

Research article

Identification of potential and novel target genes in pituitary prolactinoma by bioinformatics analysis

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Supplementary

Table 1. The statistical metrics for key differentially expressed genes (DEGs).

Agilent Id	Gene Symbol	Log FC	P Value	FDR	T value	Up/Down	Gene Name
A_23_P328074	SALL1	1.833089	2.06E-12	8.77E-08	60.26576	Up	spalt like transcription factor 1
A_23_P17522	NKX2-2	1.814078	3.68E-11	5.54E-07	42.7718	Up	NK2 homeobox 2
A_32_P149435	PTCHD1	1.891448	3.91E-11	5.54E-07	42.46841	Up	patched domain containing 1

A_23_P684 87	BMP7	1.638544	7.17E- 11	7.63E- 07	39.50907	Up	bone morphogenetic protein 7
A_23_P361 584	TMEM15 4	1.53654	5.79E- 10	4.13E- 06	30.7916	Up	transmembrane protein 154
A_24_P366 607	SERTM1	1.817216	5.83E- 10	4.13E- 06	30.77075	Up	serine rich and transmembrane domain containing 1
A_24_P497 464	SOX9- AS1	1.905462	9.38E- 10	5.7E- 06	29.06852	Up	SOX9 antisense RNA 1
A_33_P324 0747	FAM83F	1.788916	1.62E- 09	8.1E- 06	27.23397	Up	family with sequence similarity 83 member F
A_32_P459 5	SGCD	2.094348	1.81E- 09	8.1E- 06	26.87211	Up	sarcoglycan delta
A_32_P182 299	C1orf168	1.588213	1.93E- 09	8.1E- 06	26.65684	Up	chromosome 1 open reading frame 168
A_24_P352 28	GRHL2	1.574365	2.1E-09	8.1E- 06	26.40034	Up	grainyhead like transcription factor 2
A_23_P809 74	TDO2	1.745047	2.66E- 09	9.04E- 06	25.6513	Up	tryptophan 2,3-dioxygenase
A_23_P299 65	SMR3B	1.759372	2.76E- 09	9.04E- 06	25.54097	Up	submaxillary gland androgen regulated protein 3B
A_23_P167 159	SCRGI	2.129388	3.06E- 09	9.29E- 06	25.23178	Up	stimulator of chondrogenesis 1
A_24_P331 830	KAZN	1.227017	3.59E- 09	1.02E- 05	24.75271	Up	kazrin, periplakin interacting protein
A_23_P145 514	IL20RA	1.535447	3.86E- 09	1.03E- 05	24.53233	Up	interleukin 20 receptor subunit alpha
A_23_P328 709	CLRN1	1.340457	5.2E-09	1.27E- 05	23.67443	Up	clarin 1
A_23_P216 756	FCN2	2.077085	5.38E- 09	1.27E- 05	23.57765	Up	ficolin 2
A_24_P709 476	LINC011 02	1.480536	6.97E- 09	1.56E- 05	22.85332	Up	long intergenic non-protein coding RNA 1102
A_23_P380 526	DPPA4	1.231647	8.6E-09	1.78E- 05	22.28297	Up	developmental pluripotency associated 4
A_24_P492 60	SPTLC3	1.719134	8.8E-09	1.78E- 05	22.2211	Up	serine palmitoyltransferase long chain base subunit 3
A_23_P430 728	ATP4A	1.108847	1.14E- 08	2.2E- 05	21.5462	Up	ATPase H ⁺ /K ⁺ transporting alpha subunit
A_33_P325 0178	IQCJ	1.326735	1.73E- 08	3.2E- 05	20.48275	Up	IQ motif containing J
A_19_P003 31971	MIR503H G	1.447267	2.34E- 08	4.14E- 05	19.75227	Up	MIR503 host gene
A_33_P323 6833	GPR12	1.701415	2.66E- 08	4.53E- 05	19.44286	Up	G protein-coupled receptor 12
A_32_P194 312	SDK2	1.254756	4.19E- 08	6.6E- 05	18.40361	Up	sidekick cell adhesion molecule 2
A_33_P323 4060	SEPT14	1.389704	4.95E- 08	7.45E- 05	18.03658	Up	septin 14

A_33_P360 8210	MIR31H G	1.48494	5.52E- 08	7.45E- 05	17.79865	Up	MIR31 host gene
A_23_P111 402	RSPO3	1.785412	5.6E-08	7.45E- 05	17.76502	Up	R-spondin 3
A_23_P667 39	SLC13A5	1.374669	7.12E- 08	9.03E- 05	17.25669	Up	solute carrier family 13 member 5
A_23_P117 464	TPPP2	1.134536	7.49E- 08	9.03E- 05	17.15035	Up	tubulin polymerization promoting protein family member 2
A_24_P206 624	FGFR2	1.045116	7.8E-08	9.03E- 05	17.06439	Up	fibroblast growth factor receptor 2
A_33_P329 2432	IQCA1	1.083925	7.85E- 08	9.03E- 05	17.05136	Up	IQ motif containing with AAA domain 1
A_23_P366 58	MGST1	2.006529	8.59E- 08	9.49E- 05	16.86567	Up	microsomal glutathione S-transferase 1
A_33_P337 2954	LOC3877 20	1.229633	8.7E-08	9.49E- 05	16.83959	Up	collagen alpha-1(X) chain
A_23_P134 139	FABP7	1.539766	1E-07	0.000 105	16.54886	Up	fatty acid binding protein 7
A_23_P215 549	PON3	1.382761	1.02E- 07	0.000 105	16.52506	Up	paraoxonase 3
A_23_P374 844	GAL	1.402474	1.07E- 07	0.000 109	16.41339	Up	galanin and GMAP prepropeptide
A_33_P333 0149	PAX6	2.074082	1.27E- 07	0.000 123	16.08292	Up	paired box 6
A_33_P338 5376	SYPL2	1.302737	1.28E- 07	0.000 123	16.06335	Up	synaptophysin like 2
A_33_P334 5344	DRGX	1.08197	1.33E- 07	0.000 123	15.9954	Up	dorsal root ganglia homeobox
A_23_P127 267	LGI1	1.756456	1.33E- 07	0.000 123	15.9945	Up	leucine rich glioma inactivated 1
A_33_P340 2329	MIR503H G	1.05068	1.36E- 07	0.000 123	15.94943	Up	MIR503 host gene
A_33_P337 3273	SLC15A1	1.538301	1.64E- 07	0.000 142	15.58775	Up	solute carrier family 15 member 1
A_23_P801 62	TMPRSS 3	1.596153	1.77E- 07	0.000 148	15.44677	Up	transmembrane protease, serine 3
A_19_P003 18205	#N/A	1.577183	1.78E- 07	0.000 148	15.43499	Up	NA
A_23_P158 318	ROR2	1.473452	1.95E- 07	0.000 157	15.26237	Up	receptor tyrosine kinase like orphan receptor 2
A_24_P289 260	DACT2	1.389093	1.95E- 07	0.000 157	15.25987	Up	dishevelled binding antagonist of beta catenin 2
A_32_P111 336	AL59124 2.1	1.506199	2.32E- 07	0.000 183	14.93773	Up	NA
A_24_P555 066	SMTNL2	1.13931	2.61E- 07	0.000 202	14.72185	Up	smoothelin like 2
A_33_P331 0894	KRT40	1.57768	2.81E- 07	0.000 208	14.59126	Up	keratin 40

A_23_P214 026	FBN2	1.687663	2.83E- 07	0.000 208	14.57834	Up	fibrillin 2
A_23_P489 9	NTF4	1.441871	2.84E- 07	0.000 208	14.57475	Up	neurotrophin 4
A_23_P186 72	GBA3	0.964336	3.42E- 07	0.000 232	14.24096	Up	glucosylceramidase beta 3 (gene/pseudogene)
A_19_P003 25499	#N/A	0.933759	3.44E- 07	0.000 232	14.23364	Up	NA
A_33_P334 6073	SRL	1.279597	3.63E- 07	0.000 238	14.13739	Up	sarcalumenin
A_19_P003 21712	AC11219 8.2	1.208537	4.08E- 07	0.000 259	13.93544	Up	NA
A_33_P341 1021	SLIT1	1.437893	4.23E- 07	0.000 265	13.87466	Up	slit guidance ligand 1
A_23_P166 30	OR7A5	1.409749	5.03E- 07	0.000 31	13.58235	Up	olfactory receptor family 7 subfamily A member 5
A_33_P324 9768	DGKK	1.719184	5.8E-07	0.000 347	13.34618	Up	diacylglycerol kinase kappa
A_33_P334 2797	LOC4014 42	1.555765	6.8E-07	0.000 396	13.08512	Up	uncharacterized LOC401442
A_23_P127 495	BBOX1	1.969105	7.18E- 07	0.000 41	12.99661	Up	gamma-butyrobetaine hydroxylase 1
A_33_P372 3448	ART3	1.310074	7.36E- 07	0.000 412	12.95714	Up	ADP-ribosyltransferase 3
A_33_P327 5220	NRK	1.438252	7.49E- 07	0.000 414	12.93021	Up	Nik related kinase
A_33_P332 2400	LOC6547 80	1.529021	8.77E- 07	0.000 472	12.67915	Up	splicing factor proline/glutamine-rich
A_33_P336 3071	ITIH6	0.970677	9.01E- 07	0.000 478	12.63721	Up	inter-alpha-trypsin inhibitor heavy chain family member 6
A_19_P003 16371	AC00248 0.2	1.144117	1.1E-06	0.000 549	12.32129	Up	NA
A_33_P322 9370	ID4	1.414675	1.11E- 06	0.000 549	12.31878	Up	inhibitor of DNA binding 4, HLH protein
A_33_P328 2474	#N/A	1.105066	1.11E- 06	0.000 549	12.31117	Up	NA
A_33_P324 6026	DEFB131	1.290266	1.31E- 06	0.000 615	12.05627	Up	defensin beta 131
A_33_P340 0763	PLIN4	1.033075	1.33E- 06	0.000 616	12.03503	Up	perilipin 4
A_33_P350 4002	LINC012 99	1.129723	1.57E- 06	0.000 697	11.7883	Up	long intergenic non-protein coding RNA 1299
A_32_P324 933	LINC002 82	0.971613	1.72E- 06	0.000 748	11.65582	Up	long intergenic non-protein coding RNA 282
A_33_P324 8799	TRDN	2.047985	1.75E- 06	0.000 749	11.63034	Up	triadin
A_23_P311 895	CLIC5	1.76	1.86E- 06	0.000 777	11.54202	Up	chloride intracellular channel 5

A_33_P339 1915	BTBD17	1.379368	1.97E- 06	0.000 812	11.45968	Up	BTB domain containing 17
A_33_P331 5134	DIRC3	1.187589	2.04E- 06	0.000 812	11.41367	Up	disrupted in renal carcinoma 3
A_33_P333 6257	IRX1	1.782642	2.19E- 06	0.000 854	11.31183	Up	iroquoishomeobox 1
A_33_P331 6953	RBFOX3	2.121609	2.25E- 06	0.000 869	11.27381	Up	RNA binding protein, fox-1 homolog 3
A_23_P103 765	FCER1A	1.675704	2.5E-06	0.000 926	11.12106	Up	Fc fragment of IgE receptor Ia
A_33_P324 0094	NGEF	1.065886	2.66E- 06	0.000 969	11.03844	Up	neuronal guanine nucleotide exchange factor
A_23_P162 010	CCKBR	1.368159	2.67E- 06	0.000 969	11.03391	Up	cholecystokinin B receptor
A_23_P957 90	ITLN1	1.534417	2.72E- 06	0.000 98	11.00679	Up	intelectin 1
A_23_P383 227	S100A1	1.861029	2.85E- 06	0.001 006	10.94318	Up	S100 calcium binding protein A1
A_23_P429 09	TMEM13 9	1.402909	2.87E- 06	0.001 006	10.93278	Up	transmembrane protein 139
A_23_P158 89	CBLN2	1.141876	2.89E- 06	0.001 006	10.92424	Up	cerebellin 2 precursor
A_33_P361 9171	PMAIP1	1.187979	3.01E- 06	0.001 041	10.86654	Up	phorbol-12-myristate-13-acetate-induced protein 1
A_23_P849 7	GHRHR	1.170394	3.07E- 06	0.001 054	10.83768	Up	growth hormone releasing hormone receptor
A_33_P327 0863	XDH	1.809518	3.15E- 06	0.001 071	10.80343	Up	xanthine dehydrogenase
A_24_P595 717	TOGAR AM2	1.604949	3.4E-06	0.001 139	10.69969	Up	TOG array regulator of axonemal microtubules 2
A_33_P335 0164	CCDC17 8	1.42881	3.44E- 06	0.001 144	10.68331	Up	coiled-coil domain containing 178
A_23_P203 267	TRIM29	1.443956	3.54E- 06	0.001 159	10.64492	Up	tripartite motif containing 29
A_33_P338 9237	UGT2A2	1.479469	3.6E-06	0.001 17	10.62203	Up	UDP glucuronosyltransferase family 2 member A2
A_33_P341 2262	JAKMIP2 -AS1	1.32862	3.67E- 06	0.001 183	10.59731	Up	JAKMIP2 antisense RNA 1
A_24_P272 34	SOX5	1.659349	3.82E- 06	0.001 212	10.54464	Up	SRY-box 5
A_33_P340 9086	S100A1	1.494024	4.14E- 06	0.001 285	10.43768	Up	S100 calcium binding protein A1
A_32_P347 6	RPRML	1.611243	4.32E- 06	0.001 322	10.38091	Up	reprimin like
A_33_P377 3374	AC12003 6.5	1.753756	4.49E- 06	0.001 353	10.33104	Up	NA
A_23_P153 155	GALR1	1.619947	4.67E- 06	0.001 358	10.27926	Up	galanin receptor 1

A_23_P831 34	GAS1	1.058861	4.68E- 06	0.001 358	10.27589	Up	growth arrest specific 1
A_33_P330 8964	PPP1R17	1.085168	4.71E- 06	0.001 358	10.26698	Up	protein phosphatase 1 regulatory subunit 17
A_23_P302 060	IFNE	0.935355	4.82E- 06	0.001 371	10.23827	Up	interferon epsilon
A_23_P132 378	CELSR1	1.253634	4.83E- 06	0.001 371	10.23304	Up	cadherin EGF LAG seven-pass G-type receptor 1
A_23_P299 75	C4orf19	1.051466	5.25E- 06	0.001 459	10.12693	Up	chromosome 4 open reading frame 19
A_33_P334 5036	POMC	1.014551	5.73E- 06	0.001 563	10.01362	Up	proopiomelanocortin
A_19_P003 15473	#N/A	1.012926	6.47E- 06	0.001 71	9.859854	Up	NA
A_24_P365 721	SLC6A14	1.636424	6.82E- 06	0.001 79	9.794187	Up	solute carrier family 6 member 14
A_32_P113 066	LRAT	1.318608	6.87E- 06	0.001 793	9.784901	Up	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)
A_33_P341 5395	SPTLC3	1.309174	7.32E- 06	0.001 85	9.704786	Up	serine palmitoyltransferase long chain base subunit 3
A_23_P101 505	KLK11	1.847661	7.34E- 06	0.001 85	9.702092	Up	kallikrein related peptidase 11
A_32_P416 04	F5	1.535516	7.35E- 06	0.001 85	9.700312	Up	coagulation factor V
A_33_P336 7196	CNTNAP 2	1.605568	7.42E- 06	0.001 856	9.688935	Up	contactin associated protein-like 2
A_33_P321 5640	PI16	1.290311	7.68E- 06	0.001 911	9.645508	Up	peptidase inhibitor 16
A_24_P397 255	ENPP6	1.594549	8.75E- 06	0.002 116	9.485334	Up	ectonucleotidepyrophosphatase/phosphodiesterase 6
A_33_P321 7437	GBP6	1.036074	9.63E- 06	0.002 289	9.369347	Up	guanylate binding protein family member 6
A_33_P335 1264	OVOL3	1.050788	9.78E- 06	0.002 311	9.351444	Up	ovo like zinc finger 3
A_23_P112 327	OBP2A	1.350445	1E-05	0.002 352	9.323343	Up	odorant binding protein 2A
A_23_P752 83	RBP4	1.726183	1.04E- 05	0.002 42	9.282412	Up	retinol binding protein 4
A_33_P325 2048	PPP1R27	1.719928	1.05E- 05	0.002 445	9.263686	Up	protein phosphatase 1 regulatory subunit 27
A_23_P202 053	ITIH2	1.137137	1.1E-05	0.002 526	9.21207	Up	inter-alpha-trypsin inhibitor heavy chain 2
A_23_P328 740	NEURL3	1.378209	1.16E- 05	0.002 615	9.144984	Up	neuralized E3 ubiquitin protein ligase 3
A_23_P416 774	CLIC5	1.122275	1.19E- 05	0.002 615	9.114478	Up	chloride intracellular channel 5
A_24_P130 24	SLC16A1 2	1.528046	1.2E-05	0.002 615	9.110565	Up	solute carrier family 16 member 12

A_33_P328 7472	PPP1R27	1.441994	1.23E- 05	0.002 663	9.081115	Up	protein phosphatase 1 regulatory subunit 27
A_23_P697 38	RASL11 B	1.2602	1.25E- 05	0.002 678	9.056703	Up	RAS like family 11 member B
A_24_P339 429	KCNJ12	1.592216	1.33E- 05	0.002 794	8.983141	Up	potassium voltage-gated channel subfamily J member 12
A_33_P342 0757	AQP4	1.278225	1.34E- 05	0.002 794	8.978342	Up	aquaporin 4
A_23_P159 335	CD8B	0.96392	1.37E- 05	0.002 835	8.949807	Up	CD8b molecule
A_23_P249 03	P2RY2	0.995063	1.44E- 05	0.002 894	8.898402	Up	purinergic receptor P2Y2
A_23_P626 07	IL22RA1	1.500212	1.48E- 05	0.002 928	8.862964	Up	interleukin 22 receptor subunit alpha 1
A_33_P330 4533	RNF207	1.223159	1.67E- 05	0.003 222	8.722137	Up	ring finger protein 207
A_32_P348 44	ADAMT S18	1.549798	1.79E- 05	0.003 372	8.645032	Up	ADAM metalloproteinase with thrombospondin type 1 motif 18
A_23_P389 897	NGFR	1.465734	1.8E-05	0.003 372	8.640153	Up	nerve growth factor receptor
A_23_P501 193	KCNJ16	1.649162	1.81E- 05	0.003 381	8.632189	Up	potassium voltage-gated channel subfamily J member 16
A_23_P501 007	EFEMP1	0.963358	1.86E- 05	0.003 434	8.604817	Up	EGF containing fibulin like extracellular matrix protein 1
A_33_P335 3027	CHN2	0.959558	1.92E- 05	0.003 523	8.566558	Up	chimerin 2
A_23_P471 81	GPHA2	1.258662	1.95E- 05	0.003 562	8.549199	Up	glycoprotein hormone alpha 2
A_33_P323 2655	GHRHR	1.32053	2.15E- 05	0.003 813	8.440624	Up	growth hormone releasing hormone receptor
A_24_P280 333	KRT40	1.503725	2.2E-05	0.003 863	8.416969	Up	keratin 40
A_32_P218 355	C6orf132	1.411295	2.3E-05	0.003 978	8.367301	Up	chromosome 6 open reading frame 132
A_23_P402 765	NRAP	1.811676	2.31E- 05	0.003 978	8.362425	Up	nebulin related anchoring protein
A_33_P325 0173	IQCJ	1.201705	2.32E- 05	0.003 978	8.357898	Up	IQ motif containing J
A_24_P726 336	PHACTR 2	0.937904	2.47E- 05	0.004 2	8.289587	Up	phosphatase and actin regulator 2
A_33_P331 9880	EVC2	1.047398	2.51E- 05	0.004 259	8.269911	Up	EvCiliary complex subunit 2
A_33_P335 5508	FOXL2	1.219617	2.54E- 05	0.004 275	8.257205	Up	forkhead box L2
A_24_P385 732	SLC51A	1.228643	2.6E-05	0.004 347	8.234886	Up	solute carrier family 51 alpha subunit
A_19_P003 20141	NR2F1- AS1	1.049334	2.63E- 05	0.004 388	8.220529	Up	NR2F1 antisense RNA 1

A_23_P166 269	FAM3B	1.658734	2.81E- 05	0.004 546	8.14888	Up	family with sequence similarity 3 member B
A_24_P236 251	DLK1	1.084201	2.9E-05	0.004 667	8.116486	Up	delta like non-canonical Notch ligand 1
A_24_P503 68	BLID	0.934055	3.01E- 05	0.004 764	8.075302	Up	BH3-like motif containing, cell death inducer
A_23_P431 97	CALB1	1.816152	3.01E- 05	0.004 764	8.074442	Up	calbindin 1
A_33_P334 6766	UGT2A1	1.919609	3.08E- 05	0.004 817	8.050798	Up	UDP glucuronosyltransferase family 2 member A1 complex locus
A_19_P003 22810	#N/A	0.976388	3.19E- 05	0.004 888	8.012101	Up	NA
A_33_P327 9590	OGN	1.376373	3.24E- 05	0.004 921	7.998292	Up	osteoglycin
A_23_P212 508	TF	1.475208	3.38E- 05	0.005 067	7.952258	Up	transferrin
A_24_P655 849	SMAD9	1.578849	3.42E- 05	0.005 08	7.939515	Up	SMAD family member 9
A_19_P008 01466	LINC005 98	1.475444	3.45E- 05	0.005 08	7.930302	Up	long intergenic non-protein coding RNA 598
A_23_P401 055	SOX2	1.69957	3.47E- 05	0.005 086	7.925451	Up	SRY-box 2
A_23_P500 010	KLK12	2.06498	3.51E- 05	0.005 129	7.913013	Up	kallikrein related peptidase 12
A_24_P882 732	KRT17P1	1.106234	3.67E- 05	0.005 299	7.864481	Up	keratin 17 pseudogene 1
A_23_P170 649	SBSPON	1.314417	3.84E- 05	0.005 496	7.817453	Up	somatomedin B and thrombospondin type 1 domain containing
A_33_P334 5534	KRT14	1.187608	3.91E- 05	0.005 55	7.798667	Up	keratin 14
A_32_P930 375	DLGAP2	1.302276	3.98E- 05	0.005 631	7.780067	Up	DLG associated protein 2
A_23_P110 319	CWH43	1.018626	4.1E-05	0.005 709	7.750289	Up	cell wall biogenesis 43 C-terminal homolog
A_23_P334 798	LRRC2	0.953096	4.18E- 05	0.005 713	7.731307	Up	leucine rich repeat containing 2
A_33_P334 7397	AMOT	1.359913	4.28E- 05	0.005 822	7.705274	Up	angiomin
A_19_P003 18158	#N/A	1.004498	4.39E- 05	0.005 857	7.67955	Up	NA
A_33_P334 0981	LINC005 98	1.256571	4.45E- 05	0.005 905	7.666631	Up	long intergenic non-protein coding RNA 598
A_33_P334 0580	ZNF385C	0.953391	4.66E- 05	0.006 119	7.618782	Up	zinc finger protein 385C
A_23_P425 681	CCK	1.622521	4.79E- 05	0.006 272	7.590454	Up	cholecystokinin
A_23_P632 09	HSD11B 1	1.715094	4.83E- 05	0.006 272	7.583273	Up	hydroxysteroid 11-beta dehydrogenase 1

A_23_P971 1	HS3ST4	1.269685	4.84E- 05	0.006 272	7.581112	Up	heparansulfate-glucosamine 3-sulfotransferase 4
A_24_P691 826	WFDC21 P	0.992875	5.11E- 05	0.006 53	7.524302	Up	WAP four-disulfide core domain 21, pseudogene
A_19_P008 07452	#N/A	1.104671	5.13E- 05	0.006 53	7.520302	Up	NA
A_33_P326 7375	SGCD	1.257873	5.28E- 05	0.006 685	7.492188	Up	sarcoglycan delta
A_33_P332 9088	PRSS8	1.069842	5.57E- 05	0.006 95	7.439292	Up	protease, serine 8
A_33_P324 9229	OR3A4P	1.184305	5.63E- 05	0.006 981	7.427986	Up	olfactory receptor family 3 subfamily A member 4 pseudogene
A_32_P851 06	C6orf118	1.123262	5.67E- 05	0.007 016	7.420158	Up	chromosome 6 open reading frame 118
A_19_P008 04546	MIR503H G	2.046985	6.03E- 05	0.007 246	7.359333	Up	MIR503 host gene
A_33_P330 3810	LAD1	1.154517	6.1E-05	0.007 305	7.348491	Up	ladinin 1
A_33_P336 9098	MYL10	1.181726	6.32E- 05	0.007 474	7.311978	Up	myosin light chain 10
A_32_P173 662	CRISP2	1.011029	6.4E-05	0.007 486	7.299977	Up	cysteine rich secretory protein 2
A_33_P333 8698	IHH	1.292631	6.61E- 05	0.007 644	7.268026	Up	indian hedgehog
A_24_P395 814	CGB3	1.492903	6.68E- 05	0.007 644	7.257466	Up	chorionic gonadotropin beta subunit 3
A_33_P330 7475	AC12950 7.4	0.949086	7.03E- 05	0.007 924	7.207806	Up	NA
A_23_P236 39	MCOLN2	0.940979	7.22E- 05	0.008 078	7.182496	Up	mucolipin 2
A_32_P206 839	LOC1002 88911	1.265982	7.31E- 05	0.008 125	7.169161	Up	uncharacterized LOC100288911
A_32_P232 214	TRABD2 B	1.388547	7.41E- 05	0.008 172	7.156892	Up	TraB domain containing 2B
A_23_P241 49	SLC39A1 2	1.443756	7.43E- 05	0.008 172	7.153512	Up	solute carrier family 39 member 12
A_23_P565 78	VIT	1.322911	7.57E- 05	0.008 3	7.135859	Up	vitrin
A_23_P832 98	PRRX2	1.098103	7.63E- 05	0.008 328	7.128004	Up	paired related homeobox 2
A_23_P145 724	PPP1R17	1.564573	7.66E- 05	0.008 336	7.124207	Up	protein phosphatase 1 regulatory subunit 17
A_23_P121 28	TSHB	1.120155	7.89E- 05	0.008 5	7.095106	Up	thyroid stimulating hormone beta
A_23_P537 63	RUBCNL	1.059222	8.04E- 05	0.008 513	7.077398	Up	RUN and cysteine rich domain containing beclin 1 interacting protein like
A_23_P314 07	AGR2	1.36206	8.09E- 05	0.008 524	7.071021	Up	anterior gradient 2, protein disulphide isomerase family member

A_32_P882 40	KBTBD1 2	1.043668	8.24E- 05	0.008 575	7.053992	Up	kelch repeat and BTB domain containing 12
A_33_P329 4317	LINC021 82	1.330276	8.24E- 05	0.008 575	7.053473	Up	long intergenic non-protein coding RNA 2182
A_24_P120 934	GADD45 G	1.025983	8.38E- 05	0.008 626	7.037193	Up	growth arrest and DNA damage inducible gamma
A_33_P322 8460	FXYP3	0.948671	8.46E- 05	0.008 651	7.028524	Up	FXYP domain containing ion transport regulator 3
A_32_P116 606	LIX1	1.396555	8.51E- 05	0.008 656	7.022811	Up	limb and CNS expressed 1
A_33_P322 3898	PRSS45	1.185061	8.8E-05	0.008 806	6.991076	Up	protease, serine 45
A_23_P164 057	MFAP4	1.358535	8.97E- 05	0.008 914	6.972708	Up	microfibrillar associated protein 4
A_23_P365 31	TSPAN8	1.284499	9.06E- 05	0.008 981	6.963243	Up	tetraspanin 8
A_24_P170 983	ESPNL	0.967629	9.17E- 05	0.009 027	6.951781	Up	espin-like
A_33_P333 0791	LOC4012 20	1.563068	9.25E- 05	0.009 087	6.94327	Up	uncharacterized LOC401220
A_32_P133 072	SPON1	1.725709	9.31E- 05	0.009 105	6.936563	Up	spondin 1
A_33_P388 4230	NFIX	0.941992	9.37E- 05	0.009 105	6.930503	Up	nuclear factor I X
A_33_P327 5315	CELF2- AS1	0.940083	9.96E- 05	0.009 568	6.87276	Up	CELF2 antisense RNA 1
A_23_P320 225	EVC2	0.975087	0.00010 2	0.009 726	6.850414	Up	EvCiliary complex subunit 2
A_24_P365 975	COL8A2	1.028966	0.00010 3	0.009 729	6.840562	Up	collagen type VIII alpha 2 chain
A_33_P341 9006	GNRHR	1.703721	0.00010 5	0.009 848	6.820505	Up	gonadotropin releasing hormone receptor
A_23_P510 02	SULT1C 2	1.23956	0.00010 6	0.009 854	6.817742	Up	sulfotransferase family 1C member 2
A_19_P003 21190	LINC016 06	1.082379	0.00010 9	0.010 008	6.788943	Up	long intergenic non-protein coding RNA 1606
A_23_P838 38	CA8	1.224183	0.00011	0.010 051	6.778619	Up	carbonic anhydrase 8
A_24_P168 925	CHRD1	1.561708	0.00011 1	0.010 065	6.77067	Up	chordin like 1
A_24_P926 960	MEGF6	1.23387	0.00011 6	0.010 291	6.733096	Up	multiple EGF like domains 6
A_23_P537 0	RPRM	1.644262	0.00011 8	0.010 371	6.717833	Up	reprimin, TP53 dependent G2 arrest mediator homolog
A_23_P129 133	OCA2	1.181096	0.00011 8	0.010 371	6.714341	Up	OCA2 melanosomaltransmembrane protein
A_23_P146 855	MPPED1	1.224199	0.00011 9	0.010 437	6.706512	Up	metallophosphoesterase domain containing 1

A_23_P167 493	CARTPT	1.348534	0.00012 3	0.010 605	6.676755	Up	CART prepropeptide
A_23_P381 351	CSH1	1.395394	0.00012 3	0.010 605	6.676545	Up	chorionic somatomammotropin hormone 1
A_23_P252 462	GALNT9	0.972962	0.00012 6	0.010 73	6.651804	Up	polypeptide N-acetylgalactosaminyltransferase 9
A_23_P829 90	OGN	1.458835	0.00012 9	0.010 881	6.628807	Up	osteoglycin
A_32_P843 69	FAM153 B	1.100172	0.00013 1	0.010 897	6.618167	Up	family with sequence similarity 153 member B
A_33_P325 2394	GADD45 G	1.041451	0.00013 2	0.010 919	6.612967	Up	growth arrest and DNA damage inducible gamma
A_23_P209 978	VSNL1	1.042135	0.00013 4	0.011 037	6.599626	Up	visinin like 1
A_33_P323 1357	KISS1R	1.447717	0.00013 4	0.011 05	6.596694	Up	KISS1 receptor
A_23_P212 830	FGFR3	1.121697	0.00013 5	0.011 086	6.586685	Up	fibroblast growth factor receptor 3
A_33_P368 0789	PROSER 2-AS1	1.087472	0.00013 7	0.011 165	6.575783	Up	PROSER2 antisense RNA 1
A_33_P334 1499	WNT5A	1.252562	0.00013 7	0.011 165	6.574844	Up	Wnt family member 5A
A_23_P357 881	CD8B	1.210532	0.00013 8	0.011 213	6.569217	Up	CD8b molecule
A_23_P811 03	SFRP2	1.416148	0.00015 2	0.011 906	6.483851	Up	secreted frizzled related protein 2
A_23_P927 30	HSPB3	1.413693	0.00016 2	0.012 387	6.426669	Up	heat shock protein family B (small) member 3
A_33_P330 6267	PAX6	1.112687	0.00016 3	0.012 452	6.416123	Up	paired box 6
A_24_P345 451	CYBRD1	1.038518	0.00016 6	0.012 56	6.402632	Up	cytochrome b reductase 1
A_33_P322 8450	FXYP3	1.266019	0.00016 9	0.012 624	6.387741	Up	FXYP domain containing ion transport regulator 3
A_33_P348 0395	FLJ30901	1.022724	0.00017 2	0.012 732	6.371786	Up	uncharacterized protein FLJ30901
A_23_P138 938	PGR	1.816923	0.00017 5	0.012 856	6.35462	Up	progesterone receptor
A_19_P008 03588	#N/A	1.00275	0.00017 6	0.012 892	6.349834	Up	NA
A_23_P118 065	HSD17B 2	1.040626	0.00018 3	0.013 153	6.316724	Up	hydroxysteroid 17-beta dehydrogenase 2
A_32_P160 563	OPCML	1.365608	0.00018 5	0.013 26	6.308043	Up	opioid binding protein/cell adhesion molecule like
A_23_P317 760	FAM217 A	0.982831	0.00018 9	0.013 446	6.284687	Up	family with sequence similarity 217 member A
A_23_P763 32	RFX4	1.06413	0.00019 3	0.013 638	6.266747	Up	regulatory factor X4

