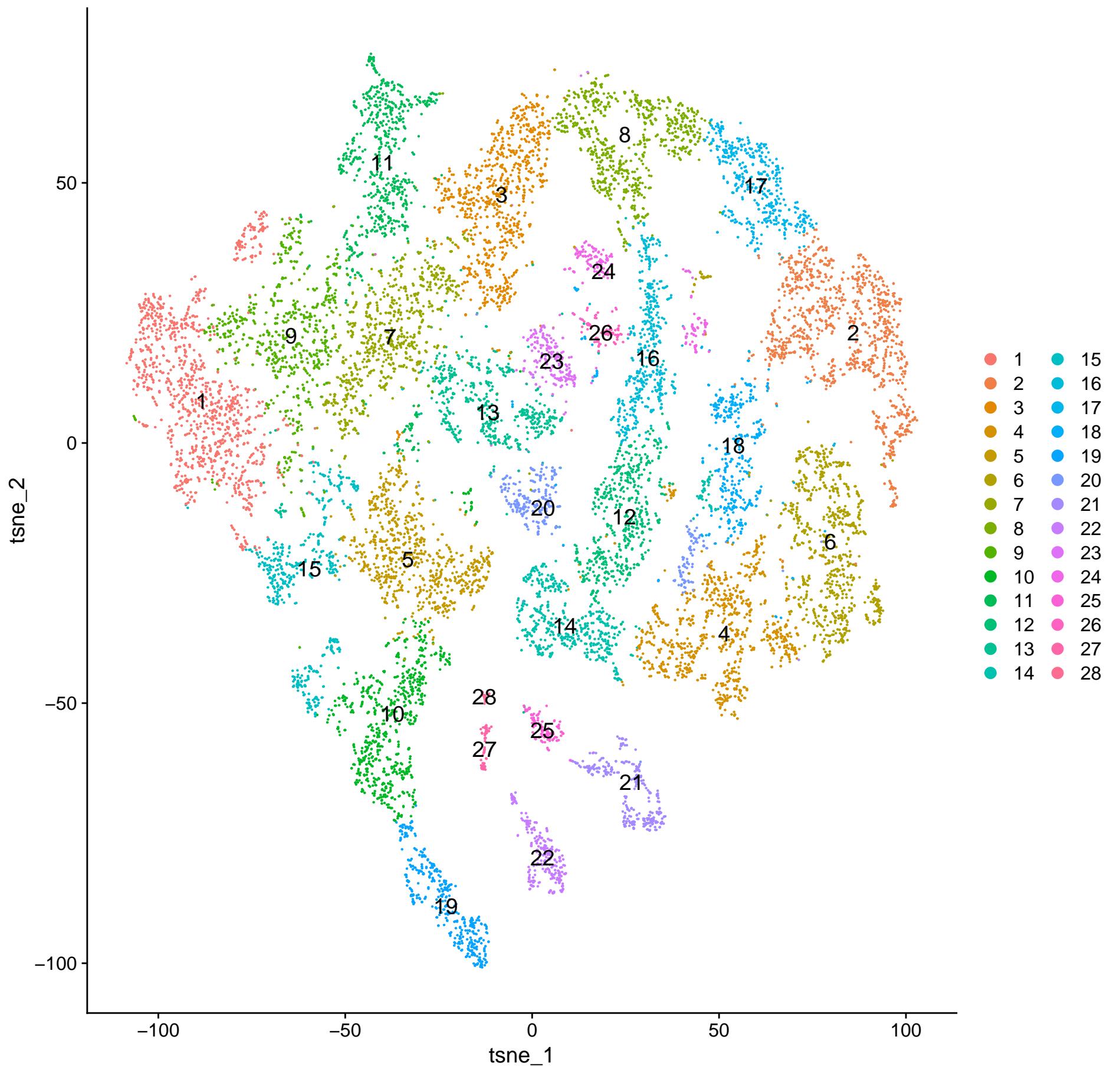
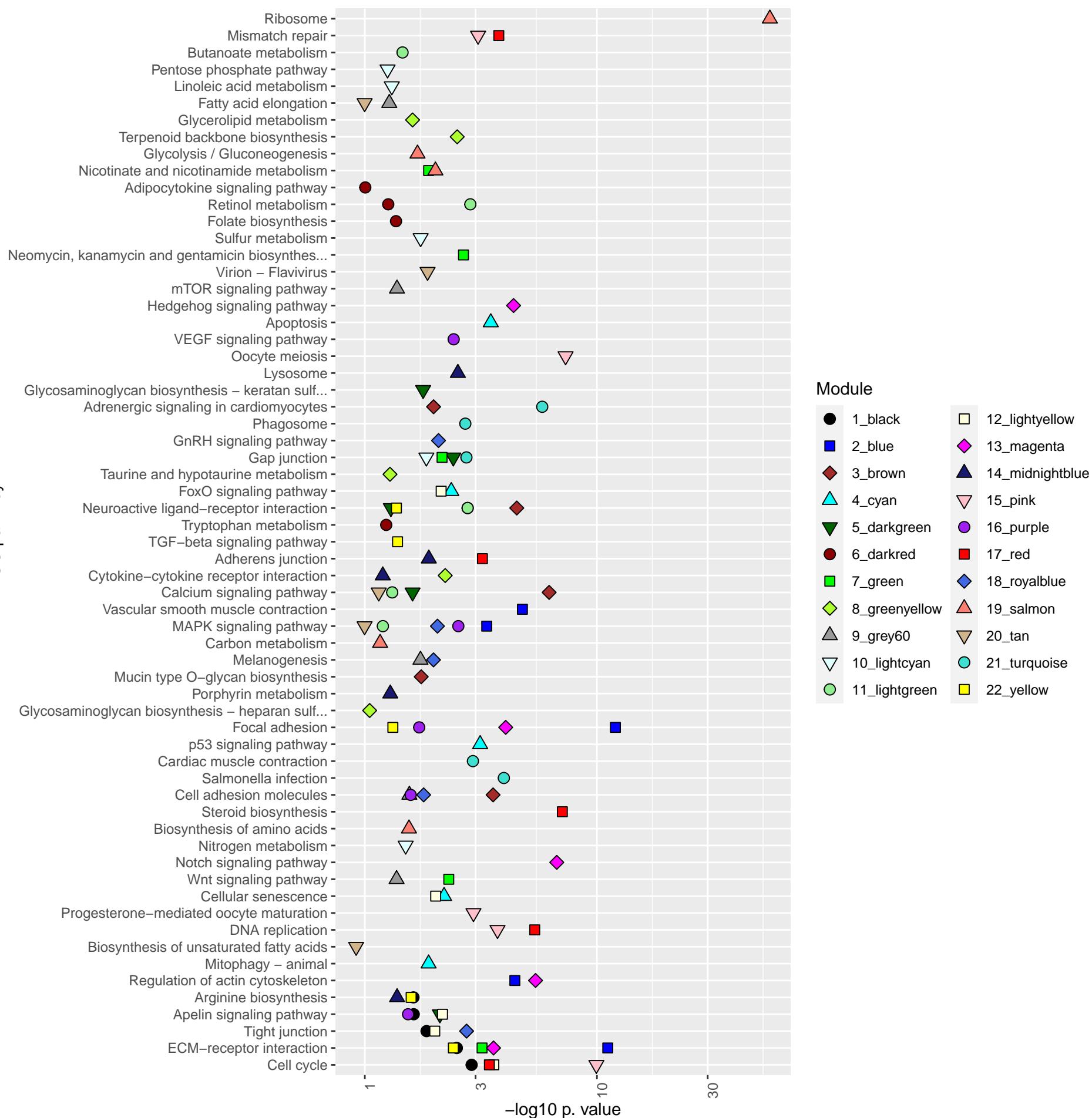
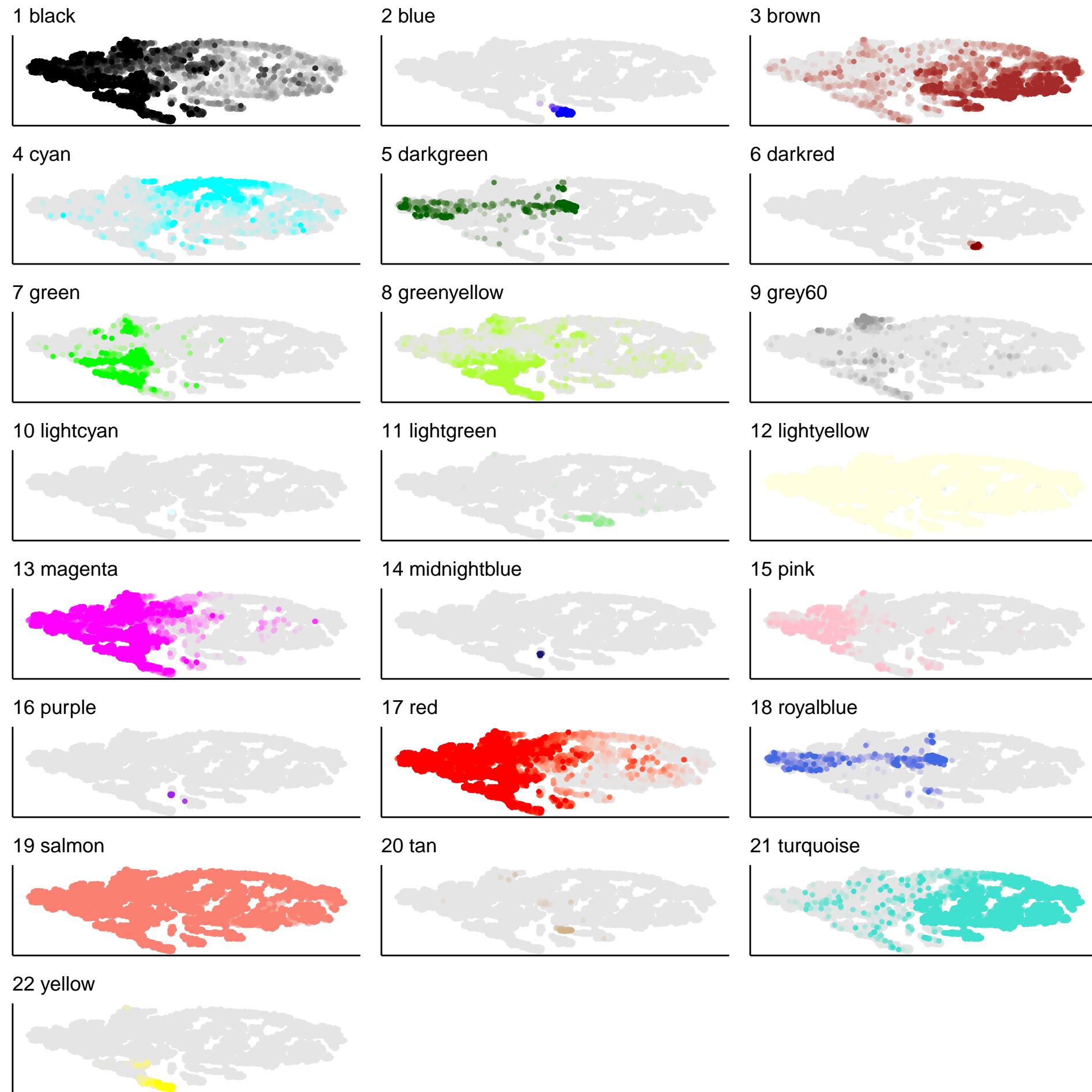


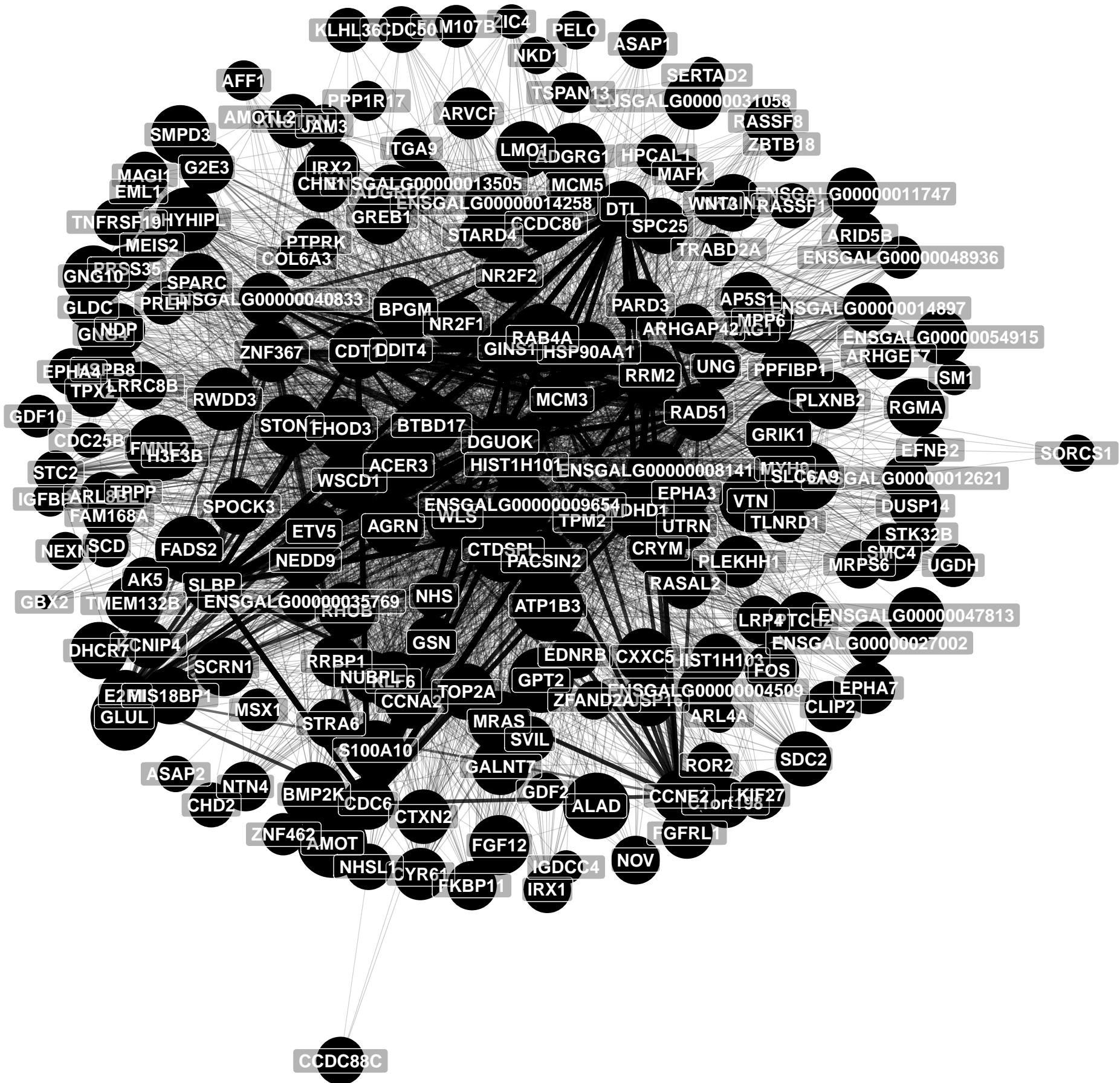
Gg-devel_int scWGCNA modules







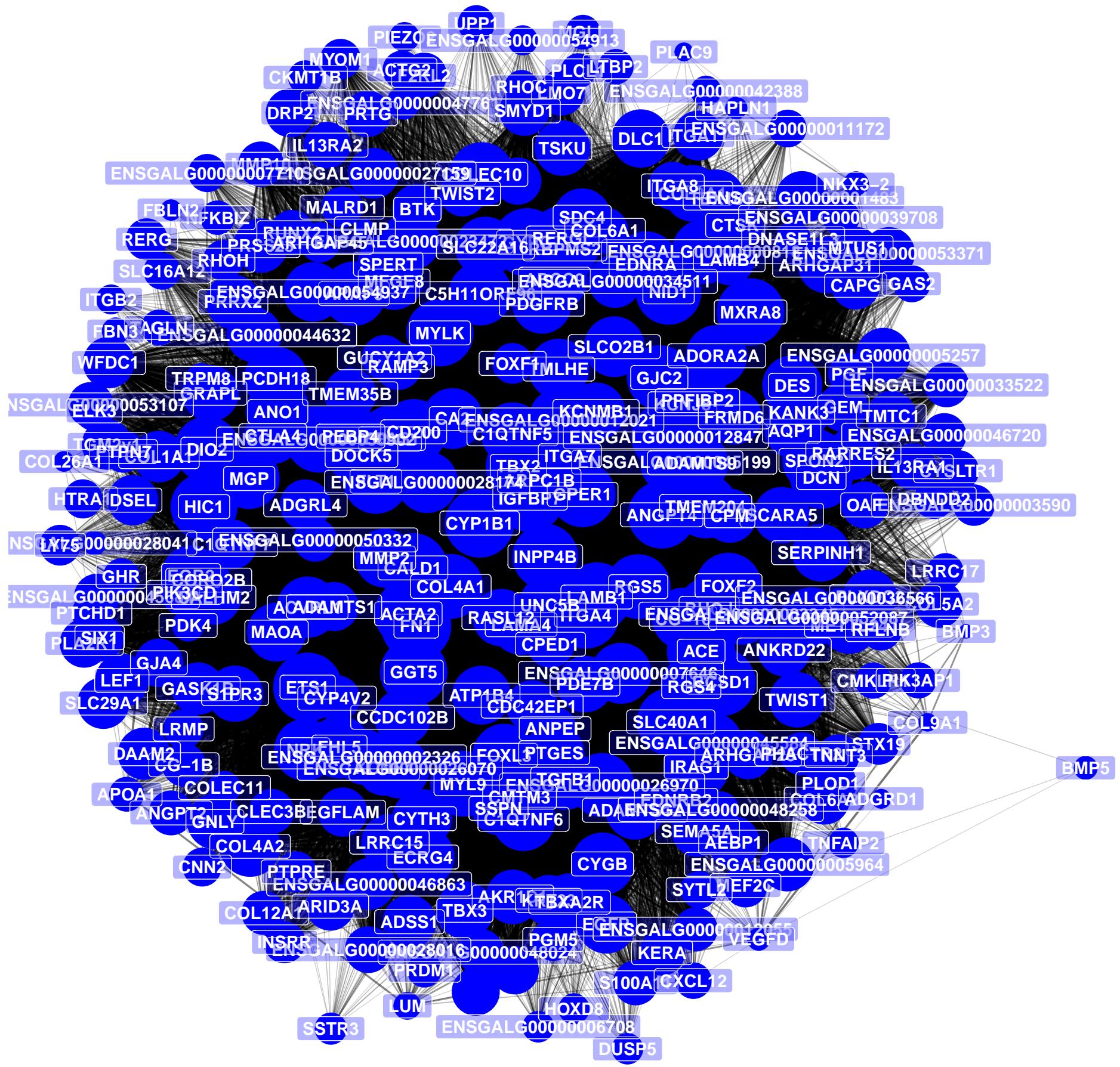




1	RRM2	SPC25	SMC4	TOP2A	DGUOK	SLC6A9	AMOT	ATP1B3
2	WDHD1	GLUL	CDT1	TPX2	CCNA2	MCM5	SLBP	ZNF367
3	GINS1	KNSTRN	SPARC	GRIK1	MCM3	CTDSPL	FADS2	DTL
4	RAD51	MIS18BP1	RAB4A	HSP90AA1	MPP6	ENSGALG00000011747	WLS	ACER3
5	VTN	RHOB	SDC2	FOS	ETV5	BPGM	GPT2	HIST1H103
6	ENSGALG00000040833	ADGRG1	TPM2	ENSGALG0000009654	ALAD	ENSGALG00000054915	PHYHIPL	ENSGALG00000008141
7	G2E3	S100A10	KLF6	MRAS	PACSIN2	PPFIBP1	FGF12	FMNL2
8	CDC6	BMP2K	RWDD3	PLXNB2	FHOD3	NOV	WSCD1	GALNT7
9	NR2F1	IRX2	STON1	SPOCK3	ENSGALG00000014258	ENSGALG00000014897	ENSGALG00000031058	CCDC80
10	HSPB8	NR2F2	E2F1	BTBD17	SCRN1	TMEM132B	NKAIN2	LMO1
11	NEDD9	EPHA3	CCNE2	GNG10	AGRN	CXXC5	CYR61	GSN
12	ARVCF	PTCH2	DHCR7	C1orf198	ENSGALG00000013505	ADGRD2	NUBPL	ENSGALG00000035769
13	RRBP1	ENSGALG00000027002	CTXN2	ARL8BL	PLEKHH1	CRYM	UNG	FAM168A
14	KCNIP4	GREB1	DUSP14	EPHA7	AP5S1	SMPD3	NDP	ARHGAP42
15	HIST1H101	LRP4	MSX1	PTPRK	RASSF8	GNG4	PARD3	MRPS6
16	CHN1	ENSGALG00000047813	DUSP16	UTRN	RGMA	FKBP11	EDNRB	CLIP2
17	ASAP1	ARID5B	HPCAL1	IRX1	FGFRL1	STRA6	KIF27	RASAL2
18	STC2	ENSGALG00000012621	LRRC8B	EPHA4	DDIT4	PRSS35	SVIL	JAG1
19	ENSGALG0000004509	AK5	ARHGEF7	MYH9	MAGI1	TNFRSF19	NHS	NTN4
20	STARD4	ROR2	KLHL36	CCDC50	RASSF1	MEIS2	ENSGALG00000048936	PRLH
21	NHSL1	CCDC88C	UGDH	IGFBP5	WNT3	CHD2	TLDNR1	ITGA9
22	JAM3	GDF10	SCD	H3F3B	PPP1R17	GLDC	TPPP	FAM107B
23	SORCS1	CDC25B	COL6A3	PELO	ZFAND2A	AFF1	NKD1	STK32B
24	GDF2	ZNF462	MAFK	EML1	TSPAN13	ASAP2	SERTAD2	ARL4A
25	ISM1	ZIC4	EFNB2	NEXN	ZBTB18	TRABD2A	IGDCC4	GBX2
26	AMOTL2							

