

Table S4 Detailed overview of the modules presented in figure S1 including gene lists and their enriched pathways

Disease	module					
AD		1				
Genes	Enrichment					
TCF12	GO	Category	Description	Count	%	Log10(P) Log10(q)
FAM107B	GO:0042552	GO Biological Processes	myelination	9	7.5	-8.09 -4.16
MTMR10	GO:0031344	GO Biological Processes	regulation of cell projection organization	17	14.17	-7.79 -4.05
DOCK5	GO:0001568	GO Biological Processes	blood vessel development	16	13.33	-6.52 -2.97
RNF13	GO:0030036	GO Biological Processes	actin cytoskeleton organization	15	12.5	-6.41 -2.97
LRRC1	GO:0061564	GO Biological Processes	axon development	13	10.83	-6.32 -2.93
FAXDC2	GO:0007420	GO Biological Processes	brain development	15	12.5	-6.02 -2.71
ZNF146	R-HSA-199418	Reactome Gene Sets	Negative regulation of the PI3K/AKT network	6	5	-5.09 -2
CERS2	R-HSA-428157	Reactome Gene Sets	Sphingolipid metabolism	5	4.17	-4.38 -1.38
MITF	GO:0031103	GO Biological Processes	axon regeneration	4	3.33	-4.13 -1.25
ENPP4	GO:0030033	GO Biological Processes	microvillus assembly	3	2.5	-3.89 -1.15
VAMP3	ko04144	KEGG Pathway	Endocytosis	7	5.83	-3.87 -1.15
QKI	GO:0007405	GO Biological Processes	neuroblast proliferation	4	3.33	-3.83 -1.13
TMEM144	GO:0021895	GO Biological Processes	cerebral cortex neuron differentiation	3	2.5	-3.78 -1.11
CCP110	GO:0007628	GO Biological Processes	adult walking behavior	3	2.5	-3.68 -1.06
KLHL32	GO:0043112	GO Biological Processes	receptor metabolic process	6	5	-3.64 -1.05
SPTLC2	GO:0007422	GO Biological Processes	peripheral nervous system development	4	3.33	-3.47 -0.99
TMEM123	GO:0007163	GO Biological Processes	establishment or maintenance of cell polarity	6	5	-3.4 -0.96
C10orf90	GO:0060326	GO Biological Processes	cell chemotaxis	7	5.83	-3.39 -0.96
TRIM59	GO:0038127	GO Biological Processes	ERBB signaling pathway	5	4.17	-3.37 -0.95
USP54	GO:0009791	GO Biological Processes	post-embryonic development	4	3.33	-3.28 -0.89
RBPJ						
SOX10						
LRP2						
SELENOP						
CLDND1						
HIP1						
AMOTL2						
NDE1						
PMP22						
CHRA1						
MYRF						
ADIPOR2						
SNX1						
MYO1E						
ABHD17B						
LAMP2						
FRYL						
REEP3						
SYPL1						
LIPA						
PREX1						
SGMS1						
FRMD5						
ATG4C						
CLCA4						
RFTN2						
FMNL2						
SALL1						
FOXN2						
PSEN1						
NPC1						
CPM						
RDX						
MAN2A1						

DBNDD2
GPR37
FRMD4B
C21orf91
PAK2
ZNF24
ARAP2
UGT8
HSPA2
SCARB2
AMER2
TMEM165
SLAIN1
CTNNA1
FGFR2
SLC12A2
CNTN2
MOB3B
TMTC2
GAB1
GLTP
TMCC3
CREB5
RAP1A
RIOK3
APOD
GPRC5B
PLD1
VEZF1
ITCH
DIP2B
CNP
SLC44A1
ERBB3
ABCA8
RHOG
PHLPP1
ENPP2
JAM3
TMEM87A
PRRG1
CHD7
SYNE3
PICALM
EVI2A
PDE1C
ERMN
LGR5
EFHD1
SOX2-OT
MTUS1
TTYH2
PLP1
SLC31A2
SHROOM4
BOK
RFFL
ANLN
MOSPD2
PIP4K2A

FAM124A
ZDHC9
MINDY1
RHOU
PXX

Disease module
AD 2

Genes	Enrichment				Count	%	Log10(P)	Log10(q)
	GO	Category	Description					
SELENBP1	R-HSA-9006934	Reactome Gene Sets	Signaling by Receptor Tyrosine Kinases		10	12.99	-5.9	-1.84
CNN3	GO:0030900	GO Biological Processes	forebrain development		9	11.69	-5.88	-1.84
SLC16A9	GO:0051961	GO Biological Processes	negative regulation of nervous system developmen		8	10.39	-5.57	-1.82
RFX4	GO:0090066	GO Biological Processes	regulation of anatomical structure size		9	11.69	-4.88	-1.49
FGFRL1	GO:0006883	GO Biological Processes	cellular sodium ion homeostasis		3	3.9	-4.8	-1.46
PAX6	GO:0035988	GO Biological Processes	chondrocyte proliferation		3	3.9	-4.73	-1.46
KCNN3	GO:0010518	GO Biological Processes	positive regulation of phospholipase activity		4	5.19	-4.58	-1.41
FAM189A2	ko04550	KEGG Pathway	Signaling pathways regulating pluripotency of stem		5	6.49	-4.38	-1.39
LINC00299	GO:0106106	GO Biological Processes	cold-induced thermogenesis		5	6.49	-4.31	-1.39
SOX9	GO:0071417	GO Biological Processes	cellular response to organonitrogen compound		8	10.39	-3.6	-0.96
SLC44A3	GO:0097191	GO Biological Processes	extrinsic apoptotic signaling pathway		5	6.49	-3.36	-0.85
AHNAK	GO:0048589	GO Biological Processes	developmental growth		8	10.39	-3.29	-0.84
NEBL	GO:0007264	GO Biological Processes	small GTPase mediated signal transduction		7	9.09	-3.29	-0.84
SH3BP2	GO:0043270	GO Biological Processes	positive regulation of ion transport		5	6.49	-2.95	-0.67
STON2	R-HSA-6806834	Reactome Gene Sets	Signaling by MET		3	3.9	-2.87	-0.63
GPR37L1	GO:0001667	GO Biological Processes	ameboidal-type cell migration		6	7.79	-2.67	-0.53
P2RY1	GO:0006637	GO Biological Processes	acyl-CoA metabolic process		3	3.9	-2.53	-0.44
LRIG1	GO:0097164	GO Biological Processes	ammonium ion metabolic process		4	5.19	-2.51	-0.44
EYA2	GO:0031349	GO Biological Processes	positive regulation of defense response		6	7.79	-2.47	-0.42
ARHGEF26	R-HSA-382551	Reactome Gene Sets	Transport of small molecules		7	9.09	-2.41	-0.37
BMPRI1B								
FIBIN								
ACSS1								
FAM167A								
AMOT								
ID4								
PHYHD1								
FGFR3								
SMOX								
GJA1								
ACOT11								
TMBIM1								
SLC25A18								
MLC1								
AGT								
CLU								
PSD2								
ZNRF3								
FADS2								
TMEM176A								
APPL2								
NOTCH2								
PLPP3								
AQP4								
NADK2								
ATP13A4								
TTPA								
PIPOX								
SLC18B1								

