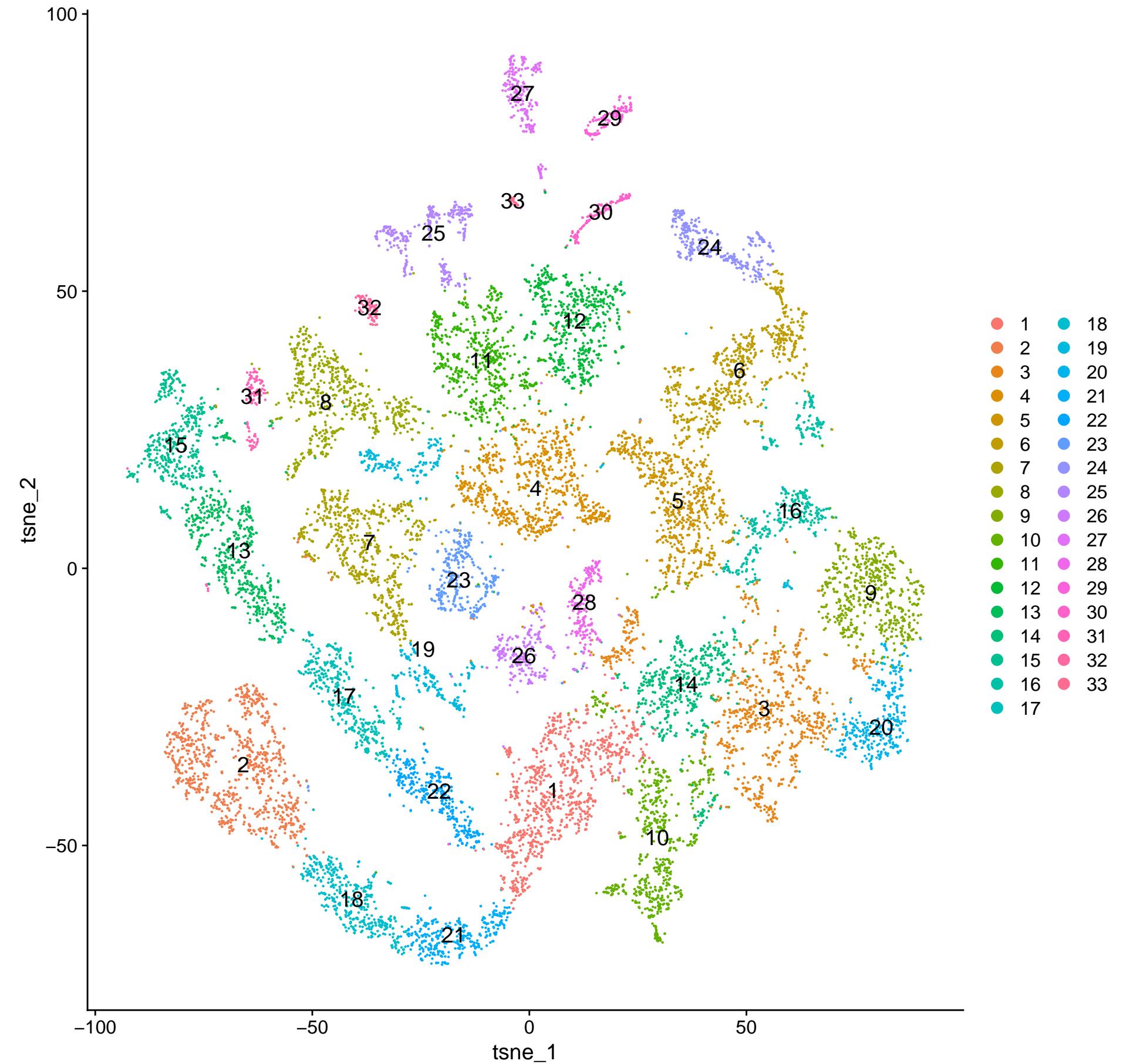


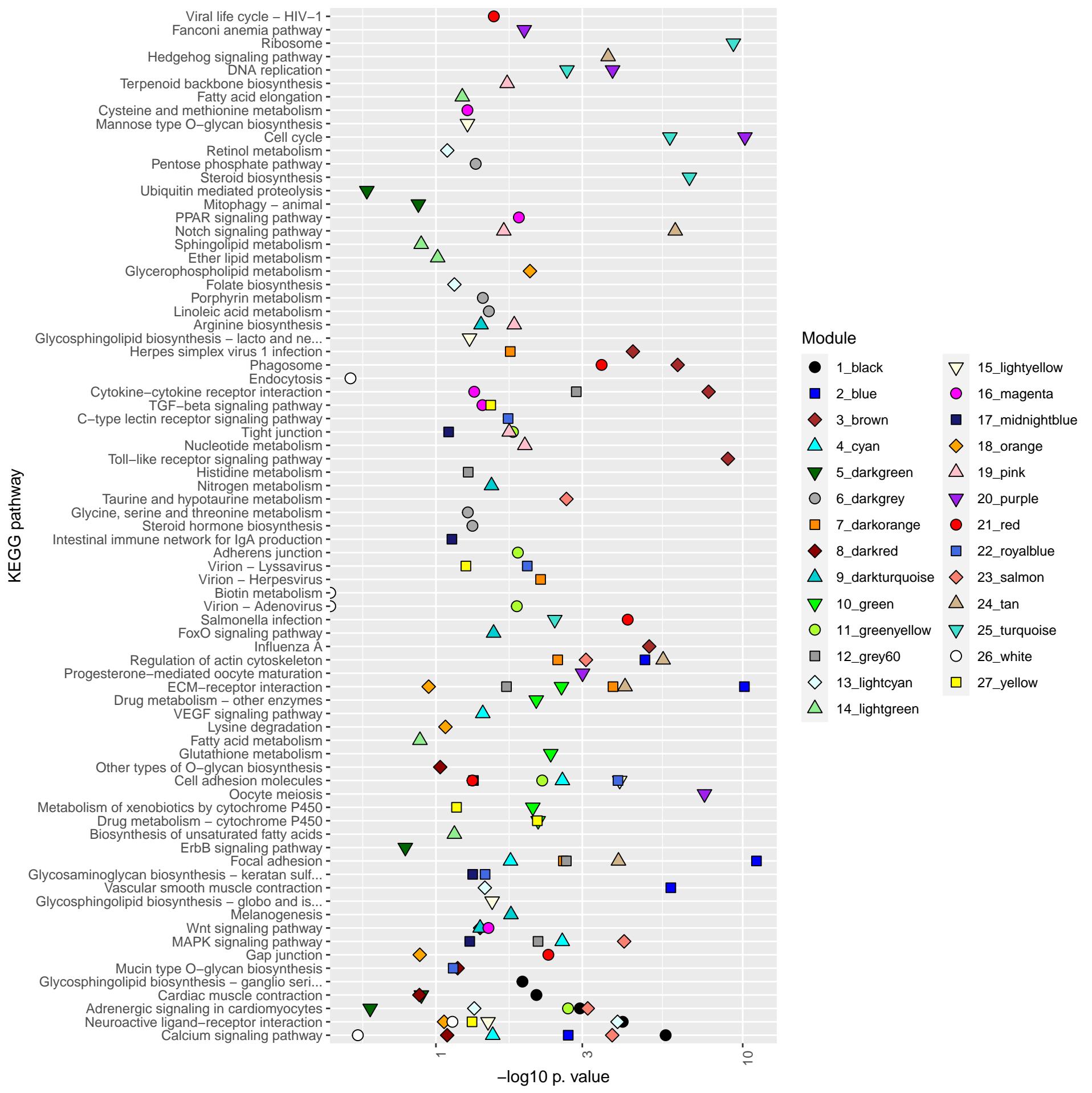
Gg-devel_int scWGCNA modules

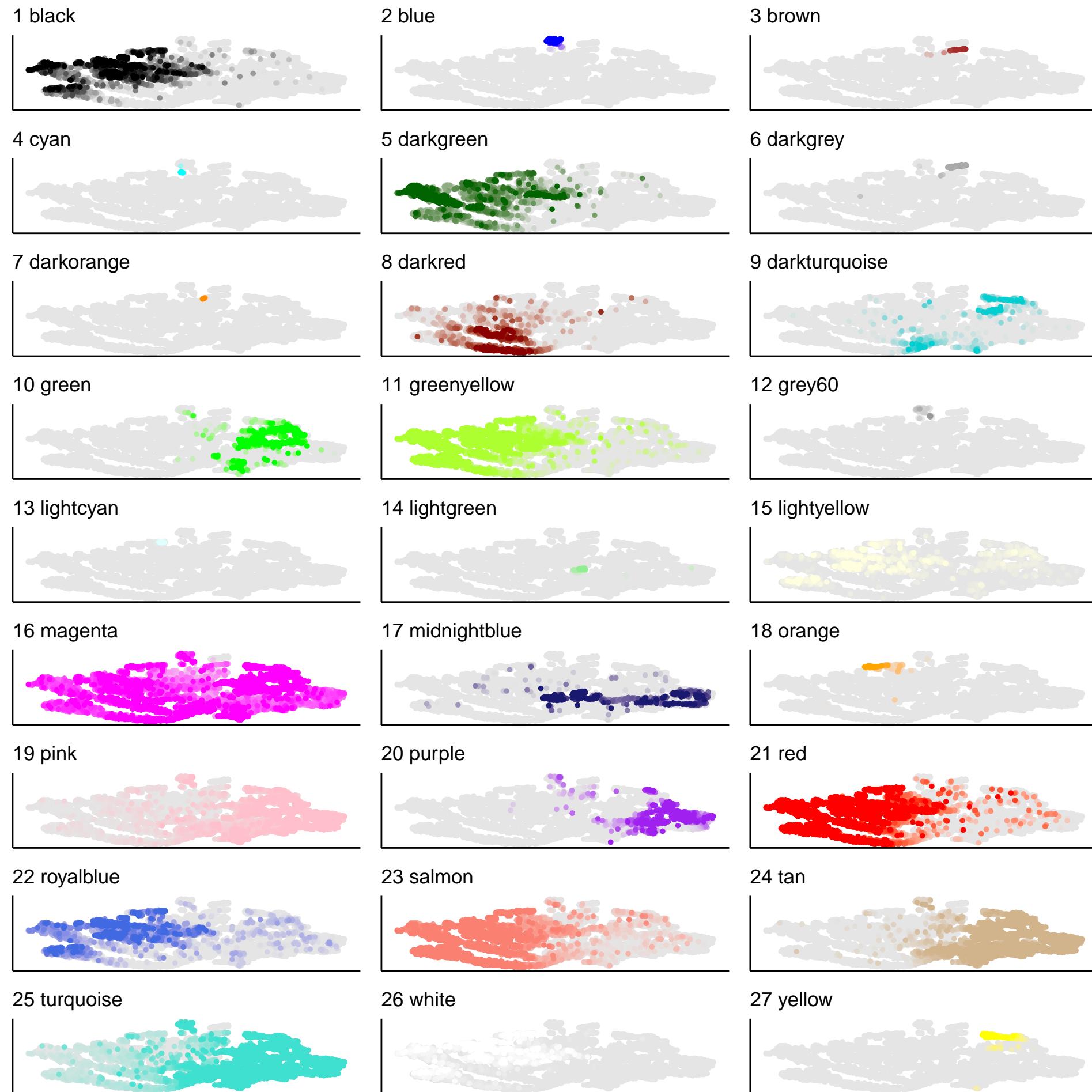


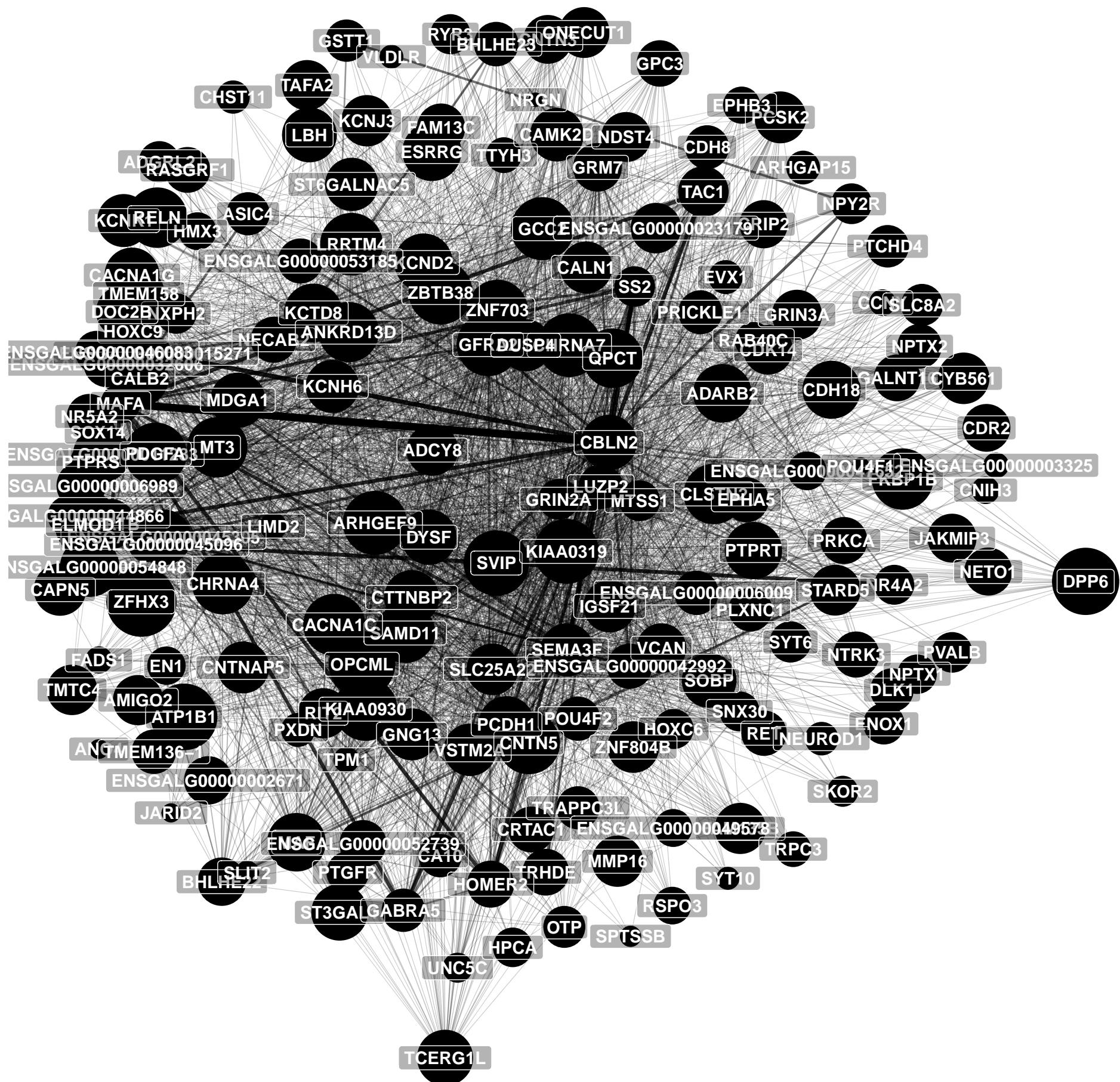


Module

●	1_black	▽	15_lightyellow
■	2_blue	●	16_magenta
◆	3_brown	■	17_midnightblue
▲	4_cyan	◆	18_orange
▼	5_darkgreen	▲	19_pink
○	6_darkgrey	▼	20_purple
□	7_darkorange	●	21_red
◆	8_darkred	■	22_royalblue
▲	9_darkturquoise	●	23_salmon
▼	10_green	△	24_tan
○	11_greenyellow	▼	25_turquoise
■	12_grey60	○	26_white
◇	13_lightcyan	■	27_yellow
▲	14_lightgreen		



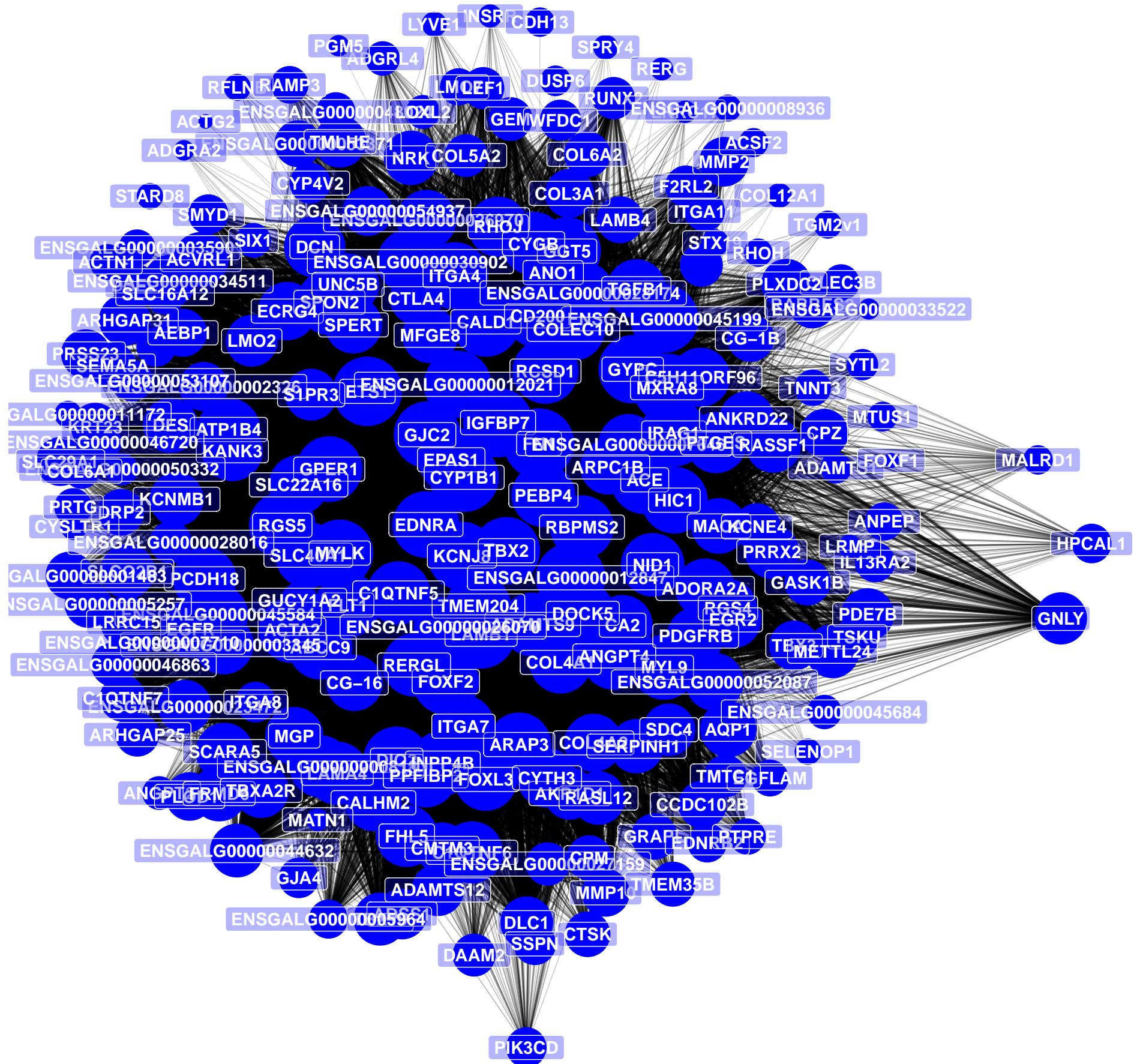




1	ZFHX3	DPP6	ATP1B1	GFRA2	KIAA0319	SVIP	CBLN2	CHRNA4
2	OPCML	ARHGEF9	RELN	KCND2	CHRNA7	LRRTM4	CACNA1C	KIAA0930
3	FKBP1B	MT3	ELMOD1	CNTN5	QPCT	ENSGALG00000032606	SEMA3F	PDGFA
4	CA10	GCC2	ESRRG	CLSTN2	ZBTB38	ANKRD13D	MAF	PTPRT
5	PCSK2	ZNF703	SLC25A22	VCAN	CTTNBP2	TAC1	PCDH1	MTSS1
6	ADARB2	CDH18	ENSGALG00000045305	TCERG1L	PRKCA	CALB2	ENSGALG00000054848	MDGA1
7	SAMD11	IGSF21	SOBP	CAMK2D	DYSF	LBH	DUSP4	ENSGALG00000011283
8	MMP16	CACNA1G	LUZP2	KCNK1	KCTD8	VSTM2A	CDK14	ENSGALG0000006009
9	SNX30	ST3GAL1	HTR1B	TMEM158	KCNJ3	NPTX2	OTP	TAFA2
10	FAM135B	GNG13	NECAB2	CAPN5	CNTN3	STARD5	CNTNAP5	DOC2B
11	TPM1	KCNH6	ENSGALG00000023179	ADCY8	TMTC4	POU4F2	ST6GALNAC5	EPHA5
12	ZNF804B	HOXC9	NDST4	GRM7	AMIGO2	GABRA5	CRIP2	RIT2
13	HOMER2	JAKMIP3	CDR2	CRTAC1	GALNT16	CALN1	ONECUT1	PXDN
14	GRIN3A	SS2	ENSGALG0000002671	TRHDE	PRICKLE1	BHLHE23	ENSGALG00000042992	TRAPPC3L
15	MAFA	PVALB	RET	ENSGALG0000006989	NTRK3	FAM13C	EN1	PLXNC1
16	ASIC4	ENSGALG00000052739	TTYH3	GPC3	NR4A2	BHLHE22	DLK1	CDH8
17	SLIT2	CYB561	NETO1	RAB40C	RASGRF1	ENSGALG00000053185	EPHB3	NPTX1
18	ENOX1	ENSGALG00000046083	NR5A2	CCNY	RSPO3	ADGRL2	SYT6	PTCHD4
19	NXPH2	PTGFR	RYR3	ENSGALG00000045096	HMX3	FADS1	ENSGALG00000044866	TRPC3
20	TMEM136-1	PTPRS	GSTT1	ENSGALG0000003325	EVX1	HPCA	ENSGALG00000015271	CHST11
21	SLC8A2	ENSGALG00000047652	GRIN2A	SPTSSB	NPY2R	ENSGALG00000049578	HOXC6	SOX14
22	LIMD2	UNC5C	SKOR2	NEUROD1	ARHGAP15	CNIH3	SYT10	POU4F1
23	VLDLR	JARID2	ANO4	NRGN				

