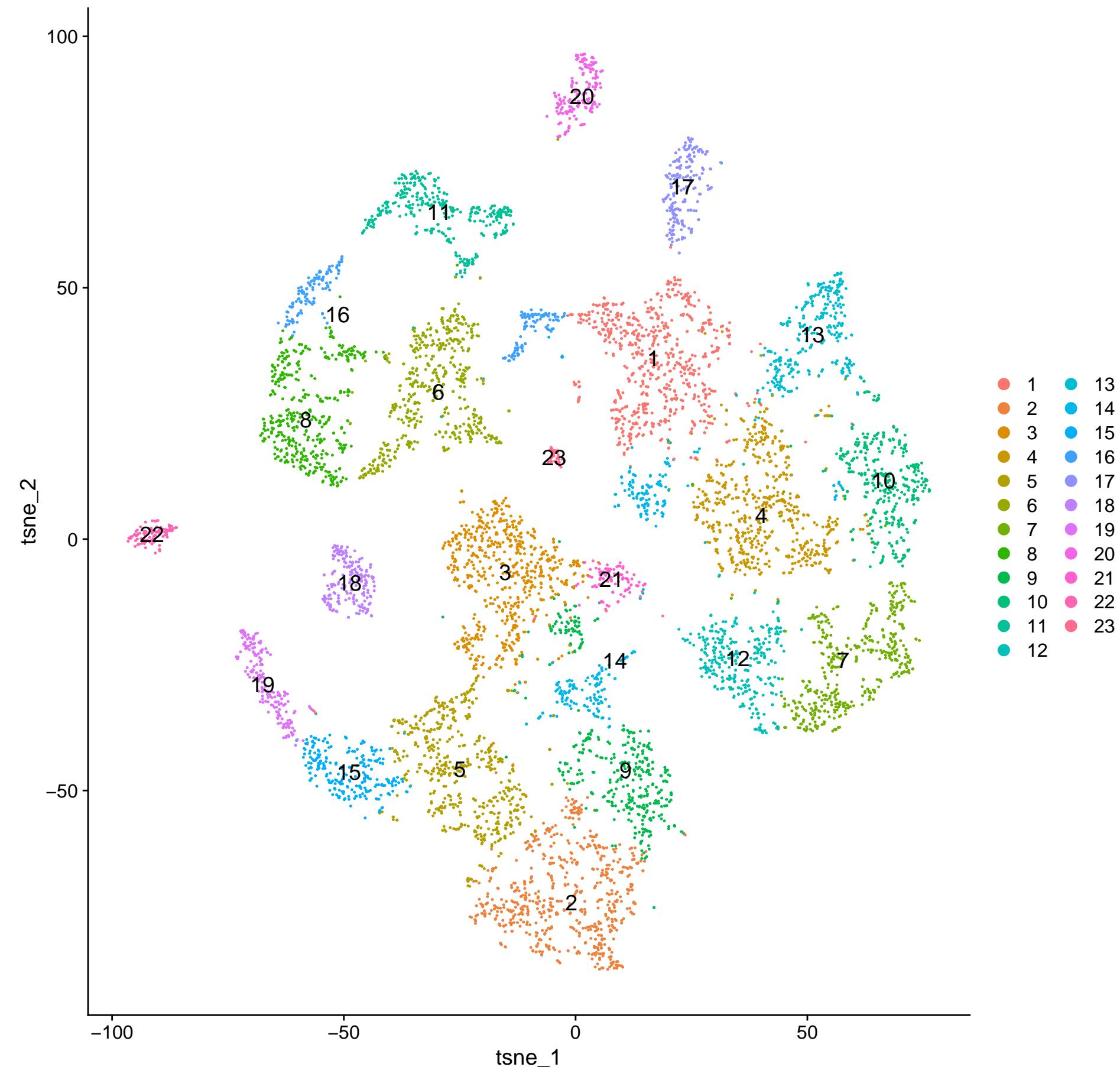
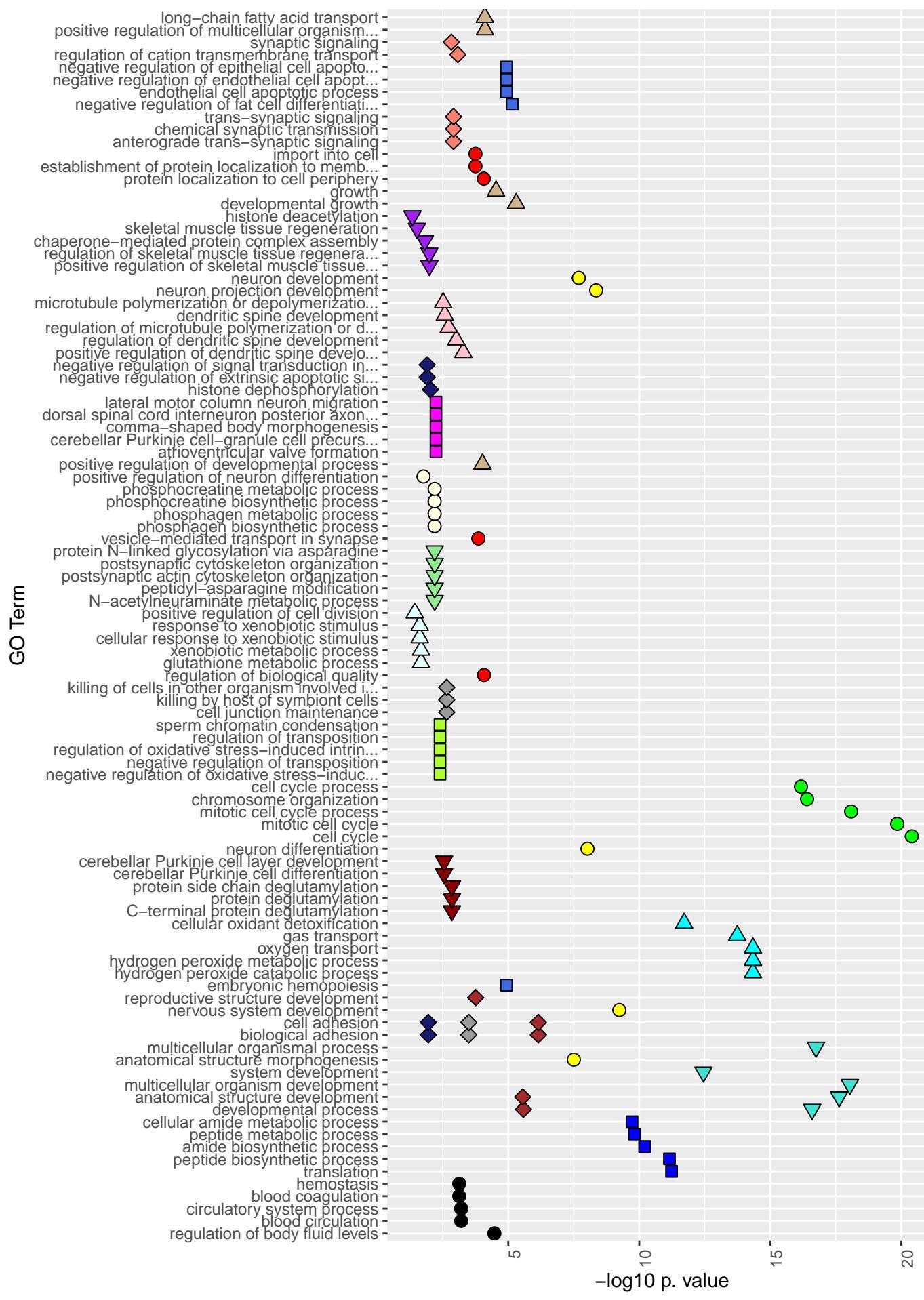


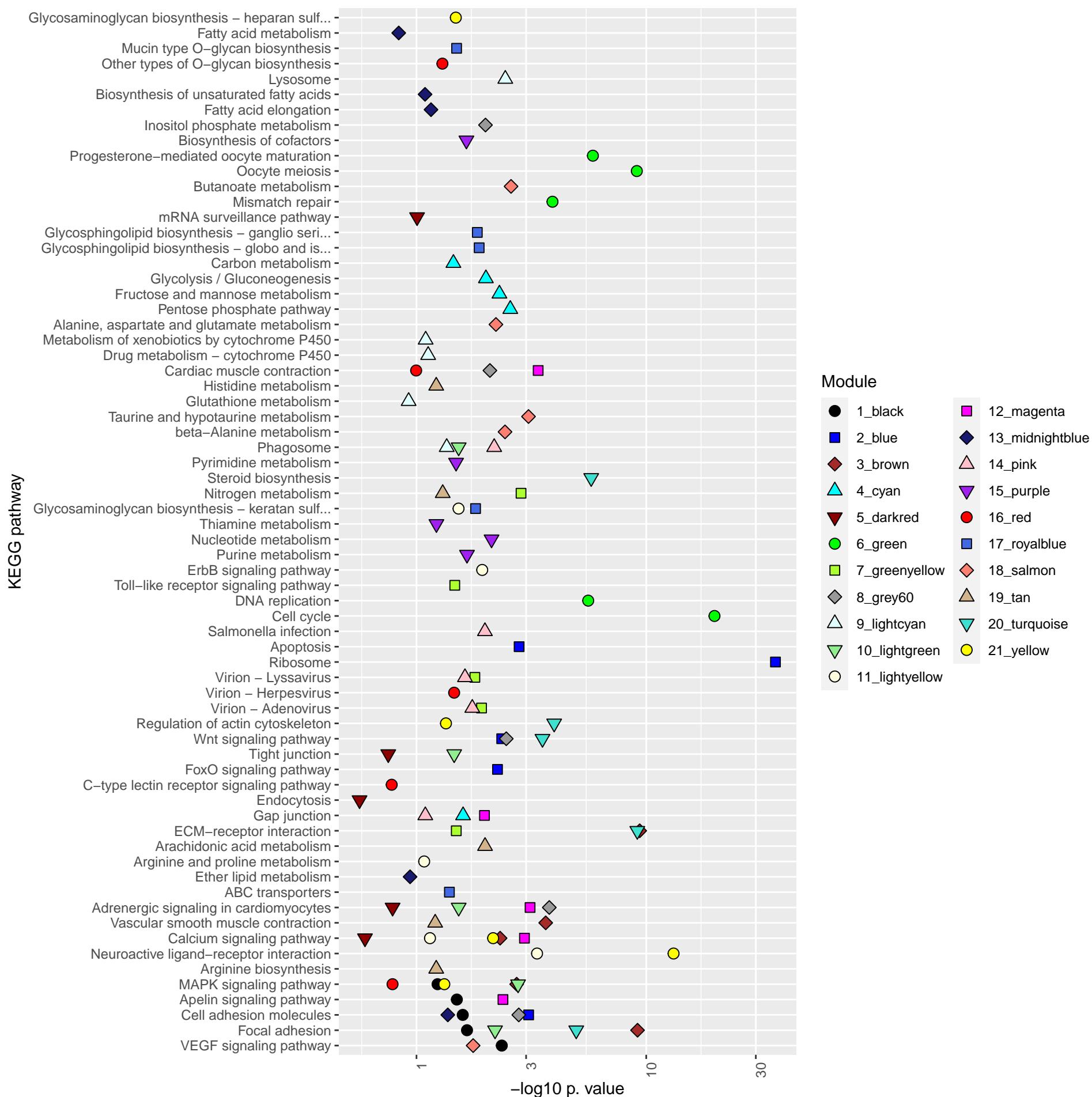