EZR
 TRIL
 OBI1-AS1
 AHCYL1
 F3
 ADCYAP1R1
 SCARA3
 LIX1
 PLSCR4
 ADGRA3
 OTX1
 IL17D
 CDC42EP4
 TP53BP2
 SEMA4B
 GOLIM4
 TNS3
 DOCK7
 NEK6
 PRDM16
 ATP1B2
 EMX2
 PRDX6
 VAC14-AS1
 NTRK2
 ADD3
 ATP1A2

Disease	module
AD	3

Genes	Enrichment				Count	%	Log10(P)	Log10(q)
TCF12	GO	Category	Description					
FAM107B	GO:0042552	GO Biological Processes	myelination		7	9.33	-7.06	-3.15
MTMR10	GO:0120035	GO Biological Processes	regulation of plasma membrane bounded cell proje		11	14.67	-5.47	-1.76
DOCK5	ko00600	KEGG Pathway	Sphingolipid metabolism		4	5.33	-5.11	-1.54
RNF13	GO:0030900	GO Biological Processes	forebrain development		8	10.67	-4.99	-1.52
LRRC1	GO:0010720	GO Biological Processes	positive regulation of cell development		9	12	-4.67	-1.28
FAXDC2	GO:0007405	GO Biological Processes	neuroblast proliferation		4	5.33	-4.63	-1.28
ZNF146	GO:0001568	GO Biological Processes	blood vessel development		10	13.33	-4.3	-1.14
CERS2	GO:0003281	GO Biological Processes	ventricular septum development		4	5.33	-4.28	-1.14
MITF	GO:0009791	GO Biological Processes	post-embryonic development		4	5.33	-4.07	-1.06
ENPP4	GO:0030036	GO Biological Processes	actin cytoskeleton organization		9	12	-3.94	-1.02
VAMP3	ko04142	KEGG Pathway	Lysosome		4	5.33	-3.47	-0.78
QKI	GO:0006486	GO Biological Processes	protein glycosylation		5	6.67	-3.21	-0.64
TMEM144	R-HSA-8856828	Reactome Gene Sets	Clathrin-mediated endocytosis		4	5.33	-3.19	-0.64
CCP110	M295	Canonical Pathways	SIG PIP3 SIGNALING IN CARDIAC MYOCTES		3	4	-3.11	-0.59
KLHL32	GO:0051298	GO Biological Processes	centrosome duplication		3	4	-3.07	-0.56
SPTLC2	GO:0007626	GO Biological Processes	locomotory behavior		4	5.33	-2.69	-0.32
TMEM123	GO:0006835	GO Biological Processes	dicarboxylic acid transport		3	4	-2.62	-0.28
C10orf90	GO:0090066	GO Biological Processes	regulation of anatomical structure size		6	8	-2.56	-0.24
TRIM59	GO:0034446	GO Biological Processes	substrate adhesion-dependent cell spreading		3	4	-2.53	-0.23
USP54	GO:0007163	GO Biological Processes	establishment or maintenance of cell polarity		4	5.33	-2.52	-0.22
RBPJ								
SOX10								
LRP2								
SELENOP								
CLDND1								
HIP1								
AMOTL2								

NDE1
PMP22
CHRA1
MYRF
ADIPOR2
SNX1
MYO1E
ABHD17B
LAMP2
FRYL
REEP3
SYPL1
LIPA
PREX1
SGMS1
FRMD5
ATG4C
CLCA4
RFTN2
FMNL2
SALL1
FOXN2
PSEN1
NPC1
CPM
RDX
MAN2A1
DBNDD2
GPR37
FRMD4B
C21orf91
PAK2
ZNF24
ARAP2
UGT8
HSPA2
SCARB2
AMER2
TMEM165
SLAIN1
CTNNA1
FGFR2
SLC12A2
CNTN2
MOB3B
TMTC2
GAB1

Disease module
Depression 1

Genes	Enrichment	Category	Description	Count	%	Log10(P)	Log10(q)
SEMA6B	GO			103	24.82	-69.62	-65.28
GABBR2	GO:0099537	GO Biological Processes	trans-synaptic signaling	63	15.18	-44.12	-40.47
GUCY1B1	R-HSA-112316	Reactome Gene Sets	Neuronal System	64	15.42	-43.76	-40.19
GRIN2B	GO:0050808	GO Biological Processes	synapse organization	71	17.11	-38.87	-35.48
THY1	GO:0048812	GO Biological Processes	neuron projection morphogenesis	37	8.92	-27.6	-24.53
FAXC	GO:0099003	GO Biological Processes	vesicle-mediated transport in synapse	48	11.57	-26.45	-23.45
SSTR3	GO:0042391	GO Biological Processes	regulation of membrane potential	49	11.81	-21.25	-18.45
SEZ6L2	GO:0007610	GO Biological Processes	behavior				

