

Bioinformatics analyses combined microarray identify the differentially expressed microRNAs in periventricular leukomalacia

Yang YANG^{1*}, Jing-jing PAN^{2*}, Yun FENG¹, Xiao-yu ZHOU¹

¹ Department of Neonatology, Nanjing Children's Hospital, Nanjing, Jiangsu, P.R. China

² Department of Pediatrics, Jiangsu Province People's Hospital, Nanjing, Jiangsu, P.R. China

*These authors contributes equally to this work.

Correspondence to: Dr Xiao-yu Zhou or Dr Yun Feng
Department of Neonatology, Nanjing Children's Hospital
72 Guangzhou Road, Nanjing, Jiangsu 210008, P.R. China.
TEL: +86 025-83117201; E-MAIL: yy860507@126.com

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Abstract

OBJECTIVES: With the improvement of premature infant cure rate and livability, the incidence of PVL has been one of the main reasons for premature infant nervous system sequelae. miRNAs are important in the regulation of cell growth, differentiation, apoptosis and carcinogenesis. The aim of the present study was to identify differentially expressed miRNAs between PVL and normal tissues.

METHODS: The target genes of significant miRNA were retrieved from the miRecords database. Furthermore, GO analysis and biological process interaction network was constructed using the BiNGO and Cytoscape software. Finally, KEGG analysis from DAVID was used to find meaningful signaling pathway.

RESULTS: In conclusion, this study identified 16 differentially expressed miRNAs, which may be important in the progression of PVL and miRNA 141 demonstrated the greatest quantity of target genes. In addition, Hdac4, Lamc1, Irs1 and Zeb1 are the most frequently appeared ones among proved genes. Wnt signaling pathway and Neurotrophin signaling pathway were identified to be significantly associated with PVL.

CONCLUSION: This work may bring some new hints for the pathogenesis of PVL in the future work. However, further investigation regarding the specific function is required.

INTRODUCTION

With the improvement of premature infant cure rate and livability, the incidence of PVL, which is one of the main reasons for premature infant nervous system sequelae, also increased significantly. Currently, it is reported that the incidence of PVL in very low birth weight (VLBW) infants

has already reached 4.2% (71/1680) in Taiwan (Tsai *et al.* 2015). Compared to that, the incidence of mainland in China was 2.3% (112/4933) in a survey performed by ten large hospitals of seven Chinese cities (Chen *et al.* 2011). The pathogeny of PVL is extremely complicated. It is basically characterized by two components: (1) focal necrosis in the periventricular region and (2) diffuse reactive

gliosis in the surrounding white matter (Folkerth 2006). However, the detailed mechanism is still not clear to date.

MiRNAs are important kinds of short endogenous RNAs found in recent years, through the way of direct decomposition of target mRNAs or suppress their translation regulate gene expression in transcription level, they play a very important role in development sequence, stem cells, signal transduction, cell growth and the occurrence of the tumor biological processes such necessary biological processes (Sayed & Abdellatif 2011). There're a few miRNA studies involved in brain diseases and normal brain development. But in point of PVL, rare miRNA studies have been reported.

In view of this situation, the aim of the present study was to identify the miRNAs, which may be important in the progression of PVL and to analyze their involvement in this process. In addition, an interaction network was constructed using the Search Tools for the Database for Annotation, Visualization and Integrated Discovery (DAVID) database and Cytoscape software. We hope this study maybe helpful for the new exploration of PVL pathogenesis such as the identification of new therapeutic targets.

MATERIALS AND METHODS

Wistar rats

All healthy adult rats (16 female rats and 16 male rats in total) were maintained in a specific pathogen-free animal facility at the animal center of Nanjing Medical University. These 16 mature pregnant wistar rats were then divided into PVL group (n=8) and control group (n=8) according to the randomized controlled standard. All procedures in this study followed the protocols approved by the Nanjing Medical University Animal Care and Use committee. The modeling and experimental methods are based on the previous reports (Guo *et al.* 2013; Bell & Hallenbeck 2002). Finally, in PVL group and control group, there were 70 and 82 neonatal rats, respectively.

Microarray analysis

After RNA isolation from neonatal brain tissues, the miRCURY™ Hy3™/Hy5™ Power Labeling Kit (Exiqon, Vedbaek, Denmark) was used according to the manufacturer's guideline for miRNA labeling. Specific methods of microarray were performed as our previous report described (Bell & Hallenbeck 2002). Differentially expressed miRNAs were identified through fold change filtering and false discovery rate (fold change ≥ 2.0 ; false discovery rate < 0.05).

Predicting the target genes of differentially expressed miRNAs

The miRecords database (<http://miRecords.umn.edu/miRecords>), which is a resource for animal miRNA-target interactions, was used to analyze the target genes

of the specific miRNAs. miRecords integrates the predicted targets of the following miRNA target prediction tools: DIANA-microT (<http://diana.cslab.ece.ntua.gr/microT>), MicroInspector (<http://bioinfo.uni-plovdiv.bg/microinspector>), miRanda (<http://www.microrna.org/microrna/home.do>), MirTarget2 (<http://mirdb.org/miRDB>), miTarget™ (<http://cbit.snu.ac.kr/~miTarget>), NBmiRTar (<http://wotan.wistar.upenn.edu/NBmiRTar/login.php>), PicTar (<http://pictar.bio.nyu.edu>), PITA (<http://genie.weizmann.ac.il/index.html>), RNA22 (<http://cbcsrv.watson.ibm.com/rna22.html>), RNAhybrid (<http://bibiserv.techfak.uni-bielefeld.de/rnahybrid>) and TargetScan (<http://www.targetscan.org>). The genes that were predicted by at least three of the 10 databases were selected as miRNA targets for subsequent analysis to reduce the quantity of false-positive results.

Network analysis and functional annotation

As an open source learning biological information processing software, Cytoscape (<http://www.cytoscape.org>) can be used for the information integration of biological molecules, genes, and etc. Therefore, this software was used to visualize these associations and the mined modules. Annotation was performed by the plugin (BiNGO v2.44) of Cytoscape software. Significance analysis including biological process was analyzed through this plugin.

KEGG pathway

The Database for Annotation, Visualization and Integrated Discovery (DAVID; <http://david.abcc.ncifcrf.gov/>) includes a broad selection of functional annotation tools for understanding the biological significance of numerous genes. In the current study, database of Kyoto Encyclopedia of Genes and Genomes (KEGG) from DAVID was used to label the function of genes and perform the pathway enrichment analysis. Through Fisher Exact Test with the software, P value was calculated with a significant value of 0.05

Statistical analysis

An independent sample *t*-test was used to identify the differentially expressed miRNAs between the PVL group and healthy control subjects, and $p < 0.05$ was considered to indicate a statistically significant difference.

RESULTS

Identification of differentially expressed miRNAs

Raw data of miRNA expression was obtained from above experiments and a strict filter rule was applied (fold change ≥ 2.0 ; false discovery rate < 0.05). Finally, 35 miRNAs exhibited significant differential expression (Table 1).

Target gene prediction

Since miRNAs regulate the post-transcriptional regression of target genes, the putative target genes of specific

Tab.1. Differentially expressed miRNAs between the LPS/control groups in three chips.

Up miRNA (24)	Fold Change				MFC*	Down miRNA (11)	Fold Change			
	Chip 1	Chip 2	Chip 3	Chip 1			Chip 2	Chip 3	MFC*	
<i>Rno-miR-144</i>	/	11.8020	15.3260	13.5640		<i>Rno-miR-141</i>	/	0.0097	/	0.0097
<i>Rno-miR-451</i>	18.9200	6.2905	9.9270	11.7125		<i>Rno-miR-10a-5p</i>	/	0.0423	/	0.0423
<i>Rno-miR-199a-3p</i>	/	2.3725	7.0036	4.6881		<i>Rno-miR-200b</i>	0.0326	0.0494	0.0735	0.0518
<i>Rno-miR-411</i>	3.7417	/	/	3.7417		<i>Rno-miR-142-5p</i>	0.0895	0.0877	/	0.0886
<i>Rno-miR-135a</i>	2.7896	/	/	2.7896		<i>Rno-miR-192</i>	/	0.0913	/	0.0913
<i>Rno-miR-449a</i>	1.8114	3.6110	/	2.7112		<i>Rno-miR-194</i>	0.1405	0.0917	/	0.1161
<i>Rno-miR-291a-3p</i>	3.3069	1.7701	/	2.5385		<i>Rno-miR-29b</i>	0.1550	0.2788	/	0.2169
<i>Rno-miR-20b-5p</i>	2.4710	/	/	2.4710		<i>Rno-miR-300-5p</i>	0.3719	/	/	0.3719
<i>Rno-miR-199a-5p</i>	1.5536	3.3857	/	2.4697		<i>Rno-miR-214</i>	0.4615	/	/	0.4615
<i>Rno-let-7d*</i>	2.3962	/	/	2.3962		<i>Rno-miR-294</i>	0.3928	/	0.5522	0.4725
<i>Rno-miR-124*</i>	2.3603	/	/	2.3603		<i>Rno-miR-29a</i>	0.3590	0.4761	0.6583	0.4978
<i>Rno-miR-126*</i>	/	2.1846	2.5139	2.3493		<i>Rno-miR-29a</i>	0.3590	0.4761	0.6583	0.4978
<i>Rno-miR-495</i>	2.2056	/	/	2.2056						
<i>Rno-miR-142-3p</i>	2.1627	/	/	2.1627						
<i>Rno-miR-186</i>	2.1562	/	/	2.1562						
<i>Rno-miR-675</i>	2.1486	/	/	2.1486						
<i>Rno-miR-329</i>	2.1400	/	/	2.1400						
<i>Rno-miR-708*</i>	2.0997	/	/	2.0997						
<i>Rno-miR-137</i>	2.0741	/	/	2.0741						
<i>Rno-miR-128</i>	2.0426	/	/	2.0426						
<i>Rno-miR-339-5p</i>	2.0074	/	/	2.0074						

*MFC: Mean Fold Change

miRNAs were retrieved from miRecords, which selects the target genes that have been retrieved by at least three databases. Furthermore, these target genes were searched for using PubMed. And a large list of target genes were identified to be close to PVL, some were already confirmed by references (Table 2).

Network analysis and functional annotation

The target genes of 16 differentially expressed miRNAs were input into BiNGO of Cytoscape software. Biological process was analyzed and 404 functional GO terms were collected at last. Functional analysis demonstrated that these genes were identified to be associated with the GO categories of brain development, generation of neurons, response to hypoxia, cell differentiation, cell death and etc (see Attachment). The Cytoscape was then used to visualize these associations (Figure 1).

KEGG pathway

KEGG from DAVID was used to label the function of genes and perform the pathway enrichment analysis. Finally, 9 significant pathways including wnt signal-

ing pathway and neurotrophin signaling pathway were acquired (Table 3).

DISCUSSION

In the present study, 35 differentially expressed miRNAs were first identified to exhibit a regulatory function in PVL. As a result of retrieving the target genes of the miRNAs from miRecords, a few of predicted targets of 16 significant miRNAs were found to be associated with PVL at last (showed in Table 1 and 2).

Though there haven't been miRNA studies reported directly related to PVL to date, some miRNA researches have already clarified how this small RNA participated in brain damage and neural development, such as miRNA-10a-5p, miRNA-29a/b and etc. Prins *et al.* (2014) once proved that the expression level of miRNA-10a-5p changed significantly in the dorsal and ventral hippocampus of rats during normal pubertal development and repeated binge-EtOH exposure. Similarly, miRNA-29 family is also an important kind of brain-specific miRNA, which is strongly expressed in neural

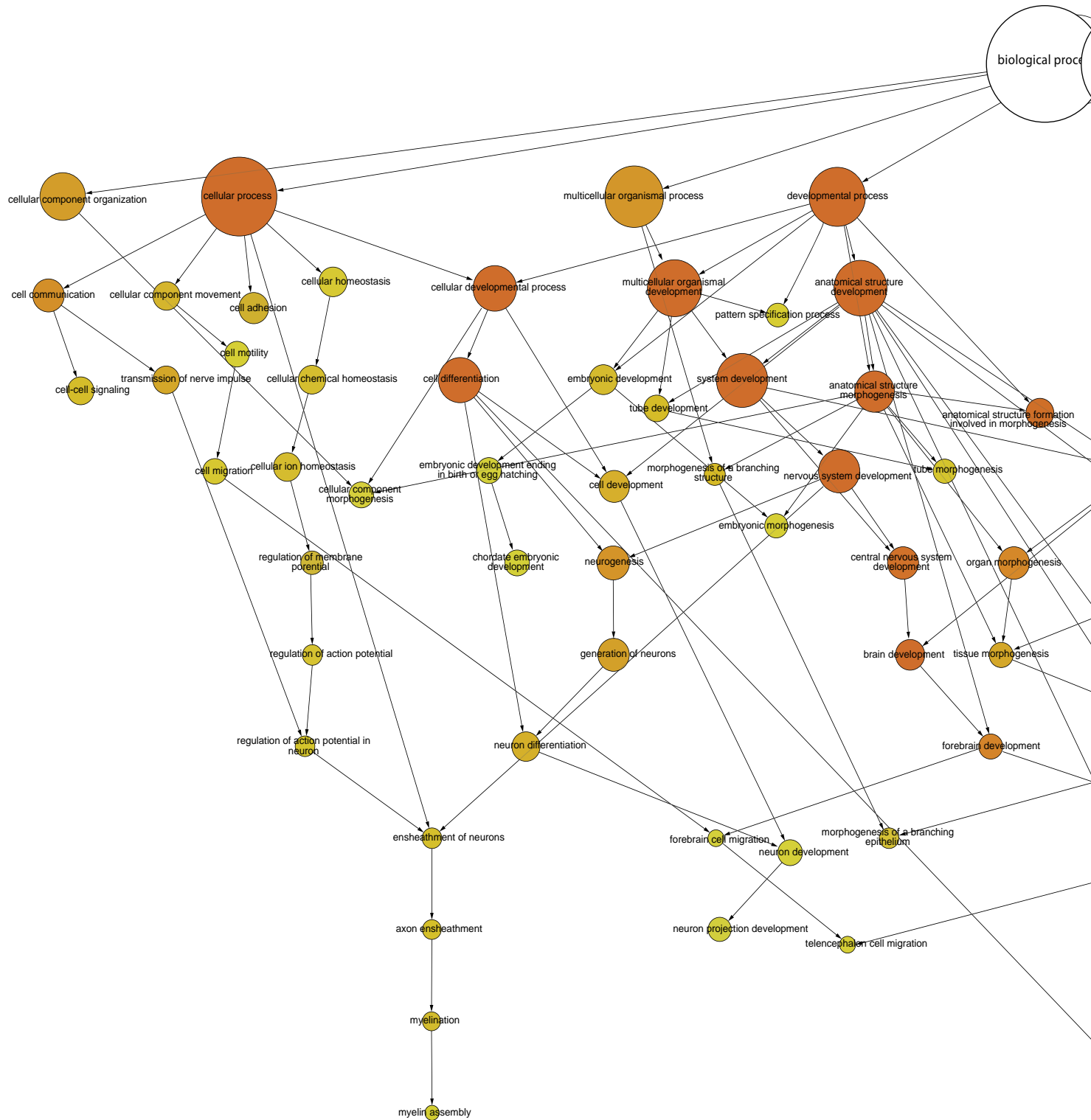
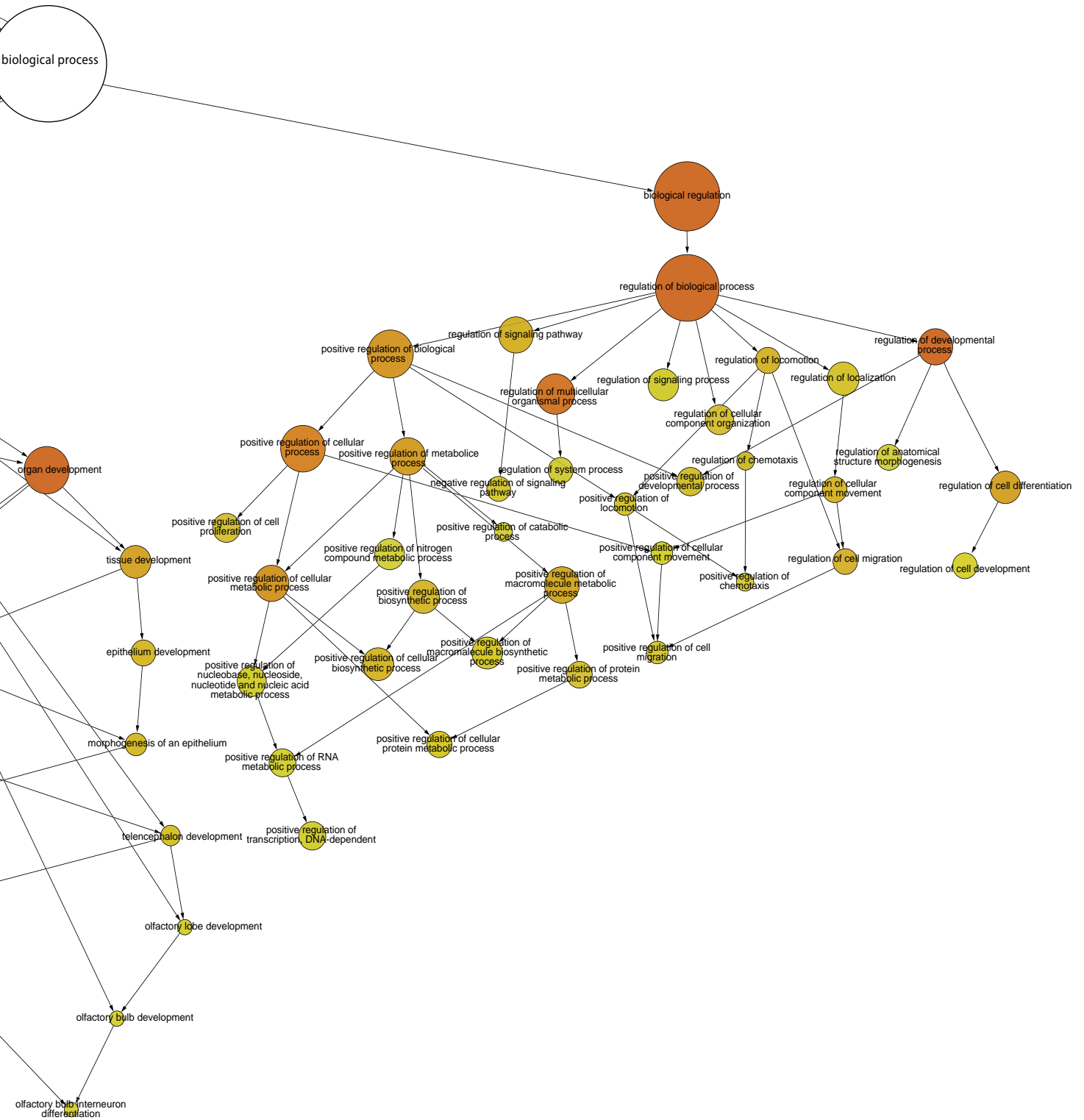


Fig. 1. The visualization of GO terms by the Cytoscape.



Tab. 2. Target genes of differentially expressed miRNA

miRNAs	Target genes related to brain disease by reference*
mir-10a-5p	Agtrl1; Bdnf ;Cisd2;Cln8; Csmd1 ;Elavl2;Fads1;Gpr177;Gsx2;Hs6st2;Lrrk1;Pitpnb;Pklr;Slc38a2;Slc7a5;Tusc5
mir-29a	Abcb6;Abcg8;Agrn;Atp1b1;Blmh; Bmf ; Ccna2 ; Cd93 ;Cerk;Cldn1;Col;Dusp2;Gpr;Grip1;Has3; Hdac4 ;Hmgcr;Hmgn3;lreb2; Lamc1 ;Moap1;Nav1; Nfia ;Oxr1; Pmp22 ;Ric8;Rmnd5a;Smtnl2;Snx;Spna2;Tpm1;Zfp
mir-29b	Abcb6;Abcg8;Agrn;Atp1b1;Blmh;Bmf;Ccna2;Cd93;Cerk;Cldn1; Col ; Dnmt3b ; Dusp2 ;Gpr;Grip1;Has3; Hdac4 ;Hmgcr;Hmgn3;lreb2; Lamc1 ;Moap1;Nav1;Nfia;Oxr1;Paip2;Pmp22;Ric8;Rmnd5a;Senp1;Smtnl2;Snx;Spna2;Tpm1;Zfp
mir-135a	Abca8a;Adcyap1;Anxa7;Btdb10;Ceacam1;Cplx1;Cxcl12;Fam;Grid2;Gypc; Heatr5b ; Hif1a9 ;Hmbox1; Hoxa10 ;Hs3st2;lgf2bp2;Impa1;Itm2b;Klf4;Lrrn1;Man2a1;Mmp16;Mrpl19; Nr3c2 ;Nudt4;Pola1;Rbak;Rnf138;Rpl28;Rspo2; Siah1a ;Slc;Smarce1;Sqstm1;Taf1;Tgm6;Tmod1;Trpm4;Trpm7;Ttrap;Ube3c;Zbtb43;Zdhhc6;Zfp;Zyg11b
mir-137	Atp1b1;Cacnb2;Cd93;Col11a1; Ctbp1 ;Ctsf;Dhd1;Egr2;Ehd4;Eif2s3x;Fam98a;Hey2;Hmgn3;Hsd3b1;Kcnc3;Kcnk6;Lamc2;Lgr4;Mapkapk2;Msi2;Myo1d;Oxr1;Pde7a;Ppil5;Rab11b;Ranbp2;Rnf138;Rrm1;Scarb1;Scn1a;Serp1;Serpina5;Slc;Snrk;Snx25;Sox9;Sv2a;Synj1;Tmem55a;Tsnax;Ube3c;Ubx4;Ulk2;Zfp
mir-139-5p	Acat1;Aplp2;Arl8b;Atp2b2;Cdc25a;Ciapin1;Dmd;Ebag9;Elavl2;Ets1;F2r;Fbxo9;Fhl1; Gclc ;Gdf10;Gnb4;Gpc4;Gpr56;Hoxb2;Iifit3; Irs1 ;Kcnd2;Kcnj6;Kif11;Lgals7;Manba;Mast4;Nalcn;Ndfip1;Ndrgr4;Nptn;Nxph1;Pafah1b1;Parg;Plcb1;Plp1;Pmp22;Ppp2ca;Pura;Rad21;Scd1;Serpini1;Slc;Syn2;Tbc1d5;Tgif1;Tmop;Tnpo1;Tspan12;Wdr4;Zeb1
mir-144	Abi2;Acdb3;Agrn;Ahcy;Ank2;Arl6ip6;Atp2b2; Cask ;Cct2;Cdh11;Cyp2c;Dnah7;Ets1;Fat4;Fbxl3;Fmr1;Gdf10;Gria2;Hdgfrp3;Hsp90aa1;Hat1;Ibsp; Ihd2 ; Irs1 ;Itsn2;Kcnab1;Lbxcor1;Lsm14a;Magel2; Map3k8 ;Mapk6; Nfe2l2 ;Nln;Nrg1;Pcdh18;Pdcl;Pde3b; Pla2g4a ;Pura;Rab6a;Rap1a;Rarb;Rfxdc2;Serpini1; Robo2 ;Scfd1;Serpini1;Slc;Sgpp1;Smarca1;Smpd3;Srr;Ssb;Suclg2;Tec;Tnpo1;Tspan12;Tspan3;Ube;Usp46;Vps4b;Zdhhc17; Zeb1 ;Zfp;Zfr;Zranb2
mir-142-3p	Acs14;Ank3; Arntl ;Atp2a2;Cask;Foxm1; Ghr ;Med20;Pawr;Pcaf;Rai14;Serinc1;Slc;Stx12;Tsen34
mir-142-5p	Apbb1ip;Brwd3;Cdh11;Crot;Cxcr7;Elavl4;FAM120C;Fmr1;Garn1;Gas7;Gpr88;Grsf1;Kdr;Lrp12;Lrp2;Nt5e;Ranbp2;Rnh1;Sfrp1;Sft2d1;Shank2;Slc18a2;Sostdc1;Sstr1;Surf4;Tdo2;Tns1;Uba3;Ube2d3;Ube2v2;Usp9x;Zfp
mir-141	Actn1;Agrt1a;Ak2;Akap6;Aldh1a1;Apbb2;Arf2;Arhgef5;Arl6ip1;Astn1;Atp1b3;Atp6v1;Atxn7a;Bcat1;Bicd2;Cacna1b;Calcr;Ccnd100;Cd28;Cdc2l5;Cdc42bpb;Chm;Chp;Cdon;Cdca5;Clasp2;Cno;Crot;Ctnnd2; Cxcl12 ;Cxcl3; Cyp26b1 ;Dcx;Dek; Dlc1 ; Dlx5 ;Dr1;Dusp5;Edem1;Efn1;Eif2s3x;Elavl2;Fam49b;Fbxl10;Fen1;Fkbp5;Grb2;Gucy1a3;H2afz;Has2;Ids;lfrd1;lgf2bp2;ll13ra2;lpmk;lrs2;Khdrbs;Kidins220;Lass6;Leng8;Mme;Myh10;Myt11;Nap1l3;Narg2;Nars2;Nlgn2;Nr3c1;Ntrk2;Nub1;Optn;Pcdh19;Pcdh9; Pitx2 ;Pou3f3;Ppt2;Prkd1;Prlr;Prmt3;Rapgef5;Rsad2;Sdc2;Serp1;Serpinb2;Slc;Snip1;Srp72; Stat4 ; Stat5a ;Stk25;Stxbp1;Trp63;Ttr;Txnip;Ulk2;Unc5c;Wdr44; Zeb1 ;Zfp
mir-186	Ablim1;Acs14;Aftph;Asah1;Aspa;Atad2;Atg9a;Best1;Bet1;Bicd2;Btf3;Cast;Cbfb; Ccnd1 ;Cdh11;Chp;Chrna5;Chrn3;Cntnap1;Col14a1;Col5a2;Cpox;Crebbp;Csmd1;Csn2;Ctsb;Cugbp1;Cux1;Cxcl13;Dazl;Dcx;Dek;Derl1;Dok6;Dr1;Drg1;Dynlt3;Ebag9;Eif2c1;Eif4b;Eif5;Ern1;Fasl;Foxd1;Foxp2;Frm4b;Fzd6;Gbe1;Gclm;Gnal;Hyou1;Ids;lgsf1;ll13ra1;lnsm1;ltga6;ltsn2;Kcnc2;Kcnj1;Kcnq3;Kif11;Kif2a;Kihl2;Lipc;Lppr4;Lrp2;Mcf2;Mfn2;Mmp16;Mpp3;Mrs2;Mtf2;Mut;Mxi1;Nars;Ncor1;Nkx2-1;Nlrp3;Nova1;Nxph1
mir-187	Masp1;Slit2;Tgfb3;Zcchc9
mir-192	Alcam;Bcr;Emp2;Ereg;F2r;Fndc3b;Gjb2;Hnrnp1;Kcnc1;Kidins220;Lphn3;Pdha1;Ppm2c;Ppp2r3a;Ryr3;Scn4b;Sh2b3;Slc10a2;Vcam1;Wdr44; Wnk1
mir-194	Acdb3;Adam17;Api5;Aqp8;Arl6ip6; Atf3 ;Atxn1;Bicd2;Cask;Cend1;Chd4;Cln5;Col14a1;Crim1;Cyp51;Dtna;Edn1;Enox1;F2r;Fdf1;Fmr1;Gmfb;Gnptg;Grhl2;Hbegf;Lrrfip1;Med20;Med4;Nbr1;Nrn1;Nxph1;Ostm1;Paip2;Pdhhb;Pja2;Ripk2;Sfrs10;Sgk3;Slc;Smarcc1;Sod2;Sox11;Stau2;Stx1b;Sumo2;Tfb2m;Tmem161b;Ube2v2;Uhmk1;Wnt5a
mir-329	Acvr1b;Adamts1;Adnp2;Bnip3l;Ccdc91;Cltc;Crmp1;Cyp26b1;Dnajb9; E2f1 ;Eno2;Epha4;F11r;Frzb;Fut7;Fxr2;Gga1;ll13ra1;lnsr;ltga2;Kihl2;Nbr1;Neo1;Nlk;Panx1
mir-339-5p	Abp1;Acot2;Adam7;Aoc3;Cdh6;Csmd1;Cxcl16;Eml5;Fhl1;Hdgfrp3;Hhip;Ier5;Jam2;L3mbt2;Lamc1;Mafk;Nfx1;Nid1;Nphp3;Nrxn1;Ocln;Ogt;Pafah1b1;Pnpt1;Prkg2;Rab15;Rasd2;S1pr1;Scn4a;Sema3c;Slc;Stat5a;Stil;Sult1b1;Suox;Tect2;Traff7;Ttpa;Txnip; Unc5c ;Vat1;Vegfb;Vom2r75;Vps33a;Vps4b;Zbtb41;Zfp382

*Target genes in bold italics were already confirmed by literature.

development and highly enriched in neurons of the olfactory bulb, the hippocampus and in the Purkinje cells of the cerebellum. Roshan *et al.* (2014) reported that miRNA-29 is a key determinant of neuronal cell survival in brain, and knockdown of miRNA-29 could result in neuronal cell death and ataxia in mice. In addition, Ouyang *et al.* (2014) demonstrated that miRNA-29a might emerge as a strategy for protection against ischemia-reperfusion injury. As is known to all, PVL is characterized by hypoxic ischemic necrotic lesions

leading to non-selective destruction of all cellular elements, including glia and blood vessels (Volpe 2009; Gilles & Gomez 2005). The immature white matter of both human beings and rodents is highly sensitive to altered oxygen tension during a critical developmental window prior to the onset of myelination (Wellmann *et al.* 2005). So, these new found miRNAs may be involved in PVL through the above pathological and physiological processes, although the exact mechanism is still not clear yet.