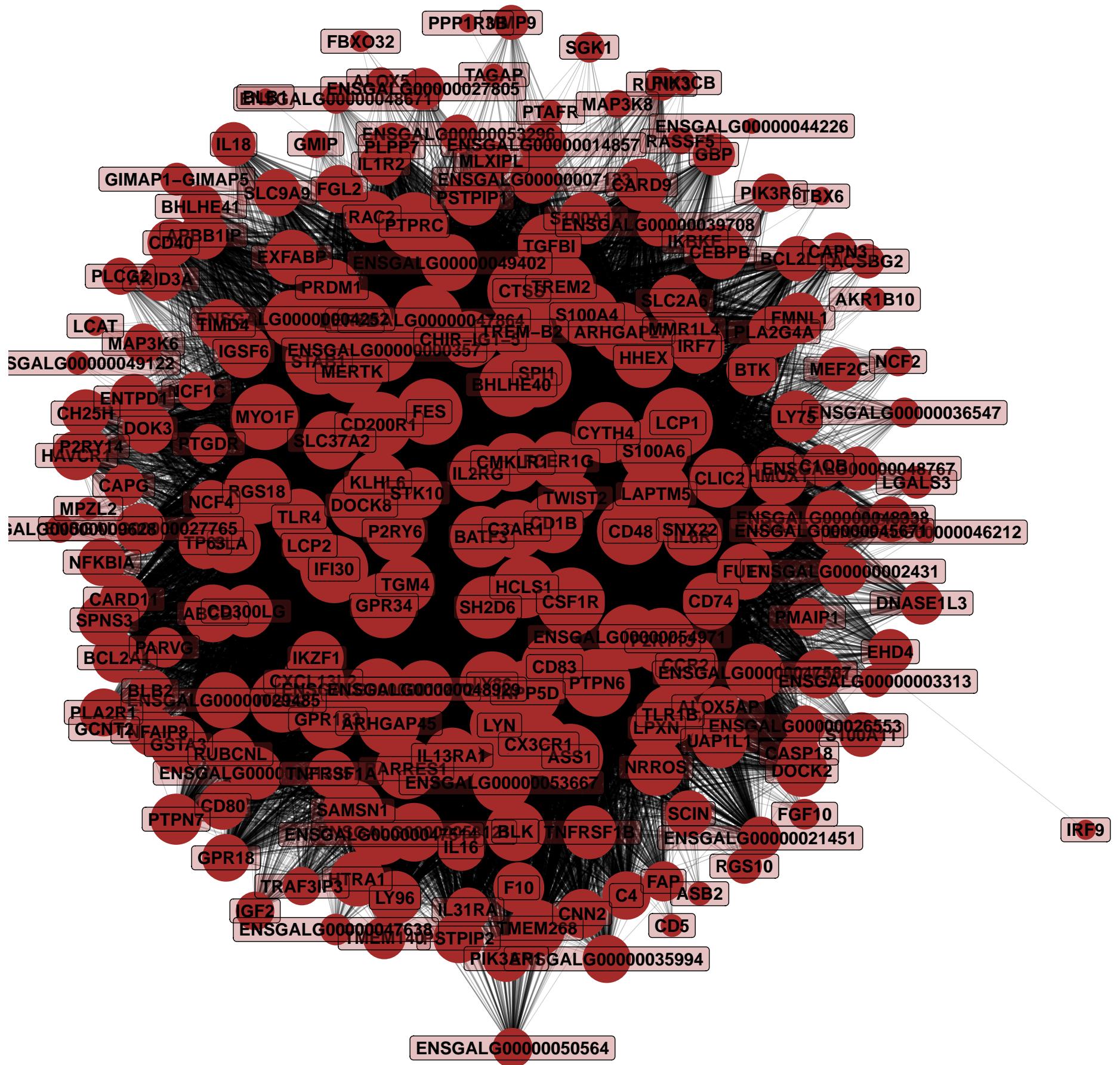
	Term	Ont	N	n	Adj. p-value
GO:0007399	nervous system development	BP	258	15	1.553e-06
GO:0048856	anatomical structure development	BP	623	23	7.007e-06
GO:0032502	developmental process	BP	655	23	1.575e-05
GO:0032501	multicellular organismal process	BP	711	24	1.94e-05
GO:0048731	system development	BP	483	19	1.965e-05
GO:0007275	multicellular organism development	BP	577	21	2.248e-05
GO:0048699	generation of neurons	BP	180	11	2.546e-05
GO:0022008	neurogenesis	BP	183	11	2.967e-05
GO:0030182	neuron differentiation	BP	165	9	0.0003294
GO:0009653	anatomical structure morphogenesis	BP	292	12	0.0004805

	Pathway	N	DE	P.DE
<i>path:gga04020</i>	Calcium signaling pathway	201	13	2.464e-06
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	281	13	8.677e-05
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	7	0.001132
<i>path:gga04260</i>	Cardiac muscle contraction	59	4	0.007482
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	2	0.01218
<i>path:gga04912</i>	GnRH signaling pathway	76	4	0.01777
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis – heparan sulfate / heparin	21	2	0.03063
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	2	0.05532
<i>path:gga04371</i>	Apelin signaling pathway	111	4	0.05859
<i>path:gga04540</i>	Gap junction	79	3	0.08572



	Term	Ont	N	n	Adj. p-value
GO:0048856	anatomical structure development	BP	623	31	4.403e-08
GO:0009653	anatomical structure morphogenesis	BP	292	20	9.046e-08
GO:0032502	developmental process	BP	655	31	1.36e-07
GO:0048646	anatomical structure formation involved in morphogenesis	BP	128	12	1.468e-06
GO:0022610	biological adhesion	BP	143	12	4.72e-06
GO:0007155	cell adhesion	BP	143	12	4.72e-06
GO:0030154	cell differentiation	BP	417	21	6.465e-06
GO:0032501	multicellular organismal process	BP	711	29	7.074e-06
GO:0048869	cellular developmental process	BP	426	21	8.968e-06
GO:0007275	multicellular organism development	BP	577	25	1.16e-05

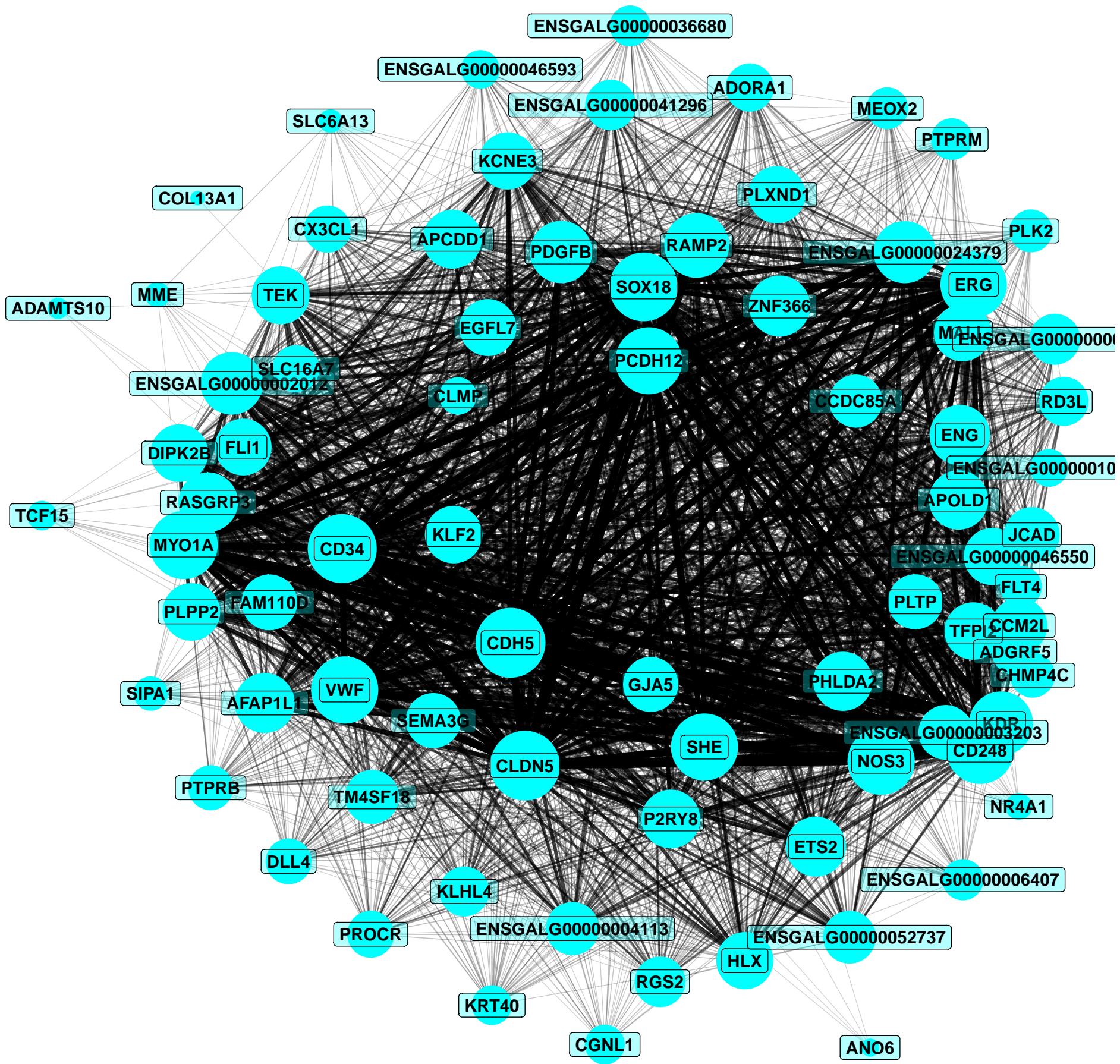
	Pathway	N	DE	P.DE
<i>path:gga04510</i>	Focal adhesion	172	20	8.178e-12
<i>path:gga04512</i>	ECM–receptor interaction	68	13	7.451e-11
<i>path:gga04270</i>	Vascular smooth muscle contraction	106	11	1.482e-06
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	13	1.577e-05
<i>path:gga04020</i>	Calcium signaling pathway	201	10	0.001999
<i>path:gga04520</i>	Adherens junction	69	5	0.005806
<i>path:gga00360</i>	Phenylalanine metabolism	12	2	0.01634
<i>path:gga04010</i>	MAPK signaling pathway	239	9	0.01881
<i>path:gga04514</i>	Cell adhesion molecules	99	5	0.02483
<i>path:gga00310</i>	Lysine degradation	50	3	0.05046



1	CSF1R	SPI1	CTSS	LAPTM5	LCP1	IFI30	RGS18	ENSGALG00000047864
2	S100A4	PTPN6	S100A6	P2RY13	TREM2	MYO1F	CD48	CD83
3	INPP5D	ITGB2	HCLS1	CD200R1	ASS1	ENSGALG00000053121	FYB	LY86
4	SAMSN1	HHEX	CXCL13L2	PTPRC	STAB1	ENSGALG00000000357	FES	CD1B
5	CCL4v1	BLK	TMEM268	C3AR1	ENSGALG00000053667	CCR2	S100A12	GSTA3
6	CX3CR1	GPR34	ARHGAP45	CYTH4	ENSGALG00000011872	CHIR-IG1-5	RARRES1	LITAF
7	DOCK8	BATF3	ARHGAP27	ABCB1	HMOX1	ENSGALG0000004252	TREM-B2	LY96
8	SH2D6	ENSGALG00000054971	P2RY6	TLR4	SLA	ENSGALG00000048929	ENSGALG00000047514	GPR183
9	MMR1L4	KLHL6	ENSGALG00000047587	BHLHE40	CLIC2	IGSF6	PRDM1	ENSGALG00000021451
10	TGFBI	IL13RA1	LCP2	BCL2A1	IL2RG	ENSGALG00000048338	C1QB	MERTK
11	FUT7	CEBPB	TLR1B	RAC2	SLC37A2	ENSGALG00000049402	TGM4	ENSGALG00000048767
12	FGL2	IL16	CD74	TIMD4	NRROS	CMKLR1	CARD11	LPXN
13	LYN	PSTPIP2	BTK	FMNL1	EXFABP	SPNS3	TP63	ENSGALG00000021395
14	CNN2	FCER1G	ENSGALG00000026553	HTRA1	CD300LG	ENSGALG00000029485	UAP1L1	NCF4
15	ENSGALG00000035994	IL6R	SLC2A6	HAVCR1	PLA2G4A	DNASE1L3	ADAP2	DOCK2
16	STK10	TNFRSF1A	IKZF1	IRF7	DOK3	BCL2L15	C4	APBB1IP
17	CH25H	CARD9	CD80	RUBCNL	LY75	GBP	PSTPIP1	PTPN7
18	GPR18	BHLHE41	ENSGALG0000002431	PLA2R1	SLC9A9	PTGDR	CASP18	TNFAIP8
19	TWIST2	ENSGALG0000007123	S100A11	ENSGALG00000047638	CD40	ENSGALG00000045671	ENSGALG00000027765	F10
20	MAP3K6	ARID3A	CAPN3	SCIN	FAP	ENTPD1	IL1R2	NFKBIA
21	PARVG	IL18	ALOX5AP	EHD4	PTAFR	TNFRSF1B	IL31RA	PLPP7
22	RGS10	PLCG2	ENSGALG00000053296	ENSGALG00000014857	ENSGALG00000050564	MAP3K8	PIK3R6	ENSGALG00000039708
23	MEF2C	TRAF3IP3	ENSGALG0000003313	CAPG	MLXIPL	IGF2	NCF1C	BLB2
24	TMEM140	MMP9	ENSGALG00000046212	NCF2	LGALS3	ENSGALG00000027805	SGK1	RUNX3
25	ALOX5	PMAIP1	RASSF5	SNX22	PIK3AP1	P2RY14	GMIP	ENSGALG00000036547
26	GIMAP1-GIMAP5	ACSBG2	TBX6	ENSGALG00000048671	FGF10	TAGAP	MPZL2	CD5
27	IKBKE	ENSGALG00000049122	AKR1B10	PIK3CB	ENSGALG00000044226	ENSGALG00000009628	ASB2	BLB1
28	LCAT	PPP1R3B	FBXO32	IRF9	GCNT2			

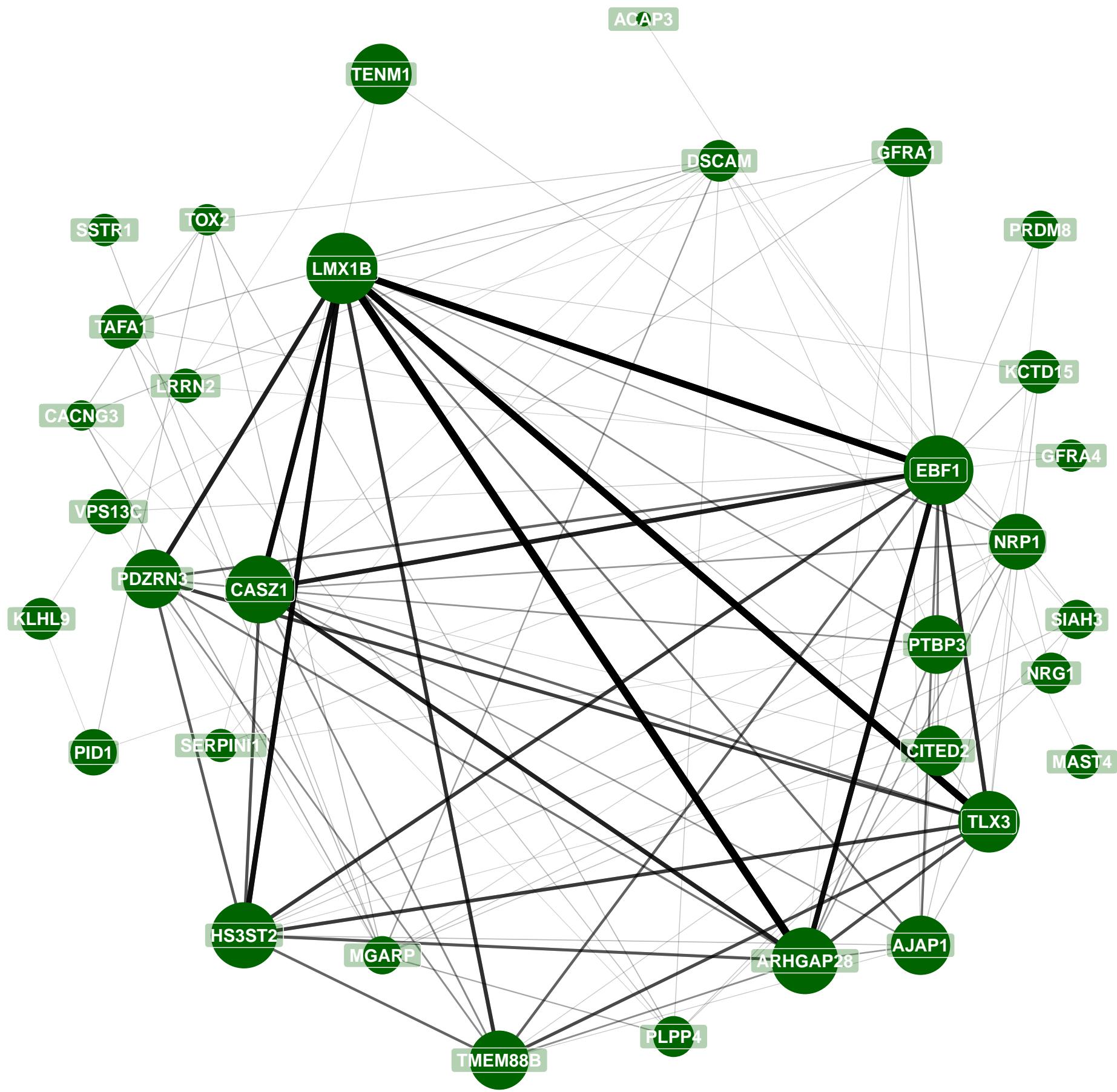
	Term	Ont	N	n	Adj. p-value
GO:0006952	defense response	BP	91	10	1.816e–06
GO:0006954	inflammatory response	BP	49	7	1.166e–05
GO:0002376	immune system process	BP	169	12	1.699e–05
GO:0098542	defense response to other organism	BP	61	7	5.037e–05
GO:0009607	response to biotic stimulus	BP	77	7	0.0002239
GO:0043207	response to external biotic stimulus	BP	77	7	0.0002239
GO:0051707	response to other organism	BP	77	7	0.0002239
GO:0044419	biological process involved in interspecies interaction between organisms	BP	88	7	0.0005098
GO:0009605	response to external stimulus	BP	192	10	0.001036
GO:0006950	response to stress	BP	319	13	0.001863

	Pathway	N	DE	P.DE
<i>path:gga04620</i>	Toll-like receptor signaling pathway	71	12	1.126e-09
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	151	15	1.813e-08
<i>path:gga04145</i>	Phagosome	125	12	7.281e-07
<i>path:gga05164</i>	Influenza A	111	10	1.104e-05
<i>path:gga05168</i>	Herpes simplex virus 1 infection	129	10	4.106e-05
<i>path:gga04623</i>	Cytosolic DNA–sensing pathway	42	6	5.018e-05
<i>path:gga04621</i>	NOD–like receptor signaling pathway	116	9	9.923e-05
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	82	7	0.0003309
<i>path:gga04672</i>	Intestinal immune network for IgA production	22	4	0.0003691
<i>path:gga04210</i>	Apoptosis	115	8	0.0005079



	Term	Ont	N	n	Adj. p-value
GO:0035590	purinergic nucleotide receptor signaling pathway	BP	7	2	0.0006861
GO:0050728	negative regulation of inflammatory response	BP	8	2	0.0009113
GO:0031348	negative regulation of defense response	BP	11	2	0.00177
GO:0050878	regulation of body fluid levels	BP	11	2	0.00177
GO:0060982	coronary artery morphogenesis	BP	1	1	0.005808
GO:0001712	ectodermal cell fate commitment	BP	1	1	0.005808
GO:0003094	glomerular filtration	BP	1	1	0.005808
GO:0070254	mucus secretion	BP	1	1	0.005808
GO:1900453	negative regulation of long-term synaptic depression	BP	1	1	0.005808
GO:0070256	negative regulation of mucus secretion	BP	1	1	0.005808

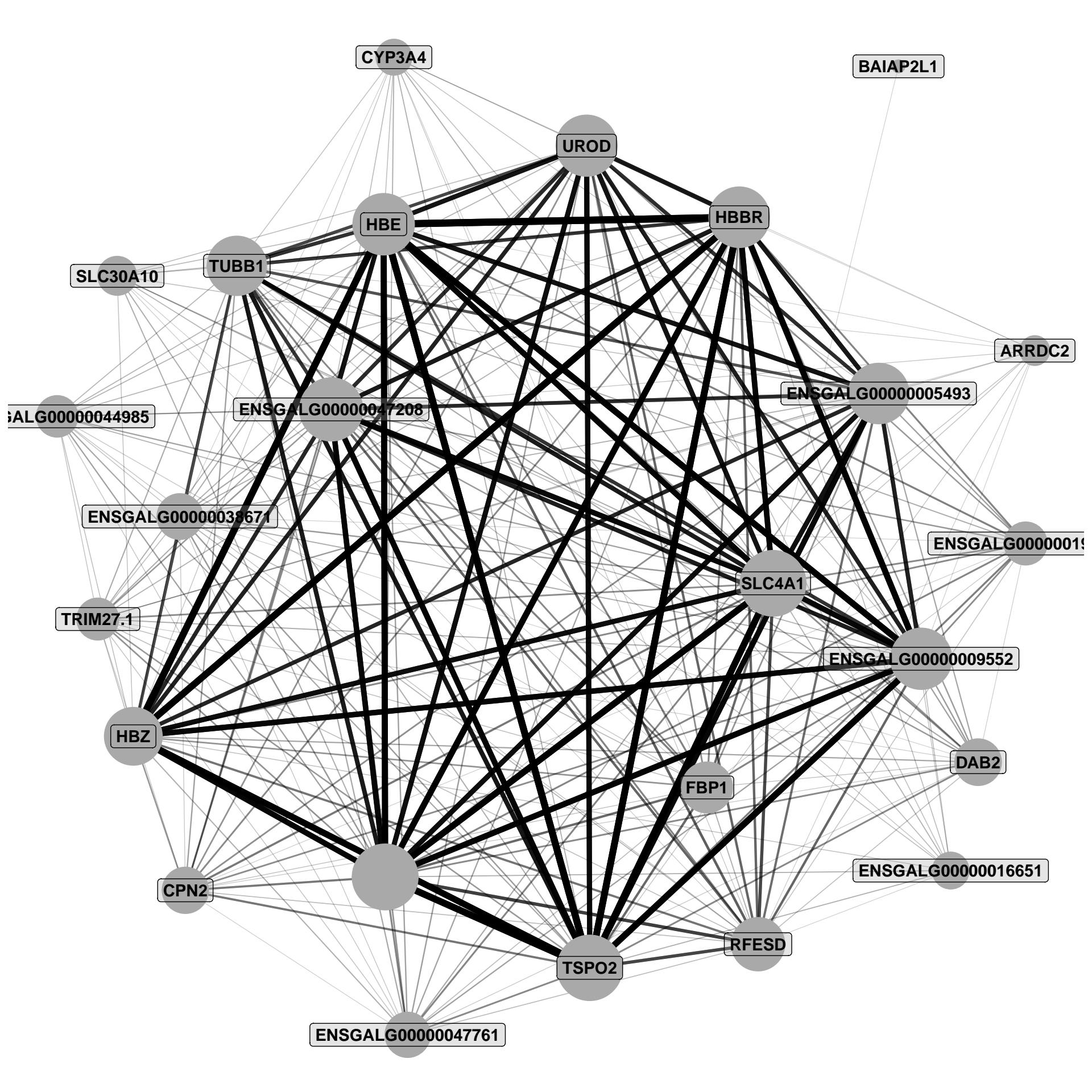
	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	99	4	0.002608
<i>path:gga04010</i>	MAPK signaling pathway	239	6	0.002626
<i>path:gga04510</i>	Focal adhesion	172	4	0.01777
<i>path:gga04020</i>	Calcium signaling pathway	201	4	0.02941
<i>path:gga04370</i>	VEGF signaling pathway	53	2	0.03792
<i>path:gga04520</i>	Adherens junction	69	2	0.06086
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	4	0.08062
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.09434
<i>path:gga04270</i>	Vascular smooth muscle contraction	106	2	0.1262
<i>path:gga04371</i>	Apelin signaling pathway	111	2	0.136