A_23_P428 11	AGR3	1.186616	0.00019 6	0.013 804	6.253129	Up	anterior gradient 3, protein disulphide isomerase family member
A_24_P940 644	SLIT1	1.673787	0.00020 1	0.013 821	6.233263	Up	slit guidance ligand 1
A_23_P268 47	SOX9	1.113591	0.00020 4	0.013 95	6.220577	Up	SRY-box 9
A_33_P335 1681	DEUP1	1.483472	0.00021	0.014 139	6.195544	Up	deuterosome assembly protein 1
A_23_P344 408	CSHL1	1.2167	0.00021 5	0.014 376	6.173456	Up	chorionic somatomammotropin hormone like 1
A_32_P111 639	CHST9	1.181236	0.00022 2	0.014 537	6.146767	Up	carbohydrate sulfotransferase 9
A_33_P324 8405	NRK	1.148294	0.00022 3	0.014 561	6.141927	Up	Nik related kinase
A_33_P324 5238	SULT1C 2	1.01799	0.00022 6	0.014 718	6.130746	Up	sulfotransferase family 1C member 2
A_23_P750 63	DYDC2	1.077759	0.00023	0.014 886	6.113345	Up	DPY30 domain containing 2
A_33_P341 0121	CFAP74	1.034589	0.00023 4	0.015 035	6.098098	Up	cilia and flagella associated protein 74
A_23_P396 05	SULT1C 4	1.072548	0.00023 6	0.015 056	6.090655	Up	sulfotransferase family 1C member 4
A_23_P251 132	SNTG2	1.884616	0.00023 7	0.015 081	6.086334	Up	syntrophin gamma 2
A_33_P342 3420	ZNF750	1.064614	0.00023 9	0.015 087	6.082126	Up	zinc finger protein 750
A_33_P325 8046	TAC4	1.141906	0.00024 2	0.015 181	6.071276	Up	tachykinin 4 (hemokinin)
A_23_P136 116	AGMO	1.074353	0.00024 2	0.015 181	6.070326	Up	alkylglycerolmonooxygenase
A_33_P331 7253	PTER	1.057567	0.00024 7	0.015 377	6.050692	Up	phosphotriesterase related
A_23_P431 139	CTRB1	1.081155	0.00024 9	0.015 428	6.043694	Up	chymotrypsinogen B1
A_23_P182 82	DLEC1	1.106803	0.00025 5	0.015 611	6.024776	Up	deleted in lung and esophageal cancer 1
A_23_P311 24	COL21A 1	1.493919	0.00025 8	0.015 701	6.015768	Up	collagen type XXI alpha 1 chain
A_19_P003 20685	LINC018 52	0.977693	0.00025 8	0.015 701	6.013804	Up	long intergenic non-protein coding RNA 1852
A_19_P008 05833	ATF7IP2	1.079212	0.00025 9	0.015 703	6.010456	Up	activating transcription factor 7 interacting protein 2
A_33_P324 9534	NEFM	1.748709	0.00026 6	0.015 898	5.989561	Up	neurofilament medium
A_19_P003 16370	AC00248 0.2	1.245626	0.00027 7	0.016 233	5.953808	Up	NA
A_23_P124 619	S100A14	1.025455	0.00027 8	0.016 296	5.94929	Up	S100 calcium binding protein A14

A_33_P335 4414	AOX1	1.169692	0.00028 3	0.016 493	5.934365	Up	aldehyde oxidase 1
A_32_P158 966	KLRF1	0.936194	0.00028 5	0.016 572	5.92911	Up	killer cell lectin like receptor F1
A_33_P335 2906	KCNIP4- IT1	1.113185	0.00028 9	0.016 663	5.916334	Up	KCNIP4 intronic transcript 1
A_33_P342 0224	ENTPD8	0.994821	0.00029 6	0.016 851	5.896821	Up	ectonucleoside triphosphate diphosphohydrolase 8
A_23_P363 255	CCDC68	1.63892	0.00029 8	0.016 851	5.892889	Up	coiled-coil domain containing 68
A_33_P329 7562	IRX2	0.941375	0.00029 8	0.016 851	5.89031	Up	iroquoishomeobox 2
A_33_P336 8646	CNKSR3	1.102873	0.00030 3	0.016 944	5.878301	Up	CNKSR family member 3
A_23_P777 31	CRYM	0.956236	0.00030 9	0.017 112	5.860011	Up	crystallin mu
A_33_P329 8810	FFAR3	1.175134	0.00031 1	0.017 186	5.855259	Up	free fatty acid receptor 3
A_33_P342 3874	MYZAP	1.382209	0.00031 5	0.017 267	5.845554	Up	myocardial zonulaadherens protein
A_23_P815 90	PDE6A	1.325565	0.00031 7	0.017 267	5.840506	Up	phosphodiesterase 6A
A_23_P118 615	ABCA8	1.154317	0.00033 5	0.017 778	5.793871	Up	ATP binding cassette subfamily A member 8
A_19_P003 17324	#N/A	1.111694	0.00033 6	0.017 778	5.791414	Up	NA
A_23_P122 924	INHBA	0.971104	0.00033 6	0.017 778	5.790115	Up	inhibin beta A subunit
A_33_P326 0125	LDLRAD 2	1.408377	0.00033 7	0.017 778	5.78717	Up	low density lipoprotein receptor class A domain containing 2
A_33_P328 1667	CNTNAP 3	0.947904	0.00033 9	0.017 833	5.781984	Up	contactin associated protein-like 3
A_32_P843 73	FAM153 C	1.604174	0.00035 3	0.018 266	5.74907	Up	family with sequence similarity 153, member C, pseudogene
A_33_P384 7514	C6orf141	1.000679	0.00035 3	0.018 268	5.74794	Up	chromosome 6 open reading frame 141
A_24_P341 55	RUNX1	1.245442	0.00036 43	0.018	5.732384	Up	runt related transcription factor 1
A_33_P335 4429	TRIM71	0.994075	0.00036 7	0.018 648	5.715808	Up	tripartite motif containing 71
A_23_P100 642	PNMT	1.853774	0.00036 7	0.018 648	5.715693	Up	phenylethanolamine N-methyltransferase
A_23_P101 72	PRSS50	1.758832	0.00037 72	0.018	5.708555	Up	protease, serine 50
A_24_P142 503	SLC47A1	1.008499	0.00037 7	0.018 89	5.69512	Up	solute carrier family 47 member 1
A_33_P328 9371	PHACTR 3	1.093945	0.00037 8	0.018 958	5.690962	Up	phosphatase and actin regulator 3

A_33_P342 1118	IL20RA	1.257448	0.00038 6	0.019 195	5.675376	Up	interleukin 20 receptor subunit alpha
A_23_P137 573	LEFTY2	1.262989	0.00038 9	0.019 237	5.667495	Up	left-right determination factor 2
A_23_P113 777	ITGBL1	1.325051	0.00039 5	0.019 372	5.654497	Up	integrin subunit beta like 1
A_33_P327 4084	RHBDL3	1.138528	0.00040 8	0.019 769	5.628682	Up	rhomboid like 3
A_23_P207 194	GH1	1.18446	0.00041 3	0.019 911	5.618101	Up	growth hormone 1
A_24_P943 781	CPED1	1.074957	0.00041 4	0.019 933	5.616267	Up	cadherin like and PC-esterase domain containing 1
A_33_P330 7500	STRA6	1.085733	0.00041 6	0.020 011	5.612103	Up	stimulated by retinoic acid 6
A_33_P338 0642	FRAS1	1.087367	0.00041 8	0.020 041	5.608323	Up	Fraser extracellular matrix complex subunit 1
A_33_P339 4833	FOXL2N B	1.814458	0.00041 8	0.020 041	5.608183	Up	FOXL2 neighbor
A_32_P780 817	CT45A1	1.206224	0.00042 9	0.020 315	5.586514	Up	cancer/testis antigen family 45 member A1
A_24_P513 75	#N/A	1.182894	0.00043 2	0.020 315	5.58114	Up	NA
A_33_P328 9121	C2orf40	1.024588	0.00043 3	0.020 315	5.579578	Up	chromosome 2 open reading frame 40
A_23_P500 501	FGFR3	1.024692	0.00043 4	0.020 315	5.578659	Up	fibroblast growth factor receptor 3
A_33_P325 2281	EYA4	1.461336	0.00044 41	0.020	5.566737	Up	EYA transcriptional coactivator and phosphatase 4
A_33_P341 5247	TNFRSF 14-AS1	1.033693	0.00044 3	0.020 438	5.560127	Up	TNFRSF14 antisense RNA 1
A_33_P326 8783	AMZ1	1.291381	0.00044 4	0.020 438	5.558504	Up	archaelysin family metalloproteinase 1
A_19_P003 16453	AL03338 4.1	1.046682	0.00044 6	0.020 479	5.556002	Up	NA
A_33_P327 5846	CACNA1 A	1.199152	0.00046 4	0.020 678	5.524021	Up	calcium voltage-gated channel subunit alpha1 A
A_32_P202 013	FAM196 A	1.104724	0.00046 5	0.020 688	5.521658	Up	family with sequence similarity 196 member A
A_24_P330 518	CA12	1.139863	0.00046 9	0.020 745	5.51508	Up	carbonic anhydrase 12
A_24_P824 66	GAS7	1.085699	0.00047 745	0.020	5.513526	Up	growth arrest specific 7
A_24_P719 04	HPGD	1.396742	0.00047 2	0.020 815	5.509054	Up	hydroxyprostaglandin dehydrogenase 15- (NAD)
A_19_P003 16914	AL16040 8.4	1.192461	0.00048 964	0.020	5.494857	Up	NA
A_23_P233	FMO5	1.160289	0.00048 9	0.021 19	5.480019	Up	flavin containing monooxygenase 5

A_23_P150 555	SCGB1D 2	1.294842	0.00049 3	0.021 282	5.473241	Up	secretoglobin family 1D member 2
A_23_P392 51	PLIN5	1.34129	0.00049 4	0.021 282	5.472734	Up	perilipin 5
A_24_P498 652	KCNA1	1.463762	0.00049 9	0.021 368	5.463722	Up	potassium voltage-gated channel subfamily A member 1
A_32_P169 179	MSX2P1	1.197032	0.00051 4	0.021 729	5.440466	Up	mshhomeobox 2 pseudogene 1
A_23_P415 974	ALDOB	1.370957	0.00051 7	0.021 761	5.436053	Up	aldolase, fructose-bisphosphate B
A_23_P152 3	RHOD	1.601066	0.00052 3	0.021 814	5.426643	Up	ras homolog family member D
A_33_P327 3777	GJB7	1.405572	0.00052 4	0.021 814	5.42471	Up	gap junction protein beta 7
A_23_P118 894	PRR15L	0.938926	0.00052 9	0.021 921	5.417484	Up	proline rich 15 like
A_23_P156 025	IRX2	1.76183	0.00053 7	0.022 073	5.404917	Up	iroquoishomeobox 2
A_23_P205 959	ALDH1A 3	1.435514	0.00054 5	0.022 276	5.393236	Up	aldehyde dehydrogenase 1 family member A3
A_23_P319 859	EYA2	1.179968	0.00054 7	0.022 323	5.389659	Up	EYA transcriptional coactivator and phosphatase 2
A_23_P667 98	KRT19	0.946886	0.00055 5	0.022 454	5.378419	Up	keratin 19
A_19_P008 00509	#N/A	1.027445	0.00055 6	0.022 454	5.37672	Up	NA
A_23_P134 914	LY6H	1.829315	0.00055 9	0.022 496	5.373259	Up	lymphocyte antigen 6 family member H
A_33_P335 8750	MYBPH L	1.079067	0.00055 9	0.022 496	5.372754	Up	myosin binding protein H like
A_23_P124 642	RASGRP 1	0.942131	0.00056 3	0.022 525	5.367106	Up	RAS guanyl releasing protein 1
A_24_P216 014	GH2	2.09163	0.00057 2	0.022 752	5.353925	Up	growth hormone 2
A_23_P304 489	FAM19A 5	1.339382	0.00057 5	0.022 762	5.350333	Up	family with sequence similarity 19 member A5, C-C motif chemokine like
A_23_P131 935	FERMT1	1.051911	0.00058 7	0.023 011	5.333832	Up	fermitin family member 1
A_33_P333 9138	RPRML	0.963599	0.00059 7	0.023 299	5.319449	Up	reprimin like
A_33_P353 3325	ASXL3	1.030682	0.00060 2	0.023 401	5.313045	Up	additional sex combs like 3, transcriptional regulator
A_19_P008 01490	LINC025 62	1.317451	0.00060 8	0.023 525	5.305686	Up	long intergenic non-protein coding RNA 2562
A_33_P341 5888	TEPP	1.140263	0.00061 3	0.023 662	5.298433	Up	testis, prostate and placenta expressed
A_23_P216 18	PDZRN3	1.396019	0.00061 5	0.023 699	5.296458	Up	PDZ domain containing ring finger 3

A_33_P334 0199	AC09657 7.1	0.958785	0.00062 3	0.023 872	5.286379	Up	NA
A_24_P469 11	KCNS2	1.033156	0.00063 2	0.024 042	5.275064	Up	potassium voltage-gated channel modifier subfamily S member 2
A_24_P561 341	ALKAL2	1.48007	0.00063 7	0.024 11	5.268559	Up	ALK and LTK ligand 2
A_33_P328 2005	VANGL2	1.487347	0.00064 5	0.024 339	5.25835	Up	VANGL planar cell polarity protein 2
A_33_P327 7890	WASIR1	0.992418	0.00064 8	0.024 395	5.255051	Up	WASH and IL9R antisense RNA 1
A_33_P335 3471	GRIK1- AS1	0.971052	0.00065 4	0.024 51	5.247831	Up	GRIK1 antisense RNA 1
A_32_P225 816	PRDM16	1.315384	0.00065 7	0.024 583	5.244556	Up	PR/SET domain 16
A_23_P148 609	PLAC1	0.962204	0.00065 8	0.024 583	5.242831	Up	placenta specific 1
A_33_P327 1121	SH3BP4	1.281724	0.00066	0.024 583	5.240632	Up	SH3 domain binding protein 4
A_23_P217 379	COL4A6	1.479885	0.00066	0.024 583	5.239941	Up	collagen type IV alpha 6 chain
A_33_P328 5965	NEURO D1	1.700584	0.00066 2	0.024 605	5.238558	Up	neuronal differentiation 1
A_33_P328 8844	IL6R	1.168827	0.00066 3	0.024 62	5.236673	Up	interleukin 6 receptor
A_23_P312 271	TEX26	1.26024	0.00066 3	0.024 62	5.236465	Up	testis expressed 26
A_33_P329 8326	FSHB	2.112742	0.00066 4	0.024 62	5.235787	Up	follicle stimulating hormone beta subunit
A_23_P207 154	CSH2	1.34608	0.00066 4	0.024 62	5.235296	Up	chorionic somatomammotropin hormone 2
A_33_P332 1382	CNTNAP 3B	1.057166	0.00067 7	0.024 843	5.220864	Up	contactin associated protein like 3B
A_23_P159 893	CHRD1	1.077118	0.00067 7	0.024 843	5.220658	Up	chordin like 1
A_33_P351 9250	NWD1	1.146885	0.00068 7	0.025 088	5.208883	Up	NACHT and WD repeat domain containing 1
A_33_P333 3158	CPXM2	1.235098	0.00069 8	0.025 302	5.196075	Up	carboxypeptidase X, M14 family member 2
A_33_P328 3122	WWC2	0.99086	0.00071 6	0.025 673	5.176277	Up	WW and C2 domain containing 2
A_24_P254 506	PAGE4	1.146619	0.00071 6	0.025 673	5.176022	Up	PAGE family member 4
A_23_P136 777	APOD	1.229853	0.00071 7	0.025 673	5.174762	Up	apolipoprotein D
A_23_P309 83	GJB7	1.662038	0.00073 9	0.026 039	5.151262	Up	gap junction protein beta 7
A_33_P327 3490	TRBV20 OR9-2	0.942031	0.00075 5	0.026 226	5.134727	Up	T-cell receptor beta variable 20/OR9-2 (non- functional)

A_23_P232 92	RXRG	1.363857	0.00076 4	0.026 479	5.125969	Up	retinoid X receptor gamma
A_23_P340 263	RNF175	1.370623	0.00077 2	0.026 711	5.117906	Up	ring finger protein 175
A_23_P398 189	IGSF11	1.162188	0.00077 6	0.026 797	5.113508	Up	immunoglobulin superfamily member 11
A_32_P187 571	SCN2B	1.633253	0.00078 6	0.026 893	5.103165	Up	sodium voltage-gated channel beta subunit 2
A_23_P125 680	TMEM25 5A	1.375195	0.00079 1	0.026 979	5.098126	Up	transmembrane protein 255A
A_23_P143 348	OVOL2	1.504252	0.00079 2	0.026 979	5.097858	Up	ovo like zinc finger 2
A_32_P607 16	CCDC15 8	1.039562	0.00079 3	0.026 979	5.096324	Up	coiled-coil domain containing 158
A_32_P141 418	ARMC4	1.39728	0.0008 047	0.027	5.090047	Up	armadillo repeat containing 4
A_33_P323 6676	C9orf152	1.121102	0.00083 1	0.027 66	5.060268	Up	chromosome 9 open reading frame 152
A_23_P381 746	ASXL3	1.378008	0.00086	0.028 195	5.033829	Up	additional sex combs like 3, transcriptional regulator
A_23_P114 713	CYP4B1	1.134734	0.00087 8	0.028 48	5.018238	Up	cytochrome P450 family 4 subfamily B member 1
A_23_P392 317	DLGAP2	1.280103	0.00087 9	0.028 513	5.016681	Up	DLG associated protein 2
A_33_P332 0197	ALKAL2	1.220161	0.00088 9	0.028 637	5.008349	Up	ALK and LTK ligand 2
A_23_P110 462	PCDHB1	0.960895	0.00091 3	0.029 158	4.987739	Up	protocadherin beta 1
A_23_P150 595	TPH1	0.948973	0.00092 4	0.029 301	4.978952	Up	tryptophan hydroxylase 1
A_23_P154 037	AOX1	1.062065	0.00094 4	0.029 642	4.96208	Up	aldehyde oxidase 1
A_23_P864 70	CH25H	0.971876	0.00096 6	0.030 028	4.944873	Up	cholesterol 25-hydroxylase
A_33_P328 3824	SLC39A8	1.133024	0.00098	0.030 38	4.93375	Up	solute carrier family 39 member 8
A_23_P143 526	S100B	1.144173	0.00099 9	0.030 653	4.91915	Up	S100 calcium binding protein B
A_33_P329 2646	MALRD1	1.208959	0.00100 4	0.030 7	4.915254	Up	MAM and LDL receptor class A domain containing 1
A_32_P348 26	B3GALT 5-AS1	1.541162	0.00101 3	0.030 874	4.908374	Up	B3GALT5 antisense RNA 1
A_33_P331 9022	CLEC9A	0.985478	0.00101 4	0.030 874	4.907676	Up	C-type lectin domain containing 9A
A_24_P190 472	SLPI	1.126312	0.00102 3	0.031 057	4.900711	Up	secretory leukocyte peptidase inhibitor
A_32_P491 99	PGR	1.356832	0.00105 1	0.031 385	4.880628	Up	progesterone receptor

A_33_P335 2467	SSTR2	1.022938	0.00105 1	0.031 385	4.880106	Up	somatostatin receptor 2
A_19_P003 21962	AP00047 3.1	1.1851	0.00106 3	0.031 601	4.871734	Up	NA
A_24_P236 235	FLRT2	0.96055	0.00110 2	0.032 397	4.844468	Up	fibronectinleucine rich transmembrane protein 2
A_33_P323 2498	C2orf71	0.973752	0.00111 5	0.032 517	4.835307	Up	chromosome 2 open reading frame 71
A_23_P133 1	COL13A 1	1.167848	0.00113 9	0.032 752	4.819329	Up	collagen type XIII alpha 1 chain
A_33_P337 3259	CACNA2 D3	1.461394	0.00115 1	0.032 92	4.811744	Up	calcium voltage-gated channel auxiliary subunit alpha2delta 3
A_23_P736 32	NR0B1	1.455678	0.00115 7	0.032 92	4.807777	Up	nuclear receptor subfamily 0 group B member 1
A_23_P210 92	CALB2	1.452992	0.00117 5	0.033 199	4.796121	Up	calbindin 2
A_23_P146 274	STMN2	1.55252	0.00119 2	0.033 466	4.785019	Up	stathmin 2
A_23_P127 781	SCGB1D 1	1.242168	0.00119 3	0.033 466	4.784787	Up	secretoglobin family 1D member 1
A_23_P213 336	FGF1	0.986971	0.00120 5	0.033 585	4.777304	Up	fibroblast growth factor 1
A_23_P482 29	KCNA1	1.237757	0.00121 8	0.033 83	4.769327	Up	potassium voltage-gated channel subfamily A member 1
A_23_P110 052	FOXL2	1.411075	0.00126 5	0.034 5	4.740819	Up	forkhead box L2
A_23_P308 483	MAP3K1 5	1.119098	0.00127 6	0.034 639	4.734086	Up	mitogen-activated protein kinase kinasekinase 15
A_33_P330 4082	AC10087 2.1	1.03319	0.00127 7	0.034 639	4.733848	Up	NA
A_33_P322 7269	GATA3- AS1	1.53053	0.00129 6	0.034 887	4.722827	Up	GATA3 antisense RNA 1
A_24_P326 491	MKX	1.009479	0.00129 8	0.034 889	4.721501	Up	mohawkhomeobox
A_23_P434 398	TXLNB	1.116641	0.00134 6	0.035 471	4.694487	Up	taxilin beta
A_33_P370 9150	T	0.957229	0.00135 4	0.035 473	4.690142	Up	T brachyury transcription factor
A_33_P352 7317	LOC1486 38	1.189409	0.00135 4	0.035 473	4.689917	Up	uncharacterized LOC148638
A_32_P183 765	ERBB4	1.80022	0.00140 9	0.036 262	4.66067	Up	erb-b2 receptor tyrosine kinase 4
A_19_P008 11193	#N/A	0.967772	0.00141	0.036 262	4.660162	Up	NA
A_23_P129 835	PPP1R1B	1.133206	0.00141 9	0.036 362	4.655157	Up	protein phosphatase 1 regulatory inhibitor subunit 1B
A_23_P799 68	PCSK2	1.403328	0.00143 7	0.036 661	4.645726	Up	proproteinconvertasesubtilisin/kexin type 2

A_33_P340 5459	FNDC11	1.20722	0.00144 6	0.036 818	4.641233	Up	fibronectin type III domain containing 11
A_23_P320 261	DMKN	0.95874	0.00147 5	0.037 025	4.626565	Up	dermokine
A_23_P200 780	TGFBR3	1.016642	0.00148	0.037 043	4.623865	Up	transforming growth factor beta receptor 3
A_23_P638 1	MN1	0.940638	0.00149 7	0.037 402	4.615481	Up	MN1 proto-oncogene, transcriptional regulator
A_33_P341 1035	SLIT1	1.425281	0.00150 4	0.037 429	4.612055	Up	slit guidance ligand 1
A_23_P210 581	KCNG1	0.947554	0.00156 2	0.038 407	4.584504	Up	potassium voltage-gated channel modifier subfamily G member 1
A_23_P543 40	MEGF11	1.058389	0.00158 2	0.038 509	4.575181	Up	multiple EGF like domains 11
A_23_P735 71	MUM1L1	1.588137	0.00158 9	0.038 563	4.571829	Up	MUM1 like 1
A_33_P384 6653	KRT19P2	1.050094	0.00166 6	0.039 613	4.537271	Up	keratin 19 pseudogene 2
A_23_P116 85	PLA2G4 A	0.933455	0.00167 7	0.039 754	4.532537	Up	phospholipase A2 group IVA
A_23_P139 687	ERP27	0.966953	0.00168 8	0.039 785	4.52741	Up	endoplasmic reticulum protein 27
A_33_P335 1279	GPR37L1	0.966182	0.00169 7	0.039 868	4.523641	Up	G protein-coupled receptor 37 like 1
A_33_P331 1503	SMR3B	0.956584	0.00170 2	0.039 925	4.521576	Up	submaxillary gland androgen regulated protein 3B
A_33_P333 6686	CLIC3	0.9489	0.00171 4	0.040 04	4.51625	Up	chloride intracellular channel 3
A_23_P421 306	SYT12	1.356431	0.00172 1	0.040 069	4.513554	Up	synaptotagmin 12
A_33_P321 9939	CUBN	0.988697	0.00175	0.040 474	4.501436	Up	cubilin
A_32_P340 46	HFM1	1.161494	0.00175 1	0.040 474	4.500666	Up	HFM1, ATP dependent DNA helicase homolog
A_33_P345 9365	LINC008 80	1.060831	0.00175 6	0.040 509	4.498854	Up	long intergenic non-protein coding RNA 880
A_23_P377 094	PNMA3	1.024371	0.00184 6	0.041 758	4.462341	Up	paraneoplastic Ma antigen 3
A_33_P334 3182	IQCA1	1.174187	0.00185	0.041 796	4.461004	Up	IQ motif containing with AAA domain 1
A_33_P372 9375	#N/A	1.126453	0.00185 4	0.041 826	4.459231	Up	NA
A_33_P336 7126	ARHGEF 28	0.948291	0.00185 7	0.041 848	4.458083	Up	Rho guanine nucleotide exchange factor 28
A_33_P338 7766	LINC009 08	1.113277	0.00189	0.042 112	4.445516	Up	long intergenic non-protein coding RNA 908
A_24_P187 799	CPED1	0.969089	0.00189 8	0.042 255	4.442173	Up	cadherin like and PC-esterase domain containing 1

A_33_P339 2829	ESPNL	1.098479	0.00193 8	0.042 586	4.4272	Up	espin-like
A_23_P691 54	FAM198 A	1.114636	0.00193 9	0.042 586	4.426766	Up	family with sequence similarity 198 member A
A_33_P321 4988	EFCAB1	1.067562	0.00196	0.042 762	4.419076	Up	EF-hand calcium binding domain 1
A_23_P344 568	FAM124 A	1.051178	0.00204 2	0.043 747	4.389351	Up	family with sequence similarity 124 member A
A_23_P117 851	CPLX3	1.042413	0.00211 1	0.044 804	4.365519	Up	complexin 3
A_33_P377 2150	ADARB2	1.299361	0.00212	0.044 804	4.362717	Up	adenosine deaminase, RNA specific B2 (inactive)
A_33_P324 6883	DMKN	1.021837	0.00212 2	0.044 804	4.361736	Up	dermokine
A_33_P328 2213	#N/A	1.051166	0.00212 4	0.044 805	4.361056	Up	NA
A_19_P008 10522	#N/A	1.16815	0.00213 1	0.044 805	4.358693	Up	NA
A_23_P102 32	BANK1	1.035706	0.00218 1	0.045 387	4.342172	Up	B-cell scaffold protein with ankyrin repeats 1
A_23_P338 534	HIF3A	1.003302	0.00220 3	0.045 626	4.335127	Up	hypoxia inducible factor 3 alpha subunit
A_23_P146 294	EFCAB1	1.496561	0.00224	0.045 987	4.323259	Up	EF-hand calcium binding domain 1
A_24_P929 322	FLJ42393	1.329889	0.00225	0.046 061	4.319918	Up	uncharacterized LOC401105
A_24_P418 203	CNTNAP 3	1.053068	0.00225 3	0.046 061	4.319016	Up	contactin associated protein-like 3
A_23_P768 4	CCNJL	1.325275	0.00225 3	0.046 061	4.319	Up	cyclin J like
A_33_P341 2428	ADAM32	0.990478	0.00228 1	0.046 295	4.310264	Up	ADAM metalloproteinase domain 32
A_23_P307 844	PHYHD1	1.331487	0.00231 9	0.046 753	4.298482	Up	phytanoyl-CoA dioxygenase domain containing 1
A_33_P322 0207	ARMC3	1.169263	0.00234 9	0.047 043	4.289263	Up	armadillo repeat containing 3
A_32_P313 405	LAMA1	1.220699	0.00236 3	0.047 061	4.284963	Up	laminin subunit alpha 1
A_33_P326 1408	TMIE	0.93458	0.00236 3	0.047 061	4.284906	Up	transmembrane inner ear
A_33_P325 8542	SPINK8	0.974261	0.00238 6	0.047 221	4.278059	Up	serine peptidase inhibitor, Kazal type 8 (putative)
A_33_P328 5629	DNAI2	1.079141	0.00238 7	0.047 221	4.277946	Up	dynein axonemal intermediate chain 2
A_33_P321 5729	RPS3AP1 4	1.011099	0.00242 9	0.047 738	4.265334	Up	ribosomal protein S3a pseudogene 14
A_23_P641 21	KIAA154 9L	1.381953	0.00253	0.048 635	4.236572	Up	KIAA1549 like

A_23_P802 42	SEZ6L	1.445032	0.00253 3	0.048 676	4.235657	Up	seizure related 6 homolog like
A_33_P330 2453	LINC002 42	1.002045	0.00259 2	0.049 393	4.219266	Up	long intergenic non-protein coding RNA 242
A_24_P334 46	KRTAP5- AS1	-1.18091	7.62E- 08	9.03E- 05	-17.1132	Down	KRTAP5-1/KRTAP5-2 antisense RNA 1
A_33_P325 9028	TRIM24	-0.41581	1.15E- 06	0.000 557	-12.2547	Down	tripartite motif containing 24
A_33_P321 2684	#N/A	-0.76271	1.64E- 06	0.000 718	-11.7307	Down	NA
A_23_P139 099	OR4A15	-0.42416	2.37E- 06	0.000 899	-11.2005	Down	olfactory receptor family 4 subfamily A member 15
A_23_P159 974	KLHL13	-0.37716	3.9E-06	0.001 22	-10.5164	Down	kelch like family member 13
A_33_P326 9503	KRT87P	-0.94844	4.21E- 06	0.001 298	-10.4139	Down	keratin 87 pseudogene
A_19_P008 02970	ZRANB2 -AS1	-0.56876	4.36E- 06	0.001 326	-10.3675	Down	ZRANB2 antisense RNA 1
A_19_P003 23612	#N/A	-0.41168	4.64E- 06	0.001 358	-10.2869	Down	NA
A_19_P003 26199	SINHCA F	-0.52736	4.72E- 06	0.001 358	-10.2635	Down	SIN3-HDAC complex associated factor
A_23_P254 831	MAGEB2	-0.36511	5.16E- 06	0.001 443	-10.1497	Down	MAGE family member B2
A_19_P003 27423	#N/A	-0.74048	5.89E- 06	0.001 597	-9.97785	Down	NA
A_19_P008 00667	LINC003 98	-0.31923	6.4E-06	0.001 71	-9.87313	Down	long intergenic non-protein coding RNA 398
A_19_P008 11704	#N/A	-0.49672	6.45E- 06	0.001 71	-9.86335	Down	NA
A_33_P325 7910	C3orf80	-1.01528	9.53E- 06	0.002 277	-9.38237	Down	chromosome 3 open reading frame 80
A_19_P003 15872	#N/A	-0.56281	1.14E- 05	0.002 6	-9.16497	Down	NA
A_23_P121 596	PPBP	-1.54696	1.17E- 05	0.002 615	-9.13962	Down	pro-platelet basic protein
A_23_P259 586	TTK	-1.24521	1.18E- 05	0.002 615	-9.12483	Down	TTK protein kinase
A_23_P328 145	FAM71D	-0.93751	1.24E- 05	0.002 678	-9.06826	Down	family with sequence similarity 71 member D
A_19_P003 26831	#N/A	-0.74662	1.25E- 05	0.002 678	-9.06195	Down	NA
A_23_P382 682	NOXRE D1	-0.73831	1.4E-05	0.002 852	-8.92458	Down	NADP dependent oxidoreductase domain containing 1
A_33_P323 5048	TRIM77	-0.40971	1.46E- 05	0.002 909	-8.88124	Down	tripartite motif containing 77
A_23_P118 834	TOP2A	-1.2832	1.69E- 05	0.003 223	-8.71249	Down	topoisomerase (DNA) II alpha