CAMKV	GO:0016358	GO Biological Processes	dendrite development	32	7.71	-20.07	-17.37
TMEM35A	GO:0007420	GO Biological Processes	brain development	51	12.29	-18.64	-16.05
LINGO1	GO:0060078	GO Biological Processes	regulation of postsynaptic membrane potential	24	5.78	-17.76	-15.2
SV2B	GO:0044057	GO Biological Processes	regulation of system process	43	10.36	-16.12	-13.61
PAK3	ko04020	KEGG Pathway	Calcium signaling pathway	24	5.78	-15.35	-12.87
CLTC	R-HSA-422475	Reactome Gene Sets	Axon guidance	39	9.4	-15.05	-12.59
ELMOD1	GO:0048168	GO Biological Processes	regulation of neuronal synaptic plasticity	15	3.61	-14.97	-12.52
CYFIP2	GO:1990138	GO Biological Processes	neuron projection extension	22	5.3	-13.84	-11.43
PCLO	GO:0036465	GO Biological Processes	synaptic vesicle recycling	15	3.61	-12.63	-10.27
TRIM37	GO:0050905	GO Biological Processes	neuromuscular process	16	3.86	-11.29	-8.97
CAMK1D	GO:0021700	GO Biological Processes	developmental maturation	24	5.78	-10.96	-8.69
GRAMD1B	R-HSA-9617324	Reactome Gene Sets	Negative regulation of NMDA receptor-mediated n	9	2.17	-10.88	-8.6
SLC12A5	GO:0140029	GO Biological Processes	exocytic process	14	3.37	-10.46	-8.21
ISLR2							
LRPPRC							
SNX32							
ATXN10							
UNC5A							
PGM2L1							
NCDN							
TMEM167B							
NAP1L2							
SCAMP5							
DMRTC1B							
CORO2A							
LARP1							
UBE2K							
ACTL6B							
NRGN							
DIRAS2							
RFPL1S							
PRKCG							
SCN8A							
KCNA2							
KCTD16							
ATAD1							
SLC9A7P1							
MYH10							
SCN2A							
PNMA8B							
CLSTN2							
ARF1							
DENND4A							
CACNG8							
UNC80							
DLGAP2							
AL365361.1							
SYNGR1							
ICAM5							
BICDL1							
YWHAH							
PPM1E							
MAP3K9							
DNM1							
SYBU							
NPM2							
KLHL29							
SYT3							
ADD2							
KRT222							

TIMM17A
RSPO3
PCMT1
SYT5
PACSIN1
FGF12
PPP2R5E
CACNA1E
NWD2
SHANK1
SIPA1L1
CAMK4
ADGRL1
CAMKK1
SYT1
MYT1L
CHD5
CLSTN3
SYNJ1
SMIM10L2A
HIPK4
BSN
IQSEC3
SYNGR3
TMEM63C
CA7
UCHL1
ATCAY
PPP3R1
FBXO34
KCNA1
KCNH5
AC004816.1
CNGB1
PCDH8
BCAS4
CAND1
RAB15
RAB3A
BASP1
MCTP1
CACNB1
CHGB
GOT1
DYNC1LI1
NCS1
SYN2
VSNL1
TOMM34
NRIP3
STX1B
NCEH1
CADPS
CALM1
ARF3
NRXN2
WDR7
CHGA
XK
LHFPL4

AGAP2
KIAA0319
GALNT9
GLS
SSTR2
CPEB3
AMIGO1
LRFN1
RAB3C
L1CAM
PRRT2
CAP2
PTPRN
PNMA2
PGAM1
EMX1
CKMT1B
DISP2
NAPB
GLRB
GALNT17
SCRT1
CKMT1A
SLC25A23
NSF
KCNAB1
ANXA6
MAGEE1
ZCCHC12
PRKCE
STMN3
PGBD5
AP3B2
AAGAB
KIAA1549L
MAST1
ENC1
FBXO11
VDAC3
SNCB
KCNQ2
PCDHGC5
RBFox1
PPP3CB
PHF24
RGS7
FBXO41
HPRT1
CNTNAP1
TBC1D9
SUSD4
JAKMIP1
MAP2K1
SRRM3
GPRASP2
CHN1
CDK5R1
DAGLA
RBFox3
DLGAP1

KIT
PDE2A
SH2D5
B4GAT1
PNMA3
BDNF
EPHA5
NDFIP1
PTPN5
MAP2K4
SYN1
PPP3CA
CAMK2B
ADAM23
ATP8A2
PCSK2
PIANP
C4orf50
ADGRA1
BAIAP2
GABRB3
CELF5
USP33
ATP2B2
MAP2
PSMA4
PRICKLE2
MAL2
MTUS2
UBE2QL1
SLC4A3
RUSC2
RAB6B
ELFN2
YWHAG
CHRM3
SPTBN2
AFF2
FAM234B
SCN3B
ARHGEF9
WASL
MCU
CDH9
MRTFA
CPNE9
VPS26B
STXBP1
TUBA8
KIF3A
ABCG4
ELAVL4
SLC25A3
CNNM1
PLXNA4
SYNPR
STMN2
CELF4
CPNE4
ATP5F1C

