DOI: 10.4081/itjm.2024.1830

SUPPLEMENTARY MATERIAL

Screening of the key genes and signaling pathways for schizophrenia using bioinformatics and next generation sequencing data analysis

Iranna Kottursh etti,[1] Basavaraj Vastrad,[2] Veena Kori,[3]
Chanabasayya Vastrad,[4] Shivakumar Kotrashetti[4]

[1]Department of Panchakarma, Rajiv Gandhi Education Society's Ayurvedic Medical College, Hospital and PG Research Center, Ron, Karnataka; [2]Department of Pharmaceutical Chemistry, K.L.E. College of Pharmacy, Gadag, Karnataka; [3]Department of Dravya Guna Vignan, D G Melmalagi Ayurvedic Medical College, Gadag, Karnataka; [4]Biostatistics and Bioinformatics, Chanabasava Nilaya, Bharthinagar, Dharwad, Karnataka, India.

Correspondence: Chanabasayya Vastrad, Biostatistics and Bioinformatics, Chanabasava Nilaya, Bharthinagar, Dharwad 580001, Karnataka, India.
Tel.: +919480073398
E-mail: channu.vastrad@gmail.com

Key words: differentially expressed genes, schizophrenia, bioinformatics analysis, protein-protein interaction, GO and pathway enrichment analyses.

Supplementary Table 1. The statistical metrics for key differentially expressed genes.

Gene Symbol	logFC	pValue	tvalue	Regulation	Gene Name
HOXC11	4.898271	1.97E-05	4.268315	Up	homeobox C11
HOTAIR	4.343866	1.33E-05	4.355707	Up	HOX transcript antisense RNA
HOXC-AS3	4.235228	2.17E-05	4.246415	Up	HOXC cluster antisense RNA 3
HOXD11	4.022462	1.69E-08	5.641522	Up	homeobox D11
GOLGA6L9	3.297534	0.002131	3.071325	Up	golgin A6 family like 9
RN7SL471P	3.04278	7.30E-05	3.966132	Up	RNA, 7SL, cytoplasmic 471, pseudogene
SLC15A1	3.030915	3.48E-06	4.640516	Up	solute carrier family 15 member 1
HOXD10	3.01674	6.09E-09	5.814387	Up	homeobox D10
CCL11	2.951088	0.007549	2.671613	Up	C-C motif chemokine ligand 11
SLFN11	2.925653	1.97E-11	6.708497	Up	schlafen family member 11
FOLH1	2.909564	6.85E-06	4.498435	Up	folate hydrolase 1
HOXC10	2.826082	0.000177	3.750439	Up	homeobox C10
SIX1	2.744972	3.24E-09	5.919202	Up	SIX homeobox 1
MYCT1	2.702087	0.013958	2.458355	Up	MYC target 1
CYP2C8	2.678177	0.000404	3.537325	Up	cytochrome P450 family 2 subfamily C member 8
XCL1	2.592006	4.89E-05	4.060654	Up	X-C motif chemokine ligand 1
QRSL1P1	2.570247	0.000104	3.880957	Up	QRSL1 pseudogene 1
HLA-DMB	2.454265	2.30E-06	4.724699	Up	major histocompatibility complex, class II, DM beta
VAX1	2.418188	0.000368	3.561717	Up	ventral anterior homeobox 1
SLCO6A1	2.379212	1.69E-05	4.301859	Up	solute carrier organic anion transporter family member 6A1
NDUFB4P5	2.337488	0.035871	2.098387	Up	NADH:ubiquinoneoxidoreductase subunit B4 pseudogene 5
VIP	2.306657	0.001007	3.288533	Up	vasoactive intestinal peptide
XCL2	2.290334	0.012469	2.498596	Up	X-C motif chemokine ligand 2
RPL7AP19	2.271062	0.027467	2.204813	Up	ribosomal protein L7a pseudogene 19
MALL	2.251002	2.71E-06	4.691936	Up	mal, T cell differentiation protein like
HOXC5	2.238585	0.001676	3.142376	Up	homeobox C5
TGM5	2.223124	0.001485	3.177659	Up	transglutaminase 5
HRH1	2.21074	2.23E-05	4.24002	Up	histamine receptor H1
GATA6	2.187587	0.001896	3.106019	Up	GATA binding protein 6
TMCO4	2.112989	2.73E-05	4.194505	Up	transmembrane and coiled-coil domains 4
FRZB	2.053298	8.19E-09	5.764566	Up	frizzled related protein
RN7SL834P	2.043651	0.029496	2.176796	Up	RNA, 7SL, cytoplasmic 834, pseudogene
CPQ	2.038515	7.77E-10	6.149559	Up	carboxypeptidase Q
HOXC-AS2	2.031851	0.015923	2.410681	Up	HOXC cluster antisense RNA 2
CALCRL	2.006166	4.12E-09	5.879263	Up	calcitonin receptor like receptor
SLC6A10P	1.994697	0.000202	3.715976	Up	solute carrier family 6 member 10, pseudogene
CPLX4	1.989809	0.020525	2.316618	Up	complexin 4
GBP2	1.985256	1.38E-09	6.057853	Up	guanylate binding protein 2
CD40	1.98021	1.74E-05	4.296057	Up	CD40 molecule
CACNG3	1.959446	0.007084	2.692859	Up	calcium voltage-gated channel auxiliary subunit gamma 3
NT5E	1.956445	9.32E-08	5.339462	Up	5'-nucleotidase ecto

ZFP92	1.945558	0.021786	2.294079	Up	ZFP92 zinc finger protein
SLC16A6	1.931421	3.99E-07	5.069526	Up	solute carrier family 16 member 6
PLAAT5	1.930981	2.82E-05	4.187878	Up	phospholipase A and acyltransferase 5
COL21A1	1.927077	1.32E-06	4.837166	Up	collagen type XXI alpha 1 chain
TMED11P	1.925349	0.000714	3.384243	Up	transmembrane p24 trafficking protein 11, pseudogene
CSPG4BP	1.924566	0.001403	3.194028	Up	chondroitin sulfate proteoglycan family member 4B, pseudogene
CD163	1.908506	0.001078	3.269412	Up	CD163 molecule
C10orf55	1.890256	3.82E-06	4.621061	Up	chromosome 10 putative open reading frame 55
WT1	1.862582	0.007801	2.660543	Up	WT1 transcription factor
PCDHGA3	1.818544	4.41E-05	4.084942	Up	protocadherin gamma subfamily A, 3
TFAP2B	1.808364	0.000622	3.421912	Up	transcription factor AP-2 beta
RNA5SP433	1.801421	0.047515	1.981683	Up	RNA, 5S ribosomal pseudogene 433
ACSM6	1.800393	0.000156	3.781356	Up	acyl-CoA synthetase medium chain family member 6
FIBCD1	1.798821	2.54E-05	4.211349	Up	fibrinogen C domain containing 1
ZC2HC1B	1.796064	1.34E-08	5.68138	Up	zinc finger C2HC-type containing 1B
SLC5A12	1.790089	5.31E-05	4.041434	Up	solute carrier family 5 member 12
DIRAS3	1.784865	3.38E-06	4.646041	Up	DIRAS family GTPase 3
HFE	1.776487	3.16E-10	6.290684	Up	homeostatic iron regulator
HOXB7	1.758192	0.01209	2.509496	Up	homeobox B7
PRSS56	1.751231	0.002285	3.050451	Up	serine protease 56
MEDAG	1.75069	0.000959	3.302174	Up	mesenteric estrogen dependent adipogenesis
HOXB-AS4	1.747643	0.008551	2.629486	Up	HOXB cluster antisense RNA 4
NKX2-5	1.743022	0.000259	3.653617	Up	NK2 homeobox 5
IGFBP7	1.742838	0.000281	3.63179	Up	insulin like growth factor binding protein 7
SHE	1.730331	0.000737	3.375514	Up	Src homology 2 domain containing E
IFNA8	1.725004	0.005174	2.796018	Up	interferon alpha 8
HOXC8	1.703115	0.009157	2.606146	Up	homeobox C8
OCIAD2	1.697957	2.18E-06	4.73567	Up	OCIA domain containing 2
NPY2R	1.68715	4.93E-06	4.567756	Up	neuropeptide Y receptor Y2
SERF1AP1	1.681452	0.008976	2.612957	Up	small EDRK-rich factor 1A pseudogene 1
OSMR	1.678002	3.47E-06	4.641042	Up	oncostatin M receptor
FIBIN	1.669976	2.99E-05	4.174072	Up	fin bud initiation factor homolog
HOXC6	1.665308	0.012417	2.500053	Up	homeobox C6
HLA-F	1.664351	0.002204	3.061276	Up	major histocompatibility complex, class I, F
SPOCD1	1.654795	1.03E-05	4.410074	Up	SPOC domain containing 1
TAC1	1.650207	0.002971	2.970734	Up	tachykinin precursor 1
PDE1C	1.637478	2.30E-06	4.725097	Up	phosphodiesterase 1C
HCG11	1.625647	2.11E-05	4.252765	Up	HLA complex group 11
RN7SL547P	1.615254	0.038124	2.073514	Up	RNA, 7SL, cytoplasmic 547, pseudogene
HTR1F	1.614061	0.001093	3.265383	Up	5-hydroxytryptamine receptor 1F
SP100	1.608891	4.36E-05	4.087366	Up	SP100 nuclear antigen
HBE1	1.608398	0.001416	3.191309	Up	hemoglobin subunit epsilon 1

AGBL2	1.605939	1.18E-06	4.858749	Up	AGBL carboxypeptidase 2
CCL2	1.602312	0.000167	3.76387	Up	C-C motif chemokine ligand 2
AQP5	1.600402	2.23E-06	4.731448	Up	aquaporin 5
DMKN	1.595573	0.000832	3.341947	Up	dermokine
POSTN	1.59239	0.005005	2.806701	Up	periostin
HOXC4	1.587288	0.006788	2.707087	Up	homeobox C4
TMOD1	1.586498	0.000428	3.521997	Up	tropomodulin 1
RHOD	1.582593	0.00094	3.307898	Up	ras homolog family member D
LRIT1	1.578177	0.017769	2.370397	Up	leucine rich repeat, Ig-like and transmembrane domains 1
FNDC7	1.576858	7.17E-05	3.97066	Up	fibronectin type III domain containing 7
WNT2B	1.573388	1.12E-07	5.30616	Up	Wnt family member 2B
TGFBI	1.555596	0.000237	3.676023	Up	transforming growth factor beta induced
IL1RL2	1.552643	0.013172	2.479078	Up	interleukin 1 receptor like 2
HLA-DMA	1.548771	1.68E-09	6.026072	Up	major histocompatibility complex, class II, DM alpha
GRHL3	1.543178	4.29E-07	5.055682	Up	grainyhead like transcription factor 3
HLA-DRA	1.541409	0.002674	3.002932	Up	major histocompatibility complex, class II, DR alpha
COL1A2	1.541364	0.009226	2.603548	Up	collagen type I alpha 2 chain
HSD17B7P2	1.53774	0.00015	3.791173	Up	hydroxysteroid 17-beta dehydrogenase 7 pseudogene 2
C6orf15	1.53427	0.015673	2.416443	Up	chromosome 6 open reading frame 15
SFTA3	1.531258	0.010145	2.57083	Up	surfactant associated 3
APOL3	1.525001	0.001116	3.259628	Up	apolipoprotein L3
CXCL6	1.523995	4.71E-05	4.069556	Up	C-X-C motif chemokine ligand 6
PRDM12	1.513799	0.001557	3.163756	Up	PR/SET domain 12
SCGN	1.513701	0.001619	3.152446	Up	secretagogin, EF-hand calcium binding protein
RUNX1	1.504621	0.000297	3.618076	Up	RUNX family transcription factor 1
CHI3L2	1.501221	0.002128	3.071785	Up	chitinase 3 like 2
SLFN12L	1.486221	0.01677	2.391717	Up	schlafen family member 12 like
RNF212	1.481639	0.002795	2.989428	Up	ring finger protein 212
TFF3	1.475679	0.006518	2.720512	Up	trefoil factor 3
HES3	1.473573	0.001149	3.251259	Up	hes family bHLH transcription factor 3
PPY	1.465516	0.017566	2.374643	Up	pancreatic polypeptide
TMPRSS15	1.463188	0.000152	3.78703	Up	transmembrane serine protease 15
IRX4	1.46149	0.002825	2.986178	Up	iroquoishomeobox 4
FAM86LP	1.457415	0.016417	2.399517	Up	family with sequence similarity 86, member A pseudogene
FLJ12825	1.455014	0.000272	3.640183	Up	uncharacterized LOC440101
PTHLH	1.440366	0.000229	3.684348	Up	parathyroid hormone like hormone
FAM86MP	1.431947	0.012907	2.486313	Up	family with sequence similarity 86, member A pseudogene
PI16	1.426746	0.001414	3.191848	Up	peptidase inhibitor 16
RNA5SP328	1.42389	0.015563	2.419007	Up	RNA, 5S ribosomal pseudogene 328
ASPA	1.422651	0.008699	2.623647	Up	aspartoacylase
RPL31P25	1.418218	0.009834	2.581629	Up	ribosomal protein L31 pseudogene 25
NOS1	1.417119	0.00349	2.920921	Up	nitric oxide synthase 1
GPR132	1.415798	0.004956	2.809897	Up	G protein-coupled receptor 132

CCNO	1.41103	0.000141	3.805588	Up	cyclin O
SEPTIN7P9	1.409701	1.05E-05	4.405693	Up	septin 7 pseudogene 9
ACCS	1.409643	0.014983	2.432791	Up	1-aminocyclopropane-1-carboxylate synthase homolog (inactive)
DCSTAMP	1.405278	0.04318	2.021965	Up	dendrocyte expressed seven transmembrane protein
SNORA15B-1	1.400077	9.68E-05	3.89838	Up	small nucleolar RNA, H/ACA box 15B-1
XDH	1.399972	0.034904	2.109471	Up	xanthine dehydrogenase
TBX15	1.398051	0.006964	2.69854	Up	T-box transcription factor 15
MPV17L	1.396255	0.001115	3.259701	Up	MPV17 mitochondrial inner membrane protein like
DKK2	1.392324	0.004217	2.861445	Up	dickkopf WNT signaling pathway inhibitor 2
IL18R1	1.392323	0.001788	3.123404	Up	interleukin 18 receptor 1
LRRC37A2	1.391118	0.001701	3.138037	Up	leucine rich repeat containing 37 member A2
LBX1	1.390378	0.008988	2.612527	Up	ladybird homeobox 1
ADAM12	1.38798	2.68E-05	4.199333	Up	ADAM metallopeptidase domain 12
EDN3	1.386348	0.022919	2.274782	Up	endothelin 3
PCDHGC3	1.384514	5.19E-07	5.019079	Up	protocadherin gamma subfamily C, 3
CASP4	1.381904	0.006208	2.7366	Up	caspase 4
NPPC	1.366619	0.00071	3.385683	Up	natriuretic peptide C
RNA5SP454	1.356678	0.013819	2.461928	Up	RNA, 5S ribosomal pseudogene 454
NEK11	1.355793	8.22E-06	4.459305	Up	NIMA related kinase 11
COL1A1	1.354731	0.015144	2.428919	Up	collagen type I alpha 1 chain
FAM225A	1.352155	0.010865	2.547	Up	family with sequence similarity 225 member A
IL1R1	1.345184	0.004544	2.837707	Up	interleukin 1 receptor type 1
HOXD9	1.341337	0.002842	2.984367	Up	homeobox D9
ABCG2	1.335451	0.009003	2.611948	Up	ATP binding cassette subfamily G member 2 (Junior blood group)
RPL23AP4	1.334899	0.009251	2.602619	Up	ribosomal protein L23a pseudogene 4
SELL	1.334733	0.005049	2.803878	Up	selectin L
ZC3HAV1L	1.33441	7.34E-05	3.965074	Up	zinc finger CCCH-type containing, antiviral 1 like
SLFN5	1.331212	8.06E-05	3.942501	Up	schlafen family member 5
GJC3	1.329068	0.005184	2.795398	Up	gap junction protein gamma 3
OTOGL	1.328821	0.00018	3.745201	Up	otogelin like
SIX2	1.32791	0.034012	2.119933	Up	SIX homeobox 2
LAMA2	1.327215	0.000381	3.553033	Up	laminin subunit alpha 2
CSRP1	1.31334	0.001083	3.26798	Up	cysteine and glycine rich protein 1
IL13RA2	1.304917	0.008503	2.631433	Up	interleukin 13 receptor subunit alpha 2
RASL12	1.302584	0.004547	2.837486	Up	RAS like family 12
GPR176	1.300926	1.33E-05	4.354606	Up	G protein-coupled receptor 176
STING1	1.298187	0.002367	3.039896	Up	stimulator of interferon response cGAMPinteractor 1
TMPRSS2	1.295607	0.049481	1.964419	Up	transmembrane serine protease 2
IFITM2	1.284938	0.00048	3.491856	Up	interferon induced transmembrane protein 2
ITGA1	1.284679	0.002749	2.994547	Up	integrin subunit alpha 1
TACSTD2	1.284299	0.017646	2.37296	Up	tumor associated calcium signal transducer 2
MR1	1.282264	0.00086	3.332719	Up	major histocompatibility complex, class I-related

NPY5R	1.279438	0.00802	2.651235	Up	neuropeptide Y receptor Y5
EGFLAM	1.273544	0.000549	3.455766	Up	EGF like, fibronectin type III and laminin G domains
SYNPO	1.268369	0.002674	3.002946	Up	synaptopodin
ADIRF	1.265222	0.012958	2.48491	Up	adipogenesis regulatory factor
SNX2P2	1.262733	0.009481	2.59421	Up	sorting nexin 2 pseudogene 2
HERC2P5	1.262077	0.000218	3.696672	Up	HERC2 pseudogene 5
CARD16	1.258236	0.009731	2.585228	Up	caspase recruitment domain family member 16
XAF1	1.247054	0.020459	2.317816	Up	XIAP associated factor 1
NINJ2	1.230325	0.001328	3.209865	Up	ninjurin 2
RPL17P26	1.229943	0.015562	2.419018	Up	ribosomal protein L17 pseudogene 26
ACE	1.228595	0.002952	2.972727	Up	angiotensin I converting enzyme
TBX1	1.226711	0.000528	3.466381	Up	T-box transcription factor 1
RPL23AP21	1.226451	0.000238	3.674781	Up	ribosomal protein L23a pseudogene 21
CD164L2	1.218206	0.0303	2.166148	Up	CD164 molecule like 2
PRR35	1.217067	0.001271	3.222476	Up	proline rich 35
GSDMD	1.216441	0.000406	3.536344	Up	gasdermin D
KCNN4	1.216439	5.24E-06	4.554854	Up	potassium calcium-activated channel subfamily N member 4
NMI	1.210872	0.002266	3.052889	Up	N-myc and STAT interactor
HTR1B	1.208402	0.026029	2.225779	Up	5-hydroxytryptamine receptor 1B
CTSO	1.20779	1.41E-05	4.342287	Up	cathepsin O
RAB38	1.204881	0.002077	3.078927	Up	RAB38, member RAS oncogene family
APOL1	1.202899	0.001544	3.166258	Up	apolipoprotein L1
ACTG2	1.195578	0.003638	2.907942	Up	actin gamma 2, smooth muscle
PRKCB	1.194572	0.006407	2.726214	Up	protein kinase C beta
ASS1	1.19296	0.000202	3.715892	Up	argininosuccinate synthase 1
ECM2	1.181928	0.001171	3.245868	Up	extracellular matrix protein 2
MLIP	1.178021	0.005459	2.778598	Up	muscular LMNA interacting protein
DNAAF1	1.177266	0.006799	2.706554	Up	dynein axonemal assembly factor 1
CTSC	1.177139	0.003436	2.925777	Up	cathepsin C
FLNC	1.166818	0.000195	3.724963	Up	filamin C
CACNA1A	1.165898	0.003361	2.932645	Up	calcium voltage-gated channel subunit alpha1 A
ECEL1	1.162242	0.008408	2.63523	Up	endothelin converting enzyme like 1
QPCT	1.162054	0.004276	2.857078	Up	glutaminyl-peptide cyclotransferase
DLX6	1.160462	0.020952	2.308847	Up	distal-less homeobox 6
NGB	1.156325	0.048193	1.975663	Up	neuroglobin
KCNE1	1.15597	0.006753	2.708799	Up	potassium voltage-gated channel subfamily E regulatory subunit 1
COL8A2	1.154069	0.004772	2.822062	Up	collagen type VIII alpha 2 chain
MARVELD2	1.152311	5.40E-07	5.011386	Up	MARVEL domain containing 2
MARCHF11	1.149063	0.009633	2.588741	Up	membrane associated ring-CH-type finger 11
NPR3	1.146702	0.002646	3.006171	Up	natriuretic peptide receptor 3
RNU7-13P	1.145606	0.017106	2.384422	Up	RNA, U7 small nuclear 13 pseudogene
CARD6	1.144436	0.000511	3.475044	Up	caspase recruitment domain family member 6

