG2, AKT1, RAC1, SKP2, MAP2K7, JAK3, IKBE, JAK1, LYN, MAP2K3, SYK, STAT1, STAT3, TYK2, NFKB1, DDB2, NFKB2, NCOR2, NFKBIA, CCNA2, SNW1, CDK6, CCNE1, CDK4, CDK2, BTK, BAX, CALR, TP53, CD44, MYD88	6.510319	4.48E-22	1.95E-22
KEGG_PATHWAY	hsa04662:B cell receptor signaling pathway	31	2.91E-22	GSK3B, PIK3CD, BCL10, RELA, CD79B, CD79A, PPP3CA, NRAS, AKT2, CD19, INPP5D, PLCG2, RAC2, AKT1, MAPK1, MAPK3, LYN, MAP2K1, MAP2K2, SYK, PRKCB, NFATC2, NFKB1, NFKBIA, BTK, GRB2, PTPN6, RAF1, FCGR2B, CARD11	10.00475	1.60E-20	6.93E-21
KEGG_PATHWAY	hsa05215:Prostate cancer	29	5.85E-19	RB1, GSK3B, HSP90AB1, ARAF, PIK3CD, RELA, NRAS, PLAU, AKT2, CREB3L2, E2F1, AKT1, MAPK1, EP300, MAPK3, MAP2K1, CREBBP, HSP90AA1, MAP2K2, MMP9, MTOR, NFKB1, NFKBIA, CREB1, CCNE1, CDK2, GRB2, RAF1, TP53	8.690759	2.67E-17	1.16E-17
KEGG_PATHWAY	hsa05166:Human T-cell leukemia virus 1 infection	41	1.19E-18	RB1, SRF, PIK3CD, BUB1B, ETS1, TNF, RELA, ICAM1, PPP3CA, CCND3, NRAS, CCND2, PTTG1, CHEK2, AKT2, CHEK1, CREB3L2, E2F1, AKT1, MAPK1, EP300, PRKACA, JAK3, JAK1, MAPK3, MAP2K1, CREBBP, MAP2K2, NFATC2, NFKB1, NFKB2, NFKBIA, CCNA2, CREB1, CCNE1, CDK4, CDK2, BAX, CALR, TP53, MAD2L1	5.399639	4.67E-17	2.03E-17
KEGG_PATHWAY	hsa04110:Cell cycle	34	1.31E-17	RB1, YWHAE, GSK3B, PCNA, PRKDC, HDAC1, BUB1B, TTK, AURKB, CCND3, CCND2, PPP2R1B, PTTG1, PPP2R1A, CHEK2, CHEK1, E2F1, EP300, SKP2, CREBBP, SMC1A, CDC25A, NDC80, CCNA2, WEE1, STAG2, TFDP1, CDK6, CCNE1, CDK4, CDK2, CDK1, TP53, MAD2L1	6.319862	4.47E-16	1.94E-16
KEGG_PATHWAY	hsa05212:Pancreatic cancer	25	2.20E-17	RB1, ARAF, PIK3CD, RELA, CDC42, AKT2, E2F1, RAC2, AKT1, MAPK1, RAC1, JAK1, MAPK3, MAP2K1, STAT1, STAT3, MTOR, NFKB1, DDB2, RAD51, CDK6, CDK4, BAX, RAF1, TP53	9.535315	6.04E-16	2.62E-16
KEGG_PATHWAY	hsa05220:Chronic myeloid leukemia	25	2.20E-17	RB1, HDAC1, ARAF, PIK3CD, CBL, RELA, NRAS, AKT2, E2F1, AKT1, MAPK1, MAPK3, MAP2K1, MAP2K2, PTPN11, NFKB1, RUNX1, DDB2, NFKBIA, CDK6, CDK4, BAX, GRB2, RAF1, TP53	9.535315	6.04E-16	2.62E-16
KEGG_PATHWAY	hsa05167:Kaposi sarcoma-associated herpesvirus infection	37	3.25E-17	RB1, GSK3B, PIK3CD, HIF1A, RELA, ICAM1, PPP3CA, NRAS, AKT2, E2F1, PLCG2, AKT1, MAPK1, EP300, RAC1, MAP2K7, IKBE, JAK1, MAPK3, LYN, MAP2K1, CREBBP, MAP2K2, SYK, STAT1, STAT3, NFATC2, TYK2, MTOR, NFKB1, NFKBIA, CREB1, CDK6, CDK4, BAX, RAF1, TP53	5.544105	8.09E-16	3.51E-16
KEGG_PATHWAY	hsa05223:Non-small cell lung cancer	24	7.97E-17	RB1, MAP2K1, MAP2K2, PRKCB, STAT3, ARAF, PIK3CD, DDB2, EML4, NRAS, CDK6, CDK4, AKT2, KIF5B, E2F1, PLCG2, BAX, AKT1, MAPK1, GRB2, RAF1, JAK3, TP53, MAPK3	9.655486	1.82E-15	7.91E-16
KEGG_PATHWAY	hsa04218:Cellular senescence	33	8.83E-17	RB1, MRE11, SERPINE1, PIK3CD, ETS1, RELA, PPP3CA, CCND3, NRAS, CCND2, CHEK2, AKT2, CHEK1, E2F1, AKT1, MAPK1, MAPK3, MAP2K3, MAP2K1, MAP2K2, IGFBP3, NFATC2, CDC25A, MTOR, NFKB1, CCNA2, CDK6, CCNE1, CDK4, CDK2, CDK1, RAF1, TP53	6.173054	1.86E-15	8.08E-16
KEGG_PATHWAY	hsa05235:PD-L1 expression and PD-1 checkpoint pathway in cancer	26	1.00E-16	PIK3CD, RASGRP1, HIF1A, RELA, PPP3CA, NRAS, AKT2, AKT1, MAPK1, JAK1, MAPK3, MAP2K3, MAP2K1, MAP2K2, CSNK2A1, STAT1, STAT3, NFATC2, PTPN11, MTOR, NFKB1, EML4, NFKBIA, PTPN6, RAF1, MYD88	8.484312	1.97E-15	8.54E-16
KEGG_PATHWAY	hsa04660:T cell receptor signaling pathway	29	3.16E-16	GSK3B, PIK3CD, BCL10, RASGRP1, TNF, RELA, CDC42, PPP3CA, PAK1, NRAS, PPP2R1B, PPP2R1A, AKT2, AKT1, MAPK1, MAP2K7, MAPK3, MAP2K1, MAP2K2, NFATC2, PTPN11, RHOA, NFKB1, NFKBIA, CDK4, GRB2, PTPN6, RAF1, CARD11	6.981101	5.77E-15	2.51E-15
KEGG_PATHWAY	hsa05211:Renal cell carcinoma	23	4.05E-16	MAP2K1, CREBBP, FH, MAP2K2, PRCC, TFE3, ARAF, PIK3CD, PTPN11, ETS1, HIF1A, CDC42, PAK1, NRAS, AKT2, AKT1, EP300, MAPK1, GRB2, VHL, RAC1, RAF1, MAPK3	9.649739	6.94E-15	3.01E-15
KEGG_PATHWAY	hsa05165:Human papillomavirus infection	45	3.53E-15	RB1, GSK3B, HDAC1, PIK3CD, PSEN1, TNF, RELA, CDC42, CCND3, NRAS, CCND2, PPP2R1B, PPP2R1A, AKT2, CREB3L2, E2F1, SPP1, AKT1, MAPK1, EP300, PRKACA, IKBE, JAK1, MAPK3, MAP2K1, CREBBP, MAP2K2, STAT1, TYK2, MTOR, NFKB1, CCNA2, PKM, CREB1, CDK6, CCNE1, CDK4, IRF1, MFNG, CDK2, GNAS, BAX, GRB2, RAF1, TP53	3.968753	5.69E-14	2.47E-14
KEGG_PATHWAY	hsa05160:Hepatitis C	31	8.84E-15	RB1, YWHAE, GSK3B, ARAF, PIK3CD, TNF, RELA, NRAS, PPP2R1B, PPP2R1A, AKT2, E2F1, AKT1, MAPK1, IKBE, JAK1, MAPK3, MAP2K1, MAP2K2, STAT1, STAT3, TYK2, NFKB1, NFKBIA, CDK6, CDK4, CDK2, BAX, GRB2, RAF1, TP53	5.725987	1.35E-13	5.85E-14
KEGG_PATHWAY	hsa04722:Neurotrophin signaling pathway	27	1.86E-14	YWHAE, GSK3B, PIK3CD, PSEN1, RELA, CDC42, RPS6KA3, NRAS, AKT2, RPS6KA1, PLCG2, AKT1, MAPK1, RAC1, MAP2K7, MAPK3, MAP2K1, MAP2K2, PRKCD, PTPN11, RHOA, NFKB1, NFKBIA, BAX, GRB2, RAF1, TP53	6.607973	2.68E-13	1.16E-13
KEGG_PATHWAY	hsa05163:Human cytomegalovirus infection	36	2.49E-14	RB1, GSK3B, PIK3CD, TNF, RELA, PPP3CA, NRAS, AKT2, CREB3L2, E2F1, RAC2, AKT1, MAPK1, RAC1, PRKACA, JAK1, MAPK3, MAP2K1, MAP2K2, PRKCB, STAT3, NFATC2, RHOA, MTOR, NFKB1, NFKBIA, CREB1, CDK6, SP1, CDK4, GNAS, BAX, GRB2, CALR, RAF1, TP53	4.678211	3.42E-13	1.48E-13
KEGG_PATHWAY	hsa04625:C-type lectin receptor signaling pathway	25	5.51E-14	PIK3CD, BCL10, TNF, RELA, PPP3CA, PAK1, NRAS, AKT2, PLCG2, AKT1, MAPK1, IKBE, MAPK3, SYK, STAT1, PRKCD, NFATC2, PTPN11, RHOA, NFKB1, NFKB2, NFKBIA, IRF1, BCL3, RAF1	6.992564	7.19E-13	3.12E-13
KEGG_PATHWAY	hsa05214:Glioma	21	4.28E-13	RB1, MAP2K1, MAP2K2, PRKCB, ARAF, PIK3CD, MTOR, DDB2, NRAS, CDK6, CDK4, AKT2, E2F1, PLCG2, BAX, AKT1, MAPK1, GRB2, RAF1, TP53, MAPK3	8.115055	5.33E-12	2.32E-12
KEGG_PATHWAY	hsa04664:Fc epsilon RI signaling pathway	20	6.85E-13	LYN, MAP2K3, MAP2K1, MAP2K2, SYK, PIK3CD, TNF, NRAS, AKT2, INPP5D, BTK, PLCG2, RAC2, AKT1, MAPK1, GRB2, RAC1, RAF1, MAP2K7, MAPK3	8.512687	8.16E-12	3.54E-12
KEGG_PATHWAY	hsa05207:Chemical carcinogenesis - receptor activation	33	1.07E-12	RB1, HSP90AB1, NR1I3, PIK3CD, AHR, RELA, RPS6KA3, CCND3, NRAS, AKT2, RPS6KA1, CREB3L2, E2F1, AKT1, MAPK1, PRKACA, IKBE, MAPK3, MAP2K1, HSP90AA1, MAP2K2, PRKCB, STAT3, AIP, CDC25A, MTOR, NFKB1, CREB1, BCL6, GNAS, GRB2, RAF1, KPNB1	4.507765	1.22E-11	5.29E-12

KEGG_PATHWAY	hsa04613:Neutrophil extracellular trap formation	31	1.57E-12	H2AX, HDAC3, HDAC1, PIK3CD, HMGB1, H2AC16, H2AC17, RELA, HDAC6, H2AC11, AKT2, PLCG2, RAC2, AKT1, MAPK1, H3C2, RAC1, MAPK3, MAP2K1, MAP2K2, H4C9, SYK, H2AC6, PRKCB, H2BC4, H2BC17, MTOR, NFKB1, H2BC12, H2BC11, RAF1	4.741833	1.72E-11	7.47E-12
KEGG_PATHWAY	hsa05162:Measles	26	5.11E-12	GSK3B, TNFAIP3, PIK3CD, RELA, CCND3, CCND2, AKT2, AKT1, JAK3, IKKBE, JAK1, CSNK2A1, STAT1, STAT3, MSN, TYK2, NFKB1, NFKBIA, CDK6, CCNE1, CDK4, CDK2, BAX, FCGR2B, TP53, MYD88	5.493439	5.39E-11	2.34E-11
KEGG_PATHWAY	hsa05221:Acute myeloid leukemia	19	5.90E-12	MAP2K1, MAP2K2, BCL2A1, STAT3, ARAF, PIK3CD, MTOR, RELA, NFKB1, RUNX1, CCNA2, NRAS, AKT2, PIM1, AKT1, MAPK1, GRB2, RAF1, MAPK3	8.20598	5.98E-11	2.60E-11
KEGG_PATHWAY	hsa05210:Colorectal cancer	21	6.65E-12	GSK3B, MAP2K1, MAP2K2, ARAF, PIK3CD, MLH1, RHOA, MTOR, DDB2, NRAS, MSH2, AKT2, RAC2, BAX, AKT1, MAPK1, GRB2, RAC1, RAF1, TP53, MAPK3	7.089014	6.51E-11	2.83E-11
KEGG_PATHWAY	hsa05205:Proteoglycans in cancer	31	7.81E-12	ARAF, PIK3CD, CBL, HIF1A, TNF, CDC42, PAK1, NRAS, PLAU, AKT2, PLCG2, AKT1, MAPK1, RAC1, PRKACA, MAPK3, MAP2K1, MAP2K2, PRKCB, STAT3, MSN, PTPN11, MMP9, RHOA, MTOR, GRB2, PTPN6, EZR, RAF1, TP53, CD44	4.462901	7.38E-11	3.21E-11
KEGG_PATHWAY	hsa01522:Endocrine resistance	22	1.02E-11	RB1, MAP2K1, MAP2K2, ARAF, PIK3CD, MMP9, MTOR, NRAS, SP1, CDK4, CARM1, AKT2, E2F1, GNAS, BAX, AKT1, MAPK1, GRB2, RAF1, PRKACA, TP53, MAPK3	6.526394	9.09E-11	3.95E-11
KEGG_PATHWAY	hsa05202:Transcriptional misregulation in cancer	30	1.03E-11	BCL2A1, MAX, HDAC1, DOT1L, PRCC, MLLT1, RELA, CCND2, PLAU, SIN3A, NSD2, H3C2, SS18, FUS, IGFBP3, TFE3, PAX5, MMP9, FLI1, NFKB1, ETV6, RUNX1, DDB2, CCNA2, BCL6, SP1, EWSR1, BAX, TP53, BIRC3	4.565094	9.09E-11	3.95E-11
KEGG_PATHWAY	hsa04935:Growth hormone synthesis, secretion and action	24	1.37E-11	MAP2K3, GSK3B, MAP2K1, CREBBP, MAP2K2, PRKCB, STAT1, IGFBP3, STAT3, PIK3CD, MTOR, NRAS, CREB1, AKT2, CREB3L2, PLCG2, GNAS, AKT1, EP300, MAPK1, GRB2, RAF1, PRKACA, MAPK3	5.777643	1.17E-10	5.09E-11
KEGG_PATHWAY	hsa05135:Yersinia infection	25	2.92E-11	GSK3B, PIK3CD, TNF, RELA, CDC42, RPS6KA3, AKT2, RPS6KA1, RAC2, AKT1, MAPK1, RAC1, MAP2K7, WASF2, MAPK3, MAP2K3, GIT2, MAP2K1, MAP2K2, NFATC2, RHOA, NFKB1, NFKBIA, ARHGEF7, MYD88	5.320429	2.43E-10	1.05E-10
KEGG_PATHWAY	hsa05417:Lipid and atherosclerosis	31	3.43E-11	GSK3B, HSP90AB1, PIK3CD, TNF, RELA, ICAM1, CDC42, PPP3CA, NRAS, AKT2, AKT1, MAPK1, RAC1, MAP2K7, IKKBE, MAPK3, LYN, MAP2K3, XBP1, HSP90AA1, HSPA5, STAT3, NFATC2, SOD2, MMP9, RHOA, NFKB1, NFKBIA, BAX, TP53, MYD88	4.214962	2.77E-10	1.20E-10
KEGG_PATHWAY	hsa04933:AGE-RAGE signaling pathway in diabetic complications	21	1.22E-10	PRKCB, STAT1, PRKCD, STAT3, SERPINE1, PIK3CD, TNF, RELA, NFKB1, ICAM1, CDC42, NRAS, CDK4, AKT2, PIM1, PLCG2, BAX, AKT1, MAPK1, RAC1, MAPK3	6.106378	9.52E-10	4.14E-10
KEGG_PATHWAY	hsa04380:Osteoclast differentiation	24	3.38E-10	MAP2K1, SYK, STAT1, NFATC2, PIK3CD, TYK2, TNF, RELA, NFKB1, NFKB2, NFKBIA, PPP3CA, CREB1, AKT2, BTK, PLCG2, AKT1, MAPK1, GRB2, RAC1, FCGR2B, MAP2K7, JAK1, MAPK3	4.963736	2.58E-09	1.12E-09
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	39	3.75E-10	YWHAE, GSK3B, CSF3R, HSP90AB1, PIK3CD, RELA, RPTOR, CCND3, STK11, NRAS, TCL1A, CCND2, PPP2R1B, PPP2R1A, AKT2, CD19, CREB3L2, SPP1, AKT1, MAPK1, RAC1, JAK3, JAK1, MCL1, MAPK3, MAP2K1, HSP90AA1, MAP2K2, SYK, MTOR, NFKB1, CREB1, CDK6, CCNE1, CDK4, CDK2, GRB2, RAF1, TP53	3.164039	2.78E-09	1.21E-09
KEGG_PATHWAY	hsa04659:Th17 cell differentiation	21	4.31E-10	HSP90AA1, HSP90AB1, STAT1, STAT3, NFATC2, TYK2, AHR, HIF1A, MTOR, RELA, NFKB1, RUNX1, NFKBIA, PPP3CA, IRF4, IL21R, MAPK1, STAT6, JAK3, JAK1, MAPK3	5.710594	3.11E-09	1.35E-09
KEGG_PATHWAY	hsa04666:Fc gamma R-mediated phagocytosis	20	5.26E-10	LYN, MAP2K1, SYK, PRKCB, PRKCD, PIK3CD, DNM2, CDC42, PAK1, AKT2, INPP5D, PLCG2, RAC2, AKT1, MAPK1, RAC1, FCGR2B, RAF1, WASF2, MAPK3	5.993627	3.69E-09	1.60E-09
KEGG_PATHWAY	hsa05170:Human immunodeficiency virus 1 infection	29	5.92E-10	PIK3CD, TNF, RELA, PPP3CA, PAK1, NRAS, AKT2, CHEK1, PLCG2, RAC2, AKT1, MAPK1, RAC1, MAP2K7, MAPK3, MAP2K3, MAP2K1, MAP2K2, PRKCB, NFATC2, MTOR, NFKB1, NFKBIA, WEE1, CDK1, BAX, CALR, RAF1, MYD88	3.998565	4.06E-09	1.76E-09
KEGG_PATHWAY	hsa05164:Influenza A	26	6.07E-10	PIK3CD, TNF, RELA, ICAM1, CCND3, AKT2, AKT1, MAPK1, EP300, IKKBE, JAK1, MAPK3, MAP2K1, CREBBP, MAP2K2, PRKCB, STAT1, TYK2, NFKB1, NFKBIA, CDK6, CDK4, BAX, NUP98, RAF1, MYD88	4.439465	4.06E-09	1.76E-09
KEGG_PATHWAY	hsa04919:Thyroid hormone signaling pathway	22	6.42E-10	GSK3B, MAP2K1, CREBBP, MAP2K2, HDAC3, PRKCB, STAT1, HDAC1, PIK3CD, HIF1A, MTOR, NRAS, SIN3A, AKT2, PLCG2, AKT1, EP300, MAPK1, RAF1, PRKACA, TP53, MAPK3	5.296008	4.19E-09	1.82E-09
KEGG_PATHWAY	hsa05213:Endometrial cancer	16	6.67E-10	GSK3B, MAP2K1, MAP2K2, ARAF, PIK3CD, MLH1, DDB2, NRAS, AKT2, BAX, AKT1, MAPK1, GRB2, RAF1, TP53, MAPK3	7.964412	4.25E-09	1.85E-09
KEGG_PATHWAY	hsa04370:VEGF signaling pathway	16	8.63E-10	MAP2K1, MAP2K2, PRKCB, NFATC2, PIK3CD, CDC42, PPP3CA, NRAS, AKT2, PLCG2, RAC2, AKT1, MAPK1, RAC1, RAF1, MAPK3	7.831672	5.37E-09	2.33E-09
KEGG_PATHWAY	hsa01521:EGFR tyrosine kinase inhibitor resistance	18	9.82E-10	GSK3B, MAP2K1, MAP2K2, PRKCB, STAT3, ARAF, PIK3CD, MTOR, NRAS, AKT2, PLCG2, BAX, AKT1, MAPK1, GRB2, RAF1, JAK1, MAPK3	6.607973	5.98E-09	2.60E-09
KEGG_PATHWAY	hsa04917:Prolactin signaling pathway	17	1.23E-09	GSK3B, MAP2K1, MAP2K2, STAT1, STAT3, PIK3CD, RELA, NFKB1, NRAS, CCND2, IRF1, AKT2, AKT1, MAPK1, GRB2, RAF1, MAPK3	7.031959	7.18E-09	3.12E-09
KEGG_PATHWAY	hsa05230:Central carbon metabolism in cancer	17	1.23E-09	MAP2K1, MAP2K2, IDH1, IDH2, PIK3CD, HIF1A, MTOR, SLC7A5, NRAS, PKM, AKT2, AKT1, MAPK1, RAF1, TP53, PDK1, MAPK3	7.031959	7.18E-09	3.12E-09
KEGG_PATHWAY	hsa05222:Small cell lung cancer	19	1.56E-09	RB1, MAX, PIK3CD, RELA, NFKB1, CKS1B, DDB2, NFKBIA, CDK6, CCNE1, CDK4, AKT2, CDK2, E2F1, BAX, AKT1, SKP2, TP53, BIRC3	6.000071	8.92E-09	3.87E-09
KEGG_PATHWAY	hsa05216:Thyroid cancer	13	1.62E-09	MAP2K1, MAP2K2, TPM3, NCOA4, DDB2, NRAS, TFG, TPR, CCDC6, BAX, MAPK1, TP53, MAPK3	10.31876	9.08E-09	3.94E-09
KEGG_PATHWAY	hsa05218:Melanoma	17	1.91E-09	RB1, MAP2K1, MAP2K2, ARAF, PIK3CD, DDB2, NRAS, CDK6, CDK4, AKT2, E2F1, BAX, AKT1, MAPK1, RAF1, TP53, MAPK3	6.839303	1.05E-08	4.54E-09
KEGG_PATHWAY	hsa04668:TNF signaling pathway	21	2.57E-09	MAP2K3, MAP2K1, RHBDF2, PIK3CD, TNFAIP3, TNF, MMP9, RELA, NFKB1, ICAM1, NFKBIA, CREB1, IRF1, AKT2, BCL3, CREB3L2, AKT1, MAPK1, MAP2K7, BIRC3, MAPK3	5.182724	1.38E-08	5.99E-09
KEGG_PATHWAY	hsa04012:ErbB signaling pathway	18	3.20E-09	GSK3B, MAP2K1, MAP2K2, PRKCB, ARAF, PIK3CD, CBL, MTOR, PAK1, NRAS, AKT2, PLCG2, AKT1, MAPK1, GRB2, RAF1, MAP2K7, MAPK3	6.146952	1.69E-08	7.33E-09
KEGG_PATHWAY	hsa04066:HIF-1 signaling pathway	20	3.46E-09	MAP2K1, CREBBP, MAP2K2, TFRC, PRKCB, STAT3, SERPINE1, PIK3CD, HIF1A, MTOR, RELA, NFKB1, AKT2, PLCG2, AKT1, EP300, MAPK1, VHL, PDK1, MAPK3	5.388765	1.75E-08	7.61E-09
KEGG_PATHWAY	hsa04620:Toll-like receptor signaling pathway	20	3.46E-09	MAP2K3, MAP2K1, MAP2K2, STAT1, PIK3CD, TYK2, TNF, RELA, NFKB1, NFKBIA, AKT2, SPP1, AKT1, MAPK1, RAC1, MAP2K7, IKKBE, MYD88, JAK1, MAPK3	5.388765	1.75E-08	7.61E-09
KEGG_PATHWAY	hsa05206:MicroRNAs in cancer	34	4.92E-09	DNMT1, HDAC1, PIK3CD, RPTOR, NRAS, CCND2, PLAU, E2F1, PLCG2, PIM1, MAPK1, EP300, TP63, MCL1, MAPK3, MAP2K1, CREBBP, MAP2K2, PRKCB, STAT3, MMP9, RHOA, CDC25A, MTOR, NFKB1, FOXP1, CDK6, CCNE1, GRB2, EZR, RAF1, TP53, CD44, EZH2	3.200443	2.45E-08	1.06E-08
KEGG_PATHWAY	hsa04062:Chemokine signaling pathway	26	6.99E-09	GSK3B, PIK3CD, RELA, CDC42, PAK1, NRAS, AKT2, PLCG2, RAC2, AKT1, MAPK1, RAC1, PRKACA, JAK3, MAPK3, LYN, MAP2K1, PRKCB, STAT1, PRKCD, STAT3, RHOA, NFKB1, NFKBIA, GRB2, RAF1	3.956415	3.42E-08	1.49E-08
KEGG_PATHWAY	hsa04064:NF-kappa B signaling pathway	19	1.19E-08	LYN, SYK, CSNK2A1, BCL2A1, PRKCB, TNFAIP3, BCL10, TNF, RELA, NFKB1, ICAM1, NFKB2, NFKBIA, PLAU, BTK, PLCG2, MYD88, CARD11, BIRC3	5.314349	5.71E-08	2.48E-08

KEGG_PATHWAY	hsa05225:Hepatocellular carcinoma	24	1.24E-08	RB1, GSK3B, MAP2K1, MAP2K2, SMARCB1, PRKCB, ARAF, PIK3CD, ARID1A, MTOR, DDB2, NRAS, CDK6, CDK4, AKT2, E2F1, PLCG2, BAX, AKT1, MAPK1, GRB2, RAF1, TP53, MAPK3	4.146179	5.80E-08	2.52E-08
KEGG_PATHWAY	hsa04650:Natural killer cell mediated cytotoxicity	21	1.25E-08	MAP2K1, MAP2K2, SYK, PRKCB, ARAF, NFATC2, PIK3CD, PTPN11, TNF, ICAM1, PPP3CA, PAK1, NRAS, PLCG2, RAC2, MAPK1, GRB2, PTPN6, RAC1, RAF1, MAPK3	4.744186	5.80E-08	2.52E-08
KEGG_PATHWAY	hsa04068:FoxO signaling pathway	21	1.63E-08	MAP2K1, CREBBP, MAP2K2, PRMT1, STAT3, ARAF, PIK3CD, SOD2, STK11, NRAS, CCND2, BCL6, AKT2, CDK2, AKT1, EP300, MAPK1, GRB2, SKP2, RAF1, MAPK3	4.672304	7.45E-08	3.24E-08
KEGG_PATHWAY	hsa05034:Alcoholism	25	1.90E-08	H2AX, HDAC3, HDAC1, ARAF, H2AC16, H2AC17, HDAC6, H2AC11, NRAS, CREB3L2, MAPK1, H3C2, PRKACA, MAPK3, MAP2K1, H4C9, H2AC6, H2BC4, H2BC17, H2BC12, CREB1, H2BC11, GNAS, GRB2, RAF1	3.905422	8.51E-08	3.70E-08
KEGG_PATHWAY	hsa05131:Shigellosis	29	2.07E-08	GSK3B, PIK3CD, U2AF1, BCL10, TNF, RELA, CDC42, RPTOR, AKT2, PLCG2, AKT1, MAPK1, H3C2, RAC1, WASF2, MAPK3, FNBP1, SEPTIN2, PRKCD, SEPTIN6, SEPTIN9, RHOA, MTOR, NFKB1, NFKBIA, BAX, TP53, CD44, MYD88	3.420459	9.17E-08	3.98E-08
KEGG_PATHWAY	hsa05224:Breast cancer	22	2.34E-08	RB1, GSK3B, MAP2K1, MAP2K2, ARAF, PIK3CD, MTOR, DDB2, NFKB2, NRAS, CDK6, SP1, CDK4, AKT2, E2F1, BAX, AKT1, MAPK1, GRB2, RAF1, TP53, MAPK3	4.365628	1.02E-07	4.41E-08
KEGG_PATHWAY	hsa04071:Sphingolipid signaling pathway	20	2.38E-08	MAP2K1, MAP2K2, PRKCB, PIK3CD, TNF, RHOA, RELA, NFKB1, NRAS, PPP2R1B, PPP2R1A, AKT2, RAC2, BAX, AKT1, MAPK1, RAC1, RAF1, TP53, MAPK3	4.814553	1.02E-07	4.42E-08
KEGG_PATHWAY	hsa04914:Progesterone-mediated oocyte maturation	19	2.93E-08	MAP2K1, HSP90AA1, HSP90AB1, ARAF, PIK3CD, CDC25A, AURKA, CCNA2, RPS6KA3, AKT2, RPS6KA1, CDK2, CDK1, AKT1, MAPK1, RAF1, PRKACA, MAD2L1, MAPK3	5.027087	1.24E-07	5.37E-08
KEGG_PATHWAY	hsa05219:Bladder cancer	12	7.29E-08	RB1, MAP2K1, NRAS, MAP2K2, CDK4, ARAF, E2F1, MAPK1, RAF1, TP53, MMP9, MAPK3	8.595738	3.03E-07	1.31E-07
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	31	9.26E-08	MAX, SRF, RASGRF1, ARAF, RASGRP1, TNF, RELA, CDC42, PPP3CA, RPS6KA3, PAK1, NRAS, AKT2, RPS6KA1, RAC2, AKT1, MAPK1, RAC1, MAP2K7, PRKACA, MAPK3, MAP2K3, MAP2K1, MAP2K2, PRKCB, NFKB1, NFKB2, GRB2, RAF1, TP53, MYD88	3.034773	3.79E-07	1.64E-07
KEGG_PATHWAY	hsa05132:Salmonella infection	28	9.49E-08	CYFIP2, HSP90AB1, PIK3CD, TNF, RELA, CDC42, PAK1, AKT2, KIF5B, AKT1, MAPK1, RAC1, MAP2K7, MAPK3, MAP2K3, MAP2K1, HSP90AA1, MAP2K2, RHOA, NFKB1, DNMT2, NFKBIA, ABI1, BAX, PLEKHM2, RAF1, MYD88, BIRC3	3.276198	3.83E-07	1.66E-07
KEGG_PATHWAY	hsa04931:Insulin resistance	18	1.29E-07	GSK3B, PRKCB, PRKCD, STAT3, PIK3CD, PTPN11, TNF, MTOR, RELA, NFKB1, PTPA, NFKBIA, RPS6KA3, CREB1, AKT2, RPS6KA1, CREB3L2, AKT1	4.849889	5.14E-07	2.23E-07
KEGG_PATHWAY	hsa05226:Gastric cancer	21	1.46E-07	RB1, GSK3B, MAP2K1, MAP2K2, ARAF, PIK3CD, MLH1, MTOR, DDB2, NRAS, CCNE1, AKT2, CDK2, E2F1, BAX, AKT1, MAPK1, GRB2, RAF1, TP53, MAPK3	4.111628	5.73E-07	2.49E-07
KEGG_PATHWAY	hsa04115:p53 signaling pathway	15	1.72E-07	IGFBP3, SERPINE1, DDB2, CCND3, CDK6, CCND2, CCNE1, CDK4, CHEK2, CHEK1, CDK2, CDK1, BAX, TP53, GTSF1	5.873754	6.65E-07	2.89E-07
KEGG_PATHWAY	hsa05231:Choline metabolism in cancer	17	1.84E-07	MAP2K1, MAP2K2, PRKCB, PIK3CD, HIF1A, MTOR, NRAS, SP1, AKT2, RAC2, AKT1, MAPK1, GRB2, RAC1, RAF1, WASF2, MAPK3	5.043122	7.00E-07	3.04E-07
KEGG_PATHWAY	hsa04630:JAK-STAT signaling pathway	22	2.17E-07	CREBBP, CSF3R, STAT1, STAT3, PIK3CD, PTPN11, TYK2, MTOR, CCND3, CCND2, AKT2, PIM1, IL21R, AKT1, EP300, GRB2, PTPN6, STAT6, RAF1, JAK3, JAK1, MCL1	3.84591	8.16E-07	3.55E-07
KEGG_PATHWAY	hsa04720:Long-term potentiation	14	2.98E-07	MAP2K1, CREBBP, MAP2K2, PRKCB, ARAF, RPS6KA3, PPP3CA, NRAS, RPS6KA1, EP300, MAPK1, RAF1, PRKACA, MAPK3	6.136758	1.10E-06	4.80E-07
KEGG_PATHWAY	hsa04150:mTOR signaling pathway	21	3.47E-07	GSK3B, MAP2K1, MAP2K2, PRKCB, PIK3CD, TNF, RHOA, MTOR, RPTOR, SLC7A5, RPS6KA3, STK11, NRAS, AKT2, RPS6KA1, AKT1, MAPK1, GRB2, SKP2, RAF1, MAPK3	3.903444	1.27E-06	5.50E-07
KEGG_PATHWAY	hsa04926:Relaxin signaling pathway	19	3.52E-07	MAP2K1, MAP2K2, PIK3CD, MMP9, RELA, NFKB1, NFKBIA, NRAS, CREB1, AKT2, CREB3L2, GNAS, AKT1, MAPK1, GRB2, RAF1, MAP2K7, PRKACA, MAPK3	4.292359	1.27E-06	5.50E-07
KEGG_PATHWAY	hsa04915:Estrogen signaling pathway	19	9.67E-07	MAP2K1, HSP90AA1, MAP2K2, HSP90AB1, PRKCD, PIK3CD, MMP9, NRAS, CREB1, SP1, AKT2, CREB3L2, GNAS, AKT1, MAPK1, GRB2, RAF1, PRKACA, MAPK3	4.014436	3.44E-06	1.49E-06
KEGG_PATHWAY	hsa04014:Ras signaling pathway	25	1.64E-06	RASGRF1, PIK3CD, RASAL1, ETS1, RASGRP1, RELA, CDC42, PAK1, NRAS, AKT2, PLCG2, RAC2, AKT1, MAPK1, RAC1, PRKACA, MAPK3, MAP2K1, MAP2K2, PRKCB, PTPN11, RHOA, NFKB1, GRB2, RAF1	3.084955	5.76E-06	2.50E-06
KEGG_PATHWAY	hsa04211:Longevity regulating pathway	15	1.76E-06	PIK3CD, SOD2, MTOR, RELA, NFKB1, RPTOR, STK11, NRAS, CREB1, AKT2, CREB3L2, BAX, AKT1, PRKACA, TP53	4.894795	6.09E-06	2.64E-06
KEGG_PATHWAY	hsa05208:Chemical carcinogenesis - reactive oxygen species	24	2.33E-06	MAP2K1, MAP2K2, PRKCD, ARAF, PIK3CD, PTPN11, SDHC, AHR, SDHA, SOD2, HIF1A, SDHB, RELA, NFKB1, NFKBIA, NRAS, AKT2, AKT1, MAPK1, GRB2, RAC1, RAF1, MAP2K7, MAPK3	3.118808	7.97E-06	3.46E-06
KEGG_PATHWAY	hsa05152:Tuberculosis	21	2.80E-06	CD74, CREBBP, SYK, STAT1, BCL10, TNF, RHOA, RELA, NFKB1, PPP3CA, CREB1, AKT2, BAX, AKT1, EP300, MAPK1, FCGR2B, RAF1, MYD88, JAK1, MAPK3	3.426357	9.48E-06	4.12E-06
KEGG_PATHWAY	hsa04210:Apoptosis	18	3.19E-06	MAP2K1, MAP2K2, BCL2A1, PIK3CD, TNF, RELA, NFKB1, NFKBIA, NRAS, AKT2, BAX, AKT1, MAPK1, RAF1, TP53, MCL1, BIRC3, MAPK3	3.887043	1.07E-05	4.63E-06
KEGG_PATHWAY	hsa04730:Long-term depression	12	4.45E-06	LYN, MAP2K1, NRAS, MAP2K2, PPP2R1B, PRKCB, PPP2R1A, ARAF, GNAS, MAPK1, RAF1, MAPK3	5.873754	1.47E-05	6.38E-06
KEGG_PATHWAY	hsa04934:Cushing syndrome	19	4.75E-06	RB1, GSK3B, MAP2K1, FH, MAP2K2, AIP, AHR, CREB1, CDK6, CCNE1, SP1, CDK4, CDK2, CREB3L2, E2F1, GNAS, MAPK1, PRKACA, MAPK3	3.600043	1.55E-05	6.73E-06
KEGG_PATHWAY	hsa05142:Chagas disease	15	8.98E-06	SERPINE1, PIK3CD, TNF, RELA, NFKB1, NFKBIA, PPP2R1B, PPP2R1A, AKT2, GNAS, AKT1, MAPK1, CALR, MYD88, MAPK3	4.277005	2.90E-05	1.26E-05
KEGG_PATHWAY	hsa04912:GnRH signaling pathway	14	1.38E-05	MAP2K3, MAP2K1, MAP2K2, PRKCB, PRKCD, CDC42, NRAS, GNAS, MAPK1, GRB2, RAF1, MAP2K7, PRKACA, MAPK3	4.421105	4.40E-05	1.91E-05
KEGG_PATHWAY	hsa04910:Insulin signaling pathway	17	1.65E-05	GSK3B, MAP2K1, MAP2K2, ARAF, PIK3CD, CBL, MTOR, RPTOR, NRAS, PRKAR1A, AKT2, AKT1, MAPK1, GRB2, RAF1, PRKACA, MAPK3	3.617892	5.19E-05	2.25E-05
KEGG_PATHWAY	hsa04114:Oocyte meiosis	17	1.81E-05	YWHAE, MAP2K1, SMC1A, AURKA, RPS6KA3, PPP3CA, PPP2R1B, PTTG1, CCNE1, PPP2R1A, RPS6KA1, CDK2, CDK1, MAPK1, PRKACA, MAD2L1, MAPK3	3.591864	5.62E-05	2.44E-05
KEGG_PATHWAY	hsa05145:Toxoplasmosis	15	2.15E-05	MAP2K3, STAT1, STAT3, TYK2, TNF, RELA, NFKB1, NFKBIA, AKT2, AKT1, MAPK1, MYD88, JAK1, BIRC3, MAPK3	3.968753	6.62E-05	2.87E-05
KEGG_PATHWAY	hsa04217:Necroptosis	18	2.62E-05	H2AX, HSP90AA1, HSP90AB1, H2AC6, STAT1, STAT3, TNFAIP3, TYK2, HMGB1, H2AC16, TNF, H2AC17, H2AC11, BAX, STAT6, JAK3, JAK1, BIRC3	3.324767	7.99E-05	3.47E-05
KEGG_PATHWAY	hsa04916:Melanogenesis	14	3.40E-05	GSK3B, MAP2K1, CREBBP, MAP2K2, PRKCB, NRAS, CREB1, CREB3L2, GNAS, EP300, MAPK1, RAF1, PRKACA, MAPK3	4.070919	1.02E-04	4.45E-05
KEGG_PATHWAY	hsa01524:Platinum drug resistance	12	4.04E-05	TOP2A, MSH2, AKT2, ERCC1, BAX, MAPK1, PIK3CD, AKT1, MLH1, TP53, BIRC3, MAPK3	4.699003	1.20E-04	5.23E-05
KEGG_PATHWAY	hsa04072:Phospholipase D signaling pathway	17	4.30E-05	MAP2K1, MAP2K2, SYK, PIK3CD, PTPN11, RHOA, MTOR, DNMT2, NRAS, AKT2, PLCG2, GNAS, AKT1, MAPK1, GRB2, RAF1, MAPK3	3.350799	1.27E-04	5.50E-05
KEGG_PATHWAY	hsa04510:Focal adhesion	20	5.81E-05	GSK3B, MAP2K1, PRKCB, RASGRF1, PIK3CD, RHOA, CDC42, CCND3, PAK1, CCND2, AKT2, SPP1, RAC2, AKT1, MAPK1, GRB2, RAC1, RAF1, BIRC3, MAPK3	2.893475	1.69E-04	7.34E-05
KEGG_PATHWAY	hsa05100:Bacterial invasion of epithelial cells	12	5.86E-05	CDC42, SEPTIN2, CLTC, SEPTIN6, CLTA, PIK3CD, RAC1, SEPTIN9, CBL, WASF2, RHOA, DNMT2	4.518272	1.69E-04	7.34E-05

KEGG_PATHWAY	hsa04929:GnRH secretion	11	5.96E-05	MAP2K1, NRAS, MAP2K2, PRKCB, AKT2, SPP1, MAPK1, PIK3CD, AKT1, RAF1, MAPK3	4.9701	1.70E-04	7.39E-05
KEGG_PATHWAY	hsa04024:cAMP signaling pathway	21	8.18E-05	MAP2K1, CREBBP, MAP2K2, PIK3CD, RHOA, RELA, NFKB1, NFKBIA, PAK1, CREB1, AKT2, CREB3L2, RAC2, GNAS, AKT1, EP300, MAPK1, RAC1, RAF1, PRKACA, MAPK3	2.728957	2.31E-04	1.00E-04
KEGG_PATHWAY	hsa04310:Wnt signaling pathway	18	8.30E-05	GSK3B, CREBBP, CSNK2A1, PRKCB, NFATC2, PSEN1, RHOA, CCAR2, PPP3CA, CCND3, CCND2, TBL1XR1, CCDC88C, RAC2, EP300, RAC1, PRKACA, TP53	3.038149	2.32E-04	1.01E-04
KEGG_PATHWAY	hsa04920:Adipocytokine signaling pathway	11	1.14E-04	NFKBIA, STK11, AKT2, STAT3, AKT1, PTPN11, ACSL3, TNF, RELA, NFKB1, MTOR	4.615093	3.15E-04	1.37E-04
KEGG_PATHWAY	hsa05130:Pathogenic Escherichia coli infection	19	1.81E-04	CYFIP2, PTPN11, TNF, RHOA, RELA, NFKB1, CDC42, NFKBIA, PAK1, ABI1, BAX, MAPK1, PTPN6, RAC1, EZR, WASF2, MYD88, MYO1F, MAPK3	2.748801	4.97E-04	2.16E-04
KEGG_PATHWAY	hsa04621:NOD-like receptor signaling pathway	18	2.28E-04	YWHAE, HSP90AA1, HSP90AB1, STAT1, PRKCD, TNFAIP3, TYK2, TNF, RHOA, RELA, NFKB1, NFKBIA, MAPK1, IKBKE, MYD88, JAK1, BIRC3, MAPK3	2.797026	6.20E-04	2.69E-04
KEGG_PATHWAY	hsa05140:Leishmaniasis	11	2.55E-04	NFKBIA, STAT1, PRKCB, MAPK1, PTPN6, TNF, RELA, NFKB1, MYD88, JAK1, MAPK3	4.195539	6.85E-04	2.98E-04
KEGG_PATHWAY	hsa04658:Th1 and Th2 cell differentiation	12	2.66E-04	NFKBIA, PPP3CA, STAT1, NFATC2, MAPK1, STAT6, TYK2, JAK3, RELA, NFKB1, JAK1, MAPK3	3.830709	7.07E-04	3.07E-04
KEGG_PATHWAY	hsa04350:TGF-beta signaling pathway	13	2.83E-04	CREBBP, TFR3, HDAC1, TNF, RHOA, TFDP1, PPP2R1B, SP1, PPP2R1A, SIN3A, EP300, MAPK1, MAPK3	3.53513	7.45E-04	3.24E-04
KEGG_PATHWAY	hsa05418:Fluid shear stress and atherosclerosis	15	2.96E-04	HSP90AA1, HSP90AB1, PIK3CD, TNF, MMP9, RHOA, RELA, NFKB1, ICAM1, AKT2, RAC2, AKT1, RAC1, MAP2K7, TP53	3.124337	7.73E-04	3.36E-04
KEGG_PATHWAY	hsa04810:Regulation of actin cytoskeleton	20	3.01E-04	CYFIP2, MAP2K1, MAP2K2, ARAF, PIK3CD, MSN, RHOA, CDC42, PAK1, NRAS, AKT2, RAC2, AKT1, MAPK1, RAC1, EZR, RAF1, ARHGEF7, WASF2, MAPK3	2.553806	7.79E-04	3.38E-04
KEGG_PATHWAY	hsa04657:IL-17 signaling pathway	12	3.53E-04	NFKBIA, GSK3B, HSP90AA1, HSP90AB1, TNFAIP3, MAPK1, TNF, IKBKE, MMP9, RELA, NFKB1, MAPK3	3.709739	9.03E-04	3.92E-04
KEGG_PATHWAY	hsa00020:Citrate cycle (TCA cycle)	7	4.33E-04	FH, MDH1, IDH1, IDH2, SDHC, SDHA, SDHB	6.852713	0.001099	4.77E-04
KEGG_PATHWAY	hsa03460:Fanconi anemia pathway	9	4.86E-04	FANCI, RAD51, RAD51C, FANCL, FANCD2, ERCC1, RPA3, MLH1, FANCG	4.805799	0.001222	5.31E-04
KEGG_PATHWAY	hsa04022:cGMP-PKG signaling pathway	16	5.05E-04	MAP2K1, MAP2K2, MEK2B, SRF, NFATC2, RHOA, PPP3CA, CREB1, AKT2, CREB3L2, AKT1, MAPK1, RAF1, MEK2D, GTF2I, MAPK3	2.830725	0.00125	5.43E-04
KEGG_PATHWAY	hsa04928:Parathyroid hormone synthesis, secretion and action	13	5.06E-04	MAP2K1, PRKCB, ARAF, RHOA, CREB1, SP1, CREB3L2, GNAS, MAPK1, RAF1, PRKACA, MEK2D, MAPK3	3.319948	0.00125	5.43E-04
KEGG_PATHWAY	hsa04140:Autophagy - animal	16	6.10E-04	MAP2K1, MAP2K2, PRKCD, PIK3CD, HMGB1, HIF1A, MTOR, RPTOR, STK11, NRAS, AKT2, AKT1, MAPK1, RAF1, PRKACA, MAPK3	2.780475	0.001492	6.48E-04
KEGG_PATHWAY	hsa05010:Alzheimer disease	27	7.65E-04	GSK3B, ARAF, PIK3CD, PSEN1, TNF, RELA, APH1A, PPP3CA, NCSTN, NRAS, PSMD2, AKT2, KIF5B, AKT1, MAPK1, MAP2K7, MAPK3, XBP1, MAP2K1, MAP2K2, CSNK2A1, SDHC, SDHA, SDHB, MTOR, NFKB1, RAF1	2.028023	0.001856	8.06E-04
KEGG_PATHWAY	hsa03430:Mismatch repair	6	8.85E-04	POLD4, PCNA, MSH2, POLD1, RPA3, MLH1	7.661418	0.002128	9.24E-04
KEGG_PATHWAY	hsa04371:Apelin signaling pathway	14	9.17E-04	MAP2K1, MAP2K2, MEK2B, SERPINE1, MTOR, NRAS, AKT2, SPP1, AKT1, MAPK1, RAF1, PRKACA, MEK2D, MAPK3	2.936877	0.002185	9.49E-04
KEGG_PATHWAY	hsa04922:Glucagon signaling pathway	12	9.76E-04	PPP3CA, CREBBP, PKM, CREB1, PPP4C, PRMT1, AKT2, CREB3L2, GNAS, EP300, AKT1, PRKACA	3.293694	0.002306	0.00100
KEGG_PATHWAY	hsa04611:Platelet activation	13	0.00107	LYN, SYK, PIK3CD, RASGRP1, RHOA, AKT2, BTK, PLCG2, GNAS, AKT1, MAPK1, PRKACA, MAPK3	3.054352	0.002488	0.00108
KEGG_PATHWAY	hsa04540:Gap junction	11	0.001071	MAP2K1, NRAS, MAP2K2, PRKCB, CDK1, GNAS, MAPK1, GRB2, RAF1, PRKACA, MAPK3	3.511483	0.002488	0.00108
KEGG_PATHWAY	hsa04213:Longevity regulating pathway - multiple species	9	0.0011	RPTOR, NRAS, HDAC1, AKT2, PIK3CD, AKT1, SOD2, PRKACA, MTOR	4.263209	0.002511	0.0011
KEGG_PATHWAY	hsa04330:Notch signaling pathway	9	0.0011	APH1A, NCOR2, NCSTN, CREBBP, SNW1, HDAC1, MFNG, EP300, PSEN1	4.263209	0.002511	0.0011
KEGG_PATHWAY	hsa04520:Adherens junction	11	0.001165	CDC42, CREBBP, CSNK2A1, RAC2, EP300, MAPK1, PTPN6, RAC1, WASF2, RHOA, MAPK3	3.473726	0.002639	0.00116
KEGG_PATHWAY	hsa04550:Signaling pathways regulating pluripotency of stem cells	14	0.001191	GSK3B, MAP2K1, MAP2K2, STAT3, PIK3CD, NRAS, AKT2, AKT1, MAPK1, GRB2, RAF1, JAK3, JAK1, MAPK3	2.855297	0.002675	0.00119
KEGG_PATHWAY	hsa05415:Diabetic cardiomyopathy	17	0.001633	GSK3B, PRKCB, PRKCD, PIK3CD, SDHC, SDHA, SDHB, MMP9, MTOR, RELA, NFKB1, PTPA, SP1, AKT2, RAC2, AKT1, RAC1	2.435459	0.003637	0.00163
KEGG_PATHWAY	hsa04670:Leukocyte transendothelial migration	12	0.001891	CDC42, PRKCB, PLCG2, RAC2, PIK3CD, MSN, PTPN11, RAC1, EZR, MMP9, RHOA, ICAM1	3.038149	0.004179	0.00189
KEGG_PATHWAY	hsa03082:ATP-dependent chromatin remodeling	12	0.002026	H2AX, H2AC11, SS18, SMARCB1, H2AC6, HDAC1, EP400, BAZ2A, ARID1A, PHF6, H2AC16, H2AC17	3.012182	0.004441	0.00202
KEGG_PATHWAY	hsa04932:Non-alcoholic fatty liver disease	14	0.002595	GSK3B, XBP1, PIK3CD, SDHC, SDHA, TNF, SDHB, RELA, NFKB1, CDC42, AKT2, BAX, AKT1, RAC1	2.618871	0.005644	0.00259
KEGG_PATHWAY	hsa05120:Epithelial cell signaling in Helicobacter pylori infection	9	0.00266	LYN, CDC42, NFKBIA, PAK1, PLCG2, PTPN11, RAC1, RELA, NFKB1	3.722802	0.005694	0.00266
KEGG_PATHWAY	hsa04714:Thermogenesis	18	0.00266	MAP2K3, SMARCB1, KDM1A, SDHC, ACSL3, ARID1A, SDHA, SDHB, MTOR, RPTOR, RPS6KA3, NRAS, CREB1, RPS6KA1, CREB3L2, GNAS, GRB2, PRKACA	2.249523	0.005694	0.00266
KEGG_PATHWAY	hsa05020:Prion disease	20	0.002908	GSK3B, HSPA5, CSNK2A1, PRKCD, PIK3CD, SDHC, SDHA, TNF, SDHB, PPP3CA, CREB1, PSMD2, KIF5B, CREB3L2, RAC2, BAX, MAPK1, RAC1, PRKACA, MAPK3	2.112861	0.006176	0.00290
KEGG_PATHWAY	hsa05014:Amyotrophic lateral sclerosis	24	0.003776	MAP2K3, NUP214, XBP1, POM121, NUP107, HSPA5, FUS, SDHC, SDHA, TNF, SDHB, MTOR, HDAC6, NUP93, PPP3CA, PSMD2, KIF5B, TPR, HNRNPA2B1, BAX, SRSF3, NUP98, RAC1, TP53	1.899867	0.007959	0.00377
KEGG_PATHWAY	hsa04360:Axon guidance	15	0.00392	GSK3B, NFATC2, PIK3CD, PTPN11, RHOA, CDC42, PPP3CA, PAK1, NRAS, PLCG2, RAC2, MAPK1, RAC1, RAF1, MAPK3	2.394193	0.008199	0.00392
KEGG_PATHWAY	hsa05133:Pertussis	9	0.004781	IRF1, IRF8, MAPK1, TNF, RELA, RHOA, NFKB1, MYD88, MAPK3	3.388704	0.009924	0.00478
KEGG_PATHWAY	hsa04930:Type II diabetes mellitus	7	0.004835	PKM, PRKCD, MAPK1, PIK3CD, TNF, MTOR, MAPK3	4.374072	0.00996	0.00483
KEGG_PATHWAY	hsa04530:Tight junction	14	0.005137	PCNA, MSN, RHOA, RUNX1, CDC42, STK11, PPP2R1B, PPP2R1A, CDK4, NF2, RAC1, EZR, MAP2K7, PRKACA	2.418605	0.010485	0.00513

KEGG_PATHWAY	hsa04728:Dopaminergic synapse	12	0.005166	GSK3B, PPP3CA, CREB1, PPP2R1B, PRKCB, PPP2R1A, AKT2, KIF5B, CREB3L2, GNAS, AKT1, PRKACA	2.669888	0.010485	0.005166
KEGG_PATHWAY	hsa03420:Nucleotide excision repair	8	0.005251	POLD4, PCNA, POLD1, ERCC1, RPA3, ERCC2, MNAT1, DDB2	3.729368	0.010578	0.005251
KEGG_PATHWAY	hsa04725:Cholinergic synapse	11	0.005596	MAP2K1, NRAS, CREB1, PRKCB, AKT2, CREB3L2, MAPK1, PIK3CD, AKT1, PRKACA, MAPK3	2.809187	0.011193	0.005596
KEGG_PATHWAY	hsa04015:Rap1 signaling pathway	16	0.005713	MAP2K3, MAP2K1, MAP2K2, PRKCB, PIK3CD, RHOA, CDC42, NRAS, AKT2, RAC2, GNAS, AKT1, MAPK1, RAC1, RAF1, MAPK3	2.216511	0.011343	0.005713
KEGG_PATHWAY	hsa03083:Polycomb repressive complex	9	0.006956	SUZ12, CREBBP, TFDP1, MAX, EED, HDAC1, EP300, AURKB, EZH2	3.184566	0.013711	0.006956
KEGG_PATHWAY	hsa05022:Pathways of neurodegeneration - multiple diseases	28	0.007089	GSK3B, ARAF, PSEN1, TNF, RELA, PPP3CA, NRAS, PSMD2, KIF5B, MAPK1, RAC1, MAP2K7, MAPK3, MAP2K3, XBP1, MAP2K1, MAP2K2, HSPA5, CSNK2A1, PRKCB, FUS, SDHC, SDHA, SDHB, MTOR, NFKB1, BAX, RAF1	1.702537	0.013814	0.007089
KEGG_PATHWAY	hsa05171:Coronavirus disease - COVID-19	17	0.007109	SYK, PRKCB, STAT1, RPL22, STAT3, PIK3CD, TYK2, TNF, RELA, NFKB1, NFKBIA, PLCG2, MAPK1, IKBKE, MYD88, JAK1, MAPK3	2.097769	0.013814	0.007109
KEGG_PATHWAY	hsa05322:Systemic lupus erythematosus	12	0.007572	H2BC12, H2AX, H2AC11, H4C9, H2AC6, H2BC11, H2BC4, H3C2, TNF, H2AC16, H2BC17, H2AC17	2.535433	0.01461	0.007572
KEGG_PATHWAY	hsa04152:AMPK signaling pathway	11	0.008415	RPTOR, CCNA2, STK11, CREB1, PPP2R1B, PPP2R1A, AKT2, CREB3L2, PIK3CD, AKT1, MTOR	2.648004	0.016123	0.008415
KEGG_PATHWAY	hsa03450:Non-homologous end-joining	4	0.008593	XRCC6, FEN1, MRE11, PRKDC	9.036545	0.01635	0.008593
KEGG_PATHWAY	hsa04137:Mitophagy - animal	10	0.009198	NRAS, CSNK2A1, SP1, TFE3, TFEB, HUWE1, E2F1, HIF1A, TP53, RELA	2.797026	0.017381	0.009198
KEGG_PATHWAY	hsa05016:Huntington disease	20	0.009479	CREBBP, HDAC1, CLTC, CLTA, SDHC, SDHA, SOD2, SDHB, MTOR, CREB1, SP1, SIN3A, PSMD2, KIF5B, CREB3L2, BAX, EP300, MAP2K7, TP53, RCOR1	1.888667	0.01779	0.009479
KEGG_PATHWAY	hsa03440:Homologous recombination	6	0.011993	POLD4, RAD51, RAD51C, MRE11, POLD1, RPA3	4.297869	0.022354	0.011993
KEGG_PATHWAY	hsa04921:Oxytocin signaling pathway	12	0.015604	PPP3CA, MAP2K1, NRAS, MAP2K2, PRKCB, GNAS, NFATC2, MAPK1, RAF1, PRKACA, RHOA, MAPK3	2.288476	0.028756	0.015604
KEGG_PATHWAY	hsa04270:Vascular smooth muscle contraction	11	0.015637	MAP2K1, MAP2K2, PRKCB, PRKCD, ARAF, GNAS, MAPK1, RAF1, PRKACA, RHOA, MAPK3	2.410869	0.028756	0.015637
KEGG_PATHWAY	hsa03410:Base excision repair	6	0.01601	POLD4, FEN1, PCNA, POLD1, HMG1, MUTYH	4.004832	0.029245	0.01601
KEGG_PATHWAY	hsa01523:Antifolate resistance	5	0.017769	ATIC, TYMS, TNF, RELA, NFKB1	4.894795	0.032243	0.017769
KEGG_PATHWAY	hsa05321:Inflammatory bowel disease	7	0.022445	STAT1, STAT3, IL21R, STAT6, TNF, RELA, NFKB1	3.162791	0.04046	0.022445
KEGG_PATHWAY	hsa05030:Cocaine addiction	6	0.024531	CREB1, CREB3L2, GNAS, PRKACA, RELA, NFKB1	3.596176	0.043679	0.024531
KEGG_PATHWAY	hsa04936:Alcoholic liver disease	11	0.024549	MAP2K3, NFKBIA, GSK3B, AKT2, AKT1, MAP2K7, TNF, IKBKE, RELA, NFKB1, MYD88	2.243448	0.043679	0.024549
KEGG_PATHWAY	hsa05031:Amphetamine addiction	7	0.029145	PPP3CA, CREB1, HDAC1, PRKCB, CREB3L2, GNAS, PRKACA	2.979441	0.051521	0.029145
KEGG_PATHWAY	hsa04141:Protein processing in endoplasmic reticulum	12	0.029906	XBP1, HSP90AA1, GANAB, HSP90AB1, RPN2, HSPA5, RPN1, BAX, CALR, MAP2K7, SEC31A, HERPUD1	2.07309	0.052527	0.029906
KEGG_PATHWAY	hsa03030:DNA replication	5	0.032626	POLD4, FEN1, PCNA, POLD1, RPA3	4.078996	0.05694	0.032626
KEGG_PATHWAY	hsa04961:Endocrine and other factor-regulated calcium reabsorption	6	0.033122	PRKCB, CLTC, GNAS, CLTA, PRKACA, DNMT2	3.324767	0.057439	0.033122
KEGG_PATHWAY	hsa04261:Adrenergic signaling in cardiomyocytes	11	0.036647	CREB1, PPP2R1B, TPM3, PPP2R1A, AKT2, CREB3L2, GNAS, MAPK1, AKT1, PRKACA, MAPK3	2.097769	0.063152	0.036647
KEGG_PATHWAY	hsa04148:Efferocytosis	11	0.039489	MAP2K1, MAP2K2, CREB1, NFATC2, MAPK1, PTPN6, PTPN11, RAC1, CALR, HIF1A, MAPK3	2.070875	0.067625	0.039489
KEGG_PATHWAY	hsa05134:Legionellosis	6	0.040655	NFKBIA, TNF, RELA, NFKB1, MYD88, NFKB2	3.146654	0.069189	0.040655
KEGG_PATHWAY	hsa04726:Serotonergic synapse	9	0.041536	MAP2K1, NRAS, PRKCB, ARAF, GNAS, MAPK1, RAF1, PRKACA, MAPK3	2.298426	0.070252	0.041536

Suppl. Table S5.3. Functional terms with FDR ≤0.055 for 63 genes upregulated in PT-DLBCL with wild-type vs. mutated *MYD88* RNA

Category	Term	Count	P Value	Genes	Fold Enrichment	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	13	2.83E-08	NTRK2, ANGPT1, CEBPE, EGF, SOX11, IGF1, GATA2, NGF, AR, FGF9, ID4, CD28, ERCC6	8.400196	2.36E-05	2.32E-05
KEGG_PATHWAY	hsa04015:Rap1 signaling pathway	7	1.61E-04	ANGPT1, FGF9, CDH1, EGF, IGF1, NGF, PLCB1	8.107966	0.023796	0.022663
KEGG_PATHWAY	hsa05226:Gastric cancer	6	2.83E-04	TGFB2, CDKN2B, APC, FGF9, CDH1, EGF	9.822222	0.023796	0.022663
GOTERM_MF_DIRECT	GO:0008083~growth factor activity	6	1.36E-04	TGFB2, FGF9, EGF, IGF1, FGF13, NGF	11.89769	0.027838	0.027838
KEGG_PATHWAY	hsa05200:Pathways in cancer	9	9.15E-04	AR, TGFB2, CDKN2B, APC, FGF9, CDH1, EGF, IGF1, PLCB1	4.146341	0.043137	0.041083
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	7	0.001027	NTRK2, TGFB2, ANGPT1, FGF9, EGF, IGF1, NGF	5.72963	0.043137	0.041083
GOTERM_BP_DIRECT	GO:0048009~insulin-like growth factor receptor signaling pathway	4	1.18E-04	GHR, AR, IGF1, PLCB1	41.1125	0.045084	0.044326
GOTERM_BP_DIRECT	GO:0007399~nervous system development	8	2.27E-04	TENM1, NTRK2, ACVR1C, NAV3, APC, SOX11, FGF13, KALRN	6.355556	0.045084	0.044326

GOTERM_BP_DIRECT	GO:0043410~positive regulation of MAPK cascade	6	2.46E-04	NTRK2, AR, FGF9, EGF, FRS2, IGF1	10.49681	0.045084	0.044326
GOTERM_BP_DIRECT	GO:0051897~positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	6	2.71E-04	NTRK2, TGFβ2, ANGPT1, EGF, CD28, IGF1	10.27813	0.045084	0.044326
KEGG_PATHWAY	hsa04014:Ras signaling pathway	6	0.002275	NTRK2, ANGPT1, FGF9, EGF, IGF1, NGF	6.190476	0.056344	0.053661
KEGG_PATHWAY	hsa04550:Signaling pathways regulating pluripotency of stem cells	5	0.002389	ACVR1C, APC, ID4, LIFR, IGF1	8.526235	0.056344	0.053661
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	7	0.00268	GHR, NTRK2, ANGPT1, FGF9, EGF, IGF1, NGF	4.748312	0.056344	0.053661
KEGG_PATHWAY	hsa05218:Melanoma	4	0.002926	FGF9, CDH1, EGF, IGF1	13.4551	0.056344	0.053661
KEGG_PATHWAY	hsa04020:Calcium signaling pathway	6	0.003018	NTRK2, FGF9, EGF, NGF, PLCB1, RYR3	5.800525	0.056344	0.053661
UP_KW_MOLECULAR_FUNCTION	KW-0339~Growth factor	5	0.001397	TGFβ2, FGF9, EGF, IGF1, NGF	10.00758	0.054499	0.054499
GOTERM_BP_DIRECT	GO:0001764~neuron migration	5	4.29E-04	NTRK2, CEP85L, CCK, GATA2, FGF13	13.93644	0.059555	0.058554

Table S6.1. Thirteen up-regulated and 121 down-regulated genes in PT-DLBCL with ≥3CNVs (corresponding to the 4th heatmap in Figure 2)

Gene ID	Gene Name	Score(d)	Fold Change	q-value(%)	local fdr(%)
BCL11A	BCL11 transcription factor A(BCL11A)	5.003049	1.699294	0	2.590674
BCL2	BCL2 apoptosis regulator(BCL2)	4.742866	2.186146	0	2.171841
CENPF	centromere protein F(CENPF)	3.84346	1.526171	1.275811	1.014176
CIP2A	CIP2A (Cellular Inhibitor Of PP2A)	3.635543	1.453009	1.937342	1.082821
CARD11	caspase recruitment domain family member 11(CARD11)	3.44116	1.50562	4.667927	1.522316
TCL6	TCL6 (T Cell Leukemia/Lymphoma 6)	3.341012	1.995004	4.667927	1.961305
BRCA2	BRCA2 DNA repair associated(BRCA2)	3.191502	1.384115	6.879542	2.984477
CPSF6	cleavage and polyadenylation specific factor 6(CPSF6)	3.188685	1.218101	6.879542	3.008715
MYC	MYC (MYC Proto-Oncogene, BHLH Transcription Factor)	3.17289	1.595965	6.879542	3.148361
TCL1A	TCL1 family AKT coactivator A(TCL1A)	3.158934	2.285494	6.879542	3.27712
LYN	LYN proto-oncogene, Src family tyrosine kinase(LYN)	3.084349	1.428092	6.879542	4.055533
ST6GAL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1(ST6GAL1)	3.079431	1.407714	6.879542	4.112452
CHEK1	checkpoint kinase 1(CHEK1)	3.065027	1.35685	6.879542	4.283342
GAS7	growth arrest specific 7(GAS7)	-7.73175	0.425209	0	0
INPP4B	inositol polyphosphate-4-phosphatase type II B(INPP4B)	-5.16876	0.495793	0	0
DPYD	dihydropyrimidine dehydrogenase(DPYD)	-4.97809	0.579295	0	0
CSF1R	colony stimulating factor 1 receptor(CSF1R)	-4.87917	0.534831	0	0
WDFY3	WD repeat and FYVE domain containing 3(WDFY3)	-4.80139	0.580577	0	0
STAT4	signal transducer and activator of transcription 4(STAT4)	-4.789	0.488201	0	0
CD28	CD28 molecule(CD28)	-4.56338	0.49738	0	0
DDR2	discoidin domain receptor tyrosine kinase 2(DDR2)	-4.48877	0.545319	0	0
GBP2	guanylate binding protein 2(GBP2)	-4.33604	0.61764	0	0
PDCD1LG2	programmed cell death 1 ligand 2(PDCD1LG2)	-4.29494	0.433783	0	0
ITK	IL2 inducible T cell kinase(ITK)	-4.28846	0.519254	0	0
CYP11B1	cytochrome P450 family 1 subfamily B member 1(CYP11B1)	-4.23322	0.532902	0	0
PRRX1	paired related homeobox 1(PRRX1)	-4.21845	0.515064	0	0
MYO1F	myosin IF(MYO1F)	-4.20408	0.564843	0	0
INPP5A	inositol polyphosphate-5-phosphatase A(INPP5A)	-4.18289	0.499063	0	0
PLCB4	phospholipase C beta 4(PLCB4)	-4.07981	0.484236	0	0

IL1R1	interleukin 1 receptor type 1(IL1R1)	-4.0153	0.602204	0	0
IL7R	interleukin 7 receptor(IL7R)	-4.0143	0.541943	0	0
CSF3R	colony stimulating factor 3 receptor(CSF3R)	-4.01404	0.5581	0	0
GATA3	GATA binding protein 3(GATA3)	-3.9774	0.484616	0	0
ARRDC4	arrestin domain containing 4(ARRDC4)	-3.9682	0.524457	0	0
TCF7L2	transcription factor 7 like 2(TCF7L2)	-3.95779	0.582257	0	0
TUSC3	tumor suppressor candidate 3(TUSC3)	-3.93866	0.502728	0	0
CSF1	colony stimulating factor 1(CSF1)	-3.87459	0.576645	0	0
ABCC3	ATP binding cassette subfamily C member 3(ABCC3)	-3.8665	0.509413	0	0
KLF4	KLF transcription factor 4(KLF4)	-3.82101	0.496883	0	0
FLNA	filamin A(FLNA)	-3.7878	0.615495	0	0
EGR2	early growth response 2(EGR2)	-3.62726	0.578941	0	0
DST	dystonin(DST)	-3.62531	0.637398	0	0
FSTL3	follistatin like 3(FSTL3)	-3.60027	0.57332	0	0
FGFR1	fibroblast growth factor receptor 1(FGFR1)	-3.58045	0.593689	0	0
BIN1	bridging integrator 1(BIN1)	-3.57164	0.593162	0	0
CDC14B	cell division cycle 14B(CDC14B)	-3.55256	0.55275	0	0
AXL	AXL receptor tyrosine kinase(AXL)	-3.53941	0.558409	0	0
ITGAV	integrin subunit alpha V(ITGAV)	-3.53919	0.648946	0	0
RASGEF1A	RasGEF domain family member 1A(RASGEF1A)	-3.52815	0.583098	0	0
CD8A	CD8 subunit alpha(CD8A)	-3.52107	0.527067	0	0
LMO2	LIM domain only 2(LMO2)	-3.51591	0.476593	0	0
ROBO1	roundabout guidance receptor 1(ROBO1)	-3.51129	0.590286	0	0
DOCK1	dedicator of cytokinesis 1(DOCK1)	-3.48463	0.673674	0	0
HTRA1	HtrA serine peptidase 1(HTRA1)	-3.4615	0.525616	0	0
SRC	SRC proto-oncogene, non-receptor tyrosine kinase(SRC)	-3.43094	0.616971	0	0
SH3D19	SH3 domain containing 19(SH3D19)	-3.42774	0.537859	0	0
SOD2	superoxide dismutase 2(SOD2)	-3.41294	0.586688	0	0
MAF	MAF bZIP transcription factor(MAF)	-3.41001	0.575323	0	0
AKAP12	A-kinase anchoring protein 12(AKAP12)	-3.40766	0.529141	0	0
ABLIM1	actin binding LIM protein 1(ABLIM1)	-3.39463	0.644774	0	0
HSPA1A	heat shock protein family A (Hsp70) member 1A(HSPA1A)	-3.3606	0.607103	0	0
DAB2IP	DAB2 interacting protein(DAB2IP)	-3.35741	0.571554	0	0
SMAD3	SMAD family member 3(SMAD3)	-3.3373	0.697319	0	0
IL15	interleukin 15(IL15)	-3.3358	0.591797	0	0
ACVR1B	activin A receptor type 1B(ACVR1B)	-3.33176	0.632625	0	0
EDIL3	EGF like repeats and discoidin domains 3(EDIL3)	-3.32123	0.540744	0	0
KSR1	kinase suppressor of ras 1(KSR1)	-3.31717	0.661151	0	0
JUN	Jun proto-oncogene, AP-1 transcription factor subunit(JUN)	-3.31475	0.609798	0	0
PRF1	perforin 1(PRF1)	-3.31271	0.576159	0	0
YAP1	Yes1 associated transcriptional regulator(YAP1)	-3.30096	0.564922	0	0
LIFR	LIF receptor subunit alpha(LIFR)	-3.29446	0.632636	0	0
FOXO4	forkhead box O4(FOXO4)	-3.28452	0.626019	0	0
CRTC3	CREB regulated transcription coactivator 3(CRTC3)	-3.26715	0.653763	0	0
ACSL6	acyl-CoA synthetase long chain family member 6(ACSL6)	-3.24579	0.589485	0	0
ALDH1A1	aldehyde dehydrogenase 1 family member A1(ALDH1A1)	-3.23265	0.55775	0	0
CTNNA1	catenin alpha 1(CTNNA1)	-3.21472	0.782698	0	0

S1PR2	sphingosine-1-phosphate receptor 2(S1PR2)	-3.19641	0.595692	0	0
APOD	apolipoprotein D(APOD)	-3.19008	0.482136	0	0
BCL11B	BCL11 transcription factor B(BCL11B)	-3.17642	0.605254	0	0
GSN	gelsolin(GSN)	-3.14265	0.623311	0	0
EXT2	exostosin glycosyltransferase 2(EXT2)	-3.14262	0.746182	0	0
FOS	Fos proto-oncogene, AP-1 transcription factor subunit(FOS)	-3.13071	0.502329	0	0
SDC4	syndecan 4(SDC4)	-3.12139	0.566795	0	0.052321
EXT1	exostosin glycosyltransferase 1(EXT1)	-3.12069	0.732549	0	0.056916
EGFR	epidermal growth factor receptor(EGFR)	-3.11609	0.553698	0	0.087368
RTKL1-TNFRSF6B	RTKL1-TNFRSF6B readthrough (NMD candidate)(RTKL1-TNFRSF6B)	-3.10125	0.657124	0	0.188321
PLPP3	PLPP3 (Phospholipid Phosphatase 3)	-3.09833	0.632892	0	0.208657
CDH11	cadherin 11(CDH11)	-3.0847	0.654946	0	0.30579
DCN	decorin(DCN)	-3.07233	0.545416	0	0.397095
SEPTIN5	SEPTIN5 (Septin 5)	-3.04696	0.551544	0	0.593886
GNAQ	G protein subunit alpha q(GNAQ)	-3.04245	0.69634	0	0.630251
ETV5	ETS variant transcription factor 5(ETV5)	-3.03982	0.677281	0	0.651623
ALDH2	aldehyde dehydrogenase 2 family member(ALDH2)	-3.03554	0.617963	0	0.686777
SH3GL1	SH3 domain containing GRB2 like 1, endophilin A2(SH3GL1)	-3.03003	0.681031	0	0.732557
AR	androgen receptor(AR)	-3.01898	0.607322	0	0.826325
SNX9	sorting nexin 9(SNX9)	-3.00297	0.677102	0	0.966713
SMO	smoothened, frizzled class receptor(SMO)	-2.99078	0.60544	0	1.07739
ASPH	aspartate beta-hydroxylase(ASPH)	-2.98485	0.705486	0	1.13231
TGFB1	transforming growth factor beta induced(TGFB1)	-2.9837	0.616631	0	1.143157
NOTCH3	notch receptor 3(NOTCH3)	-2.98355	0.667637	0	1.144503
CHST11	carbohydrate sulfotransferase 11(CHST11)	-2.98213	0.70522	0	1.157836
DNMT3A	DNA methyltransferase 3 alpha(DNMT3A)	-2.96207	0.70557	0	1.350956
PLCG1	phospholipase C gamma 1(PLCG1)	-2.95011	0.727951	0	1.470468
COL6A3	collagen type VI alpha 3 chain(COL6A3)	-2.94954	0.69761	0	1.476271
CD274	CD274 molecule(CD274)	-2.94835	0.561922	0	1.488321
CTLA4	cytotoxic T-lymphocyte associated protein 4(CTLA4)	-2.93974	0.57812	0	1.576804
TGFB3	transforming growth factor beta 3(TGFB3)	-2.93431	0.658469	0	1.633484
MITF	melanocyte inducing transcription factor(MITF)	-2.93014	0.591915	0	1.677511
PRKCA	protein kinase C alpha(PRKCA)	-2.9157	0.69721	0	1.833017
FASLG	Fas ligand(FASLG)	-2.90182	0.543217	0	1.987237
CCDC28A	coiled-coil domain containing 28A(CCDC28A)	-2.85878	0.683433	0.606472	2.49592
SGK1	serum/glucocorticoid regulated kinase 1(SGK1)	-2.85862	0.6482	0.606472	2.497811
CACNA2D3	calcium voltage-gated channel auxiliary subunit alpha2delta 3(CACNA2D3)	-2.85856	0.508849	0.606472	2.498643
ATF3	activating transcription factor 3(ATF3)	-2.83377	0.576415	0.606472	2.813145
SHTN1	SHTN1 (Shootin 1)	-2.83317	0.691805	0.606472	2.820886
GRB10	growth factor receptor bound protein 10(GRB10)	-2.83119	0.664466	0.606472	2.846743
DLL1	delta like canonical Notch ligand 1(DLL1)	-2.82891	0.63537	0.606472	2.876713
ASMTL	acetylserotonin O-methyltransferase like(ASMTL)	-2.81082	0.713868	0.606472	3.118754
BICC1	BicC family RNA binding protein 1(BICC1)	-2.80255	0.60813	0.606472	3.232301
MAP3K6	mitogen-activated protein kinase kinase kinase 6(MAP3K6)	-2.79572	0.672251	0.606472	3.327489
TEAD1	TEA domain transcription factor 1(TEAD1)	-2.78796	0.670607	0.606472	3.437186
NFIB	nuclear factor I B(NFIB)	-2.78601	0.685021	0.606472	3.465095

RUNX2	RUNX family transcription factor 2(RUNX2)	-2.77988	0.622512	0.606472	3.553192
PPFIBP1	PPFIA binding protein 1(PPFIBP1)	-2.77435	0.675735	0.606472	3.633615
PLA2G5	phospholipase A2 group V(PLA2G5)	-2.77303	0.581911	0.606472	3.65295
ZBTB16	zinc finger and BTB domain containing 16(ZBTB16)	-2.76756	0.538092	0.606472	3.733542
EML1	EMAP like 1(EML1)	-2.74417	0.642364	0.606472	4.087763
NDRG1	N-myc downstream regulated 1(NDRG1)	-2.73749	0.648429	0.606472	4.191818
FHL2	four and a half LIM domains 2(FHL2)	-2.73326	0.581578	0.606472	4.258264
RAC3	Rac family small GTPase 3(RAC3)	-2.73075	0.566874	0.606472	4.297984
PSD3	pleckstrin and Sec7 domain containing 3(PSD3)	-2.7206	0.617243	0.606472	4.460459
TEAD3	TEA domain transcription factor 3(TEAD3)	-2.70804	0.624703	0.606472	4.665741
EPHB6	EPH receptor B6(EPHB6)	-2.70409	0.599088	0.606472	4.73125
PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta(PPP2R2B)	-2.69637	0.60657	0.606472	4.860532

Suppl. Table S6.2 Significantly enriched functional terms with FDR ≤ 0.05 by DAVID functional annotation tool for 121 genes downregulated in PT-DLBCL with ≥ 3 CNVs