1	LMX1B	HS3ST2	EBF1	CASZ1	TLX3	ARHGAP28	TENM1	NRP1
2	PDZRN3	TMEM88B	AJAP1	PTBP3	GFRA1	CITED2	PID1	KCTD15
3	TAFA1	PRDM8	DSCAM	PLPP4	VPS13C	SERPINI1	KLHL9	NRG1
4	GFRA4	SSTR1	SIAH3	MAST4	MGARP	LRRN2	TOX2	CACNG3
5	ACAP3							

	Term	Ont	N	n	Adj. p-value
GO:0007399	nervous system development	BP	258	7	1.475e-06
GO:0031346	positive regulation of cell projection organization	BP	31	3	4.681e-05
GO:0051491	positive regulation of filopodium assembly	BP	6	2	7.579e-05
GO:0048731	system development	BP	483	7	8.692e-05
GO:0046847	filopodium assembly	BP	10	2	0.0002261
GO:0051489	regulation of filopodium assembly	BP	10	2	0.0002261
GO:0007275	multicellular organism development	BP	577	7	0.0002622
GO:0120035	regulation of plasma membrane bounded cell projection organization	BP	56	3	0.0002777
GO:0031344	regulation of cell projection organization	BP	57	3	0.0002927
GO:0120034	positive regulation of plasma membrane bounded cell projection assembly	BP	12	2	0.0003306

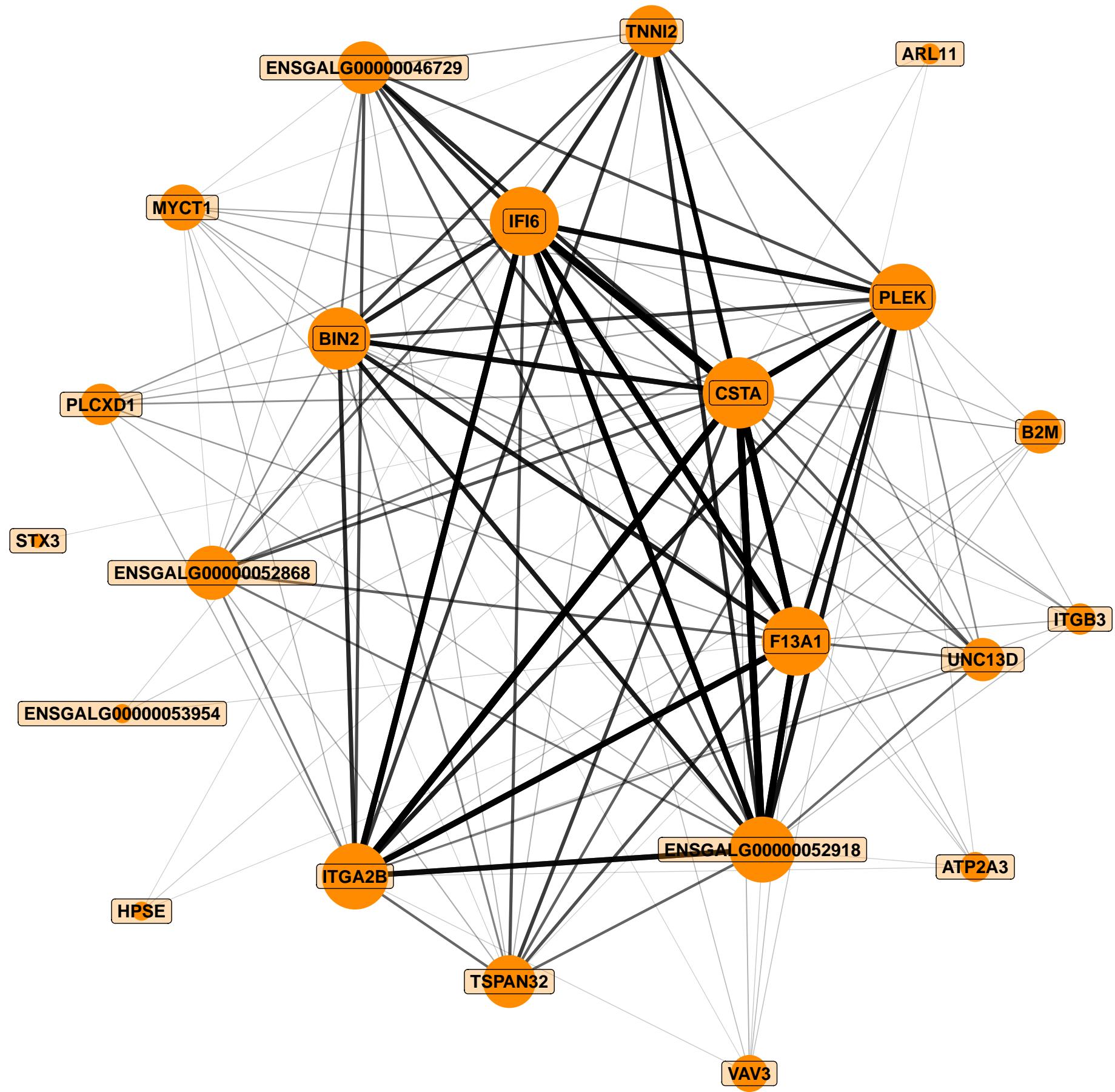
	Pathway	N	DE	P.DE
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.1269
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.1329
<i>path:gga04012</i>	ErbB signaling pathway	76	1	0.1605
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	1	0.2452
<i>path:gga04120</i>	Ubiquitin mediated proteolysis	127	1	0.2539
<i>path:gga04144</i>	Endocytosis	218	1	0.3962
<i>path:gga04010</i>	MAPK signaling pathway	239	1	0.4251
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	1	0.479
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1



1	NA	SLC4A1	TSPO2	HBE	ENSGALG00000047208	ENSGALG0000009552	HBZ	HBBR
2	TUBB1	ENSGALG00000005493	FBP1	RFESD	TRIM27.1	UROD	CPN2	ENSGALG00000038671
3	CYP3A4	ENSGALG00000044985	DAB2	ENSGALG00000047761	SLC30A10	ENSGALG00000016651	ENSGALG00000019312	ARRDC2
4	BAIAP2L1							

	Term	Ont	N	n	Adj. p-value
GO:0042744	hydrogen peroxide catabolic process	BP	7	3	1.888e-07
GO:0042743	hydrogen peroxide metabolic process	BP	7	3	1.888e-07
GO:0015671	oxygen transport	BP	7	3	1.888e-07
GO:0015669	gas transport	BP	8	3	3.018e-07
GO:0098869	cellular oxidant detoxification	BP	14	3	1.948e-06
GO:1990748	cellular detoxification	BP	16	3	2.989e-06
GO:0097237	cellular response to toxic substance	BP	16	3	2.989e-06
GO:0098754	detoxification	BP	17	3	3.625e-06
GO:0072593	reactive oxygen species metabolic process	BP	18	3	4.345e-06
GO:0009636	response to toxic substance	BP	20	3	6.056e-06

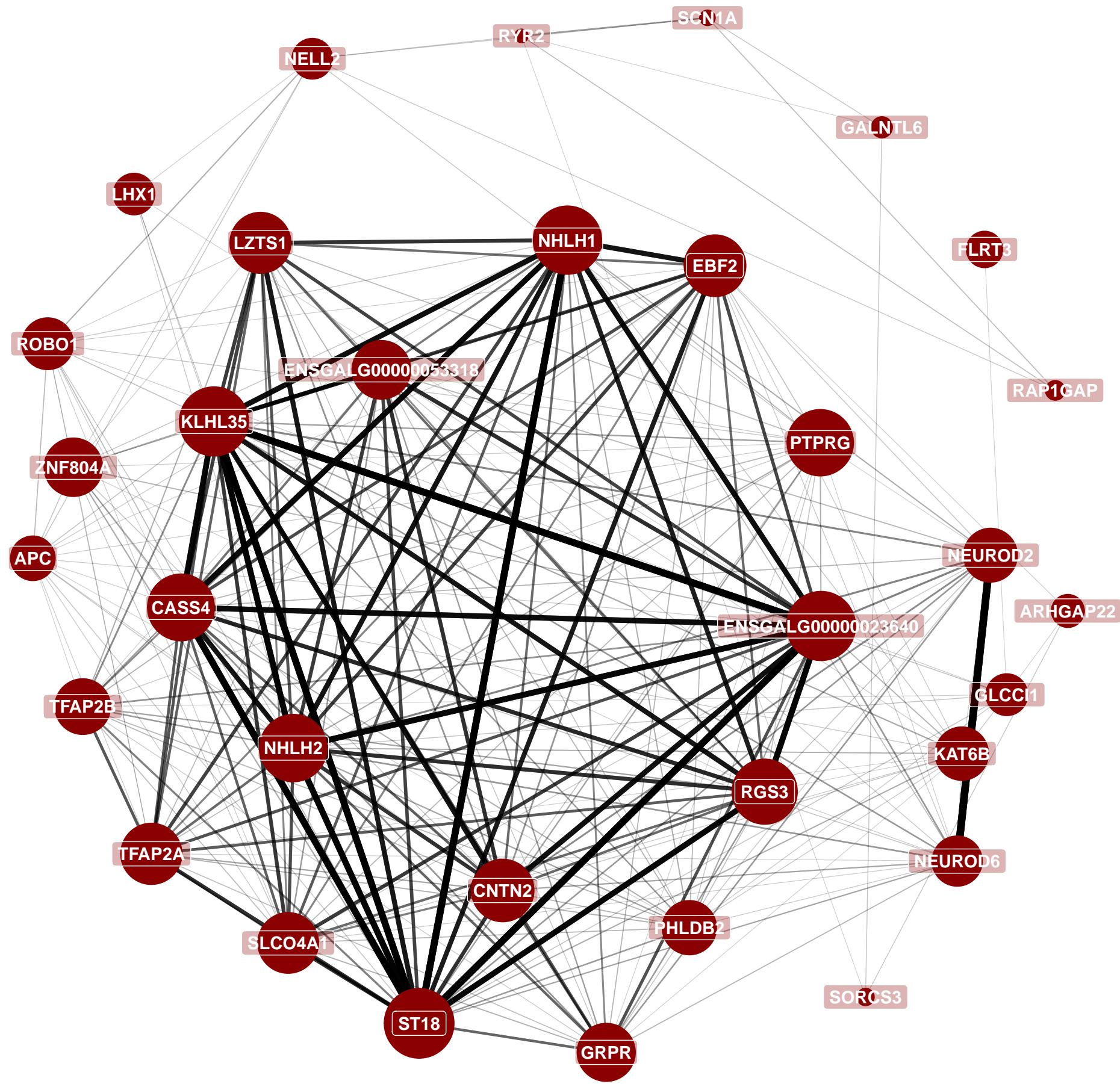
	Pathway	N	DE	P.DE
<i>path:gga00591</i>	Linoleic acid metabolism	18	1	0.03253
<i>path:gga00860</i>	Porphyrin metabolism	21	1	0.03785
<i>path:gga00030</i>	Pentose phosphate pathway	25	1	0.0449
<i>path:gga00140</i>	Steroid hormone biosynthesis	27	1	0.04841
<i>path:gga00260</i>	Glycine, serine and threonine metabolism	30	1	0.05364
<i>path:gga00830</i>	Retinol metabolism	30	1	0.05364
<i>path:gga00051</i>	Fructose and mannose metabolism	34	1	0.06058
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	46	1	0.08112
<i>path:gga04540</i>	Gap junction	79	1	0.1354
<i>path:gga01200</i>	Carbon metabolism	95	1	0.1606



1	CSTA	IFI6	ENSGALG00000046729	BIN2	ITGA2B	ENSGALG00000052918	F13A1	PLEK
2	TNNI2	UNC13D	MYCT1	ITGB3	ATP2A3	ENSGALG00000052868	TSPAN32	B2M
3	VAV3	HPSE	STX3	PLCXD1	ARL11	ENSGALG00000053954		

	Term	Ont	N	n	Adj. p-value
GO:0019883	antigen processing and presentation of endogenous antigen	BP	1	1	0.001605
GO:0002483	antigen processing and presentation of endogenous peptide antigen	BP	1	1	0.001605
GO:0019885	antigen processing and presentation of endogenous peptide antigen via MHC class I	BP	1	1	0.001605
GO:0071281	cellular response to iron ion	BP	1	1	0.001605
GO:0030200	heparan sulfate proteoglycan catabolic process	BP	1	1	0.001605
GO:2000978	negative regulation of forebrain neuron differentiation	BP	1	1	0.001605
GO:1900121	negative regulation of receptor binding	BP	1	1	0.001605
GO:0071800	podosome assembly	BP	1	1	0.001605
GO:0090343	positive regulation of cell aging	BP	1	1	0.001605
GO:2000774	positive regulation of cellular senescence	BP	1	1	0.001605

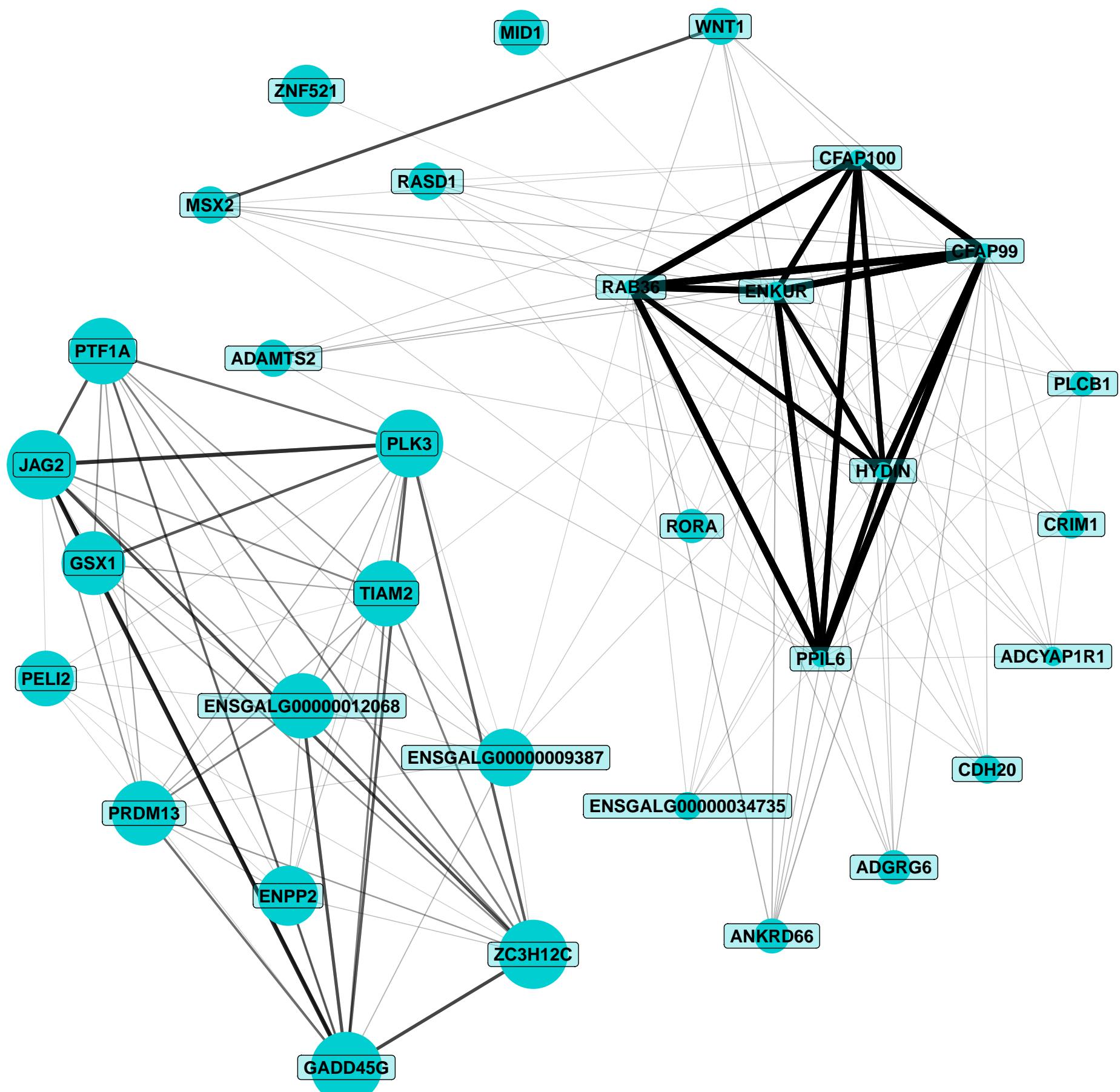
	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	68	3	0.000167
<i>path:gga04510</i>	Focal adhesion	172	3	0.002494
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	3	0.003208
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.006405
<i>path:gga05168</i>	Herpes simplex virus 1 infection	129	2	0.01792
<i>path:gga00531</i>	Glycosaminoglycan degradation	15	1	0.02382
<i>path:gga04130</i>	SNARE interactions in vesicular transport	28	1	0.04402
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.0906
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	1	0.1787
<i>path:gga04145</i>	Phagosome	125	1	0.1827



1	NHLH1	ST18	ENSGALG00000023640	KLHL35	TFAP2A	NHLH2	RGS3	CASS4
2	CNTN2	EBF2	PTPRG	LZTS1	NEUROD6	TFAP2B	ZNF804A	SLCO4A1
3	NEUROD2	ENSGALG00000053318	GRPR	PHLDB2	KAT6B	ROBO1	LHX1	APC
4	GLCCI1	NELL2	FLRT3	ARHGAP22	RAP1GAP	GALNTL6	SCN1A	SORCS3
5	RYR2							

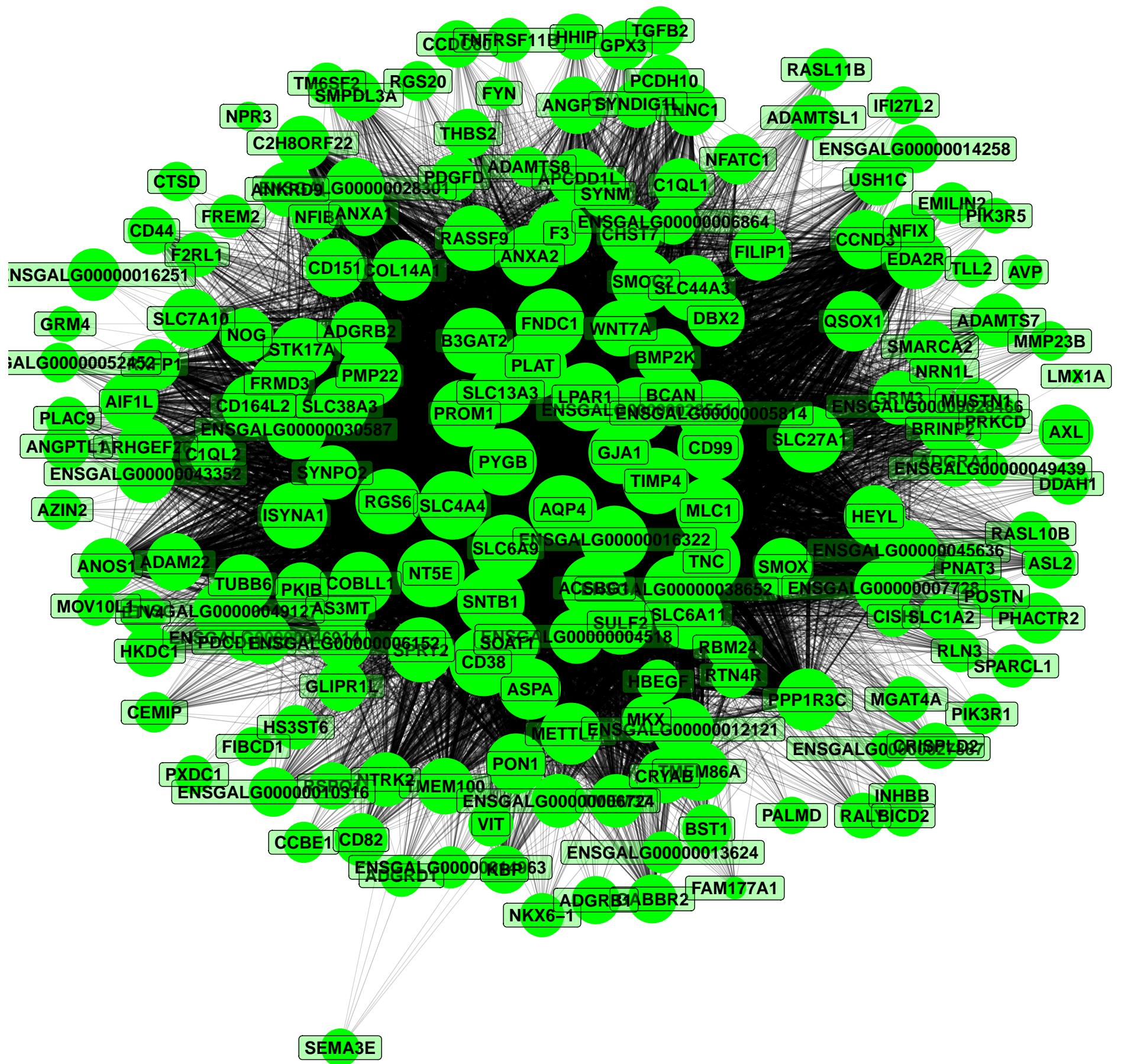
Term	Ont	N	n
cerebellar Purkinje cell–granule cell precursor cell signaling involved in regulation of granule cell precursor cell proliferation	BP	1	1
comma-shaped body morphogenesis	BP	1	1
dorsal spinal cord interneuron posterior axon guidance	BP	1	1
forebrain regionalization	BP	1	1
lateral motor column neuron migration	BP	1	1
motor neuron migration	BP	1	1
positive regulation of anterior head development	BP	1	1
positive regulation of epithelial cell differentiation involved in kidney development	BP	1	1
positive regulation of nephron tubule epithelial cell differentiation	BP	1	1
presynaptic membrane organization	BP	1	1

	Pathway	N	DE	P.DE
<i>path:gga04310</i>	Wnt signaling pathway	135	2	0.04043
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	1	0.06654
<i>path:gga04020</i>	Calcium signaling pathway	201	2	0.08167
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	1	0.09281
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.1309
<i>path:gga04514</i>	Cell adhesion molecules	99	1	0.21
<i>path:gga04371</i>	Apelin signaling pathway	111	1	0.2323
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	1	0.2523
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	1	0.3618
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	281	1	0.4902



