Table S1. Top 54 genes from DESeq2 differential expression analysis (high vs low TB)

No.	Gene	BaseMean	Log*FC*	LfcSE	Stat	*P* value	Adj. *P* val
1	*TFF3_7048*	100.2766	22.7309	3.9052	5.8207	5.86E-09	8.52E-05
2	*LNX1_18397*	169.9208	10.8022	2.0284	5.3255	1.01E-07	0.0007
3	*ZFP42_89799*	35.4992	21.2967	4.0543	5.2528	1.50E-07	0.0007
4	*PCDHB3_25298*	527.0177	6.1554	1.2160	5.0621	4.15E-07	0.0010
5	*XAGE2_87736*	40.7714	21.4984	4.2514	5.0567	4.26E-07	0.0010
6	*SLCO1A2_26370*	126.7118	-7.4639	1.4845	-5.0278	4.96E-07	0.0010
7	*ABCC12_87981*	37.2130	21.3627	4.2515	5.0247	5.04E-07	0.0010
8	*ITIH6_89568*	58.8126	20.5589	4.2215	4.8701	1.12E-06	0.0020
9	*GARNL3_27252*	29.4009	8.2978	1.7722	4.6822	2.84E-06	0.0043
10	*DNAJC22_16620*	510.5320	7.5441	1.6137	4.6750	2.94E-06	0.0043
11	*CYP4F8_24089*	11.6840	19.7575	4.2531	4.6454	3.39E-06	0.0045
12	*PRICKLE2_19595*	279.7679	4.5500	0.9861	4.6141	3.95E-06	0.0048
13	*DLX5_18350*	26.3851	19.3679	4.2518	4.5552	5.23E-06	0.0059
14	*TBX1_16353*	116.8381	7.7451	1.7185	4.5068	6.58E-06	0.0068
15	*ZNF235_10960*	183.4985	9.4889	2.1114	4.4941	6.99E-06	0.0068
16	*SNPH_17872*	367.9773	7.2030	1.6376	4.3985	1.09E-05	0.0099
17	*ADRA2C_22752*	63.3501	9.3604	2.1451	4.3635	1.28E-05	0.0109
18	*NGFR_17440*	75.3601	8.1333	1.8735	4.3412	1.42E-05	0.0114
19	*LRIT3_21714*	69.7873	8.0793	1.8664	4.3289	1.50E-05	0.0115
20	*TBX15_88894*	37.6973	8.6460	2.0065	4.3090	1.64E-05	0.0115
21	*CNPY4_25551*	32.5042	8.4343	1.9583	4.3070	1.65E-05	0.0115
22	*KRT18_92564*	58.8148	9.2841	2.1657	4.2868	1.81E-05	0.0116
23	*ADAMTSL4_24568*	412.1653	-3.6595	0.8558	-4.2762	1.90E-05	0.0116
24	*MMAA_11927*	37.2466	8.6287	2.0189	4.2739	1.92E-05	0.0116
25	*ATP7A_16851*	448.4429	1.8820	0.4533	4.1521	3.29E-05	0.0192

No.	Gene	BaseMean	Log*FC*	LfcSE	Stat	*P* value	Adj. *P* val
26	*EPHX4_10710*	71.8036	8.0959	1.9691	4.1115	3.93E-05	0.0214
27	*SERHL2_28292*	160.2545	7.0156	1.7074	4.1089	3.98E-05	0.0214
28	*CLCA2_28548*	596.6705	10.1744	2.4879	4.0896	4.32E-05	0.0224
29	*ADM5_20591*	60.2682	9.2889	2.2768	4.0798	4.51E-05	0.0226
30	*RNF144A_20926*	25.1246	8.0688	1.9816	4.0718	4.66E-05	0.0226
31	*ASIC1_24534*	30.7543	8.3561	2.0668	4.0429	5.28E-05	0.0246
32	*FGF10_22305*	74.1265	8.1139	2.0101	4.0366	5.42E-05	0.0246
33	*ATP5MPL_25583*	23.4178	7.9671	1.9873	4.0091	6.09E-05	0.0262
34	*ZBED9_25756*	93.8835	8.4746	2.1146	4.0076	6.13E-05	0.0262
35	*FRMD6_15845*	581.8674	2.1082	0.5281	3.9918	6.56E-05	0.0266
36	*ANTXR1_20910*	344.9783	2.4624	0.6170	3.9907	6.59E-05	0.0266
37	*VWA2_13854*	46.0271	8.9085	2.2437	3.9705	7.17E-05	0.0282
38	*CECR2_18607*	128.8237	7.9660	2.0179	3.9476	7.89E-05	0.0288
39	*TIGD4_24615*	29.3269	8.2845	2.1014	3.9425	8.07E-05	0.0288
40	*SLC46A3_14686*	332.4674	2.4519	0.6223	3.9401	8.15E-05	0.0288
41	*ROBO2_18609*	25.3409	8.0708	2.0490	3.9388	8.19E-05	0.0288
42	*CERS1_33991*	38.2728	8.6613	2.2010	3.9352	8.31E-05	0.0288
43	*SOCS2_6660*	120.7801	6.1865	1.5767	3.9237	8.72E-05	0.0295
44	*FAM110C_20024*	126.0239	4.8362	1.2400	3.9000	9.62E-05	0.0315
45	*SUSD2_21594*	49.9458	9.0469	2.3231	3.8942	9.85E-05	0.0315
46	*CEACAM6_26148*	189.6564	9.4731	2.4343	3.8914	9.97E-05	0.0315
47	*APOD_357*	317.7515	6.0218	1.5518	3.8804	0.0001	0.0323
48	*HOXA7_14600*	60.1866	7.8951	2.0438	3.8629	0.0001	0.0339
49	*PRSS12_15990*	212.5453	-6.3604	1.6507	-3.8532	0.0001	0.0346
50	*LRRCC1_13038*	722.5999	-3.4043	0.8943	-3.8066	0.0001	0.0410
51	*PCDHB13_25302*	30.4862	8.3417	2.2091	3.7761	0.0002	0.0454
52	*CNTN1_18508*	52.0418	9.1069	2.4209	3.7618	0.0002	0.0463

No.	Gene	BaseMean	Log*FC*	LfcSE	Stat	*P* value	Adj. *P* val
53	*EDIL3_13279*	186.2908	4.0180	1.0682	3.7615	0.0002	0.0463
54	*SLC43A2_12845*	58.5422	5.7444	1.5318	3.7501	0.0002	0.0476

Genes were selected using Adj. *P* val < 0.05 and |log*FC*| > 1.5. Gene labels may include platform-specific identifiers.

Abbreviations: Adj. *P* value, Benjamini–Hochberg–adjusted *P* value; DE, differential expression; LfcSE, standard error of log*FC*; Log*FC*, log fold change; TB, tumor budding; TNBC, triple-negative breast cancer.

Table S2. Top 188 genes ranked by mutual information (MI) with TB class

No.	Gene	MI score	No.	Gene	MI score	No.	Gene	MI score	No.	Gene	MI score
1	*CKS1B_1362*	0.4293	51	*KCP_88561*	0.4293	101	*ANXA8_17897*	0.4293	151	*KNCN_88978*	0.4293
2	*ARPP19_466*	0.4293	52	*ZFP57_89960*	0.4293	102	*GNL3_18049*	0.4293	152	*FOXD2_89074*	0.4293
3	*SLC45A3_12258*	0.4293	53	*VIM_18185*	0.4293	103	*COX5B_18008*	0.4293	153	*NKX2-5_89148*	0.4293
4	*VASH2_12681*	0.4293	54	*NDUFV1_90568*	0.4293	104	*ZNF816_18216*	0.4293	154	*IGHD_89462*	0.4293
5	*LRRCC1_13038*	0.4293	55	*TMEM189_27973*	0.4293	105	*SPRY1_18786*	0.4293	155	*REEP3_89598*	0.4293
6	*EDIL3_13279*	0.4293	56	*MMP3_4216*	0.4293	106	*TNFSF13B_19280*	0.4293	156	*GNB1L_89611*	0.4293
7	*HAND2_13573*	0.4293	57	*TBC1D30_28455*	0.4293	107	*CD38_19506*	0.4293	157	*GBP5_89721*	0.4293
8	*KIF19_14414*	0.4293	58	*ANGPTL4_28320*	0.4293	108	*PRICKLE2_19595*	0.4293	158	*EDN2_89854*	0.4293
9	*SLC46A3_14686*	0.4293	59	*SIGLEC11_27854*	0.4293	109	*STAR_19847*	0.4293	159	*MEDAG_90476*	0.4293
10	*ZBTB42_15005*	0.4293	60	*CCDC130_1019*	0.4293	110	*USP30_19866*	0.4293	160	*APOBEC3D_90589*	0.4293
11	*IRF4_15768*	0.4293	61	*IDO1_3210*	0.4293	111	*FAM110C_20024*	0.4293	161	*PRCP_90646*	0.4293
12	*S100A7A_16138*	0.4293	62	*MCM3_4072*	0.4293	112	*MGAM_20192*	0.4293	162	*ZNF724_90804*	0.4293
13	*NXF1_16209*	0.4293	63	*ITGB5_3450*	0.4293	113	*IGSF8_20178*	0.4293	163	*RBM39_92712*	0.4293
14	*TM6SF1_16943*	0.4293	64	*RAB31_5670*	0.4293	114	*DROSHA_20431*	0.4293	164	*DCAF8_91694*	0.4293
15	*NGFR_17440*	0.4293	65	*SLC25A4_6406*	0.4293	115	*OR1N2_20569*	0.4293	165	*GPS1_93022*	0.4293
16	*TTBK1_17884*	0.4293	66	*SQSTM1_6740*	0.4293	116	*MAFG_20735*	0.4293	166	*CDK16_92460*	0.4293
17	*C3orf70_17965*	0.4293	67	*USP7_7602*	0.4293	117	*AP5B1_21108*	0.4293	167	*SRCAP_90788*	0.4293
18	*SFTPA1_17909*	0.4293	68	*UBAP2L_7462*	0.4293	118	*LILRB1_21244*	0.4293	168	*BTN3A2_26908*	0.4293
19	*NOL6_18053*	0.4293	69	*MRFAP1L1_10556*	0.4293	119	*SLC5A9_21712*	0.4293	169	*DNM2_91616*	0.4293
20	*IFT27_18625*	0.4293	70	*ODAM_10470*	0.4293	120	*DCT_22118*	0.4293	170	*IL15RA_27350*	0.4293
21	*HMSD_18693*	0.4293	71	*FBXL5_10590*	0.4293	121	*MFAP3_22545*	0.4293	171	*TRIM13_28005*	0.4293
22	*MPP3_18952*	0.4293	72	*PHF23_11187*	0.4293	122	*GDF11_22582*	0.4293	172	*ZNF761_92911*	0.4293
23	*CREBRF_19339*	0.4293	73	*PPDPF_11184*	0.4293	123	*TMC6_22569*	0.4293	173	*DGCR6_15534*	0.4293
24	*PATJ_20019*	0.4293	74	*CRAT_11181*	0.4293	124	*ZNF74_22843*	0.4293	174	*EDNRA_88670*	0.4293
25	*TACR1_20733*	0.4293	75	*RGS10_11311*	0.4293	125	*SGMS2_22813*	0.4293	175	*DLGAP1_27117*	0.4293

No.	Gene	MI score	No.	Gene	MI score	No.	Gene	MI score	No.	Gene	MI score
26	*B4GALT6_20855*	0.4293	76	*ZBTB17_11403*	0.4293	126	*TRMT10A_22971*	0.4293	176	*DDTL_23438*	0.4293
27	*SACS_22437*	0.4293	77	*PROCA1_11481*	0.4293	127	*TDRD9_23073*	0.4293	177	*ERO1B_15346*	0.4293
28	*ASGR2_22847*	0.4293	78	*GPC4_11583*	0.4293	128	*RNF213_23156*	0.4293	178	*LSMEM1_27464*	0.4293
29	*ZCCHC4_23037*	0.4293	79	*ACVR1C_12053*	0.4293	129	*KDM5C_23222*	0.4293	179	*TK2_27960*	0.4293
30	*SEC16B_23083*	0.4293	80	*PCNX4_12317*	0.4293	130	*FAM81B_23460*	0.4293	180	*ZNF595_28126*	0.4293
31	*ASAP3_23766*	0.4293	81	*UPK3B_12812*	0.4293	131	*TANC2_23794*	0.4293	181	*BCL2A1_17331*	0.4293
32	*KIAA1324_24270*	0.4293	82	*EPS8L1_12856*	0.4293	132	*GAGE_23922*	0.4293	182	*LRIT3_21714*	0.4293
33	*DALRD3_24506*	0.4293	83	*RSF1_13470*	0.4293	133	*ZNF697_24100*	0.4293	183	*USH1C_11650*	0.4293
34	*BRSK2_24555*	0.4293	84	*SVBP_14145*	0.4293	134	*SPINK5_24227*	0.4293	184	*ATP6V0A1_11775*	0.4293
35	*COLEC12_24531*	0.4293	85	*SLC12A2_14584*	0.4293	135	*SUGP1_24642*	0.4293	185	*FUT3_25568*	0.4293
36	*FAM83G_24995*	0.4293	86	*IFIH1_14815*	0.4293	136	*DNLZ_25707*	0.4293	186	*CYP11A1_1693*	0.4293
37	*CCDC69_24986*	0.4293	87	*ZSCAN21_15202*	0.4293	137	*DSC3_25779*	0.4293	187	*FOXG1_2475*	0.4293
38	*PARS2_25040*	0.4293	88	*THSD1_15269*	0.4293	138	*NAV3_26097*	0.4293	188	*RHOXF1_5843*	0.4293
39	*USP2_25436*	0.4293	89	*UPRT_15417*	0.4293	139	*TAS2R5_26393*	0.4293			
40	*SCARF2_26255*	0.4293	90	*CRY1_15619*	0.4293	140	*DNAJC28_26653*	0.4293			
41	*MAGEB4_27479*	0.4293	91	*MOV10_15708*	0.4293	141	*MYO9A_26663*	0.4293			
42	*FAM166A_28865*	0.4293	92	*CXCL5_15735*	0.4293	142	*LRRC70_27457*	0.4293			
43	*FCHO1_28745*	0.4293	93	*FRMD6_15845*	0.4293	143	*FBXO32_28461*	0.4293			
44	*FAM193A_28885*	0.4293	94	*STN1_16142*	0.4293	144	*PIGBOS1_33704*	0.4293			
45	*NBPF8_34048*	0.4293	95	*HOXB13_16208*	0.4293	145	*ZKSCAN7_33685*	0.4293			
46	*TMEM42_87522*	0.4293	96	*ZNF746_16282*	0.4293	146	*DAP_33810*	0.4293			
47	*OR13A1_87645*	0.4293	97	*ISM1_16436*	0.4293	147	*TRGV8_88081*	0.4293			
48	*PGK2_88355*	0.4293	98	*ELK1_16569*	0.4293	148	*CPSF4L_88631*	0.4293			
49	*UBA7_88387*	0.4293	99	*ATP7A_16851*	0.4293	149	*ANP32D_88632*	0.4293			
50	*TRBV30_88551*	0.4293	100	*TNFRSF12A_17257*	0.4293	150	*TRBV27_88690*	0.4293			

MI was computed between each gene’s expression and the binary TB label; higher MI indicates greater class discriminability. Ties at the maximum score reflect the ranking behavior of the estimator.

Abbreviations: MI, mutual information; TB, tumor budding; TNBC, triple-negative breast cancer.