Tab. 3. Pathway enrichment analysis related to PVL by KEGG.

Description	p-value	Benjamini	Genes in test set
ECM-receptor interaction	2.7E-3	3.3E-1	AGRN;COL5A2;COL11A1;IBSP;ITGA2;ITGA6;LAMC1;LAMC2;SV2A;SDC2
Aldosterone-regulated sodium reabsorption	4.4E-3	2.9E-1	ATP1B1;ATP1B3; INSR;IRS1;IRS2; NR3C2;KCNJ1
Cell adhesion molecules	7.8E-3	3.3E-1	CD28;F11R;ALCAM;CLDN1;CNTNAP1;ITGA6;JAM2;NEO1;NRXN1;NLGN2;OCLN; SDC2;VCAM1
Pathways in cancer	2.3E-2	5.8E-1	CTBP1;CREBBP;E2F1;HHIP;ACVR1B;BCR;CCND1;FZD6;GRB2;HIF1A;ITGA2;ITGA6;LAMC1;LAMC2;RAR;STAT1; STAT4;STAT5A;DNAJC4;VEGFB; WNT5A
Lysosome	2.7E-2	5.7E-1	ATP6V0A2;TECT2;ASAH1;CTSB;CTSF;CLN5;CLTC;GGA1;IDS;MANBA;PPT2
Long-term depression	3.5E-2	6.0E-1	GRIA2;GRID2; GUCY1A3;PLA2G4A; PLCB1;PRKG2; PPP2CA
Wnt signaling pathway	4.0E-2	5.8E-1	CTBP1;CREBBP;CHP;RGD1564956;CCND1;FZD6;NLK;PLCB1;PPP2CA;SFRP1; SIAH1A; WNT5A
Neurotrophin signaling pathway	4.1E-2	5.5E-1	RAP1A;SH2B3;BDNF;GRB2;IRS1;IRS2;KIDINS220;MAPKAPK2;NTRK2; RIPK2
Valine, leucine and isoleucine biosynthesis	5.0E-2	5.8E-1	BCAT1; PHDB;PDHA1

Beside these significant miRNAs, the target gene is another key point we emphasize. (1) Firstly, miRecords was used to screen the potential target genes, and miRNA-141 has the greatest quantity of predicted target genes (99 genes, showed in Table 2). Although there is no direct evidence in the aspect of PVL, Lee *et al.* (2012) observed that the inhibition of miRNA-141 activities in SHSY5Y cells makes these cells more tolerant to oxygen glucose deprivation-induced cell death. This may indirectly indicated that miRNA-141 may be involved in the progression of PVL by the similar mechanism. (2) Secondly, 41 above-mentioned genes had already been confirmed close to brain diseases by literature search (see genes in bold italics of Table 2). (3) Furthermore, among these proved genes, Hdac4, Lamc1, Irs1 and Zeb1 are the most frequently appeared ones. Interestingly, they are also proved closely related to hypoxic ischemic brain damage (Qian *et al.* 2006; Buga *et al.* 2014; Joseph *et al.* 2015; Minchenko *et al.* 2013). For example, Qian *et al.* proved that inhibition by small interfering RNA of HDAC4 could reduce HIF-1 alpha protein expression and its transcriptional activity (Qian *et al.* 2006). Moreover, Buga *et al.* found Lamc1 was one of the “New-for-stroke” genes that were linked to the increased vasculature density in young animal’s brains (Buga *et al.* 2014).

Through BiNGO and Cytoscape, various biological processes including neurogenesis and generation of neurons related to nervous system development were found under pathological and physiological conditions (see Attachment). Subsequently, several meaningful pathways were acquired by KEGG analysis (show in Table 3). Thereinto, Wnt signaling pathway attract our attention at first glance, Wang *et al.* once found hyperbaric oxygen treatment could promote the proliferation of neural stem cells in hypoxia-ischemia brain damage neonatal rats, which is correlated with the activation of

Wnt signaling (Wang *et al.* 2007). Neurotrophin signaling pathway is another interesting pathway, Galvin *et al.* reported that continuous low-dose treatment with brain-derived neurotrophic factor or neurotrophin-3 protects striatal medium spiny neurons from mild neonatal hypoxia/ischemia (Galvin & Oorschot 2003). These results suggested the potential pathways PVL involved in, though there haven’t direct evidences.

In conclusion, the current study identified 16 differentially expressed miRNAs, which may be important in the progression of PVL and miRNA-141 demonstrated the greatest quantity of target genes. In addition, Hdac4, Lamc1, Irs1 and Zeb1 are the most frequently appeared ones among proved genes. Wnt signaling pathway and Neurotrophin signaling pathway were identified to be significantly associated with PVL. However, further investigation regarding the specific function is required.

Conflicts of interest

The authors declare no conflict of interest.

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Supplement: GO functional analysis.

GO-ID	Description	p-value	Corr-p	Gene Name
48856	Developmental process	5.0397E-27	1.6323E-23	CAST DLC1 HMGR EFNA1 STAT5A EDN1 PITPNB PDE3B CXCL12 SLC7A5 CIAPIN1 CBFβ LPHN3 ATP2B2 ASPA BDNF S1PR1 ANK2 ANK3 SOSTDC1 TRP63 ROBO2 UNC5C RARB IFRD1 INSR CCNA2 PITX2 BCR IRS1 VEGFB SSTR1 AGTR1A SIAH1A GPR56 NPTN TGIF1 ADAMTS1 LAMC1 PMP22 SMARCA1 WNT5A IBSP GCLC LPPR4 GRB2 RIC8 UBE2V2 SOX9 NRN1 GCLM ACAT1 UHMK1 ADCYAP1 ALCAM NPHP3 NDRG4 CRMP1 DMD SRR HOXA10 BTF3 NKX2-1 AGRN DNMT3B NOVA1 TEC SCD1 GSX2 CUGBP1 CREBBP LGALS7 IREB2 ITGA2 MAFK GAS7 SHANK2 FOXP2 KDR PCDH18 EPHA4 HDAC4 PLA2G4A ATF3 ITGA6 SFRP1 ETS1 CXCL13 DLX5 NTRK2 TGFB3 NCOR1 KLF4 TMD01 E2F1 GRIP1 TSNA X SYNJ1 TTPA ZEB1 LGR4 ASAH1 SDC2 ACVR1B TSPAN12 HEY2 CCDC100 SEMA3C GUCY1A3 CNTNAP1 NRG1 COL11A1 GHR KIF2A CTBP1 HSP90AA1 EGR2 SOX11 PCDH9 OSTM1 GPR177 ZFR SLIT2 PURA MFN2 MYT1L MAN2A1 CCND1 EREG CLDN1 CTSB CUX1 CLN8 AOC3 SERP1 CALCR FOXM1 CTNND2 RSAD2 ABI2 NEO1 CDH6 VCAM1 ALDH1A1 SQSTM1 PPP2CA CYP26B1 CHM POU3F3 FASL DAZL PAFAH1B1 ACSL4 DCX FOXD1 CD28 TXNIP PLP1 GRSF1 NID1 COL5A2 FZD6 GJB2 SOD2 CDON SLC18A2 HBEGF GDF10 LIPC LRP2 SMPD3 CSN2 F2R
7275	Anatomical structure development	3.6790E-25	5.9582E-22	CAST DLC1 EFNA1 STAT5A EDN1 PDE3B CXCL12 SLC7A5 CIAPIN1 CBFβ LPHN3 ATP2B2 ASPA BDNF S1PR1 ANK2 ANK3 SOSTDC1 ROBO2 RARB IFRD1 INSR CCNA2 PITX2 BCR IRS1 VEGFB AGTR1A SSTR1 GPR56 NPTN TGIF1 ADAMTS1 LAMC1 SMARCA1 PMP22 WNT5A IBSP GCLC LPPR4 GRB2 UBE2V2 SOX9 NRN1 GCLM ACAT1 UHMK1 ADCYAP1 ALCAM NPHP3 CRMP1 DMD SRR HOXA10 NKX2-1 AGRN DNMT3B NOVA1 TEC GSX2 CUGBP1 CREBBP ITGA2 MAFK GAS7 SHANK2 FOXP2 PCDH18 KDR EPHA4 HDAC4 PLA2G4A ITGA6 SFRP1 ETS1 CXCL13 DLX5 NTRK2 TGFB3 NCOR1 KLF4 TMD01 E2F1 GRIP1 SYNJ1 TTPA ZEB1 LGR4 ASAH1 SDC2 ACVR1B TSPAN12 HEY2 CCDC100 SEMA3C GUCY1A3 CNTNAP1 NRG1 COL11A1 GHR KIF2A HSP90AA1 EGR2 SOX11 PCDH9 OSTM1 GPR177 ZFR SLIT2 PURA MFN2 MYT1L MAN2A1 CCND1 EREG CLDN1 CTSB CUX1 CLN8 SERP1 CALCR CTNND2 RSAD2 ABI2 NEO1 CDH6 VCAM1 ALDH1A1 PPP2CA CYP26B1 CHM POU3F3 FASL DAZL PAFAH1B1 ACSL4 DCX FOXD1 CD28 TXNIP PLP1 GRSF1 NID1 COL5A2 FZD6 GJB2 SOD2 CDON HBEGF GDF10 LIPC LRP2 CSN2 F2R
48731	Culticellular organismal development	8.6793E-25	9.3708E-22	CAST DLC1 HMGR EFNA1 STAT5A EDN1 PITPNB PDE3B CXCL12 SLC7A5 CIAPIN1 CBFβ LPHN3 ATP2B2 ASPA BDNF S1PR1 ANK2 ANK3 SOSTDC1 ROBO2 UNC5C RARB IFRD1 INSR CCNA2 PITX2 BCR IRS1 VEGFB AGTR1A SSTR1 SIAH1A GPR56 NPTN TGIF1 ADAMTS1 LAMC1 PMP22 WNT5A IBSP GCLC LPPR4 GRB2 RIC8 UBE2V2 SOX9 NRN1 GCLM ACAT1 UHMK1 ADCYAP1 ALCAM NPHP3 NDRG4 CRMP1 DMD SRR HOXA10 BTF3 NKX2-1 AGRN DNMT3B NOVA1 TEC GSX2 IREB2 ITGA2 MAFK GAS7 SHANK2 FOXP2 KDR PCDH18 EPHA4 HDAC4 PLA2G4A ITGA6 SFRP1 ETS1 CXCL13 DLX5 NTRK2 TGFB3 NCOR1 KLF4 E2F1 GRIP1 TSNA X SYNJ1 TTPA ZEB1 LGR4 ASAH1 SDC2 ACVR1B TSPAN12 HEY2 CCDC100 SEMA3C GUCY1A3 CNTNAP1 NRG1 COL11A1 GHR KIF2A HSP90AA1 EGR2 SOX11 PCDH9 OSTM1 GPR177 ZFR SLIT2 PURA MYT1L MAN2A1 CCND1 EREG CLDN1 CTSB CUX1 CLN8 SERP1 CALCR CTNND2 RSAD2 ABI2 CDH6 VCAM1 ALDH1A1 PPP2CA CYP26B1 CHM POU3F3 FASL PAFAH1B1 ACSL4 DCX FOXD1 CD28 TXNIP PLP1 GRSF1 NID1 COL5A2 FZD6 GJB2 SOD2 CDON SLC18A2 HBEGF GDF10 LIPC LRP2 SMPD3 CSN2 F2R
7399	System development	3.1631E-23	2.5613E-20	CAST DLC1 EFNA1 STAT5A EDN1 PDE3B CXCL12 SLC7A5 CIAPIN1 CBFβ LPHN3 ATP2B2 ASPA BDNF S1PR1 ANK2 ANK3 SOSTDC1 ROBO2 RARB IFRD1 INSR CCNA2 PITX2 BCR IRS1 VEGFB AGTR1A SSTR1 GPR56 NPTN TGIF1 ADAMTS1 LAMC1 SMARCA1 PMP22 WNT5A IBSP LPPR4 GRB2 UBE2V2 SOX9 NRN1 ACAT1 UHMK1 ADCYAP1 ALCAM NPHP3 CRMP1 DMD SRR HOXA10 NKX2-1 AGRN DNMT3B NOVA1 TEC GSX2 ITGA2 MAFK SHANK2 GAS7 FOXP2 PCDH18 KDR HDAC4 EPHA4 PLA2G4A ITGA6 SFRP1 CXCL13 ETS1 DLX5 NTRK2 TGFB3 NCOR1 KLF4 E2F1 GRIP1 SYNJ1 TTPA ZEB1 LGR4 ASAH1 SDC2 ACVR1B TSPAN12 HEY2 CCDC100 SEMA3C CNTNAP1 NRG1 COL11A1 GHR KIF2A HSP90AA1 EGR2 SOX11 PCDH9 OSTM1 GPR177 ZFR SLIT2 PURA MYT1L MAN2A1 CCND1 EREG CLDN1 CTSB CUX1 CLN8 SERP1 CALCR RSAD2 ABI2 CDH6 VCAM1 ALDH1A1 PPP2CA CHM POU3F3 FASL PAFAH1B1 ACSL4 DCX FOXD1 CD28 TXNIP PLP1 GRSF1 NID1 COL5A2 FZD6 GJB2 SOD2 HBEGF GDF10 LIPC LRP2 CSN2 F2R
48513	Nervous system development	1.9999E-17	1.2955E-14	CAST DLC1 E2F1 GRIP1 EFNA1 SYNJ1 ZEB1 CXCL12 SLC7A5 SDC2 ACVR1B LPHN3 ATP2B2 ASPA BDNF S1PR1 ANK2 ANK3 CCDC100 SEMA3C CNTNAP1 ROBO2 RARB NRG1 IFRD1 KIF2A PITX2 HSP90AA1 EGR2 BCR SOX11 PCDH9 SLIT2 PURA MYT1L SSTR1 GPR56 CLDN1 NPTN TGIF1 LAMC1 CUX1 SMARCA1 PMP22 CLN8 WNT5A LPPR4 ABI2 UBE2V2 NRN1 ACAT1 UHMK1 ADCYAP1 ALCAM CRMP1 DMD SRR POU3F3 NKX2-1 PAFAH1B1 AGRN ACSL4 DCX DNMT3B NOVA1 PLP1 GSX2 MAFK GAS7 SHANK2 FOXP2 FZD6 SOD2 KDR PCDH18 EPHA4 ETS1 DLX5 NTRK2 HBEGF GDF10 NCOR1 CSN2
48869	Organ development	5.2988E-16	2.8605E-13	DLC1 EFNA1 STAT5A EDN1 PDE3B CXCL12 CIAPIN1 CBFβ LPHN3 ATP2B2 S1PR1 SOSTDC1 ROBO2 RARB INSR CCNA2 PITX2 BCR IRS1 VEGFB AGTR1A SSTR1 GPR56 TGIF1 ADAMTS1 SMARCA1 IBSP WNT5A GRB2 SOX9 ACAT1 ADCYAP1 NPHP3 DMD HOXA10 SRR NKX2-1 AGRN TEC GSX2 ITGA2 SHANK2 PCDH18 KDR FOXP2 PLA2G4A SFRP1 ITGA6 CXCL13 ETS1 DLX5 NTRK2 TGFB3 NCOR1 KLF4 E2F1 SYNJ1 TTPA ZEB1 ASAH1 LGR4 TSPAN12 ACVR1B CCDC100 HEY2 SEMA3C NRG1 COL11A1 GHR EGR2 SOX11 PCDH9 OSTM1 GPR177 ZFR SLIT2 MAN2A1 CCND1 EREG CTSB CUX1 CLN8 SERP1 CALCR ABI2 CDH6 ALDH1A1 VCAM1 PPP2CA CHM POU3F3 PAFAH1B1 FASL FOXD1 CD28 TXNIP GRSF1 NID1 COL5A2 SOD2 GJB2 FZD6 GDF10 LIPC LRP2 F2R
9653	Cellular developmental process	2.6317E-13	1.2075E-10	CAST EFNA1 TSNA X SYNJ1 EDN1 CXCL12 SLC7A5 CBFβ SDC2 ATP2B2 ASPA BDNF S1PR1 ANK2 ANK3 HEY2 CCDC100 SEMA3C ROBO2 RARB NRG1 IFRD1 COL11A1 INSR KIF2A PITX2 CTBP1 HSP90AA1 EGR2 SOX11 OSTM1 SLIT2 MFN2 MYT1L CCND1 EREG SSTR1 NPTN TGIF1 LAMC1 CUX1 PMP22 CLN8 CALCR WNT5A LPPR4 GRB2 ABI2 UBE2V2 NEO1 UHMK1 ADCYAP1 ALCAM SQSTM1 CRMP1 DMD CYP26B1 HOXA10 NKX2-1 FASL DAZL PAFAH1B1 AGRN ACSL4 DCX DNMT3B CD28 TXNIP SCD1 PLP1 GSX2 CUGBP1 CREBBP LGALS7 ITGA2 GAS7 SOD2 KDR EPHA4 HDAC4 ATF3 ITGA6 SFRP1 CDON DLX5 NTRK2 TGFB3 GDF10 NCOR1 KLF4 CSN2 F2R TMD01
9987	Anatomical structure morphogenesis	2.9823E-13	1.2075E-10	CAST DLC1 EFNA1 STAT5A EDN1 ZEB1 CXCL12 LGR4 SDC2 TSPAN12 S1PR1 ANK2 ANK3 SOSTDC1 HEY2 SEMA3C GUCY1A3 ROBO2 RARB NRG1 COL11A1 INSR CCNA2 GHR PITX2 EGR2 GPR177 SLIT2 MFN2 VEGFB CCND1 TGIF1 ADAMTS1 LAMC1 PMP22 SERP1 WNT5A GCLC LPPR4 GRB2 CTNND2 NEO1 GCLM VCAM1 ALCAM ALDH1A1 DMD CYP26B1 HOXA10 NKX2-1 FASL PAFAH1B1 FOXD1 TEC GSX2 GRSF1 ITGA2 GAS7 COL5A2 FZD6 SOD2 KDR EPHA4 ITGA6 SFRP1 ETS1 CDON DLX5 NTRK2 TGFB3 LRP2 KLF4 TMD01