Gg_ctrl_int scWGCNA modules

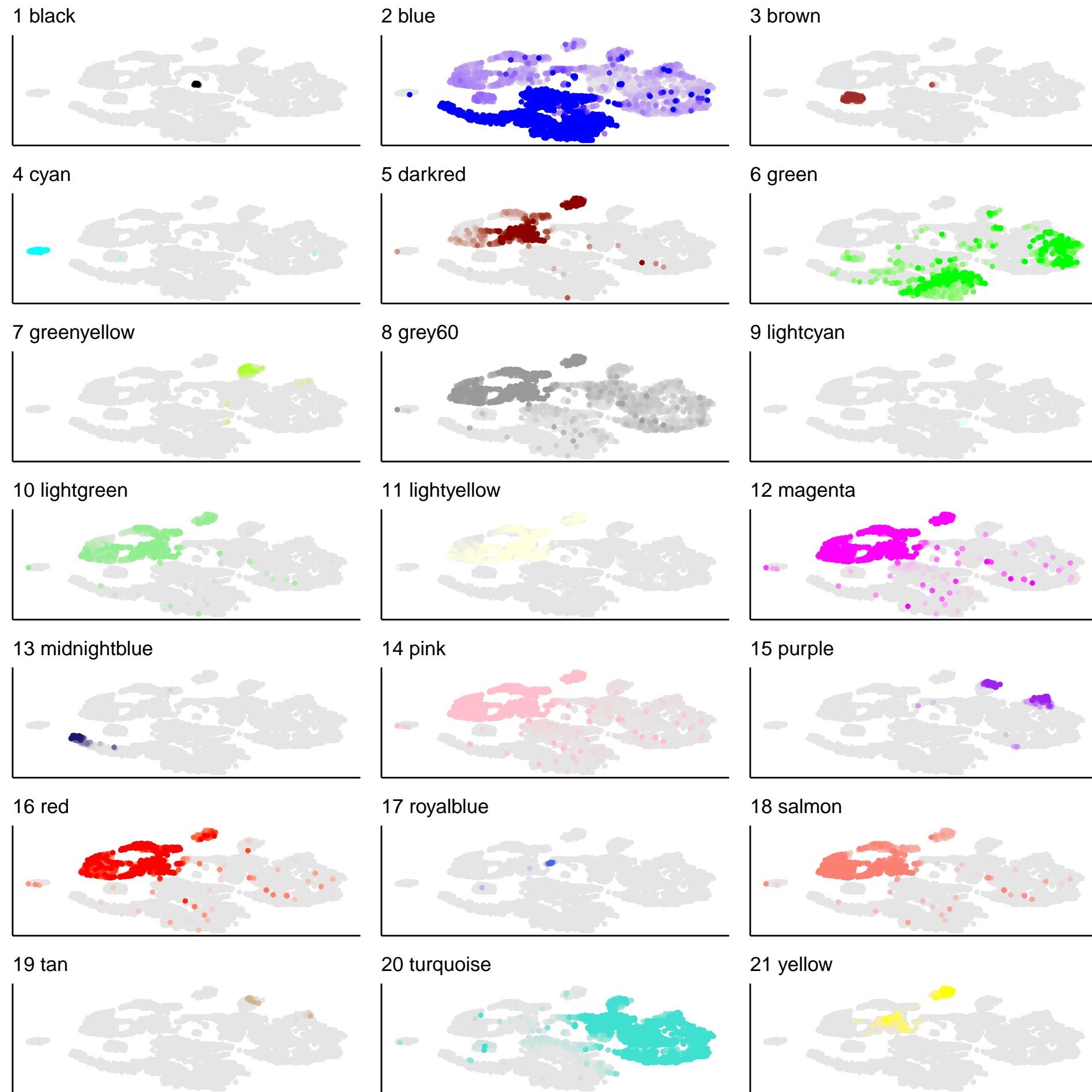


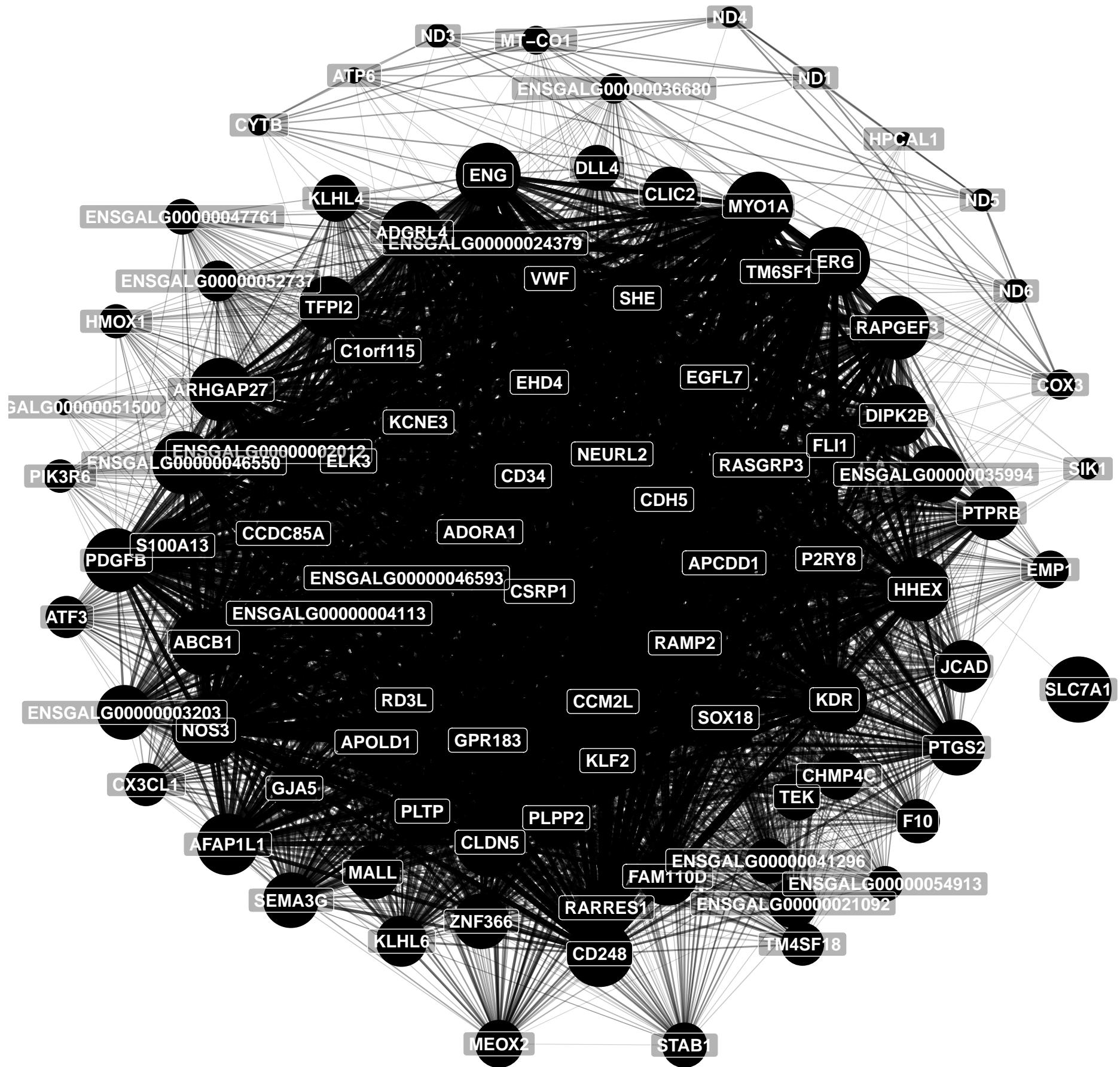


Module

