Supplementary Section

Molecular pathology associated with altered synaptic transcriptome in the dorsolateral prefrontal cortex of depressed subjects

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Table S1. Demographic and clinical characteristics of control and MDD subjects

		Control	**MDD**	**p-value**
Number of subjects		15	15	N/A
Age (Year)		57.0 ± 15.0	57.9 ± 14.0	0.87
Gender	Male	8	7	N/A
	Female	7	8	
Postmortem interval (Hour)		18.1 ± 6.0	17.8 ± 6.8	0.87
Brain pH		6.3 ± 0.8	6.5 ± 0.5	0.40
Race (white: black:other)		14: 1: 0	15: 0: 0	N/A
Drug abuse		0	1	N/A
Alcohol abuse		0	3	N/A
Antidepressant drugs		0	6 (Amitriptyline, paroxetine, alprazolam, quetiapine, quetiapine quetiapine, doxepine, bupropion, trazodone)	N/A
Suicide		0	0	N/A
Cause of death		Pulmonary embolism, lymphoma, cardiac failure, lung cancer, acute myocardial infarction, cardiopulmonary arrest, cerebrovascular accident, colon cancer, leukemia, renal failure, cardiac arrest	Cardiopulmonary arrest, pneumonia, cerebrovascular accident, cardiac failure, cardiac arrest, leukemia, heart disease, multiple vehicle accident, liver failure	

Values denote mean ± standard deviation. MDD: Major Depressive Disorder, N/A: not applicable.

Table S2. Primer sequences for qPCR-based mRNA expression analysis

Primers		**Sequences**
RASD1	Forward	TCTGCCCTCCCAAAACTAAGC
	Reverse	TCCATGTTGACACCGGAACT
H1FX	Forward	CGGGTCCTCTCAGTCTTTCC
	Reverse	CAAGGCCGAGAGCCAATAGA
SYN1	Forward	CCCTACTGTTGAGCCCCTTC
	Reverse	ATCCTTGTGGGGCTAGGTGT
IGFBP4	Forward	GACCCACTCCCAAAGCTCAG
	Reverse	CAACCAAGCAGATGGTGCAA
SYN2	Forward	AGCTGACGGTGGTATTGCTT
	Reverse	GACTGACACCACCCTGTAGC
HPSD1	Forward	TGCTGTCATTGTCCATGCCTA
	Reverse	ACATGGCTCTTGTACCCAGT
RBBP4	Forward	TGGCACATCAATCCGCACT
	Reverse	GCATGGCTGGGCACTAAAAA
ZFN32	Forward	GAGACACCCTATCTGTGCGG
	Reverse	AAGTGGTCAAAGGGTGAGCC
TLR2	Forward	ACTACGTGGATGTACCGTCA
	Reverse	AAACAGCACCCCAGACAAAA
ZFP36	Forward	TGCCAAACCCCACCCATAAA
	Reverse	TACAAGGGAAGCAGACGACC
IRF1	Forward	CACCAGGGCTGTCAGTTGAT
	Reverse	TGGAGCAGCATCTGTGTGTT
ELK1	Forward	TGGAGTTGGGAGGGAGGAAT
	Reverse	AAATCACCAACCCCCAGGTC
HES5	Forward	AGAGTCCCTGCCGTTTTAGG
	Reverse	GCCCCGGCACTACAAATATC
ASPDH	Forward	GGCTTCGATGGGGTGATTGG
	Reverse	CCGCTCAGCTCTACATCCAC
CYB561D1	Forward	ATGCTCCTGTGTCTGGTTGG
	Reverse	ACACCAGTGATAGGGACGGA
FUT9	Forward	GCATCCTGGGAGCAAAGCAT
	Reverse	TGGTTGGTAAAGTCGGCGTC

GAPDH	Forward	CCACATCGCTGAGACACCAT
	Reverse	AGTTAAAAGCAGCCCTGGTGA
ACTB	Forward	AGTCATTCCAAATATGAGATGCGTT
	Reverse	TGCTATCACCTCCCCTGTGT
18s rRNA	Forward	CGGCGACGACCCATTCGAAC
	Reverse	GAATCGAACCCTGATTCCCCGTC

Table S3. All significantly up- and down-regulated genes in the total fraction

Gene symbol	Ensemble ID	Locus	Fold change	p-Value	q-Value
Up-regulated genes					
TMEM189-UBE2V1	ENSG00000124208.16_3	chr20:48697661-48770174	2.093301568	0.028970933	0.998154148
HNRNPUL2-BSCL2	ENSG00000234857.2_3	chr11:62457747-62494856	1.862368887	0.029806405	0.998154148
SPI1	ENSG00000066336.11_2	chr11:47376411-47400127	1.674116789	0.016973309	0.998154148
RASD1	ENSG00000108551.4_2	chr17:17397751-17399709	1.671422929	0.008487038	0.998154148
HIST1H1D	ENSG00000124575.6_2	chr6:26234496-26235161	1.6182264	0.021265941	0.998154148
HSPA2	ENSG00000126803.9_3	chr14:65002623-65012891	1.587199534	0.03068192	0.998154148
OLFML3	ENSG00000116774.11_2	chr1:114522013-114578194	1.566558294	0.015948973	0.998154148
H1FX	ENSG00000184897.5_2	chr3:129033614-129035120	1.557723521	0.007713264	0.998154148
TMEM119	ENSG00000183160.8_4	chr12:108983622-108992096	1.533970067	0.027726499	0.998154148
SYN2	ENSG00000157152.16_3	chr3:12045876-12232900	1.529728606	0.025668161	0.998154148
SLC2A5	ENSG00000142583.17_3	chr1:9095166-9148537	1.524777663	0.0259714	0.998154148
MGP	ENSG00000111341.9_2	chr12:15034115-15038860	1.520322977	0.026291557	0.998154148
CD248	ENSG00000174807.3_2	chr11:66081958-66084515	1.517306136	0.012513065	0.998154148
SYN1	ENSG00000008056.13_3	chrX:47431297-47479342	1.514899142	0.010820886	0.998154148
ADAMTS2	ENSG00000087116.14_3	chr5:178537852-178772431	1.504012857	0.023024431	0.998154148
SELENON	ENSG00000162430.16_3	chr1:26126667-26144715	1.502459486	0.018145924	0.998154148
EHD1	ENSG00000110047.17_2	chr11:64619114-64655768	1.499851368	0.00026562	0.998154148
ELK1	ENSG00000126767.17_2	chrX:47494920-47510003	1.485837489	0.005823038	0.998154148
OLFML2B	ENSG00000162745.10_2	chr1:161952982-161993644	1.484633409	0.038133823	0.998154148
IGFBP4	ENSG00000141753.6_2	chr17:38599713-38613983	1.484402089	0.020842833	0.998154148
ABI3	ENSG00000108798.8_3	chr17:47287589-47300587	1.479444697	0.020125555	0.998154148
RCN3	ENSG00000142552.7_2	chr19:50030875-50050219	1.468428048	0.017645622	0.998154148
C1QL1	ENSG00000131094.3_2	chr17:43037061-43045439	1.462663912	0.001072586	0.998154148
CXCL16	ENSG00000161921.14_3	chr17:4636821-4643217	1.459074103	0.036379211	0.998154148
LY6H	ENSG00000176956.12_2	chr8:144239331-144242128	1.451994387	0.038359705	0.998154148
ZNF580	ENSG00000213015.8_3	chr19:56146382-56154835	1.451031456	0.018192279	0.998154148
WAS	ENSG00000015285.10_2	chrX:48534985-48549818	1.441728224	0.02891499	0.998154148
CITED4	ENSG00000179862.6_2	chr1:41326723-41328038	1.441314287	0.017935839	0.998154148
ANKRD63	ENSG00000230778.1_3	chr15:40573645-40574787	1.440832847	0.003236504	0.998154148
CPVL	ENSG00000106066.14_3	chr7:29034847-29235067	1.42116355	0.006864688	0.998154148

MACROD1	ENSG00000133315.10_3	chr11:63766030-63933578	1.416687846	0.004172901	0.998154148
TGFB1	ENSG00000105329.9_2	chr19:41807492-41859816	1.407438515	0.048264988	0.998154148
UTS2R	ENSG00000181408.3_2	chr17:80332106-80333462	1.396622228	0.003928235	0.998154148
TMEM250	ENSG00000238227.7_4	chr9:139006427-139010709	1.391864223	0.013786587	0.998154148
GPR150	ENSG00000178015.4_2	chr5:94955782-94957846	1.388163585	0.015277308	0.998154148
CHTF8	ENSG00000168802.12_3	chr16:69151913-69166487	1.387747039	0.039828071	0.998154148
APBB1IP	ENSG00000077420.15_2	chr10:26727132-26856732	1.384906718	0.043917747	0.998154148
BBC3	ENSG00000105327.17_3	chr19:47724079-47736023	1.384812475	0.006357654	0.998154148
ELN	ENSG00000049540.16_3	chr7:73442119-73484237	1.384729315	0.021770765	0.998154148
RPRM	ENSG00000177519.3_3	chr2:154333852-154335322	1.375723414	0.036936666	0.998154148
RAMP2	ENSG00000131477.10_2	chr17:40910465-40915059	1.374749528	0.047896512	0.998154148
PRRT1	ENSG00000204314.10_2	chr6:32116136-32122150	1.364997463	0.02346281	0.998154148
MAFB	ENSG00000204103.3_2	chr20:39314488-39317880	1.363526305	0.046257386	0.998154148
RTP5	ENSG00000188011.5_2	chr2:242811752-242815975	1.358591765	0.025310842	0.998154148
FAM219A	ENSG00000164970.14_2	chr9:34398182-34458568	1.35646382	0.03572463	0.998154148
PIK3IP1	ENSG00000100100.12_3	chr22:31677579-31688520	1.354405462	0.049762571	0.998154148
LIN37	ENSG00000267796.7_3	chr19:36239262-36245420	1.349361952	0.001828053	0.998154148
LYL1	ENSG00000104903.4_2	chr19:13209847-13213975	1.344030589	0.011272836	0.998154148
LTBP2	ENSG00000119681.11_3	chr14:74964873-75079081	1.342039282	0.035090986	0.998154148
CD37	ENSG00000104894.11_2	chr19:49838428-49846592	1.338776193	0.029333429	0.998154148
CSF3R	ENSG00000119535.17_3	chr1:36931644-36948879	1.33853256	0.018379734	0.998154148
WIPF3	ENSG00000122574.10_2	chr7:29846102-29956682	1.33549892	0.007525526	0.998154148
ATF5	ENSG00000169136.10_3	chr19:50431959-50437192	1.33248749	0.025364887	0.998154148
PRR36	ENSG00000183248.11_2	chr19:7933605-7939264	1.32961583	0.045489483	0.998154148
FAM212A	ENSG00000185614.4_2	chr3:49840687-49842463	1.329368537	0.035084598	0.998154148
SYK	ENSG00000165025.14_2	chr9:93564069-93660831	1.328146351	0.03231606	0.998154148
HK3	ENSG00000160883.10_2	chr5:176307870-176326333	1.32356396	0.013421451	0.998154148
KCNQ1	ENSG00000053918.15_3	chr11:2465914-2870339	1.321441032	0.01270184	0.998154148
NFAM1	ENSG00000235568.6_2	chr22:42776416-42828401	1.320979112	0.02182532	0.998154148
PLPPR2	ENSG00000105520.10_2	chr19:11466062-11476374	1.319630942	0.032818037	0.998154148
GYPC	ENSG00000136732.14_3	chr2:127413509-127454251	1.31916622	0.024361129	0.998154148
GMIP	ENSG00000089639.10_2	chr19:19740285-19754476	1.315489247	0.026706664	0.998154148
IL10RA	ENSG00000110324.10_3	chr11:117857063-117873752	1.311978622	0.017003244	0.998154148
DBN1	ENSG00000113758.13_4	chr5:176883609-176901402	1.309833374	0.017928644	0.998154148
CHGA	ENSG00000100604.12_4	chr14:93389425-93401638	1.309101639	0.023071499	0.998154148

MOGS	ENSG00000115275.11_3	chr2:74688184-74692537	1.308928336	0.00086767	0.998154148
TRNP1	ENSG00000253368.3_3	chr1:27320198-27327389	1.308170907	0.006174039	0.998154148
ADGRE5	ENSG00000123146.19_3	chr19:14491313-14519537	1.307845624	0.032162814	0.998154148
ARHGAP4	ENSG00000089820.15_3	chrX:153172821-153200452	1.306522635	0.008621848	0.998154148
SLC9A1	ENSG00000090020.10_2	chr1:27425306-27493472	1.304350275	0.034164689	0.998154148
UCP2	ENSG00000175567.8_3	chr11:73685712-73694352	1.303259123	0.037705574	0.998154148
HLA-DMB	ENSG00000242574.8_3	chr6:32902406-32908847	1.295387797	0.040308265	0.998154148
PPP1R18	ENSG00000146112.11_2	chr6:30644166-30655672	1.294455305	0.019709809	0.998154148
OSCAR	ENSG00000170909.13_2	chr19:54597933-54606000	1.294417495	0.01439321	0.998154148
FBXL18	ENSG00000155034.18_3	chr7:5470966-5553429	1.294226449	0.043758874	0.998154148
PNRC1	ENSG00000146278.10_2	chr6:89790470-89794879	1.293081969	0.016021982	0.998154148
TOX2	ENSG00000124191.17_2	chr20:42543504-42698256	1.292475229	0.034361075	0.998154148
TMEM184B	ENSG00000198792.12_3	chr22:38615298-38669040	1.290343169	0.049882827	0.998154148
TICAM1	ENSG00000127666.9_2	chr19:4815944-4831716	1.28926153	0.009868033	0.998154148
PCDHGA12	ENSG00000253159.2_3	chr5:140810156-140892546	1.288172369	0.041662243	0.998154148
ZNF687	ENSG00000143373.17_2	chr1:151254094-151264656	1.287295596	0.003434986	0.998154148
UNC93B1	ENSG00000110057.7_3	chr11:67758575-67772452	1.286261619	0.036635069	0.998154148
CMTM3	ENSG00000140931.19_3	chr16:66637777-66647795	1.285256771	0.038392308	0.998154148
CD34	ENSG00000174059.16_4	chr1:208054317-208084747	1.284705424	0.042190788	0.998154148
AC098850.4	ENSG00000266302.6_4	chr17:16593575-16707767	1.283861168	0.038597569	0.998154148
PRAM1	ENSG00000133246.11_2	chr19:8554940-8567996	1.282315029	0.015367944	0.998154148
SLC26A11	ENSG00000181045.14_3	chr17:78193498-78227299	1.279903414	0.034304306	0.998154148
RIN1	ENSG00000174791.10_2	chr11:66097713-66104311	1.275899205	0.005839098	0.998154148
KDELR1	ENSG00000105438.8_2	chr19:48885827-48894810	1.274793024	0.028182492	0.998154148
CEBPA	ENSG00000245848.2_2	chr19:33790840-33793470	1.273480242	0.045344695	0.998154148
CORO7	ENSG00000262246.5_4	chr16:4404543-4475706	1.272891144	0.035288201	0.998154148
TMEM175	ENSG00000127419.16_3	chr4:926175-952444	1.272863271	0.01349447	0.998154148
MED25	ENSG00000104973.16_3	chr19:50321536-50342073	1.270681745	0.016535929	0.998154148
TEF	ENSG00000167074.14_2	chr22:41763337-41795330	1.269899857	0.029924034	0.998154148
FYB1	ENSG00000082074.15_4	chr5:39105338-39274630	1.269899446	0.025860073	0.998154148
TMUB1	ENSG00000164897.12_2	chr7:150778167-150780633	1.267646457	0.017216651	0.998154148
FLOT1	ENSG00000137312.14_2	chr6:30695486-30710510	1.266533143	0.025381547	0.998154148
WDR81	ENSG00000167716.18_3	chr17:1619817-1641893	1.265851309	0.010695608	0.998154148
FAM234A	ENSG00000167930.15_3	chr16:284545-318970	1.264069786	0.04141908	0.998154148
ARHGEF25	ENSG00000240771.6_2	chr12:58003963-58013162	1.262795045	0.027200013	0.998154148