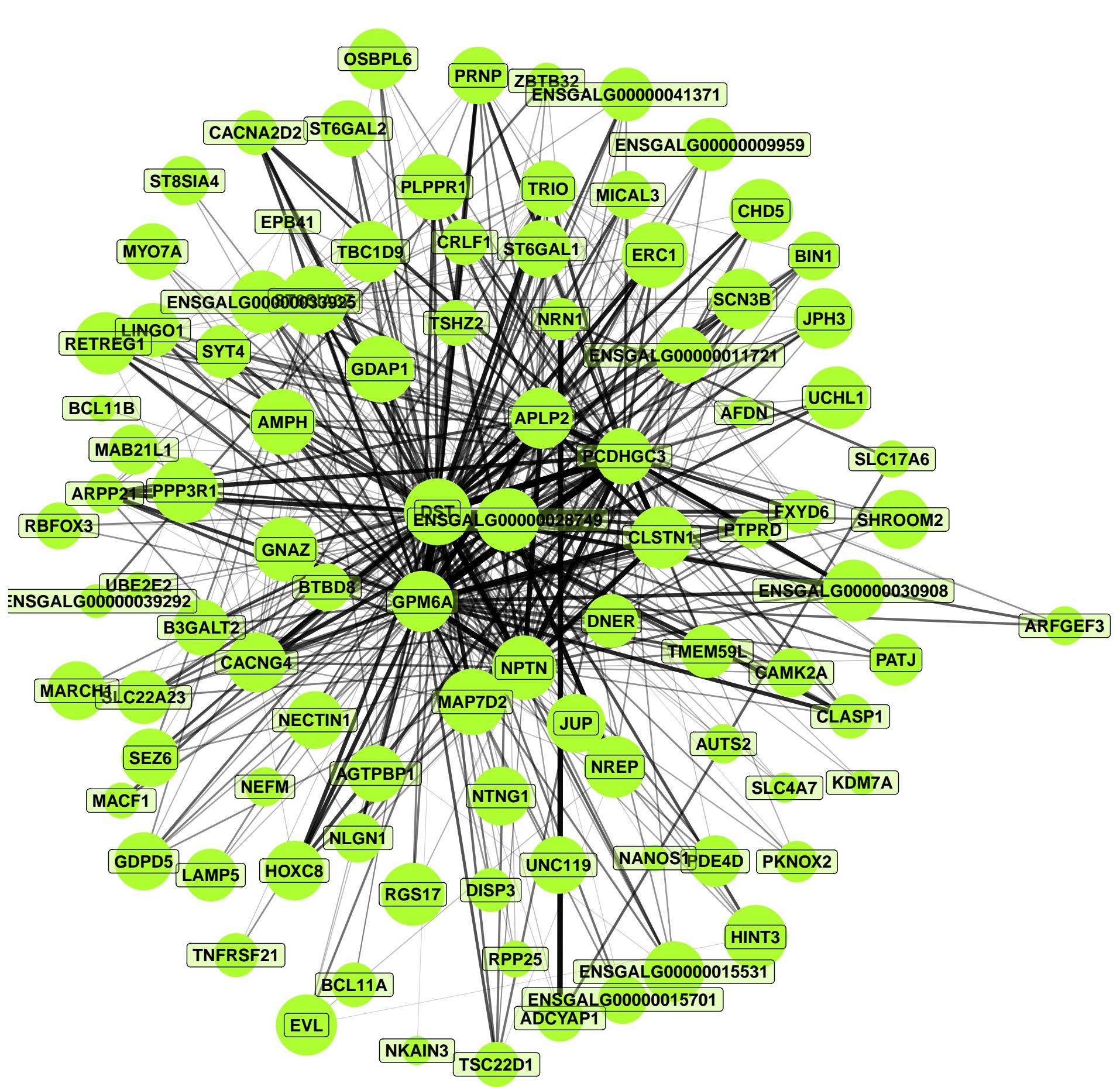
	Term	Ont	N	n	Adj. p-value
GO:0006538	glutamate catabolic process	BP	1	1	0.002369
GO:0043649	dicarboxylic acid catabolic process	BP	2	1	0.004733
GO:0009065	glutamine family amino acid catabolic process	BP	2	1	0.004733
GO:0006536	glutamate metabolic process	BP	3	1	0.007091
GO:0072350	tricarboxylic acid metabolic process	BP	4	1	0.009444
GO:0048263	determination of dorsal identity	BP	5	1	0.01179
GO:0048262	determination of dorsal/ventral asymmetry	BP	5	1	0.01179
GO:0043648	dicarboxylic acid metabolic process	BP	5	1	0.01179
GO:1901606	alpha–amino acid catabolic process	BP	6	1	0.01413
GO:0006541	glutamine metabolic process	BP	6	1	0.01413

	Pathway	N	DE	P.DE
<i>path:gga04916</i>	Melanogenesis	86	2	0.01755
<i>path:gga04068</i>	FoxO signaling pathway	112	2	0.02873
<i>path:gga00910</i>	Nitrogen metabolism	13	1	0.03038
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.03954
<i>path:gga04310</i>	Wnt signaling pathway	135	2	0.04043
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	1	0.07318
<i>path:gga00565</i>	Ether lipid metabolism	36	1	0.08195
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.1163
<i>path:gga04115</i>	p53 signaling pathway	62	1	0.1371
<i>path:gga00562</i>	Inositol phosphate metabolism	66	1	0.1452



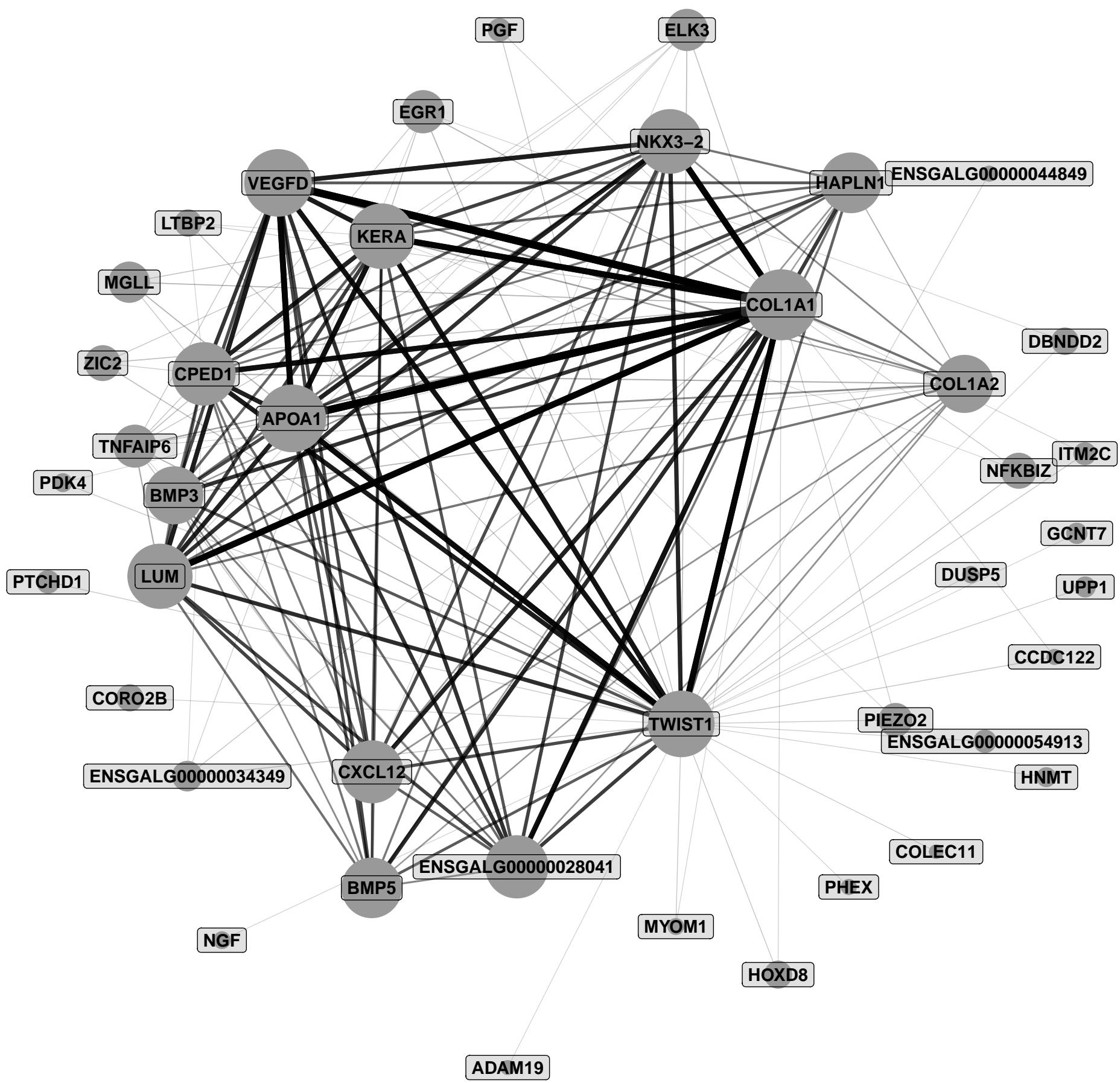
	Term	Ont	N	n	Adj. p-value
GO:0050793	regulation of developmental process	BP	214	12	5.249e-05
GO:0051241	negative regulation of multicellular organismal process	BP	70	7	5.7e-05
GO:0050790	regulation of catalytic activity	BP	229	12	0.0001006
GO:0051239	regulation of multicellular organismal process	BP	202	11	0.0001401
GO:0044092	negative regulation of molecular function	BP	82	7	0.0001568
GO:0048731	system development	BP	483	18	0.0001695
GO:0048513	animal organ development	BP	321	14	0.0001887
GO:0045597	positive regulation of cell differentiation	BP	85	7	0.0001964
GO:0006928	movement of cell or subcellular component	BP	178	10	0.0002192
GO:0071621	granulocyte chemotaxis	BP	9	3	0.0002194

	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	68	5	0.002716
<i>path:gga00480</i>	Glutathione metabolism	47	4	0.004294
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	28	3	0.007024
<i>path:gga00983</i>	Drug metabolism – other enzymes	55	4	0.007525
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	30	3	0.008527
<i>path:gga00760</i>	Nicotinate and nicotinamide metabolism	32	3	0.01021
<i>path:gga00330</i>	Arginine and proline metabolism	39	3	0.0175
<i>path:gga00532</i>	Glycosaminoglycan biosynthesis – chondroitin sulfate / dermatan sulfate	17	2	0.02352
<i>path:gga04540</i>	Gap junction	79	4	0.02557
<i>path:gga04510</i>	Focal adhesion	172	6	0.03544



	Term	Ont	N	n	Adj. p-value
GO:0097503	sialylation	BP	5	2	0.0005251
GO:0045664	regulation of neuron differentiation	BP	24	3	0.0006926
GO:1904377	positive regulation of protein localization to cell periphery	BP	7	2	0.001092
GO:0030182	neuron differentiation	BP	165	6	0.001335
GO:1904375	regulation of protein localization to cell periphery	BP	8	2	0.001449
GO:0048699	generation of neurons	BP	180	6	0.002078
GO:0022008	neurogenesis	BP	183	6	0.002258
GO:1903829	positive regulation of cellular protein localization	BP	15	2	0.005256
GO:0007204	positive regulation of cytosolic calcium ion concentration	BP	15	2	0.005256
GO:0099173	postsynapse organization	BP	16	2	0.005978

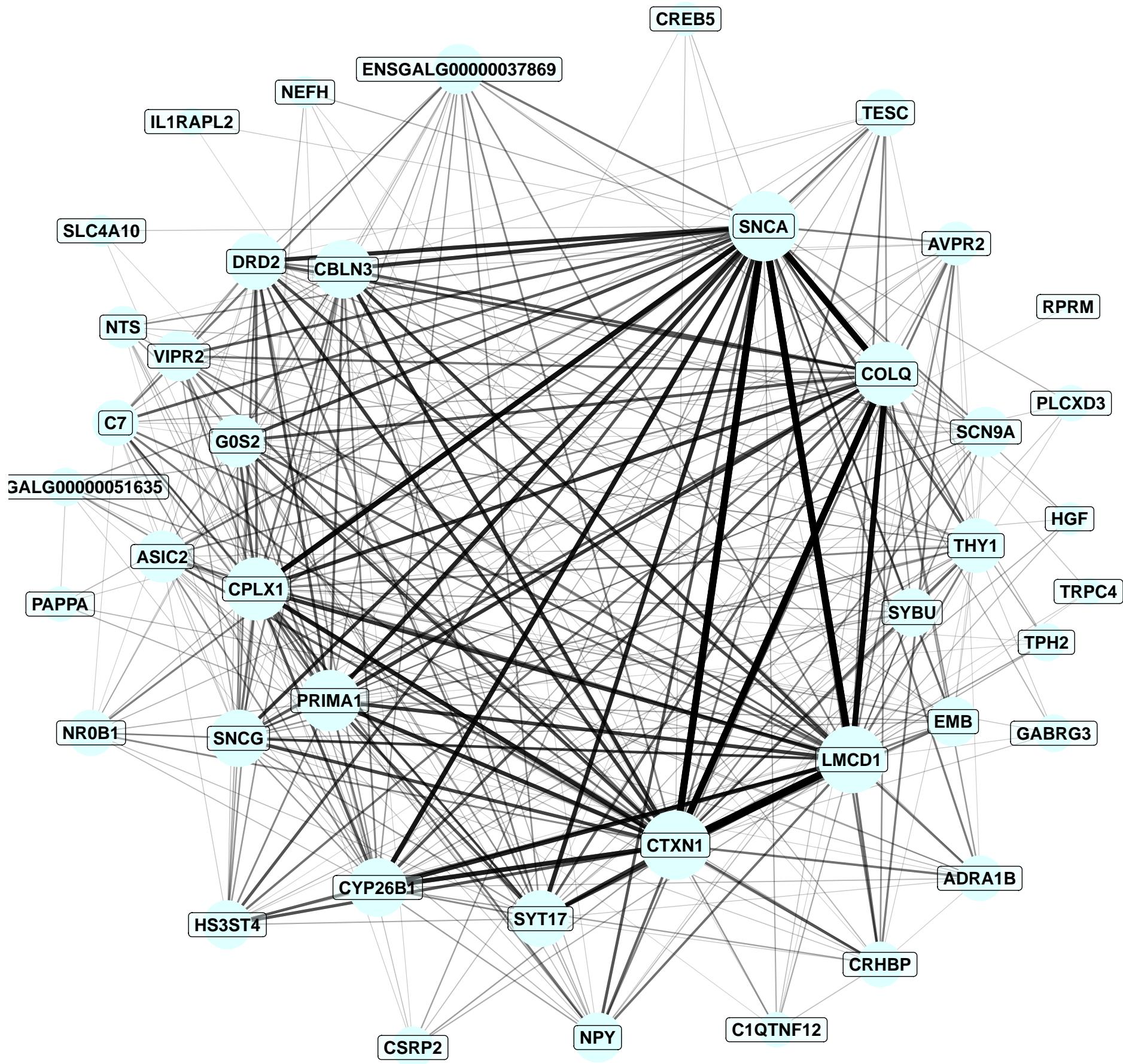
	Pathway	N	DE	P.DE
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	5	0.002018
<i>path:gga04514</i>	Cell adhesion molecules	99	4	0.00602
<i>path:gga04520</i>	Adherens junction	69	3	0.01414
<i>path:gga03267</i>	Virion – Adenovirus	2	1	0.01462
<i>path:gga04530</i>	Tight junction	133	4	0.01651
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.02903
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	2	0.03629
<i>path:gga00510</i>	N-Glycan biosynthesis	45	2	0.043
<i>path:gga04260</i>	Cardiac muscle contraction	59	2	0.06962
<i>path:gga00601</i>	Glycosphingolipid biosynthesis – lacto and neolacto series	21	1	0.1434



1	COL1A1	APOA1	TWIST1	LUM	CPED1	KERA	VEGFD	CXCL12
2	NKX3–2	COL1A2	ENSGALG00000028041	BMP5	HAPLN1	EGR1	BMP3	ELK3
3	DBNDD2	TNFAIP6	CORO2B	PIEZ02	MGLL	LTBP2	ZIC2	PTCHD1
4	ENSGALG00000034349	HOXD8	CCDC122	NFKBIZ	MYOM1	ITM2C	UPP1	PDK4
5	COLEC11	NGF	ENSGALG00000044849	DUSP5	PGF	HNMT	PHEX	ENSGALG00000054913
6	GCNT7	ADAM19						

	Term	Ont	N	n	Adj. p-value
GO:0019221	cytokine-mediated signaling pathway	BP	19	2	0.001661
GO:0032501	multicellular organismal process	BP	711	8	0.001664
GO:0060352	cell adhesion molecule production	BP	1	1	0.00321
GO:0098759	cellular response to interleukin-8	BP	1	1	0.00321
GO:0070508	cholesterol import	BP	1	1	0.00321
GO:0034113	heterotypic cell–cell adhesion	BP	1	1	0.00321
GO:0034380	high-density lipoprotein particle assembly	BP	1	1	0.00321
GO:0060354	negative regulation of cell adhesion molecule production	BP	1	1	0.00321
GO:0034115	negative regulation of heterotypic cell–cell adhesion	BP	1	1	0.00321
GO:0032691	negative regulation of interleukin-1 beta production	BP	1	1	0.00321

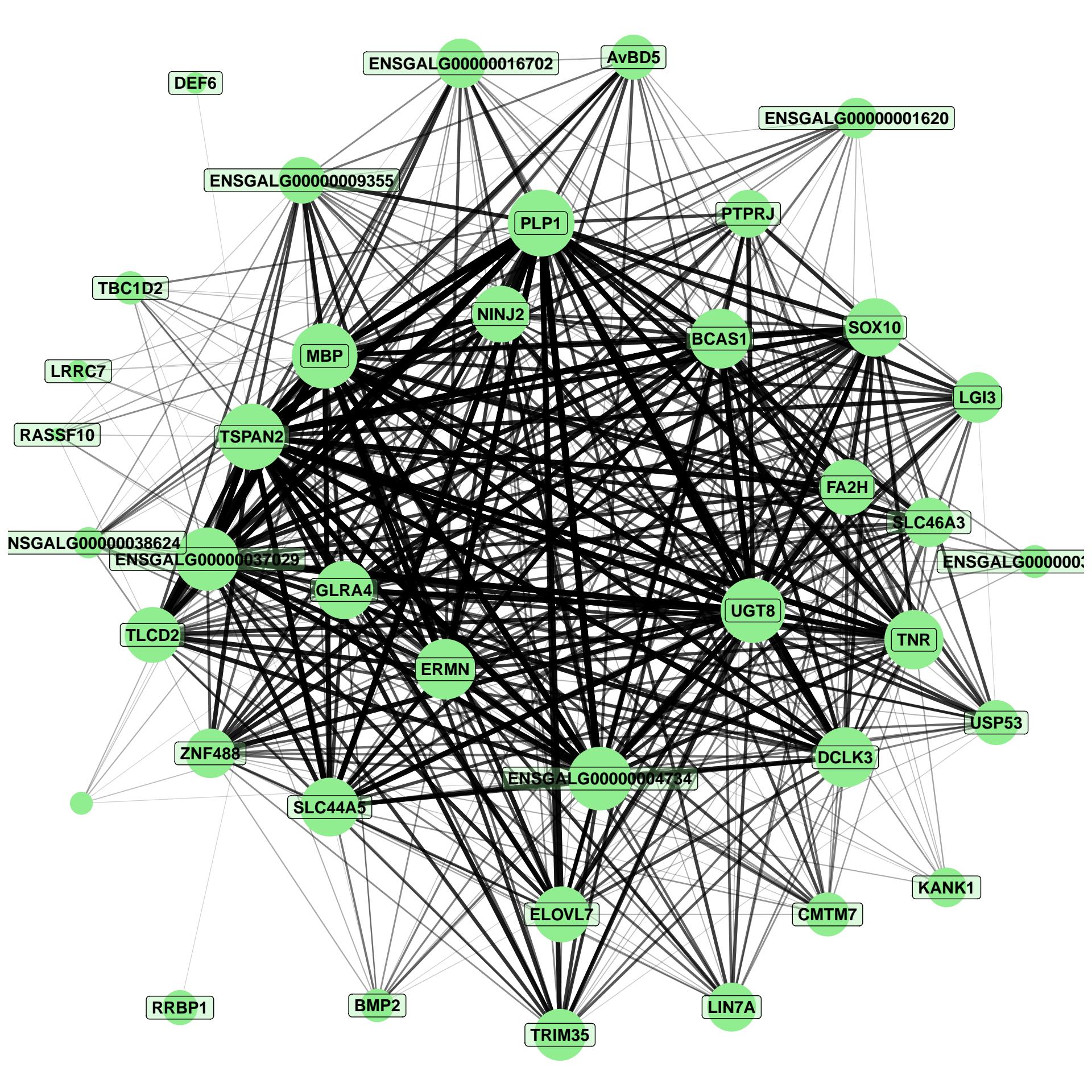
	Pathway	N	DE	P.DE
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	151	4	0.001357
<i>path:gga04510</i>	Focal adhesion	172	4	0.002186
<i>path:gga04010</i>	MAPK signaling pathway	239	4	0.007052
<i>path:gga04512</i>	ECM–receptor interaction	68	2	0.02004
<i>path:gga00340</i>	Histidine metabolism	17	1	0.05322
<i>path:gga04672</i>	Intestinal immune network for IgA production	22	1	0.06834
<i>path:gga04020</i>	Calcium signaling pathway	201	2	0.1358
<i>path:gga00561</i>	Glycerolipid metabolism	53	1	0.157
<i>path:gga00240</i>	Pyrimidine metabolism	54	1	0.1597
<i>path:gga00983</i>	Drug metabolism – other enzymes	55	1	0.1624



1	SNCA	COLQ	CTXN1	DRD2	SYT17	CYP26B1	LMCD1	CPLX1
2	SNCG	PRIMA1	G0S2	C7	CBLN3	HS3ST4	THY1	SYBU
3	VIPR2	SCN9A	ENSGALG00000037869	TESC	GABRG3	PLCXD3	EMB	NTS
4	CREB5	NEFH	ASIC2	ADRA1B	NR0B1	IL1RAPL2	NPY	AVPR2
5	SLC4A10	HGF	RPRM	CSRP2	TRPC4	TPH2	ENSGALG00000051635	CRHBP
6	PAPPA	C1QTNF12						

	Term	Ont	N	n	Adj. p-value
GO:1904064	positive regulation of cation transmembrane transport	BP	4	2	4.651e-05
GO:0034767	positive regulation of ion transmembrane transport	BP	6	2	0.0001159
GO:0034764	positive regulation of transmembrane transport	BP	6	2	0.0001159
GO:1904062	regulation of cation transmembrane transport	BP	11	2	0.0004211
GO:0006469	negative regulation of protein kinase activity	BP	20	2	0.001432
GO:0033673	negative regulation of kinase activity	BP	21	2	0.001579
GO:0051348	negative regulation of transferase activity	BP	24	2	0.002065
GO:0001933	negative regulation of protein phosphorylation	BP	26	2	0.002423
GO:0034765	regulation of ion transmembrane transport	BP	28	2	0.002808
GO:0030854	positive regulation of granulocyte differentiation	BP	1	1	0.002828