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
65007	Cellular process	6.3395E-13	2.2207E-10	DLC1 HMG3 ATP1B1 EIF2C1 ATP1B3 AQP8 EFNA1 STAT5A EDN1 SNIP1 CCT2 PRKG2 CIAPIN1 VPS33A ATP2B2 BDNF S1PR1 MAP3K8 VPS4B GRID2 H2AFZ OGT PDHA1 RARB CDCA5 PITX2 BCR SUCLG2 WNK1 OPTN MAPK6 SSTR1 SULT1B1 RYR3 SIAH1A NPTN TGIF1 RAB15 LAMC2 ARL8B LAMC1 SRP72 PMP22 IBSP SCN1A AHY LPPR4 PPT2 MME UHMK1 ADCYAP1 ALCAM STX12 CRMP1 SERINC1 DMD IDH2 HOXA10 NKX2-1 SFRS10 AGRN DNMT3B SCD1 CUGBP1 CREBBP LGALS7 NDFIP1 GAS7 PCDH19 KDR TECT2 EPHA4 PLA2G4A GBE1 COL14A1 SFRP1 ATP2A2 ETS1 ARF2 DLX5 NTRK2 UBA3 TGFBR3 NCOR1 KLF4 TMOD1 CDC42BPB NARS KCNAB1 TSNAX SYNJ1 NAP1L3 ZEB1 LSM14A PARG SEMA3C GUCY1A3 RAB6A NTSE COL11A1 CEACAM1 GHR CTBP1 EIF2S3X OSTM1 STX1B SLIT2 MAST4 ZDHHC17 MED4 CCND1 SENP1 EREG RRM1 ADAM17 SPNA2 GNB4 CLN8 SERP1 BCAT1 HSD3B1 FUT7 CXCL3 BET1 POLA1 AB12 NEO1 ITM2B EDEM1 SFT2D1 SUMO2 IGSF11 STAT4 SNRK SQSTM1 FAT4 PPP2CA CHM MRPL19 RAB11B FASL DAZL CHP ACSL4 FEN1 CD28 NUB1 NLK FADS1 NLGN2 NID1 RPL28 MANBA GJB2 SOD2 DUSP5 DUSP2 GRIA2 CDON MCFD2 USP46 LRP2 CDH11 CAST KCNC2 GNPTG KCNC1 OCLN KCNC3 HMGR ERIF5 CASK PDE3B CNO CXCL12 SLC7A5 PDHB CBFBD FDT1 CYP2C ASPA ANK2 ANK3 CPOX TRP63 TFB2M ROBO2 NALCN UNC5C IFRD1 INSR IRS2 ATG9A KCND2 STK25 NUDT4 ACTN1 ARNTL IRS1 HIF1A AGTR1A NBR1 GPR56 RIPK2 NFE2L2 SMARCA1 LRRK1 CROT ARL6IP1 WNT5A GCLC DERL1 PANX1 GRB2 PNPT1 ASTN1 UBE2V2 MAPKAPK2 GCLM HNRNP1 UBE2D3 MRS2 SRR SCARB1 CLASP2 TRAF7 NOVA1 TEC TAF1 GSX2 IREB2 AK2 ITGA2 SSB ABCB6 HDAC4 DNAJB9 ATF3 ITGA6 ULK2 SMARCC1 TMPO CACNA1B MYH10 E2F1 IMPA1 SGPP1 TTPA ACOT2 PAWR CLTC SDC2 PRMT3 ACVR1B TDO2 KCNQ3 CD93 NARS2 HEY2 CCDC100 CNTNAP1 RANBP2 SV2A PLCB1 NRG1 KIF2A EBAG9 TRPM4 HSP90AA1 EGR2 KIF11 SGK3 TRPM7 SOX11 STXBP1 PCDH9 NRXN1 PPM2C PURA PRKD1 MFN2 MYT1L MAN2A1 PDCL PKLR ERN1 CLDN1 CTSB CUX1 AOC3 TTRAP CALCR ABLIM1 CPLX1 FKBP5 USP9X CTNND2 HAT1 UBE3C NR3C1 DNAH7 CDH6 VCAM1 ALDH1A1 ANXA7 CYP26B1 SYN2 ENO2 POU3F3 CDC2L5 PAFAH1B1 TGM6 DCX CHD4 EHD4 TSEN34 TXNIP PLP1 L3MBTL2 SNX25 SLC10A2 COL5A2 CDC25A ATXN1 SCFD1 PRLR SLC18A2 ZRANB2 GDF10 PCAF LIPC GGA1 NFIA SCN4A SMPD3 CSN2 F2R
30154	Biological regulation	6.8563E-13	2.2207E-10	DLC1 EIF2C1 MASP1 EFNA1 STAT5A EDN1 SNIP1 ITSN2 MXI1 CIAPIN1 MED20 BDNF S1PR1 SOSTDC1 MAP3K8 GRID2 RAPGEF5 PDHA1 RARB CCNA2 PITX2 BCR WNK1 VEGFB SULT1B1 RYR3 SIAH1A NPTN TGIF1 RAB15 ARL8B PMP22 SCN1A MME UHMK1 ADCYAP1 NPHP3 STX12 DMD SERINC1 HOXA10 NKX2-1 AGRN DNMT3B SCD1 PAIP2 CUGBP1 CREBBP NDFIP1 LGALS7 SERPINI1 GAS7 KDR ABCG8 PLA2G4A KCNJ6 ATP2A2 SFRP1 ARF2 ETS1 DLX5 UBA3 NTRK2 TGFBR3 NCOR1 KLF4 SYNJ1 ZEB1 SERPINA5 GUCY1A3 PARG HHIP RAB6A IL13RA1 NTSE CEACAM1 GHR CTBP1 ARHGEF5 STX1B SLIT2 GNAL CCND1 MED4 ZDHHC17 EREG ADAM17 GNB4 SPNA2 WDR44 CLN8 RASD2 SERP1 HSD3B1 NEO1 ITM2B IGSF11 SUMO2 STAT4 SNRK SQSTM1 TBC1D5 RAB11B CHM DAZL FASL CERK CHP FOXD1 CD28 NLGN2 NID1 SOD2 DUSP5 GRIA2 RBAK BNIP3L HBEGF LRP2 CAST HMGR PDE3B CXCL12 LASS6 CBFBD PDHB TTR ASPA CISD2 RAD21 ANK2 ANK3 TRP63 TFB2M ROBO2 UNC5C INSR FNDC3B API5 IRS2 KCND2 FMR1 ACTN1 ARNTL AGTRL1 IRS1 HIF1A SMARCE1 AGTR1A AKAP6 RIPK2 RFXDC2 NFE2L2 SMARCA1 LRRK1 WNT5A GCLC PANX1 GRB2 UBE2V2 MAPKAPK2 GCLM UBE2D3 SCARB1 CLASP2 TRAF7 BMF TEC TAF1 GSX2 IREB2 ITGA2 FOXP2 HDAC4 HOXB2 ATF3 DNAJB9 ITGA6 PDE7A SMARCC1 CXCL16 RAP1A CACNA1B E2F1 IMPA1 PAWR ACVR1B TSPAN12 GARNL1 HEY2 CCDC100 CNTNAP1 SV2A LRRFIP1 NRG1 NFX1 HSP90AA1 EGR2 SOX11 DYNL3 STXBP1 NLRP3 PPM2C PURA MFN2 MYT1L ERN1 CLDN1 CTSB CUX1 AOC3 CALCR CYP51 CPLX1 FOXM1 CTNND2 NR3C2 RNH1 RSAD2 HAT1 NR3C1 TPM1 VCAM1 ALDH1A1 CYP26B1 SYN2 POU3F3 LBXCOR1 PAFAH1B1 CRIM1 CHD4 EHD4 TXNIP ZFP382 PLP1 L3MBTL2 HMBX1 ATXN1 ADNP2 SCFD1 PRLR DR1 SLC18A2 GDF10 PCAF LIPC NFIA SMPD3 F2R
10033	Cell differentiation	1.0057E-12	2.9613E-10	CAST EFNA1 TSNAX SYNJ1 EDN1 CXCL12 SLC7A5 CBFBD SDC2 ATP2B2 ASPA BDNF S1PR1 HEY2 CCDC100 SEMA3C ROBO2 RARB NRG1 IFRD1 COL11A1 INSR KIF2A PITX2 CTBP1 HSP90AA1 EGR2 SOX11 OSTM1 SLIT2 MYT1L CCND1 EREG SSTR1 NPTN TGIF1 LAMC1 CUX1 PMP22 CLN8 CALCR WNT5A LPPR4 GRB2 AB12 UBE2V2 NEO1 UHMK1 ADCYAP1 ALCAM SQSTM1 CRMP1 DMD CYP26B1 HOXA10 NKX2-1 FASL DAZL PAFAH1B1 AGRN ACSL4 DCX DNMT3B CD28 TXNIP SCD1 PLP1 GSX2 CUGBP1 CREBBP LGALS7 ITGA2 GAS7 SOD2 KDR EPHA4 HDAC4 ATF3 ITGA6 SFRP1 CDON DLX5 NTRK2 TGFBR3 GDF10 NCOR1 KLF4 CSN2 F2R TMOD1
50789	Response to organic substance	3.6144E-12	9.7559E-10	DLC1 E2F1 AQP8 STAT5A SYNJ1 SNIP1 ACOT2 PDE3B DEK ZEB1 CXCL12 ASAH1 SDC2 BDNF ANK2 ANK3 VPS4B CHRNAS GUCY1A3 ROBO2 INSR CCNA2 GHR IRS2 HSP90AA1 EGR2 IRS1 SLIT2 CCND1 HIF1A EREG SSTR1 AGTR1A RYR3 PKLR ERN1 RIPK2 ADAM17 TGIF1 GNB4 CTSB NFE2L2 CROT SERP1 CALCR WNT5A GCLC DERL1 PANX1 GRB2 FOXM1 NR3C1 ACAT1 ADCYAP1 ALDH1A1 ANXA7 STAT4 ENO2 SRR NKX2-1 SCARB1 FASL PAFAH1B1 ACSL4 TXNIP NUB1 FADS1 ITGA2 SOD2 HDAC4 PLA2G4A SFRP1 ATP2A2 ETS1 CXCL16 SLC18A2 TGFBR3 GDF10 PCAF LIPC NFIA F2R CACNA1B
50794	Regulation of biological process	8.4678E-12	2.1098E-9	DLC1 EIF2C1 MASP1 EFNA1 STAT5A EDN1 SNIP1 ITSN2 MXI1 CIAPIN1 MED20 BDNF S1PR1 SOSTDC1 MAP3K8 GRID2 RAPGEF5 PDHA1 RARB CCNA2 PITX2 BCR WNK1 VEGFB SIAH1A NPTN TGIF1 RAB15 ARL8B PMP22 MME UHMK1 ADCYAP1 NPHP3 STX12 DMD HOXA10 NKX2-1 AGRN DNMT3B SCD1 PAIP2 CUGBP1 CREBBP NDFIP1 LGALS7 SERPINI1 GAS7 KDR ABCG8 PLA2G4A ATP2A2 SFRP1 ARF2 ETS1 DLX5 UBA3 NTRK2 TGFBR3 NCOR1 KLF4 SYNJ1 ZEB1 SERPINA5 GUCY1A3 PARG HHIP RAB6A IL13RA1 NTSE CEACAM1 GHR CTBP1 ARHGEF5 STX1B SLIT2 GNAL CCND1 MED4 ZDHHC17 EREG ADAM17 GNB4 SPNA2 WDR44 CLN8 RASD2 SERP1 NEO1 ITM2B IGSF11 SUMO2 STAT4 SNRK SQSTM1 TBC1D5 RAB11B CHM DAZL FASL CERK CHP FOXD1 CD28 NLGN2 NID1 SOD2 DUSP5 GRIA2 BNIP3L RBAK HBEGF CAST HMGR PDE3B CXCL12 LASS6 CBFBD PDHB ASPA CISD2 RAD21 ANK2 ANK3 TRP63 TFB2M ROBO2 UNC5C INSR FNDC3B API5 IRS2 FMR1 ACTN1 ARNTL IRS1 HIF1A SMARCE1 AGTR1A RIPK2 AKAP6 RFXDC2 NFE2L2 SMARCA1 LRRK1 WNT5A GCLC PANX1 GRB2 UBE2V2 MAPKAPK2 GCLM UBE2D3 SCARB1 TRAF7 CLASP2 BMF TEC TAF1 GSX2 IREB2 ITGA2 FOXP2 HDAC4 HOXB2 ATF3 DNAJB9 ITGA6 PDE7A SMARCC1 CXCL16 RAP1A CACNA1B E2F1 IMPA1 PAWR ACVR1B TSPAN12 GARNL1 CCDC100 HEY2 CNTNAP1 LRRFIP1 NRG1 NFX1 HSP90AA1 EGR2 SOX11 DYNL3 STXBP1 NLRP3 PPM2C PURA MFN2 MYT1L ERN1 CTSB CUX1 AOC3 CALCR CYP51 FOXM1 CTNND2 NR3C2 RNH1 RSAD2 HAT1 NR3C1 TPM1 VCAM1 ALDH1A1 SYN2 POU3F3 LBXCOR1 PAFAH1B1 CRIM1 CHD4 EHD4 TXNIP ZFP382 L3MBTL2 HMBX1 ATXN1 ADNP2 SCFD1 PRLR DR1 GDF10 PCAF NFIA F2R

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
7420	Regulation of cellular process	2.0157E-11	4.6635E-9	DLG1 EIF2C1 EFNA1 STAT5A EDN1 SNIP1 ITSN2 MXI1 CIAPIN1 MED20 BDNF S1PR1 SOSTDC1 MAP3K8 GRID2 RAPGEF5 PDHA1 RARB CCNA2 PITX2 BCR WNK1 VEGFB NPTN TGIF1 RAB15 ARL8B PMP22 MME UHMK1 ADCYAP1 NPHP3 DMD HOXA10 NKX2-1 AGRN DNMT3B PAIP2 CUGBP1 CREBBP NDFIP1 LGALS7 SERPINI1 GAS7 KDR PLA2G4A SFRP1 ARF2 ETS1 DLX5 UBA3 NTRK2 TGFBR3 NCOR1 KLF4 SYNJ1 ZEB1 SERPINA5 GUCY1A3 PARG HHIP RAB6A IL13RA1 CEACAM1 GHR CTBP1 ARHGGEF5 STX1B SLIT2 GNAL CCND1 MED4 ZDHHC17 EREG ADAM17 GNB4 SPNA2 WDR44 CLN8 RASD2 SERP1 NEO1 ITM2B SUMO2 STAT4 SNRK SQSTM1 TBC1D5 RAB11B CHM DAZL FASL CERK CHP FOXD1 CD28 NLGN2 NID1 SOD2 DUSP5 GRIA2 BNIP3L RBAK HBEGF CAST HMGCRC PDE3B CXCL12 LASS6 CBFH PDHB ASPA CISD2 RAD21 ANK2 ANK3 TRP63 TFB2M ROBO2 UNC5C INSR FNDC3B API5 IRS2 FMR1 ACTN1 ARNTL IRS1 HIF1A SMARCE1 AGTR1A RIPK2 AKAP6 RFXDC2 NFE2L2 SMARCA1 LRRK1 WNT5A GCLC PANX1 GRB2 UBE2V2 MAPKAPK2 GCLM SCARB1 TRAF7 CLASP2 BMF TEC TAF1 GSX2 IREB2 ITGA2 FOXP2 HDAC4 ATF3 DNAJB9 HOXB2 ITGA6 PDE7A SMARCC1 CXCL16 RAPIA CACNA1B E2F1 IMPA1 PAWR ACVR1B CCDC100 HEY2 GARNL1 CNTNAP1 LRRFIP1 NRG1 NFX1 EGR2 HSP90AA1 SOX11 DYLNLT3 STXB1 NLRP3 PPM2C PURA MFN2 MYT1L ERN1 CTSB CUX1 AOC3 CALCR FOXM1 CTNND2 NR3C2 HAT1 NR3C1 TPM1 VCAM1 ALDH1A1 SYN2 POU3F3 LBXCOR1 PAFAH1B1 CRIM1 CHD4 EHD4 TXNIP ZFP382 L3MBTL2 HMBOX1 ATXN1 ADNP2 SCFD1 PRLR DR1 GDF10 PCAF NFIA F2R
50793	Brain development	3.5305E-10	7.6236E-8	WNT5A E2F1 DLG1 SYNJ1 ZEB1 CXCL12 ACAT1 ADCYAP1 LPHN3 ATP2B2 S1PR1 CCDC100 SRR POU3F3 NKX2-1 ROBO2 PAFAH1B1 RARB PITX2 EGR2 BCR GSX2 PCDH9 SHANK2 SLIT2 FOXP2 PCDH18 SSTR1 ETS1 DLX5 GPR56 GDF10 SMARCA1 NCOR1
7417	Regulation of developmental process	6.0464E-10	1.2240E-7	DLG1 HMGCRC EFNA1 SYNJ1 EDN1 ZEB1 CXCL12 ACVR1B TSPAN12 ASPA BDNF HEY2 ROBO2 RARB NRG1 INSR FNDC3B GHR EGR2 SLIT2 CCND1 EREG AGTR1A NPTN RIPK2 TGIF1 NFE2L2 CALCR WNT5A RNH1 RSAD2 UBE2V2 ADCYAP1 NPHP3 HOXA10 NKX2-1 PAFAH1B1 FASL AGRN DNMT3B FOXD1 CD28 CREBBP NDFIP1 GAS7 SOD2 KDR HDAC4 PLA2G4A SFRP1 ETS1 DLX5 NTRK2 TGFBR3 GDF10 KLF4
51239	Central nerve system development	9.9372E-10	1.8933E-7	WNT5A DLG1 E2F1 SYNJ1 ZEB1 ACAT1 CXCL12 ADCYAP1 ACVR1B LPHN3 ATP2B2 ASPA S1PR1 CCDC100 SRR POU3F3 NKX2-1 ROBO2 PAFAH1B1 RARB PITX2 PLP1 EGR2 BCR GSX2 SOX11 PCDH9 SHANK2 SLIT2 FOXP2 PCDH18 ETS1 SSTR1 DLX5 GPR56 GDF10 SMARCA1 NCOR1 CLN8
48646	Regulation of multicellular organismal process	1.0621E-9	1.9112E-7	HMGCRC EFNA1 SYNJ1 EDN1 ZEB1 CXCL12 ACVR1B TSPAN12 ASPA BDNF SERPINA5 HEY2 GUCY1A3 ROBO2 RARB INSR GHR EGR2 STXB1 NLRP3 SLIT2 CCND1 HIF1A EREG AGTR1A SH1A1 NPTN RIPK2 ADAM17 TGIF1 NFE2L2 CALCR WNT5A PANX1 CTNND2 RNH1 RSAD2 UBE2V2 ADCYAP1 SYN2 HOXA10 NKX2-1 FASL PAFAH1B1 AGRN DNMT3B FOXD1 CD28 GSX2 CUGBP1 NDFIP1 ITGA2 NLGN2 KDR ABCG8 HDAC4 PLA2G4A GRIA2 ATP2A2 SFRP1 ETS1 DLX5 NTRK2 HBEGF TGFBR3 GDF10 NCOR1 KLF4 F2R CACNA1B
19222	Anatomical structure formation involved in morphogenesis	1.2025E-9	2.0499E-7	CAST DLG1 GRB2 EFNA1 EDN1 NEO1 CXCL12 ALDH1A1 TSPAN12 S1PR1 ANK2 ANK3 NKX2-1 SEMA3C PAFAH1B1 PITX2 EGR2 GPR177 SLIT2 FZD6 VEGFB SFRP1 ETS1 CDON DLX5 TGFBR3 TGIF1 ADAMTS1 PMP22 TMOD1
31323	Regulation of metabolic process	3.2306E-9	5.1273E-7	CAST DLG1 EIF2C1 HMGCRC EFNA1 STAT5A EDN1 SNIP1 PDE3B MXI1 LASS6 MED20 PDHB CBFH CISD2 RAD21 S1PR1 TRP63 TFB2M PDHA1 RARB INSR PITX2 IRS2 FMR1 WNK1 ARNTL IRS1 HIF1A SMARCE1 AGTR1A NPTN AKAP6 RIPK2 TGIF1 RFXDC2 NFE2L2 SMARCA1 WNT5A GCLC UBE2V2 MAPKAPK2 UHMK1 ADCYAP1 UBE2D3 STX12 DMD HOXA10 NKX2-1 TRAF7 AGRN DNMT3B TAF1 GSX2 PAIP2 CUGBP1 CREBBP IREB2 NDFIP1 ITGA2 FOXP2 HDAC4 PLA2G4A HOXB2 ATF3 ETS1 SMARCC1 DLX5 UBA3 NTRK2 TGFBR3 NCOR1 KLF4 E2F1 PAWR ZEB1 ACVR1B SERPINA5 GARNL1 HEY2 GUCY1A3 PARG LRRFIP1 NRG1 CEACAM1 GHR NFX1 CTBP1 HSP90AA1 EGR2 SOX11 STXB1 NLRP3 PPM2C SLIT2 PURA MYT1L GNAL CCND1 MED4 EREG ERN1 ADAM17 CUX1 RASD2 SERP1 CALCR CYP51 FOXM1 CTNND2 NR3C2 HAT1 NEO1 NR3C1 TPM1 SUMO2 STAT4 SQSTM1 CHM TBC1D5 POU3F3 LBXCOR1 DAZL PAFAH1B1 CERK FOXD1 CHD4 CD28 TXNIP ZFP382 L3MBTL2 HMBOX1 SOD2 ATXN1 DUSP5 ADNP2 PRLR GRIA2 DR1 RBAK BNIP3L HBEGF NFIA F2R
48522	Regulation of cellular metabolic process	3.3243E-9	5.1273E-7	DLG1 EIF2C1 HMGCRC EFNA1 STAT5A EDN1 SNIP1 MXI1 LASS6 MED20 PDHB CBFH CISD2 RAD21 S1PR1 TRP63 TFB2M PDHA1 RARB INSR PITX2 IRS2 FMR1 WNK1 ARNTL IRS1 HIF1A SMARCE1 AGTR1A NPTN AKAP6 RIPK2 TGIF1 RFXDC2 NFE2L2 SMARCA1 WNT5A GCLC UBE2V2 MAPKAPK2 UHMK1 ADCYAP1 DMD HOXA10 NKX2-1 TRAF7 AGRN DNMT3B TAF1 GSX2 PAIP2 CUGBP1 CREBBP IREB2 NDFIP1 ITGA2 FOXP2 HDAC4 PLA2G4A HOXB2 ATF3 ETS1 SMARCC1 DLX5 UBA3 NTRK2 TGFBR3 NCOR1 KLF4 E2F1 PAWR ZEB1 ACVR1B SERPINA5 GARNL1 HEY2 GUCY1A3 PARG LRRFIP1 NRG1 CEACAM1 GHR NFX1 CTBP1 HSP90AA1 EGR2 SOX11 NLRP3 PPM2C SLIT2 PURA MYT1L GNAL CCND1 MED4 EREG ERN1 ADAM17 CUX1 RASD2 SERP1 CALCR FOXM1 CTNND2 NR3C2 HAT1 NR3C1 NEO1 TPM1 SUMO2 STAT4 SQSTM1 CHM TBC1D5 POU3F3 LBXCOR1 DAZL PAFAH1B1 CERK FOXD1 CHD4 CD28 TXNIP ZFP382 L3MBTL2 HMBOX1 SOD2 ATXN1 DUSP5 ADNP2 PRLR GRIA2 DR1 RBAK HBEGF NFIA F2R
30900	Positive regulation of cellular process	4.8209E-9	7.0976E-7	DLG1 EDN1 CXCL12 CBFH ASPA S1PR1 TRP63 ROBO2 RARB CCNA2 INSR FNDC3B PITX2 IRS2 ARNTL IRS1 VEGFB HIF1A AGTR1A NPTN TGIF1 RIPK2 NFE2L2 SMARCA1 WNT5A GCLC PANX1 MME UBE2V2 UHMK1 ADCYAP1 HOXA10 NKX2-1 TRAF7 AGRN DNMT3B TAF1 CREBBP NDFIP1 LGALS7 ITGA2 KDR HDAC4 PLA2G4A ATF3 ITGA6 ETS1 SMARCC1 CXCL16 DLX5 NTRK2 TGFBR3 NCOR1 KLF4 CACNA1B E2F1 SYNJ1 PAWR ZEB1 ACVR1B HEY2 GUCY1A3 PARG NRG1 IL13RA1 GHR EGR2 HSP90AA1 SOX11 NLRP3 SLIT2 PURA CCND1 ZDHHC17 EREG ADAM17 RASD2 SERP1 AOC3 FOXM1 NR3C1 ITM2B ALDH1A1 VCAM1 SQSTM1 POU3F3 DAZL PAFAH1B1 FASL FOXD1 CD28 TXNIP NID1 SOD2 ATXN1 GRIA2 BNIP3L HBEGF GDF10 NFIA F2R
71310	Forebrain development	7.4562E-9	1.0500E-6	WNT5A DLG1 E2F1 GSX2 PCDH9 ZEB1 CXCL12 SLIT2 FOXP2 ADCYAP1 ETS1 SSTR1 DLX5 CCDC100 POU3F3 NKX2-1 ROBO2 PAFAH1B1 RARB NCOR1 PITX2
9887	Cellular response to organic substance	9.2155E-9	1.2437E-6	WNT5A DLG1 E2F1 DERL1 GRB2 AQP8 SNIP1 PDE3B ZEB1 ADCYAP1 ROBO2 PAFAH1B1 INSR GHR IRS2 ITGA2 IRS1 SLIT2 SOD2 CCND1 HIF1A SFRP1 SSTR1 AGTR1A PKLR ERN1 TGIF1 PCAF GNB4 NFE2L2 LIPC SERP1

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
7154	Organ morphogenesis	1.5829E-8	2.0508E-6	WNT5A DLC1 GRB2 EFNA1 EDN1 ZEB1 CXCL12 ALDH1A1 TSPAN12 SOSTDC1 HOXA10 SEMA3C NKX2-1 FASL PAFAH1B1 RARB COL11A1 INSR FOXD1 CCNA2 GHR PITX2 GSX2 GRSF1 ITGA2 GPR177 COL5A2 SLIT2 FZD6 CCND1 ITGA6 SFRP1 DLX5 NTRK2 TGFBR3 TGIF1 ADAMTS1 LRP2 KLF4 SERP1
31325	Cell communication	3.8927E-8	4.7230E-6	CAST SCN1A CPLX1 PANX1 EDN1 UBE2V2 ADCYAP1 ASPA BDNF S1PR1 ANK2 SQSTM1 ANK3 DMD SYN2 HOXA10 GRID2 NKX2-1 CNTNAP1 PAFAH1B1 AGRN NRG1 PLP1 EGR2 ATG9A SGK3 FADS1 SNX25 STX1B GJB2 ATXN1 ITGA6 GRIA2 EREG NBR1 NTRK2 SLC18A2 CLDN1 RAB15 LRP2 PMP22 CLN8 SMPD3
48519	Positive regulation of cellular metabolic process	4.0224E-8	4.7230E-6	E2F1 DLC1 PAWR ZEB1 CBFEB ACVR1B S1PR1 TRP63 GUCY1A3 PARG RARB INSR GHR PITX2 IRS2 HSP90AA1 EGR2 SOX11 ARNTL IRS1 CCND1 HIF1A EREG AGTR1A NPTN ADAM17 RIPK2 NFE2L2 SMARCA1 RASD2 SERP1 WNT5A GCLC UBE2V2 NR3C1 UHMK1 ADCYAP1 SQSTM1 POU3F3 NKX2-1 DAZL AGRN DNMT3B CD28 TAF1 CREBBP NDFIP1 ITGA2 SOD2 ATXN1 HDAC4 PLA2G4A ETS1 SMARCC1 DLX5 NCOR1 NFIA KLF4 F2R
51179	Negative regulation of biological process	4.0870E-8	4.7230E-6	DLC1 EIF2C1 EDN1 SNIP1 PDE3B ZEB1 PAWR MX1 CIAPIN1 ACVR1B BDNF S1PR1 SERPINA5 SOSTDC1 HEY2 TRP63 GRID2 GUCY1A3 ROBO2 HHIP RARB NRG1 NT5E INSR API5 IRS2 FMR1 ACTN1 NLRP3 IRS1 SLIT2 PURA MFN2 CCND1 EREG SMARCE1 RIPK2 ADAM17 TGIF1 SPNA2 CTSB CUX1 PMP22 CLN8 RASD2 CALCR WNT5A GCLC FOXM1 HAT1 UBE2V2 NR3C1 TPM1 GCLM UHMK1 ADCYAP1 SUMO2 NPHP3 SQSTM1 POU3F3 NKX2-1 LBXCOR1 FASL PAFAH1B1 CLASP2 FOXD1 DNMT3B TXNIP SCD1 ZFP382 PAIP2 HMBBOX1 CREBBP NDFIP1 FOXF2 SOD2 ATXN1 ABCG8 DUSP5 HDAC4 DNAJB9 SFRP1 ATP2A2 ETS1 DLX5 BNIP3L UBA3 HBEGF TGFBR3 PCAF NCOR1 KLF4 F2R
48518	Localization	4.2287E-8	4.7230E-6	KCNC2 GNPTG CAST KCNC1 ATP1B1 KCNC3 ATP1B3 AQP8 EDN1 PITPNB CASK CNO CXCL12 SLC7A5 VPS33A TTR ATP2B2 ANK3 KCNK6 VPS4B GRID2 CHRNAS NALCN CDCA5 ATG9A KCND2 FMR1 WNK1 ARNTL OPTN BICD2 AGTR1A RYR3 RAB15 LAMC1 SRP72 CROT ARL6IP1 WNT5A SCN1A SLC38A2 DERL1 PANX1 GRB2 ASTN1 CACNB2 CCDC91 ADCYAP1 KCNJ1 MRS2 STX12 SERINC1 NKX2-1 SCARB1 CLASP2 DNMT3B ITGA2 ABCB6 TECT2 ABCG8 KCNJ6 ITGA6 ATP2A2 ARF2 ETS1 NTRK2 CHRNB3 MYH10 CACNA1B GRIP1 KCNAB1 SYNJ1 CLTC KCNQ3 CCDC100 SEMA3C RANBP2 SV2A RAB6A NRG1 GHR TRPM4 HSP90AA1 TRPM7 STXBP1 STX1B SLIT2 MFN2 ZDHHC17 ADAM17 CUX1 CLN8 AOC3 SERP1 CPLX1 CXCL3 BET1 ABI2 STAU2 VCAM1 SFT2D1 SUMO2 BEST1 SYN2 RAB11B CHM POU3F3 PAFAH1B1 CHP ACSL4 DCX EHD4 TXNIP FADS1 SLC10A2 ATXN1 SCFD1 GRIA2 MCFD2 SLC18A2 SCN4B LRP2 GGA1 SCN4A SMPD3 F2R
22008	Positive regulation of biological process	6.4596E-8	6.9742E-6	DLC1 MASP1 HMGCR EDN1 CXCL12 CBFEB ASPA S1PR1 TRP63 ROBO2 RARB INSR CCNA2 FND3B PITX2 IRS2 ARNTL IRS1 VEGFB HIF1A AGTR1A NPTN TGIF1 RIPK2 NFE2L2 SMARCA1 WNT5A GCLC PANX1 MME UBE2V2 UHMK1 ADCYAP1 HOXA10 NKX2-1 SCARB1 TRAF7 AGRN DNMT3B TAF1 CUGBP1 CREBBP NDFIP1 LGALS7 ITGA2 KDR HDAC4 PLA2G4A ATF3 ITGA6 ETS1 SMARCC1 CXCL16 DLX5 NTRK2 TGFBR3 NCOR1 KLF4 CACNA1B E2F1 SYNJ1 PAWR ZEB1 ACVR1B HEY2 GUCY1A3 PARG NRG1 IL13RA1 GHR EGR2 HSP90AA1 SOX11 NLRP3 SLIT2 PURA CCND1 ZDHHC17 EREG ADAM17 RASD2 AOC3 SERP1 FOXM1 NR3C1 ITM2B VCAM1 ALDH1A1 SQSTM1 POU3F3 DAZL PAFAH1B1 FASL FOXD1 CD28 TXNIP NID1 SOD2 ATXN1 GRIA2 BNIP3L HBEGF GDF10 NFIA F2R
32501	Neurogenesis	7.1659E-8	7.4872E-6	WNT5A LPPR4 EFNA1 SYNJ1 ABI2 UBE2V2 CXCL12 UHMK1 SDC2 ADCYAP1 ALCAM ATP2B2 ASPA BDNF S1PR1 CRMP1 DMD CCDC100 NKX2-1 ROBO2 PAFAH1B1 RARB ACSL4 NRG1 DCX IFRD1 DNMT3B PLP1 HSP90AA1 EGR2 GSX2 SOX11 GAS7 SLIT2 SOD2 KDR EPHA4 DLX5 NTRK2 NPTN TGIF1 LAMC1 CUX1 CLN8 CSN2
9893	Multicellular organismal process	9.5903E-8	9.7071E-6	CAST DLC1 HMGCR EFNA1 STAT5A EDN1 PITPNB PDE3B CXCL12 SLC7A5 CIAPIN1 CBFEB LPHN3 ATP2B2 ASPA BDNF S1PR1 ANK2 ANK3 SOSTDC1 CHRNAS GRID2 TRP63 ROBO2 RARB UNC5C IFRD1 CCNA2 ADAM7 INSR PITX2 BCR WNK1 AGTRL1 IRS1 VEGFB SSTR1 AGTR1A SIAH1A RYR3 GPR56 NPTN RAB15 TGIF1 ADAMTS1 LAMC1 PMP22 SMARCA1 WNT5A IBSP SCN1A GCLC LPPR4 GRB2 RIC8 UBE2V2 SOX9 NRN1 GCLM ACAT1 UHMK1 ADCYAP1 ALCAM NPHP3 NDRG4 CRMP1 DMD SRR HOXA10 BTF3 NKX2-1 SCARB1 AGRN DNMT3B NOVA1 TEC GSX2 CUGBP1 IREB2 ITGA2 MAFK GAS7 SHANK2 FOXF2 KDR PCDH18 ABCG8 EPHA4 HDAC4 PLA2G4A ITGA6 SFRP1 ETS1 CXCL13 DLX5 NTRK2 TGFBR3 NCOR1 KLF4 E2F1 GRIP1 TSNAX SYNJ1 TTPA ACOT2 ZEB1 PAWR LGR4 ASAH1 SDC2 ACVR1B TSPAN12 SERPINA5 HEY2 CCDC100 SEMA3C GUCY1A3 CNTNAP1 PLCB1 NRG1 COL11A1 GHR KIF2A HSP90AA1 EGR2 SOX11 STXBP1 PCDH9 MMP16 OSTM1 GPR177 STX1B ZFR SLIT2 PURA MYT1L MAN2A1 CCND1 EREG PDCL CLDN1 GNB4 CTSB CUX1 CLN8 AOC3 SERP1 CALCR CPLX1 CTNND2 RSAD2 ABI2 TPM1 CDH6 VCAM1 ALDH1A1 PPP2CA CYP26B1 SYN2 CHM POU3F3 FASL DAZL PAFAH1B1 ACSL4 DCX FOXD1 CD28 TXNIP PLP1 GRSF1 NLGN2 NID1 COL5A2 FZD6 GJB2 SOD2 ATXN1 GRIA2 CDON SLC18A2 HBEGF GDF10 LIPC LRP2 SMPD3 CSN2 F2R
10629	Positive regulation of metabolic process	1.1089E-7	1.0884E-5	E2F1 DLC1 PAWR ZEB1 CBFEB ACVR1B S1PR1 TRP63 GUCY1A3 PARG RARB INSR GHR PITX2 IRS2 HSP90AA1 EGR2 SOX11 ARNTL IRS1 CCND1 HIF1A EREG AGTR1A NPTN RIPK2 ADAM17 NFE2L2 SMARCA1 RASD2 SERP1 WNT5A GCLC UBE2V2 NR3C1 UHMK1 ADCYAP1 SQSTM1 POU3F3 NKX2-1 DAZL AGRN DNMT3B FOXD1 CD28 TAF1 CREBBP NDFIP1 ITGA2 SOD2 ATXN1 HDAC4 PLA2G4A ETS1 SMARCC1 DLX5 NCOR1 NFIA KLF4 F2R
10646	Negative regulation of gene expression	1.5303E-7	1.4578E-5	GCLC EIF2C1 SNIP1 HAT1 ZEB1 MX1 SUMO2 HEY2 TRP63 POU3F3 LBXCOR1 NKX2-1 RARB NRG1 INSR FOXD1 DNMT3B TXNIP ZFP382 HMBBOX1 NDFIP1 SLIT2 FOXF2 PURA ATXN1 DUSP5 HDAC4 SMARCE1 EREG DLX5 BNIP3L UBA3 TGIF1 CUX1 NCOR1 KLF4
16043	Regulation of cell communication	1.6699E-7	1.5453E-5	DLC1 HMGCR EFNA1 EDN1 PDE3B PAWR ITS2 CXCL12 ACVR1B BDNF S1PR1 SOSTDC1 GARNL1 HEY2 TRP63 RAPGEF5 HHIP NRG1 INSR CEACAM1 GHR EGR2 BCR ARHGEF5 STXBP1 IRS1 SLIT2 MFN2 CCND1 ZDHHC17 EREG NPTN AKAP6 RIPK2 TGIF1 ADAM17 SERP1 WNT5A GRB2 FOXM1 CTNND2 NR3C1 ADCYAP1 SQSTM1 SYN2 TBC1D5 LBXCOR1 NKX2-1 FASL PAFAH1B1 TRAF7 FOXD1 NDFIP1 ITGA2 NLGN2 KDR ATXN1 GRIA2 SFRP1 NTRK2 HBEGF TGFBR3 NCOR1 KLF4 F2R CACNA1B