HTR5A
PFN2
LPCAT4
KCND3
SLC25A22
TMEM178B
GABRG2
AREL1
INPP5J
TMEM130
WDR47
C11orf87
ATP2B3
IMMT
AL353746.1
NEXMIF
ADGRB2
EEF1A2
MDH2
KCNC2
PTK2B
ARHGAP44
MAP7D2
CACNB4
RPAP3
FLRT3
INA
PPP4R4
CHRNA2
CACNG3
SLC4A10
FRMPD4
AC016717.2
AMER3
RNF165
MOAP1
NDRG4
HTR7
PPP2CA
RIMS3
HOOK1
TSPAN18
SLC6A17
CHRM1
KCNIP2
SYT4
ADRA1D
KCNJ3
RAB27B
NPTX1
GABRB2
KCNJ6
SMPD3
RTN4RL1
AJAP1
SMIM10L2B
NCKAP1
AC090578.1
OLFM3
RIMBP2

MLLT11
PPFIA4
FOXG1
NEFM
ATP5F1B
PRKAR1B
GRIN1
ADAM11
ATP6V1C1
SV2A
ATP5F1A
ITPKA
MICAL2
SH3GL2
SYT7
FEM1B
ST8SIA3
NELL2
RTN4RL2
B4GALT6
GFOD1
SVOP
SHANK3
WNK2
CLVS2
KCNB2
PSMD12
EPHA4
LRFN5
GABRA1
NPTN
FBXL16
SLC17A7
PLXNA1
ATP1A3
AAK1
CIT
UNC13A
TSPYL1
SYT13
SPTSSB
ATP2B1
SNX10
LRTM2
CDK5R2
STUM
SEPTIN3
CNKSR2
KCNT1
SNAP25
ATP5PB
KIAA0513
IGSF21
GLS2
CDK14
PHYHIP
VAPA
CELF2
TMEM155
NEFL

HPCAL4
TIMM23
RLIM
DLG4
NMNAT2
KCNA3
SLC9A6
INPP5F
FBLL1
GRIK5
PRKN
KCNA3
OPRL1
ADARB1
GRM1
TBC1D30
GABRA5
ANKRD34A
WASF1
ARHGEF3
ROBO2
OCRL
SRRM4
SNAP91
COPS4
AVL9
AC008105.1
DLG3
MAST3
SCN2B
CACNA1B
PHACTR1
PSMD1
VDAC2
MDH1
LINC01106
ELOVL4
FAM131A
HCN1
NSMF
B4GALNT1
GRK3
SULT4A1
PJA2
RALYL
OPA1
CAMSAP3
SYP
ACTR1A
RTBDN
SHANK2
RBFOX2

Disease **module**
Depression 2

Genes	Enrichment		Description		Count	%	Log10(P)	Log10(q)
RNF125	GO	Category	Description					
PIEZO2	GO:0007272	GO Biological Processes	ensheathment of neurons		26	8.58	-24.02	-19.98
PLCL1	GO:0031344	GO Biological Processes	regulation of cell projection organization		32	10.56	-10.58	-7.14

LINC01792	GO:0014013	GO Biological Processes	regulation of gliogenesis	14	4.62	-9.89	-6.66
SMARCC1	GO:0010720	GO Biological Processes	positive regulation of cell development	24	7.92	-7.73	-4.73
FAM124A	GO:0050768	GO Biological Processes	negative regulation of neurogenesis	17	5.61	-7.55	-4.59
HIPK2	GO:0030036	GO Biological Processes	actin cytoskeleton organization	26	8.58	-7.14	-4.24
REEP3	GO:0007420	GO Biological Processes	brain development	26	8.58	-6.54	-3.7
RASSF2	R-HSA-9675108	Reactome Gene Sets	Nervous system development	21	6.93	-5.81	-3.03
CENPB	GO:0008610	GO Biological Processes	lipid biosynthetic process	24	7.92	-5.75	-2.99
BRCA1	GO:0007422	GO Biological Processes	peripheral nervous system development	8	2.64	-5.72	-2.97
PSEN1	GO:0038127	GO Biological Processes	ERBB signaling pathway	10	3.3	-5.34	-2.61
ARHGEF37	ko00565	KEGG Pathway	Ether lipid metabolism	6	1.98	-5.06	-2.38
PLAAT3	GO:0051272	GO Biological Processes	positive regulation of cellular component movement	20	6.6	-4.88	-2.23
GPR62	GO:0032528	GO Biological Processes	microvillus organization	5	1.65	-4.71	-2.09
NIFK-AS1	R-HSA-199418	Reactome Gene Sets	Negative regulation of the PI3K/AKT network	8	2.64	-4.57	-1.98
ST18	GO:0048708	GO Biological Processes	astrocyte differentiation	7	2.31	-4.48	-1.92
FOXN2	GO:0051597	GO Biological Processes	response to methylmercury	3	0.99	-4.37	-1.84
RDX	GO:0008360	GO Biological Processes	regulation of cell shape	9	2.97	-4.27	-1.77
SEMA6A	GO:0030031	GO Biological Processes	cell projection assembly	19	6.27	-4.26	-1.76
LINC01630	GO:0070444	GO Biological Processes	oligodendrocyte progenitor proliferation	3	0.99	-4.17	-1.71
NUDT16							
MTUS1							
CLCA4							
TMEM165							
ZNF536							
FEZ1							
FGF1							
RNF141							
URI1							
SELENOP							
NPC1							
ZDHHC9							
PLP1							
GLTP							
DYNC1LI2							
ERBIN							
CNP							
FRYL							
CUEDC1							
NKX6-2							
MYRF							
DBNDD2							
MARCKSL1							
PICALM							
KIF1C							
LGR5							
PLEKHB1							
AC096564.1							
SLC31A2							
ZCCHC24							
SEMA3B							
EFCAB14							
QKI							
COL9A3							
ATP10B							
MYO1E							
MINDY1							
KIF13A							
BOK							
PXK							
MOB3B							
DIP2B							