DHX58	1.143477	0.001086	3.267156	Up	DExH-box helicase 58
XKR8	1.140296	2.21E-07	5.180742	Up	XK related 8
ZP3	1.139445	7.79E-05	3.950777	Up	zonapellucida glycoprotein 3
HCFC2P1	1.138319	0.002792	2.989728	Up	host cell factor C2 pseudogene 1
IFITM1	1.137449	0.01214	2.508036	Up	interferon induced transmembrane protein 1
IL12RB1	1.13432	0.040794	2.04562	Up	interleukin 12 receptor subunit beta 1
ITGA11	1.133461	0.03143	2.151584	Up	integrin subunit alpha 11
GBP1	1.131968	0.008031	2.65075	Up	guanylate binding protein 1
COL12A1	1.131652	0.03761	2.079075	Up	collagen type XII alpha 1 chain
AZGP1	1.131579	0.011866	2.516103	Up	alpha-2-glycoprotein 1, zinc-binding
CYP1B1	1.128268	0.008966	2.613359	Up	cytochrome P450 family 1 subfamily B member 1
CAVIN2	1.126568	0.012558	2.496069	Up	caveolae associated protein 2
ASIC2	1.1236	0.035379	2.103994	Up	acid sensing ion channel subunit 2
PRRX1	1.121091	0.02329	2.268639	Up	paired related homeobox 1
WNT7B	1.117618	0.007756	2.6625	Up	Wnt family member 7B
PKHD1L1	1.116224	0.000262	3.650509	Up	PKHD1 like 1
COL14A1	1.113043	0.002762	2.99307	Up	collagen type XIV alpha 1 chain
RPH3A	1.109221	0.032519	2.13797	Up	rabphilin 3A
GUSBP5	1.107864	0.002953	2.972541	Up	GUSB pseudogene 5
CD34	1.103781	0.026033	2.225724	Up	CD34 molecule
HLA-DPA1	1.103089	0.003703	2.902434	Up	major histocompatibility complex, class II, DP alpha 1
A2M	1.100216	0.013247	2.47706	Up	alpha-2-macroglobulin
KIF25	1.099057	0.010175	2.569826	Up	kinesin family member 25
RNU6-959P	1.090088	0.044174	2.012441	Up	RNA, U6 small nuclear 959, pseudogene
MEOX2	1.088731	0.031641	2.148914	Up	mesenchyme homeobox 2
ST14	1.088543	0.017937	2.366909	Up	ST14 transmembrane serine protease matriptase
ZNF311	1.081017	0.000167	3.764354	Up	zinc finger protein 311
GBP3	1.074923	0.000699	3.390109	Up	guanylate binding protein 3
CDKN2A	1.074858	0.000149	3.79353	Up	cyclin dependent kinase inhibitor 2A
ADGRL4	1.073998	0.007821	2.659685	Up	adhesion G protein-coupled receptor L4
RNU6-726P	1.073601	0.032288	2.140821	Up	RNA, U6 small nuclear 726, pseudogene
RPLP0P2	1.072276	0.032266	2.141103	Up	ribosomal protein lateral stalk subunit P0 pseudogene 2
PHF11	1.072147	7.39E-06	4.482013	Up	PHD finger protein 11
ANKRD60	1.068293	0.008925	2.614912	Up	ankyrin repeat domain 60
CFI	1.066543	0.037873	2.076231	Up	complement factor I
IGFN1	1.065001	0.049432	1.964843	Up	immunoglobulin like and fibronectin type III domain containing 1
CXCL16	1.064115	1.08E-06	4.876456	Up	C-X-C motif chemokine ligand 16
LGALS1	1.059792	0.000468	3.498472	Up	galectin 1
MAL	1.056875	0.032681	2.135975	Up	mal, T cell differentiation protein
ESPN	1.056317	0.016618	2.395053	Up	espin
OLFML2B	1.055317	0.000987	3.294218	Up	olfactomedin like 2B
SNORD93	1.054771	0.039609	2.057806	Up	small nucleolar RNA, C/D box 93

KLF2P2	1.051194	0.021537	2.298443	Up	Kruppel like factor 2 pseudogene 2
EPSTI1	1.050737	0.017424	2.377634	Up	epithelial stromal interaction 1
KIAA1755	1.04981	0.01313	2.480225	Up	KIAA1755
GOLGA8O	1.049004	7.21E-06	4.487348	Up	golgin A8 family member O
PLXNA4	1.048315	0.015522	2.419971	Up	plexin A4
MRGPRE	1.042708	0.033686	2.123816	Up	MAS related GPR family member E
NIBAN1	1.04015	0.001262	3.224567	Up	niban apoptosis regulator 1
EPHA6	1.039954	0.006107	2.741963	Up	EPH receptor A6
ARHGAP29	1.03917	8.00E-05	3.944356	Up	Rho GTPase activating protein 29
NPIPA7	1.03895	0.026969	2.211964	Up	nuclear pore complex interacting protein family member A7
ZNF37CP	1.037984	0.014049	2.456011	Up	zinc finger protein 37C, pseudogene
RPS3AP19	1.036667	0.046588	1.990023	Up	RPS3A pseudogene 19
SPINT1	1.036277	0.019858	2.329024	Up	serine peptidase inhibitor, Kunitz type 1
MAP1LC3C	1.035186	0.016513	2.397369	Up	microtubule associated protein 1 light chain 3 gamma
CDH9	1.033504	0.011441	2.528921	Up	cadherin 9
PCDHGB6	1.033429	6.14E-05	4.007346	Up	protocadherin gamma subfamily B, 6
PSMB9	1.031235	0.001789	3.123149	Up	proteasome 20S subunit beta 9
FAM41C	1.030156	0.045761	1.997594	Up	family with sequence similarity 41 member C
C1R	1.026674	0.007638	2.667649	Up	complement C1r
MSLNL	1.025467	0.006535	2.719641	Up	mesothelin like
CDCP1	1.025077	0.002931	2.974936	Up	CUB domain containing protein 1
SERPINE1	1.022566	0.00497	2.808988	Up	serpin family E member 1
GLMP	1.019681	7.24E-09	5.785314	Up	glycosylated lysosomal membrane protein
RGCC	1.015171	0.011058	2.540873	Up	regulator of cell cycle
RNU6-1029P	1.011226	0.03873	2.067047	Up	RNA, U6 small nuclear 1029, pseudogene
HTR7	1.008107	0.042798	2.025673	Up	5-hydroxytryptamine receptor 7
AZGP1P2	1.005827	0.0201	2.324478	Up	AZGP1 pseudogene 2
CD44	0.99529	0.005402	2.782053	Up	CD44 molecule (Indian blood group)
ACOT4	0.993271	0.024119	2.25523	Up	acyl-CoA thioesterase 4
TSKS	0.990041	0.025156	2.238999	Up	testis specific serine kinase substrate
FABP4	0.987849	0.035514	2.102451	Up	fatty acid binding protein 4
ZNF804B	0.984365	0.043306	2.02075	Up	zinc finger protein 804B
HSPA1L	0.984234	0.00034	3.582942	Up	heat shock protein family A (Hsp70) member 1 like
SYTL5	0.981131	0.008138	2.646276	Up	synaptotagmin like 5
TRIM4	0.980584	0.015001	2.432363	Up	tripartite motif containing 4
ITGB3	0.977872	0.001026	3.283409	Up	integrin subunit beta 3
ACSS3	0.976362	0.000233	3.679929	Up	acyl-CoA synthetase short chain family member 3
COL9A2	0.973538	8.61E-06	4.449512	Up	collagen type IX alpha 2 chain
ALOX5AP	0.973201	0.031383	2.152185	Up	arachidonate 5-lipoxygenase activating protein
DAND5	0.97187	0.002745	2.994984	Up	DAN domain BMP antagonist family member 5
GDF6	0.970766	0.013537	2.469331	Up	growth differentiation factor 6
NOC2LP1	0.97065	0.018089	2.363788	Up	NOC2 like nucleolar associated transcriptional repressor pseudogene 1

ZNF630	0.970199	0.023882	2.25903	Up	zinc finger protein 630
SFRP4	0.970003	0.007513	2.673188	Up	secreted frizzled related protein 4
PLAAT4	0.969644	0.032132	2.142764	Up	phospholipase A and acyltransferase 4
PRDM7	0.969511	0.032915	2.133113	Up	PR/SET domain 7
FZD6	0.96556	6.71E-08	5.398791	Up	frizzled class receptor 6
POU4F1	0.964991	0.031962	2.144886	Up	POU class 4 homeobox 1
FBXO43	0.964302	0.000145	3.79968	Up	F-box protein 43
HLA-DOA	0.962199	0.018822	2.34904	Up	major histocompatibility complex, class II, DO alpha
SULT1A1	0.961801	0.014663	2.440602	Up	sulfotransferase family 1A member 1
SKOR1	0.960005	0.00068	3.397414	Up	SKI family transcriptional corepressor 1
C6orf141	0.957227	0.004793	2.820604	Up	chromosome 6 open reading frame 141
ISM1	0.949276	0.003276	2.940569	Up	isthmin 1
GRAMD2B	0.947801	0.003355	2.933167	Up	GRAM domain containing 2B
FAM180A	0.947262	0.01894	2.346704	Up	family with sequence similarity 180 member A
RGS22	0.942185	0.027424	2.205425	Up	regulator of G protein signaling 22
CASS4	0.94091	0.000144	3.800454	Up	Cas scaffold protein family member 4
SERF1A	0.936156	0.018613	2.353202	Up	small EDRK-rich factor 1A
GTF2A1L	0.935556	0.011314	2.532835	Up	general transcription factor IIA subunit 1 like
ME1	0.933874	0.013018	2.483271	Up	malic enzyme 1
IL4R	0.929502	0.026952	2.212208	Up	interleukin 4 receptor
RUNX2	0.92907	0.002095	3.07636	Up	RUNX family transcription factor 2
OR51B5	0.928957	0.01277	2.490107	Up	olfactory receptor family 51 subfamily B member 5
KAT7P1	0.927886	0.003784	2.895632	Up	KAT7 pseudogene 1
OR2B7P	0.926405	0.009189	2.604939	Up	olfactory receptor family 2 subfamily B member 7 pseudogene
PLAAT2	0.925346	0.00828	2.640438	Up	phospholipase A and acyltransferase 2
GNGT1	0.924752	0.042556	2.028046	Up	G protein subunit gamma transducin 1
CASP1	0.921583	0.048762	1.970669	Up	caspase 1
IL31RA	0.919419	0.009727	2.585386	Up	interleukin 31 receptor A
ZNF441	0.916076	0.023812	2.260151	Up	zinc finger protein 441
FCF1P10	0.913922	0.026425	2.219912	Up	FCF1 pseudogene 10
SLC27A6	0.909574	0.01788	2.368084	Up	solute carrier family 27 member 6
GOLGA8J	0.906514	0.011966	2.513149	Up	golgin A8 family member J
CCR4	0.904356	0.033251	2.129038	Up	C-C motif chemokine receptor 4
ZNF385D-AS2	0.899038	0.023228	2.269656	Up	ZNF385D antisense RNA 2
SH3BP5	0.898355	0.000616	3.42457	Up	SH3 domain binding protein 5
GLIPR1	0.89599	2.48E-06	4.710138	Up	GLI pathogenesis related 1
CPA4	0.894784	0.0018	3.121337	Up	carboxypeptidase A4
TACR3	0.893161	0.024572	2.248066	Up	tachykinin receptor 3
HMGB1P49	0.893092	0.047374	1.982945	Up	high mobility group box 1 pseudogene 49
CD96	0.891476	0.007884	2.656979	Up	CD96 molecule
MYD88	0.89108	0.000317	3.601263	Up	MYD88 innate immune signal transduction adaptor
MYOF	0.888551	0.002589	3.012782	Up	myoferlin
TGM2	0.887612	0.002211	3.060356	Up	transglutaminase 2

CPNE8	0.883617	0.002936	2.974366	Up	copine 8
LHCGR	0.879744	0.007135	2.690472	Up	luteinizing hormone/choriogonadotropin receptor
KCNS1	0.878869	0.008903	2.615773	Up	potassium voltage-gated channel modifier subfamily S member 1
FHP1	0.878294	0.035758	2.099663	Up	fumaratehydratasepseudogene 1
CBR3	0.87732	0.000922	3.313395	Up	carbonyl reductase 3
NR0B2	0.87712	0.0433	2.020807	Up	nuclear receptor subfamily 0 group B member 2
ANO3	0.872497	0.001316	3.212514	Up	anoctamin 3
MYL9	0.87151	0.045011	2.004554	Up	myosin light chain 9
TMEM106A	0.866451	2.46E-10	6.329434	Up	transmembrane protein 106A
RNU6-687P	0.86625	0.019829	2.329571	Up	RNA, U6 small nuclear 687, pseudogene
BMPR1B-DT	0.863667	0.021341	2.301896	Up	BMPR1B divergent transcript
DRD3	0.863242	0.021416	2.300572	Up	dopamine receptor D3
ANO9	0.861061	0.005993	2.748177	Up	anoctamin 9
IFITM3	0.86035	0.004067	2.872921	Up	interferon induced transmembrane protein 3
EEF1G	0.858472	0.039754	2.056293	Up	eukaryotic translation elongation factor 1 gamma
FAM83G	0.855806	0.012428	2.499745	Up	family with sequence similarity 83 member G
EEF1DP4	0.855636	0.009495	2.593686	Up	eukaryotic translation elongation factor 1 delta pseudogene 4
RNVU1-24	0.855385	0.018668	2.352087	Up	RNA, variant U1 small nuclear 24
CYBA	0.853354	0.006325	2.730463	Up	cytochrome b-245 alpha chain
APOBR	0.851895	0.041392	2.039585	Up	apolipoprotein B receptor
GPX7	0.851795	0.007131	2.690652	Up	glutathione peroxidase 7
STAT6	0.851603	0.002103	3.075356	Up	signal transducer and activator of transcription 6
MAFA	0.848754	0.02714	2.209496	Up	MAF bZIP transcription factor A
APOL6	0.848622	0.01668	2.393678	Up	apolipoprotein L6
RNFT1-DT	0.844656	0.02108	2.306553	Up	RNFT1 divergent transcript
RPL7AP76	0.844634	4.51E-05	4.079655	Up	ribosomal protein L7a pseudogene 76
RCAN2	0.843119	0.036578	2.090443	Up	regulator of calcineurin 2
SP140L	0.842254	0.007743	2.663088	Up	SP140 nuclear body protein like
GEM	0.842048	0.000666	3.403024	Up	GTP binding protein overexpressed in skeletal muscle
OR1F12P	0.840129	0.000405	3.536566	Up	olfactory receptor family 1 subfamily F member 12, pseudogene
CCDC3	0.838864	0.002766	2.992625	Up	coiled-coil domain containing 3
CALY	0.837896	0.01121	2.536095	Up	calcyon neuron specific vesicular protein
STON1-GTF2A1L	0.83658	0.001521	3.170674	Up	STON1-GTF2A1L readthrough
TLL2	0.832119	0.004082	2.871767	Up	tolloid like 2
COL25A1	0.831375	0.003574	2.91352	Up	collagen type XXV alpha 1 chain
NALCN	0.829186	0.012284	2.503886	Up	sodium leak channel, non-selective
OCLN	0.828695	0.012457	2.498925	Up	occludin
IGFL3	0.828476	0.028113	2.195703	Up	IGF like family member 3
BNC2	0.828177	0.007348	2.680641	Up	basonuclin 2
RCN3	0.827443	5.29E-05	4.042488	Up	reticulocalbin 3
SDCBPP3	0.824964	0.040747	2.046098	Up	syndecan binding protein pseudogene 3
BMS1P9	0.824166	0.008558	2.629238	Up	BMS1 pseudogene 9

SMIM10	0.823922	0.009928	2.578331	Up	small integral membrane protein 10
FILIP1L	0.822723	0.000886	3.324344	Up	filamin A interacting protein 1 like
UNC5C	0.820722	0.004569	2.835921	Up	unc-5 netrin receptor C
FOXC1	0.817691	0.025622	2.231901	Up	forkhead box C1
RPL35P5	0.817636	0.015828	2.412865	Up	ribosomal protein L35 pseudogene 5
SCG2	0.816824	0.023131	2.271268	Up	secretogranin II
MYC	0.81373	0.00085	3.336139	Up	MYC proto-oncogene, bHLH transcription factor
GIPC3	0.813333	0.002221	3.05903	Up	GIPC PDZ domain containing family member 3
HES2	0.811388	0.028617	2.188717	Up	hes family bHLH transcription factor 2
RN7SL368P	0.811158	0.035337	2.104474	Up	RNA, 7SL, cytoplasmic 368, pseudogene
MRI1	0.808081	2.52E-05	4.212668	Up	methylthioribose-1-phosphate isomerase 1
RPL3P11	0.808078	0.048459	1.973322	Up	ribosomal protein L3 pseudogene 11
RGPD8	0.807716	4.95E-06	4.566976	Up	RANBP2 like and GRIP domain containing 8
MRPL35P2	0.807691	0.000785	3.357878	Up	mitochondrial ribosomal protein L35 pseudogene 2
TUBA4A	0.806898	0.019051	2.344523	Up	tubulin alpha 4a
HMGB3P10	0.806368	0.028904	2.18479	Up	high mobility group box 3 pseudogene 10
PPP1R3B	0.802382	0.00085	3.335854	Up	protein phosphatase 1 regulatory subunit 3B
GBGT1	0.802196	0.003077	2.959985	Up	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1 (FORS blood group)
NWD1	0.800442	0.040343	2.05022	Up	NACHT and WD repeat domain containing 1
FN1	0.798295	0.018318	2.359125	Up	fibronectin 1
BMS1P11	0.797028	0.00124	3.229491	Up	BMS1 pseudogene 11
WFDC13	0.795424	0.0368	2.087977	Up	WAP four-disulfide core domain 13
ABCC12	0.794022	0.049724	1.962333	Up	ATP binding cassette subfamily C member 12
TLR6	0.793029	0.008005	2.651865	Up	toll like receptor 6
RASSF3	0.792661	0.003706	2.902194	Up	Ras association domain family member 3
NPY1R	0.792123	0.023618	2.26329	Up	neuropeptide Y receptor Y1
COPZ2	0.790257	0.002516	3.021452	Up	COPI coat complex subunit zeta 2
LAMC3	0.790129	0.047954	1.977773	Up	laminin subunit gamma 3
RPL23AP47	0.789642	0.02498	2.241717	Up	ribosomal protein L23a pseudogene 47
ADAMTS7P4	0.789358	0.046296	1.992685	Up	ADAMTS7 pseudogene 4
OSR2	0.788286	0.022748	2.277642	Up	odd-skipped related transciption factor 2
ANXA1	0.785827	0.009117	2.607651	Up	annexin A1
LRRN4CL	0.785428	0.012466	2.498657	Up	LRRN4 C-terminal like
TENT5C	0.78216	0.041062	2.042905	Up	terminal nucleotidyltransferase 5C
ATL3	0.781338	2.11E-05	4.253272	Up	atlastinGTPase 3
RAMP1	0.781158	0.009974	2.576745	Up	receptor activity modifying protein 1
FOSL2	0.780747	0.01036	2.563586	Up	FOS like 2, AP-1 transcription factor subunit
VRK2	0.780355	0.016595	2.395553	Up	VRK serine/threonine kinase 2
SLC9A7	0.77913	0.003176	2.950171	Up	solute carrier family 9 member A7
ECHDC3	0.778864	0.043866	2.015369	Up	enoyl-CoA hydratase domain containing 3
SPNS3	0.777823	0.044342	2.010846	Up	sphingolipid transporter 3 (putative)
TFPI2-DT	0.777201	0.044037	2.013741	Up	TFPI2 divergent transcript