A_33_P324 2649	KIF18A	-1.15029	1.7E-05	0.003 236	-8.70182	Down	kinesin family member 18A
A_23_P686 10	TPX2	-0.6427	1.98E-05	0.003 585	-8.53261	Down	TPX2, microtubule nucleation factor
A_19_P003 23829	#N/A	-0.90037	2.08E-05	0.003 738	-8.47651	Down	NA
A_19_P003 30864	#N/A	-1.06535	2.11E-05	0.003 766	-8.46369	Down	NA
A_19_P008 01104	#N/A	-0.54282	2.66E-05	0.004 416	-8.20936	Down	NA
A_23_P212 284	POC1A	-0.3445	2.71E-05	0.004 457	-8.18814	Down	POC1 centriolar protein A
A_19_P008 13027	#N/A	-0.38569	2.75E-05	0.004 497	-8.17297	Down	NA
A_33_P332 5502	ARHGAP 29	-0.93195	2.78E-05	0.004 538	-8.15889	Down	Rho GTPase activating protein 29
A_23_P315 815	NRG1	-0.34435	2.93E-05	0.004 679	-8.10578	Down	neuregulin 1
A_33_P333 5825	PLCD4	-0.74316	3.14E-05	0.004 861	-8.02939	Down	phospholipase C delta 4
A_33_P335 4001	CADPS2	-0.29264	3.19E-05	0.004 888	-8.01287	Down	calcium dependent secretion activator 2
A_33_P378 8618	ACER2	-0.29305	3.24E-05	0.004 921	-7.99726	Down	alkaline ceramidase 2
A_24_P193 592	CCNF	-0.96239	3.27E-05	0.004 954	-7.98653	Down	cyclin F
A_33_P357 6853	NIFK- AS1	-0.43661	3.3E-05	0.004 986	-7.97595	Down	NIFK antisense RNA 1
A_33_P325 0015	#N/A	-0.54203	3.63E-05	0.005 271	-7.87712	Down	NA
A_19_P008 08523	#N/A	-0.31475	3.87E-05	0.005 513	-7.80907	Down	NA
A_23_P575 88	GTSE1	-0.80101	4.28E-05	0.005 822	-7.70706	Down	G2 and S-phase expressed 1
A_23_P366 983	TRHDE	-0.85404	4.36E-05	0.005 857	-7.6877	Down	thyrotropin releasing hormone degrading enzyme
A_33_P340 5680	ARHGEF 3-AS1	-0.50887	4.6E-05	0.006 063	-7.63133	Down	ARHGEF3 antisense RNA 1
A_24_P911 676	SOX4	-0.48583	4.82E-05	0.006 272	-7.58518	Down	SRY-box 4
A_19_P008 07368	#N/A	-0.29663	5.04E-05	0.006 496	-7.53945	Down	NA
A_19_P003 20026	DLEU1	-0.42962	5.06E-05	0.006 498	-7.53609	Down	deleted in lymphocytic leukemia 1 (non-protein coding)
A_19_P003 25235	#N/A	-0.6208	5.14E-05	0.006 53	-7.51885	Down	NA
A_19_P003 21005	#N/A	-0.9916	5.6E-05	0.006 971	-7.43242	Down	NA

A_23_P118 174	PLK1	-0.46167	5.73E- 05	0.007 069	-7.40971	Down	polo like kinase 1
A_33_P327 1945	HAUS6	-0.41613	5.81E- 05	0.007 101	-7.3965	Down	HAUS augmin like complex subunit 6
A_19_P003 24653	GPALPP 1	-0.33064	6.19E- 05	0.007 399	-7.33303	Down	GPALPP motifs containing 1
A_23_P124 417	BUB1	-1.18787	6.27E- 05	0.007 429	-7.32071	Down	BUB1 mitotic checkpoint serine/threonine kinase
A_24_P145 629	SERINC2	-0.77141	6.37E- 05	0.007 486	-7.30502	Down	serine incorporator 2
A_33_P323 0548	KIF14	-1.33322	6.4E-05	0.007 486	-7.29949	Down	kinesin family member 14
A_33_P359 8466	HSP90A B6P	-0.61836	6.54E- 05	0.007 624	-7.27875	Down	heat shock protein 90 alpha family class B member 6, pseudogene
A_24_P122 746	VWA1	-0.91594	6.68E- 05	0.007 644	-7.25822	Down	von Willebrand factor A domain containing 1
A_33_P342 1973	FRMPD3	-0.97088	6.84E- 05	0.007 761	-7.23466	Down	FERM and PDZ domain containing 3
A_23_P185 79	PTTG2	-0.3236	7.36E- 05	0.008 159	-7.16262	Down	pituitary tumor-transforming 2
A_19_P003 29691	RANP3	-0.44835	7.63E- 05	0.008 328	-7.12757	Down	RAN, member RAS oncogene family pseudogene 3
A_33_P337 7529	HOXA4	-0.54254	8.02E- 05	0.008 513	-7.08014	Down	homeobox A4
A_33_P331 8424	#N/A	-0.32148	8.12E- 05	0.008 532	-7.06767	Down	NA
A_24_P219 114	SEL1L	-0.34542	8.34E- 05	0.008 626	-7.04271	Down	SEL1L ERAD E3 ligase adaptor subunit
A_33_P335 0488	NUSAP1	-0.45817	8.45E- 05	0.008 651	-7.02997	Down	nucleolar and spindle associated protein 1
A_33_P334 3720	CELA3A	-0.49673	8.54E- 05	0.008 656	-7.01888	Down	chymotrypsin like elastase family member 3A
A_19_P003 31977	#N/A	-0.4191	8.65E- 05	0.008 717	-7.00758	Down	NA
A_32_P160 561	DOK6	-0.68558	9.11E- 05	0.008 995	-6.9574	Down	docking protein 6
A_33_P341 8466	AC02229 6.1	-0.35285	9.32E- 05	0.009 105	-6.93602	Down	NA
A_19_P003 31084	#N/A	-0.48869	9.37E- 05	0.009 105	-6.93101	Down	NA
A_19_P003 22169	#N/A	-0.61999	0.00010 3	0.009 726	-6.84557	Down	NA
A_33_P326 3002	TMEM26 2	-0.63529	0.00010 4	0.009 737	-6.83519	Down	transmembrane protein 262
A_33_P328 4345	NRG1	-0.32711	0.00010 6	0.009 862	-6.81496	Down	neuregulin 1
A_23_P819 26	PSORS1 C2	-0.36148	0.00010 7	0.009 869	-6.80951	Down	psoriasis susceptibility 1 candidate 2

A_19_P003 32459	DHX15	-1.24559	0.00010 8	0.009 961	-6.79737	Down	DEAH-box helicase 15
A_23_P352 19	NEK2	-1.05848	0.00010 9	0.010 008	-6.78932	Down	NIMA related kinase 2
A_33_P326 0511	CICP24	-0.35944	0.00010 9	0.010 009	-6.78677	Down	capicua transcriptional repressor pseudogene 24
A_33_P340 3429	LRRC69	-0.4054	0.00011 2	0.010 141	-6.76056	Down	leucine rich repeat containing 69
A_23_P366 24	TAS2R7	-0.56665	0.00011 3	0.010 184	-6.75124	Down	taste 2 receptor member 7
A_24_P314 571	SPC24	-1.03137	0.00011 7	0.010 371	-6.72365	Down	SPC24, NDC80 kinetochore complex component
A_19_P008 07332	#N/A	-0.86237	0.00011 8	0.010 371	-6.71561	Down	NA
A_19_P008 07314	#N/A	-0.30162	0.00011 8	0.010 371	-6.7145	Down	NA
A_33_P321 1014	#N/A	-0.6112	0.00012 1	0.010 554	-6.68923	Down	NA
A_33_P335 4067	AC09282 1.2	-0.31328	0.00012 4	0.010 658	-6.66572	Down	NA
A_19_P008 01050	#N/A	-0.48588	0.00012 5	0.010 685	-6.65847	Down	NA
A_23_P700 07	HMMR	-0.49422	0.00013	0.010 887	-6.62632	Down	hyaluronan mediated motility receptor
A_33_P377 0642	LINC009 29	-0.84694	0.00013	0.010 887	-6.62288	Down	long intergenic non-protein coding RNA 929
A_19_P003 17247	PTP4A1	-0.3095	0.00013 5	0.011 079	-6.58899	Down	protein tyrosine phosphatase type IVA, member 1
A_19_P003 28255	#N/A	-0.29491	0.00013 6	0.011 131	-6.58118	Down	NA
A_23_P193 69	CARMIL 1	-0.377	0.00014 3	0.011 485	-6.53694	Down	capping protein regulator and myosin 1 linker 1
A_33_P332 2125	DAZAP2	-0.33412	0.00014 5	0.011 604	-6.52583	Down	DAZ associated protein 2
A_33_P333 3177	#N/A	-0.62324	0.00014 6	0.011 665	-6.51937	Down	NA
A_23_P104 651	CDCA5	-0.36513	0.00014 6	0.011 689	-6.51579	Down	cell division cycle associated 5
A_19_P003 28658	#N/A	-0.32397	0.00014 8	0.011 752	-6.5092	Down	NA
A_19_P003 19194	#N/A	-0.87023	0.00015 2	0.011 91	-6.48015	Down	NA
A_19_P003 30750	#N/A	-0.48391	0.00015 3	0.011 91	-6.47897	Down	NA
A_19_P008 00106	#N/A	-0.51725	0.00015 5	0.012 049	-6.46641	Down	NA
A_19_P008 00448	#N/A	-0.46945	0.00015 6	0.012 123	-6.45755	Down	NA

A_33_P320 9703	#N/A	-0.38403	0.00015 9	0.012 272	-6.44165	Down	NA
A_19_P008 01014	ANTXR2	-0.33022	0.00016 6	0.012 56	-6.40275	Down	anthrax toxin receptor 2
A_19_P003 27255	#N/A	-0.33261	0.00016 8	0.012 611	-6.39321	Down	NA
A_19_P003 21594	FBXL5	-0.89313	0.00017 633	0.012	-6.38353	Down	F-box and leucine rich repeat protein 5
A_33_P342 0704	#N/A	-0.3589	0.00017 666	0.012	-6.37957	Down	NA
A_33_P331 6903	RBPMS- AS1	-0.40474	0.00017 5	0.012 856	-6.35387	Down	RBPMS antisense RNA 1
A_23_P300 100	PLA2G2 D	-0.52315	0.00017 9	0.012 985	-6.33706	Down	phospholipase A2 group IID
A_33_P329 5077	AC09216 2.1	-0.32979	0.00018 2	0.013 153	-6.31903	Down	NA
A_33_P337 5334	DAB1	-1.09252	0.00018 6	0.013 284	-6.30295	Down	DAB1, reelin adaptor protein
A_23_P113 97	TTTY13	-0.69508	0.00018 6	0.013 284	-6.3019	Down	testis-specific transcript, Y-linked 13 (non-protein coding)
A_23_P346 884	RBPJL	-0.32051	0.00019 5	0.013 736	-6.25896	Down	recombination signal binding protein for immunoglobulin kappa J region like
A_19_P008 04053	#N/A	-0.35416	0.00019 7	0.013 821	-6.24831	Down	NA
A_19_P003 22074	#N/A	-0.36755	0.0002 821	0.013	-6.23712	Down	NA
A_19_P003 27072	#N/A	-0.34689	0.00020 1	0.013 821	-6.23408	Down	NA
A_33_P338 6344	FANCA	-0.32132	0.00020 4	0.013 95	-6.22023	Down	Fanconianemia complementation group A
A_33_P334 0468	CENPI	-0.73725	0.00020 5	0.014 011	-6.21277	Down	centromere protein I
A_19_P003 30152	#N/A	-0.44423	0.00020 6	0.014 017	-6.21017	Down	NA
A_19_P008 00639	#N/A	-0.48611	0.00020 7	0.014 064	-6.20523	Down	NA
A_19_P003 31152	#N/A	-0.61926	0.00021 139	0.014	-6.19498	Down	NA
A_19_P008 11393	#N/A	-0.30534	0.00021 5	0.014 373	-6.17502	Down	NA
A_33_P330 4268	LOC6433 27	-0.67616	0.00021 6	0.014 405	-6.16802	Down	uncharacterized LOC643327
A_33_P321 4690	NLGN1	-0.39399	0.00021 9	0.014 495	-6.15644	Down	neuroligin 1
A_33_P329 0729	POU3F2	-1.77448	0.00021 9	0.014 495	-6.15601	Down	POU class 3 homeobox 2
A_23_P425 332	PPP4R4	-0.37974	0.00021 9	0.014 495	-6.15533	Down	protein phosphatase 4 regulatory subunit 4

A_33_P334 5469	GPR6	-0.42562	0.00022	0.014	-6.148	Down	G protein-coupled receptor 6
A_23_P414 211	PAX4	-0.32483	0.00022	0.014	-6.14213	Down	paired box 4
A_33_P341 3224	AC09275 5.2	-0.39132	0.00022	0.014	-6.12784	Down	NA
A_19_P003 16773	#N/A	-0.95664	0.00022	0.014	-6.12671	Down	NA
A_33_P324 8610	ASXL2	-0.31774	0.00022	0.014	-6.12588	Down	additional sex combs like 2, transcriptional regulator
A_19_P003 20549	#N/A	-0.35255	0.00023	0.014	-6.11129	Down	NA
A_33_P324 3454	IGFL3	-1.0725	0.00023	0.014	-6.10166	Down	IGF like family member 3
A_33_P341 6414	PSAT1P1	-0.62563	0.00023	0.015	-6.09036	Down	phosphoserine aminotransferase 1 pseudogene 1
A_33_P330 7144	GRIK2	-0.39339	0.00023	0.015	-6.08797	Down	glutamate ionotropic receptor kainate type subunit 2
A_23_P600 16	PTTG3P	-0.61312	0.00024	0.015	-6.07843	Down	pituitary tumor-transforming 3, pseudogene
A_33_P323 0254	NCAPG	-0.80641	0.00024	0.015	-6.06626	Down	non-SMC condensin I complex subunit G
A_33_P326 5549	SLC19A1	-0.38232	0.00024	0.015	-6.0618	Down	solute carrier family 19 member 1
A_33_P362 9151	#N/A	-0.30303	0.00025	0.015	-6.03643	Down	NA
A_32_P645 98	LINC021 56	-0.97878	0.00025	0.015	-6.03164	Down	long intergenic non-protein coding RNA 2156
A_23_P166 993	EPHB1	-0.48094	0.00025	0.015	-6.02497	Down	EPH receptor B1
A_24_P141 707	INHBE	-0.87769	0.00025	0.015	-6.01625	Down	inhibin beta E subunit
A_19_P003 24607	XIST_EX ON1	-0.52726	0.00025	0.015	-6.01367	Down	X-chromosome inactivation gene exon 1
A_23_P112 187	FIBCD1	-0.32728	0.00025	0.015	-6.01152	Down	fibrinogen C domain containing 1
A_19_P003 30161	RGS5	-0.31195	0.00026	0.015	-6.00355	Down	regulator of G protein signaling 5
A_19_P008 10938	#N/A	-0.47038	0.00026	0.015	-5.99368	Down	NA
A_33_P367 1729	FLJ44715	-0.66365	0.00026	0.015	-5.98817	Down	uncharacterized LOC386671
A_23_P630 32	GUCA2B	-0.45895	0.00026	0.016	-5.97986	Down	guanylatecyclase activator 2B
A_23_P657 57	CCNB2	-0.68899	0.00027	0.016	-5.97008	Down	cyclin B2
A_33_P322 1761	KMT2B	-0.33926	0.00027	0.016	-5.96538	Down	lysine methyltransferase 2B

A_23_P342 138	ADAMT SL1	-0.30204	0.00027 4	0.016 143	-5.96357	Down	ADAMTS like 1
A_19_P003 29997	#N/A	-0.77956	0.00027 5	0.016 166	-5.95971	Down	NA
ERCC- 00126_533	#N/A	-0.61974	0.00028	0.016 335	-5.94611	Down	NA
A_19_P008 07001	#N/A	-0.59089	0.00028 1	0.016 399	-5.9404	Down	NA
ERCC- 00014_76	#N/A	-0.58213	0.00028 9	0.016 663	-5.9164	Down	NA
A_19_P003 30883	#N/A	-0.44021	0.00029 4	0.016 851	-5.90168	Down	NA
A_19_P008 06769	LINC011 22	-0.33078	0.00029 7	0.016 851	-5.8936	Down	long intergenic non-protein coding RNA 1122
A_33_P330 0152	#N/A	-0.3139	0.00029 7	0.016 851	-5.89333	Down	NA
A_33_P325 5001	LINC006 91	-0.67432	0.00029 9	0.016 851	-5.88871	Down	long intergenic non-protein coding RNA 691
A_32_P204 376	ANKRD2 0A2	-0.82794	0.0003	0.016 851	-5.88524	Down	ankyrin repeat domain 20 family member A2
A_19_P003 25303	#N/A	-0.29931	0.00030 2	0.016 931	-5.88008	Down	NA
A_24_P438 10	FAM83A	-1.14146	0.00030 7	0.017 077	-5.86726	Down	family with sequence similarity 83 member A
A_33_P329 6281	#N/A	-1.00736	0.00030 8	0.017 112	-5.86396	Down	NA
A_33_P339 5733	AL04979 5.1	-0.52782	0.00030 9	0.017 112	-5.86154	Down	NA
A_33_P322 9552	LRFN1	-0.3534	0.00030 9	0.017 112	-5.86091	Down	leucine rich repeat and fibronectin type III domain containing 1
A_19_P008 11105	#N/A	-0.35467	0.00030 9	0.017 112	-5.86002	Down	NA
A_23_P201 022	PKLR	-0.29705	0.00031 5	0.017 267	-5.84461	Down	pyruvate kinase, liver and RBC
A_33_P384 0512	SLC25A1 5	-0.30272	0.00031 7	0.017 267	-5.83945	Down	solute carrier family 25 member 15
A_33_P338 9758	#N/A	-0.38846	0.00031 7	0.017 267	-5.83831	Down	NA
A_24_P367 410	GABRQ	-0.68191	0.00031 9	0.017 276	-5.83492	Down	gamma-aminobutyric acid type A receptor theta subunit
A_19_P003 24404	#N/A	-0.32077	0.00032 2	0.017 376	-5.82646	Down	NA
A_23_P206 059	PRC1	-0.3017	0.00032 4	0.017 42	-5.82114	Down	protein regulator of cytokinesis 1
A_23_P140 83	AMIGO2	-0.44866	0.00032 6	0.017 507	-5.81479	Down	adhesion molecule with Ig like domain 2
A_24_P587 443	AC02527 8.1	-0.61913	0.00032 9	0.017 606	-5.80688	Down	NA

A_33_P324 8028	#N/A	-0.68935	0.00033 3	0.017 746	-5.79811	Down	NA
A_33_P327 4001	SUMO2P 8	-0.31129	0.00033 6	0.017 778	-5.79043	Down	SUMO2 pseudogene 8
A_23_P573 79	CDC45	-0.42634	0.00033 7	0.017 778	-5.78764	Down	cell division cycle 45
A_23_P254 733	CENPU	-0.53283	0.00034	0.017 833	-5.78005	Down	centromere protein U
A_24_P983 3	PRDM11	-0.38799	0.00034 1	0.017 833	-5.77904	Down	PR/SET domain 11
A_33_P331 1543	#N/A	-0.42903	0.00034 4	0.017 933	-5.7716	Down	NA
A_33_P321 6272	LOC1001 33920	-0.29115	0.00034 8	0.018 14	-5.75995	Down	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like pseudogene
A_19_P008 02008	#N/A	-0.36753	0.00035 2	0.018 266	-5.75094	Down	NA
A_19_P008 06281	#N/A	-0.45576	0.00035 5	0.018 351	-5.74313	Down	NA
A_19_P008 00105	#N/A	-0.48555	0.00035 8	0.018 376	-5.73826	Down	NA
A_23_P363 97	CYP27B1	-0.41362	0.00037	0.018 715	-5.70973	Down	cytochrome P450 family 27 subfamily B member 1
A_24_P227 091	KIF11	-0.32887	0.00037 4	0.018 869	-5.70094	Down	kinesin family member 11
A_33_P341 3518	#N/A	-0.44929	0.00037 5	0.018 883	-5.69938	Down	NA
A_33_P333 7124	LL22NC0 3-63E9.3	-0.34339	0.00037 6	0.018 89	-5.69708	Down	uncharacterized LOC648691
A_19_P008 11963	#N/A	-0.4231	0.00038 1	0.019 036	-5.68577	Down	NA
A_19_P008 01430	#N/A	-0.33418	0.00038 2	0.019 068	-5.68342	Down	NA
A_24_P941 759	G2E3	-0.2988	0.00038 6	0.019 195	-5.6742	Down	G2/M-phase specific E3 ubiquitin protein ligase
A_33_P323 7364	RPL36P2 0	-0.39151	0.00038 8	0.019 229	-5.67001	Down	ribosomal protein L36 pseudogene 20
A_33_P337 4030	LOC1001 32197	-0.31421	0.00039 3	0.019 342	-5.65903	Down	uncharacterized LOC100132197
A_19_P008 07621	LINC013 55	-0.3223	0.00040 3	0.019 654	-5.63861	Down	long intergenic non-protein coding RNA 1355
ERCC- 00085_231	#N/A	-0.8721	0.00040 3	0.019 654	-5.63845	Down	NA
A_33_P334 6643	#N/A	-0.65369	0.00040 3	0.019 654	-5.63821	Down	NA
A_33_P334 2469	OR6T1	-0.39762	0.00040 5	0.019 687	-5.63402	Down	olfactory receptor family 6 subfamily T member 1
A_23_P218 827	POLQ	-0.61577	0.00040 6	0.019 694	-5.63275	Down	DNA polymerase theta

A_33_P326 8734	COL5A1- AS1	-0.30006	0.00041 1	0.019 894	-5.62161	Down	COL5A1 antisense RNA 1
A_23_P250 136	GRIK2	-0.50891	0.00041 2	0.019 894	-5.61973	Down	glutamate ionotropic receptor kainate type subunit 2
A_33_P339 8411	RASSF3	-0.78014	0.00041 9	0.020 052	-5.60582	Down	Ras association domain family member 3
A_19_P003 24378	#N/A	-1.09872	0.00042 5	0.020 173	-5.59533	Down	NA
A_19_P003 26161	#N/A	-0.31777	0.00043 2	0.020 315	-5.58176	Down	NA
A_32_P629 97	PBK	-1.44872	0.00043 3	0.020 315	-5.58052	Down	PDZ binding kinase
A_33_P330 4452	SLC12A5 -AS1	-0.71833	0.00043 3	0.020 315	-5.57988	Down	SLC12A5 and MMP9 antisense RNA 1
A_24_P413 884	CENPA	-1.04472	0.00043 5	0.020 351	-5.57587	Down	centromere protein A
A_33_P333 5576	#N/A	-0.30201	0.00043 6	0.020 351	-5.57466	Down	NA
A_32_P470 728	GSX1	-0.37056	0.00044 3	0.020 438	-5.56016	Down	GS homeobox 1
A_19_P008 04762	#N/A	-0.48298	0.00044 9	0.020 53	-5.55088	Down	NA
A_32_P233 950	DPPA5	-0.82268	0.00044 9	0.020 53	-5.55041	Down	developmental pluripotency associated 5
A_33_P341 8185	LYNX1	-0.5229	0.00045 7	0.020 64	-5.53525	Down	Ly6/neurotoxin 1
A_33_P336 0271	EVX2	-0.52194	0.00045 8	0.020 64	-5.53386	Down	even-skipped homeobox 2
A_24_P690 811	ASPDH	-0.41954	0.00046 3	0.020 678	-5.52511	Down	aspartate dehydrogenase domain containing
A_33_P322 8709	KRTAP5- 7	-0.35642	0.00046 4	0.020 678	-5.52349	Down	keratin associated protein 5–7
A_19_P003 31839	#N/A	-0.29212	0.00047 745	0.020	-5.51346	Down	NA
A_19_P003 31107	#N/A	-0.80169	0.00047 4	0.020 853	-5.50635	Down	NA
A_23_P883 31	DLGAP5	-0.90972	0.00047 5	0.020 853	-5.50474	Down	DLG associated protein 5
A_33_P325 8392	EDN1	-0.3889	0.00047 5	0.020 853	-5.50367	Down	endothelin 1
A_19_P008 04522	#N/A	-0.57	0.00047 6	0.020 853	-5.50304	Down	NA
A_19_P003 17565	#N/A	-0.46065	0.00047 6	0.020 853	-5.50268	Down	NA
A_19_P008 02508	#N/A	-0.59414	0.00047 7	0.020 888	-5.49991	Down	NA
A_19_P008 03716	#N/A	-0.79278	0.00048 4	0.021 054	-5.4892	Down	NA

A_19_P003 20023	#N/A	-0.53921	0.00049 5	0.021 302	-5.47115	Down	NA
A_19_P003 20253	#N/A	-0.4143	0.00050 4	0.021 479	-5.45555	Down	NA
A_19_P003 15793	AL13878 1.1	-0.49995	0.00050 7	0.021 538	-5.45163	Down	NA
A_19_P003 20113	#N/A	-1.04798	0.00050 8	0.021 586	-5.44901	Down	NA
A_19_P003 22033	#N/A	-0.67146	0.00051 8	0.021 761	-5.43368	Down	NA
A_19_P003 32215	#N/A	-0.31011	0.00052 814	0.021	-5.43076	Down	NA
A_19_P008 08792	#N/A	-0.31009	0.00052 3	0.021 814	-5.42635	Down	NA
A_19_P008 04356	RNU6- 485P	-0.54041	0.00052 5	0.021 814	-5.42362	Down	RNA, U6 small nuclear 485, pseudogene
A_19_P008 08315	#N/A	-0.41158	0.00053 2	0.021 983	-5.41287	Down	NA
A_19_P003 17210	#N/A	-0.53067	0.00053 5	0.022 069	-5.40738	Down	NA
A_23_P256 956	KIF20A	-0.95407	0.00053 6	0.022 073	-5.40566	Down	kinesin family member 20A
A_19_P003 25343	#N/A	-0.32421	0.00054 4	0.022 276	-5.39456	Down	NA
A_33_P321 7357	LINC014 15	-0.53677	0.00054 5	0.022 276	-5.39301	Down	long intergenic non-protein coding RNA 1415
A_23_P153 183	CNKSR2	-0.3422	0.00055 384	0.022	-5.38593	Down	connector enhancer of kinase suppressor of Ras 2
A_24_P918 175	LOC6535 81	-0.5441	0.00055 1	0.022 408	-5.3843	Down	uncharacterized LOC653581
A_33_P325 9440	GOLGA6 A	-0.6024	0.00055 5	0.022 454	-5.37827	Down	golgin A6 family member A
A_19_P003 22834	#N/A	-0.52403	0.00056 8	0.022 671	-5.35948	Down	NA
A_24_P228 228	B4GALT 6	-0.29383	0.00057 3	0.022 761	-5.35212	Down	beta-1,4-galactosyltransferase 6
A_33_P329 9110	ARHGAP 42	-0.53734	0.00057 6	0.022 762	-5.34871	Down	Rho GTPase activating protein 42
A_32_P816 76	LINC005 99	-0.78125	0.00057 6	0.022 762	-5.34835	Down	long intergenic non-protein coding RNA 599
A_19_P003 21820	#N/A	-0.74238	0.00058 7	0.023 011	-5.33401	Down	NA
A_32_P489 662	KRT28	-0.76908	0.00059 1	0.023 113	-5.32808	Down	keratin 28
A_19_P003 23720	#N/A	-0.58573	0.00059 1	0.023 113	-5.32801	Down	NA
A_24_P498 96	GDPD4	-0.51369	0.0006 374	0.023	-5.31609	Down	glycerophosphodiesterphosphodiesterase domain containing 4

A_19_P003 17028	#N/A	-0.43091	0.0006	0.023 374	-5.31543	Down	NA
A_19_P008 07254	#N/A	-0.44738	0.00060 7	0.023 523	-5.30748	Down	NA
A_33_P339 7935	CALML3 -AS1	-0.33578	0.00060 7	0.023 523	-5.30746	Down	CALML3 antisense RNA 1
A_33_P330 7903	CDKN3	-0.66678	0.00061 3	0.023 662	-5.29862	Down	cyclin dependent kinase inhibitor 3
A_19_P003 24976	#N/A	-0.71172	0.00061 7	0.023 765	-5.29352	Down	NA
A_23_P253 752	MTFR2	-0.604	0.00062 2	0.023 868	-5.28721	Down	mitochondrial fission regulator 2
A_32_P890 614	LOC1002 68168	-0.58393	0.00062 4	0.023 883	-5.28531	Down	uncharacterized LOC100268168
A_33_P338 6414	DCAF4L 2	-0.56011	0.00062 7	0.023 974	-5.28158	Down	DDB1 and CUL4 associated factor 4 like 2
A_33_P326 1695	TEX22	-0.57797	0.00062 9	0.024 007	-5.27886	Down	testis expressed 22
A_32_P812 268	CALHM1	-0.71959	0.00063 4	0.024 08	-5.27239	Down	calcium homeostasis modulator 1
A_23_P421 436	ADD2	-0.42187	0.00064 5	0.024 339	-5.25827	Down	adducin 2
A_19_P008 08731	#N/A	-0.32277	0.00065 4	0.024 51	-5.24812	Down	NA
A_33_P342 2732	LOC1001 31180	-0.49937	0.00065 9	0.024 583	-5.24219	Down	uncharacterized LOC100131180
A_23_P486 69	CDKN3	-0.49224	0.00066 583	0.024	-5.24078	Down	cyclin dependent kinase inhibitor 3
A_33_P325 1727	RYR2	-0.45157	0.00066 7	0.024 715	-5.23158	Down	ryanodine receptor 2
A_33_P325 2444	#N/A	-0.59301	0.00067 1	0.024 806	-5.22785	Down	NA
A_19_P003 23152	#N/A	-0.4622	0.00067 2	0.024 806	-5.22606	Down	NA
A_19_P003 16888	#N/A	-0.47099	0.00067 4	0.024 821	-5.22358	Down	NA
A_33_P332 3979	LOC3398 74	-0.3826	0.00067 7	0.024 843	-5.22	Down	uncharacterized LOC339874
A_33_P326 1530	AC08749 1.1	-1.00413	0.00068 9	0.025 123	-5.20636	Down	NA
A_32_P509 677	C20orf20 3	-0.77482	0.00069 7	0.025 302	-5.19763	Down	chromosome 20 open reading frame 203
A_19_P003 16667	LINC020 99	-0.33593	0.00070 4	0.025 461	-5.18922	Down	long intergenic non-protein coding RNA 2099
A_19_P003 24450	#N/A	-0.38324	0.00070 9	0.025 533	-5.18432	Down	NA
A_33_P340 7103	YTHDF1	-0.33159	0.00072 4	0.025 806	-5.1674	Down	YTH N6-methyladenosine RNA binding protein 1