	Term	Ont	N	n	Adj. p-value
GO:0051129	negative regulation of cellular component organization	BP	62	9	2.171e-07
GO:0007167	enzyme linked receptor protein signaling pathway	BP	127	11	2.001e-06
GO:0051128	regulation of cellular component organization	BP	209	13	9.52e-06
GO:0010977	negative regulation of neuron projection development	BP	13	4	2.61e-05
GO:0051173	positive regulation of nitrogen compound metabolic process	BP	300	15	2.676e-05
GO:0051336	regulation of hydrolase activity	BP	111	9	2.963e-05
GO:0065009	regulation of molecular function	BP	267	14	2.968e-05
GO:0048519	negative regulation of biological process	BP	498	20	3.011e-05
GO:0007049	cell cycle	BP	207	12	4.231e-05
GO:0048523	negative regulation of cellular process	BP	469	19	4.272e-05

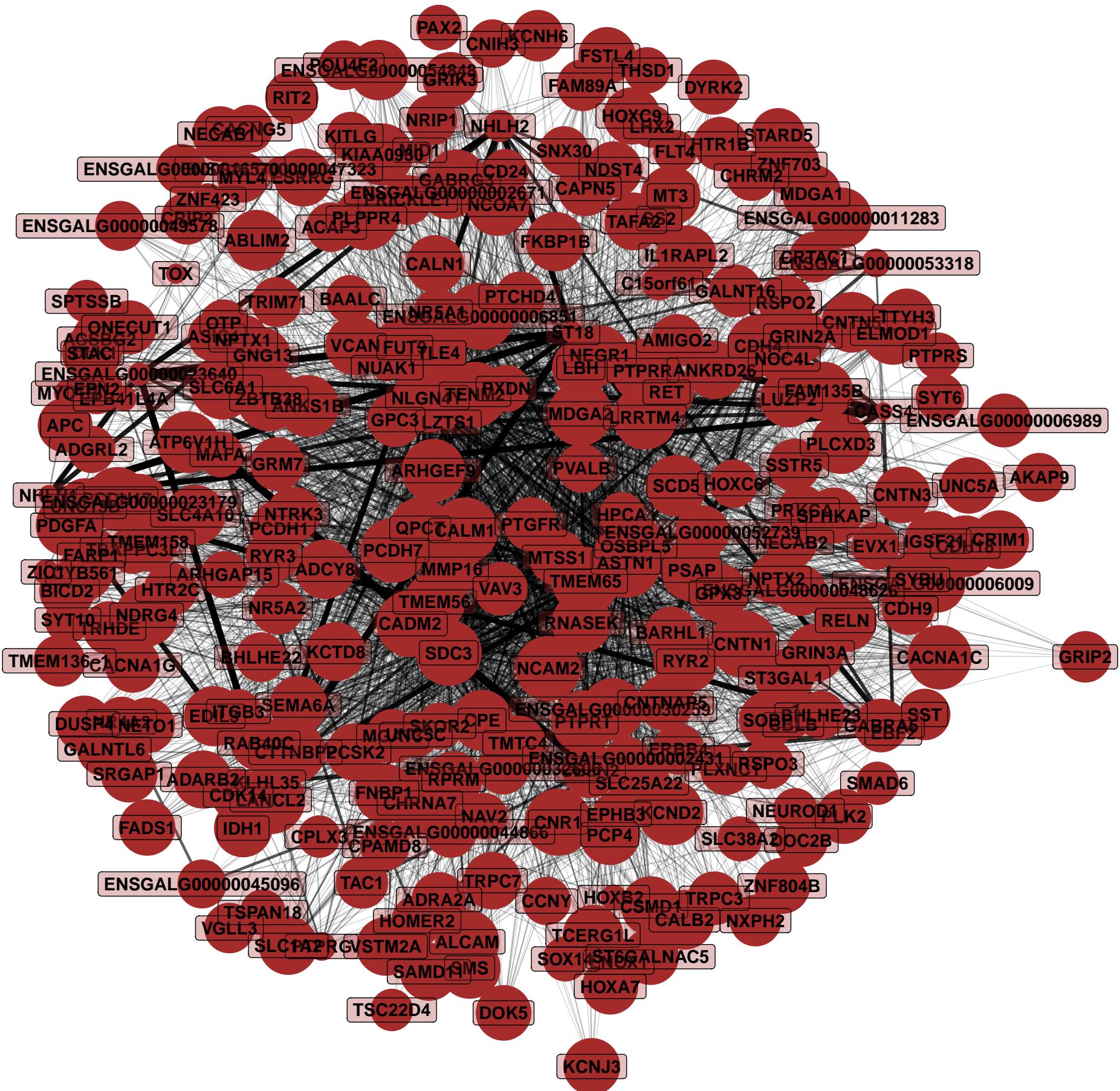
	Pathway	N	DE	P.DE
<i>path:gga04110</i>	Cell cycle	115	7	0.001302
<i>path:gga04512</i>	ECM–receptor interaction	70	5	0.003227
<i>path:gga04530</i>	Tight junction	138	6	0.01429
<i>path:gga04371</i>	Apelin signaling pathway	114	5	0.02375
<i>path:gga00220</i>	Arginine biosynthesis	17	2	0.02398
<i>path:gga01232</i>	Nucleotide metabolism	79	4	0.02645
<i>path:gga00240</i>	Pyrimidine metabolism	56	3	0.04582
<i>path:gga04810</i>	Regulation of actin cytoskeleton	192	6	0.05755
<i>path:gga04137</i>	Mitophagy – animal	62	3	0.05881
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	28	2	0.06021



1	GYPC	CYP1B1	LAMB1	ACTA2	HIC1	DIO2	ACE	KCNJ8
2	ENSGALG00000012847	GGT5	FN1	CALD1	MXRA8	FOXF2	RCSD1	ENSGALG00000030902
3	ENSGALG00000045199	ENSGALG00000012021	TBX2	MYL9	ARAP3	COL1A1	SLC40A1	ENSGALG0000000818
4	GPER1	IGFBP7	ABCC9	RGS5	SPON2	ETS1	FLT1	ANGPT4
5	IRAG1	GJC2	TMEM204	ENSGALG00000007646	ANO1	COLEC10	CD200	RBPMS2
6	DOCK5	DCN	NRK	C1QTNF5	INPP4B	ITGA4	ARPC1B	FOXL3
7	COL4A1	PEBP4	EPAS1	LAMA4	ENSGALG00000023472	MYLK	SPERT	RERGL
8	ACVRL1	ENSGALG00000045584	ECRG4	COL4A2	CA2	EDNRA	ADAMTS9	ITGA7
9	PPFIBP2	EGR2	RHOJ	C5H11ORF96	FHL5	C1QTNF6	MMP2	TBX3
10	ADORA2A	TWIST1	CYGB	ATP1B4	NID1	ENSGALG00000026970	DLC1	AKR1D1
11	MGP	KANK3	ENSGALG00000028174	EGFR	ENSGALG00000026070	SLCO2B1	UNC5B	PCDH18
12	ARHGAP31	ADAMTS12	KCNE4	DES	AQP1	PTGES	MFGE8	MAOA
13	SLC22A16	SCARA5	RGS4	PDGFRB	ENSGALG00000052087	FRMD6	KCNMB1	CG-16
14	PDE7B	CTLA4	PRSS23	TBXA2R	COL3A1	PRRX2	ENSGALG00000003345	SERPINH1
15	TGFB1	SDC4	ENSGALG00000002326	TMLHE	ENSGALG00000034511	CCDC102B	ENSGALG00000005257	RASL12
16	S1PR3	GEM	TBX18	ENSGALG00000044632	ENSGALG00000005964	ENSGALG00000054937	CYTH3	RARRES2
17	CTSK	CALHM2	ARHGAP25	CMTM3	GRAPL	LRRC15	GJA4	ANKRD22
18	COL6A2	ENSGALG00000046863	AEBP1	KRT23	LEF1	GNLY	KERA	CG-1B
19	ADGRL4	METTL24	ENSGALG0000001483	ENSGALG00000053371	EGFLAM	SLC29A1	NA	GASK1B
20	C1QTNF7	ENSGALG00000003590	CPED1	F2RL2	PLXDC2	SSPN	RUNX2	PLOD1
21	SEMA5A	ENSGALG00000027159	ADSS1	COL5A2	TSKU	BTK	MMP10	NA
22	NA	ENSGALG00000045684	TMEM35B	LAMB4	DAAM2	WFDC1	ITGA8	COL6A1
23	ITGA11	CDC42EP1	IL13RA2	RAMP3	ANPEP	CAPG	ENSGALG00000050332	EDNRB2
24	TGM2v1	PRTG	ENSGALG00000048024	CYP4V2	ENSGALG00000028016	CLEC3B	LMO7	DSEL
25	COL12A1	S100A11	TWIST2	TMTC1	PLA2R1	PIK3CD	SMYD1	ANGPT2
26	CPM	ENSGALG00000046720	IL13RA1	DRP2	ARID3A	SLC16A12	ENSGALG00000012055	CORO2B
27	STX19	GUCY1A2	ENSGALG0000003522	ENSGALG00000053107	SYTL2	MEF2C	PHACTR2	DBNDD2
28	MALRD1	ARHGAP45	CMKLR1	RFLNB	PTPRE	APOA1	ADAMTS1	SIX1
29	CYSLTR1	ENSGALG00000007710	ELK3	TNNT3	LRRC17	RHOH	OAF	PGM5
30	GAS2	INSRR	HTRA1	MTUS1	CNN2	FOXF1	LY75	PLCL1
31	ENSGALG00000011172	RHOC	MYOM1	LTBP2	ENSGALG00000048258	RERG	LRMP	PTCHD1
32	PIK3AP1	PTPN7	PRDM1	PIEZ02	CXCL12	UPP1	NFKBIZ	GHR
33	PGF	ACTG2	SSTR3	MGLL	ENSGALG00000039708	CKMT1B	ENSGALG00000047761	PDK4
34	HOXD8	DNASE1L3	DUSP5	LUM	ITGB2	TRPM8	COLEC11	ENSGALG00000042388
35	ENSGALG00000054913	ENSGALG0000006708	TNFAIP2	TAGLN	BMP5	VEGFD	FBN3	NKX3-2
36	FBLN2	COL9A1	ENSGALG00000028041	ADGRD1	PLAC9	COL26A1	HAPLN1	ENSGALG00000036566
37	CLMP	BMP3						

	Term	Ont	N	n	Adj. p-value
GO:0048856	anatomical structure development	BP	648	34	3.466e-07
GO:0032502	developmental process	BP	680	34	1.045e-06
GO:0022610	biological adhesion	BP	148	13	9.838e-06
GO:0007155	cell adhesion	BP	148	13	9.838e-06
GO:0009653	anatomical structure morphogenesis	BP	307	19	1.641e-05
GO:0045229	external encapsulating structure organization	BP	33	6	4.604e-05
GO:0030198	extracellular matrix organization	BP	33	6	4.604e-05
GO:0043062	extracellular structure organization	BP	33	6	4.604e-05
GO:0032501	multicellular organismal process	BP	741	31	0.0001034
GO:0007275	multicellular organism development	BP	598	26	0.0002109

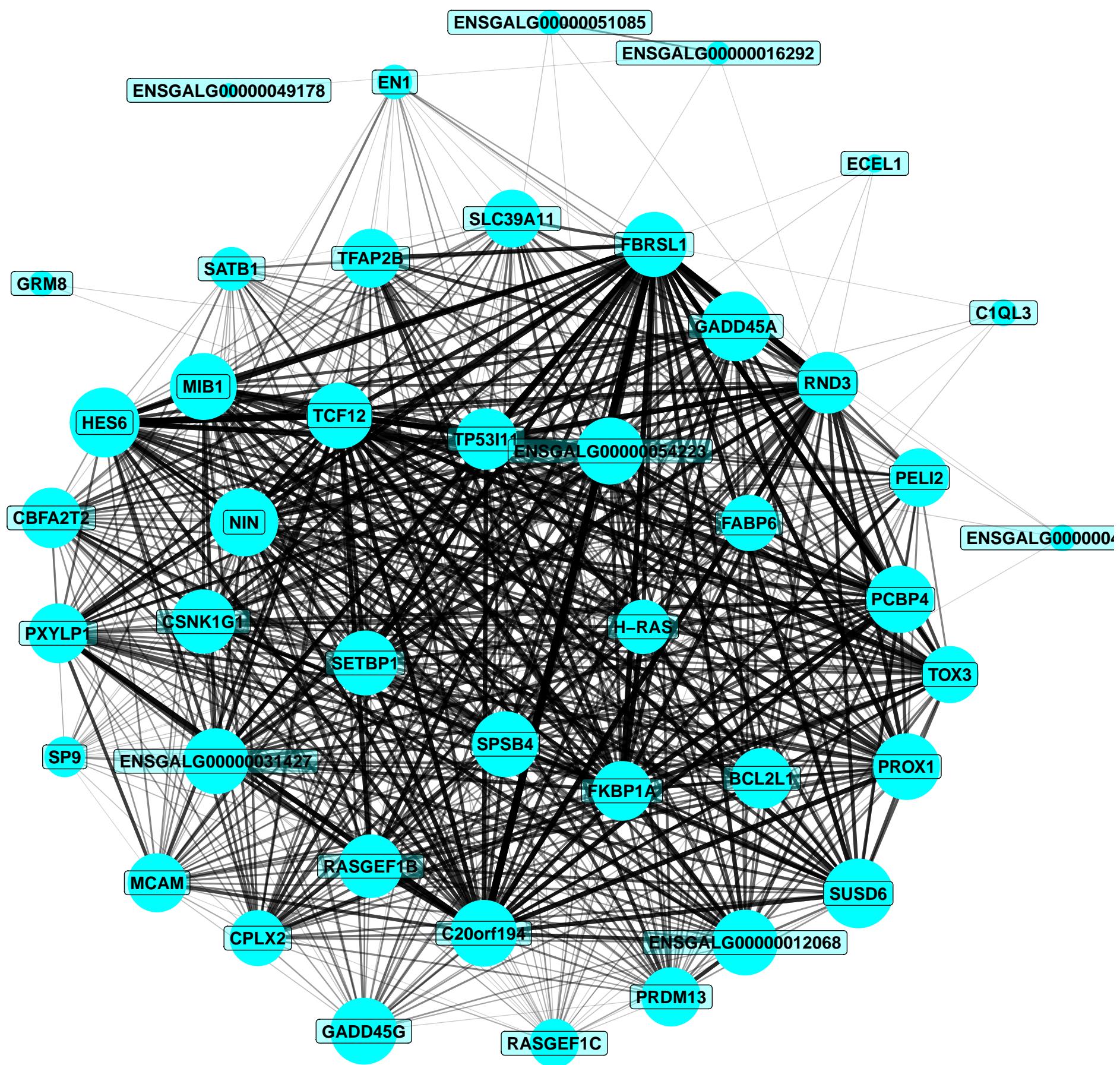
	Pathway	N	DE	P.DE
<i>path:gga04510</i>	Focal adhesion	175	23	9.734e-13
<i>path:gga04512</i>	ECM–receptor interaction	70	15	7.327e-12
<i>path:gga04270</i>	Vascular smooth muscle contraction	112	11	1.674e-05
<i>path:gga04810</i>	Regulation of actin cytoskeleton	192	14	3.724e-05
<i>path:gga04010</i>	MAPK signaling pathway	243	14	0.0004462
<i>path:gga04020</i>	Calcium signaling pathway	209	11	0.003624
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	164	9	0.00628
<i>path:gga04520</i>	Adherens junction	69	5	0.01294
<i>path:gga04672</i>	Intestinal immune network for IgA production	30	3	0.02237
<i>path:gga00360</i>	Phenylalanine metabolism	12	2	0.02366



1	ASTN1	CNTN1	SDC3	NLGN4Y	CPE	MDGA2	CNR1	SLC6A1
2	ALCAM	ENSGALG0000006851	TMEM65	KCND2	PSAP	CADM2	SEMA6A	NCAM2
3	LANCL2	NDRG4	SLC25A22	PCDH7	TENM2	CDH4	CALM1	VCAN
4	PTPRT	LRRTM4	SCD5	ANKS1B	MTSS1	RELN	ENSGALG0000006009	RYR2
5	PLPPR4	PCDH17	ARHGEF9	PCSK2	GRIK3	CACNA1C	FUT9	CHRNA7
6	ZBTB38	PTPRR	ENSGALG0000030259	ATP6V1H	NEGR1	CRIM1	NCOA7	MT3
7	IGSF21	PCP4	SYBU	PDGFA	ELMOD1	CTTNBP2	KIAA0930	LUZP2
8	FADS1	GPX3	CNTN5	ZNF703	TCERG1L	IDH1	SMS	MDGA1
9	ENSGALG0000011283	QPCT	EDIL3	FNBP1	TMEM56	GABRG3	SLC1A2	ABLIM2
10	ADCY8	VSTM2A	FKBP1B	CDH18	OSBPL5	CBLN2	TTYH3	TAFA2
11	BICD2	RNASEK	IL1RAPL2	CALB2	RSPO2	ADARB2	PCDH1	GRIN3A
12	CSMD1	ENSGALG0000054848	ANKRD26	ESRRG	SLC4A10	SOBP	PLCXD3	RAB40C
13	FARP1	LBH	TLE4	SRGAP1	HOXC9	TMEM158	UNC13B	UNC5A
14	SAMD11	FSTL4	MGAT3	KCTD8	CNTNAP5	DUSP4	PLK2	DYRK2
15	SPHKAP	ENSGALG0000032606	ENSGALG0000023179	MMP16	TRPC7	FAM135B	RPRM	ZNF804B
16	NDST4	SNX30	SST	RET	CALN1	DOK5	CNTN3	CDK14
17	APC	DLK1	KCNJ3	ST3GAL1	ADRA2A	NETO1	RYR3	NTRK3
18	CACNA1G	ST6GALNAC5	GALNTL6	GRM7	STARD5	CAPN5	PRKCA	EPN2
19	GPC3	NECAB1	STAC	TMTC4	BARHL1	TAC1	TRHDE	ACSBG2
20	FAM89A	HTR2C	ONECUT1	RSPO3	GABRA5	GNG13	VAV3	RIT2
21	GRIP2	ERBB4	HTR1B	CCNY	ENSGALG0000002671	GALNT16	PXDN	CYB561
22	NECAB2	TRPC3	HOMER2	ENSGALG0000006989	KCNH6	ASIC4	NOC4L	PTGFR
23	NR4A2	AMIGO2	NXPH2	DOC2B	ENSGALG00000052739	NPTX2	SS2	ENSGALG0000048626
24	HOXA7	CRIP2	PRICKLE1	PLXNC1	OTP	TRIM71	EPHB3	PVALB
25	KITLG	ACAP3	POU4F2	NPTX1	CDH9	CACNG5	SSTR5	BAALC
26	NRIP1	ENSGALG0000016570	VGLL3	NR5A2	ENSGALG0000049578	CRTAC1	GRIN2A	CPAMD8
27	TMEM136-1	PTCHD4	ENSGALG0000045096	ENSGALG0000044866	TSPAN18	TRAPPCL	EVX1	ADGRL2
28	AKAP9	NAV2	SYT6	ENOX1	CHRM2	CNIH3	BHLHE23	SYT10
29	SKOR2	MAFA	PAX2	HPCA	CD24	MYL4	SLC38A2	NR5A1
30	SPTSSB	UNC5C	SMAD6	BHLHE22	THSD1	ITGB3	NEUROD1	HOXC6
31	SOX14	ARHGAP15	PTPRS	LHX2	ENSGALG0000002431	FLT4	TSC22D4	CPLX3
32	C15orf61	PTPRG	CBLB	ZNF423	NHLH2	NUAK1	KLHL35	MID1
33	ENSGALG0000053318	MYO1B	EPB41L4A	HOXB2	ENSGALG0000047323	EBF2	ENSGALG0000023640	CASS4
34	ST18	LZTS1	TOX	NHLH1	ZIC1			