Table S3. Enriched pathways among diffusion-ranked PPI neighbors of the 7 biomarkers (GO Biological Processes and KEGG)

Terms	Group	Description	Symbols	Pathway size	Gene ratio	*P* value
GO:0035567	1	non-canonical Wnt signaling pathway	*DVL1, DVL3, CELSR3, CELSR2, FZD2, PTK7, RYK, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9, CELSR1, DAAM1, VANGL2, VANGL1,* ***PRICKLE2***	52	0.3654	4.00E-29
GO:0060071	1	Wnt signaling pathway, planar cell polarity pathway	*DVL1, DVL3, CELSR3, CELSR2, FZD2, PTK7, RYK, WNT11, FZD3, FZD1, FZD6, FZD7, CELSR1, DAAM1, VANGL2, VANGL1,* ***PRICKLE2***	37	0.4595	2.72E-28
hsa04310	1	Wnt signaling pathway	*CSNK1E, DVL1, DVL3, FZD2, PRICKLE3, RYK, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9, DAAM1, DAAM2, INVS, PRICKLE4, VANGL2, VANGL1, NKD2,* ***PRICKLE2***	174	0.1207	5.53E-21
GO:0016055	1	Wnt signaling pathway	*CSNK1E, DVL1, DVL3, CELSR3, CELSR2, FZD2, PTK7, RYK, STK4, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9, CELSR1, DAAM1, DAAM2, INVS, VANGL2, VANGL1, NKD2,* ***PRICKLE2***	278	0.0863	2.38E-20
GO:0198738	1	cell-cell signaling by wnt	*CSNK1E, DVL1, DVL3, CELSR3, CELSR2, FZD2, PTK7, RYK, STK4, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9, CELSR1, DAAM1, DAAM2, INVS, VANGL2, VANGL1, NKD2,* ***PRICKLE2***	278	0.0863	2.38E-20
GO:0000041	2	transition metal ion transport	***ATP7A****, ATP7B, SLC31A1, SLC31A2, CP, SLC30A1, SLC30A4, HEPH, SLC30A9, CUTC, SLC30A6, SLC30A5, SLC30A7, HEPHL1*	97	0.1443	1.72E-15
GO:0006825	3	copper ion transport	***ATP7A****, ATP7B, SLC31A1, SLC31A2, CP, HEPH, CUTC, HEPHL1*	18	0.4444	8.95E-14
GO:0060070	1	canonical Wnt signaling pathway	*CSNK1E, DVL1, DVL3, FZD2, RYK, STK4, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9*	103	0.1262	1.08E-13
GO:0007601	4	visual perception	*CACNA1F, COL11A1, GNAT1, GRM6, TRPM1, RDH5, GRK1, RS1, SLC24A1, RRH, CABP4, NYX, CACNA2D4,* ***LRIT3****, RGS9BP, GPR179*	219	0.0731	8.30E-13

Terms	**Group**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0050953	4	sensory perception of light stimulus	*CACNA1F, COL11A1, GNAT1, GRM6, TRPM1, RDH5, GRK1, RS1, SLC24A1, RRH, CABP4, NYX, CACNA2D4,* ***LRIT3****, RGS9BP, GPR179*	223	0.0717	1.10E-12
hsa05217	1	Basal cell carcinoma	*DVL1, DVL3, FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9*	63	0.1587	7.51E-12
GO:0055070	3	copper ion homeostasis	***ATP7A****, ATP7B, SLC31A1, SLC31A2, CP, MT2A, CUTC*	20	0.3500	2.57E-11
GO:0098771	2	inorganic ion homeostasis	***ATP7A****, ATP7B, SLC31A1, SLC31A2, CP, HRC, MC3R, MT1A, MT2A, SLC30A1, FZD9, SLC24A1, SLC30A9, CUTC, SLC30A5, ATP13A3, TMEM178A, SLC30A7, HEPHL1*	430	0.0442	4.00E-11
GO:0001736	1	establishment of planar polarity	*PTK7, FZD3, FZD6, CELSR1, INTU, WDPCP, VANGL2*	26	0.2692	2.11E-10
GO:0007164	1	establishment of tissue polarity	*PTK7, FZD3, FZD6, CELSR1, INTU, WDPCP, VANGL2*	26	0.2692	2.11E-10
GO:0009583	4	detection of light stimulus	*CACNA1F, GNAT1, GRM6, GRK1, RS1, RRH, CABP4, CACNA2D4, RGS9BP*	63	0.1429	2.30E-10
GO:0021915	1	neural tube development	*DVL1, DVL3, FZD2, PTK7, STK4, FZD3, FZD1, FZD6, CELSR1, INTU, WDPCP, VANGL2*	157	0.0764	3.84E-10
hsa04390	1	Hippo signaling pathway	*CSNK1E, DVL1, DVL3, FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9, NKD2*	157	0.0764	3.84E-10
GO:0055080	2	monoatomic cation homeostasis	***ATP7A****, ATP7B, SLC31A1, SLC31A2, CP, HRC, MC3R, MT1A, MT2A, SLC30A1, FZD9, SLC24A1, SLC30A9, CUTC, SLC30A5, ATP13A3, TMEM178A, SLC30A7, HEPHL1*	497	0.0382	4.60E-10
GO:0009584	4	detection of visible light	*CACNA1F, GNAT1, GRM6, GRK1, RS1, RRH, CACNA2D4, RGS9BP*	47	0.1702	5.50E-10
GO:0006878	3	intracellular copper ion homeostasis	***ATP7A****, ATP7B, SLC31A1, SLC31A2, CP, MT2A*	17	0.3529	6.79E-10
GO:0072175	1	epithelial tube formation	*DVL1, DVL3, FZD2, PTK7, STK4, FZD3, FZD1, FZD6, CELSR1, VANGL2, CEP290*	130	0.0846	7.11E-10

Terms	**Group**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
hsa04916	1	Melanogenesis	*DVL1, DVL3, FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9*	101	0.0990	9.18E-10
GO:0009581	4	detection of external stimulus	*CACNA1F, COL11A1, GNAT1, GRM6,* ***NGFR****, GRK1, RS1, RRH, CABP4, CACNA2D4, RGS9BP*	134	0.0821	9.84E-10
GO:0001841	1	neural tube formation	*DVL1, DVL3, FZD2, PTK7, STK4, FZD3, FZD1, FZD6, CELSR1, VANGL2*	102	0.0980	1.01E-09
GO:0009582	4	detection of abiotic stimulus	*CACNA1F, COL11A1, GNAT1, GRM6,* ***NGFR****, GRK1, RS1, RRH, CABP4, CACNA2D4, RGS9BP*	137	0.0803	1.25E-09
GO:0030003	2	intracellular monoatomic cation homeostasis	***ATP7A****, ATP7B, SLC31A1, SLC31A2, CP, HRC, MT1A, MT2A, SLC30A1, FZD9, SLC24A1, SLC30A9, SLC30A5, ATP13A3, TMEM178A, SLC30A7, HEPHL1*	423	0.0402	1.87E-09
GO:0035148	1	tube formation	*DVL1, DVL3, FZD2, PTK7, STK4, FZD3, FZD1, FZD6, CELSR1, VANGL2, CEP290*	144	0.0764	2.12E-09
GO:0006882	2	intracellular zinc ion homeostasis	*ATP7B, MT1A, MT2A, SLC30A1, SLC30A9, SLC30A5, SLC30A7*	36	0.1944	2.54E-09
GO:0006873	2	intracellular monoatomic ion homeostasis	***ATP7A****, ATP7B, SLC31A1, SLC31A2, CP, HRC, MT1A, MT2A, SLC30A1, FZD9, SLC24A1, SLC30A9, SLC30A5, ATP13A3, TMEM178A, SLC30A7, HEPHL1*	432	0.0394	2.57E-09
hsa04978	5	Mineral absorption	***ATP7A****, ATP7B, SLC31A1, MT1A, MT2A, SLC30A1, HEPH, HEPHL1*	60	0.1333	4.18E-09
GO:0090178	1	regulation of establishment of planar polarity involved in neural tube closure	*DVL1, DVL3, FZD2, PTK7, FZD1*	11	0.4545	4.24E-09
GO:0062111	2	zinc ion import into organelle	*SLC30A1, SLC30A4, SLC30A6, SLC30A5, SLC30A7*	11	0.4545	4.24E-09
hsa04934	1	Cushing syndrome	*CACNA1F, DVL1, DVL3, FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9*	155	0.0710	4.62E-09

Terms	Group	Description	Symbols	Pathway size	Gene ratio	*P* value
GO:0001843	1	neural tube closure	*DVL1, DVL3, FZD2, PTK7, FZD3, FZD1, FZD6, CELSR1, VANGL2*	89	0.1011	5.38E-09
GO:0001838	1	embryonic epithelial tube formation	*DVL1, DVL3, FZD2, PTK7, STK4, FZD3, FZD1, FZD6, CELSR1, VANGL2*	122	0.0820	5.87E-09
GO:0060606	1	tube closure	*DVL1, DVL3, FZD2, PTK7, FZD3, FZD1, FZD6, CELSR1, VANGL2*	90	0.1000	5.94E-09
GO:0002009	1	morphogenesis of an epithelium	***ATP7A***, *DVL1, DVL3, FZD2,* ***NGFR***, *PTK7, STK4, WNT11, FZD3, FZD1, FZD6, CELSR1, INTU, WDPCP, RIPK4, VANGL2, CEP290*	458	0.0371	6.13E-09
GO:0014020	1	primary neural tube formation	*DVL1, DVL3, FZD2, PTK7, FZD3, FZD1, FZD6, CELSR1, VANGL2*	95	0.0947	9.62E-09
GO:0060828	7	regulation of canonical Wnt signaling pathway	*CSNK1E, PTK7, STK4, WNT11, FZD1, FZD6, FZD7, FZD9, PTPRU, ANKRD6, DAAM2, INVS, NKD2*	268	0.0485	1.79E-08
GO:0090175	1	regulation of establishment of planar polarity	*DVL1, DVL3, FZD2, PTK7, FZD1*	14	0.3571	1.81E-08
GO:0071577	2	zinc ion transmembrane transport	*SLC30A1, SLC30A4, SLC30A9, SLC30A6, SLC30A5, SLC30A7*	28	0.2143	1.95E-08
GO:0090596	1	sensory organ morphogenesis	*COL11A1, DVL1, FZD2, GNAT1, PTK7, RS1, FZD3, FZD6, FJX1, INTU, WDPCP, CABP4, CEP290*	275	0.0473	2.43E-08
GO:0001738	1	morphogenesis of a polarized epithelium	*PTK7, FZD3, FZD6, CELSR1, INTU, WDPCP, VANGL2*	49	0.1429	2.44E-08
GO:0006829	2	zinc ion transport	*SLC30A1, SLC30A4, SLC30A9, SLC30A6, SLC30A5, SLC30A7*	29	0.2069	2.45E-08
hsa04550	1	Signaling pathways regulating pluripotency of stem cells	*DVL1, DVL3, FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9*	143	0.0699	2.72E-08
GO:0016331	1	morphogenesis of embryonic epithelium	*DVL1, DVL3, FZD2, PTK7, STK4, FZD3, FZD1, FZD6, CELSR1, VANGL2*	144	0.0694	2.90E-08
GO:0010043	5	response to zinc ion	***ATP7A***, *MT1A, MT2A, MTF1, PAM, SLC30A1, SLC30A4*	51	0.1373	3.25E-08

Terms	**Group**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
hsa05224	1	Breast cancer	*DVL1, DVL3, FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9*	147	0.0680	3.53E-08
hsa05226	1	Gastric cancer	*DVL1, DVL3, FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9*	149	0.0671	4.02E-08
hsa04150	1	mTOR signaling pathway	*DVL1, DVL3, FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9*	156	0.0641	6.21E-08
hsa05225	1	Hepatocellular carcinoma	*DVL1, DVL3, FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9*	168	0.0595	1.25E-07
GO:0048667	6	cell morphogenesis involved in neuron differentiation	*DVL1, CELSR3, CELSR2, **NGFR**, PTK7, RYK, FZD3, SEMA6B, NTNG1, WDPCP, CNTN5, PLXNA3, CABP4, VANGL2, PLXNA4*	440	0.0341	1.49E-07
GO:0007411	6	axon guidance	*DVL1, CELSR3, **NGFR**, PTK7, RYK, FZD3, SEMA6B, CNTN5, PLXNA3, VANGL2, PLXNA4*	225	0.0489	2.13E-07
GO:0097485	6	neuron projection guidance	*DVL1, CELSR3, **NGFR**, PTK7, RYK, FZD3, SEMA6B, CNTN5, PLXNA3, VANGL2, PLXNA4*	225	0.0489	2.13E-07
GO:0050908	4	detection of light stimulus involved in visual perception	*CACNA1F, GNAT1, GRM6, CACNA2D4, RGS9BP*	22	0.2273	2.28E-07
GO:0050962	4	detection of light stimulus involved in sensory perception	*CACNA1F, GNAT1, GRM6, CACNA2D4, RGS9BP*	22	0.2273	2.28E-07
GO:0030111	7	regulation of Wnt signaling pathway	*CSNK1E, PTK7, STK4, WNT11, FZD1, FZD6, FZD7, FZD9, PTPRU, ANKRD6, DAAM2, INVS, NKD2*	342	0.0380	3.04E-07
GO:0042472	1	inner ear morphogenesis	*COL11A1, DVL1, FZD2, PTK7, FZD3, FZD6, WDPCP, CEP290*	105	0.0762	3.57E-07
GO:0060562	1	epithelial tube morphogenesis	*DVL1, DVL3, FZD2, PTK7, STK4, WNT11, FZD3, FZD1, FZD6, CELSR1, VANGL2, CEP290*	314	0.0382	8.29E-07
GO:0042471	1	ear morphogenesis	*COL11A1, DVL1, FZD2, PTK7, FZD3, FZD6, WDPCP, CEP290*	126	0.0635	1.44E-06

Terms	Group	Description	Symbols	Pathway size	Gene ratio	*P* value
GO:0030178	7	negative regulation of Wnt signaling pathway	*CSNK1E, STK4, WNT11, FZD1, FZD6, PTPRU, ANKRD6, INVS, NKD2*	177	0.0508	2.01E-06
GO:0048812	6	neuron projection morphogenesis	***ATP7A***, *DVL1, CELSR3, CELSR2,* ***NGFR***, *PTK7, RYK, FZD3, SEMA6B, NTNG1, CNTN5, PLXNA3, VANGL2, PLXNA4*	484	0.0289	2.71E-06
GO:0048562	1	embryonic organ morphogenesis	*COL11A1, DVL1, FZD2, HOXD3, PTK7, WNT11, FZD3, FZD6, WDPCP, VANGL2, CEP290*	295	0.0373	3.04E-06
GO:0120039	6	plasma membrane bounded cell projection morphogenesis	***ATP7A***, *DVL1, CELSR3, CELSR2,* ***NGFR***, *PTK7, RYK, FZD3, SEMA6B, NTNG1, CNTN5, PLXNA3, VANGL2, PLXNA4*	489	0.0286	3.05E-06
GO:2000179	12	positive regulation of neural precursor cell proliferation	*HAPLN1, RYK, FZD3, FZD9, HAPLN3, HAPLN4*	64	0.0938	3.22E-06
GO:0048858	6	cell projection morphogenesis	***ATP7A***, *DVL1, CELSR3, CELSR2,* ***NGFR***, *PTK7, RYK, FZD3, SEMA6B, NTNG1, CNTN5, PLXNA3, VANGL2, PLXNA4*	494	0.0283	3.43E-06
GO:0007409	6	axonogenesis	*DVL1, CELSR3,* ***NGFR***, *PTK7, RYK, FZD3, SEMA6B, NTNG1, CNTN5, PLXNA3, VANGL2, PLXNA4*	366	0.0328	4.05E-06
GO:0090090	7	negative regulation of canonical Wnt signaling pathway	*STK4, WNT11, FZD1, FZD6, PTPRU, ANKRD6, INVS, NKD2*	145	0.0552	4.12E-06
GO:0009416	4	response to light stimulus	*CACNA1F, GNAT1, GRM6, TRPM1, GRK1, RS1, SLC24A1, RRH, CABP4, CACNA2D4, RGS9BP*	315	0.0349	5.68E-06
hsa05205	1	Proteoglycans in cancer	*FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9, MRAS*	203	0.0443	6.16E-06
hsa05010	1	Alzheimer disease	*CACNA1F, CSNK1E, DVL1, DVL3, FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9*	384	0.0313	6.58E-06
GO:0048568	1	embryonic organ development	*COL11A1, DVL1, FZD2, HOXD3, PTK7, STK4, WNT11, FZD3, FZD6, WDPCP, VANGL2, CEP290, PLXNA4*	452	0.0288	6.61E-06
GO:0007602	4	phototransduction	*GNAT1, GRK1, RS1, RRH, CABP4*	42	0.1190	6.66E-06

Terms	**Group**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0098742	13	cell-cell adhesion via plasma-membrane adhesion molecules	*CELSR3, CELSR2, PTK7, CELSR1, NTNG1, ADGRL1, ADGRL3, PCDH11X, FAT4, AMIGO3*	261	0.0383	6.80E-06
GO:0097501	5	stress response to metal ion	***ATP7A***, *MT1A, MT2A, SLC30A1*	21	0.1905	8.43E-06
GO:0061687	5	detoxification of inorganic compound	***ATP7A***, *MT1A, MT2A, SLC30A1*	22	0.1818	1.03E-05
GO:0050808	11	synapse organization	*DVL1, PTK7, RYK, FZD1, FZD9, NTNG1, ADGRL3, CNTN5, PLXNA4, ELFN1, HAPLN4*	337	0.0326	1.07E-05
hsa05022	1	Pathways of neurodegeneration - multiple diseases	*CACNA1F, CSNK1E, DVL1, DVL3, FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9, CCS*	476	0.0273	1.15E-05
GO:0061564	6	axon development	*DVL1, CELSR3,* ***NGFR****, PTK7, RYK, FZD3, SEMA6B, NTNG1, CNTN5, PLXNA3, VANGL2, PLXNA4*	421	0.0285	1.65E-05
GO:2000027	1	regulation of animal organ morphogenesis	*DVL1, DVL3, FZD2,* ***NGFR****, PTK7, FZD1*	89	0.0674	2.19E-05
GO:0060021	1	roof of mouth development	*FZD2, WNT11, FZD1, INTU, WDPCP, WFIKKN2*	91	0.0659	2.48E-05
GO:0098754	5	detoxification	***ATP7A***, *ATP7B, CP, MT1A, MT2A, SLC30A1, CCS*	138	0.0507	2.87E-05
GO:0048839	1	inner ear development	*COL11A1, DVL1, FZD2, PTK7, FZD3, FZD6, WDPCP, CEP290*	194	0.0412	3.42E-05
GO:0046686	5	response to cadmium ion	***ATP7A***, *MT1A, MT2A, MTF1, SLC30A1*	60	0.0833	3.90E-05
GO:2000177	12	regulation of neural precursor cell proliferation	*HAPLN1, RYK, FZD3, FZD9, HAPLN3, HAPLN4*	102	0.0588	4.74E-05
hsa05165	1	Human papillomavirus infection	*DVL1, DVL3, FZD2, WNT11, FZD3, FZD1, FZD6, FZD7, FZD8, FZD9*	331	0.0302	5.20E-05
GO:0060491	17	regulation of cell projection assembly	***ATP7A***, *DAAM2, SH3YL1, INTU, WDPCP, CEP120, MAPK15,* ***FAM110C***	206	0.0388	5.23E-05