A_33_P338 2648	RBMV1B	-0.46814	0.00072 6	0.025 851	-5.16537	Down	RNA binding motif protein, Y-linked, family 1, member B
A_33_P334 8328	#N/A	-0.45257	0.00072 7	0.025 87	-5.16416	Down	NA
A_23_P151 150	FOXM1	-0.63036	0.00073 1	0.025 919	-5.16005	Down	forkhead box M1
A_19_P008 11940	#N/A	-0.41876	0.00073 3	0.025 954	-5.15836	Down	NA
A_19_P008 00868	#N/A	-0.32832	0.00075 1	0.026 166	-5.13882	Down	NA
A_23_P108 3	GJA4	-0.54207	0.00075 2	0.026 166	-5.1378	Down	gap junction protein alpha 4
A_33_P321 7619	AC07892 3.1	-0.55897	0.00078 2	0.026 859	-5.10793	Down	NA
A_33_P329 8173	DEFA7P	-0.44812	0.00078 3	0.026 893	-5.10632	Down	defensin alpha 7, pseudogene
A_24_P794 03	PF4	-0.6126	0.00078 5	0.026 893	-5.10463	Down	platelet factor 4
A_33_P330 0142	ANKFY1	-0.30215	0.00078 5	0.026 893	-5.10422	Down	ankyrin repeat and FYVE domain containing 1
A_23_P140 35	AKAP3	-0.92292	0.00079 2	0.026 979	-5.09727	Down	A-kinase anchoring protein 3
A_32_P168 349	#N/A	-0.4856	0.00079 3	0.026 979	-5.09635	Down	NA
A_33_P330 9999	DCAF12 L2	-0.32282	0.00079 7	0.027 003	-5.09317	Down	DDB1 and CUL4 associated factor 12 like 2
A_32_P731 6	BDNF	-1.4327	0.00079 8	0.027 03	-5.09156	Down	brain derived neurotrophic factor
A_19_P003 23487	#N/A	-0.33195	0.00080 2	0.027 092	-5.08752	Down	NA
A_23_P118 815	BIRC5	-0.45791	0.00080 8	0.027 224	-5.08189	Down	baculoviral IAP repeat containing 5
A_19_P003 18567	#N/A	-0.43335	0.00081 6	0.027 426	-5.07411	Down	NA
A_33_P338 5006	SLC39A5	-0.44216	0.00081 7	0.027 426	-5.0737	Down	solute carrier family 39 member 5
A_19_P008 09507	#N/A	-0.98202	0.00082	0.027 463	-5.0702	Down	NA
A_19_P003 21075	PVT1	-1.26911	0.00082 9	0.027 66	-5.06179	Down	Pvt1 oncogene (non-protein coding)
A_33_P334 9265	GLYATL 3	-0.50093	0.00083 8	0.027 779	-5.05349	Down	glycine-N-acyltransferase like 3
A_33_P337 4443	L1CAM	-0.56749	0.00084 2	0.027 859	-5.05006	Down	L1 cell adhesion molecule
A_33_P331 4301	SV2C	-0.47211	0.00084 3	0.027 861	-5.04938	Down	synaptic vesicle glycoprotein 2C
A_23_P809 02	KIF15	-0.4448	0.00085 3	0.028 079	-5.04014	Down	kinesin family member 15

A_23_P143 994	FANCD2	-0.60919	0.00085 8	0.028 18	-5.03582	Down	Fanconianemia complementation group D2
A_19_P003 19532	LINC009 63	-0.30593	0.00086	0.028 195	-5.03397	Down	long intergenic non-protein coding RNA 963
A_32_P186 474	RACGAP 1	-0.42374	0.00086 1	0.028 195	-5.03302	Down	RacGTPase activating protein 1
A_33_P334 6635	FAM20C	-0.51837	0.00086 7	0.028 288	-5.02725	Down	FAM20C, golgi associated secretory pathway kinase
A_23_P743 49	NUF2	-0.61002	0.00087 3	0.028 388	-5.0222	Down	NUF2, NDC80 kinetochore complex component
A_19_P003 21690	AL39075 5.1	-0.8147	0.00087 8	0.028 48	-5.01818	Down	NA
A_19_P003 24561	#N/A	-0.30458	0.00088 9	0.028 637	-5.00807	Down	NA
A_33_P335 4783	#N/A	-0.43482	0.00090 1	0.028 915	-4.99774	Down	NA
A_33_P322 0475	QSOX1	-0.34597	0.00091 1	0.029	-4.99053	Down	quiescin sulphydryl oxidase 1
A_19_P003 16565	TSIX	-0.70329	0.00091 8	0.029 195	-4.9834	Down	TSIX transcript, XIST antisense RNA
A_33_P323 0189	SLITRK6	-0.43506	0.00092 1	0.029 279	-4.98064	Down	SLIT and NTRK like family member 6
A_19_P003 23540	#N/A	-0.29165	0.00092 4	0.029 301	-4.97835	Down	NA
A_33_P359 1761	FAM91A 1	-0.29173	0.00092 9	0.029 399	-4.97455	Down	family with sequence similarity 91 member A1
A_19_P003 24420	H19_1	-0.3534	0.00093 9	0.029 592	-4.9662	Down	H19 conserved region 1
A_33_P326 9854	AL66286 0.1	-0.35472	0.00094	0.029 592	-4.96563	Down	NA
A_19_P003 15768	#N/A	-0.36314	0.00094 2	0.029 63	-4.96409	Down	NA
A_23_P103 532	GPR161	-0.44277	0.00094 3	0.029 642	-4.96303	Down	G protein-coupled receptor 161
A_19_P003 21398	AC13125 4.3	-0.52376	0.00094 8	0.029 73	-4.95867	Down	NA
A_19_P003 17780	LINC015 39	-0.87469	0.00095	0.029 758	-4.95741	Down	long intergenic non-protein coding RNA 1539
A_23_P500 000	SCEL	-0.88136	0.00096	0.029 949	-4.94922	Down	sciellin
A_33_P338 9230	CXCR3	-0.34048	0.00096 1	0.029 949	-4.9487	Down	C-X-C motif chemokine receptor 3
A_33_P326 7320	RFT1	-0.30228	0.00096 4	0.029 993	-4.94632	Down	RFT1 homolog
A_19_P003 22508	AL35511 2.1	-0.72741	0.00097 4	0.030 261	-4.93841	Down	NA
A_33_P327 1276	PSG5	-0.53567	0.00098 2	0.030 383	-4.93212	Down	pregnancy specific beta-1-glycoprotein 5

A_19_P003 20343	AC09118 2.1	-0.29208	0.00098 2	0.030 383	-4.93201	Down	NA
A_23_P887 31	RAD51	-0.39275	0.00099 8	0.030 653	-4.91932	Down	RAD51 recombinase
A_33_P330 2025	ADAMT SL1	-0.46865	0.00099 9	0.030 653	-4.91862	Down	ADAMTS like 1
A_23_P116 97	HMGB4	-0.58702	0.00100 5	0.030 726	-4.91408	Down	high mobility group box 4
A_33_P323 6218	AC23372 4.12	-0.31016	0.00102 027	0.031	-4.90284	Down	NA
A_23_P150 935	TROAP	-0.33946	0.00102 5	0.031 057	-4.89966	Down	trophinin associated protein
A_19_P008 00553	#N/A	-0.4439	0.00102 7	0.031 057	-4.89751	Down	NA
A_33_P323 7744	SBK3	-0.30291	0.00102 8	0.031 057	-4.89705	Down	SH3 domain binding kinase family member 3
A_33_P339 9634	RASSF10	-0.42863	0.00102 8	0.031 057	-4.89694	Down	Ras association domain family member 10
A_33_P329 3138	SYPL1P2	-0.34807	0.00102 9	0.031 057	-4.89668	Down	synaptophysin like 1 pseudogene 2
A_33_P336 2178	PROX2	-0.52367	0.00104 2	0.031 306	-4.88685	Down	prosperohomeobox 2
A_33_P321 0418	SLC5A10	-0.36279	0.00104 5	0.031 339	-4.88498	Down	solute carrier family 5 member 10
A_19_P003 17612	LINC002 11	-0.39501	0.00104 7	0.031 385	-4.88288	Down	long intergenic non-protein coding RNA 211
A_19_P008 01257	#N/A	-0.66576	0.00105 385	0.031	-4.88109	Down	NA
A_23_P571 10	SLC52A3	-0.69684	0.00105 1	0.031 385	-4.88057	Down	solute carrier family 52 member 3
A_19_P003 29700	#N/A	-0.31138	0.00108 5	0.032 116	-4.8563	Down	NA
A_19_P008 02359	#N/A	-0.45195	0.00110 5	0.032 437	-4.84251	Down	NA
A_33_P341 9399	ZC3H12 D	-0.50596	0.00110 6	0.032 437	-4.84152	Down	zinc finger CCCH-type containing 12D
A_33_P342 3590	LOC1001 29275	-0.30291	0.00110 9	0.032 48	-4.83993	Down	uncharacterized LOC100129275
A_19_P008 13611	#N/A	-0.6284	0.00111 7	0.032 517	-4.83402	Down	NA
A_33_P380 7062	HJURP	-0.92005	0.00112 2	0.032 573	-4.83105	Down	Holliday junction recognition protein
A_19_P008 03592	#N/A	-0.30787	0.00112 3	0.032 575	-4.83036	Down	NA
ERCC-001 20_69	#N/A	-0.36448	0.00112 4	0.032 575	-4.82936	Down	NA
A_19_P003 26471	#N/A	-0.41537	0.00113 6	0.032 752	-4.82119	Down	NA

A_19_P003 27444	#N/A	-0.90056	0.00113 9	0.032 752	-4.81923	Down	NA
A_24_P153 25	XKR6	-0.40376	0.00114 4	0.032 822	-4.81636	Down	XK related 6
A_23_P216 118	UNC5D	-0.33057	0.00114 7	0.032 88	-4.81426	Down	unc-5 netrin receptor D
A_23_P124 300	BCO1	-0.39361	0.00115 5	0.032 92	-4.80866	Down	beta-carotene oxygenase 1
A_19_P008 09534	#N/A	-0.8039	0.00115 6	0.032 92	-4.80844	Down	NA
A_33_P325 0944	C1orf189	-0.54453	0.00115 6	0.032 92	-4.80833	Down	chromosome 1 open reading frame 189
A_33_P325 3139	VN1R33 P	-0.69788	0.00115 9	0.032 92	-4.80636	Down	vomeroneasal 1 receptor 33 pseudogene
A_19_P003 25561	LINC018 14	-0.31826	0.00117 4	0.033 199	-4.7967	Down	long intergenic non-protein coding RNA 1814
A_24_P322 353	PSTPIP2	-0.38392	0.00117 5	0.033 199	-4.79573	Down	proline-serine-threonine phosphatase interacting protein 2
A_23_P431 505	XKR6	-0.45688	0.00118 1	0.033 313	-4.79232	Down	XK related 6
A_33_P332 0022	GALNTL 6	-0.3736	0.00118 4	0.033 352	-4.79001	Down	polypeptide N- acetylgalactosaminyltransferase-like 6
A_19_P008 10308	#N/A	-0.52859	0.00118 5	0.033 352	-4.78995	Down	NA
A_23_P376 036	EXD1	-0.69087	0.00119 7	0.033 513	-4.7819	Down	exonuclease 3'-5' domain containing 1
A_32_P700 56	SPATA4 2	-1.07945	0.00120 3	0.033 572	-4.77858	Down	spermatogenesis associated 42 (non-protein coding)
A_24_P924 816	SLC2A13	-0.83023	0.00121 1	0.033 718	-4.77338	Down	solute carrier family 2 member 13
A_19_P003 26183	#N/A	-0.50802	0.00121 4	0.033 752	-4.77163	Down	NA
A_23_P126 888	KIF21B	-0.35514	0.00122 2	0.033 852	-4.76647	Down	kinesin family member 21B
A_33_P325 2083	GRIP1	-0.30525	0.00123 5	0.034 03	-4.75838	Down	glutamate receptor interacting protein 1
A_33_P323 1908	POU3F3	-1.22314	0.00124 5	0.034 205	-4.75272	Down	POU class 3 homeobox 3
A_23_P305 245	C3orf80	-0.92969	0.00124 6	0.034 205	-4.75191	Down	chromosome 3 open reading frame 80
A_23_P981 47	CPN1	-0.39421	0.00125 238	0.034	-4.74955	Down	carboxypeptidase N subunit 1
A_23_P510 85	SPC25	-0.89359	0.00126 5	0.034 5	-4.74067	Down	SPC25, NDC80 kinetochore complex component
A_33_P329 4911	C12ORF6 6	-0.75124	0.00127 2	0.034 57	-4.73677	Down	chromosome 12 open reading frame 66
A_23_P944 22	MELK	-1.00289	0.00128 9	0.034 824	-4.72646	Down	maternal embryonic leucine zipper kinase

A_23_P944 94	TLE4	-0.40005	0.00129	0.034 824	-4.7262	Down	transducin like enhancer of split 4
A_23_P133 123	MND1	-0.49815	0.00129	0.034 824	-4.72607	Down	meiotic nuclear divisions 1
A_23_P113 283	ZMAT3	-0.30962	0.00130 8	0.035 031	-4.71552	Down	zinc finger matrin-type 3
A_19_P003 21002	#N/A	-0.66499	0.00131 5	0.035 072	-4.71182	Down	NA
A_24_P202 319	ATP2A3	-0.53341	0.00131 7	0.035 08	-4.71075	Down	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 3
A_19_P008 08287	#N/A	-0.58374	0.00131 9	0.035 104	-4.70957	Down	NA
A_19_P003 22255	AC02703 1.2	-0.30074	0.00132 4	0.035 191	-4.70652	Down	NA
A_23_P113 382	GRIP1	-0.48946	0.00133	0.035 335	-4.70303	Down	glutamate receptor interacting protein 1
A_33_P338 7831	CENPM	-0.34165	0.00133 5	0.035 41	-4.70031	Down	centromere protein M
A_19_P008 12133	#N/A	-0.46632	0.00133 7	0.035 432	-4.69913	Down	NA
A_33_P330 7133	GRIK2	-0.39228	0.00134	0.035 451	-4.6979	Down	glutamate ionotropic receptor kainate type subunit 2
A_33_P326 5872	AC00245 4.1	-0.41286	0.00134 1	0.035 467	-4.697	Down	NA
A_33_P323 3085	AL04977 5.3	-0.76663	0.00134 3	0.035 471	-4.69629	Down	NA
A_33_P322 9276	ZSCAN2	-0.34477	0.00134 7	0.035 471	-4.69368	Down	zinc finger and SCAN domain containing 2
A_23_P305 581	GPR26	-0.92643	0.00135 4	0.035 473	-4.68974	Down	G protein-coupled receptor 26
A_33_P336 3245	NXPH4	-0.59888	0.00135 6	0.035 473	-4.68905	Down	neurexophilin 4
A_33_P337 8972	UNC5D	-0.48731	0.00136 4	0.035 577	-4.68463	Down	unc-5 netrin receptor D
A_19_P003 15659	#N/A	-0.50683	0.00136 4	0.035 577	-4.68448	Down	NA
A_33_P330 1291	FOXB2	-0.65239	0.00136 7	0.035 577	-4.68318	Down	forkhead box B2
A_33_P327 3732	BX64963 2.1	-0.29717	0.00137 4	0.035 707	-4.67918	Down	NA
A_33_P335 4291	RNF215	-0.40503	0.00137 5	0.035 711	-4.67845	Down	ring finger protein 215
A_19_P003 20972	STMN1	-0.29389	0.00137 6	0.035 711	-4.67818	Down	stathmin 1
A_23_P202 894	ACRV1	-0.7613	0.00138	0.035 747	-4.67571	Down	acrosomal vesicle protein 1
A_33_P321 2316	#N/A	-0.3866	0.00138	0.035 747	-4.67563	Down	NA

A_19_P003 17630	AC00722 1.1	-0.88118	0.00139 5	0.036 006	-4.668	Down	NA
A_19_P003 28506	#N/A	-0.31695	0.00141 9	0.036 362	-4.65535	Down	NA
A_23_P422 933	ARHGAP 20	-0.36989	0.00142 9	0.036 533	-4.64983	Down	Rho GTPase activating protein 20
A_32_P151 800	FAM72D	-0.61437	0.00144	0.036 674	-4.64458	Down	family with sequence similarity 72 member D
A_19_P008 10205	CCNB2P 1	-0.39557	0.00144 9	0.036 853	-4.63977	Down	cyclin B2 pseudogene 1
A_24_P149 74	HTR3D	-0.5183	0.00146 6	0.036 934	-4.63098	Down	5-hydroxytryptamine receptor 3D
A_23_P181 52	ATP2B2	-0.37455	0.00147 3	0.037 025	-4.62743	Down	ATPase plasma membrane Ca ²⁺ transporting 2
A_19_P003 21410	CCNG2	-0.46522	0.00148	0.037 043	-4.6241	Down	cyclin G2
A_19_P008 03108	#N/A	-0.77984	0.00150 2	0.037 422	-4.61306	Down	NA
A_23_P463 09	RCC1	-0.30159	0.00153 9	0.038 129	-4.59539	Down	regulator of chromosome condensation 1
A_23_P596 54	NPVF	-0.82435	0.00154	0.038 143	-4.5947	Down	neuropeptide VF precursor
A_33_P331 1755	KIF23	-0.8856	0.00154 4	0.038 198	-4.59276	Down	kinesin family member 23
A_24_P228 00	PSG11	-0.71926	0.00154 6	0.038 198	-4.59192	Down	pregnancy specific beta-1-glycoprotein 11
A_33_P321 0762	ADAMT S7	-0.32513	0.00154 9	0.038 203	-4.59046	Down	ADAM metalloproteinase with thrombospondin type 1 motif 7
A_33_P340 3075	PRR11	-0.3487	0.00155 9	0.038 381	-4.58586	Down	proline rich 11
A_33_P323 6077	CLRN2	-0.46427	0.00156	0.038 397	-4.58513	Down	clarin 2
A_33_P335 6816	LCE1B	-0.72876	0.00157 3	0.038 509	-4.57935	Down	late cornified envelope 1B
A_19_P008 13597	#N/A	-0.54523	0.00157 4	0.038 509	-4.57879	Down	NA
A_19_P008 00229	CRNDE	-0.91999	0.00157 7	0.038 509	-4.57744	Down	colorectal neoplasia differentially expressed
A_24_P357 468	TRAV8-2	-0.29523	0.00157 9	0.038 509	-4.57665	Down	T-cell receptor alpha variable 8-2
A_19_P003 29473	#N/A	-0.31401	0.00158	0.038 509	-4.57618	Down	NA
A_19_P003 22479	LINC018 29	-0.63842	0.00158 2	0.038 509	-4.57496	Down	long intergenic non-protein coding RNA 1829
A_19_P003 28410	#N/A	-0.83049	0.00158 5	0.038 521	-4.57347	Down	NA
A_33_P339 0187	NHLRC4	-0.84198	0.00159 6	0.038 662	-4.5687	Down	NHL repeat containing 4

A_23_P484 14	CCNA1	-0.39159	0.00160 2	0.038 728	-4.56561	Down	cyclin A1
A_33_P330 2681	TLE4	-0.37711	0.00162 3	0.039 071	-4.55641	Down	transducin like enhancer of split 4
A_33_P377 2739	LINC003 09	-0.82706	0.00163 8	0.039 28	-4.54961	Down	long intergenic non-protein coding RNA 309
A_33_P333 6552	AC06395 2.1	-1.05823	0.00165 5	0.039 498	-4.54185	Down	NA
A_33_P390 1921	PARPBP	-0.63626	0.00166 8	0.039 656	-4.53606	Down	PARP1 binding protein
A_33_P323 0188	#N/A	-0.85776	0.00167	0.039 673	-4.53535	Down	NA
A_23_P207 354	HIGD1B	-0.74427	0.00167 3	0.039 727	-4.53395	Down	HIG1 hypoxia inducible domain family member 1B
A_19_P003 16321	#N/A	-0.63455	0.00167 8	0.039 754	-4.53181	Down	NA
A_19_P003 15956	OXR1	-0.4835	0.00168 6	0.039 774	-4.5284	Down	oxidation resistance 1
A_23_P599 88	SLC35G5	-0.29464	0.00168 6	0.039 774	-4.52825	Down	solute carrier family 35 member G5
A_23_P318 16	DEFA3	-1.15384	0.00169 4	0.039 849	-4.5248	Down	defensin alpha 3
A_33_P340 0918	DISC1	-0.47671	0.00170 4	0.039 925	-4.5206	Down	disrupted in schizophrenia 1
A_19_P008 04027	#N/A	-0.60459	0.00171 9	0.040 069	-4.51438	Down	NA
A_19_P003 29041	#N/A	-0.56472	0.00172	0.040 069	-4.51368	Down	NA
A_33_P322 1019	ZAN	-0.31361	0.00175 5	0.040 509	-4.49904	Down	zonadhesin (gene/pseudogene)
A_33_P327 4731	CLTC	-0.79472	0.00175 9	0.040 546	-4.49749	Down	clathrin heavy chain
A_23_P357 794	MTBP	-0.50871	0.00177 2	0.040 725	-4.49222	Down	MDM2 binding protein
A_19_P008 10560	#N/A	-0.48498	0.00177 7	0.040 786	-4.49004	Down	NA
A_19_P003 20185	#N/A	-0.38737	0.00178 9	0.040 916	-4.48506	Down	NA
A_23_P251 486	COLEC1 0	-0.75326	0.00179 7	0.040 993	-4.48197	Down	collectin subfamily member 10
A_23_P426 835	LOC7296 52	-0.46781	0.00179 9	0.041 013	-4.48122	Down	uncharacterized LOC729652
A_33_P333 8047	PNPLA7	-0.35602	0.00180 2	0.041 058	-4.48005	Down	patatin like phospholipase domain containing 7
A_33_P323 8182	LINC005 88	-0.73748	0.00180 3	0.041 075	-4.47935	Down	long intergenic non-protein coding RNA 588
A_33_P321 0827	RAD51D	-0.32694	0.00182	0.041 335	-4.47282	Down	RAD51 paralog D

A_33_P330 2662	TLE4	-0.46781	0.00184 6	0.041 758	-4.46245	Down	transducin like enhancer of split 4
A_24_P119 609	MYO1D	-0.33354	0.00185 7	0.041 848	-4.45822	Down	myosin ID
A_33_P321 4550	CXCR2	-0.69558	0.00185 9	0.041 851	-4.45717	Down	C-X-C motif chemokine receptor 2
A_19_P003 28681	#N/A	-0.48834	0.00187 3	0.041 976	-4.45179	Down	NA
A_23_P114 210	POU3F4	-0.72576	0.00188	0.042 085	-4.44914	Down	POU class 3 homeobox 4
A_23_P212 595	DCAF1	-0.51936	0.00188	0.042 085	-4.44902	Down	DDB1 and CUL4 associated factor 1
A_32_P279 17	KIF26A	-0.39357	0.00188 5	0.042 112	-4.44716	Down	kinesin family member 26A
A_33_P328 4247	GYG2P1	-0.35135	0.00188 7	0.042 112	-4.44634	Down	glycogenin 2 pseudogene 1
A_33_P322 3602	SATL1	-1.01787	0.00188 9	0.042 112	-4.44575	Down	spermidine/spermine N1-acetyl transferase-like 1
A_33_P335 7773	LINC013 11	-0.64577	0.00189 9	0.042 255	-4.44192	Down	long intergenic non-protein coding RNA 1311
A_19_P008 00783	#N/A	-0.34959	0.0019	0.042 26	-4.44147	Down	NA
A_33_P330 7267	VWF	-1.17271	0.00190 5	0.042 285	-4.43963	Down	von Willebrand factor
A_19_P008 02201	CCNB2P 1	-0.32921	0.00191 2	0.042 367	-4.43691	Down	cyclin B2 pseudogene 1
A_23_P323 898	ZSCAN1 2	-0.32731	0.00192 1	0.042 445	-4.43356	Down	zinc finger and SCAN domain containing 12
A_23_P116 587	OMP	-0.39895	0.00192 1	0.042 445	-4.43341	Down	olfactory marker protein
A_33_P337 7519	HOXA6	-0.30358	0.00193 6	0.042 586	-4.42808	Down	homeobox A6
A_19_P008 08893	#N/A	-0.39011	0.00193 7	0.042 586	-4.42764	Down	NA
A_33_P339 1126	SPINK5	-0.73247	0.00193 9	0.042 586	-4.4269	Down	serine peptidase inhibitor, Kazal type 5
A_24_P276 385	SPACA5	-0.33114	0.00194 3	0.042 617	-4.42524	Down	sperm acrosome associated 5
A_24_P203 315	CNIH2	-0.36997	0.00195 5	0.042 739	-4.42083	Down	cornichon family AMPA receptor auxiliary protein 2
A_33_P327 8053	MYBPC1	-0.40909	0.00195 6	0.042 739	-4.42059	Down	myosin binding protein C, slow type
A_33_P331 1235	ANKDD1 B	-0.52417	0.00196 7	0.042 841	-4.41666	Down	ankyrin repeat and death domain containing 1B
A_19_P008 13205	#N/A	-0.39074	0.00197	0.042 878	-4.41527	Down	NA
A_33_P321 4446	RFC3	-0.37587	0.00198 1	0.043 063	-4.41143	Down	replication factor C subunit 3

A_19_P003 21076	PVT1	-0.46956	0.00199 2	0.043 214	-4.40743	Down	Pvt1 oncogene (non-protein coding)
A_19_P003 21010	LINC011 33	-0.35717	0.00200 8	0.043 379	-4.40148	Down	long intergenic non-protein coding RNA 1133
A_33_P325 6287	FAM95B 1	-0.73977	0.00201 1	0.043 38	-4.40064	Down	family with sequence similarity 95 member B1
A_33_P334 8794	FAM231 A	-0.29791	0.00202 7	0.043 605	-4.39472	Down	family with sequence similarity 231 member A
A_33_P323 3886	#N/A	-0.46784	0.00205 2	0.043 878	-4.38587	Down	NA
A_19_P008 04574	#N/A	-0.3931	0.00206 5	0.044 095	-4.38161	Down	NA
A_19_P003 24503	#N/A	-0.31167	0.00207 4	0.044 256	-4.37826	Down	NA
A_33_P331 4341	KIAA195 8	-0.42171	0.00210 1	0.044 677	-4.36894	Down	KIAA1958
A_33_P338 1613	#N/A	-0.32689	0.00211 6	0.044 804	-4.36394	Down	NA
A_33_P339 1418	TMEM40	-0.29537	0.00211 7	0.044 804	-4.36359	Down	transmembrane protein 40
A_23_P148 541	CTAG1A	-1.15888	0.00212 7	0.044 805	-4.36026	Down	cancer/testis antigen 1A
A_19_P003 21443	AC01874 2.1	-0.70496	0.00213 1	0.044 805	-4.35898	Down	NA
A_19_P008 12873	#N/A	-0.7287	0.00213 5	0.044 826	-4.35764	Down	NA
A_33_P371 9083	CHRNA7	-0.31719	0.00213 9	0.044 894	-4.3562	Down	cholinergic receptor nicotinic alpha 7 subunit
A_24_P740 70	PARD6G	-0.31074	0.00214 6	0.044 971	-4.3539	Down	Par-6 family cell polarity regulator gamma
A_19_P003 17759	AC10446 1.1	-0.89737	0.00215 1	0.045 027	-4.35231	Down	NA
A_33_P334 5309	PRSS56	-0.35326	0.00215 8	0.045 125	-4.34969	Down	protease, serine 56
A_19_P008 04601	TSSC2	-0.58666	0.00216 3	0.045 173	-4.34823	Down	tumor suppressing subtransferable candidate 2 pseudogene
A_19_P003 29437	#N/A	-0.59541	0.00216 5	0.045 202	-4.34741	Down	NA
A_23_P429 491	DDIAS	-0.4245	0.00219 1	0.045 511	-4.33903	Down	DNA damage induced apoptosis suppressor
A_32_P196 115	ZSCAN2 5	-0.29268	0.00219 6	0.045 572	-4.33738	Down	zinc finger and SCAN domain containing 25
A_23_P208 240	ZNF160	-0.37222	0.00221 5	0.045 759	-4.33107	Down	zinc finger protein 160
A_19_P003 26743	AL12165 5.1	-0.3691	0.00222 3	0.045 831	-4.32845	Down	NA
A_33_P340 7631	AC13356 5.1	-0.65338	0.00222 6	0.045 834	-4.32755	Down	NA

A_33_P329 6181	CCL3L3	-0.572	0.00222 7	0.045 834	-4.32736	Down	C-C motif chemokine ligand 3 like 3
A_19_P008 02881	#N/A	-0.41452	0.00222 8	0.045 845	-4.32685	Down	NA
A_19_P003 24996	#N/A	-0.29106	0.00223 3	0.045 897	-4.32536	Down	NA
A_32_P620 90	CCDC18 2	-0.31268	0.00225 5	0.046 061	-4.32007	Down	coiled-coil domain containing 182
A_33_P326 7270	TCEANC 2	-0.33479	0.00225 6	0.046 08	-4.31822	Down	transcription elongation factor A N-terminal and central domain containing 2
A_23_P717 27	CKS2	-0.30604	0.00225 6	0.046 08	-4.31802	Down	CDC28 protein kinase regulatory subunit 2
A_32_P120 791	LOC7279 16	-0.38371	0.00226 1	0.046 11	-4.31653	Down	uncharacterized LOC727916
A_23_P515 80	HSD3B2	-0.56617	0.00226 3	0.046 111	-4.31586	Down	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2
A_33_P341 5156	#N/A	-0.44703	0.00227 2	0.046 219	-4.31314	Down	NA
A_33_P341 9567	RAD21L 1	-0.49999	0.00228 295	0.046	-4.31051	Down	RAD21 cohesin complex component like 1
A_23_P118 158	HS3ST2	-0.78188	0.00228 3	0.046 327	-4.30943	Down	heparansulfate-glucosamine 3-sulfotransferase 2
A_24_P838 99	GRM5	-0.6979	0.00229 1	0.046 451	-4.30718	Down	glutamate metabotropic receptor 5
A_33_P334 3496	OR5M1	-1.13651	0.00229 9	0.046 535	-4.30454	Down	olfactory receptor family 5 subfamily M member 1
A_23_P252 388	SPEF2	-0.34362	0.00232 9	0.046 876	-4.29526	Down	sperm flagellar 2
A_33_P325 4579	KRTAP1- 5	-0.53907	0.00233 9	0.046 96	-4.29225	Down	keratin associated protein 1-5
A_33_P334 0926	KIR3DX 1	-0.35799	0.00235 4	0.047 043	-4.28758	Down	killer cell immunoglobulin like receptor, three Ig domains X1
A_33_P330 5456	SSU72P2	-0.8223	0.00235 5	0.047 043	-4.28742	Down	SSU72 pseudogene 2
A_33_P328 1041	#N/A	-0.30238	0.00235 7	0.047 054	-4.28686	Down	NA
A_24_P944 973	EYS	-0.99854	0.00236 6	0.047 061	-4.28409	Down	eyes shut homolog (Drosophila)
A_33_P327 8896	#N/A	-0.3572	0.00238 1	0.047 187	-4.27953	Down	NA
A_33_P331 5979	OR4Q3	-0.71413	0.00240 9	0.047 533	-4.27135	Down	olfactory receptor family 4 subfamily Q member 3
A_19_P003 20885	AC09118 2.1	-0.34391	0.00241 2	0.047 55	-4.27044	Down	NA
A_33_P331 1676	LINC007 03	-0.70239	0.00243 8	0.047 883	-4.26282	Down	long intergenic non-protein coding RNA 703
A_33_P336 3690	LINC011 82	-0.7252	0.00243 9	0.047 883	-4.26253	Down	long intergenic non-protein coding RNA 1182

A_33_P321 3982	OR13J1	-0.85672	0.00244 2	0.047 9	-4.26162	Down	olfactory receptor family 13 subfamily J member 1
A_23_P401 024	LINC003 04	-0.35474	0.00244 7	0.047 944	-4.26028	Down	long intergenic non-protein coding RNA 304
A_24_P297 537	MAMST R	-0.40407	0.00245 1	0.047 944	-4.2591	Down	MEF2 activating motif and SAP domain containing transcriptional regulator
A_23_P110 802	CENPH	-0.52312	0.00245 7	0.047 944	-4.25737	Down	centromere protein H
A_23_P580 09	C3orf52	-0.46294	0.00246 1	0.047 975	-4.25616	Down	chromosome 3 open reading frame 52
A_24_P472 007	UNC13A	-0.32027	0.00247 4	0.048 119	-4.25251	Down	unc-13 homolog A
A_24_P221 485	PSAT1P3	-0.97228	0.00248 8	0.048 29	-4.2483	Down	phosphoserine aminotransferase 1 pseudogene
A_33_P329 8267	RUFY4	-0.33366	0.00248 9	0.048 29	-4.24805	Down	RUN and FYVE domain containing 4
A_33_P336 7606	FLJ13224	-0.47084	0.00249 3	0.048 337	-4.24705	Down	uncharacterized LOC79857
A_24_P361 427	TBC1D2 9	-0.37791	0.00251 5	0.048 568	-4.24082	Down	TBC1 domain family member 29
A_33_P325 6317	MYT1L- AS1	-0.71248	0.00251 7	0.048 568	-4.24024	Down	MYT1L antisense RNA 1
A_19_P003 17146	AC00611 6.8	-0.29745	0.00252	0.048 568	-4.23944	Down	NA
A_33_P323 6846	GPR17	-0.61794	0.00252 1	0.048 568	-4.23892	Down	G protein-coupled receptor 17
A_33_P337 2376	#N/A	-0.48123	0.00252 2	0.048 568	-4.2387	Down	NA
A_33_P332 8921	LINC005 96	-0.29513	0.00252 4	0.048 568	-4.23823	Down	long intergenic non-protein coding RNA 596
A_19_P003 15998	#N/A	-1.11027	0.00255 4	0.048 927	-4.22988	Down	NA
A_33_P341 7474	CR38165 3.2	-1.16255	0.00255 4	0.048 927	-4.22977	Down	NA
A_33_P341 9577	RAD21L 1	-0.45966	0.00255 8	0.048 97	-4.22884	Down	RAD21 cohesin complex component like 1
A_19_P008 01549	#N/A	-0.40986	0.00258	0.049 254	-4.22271	Down	NA
A_33_P332 5330	#N/A	-0.6559	0.00258 2	0.049 254	-4.2222	Down	NA
A_33_P329 2565	OR11H7	-0.35919	0.00259 7	0.049 431	-4.21804	Down	olfactory receptor family 11 subfamily H member 7 (gene/pseudogene)
A_33_P324 4096	CASK	-0.39817	0.00261 8	0.049 598	-4.2122	Down	calcium/calmodulin dependent serine protein kinase
A_33_P341 4107	AC12359 5.1	-0.86069	0.00261 9	0.049 598	-4.21197	Down	NA
A_19_P003 22418	OXR1	-0.41218	0.00262 1	0.049 598	-4.21162	Down	oxidation resistance 1

A_19_P008	AC00941	-0.64286	0.00263	0.049	-4.20802	Down	NA
02684	3.1		4	766			
A_33_P340	C7orf65	-0.62876	0.00264	0.049	-4.20474	Down	chromosome 7 open reading frame 65
1397			6	904			

Table 2. The enriched pathway terms of the up-regulated differentially expressed genes.