EVI2A
EDIL3
ELOVL1
VEZF1
SHTN1
CTNNA3
TCFL5
ZBTB47
TF
GPR37
BCAS1
PHACTR3-AS1
LRP2
TRIM41
PTPN11
ATF7
GM2A
FGFR2
OTUD7B
COL9A2
SLC35A5
KLHL32
AIF1L
C21orf91
SPOCK3
MAP4K4
SUN2
ZFP91
CCP110
ZNF621
HSPA2
RHOG
CMTM5
LDB3
FOLH1
FADS1
CHADL
SCARB2
MOSPD2
CDK19
DENND5A
NDE1
TMTC2
ENPP2
FADS2
CDC42EP1
FAM107B
S100B
TMEM144
CLDN11
CPM
AGTPBP1
PCBP4
CDK18
MAN2A1
LPAR1
ANP32B
ANKIB1
ADIPOR2
CPOX

MOBP
SH3PXD2A
LLGL1
PLLP
C10orf90
GJC2
TRIM59
PAQR6
LAMP2
SCD
CYP27A1
PRR18
MAP6D1
SLC48A1
SLAIN1
PLD1
WNK1
FOXO4
MAG
DAAM2
AIDAP2
TMEM63A
LACC1
VRK2
LINC00320
ITCH
CD9
KLK6
ABCA8
FAM222A
SLC11A2
RHOU
DOCK5
TMC7
RNF13
ALCAM
RTKN
TP53TG5
SLC44A1
HIP1
COL4A5
GAL3ST1
CNDP1
EFHD1
TMEM98
PHLPP1
SLC45A3
KEL
CERS2
CREB5
FRMD4B
ZEB2
NIPAL4
LHPP
NEK7
PLEKHH1
MTURN
RASGRP3
IFIT2
SLCO1A2

USP54
ATG4C
CAPN3
TJAP1
TMEM123
AC026691.1
FAXDC2
PHF10
TP53INP2
HDAC11
VAMP3
PRR5L
PLPP2
PREX1
PIP4K2A
SHROOM4
SYNGR2
TBC1D12
PHLDB1
AL035106.1
RFFL
ERMN
SOX10
GJB1
SPAG9
PACC1
OPALIN
PADI2
TMEM125
HPN-AS1
TMCC3
FAM178B
KIAA1755
CDH19
IP6K3
LRRC1
JAM3
TIAF1
VWA1
HOXD1
ASPA
S1PR5
COBL
SALL1
NINJ2
SIRT2
SNX6
PCSK6
CARNS1
TSPAN15
SYPL1
NEO1
TMEM87A
GLDN
PAQR4
AMER2
SOX8
LIPE
ITGA2
SOX2-OT

CHRA1
KIF13B
TRPV5
GPRC5B
ALAD
SECISBP2L
DYNC1I2
FNBP1
PPP1R14A
UGT8
MVB12B
SEPTIN10
PMP22
GAB1
MTMR10
CLDND1
PTP4A2
ABHD17B
MAL
EFS
LIPA
CERCAM
FA2H
GPIHBP1
PDE8A
GAB2
PAIP2B
DOCK1
SEPTIN4
GDF11
SOS2
MBP
ZNF664
SPTLC2
CBR1
FBXW4
MOG
MAP4
RNASE1
SH3TC2
ANLN
TMTC4
TFEB
TTYH2
ERBB3
C22orf46
ANKRD40
AC016597.2
TCEANC2
SLC12A2
PRRG1
MYO1D
CPB2-AS1
KIF5B
WIPF1
PLXNB3
MCM7
CNTN2
PLEKHG3
PDE1C

TMEM38B
SEPTIN7
KLHL4
TCP11L2
DNAH17

Disease **module**
Depression 3

Genes	Enrichment			Count	%	Log10(P)	Log10(q)
ALOX5AP	GO	Category	Description				
CD300A	GO:0002274	GO Biological Processes	myeloid leukocyte activation	56	32.56	-47.15	-42.8
HCK	GO:0002694	GO Biological Processes	regulation of leukocyte activation	46	26.74	-36.12	-32.62
PIK3AP1	GO:0002253	GO Biological Processes	activation of immune response	48	27.91	-34.66	-31.27
IL10RA	ko05150	KEGG Pathway	Staphylococcus aureus infection	21	12.21	-31.94	-28.68
DOCK8	R-HSA-1280218	Reactome Gene Sets	Adaptive Immune System	46	26.74	-31.91	-28.68
MPEG1	GO:0001819	GO Biological Processes	positive regulation of cytokine production	37	21.51	-29.66	-26.72
LAT2	GO:0006909	GO Biological Processes	phagocytosis	32	18.6	-26.22	-23.49
TFEC	hsa04380	KEGG Pathway	Osteoclast differentiation	22	12.79	-24.19	-21.52
AC093627.7	GO:0002521	GO Biological Processes	leukocyte differentiation	33	19.19	-22.7	-20.07
ADAP2	GO:0050900	GO Biological Processes	leukocyte migration	32	18.6	-22.12	-19.52
ITGB2	GO:0071216	GO Biological Processes	cellular response to biotic stimulus	24	13.95	-21.21	-18.63
APBB1P	GO:0032103	GO Biological Processes	positive regulation of response to external stimulus	25	14.53	-19.1	-16.63
LPCAT2	GO:0002683	GO Biological Processes	negative regulation of immune system process	27	15.7	-17.33	-14.9
HLA-DQA1	GO:0042116	GO Biological Processes	macrophage activation	15	8.72	-16.17	-13.78
LINC02712	GO:0031349	GO Biological Processes	positive regulation of defense response	26	15.12	-15.55	-13.18
PTAFR	GO:0002886	GO Biological Processes	regulation of myeloid leukocyte mediated immunity	12	6.98	-14.77	-12.46
C1QB	GO:0030098	GO Biological Processes	lymphocyte differentiation	21	12.21	-13.85	-11.59
LAIR1	GO:0098883	GO Biological Processes	synapse pruning	7	4.07	-13.02	-10.84
SCIN	GO:0042089	GO Biological Processes	cytokine biosynthetic process	11	6.4	-12.13	-10
ITGAX	R-HSA-9658195	Reactome Gene Sets	Leishmania infection	16	9.3	-11.34	-9.29
TBXAS1							
LINC01736							
GPR34							
OTULINL							
FGD2							
STAB1							
C1QC							
HPGDS							
PIK3R5							
CCR1							
SLC1A5							
ABI3							
PLCB2							
C1orf162							
HLA-DMA							
PTPN6							
MS4A6A							
TNFRSF1B							
PTPRC							
WAS							
TNFRSF13C							
RASAL3							
SAMSN1							
HCLS1							
RNASET2							
LILRA1							
CSF2RB							
PLCG2							
FCGR3A							