	Term	Ont	N	n	Adj. p-value
GO:0022610	biological adhesion	BP	148	15	1.648e-07
GO:0007155	cell adhesion	BP	148	15	1.648e-07
GO:0048699	generation of neurons	BP	185	14	1.372e-05
GO:0007399	nervous system development	BP	266	17	1.563e-05
GO:0022008	neurogenesis	BP	188	14	1.646e-05
GO:0009653	anatomical structure morphogenesis	BP	307	17	9.502e-05
GO:0030182	neuron differentiation	BP	169	12	0.0001049
GO:0048666	neuron development	BP	129	10	0.0001935
GO:0048731	system development	BP	501	22	0.0002771
GO:0000904	cell morphogenesis involved in differentiation	BP	89	8	0.0003108

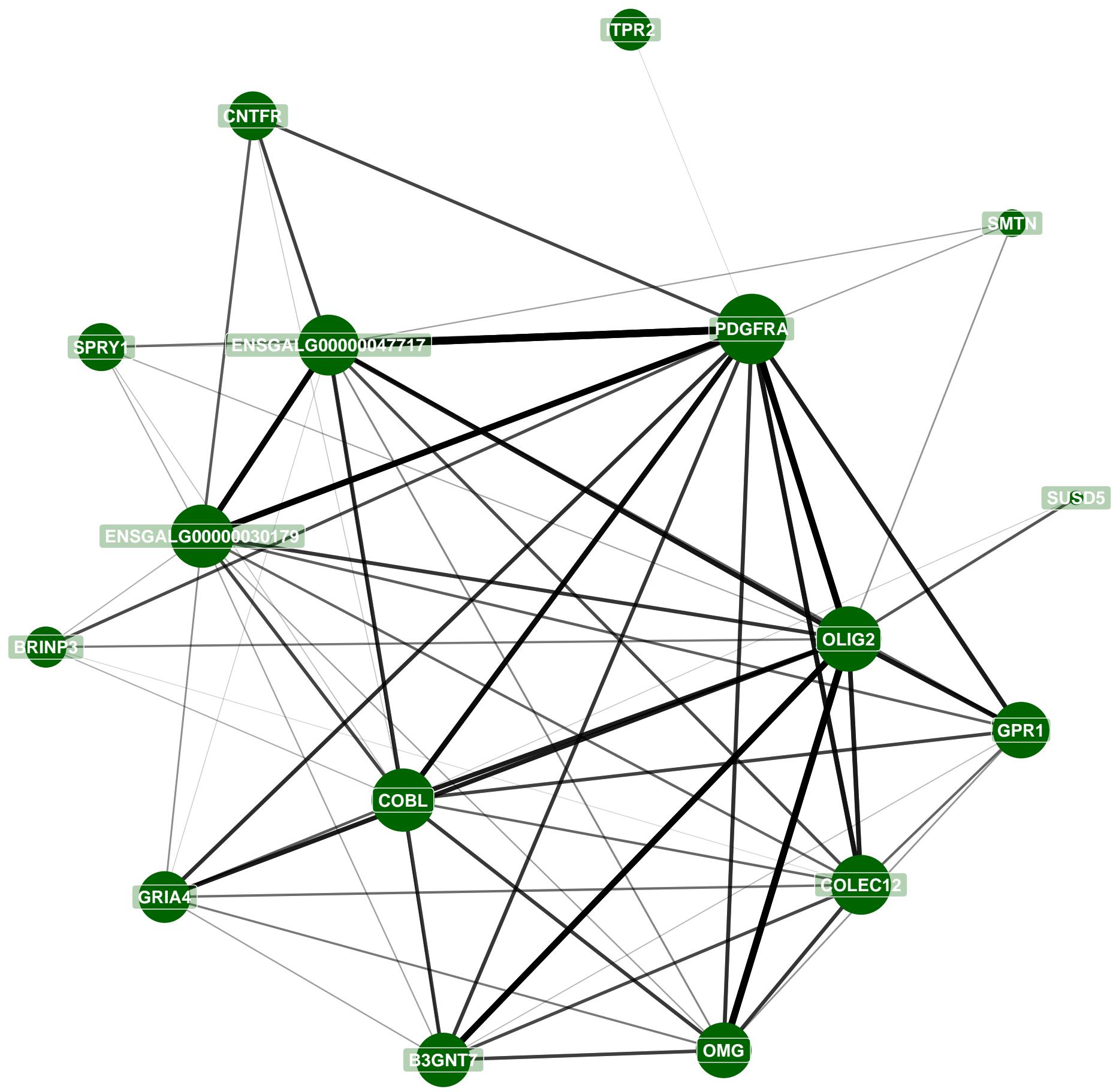
	Pathway	N	DE	P.DE
<i>path:gga04020</i>	Calcium signaling pathway	209	17	5.956e-07
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	309	18	3.054e-05
<i>path:gga04514</i>	Cell adhesion molecules	110	9	0.0002694
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	125	7	0.01051
<i>path:gga00512</i>	Mucin type O–glycan biosynthesis	29	3	0.0178
<i>path:gga04310</i>	Wnt signaling pathway	139	7	0.01798
<i>path:gga04010</i>	MAPK signaling pathway	243	10	0.01939
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	2	0.02144
<i>path:gga04371</i>	Apelin signaling pathway	114	6	0.0228
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	2	0.02502



1	PROX1	GADD45G	NIN	HES6	GADD45A	SUSD6	ENSGALG00000012068	ENSGALG00000054223
2	C20orf194	TCF12	FBRSL1	RND3	RASGEF1B	PCBP4	MIB1	ENSGALG00000031427
3	SPSB4	PXYLP1	SETBP1	TP53I11	TFAP2B	FABP6	CSNK1G1	MCAM
4	TOX3	FKBP1A	PRDM13	BCL2L1	CBFA2T2	CPLX2	PELI2	H-RAS
5	SLC39A11	SATB1	RASGEF1C	SP9	EN1	ENSGALG00000049455	GRM8	C1QL3
6	ENSGALG00000016292	ENSGALG00000051085	ENSGALG00000049178	ECEL1				

	Term	Ont	N	n	Adj. p-value
GO:0071480	cellular response to gamma radiation	BP	7	2	0.0001603
GO:0010332	response to gamma radiation	BP	8	2	0.0002134
GO:0071479	cellular response to ionizing radiation	BP	10	2	0.0003418
GO:0043524	negative regulation of neuron apoptotic process	BP	15	2	0.0007904
GO:1901215	negative regulation of neuron death	BP	17	2	0.00102
GO:0010212	response to ionizing radiation	BP	20	2	0.001418
GO:0071478	cellular response to radiation	BP	21	2	0.001564
GO:0043523	regulation of neuron apoptotic process	BP	21	2	0.001564
GO:0097193	intrinsic apoptotic signaling pathway	BP	23	2	0.001878
GO:0051402	neuron apoptotic process	BP	23	2	0.001878

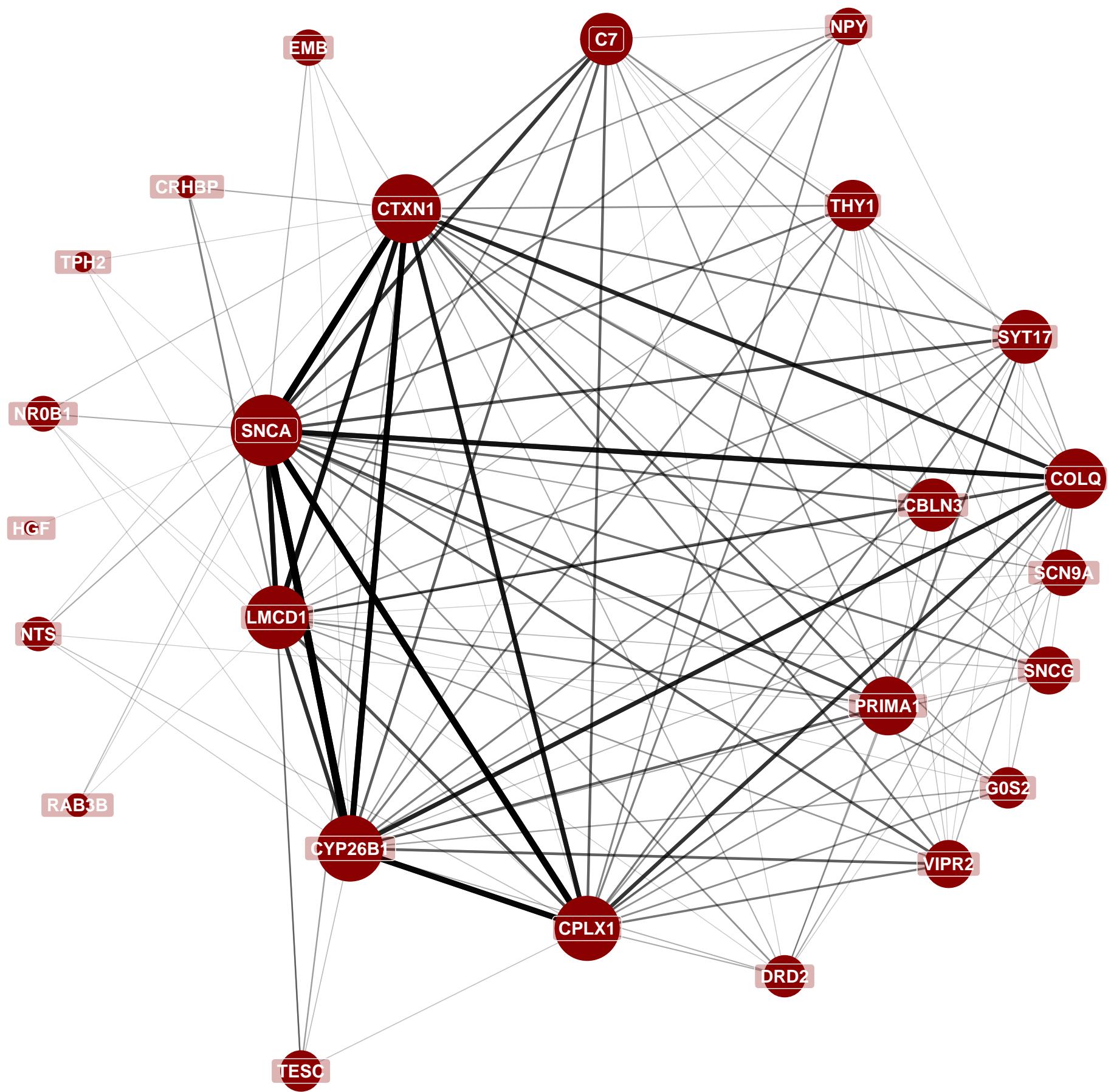
	Pathway	N	DE	P.DE
<i>path:gga04210</i>	Apoptosis	118	4	0.0003245
<i>path:gga04115</i>	p53 signaling pathway	63	3	0.0007257
<i>path:gga04068</i>	FoxO signaling pathway	118	3	0.004386
<i>path:gga04218</i>	Cellular senescence	135	3	0.006376
<i>path:gga04137</i>	Mitophagy – animal	62	2	0.0131
<i>path:gga04010</i>	MAPK signaling pathway	243	3	0.03054
<i>path:gga04110</i>	Cell cycle	115	2	0.04139
<i>path:gga04140</i>	Autophagy – animal	126	2	0.04878
<i>path:gga04340</i>	Hedgehog signaling pathway	48	1	0.1267
<i>path:gga04370</i>	VEGF signaling pathway	54	1	0.1414



1	PDGFRA	OLIG2	ENSGALG00000047717	COLEC12	COBL	OMG	ENSGALG00000030179	B3GNT7
2	GPR1	GRIA4	SMTN	CNTFR	SPRY1	ITPR2	SUSD5	BRINP3
3								

	Term	Ont	N	n	Adj. p-value
GO:0021780	glial cell fate specification	BP	1	1	0.001184
GO:0021779	oligodendrocyte cell fate commitment	BP	1	1	0.001184
GO:0021778	oligodendrocyte cell fate specification	BP	1	1	0.001184
GO:0035790	platelet-derived growth factor receptor-alpha signaling pathway	BP	1	1	0.001184
GO:0021529	spinal cord oligodendrocyte cell differentiation	BP	1	1	0.001184
GO:0021530	spinal cord oligodendrocyte cell fate specification	BP	1	1	0.001184
GO:0021794	thalamus development	BP	1	1	0.001184
GO:0070120	ciliary neurotrophic factor-mediated signaling pathway	BP	2	1	0.002367
GO:0021781	glial cell fate commitment	BP	2	1	0.002367
GO:0048714	positive regulation of oligodendrocyte differentiation	BP	3	1	0.003549

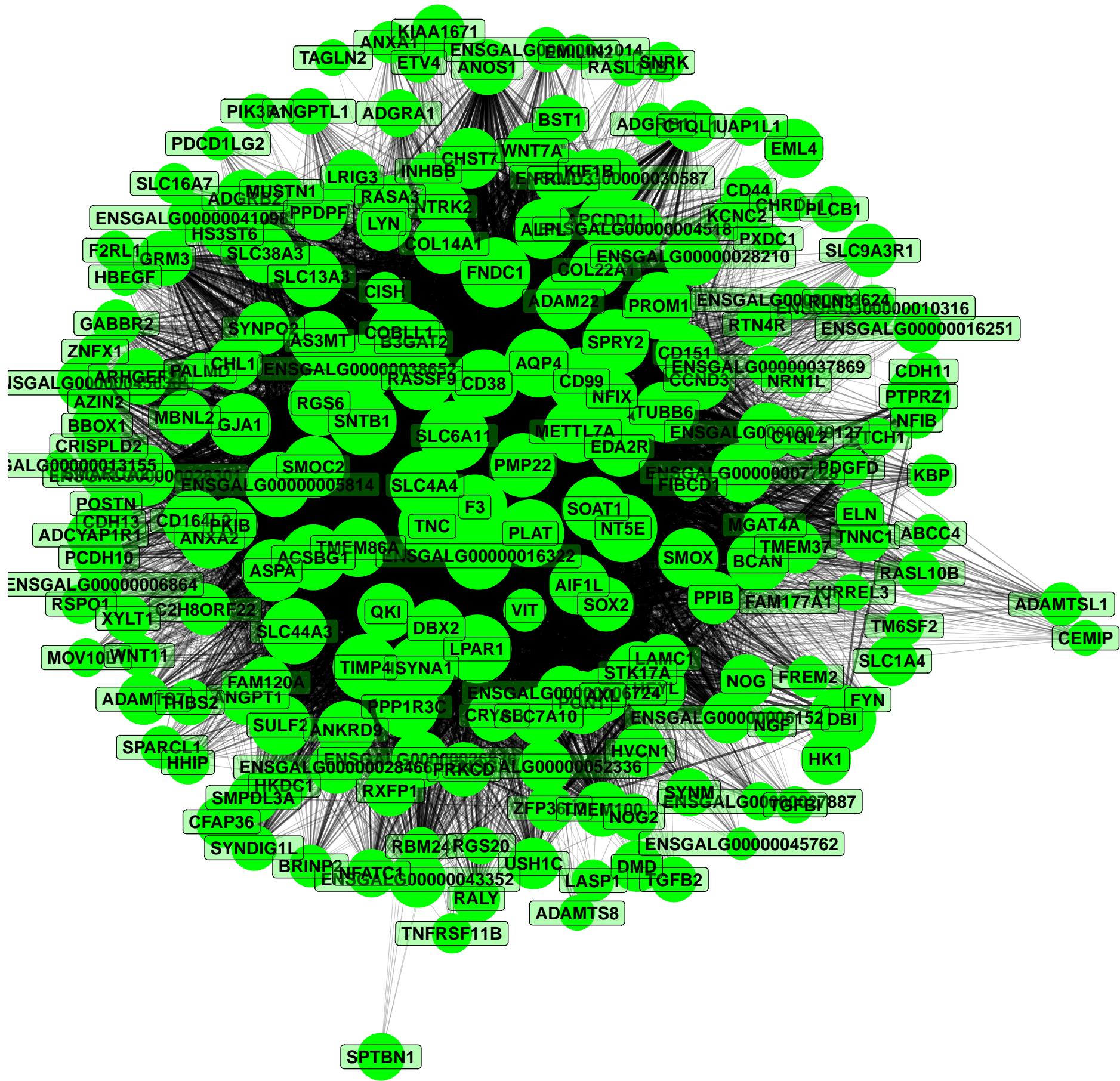
	Pathway	N	DE	P.DE
<i>path:gga04540</i>	Gap junction	80	2	0.003938
<i>path:gga04371</i>	Apelin signaling pathway	114	2	0.00784
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.01646
<i>path:gga04020</i>	Calcium signaling pathway	209	2	0.02478
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	309	2	0.05067
<i>path:gga04912</i>	GnRH signaling pathway	78	1	0.08853
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	85	1	0.0961
<i>path:gga04070</i>	Phosphatidylinositol signaling system	88	1	0.09933
<i>path:gga04114</i>	Oocyte meiosis	98	1	0.11
<i>path:gga04514</i>	Cell adhesion molecules	110	1	0.1227



1	SNCA	COLQ	SYT17	DRD2	CTXN1	CYP26B1	CPLX1	LMCD1
2	C7	G0S2	SNCG	PRIMA1	CBLN3	VIPR2	SCN9A	THY1
3	EMB	NTS	TESC	NPY	NR0B1	HGF	RAB3B	TPH2
4	CRHBP							

	Term	Ont	N	n	Adj. p-value
GO:1904064	positive regulation of cation transmembrane transport	BP	5	2	2.764e-05
GO:0034767	positive regulation of ion transmembrane transport	BP	8	2	7.715e-05
GO:0034764	positive regulation of transmembrane transport	BP	8	2	7.715e-05
GO:1904062	regulation of cation transmembrane transport	BP	12	2	0.0001811
GO:0006469	negative regulation of protein kinase activity	BP	20	2	0.000517
GO:0033673	negative regulation of kinase activity	BP	21	2	0.0005709
GO:0051348	negative regulation of transferase activity	BP	24	2	0.000748
GO:0001933	negative regulation of protein phosphorylation	BP	26	2	0.0008789
GO:0042326	negative regulation of phosphorylation	BP	31	2	0.001251
GO:0034765	regulation of ion transmembrane transport	BP	31	2	0.001251

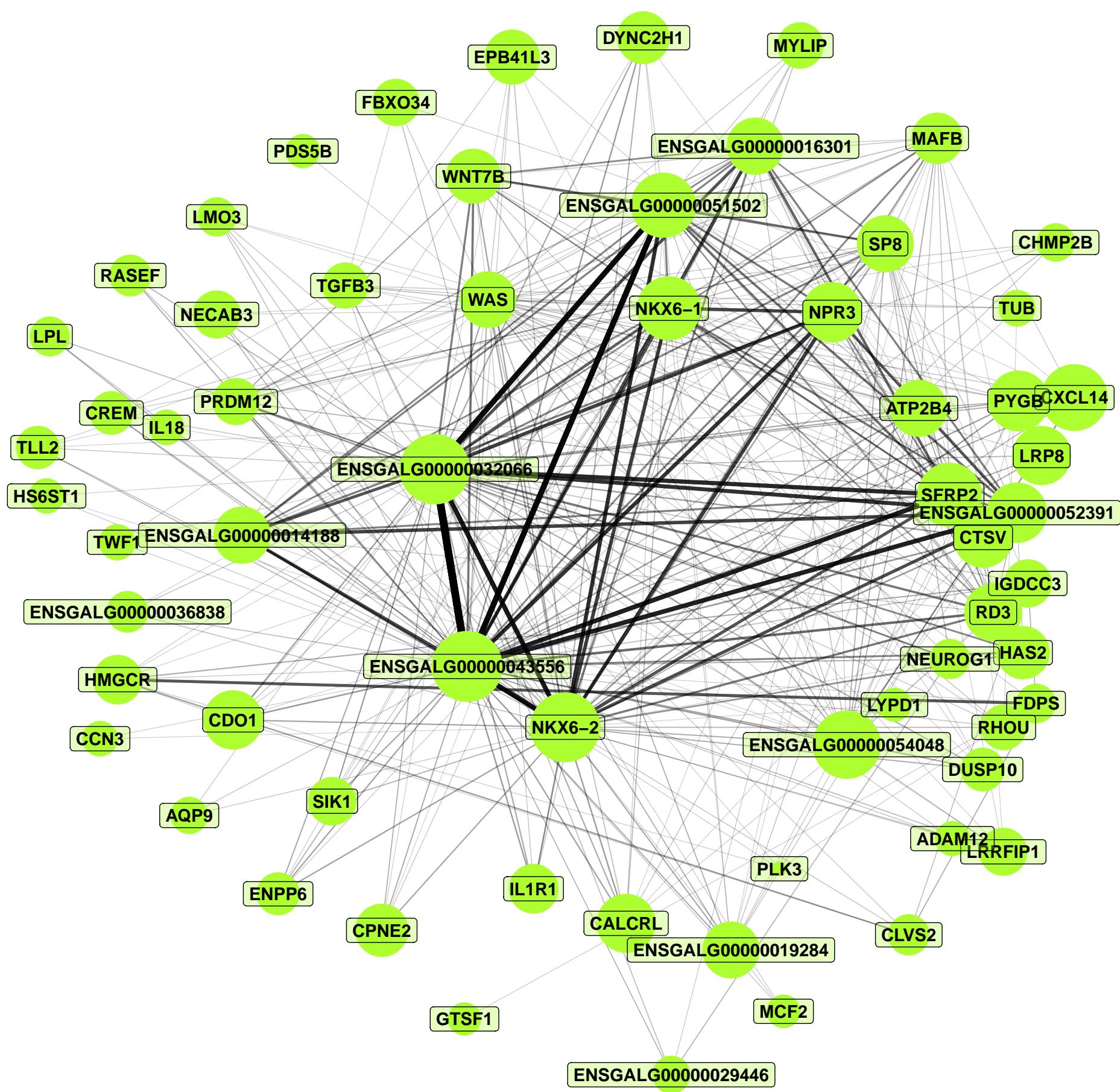
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	309	4	0.001685
<i>path:gga00790</i>	Folate biosynthesis	26	1	0.04337
<i>path:gga00830</i>	Retinol metabolism	33	1	0.05474
<i>path:gga00380</i>	Tryptophan metabolism	35	1	0.05796
<i>path:gga04920</i>	Adipocytokine signaling pathway	61	1	0.09893
<i>path:gga04540</i>	Gap junction	80	1	0.1278
<i>path:gga04510</i>	Focal adhesion	175	1	0.2593
<i>path:gga04810</i>	Regulation of actin cytoskeleton	192	1	0.2807
<i>path:gga04020</i>	Calcium signaling pathway	209	1	0.3015
<i>path:gga04010</i>	MAPK signaling pathway	243	1	0.3415