BIOCYC							
Pathway ID	Pathway Name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
545296	retinoate biosynthesis II	1.62E-03	4.52E-02	1.78E-01	4.52E-02	02	XDH,RBP4
545295	retinoate biosynthesis I	7.21E-03	1.01E-01	3.97E-01	2.02E-01	02	ALDH1A3,RBP4
142437	nicotine degradation IV	1.13E-02	1.06E-01	4.16E-01	3.18E-01	02	FMO5,AOX1
545294	the visual cycle I (vertebrates)	2.51E-02	1.54E-01	6.05E-01	7.02E-01	02	LRAT,RBP4
545293	retinol biosynthesis	3.18E-02	1.54E-01	6.05E-01	8.89E-01	02	LRAT,RBP4
142238	catecholamine biosynthesis	3.30E-02	1.54E-01	6.05E-01	9.24E-01	01	PNMT
545318	L-carnitine biosynthesis	4.91E-02	1.72E-01	6.74E-01	1.00E+00	01	BBOX1
545363	guanosine nucleotides degradation	4.91E-02	1.72E-01	6.74E-01	1.00E+00	01	XDH
KEGG							
1026136	Signaling pathways regulating pluripotency of stem cells	5.18E-04	5.12E-02	2.94E-01	8.97E-02	09	FGFR3,FGFR2,WNT5A,ID4,SOX2,INHBA,LEFTY2,PAX6,SMAD9
83053	Neuroactive ligand-receptor interaction	7.68E-04	5.12E-02	2.94E-01	1.33E-01	13	TSHB,CSH1,CSH2,FSHB,GALR1,SSTR2,GH1,GH2,GHRHR,KISS1R,GNRHR,CCKBR,P2RY2
83032	Drug metabolism - cytochrome P450	1.06E-03	5.12E-02	2.94E-01	1.84E-01	06	UGT2A2,MGST1,ALDH1A3,FMO5,AOX1,UGT2A1
83077	Jak-STAT signaling pathway	1.18E-03	5.12E-02	2.94E-01	2.05E-01	09	AOX1,CSH1,CSH2,IFNE,IL6R,IL20RA,IL22RA1,GH1,GH2
83031	Metabolism of xenobiotics by cytochrome P450	7.71E-03	2.56E-01	1.00E+00	1.00E+00	05	UGT2A2,MGST1,HSD11B1,ALDH1A3,UGT2A1
83096	Maturity onset diabetes of the young	8.89E-03	2.56E-01	1.00E+00	1.00E+00	03	NEUROD1,NKX2-2,PAX6
673221	Chemical carcinogenesis	1.18E-02	2.80E-01	1.00E+00	1.00E+00	05	UGT2A2,MGST1,HSD11B1,ALDH1A3,UGT2A1

83064	TGF-beta signaling pathway	1.29E-02	2.80E-01	1.00E+00	1.00E+00	05	ID4,INHBA,BMP7,LEFTY2, SMAD9
82940	Steroid hormone biosynthesis	1.57E-02	2.95E-01	1.00E+00	1.00E+00	04	UGT2A2,HSD11B1,HSD17B 2,UGT2A1
172847	Protein digestion and absorption	1.70E-02	2.95E-01	1.00E+00	1.00E+00	05	COL4A6,COL13A1,SLC15A 1,CTRB1,COL21A1
Pathway Interaction Database							
137983	ALK2 signaling events	1.37E-02	5.30E-01	1.00E+00	6.72E-01	02	BMP7,SMAD9
137948	BMP receptor signaling	2.16E-02	5.30E-01	1.00E+00	1.00E+00	03	BMP7,CHRD1,SMAD9
REACTOME							
1268753	Peptide hormone biosynthesis	2.15E-06	1.11E-03	7.59E-03	1.11E-03	05	CGB3,TSHB,POMC,FSHB,I NHBA
1268754	Glycoprotein hormones	3.31E-05	8.15E-03	5.56E-02	1.71E-02	04	CGB3,TSHB,FSHB,INHBA
1269559	Hormone ligand-binding receptors	4.72E-05	8.15E-03	5.56E-02	2.44E-02	04	TSHB,FSHB,GPHA2,GNRH R
1269328	Prolactin receptor signaling	1.16E-04	1.38E-02	9.41E-02	5.98E-02	04	CSH1,CSHL1,GH1,GH2
1268746	Peptide hormone metabolism	1.33E-04	1.38E-02	9.41E-02	6.89E-02	08	PCSK2,CGB3,TSHB,POMC, FSHB,INHBA,GH1,PAX6
1269327	Growth hormone receptor signaling	7.14E-04	6.16E-02	4.21E-01	3.70E-01	04	CSH1,CSHL1,GH1,GH2
1269545	Class A/1 (Rhodopsin-like receptors)	9.87E-04	7.30E-02	4.99E-01	5.11E-01	14	GPR37L1,TSHB,POMC,FSH B,GALR1,GPHA2,SSTR2,KI SS1R,GNRHR,FFAR3,CCK, CCKBR,GAL,P2RY2
1270347	POU5F1 (OCT4), SOX2, NANOG activate genes related to proliferation	1.15E-03	7.42E-02	5.07E-01	5.93E-01	03	SALL1,SOX2,DPPA4
1269544	GPCR ligand binding	1.56E-03	8.98E-02	6.13E-01	8.08E-01	17	GPR37L1,TSHB,WNT5A,PO MC,FSHB,IHH,GALR1,GPH A2,SSTR2,GHRHR,KISS1R, GNRHR,FFAR3,CCK,CCKB R,GAL,P2RY2
1270340	Regulation of gene expression in endocrine-committed (NEUROG3+) progenitor cells	2.66E-03	1.23E-01	8.36E-01	1.00E+00	02	NEUROD1,NKX2-2
GenMAPP							
MAP00350	Tyrosine metabolism	1.32E-02	2.47E-01	8.99E-01	2.78E-01	03	ALDH1A3,PNMT,AOX1

MAP00150	Androgen and estrogen metabolism	3.18E-02	2.47E-01	8.99E-01	6.67E-01	02	HSD11B1,HSD17B2
MAP00380	Tryptophan metabolism	4.08E-02	2.47E-01	8.99E-01	8.56E-01	03	AOX1,CYP4B1,TDO2
MAP00910	Nitrogen metabolism	4.70E-02	2.47E-01	8.99E-01	9.86E-01	02	CA8,CA12
MSigDB C2 BIOCARTE (v6.0)							
M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	1.18E-09	5.44E-08	2.40E-07	5.44E-08	45	S100A14,VIT,S100A1,S100B,MFAP4,FBN2,EFEMP1,FCN2,SBSPON,SPON1,FGF1,ITIH6,COL4A6,COL8A2,FRAS1,SFRP2,COL13A1,ITLN1,WNT5A,ADAM32,CSH1,CSH2,CSHL1,SLIT1,SLPI,IFNE,IHH,MEGF11,INHBA,LAMA1,ITIH2,GH1,GH2,BMP7,COL21A1,ADAMTS18,CHRD1,CLEC9A,NTF4,OGN,LEFTY2,RSPO3,MEGF6,CBLN2,LGI1
M5883	Genes encoding secreted soluble factors	2.79E-07	6.41E-06	2.83E-05	1.28E-05	21	S100A14,S100A1,S100B,FGF1,SFRP2,WNT5A,CSH1,CSH2,CSHL1,IFNE,IHH,MEGF11,INHBA,GH1,GH2,BMP7,CHRD1,NTF4,LEFTY2,MEGF6,CBLN2
M5884	Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans	1.42E-05	2.18E-04	9.63E-04	6.54E-04	16	VIT,MFAP4,FBN2,EFEMP1,SBSPON,SPON1,COL4A6,COL8A2,FRAS1,COL13A1,SLIT1,LAMA1,COL21A1,OGN,RSPO3,LGI1
M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors	1.94E-05	2.23E-04	9.84E-04	8.91E-04	29	S100A14,S100A1,S100B,FCN2,FGF1,ITIH6,SFRP2,ITLN1,WNT5A,ADAM32,CSH1,CSH2,CSHL1,SLPI,IFNE,IHH,MEGF11,INHBA,ITIH2,GH1,GH2,BMP7,ADAMTS18,CHRD1,CLEC9A,NTF4,LEFTY2,MEGF6,CBLN2
M3008	Genes encoding structural ECM glycoproteins	4.35E-04	4.00E-03	1.77E-02	2.00E-02	11	VIT,MFAP4,FBN2,EFEMP1,SBSPON,SPON1,FRAS1,SLIT1,LAMA1,RSPO3,LGI1

M4557	Biosynthesis of neurotransmitters	3.95E-03	3.03E-02	1.34E-01	1.82E-01	02	PNMT,TPH1
M3005	Genes encoding collagen proteins	5.99E-03	3.94E-02	1.74E-01	2.76E-01	04	COL4A6,COL8A2,COL13A1, COL21A1
M16518	Wnt/Ca2+/cyclic GMP signaling.	4.30E-02	2.47E-01	1.00E+00	1.00E+00	02	PDE6A,TF
PantherDB							
P02723	Adenine and hypoxanthine salvage pathway	5.47E-03	2.19E-01	9.36E-01	2.19E-01	02	AOX1,XDH
P04371	5-Hydroxytryptamine biosynthesis	4.91E-02	6.50E-01	1.00E+00	1.00E+00	01	TPH1
Pathway Ontology							
PW:0000365	melanocortin system	1.13E-02	1.52E-01	6.35E-01	4.08E-01	02	PCSK2,POMC
PW:0000040	androgen and estrogen metabolic	1.37E-02	1.52E-01	6.35E-01	4.94E-01	02	HSD11B1,UGT2A1
PW:0000371	calcium homeostasis	1.69E-02	1.52E-01	6.35E-01	6.09E-01	01	S100A1
PW:0000138	Vitamin B6 metabolic	1.69E-02	1.52E-01	6.35E-01	6.09E-01	01	AOX1
PW:0000200	the planar cell polarity Wntsignaling	2.51E-02	1.80E-01	7.53E-01	9.02E-01	02	CELSR1,VANG12
PW:0000190	porphyrin and chlorophyll metabolic	4.91E-02	2.07E-01	8.63E-01	1.00E+00	01	UGT2A1
SMPDB							
SMP00063	Tryptophan Metabolism	2.59E-03	1.16E-01	5.13E-01	1.19E-01	03	AOX1,TDO2,TPH1
SMP00220	Xanthine Dehydrogenase Deficiency (Xanthinuria)	1.69E-02	1.16E-01	5.13E-01	7.78E-01	01	XDH
SMP00203	Molybdenum Cofactor Deficiency	1.69E-02	1.16E-01	5.13E-01	7.78E-01	01	XDH
SMP00246	Pirenzepine Pathway	3.18E-02	1.16E-01	5.13E-01	1.00E+00	02	ATP4A,CCKBR
SMP00232	Cimetidine Pathway	3.18E-02	1.16E-01	5.13E-01	1.00E+00	02	ATP4A,CCKBR
SMP00028	Caffeine Metabolism	3.30E-02	1.16E-01	5.13E-01	1.00E+00	01	XDH
SMP00233	Nizatidine Pathway	3.53E-02	1.16E-01	5.13E-01	1.00E+00	02	ATP4A,CCKBR
SMP00226	Omeprazole Pathway	3.53E-02	1.16E-01	5.13E-01	1.00E+00	02	ATP4A,CCKBR

SMP00231	Famotidine Pathway	3.53E-02	1.16E-01	5.13E-01	1.00E+00	02	ATP4A,CCKBR
SMP00227	Lansoprazole Pathway	3.53E-02	1.16E-01	5.13E-01	1.00E+00	02	ATP4A,CCKBR

Table 3 The enriched pathway terms of the down-regulated differentially expressed genes

BIOCYC							
Pathway ID	Pathway Name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
545291	vitamin D3 biosynthesis	2.55E-02	2.81E-01	8.48E-01	2.81E-01	01	CYP27B1
KEGG							
83054	Cell cycle	1.09E-03	1.56E-01	8.62E-01	1.56E-01	07	TTK,CDC45,PLK1,PTTG2,BUB1,CCNA1,CCNB2
169306	Pancreatic secretion	7.88E-03	5.44E-01	1.00E+00	1.00E+00	05	RYR2,ATP2A3,ATP2B2,PLA2G2D,CELA3A
83055	p53 signaling pathway	1.19E-02	5.44E-01	1.00E+00	1.00E+00	04	GTSE1,CCNG2,ZMAT3,CCNB2
413367	Lactosylceramide biosynthesis	2.55E-02	5.44E-01	1.00E+00	1.00E+00	01	B4GALT6
413391	Cholecalciferol biosynthesis	2.55E-02	5.44E-01	1.00E+00	1.00E+00	01	CYP27B1
83050	Calcium signaling pathway	3.01E-02	5.44E-01	1.00E+00	1.00E+00	06	CHRNA7,RYR2,ATP2A3,ATP2B2,PLCD4,GRM5
377262	Fanconianemia pathway	3.36E-02	5.44E-01	1.00E+00	1.00E+00	03	FANCA,FANCD2,RAD51
119304	Progesterone-mediated oocyte maturation	3.51E-02	5.44E-01	1.00E+00	1.00E+00	04	PLK1,BUB1,CCNA1,CCNB2
199556	Vitamin digestion and absorption	3.77E-02	5.44E-01	1.00E+00	1.00E+00	02	SLC19A1,SLC52A3
413396	Steroid hormone biosynthesis, cholesterol =>progenolone => progesterone	3.81E-02	5.44E-01	1.00E+00	1.00E+00	01	HSD3B2
83096	Maturity onset diabetes of the young	4.36E-02	5.67E-01	1.00E+00	1.00E+00	02	PKLR,PAX4
Pathway Interaction Database							
138080	Aurora B signaling	1.16E-09	4.30E-08	1.81E-07	4.30E-08	09	CENPA,KLHL13,KIF23,BIRC5,RACGAP1,NCAPG,BUB1,STMN1,KIF20A
137935	FOXM1 transcription factor network	6.86E-06	1.27E-04	5.33E-04	2.54E-04	06	CENPA,PLK1,FOXM1,BIRC5,NEK2,CCNB2

138007	PLK1 signaling events	1.93E-05	2.38E-04	1.00E-03	7.15E-04	06	PLK1,SPC24,TPX2,BUB1,CENPU,KIF20A
137925	Aurora A signaling	6.31E-04	5.83E-03	2.45E-02	2.33E-02	04	CENPA,BIRC5,TPX2,DLGAP5
137959	BARD1 signaling events	5.96E-03	4.41E-02	1.85E-01	2.20E-01	03	FANCA,FANCD2,RAD51
REACTOME							
1269820	Mitotic Prometaphase	1.04E-11	5.07E-09	3.43E-08	5.07E-09	15	KIF18A,CENPA,SPC25,CENPM,PLK1,BIRC5,SPC24,CENPH,CENPI,CDCA5,NUF2,NCAPG,BUB1,CENPU,CCNB2
1269821	Resolution of Sister Chromatid Cohesion	4.85E-11	1.18E-08	7.97E-08	2.36E-08	14	KIF18A,CENPA,SPC25,CENPM,PLK1,BIRC5,SPC24,CENPH,CENPI,CDCA5,NUF2,BUB1,CENPU,CCNB2
1269741	Cell Cycle	2.94E-10	4.76E-08	3.22E-07	1.43E-07	30	KIF18A,CENPA,HJURP,SPC25,MND1,HMMR,CDC45,CENPM,PLK1,FOXM1,KIF23,GTSE1,BIRC5,SPC24,CENPH,CENPI,TPX2,CDCA5,HAUS6,NUF2,NEK2,NCAPG,BUB1,CCNA1,RAD51,CENPU,RFC3,KIF20A,CCNB2,TOP2A
1269763	Cell Cycle, Mitotic	4.25E-10	5.16E-08	3.49E-07	2.07E-07	27	KIF18A,CENPA,SPC25,HMMR,CDC45,CENPM,PLK1,FOXM1,KIF23,GTSE1,BIRC5,SPC24,CENPH,CENPI,TPX2,CDCA5,HAUS6,NUF2,NEK2,NCAPG,BUB1,CCNA1,CENPU,RFC3,KIF20A,CCNB2,TOP2A
1269519	RHO GTPases Activate Formins	3.21E-08	3.12E-06	2.11E-05	1.56E-05	12	KIF18A,CENPA,SPC25,CENPM,PLK1,BIRC5,SPC24,CENPH,CENPI,NUF2,BUB1,CENPU
1269378	Kinesins	6.18E-08	5.01E-06	3.39E-05	3.00E-05	08	KIF18A,KIF23,RACGAP1,KIF21B,KIF26A,KIF15,KIF11,KIF20A
1269826	Separation of Sister Chromatids	2.79E-07	1.94E-05	1.31E-04	1.36E-04	13	KIF18A,CENPA,SPC25,CENPM,PLK1,BIRC5,SPC24,CENPH,CENPI,CD

									CA5,NUF2,BUB1,CENP U
1269810	M Phase			5.07E- 07	2.98E-05	2.01E-04	2.46E-04	17	KIF18A,CENPA,SPC25, CENPM,PLK1,KIF23,BI RC5,SPC24,CENPH,CE NPI,CDCA5,NUF2,NCA PG,BUB1,CENPU,KIF20 A,CCNB2
1269825	Mitotic Anaphase			5.75E- 07	2.98E-05	2.01E-04	2.79E-04	13	KIF18A,CENPA,SPC25, CENPM,PLK1,BIRC5,SP C24,CENPH,CENPI,CD CA5,NUF2,BUB1,CENP U
1269823	Mitotic Metaphase and Anaphase			6.12E- 07	2.98E-05	2.01E-04	2.98E-04	13	KIF18A,CENPA,SPC25, CENPM,PLK1,BIRC5,SP C24,CENPH,CENPI,CD CA5,NUF2,BUB1,CENP U
1269799	G2/M Transition			6.15E- 04	1.42E-02	9.62E-02	2.99E-01	09	HMMR,PLK1,FOXMI,G TSE1,TPX2,HAUS6,NE K2,CCNA1,CCNB2
MSigDB C2 BIOCARTA (v6.0)									
M17370	Role of Ran in mitotic spindle regulation			2.34E- 04	8.19E-03	3.40E-02	8.19E-03	03	RCC1,TPX2,KIF15
M16334	Eph Kinases and ephrins support platelet aggregation			6.90E- 03	1.21E-01	5.01E-01	2.42E-01	02	L1CAM,EPHB1
M9703	Role of BRCA1, BRCA2 and ATR in Cancer Susceptibility			2.94E- 02	3.43E-01	1.00E+00	1.00E+00	02	FANCD2,RAD51
PantherDB									
P00031	Inflammation mediated by chemokine and cytokine signaling pathway			1.17E- 02	3.74E-01	1.00E+00	3.74E-01	07	PF4,VWF,CCL3L3,CAS K,CXCR2,CXCR3,PLCD 4
Pathway Ontology									
PW:0000194	O-Glycans biosynthetic			1.30E- 02	5.02E-02	1.95E-01	3.52E-01	01	B4GALT6
PW:0000164	ganglioside biosynthetic			1.30E- 02	5.02E-02	1.95E-01	3.52E-01	01	B4GALT6
PW:0000196	globoside metabolic			1.30E- 02	5.02E-02	1.95E-01	3.52E-01	01	B4GALT6
PW:0000197	glycosphingolipid metabolic			1.30E- 02	5.02E-02	1.95E-01	3.52E-01	01	B4GALT6
PW:0000161	glycosylphosphatidylinosit ol anchor biosynthetic			1.30E- 02	5.02E-02	1.95E-01	3.52E-01	01	B4GALT6
PW:0000162	glycosphingolipid biosynthetic-lactoseries			1.30E- 02	5.02E-02	1.95E-01	3.52E-01	01	B4GALT6

PW:0000163	glycosphingolipid biosynthetic-neolactoseries	1.30E-02	5.02E-02	1.95E-01	3.52E-01	01	B4GALT6
PW:0000192	N-Glycans biosynthetic	2.55E-02	8.04E-02	3.13E-01	6.90E-01	01	B4GALT6
PW:0000017	Huntington disease	2.68E-02	8.04E-02	3.13E-01	7.24E-01	02	CLTC,BDNF
SMPDB							
SMP00266	Eptifibatide Pathway	9.96E-03	9.96E-03	1.05E-01	4.94E-01	02	RYR2,PLCD4
SMP00261	Ticlopidine Pathway	9.96E-03	9.96E-03	1.05E-01	4.94E-01	02	RYR2,PLCD4
SMP00265	Abciximab Pathway	9.96E-03	9.96E-03	1.05E-01	4.94E-01	02	RYR2,PLCD4
SMP00264	Dipyridamole Pathway	9.96E-03	9.96E-03	1.05E-01	4.94E-01	02	RYR2,PLCD4
SMP00263	Cilostazol Pathway	9.96E-03	9.96E-03	1.05E-01	4.94E-01	02	RYR2,PLCD4
SMP00267	Tirofiban Pathway	9.96E-03	9.96E-03	1.05E-01	4.94E-01	02	RYR2,PLCD4
SMP00336	Vitamin A Deficiency	1.30E-02	1.30E-02	1.17E-01	5.54E-01	01	BCO1
SMP00260	Clopidogrel Pathway	2.19E-02	2.19E-02	1.73E-01	8.17E-01	02	RYR2,PLCD4
SMP00367	Carvedilol Pathway	2.94E-02	2.94E-02	1.85E-01	8.75E-01	02	RYR2,PLCD4
SMP00368	Labetalol Pathway	2.94E-02	2.94E-02	1.85E-01	8.75E-01	02	RYR2,PLCD4

Table 4. The enriched GO terms of the up-regulated differentially expressed genes.

GO ID	CATEGORY	GO Name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene Count	Gene
GO:0090596	BP	sensory organ morphogenesis	1.00E-12	4.43E-09	3.97E-08	4.43E-09	28	EYA4,FBN2,EFEMP1,SALL1,CLIC5,TMIE,FGFR3,FGFR2,ALDH1A3,CLRN1,PRRX2,COL8A2,SDK2,WNT5A,CELSR1,IHH,MEGF11,SOX2,SOX9,GAS1,BMP7,FOXL2,STRAB6,CALB1,ROR2,RBP4,VANGL2,PAX6

GO:004856	BP	embryonic organ morphogenesis	1.04E-11	2.29E-08	2.06E-07	4.58E-08	28	EYA4,GRHL2,OVOL2,FBN2,EFEMP1,SALL1,CLIC5,TMIE,FGFR2,ALDH1A3,CLRN1,PRRX2,WNT5A,CELSR1,IHH,RNF207,SOX2,SOX9,GAS1,BMP7,NEUROD1,FOXL2,TBXT,STRA6,ROR2,RBP4,VANGNL2,PAX6
GO:004856	BP	embryonic organ development	5.52E-11	7.17E-08	6.43E-07	2.44E-07	33	EYA4,GRHL2,OVOL2,FBN2,EFEMP1,SALL1,CLIC5,TMIE,FGFR2,ALDH1A3,CLRN1,PRRX2,WNT5A,CELSR1,IHH,RNF207,SOX2,SOX9,PLAC1,GAS1,BMP7,NEUROD1,FOXL2,NRK,TBXT,STRA6,KRT19,ROR2,RBP4,RUNX1,VANGNL2,RSPO3,PAX6
GO:000742	BP	sensory organ development	6.48E-11	7.17E-08	6.43E-07	2.87E-07	37	EYA4,PDE6A,GRHL2,FBN2,EFEMP1,SALL1,CLIC5,TMIE,FGFR3,FGFR2,ALDH1A3,CLRN1,PRRX2,COL8A2,SDK2,WNT5A,CELSR1,IHH,PRDM16,MEGF11,SOX2,SOX9,INHBA,GAS1,LAMA1,BMP7,NEUROD1,FOXL2,ADAMTS18,CHRD1,STRA6,CALB1,NTF4,ROR2,RBP4,VANGNL2,PAX6
GO:004859	BP	embryonic morphogenesis	7.43E-10	6.57E-07	5.89E-06	3.29E-06	37	EYA4,EYA2,GRHL2,OVOL2,FBN2,EFEMP1,SALL1,CLIC5,TMIE,AMOT,FGFR2,ALDH1A3,CLRN1,PRRX2,FRAS1,SFRP2,WNT5A,TRIM71,IRX1,CELSR1,IHH,RNF207,SOX2,SOX9,INHBA,GAS1,BMP7,NEUROD1,FOXL2,TBXT,STRA6,ROR2,RBP4,VANGNL2,RSPO3,PAX6,IRX2
GO:000988	BP	animal organ morphogenesis	3.37E-09	2.28E-06	2.05E-05	1.49E-05	50	EYA4,GRHL2,PGR,OVOL2,FBN2,EFEMP1,SALL1,CLIC5,TMIE,FGF1,FGFR3,FGFR2,FRLT2,ALDH1A3,CLRN1,PRRX2,COL8A2,FRAS1,SDK2,

								SFRP2,COL13A1,WNT5A,ID4,IRX1,CELSR1,SLIT1,IHH,RNF207,MEGF11,SOX2,SOX9,INHBA,GAS1,LAMA1,BMP7,NEUROD1,FOXL2,NGFR,TBXT,STRA6,CALB1,NTF4,ROR2,RBP4,VANGL2,RSPO3,TGFBR3,PAX6,LY6H,IRX2
GO:0048592	BP	eye morphogenesis	3.61E-09	2.28E-06	2.05E-05	1.60E-05	18	FBN2,EFEMP1,FGFR3,ALDH1A3,COL8A2,SDK2,WNT5A,IHH,MEGF11,SOX2,SOX9,GAS1,BMP7,FOXL2,STRA6,CALB1,RBP4,PAX6
GO:009790	BP	embryo development	5.07E-09	2.80E-06	2.51E-05	2.24E-05	50	LRAT,ERBB4,EYA4,EYA2,GRHL2,OVOL2,FBN2,EFEMP1,SALL1,CLIC5,TMIE,AMOT,FGFR2,ALDH1A3,HSD17B2,CLRN1,PRRX2,FRAS1,SFRP2,WNT5A,TRIM71,IRX1,CELSR1,IHH,RNF207,SOX2,SOX5,SOX9,PLAC1,INHBA,GAS1,LAMA1,DLK1,BMP7,NEUROD1,FOXL2,NRK,TBXT,STRA6,KRT19,ROR2,RBP4,RUNX1,CUBN,VANGL2,RSPO3,TGFBR3,P2RY2,PAX6,IRX2
GO:0060429	BP	epithelium development	7.84E-09	3.85E-06	3.45E-05	3.47E-05	54	ERBB4,DACT2,PTER,GRHL2,PGR,OVOL2,SALL1,CLIC5,NR0B1,FGF1,FGFR3,FGFR2,ALDH1A3,CLRN1,DEUP1,FRAS1,SFRP2,WNT5A,AGR2,ID4,XDH,TRIM71,IRX1,CELSR1,IHH,RNF207,SOX2,SOX9,PRSS8,INHBA,GAS1,LAMA1,BMP7,NEUROD1,FOXL2,NGFR,TBXT,NKX2-2,KAZN,STRA6,KRT14,CALB1,NTF4,ROR2,OCA2,RUNX1,VANGL2,RSPO3,TGFBR3,ZNF750,GAL,PAX6,IRX2,SMAD9
GO:0072089	BP	stem cell proliferation	1.16E-08	5.13E-06	4.60E-05	5.13E-05	17	OVOL2,FGFR2,PRRX2,SFRP2,WNT5A,ID4,TRIM71,CSHL1,IHH,SOX2,SOX5,SOX9,GAS1,BMP7,KCNA1,RUNX1,

								PAX6
GO:0031012	CC	extracellular matrix	1.21E-08	4.58E-06	2.98E-05	4.58E-06	28	VIT,MFAP4,FBN2,EFEMP1,SBSPON,SPON1,FGF1,FGFR2,FLRT2,COL4A6,COL8A2,FRAS1,SFRP2,WNT5A,SLIT1,SLPI,IHH,LAMA1,BMP7,COL21A1,ADAMTS18,CPXM2,LAD1,RUNX1,OGN,TF,LEFTY2,TGFBR3
GO:005615	CC	extracellular space	1.37E-07	2.60E-05	1.69E-04	5.19E-05	55	PCSK2,CRISP2,SCRG1,TAC4,F5,S100B,EFEMP1,FCN2,SPON1,FGF1,FLRT2,SPINK8,SFRP2,PI16,WNT5A,AGR2,POMC,PON3,XDH,APOD,CARTPT,SCGB1D2,SCGB1D1,CSHL1,ASIP,SLIT1,SLPI,C2orf40,IFNE,IHH,CTRB1,ATP4A,IL6R,PRSS8,INHBA,LAMA1,DLK1,ITIH2,SMR3B,GH1,BMP7,KLK11,CPXM2,RBP4,KLK12,FAM3B,OGN,TF,CCK,LEFTY2,TGFBR3,GAL,DMKN,CBLN2,LGI1
GO:004420	CC	extracellular matrix component	2.57E-04	3.26E-02	2.13E-01	9.78E-02	10	MFAP4,FBN2,EFEMP1,COL4A6,COL8A2,FRAS1,LAMA1,LAD1,RUNX1,TF
GO:005604	CC	basement membrane	8.42E-04	8.00E-02	5.21E-01	3.20E-01	08	EFEMP1,COL4A6,COL8A2,FRAS1,LAMA1,LAD1,RUNX1,TF
GO:0043204	CC	perikaryon	1.16E-03	8.84E-02	5.76E-01	4.42E-01	09	PCSK2,PGR,RBFOX3,PNMT,CNTNAP2,KCNA1,NGFR,CACNA1A,CCK
GO:0005788	CC	endoplasmic reticulum lumen	1.46E-03	9.27E-02	6.04E-01	5.56E-01	11	TRDN,F5,SPON1,SRL,COL4A6,COL8A2,COL13A1,WNT5A,ERP27,COL21A1,NTF4
GO:0034703	CC	cation channel complex	4.96E-03	2.47E-01	1.00E+00	1.00E+00	09	TRDN,SCN2B,CNTNAP2,CACNA2D3,KCNA1,KCNG1,KCNJ16,KCNS2,CACNA1A
GO:0005783	CC	endoplasmic reticulum	7.05E-03	2.47E-01	1.00E+00	1.00E+00	45	SPTLC3,LRAT,CPED1,TRDN,F5,PGR,S100A1,MGST1,SPON1,TMPRSS3,SRL,PLA2G4A,FGFR3,FLRT2,HSD11B1,HSD17B2,SLC51A,FXD3,ALDOB,COL4A6,COL8A2,COL13A1,FMO5,WNT5A,AGR2

									,XDH,APOD,CSH1,CSH2,AGMO,PRSS50,CYP4B1,KCNA1,ERP27,COL21A1,NGFR,NTF4,CH25H,AGR3,OCA2,RNF175,CUBN,TGFBR3,RASGRP1,SEZ6L
GO:0090665	CC	glycoprotein complex	7.07E-03	2.47E-01	1.00E+00	1.00E+00	03		SGCD,KRT19,SNTG2
GO:031226	CC	intrinsic component of plasma membrane	0.02817	3.24E-01	1.00E+00	1.00E+00	42		KLRF1,FCER1A,SCN2B,FGFR3,FGFR2,FLRT2,FXRD3,COL13A1,SGCD,AQP4,CELSR1,ART3,SLC15A1,CNTNAP2,SLC13A5,ATP4A,IL6R,TRABD2B,PRSS8,GALR1,GAS1,SSTR2,SLC16A12,SLC39A8,KCNA1,KISS1R,KCNJ12,KCNJ16,NGFR,KCNJ2,GNRHR,GPR12,FFAR3,ROR2,CCKBR,TGFBR3,SLC39A12,CD8B,P2RY2,TSPAN8,SLC6A14
GO:005179	MF	hormone activity	4.87E-08	3.94E-05	2.87E-04	3.94E-05	14		CGB3,TSHB,POMC,CARTPT,CSH1,CSH2,CSHL1,FSHB,INHBA,GPHA2,GH1,GH2,CCCK,GAL
GO:005102	MF	signaling receptor binding	4.24E-06	1.71E-03	1.25E-02	3.43E-03	54		ERBB4,CGB3,S100A14,TSHB,TAC4,TRDN,PGR,S100B,EFEMP1,PPP1R1B,NR0B1,NGEF,FGF1,FLRT2,SFRP2,WNT5A,AGR2,POMC,ALKAL2,CARTPT,CSH1,CSH2,CSHL1,ASIP,FSHB,SLIT1,RASL11B,IFNE,IHH,IL6R,INHBA,LAMA1,GPHA2,GH1,GH2,BMP7,FOXL2,NGFR,NTF4,ROR2,FAM3B,OGN,TF,CCK,CCKBR,LEFTY2,RSPO3,TGFBR3,GAL,CD8B,P2RY2,TSPAN8,SNTG2,LGI1
GO:004854	MF	xanthine dehydrogenase activity	3.25E-04	6.58E-02	4.79E-01	2.63E-01	2		AOX1,XDH
GO:016726	MF	oxidoreductase activity, acting on	3.25E-04	6.58E-02	4.79E-01	2.63E-01	2		AOX1,XDH

		CH or CH2 groups, NAD or NADP as acceptor						
GO:004864	MF	protein phosphatase inhibitor activity	5.51E-04	8.91E-02	6.48E-01	4.46E-01	5	PPP1R1B,PHACTR3,PHACTR2,PPP1R17,PPP1R27
GO:019212	MF	phosphatase inhibitor activity	7.87E-04	1.04E-01	7.58E-01	6.37E-01	5	PPP1R1B,PHACTR3,PHACTR2,PPP1R17,PPP1R27
GO:044548	MF	S100 protein binding	1.42E-03	1.04E-01	7.58E-01	1.00E+00	3	S100A1,S100B,FGF1
GO:008236	MF	serine-type peptidase activity	1.45E-03	1.04E-01	7.58E-01	1.00E+00	12	PCSK2,F5,FCN2,TMPRSS3,PRSS45,PRSS50,CTRB1,PRSS8,RHBDL3,KLK11,CPXM2,KLK12
GO:017171	MF	serine hydrolase activity	1.61E-03	1.04E-01	7.58E-01	1.00E+00	12	PCSK2,F5,FCN2,TMPRSS3,PRSS45,PRSS50,CTRB1,PRSS8,RHBDL3,KLK11,CPXM2,KLK12
GO:004252	MF	serine-type endopeptidase activity	1.77E-03	1.04E-01	7.58E-01	1.00E+00	11	PCSK2,F5,FCN2,TMPRSS3,PRSS45,PRSS50,CTRB1,PRSS8,RHBDL3,KLK11,KLK12
GO:031781	MF	type 3 melanocortin receptor binding	1.87E-03	1.04E-01	7.58E-01	1.00E+00	2	POMC,ASIP

Note: Biological Process(BP), Cellular Component(CC) and Molecular Functions (MF).