Terms	Group	Description	Symbols	Pathway size	Gene ratio	*P* value
GO:0048841	6	regulation of axon extension involved in axon guidance	*RYK, SEMA6B, PLXNA3, PLXNA4*	34	0.1176	6.13E-05
GO:0007603	4	phototransduction, visible light	*GNAT1, GRK1, RS1*	13	0.2308	6.74E-05
GO:0060026	18	convergent extension	*DVL1, PTK7, WNT11*	13	0.2308	6.74E-05
GO:0034329	11	cell junction assembly	*DVL1, RYK, WNT11, FZD1, ADGRL3, RHOD, CNTN5, ILDR1, HAPLN4*	283	0.0318	8.38E-05
GO:0043583	1	ear development	*COL11A1, DVL1, FZD2, PTK7, FZD3, FZD6, WDPCP, CEP290*	221	0.0362	8.55E-05
GO:0002052	12	positive regulation of neuroblast proliferation	*HAPLN1, FZD3, HAPLN3, HAPLN4*	37	0.1081	8.60E-05
GO:0009314	4	response to radiation	*CACNA1F, GNAT1, GRM6, TRPM1, GRK1, RS1, SLC24A1, RRH, CABP4, CACNA2D4, RGS9BP*	424	0.0259	8.64E-05
GO:0046688	5	response to copper ion	***ATP7A**, ATP7B, MT1A, MT2A*	38	0.1053	9.57E-05
GO:0007416	11	synapse assembly	*DVL1, RYK, FZD1, ADGRL3, CNTN5, HAPLN4*	117	0.0513	0.000102
GO:0031346	6	positive regulation of cell projection organization	***ATP7A**, DVL1, DVL3, LTK, PTK7, FZD1, PLXNA3, PLXNA4, CEP120, ALKAL2*	360	0.0278	0.000104
GO:0150011	15	regulation of neuron projection arborization	*DVL1, DVL3, NTNG1*	15	0.2000	0.000106
GO:0070509	19	calcium ion import	*CACNA1F, TRPM1, SLC30A1, SLC24A1*	40	0.1000	0.000117
GO:0010273	5	detoxification of copper ion	***ATP7A**, MT1A, MT2A*	16	0.1875	0.000130
GO:1990169	5	stress response to copper ion	***ATP7A**, MT1A, MT2A*	16	0.1875	0.000130
GO:0009636	5	response to toxic substance	***ATP7A**, ATP7B, CP, MT1A, MT2A, SLC30A1, SLC30A4, CCS*	240	0.0333	0.000151
GO:0001942	17	hair follicle development	***ATP7A**, **NGFR**, FZD3, FZD6, INTU*	80	0.0625	0.000155

Terms	**Group**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
hsa04360	6	Axon guidance	*RYK, FZD3, SEMA6B, NTNG1, RHOD, PLXNA3, PLXNA4*	182	0.0385	0.000164
GO:0010975	6	regulation of neuron projection development	*DVL1, LTK, PTK7, RYK, FZD1, SEMA6B, NTNG1, PLXNA3, PLXNA4, ALKAL2, AMIGO3*	460	0.0239	0.000176
GO:0009642	4	response to light intensity	*GNAT1, RS1, SLC24A1*	18	0.1667	0.000188
GO:0022404	17	molting cycle process	*ATP7A, NGFR, FZD3, FZD6, INTU*	84	0.0595	0.000195
GO:0022405	17	hair cycle process	*ATP7A, NGFR, FZD3, FZD6, INTU*	84	0.0595	0.000195
GO:0050919	6	negative chemotaxis	*RYK, SEMA6B, PLXNA3, PLXNA4*	46	0.0870	0.000203
GO:0051960	12	regulation of nervous system development	*HAPLN1, PCM1, RYK, FZD3, SEMA6B, DAAM2, PLXNA3, PLXNA4, HAPLN3, AMIGO3, HAPLN4*	468	0.0235	0.000204
GO:0050767	12	regulation of neurogenesis	*HAPLN1, PCM1, RYK, FZD3, SEMA6B, DAAM2, PLXNA3, PLXNA4, HAPLN3, HAPLN4*	393	0.0254	0.000212
GO:0099054	11	presynapse assembly	*DVL1, FZD1, CNTN5*	19	0.1579	0.000222
GO:0006874	20	intracellular calcium ion homeostasis	*ATP7B, HRC, SLC30A1, FZD9, SLC24A1, ATP13A3, TMEM178A*	200	0.0350	0.000292
GO:0001764	13	neuron migration	*CELSR2, PCM1, FZD3, CELSR1, ADGRL3, PLXNA3*	142	0.0423	0.000293
GO:0120032	17	regulation of plasma membrane bounded cell projection assembly	*ATP7A, DAAM2, SH3YL1, INTU, WDPCP, CEP120, MAPK15*	204	0.0343	0.000329
GO:1902692	12	regulation of neuroblast proliferation	*HAPLN1, FZD3, HAPLN3, HAPLN4*	53	0.0755	0.000353
GO:0042303	17	molting cycle	*ATP7A, NGFR, FZD3, FZD6, INTU*	96	0.0521	0.000364
GO:0042633	17	hair cycle	*ATP7A, NGFR, FZD3, FZD6, INTU*	96	0.0521	0.000364
GO:0090103	1	cochlea morphogenesis	*DVL1, FZD2, PTK7*	24	0.1250	0.000453
GO:0071294	5	cellular response to zinc ion	*MT1A, MT2A, MTF1*	24	0.1250	0.000453

Terms	Group	Description	Symbols	Pathway size	Gene ratio	*P* value
GO:1905515	9	non-motile cilium assembly	*PCM1, INTU, VANGL2, CEP290*	57	0.0702	0.000466
GO:0061351	1	neural precursor cell proliferation	*PCM1, FZD3, FZD6, FZD9, CEP120*	103	0.0485	0.000503
GO:0099172	11	presynapse organization	*DVL1, FZD1, CNTN5*	25	0.1200	0.000513
GO:0062009	1	secondary palate development	*FZD2, WNT11, FZD1*	26	0.1154	0.000577
GO:0071280	5	cellular response to copper ion	***ATP7A***, *MT1A, MT2A*	26	0.1154	0.000577
GO:0055074	20	calcium ion homeostasis	*ATP7B, HRC, SLC30A1, FZD9, SLC24A1, ATP13A3, TMEM178A*	227	0.0308	0.000622
GO:0007156	13	homophilic cell adhesion via plasma membrane adhesion molecules	*CELSR3, CELSR2, PTK7, CELSR1, PCDH11X, FAT4*	167	0.0359	0.000691
GO:0048843	6	negative regulation of axon extension involved in axon guidance	*RYK, SEMA6B, PLXNA3*	28	0.1071	0.000720
GO:0098703	19	calcium ion import across plasma membrane	*CACNA1F, TRPM1, SLC24A1*	28	0.1071	0.000720
hsa04744	4	Phototransduction	*GNAT1, GRK1, SLC24A1*	29	0.1034	0.000800
GO:1902656	19	calcium ion import into cytosol	*CACNA1F, TRPM1, SLC24A1*	29	0.1034	0.000800
GO:0071482	4	cellular response to light stimulus	*GNAT1, TRPM1, GRK1, RS1, RRH*	115	0.0435	0.000829
GO:0098773	17	skin epidermis development	***ATP7A***, ***NGFR***, *FZD3, FZD6, INTU*	115	0.0435	0.000829
GO:0071300	18	cellular response to retinoic acid	*LTK, PTK7, WNT11, FZD7*	68	0.0588	0.000911

Terms	**Group**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0021602	6	cranial nerve morphogenesis	*HOXD3, PLXNA3, PLXNA4*	31	0.0968	0.000974
GO:0045926	6	negative regulation of growth	*MT1A, MT2A, RYK, STK4, WNT11, SEMA6B, PLXNA3*	247	0.0283	0.001019
GO:0031069	17	hair follicle morphogenesis	***ATP7A***, ***NGFR***, *INTU*	33	0.0909	0.001172
GO:0003281	1	ventricular septum development	*FZD2, PTK7, WNT11, FZD1*	74	0.0541	0.001250
GO:1902017	17	regulation of cilium assembly	*INTU, WDPCP, CEP120, MAPK15*	74	0.0541	0.001250
GO:0003231	1	cardiac ventricle development	*COL11A1, FZD2, PTK7, WNT11, FZD1*	127	0.0394	0.001293
GO:0060271	9	cilium assembly	*CELSR2, PCM1, OFD1, INTU, WDPCP, CEP83, VANGL2, CEP290*	336	0.0238	0.001385
GO:0040007	18	growth	*DVL1, GNAT1, PTK7, RYK, STK4, WNT11, FZD7, FZD9, PLXNA3*	424	0.0212	0.001563
GO:0048589	18	developmental growth	*DVL1, GNAT1, PTK7, RYK, STK4, WNT11, FZD7, FZD9, PLXNA3*	424	0.0212	0.001563
GO:0071276	5	cellular response to cadmium ion	***ATP7A***, *MT1A, MT2A*	37	0.0811	0.001638
GO:0048730	17	epidermis morphogenesis	***ATP7A***, ***NGFR***, *INTU*	37	0.0811	0.001638
GO:0003151	1	outflow tract morphogenesis	*DVL1, FZD2, WNT11, FZD1*	80	0.0500	0.001668
GO:0120031	9	plasma membrane bounded cell projection assembly	*CELSR2, PCM1, OFD1, INTU, RHOD, WDPCP, CEP83, VANGL2, CEP290*	431	0.0209	0.001747
GO:0060560	18	developmental growth involved in morphogenesis	*DVL1, PTK7, RYK, WNT11, PLXNA3*	137	0.0365	0.001806

Terms	Group	Description	Symbols	Pathway size	Gene ratio	*P* value
GO:0010038	5	response to metal ion	***ATP7A***, *ATP7B, MT1A, MT2A, MTF1, PAM, SLC30A1, SLC30A4*	360	0.0222	0.002130
GO:0030031	9	cell projection assembly	*CELSR2, PCM1, OFD1, INTU, RHOD, WDPCP, CEP83, VANGL2, CEP290*	444	0.0203	0.002135
GO:0071526	6	semaphorin-plexin signaling pathway	*SEMA6B, PLXNA3, PLXNA4*	41	0.0732	0.002207
GO:0030901	1	midbrain development	*RYK, FZD3, FZD1, FZD6*	88	0.0455	0.002366
GO:0044782	9	cilium organization	*CELSR2, PCM1, OFD1, INTU, WDPCP, CEP83, VANGL2, CEP290*	368	0.0217	0.002438
GO:0010721	6	negative regulation of cell development	*PCM1, RYK, SEMA6B, DAAM2, TMEM176A, PLXNA3, TMEM178A*	288	0.0243	0.002439
GO:0060412	1	ventricular septum morphogenesis	*FZD2, WNT11, FZD1*	43	0.0698	0.002531
GO:0050768	6	negative regulation of neurogenesis	*PCM1, RYK, SEMA6B, DAAM2, PLXNA3*	149	0.0336	0.002603
GO:0051962	12	positive regulation of nervous system development	*HAPLN1, FZD3, PLXNA3, PLXNA4, HAPLN3, AMIGO3, HAPLN4*	294	0.0238	0.002735
GO:0030516	6	regulation of axon extension	*RYK, SEMA6B, PLXNA3, PLXNA4*	92	0.0435	0.002780
GO:0030517	6	negative regulation of axon extension	*RYK, SEMA6B, PLXNA3*	46	0.0652	0.003071
GO:0048483	6	autonomic nervous system development	*FZD3, PLXNA3, PLXNA4*	46	0.0652	0.003071
hsa00860	10	Porphyrin metabolism	*CP, HEPH, HEPHL1*	46	0.0652	0.003071
GO:0048675	18	axon extension	*DVL1, RYK, PLXNA3*	46	0.0652	0.003071
GO:0051961	6	negative regulation of nervous system development	*PCM1, RYK, SEMA6B, DAAM2, PLXNA3*	155	0.0323	0.003085

Terms	**Group**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0021675	6	nerve development	*HOXD3*, ***NGFR***, *PLXNA3, PLXNA4*	97	0.0412	0.003364
GO:0010976	6	positive regulation of neuron projection development	*DVL1, LTK, PTK7, FZD1, ALKAL2*	161	0.0311	0.003628
GO:0042073	17	intraciliary transport	*PCM1, INTU, WDPCP*	49	0.0612	0.003676
GO:0090102	1	cochlea development	*DVL1, FZD2, PTK7*	50	0.0600	0.003892
GO:0003205	1	cardiac chamber development	*COL11A1, FZD2, PTK7, WNT11, FZD1*	168	0.0298	0.004345
GO:0030900	6	forebrain development	***ATP7A***, *PCM1, RYK, SEMA6B, PLXNA3, FAT4, PLXNA4, CEP120*	407	0.0197	0.004475
GO:0045197	18	establishment or maintenance of epithelial cell apical/basal polarity	*PTK7, WNT11, PDZD11*	53	0.0566	0.004588
GO:0032526	18	response to retinoic acid	*LTK, PTK7, WNT11, FZD7*	106	0.0377	0.004617
GO:0071478	4	cellular response to radiation	*GNAT1, TRPM1, GRK1, RS1, RRH*	172	0.0291	0.004797
GO:0006826	10	iron ion transport	*CP, HEPH, HEPHL1*	54	0.0556	0.004836
GO:0050769	12	positive regulation of neurogenesis	*HAPLN1, FZD3, PLXNA3, PLXNA4, HAPLN3, HAPLN4*	246	0.0244	0.004840
GO:0022604	15	regulation of cell morphogenesis	*DVL1, DVL3, NTNG1, WDPCP, PLXNA3, PLXNA4*	246	0.0244	0.004840
GO:0003279	1	cardiac septum development	*FZD2, PTK7, WNT11, FZD1*	108	0.0370	0.004933
GO:0061387	6	regulation of extent of cell growth	*RYK, SEMA6B, PLXNA3, PLXNA4*	109	0.0367	0.005096
GO:1901800	15	positive regulation of proteasomal protein catabolic process	*CSNK1E, DVL1, NKD2, TMEM259*	109	0.0367	0.005096

Terms	**Group**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0008544	17	epidermis development	***ATP7A***, ***NGFR***, *STK4, FZD3, FZD6, INTU, WDPCP*	335	0.0209	0.005557
GO:0035088	18	establishment or maintenance of apical/basal cell polarity	*PTK7, WNT11, PDZD11*	57	0.0526	0.005627
GO:0061245	18	establishment or maintenance of bipolar cell polarity	*PTK7, WNT11, PDZD11*	57	0.0526	0.005627
GO:0042733	17	embryonic digit morphogenesis	*FZD6, INTU, WDPCP*	58	0.0517	0.005906
GO:0048640	6	negative regulation of developmental growth	*RYK, STK4, SEMA6B, PLXNA3*	114	0.0351	0.005966
GO:0051480	20	regulation of cytosolic calcium ion concentration	*HRC, FZD9, TMEM178A*	59	0.0508	0.006194
GO:0003007	1	heart morphogenesis	*COL11A1, DVL1, FZD2, WNT11, FZD1, VANGL2*	263	0.0228	0.006651
GO:0008361	6	regulation of cell size	***ATP7A***, *RYK, SEMA6B, PLXNA3, PLXNA4*	188	0.0266	0.006942
GO:0061136	15	regulation of proteasomal protein catabolic process	*CSNK1E, DVL1, RYBP, NKD2, TMEM259*	189	0.0265	0.007095
GO:0021545	6	cranial nerve development	*HOXD3, PLXNA3, PLXNA4*	64	0.0469	0.007759
GO:0030198	14	extracellular matrix organization	***ATP7A***, *COL11A1, MATN3, KAZALD1, EGFLAM, COL22A1*	274	0.0219	0.008057
GO:0021537	6	telencephalon development	*RYK, SEMA6B, PLXNA3, FAT4, PLXNA4, CEP120*	275	0.0218	0.008195
GO:0043062	14	extracellular structure organization	***ATP7A***, *COL11A1, MATN3, KAZALD1, EGFLAM, COL22A1*	275	0.0218	0.008195
GO:0032434	15	regulation of proteasomal ubiquitin-dependent protein catabolic process	*CSNK1E, DVL1, RYBP, NKD2*	125	0.0320	0.008215

Terms	**Group**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0045229	14	external encapsulating structure organization	***ATP7A***, *COL11A1, MATN3, KAZALD1, EGFLAM, COL22A1*	276	0.0217	0.008335
GO:0050771	6	negative regulation of axonogenesis	*RYK, SEMA6B, PLXNA3*	66	0.0455	0.008444
GO:0003206	1	cardiac chamber morphogenesis	*COL11A1, FZD2, WNT11, FZD1*	127	0.0315	0.008676
GO:0043588	17	skin development	***ATP7A***, ***NGFR***, *STK4, FZD3, FZD6, INTU*	279	0.0215	0.008763
GO:1903052	15	positive regulation of proteolysis involved in protein catabolic process	*CSNK1E, DVL1, NKD2, TMEM259*	131	0.0305	0.009648
GO:0050922	6	negative regulation of chemotaxis	*RYK, SEMA6B, PLXNA3*	70	0.0429	0.009917

Pathways were restricted to sizes 10–500 genes and retained at an adjusted $P < 0.01$. “Group” indexes correspond to Metascape clusters. Gene ratio denotes input hits divided by pathway size.

Abbreviations: Gene ratio, fraction of input genes annotated to a pathway; GO, Gene Ontology; GO BP, Gene Ontology Biological Process; KEGG, Kyoto Encyclopedia of Genes and Genomes; PPI, protein–protein interaction; TB, tumor budding; TNBC, triple-negative breast cancer.