CENPVL3	ENSG00000224109.2_3	chrX:51360907-51361770	1.262008089	0.003213071	0.998154148
ECHDC3	ENSG00000134463.14_3	chr10:11784365-11806069	1.261969349	0.013525789	0.998154148
GRAMD1A	ENSG00000089351.14_3	chr19:35485688-35517375	1.261513464	0.024511043	0.998154148
SNX12	ENSG00000147164.11_3	chrX:70276182-70293276	1.25945196	0.039287017	0.998154148
YPEL3	ENSG00000090238.11_3	chr16:30103635-30108236	1.258496379	0.029936041	0.998154148
SF3A2	ENSG00000104897.9_4	chr19:2236503-2248678	1.258299145	0.028933528	0.998154148
CHMP1A	ENSG00000131165.14_2	chr16:89710839-89724253	1.257199374	0.04261408	0.998154148
MS4A6A	ENSG00000110077.14_4	chr11:59939487-59952139	1.256880221	0.039990751	0.998154148
ZDHHC22	ENSG00000177108.5_3	chr14:77597613-77609077	1.256360962	0.029680791	0.998154148
VPREB3	ENSG00000128218.7_2	chr22:24094930-24096655	1.25634214	0.039219667	0.998154148
EPN3	ENSG00000049283.17_3	chr17:48609904-48621111	1.256337547	0.016817627	0.998154148
Z98749.3	ENSG00000283900.1_2	chr22:38687924-38794527	1.255492154	0.011959624	0.998154148
CARMIL2	ENSG00000159753.13_3	chr16:67678822-67691472	1.254393365	0.048002407	0.998154148
TNFRSF10C	ENSG00000173535.13_2	chr8:22941868-22974950	1.253632774	0.00711036	0.998154148
ZNF503	ENSG00000165655.16_3	chr10:77157588-77161664	1.252966607	0.005541633	0.998154148
FRAT1	ENSG00000165879.8_2	chr10:99079024-99081672	1.25216659	0.000854185	0.998154148
CPNE5	ENSG00000124772.11_2	chr6:36708552-36807778	1.251748722	0.03135507	0.998154148
IRF2BPL	ENSG00000119669.4_2	chr14:77490886-77495042	1.250817775	0.014276884	0.998154148
TBXA2R	ENSG00000006638.11_2	chr19:3594504-3606838	1.249929615	0.005014844	0.998154148
MAPK8IP2	ENSG00000008735.13_2	chr22:51039114-51052409	1.249348402	0.035938689	0.998154148
PLPP1	ENSG00000067113.16_3	chr5:54720682-54830878	1.248928976	0.030956819	0.998154148
TBC1D10B	ENSG00000169221.13_2	chr16:30368423-30381585	1.24884791	0.047418348	0.998154148
IQSEC2	ENSG00000124313.13_3	chrX:53255010-53350526	1.246952196	0.040924259	0.998154148
PILRA	ENSG00000085514.15_4	chr7:99965153-99997722	1.245500464	0.045633292	0.998154148
IRF3	ENSG00000126456.15_3	chr19:50162826-50169132	1.244512894	0.016169615	0.998154148
H1F0	ENSG00000189060.5_2	chr22:38201100-38203443	1.242274521	0.019109489	0.998154148
ZGPAT	ENSG00000197114.11_3	chr20:62338817-62367494	1.242126229	0.047414749	0.998154148
MAP2K2	ENSG00000126934.13_2	chr19:4090319-4124126	1.241750844	0.026266732	0.998154148
ZC3H3	ENSG00000014164.6_2	chr8:144519825-144623623	1.241674282	0.032984036	0.998154148
HSD11B2	ENSG00000176387.6_2	chr16:67464555-67471456	1.240862038	0.02640214	0.998154148
MAP7D1	ENSG00000116871.15_4	chr1:36621180-36646450	1.240647838	0.046467479	0.998154148
DMRTC1B	ENSG00000184911.14_4	chrX:71996833-72068636	1.239681166	0.014131602	0.998154148
DCAF15	ENSG00000132017.10_3	chr19:14063304-14072261	1.239627615	0.027237674	0.998154148
NEURL2	ENSG00000124257.6_2	chr20:44517264-44519926	1.237648385	0.045806968	0.998154148
MEF2D	ENSG00000116604.17_3	chr1:156433519-156470620	1.236800814	0.022173543	0.998154148

ATN1	ENSG00000111676.14_2	chr12:7033626-7051484	1.236547688	0.049947864	0.998154148
FAM46B	ENSG00000158246.7_2	chr1:27331511-27339327	1.236543611	0.038720862	0.998154148
ZNF414	ENSG00000133250.13_2	chr19:8574562-8579048	1.236031808	0.038160921	0.998154148
EPN1	ENSG00000063245.14_3	chr19:56186592-56221224	1.235537574	0.029422358	0.998154148
RNF26	ENSG00000173456.4_2	chr11:119205237-119208023	1.233283602	0.034126728	0.998154148
DMRTC1	ENSG00000269502.5_3	chrX:72091859-72163643	1.232011759	0.027055565	0.998154148
HPCAL1	ENSG00000115756.12_3	chr2:10443015-10567743	1.231646799	0.046724564	0.998154148
PARVG	ENSG00000138964.16_3	chr22:44568836-44615413	1.231528349	0.032680199	0.998154148
TIMM29	ENSG00000142444.6_2	chr19:11039409-11044211	1.231360932	0.032175143	0.998154148
CHST1	ENSG00000175264.7_2	chr11:45670427-45687172	1.230542227	0.008799872	0.998154148
LILRB4	ENSG00000186818.12_3	chr19:55155340-55181810	1.22892909	0.041270466	0.998154148
FAM189B	ENSG00000160767.20_3	chr1:155216996-155225274	1.227694877	0.04889218	0.998154148
FAM214B	ENSG00000005238.19_2	chr9:35104109-35116338	1.226832726	0.016761706	0.998154148
LOXL1	ENSG00000129038.15_2	chr15:74218330-74244478	1.226007718	0.012127077	0.998154148
PLCB2	ENSG00000137841.11_3	chr15:40570377-40600136	1.224290889	0.040442992	0.998154148
CBX4	ENSG00000141582.14_3	chr17:77806955-77813228	1.219360485	0.018393571	0.998154148
REEP4	ENSG00000168476.11_3	chr8:21995533-21999464	1.219224627	0.048826155	0.998154148
TMEM219	ENSG00000149932.16_2	chr16:29952206-29984373	1.218901567	0.045031882	0.998154148
NUCB1	ENSG00000104805.15_4	chr19:49403307-49426629	1.218433803	0.043787086	0.998154148
SCAF1	ENSG00000126461.14_4	chr19:50145382-50161899	1.213257723	0.01796601	0.998154148
CCDC92	ENSG00000119242.8_3	chr12:124403207-124457378	1.212157757	0.034289623	0.998154148
RAB8A	ENSG00000167461.11_3	chr19:16222439-16245044	1.210984893	0.04918032	0.998154148
CCDC120	ENSG00000147144.12_3	chrX:48911101-48927509	1.2108742	0.023224527	0.998154148
IFFO1	ENSG00000010295.19_3	chr12:6647541-6665249	1.210380167	0.026730574	0.998154148
CC2D1A	ENSG00000132024.17_3	chr19:14017014-14041692	1.210156098	0.034319422	0.998154148
PRR19	ENSG00000188368.9_4	chr19:42806250-42814973	1.208071838	0.011187886	0.998154148
ATXN2L	ENSG00000168488.18_3	chr16:28834356-28848558	1.205998217	0.00826407	0.998154148
MARCH9	ENSG00000139266.5_2	chr12:58148881-58154190	1.205933707	0.048561097	0.998154148
FHL3	ENSG00000183386.9_2	chr1:38462442-38471278	1.205539088	0.049611821	0.998154148
IL27RA	ENSG00000104998.3_2	chr19:14142560-14164028	1.205413768	0.038545702	0.998154148
ZNF777	ENSG00000196453.7_2	chr7:149128454-149158214	1.205124237	0.035023567	0.998154148
BAG1	ENSG00000107262.19_4	chr9:33247818-33264718	1.20502387	0.03454745	0.998154148
PALM3	ENSG00000187867.8_2	chr19:14164177-14169971	1.203993191	0.016492135	0.998154148
EFEMP2	ENSG00000172638.12_3	chr11:65633912-65641063	1.203885941	0.0409432	0.998154148
KDF1	ENSG00000175707.8_2	chr1:27276053-27286897	1.2031965	0.028941187	0.998154148

FAIM2	ENSG00000135472.8_2	chr12:50260679-50298000	1.201533467	0.046380128	0.998154148
AC011897.1	ENSG00000265629.1	chr2:14775215-14790933	1.200024946	0.047682398	0.998154148
MISP3	ENSG00000141854.9_3	chr19:14183348-14185874	1.197526506	0.035501877	0.998154148
STIM1	ENSG00000167323.11_3	chr11:3875757-4114440	1.19676625	0.04960973	0.998154148
AQP9	ENSG00000103569.9_3	chr15:58430368-58478110	1.196477072	0.044175948	0.998154148
FCHSD1	ENSG00000197948.10_2	chr5:141018869-141030986	1.195007475	0.026266905	0.998154148
DENND1C	ENSG00000205744.9_3	chr19:6467218-6482568	1.193688939	0.028619529	0.998154148
DPH2	ENSG00000132768.13_2	chr1:44435672-44439041	1.192547301	0.028123128	0.998154148
GOLGA7B	ENSG00000155265.10_2	chr10:99609996-99631337	1.190980819	0.049999209	0.998154148
AKAP8	ENSG00000105127.8_2	chr19:15464196-15490609	1.189835679	0.013836201	0.998154148
AL049844.1	ENSG00000257065.1_4	chr6:144128229-144165754	1.189584861	0.031421592	0.998154148
ZSWIM8	ENSG00000214655.10_3	chr10:75545340-75561555	1.188953944	0.045516401	0.998154148
MINK1	ENSG00000141503.15_3	chr17:4736683-4801356	1.187427802	0.042404185	0.998154148
KIAA1211	ENSG00000109265.13_4	chr4:56915239-57194791	1.180047447	0.039572492	0.998154148
CNOT3	ENSG00000088038.17_3	chr19:54641444-54659419	1.179581851	0.022284019	0.998154148
KCNK13	ENSG00000152315.4_3	chr14:90528109-90652201	1.179488039	0.046428605	0.998154148
FIGNL2	ENSG00000261308.2_2	chr12:52211624-52242550	1.178955985	0.00427692	0.998154148
SYVN1	ENSG00000162298.18_3	chr11:64889252-64902004	1.178337248	0.047129168	0.998154148
USP2	ENSG00000036672.15_3	chr11:119225925-119252436	1.17750312	0.035917434	0.998154148
CHERP	ENSG00000085872.14_3	chr19:16628700-16653341	1.174176363	0.020499741	0.998154148
MKL1	ENSG00000196588.14_3	chr22:40806285-41032706	1.172087662	0.040356872	0.998154148
FRAT2	ENSG00000181274.6_2	chr10:99092254-99094466	1.170560935	0.039615989	0.998154148
MAPK8IP1	ENSG00000121653.11_2	chr11:45907202-45928016	1.170325522	0.031905401	0.998154148
PHF13	ENSG00000116273.5_2	chr1:6673745-6684093	1.17024421	0.009403881	0.998154148
CDIPT	ENSG00000103502.13_2	chr16:29869678-29875057	1.169565208	0.022727541	0.998154148
RSPO4	ENSG00000101282.8_2	chr20:939095-982907	1.165890678	0.012402888	0.998154148
VSTM2B	ENSG00000187135.7_2	chr19:30017406-30055386	1.164958043	0.043166071	0.998154148
ALDH3B1	ENSG00000006534.15_2	chr11:67776048-67796749	1.164038261	0.049171069	0.998154148
GCK	ENSG00000106633.15_2	chr7:44183870-44237769	1.16275176	0.038666542	0.998154148
ADPRHL1	ENSG00000153531.13_3	chr13:114053925-114107839	1.16130856	0.045462974	0.998154148
ZMYND15	ENSG00000141497.13_2	chr17:4643310-4649414	1.156489742	0.036519367	0.998154148
CALHM2	ENSG00000138172.10_2	chr10:105206543-105212159	1.156295872	0.037591175	0.998154148
TINCR	ENSG00000223573.6_3	chr19:5558178-5568045	1.154064039	0.037996827	0.998154148
HTR1D	ENSG00000179546.4_3	chr1:23518388-23521222	1.152832868	0.007321327	0.998154148
UNK	ENSG00000132478.9_3	chr17:73780852-73821880	1.145287907	0.048767977	0.998154148

C19orf57	ENSG00000132016.11_2	chr19:13993161-14017265	1.141675582	0.01483579	0.998154148
ZDHHC7	ENSG00000153786.12_3	chr16:85007787-85045141	1.138777196	0.042348993	0.998154148
PSD4	ENSG00000125637.15_3	chr2:113914902-113966973	1.136417941	0.032569402	0.998154148
ARHGAP27	ENSG00000159314.11_3	chr17:43471268-43511787	1.13016636	0.047166984	0.998154148
AC245033.1	ENSG00000260836.1_4	chr15:83208783-83224682	1.117217036	0.035776861	0.998154148
SPPL3	ENSG00000157837.15_3	chr12:121200313-121342174	1.116406511	0.025117764	0.998154148
CIZ1	ENSG00000148337.20_3	chr9:130928343-130966662	1.107052403	0.012425977	0.998154148
Down-regulated genes					
ITGAE	ENSG00000083457.11_2	chr17:3617922-3704537	0.937559176	0.039233262	0.998154148
MTO1	ENSG00000135297.15_2	chr6:74171301-74218959	0.910465468	0.034373979	0.998154148
PRDM5	ENSG00000138738.10_3	chr4:121606074-121844025	0.90842461	0.019908993	0.998154148
CMC2	ENSG00000103121.8_3	chr16:81000345-81053875	0.904900431	0.010098337	0.998154148
AFG1L	ENSG00000135537.16_4	chr6:108616098-108847999	0.901369232	0.03136285	0.998154148
CEP83	ENSG00000173588.14_3	chr12:94700225-94853764	0.901204785	0.041106844	0.998154148
TECTA	ENSG00000109927.9_3	chr11:120971882-121062202	0.90053653	0.044549134	0.998154148
C1orf131	ENSG00000143633.12_3	chr1:231359509-231376933	0.899590718	0.024883933	0.998154148
HAUS1	ENSG00000152240.12_2	chr18:43684298-43708299	0.897269659	0.032566167	0.998154148
PIN4	ENSG00000102309.12_3	chrX:71401203-71522776	0.897010706	0.041540967	0.998154148
AP3S2	ENSG00000157823.16_3	chr15:90373831-90437870	0.893331601	0.035023666	0.998154148
TMEM116	ENSG00000198270.12_4	chr12:112369086-112450989	0.89259114	0.034579064	0.998154148
EFCAB6	ENSG00000186976.14_3	chr22:43924624-44208217	0.891949763	0.048979378	0.998154148
COG2	ENSG00000135775.13_2	chr1:230778235-230829728	0.891376761	0.049634007	0.998154148
APLF	ENSG00000169621.9_4	chr2:68694693-68882994	0.888731908	0.03550356	0.998154148
PROM1	ENSG00000007062.11_3	chr4:15964699-16086001	0.887604983	0.045747121	0.998154148
PCDHA8	ENSG00000204962.5_3	chr5:140220772-140391929	0.886855433	0.049626064	0.998154148
GTF2E1	ENSG00000153767.9_3	chr3:120461484-120501916	0.883307979	0.043196557	0.998154148
ZNF101	ENSG00000181896.11_3	chr19:19779605-19794318	0.883139347	0.02450328	0.998154148
PTRH2	ENSG00000141378.14_2	chr17:57751997-57784987	0.882647994	0.025902767	0.998154148
CBFA2T2	ENSG00000078699.21_2	chr20:32077881-32237842	0.881911109	0.044382759	0.998154148
KIAA0907	ENSG00000132680.10_3	chr1:155882834-155904191	0.881518112	0.043701589	0.998154148
HYKK	ENSG00000188266.13_2	chr15:78799906-78829714	0.880072407	0.02921606	0.998154148
ZNF229	ENSG00000278318.4_3	chr19:44921685-44952766	0.879799197	0.020186005	0.998154148
B3GALNT2	ENSG00000162885.12_2	chr1:235613238-235667781	0.879109274	0.032853327	0.998154148
NBPF3	ENSG00000142794.18_3	chr1:21766621-21811498	0.87876567	0.039145107	0.998154148
C2orf42	ENSG00000115998.7_3	chr2:70377012-70475747	0.878397634	0.045605554	0.998154148