Category	Term	Count	P Value	Genes	Fold Enrichment	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription by RNA polymerase II GO:1902895~positive regulation of miRNA transcription	33	7.65E-13	YAP1, NOTCH3, CRT3, GATA3, FOXO4, DLL1, EGFR, FSTL3, STAT4, TEAD1, TEAD3, TCF7L2, JUN, EGR2, SMAD3, PRRX1, BCL11B, TGF3, ZBTB16, LMO2, DAB2IP, MITF, FOS, KLF4, ETV5, RUNX2, DCN, AR, MAF, SMO, NFIB, CD28, ATF3	4.431529	1.23E-09	1.19E-09
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription by RNA polymerase II GO:0008285~negative regulation of cell population proliferation	9	2.21E-09	NOTCH3, AR, JUN, SMAD3, FOS, GATA3, KLF4, TEAD1, EGFR	25.3	1.78E-06	1.72E-06
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription by RNA polymerase II GO:0008285~negative regulation of cell population proliferation	23	3.85E-08	YAP1, TCF7L2, NOTCH3, JUN, SMAD3, PRRX1, ZBTB16, DNMT3A, DAB2IP, FHL2, FASLG, MITF, GATA3, KLF4, ETV5, AR, MAF, SMO, NFIB, BIN1, ATF3, HSPA1A, FGFR1	4.028384	1.56E-05	1.51E-05
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression GO:0010467~gene expression	16	3.88E-08	CSF1R, SMAD3, BCL11B, TGF3, ZBTB16, DAB2IP, GATA3, FOXO4, KLF4, SOD2, DLL1, NDRG1, AR, ASPH, CYP1B1, HSPA1A	6.218126	1.56E-05	1.51E-05
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression GO:0010467~gene expression	17	4.91E-08	YAP1, GSN, SMAD3, CSF1, MITF, KLF4, ACVR1B, DLL1, RUNX2, ROBO1, AR, MAF, SMO, CD28, IL7R, ATF3, HSPA1A	5.633268	1.58E-05	1.53E-05
GOTERM_BP_DIRECT	GO:0010467~gene expression GO:0051897~positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	9	1.85E-06	EXT1, EXT2, EGR2, SMO, NFIB, GRB10, IL7R, RUNX2, FGFR1	10.76596	4.64E-04	4.47E-04
GOTERM_BP_DIRECT	GO:0051897~positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction GO:0007169~cell surface receptor protein tyrosine kinase signaling pathway	10	2.02E-06	TCF7L2, CSF1R, SRC, AXL, CD28, GATA3, DCN, EGFR, FGFR1, DDR2	8.784722	4.64E-04	4.47E-04
GOTERM_BP_DIRECT	GO:0007169~cell surface receptor protein tyrosine kinase signaling pathway GO:0045893~positive regulation of DNA-templated transcription	8	4.15E-06	CSF1R, CSF1, SRC, CD8A, AXL, EGFR, FGFR1, DDR2	12.15616	7.68E-04	7.40E-04
GOTERM_BP_DIRECT	GO:0045893~positive regulation of DNA-templated transcription GO:0002067~glandular epithelial cell differentiation	17	4.29E-06	YAP1, CD274, EGR2, JUN, SMAD3, TGF3, ZBTB16, MITF, GATA3, FOS, KLF4, EGFR, RUNX2, AR, ASPH, NFIB, TEAD1	4.021505	7.68E-04	7.40E-04
GOTERM_BP_DIRECT	GO:0002067~glandular epithelial cell differentiation GO:0007275~multicellular organism development	4	6.81E-06	EXT1, YAP1, NFIB, KLF4	96.38095	0.001098	0.001057
GOTERM_BP_DIRECT	GO:0007275~multicellular organism development GO:0008284~positive regulation of cell population proliferation	7	8.21E-06	CSF1R, AXL, CDH11, EGFR, FSTL3, FGFR1, DDR2	14.57613	0.001116	0.001075
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell population proliferation GO:0043066~negative regulation of apoptosis	14	8.81E-06	CSF1R, CSF1, TGF3, IL15, FASLG, LIFR, DLL1, EGFR, AR, ITGAV, S1PR2, IL7R, FLNA, HSPA1A, DDR2	4.666667	0.001116	0.001075
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptosis GO:0007165~signal transduction	14	9.00E-06	CSF1R, SMAD3, SRC, FHL2, MITF, SOD2, EGFR, SMO, CHST11, AXL, CD28, CD274, ITK, CSF1R, CSF3R, IL15, SRC, FASLG, GATA3, ACVR1B, NDRG1, EGFR, AKAP12, AR, INPP4B, AXL, RAC3, MAP3K6, IL7R, DOCK1, HSPA1A, SH3GL1, DDR2	4.657462	0.001116	0.001075
GOTERM_BP_DIRECT	GO:0007165~signal transduction GO:0007155~cell adhesion	22	1.01E-05	CSF3R, DST, SRC, PRKCA, ROBO1, PPFIBP1, CDH11, CTNNA1, CYP1B1, COL6A3, ITGAV, TGFBI, EDIL3, DDR2	2.992473	0.001162	0.001119
GOTERM_BP_DIRECT	GO:0007155~cell adhesion GO:0001503~ossification	14	1.11E-05	EXT1, EXT2, CDH11, EGFR, RUNX2, FSTL3, DDR2	4.567376	0.00117	0.001127
GOTERM_BP_DIRECT	GO:0001503~ossification GO:0030097~hemopoiesis	7	1.16E-05	EXT1, EXT2, CDH11, EGFR, RUNX2, FSTL3, DDR2	13.72868	0.00117	0.001127
GOTERM_BP_DIRECT	GO:0030097~hemopoiesis GO:0048469~cell maturation	6	3.72E-05	CSF1R, ZBTB16, IL7R, SOD2, DLL1, RUNX2	15.8125	0.003528	0.003399
GOTERM_BP_DIRECT	GO:0048469~cell maturation	5	4.07E-05	IL15, AXL, GATA3, RUNX2, FGFR1	25.55556	0.003641	0.003508

GOTERM_BP_DIRECT	GO:0001701~in utero embryonic development	9	4.91E-05	AR, SMAD3, SMO, CHST11, TGFB3, GATA3, PLCG1, ACVR1B, FGFR1	6.868778	0.004165	0.004013
GOTERM_BP_DIRECT	GO:2001237~negative regulation of extrinsic apoptotic signaling pathway	5	7.95E-05	YAP1, TCF7L2, AR, SRC, ITGAV	21.62393	0.00641	0.006176
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	10	1.21E-04	JUN, BIN1, TGFB3, SRC, ZBTB16, DAB2IP, HTRA1, CTLA4, CYP1B1, FASLG	5.238095	0.0093	0.00896
GOTERM_BP_DIRECT	GO:0042130~negative regulation of T cell proliferation	5	1.81E-04	CD274, SDC4, CTLA4, PLA2G5, PDCD1LG2	17.56944	0.013236	0.012752
GOTERM_BP_DIRECT	GO:0050673~epithelial cell proliferation	5	2.12E-04	YAP1, AR, SMO, EGFR, RUNX2	16.86667	0.014231	0.01371
GOTERM_BP_DIRECT	GO:0018108~peptidyl-l-tyrosine phosphorylation	5	2.12E-04	CSF1R, SRC, EGFR, FGFR1, DDR2	16.86667	0.014231	0.01371
GOTERM_BP_DIRECT	GO:0042127~regulation of cell population proliferation	7	2.34E-04	JUN, CHST11, KSR1, TGFB3, STAT4, MITF, SGK1	8.031746	0.015057	0.014506
GOTERM_BP_DIRECT	GO:0016477~cell migration	9	2.58E-04	SDC4, RASGEF1A, AXL, CDH11, CTNNA1, ITGAV, PLCG1, DOCK1, FGFR1	5.402135	0.015978	0.015393
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	9	2.97E-04	CD274, CSF1R, SMAD3, SMO, CSF1, ITGAV, PRKCA, SOD2, EGFR	5.289199	0.017265	0.016633
GOTERM_BP_DIRECT	GO:0033674~positive regulation of kinase activity	5	3.07E-04	CSF1R, AXL, EGFR, FGFR1, DDR2	15.33333	0.017265	0.016633
GOTERM_BP_DIRECT	GO:0007179~transforming growth factor beta receptor signaling pathway	6	3.11E-04	JUN, SMAD3, CHST11, TGFB3, SRC, FOS	10.12	0.017265	0.016633
GOTERM_BP_DIRECT	GO:0002062~chondrocyte differentiation	5	3.76E-04	EXT2, NFIB, TGFB1, RUNX2, FGFR1	14.54023	0.020229	0.019489
GOTERM_BP_DIRECT	GO:0060395~SMAD protein signal transduction	4	4.66E-04	JUN, SMAD3, FOS, RUNX2	25.94872	0.024243	0.023355
GOTERM_BP_DIRECT	GO:0006366~transcription by RNA polymerase II	8	4.82E-04	AR, MAF, PRRX1, BCL11B, CD28, FOS, GATA3, KLF4	5.741844	0.024284	0.023395
GOTERM_BP_DIRECT	GO:0050679~positive regulation of epithelial cell proliferation	5	7.30E-04	YAP1, TCF7L2, SMO, EGFR, RUNX2	12.22222	0.035659	0.034354
GOTERM_BP_DIRECT	GO:0050852~T cell receptor signaling pathway	6	7.72E-04	ITK, CD8A, CD28, CTLA4, GATA3, PLCG1	8.295082	0.036603	0.035263
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	8	8.18E-04	DAB2IP, CYP1B1, FLNA, ITGAV, PRKCA, APOD, TGFB1, FGFR1	5.250324	0.037671	0.036292
GOTERM_BP_DIRECT	GO:0030225~macrophage differentiation	4	9.49E-04	CSF1R, CSF1, IL15, GATA3	20.44444	0.042515	0.040959
GOTERM_BP_DIRECT	GO:0008217~regulation of blood pressure	5	0.001102	EXT1, EXT2, SOD2, SGK1, DLL1	10.95238	0.048024	0.046266
GOTERM_BP_DIRECT	GO:0042060~wound healing	5	0.001157	EXT1, YAP1, SMAD3, SDC4, DST	10.81197	0.049066	0.04727
GOTERM_BP_DIRECT	GO:0071356~cellular response to tumor necrosis factor	6	0.001256	AKAP12, DAB2IP, CYP1B1, FOS, GATA3, GBP2, EPHB6, ITK, CSF3R, CSF1, TUSC3, PRF1, FASLG, ROBO1, AKAP12, RASGEF1A, GRB10, CTLA4, RAC3, ITGAV, SH3D19, ABCC3, ARRD4, DST, IL1R1, ACSL6, LIFR, PRKCA, PDCD1LG2, AR, PLCB4, ASPH, SMO, BIN1, CD8A, CDH11, WDFY3, SGK1, DOCK1, DDR2, GAS7, CSF1R, CD274, NOTCH3, SDC4, SRC, HTRA1, PLA2G5, ACVR1B, NDRG1, DLL1, EGFR, INPP5A, CTNNA1, FLNA, SNX9, S1PR2, PLCG1, GSN, SMAD3, TGFB3, DAB2IP, PPFIBP1, AXL, GNAQ, CD28, TGFB1, IL7R, MYO1F, FGFR1, HSPA1A	7.441176	0.051923	0.050023
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	65	5.36E-11	NOTCH3, CSF1R, CSF3R, SMAD3, SRC, CD8A, AXL, LIFR, ACVR1B, EGFR, FGFR1, DDR2	2.092976	1.34E-08	1.22E-08
GOTERM_CC_DIRECT	GO:0043235~receptor or complex	12	4.73E-08	GSN, SDC4, DST, SRC, FHL2, EGFR, AKAP12, PPFIBP1, CTNNA1, FLNA, RAC3, ITGAV, HSPA1A, DDR2	9.603218	5.94E-06	5.39E-06
GOTERM_CC_DIRECT	GO:0005925~focal adhesion	14	8.26E-07	EPHB6, ITK, CRT3, PRF1, AKAP12, RASGEF1A, GRB10, RAC3, ITGAV, SH3D19, SH3GL1, KSR1, DST, IL15, ASMTL, PRKCA, FOS, EML1, RUNX2, AR, INPP4B, PLCB4, BIN1, DPYD, ALDH1A1, WDFY3, SGK1, DOCK1, YAP1, NOTCH3, SRC, HTRA1, FOXO4, ACVR1B, NDRG1, CTNNA1, STAT4, FLNA, SNX9, PLCG1, GBP2, GSN, SMAD3, PRRX1, ZBTB16, DAB2IP, KLF4, PPFIBP1, PPP2R2B, CD28, IL7R, MYO1F, FGFR1, HSPA1A	5.795046	6.91E-05	6.28E-05
GOTERM_CC_DIRECT	GO:0005829~cytosol	54	9.03E-06	CD274, ABLIM1, GSN, DST, BIN1, AXL, CTNNA1, FLNA, MYO1F, DDR2	1.721235	5.67E-04	5.15E-04
GOTERM_CC_DIRECT	GO:0015629~actin cytoskeleton	10	2.57E-05	TCF7L2, EGR2, JUN, SMAD3, PRRX1, MITF, GATA3, FOXO4, FOS, KLF4, ETV5, RUNX2, AR, MAF, NFIB, STAT4, TEAD1, ATF3, TEAD3	6.407841	0.001292	0.001174
GOTERM_CC_DIRECT	GO:0000785~chromatin	19	6.00E-05	CD274, CSF3R, IL1R1, CD8A, CD28, CTLA4, FASLG, ITGAV, LIFR, PDCD1LG2, IL7R	2.959469	0.002508	0.002279
GOTERM_CC_DIRECT	GO:0009897~external side of plasma membrane	11	1.32E-04	YAP1, CD274, CSF1R, ITK, NOTCH3, CRT3, SRC, FHL2, GATA3, FOXO4, FSTL3, CDC14B, STAT4, GBP2, TEAD1, TEAD3, SH3D19, TCF7L2, JUN, EGR2, SMAD3, PRRX1, DST, IL15, LMO2, DNMT3A, PRKCA, MITF, FOS, KLF4, ETV5, RUNX2, AR, NFIB, WDFY3, SGK1, IL7R, DOCK1, ATF3, HSPA1A	4.616932	0.004661	0.004234
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	40	1.49E-04	KSR1, SRC, PSD3, ITGAV, PLCG1, EGFR	1.787199	0.004661	0.004234
GOTERM_CC_DIRECT	GO:0032587~ruffle membrane	6	2.52E-04	EPHB6, NOTCH3, CSF3R, CSF1, HTRA1, PRF1, FASLG, PLA2G5, DLL1, FSTL3, FLNA, APOD, GSN, TGFB3, IL15, IL1R1, PDCD1LG2, DCN, CD8A, CDH11, COL6A3, TGFB1, IL7R, FGFR1, HSPA1A	10.59178	0.00704	0.006395
GOTERM_CC_DIRECT	GO:0005576~extracellular region	25	4.12E-04		2.142555	0.010338	0.009391

GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	26	4.88E-04	CD274, SDC4, SRC, HTRA1, FASLG, NDRG1, ALDH2, FLNA, RAC3, APOD, ITGAV, SNX9, EDIL3, GSN, LIFR, PRKCA, SOD2, EXT2, SMO, AXL, GNAQ, ALDH1A1, CDH11, COL6A3, TGFB1, HSPA1A	2.073325	0.011128	0.010108
GOTERM_CC_DIRECT	GO:0044300~cerebellar mossy fiber	3	6.20E-04	BIN1, NFIB, DAB2IP	77.16872	0.012964	0.011776
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytoplasm	13	0.001	CSF1, SRC, FASLG, PRKCA, EML1, NDRG1, EGFR, FLNA, CTLA4, RAC3, APOD, GBP2, HSPA1A	3.075932	0.019317	0.017547
GOTERM_CC_DIRECT	GO:0005667~transcription regulator complex	7	0.002428	JUN, SMAD3, LMO2, KLF4, TEAD1, RUNX2, TEAD3	5.123668	0.042435	0.038547
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	47	0.002536	YAP1, CRT3, SRC, FOXO4, NDRG1, EGFR, ROBO1, CDC14B, AKAP12, ABLIM1, GRB10, CTNNA1, STAT4, FLNA, APOD, SNX9, S1PR2, PLCG1, GBP2, SH3GL1, ARRD4, EGR2, GSN, SMAD3, KSR1, DST, IL15, DNMT3A, DAB2IP, PRKCA, MITF, RUNX2, BICC1, AR, INPP4B, MAF, BIN1, GNAQ, DPYD, ALDH1A1, CDH11, WDFY3, SGK1, DOCK1, MYO1F, GAS7, HSPA1A	1.470774	0.042435	0.038547
GOTERM_CC_DIRECT	GO:0098978~glutamate synapse	9	0.002706	PLCB4, BIN1, SRC, CDH11, RAC3, FLNA, PLCG1, DOCK1, SH3GL1	3.751257	0.042447	0.038557
GOTERM_CC_DIRECT	GO:0009986~cell surface	11	0.003416	EPHB6, NOTCH3, CSF1R, SDC4, TGF3, AXL, CD28, ITGAV, ACVR1B, EGFR, ROBO1	3.014709	0.050432	0.045811
GOTERM_MF_DIRECT	GO:0061629~RNA polymerase II-specific DNA-binding transcription factor binding	12	1.58E-08	TCF7L2, AR, EGR2, JUN, SMAD3, PRRX1, LMO2, DNMT3A, FOS, GATA3, KLF4, TEAD3	10.66912	4.37E-06	4.08E-06
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	32	2.70E-08	NOTCH3, CSF1, SDC4, HTRA1, FHL2, PRF1, GATA3, FOXO4, EGFR, ROBO1, GRB10, CTNNA1, STAT4, SNX9, GBP2, SH3GL1, JUN, SMAD3, TGF3, ZBTB16, LMO2, DNMT3A, DAB2IP, FOS, SOD2, MAF, BIN1, CD28, TGFBI, ATF3, GAS7, FGFR1	3.013807	4.37E-06	4.08E-06
GOTERM_MF_DIRECT	GO:0005515~protein binding	104	4.42E-08	EPHB6, CRT3, CSF3R, CSF1, PRF1, CCDC28A, CDC14B, GRB10, CYP1B1, MAP3K6, SH3GL1, ARRD4, IL1R1, LMO2, LIFR, MITF, PRKCA, EML1, RUNX2, AR, INPP4B, MAF, SMO, BIN1, CD8A, WDFY3, ATF3, CSF1R, CD274, NOTCH3, SDC4, HTRA1, GATA3, FOXO4, NDRG1, INPP5A, APOD, SNX9, PLCG1, JUN, EGR2, SMAD3, BCL11B, TGF3, ZBTB16, EXT1, EXT2, PPFIBP1, GNAQ, CD28, TGFBI, IL7R, FGFR1, ITK, FHL2, FASLG, ROBO1, AKAP12, CTLA4, RAC3, ITGAV, TEAD1, TEAD3, SH3D19, KSR1, DST, IL15, DNMT3A, ASMTL, FOS, PDCD1LG2, ETV5, DCN, PLCB4, ASPH, DPYD, ALDH1A1, SGK1, DOCK1, DDR2, GAS7, YAP1, SRC, ACVR1B, DLL1, EGFR, FSTL3, ABLIM1, STAT4, CTNNA1, FLNA, S1PR2, GBP2, TCF7L2, GSN, PRRX1, DAB2IP, KLF4, SOD2, AXL, PPP2R2B, NFIB, MYO1F, HSPA1A	1.333989	4.37E-06	4.08E-06
GOTERM_MF_DIRECT	GO:0001228~DNA-binding transcription activator activity, RNA polymerase II-specific	17	4.83E-08	EGR2, JUN, SMAD3, PRRX1, BCL11B, ZBTB16, MITF, GATA3, FOXO4, FOS, KLF4, ETV5, RUNX2, AR, MAF, NFIB, ATF3	5.641146	4.37E-06	4.08E-06
GOTERM_MF_DIRECT	GO:0003700~DNA-binding transcription factor activity	17	1.51E-07	TCF7L2, EGR2, JUN, SMAD3, BCL11B, ZBTB16, GATA3, FOXO4, FOS, KLF4, ETV5, RUNX2, AR, STAT4, TEAD1, ATF3, TEAD3	5.188591	1.10E-05	1.02E-05
GOTERM_MF_DIRECT	GO:0000976~transcription cis-regulatory region binding	11	2.37E-06	YAP1, TCF7L2, AR, EGR2, JUN, SMAD3, FOS, GATA3, KLF4, ATF3, ETV5	7.375104	1.43E-04	1.33E-04
GOTERM_MF_DIRECT	GO:0045296~cadherin binding	12	6.16E-06	NOTCH3, PPFIBP1, SRC, CDH11, DAB2IP, CTNNA1, FLNA, SNX9, NDRG1, EGFR, SH3GL1, HSPA1A	5.860056	3.18E-04	2.97E-04
GOTERM_MF_DIRECT	GO:0000978~RNA polymerase II cis-regulatory region sequence-specific DNA binding	22	2.56E-05	YAP1, TCF7L2, EGR2, JUN, SMAD3, PRRX1, BCL11B, ZBTB16, DNMT3A, MITF, GATA3, FOXO4, FOS, KLF4, RUNX2, AR, MAF, NFIB, STAT4, TEAD1, ATF3, TEAD3	2.813957	0.001156	0.00108
GOTERM_MF_DIRECT	GO:0008013~beta-catenin binding	7	5.59E-05	TCF7L2, AR, SMAD3, CDH11, CTNNA1, FOXO4, KLF4	10.41048	0.002133	0.001992
GOTERM_MF_DIRECT	GO:0005178~integrin binding	8	5.89E-05	DST, SRC, ITGAV, PRKCA, TGFBI, S1PR2, EDIL3, EGFR	8.078678	0.002133	0.001992
GOTERM_MF_DIRECT	GO:0004714~transmembrane receptor protein tyrosine kinase activity	5	8.95E-05	CSF1R, SRC, AXL, EGFR, DDR2	20.97349	0.0027	0.002521
GOTERM_MF_DIRECT	GO:0019838~growth factor binding	5	8.95E-05	CSF1R, SRC, HTRA1, LIFR, ACVR1B	20.97349	0.0027	0.002521
GOTERM_MF_DIRECT	GO:1990837~sequence-specific double-stranded DNA binding	13	1.52E-04	EGR2, JUN, BCL11B, GATA3, FOXO4, FOS, KLF4, ETV5, RUNX2, MAF, NFIB, TEAD1, ATF3	3.7977	0.004232	0.003952
GOTERM_MF_DIRECT	GO:0019899~enzyme binding	10	4.41E-04	NOTCH3, AR, JUN, SRC, ACSL6, PRKCA, FOXO4, SOD2, EGFR, HSPA1A	4.397667	0.011412	0.010655
GOTERM_MF_DIRECT	GO:0000981~DNA-binding transcription factor activity, RNA polymerase II-specific	20	5.14E-04	TCF7L2, EGR2, JUN, SMAD3, PRRX1, ZBTB16, MITF, GATA3, FOXO4, FOS, KLF4, ETV5, RUNX2, AR, MAF, NFIB, STAT4, TEAD1, ATF3, TEAD3	2.407553	0.012401	0.011579
GOTERM_MF_DIRECT	GO:0051015~actin filament binding	8	6.08E-04	ABLIM1, GSN, BIN1, CTNNA1, FLNA, EGFR, MYO1F, GAS7	5.522134	0.013247	0.012369
GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	14	6.22E-04	CSF1R, SMAD3, CSF1, DST, ZBTB16, DAB2IP, ACSL6, EXT1, DPYD, FLNA, SNX9, GBP2, ATF3, FGFR1	3.05374	0.013247	0.012369
GOTERM_MF_DIRECT	GO:0043425~bHLH transcription factor binding	4	7.07E-04	SMAD3, LMO2, FHL2, RUNX2	22.56458	0.014214	0.013271
GOTERM_MF_DIRECT	GO:0071837~HMG box domain binding	3	0.00272	EGR2, PRRX1, GATA3	37.75228	0.051815	0.048379
KEGG_PATHWAY	hsa05200:Pathways in cancer	26	1.93E-10	CSF1R, NOTCH3, CSF3R, FASLG, DLL1, EGFR, CTNNA1, STAT4, RAC3, ITGAV, PLCG1, TCF7L2, JUN, SMAD3, TGF3, IL15, ZBTB16, PRKCA, MITF, FOS, AR, PLCB4, SMO, GNAQ, IL7R, FGFR1	4.49187	4.68E-08	3.74E-08

KEGG_PATHWAY	hsa04010:MAPK signaling pathway	15	3.41E-06	CSF1R, JUN, CSF1, IL1R1, TGFβ3, CACNA2D3, FASLG, PRKCA, FOS, EGFR, FLNA, RAC3, MAP3K6, HSPA1A, FGFR1	4.604167	4.14E-04	3.30E-04
KEGG_PATHWAY	hsa04928:Parathyroid hormone synthesis, secretion and action	9	3.05E-05	PLCB4, GNAQ, PRKCA, FOS, GATA3, SGK1, EGFR, RUNX2, FGFR1	7.206522	0.002467	0.001969
KEGG_PATHWAY	hsa04658:Th1 and Th2 cell differentiation	8	5.52E-05	NOTCH3, JUN, MAF, STAT4, FOS, GATA3, PLCG1, DLL1	8.007246	0.00306	0.002443
KEGG_PATHWAY	hsa05205:Proteoglycans in cancer	11	6.30E-05	SMO, SDC4, SRC, FLNA, FASLG, ITGAV, PRKCA, PLCG1, DCN, EGFR, FGFR1	4.965278	0.00306	0.002443
KEGG_PATHWAY	hsa04014:Ras signaling pathway	11	2.25E-04	CSF1R, CSF1, KSR1, RAC3, FASLG, PRKCA, PLCG1, PLA2G5, FOXO4, EGFR, FGFR1	4.255952	0.009116	0.007278
KEGG_PATHWAY	hsa04660:T cell receptor signaling pathway	8	3.25E-04	ITK, JUN, PPP2R2B, CD8A, CD28, CTLA4, FOS, PLCG1	6.038251	0.009473	0.007563
KEGG_PATHWAY	hsa05210:Colorectal cancer	7	3.29E-04	TCF7L2, JUN, SMAD3, TGFβ3, RAC3, FOS, EGFR	7.409004	0.009473	0.007563
KEGG_PATHWAY	hsa05161:Hepatitis B	9	3.51E-04	EGR2, JUN, SMAD3, TGFβ3, SRC, STAT4, FASLG, PRKCA, FOS	5.084356	0.009473	0.007563
KEGG_PATHWAY	hsa04015:Rap1 signaling pathway	10	4.36E-04	CSF1R, PLCB4, CSF1, SRC, GNAQ, RAC3, PRKCA, PLCG1, EGFR, FGFR1	4.343553	0.009791	0.007817
KEGG_PATHWAY	hsa04520:Adherens junction	7	4.72E-04	TCF7L2, SMAD3, SRC, CTNNA1, RAC3, EGFR, FGFR1	6.931004	0.009791	0.007817
KEGG_PATHWAY	hsa05323:Rheumatoid arthritis	7	5.00E-04	JUN, CSF1, IL15, TGFβ3, CD28, CTLA4, FOS	6.85727	0.009791	0.007817
KEGG_PATHWAY	hsa04068:FoxO signaling pathway	8	5.24E-04	SMAD3, TGFβ3, FASLG, FOXO4, IL7R, SOD2, SGK1, EGFR	5.580808	0.009791	0.007817
KEGG_PATHWAY	hsa05321:Inflammatory bowel disease	6	6.40E-04	JUN, SMAD3, MAF, TGFβ3, STAT4, GATA3	8.5	0.011074	0.008841
KEGG_PATHWAY	hsa05135:Yersinia infection	8	6.84E-04	JUN, SRC, CD8A, GNAQ, RAC3, FOS, PLCG1, DOCK1	5.338164	0.011074	0.008841
KEGG_PATHWAY	hsa05142:Chagas disease	7	8.13E-04	JUN, PLCB4, PPP2R2B, TGFβ3, GNAQ, FASLG, FOS	6.258091	0.012346	0.009856
KEGG_PATHWAY	hsa04921:Oxytocin signaling pathway	8	0.001303	JUN, PLCB4, SRC, GNAQ, CACNA2D3, PRKCA, FOS, EGFR	4.78355	0.018628	0.014872
KEGG_PATHWAY	hsa04390:Hippo signaling pathway	8	0.001457	YAP1, TCF7L2, SMAD3, PPP2R2B, TGFβ3, CTNNA1, TEAD1, TEAD3	4.692144	0.018947	0.015126
KEGG_PATHWAY	hsa04510:Focal adhesion	9	0.001481	JUN, SRC, RAC3, FLNA, COL6A3, ITGAV, PRKCA, DOCK1, EGFR	4.082512	0.018947	0.015126
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	12	0.001663	CSF1R, CSF3R, CSF1, PPP2R2B, COL6A3, FASLG, ITGAV, PRKCA, IL7R, SGK1, EGFR, FGFR1	3.052486	0.020206	0.016132
KEGG_PATHWAY	hsa05207:Chemical carcinogenesis - receptor activation	9	0.002129	AR, JUN, SRC, CYP1B1, PRKCA, FOS, KLF4, DLL1, EGFR	3.854651	0.024204	0.019323
KEGG_PATHWAY	hsa05417:Lipid and atherosclerosis	9	0.002191	JUN, PLCB4, SRC, FASLG, PRKCA, FOS, PLCG1, SOD2, HSPA1A	3.836806	0.024204	0.019323
KEGG_PATHWAY	hsa05235:PD-L1 expression and PD-1 checkpoint pathway in cancer	6	0.002759	CD274, JUN, CD28, FOS, PLCG1, EGFR	6.138889	0.029153	0.023274
KEGG_PATHWAY	hsa05163:Human cytomegalovirus infection	9	0.002901	PLCB4, IL1R1, SRC, GNAQ, RAC3, FASLG, ITGAV, PRKCA, EGFR	3.667035	0.029373	0.02345
KEGG_PATHWAY	hsa04912:GnRH signaling pathway	6	0.003182	JUN, PLCB4, SRC, GNAQ, PRKCA, EGFR	5.94086	0.030666	0.024482
KEGG_PATHWAY	hsa04360:Axon guidance	8	0.003574	EPHB6, ABLIM1, SMO, SRC, RAC3, PRKCA, PLCG1, ROBO1	4.003623	0.030666	0.024482
KEGG_PATHWAY	hsa04915:Estrogen signaling pathway	7	0.00375	JUN, PLCB4, SRC, GNAQ, FOS, EGFR, HSPA1A	4.63729	0.030666	0.024482
KEGG_PATHWAY	hsa05418:Fluid shear stress and atherosclerosis	7	0.004023	JUN, SDC4, IL1R1, SRC, RAC3, ITGAV, FOS	4.571513	0.030666	0.024482
KEGG_PATHWAY	hsa01522:Endocrine resistance	6	0.004164	NOTCH3, JUN, SRC, FOS, DLL1, EGFR	5.580808	0.030666	0.024482
KEGG_PATHWAY	hsa04640:Hematopoietic cell lineage	6	0.004164	CSF1R, CSF3R, CSF1, IL1R1, CD8A, IL7R	5.580808	0.030666	0.024482
KEGG_PATHWAY	hsa04750:Inflammatory mediator regulation of TRP channels	6	0.004164	PLCB4, IL1R1, SRC, GNAQ, PRKCA, PLCG1	5.580808	0.030666	0.024482
KEGG_PATHWAY	hsa05231:Choline metabolism in cancer	6	0.004164	JUN, RAC3, PRKCA, FOS, PLCG1, EGFR	5.580808	0.030666	0.024482
KEGG_PATHWAY	hsa04380:Osteoclast differentiation	7	0.004165	CSF1R, JUN, CSF1, IL1R1, FHL2, MITF, FOS	4.539319	0.030666	0.024482
KEGG_PATHWAY	hsa04933:AGE-RAGE signaling pathway in diabetic complications	6	0.004534	JUN, PLCB4, SMAD3, TGFβ3, PRKCA, PLCG1	5.470297	0.031342	0.025022
KEGG_PATHWAY	hsa04060:Cytokine-cytokine receptor interaction	10	0.004616	CSF1R, CSF3R, CSF1, IL15, IL1R1, TGFβ3, FASLG, LIFR, IL7R, ACVR1B	3.090045	0.031342	0.025022
KEGG_PATHWAY	hsa05202:Transcriptional misregulation in cancer	8	0.004643	CSF1R, MAF, BCL11B, ZBTB16, LMO2, MITF, ETV5, RUNX2	3.816926	0.031342	0.025022
KEGG_PATHWAY	hsa05224:Breast cancer	7	0.005094	TCF7L2, NOTCH3, JUN, FOS, DLL1, EGFR, FGFR1	4.355293	0.033455	0.026709
KEGG_PATHWAY	hsa04659:Th17 cell differentiation	6	0.006018	JUN, SMAD3, IL1R1, FOS, GATA3, PLCG1	5.115741	0.038483	0.030723
KEGG_PATHWAY	hsa04514:Cell adhesion molecules	7	0.006763	CD274, SDC4, CD8A, CD28, CTLA4, ITGAV, PDCD1LG2	4.105626	0.042138	0.033641

KEGG_PATHWAY	hsa05143:African trypanosomiasis	4	0.007172	PLCB4, GNAQ, FASLG, PRKCA	9.954955	0.043571	0.034785
KEGG_PATHWAY	hsa04071:Sphingolipid signaling pathway	6	0.009955	PLCB4, PPP2R2B, GNAQ, RAC3, PRKCA, S1PR2	4.528689	0.056523	0.045125
KEGG_PATHWAY	hsa04919:Thyroid hormone signaling pathway	6	0.009955	NOTCH3, PLCB4, SRC, ITGAV, PRKCA, PLCG1	4.528689	0.056523	0.045125
KEGG_PATHWAY	hsa05166:Human T-cell leukemia virus 1 infection	8	0.010002	EGR2, JUN, CRTCS, SMAD3, IL15, IL1R1, TGFβ3, FOS	3.303438	0.056523	0.045125
KEGG_PATHWAY	hsa01521:EGFR tyrosine kinase inhibitor resistance	5	0.010627	SRC, AXL, PRKCA, PLCG1, EGFR	5.755208	0.058692	0.046857
UP_KW_CELLULAR_COMPONENT	KW-1003~Cell membrane	43	1.95E-04	CD274, CSF1R, NOTCH3, CSF3R, CSF1, SRC, HTRA1, PRF1, FASLG, PLA2G5, ACVR1B, NDRG1, DLL1, EGFR, ROBO1, INPP5A, PSD3, CTNNA1, CTLA4, RAC3, ITGAV, SNX9, S1PR2, ABCG3, ARDC4, KSR1, DST, IL1R1, DAB2IP, LIFR, PRKCA, PDCD1LG2, PLCB4, SMO, BIN1, CD8A, AXL, GNAQ, CDH11, SGK1, IL7R, FGFR1, DDR2	1.701271	0.004877	0.004292
UP_KW_CELLULAR_COMPONENT	KW-0964~Secreted	26	0.001534	EPHB6, CD274, CSF3R, CSF1, SDC4, HTRA1, PRF1, FASLG, PLA2G5, EGFR, FSTL3, APOD, EDIL3, GSN, TGFβ3, IL15, IL1R1, LIFR, PDCD1LG2, DCN, EXT2, CD8A, COL6A3, TGFβ1, IL7R, HSPA1A	1.9106	0.019176	0.016875
UP_KW_DISEASE	KW-0656~Proto-oncogene	15	9.75E-06	YAP1, CSF1R, JUN, SRC, ZBTB16, LMO2, PRKCA, FOXO4, FOS, EGFR, FSTL3, MAF, AXL, GAS7, SH3GL1	4.099574	4.19E-04	4.19E-04
UP_KW_DOMAIN	KW-0728~SH3 domain	11	2.99E-06	ITK, DST, BIN1, SRC, SNX9, PLCG1, DOCK1, MYO1F, SH3D19, SH3GL1, GAS7	7.113548	6.28E-05	5.98E-05
UP_KW_MOLECULAR_FUNCTION	KW-0829~Tyrosine-protein kinase	7	3.07E-04	ITK, CSF1R, SRC, AXL, EGFR, FGFR1, DDR2	7.551996	0.012954	0.012954
UP_KW_MOLECULAR_FUNCTION	KW-0010~Activator	16	5.29E-04	YAP1, TCF7L2, NOTCH3, EGR2, JUN, CRTCS, MITF, GATA3, FOXO4, KLF4, AR, MAF, NFIB, STAT4, TEAD1, TEAD3	2.761873	0.012954	0.012954

Suppl. Table S7. significantly differentially expressed 318 genes between ≥7cm primary testicular DLBCL tumors and <7cm tumors (corresponding to Supplementary Figure 1C heatmap)

Gene Name	Gene ID	Gene Name	Score(d)	Fold Change	q-value(%)	local fdr(%)
UBE2C	UBE2C	UBE2C (Ubiquitin Conjugating Enzyme E2 C)	4.596951	1.67347	0.958111	3.805826
TFDP1	TFDP1	TFDP1 (Transcription Factor Dp-1)	4.175429	1.424869	2.136115	4.020332
DPM1	DPM1	DPM1 (Dolichyl-Phosphate Mannosyltransferase Subunit 1, Catalytic)	3.997619	1.434676	2.136115	4.224464
POLR2H	POLR2H	POLR2H (RNA Polymerase II, I And III Subunit H)	3.939905	1.498114	2.136115	4.319492
PRRX1	PRRX1	paired related homeobox 1(PRRX1)	-5.78741	0.404256	0	0.021786
FHL2	FHL2	four and a half LIM domains 2(FHL2)	-5.22528	0.367018	0	0.015895
ALDH1A1	ALDH1A1	aldehyde dehydrogenase 1 family member A1(ALDH1A1)	-5.13788	0.428335	0	0.012574
CDC14B	CDC14B	cell division cycle 14B(CDC14B)	-5.07794	0.441948	0	0.009529
SEPTIN5	SEPTIN5	septin 5(SEPTIN5)	-5.04582	0.382387	0	0.007596
PEG3	PEG3	paternally expressed 3(PEG3)	-5.04044	0.259443	0	0.00725
MLF1	MLF1	myeloid leukemia factor 1(MLF1)	-4.92683	0.287503	0	0
PPFIBP1	PPFIBP1	PPFIA binding protein 1(PPFIBP1)	-4.7161	0.543531	0	0
YAP1	YAP1	Yes1 associated transcriptional regulator(YAP1)	-4.61357	0.469256	0	0
SERPINF1	SERPINF1	serpin family F member 1(SERPINF1)	-4.61132	0.49367	0	0
PTK7	PTK7	protein tyrosine kinase 7 (inactive)(PTK7)	-4.60982	0.438693	0	0
BIN1	BIN1	bridging integrator 1(BIN1)	-4.55222	0.492761	0	0
MYH11	MYH11	myosin heavy chain 11(MYH11)	-4.5225	0.309879	0	0
EPHB6	EPHB6	EPH receptor B6(EPHB6)	-4.51623	0.45082	0	0
ACE	ACE	angiotensin I converting enzyme(ACE)	-4.48942	0.513107	0	0
SMARCA1	SMARCA1	SNF2 related chromatin remodeling ATPase 1(SMARCA1)	-4.44442	0.426066	0	0
WWTR1	WWTR1	WW domain containing transcription regulator 1(WWTR1)	-4.44292	0.537533	0	0
NOTCH2	NOTCH2	notch receptor 2(NOTCH2)	-4.4323	0.709204	0	0
GNAQ	GNAQ	G protein subunit alpha q(GNAQ)	-4.41267	0.60677	0	0
GATA6	GATA6	GATA binding protein 6(GATA6)	-4.4058	0.459774	0	0
TUSC3	TUSC3	tumor suppressor candidate 3(TUSC3)	-4.37879	0.457849	0	0

WT1	WT1	WT1 transcription factor(WT1)	-4.34598	0.383086	0	0
WNT2B	WNT2B	Wnt family member 2B(WNT2B)	-4.32277	0.403163	0	0
SFRP4	SFRP4	secreted frizzled related protein 4(SFRP4)	-4.30878	0.383607	0	0
FGFR3	FGFR3	fibroblast growth factor receptor 3(FGFR3)	-4.30829	0.491553	0	0
ROBO1	ROBO1	roundabout guidance receptor 1(ROBO1)	-4.30508	0.545369	0	0
HTRA1	HTRA1	HtrA serine peptidase 1(HTRA1)	-4.29712	0.453194	0	0
SH3D19	SH3D19	SH3 domain containing 19(SH3D19)	-4.2562	0.475789	0	0
DOCK1	DOCK1	dedicator of cytokinesis 1(DOCK1)	-4.22408	0.623373	0	0
PLAT	PLAT	plasminogen activator, tissue type(PLAT)	-4.20856	0.461529	0	0
ZNF703	ZNF703	zinc finger protein 703(ZNF703)	-4.16253	0.547631	0	0
ARRDC4	ARRDC4	arrestin domain containing 4(ARRDC4)	-4.16104	0.508934	0	0
CNTN1	CNTN1	contactin 1(CNTN1)	-4.15604	0.37783	0	0
DCN	DCN	decorin(DCN)	-4.1409	0.459471	0	0
PLCB4	PLCB4	phospholipase C beta 4(PLCB4)	-4.10657	0.466637	0	0
KSR1	KSR1	kinase suppressor of ras 1(KSR1)	-4.09903	0.613687	0	0
ATP8A2	ATP8A2	ATPase phospholipid transporting 8A2(ATP8A2)	-4.08737	0.365972	0	0
TCF7L2	TCF7L2	transcription factor 7 like 2(TCF7L2)	-4.07171	0.566099	0	0
TSC1	TSC1	TSC complex subunit 1(TSC1)	-4.06573	0.789767	0	0
ERBB2	ERBB2	erb-b2 receptor tyrosine kinase 2(ERBB2)	-4.05858	0.54465	0	0
LTBP1	LTBP1	latent transforming growth factor beta binding protein 1(LTBP1)	-4.0358	0.530396	0	0
RASGEF1A	RASGEF1A	RasGEF domain family member 1A(RASGEF1A)	-4.0257	0.537577	0	0
CEBPD	CEBPD	CCAAT enhancer binding protein delta(CEBPD)	-3.97591	0.526407	0	0
ITGAV	ITGAV	integrin subunit alpha V(ITGAV)	-3.96281	0.631792	0	0
AR	AR	androgen receptor(AR)	-3.92163	0.528782	0	0
LAMA1	LAMA1	laminin subunit alpha 1(LAMA1)	-3.88006	0.464016	0	0
GSN	GSN	gelsolin(GSN)	-3.8748	0.596412	0	0
CDKL5	CDKL5	cyclin dependent kinase like 5(CDKL5)	-3.87455	0.493343	0	0
SHC2	SHC2	SHC adaptor protein 2(SHC2)	-3.87443	0.490774	0	0
YPEL5	YPEL5	yippee like 5(YPEL5)	-3.85136	0.718137	0	0
ATL1	ATL1	atlastin GTPase 1(ATL1)	-3.83578	0.453081	0	0
RANBP17	RANBP17	RAN binding protein 17(RANBP17)	-3.81255	0.496972	0	0
FBN2	FBN2	fibrillin 2(FBN2)	-3.8074	0.498906	0	0
MIPOL1	MIPOL1	mirror-image polydactyly 1(MIPOL1)	-3.76548	0.529922	0	0
AKAP12	AKAP12	A-kinase anchoring protein 12(AKAP12)	-3.76112	0.497962	0	0
SRC	SRC	SRC proto-oncogene, non-receptor tyrosine kinase(SRC)	-3.76002	0.613279	0	0
NGFR	NGFR	nerve growth factor receptor(NGFR)	-3.73966	0.5465	0	0
DDR2	DDR2	discoidin domain receptor tyrosine kinase 2(DDR2)	-3.73878	0.620342	0	0
CDH11	CDH11	cadherin 11(CDH11)	-3.73024	0.622344	0	0
PTPRK	PTPRK	protein tyrosine phosphatase receptor type K(PTPRK)	-3.72951	0.578169	0	0
SMAD3	SMAD3	SMAD family member 3(SMAD3)	-3.71698	0.661237	0	0
GNA11	GNA11	G protein subunit alpha 11(GNA11)	-3.71692	0.568189	0	0
GATA3	GATA3	GATA binding protein 3(GATA3)	-3.70178	0.506462	0	0
EGFR	EGFR	epidermal growth factor receptor(EGFR)	-3.67684	0.501763	0	0
MAFB	MAFB	MAF bZIP transcription factor B(MAFB)	-3.67372	0.599792	0	0

APOD	APOD	apolipoprotein D(APOD)	-3.66843	0.423532	0	0
HDAC5	HDAC5	histone deacetylase 5(HDAC5)	-3.62444	0.701272	0	0
EPHA3	EPHA3	EPH receptor A3(EPHA3)	-3.61951	0.469119	0	0
USP6	USP6	ubiquitin specific peptidase 6(USP6)	-3.61717	0.448559	0	0
TACC2	TACC2	transforming acidic coiled-coil containing protein 2(TACC2)	-3.61013	0.503949	0	0
BRD3	BRD3	bromodomain containing 3(BRD3)	-3.60208	0.737385	0	0
BICC1	BICC1	BicC family RNA binding protein 1(BICC1)	-3.59273	0.527694	0	0
LRIG3	LRIG3	leucine rich repeats and immunoglobulin like domains 3(LRIG3)	-3.58809	0.544924	0	0
OMD	OMD	osteomodulin(OMD)	-3.57718	0.435552	0	0
MAF	MAF	MAF bZIP transcription factor(MAF)	-3.57511	0.571075	0	0
AKR1C3	AKR1C3	aldo-keto reductase family 1 member C3(AKR1C3)	-3.55847	0.443838	0	0
LIFR	LIFR	LIF receptor subunit alpha(LIFR)	-3.55439	0.613226	0	0
S1PR2	S1PR2	sphingosine-1-phosphate receptor 2(S1PR2)	-3.52124	0.554479	0	0
CRTC3	CRTC3	CREB regulated transcription coactivator 3(CRTC3)	-3.51639	0.639527	0	0
ARHGAP20	ARHGAP20	Rho GTPase activating protein 20(ARHGAP20)	-3.50788	0.489529	0	0
RICTOR	RICTOR	RPTOR independent companion of MTOR complex 2(RICTOR)	-3.49816	0.824053	0	0
AKT3	AKT3	AKT serine/threonine kinase 3(AKT3)	-3.49501	0.58664	0	0
EPCAM	EPCAM	epithelial cell adhesion molecule(EPCAM)	-3.49146	0.367264	0	0
TEAD3	TEAD3	TEA domain transcription factor 3(TEAD3)	-3.49106	0.545788	0	0
GHR	GHR	growth hormone receptor(GHR)	-3.47868	0.460791	0	0
SULF1	SULF1	sulfatase 1(SULF1)	-3.47155	0.580095	0	0
CTNNA1	CTNNA1	catenin alpha 1(CTNNA1)	-3.46249	0.794177	0	0
ABCC3	ABCC3	ATP binding cassette subfamily C member 3(ABCC3)	-3.45291	0.540475	0	0
CDH1	CDH1	cadherin 1(CDH1)	-3.44119	0.479824	0	0
HGF	HGF	hepatocyte growth factor(HGF)	-3.43463	0.497013	0	0
SNX29	SNX29	sorting nexin 29(SNX29)	-3.43099	0.717902	0	0
TEAD1	TEAD1	TEA domain transcription factor 1(TEAD1)	-3.43076	0.607046	0	0
BMP4	BMP4	bone morphogenetic protein 4(BMP4)	-3.41833	0.473158	0	0
BCR	BCR	BCR activator of RhoGEF and GTPase(BCR)	-3.39629	0.653543	0	0
GLI3	GLI3	GLI family zinc finger 3(GLI3)	-3.39434	0.549527	0	0
ID1	ID1	inhibitor of DNA binding 1(ID1)	-3.38625	0.526928	0	0
VGLL3	VGLL3	vestigial like family member 3(VGLL3)	-3.37786	0.606793	0	0
EYA1	EYA1	EYA transcriptional coactivator and phosphatase 1(EYA1)	-3.37638	0.510154	0	0
NFIB	NFIB	nuclear factor I B(NFIB)	-3.37484	0.637207	0	0
AXL	AXL	AXL receptor tyrosine kinase(AXL)	-3.3697	0.56073	0	0
BAIAP2L1	BAIAP2L1	BAR/IMD domain containing adaptor protein 2 like 1(BAIAP2L1)	-3.36687	0.494487	0	0
INPP5A	INPP5A	inositol polyphosphate-5-phosphatase A(INPP5A)	-3.36517	0.555707	0	0
MKL2	MRTFB	MRTFB (Myocardin Related Transcription Factor B)	-3.35767	0.763873	0	0
NCAM1	NCAM1	neural cell adhesion molecule 1(NCAM1)	-3.35663	0.528165	0	0
IL7R	IL7R	interleukin 7 receptor(IL7R)	-3.34926	0.58846	0	0
DLEC1	DLEC1	DLEC1 cilia and flagella associated protein(DLEC1)	-3.34118	0.441375	0	0
IGF1	IGF1	insulin like growth factor 1(IGF1)	-3.33227	0.426225	0	0

CHN1	CHN1	chimerin 1(CHN1)	-3.32916	0.524341	0	0
ANGPT1	ANGPT1	angiopoietin 1(ANGPT1)	-3.32202	0.512494	0	0
SORT1	SORT1	sortilin 1(SORT1)	-3.31827	0.549192	0	0
FLNA	FLNA	filamin A(FLNA)	-3.30752	0.66355	0	0
ERBB4	ERBB4	erb-b2 receptor tyrosine kinase 4(ERBB4)	-3.28783	0.487538	0	0
TGFB3	TGFB3	transforming growth factor beta 3(TGFB3)	-3.28666	0.63015	0	0
CTNND2	CTNND2	catenin delta 2(CTNND2) colony stimulating factor 1 receptor(CSF1R)	-3.28002	0.495213	0	0
CSF1R	CSF1R		-3.2695	0.637291	0	0
FZD7	FZD7	frizzled class receptor 7(FZD7)	-3.24205	0.558701	0	0
IL1R1	IL1R1	interleukin 1 receptor type 1(IL1R1) piccolo presynaptic cytomatrix protein(PCLO)	-3.24069	0.679351	0	0
PCLO	PCLO		-3.24063	0.41152	0	0
AK5	AK5	adenylate kinase 5(AK5)	-3.2399	0.519515	0	0
HEPH	HEPH	hephaestin(HEPH)	-3.22292	0.604242	0	0
PAK3	PAK3	p21 (RAC1) activated kinase 3(PAK3)	-3.20994	0.491462	0	0
MYO18A	MYO18A	myosin XVIII A(MYO18A) protein tyrosine phosphatase receptor type O(PTPRO)	-3.20854	0.768073	0	0
PTPRO	PTPRO		-3.2009	0.577213	0	0
CCND1	CCND1	cyclin D1(CCND1)	-3.19814	0.591885	0	0
AFF4	AFF4	ALF transcription elongation factor 4(AFF4) oxidized low density lipoprotein receptor 1(OLR1)	-3.18872	0.861881	0	0
OLR1	OLR1		-3.18057	0.531544	0	0
SPRY2	SPRY2	sprouty RTK signaling antagonist 2(SPRY2)	-3.17892	0.597668	0	0
ATRNL1	ATRNL1	attractin like 1(ATRNL1)	-3.17833	0.397397	0	0
SDC4	SDC4	syndecan 4(SDC4)	-3.17708	0.574645	0	0
SNCG	SNCG	synuclein gamma(SNCG)	-3.17315	0.50025	0	0
FLNC	FLNC	filamin C(FLNC)	-3.16559	0.537161	0	0
RUNX2	RUNX2	RUNX family transcription factor 2(RUNX2)	-3.16056	0.582492	0	0
MYO1F	MYO1F	myosin IF(MYO1F)	-3.15476	0.65046	0	0
NPM2	NPM2	nucleophosmin/nucleoplasmin 2(NPM2) ASPSCR1 tether for SLC2A4, UBX domain containing(ASPSCR1)	-3.15297	0.494151	0	0
ASPSCR1	ASPSCR1		-3.14707	0.662744	0	0
MUC1	MUC1	mucin 1, cell surface associated(MUC1)	-3.14352	0.508106	0	0
NBEAP1	NBEAP1	neurobeachin pseudogene 1(NBEAP1)	-3.13821	0.409574	0	0
SNX9	SNX9	sorting nexin 9(SNX9)	-3.13312	0.672785	0	0
ELN	ELN	elastin(ELN)	-3.12262	0.491452	0	0
DST	DST	dystonin(DST)	-3.12185	0.677355	0	0
ZNF521	ZNF521	zinc finger protein 521(ZNF521)	-3.12073	0.572857	0	0
TFAP2A	TFAP2A	transcription factor AP-2 alpha(TFAP2A)	-3.1137	0.641378	0	0.008009
ERG	ERG	ETS transcription factor ERG(ERG) platelet derived growth factor receptor alpha(PDGFR)	-3.10372	0.62924	0	0.028169
PDGFRA	PDGFRA		-3.09664	0.626435	0	0.042875
NCOA2	NCOA2	nuclear receptor coactivator 2(NCOA2)	-3.09664	0.828726	0	0.042886
CEP170B	CEP170B	centrosomal protein 170B(CEP170B)	-3.0951	0.594492	0	0.04612
CD28	CD28	CD28 molecule(CD28)	-3.09152	0.615444	0.259913	0.053733
FGF13	FGF13	fibroblast growth factor 13(FGF13)	-3.08897	0.532732	0.259913	0.059215
HIP1	HIP1	huntingtin interacting protein 1(HIP1) WD repeat and FYVE domain containing 3(WDFY3)	-3.08272	0.695925	0.259913	0.072825
WDFY3	WDFY3		-3.07762	0.714117	0.259913	0.084149
GLI1	GLI1	GLI family zinc finger 1(GLI1)	-3.06417	0.562852	0.259913	0.114886

TGFB1	TGFB1	transforming growth factor beta induced(TGFB1)	-3.06276	0.6373	0.259913	0.118178
LPAR1	LPAR1	lysophosphatidic acid receptor 1(LPAR1)	-3.05844	0.584886	0.259913	0.12839
PRRX2	PRRX2	paired related homeobox 2(PRRX2)	-3.05843	0.676785	0.259913	0.128422
CRTC1	CRTC1	CREB regulated transcription coactivator 1(CRTC1)	-3.05509	0.69189	0.259913	0.1364
MYCL	MYCL	MYCL proto-oncogene, bHLH transcription factor(MYCL)	-3.04605	0.54761	0.259913	0.158416
GPC3	GPC3	glypican 3(GPC3)	-3.03817	0.51482	0.259913	0.178131
PSD3	PSD3	pleckstrin and Sec7 domain containing 3(PSD3)	-3.03137	0.589171	0.259913	0.195513
CD8A	CD8A	CD8 subunit alpha(CD8A)	-3.02676	0.564558	0.259913	0.207499
ALDH2	ALDH2	aldehyde dehydrogenase 2 family member(ALDH2)	-3.01515	0.625161	0.259913	0.238418
CTLA4	CTLA4	cytotoxic T-lymphocyte associated protein 4(CTLA4)	-3.01459	0.571507	0.259913	0.239926
GNAI1	GNAI1	G protein subunit alpha i1(GNAI1)	-3.01019	0.553664	0.259913	0.251965
ITK	ITK	IL2 inducible T cell kinase(ITK)	-3.00868	0.603155	0.259913	0.256109
FGFR1	FGFR1	fibroblast growth factor receptor 1(FGFR1)	-3.0084	0.653104	0.259913	0.256887
EML1	EML1	EMAP like 1(EML1)	-3.00433	0.604538	0.259913	0.268206
CACNA2D3	CACNA2D3	calcium voltage-gated channel auxiliary subunit alpha2delta 3(CACNA2D3)	-2.98515	0.488479	0.259913	0.323305
STAT4	STAT4	signal transducer and activator of transcription 4(STAT4)	-2.98267	0.603204	0.259913	0.33065
LPP	LPP	LIM domain containing preferred translocation partner in lipoma(LPP)	-2.97154	0.732022	0.259913	0.364258
COL6A3	COL6A3	collagen type VI alpha 3 chain(COL6A3)	-2.96857	0.700954	0.259913	0.373417
BCL11B	BCL11B	BCL11 transcription factor B(BCL11B)	-2.96767	0.620224	0.259913	0.376178
FOXO3	FOXO3	forkhead box O3(FOXO3)	-2.96641	0.686678	0.259913	0.380108
FLT3	FLT3	fms related receptor tyrosine kinase 3(FLT3)	-2.96432	0.577644	0.259913	0.386611
ZBTB16	ZBTB16	zinc finger and BTB domain containing 16(ZBTB16)	-2.96095	0.516821	0.259913	0.397209
MDS2	MDS2	myelodysplastic syndrome 2 translocation associated(MDS2)	-2.96067	0.553481	0.259913	0.398092
PBX1	PBX1	PBX homeobox 1(PBX1)	-2.96018	0.600862	0.259913	0.399636
AUTS2	AUTS2	activator of transcription and developmental regulator AUTS2(AUTS2)	-2.95814	0.5163	0.259913	0.406111
AFF1	AFF1	ALF transcription elongation factor 1(AFF1)	-2.95633	0.787392	0.259913	0.411859
HDAC4	HDAC4	histone deacetylase 4(HDAC4)	-2.95109	0.732839	0.259913	0.428746
PPP3CC	PPP3CC	protein phosphatase 3 catalytic subunit gamma(PPP3CC)	-2.94938	0.757226	0.259913	0.434301
HES1	HES1	hes family bHLH transcription factor 1(HES1)	-2.93956	0.548698	0.259913	0.466665
NCOR2	NCOR2	nuclear receptor corepressor 2(NCOR2)	-2.93698	0.803646	0.259913	0.475312
GPHN	GPHN	gephyrin(GPHN)	-2.93148	0.582636	0.259913	0.493944
DIRAS3	DIRAS3	DIRAS family GTPase 3(DIRAS3)	-2.92772	0.487293	0.259913	0.506846
KANK1	KANK1	KN motif and ankyrin repeat domains 1(KANK1)	-2.92637	0.555472	0.259913	0.511494
DNM3	DNM3	dynamin 3(DNM3)	-2.92489	0.594585	0.259913	0.516631
ZFPM2	ZFPM2	zinc finger protein, FOG family member 2(ZFPM2)	-2.92228	0.518534	0.259913	0.52572
SERP2	SERP2	stress associated endoplasmic reticulum protein family member 2(SERP2)	-2.92082	0.504633	0.259913	0.530818
SOCS2	SOCS2	suppressor of cytokine signaling 2(SOCS2)	-2.91979	0.609988	0.259913	0.534457
HSPA2	HSPA2	heat shock protein family A (Hsp70) member 2(HSPA2)	-2.90871	0.480396	0.259913	0.573925
SLC34A2	SLC34A2	solute carrier family 34 member 2(SLC34A2)	-2.90139	0.584146	0.259913	0.600654
ADD3	ADD3	adducin 3(ADD3)	-2.90069	0.796204	0.259913	0.603211

GRID1	GRID1	glutamate ionotropic receptor delta type subunit 1(GRID1)	-2.90054	0.631512	0.259913	0.603781
MYH9	MYH9	myosin heavy chain 9(MYH9)	-2.89414	0.762218	0.259913	0.627559
DMRT1	DMRT1	doublesex and mab-3 related transcription factor 1(DMRT1)	-2.88362	0.527201	0.259913	0.667473
NOTCH3	NOTCH3	notch receptor 3(NOTCH3)	-2.88278	0.683731	0.259913	0.670726
FSTL3	FSTL3	follistatin like 3(FSTL3)	-2.88195	0.636917	0.259913	0.673909
LRRC37B	LRRC37B	leucine rich repeat containing 37B(LRRC37B)	-2.87617	0.681398	0.259913	0.696374
KLF4	KLF4	KLF transcription factor 4(KLF4)	-2.8753	0.585985	0.259913	0.699781
GAS7	GAS7	growth arrest specific 7(GAS7)	-2.87207	0.695013	0.259913	0.712494
IGF1R	IGF1R	insulin like growth factor 1 receptor(IGF1R)	-2.8694	0.65949	0.259913	0.723052
CDKN1C	CDKN1C	cyclin dependent kinase inhibitor 1C(CDKN1C)	-2.85772	0.579724	0.259913	0.770117
HECW1	HECW1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1(HECW1)	-2.85185	0.540549	0.259913	0.794252
TRAF5	TRAF5	TNF receptor associated factor 5(TRAF5)	-2.84865	0.745621	0.259913	0.807575
LHFP	LHFP	LHFP	-2.84824	0.634281	0.259913	0.809274
KDM6A	KDM6A	lysine demethylase 6A(KDM6A)	-2.84508	0.812865	0.259913	0.822527
DAB2IP	DAB2IP	DAB2 interacting protein(DAB2IP)	-2.84467	0.62353	0.259913	0.824225
PLAU	PLAU	plasminogen activator, urokinase(PLAU)	-2.84267	0.626814	0.259913	0.832654
COL1A2	COL1A2	collagen type I alpha 2 chain(COL1A2)	-2.83728	0.601407	0.259913	0.855604
ITGA7	ITGA7	integrin subunit alpha 7(ITGA7)	-2.83308	0.622585	0.259913	0.873655
MAML1	MAML1	mastermind like transcriptional coactivator 1(MAML1)	-2.82549	0.800067	0.259913	0.906709
CAMK2B	CAMK2B	calcium/calmodulin dependent protein kinase II beta(CAMK2B)	-2.82205	0.588657	0.259913	0.921872
CDKN1B	CDKN1B	cyclin dependent kinase inhibitor 1B(CDKN1B)	-2.82177	0.793009	0.259913	0.923123
CSF1	CSF1	colony stimulating factor 1(CSF1)	-2.8139	0.677035	0.259913	0.958273
PIK3R1	PIK3R1	phosphoinositide-3-kinase regulatory subunit 1(PIK3R1)	-2.80493	0.825593	0.410619	0.99908
NTRK3	NTRK3	neurotrophic receptor tyrosine kinase 3(NTRK3)	-2.79434	0.562651	0.410619	1.048303
EGR1	EGR1	early growth response 1(EGR1)	-2.7927	0.630623	0.410619	1.056008
PPP1R13B	PPP1R13B	protein phosphatase 1 regulatory subunit 13B(PPP1R13B)	-2.7819	0.717953	0.410619	1.10749
LCK	LCK	LCK proto-oncogene, Src family tyrosine kinase(LCK)	-2.7722	0.656269	0.410619	1.154792
IL13RA2	IL13RA2	interleukin 13 receptor subunit alpha 2(IL13RA2)	-2.76942	0.563107	0.410619	1.168471
CTSA	CTSA	cathepsin A(CTSA)	-2.76703	0.697051	0.410619	1.180332
SORBS2	SORBS2	sorbin and SH3 domain containing 2(SORBS2)	-2.76544	0.5665	0.410619	1.188245
SRGAP3	SRGAP3	SLIT-ROBO Rho GTPase activating protein 3(SRGAP3)	-2.76005	0.716818	0.410619	1.215329
TENM1	TENM1	teneurin transmembrane protein 1(TENM1)	-2.75841	0.551644	0.410619	1.223623
ELOVL2	ELOVL2	ELOVL fatty acid elongase 2(ELOVL2)	-2.7583	0.623245	0.410619	1.224171
PPP2CB	PPP2CB	protein phosphatase 2 catalytic subunit beta(PPP2CB)	-2.75514	0.776003	0.410619	1.240226
PPFIA2	PPFIA2	PTPRF interacting protein alpha 2(PPFIA2)	-2.75247	0.56039	0.410619	1.253846
ITGA8	ITGA8	integrin subunit alpha 8(ITGA8)	-2.74386	0.587185	0.410619	1.298314
GPR124	ADGRA2	ADGRA2 (Adhesion G Protein-Coupled Receptor A2)	-2.74323	0.665559	0.410619	1.301627
PLA2G2A	PLA2G2A	phospholipase A2 group IIA(PLA2G2A)	-2.73304	0.480788	0.410619	1.355355
LOX	LOX	lysyl oxidase(LOX)	-2.72418	0.666311	0.410619	1.402917
PDGFRB	PDGFRB	platelet derived growth factor receptor beta(PDGFRB)	-2.72289	0.707671	0.410619	1.409918

AKAP6	AKAP6	A-kinase anchoring protein 6(AKAP6)	-2.71728	0.558665	0.410619	1.440576
PLA2G5	PLA2G5	phospholipase A2 group V(PLA2G5)	-2.7157	0.579752	0.410619	1.449271
WIF1	WIF1	WNT inhibitory factor 1(WIF1)	-2.71544	0.602854	0.410619	1.450682
IL15	IL15	interleukin 15(IL15)	-2.71286	0.630957	0.410619	1.464935
TGFB2	TGFB2	transforming growth factor beta 2(TGFB2)	-2.71165	0.725263	0.410619	1.471656
PDGFB	PDGFB	platelet derived growth factor subunit B(PDGFB)	-2.7079	0.668806	0.410619	1.492559
CLTCL1	CLTCL1	clathrin heavy chain like 1(CLTCL1)	-2.70276	0.605161	0.410619	1.521428
KLK2	KLK2	kallikrein related peptidase 2(KLK2)	-2.67788	0.614271	0.410619	1.665332
SPTAN1	SPTAN1	spectrin alpha, non-erythrocytic 1(SPTAN1)	-2.67547	0.831023	0.410619	1.679587
PPARG	PPARG	peroxisome proliferator activated receptor gamma(PPARG)	-2.6722	0.595597	0.410619	1.699137
CEBPA	CEBPA	CCAAT enhancer binding protein alpha(CEBPA)	-2.67157	0.571983	0.410619	1.70287
LFNG	LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase(LFNG)	-2.66041	0.64283	0.410619	1.770403
PHF1	PHF1	PHD finger protein 1(PHF1)	-2.63758	0.718696	0.410619	1.912946
KIAA1598	SHTN1	SHTN1 (Shootin 1)	-2.6354	0.730168	0.410619	1.926905
CCNB3	CCNB3	cyclin B3(CCNB3)	-2.6259	0.552813	0.410619	1.988247
PLCB1	PLCB1	phospholipase C beta 1(PLCB1)	-2.61634	0.6736	0.410619	2.051004
PRKG2	PRKG2	protein kinase cGMP-dependent 2(PRKG2)	-2.60439	0.592993	0.542929	2.130967
ETV1	ETV1	ETS variant transcription factor 1(ETV1)	-2.60295	0.622918	0.542929	2.140705
DNMT3A	DNMT3A	DNA methyltransferase 3 alpha(DNMT3A)	-2.5999	0.726765	0.542929	2.161472
NDRG1	NDRG1	N-myc downstream regulated 1(NDRG1)	-2.59911	0.681715	0.542929	2.166853
BCAS3	BCAS3	BCAS3 microtubule associated cell migration factor(BCAS3)	-2.58701	0.787834	0.542929	2.250313
PPP2R2B	PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta(PPP2R2B)	-2.58489	0.605127	0.542929	2.265128
RGS7	RGS7	regulator of G protein signaling 7(RGS7)	-2.58324	0.546939	0.542929	2.276755
GRB10	GRB10	growth factor receptor bound protein 10(GRB10)	-2.5786	0.688453	0.542929	2.30941
ASPH	ASPH	aspartate beta-hydroxylase(ASPH)	-2.57351	0.731058	0.542929	2.345598
ERBB3	ERBB3	erb-b2 receptor tyrosine kinase 3(ERBB3)	-2.56662	0.528146	0.542929	2.395117
CAMK2G	CAMK2G	calcium/calmodulin dependent protein kinase II gamma(CAMK2G)	-2.56548	0.714931	0.542929	2.403319
FAM127C	RTL8B	RTL8B (Retrotransposon Gag Like 8B)	-2.56448	0.73116	0.542929	2.410566
CREB3L1	CREB3L1	cAMP responsive element binding protein 3 like 1(CREB3L1)	-2.56448	0.612682	0.542929	2.410617
COL1A1	COL1A1	collagen type I alpha 1 chain(COL1A1)	-2.56258	0.605779	0.542929	2.424391
CPS1	CPS1	carbamoyl-phosphate synthase 1(CPS1)	-2.56145	0.613721	0.542929	2.432603
TSHR	TSHR	thyroid stimulating hormone receptor(TSHR)	-2.55293	0.508187	0.542929	2.495208
MTUS2	MTUS2	microtubule associated scaffold protein 2(MTUS2)	-2.55234	0.518758	0.542929	2.49958
PRKCG	PRKCG	protein kinase C gamma(PRKCG)	-2.54488	0.648637	0.542929	2.555153
DACH1	DACH1	dachshund family transcription factor 1(DACH1)	-2.53953	0.64294	0.542929	2.595436
EYA2	EYA2	EYA transcriptional coactivator and phosphatase 2(EYA2)	-2.53548	0.475322	0.542929	2.62623
LINC00982	PRDM16-DT	PRDM16-DT (PRDM16 Divergent Transcript)	-2.53284	0.558742	0.542929	2.646379
ARFRP1	ARFRP1	ARF related protein 1(ARFRP1)	-2.51954	0.733953	0.542929	2.749392
FLT4	FLT4	fms related receptor tyrosine kinase 4(FLT4)	-2.5174	0.704595	0.542929	2.766127
PTK2	PTK2	protein tyrosine kinase 2(PTK2)	-2.51254	0.705848	0.542929	2.804509
SQSTM1	SQSTM1	sequestosome 1(SQSTM1)	-2.50517	0.811138	0.542929	2.863237

MAPK3	MAPK3	mitogen-activated protein kinase 3(MAPK3)	-2.49588	0.732007	0.542929	2.938308
POMGNT1	POMGNT1	protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-)(POMGNT1)	-2.49558	0.800287	0.542929	2.940723
HOXA3	HOXA3	homeobox A3(HOXA3)	-2.49244	0.676991	0.542929	2.966364
IGFBP2	IGFBP2	insulin like growth factor binding protein 2(IGFBP2)	-2.49002	0.6273	0.542929	2.986204
PPARGC1A	PPARGC1A	PPARG coactivator 1 alpha(PPARGC1A)	-2.48623	0.605433	0.542929	3.017483
RHOD	RHOD	ras homolog family member D(RHOD)	-2.4845	0.627575	0.542929	3.031842
RET	RET	ret proto-oncogene(RET)	-2.47782	0.661782	0.542929	3.087552
NEURL1	NEURL1	neuralized E3 ubiquitin protein ligase 1(NEURL1)	-2.47596	0.645225	0.542929	3.103211
HEY1	HEY1	hes related family bHLH transcription factor with YRPW motif 1(HEY1)	-2.47298	0.583272	0.542929	3.128338
PSEN1	PSEN1	presenilin 1(PSEN1)	-2.45695	0.867533	0.542929	3.265661
PPP3R2	PPP3R2	protein phosphatase 3 regulatory subunit B, beta(PPP3R2)	-2.44528	0.558404	0.542929	3.367826
ACSL6	ACSL6	acyl-CoA synthetase long chain family member 6(ACSL6)	-2.44357	0.661322	0.542929	3.383021
FGFR4	FGFR4	fibroblast growth factor receptor 4(FGFR4)	-2.43303	0.647709	0.958111	3.477252
DCLK2	DCLK2	doublecortin like kinase 2(DCLK2)	-2.43076	0.593004	0.958111	3.497761
GPR34	GPR34	G protein-coupled receptor 34(GPR34)	-2.42802	0.618395	0.958111	3.52261
MAP2	MAP2	microtubule associated protein 2(MAP2)	-2.42785	0.574544	0.958111	3.52413
EDIL3	EDIL3	EGF like repeats and discoidin domains 3(EDIL3)	-2.41999	0.625244	0.958111	3.596011
JARID2	JARID2	jumonji and AT-rich interaction domain containing 2(JARID2)	-2.41183	0.807699	0.958111	3.671591
MYBL1	MYBL1	MYB proto-oncogene like 1(MYBL1)	-2.40865	0.570602	0.958111	3.701328
PIK3CG	PIK3CG	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma(PIK3CG)	-2.4007	0.761143	0.958111	3.776323
SH3GL2	SH3GL2	SH3 domain containing GRB2 like 2, endophilin A1(SH3GL2)	-2.39291	0.622383	0.958111	3.85072
KALRN	KALRN	kalirin RhoGEF kinase(KALRN)	-2.38965	0.656998	0.958111	3.882101
LRP1B	LRP1B	LDL receptor related protein 1B(LRP1B)	-2.38825	0.616915	0.958111	3.895626
STAT5A	STAT5A	signal transducer and activator of transcription 5A(STAT5A)	-2.38587	0.789118	0.958111	3.918767
PLAG1	PLAG1	PLAG1 zinc finger(PLAG1)	-2.38144	0.629904	0.958111	3.961931
NGF	NGF	nerve growth factor(NGF)	-2.37997	0.572455	0.958111	3.976338
SMAD6	SMAD6	SMAD family member 6(SMAD6)	-2.3653	0.626244	0.958111	4.121967
IKZF2	IKZF2	IKAROS family zinc finger 2(IKZF2)	-2.36494	0.731035	0.958111	4.125531
IRS2	IRS2	insulin receptor substrate 2(IRS2)	-2.36048	0.684918	0.958111	4.170492
LRRC7	LRRC7	leucine rich repeat containing 7(LRRC7)	-2.35955	0.602252	0.958111	4.179911
CXXC4	CXXC4	CXXC finger protein 4(CXXC4)	-2.35639	0.658277	0.958111	4.212021
APLP2	APLP2	amyloid beta precursor like protein 2(APLP2)	-2.35433	0.832068	0.958111	4.233024
MAPK8IP2	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2(MAPK8IP2)	-2.35322	0.697068	0.958111	4.244385
SFRP2	SFRP2	secreted frizzled related protein 2(SFRP2)	-2.34115	0.516434	0.958111	4.369067
KIAA1549	KIAA1549	KIAA1549(KIAA1549)	-2.33852	0.65075	0.958111	4.396602
ZMYND11	ZMYND11	zinc finger MYND-type containing 11(ZMYND11)	-2.3302	0.818266	0.958111	4.484274
PPAP2B	PLPP3	PLPP3 (Phospholipid Phosphatase 3)	-2.3222	0.72516	0.958111	4.569787
FZD2	FZD2	frizzled class receptor 2(FZD2)	-2.31455	0.696682	0.958111	4.652478
ENPP2	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2(ENPP2)	-2.29767	0.677162	0.958111	4.83871
PROM1	PROM1	prominin 1(PROM1)	-2.2918	0.613649	0.958111	4.90455

NFATC2	NFATC2	nuclear factor of activated T cells 2(NFATC2)	-2.29088	0.820917	0.958111	4.914999
PPP1R13L	PPP1R13L	protein phosphatase 1 regulatory subunit 13 like(PPP1R13L)	-2.28754	0.735941	0.958111	4.95281

Suppl. Table S8.1 significantly differentially expressed 166 genes between primary testicular DLBCL and systemic DLBCL with mutated *MYD88* RNA (corresponding to heatmap in Figure 2H)

Gene Name	Gene Name	Score(d)	Fold Change	q-value(%)	local fdr(%)
WT1	WT1 transcription factor(WT1)	7.004197	3.87454	0	0.136649
MYH11	myosin heavy chain 11(MYH11)	6.683419	4.741474	0	0.107874
KMT2D	lysine methyltransferase 2D(KMT2D)	5.975887	1.38929	0	0
CEBPD	CCAAT enhancer binding protein delta(CEBPD)	5.909311	2.151772	0	0
FSTL3	folliculin like 3(FSTL3)	5.795122	2.103474	0	0
TCL1A	TCL1 family AKT coactivator A(TCL1A)	5.724054	4.154233	0	0
RASAL1	RAS protein activator like 1(RASAL1)	5.626188	2.688182	0	0
PLA2G5	phospholipase A2 group V(PLA2G5)	5.340147	2.340712	0	0
GAB1	GRB2 associated binding protein 1(GAB1)	5.311036	1.866645	0	0
IGFBP2	insulin like growth factor binding protein 2(IGFBP2)	5.08693	2.338625	0	0
ZNF444	zinc finger protein 444(ZNF444)	4.81859	1.908072	0	0
AMH	anti-Mullerian hormone(AMH)	4.728996	1.831696	0	0
ARID1A	AT-rich interaction domain 1A(ARID1A)	4.649484	1.249161	0	0
RERG	RAS like estrogen regulated growth inhibitor(RERG)	4.023763	1.9668	0	0
CAMTA1	calmodulin binding transcription activator 1(CAMTA1)	3.932429	1.282204	0	0
CKB	creatine kinase B(CKB)	3.844675	2.178814	0	0
IRS1	insulin receptor substrate 1(IRS1)	3.781051	1.42929	0	0
CDK4	cyclin dependent kinase 4(CDK4)	3.758489	1.315305	0	0
PATZ1	POZ/BTB and AT hook containing zinc finger 1(PATZ1)	3.728995	1.248882	0	0
EP400	E1A binding protein p400(EP400)	3.679033	1.18434	0	0
MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase(MFNG)	3.66962	1.450826	0	0
TP53	tumor protein p53(TP53)	3.669461	1.435291	0	0
PEG3	paternally expressed 3(PEG3)	3.663193	2.371438	0	0
SUFU	SUFU negative regulator of hedgehog signaling(SUFU)	3.614029	1.367225	0	0
WDR90	WD repeat domain 90(WDR90)	3.607248	1.467342	0	0
FCGBP	Fc gamma binding protein(FCGBP)	3.6026	1.8523	0	0
MALAT1	metastasis associated lung adenocarcinoma transcript 1(MALAT1)	3.498101	12.24507	0	0
AR	androgen receptor(AR)	3.463697	1.578773	0	0
RUNX1T1	RUNX1 partner transcriptional co-repressor 1(RUNX1T1)	3.440081	2.053486	0	0.086445
LAMA1	laminin subunit alpha 1(LAMA1)	3.39696	1.765292	0	0.329449
PRCC	proline rich mitotic checkpoint control factor(PRCC)	3.383639	1.197854	0	0.409519
MEF2D	myocyte enhancer factor 2D(MEF2D)	3.37438	1.320617	0	0.4666
RASGRF2	Ras protein specific guanine nucleotide releasing factor 2(RASGRF2)	3.338104	1.614414	0	0.701786
FBXO31	F-box protein 31(FBXO31)	3.336421	1.260512	0	0.713149
USP5	ubiquitin specific peptidase 5(USP5)	3.312998	1.222425	0	0.875608
TP63	tumor protein p63(TP63)	3.287759	1.762697	0.679492	1.059762
FHL2	four and a half LIM domains 2(FHL2)	3.28741	1.738599	0.679492	1.062382
ELN	elastin(ELN)	3.270843	1.895119	0.679492	1.188605
BTG1	BTG anti-proliferation factor 1(BTG1)	3.265123	1.274603	0.679492	1.233167