ENPP7P3	0.776458	0.045097	2.003746	Up	ectonucleotidepyrophosphatase/phosphodiesterase 7 pseudogene 3
SLC46A3	0.776346	0.025998	2.226249	Up	solute carrier family 46 member 3
ZMYND15	0.773003	0.004503	2.840571	Up	zinc finger MYND-type containing 15
DDX60L	0.772054	0.005471	2.777936	Up	DExD/H-box 60 like
DPF3	0.77163	0.003147	2.953018	Up	double PHD fingers 3
NPIPB2	0.768363	0.001367	3.201493	Up	nuclear pore complex interacting protein family member B2
CAV1	0.767048	0.003652	2.906767	Up	caveolin 1
EFEMP1	0.765741	0.045274	2.002097	Up	EGF containing fibulin extracellular matrix protein 1
RGS4	0.764556	0.008909	2.615511	Up	regulator of G protein signaling 4
SPOCK2	0.763617	0.030611	2.162094	Up	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 2
TPM2	0.758071	0.003317	2.936755	Up	tropomyosin 2
MMP23B	0.756953	0.01342	2.472428	Up	matrix metallopeptidase 23B
ALPK2	0.754178	0.040235	2.051332	Up	alpha kinase 2
COL24A1	0.753791	0.007064	2.693826	Up	collagen type XXIV alpha 1 chain
CCDC103	0.752517	0.02837	2.192128	Up	coiled-coil domain containing 103
TBXA2R	0.751708	0.011133	2.538507	Up	thromboxane A2 receptor
GMPR	0.749609	0.022529	2.281332	Up	guanosine monophosphate reductase
TNFAIP2	0.746278	0.007376	2.679391	Up	TNF alpha induced protein 2
TMIGD2	0.74321	0.013339	2.474575	Up	transmembrane and immunoglobulin domain containing 2
GDF5	0.740609	0.001925	3.101543	Up	growth differentiation factor 5
KRT8	0.739809	0.027373	2.206151	Up	keratin 8
OR2B8P	0.737212	0.021743	2.294825	Up	olfactory receptor family 2 subfamily B member 8 pseudogene
UBL5P4	0.736837	0.005195	2.794691	Up	ubiquitin like 5 pseudogene 4
APCDD1L-DT	0.736205	0.005149	2.797538	Up	APCDD1L divergent transcript
HBG2	0.730909	0.004013	2.877145	Up	hemoglobin subunit gamma 2
GPD2	0.725371	0.003769	2.896862	Up	glycerol-3-phosphate dehydrogenase 2
DOCK5	0.723514	0.004201	2.862656	Up	dedicator of cytokinesis 5
NFE2	0.722542	0.04813	1.97622	Up	nuclear factor, erythroid 2
MAP1LC3A	0.721971	0.002873	2.980965	Up	microtubule associated protein 1 light chain 3 alpha
COBL	0.71922	0.029373	2.178442	Up	cordon-bleu WH2 repeat protein
FOXH1	0.718813	0.000444	3.512166	Up	forkhead box H1
TMEM255A	0.717295	0.041207	2.041443	Up	transmembrane protein 255A
S100A16	0.71636	0.000495	3.483223	Up	S100 calcium binding protein A16
NQO1	0.715675	0.011684	2.521555	Up	NAD(P)H quinone dehydrogenase 1
ERRFI1	0.714857	0.010045	2.574293	Up	ERBB receptor feedback inhibitor 1
COL6A2	0.714049	0.006851	2.703984	Up	collagen type VI alpha 2 chain
SLC38A8	0.713697	0.027684	2.201732	Up	solute carrier family 38 member 8
CHST8	0.711721	0.045083	2.003875	Up	carbohydrate sulfotransferase 8
SLC13A5	0.711178	0.017847	2.368769	Up	solute carrier family 13 member 5
TNFSF4	0.709524	0.002183	3.064135	Up	TNF superfamily member 4
TMEM35B	0.708823	0.001478	3.178967	Up	transmembrane protein 35B
SHISAL2A	0.7086	0.013605	2.467523	Up	shisa like 2A

WNT9B	0.70813	0.046715	1.988872	Up	Wnt family member 9B
LOX	0.706987	0.012043	2.51088	Up	lysyl oxidase
SSH3	0.705198	0.004019	2.876667	Up	slingshot protein phosphatase 3
TLE6	0.704726	0.007633	2.667878	Up	TLE family member 6, subcortical maternal complex member
RPL23AP87	0.703686	0.002888	2.979444	Up	ribosomal protein L23a pseudogene 87
LPCAT2	0.701804	0.003836	2.89133	Up	lysophosphatidylcholineacyltransferase 2
SMOC2	0.700767	0.02619	2.223377	Up	SPARC related modular calcium binding 2
FCGR1A	0.699392	0.042265	2.0309	Up	Fc gamma receptor Ia
LTBP2	0.697873	0.002412	3.034175	Up	latent transforming growth factor beta binding protein 2
SPARCL1	0.696516	0.042594	2.027671	Up	SPARC like 1
SPHK1	0.695806	0.012058	2.51043	Up	sphingosine kinase 1
PTGES3L-AARSD1	0.694537	0.006416	2.725723	Up	PTGES3L-AARSD1 readthrough
CCDC200	0.692533	2.97E-05	4.175732	Up	coiled-coil domain containing 200
RPS6P11	0.691935	0.039315	2.060879	Up	ribosomal protein S6 pseudogene 11
S100A5	0.691224	0.014288	2.449937	Up	S100 calcium binding protein A5
ZNF676	-7.11702	2.94E-19	-8.97086	Down	zinc finger protein 676
OR4A16	-4.9484	0.000151	-3.78974	Down	olfactory receptor family 4 subfamily A member 16
VN1R85P	-3.6006	3.52E-05	-4.1369	Down	vomeronasal 1 receptor 85 pseudogene
OR4A11P	-3.53862	0.02636	-2.22087	Down	olfactory receptor family 4 subfamily A member 11 pseudogene
BNIP3P30	-3.5377	3.31E-05	-4.15132	Down	BCL2 interacting protein 3 pseudogene 30
OLIG2	-3.51763	3.82E-10	-6.26116	Down	oligodendrocyte transcription factor 2
FEZF2	-3.49417	3.46E-05	-4.14103	Down	FEZ family zinc finger 2
HYAL4	-3.30364	7.21E-07	-4.95556	Down	hyaluronidase 4
ZNF98	-3.21622	0.001588	-3.15812	Down	zinc finger protein 98
CRH	-3.18656	7.10E-08	-5.38859	Down	corticotropin releasing hormone
ACAN	-3.16463	2.30E-09	-5.97541	Down	aggrecan
GABRA4	-3.15784	4.75E-05	-4.06764	Down	gamma-aminobutyric acid type A receptor subunit alpha4
HAPLN1	-3.14928	1.08E-06	-4.87656	Down	hyaluronan and proteoglycan link protein 1
ZNF99	-3.04065	0.01023	-2.56797	Down	zinc finger protein 99
MAGEA4	-3.00621	0.030705	-2.16088	Down	MAGE family member A4
TRIM49B	-2.85033	0.001756	-3.12861	Down	tripartite motif containing 49B
RNU6-81P	-2.84153	0.003379	-2.93098	Down	RNA, U6 small nuclear 81, pseudogene
XRCC6P5	-2.80462	1.34E-05	-4.35305	Down	X-ray repair cross complementing 6 pseudogene 5
FOXG1	-2.79574	3.09E-05	-4.16677	Down	forkhead box G1
TFAP2D	-2.74862	0.000218	-3.69705	Down	transcription factor AP-2 delta
ALPI	-2.73025	0.013044	-2.48255	Down	alkaline phosphatase, intestinal
ISL1	-2.68479	1.00E-05	-4.41697	Down	ISL LIM homeobox 1
HTR2C	-2.64259	0.000112	-3.86194	Down	5-hydroxytryptamine receptor 2C
DUXAP9	-2.60154	7.15E-05	-3.97134	Down	double homeobox A pseudogene 9
TNNT2	-2.58586	0.000528	-3.466	Down	troponin T2, cardiac type
OTX2	-2.55188	1.64E-05	-4.30848	Down	orthodenticlehomeobox 2
EMX2	-2.53058	0.000538	-3.46106	Down	empty spiracles homeobox 2

GPR12	-2.52202	0.000338	-3.58391	Down	G protein-coupled receptor 12
MAGEC2	-2.50757	0.036332	-2.09319	Down	MAGE family member C2
ANKRD20A17P	-2.50105	0.001375	-3.19975	Down	ankyrin repeat domain 20 family member A17, pseudogene
MAGEC1	-2.34596	0.008937	-2.61446	Down	MAGE family member C1
CHRM1	-2.32202	0.007776	-2.66166	Down	cholinergic receptor muscarinic 1
LMX1A	-2.28962	0.002046	-3.08349	Down	LIM homeobox transcription factor 1 alpha
HSPA2	-2.27247	4.56E-07	-5.04405	Down	heat shock protein family A (Hsp70) member 2
SLITRK2	-2.26532	1.01E-06	-4.88887	Down	SLIT and NTRK like family member 2
PPP1R12BP1	-2.26307	0.007573	-2.67055	Down	protein phosphatase 1 regulatory subunit 12B pseudogene 1
SLC6A11	-2.25909	1.87E-05	-4.2799	Down	solute carrier family 6 member 11
BMS1P17	-2.25382	0.011679	-2.52169	Down	BMS1 pseudogene 17
RHAG	-2.25082	0.008664	-2.62505	Down	Rh associated glycoprotein
OLIG1	-2.23152	0.001331	-3.2093	Down	oligodendrocyte transcription factor 1
LHFPL3	-2.21415	2.18E-06	-4.73562	Down	LHFPL tetraspan subfamily member 3
RNA5SP135	-2.19078	0.015187	-2.42789	Down	RNA, 5S ribosomal pseudogene 135
ANKRD66	-2.17421	0.048832	-1.97006	Down	ankyrin repeat domain 66
ICE2P2	-2.17272	0.004628	-2.83187	Down	interactor of little elongation complex ELL subunit 2 pseudogene 2
EOMES	-2.11577	6.20E-05	-4.00517	Down	eomesodermin
MPPED1	-2.11176	6.11E-05	-4.00861	Down	metallophosphoesterase domain containing 1
HSP90AB7P	-2.07068	0.025818	-2.22894	Down	heat shock protein 90 alpha family class B member 7, pseudogene
OR7E154P	-2.04934	0.000957	-3.30289	Down	olfactory receptor family 7 subfamily E member 154 pseudogene
CLIC6	-2.04148	0.000376	-3.55666	Down	chloride intracellular channel 6
EMX2OS	-2.03789	0.006675	-2.71262	Down	EMX2 opposite strand/antisense RNA
LHX2	-2.01128	9.69E-05	-3.89832	Down	LIM homeobox 2
RNASE6	-2.00857	0.000224	-3.69016	Down	ribonuclease A family member k6
ACTG1P12	-2.00201	0.007316	-2.68213	Down	actin gamma 1 pseudogene 12
USP17L1	-1.99938	0.002363	-3.04039	Down	ubiquitin specific peptidase 17 like family member 1
RNASE1	-1.99669	0.049172	-1.9671	Down	ribonuclease A family member 1, pancreatic
OTX1	-1.98896	6.25E-06	-4.5179	Down	orthodenticlehomeobox 1
HGF	-1.97434	0.000219	-3.69647	Down	hepatocyte growth factor
DMBX1	-1.97135	0.008425	-2.63456	Down	diencephalon/mesencephalon homeobox 1
CRYGD	-1.93869	0.00268	-3.00221	Down	crystallin gamma D
C1orf210	-1.93773	0.00044	-3.5147	Down	chromosome 1 open reading frame 210
EDDM3A	-1.9256	0.002163	-3.06693	Down	epididymal protein 3A
CCKBR	-1.91739	0.000446	-3.51151	Down	cholecystokinin B receptor
ISL1-DT	-1.90158	0.001007	-3.28845	Down	ISL1 divergent transcript
C18orf63	-1.83706	0.021613	-2.29711	Down	chromosome 18 open reading frame 63
SNORD114-10	-1.81058	0.03981	-2.05572	Down	small nucleolar RNA, C/D box 114-10
SIRPB1	-1.76765	0.000651	-3.40945	Down	signal regulatory protein beta 1
HCAR2	-1.76743	0.00049	-3.48607	Down	hydroxycarboxylic acid receptor 2
SNORD114-2	-1.7594	0.040804	-2.04552	Down	small nucleolar RNA, C/D box 114-2
SLITRK4	-1.74748	0.000915	-3.31552	Down	SLIT and NTRK like family member 4

HMGN1P13	-1.74219	0.002206	-3.06099	Down	high mobility group nucleosome binding domain 1 pseudogene 13
ZNF300P1	-1.73429	0.004733	-2.82468	Down	zinc finger protein 300 pseudogene 1
IBSP	-1.73197	0.019658	-2.33282	Down	integrin binding sialoprotein
PTH2R	-1.71303	2.56E-05	-4.20941	Down	parathyroid hormone 2 receptor
ALKAL1	-1.70506	0.000956	-3.3033	Down	ALK and LTK ligand 1
SHISA3	-1.70276	0.000273	-3.63992	Down	shisa family member 3
TAFA1	-1.69708	0.000821	-3.3456	Down	TAFA chemokine like family member 1
CTB-1I21.1	-1.68482	0.000352	-3.57344	Down	uncharacterized CTB-1I21.1
RNA5SP220	-1.67863	0.008286	-2.64018	Down	RNA, 5S ribosomal pseudogene 220
DUXAP10	-1.67837	0.0019	-3.1055	Down	double homeobox A pseudogene 10
EDDM3B	-1.67744	0.008676	-2.62457	Down	epididymal protein 3B
LHX9	-1.66892	0.000593	-3.43476	Down	LIM homeobox 9
SP5	-1.66855	0.000142	-3.80459	Down	Sp5 transcription factor
ALDH1A1	-1.66388	0.003909	-2.8854	Down	aldehyde dehydrogenase 1 family member A1
ADRA2A	-1.65618	0.000823	-3.34479	Down	adrenoceptor alpha 2A
XIST	-1.60879	0.037816	-2.07684	Down	X inactive specific transcript
MS4A7	-1.59452	0.037366	-2.08174	Down	membrane spanning 4-domains A7
RPL34P22	-1.57439	0.005644	-2.7678	Down	ribosomal protein L34 pseudogene 22
DMRT3	-1.55645	0.011031	-2.54171	Down	doublesex and mab-3 related transcription factor 3
CAPN8	-1.55643	0.000666	-3.40304	Down	calpain 8
RNU6-440P	-1.55361	0.011004	-2.54257	Down	RNA, U6 small nuclear 440, pseudogene
MYADML	-1.55259	0.011297	-2.53337	Down	myeloid associated differentiation marker like (pseudogene)
TNFSF9	-1.54643	3.05E-05	-4.16949	Down	TNF superfamily member 9
TBL1Y	-1.54287	0.022511	-2.28163	Down	transducin beta like 1 Y-linked
PCAT2	-1.53359	0.007061	-2.69397	Down	prostate cancer associated transcript 2
RNU6-1049P	-1.53326	0.002341	-3.04323	Down	RNA, U6 small nuclear 1049, pseudogene
HOXA13	-1.52381	0.02589	-2.22786	Down	homeobox A13
RNA5SP193	-1.51621	0.000619	-3.42301	Down	RNA, 5S ribosomal pseudogene 193
KLHL40	-1.51418	0.046354	-1.99216	Down	kelch like family member 40
RNU6-127P	-1.50257	0.01328	-2.47618	Down	RNA, U6 small nuclear 127, pseudogene
RBM17P3	-1.49668	0.000183	-3.741	Down	RNA binding motif protein 17 pseudogene 3
IL33	-1.49464	0.003937	-2.88315	Down	interleukin 33
IRS4	-1.4938	0.009188	-2.605	Down	insulin receptor substrate 4
CXCL13	-1.49229	0.016814	-2.39075	Down	C-X-C motif chemokine ligand 13
DSC1	-1.49117	0.000407	-3.53546	Down	desmocollin 1
DUXAP8	-1.4829	0.007107	-2.69178	Down	double homeobox A pseudogene 8
SAMSN1	-1.4807	0.007589	-2.66981	Down	SAM domain, SH3 domain and nuclear localization signals 1
CBLN2	-1.47795	0.016142	-2.40568	Down	cerebellin 2 precursor
SLC66A1L	-1.47352	0.019969	-2.32692	Down	solute carrier family 66 member 1 like
SYK	-1.46819	0.023485	-2.26545	Down	spleen associated tyrosine kinase
MT1H	-1.46419	0.040831	-2.04524	Down	metallothionein 1H
GCG	-1.45329	0.009435	-2.59587	Down	glucagon

RN7SKP226	-1.44953	0.002418	-3.03347	Down	RN7SK pseudogene 226
BRWD1P3	-1.44724	0.036353	-2.09295	Down	bromodomain and WD repeat domain containing 1 pseudogene 3
RN7SL89P	-1.43382	0.013798	-2.46247	Down	RNA, 7SL, cytoplasmic 89, pseudogene
ADRA2C	-1.42755	0.000422	-3.52594	Down	adrenoceptor alpha 2C
MRLN	-1.42486	0.00222	-3.05907	Down	myoregulin
RPL31P37	-1.42447	0.021322	-2.30223	Down	ribosomal protein L31 pseudogene 37
MIOXP1	-1.40543	0.001741	-3.13112	Down	myo-inositol oxygenasepseudogene 1
H1-1	-1.40448	0.002126	-3.07207	Down	H1.1 linker histone, cluster member
SLC17A7	-1.40245	1.59E-05	-4.31614	Down	solute carrier family 17 member 7
GABRA2	-1.39622	0.006842	-2.70443	Down	gamma-aminobutyric acid type A receptor subunit alpha2
PTPRT	-1.377	0.011468	-2.5281	Down	protein tyrosine phosphatase receptor type T
RNU6-421P	-1.37295	0.009135	-2.60696	Down	RNA, U6 small nuclear 421, pseudogene
ADRB1	-1.37084	0.000332	-3.58885	Down	adrenoceptor beta 1
TFAP2A	-1.36834	0.001639	-3.1488	Down	transcription factor AP-2 alpha
GRIK3	-1.36563	0.005618	-2.7693	Down	glutamate ionotropic receptor kainate type subunit 3
NR2E1	-1.36083	0.024602	-2.2476	Down	nuclear receptor subfamily 2 group E member 1
SMG1P4	-1.36	3.09E-08	-5.53624	Down	SMG1 pseudogene 4
C5orf58	-1.35574	0.002748	-2.99461	Down	chromosome 5 open reading frame 58
ADGRF2	-1.35218	0.002923	-2.97577	Down	adhesion G protein-coupled receptor F2
FAM162B	-1.34867	0.005921	-2.75211	Down	family with sequence similarity 162 member B
MICB	-1.34272	0.002377	-3.03852	Down	MHC class I polypeptide-related sequence B
TAFA4	-1.34191	0.00183	-3.11651	Down	TAFA chemokine like family member 4
CMKLR1	-1.34057	0.023417	-2.26656	Down	chemerin chemokine-like receptor 1
RNY3	-1.32938	0.01055	-2.55727	Down	RNA, Ro60-associated Y3
KCNK17	-1.32639	0.041392	-2.03958	Down	potassium two pore domain channel subfamily K member 17
PCDHGA7	-1.32477	2.20E-05	-4.24329	Down	protocadherin gamma subfamily A, 7
C1GALT1C1L	-1.32374	0.016822	-2.39057	Down	C1GALT1 specific chaperone 1 like
FZD8	-1.31904	0.000349	-3.57575	Down	frizzled class receptor 8
LIPM	-1.3006	0.043771	-2.01628	Down	lipase family member M
RNU6-358P	-1.29702	0.032373	-2.13977	Down	RNA, U6 small nuclear 358, pseudogene
SHOX2	-1.28973	0.000971	-3.29881	Down	short stature homeobox 2
ASS1P14	-1.28427	0.042831	-2.02535	Down	argininosuccinatesynthetase 1 pseudogene 14
SH3TC2	-1.27914	0.000657	-3.40673	Down	SH3 domain and tetratricopeptide repeats 2
ONECUT1	-1.27854	0.001074	-3.27051	Down	one cut homeobox 1
RN7SKP106	-1.27832	0.003537	-2.91676	Down	RN7SK pseudogene 106
ANKRD20A11P	-1.27576	0.016995	-2.38682	Down	ankyrin repeat domain 20 family member A11, pseudogene
RNU6-912P	-1.27173	0.016029	-2.40825	Down	RNA, U6 small nuclear 912, pseudogene
RPL37P14	-1.26962	0.04076	-2.04596	Down	ribosomal protein L37 pseudogene 14
RNY3P9	-1.26613	0.031535	-2.15026	Down	RNY3 pseudogene 9
OR7E136P	-1.26492	0.036356	-2.09293	Down	olfactory receptor family 7 subfamily E member 136 pseudogene
MTCYBP44	-1.25176	0.019371	-2.33831	Down	MT-CYB pseudogene 44
C10orf88B	-1.25025	0.008338	-2.63806	Down	C10orf88B (pseudogene)