MILR1
HLA-DRB1
ITGAL
FOLR2
SUSD3
CARD11
TAL1
PYCARD
SIGLEC8
RBM47
IL1B
TYROBP
PLD4
RNASE2
MSR1
MAF
PLEK
SELPLG
HLA-DOA
CYTL1
OLFML3
CD68
RGS10
RNASE6
SASH3
RUNX1
CD53
PIK3CG
IL18
IFI30
UCP2
HAVCR2
TNFAIP8L2
EVI2B
LCP2
LPAR5
NCF4
MS4A4A
DOCK2
CCR5
WDFY4
AL357522.1
RGS18
CSF1R
LILRB1
HLA-DMB
FCGR1A
TMC8
CYBB
FCGR1CP
EBI3
P2RY12
TGFB1
TLR7
C3
AOAH
CYBA
PALD1
RAB3IL1
LGALS9

C3AR1
NCF2
LAPTM5
CD86
HLA-DRA
HLA-DPA1
TLR6
TREM2
DEF6
GAL3ST4
NCKAP1L
HCST
FPR1
LY86
FYB1
IRF8
CD84
FCER1G
PSTPIP2
CD14
ADORA3
CX3CR1
PRAM1
CD37
CLEC9A
CD74
CYTH4
CMKLR1
BLNK
VSIG4
SYK
BTK
SLC2A5
RAC2
IKZF1
CLEC7A
MYO1F
P2RY13
CD4
ADAM28
LST1
KCNQ1
GPR65
LILRB4
CTSS
IRF5
TGFB1
RHBDF2
BIN2
TLR2
HAMP
TMIGD3
FCGR2A
SERPINA1
TMEM119
CD33
TLR1
ITGAM
SIGLEC9
C1QA

FCGR1B
S100A11
ALOX5
IGSF6
AIF1

Disease **module**
Depression 4

Genes	Enrichment			Count	%	Log10(P)	Log10(q)
MRPL54	GO	Category	Description				
C19orf53	ko00190	KEGG Pathway	Oxidative phosphorylation	50	29.07	-77.06	-72.71
POLR2L	GO:1902600	GO Biological Processes	proton transmembrane transport	22	12.79	-22.85	-20.17
TRIR	R-HSA-72766	Reactome Gene Sets	Translation	22	12.79	-17.06	-14.4
COX6A1	R-HSA-5628897	Reactome Gene Sets	TP53 Regulates Metabolic Genes	14	8.14	-15.7	-13.11
SNRPC	R-HSA-8953854	Reactome Gene Sets	Metabolism of RNA	28	16.28	-14.88	-12.32
ATP5MC3	CORUM:2920	CORUM	Respiratory chain complex I (lambda subunit) mitoc	8	4.65	-13.67	-11.2
CUTA	ko03010	KEGG Pathway	Ribosome	14	8.14	-12.14	-9.68
UQCRH	CORUM:2905	CORUM	Respiratory chain complex I (intermediate), mitoch	5	2.91	-8.43	-6.08
ATP5MG	R-HSA-1268020	Reactome Gene Sets	Mitochondrial protein import	8	4.65	-8.24	-5.9
POP7	GO:0006626	GO Biological Processes	protein targeting to mitochondrion	9	5.23	-7.96	-5.62
DDT	R-HSA-72165	Reactome Gene Sets	mRNA Splicing - Minor Pathway	7	4.07	-7.51	-5.19
ATOX1	R-HSA-180585	Reactome Gene Sets	Vif-mediated degradation of APOBEC3G	7	4.07	-7.39	-5.08
ATP5ME	CORUM:6442	CORUM	Cytochrome c oxidase, mitochondrial	4	2.33	-5.88	-3.71
LAMTOR2	GO:0006122	GO Biological Processes	mitochondrial electron transport, ubiquinol to cyto	4	2.33	-5.75	-3.6
SERF2	GO:0045116	GO Biological Processes	protein neddylation	4	2.33	-5.63	-3.5
NDUFA7	CORUM:7556	CORUM	PRAME complex	3	1.74	-5.11	-3.02
COX6C	R-HSA-9639288	Reactome Gene Sets	Amino acids regulate mTORC1	5	2.91	-4.65	-2.63
SNX3	R-HSA-8950505	Reactome Gene Sets	Gene and protein expression by JAK-STAT signaling	4	2.33	-4.06	-2.13
COX5B	GO:0051881	GO Biological Processes	regulation of mitochondrial membrane potential	5	2.91	-4.02	-2.1
COX4I1	GO:0042273	GO Biological Processes	ribosomal large subunit biogenesis	5	2.91	-4.02	-2.1
RPP21							
TIMM10							
SOD1							
RPS21							
EDF1							
NOP10							
NDUFA6							
MICOS13							
RPS28							
RBX1							
ATP5IF1							
BEX3							
COX8A							
SLIRP							
NDUFA12							
MIF							
MICOS10							
SF3B5							
ATP5F1E							
RANGRF							
RPL26L1							
RTRAF							
POLR2K							
NCBP2AS2							
ZMAT2							
NDUFA4							
NDUFB9							
MAPKAPK5-AS1							
PEBP1							