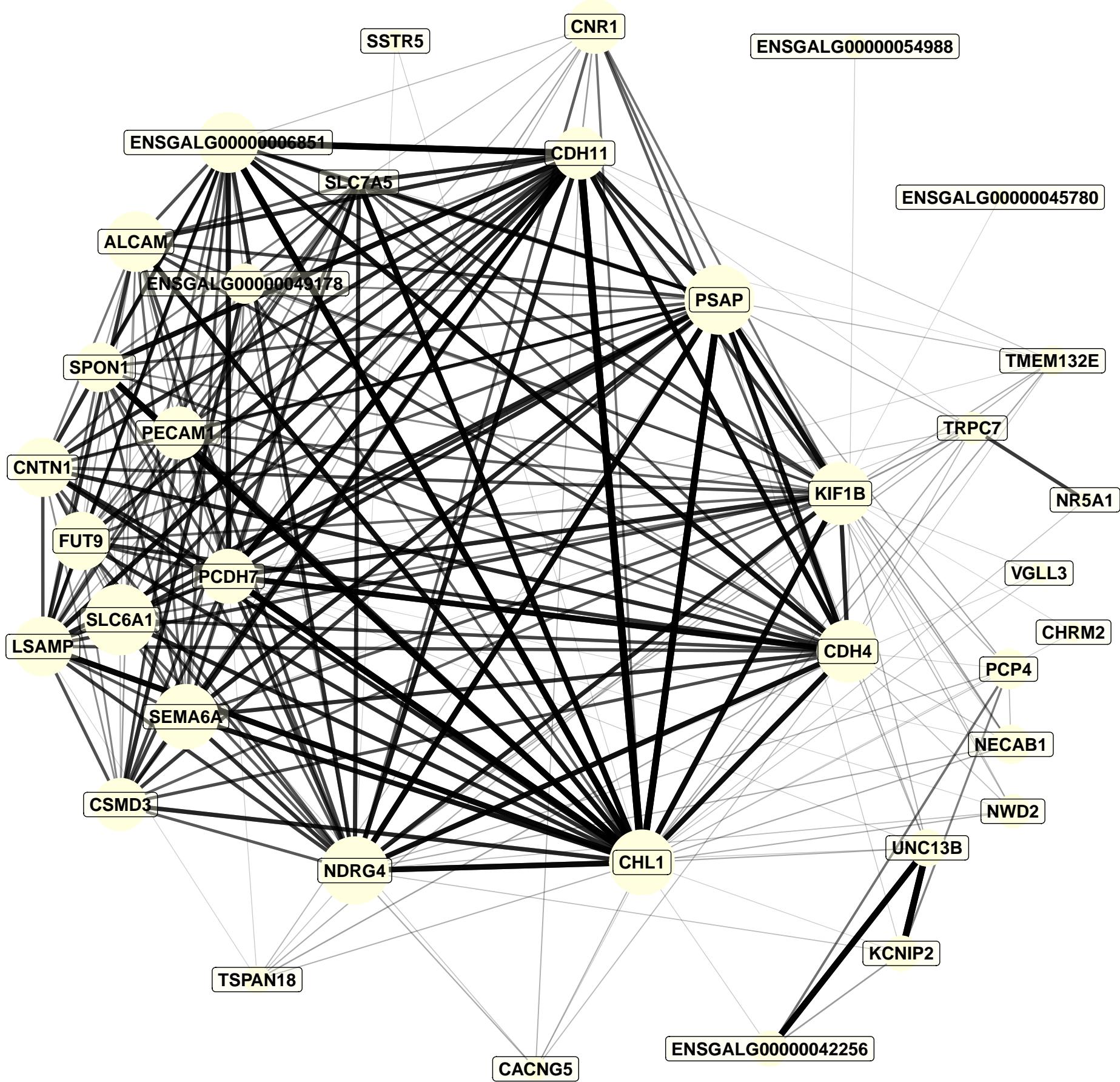
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	6	0.0001235
<i>path:gga04270</i>	Vascular smooth muscle contraction	106	2	0.03602
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	2	0.04645
<i>path:gga00790</i>	Folate biosynthesis	26	1	0.07104
<i>path:gga00830</i>	Retinol metabolism	30	1	0.08153
<i>path:gga00380</i>	Tryptophan metabolism	33	1	0.08932
<i>path:gga04020</i>	Calcium signaling pathway	201	2	0.1103
<i>path:gga04920</i>	Adipocytokine signaling pathway	58	1	0.1518
<i>path:gga04540</i>	Gap junction	79	1	0.201
<i>path:gga00230</i>	Purine metabolism	113	1	0.2748



1	PLP1	MBP	TSPAN2	BCAS1	SOX10	UGT8	ENSGALG00000004734	ZNF488
2	GLRA4	ENSGALG00000037029	FA2H	ERMN	TNR	DCLK3	PTPRJ	ELOVL7
3	NINJ2	SLC44A5	USP53	TLCD2	KANK1	LGI3	ENSGALG00000009355	TRIM35
4	CMTM7	AvBD5	BMP2	ENSGALG00000016702	LIN7A	SLC46A3	ENSGALG00000001620	NA
5	DEF6	TBC1D2	RRBP1	ENSGALG00000038624	LRRC7	RASSF10	ENSGALG00000038783	

	Term	Ont	N	n	Adj. p-value
GO:0008366	axon ensheathment	BP	12	3	4.499e-06
GO:0007272	ensheathment of neurons	BP	12	3	4.499e-06
GO:0042552	myelination	BP	12	3	4.499e-06
GO:0032291	axon ensheathment in central nervous system	BP	2	2	7.78e-06
GO:0022010	central nervous system myelination	BP	2	2	7.78e-06
GO:0014003	oligodendrocyte development	BP	2	2	7.78e-06
GO:0021782	glial cell development	BP	5	2	7.739e-05
GO:0048709	oligodendrocyte differentiation	BP	9	2	0.0002766
GO:0010001	glial cell differentiation	BP	21	2	0.001579
GO:0042063	gliogenesis	BP	25	2	0.00224

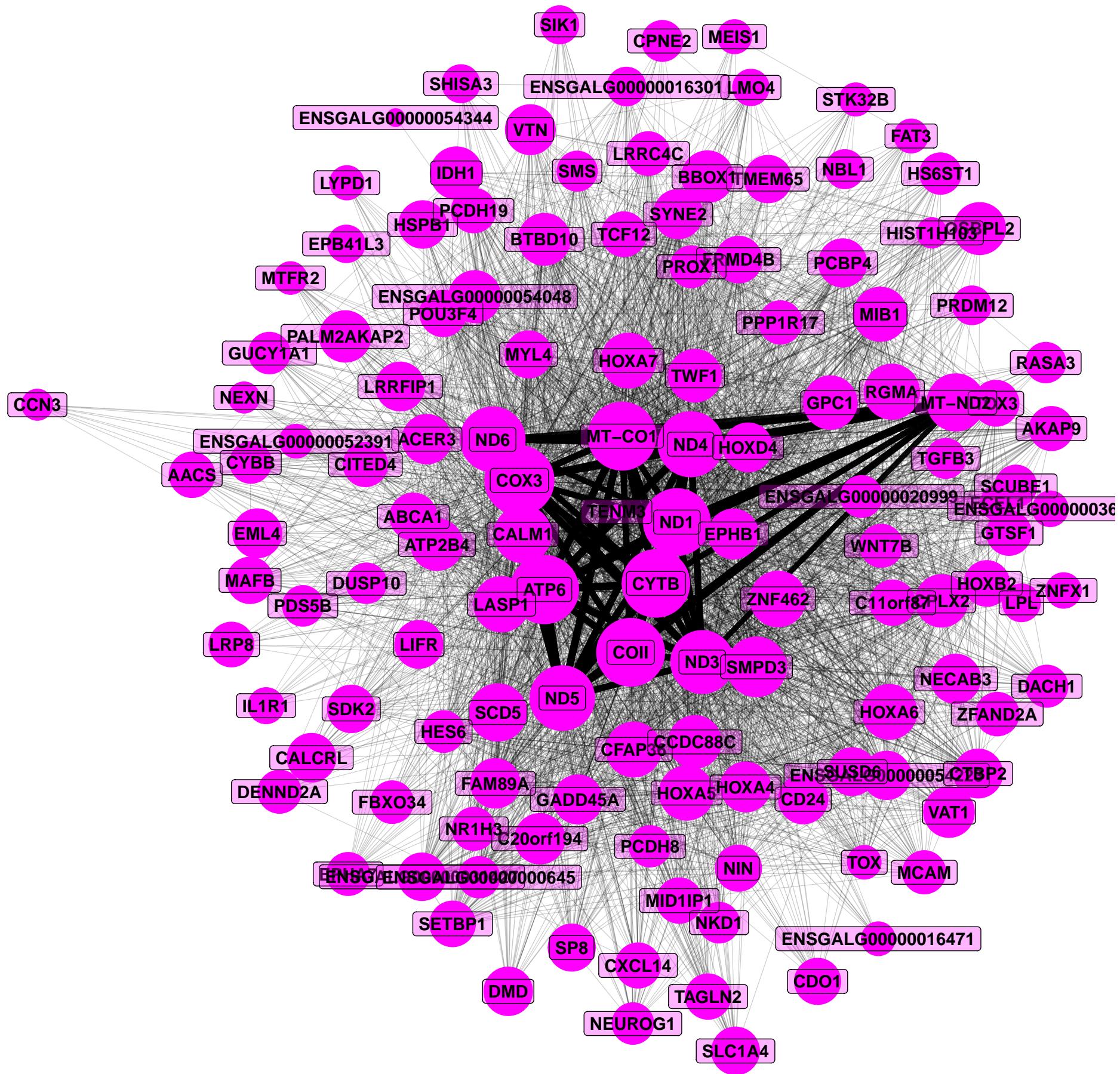
	Pathway	N	DE	P.DE
<i>path:gga00062</i>	Fatty acid elongation	22	1	0.06044
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	26	1	0.07104
<i>path:gga00565</i>	Ether lipid metabolism	36	1	0.09704
<i>path:gga00600</i>	Sphingolipid metabolism	48	1	0.1273
<i>path:gga01212</i>	Fatty acid metabolism	49	1	0.1298
<i>path:gga04512</i>	ECM–receptor interaction	68	1	0.1756
<i>path:gga04520</i>	Adherens junction	69	1	0.1779
<i>path:gga03015</i>	mRNA surveillance pathway	72	1	0.1849
<i>path:gga04350</i>	TGF–beta signaling pathway	83	1	0.21
<i>path:gga04514</i>	Cell adhesion molecules	99	1	0.2453



1	SLC6A1	PSAP	SEMA6A	NDRG4	CHL1	SPON1	ALCAM
2	CNTN1	ENSGALG0000006851	CDH11	KIF1B	CNR1	LSAMP	PCDH7
3	CSMD3	PECAM1	SLC7A5	PCP4	ENSGALG0000049178	UNC13B	NECAB1
4	TSPAN18	NWD2	TMEM132E	KCNIP2	CACNG5	SSTR5	ENSGALG0000042256
5	CHRM2	NR5A1	ENSGALG0000054988	ENSGALG0000045780			VGLL3

	Term	Ont	N	n	Adj. p-value
GO:0022610	biological adhesion	BP	143	6	1.332e-06
GO:0007155	cell adhesion	BP	143	6	1.332e-06
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	BP	21	3	1.885e-05
GO:0098742	cell–cell adhesion via plasma–membrane adhesion molecules	BP	30	3	5.664e-05
GO:0007193	adenylate cyclase–inhibiting G protein–coupled receptor signaling pathway	BP	5	2	6.139e-05
GO:0098609	cell–cell adhesion	BP	66	3	0.0006002
GO:0007188	adenylate cyclase–modulating G protein–coupled receptor signaling pathway	BP	19	2	0.001027
GO:0007197	adenylate cyclase–inhibiting G protein–coupled acetylcholine receptor signaling pathway	BP	1	1	0.002522
GO:0098664	G protein–coupled serotonin receptor signaling pathway	BP	1	1	0.002522
GO:0007210	serotonin receptor signaling pathway	BP	1	1	0.002522

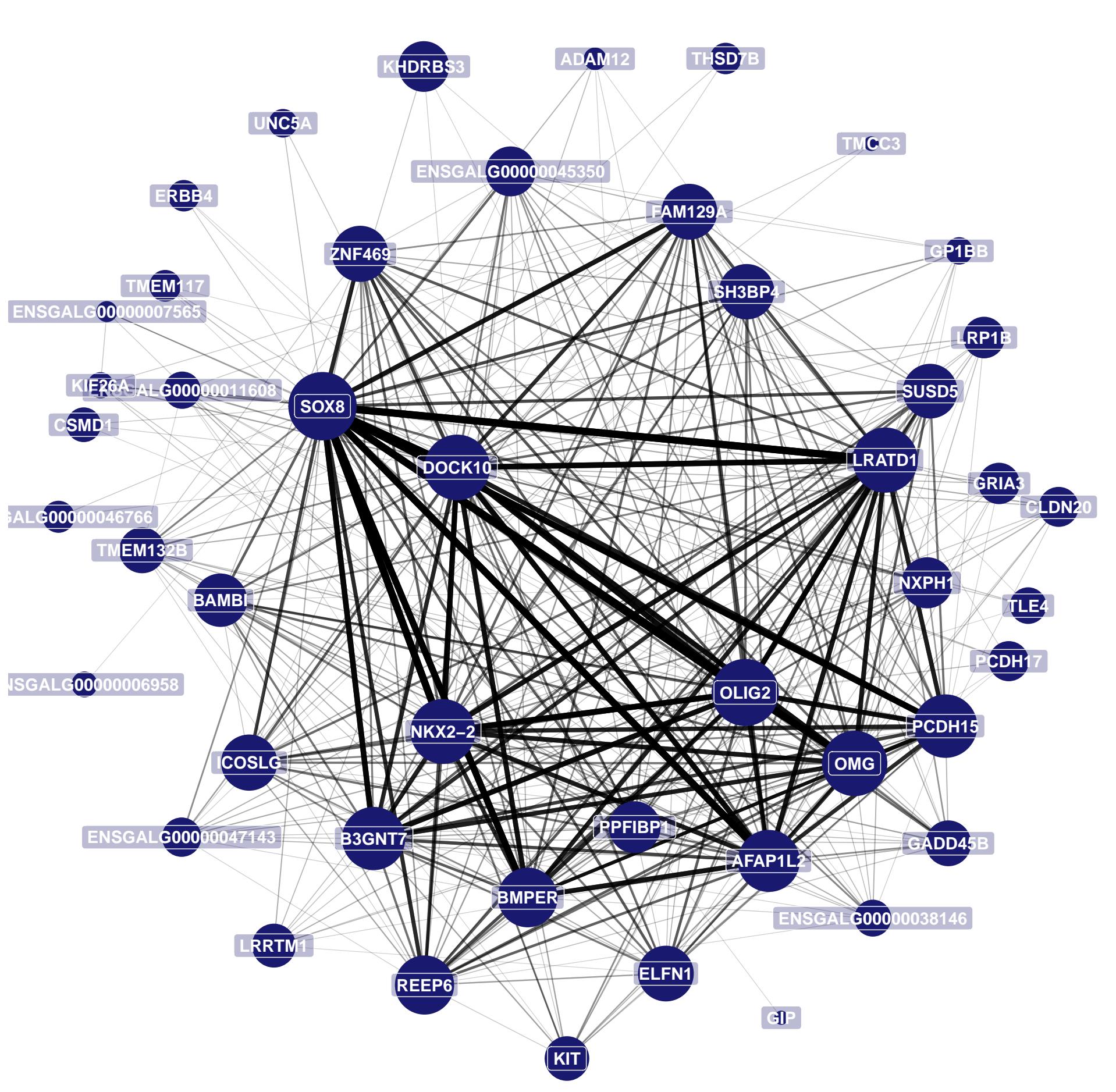
	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	99	4	0.0001066
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	1	0.02986
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	3	0.03327
<i>path:gga00601</i>	Glycosphingolipid biosynthesis – lacto and neolacto series	21	1	0.05169
<i>path:gga00515</i>	Mannose type O-glycan biosynthesis	22	1	0.05408
<i>path:gga00600</i>	Sphingolipid metabolism	48	1	0.1143
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.1387
<i>path:gga04142</i>	Lysosome	113	1	0.2492
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	1	0.2662
<i>path:gga04150</i>	mTOR signaling pathway	135	1	0.2901



1	COX3	MT-CO1	CYTB	ATP6	COII	ND1	ND5	ND4
2	ND6	ND3	MT-ND2	CALM1	SMPD3	SCD5	LASP1	CFAP36
3	ZNF462	HOXA7	GPC1	IDH1	ENSGALG00000054048	HOXA6	HOXA5	VTN
4	MAFB	CXCL14	RGMA	OSBPL2	ATP2B4	MIB1	CPLX2	LIFR
5	VAT1	BBOX1	ACER3	TWF1	FAM89A	BTBD10	SLC1A4	CCDC88C
6	SYNE2	TMEM65	HOXA4	MYL4	CD24	DMD	AKAP9	PALM2AKAP2
7	EPHB1	CTBP2	ENSGALG00000020999	HOXD4	SP8	LRRFIP1	EML4	HSPB1
8	GADD45A	C20orf194	CALCRL	POU3F4	TGFB3	SDK2	PDS5B	NECAB3
9	LRRC4C	AACS	GUCY1A1	TAGLN2	CDO1	HOXB2	LRP8	SUSD6
10	NIN	FRMD4B	PCBP4	EPHA7	ENSGALG00000054223	PCDH19	SMS	TOX3
11	C11orf87	ABCA1	MID1IP1	DENND2A	PCDH8	NR1H3	FBXO34	WNT7B
12	DACH1	ENSGALG00000031427	GTSF1	HS6ST1	SETBP1	PPP1R17	LMO4	CITED4
13	EPB41L3	TCF12	MCAM	ENSGALG00000016301	CPNE2	NEUROG1	RASA3	NKD1
14	FAT3	ENSGALG0000000645	SCUBE1	ZFAND2A	PROX1	CYBB	NBL1	MTFR2
15	SHISA3	PRDM12	SIK1	HIST1H103	HES6	DUSP10	ENSGALG00000036838	MEIS1
16	ECEL1	ENSGALG00000052391	IL1R1	ZNFX1	LYPD1	LPL	STK32B	TENM3
17	CCN3	ENSGALG00000016471	TOX	NEXN	ENSGALG00000054344			

	Term	Ont	N	n	Adj. p-value
GO:0048568	embryonic organ development	BP	63	8	8.251e-08
GO:0048562	embryonic organ morphogenesis	BP	46	7	1.53e-07
GO:0003002	regionalization	BP	51	7	3.19e-07
GO:0007275	multicellular organism development	BP	577	19	7.944e-07
GO:0048598	embryonic morphogenesis	BP	87	8	1.042e-06
GO:0007389	pattern specification process	BP	61	7	1.117e-06
GO:0032501	multicellular organismal process	BP	711	21	1.142e-06
GO:0032502	developmental process	BP	655	20	1.279e-06
GO:0048731	system development	BP	483	17	1.307e-06
GO:0009790	embryo development	BP	121	9	1.31e-06

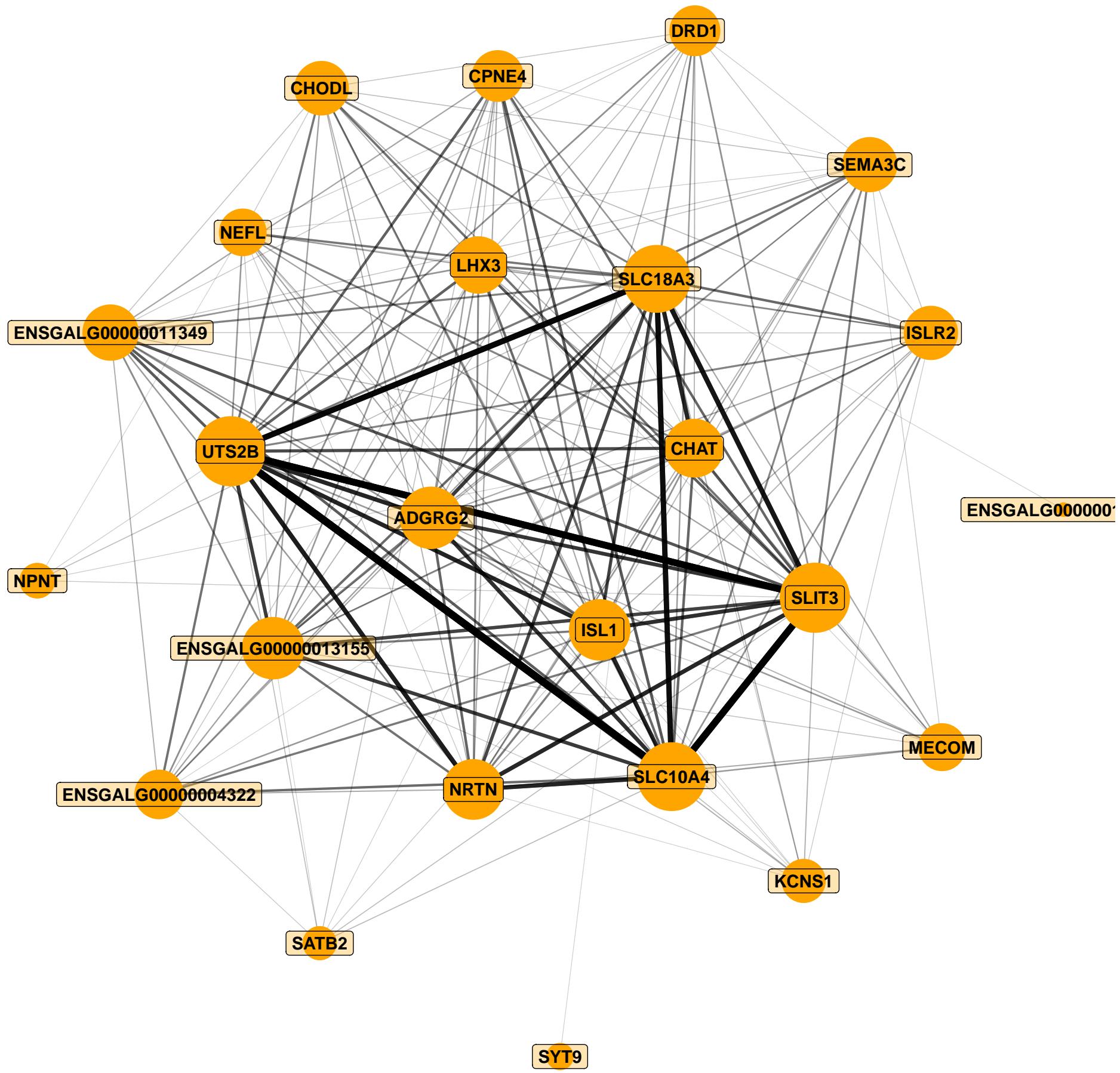
	Pathway	N	DE	P.DE
<i>path:gga03320</i>	PPAR signaling pathway	56	3	0.01369
<i>path:gga04310</i>	Wnt signaling pathway	135	4	0.03288
<i>path:gga04350</i>	TGF–beta signaling pathway	83	3	0.0382
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	151	4	0.04646
<i>path:gga00270</i>	Cysteine and methionine metabolism	42	2	0.05413
<i>path:gga04010</i>	MAPK signaling pathway	239	5	0.06324
<i>path:gga00480</i>	Glutathione metabolism	47	2	0.06605
<i>path:gga00600</i>	Sphingolipid metabolism	48	2	0.06853
<i>path:gga04270</i>	Vascular smooth muscle contraction	106	3	0.06938
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	3	0.09607