1	TNC	SLC6A11	FNDC1	AQP4	CD38	SLC4A4	NT5E	ENSGALG00000038652
2	SNTB1	LPAR1	ENSGALG00000016322	PMP22	PLAT	ISYNA1	BCAN	PROM1
3	GJA1	ACSBG1	RGS6	TIMP4	B3GAT2	CD99	SMOC2	SLC13A3
4	DBI	RASSF9	SLC44A3	SULF2	F3	HEYL	PTPRZ1	PON1
5	ENSGALG0000005814	SPRY2	APCDD1L	COBL1	METTL7A	COL14A1	DBX2	PPP1R3C
6	TUBB6	ANXA2	STK17A	AIF1L	SOAT1	ASPA	CD164L2	NFIX
7	ANGPT1	QKI	SYNPO2	LAMC1	CHST7	SLC7A10	CRYAB	ENSGALG00000028301
8	ENSGALG00000030587	ENSGALG00000028210	SOX2	SLC38A3	EDA2R	CD151	ALPL	FRMD3
9	ENSGALG0000007728	ENSGALG00000045636	ENSGALG00000026836	SMOX	ANOS1	EML4	AS3MT	ANKRD9
10	SLC9A3R1	CCND3	NOG	WNT7A	ENSGALG00000043352	TNNC1	ENSGALG00000049127	ARHGEF26
11	PRKCD	ADGRB2	ENSGALG0000004518	ENSGALG0000006724	RSPO1	FAM120A	KIAA1671	PPIB
12	TGFB2	LYN	LRIG3	SLC1A4	GRM3	TMEM86A	ADAM22	TMEM100
13	ZFP36L2	COL22A1	ENSGALG00000028466	CHL1	C2H8ORF22	USH1C	PPDPF	CDH13
14	ADAMTS7	PKIB	AXL	PCDH10	C1QL1	SMPDL3A	HVCN1	TMEM37
15	ENSGALG00000052336	PLCB1	HKDC1	NTRK2	NOG2	SYNM	DMD	MBNL2
16	SMARCA2	RXFP1	SPARCL1	NFATC1	NFIB	CFAP36	BBOX1	ANGPTL1
17	ENSGALG00000041098	VIT	XYLT1	ENSGALG0000006152	BRINP2	SYNDIG1L	BST1	ENSGALG00000016251
18	HS3ST6	KCNC2	ENSGALG00000010316	F2RL1	C1QL2	PTCH1	RALY	ADGRA1
19	ELN	CRISPLD2	ETV4	HHIP	ENSGALG00000037869	ADCYAP1R1	TNFRSF11B	GABBR2
20	RBM24	CD44	HK1	PDGFD	SPTBN1	ADGRB1	CDH11	KBP
21	THBS2	LASP1	ADAMTSL1	ENSGALG00000041014	ANXA1	MGAT4A	EMILIN2	ENSGALG0000006864
22	KIF1B	WNT11	RASL10B	TGFBI	MUSTN1	TM6SF2	RTN4R	RASA3
23	POSTN	CEMIP	PIK3R1	ENSGALG00000013155	INHBB	KIRREL3	CISH	RASL11B
24	TAGLN2	FYN	SNRK	FREM2	ABCC4	HBEGF	FAM177A1	ENSGALG00000013624
25	CHRDL1	SLC16A7	UAP1L1	RLN3	MOV10L1	NRN1L	ENSGALG00000027887	FIBCD1
26	ADAMTS8	PXDC1	NGF	PALMD	AZIN2	RGS20	ENSGALG00000045762	ZNFX1
27	PDCD1LG2							

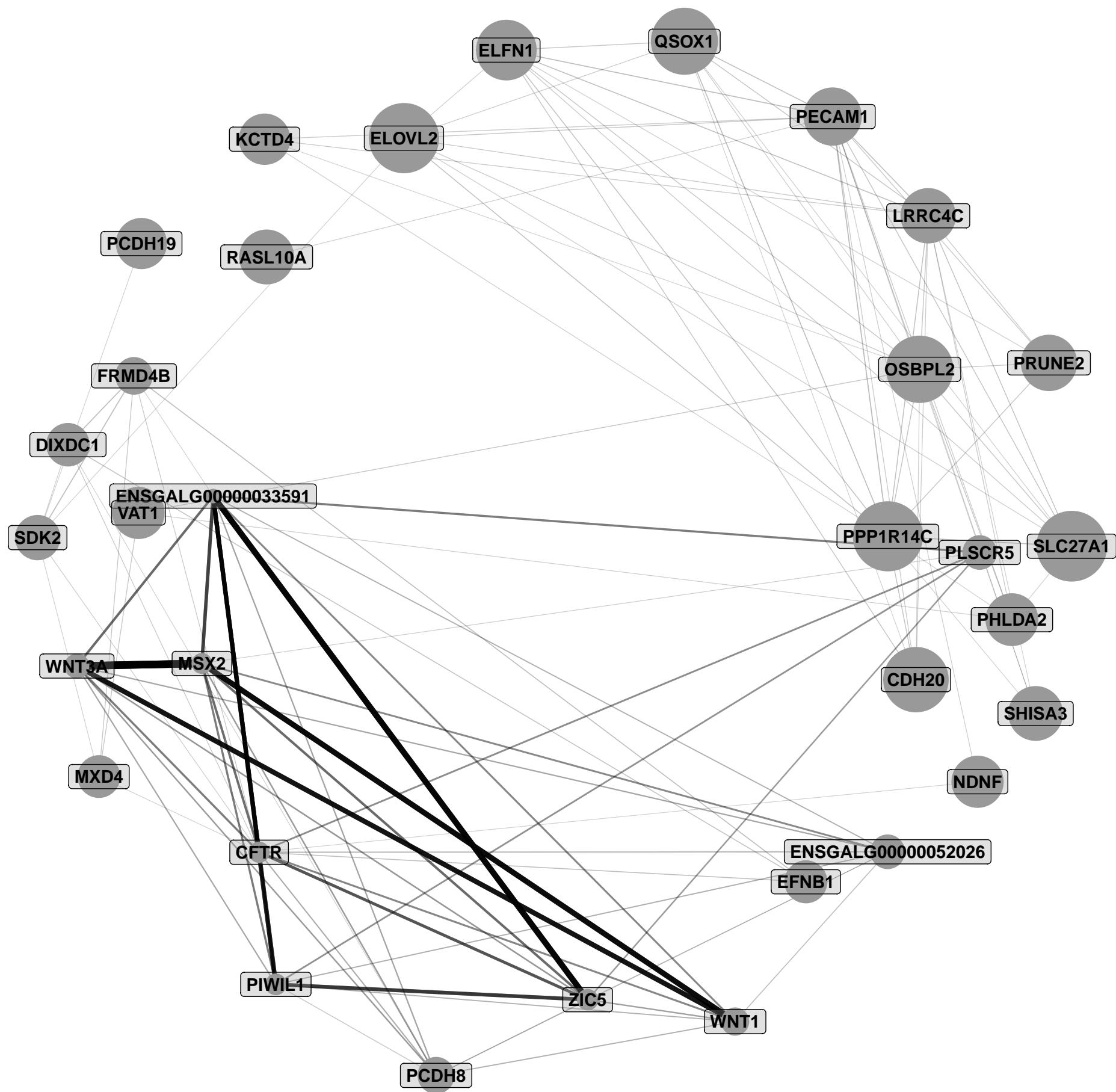
	Term	Ont	N	n	Adj. p-value
GO:0050793	regulation of developmental process	BP	224	14	7.283e-06
GO:0007275	multicellular organism development	BP	598	24	1.107e-05
GO:0023051	regulation of signaling	BP	273	15	1.61e-05
GO:0007167	enzyme linked receptor protein signaling pathway	BP	127	10	2.137e-05
GO:0048731	system development	BP	501	21	2.148e-05
GO:0030199	collagen fibril organization	BP	12	4	2.229e-05
GO:0051246	regulation of protein metabolic process	BP	248	14	2.301e-05
GO:0006928	movement of cell or subcellular component	BP	186	12	2.426e-05
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	BP	81	8	2.846e-05
GO:0048870	cell motility	BP	132	10	2.988e-05

	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	70	6	0.0006301
<i>path:gga00524</i>	Neomycin, kanamycin and gentamicin biosynthesis	5	2	0.002181
<i>path:gga04310</i>	Wnt signaling pathway	139	7	0.005015
<i>path:gga04540</i>	Gap junction	80	5	0.00705
<i>path:gga00760</i>	Nicotinate and nicotinamide metabolism	33	3	0.01309
<i>path:gga01250</i>	Biosynthesis of nucleotide sugars	35	3	0.01537
<i>path:gga04510</i>	Focal adhesion	175	7	0.01659
<i>path:gga00330</i>	Arginine and proline metabolism	40	3	0.02197
<i>path:gga00532</i>	Glycosaminoglycan biosynthesis – chondroitin sulfate / dermatan sulfate	17	2	0.02635
<i>path:gga00520</i>	Amino sugar and nucleotide sugar metabolism	46	3	0.03163



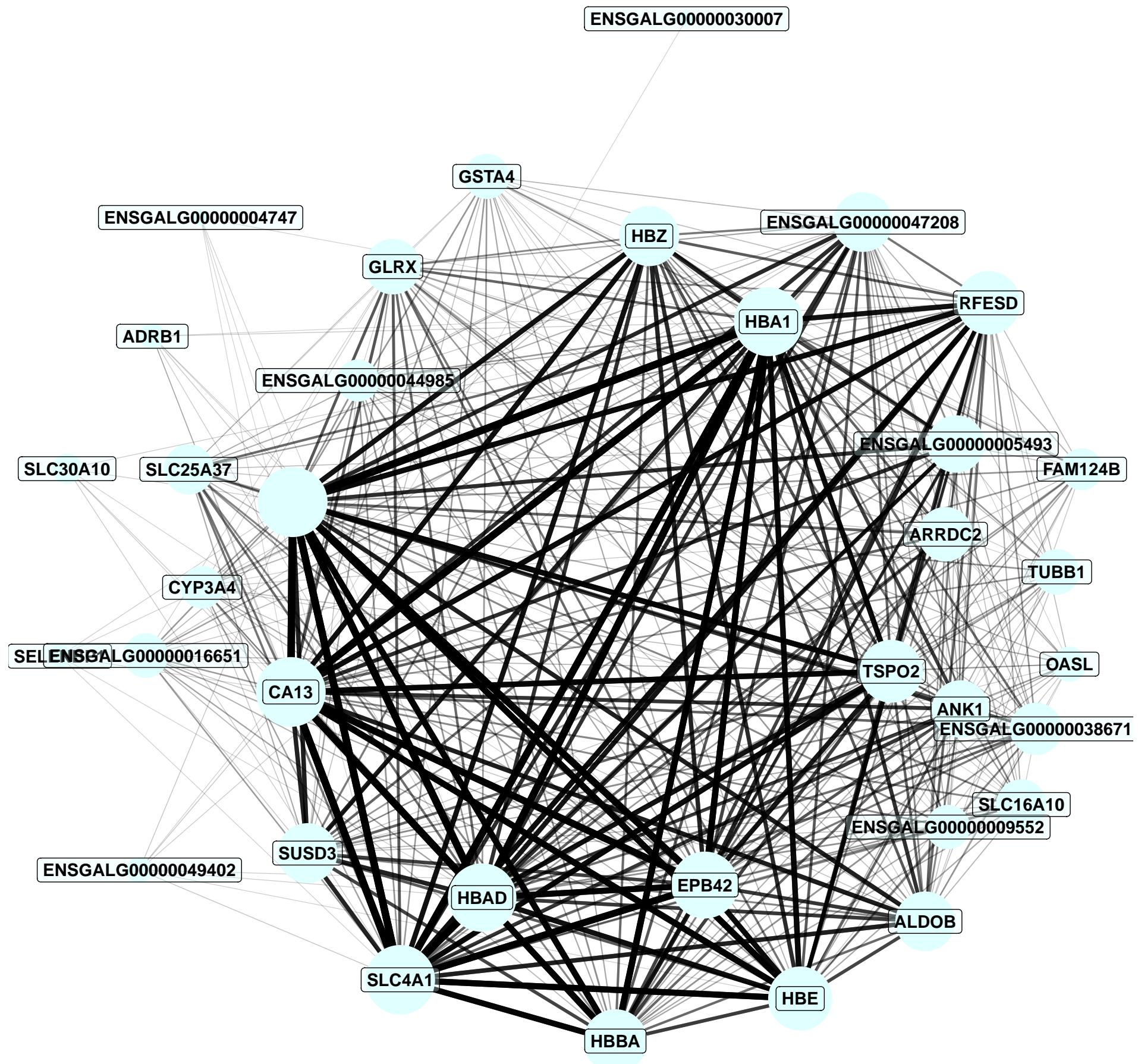
	Term	Ont	N	n	Adj. p-value
GO:0060317	cardiac epithelial to mesenchymal transition	BP	11	2	0.00104
GO:0001817	regulation of cytokine production	BP	47	3	0.001175
GO:0032501	multicellular organismal process	BP	741	10	0.001443
GO:0001816	cytokine production	BP	51	3	0.00149
GO:0032502	developmental process	BP	680	9	0.002905
GO:0030154	cell differentiation	BP	435	7	0.003028
GO:0048869	cellular developmental process	BP	444	7	0.003392
GO:0001775	cell activation	BP	73	3	0.004154
GO:0021560	abducens nerve development	BP	1	1	0.004441
GO:0021599	abducens nerve formation	BP	1	1	0.004441

	Pathway	N	DE	P.DE
<i>path:gga00900</i>	Terpenoid backbone biosynthesis	19	2	0.003159
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	164	4	0.006022
<i>path:gga00561</i>	Glycerolipid metabolism	55	2	0.02477
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	1	0.05203
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis – heparan sulfate / heparin	21	1	0.0893
<i>path:gga00040</i>	Pentose and glucuronate interconversions	21	1	0.0893
<i>path:gga04217</i>	Necroptosis	114	2	0.09113
<i>path:gga04010</i>	MAPK signaling pathway	243	3	0.09335
<i>path:gga04068</i>	FoxO signaling pathway	118	2	0.0966
<i>path:gga05164</i>	Influenza A	121	2	0.1008



	Term	Ont	N	n	Adj. p-value
GO:0048263	determination of dorsal identity	BP	6	2	8.105e-05
GO:0048262	determination of dorsal/ventral asymmetry	BP	6	2	8.105e-05
GO:0007275	multicellular organism development	BP	598	7	0.0004111
GO:0009953	dorsal/ventral pattern formation	BP	16	2	0.0006389
GO:0048856	anatomical structure development	BP	648	7	0.0006656
GO:0009855	determination of bilateral symmetry	BP	17	2	0.000723
GO:0009799	specification of symmetry	BP	17	2	0.000723
GO:0032502	developmental process	BP	680	7	0.0008858
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	BP	22	2	0.001219
GO:0032501	multicellular organismal process	BP	741	7	0.001464

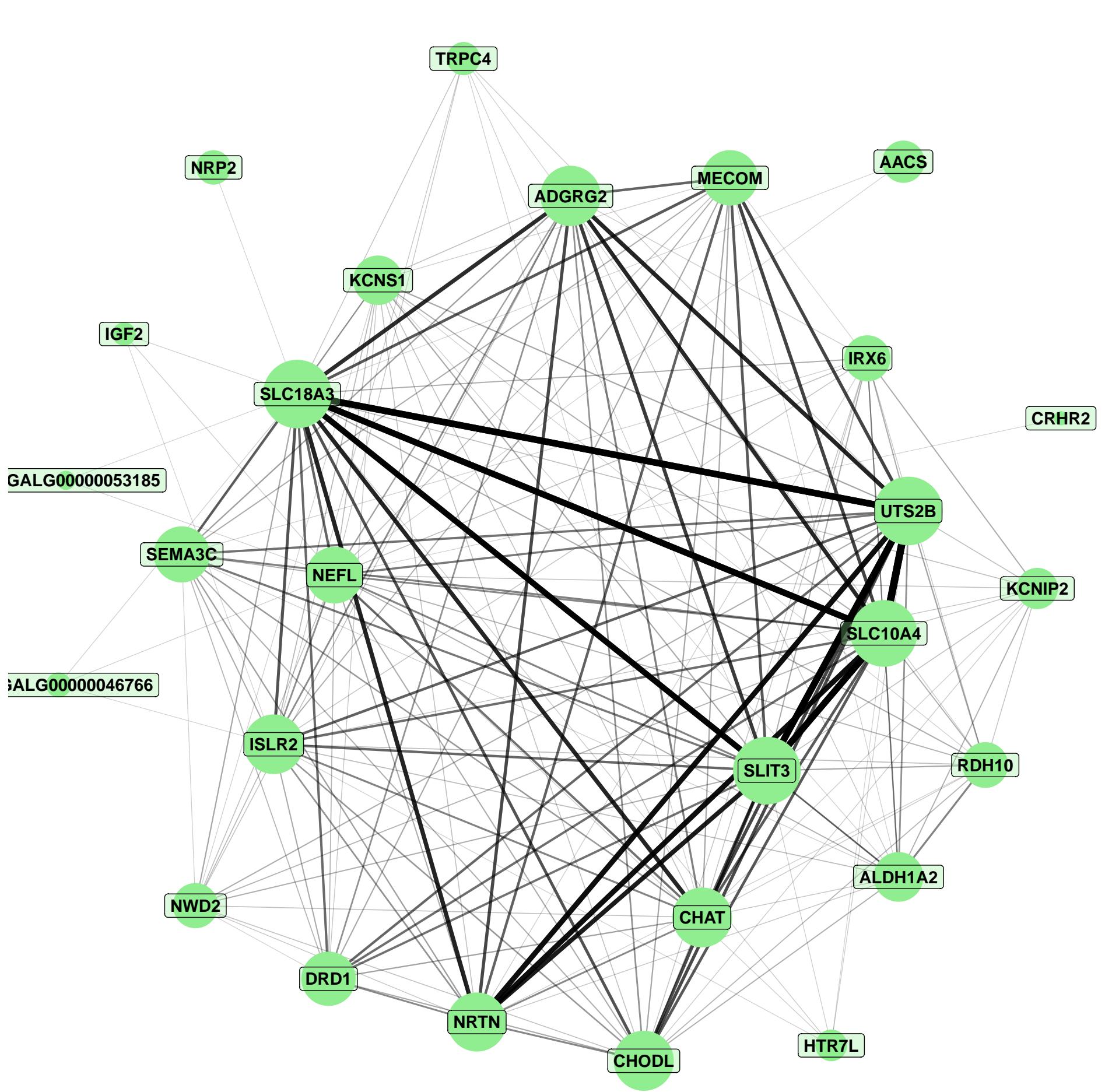
	Pathway	N	DE	P.DE
<i>path:gga04916</i>	Melanogenesis	88	2	0.01833
<i>path:gga04514</i>	Cell adhesion molecules	110	2	0.0278
<i>path:gga04150</i>	mTOR signaling pathway	138	2	0.04208
<i>path:gga04310</i>	Wnt signaling pathway	139	2	0.04263
<i>path:gga00062</i>	Fatty acid elongation	23	1	0.05312
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	28	1	0.06431
<i>path:gga02010</i>	ABC transporters	37	1	0.08411
<i>path:gga01212</i>	Fatty acid metabolism	51	1	0.1141
<i>path:gga03320</i>	PPAR signaling pathway	59	1	0.1308
<i>path:gga04530</i>	Tight junction	138	1	0.2803