Table S4. Pathways enriched from *NGFR*/*EDIL3* seed-based network diffusion

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
M153	1	Canonical Pathways	PID P75 NTR PATHWAY	*ARHGDIA, BAD, MAG, NDN, NGF,* ***NGFR****, NTF3, NTF4, OMG, SORT1, SMPD2, ADAM17, RIPK2, MAGED1, ZNF274, PRDM4, NCSTN, BEX3, MAGEH1, APH1A, PSENEN, BEX1, RTN4, RTN4R, APH1B*	68	0.36764706	3.20E-38
hsa04151	2	KEGG Pathway	PI3K-Akt signaling pathway	*ANGPT1, ANGPT2, BAD, COL4A1, COL9A1, COL9A2, COL9A3, COMP, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, EGF, EREG, FGF1, VEGFD, GDNF, ITGA9, ITGAV, ITGB3, ITGB5, NGF,* ***NGFR****, NTF3, NTF4, NTRK2, PDGFA, PDGFB, PGF, VEGFB, VEGFC, VTN, FGF23, MAGI1, FGF19, FGF21, ANGPT4, PDGFC, PDGFD*	362	0.11049724	5.04E-38
WP4172	2	WikiPathways	PI3K Akt signaling	*ANGPT1, ANGPT2, BAD, COL4A1, COL9A1, COL9A2, COL9A3, COMP, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, EGF, FGF1, VEGFD, ITGA9, ITGAV, ITGB3, ITGB5, NGF,* ***NGFR****, NTF3, NTF4, NTRK2, PDGFA, PDGFB, PGF, VEGFB, VEGFC, VTN, FGF23, FGF19, FGF21, ANGPT4, PDGFC, PDGFD*	340	0.10882353	6.49E-35
GO:0007169	2	GO Biological Processes	cell surface receptor protein tyrosine kinase signaling pathway	*ANGPT1, ANGPT2, COL4A1, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, EGF, EREG, FGF1, VEGFD, GDNF, GFRA1, GFRA2, HCK, ITGB3, NDN, NGF,* ***NGFR****, NTF3, NTF4, NTRK2, NTRK3, PDGFA, PDGFB, PGF, SORT1, ADAM17, VEGFB, VEGFC, FGF23, TRADD, FGF19, SHC2, FGF21, SHC3, PDGFC, PDGFD, SHC4*	453	0.08830022	4.04E-34
hsa04014	2	KEGG Pathway	Ras signaling pathway	*ANGPT1, ANGPT2, BAD, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, EGF, FGF1, VEGFD, NGF,* ***NGFR****, NTF3, NTF4, NTRK2, PDGFA, PDGFB, PGF, STK4, VEGFB, VEGFC, FGF23, FGF19, SHC2, FGF21, ANGPT4, SHC3, PDGFC, PDGFD, SHC4*	238	0.1302521	9.17E-32

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
hsa04010	2	KEGG Pathway	MAPK signaling pathway	*ANGPT1, ANGPT2, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, EGF, EREG, FGF1, VEGFD, GDNF, MEF2C, NGF,* ***NGFR****, NTF3, NTF4, NTRK2, PDGFA, PDGFB, PGF, STK4, VEGFB, VEGFC, MAP3K12, FGF23, TRADD, FGF19, FGF21, IRAK4, ANGPT4, PDGFC, PDGFD*	300	0.11	2.58E-31
WP3932	2	WikiPathways	Focal adhesion PI3K Akt mTOR signaling	*ANGPT1, ANGPT2, BAD, COL4A1, COL11A1, COMP, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, EGF, FGF1, VEGFD, ITGA9, ITGAV, ITGB2, ITGB3, ITGB5, NGF,* ***NGFR****, PDGFA, PDGFB, PGF, VEGFB, VEGFC, VTN, FGF19, FGF21, ANGPT4, PDGFC, PDGFD*	304	0.10526316	9.24E-30
hsa04722	3	KEGG Pathway	Neurotrophin signaling pathway	*ARHGDIA, ARHGDIB, ARHGDIG, BAD, IRAK2, NGF,* ***NGFR****, NTF3, NTF4, NTRK2, NTRK3, SORT1, RIPK2, MAGED1, ZNF274, PRDM4, IRAK3, SHC2, BEX3, IRAK4, SHC3, KIDINS220, SHC4*	120	0.19166667	8.14E-28
hsa04015	2	KEGG Pathway	Rap1 signaling pathway	*ANGPT1, ANGPT2, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, EGF, FGF1, VEGFD, ITGB2, ITGB3, NGF,* ***NGFR****, PDGFA, PDGFB, PGF, VEGFB, VEGFC, FGF23, MAGI1, FGF19, FGF21, ANGPT4, PDGFC, PDGFD*	212	0.12264151	4.77E-26
R-HSA-193704	1	Reactome Gene Sets	p75 NTR receptor-mediated signalling	*ARHGDIA, BAD, CASP2, MAG, NGF, OMG, SMPD2, ADAM17, RIPK2, MAGED1, PRDM4, NCSTN, ITGB3BP, BEX3, APH1A, PSENEN, RTN4, RTN4R, APH1B, LINGO1*	94	0.21276596	2.68E-25
WP5087	2	WikiPathways	Pleural mesothelioma	*ANGPT1, ANGPT2, COL4A1, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, EGF, FGF1, VEGFD, ITGAV, ITGB2, ITGB3, MDK, NGF,* ***NGFR****, NTF3, NTF4, NTRK2, PDGFA, PDGFB, PGF, VEGFB, VEGFC, FGF23, FGF19, FGF21, ANGPT4, PDGFC, PDGFD, RASSF4*	439	0.07289294	1.01E-24

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
hsa04510	2	KEGG Pathway	Focal adhesion	*BAD, COL4A1, COL9A1, COL9A2, COL9A3, COMP, EGF, VEGFD, ITGA9, ITGAV, ITGB3, ITGB5, PDGFA, PDGFB, PGF, VEGFB, VEGFC, VTN, SHC2, SHC3, PDGFC, PDGFD, SHC4*	203	0.11330049	2.44E-22
R-HSA-73887	1	Reactome Gene Sets	Death Receptor Signaling	*ARHGDIA, BAD, CASP2, MAG, NGF, OMG, SMPD2, ADAM17, RIPK2, MAGED1, PRDM4, NCSTN, ITGB3BP, BEX3, APH1A, PSENEN, RTN4, RTN4R, APH1B, LINGO1*	132	0.15151515	3.76E-22
WP306	2	WikiPathways	Focal adhesion	*BAD, COL4A1, COMP, EGF, VEGFD, HCK, ITGA9, ITGAV, ITGB3, ITGB5, PDGFA, PDGFB, PGF, VEGFB, VEGFC, VTN, SHC2, SHC3, PDGFC, PDGFD, SHC4*	199	0.10552764	7.88E-20
M5883	2	Canonical Pathways	NABA SECRETED FACTORS	*ANGPT1, ANGPT2, CNTF, EGF, EREG, FGF1, VEGFD, GDNF, IL17A, MDK, NGF, NTF3, NTF4, PDGFA, PDGFB, PGF, VEGFB, VEGFC, FGF23, FGF19, FGF21, ANGPT4, PDGFC, PDGFD*	343	0.06997085	2.57E-18
GO:0043410	2	GO Biological Processes	positive regulation of MAPK cascade	*ANGPT1, EFNA1, EGF, FGF1, GAS6, ICAM1, ITGB3, MEF2C, NGF, NTF3, NTRK2, NTRK3, PDGFA, PDGFB, VEGFB, MAP3K12, FGF23, RIPK2, TRAF4, FGF19, EDAR, FGF21, TNFRSF19, PDGFC, EDA2R, PDGFD*	474	0.05485232	3.61E-17
GO:0048514	2	GO Biological Processes	blood vessel morphogenesis	*ANGPT1, ANGPT2, COL4A1, COMP, EFNA1, EGF, EREG, FGF1, VEGFD, RBPJ, ITGAV, ITGB3, MFGE8, NRCAM, NTRK2, PDGFA, PDGFB, PGF, STK4, TGFBR3, VEGFB, VEGFC, ANGPT4, RTN4*	445	0.05393258	9.36E-16
R-HSA-3000178	5	Reactome Gene Sets	ECM proteoglycans	*COL4A1, COL9A1, COL9A2, COL9A3, COMP, HAPLN1, ITGA9, ITGAV, ITGB3, ITGB5, MATN1, MATN3, VTN*	76	0.17105263	1.59E-15
GO:0001525	2	GO Biological Processes	angiogenesis	*ANGPT1, ANGPT2, COL4A1, EFNA1, EGF, EREG, FGF1, VEGFD, RBPJ, ITGAV, ITGB3, MFGE8, NRCAM, PDGFA, PDGFB, PGF, STK4, VEGFB, VEGFC, ANGPT4, RTN4*	352	0.05965909	8.98E-15

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
WP2380	3	WikiPathways	Brain derived neurotrophic factor BDNF signaling	*BAD, MEF2C, NGF,* ***NGFR****, NTF3, NTRK2, NTRK3, SORT1, ADAM17, RANBP9, SHC2, SHC3, KIDINS220, LINGO1, SHC4*	137	0.10948905	9.88E-15
R-HSA-1474244	5	Reactome Gene Sets	Extracellular matrix organization	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1, COMP, HAPLN1, ICAM1, ITGA9, ITGAV, ITGB2, ITGB3, ITGB5, MATN1, MATN3, PDGFA, PDGFB, ADAM17, VTN, NCSTN*	318	0.06289308	1.49E-14
hsa04020	2	KEGG Pathway	Calcium signaling pathway	*EGF, FGF1, VEGFD, GDNF, HRC, NGF, NTRK2, NTRK3, NTSR1, PDGFA, PDGFB, VEGFB, VEGFC, FGF23, FGF19, FGF21, PDGFC, PDGFD*	254	0.07086614	4.23E-14
GO:0038179	3	GO Biological Processes	neurotrophin signaling pathway	*GFRA1, NDN, NGF, NTF3, NTF4, NTRK2, NTRK3, SORT1, KIDINS220*	28	0.32142857	7.49E-14
GO:0001934	7	GO Biological Processes	positive regulation of protein phosphorylation	*ANGPT1, CNTF, EFNA1, EFNA5, EGF, EREG, FGF1, GAS6, PDGFA, PDGFB, STK4, VEGFB, RIPK2, TRAF4, FGF19, SEMA4D, ANGPT4*	231	0.07359307	1.19E-13
R-HSA-216083	5	Reactome Gene Sets	Integrin cell surface interactions	*COL4A1, COL9A1, COL9A2, COL9A3, COMP, ICAM1, ITGA9, ITGAV, ITGB2, ITGB3, ITGB5, VTN*	84	0.14285714	1.91E-13
GO:0070374	2	GO Biological Processes	positive regulation of ERK1 and ERK2 cascade	*ANGPT1, FGF1, GAS6, ICAM1, ITGB3, NGF, PDGFA, PDGFB, VEGFB, MAP3K12, FGF23, RIPK2, FGF19, FGF21, PDGFC, PDGFD*	201	0.07960199	1.92E-13
GO:0042327	7	GO Biological Processes	positive regulation of phosphorylation	*ANGPT1, CNTF, EFNA1, EFNA5, EGF, EREG, FGF1, GAS6, PDGFA, PDGFB, STK4, VEGFB, RIPK2, TRAF4, FGF19, SEMA4D, ANGPT4*	254	0.06692913	5.60E-13
GO:0051897	2	GO Biological Processes	positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	*ANGPT1, EFNA5, EGF, GAS6, IL17A, NGF, NTF3, NTRK2, NTRK3, PDGFA, PDGFB, VEGFB, SEMA4D, PDGFC, RTN4, PDGFD*	217	0.07373272	6.27E-13

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
GO:0061564	4	GO Biological Processes	axon development	*ALCAM, CNP, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, GDNF, MAG, NDN, NGF,* ***NGFR****, NRCAM, NTRK3, ADAM17, SEMA4D, TNFRSF21, PLXNA3, PRDM8, RTN4, RTN4R*	441	0.04761905	7.18E-13
GO:0070372	2	GO Biological Processes	regulation of ERK1 and ERK2 cascade	*ANGPT1, CRYBA1, FGF1, GAS6, ICAM1, ITGB3, NGF, PDGFA, PDGFB, VEGFB, MAP3K12, FGF23, RIPK2, FGF19, RANBP9, FGF21, PDGFC, PDGFD*	303	0.05940594	8.61E-13
GO:0006935	2	GO Biological Processes	chemotaxis	*ANGPT1, EFNA5, VEGFD, GAS6, GDNF, HOXB9, ITGA9, ITGAV, ITGB2, ITGB3, MDK, NTF3, PDGFA, PDGFB, PGF, VEGFB, VEGFC, SEMA4D, PLXNA3*	350	0.05428571	9.59E-13
GO:0042330	2	GO Biological Processes	taxis	*ANGPT1, EFNA5, VEGFD, GAS6, GDNF, HOXB9, ITGA9, ITGAV, ITGB2, ITGB3, MDK, NTF3, PDGFA, PDGFB, PGF, VEGFB, VEGFC, SEMA4D, PLXNA3*	352	0.05397727	1.06E-12
GO:0010562	7	GO Biological Processes	positive regulation of phosphorus metabolic process	*ANGPT1, CNTF, EFNA1, EFNA5, EGF, EREG, FGF1, GAS6, NTSR1, PDGFA, PDGFB, STK4, VEGFB, RIPK2, TRAF4, FGF19, SEMA4D, ANGPT4*	320	0.05625	2.16E-12
GO:0045937	7	GO Biological Processes	positive regulation of phosphate metabolic process	*ANGPT1, CNTF, EFNA1, EFNA5, EGF, EREG, FGF1, GAS6, NTSR1, PDGFA, PDGFB, STK4, VEGFB, RIPK2, TRAF4, FGF19, SEMA4D, ANGPT4*	320	0.05625	2.16E-12
GO:0050678	8	GO Biological Processes	regulation of epithelial cell proliferation	*BAD, EGF, EREG, FGF1, RBPJ, IL17A, ITGB3, MDK, MEF2C,* ***NGFR****, PDGFB, STK4, ADAM17, TGFBR3, VEGFB, VEGFC, MAGED1, CNMD, ITGB3BP, RTN4*	416	0.04807692	2.19E-12
GO:0040011	2	GO Biological Processes	locomotion	*ANGPT1, EFNA5, VEGFD, GAS6, GDNF, HOXB9, ITGA9, ITGAV, ITGB2, ITGB3, MDK, NTF3, PDGFA, PDGFB, PGF, VEGFB, VEGFC, SEMA4D, PLXNA3*	376	0.05053192	3.37E-12

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
R-HSA-2219528	9	Reactome Gene Sets	PI3K/AKT Signaling in Cancer	*BAD, EGF, EREG, FGF1, NTF3, NTF4, NTRK2, NTRK3, PDGFA, PDGFB, FGF23, FGF19*	112	0.10714286	6.41E-12
R-HSA-2219530	9	Reactome Gene Sets	Constitutive Signaling by Aberrant PI3K in Cancer	*EGF, EREG, FGF1, NTF3, NTF4, NTRK2, NTRK3, PDGFA, PDGFB, FGF23, FGF19*	86	0.12790698	6.91E-12
R-HSA-6811558	9	Reactome Gene Sets	PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	*EGF, EREG, FGF1, NTF3, NTF4, NTRK2, NTRK3, PDGFA, PDGFB, FGF23, FGF19, IRAK4*	114	0.10526316	7.93E-12
GO:0051896	2	GO Biological Processes	regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	*ANGPT1, CRYBA1, EFNA5, EGF, GAS6, IL17A, NGF, NTF3, NTRK2, NTRK3, PDGFA, PDGFB, VEGFB, SEMA4D, PDGFC, RTN4, PDGFD*	311	0.05466238	1.42E-11
R-HSA-199418	9	Reactome Gene Sets	Negative regulation of the PI3K/AKT network	*EGF, EREG, FGF1, NTF3, NTF4, NTRK2, NTRK3, PDGFA, PDGFB, FGF23, FGF19, IRAK4*	121	0.09917355	1.62E-11
GO:0048667	4	GO Biological Processes	cell morphogenesis involved in neuron differentiation	*ALCAM, CNP, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, GDNF, MEF2C, NDN, NGF,* ***NGFR****, NRCAM, NTRK3, ADAM17, SEMA4D, PLXNA3, PRDM8, KIDINS220, RTN4R*	465	0.04301075	1.64E-11
M5884	10	Canonical Pathways	NABA CORE MATRISOME	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1, COMP, HAPLN1, GAS6, MATN1, MATN3, MFGE8, VTN, CILP,* ***EDIL3****, HAPLN3, CILP2*	275	0.05818182	2.29E-11
R-HSA-3928665	4	Reactome Gene Sets	EPH-ephrin mediated repulsion of cells	*EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, NCSTN, APH1A, PSENEN, APH1B*	51	0.17647059	2.92E-11
GO:0031401	7	GO Biological Processes	positive regulation of protein modification process	*ANGPT1, CNTF, EFNA1, EFNA5, EGF, EREG, FGF1, GAS6, NGF, PDGFA, PDGFB, STK4, VEGFB, RIPK2, TRAF4, FGF19, SEMA4D, ANGPT4*	375	0.048	2.99E-11
hsa05218	9	KEGG Pathway	Melanoma	*BAD, EGF, FGF1, PDGFA, PDGFB, FGF23, FGF19, FGF21, PDGFC, PDGFD*	73	0.1369863	3.16E-11

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
R-HSA-204998	11	Reactome Gene Sets	Cell death signalling via NRAGE, NRIF and NADE	*BAD, CASP2, NGF, MAGED1, NCSTN, ITGB3BP, BEX3, APH1A, PSENEN, APH1B*	73	0.1369863	3.16E-11
GO:0051781	12	GO Biological Processes	positive regulation of cell division	*EREG, FGF1, VEGFD, MDK, PDGFA, PDGFB, PGF, VEGFB, VEGFC, PDGFC, PDGFD*	99	0.11111111	3.32E-11
M160	5	Canonical Pathways	PID AVB3 INTEGRIN PATHWAY	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1, ITGAV, ITGB3, MFGE8, VTN,* ***EDIL3***	74	0.13513514	3.64E-11
GO:0007409	4	GO Biological Processes	axonogenesis	*ALCAM, CNP, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, GDNF, NDN, NGF,* ***NGFR****, NRCAM, NTRK3, ADAM17, SEMA4D, PLXNA3, PRDM8, RTN4R*	383	0.04699739	4.23E-11
GO:0001932	7	GO Biological Processes	regulation of protein phosphorylation	*ANGPT1, CNTF, EFNA1, EFNA5, EGF, EREG, FGF1, GAS6, ITGB2, PDGFA, PDGFB, STK4, VEGFB, RIPK2, TRAF4, FGF19, SEMA4D, ANGPT4*	387	0.04651163	5.01E-11
R-HSA-5663202	9	Reactome Gene Sets	Diseases of signal transduction by growth factor receptors and second messengers	*BAD, EGF, EREG, FGF1, RBPJ, ITGB3, NTF3, NTF4, NTRK2, NTRK3, PDGFA, PDGFB, ADAM17, FGF23, FGF19, NCSTN, APH1A, PSENEN, APH1B*	452	0.0420354	8.00E-11
hsa01521	13	KEGG Pathway	EGFR tyrosine kinase inhibitor resistance	*BAD, EGF, GAS6, PDGFA, PDGFB, SHC2, SHC3, PDGFC, PDGFD, SHC4*	80	0.125	8.07E-11
GO:0050920	12	GO Biological Processes	regulation of chemotaxis	*ANGPT2, FGF1, VEGFD, GAS6, MDK, NTF3, NTRK3, PDGFB, PGF, ADAM17, VEGFB, VEGFC, PLXNA3, PDGFD*	214	0.06542056	9.03E-11
WP4806	13	WikiPathways	EGFR tyrosine kinase inhibitor resistance	*BAD, EGF, GAS6, PDGFA, PDGFB, SHC2, SHC3, PDGFC, PDGFD, SHC4*	84	0.11904762	1.33E-10
GO:0043524	15	GO Biological Processes	negative regulation of neuron apoptotic process	*ANGPT1, CNTF, CNTFR, GDNF, MAG, MDK, MEF2C, NGF, NTF3, NTF4, NTRK2, VEGFB, MAP3K12*	181	0.0718232	1.36E-10