MIB1	MIB E3 ubiquitin protein ligase 1(MIB1)	3.196865	1.200169	0.679492	1.805181
BAZ2A	bromodomain adjacent to zinc finger domain 2A(BAZ2A)	3.189654	1.158899	0.679492	1.870053
MDC1	mediator of DNA damage checkpoint 1(MDC1)	3.177216	1.214202	0.679492	1.984026
PFDN5	prefoldin subunit 5(PFDN5)	3.149359	1.313807	0.679492	2.248866
DMRT1	doublesex and mab-3 related transcription factor 1(DMRT1)	3.107828	1.77898	0.679492	2.669022
ERBB4	erb-b2 receptor tyrosine kinase 4(ERBB4)	3.07563	1.713758	1.150428	3.016305
DTX1	deltex E3 ubiquitin ligase 1(DTX1)	3.074217	1.917378	1.150428	3.03199
CTDSP2	CTD small phosphatase 2(CTDSP2)	3.053941	1.20275	1.150428	3.261167
MAFB	MAF bZIP transcription factor B(MAFB)	3.049341	1.418234	1.150428	3.314254
NCAM1	neural cell adhesion molecule 1(NCAM1)	3.048723	1.572951	1.150428	3.321424
NACA	nascent polypeptide associated complex subunit alpha(NACA)	3.033026	1.33286	1.150428	3.50582
DGKZ	diacylglycerol kinase zeta(DGKZ)	3.025116	1.25147	1.150428	3.600562
RCSD1	RCSD domain containing 1(RCSD1)	3.019027	1.353591	1.150428	3.674321
PPP2CB	protein phosphatase 2 catalytic subunit beta(PPP2CB)	3.010992	1.202149	1.150428	3.77278
DAB2IP	DAB2 interacting protein(DAB2IP)	3.007392	1.560701	1.150428	3.817304
CIC	capicua transcriptional repressor(CIC)	2.987402	1.276603	1.150428	4.069253
ATG13	autophagy related 13(ATG13)	2.985717	1.234683	1.150428	4.090853
DACH1	dachshund family transcription factor 1(DACH1)	2.980665	1.456404	1.150428	4.155968
TNC	tenascin C(TNC)	-8.1153	0.444794	0	0
KDM6A	lysine demethylase 6A(KDM6A)	-7.57791	0.668811	0	0.03271
NDE1	nudE neurodevelopment protein 1(NDE1)	-7.17788	0.680318	0	0.066714
ZRSR2	zinc finger CCCH-type, RNA binding motif and serine/arginine rich 2(ZRSR2)	-6.47894	0.646509	0	0.09774
SEPTIN6	septin 6(SEPTIN6)	-6.38668	0.604708	0	0.093879
JAK1	Janus kinase 1(JAK1)	-6.05824	0.686637	0	0.048973
KDM4C	lysine demethylase 4C(KDM4C)	-5.98371	0.730209	0	0.029888
CD44	CD44 molecule (IN blood group)(CD44)	-5.83206	0.523332	0	0
NCOA3	nuclear receptor coactivator 3(NCOA3)	-5.25785	0.716583	0	0
GPHN	gephyrin(GPHN)	-5.10891	0.451953	0	0
CHL1	cell adhesion molecule L1 like(CHL1)	-5.10194	0.395824	0	0
ST6GAL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1(ST6GAL1)	-5.02039	0.662606	0	0
TMEM30A	transmembrane protein 30A(TMEM30A)	-4.90544	0.695727	0	0
OGA	OGA (O-GlcNAcase)	-4.87401	0.761196	0	0
BIRC3	baculoviral IAP repeat containing 3(BIRC3)	-4.69056	0.616726	0	0
IL7R	interleukin 7 receptor(IL7R)	-4.66982	0.501399	0	0
TFRC	transferrin receptor(TFRC)	-4.66913	0.622615	0	0
IL2RA	interleukin 2 receptor subunit alpha(IL2RA)	-4.66421	0.513498	0	0
CD58	CD58 molecule(CD58)	-4.6069	0.577725	0	0
FAS	Fas cell surface death receptor(FAS)	-4.58068	0.656517	0	0
RICTOR	RPTOR independent companion of MTOR complex 2(RICTOR)	-4.50076	0.787831	0	0
HIF1A	hypoxia inducible factor 1 subunit alpha(HIF1A)	-4.49736	0.723659	0	0
CHD2	chromodomain helicase DNA binding protein 2(CHD2)	-4.48983	0.771007	0	0
OFD1	OFD1 centriole and centriolar satellite protein(OFD1)	-4.44532	0.74158	0	0
RBM6	RNA binding motif protein 6(RBM6)	-4.40603	0.773725	0	0
HAS2	hyaluronan synthase 2(HAS2)	-4.34259	0.502117	0	0
IL6	interleukin 6(IL6)	-4.32982	0.452483	0	0
CHMP2B	charged multivesicular body protein 2B(CHMP2B)	-4.31872	0.784768	0	0
TAF1	TATA-box binding protein associated factor 1(TAF1)	-4.31666	0.837635	0	0

WDR70	WD repeat domain 70(WDR70)	-4.286	0.805369	0	0
ZNF217	zinc finger protein 217(ZNF217)	-4.24895	0.794164	0	0
LPXN	leupaxin(LPXN)	-4.21911	0.747823	0	0
IL1B	interleukin 1 beta(IL1B)	-4.20545	0.466083	0	0
KDM5C	lysine demethylase 5C(KDM5C)	-4.2	0.770829	0	0
CDH1	cadherin 1(CDH1)	-4.19235	0.471552	0	0
RPN1	ribophorin I(RPN1)	-4.18053	0.764315	0	0
HSPA1A	heat shock protein family A (Hsp70) member 1A(HSPA1A)	-4.13271	0.564342	0	0
RASGRP1	RAS guanyl releasing protein 1(RASGRP1)	-4.08647	0.667468	0	0
CD22	CD22 molecule(CD22)	-4.04201	0.595289	0	0
VEGFA	vascular endothelial growth factor A(VEGFA)	-3.98046	0.58579	0	0
SOD2	superoxide dismutase 2(SOD2)	-3.9581	0.626702	0	0
VTI1A	vesicle transport through interaction with t-SNAREs 1A(VTI1A)	-3.93359	0.703139	0	0
TNFAIP3	TNF alpha induced protein 3(TNFAIP3)	-3.93005	0.734647	0	0
PRRX1	paired related homeobox 1(PRRX1)	-3.83083	0.601167	0	0
CALR	calreticulin(CALR)	-3.82552	0.765521	0	0
NDRG1	N-myc downstream regulated 1(NDRG1)	-3.79482	0.639202	0	0
LMBRD1	LMBR1 domain containing 1(LMBRD1)	-3.78676	0.74161	0	0
MDS2	myelodysplastic syndrome 2 translocation associated(MDS2)	-3.7694	0.486841	0	0
FRYL	FRY like transcription coactivator(FRYL)	-3.76412	0.869205	0	0
SNX9	sorting nexin 9(SNX9)	-3.73516	0.684037	0	0
PTGS2	prostaglandin-endoperoxide synthase 2(PTGS2)	-3.64461	0.572169	0	0
BCL10	BCL10 immune signaling adaptor(BCL10)	-3.63841	0.826327	0	0
VHL	von Hippel-Lindau tumor suppressor(VHL)	-3.61585	0.798853	0	0
VCAM1	vascular cell adhesion molecule 1(VCAM1)	-3.60057	0.690567	0	0
KLHL6	kelch like family member 6(KLHL6)	-3.54978	0.625542	0	0
TEC	tec protein tyrosine kinase(TEC)	-3.54004	0.693492	0	0
TNF	tumor necrosis factor(TNF)	-3.53231	0.582425	0	0
MMP7	matrix metalloproteinase 7(MMP7)	-3.52505	0.407674	0	0
TENT5C	TENT5C (Terminal Nucleotidyltransferase 5C)	-3.51101	0.635672	0	0
SMC1A	structural maintenance of chromosomes 1A(SMC1A)	-3.50758	0.787688	0	0
TCF12	transcription factor 12(TCF12)	-3.49388	0.788946	0	0
TGFBR2	transforming growth factor beta receptor 2(TGFBR2)	-3.48062	0.753386	0	0
GOSR1	golgi SNAP receptor complex member 1(GOSR1)	-3.46073	0.817574	0	0
CHN1	chimerin 1(CHN1)	-3.45379	0.613697	0	0
RHOH	ras homolog family member H(RHOH)	-3.44976	0.726334	0	0
CXCL8	C-X-C motif chemokine ligand 8(CXCL8)	-3.41514	0.454355	0	0
NDUFAF1	NADH:ubiquinone oxidoreductase complex assembly factor 1(NDUFAF1)	-3.34889	0.775634	0	0
IL21R	interleukin 21 receptor(IL21R)	-3.34787	0.71329	0	0
PIK3CB	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit beta(PIK3CB)	-3.31802	0.838735	0	0
PLAU	plasminogen activator, urokinase(PLAU)	-3.31374	0.642615	0	0
IRAG2	IRAG2 (Inositol 1,4,5-Triphosphate Receptor Associated 2)	-3.29062	0.64638	0	0
LPAR1	lysophosphatidic acid receptor 1(LPAR1)	-3.25405	0.658796	0	0
MSH3	mutS homolog 3(MSH3)	-3.25047	0.841654	0	0
TOP1	DNA topoisomerase I(TOP1)	-3.24079	0.788903	0	0
MSN	moesin(MSN)	-3.24001	0.78308	0	0

HHEX	hematopoietically expressed homeobox(HHEX)	-3.21953	0.694098	0	0.124923
ABCC3	ATP binding cassette subfamily C member 3(ABCC3)	-3.21692	0.633596	0	0.146822
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2(ENPP2)	-3.20769	0.655714	0	0.225116
HSPA5	heat shock protein family A (Hsp70) member 5(HSPA5)	-3.17852	0.829529	0	0.483845
LMO2	LIM domain only 2(LMO2)	-3.16935	0.591439	0	0.568704
PRDM1	PR/SET domain 1(PRDM1)	-3.15873	0.661418	0	0.669132
PHF6	PHD finger protein 6(PHF6)	-3.15475	0.77828	0	0.707339
TPM4	tropomyosin 4(TPM4)	-3.15094	0.771413	0	0.744333
BAIAP2L1	BAR/IMD domain containing adaptor protein 2 like 1(BAIAP2L1)	-3.1121	0.525563	0	1.138173
NEDD4	NEDD4 E3 ubiquitin protein ligase(NEDD4)	-3.10077	0.736789	0	1.259221
ATRX	ATRX chromatin remodeler(ATRX)	-3.08677	0.837212	0	1.412677
MNAT1	MNAT1 component of CDK activating kinase(MNAT1)	-2.97467	0.842691	0	2.805218
CEP43	CEP43 (Centrosomal Protein 43)	-2.9533	0.789029	0	3.1052
SFRP2	secreted frizzled related protein 2(SFRP2)	-2.94434	0.488207	0	3.234434
DNAJB1	DnaJ heat shock protein family (Hsp40) member B1(DNAJB1)	-2.93824	0.730649	0	3.323631
THRAP3	thyroid hormone receptor associated protein 3(THRAP3)	-2.92638	0.897872	0	3.499685
PTK2B	protein tyrosine kinase 2 beta(PTK2B)	-2.92009	0.804992	0	3.594627
LASP1	LIM and SH3 protein 1(LASP1)	-2.91861	0.810524	0	3.617075
LAMP2	lysosomal associated membrane protein 2(LAMP2)	-2.91481	0.759734	0	3.675064
WSB1	WD repeat and SOCS box containing 1(WSB1)	-2.89349	0.812931	0	4.007426
RMI2	RecQ mediated genome instability 2(RMI2)	-2.88494	0.72381	0.679492	4.144021
CD19	CD19 molecule(CD19)	-2.88181	0.66827	0.679492	4.194588
TNFRSF10D	TNF receptor superfamily member 10d(TNFRSF10D)	-2.8767	0.726822	0.679492	4.277564
CD274	CD274 molecule(CD274)	-2.87639	0.59617	0.679492	4.282699
ELF4	E74 like ETS transcription factor 4(ELF4)	-2.87233	0.817117	0.679492	4.349149
TET2	tet methylcytosine dioxygenase 2(TET2)	-2.86872	0.852862	0.679492	4.40873
CHEK2	checkpoint kinase 2(CHEK2)	-2.8655	0.768576	0.679492	4.462039
PMS2	PMS1 homolog 2, mismatch repair system component(PMS2)	-2.86268	0.856542	0.679492	4.509055
DDX3X	DEAD-box helicase 3 X-linked(DDX3X)	-2.86074	0.868258	0.679492	4.541583
SDC4	syndecan 4(SDC4)	-2.86025	0.673615	0.679492	4.549729
DDX6	DEAD-box helicase 6(DDX6)	-2.85474	0.854107	0.679492	4.64261
HEY1	hes related family bHLH transcription factor with YRPW motif 1(HEY1)	-2.85376	0.619519	0.679492	4.659196
EML4	EMAP like 4(EML4)	-2.83786	0.858279	0.679492	4.932107
DLL1	delta like canonical Notch ligand 1(DLL1)	-2.83459	0.72232	0.679492	4.989084

Suppl. Table S8.2 Significantly enriched functional terms with FDR ≤ 0.05 by DAVID functional annotation tool for 57 genes upregulated in primary testicular DLBCL compared with systemic DLBCL

Category	Term associated with 57 upregulated genes	Count	P Value	Genes	Fold Enrichment	Benjamini	FDR
UP_KW_CELLULAR_COMPONENT	KW-0539~Nucleus	33	1.41E-06	KMT2D, MDC1, CEBPD, PRCC, FHL2, DTX1, BAZ2A, FSTL3, PPP2CB, TCL1A, DACH1, ERBB4, SUFU, EP400, CAMTA1, PATZ1, CIC, ZNF444, MEF2D, TP63, RUNX1T1, DMRT1, PEG3, ARID1A, DGKZ, AR, MAFB, WT1, NACA, CDK4, CTDSP2, PFDN5, TP53	2.062716	2.54E-05	2.54E-05
GOTERM_CC_DIRECT	GO:0005634~nucleus	34	4.60E-06	KMT2D, MDC1, BTG1, CEBPD, IRS1, PRCC, FHL2, BAZ2A, RERG, FSTL3, PPP2CB, DACH1, ERBB4, SUFU, CAMTA1, PATZ1, CIC, ZNF444, MEF2D, TP63, RUNX1T1, USP5, DMRT1, PEG3, ARID1A, DGKZ, AR, MAFB, WT1, NACA, CDK4, MALAT1, PFDN5, TP53	2.017638	5.47E-04	5.47E-04
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription by RNA polymerase II	13	1.07E-05	DMRT1, PEG3, DAB2IP, FHL2, AR, DACH1, MAFB, WT1, NACA, SUFU, PATZ1, TP53, TP63	4.757121	0.006703	0.006651
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	26	1.33E-05	KMT2D, MDC1, BTG1, CEBPD, IRS1, PRCC, FHL2, DTX1, RERG, FSTL3, TCL1A, DACH1, ERBB4, SUFU, EP400, PATZ1, CIC, MEF2D, TP63, RUNX1T1, ARID1A, AR, WT1, CDK4, CTDSP2, TP53	2.36412	7.92E-04	7.92E-04

UP_KW_BIOLOGICAL_PROCESS	KW-0805~Transcription regulation GO:0045892~negative regulation of DNA-templated transcription	21	1.77E-05	KMT2D, DMRT1, CEBPD, FHL2, BAZ2A, ARID1A, FSTL3, AR, DACH1, MAFB, WT1, ERBB4, NACA, CAMTA1, PATZ1, CIC, ZNF444, MEF2D, TP53, TP63, RUNX1T1	2.554012	4.93E-04	4.93E-04
GOTERM_BP_DIRECT		10	2.66E-05	DACH1, CEBPD, WT1, DAB2IP, CIC, PATZ1, PFDN5, TP53, TP63, RUNX1T1	6.149963	0.006703	0.006651
UP_KW_BIOLOGICAL_PROCESS	KW-0804~Transcription GO:0045944~positive regulation of transcription by RNA polymerase II GO:0045893~positive regulation of DNA-templated transcription GO:0008285~negative regulation of cell population proliferation GO:0006357~regulation of transcription by RNA polymerase II GO:0000981~DNA-binding transcription factor activity, RNA polymerase II-specific GO:0001228~DNA-binding transcription activator activity, RNA polymerase II-specific	21	2.74E-05	KMT2D, DMRT1, CEBPD, FHL2, BAZ2A, ARID1A, FSTL3, AR, DACH1, MAFB, WT1, ERBB4, NACA, CAMTA1, PATZ1, CIC, ZNF444, MEF2D, TP53, TP63, RUNX1T1	2.483039	4.93E-04	4.93E-04
GOTERM_BP_DIRECT		14	3.11E-05	KMT2D, DMRT1, PEG3, CEBPD, DAB2IP, FSTL3, AR, MAFB, WT1, NACA, CAMTA1, MEF2D, TP53, TP63	3.927946	0.006703	0.006651
GOTERM_BP_DIRECT		10	1.43E-04	AR, MAFB, ERBB4, WT1, EP400, DTX1, ARID1A, PATZ1, TP53, TP63	4.942396	0.023137	0.022958
GOTERM_BP_DIRECT		8	1.93E-04	AR, BTG1, ERBB4, WT1, DAB2IP, ATG13, TP53, RERG	6.495721	0.025036	0.024843
GOTERM_BP_DIRECT		14	3.72E-04	DMRT1, PEG3, CEBPD, ARID1A, FSTL3, DACH1, MAFB, WT1, CTDSP2, CAMTA1, CIC, ZNF444, TP53, TP63	3.071918	0.040063	0.039753
GOTERM_MF_DIRECT		13	4.33E-04	DMRT1, PEG3, CEBPD, AR, DACH1, MAFB, WT1, PATZ1, CIC, ZNF444, MEF2D, TP53, TP63	3.239637	0.04643	0.044562
GOTERM_MF_DIRECT		8	5.34E-04	AR, MAFB, DMRT1, CEBPD, WT1, MEF2D, TP53, TP63	5.495605	0.04643	0.044562
GOTERM_CC_DIRECT	GO:0005829~cytosol	28	5.71E-04	IRS1, RASGRF2, DTX1, BAZ2A, RASAL1, RCDSD1, RERG, PPP2CB, TCL1A, DACH1, ERBB4, SUFU, CAMTA1, NCAM1, MYH11, CKB, USP5, DAB2IP, GAB1, DGKZ, ATG13, FBXO31, MIB1, AR, WT1, CDK4, PFDN5, TP53	1.8163	0.022655	0.022655
UP_KW_MOLECULAR_FUNCTION	KW-0010~Activator GO:0016607~nuclear speck	10	6.65E-04	AR, DACH1, MAFB, CEBPD, ERBB4, NACA, CAMTA1, MEF2D, TP53, TP63	3.904433	0.017036	0.017036
GOTERM_CC_DIRECT	KW-0238~DNA-binding	7	0.001025	AR, DACH1, WT1, PRCC, EP400, BAZ2A, DGKZ	5.937662	0.030479	0.030479
UP_KW_MOLECULAR_FUNCTION		17	0.001065	DMRT1, CEBPD, BAZ2A, ARID1A, AR, DACH1, MAFB, WT1, NACA, EP400, PATZ1, CIC, ZNF444, MEF2D, TP53, TP63, RUNX1T1	2.28067	0.017036	0.017036

Suppl. Table S8.3 Significantly enriched functional terms with FDR ≤ 0.05 by DAVID functional annotation tool for 109 genes downregulated in primary testicular DLBCL compared with systemic DLBCL

Category	Term associated with 109 downregulated genes	Count	P Value	Genes	Fold Enrichment	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression GO:0043066~negative regulation of apoptotic process	18	2.07E-09	DDX3X, CXCL8, TFRC, TCF12, TNC, MSN, PIK3CB, PRDM1, DLL1, HIF1A, TNF, VEGFA, IL6, IL1B, CALR, IL7R, HSPA1A, KDM6A	6.46169	3.14E-06	3.07E-06
GOTERM_BP_DIRECT	GO:0009410~response to xenobiotic stimulus	16	9.83E-08	DDX3X, HSPA5, TFRC, SOD2, TNF, TNFRSF10D, VEGFA, IL6, FAS, PTK2B, RICTOR, VHL, MNAT1, CD44, HSPA1A, BIRC3	5.766382	7.45E-05	7.28E-05
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription by RNA polymerase II GO:0045429~positive regulation of nitric oxide biosynthetic process GO:0010573~vascular endothelial growth factor production	11	1.23E-06	SFRP2, MMP7, CDH1, PMS2, PTK2B, CALR, TOP1, SOD2, PTGS2, TNF, TGFB2	7.913167	6.21E-04	6.08E-04
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell population proliferation GO:0032757~positive regulation of interleukin-8 production GO:0030335~positive regulation of cell migration GO:0033138~positive regulation of peptidyl-serine phosphorylation	22	3.27E-06	KDM4C, DDX3X, HSPA5, PRRX1, NCOA3, ATRX, LMO2, TCF12, TET2, DLL1, HIF1A, TNF, VEGFA, HHEX, IL6, SFRP2, HEY1, THRAP3, ELF4, IL1B, KDM6A, TAF1	3.200548	0.001187	0.00116
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	6	3.91E-06	IL1B, PTK2B, PIK3CB, SOD2, PTGS2, TNF	24.91667	0.001187	0.00116
GOTERM_BP_DIRECT	GO:0030155~regulation of cell adhesion	4	5.34E-06	IL6, IL1B, HIF1A, TNF	104.4127	0.001349	0.001319
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell population proliferation GO:0000122~negative regulation of transcription by RNA polymerase II GO:0045766~positive regulation of angiogenesis	6	1.69E-05	CXCL8, PLAU, TNC, PTK2B, DLL1, JAK1	18.58192	0.003658	0.003576
GOTERM_BP_DIRECT		13	1.93E-05	KDM4C, TNC, DLL1, TGFB2, VEGFA, IL6, SFRP2, IL1B, PTK2B, HAS2, CALR, IL7R, CEP43	4.694444	0.003658	0.003576
GOTERM_BP_DIRECT		6	2.52E-05	IL6, IL1B, BCL10, CD58, TNF, HSPA1A	17.13021	0.004019	0.003929
GOTERM_BP_DIRECT		10	2.65E-05	CD274, MMP7, HSPA5, PLAU, IL1B, PTK2B, HAS2, SOD2, CEP43, VEGFA	6.366628	0.004019	0.003929
GOTERM_BP_DIRECT		6	4.78E-05	IL6, SFRP2, TFRC, PTGS2, TNF, CD44	15.01826	0.006427	0.006282
GOTERM_BP_DIRECT		8	5.09E-05	VCAM1, TFRC, PLAU, PTK2B, SOD2, HIF1A, TNF, VEGFA	8.258632	0.006427	0.006282
GOTERM_BP_DIRECT		11	1.25E-04	IL6, SFRP2, CXCL8, IL1B, PTK2B, VHL, SOD2, PTGS2, DLL1, NDRG1, HSPA1A	4.631208	0.014622	0.014294
GOTERM_BP_DIRECT		16	2.14E-04	KDM5C, PRRX1, PRDM1, PHF6, TNF, VEGFA, DNAJB1, HHEX, HEY1, NEDD4, ZNF217, VHL, CALR, HSPA1A, KDM6A, TAF1	3.035883	0.023167	0.022647
GOTERM_BP_DIRECT		7	2.63E-04	SFRP2, CXCL8, IL1B, PTK2B, HIF1A, TGFB2, VEGFA	7.846967	0.025698	0.025122

GOTERM_BP_DIRECT	GO:0010629~negative regulation of gene expression	9	2.87E-04	DDX3X, SFRP2, CXCL8, VHL, PRDM1, HIF1A, TNF, TAF1, VEGFA	5.304839	0.025698	0.025122
GOTERM_BP_DIRECT	GO:0031622~positive regulation of fever generation	3	2.88E-04	IL1B, PTGS2, TNF	109.6333	0.025698	0.025122
GOTERM_BP_DIRECT	GO:0048844~artery morphogenesis	4	3.27E-04	PRRX1, PRDM1, TGFB2, VEGFA	29.23556	0.026821	0.026219
GOTERM_BP_DIRECT	GO:0042102~positive regulation of T cell proliferation	5	3.36E-04	CD274, IL6, VCAM1, TFRC, IL1B	14.97723	0.026821	0.026219
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	9	3.70E-04	IL6, DDX3X, SFRP2, LPAR1, FAS, BCL10, PTGS2, TNF, TNFRSF10D	5.107143	0.028075	0.027445
GOTERM_BP_DIRECT	GO:0031175~neuron projection development	6	5.76E-04	IL6, CDH1, NEDD4, TNC, PTK2B, FRYL	8.841398	0.041575	0.040642
GOTERM_BP_DIRECT	GO:0071222~cellular response to lipopolysaccharide	7	6.11E-04	CD274, IL6, CXCL8, IL1B, TNFAIP3, BCL10, TNF	6.696626	0.04212	0.041175
GOTERM_BP_DIRECT	GO:0010575~positive regulation of vascular endothelial growth factor production	4	6.86E-04	IL6, IL1B, PTGS2, HIF1A	22.84028	0.045188	0.044175
UP_KW_BIOLOGICAL_PROCESS	KW-0945~Host-virus interaction	15	4.53E-04	DDX3X, HSPA5, TFRC, OGA, SEPTIN6, MSN, TENT5C, HIF1A, LMBRD1, CHEK2, NEDD4, RICTOR, TOP1, HSPA1A, TAF1	2.928389	0.028567	0.028567
GOTERM_CC_DIRECT	GO:0009897~external side of plasma membrane	13	2.28E-06	CD274, VCAM1, TFRC, TNF, TGFB2, PLAU, CD19, IL2RA, IL21R, FAS, CALR, IL7R, CD22	5.806783	2.48E-04	2.40E-04
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	30	2.58E-06	CD274, DDX3X, SDC4, TFRC, TNFAIP3, NDRG1, DNAJB1, BAIAP2L1, CHL1, PLAU, CDH1, CD19, LAMP2, SNX9, CD58, MMP7, VCAM1, TPM4, HSPA5, NCOA3, MSN, SOD2, THRAP3, NEDD4, CHMP2B, FAS, CALR, CD44, CD22, HSPA1A	2.545933	2.48E-04	2.40E-04
GOTERM_CC_DIRECT	GO:0005925~focal adhesion	13	2.63E-06	TPM4, HSPA5, SDC4, TNC, MSN, LASP1, PLAU, PTK2B, LPXN, CALR, CD44, JAK1, HSPA1A	5.72669	2.48E-04	2.40E-04
GOTERM_CC_DIRECT	GO:0009986~cell surface	15	7.40E-06	VCAM1, HSPA5, SDC4, TFRC, LPAR1, MSN, TNF, TNFRSF10D, VEGFA, PLAU, FAS, CD58, CALR, CD44, CD22	4.374974	5.23E-04	5.07E-04
GOTERM_CC_DIRECT	GO:0005829~cytosol	49	7.35E-05	DDX6, KDM5C, DDX3X, RPN1, GOSR1, TNFAIP3, PIK3CB, BCL10, RASGRP1, HIF1A, NDRG1, GPHN, DNAJB1, BAIAP2L1, CHN1, VTI1A, PTK2B, PMS2, LPXN, RICTOR, SNX9, VHL, JAK1, OFD1, RMI2, WSB1, TPM4, PRRX1, HSPA5, NCOA3, NDE1, OGA, MSN, SMC1A, TGFB2, EML4, TEC, IL1B, NEDD4, CHMP2B, FAS, NDUFAF1, CALR, IL7R, CEP43, CD44, BIRC3, HSPA1A	1.662165	0.004159	0.004027
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	46	5.52E-04	CD274, DDX3X, SDC4, TFRC, LPAR1, PIK3CB, RASGRP1, TNF, NDRG1, DLL1, GPHN, BAIAP2L1, CHL1, PLAU, CDH1, CD19, LAMP2, ENPP2, IL21R, PTK2B, HAS2, LPXN, SNX9, VHL, CD58, JAK1, ABCC3, TMEM30A, VCAM1, HSPA5, IRAG2, RHOH, MSN, TGFB2, TNFRSF10D, LMBRD1, TEC, IL2RA, NEDD4, CHMP2B, FAS, IL7R, CD44, CD22, HSPA1A	1.576305	0.020976	0.020309
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytoplasm	13	5.70E-04	TFRC, MSN, BCL10, NDRG1, CDH1, NEDD4, LAMP2, VTI1A, PTK2B, LPXN, CALR, CEP43, HSPA1A	3.273469	0.020976	0.020309
GOTERM_CC_DIRECT	GO:0005912~adherens junction	7	5.93E-04	BAIAP2L1, CDH1, LPXN, MSN, DLL1, NDRG1, VEGFA	6.740538	0.020976	0.020309
GOTERM_CC_DIRECT	GO:0005634~nucleus	49	7.21E-04	KDM5C, DDX3X, TNFAIP3, PIK3CB, PRDM1, CHD2, PHF6, HHEX, HEY1, CHEK2, JAK1, RBM6, KDM6A, OFD1, RMI2, NCOA3, TCF12, ATRX, LMO2, TET2, SMC1A, TENT5C, ELF4, MSH3, THRAP3, TOP1, BIRC3, DDX6, BCL10, HIF1A, NDRG1, DNAJB1, WDR70, PTK2B, PMS2, LPXN, VHL, KDM4C, PRRX1, HSPA5, OGA, MSN, VEGFA, NEDD4, ZNF217, CALR, CEP43, TAF1, HSPA1A	1.520578	0.022658	0.021937
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	36	8.19E-04	CD274, KDM5C, DDX3X, PIK3CB, PRDM1, PHF6, HIF1A, DNAJB1, BAIAP2L1, HEY1, WDR70, CHEK2, PMS2, VHL, KDM6A, ZRSR2, RMI2, KDM4C, PRRX1, NCOA3, TCF12, ATRX, LMO2, TET2, SMC1A, TENT5C, ELF4, MSH3, THRAP3, ZNF217, TOP1, MNAT1, IL7R, BIRC3, TAF1, HSPA1A	1.711776	0.023166	0.022429
GOTERM_CC_DIRECT	GO:0005856~cytoskeleton	10	0.001475	LASP1, BAIAP2L1, TEC, TPM4, PTK2B, MSN, RHOH, GPHN, JAK1	3.699302	0.03796	0.036753
GOTERM_CC_DIRECT	GO:0000776~kinetochore	6	0.001768	NDE1, CHMP2B, SEPTIN6, SMC1A, MNAT1, PHF6	6.884689	0.041696	0.04037
GOTERM_MF_DIRECT	GO:0005515~protein binding	95	7.57E-08	KDM5C, DDX3X, CXCL8, TFRC, TNC, TNFAIP3, PIK3CB, PRDM1, CHD2, PHF6, TNF, GPHN, HHEX, LASP1, BAIAP2L1, HEY1, PLAU, CDH1, CHEK2, LAMP2, JAK1, RBM6, KDM6A, OFD1, RMI2, STGAL1, WSB1, MMP7, TPM4, NCOA3, TCF12, ATRX, LMO2, TET2, RHOH, SMC1A, TENT5C, TGFB2, EML4, LMBRD1, ELF4, MSH3, THRAP3, IL1B, TOP1, CD44, BIRC3, CD274, DDX6, SDC4, RPN1, LPAR1, BCL10, PTGS2, HIF1A, NDRG1, DLL1, DNAJB1, CHN1, IL21R, VTI1A, PTK2B, PMS2, LPXN, HAS2, RICTOR, SNX9, VHL, CD58, ZRSR2, TMEM30A, PRRX1, HSPA5, NDE1, SEPTIN6, MSN, SOD2, TNFRSF10D, VEGFA, IL6, TEC, KLHL6, IL2RA, NEDD4, CHMP2B, ZNF217, FAS, NDUFAF1, CALR, MNAT1, IL7R, CEP43, CD22, TAF1, HSPA1A	1.343819	2.52E-05	2.44E-05
GOTERM_MF_DIRECT	GO:0019899~enzyme binding	13	9.50E-07	KDM4C, HSPA5, MSN, PTGS2, SOD2, PHF6, HIF1A, WDR70, MSH3, NEDD4, LAMP2, VHL, HSPA1A	6.304693	1.58E-04	1.53E-04
GOTERM_MF_DIRECT	GO:0045296~cadherin binding	10	9.62E-05	DDX6, DNAJB1, LASP1, DDX3X, HSPA5, CDH1, CHMP2B, SNX9, NDRG1, HSPA1A	5.385409	0.010674	0.010322
GOTERM_MF_DIRECT	GO:0019904~protein domain specific binding	8	1.96E-04	DDX6, HSPA5, IL1B, NEDD4, LAMP2, CHMP2B, TOP1, HIF1A	6.651105	0.01629	0.015752
GOTERM_MF_DIRECT	GO:0005524~ATP binding	21	2.45E-04	ABCC3, DDX6, DDX3X, HSPA5, ATRX, PIK3CB, CHD2, SMC1A, GPHN, TGFB2, TEC, THRAP3, MSH3, CHEK2, PTK2B, PMS2, TOP1, JAK1, HSPA1A, TAF1	2.458556	0.016312	0.015773
GOTERM_MF_DIRECT	GO:0031625~ubiquitin protein ligase binding	9	3.19E-04	HSPA5, CHEK2, PTK2B, SNX9, BCL10, CALR, HIF1A, JAK1, HSPA1A	5.220903	0.017693	0.017109
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	22	4.38E-04	OFD1, ZRSR2, KDM5C, TPM4, SDC4, TFRC, NDE1, LMO2, OGA, TNFAIP3, BCL10, SOD2, RASGRP1, TNF, GPHN, VEGFA, CDH1, CHEK2, FAS, HAS2, SNX9, KDM6A	2.285001	0.020824	0.020136
GOTERM_MF_DIRECT	GO:0048018~receptor ligand activity	5	6.29E-04	CD274, SFRP2, DLL1, HSPA1A, VEGFA	12.70502	0.026185	0.02532
KEGG_PATHWAY	hsa05200:Pathways in cancer	21	2.65E-08	CXCL8, NCOA3, LPAR1, PIK3CB, PTGS2, DLL1, RASGRP1, HIF1A, TGFB2, VEGFA, EML4, IL6, HEY1, CDH1, MSH3, IL2RA, FAS, VHL, IL7R, JAK1, BIRC3	4.353659	5.56E-06	4.27E-06
KEGG_PATHWAY	hsa04640:Hematopoietic cell lineage	9	2.52E-06	IL6, TFRC, IL1B, CD19, IL2RA, IL7R, TNF, CD44, CD22	10.04545	2.65E-04	2.03E-04

KEGG_PATH WAY	hsa04064:NF-kappa B signaling pathway	9	3.93E-06	VCAM1, CXCL8, PLAU, IL1B, TNFAIP3, BCL10, PTGS2, TNF, BIRC3	9.471429	2.75E-04	2.11E-04
KEGG_PATH WAY	hsa04668:TNF signaling pathway	9	1.00E-05	IL6, VCAM1, IL1B, FAS, TNFAIP3, PIK3CB, PTGS2, TNF, BIRC3	8.357143	4.98E-04	3.81E-04
KEGG_PATH WAY	hsa05169:Epstein-Barr virus infection	11	1.18E-05	IL6, CD19, NEDD4, FAS, TNFAIP3, CD58, CALR, PIK3CB, TNF, CD44, JAK1	5.987685	4.98E-04	3.81E-04
KEGG_PATH WAY	hsa05163:Human cytomegalovirus infection	11	3.01E-05	IL6, CXCL8, IL1B, FAS, PTK2B, CALR, PIK3CB, PTGS2, TNF, JAK1, VEGFA	5.378319	8.08E-04	6.19E-04
KEGG_PATH WAY	hsa04933:AGE-RAGE signaling pathway in diabetic complications	8	3.05E-05	IL6, VCAM1, CXCL8, IL1B, PIK3CB, TNF, TGFBR2, VEGFA	8.752475	8.08E-04	6.19E-04
KEGG_PATH WAY	hsa05162:Measles	9	3.11E-05	IL6, IL1B, IL2RA, FAS, TNFAIP3, MSN, PIK3CB, JAK1, HSPA1A	7.154676	8.08E-04	6.19E-04
KEGG_PATH WAY	hsa05142:Chagas disease	8	3.46E-05	IL6, CXCL8, IL1B, FAS, CALR, PIK3CB, TNF, TGFBR2	8.582524	8.08E-04	6.19E-04
KEGG_PATH WAY	hsa05161:Hepatitis B	9	9.66E-05	IL6, DDX3X, CXCL8, FAS, PTK2B, PIK3CB, TNF, JAK1, TGFBR2	6.101227	0.002029	0.001555
KEGG_PATH WAY	hsa05417:Lipid and atherosclerosis	10	1.23E-04	IL6, VCAM1, CXCL8, HSPA5, IL1B, FAS, PIK3CB, SOD2, TNF, HSPA1A	5.115741	0.002342	0.001795
KEGG_PATH WAY	hsa05143:African trypanosomiasis	5	3.12E-04	IL6, VCAM1, IL1B, FAS, TNF	14.93243	0.005458	0.004185
KEGG_PATH WAY	hsa04659:Th17 cell differentiation	7	3.90E-04	IL6, IL1B, IL2RA, IL21R, HIF1A, JAK1, TGFBR2	7.162037	0.006303	0.004832
KEGG_PATH WAY	hsa05205:Proteoglycans in cancer	9	4.49E-04	SDC4, PLAU, FAS, MSN, PIK3CB, HIF1A, TNF, CD44, VEGFA	4.875	0.006736	0.005164
KEGG_PATH WAY	hsa05166:Human T-cell leukemia virus 1 infection	9	8.09E-04	IL6, MMP7, CHEK2, IL2RA, CALR, PIK3CB, TNF, JAK1, TGFBR2	4.459641	0.010946	0.008392
KEGG_PATH WAY	hsa05164:influenza A	8	8.34E-04	DNAJB1, IL6, CXCL8, IL1B, FAS, PIK3CB, TNF, JAK1	5.139535	0.010946	0.008392
KEGG_PATH WAY	hsa05144:Malaria	5	9.96E-04	IL6, VCAM1, CXCL8, IL1B, TNF	11.05	0.012305	0.009434
KEGG_PATH WAY	hsa05235:PD-L1 expression and PD-1 checkpoint pathway in cancer	6	0.001219	EMIL4, CD274, PIK3CB, HIF1A, RASGRP1, JAK1	7.366667	0.01422	0.010902
KEGG_PATH WAY	hsa04060:Cytokine-cytokine receptor interaction	10	0.001291	IL6, CXCL8, IL1B, IL2RA, IL21R, FAS, IL7R, TNF, TGFBR2, TNFRSF10D	3.708054	0.014272	0.010942
KEGG_PATH WAY	hsa05134:Legionellosis	5	0.001526	IL6, CXCL8, IL1B, TNF, HSPA1A	9.866071	0.015521	0.0119
KEGG_PATH WAY	hsa04657:IL-17 signaling pathway	6	0.001552	IL6, CXCL8, IL1B, TNFAIP3, PTGS2, TNF	6.978947	0.015521	0.0119
KEGG_PATH WAY	hsa05202:Transcriptional misregulation in cancer	8	0.001631	IL6, HHEX, CXCL8, PLAU, LMO2, TGFBR2, BIRC3, KDM6A	4.580311	0.015565	0.011933
KEGG_PATH WAY	hsa05167:Kaposi sarcoma-associated herpesvirus infection	8	0.001781	IL6, CXCL8, FAS, PIK3CB, PTGS2, HIF1A, JAK1, VEGFA	4.510204	0.016263	0.012469
KEGG_PATH WAY	hsa01523:Antifolate resistance	4	0.002344	ABCC3, IL6, IL1B, TNF	14.73333	0.020275	0.015544
KEGG_PATH WAY	hsa04625:C-type lectin receptor signaling pathway	6	0.002414	IL6, IL1B, BCL10, PIK3CB, PTGS2, TNF	6.314286	0.020275	0.015544
KEGG_PATH WAY	hsa04066:HIF-1 signaling pathway	6	0.002841	IL6, TFRC, VHL, PIK3CB, HIF1A, VEGFA	6.082569	0.021775	0.016694
KEGG_PATH WAY	hsa04620:Toll-like receptor signaling pathway	6	0.002841	IL6, CXCL8, IL1B, PIK3CB, TNF, JAK1	6.082569	0.021775	0.016694
KEGG_PATH WAY	hsa04217:Necroptosis	7	0.002903	IL1B, CHMP2B, FAS, TNFAIP3, TNF, JAK1, BIRC3	4.86478	0.021775	0.016694
KEGG_PATH WAY	hsa04621:NOD-like receptor signaling pathway	7	0.006737	IL6, CXCL8, IL1B, TNFAIP3, TNF, JAK1, BIRC3	4.092593	0.047367	0.036314
KEGG_PATH WAY	hsa05132:Salmonella infection	8	0.006973	IL6, CXCL8, IL1B, RHOH, SNX9, PIK3CB, TNF, BIRC3	3.521912	0.047367	0.036314
KEGG_PATH WAY	hsa05332:Graft-versus-host disease	4	0.006992	IL6, IL1B, FAS, TNF	10.04545	0.047367	0.036314
KEGG_PATH WAY	hsa05135:Yersinia infection	6	0.007716	IL6, CXCL8, IL1B, PTK2B, PIK3CB, TNF	4.804348	0.050634	0.038819
KEGG_PATH WAY	hsa05418:Fluid shear stress and atherosclerosis	6	0.008429	VCAM1, SDC4, IL1B, PIK3CB, TNF, VEGFA	4.702128	0.053594	0.041088
KEGG_PATH WAY	hsa04380:Osteoclast differentiation	6	0.008677	TEC, IL1B, PIK3CB, TNF, JAK1, TGFBR2	4.669014	0.053594	0.041088
KEGG_PATH WAY	hsa05130:Pathogenic Escherichia coli infection	7	0.00943	IL6, BAIAP2L1, CXCL8, IL1B, LPAR1, FAS, TNF	3.810345	0.056579	0.043377
KEGG_PATH WAY	hsa05323:Rheumatoid arthritis	5	0.009815	IL6, CXCL8, IL1B, TNF, VEGFA	5.87766	0.057253	0.043894

Suppl. Table S9.1. Significantly differentially expressed 743 genes between MCD cases in clusters 1, 2, or 5 and MCD cases in clusters 3 or 4 (corresponding to the heatmap in Figure 3)

Gene ID	Gene Name	Score(d)	Fold Change	q-value(%)	local fdr(%)
NACA	nascent polypeptide associated complex subunit alpha(NACA)	3.923406	2.493193	0	0.184468
NPM1	nucleophosmin 1(NPM1)	3.876255	2.19609	0	0.173193
GAS5	GAS5 (Growth Arrest Specific 5)	3.576439	3.688053	0	0.091378
PRKCB	protein kinase C beta(PRKCB)	3.256585	2.261282	0	0
TBL1XR1	TBL1X/Y related 1(TBL1XR1)	3.22668	2.117741	0	0
IRF8	interferon regulatory factor 8(IRF8)	3.216764	2.191972	0	0

DEK	DEK proto-oncogene(DEK)	3.16936	2.080698	0	0
RPS21	ribosomal protein S21(RPS21)	3.15839	3.453446	0	0
PLCG2	phospholipase C gamma 2(PLCG2)	3.153581	2.049794	0	0
USP7	ubiquitin specific peptidase 7(USP7)	3.140326	1.843148	0	0
SET	SET nuclear proto-oncogene(SET)	3.04698	1.939406	0	0
RPL22	ribosomal protein L22(RPL22)	3.036884	2.324695	0	0
BTK	Bruton tyrosine kinase(BTK)	3.0075	2.045943	0	0
HSPA4	heat shock protein family A (Hsp70) member 4(HSPA4)	2.999556	2.130632	0	0
U2AF1	U2 small nuclear RNA auxiliary factor 1(U2AF1)	2.967662	2.37626	0	0
KTN1	kinectin 1(KTN1)	2.946842	1.853176	0	0
HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1(HNRNPA2B1)	2.943291	2.163488	0	0
TCL1A	TCL1 family AKT coactivator A(TCL1A)	2.900919	3.205194	0	0
CYFIP2	cytoplasmic FMR1 interacting protein 2(CYFIP2)	2.899219	1.765597	0	0
SUZ12	SUZ12 polycomb repressive complex 2 subunit(SUZ12)	2.873482	1.598939	0	0
PAX5	paired box 5(PAX5)	2.872297	1.884712	0	0
LYN	LYN proto-oncogene, Src family tyrosine kinase(LYN)	2.868041	1.666989	0	0
RAC2	Rac family small GTPase 2(RAC2)	2.801305	2.272469	0	0
FOXP1	forkhead box P1(FOXP1)	2.795895	1.69853	0	0
GMPS	guanine monophosphate synthase(GMPS)	2.775733	1.831943	0	0
PFDN5	prefoldin subunit 5(PFDN5)	2.769707	2.15577	0	0
XRCC6	X-ray repair cross complementing 6(XRCC6)	2.76802	1.736475	0	0
TOP2A	DNA topoisomerase II alpha(TOP2A)	2.766409	1.657436	0	0
PRKDC	protein kinase, DNA-activated, catalytic subunit(PRKDC)	2.760233	1.628163	0	0
SYK	spleen associated tyrosine kinase(SYK)	2.746948	1.705805	0	0
TYMS	thymidylate synthetase(TYMS)	2.734307	1.908484	0	0
RB1	RB transcriptional corepressor 1(RB1)	2.719372	2.098342	0	0
HDAC2	histone deacetylase 2(HDAC2)	2.693591	1.760118	0	0
SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5(SMARCA5)	2.688086	1.774262	0	0
XPO1	exportin 1(XPO1)	2.684601	1.733231	0	0
RAD21	RAD21 cohesin complex component(RAD21)	2.680223	1.643719	0	0
PTEN	phosphatase and tensin homolog(PTEN)	2.673207	1.732461	0	0
SFPQ	splicing factor proline and glutamine rich(SFPQ)	2.66997	1.573093	0	0
STAG2	STAG2 cohesin complex component(STAG2)	2.669666	1.59416	0	0
PRKAR1A	protein kinase cAMP-dependent type I regulatory subunit alpha(PRKAR1A)	2.668829	1.721799	0	0
HMGA1	high mobility group AT-hook 1(HMGA1)	2.668619	2.19001	0	0
TOP1	DNA topoisomerase I(TOP1)	2.652002	1.843421	0	0
TTK	TTK protein kinase(TTK)	2.597967	1.798328	0	0
CDK1	cyclin dependent kinase 1(CDK1)	2.583681	1.799315	0	0
NFKB1	nuclear factor kappa B subunit 1(NFKB1)	2.58277	1.681356	0	0
CAPRIN1	cell cycle associated protein 1(CAPRIN1)	2.581476	1.745059	0	0
PCNA	proliferating cell nuclear antigen(PCNA)	2.564136	1.905833	0	0
MELK	maternal embryonic leucine zipper kinase(MELK)	2.55557	1.815189	0	0
INPP5D	inositol polyphosphate-5-phosphatase D(INPP5D)	2.523042	1.711919	0	0
HSP90AB1	heat shock protein 90 alpha family class B member 1(HSP90AB1)	2.515505	1.564428	0.046128	0
SMC1A	structural maintenance of chromosomes 1A(SMC1A)	2.509217	1.645352	0.046128	0
NUP107	nucleoporin 107(NUP107)	2.502086	1.755498	0.046128	0

ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase(ATIC)	2.488885	1.672076	0.046128	0
DNMT1	DNA methyltransferase 1(DNMT1)	2.484558	1.635273	0.046128	0
NONO	non-POU domain containing octamer binding(NONO)	2.482021	1.881713	0.046128	0
H3C2	H3C2 (H3 Clustered Histone 2)	2.457109	2.287829	0.046128	0
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B(BUB1B)	2.454558	1.74312	0.046128	0
FUS	FUS RNA binding protein(FUS)	2.42431	1.732918	0.046128	0
CCNA2	cyclin A2(CCNA2)	2.417395	1.731686	0.046128	0
ATM	ATM serine/threonine kinase(ATM)	2.415933	1.507536	0.046128	0
CARD11	caspase recruitment domain family member 11(CARD11)	2.412458	1.659741	0.046128	0
GTF2I	general transcription factor Ili(GTF2I)	2.408683	1.624135	0.046128	0
ABI1	abl interactor 1(ABI1)	2.401879	1.496113	0.046128	0
MRE11	MRE11 (MRE11 Homolog, Double Strand Break Repair Nuclease)	2.399075	1.596706	0.046128	0
FIP1L1	factor interacting with PAPOLA and CPSF1(FIP1L1)	2.385067	1.503064	0.046128	0
POLD1	DNA polymerase delta 1, catalytic subunit(POLD1)	2.382314	1.806494	0.046128	0
MSI2	musashi RNA binding protein 2(MSI2)	2.376765	1.792876	0.046128	0
TFRC	transferrin receptor(TFRC)	2.373926	1.843088	0.046128	0
PTPN2	protein tyrosine phosphatase non-receptor type 2(PTPN2)	2.371633	1.744083	0.046128	0
FANCI	FA complementation group I(FANCI)	2.366483	1.533849	0.046128	0
NCOA3	nuclear receptor coactivator 3(NCOA3)	2.344046	1.478298	0.085499	0
SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1(SMARCB1)	2.34115	1.845985	0.085499	0
KPNB1	karyopherin subunit beta 1(KPNB1)	2.315156	1.562114	0.085499	0
SARNP	SAP domain containing ribonucleoprotein(SARNP)	2.297878	1.952204	0.085499	0
TOP2B	DNA topoisomerase II beta(TOP2B)	2.292366	1.552999	0.085499	0
YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon(YWHAE)	2.291696	1.654136	0.085499	0
PRMT1	protein arginine methyltransferase 1(PRMT1)	2.287454	1.718632	0.085499	0
POU2AF1	POU class 2 homeobox associating factor 1(POU2AF1)	2.285029	1.752503	0.085499	0
H2BC4	H2BC4 (H2B Clustered Histone 4)	2.270187	2.168008	0.085499	0
CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase(CAD)	2.263745	1.558847	0.085499	0
FNBP1	formin binding protein 1(FNBP1)	2.261759	1.744725	0.085499	0
LRPPRC	leucine rich pentatricopeptide repeat containing(LRPPRC)	2.249226	1.517534	0.085499	0
DDX3X	DEAD-box helicase 3 X-linked(DDX3X)	2.248289	1.541582	0.085499	0
ZNF207	zinc finger protein 207(ZNF207)	2.225004	1.541699	0.085499	0
IRF4	interferon regulatory factor 4(IRF4)	2.224526	1.855881	0.085499	0
CNTRL	centriolin(CNTRL)	2.219932	1.433707	0.085499	0
SEPTIN2	SEPTIN2 (Septin 2)	2.208294	1.792689	0.085499	0
TCEA1	transcription elongation factor A1(TCEA1)	2.207877	1.501914	0.085499	0
CD79A	CD79a molecule(CD79A)	2.201403	1.876869	0.085499	0
EZH2	enhancer of zeste 2 polycomb repressive complex 2 subunit(EZH2)	2.198084	1.46901	0.085499	0
IKZF1	IKAROS family zinc finger 1(IKZF1)	2.188895	1.436489	0.085499	0
CEP43	CEP43 (Centrosomal Protein 43)	2.187978	1.627551	0.085499	0
EIF4A2	eukaryotic translation initiation factor 4A2(EIF4A2)	2.181607	1.508881	0.085499	0
SMC3	structural maintenance of chromosomes 3(SMC3)	2.179659	1.4937	0.085499	0
PTPN6	protein tyrosine phosphatase non-receptor type 6(PTPN6)	2.164704	1.536437	0.160999	0
AFF3	ALF transcription elongation factor 3(AFF3)	2.150048	1.686426	0.160999	0
RAD50	RAD50 double strand break repair protein(RAD50)	2.136962	1.563056	0.160999	0

PTPN11	protein tyrosine phosphatase non-receptor type 11(PTPN11)	2.135441	1.601984	0.160999	0
CEP57	centrosomal protein 57(CEP57)	2.129078	1.544958	0.160999	0
HERPUD1	homocysteine inducible ER protein with ubiquitin like domain 1(HERPUD1)	2.12513	1.538485	0.160999	0
SH3BP1	SH3 domain binding protein 1(SH3BP1)	2.11553	1.821497	0.160999	0
NDC80	NDC80 kinetochore complex component(NDC80)	2.115312	1.555957	0.160999	0
CENPU	centromere protein U(CENPU)	2.112997	1.840608	0.160999	0
FANCD2	FA complementation group D2(FANCD2)	2.110721	1.471796	0.160999	0
U2AF2	U2 small nuclear RNA auxiliary factor 2(U2AF2)	2.099703	1.557384	0.160999	0
RAP1GDS1	Rap1 GTPase-GDP dissociation stimulator 1(RAP1GDS1)	2.069841	1.561438	0.160999	0
MAPK1	mitogen-activated protein kinase 1(MAPK1)	2.064341	1.615282	0.160999	0
IRAG2	IRAG2 (Inositol 1,4,5-Triphosphate Receptor Associated 2)	2.063872	1.802586	0.160999	0
SRSF2	serine and arginine rich splicing factor 2(SRSF2)	2.062062	1.549432	0.160999	0
WDR1	WD repeat domain 1(WDR1)	2.056324	1.67207	0.160999	0
MKI67	marker of proliferation Ki-67(MKI67)	2.052359	1.498231	0.160999	0
CD79B	CD79b molecule(CD79B)	2.046652	1.707574	0.160999	0
IKZF3	IKAROS family zinc finger 3(IKZF3)	2.045376	1.400986	0.160999	0
SF3B1	splicing factor 3b subunit 1(SF3B1)	2.043781	1.439552	0.160999	0
BTG1	BTG anti-proliferation factor 1(BTG1)	2.038792	1.493468	0.160999	0
KIF5B	kinesin family member 5B(KIF5B)	2.037525	1.603725	0.160999	0
HOOK3	hook microtubule tethering protein 3(HOOK3)	2.036562	1.539152	0.160999	0
MDM4	MDM4 regulator of p53(MDM4)	2.034737	1.413443	0.160999	0
PPP3R1	protein phosphatase 3 regulatory subunit B, alpha(PPP3R1)	2.034714	1.566287	0.160999	0
TPR	translocated promoter region, nuclear basket protein(TPR)	2.028398	1.429469	0.160999	0
TFDP1	transcription factor Dp-1(TFDP1)	2.022215	1.488307	0.160999	0
EZR	ezrin(EZR)	2.021334	1.637305	0.160999	0
AKT2	AKT serine/threonine kinase 2(AKT2)	2.002694	1.703608	0.261736	0
MAD2L1	mitotic arrest deficient 2 like 1(MAD2L1)	2.001665	1.637565	0.261736	0
GNAS	GNAS complex locus(GNAS)	1.973089	1.505725	0.261736	0
KRAS	KRAS proto-oncogene, GTPase(KRAS)	1.972423	1.561573	0.261736	0
SRSF3	serine and arginine rich splicing factor 3(SRSF3)	1.968419	1.435763	0.261736	0
FBXO11	F-box protein 11(FBXO11)	1.965293	1.572781	0.261736	0
HUWE1	HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1(HUWE1)	1.961784	1.496804	0.261736	0
BCL2A1	BCL2 related protein A1(BCL2A1)	1.956293	1.613476	0.261736	0
MBNL1	muscleblind like splicing regulator 1(MBNL1)	1.951888	1.534308	0.261736	0
COX6C	cytochrome c oxidase subunit 6C(COX6C)	1.950841	1.682315	0.261736	0
SEPTIN6	septin 6(SEPTIN6)	1.946366	1.493253	0.261736	0
GIT2	GIT ArfGAP 2(GIT2)	1.944845	1.420569	0.261736	0
NRAS	NRAS proto-oncogene, GTPase(NRAS)	1.942985	1.476037	0.261736	0
LPXN	leupaxin(LPXN)	1.93849	1.427427	0.261736	0
GRB2	growth factor receptor bound protein 2(GRB2)	1.937478	1.553353	0.261736	0
KDM1A	lysine demethylase 1A(KDM1A)	1.927166	1.428659	0.261736	0
RPS6KA3	ribosomal protein S6 kinase A3(RPS6KA3)	1.90857	1.587544	0.261736	0
H2AC17	H2AC17 (H2A Clustered Histone 17)	1.90586	1.556024	0.261736	0
DDX5	DEAD-box helicase 5(DDX5)	1.884649	1.428793	0.261736	0
CCNG1	cyclin G1(CCNG1)	1.87705	1.438149	0.426136	0
MAPRE1	microtubule associated protein RP/EB family member 1(MAPRE1)	1.868951	1.569434	0.426136	0

LCP1	lymphocyte cytosolic protein 1(LCP1)	1.863382	1.527284	0.426136	0
IDH2	isocitrate dehydrogenase (NADP(+)) 2(IDH2)	1.856479	1.599014	0.426136	0
MAP3K7	mitogen-activated protein kinase kinase kinase 7(MAP3K7)	1.854329	1.365365	0.426136	0
CCND2	cyclin D2(CCND2)	1.853771	1.811562	0.426136	0
FANCL	FA complementation group L(FANCL)	1.851665	1.572213	0.426136	0
GRHPR	glyoxylate and hydroxypyruvate reductase(GRHPR)	1.847591	1.76459	0.426136	0
LASP1	LIM and SH3 protein 1(LASP1)	1.847271	1.463621	0.426136	0
CHD2	chromodomain helicase DNA binding protein 2(CHD2)	1.842282	1.356198	0.426136	0
ST6GAL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1(ST6GAL1)	1.84006	1.41522	0.426136	0
RPS6KA1	ribosomal protein S6 kinase A1(RPS6KA1)	1.833809	1.553566	0.426136	0
CUX1	cut like homeobox 1(CUX1)	1.826051	1.416651	0.426136	0
NUP93	nucleoporin 93(NUP93)	1.825264	1.388273	0.426136	0
BCL11A	BCL11 transcription factor A(BCL11A)	1.817639	1.430997	0.426136	0
DDX6	DEAD-box helicase 6(DDX6)	1.801573	1.366706	0.426136	0
PTBP1	polypyrimidine tract binding protein 1(PTBP1)	1.797198	1.49755	0.426136	0
HDAC1	histone deacetylase 1(HDAC1)	1.795779	1.451848	0.426136	0
SS18	SS18 subunit of BAF chromatin remodeling complex(SS18)	1.795724	1.548672	0.426136	0
PKM	pyruvate kinase M1/2(PKM)	1.794247	1.618832	0.426136	0
TMEM230	transmembrane protein 230(TMEM230)	1.79053	1.516286	0.426136	0
PICALM	phosphatidylinositol binding clathrin assembly protein(PICALM)	1.786465	1.526474	0.426136	0.030801
H2BC12	H2BC12 (H2B Clustered Histone 12)	1.784287	1.639452	0.426136	0.054408
ETS1	ETS proto-oncogene 1, transcription factor(ETS1)	1.772045	1.399763	0.426136	0.190877
CPSF6	cleavage and polyadenylation specific factor 6(CPSF6)	1.767669	1.347521	0.426136	0.241254
CARMIL2	CARMIL2 (Capping Protein Regulator And Myosin 1 Linker 2)	1.764753	1.512142	0.426136	0.275292
ARHGEF7	Rho guanine nucleotide exchange factor 7(ARHGEF7)	1.763797	1.436562	0.426136	0.286529
CALR	calreticulin(CALR)	1.762277	1.408273	0.426136	0.304497
RABEP1	rabaptin, RAB GTPase binding effector protein 1(RABEP1)	1.756328	1.461366	0.426136	0.375778
PHB1	PHB1 (Prohibitin 1)	1.747713	1.514054	0.641617	0.481849
FANCA	FA complementation group A(FANCA)	1.742715	1.491696	0.641617	0.544959
TPM3	tropomyosin 3(TPM3)	1.742147	1.478752	0.641617	0.552207
ELP2	elongator acetyltransferase complex subunit 2(ELP2)	1.732914	1.364631	0.641617	0.672087
CBFA2T3	CBFA2/RUNX1 partner transcriptional co-repressor 3(CBFA2T3)	1.732692	1.662824	0.641617	0.675023
ERCC2	ERCC excision repair 2, TFIIH core complex helicase subunit(ERCC2)	1.732378	1.598292	0.641617	0.679175
RHOA	ras homolog family member A(RHOA)	1.729411	1.405221	0.641617	0.718623
UBE2C	ubiquitin conjugating enzyme E2 C(UBE2C)	1.722463	1.440857	0.641617	0.81267
EED	embryonic ectoderm development(EED)	1.71272	1.382132	0.641617	0.948475
PHF6	PHD finger protein 6(PHF6)	1.707188	1.390551	0.641617	1.027658
ZC3H7A	zinc finger CCCH-type containing 7A(ZC3H7A)	1.702756	1.322274	0.641617	1.092186
CDC42	cell division cycle 42(CDC42)	1.691446	1.510205	0.641617	1.261337
CCDC88C	coiled-coil domain containing 88C(CCDC88C)	1.685251	1.369536	0.641617	1.356736
MDM2	MDM2 proto-oncogene(MDM2)	1.679754	1.438814	0.641617	1.443049
CDK7	cyclin dependent kinase 7(CDK7)	1.674923	1.405627	0.641617	1.520209
NIN	ninein(NIN)	1.66202	1.343329	0.641617	1.732298
WEE1	WEE1 G2 checkpoint kinase(WEE1)	1.651928	1.390119	0.641617	1.90439
BAX	BCL2 associated X, apoptosis regulator(BAX)	1.646754	1.486127	0.641617	1.994755
GOSR1	golgi SNAP receptor complex member 1(GOSR1)	1.646289	1.446089	0.641617	2.00295

FGFR1OP2	FGFR1 oncogene partner 2(FGFR1OP2)	1.638452	1.404769	0.641617	2.142854
EWSR1	EWS RNA binding protein 1(EWSR1)	1.628062	1.308715	1.010005	2.333583
FH	fumarate hydratase(FH)	1.625036	1.412973	1.010005	2.390269
VTI1A	vesicle transport through interaction with t-SNAREs 1A(VTI1A)	1.612448	1.428257	1.010005	2.631713
CCDC6	coiled-coil domain containing 6(CCDC6)	1.607038	1.386731	1.010005	2.738268
CHEK1	checkpoint kinase 1(CHEK1)	1.605535	1.371194	1.010005	2.768188
PPP4C	protein phosphatase 4 catalytic subunit(PPP4C)	1.591823	1.511394	1.010005	3.047153
CLTA	clathrin light chain A(CLTA)	1.590539	1.459284	1.010005	3.073832
ARID1A	AT-rich interaction domain 1A(ARID1A)	1.584337	1.278889	1.010005	3.204134
VHL	von Hippel-Lindau tumor suppressor(VHL)	1.58282	1.356884	1.010005	3.236369
UTP4	UTP4 (UTP4 Small Subunit Processome Component)	1.579506	1.341894	1.010005	3.307237
GAB1	GRB2 associated binding protein 1(GAB1)	1.575636	1.474338	1.010005	3.390855
POLR2H	RNA polymerase II, I and III subunit H(POLR2H)	1.575462	1.425475	1.010005	3.394623
CD74	CD74 molecule(CD74)	1.561596	1.629986	1.010005	3.701829
EPS15	epidermal growth factor receptor pathway substrate 15(EPS15)	1.559423	1.323248	1.010005	3.751041
SNX29	sorting nexin 29(SNX29)	1.552459	1.425449	1.010005	3.910719
SNHG5	SNHG5 (Small Nucleolar RNA Host Gene 5)	1.546552	1.856404	1.010005	4.048557
OFD1	OFD1 centriole and centriolar satellite protein(OFD1)	1.539937	1.407333	1.010005	4.205534
CXCR4	C-X-C motif chemokine receptor 4(CXCR4)	1.535243	1.385945	1.010005	4.318577
CNOT2	CCR4-NOT transcription complex subunit 2(CNOT2)	1.529303	1.299774	1.010005	4.463679
HSP90AA1	heat shock protein 90 alpha family class A member 1(HSP90AA1)	1.527969	1.351657	1.010005	4.49658
PRKCD	protein kinase C delta(PRKCD)	1.522068	1.347472	1.434313	4.643445
PTPRA	protein tyrosine phosphatase receptor type A(PTPRA)	1.511951	1.38877	1.434313	4.900503
ZC3H7B	zinc finger CCCH-type containing 7B(ZC3H7B)	1.51135	1.418657	1.434313	4.915993
FGFR2	fibroblast growth factor receptor 2(FGFR2)	-5.14176	0.197448	0	0
MALAT1	metastasis associated lung adenocarcinoma transcript 1(MALAT1)	-5.11111	0.009966	0	0
WNT2B	Wnt family member 2B(WNT2B)	-4.84416	0.205688	0	0.002061
PC	pyruvate carboxylase(PC)	-4.6622	0.277447	0	0.021017
SERP2	stress associated endoplasmic reticulum protein family member 2(SERP2)	-4.47447	0.226374	0	0.044243
EGFR	epidermal growth factor receptor(EGFR)	-4.34036	0.291632	0	0.063098
EDIL3	EGF like repeats and discoidin domains 3(EDIL3)	-4.31035	0.292646	0	0.067501
BICC1	BicC family RNA binding protein 1(BICC1)	-4.29065	0.306107	0	0.070413
ID4	inhibitor of DNA binding 4(ID4)	-4.28992	0.253057	0	0.070522
TACC2	transforming acidic coiled-coil containing protein 2(TACC2)	-4.2878	0.28395	0	0.070835
LRIG3	leucine rich repeats and immunoglobulin like domains 3(LRIG3)	-4.24632	0.316105	0	0.076976
DLEC1	DLEC1 cilia and flagella associated protein(DLEC1)	-4.24392	0.222617	0	0.077331
ZFPM2	zinc finger protein, FOG family member 2(ZFPM2)	-4.19744	0.254821	0	0.084133
ETV1	ETS variant transcription factor 1(ETV1)	-4.17338	0.32594	0	0.087585
GNAI1	G protein subunit alpha i1(GNAI1)	-4.15859	0.282284	0	0.089675
HSPA2	heat shock protein family A (Hsp70) member 2(HSPA2)	-4.15467	0.240944	0	0.090225
CEP170B	centrosomal protein 170B(CEP170B)	-4.10091	0.336052	0	0.097507
ARHGAP20	Rho GTPase activating protein 20(ARHGAP20)	-4.05379	0.273449	0	0.103368
CNTN1	contactin 1(CNTN1)	-4.04218	0.247787	0	0.104712
KLF4	KLF transcription factor 4(KLF4)	-4.02982	0.325049	0	0.106096
FGF13	fibroblast growth factor 13(FGF13)	-4.01683	0.285127	0	0.107488
PTK7	protein tyrosine kinase 7 (inactive)(PTK7)	-3.99005	0.322573	0	0.110139

FLNC	filamin C(FLNC)	-3.97436	0.296122	0	0.111538
DST	dystonin(DST)	-3.96864	0.417081	0	0.112016
GLI3	GLI family zinc finger 3(GLI3)	-3.95722	0.327264	0	0.11292
EPOR	erythropoietin receptor(EPOR)	-3.95031	0.341797	0	0.113431
PPFIA2	PTPRF interacting protein alpha 2(PPFIA2)	-3.94422	0.279898	0	0.113859
ERBB4	erb-b2 receptor tyrosine kinase 4(ERBB4)	-3.93041	0.293327	0	0.114746
NTRK2	neurotrophic receptor tyrosine kinase 2(NTRK2)	-3.91685	0.294417	0	0.115499
ZNF521	zinc finger protein 521(ZNF521)	-3.89406	0.317522	0	0.116482
PCLO	piccolo presynaptic cytomatrix protein(PCLO)	-3.88672	0.211513	0	0.11672
NAV3	neuron navigator 3(NAV3)	-3.87236	0.331194	0	0.117066
SLC45A3	solute carrier family 45 member 3(SLC45A3)	-3.8707	0.317089	0	0.117096
ACSL6	acyl-CoA synthetase long chain family member 6(ACSL6)	-3.86482	0.37838	0	0.117183
KALRN	kalirin RhoGEF kinase(KALRN)	-3.8644	0.337432	0	0.117188
NCAM1	neural cell adhesion molecule 1(NCAM1)	-3.85613	0.31535	0	0.11726
BRSK1	BR serine/threonine kinase 1(BRSK1)	-3.85143	0.358171	0	0.117276
TENM1	teneurin transmembrane protein 1(TENM1)	-3.84791	0.287558	0	0.117275
GHR	growth hormone receptor(GHR)	-3.84417	0.266892	0	0.117263
SFRP2	secreted frizzled related protein 2(SFRP2)	-3.82952	0.222427	0	0.117091
LAMA1	laminin subunit alpha 1(LAMA1)	-3.8282	0.312208	0	0.117066
ITGB3	integrin subunit beta 3(ITGB3)	-3.81798	0.359196	0	0.116813
PAPPA	pappalysin 1(PAPPA)	-3.81552	0.335753	0	0.116737
FBN2	fibrillin 2(FBN2)	-3.81433	0.33653	0	0.116698
RYR3	ryanodine receptor 3(RYR3)	-3.79191	0.282337	0	0.115688
AR	androgen receptor(AR)	-3.7905	0.367776	0	0.115606
HAS2	hyaluronan synthase 2(HAS2)	-3.78292	0.257041	0	0.11513
LIFR	LIF receptor subunit alpha(LIFR)	-3.77588	0.409718	0	0.114629
MAP2	microtubule associated protein 2(MAP2)	-3.76791	0.265746	0	0.11399
NGFR	nerve growth factor receptor(NGFR)	-3.7574	0.355848	0	0.113033
ESR1	estrogen receptor 1(ESR1)	-3.74356	0.308665	0	0.111561
ROS1	ROS proto-oncogene 1, receptor tyrosine kinase(ROS1)	-3.73627	0.263015	0	0.110687
LTBP1	latent transforming growth factor beta binding protein 1(LTBP1)	-3.72884	0.37666	0	0.109724
TRHDE	thyrotropin releasing hormone degrading enzyme(TRHDE)	-3.72033	0.302578	0	0.108527
GAS1	growth arrest specific 1(GAS1)	-3.71359	0.375465	0	0.107507
SORBS2	sorbin and SH3 domain containing 2(SORBS2)	-3.70665	0.308859	0	0.10639
EPHB6	EPH receptor B6(EPHB6)	-3.69767	0.345572	0	0.10484
NTRK3	neurotrophic receptor tyrosine kinase 3(NTRK3)	-3.66779	0.32189	0	0.098804
INHBA	inhibin subunit beta A(INHBA)	-3.66583	0.289861	0	0.09836
FZD8	frizzled class receptor 8(FZD8)	-3.66518	0.325728	0	0.09821
PLAT	plasminogen activator, tissue type(PLAT)	-3.66097	0.353836	0	0.097228
RANBP17	RAN binding protein 17(RANBP17)	-3.65769	0.343459	0	0.096444
FGF1	fibroblast growth factor 1(FGF1)	-3.64014	0.329298	0	0.091934
WT1	WT1 transcription factor(WT1)	-3.63594	0.300623	0	0.090777
VGLL3	vestigial like family member 3(VGLL3)	-3.62942	0.375111	0	0.088915
FGF10	fibroblast growth factor 10(FGF10)	-3.62381	0.228044	0	0.087255
PDGFRA	platelet derived growth factor receptor alpha(PDGFRA)	-3.62098	0.396882	0	0.086395
RELN	reelin(RELN)	-3.61914	0.328146	0	0.085828
HGF	hepatocyte growth factor(HGF)	-3.61664	0.324646	0	0.085044

JAG2	jagged canonical Notch ligand 2(JAG2)	-3.61268	0.395502	0	0.083787
GNA11	G protein subunit alpha 11(GNA11)	-3.60594	0.387506	0	0.081572
PAK3	p21 (RAC1) activated kinase 3(PAK3)	-3.59273	0.295258	0	0.076979
ARRDC4	arrestin domain containing 4(ARRDC4)	-3.59088	0.386708	0	0.076307
FZD7	frizzled class receptor 7(FZD7)	-3.57798	0.338448	0	0.071438
MN1	MN1 proto-oncogene, transcriptional regulator(MN1)	-3.57547	0.376407	0	0.070453
DACH1	dachshund family transcription factor 1(DACH1)	-3.57351	0.363975	0	0.069672
DNM1	dynamin 1(DNM1)	-3.56176	0.368566	0	0.064828
SH3D19	SH3 domain containing 19(SH3D19)	-3.54718	0.395902	0	0.058407
PBX1	PBX homeobox 1(PBX1)	-3.54649	0.37994	0	0.058092
KCNB1	potassium voltage-gated channel subfamily B member 1(KCNB1)	-3.53532	0.262884	0	0.052833
PEG3	paternally expressed 3(PEG3)	-3.53073	0.250658	0	0.050588
FRMPD4	FERM and PDZ domain containing 4(FRMPD4)	-3.52671	0.329299	0	0.048585
ERBB3	erb-b2 receptor tyrosine kinase 3(ERBB3)	-3.51812	0.265414	0	0.044173
MAF	MAF bZIP transcription factor(MAF)	-3.50805	0.405545	0	0.038779
CACNA1G	calcium voltage-gated channel subunit alpha1 G(CACNA1G)	-3.50805	0.338603	0	0.038775
ZNF703	zinc finger protein 703(ZNF703)	-3.50686	0.413957	0	0.038125
YAP1	Yes1 associated transcriptional regulator(YAP1)	-3.5013	0.3887	0	0.035019
LINGO2	leucine rich repeat and Ig domain containing 2(LINGO2)	-3.50024	0.264041	0	0.034418
KIAA1549	KIAA1549(KIAA1549)	-3.49781	0.350365	0	0.033037
GPC3	glypican 3(GPC3)	-3.49204	0.310517	0	0.029684
PDE4DIP	phosphodiesterase 4D interacting protein(PDE4DIP)	-3.48969	0.415042	0	0.028296
ITGA7	integrin subunit alpha 7(ITGA7)	-3.48722	0.371264	0	0.026819
PROM1	prominin 1(PROM1)	-3.48153	0.321617	0	0.023365
IL12RB2	interleukin 12 receptor subunit beta 2(IL12RB2)	-3.48126	0.354727	0	0.023197
FOSB	FosB proto-oncogene, AP-1 transcription factor subunit(FOSB)	-3.47121	0.29506	0	0.016882
TEAD1	TEA domain transcription factor 1(TEAD1)	-3.46976	0.431269	0	0.015949
ELOVL2	ELOVL fatty acid elongase 2(ELOVL2)	-3.46725	0.391966	0	0.014317
OMD	osteomodulin(OMD)	-3.46251	0.296925	0	0.011194
PPARGC1A	PPARG coactivator 1 alpha(PPARGC1A)	-3.45871	0.335126	0	0.008648
PSD3	pleckstrin and Sec7 domain containing 3(PSD3)	-3.45198	0.374306	0	0.004042
ZBTB16	zinc finger and BTB domain containing 16(ZBTB16)	-3.44379	0.316223	0	0
AKAP12	A-kinase anchoring protein 12(AKAP12)	-3.44012	0.361982	0	0
EPHA2	EPH receptor A2(EPHA2)	-3.43999	0.369047	0	0
LPAR1	lysophosphatidic acid receptor 1(LPAR1)	-3.43677	0.385095	0	0
MAGEE1	MAGE family member E1(MAGEE1)	-3.43305	0.343565	0	0
GATA3	GATA binding protein 3(GATA3)	-3.43212	0.369101	0	0
PRSS8	serine protease 8(PRSS8)	-3.43122	0.321923	0	0
PRDM16	PR/SET domain 16(PRDM16)	-3.40539	0.364693	0	0
CLTCL1	clathrin heavy chain like 1(CLTC1)	-3.40301	0.360584	0	0
HES1	hes family bHLH transcription factor 1(HES1)	-3.39971	0.329395	0	0
RGS7	regulator of G protein signaling 7(RGS7)	-3.38605	0.328668	0	0
ROBO1	roundabout guidance receptor 1(ROBO1)	-3.38222	0.42432	0	0
FGFR3	fibroblast growth factor receptor 3(FGFR3)	-3.37314	0.393123	0	0
ANGPT1	angiotensinogen 1(ANGPT1)	-3.36446	0.34573	0	0
AKR1C3	aldo-keto reductase family 1 member C3(AKR1C3)	-3.36208	0.312921	0	0
PTGS2	prostaglandin-endoperoxide synthase 2(PTGS2)	-3.3432	0.34738	0	0

MLF1	myeloid leukemia factor 1(MLF1)	-3.33883	0.29037	0	0
GATA6	GATA binding protein 6(GATA6)	-3.33577	0.380257	0	0
BAIAP2L1	BAR/IMD domain containing adaptor protein 2 like 1(BAIAP2L1)	-3.33011	0.32743	0	0
SPRY4	sprouty RTK signaling antagonist 4(SPRY4)	-3.31901	0.398595	0	0
PLA2G5	phospholipase A2 group V(PLA2G5)	-3.29377	0.37048	0	0
SHC2	SHC adaptor protein 2(SHC2)	-3.29015	0.378149	0	0
DAB2IP	DAB2 interacting protein(DAB2IP)	-3.28857	0.395986	0	0
SMAD6	SMAD family member 6(SMAD6)	-3.28105	0.349041	0	0
MB21D2	Mab-21 domain containing 2(MB21D2)	-3.27697	0.352825	0	0
LHX4	LIM homeobox 4(LHX4)	-3.27202	0.310422	0	0
EDNRB	endothelin receptor type B(EDNRB)	-3.27012	0.349693	0	0
ADGRA2	ADGRA2 (Adhesion G Protein-Coupled Receptor A2)	-3.26643	0.430834	0	0
TNFRSF11A	TNF receptor superfamily member 11a(TNFRSF11A)	-3.26368	0.348208	0	0
RERG	RAS like estrogen regulated growth inhibitor(RERG)	-3.25551	0.354722	0	0
ACVR1B	activin A receptor type 1B(ACVR1B)	-3.25354	0.433982	0	0
PPP3R2	protein phosphatase 3 regulatory subunit B, beta(PPP3R2)	-3.23243	0.327775	0	0
HTRA1	HtrA serine peptidase 1(HTRA1)	-3.22849	0.405329	0	0
RNF217-AS1	RNF217-AS1 (RNF217 Antisense RNA 1 (Head To Head))	-3.22559	0.353942	0	0
PTPRK	protein tyrosine phosphatase receptor type K(PTPRK)	-3.22498	0.434837	0	0
PLCB4	phospholipase C beta 4(PLCB4)	-3.22131	0.403956	0	0
CSF1	colony stimulating factor 1(CSF1)	-3.20536	0.452461	0	0
DOCK1	dedicator of cytokinesis 1(DOCK1)	-3.20431	0.517037	0	0
EYA1	EYA transcriptional coactivator and phosphatase 1(EYA1)	-3.20327	0.339493	0	0
HEPH	hephaestin(HEPH)	-3.1979	0.419694	0	0
IL13RA2	interleukin 13 receptor subunit alpha 2(IL13RA2)	-3.19781	0.369081	0	0
EML1	EMAP like 1(EML1)	-3.19312	0.440261	0	0
BMP4	bone morphogenetic protein 4(BMP4)	-3.18834	0.316536	0	0
CREB3L1	cAMP responsive element binding protein 3 like 1(CREB3L1)	-3.18171	0.376733	0	0
DKK4	dickkopf WNT signaling pathway inhibitor 4(DKK4)	-3.17299	0.299069	0	0
PRDM7	PR/SET domain 7(PRDM7)	-3.17221	0.325509	0	0
DDR2	discoidin domain receptor tyrosine kinase 2(DDR2)	-3.17185	0.466641	0	0
DIRAS3	DIRAS family GTPase 3(DIRAS3)	-3.16091	0.310633	0	0
AK5	adenylate kinase 5(AK5)	-3.15885	0.355617	0	0
NUTM1	NUT midline carcinoma family member 1(NUTM1)	-3.1567	0.282299	0	0
HOXA11	homeobox A11(HOXA11)	-3.15052	0.342232	0	0
MECOM	MDS1 and EVI1 complex locus(MECOM)	-3.14886	0.39179	0	0
HOXD9	homeobox D9(HOXD9)	-3.14815	0.375732	0	0
IGF1	insulin like growth factor 1(IGF1)	-3.14775	0.299593	0	0
PAX8	paired box 8(PAX8)	-3.14022	0.39959	0	0
ACVR1C	activin A receptor type 1C(ACVR1C)	-3.14014	0.332994	0	0
GLI1	GLI family zinc finger 1(GLI1)	-3.1377	0.375968	0	0
NGF	nerve growth factor(NGF)	-3.136	0.321615	0	0
LRRC7	leucine rich repeat containing 7(LRRC7)	-3.13461	0.339799	0	0
ELN	elastin(ELN)	-3.13336	0.340494	0	0
MYH11	myosin heavy chain 11(MYH11)	-3.13144	0.324617	0	0
MITF	melanocyte inducing transcription factor(MITF)	-3.12464	0.390027	0	0