1	SLC4A1	NA	CA13	HBAD	HBA1	EPB42	HBE	RFESD
2	TSPO2	HBBA	ALDOB	SUSD3	ENSGALG00000047208	ANK1	GLRX	ENSGALG0000005493
3	HBZ	CYP3A4	ENSGALG00000044985	ARRDC2	SLC25A37	ENSGALG0000009552	TUBB1	GSTA4
4	ENSGALG00000038671	SLC16A10	FAM124B	ENSGALG00000016651	ADRB1	SLC30A10	ENSGALG00000030007	OASL
5	ENSGALG0000004747	ENSGALG00000049402	SELENBP1					

	Term	Ont	N	n	Adj. p-value
GO:0042744	hydrogen peroxide catabolic process	BP	7	5	9.49e-13
GO:0042743	hydrogen peroxide metabolic process	BP	7	5	9.49e-13
GO:0015671	oxygen transport	BP	7	5	9.49e-13
GO:0015669	gas transport	BP	8	5	2.527e-12
GO:0098869	cellular oxidant detoxification	BP	14	5	8.946e-11
GO:1990748	cellular detoxification	BP	16	5	1.946e-10
GO:0097237	cellular response to toxic substance	BP	16	5	1.946e-10
GO:0098754	detoxification	BP	17	5	2.752e-10
GO:0009636	response to toxic substance	BP	20	5	6.862e-10
GO:0072593	reactive oxygen species metabolic process	BP	21	5	8.991e-10

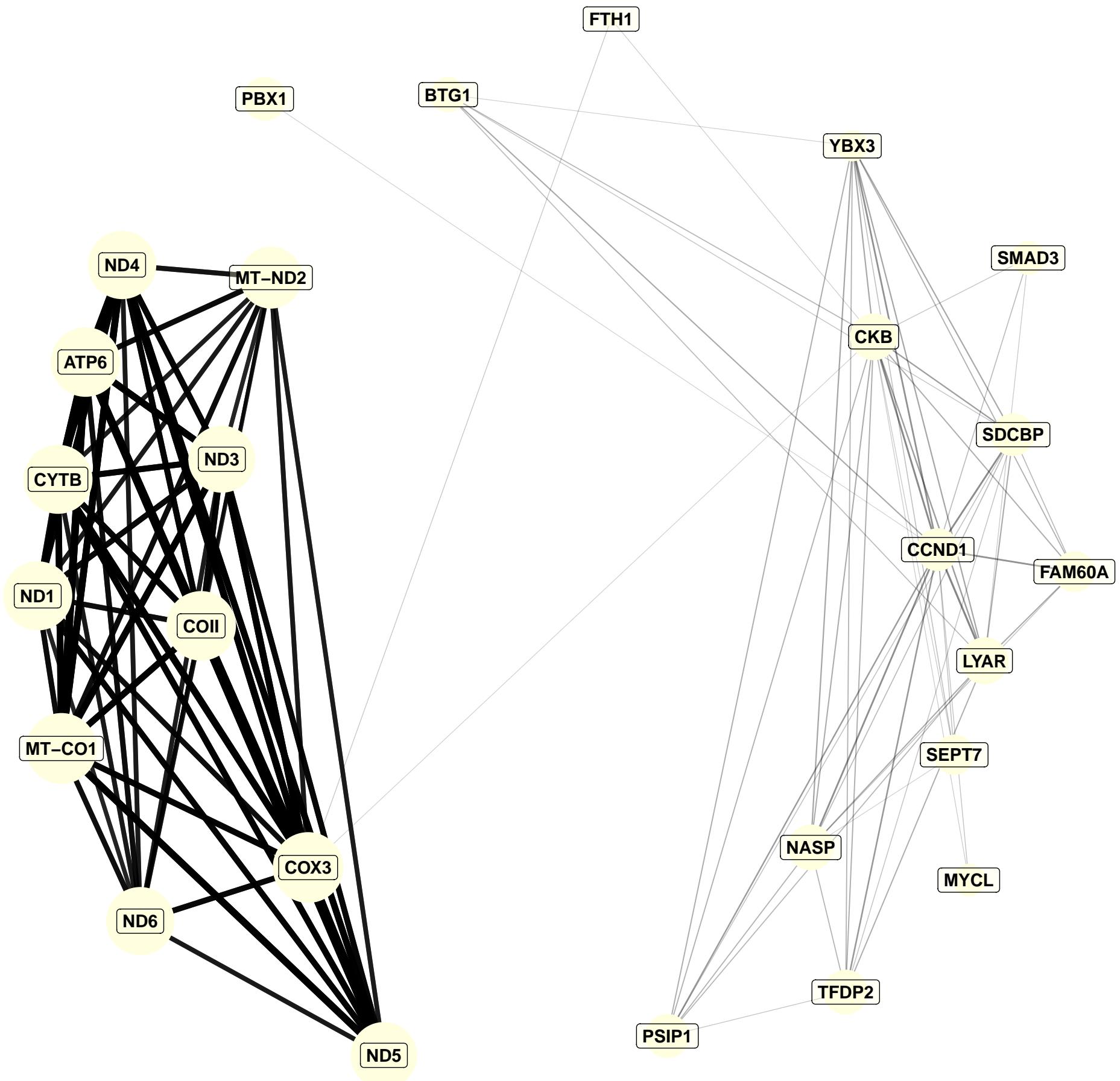
	Pathway	N	DE	P.DE
<i>path:gga04540</i>	Gap junction	80	2	0.01441
<i>path:gga00920</i>	Sulfur metabolism	8	1	0.01821
<i>path:gga00910</i>	Nitrogen metabolism	14	1	0.03166
<i>path:gga00591</i>	Linoleic acid metabolism	22	1	0.04932
<i>path:gga00030</i>	Pentose phosphate pathway	25	1	0.05586
<i>path:gga00140</i>	Steroid hormone biosynthesis	28	1	0.06236
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	1	0.06451
<i>path:gga01100</i>	Metabolic pathways	1279	6	0.0673
<i>path:gga00260</i>	Glycine, serine and threonine metabolism	31	1	0.06881
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	31	1	0.06881



1	SLC18A3	UTS2B	SLC10A4	SLIT3	CHAT	ISLR2	NEFL	ADGRG2
2	NRTN	CHODL	DRD1	SEMA3C	ALDH1A2	KCNS1	IRX6	MECOM
3	NRP2	KCNIP2	RDH10	NWD2	AACS	HTR7L	TRPC4	IGF2
4	ENSGALG00000053185	ENSGALG00000046766	CRHR2					

	Term	Ont	N	n	Adj. p-value
GO:0043434	response to peptide hormone	BP	31	2	0.001251
GO:1901652	response to peptide	BP	35	2	0.001594
GO:0016102	diterpenoid biosynthetic process	BP	1	1	0.001702
GO:0031017	exocrine pancreas development	BP	1	1	0.001702
GO:0038028	insulin receptor signaling pathway via phosphatidylinositol 3-kinase	BP	1	1	0.001702
GO:2000467	positive regulation of glycogen (starch) synthase activity	BP	1	1	0.001702
GO:0048633	positive regulation of skeletal muscle tissue growth	BP	1	1	0.001702
GO:2000465	regulation of glycogen (starch) synthase activity	BP	1	1	0.001702
GO:0002138	retinoic acid biosynthetic process	BP	1	1	0.001702
GO:0010817	regulation of hormone levels	BP	47	2	0.002861

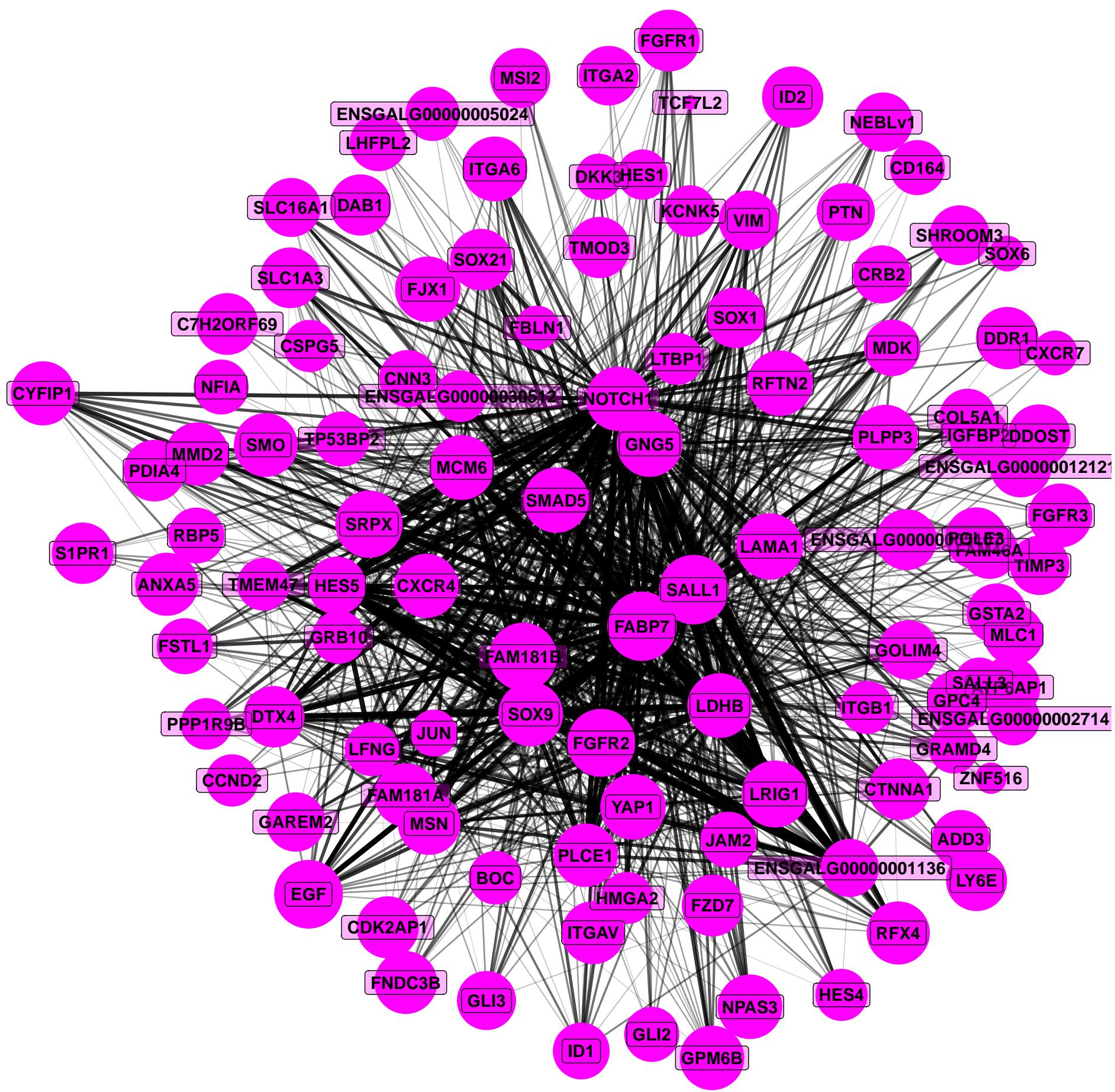
	Pathway	N	DE	P.DE
<i>path:gga00830</i>	Retinol metabolism	33	2	0.001418
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	309	4	0.001685
<i>path:gga00650</i>	Butanoate metabolism	21	1	0.03517
<i>path:gga04020</i>	Calcium signaling pathway	209	2	0.04871
<i>path:gga04010</i>	MAPK signaling pathway	243	2	0.06364
<i>path:gga00280</i>	Valine, leucine and isoleucine degradation	43	1	0.07075
<i>path:gga00310</i>	Lysine degradation	50	1	0.08181
<i>path:gga04540</i>	Gap junction	80	1	0.1278
<i>path:gga00564</i>	Glycerophospholipid metabolism	88	1	0.1397
<i>path:gga01100</i>	Metabolic pathways	1279	4	0.1677



1	MT-CO1	COX3	ATP6	ND1	COII	CYTB	ND4	ND5
2	ND3	ND6	MT-ND2	FTH1	SEPT7	NASP	PBX1	CKB
3	LYAR	CCND1	PSIP1	TFDP2	SDCBP	YBX3	FAM60A	BTG1
4	SMAD3	MYCL						

	Term	Ont	N	n	Adj. p-value
GO:0045930	negative regulation of mitotic cell cycle	BP	22	3	1.684e-06
GO:0007346	regulation of mitotic cell cycle	BP	36	3	7.735e-06
GO:0045786	negative regulation of cell cycle	BP	46	3	1.633e-05
GO:0042127	regulation of cell population proliferation	BP	154	4	2.01e-05
GO:0008283	cell population proliferation	BP	179	4	3.629e-05
GO:0008285	negative regulation of cell population proliferation	BP	64	3	4.43e-05
GO:0007050	cell cycle arrest	BP	13	2	8.912e-05
GO:0048523	negative regulation of cellular process	BP	469	5	0.000111
GO:0048519	negative regulation of biological process	BP	498	5	0.0001474
GO:0048522	positive regulation of cellular process	BP	512	5	0.0001679

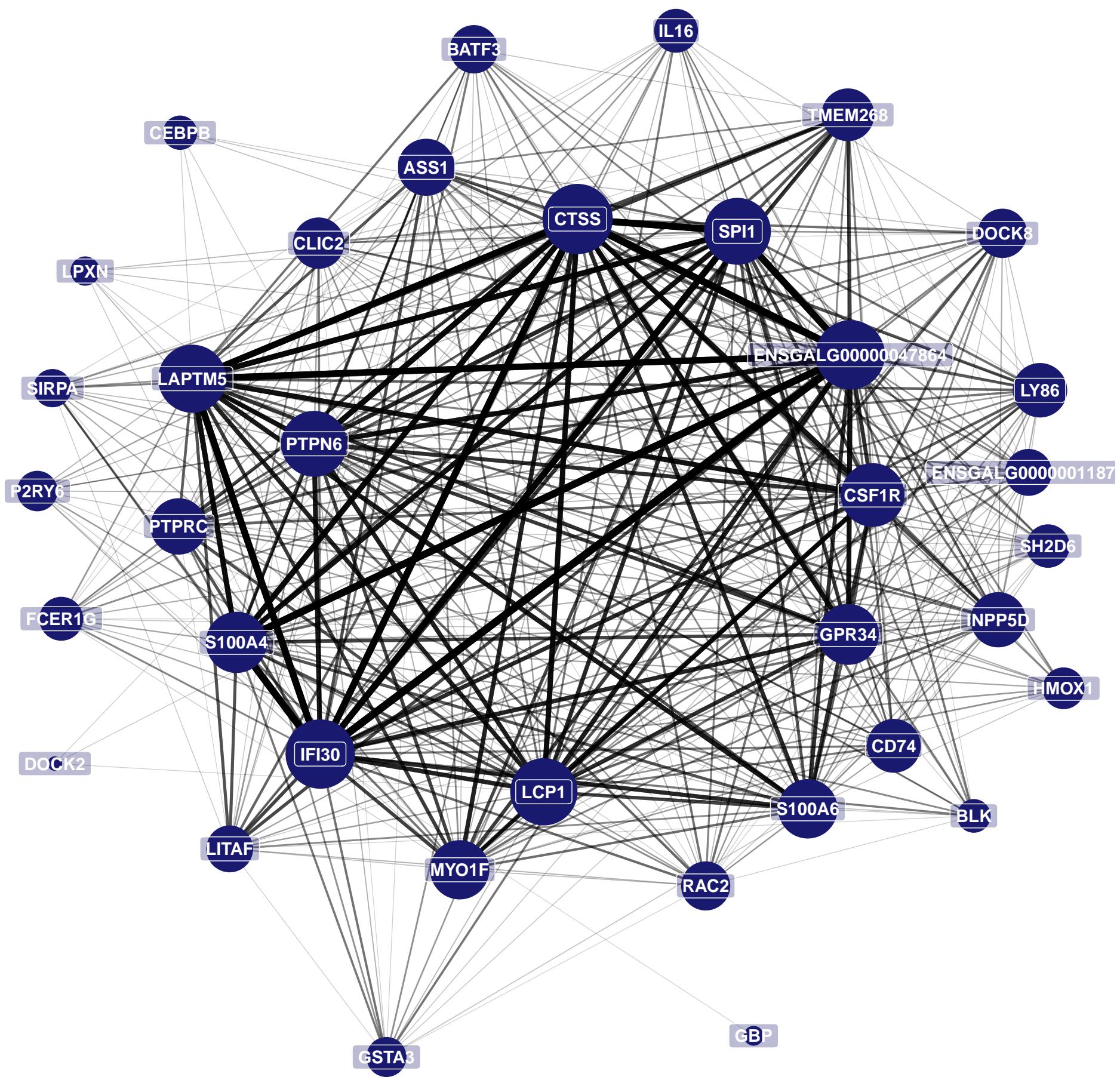
	Pathway	N	DE	P.DE
<i>path:gga04110</i>	Cell cycle	115	3	0.0002537
<i>path:gga04371</i>	Apelin signaling pathway	114	2	0.006898
<i>path:gga04068</i>	FoxO signaling pathway	118	2	0.007374
<i>path:gga04218</i>	Cellular senescence	135	2	0.009557
<i>path:gga04530</i>	Tight junction	138	2	0.009969
<i>path:gga04310</i>	Wnt signaling pathway	139	2	0.01011
<i>path:gga04216</i>	Ferroptosis	34	1	0.03711
<i>path:gga00330</i>	Arginine and proline metabolism	40	1	0.04352
<i>path:gga04340</i>	Hedgehog signaling pathway	48	1	0.05201
<i>path:gga03250</i>	Viral life cycle – HIV-1	49	1	0.05307



1	FABP7	EGF	SLC1A3	NOTCH1	SALL1	SOX9	SRPX	FGFR2
2	PLPP3	LRIG1	GNG5	FGFR3	HES5	FAM181B	PTN	ID1
3	MCM6	MSN	LDHB	YAP1	GSTA2	ENSGALG00000001136	CXCR4	RFX4
4	SMAD5	LAMA1	MLC1	PLCE1	DDR1	NEBLv1	S1PR1	FJX1
5	FAM181A	ANXA5	VIM	TIMP3	DTX4	ITGA6	RFTN2	GPM6B
6	GLI3	FZD7	COL5A1	ENSGALG00000030512	NPAS3	CTNNA1	FNDC3B	CYFIP1
7	FSTL1	MDK	ID2	MMD2	SOX21	SMO	DAB1	IGFBP2
8	SOX1	ITGAV	LFNG	ENSGALG00000005024	SHROOM3	LY6E	NFIA	GOLIM4
9	TMOD3	LHFPL2	CDK2AP1	ITGB1	DDOST	PDIA4	FGFR1	ENSGALG00000012121
10	TMEM47	CRB2	MSI2	POLE3	JAM2	ATP6AP1	BOC	ITGA2
11	PPP1R9B	C7H2ORF69	GPC4	GAREM2	ENSGALG00000005107	HES1	ADD3	HES4
12	CNN3	SLC16A1	RBP5	DKK3	TP53BP2	HMGA2	GLI2	FAM46A
13	ENSGALG0000002714	JUN	CD164	KCNK5	CCND2	GRB10	GRAMD4	LTBP1
14	CSPG5	SALL3	CXCR7	FBLN1	TCF7L2	SOX6	ZNF516	

	Term	Ont	N	n	Adj. p-value
GO:0007166	cell surface receptor signaling pathway	BP	272	17	6.428e-11
GO:0023052	signaling	BP	529	22	2.186e-10
GO:0007154	cell communication	BP	536	22	2.806e-10
GO:0007165	signal transduction	BP	493	21	3.867e-10
GO:0051716	cellular response to stimulus	BP	677	23	4.084e-09
GO:0050896	response to stimulus	BP	807	24	2.363e-08
GO:0007275	multicellular organism development	BP	598	20	6.379e-08
GO:0050789	regulation of biological process	BP	1130	28	6.482e-08
GO:0032501	multicellular organismal process	BP	741	22	1.043e-07
GO:0048856	anatomical structure development	BP	648	20	2.345e-07