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
9605	Cellular component organization	2.1813E-7	1.9625E-5	DLC1 CAST HMG3N CASK CNO CXCL12 ANK2 ANK3 TRP63 VPS4B H2AFZ TFB2M ROBO2 OGT INSR CDCA5 ATG9A KCND2 ACTN1 OPTN IRS1 NBR1 LAMC2 ARL8B LAMC1 SMARCA1 PMP22 IBSP LPPR4 GRB2 ACAT1 UHMK1 ALCAM NPHP3 DMD SRR NKX2-1 SCARB1 AGRN CLASP2 DNMT3B TAF1 CUGBP1 CREBBP GAS7 KDR HDAC4 EPHA4 ITGA6 ETS1 SMARCC1 DLX5 TGFBR3 CHRNB3 TMPO NCOR1 CDC42BPB TMOD1 SYNJ1 NAP1L3 CLTC SDC2 LSM14A CCDC100 NRG1 COL11A1 KIF2A GHR CTBP1 KIF11 EGR2 HSP90AA1 STXB1 NRXN1 SLIT2 MFN2 MAN2A1 MED4 SPNA2 CLN8 ABLM1 HAT1 ABI2 NR3C1 ALDH1A1 ANXA7 SQSTM1 PAFAH1B1 FASL ACSL4 CHD4 EHD4 L3MBTL2 NLGN2 NID1 COL5A2 CDC25A SOD2 PRLR GRIA2 LIPC LRP2 F2R
80090	Response to external stimulus	2.5276E-7	2.2127E-5	AHCY HMGCR CXCL3 STAT5A SYNJ1 TTPA ACOT2 HAT1 ZEB1 CXCL12 ACAT1 ADCYAP1 VCAM1 ALDH1A1 SQSTM1 GRID2 PARG ACSL4 COL11A1 INSR GHR TXNIP SUOX ATG9A FADS1 ITGA2 SLIT2 SOD2 ABCG8 CCND1 PLA2G4A ITGA6 ETS1 SSTR1 AGTR1A NBR1 CXCL16 PKLR CTSB LIPC LRP2 KLF4
10604	Regulation of primary metabolic process	2.9416E-7	2.5073E-5	DLC1 CAST EIF2C1 STAT5A EDN1 SNIP1 PDE3B MXI1 MED20 LASS6 CBFβ S1PR1 RAD21 TRP63 TFB2M RARB INSR PITX2 IRS2 FMR1 ARNTL IRS1 HIF1A SMARCE1 AGTR1A NPTN TGIF1 RIPK2 RFXDC2 NFE2L2 SMARCA1 WNT5A GCLC UBE2V2 MAPKAPK2 UHMK1 ADCYAP1 UBE2D3 DMD HOXA10 NKX2-1 AGRN DNMT3B TAF1 GSX2 PAIP2 CUGBP1 CREBBP IREB2 NDFIP1 ITGA2 FOXP2 HDAC4 PLA2G4A HOXB2 ATF3 ETS1 SMARCC1 DLX5 UBA3 NTRK2 TGFBR3 NCOR1 KLF4 E2F1 PAWR ZEB1 ACVR1B SERPINA5 GARNL1 HEY2 GUCY1A3 PARG LRRFIP1 NRG1 GHR NFX1 CTBP1 EGR2 SOX11 NLRP3 SLIT2 PURA MYT1L GNAL CCND1 MED4 EREG ADAM17 CUX1 RASD2 SERP1 CALCR CYP51 FOXM1 CTNND2 NR3C2 HAT1 NR3C1 NEO1 TPM1 SUMO2 STAT4 SQSTM1 TBC1D5 CHM POU3F3 LBXCOR1 DAZL PAFAH1B1 FOXD1 CHD4 CD28 TXNIP ZFP382 L3MBTL2 HMBOX1 SOD2 ATXN1 DUSP5 ADNP2 DR1 RBAK NFIA F2R
48699	Positive regulation of macromolecule metabolic process	3.3157E-7	2.7538E-5	E2F1 DLC1 PAWR ZEB1 CBFβ ACVR1B S1PR1 TRP63 PARG RARB INSR GHR PITX2 IRS2 EGR2 SOX11 ARNTL IRS1 CCND1 HIF1A EREG AGTR1A NPTN ADAM17 RIPK2 NFE2L2 SMARCA1 RASD2 SERP1 WNT5A GCLC UBE2V2 NR3C1 UHMK1 SQSTM1 POU3F3 NKX2-1 DAZL AGRN DNMT3B FOXD1 CD28 TAF1 CREBBP NDFIP1 ITGA2 ATXN1 HDAC4 ETS1 SMARCC1 DLX5 NCOR1 NFIA KLF4 F2R
31326	Generation of neurons	3.4310E-7	2.7783E-5	WNT5A LPPR4 EFNA1 SYNJ1 ABI2 UBE2V2 CXCL12 UHMK1 SDC2 ADCYAP1 ALCAM ATP2B2 ASPA BDNF S1PR1 CRMP1 DMD NKX2-1 ROBO2 PAFAH1B1 ACSL4 NRG1 DCX IFRD1 DNMT3B HSP90AA1 EGR2 GSX2 GAS7 SLIT2 SOD2 KDR EPHA4 DLX5 NTRK2 NPTN TGIF1 LAMC1 CUX1 CLN8 CSN2
31667	Regulation of cellular biosynthetic process	4.0981E-7	3.2076E-5	EIF2C1 STAT5A EDN1 SNIP1 MXI1 MED20 LASS6 CBFβ PDHB S1PR1 RAD21 TRP63 TFB2M PDHA1 RARB INSR PITX2 IRS2 FMR1 ARNTL IRS1 HIF1A SMARCE1 TGIF1 RIPK2 RFXDC2 NFE2L2 SMARCA1 WNT5A GCLC UHMK1 ADCYAP1 DMD HOXA10 NKX2-1 AGRN DNMT3B TAF1 GSX2 PAIP2 CREBBP IREB2 ITGA2 FOXP2 HDAC4 PLA2G4A ATF3 HOXB2 ETS1 SMARCC1 DLX5 UBA3 NTRK2 TGFBR3 NCOR1 KLF4 E2F1 PAWR ZEB1 ACVR1B HEY2 GUCY1A3 LRRFIP1 NRG1 NFX1 CTBP1 EGR2 HSP90AA1 SOX11 NLRP3 PPM2C PURA GNAL MYT1L MED4 EREG CUX1 SERP1 CALCR FOXM1 NR3C2 CTNND2 HAT1 NR3C1 NEO1 SUMO2 STAT4 POU3F3 LBXCOR1 DAZL FOXD1 CHD4 CD28 TXNIP ZFP382 L3MBTL2 HMBOX1 SOD2 ATXN1 DUSP5 ADNP2 DR1 RBAK HBEGF NFIA F2R
45595	Response to nutrient levels	4.2167E-7	3.2076E-5	AHCY HMGCR STAT5A SYNJ1 TTPA ACOT2 HAT1 ZEB1 ACAT1 ADCYAP1 VCAM1 ALDH1A1 SQSTM1 ACSL4 INSR GHR SUOX ATG9A FADS1 ITGA2 SLIT2 SOD2 ABCG8 CCND1 PLA2G4A SSTR1 NBR1 PKLR LIPC LRP2 KLF4
9889	Regulation of cell differentiation	4.2582E-7	3.2076E-5	WNT5A EFNA1 SYNJ1 EDN1 UBE2V2 ZEB1 CXCL12 ADCYAP1 ACVR1B NPHP3 ASPA HOXA10 NKX2-1 ROBO2 PAFAH1B1 RARB AGRN NRG1 DNMT3B FNDC3B GHR CREBBP NDFIP1 SLIT2 SOD2 KDR HDAC4 CCND1 SFRP1 EREG ETS1 DLX5 NTRK2 NPTN RIPK2 TGFBR3 TGIF1 GDF10 KLF4
9991	Regulation of biosynthetic process	4.7340E-7	3.4849E-5	EIF2C1 STAT5A EDN1 SNIP1 MXI1 MED20 LASS6 CBFβ PDHB S1PR1 RAD21 TRP63 TFB2M PDHA1 RARB INSR PITX2 IRS2 FMR1 ARNTL IRS1 HIF1A SMARCE1 TGIF1 RIPK2 RFXDC2 NFE2L2 SMARCA1 WNT5A GCLC UHMK1 ADCYAP1 DMD HOXA10 NKX2-1 AGRN DNMT3B TAF1 GSX2 PAIP2 CREBBP IREB2 ITGA2 FOXP2 HDAC4 PLA2G4A ATF3 HOXB2 ETS1 SMARCC1 DLX5 UBA3 NTRK2 TGFBR3 NCOR1 KLF4 E2F1 PAWR ZEB1 ACVR1B HEY2 GUCY1A3 LRRFIP1 NRG1 NFX1 CTBP1 EGR2 HSP90AA1 SOX11 NLRP3 PPM2C PURA GNAL MYT1L MED4 EREG CUX1 SERP1 CYP51 CALCR FOXM1 NR3C2 CTNND2 HAT1 NR3C1 NEO1 SUMO2 STAT4 POU3F3 LBXCOR1 DAZL FOXD1 CHD4 CD28 TXNIP ZFP382 L3MBTL2 HMBOX1 SOD2 ATXN1 DUSP5 ADNP2 DR1 RBAK HBEGF NFIA F2R
9888	Response to extracellular stimulus	5.1406E-7	3.7001E-5	AHCY HMGCR STAT5A SYNJ1 TTPA ACOT2 HAT1 ZEB1 ACAT1 ADCYAP1 VCAM1 ALDH1A1 SQSTM1 ACSL4 INSR GHR SUOX ATG9A FADS1 ITGA2 SLIT2 SOD2 ABCG8 CCND1 PLA2G4A ITGA6 SSTR1 NBR1 PKLR LIPC LRP2 KLF4
60255	Tissue development	5.7877E-7	4.0753E-5	WNT5A IBSP DLC1 GRB2 EDN1 ZEB1 SOX9 CXCL12 ACAT1 ALDH1A1 ACVR1B S1PR1 PPP2CA DMD HOXA10 SEMA3C NKX2-1 RARB AGRN NRG1 COL11A1 FOXD1 TEC GHR PITX2 TXNIP GRSF1 ITGA2 GPR177 COL5A2 SLIT2 FZD6 CCND1 PLA2G4A SFRP1 DLX5 TGFBR3 TGIF1 CTSB KLF4 F2R
19226	Regulation of macromolecule metabolic process	7.0189E-7	4.8370E-5	DLC1 CAST EIF2C1 STAT5A EDN1 SNIP1 MXI1 MED20 LASS6 CBFβ S1PR1 RAD21 TRP63 TFB2M RARB INSR PITX2 IRS2 FMR1 ARNTL IRS1 HIF1A SMARCE1 AGTR1A NPTN TGIF1 RIPK2 RFXDC2 NFE2L2 SMARCA1 WNT5A GCLC UBE2V2 MAPKAPK2 UHMK1 UBE2D3 STX12 DMD HOXA10 NKX2-1 AGRN DNMT3B TAF1 GSX2 PAIP2 CUGBP1 CREBBP IREB2 NDFIP1 ITGA2 FOXP2 HDAC4 HOXB2 ATF3 ETS1 SMARCC1 DLX5 UBA3 TGFBR3 NCOR1 KLF4 E2F1 PAWR ZEB1 ACVR1B SERPINA5 HEY2 PARG LRRFIP1 NRG1 NFX1 GHR CTBP1 EGR2 SOX11 STXB1 NLRP3 SLIT2 PURA MYT1L CCND1 MED4 EREG ADAM17 CUX1 RASD2 SERP1 CALCR FOXM1 CTNND2 NR3C2 HAT1 NR3C1 NEO1 SUMO2 STAT4 SQSTM1 POU3F3 LBXCOR1 DAZL FOXD1 CHD4 CD28 TXNIP ZFP382 L3MBTL2 HMBOX1 SOD2 ATXN1 DUSP5 ADNP2 GRIA2 DR1 BNIP3L RBAK HBEGF NFIA F2R
48729	Transmission of nerve impulse	7.8337E-7	5.2861E-5	CAST SCN1A PLP1 CPLX1 EGR2 UBE2V2 STX1B ADCYAP1 ATXN1 BDNF ASPA S1PR1 GRIA2 ANK2 ANK3 DMD SYN2 GRID2 CLDN1 RAB15 CNTNAP1 PAFAH1B1 AGRN PMP22 NRG1 CLN8

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
42127	Tissue morphogenesis	8.7979E-7	5.8156E-5	WNT5A DLC1 GRB2 EDN1 GRSF1 ITGA2 GPR177 CXCL12 SLIT2 FZD6 ALDH1A1 SFRP1 HOXA10 SEMA3C TGIF1 TGFBR3 NKX2-1 COL11A1 FOXD1 KLF4 PITX2
9719	Regulation of cell proliferation	1.2425E-6	8.0486E-5	WNT5A DLC1 FOXM1 EDN1 NR3C2 MME ZEB1 PAWR NR3C1 CXCL12 ADCYAP1 VCAM1 S1PR1 HEY2 FASL RARB IL13RA1 INSR CCNA2 CD28 PITX2 TXNIP NDFIP1 ITGA2 IRS1 SLIT2 SOD2 KDR PURA MFN2 HDAC4 PLA2G4A CCND1 HIF1A ATF3 EREG ETS1 DLX5 RIPK2 ADAM17 TGFBR3 TGIF1 PCAF PMP22 KLF4 F2R
48878	Response to endogenous stimulus	1.3210E-6	8.3896E-5	CALCR WNT5A DLC1 GCLC GRB2 FOXM1 ACOT2 PDE3B ZEB1 CXCL12 ACAT1 ADCYAP1 ALDH1A1 BDNF ENO2 NKX2-1 ROBO2 CCNA2 INSR GHR TXNIP IRS2 HSP90AA1 EGR2 FADS1 ITGA2 IRS1 SLIT2 PLA2G4A CCND1 HIF1A SFRP1 ATP2A2 EREG ETS1 SSTR1 AGTR1A PKLR SLC18A2 ADAM17 TGFBR3 GDF10 PCAF GNB4 CTSB LIPC CROT CACNA1B
31328	Chemical homeostasis	1.4451E-6	9.0012E-5	CALCR SCN1A EDN1 PDE3B ADCYAP1 ASPA BDNF S1PR1 ANK2 ANK3 GRID2 CNTNAP1 SCARB1 FASL SV2A NRG1 INSR PLP1 EGR2 KCND2 IREB2 NDFIP1 SOD2 KDR ATXN1 ABCG8 PLA2G4A HIF1A ATP2A2 AGTR1A RYR3 SLC18A2 CLDN1 NPTN LIPC PMP22 NCOR1 F2R
7155	Positive regulation of cellular biosynthetic process	1.8713E-6	1.1190E-4	WNT5A E2F1 ZEB1 PAWR NR3C1 CBFH UHMK1 ADCYAP1 ACVR1B S1PR1 TRP63 POU3F3 GUCY1A3 NKX2-1 DAZL RARB AGRN INSR CD28 PITX2 TAF1 IRS2 HSP90AA1 EGR2 SOX11 CREBBP ITGA2 ARNTL IRS1 SOD2 ATXN1 HDAC4 PLA2G4A HIF1A EREG ETS1 DLX5 SMARCC1 NFE2L2 SMARCA1 NFIA KLF4 F2R SERP1
22610	Biological adhesion	1.9011E-6	1.1190E-4	IBSP DLC1 CTNND2 ASTN1 NEO1 CDH6 ALCAM VCAM1 IGSF11 CD93 FAT4 CNTNAP1 SCARB1 ROBO2 COL11A1 CEACAM1 STXBP1 ITGA2 NLGN2 ACTN1 PCDH9 NID1 NRXN1 PCDH19 SLIT2 COL14A1 ITGA6 CDON GPR56 CLDN1 NPTN ADAM17 LAMC2 LAMC1 AOC3 CDH11
48468	Cell adhesion	1.9011E-6	1.1190E-4	IBSP DLC1 CTNND2 ASTN1 NEO1 CDH6 ALCAM VCAM1 IGSF11 CD93 FAT4 CNTNAP1 SCARB1 ROBO2 COL11A1 CEACAM1 STXBP1 ITGA2 NLGN2 ACTN1 PCDH9 NID1 NRXN1 PCDH19 SLIT2 COL14A1 ITGA6 CDON GPR56 CLDN1 NPTN ADAM17 LAMC2 LAMC1 AOC3 CDH11
30182	Cell development	1.9347E-6	1.1190E-4	LPPR4 EDN1 ABI2 CXCL12 CFBF SDC2 UHMK1 ALCAM ASPA CRMP1 DMD SEMA3C NKX2-1 ROBO2 FASL DAZL PAFAH1B1 AGRN ACSL4 COL11A1 PLP1 EGR2 SOX11 CUGBP1 CREBBP GAS7 SLIT2 SOD2 KDR EPHA4 HDAC4 EREG DLX5 NTRK2 TGFBR3 LAMC1 KLF4 F2R TMOD1
10558	Neuron differentiation	2.0173E-6	1.1463E-4	WNT5A LPPR4 EFNA1 ABI2 CXCL12 SDC2 UHMK1 ALCAM ATP2B2 BDNF S1PR1 CRMP1 DMD NKX2-1 ROBO2 PAFAH1B1 NRG1 ACSL4 EGR2 GSX2 GAS7 SLIT2 SOD2 KDR EPHA4 DLX5 NTRK2 LAMC1 CUX1 CLN8 CSN2
65008	Negative regulation of macromolecule biosynthetic process	2.2236E-6	1.2418E-4	GCLC EIF2C1 EDN1 HAT1 ZEB1 MXI1 SUMO2 HEY2 TRP63 POU3F3 LBXCOR1 NKX2-1 RARB NRG1 FOXD1 DNMT3B TXNIP ZFP382 PAIP2 HMBOX1 FMR1 FOXP2 PURA ATXN1 DUSP5 HDAC4 SMARCE1 EREG DLX5 UBA3 HBEGF TGIF1 CUX1 NCOR1 KLF4
48523	Regulation of biological quality	2.4127E-6	1.3245E-4	CAST DLC1 EDN1 PDE3B CXCL12 ACVR1B TTR ASPA BDNF S1PR1 ANK2 ANK3 GRID2 GUCY1A3 CNTNAP1 SV2A NRG1 INSR EGR2 KCND2 STXBP1 WNK1 AGTRL1 SLIT2 HIF1A AGTR1A SULT1B1 RYR3 CLDN1 NPTN ADAM17 RAB15 SPNA2 PMP22 CLN8 AOC3 CALCR SCN1A CPLX1 GCLC HSD3B1 CTNND2 UBE2V2 TPM1 GCLM ADCYAP1 ALDH1A1 STX12 DMD CYP26B1 SYN2 NKX2-1 SCARB1 FASL PAFAH1B1 AGRN PLP1 IREB2 NDFIP1 ITGA2 GAS7 SOD2 KDR ATXN1 ABCG8 PLA2G4A KCNJ6 ATP2A2 CXCL16 SLC18A2 TGFBR3 HBEGF LIPC LRP2 NCOR1 SMPD3 F2R
70887	Negative regulation of cellular process	2.9384E-6	1.5771E-4	DLC1 EIF2C1 EDN1 PDE3B ZEB1 PAWR MXI1 CIAPIN1 ACVR1B S1PR1 SERPINA5 SOSTDC1 HEY2 TRP63 HHIP RARB NRG1 INSR APIS FMR1 ACTN1 IRS1 SLIT2 PURA MFN2 CCND1 EREG SMARCE1 RIPK2 ADAM17 TGIF1 SPNA2 CTSB CUX1 PMP22 CLN8 RASD2 WNT5A GCLC FOXM1 HAT1 UBE2V2 NR3C1 TPM1 GCLM UHMK1 ADCYAP1 SUMO2 NPHP3 SQSTM1 POU3F3 LBXCOR1 NKX2-1 PAFAH1B1 CLASP2 FOXD1 DNMT3B TXNIP ZFP382 PAIP2 HMBOX1 CREBBP NDFIP1 FOXP2 SOD2 ATXN1 DUSP5 HDAC4 DNAJB9 SFRP1 ETS1 DLX5 BNIP3L UBA3 HBEGF TGFBR3 PCAF NCOR1 KLF4 F2R
30334	Cellular response to chemical stimulus	2.9702E-6	1.5771E-4	WNT5A DLC1 E2F1 DERL1 GRB2 AQP8 CXCL3 SNIP1 PDE3B ZEB1 ADCYAP1 CYP2C ROBO2 PAFAH1B1 INSR GHR IRS2 ITGA2 IRS1 SLIT2 SOD2 CCND1 HIF1A SFRP1 SSTR1 AGTR1A ETS1 PKLR ERN1 TGIF1 PCAF GNB4 NFE2L2 LIPC SERP1
9891	Regulation of cell migration	3.2274E-6	1.6838E-4	WNT5A DLC1 EFNA1 EDN1 ITGA2 CXCL12 IRS1 SLIT2 KDR S1PR1 ETS1 CXCL16 ADAM17 NKX2-1 TGFBR3 HBEGF WDR44 INSR F2R AOC3 PITX2
10468	Positive regulation of biosynthetic process	3.2750E-6	1.6838E-4	WNT5A E2F1 ZEB1 PAWR NR3C1 CBFH UHMK1 ADCYAP1 ACVR1B S1PR1 TRP63 POU3F3 GUCY1A3 NKX2-1 DAZL RARB AGRN INSR CD28 PITX2 TAF1 IRS2 HSP90AA1 EGR2 SOX11 CREBBP ITGA2 ARNTL IRS1 SOD2 ATXN1 HDAC4 PLA2G4A HIF1A EREG ETS1 DLX5 SMARCC1 NFE2L2 SMARCA1 NFIA KLF4 F2R SERP1
35466	Regulation of membrane potential	3.4874E-6	1.7609E-4	EIF2C1 STAT5A SNIP1 MXI1 MED20 LASS6 CBFH S1PR1 RAD21 TRP63 TFB2M RARB INSR PITX2 FMR1 ARNTL HIF1A SMARCE1 TGIF1 RIPK2 NFE2L2 RFXDC2 SMARCA1 WNT5A GCLC MAPKAPK2 UHMK1 STX12 DMD HOXA10 NKX2-1 AGRN DNMT3B TAF1 GSX2 PAIP2 CUGBP1 CREBBP IREB2 NDFIP1 ITGA2 FOXP2 HDAC4 ATF3 HOXB2 ETS1 SMARCC1 DLX5 UBA3 TGFBR3 NCOR1 KLF4 E2F1 PAWR ZEB1 ACVR1B HEY2 LRRFIP1 NRG1 NFX1 CTBP1 EGR2 SOX11 STXBP1 NLRP3 SLIT2 PURA MYT1L MED4 EREG CUX1 SERP1 CALCR FOXM1 NR3C2 CTNND2 HAT1 NR3C1 NEO1 SUMO2 STAT4 LBXCOR1 POU3F3 DAZL FOXD1 CHD4 TXNIP ZFP382 L3MBTL2 HMBOX1 SOD2 DUSP5 ATXN1 ADNP2 DR1 BNIP3L RBAK NFIA F2R
51270	Regulation of locomotion	3.5338E-6	1.7609E-4	DLC1 HMGR EFNA1 EDN1 PAWR ITS2 ZEB1 ACVR1B S1PR1 SOSTDC1 GARNL1 HEY2 TRP63 RAPGEF5 NRG1 INSR CEACAM1 GHR BCR ARHGEF5 IRS1 SLIT2 MFN2 CCND1 ZDHHC17 EREG NPTN TGIF1 ADAM17 RIPK2 AKAP6 WNT5A GRB2 FOXM1 NR3C1 ADCYAP1 SQSTM1 TBC1D5 LBXCOR1 NKX2-1 PAFAH1B1 FASL TRAF7 FOXD1 NDFIP1 KDR ATXN1 SFRP1 HBEGF TGFBR3 NCOR1 KLF4 F2R
31327	Negative regulation of transcription	4.2809E-6	2.1009E-4	WNT5A DLC1 EFNA1 EDN1 ITGA2 ACTN1 CXCL12 IRS1 SLIT2 KDR S1PR1 ETS1 CXCL16 ADAM17 NKX2-1 TGFBR3 HBEGF WDR44 INSR F2R AOC3 PITX2