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
R-HSA-5673001	9	Reactome Gene Sets	RAF/MAP kinase cascade	*ANGPT1, EGF, EREG, FGF1, GDNF, GFRA1, GFRA2, ITGB3, PDGFA, PDGFB, FGF23, FGF19, RANBP9, SHC2, SHC3*	266	0.05639098	1.53E-10
M187	3	Canonical Pathways	PID TRKR PATHWAY	*NGF, **NGFR**, NTF3, NTF4, NTRK2, NTRK3, MAGED1, SHC2, SHC3*	61	0.14754098	1.58E-10
GO:0050926	12	GO Biological Processes	regulation of positive chemotaxis	*ANGPT2, VEGFD, NTF3, NTRK3, PGF, VEGFB, VEGFC*	26	0.26923077	1.98E-10
R-HSA-5684996	9	Reactome Gene Sets	MAPK1/MAPK3 signaling	*ANGPT1, EGF, EREG, FGF1, GDNF, GFRA1, GFRA2, ITGB3, PDGFA, PDGFB, FGF23, FGF19, RANBP9, SHC2, SHC3*	272	0.05514706	2.08E-10
hsa04512	5	KEGG Pathway	ECM-receptor interaction	*COL4A1, COL9A1, COL9A2, COL9A3, COMP, ITGA9, ITGAV, ITGB3, ITGB5, VTN*	89	0.11235955	2.38E-10
hsa04810	9	KEGG Pathway	Regulation of actin cytoskeleton	*EGF, FGF1, ITGA9, ITGAV, ITGB2, ITGB3, ITGB5, PDGFA, PDGFB, FGF23, FGF19, FGF21, PDGFC, PDGFD*	232	0.06034483	2.62E-10
R-HSA-205043	11	Reactome Gene Sets	NRIF signals cell death from the nucleus	*NGF, NCSTN, ITGB3BP, APH1A, PSENEN, APH1B*	15	0.4	2.63E-10
GO:0042325	7	GO Biological Processes	regulation of phosphorylation	*ANGPT1, CNTF, EFNA1, EFNA5, EGF, EREG, FGF1, GAS6, ITGB2, PDGFA, PDGFB, STK4, VEGFB, RIPK2, TRAF4, FGF19, SEMA4D, ANGPT4*	431	0.04176334	2.86E-10
GO:0033627	16	GO Biological Processes	cell adhesion mediated by integrin	*ICAM1, ITGAV, ITGB2, ITGB3, ITGB5, ADAM17, VTN*	29	0.24137931	4.63E-10
WP382	9	WikiPathways	MAPK signaling	*EGF, FGF1, MEF2C, NGF, NTF3, NTF4, NTRK2, PDGFA, PDGFB, STK4, MAP3K12, FGF23, FGF19, FGF21*	247	0.05668016	5.96E-10
GO:0009611	17	GO Biological Processes	response to wounding	*ANGPT1, ANGPT2, CLIC1, COMP, EREG, FGF1, GAS6, IL17A, ITGAV, ITGB3, ITGB5, MAG, MDK, NTRK3, PDGFA, PDGFB, ADAM17, ANGPT4*	461	0.03904555	8.36E-10

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
R-HSA-5683057	9	Reactome Gene Sets	MAPK family signaling cascades	*ANGPT1, EGF, EREG, FGF1, GDNF, GFRA1, GFRA2, ITGB3, PDGFA, PDGFB, FGF23, FGF19, RANBP9, SHC2, SHC3*	311	0.04823151	1.32E-09
GO:0043523	15	GO Biological Processes	regulation of neuron apoptotic process	*ANGPT1, CASP2, CNTF, CNTFR, GDNF, MAG, MDK, MEF2C, NGF, NTF3, NTF4, NTRK2, VEGFB, MAP3K12*	264	0.0530303	1.42E-09
GO:1903034	18	GO Biological Processes	regulation of response to wounding	*ANGPT1, ANGPT2, CNTF, IL17A, MDK, NTRK3, PDGFA, PDGFB, ADAM17, VEGFB, VTN, RTN4R*	179	0.06703911	1.56E-09
GO:0050918	12	GO Biological Processes	positive chemotaxis	*ANGPT1, VEGFD, GDNF, NTF3, PDGFB, PGF, VEGFB, VEGFC*	54	0.14814815	1.63E-09
GO:0050679	8	GO Biological Processes	positive regulation of epithelial cell proliferation	*BAD, EGF, FGF1, RBPJ, IL17A, ITGB3, MDK, PDGFB, ADAM17, VEGFB, VEGFC, ITGB3BP, RTN4*	222	0.05855856	1.68E-09
WP5078	12	WikiPathways	T cell modulation and desmoplasia in pancreatic cancer	*VEGFD, PDGFA, PDGFB, PGF, VEGFB, VEGFC, PDGFC, PDGFD*	55	0.14545455	1.90E-09
GO:0050921	12	GO Biological Processes	positive regulation of chemotaxis	*VEGFD, GAS6, MDK, NTF3, NTRK3, PDGFB, PGF, ADAM17, VEGFB, VEGFC, PDGFD*	145	0.07586207	2.08E-09
M100	3	Canonical Pathways	PID SHP2 PATHWAY	*ANGPT1, EGF, NGF, NTF3, NTF4, NTRK2, NTRK3, PDGFB*	57	0.14035088	2.55E-09
WP5265	3	WikiPathways	Neurogenesis regulation in the olfactory epithelium	*IL17A, MEF2C, NGF,* ***NGFR****, NTRK2, NTRK3, RTN4, RTN4R*	57	0.14035088	2.55E-09
GO:0048146	13	GO Biological Processes	positive regulation of fibroblast proliferation	*EREG, GAS6, ITGB3,* ***NGFR****, PDGFA, PDGFB, PDGFC, PDGFD*	57	0.14035088	2.55E-09
R-HSA-186797	5	Reactome Gene Sets	Signaling by PDGF	*COL4A1, COL9A1, COL9A2, COL9A3, PDGFA, PDGFB, PDGFC, PDGFD*	58	0.13793103	2.95E-09

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
hsa05165	5	KEGG Pathway	Human papillomavirus infection	*BAD, COL4A1, COL9A1, COL9A2, COL9A3, COMP, EGF, RBPJ, ITGA9, ITGAV, ITGB3, ITGB5, VTN, TRADD, MAGI1*	333	0.04504505	3.35E-09
GO:0002687	12	GO Biological Processes	positive regulation of leukocyte migration	*VEGFD, GAS6, ICAM1, ITGB3, MDK, PGF, ADAM17, VEGFB, VEGFC, RTN4, PDGFD*	152	0.07236842	3.42E-09
GO:0097191	19	GO Biological Processes	extrinsic apoptotic signaling pathway	*BAD, CASP2, ITGAV, NGF,* ***NGFR****, SORT1, STK4, TRADD, SIVA1, BEX3*	117	0.08547009	3.58E-09
R-HSA-9839383	11	Reactome Gene Sets	TGFBR3 PTM regulation	*TGFBR3, NCSTN, APH1A, PSENEN, APH1B*	11	0.45454546	4.05E-09
R-HSA-2682334	4	Reactome Gene Sets	EPH-Ephrin signaling	*EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, NCSTN, APH1A, PSENEN, APH1B*	91	0.0989011	6.06E-09
R-HSA-419037	5	Reactome Gene Sets	NCAM1 interactions	*COL4A1, COL9A1, COL9A2, COL9A3, GDNF, GFRA1, GFRA2*	42	0.16666667	7.48E-09
GO:0050927	12	GO Biological Processes	positive regulation of positive chemotaxis	*VEGFD, NTF3, NTRK3, PGF, VEGFB, VEGFC*	25	0.24	8.83E-09
R-HSA-1257604	9	Reactome Gene Sets	PIP3 activates AKT signaling	*BAD, EGF, EREG, FGF1, NTF3, NTF4, NTRK2, NTRK3, PDGFA, PDGFB, FGF23, FGF19, IRAK4*	262	0.04961832	1.23E-08
R-HSA-166520	20	Reactome Gene Sets	Signaling by NTRKs	*MEF2C, NGF, NTF3, NTF4, NTRK2, NTRK3, PCSK6, SHC2, SHC3, KIDINS220*	133	0.07518797	1.24E-08
GO:0038180	3	GO Biological Processes	nerve growth factor signaling pathway	*NGF, NTF3, NTF4, SORT1, KIDINS220*	14	0.35714286	1.73E-08
GO:0050930	12	GO Biological Processes	induction of positive chemotaxis	*VEGFD, NTF3, PGF, VEGFB, VEGFC*	15	0.33333333	2.58E-08
GO:0007411	4	GO Biological Processes	axon guidance	*ALCAM, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, GDNF,* ***NGFR****, NRCAM, ADAM17, SEMA4D, PLXNA3*	233	0.05150215	3.02E-08

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
GO:1990090	3	GO Biological Processes	cellular response to nerve growth factor stimulus	*NGF, NTF3, NTF4, NTRK2, NTRK3, SORT1, KIDINS220*	51	0.1372549	3.06E-08
GO:0097485	4	GO Biological Processes	neuron projection guidance	*ALCAM, EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, GDNF,* ***NGFR****, NRCAM, ADAM17, SEMA4D, PLXNA3*	234	0.05128205	3.16E-08
GO:0051302	12	GO Biological Processes	regulation of cell division	*EREG, FGF1, VEGFD, MDK, PDGFA, PDGFB, PGF, VEGFB, VEGFC, PDGFC, PDGFD*	190	0.05789474	3.50E-08
GO:0050730	7	GO Biological Processes	regulation of peptidyl-tyrosine phosphorylation	*ANGPT1, CNTF, EFNA1, EFNA5, ITGB2, VEGFB, RIPK2, ANGPT4*	79	0.10126582	3.59E-08
GO:0010594	8	GO Biological Processes	regulation of endothelial cell migration	*ANGPT1, ANGPT2, EFNA1, EGF, FGF1, ITGB3, MEF2C, PDGFB, ADAM17, TGFBR3, VEGFC, ANGPT4*	239	0.05020921	3.99E-08
GO:0050731	7	GO Biological Processes	positive regulation of peptidyl-tyrosine phosphorylation	*ANGPT1, CNTF, EFNA1, EFNA5, VEGFB, RIPK2, ANGPT4*	53	0.13207547	4.03E-08
R-HSA-1251985	11	Reactome Gene Sets	Nuclear signaling by ERBB4	*EREG, ADAM17, NCSTN, APH1A, PSENEN, APH1B*	32	0.1875	4.36E-08
GO:1990089	3	GO Biological Processes	response to nerve growth factor	*NGF, NTF3, NTF4, NTRK2, NTRK3, SORT1, KIDINS220*	54	0.12962963	4.61E-08
GO:0042987	11	GO Biological Processes	amyloid precursor protein catabolic process	*ADAM17, NCSTN, APH1A, PSENEN, APH1B*	17	0.29411765	5.27E-08
GO:0007219	11	GO Biological Processes	Notch signaling pathway	*HOXD3, RBPJ, IL17A, ADAM17, NCSTN, APH1A, ANGPT4, PSENEN, APH1B*	118	0.07627119	5.99E-08
R-HSA-9006925	9	Reactome Gene Sets	Intracellular signaling by second messengers	*BAD, EGF, EREG, FGF1, NTF3, NTF4, NTRK2, NTRK3, PDGFA, PDGFB, FGF23, FGF19, IRAK4*	304	0.04276316	7.07E-08

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
R-HSA-1236394	11	Reactome Gene Sets	Signaling by ERBB4	*EGF, EREG, ADAM17, NCSTN, APH1A, PSENEN, APH1B*	58	0.12068966	7.66E-08
R-HSA-1980145	11	Reactome Gene Sets	Signaling by NOTCH2	*RBPJ, MDK, NCSTN, APH1A, PSENEN, APH1B*	35	0.17142857	7.69E-08
GO:0019221	14	GO Biological Processes	cytokine-mediated signaling pathway	*BAD, CNTF, CNTFR, EREG, HCK, IL17A, IRAK2, PDGFB, TRADD, RIPK2, EDAR, IRAK3, IRAK4, TNFRSF19, EDA2R*	427	0.03512881	9.00E-08
R-HSA-375165	5	Reactome Gene Sets	NCAM signaling for neurite out-growth	*COL4A1, COL9A1, COL9A2, COL9A3, GDNF, GFRA1, GFRA2*	63	0.11111111	1.37E-07
GO:0048145	13	GO Biological Processes	regulation of fibroblast proliferation	*EREG, GAS6, ITGB3,* ***NGFR****, PDGFA, PDGFB, PDGFC, PDGFD*	94	0.08510638	1.41E-07
GO:1903035	18	GO Biological Processes	negative regulation of response to wounding	*ANGPT1, ANGPT2, IL17A, MDK, PDGFA, PDGFB, VTN, RTN4R*	97	0.08247423	1.81E-07
GO:0010595	8	GO Biological Processes	positive regulation of endothelial cell migration	*ANGPT1, EGF, FGF1, ITGB3, PDGFB, ADAM17, TGFBR3, VEGFC, ANGPT4*	136	0.06617647	2.03E-07
M174	16	Canonical Pathways	PID UPA UPAR PATHWAY	*ITGAV, ITGB2, ITGB3, ITGB5, VTN, PDGFD*	42	0.14285714	2.40E-07
hsa04820	5	KEGG Pathway	Cytoskeleton in muscle cells	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1, COMP, ITGA9, ITGAV, ITGB3, ITGB5, PDLIM1*	232	0.04741379	2.65E-07
GO:0042060	17	GO Biological Processes	wound healing	*ANGPT1, ANGPT2, CLIC1, COMP, EREG, FGF1, GAS6, ITGAV, ITGB3, ITGB5, PDGFA, ADAM17, ANGPT4*	341	0.03812317	2.65E-07
GO:0002685	12	GO Biological Processes	regulation of leukocyte migration	*VEGFD, GAS6, ICAM1, ITGB3, MDK, PGF, ADAM17, VEGFB, VEGFC, RTN4, PDGFD*	233	0.0472103	2.76E-07

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
GO:0031589	16	GO Biological Processes	cell-substrate adhesion	*ANGPT1, EFNA1, GAS6, HOXD3, ITGA9, ITGAV, ITGB2, ITGB3, ITGB5, VTN*	185	0.05405405	2.81E-07
GO:0050919	16	GO Biological Processes	negative chemotaxis	*EFNA5, ITGAV, ITGB3, PDGFA, SEMA4D, PLXNA3*	44	0.13636364	3.19E-07
GO:0008625	19	GO Biological Processes	extrinsic apoptotic signaling pathway via death domain receptors	*BAD, NGF, SORT1, STK4, TRADD, BEX3*	45	0.13333333	3.66E-07
GO:0045766	8	GO Biological Processes	positive regulation of angiogenesis	*ANGPT2, FGF1, ITGB2, ITGB3, MDK, VEGFB, VEGFC, CLIC3, ANGPT4, RTN4*	191	0.05235602	3.78E-07
GO:0042982	11	GO Biological Processes	amyloid precursor protein metabolic process	*ADAM17, NCSTN, APH1A, PSENEN, APH1B*	25	0.2	4.34E-07
R-HSA-2979096	11	Reactome Gene Sets	NOTCH2 Activation and Transmission of Signal to the Nucleus	*MDK, NCSTN, APH1A, PSENEN, APH1B*	25	0.2	4.34E-07
R-HSA-9013507	11	Reactome Gene Sets	NOTCH3 Activation and Transmission of Signal to the Nucleus	*EGF, NCSTN, APH1A, PSENEN, APH1B*	25	0.2	4.34E-07
GO:1904018	8	GO Biological Processes	positive regulation of vasculature development	*ANGPT2, FGF1, ITGB2, ITGB3, MDK, VEGFB, VEGFC, CLIC3, ANGPT4, RTN4*	195	0.05128205	4.57E-07
R-HSA-9013700	11	Reactome Gene Sets	NOTCH4 Activation and Transmission of Signal to the Nucleus	*NCSTN, APH1A, PSENEN, APH1B*	11	0.36363636	4.71E-07
M47	16	Canonical Pathways	PID INTEGRIN CS PATHWAY	*ITGA9, ITGAV, ITGB2, ITGB3, ITGB5*	26	0.19230769	5.35E-07

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
WP2848	13	WikiPathways	Pluripotent stem cell differentiation pathway	*CNTF, EGF, FGF1, NTF4, PDGFA, PDGFB*	48	0.125	5.43E-07
GO:0045765	8	GO Biological Processes	regulation of angiogenesis	*ANGPT2, EFNA1, EFNA3, FGF1, ITGB2, ITGB3, MDK, VEGFB, VEGFC, CLIC3, CNMD, ANGPT4, RTN4*	365	0.03561644	5.72E-07
R-HSA-9012852	11	Reactome Gene Sets	Signaling by NOTCH3	*EGF, RBPJ, NCSTN, APH1A, PSENEN, APH1B*	49	0.12244898	6.16E-07
GO:1900047	18	GO Biological Processes	negative regulation of hemostasis	*ANGPT1, ANGPT2, COMP, PDGFA, PDGFB, VTN*	49	0.12244898	6.16E-07
GO:0031293	11	GO Biological Processes	membrane protein intracellular domain proteolysis	*NCSTN, APH1A, PSENEN, APH1B*	12	0.33333333	7.04E-07
GO:0043535	8	GO Biological Processes	regulation of blood vessel endothelial cell migration	*ANGPT1, ANGPT2, EFNA1, MEF2C, PDGFB, ADAM17, TGFBR3, VEGFC, ANGPT4*	159	0.05660377	7.64E-07
GO:1901342	8	GO Biological Processes	regulation of vasculature development	*ANGPT2, EFNA1, EFNA3, FGF1, ITGB2, ITGB3, MDK, VEGFB, VEGFC, CLIC3, CNMD, ANGPT4, RTN4*	375	0.03466667	7.74E-07
GO:0048013	4	GO Biological Processes	ephrin receptor signaling pathway	*EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, NTRK3*	51	0.11764706	7.85E-07
WP2431	6	WikiPathways	Spinal cord injury	*COL4A1, GDNF, ICAM1, MAG,* ***NGFR****, OMG, RTN4, RTN4R*	120	0.06666667	9.29E-07
R-HSA-3928663	4	Reactome Gene Sets	EPHA-mediated growth cone collapse	*EFNA1, EFNA2, EFNA3, EFNA4, EFNA5*	29	0.17241379	9.51E-07
WP61	11	WikiPathways	Notch signaling	*RBPJ, ADAM17, NCSTN, APH1A, PSENEN, APH1B*	54	0.11111111	1.11E-06
R-HSA-2122948	11	Reactome Gene Sets	Activated NOTCH1 Transmits Signal to the Nucleus	*ADAM17, NCSTN, APH1A, PSENEN, APH1B*	31	0.16129032	1.35E-06