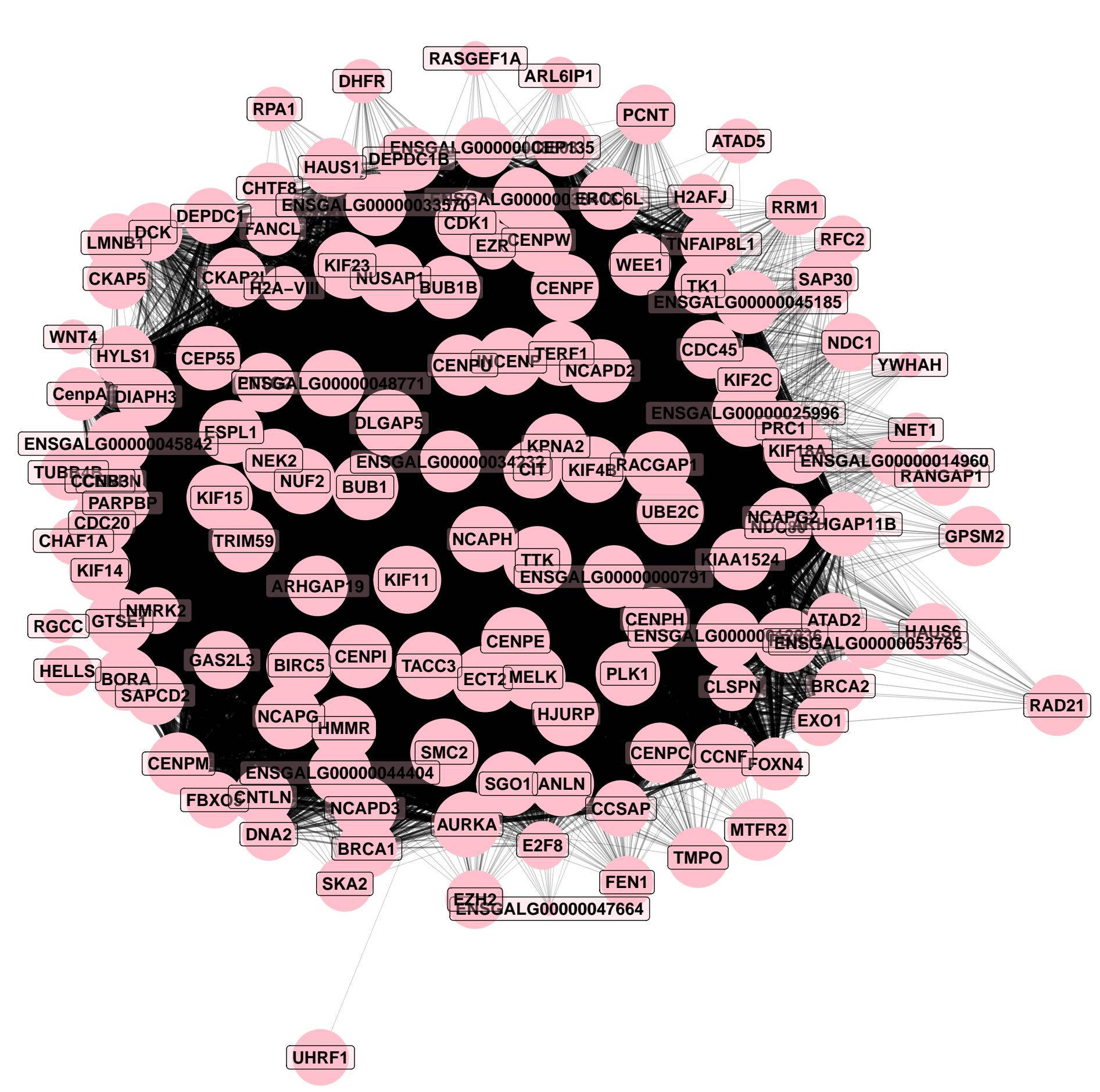
	Pathway	N	DE	P.DE
<i>path:gga04330</i>	Notch signaling pathway	52	7	1.936e-07
<i>path:gga04810</i>	Regulation of actin cytoskeleton	192	10	3.64e-06
<i>path:gga04340</i>	Hedgehog signaling pathway	48	5	4.232e-05
<i>path:gga04510</i>	Focal adhesion	175	8	9e-05
<i>path:gga04512</i>	ECM–receptor interaction	70	5	0.0002595
<i>path:gga04350</i>	TGF–beta signaling pathway	87	4	0.005516
<i>path:gga04310</i>	Wnt signaling pathway	139	5	0.005539
<i>path:gga04020</i>	Calcium signaling pathway	209	6	0.007213
<i>path:gga04514</i>	Cell adhesion molecules	110	4	0.01242
<i>path:gga04520</i>	Adherens junction	69	3	0.01866



1	S100A4	LAPTM5	CTSS	CSF1R	ENSGALG00000047864	SPI1	IFI30	LCP1
2	MYO1F	TMEM268	INPP5D	S100A6	PTPN6	LY86	LITAF	ASS1
3	PTPRC	BLK	BATF3	DOCK8	GSTA3	RAC2	GPR34	CLIC2
4	ENSGALG00000011872	SH2D6	CEBPB	CD74	P2RY6	HMOX1	SIRPA	DOCK2
5	LPXN	IL16	FCER1G	GBP				

	Term	Ont	N	n	Adj. p-value
GO:0015698	inorganic anion transport	BP	12	2	0.0003994
GO:0006575	cellular modified amino acid metabolic process	BP	25	2	0.001779
GO:0007202	activation of phospholipase C activity	BP	1	1	0.002517
GO:0000053	argininosuccinate metabolic process	BP	1	1	0.002517
GO:0071380	cellular response to prostaglandin E stimulus	BP	1	1	0.002517
GO:0071379	cellular response to prostaglandin stimulus	BP	1	1	0.002517
GO:0106106	cold-induced thermogenesis	BP	1	1	0.002517
GO:0042167	heme catabolic process	BP	1	1	0.002517
GO:0006788	heme oxidation	BP	1	1	0.002517
GO:0006817	phosphate ion transport	BP	1	1	0.002517

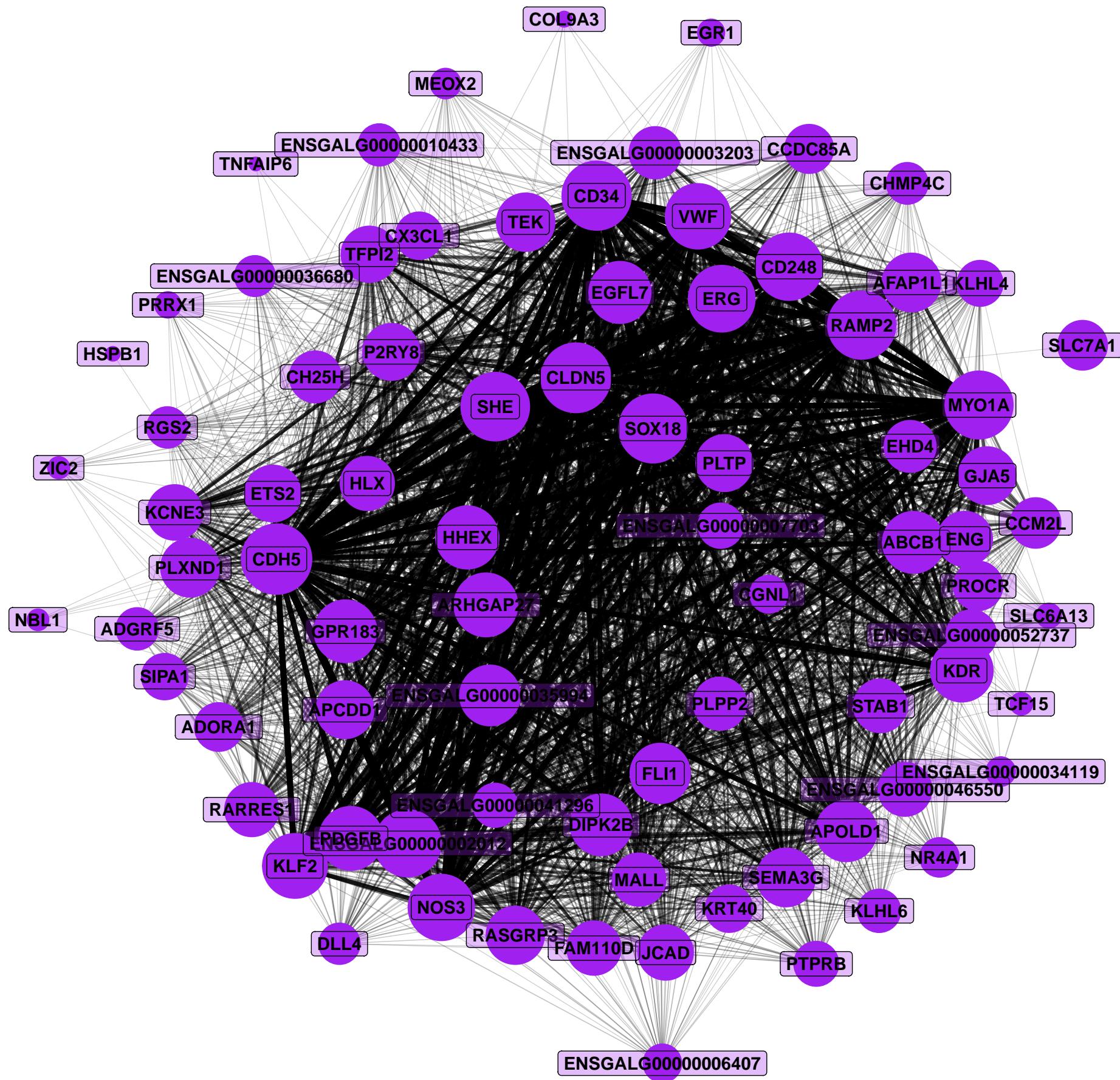
	Pathway	N	DE	P.DE
<i>path:gga04142</i>	Lysosome	116	3	0.00304
<i>path:gga04520</i>	Adherens junction	69	2	0.01298
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.04196
<i>path:gga00860</i>	Porphyrin metabolism	21	1	0.05158
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	164	2	0.0638
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	1	0.07054
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	31	1	0.07522
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	1	0.07755
<i>path:gga04216</i>	Ferroptosis	34	1	0.0822
<i>path:gga00480</i>	Glutathione metabolism	47	1	0.1119



1	CENPE	NUSAP1	CENPF	KIF11	SMC2	ENSGALG00000025996	UBE2C	TTK
2	NDC80	KIF4B	KPNA2	INCENP	DLGAP5	TACC3	KIF15	ENSGALG00000048771
3	KIF23	BUB1	RACGAP1	GTSE1	CDK1	KIF18A	ECT2	BIRC5
4	AURKA	NUF2	PLK1	ENSGALG00000012836	KIF2C	CENPW	ANLN	SGO1
5	BUB1B	HMMR	NCAPG	PBK	CENPH	CDC20	ENSGALG00000038416	CEP55
6	NCAPH	TERF1	MELK	ENSGALG00000045185	ARHGAP11B	CCNF	ENSGALG00000044404	CENPI
7	DEPDC1B	ESPL1	HJURP	NEK2	BRCA1	ERCC6L	PTTG2	ENSGALG00000045842
8	TK1	NCAPD2	BORA	NCAPD3	CENPN	ENSGALG00000034232	ENSGALG0000000791	TRIM59
9	UHRF1	KIAA1524	CENPC	WEE1	DIAPH3	CENPU	HAUS1	KIF14
10	CENPM	TNFAIP8L1	CDC45	NCAPG2	HYLS1	MTFR2	ENSGALG00000033570	ARHGAP19
11	CNTLN	RRM1	GPSM2	ENSGALG0000008803	DEPDC1	GAS2L3	NDC1	RAD21
12	CCNB3	DNA2	SAPCD2	RANGAP1	TMPO	CIT	CHTF8	CEP135
13	DCK	BRCA2	SAP30	CenpA	HELLS	CKAP2L	FEN1	ATAD2
14	HAUS6	FANCL	FBXO5	PCNT	EXO1	FOXN4	LMNB1	PRC1
15	CLSPN	CCSAP	CKAP5	PARPBP	RFC2	EZH2	TUBB4B	NMRK2
16	SKA2	E2F8	H2AFJ	EZR	CHAF1A	ATAD5	DHFR	ENSGALG00000053765
17	ENSGALG0000014960	RPA1	H2A-VIII	NET1	RGCC	ENSGALG00000047664	RASGEF1A	WNT4
18	YWHAH	ARL6IP1						

	Term	Ont	N	n	Adj. p-value
GO:0007049	cell cycle	BP	207	17	2.412e-11
GO:0051276	chromosome organization	BP	178	16	2.473e-11
GO:0051383	kinetochore organization	BP	10	6	1.81e-10
GO:0000278	mitotic cell cycle	BP	101	12	3.382e-10
GO:1903047	mitotic cell cycle process	BP	78	10	5.014e-09
GO:0022402	cell cycle process	BP	129	12	5.857e-09
GO:0007059	chromosome segregation	BP	43	8	8.718e-09
GO:1902850	microtubule cytoskeleton organization involved in mitosis	BP	21	6	4.272e-08
GO:0034508	centromere complex assembly	BP	12	5	6.925e-08
GO:0006996	organelle organization	BP	440	19	7.532e-08

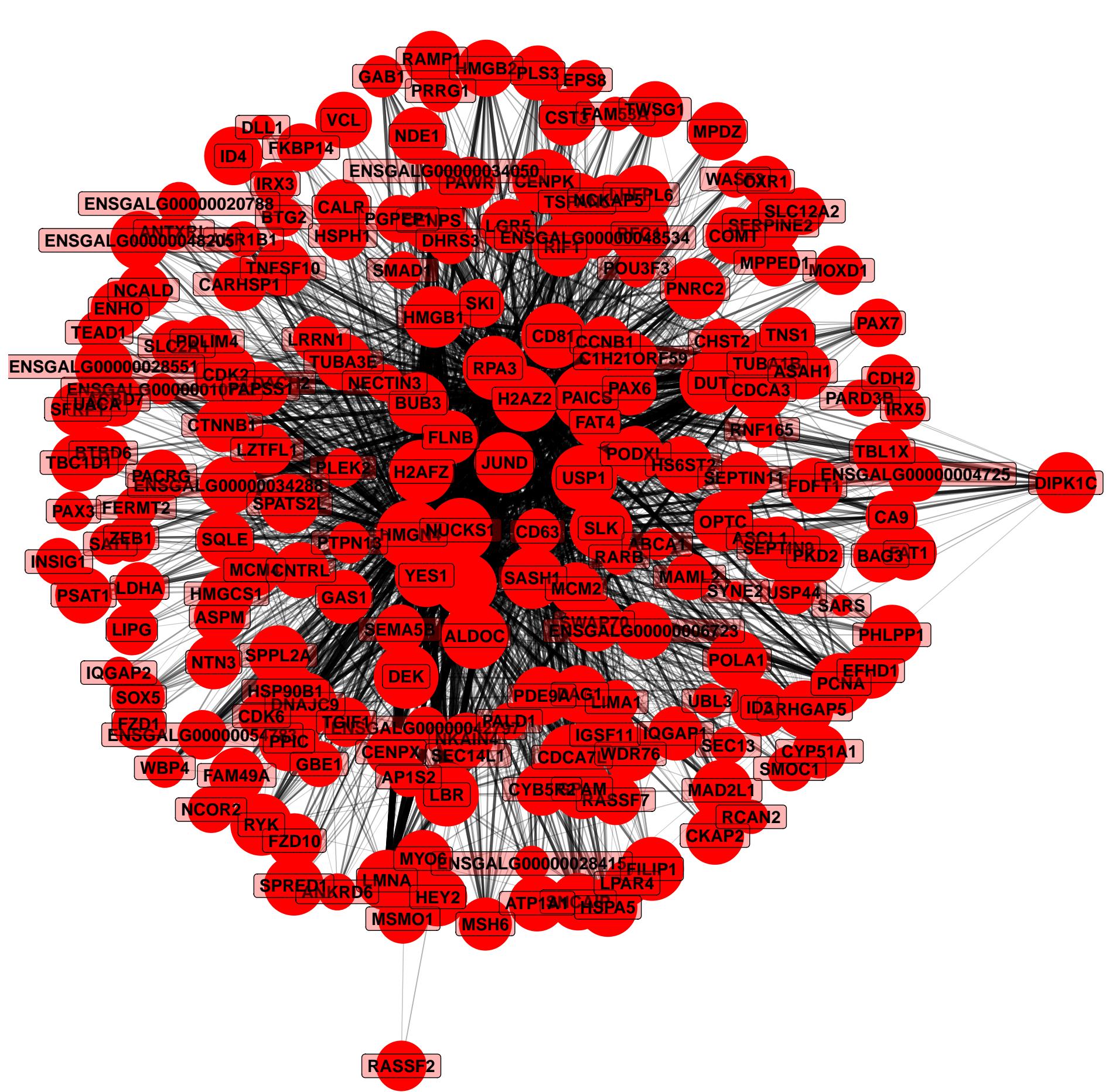
	Pathway	N	DE	P.DE
<i>path:gga04110</i>	Cell cycle	115	13	1.133e–10
<i>path:gga04114</i>	Oocyte meiosis	98	10	4.713e–08
<i>path:gga03030</i>	DNA replication	29	4	0.0001866
<i>path:gga03430</i>	Mismatch repair	19	3	0.000841
<i>path:gga04914</i>	Progesterone–mediated oocyte maturation	79	5	0.001153
<i>path:gga03460</i>	Fanconi anemia pathway	48	4	0.00132
<i>path:gga03440</i>	Homologous recombination	36	3	0.005476
<i>path:gga00240</i>	Pyrimidine metabolism	56	3	0.0184
<i>path:gga04120</i>	Ubiquitin mediated proteolysis	128	4	0.03941
<i>path:gga01232</i>	Nucleotide metabolism	79	3	0.04455



1	CDH5	RAMP2	CD248	MYO1A	NOS3	ERG	CD34	APOLD1
2	ENSGALG0000002012	SHE	SOX18	CLDN5	ABCB1	P2RY8	KLF2	DIPK2B
3	ARHGAP27	EGFL7	FLI1	HHEX	VWF	GPR183	MALL	PDGFB
4	KDR	AFAP1L1	RASGRP3	GJA5	PLPP2	CCM2L	TEK	ENG
5	HLX	ENSGALG00000035994	ENSGALG00000052737	FAM110D	RARRES1	KCNE3	ENSGALG00000046550	STAB1
6	APCDD1	SEMA3G	CX3CL1	ENSGALG0000003203	JCAD	TFPI2	EHD4	ENSGALG00000041296
7	PLXND1	ADORA1	CH25H	CCDC85A	KLHL6	PLTP	ENSGALG0000007703	KLHL4
8	ADGRF5	KRT40	PROCR	ETS2	PTPRB	DLL4	RGS2	ENSGALG0000006407
9	CGNL1	CHMP4C	SLC7A1	SIPA1	ENSGALG00000036680	MEOX2	ENSGALG0000010433	NR4A1
10	EGR1	ZIC2	TCF15	SLC6A13	NBL1	TNFAIP6	ENSGALG00000034119	HSPB1
11	PRRX1	COL9A3						

	Term	Ont	N	n	Adj. p-value
GO:0048844	artery morphogenesis	BP	3	2	0.0001009
GO:0060840	artery development	BP	4	2	0.000201
GO:0032501	multicellular organismal process	BP	741	13	0.000336
GO:0035590	purinergic nucleotide receptor signaling pathway	BP	7	2	0.0006957
GO:0048585	negative regulation of response to stimulus	BP	127	5	0.0008769
GO:0010646	regulation of cell communication	BP	271	7	0.001024
GO:0007166	cell surface receptor signaling pathway	BP	272	7	0.001046
GO:0023051	regulation of signaling	BP	273	7	0.001068
GO:0050728	negative regulation of inflammatory response	BP	10	2	0.001474
GO:0050878	regulation of body fluid levels	BP	11	2	0.001795