DCAF8L1	-1.24249	0.014911	-2.43454	Down	DDB1 and CUL4 associated factor 8 like 1
MUC3A	-1.23766	0.004634	-2.83146	Down	mucin 3A, cell surface associated
RPS19P6	-1.23671	0.046021	-1.9952	Down	ribosomal protein S19 pseudogene 6
SCAT8	-1.22904	0.045237	-2.00245	Down	S-phase cancer associated transcript 8
RN7SKP5	-1.22147	0.032818	-2.13431	Down	RN7SK pseudogene 5
RPSAP3	-1.21815	0.039218	-2.06189	Down	ribosomal protein SA pseudogene 3
GPR101	-1.21811	0.006864	-2.70339	Down	G protein-coupled receptor 101
DEFB1	-1.21803	0.024987	-2.24161	Down	defensin beta 1
MNX1	-1.21578	0.001035	-3.28092	Down	motor neuron and pancreas homeobox 1
LEMD1	-1.19143	4.32E-06	-4.59526	Down	LEM domain containing 1
NPC1L1	-1.18146	0.002089	-3.07729	Down	NPC1 like intracellular cholesterol transporter 1
MEG3	-1.18052	0.002172	-3.06564	Down	maternally expressed 3
LRRC61	-1.17319	0.000646	-3.41164	Down	leucine rich repeat containing 61
RNU6-693P	-1.17272	0.036746	-2.08858	Down	RNA, U6 small nuclear 693, pseudogene
RPS3AP24	-1.16788	0.026107	-2.22462	Down	RPS3A pseudogene 24
SCUBE1	-1.16271	0.001437	-3.18703	Down	signal peptide, CUB domain and EGF like domain containing 1
GDA	-1.15464	0.007776	-2.66163	Down	guanine deaminase
SNX31	-1.14054	0.016325	-2.40157	Down	sorting nexin 31
DPPA5	-1.13939	0.030934	-2.15791	Down	developmental pluripotency associated 5
RNU6-1287P	-1.13125	0.034033	-2.11968	Down	RNA, U6 small nuclear 1287, pseudogene
HMGN1P33	-1.12829	0.021083	-2.3065	Down	high mobility group nucleosome binding domain 1 pseudogene 33
CAT	-1.12539	1.02E-05	-4.41241	Down	catalase
EVX2	-1.12164	0.019495	-2.33594	Down	even-skipped homeobox 2
LAMA3	-1.11716	0.001165	-3.24736	Down	laminin subunit alpha 3
NCR3	-1.11578	0.026318	-2.22149	Down	natural cytotoxicity triggering receptor 3
GPR78	-1.10902	0.036165	-2.09506	Down	G protein-coupled receptor 78
RNA5SP133	-1.10521	0.009302	-2.60075	Down	RNA, 5S ribosomal pseudogene 133
NNAT	-1.10418	0.000198	-3.721	Down	neuronatin
TAS2R41	-1.10196	0.038548	-2.06898	Down	taste 2 receptor member 41
TNP1	-1.09669	0.007137	-2.69037	Down	transition protein 1
POU3F4	-1.09504	0.007683	-2.66571	Down	POU class 3 homeobox 4
TGM3	-1.09442	0.004201	-2.86268	Down	transglutaminase 3
CHAT	-1.08934	0.001793	-3.12257	Down	choline O-acetyltransferase
SPATA31C1	-1.08635	0.034761	-2.11113	Down	SPATA31 subfamily C member 1
COL15A1	-1.08429	0.015955	-2.40995	Down	collagen type XV alpha 1 chain
CDH5	-1.08348	0.001601	-3.15575	Down	cadherin 5
FYB2	-1.08276	6.66E-05	-3.98803	Down	FYN binding protein 2
STXBP6	-1.07804	0.028361	-2.19226	Down	syntaxin binding protein 6
LRRC3B	-1.0724	0.016711	-2.393	Down	leucine rich repeat containing 3B
DSC2	-1.06749	0.001254	-3.22624	Down	desmocollin 2
CCDC63	-1.06707	0.049444	-1.96474	Down	coiled-coil domain containing 63
CYP4F3	-1.06369	0.037955	-2.07535	Down	cytochrome P450 family 4 subfamily F member 3

HDGFL1	-1.06317	0.048943	-1.96909	Down	HDGF like 1
EEF1A1P40	-1.06122	0.022663	-2.27907	Down	eukaryotic translation elongation factor 1 alpha 1 pseudogene 40
DISC1FP1	-1.05779	0.001354	-3.20431	Down	DISC1 fusion partner 1
RPS3AP23	-1.05384	0.043741	-2.01657	Down	RPS3A pseudogene 23
RSPO2	-1.05012	0.012439	-2.49944	Down	R-spondin 2
ODF4	-1.04997	0.029763	-2.17323	Down	outer dense fiber of sperm tails 4
POU5F1B	-1.04962	0.007686	-2.66554	Down	POU class 5 homeobox 1B
MTND5P3	-1.04011	0.026639	-2.21676	Down	MT-ND5 pseudogene 3
BRINP2	-1.03324	0.032564	-2.13741	Down	BMP/retinoic acid inducible neural specific 2
EMBP1	-1.03188	1.44E-08	-5.66911	Down	embiginpseudogene 1
C1orf115	-1.01782	5.73E-05	-4.02347	Down	chromosome 1 open reading frame 115
RNU6-708P	-1.00854	0.030361	-2.16535	Down	RNA, U6 small nuclear 708, pseudogene
C10orf53	-1.0076	0.006317	-2.73084	Down	chromosome 10 open reading frame 53
LMAN1L	-1.00428	0.039301	-2.06102	Down	lectin, mannose binding 1 like
GABRR1	-1.00395	0.03521	-2.10593	Down	gamma-aminobutyric acid type A receptor subunit rho1
KRT18P14	-1.00121	0.012953	-2.48506	Down	keratin 18 pseudogene 14
SCUBE1-AS2	-0.99777	0.042493	-2.02866	Down	SCUBE1 antisense RNA 2
ALS2CL	-0.99293	0.027933	-2.19822	Down	ALS2 C-terminal like
TMPRSS3	-0.9905	0.017481	-2.37644	Down	transmembrane serine protease 3
PCSK9	-0.98736	0.005713	-2.76381	Down	proproteinconvertasesubtilisin/kexin type 9
TPRXL	-0.98405	0.038522	-2.06926	Down	tetrapeptide repeat homeobox like (pseudogene)
RORB	-0.98356	0.002318	-3.04619	Down	RAR related orphan receptor B
RN7SKP276	-0.9825	0.034277	-2.1168	Down	RN7SK pseudogene 276
SCN5A	-0.9768	0.008635	-2.62618	Down	sodium voltage-gated channel alpha subunit 5
BNIP3P22	-0.97232	0.004527	-2.8389	Down	BCL2 interacting protein 3 pseudogene 22
PLEK	-0.96687	0.020126	-2.32399	Down	pleckstrin
C1QL3	-0.95974	0.00541	-2.78158	Down	complement C1q like 3
DGKG	-0.94784	0.01035	-2.56391	Down	diacylglycerol kinase gamma
POU2F3	-0.94315	0.009738	-2.58499	Down	POU class 2 homeobox 3
LY75	-0.94092	0.004117	-2.86902	Down	lymphocyte antigen 75
ANP32BP1	-0.93884	0.02387	-2.25922	Down	acidic nuclear phosphoprotein 32 family member B pseudogene 1
ROR2	-0.93702	0.01125	-2.53485	Down	receptor tyrosine kinase like orphan receptor 2
FOXF1	-0.93408	0.046207	-1.99349	Down	forkhead box F1
JPH1	-0.93321	0.000891	-3.32288	Down	junctophilin 1
SMCO1	-0.93312	0.035184	-2.10624	Down	single-pass membrane protein with coiled-coil domains 1
RPL7P18	-0.93193	0.002384	-3.0377	Down	ribosomal protein L7 pseudogene 18
DSC3	-0.93028	0.0037	-2.90266	Down	desmocollin 3
GADL1	-0.92643	0.043981	-2.01427	Down	glutamate decarboxylase like 1
STRIT1	-0.92474	0.029015	-2.18328	Down	small transmembrane regulator of ion transport 1
SYNDIG1L	-0.92352	0.019969	-2.32692	Down	synapse differentiation inducing 1 like
ANGPT4	-0.92291	0.012855	-2.48776	Down	angiopoietin 4
VN1R2	-0.92084	0.010317	-2.56504	Down	vomeronasal 1 receptor 2

DACT2	-0.91908	0.015192	-2.42777	Down	dishevelled binding antagonist of beta catenin 2
LEMD1-DT	-0.90881	0.000445	-3.51213	Down	LEMD1 divergent transcript
CTSF	-0.90751	0.024104	-2.25547	Down	cathepsin F
CASC8	-0.90377	0.023784	-2.2606	Down	cancer susceptibility 8
LMOD2	-0.90328	0.014026	-2.45659	Down	leiomodin 2
LRRC31	-0.90303	0.029479	-2.17703	Down	leucine rich repeat containing 31
EDA	-0.89979	0.001237	-3.23027	Down	ectodysplasin A
MYOM2	-0.89959	1.31E-05	-4.35866	Down	myomesin 2
MOBP	-0.89751	0.018232	-2.36086	Down	myelin associated oligodendrocyte basic protein
ZNF578	-0.89445	0.001473	-3.17985	Down	zinc finger protein 578
RHBDF1P1	-0.89405	0.006186	-2.73776	Down	RHBDF1 pseudogene 1
PCDHB5	-0.89152	0.000217	-3.69832	Down	protocadherin beta 5
POTEE	-0.8891	0.019012	-2.3453	Down	POTE ankyrin domain family member E
RARRES2P3	-0.87949	0.002596	-3.01192	Down	retinoic acid receptor responder 2 pseudogene 3
RN7SL526P	-0.87881	0.003787	-2.89538	Down	RNA, 7SL, cytoplasmic 526, pseudogene
NTNG2	-0.87623	0.003264	-2.94169	Down	netrin G2
FOXL1	-0.87361	0.025795	-2.22928	Down	forkhead box L1
TRPC2	-0.87314	0.021797	-2.29388	Down	transient receptor potential cation channel subfamily C member 2 (pseudogene)
GRASLND	-0.87003	8.07E-05	-3.94229	Down	glycosaminoglycan regulatory associated long non-coding RNA
WNT10B	-0.8698	0.001336	-3.20819	Down	Wnt family member 10B
RNU7-7P	-0.86771	0.018591	-2.35363	Down	RNA, U7 small nuclear 7 pseudogene
SEPHS1P6	-0.86616	0.048518	-1.97281	Down	selenophosphatesynthetase 1 pseudogene 6
MROH5	-0.86591	0.047302	-1.98358	Down	maestro heat like repeat family member 5 (gene/pseudogene)
AANAT	-0.86575	0.036606	-2.09013	Down	aralkylamine N-acetyltransferase
RNA5SP342	-0.86469	0.025643	-2.23158	Down	RNA, 5S ribosomal pseudogene 342
RN7SL717P	-0.86302	0.02247	-2.28234	Down	RNA, 7SL, cytoplasmic 717, pseudogene
ZNF726	-0.86085	0.004736	-2.82446	Down	zinc finger protein 726
TRIM58	-0.85454	0.037425	-2.08109	Down	tripartite motif containing 58
FRMD7	-0.85437	0.01245	-2.49911	Down	FERM domain containing 7
HMX3	-0.85129	0.040838	-2.04517	Down	H6 family homeobox 3
RPL27P5	-0.84781	0.017459	-2.3769	Down	ribosomal protein L27 pseudogene 5
SRPX	-0.84765	0.00099	-3.2933	Down	sushi repeat containing protein X-linked
GPA33	-0.84679	0.016672	-2.39386	Down	glycoprotein A33
CA4	-0.84652	0.027533	-2.20387	Down	carbonic anhydrase 4
CDH13	-0.84204	0.016709	-2.39305	Down	cadherin 13
PRR5-ARHGAP8	-0.83996	0.041487	-2.03863	Down	PRR5-ARHGAP8 readthrough
KIF26A	-0.83873	0.007932	-2.65495	Down	kinesin family member 26A
NEUROG2	-0.83864	0.019188	-2.34185	Down	neurogenin 2
SNTG2	-0.8364	0.036064	-2.0962	Down	syntrophin gamma 2
DSCAM	-0.82994	0.023129	-2.2713	Down	DS cell adhesion molecule
PCP4	-0.82956	0.016492	-2.39785	Down	Purkinje cell protein 4
NPIPB8	-0.82757	0.008158	-2.64546	Down	nuclear pore complex interacting protein family member B8

ITIH1	-0.82093	0.027546	-2.20369	Down	inter-alpha-trypsin inhibitor heavy chain 1
KCNQ5	-0.81899	0.010055	-2.57393	Down	potassium voltage-gated channel subfamily Q member 5
RPL26P26	-0.81781	0.001341	-3.207	Down	ribosomal protein L26 pseudogene 26
PCAT1	-0.81754	0.041786	-2.03564	Down	prostate cancer associated transcript 1
RAD51AP2	-0.81667	0.012036	-2.51109	Down	RAD51 associated protein 2
GRIP2	-0.81603	0.002305	-3.04779	Down	glutamate receptor interacting protein 2
PRB4	-0.81483	0.001474	-3.17968	Down	proline rich protein BstNI subfamily 4
PPFIBP2	-0.81282	0.005479	-2.77744	Down	PPFIA binding protein 2
FAM153A	-0.81214	0.049418	-1.96497	Down	family with sequence similarity 153 member A
SEPTIN12	-0.80746	0.021089	-2.30638	Down	septin 12
IFI30	-0.80607	0.047809	-1.97906	Down	IFI30 lysosomalthiolreductase
RNU1-77P	-0.80293	0.01294	-2.4854	Down	RNA, U1 small nuclear 77, pseudogene
ANKRD7	-0.80271	0.040004	-2.05371	Down	ankyrin repeat domain 7
KHDRBS2	-0.80042	0.011087	-2.53994	Down	KH RNA binding domain containing, signal transduction associated 2
ALDH3A1	-0.80006	0.045815	-1.9971	Down	aldehyde dehydrogenase 3 family member A1
KCNJ1	-0.79497	0.038322	-2.07139	Down	potassium inwardly rectifying channel subfamily J member 1
RNU6ATAC23P	-0.79421	0.005014	-2.8061	Down	RNA, U6atac small nuclear 23, pseudogene
ANG	-0.79411	0.009912	-2.5789	Down	angiogenin
CTTNBP2	-0.79285	0.004113	-2.86939	Down	cortactin binding protein 2
SLC28A2	-0.78997	0.002288	-3.05001	Down	solute carrier family 28 member 2
ZNF135	-0.78884	0.000104	-3.88115	Down	zinc finger protein 135
PCDHGA6	-0.78671	0.007156	-2.68949	Down	protocadherin gamma subfamily A, 6
RNU6-1115P	-0.78575	0.045881	-1.99648	Down	RNA, U6 small nuclear 1115, pseudogene
TMEM100	-0.7833	0.00473	-2.82487	Down	transmembrane protein 100
RASGEF1B	-0.78268	0.022162	-2.28758	Down	RasGEF domain family member 1B
HJV	-0.78121	0.005745	-2.76197	Down	hemojuvelin BMP co-receptor
HPD	-0.78117	0.034279	-2.11678	Down	4-hydroxyphenylpyruvate dioxygenase
GUCY1B2	-0.77789	0.046244	-1.99316	Down	guanylatecyclase 1 soluble subunit beta 2 (pseudogene)
PCDHB18P	-0.7771	6.30E-05	-4.00126	Down	protocadherin beta 18 pseudogene
GDF15	-0.776	0.021902	-2.29206	Down	growth differentiation factor 15
KLHL31	-0.77152	0.025835	-2.22869	Down	kelch like family member 31
RAD21L1	-0.77093	0.009461	-2.59493	Down	RAD21 cohesin complex component like 1
CAV3	-0.77072	0.001194	-3.24021	Down	caveolin 3
AGBL4	-0.77054	0.0057	-2.76457	Down	AGBL carboxypeptidase 4
THEMIS	-0.76962	0.017239	-2.38157	Down	thymocyte selection associated
WDR87	-0.76812	0.019958	-2.32714	Down	WD repeat domain 87
TPSG1	-0.76649	0.003338	-2.93476	Down	tryptase gamma 1
CDON	-0.76142	0.000325	-3.5942	Down	cell adhesion associated, oncogene regulated
LRIT2	-0.75835	0.026021	-2.2259	Down	leucine rich repeat, Ig-like and transmembrane domains 2
KLHDC7B	-0.75671	0.028737	-2.18708	Down	kelch domain containing 7B
DLGAP1-AS3	-0.75372	0.03746	-2.08071	Down	DLGAP1 antisense RNA 3
GTF2IP14	-0.75288	4.11E-10	-6.24997	Down	general transcription factor IIipseudogene 14