NBEAP1	neurobeachin pseudogene 1(NBEAP1)	-3.11582	0.2901	0	0
CDKN1C	cyclin dependent kinase inhibitor 1C(CDKN1C)	-3.11535	0.369355	0	0
SLCO1B3	solute carrier organic anion transporter family member 1B3(SLCO1B3)	-3.11409	0.344818	0	0
CCNB3	cyclin B3(CCNB3)	-3.11221	0.326272	0	0
GATA2	GATA binding protein 2(GATA2)	-3.10683	0.393026	0	0
NOTCH3	notch receptor 3(NOTCH3)	-3.10392	0.478924	0	0
DGKB	diacylglycerol kinase beta(DGKB)	-3.08413	0.362094	0	0
GRIN2A	glutamate ionotropic receptor NMDA type subunit 2A(GRIN2A)	-3.08351	0.375045	0	0
BCL11B	BCL11 transcription factor B(BCL11B)	-3.07355	0.437307	0	0
SOCS2	suppressor of cytokine signaling 2(SOCS2)	-3.06942	0.429272	0	0
PRKG2	protein kinase cGMP-dependent 2(PRKG2)	-3.06516	0.369632	0	0
MUC1	mucin 1, cell surface associated(MUC1)	-3.06382	0.380603	0	0
WDFY3	WD repeat and FYVE domain containing 3(WDFY3)	-3.05769	0.535513	0	0
DNM3	dynamamin 3(DNM3)	-3.05281	0.427943	0	0
HEY1	hes related family bHLH transcription factor with YRPW motif 1(HEY1)	-3.04061	0.350827	0	0
KIT	KIT proto-oncogene, receptor tyrosine kinase(KIT)	-3.03599	0.417987	0	0
RET	ret proto-oncogene(RET)	-3.03495	0.412277	0	0
GRB10	growth factor receptor bound protein 10(GRB10)	-3.03407	0.456278	0	0
COL11A1	collagen type XI alpha 1 chain(COL11A1)	-3.03072	0.333214	0	0
PAK5	PAK5 (P21 (RAC1) Activated Kinase 5)	-3.03002	0.346192	0	0
LEFTY2	left-right determination factor 2(LEFTY2)	-3.02237	0.398027	0	0
PRKACG	protein kinase cAMP-activated catalytic subunit gamma(PRKACG)	-3.02171	0.377095	0	0
IGFBP2	insulin like growth factor binding protein 2(IGFBP2)	-3.02058	0.413192	0	0
RNF43	ring finger protein 43(RNF43)	-3.01526	0.409824	0	0
EPHA7	EPH receptor A7(EPHA7)	-3.00381	0.312984	0	0
EPHA3	EPH receptor A3(EPHA3)	-2.99884	0.36624	0	0
JUN	Jun proto-oncogene, AP-1 transcription factor subunit(JUN)	-2.98727	0.494427	0	0
TPO	thyroid peroxidase(TPO)	-2.98594	0.378414	0	0
FZD2	frizzled class receptor 2(FZD2)	-2.98563	0.435489	0	0
SRGAP3	SLIT-ROBO Rho GTPase activating protein 3(SRGAP3)	-2.98241	0.518485	0	0
IL1RAP	interleukin 1 receptor accessory protein(IL1RAP)	-2.97901	0.414274	0	0
SDC4	syndecan 4(SDC4)	-2.97538	0.430223	0	0
CCK	cholecystokinin(CCK)	-2.97462	0.309849	0	0
SH3GL2	SH3 domain containing GRB2 like 2, endophilin A1(SH3GL2)	-2.97379	0.390116	0	0
DUSP26	dual specificity phosphatase 26(DUSP26)	-2.97324	0.340754	0	0
PRKCG	protein kinase C gamma(PRKCG)	-2.97129	0.404179	0	0
NTF3	neurotrophin 3(NTF3)	-2.96842	0.265675	0	0
TEAD4	TEA domain transcription factor 4(TEAD4)	-2.9669	0.354156	0	0
AXL	AXL receptor tyrosine kinase(AXL)	-2.96383	0.441637	0	0
PPARG	peroxisome proliferator activated receptor gamma(PPARG)	-2.96137	0.36729	0	0
ALK	ALK receptor tyrosine kinase(ALK)	-2.96015	0.376846	0	0
DLL1	delta like canonical Notch ligand 1(DLL1)	-2.95165	0.449952	0	0
PRDM16-DT	PRDM16-DT (PRDM16 Divergent Transcript)	-2.94137	0.338311	0	0
HOXA3	homeobox A3(HOXA3)	-2.9385	0.437235	0	0
XKR3	XK related 3(XKR3)	-2.93579	0.288945	0	0
SNCG	synuclein gamma(SNCG)	-2.92921	0.375459	0	0

GRID1	glutamate ionotropic receptor delta type subunit 1(GRID1)	-2.92188	0.441602	0	0
FLT4	fms related receptor tyrosine kinase 4(FLT4)	-2.91586	0.486401	0	0
BDNF	brain derived neurotrophic factor(BDNF)	-2.91486	0.316299	0	0
FGFR4	fibroblast growth factor receptor 4(FGFR4)	-2.91246	0.413234	0	0
ADGRG7	ADGRG7 (Adhesion G Protein-Coupled Receptor G7)	-2.91196	0.354103	0	0
WNT11	Wnt family member 11(WNT11)	-2.90879	0.385439	0	0
IRS4	insulin receptor substrate 4(IRS4)	-2.90419	0.339356	0	0
TET1	tet methylcytosine dioxygenase 1(TET1)	-2.89848	0.458479	0	0
NTRK1	neurotrophic receptor tyrosine kinase 1(NTRK1)	-2.89652	0.416138	0	0
P2RY8	P2Y receptor family member 8(P2RY8)	-2.89545	0.430832	0	0
VEGFD	VEGFD (Vascular Endothelial Growth Factor D)	-2.89485	0.434462	0	0
TEAD3	TEA domain transcription factor 3(TEAD3)	-2.89016	0.439456	0	0
WWTR1	WW domain containing transcription regulator 1(WWTR1)	-2.89011	0.511842	0	0
MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2(MAPK8IP2)	-2.86555	0.456319	0	0
NPM2	nucleophosmin/nucleoplasmin 2(NPM2)	-2.86547	0.349489	0	0
ABCC3	ATP binding cassette subfamily C member 3(ABCC3)	-2.86405	0.429142	0	0
SPRY2	sprouty RTK signaling antagonist 2(SPRY2)	-2.85861	0.453178	0	0
HNF1A	HNF1 homeobox A(HNF1A)	-2.85539	0.440231	0	0
EPHA5	EPH receptor A5(EPHA5)	-2.85368	0.353059	0	0
EGR4	early growth response 4(EGR4)	-2.84924	0.39852	0	0
IGF1R	insulin like growth factor 1 receptor(IGF1R)	-2.849	0.505567	0	0
CPS1	carbamoyl-phosphate synthase 1(CPS1)	-2.84878	0.416907	0	0
CAV1	caveolin 1(CAV1)	-2.84428	0.465803	0	0
CEBPA	CCAAT enhancer binding protein alpha(CEBPA)	-2.84139	0.386525	0	0
CYP2C19	cytochrome P450 family 2 subfamily C member 19(CYP2C19)	-2.83538	0.353273	0	0
OLR1	oxidized low density lipoprotein receptor 1(OLR1)	-2.83535	0.385654	0	0
NTF4	neurotrophin 4(NTF4)	-2.83366	0.312267	0	0
CTNND2	catenin delta 2(CTNND2)	-2.83362	0.380756	0	0
RUNX2	RUNX family transcription factor 2(RUNX2)	-2.8335	0.446175	0	0
GATA1	GATA binding protein 1(GATA1)	-2.8265	0.399642	0	0
MLLT11	MLLT11 transcription factor 7 cofactor(MLLT11)	-2.82216	0.408407	0	0
MTUS2	microtubule associated scaffold protein 2(MTUS2)	-2.82141	0.321966	0	0
ITGA8	integrin subunit alpha 8(ITGA8)	-2.81671	0.419729	0	0
CAMK2B	calcium/calmodulin dependent protein kinase II beta(CAMK2B)	-2.80843	0.426068	0	0
SPECC1	sperm antigen with calponin homology and coiled-coil domains 1(SPECC1)	-2.80761	0.524936	0	0
RUNX1T1	RUNX1 partner transcriptional co-repressor 1(RUNX1T1)	-2.80648	0.368023	0	0
MIPOL1	mirror-image polydactyly 1(MIPOL1)	-2.79906	0.449342	0	0
SRRM3	serine/arginine repetitive matrix 3(SRRM3)	-2.79127	0.504575	0	0
NOTCH4	notch receptor 4(NOTCH4)	-2.78887	0.512245	0	0
CDH1	cadherin 1(CDH1)	-2.78722	0.389542	0	0
TAL1	TAL bHLH transcription factor 1, erythroid differentiation factor(TAL1)	-2.78642	0.495263	0	0
LRP5	LDL receptor related protein 5(LRP5)	-2.78406	0.481603	0	0
CBLC	Cbl proto-oncogene C(CBLC)	-2.78183	0.424737	0	0
TMPRSS2	transmembrane serine protease 2(TMPRSS2)	-2.77292	0.500701	0	0
MAP3K6	mitogen-activated protein kinase kinase kinase 6(MAP3K6)	-2.76939	0.502169	0	0
PAX3	paired box 3(PAX3)	-2.76673	0.295333	0	0

IRS2	insulin receptor substrate 2(IRS2)	-2.76263	0.460205	0	0
GABRG2	gamma-aminobutyric acid type A receptor subunit gamma2(GABRG2)	-2.75174	0.392451	0	0
PRMT8	protein arginine methyltransferase 8(PRMT8)	-2.75118	0.418913	0	0
EPHA10	EPH receptor A10(EPHA10)	-2.75067	0.34733	0	0
CDH11	cadherin 11(CDH11)	-2.74905	0.527404	0	0
HLF	HLF transcription factor, PAR bZIP family member(HLF)	-2.74879	0.400814	0	0
LGR5	leucine rich repeat containing G protein-coupled receptor 5(LGR5)	-2.74431	0.352595	0	0
TRPS1	transcriptional repressor GATA binding 1(TRPS1)	-2.74399	0.574192	0	0
TGFB3	transforming growth factor beta 3(TGFB3)	-2.73609	0.494095	0	0
WNT16	Wnt family member 16(WNT16)	-2.73422	0.341888	0	0
TFAP2A	transcription factor AP-2 alpha(TFAP2A)	-2.73376	0.481501	0	0
MYCL	MYCL proto-oncogene, bHLH transcription factor(MYCL)	-2.72931	0.405936	0	0
PPP2R2B	protein phosphatase 2 regulatory subunit Bbeta(PPP2R2B)	-2.72516	0.437099	0	0
TAL2	TAL bHLH transcription factor 2(TAL2)	-2.72106	0.352763	0	0
NODAL	nodal growth differentiation factor(NODAL)	-2.71586	0.380886	0	0
CHN1	chimerin 1(CHN1)	-2.71542	0.409998	0	0
GPHN	gephyrin(GPHN)	-2.71037	0.449343	0	0
NEURL1	neuralized E3 ubiquitin protein ligase 1(NEURL1)	-2.70237	0.457417	0	0
DMRT1	doublesex and mab-3 related transcription factor 1(DMRT1)	-2.70202	0.393351	0	0
BTBD18	BTB domain containing 18(BTBD18)	-2.69624	0.331315	0	0
HMG2P46	high mobility group nucleosomal binding domain 2 pseudogene 46(HMG2P46)	-2.69427	0.344395	0	0
WNT7B	Wnt family member 7B(WNT7B)	-2.68223	0.441654	0	0
IBSP	integrin binding sialoprotein(IBSP)	-2.68023	0.331233	0	0
CDC14B	cell division cycle 14B(CDC14B)	-2.67989	0.481742	0	0
LHX2	LIM homeobox 2(LHX2)	-2.67207	0.41127	0	0
SMO	smoothened, frizzled class receptor(SMO)	-2.67165	0.458588	0	0
GRM3	glutamate metabotropic receptor 3(GRM3)	-2.66923	0.345644	0	0
ACVR2A	activin A receptor type 2A(ACVR2A)	-2.66789	0.46143	0	0
GAS7	growth arrest specific 7(GAS7)	-2.66699	0.548963	0	0
TGFBR3	transforming growth factor beta receptor 3(TGFBR3)	-2.66533	0.47579	0	0
SOX2	SOX-box transcription factor 2(SOX2)	-2.665	0.437154	0	0
GRM1	glutamate metabotropic receptor 1(GRM1)	-2.6629	0.386625	0	0
PLAU	plasminogen activator, urokinase(PLAU)	-2.6626	0.48918	0	0
LINC00598	LINC00598 (Long Intergenic Non-Protein Coding RNA 598)	-2.65976	0.370598	0	0
RHOD	ras homolog family member D(RHOD)	-2.65906	0.429855	0	0
AKAP6	A-kinase anchoring protein 6(AKAP6)	-2.65885	0.404696	0	0
TGFB2	transforming growth factor beta 2(TGFB2)	-2.65503	0.539542	0	0
CXXC4	CXXC finger protein 4(CXXC4)	-2.65374	0.442211	0	0
FOXL2	forkhead box L2(FOXL2)	-2.65129	0.440575	0	0
SEPTIN5	septin 5(SEPTIN5)	-2.64659	0.447212	0	0
PTPRR	protein tyrosine phosphatase receptor type R(PTPRR)	-2.64343	0.378765	0	0
CDX2	caudal type homeobox 2(CDX2)	-2.64241	0.468889	0	0
FHL2	four and a half LIM domains 2(FHL2)	-2.641	0.430307	0	0
ATL1	atlastin GTPase 1(ATL1)	-2.63965	0.421	0	0
LOX	lysyl oxidase(LOX)	-2.63577	0.491265	0	0
KSR1	kinase suppressor of ras 1(KSR1)	-2.63445	0.555773	0	0

ACSBG1	acyl-CoA synthetase bubblegum family member 1(ACSBG1)	-2.63205	0.415088	0	0
ATRNL1	attractin like 1(ATRNL1)	-2.62953	0.35638	0	0
SFRP4	secreted frizzled related protein 4(SFRP4)	-2.6204	0.415976	0	0
PAX7	paired box 7(PAX7)	-2.61457	0.346971	0	0
NEDD4	NEDD4 E3 ubiquitin protein ligase(NEDD4)	-2.61456	0.511567	0	0
CCND1	cyclin D1(CCND1)	-2.61412	0.47735	0	0
STYK1	serine/threonine/tyrosine kinase 1(STYK1)	-2.61363	0.492223	0	0
ERG	ETS transcription factor ERG(ERG)	-2.60842	0.498374	0	0
ACKR3	atypical chemokine receptor 3(ACKR3)	-2.60795	0.450183	0	0
KLK2	kallikrein related peptidase 2(KLK2)	-2.60635	0.442772	0	0
SLC34A2	solute carrier family 34 member 2(SLC34A2)	-2.60634	0.444816	0	0
FSTL3	folliculin like 3(FSTL3)	-2.5997	0.493531	0	0
FLT3LG	fms related receptor tyrosine kinase 3 ligand(FLT3LG)	-2.59474	0.451677	0	0
FLT3	fms related receptor tyrosine kinase 3(FLT3)	-2.58547	0.449125	0	0
GDF6	growth differentiation factor 6(GDF6)	-2.5844	0.487412	0	0
ERBB2	erb-b2 receptor tyrosine kinase 2(ERBB2)	-2.57734	0.510539	0	0
DKK1	dickkopf WNT signaling pathway inhibitor 1(DKK1)	-2.57724	0.363746	0	0
NOS3	nitric oxide synthase 3(NOS3)	-2.5712	0.473651	0	0
CYP1B1	cytochrome P450 family 1 subfamily B member 1(CYP1B1)	-2.57002	0.508732	0	0
NUTM2A	NUT family member 2A(NUTM2A)	-2.56825	0.499021	0	0
WIF1	WNT inhibitory factor 1(WIF1)	-2.56799	0.446075	0	0
TCTA	T cell leukemia translocation altered(TCTA)	-2.56539	0.515598	0	0
PTCRA	pre T cell antigen receptor alpha(PTCRA)	-2.56495	0.373162	0	0
IL3	interleukin 3(IL3)	-2.56268	0.42606	0	0
FGF4	fibroblast growth factor 4(FGF4)	-2.55483	0.451995	0	0
SCN8A	sodium voltage-gated channel alpha subunit 8(SCN8A)	-2.55352	0.430268	0	0
PIK3R2	phosphoinositide-3-kinase regulatory subunit 2(PIK3R2)	-2.54735	0.583198	0	0
LMO1	LIM domain only 1(LMO1)	-2.5459	0.456583	0	0
PRG2	proteoglycan 2, pro eosinophil major basic protein(PRG2)	-2.54377	0.355313	0	0
MET	MET proto-oncogene, receptor tyrosine kinase(MET)	-2.54367	0.423906	0	0
ACER1	alkaline ceramidase 1(ACER1)	-2.54317	0.444069	0	0
IL1R1	interleukin 1 receptor type 1(IL1R1)	-2.543	0.58091	0	0
HOXD13	homeobox D13(HOXD13)	-2.53684	0.405978	0	0
KANK1	KN motif and ankyrin repeat domains 1(KANK1)	-2.53554	0.441457	0	0
CDKN2A	cyclin dependent kinase inhibitor 2A(CDKN2A)	-2.53517	0.444032	0	0
LRP1B	LDL receptor related protein 1B(LRP1B)	-2.52619	0.415575	0	0
GNA12	G protein subunit alpha 12(GNA12)	-2.51838	0.540972	0	0
S1PR2	sphingosine-1-phosphate receptor 2(S1PR2)	-2.50542	0.493711	0	0
TSHR	thyroid stimulating hormone receptor(TSHR)	-2.50503	0.379718	0	0
PDGFRB	platelet derived growth factor receptor beta(PDGFRB)	-2.50375	0.523519	0	0
CACNA2D3	calcium voltage-gated channel auxiliary subunit alpha2delta 3(CACNA2D3)	-2.50344	0.41488	0	0
TLX1	T cell leukemia homeobox 1(TLX1)	-2.50261	0.426205	0	0
MMP7	matrix metalloproteinase 7(MMP7)	-2.49905	0.363601	0	0
MYCN	MYCN proto-oncogene, bHLH transcription factor(MYCN)	-2.49178	0.44424	0	0
HOXC13	homeobox C13(HOXC13)	-2.48277	0.400847	0	0
PPFIBP1	PPFIA binding protein 1(PPFIBP1)	-2.48193	0.536768	0	0

LNP1	leukemia NUP98 fusion partner 1(LNP1)	-2.47785	0.445934	0	0
TIAM1	TIAM Rac1 associated GEF 1(TIAM1)	-2.46817	0.529802	0	0
TAF5	TAF5 (TAF Chemokine Like Family Member 5)	-2.46488	0.554268	0	0
LAMA5	laminin subunit alpha 5(LAMA5)	-2.45984	0.571107	0	0
TNFRSF10D	TNF receptor superfamily member 10d(TNFRSF10D)	-2.43889	0.521112	0	0
FOXO3	forkhead box O3(FOXO3)	-2.43847	0.556582	0	0
FOSL1	FOS like 1, AP-1 transcription factor subunit(FOSL1)	-2.43707	0.443791	0	0
MPL	MPL proto-oncogene, thrombopoietin receptor(MPL)	-2.43578	0.485699	0	0
ALDH2	aldehyde dehydrogenase 2 family member(ALDH2)	-2.4348	0.503669	0	0
CCN6	CCN6 (Cellular Communication Network Factor 6)	-2.43162	0.333527	0	0
FOS	Fos proto-oncogene, AP-1 transcription factor subunit(FOS)	-2.42957	0.428488	0	0
SOX11	SRY-box transcription factor 11(SOX11)	-2.42762	0.551311	0	0
SLC1A2	solute carrier family 1 member 2(SLC1A2)	-2.42622	0.546939	0	0
ROBO2	roundabout guidance receptor 2(ROBO2)	-2.42428	0.421952	0	0
HOXC11	homeobox C11(HOXC11)	-2.42345	0.40742	0	0
PLPP3	PLPP3 (Phospholipid Phosphatase 3)	-2.42314	0.549243	0	0
FUT1	fucosyltransferase 1 (H blood group)(FUT1)	-2.4048	0.456233	0	0
WNT5B	Wnt family member 5B(WNT5B)	-2.40474	0.417559	0	0
CRADD	CASP2 and RIPK1 domain containing adaptor with death domain(CRADD)	-2.404	0.502271	0	0
IL15	interleukin 15(IL15)	-2.40325	0.510215	0	0
IL13	interleukin 13(IL13)	-2.40307	0.461483	0	0
CDKL5	cyclin dependent kinase like 5(CDKL5)	-2.39563	0.464815	0	0
KDR	kinase insert domain receptor(KDR)	-2.39247	0.583356	0	0
FGF23	fibroblast growth factor 23(FGF23)	-2.38874	0.501198	0	0
ZNF331	zinc finger protein 331(ZNF331)	-2.38559	0.530859	0	0
EGF	epidermal growth factor(EGF)	-2.38385	0.431464	0	0
LMO2	LIM domain only 2(LMO2)	-2.37769	0.455261	0	0
AUTS2	activator of transcription and developmental regulator AUTS2(AUTS2)	-2.37624	0.452059	0	0
FLCN	folliculin(FLCN)	-2.37592	0.580182	0	0
LINC01565	LINC01565 (Long Intergenic Non-Protein Coding RNA 1565)	-2.36948	0.484225	0	0
IL1B	interleukin 1 beta(IL1B)	-2.3694	0.435804	0	0
AGR3	anterior gradient 3, protein disulphide isomerase family member(AGR3)	-2.36665	0.494603	0	0
PPP1R13B	protein phosphatase 1 regulatory subunit 13B(PPP1R13B)	-2.36183	0.585897	0	0
DCN	decorin(DCN)	-2.35634	0.476357	0	0
NKX2-1	NK2 homeobox 1(NKX2-1)	-2.35591	0.454607	0	0
HECW1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1(HECW1)	-2.35562	0.443745	0	0
LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase(LFNG)	-2.35472	0.507491	0	0
PTCH1	patched 1(PTCH1)	-2.35216	0.554845	0	0
SOX10	SRY-box transcription factor 10(SOX10)	-2.35173	0.569884	0	0
PRRX1	paired related homeobox 1(PRRX1)	-2.35085	0.527948	0	0
DMRTA2	DMRT like family A2(DMRTA2)	-2.34995	0.516693	0	0
EPO	erythropoietin(EPO)	-2.34744	0.502693	0	0
SETBP1	SET binding protein 1(SETBP1)	-2.34494	0.580754	0	0
WNT4	Wnt family member 4(WNT4)	-2.34182	0.521589	0	0
CSF3	colony stimulating factor 3(CSF3)	-2.33883	0.481756	0	0

PDGFD	platelet derived growth factor D(PDGFD)	-2.33487	0.522788	0	0
FOXO4	forkhead box O4(FOXO4)	-2.32606	0.548476	0	0
PLCB1	phospholipase C beta 1(PLCB1)	-2.31302	0.555627	0	0
CDKN1A	cyclin dependent kinase inhibitor 1A(CDKN1A)	-2.31038	0.55362	0	0
WNT10B	Wnt family member 10B(WNT10B)	-2.30541	0.495753	0	0
EGR2	early growth response 2(EGR2)	-2.30497	0.530179	0	0
ASTN2	astrotactin 2(ASTN2)	-2.30335	0.503487	0	0
GFAP	glial fibrillary acidic protein(GFAP)	-2.29355	0.457946	0	0
ECT2L	epithelial cell transforming 2 like(ECT2L)	-2.28294	0.495783	0	0
PCNA-AS1	PCNA-AS1 (PCNA Antisense RNA 1)	-2.26961	0.365529	0	0
EXT1	exostosin glycosyltransferase 1(EXT1)	-2.26578	0.624032	0	0
FGFR1	fibroblast growth factor receptor 1(FGFR1)	-2.26365	0.550718	0	0
NAB2	NGFI-A binding protein 2(NAB2)	-2.26006	0.523173	0	0
NR6A1	nuclear receptor subfamily 6 group A member 1(NR6A1)	-2.25856	0.49958	0	0
FGF19	fibroblast growth factor 19(FGF19)	-2.25815	0.533537	0	0
CAMK2A	calcium/calmodulin dependent protein kinase II alpha(CAMK2A)	-2.25627	0.539495	0	0
FGF3	fibroblast growth factor 3(FGF3)	-2.25419	0.530683	0	0
IRS1	insulin receptor substrate 1(IRS1)	-2.25152	0.581165	0	0
MATK	megakaryocyte-associated tyrosine kinase(MATK)	-2.24783	0.509591	0	0
FGF6	fibroblast growth factor 6(FGF6)	-2.24561	0.511898	0	0
CEBPE	CCAAT enhancer binding protein epsilon(CEBPE)	-2.24035	0.444728	0	0
ALDH1A1	aldehyde dehydrogenase 1 family member A1(ALDH1A1)	-2.23904	0.521651	0	0
EXT2	exostosin glycosyltransferase 2(EXT2)	-2.23119	0.642868	0	0
DNMT3A	DNA methyltransferase 3 alpha(DNMT3A)	-2.23073	0.597187	0	0
FZD10	frizzled class receptor 10(FZD10)	-2.22399	0.468977	0	0
SSX1	SSX family member 1(SSX1)	-2.22298	0.519795	0	0
DKK2	dickkopf WNT signaling pathway inhibitor 2(DKK2)	-2.22003	0.487053	0	0
AMH	anti-Mullerian hormone(AMH)	-2.21076	0.531373	0	0
FCGBP	Fc gamma binding protein(FCGBP)	-2.21061	0.470213	0	0
TBX15	T-box transcription factor 15(TBX15)	-2.20484	0.445586	0	0
WNT6	Wnt family member 6(WNT6)	-2.19563	0.521673	0	0
CDX1	caudal type homeobox 1(CDX1)	-2.19368	0.563058	0	0
LHFPL6	LHFPL6 (LHFPL Tetraspan Subfamily Member 6)	-2.19092	0.540833	0	0
SORT1	sortilin 1(SORT1)	-2.1888	0.520977	0	0
CDKN2B	cyclin dependent kinase inhibitor 2B(CDKN2B)	-2.18683	0.6107	0	0
SULF1	sulfatase 1(SULF1)	-2.17837	0.566829	0	0
ETV4	ETS variant transcription factor 4(ETV4)	-2.17235	0.506513	0	0
ATP8A2	ATPase phospholipid transporting 8A2(ATP8A2)	-2.17087	0.446875	0	0
NOD1	nucleotide binding oligomerization domain containing 1(NOD1)	-2.16785	0.613697	0	0
NKX2-5	NK2 homeobox 5(NKX2-5)	-2.16735	0.423001	0	0
INPP4B	inositol polyphosphate-4-phosphatase type II B(INPP4B)	-2.16619	0.583764	0	0
IL2	interleukin 2(IL2)	-2.16523	0.47229	0	0
PPP1R13L	protein phosphatase 1 regulatory subunit 13 like(PPP1R13L)	-2.16085	0.573614	0	0
NFIB	nuclear factor I B(NFIB)	-2.15966	0.589648	0	0
TUSC3	tumor suppressor candidate 3(TUSC3)	-2.15862	0.54479	0	0
DUSP9	dual specificity phosphatase 9(DUSP9)	-2.15803	0.558077	0	0

ATF3	activating transcription factor 3(ATF3)	-2.1545	0.49854	0	0
SRC	SRC proto-oncogene, non-receptor tyrosine kinase(SRC)	-2.15433	0.592151	0	0
WNT8B	Wnt family member 8B(WNT8B)	-2.15166	0.493726	0	0
TCF7L2	transcription factor 7 like 2(TCF7L2)	-2.1515	0.581304	0	0
MAFB	MAF bZIP transcription factor B(MAFB)	-2.12799	0.589844	0	0
COL6A3	collagen type VI alpha 3 chain(COL6A3)	-2.12308	0.610004	0	0
FGF9	fibroblast growth factor 9(FGF9)	-2.12185	0.52429	0	0
C10orf55	chromosome 10 putative open reading frame 55(C10orf55)	-2.12061	0.59369	0	0
HMG2	high mobility group AT-hook 2(HMG2)	-2.11494	0.493604	0	0
DDIT3	DNA damage inducible transcript 3(DDIT3)	-2.10535	0.549167	0	0
TLX3	T cell leukemia homeobox 3(TLX3)	-2.10306	0.551199	0	0
ZFTA	ZFTA (Zinc Finger Translocation Associated)	-2.0992	0.60921	0	0
FGF8	fibroblast growth factor 8(FGF8)	-2.09418	0.492634	0	0
RTL8B	RTL8B (Retrotransposon Gag Like 8B)	-2.09374	0.607332	0	0
HOXD11	homeobox D11(HOXD11)	-2.08658	0.487511	0	0
IL7R	interleukin 7 receptor(IL7R)	-2.06814	0.567283	0	0
PRF1	perforin 1(PRF1)	-2.06437	0.572166	0	0
DACH2	dachshund family transcription factor 2(DACH2)	-2.06253	0.519233	0	0
AHRR	aryl hydrocarbon receptor repressor(AHRR)	-2.05392	0.599185	0	0
DLL3	delta like canonical Notch ligand 3(DLL3)	-2.04768	0.474579	0	0
CSF3R	colony stimulating factor 3 receptor(CSF3R)	-2.04603	0.590763	0	0
PLAG1	PLAG1 zinc finger(PLAG1)	-2.04037	0.511107	0	0
USP6	ubiquitin specific peptidase 6(USP6)	-2.03922	0.478689	0	0
FCRL4	Fc receptor like 4(FCRL4)	-2.03504	0.479526	0	0
HOXA9	homeobox A9(HOXA9)	-2.03215	0.510128	0	0
PRKCA	protein kinase C alpha(PRKCA)	-2.03149	0.604067	0	0
FGF2	fibroblast growth factor 2(FGF2)	-2.02971	0.599784	0	0
CD28	CD28 molecule(CD28)	-2.02311	0.587093	0	0
PRRX2	paired related homeobox 2(PRRX2)	-2.01332	0.58599	0	0
NR4A3	nuclear receptor subfamily 4 group A member 3(NR4A3)	-2.01116	0.529	0	0
CHST11	carbohydrate sulfotransferase 11(CHST11)	-2.01017	0.631096	0	0
CACNA1F	calcium voltage-gated channel subunit alpha1 F(CACNA1F)	-2.00118	0.610572	0	0
TLR4	toll like receptor 4(TLR4)	-1.99878	0.654187	0	0
MYBL1	MYB proto-oncogene like 1(MYBL1)	-1.99251	0.483045	0	0
APOD	apolipoprotein D(APOD)	-1.98821	0.46729	0	0
AMER1	APC membrane recruitment protein 1(AMER1)	-1.983	0.585565	0	0
KLK7	kallikrein related peptidase 7(KLK7)	-1.98119	0.530907	0	0
VEGFC	vascular endothelial growth factor C(VEGFC)	-1.97583	0.573889	0	0
ZIC2	Zic family member 2(ZIC2)	-1.97561	0.578417	0	0
CEBPD	CCAAT enhancer binding protein delta(CEBPD)	-1.96989	0.575374	0	0
FZD6	frizzled class receptor 6(FZD6)	-1.96776	0.579004	0	0
FGF14	fibroblast growth factor 14(FGF14)	-1.96735	0.539532	0	0
MNX1	motor neuron and pancreas homeobox 1(MNX1)	-1.95844	0.560895	0	0
NOTCH2	notch receptor 2(NOTCH2)	-1.95471	0.693716	0	0
CCT6B	chaperonin containing TCP1 subunit 6B(CCT6B)	-1.9452	0.521849	0	0
RASGEF1A	RasGEF domain family member 1A(RASGEF1A)	-1.94462	0.586695	0	0

ATP1B4	ATPase Na+/K+ transporting family member beta 4(ATP1B4)	-1.94169	0.530396	0	0
FASLG	Fas ligand(FASLG)	-1.94065	0.539192	0	0
FEV	FEV transcription factor, ETS family member(FEV)	-1.94049	0.638987	0	0
TNF	tumor necrosis factor(TNF)	-1.93876	0.561012	0	0
TMT1B	TMT1B (Thiol Methyltransferase 1B)	-1.93794	0.493972	0	0
NUTM2B	NUT family member 2B(NUTM2B)	-1.91855	0.59461	0	0
PIMREG	PIMREG (PICALM Interacting Mitotic Regulator)	-1.91025	0.558851	0	0
TIRAP	TIR domain containing adaptor protein(TIRAP)	-1.89718	0.573808	0	0
PDGFA	platelet derived growth factor subunit A(PDGFA)	-1.8966	0.555005	0	0
BCL9	BCL9 transcription coactivator(BCL9)	-1.89649	0.678542	0	0
ERCC4	ERCC excision repair 4, endonuclease catalytic subunit(ERCC4)	-1.88518	0.639989	0	0
FZD3	frizzled class receptor 3(FZD3)	-1.88439	0.592698	0	0
KIAA0232	KIAA0232(KIAA0232)	-1.8832	0.700096	0	0
ZNF444	zinc finger protein 444(ZNF444)	-1.88298	0.566285	0	0
ACE	angiotensin I converting enzyme(ACE)	-1.88271	0.607453	0	0
STAT4	signal transducer and activator of transcription 4(STAT4)	-1.87882	0.609328	0	0
PDGFB	platelet derived growth factor subunit B(PDGFB)	-1.87609	0.621043	0	0
PAK6	p21 (RAC1) activated kinase 6(PAK6)	-1.85509	0.564959	0	0
ITK	IL2 inducible T cell kinase(ITK)	-1.85046	0.6234	0	0.02001
GRIN2B	glutamate ionotropic receptor NMDA type subunit 2B(GRIN2B)	-1.84938	0.490689	0	0.037641
ABL2	ABL proto-oncogene 2, non-receptor tyrosine kinase(ABL2)	-1.84617	0.671105	0	0.090884
LRRC37B	leucine rich repeat containing 37B(LRRC37B)	-1.8426	0.659513	0	0.150715
INPP5A	inositol polyphosphate-5-phosphatase A(INPP5A)	-1.8401	0.593394	0	0.193007
TNC	tenascin C(TNC)	-1.83924	0.659385	0	0.207738
HES5	hes family bHLH transcription factor 5(HES5)	-1.83703	0.670276	0	0.24565
PER1	period circadian regulator 1(PER1)	-1.81772	0.64923	0	0.591158
HSPA1A	heat shock protein family A (Hsp70) member 1A(HSPA1A)	-1.81761	0.626353	0	0.593363
DLL4	delta like canonical Notch ligand 4(DLL4)	-1.80607	0.595996	0	0.811962
DPYD	dihydropyrimidine dehydrogenase(DPYD)	-1.80513	0.664669	0	0.830278
HOXA13	homeobox A13(HOXA13)	-1.78852	0.536669	0	1.162397
CHL1	cell adhesion molecule L1 like(CHL1)	-1.77456	0.553043	0	1.457143
TLL2	tolloid like 2(TLL2)	-1.76639	0.660688	0	1.636067
SH2D5	SH2 domain containing 5(SH2D5)	-1.76193	0.658602	0	1.73592
OLIG1	oligodendrocyte transcription factor 1(OLIG1)	-1.75387	0.675056	0	1.920312
DGKI	diacylglycerol kinase iota(DGKI)	-1.74853	0.588613	0	2.045182
RAC3	Rac family small GTPase 3(RAC3)	-1.7481	0.549802	0	2.055321
BHLHE22	basic helix-loop-helix family member e22(BHLHE22)	-1.73224	0.609273	0.046128	2.439561
EGR1	early growth response 1(EGR1)	-1.7276	0.606515	0.046128	2.555726
ID1	inhibitor of DNA binding 1(ID1)	-1.72663	0.587428	0.046128	2.580175
CILK1	CILK1 (Ciliogenesis Associated Kinase 1)	-1.72186	0.674719	0.046128	2.701797
FANCE	FA complementation group E(FANCE)	-1.69757	0.612533	0.046128	3.349458
BCORL1	BCL6 corepressor like 1(BCORL1)	-1.68482	0.689382	0.046128	3.708931
TNFRSF6B	TNF receptor superfamily member 6b(TNFRSF6B)	-1.67925	0.614369	0.046128	3.870206
ADM	adrenomedullin(ADM)	-1.67614	0.591311	0.046128	3.961431
CANT1	calcium activated nucleotidase 1(CANT1)	-1.6608	0.702461	0.046128	4.423608
ITPKA	inositol-trisphosphate 3-kinase A(ITPKA)	-1.65655	0.631384	0.046128	4.555268

HDAC5	histone deacetylase 5(HDAC5)	-1.64968	0.716633	0.046128	4.771751
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Suppl. Table S9.2 Significantly enriched terms and pathways analyzed by DAVID functional annotation tool for 213 upregulated in clusters 3 and 4 (corresponding to the 1st enrichment plot in Figure 3)

Category	Term	Count	P Value	Genes	Fold Enrichment	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0006338~chromatin remodeling GO:0050853~B cell receptor signaling pathway	23	1.61E-11	RB1, SS18, NPM1, HDAC2, SMARCB1, KDM1A, PRKCB, PRMT1, PRKDC, HDAC1, NCOA3, SMARCA5, HUUWE1, DEK, ARID1A, SFPQ, IRF4, CHEK1, CDK1, ATM, TOP1, MAP3K7, SF3B1	6.301291	3.20E-08	3.11E-08
GOTERM_BP_DIRECT	GO:0051301~cell division	11	8.06E-10	LYN, CD79B, CD79A, SYK, PRKCB, BTK, PLCG2, MAPK1, PTPN6, GRB2, NFKB1	16.94567	8.03E-07	7.80E-07
GOTERM_BP_DIRECT	GO:0035556~intracellular signal transduction	20	3.06E-08	RB1, UBE2C, CLTA, BUB1B, SMC3, SMC1A, NDC80, CCNA2, WEE1, CDK7, STAG2, CCND2, RAD21, CCNG1, TPR, CNTRL, ZNF207, CDK1, MAPRE1, MAD2L1, YWHAE, SS18, DDX3X, SYK, TFRC, PRKCB, PRKCD, PTPN11, RPS6KA3, TCL1A, MELK, PRKAR1A, AKT2, INPP5D, RPS6KA1, CHEK1, BTK, PLCG2, MAPK1, PTPN6, ARHGEF7	4.881633	1.87E-05	1.82E-05
GOTERM_BP_DIRECT	GO:000122~negative regulation of transcription by RNA polymerase II	21	3.76E-08	RB1, DDY5, DNMT1, HDAC2, PHB1, PCNA, KDM1A, HDAC1, PHF6, CUX1, TPR, VHL, SUZ12, EED, BCL11A, PAX5, NFKB1, FOXF1, SFPQ, TBL1XR1, NACA, SARNP, CNOT2, HNRNPA2B1, MDM2, IRF8, MDM4, CALR, EZR, PTPN2, EZH2	4.568056	1.87E-05	1.82E-05
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription by RNA polymerase II	31	1.13E-07	RB1, TOP2A, HDAC2, SMARCB1, DDX3X, KDM1A, PRKDC, HDAC1, ETS1, IKZF3, RPS6KA3, PPP3R1, RPS6KA1, SF3B1, GTF2I, SS18, NPM1, XRCC6, BCL11A, NCOA3, SMARCA5, HMGA1, PAX5, DEK, NFKB1, SFPQ, CDK7, PKM, TFDP1, IRF4, TBL1XR1, NACA, POU2AF1, IRF8, TCEA1, ATM	3.025041	4.44E-05	4.31E-05
GOTERM_BP_DIRECT	GO:0006974~DNA damage response	36	1.34E-07	LYN, TOP2A, FH, MRE11, PRMT1, FANCL, PRKDC, PRKCD, SMARCA5, CHD2, FOXF1, RAD50, ERCC2, CHEK1, CDK1, MAPK1, ATM	2.693449	4.44E-05	4.31E-05
GOTERM_BP_DIRECT	GO:0030183~B cell differentiation	17	1.88E-07	CD79B, TOP2B, CD79A, SYK, PLCG2, PAX5, IKZF3, CARD11, PTPN2, EZH2	5.20363	5.36E-05	5.21E-05
GOTERM_BP_DIRECT	GO:0007094~mitotic spindle assembly checkpoint signaling	10	4.75E-07	CD79B, TOP2B, CD79A, SYK, PLCG2, PAX5, IKZF3, CARD11, PTPN2, EZH2	10.44127	1.18E-04	1.15E-04
GOTERM_BP_DIRECT	GO:0006281~DNA repair	7	7.75E-07	TPR, ZNF207, BUB1B, TTK, ATM, NDC80, MAD2L1	21.21935	1.72E-04	1.67E-04
GOTERM_BP_DIRECT	GO:0007049~cell cycle	15	1.04E-06	FANCI, NPM1, FH, MRE11, FANCL, NONO, SMARCA5, FANCA, SMC3, SMC1A, CDK7, RAD50, POLD1, CHEK1, CDK1	5.279294	2.08E-04	2.02E-04
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	16	2.03E-06	RB1, FANCI, SMARCB1, PRKCD, CLTA, IKZF1, MKI67, RPS6KA3, CDK7, TFDP1, RPS6KA1, CHEK1, CNTRL, MDM2, MAPK1, MDM4	4.640564	3.45E-04	3.35E-04
GOTERM_BP_DIRECT	GO:0016310~phosphorylation	20	2.08E-06	CD74, NPM1, HDAC2, MRE11, DDX3X, HSP90AB1, BCL2A1, TFRC, PRKDC, HDAC1, NFKB1, RPS6KA3, CCND2, CCNG1, RPS6KA1, MDM2, CDK1, MDM4, VHL, MAD2L1	3.70696	3.45E-04	3.35E-04
GOTERM_BP_DIRECT	GO:0018105~peptidyl-serine phosphorylation	22	4.02E-06	LYN, GIT2, SYK, PRKCB, PRKDC, PRKCD, BUB1B, TTK, RPS6KA3, WEE1, CDK7, PKM, MELK, PRKAR1A, AKT2, RPS6KA1, CHEK1, BTK, CDK1, MAPK1, TOP1, MAP3K7	3.26599	6.16E-04	5.99E-04
GOTERM_BP_DIRECT	GO:0045892~negative regulation of DNA-templated transcription	11	6.93E-06	RPS6KA3, PRKDC, PRKCB, AKT2, RPS6KA1, PRKCD, CDK1, MAPK1, TTK, ATM, TOP1	6.583985	9.86E-04	9.58E-04
GOTERM_BP_DIRECT	GO:0007059~chromosome segregation	20	1.19E-05	RB1, XRCC6, HDAC2, PHB1, SET, KDM1A, EED, HDAC1, NONO, HMGA1, IKZF1, CBF2A3, FOXF1, SFPQ, MDM2, SRSF2, MDM4, CALR, PFDN5, EZH2	3.27998	0.001578	0.001533
GOTERM_BP_DIRECT	GO:0048511~rhythmic process	9	1.49E-05	TOP2A, CENPU, DDX3X, STAG2, RAD21, ERCC2, TTK, TOP1, NDC80	8.132143	0.001858	0.001806
GOTERM_BP_DIRECT	GO:0034087~establishment of mitotic sister chromatid cohesion	8	2.05E-05	TOP2A, USP7, SFPQ, DDX5, PRKDC, CDK1, TOP1, EZH2	9.516094	0.002406	0.002339
GOTERM_BP_DIRECT	GO:0031507~heterochromatin formation	4	3.97E-05	STAG2, RAD21, SMC1A, SMC3	53.69796	0.004394	0.00427
GOTERM_BP_DIRECT	GO:0050821~protein stabilization	7	4.93E-05	RB1, HDAC2, EED, HDAC1, SMARCA5, H2AC17, EZH2	10.60968	0.005063	0.004921
GOTERM_BP_DIRECT	GO:0042752~regulation of circadian rhythm	12	5.09E-05	CD74, USP7, HSP90AA1, PHB1, CDK7, HSP90AB1, PRKCD, PTEN, ZNF207, MDM4, VHL, CALR	4.718231	0.005063	0.004921
GOTERM_BP_DIRECT	GO:0070301~cellular response to hydrogen peroxide	7	7.65E-05	TOP2A, USP7, SFPQ, PRKDC, NONO, CDK1, EZH2	9.81791	0.007258	0.007053
GOTERM_BP_DIRECT	GO:0007062~sister chromatid cohesion	7	8.32E-05	TOP2B, HDAC2, PCNA, PRKCD, MDM2, CDK1, EZH2	9.673529	0.007532	0.00732
GOTERM_BP_DIRECT	GO:0038095~Fc-epsilon receptor signaling pathway	5	1.10E-04	MRE11, STAG2, RAD21, SMC1A, SMC3	19.57738	0.009126	0.008869
GOTERM_BP_DIRECT	GO:1902459~positive regulation of stem cell population maintenance	5	1.10E-04	LYN, SYK, BTK, PLCG2, MAP3K7	19.57738	0.009126	0.008869
GOTERM_BP_DIRECT	GO:0090307~mitotic spindle assembly	6	1.36E-04	SS18, HDAC2, SMARCB1, HDAC1, NCOA3, ARID1A	11.99635	0.010807	0.010503
GOTERM_BP_DIRECT	GO:0006468~protein phosphorylation	6	1.50E-04	STAG2, ZNF207, SMC1A, SMC3, RHOA, KPNB1	11.74643	0.011501	0.011177
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	14	1.97E-04	LYN, SYK, PRKCB, PRKDC, PRKCD, WEE1, CDK7, MELK, RPS6KA1, CHEK1, BTK, CDK1, MAPK1, ATM	3.498936	0.014526	0.014118
GOTERM_BP_DIRECT	GO:0006366~transcription by RNA polymerase II	18	2.06E-04	CDK1, PRKCB, PRKCD, PTEN, CXCR4, BUB1B, NFKB1, MELK, RABEP1, INPP5D, RAD21, ERCC2, CHEK1, MDM2, CDK1, BAX, MAPK1, MAP3K7	2.852421	0.014544	0.014135
GOTERM_BP_DIRECT	GO:0018107~peptidyl-threonine phosphorylation	11	2.12E-04	RB1, CDK7, TFDP1, ERCC2, TCEA1, PAX5, DEK, POLR2H, ETS1, NFKB1, GTF2I	4.398663	0.014544	0.014135
GOTERM_BP_DIRECT		6	2.87E-04	PRKDC, CAD, CHEK1, PRKCD, CDK1, MAPK1	10.25143	0.019071	0.018535

GOTERM_BP_DIRECT	GO:0008380~RNA splicing	10	3.01E-04	PTBP1, SFPO, MBNL1, FUS, U2AF2, PRMT1, NONO, SRSF2, U2AF1, SF3B1	4.675195	0.019125	0.018587
GOTERM_BP_DIRECT	GO:0045740~positive regulation of DNA replication	5	3.07E-04	CDC42, WEE1, PCNA, SMARCA5, CDK1	15.15668	0.019125	0.018587
GOTERM_BP_DIRECT	GO:0034644~cellular response to UV	6	3.40E-04	NPM1, PCNA, KDM1A, POLD1, PRKCD, BAX	9.891729	0.020514	0.019937
GOTERM_BP_DIRECT	GO:0034605~cellular response to heat	6	4.32E-04	LYN, YWHAE, HSP90AA1, HDAC2, HSP90AB1, TPR	9.397143	0.024441	0.023754
GOTERM_BP_DIRECT	GO:0045597~positive regulation of cell differentiation	6	4.32E-04	RPS6KA3, SMARCB1, HSP90AB1, RPS6KA1, VHL, ARID1A	9.397143	0.024441	0.023754
GOTERM_BP_DIRECT	GO:0002218~activation of innate immune response	5	4.42E-04	XRCC6, SFPO, HSP90AA1, PRKDC, NONO	13.81933	0.024441	0.023754
GOTERM_BP_DIRECT	GO:0006406~mRNA export from nucleus	6	5.03E-04	NUP107, XPO1, SARNP, TPR, HNRNPA2B1, SRSF3	9.094009	0.027092	0.02633
GOTERM_BP_DIRECT	GO:0031100~animal organ regeneration	5	6.14E-04	CCNA2, ATIC, CAD, CDK1, LCP1	12.69884	0.032168	0.031263
GOTERM_BP_DIRECT	GO:0034089~establishment of meiotic sister chromatid cohesion	3	6.60E-04	RAD21, SMC1A, SMC3	70.47857	0.033718	0.03277
GOTERM_BP_DIRECT	GO:0007095~mitotic G2 DNA damage checkpoint signaling	5	6.81E-04	MRE11, CCNG1, CHEK1, CDK1, ATM	12.36466	0.033874	0.032921
GOTERM_BP_DIRECT	GO:0042981~regulation of apoptotic process	10	7.06E-04	HSP90AA1, PHB1, BAX, PTPN6, ATM, CALR, ETS1, IKZF3, FBXO11, CARD11	4.158028	0.03428	0.033316
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell population proliferation	14	7.65E-04	LYN, NPM1, PHB1, SMARCB1, BTG1, PTEN, HMGA1, ETS1, CBFA2T3, ABI1, MDM4, PTPN6, VHL, PTPN2	3.031336	0.036285	0.035264
GOTERM_BP_DIRECT	GO:0006357~regulation of transcription by RNA polymerase II	32	8.14E-04	RB1, DDX5, SMARCB1, KDM1A, HDAC1, IKZF1, CHD2, ETS1, IKZF3, CUX1, RAD21, MAPK1, SS18, PRKCB, BCL11A, FUS, SMARCA5, ELP2, PAX5, DEK, ARID1A, RHOA, NFKB1, FOXP1, TFDP1, PRKAR1A, IRF4, TBL1XR1, CNOT2, ERCC2, CDK1, IRF8	1.872407	0.037671	0.036611
GOTERM_BP_DIRECT	GO:0030889~negative regulation of B cell proliferation	4	8.50E-04	LYN, INPP5D, BTK, ATM	20.88254	0.038448	0.037367
GOTERM_BP_DIRECT	GO:0034504~protein localization to nucleus	5	9.11E-04	YWHAE, XPO1, RAP1GDS1, MDM2, CALR	11.45993	0.040299	0.039166
GOTERM_BP_DIRECT	GO:0008286~insulin receptor signaling pathway	6	9.38E-04	PTPRA, AKT2, GAB1, MAPK1, GRB2, PTPN2	7.941247	0.040603	0.039461
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell population proliferation	15	0.001041	LYN, SUZ12, SS18, NPM1, HDAC2, PRMT1, HDAC1, PTEN, TTK, CCND2, MDM2, PTPN6, CALR, CEP43, EZH2	2.785714	0.044083	0.042843
GOTERM_BP_DIRECT	GO:0060789~hair follicle placode formation	3	0.001093	HDAC2, HDAC1, GNAS	56.38286	0.044083	0.042843
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	15	0.001105	CD74, DNMT1, PHB1, DDX3X, TFRC, BCL11A, HDAC1, ETS1, MDM2, CDK1, PLCG2, KRAS, ATM, CALR, EZR	2.769296	0.044083	0.042843
GOTERM_BP_DIRECT	GO:0006397~mRNA processing	10	0.001107	PTBP1, SFPO, MBNL1, CPSF6, FIP1L1, U2AF2, NONO, HNRNPA2B1, SRSF2, U2AF1	3.899229	0.044083	0.042843
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	123	4.57E-36	RB1, PHB1, MRE11, SMARCB1, KDM1A, IKZF1, SMC3, MKI67, IKZF3, ETS1, RPS6KA3, TCL1A, CCND2, AKT2, RPS6KA1, CHEK1, ZNF207, GTF2I, MBNL1, USP7, PRKCB, PRKCD, FBXO11, FOXF1, EWSR1, TBL1XR1, FANCD2, SARNP, SRSF2, BTK, KPNB1, DDX6, DDX5, DNMT1, SET, PRKDC, PPP4C, RAD21, TPR, LPXN, H3C2, LYN, XRCC6, CPSF6, UBE2C, FANCL, BCL11A, FUS, HSPA4, NONO, SMARCA5, HMGA1, FANCA, NDC80, NFKB1, CDK7, STAG2, NACA, CNOT2, MDM2, CDK1, GNAS, GRB2, MDM4, ATM, CALR, EZH2, PICALM, YWHAE, CEP57, TOP2A, TOP2B, DDX3X, BTG1, HSP90AB1, PTEN, AFF3, CHD2, PHF6, PTBP1, XPO1, ZC3H7A, ZC3H7B, CNTRL, OFD1, SS18, HSP90AA1, SYK, EED, PRMT1, NCOA3, CAD, PAX5, SMC1A, ARID1A, CBFA2T3, RHOA, CCNA2, H2BC12, SFPO, TFDP1, PKM, IRF4, IRF8, TOP1, PFDNS, FH, HDAC2, PCNA, HDAC1, RAP1GDS1, TTK, TYMS, SH3BP1, CUX1, U2AF2, POLD1, MAPK1, VHL, POLR2H, EPS15, SF3B1, SUZ12, CENPU, CD74, NPM1, SEPTIN2, H2BC4, HUWE1, ELP2, PTPN11, DEK, LRPPRC, WEE1, RAD50, ERCC2, ABI1, HNRNPA2B1, CCNG1, TCEA1, BAX, PTPN6, CEP43, PTPN2, MAD2L1	3.035686	2.03E-33	1.83E-33
GOTERM_CC_DIRECT	GO:0005634~nucleus	149	4.03E-35	RB1, CYFIP2, PHB1, MRE11, SMARCB1, KDM1A, BUB1B, IKZF1, SMC3, MKI67, IKZF3, ETS1, H2AC17, RPS6KA3, CCND2, AKT2, RPS6KA1, CHEK1, ZNF207, MAP3K7, GTF2I, MBNL1, USP7, PRKCB, RPL22, PRKCD, FBXO11, FOXF1, EWSR1, TBL1XR1, FANCD2, SARNP, SRSF2, BTK, KPNB1, DDX6, DDX5, DNMT1, SET, PRKDC, PPP4C, RAD21, TPR, LPXN, H3C2, LYN, XRCC6, CPSF6, UBE2C, FANCL, BCL11A, FUS, HSPA4, NONO, SMARCA5, HMGA1, FANCA, NDC80, NFKB1, CDK7, STAG2, NACA, CNOT2, MDM2, CDK1, GNAS, GRB2, MDM4, ATM, CALR, EZH2, PICALM, YWHAE, CEP57, TOP2A, TOP2B, DDX3X, BTG1, HSP90AB1, PTEN, AFF3, CHD2, PHF6, PTBP1, XPO1, ZC3H7A, ZC3H7B, CNTRL, OFD1, SS18, HSP90AA1, SYK, EED, PRMT1, NCOA3, CAD, PAX5, SMC1A, ARID1A, CBFA2T3, RHOA, CCNA2, H2BC12, SFPO, TFDP1, PKM, IRF4, IRF8, TOP1, PFDNS, FH, HDAC2, PCNA, HDAC1, RAP1GDS1, TTK, TYMS, SH3BP1, CUX1, U2AF2, POLD1, MAPK1, VHL, POLR2H, EPS15, SF3B1, SUZ12, CENPU, CD74, NPM1, SEPTIN2, H2BC4, HUWE1, ELP2, PTPN11, DEK, LRPPRC, WEE1, RAD50, ERCC2, ABI1, HNRNPA2B1, CCNG1, TCEA1, BAX, PTPN6, CEP43, PTPN2, MAD2L1	2.399971	8.95E-33	8.08E-33
GOTERM_CC_DIRECT	GO:0005829~cytosol	138	1.62E-31	UBE2C, FANCL, BCL11A, HSPA4, IDH2, HMGA1, FANCA, HOOK3, NDC80,	2.429765	2.40E-29	2.17E-29

					NFKB1, GRHPR, CDK7, STAG2, CAPRIN1, CNOT2, MDM2, CDK1, GNAS, GRB2, ATM, CALR, RPS21, PICALM, YWHAE, CEP57, TOP2B, DDX3X, HSP90AB1, WDR1, PTEN, CLTA, AFF3, XPO1, ATIC, CNTRL, RAC2, OFD1, HSP90AA1, SYK, EED, PRMT1, NCOA3, CAD, GAB1, SMC1A, RHOA, CCNA2, H2BC12, SFPQ, TFDP1, PKM, IRF4, IRF8, LCP1, MAPRE1, ARHGEF7, PFDN5, FH, BCL2A1, HDAC1, RAP1GDS1, GOSR1, TYMS, CDC42, NRAS, SH3BP1, FIP1L1, CUX1, POLD1, MAPK1, VHL, POLR2H, EPS15, CENPU, NPM1, H2BC4, HUWE1, ELP2, PTPN11, ERCC2, AB1, CCDC6, BAX, KRAS, PTPN6, CEP43, PTPN2, MAD2L1, CYFIP2, PHB1, MRE11, BUB1B, MSI2, IKZF3, ETS1, RPS6KA3, CCND2, AKT2, KIF5B, RPS6KA1, CHEK1, ZNF207, MAP3K7, GTF2I, MBNL1, PRKCB, RPL22, PRKCD, IRAG2, FBXO11, MELK, EWSR1, PRKAR1A, BTK, SRSF3, EZR, CARD11, KPNB1, DDX6, DDX5, SET, PPP4C, TPR, PLCG2, LPXN, FANCI, LYN, CARMIL2, CPSF6, BCL11A, FUS, FANCA, HOOK3, NDC80, NFKB1, GRHPR, CDK7, NACA, CAPRIN1, CNOT2, CCDC88C, MDM2, CDK1, GNAS, GRB2, ATM, CALR, RPS21, YWHAE, CEP57, TOP2A, DDX3X, BTG1, HSP90AB1, PTEN, LASP1, XPO1, HSP90AA1, SYK, PRMT1, NCOA3, CAD, GAB1, CCNA2, TFDP1, PKM, IRF8, LCP1, ARHGEF7, PFDN5, FH, HDAC2, BCL2A1, HDAC1, CXCR4, TTK, TYMS, CDC42, MAPK1, EPS15, CD74, NPM1, SEPTIN2, HUWE1, ELP2, PTPN11, WEE1, ERCC2, HNRNPA2B1, CCNG1, BAX, KRAS, PTPN6, PTPN2, MAD2L1			
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	107	9.00E-13			1.84957	9.99E-11	9.03E-11
GOTERM_CC_DIRECT	GO:0032991~protein-containing complex	29	2.63E-10			4.216952	2.34E-08	2.11E-08
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	52	1.69E-08			2.290531	1.08E-06	9.74E-07
GOTERM_CC_DIRECT	GO:0005813~centrosome	26	1.70E-08			3.853964	1.08E-06	9.74E-07
GOTERM_CC_DIRECT	GO:0000785~chromatin	34	5.02E-08			2.92535	2.79E-06	2.52E-06
GOTERM_CC_DIRECT	GO:0000776~kinetochore	13	1.24E-07			7.742543	6.11E-06	5.52E-06
GOTERM_CC_DIRECT	GO:0000781~chromosome, telomeric region	13	1.82E-07			7.474016	8.09E-06	7.31E-06
GOTERM_CC_DIRECT	GO:0005694~chromosome	15	2.94E-07			5.873735	1.19E-05	1.07E-05
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytoplasm	25	7.09E-07			3.267474	2.60E-05	2.35E-05
GOTERM_CC_DIRECT	GO:0016363~nuclear matrix	11	7.61E-07			8.416007	2.60E-05	2.35E-05
GOTERM_CC_DIRECT	GO:0005925~focal adhesion	18	1.97E-06			4.115665	6.24E-05	5.64E-05
GOTERM_CC_DIRECT	GO:0005819~spindle	11	3.36E-06			7.150856	9.94E-05	8.98E-05
GOTERM_CC_DIRECT	GO:0097431~mitotic spindle pole	7	7.13E-06			14.81348	1.98E-04	1.79E-04
GOTERM_CC_DIRECT	GO:0030892~mitotic cohesin complex	4	1.93E-05			66.30794	5.05E-04	4.56E-04
GOTERM_CC_DIRECT	GO:0005730~nucleolus	32	2.57E-05			2.273415	6.35E-04	5.74E-04
GOTERM_CC_DIRECT	GO:1904813~ficolin-1-rich granule lumen	9	3.80E-05			7.161257	8.87E-04	8.01E-04
GOTERM_CC_DIRECT	GO:0000307~cyclin-dependent protein kinase holoenzyme complex	6	7.56E-05			13.56299	0.001678	0.001516
GOTERM_CC_DIRECT	GO:0042382~paraspeckles	4	1.54E-04			36.16797	0.003247	0.002933
GOTERM_CC_DIRECT	GO:0034774~secretory granule lumen	8	1.69E-04			6.859442	0.003401	0.003072
GOTERM_CC_DIRECT	GO:0008278~cohesin complex	4	2.03E-04			33.15397	0.003924	0.003544
GOTERM_CC_DIRECT	GO:1990391~DNA repair complex	4	2.62E-04			30.60366	0.004686	0.004232
GOTERM_CC_DIRECT	GO:1990904~ribonucleoprotein complex	10	2.76E-04			4.736281	0.004686	0.004232
GOTERM_CC_DIRECT	GO:0016514~SWI/SNF complex	5	2.81E-04			15.54092	0.004686	0.004232
GOTERM_CC_DIRECT	GO:0005938~cell cortex	9	2.86E-04			5.360222	0.004686	0.004232
GOTERM_CC_DIRECT	GO:0005635~nuclear envelope	10	2.96E-04			4.691599	0.004686	0.004232
GOTERM_CC_DIRECT	GO:0000775~chromosome, centromeric region	6	3.61E-04			9.783138	0.005525	0.00499
GOTERM_CC_DIRECT	GO:0035098~ESC/E(Z) complex	4	5.02E-04			24.86548	0.007435	0.006715
GOTERM_CC_DIRECT	GO:0032993~protein-DNA complex	5	6.09E-04			12.75153	0.008722	0.007877
GOTERM_CC_DIRECT	GO:0000794~condensed nuclear chromosome	5	7.38E-04			12.1295	0.010242	0.00925
GOTERM_CC_DIRECT	GO:0001650~fibrillar center	8	8.64E-04			5.234837	0.011627	0.010501

				YWHAE, CYFIP2, PHB1, NUP107, DDX3X, HSP90A1, TFRC, CLTA, MKI67, HERPUD1, PTBP1, ATIC, XPO1, KIF5B, CNTRL, GTF21, OFD1, HSP90AA1, EED, CAD, IRAG2, RHOA, NUP93, MELK, PRKAR1A, IRF4, TBL1XR1, EZR, KPNB1, DDX6, DDX5, HDAC2, PRKDC, GOSR1, CXCR4, TTK, CDC42, NRAS, POLD1, RAD21, LPXN, H3C2, EPS15, FANCI, CD74, NPM1, CARMIL2, XRCC6, CPSF6, FANCL, FUS, NONO, HUWE1, TMEM230, LRPPRC, NDC80, KTN1, RAD50, STAG2, PTPRA, CAPRIN1, CNOT2, HNRNPA2B1, CDK1, GNAS, BAX, KRAS, PTPN6, CALR, PTPN2, PICALM	1.398929	0.01841	0.016627
GOTERM_CC_DIRECT	GO:0016020~membrane	71	0.00141				
GOTERM_CC_DIRECT	GO:0030893~meiotic cohesin complex	3	0.002025	RAD21, SMC1A, SMC3	42.62653	0.024969	0.022551
GOTERM_CC_DIRECT	GO:0019815~B cell receptor complex	3	0.002025	CD79B, CD79A, SYK	42.62653	0.024969	0.022551
GOTERM_CC_DIRECT	GO:0031252~cell leading edge	5	0.002382	CARMIL2, DDX3X, SH3BP1, CAPRIN1, CXCR4	8.880527	0.028587	0.025819
GOTERM_CC_DIRECT	GO:0110016~B-WICH complex	3	0.002682	SMARCA5, DEK, SF3B1	37.29821	0.031333	0.028298
GOTERM_CC_DIRECT	GO:0000793~condensed chromosome	4	0.002979	TOP2A, FANCD2, SMARCA5, MKI67	13.71888	0.033911	0.030627
GOTERM_CC_DIRECT	GO:0030027~lamellipodium	8	0.003563	CARMIL2, DDX3X, SH3BP1, CAPRIN1, ABI1, RAC2, ARHGEF7, RHOA	4.080488	0.039348	0.035537
GOTERM_CC_DIRECT	GO:0035861~site of double-strand break	6	0.003633	FH, RAD50, MRE11, CNTRL, SMARCA5, ATM	5.8507	0.039348	0.035537
GOTERM_CC_DIRECT	GO:0072686~mitotic spindle	7	0.003798	CDC42, NIN, TBL1XR1, TPR, CDK1, MAPK1, MAD2L1	4.704279	0.040156	0.036267
GOTERM_CC_DIRECT	GO:0005721~pericentric heterochromatin	4	0.003955	DNMT1, SMARCA5, IKZF1, EZH2	12.43274	0.040842	0.036886
GOTERM_CC_DIRECT	GO:0005677~chromatin silencing complex	3	0.004253	SUZ12, SMARCA5, EZH2	29.83857	0.042616	0.038489
GOTERM_CC_DIRECT	GO:0005657~replication fork	4	0.004319	DNMT1, PCNA, MRE11, CHEK1 RB1, CYFIP2, EIF4A2, PHB1, NUP107, SMARCB1, TFRC, IKZF1, MKI67, SMC3, IKZF3, H2AC17, RPS6KA3, TCL1A, AKT2, FGFR1OP2, RPS6KA1, CHEK1, MBNL1, STG6A1, FNBP1, PRKCB, RPL22, PRKCD, NUP93, EWSR1, PRKAR1A, SARNP, BTK, EZR, SET, PRKDC, CD79B, CD79A, PPP3R1, PPP4C, INPP5D, RAD21, PLCG2, VTI1A, H3C2, LYN, XRCC6, SMARCA5, STAG2, CDC8C8C, GRB2, ATM, CALR, RPS21, EZH2, CEP57, TOP2A, TOP2B, BTG1, CLTA, PHF6, HERPUD1, XPO1, CNTRL, RAC2, OFD1, SS18, SYK, PRMT1, NCOA3, GAB1, PAX5, CBFA2T3, RHOA, ARHGEF7, MAPRE1, FH, PCNA, CXCR4, NRAS, EPS15, SF3B1, SUZ12, GIT2, CENPU, CD74, NPM1, UTP4, SEPTIN2, H2BC4, HUWE1, SEPTIN6, COX6C, LRPPRC, KTN1, HNRNPA2B1, ABI1, CCNG1, CCDC6, TCEA1, CEP43, MAD2L1, MRE11, KDM1A, BUB1B, MSI2, ETS1, CCND2, KIF5B, ZNF207, MAP3K7, GTF21, USP7, TPM3, FBXO11, FOXF1, MELK, FANCD2, TBL1XR1, SRSF2, SRSF3, KPNB1, CARD11, DDX6, DDX5, DNMT1, TPR, LPXN, FANCI, CPSF6, HSPA4, UBE2C, FANCL, FUS, NONO, HMGA1, FANCA, HOOK3, NDC80, NFKB1, GRHPR, CDK7, NACA, PTPRA, CNOT2, CAPRIN1, MDM2, GNAS, CDK1, MDM4, PICALM, YWHAE, DDX3X, HSP90A1, PTEN, CHD2, PTBP1, LASP1, ZC3H7B, HSP90AA1, EED, CAD, SMC1A, ARID1A, H2BC12, CCNA2, SFPO, PKM, TFDP1, RABEP1, IRF4, IRF8, TOP1, PFDN5, HDAC2, BCL2A1, HDAC1, RAP1GDS1, TTK, U2AF1, CDC42, SH3BP1, FIP1L1, U2AF2, POLD1, MAPK1, VHL, PTPN11, DEK, WEE1, RAD50, NIN, POU2AF1, ERCC2, BAX, PTPN6, KRAS, PTPN2	12.05599	0.042616	0.038489
GOTERM_MF_DIRECT	GO:0005515~protein binding	194	1.39E-19	EIF4A2, YWHAE, TOP2A, DDX3X, HSP90A1, TFRC, MSI2, MKI67, CHD2, PHF6, PTBP1, XPO1, ZC3H7A, ZC3H7B, ZNF207, MBNL1, HSP90AA1, PRMT1, RPL22, SMC1A, SFPO, PKM, EWSR1, SARNP, SRSF2, SRSF3, TOP1, EZR, MAPRE1, KPNB1, DDX6, DDX5, DNMT1, HDAC2, PRKDC, U2AF1, FIP1L1, U2AF2, TPR, SF3B1, NPM1, XRCC6, CPSF6, UTP4, FUS, NONO, HMGA1, HUWE1, DEK, LRPPRC, KTN1, CAPRIN1, HNRNPA2B1, GRB2, CALR, RPS21	1.398245	6.84E-17	6.20E-17
GOTERM_MF_DIRECT	GO:0003723~RNA binding	56	7.39E-17	RB1, CEP57, YWHAE, MRE11, SMARCB1, HSP90A1, KDM1A, TFRC, PTEN, IKZF1, MSI2, IKZF3, ETS1, TCL1A, KIF5B, FGFR1OP2, MAP3K7, OFD1, HSP90AA1, FNBP1, EED, PRMT1, RPL22, CAD, FOXF1, EWSR1, BTK, EZR, MAPRE1, PCNA, TTK, CD79B, CDC42, CD79A, MAPK1, CD74, FUS, SEPTIN2, NONO, H2BC4, HOOK3, NDC80, NFKB1, RAD50, CCDC8C8C, HNRNPA2B1, CCDC6, MDM2, BAX, KRAS, GRB2, ATM, MAD2L1	3.537961	1.82E-14	1.65E-14
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	53	8.14E-12	TOP2A, TOP2B, DNMT1, SMARCB1, MRE11, SET, DDX3X, PCNA, IKZF1, MKI67, CHD2, ETS1, PHF6, H2AC17, POLD1, RAD21, ZNF207, MAPK1, H3C2, GTF21, FANCI, XRCC6, FUS, NONO, H2BC4, SMARCA5, HMGA1, HUWE1, DEK, ARID1A, SMC1A, H2BC12, SFPO, RAD50, NACA, POU2AF1, SARNP, TCEA1, ATM, CALR, TOP1	2.804814	1.33E-09	1.21E-09
GOTERM_MF_DIRECT	GO:0003677~DNA binding	41	5.16E-11	LYN, YWHAE, DDX5, HDAC2, PHB1, BTG1, PCNA, KDM1A, PRMT1, PRKDC, HDAC1, PRKCD, CAD, PTEN, HMGA1, PHF6, H2AC17, U2AF2, POLD1, MDM2, MDM4, VHL, KPNB1	3.257456	6.33E-09	5.74E-09
GOTERM_MF_DIRECT	GO:0019899~enzyme binding	23	1.17E-10	TOP2A, EIF4A2, TOP2B, DDX6, DDX5, DDX3X, HSP90A1, PRKDC, GMPS, BUB1B, TTK, MKI67, CHD2, SMC3, RPS6KA3, AKT2, KIF5B, CHEK1, RPS6KA1, CNTRL, MAPK1, MAP3K7, GTF21, LYN, XRCC6, HSP90AA1, SYK, PRKCB, HSPA4, UBE2C, PRKCD, CAD, SMARCA5, HOOK3, SMC1A, WEE1, CDK7, RAD50, PKM, MELK, CAPRIN1, ERCC2, CDK1, BTK, KRAS, ATM, TOP1	5.683461	1.15E-08	1.04E-08
GOTERM_MF_DIRECT	GO:0005524~ATP binding	47	1.96E-10	TOP2A, TOP2B, DNMT1, HDAC2, SET, PCNA, KDM1A, CHD2, SMC3, POLD1, RAD21, TPR, NPM1, PRKCB, FUS, NONO, SMARCA5, HMGA1, SMC1A, NFKB1, SFPO, STAG2, SARNP, CDK1, TOP1, EZH2	2.803646	1.60E-08	1.45E-08
GOTERM_MF_DIRECT	GO:0003682~chromatin binding	26	5.34E-10	YWHAE, DDX6, PRKDC, IKZF1, CCNA2, PPP3R1, RABEP1, TFDP1, PRKAR1A, CHEK1, MDM2, GRB2, TOP1, EZR, KPNB1	4.569826	3.74E-08	3.39E-08
GOTERM_MF_DIRECT	GO:0019904~protein domain specific binding	15	1.10E-07	NPM1, HSP90A1, SYK, TFRC, BCL11A, PRKCD, ELP2, PTPN11, RHOA, CDC42, CCNA2, RPS6KA3, TCL1A, CCND2, PLCG2, RAC2, GRB2, PTPN6, MAPRE1, ARHGEF7, CEP43, PTPN2	6.35418	6.73E-06	6.10E-06
GOTERM_MF_DIRECT	GO:0019901~protein kinase binding	22	1.37E-07	YWHAE, DDX6, MRE11, DDX3X, HSP90A1, SEPTIN2, PTPN11, KTN1, LASP1, PKM, ATIC, KIF5B, ABI1, H3C2, EZR, MAPRE1, EPS15, PICALM	4.028533	7.49E-06	6.79E-06
GOTERM_MF_DIRECT	GO:0045296~cadherin binding	18	1.54E-07	SYK, PRKCB, PRKDC, PRKCD, BUB1B, TTK, RPS6KA3, CDK7, MELK, AKT2, RPS6KA1, CHEK1, CDK1, MAPK1, ATM, TOP1, MAP3K7, GTF21	4.93919	7.54E-06	6.83E-06
GOTERM_MF_DIRECT	GO:0004674~protein serine/threonine kinase activity	18	9.68E-07		4.331488	4.32E-05	3.92E-05
GOTERM_MF_DIRECT	GO:1990841~promoter-specific chromatin binding	8	8.74E-06	SUZ12, DDX5, DNMT1, HDAC2, KDM1A, HDAC1, IKZF3, EZH2	10.81457	3.58E-04	3.24E-04