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
WP322	16	WikiPathways	Osteoblast signaling	*ITGAV, ITGB3, PDGFB, FGF23*	14	0.28571429	1.41E-06
GO:0014910	13	GO Biological Processes	regulation of smooth muscle cell migration	*ITGB3, MDK, MEF2C, PDGFA, PDGFB, VTN, PDGFD*	89	0.07865169	1.49E-06
R-HSA-114608	2	Reactome Gene Sets	Platelet degranulation	*EGF, VEGFD, GAS6, ITGB3, PDGFA, PDGFB, VEGFB, VEGFC*	129	0.0620155	1.61E-06
R-HSA-2644602	11	Reactome Gene Sets	Signaling by NOTCH1 PEST Domain Mutants in Cancer	*RBPJ, ADAM17, NCSTN, APH1A, PSENEN, APH1B*	58	0.10344828	1.70E-06
R-HSA-2644603	11	Reactome Gene Sets	Signaling by NOTCH1 in Cancer	*RBPJ, ADAM17, NCSTN, APH1A, PSENEN, APH1B*	58	0.10344828	1.70E-06
R-HSA-2644606	11	Reactome Gene Sets	Constitutive Signaling by NOTCH1 PEST Domain Mutants	*RBPJ, ADAM17, NCSTN, APH1A, PSENEN, APH1B*	58	0.10344828	1.70E-06
R-HSA-2894858	11	Reactome Gene Sets	Signaling by NOTCH1 HD+PEST Domain Mutants in Cancer	*RBPJ, ADAM17, NCSTN, APH1A, PSENEN, APH1B*	58	0.10344828	1.70E-06
R-HSA-2894862	11	Reactome Gene Sets	Constitutive Signaling by NOTCH1 HD+PEST Domain Mutants	*RBPJ, ADAM17, NCSTN, APH1A, PSENEN, APH1B*	58	0.10344828	1.70E-06
R-HSA-76005	2	Reactome Gene Sets	Response to elevated platelet cytosolic Ca2+	*EGF, VEGFD, GAS6, ITGB3, PDGFA, PDGFB, VEGFB, VEGFC*	134	0.05970149	2.14E-06
M177	4	Canonical Pathways	PID EPHA FWDPATHWAY	*EFNA1, EFNA2, EFNA3, EFNA5, HCK*	34	0.14705882	2.17E-06

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
WP5406	6	WikiPathways	13q12 12 copy number variation	*MAG, TNFRSF19, RTN4, RTN4R, LINGO1*	34	0.14705882	2.17E-06
GO:0001936	8	GO Biological Processes	regulation of endothelial cell proliferation	*EGF, ITGB3, MDK, MEF2C,* ***NGFR****, PDGFB, ADAM17, VEGFB, CNMD*	181	0.04972376	2.24E-06
R-HSA-202733	17	Reactome Gene Sets	Cell surface interactions at the vascular wall	*ANGPT1, ANGPT2, GAS6, ITGAV, ITGB2, ITGB3, MAG, ANGPT4*	135	0.05925926	2.26E-06
hsa04330	11	KEGG Pathway	Notch signaling pathway	*RBPJ, ADAM17, NCSTN, APH1A, PSENEN, APH1B*	62	0.09677419	2.53E-06
GO:0035313	16	GO Biological Processes	wound healing, spreading of epidermal cells	*ITGAV, ITGB3, ITGB5, ADAM17*	16	0.25	2.54E-06
GO:0002690	12	GO Biological Processes	positive regulation of leukocyte chemotaxis	*VEGFD, GAS6, MDK, PGF, ADAM17, VEGFB, VEGFC*	97	0.07216495	2.67E-06
GO:0007229	16	GO Biological Processes	integrin-mediated signaling pathway	*HCK, ITGA9, ITGAV, ITGB2, ITGB3, ITGB5, VTN*	98	0.07142857	2.86E-06
R-HSA-1442490	5	Reactome Gene Sets	Collagen degradation	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1, ADAM17*	64	0.09375	3.06E-06
M251	11	Canonical Pathways	PID SYNDECAN 3 PATHWAY	*NCSTN, APH1A, PSENEN, APH1B*	17	0.23529412	3.30E-06
M212	16	Canonical Pathways	PID INTEGRIN5 PATHWAY	*ITGAV, ITGB5, VTN,* ***EDIL3***	17	0.23529412	3.30E-06
GO:0048008	13	GO Biological Processes	platelet-derived growth factor receptor signaling pathway	*ITGB3, PDGFA, PDGFB, PDGFC, PDGFD*	37	0.13513514	3.35E-06
GO:0002040	12	GO Biological Processes	sprouting angiogenesis	*ANGPT1, VEGFD, PGF, VEGFB, VEGFC, RTN4*	66	0.09090909	3.66E-06

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0001666	12	GO Biological Processes	response to hypoxia	*ANGPT2, BAD, VEGFD, PGF, ADAM17, TGFBR3, VEGFB, VEGFC, PDLIM1, ANGPT4, RTN4*	304	0.03618421	3.72E-06
GO:0031663	14	GO Biological Processes	lipopolysaccharide-mediated signaling pathway	*HCK, IRAK2, RIPK2, IRAK3, IRAK4*	38	0.13157895	3.84E-06
M3008	10	Canonical Pathways	NABA ECM GLYCOPROTEINS	*COMP, GAS6, MATN1, MATN3, MFGE8, VTN, CILP,* ***EDIL3****, CILP2*	196	0.04591837	4.31E-06
GO:0033619	11	GO Biological Processes	membrane protein proteolysis	*ADAM17, NCSTN, APH1A, PSENEN, APH1B*	39	0.12820513	4.38E-06
hsa05224	9	KEGG Pathway	Breast cancer	*EGF, FGF1, FGF23, FGF19, SHC2, FGF21, SHC3, SHC4*	148	0.05405405	4.49E-06
hsa04072	13	KEGG Pathway	Phospholipase D signaling pathway	*EGF, PDGFA, PDGFB, SHC2, SHC3, PDGFC, PDGFD, SHC4*	149	0.05369128	4.72E-06
hsa05226	9	KEGG Pathway	Gastric cancer	*EGF, FGF1, FGF23, FGF19, SHC2, FGF21, SHC3, SHC4*	150	0.05333333	4.96E-06
R-HSA-194138	12	Reactome Gene Sets	Signaling by VEGF	*VEGFD, ITGAV, ITGB3, PGF, VEGFB, VEGFC, SHC2*	108	0.06481482	5.46E-06
GO:0036293	12	GO Biological Processes	response to decreased oxygen levels	*ANGPT2, BAD, VEGFD, PGF, ADAM17, TGFBR3, VEGFB, VEGFC, PDLIM1, ANGPT4, RTN4*	317	0.03470032	5.54E-06
GO:1900046	18	GO Biological Processes	regulation of hemostasis	*ANGPT1, ANGPT2, COMP, PDGFA, PDGFB, VTN*	72	0.08333333	6.11E-06
GO:0090287	8	GO Biological Processes	regulation of cellular response to growth factor stimulus	*ANGPT1, FGF1, RBPJ, ITGB3,* ***NGFR****, PCSK6, ADAM17, TGFBR3, VEGFB, VEGFC, VTN, CILP*	385	0.03116883	6.16E-06
WP4262	9	WikiPathways	Breast cancer pathway	*EGF, FGF1, FGF23, FGF19, SHC2, FGF21, SHC3, SHC4*	155	0.0516129	6.31E-06

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
R-HSA-1980143	11	Reactome Gene Sets	Signaling by NOTCH1	*RBPJ, ADAM17, NCSTN, APH1A, PSENEN, APH1B*	74	0.08108108	7.17E-06
R-HSA-9006936	11	Reactome Gene Sets	Signaling by TGFB family members	*ITGAV, ITGB3, ITGB5, TGFBR3, NCSTN, APH1A, PSENEN, APH1B*	158	0.05063291	7.27E-06
M3005	5	Canonical Pathways	NABA COLLAGENS	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1*	44	0.11363636	8.06E-06
R-HSA-8948216	5	Reactome Gene Sets	Collagen chain trimerization	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1*	44	0.11363636	8.06E-06
hsa05214	13	KEGG Pathway	Glioma	*EGF, PDGFA, PDGFB, SHC2, SHC3, SHC4*	76	0.07894737	8.37E-06
WP268	11	WikiPathways	Notch signaling	*RBPJ, ADAM17, NCSTN, APH1A, APH1B*	45	0.11111111	9.02E-06
WP3931	9	WikiPathways	Embryonic stem cell pluripotency pathways	*EGF, FGF1, PDGFA, PDGFB, FGF23, FGF19, FGF21*	118	0.05932203	9.80E-06
GO:0097190	19	GO Biological Processes	apoptotic signaling pathway	*BAD, CASP2, ITGAV, NGF, **NGFR**, SORT1, STK4, TRADD, SIVA1, BEX3, EDA2R*	337	0.03264095	9.84E-06
GO:0038084	12	GO Biological Processes	vascular endothelial growth factor signaling pathway	*VEGFD, PGF, VEGFB, VEGFC*	22	0.18181818	9.90E-06
M198	5	Canonical Pathways	PID SYNDECAN 1 PATHWAY	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1*	46	0.10869565	1.01E-05
M70	11	Canonical Pathways	PID PS1 PATHWAY	*RBPJ, NCSTN, APH1A, PSENEN, APH1B*	46	0.10869565	1.01E-05
R-HSA-9839373	11	Reactome Gene Sets	Signaling by TGFBR3	*TGFBR3, NCSTN, APH1A, PSENEN, APH1B*	46	0.10869565	1.01E-05
GO:0044409	16	GO Biological Processes	symbiont entry into host	*GAS6, ICAM1, ITGAV, ITGB3, ITGB5, MOG, SIVA1*	120	0.05833333	1.09E-05

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
GO:0046718	16	GO Biological Processes	symbiont entry into host cell	*GAS6, ICAM1, ITGAV, ITGB3, ITGB5, MOG, SIVA1*	120	0.05833333	1.09E-05
GO:0014911	13	GO Biological Processes	positive regulation of smooth muscle cell migration	*ITGB3, MDK, PDGFB, VTN, PDGFD*	47	0.10638298	1.12E-05
GO:0043536	8	GO Biological Processes	positive regulation of blood vessel endothelial cell migration	*ANGPT1, PDGFB, ADAM17, TGFBR3, VEGFC, ANGPT4*	80	0.075	1.13E-05
WP4541	16	WikiPathways	Hippo Merlin signaling dysregulation	*ITGA9, ITGAV, ITGB2, ITGB3, ITGB5,* ***NGFR****, NTRK2*	121	0.05785124	1.15E-05
GO:0070482	12	GO Biological Processes	response to oxygen levels	*ANGPT2, BAD, VEGFD, PGF, ADAM17, TGFBR3, VEGFB, VEGFC, PDLIM1, ANGPT4, RTN4*	344	0.03197674	1.19E-05
GO:0035987	16	GO Biological Processes	endodermal cell differentiation	*COL11A1, ITGAV, ITGB2, ITGB5, VTN*	48	0.10416667	1.25E-05
GO:0030195	18	GO Biological Processes	negative regulation of blood coagulation	*ANGPT1, ANGPT2, PDGFA, PDGFB, VTN*	48	0.10416667	1.25E-05
GO:0006509	11	GO Biological Processes	membrane protein ectodomain proteolysis	*ADAM17, NCSTN, APH1A, PSENEN*	24	0.16666667	1.42E-05
GO:0050435	11	GO Biological Processes	amyloid-beta metabolic process	*NCSTN, APH1A, PSENEN, APH1B*	24	0.16666667	1.42E-05
GO:0002688	12	GO Biological Processes	regulation of leukocyte chemotaxis	*VEGFD, GAS6, MDK, PGF, ADAM17, VEGFB, VEGFC*	126	0.05555556	1.50E-05
hsa04012	20	KEGG Pathway	ErbB signaling pathway	*BAD, EGF, EREG, SHC2, SHC3, SHC4*	86	0.06976744	1.71E-05

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
hsa04926	12	KEGG Pathway	Relaxin signaling pathway	*COL4A1, VEGFD, VEGFB, VEGFC, SHC2, SHC3, SHC4*	130	0.05384615	1.84E-05
GO:0050819	18	GO Biological Processes	negative regulation of coagulation	*ANGPT1, ANGPT2, PDGFA, PDGFB, VTN*	52	0.09615385	1.85E-05
WP673	20	WikiPathways	ErbB signaling	*BAD, EGF, EREG, SHC2, SHC3, SHC4*	90	0.06666667	2.22E-05
R-HSA-3000170	16	Reactome Gene Sets	Syndecan interactions	*ITGAV, ITGB3, ITGB5, VTN*	27	0.14814815	2.32E-05
GO:0050878	17	GO Biological Processes	regulation of body fluid levels	*ANGPT1, ANGPT2, ATP7B, CLIC1, COMP, GAS6, ITGB3, PDGFA, PDGFB, VTN, ANGPT4*	370	0.02972973	2.34E-05
GO:0007160	16	GO Biological Processes	cell-matrix adhesion	*HOXD3, ITGA9, ITGAV, ITGB2, ITGB3, ITGB5, VTN*	137	0.05109489	2.59E-05
R-HSA-1474228	5	Reactome Gene Sets	Degradation of the extracellular matrix	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1, ADAM17, NCSTN*	138	0.05072464	2.71E-05
GO:0001706	16	GO Biological Processes	endoderm formation	*COL11A1, ITGAV, ITGB2, ITGB5, VTN*	58	0.0862069	3.17E-05
R-HSA-449147	14	Reactome Gene Sets	Signaling by Interleukins	*CNTF, CNTFR, HCK, ICAM1, IL17A, IRAK2, ITGB2, MEF2C, NDN, RIPK2, IRAK3, IRAK4*	455	0.02637363	3.22E-05
GO:0021675	3	GO Biological Processes	nerve development	*HOXD3, NGF,* ***NGFR****, NTF3, NTF4, PLXNA3*	97	0.06185567	3.40E-05
GO:0043085	7	GO Biological Processes	positive regulation of catalytic activity	*ANGPT1, EREG, FGF1, GAS6, PDGFB, FGF23, TRAF4, SEMA4D, PSENEN, RTN4R*	318	0.03144654	3.44E-05
GO:0008543	9	GO Biological Processes	fibroblast growth factor receptor signaling pathway	*FGF1,* ***NGFR****, FGF23, FGF19, FGF21*	59	0.08474576	3.44E-05

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
M17	11	Canonical Pathways	PID NOTCH PATHWAY	*RBPJ, NCSTN, APH1A, PSENEN, APH1B*	59	0.08474576	3.44E-05
GO:0044319	16	GO Biological Processes	wound healing, spreading of cells	*ITGAV, ITGB3, ITGB5, ADAM17*	30	0.13333333	3.57E-05
GO:0090505	16	GO Biological Processes	epiboly involved in wound healing	*ITGAV, ITGB3, ITGB5, ADAM17*	30	0.13333333	3.57E-05
R-HSA-2022090	5	Reactome Gene Sets	Assembly of collagen fibrils and other multimeric structures	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1*	60	0.08333333	3.74E-05
GO:0072124	13	GO Biological Processes	regulation of glomerular mesangial cell proliferation	*ITGB3, PDGFB, PDGFD*	11	0.27272727	3.82E-05
GO:0090504	16	GO Biological Processes	epiboly	*ITGAV, ITGB3, ITGB5, ADAM17*	31	0.12903226	4.08E-05
GO:0016485	11	GO Biological Processes	protein processing	*CASP2, COMP, PCSK6, ADAM17, NCSTN, APH1A, PSENEN, APH1B*	201	0.039801	4.13E-05
WP185	16	WikiPathways	Integrin mediated cell adhesion	*ITGA9, ITGAV, ITGB2, ITGB3, ITGB5, SHC3*	102	0.05882353	4.51E-05
WP51	9	WikiPathways	Regulation of actin cytoskeleton	*EGF, FGF1, PDGFA, PDGFB, FGF23, FGF19, FGF21*	150	0.04666667	4.62E-05
hsa05215	13	KEGG Pathway	Prostate cancer	*BAD, EGF, PDGFA, PDGFB, PDGFC, PDGFD*	106	0.05660377	5.60E-05
WP5090	16	WikiPathways	Complement system in neuronal development and plasticity	*GAS6, ITGAV, ITGB2, ITGB3, MFGE8, VTN*	107	0.05607477	5.90E-05