Table 5. The enriched GO terms of the down-regulated differentially expressed genes.

GO ID	CATEGORY	GO Name	P Value	FDR B&H	FDR B&Y	Bonferro ni	Gene Count	Gene
GO:0000280	BP	nuclear division	2.87E-18	6.44E-15	5.58E-14	9.45E-15	41	NUSAP1,KIF18A,SPC25,RCC1,TTK,FANCA,FANCD2,CKS2,KLHL13,CLTC,PLK1,KIF23,BIRC5,SPC24,CENPH,TPX2,RACGAP1,MTBP,CDCA5,PTTG2,HAUS6,DLGAP5,PBK,RAD21L1,NUF2,NEK2,PTTG3P,NCAPG,KIF15,BUB1,CCNA1,KIF14,KIF11,RAD51,RAD51D,PRC1,EDN1,CCNF,CCNG2,CCNB2,TOP2A

GO:0048285	BP	organelle fission	3.91E-18	6.44E- 15	5.58E- 14	1.29E-14	42	NUSAP1,KIF18A,SPC25,RCC1, TTK,FANCA,FANCD2,CKS2,K LHL13,CLTC,PLK1,KIF23,BIRC 5,SPC24,CENPH,TPX2,RACGA P1,MTBP,MTRF2,CDCA5,PTTG 2,HAUS6,DLGAP5,PBK,RAD21 L1,NUF2,NEK2,PTTG3P,NCAP G,KIF15,BUB1,CCNA1,KIF14,K IF11,RAD51,RAD51D,PRC1,ED N1,CCNF,CCNG2,CCNB2,TOP2 A
GO:0007059	BP	chromoso me segregatio n	1.04E-17	1.14E- 14	9.91E- 14	3.43E-14	31	NUSAP1,KIF18A,CENPA,HJUR P,SPC25,RCC1,TTK,FANCD2,C ENPM,PLK1,KIF23,BIRC5,SPC2 4,CENPH,CENPI,RACGAP1,MT BP,CDCA5,PTTG2,DLGAP5,RA D21L1,NUF2,NEK2,PTTG3P,NC APG,BUB1,KIF14,KIF11,CENP U,PRC1,TOP2A
GO:0098813	BP	nuclear chromoso me segregatio n	8.97E-17	7.37E- 14	6.40E- 13	2.95E-13	28	NUSAP1,KIF18A,CENPA,SPC25 ,TTK,FANCD2,CENPM,PLK1,K IF23,BIRC5,SPC24,CENPH,CEN PI,RACGAP1,MTBP,CDCA5,PT TG2,DLGAP5,RAD21L1,NUF2, NEK2,PTTG3P,NCAPG,BUB1,K IF14,CENPU,PRC1,TOP2A
GO:0022402	BP	cell cycle process	1.35E-15	8.90E- 13	7.72E- 12	4.45E-12	58	NUSAP1,CDKN3,KIF18A,CENP A,SPC25,RCC1,HMMR,TTK,CD C45,FANCA,FANCD2,CKS2,CE NPM,KLHL13,ZC3H12D,CLTC, PLK1,FOXMI,KIF23,GTSE1,BI RC5,SPC24,CENPH,CENPI,TPX 2,RACGAP1,MTBP,CDCA5,PTT G2,SOX4,HAUS6,CYP27B1,DL GAP5,PBK,RAD21L1,NUF2,ME LK,NEK2,PTTG3P,NCAPG,KIF 15,BUB1,CCNA1,KIF14,SLC39 A5,KIF11,RAD51,RAD51D,CEN PU,STMN1,PRC1,EDN1,KIF20A ,CCNF,CCNG2,DDIAS,CCNB2, TOP2A
GO:0000819	BP	sister chromatid segregatio n	2.90E-15	1.59E- 12	1.38E- 11	9.53E-12	24	NUSAP1,KIF18A,CENPA,SPC25 ,TTK,CENPM,PLK1,KIF23,BIR C5,SPC24,CENPH,CENPI,RACG AP1,MTBP,CDCA5,DLGAP5,N UF2,NEK2,NCAPG,BUB1,KIF14

GO:1903047	BP	mitotic cell cycle process	2.55E-14	1.20E-11	1.04E-10	8.38E-11	45	,CENPU,PRC1,TOP2A NUSAP1,CDKN3,KIF18A,CENP A,SPC25,RCC1,HMMR,TTK,CD C45,CKS2,KLHL13,ZC3H12D,C LTC,PLK1,FOXM1,KIF23,GTSE 1,BIRC5,SPC24,CENPH,TPX2,R ACGAP1,MTBP,CDCA5,SOX4, HAUS6,DLGAP5,PBK,NUF2,M ELK,NEK2,NCAPG,KIF15,BUB 1,CCNA1,KIF14,KIF11,STMN1, PRC1,EDN1,KIF20A,CCNF,CC NG2,CCNB2,TOP2A
GO:0007049	BP	cell cycle	3.07E-14	1.26E-11	1.09E-10	1.01E-10	64	NUSAP1,CDKN3,KIF18A,CENP A,EXD1,HJURP,SPC25,RCC1,M ND1,HMMR,TTK,CDC45,FANC A,FANCD2,CKS2,CENPM,KLH L13,ZC3H12D,CLTC,PLK1,FOX M1,KIF23,GTSE1,BIRC5,SPC24, CENPH,CENPI,TPX2,RACGAP1 ,MTBP,PRR11,CDCA5,PTTG2,S OX4,HAUS6,CYP27B1,DLGAP5 ,PBK,RAD21L1,PARD6G,NUF2, MELK,PTP4A1,NEK2,PTTG3P, NCAPG,KIF15,BUB1,CCNA1,KI F14,SLC39A5,KIF11,RAD51,RA D51D,CENPU,STMN1,PRC1,ED N1,KIF20A,CCNF,CCNG2,DDI AS,CCNB2,TOP2A
GO:0000278	BP	mitotic cell cycle	5.56E-13	2.03E-10	1.76E-09	1.83E-09	45	NUSAP1,CDKN3,KIF18A,CENP A,SPC25,RCC1,HMMR,TTK,CD C45,CKS2,KLHL13,ZC3H12D,C LTC,PLK1,FOXM1,KIF23,GTSE 1,BIRC5,SPC24,CENPH,TPX2,R ACGAP1,MTBP,CDCA5,SOX4, HAUS6,DLGAP5,PBK,NUF2,M ELK,NEK2,NCAPG,KIF15,BUB 1,CCNA1,KIF14,KIF11,STMN1, PRC1,EDN1,KIF20A,CCNF,CC NG2,CCNB2,TOP2A
GO:0051301	BP	cell division	2.86E-12	9.41E-10	8.16E-09	9.41E-09	35	NUSAP1,SPC25,RCC1,TTK,CK S2,KLHL13,PLK1,KIF23,BIRC5, POU3F2,POU3F3,PPBP,SPC24,T PX2,RACGAP1,MTBP,CDCA5, HAUS6,DLGAP5,PARD6G,NUF 2,NEK2,NCAPG,BUB1,CCNA1, KIF14,KIF11,STMN1,PRC1,ED

									N1,KIF20A,CCNF,CCNG2,CCNB2,TOP2A
GO:0000793	CC	condensed chromosome	5.65E-11	2.22E-08	1.46E-07	2.22E-08	19		CENPA,HJURP,SPC25,RCC1,FANCD2,CENPM,PLK1,BIRC5,SPC24,CENPH,CDCA5,RAD21L1,NUF2,NEK2,NCAPG,BUB1,RAD51,CENPU,TOP2A
GO:0000776	CC	kinetochore	1.20E-10	2.36E-08	1.55E-07	4.72E-08	15		KIF18A,CENPA,HJURP,SPC25,CENPM,PLK1,BIRC5,SPC24,CENPH,CENPI,MTBP,NUF2,NEK2,BUB1,CENPU
GO:0000775	CC	chromosome, centromeric region	4.29E-09	5.33E-07	3.49E-06	1.69E-06	16		KIF18A,CENPA,HJURP,SPC25,CENPM,PLK1,BIRC5,SPC24,CENPH,CENPI,MTBP,CDCA5,NUF2,NEK2,BUB1,CENPU
GO:0000777	CC	condensed chromosome kinetochore	5.42E-09	5.33E-07	3.49E-06	2.13E-06	12		CENPA,HJURP,SPC25,CENPM,PLK1,BIRC5,SPC24,CENPH,NUF2,NEK2,BUB1,CENPU
GO:0005819	CC	spindle	7.20E-09	5.66E-07	3.71E-06	2.83E-06	20		NUSAP1,KIF18A,TTK,CLTC,PLK1,KIF23,POC1A,BIRC5,TPX2,RACGAP1,HAUS6,DLGAP5,PTP4A1,NEK2,KIF15,KIF14,KIF11,RASSF10,PRC1,KIF20A
GO:0000779	CC	condensed chromosome, centromeric region	1.72E-08	1.13E-06	7.38E-06	6.76E-06	12		CENPA,HJURP,SPC25,CENPM,PLK1,BIRC5,SPC24,CENPH,NUF2,NEK2,BUB1,CENPU
GO:0005871	CC	kinesin complex	4.58E-08	2.57E-06	1.69E-05	1.80E-05	09		KIF18A,KIF23,KIF21B,KIF26A,DISC1,KIF15,KIF14,KIF11,KIF20A
GO:0015630	CC	microtubule cytoskeleton	1.43E-07	7.01E-06	4.59E-05	5.61E-05	38		NUSAP1,KIF18A,SPEF2,TTK,CDCA5,CLTC,C12orf66,PLK1,KIF23,POC1A,GTSE1,BIRC5,TPX2,RACGAP1,KIF21B,HAUS6,KIF26A,DISC1,DLGAP5,DAB1,PTP4A1,NEK2,NCAPG,KIF15,CCNA1,KIF14,RASSF3,KIF11,RAD51,RAD51D,CENPU,RASSF10,STMN1,PRC1,KIF20A,CCNF,CCNB2,TOP2A
GO:0005694	CC	chromosome	4.51E-07	1.97E-05	1.29E-04	1.77E-04	33		NUSAP1,KIF18A,CENPA,HJURP,SPC25,RCC1,CDC45,FANCD2,SIN3CAF,CENPM,CLTC,PLK1,

									BIRC5,SPC24,CENPH,CENPI,M TBP,POLQ,CDCA5,HMGB4,RA D21L1,NUF2,TRIM24,NEK2,NC APG,BUB1,PARPBP,RAD51,RA D51D,CENPU,RFC3,ASXL2,TO P2A
GO:0044430	CC	cytoskelet al part	9.84E-07	3.65E- 05	2.39E- 04	3.87E-04	44		NUSAP1,KIF18A,SPEF2,TTK,A DD2,CDC45,CLTC,PLK1,KIF23, POC1A,CARMIL1,GTSE1,BIRC 5,KRT87P,TPX2,RACGAP1,MY BPC1,KIF21B,HAUS6,MYO1D, KIF26A,DISC1,DLGAP5,DAB1, PTP4A1,NEK2,NCAPG,KIF15,K IF14,RASSF3,KRTAP5- 7,KIF11,RAD51,RAD51D,KRT2 8,CENPU,RASSF10,STMN1,PR C1,KIF20A,CCNF,CCNB2,KRT AP1-5,TOP2A
GO:0008017	MF	microtubu le binding	6.06E-06	2.40E- 03	1.73E- 02	4.63E-03	13		NUSAP1,KIF18A,PLK1,KIF23,B IRC5,RACGAP1,KIF21B,KIF26 A,KIF15,KIF14,KIF11,PRC1,KIF 20A
GO:0003777	MF	microtubu le motor activity	8.30E-06	2.40E- 03	1.73E- 02	6.34E-03	08		KIF18A,KIF23,KIF21B,KIF26A, KIF15,KIF14,KIF11,KIF20A
GO:0015631	MF	tubulin binding	9.41E-06	2.40E- 03	1.73E- 02	7.19E-03	15		NUSAP1,KIF18A,PLK1,KIF23,B IRC5,RACGAP1,KIF21B,KIF26 A,KIF15,KIF14,KIF11,RAD51D, STMN1,PRC1,KIF20A
GO:0008574	MF	ATP- dependent microtubu le motor activity, plus-end- directed	6.32E-05	1.05E- 02	7.57E- 02	4.83E-02	04		KIF18A,KIF26A,KIF14,KIF11
GO:0003774	MF	motor activity	6.86E-05	1.05E- 02	7.57E- 02	5.24E-02	09		KIF18A,KIF23,KIF21B,MYO1D, KIF26A,KIF15,KIF14,KIF11,KIF 20A
GO:1990939	MF	ATP- dependent microtubu le motor activity	1.01E-04	1.14E- 02	8.19E- 02	7.71E-02	04		KIF18A,KIF26A,KIF14,KIF11
GO:0016887	MF	ATPase activity	1.04E-04	1.14E- 02	8.19E- 02	7.95E-02	17		KIF18A,KIF23,POLQ,ATP2A3,A TP2B2,KIF21B,MYO1D,KIF26A

									,DHX15,KIF15,KIF14,KIF11,RA D51,RAD51D,RFC3,KIF20A,TO P2A
GO:0043142	MF	single- stranded DNA- dependent ATPase activity	7.57E-04	6.64E- 02	4.79E- 01	5.79E-01	03		POLQ,RAD51,RFC3
GO:0030165	MF	PDZ domain binding	8.28E-04	6.64E- 02	4.79E- 01	6.33E-01	07		ARHGAP29,NLGN1,CASK,ATP 2B2,KIF14,L1CAM,GRIK2
GO:0044877	MF	protein- containing complex binding	8.70E-04	6.64E- 02	4.79E- 01	6.64E-01	37		NUSAP1,DOK6,KIF18A,NRG1, CENPA,RBPJL,RCC1,ADD2,CD C45,CKS2,PLK1,KIF23,VWF,C ARMIL1,BIRC5,CASK,CENPH, RACGAP1,POLQ,CDCA5,KIF21 B,MYO1D,KIF26A,DISC1,TRIM 24,YTHDF1,PRDM11,KIF15,KIF 14,KIF11,RAD51,L1CAM,PRC1, KIF20A,TLE4,TOP2A,EPHB1

Note: Biological Process(BP), Cellular Component(CC) and Molecular Functions (MF).

Table 6. Topology table for up and down regulated genes.

Category	Node	Degree	Betweenness	Stress	Closeness	Clustering Coefficient
Up	SALL1	20	6.73E-03	599040	0.270852	0.026316
Up	BMP7	42	1.85E-02	2547692	0.241805	0
Up	FAM83F	2	5.08E-04	43304	0.20099	0
Up	SGCD	8	3.55E-03	808402	0.171417	0
Up	C1orf168	1	0.00E+00	0	1	0
Up	GRHL2	7	1.70E-03	324668	0.243088	0
Up	TDO2	18	3.51E-03	741118	0.221367	0
Up	SMR3B	11	2.91E-03	241848	0.209856	0
Up	SCRG1	1	0.00E+00	0	0.171291	0
Up	IL20RA	36	1.30E-02	3240444	0.233049	0
Up	FCN2	7	2.56E-03	197754	0.189402	0
Up	DPPA4	105	5.28E-02	8404518	0.278355	1.90E-04
Up	ATP4A	91	4.54E-02	4727962	0.263514	0
Up	GPR12	2	5.02E-04	50910	0.215258	0
Up	SDK2	11	1.32E-03	347148	0.206891	0
Up	SEPT14	9	3.56E-03	546322	0.189457	0
Up	RSPO3	5	2.03E-03	178044	0.172718	0
Up	SLC13A5	2	1.07E-04	16672	0.203829	0
Up	FGFR2	93	5.79E-02	6781948	0.291174	0.003175
Up	MGST1	7	1.66E-03	259370	0.209421	0

Up	FABP7	10	3.53E-03	348144	0.198368	0
Up	PON3	2	1.00E+00	2	1	0
Up	GAL	9	2.89E-03	341670	0.219065	0
Up	PAX6	49	2.00E-02	1487900	0.266617	0.002775
Up	SYPL2	12	3.97E-03	648624	0.216559	0
Up	LGI1	2	5.08E-04	71602	0.185225	0
Up	SLC15A1	64	2.63E-02	6462618	0.251196	0
Up	TMPRSS3	33	1.58E-02	3314720	0.24797	0
Up	ROR2	49	1.54E-02	2469916	0.257031	0
Up	DACT2	4	1.06E-03	191246	0.177576	0
Up	SMTNL2	16	4.38E-03	927394	0.241701	0
Up	KRT40	313	1.59E-01	22565808	0.304829	0
Up	FBN2	24	6.88E-03	1381044	0.220957	0
Up	NTF4	5	2.03E-03	147964	0.13475	0
Up	GBA3	2	5.08E-04	52696	0.148844	0
Up	SLIT1	2	5.08E-04	49644	0.176676	0
Up	OR7A5	1	0.00E+00	0	0.214321	0
Up	BBOX1	19	6.49E-03	440000	0.226003	0
Up	ART3	24	8.13E-03	976682	0.239993	0
Up	ID4	13	3.35E-03	782844	0.231447	0
Up	PLIN4	3	7.56E-05	37378	0.213461	0
Up	TRDN	37	1.31E-02	2095642	0.247674	0
Up	CLIC5	8	2.39E-03	360044	0.208391	0
Up	IRX1	1	0.00E+00	0	0.200969	0
Up	FCER1A	3	3.26E-05	5636	0.185557	0
Up	NGEF	21	7.48E-03	1282594	0.208005	0
Up	CCKBR	17	6.42E-03	1313620	0.225189	0
Up	ITLN1	11	3.22E-03	584478	0.223274	0
Up	S100A1	23	5.90E-03	824942	0.251533	0
Up	TMEM139	3	3.55E-03	258886	0.184289	0
Up	PMAIP1	14	4.74E-03	615246	0.230621	0
Up	GHRHR	1	0.00E+00	0	1	0
Up	XDH	2	5.08E-04	44858	0.200601	0
Up	TRIM29	104	6.13E-02	9041322	0.297553	0
Up	UGT2A2	1	0.00E+00	0	1	0
Up	SOX5	37	1.43E-02	1508376	0.275378	0
Up	S100A1	23	5.90E-03	824942	0.251533	0
Up	GALR1	1	0.00E+00	0	0.179707	0
Up	GAS1	3	1.01E-03	43314	0.226575	0
Up	PPP1R17	1	0.00E+00	0	0.214321	0
Up	IFNE	10	2.80E-03	416368	0.217901	0
Up	CELSR1	17	4.71E-03	588542	0.223388	0
Up	C4orf19	7	5.94E-04	75814	0.20404	0
Up	POMC	13	5.46E-03	738136	0.221941	0
Up	LRAT	3	0.00E+00	0	1	0
Up	KLK11	27	1.36E-02	2408872	0.236335	0

Up	F5	15	4.61E-03	881738	0.220265	0
Up	CNTNAP2	8	2.06E-03	345082	0.217348	0
Up	ENPP6	40	1.39E-02	3610524	0.233408	0
Up	GBP6	3	1.02E-03	53086	0.167077	0
Up	OBP2A	7	3.04E-03	662994	0.170129	0
Up	RBP4	15	4.72E-03	550068	0.226992	0
Up	PPP1R27	1	0.00E+00	0	0.166294	0
Up	ITIH2	16	5.09E-03	851246	0.219884	0
Up	NEURL3	1	0.00E+00	0	1	0
Up	CLIC5	8	2.39E-03	360044	0.208391	0
Up	PPP1R27	1	0.00E+00	0	0.166294	0
Up	RASL11B	6	1.08E-03	251748	0.233312	0
Up	KCNJ12	17	4.14E-03	1228964	0.207786	0
Up	AQP4	3	5.64E-04	54624	0.198508	0
Up	CD8B	2	5.08E-04	43304	0.20099	0
Up	P2RY2	4	9.10E-04	137648	0.233077	0
Up	IL22RA1	7	2.15E-03	456438	0.199181	0
Up	RNF207	4	6.33E-04	99124	0.213496	0
Up	ADAMTS18	5	7.80E-04	175548	0.216858	0
Up	NGFR	46	1.93E-02	2626710	0.258024	0
Up	KCNJ16	1	0.00E+00	0	1	0
Up	EFEMP1	56	3.53E-02	3383126	0.271749	0
Up	CHN2	13	3.42E-03	578204	0.234506	0
Up	GPHA2	21	6.38E-03	1083752	0.214718	0
Up	GHRHR	1	0.00E+00	0	1	0
Up	KRT40	313	1.59E-01	22565808	0.304829	0
Up	C6orf132	1	0.00E+00	0	0.195135	0
Up	NRAP	7	2.54E-03	723962	0.182437	0
Up	PHACTR2	16	5.85E-03	1042524	0.242609	0
Up	EVC2	86	4.01E-02	3002590	0.269961	0
Up	FOXL2	70	2.86E-02	8356260	0.257889	0
Up	FAM3B	9	5.47E-03	400338	0.24077	0
Up	DLK1	69	3.09E-02	5339202	0.257485	0
Up	BLID	12	2.22E-03	427182	0.219345	0
Up	CALB1	8	1.87E-03	281870	0.227635	0
Up	OGN	10	3.36E-03	588086	0.221218	0
Up	TF	59	3.30E-02	5546776	0.282609	0
Up	SMAD9	114	7.87E-02	8103704	0.303093	0
Up	SOX2	355	2.07E-01	37524600	0.318174	0
Up	KRT14	53	2.76E-02	6537242	0.277277	0
Up	DLGAP2	14	8.62E-03	607018	0.259128	0
Up	LRRC2	2	1.61E-05	2042	0.164853	0
Up	AMOT	111	6.81E-02	13889668	0.286702	0
Up	ZNF385C	7	2.12E-03	396460	0.198308	0
Up	CCK	2	5.08E-04	109288	0.183825	0
Up	HSD11B1	16	5.27E-03	800492	0.218251	0

Up	SGCD	8	3.55E-03	808402	0.171417	0
Up	PRSS8	1	0.00E+00	0	1	0
Up	C6orf118	5	1.11E-03	182260	0.220228	0
Up	LAD1	7	2.00E-03	282468	0.222492	0
Up	MYL10	3	3.70E-04	73004	0.215777	0
Up	CRISP2	5	2.02E-03	232114	0.218082	0
Up	IHH	2	5.08E-04	70496	0.159532	0
Up	MCOLN2	1	0.00E+00	0	1	0
Up	SLC39A12	70	3.22E-02	4986186	0.249178	0
Up	VIT	2	5.08E-04	69608	0.209376	0
Up	PPP1R17	1	0.00E+00	0	0.214321	0
Up	TSHB	15	6.40E-03	1264174	0.237848	0
Up	GADD45G	56	2.74E-02	5419566	0.271843	0
Up	FXYD3	7	1.80E-03	219094	0.20662	0
Up	LIX1	2	1.00E+00	2	1	0
Up	PRSS45	3	1.00E+00	6	1	0
Up	MFAP4	6	1.38E-03	246964	0.216631	0
Up	SPON1	3	1.02E-03	109098	0.214367	0
Up	NFIX	22	5.02E-03	1428620	0.232403	0
Up	COL8A2	18	6.18E-03	653142	0.221205	0
Up	GNRHR	1	0.00E+00	0	1	0
Up	SULT1C2	10	4.91E-03	344354	0.215375	0
Up	CA8	33	1.30E-02	1324240	0.262215	0
Up	CHRD1	6	7.97E-04	108788	0.198089	0
Up	MEGF6	6	1.43E-03	100130	0.228083	0
Up	RPRM	9	3.81E-03	39669	0.211331	0
Up	OCA2	3	8.78E-05	7862	0.168788	0
Up	MPPED1	26	8.03E-03	1622472	0.222492	0
Up	CARTPT	3	1.00E+00	6	1	0
Up	CSH1	13	5.61E-03	475316	0.257014	0
Up	GALNT9	1	0.00E+00	0	0.189969	0
Up	OGN	10	3.36E-03	588086	0.221218	0
Up	FAM153B	14	5.40E-03	935250	0.2049	0
Up	GADD45G	56	2.74E-02	5419566	0.271843	0
Up	VSNL1	10	1.31E-03	162184	0.199151	0
Up	KISS1R	3	1.02E-03	144830	0.182319	0
Up	FGFR3	49	2.12E-02	2766462	0.268434	0
Up	WNT5A	22	7.80E-03	881282	0.206349	0
Up	CD8B	2	5.08E-04	43304	0.20099	0
Up	SFRP2	17	3.65E-03	988952	0.223769	0
Up	HSPB3	24	9.14E-03	1066592	0.24811	0
Up	PAX6	49	2.00E-02	1487900	0.266617	0.002775
Up	CYBRD1	21	7.61E-03	1486198	0.221255	0
Up	FXYD3	7	1.80E-03	219094	0.20662	0
Up	PGR	68	3.40E-02	5124700	0.28689	0
Up	HSD17B2	2	5.08E-04	61020	0.152911	0

Up	OPCML	11	9.23E-03	415810	0.253949	0
Up	RFX4	4	5.08E-04	68768	0.194519	0
Up	AGR3	14	3.65E-03	622642	0.231135	0
Up	SLIT1	2	5.08E-04	49644	0.176676	0
Up	SOX9	19	4.66E-03	1135172	0.228918	0
Up	CSHL1	3	1.02E-03	142558	0.195484	0
Up	CHST9	4	4.30E-04	57912	0.2136	0
Up	SULT1C2	10	4.91E-03	344354	0.215375	0
Up	DYDC2	1	0.00E+00	0	1	0
Up	SLIT1	4	1.52E-03	98748	0.177265	0
Up	SNTG2	14	4.17E-03	686616	0.201051	0
Up	ZNF750	1	0.00E+00	0	0.196381	0
Up	TAC4	3	1.00E+00	6	1	0
Up	PTER	14	4.59E-03	989784	0.223477	0
Up	CTRB1	2	1.00E+00	2	1	0
Up	COL21A1	2	0.00E+00	0	0	0
Up	ATF7IP2	4	7.03E-04	79612	0.215258	0
Up	NEFM	50	2.12E-02	4143078	0.272012	0
Up	S100A14	21	8.84E-03	986808	0.265288	0
Up	AOX1	6	1.58E-03	130420	0.202895	0
Up	KLRF1	5	6.70E-04	77804	0.192503	0
Up	CCDC68	13	5.14E-03	436104	0.208269	0
Up	CNKSR3	9	2.74E-03	263976	0.196244	0
Up	CRYM	4	5.65E-04	44096	0.209666	0
Up	MYZAP	1	0.00E+00	0	0.213484	0
Up	PDE6A	4	1.43E-04	8434	0.238597	0
Up	INHBA	8	2.57E-03	734598	0.176407	0
Up	CNTNAP3	33	1.34E-02	1433542	0.235939	0
Up	FAM153C	2	5.08E-04	85808	0.170078	0
Up	C6orf141	74	3.72E-02	9207512	0.260292	0
Up	RUNX1	79	3.50E-02	4622022	0.286015	0
Up	TRIM71	17	6.52E-03	713150	0.220623	0
Up	PNMT	3	5.88E-04	55878	0.215493	0
Up	PRSS50	25	9.88E-03	1981826	0.256663	0
Up	SLC47A1	27	1.28E-02	765214	0.222832	0
Up	PHACTR3	29	1.17E-02	1887264	0.234506	0
Up	IL20RA	36	1.30E-02	3240444	0.233049	0
Up	LEFTY2	3	1.02E-03	95398	0.147528	0
Up	RHBDL3	4	1.52E-03	323400	0.165874	0
Up	GH1	85	3.79E-02	5815610	0.26716	0
Up	STRA6	2	5.08E-04	57684	0.184652	0
Up	FRAS1	33	1.76E-02	1896950	0.244978	0
Up	CT45A1	3	1.00E+00	6	1	0
Up	FGFR3	49	2.12E-02	2766462	0.268434	0
Up	EYA4	26	6.49E-03	1286994	0.239075	0
Up	AMZ1	12	3.35E-03	644006	0.193934	0