COQ5	ENSG00000110871.14_3	chr12:120941077-120972237	0.877445918	0.04988016	0.998154148
TCAIM	ENSG00000179152.19_2	chr3:44379611-44450943	0.876255874	0.022788154	0.998154148
ZGRF1	ENSG00000138658.15_3	chr4:113460489-113558151	0.874672595	0.041201931	0.998154148
CCDC148	ENSG00000153237.17_2	chr2:159027593-159313265	0.874317573	0.040879138	0.998154148
ZNF470	ENSG00000197016.11_3	chr19:57078880-57100279	0.873837764	0.033241111	0.998154148
CLCN5	ENSG00000171365.15_3	chrX:49687225-49863892	0.872365383	0.015183493	0.998154148
LLPH	ENSG00000139233.6_3	chr12:66510335-66524548	0.868196543	0.007871643	0.998154148
INTS6L	ENSG00000165359.15_3	chrX:134654568-134716435	0.868061629	0.042315812	0.998154148
SRBD1	ENSG00000068784.12_2	chr2:45615819-45839304	0.867425699	0.033605132	0.998154148
ZNF420	ENSG00000197050.10_3	chr19:37498759-37621216	0.867158359	0.038245875	0.998154148
ZNF28	ENSG00000198538.10_3	chr19:53300662-53360853	0.867002109	0.049143936	0.998154148
BRAP	ENSG00000089234.15_3	chr12:112079950-112123790	0.866498758	0.006329511	0.998154148
COX20	ENSG00000203667.9_2	chr1:244998624-245008359	0.865615572	0.041589931	0.998154148
ZNF330	ENSG00000109445.10_3	chr4:142142041-142155851	0.863654627	0.04641773	0.998154148
ZNF804B	ENSG00000182348.6_2	chr7:88388682-88966371	0.86354437	0.00437694	0.998154148
WDR78	ENSG00000152763.16_2	chr1:67278568-67390570	0.863384059	0.027051146	0.998154148
ST6GAL2	ENSG00000144057.15_3	chr2:107418056-107503564	0.863107417	0.036827037	0.998154148
INTS13	ENSG00000064102.14_2	chr12:27058114-27091259	0.862602546	0.033613575	0.998154148
ING3	ENSG00000071243.15_2	chr7:120590803-120617270	0.862200451	0.020259214	0.998154148
FAM184B	ENSG00000047662.4_2	chr4:17630929-17783135	0.861703971	0.030293451	0.998154148
ZNF749	ENSG00000186230.6_3	chr19:57946697-57956853	0.861197561	0.049969053	0.998154148
NRF1	ENSG00000106459.14_2	chr7:129251555-129396922	0.861126787	0.029941728	0.998154148
ZNF571	ENSG00000180479.13_2	chr19:38045684-38085691	0.859541772	0.038220795	0.998154148
HAT1	ENSG00000128708.12_2	chr2:172778958-172848596	0.859147955	0.032231134	0.998154148
SNX25	ENSG00000109762.15_2	chr4:186125391-186291339	0.859118875	0.018687806	0.998154148
SYDE2	ENSG00000097096.8_2	chr1:85622556-85666729	0.856872991	0.035663879	0.998154148
EXOSC8	ENSG00000120699.12_3	chr13:37572953-37583750	0.8565462	0.042749302	0.998154148
C5	ENSG00000106804.7_2	chr9:123714613-123812554	0.856292725	0.011729918	0.998154148
WNK3	ENSG00000196632.10_3	chrX:54219256-54385075	0.855529679	0.036951048	0.998154148
ZBTB26	ENSG00000171448.8_2	chr9:125677845-125693779	0.855460372	0.048767298	0.998154148
ZNF143	ENSG00000166478.9_3	chr11:9481866-9550071	0.855069345	0.016542077	0.998154148
TMEM138	ENSG00000149483.11_2	chr11:61129473-61136981	0.854565311	0.02570802	0.998154148
RPIA	ENSG00000153574.8_2	chr2:88991162-89050452	0.853072317	0.036995561	0.998154148
SPRED2	ENSG00000198369.9_3	chr2:65537985-65659771	0.852810015	0.04134861	0.998154148
ZNF549	ENSG00000121406.8_2	chr19:58038693-58068910	0.852415333	0.027971884	0.998154148

TBCCD1	ENSG00000113838.12_3	chr3:186263862-186288332	0.852282031	0.022906767	0.998154148
ZSCAN21	ENSG00000166529.14_2	chr7:99647397-99662661	0.852144054	0.005769904	0.998154148
ZNF10	ENSG00000256223.5_3	chr12:133707161-133736051	0.852033858	0.049823058	0.998154148
SEL1L3	ENSG00000091490.10_3	chr4:25749049-25865382	0.851896384	0.030046817	0.998154148
GNPAT	ENSG00000116906.11_3	chr1:231376953-231413719	0.851323487	0.046747047	0.998154148
PYROXD1	ENSG00000121350.15_2	chr12:21590549-21624186	0.850813366	0.026805023	0.998154148
DCAF17	ENSG00000115827.13_3	chr2:172290727-172341562	0.850640374	0.022532351	0.998154148
DHFR2	ENSG00000178700.7_3	chr3:93766680-93782233	0.850253114	0.011485906	0.998154148
ZNF322	ENSG00000181315.10_3	chr6:26634611-26659980	0.850106466	0.039396684	0.998154148
WASHC3	ENSG00000120860.10_3	chr12:102406705-102455927	0.850001287	0.024321285	0.998154148
S100PBP	ENSG00000116497.17_3	chr1:33282368-33324480	0.849946658	0.045894145	0.998154148
THADA	ENSG00000115970.18_3	chr2:43457975-43823185	0.84859352	0.013666855	0.998154148
NUDT15	ENSG00000136159.3_2	chr13:48611703-48621358	0.848000137	0.041287143	0.998154148
CNTNAP3B	ENSG00000154529.10	chr9:43684902-43924049	0.847475962	0.039200767	0.998154148
POLR1B	ENSG00000125630.15_2	chr2:113299492-113334727	0.847428265	0.021118645	0.998154148
TTPA	ENSG00000137561.4_2	chr8:63961112-63998612	0.84488278	0.037238954	0.998154148
RBM34	ENSG00000188739.14_3	chr1:235294498-235324772	0.844852633	0.025783746	0.998154148
SOX6	ENSG00000110693.17_3	chr11:15987995-16761138	0.844156122	0.016625836	0.998154148
ZNF610	ENSG00000167554.14_2	chr19:52839498-52871031	0.843991324	0.024844326	0.998154148
KIAA1143	ENSG00000163807.5_2	chr3:44779153-44803154	0.843458346	0.047586775	0.998154148
FAAH2	ENSG00000165591.6_2	chrX:57313139-57515629	0.842938279	0.033542833	0.998154148
UBXN8	ENSG00000104691.14_3	chr8:30589764-30624522	0.842705342	0.03706639	0.998154148
NECTIN3	ENSG00000177707.10_3	chr3:110788918-110994410	0.841803775	0.021271187	0.998154148
FXN	ENSG00000165060.11_3	chr9:71650175-71715094	0.841145026	0.006870013	0.998154148
MNAT1	ENSG00000020426.10_3	chr14:61201460-61436671	0.84060604	0.03447681	0.998154148
SDHC	ENSG00000143252.14_2	chr1:161284047-161345130	0.840134938	0.017708017	0.998154148
ZNF761	ENSG00000160336.14_3	chr19:53935246-53961515	0.83957076	0.042689333	0.998154148
ZNF468	ENSG00000204604.9_3	chr19:53341261-53360902	0.838670553	0.0214953	0.998154148
KLHL20	ENSG00000076321.10_3	chr1:173684080-173755840	0.83782626	0.011677379	0.998154148
U2AF1L5	ENSG00000275895.6_4	chr21:44513066-44527693	0.837420787	0.033815163	0.998154148
NT5E	ENSG00000135318.11_3	chr6:86159302-86205509	0.835936472	0.015883428	0.998154148
ZNF415	ENSG00000170954.11_4	chr19:53611132-53636330	0.835774411	0.036544448	0.998154148
ZNF883	ENSG00000228623.5_1	chr9:115720002-115812323	0.835513559	0.035661451	0.998154148
BDNF	ENSG00000176697.18_3	chr11:27676440-27743605	0.835200945	0.03308505	0.998154148
TIMMDC1	ENSG00000113845.9_2	chr3:119217379-119243937	0.835075439	0.022781485	0.998154148

EPB41L5	ENSG00000115109.13_2	chr2:120770581-120936695	0.834755246	0.039226633	0.998154148
FAM206A	ENSG00000119328.11_2	chr9:111696461-111713024	0.833922498	0.026167117	0.998154148
PRKD1	ENSG00000184304.14_4	chr14:30045685-30661104	0.831883887	0.028437524	0.998154148
CWC25	ENSG00000273559.4_2	chr17:36956687-36981734	0.831754483	0.010681401	0.998154148
MARC1	ENSG00000186205.12_3	chr1:220960101-220992999	0.831715965	0.018499295	0.998154148
KIAA0586	ENSG00000100578.14_4	chr14:58894103-59018007	0.831543164	0.034692463	0.998154148
PLPBP	ENSG00000147471.11_4	chr8:37620111-37637285	0.831473656	0.043022808	0.998154148
LRP2BP	ENSG00000109771.15_2	chr4:186285033-186317053	0.830633737	0.040152033	0.998154148
FBXO16	ENSG00000214050.7_3	chr8:28205804-28347835	0.829598375	0.02478746	0.998154148
PAAF1	ENSG00000175575.12_2	chr11:73587744-73642169	0.829479609	0.007253391	0.998154148
KIF27	ENSG00000165115.14_2	chr9:86451613-86536380	0.828087838	0.030180324	0.998154148
VWC2L	ENSG00000174453.9_3	chr2:215275789-215443683	0.82793781	0.0294608	0.998154148
PXMP2	ENSG00000176894.9_3	chr12:133264192-133281577	0.827659652	0.041337544	0.998154148
TNNT1	ENSG00000105048.16_2	chr19:55644162-55660722	0.827234609	0.036510138	0.998154148
DCHS2	ENSG00000197410.12_1	chr4:155153189-155412868	0.827081705	0.02899233	0.998154148
BRD7	ENSG00000166164.15_3	chr16:50347398-50402845	0.826976017	0.034620297	0.998154148
PEX12	ENSG00000108733.9_3	chr17:33901814-33905882	0.826933835	0.025111113	0.998154148
ZNF562	ENSG00000171466.9_3	chr19:9752484-9785762	0.826073297	0.028263248	0.998154148
MSH6	ENSG00000116062.14_3	chr2:47922669-48037240	0.824938523	0.023279416	0.998154148
MRPS22	ENSG00000175110.11_3	chr3:138724648-139076065	0.823281569	0.003584798	0.998154148
COMMD10	ENSG00000145781.8_2	chr5:115420688-115748459	0.82320552	0.019276292	0.998154148
S100A13	ENSG00000189171.14_3	chr1:153591263-153603836	0.822323012	0.016706959	0.998154148
TSPAN12	ENSG00000106025.8_2	chr7:120427374-120498456	0.821454208	0.032565656	0.998154148
MRPL47	ENSG00000136522.13_2	chr3:179306073-179322442	0.820240262	0.034058717	0.998154148
RBM28	ENSG00000106344.8_3	chr7:127937738-127983962	0.820027942	0.0409239	0.998154148
SMG7	ENSG00000116698.21_3	chr1:183441351-183567381	0.819881274	0.032186278	0.998154148
C12orf49	ENSG00000111412.5_2	chr12:117147990-117175875	0.819357723	0.017175047	0.998154148
SLC25A33	ENSG00000171612.6_3	chr1:9599541-9645237	0.819276085	0.041476807	0.998154148
LYRM2	ENSG00000083099.10_2	chr6:90277863-90348472	0.817864529	0.008061349	0.998154148
PHACTR2	ENSG00000112419.14_3	chr6:143857982-144152322	0.817641259	0.02680242	0.998154148
ADHFE1	ENSG00000147576.15_3	chr8:67342420-67383836	0.817189796	0.008036173	0.998154148
ZNF334	ENSG00000198185.11_3	chr20:45128269-45142198	0.816737908	0.019624702	0.998154148
TAF11	ENSG00000064995.16_2	chr6:34845555-34855866	0.816081323	0.025533362	0.998154148
UBXN2A	ENSG00000173960.13_3	chr2:24150155-24227779	0.815206282	0.008464835	0.998154148
ZNF614	ENSG00000142556.18_3	chr19:52516018-52533493	0.812879662	0.011409011	0.998154148

UTP6	ENSG00000108651.9_2	chr17:30187918-30228784	0.812707045	0.018120549	0.998154148
PLCH1	ENSG00000114805.16_3	chr3:155093369-155462856	0.812145362	0.044987961	0.998154148
PRELID3A	ENSG00000141391.13_3	chr18:12407895-12432237	0.810555804	0.022078299	0.998154148
ZFP3	ENSG00000180787.5_2	chr17:4981543-4999669	0.809872741	0.005821418	0.998154148
NDUFAF7	ENSG00000003509.15_2	chr2:37458774-37480546	0.809738934	0.028668135	0.998154148
LRRC6	ENSG00000129295.8_2	chr8:133584201-133687863	0.807175474	0.048213135	0.998154148
ZW10	ENSG00000086827.8_3	chr11:113603909-113644533	0.807066572	0.014907383	0.998154148
MIS12	ENSG00000167842.15_2	chr17:5389605-5394134	0.806987816	0.008428619	0.998154148
TRIB2	ENSG00000071575.11_2	chr2:12857015-12882860	0.804887983	0.040491981	0.998154148
AC004076.1	ENSG00000268163.1_4	chr19:57949338-57988904	0.804581253	0.017412907	0.998154148
RGPD3	ENSG00000153165.18_2	chr2:107007746-107084832	0.803091307	0.043208367	0.998154148
AL121845.3	ENSG00000273154.3_4	chr20:62340216-62370456	0.80126645	0.037421084	0.998154148
SRP19	ENSG00000153037.13_3	chr5:112196919-112205485	0.800697338	0.0489681	0.998154148
HSD17B6	ENSG00000025423.11_3	chr12:57145945-57181574	0.800373574	0.039449677	0.998154148
AC018630.6	ENSG00000275778.1_4	chr12:10998448-11324197	0.800002824	0.015909879	0.998154148
RPF2	ENSG00000197498.12_2	chr6:111303218-111349466	0.79908781	0.044183911	0.998154148
PAK1IP1	ENSG00000111845.4_2	chr6:10694928-10710015	0.797721913	0.013261023	0.998154148
VWA8	ENSG00000102763.17_3	chr13:42140973-42535256	0.797470431	0.007075448	0.998154148
SPRY2	ENSG00000136158.11_3	chr13:80910111-80915086	0.795991401	0.011348033	0.998154148
ETV1	ENSG00000006468.13_2	chr7:13930853-14031050	0.793589732	0.02766108	0.998154148
PDSS1	ENSG00000148459.15_3	chr10:26986588-27035727	0.791703822	0.01275175	0.998154148
ZNF302	ENSG00000089335.20_3	chr19:35168544-35177302	0.791464577	0.025360148	0.998154148
USPL1	ENSG00000132952.11_2	chr13:31191830-31234907	0.788301055	0.041974079	0.998154148
USP18	ENSG00000184979.9_2	chr22:18632666-18660164	0.787897784	0.003205706	0.998154148
CEBPZ	ENSG00000115816.14_3	chr2:37428755-37458856	0.787511339	0.045209765	0.998154148
BLZF1	ENSG00000117475.13_2	chr1:169337208-169365778	0.786436941	0.033047401	0.998154148
SELENOT	ENSG00000198843.12_3	chr3:150320662-150348232	0.780810525	0.030589203	0.998154148
MPHOSPH8	ENSG00000196199.13_2	chr13:20207821-20247599	0.778988661	0.039299165	0.998154148
ZNF484	ENSG00000127081.13_2	chr9:95607313-95640320	0.778441553	0.032061778	0.998154148
C8orf4	ENSG00000176907.4_2	chr8:40010974-40012827	0.77821368	0.006847759	0.998154148
PDCD6IP	ENSG00000170248.13_2	chr3:33839844-33911199	0.777223064	0.006442322	0.998154148
TMEM254	ENSG00000133678.13_3	chr10:81838402-81852313	0.776132899	0.00496647	0.998154148
TAS2R5	ENSG00000127366.5_2	chr7:141490017-141491167	0.775416025	0.042789881	0.998154148
LRRC37A	ENSG00000176681.14_2	chr17:44370099-44415160	0.774183314	0.0381071	0.998154148
SLC4A8	ENSG00000050438.16_2	chr12:51785101-51909547	0.772767428	0.041781165	0.998154148