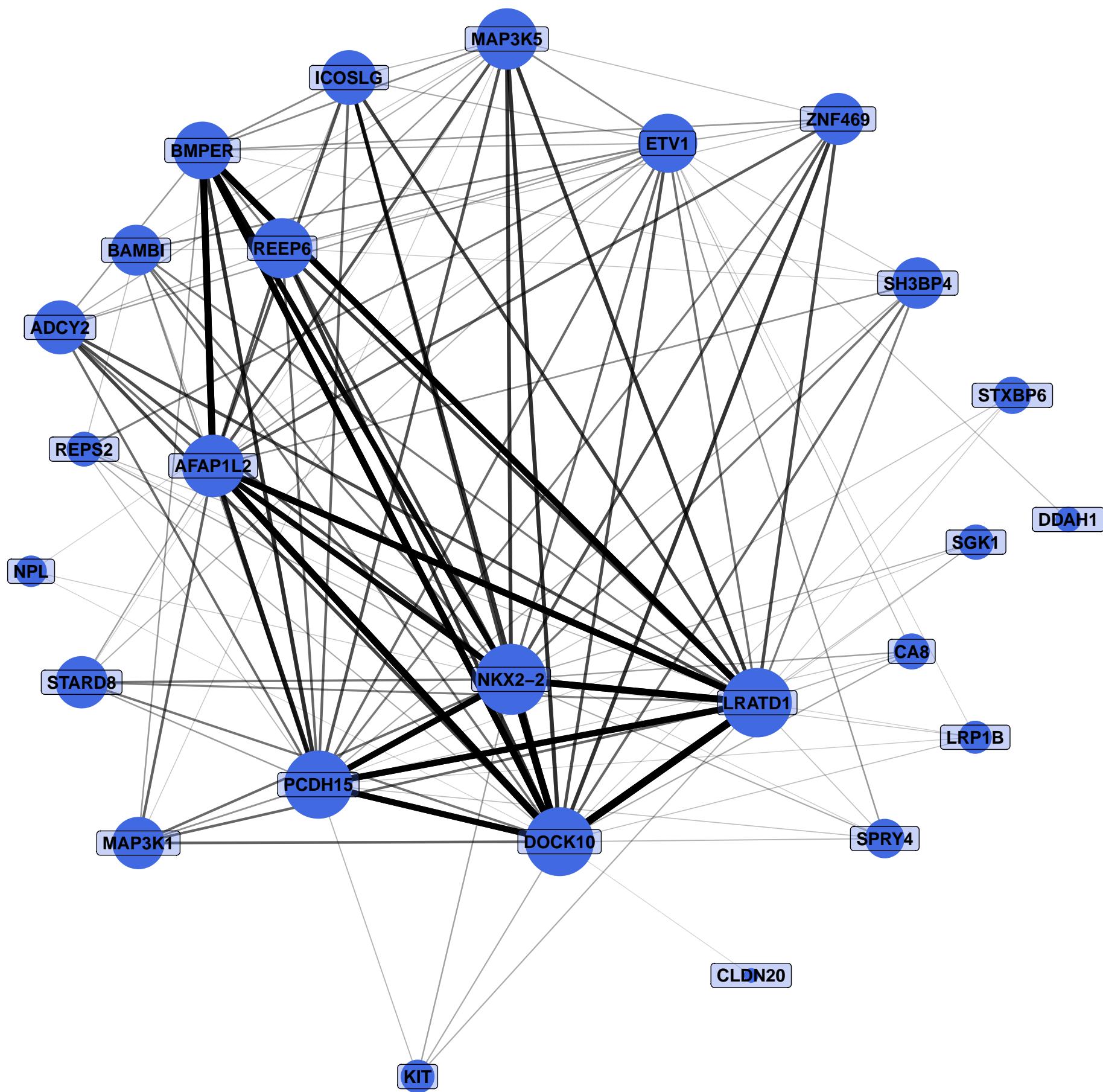
	Pathway	N	DE	P.DE
<i>path:gga04010</i>	MAPK signaling pathway	243	6	0.002961
<i>path:gga04370</i>	VEGF signaling pathway	54	3	0.003852
<i>path:gga04510</i>	Focal adhesion	175	4	0.01927
<i>path:gga04514</i>	Cell adhesion molecules	110	3	0.02657
<i>path:gga04371</i>	Apelin signaling pathway	114	3	0.02912
<i>path:gga00120</i>	Primary bile acid biosynthesis	11	1	0.0625
<i>path:gga04512</i>	ECM–receptor interaction	70	2	0.06318
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.09494
<i>path:gga04020</i>	Calcium signaling pathway	209	3	0.1235
<i>path:gga04530</i>	Tight junction	138	2	0.1931



1	HMGN4	LBR	NUCKS1	CD81	HMGB2	H2AZ2	DUT	PCNA
2	PAICS	CENPK	SASH1	DEK	H2AFZ	TUBA1B	CDK2	CKAP2
3	CDCA3	USP1	IGSF11	NA	FILIP1	DNAJC9	RPA3	ALDOC
4	MAD2L1	YES1	ID3	CENPS	SEPTIN9	SLK	TUBA3E	CDCA7L
5	BUB3	SERPINE2	JUND	CST3	HMGB1	SWAP70	OPTC	ENSGALG00000028551
6	LMNA	PAPSS1	ARHGAP5	DIPK1C	GPAM	NDE1	PNRC2	ACBD7
7	RYK	CCNB1	ASPM	FZD10	PAX6	SPRED1	PODXL	MCM2
8	LGR5	RAMP1	ENHO	SPPL2A	POLA1	HSP90B1	HEY2	RIF1
9	GAS1	HSPA5	ID4	COMT	ENSGALG00000054783	RFC1	TSPAN3	VCL
10	ENSGALG00000034288	TBL1X	LHFPL6	PHLPP1	SPATS2L	HS6ST2	TNFSF10	PDE9A
11	TBC1D1	PPIC	DAG1	PSAT1	SNCAIP	TNS1	MYO6	WDR76
12	FAT1	FAM49A	CDK6	SEPTIN11	ENSGALG00000010722	PACRG	ATP1A1	SLC2A1
13	MPDZ	ENSGALG00000048205	ENSGALG0000006723	FLNB	CTNNB1	ZEB1	SEMA5B	ENSGALG0000004725
14	TWSG1	PAX7	LIPG	ASAHI	SFRP1	MSH6	MCM4	EFHD1
15	SOX5	LRRN1	BTBD6	NKAIN4	FZD1	CA9	NCALD	PLS3
16	FDFT1	GBE1	CNTRL	ANTXRL	CYB5R2	SMOC1	CENPX	NTN3
17	CARHSP1	SQLE	GAB1	FERMT2	AKR1B1	CALR	MOXD1	HMGCS1
18	NCKAP5	MAML2	RASSF7	CD63	BAG3	ASCL1	LDHA	ENSGALG00000028415
19	PDLIM4	CYP51A1	PKD2	NCOR2	TGIF1	TEAD1	UBL3	LZTFL1
20	PAWR	IQGAP1	SAT1	C1H21ORF59	RASSF2	OXR1	PGPEP1	PAX3
21	IRX3	SKI	CDH2	MSMO1	HSPH1	FKBP14	NECTIN3	FAT4
22	CHST2	INSIG1	MPPED1	LIMA1	SLC12A2	DHRS3	POU3F3	LPAR4
23	EPS8	PTPN13	PRRG1	BTG2	UACA	ENSGALG00000034050	AP1S2	USP44
24	RNF165	ENSGALG00000020788	SEC13	ENSGALG00000042797	ENSGALG00000048534	WBP4	IRX5	PLEK2
25	WASF3	ANKRD6	IQGAP2	PARD3B	SMAD1	RCAN2	PALD1	ABCA1
26	DLL1	FAM53A	RARB	SEC14L1	SARS	DACH2	SYNE2	

	Term	Ont	N	n	Adj. p-value
GO:0016126	sterol biosynthetic process	BP	9	5	9.189e-08
GO:1901617	organic hydroxy compound biosynthetic process	BP	27	6	2.574e-06
GO:0006694	steroid biosynthetic process	BP	16	5	2.921e-06
GO:1901360	organic cyclic compound metabolic process	BP	688	27	5.44e-06
GO:0016125	sterol metabolic process	BP	19	5	7.492e-06
GO:0008150	biological_process	BP	1957	53	1.222e-05
GO:1901576	organic substance biosynthetic process	BP	681	26	1.339e-05
GO:0009987	cellular process	BP	1870	51	1.557e-05
GO:0009058	biosynthetic process	BP	690	26	1.683e-05
GO:1901362	organic cyclic compound biosynthetic process	BP	463	20	2.561e-05

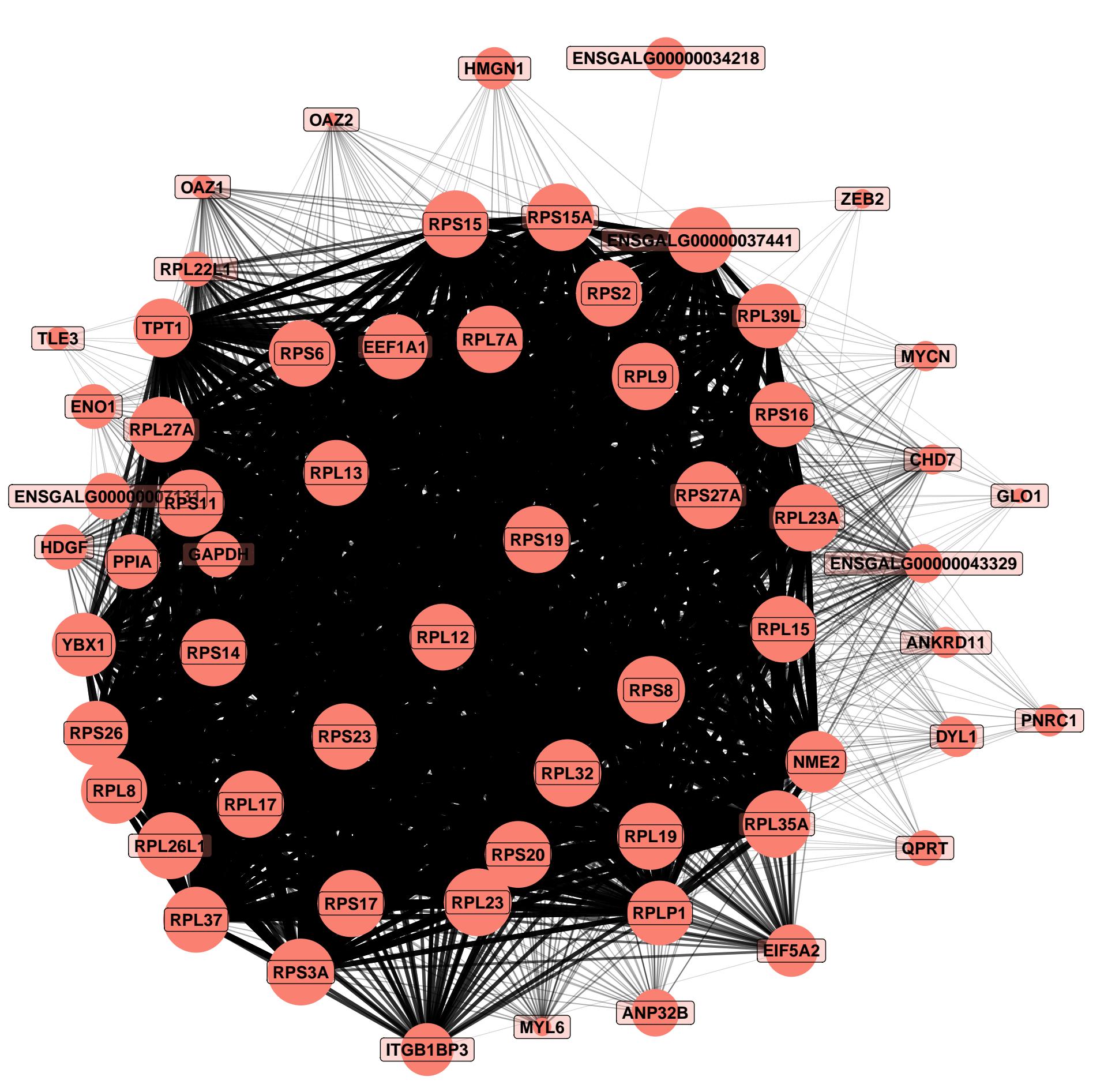
	Pathway	N	DE	P.DE
<i>path:gga00100</i>	Steroid biosynthesis	16	6	8.005e-08
<i>path:gga03030</i>	DNA replication	29	6	4.028e-06
<i>path:gga03430</i>	Mismatch repair	19	4	0.0001669
<i>path:gga04110</i>	Cell cycle	115	8	0.0003619
<i>path:gga04520</i>	Adherens junction	69	6	0.0006142
<i>path:gga04310</i>	Wnt signaling pathway	139	7	0.005287
<i>path:gga03460</i>	Fanconi anemia pathway	48	4	0.005947
<i>path:gga05132</i>	Salmonella infection	223	9	0.007035
<i>path:gga04330</i>	Notch signaling pathway	52	4	0.007896
<i>path:gga03420</i>	Nucleotide excision repair	37	3	0.01832



1	NKX2-2	DOCK10	LRATD1	AFAP1L2	PCDH15	BMPER	REEP6	MAP3K5
2	ETV1	BAMBI	ZNF469	ADCY2	SH3BP4	ICOSLG	MAP3K1	STARD8
3	SGK1	LRP1B	SPRY4	KIT	CA8	STXBP6	NPL	REPS2
4	DDAH1	CLDN20						

	Term	Ont	N	n	Adj. p-value
GO:0050954	sensory perception of mechanical stimulus	BP	15	2	0.0003131
GO:0007605	sensory perception of sound	BP	15	2	0.0003131
GO:0046348	amino sugar catabolic process	BP	1	1	0.001776
GO:0036018	cellular response to erythropoietin	BP	1	1	0.001776
GO:0036216	cellular response to stem cell factor stimulus	BP	1	1	0.001776
GO:0097067	cellular response to thyroid hormone stimulus	BP	1	1	0.001776
GO:0038162	erythropoietin-mediated signaling pathway	BP	1	1	0.001776
GO:0038093	Fc receptor signaling pathway	BP	1	1	0.001776
GO:0035701	hematopoietic stem cell migration	BP	1	1	0.001776
GO:0038109	Kit signaling pathway	BP	1	1	0.001776

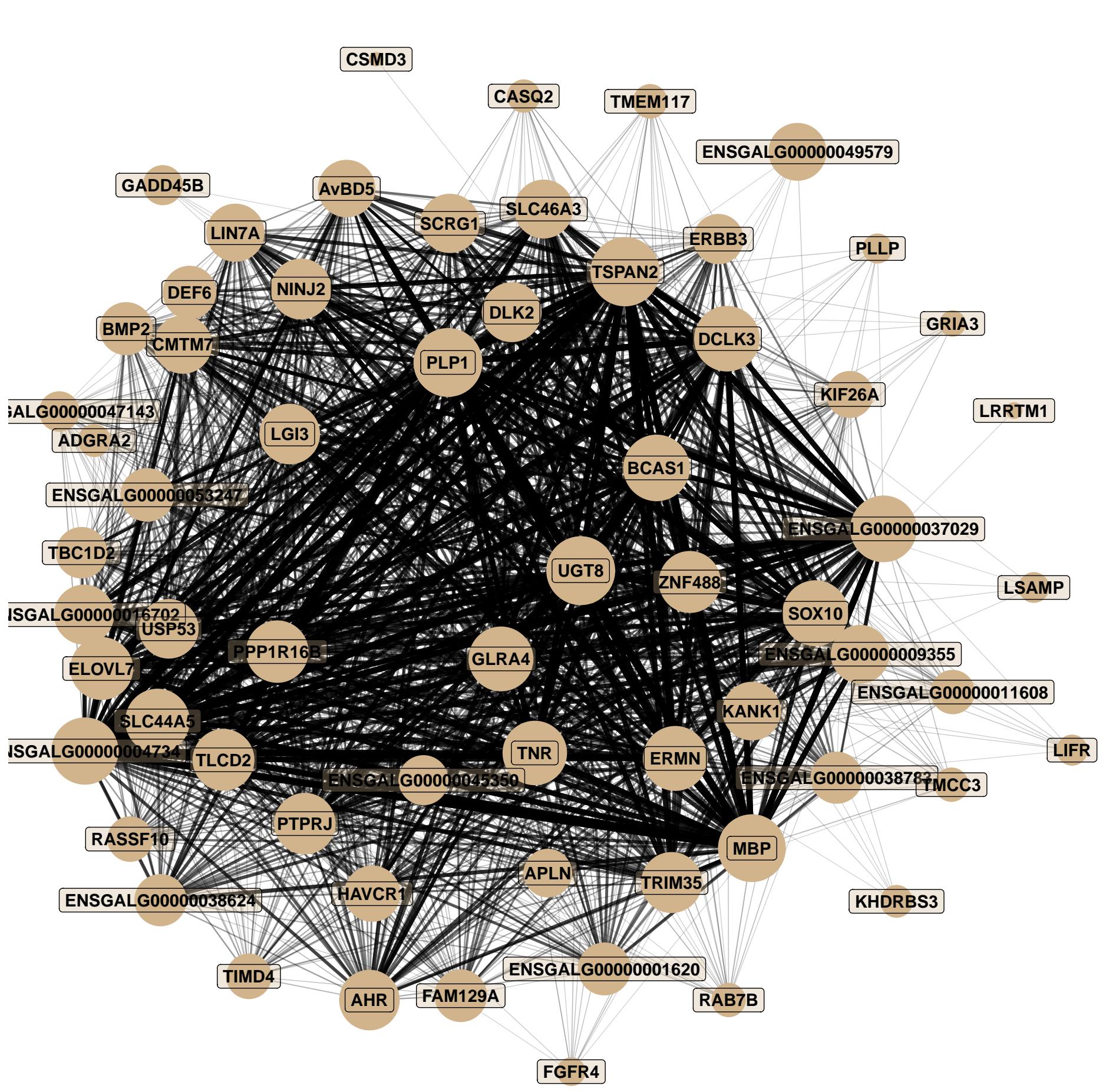
	Pathway	N	DE	P.DE
<i>path:gga04530</i>	Tight junction	138	3	0.001804
<i>path:gga04912</i>	GnRH signaling pathway	78	2	0.008365
<i>path:gga04010</i>	MAPK signaling pathway	243	3	0.0088
<i>path:gga04916</i>	Melanogenesis	88	2	0.01055
<i>path:gga04514</i>	Cell adhesion molecules	110	2	0.01613
<i>path:gga00910</i>	Nitrogen metabolism	14	1	0.0246
<i>path:gga04672</i>	Intestinal immune network for IgA production	30	1	0.052
<i>path:gga00520</i>	Amino sugar and nucleotide sugar metabolism	46	1	0.07866
<i>path:gga04622</i>	RIG-I-like receptor signaling pathway	49	1	0.08358
<i>path:gga04914</i>	Progesterone-mediated oocyte maturation	79	1	0.1314



1	RPS8	RPS15A	RPS27A	RPL32	RPL23	RPS17	ENSGALG00000037441	RPS14
2	RPS15	RPL35A	RPS11	RPL17	RPL26L1	RPS19	RPL9	RPS2
3	RPS6	RPS20	RPS23	RPL7A	RPS3A	RPL23A	RPL19	RPS16
4	RPL13	RPL12	RPL15	RPL37	RPL8	RPL27A	RPLP1	RPL39L
5	RPS26	YBX1	EEF1A1	TPT1	NME2	PPIA	ITGB1BP3	GAPDH
6	ANP32B	EIF5A2	ENSGALG0000007131	ENO1	HDGF	ENSGALG00000043329	DYL1	RPL22L1
7	PNRC1	HMGN1	ENSGALG00000034218	MYL6	QPRT	OAZ1	CHD7	GLO1
8	OAZ2	ANKRD11	ZEB2	MYCN	TLE3			