GOTERM_MF_DIRECT	GO:0097110~scaffold protein binding	8	1.06E-05	LYN, YWHAE, XRCC6, HSP90AA1, SYK, PLCG2, MAP3K7, PHF6	10.50558	4.01E-04	3.63E-04
GOTERM_MF_DIRECT	GO:0001784~phosphotyrosine residue binding	7	2.51E-05	LYN, SYK, PLCG2, MAPK1, PTPN6, PTPN11, GRB2	11.91605	8.81E-04	7.98E-04
GOTERM_MF_DIRECT	GO:0003729~mRNA binding	13	3.89E-05	DDX6, HSP90AA1, CPSF6, DDX3X, NONO, MSI2, TYMS, PTBP1, PKM, CAPRIN1, TPR, CALR, SF3B1	4.442415	0.001272	0.001153
GOTERM_MF_DIRECT	GO:0106310~protein serine kinase activity	15	4.81E-05	PRKCB, PRKDC, PRKCD, BUB1B, TTK, RPS6KA3, CDK7, MELK, AKT2, RPS6KA1, CHEK1, CDK1, MAPK1, ATM, MAP3K7	3.767369	0.001475	0.001336
GOTERM_MF_DIRECT	GO:0097718~disordered domain specific binding	6	5.32E-05	RB1, HSP90AA1, HSP90AB1, NCOA3, MDM2, EZR	14.51429	0.001537	0.001393
GOTERM_MF_DIRECT	GO:0003712~transcription coregulator activity	9	6.57E-05	BTG1, EWSR1, BCL11A, FUS, CNOT2, POU2AF1, HMGA1, LPXN, NFKB1	6.618514	0.001793	0.001625
GOTERM_MF_DIRECT	GO:0070182~DNA polymerase binding	5	8.38E-05	FANCI, HSP90AA1, PCNA, HSP90AB1, FANCD2	20.89177	0.002166	0.001963
GOTERM_MF_DIRECT	GO:0042826~histone deacetylase binding	9	9.65E-05	YWHAE, SFPQ, HSP90AA1, HDAC2, PHB1, HSP90AB1, HDAC1, IKZF3, PHF6	6.267532	0.002368	0.002146
GOTERM_MF_DIRECT	GO:0004715~non-membrane spanning protein tyrosine kinase activity	6	1.35E-04	LYN, WEE1, MELK, SYK, PRKCD, BTK	11.99006	0.003168	0.002871
GOTERM_MF_DIRECT	GO:0050681~nuclear androgen receptor binding	5	1.66E-04	DDX5, KDM1A, PRKCB, CALR, FOXP1	17.67766	0.003695	0.003349
GOTERM_MF_DIRECT	GO:0001222~transcription corepressor binding	6	1.84E-04	SUZ12, EED, HDAC1, CNOT2, ETS1, EZH2	11.25598	0.003919	0.003552
GOTERM_MF_DIRECT	GO:0023026~MHC class II protein complex binding	5	1.93E-04	YWHAE, CD74, HSP90AA1, PKM, HSP90AB1	17.02293	0.003943	0.003573
GOTERM_MF_DIRECT	GO:0003713~transcription coactivator activity	12	2.27E-04	SS18, NPM1, PKM, SMARCB1, KDM1A, FUS, NACA, IRF4, NCOA3, POU2AF1, HMGA1, ARID1A	3.982259	0.004453	0.004036
GOTERM_MF_DIRECT	GO:0030374~nuclear receptor coactivator activity	6	4.08E-04	SS18, KDM1A, PRKCB, NCOA3, HMGA1, ETS1	9.50936	0.0077	0.006978
GOTERM_MF_DIRECT	GO:0017124~SH3 domain binding	8	4.49E-04	LYN, SH3BP1, INPP5D, ABI1, CCDG6, PTPN6, GRB2, EPS15	5.836432	0.00816	0.007395
GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	20	5.35E-04	CEP57, TOP2A, NPM1, STG6A1, HSP90AA1, HSP90AB1, BCL2A1, TFRC, BCL11A, TYMS, IKZF3, GRHPR, SFPQ, PKM, RABEP1, ATIC, TPR, BAX, CEP43, MAD2L1	2.451302	0.009382	0.008503
GOTERM_MF_DIRECT	GO:0140297~DNA-binding transcription factor binding	9	5.86E-04	RB1, NPM1, TFDP1, KDM1A, BCL11A, HDAC1, RAD21, VHL, MAP3K7	4.809967	0.009565	0.008669
GOTERM_MF_DIRECT	GO:0043021~ribonucleoprotein complex binding	5	5.99E-04	TOP2B, DDX5, MDM2, PHF6, EZH2	12.7672	0.009565	0.008669
GOTERM_MF_DIRECT	GO:0031625~ubiquitin in protein ligase binding	12	6.04E-04	LYN, RB1, YWHAE, HSP90AA1, HSP90AB1, FANCL, PRKAR1A, MDM2, CXCR4, CALR, MAP3K7, LRPPRC	3.546899	0.009565	0.008669
GOTERM_MF_DIRECT	GO:0003678~DNA helicase activity	5	8.16E-04	XRCC6, RAD50, DDX3X, MRE11, ERCC2	11.7851	0.012522	0.011349
GOTERM_MF_DIRECT	GO:0046982~protein heterodimerization activity	13	8.88E-04	YWHAE, TOP2A, PHB1, BCL2A1, BCL11A, H2BC4, SMC3, SMC1A, IKZF3, H2AC17, H2BC12, BAX, H3C2	3.161401	0.012859	0.011654
GOTERM_MF_DIRECT	GO:0035591~signaling adaptor activity	6	9.08E-04	YWHAE, DDX3X, SYK, CAPRIN1, ABI1, GAB1	7.993375	0.012859	0.011654
GOTERM_MF_DIRECT	GO:0016887~ATP hydrolysis activity	14	9.34E-04	EIF4A2, DDX6, XRCC6, DDX5, HSP90AA1, DDX3X, HSP90AB1, SMARCA5, SMC3, CHD2, SMC1A, RAD50, KIF5B, ERCC2	2.965284	0.012859	0.011654
GOTERM_MF_DIRECT	GO:0004713~protein tyrosine kinase activity	7	9.43E-04	LYN, WEE1, PKM, SYK, BTK, TTK, MAP3K7	6.187179	0.012859	0.011654
GOTERM_MF_DIRECT	GO:0043015~gamma-tubulin binding	5	9.88E-04	OFD1, LYN, CEP57, DDX3X, ARHGEF7	11.21022	0.013111	0.011882
GOTERM_MF_DIRECT	GO:0002039~p53 binding	6	0.001034	USP7, SMARCB1, KDM1A, HDAC1, MDM2, MDM4	7.768209	0.013268	0.012025
GOTERM_MF_DIRECT	GO:0042393~histone binding	10	0.001054	NPM1, HDAC2, FH, SET, TBL1XR1, PRKCB, SMARCA5, DEK, CHD2, PHF6	3.928368	0.013268	0.012025
GOTERM_MF_DIRECT	GO:0003714~transcription corepressor activity	9	0.001813	RB1, PHB1, TBL1XR1, HDAC1, SRSF2, VHL, PFDNS, CBFA2T3, EZH2	4.035679	0.02225	0.020165
GOTERM_MF_DIRECT	GO:0140031~phosphorylation-dependent protein binding	3	0.003129	LYN, PLCG2, PTPN6	34.47143	0.037475	0.033964
GOTERM_MF_DIRECT	GO:0008094~ATP-dependent activity, acting on DNA	4	0.003714	TOP2A, XRCC6, CDK7, SMARCA5	12.67915	0.043424	0.039356
GOTERM_MF_DIRECT	GO:0070878~primary miRNA binding	3	0.003995	DDX5, SRSF3, EZH2	30.64127	0.045614	0.04134
GOTERM_MF_DIRECT	GO:0042054~histone methyltransferase activity	4	0.004498	SUZ12, EED, PRMT1, EZH2	11.86114	0.050188	0.045486
GOTERM_MF_DIRECT	GO:0008353~RNA polymerase II CTD heptapeptide repeat kinase activity	3	0.004958	CDK7, CDK1, MAPK1, RB1, YWHAE, HDAC2, PCNA, PRKDC, HDAC1, BUB1B, TTK, SMC3, SMC1A, NDC80, CCNA2, WEE1, CDK7, STAG2, TFDP1, CCND2, RAD21, CHEK1, MDM2, CDK1, ATM, MAD2L1	27.57714	0.054096	0.049028
KEGG_PATHWAY	hsa04110:Cell cycle	23	4.62E-14		8.093305	1.15E-11	7.02E-12

KEGG_PATHWAY	hsa04662:B cell receptor signaling pathway	18	3.00E-13	LYN, SYK, PRKCB, NFKB1, CD79B, CD79A, NRAS, PPP3R1, AKT2, INPP5D, BTK, PLCG2, RAC2, MAPK1, KRAS, GRB2, PTPN6, CARD11	10.9973	3.74E-11	2.28E-11
KEGG_PATHWAY	hsa05203:Viral carcinogenesis	24	1.28E-12	LYN, RB1, YWHA, USP7, HDAC2, DDX3X, SYK, HDAC1, H2BC4, RHOA, NFKB1, CDC42, H2BC12, CCNA2, NRAS, PKM, CCND2, CHEK1, MDM2, CDK1, BAX, MAPK1, KRAS, GRB2	6.508974	1.06E-10	6.47E-11
KEGG_PATHWAY	hsa04722:Neurotrophin signaling pathway	16	2.92E-09	YWHA, PRKCD, GAB1, PTPN11, RHOA, NFKB1, CDC42, RPS6KA3, NRAS, AKT2, RPS6KA1, PLCG2, BAX, MAPK1, KRAS, GRB2	7.412998	1.82E-07	1.11E-07
KEGG_PATHWAY	hsa04218:Cellular senescence	17	1.70E-08	RB1, MRE11, PTEN, ETS1, NFKB1, CCNA2, NRAS, PPP3R1, RAD50, CCND2, AKT2, CHEK1, MDM2, CDK1, MAPK1, KRAS, ATM	6.02011	8.49E-07	5.18E-07
KEGG_PATHWAY	hsa05200:Pathways in cancer	30	5.52E-08	RB1, FH, HDAC2, HSP90AB1, HDAC1, PTEN, CXCR4, ETS1, CDC42, NRAS, CCND2, AKT2, TPR, PLCG2, RAC2, MAPK1, VHL, HSP90AA1, TPM3, PRKCB, NCOA3, RHOA, NFKB1, CCNA2, GNAS, CCDC6, MDM2, BAX, KRAS, GRB2	3.129314	2.29E-06	1.40E-06
KEGG_PATHWAY	hsa05220:Chronic myeloid leukemia	12	1.02E-07	RB1, HDAC2, NRAS, HDAC1, AKT2, MDM2, BAX, MAPK1, PTPN11, KRAS, GRB2, NFKB1	8.664543	3.61E-06	2.20E-06
KEGG_PATHWAY	hsa04664:Fc epsilon RI signaling pathway	11	3.44E-07	LYN, NRAS, SYK, AKT2, INPP5D, BTK, PLCG2, RAC2, MAPK1, KRAS, GRB2	8.863367	1.07E-05	6.53E-06
KEGG_PATHWAY	hsa05211:Renal cell carcinoma	11	3.95E-07	CDC42, NRAS, FH, AKT2, GAB1, MAPK1, PTPN11, KRAS, GRB2, VHL, ETS1	8.736748	1.08E-05	6.59E-06
KEGG_PATHWAY	hsa05166:Human T-cell leukemia virus 1 infection	18	4.33E-07	RB1, PTEN, BUB1B, ETS1, NFKB1, CCNA2, NRAS, PPP3R1, XPO1, CCND2, AKT2, CHEK1, BAX, MAPK1, KRAS, ATM, CALR, MAD2L1	4.487689	1.08E-05	6.59E-06
KEGG_PATHWAY	hsa05214:Glioma	11	8.67E-07	RB1, NRAS, PRKCB, AKT2, PTEN, MDM2, PLCG2, BAX, MAPK1, KRAS, GRB2	8.047004	1.96E-05	1.20E-05
KEGG_PATHWAY	hsa05170:Human immunodeficiency virus 1 infection	17	1.18E-06	PRKCB, CXCR4, NFKB1, WEE1, NRAS, PPP3R1, AKT2, CHEK1, CDK1, PLCG2, RAC2, BAX, MAPK1, KRAS, ATM, CALR, MAP3K7	4.437358	2.44E-05	1.49E-05
KEGG_PATHWAY	hsa04660:T cell receptor signaling pathway	13	1.67E-06	PTPN11, RHOA, NFKB1, CDC42, NRAS, PPP3R1, AKT2, MAPK1, KRAS, GRB2, PTPN6, MAP3K7, CARD11	5.924322	3.19E-05	1.95E-05
KEGG_PATHWAY	hsa04625:C-type lectin receptor signaling pathway	12	2.46E-06	NRAS, PPP3R1, SYK, AKT2, PRKCD, MDM2, PLCG2, MAPK1, PTPN11, KRAS, RHOA, NFKB1	6.353998	4.38E-05	2.67E-05
KEGG_PATHWAY	hsa05206:MicroRNAs in cancer	20	2.72E-06	DNMT1, HDAC2, PRKCB, HDAC1, PTEN, RHOA, NFKB1, FOXF1, NRAS, CCND2, CCNG1, MDM2, PLCG2, MAPK1, MDM4, KRAS, GRB2, ATM, EZR, EZH2	3.563941	4.51E-05	2.76E-05
KEGG_PATHWAY	hsa05169:Epstein-Barr virus infection	16	3.18E-06	LYN, RB1, USP7, HDAC2, SYK, HDAC1, NFKB1, CCNA2, CCND2, AKT2, MDM2, BTK, PLCG2, BAX, CALR, MAP3K7	4.382068	4.94E-05	3.02E-05
KEGG_PATHWAY	hsa05223:Non-small cell lung cancer	10	5.41E-06	RB1, NRAS, PRKCB, AKT2, KIF5B, PLCG2, BAX, MAPK1, KRAS, GRB2	7.616094	7.93E-05	4.84E-05
KEGG_PATHWAY	hsa05202:Transcriptional misregulation in cancer	15	8.50E-06	SS18, DDX5, HDAC2, BCL2A1, FUS, HDAC1, PAX5, NFKB1, CCNA2, CCND2, EWSR1, MDM2, BAX, ATM, H3C2	4.321048	1.18E-04	7.18E-05
KEGG_PATHWAY	hsa05215:Prostate cancer	11	9.09E-06	RB1, HSP90AA1, NRAS, HSP90AB1, AKT2, PTEN, MDM2, MAPK1, KRAS, GRB2, NFKB1	6.240534	1.19E-04	7.27E-05
KEGG_PATHWAY	hsa04370:VEGF signaling pathway	9	1.01E-05	CDC42, NRAS, PPP3R1, PRKCB, AKT2, PLCG2, RAC2, MAPK1, KRAS	8.339623	1.26E-04	7.71E-05
KEGG_PATHWAY	hsa01521:EGFR tyrosine kinase inhibitor resistance	10	1.16E-05	NRAS, PRKCB, AKT2, PTEN, GAB1, PLCG2, BAX, MAPK1, KRAS, GRB2	6.949686	1.33E-04	8.14E-05
KEGG_PATHWAY	hsa05163:Human cytomegalovirus infection	16	1.18E-05	RB1, PRKCB, CXCR4, RHOA, NFKB1, NRAS, PPP3R1, AKT2, MDM2, RAC2, GNAS, BAX, MAPK1, KRAS, GRB2, CALR	3.936105	1.33E-04	8.14E-05
KEGG_PATHWAY	hsa05205:Proteoglycans in cancer	15	1.60E-05	DDX5, PRKCB, GAB1, PTPN11, RHOA, CDC42, NRAS, AKT2, MDM2, PLCG2, MAPK1, KRAS, GRB2, PTPN6, EZR	4.08805	1.73E-04	1.06E-04
KEGG_PATHWAY	hsa05161:Hepatitis B	13	3.31E-05	RB1, DDX3X, PCNA, PRKCB, NFKB1, CCNA2, NRAS, AKT2, BAX, MAPK1, KRAS, GRB2, MAP3K7	4.434155	3.44E-04	2.10E-04
KEGG_PATHWAY	hsa05131:Shigellosis	16	3.70E-05	FNBP1, SEPTIN2, PRKCD, SEPTIN6, U2AF1, RHOA, NFKB1, CDC42, AKT2, MDM2, PLCG2, BAX, MAPK1, ATM, H3C2, MAP3K7	3.572529	3.59E-04	2.19E-04
KEGG_PATHWAY	hsa04613:Neutrophil extracellular trap formation	14	3.75E-05	HDAC2, SYK, PRKCB, HDAC1, H2BC4, H2AC17, NFKB1, H2BC12, AKT2, PLCG2, RAC2, MAPK1, H3C2, MAP3K7	4.053983	3.59E-04	2.19E-04
KEGG_PATHWAY	hsa04062:Chemokine signaling pathway	14	3.96E-05	LYN, PRKCB, PRKCD, CXCR4, RHOA, NFKB1, CDC42, NRAS, AKT2, PLCG2, RAC2, MAPK1, KRAS, GRB2	4.032978	3.65E-04	2.23E-04
KEGG_PATHWAY	hsa05216:Thyroid cancer	7	4.36E-05	NRAS, TPM3, TPR, CCDC6, BAX, MAPK1, KRAS	10.51844	3.88E-04	2.37E-04
KEGG_PATHWAY	hsa05225:Hepatocellular carcinoma	13	5.01E-05	RB1, SMARCB1, PRKCB, PTEN, GAB1, ARID1A, NRAS, AKT2, PLCG2, BAX, MAPK1, KRAS, GRB2	4.251572	4.30E-04	2.62E-04
KEGG_PATHWAY	hsa04115:p53 signaling pathway	9	5.33E-05	CCND2, CCNG1, CHEK1, PTEN, MDM2, CDK1, BAX, MDM4, ATM	6.671698	4.42E-04	2.70E-04
KEGG_PATHWAY	hsa04666:Fc gamma R-mediated phagocytosis	10	6.00E-05	LYN, CDC42, SYK, PRKCB, AKT2, INPP5D, PRKCD, PLCG2, RAC2, MAPK1	5.673213	4.82E-04	2.94E-04
KEGG_PATHWAY	hsa01522:Endocrine resistance	10	6.50E-05	RB1, NRAS, AKT2, NCOA3, MDM2, GNAS, BAX, MAPK1, KRAS, GRB2	5.615908	5.06E-04	3.09E-04
KEGG_PATHWAY	hsa04933:AGE-RAGE signaling pathway in diabetic complications	10	7.61E-05	CDC42, NRAS, PRKCB, AKT2, PRKCD, PLCG2, BAX, MAPK1, KRAS, NFKB1	5.504701	5.74E-04	3.50E-04
KEGG_PATHWAY	hsa05165:Human papillomavirus infection	18	8.98E-05	RB1, HDAC2, HDAC1, PTEN, NFKB1, CDC42, CCNA2, NRAS, PKM, CCND2, AKT2, MDM2, GNAS, BAX, MAPK1, KRAS, GRB2, ATM	3.005269	6.57E-04	4.01E-04
KEGG_PATHWAY	hsa04064:NF-kappa B signaling pathway	10	1.03E-04	LYN, SYK, BCL2A1, PRKCB, BTK, PLCG2, ATM, MAP3K7, CARD11, NFKB1	5.294999	7.33E-04	4.47E-04
KEGG_PATHWAY	hsa04650:Natural killer cell mediated cytotoxicity	11	1.06E-04	NRAS, PPP3R1, SYK, PRKCB, PLCG2, RAC2, MAPK1, PTPN11, KRAS, GRB2	4.704403	7.33E-04	4.47E-04
KEGG_PATHWAY	hsa05207:Chemical carcinogenesis - receptor activation	14	1.20E-04	RB1, HSP90AA1, HSP90AB1, PRKCB, NFKB1, RPS6KA3, NRAS, AKT2, RPS6KA1, GNAS, MAPK1, KRAS, GRB2, KPNB1	3.620301	7.89E-04	4.82E-04
KEGG_PATHWAY	hsa04068:FoxO signaling pathway	11	1.20E-04	USP7, NRAS, CCND2, PRMT1, AKT2, PTEN, MDM2, MAPK1, KRAS, GRB2, ATM	4.633124	7.89E-04	4.82E-04

KEGG_PATHWAY	hsa05417:Lipid and atherosclerosis	14	1.26E-04	LYN, HSP90AA1, HSP90AB1, HSPA4, RHOA, NFKB1, CDC42, NRAS, PPP3R1, AKT2, BAX, MAPK1, KRAS, MAP3K7	3.603541	8.02E-04	4.89E-04
KEGG_PATHWAY	hsa04914:Progesterone-mediated oocyte maturation	10	1.58E-04	CCNA2, RPS6KA3, HSP90AA1, HSP90AB1, AKT2, RPS6KA1, CDK1, MAPK1, KRAS, MAD2L1	5.008782	9.84E-04	6.01E-04
KEGG_PATHWAY	hsa05135:Yersinia infection	11	1.74E-04	CDC42, RPS6KA3, GIT2, AKT2, RPS6KA1, RAC2, MAPK1, ARHGEF7, MAP3K7, RHOA, NFKB1	4.431684	0.001057	6.45E-04
KEGG_PATHWAY	hsa05235:PD-L1 expression and PD-1 checkpoint pathway in cancer	9	1.95E-04	NRAS, PPP3R1, AKT2, PTEN, MAPK1, PTPN6, PTPN11, KRAS, NFKB1	5.559748	0.001148	7.01E-04
KEGG_PATHWAY	hsa05221:Acute myeloid leukemia	8	1.98E-04	CCNA2, NRAS, BCL2A1, AKT2, MAPK1, KRAS, GRB2, NFKB1	6.540881	0.001148	7.01E-04
KEGG_PATHWAY	hsa05218:Melanoma	8	3.09E-04	RB1, NRAS, AKT2, PTEN, MDM2, BAX, MAPK1, KRAS	6.092875	0.001697	0.001036
KEGG_PATHWAY	hsa04919:Thyroid hormone signaling pathway	10	3.23E-04	HDAC2, NRAS, HDAC1, PRKCB, AKT2, NCOA3, MDM2, PLCG2, MAPK1, KRAS	4.557171	0.001697	0.001036
KEGG_PATHWAY	hsa04071:Sphingolipid signaling pathway	10	3.23E-04	NRAS, PRKCB, AKT2, PTEN, RAC2, BAX, MAPK1, KRAS, RHOA, NFKB1	4.557171	0.001697	0.001036
KEGG_PATHWAY	hsa04072:Phospholipase D signaling pathway	11	3.25E-04	NRAS, SYK, AKT2, GAB1, PLCG2, GNAS, MAPK1, PTPN11, KRAS, GRB2, RHOA	4.104512	0.001697	0.001036
KEGG_PATHWAY	hsa04014:Ras signaling pathway	14	3.27E-04	PRKCB, GAB1, PTPN11, ETS1, RHOA, NFKB1, CDC42, NRAS, AKT2, PLCG2, RAC2, MAPK1, KRAS, GRB2	3.27044	0.001697	0.001036
KEGG_PATHWAY	hsa05212:Pancreatic cancer	8	4.30E-04	RB1, CDC42, AKT2, RAC2, BAX, MAPK1, KRAS, NFKB1	5.776362	0.002185	0.001334
KEGG_PATHWAY	hsa05213:Endometrial cancer	7	6.11E-04	NRAS, AKT2, PTEN, BAX, MAPK1, KRAS, GRB2	6.596312	0.003043	0.001858
KEGG_PATHWAY	hsa04915:Estrogen signaling pathway	10	8.39E-04	HSP90AA1, NRAS, HSP90AB1, AKT2, NCOA3, PRKCD, GNAS, MAPK1, KRAS, GRB2	3.999819	0.004023	0.002456
KEGG_PATHWAY	hsa04012:ErbB signaling pathway	8	8.40E-04	NRAS, PRKCB, AKT2, GAB1, PLCG2, MAPK1, KRAS, GRB2	5.171859	0.004023	0.002456
KEGG_PATHWAY	hsa05210:Colorectal cancer	8	9.00E-04	NRAS, AKT2, RAC2, BAX, MAPK1, KRAS, GRB2, RHOA	5.112412	0.004229	0.002582
KEGG_PATHWAY	hsa04720:Long-term potentiation	7	0.001204	RPS6KA3, NRAS, PPP3R1, PRKCB, RPS6KA1, MAPK1, KRAS	5.808692	0.00555	0.003388
KEGG_PATHWAY	hsa04912:GnRH signaling pathway	8	0.001335	CDC42, NRAS, PRKCB, PRKCD, GNAS, MAPK1, KRAS, GRB2	4.782579	0.006044	0.003689
KEGG_PATHWAY	hsa03450:Non-homologous end-joining	4	0.001405	XRCC6, RAD50, MRE11, PRKDC	17.10692	0.006245	0.003812
KEGG_PATHWAY	hsa05230:Central carbon metabolism in cancer	7	0.001629	NRAS, PKM, AKT2, IDH2, PTEN, MAPK1, KRAS	5.481442	0.006995	0.00427
KEGG_PATHWAY	hsa04917:Prolactin signaling pathway	7	0.001629	NRAS, CCND2, AKT2, MAPK1, KRAS, GRB2, NFKB1	5.481442	0.006995	0.00427
KEGG_PATHWAY	hsa05034:Alcoholism	11	0.001959	H2BC12, HDAC2, NRAS, HDAC1, H2BC4, GNAS, MAPK1, KRAS, GRB2, H3C2, H2AC17	3.253044	0.00827	0.005048
KEGG_PATHWAY	hsa04150:mTOR signaling pathway	10	0.00205	RPS6KA3, NRAS, PRKCB, AKT2, RPS6KA1, PTEN, MAPK1, KRAS, GRB2, RHOA	3.518828	0.008507	0.005193
KEGG_PATHWAY	hsa01524:Platinum drug resistance	7	0.002161	TOP2A, TOP2B, AKT2, MDM2, BAX, MAPK1, ATM	5.189099	0.00882	0.005384
KEGG_PATHWAY	hsa05167:Kaposi sarcoma-associated herpesvirus infection	11	0.002659	LYN, RB1, NRAS, PPP3R1, SYK, AKT2, PLCG2, BAX, MAPK1, KRAS, NFKB1	3.120267	0.01068	0.006519
KEGG_PATHWAY	hsa04931:Insulin resistance	8	0.003313	RPS6KA3, PRKCB, AKT2, RPS6KA1, PRKCD, PTEN, PTPN11, NFKB1	4.080549	0.013093	0.007992
KEGG_PATHWAY	hsa04114:Oocyte meiosis	9	0.0034	YWHAE, RPS6KA3, PPP3R1, RPS6KA1, CDK1, MAPK1, SMC1A, SMC3, MAD2L1	3.599837	0.013118	0.008008
KEGG_PATHWAY	hsa05130:Pathogenic Escherichia coli infection	11	0.003424	CDC42, CYFIP2, ABI1, BAX, MAPK1, PTPN6, PTPN11, EZR, MAP3K7, RHOA, NFKB1	3.012672	0.013118	0.008008
KEGG_PATHWAY	hsa03083:Polycomb repressive complex	7	0.003604	SUZ12, USP7, HDAC2, TFDP1, EED, HDAC1, EZH2	4.688944	0.013597	0.0083
KEGG_PATHWAY	hsa04380:Osteoclast differentiation	9	0.003873	PPP3R1, SYK, AKT2, BTK, PLCG2, MAPK1, GRB2, MAP3K7, NFKB1	3.523784	0.014395	0.008787
KEGG_PATHWAY	hsa04730:Long-term depression	6	0.004238	LYN, NRAS, PRKCB, GNAS, MAPK1, KRAS	5.559748	0.015518	0.009473
KEGG_PATHWAY	hsa04670:Leukocyte transendothelial migration	8	0.004674	CDC42, PRKCB, PLCG2, RAC2, CXCR4, PTPN11, EZR, RHOA	3.834309	0.016868	0.010297
KEGG_PATHWAY	hsa03082:ATP-dependent chromatin remodeling	8	0.004899	SS18, HDAC2, SMARCB1, HDAC1, SMARCA5, ARID1A, PHF6, H2AC17	3.801537	0.017426	0.010637
KEGG_PATHWAY	hsa05224:Breast cancer	9	0.004972	RB1, NRAS, AKT2, NCOA3, PTEN, BAX, MAPK1, KRAS, GRB2	3.380928	0.017438	0.010645
KEGG_PATHWAY	hsa05132:Salmonella infection	12	0.005292	CDC42, CYFIP2, HSP90AA1, HSP90AB1, AKT2, KIF5B, ABI1, BAX, MAPK1, MAP3K7, RHOA, NFKB1	2.658047	0.0183	0.011171
KEGG_PATHWAY	hsa04360:Axon guidance	10	0.005668	CDC42, NRAS, PPP3R1, PLCG2, RAC2, MAPK1, CXCR4, PTPN11, KRAS, RHOA	3.021602	0.019334	0.011802
KEGG_PATHWAY	hsa05219:Bladder cancer	5	0.005949	RB1, NRAS, MDM2, MAPK1, KRAS	6.780181	0.019832	0.012106
KEGG_PATHWAY	hsa04540:Gap junction	7	0.005973	NRAS, PRKCB, CDK1, GNAS, MAPK1, KRAS, GRB2	4.230243	0.019832	0.012106
KEGG_PATHWAY	hsa04935:Growth hormone synthesis, secretion and action	8	0.006146	NRAS, PRKCB, AKT2, PLCG2, GNAS, MAPK1, KRAS, GRB2	3.645737	0.020136	0.012292
KEGG_PATHWAY	hsa04611:Platelet activation	8	0.007	LYN, SYK, AKT2, BTK, PLCG2, GNAS, MAPK1, RHOA	3.558239	0.022636	0.013818
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	13	0.007435	PRKCB, NFKB1, CDC42, RPS6KA3, NRAS, PPP3R1, AKT2, RPS6KA1, RAC2, MAPK1, KRAS, GRB2, MAP3K7	2.409224	0.023734	0.014488

KEGG_PATHWAY	hsa05160:Hepatitis C	9	0.007592	RB1, YWHAE, NRAS, AKT2, BAX, MAPK1, KRAS, GRB2, NFKB1	3.147027	0.023929	0.014607
KEGG_PATHWAY	hsa04810:Regulation of actin cytoskeleton	11	0.008148	CDC42, CYFIP2, NRAS, AKT2, RAC2, MAPK1, CXCR4, KRAS, EZR, ARHGEF7, RHOA	2.65901	0.025359	0.01548
KEGG_PATHWAY	hsa05231:Choline metabolism in cancer	7	0.00848	NRAS, PRKCB, AKT2, RAC2, MAPK1, KRAS, GRB2	3.931135	0.026068	0.015913
KEGG_PATHWAY	hsa04210:Apoptosis	8	0.010897	NRAS, BCL2A1, AKT2, BAX, MAPK1, KRAS, ATM, NFKB1	3.27044	0.03309	0.0202
KEGG_PATHWAY	hsa05100:Bacterial invasion of epithelial cells	6	0.012688	CDC42, SEPTIN2, GAB1, SEPTIN6, CLTA, RHOA	4.27673	0.037876	0.023121
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	14	0.012778	YWHAE, HSP90AA1, HSP90AB1, SYK, PTEN, NFKB1, TCL1A, NRAS, CCND2, AKT2, MDM2, MAPK1, KRAS, GRB2	2.150179	0.037876	0.023121
KEGG_PATHWAY	hsa04066:HIF-1 signaling pathway	7	0.013261	TFRC, PRKCB, AKT2, PLCG2, MAPK1, VHL, NFKB1	3.570481	0.038846	0.023714
KEGG_PATHWAY	hsa05226:Gastric cancer	8	0.017885	RB1, NRAS, AKT2, GAB1, BAX, MAPK1, KRAS, GRB2	2.965199	0.051782	0.03161
KEGG_PATHWAY	hsa05208:Chemical carcinogenesis - reactive oxygen species	10	0.019949	NRAS, AKT2, PRKCD, PTEN, MAPK1, PTPN11, KRAS, GRB2, COX6C, NFKB1	2.460066	0.057096	0.034854
KEGG_PATHWAY	hsa04213:Longevity regulating pathway - multiple species	5	0.02459	HDAC2, NRAS, HDAC1, AKT2, KRAS	4.483668	0.069578	0.042473
KEGG_PATHWAY	hsa04714:Thermogenesis	10	0.024944	RPS6KA3, NRAS, SMARCB1, KDM1A, RPS6KA1, GNAS, KRAS, GRB2, ARID1A, COX6C	2.36585	0.069786	0.0426
KEGG_PATHWAY	hsa04520:Adherens junction	6	0.025284	CDC42, RAC2, MAPK1, PTPN6, MAP3K7, RHOA	3.586934	0.069954	0.042703
KEGG_PATHWAY	hsa03420:Nucleotide excision repair	5	0.025903	CDK7, PCNA, POLD1, ERCC2, POLR2H	4.412499	0.070876	0.043266
KEGG_PATHWAY	hsa04929:GnRH secretion	5	0.028653	NRAS, PRKCB, AKT2, MAPK1, KRAS	4.27673	0.076911	0.04695
KEGG_PATHWAY	hsa04926:Relaxin signaling pathway	7	0.028866	NRAS, AKT2, GNA5, MAPK1, KRAS, GRB2, NFKB1	2.993711	0.076911	0.04695
KEGG_PATHWAY	hsa04510:Focal adhesion	9	0.029035	CDC42, CCND2, PRKCB, AKT2, PTEN, RAC2, MAPK1, GRB2, RHOA	2.464913	0.076911	0.04695
UP_KW_BIOLOGICAL_PROCESS	KW-0945~Host-virus interaction	39	2.08E-13	RB1, YWHAE, EIF4A2, PHB1, SMARCB1, MRE11, SET, DDX3X, PCNA, TFRC, CXCR4, XPO1, ZC3H7B, RPS6KA1, MAPK1, EPS15, MAP3K7, LYN, CENPU, USP7, NPM1, XRCC6, HSP90AA1, SYK, EED, SMARCA5, SEPTIN6, RHOA, CCNA2, RAD50, ERCC2, ABI1, HNRNPA2B1, CDK1, MDM2, BAX, GRB2, TOP1, KPNB1, RB1, SMARCB1, CLTA, BUB1B, IKZF1, MKI67, SMC3, RPS6KA3, CCND2, RAD21, TPR, CHEK1, RPS6KA1, CNTRL, ZNF207, MAPK1, FANCI, UBE2C, SEPTIN2, PRKCD, SEPTIN6, SMC1A, RHOA, NDC80, CCNA2, WEE1, CDK7, RAD50, MELK, STAG2, TFDP1, FANCD2, CCNG1, CDK1, ATM, MAPRE1, MAD2L1	3.970392	1.37E-11	1.17E-11
UP_KW_BIOLOGICAL_PROCESS	KW-0131~Cell cycle	37	4.41E-12	FANCI, USP7, XRCC6, FH, MRE11, PCNA, FANCL, PRKDC, NONO, HUWE1, FANCA, SMC3, SMC1A, SFPQ, CDK7, RAD50, FANCD2, POLD1, RAD21, ERCC2, CHEK1	3.783231	1.46E-10	1.24E-10
UP_KW_BIOLOGICAL_PROCESS	KW-0234~DNA repair	21	2.00E-07	UBE2C, SEPTIN2, SEPTIN6, CLTA, BUB1B, SMC3, SMC1A, NDC80, RHOA, CCNA2, WEE1, CDK7, STAG2, CCND2, RAD21, CCNG1, TPR, CNTRL, ZNF207, CDK1, MAPRE1, MAD2L1	4.052619	4.40E-06	3.73E-06
UP_KW_BIOLOGICAL_PROCESS	KW-0132~Cell division	22	4.31E-07	FANCI, USP7, XRCC6, FH, MRE11, PCNA, FANCL, PRKDC, NONO, HUWE1, FANCA, SMC3, SMC1A, SFPQ, CDK7, RAD50, FANCD2, POLD1, RAD21, ERCC2, CHEK1, ATM	3.697126	7.10E-06	6.03E-06
UP_KW_BIOLOGICAL_PROCESS	KW-0227~DNA damage	22	9.58E-07	UBE2C, SEPTIN2, CLTA, BUB1B, SMC3, SMC1A, NDC80, CCNA2, WEE1, STAG2, RAD21, CCNG1, TPR, ZNF207, CDK1, MAPRE1, MAD2L1	3.520271	1.27E-05	1.07E-05
UP_KW_BIOLOGICAL_PROCESS	KW-0498~Mitosis	17	3.72E-06	TOP2A, USP7, SFPQ, DDX5, HDAC2, PRKDC, HDAC1, NONO, HUWE1, TOP1, EZH2	4.089629	4.10E-05	3.48E-05
UP_KW_BIOLOGICAL_PROCESS	KW-0090~Biological rhythms	12	8.89E-06	CYFIP2, DDX3X, BCL2A1, PRKCB, PRKCD, PTEN, BUB1B, NFKB1, MELK, RABEP1, AKT2, INPP5D, RAD21, MDM2, BTK, CDK1, BAX, MAPK1, MAP3K7	5.619632	8.39E-05	7.12E-05
UP_KW_BIOLOGICAL_PROCESS	KW-0053~Apoptosis	19	7.56E-04	RB1, SMARCB1, DDX3X, KDM1A, IKZF1, AFF3, CHD2, IKZF3, ETS1, PHF6, MAP3K7, GTF2I, SS18, EED, PRKCB, NCOA3, PAX5, ARID1A, CBFA2T3, FOXF1, SFPQ, TFDP1, IRF4, EWSR1, TBL1XR1, SARNP, BTK, IRF8, DDX5, DNMT1, HDAC2, HDAC1, CUX1, RAD21, LPXN, MAPK1, SUZ12, CENPU, XRCC6, UTP4, BCL11A, NONO, HMGA1, LRPPRC, NFKB1, CDK7, NACA, POU2AF1, CNOT2, ERCC2, TCEA1, EZH2	2.431079	0.006235	0.005291
UP_KW_BIOLOGICAL_PROCESS	KW-0805~Transcription regulation	52	0.001189	RB1, SMARCB1, DDX3X, KDM1A, IKZF1, AFF3, CHD2, IKZF3, ETS1, PHF6, MAP3K7, GTF2I, SS18, EED, PRKCB, NCOA3, PAX5, ARID1A, CBFA2T3, FOXF1, SFPQ, TFDP1, IRF4, EWSR1, TBL1XR1, SARNP, BTK, IRF8, DDX5, DNMT1, HDAC2, HDAC1, CUX1, RAD21, LPXN, MAPK1, POLR2H, SUZ12, CENPU, XRCC6, UTP4, BCL11A, NONO, HMGA1, LRPPRC, NFKB1, CDK7, NACA, POU2AF1, CNOT2, ERCC2, TCEA1, EZH2	1.513157	0.008428	0.007151
UP_KW_BIOLOGICAL_PROCESS	KW-0804~Transcription	53	0.001277	RB1, SMARCB1, DDX3X, KDM1A, IKZF1, AFF3, CHD2, IKZF3, ETS1, PHF6, MAP3K7, GTF2I, SS18, EED, PRKCB, NCOA3, PAX5, ARID1A, CBFA2T3, FOXF1, SFPQ, TFDP1, IRF4, EWSR1, TBL1XR1, SARNP, BTK, IRF8, DDX5, DNMT1, HDAC2, HDAC1, CUX1, RAD21, LPXN, MAPK1, POLR2H, SUZ12, CENPU, XRCC6, UTP4, BCL11A, NONO, HMGA1, LRPPRC, NFKB1, CDK7, NACA, POU2AF1, CNOT2, ERCC2, TCEA1, EZH2	1.499398	0.008428	0.007151
UP_KW_BIOLOGICAL_PROCESS	KW-0509~mRNA transport	8	0.001484	NUP93, NUP107, XPO1, SARNP, TPR, HNRNPA2B1, SRSF3, LRPPRC	4.72238	0.008901	0.007553
UP_KW_BIOLOGICAL_PROCESS	KW-0159~Chromosome partition	5	0.004291	DDX3X, STAG2, RAD21, ERCC2, ZNF207	7.472915	0.023603	0.020026
UP_KW_CELLULAR_COMPONENT	KW-0539~Nucleus	146	2.37E-30	RB1, CYFIP2, PHB1, MRE11, NUP107, SMARCB1, KDM1A, BUB1B, IKZF1, SMC3, MKI67, IKZF3, ETS1, H2AC17, RPS6KA3, TCL1A, CCND2, AKT2, RPS6KA1, CHEK1, ZNF207, GTF2I, MBNL1, USP7, PRKCB, PRKCD, IRAG2, FBXO11, FOXF1, NUP93, EWSR1, TBL1XR1, FANCD2, SARNP, SRSF2, BTK, SRSF3, KPNB1, DDX6, DDX5, DNMT1, SET, PRKDC, PPP4C, RAD21, TPR, LPXN, H3C2, FANCI, LYN, XRCC6, CPSF6, FANCL, BCL11A, FUS, NONO, SMARCA5, HMGA1, FANCA, NDC80, NFKB1, CDK7, STAG2, NACA, CNOT2, MDM2, CDK1, GRB2, MDM4, ATM, EZH2, PICALM, YWHAE, CEP57, TOP2A, TOP2B, DDX3X, HSP90AB1, PTEN, AFF3, CHD2, PHF6, PTBP1, XPO1, ZC3H7A, ZC3H7B, CNTRL, OFD1, SS18, HSP90AA1, EED, PRMT1, NCOA3, CAD, PAX5, SMC1A, ARID1A, CBFA2T3, RHOA, CCNA2, H2BC12, SFPQ, TFDP1, PKM, IRF4, IRF8, TOP1, PFDN5, FH, HDAC2, PCNA, HDAC1, RAP1GDS1, U2AF1, TYMS, SH3BP1, FIP1L1, CUX1, U2AF2, POLD1, MAPK1, VHL, POLR2H, SF3B1, SUZ12, CENPU, NPM1, UTP4, H2BC4, HUWE1, ELP2, PTPN11, DEK, LRPPRC, WEE1, RAD50, POU2AF1, ERCC2, ABI1, HNRNPA2B1, CCNG1, TCEA1, BAX, PTPN6, PTPN2, MAD2L1	2.202816	8.78E-29	7.83E-29

UP_KW_CELLULAR_C OMPONENT	KW-0963~Cytoplasm	121	1.85E-15	CYFIP2, PHB1, BUB1B, IKZF1, MSI2, IKZF3, ETS1, RPS6KA3, TCL1A, CCND2, AKT2, KIF5B, FGFR1OP2, RPS6KA1, CHEK1, ZNF207, MAP3K7, GTF2I, MBNL1, USP7, TPM3, FNBP1, PRKCB, RPL22, PRKCD, IRAG2, EWSR1, BTK, SRSF3, EZR, CARD11, KPNB1, DDX6, DDX5, SET, GMPS, PPP3R1, PPP4C, INPP5D, RAD21, TPR, LPXN, FANCI, LYN, CARMIL2, CPSF6, FANCL, BCL11A, HSPA4, FANCA, HOOK3, NFKB1, CDK7, NACA, CAPRIN1, CNOT2, CCDC88C, MDM2, CDK1, GRB2, ATM, CALR, RPS21, YWHAE, CEP57, TOP2A, DDX3X, HSP90AB1, WDR1, PTEN, CLTA, LASP1, XPO1, ATIC, CNTRL, RAC2, OFD1, HSP90AA1, SYK, PRMT1, NCOA3, CAD, RHOA, CCNA2, SFPO, TFDP1, RABEP1, PKM, IRF8, LCP1, MAPRE1, ARHGEF7, PFDN5, FH, HDAC2, BCL2A1, RAP1GDS1, TYMS, CDC42, SH3BP1, MAPK1, VHL, EPS15, CENPU, NPM1, SEPTIN2, HUWE1, SEPTIN6, ELP2, PTPN11, NIN, ERCC2, ABI1, HNRNPA2B1, CCDC6, BAX, KRAS, PTPN6, CEP43, PTPN2, MAD2L1	1.84229	3.41E-14	3.05E-14
UP_KW_CELLULAR_C OMPONENT	KW-0158~Chromosome	35	2.16E-14	FH, MRE11, NUP107, KDM1A, BUB1B, MKI67, SMC3, PHF6, H2AC17, RAD21, TPR, CHEK1, CNTRL, ZNF207, H3C2, CENPU, USP7, XRCC6, UTP4, EED, BCL11A, SEPTIN2, NONO, H2BC4, SMARCA5, HMGA1, IRAG2, SEPTIN6, SMC1A, FBXO11, NDC80, H2BC12, RAD50, STAG2, MAD2L1	4.933729	2.67E-13	2.38E-13
UP_KW_CELLULAR_C OMPONENT	KW-0137~Centromere	14	1.28E-08	CENPU, NUP107, SEPTIN2, SEPTIN6, BUB1B, SMC3, SMC1A, PHF6, NDC80, STAG2, RAD21, TPR, ZNF207, MAD2L1	8.360671	1.18E-07	1.05E-07
UP_KW_CELLULAR_C OMPONENT	KW-0995~Kinetochore	11	2.98E-07	CENPU, NUP107, SEPTIN2, TPR, ZNF207, SEPTIN6, BUB1B, SMC1A, PHF6, NDC80, MAD2L1	9.259301	2.21E-06	1.97E-06
UP_KW_CELLULAR_C OMPONENT	KW-0206~Cytoskeleton	37	3.42E-06	CEP57, DDX3X, WDR1, CLTA, BUB1B, CDC42, LASP1, PPP4C, KIF5B, INPP5D, RAD21, TPR, CHEK1, CNTRL, ZNF207, MAPK1, OFD1, NPM1, CARMIL2, TPM3, FNBP1, SEPTIN2, IRAG2, SEPTIN6, HOOK3, RHOA, NIN, ERCC2, ABI1, CDK1, CCDC6, ATM, LCP1, EZR, MAPRE1, CEP43, MAD2L1	2.29973	2.11E-05	1.88E-05
UP_KW_MOLECULA R_FUNCTION	KW-0678~Repressor	24	8.86E-06	RB1, SUZ12, CENPU, DNMT1, HDAC2, KDM1A, EED, BCL11A, HDAC1, NONO, IKZF1, CBFA2T3, FOXP1, PTBP1, SFPO, CUX1, TBL1XR1, U2AF2, EWSR1, CNOT2, RAD21, IRF8, MAPK1, EZH2	2.857589	3.03E-04	2.49E-04
UP_KW_MOLECULA R_FUNCTION	KW-0694~RNA-binding	26	1.45E-05	EIF4A2, DDX6, DDX5, DDX3X, U2AF1, MSI2, PTBP1, XPO1, FIP1L1, ZC3H7A, U2AF2, SF3B1, NPM1, MBNL1, CPSF6, FUS, NONO, RPL22, LRPPRC, SFPO, EWSR1, SARNP, CAPRIN1, HNRNPA2B1, SRSF2, SRSF3	2.621676	3.03E-04	2.49E-04
UP_KW_MOLECULA R_FUNCTION	KW-0156~Chromatin regulator	16	1.78E-05	RB1, SUZ12, DNMT1, HDAC2, SMARCB1, KDM1A, PRKCB, EED, HDAC1, SMARCA5, DEK, IKZF1, ARID1A, CHD2, TBL1XR1, EZH2	3.822138	3.03E-04	2.49E-04
UP_KW_MOLECULA R_FUNCTION	KW-0238~DNA-binding	49	4.69E-05	RB1, TOP2A, TOP2B, SMARCB1, DDX3X, IKZF1, AFF3, MKI67, CHD2, IKZF3, ETS1, PHF6, H2AC17, ZNF207, GTF2I, PAX5, ARID1A, FOXP1, H2BC12, SFPO, TFDP1, IRF4, SARNP, IRF8, TOP1, DNMT1, SET, PCNA, PRKDC, CUX1, POLD1, RAD21, MAPK1, H3C2, POLR2H, FANCI, XRCC6, FUS, NONO, H2BC4, HMGA1, HUWE1, DEK, LRPPRC, NFKB1, NACA, ERCC2, TCEA1, ATM	1.758569	5.98E-04	4.92E-04
UP_KW_MOLECULA R_FUNCTION	KW-0418~Kinase	24	1.29E-04	LYN, GIT2, SYK, PRKCB, PRKDC, PRKCD, BUB1B, TTK, HOOK3, RPS6KA3, WEE1, CDK7, PKM, MELK, PRKAR1A, AKT2, RPS6KA1, CHEK1, BTK, CDK1, MAPK1, ATM, MAP3K7, GTF2I	2.407188	0.001312	0.001081
UP_KW_MOLECULA R_FUNCTION	KW-0723~Serine/threonine-protein kinase	16	2.39E-04	PRKCB, PRKDC, PRKCD, BUB1B, TTK, RPS6KA3, CDK7, MELK, AKT2, RPS6KA1, CHEK1, CDK1, MAPK1, ATM, MAP3K7, GTF2I	3.036636	0.002029	0.001671
UP_KW_MOLECULA R_FUNCTION	KW-0347~Helicase	8	0.003244	EIF4A2, DDX6, XRCC6, DDX5, DDX3X, ERCC2, SMARCA5, CHD2	4.121149	0.021933	0.018063
UP_KW_MOLECULA R_FUNCTION	KW-0799~Topoisomerase	3	0.003441	TOP2A, TOP2B, TOP1	32.45405	0.021933	0.018063
UP_KW_MOLECULA R_FUNCTION	KW-0010~Activator	19	0.006735	S518, XRCC6, DNMT1, SMARCB1, NONO, NCOA3, IKZF1, AFF3, NFKB1, PTBP1, SFPO, TFDP1, TBL1XR1, IRF4, NACA, POU2AF1, RAD21, IRF8, LPXN	1.984546	0.038165	0.03143

Suppl. Table S9.3 Significantly enriched terms and pathways analyzed by DAVID functional annotation tool for 530 genes upregulated in clusters 1, 2, and 5 (corresponding to the 2nd enrichment plot in Figure 3)

Category	Term	Count	P Value	Genes	Fold Enrichment	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription by RNA polymerase II	130	2.41E-44	CSF3, FGF1, HOXA13, FGF2, TNF, FGF4, SOX2, HOXA9, CREB3L1, LMO1, HGF, LMO2, SOX11, MTF, HNF1A, SOX10, RUNX2, AR, MYCN, SFRP2, MAF, SMO, DDIT3, ERG, ZFPM2, ATF3, NOTCH2, NOTCH3, NOTCH4, GATA6, PIK3R2, GATA3, BHLHE22, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, NKX2-5, PPARGC1A, TFAP2A, WWTR1, EGR1, JUN, EGR2, BCL11B, EGR4, AUTS2, TGFBR3, ZBTB16, HMGA2, INHBA, IGF1, ESR1, PBX1, IL2, FOSL1, BMP4, BCL9, NR4A3, MAFB, LHX2, TLX1, FEV, ID4, CD28, LHX4, HOXD9, FGFR2, NODAL, FGF10, HOXC13, GLI1, HOXC11, GLI3, MECOM, HEY1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, PEG3, TET1, PAX3, ETV1, FOXL2, OLIG1, FOS, ETV4, DCN, PAX8, TAL1, IL1B, ITGA8, PPARG, MET, TLR4, YAP1, CEBPA, HDAC5, HLF, CEBPD, CEBPE, PLAG1, LRP5, HOXD13, DLL1, EGFR, FSTL3, MUC1, STAT4, HES1, HESS, TCF7L2, PRRX1, CDX2, EYA1, DMRT1, CDKN2A, CDX1, DAB2IP, KLF4, ACVR2A, PER1, NR6A1, WT1, NFIB, FOSB	4.036624	9.00E-41	8.29E-41
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell population proliferation	76	7.52E-36	CSF3, CSF1, EPO, FLT3, IRS1, FLT4, TNC, ADM, IRS2, FASLG, GLI1, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, FGF8, EDNRB, FGF9, KDR, PDGFRB, PDGFRA, IL15, MATK, FLT3LG, LIFR, TIAM1, AR, SFRP2, IL18, ATF3, PDGFB, LRP5, PDGFA, TNFRSF11A, DLL1, EGFR, ERBB3, ERBB4, PDGFD, ZNF703, ERBB2, NTF3, HAS2, HES1, S1PR2, NKX2-5, FGF23, HESS, IL12RB2, NTRK2, WWTR1, TGFBR2, CDX2, EGR4, TGFBR3, EGF, NTRK3, AKR1C3, VEGFC, VEGFD, IGF1, EPOR, TSHR, IL2, BMP4, FOSL1, IL3, FGF19, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1	5.857708	1.40E-32	1.29E-32
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	74	6.30E-34	RET, CSF1, ITGB3, TNC, FGF1, FGF2, TNF, FGF3, FGF4, ROBO1, FGF6, FGF8, FGF9, AMH, IL13, SOX11, MTF, WNT16, NGF, SOX10, DKK1, RUNX2, TGFBR3, SFRP4, AR, MYCN, MAF, SMO, IL1B, PPARG, TLR4, ATF3, YAP1, CEBPA, CEBPE, PLAG1, PDGFB, GATA2, ACVR1B, DLL1, DLL4, WNT6, ERBB3, ERBB2, NKX2-1, HES1, NKX2-5, FGF23, PPARGC1A, TFAP2A, EGR1, NTRK2, ANGPT1, CDKN2A, EGF, NOS3, NTRK3, CAV1, HMGA2, IGF1, INHBA, KLF4, BMP4, WT1, FEV, FGF19, CD28, ID4, CNTN1, SPRY2, FGFR4, IL7R, FGF10, HSPA1A	5.669941	7.84E-31	7.22E-31
GOTERM_BP_DIRECT	GO:0060070~canonical Wnt signaling pathway	34	3.85E-26	YAP1, WNT2B, LRP5, WNT8B, GATA3, FZD10, FOXO3, FGF2, WNT6, EDNRB, WNT11, FGF9, ADGRA2, GPC3, WNT4, TCF7L2, WNT10B, FZD3, FZD2, WNT5B, EGF, FZD7, CAV1, WNT7B, FZD6, FZD8, KLF4, WNT16, DKK1, LRP1B, EXT1, SFRP4, BCL9, SFRP2	11.83929	3.59E-23	3.31E-23

GOTERM_BP_DIRECT	GO:000122~negative regulation of transcription by RNA polymerase II	88	2.03E-25	EPO, FHL2, FASLG, TNF, GLI3, SOX2, FLCN, DACH1, EDNRB, HEY1, FGF9, CCND1, PPP1R13L, TRPS1, CREB3L1, MNX1, SSX1, LMO1, PEG3, DNMT3A, TET1, SOX11, FOXL2, MITF, HNF1A, DUSP26, SOX10, DKK1, AR, MAF, SMO, TAL1, DDIT3, PPARG, BCORL1, ZFPM2, ATF3, YAP1, NOTCH2, CEBPA, HDAC5, NOTCH3, NOTCH4, GATA6, GATA3, FOXO3, GATA2, GATA1, DLL4, PRDM16, NKX2-1, HES1, NKX2-5, HES5, TFAP2A, TCF7L2, EGR1, WNT10B, WWTR1, JUN, PRRX1, CDX2, MAGEE1, DMRT1, ZBTB16, CAV1, PTCH1, DAB2IP, HMGA2, KLF4, ESR1, BMP4, TBX15, PER1, NR4A3, MAFB, NR6A1, NFIB, WT1, NEDD4, ID1, ID4, FOSB, HOXD9, FGFR2, NODAL, FGF1, HSPA1A	3.563863	1.51E-22	1.39E-22
GOTERM_BP_DIRECT	GO:0051897~positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	41	3.88E-25	RET, CSF3, FLT3, IRS1, SRC, PDGFB, PDGFA, IRS2, GATA3, FGF2, TNF, EGFR, IGF1R, RELN, ERBB3, ERBB4, PDGFD, KDR, PDGFRB, NTRK1, TCF7L2, PDGFRA, NTRK2, TGF2, ANGPT1, EGF, HGF, NTRK3, AKR1C3, HNF1A, IGF1, WNT16, DCN, AXL, NEDD4, KIT, CD28, SPRY2, FGFR3, FGFR1, DDR2	8.328125	2.41E-22	2.22E-22
GOTERM_BP_DIRECT	GO:0045893~positive regulation of DNA-templated transcription	74	1.44E-24	CDKN1C, RET, EPO, HOXC13, GLI1, FGF2, TNF, GLI3, HOXA11, SOX2, MECOM, ZIC2, CDH1, TEAD1, MYBL1, PAX3, FOXL2, MITF, HNF1A, FOS, SOX10, RUNX2, AR, MYCN, PAX8, TAL1, IL1B, DDIT3, PPARG, PLCB1, YAP1, NOTCH4, PDGFB, GATA6, LRP5, GATA3, FOXO3, GATA1, EGFR, WNT6, WNT11, ERBB4, PRDM16, NKX2-1, NKX2-5, FGF23, PPARGC1A, HES5, WNT4, TFAP2A, EGR1, JUN, EGR2, FZD2, TGF2, CDKN2A, EGF, FZD7, ZBTB16, PTCH1, HMGA2, PDE4DIP, IGF1, INHBA, GDF6, KLF4, ESR1, BMP4, MLLT11, TBX15, MAFB, LHX2, NFIB, WT1	4.047686	7.69E-22	7.08E-22
GOTERM_BP_DIRECT	GO:0007169~cell surface receptor protein tyrosine kinase signaling pathway	32	7.61E-24	RET, ALK, SHC2, CSF1, FLT3, SRC, FLT4, EGFR, NTF4, ERBB3, ERBB4, ERBB2, NTF3, KDR, ROS1, PDGFRB, NTRK1, PDGFRA, NTRK2, BDNF, NTRK3, STYK1, NGF, AXL, PTK7, FGFR4, MET, FGFR3, FGFR2, FGFR1, EPHA2, DDR2	11.24324	3.55E-21	3.27E-21
GOTERM_BP_DIRECT	GO:0007275~multicellular organism development	28	3.20E-23	RET, ALK, FLT3, FLT4, EGFR, IGF1R, FSTL3, ERBB3, ERBB4, CDH1, ERBB2, KDR, ROS1, PDGFRB, NTRK1, PDGFRA, NTRK2, NTRK3, AXL, KIT, CDH11, FGFR4, MET, FGFR3, FGFR2, FGFR1, EPHA2, DDR2	13.48148	1.33E-20	1.22E-20
GOTERM_BP_DIRECT	GO:0033674~positive regulation of kinase activity	24	1.25E-22	PDGFRB, ALK, NTRK1, RET, PDGFRA, NTRK2, FLT3, FLT4, NTRK3, EGFR, IGF1R, ERBB3, AXL, ERBB4, ERBB2, KDR, FGFR4, MET, ROS1, FGFR3, FGFR2, EPHA2, FGFR1, DDR2	17.01818	4.67E-20	4.30E-20
GOTERM_BP_DIRECT	GO:0045165~cell fate commitment	24	3.39E-22	WNT10B, WNT2B, WNT5B, WNT7B, GATA6, WNT8B, MITF, GATA3, GATA2, WNT16, GATA1, SOX2, EXT1, WNT6, FGF8, WNT11, TAL1, ERBB4, KDR, SPRY2, GAS1, PPARG, FGFR2, WNT4	16.42105	1.15E-19	1.06E-19
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	39	2.38E-20	NOTCH2, EPO, SRC, FLT4, ITGB3, PDGFB, PDGFA, NOD1, PLA2G5, TNFRSF11A, FGF1, FGF2, TNF, EGFR, FGF4, AKAP12, FGF8, ERBB4, PDGFD, KDR, FGF23, PDGFRB, NTRK1, PDGFRA, ANGPT1, PRKCA, IGF1, INHBA, TIRAP, BMP4, FGF19, SPRY2, ACKR3, FGFR4, FGFR3, TLR4, FGFR2, NODAL, FGF10	6.671053	7.40E-18	6.82E-18
GOTERM_BP_DIRECT	GO:1902895~positive regulation of miRNA transcription	23	3.33E-20	NOTCH2, NGFR, EGR1, NOTCH3, TGF2, JUN, PDGFB, GATA3, FOS, GATA2, KLF4, FOXO3, SMAD6, FGF2, TNF, EGFR, BMP4, FOSL1, AR, MYCN, WT1, PPARG, TEAD1	14.95	9.56E-18	8.81E-18
GOTERM_BP_DIRECT	GO:0043410~positive regulation of MAPK cascade	35	1.73E-19	RET, FLT3, FLT4, PDGFB, LPAR1, PDGFA, FGF2, TNF, FGF3, GRM1, FGF4, IGF1R, SOX2, FGF6, FGF8, FGF9, ERBB2, KDR, FGF23, WNT4, NTRK2, KSR1, TGF2, EGF, FZD7, HGF, DAB2IP, IGF1, AR, FGF19, KIT, FGFR3, FGFR2, FGF10, FGFR1	7.260638	4.63E-17	4.26E-17
GOTERM_BP_DIRECT	GO:0001934~positive regulation of protein phosphorylation	36	4.08E-19	CDKN1A, FLT4, ITGB3, FGF1, FGF2, TNF, FGF3, EGFR, FGF4, FGF6, FGF8, RELN, EDNRB, FGF9, CCND1, ERBB4, ERBB2, KDR, FGF23, NTRK1, NTRK2, EPHA7, ANGPT1, HGF, NTRK3, VEGFC, FZD8, VEGFD, HNF1A, INHBA, HSPA2, ACVR2A, BMP4, IL1B, FGF19, FGF10	6.815534	1.02E-16	9.36E-17
GOTERM_BP_DIRECT	GO:0007165~signal transduction	89	1.02E-18	RET, ALK, TENM1, ITK, PTPRR, CSF3R, EPO, IRS1, CTNND2, IRS4, CBLC, ADM, IRS2, FASLG, PTPRK, FGF1, FGF2, FGF3, IGF1R, FGF4, AKAP12, FGF9, CHL1, PLA2, CCN6, PRKG2, RAC3, MAP3K6, SH3GL2, PDGFRB, IL15, IL13, MATK, FLT3LG, RHOD, GABRG2, AR, INPP4B, IL1B, KIT, ITPKA, PPARG, ERG, PLPP3, PLCB1, DOCK1, MET, CILK1, DDR2, FBN2, CAMK2B, SRC, WNT8B, NOD1, PIK3R2, GATA3, TNFRSF11A, ACVR1B, TRHDE, KALRN, EGFR, DLL4, ARHGAP20, WNT11, ERBB3, ERBB4, WIF1, GNA11, ERBB2, NTF3, GNA12, CHN1, ABL2, SRGAP3, LEFTY2, PAK5, VEGFC, CCK, IGF1, ESR1, EPOR, TNFRSF10D, NR4A3, FGF14, AXL, PTK7, FGF13, IL7R, HSPA1A	2.799194	2.38E-16	2.20E-16
GOTERM_BP_DIRECT	GO:0043406~positive regulation of MAP kinase activity	20	4.63E-17	PDGFRB, TENM1, FLT3, EGF, NTRK3, PDGFB, PDGFA, FGF1, FGF2, TNF, EGFR, ROBO1, GHR, IL1B, PDGFD, KIT, NTF3, ERBB2, TLR4, FGFR1	14.18182	1.02E-14	9.37E-15
GOTERM_BP_DIRECT	GO:0018108~peptidyl-tyrosine phosphorylation	18	2.97E-15	PDGFRB, NTRK1, PDGFRA, FLT3, SRC, FLT4, PDGFB, EGFR, RELN, ERBB4, ERBB2, KDR, ABL2, FGF4, FGFR2, EPHA3, FGFR1, DDR2	14.04	6.16E-13	5.67E-13
GOTERM_BP_DIRECT	GO:0030182~neuron differentiation	28	1.22E-14	HDAC5, BRSK1, WNT2B, WNT8B, FZD10, SOX2, WNT6, FGF8, WNT11, CCND1, ERBB2, WNT4, NTRK2, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, DNMT3A, FZD8, SOX11, WNT16, RUNX2, LHX2, LHX4, MET, EPHA2	6.658537	2.40E-12	2.21E-12
GOTERM_BP_DIRECT	GO:0072089~stem cell proliferation	17	4.11E-14	RNF43, PRRX1, WNT7B, PTCH1, FGF2, GLI3, RUNX2, PBX1, FGF4, FGF8, WNT11, FGF9, NFIB, HOXA3, KDR, FGF10, FGFR1	13.53061	7.31E-12	6.73E-12
GOTERM_BP_DIRECT	GO:0051781~positive regulation of cell division	17	4.11E-14	TGF2, TGF3, PDGFB, VEGFC, PDGFA, VEGFD, FGF1, FGF2, FGF3, FGF4, FGF6, FGF8, FGF9, TAL1, IL1B, PDGFD, FGFR2	13.53061	7.31E-12	6.73E-12
GOTERM_BP_DIRECT	GO:0008543~fibroblast growth factor receptor signaling pathway	18	4.98E-14	NGFR, FGF1, FGF2, FGF3, FGF4, EXT1, FGF6, FGF8, FGF9, FGF19, SPRY2, FGFR4, FGF23, FGFR3, FGFR2, FGF10, FGFR1, WNT4	12.10345	8.45E-12	7.78E-12
GOTERM_BP_DIRECT	GO:0006357~regulation of transcription by RNA polymerase II	93	1.36E-13	ZNF331, EPO, HOXC13, DACH2, GLI1, HOXA13, HOXC11, GLI3, HOXA11, HOXA9, DACH1, HEY1, MECOM, ZIC2, PPP1R13L, TRPS1, CREB3L1, HOXA3, ZNF444, ZNF521, TEAD1, TEAD3, TEAD4, PEG3, PAX3, FOXL2, MITF, ETV1, HNF1A, FOS, SOX10, ETV4, RUNX2, MYCL, DMRTA2, MYCN, MAF, PAX8, TAL2, PAX7, TAL1, DDIT3, AHRR, PPARG, ERG, ATF3, VGLL3, CEBPA, HLF, CEBPD, CEBPE, HOXD13, FOXO4, FOXO3, HOXD11, FSTL3, PRDM16, NKX2-1, STAT4, HES1, NKX2-5, HES5, TFAP2A, TCF7L2, EGR1, JUN, EGR2, PRRX1, CDX2, EGR4, DMRT1, CDX1, ZBTB16, PRRX2, INHBA, KLF4, SMAD6, ESR1, PBX1, FOSL1, TBX15, NR4A3, MAFB, NR6A1, TLX3, LHX2, NFIB, WT1, FEV, TLX1, FOSB, LHX4, HOXD9	2.258406	2.21E-11	2.04E-11
GOTERM_BP_DIRECT	GO:0009887~animal organ morphogenesis	24	4.65E-13	NOTCH2, LAMA5, CDX2, CDX1, ELN, PTCH1, VEGFC, PDGFA, PAX3, FGF1, FGF2, DCN, FGF3, PBX1, FGF4, LFNG, FGF6, FGF8, FGF9, FGF19, LHX4, FGF23, FGFR2, FGF10	6.985075	7.24E-11	6.67E-11
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell population proliferation	42	6.22E-13	TENM1, CEBPA, CDKN1A, ATP8A2, ADM, GATA3, FOXO4, PTPRK, PTGS2, DLL1, GATA1, RERG, DLL4, ERBB4, CCN6, CYP1B1, TFAP2A, NTRK1, TGF2, CDKN2B, BCL11B, TGF3, CDKN2A, NOS3, ZBTB16, DAB2IP, DLEC1, INHBA, NGF, KLF4, SMAD6, BMP4, FOSL1, SFRP4, AR, SFRP2, WT1, IL1B, NEUR1, SPRY2, ACKR3, HSPA1A	3.774194	9.29E-11	8.56E-11

GOTERM_BP_DIRECT	GO:0042060~wound healing	19	8.44E-13	YAP1, NOTCH2, PDGFRA, CDKN1A, TGF2, SDC4, DST, ITGB3, NOTCH4, PDGFA, IGF1, FGF1, FGF2, EXT1, ERBB3, PTK7, ERBB2, PLPP3, FGF10	9.5	1.21E-10	1.12E-10
GOTERM_BP_DIRECT	GO:0050673~epithelial cell proliferation	16	1.06E-12	YAP1, EYA1, EGF, HGF, FGF1, EGFR, RUNX2, BMP4, FLCN, AR, SMO, KIT, KDR, GPC3, NKX2-5, FGF10	12.48	1.42E-10	1.31E-10
GOTERM_BP_DIRECT	GO:0045669~positive regulation of osteoblast differentiation	19	1.07E-12	YAP1, FBN2, WWTR1, WNT10B, CEBPA, CEBPD, HGF, WNT7B, LRP5, SOX11, IGF1, FGF2, GLI3, ACVR2A, RUNX2, BMP4, SFRP2, WNT4, DDR2	9.379747	1.42E-10	1.31E-10
GOTERM_BP_DIRECT	GO:0071300~cellular response to retinoic acid	18	1.49E-12	YAP1, RET, WNT10B, WNT5B, FZD7, WNT7B, TNC, WNT8B, FZD10, KLF4, TNF, WNT6, WNT11, PTK7, ABL2, PPARG, FGFR2, EPHA3	10.02857	1.92E-10	1.77E-10
GOTERM_BP_DIRECT	GO:0001658~branching involved in ureteric bud morphogenesis	15	2.46E-12	LAMA5, EYA1, PTCH1, HOXD11, FGF2, GLI3, PBX1, HOXA11, BMP4, WNT6, FGF8, PAX8, WT1, GPC3, WNT4	13.29545	3.06E-10	2.82E-10
GOTERM_BP_DIRECT	GO:0048661~positive regulation of smooth muscle cell proliferation	16	3.72E-12	PDGFRB, NOTCH3, ITGB3, IL13, PDGFB, IGF1, PTGS2, FGF2, TNF, EGFR, IGF1R, BMP4, NR4A3, PDGFD, TLR4, HES5	11.55556	4.48E-10	4.13E-10
GOTERM_BP_DIRECT	GO:0007411~axon guidance	28	4.37E-12	EPHB6, ROBO2, RET, NOTCH2, NOTCH3, EPHA10, GATA3, KALRN, GLI3, RELN, CHL1, NKX2-1, NCAM1, NTRK1, EPHA5, NGFR, EPHA7, BDNF, NTRK3, ETV1, EXT1, LHX2, PTK7, KIT, CNTN1, FGFR2, EPHA3, EPHA2	5.25	5.10E-10	4.70E-10
GOTERM_BP_DIRECT	GO:0016310~phosphorylation	50	5.59E-12	RET, ALK, ITK, CDKN1A, FLT3, FLT4, IGF1R, PLAUR, PRKACG, KDR, PRKG2, PDGFRB, PRKCG, EPHA5, EPHA7, CDKL5, KSR1, MATK, PRKCA, MAPK8IP2, KIT, ITPKA, MET, CILK1, EPHA2, CAMK2B, BRSK1, EPHA10, SRC, CAMK2A, AKAP6, AK5, KALRN, EGFR, ERBB3, ERBB4, ERBB2, PAK6, PAK3, PAK5, NTRK1, NTRK2, NTRK3, STYK1, ACVR2A, AXL, FGFR4, FGFR3, FGFR2, FGFR1	3.080569	6.33E-10	5.83E-10
GOTERM_BP_DIRECT	GO:0090090~negative regulation of canonical Wnt signaling pathway	24	1.23E-11	AMER1, EGRI, WWTR1, TCF7L2, CAV1, FZD6, IGFBP2, DAB2IP, FOXO3, GLI1, SOX10, DKK1, GLI3, BICC1, DKK2, SOX2, DKK4, SFRP4, SFRP2, WNT11, DDIT3, HECW1, GPC3, NKX2-5	6	1.35E-09	1.24E-09
GOTERM_BP_DIRECT	GO:0050679~positive regulation of epithelial cell proliferation	17	1.47E-11	YAP1, TCF7L2, EYA1, IGF1, FGF1, FGF2, EGFR, RUNX2, BMP4, NR4A3, FGF9, SMO, ERBB2, NKX2-5, NODAL, FGFR2, FGF10	9.608696	1.54E-09	1.42E-09
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	32	1.49E-11	RET, CSF1, FLT4, PDGFB, PDGFA, FGF1, GLI1, EGFR, IGF1R, PLAUR, PDGFD, ZNF703, NTF3, KDR, HAS2, PDGFRB, PDGFRA, MMP7, WNT5B, EGF, HGF, CAV1, NTRK3, PRKCA, IGF1, RHOD, TIAM1, SMO, IL1B, KIT, SPRY2, EPHA2	4.348432	1.54E-09	1.42E-09
GOTERM_BP_DIRECT	GO:0042475~odontogenesis of dentin-containing tooth	16	1.52E-11	JAG2, PDGFRA, NGFR, LAMA5, BCL11B, GATA6, TNC, ADM, GLI3, ACVR2A, RUNX2, FGF4, BMP4, WNT6, SMO, FGF10	10.57627	1.54E-09	1.42E-09
GOTERM_BP_DIRECT	GO:0009410~response to xenobiotic stimulus	30	1.76E-11	RET, HDAC5, CDKN1A, SRC, GATA6, SLC1A2, FOXO3, PTGS2, TNF, GRIN2A, FGF8, CCND1, CDH1, GNA12, AMH, NTRK1, FZD3, MMP7, ACE, PTCH1, IGFBP2, DNMT3A, VEGFC, FOS, FOSL1, SFRP2, CPS1, LOX, FOSB, PPARG	4.606299	1.73E-09	1.59E-09
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	43	2.35E-11	NOTCH2, CDKN1A, TNFRSF6B, SRC, FLT4, GATA6, FHL2, TNF, GATA1, EGFR, GLI3, FGF4, IGF1R, SOCS2, EDNRB, ERBB3, CHST11, ERBB4, ERBB2, KDR, NKX2-5, TFAP2A, NTRK1, ANGPT1, HGF, HMGA2, MITF, HNF1A, IGF1, SMAD6, SOX10, DKK1, IL2, TNFRSF10D, SMO, WT1, PAX7, AXL, CD28, SPRY2, LHX4, HSPA1A, DDR2	3.307692	2.25E-09	2.07E-09
GOTERM_BP_DIRECT	GO:0010467~gene expression	22	7.95E-11	EGR2, PDGFB, GATA6, LRP5, RUNX2, GFAP, GRM3, EXT1, FOSL1, EXT2, EDNRB, SMO, NFIB, DDIT3, HOXA3, GRB10, NKX2-1, CNTN1, IL7R, ROS1, TLR4, FGFR1	6.085106	7.42E-09	6.83E-09
GOTERM_BP_DIRECT	GO:0045892~negative regulation of DNA-templated transcription	45	9.24E-11	CDKN1C, CEBPA, HDAC5, CEBPD, GATA6, PDGFB, GATA3, PTPRK, TNF, GLI3, DACH1, WNT11, MECOM, HEY1, ZIC2, CREB3L1, ZNF703, PRDM16, NKX2-1, HES1, NKX2-5, WNT4, RUNX1T1, TFAP2A, TCF7L2, JUN, CDKN2A, ZBTB16, DNMT3A, DAB2IP, HMGA2, FOXL2, KLF4, RUNX2, BMP4, ZFTA, PER1, SFRP2, WT1, DDIT3, ID1, ID4, PPARG, PLCB1, ZFPM2	3.062827	8.33E-09	7.67E-09
GOTERM_BP_DIRECT	GO:0042472~inner ear morphogenesis	15	9.37E-11	TFAP2A, FZD3, ATP8A2, PRRX1, COL11A1, FZD6, GATA3, GATA2, MAFB, PAX8, FGF9, ITGA8, SPRY2, FGFR2, FGFR1	10.44643	8.33E-09	7.67E-09
GOTERM_BP_DIRECT	GO:0010629~negative regulation of gene expression	32	1.08E-10	YAP1, NOTCH2, CDKN1A, PLAG1, SRC, PDGFB, GATA2, ACVR1B, FGF2, TNF, ROBO1, DLL4, CREB3L1, KDR, HES1, ROS1, SH3GL2, WNT4, TGF2, ACE, SOX11, IGF1, KLF4, ESR1, BMP4, MYCN, SFRP2, PC, SMO, FGF19, CD28, PPARG	4.025806	9.39E-09	8.64E-09
GOTERM_BP_DIRECT	GO:0030154~cell differentiation	49	2.03E-10	FGF1, FGF2, FGF3, FGF4, FGF6, FGF9, ZIC2, ROS1, MYBL1, FOXL2, ETV1, DLEC1, ETV4, SFRP4, SFRP2, PPARG, ERG, ZFPM2, CAMK2B, SRC, NOTCH4, DLL1, FSTL3, DLL3, ACVR1C, GNA12, NKX2-1, NKX2-5, FGF23, JAG2, NTRK1, NTRK2, CDX2, ANGPT1, EYA1, CDX1, BTBD18, NTRK3, CAV1, INHBA, SMAD6, ACER1, FEV, FGF19, ID1, ID4, TLL2, FGF10, FGFR1	2.818584	1.72E-08	1.59E-08
GOTERM_BP_DIRECT	GO:0030324~lung development	17	2.36E-10	PDGFRA, LAMA5, CEBPA, NOS3, WNT7B, FGF1, GLI1, FGF2, EGFR, GLI3, FGF9, LOX, NKX2-1, GPC3, HES1, ZFPM2, FGFR2	8.085366	1.95E-08	1.80E-08
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	32	2.79E-10	NOTCH2, SRC, HTRA1, LPAR1, ADM, NOD1, FASLG, FOXO3, PTGS2, TNF, FLCN, GRIN2A, ACVR1C, CYP1B1, WNT10B, JUN, ACE, CRADD, TGF2, CDKN2A, ZBTB16, DAB2IP, FOXL2, TNFRSF10D, BMP4, MLLT11, FOSL1, SFRP4, SFRP2, WT1, NEURL1, PPARG	3.875776	2.26E-08	2.08E-08
GOTERM_BP_DIRECT	GO:0045747~positive regulation of Notch signaling pathway	14	3.39E-10	JAG2, ROBO2, YAP1, TGF2, NOS3, SRC, DLL1, ROBO1, DLL4, LFNG, KIT, HES1, HES5, FGF10	10.70588	2.67E-08	2.46E-08
GOTERM_BP_DIRECT	GO:0045444~fat cell differentiation	17	3.44E-10	TCF7L2, WNT10B, CEBPA, EGR2, WNT5B, CEBPD, HMGA2, GATA2, KLF4, GDF6, SMAD6, NR4A3, MAFB, CCND1, ID4, PLCB1, ZFPM2	7.892857	2.67E-08	2.46E-08
GOTERM_BP_DIRECT	GO:2000648~positive regulation of stem cell proliferation	13	3.81E-10	PRRX1, HMGA2, SOX11, FGF2, RUNX2, PBX1, FGF4, FGF8, FGF9, HOXA3, KDR, FGF10, FGFR1	12.07143	2.90E-08	2.68E-08
GOTERM_BP_DIRECT	GO:0008584~male gonad development	19	5.04E-10	TGF2, ACE, WNT2B, GATA6, AKR1C3, GATA3, INHBA, ESR1, GATA1, HOXA11, AR, HOXA9, SFRP2, FGF9, WT1, PRKACG, KIT, CYP1B1, WNT4	6.616071	3.77E-08	3.47E-08
GOTERM_BP_DIRECT	GO:0001701~in utero embryonic development	26	5.43E-10	NOTCH2, CDKN1A, PTPRR, GATA6, GATA3, ACVR1B, GATA1, GLI3, FLCN, CHST11, GNA12, JAG2, SLC34A2, PDGFRA, ANGPT1, TGF2, NOS3, PTCH1, WNT7B, SOX10, FOSL1, AR, SMO, ZFPM2, FGFR2, FGFR1	4.588235	3.97E-08	3.66E-08
GOTERM_BP_DIRECT	GO:0006468~protein phosphorylation	34	8.12E-10	EPHB6, RET, CAMK2B, BRSK1, ITK, EPHA10, SRC, CAMK2A, PDGFB, ACVR1B, KALRN, ACVR1C, WNT11, ERBB2, PRKG2, ABL2, PAK6, PAK3, MAP3K6, ROS1, PAK5, PRKCG, NTRK1, EPHA5, EPHA7, CDKL5, STYK1, MATK, PRKCA, ACVR2A, ERG, CILK1, EPHA3, FGFR1	3.526596	5.83E-08	5.37E-08