DPH3	ENSG00000154813.9_2	chr3:16299485-16306479	0.771048729	0.00336707	0.998154148
TMEM126A	ENSG00000171202.6_2	chr11:85359011-85367591	0.768098469	0.029954166	0.998154148
FGD6	ENSG00000180263.13_3	chr12:95470525-95611258	0.767550409	0.032563425	0.998154148
BDH2	ENSG00000164039.14_3	chr4:104000592-104021040	0.76618433	0.026098732	0.998154148
AL513165.2	ENSG00000256966.6_4	chr9:37512544-37592466	0.765501781	0.037636186	0.998154148
ZNF32	ENSG00000169740.13_2	chr10:44139307-44144304	0.764235273	0.008265639	0.998154148
ENDOU	ENSG00000111405.8_2	chr12:48103517-48119350	0.76297606	0.008070261	0.998154148
SLN	ENSG00000170290.3_2	chr11:107578104-107590419	0.762697314	0.030907623	0.998154148
OR2W3	ENSG00000238243.3_2	chr1:248058889-248059833	0.761683655	0.021253529	0.998154148
DNAJA4	ENSG00000140403.12_2	chr15:78556428-78574538	0.76013059	0.040997887	0.998154148
LRRC37A2	ENSG00000238083.7_2	chr17:44588877-44633016	0.75918872	0.029176016	0.998154148
CCDC167	ENSG00000198937.8_2	chr6:37450696-37467698	0.758738525	0.049893105	0.998154148
OTOGL	ENSG00000165899.10_2	chr12:80603233-80772870	0.758383143	0.0073387	0.998154148
FP15737	ENSG00000215298.3	chr8:23430157-23432974	0.751653359	0.029617859	0.998154148
ACAD11	ENSG00000240303.7_3	chr3:132276982-132379567	0.750470175	0.048358226	0.998154148
RBBP4	ENSG00000162521.18_3	chr1:33116743-33151812	0.749822389	0.020815195	0.998154148
HSPD1	ENSG00000144381.16_3	chr2:198351305-198381461	0.745771365	0.023242035	0.998154148
TOGARAM1	ENSG00000198718.12_3	chr14:45431411-45543634	0.743039018	0.009521289	0.998154148
GSTM5	ENSG00000134201.10_3	chr1:110254877-110318050	0.740939805	0.035152072	0.998154148
FSBP	ENSG00000265817.2_3	chr8:95384398-95449180	0.739829097	0.019761943	0.998154148
PPARA	ENSG00000186951.16_3	chr22:46546424-46639653	0.736169585	0.044314345	0.998154148
QSER1	ENSG00000060749.14_2	chr11:32914724-33014862	0.735464221	0.038886837	0.998154148
FABP6	ENSG00000170231.15_2	chr5:159614374-159665742	0.731863888	0.028418238	0.998154148
ZNF709	ENSG00000242852.6_3	chr19:12571998-12624668	0.71556927	0.007476814	0.998154148
RALB	ENSG00000144118.13_3	chr2:120997640-121052289	0.714954298	0.025116048	0.998154148
DUSP6	ENSG00000139318.7_2	chr12:89741009-89747048	0.713571153	0.024744029	0.998154148
MDM4	ENSG00000198625.12_2	chr1:204485507-204527248	0.70941623	0.013522487	0.998154148
FCF1	ENSG00000119616.11_2	chr14:75179847-75205323	0.702405537	0.008291242	0.998154148
NME1-NME2	ENSG00000011052.21_3	chr17:49230951-49249105	0.651236153	0.049573833	0.998154148
MKLN1	ENSG00000128585.17_3	chr7:130794855-131181395	0.630768248	0.014691013	0.998154148
AL662899.3	ENSG00000263020.6_4	chr6:31633879-31641323	0.522821095	0.014578824	0.998154148
AD000671.1	ENSG00000188223.9_4	chr19:36236579-36245420	0.491543271	0.015996805	0.998154148

Table S4. All significantly up- and down-regulated genes in the synaptic fraction

Gene symbol	Ensemble ID	Locus	Fold change	p-Value	q-Value
Up-regulated genes					
ZFP36	ENSG00000128016.5_2	chr19:39897453-39900052	2.1776576	0.0275288	0.999912394
C1QB	ENSG00000173369.15_2	chr1:22979255-22988031	2.0394579	0.0465707	0.999912394
CHTF8	ENSG00000168802.12_3	chr16:69151913-69166487	1.8470062	0.0174307	0.999912394
RASD1	ENSG00000108551.4_2	chr17:17397751-17399709	1.8322651	0.0081353	0.999912394
CEBPD	ENSG00000221869.4_2	chr8:48649471-48651648	1.7427126	0.0399716	0.999912394
TMEM88B	ENSG00000205116.3_2	chr1:1361508-1363167	1.7405742	0.0093953	0.999912394
KIF19	ENSG00000196169.14_2	chr17:72322349-72351959	1.7176642	0.0061926	0.999912394
MOG	ENSG00000204655.11_3	chr6:29624758-29640149	1.6982876	0.0446928	0.999912394
S100A9	ENSG00000163220.10_2	chr1:153330330-153333503	1.6963496	0.0214211	0.999912394
RGS16	ENSG00000143333.6_2	chr1:182567758-182573543	1.6860759	0.020914	0.999912394
HAPLN2	ENSG00000132702.12_2	chr1:156589086-156595517	1.660522	0.0399065	0.999912394
CX3CL1	ENSG00000006210.6_2	chr16:57406370-57418960	1.6509677	0.0164296	0.999912394
GALNT15	ENSG00000131386.17_2	chr3:16216156-16273499	1.6278187	0.0268205	0.999912394
SLC2A5	ENSG00000142583.17_3	chr1:9095166-9148537	1.6249166	0.003212	0.999912394
ADNP2	ENSG00000101544.8_2	chr18:77866915-77905406	1.5810882	0.0164974	0.999912394
CD68	ENSG00000129226.13_3	chr17:7482785-7485431	1.5771296	0.0423986	0.999912394
FPR1	ENSG00000171051.8_3	chr19:52248425-52307363	1.5668887	0.007887	0.999912394
CDC42EP1	ENSG00000128283.6_4	chr22:37956454-37965412	1.5649011	0.0222008	0.999912394
TYROBP	ENSG00000011600.11_2	chr19:36395303-36399197	1.5585077	0.022949	0.999912394
PRIMA1	ENSG00000175785.12_2	chr14:94184644-94254827	1.5531521	0.0295804	0.999912394
SMOC1	ENSG00000198732.10_2	chr14:70320848-70499083	1.5367045	0.0062641	0.999912394
HIST1H3D	ENSG00000197409.7_3	chr6:26197068-26197478	1.5350196	0.0125672	0.999912394
AL136376.1	ENSG00000269279.1	chr1:116915890-116926718	1.5307629	0.0418539	0.999912394
CBR1	ENSG00000159228.12_2	chr21:37442239-37445464	1.5095717	0.0023686	0.999912394
AC006486.1	ENSG00000268643.1_4	chr19:42738735-42759284	1.5061942	0.0058379	0.999912394
PRR18	ENSG00000176381.5_3	chr6:166718788-166721936	1.5019354	0.0063391	0.999912394
EDIL3	ENSG00000164176.12_3	chr5:83236373-83680611	1.4997978	0.0429222	0.999912394
ITGB2	ENSG00000160255.17_3	chr21:46305868-46351904	1.4975076	0.0450782	0.999912394
GPIHBP1	ENSG00000277494.1_2	chr8:144295068-144299044	1.4970042	0.0161025	0.999912394
RTKN	ENSG00000114993.16_2	chr2:74652963-74669549	1.4941954	0.0054524	0.999912394

SLC11A1	ENSG00000018280.16_2	chr2:219246752-219261617	1.478482	0.0411049	0.999912394
SPI1	ENSG00000066336.11_2	chr11:47376411-47400127	1.4699304	0.0291721	0.999912394
LDB3	ENSG00000122367.19_3	chr10:88428206-88495825	1.4638139	0.0148954	0.999912394
RHOU	ENSG00000116574.5_2	chr1:228870824-228882416	1.4572597	0.0028964	0.999912394
HCLS1	ENSG00000180353.10_2	chr3:121350246-121379774	1.4534723	0.0302514	0.999912394
GPX1	ENSG00000233276.3_3	chr3:49394609-49396033	1.4522081	0.0247716	0.999912394
AC073896.1	ENSG00000144785.8_4	chr12:56679700-56709843	1.4457229	0.0296458	0.999912394
SH3PXD2B	ENSG00000174705.12_3	chr5:171752004-171881527	1.4452584	0.0450207	0.999912394
TSPAN15	ENSG00000099282.9_3	chr10:71211229-71267425	1.4395893	0.0331081	0.999912394
FERMT3	ENSG00000149781.12_3	chr11:63974150-63991358	1.4365096	0.039016	0.999912394
ECHDC3	ENSG00000134463.14_3	chr10:11784365-11806069	1.4311422	0.0008299	0.999912394
DEF6	ENSG00000023892.10_2	chr6:35265629-35289548	1.422364	0.0065991	0.999912394
PHLDB1	ENSG00000019144.18_3	chr11:118477155-118528748	1.411454	0.0223944	0.999912394
CXCL16	ENSG00000161921.14_3	chr17:4636821-4643217	1.4082337	0.0339933	0.999912394
HBEGF	ENSG00000113070.7_2	chr5:139712428-139726216	1.4071037	0.0178945	0.999912394
MAP2K3	ENSG00000034152.18_3	chr17:21187984-21218552	1.4012996	0.0122844	0.999912394
AKIRIN1	ENSG00000174574.15_3	chr1:39456895-39471731	1.394551	0.0175371	0.999912394
INSIG1	ENSG00000186480.12_3	chr7:155089486-155101945	1.3942983	0.0419544	0.999912394
PIM1	ENSG00000137193.13_2	chr6:37137979-37143202	1.3910995	0.0439518	0.999912394
CD59	ENSG00000085063.14_3	chr11:33719807-33757991	1.3892392	0.0317052	0.999912394
OPALIN	ENSG00000197430.10_2	chr10:98102973-98119122	1.3824273	0.0413411	0.999912394
SHROOM4	ENSG00000158352.15_2	chrX:50334647-50557302	1.3807606	0.0400913	0.999912394
DBNDD2	ENSG00000244274.7_3	chr20:44034697-44039250	1.3799971	0.0368782	0.999912394
GPNMB	ENSG00000136235.15_3	chr7:23275586-23314727	1.3790575	0.0212324	0.999912394
TRAF4	ENSG00000076604.14_3	chr17:27071002-27077976	1.3779663	0.0069576	0.999912394
SIGLEC9	ENSG00000129450.8_2	chr19:51628165-51639908	1.3767954	0.0321491	0.999912394
GSN	ENSG00000148180.19_3	chr9:123970072-124095121	1.3707911	0.0346081	0.999912394
PDE4B	ENSG00000184588.17_3	chr1:66258197-66840262	1.3698842	0.0454108	0.999912394
ELOVL1	ENSG00000066322.14_3	chr1:43829068-43833745	1.3657649	0.047326	0.999912394
H1F0	ENSG00000189060.5_2	chr22:38201100-38203443	1.3602022	0.0042927	0.999912394
SGK2	ENSG00000101049.14_3	chr20:42187608-42216877	1.3572334	0.0484886	0.999912394
WIPF1	ENSG00000115935.17_4	chr2:175424300-175547644	1.353282	0.0052749	0.999912394
PXDC1	ENSG00000168994.13_2	chr6:3722848-3752260	1.3525253	0.0457249	0.999912394
C5AR1	ENSG00000197405.7_3	chr19:47793280-47825323	1.3483603	0.0297668	0.999912394
RNASET2	ENSG00000026297.15_3	chr6:167342992-167370679	1.3462312	0.0442161	0.999912394

ZBED3	ENSG00000132846.5_4	chr5:76367897-76383148	1.3454267	0.0008996	0.999912394
PIP4K2A	ENSG00000150867.13_3	chr10:22823778-23003484	1.3430789	0.0118545	0.999912394
GSG1L	ENSG00000169181.12_4	chr16:27798856-28074830	1.3406162	0.0007414	0.999912394
SNU13	ENSG00000100138.13_2	chr22:42069934-42086508	1.338581	0.0128383	0.999912394
RASSF2	ENSG00000101265.15_2	chr20:4760669-4804291	1.3380231	0.0125459	0.999912394
CDKN1C	ENSG00000129757.12_2	chr11:2904443-2907111	1.3369348	0.0446486	0.999912394
ZBTB43	ENSG00000169155.9_3	chr9:129567285-129600489	1.3366042	0.0234785	0.999912394
MTA2	ENSG00000149480.6_2	chr11:62360686-62369312	1.3318732	0.039548	0.999912394
MAL	ENSG00000172005.10_2	chr2:95691422-95719741	1.3315349	0.0474162	0.999912394
SLCO1A2	ENSG00000084453.16_3	chr12:21417534-21572528	1.3277406	0.0111242	0.999912394
SOX8	ENSG00000005513.9_2	chr16:1031808-1036979	1.3246712	0.012971	0.999912394
SERINC5	ENSG00000164300.16_2	chr5:79407474-79551898	1.3231909	0.0397174	0.999912394
SLC25A1	ENSG00000100075.9_2	chr22:19163088-19166343	1.3223847	0.0257429	0.999912394
SNAI1	ENSG00000124216.3_2	chr20:48599536-48605423	1.3216293	0.0250616	0.999912394
N4BP2L1	ENSG00000139597.17_3	chr13:32974860-33002448	1.3213328	0.0269505	0.999912394
TLR2	ENSG00000137462.6_2	chr4:154622652-154626851	1.3203869	0.0323141	0.999912394
GTF2H3	ENSG00000111358.13_3	chr12:124118286-124147153	1.3202115	0.0160122	0.999912394
OTUD7B	ENSG00000264522.5_2	chr1:149909705-149982625	1.3174402	0.0370509	0.999912394
RELA	ENSG00000173039.18_3	chr11:65421067-65430565	1.3140115	0.0256881	0.999912394
MSLN	ENSG00000102854.15_3	chr16:810762-818865	1.3129353	0.0317411	0.999912394
SPATA13	ENSG00000182957.15_3	chr13:24553944-24881212	1.3113199	0.027528	0.999912394
WASF2	ENSG00000158195.10_2	chr1:27730730-27816669	1.3082764	0.032357	0.999912394
TNFRSF10B	ENSG00000120889.12_2	chr8:22877646-22926692	1.3079724	0.0392618	0.999912394
IRF2	ENSG00000168310.10_3	chr4:185308867-185395734	1.3031339	0.0051633	0.999912394
B3GNT9	ENSG00000237172.3_2	chr16:67182008-67185117	1.3028737	0.0483316	0.999912394
MICALL1	ENSG00000100139.13_3	chr22:38301664-38338829	1.3026413	0.0102863	0.999912394
CDC42SE1	ENSG00000197622.12_2	chr1:151023447-151042801	1.3025141	0.043694	0.999912394
NUAK2	ENSG00000163545.8_2	chr1:205271187-205290919	1.2999699	0.0153594	0.999912394
SSH3	ENSG00000172830.12_3	chr11:67070919-67080078	1.2998803	0.0098709	0.999912394
TFEB	ENSG00000112561.17_3	chr6:41651716-41703997	1.2944792	0.0053913	0.999912394
PTPRH	ENSG00000080031.9_3	chr19:55692616-55720874	1.2943289	0.0371086	0.999912394
FCHSD1	ENSG00000197948.10_2	chr5:141018869-141030986	1.2928176	0.0212076	0.999912394
PTPRC	ENSG00000081237.18_3	chr1:198607801-198726412	1.2926396	0.0250106	0.999912394
IRF1	ENSG00000125347.13_3	chr5:131817301-131826490	1.2895121	0.049636	0.999912394
NFAM1	ENSG00000235568.6_2	chr22:42776416-42828401	1.2886583	0.0359893	0.999912394