1	OLIG2	SOX8	NKX2-2	DOCK10	OMG	LRATD1	AFAP1L2	B3GNT7
2	PCDH15	BMPER	REEP6	SUSD5	NXPH1	ZNF469	BAMBI	ELFN1
3	FAM129A	ICOSLG	SH3BP4	PPFIBP1	KHDRBS3	ENSGALG00000045350	TMEM132B	KIT
4	LRP1B	LRRTM1	GADD45B	GRIA3	PCDH17	ENSGALG00000047143	CLDN20	TLE4
5	CSMD1	ERBB4	THSD7B	ENSGALG00000011608	ENSGALG00000046766	ENSGALG00000038146	TMEM117	ENSGALG00000006958
6	ADAM12	UNC5A	GP1BB	KIF26A	TMCC3	GIP	ENSGALG00000007565	

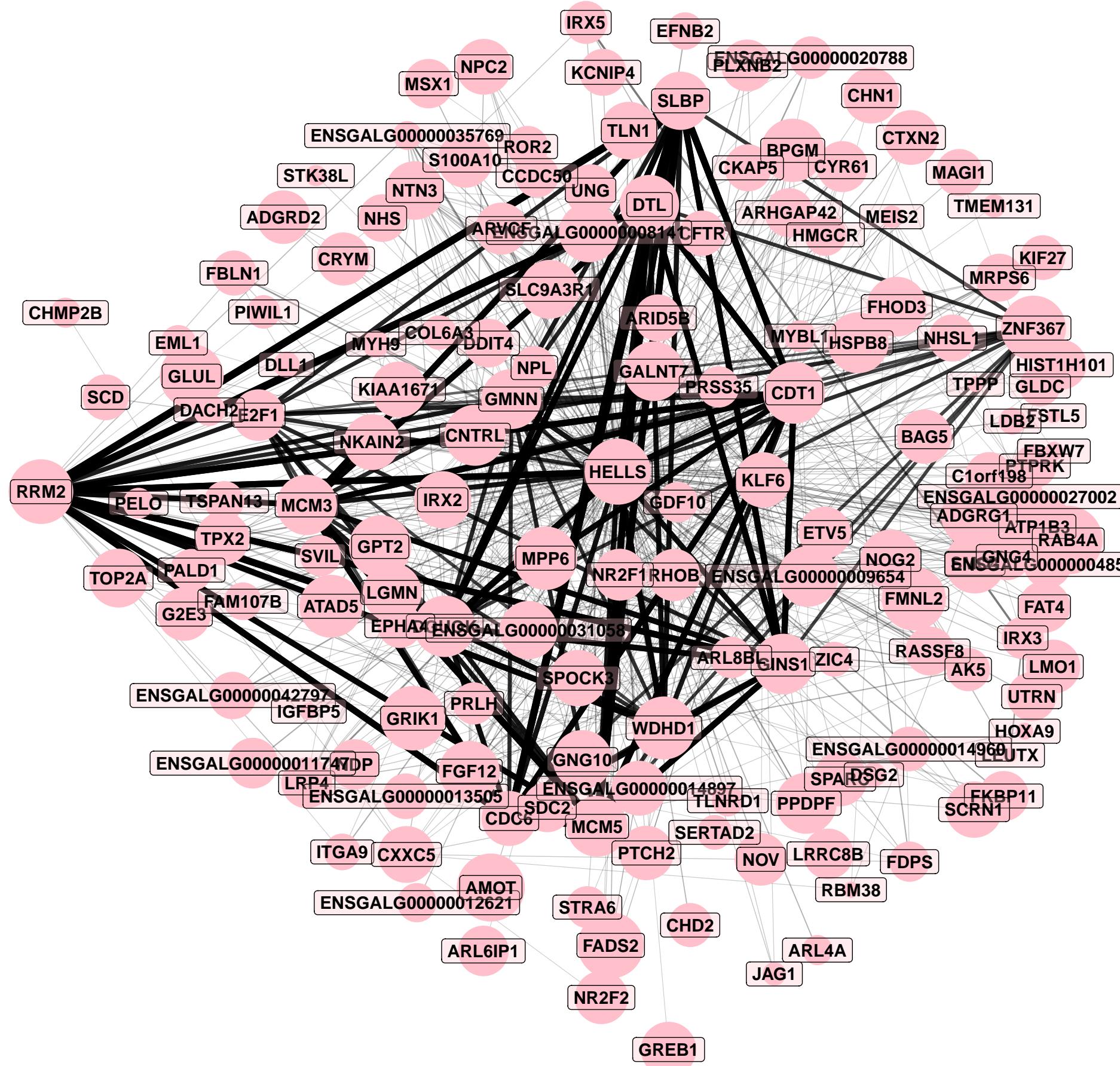
	Term	Ont	N	n	Adj. p-value
GO:0048709	oligodendrocyte differentiation	BP	9	2	0.0004285
GO:0050954	sensory perception of mechanical stimulus	BP	15	2	0.001233
GO:0007605	sensory perception of sound	BP	15	2	0.001233
GO:0010001	glial cell differentiation	BP	21	2	0.002433
GO:0042063	gliogenesis	BP	25	2	0.003445
GO:0036018	cellular response to erythropoietin	BP	1	1	0.003515
GO:0036216	cellular response to stem cell factor stimulus	BP	1	1	0.003515
GO:0097067	cellular response to thyroid hormone stimulus	BP	1	1	0.003515
GO:0038162	erythropoietin-mediated signaling pathway	BP	1	1	0.003515
GO:0038093	Fc receptor signaling pathway	BP	1	1	0.003515

	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	99	2	0.04729
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.04813
<i>path:gga04010</i>	MAPK signaling pathway	239	3	0.05143
<i>path:gga04672</i>	Intestinal immune network for IgA production	22	1	0.07461
<i>path:gga04530</i>	Tight junction	133	2	0.07945
<i>path:gga04310</i>	Wnt signaling pathway	135	2	0.08151
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.1676
<i>path:gga04115</i>	p53 signaling pathway	62	1	0.1966
<i>path:gga04512</i>	ECM–receptor interaction	68	1	0.2134
<i>path:gga03015</i>	mRNA surveillance pathway	72	1	0.2245



	Term	Ont	N	n	Adj. p-value
GO:0021520	spinal cord motor neuron cell fate specification	BP	2	2	2.956e-06
GO:0048665	neuron fate specification	BP	3	2	8.857e-06
GO:0021983	pituitary gland development	BP	7	2	6.173e-05
GO:0021522	spinal cord motor neuron differentiation	BP	7	2	6.173e-05
GO:0021536	diencephalon development	BP	8	2	8.223e-05
GO:0048663	neuron fate commitment	BP	8	2	8.223e-05
GO:0021515	cell differentiation in spinal cord	BP	10	2	0.0001319
GO:0021517	ventral spinal cord development	BP	12	2	0.000193
GO:0001708	cell fate specification	BP	13	2	0.0002278
GO:0035270	endocrine system development	BP	17	2	0.0003956

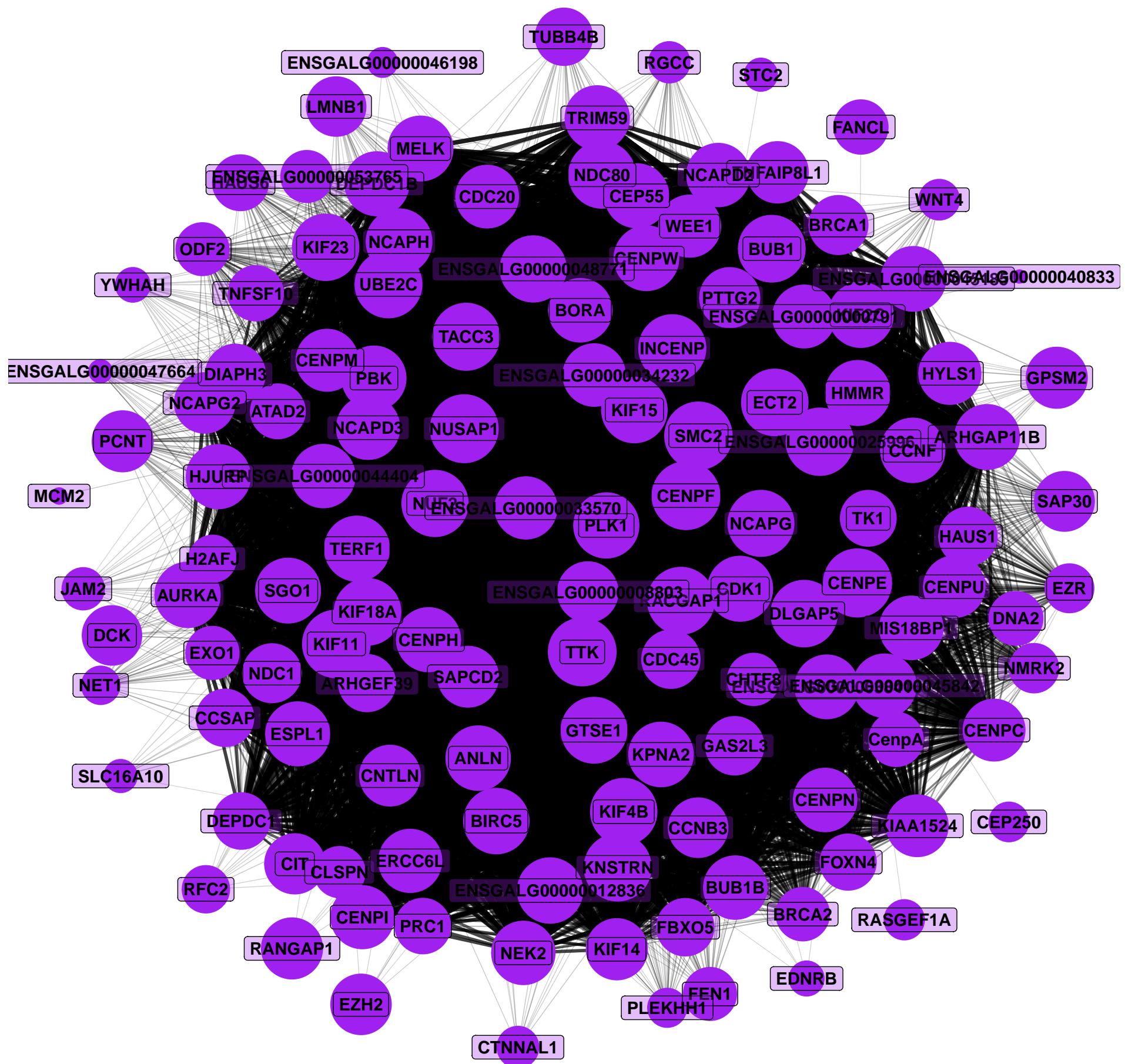
	Pathway	N	DE	P.DE
<i>path:gga00564</i>	Glycerophospholipid metabolism	84	2	0.00944
<i>path:gga00310</i>	Lysine degradation	50	1	0.08436
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	2	0.08654
<i>path:gga04512</i>	ECM–receptor interaction	68	1	0.113
<i>path:gga04540</i>	Gap junction	79	1	0.1301
<i>path:gga04020</i>	Calcium signaling pathway	201	1	0.2998
<i>path:gga04010</i>	MAPK signaling pathway	239	1	0.3458
<i>path:gga01100</i>	Metabolic pathways	1247	1	0.9003
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1



1	RRM2	HELLS	SMC4	TOP2A	DGUOK	AMOT	WDHD1	MCM5
2	CDT1	MCM3	SLBP	ATP1B3	ATAD5	ZNF367	GINS1	DTL
3	TPX2	FADS2	GLUL	RAB4A	GRIK1	SPARC	RHOB	GMNN
4	BPGM	FGF12	MPP6	ENSGALG0000009654	ADGRG1	ENSGALG00000011747	ENSGALG00000008141	GPT2
5	PPDPF	SDC2	NOG2	CDC6	FMNL2	SLC9A3R1	NOV	G2E3
6	KLF6	TLN1	ENSGALG00000027002	ETV5	ENSGALG00000031058	S100A10	CNTRL	GALNT7
7	NTN3	NR2F1	ENSGALG00000014897	LGMN	HSPB8	NR2F2	IRX2	CXXC5
8	FHOD3	SPOCK3	MSX1	GNG10	SCRN1	E2F1	KIAA1671	NPC2
9	PLXNB2	ARVCF	UNG	NKAIN2	LMO1	C1orf198	CYR61	PTCH2
10	KCNIP4	FBLN1	LRP4	BAG5	ADGRD2	RASSF8	MRPS6	CHN1
11	NDP	GREB1	CRYM	GNG4	ARHGAP42	ARL8BL	HIST1H101	IRX3
12	CTXN2	UTRN	ENSGALG00000013505	FAT4	ENSGALG00000042797	DDIT4	PTPRK	ENSGALG00000035769
13	EPHA4	FKBP11	LRRC8B	MAGI1	SVIL	NHS	MEIS2	ENSGALG00000048534
14	PALD1	NHSL1	CFTR	ARID5B	KIF27	PRSS35	JAG1	CCDC50
15	ENSGALG00000012621	IRX5	MYH9	ENSGALG00000014960	GLDC	ENSGALG00000020788	NPL	STRA6
16	MYBL1	CHD2	AK5	PRLH	SCD	CKAP5	TLNRD1	FAM107B
17	ROR2	ITGA9	SERTAD2	TSPAN13	DACH2	EFNB2	HOXA9	PELO
18	IGFBP5	ARL6IP1	FDPS	GDF10	CHMP2B	TPPP	EML1	ZIC4
19	DLL1	ARL4A	RBM38	HMGCR	LDB2	COL6A3	FSTL5	PIWIL1
20	DSG2	STK38L	FBXW7	TMEM131	LEUTX			

	Term	Ont	N	n	Adj. p-value
GO:0044238	primary metabolic process	BP	1122	31	3.2e-06
GO:0006807	nitrogen compound metabolic process	BP	1086	30	4.79e-06
GO:0071704	organic substance metabolic process	BP	1183	31	9.444e-06
GO:0008152	metabolic process	BP	1233	31	2.149e-05
GO:0044237	cellular metabolic process	BP	1175	30	2.24e-05
GO:0060255	regulation of macromolecule metabolic process	BP	625	20	3.004e-05
GO:0051171	regulation of nitrogen compound metabolic process	BP	578	19	3.354e-05
GO:0051345	positive regulation of hydrolase activity	BP	55	6	3.746e-05
GO:0080090	regulation of primary metabolic process	BP	587	19	4.138e-05
GO:0065009	regulation of molecular function	BP	260	12	4.467e-05

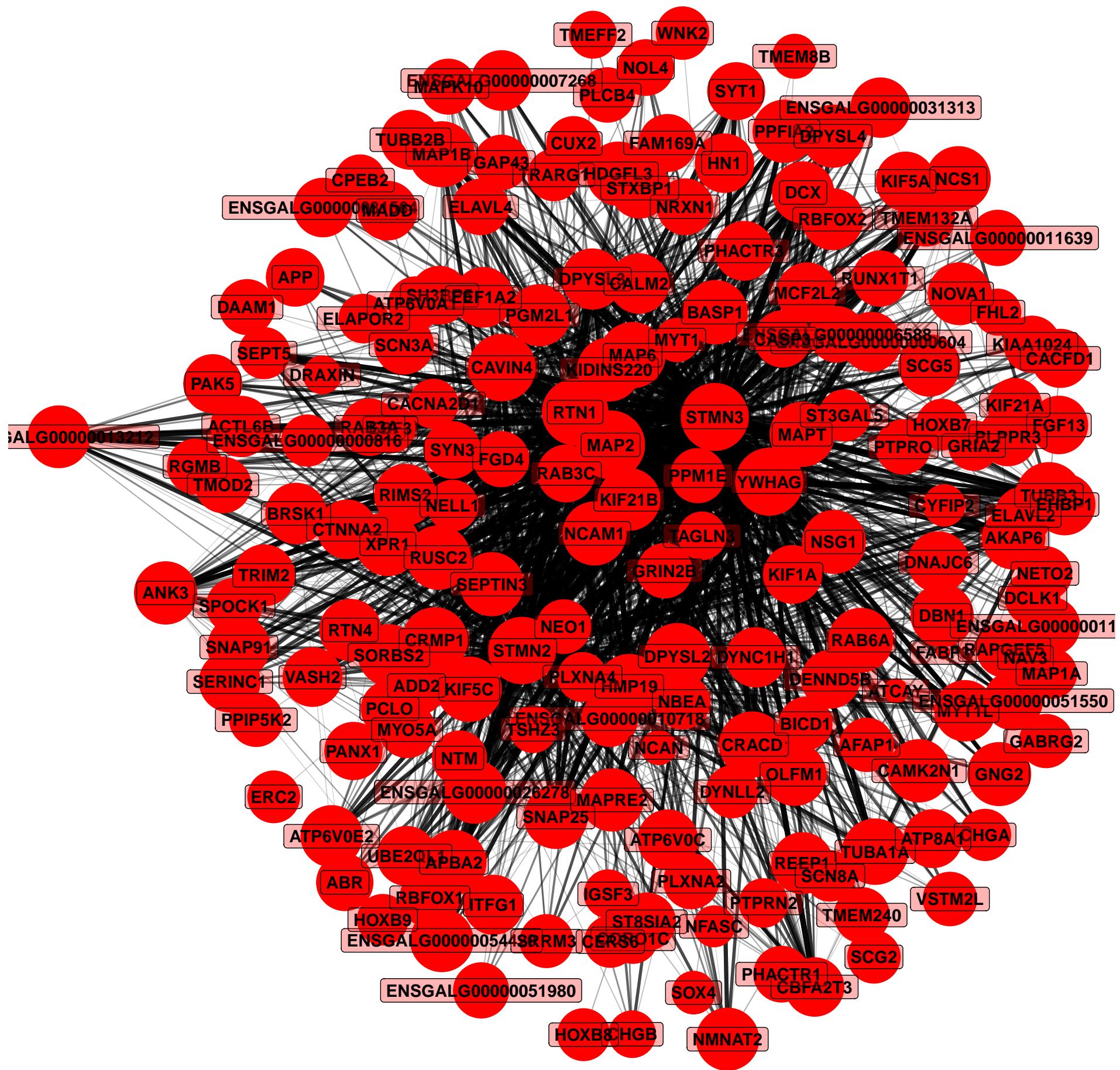
	Pathway	N	DE	P.DE
<i>path:gga01232</i>	Nucleotide metabolism	76	4	0.01125
<i>path:gga00220</i>	Arginine biosynthesis	17	2	0.01586
<i>path:gga04530</i>	Tight junction	133	5	0.01846
<i>path:gga00900</i>	Terpenoid backbone biosynthesis	19	2	0.01965
<i>path:gga04330</i>	Notch signaling pathway	52	3	0.02167
<i>path:gga00240</i>	Pyrimidine metabolism	54	3	0.02393
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	26	2	0.03545
<i>path:gga04371</i>	Apelin signaling pathway	111	4	0.03874
<i>path:gga04110</i>	Cell cycle	113	4	0.04093
<i>path:gga04512</i>	ECM–receptor interaction	68	3	0.0431



1	CENPE	CENPF	NUSAP1	KIF11	SMC2	ENSGALG00000025996	UBE2C	TTK
2	KIF4B	KPNA2	NDC80	DLGAP5	INCENP	TACC3	KNSTRN	ENSGALG00000048771
3	KIF15	BUB1	RACGAP1	GTSE1	KIF23	ECT2	KIF18A	CDK1
4	PLK1	AURKA	ENSGALG00000012836	BIRC5	NUF2	KIF2C	BUB1B	ANLN
5	HMMR	CENPW	SGO1	NCAPG	PBK	CDC20	CENPH	ENSGALG00000038416
6	NCAPH	MELK	CEP55	TERF1	ARHGAP11B	ENSGALG00000045185	ESPL1	ENSGALG00000044404
7	CCNF	CENPI	DEPDC1B	HJURP	ERCC6L	BRCA1	NEK2	PTTG2
8	ENSGALG00000045842	NCAPD2	BORA	TK1	NCAPD3	ENSGALG00000034232	CENPN	ENSGALG00000000791
9	TRIM59	MIS18BP1	KIAA1524	CENPC	WEE1	DIAPH3	CENPU	CENPM
10	KIF14	HAUS1	TNFAIP8L1	NCAPG2	HYLS1	CDC45	ENSGALG00000033570	GPSM2
11	CNTLN	NDC1	GAS2L3	DEPDC1	ENSGALG00000008803	SAPCD2	CCNB3	RANGAP1
12	DCK	CIT	DNA2	CHTF8	SAP30	BRCA2	CenpA	ATAD2
13	PCNT	FOXN4	HAUS6	FANCL	ARHGEF39	FBXO5	FEN1	LMNB1
14	EXO1	PRC1	CCSAP	CLSPN	EZH2	TNFSF10	TUBB4B	RFC2
15	NMRK2	H2AFJ	EZR	ENSGALG00000053765	ODF2	NET1	RGCC	ENSGALG00000047664
16	CTNNAL1	JAM2	RASGEF1A	WNT4	YWHAH	CEP250	SLC16A10	STC2
17	PLEKHH1	EDNRB	MCM2	ENSGALG00000046198	ENSGALG00000040833			

	Term	Ont	N	n	Adj. p-value
GO:0051383	kinetochore organization	BP	10	6	1.584e–10
GO:0000278	mitotic cell cycle	BP	99	12	2.048e–10
GO:0007049	cell cycle	BP	201	15	1.068e–09
GO:0051276	chromosome organization	BP	177	14	1.865e–09
GO:0022402	cell cycle process	BP	126	12	3.453e–09
GO:1903047	mitotic cell cycle process	BP	77	10	3.546e–09
GO:0007059	chromosome segregation	BP	43	8	7.319e–09
GO:1902850	microtubule cytoskeleton organization involved in mitosis	BP	21	6	3.747e–08
GO:0034508	centromere complex assembly	BP	12	5	6.209e–08
GO:0051301	cell division	BP	87	9	1.667e–07