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
42391	Cellular component movement	4.5328E-6	2.1649E-4	GCLC EIF2C1 EDN1 HAT1 ZEB1 MXI1 SUMO2 HEY2 TRP63 POU3F3 LBXCOR1 NKX2-1 RARB NRG1 FOXD1 DNMT3B TXNIP ZFP382 PAIP2 HMBOX1 FMR1 FOXP2 PURA ATXN1 DUSP5 HDAC4 SMARCE1 EREG DLX5 UBA3 HBEGF TGIF1 CUX1 NCOR1 KLF4
40012	Response to hormone stimulus	4.5450E-6	2.1649E-4	SCN1A PLP1 EGR2 KCND2 EDN1 SOD2 ADCYAP1 ATXN1 ASPA BDNF ANK2 ANK3 GRID2 CLDN1 CNTNAP1 PMP22 NRG1
16481	Morphogenesis of a branching structure	4.9324E-6	2.3154E-4	WNT5A DLC1 EFNA1 EDN1 ITGA2 CXCL12 IRS1 SLIT2 KDR S1PR1 ETS1 CXCL16 ADAM17 NKX2-1 TGFBR3 HBEGF ROBO2 WDR44 INSR F2R AOC3 PITX2
6928	Negative regulation of biosynthetic process	5.1463E-6	2.3813E-4	GCLC HAT1 ZEB1 MXI1 SUMO2 HEY2 TRP63 POU3F3 LBXCOR1 NKX2-1 RARB NRG1 FOXD1 DNMT3B TXNIP ZFP382 HMBOX1 PURA FOXP2 ATXN1 DUSP5 HDAC4 SMARCE1 EREG DLX5 UBA3 TGIF1 CUX1 NCOR1 KLF4
9725	Tube development	5.3989E-6	2.4630E-4	CXCL3 ASTN1 ABI2 CXCL12 VCAM1 ALCAM RAB11B POU3F3 NKX2-1 SEMA3C PAFAH1B1 ROBO2 SCARB1 CLASP2 DCX NRG1 HSP90AA1 EGR2 ITGA2 SLIT2 EPHA4 ITGA6 AGTR1A ETS1 ADAM17 LAMC1 AOC3 MYH10
1763	Morphogenesis of an epithelium	6.0459E-6	2.7198E-4	CALCR WNT5A DLC1 GCLC GRB2 FOXM1 ACOT2 PDE3B CXCL12 ACAT1 ADCYAP1 ALDH1A1 BDNF ENO2 NKX2-1 ROBO2 CCNA2 INSR GHR TXNIP IRS2 HSP90AA1 EGR2 FADS1 ITGA2 IRS1 SLIT2 PLA2G4A CCND1 HIF1A SFRP1 ATP2A2 EREG ETS1 SSTR1 AGTR1A PKLR TGFBR3 PCAF GNB4 CTSB LIPC CACNA1B
9890	Epithelium development	6.7611E-6	2.9999E-4	WNT5A GRB2 EDN1 CTNND2 CXCL12 SLIT2 SFRP1 DLX5 HOXA10 NKX2-1 SEMA3C FOXD1 PITX2
35295	Regulation of macromolecule biosynthetic process	7.4630E-6	3.2332E-4	GCLC EIF2C1 EDN1 HAT1 ZEB1 MXI1 SUMO2 HEY2 TRP63 POU3F3 LBXCOR1 NKX2-1 RARB NRG1 FOXD1 DNMT3B TXNIP ZFP382 PAIP2 HMBOX1 FMR1 FOXP2 PURA ATXN1 DUSP5 HDAC4 SMARCE1 EREG DLX5 UBA3 HBEGF TGIF1 CUX1 NCOR1 KLF4
2009	Negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	7.4867E-6	3.2332E-4	WNT5A DLC1 GCLC EDN1 GCLM CXCL12 ACAT1 LGR4 SLIT2 ASAH1 FZD6 SOD2 MAN2A1 SFRP1 HOXA10 NKX2-1 TGIF1 GUCY1A3 ROBO2 RARB CUX1 FOXD1 PITX2
60429	Positive regulation of molecular function	7.6208E-6	3.2479E-4	WNT5A DLC1 GRB2 EDN1 GRSF1 CXCL12 SLIT2 FZD6 ALDH1A1 SFRP1 HOXA10 TGIF1 NKX2-1 SEMA3C FOXD1 PITX2
10556	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	7.8065E-6	3.2838E-4	TXNIP WNT5A DLC1 GRB2 EDN1 GRSF1 CXCL12 ACAT1 SLIT2 FZD6 ALDH1A1 CCND1 S1PR1 SFRP1 DLX5 HOXA10 SEMA3C NKX2-1 TGIF1 FOXD1 PITX2
45934	Regulation of nitrogen compound metabolic process	8.0143E-6	3.3280E-4	E2F1 EIF2C1 STAT5A EDN1 SNIP1 ZEB1 PAWR MXI1 LASS6 MED20 CBFβ ACVR1B RAD21 S1PR1 HEY2 TRP63 TFB2M LRRFIP1 RARB NRG1 INSR NFX1 PITX2 CTBP1 IRS2 EGR2 SOX11 FMR1 ARNTL NLRP3 IRS1 PURA MYT1L MED4 HIF1A SMARCE1 EREG RIPK2 TGIF1 RFXDC2 NFE2L2 CUX1 SMARCA1 SERP1 WNT5A GCLC FOXM1 CTNND2 NR3C2 HAT1 NEO1 NR3C1 UHMK1 SUMO2 STAT4 DMD HOXA10 POU3F3 NKX2-1 LBXCOR1 DAZL AGRN DNMT3B FOXD1 CHD4 CD28 TXNIP TAF1 ZFP382 L3MBTL2 GSX2 PAIP2 HMBOX1 CREBBP IREB2 ITGA2 FOXP2 SOD2 ATXN1 DUSP5 HDAC4 ADNP2 HOXB2 ATF3 ETS1 DR1 DLX5 SMARCC1 UBA3 RBAK HBEGF TGFBR3 NCOR1 NFIA KLF4 F2R
44093	Establishment of localization	8.4676E-6	3.4717E-4	GCLC EDN1 HAT1 ZEB1 MXI1 SUMO2 HEY2 TRP63 POU3F3 LBXCOR1 NKX2-1 RARB NRG1 FOXD1 DNMT3B TXNIP ZFP382 HMBOX1 NDFIP1 FOXP2 PURA ATXN1 DUSP5 HDAC4 SMARCE1 EREG DLX5 UBA3 TGIF1 CUX1 NCOR1 KLF4
19219	Embryonic development	9.4752E-6	3.8363E-4	CALCR WNT5A DLC1 EFNA1 EDN1 TPM1 GCLM CXCL12 ADCYAP1 S1PR1 SERINC1 GARNL1 SCARB1 FASL CERK TRAF7 NRG1 INSR CEACAM1 GHR ITGA2 NLRP3 IRS1 PPM2C GNAL HDAC4 CCND1 PRLR EREG AGTR1A NTRK2 ERN1 AKAP6 RIPK2 ADAM17 TGFBR3 GNB4 F2R
51171	Cell-cell signaling	1.0505E-5	4.1978E-4	STAT5A SNIP1 EDN1 MXI1 MED20 LASS6 CBFβ S1PR1 RAD21 TRP63 TFB2M RARB INSR PITX2 ARNTL HIF1A SMARCE1 TGIF1 RIPK2 NFE2L2 RFXDC2 SMARCA1 WNT5A GCLC UBE2V2 MAPKAPK2 ADCYAP1 DMD HOXA10 NKX2-1 AGRN DNMT3B TAF1 GSX2 CUGBP1 CREBBP NDFIP1 FOXP2 HDAC4 ATF3 HOXB2 ETS1 SMARCC1 DLX5 UBA3 NTRK2 TGFBR3 NCOR1 KLF4 E2F1 PAWR ZEB1 ACVR1B HEY2 GARNL1 GUCY1A3 PARG LRRFIP1 NRG1 NFX1 CTBP1 EGR2 SOX11 NLRP3 PURA GNAL MYT1L MED4 EREG CUX1 CALCR FOXM1 NR3C2 CTNND2 HAT1 NR3C1 NEO1 TPM1 SUMO2 STAT4 TBC1D5 CHM LBXCOR1 POU3F3 PAFAH1B1 FOXD1 CHD4 CD28 TXNIP ZFP382 L3MBTL2 HMBOX1 SOD2 DUSP5 ATXN1 ADNP2 DR1 RBAK NFIA F2R
51234	Negative regulation of nitrogen compound metabolic process	1.0627E-5	4.1978E-4	STAT5A SNIP1 EDN1 MXI1 MED20 LASS6 CBFβ S1PR1 RAD21 TRP63 TFB2M RARB INSR PITX2 ARNTL HIF1A SMARCE1 TGIF1 RIPK2 NFE2L2 RFXDC2 SMARCA1 WNT5A GCLC UBE2V2 MAPKAPK2 ADCYAP1 DMD HOXA10 NKX2-1 AGRN DNMT3B TAF1 GSX2 CUGBP1 CREBBP NDFIP1 FOXP2 HDAC4 ATF3 HOXB2 ETS1 SMARCC1 DLX5 UBA3 NTRK2 TGFBR3 NCOR1 KLF4 E2F1 PAWR ZEB1 ACVR1B HEY2 GARNL1 GUCY1A3 PARG LRRFIP1 NRG1 NFX1 CTBP1 EGR2 HSP90AA1 SOX11 NLRP3 PURA GNAL MYT1L MED4 EREG CUX1 CALCR FOXM1 NR3C2 CTNND2 HAT1 NR3C1 NEO1 TPM1 SUMO2 STAT4 TBC1D5 CHM LBXCOR1 POU3F3 PAFAH1B1 FOXD1 CHD4 CD28 TXNIP ZFP382 L3MBTL2 HMBOX1 SOD2 ATXN1 DUSP5 ADNP2 DR1 RBAK NFIA F2R
9790	Negative regulation of macromolecule metabolic process	1.0935E-5	4.2673E-4	GNPTG KCNC2 CAST KCNC1 ATP1B1 KCNC3 ATP1B3 AQP8 EDN1 PITPNB CASK CNO SLC7A5 VPS33A ATP2B2 TTR ANK3 KCNK6 VPS4B GRID2 CHRNAS NALCN CDCA5 ATG9A KCND2 FMR1 WNK1 OPTN ARNTL BICD2 AGTR1A RYR3 RAB15 SRP72 CROT ARLGIP1 SCN1A DERL1 SLC38A2 PANX1 GRB2 CACNB2 CCDC91 ADCYAP1 KCNJ1 MRS2 STX12 SERINC1 SCARB1 ITGA2 ABCB6 TECT2 ABCG8 KCNJ6 ATP2A2 ARF2 NTRK2 CHRN3 MYH10 CACNA1B KCNAB1 SYNJ1 CLTC KCNQ3 RAB6A SV2A RANBP2 NRG1 GHR TRPM4 TRPM7 STXB1 STX1B MFN2 ZDHHC17 CUX1 CLN8 SERP1 CPLX1 BET1 STAU2 SFT2D1 BEST1 SYN2 RAB11B CHM PAFAH1B1 CHP ACSL4 EHD4 TXNIP FADS1 SLC10A2 ATXN1 SCFD1 GRIA2 MCFD2 SLC18A2 SCN4B GGA1 LRP2 SMPD3 SCN4A F2R

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
7267	Signal transmission	1.1428E-5	4.4066E-4	WNT5A DLC1 GRB2 HMGCR EFNA1 RIC8 EDN1 PITPNB TTPA ZEB1 ALDH1A1 VCAM1 ACVR1B CYP26B1 HOXA10 BTF3 SEMA3C RARB NRG1 ACSL4 DNMT3B COL11A1 PITX2 GRSF1 GPR177 SLIT2 FZD6 MAN2A1 SFRP1 CDON DLX5 TGFBF3 TGIF1
51172	Signaling process	1.2033E-5	4.5853E-4	CAST CPLX1 PANX1 EDN1 UBE2V2 ADCYAP1 BDNF DMD SYN2 GRID2 HOXA10 NKX2-1 PAFAH1B1 AGRN NRG1 STX1B GJB2 ATXN1 EREG GRIA2 NTRK2 SLC18A2 RAB15 LRP2 CLN8 SMPD3
10605	Myelination	1.2885E-5	4.8530E-4	GCLC EDN1 HAT1 ZEB1 MX1 SUMO2 HEY2 TRP63 POU3F3 LBXCOR1 NKX2-1 RARB NRG1 FOXD1 DNMT3B TXNIP ZFP382 HMBOX1 NDFIP1 FOXP2 PURA ATXN1 DUSP5 HDAC4 SMARCE1 EREG DLX5 UBA3 TGIF1 CUX1 NCOR1 KLF4
23046	Cellular iron homeostasis	1.3787E-5	5.1328E-4	GCLC EIF2C1 EDN1 SNIP1 HAT1 ZEB1 MX1 SUMO2 SERPINA5 HEY2 TRP63 POU3F3 NKX2-1 LBXCOR1 RARB NRG1 FOXD1 DNMT3B INSR TXNIP ZFP382 PAIP2 HMBOX1 FMR1 NDFIP1 SLIT2 FOXP2 PURA ATXN1 DUSP5 HDAC4 EREG SMARCE1 DLX5 BNIP3L UBA3 HBEFG TGIF1 CUX1 NCOR1 KLF4 RASD2
23060	Positive regulation of cell proliferation	1.4188E-5	5.1634E-4	CAST DLC1 IMPA1 EFNA1 STAT5A EDN1 SNIP1 PDE3B ACVR1B ASPA BDNF S1PR1 ANK2 ANK3 MAP3K8 GRID2 CNTNAP1 RAB6A UNC5C NRG1 CCNA2 INSR CEACAM1 GHR EGR2 BCR WNK1 STX1B IRS1 GNAL CCND1 HIF1A EREG AGTR1A CLDN1 RAB15 GNB4 ARL8B PMP22 CLN8 LRRK1 RASD2 CALCR WNT5A SCN1A CPLX1 GRB2 UBE2V2 MAPKAPK2 ADCYAP1 STAT4 DMD SYN2 RAB11B FASL PAFAH1B1 CHP AGRN TRAF7 TEC PLP1 ATXN1 GRIA2 ARF2 PDE7A NTRK2 SLC18A2 RAP1A TGFBF3 LRP2 SMPD3 F2R
42552	Cell proliferation	1.4188E-5	5.1634E-4	CAST DLC1 IMPA1 EFNA1 STAT5A EDN1 SNIP1 PDE3B ACVR1B ASPA BDNF S1PR1 ANK2 ANK3 MAP3K8 GRID2 CNTNAP1 RAB6A UNC5C NRG1 CCNA2 INSR CEACAM1 GHR EGR2 BCR WNK1 STX1B IRS1 GNAL CCND1 HIF1A EREG AGTR1A CLDN1 RAB15 GNB4 ARL8B PMP22 CLN8 LRRK1 RASD2 CALCR WNT5A SCN1A CPLX1 GRB2 UBE2V2 MAPKAPK2 ADCYAP1 STAT4 DMD SYN2 RAB11B FASL PAFAH1B1 CHP AGRN TRAF7 TEC PLP1 ATXN1 GRIA2 ARF2 PDE7A NTRK2 SLC18A2 RAP1A TGFBF3 LRP2 SMPD3 F2R
6873	Cellular chemical homeostasis	1.4729E-5	5.2834E-4	PLP1 ASPA EGR2 ANK2 ANK3 CLDN1 CNTNAP1 NRG1 PMP22
8284	Positive regulation of macromolecule biosynthetic process	1.4844E-5	5.2834E-4	CALCR SCN1A EDN1 ADCYAP1 ASPA BDNF S1PR1 ANK2 ANK3 GRID2 FASL CNTNAP1 SV2A NRG1 PLP1 EGR2 KCND2 IREB2 NDFIP1 KDR SOD2 ATXN1 ATP2A2 AGTR1A RYR3 CLDN1 NPTN PMP22 F2R
8283	Axon ensheathment	1.5447E-5	5.4383E-4	WNT5A FOXM1 EDN1 MME CXCL12 ADCYAP1 VCAM1 S1PR1 HEY2 FASL IL13RA1 INSR CCNA2 CD28 ITGA2 IRS1 PURA KDR HDAC4 CCND1 PLA2G4A ATF3 HIF1A EREG ETS1 DLX5 RIPK2 TGIF1 ADAM17 F2R
55082	Ensheathment of neurons	1.6340E-5	5.6908E-4	WNT5A SOX11 CREBBP POLA1 LGALS7 ITGA2 CXCL12 LGR4 CCND1 STAT4 EREG DLX5 CCDC100 POU3F3 RIPK2 TGFBF3 SCARB1 GNB4 PAFAH1B1 IFRD1
10557	Positive regulation of developmental process	1.8047E-5	6.2186E-4	CALCR SCN1A EDN1 ADCYAP1 ASPA BDNF S1PR1 ANK2 ANK3 GRID2 FASL CNTNAP1 SV2A NRG1 PLP1 EGR2 KCND2 IREB2 NDFIP1 KDR SOD2 ATXN1 ATP2A2 AGTR1A RYR3 CLDN1 NPTN PMP22 F2R
7272	Rhythmic process	1.8697E-5	6.3746E-4	WNT5A E2F1 ZEB1 PAWR NR3C1 CBFβ UHMK1 ACVR1B S1PR1 TRP63 POU3F3 NKX2-1 DAZL RARB AGRN INSR CD28 PITX2 TAF1 IRS2 EGR2 SOX11 CREBBP ITGA2 ARNTL IRS1 ATXN1 HDAC4 HIF1A EREG ETS1 DLX5 SMARCC1 NFE2L2 SMARCA1 NFIA KLF4 F2R SERP1
8366	Development of primary sexual characteristics	2.0985E-5	7.0073E-4	PLP1 ASPA EGR2 ANK2 ANK3 CLDN1 CNTNAP1 NRG1 PMP22
51094	Transport	2.0985E-5	7.0073E-4	PLP1 ASPA EGR2 ANK2 ANK3 CLDN1 CNTNAP1 NRG1 PMP22
48511	Positive regulation of catalytic activity	2.2051E-5	7.2882E-4	WNT5A HMGCR SYNJ1 UBE2V2 CXCL12 ACVR1B ASPA HEY2 HOXA10 PAFAH1B1 ROBO2 NRG1 INSR FOXD1 DNMT3B FND3B GHR KDR PLA2G4A EREG AGTR1A ETS1 DLX5 NPTN RIPK2 TGIF1 GDF10
45137	Cellular response to endogenous stimulus	2.4935E-5	8.1582E-4	WNT5A EGR2 AHY HS3ST2 ARNTL SLIT2 ADCYAP1 ALDH1A1 PLA2G4A EREG ETS1 GDF10 NKX2-1 ROBO2 ADAMTS1 LIPC NCOR1
6810	Telencephalon development	2.5862E-5	8.3766E-4	WNT5A LGR4 SLIT2 ADCYAP1 CDH6 KDR GJB2 ACVR1B CCND1 PLA2G4A EREG NKX2-1 ADAMTS1 ROBO2
43085	Regulation of localization	2.8562E-5	9.1597E-4	GNPTG KCNC2 CAST KCNC1 ATP1B1 KCNC3 ATP1B3 AQP8 EDN1 PITPNB CASK CNO SLC7A5 VPS33A ATP2B2 TTR KCNK6 VPS4B GRID2 CHRNAS NALCN ATG9A KCND2 FMR1 WNK1 OPTN ARNTL BICD2 AGTR1A RYR3 RAB15 SRP72 CROT ARL6IP1 SCN1A DERL1 SLC38A2 PANX1 GRB2 CACNB2 CCDC91 ADCYAP1 KCNJ1 MRS2 STX12 SERINC1 SCARB1 ABCB6 TECT2 ABCG8 KCNJ6 ATP2A2 ARF2 NTRK2 CHRN3 MYH10 CACNA1B KCNAB1 SYNJ1 CLTC KCNQ3 RAB6A SV2A RANBP2 NRG1 GHR TRPM4 TRPM7 STXB1 STX1B MFN2 ZDHHC17 CUX1 CLN8 SERP1 CPLX1 BET1 STAU2 SFT2D1 BEST1 SYN2 RAB11B CHM PAFAH1B1 CHP ACSL4 EHD4 TXNIP FADS1 SLC10A2 ATXN1 SCFD1 GRIA2 MCFD2 SLC18A2 SCN4B GGA1 LRP2 SMPD3 SCN4A F2R
71495	Response to oxygen levels	2.9634E-5	9.3782E-4	CALCR DLC1 EFNA1 EDN1 TPM1 GCLM ADCYAP1 S1PR1 SERINC1 GARNL1 SCARB1 FASL CERK TRAF7 NRG1 INSR CEACAM1 GHR ITGA2 NLRP3 IRS1 PPM2C GNAL CCND1 PRLR EREG AGTR1A NTRK2 ERN1 ADAM17 AKAP6 GNB4 F2R
21537	Response to hypoxia	2.9822E-5	9.3782E-4	DLC1 IRS2 GRB2 ITGA2 PDE3B ZEB1 IRS1 SLIT2 ADCYAP1 HIF1A SFRP1 SSTR1 AGTR1A PKLR PCAF ROBO2 GNB4 LIPC INSR GHR
32879	Regulation of action potential in neuron	3.1049E-5	9.6699E-4	GSX2 DLX5 CCDC100 POU3F3 NKX2-1 ROBO2 PAFAH1B1 RARB CXCL12 SLIT2 FOXP2