OTOF	-0.75205	0.044326	-2.01099	Down	otoferlin
RN7SL581P	-0.75125	0.039671	-2.05715	Down	RNA, 7SL, cytoplasmic 581, pseudogene
OPRD1	-0.7493	0.045654	-1.99857	Down	opioid receptor delta 1
LGI1	-0.74369	0.037802	-2.077	Down	leucine rich glioma inactivated 1
CACNA2D4	-0.73902	0.000415	-3.53044	Down	calcium voltage-gated channel auxiliary subunit alpha2delta 4
RN7SKP29	-0.73893	0.015062	-2.43089	Down	RN7SK pseudogene 29
RPS10P9	-0.73685	0.026446	-2.21959	Down	ribosomal protein S10 pseudogene 9
ZNF300	-0.73621	0.003258	-2.94226	Down	zinc finger protein 300
LY6E	-0.736	0.048421	-1.97366	Down	lymphocyte antigen 6 family member E
PGAM1P5	-0.73363	0.007632	-2.66792	Down	phosphoglyceratemutase 1 pseudogene 5
RAPGEF5	-0.73338	0.005008	-2.8065	Down	Rap guanine nucleotide exchange factor 5
PLAAT1	-0.73279	0.011737	-2.51995	Down	phospholipase A and acyltransferase 1
TAS2R43	-0.73149	0.009149	-2.60643	Down	taste 2 receptor member 43
GCM1	-0.73145	0.027506	-2.20426	Down	glial cells missing transcription factor 1
PKD1P2	-0.7314	0.032521	-2.13794	Down	polycystin 1, transient receptor potential channel interacting pseudogene 2
PCDHGA10	-0.73081	0.014395	-2.44726	Down	protocadherin gamma subfamily A, 10
ISLR2	-0.73079	0.048508	-1.97289	Down	immunoglobulin superfamily containing leucine rich repeat 2
MSL3P1	-0.72722	0.043168	-2.02208	Down	MSL complex subunit 3 pseudogene 1
UNC5A	-0.72529	0.036432	-2.09207	Down	unc-5 netrin receptor A
RN7SL748P	-0.7251	0.012903	-2.48644	Down	RNA, 7SL, cytoplasmic 748, pseudogene
SLC1A2	-0.72429	0.016932	-2.38817	Down	solute carrier family 1 member 2
ATP13A5	-0.71815	0.02272	-2.27811	Down	ATPase 13A5
RPL23P8	-0.71591	0.019376	-2.33822	Down	ribosomal protein L23 pseudogene 8
RYR1	-0.71439	0.035406	-2.10369	Down	ryanodine receptor 1
ALKBH3	-0.71346	1.12E-12	-7.11527	Down	alkB homolog 3, alpha-ketoglutarate dependent dioxygenase
RN7SL104P	-0.71213	0.008015	-2.65145	Down	RNA, 7SL, cytoplasmic 104, pseudogene
IRGM	-0.71191	0.002662	-3.00433	Down	immunity related GTPase M
LEXM	-0.71152	0.015554	-2.41922	Down	lymphocyte expansion molecule
LRRIQ4	-0.71022	0.025189	-2.23848	Down	leucine rich repeats and IQ motif containing 4
TRPC3	-0.70533	0.005912	-2.7526	Down	transient receptor potential cation channel subfamily C member 3
RNU7-124P	-0.70469	0.001562	-3.16297	Down	RNA, U7 small nuclear 124 pseudogene
IP6K3	-0.69959	0.045926	-1.99607	Down	inositol hexakisphosphate kinase 3
PDE2A	-0.69834	0.008263	-2.64113	Down	phosphodiesterase 2A
RNA5SP109	-0.6977	0.043888	-2.01516	Down	RNA, 5S ribosomal pseudogene 109
ARMC8P1	-0.69731	0.037812	-2.07689	Down	armadillo repeat containing 8 pseudogene 1
TRMT9B	-0.69629	0.014231	-2.45138	Down	tRNAmethyltransferase 9B (putative)
RGS9BP	-0.69157	0.046627	-1.98967	Down	regulator of G protein signaling 9 binding protein
SEC14L1P1	-0.68911	1.19E-08	-5.70135	Down	SEC14 like 1 pseudogene 1
GOLGA6L3	-0.68709	0.014706	-2.43953	Down	golgin A6 family like 3
RPL27P4	-0.68327	0.036206	-2.09461	Down	ribosomal protein L27 pseudogene 4
SLCO5A1	-0.68297	0.004154	-2.86624	Down	solute carrier organic anion transporter family member 5A1
ST6GAL1	-0.68288	0.00085	-3.33613	Down	ST6 beta-galactoside alpha-2,6-sialyltransferase 1

PDE11A	-0.68286	0.015896	-2.41129	Down	phosphodiesterase 11A
ENPP7	-0.68156	0.008709	-2.62325	Down	ectonucleotidepyrophosphatase/phosphodiesterase 7
RPS10P30	-0.68109	0.008674	-2.62464	Down	ribosomal protein S10 pseudogene 30
RNA5SP152	-0.67969	0.011896	-2.51522	Down	RNA, 5S ribosomal pseudogene 152
SLC14A1	-0.67816	0.031216	-2.15431	Down	solute carrier family 14 member 1 (Kidd blood group)
EMX1	-0.67802	0.026882	-2.21323	Down	empty spiracles homeobox 1
RNU2-13P	-0.67692	0.028218	-2.19425	Down	RNA, U2 small nuclear 13, pseudogene
RAP1GAP2	-0.6766	0.013764	-2.46337	Down	RAP1 GTPase activating protein 2
CCDC152	-0.67595	0.026416	-2.22005	Down	coiled-coil domain containing 152
RN7SL546P	-0.6759	0.038307	-2.07155	Down	RNA, 7SL, cytoplasmic 546, pseudogene
LHX4	-0.67483	0.019933	-2.32761	Down	LIM homeobox 4
GOLGA6L7	-0.67087	0.030739	-2.16043	Down	golgin A6 family like 7
C1orf167	-0.67085	0.032358	-2.13996	Down	chromosome 1 open reading frame 167
RNU6-1324P	-0.66885	0.04257	-2.0279	Down	RNA, U6 small nuclear 1324, pseudogene
NAPSB	-0.66521	0.005426	-2.78059	Down	napsin B aspartic peptidase, pseudogene
AKR1D1	-0.66508	0.030302	-2.16612	Down	aldo-ketoreductase family 1 member D1
ACTN3	-0.66479	0.027553	-2.2036	Down	actinin alpha 3
C15orf32	-0.66358	0.001352	-3.20481	Down	chromosome 15 putative open reading frame 32
SSUH2	-0.66238	0.018543	-2.35458	Down	ssu-2 homolog
TTC34	-0.6612	0.049153	-1.96726	Down	tetratricopeptide repeat domain 34
SCML4	-0.66058	0.044237	-2.01183	Down	Scmpolycomb group protein like 4
RPS3P1	-0.65871	0.00622	-2.73593	Down	ribosomal protein S3 pseudogene 1
FAM107A	-0.65748	0.041982	-2.0337	Down	family with sequence similarity 107 member A
TMEM105	-0.65676	0.047109	-1.98532	Down	TMEM105 long non-coding RNA
TCEAL7	-0.65506	0.045049	-2.0042	Down	transcription elongation factor A like 7
TSBP1	-0.65421	0.036985	-2.08592	Down	testis expressed basic protein 1
LAMP5	-0.65331	0.033244	-2.12912	Down	lysosomal associated membrane protein family member 5
HAPLN3	-0.65097	0.014014	-2.45692	Down	hyaluronan and proteoglycan link protein 3
KLHL14	-0.64899	0.024942	-2.24229	Down	kelch like family member 14
RAG2	-0.6487	0.000937	-3.30886	Down	recombination activating 2
ZSCAN1	-0.64859	0.005678	-2.76583	Down	zinc finger and SCAN domain containing 1
TMSB4XP3	-0.64037	0.043105	-2.02269	Down	TMSB4X pseudogene 3
ADH1B	-0.63971	0.041479	-2.03871	Down	alcohol dehydrogenase 1B (class I), beta polypeptide
OR9A2	-0.63879	0.018969	-2.34614	Down	olfactory receptor family 9 subfamily A member 2
SMTNL2	-0.63759	0.041003	-2.0435	Down	smoothelin like 2
TMSB15A	-0.63642	0.032516	-2.13801	Down	thymosin beta 15A
SEMA3F	-0.62684	0.007664	-2.66651	Down	semaphorin 3F
FUT9	-0.62428	0.034386	-2.11551	Down	fucosyltransferase 9
RNU6-874P	-0.62413	0.00378	-2.89598	Down	RNA, U6 small nuclear 874, pseudogene
DPY19L2P1	-0.62395	0.007057	-2.69416	Down	DPY19L2 pseudogene 1
PRXL2AP1	-0.62366	0.014532	-2.44383	Down	peroxiredoxin like 2A pseudogene 1
ANKRD44-IT1	-0.62318	0.024519	-2.2489	Down	ANKRD44 intronic transcript 1
RNU6-766P	-0.623	0.012621	-2.4943	Down	RNA, U6 small nuclear 766, pseudogene

TREML1	-0.62108	0.032561	-2.13745	Down	triggering receptor expressed on myeloid cells like 1
TXLNB	-0.62074	0.020918	-2.30947	Down	taxilin beta
RN7SL202P	-0.62025	0.022812	-2.27657	Down	RNA, 7SL, cytoplasmic 202, pseudogene
RNU4-51P	-0.6138	0.02023	-2.32205	Down	RNA, U4 small nuclear 51, pseudogene
EEF1A1P24	-0.61326	0.047621	-1.98074	Down	eukaryotic translation elongation factor 1 alpha 1 pseudogene 24
TP53I11	-0.61224	0.004167	-2.86522	Down	tumor protein p53 inducible protein 11
EDARADD	-0.61156	0.031414	-2.15178	Down	EDAR associated death domain
SULT1C3	-0.60959	0.03322	-2.12941	Down	sulfotransferase family 1C member 3
CFAP251	-0.60771	0.015022	-2.43184	Down	cilia and flagella associated protein 251
PCDHA6	-0.60654	0.00176	-3.12797	Down	protocadherin alpha 6
MROH3P	-0.60647	0.038209	-2.07261	Down	maestro heat like repeat family member 3, pseudogene
C6orf132	-0.60507	0.025681	-2.231	Down	chromosome 6 open reading frame 132
CLVS2	-0.60398	0.018641	-2.35263	Down	clavesin 2
ERICH2	-0.60086	0.042608	-2.02753	Down	glutamate rich 2
CUX2	-0.60049	0.029097	-2.18217	Down	cut like homeobox 2
TEX15	-0.59947	0.027521	-2.20404	Down	testis expressed 15, meiosis and synapsis associated
RNU6-886P	-0.59911	0.023786	-2.26057	Down	RNA, U6 small nuclear 886, pseudogene
SRRM1P1	-0.59868	0.017647	-2.37295	Down	serine/arginine repetitive matrix 1 pseudogene 1
CDK18	-0.59848	0.020044	-2.32552	Down	cyclin dependent kinase 18
KCNH7	-0.59766	0.03817	-2.07302	Down	potassium voltage-gated channel subfamily H member 7
RAI2	-0.59669	0.026112	-2.22454	Down	retinoic acid induced 2
CDHR1	-0.59623	0.024512	-2.24902	Down	cadherin related family member 1
VN1R5	-0.59545	0.027954	-2.19793	Down	vomeronasal 1 receptor 5 (gene/pseudogene)
ROBO4	-0.59085	0.026777	-2.21476	Down	roundabout guidance receptor 4
PKIB	-0.58954	0.001746	-3.13035	Down	cAMP-dependent protein kinase inhibitor beta
RN7SL612P	-0.58842	0.026344	-2.2211	Down	RNA, 7SL, cytoplasmic 612, pseudogene
RNU7-119P	-0.58831	0.011385	-2.53065	Down	RNA, U7 small nuclear 119 pseudogene
POU6F2	-0.58541	0.034262	-2.11698	Down	POU class 6 homeobox 2
RPL39L	-0.58453	0.042307	-2.03049	Down	ribosomal protein L39 like
SLC2A4	-0.57929	0.039115	-2.06297	Down	solute carrier family 2 member 4
RNU5B-1	-0.57784	0.023129	-2.2713	Down	RNA, U5B small nuclear 1
KLHL34	-0.57588	0.019021	-2.34511	Down	kelch like family member 34
TMEM200A	-0.57538	0.022424	-2.28311	Down	transmembrane protein 200A
SPTSSB	-0.57518	0.038215	-2.07254	Down	serine palmitoyltransferase small subunit B
DRD2	-0.57326	0.049361	-1.96546	Down	dopamine receptor D2
GP6	-0.57252	0.023024	-2.27304	Down	glycoprotein VI platelet
GPR143	-0.56822	0.009054	-2.60999	Down	G protein-coupled receptor 143
MTCO1P42	-0.56711	0.049435	-1.96482	Down	MT-CO1 pseudogene 42
KRT18P55	-0.56685	0.041601	-2.03749	Down	keratin 18 pseudogene 55
RAB33A	-0.56676	0.011055	-2.54096	Down	RAB33A, member RAS oncogene family
FBN3	-0.56641	0.025282	-2.23707	Down	fibrillin 3
ZNF732	-0.56276	0.037319	-2.08226	Down	zinc finger protein 732

RASGRP1	-0.55299	0.001768	-3.12673	Down	RAS guanyl releasing protein 1
GALNT12	-0.55288	0.032481	-2.13845	Down	polypeptide N-acetylgalactosaminyltransferase 12
RNU6-1322P	-0.55059	0.02326	-2.26914	Down	RNA, U6 small nuclear 1322, pseudogene
RN7SKP57	-0.55	0.006178	-2.73816	Down	RN7SK pseudogene 57
TRPM5	-0.54916	0.00255	-3.01738	Down	transient receptor potential cation channel subfamily M member 5
SASH3	-0.54756	0.033581	-2.12506	Down	SAM and SH3 domain containing 3
SLC9A2	-0.54227	0.016119	-2.40622	Down	solute carrier family 9 member A2
PRB3	-0.54066	0.036584	-2.09037	Down	proline rich protein BstNI subfamily 3
ABI3BP	-0.53992	0.015516	-2.4201	Down	ABI family member 3 binding protein
RN7SL655P	-0.53949	0.015039	-2.43143	Down	RNA, 7SL, cytoplasmic 655, pseudogene
SERF1A	-0.53521	2.58E-05	-4.20774	Down	small EDRK-rich factor 1A
SNORA80C	-0.53346	0.044609	-2.00832	Down	small nucleolar RNA, H/ACA box 80C
RNVU1-14	-0.53303	0.039922	-2.05455	Down	RNA, variant U1 small nuclear 14
KCNK2	-0.52856	0.049137	-1.9674	Down	potassium two pore domain channel subfamily K member 2
TAL2	-0.52773	0.024421	-2.25044	Down	TAL bHLH transcription factor 2
RN7SL144P	-0.52721	0.00837	-2.63676	Down	RNA, 7SL, cytoplasmic 144, pseudogene
RNU6-789P	-0.52638	0.004501	-2.84075	Down	RNA, U6 small nuclear 789, pseudogene
ALG1L11P	-0.52635	0.029628	-2.17502	Down	ALG1 like 11, pseudogene
AIMP1P1	-0.52507	0.027398	-2.2058	Down	aminoacyltRNAsynthetase complex interacting multifunctional protein 1 pseudogene 1
BTK	-0.52338	0.045773	-1.99748	Down	Bruton tyrosine kinase
STAC2	-0.52123	0.040988	-2.04365	Down	SH3 and cysteine rich domain 2
APOBEC3G	-0.5198	0.04713	-1.98513	Down	apolipoprotein B mRNA editing enzyme catalytic subunit 3G
IFTAP	-0.51952	0.010193	-2.56921	Down	intraflagellar transport associated protein
MGAM	-0.51866	0.034483	-2.11438	Down	maltase-glucoamylase
GUSBP9	-0.51811	0.000604	-3.42992	Down	GUSB pseudogene 9
BMP8B	-0.51759	0.000204	-3.71363	Down	bone morphogenetic protein 8b
RNU4-87P	-0.51628	0.00904	-2.61054	Down	RNA, U4 small nuclear 87, pseudogene
ZP1	-0.51085	0.020208	-2.32247	Down	zonapellucida glycoprotein 1
MAPK13	-0.51068	0.019353	-2.33866	Down	mitogen-activated protein kinase 13

Supplementary Table 2. The enriched gene ontology terms of the up and down regulated differentially expressed genes.

GO ID	CATEGORY	GO Name	adjusted_p_value	negative_log10_of_adjusted_p_value	Gene Count	Gene
			Up regulated genes			
GO:0032501	BP	multicellular organismal process	3.51E-13	12.45473123	213	HOXC11,HOXD11,HOXD10,CCL11,HOXC10,SIX1,MYCT1,XCL1,HLA-DMB,VAX1,VIP,XCL2,MALL,HOXC5,HRH1,GATA6,FRZB,CALCRL,CPLX4,CD40,CACNG3,WT1,PCDHGA3,TFAP2B,HFE,HOXB7,PRSS56,NKX2-5,IGFBP7,IFNA8,HOXC8,OCIAD2,NPY2R,HOXC6,HLA-F,SPOCD1,TAC1,SP100,CCL2,AQP5,HOXC4,TMOD1,WNT2B,TGFBI,IL1RL2,HLA-DMA,GRHL3,HLA-DRA,COL1A2,CXCL6,PRDM12,RUNX1,TFF3,HES3,PPY,IRX4,PTHLH,PI16,ASPA,NOS1,DCSTAMP,XDH,TBX15,DKK2,IL18R1,LBX1,ADAM12,EDN3,PCDHGC3,NPPC,COL1A1,IL1R1,HOXD9,ABCG2,GJC3,OTOGL,SIX2,LAMA2,CSRP1,IL13RA2,GPR176,STING1,ITGA1,TACSTD2,MR1,NPY5R,CARD16,NINJ2,ACE,TBX1,GSDMD,KCNN4,NMI,HTR1B,ACTG2,PRKCB,ASS1,MLIP,DNAAF1,CTSC,ECEL1,DLX6,KCNE1,COL8A2,MARVELD2,NPR3,DHX58,XKR8,ZP3,IFITM1,IL12RB1,ITGA11,GBP1,COL12A1,AZGP1,CYP1B1,ASIC2,PRRX1,WNT7B,PKHD1L1,CD34,HLA-DPA1,A2M,MEOX2,ST14,CDKN2A,IGFN1,LGALS1,MAL,ESPN,PLXNA4,EPHA6,SPINT1,CDH9,PCDHGB6,SERPINE1,RGCC,HTR7,CD44,FABP4,ITGB3,COL9A2,ALOX5AP,DAND5,GDF6,SFRP4,PLAAT4,FZD6,POU4F1,HLA-DOA,ISM1,GTF2A1L,IL4R,RUNX2,OR51B5,GNGT1,CASP1,IL31RA,CCR4,TACR3,CD96,MYD88,MYOF,TGM2,LHCGR,CBR3,MYL9,TMEM106A,DRD3,CYBA,STAT6,TLL2,OCLN,BNC2,RCN3,UNC5C,FOXC1,SCG2,MYC,HES2,FN1,TLR6,NPY1R,LAMC3,OSR2,ANXA1,TENT5C,RAMP1,ZMYND15,DPF3,CAV1,EFEMP1,RGS4,SPOCK2,TPM2,ALPK2,CCDC103,TBXA2R,TNFAIP2,TMIGD2,GDF5,KRT8,DOCK5,COBL,FOXH1,ERRFI1,CHST8,TNFSF4,WNT9B,LOX,TLE6,SMOC2,SPHK1
GO:0032502	BP	developmental process	4.25E-11	10.37134879	182	HOXC11,HOXD11,HOXD10,CCL11,HOXC10,SIX1,VAX1,MALL,HOXC5,TGM5,GATA6,FRZB,CPQ,CALCRL,CD40,WT1,PCDHGA3,TFAP2B,HOXB7,PRSS56,MEDAG,NKX2-5,IGFBP7,IFNA8,HOXC8,NPY2R,HOXC6,SPOCD1,SP100,CCL2,AQP5,POSTN,HOXC4,TMOD1,RHOD,WNT2B,TGFBI,IL1RL2,GRHL3,HLA-DRA,COL1A2,PRDM12,RUNX1,HES3,IRX4,PTHLH,PI16,ASPA,NOS1,CCNO,DCSTAMP,XDH,TBX15,D