GOTERM_BP_DIRECT	GO:0009653~anatomical structure morphogenesis	21	1.16E-09	FBN2, EYA1, GATA6, SOX11, FOXL2, GATA3, HOXC13, GATA2, FGF1, SMAD6, SOX10, GATA1, FGF3, HOXA11, SOX2, FGF8, PAX8, PAX7, CLTC1, GPC3, ZFPM2	5.571429	8.20E-08	7.55E-08
GOTERM_BP_DIRECT	GO:0046777~protein autophosphorylation	21	1.48E-09	PDGFRB, ALK, CAMK2B, NTRK1, PDGFRA, NTRK2, CDKL5, FLT3, SRC, FLT4, CAMK2A, ACVR1B, EGFR, IGF1R, ERBB4, KIT, KDR, FGFR4, FGFR2, FGFR1, DDR2	5.496644	1.02E-07	9.44E-08
GOTERM_BP_DIRECT	GO:0046579~positive regulation of Ras protein signal transduction	10	2.60E-09	NTRK1, NOTCH2, RASGEF1A, CSF1, EPO, SRC, IGF1, NGF, DGKI, FGF10	16.95652	1.77E-07	1.63E-07
GOTERM_BP_DIRECT	GO:0045840~positive regulation of mitotic nuclear division	11	3.02E-09	PDGFRB, FGF8, DMRT1, EGF, IL1B, PDGFB, LRP5, CD28, IGF1, TNF, HOXA13	13.83871	2.01E-07	1.85E-07
GOTERM_BP_DIRECT	GO:0009952~anterior/posterior pattern specification	17	3.67E-09	ZBTB16, LRP5, HOXD13, HOXC13, HOXC11, GLI3, ACVR2A, PBX1, HOXA11, HOXA9, HEY1, SMO, WIF1, HOXA3, HES1, HOXD9, HES5	6.765306	2.40E-07	2.21E-07
GOTERM_BP_DIRECT	GO:0001759~organ induction	8	4.89E-09	BMP4, FGF8, FGF1, FGF2, HOXC11, FGFR1, HOXA11, FGF10	26	3.15E-07	2.90E-07
GOTERM_BP_DIRECT	GO:0003148~outflow tract septum morphogenesis	10	6.22E-09	BMP4, ROBO2, TGF2, FGF8, GATA6, ZFPM2, NKX2-5, SMAD6, FGFR2, ROBO1	15.6	3.94E-07	3.63E-07
GOTERM_BP_DIRECT	GO:0030097~hemopoiesis	14	6.91E-09	NOTCH2, TGF2, ANGPT1, FLT3, NOTCH4, ZBTB16, DLL1, EPOR, RUNX2, FLCN, TAL1, KIT, NKX2-5, IL7R	8.53125	4.30E-07	3.96E-07
GOTERM_BP_DIRECT	GO:0001942~hair follicle development	12	7.59E-09	LAMA5, TGF2, FZD3, LHX2, FZD6, PDGFA, INHBA, HOXC13, ACVR1B, LGR5, DKK1, EGFR	10.88372	4.64E-07	4.28E-07
GOTERM_BP_DIRECT	GO:0006366~transcription by RNA polymerase II	25	9.35E-09	CEBPB, HOXD13, GATA3, GATA2, FGF2, HOXA13, GATA1, NKX2-5, WNT10B, PRRX1, BCL11B, ETV1, HNF1A, INHBA, FOS, KLF4, ESR1, IL2, BMP4, BCL9, AR, MAF, TAL1, CD28, FOSB	4.148936	5.63E-07	5.19E-07
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	26	1.24E-08	FLT4, PDGFA, FGF1, PTGS2, DLL4, FGF6, FGF9, HEY1, HOXA3, KDR, CYP1B1, APOD, PDGFRB, ANGPT1, EGF, NOS3, CAV1, DAB2IP, FZD8, PRKCA, TAL1, ID1, ACKR3, FGFR2, FGF10, FGFR1	3.945525	7.26E-07	6.69E-07
GOTERM_BP_DIRECT	GO:0042531~positive regulation of tyrosine phosphorylation of STAT protein	14	1.24E-08	EPO, IL15, FLT3, IL13, IGF1, TNF, IL2, GHR, IL3, ERBB4, KIT, HES1, FGFR3, HES5	8.149254	7.26E-07	6.69E-07
GOTERM_BP_DIRECT	GO:0090263~positive regulation of canonical Wnt signaling pathway	18	1.62E-08	YAP1, AMER1, KANK1, WNT10B, SRC, EGF, FGF2, EGFR, DKK2, SFRP4, SFRP2, FGF9, ADGRA2, PTK7, GPC3, LGR5, FGFR2, FGF10	5.707317	9.30E-07	8.56E-07
GOTERM_BP_DIRECT	GO:0014911~positive regulation of smooth muscle cell migration	9	2.64E-08	PDGFRB, SRC, ITGB3, PDGFB, CYP1B1, HAS2, IGF1, FOXO4, TLR4	16.71429	1.48E-06	1.36E-06
GOTERM_BP_DIRECT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	15	2.66E-08	CSF3, ANGPT1, IL15, SRC, EGF, ITGB3, IGF1, GATA1, GHR, IL3, FGF8, RELN, NTF3, PLPP3, FGF10	6.964286	1.48E-06	1.36E-06
GOTERM_BP_DIRECT	GO:0060412~ventricular septum morphogenesis	11	2.74E-08	TGFB3, ROBO2, TGF2, WNT11, HEY1, NOS3, HES1, SOX11, ZFPM2, NKX2-5, ROBO1	11.28947	1.50E-06	1.38E-06
GOTERM_BP_DIRECT	GO:0033138~positive regulation of peptidyl-serine phosphorylation	14	3.68E-08	TENM1, NTRK2, ANGPT1, BDNF, NTRK3, CAV1, NGF, PTGS2, TNF, EGFR, NTF4, SFRP2, NTF3, SPRY2	7.479452	1.99E-06	1.83E-06
GOTERM_BP_DIRECT	GO:0001649~osteoblast differentiation	18	3.75E-08	WWTR1, WNT10B, FHL2, TNC, GLI1, FGF2, GLI3, RUNX2, SOX2, BMP4, WNT11, FGF9, LOX, SMO, IBSP, CREB3L1, ID4, EPHA2	5.4	2.00E-06	1.84E-06
GOTERM_BP_DIRECT	GO:0001656~metanephros development	10	3.89E-08	BMP4, ROBO2, FGF8, EYA1, ITGA8, GDF6, HOXC11, GLI3, HOXA11, FGF10, FZD2, IL15, PDGFA, FASLG, INHBA, TNFRSF11A, TRHDE, GATA1, IL2, FGF3, TSHR, FGF4, IL3, AR, FGF14, SFRP2, FGF9, IL1B, CCN6, NTF3, AMH, FGF13, FGFR3, FGFR2	13	2.03E-06	1.87E-06
GOTERM_BP_DIRECT	GO:0007267~cell-cell signaling	24	3.91E-08		4	2.03E-06	1.87E-06
GOTERM_BP_DIRECT	GO:0030326~embryonic limb morphogenesis	11	4.69E-08	NOTCH2, FBN2, TGF2, PRRX1, FGF9, PTCH1, HNF1A, DKK1, PBX1, FGFR1, HOXA11	10.725	2.40E-06	2.21E-06
GOTERM_BP_DIRECT	GO:0048013~ephrin receptor signaling pathway	12	5.22E-08	NTRK1, EPHB6, EPHA5, TIAM1, EPHA7, EPHA10, SRC, CHN1, PAK3, KALRN, EPHA3, EPHA2	9.176471	2.63E-06	2.43E-06
GOTERM_BP_DIRECT	GO:0001570~vasculogenesis	13	8.13E-08	YAP1, NTRK2, CAV1, ADM, HOXA13, SMO, WT1, KDR, ACKR3, HAS2, NKX2-5, ZFPM2, EPHA2	7.8	4.05E-06	3.73E-06
GOTERM_BP_DIRECT	GO:0140467~integrated stress response signaling	9	8.92E-08	FOSL1, CEBPA, JUN, MAF, MAFB, CEBPD, CEBPE, DDIT3, FOS	14.625	4.38E-06	4.04E-06
GOTERM_BP_DIRECT	GO:0060045~positive regulation of cardiac muscle cell proliferation	10	9.78E-08	TGFB3, YAP1, FGF9, ERBB4, GATA6, ZFPM2, GLI1, FGF2, FGFR2, FGFR1	11.81818	4.69E-06	4.32E-06
GOTERM_BP_DIRECT	GO:0048146~positive regulation of fibroblast proliferation	12	9.79E-08	PDGFRA, NGFR, CDKN1A, PDGFG, ITGB3, PDGFB, PDGFA, IGF1, ESR1, EGFR, DDR2, FGF10	8.666667	4.69E-06	4.32E-06
GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	18	1.02E-07	ACE, EPO, NOS3, IL13, FASLG, ADM, FOS, TNFRSF11A, PTGS2, SMAD6, TIRAP, AKAP12, CPS1, IL1B, TLR4, FGFR2, IL12RB2, FGF10	5.05036	4.82E-06	4.44E-06
GOTERM_BP_DIRECT	GO:0007399~nervous system development	32	1.06E-07	CAMK2B, NOTCH2, TENM1, LRP5, WNT8B, ACVR1B, FGF2, KALRN, ROBO1, ACVR1C, EDNRB, ERBB4, NTF3, HES1, NTRK1, NTRK2, BDNF, NTRK3, PAX3, SOX11, INHBA, FOS, IL3, FGF14, NAV3, AXL, FGF19, SCN8A, NEUR1, ITGA8, FGF13, MET	3.014493	4.94E-06	4.55E-06
GOTERM_BP_DIRECT	GO:0035162~embryonic hemopoiesis	8	1.07E-07	IL3, TPO, TAL1, KIT, KDR, FLT3LG, GATA3, PBX1	18.35294	4.95E-06	4.56E-06

GOTERM_BP_DIRECT	GO:0007420~brain development	22	1.14E-07	ROBO2, EGR2, EPHA7, PTCH1, SOX11, IRS2, GRIN2B, EML1, EPOR, PBX1, SOX2, GRIN2A, RELN, ZIC2, CHL1, NFIB, NKX2-1, CNTN1, NCAM1, APOD, NODAL, HES5	4.085714	5.14E-06	4.73E-06
GOTERM_BP_DIRECT	GO:0010976~positive regulation of neuron projection development	17	1.14E-07	CAMK2B, NTRK1, RET, NTRK2, ATP8A2, EPO, BDNF, NTRK3, DAB2IP, RELN, LRRC7, PTK7, CNTN1, ABL2, EPHA3, FGFR1, DDR2	5.346774	5.14E-06	4.73E-06
GOTERM_BP_DIRECT	GO:0050680~negative regulation of epithelial cell proliferation	12	1.20E-07	SOX2, CDKN1C, TGFBF3, BMP4, WNT10B, FLCN, AR, TGFB2, CDKN2B, SFRP2, DAB2IP, GPC3	8.509091	5.25E-06	4.84E-06
GOTERM_BP_DIRECT	GO:0035019~somatic stem cell population maintenance	12	1.20E-07	SOX2, YAP1, BCL9, CDX2, KIT, LRP5, HES1, GATA2, KLF4, NODAL, FGF4, FGF10	8.509091	5.25E-06	4.84E-06
GOTERM_BP_DIRECT	GO:0002053~positive regulation of mesenchymal cell proliferation	9	1.28E-07	SMO, PRRX1, FGF9, LRP5, KDR, PDGFA, IRS2, FGFR2, FGFR1	14.04	5.57E-06	5.13E-06
GOTERM_BP_DIRECT	GO:0002062~chondrocyte differentiation	12	2.12E-07	BMP4, EXT2, WNT10B, WNT2B, WNT5B, FGF9, NFIB, HMGA2, FGFR3, GLI3, RUNX2, FGFR1	8.068966	9.11E-06	8.39E-06
GOTERM_BP_DIRECT	GO:0007422~peripheral nervous system development	9	2.52E-07	NTF4, EGR2, EDNRB, ERBB3, BDNF, SCN8A, NTF3, NGF, SOX10	13	1.07E-05	9.84E-06
GOTERM_BP_DIRECT	GO:0030334~regulation of cell migration	16	2.76E-07	LAMA5, LAMA1, TNC, FGF1, FGF2, FGF3, FGF4, FGF6, FGF8, FGF9, ERBB4, FGF19, RAC3, MET, FGF23, FGF10	5.37931	1.16E-05	1.07E-05
GOTERM_BP_DIRECT	GO:0016477~cell migration	25	2.82E-07	LAMA5, SDC4, ITGB3, PTPRK, RASGEF1A, ERBB4, CDH1, KDR, GPC3, HES1, PAK5, TGFB2, MATK, RHOD, TGFBF3, TIAM1, AXL, PTK7, CDH11, FGFR4, DOCK1, MET, EPHA3, FGFR1, EPHA2	3.469751	1.17E-05	1.08E-05
GOTERM_BP_DIRECT	GO:0003180~aortic valve morphogenesis	10	2.88E-07	DLL4, BMP4, ROBO2, HEY1, NOS3, ELN, GATA3, NKX2-5, SMAD6, ROBO1	10.54054	1.18E-05	1.09E-05
GOTERM_BP_DIRECT	GO:0035567~non-canonical Wnt signaling pathway	9	3.45E-07	SFRP4, FZD3, SFRP2, FZD2, FZD7, FZD6, FZD8, FZD10, WNT4	12.53571	1.40E-05	1.29E-05
GOTERM_BP_DIRECT	GO:0050918~positive chemotaxis	11	4.52E-07	BMP4, FGF8, ANGPT1, HGF, NTF3, PDGFB, VEGFC, VEGFD, FGF2, MET, FGF10	8.58	1.81E-05	1.67E-05
GOTERM_BP_DIRECT	GO:0003184~pulmonary valve morphogenesis	8	5.87E-07	NOTCH2, BMP4, ROBO2, TGFB2, HEY1, NOS3, SMAD6, ROBO1	14.85714	2.33E-05	2.15E-05
GOTERM_BP_DIRECT	GO:0030217~T cell differentiation	10	7.41E-07	JAG2, LFNG, DLL4, EGR1, WNT10B, KIT, PIK3R2, GATA3, IL2, RUNX2	9.512195	2.91E-05	2.68E-05
GOTERM_BP_DIRECT	GO:0051091~positive regulation of DNA-binding transcription factor activity	14	7.88E-07	HDAC5, FZD2, TNFRSF11A, ESR1, TNF, ZIC2, IL1B, DDIT3, KIT, PPARG, PLPP3, PPARGC1A, NODAL, DDR2	5.808511	3.06E-05	2.82E-05
GOTERM_BP_DIRECT	GO:0048010~vascular endothelial growth factor receptor signaling pathway	9	8.17E-07	FGF9, SRC, AXL, FLT4, KDR, VEGFC, VEGFD, SULF1, FGF10	11.32258	3.14E-05	2.89E-05
GOTERM_BP_DIRECT	GO:0010595~positive regulation of endothelial cell migration	12	8.33E-07	ANGPT1, ADGRA2, EGF, FLT4, ITGB3, KDR, PRKCA, GATA3, PLPP3, FGF1, FGF2, FUT1	7.090909	3.14E-05	2.89E-05
GOTERM_BP_DIRECT	GO:0009611~response to wounding	12	8.33E-07	SOX2, FOSL1, TGFB2, GRIN2A, DST, NFIB, DDIT3, PDGFB, SLC1A2, TNC, PDGFA, GLI1	7.090909	3.14E-05	2.89E-05
GOTERM_BP_DIRECT	GO:0001837~epithelial to mesenchymal transition	11	9.60E-07	TGFBF3, TGFB2, WNT11, NOTCH4, HGF, HMGA2, NCAM1, IGF1, FGFR2, FGFR1, WNT4	7.944444	3.58E-05	3.30E-05
GOTERM_BP_DIRECT	GO:0042127~regulation of cell population proliferation	17	1.19E-06	JAG2, TFAP2A, ALK, TGFB2, JUN, MMP7, KSR1, TGFB3, HOXD13, MITF, ERBB3, CHST11, TAL1, PLAUG, KIT, STAT4, LGR5	4.510204	4.41E-05	4.06E-05
GOTERM_BP_DIRECT	GO:0043627~response to estrogen	11	1.36E-06	SLC34A2, TGFB3, EPO, CAV1, IGFBP2, GATA6, PPARG, GATA3, SMAD6, ESR1, HOXA11	7.660714	4.94E-05	4.55E-05
GOTERM_BP_DIRECT	GO:0048469~cell maturation	9	1.38E-06	IL15, AXL, HES1, PPARG, GATA3, SOX10, HES5, RUNX2, FGFR1	10.63636	4.94E-05	4.55E-05
GOTERM_BP_DIRECT	GO:0048008~platelet-derived growth factor receptor signaling pathway	9	1.38E-06	PDGFRB, PDGFRA, NR4A3, SRC, PDGFD, ITGB3, PDGFB, PDGFA, PLAT	10.63636	4.94E-05	4.55E-05
GOTERM_BP_DIRECT	GO:0050804~modulation of chemical synaptic transmission	13	1.47E-06	EPHA7, CDKL5, DGKB, GRID1, BDNF, NGF, DNM1, NTF4, AKAP12, RELN, PLCB4, NTF3, CDH11	6.035714	5.22E-05	4.81E-05
GOTERM_BP_DIRECT	GO:0030336~negative regulation of cell migration	19	1.59E-06	NGFR, KANK1, TET1, MITF, PTPRK, FOXO3, SULF1, ROBO1, TGFBF3, DACH1, SFRP2, WNT11, NAV3, CDH1, CDH11, NKX2-1, CYP1B1, SRGAP3, WNT4	3.962567	5.61E-05	5.16E-05
GOTERM_BP_DIRECT	GO:0043524~negative regulation of neuron apoptotic process	17	1.71E-06	PRKCG, NTRK1, NTRK2, ANGPT1, TGFB3, BDNF, CBLC, NGF, NTF4, FGF8, ERBB3, CCND1, CHL1, AXL, NTF3, KDR, PPARGC1A	4.390728	5.96E-05	5.49E-05
GOTERM_BP_DIRECT	GO:0048568~embryonic organ development	9	1.76E-06	TEAD4, WNT7B, PTCH1, GATA3, ZFPM2, TEAD1, FGFR2, PBX1, TEAD3	10.32353	6.08E-05	5.60E-05
GOTERM_BP_DIRECT	GO:0030509~BMP signaling pathway	13	1.90E-06	NOTCH2, EGR1, GDF6, SMAD6, ACVR2A, RUNX2, TGFBF3, BMP4, EXT1, SFRP2, HES1, PPARG, HES5	5.895349	6.50E-05	5.99E-05
GOTERM_BP_DIRECT	GO:0001764~neuron migration	15	1.97E-06	NTRK2, CDKL5, AUTS2, CCK, GATA3, GATA2, RELN, TLX3, CHL1, AXL, KIT, ASTN2, FGF13, FGFR2, FGFR1	4.957627	6.70E-05	6.17E-05

GOTERM_BP_DIRECT	GO:0048589~developmental growth	8	2.22E-06	CHST11, NOTCH4, GAS1, ADM, GATA3, SOX10, GLI3, HOXA11	12.48	7.47E-05	6.88E-05
GOTERM_BP_DIRECT	GO:0045665~negative regulation of neuron differentiation	11	2.25E-06	SOX2, NOTCH3, HEY1, TLX3, ID4, HES1, FOXO3, DLL1, GLI3, HES5, PBX1	7.271186	7.49E-05	6.90E-05
GOTERM_BP_DIRECT	GO:0046330~positive regulation of JNK cascade	14	2.27E-06	FZD7, FLT4, WNT7B, DAB2IP, NOD1, FZD10, WNT16, TNF, DKK1, TIRAP, IL1B, FGF19, PLCB1, TLR4	5.300971	7.50E-05	6.91E-05
GOTERM_BP_DIRECT	GO:0019221~cytokine-mediated signaling pathway	17	2.42E-06	CEBPA, CSF3, CSF3R, FLT3, IRS1, CAV1, LIFR, INHBA, EPOR, GHR, FOSL1, IL1B, KIT, STAT4, IL13RA2, IL7R, IL12RB2	4.277419	7.91E-05	7.29E-05
GOTERM_BP_DIRECT	GO:2000573~positive regulation of DNA biosynthetic process	7	2.65E-06	PDGFRB, HGF, PDGFB, CYP1B1, FGFR4, TNF, FGF2	16.05882	8.62E-05	7.94E-05
GOTERM_BP_DIRECT	GO:0031100~animal organ regeneration	9	3.50E-06	TGFBR3, CDKN1A, ACE, NR4A3, FLT3, AXL, ADM, PPARG, GATA1	9.486486	1.13E-04	1.04E-04
GOTERM_BP_DIRECT	GO:0060065~uterus development	7	3.90E-06	TGFB2, HOXA9, SRC, FOXL2, GATA3, ESR1, HOXA11	15.16667	1.23E-04	1.13E-04
GOTERM_BP_DIRECT	GO:0060749~mammary gland alveolus development	7	3.90E-06	SOCS2, AR, CCND1, ERBB4, EGF, TNFRSF11A, ESR1	15.16667	1.23E-04	1.13E-04
GOTERM_BP_DIRECT	GO:0009954~proximal/distal pattern formation	8	3.93E-06	HOXA9, GLI1, DLL1, HOXD9, HOXC11, GLI3, PBX1, HOXA11	11.55556	1.23E-04	1.13E-04
GOTERM_BP_DIRECT	GO:0001823~mesonephros development	6	4.38E-06	BMP4, FGF8, PAX8, ZBTB16, GATA3, FGF10	21.27273	1.36E-04	1.25E-04
GOTERM_BP_DIRECT	GO:0043491~phosphatidylinositol 3-kinase/protein kinase B signal transduction	12	4.58E-06	FLCN, ERBB3, IRS1, ERBB2, CD28, COL6A3, PIK3R2, GATA3, TNF, FGF2, EPHA2, IGF1R	6	1.41E-04	1.30E-04
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	17	4.67E-06	NTRK1, NOS3, ITGB3, GATA6, VEGFC, HMGA2, ADM, VEGFD, PRKCA, GATA2, FGF1, FGF2, SFRP2, IL1B, KDR, CYP1B1, NODAL	4.067485	1.43E-04	1.32E-04
GOTERM_BP_DIRECT	GO:0060391~positive regulation of SMAD protein signal transduction	9	5.32E-06	TGFBR3, BMP4, TGFB2, TGFB3, INHBA, GDF6, AMH, NODAL, ACVR2A	9	1.62E-04	1.49E-04
GOTERM_BP_DIRECT	GO:0070371~ERK1 and ERK2 cascade	10	6.06E-06	FLCN, EGF, GRB10, SPRY2, NOD1, FGF2, FGF23, TLR4, DUSP9, FGF10	7.5	1.82E-04	1.68E-04
GOTERM_BP_DIRECT	GO:1904707~positive regulation of vascular associated smooth muscle cell proliferation	10	7.13E-06	JUN, NR4A3, FGF9, SRC, PDGFB, IGF1, TNF, FGF2, FGFR2, DDR2	7.358491	2.13E-04	1.96E-04
GOTERM_BP_DIRECT	GO:0042733~embryonic digit morphogenesis	10	8.37E-06	BMP4, SFRP2, CHST11, ZBTB16, GNA12, LRP5, HOXD13, HOXC11, GLI3, HOXA11	7.222222	2.48E-04	2.28E-04
GOTERM_BP_DIRECT	GO:0007179~transforming growth factor beta receptor signaling pathway	13	9.43E-06	TGFB2, JUN, TGFB3, SRC, PTPRK, FOS, SMAD6, TGFBR3, FLCN, CHST11, ID1, ITGA8, NODAL	5.07	2.77E-04	2.55E-04
GOTERM_BP_DIRECT	GO:0007405~neuroblast proliferation	9	9.55E-06	DMRTA2, SMO, ID4, ACSL6, GATA2, FGF2, SOX10, EML1, GLI3	8.357143	2.79E-04	2.57E-04
GOTERM_BP_DIRECT	GO:0048701~embryonic cranial skeleton morphogenesis	8	1.06E-05	BMP4, TFAP2A, TBX15, PDGFRA, PRRX1, NODAL, FGFR2, RUNX2	10.06452	3.02E-04	2.78E-04
GOTERM_BP_DIRECT	GO:0045664~regulation of neuron differentiation	8	1.06E-05	NTF4, ALK, RELN, BCL11B, EYA1, BDNF, NTF3, NGF	10.06452	3.02E-04	2.78E-04
GOTERM_BP_DIRECT	GO:0060071~Wnt signaling pathway, planar cell polarity pathway	8	1.06E-05	TIAM1, FZD3, FZD2, WNT11, FZD7, WNT7B, FZD6, GPC3	10.06452	3.02E-04	2.78E-04
GOTERM_BP_DIRECT	GO:0001709~cell fate determination	7	1.07E-05	NOTCH2, NOTCH4, PTCH1, HES1, GATA3, GATA2, DLL1	13	3.02E-04	2.78E-04
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	32	1.14E-05	ROBO2, CSF3R, SRC, LAMA1, CTNND2, ITGB3, TNC, PTPRK, ROBO1, RELN, IBSP, CHL1, CCN6, CYP1B1, ABL2, NCAM1, HES1, EDIL3, HES5, DST, OMD, PRKCA, IL2, PPFIBP1, PTK7, CDH11, CNTN1, COL6A3, ACKR3, EPHA3, EPHA2, DDR2	2.413926	3.20E-04	2.94E-04
GOTERM_BP_DIRECT	GO:0046427~positive regulation of receptor signaling pathway via JAK-STAT	9	1.15E-05	GHR, ERBB4, KIT, CAMK2A, CYP1B1, HES1, IL7R, TNF, HES5	8.162791	3.20E-04	2.94E-04
GOTERM_BP_DIRECT	GO:0001822~kidney development	14	1.25E-05	TFAP2A, TGFB2, ACE, SOX11, GATA3, SULF1, BICC1, BMP4, PAX8, WT1, PTK7, ITGA8, HAS2, WNT4	4.55	3.46E-04	3.19E-04
GOTERM_BP_DIRECT	GO:0007613~memory	12	1.34E-05	NTF4, GRIN2A, BDNF, NTF3, ITGA8, PAK6, FGF13, NGF, PLCB1, PTGS2, KALRN, PAK5	5.37931	3.68E-04	3.39E-04
GOTERM_BP_DIRECT	GO:0060449~bud elongation involved in lung branching	5	1.40E-05	BMP4, YAP1, SPRY2, FGFR2, FGF10	27.85714	3.75E-04	3.45E-04
GOTERM_BP_DIRECT	GO:0002067~glandular epithelial cell differentiation	5	1.40E-05	EXT1, YAP1, NFIB, CAV1, KLF4	27.85714	3.75E-04	3.45E-04
GOTERM_BP_DIRECT	GO:0045937~positive regulation of phosphate metabolic process	5	1.40E-05	PDGFRB, FLT3, FLT4, KIT, KDR	27.85714	3.75E-04	3.45E-04

GOTERM_BP_DIRECT	GO:0001938~positive regulation of endothelial cell proliferation	11	1.43E-05	BMP4, EGF, FLT4, ITGB3, PDGFB, KDR, VEGFC, VEGFD, PRKCA, FGF2, FGF10	5.958333	3.80E-04	3.50E-04
GOTERM_BP_DIRECT	GO:0040037~negative regulation of fibroblast growth factor receptor signaling pathway	7	1.43E-05	NGFR, CREB3L1, SPRY4, SPRY2, SULF1, FGF2, WNT4	12.40909	3.80E-04	3.50E-04
GOTERM_BP_DIRECT	GO:0030513~positive regulation of BMP signaling pathway	9	1.63E-05	NOTCH2, BMP4, GATA6, GPC3, KDR, HES1, SOX11, SULF1, HES5	7.8	4.27E-04	3.94E-04
GOTERM_BP_DIRECT	GO:0007219~Notch signaling pathway	14	1.64E-05	JAG2, NOTCH2, NOTCH3, CEBPA, NOTCH4, SORBS2, DLL1, DLL3, DLL4, HEY1, NEURL1, CNTN1, HES1, HES5	4.439024	4.27E-04	3.94E-04
GOTERM_BP_DIRECT	GO:0038180~nerve growth factor signaling pathway	6	1.78E-05	NTRK1, NTF4, SORT1, BDNF, NTF3, NGF	16.71429	4.58E-04	4.22E-04
GOTERM_BP_DIRECT	GO:0010463~mesenchymal cell proliferation	6	1.78E-05	WNT11, PRRX1, FGF9, KDR, FGFR1, FGF4	16.71429	4.58E-04	4.22E-04
GOTERM_BP_DIRECT	GO:0036120~cellular response to platelet-derived growth factor stimulus	7	1.90E-05	PDGFRB, SRC, PDGFD, ITGB3, PDGFB, HAS2, TLR4	11.86957	4.86E-04	4.47E-04
GOTERM_BP_DIRECT	GO:0045648~positive regulation of erythrocyte differentiation	8	2.04E-05	TAL1, INHBA, GATA2, FOXO3, ACVR1B, GATA1, ACVR2A, HSPA1A	9.176471	5.17E-04	4.76E-04
GOTERM_BP_DIRECT	GO:0045471~response to ethanol	13	2.08E-05	CSF3, IL13, TNC, FOS, TNFRSF11A, TNF, GRIN2B, IL2, IGF1R, GRIN2A, FOSB, FGFR2, RGS7	4.694444	5.25E-04	4.84E-04
GOTERM_BP_DIRECT	GO:0008217~regulation of blood pressure	11	2.60E-05	EXT1, EXT2, ACE, EDNRB, NOS3, GNA11, GNA12, LRP5, PPARG, PTGS2, DLL1	5.571429	6.52E-04	6.00E-04
GOTERM_BP_DIRECT	GO:0001501~skeletal system development	14	2.96E-05	JAG2, TEAD4, TGFB2, HOXD13, IGF1, HOXA13, HOXA11, DLL3, GNA11, TRPS1, CDH11, FGFR3, EPHA2, FGFR1	4.2	7.38E-04	6.80E-04
GOTERM_BP_DIRECT	GO:0070372~regulation of ERK1 and ERK2 cascade	8	3.02E-05	TIAM1, EPHA7, IL1B, ERBB2, ROS1, EGFR, FGFR2, EPHA2	8.666667	7.47E-04	6.88E-04
GOTERM_BP_DIRECT	GO:0030178~negative regulation of Wnt signaling pathway	9	3.12E-05	DKK4, SFRP4, RN43, SFRP2, FGF9, WIF1, GRB10, CXCC4, DKK1	7.163265	7.66E-04	7.06E-04
GOTERM_BP_DIRECT	GO:0032956~regulation of actin cytoskeleton organization	12	3.43E-05	PDGFRB, EPHA5, PDGFRA, BAIAP2L1, ITGB3, PDGFA, RAC3, ABL2, FZD10, PAK3, RHOD, EPHA3	4.875	8.36E-04	7.70E-04
GOTERM_BP_DIRECT	GO:0007507~heart development	18	3.45E-05	CDKN1A, TGFB2, NTRK3, PDGFB, ADM, EPOR, GLI3, BICC1, LOX, ERBB3, WT1, ERBB4, WIF1, GNA11, ERBB2, PPARG, NKX2-5, ZFPM2	3.311321	8.36E-04	7.70E-04
GOTERM_BP_DIRECT	GO:0043536~positive regulation of blood vessel endothelial cell migration	9	3.63E-05	ANGPT1, NOS3, PDGFB, KDR, VEGFC, PRKCA, GATA2, FGF2, FGFR1	7.02	8.73E-04	8.04E-04
GOTERM_BP_DIRECT	GO:0001657~ureteric bud development	8	3.65E-05	RET, BMP4, ROBO2, SDC4, WT1, SMAD6, FGFR2, FGFR1	8.432432	8.73E-04	8.04E-04
GOTERM_BP_DIRECT	GO:0060395~SMAD protein signal transduction	7	4.06E-05	WWTR1, JUN, FOS, INHBA, GDF6, SMAD6, RUNX2	10.5	9.65E-04	8.89E-04
GOTERM_BP_DIRECT	GO:0002052~positive regulation of neuroblast proliferation	8	4.37E-05	DMRTA2, FZD3, SMO, ID4, VEGFC, FGF2, SOX10, GLI3	8.210526	0.001033	9.52E-04
GOTERM_BP_DIRECT	GO:0060484~lung-associated mesenchyme development	5	4.82E-05	WNT11, FGF9, PTK7, FGFR2, FGFR1	21.66667	0.001132	0.001043
GOTERM_BP_DIRECT	GO:0035556~intracellular signal transduction	27	5.45E-05	NOTCH2, BRSK1, ITK, SHC2, DGKB, SRC, NOD1, KALRN, SOCS2, FLCN, EDNRB, ERBB2, PAK6, RAC3, PAK3, PAK5, RGS7, PRKCG, DMRT1, DAB2IP, HMGGA2, PRKCA, TGFB3, NR4A3, KIT, CILK1, DGKI	2.4375	0.001272	0.001172
GOTERM_BP_DIRECT	GO:0003151~outflow tract morphogenesis	9	5.60E-05	TGFB3, SFRP2, FZD2, WNT11, EYA1, ELN, HES1, SOX11, NKX2-5	6.622642	0.0013	0.001197
GOTERM_BP_DIRECT	GO:0001974~blood vessel remodeling	8	6.18E-05	EXT1, DLL4, ACE, FGF8, AXL, NOS3, HOXA3, FGF10	7.8	0.001416	0.001304
GOTERM_BP_DIRECT	GO:0007224~smoothened signaling pathway	11	6.18E-05	WNT10B, SMO, PRRX1, FGF9, PTCH1, GPC3, HES1, GLI1, GLI3, HES5, RUNX2	5.047059	0.001416	0.001304
GOTERM_BP_DIRECT	GO:1902894~negative regulation of miRNA transcription	7	6.36E-05	BMP4, NFIB, PDGFB, GATA6, PPARG, ESR1, TNF	9.75	0.001448	0.001334
GOTERM_BP_DIRECT	GO:0030857~negative regulation of epithelial cell differentiation	6	6.99E-05	YAP1, SMO, CCND1, CAV1, DLL1, FGF10	13	0.001555	0.001432
GOTERM_BP_DIRECT	GO:0071548~response to dexamethasone	6	6.99E-05	ACE, CPS1, EPO, PAPP, CYP11B1, FOXO3	13	0.001555	0.001432
GOTERM_BP_DIRECT	GO:0042326~negative regulation of phosphorylation	6	6.99E-05	CDKN1C, CDKN1A, CDKN2B, CDKN2A, GRB10, INHBA	13	0.001555	0.001432
GOTERM_BP_DIRECT	GO:0002063~chondrocyte development	6	6.99E-05	SFRP2, CHST11, COL11A1, SULF1, RUNX2, HOXA11	13	0.001555	0.001432

GOTERM_BP_DIRECT	GO:0060349~bone morphogenesis	7	7.85E-05	TFAP2A, SFRP4, CDX1, LRP5, HAS2, FGFR3, FGFR2	9.413793	0.001734	0.001597
GOTERM_BP_DIRECT	GO:0030949~positive regulation of vascular endothelial growth factor receptor signaling pathway	6	9.29E-05	FGF9, IL1B, ITGB3, GRB10, ROBO1, FGF10	12.31579	0.002029	0.001869
GOTERM_BP_DIRECT	GO:0032332~positive regulation of chondrocyte differentiation	6	9.29E-05	ZBTB16, PRKG2, GDF6, GLI3, RUNX2, HOXA11	12.31579	0.002029	0.001869
GOTERM_BP_DIRECT	GO:0000165~MAPK cascade	13	9.60E-05	RET, KSR1, CAV1, MAPK8IP2, DUSP9, EGFR, AR, FGF8, PAK3, MAP3K6, FGF13, FGFR3, FGFR1	4.02381	0.002071	0.001908
GOTERM_BP_DIRECT	GO:0042476~odontogenesis	7	9.60E-05	BMP4, TGFB2, FGF8, TGFB3, SRC, INHBA, FGFR2	9.1	0.002071	0.001908
GOTERM_BP_DIRECT	GO:0048856~anatomical structure development	8	1.00E-04	TFAP2A, PAX8, EYA1, PAX7, PAX3, HOXD11, HOXC11, HOXA11	7.255814	0.002145	0.001976
GOTERM_BP_DIRECT	GO:0045599~negative regulation of fat cell differentiation	9	1.08E-04	YAP1, WWTR1, WNT10B, SORT1, DDIT3, ID4, ZFPM2, TNF, RUNX1T1	6.051724	0.002299	0.002118
GOTERM_BP_DIRECT	GO:0030282~bone mineralization	9	1.08E-04	WNT11, IBSP, LOX, GPC3, PTGS2, FGFR3, GATA1, FGFR2, RUNX2	6.051724	0.002299	0.002118
GOTERM_BP_DIRECT	GO:0050808~synapse organization	10	1.11E-04	NTRK2, PTK7, WNT7B, CTNND2, SNCG, NCAM1, PAK3, FGFR4, PPFIA2, ROBO1	5.27027	0.002334	0.00215
GOTERM_BP_DIRECT	GO:0016055~Wnt signaling pathway	15	1.18E-04	AMER1, RNF43, FZD2, WNT7B, CTNND2, MITF, WNT16, CXXC4, DKK2, DKK4, CCND1, WIF1, DDIT3, RAC3, FGF10	3.461538	0.002478	0.002283
GOTERM_BP_DIRECT	GO:0060445~branching involved in salivary gland morphogenesis	5	1.21E-04	LAMA5, FGF8, LAMA1, FGFR2, FGFR1	17.72727	0.002517	0.002318
GOTERM_BP_DIRECT	GO:2000647~negative regulation of stem cell proliferation	6	1.21E-04	WNT11, NFIB, PTCH1, FGF2, GLI3, FGF10	11.7	0.002517	0.002318
GOTERM_BP_DIRECT	GO:0032868~response to insulin	10	1.36E-04	EGR1, EGR2, ACVR1C, SORT1, IRS1, IGFBP2, GRB10, ADM, FOS, TNFRSF11A	5.131579	0.002812	0.00259
GOTERM_BP_DIRECT	GO:0045785~positive regulation of cell adhesion	9	1.38E-04	IBSP, ANGPT1, LAMA1, ERBB2, PIK3R2, PRKCA, DUSP26, RHOD, TNF	5.85	0.002838	0.002614
GOTERM_BP_DIRECT	GO:0048009~insulin-like growth factor receptor signaling pathway	7	1.40E-04	GHR, AR, IRS1, GRB10, IGF1, PLCB1, IGF1R	8.53125	0.002862	0.002636
GOTERM_BP_DIRECT	GO:0071260~cellular response to mechanical stimulus	10	1.51E-04	WNT11, CRADD, IL1B, ITGB3, IL13, PTGS2, FGF2, TLR4, EGFR, IGF1R	5.064935	0.003063	0.002821
GOTERM_BP_DIRECT	GO:0048863~stem cell differentiation	8	1.55E-04	CDX2, KIT, GATA6, HMGA2, FOXO4, ESR1, RUNX2, FGFR1	6.782609	0.003113	0.002867
GOTERM_BP_DIRECT	GO:0009948~anterior/posterior axis specification	6	1.56E-04	BMP4, CDX2, CDX1, DDIT3, GPC3, LEFTY2	11.14286	0.003113	0.002867
GOTERM_BP_DIRECT	GO:0032924~activin receptor signaling pathway	6	1.56E-04	ACVR1C, FGF9, INHBA, GDF6, ACVR1B, ACVR2A	11.14286	0.003113	0.002867
GOTERM_BP_DIRECT	GO:0048333~mesodermal cell differentiation	5	1.78E-04	ITGB3, ITGA8, HMGA2, INHBA, FGFR2	16.25	0.003529	0.00325
GOTERM_BP_DIRECT	GO:0048286~lung alveolus development	8	1.79E-04	BMP4, ACE, TGFB3, FLT4, KDR, PDGFA, FGFR2, FGF10	6.638298	0.003529	0.00325
GOTERM_BP_DIRECT	GO:0030879~mammary gland development	6	1.98E-04	HOXA9, TGFB3, NOTCH4, CAV1, IRS2, HOXD9	10.63636	0.003862	0.003557
GOTERM_BP_DIRECT	GO:0048665~neuron fate specification	6	1.98E-04	DMRTA2, EYA1, TLX3, NFIB, FEV, DLL1	10.63636	0.003862	0.003557
GOTERM_BP_DIRECT	GO:0035914~skeletal muscle cell differentiation	8	2.05E-04	EGR1, DMRTA2, BCL9, EGR2, HLF, SOX11, FOS, ATF3	6.5	0.003958	0.003645
GOTERM_BP_DIRECT	GO:0048839~inner ear development	8	2.05E-04	SOX2, CEBPA, TGFB2, MAF, CEBPD, TGFB3, LGR5, HOXA13	6.5	0.003958	0.003645
GOTERM_BP_DIRECT	GO:0071679~commissural neuron axon guidance	5	2.52E-04	FZD3, SMO, NFIB, PTCH1, NCAM1	15	0.004803	0.004424
GOTERM_BP_DIRECT	GO:0060644~mammary gland epithelial cell differentiation	5	2.52E-04	SMO, ERBB4, PTCH1, ZNF703, FGF2	15	0.004803	0.004424
GOTERM_BP_DIRECT	GO:0031401~positive regulation of protein modification process	5	2.52E-04	PDGFRB, FLT3, FLT4, KIT, KDR	15	0.004803	0.004424
GOTERM_BP_DIRECT	GO:0001889~liver development	10	2.94E-04	TGFB3, CEBPA, CDKN2B, HGF, GATA6, HES1, HNF1A, MET, NODAL, WNT4	4.642857	0.005576	0.005135

GOTERM_BP_DIRECT	GO:0030325~adrenal gland development	6	3.06E-04	PDGFRA, WNT11, WT1, CYP1B1, PBX1, WNT4	9.75	0.005764	0.005309
GOTERM_BP_DIRECT	GO:0060129~thyroid-stimulating hormone-secreting cell differentiation	4	3.15E-04	FGF8, GATA2, FGF2, WNT4	26	0.005843	0.005382
GOTERM_BP_DIRECT	GO:0014807~regulation of somitogenesis	4	3.15E-04	LFNG, CDX2, CDX1, DLL1	26	0.005843	0.005382
GOTERM_BP_DIRECT	GO:0060510~type II pneumocyte differentiation	4	3.15E-04	NFIB, GATA6, NKX2-1, FGF10	26	0.005843	0.005382
GOTERM_BP_DIRECT	GO:0070555~response to interleukin-1	7	3.23E-04	GHR, IL1R1, EPO, SRC, IL1B, PRKCA, TNFRSF11A	7.378378	0.005911	0.005444
GOTERM_BP_DIRECT	GO:0046326~positive regulation of glucose import	7	3.23E-04	IRS1, FGF19, CLTCL1, SLC1A2, GPC3, IRS2, IGF1	7.378378	0.005911	0.005444
GOTERM_BP_DIRECT	GO:0032570~response to progesterone	7	3.23E-04	YAP1, FOSL1, TGFB2, TGFB3, CAV1, FOSB, FOS	7.378378	0.005911	0.005444
GOTERM_BP_DIRECT	GO:0038083~peptidyl-tyrosine autophosphorylation	5	3.46E-04	NTRK1, ALK, KDR, EGFR, IGF1R	13.92857	0.006269	0.005774
GOTERM_BP_DIRECT	GO:0042491~inner ear auditory receptor cell differentiation	5	3.46E-04	BMP4, HES1, DLL1, FGF2, HES5	13.92857	0.006269	0.005774
GOTERM_BP_DIRECT	GO:0032355~response to estradiol	10	3.51E-04	GHR, SOCS2, PTCH1, DNMT3A, IGF2BP2, WNT8B, CYP1B1, PTGS2, ESR1, FGF10	4.534884	0.006307	0.005808
GOTERM_BP_DIRECT	GO:0001503~ossification	10	3.51E-04	EXT1, EXT2, SORT1, COL11A1, CDH11, TNFRSF11A, EGFR, RUNX2, FSTL3, DDR2	4.534884	0.006307	0.005808
GOTERM_BP_DIRECT	GO:0060038~cardiac muscle cell proliferation	6	3.74E-04	TGFB3, TGFB2, FGF9, GATA6, NKX2-5, FGFR1	9.36	0.00662	0.006097
GOTERM_BP_DIRECT	GO:0021983~pituitary gland development	6	3.74E-04	SOX2, BMP4, CDH1, NKX2-1, GLI1, FGF10	9.36	0.00662	0.006097
GOTERM_BP_DIRECT	GO:0097150~neuronal stem cell population maintenance	6	3.74E-04	SOX2, PRRX1, HES1, FOXO3, DLL1, HES5	9.36	0.00662	0.006097
GOTERM_BP_DIRECT	GO:0009953~dorsal/ventral pattern formation	7	4.34E-04	FGF8, LHX2, PTCH1, TLL2, HOXD11, GLI1, HOXA11	7	0.007573	0.006975
GOTERM_BP_DIRECT	GO:2001237~negative regulation of extrinsic apoptotic signaling pathway	7	4.34E-04	BMP4, YAP1, TCF7L2, AR, SRC, IGF1, PAK5	7	0.007573	0.006975
GOTERM_BP_DIRECT	GO:0048144~fibroblast proliferation	7	4.34E-04	NGFR, CDKN1A, WNT7B, CAV1, VEGFD, ESR1, FGF10	7	0.007573	0.006975
GOTERM_BP_DIRECT	GO:0098609~cell-cell adhesion	16	4.49E-04	ROBO2, LAMA5, SRC, CTNND2, LRP5, EGFR, ROBO1, BAIAP2L1, CDH1, LRRC7, KIT, ITGA8, CNTN1, ITGA7, PLPP3, FGFR2	2.902326	0.007807	0.00719
GOTERM_BP_DIRECT	GO:0008045~motor neuron axon guidance	6	4.53E-04	EGR2, FGF8, ERBB2, CHN1, RAC3, LHX4	9	0.007839	0.00722
GOTERM_BP_DIRECT	GO:0048546~digestive tract morphogenesis	5	4.62E-04	SFRP2, GLI1, SOX10, EGFR, NODAL	13	0.007952	0.007324
GOTERM_BP_DIRECT	GO:0060326~cell chemotaxis	10	4.93E-04	PDGFRB, PDGFRA, LOX, HGF, KIT, PDGFB, LPAR1, RAC3, ACKR3, EPHA2	4.333333	0.008447	0.007779
GOTERM_BP_DIRECT	GO:0050767~regulation of neurogenesis	7	5.00E-04	DLL4, YAP1, HEY1, IL1B, HES1, DLL1, HES5	6.825	0.008481	0.007811
GOTERM_BP_DIRECT	GO:1900182~positive regulation of protein localization to nucleus	7	5.00E-04	BMP4, YAP1, WWTR1, NGFR, TCF7L2, CDKN2A, SRC	6.825	0.008481	0.007811
GOTERM_BP_DIRECT	GO:0010518~positive regulation of phospholipase activity	4	5.40E-04	PLA2G5, FGFR3, FGFR2, FGFR1	22.28571	0.008964	0.008256
GOTERM_BP_DIRECT	GO:0071393~cellular response to progesterone stimulus	4	5.40E-04	SRC, CYP1B1, SOX10, IGF1R	22.28571	0.008964	0.008256
GOTERM_BP_DIRECT	GO:2000144~positive regulation of DNA-templated transcription initiation	4	5.40E-04	FOSL1, CEBPA, JUN, MITF	22.28571	0.008964	0.008256
GOTERM_BP_DIRECT	GO:0032927~positive regulation of activin receptor signaling pathway	4	5.40E-04	FGF9, ACVR1B, NODAL, ACVR2A	22.28571	0.008964	0.008256
GOTERM_BP_DIRECT	GO:0010718~positive regulation of epithelial to mesenchymal transition	8	5.40E-04	BMP4, WWTR1, TIAM1, TCF7L2, TGFB2, TGFB3, IL1B, ZNF703	5.571429	0.008964	0.008256
GOTERM_BP_DIRECT	GO:0002244~hematopoietic progenitor cell differentiation	9	5.44E-04	BMP4, PDGFRA, CEBPD, KIT, INHBA, GATA2, DOCK1, EML1, FSTL3	4.808219	0.008964	0.008256

GOTERM_BP_DIRECT	GO:0032967~positive regulation of collagen biosynthetic process	6	5.45E-04	BMP4, TGFB3, CREB3L1, INHBA, WNT4, DDR2	8.666667	0.008964	0.008256
GOTERM_BP_DIRECT	GO:0043433~negative regulation of DNA-binding transcription factor activity	9	5.97E-04	TCF7L2, SFRP4, DDIT3, PTCH1, FZD6, ID1, HES1, ESR1, PBX1	4.743243	0.009769	0.008998
GOTERM_BP_DIRECT	GO:0009612~response to mechanical stimulus	8	6.03E-04	FOSL1, SRC, PTCH1, IGFBP2, TNC, FOSB, PPARG, TNFRSF11A	5.473684	0.009802	0.009028
GOTERM_BP_DIRECT	GO:003630~positive regulation of cell adhesion mediated by integrin	5	6.04E-04	RET, TGFB2, SFRP2, ITGB3, RAC3	12.1875	0.009802	0.009028
GOTERM_BP_DIRECT	GO:0048704~embryonic skeletal system morphogenesis	7	7.44E-04	PDGFRA, HOXA9, EYA1, COL11A1, HOXA3, SOX11, HOXD9	6.348837	0.01198	0.011034
GOTERM_BP_DIRECT	GO:0030155~regulation of cell adhesion	8	7.44E-04	JAG2, RET, LAMA5, PLA2, TNC, ABL1, DLL1, FUT1	5.288136	0.01198	0.011034
GOTERM_BP_DIRECT	GO:0048557~embryonic digestive tract morphogenesis	5	7.74E-04	PDGFRA, SOX11, GLI3, FGFR2, FGF10	11.47059	0.012399	0.011419
GOTERM_BP_DIRECT	GO:0051092~positive regulation of NF-kappaB transcription factor activity	12	8.07E-04	NTRK1, ALK, AR, IL1B, CAMK2A, NOD1, IL1RAP, TNFRSF11A, TNF, TLR4, TIRAP, HSPA1A	3.416058	0.012871	0.011854
GOTERM_BP_DIRECT	GO:0045597~positive regulation of cell differentiation	8	8.24E-04	SOX2, GHR, AR, FGF8, CDX2, PPP1R13L, CCN6, FGFR1	5.2	0.013099	0.012064
GOTERM_BP_DIRECT	GO:0003129~heart induction	4	8.48E-04	BMP4, ROBO2, DKK1, ROBO1	19.5	0.013297	0.012247
GOTERM_BP_DIRECT	GO:0010544~negative regulation of platelet activation	4	8.48E-04	PDGFRA, NOS3, PDGFB, PDGFA	19.5	0.013297	0.012247
GOTERM_BP_DIRECT	GO:0003149~membranous septum morphogenesis	4	8.48E-04	BMP4, TGFB2, FZD2, FGFR2	19.5	0.013297	0.012247
GOTERM_BP_DIRECT	GO:0048812~neuron projection morphogenesis	8	9.11E-04	NTF4, BDNF, NTF3, DAB2IP, NGF, EGFR, MNX1, GAS7	5.114754	0.014234	0.01311
GOTERM_BP_DIRECT	GO:0006919~activation of cysteine-type endopeptidase activity involved in apoptotic process	9	9.24E-04	RET, NGFR, CRADD, CDKN2A, FASLG, NOD1, PPARG, TNF, ROBO1	4.443038	0.014377	0.013241
GOTERM_BP_DIRECT	GO:0030316~osteoclast differentiation	7	9.52E-04	CSF1, GPC3, MITF, FOS, TNFRSF11A, TNF, EPHA2	6.066667	0.014689	0.013529
GOTERM_BP_DIRECT	GO:0042311~vasodilation	7	9.52E-04	EXT1, EXT2, EDNRB, CP51, NOS3, TNF, EGFR	6.066667	0.014689	0.013529
GOTERM_BP_DIRECT	GO:0051145~smooth muscle cell differentiation	5	9.75E-04	BMP4, GATA6, ITGA8, WNT4, FGF10	10.83333	0.014917	0.013738
GOTERM_BP_DIRECT	GO:0043388~positive regulation of DNA binding	5	9.75E-04	EGF, HES1, PPARG, IGF1, NGF	10.83333	0.014917	0.013738
GOTERM_BP_DIRECT	GO:0007565~female pregnancy	9	0.001004	FOSL1, ACE, TGFB3, PAPPA, IGFBP2, FOSB, ADM, FOS, TEAD3	4.3875	0.015305	0.014095
GOTERM_BP_DIRECT	GO:0030308~negative regulation of cell growth	11	0.001037	CDKN1A, TGFB2, SFRP2, WNT11, WT1, CDKN2A, PPARG, INHBA, ACVR1B, RERG, HSPA1A	3.575	0.015735	0.014492
GOTERM_BP_DIRECT	GO:0030878~thyroid gland development	6	0.001054	FGF8, PAX8, HOXA3, NKX2-1, NKX2-5, FGF10	7.548387	0.015939	0.01468
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia	12	0.001084	SRC, DNMT3A, MPL, GATA6, PPARG, MALAT1, FOS, INHBA, FOXO3, PTGS2, FGFR2, DDR2	3.295775	0.016319	0.01503
GOTERM_BP_DIRECT	GO:0051402~neuron apoptotic process	9	0.001181	NTRK1, NGFR, EPHA7, FGF8, ERBB3, ANGPT1, AXL, COL6A3, PPARGC1A	4.280488	0.017712	0.016313
GOTERM_BP_DIRECT	GO:0046849~bone remodeling	5	0.00121	NOTCH2, LRP5, MITF, WNT16, EPHA2	10.26316	0.017999	0.016577
GOTERM_BP_DIRECT	GO:0038084~vascular endothelial growth factor signaling pathway	5	0.00121	FLT3, FLT4, KDR, VEGFC, VEGFD	10.26316	0.017999	0.016577
GOTERM_BP_DIRECT	GO:0010575~positive regulation of vascular endothelial growth factor production	6	0.001224	IL1B, FLT4, CYP1B1, SULF1, PTGS2, NODAL	7.3125	0.018121	0.01669
GOTERM_BP_DIRECT	GO:0003416~endochondral bone growth	4	0.001247	EXT1, FGFR3, FGFR2, DDR2	17.33333	0.018121	0.01669
GOTERM_BP_DIRECT	GO:0060231~mesenchymal to epithelial transition	4	0.001247	WT1, FZD7, GATA3, WNT4	17.33333	0.018121	0.01669

GOTERM_BP_DIRECT	GO:0010907~positive regulation of glucose metabolic process	4	0.001247	SLC45A3, IRS1, SRC, IRS2	17.33333	0.018121	0.01669
GOTERM_BP_DIRECT	GO:1904383~response to sodium phosphate	4	0.001247	EDNRB, FGF23, RUNX2, FGFR1	17.33333	0.018121	0.01669
GOTERM_BP_DIRECT	GO:0090129~positive regulation of synapse maturation	4	0.001247	CAMK2B, RELN, NEURL1, DAB2IP	17.33333	0.018121	0.01669
GOTERM_BP_DIRECT	GO:0030199~collagen fibril organization	8	0.001332	EXT1, TGFB2, SFRP2, LOX, COL11A1, TLL2, CYP1B1, DDR2	4.8	0.019278	0.017755
GOTERM_BP_DIRECT	GO:0120163~negative regulation of cold-induced thermogenesis	7	0.001345	WNT10B, FLCN, IL15, DDIT3, ID1, ALDH1A1, TLR4	5.6875	0.019312	0.017786
GOTERM_BP_DIRECT	GO:0048538~thymus development	7	0.001345	MAFB, BCL11B, HOXA3, HES1, GATA3, PBX1, FGF10	5.6875	0.019312	0.017786
GOTERM_BP_DIRECT	GO:0030225~macrophage differentiation	6	0.001412	BMP4, CEBPA, CSF1, IL15, CEBPE, GATA3	7.090909	0.019898	0.018326
GOTERM_BP_DIRECT	GO:0003281~ventricular septum development	6	0.001412	PAX8, PTK7, HES1, GATA3, SMAD6, HOXA13	7.090909	0.019898	0.018326
GOTERM_BP_DIRECT	GO:0051968~positive regulation of synaptic transmission, glutamatergic	6	0.001412	NTRK1, GRIN2A, RELN, PTGS2, GRIN2B, EGFR	7.090909	0.019898	0.018326
GOTERM_BP_DIRECT	GO:0035924~cellular response to vascular endothelial growth factor stimulus	6	0.001412	DLL4, FLT4, DAB2IP, KDR, GAS1, SPRY2	7.090909	0.019898	0.018326
GOTERM_BP_DIRECT	GO:0035115~embryonic forelimb morphogenesis	6	0.001412	TFAP2A, HOXA9, HOXD9, HOXA13, RUNX2, HOXA11	7.090909	0.019898	0.018326
GOTERM_BP_DIRECT	GO:0045780~positive regulation of bone resorption	5	0.001482	SRC, ITGB3, PRKCA, TNFRSF11A, EGFR	9.75	0.020496	0.018877
GOTERM_BP_DIRECT	GO:0001892~embryonic placenta development	5	0.001482	CEBPA, PDGFB, GATA2, EGFR, NODAL	9.75	0.020496	0.018877
GOTERM_BP_DIRECT	GO:0021675~nerve development	5	0.001482	NTF4, NGFR, BDNF, NTF3, NGF	9.75	0.020496	0.018877
GOTERM_BP_DIRECT	GO:0007215~glutamate receptor signaling pathway	5	0.001482	GRIN2A, KCNB1, GRID1, PLCB1, GRIN2B	9.75	0.020496	0.018877
GOTERM_BP_DIRECT	GO:0030539~male genitalia development	5	0.001482	PDGFRA, FGF8, WT1, HOXD13, HOXA13	9.75	0.020496	0.018877
GOTERM_BP_DIRECT	GO:0031069~hair follicle morphogenesis	6	0.001621	EXT1, NGFR, TGFB2, SMO, FGFR2, FGF10	6.882353	0.022257	0.020498
GOTERM_BP_DIRECT	GO:0048873~homeostasis of number of cells within a tissue	6	0.001621	SMO, CSF1, NOS3, RAC3, GATA2, GATA1	6.882353	0.022257	0.020498
GOTERM_BP_DIRECT	GO:0051384~response to glucocorticoid	7	0.001668	GHR, WNT7B, IGFBP2, ADM, ACSBG1, PTGS2, TNF	5.46	0.022814	0.021012
GOTERM_BP_DIRECT	GO:0045666~positive regulation of neuron differentiation	9	0.001733	SOCS2, BMP4, EPO, SOX11, GATA2, NGF, GDF6, NKX2-5, FGFR1	4.034483	0.023586	0.021723
GOTERM_BP_DIRECT	GO:0007611~learning or memory	8	0.001737	NTRK1, PRKCG, GRIN2A, EGR2, SRC, GRIN2B, DKK1, EGFR	4.588235	0.023586	0.021723
GOTERM_BP_DIRECT	GO:0030512~negative regulation of transforming growth factor beta receptor signaling pathway	11	0.001793	TGFBR3, CHST11, TGFB3, PRDM16, HTRA1, NKX2-1, TET1, SPRY2, PPARG, SMAD6, HSPA1A	3.325581	0.024011	0.022114
GOTERM_BP_DIRECT	GO:0070886~positive regulation of calcineurin-NFAT signaling cascade	5	0.001794	PPP3R2, ERBB3, AKAP6, IGF1, TNF	9.285714	0.024011	0.022114
GOTERM_BP_DIRECT	GO:0060252~positive regulation of glial cell proliferation	5	0.001794	PLAG1, IL1B, VEGFC, TNF, EGFR	9.285714	0.024011	0.022114
GOTERM_BP_DIRECT	GO:0060037~pharyngeal system development	5	0.001794	FGF8, EYA1, PTCH1, GATA3, NKX2-5	9.285714	0.024011	0.022114
GOTERM_BP_DIRECT	GO:0048678~response to axon injury	6	0.001852	NTRK1, KCNB1, EPO, AXL, APOD, FGF2	6.685714	0.024526	0.022588
GOTERM_BP_DIRECT	GO:0051966~regulation of synaptic transmission, glutamatergic	6	0.001852	GRM3, MAPK8IP2, TNF, DKK1, DGKI, GRM1	6.685714	0.024526	0.022588
GOTERM_BP_DIRECT	GO:0060828~regulation of canonical Wnt signaling pathway	6	0.001852	AMER1, PTK7, FZD7, CTNND2, ZNF703, GPC3	6.685714	0.024526	0.022588
GOTERM_BP_DIRECT	GO:0071560~cellular response to	8	0.001891	CDKN2B, PDGFD, CAV1, FOS, FGFR2, IGF1R, WNT4, DDR2	4.521739	0.024956	0.022985

GOTERM_BP_DIRECT	transforming growth factor beta stimulus							
GOTERM_BP_DIRECT	GO:0051799~negative regulation of hair follicle development	3	0.001927	NGFR, SMO, INHBA	39	0.025077	0.023096	
GOTERM_BP_DIRECT	GO:0010966~regulation of phosphate transport	3	0.001927	ROS1, FGF23, FGFR1	39	0.025077	0.023096	
GOTERM_BP_DIRECT	GO:0035793~positive regulation of metanephric mesenchymal cell migration by platelet-derived growth factor receptor-beta signaling pathway	3	0.001927	PDGFRB, PDGFB, PDGFA	39	0.025077	0.023096	
GOTERM_BP_DIRECT	GO:2000544~regulation of endothelial cell chemotaxis to fibroblast growth factor	3	0.001927	FGF1, FGF2, FGF4	39	0.025077	0.023096	
GOTERM_BP_DIRECT	GO:0031623~receptor internalization	7	0.002047	GHR, DNM3, CAV1, NEDD4, ACKR3, ADM, DNM1	5.25	0.026543	0.024446	
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	13	0.002065	EGR1, TGF2, ACE, TGF2, EPO, CAV1, VEGFC, ADM, VEGFD, PLAT, TNF, TGF2, PLAU	2.864407	0.026683	0.024575	
GOTERM_BP_DIRECT	GO:0097192~extrinsic apoptotic signaling pathway in absence of ligand	6	0.002106	ERBB3, EYA1, IL1B, FOXO3, IL2, FGF10	6.5	0.027122	0.024979	
GOTERM_BP_DIRECT	GO:0061003~positive regulation of dendritic spine morphogenesis	5	0.002149	CAMK2B, TIAM1, RELN, ITPKA, KALRN	8.863636	0.027479	0.025308	
GOTERM_BP_DIRECT	GO:0030318~melanocyte differentiation	5	0.002149	EDNRB, KIT, MITF, SOX10, GLI3	8.863636	0.027479	0.025308	
GOTERM_BP_DIRECT	GO:0097191~extrinsic apoptotic signaling pathway	7	0.00226	MLLT11, YAP1, TGF2, FASLG, INHBA, ACVR1B, TNF	5.150943	0.028698	0.026431	
GOTERM_BP_DIRECT	GO:0048666~neuron development	7	0.00226	NTRK1, EPHA5, ALK, TENM1, TGF2, ATP8A2, PBX1	5.150943	0.028698	0.026431	
GOTERM_BP_DIRECT	GO:0030219~megakaryocyte differentiation	4	0.002358	CDKN2B, MAF, TAL1, GATA1	14.18182	0.029547	0.027213	
GOTERM_BP_DIRECT	GO:0033327~Leydig cell differentiation	4	0.002358	PDGFRA, AR, NKX2-1, AMH	14.18182	0.029547	0.027213	
GOTERM_BP_DIRECT	GO:0016331~morphogenesis of embryonic epithelium	4	0.002358	JAG2, LAMA5, VEGFC, FGFR2	14.18182	0.029547	0.027213	
GOTERM_BP_DIRECT	GO:0048660~regulation of smooth muscle cell proliferation	4	0.002358	BMP4, TCF7L2, NR4A3, ELN	14.18182	0.029547	0.027213	
GOTERM_BP_DIRECT	GO:0043407~negative regulation of MAP kinase activity	6	0.002385	IL1B, SPRY4, DAB2IP, CBLC, SPRY2, PPARG	6.324324	0.029686	0.027341	
GOTERM_BP_DIRECT	GO:2001240~negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	6	0.002385	EYA1, IL1B, TNF, GATA1, HSPA1A, FGF10	6.324324	0.029686	0.027341	
GOTERM_BP_DIRECT	GO:0021766~hippocampus development	8	0.002419	EPHA5, ALK, RELN, ID4, NKX2-1, FGF13, GLI3, IGF1R	4.333333	0.030007	0.027637	
GOTERM_BP_DIRECT	GO:0016525~negative regulation of angiogenesis	11	0.002508	TGF2, CCN6, DAB2IP, SPRY2, FASLG, PPARG, FOXO4, KLF4, SULF1, DCN, EPHA2	3.177778	0.031009	0.028559	
GOTERM_BP_DIRECT	GO:0048663~neuron fate commitment	5	0.002549	BMP4, NOTCH3, OLIG1, BHLHE22, ZNF521	8.478261	0.031209	0.028743	
GOTERM_BP_DIRECT	GO:0008589~regulation of smoothened signaling pathway	5	0.002549	PTCH1, GAS1, GLI1, FGFR2, FGF10	8.478261	0.031209	0.028743	
GOTERM_BP_DIRECT	GO:0070498~interleukin-1-mediated signaling pathway	5	0.002549	EGR1, IL1R1, IL1B, IL1RAP, PLCB1	8.478261	0.031209	0.028743	
GOTERM_BP_DIRECT	GO:2000352~negative regulation of endothelial cell apoptotic process	6	0.00269	ANGPT1, ITGB3, IL13, KDR, GATA3, GATA2	6.157895	0.03282	0.030227	
GOTERM_BP_DIRECT	GO:0045600~positive regulation of fat cell differentiation	7	0.002997	LMO1, CEBPA, SFRP2, WIF1, ZBTB16, LRP5, PPARG	4.875	0.03611	0.033257	
GOTERM_BP_DIRECT	GO:0030218~erythrocyte differentiation	7	0.002997	BMP4, TAL1, EPO, KIT, GATA3, INHBA, GATA1	4.875	0.03611	0.033257	
GOTERM_BP_DIRECT	GO:0071425~hematopoietic stem cell proliferation	5	0.002998	WNT10B, CEBPA, SFRP2, WNT2B, MECOM	8.125	0.03611	0.033257	
GOTERM_BP_DIRECT	GO:0030099~myeloid cell differentiation	5	0.002998	CEBPA, CEBPE, ZBTB16, DLL1, TIRAP	8.125	0.03611	0.033257	

GOTERM_BP_DIRECT	GO:0045595~regulation of cell differentiation	6	0.003021	TFAP2A, CEBPD, KLF4, HES5, RUNX2, FGFR1	6	0.036159	0.033302
GOTERM_BP_DIRECT	GO:0001541~ovarian follicle development	6	0.003021	LFNG, KIT, KDR, FOXL2, INHBA, AMH	6	0.036159	0.033302
GOTERM_BP_DIRECT	GO:0010936~negative regulation of macrophage cytokine production	4	0.003085	TGFB2, TGFB3, AXL, PRG2	13	0.03645	0.033571
GOTERM_BP_DIRECT	GO:0030850~prostate gland development	4	0.003085	HOXA9, PTCH1, GLI1, HOXA11	13	0.03645	0.033571
GOTERM_BP_DIRECT	GO:0060444~branching involved in mammary gland duct morphogenesis	4	0.003085	CSF1, SRC, LRP5, EPHA2	13	0.03645	0.033571
GOTERM_BP_DIRECT	GO:0072112~podocyte differentiation	4	0.003085	EXT1, EDNRB, WT1, PROM1	13	0.03645	0.033571
GOTERM_BP_DIRECT	GO:0033077~T cell differentiation in thymus	6	0.003382	MAFB, BCL11B, FZD7, FZD8, IL7R, GLI3	5.85	0.039707	0.03657
GOTERM_BP_DIRECT	GO:0008625~extrinsic apoptotic signaling pathway via death domain receptors	6	0.003382	CRADD, SORT1, DAB2IP, FASLG, NGF, TNF	5.85	0.039707	0.03657
GOTERM_BP_DIRECT	GO:0007417~central nervous system development	11	0.003436	ROBO2, NGFR, RELN, SMO, PAX8, ZIC2, TLX3, ADGRA2, ZBTB16, MNX1, SH3GL2	3.042553	0.040217	0.03704
GOTERM_BP_DIRECT	GO:0042327~positive regulation of phosphorylation	5	0.003498	AR, EGF, FZD7, GRB10, EGFR	7.8	0.04056	0.037356
GOTERM_BP_DIRECT	GO:0048844~artery morphogenesis	5	0.003498	NOTCH3, WNT11, PRRX1, HES1, HOXA13	7.8	0.04056	0.037356
GOTERM_BP_DIRECT	GO:0035329~hippo signaling	5	0.003498	TEAD4, YAP1, WWTR1, TEAD1, TEAD3	7.8	0.04056	0.037356
GOTERM_BP_DIRECT	GO:0071363~cellular response to growth factor stimulus	7	0.003579	ACVR1C, IBSP, ERBB2, PDGFB, KLF4, ACVR1B, ACVR2A	4.706897	0.041378	0.038109
GOTERM_BP_DIRECT	GO:0035264~multicellular organism growth	9	0.003661	EXT1, NOTCH2, WWTR1, AR, SMO, TAL2, PPP1R13L, PLAG1, SLC1A2	3.581633	0.042114	0.038787
GOTERM_BP_DIRECT	GO:0007595~lactation	6	0.003772	SOCS2, CCND1, ERBB4, CAV1, NEURL1, KALRN	5.707317	0.042114	0.038787
GOTERM_BP_DIRECT	GO:1900127~positive regulation of hyaluronan biosynthetic process	3	0.00379	EGF, PDGFB, HAS2	29.25	0.042114	0.038787
GOTERM_BP_DIRECT	GO:0042490~mechanoreceptor differentiation	3	0.00379	NTRK1, NTF4, NTRK2	29.25	0.042114	0.038787
GOTERM_BP_DIRECT	GO:0038162~erythropoietin-mediated signaling pathway	3	0.00379	EPO, KIT, EPOR	29.25	0.042114	0.038787
GOTERM_BP_DIRECT	GO:0072050~S-shaped body morphogenesis	3	0.00379	PAX8, HES1, HES5	29.25	0.042114	0.038787
GOTERM_BP_DIRECT	GO:1904238~pericyte cell differentiation	3	0.00379	BMP4, EPHA2, WNT4	29.25	0.042114	0.038787
GOTERM_BP_DIRECT	GO:0007386~compartment pattern specification	3	0.00379	LFNG, DLL1, DLL3	29.25	0.042114	0.038787
GOTERM_BP_DIRECT	GO:0060571~morphogenesis of an epithelial fold	3	0.00379	AR, HOXD13, EGFR	29.25	0.042114	0.038787
GOTERM_BP_DIRECT	GO:0045608~negative regulation of inner ear auditory receptor cell differentiation	3	0.00379	HES1, DLL1, HES5	29.25	0.042114	0.038787
GOTERM_BP_DIRECT	GO:0060684~epithelial-mesenchymal cell signaling	3	0.00379	BMP4, WNT6, SMO	29.25	0.042114	0.038787
GOTERM_BP_DIRECT	GO:0060486~club cell differentiation	3	0.00379	NFIB, GATA6, NKX2-1	29.25	0.042114	0.038787
GOTERM_BP_DIRECT	GO:0060665~regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling	3	0.00379	HGF, FGFR1, FGF10	29.25	0.042114	0.038787
GOTERM_BP_DIRECT	GO:0007612~learning	7	0.0039	FOSL1, NTRK2, PAK6, FGF13, PLCB1, PTGS2, PAK5	4.627119	0.043083	0.03968
GOTERM_BP_DIRECT	GO:0051450~myoblast proliferation	4	0.003934	SRC, HGF, FOS, IGF1	12	0.043083	0.03968

GOTERM_BP_DIRECT	GO:0033690~positive regulation of osteoblast proliferation	4	0.003934	ITGB3, LRP5, GATA1, IGF1R	12	0.043083	0.03968
GOTERM_BP_DIRECT	GO:0048584~positive regulation of response to stimulus	4	0.003934	PDGFRB, FLT3, FLT4, KDR	12	0.043083	0.03968
GOTERM_BP_DIRECT	GO:0061029~eyelid development in camera-type eye	4	0.003934	TFAP2A, SOX11, INHBA, EGFR	12	0.043083	0.03968
GOTERM_BP_DIRECT	GO:0007166~cell surface receptor signaling pathway	18	0.003949	IL1R1, LAMA1, FCRL4, CBLC, LIFR, INHBA, EGFR, TIRAP, TSHR, EDNRB, ADGRG7, ADGRA2, PAPPA, ERBB2, CD28, IL7R, MET, IL12RB2	2.186916	0.043121	0.039714
GOTERM_BP_DIRECT	GO:0071542~dopamine rgic neuron differentiation	5	0.004051	DMRTA2, FGF8, SMO, VEGFD, TSHR	7.5	0.043974	0.0405
GOTERM_BP_DIRECT	GO:0014003~oligodendrocyte development	5	0.004051	LPAR1, OLIG1, SOX11, SOX10, HES5	7.5	0.043974	0.0405
GOTERM_BP_DIRECT	GO:0070373~negative regulation of ERK1 and ERK2 cascade	8	0.004087	LMO1, FLCN, PTPRR, DAB2IP, SPRY2, DUSP26, TLR4, ATF3	3.949367	0.044107	0.040622
GOTERM_BP_DIRECT	GO:0001843~neural tube closure	8	0.004087	BMP4, TGFB2, FZD3, SDC4, LHX2, PTCH1, FZD6, ADM	3.949367	0.044107	0.040622
GOTERM_BP_DIRECT	GO:0042594~response to starvation	6	0.004193	CPS1, DDIT3, ADM, PPARG, FOXO3, PPARGC1A	5.571429	0.044861	0.041317
GOTERM_BP_DIRECT	GO:0030501~positive regulation of bone mineralization	6	0.004193	FBN2, BMP4, TFAP2A, WNT10B, ACVR2A, WNT4	5.571429	0.044861	0.041317
GOTERM_BP_DIRECT	GO:0045746~negative regulation of Notch signaling pathway	6	0.004193	DLL4, HEY1, NEURL1, GATA2, DLL1, DLL3	5.571429	0.044861	0.041317
GOTERM_BP_DIRECT	GO:0034446~substrate adhesion-dependent cell spreading	7	0.004242	LAMA5, SRC, LAMA1, AXL, FZD7, ITGB3, ITGA8	4.55	0.045256	0.041681
GOTERM_BP_DIRECT	GO:0007254~JNK cascade	7	0.004605	FGF14, IL1B, NOD1, MAPK8IP2, TNF, TLR4, DUSP9	4.47541	0.048993	0.045122
GOTERM_BP_DIRECT	GO:1904706~negative regulation of vascular associated smooth muscle cell proliferation	6	0.004647	BMP4, CDKN1A, TAF4, TGFB3, GNA12, PPARG	5.44186	0.049293	0.045398
GOTERM_BP_DIRECT	GO:0001933~negative regulation of protein phosphorylation	8	0.004694	WWTR1, CDKN1A, SMO, ANGPT1, NTRK3, PLPP3, IL2, SH3GL2	3.851852	0.049654	0.045731
GOTERM_BP_DIRECT	GO:0062009~secondary palate development	4	0.004913	TGFBR3, TGFB2, WNT11, TGFB3	11.14286	0.051389	0.047329
GOTERM_BP_DIRECT	GO:0060317~cardiac epithelial to mesenchymal transition	4	0.004913	TGFBR3, TGFB2, HEY1, WNT16	11.14286	0.051389	0.047329
GOTERM_BP_DIRECT	GO:2001028~positive regulation of endothelial cell chemotaxis	4	0.004913	KDR, FGF2, MET, FGFR1	11.14286	0.051389	0.047329
GOTERM_BP_DIRECT	GO:0043068~positive regulation of programmed cell death	4	0.004913	NTRK1, BMP4, CDKN1A, TNF	11.14286	0.051389	0.047329
GOTERM_BP_DIRECT	GO:0045429~positive regulation of nitric oxide biosynthetic process	6	0.005134	IL1B, KLF4, PTGS2, ESR1, TNF, TLR4	5.318182	0.053553	0.049322
GOTERM_BP_DIRECT	GO:0000902~cell morphogenesis	9	0.005251	YAP1, TGFB2, RELN, DMRT1, CDH1, HGF, CDH11, IL7R, DKK1	3.375	0.054618	0.050303
GOTERM_BP_DIRECT	GO:0035116~embryonic hindlimb morphogenesis	5	0.00533	BMP4, FGF8, ZBTB16, GPC3, FGF4 RET, ALK, NOTCH2, NOTCH3, CSF3R, FLT3, SRC, FLT4, ITGB3, LRP5, PTPRK, ACVR1B, EGFR, IGF1R, GHR, ERBB3, ERBB4, ERBB2, KDR, OLR1, IL13RA2, ROS1, IL12RB2, PDGFRB, NTRK1, PDGFRA, NTRK2, NTRK3, STYK1, LIFR, TSHR, ACVR2A, LRP1B, TGFB3, AXL, PTK7, KIT, PPARG, FGFR4, MET, FGFR3, TLR4, FGFR2, FGFR1, EPHA2, DDR2	6.964286	0.055279	0.050912
GOTERM_CC_DIRECT	GO:0043235~receptor complex	46	5.32E-28	HOXC13, HOXA13, HOXC11, SOX2, HOXA9, HEY1, TRPS1, CREB3L1, HOXA3, TEAD1, MNX1, TEAD3, TEAD4, PAX3, SOX11, FOXL2, MITF, ETV1, OLIG1, HNF1A, FOS, SOX10, ETV4, RUNX2, MYCL, DMRTA2, AR, MYCN, MAF, PAX8, TAL2, PAX7, TAL1, DDIT3, AHRN, PPARG, ERG, PLCB1, ZFPM2, ATF3, CEBPA, HLF, CEBPD, CEBPE, GATA6, HOXD13, BHLHE22, GATA3, FOXO4, FOXO3, HOXD11, GATA1, MUC1, NKX2-1, STAT4, HES1, NKX2-5, PPARGC1A, HES5, TFAP2A, TCF7L2, EGR1, JUN, EGR2, NPM2, PRRX1, CDX2, EGR4, DMRT1, CDX1, PRRX2, HMGA2, FANCE, KLF4, SMAD6, ESR1, PBX1, FOSL1, TBX15, NR4A3, MAFB, NR6A1, TLX3, LHX2, NFIB, FEV, TLX1, NEDD4, FOSB, LHX4, HOXD9, EPHB6, ROBO2, EPO, ITGB3, MPL, PLAT, PTPRK, FZD10, TNF, ROBO1, GHR, PLAUG, ADGRA2, ROS1, PPFIA2, FCRL4, FLT3LG, TIRAP, TGFB3, SFRP4, KIT, ITGA8, ITGA7, MET, TLR4, EPHA2, NOTCH2, NOTCH3, SDC4, NOTCH4, PDGFB, SLC1A2, LPAR1, PDGFA, ACVR1B, EGFR, WNT6, TPO, GRIN2A, WIF1, GPC3, NCAM1, PROM1, WNT4, NTRK1, NGFR, FZD3, SORT1, TGFB3, KCNB1, FZD6, HSPA2, SULF1, GRIN2B, TSHR, ACVR2A, TNFRSF10D, AXL, CD28, ACKR3, FGFR3, FGFR2, FGF10	8.275642	2.36E-25	2.18E-25
GOTERM_CC_DIRECT	GO:0000785~chromatin	91	7.93E-23	EPHB6, CSF3, TNFRSF6B, CSF3R, CSF1, EPO, TNC, PRF1, PLAT, IL1RAP, FGF1, FGF2, TNF, FGF3, FGF4, FGF6, FGF8, IBSP, FGF9, PLAUG, CDH1, CCN6, KDR, PRSS8, IL13RA2, WNT5B, IL1R1, HGF, OMD, IGF2BP2, FLT3LG, DKK1, SFRP4	3.186471	1.76E-20	1.63E-20
GOTERM_CC_DIRECT	GO:0009986~cell surface	63	6.46E-20		3.881517	9.54E-18	8.83E-18
GOTERM_CC_DIRECT	GO:0005576~extracellular region	119	3.26E-18		2.2927	3.61E-16	3.34E-16