JPT2	ENSG00000206053.12_4	chr16:1728257-1752281	1.2886282	0.0119669	0.999912394
SMAD9	ENSG00000120693.13_3	chr13:37418968-37494902	1.2882305	0.0147515	0.999912394
SH3BP4	ENSG00000130147.15_3	chr2:235860617-235964358	1.28803	0.0174714	0.999912394
INPP1	ENSG00000151689.12_2	chr2:191208196-191236391	1.2871267	0.043256	0.999912394
ELF1	ENSG00000120690.15_3	chr13:41506164-41635576	1.2832428	0.0154785	0.999912394
CORO1B	ENSG00000172725.13_3	chr11:67202981-67211292	1.2821114	0.0320307	0.999912394
CHMP2B	ENSG00000083937.8_2	chr3:87276421-87304698	1.2804737	0.0230209	0.999912394
ELK1	ENSG00000126767.17_2	chrX:47494920-47510003	1.2792851	0.0494165	0.999912394
NDRG1	ENSG00000104419.14_4	chr8:134249414-134314265	1.2788627	0.0467802	0.999912394
KIF13B	ENSG00000197892.12_2	chr8:28924796-29120641	1.2781564	0.0141405	0.999912394
FAM198A	ENSG00000144649.8_4	chr3:43020759-43101703	1.276496	0.0247417	0.999912394
TMEM98	ENSG00000006042.11_2	chr17:31254928-31272124	1.2762245	0.0481177	0.999912394
ADGRE5	ENSG00000123146.19_3	chr19:14491313-14519537	1.2758758	0.0162438	0.999912394
ADIPOR2	ENSG00000006831.9_2	chr12:1797740-1897844	1.2755488	0.0287699	0.999912394
H2AFJ	ENSG00000246705.4_3	chr12:14927317-14930936	1.2740466	0.0205642	0.999912394
DUSP16	ENSG00000111266.8_3	chr12:12627144-12715317	1.2739273	0.0112589	0.999912394
AC009690.1	ENSG00000260729.1_4	chr15:72577068-72668322	1.2736923	0.0467613	0.999912394
MSR1	ENSG00000038945.14_3	chr8:15965387-16424999	1.2736773	0.0492673	0.999912394
LCP1	ENSG00000136167.13_3	chr13:46700055-46786006	1.2736568	0.0283315	0.999912394
TMCC3	ENSG00000057704.12_3	chr12:94960900-95044338	1.2729291	0.0284203	0.999912394
BHLHE41	ENSG00000123095.5_2	chr12:26272959-26278060	1.2717088	0.0085049	0.999912394
RWDD3	ENSG00000122481.16_3	chr1:95699711-95712781	1.2711802	0.0471943	0.999912394
HNRNPA1L2	ENSG00000139675.11_3	chr13:53214921-53217931	1.2695678	0.0144244	0.999912394
C11orf57	ENSG00000150776.17_3	chr11:111944810-111955874	1.2688734	0.0100756	0.999912394
SHMT1	ENSG00000176974.19_3	chr17:18231174-18266877	1.2677934	0.0410607	0.999912394
LEMD2	ENSG00000161904.11_3	chr6:33738979-33756913	1.2642032	0.045934	0.999912394
RPS15	ENSG00000115268.9_4	chr19:1438357-1440493	1.2641858	0.0312018	0.999912394
SLA	ENSG00000155926.13_3	chr8:134048969-134115298	1.2603458	0.0320541	0.999912394
NPC2	ENSG00000119655.10_3	chr14:74942895-74960880	1.2570853	0.0346297	0.999912394
TCP11L2	ENSG00000166046.10_3	chr12:106695707-106740793	1.2566249	0.0280612	0.999912394
JMJD4	ENSG00000081692.12_2	chr1:227918126-227923112	1.2547875	0.0138267	0.999912394
ST20-MTHFS	ENSG00000259332.3_3	chr15:80137492-80216096	1.2538705	0.0465473	0.999912394
RNASE4	ENSG00000258818.3_3	chr14:21152259-21169374	1.2534573	0.0148222	0.999912394
ERRFI1	ENSG00000116285.12_2	chr1:8064464-8086368	1.2530838	0.0370586	0.999912394
SHKBP1	ENSG00000160410.14_3	chr19:41082757-41097305	1.252883	0.0349054	0.999912394

PLA2G16	ENSG00000176485.11_3	chr11:63340667-63384355	1.2526898	0.0395807	0.999912394
NDE1	ENSG00000072864.14_3	chr16:15737124-15820210	1.2505641	0.0420034	0.999912394
SF3A2	ENSG00000104897.9_4	chr19:2236503-2248678	1.2494376	0.013301	0.999912394
IL17RA	ENSG00000177663.13_2	chr22:17565844-17596584	1.2487521	0.0225229	0.999912394
TOR4A	ENSG00000198113.2_2	chr9:140172201-140177093	1.2480499	0.0192268	0.999912394
FAM228A	ENSG00000186453.12_4	chr2:24397938-24423718	1.2479403	0.0174632	0.999912394
ADRA2B	ENSG00000274286.1_2	chr2:96778623-96781984	1.2478672	0.0273155	0.999912394
H1FX	ENSG00000184897.5_2	chr3:129033614-129035120	1.2478233	0.0110975	0.999912394
WTAP	ENSG00000146457.14_2	chr6:160146617-160177351	1.2474898	0.0412624	0.999912394
TRAFD1	ENSG00000135148.11_3	chr12:112563305-112591413	1.2458801	0.0146729	0.999912394
FAM107B	ENSG00000065809.13_3	chr10:14560556-14816896	1.2447128	0.0191543	0.999912394
CCNG1	ENSG00000113328.18_2	chr5:162864575-162873157	1.2428177	0.0178573	0.999912394
CPVL	ENSG00000106066.14_3	chr7:29034847-29235067	1.2419374	0.0382903	0.999912394
FYB1	ENSG00000082074.15_4	chr5:39105338-39274630	1.2391096	0.0303154	0.999912394
PSENEN	ENSG00000205155.7_3	chr19:36236015-36238420	1.2386774	0.0445087	0.999912394
MIIP	ENSG00000116691.10_2	chr1:12079523-12092102	1.2380441	0.0292537	0.999912394
PARVG	ENSG00000138964.16_3	chr22:44568836-44615413	1.2379095	0.0213258	0.999912394
CSF3R	ENSG00000119535.17_3	chr1:36931644-36948879	1.237778	0.0238275	0.999912394
APH1A	ENSG00000117362.12_3	chr1:150237799-150241980	1.2367637	0.0093605	0.999912394
CDH19	ENSG00000071991.8_2	chr18:64168320-64271375	1.2355281	0.03839	0.999912394
LIPT2	ENSG00000175536.6_2	chr11:74202757-74204778	1.2346426	0.0380753	0.999912394
TAB2	ENSG00000055208.18_3	chr6:149539777-149732749	1.234626	0.0303709	0.999912394
PALM3	ENSG00000187867.8_2	chr19:14164177-14169971	1.2323999	0.0250486	0.999912394
TRIM62	ENSG00000116525.13_2	chr1:33611003-33647660	1.2310591	0.0237846	0.999912394
ZNF821	ENSG00000102984.14_3	chr16:71893583-71929239	1.2299161	0.0487599	0.999912394
MED30	ENSG00000164758.7_2	chr8:118532952-118552501	1.2291014	0.0479023	0.999912394
MTSS1	ENSG00000170873.18_3	chr8:125563031-125740670	1.2281944	0.0312497	0.999912394
CHD2	ENSG00000173575.20_1	chr15:93443419-93571235	1.2274986	0.0455669	0.999912394
HNRNPF	ENSG00000169813.16_3	chr10:43881065-43904614	1.227477	0.0416568	0.999912394
MYD88	ENSG00000172936.12_3	chr3:38179969-38184513	1.2266494	0.0430256	0.999912394
COL9A2	ENSG00000049089.13_3	chr1:40766159-40783488	1.2255108	0.0403993	0.999912394
EMILIN2	ENSG00000132205.10_2	chr18:2847028-2915991	1.2252446	0.0092872	0.999912394
RGL2	ENSG00000237441.9_2	chr6:33259431-33267101	1.2247001	0.0106655	0.999912394
TCF12	ENSG00000140262.17_2	chr15:57210821-57591479	1.2246067	0.0305264	0.999912394
MCM5	ENSG00000100297.15_3	chr22:35796056-35821423	1.2226446	0.0233467	0.999912394

PHC2	ENSG00000134686.18_3	chr1:33789224-33896653	1.2205689	0.0040414	0.999912394
FAM114A1	ENSG00000197712.11_2	chr4:38869298-38947360	1.2204702	0.0271639	0.999912394
TBXAS1	ENSG00000059377.16_2	chr7:139476850-139720125	1.2176727	0.0345651	0.999912394
ZNF570	ENSG00000171827.10_2	chr19:37958487-37979554	1.2173453	0.0226402	0.999912394
GDE1	ENSG00000006007.11_2	chr16:19513011-19533467	1.2167078	0.0278638	0.999912394
BMP8B	ENSG00000116985.11_3	chr1:40222854-40254533	1.2160911	0.0294302	0.999912394
SLC4A2	ENSG00000164889.13_3	chr7:150754297-150773614	1.2135736	0.0302291	0.999912394
RPS6KA2	ENSG00000071242.11_3	chr6:166822852-167319939	1.2109142	0.0109757	0.999912394
EIF3F	ENSG00000175390.13_3	chr11:7991798-8023409	1.2101928	0.0264594	0.999912394
FOXO3	ENSG00000118689.14_2	chr6:108881038-109005977	1.2096335	0.0474803	0.999912394
FBXL8	ENSG00000135722.8_3	chr16:67193834-67198473	1.2068191	0.0183952	0.999912394
ZNF217	ENSG00000171940.13_3	chr20:52183604-52226446	1.2067404	0.0063415	0.999912394
JOSD2	ENSG00000161677.11_3	chr19:51009255-51014610	1.2047893	0.0127898	0.999912394
RUNX1	ENSG00000159216.18_3	chr21:36160098-37376965	1.2047371	0.0247299	0.999912394
LACTB2	ENSG00000147592.8_2	chr8:71547553-71581409	1.1988347	0.0271241	0.999912394
BMF	ENSG00000104081.13_3	chr15:40380091-40401093	1.1977482	0.0485777	0.999912394
PPP1R35	ENSG00000160813.6_2	chr7:100032905-100034188	1.1957616	0.0338099	0.999912394
ZEB2	ENSG00000169554.18_3	chr2:145121931-145282150	1.1954504	0.0353838	0.999912394
AC018755.1	ENSG00000167765.3	chr19:52095036-52097630	1.19383	0.0488274	0.999912394
TUT1	ENSG00000149016.15_3	chr11:62342517-62359649	1.1934012	0.0438199	0.999912394
MED25	ENSG00000104973.16_3	chr19:50321536-50342073	1.1892178	0.022476	0.999912394
TMEM187	ENSG00000177854.7_3	chrX:153237778-153248646	1.1887293	0.0487107	0.999912394
DISC1	ENSG00000162946.21_4	chr1:231762561-232177018	1.1857924	0.0110872	0.999912394
NRBP2	ENSG00000185189.17_3	chr8:144915764-144923146	1.1838847	0.0368363	0.999912394
FNBP1	ENSG00000187239.16_2	chr9:132649466-132805473	1.1837077	0.0282587	0.999912394
STAT5A	ENSG00000126561.16_2	chr17:40439565-40463961	1.180101	0.0371641	0.999912394
TIFA	ENSG00000145365.10_2	chr4:113195698-113207059	1.178567	0.0376155	0.999912394
SELENOM	ENSG00000198832.10_2	chr22:31500758-31516055	1.1785199	0.0434439	0.999912394
ARL16	ENSG00000214087.8_3	chr17:79648204-79650954	1.177453	0.03142	0.999912394
GTPBP1	ENSG00000100226.15_3	chr22:39101728-39134304	1.1753528	0.0135741	0.999912394
HAUS4	ENSG00000092036.18_4	chr14:23415437-23426370	1.1747808	0.0072245	0.999912394
ARHGAP27	ENSG00000159314.11_3	chr17:43471268-43511787	1.1734611	0.0469769	0.999912394
GXYLT2	ENSG00000172986.12_3	chr3:72937224-73047289	1.1708746	0.0223666	0.999912394
MACROD1	ENSG00000133315.10_3	chr11:63766030-63933578	1.1696237	0.0475393	0.999912394
SMPDL3A	ENSG00000172594.12_2	chr6:123110194-123130865	1.1692425	0.0446456	0.999912394

BLVRB	ENSG00000090013.9_2	chr19:40953696-40971747	1.1641493	0.0294404	0.999912394
RCAN1	ENSG00000159200.17_2	chr21:35885440-35987441	1.1594898	0.0339671	0.999912394
SNIP1	ENSG00000163877.10_2	chr1:38000050-38019945	1.1587107	0.0407049	0.999912394
GTF2F2	ENSG00000188342.11_3	chr13:45694650-45859044	1.1553077	0.0138344	0.999912394
KCTD5	ENSG00000167977.8_3	chr16:2732476-2759031	1.1511217	0.0410237	0.999912394
LSM1	ENSG00000175324.9_2	chr8:38020839-38034248	1.147908	0.0453231	0.999912394
LLGL2	ENSG00000073350.13_2	chr17:73521161-73571289	1.1455037	0.0497083	0.999912394
KRBA2	ENSG00000184619.3_3	chr17:8271955-8280029	1.1452456	0.0460014	0.999912394
BAZ2A	ENSG00000076108.11_2	chr12:56989380-57030600	1.1441418	0.0482752	0.999912394
CDK19	ENSG00000155111.14_3	chr6:110931181-111137161	1.142423	0.0318343	0.999912394
WHAMM	ENSG00000156232.7_2	chr15:83478380-83504860	1.1388265	0.0204501	0.999912394
TBC1D1	ENSG00000065882.15_3	chr4:37892708-38140796	1.1370191	0.0418677	0.999912394
TCEAL3	ENSG00000196507.10_3	chrX:102862379-102884618	1.1365208	0.0453117	0.999912394
RIN3	ENSG00000100599.15_4	chr14:92980118-93155339	1.1312604	0.044281	0.999912394
RALY	ENSG00000125970.11_4	chr20:32581452-32696114	1.127119	0.0485894	0.999912394
CC2D1A	ENSG00000132024.17_3	chr19:14017014-14041692	1.1255187	0.0372756	0.999912394
UBE2D2	ENSG00000131508.15_2	chr5:138906016-139008018	1.125508	0.0484474	0.999912394
C14orf93	ENSG00000100802.14_3	chr14:23455117-23479375	1.1185911	0.0385821	0.999912394
PHF11	ENSG00000136147.17_4	chr13:50069746-50103123	1.1184468	0.0259917	0.999912394
CCDC9	ENSG00000105321.12_2	chr19:47759237-47775210	1.1153723	0.0415504	0.999912394
SPAG1	ENSG00000104450.12_2	chr8:101170134-101271506	1.1132633	0.0342163	0.999912394
KLHL36	ENSG00000135686.12_2	chr16:84682131-84701292	1.0996935	0.0386563	0.999912394
ATXN1L	ENSG00000224470.7_3	chr16:71879894-71919171	1.0728368	0.0473205	0.999912394
Down-regulated genes					
RNASEH2B	ENSG00000136104.19_3	chr13:51483814-51547881	0.9263577	0.0496634	0.999912394
DNAJC24	ENSG00000170946.14_2	chr11:31391387-31453396	0.9192889	0.0274706	0.999912394
AP3S2	ENSG00000157823.16_3	chr15:90373831-90437870	0.9112092	0.0498719	0.999912394
TET1	ENSG00000138336.8_3	chr10:70320413-70454239	0.9024881	0.0076316	0.999912394
ZSCAN29	ENSG00000140265.12_2	chr15:43650370-43663223	0.8990058	0.046785	0.999912394
ZNF713	ENSG00000178665.14_3	chr7:55955168-56009918	0.8873668	0.0164467	0.999912394
PDE7B	ENSG00000171408.13_3	chr6:136172834-136516712	0.8871713	0.0490762	0.999912394
ZFP3	ENSG00000180787.5_2	chr17:4981543-4999669	0.8855522	0.0246304	0.999912394
ISPD	ENSG00000214960.9_2	chr7:16127152-16460947	0.8830823	0.0429459	0.999912394
ASAP2	ENSG00000151693.10_3	chr2:9346894-9545812	0.8790239	0.0426633	0.999912394
LZIC	ENSG00000162441.11_2	chr1:9982171-10003465	0.8785773	0.0350735	0.999912394