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
R-HSA-187687	20	Reactome Gene Sets	Signalling to ERKs	*NGF, SHC2, SHC3, KIDINS220*	34	0.11764706	5.92E-05
GO:0016032	16	GO Biological Processes	viral process	*ATP7B, GAS6, ICAM1, ITGAV, ITGB3, ITGB5, MOG, SIVA1, ST6GALNAC3*	275	0.03272727	6.28E-05
R-HSA-1650814	5	Reactome Gene Sets	Collagen biosynthesis and modifying enzymes	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1*	67	0.07462687	6.38E-05
GO:2000351	16	GO Biological Processes	regulation of endothelial cell apoptotic process	*ANGPT1, GAS6, ICAM1, ITGB3,* ***NGFR***	67	0.07462687	6.38E-05
GO:0048010	12	GO Biological Processes	vascular endothelial growth factor receptor signaling pathway	*VEGFD, PGF, VEGFB, VEGFC*	35	0.11428571	6.65E-05
GO:0001938	8	GO Biological Processes	positive regulation of endothelial cell proliferation	*EGF, ITGB3, MDK, PDGFB, ADAM17, VEGFB*	110	0.05454546	6.88E-05
GO:0051701	16	GO Biological Processes	biological process involved in interaction with host	*GAS6, ICAM1, ITGAV, ITGB3, ITGB5, MOG, SIVA1*	160	0.04375	6.95E-05
GO:0097192	19	GO Biological Processes	extrinsic apoptotic signaling pathway in absence of ligand	*BAD, CASP2, ITGAV, NGF*	36	0.11111111	7.45E-05
WP5561	16	WikiPathways	Integrative Analysis of Treg Glial Interactions	*CNP, ITGAV, ITGB3, MOG, PDGFA, TGFBR3*	112	0.05357143	7.61E-05
GO:0006909	16	GO Biological Processes	phagocytosis	*CRYBA1, GAS6, HCK, ITGAV, ITGB2, ITGB3, MFGE8*	163	0.04294479	7.81E-05
GO:0030193	18	GO Biological Processes	regulation of blood coagulation	*ANGPT1, ANGPT2, PDGFA, PDGFB, VTN*	70	0.07142857	7.88E-05

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0043277	16	GO Biological Processes	apoptotic cell clearance	*GAS6, ITGAV, ITGB3, MFGE8*	37	0.10810811	8.31E-05
GO:2000352	16	GO Biological Processes	negative regulation of endothelial cell apoptotic process	*ANGPT1, GAS6, ICAM1, ITGB3*	37	0.10810811	8.31E-05
R-HSA-2129379	16	Reactome Gene Sets	Molecules associated with elastic fibres	*ITGAV, ITGB3, ITGB5, VTN*	37	0.10810811	8.31E-05
R-HSA-190322	9	Reactome Gene Sets	FGFR4 ligand binding and activation	*FGF1, FGF23, FGF19*	14	0.21428571	8.32E-05
R-HSA-190373	9	Reactome Gene Sets	FGFR1c ligand binding and activation	*FGF1, TGFBR3, FGF23*	14	0.21428571	8.32E-05
R-HSA-187037	20	Reactome Gene Sets	Signaling by NTRK1 (TRKA)	*MEF2C, NGF, NTRK2, SHC2, SHC3, KIDINS220*	115	0.05217391	8.81E-05
R-HSA-9013694	11	Reactome Gene Sets	Signaling by NOTCH4	*RBPJ, NCSTN, APH1A, PSENEN, APH1B*	72	0.06944444	9.02E-05
GO:0034113	16	GO Biological Processes	heterotypic cell-cell adhesion	*ITGAV, ITGB2, ITGB3, NRCAM*	38	0.10526316	9.24E-05
GO:0038034	19	GO Biological Processes	signal transduction in absence of ligand	*BAD, CASP2, ITGAV, NGF*	38	0.10526316	9.24E-05
GO:0061045	18	GO Biological Processes	negative regulation of wound healing	*ANGPT1, ANGPT2, PDGFA, PDGFB, VTN*	73	0.06849315	9.63E-05
R-HSA-157118	11	Reactome Gene Sets	Signaling by NOTCH	*EGF, RBPJ, MDK, ADAM17, NCSTN, APH1A, PSENEN, APH1B*	228	0.03508772	9.98E-05

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
WP5285	12	WikiPathways	Immune infiltration in pancreatic cancer	*VEGFD, IL17A, VEGFB, VEGFC*	39	0.1025641	0.000102477
R-HSA-5654228	9	Reactome Gene Sets	Phospholipase C-mediated cascade; FGFR4	*FGF1, FGF23, FGF19*	15	0.2	0.000103465
GO:1901722	13	GO Biological Processes	regulation of cell proliferation involved in kidney development	*ITGB3, PDGFB, PDGFD*	15	0.2	0.000103465
GO:0050818	18	GO Biological Processes	regulation of coagulation	*ANGPT1, ANGPT2, PDGFA, PDGFB, VTN*	76	0.06578947	0.000116678
GO:0002755	14	GO Biological Processes	MyD88-dependent toll-like receptor signaling pathway	*IRAK2, IRAK3, IRAK4*	16	0.1875	0.000126756
GO:0032102	18	GO Biological Processes	negative regulation of response to external stimulus	*ANGPT1, ANGPT2, HCK, IL17A, MDK, PDGFA, PDGFB, VTN, IRAK3, PLXNA3, RTN4R*	449	0.02449889	0.000131874
GO:0051216	10	GO Biological Processes	cartilage development	*COL11A1, COMP, HOXD3, MATN1, MATN3, MEF2C, CNMD*	180	0.03888889	0.000144962
GO:0001704	16	GO Biological Processes	formation of primary germ layer	*COL11A1, ITGAV, ITGB2, ITGB3, ITGB5, VTN*	126	0.04761905	0.00014573
WP4565	3	WikiPathways	Neural crest cell migration in cancer	***NGFR**, NTRK2, SORT1, KIDINS220*	43	0.09302326	0.000150789
GO:0045860	7	GO Biological Processes	positive regulation of protein kinase activity	*ANGPT1, EREG, FGF1, GAS6, PDGFB, TRAF4*	128	0.046875	0.000158835
GO:0061448	10	GO Biological Processes	connective tissue development	*COL11A1, COMP, HOXD3, MATN1, MATN3, MEF2C, PDGFB, CNMD*	245	0.03265306	0.000163544

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R-HSA-1566948	16	Reactome Gene Sets	Elastic fibre formation	*ITGAV, ITGB3, ITGB5, VTN*	44	0.09090909	0.000165061
hsa04360	4	KEGG Pathway	Axon guidance	*EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, SEMA4D, PLXNA3*	184	0.03804348	0.000166007
WP4223	20	WikiPathways	Ras signaling	*BAD, **NGFR**, NTRK2, STK4, SHC2, SHC3, SHC4*	185	0.03783784	0.000171636
WP5493	20	WikiPathways	Effect of dasatinib on the BCR ABL signaling pathway	*MEF2C, SHC2, SHC3, SHC4*	45	0.08888889	0.000180285
R-HSA-190242	9	Reactome Gene Sets	FGFR1 ligand binding and activation	*FGF1, TGFBR3, FGF23*	18	0.16666667	0.000183008
R-HSA-210993	18	Reactome Gene Sets	Tie2 Signaling	*ANGPT1, ANGPT2, ANGPT4*	18	0.16666667	0.000183008
hsa05206	4	KEGG Pathway	MicroRNAs in cancer	*EFNA1, EFNA2, EFNA3, EFNA4, EFNA5, ITGB3, PDGFA, PDGFB, SHC4*	318	0.02830189	0.000188109
GO:0007596	17	GO Biological Processes	blood coagulation	*ANGPT1, ANGPT2, CLIC1, COMP, GAS6, ITGB3, ANGPT4*	191	0.03664922	0.000208747
GO:0007492	16	GO Biological Processes	endoderm development	*COL11A1, ITGAV, ITGB2, ITGB5, VTN*	86	0.05813954	0.000209141
R-HSA-2173789	16	Reactome Gene Sets	TGF-beta receptor signaling activates SMADs	*ITGAV, ITGB3, ITGB5, TGFBR3*	47	0.08510638	0.000213731
GO:0019058	16	GO Biological Processes	viral life cycle	*GAS6, ICAM1, ITGAV, ITGB3, ITGB5, MOG, SIVA1*	193	0.03626943	0.000222464
GO:0050817	17	GO Biological Processes	coagulation	*ANGPT1, ANGPT2, CLIC1, COMP, GAS6, ITGB3, ANGPT4*	193	0.03626943	0.000222464
GO:0033674	7	GO Biological Processes	positive regulation of kinase activity	*ANGPT1, EREG, FGF1, GAS6, PDGFB, TRAF4*	137	0.04379562	0.000229795

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
R-HSA-1474290	5	Reactome Gene Sets	Collagen formation	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1*	89	0.05617978	0.000245529
GO:0044344	9	GO Biological Processes	cellular response to fibroblast growth factor stimulus	*FGF1,* ***NGFR****, FGF23, FGF19, FGF21*	89	0.05617978	0.000245529
GO:0061041	18	GO Biological Processes	regulation of wound healing	*ANGPT1, ANGPT2, PDGFA, PDGFB, VEGFB, VTN*	139	0.04316547	0.000248509
GO:0007599	17	GO Biological Processes	hemostasis	*ANGPT1, ANGPT2, CLIC1, COMP, GAS6, ITGB3, ANGPT4*	197	0.035533	0.00025208
R-HSA-5654719	9	Reactome Gene Sets	SHC-mediated cascade:FGFR4	*FGF1, FGF23, FGF19*	20	0.15	0.000253329
R-HSA-5654720	9	Reactome Gene Sets	PI-3K cascade:FGFR4	*FGF1, FGF23, FGF19*	20	0.15	0.000253329
R-HSA-167044	20	Reactome Gene Sets	Signalling to RAS	*NGF, SHC2, SHC3*	20	0.15	0.000253329
R-HSA-76002	2	Reactome Gene Sets	Platelet activation, signaling and aggregation	*EGF, VEGFD, GAS6, ITGB3, PDGFA, PDGFB, VEGFB, VEGFC*	262	0.03053435	0.000257661
GO:0060348	10	GO Biological Processes	bone development	*COMP, MATN1, MEF2C, PDGFA, RPL13, SEMA4D, PDGFC*	199	0.03517588	0.000268034
GO:0035924	12	GO Biological Processes	cellular response to vascular endothelial growth factor stimulus	*VEGFD, PGF, VEGFB, VEGFC*	50	0.08	0.000271963
GO:0044403	16	GO Biological Processes	biological process involved in symbiotic interaction	*GAS6, ICAM1, ITGAV, ITGB3, ITGB5, MOG, SIVA1*	200	0.035	0.00027631

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
hsa05418	16	KEGG Pathway	Fluid shear stress and atherosclerosis	*ICAM1, ITGAV, ITGB3, MEF2C, PDGFA, PDGFB*	142	0.04225352	0.000278807
hsa04540	13	KEGG Pathway	Gap junction	*EGF, PDGFA, PDGFB, PDGFC, PDGFD*	92	0.05434783	0.000286539
M103	16	Canonical Pathways	PID S1P S1P1 PATHWAY	*ITGAV, ITGB3, PDGFB*	21	0.14285714	0.000294193
R-HSA-445144	16	Reactome Gene Sets	Signal transduction by L1	*ITGA9, ITGAV, ITGB3*	21	0.14285714	0.000294193
GO:0048511	3	GO Biological Processes	rhythmic process	*CASP2, EREG, MDK, NGF,* ***NGFR****, NTRK2, NTRK3, MAGED1*	269	0.02973978	0.000307509
R-HSA-166016	14	Reactome Gene Sets	Toll Like Receptor 4 (TLR4) Cascade	*IRAK2, ITGB2, MEF2C, RIPK2, IRAK3, IRAK4*	145	0.04137931	0.000311932
GO:0002429	14	GO Biological Processes	immune response-activating cell surface receptor signaling pathway	*HCK, IRAK2, MEF2C, MOG, RIPK2, SIVA1, TNFRSF21, IRAK4*	270	0.02962963	0.000315233
M50	13	Canonical Pathways	PID PTP1B PATHWAY	*EGF, HCK, ITGB3, PDGFB*	52	0.07692308	0.000316605
GO:0030198	10	GO Biological Processes	extracellular matrix organization	*COL4A1, COL11A1, COMP, GAS6, MATN1, MATN3, VTN, KAZALD1*	272	0.02941177	0.000331155
R-HSA-5654712	9	Reactome Gene Sets	FRS-mediated FGFR4 signaling	*FGF1, FGF23, FGF19*	22	0.13636364	0.000339081
GO:0072012	18	GO Biological Processes	glomerulus vasculature development	*ANGPT1, ANGPT2, PDGFB*	22	0.13636364	0.000339081
GO:0043062	10	GO Biological Processes	extracellular structure organization	*COL4A1, COL11A1, COMP, GAS6, MATN1, MATN3, VTN, KAZALD1*	273	0.02930403	0.000339359

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0045229	10	GO Biological Processes	external encapsulating structure organization	*COL4A1, COL11A1, COMP, GAS6, MATN1, MATN3, VTN, KAZALD1*	275	0.02909091	0.000356264
GO:0071774	9	GO Biological Processes	response to fibroblast growth factor	*FGF1,* ***NGFR****, FGF23, FGF19, FGF21*	97	0.05154639	0.000366184
R-HSA-2404192	9	Reactome Gene Sets	Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)	*FGF1, FGF23, CILP, FGF19*	54	0.07407407	0.000366266
GO:0002011	16	GO Biological Processes	morphogenesis of an epithelial sheet	*ITGAV, ITGB3, ITGB5, ADAM17*	54	0.07407407	0.000366266
GO:0048661	13	GO Biological Processes	positive regulation of smooth muscle cell proliferation	*EREG, ITGB3, PDGFB, IRAK4, PDGFD*	98	0.05102041	0.000383936
hsa05231	13	KEGG Pathway	Choline metabolism in cancer	*EGF, PDGFA, PDGFB, PDGFC, PDGFD*	99	0.05050505	0.000402332
hsa04933	12	KEGG Pathway	AGE-RAGE signaling pathway in diabetic complications	*COL4A1, VEGFD, ICAM1, VEGFB, VEGFC*	101	0.04950495	0.00044111
GO:0010988	16	GO Biological Processes	regulation of low-density lipoprotein particle clearance	*ITGAV, ITGB3, FGF21*	24	0.125	0.00044157
GO:0061437	18	GO Biological Processes	renal system vasculature development	*ANGPT1, ANGPT2, PDGFB*	24	0.125	0.00044157
GO:0061440	18	GO Biological Processes	kidney vasculature development	*ANGPT1, ANGPT2, PDGFB*	24	0.125	0.00044157
hsa04148	16	KEGG Pathway	Efferocytosis	*GAS6, ITGAV, ITGB3, ITGB5, MFGE8, ADAM17*	157	0.03821656	0.00047644
R-HSA-9006115	3	Reactome Gene Sets	Signaling by NTRK2 (TRKB)	*NTF3, NTF4, NTRK2*	25	0.12	0.000499483

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
M118	12	Canonical Pathways	PID INTEGRIN A9B1 PATHWAY	*VEGFD, ITGA9, VEGFC*	25	0.12	0.000499483
hsa04974	5	KEGG Pathway	Protein digestion and absorption	*COL4A1, COL9A1, COL9A2, COL9A3, COL11A1*	105	0.04761905	0.000527047
GO:0070167	10	GO Biological Processes	regulation of biomineral tissue development	*COMP, GAS6, MATN1, MEF2C, FGF23*	105	0.04761905	0.000527047
GO:0051347	7	GO Biological Processes	positive regulation of transferase activity	*ANGPT1, EREG, FGF1, GAS6, PDGFB, TRAF4*	161	0.03726708	0.000544136
M226	12	Canonical Pathways	PID VEGFR1 PATHWAY	*PGF, VEGFB, SHC2*	26	0.11538462	0.000562044
GO:0036120	13	GO Biological Processes	cellular response to platelet-derived growth factor stimulus	*ITGB3, PDGFB, PDGFD*	26	0.11538462	0.000562044
GO:0032835	18	GO Biological Processes	glomerulus development	*ANGPT1, ANGPT2, MEF2C, PDGFB*	61	0.06557377	0.000584174
WP5366	6	WikiPathways	NF1 copy number variation syndrome	*EGF, NGF,* ***NGFR****, OMG, RTN4R*	109	0.04587156	0.000624996
R-HSA-977225	11	Reactome Gene Sets	Amyloid fiber formation	*MFGE8, NCSTN, APH1A, PSENEN, APH1B*	109	0.04587156	0.000624996
GO:0043124	14	GO Biological Processes	negative regulation of canonical NF-kappaB signal transduction	*IRAK2, TGFBR3, RIPK2, SIVA1, IRAK3*	109	0.04587156	0.000624996
R-HSA-5654716	9	Reactome Gene Sets	Downstream signaling of activated FGFR4	*FGF1, FGF23, FGF19*	27	0.11111111	0.000629401

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
WP3624	13	WikiPathways	Lung fibrosis	*EGF, FGF1, PDGFA, PDGFB*	63	0.06349206	0.000660355
GO:0070555	14	GO Biological Processes	response to interleukin-1	*IL17A, IRAK2, RIPK2, IRAK3, IRAK4*	111	0.04504505	0.000678797
R-HSA-166058	14	Reactome Gene Sets	MyD88:MAL(TIRAP) cascade initiated on plasma membrane	*IRAK2, MEF2C, RIPK2, IRAK3, IRAK4*	111	0.04504505	0.000678797
R-HSA-168188	14	Reactome Gene Sets	Toll Like Receptor TLR6:TLR2 Cascade	*IRAK2, MEF2C, RIPK2, IRAK3, IRAK4*	111	0.04504505	0.000678797
GO:0036119	13	GO Biological Processes	response to platelet-derived growth factor	*ITGB3, PDGFB, PDGFD*	28	0.10714286	0.000701699
GO:0070498	14	GO Biological Processes	interleukin-1-mediated signaling pathway	*IRAK2, IRAK3, IRAK4*	28	0.10714286	0.000701699
GO:0002768	14	GO Biological Processes	immune response-regulating cell surface receptor signaling pathway	*HCK, IRAK2, MEF2C, MOG, RIPK2, SIVA1, TNFRSF21, IRAK4*	305	0.02622951	0.000703622
R-HSA-168898	14	Reactome Gene Sets	Toll-like Receptor Cascades	*IRAK2, ITGB2, MEF2C, RIPK2, IRAK3, IRAK4*	170	0.03529412	0.000723761
R-HSA-168179	14	Reactome Gene Sets	Toll Like Receptor TLR1:TLR2 Cascade	*IRAK2, MEF2C, RIPK2, IRAK3, IRAK4*	114	0.04385965	0.000765901
R-HSA-181438	14	Reactome Gene Sets	Toll Like Receptor 2 (TLR2) Cascade	*IRAK2, MEF2C, RIPK2, IRAK3, IRAK4*	114	0.04385965	0.000765901
GO:0048660	13	GO Biological Processes	regulation of smooth muscle cell proliferation	*EREG, ITGB3, MEF2C, PDGFB, IRAK4, PDGFD*	172	0.03488372	0.000769266