						KK2,IL18R1,LBX1,ADAM12,EDN3,PCDHGC3,NPPC,COL1A1,HOXD9,SLFN5,GJC3,SIX2,LAMA2,CSRP1,ITGA1,TACSTD2,MR1,NPY5R,EGFLAM,ADIRF,NINJ2,ACE,TBX1,RAB38,ACTG2,PRKCB,ASS1,DNAAF1,CTSC,FLNC,DLX6,KCNE1,COL8A2,MARVELD2,NPR3,XKR8,ZP3,IFITM1,IL12RB1,ITGA11,COL12A1,CYP1B1,ASIC2,PRRX1,WNT7B,CD34,A2M,MEOX2,ST14,CDKN2A,IGFN1,LGALS1,MAL,PLXNA4,EPHA6,SPINT1,CDH9,PCDHGB6,SERPINE1,RGCC,CD44,FABP4,ITGB3,COL9A2,DAND5,GDF6,SFRP4,PLAAT4,FZD6,POU4F1,HLA-DOA,ISM1,IL4R,RUNX2,GNGT1,IL31RA,CCR4,TACR3,MYD88,MYOF,TGM2,LHCGR,NR0B2,MYL9,DRD3,STAT6,CCDC3,TLL2,BNC2,RCN3,UNC5C,FOXC1,SCG2,MYC,HES2,FN1,NPY1R,LAMC3,OSR2,ANXA1,TENT5C,RAMP1,FOSL2,ZMYND15,DPF3,CAV1,EFEMP1,RGS4,SPOCK2,ALPK2,CCDC103,TBXA2R,TNFAIP2,TMIGD2,GDF5,KRT8,DOCK5,COBL,FOXH1,NQO1,ERRFI1,CHST8,TNFSF4,WNT9B,LOX,TLE6,SMOC2,SPARCL1,SPHK1
GO:0071944	CC	cell periphery	4.88E-14	13.31116773	189	SLC15A1,FOLH1,CYP2C8,HLA-DMB,SLCO6A1,MALL,TGM5,HRH1,CALCRL,CPLX4,CD40,CACNG3,NT5E,SLC16A6,COL21A1,CD163,PCDHGA3,FIBCD1,SLC5A12,DIRAS3,HFE,IGFBP7,NPY2R,OSMR,HLA-F,HTR1F,AQP5,POSTN,TMOD1,RHOD,WNT2B,TGFBI,IL1RL2,HLA-DMA,HLA-DRA,COL1A2,C6ORF15,NOS1,GPR132,DCSTAMP,IL18R1,ADAM12,PCDHGC3,CASP4,COL1A1,IL1R1,ABCG2,SELL,GJC3,OTOGL,LAMA2,IL13RA2,RASL12,GPR176,STING1,TMPRSS2,IFITM2,ITGA1,TACSTD2,MR1,NPY5R,EGFLAM,SYNPO,NINJ2,ACE,GSDMD,KCNN4,HTR1B,RAB38,ACTG2,PRKCB,ECM2,MLIP,DNAAF1,CTSC,FLNC,CACNA1A,ECEL1,KCNE1,COL8A2,MARVELD2,NPR3,XKR8,ZP3,IFITM1,IL12RB1,ITGA11,GBP1,COL12A1,AZGP1,CAVIN2,ASIC2,WNT7B,PKHD1L1,COL14A1,RPH3A,CD34,HLA-DPA1,A2M,ST14,ADGRL4,CXCL16,LGALS1,MAL,OLFML2B,PLXNA4,MRGPRE,NIBAN1,EPHA6,SPINT1,CDH9,PCDHGB6,CDCP1,SERPINE1,HTR7,CD44,HSPA1L,SYTL5,TRIM4,ITGB3,COL9A2,FZD6,HLA-DOA,CASS4,IL4R,OR51B5,GNGT1,CASP1,IL31RA,SLC27A6,CCR4,GLIPR1,TACR3,CD96,MYD88,MYOF,TGM2,CPNE8,LHCGR,KCNS1,ANO3,MYL9,TMEM106A,DRD3,ANO9,IFITM3,CYBA,APOBR,GEM,CALY,COL25A1,NALCN,OCLN,UNC5C,FN1,TLR6,RASSF3,NPY1R,LAMC3,ANXA1,RAMP1,SLC9A7,C

						AV1,EFEMP1,RGS4,SPOCK2,MMP23B,ALPK2,COL24A1,TBXA2R,TNFAIP2,TMIGD2,GDF5,KRT8,DOCK5,COBL,S100A16,ERRFI1,COL6A2,SLC13A5,TNFSF4,LOX,TLE6,LPCAT2,SMOC2,FCGR1A,LTBP2,SPARCL1,SPHK1
GO:0110165	CC	cellular anatomical entity	0.011787503	1.928578184	392	HOXC11,HOXD11,RN7SL471P,SLC15A1,HOXD10,CCL11,SLFN11,FOLH1,HOXC10,SIX1,MYCT1,CYP2C8,XCL1,HLA-DMB,VAX1,SLCO6A1,VIP,XCL2,MALL,HOXC5,TGM5,HRH1,GATA6,TMCO4,FRZB,CPQ,CALCRL,CPLX4,GBP2,CD40,CACNG3,NT5E,ZFP92,SLC16A6,PLAAT5,COL21A1,CD163,WT1,PCDHGA3,TFAP2B,ACSM6,FIBCD1,SLC5A12,DIRAS3,HFE,HOXB7,PRSS56,MEDAG,NKX2-5,IGFBP7,IFNA8,HOXC8,OCIAD2,NPY2R,OSMR,FIBIN,HOXC6,HLA-F,SPOCD1,TAC1,PDE1C,RN7SL547P,HTR1F,SP100,HBE1,AGBL2,CCL2,AQP5,DMKN,POSTN,HOXC4,TMOD1,RHOD,LRIT1,FNDC7,WNT2B,TGFBI,IL1RL2,HLA-DMA,GRHL3,HLA-DRA,COL1A2,C6ORF15,APOL3,CXCL6,PRDM12,SCGN,RUNX1,CHI3L2,SLFN12L,RNF212,TFF3,HES3,PPY,TMPRSS15,IRX4,PTHLH,PI16,RNA5SP328,ASPA,NOS1,GPR132,CCNO,DCSTAMP,SNORA15B-1,XDH,TBX15,DKK2,IL18R1,LRRC37A2,LBX1,ADAM12,EDN3,PCDHGC3,CASP4,NPPC,NEK11,COL1A1,IL1R1,HOXD9,ABCG2,SELL,ZC3HAV1L,SLFN5,GJC3,OTOGL,SIX2,LAMA2,CSRP1,IL13RA2,RASL12,GPR176,STING1,TMPRSS2,IFITM2,ITGA1,TACSTD2,MR1,NPY5R,EGFLAM,SYNPO,ADIRF,XAF1,NINJ2,ACE,TBX1,CD164L2,GSDMD,KCNN4,NMI,HTR1B,CTSO,RAB38,APOL1,ACTG2,PRKCB,ASS1,ECM2,MLIP,DNAAF1,CTSC,FLNC,CACNA1A,ECEL1,QPCT,DLX6,NGB,KCNE1,COL8A2,MARVELD2,MARCHF11,NPR3,DHX58,XKR8,ZP3,IFITM1,IL12RB1,ITGA11,GBP1,COL12A1,AZGP1,CYP1B1,CAVIN2,ASIC2,PRRX1,WNT7B,PKHD1L1,COL14A1,RPH3A,CD34,HLA-DPA1,A2M,KIF25,RNU6-959P,MEOX2,ST14,ZNF311,GBP3,CDKN2A,ADGRL4,RNU6-726P,PHF11,CFI,IGFN1,CXCL16,LGALS1,MAL,ESPN,OLFML2B,SNORD93,PLXNA4,MRGPRE,NIBAN1,EPHA6,ARHGAP29,NPIPA7,SPINT1,MAP1LC3C,CDH9,PCDHGB6,PSMB9,C1R,MSLNL,CDCP1,SERPINE1,GLMP,RGCC,RNU6-1029P,HTR7,CD44,ACOT4,TSKS,FABP4,ZNF804B,HSPA1L,SYTL5,TRIM4,ITGB3,ACSS3,COL9A2,ALOX5AP,DAND5,GDF6,ZNF630,SFRP4,PLAAT4,PRDM7,FZD6,POU4F1,

						FBXO43,HLA-DOA,SKOR1,ISM1,GRAMD2B,FAM180A,RGS22,CASS4,GTF2A1L,ME1,IL4R,RUNX2,OR51B5,PLAAT2,GNGT1,CASP1,IL31RA,ZNF441,SLC27A6,GOLGA8J,CCR4,SH3BP5,GLIPR1,CPA4,TACR3,CD96,MYD88,MYOF,TGM2,CPNE8,LHCGR,KCNS1,CBR3,NR0B2,ANO3,MYL9,TMEM106A,DRD3,ANO9,IFITM3,EEF1G,FAM83G,RNVU1-24,CYBA,APOBR,GPX7,STAT6,MAFA,APOL6,RCAN2,SP140L,GEM,CCDC3,CALY,STON1-GTF2A1L,TLL2,COL25A1,NALCN,OCLN,IGFL3,BNC2,RCN3,SMIM10,FILIP1L,UNC5C,FOXC1,SCG2,MYC,HES2,RN7SL368P,MRI1,TUBA4A,PPP1R3B,GBGT1,NWD1,FN1,WFDC13,ABCC12,TLR6,RASSF3,NPY1R,COPZ2,LAMC3,OSR2,ANXA1,LRRN4CL,TENT5C,ATL3,RAMP1,FOSL2,VRK2,SLC9A7,ECHDC3,SPNS3,SLC46A3,ZMYND15,DDX60L,DPF3,NPIPB2,CAV1,EFEMP1,RGS4,SPOCK2,TPM2,MMP23B,ALPK2,COL24A1,CCDC103,TBXA2R,GMPR,TNFAIP2,TMIGD2,GDF5,KRT8,GPD2,DOCK5,NFE2,MAP1LC3A,COBL,FOXH1,TMEM255A,S100A16,NQO1,ERRFI1,COL6A2,SLC38A8,CHST8,SLC13A5,TNFSF4,TMEM35B,SHISAL2A,WNT9B,LOX,SSH3,TLE6,LPCAT2,SMOC2,FCGR1A,LTBP2,SPARCL1,SPHK1,PTGES3L-AARSD1,S100A5
GO:0001228	MF	DNA-binding transcription activator activity, RNA polymerase II-specific	0.003832064	2.416567232	23	HOXC11,HOXD10,HOXC10,SIX1,WT1,TFAP2B,HOXB7,NKX2-5,HOXC4,GRHL3,RUNX1,SIX2,PRRX1,MEOX2,POU4F1,RUNX2,STAT6,MAFA,FOXC1,MYC,OSR2,FOSL2,FOXH1
GO:0005102	MF	signaling receptor binding	0.006470983	2.18902973	51	CCL11,XCL1,VIP,XCL2,CACNG3,FIBCD1,HFE,IFNA8,OSMR,TAC1,CCL2,WNT2B,TGFBI,HLA-DRA,CXCL6,PPY,PTHLH,DKK2,EDN3,NPPC,IL1R1,LAMA2,ITGA1,MR1,ACE,ECM2,ZP3,IL12RB1,ITGA11,WNT7B,A2M,CXCL16,SERPINE1,FABP4,SYTL5,ITGB3,DAND5,GDF6,MYD88,NR0B2,DRD3,IGFL3,SCG2,FN1,TLR6,ANXA1,CAV1,EFEMP1,GDF5,TNFSF4,WNT9B
Down regulated genes						
GO:0050794	BP	regulation of cellular process	0.0026307	2.579928652	205	ZNF676,OR4A16,OLIG2,FEZF2,ZNF98,CRH,GABRA4,ZNF99,MAGEA4,FOXG1,TFAP2D,ISL1,HTR2C,TNNT2,OTX2,EMX2,GPR12,MAGEC2,MAGEC1,CHRM1,LMX1A,HSPA2,SLITRK2,OLIG1,EOMES,CLIC6,LHX2,OTX1,HGF,DMBX1,CCKBR,SIRPB1,HCAR2,SLITRK4,IBSP,PTH2R,ALKAL1,SHISA3,TAFA1,LHX9,SP5,ADRA2A,MS4A7,DMRT3,TNFSF9,TBL1Y,HOXA13,IL33,IRS4,C

						XCL13,SAMSN1,CBLN2,SYK,GCG,ADRA2C,MRLN,H1-1,SLC17A7,GABRA2,PTPRT,ADRB1,TFAP2A,GRIK3,NR2E1,MICB,TAFA4,CMKLR1,KCNK17,FZD8,SHOX2,SH3TC2,ONECUT1,GPR101,DEFB1,MNX1,MEG3,SCUBE1,CAT,EVX2,LAMA3,NCR3,GPR78,NNAT,TAS2R41,TNP1,POU3F4,COL15A1,CDH5,FYB2,STXBP6,DSC2,HDGFL1,RSPO2,POU5F1B,BRINP2,GABRR1,PCSK9,RORB,SCN5A,PLEK,C1QL3,DGKG,POU2F3,ROR2,FOXF1,JPH1,STRIT1,ANGPT4,VN1R2,DACT2,LMOD2,EDA,ZNF578,NTNG2,FOXL1,WNT10B,ZNF726,TRIM58,FRMD7,HMX3,SRPX,CDH13,PRR5-ARHGAP8,KIF26A,NEUROG2,DSCAM,PCP4,KCNQ5,GRIP2,IFI30,KHDRBS2,KCNJ1,ANG,CTTNBP2,ZNF135,TMEM100,RASGEF1B,HJV,GDF15,KLHL31,CAV3,AGBL4,THEMIS,CDON,OPRD1,LGI1,CACNA2D4,ZNF300,LY6E,RAPGEF5,TAS2R43,GCM1,ISLR2,UNC5A,SLC1A2,RYR1,IRGM,LRRIQ4,TRPC3,PDE2A,RGS9BP,ST6GAL1,PDE11A,ENPP7,EMX1,RAP1GAP2,LHX4,ACTN3,SCML4,FAM107A,TCEAL7,HAPLN3,RAG2,ZSCAN1,OR9A2,TMSB15A,SEMA3F,FUT9,TREML1,TP53I11,EDARADD,CUX2,TEX15,CDK18,KCNH7,ROBO4,PKIB,POU6F2,SLC2A4,DRD2,GP6,GPR143,RAB33A,ZNF732,RASGRP1,TRPM5,SASH3,ABI3BP,KCNK2,TAL2,BTK,STAC2,APOBEC3G,BMP8B,MAPK13
GO:0065007	BP	biological regulation	0.010910447	1.962157457	226	ZNF676,OR4A16,OLIG2,FEZF2,ZNF98,CRH,GABRA4,ZNF99,MAGEA4,TRIM49B,FOXG1,TFAP2D,ISL1,HTR2C,TNNT2,OTX2,EMX2,GPR12,MAGEC2,MAGEC1,CHRM1,LMX1A,HSPA2,SLITRK2,SLC6A11,OLIG1,EOMES,CLIC6,LHX2,OTX1,HGF,DMBX1,CCKBR,SIRPB1,HCAR2,SLITRK4,IBSP,PTH2R,ALKAL1,SHISA3,TAFA1,LHX9,SP5,ALDH1A1,ADRA2A,XIST,MS4A7,DMRT3,TNFSF9,TBL1Y,HOXA13,KLHL40,IL33,IRS4,CXCL13,SAMSN1,CBLN2,SYK,MT1H,GCG,ADRA2C,MRLN,H1-1,SLC17A7,GABRA2,PTPRT,ADRB1,TFAP2A,GRIK3,NR2E1,MICB,TAFA4,CMKLR1,KCNK17,FZD8,SHOX2,SH3TC2,ONECUT1,GPR101,DEFB1,MNX1,MEG3,SCUBE1,DPPA5,CAT,EVX2,LAMA3,NCR3,GPR78,NNAT,TAS2R41,TNP1,POU3F4,CHAT,COL15A1,CDH5,FYB2,STXBP6,DSC2,HDGFL1,RSPO2,POU5F1B,BRINP2,C1ORF115,GABRR1,ALS2CL,PCSK9,RORB,SCN5A,PLEK,C1QL3,DGKG,POU2F3,ROR2,FOXF1,JPH1,DSC3,STRIT1,ANGPT4,VN1R2,DACT2,LMOD2,EDA,ZNF578,PCDHB5,NTNG2,FOXL1,WNT10B,AANAT,ZNF726,TRIM58,FRMD7,HMX3,SRPX,CDH13,PRR5-

						ARHGAP8,KIF26A,NEUROG2,DSCAM,PCP4,ITIH1,KCNQ5,GRIP2,IFI30,KHDRBS2,KCNJ1,ANG,CTTNBP2,ZNF135,TMEM100,RASGEF1B,HJV,GDF15,KLHL31,CAV3,AGBL4,THEMIS,CDON,OTOF,OPRD1,LGI1,CACNA2D4,ZNF300,LY6E,RAPGEF5,TAS2R43,GCM1,ISLR2,UNC5A,SLC1A2,RYR1,IRGM,LRRIQ4,TRPC3,PDE2A,RGS9BP,ST6GAL1,PDE11A,ENPP7,EMX1,RAP1GAP2,LHX4,AKR1D1,ACTN3,SCML4,FAM107A,TCEAL7,HAPLN3,RAG2,ZSCAN1,ADH1B,OR9A2,SMTNL2,TMSB15A,SEMA3F,FUT9,TREML1,TP53I11,EDARADD,CUX2,TEX15,CDK18,KCNH7,ROBO4,PKIB,POU6F2,SLC2A4,SPTSSB,DRD2,GP6,GPR143,RAB33A,ZNF732,RASGRP1,TRPM5,SASH3,SLC9A2,ABI3BP,KCNK2,TAL2,BTK,STAC2,APOBEC3G,BMP8B,ZP1,MAPK13
GO:0071944	CC	cell periphery	1.16902E-05	4.932177245	144	OR4A16,ACAN,GABRA4,HAPLN1,ALPI,HTR2C,GPR12,CHRM1,HSPA2,SLITRK2,SLC6A11,RHAG,LHFPL3,CLIC6,C1ORF210,CCKBR,SIRPB1,HCAR2,SLITRK4,PTH2R,ALKAL1,ADRA2A,MS4A7,TNFSF9,IRS4,DSC1,SYK,ADRA2C,SLC17A7,GABRA2,PTPRT,ADRB1,GRIK3,MICB,CMKLR1,KCNK17,PCDHGA7,FZD8,SH3TC2,MUC3A,GPR101,NPC1L1,SCUBE1,CAT,LAMA3,NCR3,GPR78,TAS2R41,TGM3,COL15A1,CDH5,FYB2,STXBP6,LRRC3B,DSC2,ODF4,LMAN1L,GABRR1,PCSK9,SCN5A,PLEK,DGKG,POU2F3,LY75,ROR2,JPH1,DSC3,ANGPT4,VN1R2,CTSF,EDA,MOBP,PCDHB5,NTNG2,FRMD7,SRPX,GPA33,CA4,CDH13,SNTG2,DSCAM,ITIH1,KCNQ5,GRIP2,SEPTIN12,ALDH3A1,KCNJ1,ANG,CTTNBP2,SLC28A2,PCDHGA6,TMEM100,RASGEF1B,HJV,GDF15,CAV3,TPSG1,CDON,OTOF,OPRD1,CACNA2D4,LY6E,RAPGEF5,TAS2R43,PCDHGA10,ISLR2,UNC5A,SLC1A2,ATP13A5,RYR1,IRGM,TRPC3,PDE2A,SLCO5A1,ENPP7,SLC14A1,RAP1GAP2,ACTN3,FAM107A,LAMP5,HAPLN3,ADH1B,OR9A2,SEMA3F,TREML1,PCDHA6,KCNH7,CDHR1,ROBO4,SLC2A4,DRD2,GP6,GPR143,RAB33A,FBN3,RASGRP1,TRPM5,SLC9A2,ABI3BP,KCNK2,BTK,STAC2,MGAM,ZP1
GO:0005886	CC	plasma membrane	0.000574783	3.24049608	128	OR4A16,GABRA4,ALPI,HTR2C,GPR12,CHRM1,HSPA2,SLITRK2,SLC6A11,RHAG,LHFPL3,CLIC6,C1ORF210,CCKBR,SIRPB1,HCAR2,SLITRK4,PTH2R,ALKAL1,ADRA2A,MS4A7,TNFSF9,IRS4,DSC1,SYK,ADRA2C,SLC17A7,GABRA2,PTPRT,ADRB1,GRIK3,MICB,CMKLR1,KCNK17,PCDHGA7,FZD8,SH3TC2,MUC3A,GPR101,NPC1L1,SCUBE1,CAT,NCR3,GPR78,TAS2R41,TGM3,CDH5,FYB2,STXBP6,DSC2,ODF4,GABRR1,PCSK9,SCN5A,PLEK,DGKG,POU2F3,LY75,ROR2,JPH1,DSC