KMT5B	ENSG00000110066.14_3	chr11:67922330-67981295	0.8762556	0.0410923	0.999912394
LYRM2	ENSG00000083099.10_2	chr6:90277863-90348472	0.8757792	0.0216332	0.999912394
SGSM3	ENSG00000100359.20_3	chr22:40766595-40806293	0.874915	0.0405052	0.999912394
GIN1	ENSG00000145723.16_2	chr5:102421704-102455855	0.8702349	0.0176353	0.999912394
CDIP1	ENSG00000089486.16_3	chr16:4560676-4588829	0.8639487	0.0192545	0.999912394
MARC1	ENSG00000186205.12_3	chr1:220960101-220992999	0.863248	0.0133391	0.999912394
RNF214	ENSG00000167257.10_3	chr11:117103341-117157161	0.8631369	0.0106245	0.999912394
PCDHB7	ENSG00000113212.6_2	chr5:140552200-140555964	0.8596802	0.0464523	0.999912394
TRAPPC5	ENSG00000181029.8_3	chr19:7745729-7752589	0.8586476	0.0372299	0.999912394
SYPL2	ENSG00000143028.8_2	chr1:110009250-110024759	0.8583532	0.0025033	0.999912394
GSTM2	ENSG00000213366.12_3	chr1:110210644-110252173	0.8556602	0.0315312	0.999912394
THSD1	ENSG00000136114.15_2	chr13:52951302-52980629	0.845616	0.0217433	0.999912394
SGCD	ENSG00000170624.13_2	chr5:155297354-156194799	0.8447133	0.0351057	0.999912394
PLCB3	ENSG00000149782.11_2	chr11:64018995-64036622	0.8445156	0.0303356	0.999912394
SEL1L3	ENSG00000091490.10_3	chr4:25749049-25865382	0.8441025	0.0024603	0.999912394
SLC35A4	ENSG00000176087.14_2	chr5:139944041-139948688	0.8382002	0.0421184	0.999912394
VILL	ENSG00000136059.14_2	chr3:38029550-38048679	0.8355835	0.0189474	0.999912394
SCGB3A1	ENSG00000161055.3_2	chr5:180017103-180018540	0.8351407	0.0489781	0.999912394
TCERG1L	ENSG00000176769.9_2	chr10:132890654-133109984	0.8339763	0.0461175	0.999912394
CLUAP1	ENSG00000103351.12_3	chr16:3550924-3589048	0.8274534	0.036996	0.999912394
DPH3	ENSG00000154813.9_2	chr3:16299485-16306479	0.8206404	0.0066713	0.999912394
MON1A	ENSG00000164077.13_4	chr3:49946295-49967606	0.8193118	0.0366616	0.999912394
CACHD1	ENSG00000158966.13_2	chr1:64936475-65158741	0.8180571	0.0310342	0.999912394
NT5E	ENSG00000135318.11_3	chr6:86159302-86205509	0.8171443	0.018534	0.999912394
TRPM3	ENSG00000083067.22_3	chr9:73143979-74061820	0.8157727	0.0352362	0.999912394
SHROOM2	ENSG00000146950.12_2	chrX:9754496-9917483	0.8083461	0.0260327	0.999912394
ADHFE1	ENSG00000147576.15_3	chr8:67342420-67383836	0.8032816	0.0306443	0.999912394
AC091167.7	ENSG00000275674.1_4	chr15:90809549-90857731	0.801337	0.0433393	0.999912394
SPATA24	ENSG00000170469.10_4	chr5:138732252-138739777	0.7986994	0.0050226	0.999912394
CDH4	ENSG00000179242.15_4	chr20:59827482-60515673	0.7962247	0.019576	0.999912394
CLDN10	ENSG00000134873.9_2	chr13:96085858-96232013	0.7947775	0.0254516	0.999912394
N6AMT1	ENSG00000156239.11_2	chr21:30244513-30257693	0.794196	0.0192057	0.999912394
FUT9	ENSG00000172461.10_2	chr6:96463860-96663488	0.7924129	0.0261338	0.999912394
FZD8	ENSG00000177283.7_3	chr10:35927177-35931206	0.7911683	0.0373176	0.999912394
MTA3	ENSG00000057935.13_2	chr2:42721709-42984087	0.7883872	0.0229091	0.999912394

CISD3	ENSG00000277972.1_2	chr17:36886488-36891297	0.7833351	0.0087768	0.999912394
WNT7B	ENSG00000188064.9_3	chr22:46316242-46373009	0.7770486	0.0398209	0.999912394
MRPL34	ENSG00000130312.6_3	chr19:17403418-17417652	0.7698633	0.0371592	0.999912394
ASPDH	ENSG00000204653.9_3	chr19:51014857-51017947	0.7658521	0.0327412	0.999912394
TTPA	ENSG00000137561.4_2	chr8:63961112-63998612	0.7616707	0.0046591	0.999912394
LFNG	ENSG00000106003.12_2	chr7:2552163-2568811	0.7578215	0.0298689	0.999912394
KCNJ14	ENSG00000182324.6_3	chr19:48958766-48970237	0.7523269	0.0071809	0.999912394
CHST7	ENSG00000147119.3_2	chrX:46433219-46457843	0.7443651	0.0226256	0.999912394
CYB561D1	ENSG00000174151.14_4	chr1:110036674-110045554	0.7427098	0.0254082	0.999912394
TEN1	ENSG00000257949.6_3	chr17:73975301-73996667	0.7386488	0.0370837	0.999912394
CHP1	ENSG00000187446.11_2	chr15:41523037-41574088	0.7310931	0.0382482	0.999912394
ARNT2	ENSG00000172379.20_3	chr15:80696692-80890278	0.7235799	0.0358096	0.999912394
ACSS1	ENSG00000154930.14_2	chr20:24986866-25039616	0.7132899	0.0013848	0.999912394
HES5	ENSG00000197921.5_2	chr1:2460184-2461684	0.5447051	0.0328057	0.999912394

Table S5. Gene Ontology analysis performed with up-regulated genes (> 1.3-fold) in synaptic fraction

GO ID	Term annotated	Number of genes	Fold enrichment	p-value	FDR
Biological Process (BP)					
GO:0110089	Regulation of hippocampal neuron apoptotic process	2	99.98	3.63E-04	4.29E-02
GO:0071223	Cellular response to lipoteichoic acid	3	59.99	3.30E-05	9.85E-03
GO:0070391	Response to lipoteichoic acid	3	59.99	3.30E-05	9.67E-03
GO:0002523	Leukocyte migration involved in inflammatory response	3	46.15	6.40E-05	1.51E-02
GO:0002269	Leukocyte activation involved in inflammatory response	4	36.36	7.95E-06	4.84E-03
GO:0001774	Microglial cell activation	4	36.36	7.95E-06	4.66E-03
GO:0007250	Activation of NF-kappab-inducing kinase activity	3	33.33	1.49E-04	2.29E-02
GO:1903978	Regulation of microglial cell activation	3	29.99	1.97E-04	2.78E-02
GO:0010894	Negative regulation of steroid biosynthetic process	3	26.08	2.86E-04	3.71E-02
GO:0061900	Glial cell activation	4	25.8	2.69E-05	8.35E-03
GO:0042116	Macrophage activation	5	24.39	3.23E-06	2.43E-03
GO:0150076	Neuroinflammatory response	4	24.24	3.37E-05	9.51E-03
GO:0045939	Negative regulation of steroid metabolic process	3	24	3.58E-04	4.26E-02
GO:1901224	Positive regulation of NIK/NF-kappab signaling	5	13.16	5.26E-05	1.34E-02
GO:0030593	Neutrophil chemotaxis	5	12.19	7.41E-05	1.65E-02
GO:0071621	Granulocyte chemotaxis	5	11.23	1.07E-04	1.92E-02
GO:1901222	Regulation of NIK/NF-kappab signaling	6	11.21	2.16E-05	7.11E-03
GO:1990266	Neutrophil migration	5	10.99	1.18E-04	2.03E-02
GO:0097530	Granulocyte migration	5	10.1	1.72E-04	2.60E-02
GO:0042035	Regulation of cytokine biosynthetic process	5	9.9	1.89E-04	2.74E-02
GO:0032680	Regulation of tumor necrosis factor production	6	8.82	7.78E-05	1.71E-02
GO:1903555	Regulation of tumor necrosis factor superfamily cytokine production	6	8.57	9.07E-05	1.86E-02
GO:0030595	Leukocyte chemotaxis	6	8.51	9.42E-05	1.86E-02
GO:0002221	Pattern recognition receptor signaling pathway	5	8.13	4.52E-04	4.83E-02
GO:0097529	Myeloid leukocyte migration	5	8.06	4.68E-04	4.93E-02
GO:0051092	Positive regulation of NF-kappab transcription factor activity	6	7.89	1.40E-04	2.24E-02
GO:0030099	Myeloid cell differentiation	8	7.58	1.39E-05	5.80E-03
GO:0071219	Cellular response to molecule of bacterial origin	7	7.29	6.23E-05	1.52E-02
GO:0060326	Cell chemotaxis	7	6.83	9.26E-05	1.88E-02
GO:0034341	Response to interferon-gamma	6	6.59	3.58E-04	4.29E-02

GO:0071216	Cellular response to biotic stimulus	7	6.54	1.20E-04	2.04E-02
GO:0071222	Cellular response to lipopolysaccharide	6	6.49	3.89E-04	4.46E-02
GO:0051091	Positive regulation of DNA-binding transcription factor activity	8	6.04	6.69E-05	1.56E-02
GO:0032496	Response to lipopolysaccharide	9	5.75	3.34E-05	9.60E-03
GO:0002237	Response to molecule of bacterial origin	9	5.5	4.65E-05	1.21E-02
GO:0043312	Neutrophil degranulation	13	5.38	1.11E-06	2.52E-03
GO:0002283	Neutrophil activation involved in immune response	13	5.34	1.22E-06	2.41E-03
GO:0002446	Neutrophil mediated immunity	13	5.26	1.42E-06	2.25E-03
GO:0110053	Regulation of actin filament organization	7	5.26	4.35E-04	4.74E-02
GO:0042119	Neutrophil activation	13	5.24	1.49E-06	2.14E-03
GO:0002274	Myeloid leukocyte activation	15	5.23	2.19E-07	1.73E-03
GO:0036230	Granulocyte activation	13	5.19	1.65E-06	2.18E-03
GO:0032970	Regulation of actin filament-based process	10	5.18	2.86E-05	8.70E-03
GO:0043299	Leukocyte degranulation	13	5.15	1.80E-06	2.04E-03
GO:0002444	Myeloid leukocyte mediated immunity	13	5.05	2.22E-06	2.20E-03
GO:0002275	Myeloid cell activation involved in immune response	13	5.02	2.37E-06	2.08E-03
GO:0006954	Inflammatory response	12	4.95	6.85E-06	4.51E-03
GO:0050727	Regulation of inflammatory response	8	4.86	2.83E-04	3.70E-02
GO:0032956	Regulation of actin cytoskeleton organization	8	4.66	3.72E-04	4.36E-02
GO:1902903	Regulation of supramolecular fiber organization	8	4.51	4.65E-04	4.93E-02
GO:2001233	Regulation of apoptotic signaling pathway	9	4.49	2.10E-04	2.91E-02
GO:0002366	Leukocyte activation involved in immune response	13	4.23	1.42E-05	5.75E-03
GO:0051090	Regulation of DNA-binding transcription factor activity	9	4.21	3.30E-04	3.98E-02
GO:0002263	Cell activation involved in immune response	13	4.21	1.52E-05	5.99E-03
GO:0045055	Regulated exocytosis	14	4.03	1.10E-05	5.28E-03
GO:0002757	Immune response-activating signal transduction	11	4	1.11E-04	1.93E-02
GO:0002443	Leukocyte mediated immunity	15	3.95	6.71E-06	4.61E-03
GO:0009611	Response to wounding	11	3.91	1.36E-04	2.21E-02
GO:0002253	Activation of immune response	12	3.88	7.12E-05	1.61E-02
GO:0044089	Positive regulation of cellular component biogenesis	10	3.87	3.00E-04	3.82E-02
GO:0071396	Cellular response to lipid	10	3.82	3.28E-04	4.02E-02
GO:0002764	Immune response-regulating signaling pathway	11	3.75	1.94E-04	2.78E-02
GO:0002252	Immune effector process	20	3.73	3.79E-07	1.50E-03
GO:0051493	Regulation of cytoskeleton organization	10	3.72	4.02E-04	4.51E-02
GO:0051347	Positive regulation of transferase activity	12	3.7	1.10E-04	1.94E-02

GO:0006887	Exocytosis	14	3.58	4.02E-05	1.09E-02
GO:0045321	Leukocyte activation	16	3.55	1.20E-05	5.57E-03
GO:0006915	Apoptotic process	16	3.53	1.28E-05	5.62E-03
GO:0001817	Regulation of cytokine production	12	3.5	1.81E-04	2.67E-02
GO:0002682	Regulation of immune system process	28	3.44	5.88E-09	9.30E-05
GO:0001775	Cell activation	17	3.24	1.93E-05	6.95E-03
GO:0050776	Regulation of immune response	18	3.21	1.25E-05	5.64E-03
GO:0045087	Innate immune response	12	3.19	4.17E-04	4.61E-02
GO:1902533	Positive regulation of intracellular signal transduction	16	3.18	4.42E-05	1.16E-02
GO:0030334	Regulation of cell migration	13	3.14	2.73E-04	3.60E-02
GO:0000122	Negative regulation of transcription by RNA polymerase II	13	3.11	3.02E-04	3.82E-02
GO:0051270	Regulation of cellular component movement	15	3.1	1.05E-04	1.92E-02
GO:0051338	Regulation of transferase activity	15	3.09	1.08E-04	1.92E-02
GO:0050778	Positive regulation of immune response	13	3.08	3.27E-04	4.04E-02
GO:0012501	Programmed cell death	16	3.08	6.37E-05	1.53E-02
GO:0033993	Response to lipid	13	3.03	3.82E-04	4.44E-02
GO:0016477	Cell migration	14	2.99	2.56E-04	3.40E-02
GO:0008219	Cell death	16	2.98	9.34E-05	1.87E-02
GO:0034097	Response to cytokine	16	2.97	9.85E-05	1.85E-02
GO:0033043	Regulation of organelle organization	19	2.97	2.02E-05	6.96E-03
GO:0051707	Response to other organism	14	2.93	3.23E-04	4.02E-02
GO:0043207	Response to external biotic stimulus	14	2.92	3.29E-04	4.01E-02
GO:0051130	Positive regulation of cellular component organization	17	2.85	9.43E-05	1.84E-02
GO:0009607	Response to biotic stimulus	14	2.84	4.29E-04	4.71E-02
GO:0002684	Positive regulation of immune system process	16	2.83	1.68E-04	2.56E-02
GO:0032940	Secretion by cell	14	2.83	4.47E-04	4.84E-02
GO:0071345	Cellular response to cytokine stimulus	14	2.83	4.51E-04	4.85E-02
GO:0044093	Positive regulation of molecular function	25	2.83	1.78E-06	2.16E-03
GO:0031327	Negative regulation of cellular biosynthetic process	21	2.81	1.58E-05	6.11E-03
GO:0009890	Negative regulation of biosynthetic process	21	2.76	2.00E-05	7.04E-03
GO:0051253	Negative regulation of RNA metabolic process	18	2.75	9.06E-05	1.88E-02
GO:0045892	Negative regulation of transcription, DNA-templated	16	2.75	2.37E-04	3.22E-02
GO:0006952	Defense response	18	2.73	1.01E-04	1.85E-02
GO:0045934	Negative regulation of nucleobase-containing compound metabolic process	19	2.7	7.06E-05	1.62E-02