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0002063	10	GO Biological Processes	chondrocyte development	*COL11A1, COMP, MATN1*	29	0.10344828	0.00077908
M55	16	Canonical Pathways	PID S1P S1P3 PATHWAY	*ITGAV, ITGB3, PDGFB*	29	0.10344828	0.00077908
M72	16	Canonical Pathways	PID NECTIN PATHWAY	*ITGAV, ITGB3, PDGFB*	30	0.1	0.00086168
GO:0050820	18	GO Biological Processes	positive regulation of coagulation	*ANGPT1, ANGPT2, VTN*	30	0.1	0.00086168
GO:0007369	16	GO Biological Processes	gastrulation	*COL11A1, ITGAV, ITGB2, ITGB3, ITGB5, VTN*	176	0.03409091	0.000866885
WP3303	18	WikiPathways	RAC1 PAK1 p38 MMP2 pathway	*ANGPT1, ANGPT2, BAD, ANGPT4*	68	0.05882353	0.000881191
hsa04668	12	KEGG Pathway	TNF signaling pathway	*VEGFD, ICAM1, ADAM17, VEGFC, TRADD*	119	0.04201681	0.000929268
R-HSA-5654733	9	Reactome Gene Sets	Negative regulation of FGFR4 signaling	*FGF1, FGF23, FGF19*	31	0.09677419	0.000949635
hsa05152	14	KEGG Pathway	Tuberculosis	*BAD, IRAK2, ITGB2, TRADD, RIPK2, IRAK4*	182	0.03296703	0.001030901
R-HSA-448424	14	Reactome Gene Sets	Interleukin-17 signaling	*IL17A, IRAK2, MEF2C, RIPK2*	71	0.05633803	0.001036161
hsa04917	20	KEGG Pathway	Prolactin signaling pathway	*CYP17A1, SHC2, SHC3, SHC4*	71	0.05633803	0.001036161
GO:0007162	18	GO Biological Processes	negative regulation of cell adhesion	*ANGPT1, ANGPT2, ARHGDIG, EFNA5, MDK, SEMA4D, TNFRSF21, B4GALNT2*	326	0.02453988	0.001079812
GO:0002757	14	GO Biological Processes	immune response-activating signaling pathway	*HCK, IRAK2, MEF2C, MOG, RIPK2, SIVA1, IRAK3, TNFRSF21, IRAK4*	407	0.02211302	0.001108367

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0042490	3	GO Biological Processes	mechanoreceptor differentiation	*RBPJ, NTF4, NTRK2, NTRK3*	75	0.05333333	0.001271291
WP2118	16	WikiPathways	Arrhythmogenic right ventricular cardiomyopathy	*ITGA9, ITGAV, ITGB3, ITGB5*	75	0.05333333	0.001271291
M186	16	Canonical Pathways	PID PDGFRB PATHWAY	*ARHGDIA, HCK, ITGAV, ITGB3, PDGFB*	129	0.03875969	0.001332008
WP4217	16	WikiPathways	Ebola virus infection in host	*GAS6, ITGAV, ITGB3, MFGE8, ADAM17*	129	0.03875969	0.001332008
hsa05220	20	KEGG Pathway	Chronic myeloid leukemia	*BAD, SHC2, SHC3, SHC4*	77	0.05194805	0.001401808
WP5124	11	WikiPathways	Alzheimer 39 s disease	*BAD, ADAM17, NCSTN, APH1A, PSENEN, RTN4, APH1B*	264	0.02651515	0.001419196
R-HSA-168638	14	Reactome Gene Sets	NOD1/2 Signaling Pathway	*CASP2, IRAK2, RIPK2*	36	0.08333333	0.001474247
GO:0050830	14	GO Biological Processes	defense response to Gram-positive bacterium	*FAU, HCK, IL17A, ADAM17, RIPK2*	132	0.03787879	0.001474663
hsa04650	20	KEGG Pathway	Natural killer cell mediated cytotoxicity	*ICAM1, ITGB2, SHC2, SHC3, SHC4*	134	0.03731343	0.001575817
WP2059	11	WikiPathways	Alzheimer 39 s disease and miRNA effects	*BAD, ADAM17, NCSTN, APH1A, PSENEN, RTN4, APH1B*	269	0.02602231	0.001579299
WP3888	16	WikiPathways	VEGFA VEGFR2 signaling	*CLIC1, CNP, ICAM1, ITGAV, ITGB3, ITGB5, MEF2C, PGF, SHC2*	432	0.02083333	0.001669063
GO:0010984	16	GO Biological Processes	regulation of lipoprotein particle clearance	*ITGAV, ITGB3, FGF21*	38	0.07894737	0.001725959

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
GO:0030500	10	GO Biological Processes	regulation of bone mineralization	*COMP, MATN1, MEF2C, FGF23*	83	0.04819277	0.001849064
GO:0071347	14	GO Biological Processes	cellular response to interleukin-1	*IL17A, IRAK2, IRAK3, IRAK4*	83	0.04819277	0.001849064
hsa04915	20	KEGG Pathway	Estrogen signaling pathway	*KRT13, KRT15, SHC2, SHC3, SHC4*	139	0.03597122	0.001850944
GO:0032147	7	GO Biological Processes	activation of protein kinase activity	*ANGPT1, FGF1, GAS6*	39	0.07692308	0.00186125
GO:0007623	3	GO Biological Processes	circadian rhythm	*NGF, **NGFR**, NTRK2, NTRK3, MAGED1*	140	0.03571429	0.001909931
GO:0002062	10	GO Biological Processes	chondrocyte differentiation	*COL11A1, COMP, MATN1, MEF2C*	85	0.04705882	0.002017792
GO:0071222	14	GO Biological Processes	cellular response to lipopolysaccharide	*HCK, IRAK2, MEF2C, RIPK2, IRAK3, IRAK4*	209	0.02870813	0.002081818
hsa05412	16	KEGG Pathway	Arrhythmogenic right ventricular cardiomyopathy	*ITGA9, ITGAV, ITGB3, ITGB5*	86	0.04651163	0.002106019
R-HSA-5654743	9	Reactome Gene Sets	Signaling by FGFR4	*FGF1, FGF23, FGF19*	41	0.07317073	0.00215124
GO:0007422	3	GO Biological Processes	peripheral nervous system development	*GDNF, NGF, NTRK2, NTRK3*	87	0.04597701	0.002196874
R-HSA-190236	9	Reactome Gene Sets	Signaling by FGFR	*FGF1, TGFBR3, FGF23, FGF19*	89	0.04494382	0.002386626
GO:0034142	14	GO Biological Processes	toll-like receptor 4 signaling pathway	*IRAK2, RIPK2, IRAK4*	43	0.06976744	0.0024678

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
R-HSA-109704	9	Reactome Gene Sets	PI3K Cascade	*FGF1, FGF23, FGF19*	44	0.06818182	0.002636293
GO:0038061	14	GO Biological Processes	non-canonical NF-kappaB signal transduction	*IRAK2, TRADD, IRAK4*	44	0.06818182	0.002636293
WP4136	14	WikiPathways	Fibrin complement receptor 3 signaling	*IRAK2, ITGB2, IRAK4*	44	0.06818182	0.002636293
WP4746	16	WikiPathways	Thyroid hormones production and peripheral downstream signaling effects	*BAD, ITGAV, ITGB3, FGF21*	93	0.04301075	0.002799387
R-HSA-170834	16	Reactome Gene Sets	Signaling by TGF-beta Receptor Complex	*ITGAV, ITGB3, ITGB5, TGFBR3*	94	0.04255319	0.002909732
GO:0002253	14	GO Biological Processes	activation of immune response	*HCK, IRAK2, MEF2C, MOG, RIPK2, SIVA1, IRAK3, TNFRSF21, IRAK4*	471	0.01910828	0.002977431
GO:0002764	14	GO Biological Processes	immune response-regulating signaling pathway	*HCK, IRAK2, MEF2C, MOG, RIPK2, SIVA1, IRAK3, TNFRSF21, IRAK4*	471	0.01910828	0.002977431
GO:0140895	14	GO Biological Processes	cell surface toll-like receptor signaling pathway	*IRAK2, RIPK2, IRAK4*	46	0.06521739	0.00299418
GO:0034446	16	GO Biological Processes	substrate adhesion-dependent cell spreading	*EFNA1, ITGAV, ITGB3*	46	0.06521739	0.00299418
R-HSA-168142	14	Reactome Gene Sets	Toll Like Receptor 10 (TLR10) Cascade	*IRAK2, MEF2C, RIPK2, IRAK4*	95	0.04210526	0.003023015

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
R-HSA-168176	14	Reactome Gene Sets	Toll Like Receptor 5 (TLR5) Cascade	*IRAK2, MEF2C, RIPK2, IRAK4*	95	0.04210526	0.003023015
R-HSA-975871	14	Reactome Gene Sets	MyD88 cascade initiated on plasma membrane	*IRAK2, MEF2C, RIPK2, IRAK4*	95	0.04210526	0.003023015
GO:0071219	14	GO Biological Processes	cellular response to molecule of bacterial origin	*HCK, IRAK2, MEF2C, RIPK2, IRAK3, IRAK4*	227	0.02643172	0.003135985
GO:0045840	13	GO Biological Processes	positive regulation of mitotic nuclear division	*EGF, EREG, PDGFB*	47	0.06382979	0.003183756
WP4534	16	WikiPathways	Mechanoregulation and pathology of YAP TAZ via Hippo and non Hippo mechanisms	*ITGB2, ITGB3, ITGB5*	47	0.06382979	0.003183756
hsa04145	16	KEGG Pathway	Phagosome	*COMP, ITGAV, ITGB2, ITGB3, ITGB5*	159	0.03144654	0.003311138
GO:0002833	14	GO Biological Processes	positive regulation of response to biotic stimulus	*EREG, HCK, IL17A, IRAK2, RIPK2, IRAK3, IRAK4, RTN4*	391	0.02046036	0.003336783
R-HSA-112399	9	Reactome Gene Sets	IRS-mediated signalling	*FGF1, FGF23, FGF19*	48	0.0625	0.003380538
GO:0070527	17	GO Biological Processes	platelet aggregation	*CLIC1, COMP, ITGB3*	48	0.0625	0.003380538
hsa05410	16	KEGG Pathway	Hypertrophic cardiomyopathy	*ITGA9, ITGAV, ITGB3, ITGB5*	99	0.04040404	0.003506283
hsa01522	20	KEGG Pathway	Endocrine resistance	*BAD, SHC2, SHC3, SHC4*	99	0.04040404	0.003506283
M92	18	Canonical Pathways	PID ANGIOPOIETIN RECEPTOR PATHWAY	*ANGPT1, ANGPT2, ANGPT4*	49	0.06122449	0.00358461

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0045859	7	GO Biological Processes	regulation of protein kinase activity	*ANGPT1, EREG, FGF1, GAS6, PDGFB, TRAF4*	234	0.02564103	0.003638368
R-HSA-9020702	14	Reactome Gene Sets	Interleukin-1 signaling	*IRAK2, RIPK2, IRAK3, IRAK4*	101	0.03960396	0.003766519
R-HSA-975138	14	Reactome Gene Sets	TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	*IRAK2, MEF2C, RIPK2, IRAK4*	101	0.03960396	0.003766519
GO:0002224	14	GO Biological Processes	toll-like receptor signaling pathway	*IRAK2, IRAK3, IRAK4*	50	0.06	0.003796056
R-HSA-975155	14	Reactome Gene Sets	MyD88 dependent cascade initiated on endosome	*IRAK2, MEF2C, RIPK2, IRAK4*	102	0.03921569	0.003901417
GO:0050851	14	GO Biological Processes	antigen receptor-mediated signaling pathway	*MEF2C, MOG, RIPK2, SIVA1, TNFRSF21*	166	0.03012048	0.003977105
hsa04630	13	KEGG Pathway	JAK-STAT signaling pathway	*CNTF, CNTFR, EGF, PDGFA, PDGFB*	168	0.02976191	0.00418377
R-HSA-2428928	9	Reactome Gene Sets	IRS-related events triggered by IGF1R	*FGF1, FGF23, FGF19*	52	0.05769231	0.004241384
R-HSA-5654736	9	Reactome Gene Sets	Signaling by FGFR1	*FGF1, TGFBR3, FGF23*	52	0.05769231	0.004241384
GO:0032369	16	GO Biological Processes	negative regulation of lipid transport	*EGF, ITGAV, ITGB3*	52	0.05769231	0.004241384
hsa05414	16	KEGG Pathway	Dilated cardiomyopathy	*ITGA9, ITGAV, ITGB3, ITGB5*	105	0.03809524	0.004325662

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
R-HSA-168181	14	Reactome Gene Sets	Toll Like Receptor 7/8 (TLR7/8) Cascade	*IRAK2, MEF2C, RIPK2, IRAK4*	106	0.03773585	0.004473712
R-HSA-2428924	9	Reactome Gene Sets	IGF1R signaling cascade	*FGF1, FGF23, FGF19*	53	0.05660377	0.00447542
R-HSA-74751	9	Reactome Gene Sets	Insulin receptor signalling cascade	*FGF1, FGF23, FGF19*	54	0.05555556	0.004717135
WP195	14	WikiPathways	IL1 signaling	*IRAK2, IRAK3, IRAK4*	54	0.05555556	0.004717135
R-HSA-168138	14	Reactome Gene Sets	Toll Like Receptor 9 (TLR9) Cascade	*IRAK2, MEF2C, RIPK2, IRAK4*	109	0.03669725	0.004938264
M276	9	Canonical Pathways	PID FGF PATHWAY	*FGF1, FGF23, FGF19*	55	0.05454546	0.0049666
GO:0032496	14	GO Biological Processes	response to lipopolysaccharide	*HCK, IRAK2, MEF2C, ADAM17, RIPK2, IRAK3, IRAK4*	332	0.02108434	0.00504794
hsa04066	18	KEGG Pathway	HIF-1 signaling pathway	*ANGPT1, ANGPT2, EGF, ANGPT4*	110	0.03636364	0.005100029
GO:0002752	14	GO Biological Processes	cell surface pattern recognition receptor signaling pathway	*IRAK2, RIPK2, IRAK4*	56	0.05357143	0.005223883
R-HSA-168643	14	Reactome Gene Sets	Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways	*CASP2, IRAK2, RIPK2*	56	0.05357143	0.005223883
GO:0071216	14	GO Biological Processes	cellular response to biotic stimulus	*HCK, IRAK2, MEF2C, RIPK2, IRAK3, IRAK4*	253	0.02371542	0.005302776

Term	**Group ID**	**Category**	**Description**	**Symbols**	**Pathway size**	**Gene ratio**	***P* value**
GO:0035265	10	GO Biological Processes	organ growth	*COMP, MATN1, STK4, TGFBR3*	112	0.03571429	0.005434137
R-HSA-193648	19	Reactome Gene Sets	NRAGE signals death through JNK	*BAD, NGF, MAGED1*	57	0.05263158	0.005489051
GO:0043549	7	GO Biological Processes	regulation of kinase activity	*ANGPT1, EREG, FGF1, GAS6, PDGFB, TRAF4*	256	0.0234375	0.00560932
GO:0060350	10	GO Biological Processes	endochondral bone morphogenesis	*COMP, MATN1, MEF2C*	60	0.05	0.006332494
WP5180	11	WikiPathways	DYRK1A involvement regarding cell proliferation in brain development	*NCSTN, APH1A, PSENEN*	62	0.0483871	0.006935332
GO:0050852	14	GO Biological Processes	T cell receptor signaling pathway	*MOG, RIPK2, SIVA1, TNFRSF21*	121	0.03305785	0.007118648
GO:0051785	13	GO Biological Processes	positive regulation of nuclear division	*EGF, EREG, PDGFB*	63	0.04761905	0.007249081
R-HSA-450294	14	Reactome Gene Sets	MAP kinase activation	*IRAK2, MEF2C, RIPK2*	63	0.04761905	0.007249081
GO:0002237	14	GO Biological Processes	response to molecule of bacterial origin	*HCK, IRAK2, MEF2C, ADAM17, RIPK2, IRAK3, IRAK4*	357	0.01960784	0.007409881
GO:0045089	14	GO Biological Processes	positive regulation of innate immune response	*EREG, HCK, IRAK2, RIPK2, IRAK3, IRAK4, RTN4*	357	0.01960784	0.007409881
hsa04062	20	KEGG Pathway	Chemokine signaling pathway	*BAD, HCK, SHC2, SHC3, SHC4*	193	0.02590674	0.007452371

Term	Group ID	Category	Description	Symbols	Pathway size	Gene ratio	*P* value
GO:0007249	14	GO Biological Processes	canonical NF-kappaB signal transduction	*IRAK2, TRADD, RIPK2*	64	0.046875	0.00757112
GO:0034109	17	GO Biological Processes	homotypic cell-cell adhesion	*CLIC1, COMP, ITGB3*	65	0.04615385	0.007901497
M237	16	Canonical Pathways	PID VEGFR1 2 PATHWAY	*ITGAV, ITGB3, VTN*	69	0.04347826	0.009307325
GO:1905953	16	GO Biological Processes	negative regulation of lipid localization	*EGF, ITGAV, ITGB3*	70	0.04285714	0.009680077

Results aggregate GO, KEGG, Reactome, WikiPathways, and Canonical Pathways. Top categories include PID p75NTR, PI3K–Akt, neurotrophin signaling, nervous system development, and ECM proteoglycans; gene ratio and *P* value are reported per term.

Abbreviations: ECM, extracellular matrix; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; MAPK, mitogen-activated protein kinase; PID, Pathway Interaction Database; PI3K, phosphoinositide 3-kinase; p75NTR, p75 neurotrophin receptor; PPI, protein–protein interaction; TRK, tropomyosin receptor kinase