GOTERM_ CC_DIRECT	GO:0005886~plasma membrane	222	9.34E-16	LOX, PAPP, EPHA3, FBN2, NOTCH2, NOTCH3, EPHA10, NOTCH4, HTRA1, PDGFB, PDGFA, PLA2G5, KLK2, LTBP1, KLK7, WNT6, PDGFD, APOD, FGF23, WNT4, WNT10B, NGFR, TGF2, ACE, BDNF, TGF3, PRG2, INHBA, IGF1, IL2, BMP4, IL3, FGF19, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1, TENM1, WNT2B, FLT4, ELN, FASLG, ADM, LFNG, GHR, OLR1, AMH, MMP7, IL15, IL13, WNT16, NGF, DCN, LRRC7, IL1B, CDH11, COL6A3, MET, LAMA5, CANT1, LAMA1, COL11A1, WNT8B, TMPSR52, DLL1, FSTL3, NTF4, RELN, WNT11, ERBB4, WIF1, NTF3, GPC3, NCAM1, LEFTY2, ANGPT1, EGF, WNT7B, VEGFC, CCK, VEGFD, EPOR, TLL2, HSPA1A EPHB6, PRF1, CBL, FZD10, BAIAP2L1, EDNRB, ADGRA2, KDR, PRSS8, ARDC4, PRKCG, EPHA5, SLC34A2, EPHA7, IL1R1, ACSL6, FLT3LG, SOX11, PRKCA, DKK1, GABRG2, AR, TIAM1, BCORL1, PLPP3, EPHA3, EPHA2, SLC45A3, SDC4, EPHA10, LPAR1, PLA2G5, KALRN, GRIN2A, INPP5A, PROM1, JAG2, NGFR, WWTR1, FZD3, ACE, FZD2, MAGEE1, FZD7, FZD6, FZD8, GRIN2B, PPFIBP1, PTK7, CD28, XKR3, RET, DIRAS3, ROBO2, ITK, TENM1, PTPRR, PTPRK, ROBO1, AKAP12, CHL1, RAC3, OLR1, PRMT8, RHOD, PLCB4, LRRC7, KIT, GAS1, ACSBG1, TLR4, DDR2, GAS7, AMER1, KANK1, TMPSR52, GNAI1, EGFR, RELN, GPC3, HAS2, FLNC, PAK3, PAK5, IL12RB2, SORT1, KCNB1, WNT7B, DAB2IP, SEPTINS, SORBS2, SULF1, AXL, NEDD4, TACC2, LGR5, HSPA1A, ATP8A2, CSF3R, CSF1, DGKB, IRS1, TUSC3, CTNND2, MPL, IRS4, IRS2, IL1RAP, TNF, IGF1R, PLAU, CDH1, GRB10, ROS1, SH3GL2, RGS7, PDGFRB, PDGFRA, RNF43, USP6, WNT5B, MATK, ATP1B4, LIFR, SMO, SCN8A, WDFY3, DGKI, NOTCH2, NOTCH3, SHC2, NOTCH4, HTRA1, SLC1A2, TNFRSF11A, CYP2C19, TRHDE, FUT1, CACNA1G, WNT6, TPO, ADGRG7, SLC01B3, ABL2, WNT4, TGF3, PTCH1, CAV1, HSPA2, ESR1, LRP1B, TNFRSF10D, CPS1, CNTN1, FGF13, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1, ALK, PPP1R13B, FLT3, ITGB3, FLT4, FASLG, GPHN, RERG, GRM1, GHR, GRM3, FLCN, KIAA1549, HEPH, RASGEF1A, SH3D19, ABCC3, DST, GRID1, DNM1, TIRAP, TGFBR3, DNM3, CDH11, ITGA8, ITGA7, MET, DOCK1, CANT1, CEBPE, SRC, LRP5, NOD1, ACVR1B, DLL1, DLL3, DLL4, P2RY8, MUC1, ACVR1C, ERBB3, ERBB4, GNA11, ERBB2, GNA12, NCAM1, LRIG3, S1PR2, NTRK1, NTRK2, ANGPT1, NOS3, EGF, NTRK3, STYK1, EPOR, TSHR, ACVR2A, NEUR1L, SPRY2, ACKR3	1.606986	8.28E-14	7.66E-14
				FCGBP, CSF3, TNFRSF6B, CSF1, EPO, TNC, PLAT, FGF1, FGF2, TNF, FGF3, FGF4, FGF6, FGF8, IBSF, FGF9, PLAU, CCN6, PRSS8, IL13RA2, WNT5B, HGF, OMD, IGFBP2, FLT3LG, DKK1, DKK2, DKK4, SFRP4, SFRP2, LOX, PAPP, HTRA1, PDGFB, PDGFA, KLK2, TRHDE, KLK7, WNT6, TPO, PDGFD, APOD, PROM1, FGF23, WNT4, WNT10B, TGF2, ACE, BDNF, TGF3, INHBA, IGF1, GDF6, IL2, BMP4, IL3, FGF19, NODAL, FGF10, PTPRR, WNT2B, FASLG, ADM, GHR, AMH, MMP7, IL15, IL13, WNT16, NGF, DCN, TGFBR3, IL1B, KIT, COL6A3, TLR4, LAMA5, LAMA1, COL11A1, WNT8B, EGFR, FSTL3, NTF4, MUC1, RELN, WNT11, ERBB3, NTF3, LRIG3, LEFTY2, LINGO2, ANGPT1, EGF, WNT7B, VEGFC, CCK, VEGFD, SULF1, TSHR, TAFAS, AXL, TLL2, HSPA1A RET, ATL1, ROBO1, IGF1R, GRM3, NTF4, PCLO, CHL1, NTF3, NCAM1, PPFIA2, NTRK1, EPHA5, NTRK2, TGF2, FZD3, DST, KCNB1, BDNF, NTRK3, DAB2IP, CCK, NGF, GABRG2, DNM3, PTK7, SCN8A, ALDH1A1, CNTN1, WDFY3, FGF13, FGFR4, DGKI			
GOTERM_ CC_DIRECT	GO:0005615~extracellul ar space	103	2.05E-12	LAMA5, DGKB, FRMPD4, SRC, ITGB3, SLC1A2, LPAR1, PLAT, IL1RAP, GRM1, GRM3, GRIN2A, PCLO, ERBB4, CDH1, RAC3, SH3GL2, PPFIA2, EPHA7, CDKL5, USP6, GRID1, DNM1, DNM3, TIAM1, PLCB4, SCN8A, CDH11, ITPKA, ITGA8, PLCB1, DOCK1, DGKI CEBPA, GATA6, GATA2, DACH2, GATA1, HOXA11, SOX2, HOXA9, DACH1, NKX2- 1, NKX2-5, TEAD1, TEAD3, TEAD4, WWTR1, JUN, LMO2, HNF1A, KLF4, ESR1, RUNX2, NR4A3, NR6A1, TAL1, DDIT3 ATP8A2, IRS1, NAB2, FZD10, FGF1, HOXA13, CDC14B, HOXA11, SOX2, HOXA9, DACH1, BAIAP2L1, CCND1, CREB3L1, PRKACG, HOXA3, MNX1, LMO1, PDGFRA, CDKL5, LMO2, SOX11, MITF, PRKCA, PIMREG, SOX10, RUNX2, MYCL, AR, MYCN, WDFY3, ERG, BCORL1, ZFPM2, ATF3, EPHA3, NOTCH2, BRSK1, NOTCH3, NOTCH4, GATA6, GATA3, AK5, FOXO4, FOXO3, GATA2, KALRN, GATA1, PRDM16, NKX2-1, NKX2-5, PPARGC1A, SPECC1, TFAP2A, WWTR1, EGR1, NGFR, JUN, EGR2, EGR4, HMGA2, FANCE, SMAD6, ESR1, PBX1, FOSL1, MLT11, BCL9, NR4A3, TLX3, ID1, ID4, IL7R, HOXD9, ITK, CDKN1A, PPP1R13B, FLT4, ITGB3, FHL2, GLI1, HOXC11, RERG, GLI3, MECOM, ZIC2, HEY1, PPP1R13L, TRPS1, OLR1, ZNF521, TEAD1, MYBL1, TEAD3, SH3D19, TEAD4, DST, IL15, DNMT3A, PAX3, FOXL2, FOS, DUSP26, ETV4, PAX8, SETBP1, LRRC7, TAL1, AHRH, PPARG, DOCK1, CAMK2B, YAP1, CEBPA, HDACS, HLF, CEBPD, CEBPE, SRC, PLAG1, CAMK2A, TMPSR52, HOXD13, HOXD11, GNAI1, FSTL3, ERBB4, ERBB2, STAT4, PAK6, LRIG3, HES1, PAK5, HES5, RUNX1T1, TCF7L2, NPM2, PRRX1, CDX2, EYA1, CDKN2A, KLF4, PER1, NR6A1, ERCC4, WT1, NFIB, FOSB, TACC2, LGR5, HSPA1A	2.050814	1.52E-10	1.40E-10
GOTERM_ CC_DIRECT	GO:0030424~axon	33	1.69E-09	PRKCG, NGFR, NTRK2, FRMPD4, CTNND2, CAMK2A, MAPK8IP2, KALRN, GRIN2B, GPHN, GRM3, DNM3, GRIN2A, PLCB4, PCLO, LRRC7, PSD3, NEUR1L, PAK6, PAK3, SH2D5, DGKI RET, SRC, MPL, LPAR1, TNF, ROBO1, IGF1R, GHR, AKAP12, MAP2, GNA12, SNCG, RAC3, NCAM1, APOD, NTRK1, EPHA5, NTRK2, TGF2, FZD3, TGF3, DAB2IP, SORBS2, MAPK8IP2, TIAM1, PTK7, FGFR4	3.515254	1.07E-07	9.87E-08
GOTERM_ CC_DIRECT	GO:0098978~glutamate rgic synapse	34	1.06E-08	CEBPA, JUN, HLF, CEBPD, CEBPE, FOS, PBX1, FOSL1, MAFB, MAF, DDIT3, STAT4, PPARG, NKX2-5, ATF3 CSF3R, ITGB3, MPL, FASLG, TNFRSF11A, TNF, GHR, FGF8, PLAU, KDR, NCAM1, IL13RA2, IL12RB2, EPHA5, PDGFRA, ACE, IL1R1, IL13, FCRL4, LIFR, EPOR, TGFBR3, KIT, ITGA8, CD28, ITGA7, ACKR3, IL7R, TLR4	3.185822	5.62E-07	5.20E-07
GOTERM_ CC_DIRECT	GO:0005667~transcripti on regulator complex	25	1.14E-08	TEAD4, TCF7L2, EYA1, DDIT3, HMGA2, FOS, NKX2-5, GATA1, HOXA11 EPHB6, RET, EPHA10, CTNND2, GPHN, GRM1, NTF4, RELN, INPP5A, CHL1, MAP2, NTF3, APOD, PRKCG, NTRK1, EPHA5, NTRK2, FZD3, EPHA7, MAGEE1, KCNB1, BDNF, DAB2IP, SORBS2, NGF, PLCB4, SMO, FGF13, EPHA3, EPHA2 SOX2, HOXA9, HMGN2P46, CREB3L1, PRKACG, HOXA3, KDR, MNX1, PRKCG, SRRM3, MTUS2, SOX11, PRKCA, HNF1A, SOX10, RUNX2, SFRP4, AR, DDIT3, BCORL1, ZFPM2, ATF3, GATA6, PIK3R2, GATA3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, NKX2-5, PPARGC1A, WWTR1, EGR1, JUN, EGR2, CRADD, MAGEE1, BCL11B, BTBD18, PBX1, FOSL1, ID1, ID4, HOXD9, CDKN1C, ITK,	4.113687	5.62E-07	5.20E-07
GOTERM_ CC_DIRECT	GO:0005654~nucleopla sm	151	3.50E-08	TACC2, LGR5, HSPA1A PRKCG, NGFR, NTRK2, FRMPD4, CTNND2, CAMK2A, MAPK8IP2, KALRN, GRIN2B, GPHN, GRM3, DNM3, GRIN2A, PLCB4, PCLO, LRRC7, PSD3, NEUR1L, PAK6, PAK3, SH2D5, DGKI RET, SRC, MPL, LPAR1, TNF, ROBO1, IGF1R, GHR, AKAP12, MAP2, GNA12, SNCG, RAC3, NCAM1, APOD, NTRK1, EPHA5, NTRK2, TGF2, FZD3, TGF3, DAB2IP, SORBS2, MAPK8IP2, TIAM1, PTK7, FGFR4	1.516695	1.55E-06	1.44E-06
GOTERM_ CC_DIRECT	GO:0014069~postsynap tic density	22	7.70E-07	CEBPA, JUN, HLF, CEBPD, CEBPE, FOS, PBX1, FOSL1, MAFB, MAF, DDIT3, STAT4, PPARG, NKX2-5, ATF3 CSF3R, ITGB3, MPL, FASLG, TNFRSF11A, TNF, GHR, FGF8, PLAU, KDR, NCAM1, IL13RA2, IL12RB2, EPHA5, PDGFRA, ACE, IL1R1, IL13, FCRL4, LIFR, EPOR, TGFBR3, KIT, ITGA8, CD28, ITGA7, ACKR3, IL7R, TLR4	3.649717	3.10E-05	2.87E-05
GOTERM_ CC_DIRECT	GO:0043025~neuronal cell body	27	2.80E-06	TEAD4, TCF7L2, EYA1, DDIT3, HMGA2, FOS, NKX2-5, GATA1, HOXA11 EPHB6, RET, EPHA10, CTNND2, GPHN, GRM1, NTF4, RELN, INPP5A, CHL1, MAP2, NTF3, APOD, PRKCG, NTRK1, EPHA5, NTRK2, FZD3, EPHA7, MAGEE1, KCNB1, BDNF, DAB2IP, SORBS2, NGF, PLCB4, SMO, FGF13, EPHA3, EPHA2 SOX2, HOXA9, HMGN2P46, CREB3L1, PRKACG, HOXA3, KDR, MNX1, PRKCG, SRRM3, MTUS2, SOX11, PRKCA, HNF1A, SOX10, RUNX2, SFRP4, AR, DDIT3, BCORL1, ZFPM2, ATF3, GATA6, PIK3R2, GATA3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, NKX2-5, PPARGC1A, WWTR1, EGR1, JUN, EGR2, CRADD, MAGEE1, BCL11B, BTBD18, PBX1, FOSL1, ID1, ID4, HOXD9, CDKN1C, ITK,	2.891334	1.02E-04	9.43E-05
GOTERM_ CC_DIRECT	GO:0090575~RNA polymerase II transcription regulator complex	15	3.12E-06	CEBPA, JUN, HLF, CEBPD, CEBPE, FOS, PBX1, FOSL1, MAFB, MAF, DDIT3, STAT4, PPARG, NKX2-5, ATF3 CSF3R, ITGB3, MPL, FASLG, TNFRSF11A, TNF, GHR, FGF8, PLAU, KDR, NCAM1, IL13RA2, IL12RB2, EPHA5, PDGFRA, ACE, IL1R1, IL13, FCRL4, LIFR, EPOR, TGFBR3, KIT, ITGA8, CD28, ITGA7, ACKR3, IL7R, TLR4	4.780947	1.02E-04	9.43E-05
GOTERM_ CC_DIRECT	GO:0009897~external side of plasma membrane	29	3.22E-06	TEAD4, TCF7L2, EYA1, DDIT3, HMGA2, FOS, NKX2-5, GATA1, HOXA11 EPHB6, RET, EPHA10, CTNND2, GPHN, GRM1, NTF4, RELN, INPP5A, CHL1, MAP2, NTF3, APOD, PRKCG, NTRK1, EPHA5, NTRK2, FZD3, EPHA7, MAGEE1, KCNB1, BDNF, DAB2IP, SORBS2, NGF, PLCB4, SMO, FGF13, EPHA3, EPHA2 SOX2, HOXA9, HMGN2P46, CREB3L1, PRKACG, HOXA3, KDR, MNX1, PRKCG, SRRM3, MTUS2, SOX11, PRKCA, HNF1A, SOX10, RUNX2, SFRP4, AR, DDIT3, BCORL1, ZFPM2, ATF3, GATA6, PIK3R2, GATA3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, NKX2-5, PPARGC1A, WWTR1, EGR1, JUN, EGR2, CRADD, MAGEE1, BCL11B, BTBD18, PBX1, FOSL1, ID1, ID4, HOXD9, CDKN1C, ITK,	2.736321	1.02E-04	9.43E-05
GOTERM_ CC_DIRECT	GO:0032993~protein- DNA complex	9	4.06E-06	TEAD4, TCF7L2, EYA1, DDIT3, HMGA2, FOS, NKX2-5, GATA1, HOXA11 EPHB6, RET, EPHA10, CTNND2, GPHN, GRM1, NTF4, RELN, INPP5A, CHL1, MAP2, NTF3, APOD, PRKCG, NTRK1, EPHA5, NTRK2, FZD3, EPHA7, MAGEE1, KCNB1, BDNF, DAB2IP, SORBS2, NGF, PLCB4, SMO, FGF13, EPHA3, EPHA2 SOX2, HOXA9, HMGN2P46, CREB3L1, PRKACG, HOXA3, KDR, MNX1, PRKCG, SRRM3, MTUS2, SOX11, PRKCA, HNF1A, SOX10, RUNX2, SFRP4, AR, DDIT3, BCORL1, ZFPM2, ATF3, GATA6, PIK3R2, GATA3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, NKX2-5, PPARGC1A, WWTR1, EGR1, JUN, EGR2, CRADD, MAGEE1, BCL11B, BTBD18, PBX1, FOSL1, ID1, ID4, HOXD9, CDKN1C, ITK,	9.341234	1.17E-04	1.09E-04
GOTERM_ CC_DIRECT	GO:0030425~dendrite	30	4.24E-06	TEAD4, TCF7L2, EYA1, DDIT3, HMGA2, FOS, NKX2-5, GATA1, HOXA11 EPHB6, RET, EPHA10, CTNND2, GPHN, GRM1, NTF4, RELN, INPP5A, CHL1, MAP2, NTF3, APOD, PRKCG, NTRK1, EPHA5, NTRK2, FZD3, EPHA7, MAGEE1, KCNB1, BDNF, DAB2IP, SORBS2, NGF, PLCB4, SMO, FGF13, EPHA3, EPHA2 SOX2, HOXA9, HMGN2P46, CREB3L1, PRKACG, HOXA3, KDR, MNX1, PRKCG, SRRM3, MTUS2, SOX11, PRKCA, HNF1A, SOX10, RUNX2, SFRP4, AR, DDIT3, BCORL1, ZFPM2, ATF3, GATA6, PIK3R2, GATA3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, NKX2-5, PPARGC1A, WWTR1, EGR1, JUN, EGR2, CRADD, MAGEE1, BCL11B, BTBD18, PBX1, FOSL1, ID1, ID4, HOXD9, CDKN1C, ITK,	2.639914	1.17E-04	1.09E-04
GOTERM_ CC_DIRECT	GO:0005634~nucleus	199	7.62E-06	TEAD4, TCF7L2, EYA1, DDIT3, HMGA2, FOS, NKX2-5, GATA1, HOXA11 EPHB6, RET, EPHA10, CTNND2, GPHN, GRM1, NTF4, RELN, INPP5A, CHL1, MAP2, NTF3, APOD, PRKCG, NTRK1, EPHA5, NTRK2, FZD3, EPHA7, MAGEE1, KCNB1, BDNF, DAB2IP, SORBS2, NGF, PLCB4, SMO, FGF13, EPHA3, EPHA2 SOX2, HOXA9, HMGN2P46, CREB3L1, PRKACG, HOXA3, KDR, MNX1, PRKCG, SRRM3, MTUS2, SOX11, PRKCA, HNF1A, SOX10, RUNX2, SFRP4, AR, DDIT3, BCORL1, ZFPM2, ATF3, GATA6, PIK3R2, GATA3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, NKX2-5, PPARGC1A, WWTR1, EGR1, JUN, EGR2, CRADD, MAGEE1, BCL11B, BTBD18, PBX1, FOSL1, ID1, ID4, HOXD9, CDKN1C, ITK,	1.304495	1.97E-04	1.83E-04

				TENM1, CDKN1A, HOXC13, GLI1, HOXC11, GLI3, MECOM, HEY1, TEAD1, TEAD3, TEAD4, TET1, PAX3, FOS, DUSP9, MLF1, ZFTA, MN1, PLCB4, PAX8, TAL1, PAX7, ITPKA, AHRN, PPARG, PLCB1, VGLL3, YAP1, KANK1, HOXD11, GNAI1, EGFR, FSTL3, MIPOL1, STAT4, RUNX1T1, CDKN2B, NPM2, CDX2, DMRT1, CDKN2A, CDX1, AKR1C3, SORBS2, PER1, NR6A1, NFIB, WT1, NEDD4, FOSB, HSPA1A, ZNF331, PRDM7, IRS1, CTNND2, NAB2, FGF1, DACH2, HOXA13, FGF2, HOXA11, CDC14B, DACH1, CCND1, ZNF444, SSX1, PDGFRB, LMO1, PDGFRA, CDKL5, LMO2, MITF, MYCN, MAF, MALAT1, ERG, DGKI, NOTCH2, BRK1, NOTCH4, AK5, BHLHE22, FOXO4, FOXO3, CCNB3, TFAP2A, AUTS2, ZBTB16, HMGA2, HSPA2, FANCE, SMAD6, ESR1, MAFB, FGF14, NR4A3, TLX3, LHX2, TLX1, FEV, LHX4, FGF13, FGFR2, FGF10, FGFR1, PPP1R13B, ITGB3, FHL2, FASLG, RERG, GRM1, FLCN, ZIC2, PPP1R13L, TRPS1, ZNF521, MYBL1, PEG3, DST, DNMT3A, ETV1, FOXL2, OLIG1, DUSP26, ETV4, DMRTA2, CILK1, CEBPA, HDAC5, LAMA5, NUTM1, HLF, CEBPD, CEBPE, PLAG1, CAMK2A, CXXC4, MUC1, ERBB4, ERBB2, HES1, LRIG3, HES5, TCF7L2, EYA1, PRRX1, NOS3, PRRX2, PDE4DIP, TBX15, ERCC4, SPRY2			
GOTERM_	GO:0032587~ruffle	13	8.02E-06	KANK1, CDKL5, KSR1, SRC, ITGB3, SPRY4, EGFR, TIRAP, TIAM1, PSD3, ERBB2, SPRY2, EPHA2	5.159048	1.97E-04	1.83E-04
CC_DIRECT	membrane						
GOTERM_	GO:0062023~collagen-	27	1.10E-05	FBN2, LAMA5, WNT2B, LAMA1, COL11A1, ELN, HTRA1, PDGFB, TNC, LTBP1, RELN, GPC3, NCAM1, LEFTY2, EDIL3, TGF82, WNT5B, ANGPT1, TGF83, PRG2, SULF1, DCN, SFRP2, LOX, COL6A3, FGFR2, FGF10	2.678736	2.57E-04	2.38E-04
CC_DIRECT	containing extracellular						
GOTERM_	GO:0005796~Golgi	13	1.32E-05	WNT5B, SDC4, WNT7B, OMD, PDGFB, PDGFA, NGF, DCN, WNT6, MUC1, GPC3, FGF23, WNT4	4.917971	2.80E-04	2.59E-04
CC_DIRECT	lumen						
GOTERM_	GO:0030666~endocytic	11	1.33E-05	CAMK2B, WNT6, CSF3R, SMO, WNT5B, NOS3, WNT7B, CAV1, PTCH1, CAMK2A, WNT4	6.017101	2.80E-04	2.59E-04
CC_DIRECT	vesicle membrane						
GOTERM_	GO:0048471~perinuclea	40	1.43E-05	TENM1, CDKN1A, PTPRR, PPP1R13B, CSF1, SRC, AKAP6, FASLG, EGFR, HEPH, CDH1, ERBB2, SNCG, RAC3, APOD, ROS1, SH3GL2, PRKCG, EPHA5, NTRK2, CDKL5, MAGEE1, SORT1, KCNB1, BDNF, CAV1, PTCH1, PDE4DIP, PRKCA, SORBS2, INHBA, EML1, MLF1, DNMT3, NEDD4, NEURL1, PPARG, TLR4, DGKI, HSPA1A	2.127657	2.88E-04	2.67E-04
CC_DIRECT	r region of cytoplasm						
GOTERM_	GO:0031093~platelet	10	4.25E-05	TGF82, TGF83, EGF, HGF, PDGFB, VEGFC, PDGFA, VEGFD, IGF1, LEFTY2	5.952747	8.19E-04	7.58E-04
CC_DIRECT	alpha granule lumen						
GOTERM_	GO:0005901~caveola	10	9.30E-05	SMO, IRS1, SRC, NOS3, CAV1, PTCH1, AKAP6, FASLG, PTGS2, IGF1R	5.397158	0.001717	0.001589
CC_DIRECT							
GOTERM_	GO:0031012~extracellul	18	1.03E-04	LINGO2, FBN2, FCGBP, MMP7, LAMA1, ELN, OMD, FGF1, LTBP1, TSHR, WNT6, RELN, WNT11, CCN6, COL6A3, LRIG3, TLR4, WNT4	3.035901	0.001825	0.001689
CC_DIRECT	ar matrix						
GOTERM_	GO:0043197~dendritic	14	1.97E-04	NGFR, NTRK2, FRMPD4, CAMK2A, LPAR1, GRM3, DNMT3, TIAM1, GRIN2A, NEDD4, ITPKA, NEURL1, DGKI, PPFIA2	3.498158	0.00335	0.003101
CC_DIRECT	spine						
GOTERM_	GO:0005925~focal	25	2.23E-04	SDC4, SRC, ITGB3, FHL2, TNC, PIK3R2, EGFR, AKAP12, PLAU, GNA12, RAC3, FLNC, PDGFRB, FZD2, DST, CAV1, SPRY4, SORBS2, PPFIBP1, PTK7, ITGA8, FGFR3, HSPA1A, EPHA2, DDR2	2.326361	0.003655	0.003383
CC_DIRECT	adhesion						
GOTERM_	GO:0009925~basal	9	3.88E-04	ABCC3, ACE, ERBB3, DST, ERBB4, ERBB2, SLCO1B3, MET, EGFR	5.059835	0.006138	0.005681
CC_DIRECT	plasma membrane						
GOTERM_	GO:0005737~cytoplasm	176	6.91E-04	DGKB, IRS1, CTNND2, PLAT, FZD10, FGF1, FGF2, FGF3, CDC14B, FGF4, SOX2, FGF6, HOXA9, FGF8, CCND1, FGF9, CDH1, GRB10, SH3GL2, PPFIA2, SSX1, RGS7, PDGFRB, ARRC4, LMO1, PRKCG, PDGFA, USP6, MATK, MTUS2, MITF, PRKCA, DLEC1, HNF1A, MAPK8IP2, RUNX2, SFRP4, AR, INPP4B, MAF, DDIT3, HECW1, WDFY3, ZFPM2, DGKI, BRK1, PDGFB, LPAR1, AK5, FOXO4, FOXO3, CYP2C19, GATA2, TRHDE, KALRN, CACNA1G, SOCS2, CCNB3, MAP2, ZNF703, MYH11, APOD, SRGAP3, NKX2-5, FGF23, WNT4, WNT11, EGR1, FZD3, EGR2, ACE, FZD2, CRADD, AUTS2, BDNF, RANBP17, HSPA2, SMAD6, ESR1, GRIN2B, PBX1, GFAP, FGF14, CPS1, FGF19, ID1, ID4, FGF13, FGFR4, FGFR2, FGF10, CDKN1C, TENM1, PPP1R13B, ADM, GLI1, GPHN, GLI3, ROBO1, AKAP12, FLCN, ZIC2, HEY1, CEP170B, TEAD4, KSR1, DST, IL15, IL13, DNMT3A, DUSP26, WNT16, DUSP9, TIRAP, MLF1, DNMT1, DNMT3, DPYD, ITPKA, ALDH1A1, CDH11, AHRN, PPARG, ACSBG1, PLCB1, DOCK1, TLR4, CILK1, GAS7, CAMK2B, YAP1, HDAC5, KANK1, NUTM1, SRC, CAMK2A, AKAP6, NOD1, PTGS2, CXXC4, EGFR, GNAI1, MUC1, RELN, WNT11, GNA11, ERBB2, GNA12, STAT4, PAK6, SNCG, HES1, FLNC, S1PR2, PAK3, PAK5, NTRK2, CDKN2B, NPM2, EYA1, DMRT1, CDKN2A, NOS3, SPRY4, DAB2IP, AKR1C3, PDE4DIP, ACVR2A, BICC1, PER1, TAFAS, PC, WT1, NEDD4, TACC2, HSPA1A	1.238138	0.010556	0.00977
CC_DIRECT							
GOTERM_	GO:0005788~endoplas	19	7.67E-04	WNT5B, CSF1, FLT3, BDNF, COL11A1, WNT7B, PDGFB, TNC, PDGFA, PTGS2, LTBP1, FSTL3, BMP4, WNT6, PDGFD, GPC3, COL6A3, FGF23, WNT4	2.472974	0.011325	0.010481
CC_DIRECT	mic reticulum lumen						
GOTERM_	GO:0032991~protein-	32	8.71E-04	ALK, NOTCH2, CDKN1A, FRMPD4, ITGB3, FOXO3, PTGS2, LTBP1, EGFR, HOXA11, DLL3, TRPS1, ZNF703, GRB10, NKX2-5, RGS7, NTRK1, PDGFRA, KSR1, CDKN2A, ZBTB16, CAV1, MITF, HNF1A, MAPK8IP2, SMAD6, ESR1, AR, CPS1, NEDD4, DGKI, HSPA1A	1.89374	0.012441	0.011514
CC_DIRECT	containing complex						
GOTERM_	GO:0044294~dendritic	4	0.00112	CDKL5, MAP2, SRC, PTCH1	17.99053	0.015511	0.014356
CC_DIRECT	growth cone						
GOTERM_	GO:0030054~cell	13	0.00241	YAP1, PDGFRA, BRK1, PTPRR, DST, SRC, PTPRK, EGFR, PPP1R13L, CDH1, SCN8A, KDR, PAK6	2.814026	0.032353	0.029943
CC_DIRECT	junction						
GOTERM_	GO:0035867~alphav-	3	0.003523	ITGB3, IGF1, IGF1R	30.35901	0.045352	0.041973
CC_DIRECT	beta3 integrin-IGF-1-						
GOTERM_	GO:0097060~synaptic	6	0.003583	PRKCG, GRIN2A, SRC, GRIN2B, GPHN, DGKI	5.782669	0.045352	0.041973
CC_DIRECT	membrane						
GOTERM_	GO:0045211~postsynap	13	0.004323	MAGEE1, KCNB1, DGKB, ITGB3, LPAR1, GRIN2B, GPHN, GABRG2, GRM3, GRIN2A, ERBB4, LRRC7, CNTN1	2.618024	0.053194	0.049231
CC_DIRECT	tic membrane						

GOTERM_MF_DIRE	GO:0001228~DNA-binding transcription activator activity, RNA polymerase II-specific	67	4.66E-28	HOXC13, GLI1, HOXA13, HOXC11, SOX2, HOXA9, MECOM, CREB3L1, ZNF521, MYBL1, TEAD4, SOX11, FOXL2, MITF, ETV1, HNF1A, FOS, SOX10, ETV4, RUNX2, AR, MYCN, MAF, PAX8, DDIT3, PPARG, ERG, ATF3, NOTCH2, CEBPA, HLF, CEBPD, CEBPE, PLAG1, NOTCH4, HOXD13, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-5, TFAP2A, EGR1, JUN, EGR2, PRRX1, BCL11B, EGR4, DMRT1, CDX1, ZBTB16, KLF4, ESR1, PBX1, FOSL1, NR4A3, MAFB, NR6A1, LHX2, NFIB, WT1, FEV, TLX1, FOSB, LHX4	5.123954	3.57E-25	3.28E-25
GOTERM_MF_DIRE	GO:0008083~growth factor activity	39	4.26E-25	CSF3, CSF1, PDGFB, PDGFA, FGF1, FGF2, FGF3, FGF4, NTF4, FGF6, FGF8, FGF9, PDGFD, CCN6, NTF3, AMH, LEFTY2, FGF23, JAG2, TGFB2, TGFB3, EGF, BDNF, HGF, VEGFC, VEGFD, IGF1, INHBA, NGF, GDF6, DKK1, IL2, BMP4, IL3, FGF14, FGF19, FGF13, NODAL, FGF10	8.911648	1.63E-22	1.50E-22
GOTERM_MF_DIRE	GO:0004714~transmembrane receptor protein tyrosine kinase activity	22	1.98E-23	ALK, NTRK1, RET, PDGFRA, NTRK2, FLT3, SRC, FLT4, NTRK3, STYK1, EGFR, IGF1R, ERBB3, AXL, ERBB4, PTK7, KIT, ERBB2, KDR, ROS1, EPHA2, DDR2, ZNF331, DACH2, HOXA13, HOXA11, SOX2, HOXA9, DACH1, HOXA3, ZNF444, SOX11, MITF, HNF1A, SOX10, RUNX2, MYCL, AR, MYCN, MAF, DDIT3, ERG, ATF3, GATA6, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, NKX2-5, TFAP2A, EGR1, JUN, EGR2, BCL11B, EGR4, ZBTB16, ESR1, PBX1, FOSL1, NR4A3, MAFB, TLX3, LHX2, TLX1, FEV, HOXD9, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, PEG3, DNMT3A, TET1, PAX3, ETV1, FOXL2, FOS, ETV4, DMRTA2, PAX8, TAL2, PAX7, TAL1, PPARG, YAP1, CEBPA, HDAC5, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, MUC1, STAT4, HES5, TCF7L2, PRRX1, CDX2, DMRT1, CDX1, PRRX2, KLF4, TBX15, PER1, NR6A1, WT1, NFIB, FOSB	21.26843	5.04E-21	4.63E-21
GOTERM_MF_DIRE	GO:0000978~RNA polymerase II cis-regulatory region sequence-specific DNA binding	98	1.24E-21	HOXC13, HOXA13, HOXC11, GLI3, HOXA11, HOXA9, HEY1, CREB3L1, ZNF444, TEAD1, MNX1, PAX3, FOXL2, ETV1, FOS, SOX10, ETV4, RUNX2, DMRTA2, MYCN, MAF, PAX8, PAX7, ERG, ATF3, HLF, CEBPD, CEBPE, GATA6, HOXD13, BHLHE22, GATA3, FOXO4, FOXO3, HOXD11, GATA2, GATA1, HES1, NKX2-5, HES5, TFAP2A, EGR1, JUN, EGR2, CDX2, BCL11B, EGR4, DMRT1, CDX1, PRRX2, KLF4, ESR1, PBX1, FOSL1, TBX15, NR6A1, TLX3, NFIB, FEV, FOSB, LHX4, HOXD9, HOXC13, GLI3, SOX2, HOXA9, HEY1, MECOM, ZIC2, TRPS1, TEAD1, TEAD3, TEAD4, PAX3, SOX11, FOXL2, ETV1, HNF1A, FOS, SOX10, ETV4, RUNX2, AR, MYCN, PAX8, PAX7, TAL1, DDIT3, PPARG, ATF3, CEBPA, PLAG1, GATA6, HOXD13, BHLHE22, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, STAT4, NKX2-5, TFAP2A, TCF7L2, EGR1, JUN, EGR2, CDX2, BCL11B, EGR4, CDX1, ZBTB16, PRRX2, KLF4, ESR1, PBX1, FOSL1, WT1, HOXD9	2.888902	2.37E-19	2.18E-19
GOTERM_MF_DIRE	GO:1990837~sequence-specific double-stranded DNA binding	62	2.98E-21	YAP1, CEBPA, HDAC5, GATA6, GATA3, HOXC13, FOXO3, GLI1, TNF, GATA1, SOX2, ERBB4, CREB3L1, PRDM16, NKX2-1, NKX2-5, TFAP2A, TCF7L2, EGR1, JUN, EGR2, CDX1, HMG2, PDE4DIP, SOX11, HNF1A, FOS, KLF4, SMAD6, SOX10, PBX1, PER1, AR, PAX8, WT1, TAL1, DDIT3, AHRH, PPARG, ATF3, ZNF331, DACH2, HOXA13, HOXA11, SOX2, HOXA9, DACH1, CREB3L1, HOXA3, ZNF444, MNX1, SOX11, MITF, HNF1A, SOX10, RUNX2, MYCL, AR, MYCN, MAF, DDIT3, ERG, ATF3, GATA6, GATA3, BHLHE22, FOXO4, FOXO3, GATA2, GATA1, NKX2-1, NKX2-5, TFAP2A, EGR1, JUN, EGR2, EGR4, ZBTB16, ESR1, PBX1, FOSL1, NR4A3, MAFB, TLX3, LHX2, TLX1, FEV, LHX4, HOXD9, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, PEG3, PAX3, ETV1, FOXL2, OLIG1, FOS, ETV4, DMRTA2, PAX8, TAL2, PAX7, TAL1, AHRH, PPARG, CEBPA, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, STAT4, HES1, HES5, TCF7L2, PRRX1, CDX2, DMRT1, CDX1, PRRX2, KLF4, TBX15, NR6A1, WT1, NFIB, FOSB	4.174275	4.56E-19	4.19E-19
GOTERM_MF_DIRE	GO:0003700~DNA-binding transcription factor activity	59	4.17E-20	PDGFRB, ALK, NTRK1, RET, EPHA7, FLT3, SRC, STYK1, MATK, EGFR, IGF1R, ERBB3, AXL, ERBB4, KIT, ERBB2, KDR, ABL2, MET, ROS1, FGFR3, FGFR2, FGFR1, CSF3, WNT2B, CSF1, EPO, WNT8B, FASLG, FGF2, TNF, WNT6, WNT11, LEFTY2, WNT4, WNT10B, TGFB2, WNT5B, TGFB3, IL15, WNT7B, IL13, FLT3LG, INHBA, WNT16, GDF6, IL2, BMP4, IL3, TAFAS, IL1B, NODAL	4.150157	5.32E-18	4.89E-18
GOTERM_MF_DIRE	GO:0000976~transcription on cis-regulatory region binding	40	1.10E-19	EPHA7, FLT3, SRC, FLT4, HTRA1, LIFR, ACVR1B, ACVR2A, GHR, ACVR1C, ERBB3, KIT, ERBB2, KDR, EPHA2	6.18084	1.21E-17	1.11E-17
GOTERM_MF_DIRE	GO:0000981~DNA-binding transcription factor activity, RNA polymerase II-specific	97	2.81E-19	CEBPA, HDAC5, GATA3, GATA2, GATA1, HEY1, NKX2-1, HES1, NKX2-5, PPARGC1A, TEAD3, TCF7L2, JUN, EGR2, PRRX1, CDKN2A, LMO2, DNMT3A, HMG2, FOS, DUSP26, KLF4, AR, TAL1, DDIT3, ID4, ZFPM2	2.691099	2.69E-17	2.47E-17
GOTERM_MF_DIRE	GO:0004713~protein tyrosine kinase activity	23	3.29E-14	FRMPD4, FZD10, HOXA9, PRKACG, CREB3L1, HOXA3, CYP1B1, PRSS8, PRKCG, PRKCA, DKK1, SOX10, EML1, DKK2, GABRG2, DKK4, AR, DDIT3, HECW1, ATF3, PDGFB, GATA6, PDGFA, GATA3, GATA2, GATA1, GRIN2A, PPP3R2, PRDM16, NKX2-1, NKX2-5, PROM1, PPARGC1A, JAG2, WNT10B, NGFR, JUN, FZD3, FZD2, BTBD18, FZD7, FZD6, FZD8, GRIN2B, PBX1, MLLT11, FOSL1, PPFBP1, CDKN1C, RET, ITK, CDKN1A, ELN, HOXC13, GLI1, HOXC11, GLI3, MECOM, HEY1, OLR1, TEAD1, TEAD3, TEAD4, ELOVL2, FCRL4, TET1, PAX3, FOS, DUSP9, PLCB4, PAX8, TAL2, LRRC7, TAL1, DPYD, AHRH, GAS1, PPARG, PLCB1, GAS7, KANK1, ATL1, PTGS2, EGFR, FSTL3, MIPOL1, NTF4, CHN1, NTF3, STAT4, AGR3, HAS2, FLNC, RUNX1T1, CDKN2B, CDKN2A, KCNB1, WNT7B, SEPTIN5, DAB2IP, WT1, NFIB, FOSB, LGR5, HSPA1A, CSF3R, ATP8A2, CSF1, EPO, IRS1, CTNND2, NAB2, IRS4, TNC, IRS2, FGF1, FGF2, TNF, FGF3, CDC14B, FGF6, DACH1, IBSP, CDH1, GRB10, MB21D2, IL13RA2, MAP3K6, ROS1, SSX1, RN4F4, CDKL5, USP6, IGFBP2, MITF, MAF, SMO, ERG, TCTA, DGKI, NOTCH2, NOTCH3, SHC2, NOTCH4, FOXO4, TNFRSF11A, FOXO3, SOCS2, CLTCL1, ABL2, SRGAP3, BDNF, ZBTB16, TNFRSF10D, GFAP, BCL9, MAFB, LHX2, LHX4, ALK, PPP1R13B, FLT3, FLT4, ITGB3, FHL2, FASLG, KIAA1549, PPP1R13L, AMH, ZNF521, SH3D19, PTCRA, KSR1, DST, DNMT3A, FOXL2, DUSP26, NGF, TIRAP, ITGA7, MET, CEBPA, HDAC5, NUTM1, CANT1, CEBPD, CEBPE, SRC, LRP5, NOD1, NTRK1, NTRK2, PRRX1, ANGPT1, NTRK3, STYK1, KLF4, PC, EPHB6, TNFRSF6B, PRF1, CBLC, SOX2, BAIAP2L1, EDNRB, ADGRA2, KDR, ARRC4, EPHA5, EPHA7, IL1R1, FLT3LG, C10ORF55, MTUS2, DLEC1, HNF1A, PIMREG, MAPK8IP2, RUNX2, SFRP4, INPP4B, TIAM1, PAPP, PLPP3, ZFPM2, EPHA3, EPHA2, SDC4, EPHA10, LPAR1, PIK3R2, KALRN, INPP5A, MAP2, ZNF703, APOD, VVWTR1, EGR1, EGR2, MAGEE1, BCL11B, CRADD, EGR4, PRG2, IGF1, EXT1, ACER1, EXT2, PTK7, ID1, ID4, CD28, RTL8B, NODAL, DIRAS3, ROBO2, PTPRR, PTPRK, ROBO1, AKAP12, SERP2, RAC3, PRMT8, IL15, IL13, MLF1, MN1, IL1B, KIT, TLR4, DDR2, AMER1, YAP1, TMPPRSS2, AKAP6, GNAI1, WIF1, GPC3, PAK6, PAK3, PAK5, NPM2, CDX2, CDX1, SORT1, VEGFC, VEGFD, SORBS2, PER1, AXL, NEDD4, FCGBP, PRDM7,	8.338191	2.79E-12	2.57E-12
GOTERM_MF_DIRE	GO:0005125~cytokine activity	29	3.11E-13		5.607131	2.38E-11	2.18E-11
GOTERM_MF_DIRE	GO:0019838~growth factor binding	15	5.72E-13		14.5012	3.98E-11	3.65E-11
GOTERM_MF_DIRE	GO:0061629~RNA polymerase II-specific DNA-binding transcription factor binding	27	3.22E-12		5.532524	2.06E-10	1.89E-10
GOTERM_MF_DIRE	GO:0005515~protein binding	401	6.34E-10		1.185428	3.73E-08	3.43E-08

				MPL, PLAT, IGF1R, CCND1, PLA1, SH3GL2, PPFA2, PDGFRB, LMO1, PDGFRA, HGF, LMO2, MATK, ATP1B4, LIFR, MYCN, LOX, SCN8A, WDFY3, FBN2, SLC1A2, HTRA1, LTBP1, CCNB3, ADGRG7, MYH11, FGF23, TFAP2A, TGF2, AUTS2, TGF2, PTCH1, CAV1, HMG2, HSPA2, INHBA, SMAD6, ESR1, LRP1B, IL2, BMP4, IL3, FGF14, NR4A3, TLX3, CPS1, TLX1, FGF19, CNTN1, FGF13, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1, GPHN, GRM1, GHR, FLCN, TRPS1, MMP7, ETV1, OLIG1, ETV4, DCN, DNM1, DNM3, TGFBR3, SETBP1, ALDH1A1, DOCK1, CILK1, CAMK2B, HLF, LAMA1, CAMK2A, ACVR1B, DLL1, DLL4, MUC1, WNT11, ERBB3, ERBB4, GNA11, ERBB2, GNA12, SNCG, HES1, LRIG3, NCAM1, S1PR2, TCF7L2, EYA1, NOS3, EGF, SPRY4, PDE4DIP, CCK, EPOR, TSHR, ACVR2A, TBX15, ERCC4, PPP2R2B, NEURL1, SPRY2, ACKR3			
GOTERM_MF_DIRE	GO:0042802~identical protein binding	89	1.89E-09	ROBO2, ALK, CSF1, ITGB3, NAB2, PRF1, FHL2, FGF2, TNF, GPHN, IGF1R, ROBO1, GHR, PPP1R13L, CDH1, GRB10, KDR, PRKG2, OLR1, SH3GL2, PRMT8, GRID1, HGF, LMO2, DNMT3A, C10ORF55, HNF1A, FOS, SOX10, TIRAP, DNM1, DNM3, DMRTA2, MAF, DDIT3, PPARG, PLCB1, MET, TLR4, ATF3, GAS7, CAMK2B, CEBPA, HDAC5, NOTCH3, CEBPD, SDC4, CEBPE, ATL1, CAMK2A, HTRA1, PDGFB, PDGFA, NOD1, GATA3, FOXO4, EGFR, MIPOL1, ERBB3, ERBB2, STAT4, HAS2, FLNC, NTRK1, TFAP2A, JUN, NPM2, ANGPT1, DMRT1, TGF2, ZBTB16, CAV1, DAB2IP, SEPTIN5, SORBS2, VEGFD, INHBA, GDF6, SMAD6, ESR1, EPOR, GFAP, MAFB, PC, ERCC4, CD28, FGFR3, FGFR2, FGFR1	1.931824	1.03E-07	9.49E-08
GOTERM_MF_DIRE	GO:0017147~Wnt-protein binding	12	2.53E-09	SFRP4, FZD3, SFRP2, FZD2, WIF1, EGF, FZD7, FZD6, LRP5, FZD8, FZD10, LRP1B	11.90625	1.29E-07	1.19E-07
GOTERM_MF_DIRE	GO:0005178~integrin binding	21	1.14E-08	LAMA5, DST, SRC, ITGB3, TNC, PRKCA, IGF1, FGF1, FGF2, EGFR, GFAP, SFRP2, IBSP, IL1B, CCN6, ITGA8, KDR, ITGA7, S1PR2, PLPP3, EDIL3	4.887442	5.45E-07	5.01E-07
GOTERM_MF_DIRE	GO:0005161~platelet-derived growth factor receptor binding	8	2.55E-08	PDGFRB, PDGFRA, IL1R1, PDGFD, ITGB3, PDGFB, PDGFA, VEGFD	21.54464	1.15E-06	1.06E-06
GOTERM_MF_DIRE	GO:0043565~sequence-specific DNA binding	27	4.65E-08	HLF, PLAG1, FOXO4, FOXO3, GLI1, HOXA13, GATA1, SOX2, PRDM16, HES1, NKX2-5, PPARGC1A, TFAP2A, TCF7L2, EGR1, EGR2, EGR4, PAX3, ETV1, ETV4, ESR1, MAFB, NR6A1, WT1, PPARG, LHX4, ERG	3.571875	1.92E-06	1.76E-06
GOTERM_MF_DIRE	GO:0005109~frizzled binding	11	4.94E-08	WNT6, WNT10B, RNF43, WNT11, WNT2B, WNT5B, FZD7, WNT7B, WNT8B, WNT16, WNT4	10.63421	1.92E-06	1.76E-06
GOTERM_MF_DIRE	GO:0042813~Wnt receptor activity	9	5.27E-08	FZD3, FZD2, EGF, FZD7, FZD6, LRP5, FZD8, FZD10, LRP1B	15.42401	1.92E-06	1.76E-06
GOTERM_MF_DIRE	GO:0005104~fibroblast growth factor receptor binding	9	5.27E-08	FGF6, FGF8, FGF9, FGF19, FGF1, FGF2, FGF3, FGF4, FGF10	15.42401	1.92E-06	1.76E-06
GOTERM_MF_DIRE	GO:0019899~enzyme binding	31	6.98E-08	NOTCH2, NOTCH3, CSF3, SRC, ITGB3, FOXO4, CYP2C19, PTGS2, EGFR, FLCN, HOXA9, CCND1, NKX2-1, PDGFRB, EGR1, JUN, PRMT8, NPM2, SORT1, CAV1, ACSL6, PDE4DIP, PRKCA, HSPA2, ESR1, AR, TAL1, NEDD4, PPARG, PLCB1, HSPA1A	3.141927	2.43E-06	2.23E-06
GOTERM_MF_DIRE	GO:0015026~coreceptor activity	12	3.56E-07	TGFBR3, NGFR, PTK7, ITGB3, ERBB2, LRP5, CD28, KDR, ACKR3, IL1RAP, ACVR2A, IL12RB2	7.668432	1.19E-05	1.09E-05
GOTERM_MF_DIRE	GO:0005524~ATP binding	75	3.87E-07	EPHB6, RET, ALK, ITK, ATP8A2, FLT3, DGKB, FLT4, GPHN, IGF1R, CCT6B, PRKACG, KDR, PRKG2, MAP3K6, ROS1, ABCC3, PDGFRB, PRKCG, EPHA5, PDGFRA, EPHA7, CDKL5, KSR1, ACSL6, MATK, PRKCA, RUNX2, NAV3, SCN8A, KIT, ITPKA, ACSBG1, MET, CILK1, DGKI, EPHA3, EPHA2, DDR2, CAMK2B, BRSK1, EPHA10, SRC, CAMK2A, NOD1, AK5, ACVR1B, KALRN, EGFR, ACVR1C, ERBB3, ERBB4, ERBB2, ABL2, PAK6, LRIG3, MYH11, PAK3, PAK5, NTRK1, NTRK2, NTRK3, STYK1, KIAA0232, HSPA2, ACVR2A, PC, CPS1, AXL, PTK7, FGFR4, FGFR3, FGFR2, FGFR1, HSPA1A	1.835	1.23E-05	1.13E-05
GOTERM_MF_DIRE	GO:0001221~transcription coregulator binding	9	5.55E-06	LMO2, PPARG, FOS, GATA2, KLF4, FOXO3, ESR1, GATA1, PBX1	8.929688	1.70E-04	1.56E-04
GOTERM_MF_DIRE	GO:0008013~beta-catenin binding	14	6.87E-06	AMER1, KANK1, TCF7L2, CTNND2, PTPRK, FOXO4, KLF4, FOXO3, ESR1, GLI3, AR, BCL9, CDH1, CDH11	4.79858	2.02E-04	1.86E-04
GOTERM_MF_DIRE	GO:0048018~receptor ligand activity	11	1.68E-05	DLL4, WNT10B, RELN, SFRP2, TAFAS, EGF, WNT7B, WNT8B, DLL1, HSPA1A, WNT4	5.841329	4.61E-04	4.24E-04
GOTERM_MF_DIRE	GO:0005158~insulin receptor binding	7	1.74E-05	IRS1, SRC, IRS4, GRB10, IRS2, IGF1, IGF1R	11.99645	4.61E-04	4.24E-04
GOTERM_MF_DIRE	GO:0042056~chemoattractant activity	9	1.75E-05	BMP4, FGF8, HGF, NTF3, PDGFB, VEGFC, VEGFD, FGF2, FGF10	7.712003	4.61E-04	4.24E-04
GOTERM_MF_DIRE	GO:0005112~Notch binding	8	2.05E-05	JAG2, NOTCH2, DLL4, NOTCH3, ATRNL1, NOTCH4, DLL1, DLL3	9.140152	5.24E-04	4.81E-04
GOTERM_MF_DIRE	GO:0008046~axon guidance receptor activity	7	2.30E-05	ROBO2, NTRK2, EPHA7, PTK7, NCAM1, FGFR4, ROBO1	11.47486	5.67E-04	5.21E-04
GOTERM_MF_DIRE	GO:0008201~heparin binding	17	4.23E-05	ALK, TENM1, COL11A1, PTCH1, PRG2, FGF1, FGF2, FGF4, TGFBR3, BMP4, FGF14, FGF9, CCN6, FGFR4, FGFR2, FGF10, FGF1	3.409325	0.001012	9.30E-04
GOTERM_MF_DIRE	GO:0043548~phosphatidylinositol 3-kinase binding	6	4.37E-05	IRS1, AXL, DAB2IP, IRS4, IRS2, IGF1R	14.13867	0.001013	9.31E-04
GOTERM_MF_DIRE	GO:0005005~transmembrane-ephrin receptor activity	6	6.06E-05	EPHB6, EPHA5, EPHA7, EPHA10, EPHA3, EPHA2	13.30699	0.001363	0.001253
GOTERM_MF_DIRE	GO:0043121~neurotrophin binding	4	7.23E-05	NTRK1, NTRK2, NGFR, NTRK3	37.70313	0.001581	0.001453
GOTERM_MF_DIRE	GO:0042803~protein homodimerization activity	39	1.06E-04	CAMK2B, TENM1, CEBPA, CANT1, CSF1, FLT4, CAMK2A, PDGFB, PDGFA, NOD1, PTGS2, GHR, MECOM, ERBB4, HES1, NKX2-5, NTRK1, WWTR1, PDGFRA, NTRK2, TGF2, PRMT8, DST, ZBTB16, DAB2IP, ACSL6, MTUS2, HNF1A, DNM1, EXT1, TBX15, NR4A3, NR6A1, DDIT3, DPYD, KIT, ATF3, FGFR2, FGFR1	1.960563	0.002253	0.00207

GOTERM_MF_DIRECT	GO:0070064~proline-rich region binding	6	1.09E-04	GHR, YAP1, BAIAP2L1, CCND1, NEDD4, SH3D19 ZNF331, GLI1, HOXA13, SOX2, MECOM, ZIC2, TEAD1, DNMT3A, TET1, PAX3, FOXL2, HNF1A, SOX10, MLF1, MYCL, AR, MYCN, PAX8, SETBP1, TAL2, DDIT3, PPARG, ERG, ZFPM2, CEBPA, HLF, HOXD13, GATA3, FOXO4, FOXO3, GATA1, PRDM16, NKX2-1, LRIG3, HES1, NKX2-5, PPARGC1A, RUNX1T1, TFAP2A, EGR1, JUN, EGR2, CDKN2A, ZBTB16, HMGA2, ESR1, PBX1, NR4A3, NR6A1, ERCC4, NFIB, FOSB, LHX4	11.90625	0.002253	0.00207
GOTERM_MF_DIRECT	GO:0003677~DNA binding	53	1.34E-04	YAP1, HDAC5, GATA6, HOXD13, HOXC13, GATA2, GLI1, EGFR, GLI3, HMGN2P46, CREB3L1, HES1, NKX2-5, HES5, TFAP2A, EGR2, NPM2, AUTS2, DMRT1, DNMT3A, MITF, HNF1A, FOS, SMAD6, ESR1, AR, LHX2, TAL1, PPARG, ERG	1.727109	0.002688	0.00247
GOTERM_MF_DIRECT	GO:0003682~chromatin binding	30	1.55E-04		2.162703	0.00304	0.002793
GOTERM_MF_DIRECT	GO:0005163~nerve growth factor receptor binding	4	1.77E-04	NTF4, BDNF, NTF3, NGF	30.1625	0.003307	0.003039
GOTERM_MF_DIRECT	GO:0005007~fibroblast growth factor receptor activity	4	1.77E-04	FGFR4, FGFR3, FGFR2, FGFR1	30.1625	0.003307	0.003039
GOTERM_MF_DIRECT	GO:0140297~DNA-binding transcription factor binding	15	2.02E-04	LMO1, YAP1, HDAC5, LMO2, GATA6, FOXO4, HOXC13, SOX10, PBX1, PER1, PRDM16, ZNF703, PPARG, PPARGC1A, RUNX1T1	3.288063	0.00367	0.003373
GOTERM_MF_DIRECT	GO:0001223~transcripti on coactivator binding	8	2.51E-04	AR, GATA6, PPARG, GATA3, HNF1A, GATA2, ESR1, GATA1	6.283854	0.004471	0.004109
GOTERM_MF_DIRECT	GO:0071837~HMG box domain binding	5	2.87E-04	EGR2, PRRX1, HOXA3, PAX3, GATA3	14.5012	0.004911	0.004513
GOTERM_MF_DIRECT	GO:0017134~fibroblast growth factor binding	6	2.89E-04	TGFBR3, ITGB3, FGFR4, FGFR3, FGFR2, FGFR1	9.835598	0.004911	0.004513
GOTERM_MF_DIRECT	GO:0005004~GPI-linked ephrin receptor activity	4	3.47E-04	NTRK1, EPHA5, EPHA7, EPHA3	25.13542	0.005779	0.00531
GOTERM_MF_DIRECT	GO:0004672~protein kinase activity	19	4.49E-04	PDGFRB, PRKCG, CAMK2B, PDGFRA, CDKL5, KSR1, SRC, FLT4, CAMK2A, STYK1, PRKCA, ERBB3, CCND1, PTK7, ERBB2, PRKG2, ABL2, MET, CLK1	2.586135	0.007312	0.006719
GOTERM_MF_DIRECT	GO:0005003~ephrin receptor activity	4	5.96E-04	EPHB6, EPHA5, EPHA3, EPHA2	21.54464	0.009501	0.008731
GOTERM_MF_DIRECT	GO:0005021~vascular endothelial growth factor receptor activity	4	9.35E-04	PDGFRA, FLT3, FLT4, KDR	18.85156	0.014351	0.013188
GOTERM_MF_DIRECT	GO:0019901~protein kinase binding	27	9.38E-04	BRSK1, CDKN1A, PTPRR, GATA6, PTPRK, FOXO3, EGFR, GHR, CCND1, RAC3, IL12RB2, PDGFRB, TCF7L2, CDKN2B, CDKN2A, CAV1, DAB2IP, PDE4DIP, MAPK8IP2, NBEAP1, RHOD, ESR1, DNMT1, NR4A3, LRRC7, CD28, SPRY2	2.027857	0.014351	0.013188
GOTERM_MF_DIRECT	GO:0070888~E-box binding	8	0.001004	PER1, TAL1, HES1, OLIG1, PPARG, MITF, GATA3, BHLHE22	5.027083	0.015055	0.013835
GOTERM_MF_DIRECT	GO:0004896~cytokine receptor activity	7	0.001133	GHR, CSF3R, FLT3, LIFR, IL7R, IL13RA2, IL12RB2	5.864931	0.016669	0.015318
GOTERM_MF_DIRECT	GO:0003714~transcripti on corepressor activity	15	0.001174	YAP1, WWTR1, NAB2, DNMT3A, FHL2, HMGA2, CCND1, PPP1R13L, DDIT3, ZFPM2, BCORL1, SSK1, HSPA1A, WNT4, RUNX1T1	2.758765	0.016948	0.015575
GOTERM_MF_DIRECT	GO:0019955~cytokine binding	7	0.001274	GHR, CSF3R, KIT, LIFR, TNFRSF11A, IL13RA2, IL12RB2	5.737432	0.018053	0.016589
GOTERM_MF_DIRECT	GO:0046983~protein dimerization activity	14	0.001338	OLIG1, MITF, HNF1A, BHLHE22, MYCL, MYCN, HEY1, TAL2, TAL1, ID1, ID4, AHRH, HES1, HES5	2.853209	0.018607	0.017099
GOTERM_MF_DIRECT	GO:0140416~transcripti on regulator inhibitor activity	6	0.001421	NFIB, DDIT3, ID1, ID4, SMAD6, HSPA1A	7.069336	0.019414	0.017841
GOTERM_MF_DIRECT	GO:0001227~DNA-binding transcription repressor activity, RNA polymerase II-specific	21	0.001618	TFAP2A, JUN, PRRX1, CDX2, PEG3, ZBTB16, MITF, GATA3, FOXO3, TBX15, DACH1, HEY1, CREB3L1, TRPS1, PRDM16, HES1, PPARG, HOXD9, MNX1, HES5, ATF3	2.193257	0.021717	0.019957
GOTERM_MF_DIRECT	GO:0005516~calmoduli n binding	15	0.001837	CAMK2B, NGFR, ACE, USP6, NOS3, CAMK2A, PDE4DIP, ESR1, EGFR, RYR3, AKAP12, MAP2, ITPKA, MYH11, PLCB1	2.630451	0.024223	0.02226
GOTERM_MF_DIRECT	GO:0005102~signaling receptor binding	21	0.002102	PDGFRB, TGFBR2, WNT5B, SRC, LAMA1, HGF, CAV1, IGFBP2, FZD8, FLT3LG, FASLG, ADM, PLAT, WNT16, AR, WIF1, NTF3, ERBB2, AMH, TLR4, HSPA1A	2.145706	0.027249	0.025041
GOTERM_MF_DIRECT	GO:0005114~type II transforming growth factor beta receptor binding	4	0.002596	TGFBR3, TGFBR2, TGFBR3, AMH	13.71023	0.032561	0.029922
GOTERM_MF_DIRECT	GO:0048185~activin binding	4	0.002596	TGFBR3, ACVR1B, ACVR2A, FSTL3	13.71023	0.032561	0.029922
GOTERM_MF_DIRECT	GO:0030971~receptor tyrosine kinase binding	8	0.002695	TIAM1, SHC2, ANGPT1, ERBB2, MATK, FLT3LG, CBL, PIK3R2	4.248239	0.033254	0.030559
GOTERM_MF_DIRECT	GO:0004861~cyclin-dependent protein serine/threonine kinase inhibitor activity	4	0.003394	CDKN1C, CDKN1A, CDKN2B, CDKN2A	12.56771	0.040572	0.037284
GOTERM_MF_DIRECT	GO:0048407~platelet-derived growth factor binding	4	0.003394	PDGFRB, PDGFRA, PDGFB, PDGFA	12.56771	0.040572	0.037284

GOTERM_MF_DIRECT	GO:0005030~neurotrophin receptor activity	3	0.00405	NTRK1, NTRK2, NTRK3	28.27734	0.047668	0.043805
GOTERM_MF_DIRECT	GO:0035497~cAMP response element binding	4	0.004326	JUN, NR4A3, CREB3L1, HMGA2	11.60096	0.049399	0.045396
GOTERM_MF_DIRECT	GO:0039706~co-receptor binding	4	0.004326	DKK4, BMP4, DKK1, DKK2 CSF3R, EPO, FZD10, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, EDNRB, FGF8, CCND1, FGF9, CDH1, PRKACG, PDGFRB, PRKCG, PDGFRA, WNT5B, HGF, FLT3LG, MIF, PRKCA, AR, SMO, NOTCH2, NOTCH3, NOTCH4, PDGFB, LPAR1, PDGFA, PIK3R2, WNT6, FGF23, WNT4, JAG2, WNT10B, FZD3, TGFBR2, JUN, FZD2, TGFBR3, ZBTB16, PTC1, FZD7, FZD6, FZD8, IGF1, ESR1, IL2, BMP4, IL3, FGF19, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1, RET, ALK, CDKN1A, WNT2B, FLT3, FLT4, FASLG, GLI1, GLI3, MECOM, HEY1, RAC3, IL15, IL13, FOS, WNT16, PLCB4, PAX8, KIT, PPARG, PLCB1, MET, CAMK2B, CEBPA, LAMA5, LAMA1, CAMK2A, LRP5, WNT8B, PTGS2, DLL1, EGFR, GNAI1, DLL3, DLL4, WNT11, GNAI1, ERBB2, GNA12, STAT4, HES1, HES5, IL12RB2, RUNX1T1, NTRK1, TCF7L2, CDKN2B, CDKN2A, EGF, WNT7B, VEGFC, VEGFD, EPOR RET, PTPRR, CSF1, FLT3, FLT4, FASLG, IL1RAP, FGF1, FGF2, TNF, FGF3, IGF1R, FGF4, FGF6, FGF8, MECOM, FGF9, PRKACG, KDR, RAC3, MAP3K6, PDGFRB, PRKCG, PDGFRA, IL1R1, HGF, CACNA2D3, FLT3LG, PRKCA, FOS, NGF, MAPK8IP2, DUSP9, IL1B, DDIT3, KIT, MET, EPHA2, PDGFB, PDGFA, CACNA1F, EGFR, CACNA1G, NTF4, PPP3R2, ERBB3, ERBB4, PDGFD, ERBB2, BDNF, GNA12, FGF23, NTRK1, NTRK2, NGFR, TGFBR2, JUN, ANGPT1, TGFBR3, EGF, BDNF, VEGFC, VEGFD, IGF1, FGF19, FGFR4, FGFR3, FGFR2, FGF10, FGFR1, HSPA1A CDKN1A, WNT2B, FLT4, FZD10, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, FGF8, HEY1, FGF9, CCND1, WNT5B, FOS, WNT16, KIT, NOTCH2, NOTCH3, SHC2, NOTCH4, LRP5, WNT8B, PIK3R2, DLL1, EGFR, DLL3, DLL4, WNT6, WNT11, ERBB2, HES1, FGF23, HES5, WNT4, JAG2, TCF7L2, WNT10B, JUN, FZD3, FZD2, EGF, FZD7, WNT7B, FZD6, FZD8, IGF1, ESR1, FGF19, FGF10, FGFR1 RET, CDKN1A, CSF3, CSF3R, CSF1, EPO, FLT3, IRS1, FLT4, ITGB3, TNC, FASLG, FGF1, FGF2, FGF3, IGF1R, FGF4, GHR, FGF6, FGF8, IBSP, FGF9, CCND1, CREB3L1, KDR, PDGFRB, PDGFRA, HGF, FLT3LG, PRKCA, NGF, KIT, ITGA8, COL6A3, ITGA7, MET, TLR4, EPHA2, LAMA5, LAMA1, PDGFB, LPAR1, PDGFA, PIK3R2, FOXO3, EGFR, NTF4, RELN, ERBB3, ERBB4, PDGFD, ERBB2, NTF3, FGF23, NTRK1, NTRK2, NGFR, ANGPT1, EGF, NOS3, BDNF, VEGFC, VEGFD, IGF1, EPOR, IL2, IL3, PPP2R2B, FGF19, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1	11.60096	0.049399	0.045396
KEGG_PATHWAY	hsa05200:Pathways in cancer	112	1.66E-51	RET, PTPRR, CSF1, FLT3, FLT4, FASLG, IL1RAP, FGF1, FGF2, TNF, FGF3, IGF1R, FGF4, FGF6, FGF8, MECOM, FGF9, PRKACG, KDR, RAC3, MAP3K6, PDGFRB, PRKCG, PDGFRA, IL1R1, HGF, CACNA2D3, FLT3LG, PRKCA, FOS, NGF, MAPK8IP2, DUSP9, IL1B, DDIT3, KIT, MET, EPHA2, PDGFB, PDGFA, CACNA1F, EGFR, CACNA1G, NTF4, PPP3R2, ERBB3, ERBB4, PDGFD, ERBB2, BDNF, GNA12, FGF23, NTRK1, NTRK2, NGFR, TGFBR2, JUN, ANGPT1, TGFBR3, EGF, BDNF, VEGFC, VEGFD, IGF1, FGF19, FGFR4, FGFR3, FGFR2, FGF10, FGFR1, HSPA1A CDKN1A, WNT2B, FLT4, FZD10, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, FGF8, HEY1, FGF9, CCND1, WNT5B, FOS, WNT16, KIT, NOTCH2, NOTCH3, SHC2, NOTCH4, LRP5, WNT8B, PIK3R2, DLL1, EGFR, DLL3, DLL4, WNT6, WNT11, ERBB2, HES1, FGF23, HES5, WNT4, JAG2, TCF7L2, WNT10B, JUN, FZD3, FZD2, EGF, FZD7, WNT7B, FZD6, FZD8, IGF1, ESR1, FGF19, FGF10, FGFR1 RET, CDKN1A, CSF3, CSF3R, CSF1, EPO, FLT3, IRS1, FLT4, ITGB3, TNC, FASLG, FGF1, FGF2, FGF3, IGF1R, FGF4, GHR, FGF6, FGF8, IBSP, FGF9, CCND1, CREB3L1, KDR, PDGFRB, PDGFRA, HGF, FLT3LG, PRKCA, NGF, KIT, ITGA8, COL6A3, ITGA7, MET, TLR4, EPHA2, LAMA5, LAMA1, PDGFB, LPAR1, PDGFA, PIK3R2, FOXO3, EGFR, NTF4, RELN, ERBB3, ERBB4, PDGFD, ERBB2, NTF3, FGF23, NTRK1, NTRK2, NGFR, ANGPT1, EGF, NOS3, BDNF, VEGFC, VEGFD, IGF1, EPOR, IL2, IL3, PPP2R2B, FGF19, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1	5.159892	4.82E-49	2.96E-49
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	71	5.23E-35	RET, PTPRR, CSF1, FLT3, FLT4, FASLG, IL1RAP, FGF1, FGF2, TNF, FGF3, IGF1R, FGF4, FGF6, FGF8, MECOM, FGF9, PRKACG, KDR, RAC3, MAP3K6, PDGFRB, PRKCG, PDGFRA, IL1R1, HGF, CACNA2D3, FLT3LG, PRKCA, FOS, NGF, MAPK8IP2, DUSP9, IL1B, DDIT3, KIT, MET, EPHA2, PDGFB, PDGFA, CACNA1F, EGFR, CACNA1G, NTF4, PPP3R2, ERBB3, ERBB4, PDGFD, ERBB2, BDNF, GNA12, FGF23, NTRK1, NTRK2, NGFR, TGFBR2, JUN, ANGPT1, TGFBR3, EGF, BDNF, VEGFC, VEGFD, IGF1, FGF19, FGFR4, FGFR3, FGFR2, FGF10, FGFR1, HSPA1A CDKN1A, WNT2B, FLT4, FZD10, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, FGF8, HEY1, FGF9, CCND1, WNT5B, FOS, WNT16, KIT, NOTCH2, NOTCH3, SHC2, NOTCH4, LRP5, WNT8B, PIK3R2, DLL1, EGFR, DLL3, DLL4, WNT6, WNT11, ERBB2, HES1, FGF23, HES5, WNT4, JAG2, TCF7L2, WNT10B, JUN, FZD3, FZD2, EGF, FZD7, WNT7B, FZD6, FZD8, IGF1, ESR1, FGF19, FGF10, FGFR1 RET, CDKN1A, CSF3, CSF3R, CSF1, EPO, FLT3, IRS1, FLT4, ITGB3, TNC, FASLG, FGF1, FGF2, FGF3, IGF1R, FGF4, GHR, FGF6, FGF8, IBSP, FGF9, CCND1, CREB3L1, KDR, PDGFRB, PDGFRA, HGF, FLT3LG, PRKCA, NGF, KIT, ITGA8, COL6A3, ITGA7, MET, TLR4, EPHA2, LAMA5, LAMA1, PDGFB, LPAR1, PDGFA, PIK3R2, FOXO3, EGFR, NTF4, RELN, ERBB3, ERBB4, PDGFD, ERBB2, NTF3, FGF23, NTRK1, NTRK2, NGFR, ANGPT1, EGF, NOS3, BDNF, VEGFC, VEGFD, IGF1, EPOR, IL2, IL3, PPP2R2B, FGF19, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1	5.811481	7.61E-33	4.68E-33
KEGG_PATHWAY	hsa05224:Breast cancer	52	1.61E-34	RET, CDKN1A, CSF3, CSF3R, CSF1, EPO, FLT3, IRS1, FLT4, ITGB3, TNC, FASLG, FGF1, FGF2, FGF3, IGF1R, FGF4, GHR, FGF6, FGF8, IBSP, FGF9, CCND1, CREB3L1, KDR, PDGFRB, PDGFRA, HGF, FLT3LG, PRKCA, NGF, KIT, ITGA8, COL6A3, ITGA7, MET, TLR4, EPHA2, LAMA5, LAMA1, PDGFB, LPAR1, PDGFA, PIK3R2, FOXO3, EGFR, NTF4, RELN, ERBB3, ERBB4, PDGFD, ERBB2, NTF3, FGF23, NTRK1, NTRK2, NGFR, ANGPT1, EGF, NOS3, BDNF, VEGFC, VEGFD, IGF1, EPOR, IL2, IL3, PPP2R2B, FGF19, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1	8.627628	1.56E-32	9.59E-33
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	75	6.18E-33	CSF1, FLT3, FLT4, FASLG, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, FGF8, FGF9, PRKACG, KDR, RAC3, PDGFRB, PRKCG, PDGFRA, KSR1, HGF, FLT3LG, PRKCA, NGF, TIAM1, KIT, MET, EPHA2, SHC2, PDGFB, PDGFA, PIK3R2, PLA2G5, FOXO4, EGFR, NTF4, GRIN2A, PDGFD, NTF3, ABL2, PAK6, PAK3, FGF23, PAK5, NTRK1, NTRK2, NGFR, ANGPT1, EGF, BDNF, VEGFC, VEGFD, IGF1, GRIN2B, FGF19, FGFR4, FGFR3, FGFR2, FGF10, FGFR1	5.087477	4.50E-31	2.77E-31
KEGG_PATHWAY	hsa04014:Ras signaling pathway	59	4.88E-30	CSF1, FLT4, ITGB3, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, FGF8, FGF9, CDH1, KDR, RAC3, PDGFRB, PRKCG, PDGFRA, HGF, PRKCA, NGF, TIAM1, PLCB4, KIT, PLCB1, MET, EPHA2, SRC, PDGFB, LPAR1, PDGFA, PIK3R2, EGFR, GNAI1, GRIN2A, PDGFD, FGF23, NGFR, ANGPT1, EGF, VEGFC, VEGFD, IGF1, GRIN2B, FGF19, ID1, FGFR4, FGFR3, FGFR2, FGF10, FGFR1 CDKN1A, WNT2B, ITGB3, FASLG, FZD10, FGF2, TNF, IGF1R, CCND1, PLAU, PRKACG, KDR, PRKCG, WNT5B, HGF, PRKCA, WNT16, DCN, TIAM1, SMO, MET, TLR4, CAMK2B, SDC4, SRC, CAMK2A, WNT8B, PIK3R2, EGFR, WNT6, WNT11, ERBB3, ERBB4, ERBB2, GPC3, WNT4, WNT10B, TGFBR2, FZD3, FZD2, FZD7, WNT7B, CAV1, PTC1, FZD6, FZD8, IGF1, ESR1, FGFR1 CDKN1A, SHC2, WNT2B, LRP5, WNT8B, PIK3R2, FZD10, FGF1, FGF2, FGF3, EGFR, FGF4, FGF6, WNT6, FGF8, WNT11, FGF9, CCND1, CDH1, ERBB2, FGF23, WNT4, TCF7L2, WNT10B, TGFBR2, CDKN2B, FZD3, FZD2, WNT5B, CDX2, TGFBR3, EGF, FZD7, HGF, WNT7B, FZD6, FZD8, WNT16, FGF19, MET, FGFR2, FGF10 RET, FLT4, FGF1, FGF2, FGF3, GRM1, RYR3, FGF4, FGF6, FGF8, EDNRB, FGF9, PRKACG, KDR, PDGFRB, PRKCG, PDGFRA, HGF, PRKCA, NGF, PLCB4, ITPKA, PLCB1, MET, CAMK2B, CAMK2A, PDGFB, PDGFA, CACNA1F, EGFR, CACNA1G, GRIN2A, PPP3R2, ERBB3, ERBB4, PDGFD, GNA11, ERBB2, FGF23, NTRK1, NTRK2, EGF, NOS3, NTRK3, VEGFC, VEGFD, GRIN2B, FGF19, FGFR4, FGF3, FGF2, FGF10, FGFR1	6.087302	2.84E-28	1.75E-28
KEGG_PATHWAY	hsa04015:Rap1 signaling pathway	50	2.59E-24	CSF1, FLT4, ITGB3, FGF1, FGF2, FGF3, IGF1R, FGF4, FGF6, FGF8, FGF9, CDH1, KDR, RAC3, PDGFRB, PRKCG, PDGFRA, HGF, PRKCA, NGF, TIAM1, PLCB4, KIT, PLCB1, MET, EPHA2, SRC, PDGFB, LPAR1, PDGFA, PIK3R2, EGFR, GNAI1, GRIN2A, PDGFD, FGF23, NGFR, ANGPT1, EGF, VEGFC, VEGFD, IGF1, GRIN2B, FGF19, ID1, FGFR4, FGFR3, FGFR2, FGF10, FGFR1 CDKN1A, WNT2B, ITGB3, FASLG, FZD10, FGF2, TNF, IGF1R, CCND1, PLAU, PRKACG, KDR, PRKCG, WNT5B, HGF, PRKCA, WNT16, DCN, TIAM1, SMO, MET, TLR4, CAMK2B, SDC4, SRC, CAMK2A, WNT8B, PIK3R2, EGFR, WNT6, WNT11, ERBB3, ERBB4, ERBB2, GPC3, WNT4, WNT10B, TGFBR2, FZD3, FZD2, FZD7, WNT7B, CAV1, PTC1, FZD6, FZD8, IGF1, ESR1, FGFR1 CDKN1A, SHC2, WNT2B, LRP5, WNT8B, PIK3R2, FZD10, FGF1, FGF2, FGF3, EGFR, FGF4, FGF6, WNT6, FGF8, WNT11, FGF9, CCND1, CDH1, ERBB2, FGF23, WNT4, TCF7L2, WNT10B, TGFBR2, CDKN2B, FZD3, FZD2, WNT5B, CDX2, TGFBR3, EGF, FZD7, HGF, WNT7B, FZD6, FZD8, WNT16, FGF19, MET, FGFR2, FGF10 RET, FLT4, FGF1, FGF2, FGF3, GRM1, RYR3, FGF4, FGF6, FGF8, EDNRB, FGF9, PRKACG, KDR, PDGFRB, PRKCG, PDGFRA, HGF, PRKCA, NGF, PLCB4, ITPKA, PLCB1, MET, CAMK2B, CAMK2A, PDGFB, PDGFA, CACNA1F, EGFR, CACNA1G, GRIN2A, PPP3R2, ERBB3, ERBB4, PDGFD, GNA11, ERBB2, FGF23, NTRK1, NTRK2, EGF, NOS3, NTRK3, VEGFC, VEGFD, GRIN2B, FGF19, FGFR4, FGF3, FGF2, FGF10, FGFR1	5.791405	1.26E-22	7.73E-23
KEGG_PATHWAY	hsa05205:Proteoglycan s in cancer	49	3.42E-24	RET, CDKN1A, CSF3, CSF3R, CSF1, EPO, FLT3, IRS1, FLT4, ITGB3, TNC, FASLG, FGF1, FGF2, FGF3, IGF1R, FGF4, GHR, FGF6, FGF8, IBSP, FGF9, CCND1, CREB3L1, KDR, PDGFRB, PDGFRA, HGF, FLT3LG, PRKCA, NGF, KIT, ITGA8, COL6A3, ITGA7, MET, TLR4, EPHA2, LAMA5, LAMA1, PDGFB, LPAR1, PDGFA, PIK3R2, FOXO3, EGFR, NTF4, RELN, ERBB3, ERBB4, PDGFD, ERBB2, NTF3, FGF23, NTRK1, NTRK2, NGFR, ANGPT1, EGF, NOS3, BDNF, VEGFC, VEGFD, IGF1, EPOR, IL2, IL3, PPP2R2B, FGF19, FGFR4, IL7R, FGFR3, FGFR2, FGF10, FGFR1	5.898148	1.42E-22	8.75E-23
KEGG_PATHWAY	hsa05226:Gastric cancer	42	1.92E-23	RET, CDKN1A, CSF3, CSF3R, CSF1, EPO, FLT3, IRS1, FLT4, ITGB3, TNC, FASLG, FGF1, FGF2, FGF3, IGF1R, FGF4, GHR, FGF6, FGF8, IBSP, FGF9, CCND1, CREB3L1, KDR, PDGFRB, PDGFRA, HGF, PRKCA, NGF, PLCB4, ITPKA, PLCB1, MET, CAMK2B, CAMK2A, PDGFB, PDGFA, CACNA1F, EGFR, CACNA1G, GRIN2A, PPP3R2, ERBB3, ERBB4, PDGFD, GNA11, ERBB2, FGF23, NTRK1, NTRK2, EGF, NOS3, NTRK3, VEGFC, VEGFD, GRIN2B, FGF19, FGFR4, FGF3, FGF2, FGF10, FGFR1	6.875556	6.97E-22	4.29E-22
KEGG_PATHWAY	hsa04020:Calcium signaling pathway	53	3.78E-23	CEBPA, CDKN1A, SLC45A3, FLT3, CEBPE, TMPPRSS2, PDGFA, PLAT, HOXA11, IGF1R, HOXA9, PLAU, PROM1, RUNX1T1, SSX1, PTCRA, NTRK1, NGFR, BCL11B, EYA1, ZBTB16, LMO2, PAX3, HMGA2, ETV1, MIF, IGF1, WNT16, ETV4, MLF1, RUNX2, PBX1, IL3, MYCN, NR4A3, MAF, PAX8, TLX3, WT1, PAX7, FEV, DDIT3, TLX1, PPARG, ERG, MET CDKN1A, PDGFB, PDGFA, PIK3R2, FGF1, FGF2, FGF3, EGFR, FGF4, IGF1R, FGF6, FGF8, FGF9, CCND1, CDH1, PDGFD, FGF23, PDGFRB, PDGFRA, CDKN2A, EGF, HGF, MIF, IGF1, FGF19, MET, FGF10, FGFR1 CAMK2B, WNT2B, CTNND2, CAMK2A, LRP5, WNT8B, FZD10, CXCC4, WNT6, PPP3R2, WNT11, CCND1, WIF1, PRKACG, RAC3, WNT4, PRKCG, TCF7L2, RNF43, WNT10B, JUN, FZD3, MMP7, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, WNT16, DKK1, DKK2, DKK4, FOSL1, SFRP4, PLCB4, SFRP2, PLCB1, LGR5 WNT2B, WNT8B, PIK3R2, FZD10, ACVR1B, FGF2, IGF1R, SOX2, WNT6, ACVR1C, WNT11, LEFTY2, WNT4, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, LIFR, IGF1, INHBA, KLF4, WNT16, DUSP9, ACVR2A, BMP4, ID1, ID4, FGFR4, FGR3, FGFR2, NODAL, FGFR1 CAMK2B, WNT2B, CAMK2A, WNT8B, FZD10, GNAI1, WNT6, EDNRB, WNT11, PRKACG, CREB3L1, WNT4, PRKCG, TCF7L2, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, MIF, WNT16, PLCB4, KIT, PLCB1 LAMA5, SHC2, SRC, LAMA1, FLT4, ITGB3, PDGFB, TNC, PDGFA, PIK3R2, EGFR, IGF1R, RELN, CCND1, IBSP, PDGFD, ERBB2, KDR, PAK6, RAC3, PAK3, PAK5, PRKCG, PDGFRB, PDGFRA, JUN, EGF, HGF, CAV1, VEGFC, PRKCA, VEGFD, IGF1, ITGA8, COL6A3, ITGA7, DOCK1, MET TCF7L2, WNT10B, CDKN1A, FZD3, FZD2, WNT2B, WNT5B, FZD7, WNT7B, PTC1, FZD6, FZD8, WNT8B, FZD10, GLI1, WNT16, GLI3, BMP4, WNT6, WNT11, SMO, WNT4	5.123797	1.22E-21	7.53E-22
KEGG_PATHWAY	hsa05202:Transcriptional misregulation in cancer	46	1.52E-22	CEBPA, CDKN1A, SLC45A3, FLT3, CEBPE, TMPPRSS2, PDGFA, PLAT, HOXA11, IGF1R, HOXA9, PLAU, PROM1, RUNX1T1, SSX1, PTCRA, NTRK1, NGFR, BCL11B, EYA1, ZBTB16, LMO2, PAX3, HMGA2, ETV1, MIF, IGF1, WNT16, ETV4, MLF1, RUNX2, PBX1, IL3, MYCN, NR4A3, MAF, PAX8, TLX3, WT1, PAX7, FEV, DDIT3, TLX1, PPARG, ERG, MET CDKN1A, PDGFB, PDGFA, PIK3R2, FGF1, FGF2, FGF3, EGFR, FGF4, IGF1R, FGF6, FGF8, FGF9, CCND1, CDH1, PDGFD, FGF23, PDGFRB, PDGFRA, CDKN2A, EGF, HGF, MIF, IGF1, FGF19, MET, FGF10, FGFR1 CAMK2B, WNT2B, CTNND2, CAMK2A, LRP5, WNT8B, FZD10, CXCC4, WNT6, PPP3R2, WNT11, CCND1, WIF1, PRKACG, RAC3, WNT4, PRKCG, TCF7L2, RNF43, WNT10B, JUN, FZD3, MMP7, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, WNT16, DKK1, DKK2, DKK4, FOSL1, SFRP4, PLCB4, SFRP2, PLCB1, LGR5 WNT2B, WNT8B, PIK3R2, FZD10, ACVR1B, FGF2, IGF1R, SOX2, WNT6, ACVR1C, WNT11, LEFTY2, WNT4, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, LIFR, IGF1, INHBA, KLF4, WNT16, DUSP9, ACVR2A, BMP4, ID1, ID4, FGFR4, FGR3, FGFR2, NODAL, FGFR1 CAMK2B, WNT2B, CAMK2A, WNT8B, FZD10, GNAI1, WNT6, EDNRB, WNT11, PRKACG, CREB3L1, WNT4, PRKCG, TCF7L2, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, MIF, WNT16, PLCB4, KIT, PLCB1 LAMA5, SHC2, SRC, LAMA1, FLT4, ITGB3, PDGFB, TNC, PDGFA, PIK3R2, EGFR, IGF1R, RELN, CCND1, IBSP, PDGFD, ERBB2, KDR, PAK6, RAC3, PAK3, PAK5, PRKCG, PDGFRB, PDGFRA, JUN, EGF, HGF, CAV1, VEGFC, PRKCA, VEGFD, IGF1, ITGA8, COL6A3, ITGA7, DOCK1, MET TCF7L2, WNT10B, CDKN1A, FZD3, FZD2, WNT2B, WNT5B, FZD7, WNT7B, PTC1, FZD6, FZD8, WNT8B, FZD10, GLI1, WNT16, GLI3, BMP4, WNT6, WNT11, SMO, WNT4	5.852619	4.41E-21	2.71E-21
KEGG_PATHWAY	hsa05218:Melanoma	28	1.31E-19	CEBPA, CDKN1A, SLC45A3, FLT3, CEBPE, TMPPRSS2, PDGFA, PLAT, HOXA11, IGF1R, HOXA9, PLAU, PROM1, RUNX1T1, SSX1, PTCRA, NTRK1, NGFR, BCL11B, EYA1, ZBTB16, LMO2, PAX3, HMGA2, ETV1, MIF, IGF1, WNT16, ETV4, MLF1, RUNX2, PBX1, IL3, MYCN, NR4A3, MAF, PAX8, TLX3, WT1, PAX7, FEV, DDIT3, TLX1, PPARG, ERG, MET CDKN1A, PDGFB, PDGFA, PIK3R2, FGF1, FGF2, FGF3, EGFR, FGF4, IGF1R, FGF6, FGF8, FGF9, CCND1, CDH1, PDGFD, FGF23, PDGFRB, PDGFRA, CDKN2A, EGF, HGF, MIF, IGF1, FGF19, MET, FGF10, FGFR1 CAMK2B, WNT2B, CTNND2, CAMK2A, LRP5, WNT8B, FZD10, CXCC4, WNT6, PPP3R2, WNT11, CCND1, WIF1, PRKACG, RAC3, WNT4, PRKCG, TCF7L2, RNF43, WNT10B, JUN, FZD3, MMP7, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, WNT16, DKK1, DKK2, DKK4, FOSL1, SFRP4, PLCB4, SFRP2, PLCB1, LGR5 WNT2B, WNT8B, PIK3R2, FZD10, ACVR1B, FGF2, IGF1R, SOX2, WNT6, ACVR1C, WNT11, LEFTY2, WNT4, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, LIFR, IGF1, INHBA, KLF4, WNT16, DUSP9, ACVR2A, BMP4, ID1, ID4, FGFR4, FGR3, FGFR2, NODAL, FGFR1 CAMK2B, WNT2B, CAMK2A, WNT8B, FZD10, GNAI1, WNT6, EDNRB, WNT11, PRKACG, CREB3L1, WNT4, PRKCG, TCF7L2, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, MIF, WNT16, PLCB4, KIT, PLCB1 LAMA5, SHC2, SRC, LAMA1, FLT4, ITGB3, PDGFB, TNC, PDGFA, PIK3R2, EGFR, IGF1R, RELN, CCND1, IBSP, PDGFD, ERBB2, KDR, PAK6, RAC3, PAK3, PAK5, PRKCG, PDGFRB, PDGFRA, JUN, EGF, HGF, CAV1, VEGFC, PRKCA, VEGFD, IGF1, ITGA8, COL6A3, ITGA7, DOCK1, MET TCF7L2, WNT10B, CDKN1A, FZD3, FZD2, WNT2B, WNT5B, FZD7, WNT7B, PTC1, FZD6, FZD8, WNT8B, FZD10, GLI1, WNT16, GLI3, BMP4, WNT6, WNT11, SMO, WNT4	9.418569	3.48E-18	2.14E-18
KEGG_PATHWAY	hsa04310:Wnt signaling pathway	40	5.29E-19	CEBPA, CDKN1A, SLC45A3, FLT3, CEBPE, TMPPRSS2, PDGFA, PLAT, HOXA11, IGF1R, HOXA9, PLAU, PROM1, RUNX1T1, SSX1, PTCRA, NTRK1, NGFR, BCL11B, EYA1, ZBTB16, LMO2, PAX3, HMGA2, ETV1, MIF, IGF1, WNT16, ETV4, MLF1, RUNX2, PBX1, IL3, MYCN, NR4A3, MAF, PAX8, TLX3, WT1, PAX7, FEV, DDIT3, TLX1, PPARG, ERG, MET CDKN1A, PDGFB, PDGFA, PIK3R2, FGF1, FGF2, FGF3, EGFR, FGF4, IGF1R, FGF6, FGF8, FGF9, CCND1, CDH1, PDGFD, FGF23, PDGFRB, PDGFRA, CDKN2A, EGF, HGF, MIF, IGF1, FGF19, MET, FGF10, FGFR1 CAMK2B, WNT2B, CTNND2, CAMK2A, LRP5, WNT8B, FZD10, CXCC4, WNT6, PPP3R2, WNT11, CCND1, WIF1, PRKACG, RAC3, WNT4, PRKCG, TCF7L2, RNF43, WNT10B, JUN, FZD3, MMP7, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, WNT16, DKK1, DKK2, DKK4, FOSL1, SFRP4, PLCB4, SFRP2, PLCB1, LGR5 WNT2B, WNT8B, PIK3R2, FZD10, ACVR1B, FGF2, IGF1R, SOX2, WNT6, ACVR1C, WNT11, LEFTY2, WNT4, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, LIFR, IGF1, INHBA, KLF4, WNT16, DUSP9, ACVR2A, BMP4, ID1, ID4, FGFR4, FGR3, FGFR2, NODAL, FGFR1 CAMK2B, WNT2B, CAMK2A, WNT8B, FZD10, GNAI1, WNT6, EDNRB, WNT11, PRKACG, CREB3L1, WNT4, PRKCG, TCF7L2, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, MIF, WNT16, PLCB4, KIT, PLCB1 LAMA5, SHC2, SRC, LAMA1, FLT4, ITGB3, PDGFB, TNC, PDGFA, PIK3R2, EGFR, IGF1R, RELN, CCND1, IBSP, PDGFD, ERBB2, KDR, PAK6, RAC3, PAK3, PAK5, PRKCG, PDGFRB, PDGFRA, JUN, EGF, HGF, CAV1, VEGFC, PRKCA, VEGFD, IGF1, ITGA8, COL6A3, ITGA7, DOCK1, MET TCF7L2, WNT10B, CDKN1A, FZD3, FZD2, WNT2B, WNT5B, FZD7, WNT7B, PTC1, FZD6, FZD8, WNT8B, FZD10, GLI1, WNT16, GLI3, BMP4, WNT6, WNT11, SMO, WNT4	5.644955	1.28E-17	7.89E-18
KEGG_PATHWAY	hsa04550:Signaling pathways regulating pluripotency of stem cells	36	2.36E-18	CEBPA, CDKN1A, SLC45A3, FLT3, CEBPE, TMPPRSS2, PDGFA, PLAT, HOXA11, IGF1R, HOXA9, PLAU, PROM1, RUNX1T1, SSX1, PTCRA, NTRK1, NGFR, BCL11B, EYA1, ZBTB16, LMO2, PAX3, HMGA2, ETV1, MIF, IGF1, WNT16, ETV4, MLF1, RUNX2, PBX1, IL3, MYCN, NR4A3, MAF, PAX8, TLX3, WT1, PAX7, FEV, DDIT3, TLX1, PPARG, ERG, MET CDKN1A, PDGFB, PDGFA, PIK3R2, FGF1, FGF2, FGF3, EGFR, FGF4, IGF1R, FGF6, FGF8, FGF9, CCND1, CDH1, PDGFD, FGF23, PDGFRB, PDGFRA, CDKN2A, EGF, HGF, MIF, IGF1, FGF19, MET, FGF10, FGFR1 CAMK2B, WNT2B, CTNND2, CAMK2A, LRP5, WNT8B, FZD10, CXCC4, WNT6, PPP3R2, WNT11, CCND1, WIF1, PRKACG, RAC3, WNT4, PRKCG, TCF7L2, RNF43, WNT10B, JUN, FZD3, MMP7, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, WNT16, DKK1, DKK2, DKK4, FOSL1, SFRP4, PLCB4, SFRP2, PLCB1, LGR5 WNT2B, WNT8B, PIK3R2, FZD10, ACVR1B, FGF2, IGF1R, SOX2, WNT6, ACVR1C, WNT11, LEFTY2, WNT4, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, LIFR, IGF1, INHBA, KLF4, WNT16, DUSP9, ACVR2A, BMP4, ID1, ID4, FGFR4, FGR3, FGFR2, NODAL, FGFR1 CAMK2B, WNT2B, CAMK2A, WNT8B, FZD10, GNAI1, WNT6, EDNRB, WNT11, PRKACG, CREB3L1, WNT4, PRKCG, TCF7L2, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, MIF, WNT16, PLCB4, KIT, PLCB1 LAMA5, SHC2, SRC, LAMA1, FLT4, ITGB3, PDGFB, TNC, PDGFA, PIK3R2, EGFR, IGF1R, RELN, CCND1, IBSP, PDGFD, ERBB2, KDR, PAK6, RAC3, PAK3, PAK5, PRKCG, PDGFRB, PDGFRA, JUN, EGF, HGF, CAV1, VEGFC, PRKCA, VEGFD, IGF1, ITGA8, COL6A3, ITGA7, DOCK1, MET TCF7L2, WNT10B, CDKN1A, FZD3, FZD2, WNT2B, WNT5B, FZD7, WNT7B, PTC1, FZD6, FZD8, WNT8B, FZD10, GLI1, WNT16, GLI3, BMP4, WNT6, WNT11, SMO, WNT4	6.138889	5.28E-17	3.25E-17
KEGG_PATHWAY	hsa04916:Melanogenesis	28	1.78E-15	CEBPA, CDKN1A, SLC45A3, FLT3, CEBPE, TMPPRSS2, PDGFA, PL			