						3,VN1R2,CTSF,EDA,PCDHB5,NTNG2,FRMD7,GPA33,CA4,CDH13,SNTG2,DSCAM,KCNQ5,GRIP2,SEPTIN12,ALDH3A1,KCNJ1,SLC28A2,PCDHGA6,TMEM100,RASGEF1B,HJV,CAV3,TPSG1,CDON,OTOF,OPRD1,CACNA2D4,LY6E,RAPGEF5,TAS2R43,PCDHGA10,ISLR2,UNC5A,SLC1A2,ATP13A5,RYR1,IRGM,TRPC3,PDE2A,SLCO5A1,ENPP7,SLC14A1,RAP1GAP2,ACTN3,FAM107A,LAMP5,ADH1B,OR9A2,SEMA3F,TREML1,PCDHA6,KCNH7,CDHR1,ROBO4,SLC2A4,DRD2,GP6,GPR143,RAB33A,RASGRP1,TRPM5,SLC9A2,KCNK2,BTK,STAC2,MGAM,ZP1
GO:0003690	MF	double-stranded DNA binding	0.007621691	2.117948683	49	ZNF676,OLIG2,FEZF2,ZNF98,ZNF99,FOXG1,TFAP2D,ISL1,OTX2,EMX2,LMX1A,OLIG1,EOMES,LHX2,OTX1,DMBX1,LHX9,SP5,DMRT3,HOXA13,H1-1,TFAP2A,NR2E1,SHOX2,ONECUT1,MNX1,EVX2,POU3F4,HDGFL1,POU5F1B,RORB,POU2F3,FOXF1,ZNF578,FOXL1,ZNF726,HMX3,NEUROG2,RAD51AP2,ZNF135,ZNF300,GCM1,EMX1,LHX4,ZSCAN1,CUX2,POU6F2,ZNF732,TAL2
GO:0043565	MF	sequence-specific DNA binding	0.014223469	1.846994481	47	ZNF676,OLIG2,FEZF2,ZNF98,ZNF99,FOXG1,TFAP2D,ISL1,OTX2,EMX2,LMX1A,OLIG1,EOMES,LHX2,OTX1,DMBX1,LHX9,SP5,DMRT3,HOXA13,TFAP2A,NR2E1,SHOX2,ONECUT1,MNX1,EVX2,POU3F4,POU5F1B,RORB,POU2F3,FOXF1,ZNF578,FOXL1,ZNF726,HMX3,NEUROG2,ZNF135,ZNF300,GCM1,EMX1,LHX4,RAG2,ZSCAN1,CUX2,POU6F2,ZNF732,TAL2

Supplementary Table 3. **The enriched pathway terms of the up and down regulated differentially expressed genes.**

Pathway ID	Pathway Name	adjusted_p_value	negative_log10_of_adjusted_p_value	Gene Count	Gene
Up regulated genes					
REAC:R-HSA-500792	GPCR ligand binding	6.88E-07	6.162301143	32	CCL11,XCL1,VIP,XCL2,HRH1,CALCRL,NPY2R,TAC1,HTR1F,CCL2,WNT2B,CXCL6,PPY,PTHLH,GPR132,EDN3,NPY5R,HTR1B,WNT7B,CXCL16,HTR7,FZD6,GNGT1,CCR4,TACR3,LHCGR,DRD3,NPY1R,ANXA1,RAMP1,TBXA2R,WNT9B
REAC:R-HSA-1474244	Extracellular matrix organization	6.88E-07	6.162301143	25	COL21A1,COL1A2,ADAM12,COL1A1,LAMA2,ITGA1,COL8A2,ITGA11,COL12A1,COL14A1,A2M,SERPINE1,CD44,ITGB3,COL9A2,TLL2,COL25A1,FN1,LAMC3,EFEMP1,COL24A1,GDF5,COL6A2,LOX,LTBP2
REAC:R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	2.68237E-05	4.571481589	23	CCL11,XCL1,XCL2,HRH1,NPY2R,TAC1,HTR1F,CCL2,CXCL6,PPY,GPR132,EDN3,NPY5R,HTR1B,CXCL16,HTR7,CCR4,TACR3,LHCGR,DRD3,NPY1R,ANXA1,TBXA2R
REAC:R-HSA-1280215	Cytokine Signaling in Immune system	0.0002394	3.620875149	34	CCL11,GBP2,IFNA8,OSMR,HLA-F,SP100,CCL2,IL1RL2,HLA-DRA,COL1A2,IL18R1,IL1R1,IL13RA2,IFITM2,XAF1,GSDMD,IFITM1,IL12RB1,GBP1,HLA-DPA1,GBP3,PSMB9,CD44,IL4R,CASP1,IL31RA,MYD88,IFITM3,STAT6,MYC,FN1,ANXA1,TNFSF4,FCGR1A
REAC:R-HSA-375276	Peptide ligand-binding receptors	0.000700899	3.154344276	15	CCL11,XCL1,XCL2,NPY2R,TAC1,CCL2,CXCL6,PPY,EDN3,NPY5R,CXCL16,CCR4,TACR3,NPY1R,ANXA1
REAC:R-HSA-913531	Interferon Signaling	0.002127017	2.672228974	14	GBP2,IFNA8,HLA-F,SP100,HLA-DRA,IFITM2,XAF1,IFITM1,GBP1,HLA-DPA1,GBP3,CD44,IFITM3,FCGR1A
Down regulated genes					
REAC:R-HSA-375280	Amine ligand-binding receptors	0.001186388	2.925773188	7	HTR2C,CHRM1,ADRA2A,ADRA2C,ADRB1,DRD2,GPR143
REAC:R-HSA-372790	Signaling by GPCR	0.007766553	2.10977171	25	CRH,HTR2C,CHRM1,CCKBR,HCAR2,PTH2R,ADRA2A,CXCL13,GCG,ADRA2C,ADRB1,CMKLR1,FZD8,TAS2R41,DGKG,WNT10B,OPRD1,TAS2R43,TRPC3,PDE2A,PDE11A,DRD2,GPR143,RASGRP1,BTK
REAC:R-HSA-112316	Neuronal System	0.010991897	1.95892736	17	GABRA4,SLITRK2,SLC6A11,SLITRK4,SLC17A7,GABRA2,GRIK3,KCNK17,CHAT,GABRR1,KCNQ5,GRIP2,PPFIBP2,KCNJ1,SLC1A2,KCNH7,KCNK2
REAC:R-HSA-416476	G alpha (q) signalling events	0.17634231	0.753643474	9	HTR2C,CHRM1,CCKBR,GCG,DGKG,TRPC3,GPR143,RASGRP1,BTK
REAC:R-HSA-76002	Platelet activation, signaling and aggregation	0.24300464	0.614385434	9	HGF,ADRA2A,SYK,ADRA2C,PLEK,DGKG,TRPC3,GP6,RASGRP1

REAC:R-HSA-112315	Transmission across Chemical Synapses	0.24300464	0.614385434	9	GABRA4,SLC6A11,SLC17A7,GABRA2,GRIK3,CHAT,GABRR1,GRIP2,SLC1A2

Supplementary Table 4. Topology table for up and down regulated genes.

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	MYC	713	0.310415	41107234	0.433377
Up	FN1	689	0.293815	40890432	0.429548
Up	CDKN2A	148	0.047269	5288844	0.384072
Up	EEF1G	122	0.042026	3643566	0.383507
Up	CAV1	115	0.0405	6878160	0.344971
Up	HSPA1L	113	0.032596	7415414	0.335944
Up	MAP1LC3A	106	0.035181	9219812	0.329656
Up	A2M	102	0.038671	4484236	0.321092
Up	RUNX1	96	0.027953	3467212	0.355222
Up	CACNA1A	91	0.035096	5937950	0.317817
Up	MYD88	87	0.024098	4076800	0.341514
Up	STAT6	85	0.027432	5720414	0.329746
Up	FLNC	77	0.022556	2426120	0.357767
Up	TUBA4A	71	0.020727	2772160	0.357416
Up	TGM2	69	0.025933	2970994	0.360811
Up	NR0B2	60	0.026235	2976610	0.361455
Up	RUNX2	57	0.011225	2793000	0.327348
Up	CD44	56	0.014342	1693324	0.351795
Up	CD40	53	0.013135	1670188	0.308591
Up	PRKCB	53	0.013412	1325434	0.348799
Up	MAP1LC3C	53	0.014121	4769440	0.278661
Up	KRT8	52	0.012552	1651368	0.352577
Up	CASP4	51	0.010098	2058474	0.305693
Up	ANXA1	51	0.012751	1572884	0.350307
Up	CASP1	48	0.016877	2217626	0.320246
Up	NMI	47	0.015203	1049100	0.353432
Up	LGALS1	44	0.009749	791434	0.367726
Up	SP100	37	0.009551	1545490	0.312264
Up	COL1A1	36	0.008394	1014920	0.34432
Up	SULT1A1	36	0.009131	1242722	0.31932
Up	ASS1	36	0.011257	1026758	0.352918
Up	HLA-DRA	35	0.008744	1724256	0.311891
Up	ITGB3	33	0.007408	665718	0.299712
Up	PTGES3L-AARSD1	32	0.010914	1482042	0.31589
Up	GBP2	32	0.007139	553794	0.298485
Up	TPM2	31	0.005003	992092	0.313986
Up	SERPINE1	31	0.007023	1430922	0.321687
Up	CCL2	29	0.005091	650984	0.301821
Up	S100A16	29	0.009655	1044560	0.321007
Up	FOSL2	27	0.008462	1220104	0.317984
Up	COL1A2	26	0.003973	895308	0.318957
Up	NFE2	24	0.005793	1797082	0.281154
Up	IL1R1	24	0.004361	458608	0.316493
Up	PSMB9	24	0.006432	1021664	0.315453
Up	IL4R	23	0.005681	517958	0.344222
Up	LAMC3	23	0.006557	622902	0.308695
Up	OCLN	22	0.005495	580274	0.319097
Up	NOS1	22	0.00664	974768	0.314094
Up	WT1	21	0.004938	1799848	0.279387
Up	MEOX2	19	0.006733	395866	0.286793
Up	VRK2	18	0.003945	494672	0.312479
Up	NQO1	18	0.003884	450276	0.338156
Up	GBP1	18	0.002218	646304	0.282307
Up	GTF2A1L	18	0.005653	503070	0.264529
Up	GEM	17	0.006252	575466	0.275815
Up	HBG2	17	0.002628	1163364	0.28558
Up	DHX58	17	0.005166	1326428	0.266989
Up	HOXC8	17	0.003742	924866	0.292993
Up	TFAP2B	16	0.003332	468986	0.3196
Up	NKX2-5	15	0.005275	1289306	0.266443
Up	HOXB7	15	0.001026	415826	0.300329
Up	SH3BP5	15	0.003502	424768	0.318706
Up	SELL	15	0.003929	435998	0.317845
Up	GATA6	14	0.004497	254336	0.297851
Up	IGFBP7	14	0.004721	439072	0.308931
Up	TBXA2R	14	0.001869	367166	0.258839
Up	CCL11	14	0.002065	164722	0.284488
Up	EFEMP1	14	0.002425	231684	0.313123

Up	DOCK5	14	8.09E-04	503246	0.265202
Up	CYP2C8	13	0.002413	197708	0.282723
Up	HOXC11	13	0.003187	698564	0.287154
Up	FCGR1A	13	8.84E-04	97144	0.295318
Up	SPHK1	13	0.002514	399368	0.312318
Up	RPH3A	13	0.005499	594192	0.239286
Up	ME1	13	0.003983	323528	0.310113
Up	CYBA	12	0.003753	425394	0.309692
Up	FOXH1	12	0.001424	364336	0.28641
Up	QPCT	12	2.95E-04	89812	0.3088
Up	SIX1	11	0.003261	354146	0.309771
Up	RHOD	11	0.003903	253714	0.308069
Up	TAC1	11	0.004206	919236	0.252808
Up	ERRFI1	11	0.001711	514210	0.286793
Up	ACTG2	11	9.28E-04	252392	0.317956
Up	MYL9	10	0.001073	213044	0.313365
Up	FABP4	10	0.001824	494610	0.259151
Up	IFITM1	10	0.00171	238942	0.308852
Up	SCG2	10	0.001365	170254	0.309929
Up	RASSF3	10	0.002494	399370	0.31589
Up	PTHLH	10	8.16E-04	260708	0.28098
Up	AZGP1	10	0.001935	200850	0.315644
Up	MAL	9	9.89E-05	12454	0.284933
Up	LHCGR	9	0.00182	352424	0.235393
Up	HOXD9	9	0.002796	305862	0.242953
Up	SLFN11	9	0.001186	163668	0.307939
Up	TSKS	9	0.00151	481574	0.28909
Up	HFE	9	0.001969	221134	0.310166
Up	VIP	9	9.05E-04	280086	0.273642
Up	DPF3	9	7.14E-04	220264	0.265995
Up	RGS4	9	0.002004	232962	0.248365
Up	GDF5	9	0.001783	491850	0.265009
Up	CTSC	9	0.003107	247202	0.307731
Up	ITGA1	9	0.002779	561424	0.252161
Up	MYOF	9	0.004772	264182	0.326235
Up	NT5E	8	0.001565	159942	0.313769
Up	LOX	8	0.001838	263290	0.240676
Up	ZC3HAV1L	8	7.81E-04	192084	0.314121
Up	CSRP1	8	7.94E-04	283154	0.32064
Up	TMPRSS2	8	4.59E-04	148024	0.272435
Up	DRD3	8	0.002509	711582	0.272252
Up	IFITM3	8	4.43E-04	126806	0.309429
Up	ARHGAP29	8	0.00181	147004	0.310774
Up	CCR4	7	6.21E-04	109346	0.252931
Up	ZP3	7	0.00239	160720	0.309271
Up	XAF1	7	0.001344	272360	0.265357
Up	CDCP1	7	2.24E-04	67016	0.309271
Up	SLC27A6	7	0.0013	150364	0.309376
Up	TNFAIP2	7	0.001251	134608	0.309508
Up	SYNPO	7	5.32E-04	86028	0.308043
Up	RCN3	7	0.002741	120710	0.313123
Up	FRZB	7	0.002234	496488	0.223846
Up	TLR6	2	0	0	0.274755
Up	TGFBI	1	0	0	0.300503
Up	COL14A1	1	0	0	0.260261
Up	HOXD10	1	0	0	0.195475
Up	CFI	1	0	0	0.249692
Up	HLA-DMB	1	0	0	0.237757
Up	TACR3	1	0	0	0.201804
Up	XDH	1	0	0	0.302372
Up	CARD16	1	0	0	0.242582
Up	AGBL2	1	0	0	0.249692
Up	NEK11	1	0	0	0.302372
Up	ACSS3	1	0	0	0.249692
Up	KIF25	1	0	0	0.302372
Down	ONECUT1	248	0.103995	20071096	0.332755
Down	SYK	102	0.028975	4996254	0.340334
Down	MAPK13	96	0.0179	7197118	0.329448
Down	TFAP2A	82	0.025051	3509194	0.357206
Down	BTK	76	0.022414	3110388	0.368618

Down	KHDRBS2	49	0.008933	2433462	0.316768
Down	SLC2A4	40	0.010992	1864574	0.311544
Down	ZSCAN1	36	0.010197	3179928	0.281523
Down	IRS4	34	0.00737	1014618	0.351557
Down	HSPA2	33	0.007802	1221970	0.327789
Down	CDK18	25	0.004915	1002500	0.321971
Down	CDH5	24	0.006444	437132	0.319488
Down	CTTNBP2	23	0.004794	2924350	0.265647
Down	FAM107A	22	0.005481	1728074	0.271179
Down	GDA	20	0.005442	574062	0.311384
Down	DSC1	20	0.003744	576496	0.316191
Down	CAT	20	0.003498	819048	0.325042
Down	GP6	17	0.001927	214126	0.293606
Down	RORB	16	0.003777	785660	0.280354
Down	CAV3	16	0.002744	533494	0.287381
Down	ISL1	16	0.005951	1372458	0.283361
Down	RYR1	16	0.007187	559250	0.317845
Down	ADRB1	15	0.00445	985108	0.263611
Down	FOXG1	14	0.002424	202668	0.301347
Down	MYOM2	14	0.003356	147258	0.275149
Down	IL33	14	0.003617	294292	0.269177
Down	GCM1	14	0.002526	406854	0.316466
Down	FBN3	13	9.42E-04	268368	0.260782
Down	ADH1B	13	0.002617	313254	0.29389
Down	NR2E1	13	0.001666	564764	0.272843
Down	SCN5A	12	0.003712	344292	0.311066
Down	SAMSN1	11	9.82E-04	421748	0.276841
Down	MAGEA4	11	0.003625	358454	0.313688
Down	SLC9A2	11	0.001535	262226	0.314582
Down	APOBEC3G	11	0.00132	314414	0.315507
Down	DRD2	11	0.003965	692488	0.250705
Down	OPRD1	11	0.00294	426778	0.311119
Down	ROBO4	10	0.001821	428540	0.27319
Down	PLEK	10	0.001681	180396	0.312988
Down	ANG	10	0.002316	490036	0.280721
Down	TGM3	10	0.001694	243370	0.309876
Down	MAGEC1	9	0.003864	256148	0.307368
Down	CCKBR	9	0.001275	317674	0.283317
Down	HGF	9	0.001757	199476	0.285961
Down	LAMA3	9	0.001859	303950	0.265125
Down	PKIB	8	0.001761	169064	0.313365
Down	ROR2	8	8.65E-04	144138	0.307861
Down	MAGEC2	8	0.00223	451514	0.269018
Down	DSC2	8	0.001131	202720	0.308617
Down	ABI3BP	8	0.002201	129372	0.319013
Down	TNP1	8	0.001681	283552	0.258967
Down	TAL2	8	0.001937	364704	0.272171
Down	GABRR1	7	0.002252	180754	0.307472
Down	JPH1	7	7.45E-04	118932	0.311491
Down	EMX1	7	0.002009	215908	0.236784
Down	PPFIBP2	7	0.001284	277220	0.260094
Down	RAI2	7	0.001178	291306	0.32019
Down	DSC3	7	7.49E-04	106410	0.307783
Down	CXCL13	7	0.002564	189938	0.29154
Down	HTR2C	7	0.001334	307330	0.243619
Down	EDARADD	6	0.001115	204766	0.257177
Down	ADRA2A	6	2.37E-04	26196	0.237803
Down	TNNT2	6	0.001847	203462	0.313257
Down	EMX2	6	0.001096	181732	0.257504
Down	ALDH1A1	6	0.001355	148660	0.31404
Down	KCNJ1	6	0.00173	133968	0.309613
Down	RAG2	6	8.99E-04	88052	0.307731
Down	SEMA3F	5	0.001235	102780	0.309429
Down	GPR143	5	0.001465	285038	0.249555
Down	CDON	5	0.001102	214134	0.248044
Down	LHX2	5	5.72E-04	149514	0.212682
Down	CRH	5	0.001115	169686	0.259446
Down	MPPED1	5	6.18E-04	104820	0.246185
Down	OTX2	5	6.53E-04	126900	0.268108
Down	SERF1A	5	0.001134	170184	0.313311