Up	CACNA1A	98	5.07E-02	4392082	0.272841	0
Up	CA12	13	3.67E-03	625692	0.218106	0
Up	GAS7	28	9.64E-03	1499288	0.218894	0
Up	HPGD	1	0.00E+00	0	0.214321	0
Up	FMO5	5	9.24E-04	141874	0.217516	0
Up	SCGB1D2	9	2.67E-03	252442	0.209376	0
Up	PLIN5	6	2.54E-03	488350	0.178558	0
Up	KCNA1	7	2.68E-03	237802	0.195435	0
Up	ALDOB	28	1.11E-02	1644614	0.253084	0
Up	RHOD	19	7.80E-03	1084918	0.189786	0
Up	GJB7	51	2.16E-02	2788870	0.243992	0
Up	ALDH1A3	9	2.42E-03	378026	0.220327	0
Up	EYA2	88	4.15E-02	6323538	0.281237	0
Up	KRT19	59	2.60E-02	7305954	0.276926	0
Up	LY6H	3	5.57E-04	60178	0.176092	0
Up	MYBPHL	7	2.32E-03	246776	0.198308	0
Up	RASGRP1	4	3.51E-04	53352	0.195019	0
Up	GH2	2	8.82E-06	644	0.197325	0
Up	FERMT1	15	4.58E-03	653358	0.227097	0
Up	ASXL3	2	5.08E-04	44514	0.172627	0
Up	TEPP	1	0.00E+00	0	0.209354	0
Up	PDZRN3	11	4.13E-03	858088	0.195387	0
Up	KCNS2	1	0.00E+00	0	0.148569	0
Up	VANGL2	33	1.46E-02	1934604	0.232321	0
Up	PRDM16	6	1.44E-03	306010	0.223972	0
Up	PLAC1	20	6.67E-03	1205836	0.224957	0
Up	SH3BP4	43	1.67E-02	2668100	0.262618	0
Up	COL4A6	9	4.29E-03	288964	0.222241	0
Up	NEUROD1	15	3.84E-03	758734	0.219016	0
Up	IL6R	17	6.73E-03	876290	0.223845	0
Up	FSHB	2	1.00E+00	2	1	0
Up	CSH2	13	5.61E-03	475316	0.257014	0
Up	CNTNAP3B	16	7.15E-03	582922	0.190741	0
Up	CHRD1	6	7.97E-04	108788	0.198089	0
Up	NWD1	1	0.00E+00	0	0.175339	0
Up	WWC2	18	3.48E-03	975000	0.230041	0
Up	APOD	50	3.56E-02	2147634	0.271412	0
Up	GJB7	51	2.16E-02	2788870	0.243992	0
Up	RXRG	32	1.14E-02	2426724	0.228268	0
Up	RNF175	2	2.24E-05	1134	0.179355	0
Up	IGSF11	2	0.00E+00	0	0	0
Up	SCN2B	86	3.56E-02	7895890	0.255896	0
Up	OVOL2	1	0.00E+00	0	0.216108	0
Up	CCDC158	12	2.91E-03	441576	0.225705	0
Up	ASXL3	2	5.08E-04	44514	0.172627	0
Up	CYP4B1	2	1.00E+00	2	1	0

Up	DLGAP2	14	8.62E-03	607018	0.259128	0
Up	TPH1	7	1.87E-03	396120	0.227635	0
Up	AOX1	6	1.58E-03	130420	0.202895	0
Up	SLC39A8	26	1.05E-02	1259100	0.220179	0
Up	S100B	33	1.07E-02	1384834	0.252922	0
Up	SLPI	7	4.10E-03	388202	0.209143	0
Up	PGR	68	3.40E-02	5124700	0.28689	0
Up	SSTR2	7	2.14E-03	321652	0.229425	0
Up	FLRT2	3	0.00E+00	0	1	0
Up	C2orf71	5	2.03E-03	289652	0.182386	0
Up	COL13A1	2	0.00E+00	0	0	0
Up	CACNA2D3	1	0.00E+00	0	1	0
Up	NR0B1	15	5.59E-03	309134	0.247425	0
Up	CALB2	4	1.64E-05	1926	0.187706	0
Up	STMN2	27	1.22E-02	1546160	0.247254	0
Up	SCGB1D1	71	4.35E-02	6754916	0.254063	0
Up	FGF1	27	1.23E-02	832698	0.262916	0
Up	KCNA1	7	2.68E-03	237802	0.195435	0
Up	FOXL2	70	2.86E-02	8356260	0.257889	0
Up	MAP3K15	7	1.18E-03	196726	0.213172	0
Up	MKX	10	2.04E-03	492958	0.220302	0
Up	TXLNB	43	1.53E-02	4523946	0.233769	0
Up	T	1	0.00E+00	0	1	0
Up	ERBB4	84	3.50E-02	8327424	0.269131	0
Up	PPP1R1B	8	1.69E-03	176268	0.187885	0
Up	PCSK2	2	0.00E+00	0	0	0
Up	DMKN	7	2.21E-03	390378	0.236123	0
Up	TGFBR3	22	9.08E-03	805594	0.23413	0
Up	MN1	3	4.47E-05	9412	0.20941	0
Up	SLIT1	2	5.08E-04	49644	0.176676	0
Up	KCNG1	5	1.09E-03	200078	0.194567	0
Up	MEGF11	2	5.16E-05	7530	0.192871	0
Up	PLA2G4A	35	1.68E-02	3125428	0.264079	0
Up	ERP27	5	6.80E-04	96440	0.20941	0
Up	GPR37L1	1	0.00E+00	0	1	0
Up	SMR3B	11	2.91E-03	241848	0.209856	0
Up	CLIC3	9	3.25E-03	417244	0.21813	0
Up	SYT12	16	5.27E-03	975528	0.226783	0
Up	CUBN	10	2.40E-03	351968	0.206793	0
Up	PNMA3	5	7.32E-04	128516	0.189685	0
Up	FAM198A	3	9.84E-05	8632	0.182912	0
Up	FAM124A	29	1.00E-02	2057940	0.226796	0
Up	CPLX3	17	7.35E-03	422424	0.250732	0
Up	ADARB2	9	2.11E-03	368998	0.226171	0
Up	DMKN	7	2.21E-03	390378	0.236123	0
Up	BANK1	4	1.46E-04	22828	0.217336	0

Up	HIF3A	3	6.24E-04	67108	0.19472	0
Up	CNTNAP3	33	1.34E-02	1433542	0.235939	0
Up	CCNJL	39	1.50E-02	3448762	0.260533	0
Up	ADAM32	21	6.74E-03	1279704	0.223185	0
Up	PHYHD1	3	7.04E-04	88272	0.214905	0
Up	LAMA1	31	1.32E-02	3129918	0.248298	0
Up	DNAI2	12	3.01E-03	467486	0.2	0
Down	TRIM24	66	2.39E-02	7566812	0.292625	0
Down	KLHL13	30	8.55E-03	2607752	0.279499	0
Down	MAGEB2	46	1.08E-02	4326748	0.268579	0
Down	PPBP	22	7.30E-03	2718118	0.22063	0
Down	TTK	77	3.23E-02	12267556	0.31332	7.21E-04
Down	FAM71D	3	6.39E-05	15292	0.197561	0
Down	TOP2A	102	4.15E-02	13126864	0.323325	0.002912
Down	KIF18A	27	9.22E-03	1047074	0.272947	0.002849
Down	TPX2	45	1.33E-02	5212220	0.283324	0.00303
Down	POC1A	3	2.10E-04	38988	0.263713	0
Down	ARHGAP29	14	2.99E-03	1435976	0.254092	0
Down	NRG1	66	2.98E-02	8652224	0.277873	0
Down	PLCD4	3	1.07E-03	235394	0.224878	0
Down	CADPS2	15	4.01E-03	1430040	0.22412	0
Down	CCNF	13	2.36E-03	321772	0.266733	0
Down	GTSE1	141	5.29E-02	7085030	0.337622	0.008713
Down	TRHDE	15	4.61E-03	1973410	0.23257	0
Down	SOX4	27	1.24E-02	7096428	0.258212	0
Down	DLEU1	21	6.78E-03	2289500	0.253469	0
Down	PLK1	276	1.64E-01	39488508	0.35244	0.001016
Down	HAUS6	53	1.32E-02	7866150	0.288256	0
Down	BUB1	95	4.02E-02	4659062	0.318162	0.008649
Down	SERINC2	8	2.18E-03	1257316	0.206187	0
Down	KIF14	62	1.75E-02	10376292	0.284688	0
Down	VWA1	14	4.26E-03	366250	0.21001	0
Down	PTTG2	1	0.00E+00	0	0.224824	0
Down	SEL1L	58	2.60E-02	9557720	0.270569	0
Down	NUSAP1	35	1.32E-02	2253376	0.300363	0.008913
Down	CELA3A	12	3.00E-03	434718	0.234812	0
Down	DOK6	6	7.47E-04	300368	0.234664	0
Down	NRG1	66	2.98E-02	8652224	0.277873	0
Down	DHX15	208	9.39E-02	39966314	0.320847	0
Down	NEK2	52	1.53E-02	5682386	0.277397	0
Down	TAS2R7	14	5.78E-03	635150	0.247921	0.010989
Down	SPC24	41	1.22E-02	1425412	0.291526	0.039024
Down	HMMR	44	1.23E-02	3764124	0.283002	0.003171
Down	PTP4A1	53	2.21E-02	5500792	0.256435	0
Down	DAZAP2	99	4.35E-02	9779248	0.28839	0.003651
Down	CDCA5	55	1.97E-02	1719302	0.3	0.002903

Down	ANTXR2	12	3.86E-03	876552	0.218842	0
Down	FBXL5	41	1.34E-02	1287978	0.299253	0.006748
Down	PLA2G2D	1	0.00E+00	0	0.206084	0
Down	DAB1	67	2.85E-02	5666990	0.279457	0.007689
Down	RBPJL	2	5.37E-04	117698	0.224851	0
Down	FANCA	86	2.87E-02	13664846	0.284167	0
Down	NLGN1	11	3.82E-03	881670	0.215525	0
Down	POU3F2	10	2.82E-03	567692	0.225258	0
Down	PPP4R4	3	5.68E-04	157816	0.205041	0
Down	GPR6	2	5.37E-04	60688	0.210938	0
Down	PAX4	3	1.07E-03	234714	0.21372	0
Down	ASXL2	18	6.05E-03	1686090	0.242263	0
Down	IGFL3	1	0.00E+00	0	1	0
Down	GRIK2	13	4.44E-03	430606	0.243976	0.025641
Down	NCAPG	52	1.62E-02	5737472	0.285517	0
Down	SLC19A1	3	5.43E-04	132382	0.188974	0
Down	EPHB1	14	3.21E-03	1135208	0.242942	0
Down	INHBE	15	7.30E-03	1600282	0.257445	0
Down	FIBCD1	1	0.00E+00	0	1	0
Down	RGS5	7	2.09E-03	462166	0.237446	0
Down	CCNB2	36	8.70E-03	3365996	0.275673	0.009524
Down	ADAMTSL1	7	2.82E-03	352088	0.208506	0
Down	FAM83A	7	1.40E-03	115518	0.279038	0.047619
Down	LRFN1	20	9.73E-03	1618782	0.237416	0
Down	PKLR	19	4.89E-03	591642	0.267308	0.005848
Down	SLC25A15	15	5.26E-03	1022014	0.258069	0
Down	PRC1	29	6.84E-03	1142838	0.294452	0.031339
Down	AMIGO2	6	1.08E-03	410596	0.178235	0
Down	KIF11	134	5.97E-02	17181634	0.31282	0
Down	G2E3	6	1.27E-03	455226	0.218061	0
Down	OR6T1	1	0.00E+00	0	0.225613	0
Down	POLQ	1	0.00E+00	0	1	0
Down	GRIK2	13	4.44E-03	430606	0.243976	0.025641
Down	RASSF3	28	7.78E-03	3540288	0.258176	0
Down	PBK	107	4.20E-02	12464178	0.300775	0
Down	CENPA	88	3.07E-02	4765456	0.300799	0.006293
Down	LYNX1	1	0.00E+00	0	0.189426	0
Down	ASPDH	10	3.69E-03	974500	0.235242	0
Down	DLGAP5	23	7.53E-03	2047406	0.302705	0.019763
Down	KIF20A	38	9.99E-03	3761204	0.277108	0
Down	CNKSR2	10	2.74E-03	698616	0.245083	0
Down	GOLGA6A	1	0.00E+00	0	0.194204	0
Down	B4GALT6	4	1.00E+00	12	1	0
Down	KRT28	1	0.00E+00	0	1	0
Down	CDKN3	29	1.03E-02	1383840	0.274414	0.002849
Down	DCAF4L2	7	1.14E-03	263466	0.229603	0

Down	CALHM1	2	0.00E+00	0	0	0
Down	ADD2	17	5.29E-03	1384972	0.251723	0
Down	CDKN3	29	1.03E-02	1383840	0.274414	0.002849
Down	RYR2	28	8.08E-03	2614302	0.258642	0
Down	C20orf203	2	1.00E+00	2	1	0
Down	YTHDF1	61	2.13E-02	7937228	0.298366	0
Down	FOXM1	80	2.74E-02	8443400	0.298749	0.002331
Down	GJA4	3	1.07E-03	514922	0.181296	0
Down	PF4	11	5.89E-03	2016954	0.188248	0.027778
Down	ANKFY1	41	1.24E-02	5747558	0.26362	0
Down	AKAP3	10	3.76E-03	892188	0.240046	0
Down	DCAF12L2	11	3.30E-03	771012	0.231472	0
Down	BDNF	11	4.67E-03	1264752	0.242373	0
Down	BIRC5	61	2.10E-02	6990168	0.290549	0
Down	SLC39A5	45	1.94E-02	2952184	0.228407	0
Down	GLYATL3	1	0.00E+00	0	0.190715	0
Down	L1CAM	24	6.90E-03	2825930	0.267884	0
Down	SV2C	7	2.26E-03	545018	0.20922	0
Down	KIF15	27	7.88E-03	1833408	0.267865	0
Down	FANCD2	74	3.14E-02	6501308	0.312978	0.004813
Down	RACGAP1	89	3.18E-02	7802394	0.304263	0.005107
Down	FAM20C	12	4.87E-03	828322	0.200852	0
Down	NUF2	44	1.42E-02	2296298	0.301725	3.38E-02
Down	QSOX1	15	4.90E-03	1223750	0.241087	0
Down	SLITRK6	1	0.00E+00	0	0.206759	0
Down	FAM91A1	23	7.07E-03	2542312	0.2639	0
Down	GPR161	16	8.15E-03	864880	0.246363	0.008333
Down	SCEL	14	5.37E-03	1611186	0.249883	0
Down	CXCR3	6	2.15E-03	733476	0.158492	0.066667
Down	RFT1	21	6.86E-03	2273166	0.225517	0
Down	PSG5	4	1.24E-03	315510	0.199775	0
Down	RAD51	120	4.54E-02	8161594	0.307324	0.001883
Down	ADAMTSL1	7	2.82E-03	352088	0.208506	0
Down	HMGB4	3	6.06E-04	146328	0.226988	0
Down	TROAP	33	1.24E-02	1251972	0.293872	0.006452
Down	RASSF10	38	1.21E-02	3884098	0.259851	0
Down	ZC3H12D	1	0.00E+00	0	1	0
Down	HJURP	21	4.31E-03	873270	0.271041	0.035088
Down	XKR6	1	0.00E+00	0	0.225613	0
Down	UNC5D	1	0.00E+00	0	0.201809	0
Down	C1orf189	2	1.00E+00	2	1	0
Down	PSTPIP2	8	1.87E-03	472358	0.247427	0
Down	XKR6	1	0.00E+00	0	0.225613	0
Down	EXD1	1	0.00E+00	0	1	0
Down	KIF21B	30	9.70E-03	2431650	0.256842	0
Down	GRIP1	53	1.84E-02	6233398	0.270372	0.001569

Down	POU3F3	3	5.62E-04	84710	0.208378	0
Down	CPN1	6	1.71E-03	328228	0.22172	0
Down	SPC25	35	6.24E-03	630312	0.27207	0.052101
Down	C12ORF66	4	1.61E-03	77742	0.201711	0
Down	MELK	23	6.63E-03	1668988	0.250673	0
Down	TLE4	28	9.56E-03	2438214	0.252507	0
Down	MND1	7	2.70E-03	788252	0.224986	0
Down	ZMAT3	24	7.69E-03	2968830	0.271931	0
Down	ATP2A3	53	2.39E-02	6619182	0.256171	0
Down	GRIP1	53	1.84E-02	6233398	0.270372	0.001569
Down	CENPM	15	2.31E-03	174586	0.25524	0.114286
Down	GRIK2	13	4.44E-03	430606	0.243976	0.025641
Down	ZSCAN2	1	0.00E+00	0	1	0
Down	GPR26	1	0.00E+00	0	1	0
Down	NXPH4	4	1.61E-03	1133406	0.17246	0
Down	UNC5D	1	0.00E+00	0	0.201809	0
Down	RNF215	1	0.00E+00	0	1	0
Down	STMN1	65	2.51E-02	7293058	0.286065	4.81E-04
Down	ARHGAP20	2	1.00E-05	3872	0.219564	0
Down	FAM72D	1	0.00E+00	0	0.225613	0
Down	HTR3D	4	7.06E-04	153078	0.180646	0
Down	ATP2B2	118	5.57E-02	10270314	0.275124	2.90E-04
Down	CCNG2	11	3.40E-03	744714	0.210806	0
Down	RCC1	102	3.87E-02	10546556	0.314165	0.001941
Down	NPVF	3	3.46E-05	17228	0.217653	0
Down	KIF23	62	2.33E-02	4491558	0.306515	0.015819
Down	PSG11	4	1.12E-03	136444	0.188324	0
Down	PRR11	95	3.70E-02	16341014	0.259923	0
Down	LCE1B	22	1.04E-02	1365886	0.209408	0
Down	CCNA1	83	2.81E-02	8701494	0.2972	2.47E-03
Down	TLE4	28	9.56E-03	2438214	0.252507	0
Down	HIGD1B	3	1.00E+00	6	1	0
Down	OXR1	10	1.57E-03	396854	0.225914	0
Down	DEFA3	1	0.00E+00	0	0.184876	0
Down	DISC1	138	5.45E-02	23062588	0.288949	0
Down	CLTC	333	1.73E-01	59969246	0.345833	0.001483
Down	MTBP	7	9.00E-04	308238	0.25191	0
Down	COLEC10	14	5.78E-03	496564	0.230569	0
Down	PNPLA7	1	0.00E+00	0	1	0
Down	TLE4	28	9.56E-03	2438214	0.252507	0
Down	MYO1D	58	2.01E-02	6943106	0.297723	0
Down	CXCR2	9	2.70E-03	571596	0.206862	0
Down	POU3F4	3	3.10E-04	10712	0.214335	0
Down	KIF26A	3	5.58E-04	216568	0.213757	0
Down	VWF	20	6.90E-03	3379006	0.226877	0
Down	ZSCAN12	40	1.72E-02	4511560	0.249014	0

Down	OMP	1	0.00E+00	0	1	0
Down	SPINK5	1	0.00E+00	0	0.200236	0
Down	MYBPC1	24	1.02E-02	2208902	0.223047	0
Down	RFC3	48	1.19E-02	6744340	0.286615	0
Down	KIAA1958	14	4.06E-03	1021098	0.246641	0
Down	TMEM40	1	0.00E+00	0	1	0
Down	CTAG1A	2	5.37E-04	160340	0.182031	0
Down	CHRNA7	5	1.20E-03	315000	0.238785	0
Down	PARD6G	21	6.07E-03	2092448	0.251349	0
Down	ZNF160	4	1.00E+00	12	1	0
Down	CCL3L3	1	1.00E+00	6	1	0
Down	CKS2	36	8.66E-03	1293372	0.279227	2.50E-02
Down	HSD3B2	19	6.19E-03	434014	0.258678	0.005848
Down	RAD21L1	1	0.00E+00	0	0.198223	0
Down	HS3ST2	11	4.28E-03	1134682	0.226849	0
Down	GRM5	10	2.07E-03	756604	0.225846	0
Down	SPEF2	3	1.07E-03	311542	0.166704	0
Down	KIR3DX1	3	5.37E-04	151612	0.229872	0
Down	EYS	1	0.00E+00	0	0.217653	0
Down	CENPH	38	1.29E-02	1191544	0.293478	0.022222
Down	C3orf52	11	3.74E-03	897310	0.232454	0
Down	UNC13A	7	2.18E-03	1007070	0.215862	0
Down	RUFY4	3	5.58E-04	112984	0.219927	0
Down	GPR17	1	0.00E+00	0	1	0
Down	RAD21L1	1	0.00E+00	0	0.198223	0
Down	CASK	79	3.54E-02	8491074	0.295926	0
Down	OXR1	10	1.57E-03	396854	0.225914	0

Table 7. miRNA-target gene interaction table.

Regulation	target Genes	Degree	Top MicroRNA	Regulation	target Genes	Degree	Top MicroRNA
Up	SALL1	53	hsa-mir-548b-3p	Down	TRIM24	21	hsa-mir-4477a
Up	NKX2-2	20	hsa-mir-6829-3p	Down	KLHL13	1	hsa-mir-218-5p
Up	PTCHD1	60	hsa-mir-548a-3p	Down	MAGEB2	2	hsa-mir-98-5p
Up	BMP7	22	hsa-mir-6890-3p	Down	C3orf80	10	hsa-mir-3153
Up	TMEM154	49	hsa-mir-3187-3p	Down	PPBP	1	hsa-mir-335-5p
Up	SERTM1	13	hsa-mir-3924	Down	TTK	7	hsa-mir-376a-3p
Up	FAM83F	94	hsa-mir-612	Down	TOP2A	17	hsa-mir-708-5p
Up	SGCD	41	hsa-mir-4761-5p	Down	KIF18A	2	hsa-mir-192-5p
Up	C1orf168	2	hsa-mir-148b-3p	Down	TPX2	1	hsa-mir-193b-3p
Up	GRHL2	1	hsa-mir-26b-5p	Down	POC1A	69	hsa-mir-3605-5p
Up	SMR3B	1	hsa-mir-495-3p	Down	ARHGAP29	25	hsa-mir-6814-5p
Up	SCRG1	33	hsa-mir-1304-3p	Down	NRG1	1	hsa-mir-124-3p
Up	IL20RA	1	hsa-mir-26b-5p	Down	CADPS2	4	hsa-mir-30c-5p
Up	FCN2	8	hsa-mir-8064	Down	ACER2	46	hsa-let-7d-5p
Up	DPPA4	1	hsa-mir-26b-5p	Down	CCNF	102	hsa-mir-324-3p

Up	SPTLC3	32	hsa-mir-206	Down	GTSE1	2	hsa-mir-484
Up	ATP4A	1	hsa-mir-1289	Down	SOX4	160	hsa-mir-519a-3p
Up	SDK2	33	hsa-mir-644a	Down	DLEU1	31	hsa-mir-616-5p
Up	RSPO3	1	hsa-mir-335-5p	Down	PLK1	17	hsa-mir-3120-3p
Up	FGFR2	5	hsa-mir-19b-1-5p	Down	HAUS6	14	hsa-mir-5582-3p
Up	IQCA1	1	hsa-mir-193b-3p	Down	BUB1	67	hsa-mir-497-3p
Up	MGST1	2	hsa-mir-652-3p	Down	SERINC2	1	hsa-mir-335-5p
Up	FABP7	7	hsa-mir-6823-3p	Down	KIF14	14	hsa-mir-3133
Up	PON3	1	hsa-mir-335-5p	Down	VWA1	30	hsa-mir-592
Up	GAL	8	hsa-mir-4671-5p	Down	FRMPD3	18	hsa-mir-6511a-3p
Up	PAX6	23	hsa-mir-599	Down	SEL1L	12	hsa-mir-548as-3p
Up	SYPL2	1	hsa-mir-615-3p	Down	NUSAP1	1	hsa-let-7b-5p
Up	SLC15A1	19	hsa-mir-7977	Down	DOK6	23	hsa-mir-3679-3p
Up	TMPRSS3	2	hsa-mir-204-5p	Down	NRG1	1	hsa-mir-124-3p
Up	ROR2	3	hsa-mir-451a	Down	DHX15	7	hsa-mir-221-3p
Up	DACT2	2	hsa-mir-128-3p	Down	NEK2	2	hsa-mir-92a-3p
Up	SMTNL2	43	hsa-mir-3652	Down	TAS2R7	1	hsa-mir-142-3p
Up	FBN2	16	hsa-mir-23c	Down	SPC24	26	hsa-mir-3664-5p
Up	NTF4	1	hsa-mir-124-3p	Down	HMMR	5	hsa-mir-106b-5p
Up	SRL	2	hsa-mir-18a-3p	Down	PTP4A1	132	hsa-mir-186-5p
Up	SLIT1	33	hsa-mir-5787	Down	DAZAP2	109	hsa-mir-511-5p
Up	BBOX1	4	hsa-mir-4477a	Down	CDCA5	4	hsa-mir-331-3p
Up	ART3	2	hsa-mir-122-5p	Down	ANTXR2	60	hsa-mir-3065-5p
Up	NRK	1	hsa-mir-335-5p	Down	FBXL5	31	hsa-mir-4731-3p
Up	ID4	91	hsa-mir-4311	Down	PLA2G2D	20	hsa-mir-548au-3p
Up	PLIN4	1	hsa-mir-335-5p	Down	RBPJL	25	hsa-mir-6731-5p
Up	TRDN	17	hsa-mir-501-3p	Down	CENPI	2	hsa-mir-192-5p
Up	CLIC5	54	hsa-mir-4480	Down	NLGN1	8	hsa-mir-670-3p
Up	BTBD17	1	hsa-mir-335-5p	Down	POU3F2	19	hsa-mir-6781-5p
Up	CCKBR	3	hsa-mir-148a-3p	Down	PAX4	8	hsa-mir-4783-5p
Up	S100A1	4	hsa-mir-138-5p	Down	ASXL2	48	hsa-mir-5002-5p
Up	CBLN2	6	hsa-mir-6819-3p	Down	GRIK2	1	hsa-mir-26b-5p
Up	PMAIP1	128	hsa-mir-411-3p	Down	NCAPG	20	hsa-mir-664b-3p
Up	XDH	1	hsa-mir-26b-5p	Down	SLC19A1	9	hsa-mir-4422
Up	TRIM29	18	hsa-mir-1268a	Down	EPHB1	18	hsa-mir-548aw
Up	UGT2A2	9	hsa-mir-548u	Down	INHBE	2	hsa-mir-98-5p
Up	SOX5	38	hsa-mir-555	Down	FIBCD1	12	hsa-mir-6717-5p
Up	S100A1	4	hsa-mir-132-3p	Down	RGS5	42	hsa-mir-4255
Up	GALR1	8	hsa-mir-130b-5p	Down	GUCA2B	1	hsa-mir-335-5p
Up	GAS1	33	hsa-mir-449b-5p	Down	CCNB2	6	hsa-let-7f-5p
Up	PPP1R17	1	hsa-mir-335-5p	Down	ADAMTSL1	2	hsa-mir-25-3p
Up	IFNE	16	hsa-mir-4786-5p	Down	FAM83A	5	hsa-mir-5090
Up	CELSR1	2	hsa-mir-92a-3p	Down	LRFN1	18	hsa-mir-6887-3p
Up	C4orf19	5	hsa-mir-1273f	Down	SLC25A15	20	hsa-mir-6720-3p
Up	POMC	2	hsa-mir-488-3p	Down	GABRQ	1	hsa-mir-335-5p
Up	SLC6A14	1	hsa-mir-26b-5p	Down	PRC1	17	hsa-mir-3977

Up	LRAT	47	hsa-mir-4770	Down	AMIGO2	2	hsa-mir-155-5p
Up	SPTLC3	32	hsa-mir-6514-5p	Down	CDC45	2	hsa-mir-575
Up	KLK11	1	hsa-mir-335-5p	Down	PRDM11	1	hsa-mir-335-5p
Up	F5	4	hsa-mir-634	Down	CYP27B1	12	hsa-mir-1178-5p
Up	CNTNAP2	14	hsa-mir-571	Down	KIF11	15	hsa-mir-4495
Up	PI16	2	hsa-mir-1-1	Down	G2E3	54	hsa-mir-520g-3p
Up	ENPP6	24	hsa-mir-6077	Down	POLQ	86	hsa-mir-664a-5p
Up	GBP6	24	hsa-mir-548j-3p	Down	GRIK2	1	hsa-mir-26b-5p
Up	NEURL3	1	hsa-mir-335-5p	Down	RASSF3	3	hsa-mir-20a-3p
Up	CLIC5	54	hsa-mir-4301	Down	PBK	4	hsa-mir-4699-3p
Up	RASL11B	7	hsa-mir-3137	Down	CENPA	23	hsa-mir-4719
Up	KCNJ12	24	hsa-mir-770-5p	Down	LYNX1	1	hsa-mir-744-5p
Up	AQP4	1	hsa-mir-320a	Down	EVX2	9	hsa-mir-33b-3p
Up	P2RY2	16	hsa-mir-4433b-3p	Down	KRTAP5-7	1	hsa-mir-26b-5p
Up	IL22RA1	1	hsa-mir-26b-5p	Down	DLGAP5	21	hsa-mir-520e
Up	RNF207	10	hsa-mir-3190-5p	Down	EDN1	57	hsa-mir-379-5p
Up	ADAMTS18	16	hsa-mir-588	Down	KIF20A	5	hsa-mir-23a-3p
Up	NGFR	23	hsa-mir-6732-5p	Down	CNKSR2	10	hsa-mir-6808-3p
Up	KCNJ16	1	hsa-mir-148b-3p	Down	GOLGA6A	4	hsa-mir-450b-5p
Up	GPHA2	24	hsa-mir-1180-5p	Down	B4GALT6	19	hsa-mir-1248
Up	C6orf132	48	hsa-mir-4638-5p	Down	ARHGAP42	22	hsa-mir-6131
Up	PHACTR2	47	hsa-mir-590-3p	Down	KRT28	1	hsa-mir-1229-3p
Up	EVC2	18	hsa-mir-6873-3p	Down	CDKN3	18	hsa-mir-4695-3p
Up	FOXL2	10	hsa-mir-1253	Down	DCAF4L2	2	hsa-mir-494-3p
Up	FAM3B	1	hsa-mir-335-5p				
Up	DLK1	1	hsa-mir-15a-5p				
Up	BLID	1	hsa-mir-335-5p				
Up	UGT2A1	10	hsa-mir-4762-5p				
Up	OGN	1	hsa-mir-526b-5p				
Up	TF	2	hsa-mir-19a-3p				
Up	SMAD9	45	hsa-mir-4419b				
Up	LINC00598	209	hsa-mir-890				
Up	SOX2	15	hsa-mir-126-3p				
Up	KLK12	2	hsa-mir-1-3p				
Up	KRT14	2	hsa-mir-124-3p				
Up	DLGAP2	8	hsa-mir-20a-3p				
Up	LRRC2	46	hsa-mir-3914				
Up	AMOT	23	hsa-mir-500a-5p				
Up	LINC00598	209	hsa-mir-518a-5p				
Up	HSD11B1	2	hsa-mir-26b-5p				
Up	SGCD	41	hsa-mir-4698				
Up	PRSS8	1	hsa-mir-335-5p				
Up	C6orf118	2	hsa-mir-1-1				
Up	CRISP2	2	hsa-mir-27a-3p				
Up	IHH	22	hsa-mir-6839-5p				
Up	MCOLN2	18	hsa-mir-6731-3p				

Up	SLC39A12	1	hsa-mir-335-5p
Up	VIT	1	hsa-mir-124-3p
Up	PRRX2	1	hsa-mir-124-3p
Up	PPP1R17	1	hsa-mir-335-5p
Up	TSHB	1	hsa-mir-26b-5p
Up	AGR2	2	hsa-mir-197-3p
Up	KBTBD12	39	hsa-mir-4675
Up	GADD45G	1	hsa-mir-181a-5p
Up	LIX1	3	hsa-mir-4668-5p
Up	PRSS45	8	hsa-mir-765
Up	MFAP4	1	hsa-mir-124-3p
Up	ESPNL	1	hsa-mir-375
Up	NFIX	67	hsa-mir-4488
Up	EVC2	18	hsa-mir-1236-3p
Up	COL8A2	2	hsa-mir-124-3p
Up	GNRHR	4	hsa-mir-1-3p
Up	SULT1C2	2	hsa-mir-7-5p
Up	CA8	54	hsa-mir-646
Up	CHRD1	54	hsa-mir-583
Up	RPRM	32	hsa-mir-939-5p
Up	OCA2	12	hsa-mir-1299
Up	MPPED1	15	hsa-mir-516a-3p
Up	OGN	1	hsa-mir-526b-5p
Up	GADD45G	1	hsa-mir-181a-5p
Up	VSNL1	25	hsa-mir-6873-5p
Up	FGFR3	9	hsa-mir-425-5p
Up	WNT5A	29	hsa-mir-4680-3p
Up	SFRP2	2	hsa-mir-218-5p
Up	HSPB3	1	hsa-mir-335-5p
Up	PAX6	23	hsa-mir-223-3p
Up	CYBRD1	42	hsa-mir-4517
Up	PGR	2	hsa-mir-181a-5p
Up	HSD17B2	2	hsa-mir-124-3p
Up	OPCML	9	hsa-mir-3149
Up	AGR3	1	hsa-mir-335-5p
Up	SLIT1	33	hsa-mir-4726-5p
Up	SOX9	30	hsa-mir-1323
Up	CSHL1	1	hsa-mir-16-5p
Up	CHST9	2	hsa-mir-92a-3p
Up	NRK	1	hsa-mir-335-5p
Up	SULT1C2	2	hsa-mir-7-5p
Up	SULT1C4	10	hsa-mir-6833-3p
Up	SNTG2	1	hsa-mir-146a-5p
Up	TAC4	1	hsa-mir-335-5p
Up	AGMO	23	hsa-mir-1976
Up	PTER	2	hsa-mir-130b-3p