GO:0043085	Positive regulation of catalytic activity	19	2.68	7.97E-05	1.73E-02
GO:1902531	Regulation of intracellular signal transduction	24	2.65	9.08E-06	4.79E-03
GO:2000113	Negative regulation of cellular macromolecule biosynthetic process	18	2.64	1.48E-04	2.30E-02
GO:0010558	Negative regulation of macromolecule biosynthetic process	19	2.63	1.00E-04	1.86E-02
GO:1903507	Negative regulation of nucleic acid-templated transcription	16	2.63	3.86E-04	4.45E-02
GO:1902679	Negative regulation of RNA biosynthetic process	16	2.62	3.93E-04	4.47E-02
GO:0051240	Positive regulation of multicellular organismal process	22	2.56	3.91E-05	1.08E-02
GO:0051128	Regulation of cellular component organization	31	2.54	7.11E-07	1.87E-03
GO:0001932	Regulation of protein phosphorylation	18	2.54	2.45E-04	3.31E-02
GO:0010941	Regulation of cell death	21	2.5	8.19E-05	1.75E-02
GO:1901700	Response to oxygen-containing compound	19	2.5	1.95E-04	2.78E-02
GO:0009967	Positive regulation of signal transduction	20	2.44	1.73E-04	2.58E-02
GO:0002376	Immune system process	33	2.41	1.25E-06	2.20E-03
GO:0006955	Immune response	22	2.41	9.50E-05	1.83E-02
GO:0007166	Cell surface receptor signaling pathway	29	2.38	8.83E-06	4.81E-03
GO:0010628	Positive regulation of gene expression	23	2.34	1.26E-04	2.10E-02
GO:0045595	Regulation of cell differentiation	21	2.34	2.87E-04	3.69E-02
GO:0048584	Positive regulation of response to stimulus	28	2.33	1.69E-05	6.38E-03
GO:0031399	Regulation of protein modification process	21	2.32	3.06E-04	3.84E-02
GO:0031324	Negative regulation of cellular metabolic process	29	2.31	1.28E-05	5.49E-03
GO:0009605	Response to external stimulus	24	2.31	9.67E-05	1.84E-02
GO:0051172	Negative regulation of nitrogen compound metabolic process	26	2.26	6.07E-05	1.52E-02
GO:0051173	Positive regulation of nitrogen compound metabolic process	35	2.24	2.78E-06	2.31E-03
GO:0065009	Regulation of molecular function	36	2.21	2.15E-06	2.27E-03
GO:0031325	Positive regulation of cellular metabolic process	36	2.2	2.30E-06	2.14E-03
GO:0050793	Regulation of developmental process	28	2.19	6.10E-05	1.51E-02
GO:2000026	Regulation of multicellular organismal development	22	2.18	3.99E-04	4.51E-02
GO:0050790	Regulation of catalytic activity	25	2.17	2.18E-04	3.00E-02
GO:0010604	Positive regulation of macromolecule metabolic process	35	2.12	9.68E-06	4.94E-03
GO:0009893	Positive regulation of metabolic process	37	2.07	6.23E-06	4.48E-03
GO:0032879	Regulation of localization	28	2.07	1.84E-04	2.69E-02
GO:0051239	Regulation of multicellular organismal process	32	2.07	4.17E-05	1.12E-02
GO:0070887	Cellular response to chemical stimulus	29	2.05	1.37E-04	2.22E-02
GO:0048583	Regulation of response to stimulus	45	2.05	4.18E-07	1.32E-03
GO:0009892	Negative regulation of metabolic process	29	2.04	1.48E-04	2.32E-02

GO:0009966	Regulation of signal transduction	32	1.95	1.26E-04	2.12E-02
GO:0007165	Signal transduction	46	1.85	8.03E-06	4.54E-03
GO:0023051	Regulation of signaling	34	1.85	2.47E-04	3.31E-02
GO:0048518	Positive regulation of biological process	56	1.84	2.30E-07	1.21E-03
GO:0048522	Positive regulation of cellular process	49	1.83	2.84E-06	2.24E-03
GO:0010646	Regulation of cell communication	33	1.82	4.07E-04	4.53E-02
GO:0023052	Signaling	48	1.81	7.48E-06	4.73E-03
GO:0048731	System development	39	1.79	1.48E-04	2.33E-02
GO:0007154	Cell communication	48	1.78	9.89E-06	4.89E-03
GO:0048523	Negative regulation of cellular process	41	1.76	1.30E-04	2.13E-02
GO:0048519	Negative regulation of biological process	46	1.76	2.30E-05	7.41E-03
GO:0048856	Anatomical structure development	47	1.76	2.37E-05	7.50E-03
GO:0032502	Developmental process	49	1.72	2.15E-05	7.25E-03
GO:0007275	Multicellular organism development	42	1.69	1.99E-04	2.78E-02
GO:0051716	Cellular response to stimulus	54	1.65	1.92E-05	7.07E-03
GO:0050896	Response to stimulus	62	1.48	8.22E-05	1.73E-02
Molecular Function (MF)					
GO:0035325	Toll-like receptor binding	3	49.99	5.22E-05	4.85E-02
GO:0019901	Protein kinase binding	13	3.95	2.88E-05	4.47E-02
GO:0019900	Kinase binding	14	3.78	2.22E-05	5.16E-02
GO:0044877	Protein-containing complex binding	17	3.08	3.70E-05	4.31E-02
GO:0005515	Protein binding	81	1.36	1.71E-05	7.94E-02
Cellular Component (CC)					
GO:0002102	Podosome	4	27.58	2.12E-05	2.16E-02
GO:0030667	Secretory granule membrane	10	6.64	3.51E-06	7.14E-03
PANTHER pathway					
P00054	Toll receptor signaling pathway	6	18.75	1.33E-06	2.18E-04

Table S6. The response to stimulus, immune system process, and cell death related Gene Ontology (GO) terms of biological process based on upregulated genes (>1.3-fold) in synaptosome

GO ID	Term annotated	Fold enrichment	p-value	FDR	Number of genes
Response to stimulus related GO terms					
GO:0050896	Response to stimulus	1.48	8.22E-05	1.73E-02	62
GO:0006952	➢ defense response	6.66	1.12E-04	2.11E-02	18
GO:0006954	- inflammatory response	2.48	8.37E-06	4.16E-03	12
GO:0002523	- leukocyte migration involved in inflammatory response	46.15	6.40E-05	1.51E-02	3
GO:0002269	- leukocyte activation involved in inflammatory response	2.48	7.95E-06	4.84E-03	5
GO:0050727	- regulation of inflammatory response	4.86	2.83E-04	3.70E-02	8
GO:0150076	- neuroinflammatory response	24.24	3.37E-05	9.51E-03	4
GO:0061900	- glial cell activation	25.8	2.69E-05	8.35E-03	4
GO:0001774	- microglial cell activation	36.36	7.95E-06	4.66E-03	4
GO:1903978	- regulation of microglial cell activation	29.99	1.97E-04	2.78E-02	3
GO:0098542	- defense response to other organism	4.7	2.70E-04	3.58E-02	14
GO:0045087	- innate immune response	3.19	4.17E-04	4.61E-02	12
GO:0034341	- response to interferon-gamma	6.59	3.58E-04	4.29E-02	6
GO:0009607	➢ response to biotic stimulus	2.84	4.29E-04	4.71E-02	14
GO:0043207	- response to external biotic stimulus	2.92	3.29E-04	4.01E-02	14
GO:0009605	➢ response to external stimulus	2.31	9.67E-05	1.84E-02	24
GO:1901700	➢ response to oxygen-containing compound	7.87	3.00E-04	3.88E-02	19
Immune system process related GO terms					
GO:0002376	Immune system process	2.41	1.25E-06	2.20E-03	33
GO:0002252	➢ immune effector process	3.73	3.79E-07	1.50E-03	20
GO:0002443	- leukocyte mediated immunity	3.95	6.71E-06	4.61E-03	15
GO:0002444	- myeloid leukocyte mediated immunity	5.34	1.22E-06	2.41E-03	13
GO:0002446	- neutrophil mediated immunity	5.26	1.42E-06	2.25E-03	13
GO:0006955	➢ immune response	2.41	9.50E-05	1.83E-02	22
GO:0002263	- cell activation involved in immune response	4.21	1.52E-05	5.99E-03	13
GO:0002366	- leukocyte activation involved in immune response	4.23	1.42E-05	5.75E-03	13
GO:0002275	- myeloid cell activation involved in immune response	5.02	2.37E-06	2.08E-03	13

GO:0002283	- neutrophil activation involved in immune response	5.34	1.22E-06	2.41E-03	13
GO:0050776	- regulation of immune response	3.21	1.25E-05	5.64E-03	18
GO:0002764	- immune response-regulating signaling pathway	3.75	1.94E-04	2.78E-02	11
GO:0050778	- positive regulation of immune response	3.08	3.27E-04	4.04E-02	13
GO:0002253	➢ activation of immune response	3.88	7.12E-05	1.61E-02	12
GO:0002757	- immune response-activating signal transduction	4	1.11E-04	1.93E-02	11
GO:0002682	➢ regulation of immune system process	3.44	5.88E-09	9.30E-05	28
GO:0002684	➢ positive regulation of immune system process	2.83	1.68E-04	2.56E-02	16
Cell death related GO terms					
GO:0008219	Cell death	2.98	9.34E-05	1.87E-02	16
GO:0010941	➢ regulation of cell death	2.5	8.19E-05	1.75E-02	21
GO:0012501	➢ programmed cell death	3.08	6.37E-05	1.53E-02	16
GO:0006915	- apoptotic process	4.52	4.90E-05	1.26E-02	15
GO:0110089	- regulation of hippocampal neuron apoptotic process	99.98	3.63E-04	4.29E-02	2
GO:2001233	- regulation of apoptotic signaling pathway	4.49	2.10E-04	2.91E-02	9

Table S7. Correlation between gene expressions and confounding variables in the total fraction

Variables	**RASD1**	**H1FX**	**SYN1**	**IGFBP4**	**SYN2**	**HPSD1**	**RBBP4**	**ZFN32**
Age	r=0.049 *p*=0.86	r=0.16 *p*=0.57	r=0.39 *p*=0.15	r=-0.04 *p*=0.87	r=0.18 *p*=0.52	r=-0.02 *p*=0.92	r=0.12 *p*=0.65	r=-0.17 *p*=0.54
PMI	r=0.01 *p*=0.97	r=-0.08 *p*=0.77	r=-0.14 *p*=0.61	r=0.12 *p*=0.67	r=0.21 *p*=0.44	r=0.24 *p*=0.39	r=-0.003 *p*=0.99	r=-0.22 *p*=0.41
Brain pH	r=-0.25 *p*=0.39	r=0.13 *p*=0.64	r=0.14 *p*=0.62	r=-0.19 *p*=0.49	r=0.07 *p*=0.79	r=-0.49 *p*=0.06	r=-0.44 *p*=0.10	r=-0.17 *p*=0.55
Sex	t=1.3 *p*=0.19	t=0.83 *p*=0.42	t=1.2 *p*=0.24	t=1.4 *p*=0.17	t=0.91 *p*=0.38	t=1.4 *p*=0.17	t=1.1 *p*=0.27	t=0.20 *p*=0.84
Alcohol Abuse	t=0.26 *p*=0.79	t=1.41 *p*=0.18	t=0.68 *p*=0.51	t=1.44 *p*=0.17	t=1.26 *p*=0.23	t=1.07 *p*=0.30	t=4.38 *p*=0.001	t=2.25 *p*=0.04
Antidepressant	t=1.2 *p*=0.22	t=0.63 *p*=0.53	t=0.006 *p*=0.99	t=0.32 *p*=0.75	t=0.13 *p*=0.89	t=0.72 *p*=0.48	t=0.07 *p*=0.95	t=0.12 *p*=0.91

Values denote p-value. Ct: control, MDD: Major Depressive Disorder, dlPFC: Dorsolateral prefrontal cortex, PMI: postmortem interval, miR: microRNA. The asterisk indicates a statistically significant correlation ($p < 0.05$).

Table S8. Correlation between gene expressions and confounding variables in the synaptic fraction

Variables	TLR2	ELK1	ZFP36	IRF1	HES5	ASPDH	CYB561D1	FUT9
Age	r=-0.06 *p*=0.85	r=0.18 *p*=0.55	r=0.30 *p*=0.34	r=0.12 *p*=0.72	r=0.14 *p*=0.63	r=-0.01 *p*=0.96	r=-0.01 *p*=0.96	r=0.001 *p*=0.99
PMI	r=-0.32 *p*=0.29	r=-0.001 *p*=1	r=-0.30 *p*=0.34	r=0.05 *p*=0.87	r=0.20 *p*=0.47	r=-0.23 *p*=0.41	r=0.23 *p*=0.41	r=0.28 *p*=0.32
Brain pH	r=0.09 *p*=0.77	r=0.24 *p*=0.43	r=-0.24 *p*=0.45	r=-0.19 *p*=0.56	r=-0.18 *p*=0.52	r=-0.07 *p*=0.81	r=0.15 *p*=0.60	r=-0.19 *p*=0.51
Sex	t=0.98 *p*=0.34	t=1.2 *p*=0.25	t=0.87 *p*=0.40	t=0.77 *p*=0.45	t=0.92 *p*=0.37	t=1.6 *p*=0.13	t=0.50 *p*=0.62	t=1.1 *p*=0.26
Antidepressant	t=0.35 *p*=0.73	t=0.63 *p*=0.54	t=0.13 *p*=0.89	t=1.4 *p*=0.19	t=0.61 *p*=0.55	t=0.52 *p*=0.61	t=0.16 *p*=0.87	t=1.5 *p*=0.14
Alcohol Abuse	t=0.99 *p*=0.34	t=1.05 *p*=0.31	t=0.79 *p*=0.69	t=1.10 *p*=0.29	t=1.98 *p*=0.07	t=.35 *p*=0.73	t=0.2.19 *p*=0.05	t=1.59 *p*=0.13

Values denote p-value. Ct: control, MDD: Major Depressive Disorder. PMI: postmortem interval. The asterisk indicates a statistically significant correlation ($p < 0.05$).