PARK7
PSMB6
HSPE1
RPL34
MEA1
NDUFB8
MRPS24
PSMB10
NHP2
NDUFA13
WDR83OS
CHCHD2
NDUFAB1
GPX4
MYL6B
COPS9
UFC1
MRPL36
NDUFB3
MOCS2
NME2
PRDX5
SELENOH
UQCR10
LSM4
ATP5MC1
AURKAIP1
UBA52
COX7A2
MYL12B
RPL27
ATP5PF
PFDN5
BOLA2B
SNRPD2
DYNLL1
BUD31
SNU13
MRPL34
COX14
MRPL51
NDUFA8
MRPL20
NDUFB2
NAA38
NDUFS5
COX6B1
SMDT1
ATP5PD
MED10
LAGE3
UQCR11
COX7C
NDUFB7
NDUFA1
SPAG7
NDUFS8
TOMM7
UBL5
FAU

SDHB
MRPL14
NEDD8
NDUFA2
SMIM26
LAMTOR4
ELOB
ROMO1
SNRNP25
PSMA7
COA3
BLOC1S1
NDUFB4
ATP5PO
RNF7
NDUFS6
HINT1
PITHD1
NDUFS3
PTRHD1
NME1
NDUFA11
TMEM258
UBB
CUEDC2
MTLN
NDUFB1
MRPL57
ATP6V1D
ATP5MPL
UQCRQ
MRPS23
PET100
SSR4
IMP3
MRPL55
HAX1
NDUFB11
PPIA
NDUFB6
NDUFB10
TMEM256
LAMTOR5
BABAM1
ATP5MD
COX7B
NDUFC1
ATP6V1F
RAB5IF
MRPS12
TOMM6
TXNL4A
MRPL27
EIF3K
CACYBP
ALKBH7
TOMM22
PHPT1
ATP5MF
TIMM8B

RPL24
RNF181

Disease **module**
Depression 5

Genes	Enrichment			Count	%	Log10(P)	Log10(q)
ROPN1L	GO	Category	Description				
SLC47A2	GO:0003341	GO Biological Processes	cilium movement	32	21.77	-53.41	-49.06
C11orf16	GO:0035082	GO Biological Processes	axoneme assembly	29	19.73	-47.86	-43.81
AL390236.1	GO:0070286	GO Biological Processes	axonemal dynein complex assembly	16	10.88	-27.81	-24.42
PIH1D2	GO:0003351	GO Biological Processes	epithelial cilium movement	10	6.8	-16.24	-12.93
HYDIN	GO:0030317	GO Biological Processes	flagellated sperm motility	13	8.84	-14.43	-11.23
BBOF1	GO:0001539	GO Biological Processes	cilium or flagellum-dependent cell motility	8	5.44	-11.11	-8
DCDC2	GO:0044458	GO Biological Processes	motile cilium assembly	6	4.08	-8.75	-5.75
DYNLRB2	ko05016	KEGG Pathway	Huntington's disease	9	6.12	-6.05	-3.19
CD36	GO:0021591	GO Biological Processes	ventricular system development	3	2.04	-3.2	-0.43
TMEM232	GO:1902017	GO Biological Processes	regulation of cilium assembly	4	2.72	-3.05	-0.32
TCTEX1D1							
CFAP300							
TEKT1							
CFAP52							
BEST4							
ADGRD2							
CFAP206							
RSPH1							
TEX9							
CRNDE							
TTC6							
DTHD1							
MNS1							
DNAH12							
WDR38							
AC023300.2							
CELSR1							
MAATS1							
SPAG17							
DNAH2							
CATIP							
FHAD1							
IL5RA							
AC093689.1							
RASSF9							
LINC01765							
STOML3							
AGBL2							
LRRC23							
CFAP58							
WDR78							
PRR29							
ZNF474							
NEK11							
C1orf87							
C9orf24							
C22orf15							
DNAI2							
AL672167.1							
C7orf57							
CFAP73							
CCDC153							

SPEF2
DLEC1
RSPH4A
CCDC175
UMODL1-AS1
CFAP65
ADGB
GRAMD2A
SPATA17
MARCHF10
CFAP45
LRRIQ1
WDR63
AC104809.1
CFAP161
ANKUB1
DNAH5
CFAP43
C6orf118
AL161618.1
LRRC46
ARMC4
PPIAP45
DNAH10
DNAAF1
MAP3K19
CCDC146
C11orf88
DRC3
FANK1
CCDC60
CFAP157
FAM216B
CFAP100
AK7
LRRC71
DNAH11
FAM92B
CCDC114
AL357093.2
LRRC74B
DYDC2
FAM81B
NME9
NEK5
CFAP299
ZBBX
DNAAF3
CAPS
CFAP126
ANXA1
MUSK
CFAP70
CFAP54
CAPSL
VWA5B1
DNAH3
CFAP46
SPAG8
SPAG6

C4orf47
 EFCAB1
 CFAP53
 DNAI1
 PIH1D3
 C1orf158
 C1QTNF8
 CASC1
 C1orf194
 DNAH9
 CCDC81
 EFCAB12
 VWA3A
 TTC25
 CFAP47
 MAK
 ZMYND10
 CCDC170
 AC019330.1
 CCDC40
 ANKRD66
 NHLRC4
 FOXJ1
 IQCG
 TUBA4B
 DRC1
 FAM183A
 CFAP77
 CCDC78
 TTC29
 SPA17
 CCDC33
 AC096637.3
 VWA3B
 AC013470.2
 LRRC9
 FAM166B
 WDR93
 PIFO
 DRC7
 ARMC3
 TMEM67