Up	CTRB1	1	hsa-mir-335-5p
Up	COL21A1	2	hsa-mir-29c-3p
Up	ATF7IP2	11	hsa-mir-548c-3p
Up	NEFM	2	hsa-let-7a-5p
Up	S100A14	2	hsa-mir-16-5p
Up	AOX1	1	hsa-mir-26b-5p
Up	KLRF1	1	hsa-mir-335-5p
Up	CCDC68	10	hsa-mir-6808-5p
Up	IRX2	9	hsa-mir-607
Up	CNKSR3	138	hsa-mir-2276-3p
Up	MYZAP	22	hsa-mir-7153-3p
Up	PDE6A	34	hsa-mir-4757-5p
Up	ABCA8	2	hsa-mir-192-5p
Up	INHBA	40	hsa-mir-548i
Up	LDLRAD2	7	hsa-mir-3974
Up	CNTNAP3	4	hsa-mir-1226-3p
Up	C6orf141	22	hsa-mir-1827
Up	RUNX1	60	hsa-mir-1179
Up	TRIM71	104	hsa-mir-3607-3p
Up	PNMT	1	hsa-mir-26b-5p
Up	PRSS50	1	hsa-mir-124-3p
Up	SLC47A1	52	hsa-mir-637
Up	IL20RA	1	hsa-mir-26b-5p
Up	LEFTY2	10	hsa-mir-4267
Up	ITGBL1	18	hsa-mir-579-3p
Up	RHBDL3	4	hsa-mir-8485
Up	GH1	1	hsa-mir-7-5p
Up	FRAS1	1	hsa-mir-124-3p
Up	CT45A1	1	hsa-mir-335-5p
Up	FGFR3	9	hsa-mir-4764-5p
Up	EYA4	9	hsa-mir-203a-3p
Up	AMZ1	19	hsa-mir-1470
Up	CACNA1A	21	hsa-mir-4734
Up	FAM196A	1	hsa-mir-335-5p
Up	CA12	24	hsa-mir-2355-3p
Up	GAS7	18	hsa-mir-384
Up	HPGD	6	hsa-mir-664a-3p
Up	SCGB1D2	1	hsa-mir-26b-5p
Up	PLIN5	17	hsa-mir-1184
Up	ALDOB	2	hsa-mir-378a-3p
Up	GJB7	38	hsa-mir-653-5p
Up	PRR15L	7	hsa-mir-3679-3p
Up	IRX2	9	hsa-mir-6808-3p
Up	ALDH1A3	31	hsa-mir-1304-5p
Up	EYA2	1	hsa-mir-30a-5p
Up	KRT19	2	hsa-mir-193b-3p

Up	LY6H	17	hsa-mir-3188
Up	MYBPHL	19	hsa-mir-4304
Up	RASGRP1	13	hsa-mir-3161
Up	FERMT1	4	hsa-mir-9-5p
Up	ASXL3	28	hsa-mir-1297
Up	PDZRN3	1	hsa-mir-197-3p
Up	KCNS2	19	hsa-mir-888-3p
Up	VANGL2	34	hsa-mir-4733-5p
Up	PRDM16	6	hsa-mir-133a-3p
Up	SH3BP4	42	hsa-mir-663b
Up	COL4A6	2	hsa-mir-197-3p
Up	NEUROD1	17	hsa-mir-6738-3p
Up	IL6R	55	hsa-mir-509-5p
Up	FSHB	7	hsa-mir-3121-5p
Up	CHRD1	54	hsa-mir-4510
Up	NWD1	75	hsa-mir-548ap-3p
Up	CPXM2	14	hsa-mir-4539
Up	WWC2	39	hsa-mir-596
Up	GJB7	38	hsa-mir-642a-5p
Up	IGSF11	4	hsa-mir-3163
Up	SCN2B	46	hsa-mir-4708-5p
Up	CCDC158	15	hsa-mir-1261
Up	ASXL3	28	hsa-mir-708-3p
Up	DLGAP2	8	hsa-mir-4635
Up	AOX1	1	hsa-mir-26b-5p
Up	CH25H	1	hsa-mir-26b-5p
Up	SLC39A8	6	hsa-mir-331-3p
Up	S100B	2	hsa-mir-29a-3p
Up	SLPI	26	hsa-mir-298
Up	PGR	2	hsa-mir-126-3p
Up	SSTR2	35	hsa-mir-6787-3p
Up	C2orf71	12	hsa-mir-3065-3p
Up	COL13A1	28	hsa-mir-940
Up	CACNA2D3	15	hsa-mir-6503-3p
Up	NR0B1	1	hsa-mir-561-3p
Up	CALB2	1	hsa-mir-335-5p
Up	SCGB1D1	2	hsa-mir-26b-5p
Up	FGF1	24	hsa-mir-589-3p
Up	FOXL2	10	hsa-mir-520a-5p
Up	MKX	31	hsa-mir-548p
Up	TXLNB	27	hsa-mir-642a-5p
Up	ERBB4	7	hsa-mir-302b-3p
Up	PCSK2	25	hsa-mir-660-5p
Up	DMKN	18	hsa-mir-6720-5p
Up	TGFBR3	67	hsa-mir-548aq-3p
Up	MN1	17	hsa-mir-188-3p

Up	SLIT1	33	hsa-mir-629-3p
Up	KCNG1	1	hsa-mir-324-5p
Up	MEGF11	1	hsa-mir-335-5p
Up	PLA2G4A	35	hsa-mir-2114-5p
Up	GPR37L1	15	hsa-mir-4467
Up	SMR3B	1	hsa-mir-495-3p
Up	CLIC3	2	hsa-mir-124-3p
Up	SYT12	2	hsa-mir-146a-5p
Up	CUBN	11	hsa-mir-140-5p
Up	HFM1	11	hsa-mir-4262
Up	PNMA3	12	hsa-mir-6792-3p
Up	IQCA1	1	hsa-mir-193b-3p
Up	ESPNL	1	hsa-mir-375
Up	FAM198A	11	hsa-mir-1321
Up	EFCAB1	12	hsa-mir-1538
Up	FAM124A	9	hsa-mir-6836-3p
Up	ADARB2	30	hsa-mir-3117-5p
Up	DMKN	18	hsa-mir-6720-5p
Up	BANK1	4	hsa-mir-4662a-5p
Up	HIF3A	17	hsa-mir-210-3p
Up	EFCAB1	12	hsa-mir-6769a-3p
Up	CNTNAP3	4	hsa-mir-1226-3p
Up	CCNJL	2	hsa-let-7c-3p
Up	ADAM32	1	hsa-mir-335-5p
Up	LAMA1	1	hsa-mir-124-3p
Up	SEZ6L	10	hsa-mir-3133

Note: Degree: No of miRNA interact with target gene. We taken any one miRNA in table.

Table 8. TF-target gene interaction table.

Regulation	TF	Degree	Gene	Regulation	TF	Degree	Gene
Up	EZH2	73	IRX1	Down	CREM	10	ACER2
Up	WT1	12	ADAMTS18	Down	TRIM28	14	ARHGAP29
Up	ZNF76	22	ADARB2	Down	GATAD1	11	FLJ13224
Up	SUZ12	30	CACNA2D3	Down	SIN3A	28	ANTXR2
Up	EBF1	14	CSHL1	Down	PHF8	31	AKAP3
Up	FOSL2	10	AGR2	Down	MXD4	20	BIRC5
Up	ZNF217	9	AMZ1	Down	SAP30	31	HOXA4
Up	NFIA	11	ALDOB	Down	STAT1	7	CDCA5
Up	ZNF644	17	ATF7IP2	Down	GLI4	8	ASPDH
Up	GATA4	14	CHN2	Down	KDM5B	31	ATP2A3
Up	NR2F2	6	AOX1	Down	KDM5A	35	CCNF
Up	CREB1	14	CNKSR3	Down	ZEB1	26	C3orf52
Up	ZBTB33	25	APOD	Down	ATF1	23	CKS2
Up	TFE3	14	CNKSR3	Down	NR2C2	19	C1orf189
Up	MBD4	10	DPPA4	Down	TFDP1	26	CADPS2

Up	MYBL2	10	HSD17B2	Down	ZNF589	14	DAZAP2
Up	ZFP64	15	C6orf132	Down	POLR2H	14	CDC45
Up	ATF1	18	CCDC68	Down	ETV1	10	FAM83A
Up	GATAD2A	18	CRYM	Down	SMARCA4	12	CENPH
Up	RCOR2	13	FGFR3	Down	MAZ	34	BDNF
Up	BCL6	11	KISS1R	Down	SIRT6	12	HMMR
Up	FOXA3	15	DMKN	Down	REST	24	CDCA5
Up	YY1	9	FABP7	Down	PPARG	17	BIRC5
Up	HMG20B	16	IL6R	Down	ZNF2	21	BUB1
Up	ZNF7	2	PNMT	Down	BCL11A	22	CENPM
Up	NFIC	4	FMO5	Down	LEF1	13	CCNG2
Up	HNF4G	10	PRR15L	Down	INSM2	18	CKS2
Up	MBD1	27	DACT2	Down	BCL3	1	AMIGO2
Up	THAP1	6	FCN2	Down	NCOR1	19	CLTC
Up	RARA	6	DMKN	Down	FOSL2	6	MYBPC1
Up	ETV4	10	ITIH2	Down	ZNF335	16	CYP27B1
Up	L3MBTL2	19	AMOT	Down	TAF7	21	DAZAP2
Up	CTBP1	2	ASXL3	Down	CREB1	15	DHX15
Up	NONO	3	GRHL2	Down	GABPA	16	CLRN2
Up	PPARG	19	CSH1	Down	L3MBTL2	20	C3orf80
Up	MAZ	28	BMP7	Down	ZNF175	10	EXD1
Up	CBFB	7	FFAR3	Down	ZNF639	16	CRNDE
Up	SMAD4	14	CLIC3	Down	KLF16	22	FANCA
Up	RNF2	12	CCNJL	Down	SMAD5	31	CNIH2
Up	ATF4	4	FRAS1	Down	EED	9	KIF18A
Up	HBP1	16	LOC100288911	Down	NRF1	25	FANCA
Up	ATF3	12	C6orf141	Down	SP7	16	B4GALT6
Up	KLF11	14	LINC00242	Down	ZNF580	23	HOXA6
Up	ZNF580	19	ARMC4	Down	SMARCE1	11	KIF20A
Up	GATAD1	15	PHYHD1	Down	POLR2A	20	C20orf203
Up	CTCF	22	ATP4A	Down	DMAP1	14	FAM20C
Up	ZBTB26	16	FAM3B	Down	ZNF501	26	ARHGAP20
Up	ZNF589	11	CA12	Down	SP3	11	G2E3
Up	PKNOX1	11	CSH2	Down	SUZ12	23	CRNDE
Up	ZEB1	11	AQP4	Down	BCL11B	28	DISC1
Up	ZNF263	15	CLIC3	Down	GFI1B	10	FOXM1
Up	KLF1	17	C9orf152	Down	ZNF324	17	C1orf189
Up	ZNF558	7	ARMC3	Down	ARID4B	17	MYO1D
Up	TBX21	5	DMKN	Down	MXD3	21	DOK6
Up	ZNF324	13	WNT5A	Down	SMAD4	16	LOC339874
Up	ZNF547	2	NGFR	Down	IRF4	13	NHLRC4
Up	ZNF202	2	ARMC4	Down	PRDM10	9	MAMSTR
Up	ZNF175	8	ART3	Down	EGR1	13	NXPH4
Up	ZNF239	4	ASXL3	Down	CREB3L1	25	NUSAP1
Up	ZNF121	11	CELSR1	Down	TCF7L2	1	ASPDH
Up	TARDBP	7	MKX	Down	MTA1	15	YTHDF1

Up	SP3	19	FAM196A	Down	SREBF1	3	PARPBP
Up	PRDM2	6	CPLX3	Down	CDC5L	7	LRFN1
Up	BCOR	8	KISS1R	Down	NR2F1	18	ZSCAN12
Up	POLR2H	2	GJB7	Down	TRIM22	15	VWA1
Up	CEBPA	5	SLC6A14	Down	IKZF1	13	TROAP
Up	TRIM24	4	LDLRAD2	Down	ZNF202	6	TRHDE
Up	NR2F1	13	IL22RA1	Down	HIC1	16	TEX22
Up	ZNF384	7	ID4	Down	ID3	18	TCEANC2
Up	NCOR1	6	KAZN	Down	KLF6	12	TTK
Up	NR4A1	11	FOXL2	Down	ZNF76	27	ZRANB2-AS1
Up	GMEB2	2	PRSS8	Down	TCF7	5	SOX4
Up	THRB	11	CTRB1	Down	DRAP1	13	SERINC2
Up	TGIF2	19	NFIX	Down	KLF9	43	UNC13A
Up	NFYC	14	FMO5	Down	HCFC1	15	TRIM24
Up	ZNF512	7	CT45A1	Down	CEBPA	6	RASSF10
Up	GABPA	9	EVC2	Down	MBD1	10	PLK1
Up	ARID4B	13	PPP1R27	Down	MLX	14	ZSCAN2
Up	KDM1A	13	PLIN4	Down	NFYC	11	TPX2
Up	DMAPI	20	C1orf168	Down	KDM1A	9	SPC24
Up	KLF7	21	ENTPD8	Down	ELF1	24	RGS5
Up	GLIS2	27	KCNJ12	Down	MNT	3	PARPBP
Up	ZNF146	6	OVOL3	Down	PBX2	9	TLE4
Up	SP1	14	NTF4	Down	HBP1	15	SLC39A5
Up	ZNF488	2	FXYP3	Down	KLF8	20	RCC1
Up	BCL11A	12	KRT19	Down	KLF11	12	ZC3H12D
Up	ZNF341	19	COL13A1	Down	CHD1	20	RASSF3
Up	BCL11B	16	EYA4	Down	FOXJ2	13	TCEANC2
Up	ZBTB7A	19	SALL1	Down	TEAD3	10	TRIM24
Up	HIC1	23	FGFR2	Down	HMG3	16	KIF11
Up	ZNF501	17	FAM198A	Down	ZNF584	9	PF4
Up	SOX13	19	MGST1	Down	NCOA1	10	DAZAP2
Up	ESRRA	8	ESRRA	Down	ZKSCAN1	8	PVT1
Up	INSM2	11	PMAIP1	Down	HDAC1	12	HAUS6
Up	ZNF2	17	GAS1	Down	ZNF423	18	KLHL13
Up	ZNF610	11	ROR2	Down	ZFX	23	HMMR
Up	ETV6	1	BMP7	Down	EZH2	34	POU3F4
Up	ZNF394	15	CACNA2D3	Down	EP300	4	PBK
Up	ZNF18	12	RNF207	Down	GTF2E2	28	KIAA1958
Up	ZNF24	15	DNAI2	Down	NFRKB	12	CCNB2
Up	KLF8	11	NKX2-2	Down	HDGF	17	POLQ
Up	ELF3	14	BTBD17	Down	JUNB	6	LINC00309
Up	DIDO1	2	LEFTY2	Down	WRNIP1	24	CALHM1
Up	RERE	11	SOX9	Down	MLLT1	11	PTP4A1
Up	ZNF197	11	WWC2	Down	ZFP37	23	DISC1
Up	MLX	12	FLJ42393	Down	TBX21	8	SPC24
Up	FOSL1	11	FMO5	Down	SMC3	6	BDNF

Up	ESR1	3	LG11	Down	ZBTB17	8	POU3F3
Up	ZFP2	12	STRA6	Down	EHMT2	1	BDNF
Up	POLR2A	7	LDLRAD2	Down	MYNN	21	C20orf203
Up	NFIL3	11	NEURL3	Down	KLF13	11	INHBE
Up	KLF16	21	GH2	Down	FOSL1	18	PTP4A1
Up	KLF4	16	GADD45G	Down	CTCF	12	PKLR
Up	REST	13	RHBDL3	Down	ZNF644	17	MAMSTR
Up	RAD21	17	RBP4	Down	SSRP1	9	TRIM24
Up	MXD3	14	S100A1	Down	RERE	18	PTTG2
Up	SCRT1	7	GPR37L1	Down	CEBPG	7	MTBP
Up	ZNF335	10	RPRML	Down	ZHX2	11	LOC339874
Up	ELF1	11	DLEC1	Down	ETS1	18	CNIH2
Up	GATA2	7	CA8	Down	SCRT2	6	SLC52A3
Up	KLF9	26	CCKBR	Down	GMEB2	15	ZSCAN12
Up	RXRB	11	TMEM139	Down	MYC	5	FANCA
Up	DPF2	6	GRHL2	Down	SCRT1	3	STMN1
Up	NR2F6	15	PTER	Down	THRB	12	SLC25A15
Up	ZNF71	10	EFEMP1	Down	ZNF197	18	RASSF10
Up	ZNF101	7	RNF207	Down	ZBTB7A	28	QSOX1
Up	JUN	2	C6orf141	Down	MXI1	6	HJURP
Up	ZNF623	5	HIF3A	Down	ZNF394	24	ZNF160
Up	ZNF140	1	C6orf141	Down	ZBTB40	7	G2E3
Up	ZNF292	1	C6orf141	Down	E2F4	14	FANCD2
Up	ZNF264	2	OVOL3	Down	RNF2	9	PNPLA7
Up	CUX1	9	SYT12	Down	ZNF407	8	CCNB2
Up	GFI1B	6	TGFBR3	Down	ZBTB11	21	RAD51
Up	ZNF382	9	KCNG1	Down	MAFG	3	CLTC
Up	PRDM12	1	C6orf141	Down	POU5F1	2	BUB1
Up	FOS	3	IL6R	Down	RCOR2	10	CDKN3
Up	PRDM10	14	STRA6	Down	NR4A1	12	C20orf203
Up	TEAD3	14	TF	Down	TFAP4	16	RFT1
Up	IRF1	10	TEPP	Down	ZNF101	11	CADPS2
Up	SIRT6	5	CA8	Down	ZNF341	11	NXPH4
Up	MIXL1	3	MYBPHL	Down	MEF2D	12	RCC1
Up	ZBTB11	9	SLC39A8	Down	YY1	10	KIF18A
Up	CREB3L1	9	RASL11B	Down	EBF1	8	KIR3DX1
Up	TFDP1	29	VSNL1	Down	TSHZ1	11	PKLR
Up	HMBOX1	5	TMEM154	Down	PKNOX1	4	LYNX1
Up	BHLHE40	7	PPP1R27	Down	WT1	15	RAD21L1
Up	BACH1	3	PNMT	Down	FOXA3	14	FOXMI
Up	FOXJ2	7	S100B	Down	PRDM1	10	PRDM1
Up	SMARCA4	5	FAM83F	Down	ZNF610	16	SLC19A1
Up	SIN3A	17	PAX6	Down	ZNF18	17	DISC1
Up	ZBTB40	6	HPGD	Down	KLF7	20	NHLRC4
Up	ID3	13	SRL	Down	ZBTB33	15	HOXA6
Up	TRIM28	4	FBN2	Down	GLIS2	19	ZBTB33

Up	HDAC1	13	GADD45G	Down	KLF4	8	PRR11
Up	SMARCE1	8	CYBRD1	Down	SUPT5H	7	EVX2
Up	GLI4	4	RUNX1	Down	ARNT	6	CDC45
Up	SCRT2	3	PDE6A	Down	EGR2	13	FLJ13224
Up	GLIS1	15	STRA6	Down	ZNF382	6	HOXA4
Up	EGR2	15	RPRM	Down	RFX1	7	OMP
Up	ATF2	4	CH25H	Down	ELK1	23	ZMAT3
Up	HHEX	5	SOX9	Down	ZNF71	17	NUF2
Up	STAT3	5	CLEC9A	Down	DDX20	16	TSSC2
Up	CEBPG	14	TSPAN8	Down	SP1	25	LOC100268168
Up	HCFC1	4	CLIC3	Down	TEAD2	1	CDC45
Up	TFAP4	14	TRIM71	Down	SMARCA5	13	RAD21L1
Up	NR2C2	10	MFAP4	Down	ZNF83	9	MAMSTR
Up	HMGN3	8	ENTPD8	Down	ZNF24	22	MTBP
Up	FOXM1	7	NTF4	Down	DNMT1	5	KIF20A
Up	EGR1	7	RHOD	Down	GTF2A2	7	FAM83A
Up	IRF4	7	KISS1R	Down	E2F5	13	DHX15
Up	DRAP1	14	NEURL3	Down	IRF2	7	CNIH2
Up	SP7	10	PPP1R27	Down	HMBOX1	5	CLTC
Up	NCOA1	3	TMPRSS3	Down	CREB3	4	MYO1D
Up	CREM	8	S100A14	Down	ZNF623	9	TCEANC2
Up	HMG20A	12	ZNF385C	Down	JUND	8	MYBPC1
Up	LEF1	3	TF	Down	MBD2	9	PRR11
Up	DNMT1	1	CNKSR3	Down	ATF3	12	CRNDE
Up	ZNF423	18	PPP1R1B	Down	MIXL1	6	SLC35G5
Up	TEAD1	9	SPTLC3	Down	ZNF512	7	HTR3D
Up	ADNP	8	RNF207	Down	ATF2	6	NLGN1
Up	HES1	5	GADD45G	Down	ZFP2	23	GPR161
Up	ARNT	2	TEPP	Down	MAFK	5	STMN1
Up	ZFP37	13	RASGRP1	Down	KLF1	21	ZBTB33
Up	ZBTB17	4	KRT19	Down	HDAC8	1	CDC45
Up	MYNN	10	KISS1R	Down	ETS2	2	TRIM24
Up	ARID1B	7	PON3	Down	RELA	3	PKLR
Up	RFXANK	8	PRSS8	Down	NR2F6	22	QSOX1
Up	ZNF143	4	COL13A1	Down	HES1	2	KIF15
Up	SP2	17	EFCAB1	Down	ZHX1	2	TSSC2
Up	CDC5L	5	PTER	Down	TSC22D4	1	CDC45
Up	ZNF16	4	RUNX1	Down	BACH1	6	ZSCAN12
Up	PRDM1	4	TGFBR3	Down	DIDO1	4	CYP27B1
Up	TRIM22	6	SULT1C4	Down	CUX1	7	PVT1
Up	GTF2F1	11	SYT12	Down	ETV6	3	PRR11
Up	TSHZ1	5	KRT19P2	Down	ARID1B	12	RACGAP1
Up	RFX1	5	PGR	Down	ZNF207	15	RAD51D
Up	PTTG1	1	CRISP2	Down	IRF1	24	CENPH
Up	MEF2D	8	PDE6A	Down	GATA4	6	TPX2
Up	SSRP1	15	TRIM71	Down	NFIA	9	VWA1

Up	NRF1	14	SALL1	Down	TGIF2	13	PLK1
Up	KDM5A	2	CRYM	Down	CBFB	9	PSTPIP2
Up	RCOR1	6	GRHL2	Down	TFE3	14	DISC1
Up	HDAC2	5	ESPNL	Down	ZFP64	9	G2E3
Up	HDAC6	5	SSTR2	Down	SIN3B	9	PTP4A1
Up	SMARCA5	11	GH2	Down	GTF2F1	17	CNIH2
Up	E2F5	11	CSH2	Down	ZBTB26	11	SOX4
Up	HDGF	6	CSHL1	Down	CCNT2	8	PNPLA7
Up	ETV1	5	DLEC1	Down	TEAD1	8	NCAPG
Up	PYGO2	1	CYBRD1	Down	GTF2B	8	KIF11
Up	ELK1	6	FOXL2	Down	RFXANK	9	HAUS6
Up	KDM5B	11	WWC2	Down	SOX5	10	CDKN3
Up	NFRKB	7	LEFTY2	Down	NR2F2	4	SPC24
Up	MITF	2	RASGRP1	Down	GATAD2A	11	LYNX1
Up	PHF8	11	ID4	Down	THAP1	4	CLTC
Up	ZNF639	6	MYBPHL	Down	RFX3	6	CENPA
Up	SAP30	11	LOC100288911	Down	ETV4	15	HMMR
Up	CREB3	6	SRL	Down	ZNF384	13	SLITRK6
Up	KLF6	7	VANGL2	Down	SP2	20	UNC13A
Up	ZKSCAN1	5	DLK1	Down	ZNF143	11	RFC3
Up	CBX8	6	SOX2	Down	MTA2	5	FLJ13224
Up	ZNF138	1	DMKN	Down	ZNF121	6	TMEM40
Up	ZNF366	7	WNT5A	Down	BCL6	12	YTHDF1
Up	SUPT5H	5	S100B	Down	ATF4	7	RAD21L1
Up	USF2	5	SYPL2	Down	USF1	3	PNPLA7
Up	POU5F1	5	DPPA4	Down	PML	4	RCC1
Up	EHMT2	3	DRGX	Down	RAD21	16	DOK6
Up	CTBP2	26	LRAT	Down	MYBL2	4	SEL1L
Up	CEBPB	2	PMAIP1	Down	RARA	7	DLEU1
Up	SREBF2	4	MN1	Down	HMG20A	6	EXD1
Up	MTA1	7	GPR37L1	Down	MBD4	4	SEL1L
Up	CCNT2	6	FGFR3	Down	HNF4G	4	CLRN2
Up	JUND	4	KRT19	Down	HMG20B	12	RAD51
Up	KLF13	6	KISS1R	Down	NFATC1	2	PVT1
Up	MBD2	8	LGI1	Down	NONO	3	PRR11
Up	ZFX	8	PAX6	Down	PPARGC1A	1	CLTC
Up	WRNIP1	5	ERP27	Down	JUN	2	PVT1
Up	MLLT1	8	LY6H	Down	HSF1	1	CLTC
Up	ZNF584	4	EVC2	Down	SOX13	9	STMN1
Up	HLF	2	FAM217A	Down	TAL1	5	HJURP
Up	IKZF1	8	PHYHD1	Down	KAT2A	1	CLTC
Up	TEAD4	5	ITIH2	Down	ARID3A	1	CLTC
Up	CEBPD	5	SLC39A8	Down	GATA1	4	RFT1
Up	FOXA2	5	FAM83F	Down	MTA3	2	PVT1
Up	GATA1	5	OR7A5	Down	GATAD2B	3	FAM91A1
Up	ZNF8	2	FXYD3	Down	ESRRA	9	SLC39A5

Up	MAFK	3	TDO2	Down	RXRB	9	SLC25A15
Up	STAT1	2	FFAR3	Down	CTBP2	15	FOXB2
Up	MXD4	17	SH3BP4	Down	ZNF366	10	TROAP
Up	SMC3	4	FLRT2	Down	RUNX3	1	CXCR3
Up	GTF2A2	1	FOXL2	Down	SPI1	1	CXCR3
Up	MNT	1	FRAS1	Down	NFIC	3	ZC3H12D
Up	ZNF641	1	FXYD3	Down	ELF3	7	NXPH4
Up	ZNF354C	1	FXYD3	Down	ZNF558	8	NLGN1
Up	CHD1	12	IRX2	Down	MAX	4	FAM83A
Up	ZNF592	1	GRHL2	Down	ZNF547	6	SV2C
Up	ZNF207	1	GRHL2	Down	PRDM2	10	NUF2
Up	NFATC1	2	S100A14	Down	ZNF263	17	FIBCD1
Up	FOXK2	2	LY6H	Down	ZBTB1	7	PRC1
Up	GATAD2B	4	RHOD	Down	ZNF641	2	LRFN1
Up	MYC	5	SYT12	Down	TARDBP	3	SLC19A1
Up	SIX4	1	GRHL2	Down	NFIL3	9	NUSAP1
Up	MTA3	2	S100A14	Down	HDAC2	6	ZSCAN2
Up	GTF2E2	5	HSD11B1	Down	ESR1	1	EDN1
Up	TBX3	2	PNMT	Down	HDAC6	6	FANCD2
Up	EED	7	NEURL3	Down	ZNF7	4	G2E3
Up	JUNB	5	KAZN	Down	NFYB	2	PRR11
Up	YBX1	2	KCNJ12	Down	GATA2	9	KIF21B
Up	MAFF	3	KCNJ16	Down	PTRF	1	FAM83A
Up	GTF3C2	1	KISS1R	Down	CEBPD	2	FAM83A
Up	ZBTB1	3	TGFBR3	Down	FOXA2	2	TCEANC2
Up	IRF2	1	KISS1R	Down	USF2	6	L1CAM
Up	ZHX2	3	NFIX	Down	SIX4	2	PVT1
Up	CHD4	1	KISS1R	Down	TEAD4	2	FAM83A
Up	SMAD5	5	RNF207	Down	ZNF217	2	RASSF3
Up	MCM3	1	KLK11	Down	RCOR1	3	MTBP
Up	TAL1	3	TEPP	Down	GLIS1	13	PRSS56
Up	RELA	4	PNMT	Down	BCOR	11	ZAN
Up	PTRF	2	LEFTY2	Down	ADNP	12	TMEM40
Up	ARID3A	1	LY6H	Down	BHLHE40	6	TRHDE
Up	NFE2	2	TMEM139	Down	CTBP1	4	POU3F3
Up	ETS1	2	ZNF385C	Down	CEBPB	3	STMN1
Up	AEBP2	1	OVOL3	Down	CBX8	6	ZRANB2-AS1
Up	NFE2L2	2	RHOD	Down	ZNF488	1	HOXA4
Up	DDX20	3	PDE6A	Down	RXRA	1	HOXA4
Up	EP300	1	PI16	Down	ZNF264	1	HOXA6
Up	MTA2	3	RHBDL3	Down	ZNF16	1	HOXA6
Up	KAT2A	1	PMAIP1	Down	ZNF138	1	HOXA6
Up	POU2F2	1	PMAIP1	Down	ZNF707	1	INHBE
Up	TCF7	1	PMAIP1	Down	NFE2L1	1	KIAA1958
Up	PML	2	S100A1	Down	CHD4	1	KIF11
Up	NR3C1	1	PNMT	Down	TBP	4	NCAPG

Up	MAX	2	RNF207	Down	MAFF	2	KIF18A
Up	ZNF707	1	PPP1R27	Down	GATA3	5	SPEF2
Up	MXI1	2	PRSS8	Down	HLF	2	RAD21L1
Up	NFYB	1	PRR15L	Down	THRAP3	3	RCC1
Up	GATA3	1	PRR15L	Down	ZNF8	1	LRFN1
Up	DEK	2	RHOD	Down	ZNF239	2	ZNF160
Up	E2F6	1	RNF207	Down	SIX5	1	MAMSTR
Up	TAF7	2	S100A1	Down	RBBP5	2	MTBP
Up	HDAC8	1	RUNX1	Down	DPF2	5	PRC1
Up	ZNF83	1	RUNX1	Down	MITF	2	ZBTB33
Up	RUNX3	1	RUNX1	Down	SREBF2	5	PNPLA7
Up	SPI1	1	RUNX1	Down	ZNF585B	1	OXR1
Up	SREBF1	1	RUNX1	Down	NFE2	5	PF4
Up	GTF2B	1	S100A1	Down	MCM7	1	PKLR
Up	PBX2	1	SALL1	Down	FO XK2	1	PRR11
Up	ZNF407	1	SYPL2	Down	ZNF592	1	PVT1
Up	HNF4A	1	TF	Down	ZNF140	1	SLC5A10
Up	RXRA	2	TPPP2	Down	ZNF146	2	TROAP
Up	TEAD2	1	WWC2	Down	TBX3	2	ZC3H12D
				Down	HHEX	1	TPX2
				Down	CEBPZ	1	TSSC2
				Down	SP4	1	ZSCAN12

Note: Degree: No of target gene interact with TF. We taken any one target gene in table. TF transcription factors.