Table S9. Synaptic/total fraction ratio of genes in control subjects (top and bottom 20)

Gene symbol	Ensembl ID	Synaptosome/total fraction ratio	Chromosomal location	Strand
The ratio of enrichment genes top 20				
EPDR1	ENSG00000086289.11_3	8.869108	chr7:37723446-37991543	+
AC025594.2	ENSG00000272899.3_4	7.371736	chr7:128506362-128512098	+
PMP2	ENSG00000147588.6_2	7.325013	chr8:82352561-82359758	-
LYNX1	ENSG00000180155.19_2	7.18706	chr8:143852615-143859226	-
GIPC1	ENSG00000123159.15_3	6.425831	chr19:14588572-14606961	-
E2F1	ENSG00000101412.12_2	4.523676	chr20:32263489-32274210	-
AC091959.3	ENSG00000275740.1_3	4.492684	chr5:145583113-145718814	+
EBF4	ENSG00000088881.20_3	3.781456	chr20:2673524-2740754	+
GJC2	ENSG00000198835.3_2	3.732905	chr1:228337553-228347527	+
TMEM189-UBE2V1	ENSG00000124208.16_3	3.572151	chr20:48697661-48770174	-
C1QA	ENSG00000173372.16_3	3.543936	chr1:22962999-22966101	+
FIP1L1	ENSG00000145216.15_3	3.511716	chr4:54243810-54327028	+
CAVIN1	ENSG00000177469.12_3	3.456352	chr17:40554470-40575535	-
DZIP1	ENSG00000134874.17_2	3.447099	chr13:96230456-96296957	-
FLII	ENSG00000177731.15_2	3.377484	chr17:18148150-18162230	-
OGDH	ENSG00000105953.14_2	3.082193	chr7:44646171-44748665	+
DYSF	ENSG00000135636.13_2	2.67007	chr2:71680852-71913898	+
POLR2J2	ENSG00000267645.5_3	2.619659	chr7:102277496-102312088	-
GINM1	ENSG00000055211.12_2	2.53371	chr6:149887430-149912884	+
INO80B-WBP1	ENSG00000274049.4_3	2.489328	chr2:74682215-74688011	+
The ratio of depleted genes bottom 20				
C1orf64	ENSG00000183888.4_2	0.251085	chr1:16330731-16335302	+
GIMAP7	ENSG00000179144.4_2	0.249776	chr7:150211918-150218161	+
ACVRL1	ENSG00000139567.12_2	0.248565	chr12:52300692-52317145	+
GIT2	ENSG00000139436.20_3	0.243924	chr12:110367597-110434194	-
FLT1	ENSG00000102755.11_2	0.241182	chr13:28874481-29069282	-
ABCG2	ENSG00000118777.10_3	0.232325	chr4:89011416-89152474	-
FGR	ENSG00000000938.12_2	0.224675	chr1:27938575-27961788	-
CP	ENSG00000047457.13_2	0.224644	chr3:148880197-148939842	-

TM4SF1	ENSG00000169908.11_3	0.222281	chr3:149086809-149095652	-
ABCB1	ENSG00000085563.14_2	0.218971	chr7:87132949-87342639	-
CDH5	ENSG00000179776.17_3	0.218477	chr16:66400525-66438689	+
CXCL1	ENSG00000163739.4_2	0.205596	chr4:74735110-74736959	+
EDN1	ENSG00000078401.6_2	0.199844	chr6:12290596-12297427	+
POLR2J2	ENSG00000228049.7_3	0.195706	chr7:102305815-102312076	-
AC004922.1	ENSG00000284292.1_2	0.192021	chr7:98923502-98992276	+
LYNX1	ENSG00000284505.1_1	0.188766	chr8:143845752-143859640	-
GINS1	ENSG00000101003.9_2	0.182566	chr20:25388363-25433264	+
HIGD1B	ENSG00000131097.6_2	0.179365	chr17:42923721-42927848	+
CSF3	ENSG00000108342.12_2	0.172712	chr17:38171614-38174066	+
C7orf55-LUC7L2	ENSG00000269955.2_3	0.137439	chr7:139026106-139107345	+

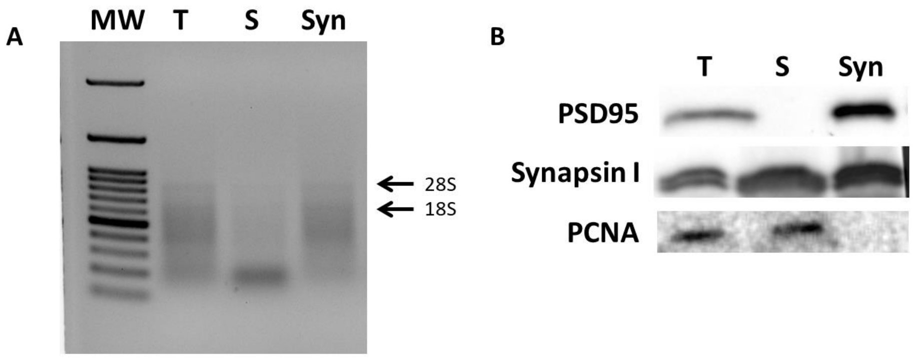

Figure S1. Verification of RNA quality with gel electrophoresis and validation of synaptosome with Western Blot. The result of western blot about validation tests and gel electrophoresis about isolated RNA. (A) An equal amount of RNAs (500 ng) was loaded in 0.8% TAE Agarose gel and stained with Ethidium Bromide. MW is 100bp plus ladder size marker. (B) An equal amount of proteins (20 ug) were loaded to subject to PAGE and blotted. MW, molecular weight; T, total fraction; S, S fraction; Syn, synaptosome.

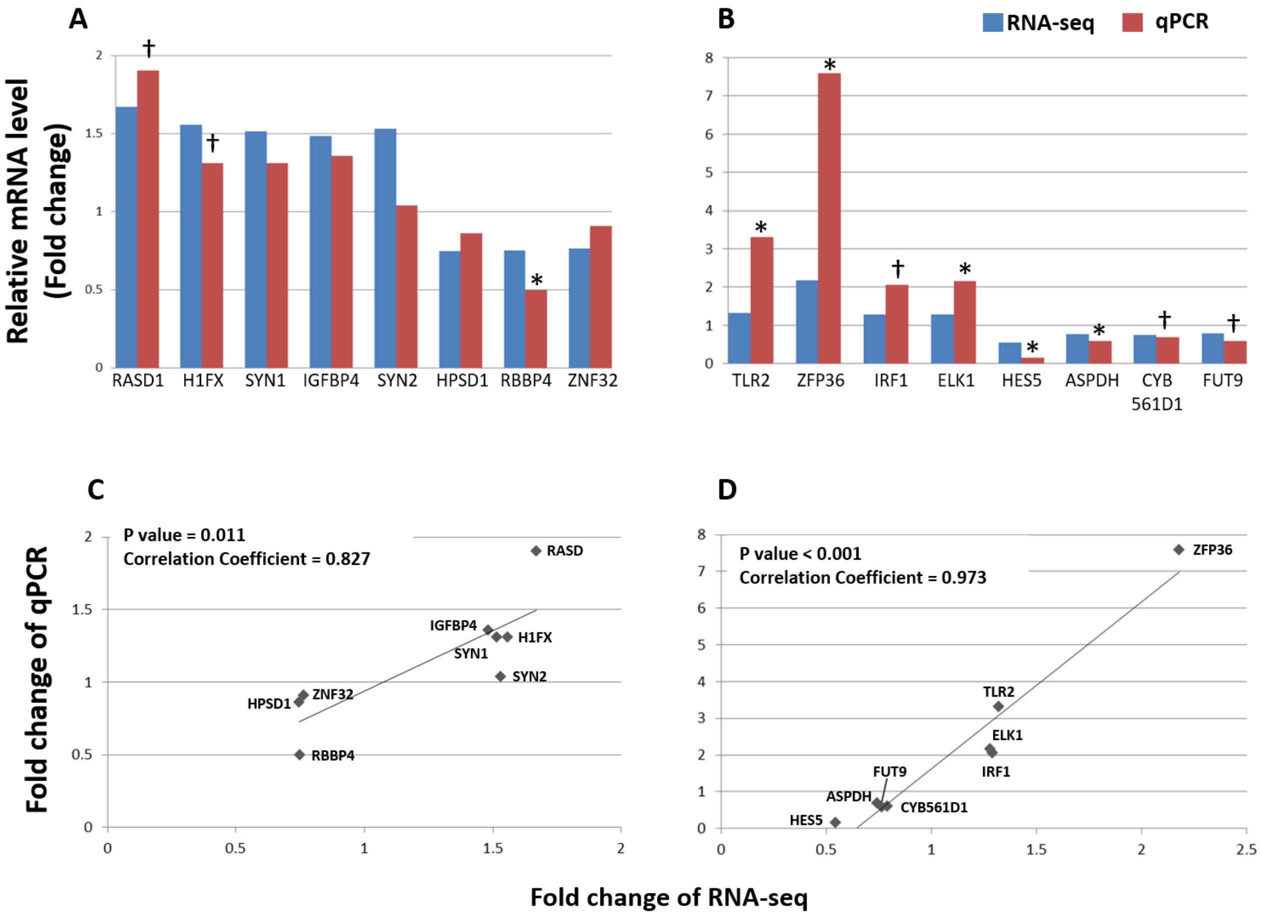

Figure S2. The fold change comparison based on relative quantification of gene expression and scatter plot of correlation between fold change of RNA-seq and qPCR. A) The gene expression differences measured by qPCR of total fraction are as follows: RASD1: t = -1.788, df = 17.5, p = 0.091; H1FX: t = -1.948, df = 28, p = 0.061; SYN1: t = -0.982, df = 28, p = 0.335; IGFBP4: t = -1.598, df = 21.3, p = 0.125; SYN2: t = -0.128, df = 28, p = 0.899; HPSD1: t = 0.801, df = 28, p = 0.430; RBBP4: t = 2.433, df = 16.3, p = 0.027; ZNF32: t = 0.787, df = 28, p = 0.438. B) The gene expression differences measured by qPCR of synaptic fraction are as follows: TLR2: t = -2.592, df = 12.5, p = 0.023; ZFP36: t = -2.411, df = 13.1, p = 0.031; IRF1: t = -1.923, df = 14.5, p = 0.074; ELK1:t = -3.220, df = 19.3, p = 0.004; HES5: t = 2.795, df = 14.2, p = 0.014; ASPDH: t = 2.593, df = 28, p = 0.015; CYB561D1: t = 1.754, df = 28, p = 0.090; FUT9: t = 1.825, df = 28, p = 0.079. Values denote average ± SEM. 'a' denotes the statistical significance between control and MDD subjects. (n=15 in control, n=15 in MDD; outliers excluded). The geometric mean (GAPDH, ACTB, and 18s rRNA) was used as normalizer. * p < 0.05, † p < 0.01. The scatter plot of correlation between fold change of qPCR and RNA-seq in total fraction (C) and synaptic fraction (D). X-axis indicates the fold change of RNA-seq, while Y-axis shows that of qPCR data (MDD/Ct). MDD, Major Depressive Disorder

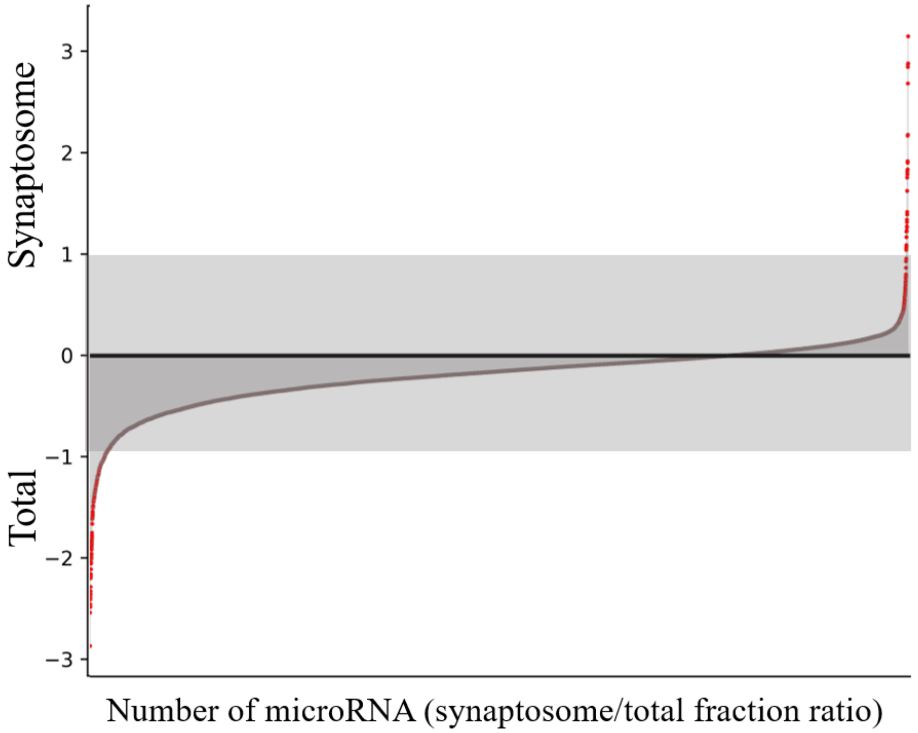

Figure S3. Enrichment ratios of synaptic fraction gene expression compared to total fraction. Gene expressions ratio of synaptic/total fraction about control subjects as measured by RNA-seq. The synaptic/total ratio are shown as log(base=2) transformed values.

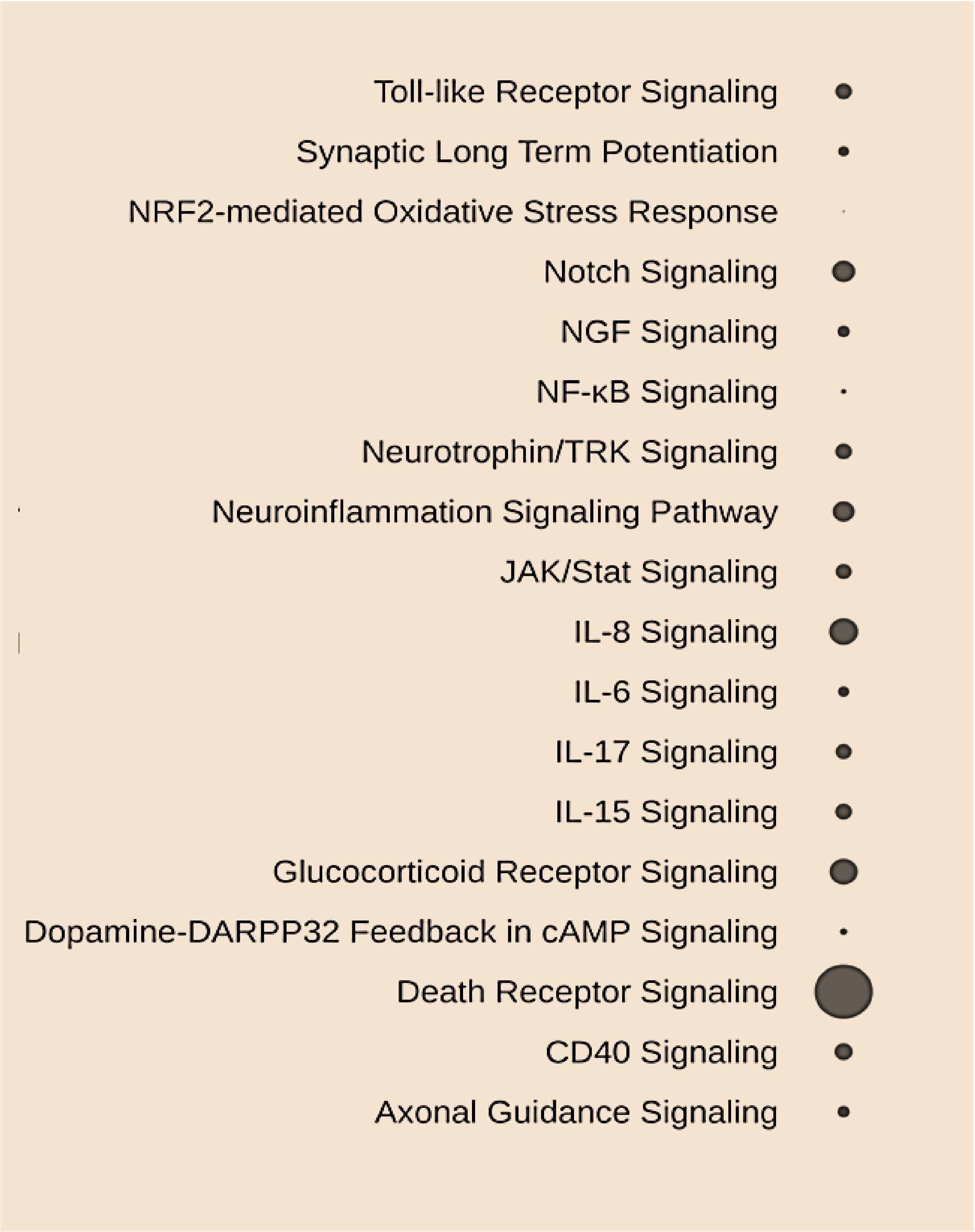

Figure S4. The result of canonical pathway in significantly altered shift genes. The analysis was performed by 119 shifted ratio genes (84 up and 35 down together). Spots/circles size is function of –log(base=10) of fisher exact test enrichment p-value.