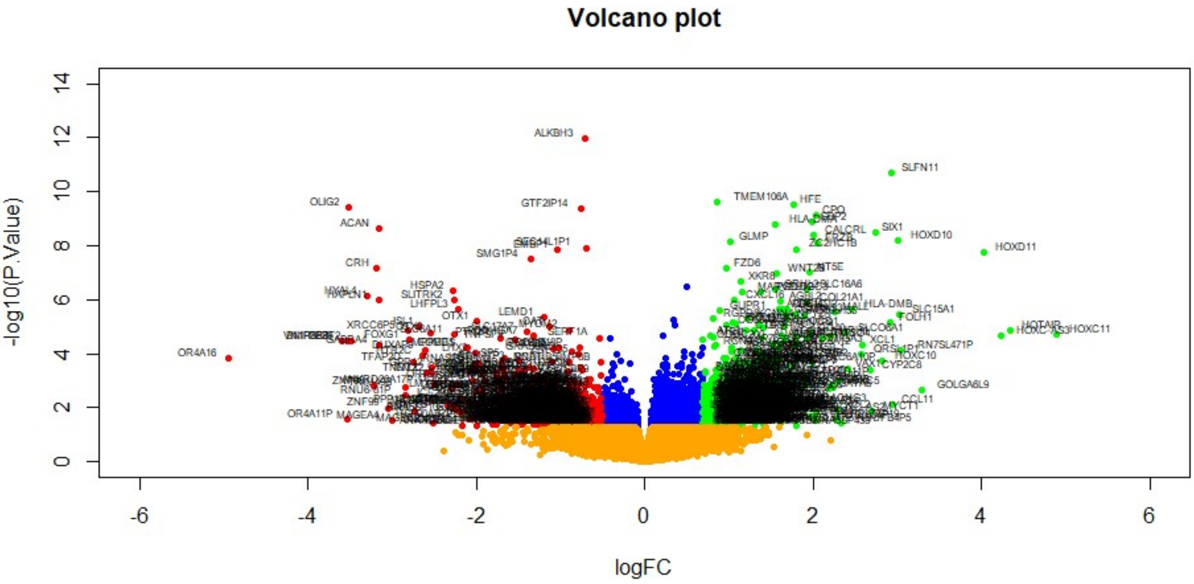
Down	HPD	5	7.94E-04	86584	0.309271
Down	IBSP	5	8.09E-04	34624	0.271098
Down	ALDH3A1	5	8.40E-04	109504	0.259114
Down	MT1H	5	0.001242	134364	0.314094
Down	FZD8	5	0.001155	202456	0.236661
Down	OTX1	5	0.00165	268444	0.198627
Down	GRIK3	5	0.001684	267902	0.23588
Down	TXLNB	5	0.001674	109700	0.307161
Down	LHX4	5	0.001645	385896	0.220903
Down	RASGRP1	4	5.93E-04	103616	0.260224
Down	CUX2	4	2.02E-04	67776	0.271968
Down	SLC1A2	4	6.01E-04	113990	0.274466
Down	TMPRSS3	4	2.60E-04	38846	0.30755
Down	ZNF300	4	4.45E-04	84152	0.314148
Down	GDF15	4	9.15E-04	158668	0.314121
Down	ITIH1	4	3.41E-04	21144	0.268523
Down	RAP1GAP2	4	4.08E-05	20462	0.307627
Down	TNFSF9	4	6.47E-04	65914	0.308278
Down	SHOX2	4	9.04E-05	21074	0.257577
Down	MICB	4	5.78E-04	72208	0.308512
Down	ALPI	4	6.55E-04	66416	0.308043
Down	PCP4	4	4.43E-05	7142	0.232288
Down	SRPX	4	0.001099	195728	0.240787
Down	LMX1A	4	1.29E-04	23564	0.256869
Down	CDHR1	3	6.01E-04	94522	0.235697
Down	KCNQ5	3	6.03E-04	93146	0.235773
Down	SIRPB1	3	7.29E-05	9782	0.315153
Down	GABRA4	3	0.001097	266474	0.244616
Down	NNAT	3	6.28E-04	109512	0.313096
Down	HAPLN1	3	1.48E-04	85880	0.313365
Down	KLHL14	3	5.49E-04	138460	0.258783
Down	CLIC6	3	5.67E-04	165968	0.214496
Down	POU2F3	3	5.73E-04	38682	0.30742
Down	GCG	3	0.001097	200710	0.213654
Down	KIF26A	3	3.65E-05	5286	0.262472
Down	PCSK9	3	0.001097	65738	0.307057
Down	GABRA2	3	1.57E-05	4184	0.237881
Down	PTPRT	3	5.53E-04	116256	0.246252
Down	CHRM1	3	5.60E-04	70892	0.19655
Down	CA4	3	2.71E-05	3890	0.247993
Down	TTC34	3	5.49E-04	151206	0.24305
Down	BMP8B	3	3.47E-06	1434	0.248959
Down	PCDHA6	3	7.14E-05	23652	0.30755
Down	GPR12	2	3.26E-06	802	0.269217
Down	GALNT12	2	5.49E-04	133238	0.244583
Down	OLIG1	1	0	0	0.241185
Down	SNTG2	1	0	0	0.237277

Supplementary Table 5. Micro-RNA-hub gene and transcript factor-hub gene topology table.

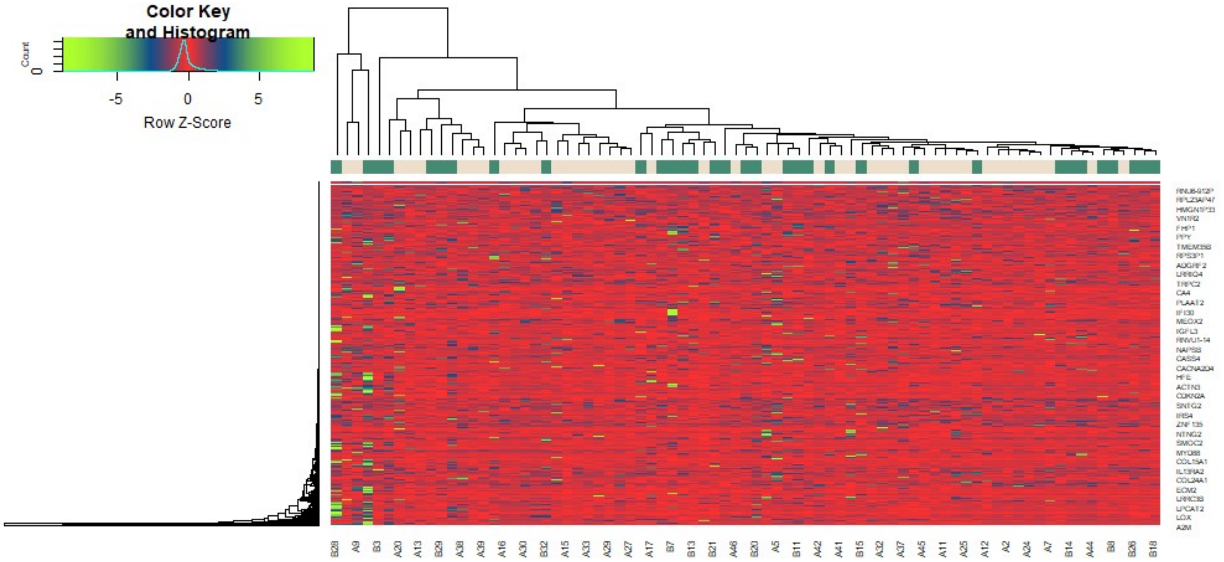
Regulation	Hub Genes	Degree	MicroRNA	Regulation	Hub Genes	Degree	TF
Up	MYC	194	hsa-mir-3157-5p	Up	STAT6	16	USF2
Up	RUNX1	125	hsa-mir-4530	Up	CDKN2A	16	SRY
Up	CAV1	115	hsa-mir-4796-3p	Up	CAV1	16	HOXA5
Up	FN1	105	hsa-mir-132-3p	Up	FN1	14	RELA
Up	CACNA1A	69	hsa-mir-10b-5p	Up	MAP1LC3A	14	JUND
Up	MYD88	35	hsa-mir-384	Up	RUNX1	14	IRF2
Up	FLNC	35	hsa-mir-129-2-3p	Up	FLNC	12	PRRX2
Up	CDKN2A	31	hsa-mir-191-5p	Up	MYD88	9	SOX10
Up	STAT6	28	hsa-mir-127-5p	Up	CACNA1A	9	GATA2
Up	TGM2	27	hsa-mir-107	Up	A2M	7	HNF4A
Up	TUBA4A	27	hsa-mir-182-5p	Up	MYC	7	CEBPB
Up	EEF1G	25	hsa-mir-342-3p	Up	TUBA4A	7	JUN
Up	HSPA1L	10	hsa-mir-101-3p	Up	HSPA1L	7	SREBF1
Up	A2M	10	hsa-mir-128-3p	Up	TGM2	7	ELK4
Up	MAP1LC3A	6	hsa-mir-22-3p	Up	EEF1G	2	ESR1
Down	IRS4	134	hsa-mir-769-3p	Down	GDA	13	GATA3
Down	TFAP2A	100	hsa-mir-4713-5p	Down	SYK	13	FOXC1
Down	HSPA2	45	hsa-mir-155-5p	Down	TFAP2A	13	PRDM1
Down	GDA	45	hsa-mir-191-5p	Down	IRS4	11	PAX2
Down	MAPK13	43	hsa-mir-4516	Down	KHDRBS2	10	PDX1
Down	SYK	42	hsa-mir-4722-3p	Down	ZSCAN1	9	REL
Down	FAM107A	39	hsa-mir-146a-3p	Down	MAPK13	9	FOS
Down	SLC2A4	35	hsa-mir-1286	Down	ONECUT1	8	ARID3A
Down	CDH5	34	hsa-mir-128-3p	Down	SLC2A4	8	MAX
Down	CTTNBP2	27	hsa-mir-15b-5p	Down	CDK18	7	NFIC
Down	CDK18	24	hsa-mir-6893-5p	Down	CDH5	7	USF1
Down	ONECUT1	16	hsa-mir-378a-5p	Down	CTTNBP2	6	TEAD1
Down	BTK	13	hsa-mir-34a-5p	Down	FAM107A	4	NFKB1
Down	KHDRBS2	4	hsa-mir-148b-3p	Down	HSPA2	4	E2F1
Down	ZSCAN1	3	hsa-mir-212-3p	Down	BTK	2	SOX5

Supplemenary Table 6. Drug-hub gene topology table.

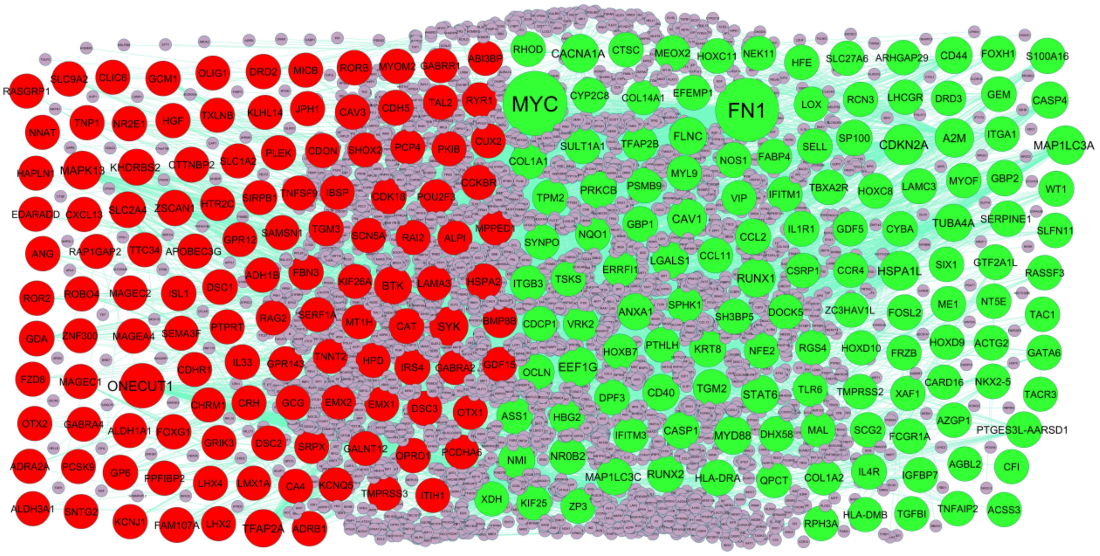
Hub Gene	Regulation	Degree	Drug
TUBA4A	Up	7	Cabazitaxel
A2M	Up	3	Becaplermin
FN1	Up	1	Ocriplasmin
SYK	Down	6	Staurosporine
BTK	Down	2	XL418
CDH5	Down	2	Lenalidomide



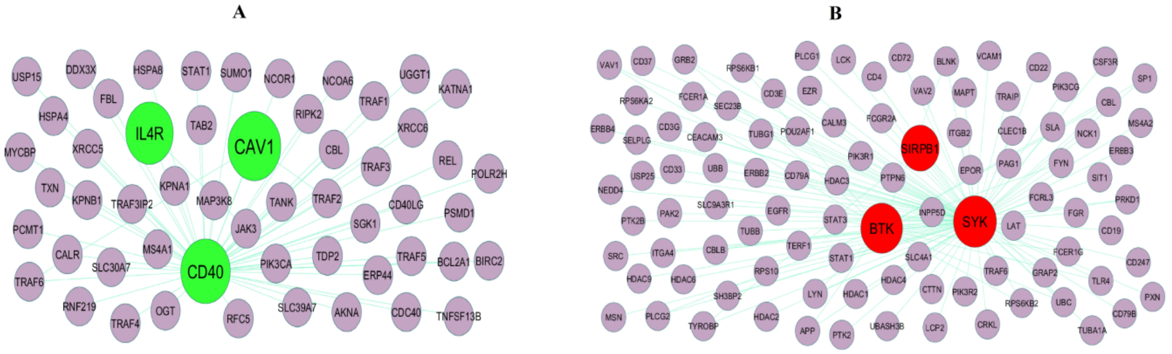
Supplementary Figure 1. Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected. Green dot represented up regulated significant genes and red dot represented down-regulated significant genes.



Supplementary Figure 2. Heat map of differentially expressed genes. Legend on the top left indicates log fold change of genes (A1 – A46 = schizophrenia samples; B1 – B33 = normal control samples).

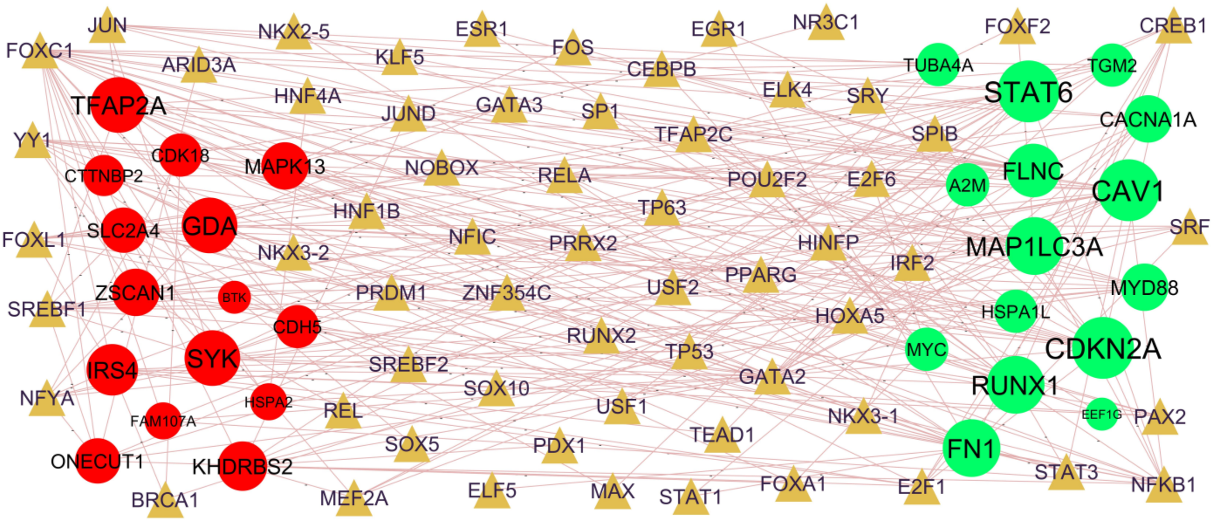


Supplementary Figure 3. Protein-protein interaction network of differentially expressed genes. Up regulated genes are marked in parrot green; down regulated genes are marked in red.

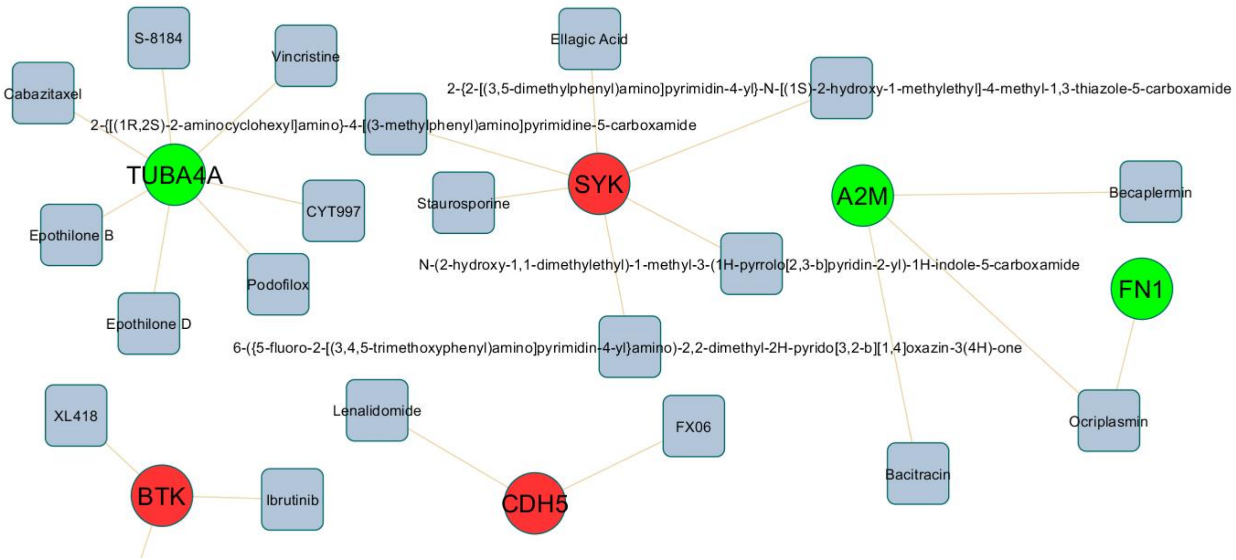


Supplementary Figure 4. Modules selected from the protein-protein interaction (PPI) network. A) The most significant module was obtained from the PPI network with 54 nodes and 56 edges for upregulated genes; B) the most significant module was obtained from the PPI network with 99 nodes and 117 edges for downregulated genes. Upregulated genes are marked in parrot green; downregulated genes are marked in red.

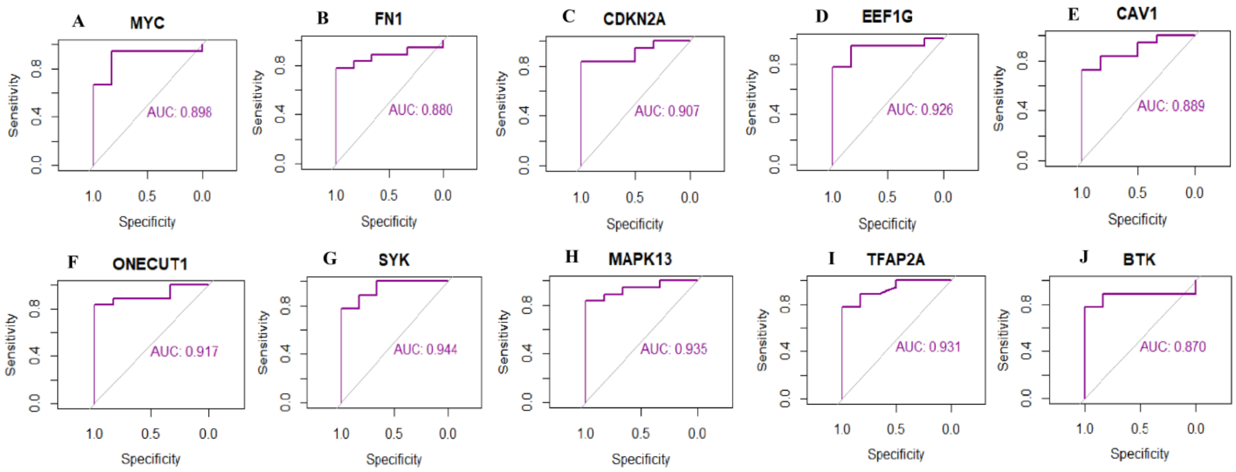
Supplementary Figure 5. Hub gene – micro-RNA regulatory network. The blue color diamond nodes represent the key miRNAs; upregulated genes are marked in green; downregulated genes are marked in red.



Supplementary Figure 6. Hub gene – transcriptor factor (TF) regulatory network. The olive color triangle nodes represent the key TFs; upregulated genes are marked in green; downregulated genes are marked in red.



Supplementary Figure 7. Hub gene – drug interaction network. The blue color rectangle nodes represent the key drugs; upregulated genes are marked in green; downregulated genes are marked in red.



Supplementary Figure 8. Receiver operating characteristic curve analyses of hub genes.