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
70482	Negative regulation of cellular metabolic process	3.8411E-5	1.1758E-3	WNT5A DLC1 PANX1 EFNA1 SYNJ1 EDN1 PDE3B CXCL12 UHMK1 ADCYAP1 S1PR1 SYN2 CCDC100 NKX2-1 SCARB1 NRG1 INSR EHD4 PITX2 IRS2 NDFIP1 STXB1 ITGA2 ACTN1 NLRP3 STX1B IRS1 SLIT2 KDR ABCG8 PLA2G4A SCFD1 ETS1 CXCL16 NTRK2 ADAM17 HBEGF TGFBR3 WDR44 F2R AOC3 SERP1 CACNA1B
1666	Cellular response to hormone stimulus	3.8512E-5	1.1758E-3	WNT5A E2F1 ATP1B1 AHY EDN1 ACOT2 ITGA2 CXCL12 SDC2 SOD2 KDR VCAM1 HYOU1 SCFD1 HIF1A ETS1 PKLR ADAM17 TGFBR3 LIPC
19228	Tube morphogenesis	3.8843E-5	1.1758E-3	E2F1 ATP1B1 AHY EDN1 ACOT2 ITGA2 CXCL12 SDC2 SOD2 KDR VCAM1 HYOU1 SCFD1 HIF1A ETS1 PKLR ADAM17 TGFBR3 LIPC
31324	Positive regulation of protein metabolic process	4.2309E-5	1.2658E-3	PLP1 ASPA SCN1A EGR2 ANK2 ANK3 CLDN1 CNTNAP1 NRG1 PMP22
32870	Negative regulation of metabolic process	4.2596E-5	1.2658E-3	GCLC EIF2C1 EDN1 HAT1 ZEB1 MXI1 SUMO2 SERPINA5 HEY2 TRP63 POU3F3 LBXCOR1 NKX2-1 RARB NRG1 FOXD1 DNMT3B INSR TXNIP ZFP382 PAIP2 HMBOX1 FMR1 NDFIP1 SLIT2 FOXF2 PURA ATXN1 DUSP5 HDAC4 EREG SMARCE1 DLX5 UBA3 HBEGF TGIF1 CUX1 NCOR1 KLF4 RASD2
35239	Positive regulation of locomotion	4.4300E-5	1.3044E-3	DLC1 IRS2 GRB2 ITGA2 PDE3B IRS1 SLIT2 ADCYAP1 HIF1A SFRP1 SSTR1 AGTR1A PKLR PCAF ROBO2 GNB4 LIPC INSR GHR
51247	Regulation of action potential	4.5825E-5	1.3372E-3	WNT5A DLC1 GCLC EDN1 GCLM CXCL12 LGR4 SLIT2 SOD2 FZD6 HOXA10 TGIF1 GUCY1A3 NKX2-1 FOXD1 PITX2
9892	Regulation of cellular component organization	4.7082E-5	1.3616E-3	WNT5A DLC1 TAF1 GCLC NDFIP1 ITGA2 UBE2V2 UHMK1 ACVR1B HDAC4 CCND1 SQSTM1 AGTR1A NPTN RIPK2 ADAM17 DAZL NCOR1 DNMT3B INSR RASD2 SERP1 GHR
40017	Negative regulation of signaling pathway	4.8299E-5	1.3732E-3	GCLC EIF2C1 SNIP1 EDN1 HAT1 PDE3B ZEB1 MXI1 SUMO2 SERPINA5 HEY2 TRP63 POU3F3 NKX2-1 LBXCOR1 RARB NRG1 FOXD1 DNMT3B INSR TXNIP ZFP382 PAIP2 HMBOX1 FMR1 NDFIP1 SLIT2 FOXF2 PURA ATXN1 DUSP5 HDAC4 EREG SMARCE1 DLX5 BNIP3L UBA3 HBEGF TGIF1 CUX1 NCOR1 KLF4 RASD2
1508	Regulation of chemotaxis	4.8332E-5	1.3732E-3	WNT5A EDN1 ITGA2 CXCL12 IRS1 SLIT2 KDR S1PR1 ETS1 CXCL16 HBEGF ADAM17 INSR F2R AOC3
51128	Transmembrane receptor protein tyrosine kinase signaling pathway	5.0239E-5	1.4150E-3	PLP1 ASPA SCN1A EGR2 KCND2 ANK2 ANK3 CLDN1 CNTNAP1 NRG1 PMP22
35467	Positive regulation of cellular protein metabolic process	5.2253E-5	1.4590E-3	DLC1 EFNA1 SYNJ1 EDN1 UBE2V2 TPM1 CXCL12 ADCYAP1 S1PR1 NKX2-1 SCARB1 ROBO2 PAFAH1B1 CLASP2 AGRN INSR DNMT3B CD28 EHD4 HSP90AA1 STXB1 ITGA2 GAS7 SLIT2 KDR PLA2G4A EREG ETS1 NTRK2 NPTN TGFBR3 SPNA2 NCOR1
50920	Ovulation cycle	5.3769E-5	1.4885E-3	WNT5A DLC1 FOXM1 PAWR NR3C1 IRS1 SLIT2 ATXN1 MFN2 CCND1 SFRP1 SOSTDC1 HEY2 TGIF1 TGFBR3 LBXCOR1 NKX2-1 NCOR1 KLF4
7169	Ion homeostasis	5.5011E-5	1.5100E-3	WNT5A S1PR1 ITGA2 ADAM17 ROBO2 CXCL12 SLIT2 KDR
32270	Cell migration	6.0548E-5	1.6480E-3	TXNIP IRS2 BCR GRB2 EFNA1 IRS1 ADCYAP1 KDR EPHA4 PRLR EREG NTRK2 ADAM17 HBEGF AGRN INSR GHR
42698	Morphogenesis of a branching epithelium	6.2962E-5	1.6908E-3	DLC1 TAF1 GCLC NDFIP1 ITGA2 UBE2V2 UHMK1 ACVR1B HDAC4 CCND1 SQSTM1 AGTR1A NPTN RIPK2 ADAM17 DAZL NCOR1 DNMT3B INSR RASD2 SERP1 GHR
50801	Regulation of catabolic process	6.3164E-5	1.6908E-3	WNT5A ALDH1A1 PLA2G4A EREG ETS1 NKX2-1 GDF10 ROBO2 ADAMTS1 SLIT2 ADCYAP1
16477	Sensory organ development	6.4767E-5	1.7195E-3	CALCR SCN1A EDN1 ADCYAP1 ASPA BDNF S1PR1 ANK2 ANK3 GRID2 FASL CNTNAP1 SV2A NRG1 PLP1 EGR2 KCND2 IREB2 NDFIP1 KDR SOD2 ATXN1 ATP2A2 AGTR1A RYR3 CLDN1 NPTN PMP22 F2R
61138	Regulation of response to external stimulus	7.0880E-5	1.8544E-3	HSP90AA1 CXCL3 ASTN1 AB12 CXCL12 SLIT2 VCAM1 ITGA6 AGTR1A POU3F3 ADAM17 NKX2-1 SEMA3C SCARB1 PAFAH1B1 CLASP2 LAMC1 NRG1 DCX AOC3
9894	Cellular homeostasis	7.0994E-5	1.8544E-3	WNT5A SFRP1 GRB2 EDN1 HOXA10 SEMA3C NKX2-1 CXCL12 FOXD1 PITX2
7423	Positive regulation of cell migration	7.9696E-5	2.0651E-3	WNT5A CAST TAF1 IRS2 GCLC NDFIP1 PDE3B UBE2V2 ARNTL TPM1 IRS1 ADCYAP1 HDAC4 CISD2 S1PR1 GARNL1 CHM TBC1D5 PAFAH1B1 INSR
32101	Female sex differentiation	8.5251E-5	2.1788E-3	EDN1 AB12 ZEB1 COL5A2 FZD6 ALDH1A1 TSPAN12 ATP2B2 DLX5 NTRK2 TGIF1 FASL RARB CUX1 COL11A1 CLN8 KLF4 PITX2
19725	Pattern specification process	8.5431E-5	2.1788E-3	WNT5A NDFIP1 ITGA2 CXCL12 SLIT2 ADCYAP1 KDR PLA2G4A S1PR1 SERPINA5 GRID2 ADAM17 ROBO2 NTSE F2R AOC3 CD28
30335	Ovulation cycle process	9.5096E-5	2.4064E-3	CALCR SCN1A GCLC EDN1 ADCYAP1 ASPA BDNF S1PR1 ANK2 ANK3 DMD GRID2 CNTNAP1 FASL SV2A NRG1 PLP1 EGR2 KCND2 IREB2 NDFIP1 KDR SOD2 ATXN1 ATP2A2 AGTR1A RYR3 CLDN1 NPTN PMP22 F2R
46660	Regulation of molecular function	9.6735E-5	2.4289E-3	WNT5A EDN1 ITGA2 CXCL12 IRS1 KDR S1PR1 ETS1 CXCL16 HBEGF ADAM17 INSR F2R AOC3
7389	Homeostatic process	1.0210E-4	2.5439E-3	WNT5A ACVR1B PLA2G4A EREG NKX2-1 ROBO2 ADAMTS1 SLIT2 CDH6 ADCYAP1
22602	Behavior	1.0291E-4	2.5444E-3	EGR2 GSX2 EDN1 GRSF1 ZEB1 GPR177 CXCL12 SFRP1 SOSTDC1 DLX5 CYP26B1 HOXA10 SEMA3C TGIF1 NKX2-1 PITX2

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
65009	Regulation of transcription	1.1475E-4	2.8156E-3	WNT5A ALDH1A1 PLA2G4A EREG ETS1 NKX2-1 ROBO2 ADAMTS1 SLIT2 ADCYAP1
42592	Reproductive developmental process	1.1690E-4	2.8284E-3	CALCR WNT5A CAST DLC1 HMGCR EDN1 TPM1 GCLM CXCL12 ADCYAP1 S1PR1 SERINC1 GARNL1 CHM TBC1D5 SCARB1 FASL PAFAH1B1 CERK TRAF7 NRG1 INSR CEACAM1 GHR NDFIP1 WNK1 ITGA2 NLRP3 IRS1 PPM2C SOD2 GNAL HDAC4 CCND1 PRLR EREG AGTR1A NTRK2 ERN1 AKAP6 RIPK2 ADAM17 TGFB3 GNB4 CTSB LRP2 CLN8 F2R
7610	Neurotransmitter receptor metabolic process	1.1701E-4	2.8284E-3	CALCR SCN1A GCLC EDN1 PDE3B ADCYAP1 ASPA BDNF S1PR1 ANK2 ANK3 DMD GRID2 CNTNAP1 SCARB1 FASL SV2A NRG1 INSR PLP1 EGR2 KCND2 IREB2 NDFIP1 ITGA2 SOD2 KDR ATXN1 ABCG8 PLA2G4A HIF1A ATP2A2 AGTR1A RYR3 SLC18A2 CLDN1 NPTN TGFB3 LIPC PMP22 NCOR1 F2R
45449	Eye development	1.1813E-4	2.8343E-3	SCN1A AHYC HMGCR CXCL3 RIC8 CTNND2 ASTN1 ABI2 CXCL12 ADCYAP1 CHRNAS NKX2-1 PAFAH1B1 NRG1 PLCB1 EGR2 SLIT2 SOD2 ATXN1 EPHA4 AGTR1A CXCL16 NTRK2 SLC18A2 CLN8 RASD2 AOC3
3006	Cell cycle phase	1.2383E-4	2.9492E-3	E2F1 STAT5A SNIP1 ZEB1 PAWR MXI1 LASS6 MED20 CFBF ACVR1B RAD21 S1PR1 HEY2 TRP63 TFB2M LRRFIP1 RARB NRG1 INSR NFX1 PITX2 CTBP1 EGR2 SOX11 ARNTL NLRP3 PURA MYT1L MED4 HIF1A SMARCE1 EREG RIPK2 TGIF1 RFXDC2 NFE2L2 CUX1 SMARCA1 WNT5A GCLC FOXM1 CTNND2 NR3C2 HAT1 NEO1 NR3C1 SUMO2 STAT4 DMD HOXA10 POU3F3 LBXCOR1 NKX2-1 AGRN DNMT3B FOXD1 CHD4 TXNIP TAF1 ZFP382 L3MBTL2 GSX2 HMBOX1 CREBBP FOXP2 SOD2 ATXN1 DUSP5 HDAC4 ADNP2 HOXB2 ATF3 ETS1 DR1 SMARCC1 DLX5 UBA3 RBAK TGFB3 NCOR1 NFIA KLF4 F2R
45213	Positive regulation of nitrogen compound metabolic process	1.2547E-4	2.9622E-3	WNT5A CUGBP1 CXCL12 LGR4 SLIT2 GJB2 ADCYAP1 CDH6 KDR ACVR1B PLA2G4A CCND1 SFRP1 EREG NKX2-1 ROBO2 ADAMTS1 DAZL PAFAH1B1 INSR
1654	Enzyme linked receptor protein signaling pathway	1.2621E-4	2.9622E-3	DMD AGRN NRG1
22403	Response to protein stimulus	1.2844E-4	2.9930E-3	ALDH1A1 ATP2B2 TSPAN12 NTRK2 ABI2 TGIF1 FASL ZEB1 RARB COL5A2 CLN8 KLF4 PITX2
51173	Positive regulation of chemotaxis	1.3258E-4	3.0674E-3	E2F1 TAF1 KIF11 POLA1 CLTC CDC25A ACVR1B CCND1 EREG SIAH1A PPP2CA CYP26B1 CCDC100 ADAM17 PAFAH1B1 CLASP2 ARL8B NCOR1 CDCA5 KIF2A
7167	Locomotory behavior	1.3428E-4	3.0847E-3	E2F1 UBE2V2 ZEB1 NR3C1 CFBF ADCYAP1 ACVR1B S1PR1 TRP63 POU3F3 PARG GUCY1A3 NKX2-1 RARB AGRN INSR CD28 PITX2 TAF1 HSP90AA1 EGR2 SOX11 CREBBP ARNTL SOD2 ATXN1 HDAC4 HIF1A EREG ETS1 SMARCC1 DLX5 NFE2L2 SMARCA1 NFIA KLF4 F2R
51789	Regulation of catalytic activity	1.3656E-4	3.1150E-3	TXNIP IRS2 BCR GRB2 EFNA1 USP9X NLK IRS1 ADCYAP1 KDR EPHA4 UBE2D3 PRLR EREG NTRK2 ADAM17 TGFB3 HBEGF AGRN INSR GHR
50921	Regulation of cell development	1.3967E-4	3.1637E-3	CCND1 DERL1 ERN1 ITGA2 TGIF1 PAFAH1B1 DEK CTSB NR3C1 NFE2L2 LIPC INSR SERP1
7626	Positive regulation of cellular component movement	1.4469E-4	3.2380E-3	WNT5A S1PR1 ITGA2 ADAM17 CXCL12 SLIT2 KDR
50790	Sex differentiation	1.4496E-4	3.2380E-3	SCN1A CXCL3 ASTN1 CXCL12 SLIT2 SOD2 ATXN1 EPHA4 AGTR1A CXCL16 SLC18A2 NKX2-1 PAFAH1B1 NRG1 CLN8 RASD2
60284	Cell junction assembly	1.4660E-4	3.2522E-3	CALCR CAST DLC1 HMGCR EFNA1 EDN1 TPM1 GCLM ADCYAP1 S1PR1 SERINC1 GARNL1 CHM TBC1D5 SCARB1 FASL PAFAH1B1 CERK TRAF7 NRG1 INSR CEACAM1 GHR WNK1 ITGA2 NLRP3 IRS1 PPM2C SOD2 GNAL CCND1 PRLR EREG AGTR1A NTRK2 ERN1 AKAP6 ADAM17 GNB4 CTSB LRP2 CLN8 F2R
51272	Cellular component morphogenesis	1.5958E-4	3.5161E-3	EFNA1 SYNJ1 EDN1 UBE2V2 CXCL12 SLIT2 KDR ADCYAP1 HDAC4 ASPA DLX5 NTRK2 HOXA10 NPTN NKX2-1 TGIF1 TGFB3 ROBO2 PAFAH1B1 AGRN DNMT3B
7548	Cell motility	1.6704E-4	3.6557E-3	WNT5A EDN1 ITGA2 CXCL12 IRS1 KDR S1PR1 ETS1 CXCL16 HBEGF ADAM17 INSR F2R AOC3
34329	Localization of cell	1.9387E-4	4.2144E-3	WNT5A LGR4 SLIT2 ADCYAP1 CDH6 KDR GJB2 ACVR1B CCND1 PLA2G4A EREG NKX2-1 ADAMTS1 ROBO2
32989	Embryonic morphogenesis	2.0458E-4	4.3525E-3	DLC1 ITGA6 ANK2 ANK3 ACTN1 LAMC2 LAMC1
48870	Cellular response to stimulus	2.0472E-4	4.3525E-3	EGR2 LPPR4 GAS7 CXCL12 SLIT2 SDC2 KDR MFN2 ALCAM EPHA4 ANK2 ANK3 DLX5 DMD NKX2-1 TGFB3 ROBO2 PAFAH1B1 LAMC1 PMP22 NRG1 TMOD1
51674	Embryonic development ending in birth	2.0560E-4	4.3525E-3	HSP90AA1 CXCL3 ASTN1 ABI2 CXCL12 SLIT2 VCAM1 ITGA6 AGTR1A ETS1 POU3F3 ADAM17 NKX2-1 SEMA3C SCARB1 PAFAH1B1 CLASP2 LAMC1 NRG1 DCX AOC3
48598	Cellular response to insulin stimulus	2.0560E-4	4.3525E-3	HSP90AA1 CXCL3 ASTN1 ABI2 CXCL12 SLIT2 VCAM1 ITGA6 AGTR1A ETS1 POU3F3 ADAM17 NKX2-1 SEMA3C SCARB1 PAFAH1B1 CLASP2 LAMC1 NRG1 DCX AOC3
51716	Positive regulation of transcription, DNA-dependent	2.0890E-4	4.3936E-3	WNT5A DLC1 GRB2 EFNA1 EDN1 GRSF1 ZEB1 GPR177 FZD6 VCAM1 ALDH1A1 CDON DLX5 CYP26B1 HOXA10 TGIF1 RARB COL11A1 PITX2

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
9792	Celencephalon cell migration	2.1165E-4	4.4227E-3	WNT5A DLC1 E2F1 DERL1 GRB2 AQP8 CXCL3 SNIP1 POLA1 PDE3B UBE2V2 ZEB1 ADCYAP1 CYP2C STAT4 SQSTM1 PARG ROBO2 FASL PAFAH1B1 INSR CHD4 GHR IRS2 ATG9A FADS1 ITGA2 IRS1 SLIT2 SOD2 CCND1 HIF1A ITGA6 SFRP1 ETS1 SSSTR1 AGTR1A NBR1 PKLR ERN1 RIPK2 TGIF1 PCAF GNB4 NFE2L2 LIPC SERP1 TTRAP
32869	Positive regulation of RNA metabolic process	2.1609E-4	4.4867E-3	DLC1 GRB2 RIC8 EDN1 PITPNB TTPA ZEB1 SLIT2 FZD6 VCAM1 ACVR1B MAN2A1 SFRP1 DLX5 BTF3 SEMA3C TGIF1 TGFBR3 ACSL4 COL11A1 PITX2
45893	Motor axon guidance	2.2180E-4	4.5758E-3	DLC1 IRS2 HIF1A GRB2 PKLR PDE3B PCAF IRS1 INSR GHR
22029	Cellular response to protein stimulus	2.3278E-4	4.7721E-3	E2F1 NR3C1 ZEB1 CBFB ACVR1B S1PR1 TRP63 POU3F3 NKX2-1 RARB AGRN PITX2 TAF1 EGR2 SOX11 CREBBP ARNTL ATXN1 HDAC4 HIF1A ETS1 SMARCC1 DLX5 NFE2L2 SMARCA1 NFIA KLF4 F2R
51254	Development of primary female sexual characteristics	2.6019E-4	5.3004E-3	POU3F3 NKX2-1 PAFAH1B1 CXCL12 SLIT2
8045	Positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2.8192E-4	5.6586E-3	E2F1 NR3C1 ZEB1 CBFB ACVR1B S1PR1 TRP63 POU3F3 NKX2-1 RARB AGRN PITX2 TAF1 EGR2 SOX11 CREBBP ARNTL ATXN1 HDAC4 HIF1A ETS1 SMARCC1 DLX5 NFE2L2 SMARCA1 NFIA KLF4 F2R
71445	Positive regulation of response to external stimulus	2.8287E-4	5.6586E-3	ALCAM EGR2 CXCL12 SLIT2
46545	Establishment of protein localization	2.8302E-4	5.6586E-3	CCND1 DERL1 ERN1 TGIF1 PAFAH1B1 NFE2L2 SERP1
45935	Regulation of protein metabolic process	2.9453E-4	5.8526E-3	ACVR1B PLA2G4A EREG NKX2-1 ROBO2 ADAMTS1 SLIT2 CDH6 ADCYAP1
32103	Cellular response to biotic stimulus	2.9981E-4	5.9075E-3	E2F1 UBE2V2 ZEB1 NR3C1 CBFB ADCYAP1 ACVR1B S1PR1 TRP63 POU3F3 PARG GUCY1A3 NKX2-1 RARB AGRN INSR CD28 PITX2 TAF1 EGR2 SOX11 CREBBP ARNTL ATXN1 HDAC4 HIF1A EREG ETS1 SMARCC1 DLX5 NFE2L2 SMARCA1 NFIA KLF4 F2R
45184	Neuron development	3.0094E-4	5.9075E-3	WNT5A PLA2G4A S1PR1 ITGA2 ADAM17 CXCL12 SLIT2 AOC3 CD28 KDR
51246	Positive regulation of multicellular organismal process	3.0946E-4	6.0382E-3	ARL6IP1 CAST GNPTG DERL1 BET1 CASK CCDC91 CLTC VPS33A SFT2D1 STX12 ANK3 RAB11B CHM RAB6A TXNIP ATG9A STXB1P1 ITGA2 ARNTL OPTN STX1B MFN2 SCFD1 ZDHHC17 GRIA2 AGTR1A ARF2 MCFD2 RAB15 SRP72 GGA1 LRP2 F2R SERP1
71216	Forebrain cell migration	3.2836E-4	6.3609E-3	WNT5A CAST DLC1 GCLC EIF2C1 EDN1 UBE2V2 UHMK1 ACVR1B UBE2D3 SQSTM1 SERPINA5 DAZL INSR DNMT3B GHR TAF1 PAIP2 FMR1 IREB2 NDFIP1 ITGA2 ARNTL SLIT2 HDAC4 CCND1 AGTR1A NPTN RIPK2 ADAM17 NCOR1 RASD2 SERP1
48666	Renal system development	3.3047E-4	6.3609E-3	WNT5A STAT4 CCND1 DERL1 ERN1 RIPK2 NFE2L2 SERP1
51240	Negative regulation of cell communication	3.3385E-4	6.3609E-3	EGR2 LPPR4 ABI2 GAS7 CXCL12 SLIT2 SDC2 UHMK1 SOD2 KDR ALCAM EPHA4 CRMP1 DLX5 DMD NTRK2 NKX2-1 ROBO2 PAFAH1B1 LAMC1 ACSL4
21885	Neuron projection development	3.3385E-4	6.3609E-3	WNT5A PANX1 CUGBP1 EDN1 ITGA2 NLRP3 ADCYAP1 KDR PLA2G4A HIF1A GRIA2 EREG AGTR1A NTRK2 HEY2 NPTN RIPK2 ADAM17 FOXD1 F2R GHR
72001	Response to nutrient	3.3788E-4	6.4001E-3	POU3F3 NKX2-1 PAFAH1B1 CXCL12 SLIT2
10648	Pituitary bulb development	3.4098E-4	6.4212E-3	WNT5A ALDH1A1 AGTR1A SOX11 HOXA10 POU3F3 ROBO2 NID1 ADAMTS1 ACAT1 SLIT2
31175	Cell cycle	3.7196E-4	6.9641E-3	WNT5A DLC1 FOXM1 PAWR NR3C1 IRS1 SLIT2 ATXN1 MFN2 CCND1 SFRP1 SOSTDC1 HEY2 TGIF1 TGFBR3 LBXCOR1 NKX2-1 HHIP NCOR1 KLF4
7584	Cellular response to unfolded protein	3.8624E-4	7.1898E-3	EGR2 LPPR4 ABI2 GAS7 CXCL12 SLIT2 SDC2 UHMK1 KDR ALCAM EPHA4 DLX5 DMD NKX2-1 ROBO2 PAFAH1B1 LAMC1 ACSL4
21772	Endoplasmic reticulum unfolded protein response	3.9151E-4	7.2463E-3	SUOX AHYC HMGCR FADS1 SYNJ1 TTPA HAT1 ITGA2 SOD2 VCAM1 ALDH1A1 ABCG8 PLA2G4A CCND1 PKLR ACSL4 LRP2 INSR KLF4
7049	Chordate embryonic development	4.1364E-4	7.5811E-3	GSX2 DLX5 ROBO2 SLIT2
6090	Pyruvate metabolic process	4.5788E-4	8.1938E-3	ATF3 PKLR ENO2 SRR PDHA1 PDHB
6464	Protein modification process	4.6393E-4	8.2564E-3	CAST GNPTG EFNA1 CASK PRKG2 PRMT3 ACVR1B MAP3K8 OGT RAB6A INSR GHR BCR STK25 SGK3 TRPM7 WNK1 PPM2C PRKD1 MAST4 MAN2A1 ZDHHC17 SENP1 MAPK6 SIAH1A ERN1 RIPK2 LRRK1 SERP1 WNT5A FUT7 USP9X HAT1 PPT2 ABI2 UBE2V2 UBE3C MAPKAPK2 UHMK1 SUMO2 UBE2D3 STAT4 SNRK PPP2CA CDC2L5 TRAF7 TGM6 TEC TAF1 NUB1 NLK CREBBP NID1 CDC25A KDR DUSP5 HDAC4 EPHA4 DUSP2 ULK2 UBA3 NTRK2 USP46 TGFBR3 PCAF F2R CDC42BPB

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
61061	Muscle structure development	4.7058E-4	8.3291E-3	CAST NE01 DMD CDON TGFB3 SEMA3C CTSB RARB AGRN NRG1 IFRD1 COL11A1 F2R PITX2 TMOD1 SERP1
6357	Regulation of transcription from RNA polymerase II promoter	4.8269E-4	8.4821E-3	E2F1 ZEB1 MXI1 MED20 CBFβ ACVR1B S1PR1 RAD21 HEY2 POU3F3 NKX2-1 RARB AGRN PITX2 TXNIP TAF1 EGR2 SOX11 CREBBP ARNTL SOD2 ATXN1 HDAC4 MED4 HIF1A ETS1 DLX5 TGIF1 CUX1 NCOR1 NFIA KLF4
44057	Regulation of system process	4.8447E-4	8.4821E-3	EGR2 GSX2 EDN1 CTNND2 STXBP1 ITGA2 NLGN2 ADCYAP1 KDR ABCG8 HDAC4 BDNF GRIA2 ATP2A2 AGTR1A SYN2 NTRK2 NPTN GUCY1A3 HBEGF KLF4 F2R CACNA1B
23051	Regulation of signaling process	5.4194E-4	9.4353E-3	WNT5A DLC1 GRB2 HMGR EFNA1 FOXM1 EDN1 ITS2 ADCYAP1 S1PR1 SQSTM1 GARNL1 TBC1D5 RAPGEF5 FASL PAFAH1B1 HHIP TRAF7 NRG1 INSR CEACAM1 GHR BCR ARHGEF5 NDFIP1 SLIT2 KDR MFN2 ZDHHC17 GRIA2 EREG AGTR1A AKAP6 RIPK2 ADAM17 HBEGF NCOR1 KLF4 F2R
6984	ER-nucleus signaling pathway	5.4474E-4	9.4353E-3	CCND1 DERL1 ATP2A2 ERN1 NFE2L2 SERP1
22603	Regulation of anatomical structure morphogenesis	5.6831E-4	9.7272E-3	WNT5A DLC1 EFNA1 EDN1 RNH1 GAS7 CXCL12 SLIT2 KDR TSPAN12 SFRP1 EREG ETS1 AGTR1A HOXA10 NKX2-1 TGFB3 ROBO2 FASL PAFAH1B1
51649	Establishment of localization in cell	5.7250E-4	9.7272E-3	ARL6IP1 GNPTG CAST CPLX1 DERL1 EDN1 BET1 CASK CNO CLTC VPS33A STX12 SYN2 VPS4B CHM PAFAH1B1 RANBP2 RAB6A CHP CDCA5 TXNIP STXBP1 ARNTL OPTN STX1B ATXN1 MFN2 SCFD1 AGTR1A NTRK2 SLC18A2 RAB15 SRP72 CUX1 GGA1 LRP2 SMPD3 F2R MYH10
32268	Regulation of cellular protein metabolic process	5.7353E-4	9.7272E-3	DLC1 GCLC EIF2C1 EDN1 UBE2V2 UHMK1 ACVR1B SQSTM1 SERPINA5 DAZL INSR DNMT3B GHR TAF1 PAIP2 FMR1 IREB2 NDFIP1 ITGA2 SLIT2 HDAC4 CCND1 AGTR1A NPTN RIPK2 ADAM17 NCOR1 RASD2 SERP1
45892	Negative regulation of transcription, DNA-dependent	5.7601E-4	9.7272E-3	TXNIP HMBOX1 HAT1 ZEB1 MXI1 FOXP2 PURA HDAC4 SMARCE1 DLX5 HEY2 TRP63 POU3F3 TGIF1 NKX2-1 RARB CUX1 NCOR1 DNMT3B FOXD1 KLF4
40011	Locomotion	5.7660E-4	9.7272E-3	HSP90AA1 CXCL3 ASTN1 ABI2 CXCL12 SLIT2 VCAM1 ITGA6 AGTR1A ETS1 CXCL16 POU3F3 ADAM17 SEMA3C NKX2-1 SCARB1 PAFAH1B1 CLASP2 LAMC1 NRG1 DCX AOC3
21988	Olfactory lobe development	5.8247E-4	9.7753E-3	GSX2 DLX5 ROBO2 SLIT2
48520	Positive regulation of behavior	5.8735E-4	9.8064E-3	WNT5A S1PR1 ITGA2 ADAM17 CXCL12 SLIT2 KDR
1554	Luteolysis	6.0144E-4	9.8360E-3	PLA2G4A ROBO2 SLIT2
7520	Myelin assembly	6.0144E-4	9.8360E-3	CAST CDON NE01
21889	Myoblast fusion	6.0144E-4	9.8360E-3	GSX2 ROBO2 SLIT2
32288	Olfactory bulb interneuron differentiation	6.0144E-4	9.8360E-3	ANK2 ANK3 PMP22
9896	Positive regulation of catabolic process	6.0431E-4	9.8360E-3	WNT5A TAF1 IRS2 GCLC NDFIP1 UBE2V2 IRS1 INSR
1655	Urogenital system development	6.0774E-4	9.8423E-3	WNT5A ALDH1A1 SFRP1 AGTR1A SOX11 HOXA10 POU3F3 ROBO2 NID1 ADAMTS1 ACAT1 SLIT2
43412	Macromolecule modification	6.1289E-4	9.8763E-3	CAST GNPTG EFNA1 CASK PRKG2 PRMT3 ACVR1B MAP3K8 TFB2M OGT RAB6A INSR GHR BCR STK25 SGK3 TRPM7 WNK1 PPM2C PRKD1 MAST4 MAN2A1 ZDHHC17 SENP1 MAPK6 SIAH1A ERN1 RIPK2 LRRK1 SERP1 WNT5A FUT7 USP9X HAT1 PPT2 ABI2 UBE2V2 UBE3C MAPKAPK2 UHMK1 SUMO2 UBE2D3 STAT4 SNRK PPP2CA CDC2L5 TRAF7 TGM6 DNMT3B TEC TAF1 NUB1 NLK CREBBP NID1 CDC25A KDR DUSP5 HDAC4 EPHA4 DUSP2 ULK2 UBA3 NTRK2 USP46 TGFB3 PCAF F2R CDC42BPB
51147	Regulation of muscle cell differentiation	6.4387E-4	1.0324E-2	HDAC4 EREG EDN1 ZEB1 AGRN NRG1
51253	Negative regulation of RNA metabolic process	6.8518E-4	1.0891E-2	TXNIP HMBOX1 HAT1 ZEB1 MXI1 FOXP2 PURA HDAC4 SMARCE1 DLX5 HEY2 TRP63 POU3F3 TGIF1 NKX2-1 RARB CUX1 NCOR1 DNMT3B FOXD1 KLF4
43687	Post-translational protein modification	6.8593E-4	1.0891E-2	CAST EFNA1 CASK PRKG2 PRMT3 ACVR1B MAP3K8 RAB6A INSR GHR BCR STK25 SGK3 TRPM7 WNK1 PPM2C PRKD1 MAST4 SENP1 MAPK6 SIAH1A ERN1 RIPK2 LRRK1 WNT5A USP9X HAT1 ABI2 UBE2V2 UBE3C MAPKAPK2 UHMK1 SUMO2 UBE2D3 STAT4 SNRK PPP2CA CDC2L5 TRAF7 TGM6 TEC TAF1 NUB1 NLK CREBBP NID1 CDC25A KDR DUSP5 HDAC4 EPHA4 DUSP2 ULK2 UBA3 NTRK2 USP46 TGFB3 F2R CDC42BPB
8406	Gonad development	7.1491E-4	1.1296E-2	WNT5A PLA2G4A CCND1 EREG NKX2-1 ROBO2 ADAMTS1 SLIT2 KDR CDH6 ADCYAP1