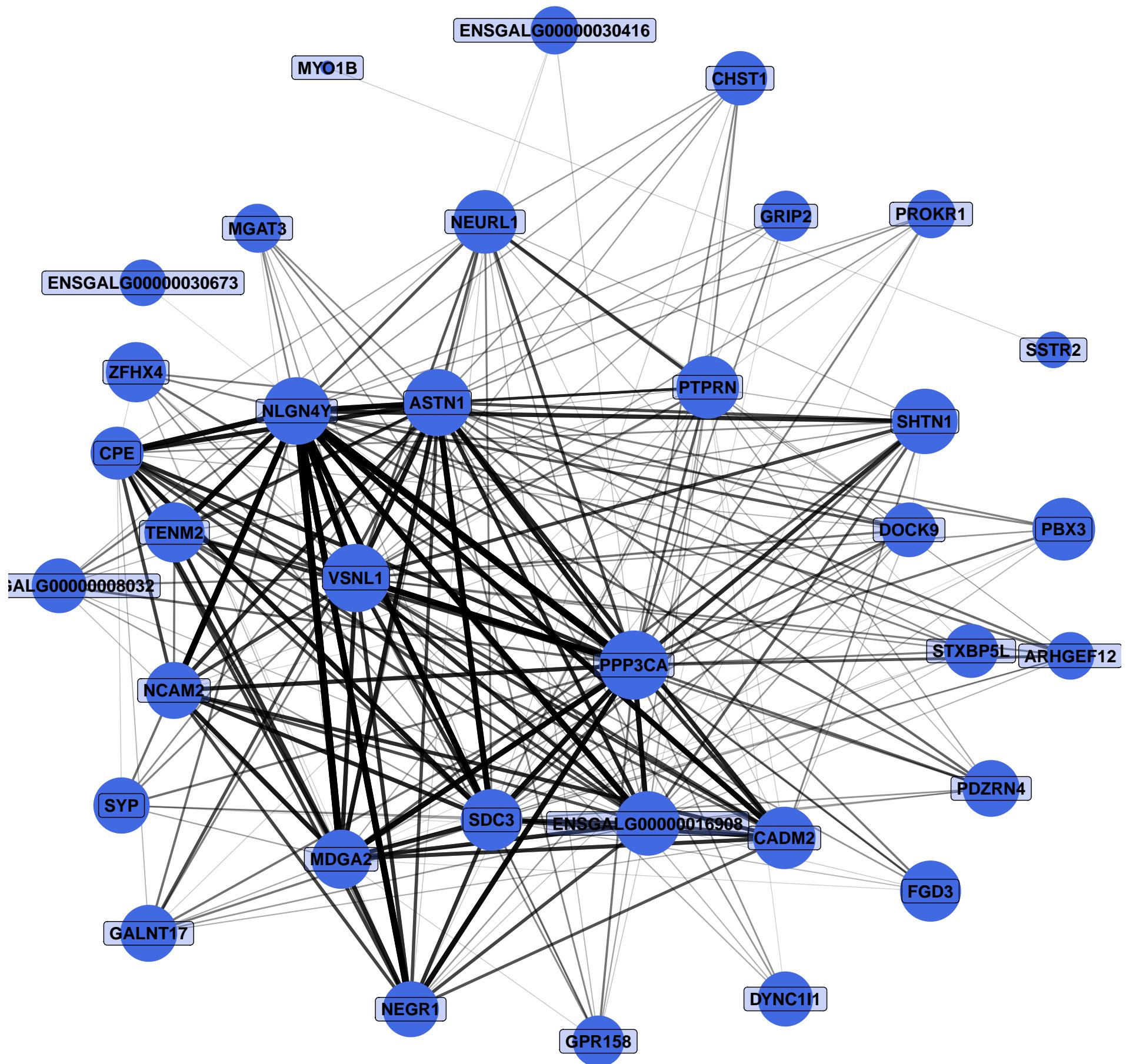
	Pathway	N	DE	P.DE
<i>path:gga04110</i>	Cell cycle	113	13	6.793e–11
<i>path:gga04114</i>	Oocyte meiosis	96	10	3.118e–08
<i>path:gga03030</i>	DNA replication	29	4	0.0001717
<i>path:gga04914</i>	Progesterone–mediated oocyte maturation	78	5	0.0009881
<i>path:gga03460</i>	Fanconi anemia pathway	48	3	0.01148
<i>path:gga03430</i>	Mismatch repair	19	2	0.01456
<i>path:gga04120</i>	Ubiquitin mediated proteolysis	127	4	0.03598
<i>path:gga03440</i>	Homologous recombination	36	2	0.04819
<i>path:gga03013</i>	Nucleocytoplasmic transport	89	3	0.05661
<i>path:gga04068</i>	FoxO signaling pathway	112	3	0.09702



1	STMN3	STMN2	CAVIN4	MAP6	YWHAG	MAP2	HMP19	RTN1
2	TUBB3	KIF5C	OLFM1	MAP1B	CRMP1	RUNX1T1	DPYSL3	DPYSL2
3	NCS1	DCX	CRACD	KIDINS220	TUBA1A	BRSK1	ANK3	XPR1
4	MAPT	NSG1	ELAVL4	SNAP25	RUSC2	SYT1	NCAM1	AKAP6
5	SEPTIN3	CAMK2N1	DPYSL4	BASP1	SNAP91	CBFA2T3	GNG2	RGMB
6	TAGLN3	PPFIA2	VASH2	MYT1L	NRXN1	KIF21B	ENSGALG00000013212	ENSGALG00000026278
7	APBA2	EEF1A2	ENSGALG00000054420	RBFOX1	RAB6A	RAB3C	SEPT5	UBE2QL1
8	DBN1	REEP1	TRIM2	MAPRE2	KIF1A	GAP43	SERINC1	RIMS2
9	SPOCK1	SORBS2	HDGFL3	APP	ST8SIA2	RTN4	EHBP1	MCF2L2
10	NOVA1	EBF3	ACTL6B	NMNAT2	SCG5	AFAP1	ATP6V0E2	CALM2
11	ENSGALG00000010718	PLXNA2	RBFOX2	ELAVL2	ENSGALG00000007268	ENSGALG00000000604	MAPK10	MYT1
12	RAPGEF5	TUBB2B	PGM2L1	SH3BP5	VSTM2L	PCLO	DENND5B	SCN3A
13	DNAJC6	PHACTR3	FGF13	KIAA1024	ATP8A1	CTNNA2	CACFD1	ATP6V0C
14	PANX1	ITFG1	KIF5A	ENSGALG00000051980	HN1	SCG2	PAK5	PHACTR1
15	TRARG1	ENSGALG00000031313	ENSGALG00000031564	PLPPR3	DYNC1H1	CHGA	ENSGALG00000051550	STXBP1
16	ADD2	GRIA2	ENSGALG00000011528	MADD	NAV3	NEO1	TMEM132A	CUX2
17	NOL4	SYN3	DAAM1	CHGB	NETO2	NCAN	ABR	TMEM240
18	IGSF3	ENSGALG0000006588	CACNA2D1	MAP1A	DYNLL2	PPM1E	SRRM3	PLXNA4
19	NBEA	FAM169A	TMOD2	KIF21A	RAB3A	ENSGALG00000011639	CPEB2	GRIN2B
20	NTM	FGD4	MYO5A	ATP6V0A1	PLCB4	TMEFF2	HOXB9	PTPRO
21	NFASC	CASP3	ELAPOR2	PTPRN2	CORO1C	DCLK1	DRAVIN	GABRG2
22	ST3GAL5	ENSGALG0000000816	HOXB8	TSHZ3	WNK2	CERS6	PPIP5K2	BICD1
23	NELL1	HOXB7	SCN8A	FHL2	ERC2	CYFIP2	SOX4	FABP3
24	TMEM8B	ATCAY						

	Term	Ont	N	n	Adj. p-value
GO:0031175	neuron projection development	BP	112	14	4.183e-10
GO:0048666	neuron development	BP	126	14	2.028e-09
GO:0120036	plasma membrane bounded cell projection organization	BP	138	14	6.711e-09
GO:0030030	cell projection organization	BP	142	14	9.734e-09
GO:0048699	generation of neurons	BP	180	15	2.821e-08
GO:0022008	neurogenesis	BP	183	15	3.523e-08
GO:0030182	neuron differentiation	BP	165	14	6.641e-08
GO:0048667	cell morphogenesis involved in neuron differentiation	BP	77	10	9.845e-08
GO:0007399	nervous system development	BP	258	17	1.054e-07
GO:0048812	neuron projection morphogenesis	BP	80	10	1.426e-07

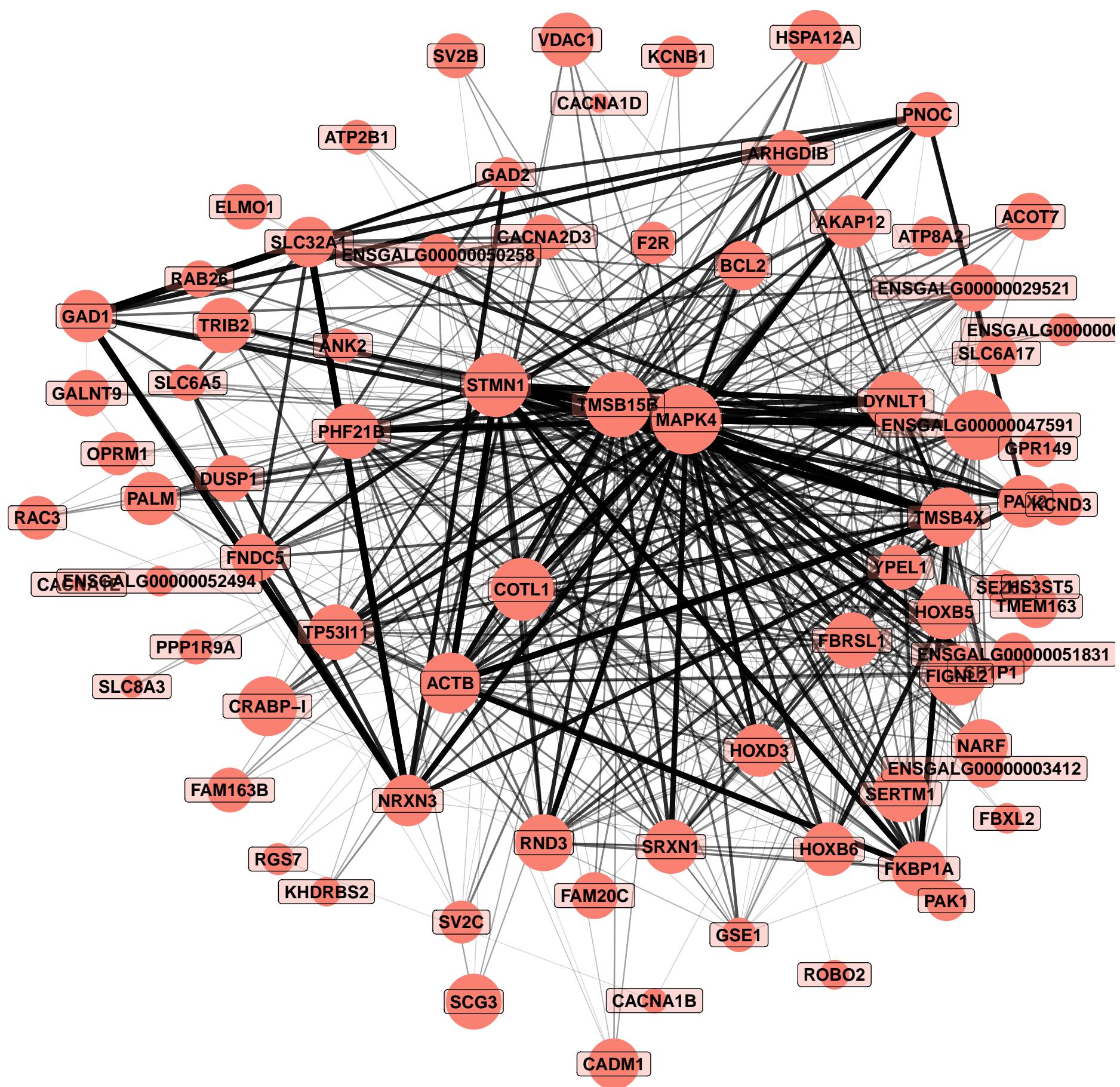
	Pathway	N	DE	P.DE
<i>path:gga05132</i>	Salmonella infection	222	12	6.055e-05
<i>path:gga04145</i>	Phagosome	125	8	0.000341
<i>path:gga04540</i>	Gap junction	79	5	0.00473
<i>path:gga03250</i>	Viral life cycle – HIV-1	48	3	0.02857
<i>path:gga04514</i>	Cell adhesion molecules	99	4	0.04843
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.0542
<i>path:gga04912</i>	GnRH signaling pathway	76	3	0.08815
<i>path:gga04070</i>	Phosphatidylinositol signaling system	85	3	0.1135
<i>path:gga04114</i>	Oocyte meiosis	96	3	0.1477
<i>path:gga00190</i>	Oxidative phosphorylation	100	3	0.1608



1	NLGN4Y	ASTN1	PPP3CA	SDC3	CPE	VSNL1	MDGA2	ENSGALG00000016908
2	CADM2	SHTN1	TENM2	ZFHX4	NEURL1	NCAM2	NEGR1	PTPRN
3	GALNT17	SYP	PBX3	FGD3	PDZRN4	ENSGALG00000008032	STXBP5L	ARHGEF12
4	DOCK9	MGAT3	DYNC1I1	GPR158	CHST1	GRIP2	PROKR1	ENSGALG00000030673
5	ENSGALG00000030416	SSTR2	MYO1B					

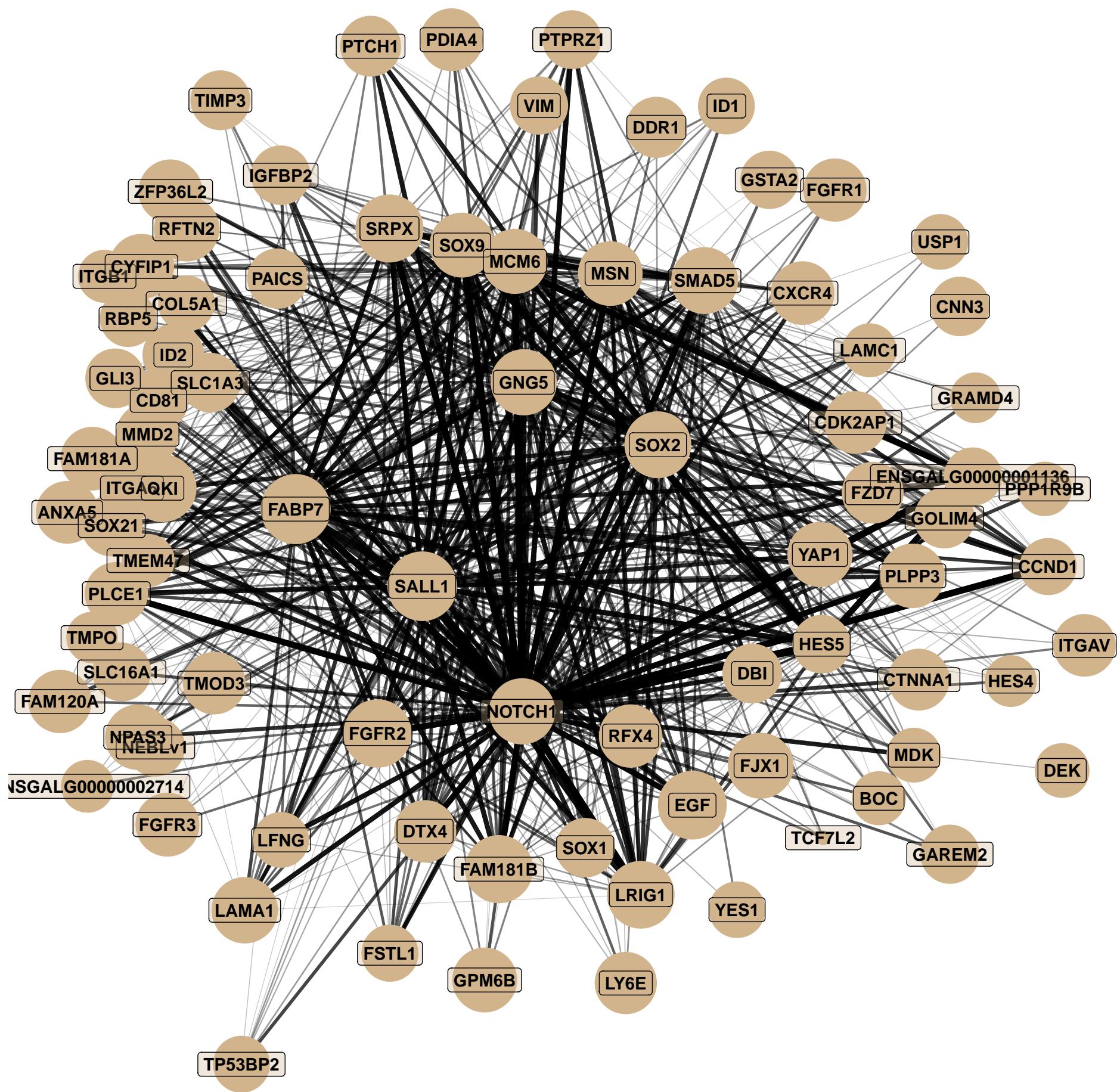
	Term	Ont	N	n	Adj. p-value
GO:0035584	calcium–mediated signaling using intracellular calcium source	BP	2	1	0.00519
GO:0003419	growth plate cartilage chondrocyte proliferation	BP	2	1	0.00519
GO:0022610	biological adhesion	BP	143	3	0.005969
GO:0007155	cell adhesion	BP	143	3	0.005969
GO:0035988	chondrocyte proliferation	BP	4	1	0.01035
GO:0007157	heterophilic cell–cell adhesion via plasma membrane cell adhesion molecules	BP	4	1	0.01035
GO:1900026	positive regulation of substrate adhesion–dependent cell spreading	BP	4	1	0.01035
GO:1900024	regulation of substrate adhesion–dependent cell spreading	BP	4	1	0.01035
GO:0010770	positive regulation of cell morphogenesis involved in differentiation	BP	6	1	0.01549
GO:0051491	positive regulation of filopodium assembly	BP	6	1	0.01549

	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	99	4	0.0001201
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.01035
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	82	2	0.01912
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.03579
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	1	0.07275
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	2	0.08541
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	1	0.1013
<i>path:gga00510</i>	N-Glycan biosynthesis	45	1	0.1107
<i>path:gga04370</i>	VEGF signaling pathway	53	1	0.129
<i>path:gga04114</i>	Oocyte meiosis	96	1	0.2217



	Term	Ont	N	n	Adj. p-value
GO:0006816	calcium ion transport	BP	30	4	2.704e-05
GO:0030001	metal ion transport	BP	40	4	8.626e-05
GO:0070588	calcium ion transmembrane transport	BP	23	3	0.0003188
GO:0060999	positive regulation of dendritic spine development	BP	6	2	0.0005049
GO:0031175	neuron projection development	BP	112	5	0.0005083
GO:0034762	regulation of transmembrane transport	BP	29	3	0.0006413
GO:0048666	neuron development	BP	126	5	0.0008682
GO:0070509	calcium ion import	BP	8	2	0.0009354
GO:0060998	regulation of dendritic spine development	BP	8	2	0.0009354
GO:0120036	plasma membrane bounded cell projection organization	BP	138	5	0.001305

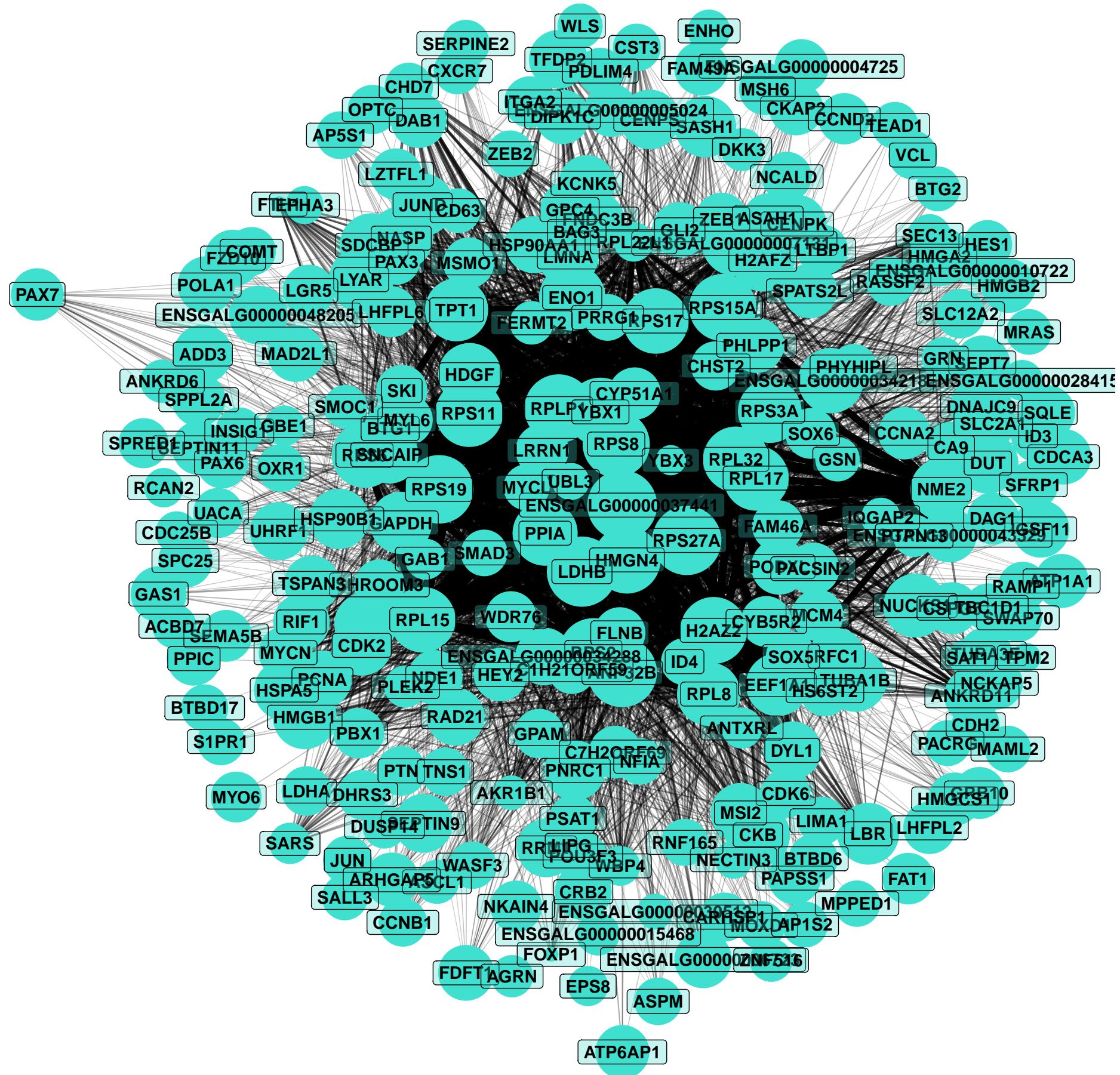
	Pathway	N	DE	P.DE
<i>path:gga04010</i>	MAPK signaling pathway	239	8	7.828e-05
<i>path:gga04020</i>	Calcium signaling pathway	201	7	0.0001761
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	5	0.0007504
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	6	0.0008267
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	2	0.002171
<i>path:gga04260</i>	Cardiac muscle contraction	59	3	0.005028
<i>path:gga00650</i>	Butanoate metabolism	21	2	0.006676
<i>path:gga00410</i>	beta-Alanine metabolism	25	2	0.009394
<i>path:gga05132</i>	Salmonella infection	222	5	0.009877
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	2	0.01512