Disease **module**
 Depression 6

Genes	Enrichment				Count	%	Log10(P)	Log10(q)
SLC4A4	GO	Category	Description		17	15.45	-9.58	-5.55
ACACB	GO:0007610	GO Biological Processes	behavior		13	11.82	-9.58	-5.55
GJB6	GO:0042063	GO Biological Processes	gliogenesis		16	14.55	-8.99	-5.34
GRAMD1C	GO:0007423	GO Biological Processes	sensory organ development		11	10	-7.87	-4.56
NOTCH2	GO:0043491	GO Biological Processes	protein kinase B signaling		16	14.55	-7.74	-4.54
ETNPPL	GO:0009611	GO Biological Processes	response to wounding		7	6.36	-7.56	-4.45
RHPN2	GO:0071260	GO Biological Processes	cellular response to mechanical stimulus		4	3.64	-7.14	-4.12
SALL2	GO:0006857	GO Biological Processes	oligopeptide transport		14	12.73	-6.41	-3.65
NTRK2	GO:0048589	GO Biological Processes	developmental growth		6	5.45	-5.84	-3.26
EYA2	GO:0022404	GO Biological Processes	molting cycle process		4	3.64	-5.72	-3.16
MYORG	ko04964	KEGG Pathway	Proximal tubule bicarbonate reclamation		8	7.27	-5.71	-3.16
SLC18B1	GO:0050679	GO Biological Processes	positive regulation of epithelial cell proliferation		11	10	-5.39	-2.91
TTPA	GO:0048871	GO Biological Processes	multicellular organismal homeostasis					

PRDM16	GO:0046320	GO Biological Processes	regulation of fatty acid oxidation	4	3.64	-5.13	-2.72
OPHN1	GO:0000904	GO Biological Processes	cell morphogenesis involved in differentiation	13	11.82	-5.08	-2.68
PRSS35	GO:0090596	GO Biological Processes	sensory organ morphogenesis	8	7.27	-4.94	-2.58
KDM3B	GO:1905332	GO Biological Processes	positive regulation of morphogenesis of an epitheli	4	3.64	-4.92	-2.57
GLI3	GO:0016054	GO Biological Processes	organic acid catabolic process	8	7.27	-4.78	-2.48
TP53BP2	GO:0030534	GO Biological Processes	adult behavior	6	5.45	-4.76	-2.47
SLC1A2	GO:0071396	GO Biological Processes	cellular response to lipid	11	10	-4.67	-2.39
KCNN3	GO:1901615	GO Biological Processes	organic hydroxy compound metabolic process	10	9.09	-4.16	-2.03
F3							
ALDH1L1							
PLPP3							
SLC9A3R1							
EDNRB							
PHKA1							
P2RY2							
P2RY1							
PPARA							
FGF2							
TRIL							
ADGRG1							
AQP4							
SLC7A11							
GLUD1							
ID4							
MRO							
AHNAK							
LINC00299							
ATP1A2							
MLC1							
MSI2							
AL109809.1							
ACSS1							
MMP28							
CYBRD1							
ZHX3							
PBXIP1							
ATP13A4-AS1							
ATP1B2							
PSD2							
CNN3							
GJA1							
PON3							
GPAM							
ZNRF3							
CNTFR							
FAM167A							
SOX21							
PAPLN							
MYO10							
RANBP3L							
EIF4EBP2							
GMNN							
SLC1A3							
METTL7A							
ALDH6A1							
SLC2A10							
SDC4							
TMEM47							
NEK6							
ADGRA3							

FGFR3
 APPL2
 PON2
 SLC15A2
 ATP13A4
 LRIG1
 PHYHD1
 AL136366.1
 TLR4
 MAPK4
 HEPH
 SALL3
 ADHFE1
 SLCO1C1
 MERTK
 ARHGAP31
 BBS2
 OBI1-AS1
 CARMIL1
 SLC25A18
 LRP4
 GPR37L1
 SOX9
 PREX2
 SDC2
 SNTA1
 DAG1
 GABRG1
 UNG
 NR2E1
 AGT
 STOX1
 APCDD1
 NPAS3
 MAOA
 EGFR
 SELENBP1
 HTRA1
 SOX21-AS1

Disease **module**
 Depression 7

Genes	Enrichment		Description	Count	%	Log10(P)	Log10(q)
MCL1	GO	Category					
FOS	R-HSA-9031628	Reactome Gene Sets	NGF-stimulated transcription	5	27.78	-10.47	-6.12
CCNL1	GO:0051412	GO Biological Processes	response to corticosterone	4	22.22	-9.24	-5.5
CSRNP1	GO:0035914	GO Biological Processes	skeletal muscle cell differentiation	5	27.78	-9.18	-5.5
CDKN1A	GO:0043435	GO Biological Processes	response to corticotropin-releasing hormone	3	16.67	-8.65	-5.15
EGR1	M115	Canonical Pathways	PID REG GR PATHWAY	4	22.22	-6.69	-3.58
IER2	GO:0010942	GO Biological Processes	positive regulation of cell death	7	38.89	-6.63	-3.54
ATF3	R-HSA-6785807	Reactome Gene Sets	Interleukin-4 and Interleukin-13 signaling	4	22.22	-6.21	-3.19
BTG2	hsa04928	KEGG Pathway	parathyroid hormone synthesis, secretion and acti	4	22.22	-6.13	-3.13
KLF6	M145	Canonical Pathways	PID P53 DOWNSTREAM PATHWAY	4	22.22	-5.8	-2.85
GADD45B	GO:0009410	GO Biological Processes	response to xenobiotic stimulus	3	16.67	-3.12	-0.7
NR4A1							
FOSB							
NR4A2							
NPAS4							
EGR2							

JUNB
NR4A3

Disease	module
Depression	8

Genes	Enrichment		Description	Count	%	Log10(P)	Log10(q)
	GO	Category					
WDTC1	GO		chromatin remodeling	3	20	-3.89	0
HDAC5	GO:0006338	GO Biological Processes	chromatin remodeling	3	20	-3.89	0
EEF2	GO:0018205	GO Biological Processes	peptidyl-lysine modification	3	20	-2.91	0
ZMIZ2							
DENND1A							
PACS2							
PRRC2A							
ZC3H7B							
TAF6							
RABL6							
SMARCC2							
SLC45A4							
TNPO2							
MLLT6							
TTBK1							