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
51252	Regulation of RNA metabolic process	7.6650E-4	1.2052E-2	E2F1 STAT5A SNIP1 ZEB1 MXI1 MED20 LASS6 CFBF ACVR1B S1PR1 RAD21 HEY2 TRP63 TFB2M RARB INSR NFX1 PITX2 EGR2 SOX11 ARNTL PURA MYT1L MED4 HIF1A SMARCE1 TGIF1 RFXDC2 NFE2L2 CUX1 SMARCA1 CALCR FOXM1 NR3C2 HAT1 MAPKAPK2 NR3C1 STAT4 HOXA10 POU3F3 NKX2-1 AGRN DNMT3B FOXD1 TXNIP TAF1 ZFP382 GSX2 CUGBP1 HMBBOX1 CREBBP FOXP2 SOD2 ATXN1 HDAC4 ADNP2 HOXB2 ATF3 ETS1 SMARCC1 DLX5 RBAK NCOR1 NFIA KLF4 F2R
51641	Cellular localization	7.7029E-4	1.2053E-2	ARL6IP1 WNT5A CAST GNPTG CPLX1 DERL1 EDN1 BET1 CASK CNO CLTC VPS33A SUMO2 STX12 SYN2 CCDC100 VPS4B CHM PAFAH1B1 RANBP2 CHP RAB6A CDCA5 TXNIP STXBP1 ARNTL OPTN STX1B ATXN1 MFN2 SCFD1 AGTR1A NTRK2 SLC18A2 RAB15 SRP72 CUX1 GGA1 LRP2 SMPD3 F2R MYH10
21795	Cerebral cortex cell migration	7.9501E-4	1.2321E-2	POU3F3 NKX2-1 PAFAH1B1 SLIT2
51482	Elevation of cytosolic calcium ion concentration involved in G-protein and IP3K pathway	7.9501E-4	1.2321E-2	S1PR1 AGTR1A EDN1 F2R
90092	Regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	8.2312E-4	1.2658E-2	WNT5A ACVR1B SOSTDC1 NKX2-1 LBXCOR1 TGFBR3 ZEB1 NR3C1 FOXD1
22402	Cell cycle process	8.2459E-4	1.2658E-2	E2F1 TAF1 KIF11 POLA1 CLTC UHMK1 CDC25A MFN2 ACVR1B CCND1 EREG SIAH1A PPP2CA CYP26B1 CCDC100 ADAM17 PAFAH1B1 CLASP2 ARL8B PMP22 NCOR1 CDCA5 MYH10 KIF2A
7044	Cell-substrate junction assembly	8.3368E-4	1.2737E-2	DLC1 ITGA6 ACTN1 LAMC2 LAMC1
23034	Intracellular signaling pathway	8.4900E-4	1.2910E-2	DLC1 CAST EFNA1 STAT5A EDN1 SNIP1 S1PR1 RAB6A NRG1 PLCB1 INSR CCNA2 GHR BCR ARHGEF5 WNK1 IRS1 PRKD1 GNAL CCND1 MED4 AGTR1A ERN1 RAB15 GNB4 NFE2L2 ARL8B LRRK1 RASD2 SERP1 WNT5A CALCR DERL1 GRB2 NR3C2 MAPKAPK2 CYP26B1 RAB11B TRAF7 CHP DCX TEC ATP2A2 PDE7A ARF2 TGFBR3 RAP1A F2R CDC42BPB
21543	Pallium development	8.6822E-4	1.3141E-2	DLX5 CCDC100 POU3F3 NKX2-1 PAFAH1B1 SLIT2 FOXP2
2685	Cerebral cortex development	8.8359E-4	1.3189E-2	WNT5A ITGA2 ADAM17 CXCL12 SLIT2 AOC3
21987	Negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	8.8359E-4	1.3189E-2	CCDC100 POU3F3 NKX2-1 PAFAH1B1 SLIT2 FOXP2
90101	Regulation of leukocyte migration	8.8359E-4	1.3189E-2	WNT5A SOSTDC1 NKX2-1 LBXCOR1 TGFBR3 NR3C1
51093	Negative regulation of developmental process	9.0149E-4	1.3394E-2	CALCR WNT5A CREBBP ZEB1 SOD2 ADCYAP1 NPHP3 HDAC4 CCND1 BDNF EREG SFRP1 DLX5 TGFBR3 NKX2-1 FASL RARB KLF4
6811	Ion transport	9.0796E-4	1.3429E-2	KCNC2 KCNC1 SCN1A ATP1B1 SLC38A2 KCNC3 PANX1 ATP1B3 KCNAB1 CACNB2 CLTC KCNJ1 ATP2B2 MRS2 KCNQ3 BEST1 KCNK6 CHRNAS VPS4B GRID2 NALCN TRPM4 KCND2 TRPM7 WNK1 SLC10A2 TECT2 KCNJ6 GRIA2 ATP2A2 RYR3 CHRNB3 SCN4B CLN8 SCN4A F2R CACNA1B
48592	Eye morphogenesis	9.8229E-4	1.4409E-2	ALDH1A1 TSPAN12 NTRK2 FASL ZEB1 RARB COL5A2
45597	Positive regulation of cell differentiation	9.8972E-4	1.4409E-2	SYNJ1 CXCL12 KDR ACVR1B ASPA ETS1 DLX5 NPTN HOXA10 RIPK2 TGIF1 GDF10 ROBO2 PAFAH1B1 NRG1 DNMT3B FNDC3B GHR
32583	Regulation of gene-specific transcription	9.9382E-4	1.4409E-2	HDAC4 TAF1 RAD21 HIF1A ETS1 DLX5 HEY2 NKX2-1 SMARCA1 NCOR1 INSR FOXD1 NFIA FOXP2
6491	N-glycan processing	1.0168E-3	1.4409E-2	GNPTG MAN2A1
60318	Definitive erythrocyte differentiation	1.0168E-3	1.4409E-2	NKX2-1 TGFBR3
21798	Forebrain dorsal/ventral pastern formation	1.0168E-3	1.4409E-2	NKX2-1 TGFBR3
10771	Negative regulation of cell morphogenesis involved in differentiation	1.0168E-3	1.4409E-2	GSX2 NKX2-1
10719	Negative regulation of epithelial to mesenchymal transition	1.0168E-3	1.4409E-2	TGFBR3 NCOR1

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
90273	Regulation of somatostatin secretion	1.0168E-3	1.4409E-2	IRS1 ADCYAP1
82	G1/S transition of mitotic cell cycle	1.0266E-3	1.4409E-2	E2F1 ACVR1B CCND1 ADAM17 CDCA5 CDC25A
768	Syncytium formation by plasma membrane fusion	1.0276E-3	1.4409E-2	CAST CDON NEO1
60216	Definitive hemopoiesis	1.0276E-3	1.4409E-2	TGFBR3 NCOR1 CBFβ
3002	Regionalization	1.0595E-3	1.4792E-2	EGR2 SFRP1 GSX2 DLX5 CYP26B1 EDN1 HOXA10 GRSF1 SEMA3C NKX2-1 TGIF1 GPR177
51130	Positive regulation of cellular component organization	1.1071E-3	1.5390E-2	HSP90AA1 SYNJ1 EDN1 ITGA2 UBE2V2 CXCL12 ADCYAP1 KDR PLA2G4A EREG NPTN ROBO2 PAFAH1B1 NCOR1 DNMT3B INSR CD28
48608	Reproductive structure development	1.1318E-3	1.5626E-2	WNT5A PLA2G4A CCND1 SFRP1 EREG NKX2-1 ROBO2 ADAMTS1 SLIT2 KDR CDH6 ADCYAP1
1822	Kidney development	1.1337E-3	1.5626E-2	ALDH1A1 AGTR1A SOX11 HOXA10 POU3F3 ROBO2 NID1 ADAMTS1 ACAT1 SLIT2
51216	Cartilage development	1.1485E-3	1.5763E-2	WNT5A DLX5 EDN1 HOXA10 ZEB1 SOX9 COL11A1 GHR
51146	Striated muscle cell differentiation	1.1825E-3	1.6161E-2	CAST CDON NEO1 AGRN RARB NRG1 F2R TMOD1 PITX2
18193	Peptidyl-amino acid modification	1.2081E-3	1.6442E-2	PRMT3 ACVR1B HDAC4 TAF1 CREBBP ABI2 PCAF RAB6A INSR UHMK1 F2R GHR
71375	Cellular responses to peptide hormone stimulus	1.2260E-3	1.6558E-2	DLC1 IRS2 HIF1A GRB2 PKLR PDE3B PCAF IRS1 INSR GHR
7268	Synaptic transmission	1.2295E-3	1.6558E-2	CAST CPLX1 UBE2V2 STX1B ADCYAP1 ATXN1 BDNF GRIA2 DMD SYN2 GRID2 RAB15 PAFAH1B1 AGRN NRG1 CLN8
32504	Multicellular organism reproduction	1.2371E-3	1.6558E-2	WNT5A E2F1 STAT5A TSNAX CXCL12 ADCYAP1 ALDH1A1 SERPINA5 CYP26B1 TRP63 NKX2-1 DAZL PAFAH1B1 ROBO2 ACSL4 ADAM7 CUGBP1 SLIT2 CCND1 PLA2G4A EREG SSTR1 ETS1 SIAH1A GDF10 ADAMTS1
48609	Reproductive process in a multicellular organism	1.2371E-3	1.6558E-2	WNT5A E2F1 STAT5A TSNAX CXCL12 ADCYAP1 ALDH1A1 SERPINA5 CYP26B1 TRP63 NKX2-1 DAZL PAFAH1B1 ROBO2 ACSL4 ADAM7 CUGBP1 SLIT2 CCND1 PLA2G4A EREG SSTR1 ETS1 SIAH1A GDF10 ADAMTS1
32787	Monocarboxylic acid metabolic process	1.2933E-3	1.7238E-2	SCD1 PLP1 FADS1 EDN1 ACOT2 SLC10A2 PDHB ALDH1A1 PLA2G4A ATF3 CYP26B1 PKLR ENO2 SRR IDH2 PDHA1 LIPC ACSL4 CROT GHR
48812	Neuron projection morphogenesis	1.3190E-3	1.7510E-2	EGR2 LPPR4 GAS7 CXCL12 SDC2 SLIT2 KDR ALCAM EPHA4 DMD DLX5 NKX2-1 ROBO2 PAFAH1B1
31644	Regulation of neurological system process	1.3530E-3	1.7888E-2	EGR2 EDN1 CTNND2 STXB1 NLGN2 ITGA2 ADCYAP1 KDR BDNF GRIA2 SYN2 NTRK2 NPTN F2R CACNA1B
21536	Diencephalon development	1.3653E-3	1.7977E-2	WNT5A ETS1 NKX2-1 NCOR1 PITX2 ADCYAP1
51969	Regulation of transmission of nerve impulse	1.3938E-3	1.8265E-2	EGR2 EDN1 CTNND2 STXB1 NLGN2 ITGA2 ADCYAP1 KDR BDNF GRIA2 SYN2 NTRK2 NPTN CACNA1B
51329	Interphase of mitotic cell cycle	1.3985E-3	1.8265E-2	E2F1 ACVR1B TAF1 CCND1 POLA1 ADAM17 CDCA5 CDC25A
45596	Negative regulation of cell differentiation	1.4247E-3	1.8532E-2	WNT5A CREBBP ZEB1 SOD2 ADCYAP1 NHPH3 HDAC4 CCND1 EREG SFRP1 DLX5 TGFBR3 NKX2-1 RARB KLF4
10647	Positive regulation of cell communication	1.4700E-3	1.9035E-2	WNT5A NDFIP1 ITGA2 IRS1 KDR ADCYAP1 ACVR1B ZDHHC17 GRIA2 EREG NTRK2 TRP63 NPTN RIPK2 ADAM17 TGFBR3 HBEGF FASL TRAF7 NRG1 FOXD1 INSR F2R GHR
22607	Cellular component assembly	1.4751E-3	1.9035E-2	CAST DLC1 GRB2 CASK NAP1L3 ACAT1 LSM14A ALDH1A1 ANK2 SQSTM1 ANK3 SRR TRP63 H2AFZ PAFAH1B1 AGRN OGT NRG1 INSR TAF1 HSP90AA1 KCND2 ATG9A CUGBP1 ACTN1 NRXN1 GAS7 IRS1 SOD2 MED4 PRLR ITGA6 NBR1 CHRNB3 TGFBR3 LAMC2 LAMC1 LIPC PMP22 NCOR1 TMOD1
50795	Regulation of behavior	1.5387E-3	1.9777E-2	WNT5A S1PR1 ITGA2 ADAM17 ROBO2 CXCL12 SLIT2 KDR
34330	Cell junction organization	1.5612E-3	1.9987E-2	DLC1 ITGA6 ANK2 ANK3 ACTN1 LAMC2 LAMC1
10628	Positive regulation of gene expression	1.5682E-3	1.9997E-2	E2F1 NR3C1 ZEB1 CBFβ ACVR1B S1PR1 TRP63 POU3F3 NKX2-1 RARB AGRN FOXD1 DNMT3B PITX2 TAF1 EGR2 SOX11 CREBBP ARNTL ATXN1 HDAC4 HIF1A ETS1 SMARCC1 DLX5 NFE2L2 SMARCA1 NFIA KLF4 F2R
6949	Syncytium formation	1.6053E-3	2.0268E-2	CAST CDON NEO1

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
51597	response to methylmercury	1.6053E-3	2.0268E-2	PLA2G4A ANK2 ANK3
9966	Regulation of signal transduction	1.6082E-3	2.0268E-2	WNT5A DLC1 GRB2 HMGR EFNA1 FOXM1 EDN1 ITSN2 ADCYAP1 S1PR1 SQSTM1 GARNL1 TBC1D5 RAPGEF5 FASL PAFAH1B1 TRAF7 HHIP NRG1 INSR CEACAM1 GHR BCR ARHGEF5 NDFIP1 SLIT2 KDR MFN2 ZDHHC17 EREG AKAP6 RIPK2 ADAM17 HBEGF NCOR1 KLF4 F2R
8104	Protein localization	1.6278E-3	2.0435E-2	ARL6IP1 WNT5A CAST GNPTG DERL1 GRIP1 BET1 CASK CCDC91 CLTC VPS33A SFT2D1 SUMO2 STX12 ANK3 CHM RAB11B RAB6A TXNIP ATG9A STXBP1 ITGA2 ARNTL OPTN STX1B MFN2 SCFD1 ZDHHC17 GRIA2 AGTR1A ARF2 MCFD2 RAB15 SRP72 LRP2 GGA1 F2R SERP1
51347	Positive regulation of transferase activity	1.6453E-3	2.0576E-2	EFNA1 EDN1 IRS1 CCND1 PRLR EREG SERINC1 ERN1 ADAM17 CERK TRAF7 NRG1 INSR CEACAM1 F2R GHR
48583	Regulation of response to stimulus	1.6534E-3	2.0597E-2	WNT5A MASP1 FOXM1 EDN1 UBE2V2 CXCL12 ADCYAP1 S1PR1 SERPINA5 GRID2 PARG ROBO2 IL13RA1 NTSE CD28 NDFIP1 ITGA2 IRS1 SLIT2 KDR PLA2G4A EREG HBEGF ADAM17 RIPK2 NCOR1 F2R AOC3
45944	Positive regulation of transcription from RNA polymerase II promoter	1.6652E-3	2.0666E-2	E2F1 TAF1 EGR2 SOX11 CREBBP ARNTL ZEB1 CBFβ ATXN1 ACVR1B HDAC4 HIF1A S1PR1 ETS1 DLX5 POU3F3 NKX2-1 RARB AGRN NFIA KLF4 PITX2
43434	Response to peptide hormone stimulus	1.6893E-3	2.0811E-2	DLC1 IRS2 EGR2 GRB2 FADS1 PDE3B CXCL12 IRS1 HIF1A ATP2A2 EREG PKLR PCAF CTSB LIPC CCNA2 INSR GHR
48754	Branching morphogenesis of a tube	1.6898E-3	2.0811E-2	WNT5A EDN1 HOXA10 NKX2-1 CXCL12 FOXD1 SLIT2 PITX2
6355	Regulation of transcription, DNA-dependent	1.7468E-3	2.1431E-2	E2F1 STAT5A SNIP1 ZEB1 MXI1 MED20 LASS6 CBFβ ACVR1B S1PR1 RAD21 HEY2 TRP63 TFB2M RARB INSR NFκB PITX2 EGR2 SOX11 ARNTL PURA MYT1L MED4 HIF1A SMARCE1 TGIF1 RFXDC2 NFE2L2 CUX1 SMARCA1 FOXM1 NR3C2 HAT1 NR3C1 STAT4 HOXA10 POU3F3 NKX2-1 AGRN DNMT3B FOXD1 TXNIP TAF1 ZFP382 GSX2 HMBOX1 CREBBP SOD2 FOXP2 ATXN1 HDAC4 ADNP2 ATF3 HOXB2 ETS1 SMARCC1 DLX5 RBAK NCOR1 NFIA KLF4 F2R
32868	Response to insulin stimulus	1.7610E-3	2.1524E-2	DLC1 IRS2 EGR2 HIF1A GRB2 FADS1 PKLR PDE3B PCAF IRS1 INSR GHR
42692	Muscle cell differentiation	1.7841E-3	2.1724E-2	CAST CDON NEO1 AGRN RARB NRG1 IFRD1 F2R TMOD1 PITX2
14070	Response to organic cyclic substance	1.8183E-3	2.2058E-2	WNT5A FADS1 ITGA2 ACAT1 SDC2 ALDH1A1 ANXA7 CCND1 RYR3 PKLR ENO2 SRR CHRNA5 GUCY1A3 CTSB LIPC NFIA GHR CACNA1B
15031	Protein transport	1.8331E-3	2.2154E-2	ARL6IP1 GNPTG CAST DERL1 BET1 CASK CCDC91 CLTC VPS33A SFT2D1 STX12 RAB11B CHM RAB6A TXNIP ATG9A STXBP1 ARNTL OPTN STX1B MFN2 SCFD1 ZDHHC17 AGTR1A ARF2 MCFD2 RAB15 SRP72 GGA1 LRP2 F2R SERP1
33036	Macromolecule localization	1.8480E-3	2.2223E-2	ARL6IP1 WNT5A CAST GNPTG DERL1 GRIP1 BET1 CASK CCDC91 CLTC VPS33A SFT2D1 SUMO2 STX12 ANK3 CHM RAB11B VPS4B SCARB1 RAB6A ACSL4 TXNIP ATG9A FMR1 STXBP1 ITGA2 ARNTL OPTN STX1B MFN2 ABCG8 ZDHHC17 SCFD1 GRIA2 ARF2 AGTR1A MCFD2 RAB15 SRP72 LRP2 GGA1 CROT F2R SERP1
51325	Interphase	1.8525E-3	2.2223E-2	E2F1 ACVR1B TAF1 CCND1 POLA1 ADAM17 CDCA5 CDC25A
51345	Positive regulation of hydrolase activity	1.9765E-3	2.3623E-2	DLC1 S1PR1 AGTR1A GARNL1 EDN1 ERN1 ITGA2 AKAP6 FASL GNB4 NLRP3 TPM1 F2R
3205	Cardiac chamber development	2.0429E-3	2.4149E-2	SEMA3C TGFB3 ADAMTS1 COL11A1 PITX2
3206	Cardiac chamber morphogenesis	2.0429E-3	2.4149E-2	SEMA3C TGFB3 ADAMTS1 COL11A1 PITX2
10927	Cellular component assembly involved in morphogenesis	2.0429E-3	2.4149E-2	ANK2 ANK3 PAFAH1B1 PMP22 TMOD1
50804	Regulation of synaptic transmission	2.0882E-3	2.4596E-2	EGR2 EDN1 STXBP1 CTNND2 NLGN2 ADCYAP1 KDR BDNF GRIA2 SYN2 NTRK2 NPTN CACNA1B
14066	Regulation of phosphoinositide 3-kinase cascade	2.1961E-3	2.5773E-2	NCOR1 KLF4 F2R KDR
32990	Cell part morphogenesis	2.2248E-3	2.6015E-2	EGR2 LPPR4 GAS7 CXCL12 SDC2 SLIT2 KDR MFN2 ALCAM EPHA4 DMD DLX5 NKX2-1 ROBO2 PAFAH1B1
6796	Phosphate metabolic process	2.2492E-3	2.6206E-2	WNT5A CAST LPPR4 IMPA1 EFNA1 SYNJ1 CASK ABI2 PRKG2 MAPKAPK2 UHMK1 ACVR1B STAT4 BDNF SNRK PPP2CA MAP3K8 CDC2L5 INSR GHR TEC TAF1 BCR STK25 SGK3 TRPM7 NLK WNK1 PPM2C CDC25A KDR TECT2 PRKD1 DUSP5 EPHA4 MAST4 DUSP2 MAPK6 ULK2 NTRK2 ERN1 RIPK2 TGFB3 LRRK1 F2R CDC42BPB
45927	Positive regulation of growth	2.2789E-3	2.6457E-2	CXCL16 CUGBP1 ADAM17 HBEGF PAFAH1B1 INSR CXCL12 SERP1 GHR