1	FABP7	EGF	NOTCH1	SLC1A3	SOX2	SALL1	SRPX	FGFR2
2	SOX9	GNG5	PLPP3	LRIG1	FGFR3	FAM181B	DBI	HES5
3	QKI	MCM6	MSN	ID1	PTPRZ1	SMAD5	YAP1	ENSGALG00000001136
4	RFX4	LAMC1	LAMA1	CXCR4	GSTA2	PLCE1	DTX4	DDR1
5	TIMP3	FJX1	NEBLv1	VIM	ANXA5	NPAS3	ZFP36L2	FZD7
6	CTNNA1	FAM181A	CD81	GPM6B	GLI3	RFTN2	CYFIP1	COL5A1
7	FAM120A	FSTL1	CCND1	SOX21	ITGA6	MDK	PTCH1	ID2
8	IGFBP2	MMD2	TMOD3	GOLIM4	CDK2AP1	LY6E	LFNG	ITGAV
9	SOX1	PDIA4	FGFR1	PAICS	ITGB1	CNN3	TMEM47	BOC
10	PPP1R9B	YES1	HES4	GAREM2	RBP5	DEK	SLC16A1	TP53BP2
11	USP1	ENSGALG0000002714	GRAMD4	TMPO	TCF7L2			

	Term	Ont	N	n	Adj. p-value
GO:0007166	cell surface receptor signaling pathway	BP	263	15	1.017e-10
GO:0007165	signal transduction	BP	477	18	9.649e-10
GO:0023052	signaling	BP	512	18	2.971e-09
GO:0007154	cell communication	BP	519	18	3.679e-09
GO:0051716	cellular response to stimulus	BP	657	20	4.042e-09
GO:0050896	response to stimulus	BP	779	21	1.312e-08
GO:0050789	regulation of biological process	BP	1098	24	5.513e-08
GO:0050794	regulation of cellular process	BP	1048	23	1.053e-07
GO:0007275	multicellular organism development	BP	577	17	1.159e-07
GO:0032502	developmental process	BP	655	18	1.317e-07

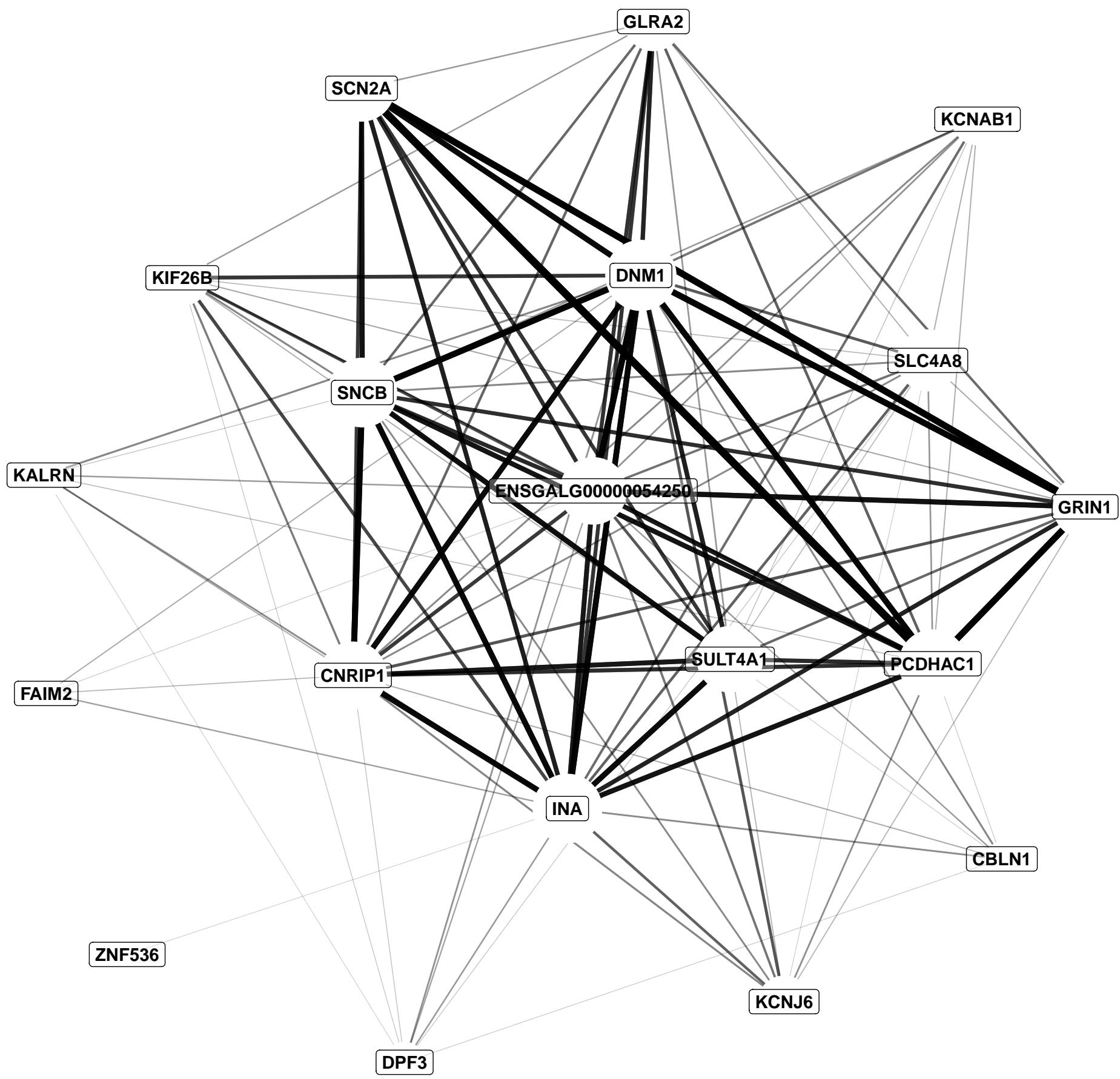
	Pathway	N	DE	P.DE
<i>path:gga04330</i>	Notch signaling pathway	52	6	9.391e-07
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	9	3.136e-06
<i>path:gga04512</i>	ECM–receptor interaction	68	5	7.338e-05
<i>path:gga04510</i>	Focal adhesion	172	7	0.0001161
<i>path:gga04340</i>	Hedgehog signaling pathway	47	4	0.0002284
<i>path:gga04520</i>	Adherens junction	69	4	0.0009948
<i>path:gga04020</i>	Calcium signaling pathway	201	6	0.001834
<i>path:gga04350</i>	TGF–beta signaling pathway	83	3	0.01622
<i>path:gga03260</i>	Virion – Human immunodeficiency virus	4	1	0.02543
<i>path:gga04514</i>	Cell adhesion molecules	99	3	0.02575



1	ENSGALG00000037441	ANP32B	LDHB	RPS2	RPLP1	HMGN4	RPS27A	RPS19
2	RPS15A	H2AZ2	RPS8	YBX1	RPS11	RPS6	RPL32	RPS17
3	NUCKS1	RPL17	RPL15	ENO1	RPS3A	CKB	PPIA	NASP
4	RPL8	H2AFZ	TPT1	EEF1A1	GAPDH	LBR	ENSGALG00000007131	NME2
5	HMGB2	PCNA	ENSGALG00000034218	NA	TUBA1B	JUND	PNRC1	HDGF
6	SASH1	HMGB1	LYAR	SDCBP	DUT	PTN	DYL1	DNAJC9
7	SEPTIN9	CDK2	LMNA	SEPT7	HMGA2	UHRF1	CDCA3	CKAP2
8	MAD2L1	IGSF11	CENPK	CENPS	PAPSS1	PODXL	SPC25	RAD21
9	MSI2	FZD10	ENSGALG0000005024	ARHGAP5	MYL6	ID3	BTG1	TFDP2
10	CST3	HSPA5	TUBA3E	ADD3	RRM1	NDE1	DAB1	CCNA2
11	FTH1	HSP90B1	YBX3	LGR5	HES1	ENSGALG00000043329	PBX1	CCNB1
12	LRRN1	GAS1	PAX6	POLA1	ZEB1	FNDC3B	LHFPL2	SEPTIN11
13	ASPM	JUN	SNCAIP	ENSGALG0000006723	ENSGALG00000034288	RIF1	DIPK1C	S1PR1
14	GPAM	TSPAN3	ENSGALG00000048205	ANKRD11	OPTC	HSP90AA1	CRB2	SWAP70
15	FAM49A	ACBD7	SERPINE2	SPPL2A	KCNK5	CDK6	CHD7	GPC4
16	PHLPP1	HS6ST2	SEMA5B	ATP6AP1	SOX6	SPRED1	PAX7	NFIA
17	ENSGALG00000030512	HEY2	ENSGALG00000028415	RFC1	ID4	ATP1A1	NKAIN4	RAMP1
18	POU3F3	ANTXRL	ZEB2	UBL3	AKR1B1	HMGCS1	SPATS2L	CCND2
19	LHFPL6	FDFT1	GLI2	FERMT2	SMAD3	FAT1	DAG1	C7H2ORF69
20	ENSGALG0000004725	NCKAP5	TNS1	COMT	VCL	ASCL1	SHROOM3	ENSGALG00000010722
21	ENHO	PPIC	CSPG5	RASSF2	PAC SIN2	CD63	SMOC1	MYCN
22	MCM4	WDR76	SKI	GRB10	SQLE	NCALD	MSH6	GRN
23	PAX3	CA9	LIPG	TEAD1	CYB5R2	FLNB	DKK3	PSAT1
24	MYO6	ITGA2	MRAS	BTBD6	MAML2	PACRG	CHST2	SLC2A1
25	TBC1D1	CXCR7	SEC13	RNF165	AP1S2	FAM46A	MSMO1	OXR1
26	LZTFL1	SFRP1	GAB1	TPM2	BTG2	SOX5	RPL22L1	C1H21ORF59
27	CYP51A1	PHYHIPL	LTBP1	LDHA	ASAHI	EPHA3	WASF3	LIMA1
28	INSIG1	PDLIM4	CDC25B	AP5S1	BAG3	SARS	ZNF516	SAT1
29	SLC12A2	CDH2	WLS	CARHSP1	GBE1	DUSP14	MOXD1	GSN
30	NECTIN3	PRRG1	BTBD17	SALL3	UACA	DHRS3	MYCL	MPPED1
31	EPS8	PTPN13	AGRN	WBP4	IQGAP2	ANKRD6	RCAN2	FOXP1
32	PLEK2	ENSGALG00000015468						

	Term	Ont	N	n	Adj. p-value
GO:0008150	biological_process	BP	1904	78	1.119e-11
GO:0009987	cellular process	BP	1823	75	2.722e-11
GO:0009058	biosynthetic process	BP	672	39	4.385e-10
GO:1901576	organic substance biosynthetic process	BP	663	38	1.077e-09
GO:0065007	biological regulation	BP	1194	54	1.38e-09
GO:0016043	cellular component organization	BP	662	37	3.641e-09
GO:0050789	regulation of biological process	BP	1098	50	5.18e-09
GO:0032501	multicellular organismal process	BP	711	38	7.441e-09
GO:0071840	cellular component organization or biogenesis	BP	683	37	8.417e-09
GO:0048856	anatomical structure development	BP	623	35	8.895e-09

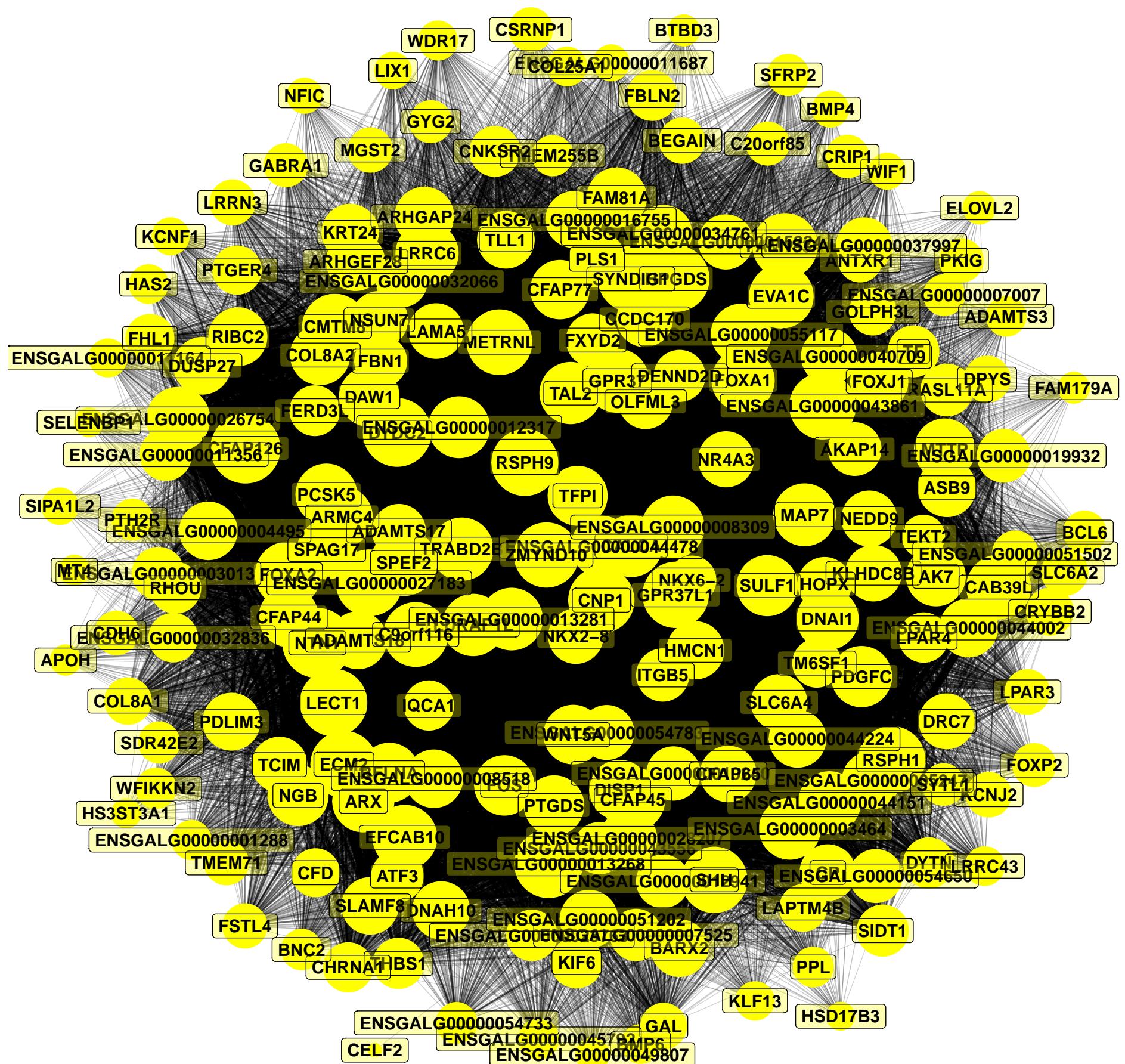
	Pathway	N	DE	P.DE
<i>path:gga03010</i>	Ribosome	114	16	4.748e–10
<i>path:gga00100</i>	Steroid biosynthesis	15	6	1.985e–07
<i>path:gga04110</i>	Cell cycle	113	12	1.628e–06
<i>path:gga03030</i>	DNA replication	29	4	0.002122
<i>path:gga05132</i>	Salmonella infection	222	11	0.003636
<i>path:gga04914</i>	Progesterone–mediated oocyte maturation	78	6	0.003735
<i>path:gga03430</i>	Mismatch repair	19	3	0.005324
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	46	4	0.01132
<i>path:gga04218</i>	Cellular senescence	134	7	0.01444
<i>path:gga04310</i>	Wnt signaling pathway	135	7	0.01499



1	DNM1	SNCB	PCDHAC1	ENSGALG00000054250	INA	GRIN1	SCN2A	CNRIP1
2	SULT4A1	SLC4A8	GLRA2	KCNAB1	KIF26B	KCNJ6	KALRN	CBLN1
3	DPF3	FAIM2	ZNF536					

	Term	Ont	N	n	Adj. p-value
GO:2001258	negative regulation of cation channel activity	BP	1	1	0.001605
GO:1902260	negative regulation of delayed rectifier potassium channel activity	BP	1	1	0.001605
GO:1901380	negative regulation of potassium ion transmembrane transport	BP	1	1	0.001605
GO:1901017	negative regulation of potassium ion transmembrane transporter activity	BP	1	1	0.001605
GO:1903817	negative regulation of voltage-gated potassium channel activity	BP	1	1	0.001605
GO:2001257	regulation of cation channel activity	BP	1	1	0.001605
GO:1902259	regulation of delayed rectifier potassium channel activity	BP	1	1	0.001605
GO:1904063	negative regulation of cation transmembrane transport	BP	2	1	0.003207
GO:0032413	negative regulation of ion transmembrane transporter activity	BP	2	1	0.003207
GO:0043267	negative regulation of potassium ion transport	BP	2	1	0.003207

	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	2	0.07384
<i>path:gga04020</i>	Calcium signaling pathway	201	1	0.2777
<i>path:gga04144</i>	Endocytosis	218	1	0.2975
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1
<i>path:gga00785</i>	Lipoic acid metabolism	3	0	1
<i>path:gga00290</i>	Valine, leucine and isoleucine biosynthesis	3	0	1
<i>path:gga03264</i>	Virion – Flavivirus	3	0	1
<i>path:gga00232</i>	Caffeine metabolism	4	0	1
<i>path:gga03266</i>	Virion – Herpesvirus	4	0	1



1	CFAP126	NTN1	LECT1	DYDC2	ECM2	SHH	FOXA2	CNP1
2	RSPH1	HPGDS	ENSGALG00000013268	ENSGALG00000043861	CALCA	ENSGALG00000055117	SULF1	SPEF2
3	ENSGALG00000027183	RSPH9	PTGDS	EVA1C	FOXA1	METRNL	FAM183A	GPR37L1
4	CAB39L	SYNDIG1	ARX	TAL2	CFAP45	ZMYND10	ENSGALG00000044478	ENSGALG00000026754
5	C9orf116	ENSGALG00000008309	LURAP1L	FOXJ1	CMTM8	GPR37	PDGFC	ENSGALG00000013281
6	FOS	NKX2–8	TRABD2B	MTTP	MAP7	EFCAB10	DNAI1	ARMC4
7	LRRC6	ENSGALG00000044151	WNT5A	COL8A2	CFAP77	ENSGALG00000003464	DAW1	KRT24
8	CFAP44	ENSGALG00000012317	AK7	PCSK5	ENSGALG00000054783	NGB	FAM81A	ENSGALG00000043556
9	RIBC2	ENSGALG00000008518	DNAH10	ENSGALG00000005247	ARHGEF28	KLHDC8B	ENSGALG00000004495	ENSGALG00000034761
10	DUSP27	RFLNA	SPAG17	ENSGALG00000044224	TCIM	SLC6A4	ENSGALG00000044002	TFPI
11	ENSGALG00000028207	DISP1	SLAMF8	ADAMTS18	OLFML3	ARHGAP24	HMCN1	TLL1
12	ENSGALG00000051202	PDLIM3	NR4A3	ASB9	RASL11A	ENSGALG00000032066	NSUN7	ENSGALG00000019932
13	ENSGALG00000037997	NKX6–2	ENSGALG00000015224	NEDD9	BARX2	HOPX	ADAMTS17	ENSGALG00000040709
14	AKAP14	LAMA5	PLS1	FXYD2	CP	ATF3	CCDC170	ITGB5
15	ENSGALG00000019240	ENSGALG00000023763	ENSGALG00000054650	ENSGALG00000003013	DRC7	GAL	CFAP65	ENSGALG00000016755
16	CFD	FOXP2	COL8A1	ENSGALG00000011356	ENSGALG00000012941	ENSGALG00000032836	LPAR4	KIF6
17	FHL1	TF	FERD3L	SFRP2	ENSGALG00000051502	CHRNA1	SIDT1	THBS1
18	DYTN	FBLN2	FBN1	RHOU	DENND2D	CNKS2	CRYBB2	GOLPH3L
19	DPYS	TM6SF1	MGST2	KCNJ2	LAPTM4B	IQCA1	ENSGALG00000007525	PTGER4
20	SLC6A2	LRRN3	BEGAIN	LPAR3	ENSGALG00000011164	CSRNP1	ANTXR1	TMEM71
21	GYG2	FSTL4	BCL6	PKIG	CDH6	GABRA1	WFIKKN2	ENSGALG0000007007
22	SDR42E2	BNC2	TEKT2	SYTL1	TMEM255B	ENSGALG0000001288	C20orf85	PTH2R
23	KLF13	NFIC	ELOVL2	LIX1	BMP4	ADAMTS3	ENSGALG00000054733	ENSGALG00000011687
24	CRIP1	LRRC43	HAS2	KCNF1	WIF1	WDR17	BMP6	SIPA1L2
25	BTBD3	PPL	COL25A1	ENSGALG00000045792	ENSGALG00000049807	FAM179A	MT4	SELENBP1
26	APOH	HSD17B3	HS3ST3A1	CELF2				

	Term	Ont	N	n	Adj. p-value
GO:0009950	dorsal/ventral axis specification	BP	2	2	0.0002032
GO:0009951	polarity specification of dorsal/ventral axis	BP	2	2	0.0002032
GO:0065001	specification of axis polarity	BP	3	2	0.0006037
GO:0071276	cellular response to cadmium ion	BP	4	2	0.001196
GO:0046686	response to cadmium ion	BP	4	2	0.001196
GO:0032501	multicellular organismal process	BP	711	21	0.001264
GO:0048856	anatomical structure development	BP	623	19	0.001499
GO:0007275	multicellular organism development	BP	577	18	0.001556
GO:0048513	animal organ development	BP	321	12	0.002241
GO:0048639	positive regulation of developmental growth	BP	19	3	0.002351

	Pathway	N	DE	P.DE
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	28	3	0.007235
<i>path:gga04350</i>	TGF–beta signaling pathway	83	4	0.03099
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	8	0.04886
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.05596
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	30	2	0.06807
<i>path:gga04512</i>	ECM–receptor interaction	68	3	0.07338
<i>path:gga04216</i>	Ferroptosis	34	2	0.08463
<i>path:gga00920</i>	Sulfur metabolism	7	1	0.09587
<i>path:gga00590</i>	Arachidonic acid metabolism	39	2	0.1068
<i>path:gga00480</i>	Glutathione metabolism	47	2	0.145