KEGG_PA THWAY	hsa01521:EGFR tyrosine kinase inhibitor resistance	24	4.09E-14	PDGFRB, PRKCG, PDGFRA, SHC2, SRC, EGF, HGF, PDGFB, PDGFA, PRKCA, PIK3R2, IGF1, FOXO3, FGF2, EGFR, IGF1R, ERBB3, AXL, PDGFD, ERBB2, KDR, MET, FGFR3, FGFR2	7.366667	7.00E-13	4.30E-13
KEGG_PA THWAY	hsa04934:Cushing syndrome	32	8.16E-14	CAMK2B, CDKN1A, WNT2B, CAMK2A, WNT8B, FZD10, CACNA1F, GNAI1, EGFR, CACNA1G, WNT6, WNT11, CCND1, PRKACG, GNA11, CREB3L1, WNT4, TCF7L2, WNT10B, CDKN2B, FZD3, FZD2, WNT5B, CDKN2A, FZD7, WNT7B, FZD6, FZD8, WNT16, PBX1, PLCB4, PLCB1	5.069534	1.32E-12	8.12E-13
KEGG_PA THWAY	hsa04390:Hippo signaling pathway	32	1.18E-13	YAP1, WNT2B, WNT8B, FZD10, FGF1, SOX2, WNT6, WNT11, CCND1, CDH1, AMH, TEAD1, WNT4, TEAD3, TEAD4, WWTR1, TCF7L2, WNT10B, TGF2, FZD3, FZD2, WNT5B, TGF2, FZD7, WNT7B, FZD6, FZD8, WNT16, GDF6, BMP4, PPP2R2B, ID1	5.004954	1.81E-12	1.11E-12
KEGG_PA THWAY	hsa05165:Human papillomavirus infection	44	9.36E-12	NOTCH2, LAMA5, NOTCH3, CDKN1A, WNT2B, LAMA1, ITGB3, NOTCH4, TNC, WNT8B, FASLG, PIK3R2, FZD10, PTGS2, TNF, EGFR, LFNG, WNT6, RELN, WNT11, CCND1, HEY1, IBSP, PRKACG, CREB3L1, HES1, HES5, WNT4, PDGFRB, TCF7L2, WNT10B, FZD3, FZD2, WNT5B, EGF, FZD7, WNT7B, FZD6, FZD8, WNT16, PPP2R2B, ITGA8, COL6A3, ITGA7	3.244578	1.36E-10	8.38E-11
KEGG_PA THWAY	hsa05225:Hepatocellular carcinoma	30	3.42E-11	CDKN1A, SHC2, WNT2B, LRP5, WNT8B, PIK3R2, FZD10, EGFR, IGF1R, WNT6, WNT11, CCND1, WNT4, PRKCG, TCF7L2, WNT10B, TGF2, FZD3, FZD2, WNT5B, TGF2, CDKN2A, FZD7, HGF, WNT7B, FZD6, FZD8, PRKCA, WNT16, MET	4.333333	4.73E-10	2.91E-10
KEGG_PA THWAY	hsa04810:Regulation of actin cytoskeleton	35	4.02E-11	SRC, ITGB3, PDGFB, LPAR1, PDGFA, PIK3R2, FGF1, FGF2, FGF3, EGFR, FGF4, FGF6, FGF8, FGF9, PDGFD, GNA12, PAK6, RAC3, MYH11, PAK3, FGF23, PAK5, PDGFRB, PDGFRA, EGF, TIAM1, FGF19, ITGA8, ITGA7, FGF4, DOCK1, FGF3, FGFR2, FGF10, FGFR1	3.736715	5.32E-10	3.27E-10
KEGG_PA THWAY	hsa05215:Prostate cancer	22	2.45E-10	PDGFRB, PDGFRA, TCF7L2, CDKN1A, EGF, PDGFB, PDGFA, TMPPSS2, PLAT, PIK3R2, IGF1, EGFR, IGF1R, AR, CCND1, PLAU, CREB3L1, PDGFD, ERBB2, ERG, FGFR2, FGFR1	5.512472	3.10E-09	1.91E-09
KEGG_PA THWAY	hsa01522:Endocrine resistance	21	2.00E-09	JAG2, NOTCH2, NOTCH3, CDKN1A, JUN, SHC2, CDKN2A, SRC, NOTCH4, PIK3R2, FOS, IGF1, DLL1, ESR1, EGFR, IGF1R, DLL3, DLL4, CCND1, PRKACG, ERBB2	5.208754	2.42E-08	1.49E-08
KEGG_PA THWAY	hsa04060:Cytokine-cytokine receptor interaction	36	1.18E-08	CSF3, TNFRSF6B, CSF3R, CSF1, EPO, MPL, FASLG, TNFRSF11A, IL1RAP, ACVR1B, TNF, GHR, ACVR1C, AMH, IL13RA2, IL12RB2, NGFR, TGF2, TGF2, IL15, IL1R1, IL13, LIFR, INHBA, NGF, GDF6, EPOR, ACVR2A, IL2, TNFRSF10D, BMP4, IL3, IL1B, ACKR3, IL7R, NODAL	2.966443	1.37E-07	8.42E-08
KEGG_PA THWAY	hsa04630:JAK-STAT signaling pathway	26	1.49E-08	CDKN1A, CSF3, CSF3R, EPO, MPL, PDGFB, PDGFA, PIK3R2, EGFR, GHR, SOCS2, CCND1, STAT4, IL13RA2, IL12RB2, PDGFRB, PDGFRA, IL15, EGF, IL13, LIFR, EPOR, IL2, GFAP, IL3, IL7R	3.800265	1.67E-07	1.03E-07
KEGG_PA THWAY	hsa04150:mTOR signaling pathway	25	1.94E-08	WNT2B, IRS1, LRP5, WNT8B, PIK3R2, FZD10, TNF, IGF1R, FLCN, WNT6, WNT11, GRB10, WNT4, PRKCG, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, PRKCA, IGF1, WNT16	3.885373	2.09E-07	1.28E-07
KEGG_PA THWAY	hsa05214:Glioma	17	4.59E-08	PDGFRB, PRKCG, CAMK2B, PDGFRA, CDKN1A, SHC2, CDKN2A, EGF, CAMK2A, PDGFB, PDGFA, PRKCA, PIK3R2, IGF1, EGFR, IGF1R, CCND1	5.49269	4.69E-07	2.88E-07
KEGG_PA THWAY	hsa04012:ErbB signaling pathway	18	4.67E-08	PRKCG, CAMK2B, CDKN1A, JUN, SHC2, SRC, EGF, CAMK2A, PRKCA, PIK3R2, EGFR, ERBB3, ERBB4, ERBB2, ABL2, PAK6, PAK3, PAK5	5.139535	4.69E-07	2.88E-07
KEGG_PA THWAY	hsa04360:Axon guidance	26	9.46E-08	EPHB6, ROBO2, CAMK2B, SRC, CAMK2A, PIK3R2, GNAI1, ROBO1, PPP3R2, PAK6, RAC3, SRGAP3, PAK3, PAK5, WNT4, EPHA5, FZD3, EPHA7, WNT5B, PTCH1, PRKCA, RHOD, SMO, MET, EPHA3, EPHA2	3.469807	9.17E-07	5.64E-07
KEGG_PA THWAY	hsa04540:Gap junction	18	1.32E-07	PDGFRB, PRKCG, PDGFRA, SRC, EGF, PDGFB, LPAR1, PDGFA, PRKCA, EGFR, GNAI1, GRM1, PLCB4, PRKACG, GNA11, PDGFD, PRKG2, PLCB1	4.804348	1.24E-06	7.64E-07
KEGG_PA THWAY	hsa05207:Chemical carcinogenesis - receptor activation	28	1.51E-07	NOTCH2, SRC, PIK3R2, CACNA1F, FGF2, DLL1, FGF3, GNAI1, EGFR, FGF4, DLL3, DLL4, FGF6, FGF8, FGF9, CCND1, PRKACG, CREB3L1, CYP1B1, PRKCG, JUN, EGF, PRKCA, FOS, KLF4, ESR1, AR, FGF10	3.197933	1.37E-06	8.43E-07
KEGG_PA THWAY	hsa04928:Parathyroid hormone synthesis, secretion and action	20	1.55E-07	PRKCG, EGR1, SLC34A2, CDKN1A, LRP5, PRKCA, GATA3, FOS, EGFR, GNAI1, RUNX2, MAFB, PLCB4, PRKACG, GNAI1, CREB3L1, GNA12, PLCB1, FGF23, FGFR1	4.270531	1.37E-06	8.43E-07
KEGG_PA THWAY	hsa04072:Phospholipase D signaling pathway	22	5.56E-07	PDGFRB, PDGFRA, SHC2, DGKB, EGF, PDGFB, LPAR1, PDGFA, PRKCA, PIK3R2, EGFR, DNMT1, GRM1, GRM3, DNMT3, PLCB4, PDGFD, KIT, GNA12, PLCB1, PLPP3, DGKI	3.625652	4.76E-06	2.93E-06
KEGG_PA THWAY	hsa05206:MicroRNAs in cancer	33	1.15E-06	NOTCH2, HDAC5, NOTCH3, CDKN1A, SLC45A3, IRS1, ITGB3, NOTCH4, PDGFB, TNC, PDGFA, IRS2, PIK3R2, PTGS2, EGFR, ERBB3, CCND1, PLAU, ERBB2, CYP1B1, PRKCG, PDGFRB, PDGFRA, TGF2, FZD3, CDKN2A, DNMT3A, HMGA2, PRKCA, SPRY2, ZFPM2, MET, FGFR3	2.597222	9.57E-06	5.89E-06
KEGG_PA THWAY	hsa04350:TGF-beta signaling pathway	18	1.43E-06	TGF2, CDKN2B, TGF2, INHBA, GDF6, ACVR1B, SMAD6, TNF, LTBP1, DCN, ACVR2A, BMP4, ACVR1C, ID1, ID4, AMH, LEFTY2, NODAL	4.092593	1.15E-05	7.09E-06
KEGG_PA THWAY	hsa05230:Central carbon metabolism in cancer	14	4.51E-06	PDGFRB, NTRK1, RET, PDGFRA, FLT3, NTRK3, PIK3R2, EGFR, KIT, ERBB2, MET, FGFR3, FGFR2, FGFR1	4.841941	3.54E-05	2.18E-05
KEGG_PA THWAY	hsa04068:FoxO signaling pathway	19	5.84E-06	CDKN1A, TGF2, CDKN2B, TGF2, IRS1, EGF, IRS4, FASLG, PIK3R2, IRS2, FOXO4, IGF1, FOXO3, EGFR, GRM1, IGF1R, CCNB3, CCND1, IL7R	3.534512	4.47E-05	2.75E-05
KEGG_PA THWAY	hsa05223:Non-small cell lung cancer	14	6.22E-06	ALK, PRKCG, RET, CDKN1A, CDKN2A, EGF, HGF, PRKCA, PIK3R2, FOXO3, EGFR, CCND1, ERBB2, MET	4.709285	4.58E-05	2.82E-05
KEGG_PA THWAY	hsa04722:Neurotrophin signaling pathway	18	6.30E-06	CAMK2B, NTRK1, NGFR, NTRK2, JUN, SHC2, SORT1, IRS1, BDNF, NTRK3, CAMK2A, MATK, FASLG, PIK3R2, NGF, FOXO3, NTF4, NTF3	3.683333	4.58E-05	2.82E-05
KEGG_PA THWAY	hsa04935:Growth hormone synthesis, secretion and action	18	7.90E-06	PRKCG, SHC2, IRS1, IRS4, PRKCA, PIK3R2, IRS2, FOS, IGF1, CACNA1F, GNAI1, GHR, SOCS2, PLCB4, PRKACG, GNA11, CREB3L1, PLCB1	3.622951	5.61E-05	3.45E-05
KEGG_PA THWAY	hsa05231:Choline metabolism in cancer	16	9.65E-06	PDGFRB, PRKCG, PDGFRA, JUN, DGKB, EGF, PDGFB, PDGFA, PRKCA, PIK3R2, FOS, EGFR, PDGFD, RAC3, PLPP3, DGKI	3.968575	6.69E-05	4.11E-05
KEGG_PA THWAY	hsa04921:Oxytocin signaling pathway	20	1.42E-05	PRKCG, CAMK2B, CDKN1A, JUN, NOS3, SRC, CAMK2A, CACNA2D3, PRKCA, FOS, CACNA1F, PTGS2, EGFR, GNAI1, RYR3, PLCB4, PPP3R2, CCND1, PRKACG, PLCB1	3.189033	9.58E-05	5.89E-05
KEGG_PA THWAY	hsa05142:Chagas disease	16	1.58E-05	TGF2, JUN, ACE, TGF2, FASLG, PIK3R2, FOS, TNF, IL2, GNAI1, PLCB4, PPP2R2B, IL1B, GNA11, PLCB1, TLR4	3.814455	1.04E-04	6.42E-05
KEGG_PA THWAY	hsa04658:Th1 and Th2 cell differentiation	15	1.82E-05	JAG2, NOTCH2, NOTCH3, JUN, IL13, GATA3, FOS, DLL1, IL2, DLL3, DLL4, MAF, PPP3R2, STAT4, IL12RB2	4.003623	1.18E-04	7.23E-05
KEGG_PA THWAY	hsa05010:Alzheimer disease	35	2.02E-05	WNT2B, CSF1, IRS1, LRP5, IRS4, WNT8B, IRS2, PIK3R2, FZD10, CACNA1F, PTGS2, TNF, RYR3, WNT6, GRIN2A, PPP3R2, WNT11, WNT4, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, WNT16, GRIN2B, DKK1, DKK2, DKK4, PLCB4, IL1B, DDIT3, PLCB1	2.198068	1.28E-04	7.88E-05
KEGG_PA THWAY	hsa04330:Notch signaling pathway	12	3.35E-05	JAG2, LFNG, PTCRA, NOTCH2, DLL4, NOTCH3, HEY1, NOTCH4, HES1, DLL1, HES5, DLL3	4.752688	2.03E-04	1.25E-04
KEGG_PA THWAY	hsa04713:Circadian entrainment	15	3.36E-05	PRKCG, CAMK2B, CAMK2A, PRKCA, FOS, GRIN2B, GNAI1, RYR3, CACNA1G, PER1, GRIN2A, PLCB4, PRKACG, PRKG2, PLCB1	3.797251	2.03E-04	1.25E-04

KEGG_PA THWAY	hsa04750:Inflammatory mediator regulation of TRP channels	15	4.24E-05	PRKCG, CAMK2B, NTRK1, IL1R1, SRC, CAMK2A, PRKCA, PIK3R2, IL1RAP, IGF1, NGF, PLCB4, PRKACG, IL1B, PLCB1	3.720539	2.51E-04	1.55E-04
KEGG_PA THWAY	hsa05163:Human cytomegalovirus infection	24	4.39E-05	PRKCG, PDGFRA, CDKN1A, IL1R1, CDKN2A, SRC, ITGB3, FASLG, PRKCA, PIK3R2, PTGS2, TNF, EGFR, GNAI1, PLCB4, PPP3R2, CCND1, PRKACG, IL1B, GNAI1, CREB3L1, GNA12, RAC3, PLCB1	2.60767	2.51E-04	1.55E-04
KEGG_PA THWAY	hsa04961:Endocrine and other factor-regulated calcium reabsorption	11	4.40E-05	DNM3, PRKCG, PLCB4, PRKACG, CLTCL1, ATP1B4, PRKCA, KLK2, PLCB1, ESR1, DNM1	5.096436	2.51E-04	1.55E-04
KEGG_PA THWAY	hsa05321:Inflammatory bowel disease	12	5.29E-05	TGFB2, JUN, MAF, TGFB3, IL1B, IL13, STAT4, GATA3, TNF, TLR4, IL2, IL12RB2	4.533333	2.96E-04	1.82E-04
KEGG_PA THWAY	hsa05418:Fluid shear stress and atherosclerosis	18	5.39E-05	JUN, SDC4, IL1R1, NOS3, SRC, ITGB3, CAV1, PDGFB, PDGFA, PLAT, PIK3R2, FOS, TNF, ACVR2A, BMP4, IL1B, KDR, RAC3	3.134752	2.96E-04	1.82E-04
KEGG_PA THWAY	hsa05022:Pathways of neurodegeneration - multiple diseases	39	6.15E-05	CAMK2B, WNT2B, CSF1, CAMK2A, LRP5, WNT8B, FASLG, FZD10, CACNA1F, PTGS2, TNF, GRM1, RYR3, WNT6, GRIN2A, PPP3R2, WNT11, WNT4, PRKCG, WNT10B, FZD3, FZD2, WNT5B, BDNF, FZD7, WNT7B, FZD6, SEPTIN5, FZD8, PRKCA, WNT16, GRIN2B, DKK1, DKK2, DKK4, PLCB4, IL1B, DDI3, PLCB1	1.982747	3.31E-04	2.04E-04
KEGG_PA THWAY	hsa05146:Amoebiasis	15	6.62E-05	PRKCG, LAMA5, TGFB2, IL1R1, TGFB3, LAMA1, PRKCA, PIK3R2, TNF, PLCB4, PRKACG, IL1B, GNA11, PLCB1, TLR4	3.576052	3.50E-04	2.15E-04
KEGG_PA THWAY	hsa05031:Amphetamine addiction	12	9.32E-05	CAMK2B, PRKCG, GRIN2A, JUN, PPP3R2, PRKACG, CREB3L1, CAMK2A, FOSB, PRKCA, FOS, GRIN2B	4.270531	4.85E-04	2.98E-04
KEGG_PA THWAY	hsa05211:Renal cell carcinoma	12	1.07E-04	FLCN, CDKN1A, TGFB2, JUN, TGFB3, HGF, PDGFB, PAK6, PIK3R2, PAK3, MET, PAK5	4.209524	5.45E-04	3.35E-04
KEGG_PA THWAY	hsa04919:Thyroid hormone signaling pathway	16	1.18E-04	PRKCG, NOTCH2, NOTCH3, SRC, ITGB3, NOTCH4, ATP1B4, PRKCA, PIK3R2, ESR1, BMP4, PLCB4, CCND1, PRKACG, PLCB1, WNT4	3.220401	5.92E-04	3.64E-04
KEGG_PA THWAY	hsa04066:HIF-1 signaling pathway	15	1.24E-04	PRKCG, CAMK2B, CDKN1A, ANGPT1, EPO, NOS3, EGF, CAMK2A, PRKCA, PIK3R2, IGF1, EGFR, IGF1R, ERBB2, TLR4	3.379205	6.10E-04	3.75E-04
KEGG_PA THWAY	hsa04730:Long-term depression	11	1.32E-04	PRKCG, PLCB4, GNA11, GNA12, PRKG2, PRKCA, IGF1, PLCB1, GNAI1, GRM1, IGF1R	4.501852	6.41E-04	3.94E-04
KEGG_PA THWAY	hsa04911:Insulin secretion	13	1.70E-04	PRKCG, CAMK2B, CAMK2A, ATP1B4, PRKCA, CCK, CACNA1F, PLCB4, PCLO, PRKACG, GNA11, CREB3L1, PLCB1	3.711886	8.05E-04	4.95E-04
KEGG_PA THWAY	hsa04640:Hematopoietic cell lineage	14	1.72E-04	CSF3, CSF3R, CSF1, IL1R1, EPO, FLT3, ITGB3, FLT3LG, TNF, EPOR, IL3, IL1B, KIT, IL7R	3.472503	8.05E-04	4.95E-04
KEGG_PA THWAY	hsa05219:Bladder cancer	9	2.02E-04	CDKN1A, CCND1, CDKN2A, CDH1, SRC, EGF, ERBB2, FGFR3, EGFR	5.390244	9.31E-04	5.73E-04
KEGG_PA THWAY	hsa04933:AGE-RAGE signaling pathway in diabetic complications	14	2.10E-04	EGR1, TGFB2, JUN, TGFB3, NOS3, VEGFC, VEGFD, PRKCA, PIK3R2, TNF, PLCB4, CCND1, IL1B, PLCB1	3.40374	9.56E-04	5.88E-04
KEGG_PA THWAY	hsa04926:Relaxin signaling pathway	16	2.41E-04	JUN, SHC2, NOS3, SRC, VEGFC, VEGFD, PRKCA, PIK3R2, FOS, EGFR, GNAI1, PLCB4, EDNRB, PRKACG, CREB3L1, PLCB1	3.022222	0.00108	6.64E-04
KEGG_PA THWAY	hsa04720:Long-term potentiation	11	3.38E-04	CAMK2B, PRKCG, GRIN2A, PLCB4, PPP3R2, PRKACG, CAMK2A, PRKCA, PLCB1, GRIN2B, GRM1	4.031509	0.001489	9.16E-04
KEGG_PA THWAY	hsa05417:Lipid and atherosclerosis	21	4.85E-04	CAMK2B, JUN, NOS3, SRC, CAMK2A, FASLG, PRKCA, PIK3R2, HSPA2, FOS, TNF, TIRAP, PLCB4, PPP3R2, IL1B, DDI3, OLR1, PPARG, PLCB1, TLR4, HSPA1A	2.387346	0.002105	0.001295
KEGG_PA THWAY	hsa05216:Thyroid cancer	8	6.16E-04	NTRK1, RET, TCF7L2, CDKN1A, CCND1, PAX8, CDH1, PPARG	5.309309	0.002637	0.001622
KEGG_PA THWAY	hsa04380:Osteoclast differentiation	16	6.28E-04	TGFB2, JUN, CSF1, IL1R1, ITGB3, FHL2, PIK3R2, MITF, FOS, TNFRSF11A, TNF, FOSL1, PPP3R2, IL1B, FOSB, PPARG	2.766823	0.002647	0.001628
KEGG_PA THWAY	hsa04370:VEGF signaling pathway	10	6.42E-04	PRKCG, SHC2, PPP3R2, SRC, NOS3, KDR, RAC3, PIK3R2, PRKCA, PTGS2	4.092593	0.002667	0.001641
KEGG_PA THWAY	hsa05030:Cocaine addiction	9	7.17E-04	GRM3, GRIN2A, JUN, BDNF, PRKACG, CREB3L1, FOSB, GRIN2B, GNAI1	4.510204	0.002937	0.001807
KEGG_PA THWAY	hsa04912:GnRH signaling pathway	12	0.001306	CAMK2B, EGR1, JUN, PLCB4, SRC, PRKACG, GNA11, CAMK2A, PRKCA, PLCB1, CACNA1F, EGFR	3.168459	0.005279	0.003247
KEGG_PA THWAY	hsa05323:Rheumatoid arthritis	12	0.001427	TGFB2, JUN, CSF1, ANGPT1, IL15, TGFB3, IL1B, CD28, FOS, TNFRSF11A, TNF, TLR4	3.134752	0.005687	0.003498
KEGG_PA THWAY	hsa04915:Estrogen signaling pathway	15	0.001504	JUN, SHC2, NOS3, SRC, PIK3R2, FOS, ESR1, EGFR, GNAI1, GRM1, PLCB4, PRKACG, CREB3L1, PLCB1, HSPA1A	2.64988	0.005913	0.003637
KEGG_PA THWAY	hsa05221:Acute myeloid leukemia	10	0.001608	TCF7L2, CEBPA, IL3, CCND1, FLT3, CEBPE, ZBTB16, KIT, PIK3R2, RUNX1T1	3.611111	0.00624	0.003839
KEGG_PA THWAY	hsa05166:Human T-cell leukemia virus 1 infection	20	0.001801	EGR1, CDKN1A, TGFB2, CDKN2B, EGR2, JUN, MMP7, IL1R1, TGFB3, CDKN2A, IL15, PIK3R2, FOS, TNF, IL2, FOSL1, PPP3R2, CCND1, PRKACG, CREB3L1	2.202292	0.006897	0.004242
KEGG_PA THWAY	hsa04925:Aldosterone synthesis and secretion	12	0.002004	CAMK2B, PRKCG, PLCB4, PRKACG, CREB3L1, GNA11, CAMK2A, ATP1B4, PRKCA, PLCB1, CACNA1F, CACNA1G	3.006803	0.007574	0.004659
KEGG_PA THWAY	hsa04024:cAMP signaling pathway	20	0.002114	CAMK2B, JUN, BDNF, PTCH1, CAMK2A, ATP1B4, PIK3R2, FOS, CACNA1F, GLI1, GRIN2B, GLI3, GNAI1, TSHR, TIAM1, GRIN2A, PRKACG, CREB3L1, RAC3, AMH	2.173058	0.007886	0.004851
KEGG_PA THWAY	hsa04725:Cholinergic synapse	13	0.002383	PRKCG, CAMK2B, CAMK2A, PRKCA, PIK3R2, FOS, CACNA1F, GNAI1, PLCB4, PRKACG, GNA11, CREB3L1, PLCB1	2.775845	0.008779	0.0054
KEGG_PA THWAY	hsa04923:Regulation of lipolysis in adipocytes	9	0.002477	IRS1, PRKACG, IRS4, PRKG2, PIK3R2, IRS2, PTGS2, GNAI1, TSHR	3.745763	0.008899	0.005474
KEGG_PA THWAY	hsa05213:Endometrial cancer	9	0.002477	TCF7L2, CDKN1A, CCND1, CDH1, EGF, ERBB2, PIK3R2, FOXO3, EGFR	3.745763	0.008899	0.005474
KEGG_PA THWAY	hsa05161:Hepatitis B	16	0.002545	PRKCG, CDKN1A, TGFB2, EGR2, JUN, TGFB3, SRC, FASLG, PRKCA, PIK3R2, FOS, TNF, TIRAP, CREB3L1, STAT4, TLR4	2.410361	0.009032	0.005556
KEGG_PA THWAY	hsa05210:Colorectal cancer	11	0.002657	TCF7L2, CDKN1A, TGFB2, JUN, CCND1, TGFB3, EGF, RAC3, PIK3R2, FOS, EGFR	3.104725	0.009314	0.005729
KEGG_PA THWAY	hsa04918:Thyroid hormone synthesis	10	0.003197	PRKCG, TPO, PLCB4, PAX8, PRKACG, CREB3L1, ATP1B4, PRKCA, PLCB1, TSHR	3.274074	0.011074	0.006812
KEGG_PA THWAY	hsa04213:Longevity regulating pathway - multiple species	9	0.003399	IRS1, PRKACG, IRS4, PIK3R2, IRS2, IGF1, FOXO3, HSPA1A, IGF1R	3.564516	0.011504	0.007077
KEGG_PA THWAY	hsa04211:Longevity regulating pathway	11	0.003412	IRS1, PRKACG, CREB3L1, IRS4, PIK3R2, IRS2, PPARG, IGF1, FOXO3, PPARGC1A, IGF1R	3.001235	0.011504	0.007077
KEGG_PA THWAY	hsa05143:African trypanosomiasis	7	0.003439	PRKCG, PLCB4, IL1B, FASLG, PRKCA, PLCB1, TNF	4.645646	0.011504	0.007077
KEGG_PA THWAY	hsa05144:Malaria	8	0.003803	CSF3, TGFB2, TGFB3, IL1B, HGF, TNF, MET, TLR4	3.928889	0.012506	0.007693
KEGG_PA THWAY	hsa05212:Pancreatic cancer	10	0.003825	CDKN1A, TGFB2, CCND1, TGFB3, CDKN2A, EGF, ERBB2, RAC3, PIK3R2, EGFR	3.189033	0.012506	0.007693

KEGG_PA THWAY	hsa04071:Sphingolipid signaling pathway	13	0.003894	PRKCG, NOS3, PRKCA, PIK3R2, TNF, GNAI1, ACER1, PLCB4, PPP2R2B, GNA12, RAC3, S1PR2, PLCB1	2.616576	0.012592	0.007746
KEGG_PA THWAY	hsa05100:Bacterial invasion of epithelial cells	10	0.004173	DNM3, SHC2, CDH1, SRC, CAV1, CLTCL1, PIK3R2, DOCK1, MET, DNM1 TGF2, ACE, TGF2, LAMA1, ITGB3, ITGA8, CACNA2D3, ITGA7, IGF1, CACNA1F,	3.148148	0.013346	0.008209
KEGG_PA THWAY	hsa05410:Hypertrophic cardiomyopathy	11	0.006741	TNF GRM3, PRKCG, GRIN2A, PLCB4, PPP3R2, PRKACG, SLC1A2, PRKCA, PLCB1, GRIN2B, GNAI1, GRM1	2.728395	0.021323	0.013116
KEGG_PA THWAY	hsa04724:Glutamatergi c synapse	12	0.006908	PRKCG, CAMK2B, CAMK2A, PRKCA, FOS, GRIN2B, GNAI1, GRIN2A, PLCB4, PPP2R2B, PRKACG, CREB3L1, PLCB1	2.562319	0.021615	0.013296
KEGG_PA THWAY	hsa04728:Dopaminergic synapse	13	0.007299	NOS3, IRS1, IRS4, ATP1B4, IRS2, CACNA1F, GNAI1, PLCB4, EDNRB, PPP3R2, GNA11, CREB3L1, GNA12, PRKG2, PLCB1	2.41835	0.022595	0.013899
KEGG_PA THWAY	hsa04022:cGMP-PKG signaling pathway	15	0.007552	SOC2, SHC2, CCND1, SRC, PIK3R2, FOS, TNFRSF11A, FOXO3, ESR1 JUN, CSF1, IL15, CREB3L1, IL1B, DAB2IP, VEGF, PIK3R2, VEGFD, FOS, PTGS2, TNF	3.112676	0.023659	0.014553
KEGG_PA THWAY	hsa04668:TNF signaling pathway	12	0.00887	LAMA5, RELN, SDC4, IBS, LAMA1, ITGB3, ITGA8, TNC, COL6A3, ITGA7 TGF2, TGF3, LAMA1, PRKACG, ITGB3, ITGA8, CACNA2D3, ITGA7, IGF1, CACNA1F, TNF	2.47619	0.026609	0.016368
KEGG_PA THWAY	hsa04512:ECM-receptor interaction	10	0.009864	ALK, JUN, PPP3R2, EGF, CD28, PIK3R2, FOS, TLR4, TIRAP, EGFR	2.759051	0.029289	0.018016
KEGG_PA THWAY	hsa05414:Dilated cardiomyopathy	11	0.010085	ITK, JUN, PPP3R2, PPP2R2B, CD28, PAK6, PIK3R2, FOS, PAK3, TNF, IL2, PAK5 CCND1, PPP2R2B, IRS1, CREB3L1, IRS4, PIK3R2, IRS2, PPARG, IGF1, FOXO3, PPARGC1A, IGF1R	2.572487	0.029643	0.018234
KEGG_PA THWAY	hsa05235:PD-L1 expression and PD-1 checkpoint pathway in cancer	10	0.01058	SOC2, IRS1, IRS4, PIK3R2, IRS2, TNF, CACNA1G EGR1, NOTCH3, HDAC5, NOS3, PLAT, GNAI1, RYR3, PLCB4, CCND1, CDH1, PRKACG, PLCB1, PPARGC1A	2.728395	0.030254	0.01861
KEGG_PA THWAY	hsa04660:T cell receptor signaling pathway	12	0.010605	ITK, JUN, PPP3R2, PPP2R2B, CD28, PAK6, PIK3R2, FOS, PAK3, TNF, IL2, PAK5 CCND1, PPP2R2B, IRS1, CREB3L1, IRS4, PIK3R2, IRS2, PPARG, IGF1, FOXO3, PPARGC1A, IGF1R	2.415301	0.030254	0.01861
KEGG_PA THWAY	hsa04152:AMPK signaling pathway	12	0.010605	SOC2, IRS1, IRS4, PIK3R2, IRS2, TNF, CACNA1G EGR1, NOTCH3, HDAC5, NOS3, PLAT, GNAI1, RYR3, PLCB4, CCND1, CDH1, PRKACG, PLCB1, PPARGC1A	2.415301	0.030254	0.01861
KEGG_PA THWAY	hsa04930:Type II diabetes mellitus	7	0.011316	SOC2, IRS1, IRS4, PIK3R2, IRS2, TNF, CACNA1G EGR1, NOTCH3, HDAC5, NOS3, PLAT, GNAI1, RYR3, PLCB4, CCND1, CDH1, PRKACG, PLCB1, PPARGC1A	3.65721	0.03197	0.019665
KEGG_PA THWAY	hsa04371:Apelin signaling pathway	13	0.01143	SOC2, IRS1, IRS4, PIK3R2, IRS2, TNF, CACNA1G EGR1, NOTCH3, HDAC5, NOS3, PLAT, GNAI1, RYR3, PLCB4, CCND1, CDH1, PRKACG, PLCB1, PPARGC1A	2.280159	0.031982	0.019673
KEGG_PA THWAY	hsa04971:Gastric acid secretion	9	0.01162	CAMK2B, PRKCG, PLCB4, PRKACG, CAMK2A, ATP1B4, PRKCA, PLCB1, GNAI1 PRKCG, PLCB4, GNA11, PIK3R2, PRKCA, PLCB1, CACNA1F, CACNA1G	2.907895	0.032204	0.019809
KEGG_PA THWAY	hsa04929:GnRH secretion	8	0.015813	PRKCG, PLCB4, GNA11, PIK3R2, PRKCA, PLCB1, CACNA1F, CACNA1G PLCB4, PRKACG, CREB3L1, GNA11, PLCB1, CACNA1F, PBX1, CACNA1G	3.022222	0.043004	0.026453
KEGG_PA THWAY	hsa04927:Cortisol synthesis and secretion	8	0.015813	PLCB4, PRKACG, CREB3L1, GNA11, PLCB1, CACNA1F, PBX1, CACNA1G PRKCG, INPP4B, INPP5A, PLCB4, DGKB, ITPKA, PIK3R2, PRKCA, PLCB1, DGKI	3.022222	0.043004	0.026453
KEGG_PA THWAY	hsa04070:Phosphatidyli nositol signaling system	10	0.0178	PRKCG, INPP4B, INPP5A, PLCB4, DGKB, ITPKA, PIK3R2, PRKCA, PLCB1, DGKI PRKCG, IRS1, ATP1B4, PIK3R2, PRKCA, IGF1	2.505669	0.047823	0.029417
KEGG_PA THWAY	hsa04960:Aldosterone- regulated sodium reabsorption	6	0.017913	PRKCG, IRS1, ATP1B4, PIK3R2, PRKCA, IGF1 PLCB4, ACE, PPP3R2, PRKACG, PRKG2, PLCB1, CACNA1F, GNAI1	3.877193	0.047823	0.029417
KEGG_PA THWAY	hsa04924:Renin secretion	8	0.021372	PLCB4, ACE, PPP3R2, PRKACG, PRKG2, PLCB1, CACNA1F, GNAI1 SMO, CCND1, PRKACG, PTCH1, GAS1, GLI1, GLI3	2.847021	0.056538	0.034778
KEGG_PA THWAY	hsa04340:Hedgehog signaling pathway	7	0.025281	SMO, CCND1, PRKACG, PTCH1, GAS1, GLI1, GLI3 EGR2, JUN, PPP3R2, KSR1, SRC, IL1B, PIK3R2, PTGS2, TNF, IL2	3.069444	0.066278	0.040769
KEGG_PA THWAY	hsa04625:C-type lectin receptor signaling pathway	10	0.02661	EGR2, JUN, PPP3R2, KSR1, SRC, IL1B, PIK3R2, PTGS2, TNF, IL2 PRKCG, JUN, FASLG, PRKCA, PIK3R2, FOS, TNF, GNAI1, CCNB3, PPP3R2, GNA11, RAC3, PAK6, PAK3, TLR4, PAK5	2.338624	0.069138	0.042528
KEGG_PA THWAY	hsa05170:Human immunodeficiency virus 1 infection	16	0.026883	PRKCG, JUN, FASLG, PRKCA, PIK3R2, FOS, TNF, GNAI1, CCNB3, PPP3R2, GNA11, RAC3, PAK6, PAK3, TLR4, PAK5 TEAD4, YAP1, WWTR1, TEAD1, TEAD3	1.844549	0.069229	0.042584
KEGG_PA THWAY	hsa04392:Hippo signaling pathway - multiple species	5	0.028477	TEAD4, YAP1, WWTR1, TEAD1, TEAD3 IL1B, CD28, PRF1, FASLG, TNF, IL2	4.233716	0.072691	0.044714
KEGG_PA THWAY	hsa04940:Type I diabetes mellitus	6	0.029168	IL1B, CD28, PRF1, FASLG, TNF, IL2 IL1B, CD28, PRF1, FASLG, TNF, IL2	3.426357	0.073807	0.0454
KEGG_PA THWAY	hsa05332:Graft-versus- host disease	6	0.031852	IL1B, CD28, PRF1, FASLG, TNF, IL2 AMER1, WNT2B, CTNND2, LRP5, WNT8B, FZD10, CXXC4, WNT6, WNT11, ADGRA2, WIF1, WNT4, TCF7L2, RNF43, WNT10B, FZD3, FZD2, WNT5B, FZD7, WNT7B, FZD6, FZD8, WNT16, DKK1, DKK2, DKK4, SFRP4, BCL9, SFRP2, PTK7, DDIT3	3.348485	0.079903	0.04915
UP_KW_B IOLOGICA L_PROCES S	KW-0879~Wnt signaling pathway	31	8.70E-14	ZNF331, CTNND2, NAB2, DACH2, HOXA13, HOXA11, SOX2, HOXA9, DACH1, CCND1, CREB3L1, HOXA3, ZNF444, MNX1, SSX1, LMO1, ATP1B4, SOX11, MITF, HNF1A, SOX10, RUNX2, AR, MYCN, MAF, DDIT3, ERG, BCORL1, ZFPM2, ATF3, NOTCH2, NOTCH3, NOTCH4, GATA6, GATA3, BHLHE22, FOXO4, FOXO3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, PPARGC1A, TFAP2A, WWTR1, EGR1, JUN, EGR2, BCL11B, EGR4, AUTS2, BTBD18, ZBTB16, HMG2, SMAD6, ESR1, PBX1, NR4A3, MAFB, LHX2, FEV, ID1, ID4, LHX4, HOXD9, FGFR1, TENM1, FHL2, FASLG, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, PPP1R13L, TRPS1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, TET1, PAX3, ETV1, FOXL2, OLIG1, ETV4, MN1, PAX8, TAL2, PAX7, TAL1, AHRR, PPARG, VGLL3, YAP1, CEBPA, HDAC5, KANK1, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, FSTL3, ERBB4, ERBB2, STAT4, HES1, HES5, RUNX1T1, TCF7L2, CDX2, EYA1, DMRT1, CDKN2A, CDX1, KLF4, TBX15, PER1, NR6A1, WT1, NFIB	5.351274	7.66E-12	7.13E-12
UP_KW_B IOLOGICA L_PROCES S	KW-0805~Transcription regulation	127	1.23E-12	ZNF331, CTNND2, NAB2, DACH2, HOXA13, HOXA11, SOX2, HOXA9, DACH1, CCND1, CREB3L1, HOXA3, ZNF444, MNX1, SSX1, LMO1, ATP1B4, SOX11, MITF, HNF1A, SOX10, RUNX2, AR, MYCN, MAF, DDIT3, ERG, BCORL1, ZFPM2, ATF3, NOTCH2, NOTCH3, NOTCH4, GATA6, GATA3, BHLHE22, FOXO4, FOXO3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, PPARGC1A, TFAP2A, WWTR1, EGR1, JUN, EGR2, BCL11B, EGR4, AUTS2, BTBD18, ZBTB16, HMG2, SMAD6, ESR1, PBX1, NR4A3, MAFB, LHX2, FEV, ID1, ID4, LHX4, HOXD9, FGFR1, TENM1, FHL2, FASLG, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, PPP1R13L, TRPS1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, TET1, PAX3, ETV1, FOXL2, OLIG1, ETV4, MN1, PAX8, TAL2, PAX7, TAL1, AHRR, PPARG, VGLL3, YAP1, CEBPA, HDAC5, KANK1, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, FSTL3, ERBB4, ERBB2, STAT4, HES1, HES5, RUNX1T1, TCF7L2, CDX2, EYA1, DMRT1, CDKN2A, CDX1, KLF4, TBX15, PER1, NR6A1, WT1, NFIB	1.798155	5.41E-11	5.04E-11
UP_KW_B IOLOGICA L_PROCES S	KW-0804~Transcription	127	9.65E-12	ZNF331, CTNND2, NAB2, DACH2, HOXA13, HOXA11, SOX2, HOXA9, DACH1, CCND1, CREB3L1, HOXA3, ZNF444, MNX1, SSX1, LMO1, ATP1B4, SOX11, MITF, HNF1A, SOX10, RUNX2, AR, MYCN, MAF, DDIT3, ERG, BCORL1, ZFPM2, ATF3, NOTCH2, NOTCH3, NOTCH4, GATA6, GATA3, BHLHE22, FOXO4, FOXO3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, PPARGC1A, TFAP2A, WWTR1, EGR1, JUN, EGR2, BCL11B, EGR4, AUTS2, BTBD18, ZBTB16, HMG2, SMAD6, ESR1, PBX1, NR4A3, MAFB, LHX2, FEV, ID1, ID4, LHX4, HOXD9, FGFR1, TENM1, FHL2, FASLG, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, PPP1R13L, TRPS1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, TET1, PAX3, ETV1, FOXL2, OLIG1, ETV4, MN1, PAX8, TAL2, PAX7, TAL1, AHRR, PPARG, VGLL3, YAP1, CEBPA, HDAC5, KANK1, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, FSTL3, ERBB4, ERBB2, STAT4, HES1, HES5, RUNX1T1, TCF7L2, CDX2, EYA1, DMRT1, CDKN2A, CDX1, KLF4, TBX15, PER1, NR6A1, WT1, NFIB	1.748186	2.83E-10	2.64E-10

UP_KW_B IOLOGICA L_PROCES S	KW-0221~Differentiation	57	1.74E-09	ROBO2, GLI1, FGF1, FGF2, FGF3, FGF4, ROBO1, FGF6, FGF8, MECOM, FGF9, ZIC2, CHL1, KDR, AMH, ZNF521, MYBL1, SOX11, FOXL2, DLIC1, MLF1, RUNX2, SFRP4, SFRP2, PAX8, TAL1, ITGA8, ZFPM2, EPHA2, GAS7, CAMK2B, NOTCH2, NOTCH3, NOTCH4, FOXO4, DLL1, DLL3, DLL4, PRDM16, FGF23, HES5, NTRK1, NTRK2, NGFR, ANGPT1, DMRT1, SORT1, BTBD18, NTRK3, VEGFC, VEGFD, HSPA2, PBX1, BMP4, AXL, FEV, TLL2	2.364331	3.82E-08	3.56E-08
UP_KW_B IOLOGICA L_PROCES S	KW-0524~Neurogenesis	24	1.41E-05	ROBO2, CAMK2B, NTRK1, EPHA5, NGFR, NTRK2, BRSK1, FZD3, EPHA7, NTRK3, PAX3, SOX11, BHLHE22, ROBO1, DLL4, ZIC2, CHL1, FEV, NEDD4, CHN1, ITGA8, FGF13, HES5, GAS7	2.818895	2.48E-04	2.31E-04
UP_KW_B IOLOGICA L_PROCES S	KW-0914~Notch signaling pathway	10	1.96E-05	JAG2, NOTCH2, DLL4, NOTCH3, HEY1, NOTCH4, NEURL1, CNTN1, DLL1, DLL3	6.448888	2.88E-04	2.68E-04
UP_KW_B IOLOGICA L_PROCES S	KW-0130~Cell adhesion	29	5.58E-04	RET, LAMA5, CSF3R, SRC, LAMA1, CTNND2, ITGB3, TNC, RELN, IBSP, CHL1, CDH1, ABL2, OLR1, NCAM1, EDIL3, DST, OMD, PRKCA, PTK7, KIT, CDH11, ITGA8, CNTN1, COL6A3, ITGA7, ACKR3, EPHA3, EPHA2	2.014622	0.007015	0.006537
UP_KW_B IOLOGICA L_PROCES S	KW-0037~Angiogenesis	13	9.09E-04	ANGPT1, FLT4, DAB2IP, VEGFC, VEGFD, PRKCA, FGF1, FGF2, DLL4, FGF6, ADGRA2, KDR, EPHA2	3.129073	0.009994	0.009313
UP_KW_C ELLULAR COMPON ENT	KW-0964~Secreted	119	2.08E-13	EPHB6, FCGBP, CSF3, TNFRSF6B, CSF3R, CSF1, EPO, TNC, PRF1, PLAT, IL1RAP, FGF1, FGF2, TNF, FGF3, FGF4, FGF6, FGF8, IBSP, FGF9, PLAU, CCN6, KDR, PRSS8, WNT5B, IL1R1, OMD, IGFBP2, FLT3LG, LIFR, DKK1, DKK2, DKK4, SFRP4, SFRP2, LOX, PAPPA, EPHA3, FBN2, SDC4, EPHA10, HTRA1, PDGFB, PDGFA, PLA2G5, LTBP1, KLK7, WNT6, PDGFD, APOD, FGF23, WNT4, WNT10B, TGFβ2, ACE, BDNF, TGFβ3, PRG2, INHBA, IGF1, GDF6, IL2, BMP4, EXT2, IL3, FGF19, FGFR4, IL7R, FGFR3, FGFR2, NODAL, FGF10, PTPRR, WNT2B, FLT4, ELN, FASLG, ADM, GHR, CHL1, OLR1, AMH, EDIL3, MMP7, IL15, IL13, WNT16, NGF, DCN, TGFβR3, IL1B, COL6A3, MET, LAMA5, LAMA1, COL11A1, WNT8B, TMPPRS2, EGFR, FSTL3, NTF4, MUC1, RELN, WNT11, ERBB3, WIF1, NTF3, NCAM1, LEFTY2, ANGPT1, WNT7B, VEGFC, CCK, VEGFD, SULF1, EPOR, TAFAS, TLL2, HSPA1A	1.974602	7.06E-12	7.06E-12
UP_KW_C ELLULAR COMPON ENT	KW-0272~Extracellular matrix	26	2.54E-07	FBN2, LAMA5, WNT2B, LAMA1, COL11A1, ELN, TNC, WNT8B, LTBP1, WNT6, RELN, WNT11, CHL1, WNT4, WNT10B, TGFβ2, MMP7, WNT5B, TGFβ3, WNT7B, OMD, WNT16, DCN, TGFβR3, BMP4, COL6A3	3.370997	4.32E-06	4.32E-06
UP_KW_C ELLULAR COMPON ENT	KW-1003~Cell membrane	152	2.12E-05	ATP8A2, CSF3R, CSF1, DGKB, MPL, IRS4, PRF1, FZD10, IL1RAP, TNF, IGF1R, EDNRB, ADGRA2, CDH1, KDR, PRSS8, ROS1, RGS7, PDGFRB, ARDC4, PRKCG, EPHA5, PDGFRA, SLC34A2, RNF43, EPHA7, USP6, IL1R1, FLT3LG, LIFR, PRKCA, GABRG2, TIAM1, SMO, SCN8A, PLPP3, DGKI, EPHA3, EPHA2, NOTCH2, NOTCH3, EPHA10, NOTCH4, HTRA1, SLC1A2, LPAR1, TNFRSF11A, PLA2G5, CACNA1G, GRIN2A, INPP5A, SLC01B3, PROM1, WWTR1, NGFR, FZD3, ACE, FZD2, MAGEE1, CAV1, PTC1, FZD7, FZD6, FZD8, ESR1, GRIN2B, CPS1, CNTN1, FGF13, FGFR4, IL7R, XKR3, FGFR3, FGFR2, FGFR1, RET, DIRAS3, ALK, TENM1, PTPRR, FLT4, ITGB3, FASLG, PTPRK, GPHN, GRM1, ROBO1, GRM3, GHR, CHL1, PSD3, OLR1, PRKG2, RAC3, ABCC3, PRMT8, KSR1, DST, GRID1, FCRL4, RHOD, TIRAP, DNMT1, TGFβR3, PLCB4, KIT, CDH11, ITGA8, GAS1, ACSBG1, TLR4, DDR2, AMER1, KANK1, CANT1, SRC, TMPPRS2, NOD1, ACVR1B, DLL1, EGFR, GNAI1, DLL4, P2RY8, MUC1, ERBB3, ERBB4, GNAI1, ERBB2, GNA12, GPC3, HAS2, NCAM1, LRIG3, S1PR2, NTRK1, NTRK2, SORT1, KCNB1, NOS3, SPRY4, DAB2IP, SORBS2, EPOR, TSHR, ACVR2A, AXL, NEDD4, NEURL1, SPRY2, ACKR3, LGR5, SOX2, HOXA9, CREB3L1, HOXA3, KDR, MNX1, SOX11, PRKCA, HNF1A, PIMREG, SOX10, RUNX2, AR, DDIT3, BCORL1, ZFPM2, ATF3, GATA6, GATA3, GATA2, GATA1, ZNF703, PRDM16, NKX2-1, NKX2-5, PPARGC1A, WWTR1, EGR1, JUN, EGR2, CRADD, MAGEE1, BCL11B, EGRA, BTBD18, RANBP17, PBX1, MLLT11, FOSL1, ID1, ID4, HOXD9, CDKN1C, ITK, TENM1, CDKN1A, HOXC13, GLI1, HOXC11, GLI3, MECOM, HEY1, TEAD1, TEAD3, TEAD4, IL15, TET1, PAX3, FOS, MLF1, MN1, PAX8, TAL1, PAX7, AHRR, PPARG, PLCB1, VGLL3, AMER1, YAP1, KANK1, HOXD13, AKAP6, PTGS2, HOXD11, GNAI1, EGFR, FSTL3, STAT4, PAK6, PAK5, RUNX1T1, NPM2, CDX2, DMRT1, CDKN2A, CDX1, SORT1, PER1, NR6A1, NFIB, WT1, NEDD4, FOSB, TACC2, HSPA1A, ZNF331, PRDM7, CTNND2, NAB2, FGF1, DACH2, HOXA13, FGF2, HOXA11, CDC14B, DACH1, CCND1, ZNF444, LMO1, RNF43, CDKL5, LMO2, ATP1B4, MTF, MYCL, MYCN, MAF, WDFY3, ERG, DGKI, NOTCH2, NOTCH3, BRSK1, NOTCH4, AK5, BHLHE22, FOXO4, FOXO3, CCNB3, SPECC1, TFAP2A, AUTS2, ZBTB16, HMGA2, FANCE, SMAD6, ESR1, BCL9, MAFB, FGF14, NR4A3, TLX3, CPS1, LHX2, TLX1, FEV, LHX4, FGF13, FGFR1, PPP1R13B, FLT4, FHL2, FASLG, FLCN, ZIC2, PPP1R13L, TRPS1, ZNF521, MYBL1, SH3D19, PEG3, DST, DNMT3A, ETV1, FOXL2, OLIG1, DUSP26, ETV4, DMRTA2, NAV3, SETBP1, CILK1, CEBPA, HDACS, NUTM1, HLF, CEBPD, CEBPE, SRC, PLAG1, MUC1, ERBB4, ERBB2, HES1, LRIG3, HES5, TCF7L2, EYA1, PRRX1, PRRX2, KLF4, TBX15, ERCC4	1.357954	2.41E-04	2.41E-04
UP_KW_C ELLULAR COMPON ENT	KW-0539~Nucleus	194	0.001515	ATP8A2, FRMPD4, CTNND2, ITGB3, GPHN, GLI3, ROBO1, FLCN, KIAA1549, PCLO, ADGRA2, PSD3, RAC3, SH3GL2, PPFA2, SSK1, PRKCG, EPHA5, PDGFRA, CDKL5, KSR1, DST, GABRG2, MLF1, DNMT1, SMO, SCN8A, ALDH1A1, WDFY3, TLR4, CILK1, DGKI, EPHA2, KANK1, BRSK1, ATL1, CAMK2A, GRIN2A, INPP5A, MAP2, ERBB2, PROM1, NTRK2, NGFR, AUTS2, KCNB1, SPRY4, DAB2IP, SORBS2, NEURL1, SPRY2, FGF13	1.197958	0.012879	0.012879
UP_KW_C ELLULAR COMPON ENT	KW-0966~Cell projection	52	0.005912	RET, ALK, FLT3, GLI1, FGF3, FGF4, FGF6, HOXA9, MECOM, CCND1, ZNF521, ROS1, SSK1, LMO1, PDGFRB, PDGFRA, USP6, LMO2, PAX3, ETV1, PRKCA, FOS, MYCN, MAF, TAL2, PAX7, TAL1, DDIT3, KIT, ERG, TCTA, MET, GAS7, YAP1, HLF, SRC, PLAG1, PDGFB, FOXO4, FOXO3, EGFR, FSTL3, PDGFD, MYH11, RUNX1T1, NTRK1, SPECC1, WWTR1, JUN, ZBTB16, STYK1, HMGA2, PBX1, IL2, MLLT11, BCL9, NR4A3, MAFB, AXL, TLX1, LHX4, FGFR2	1.459283	0.040202	0.040202
UP_KW_D ISEASE	KW-0656~Proto- oncogene	62	6.56E-27	CTNND2, FZD10, DACH2, FGF1, HOXA13, FGF2, FGF3, HOXA11, FGF4, SOX2, FGF6, HOXA9, DACH1, FGF8, FGF9, CREB3L1, HOXA3, KDR, PDGFRB, PDGFRA, RNF43, EPHA7, WNT5B, SOX11, MTF, DKK1, DKK2, DKK4, SFRP4, SFRP2, SMO, WDFY3, NOTCH2, NOTCH3, NOTCH4, PDGFB, PDGFA, FOXO4, WNT6, PDGFD, NKX2-5, WNT4, JAG2, WNT10B, NGFR, FZD3, FZD2, FZD7, FZD6, FZD8, GDF6, PBX1, BMP4, TLX3, TLX1, FEV, ID1, HOXD9, NODAL, ROBO2, WNT2B, HOXC13, GLI1, HOXC11, ROBO1, LFNG, MECOM, ZIC2, HEY1, CHL1, ZNF521, EDIL3, TET1, PAX3, OLIG1, WNT16, MLF1, MN1, PAX8, PAX7, TAL1, ITGA8, CILK1, GAS7,	4.795729	4.99E-25	4.92E-25
UP_KW_ MOLECUL AR_FUNC TION	KW-9996~Developmental protein	123	6.43E-34		3.270738	2.38E-32	2.15E-32

UP_KW_ MOLECUL AR_FUNC TION	KW-0217~Developmental protein	123	6.43E-34	CAMK2B, CEBPA, LRP5, WNT8B, HOXD13, HOXD11, DLL1, EGFR, DLL3, DLL4, RELN, WNT11, ERBB4, WIF1, LRIG3, PAK3, LEFTY2, HES5, NTRK1, NTRK2, NPM2, PRRX1, CDX2, ANGPT1, EYA1, DMRT1, CDX1, SORT1, NTRK3, WNT7B, SPRY4, PRRX2, DAB2IP, VEGFC, VEGFD, BICC1, SPRY2, ACKR3, TLL2 CTNND2, FZD10, DACH2, FGF1, HOXA13, FGF2, FGF3, HOXA11, FGF4, SOX2, FGF6, HOXA9, DACH1, FGF8, FGF9, CREB3L1, HOXA3, KDR, PDGFRB, PDGFRA, RNF43, EPHA7, WNT5B, SOX11, MITF, DKK1, DKK2, DKK4, SFRP4, SFRP2, SMO, WDFY3, NOTCH2, NOTCH3, NOTCH4, PDGFB, PDGFA, FOXO4, WNT6, PDGFD, NKX2-5, WNT4, JAG2, WNT10B, NGFR, FZD3, FZD2, FZD7, FZD6, FZD8, GDF6, PBX1, BMP4, TLX1, TLX1, FEV, ID1, HOXD9, NODAL, ROBO2, WNT2B, HOXC13, GLI1, HOXC11, ROBO1, LFNG, MECOM, ZIC2, HEY1, CHL1, ZNF521, EDIL3, TET1, PAX3, OLIG1, WNT16, MLF1, MN1, PAX8, PAX7, TAL1, ITGA8, CILK1, GAS7, CAMK2B, CEBPA, LRP5, WNT8B, HOXD13, HOXD11, DLL1, EGFR, DLL3, DLL4, RELN, WNT11, ERBB4, WIF1, LRIG3, PAK3, LEFTY2, HES5, NTRK1, NTRK2, NPM2, PRRX1, CDX2, ANGPT1, EYA1, DMRT1, CDX1, SORT1, NTRK3, WNT7B, SPRY4, PRRX2, DAB2IP, VEGFC, VEGFD, BICC1, SPRY2, ACKR3, TLL2	3.270738	2.38E-32	2.15E-32
UP_KW_ MOLECUL AR_FUNC TION	KW-0339~Growth factor	36	2.30E-21	CSF3, CSF1, PDGFB, PDGFA, FGF1, FGF2, FGF3, FGF4, NTF4, FGF6, FGF8, FGF9, PDGFD, CCN6, NTF3, AMH, LEFTY2, FGF23, TGFB2, TGFB3, EGF, BDNF, HGF, VEGFC, VEGFD, IGF1, INHBA, NGF, GDF6, IL2, BMP4, IL3, FGF14, FGF19, NODAL, FGF10	7.629305	5.46E-20	4.94E-20
UP_KW_ MOLECUL AR_FUNC TION	KW-0829~Tyrosine-protein kinase	34	2.95E-21	RET, ALK, ITK, EPHA10, FLT3, SRC, FLT4, EGFR, IGF1R, ERBB3, ERBB4, ERBB2, KDR, ABL2, ROS1, PDGFRB, NTRK1, EPHA5, PDGFRA, NTRK2, EPHA7, NTRK3, STYK1, MATK, AXL, KIT, FGFR4, MET, FGFR3, FGFR2, EPHA3, FGFR1, EPHA2, DDR2	8.19931	5.46E-20	4.94E-20
UP_KW_ MOLECUL AR_FUNC TION	KW-0497~Mitogen	15	6.36E-11	TGFB2, TGFB3, PDGFB, VEGFC, PDGFA, VEGFD, FGF1, FGF2, FGF3, FGF4, FGF6, FGF8, FGF9, IL1B, PDGFD	10.23443	9.41E-10	8.52E-10
UP_KW_ MOLECUL AR_FUNC TION	KW-0010~Activator	60	1.72E-09	GLI1, GLI3, SOX2, DACH1, ZIC2, CREB3L1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, TET1, SOX11, MITF, ETV1, HNF1A, SOX10, ETV4, MN1, AR, MYCN, MAF, DDIT3, PPARG, ZFPM2, YAP1, NOTCH2, CEBPA, NOTCH3, CEBPD, CEBPE, PLAG1, NOTCH4, GATA6, GATA3, FOXO4, FOXO3, GATA2, GATA1, ERBB4, ERBB2, PRDM16, NKX2-1, STAT4, PPARGC1A, TFAP2A, TCF7L2, EGR1, WWTR1, JUN, EGR2, CDX2, EYA1, CDX1, KLF4, ESR1, PBX1, MAFB, LHX2, NFIB	2.315099	2.12E-08	1.92E-08
UP_KW_ MOLECUL AR_FUNC TION	KW-0418~Kinase	60	7.97E-09	RET, ALK, ITK, CDKN1A, FLT3, DGKB, FLT4, IGF1R, PLAU, PRKACG, KDR, PRKG2, MAP3K6, ROS1, PDGFRB, PRKCG, EPHA5, PDGFRA, EPHA7, CDKL5, KSR1, MATK, PRKCA, MAPK8IP2, KIT, ITPKA, MET, CILK1, DGKI, EPHA3, EPHA2, DDR2, CAMK2B, BRSK1, EPHA10, SRC, CAMK2A, AKAP6, AK5, ACVR1B, KALRN, EGFR, ACVR1C, ERBB3, ERBB4, ERBB2, ABL2, PAK6, PAK3, PAK5, NTRK1, NTRK2, NTRK3, STYK1, ACVR2A, AXL, FGFR4, FGFR3, FGFR2, FGFR1	2.223109	8.43E-08	7.63E-08
UP_KW_ MOLECUL AR_FUNC TION	KW-0675~Receptor	99	2.60E-05	EPHB6, TNFRSF6B, CSF3R, IRS1, MPL, IRS2, FZD10, IL1RAP, IGF1R, EDNRB, ADGRA2, KDR, IL13RA2, ROS1, PDGFRB, EPHA5, PDGFRA, EPHA7, IL1R1, LIFR, GABRG2, AR, SMO, EPHA3, EPHA2, NOTCH2, NOTCH3, EPHA10, NOTCH4, LPAR1, TNFRSF11A, GRIN2A, ADGRG7, NGFR, FZD3, FZD2, PTCH1, FZD7, FZD6, FZD8, ESR1, GRIN2B, LRP1B, TNFRSF10D, NR4A3, PTK7, FGFR4, IL7R, FGFR3, FGFR2, FGFR1, RET, ROBO2, ALK, PTPRR, FLT3, FLT4, ITGB3, PTPRK, GRM1, RYR3, ROBO1, GRM3, GHR, OLR1, PTCRA, GRID1, FCRL4, TGFBR3, KIT, ITGA8, ITGA7, PPARG, MET, TLR4, DDR2, LRP5, ACVR1B, EGFR, P2RY8, ACVR1C, ERBB3, ERBB4, ERBB2, NCAM1, S1PR2, IL12RB2, NTRK1, NTRK2, SORT1, NTRK3, EPOR, TSHR, ACVR2A, NR6A1, AXL, ACKR3, LGR5, HSPA1A	1.489746	2.41E-04	2.18E-04
UP_KW_ MOLECUL AR_FUNC TION	KW-0238~DNA-binding	107	8.55E-05	ZNF331, DACH2, HOXA13, HOXA11, SOX2, HOXA9, DACH1, CREB3L1, HOXA3, ZNF444, MNX1, SOX11, MITF, HNF1A, SOX10, RUNX2, MYCL, AR, MYCN, MAF, DDIT3, ERG, ZFPM2, ATF3, GATA6, GATA3, FOXO4, FOXO3, GATA2, GATA1, PRDM16, NKX2-1, NKX2-5, TFAP2A, EGR1, JUN, EGR2, EGR4, ZBTB16, HMGA2, ESR1, PBX1, FOSL1, NR4A3, MAFB, TLX3, LHX2, TLX1, FEV, LHX4, HOXD9, HOXC13, GLI1, HOXC11, GLI3, MECOM, ZIC2, HEY1, TRPS1, ZNF521, TEAD1, MYBL1, TEAD3, TEAD4, DNMT3A, TET1, PAX3, ETV1, FOXL2, OLIG1, FOS, ETV4, MLF1, DMRTA2, PAX8, SETBP1, TAL2, PAX7, TAL1, AHRR, PPARG, CEBPA, HLF, CEBPD, CEBPE, PLAG1, HOXD13, HOXD11, CXXC4, STAT4, HES1, HES5, RUNX1T1, TCF7L2, PRRX1, CDX2, DMRT1, CDKN2A, CDX1, PRRX2, KLF4, TBX15, NR6A1, ERCC4, WT1, NFIB, FOSB	1.418593	7.03E-04	6.36E-04
UP_KW_ MOLECUL AR_FUNC TION	KW-0678~Repressor	36	0.006963	YAP1, TENM1, HDAC5, NAB2, FASLG, BHLHE22, DACH2, GATA1, GLI3, DACH1, CCND1, HEY1, ZIC2, PPP1R13L, TRPS1, ZNF703, PRDM16, NKX2-1, HES1, ZNF521, HES5, RUNX1T1, TCF7L2, BCL11B, ZBTB16, DNMT3A, TET1, PBX1, MAFB, MAF, DDIT3, ID1, ID4, ZFPM2, BCORL1, ATF3	1.583441	0.051527	0.046653