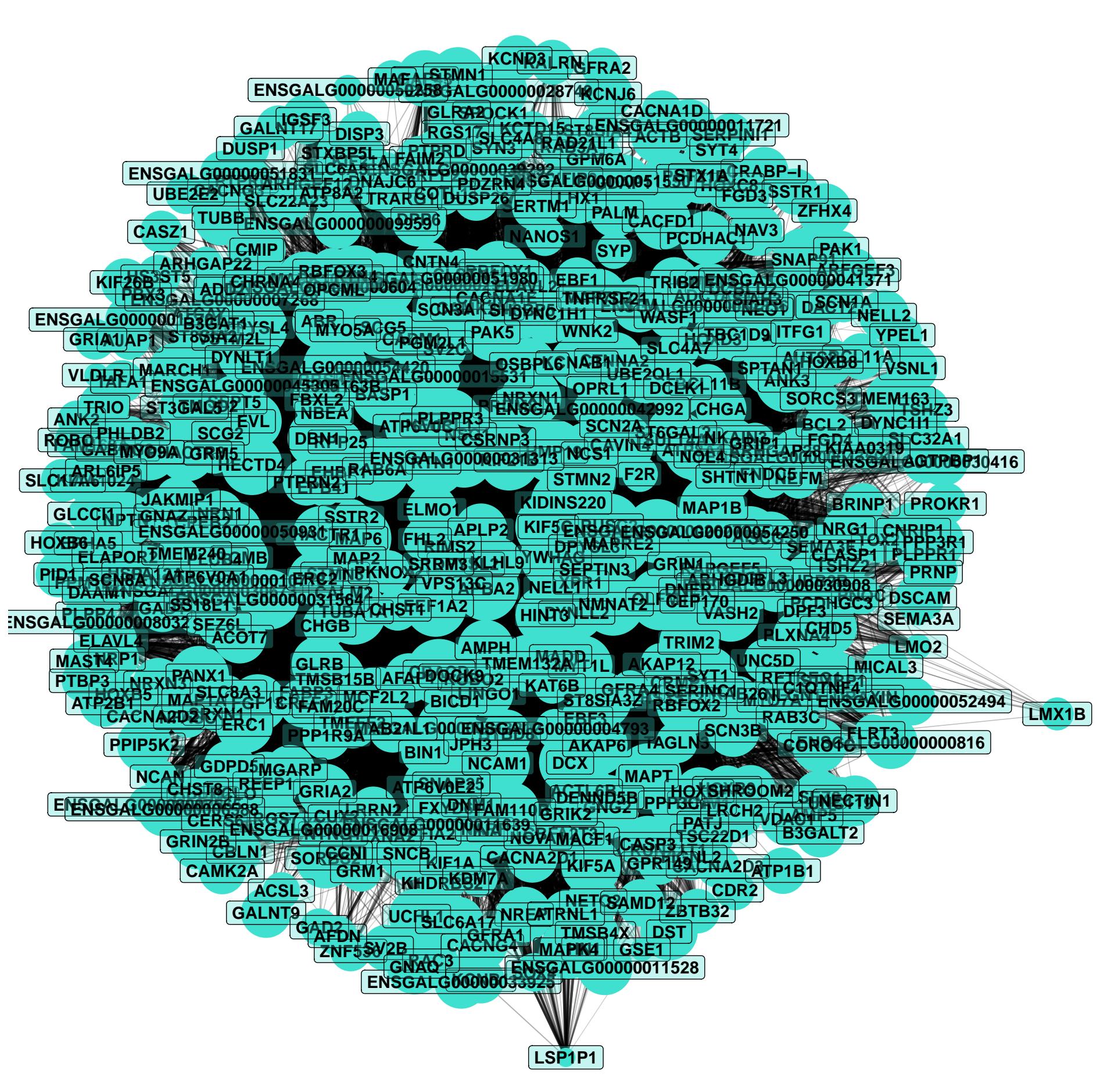
	Term	Ont	N	n	Adj. p-value
GO:0006412	translation	BP	87	13	6.593e-17
GO:0043043	peptide biosynthetic process	BP	88	13	7.71e-17
GO:0043604	amide biosynthetic process	BP	101	13	5.019e-16
GO:0006518	peptide metabolic process	BP	107	13	1.092e-15
GO:0043603	cellular amide metabolic process	BP	125	13	8.695e-15
GO:1901566	organonitrogen compound biosynthetic process	BP	209	14	3.449e-13
GO:0034641	cellular nitrogen compound metabolic process	BP	738	19	2.761e-10
GO:0010467	gene expression	BP	623	17	1.25e-09
GO:0044271	cellular nitrogen compound biosynthetic process	BP	543	15	1.214e-08
GO:0034645	cellular macromolecule biosynthetic process	BP	558	15	1.748e-08

	Pathway	N	DE	P.DE
<i>path:gga03010</i>	Ribosome	115	34	2.56e-56
<i>path:gga00760</i>	Nicotinate and nicotinamide metabolism	33	2	0.009677
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	49	2	0.02058
<i>path:gga01230</i>	Biosynthesis of amino acids	58	2	0.02819
<i>path:gga01200</i>	Carbon metabolism	95	2	0.06854
<i>path:gga01240</i>	Biosynthesis of cofactors	119	2	0.1007
<i>path:gga00620</i>	Pyruvate metabolism	34	1	0.1428
<i>path:gga03250</i>	Viral life cycle – HIV-1	49	1	0.1992
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.21
<i>path:gga00983</i>	Drug metabolism – other enzymes	56	1	0.2243



	Term	Ont	N	n	Adj. p-value
GO:0008366	axon ensheathment	BP	12	3	1.966e–05
GO:0007272	ensheathment of neurons	BP	12	3	1.966e–05
GO:0042552	myelination	BP	12	3	1.966e–05
GO:0032291	axon ensheathment in central nervous system	BP	2	2	2.072e–05
GO:0022010	central nervous system myelination	BP	2	2	2.072e–05
GO:0014003	oligodendrocyte development	BP	2	2	2.072e–05
GO:0021782	glial cell development	BP	5	2	0.0002054
GO:0048709	oligodendrocyte differentiation	BP	9	2	0.0007307
GO:0010001	glial cell differentiation	BP	21	2	0.004114
GO:0060959	cardiac neuron development	BP	1	1	0.004589

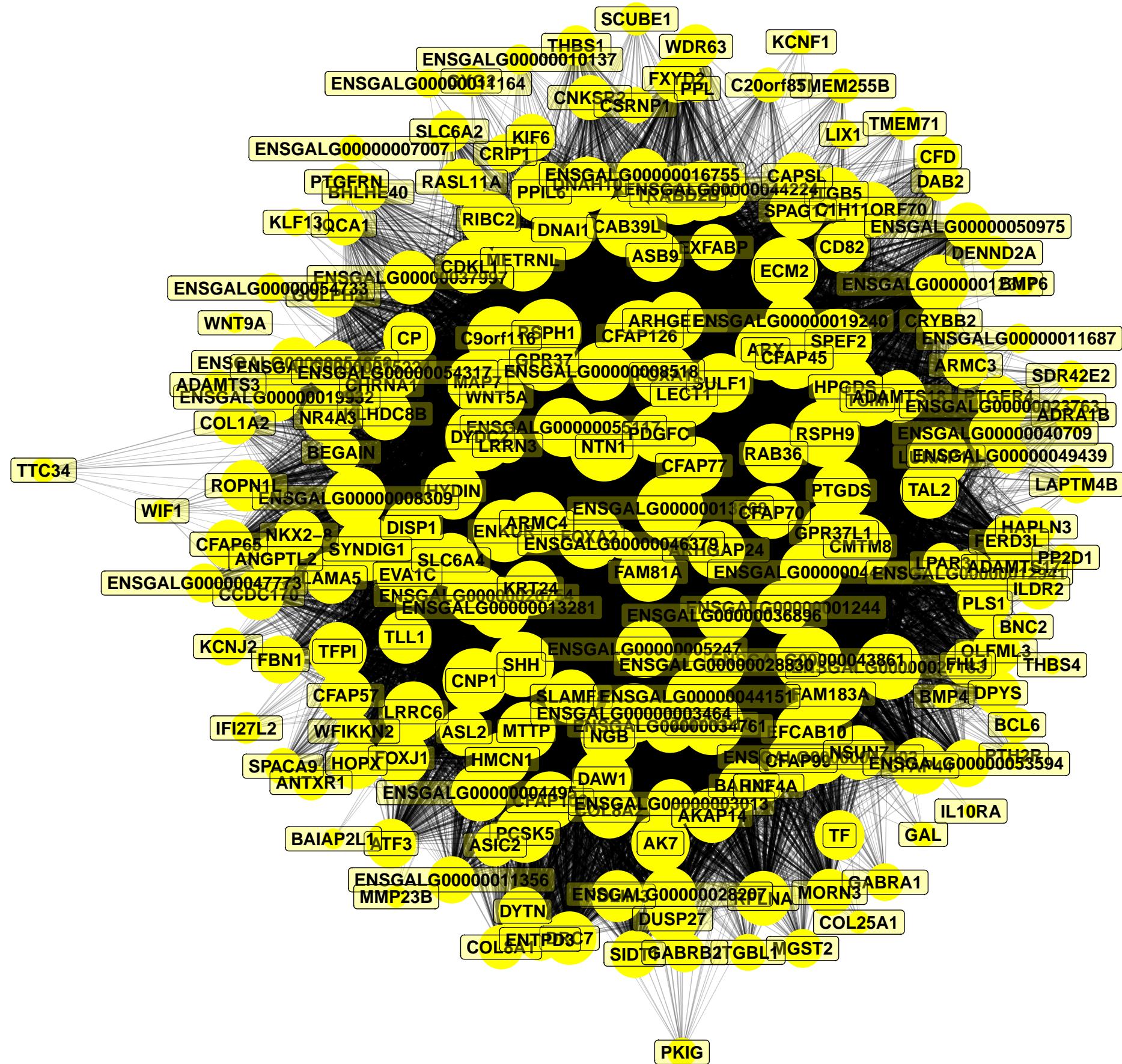
	Pathway	N	DE	P.DE
<i>path:gga03264</i>	Virion – Flavivirus	3	1	0.01371
<i>path:gga04020</i>	Calcium signaling pathway	209	3	0.07108
<i>path:gga00062</i>	Fatty acid elongation	23	1	0.1005
<i>path:gga04010</i>	MAPK signaling pathway	243	3	0.1006
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	28	1	0.121
<i>path:gga00565</i>	Ether lipid metabolism	39	1	0.1644
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	164	2	0.1735
<i>path:gga00600</i>	Sphingolipid metabolism	48	1	0.1984
<i>path:gga01212</i>	Fatty acid metabolism	51	1	0.2094
<i>path:gga04260</i>	Cardiac muscle contraction	61	1	0.2451



9	CALM2	HDGFL3	ST8SIA2	NMNAT2	TMSB15B	PCLO	ENSGALG00000007268	ACTL6B
10	TRIM2	TAGLN3	EHBP1	DBN1	SERINC1	SCN3A	ATP6V0E2	RTN4
11	ENSGALG0000000604	SORBS2	CRABP-I	RAPGEF5	ELAVL2	NOVA1	SCG5	PGM2L1
12	MAPK4	ENSGALG0000010718	VSTM2L	FGF13	LAMP5	TUBB2B	SH3BP5	ATP6V0C
13	RBFOX2	LHX1	ATP8A1	HECTD4	KIAA1024	GRIA2	CEP170	EBF3
14	DENND5B	PLPPR3	PANX1	SS18L1	PLXNA2	KIF5A	MAPK10	PHACTR3
15	DNAJC6	ADD2	STXBP1	AFAP1	CTNNA2	PAK5	ITFG1	CACFD1
16	HN1	ENSGALG0000031564	PHACTR1	ENSGALG0000028749	SCG2	MADD	ENSGALG0000031313	MAP7D2
17	UCHL1	CHGA	ENSGALG0000051550	ENSGALG0000051980	MYT1	NA	NAV3	NRXN3
18	GPM6A	TRARG1	ENSGALG0000050931	LRCH2	PCDHGC3	CHGB	DST	TMEM132A
19	IGSF3	DYNC1H1	SYN3	ENSGALG0000011528	DPP6	CUX2	TMEM240	CNRIP1
20	DNM1	CACNA2D1	ATP6V0A1	NTM	NOL4	ST8SIA3Z	ADCYAP1	NEO1
21	ENSGALG0000015531	CMIP	GRIN2B	PCDHAC1	DYNLL2	HSPA12A	APLP2	FGD4
22	ENSGALG0000030908	STMN1	INA	ENSGALG000006588	NEFM	SNCB	HINT3	RAB3A
23	NREP	NETO2	ABR	TMEFF2	ENSGALG0000011639	DAAM1	PLPPR1	NRN1
24	ENSGALG0000054250	TMOD2	PLCB4	STX1A	CSRNP3	FAM169A	SRRM3	FNDC5
25	PPM1E	NPTN	NCAN	SYT4	NBEA	PLXNA4	CPEB2	MYO5A
26	SLC32A1	ZFHX4	GDAP1	SEZ6	GAD1	ENSGALG0000000816	ERC1	GNAZ
27	KIF21A	PTPRO	PPP3R1	FAM110B	KCNAB1	OSBPL6	MYO9A	AMPH
28	GALNT9	ELAPOR2	SERTM1	COTL1	MAB21L1	GRIN1	CASP3	CACNG4
29	NTNG1	ACTB	PATJ	CORO1C	GABRG2	ELMO1	MYO7A	PTPRN2
30	TUBB	GLRB	EVL	DCLK1	ENSGALG0000030673	MAP1A	CHD5	SSTR1
31	PPP3CA	RETREG1	NFASC	ARPP21	CERS6	EBF1	NELL2	B3GALT2
32	WNK2	ST3GAL5	RGS17	LINGO1	SCN8A	OPRM1	CCNI	SULT4A1
33	UNC119	PPIP5K2	GDPD5	ERC2	SCN3B	PTPRD	ZBTB32	HOXB9
34	SEMA3F	TRIO	VDAC1	GNAQ	ENSGALG0000041371	BICD1	CBLN1	CADM1
35	ST6GAL2	ENSGALG0000033925	TSHZ3	MARCH1	NELL1	PNOc	ENSGALG0000011721	BCL11A
36	HOXC8	BTBD8	SCG3	FABP3	TMEM163	GLRA2	RAC3	CRLF1
37	SHROOM2	NRP1	ARL6IP5	ENSGALG0000009959	SPTAN1	ANK2	CLSTN1	NARF
38	FXYD6	TBC1D9	FHL2	DRAKIN	SLC4A8	TSHZ2	JPH3	NANOS1
39	ACOT7	ENSGALG0000029521	HOXB8	CACNA1E	HS3ST2	CASZ1	FIGNL2	TRIB2
40	PRNP	AGTPBP1	ARFGEF3	DNER	SLC6A17	DSCAM	PLPP4	RGS7
41	CYFIP2	TSC22D1	EPB41	NECTIN1	RPP25	CACNA2D2	VSNL1	ENSGALG0000052494
42	CAMK2A	FAIM2	KHDRBS2	SLC22A23	GALNT17	PALM	HOXB7	ENSGALG0000039292
43	TMSB4X	SERPINI1	TOX2	HOXD3	MGARP	SCN2A	OPRL1	KIF26B
44	TNFRSF21	KLHL9	ST8SIA4	PKNOX2	ENSGALG0000015701	RBFOX3	KCNB1	FGD3
45	LRRN2	SAMD12	NLGN1	CLASP1	PPP1R9A	NEURL1	MICAL3	CACNA2D3
46	BIN1	KCNJ6	AUTS2	ATP1B1	GFRA4	C1QTNF4	MAST4	SRXN1
47	DYNLT1	PBX3	DPF3	SLC4A7	MACF1	ATCAY	SOX4	ZNF536
48	EPHA5	UBE2E2	PRDM8	KCND3	KALRN	HS3ST5	AFDN	FBXL2
49	GAD2	ENSGALG0000051831	CACNG3	WASF1	PHF21B	SLC17A6	SV2B	FAM20C
50	JAKMIP1	SHTN1	DUSP26	NRG1	ATP2B1	CHRNA4	DISP3	FAM163B
51	TAFA1	ATRNL1	SCN1A	PID1	DCBLD2	ROBO2	GFRA2	PDZRN4
52	AKAP12	SEZ6L	TENM1	SLC6A5	STXBP5L	LMX1B	ATP8A2	PTBP3

	Term	Ont	N	n	Adj. p-value
GO:0007399	nervous system development	BP	266	43	2.221e-17
GO:0030182	neuron differentiation	BP	169	34	5.979e-17
GO:0048699	generation of neurons	BP	185	35	1.564e-16
GO:0022008	neurogenesis	BP	188	35	2.644e-16
GO:0031175	neuron projection development	BP	114	27	1.41e-15
GO:0048666	neuron development	BP	129	28	4.622e-15
GO:0120036	plasma membrane bounded cell projection organization	BP	140	29	5.501e-15
GO:0030030	cell projection organization	BP	144	29	1.201e-14
GO:0061564	axon development	BP	74	18	5.017e-11
GO:0048468	cell development	BP	225	31	5.43e-11

	Pathway	N	DE	P.DE
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	125	17	1.543e-06
<i>path:gga05132</i>	Salmonella infection	223	20	0.0001067
<i>path:gga04260</i>	Cardiac muscle contraction	61	8	0.001195
<i>path:gga04540</i>	Gap junction	80	9	0.001819
<i>path:gga04145</i>	Phagosome	130	12	0.001951
<i>path:gga04020</i>	Calcium signaling pathway	209	16	0.002709
<i>path:gga04514</i>	Cell adhesion molecules	110	10	0.005034
<i>path:gga04520</i>	Adherens junction	69	7	0.01003
<i>path:gga04010</i>	MAPK signaling pathway	243	16	0.01125
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	309	18	0.02345



1	CFAP126	DYDC2	LECT1	NTN1	ECM2	SHH	FOXA2	RSPH1
2	CNP1	HPGDS	ENSGALG00000013268	ENSGALG00000043861	CALCA	SPEF2	RSPH9	PTGDS
3	ENSGALG00000055117	SULF1	EVA1C	ENSGALG00000027183	FOXA1	FAM183A	PPIL6	METRNL
4	CAB39L	GPR37L1	ARX	RAB36	ENKUR	CFAP45	SYNDIG1	TAL2
5	ENSGALG00000044478	ZMYND10	CFAP100	CFAP99	ENSGALG00000026754	C9orf116	FOXJ1	ENSGALG0000008309
6	HYDIN	LURAP1L	CMTM8	ARMC4	PDGFC	ENSGALG00000013281	GPR37	DNAI1
7	NKX2–8	ENSGALG00000044151	EFCAB10	LRRC6	MAP7	MTTP	CFAP77	TRABD2B
8	ENSGALG0000008518	WNT5A	DAW1	CFAP44	ENSGALG0000003464	ENSGALG00000012317	AK7	KRT24
9	COL8A2	RIBC2	DNAH10	FAM81A	ENSGALG0000005247	PCSK5	NGB	KLHDC8B
10	ENSGALG0000004495	ENSGALG0000034761	ARHGEF28	ENSGALG0000044224	SLC6A4	SPAG17	ENSGALG00000028207	DUSP27
11	ENSGALG0000044002	RFLNA	TCIM	ENSGALG0000028830	TFPI	ENSGALG0000001244	ENSGALG00000019932	SLAMF8
12	ENSGALG0000036896	NSUN7	CDKL1	OLFML3	PDLIM3	DISP1	ASB9	ENSGALG0000015224
13	HMCN1	C1H11ORF70	ENSGALG0000037997	ARHGAP24	HOPX	TLL1	ADAMTS18	CD82
14	NR4A3	ENSGALG0000054317	ENSGALG0000040709	CFAP70	AKAP14	RASL11A	CFAP57	BARX2
15	FXYD2	PLS1	CCDC170	LAMA5	ENSGALG0000023763	ASL2	ADAMTS17	ENSGALG0000003013
16	ROPN1L	ITGB5	CP	ATF3	ENSGALG0000019240	COL1A2	ENSGALG0000054650	CFD
17	CFAP65	ENSGALG0000011356	DRC7	FHL1	ENSGALG0000016755	WDR63	GAL	ANGPTL2
18	ENSGALG0000012941	TF	KIF6	COL8A1	EXFABP	FERD3L	ASIC2	DYTN
19	CAPSL	ENSGALG0000053594	ENSGALG0000050975	MORN3	ARMC3	SIDT1	CHRNA1	THBS1
20	ILDR2	GOLPH3L	FBN1	CNKSR2	CRYBB2	DPYS	IQCA1	KCNJ2
21	MGST2	LAPTM4B	PTGER4	BEGAIN	SLC6A2	ANTXR1	LPAR3	ENTPD3
22	LRRN3	GABRB2	PTGFRN	CSRNP1	ADRA1B	DAB2	TMEM71	BHLHE40
23	ENSGALG0000011164	GYG2	ENSGALG0000010137	ITGBL1	SDR42E2	WFIKKN2	DENND2A	IFI27L2
24	BCL6	ENSGALG0000049439	HAPLN3	GABRA1	SCUBE1	PKIG	TMEM255B	SPACA9
25	ENSGALG0000007007	BNC2	KLF13	ENSGALG0000047773	LIX1	ENSGALG0000011687	PTH2R	C20orf85
26	ADAMTS3	HNF4A	CRIP1	ENSGALG0000054733	BMP4	WIF1	ENSGALG0000046379	PP2D1
27	KCNF1	TTC34	BMP6	MMP23B	COL25A1	BAIAP2L1	PPL	WNT9A
28	THBS4	IL10RA						

	Term	Ont	N	n	Adj. p-value
GO:0009950	dorsal/ventral axis specification	BP	2	2	0.0002225
GO:0009951	polarity specification of dorsal/ventral axis	BP	2	2	0.0002225
GO:0065001	specification of axis polarity	BP	3	2	0.0006608
GO:0051216	cartilage development	BP	48	5	0.0007224
GO:0061448	connective tissue development	BP	49	5	0.0007948
GO:0006953	acute-phase response	BP	5	2	0.00216
GO:0003415	chondrocyte hypertrophy	BP	5	2	0.00216
GO:0051094	positive regulation of developmental process	BP	128	7	0.003102
GO:0048639	positive regulation of developmental growth	BP	20	3	0.003112
GO:0040007	growth	BP	100	6	0.00386

	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	70	5	0.003919
<i>path:gga00220</i>	Arginine biosynthesis	17	2	0.02611
<i>path:gga04350</i>	TGF–beta signaling pathway	87	4	0.04136
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	309	9	0.04285
<i>path:gga04510</i>	Focal adhesion	175	6	0.04778
<i>path:gga00240</i>	Pyrimidine metabolism	56	3	0.05123
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.05849
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	2	0.06939
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	31	2	0.07797
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	2	0.08238