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
8344	Adult locomotory behavior	2.2915E-3	2.6508E-2	ATXN1 EPHA4 SCN1A PAFAH1B1 CXCL12 CLN8
6793	Phosphate metabolic process	2.3445E-3	2.6958E-2	WNT5A CAST LPPR4 IMPA1 EFNA1 SYNJ1 CASK ABI2 PRKG2 MAPKAPK2 UHMK1 ACVR1B STAT4 BDNF SNRK PPP2CA MAP3K8 CDC2L5 INSR GHR TEC TAF1 BCR STK25 SGK3 TRPM7 NLK WNK1 PPM2C CDC25A KDR TECT2 PRKD1 DUSP5 EPHA4 MAST4 DUSP2 MAPK6 ULK2 NTRK2 ERN1 RIPK2 TGFBR3 LRRK1 F2R CDC42BPB
45725	Positive regulation of glycogen biosynthetic process	2.3511E-3	2.6958E-2	IRS2 IRS1 INSR
279	M phase	2.3554E-3	2.6958E-2	KIF11 CLTC CDC25A EREG PPP2CA SIAH1A CYP26B1 CCDC100 PAFAH1B1 ARL8B CLASP2 CDCA5 NCOR1 KIF2A
43523	Regulation of neuron apoptosis	2.3649E-3	2.6972E-2	GCLC SNRK GRID2 FASL UBE2V2 GCLM F2R SOD2 KDR GHR
21983	Pituitary gland development	2.3881E-3	2.7141E-2	WNT5A ETS1 NKX2-1 PITX2 ADCYAP1
31329	Regulation of cellular catabolic process	2.4458E-3	2.7699E-2	TAF1 IRS2 GCLC UBE2V2 TPM1 IRS1 ADCYAP1 HDAC4 CSD2 S1PR1 GARNL1 TBC1D5 CHM PAFAH1B1 INSR
45941	Positive regulation of transcription	2.5014E-3	2.8230E-2	E2F1 NR3C1 ZEB1 CBFβ ACVR1B S1PR1 TRP63 POU3F3 NKX2-1 RARB AGRN PITX2 TAF1 EGR2 SOX11 CREBBP ARNTL ATXN1 HDAC4 HIF1A ETS1 SMARCC1 DLX5 NFE2L2 SMARCA1 NFIA KLF4 F2R
19752	Carboxylic acid metabolic process	2.5230E-3	2.8277E-2	BCAT1 AHYC GCLC NARS EDN1 ACOT2 GCLM PDHB ALDH1A1 TDO2 NARS2 CYP26B1 ENO2 IDH2 SRR PDHA1 ACSL4 GHR SCD1 PLP1 SUCLG2 FADS1 SLC10A2 PLA2G4A ATF3 PKLR MCFD2 LIPC CROT
43436	Oxoacid metabolic process	2.5230E-3	2.8277E-2	BCAT1 AHYC GCLC NARS EDN1 ACOT2 GCLM PDHB ALDH1A1 TDO2 NARS2 CYP26B1 ENO2 IDH2 SRR PDHA1 ACSL4 GHR SCD1 PLP1 SUCLG2 FADS1 SLC10A2 PLA2G4A ATF3 PKLR MCFD2 LIPC CROT
3007	Heart morphogenesis	2.6239E-3	2.9306E-2	DLC1 SEMA3C TGFBR3 ADAMTS1 COL11A1 INSR PITX2
33674	Positive regulation of kinase activity	2.6846E-3	2.9881E-2	EFNA1 EDN1 IRS1 CCND1 PRLR EREG ERN1 ADAM17 CERK TRAF7 NRG1 INSR CEACAM1 F2R GHR
43062	Extracellular structure organization	2.7076E-3	2.9984E-2	CAST IBSP NLGN2 NID1 AGRN LAMC1 NRG1 COL11A1 COL5A2 F2R
50927	Positive regulation of positive chemotaxis	2.7124E-3	2.9984E-2	S1PR1 ITGA2 CXCL12 KDR
2687	Positive regulation of leukocyte migration	2.7739E-3	3.0508E-2	WNT5A ITGA2 ADAM17 CXCL12 AOC3
6468	Protein amino acid phosphorylation	2.8592E-3	3.0508E-2	WNT5A CAST EFNA1 CASK ABI2 MAPKAPK2 PRKG2 UHMK1 ACVR1B STAT4 SNRK MAP3K8 CDC2L5 INSR GHR TEC TAF1 BCR STK25 SGK3 TRPM7 NLK WNK1 KDR PRKD1 MAST4 EPHA4 MAPK6 ULK2 NTRK2 ERN1 RIPK2 TGFBR3 LRRK1 F2R CDC42BPB
9791	Post-embryonic development	2.8906E-3	3.0508E-2	SIAH1A SLC18A2 IREB2 SEMA3C KLF4 SOD2 SERP1
6082	Organic acid metabolic process	2.8977E-3	3.0508E-2	BCAT1 AHYC GCLC NARS EDN1 ACOT2 GCLM PDHB ALDH1A1 TDO2 NARS2 CYP26B1 ENO2 IDH2 SRR PDHA1 ACSL4 GHR SCD1 PLP1 SUCLG2 FADS1 SLC10A2 PLA2G4A ATF3 PKLR MCFD2 LIPC CROT
31331	Positive regulation of cellular catabolic process	2.9019E-3	3.0508E-2	TAF1 IRS2 GCLC UBE2V2 IRS1 INSR
43112	Receptor metabolic process	2.9019E-3	3.0508E-2	GRIA2 GRB2 DMD AGRN CLTC NRG1
6271	DNA strand elongation involved in DNA replication	2.9858E-3	3.0508E-2	CLN8 SOD2
18076	N-terminal peptidyl-lysine acetylation	2.9858E-3	3.0508E-2	SEMA3C PITX2
7571	Age dependent general metabolic decline	2.9858E-3	3.0508E-2	POLA1 FEN1
1306	Age-dependent response to oxidative stress	2.9858E-3	3.0508E-2	POLA1 FEN1
32291	Ensheathment of axons in the CNS	2.9858E-3	3.0508E-2	CLN8 SOD2
45338	Farnesyl diphosphate metabolic process	2.9858E-3	3.0508E-2	WNT5A ADAM17

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
21877	Forebrain neuron fate commitment	2.9858E-3	3.0508E-2	WNT5A ADAM17
6273	Lagging strand elongation	2.9858E-3	3.0508E-2	NCOR1 KLF4
22010	Myelination in the CNS	2.9858E-3	3.0508E-2	CREBBP PCAF
14067	Negative regulation of phosphoinositide 3-kinase cascade	2.9858E-3	3.0508E-2	CREBBP PCAF
51497	Negative regulation of stress fiber assembly	2.9858E-3	3.0508E-2	DLX5 NKX2-1
18394	Peptidyl-lysine acetylation	2.9858E-3	3.0508E-2	PLP1 ASPA
10820	Positive regulation of T cell chemotaxis	2.9858E-3	3.0508E-2	PLP1 ASPA
3350	Pulmonary myocardium development	2.9858E-3	3.0508E-2	NCOR1 CD28
10819	Regulation of T cell chemotaxis	2.9858E-3	3.0508E-2	HMGCR FDF1
50923	Regulation of negative chemotaxis	2.9858E-3	3.0508E-2	ROBO2 SLIT2
45066	Regulatory T cell differentiation	2.9858E-3	3.0508E-2	DLC1 S1PR1
60841	Venous blood vessel development	2.9858E-3	3.0508E-2	SEMA3C PITX2
35556	Intracellular signal transduction	3.0274E-3	3.0836E-2	CALCR WNT5A CAST DLC1 GRB2 EFNA1 STAT5A EDN1 SNIP1 MAPKAPK2 S1PR1 RAB11B CHP RAB6A TRAF7 NRG1 INSR CCNA2 GHR TEC WNK1 IRS1 GNAL ARF2 AGTR1A PDE7A RAP1A RAB15 TGFB3 GNB4 ARL8B LRRK1 RASD2 F2R
22414	Reproductive process	3.1021E-3	3.1497E-2	WNT5A E2F1 STAT5A TSNAX CXCL12 LGR4 ADCYAP1 CDH6 ALDH1A1 ACVR1B SERPINA5 SOSTDC1 CYP26B1 TRP63 NKX2-1 ROBO2 DAZL PAFAH1B1 ACSL4 ADAM7 INSR CUGBP1 SLIT2 GJB2 KDR CCND1 PLA2G4A SFRP1 EREG ETS1 SSTR1 SIAH1A GDF10 ADAMTS1
8285	Negative regulation of cell proliferation	3.1130E-3	3.1509E-2	WNT5A DLC1 NDFIP1 PAWR ZEB1 SLIT2 SOD2 ADCYAP1 MFN2 HDAC4 EREG TGIF1 TGFB3 PCAF RARB PMP22 KLF4 F2R
70875	Positive regulation of glycogen metabolic process	3.2796E-3	3.3092E-2	IRS2 IRS1 INSR
2688	Regulation of leukocyte chemotaxis	3.3060E-3	3.3108E-2	WNT5A ADAM17 CXCL12 SLIT2
50926	Regulation of positive chemotaxis	3.3060E-3	3.3108E-2	S1PR1 ITGA2 CXCL12 KDR
48858	Cell projection morphogenesis	3.3118E-3	3.3108E-2	EGR2 LPPR4 GAS7 CXCL12 SDC2 SLIT2 KDR ALCAM EPHA4 DMD DLX5 NKX2-1 ROBO2 PAFAH1B1
10608	Posttranscriptional regulation of gene expression	3.5202E-3	3.5082E-2	CALCR STX12 EIF2C1 PAIP2 SNIP1 FMR1 STXBP1 IREB2 ITGA2 DAZL MAPKAPK2 UHMK1 SERP1
42180	Cellular ketone metabolic process	3.5958E-3	3.5501E-2	BCAT1 AHYC GCLC NARS EDN1 ACOT2 GCLM PDHB ALDH1A1 TDO2 NARS2 CYP26B1 ENO2 IDH2 SRR PDHA1 ACSL4 GHR SCD1 PLP1 SUCLG2 FADS1 SLC10A2 PLA2G4A ATF3 PKLR MCFD2 LIPC CROT
30030	Cell projection organization	3.6236E-3	3.5501E-2	EGR2 LPPR4 ABI2 GAS7 CXCL12 SLIT2 SDC2 UHMK1 KDR ALCAM EPHA4 ITGA6 DLX5 DMD NKX2-1 ROBO2 PAFAH1B1 LAMC1 ACSL4
7202	Activation of phospholipase C activity	3.6263E-3	3.5501E-2	DLC1 S1PR1 AGTR1A EDN1 GNB4 F2R
10863	Positive regulation of phospholipase C activity	3.6263E-3	3.5501E-2	DLC1 S1PR1 AGTR1A EDN1 GNB4 F2R
51262	Protein tetramerization	3.6263E-3	3.5501E-2	ALDH1A1 SRR TRP63 NRXN1 INSR SOD2
7568	Aging	3.6369E-3	3.5501E-2	HMGCR GRB2 FOXM1 FADS1 SOD2 VCAM1 PLA2G4A SLC18A2 TRP63 SRR LRP2 CLN8 SERP1 AOC3
30278	Regulation of ossification	3.6425E-3	3.5501E-2	CALCR HDAC4 PLA2G4A EGR2 SFRP1 DLX5 RSAD2 GDF10

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
16192	Vesicle-mediated transport	3.6574E-3	3.5501E-2	CPLX1 GRB2 SYNJ1 BET1 CNO CLTC VPS33A SFT2D1 STX12 VPS4B SCARB1 RAB6A CHP EHD4 GHR STXBP1 OPTN STX1B SCFD1 GRIA2 ARF2 MCFD2 SLC18A2 GGA1 LRP2 CUX1
34976	Response to endoplasmic reticulum stress	3.6774E-3	3.5501E-2	CCND1 DERL1 ERN1 NFE2L2 SERP1
8015	Blood circulation	3.6827E-3	3.5501E-2	GCLC AGTR1A EDN1 WNK1 NKX2-1 GUCY1A3 NRG1 TPM1 GCLM SLIT2 AOC3 SOD2
3013	Circulatory system process	3.6827E-3	3.5501E-2	GCLC AGTR1A EDN1 WNK1 NKX2-1 GUCY1A3 NRG1 TPM1 GCLM SLIT2 AOC3 SOD2
48584	Positive regulation of response to stimulus	3.7374E-3	3.5921E-2	WNT5A MASP1 ITGA2 UBE2V2 CXCL12 IRS1 SLIT2 KDR PLA2G4A S1PR1 EREG RIPK2 HBEGF PARG ADAM17 AOC3 CD28
6916	Anti-apoptosis	3.7695E-3	3.6122E-2	GCLC DNAJB9 SQSTM1 ETS1 BNIP3L RIPK2 ADAM17 NR3C1 CIAPIN1 API5 SOD2
1568	Blood vessel development	3.8090E-3	3.6357E-2	VEGFB S1PR1 ETS1 EFNA1 AGTR1A NTRK2 EDN1 HEY2 CHM SEMA3C TGFB3 CXCL12 SLIT2 PITX2
8585	Female gland development	3.8164E-3	3.6357E-2	PLA2G4A EREG ROBO2 ADAMTS1 SLIT2 CDH6 ADCYAP1
3	Reproduction	3.8477E-3	3.6548E-2	WNT5A E2F1 STAT5A TSNAX CXCL12 LGR4 ADCYAP1 CDH6 ALDH1A1 ACVR1B SERPINA5 SOSTDC1 CYP26B1 TRP63 NKX2-1 ROBO2 DAZL PAFAH1B1 ACSL4 ADAM7 INSR CUGBP1 SLIT2 GJB2 KDR CCND1 PLA2G4A SFRP1 EREG ETS1 SSTR1 SIAH1A GDF10 ADAMTS1
902	Cell morphogenesis	3.8869E-3	3.6812E-2	EGR2 LPPR4 GAS7 CXCL12 SLIT2 SDC2 KDR ALCAM EPHA4 DLX5 DMD TGFB3 NKX2-1 ROBO2 PAFAH1B1 LAMC1 NRG1
45840	Positive regulation of mitosis	3.9823E-3	3.7496E-2	EREG EDN1 INSR CD28
51785	Positive regulation of nuclear division	3.9823E-3	3.7496E-2	EREG EDN1 INSR CD28
40008	Regulation of growth	4.0356E-3	3.7888E-2	SCD1 ZFP382 CUGBP1 CXCL12 SLIT2 ACVR1B IGSF11 CXCL16 SIAH1A HEY2 ADAM17 HBEGF PAFAH1B1 AGRN NCOR1 INSR CRIM1 SERP1 GHR
43010	Camera-type eye development	4.0633E-3	3.8037E-2	ALDH1A1 ATP2B2 TSPAN12 ABI2 TGIF1 ZEB1 CLN8 KLF4 PITX2
42594	Response to starvation	4.1702E-3	3.8926E-2	ATG9A SQSTM1 SSTR1 NBR1 FADS1 ACAT1 ADCYAP1
51049	Regulation of transport	4.2271E-3	3.9220E-2	WNT5A PANX1 SYNJ1 EDN1 PDE3B CXCL12 UHMK1 ADCYAP1 SYN2 SCARB1 NRG1 INSR EHD4 IRS2 STXBP1 NDFIP1 ITGA2 NLRP3 IRS1 STX1B ABCG8 SCFD1 PLA2G4A NTRK2 F2R AOC3 CACNA1B SERP1
14706	Striated muscle tissue development	4.2307E-3	3.9220E-2	DMD SEMA3C TGFB3 CTSB AGRN RARB NRG1 COL11A1 F2R PITX2
1889	Liver development	4.2501E-3	3.9220E-2	ALDH1A1 MAN2A1 CCND1 ITGA2 TGFB3 LIPC ACAT1 SOD2
46777	Protein amino acid autophosphorylation	4.2501E-3	3.9220E-2	ACVR1B TAF1 BCR NTRK2 WNK1 INSR UHMK1 KDR
44281	Small molecule metabolic process	4.2855E-3	3.9434E-2	ATP1B1 IMPA1 OCLN ATP1B3 NARS SGPP1 HMGCR EDN1 TTPA ACOT2 PDE3B PDHB FDFT1 PRMT3 ATP2B2 TDO2 NARS2 VPS4B GUCY1A3 TFB2M PDHA1 RAB6A NT5E GHR SUCLG2 MAN2A1 SULT1B1 PKLR CLN8 CROT SERP1 CYP51 BCAT1 AHCY GCLC GCLM ADCYAP1 ALDH1A1 CYP26B1 ENO2 SRR IDH2 SCARB1 ACSL4 DNMT3B SCD1 PLP1 FADS1 AK2 SLC10A2 TECT2 SOD2 PLA2G4A ATF3 GBE1 ATP2A2 MCFD2 LIPC LRP2
51338	Regulation of transferase activity	4.3313E-3	3.9729E-2	EFNA1 HMGCR EDN1 WNK1 IRS1 CCND1 PRLR EREG SERINC1 ERN1 ADAM17 CERK TRAF7 NRG1 CLN8 INSR CEACAM1 F2R GHR
32940	Secretion by cell	4.3653E-3	3.9729E-2	CAST CPLX1 EDN1 STXBP1 VPS33A SCFD1 AGTR1A SYN2 NTRK2 SLC18A2 RAB15 CHP LRP2 SMPD3
80134	Regulation of response to stress	4.3696E-3	3.9729E-2	FOXM1 EDN1 NDFIP1 ITGA2 UBE2V2 SLIT2 ADCYAP1 PLA2G4A EREG SERPINA5 RIPK2 HBEGF PARG NCOR1 NT5E F2R AOC3 CD28
48854	Brain morphogenesis	4.4034E-3	3.9729E-2	ITGA6 LAMC2 LAMC1
48048	Embryonic eye morphogenesis	4.4034E-3	3.9729E-2	ALDH1A1 ZEB1 RARB
60206	Estrous cycle phase	4.4034E-3	3.9729E-2	WNT5A GSX2 PAFAH1B1
31581	Hemidesmosome assembly	4.4034E-3	3.9729E-2	WNT5A ALDH1A1 ETS1
10817	Regulation of hormone levels	4.5325E-3	4.0433E-2	ALDH1A1 TTR CPLX1 HSD3B1 KCNJ6 SULT1B1 CYP26B1 EDN1 SLC18A2 SCARB1 LRP2 SMPD3

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
44237	Cellular metabolic process	4.5341E-3	4.0433E-2	CAST GNPTG ATP1B1 OCLN EIF2C1 ATP1B3 HMGR EFNA1 STAT5A EIF5 EDN1 SNIP1 CASK PDE3B CCT2 PRKG2 PDHB FDF1 CYP2C ATP2B2 BDNF CPOX MAP3K8 VPS4B TFB2M PDHA1 OGT INSR ATG9A BCR STK25 NUDT4 SUCLG2 WNK1 MAPK6 SULT1B1 NBR1 SIAH1A RIPK2 LRRK1 CROT WNT5A GCLC DERL1 AHCY LPPR4 GRB2 PNPT1 MME PPT2 UBE2V2 MAPKAPK2 GCLM UHMK1 ADCYAP1 HNRNPL UBE2D3 SERINC1 DMD SRR IDH2 NKX2-1 SFR510 SCARB1 AGRN TRAF7 DNMT3B NOVA1 TEC SCD1 TAF1 CUGBP1 CREBBP IREB2 AK2 SSB KDR TECT2 EPHA4 HDAC4 PLA2G4A GBE1 DNAJB9 ATF3 ATP2A2 ULK2 NTRK2 UBA3 TGFBR3 CDC42BPB IMPA1 NARS SGPP1 SYNJ1 TTPA ACOT2 CLTC PRMT3 ACVR1B TDO2 NARS2 GUCY1A3 RANBP2 RAB6A PLCB1 NRG1 NT5E COL11A1 GHR EIF2S3X HSP90AA1 SGK3 TRPM7 PPM2C PURA PRKD1 MAST4 MAN2A1 ZDHHC17 MED4 SENP1 EREG PDCL RRM1 PKLR ERN1 ADAM17 CTSS CLN8 SERP1 TTRAP CALCR BCAT1 HSD3B1 FUT7 FKBP5 USP9X POLA1 HAT1 ABI2 UBE3C NR3C1 EDEM1 ALDH1A1 SUMO2 STAT4 SNRK SQSTM1 PPP2CA CYP26B1 ENO2 MRPL19 CDC2L5 TGM6 ACCL4 FEN1 TSEN34 PLP1 NUB1 NLK FADS1 NID1 SLC10A2 RPL28 MANBA CDC25A SOD2 DUSP5 DUSP2 GRIA2 MCFD2 ZRANB2 USP46 PCAF LIPC NFIA SMPD3 F2R
42176	Regulation of protein catabolic process	4.5483E-3	4.0433E-2	WNT5A CAST TAF1 GCLC NDFIP1 UBE2V2 ARNTL
19220	Regulation of phosphate metabolic process	4.5508E-3	4.0433E-2	DLC1 HMGR EFNA1 EDN1 ACVR1B SQSTM1 TRAF7 CERK NRG1 INSR CEACAM1 GHR WNK1 ITGA2 IRS1 SLIT2 ATXN1 CCND1 EREG PRLR ERN1 NPTN ADAM17 AKAP6 F2R
51174	Regulation of phosphorus metabolic process	4.5508E-3	4.0433E-2	DLC1 HMGR EFNA1 EDN1 ACVR1B SQSTM1 TRAF7 CERK NRG1 INSR CEACAM1 GHR WNK1 ITGA2 IRS1 SLIT2 ATXN1 CCND1 EREG PRLR ERN1 NPTN ADAM17 AKAP6 F2R
51259	Protein oligomerization	4.5564E-3	4.0433E-2	KCND2 GRB2 NRXN1 IRS1 ACAT1 SOD2 ALDH1A1 SQSTM1 NBR1 SRR TRP63 CHRN3 OGT LIPC INSR
61008	Hepaticobiliary system development	4.5818E-3	4.0547E-2	ALDH1A1 MAN2A1 CCND1 ITGA2 TGFBR3 LIPC ACAT1 SOD2
9607	Response to biotic stimulus	4.6916E-3	4.1406E-2	WNT5A SCD1 DERL1 TUSCS RSAD2 SOD2 STAT4 CCND1 PLA2G4A BNIP3L PKLR SRR ERN1 RIPK2 GUCY1A3 NKX2-1 PARG ADAM17 SCARB1 FASL NFE2L2 F2R SERP1
45860	Positive regulation of protein kinase activity	4.7716E-3	4.1909E-2	EFNA1 EDN1 CCND1 PRLR EREG ERN1 ADAM17 CERK TRAF7 NRG1 INSR CEACAM1 F2R GHR
90068	Positive regulation of cell cycle process	4.7744E-3	4.1909E-2	EREG EDN1 DAZL INSR CD28
31346	Positive regulation of cell projection organization	4.9329E-3	4.3076E-2	HSP90AA1 NPTN ITGA2 ROBO2 PAFAH1B1 UBE2V2 CXCL12 ADCYAP1
10518	Positive regulation of phospholipase activity	4.9534E-3	4.3076E-2	DLC1 S1PR1 AGTR1A EDN1 GNB4 F2R
3001	Generation of a signal involved in cell-cell signaling	4.9606E-3	4.3076E-2	CAST CPLX1 SYN2 NTRK2 EDN1 SLC18A2 RAB15 LRP2 SMPD3
23061	Signal release	4.9606E-3	4.3076E-2	CAST CPLX1 SYN2 NTRK2 EDN1 SLC18A2 RAB15 LRP2 SMPD3
44085	Cellular component biogenesis	5.3318E-3	4.6176E-2	CAST DLC1 GRB2 CASK NAP1L3 ACAT1 LSM14A ALDH1A1 ANK2 SQSTM1 ANK3 SRR TRP63 H2AF2 TFB2M PAFAH1B1 AGRN OGT NRG1 INSR TAF1 HSP90AA1 KCND2 ATG9A CUGBP1 ACTN1 NRXN1 GAS7 IRS1 SOD2 MED4 PRLR ITGA6 NBR1 CHRN3 TGFBR3 LAMC2 LAMC1 LIPC PMP22 NCOR1 TMOD1
60348	Bone development	5.3648E-3	4.6234E-2	IBSP HDAC4 DLX5 HOXA10 RSAD2 GDF10 COL11A1 COL5A2 CBFβ GHR
35107	Appendage morphogenesis	5.3813E-3	4.6234E-2	WNT5A DLX5 CYP26B1 HOXA10 SEMA3C RARB PITX2
35108	Limb morphogenesis	5.3813E-3	4.6234E-2	WNT5A DLX5 CYP26B1 HOXA10 SEMA3C RARB PITX2
1944	Vasculature development	5.4378E-3	4.6595E-2	VEGFB S1PR1 ETS1 EFNA1 AGTR1A NTRK2 EDN1 HEY2 CHM SEMA3C TGFBR3 CXCL12 SLIT2 PITX2
48568	Embryonic organ development	5.5326E-3	4.7282E-2	ALDH1A1 VCAM1 GRB2 EFNA1 DLX5 EDN1 TTPA ZEB1 RARB COL11A1 FZD6 PITX2
10828	Positive regulation of glucose transport	5.6028E-3	4.7334E-2	IRS2 IRS1 INSR AOC3
45765	Regulation of angiogenesis	5.697E-3	4.7334E-2	WNT5A TSPAN12 EREG ETS1 EFNA1 RNH1 FASL KDR
1569	S-adenosylhomocysteine metabolic process	5.7333E-3	4.7334E-2	EDN1 CXCL12 PITX2
10510	Cerebral cortex neuron differentiation	5.7333E-3	4.7334E-2	PDHA1 PPM2C PDHB
10559	Embryonic camera-type eye development	5.7333E-3	4.7334E-2	HBEGF PAWR INSR

Supplement: GO functional analysis - cont.

GO-ID	Description	p-value	Corr-p	Gene Name
21544	Negative regulation of small GTPase mediated signal transduction	5.7333E-3	4.7334E-2	GSX2 RARB FOXP2
21895	Patterning of blood vessel	5.7333E-3	4.7334E-2	DLX5 NKX2-1 PAFAH1B1
31076	Positive regulation of epidermal growth factor receptor signaling pathway	5.7333E-3	4.7334E-2	ALDH1A1 ZEB1 PITX2
42403	Regulation of acetyl-CoA biosynthetic process from pyruvate	5.7333E-3	4.7334E-2	TTR KCNJ6 SUL1B1
45742	Regulation of glycoprotein biosynthetic process	5.7333E-3	4.7334E-2	EREG ADAM17 FASL
46498	Subpallium development	5.7333E-3	4.7334E-2	OCLN AHCY DNMT3B
51058	Thyroid hormone metabolic process	5.7333E-3	4.7334E-2	MFN2 DLC1 SLIT2
16337	Cell-cell adhesion	5.8293E-3	4.7334E-2	ASTN1 STXBP1 PCDH9 PCDH19 SLIT2 CDH6 VCAM1 CD93 ITGA6 FAT4 CLDN1 NPTN ROBO2 COL11A1 CDH11
48660	Regulation of smooth muscle cell proliferation	5.8384E-3	4.7334E-2	MFN2 S1PR1 HIF1A EREG EDN1 ITGA2 KLF4
301	DNA strand elongation	5.8455E-3	4.7334E-2	OPTN CUX1
6422	Aspartyl-tRNA aminoacylation	5.8455E-3	4.7334E-2	NARS NARS2
21604	Cranial nerve structural organization	5.8455E-3	4.7334E-2	EGR2 DMD
22616	Forebrain morphogenesis	5.8455E-3	4.7334E-2	POLA1 FEN1
30913	Paranodal junction assembly	5.8455E-3	4.7334E-2	ANK2 ANK3
48853	Response to nitrosative stress	5.8455E-3	4.7334E-2	WNT5A GSX2
51409	Retrograde transport, vesicle recycling within Golgi	5.8455E-3	4.7334E-2	GCLC GCLM
60537	Muscle tissue development	6.0146E-3	4.8127E-2	DMD SEMA3C TGFB3 CTSB AGRN RARB NRG1 COL11A1 F2R PITX2
1657	Response to growth factor stimulus	6.0167E-3	4.8127E-2	SFRP1 HOXA10 ROBO2 RARB FOXD1 SLIT2
3018	Ureteric bud development	6.0167E-3	4.8127E-2	GCLC EDN1 GUCY1A3 GCLM SLIT2 SOD2
70848	Vascular process in circulatory system	6.0167E-3	4.8127E-2	E2F1 ACOT2 GDF10 TGIF1 FASL ZEB1
16044	Cellular membrane organization	6.0178E-3	4.8127E-2	CTBP1 HSP90AA1 GRB2 SYNJ1 STXBP1 CNO CLTC MFN2 ANXA7 GRIA2 SCARB1 PAFAH1B1 TMPO AGRN LRP2 CLN8 GHR EHD4
45732	Positive regulation of protein catabolic process	6.0856E-3	4.8550E-2	WNT5A TAF1 GCLC NDFIP1 UBE2V2
60562	Epithelial tube morphogenesis	6.1108E-3	4.8631E-2	WNT5A DLC1 HOXA10 NKX2-1 TGIF1 FOXD1 SLIT2 FZD6
61024	Membrane organization	6.2286E-3	4.9447E-2	CTBP1 HSP90AA1 GRB2 SYNJ1 STXBP1 CNO CLTC MFN2 ANXA7 GRIA2 SCARB1 PAFAH1B1 TMPO AGRN LRP2 CLN8 GHR EHD4