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



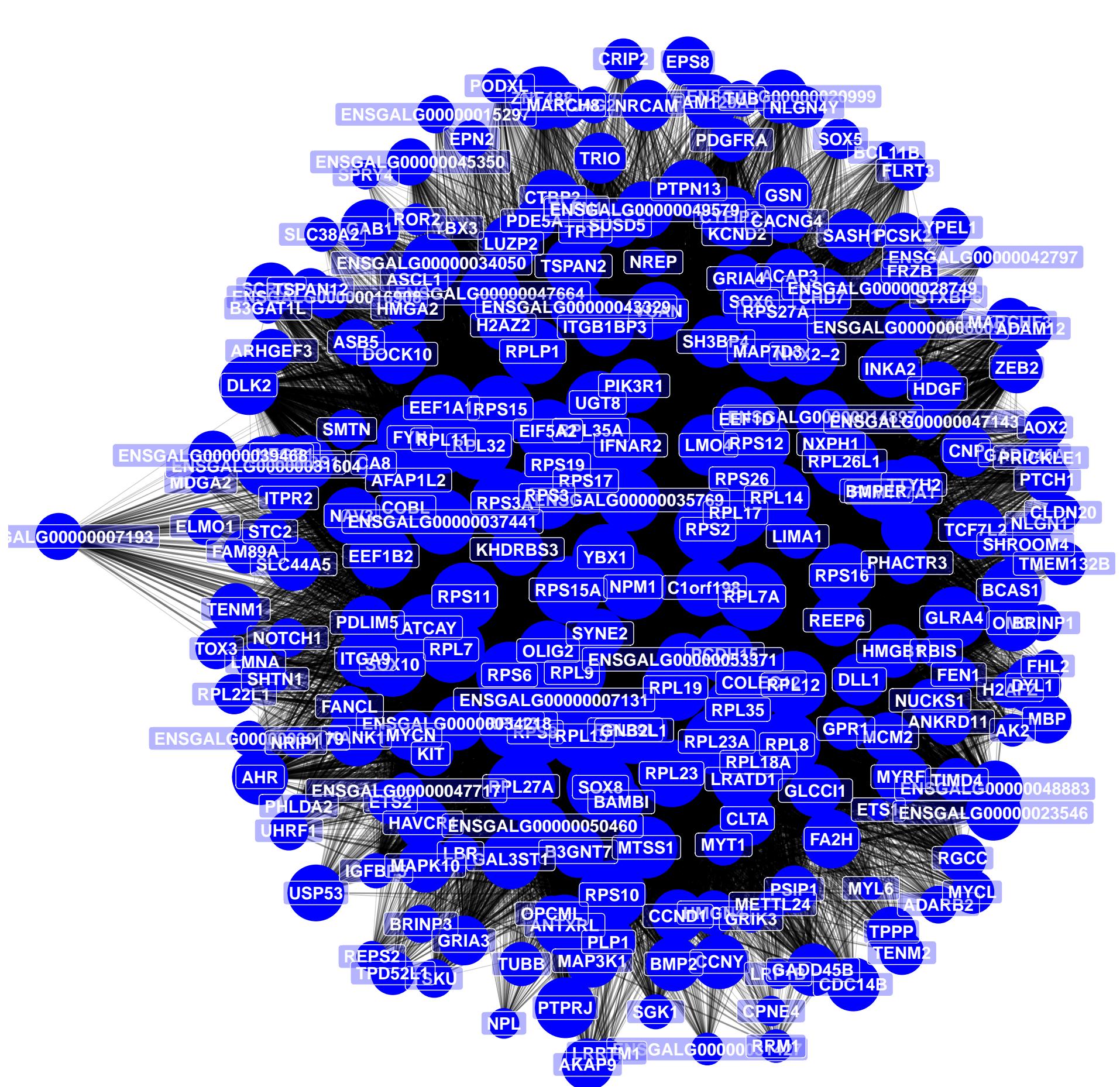




1	CDH5	VWF	RAMP2	CD34	CD248	MYO1A	ENSGALG00000002012	SHE
2	SOX18	APOLD1	NOS3	ERG	ENSGALG00000024379	ARHGAP27	CLDN5	KLF2
3	ABCB1	ENSGALG00000046550	GPR183	EGFL7	KDR	P2RY8	RASGRP3	HHEX
4	ZNF366	MALL	FLI1	TFPI2	ENG	CCM2L	FAM110D	PLPP2
5	PLTP	ADGRL4	AFAP1L1	PDGFB	DIPK2B	RD3L	S100A13	ADORA1
6	RAPGEF3	CLIC2	SEMA3G	RARRES1	SLC7A1	KLHL4	ENSGALG0000003203	CSRP1
7	ENSGALG00000052737	ENSGALG00000046593	ENSGALG00000035994	CCDC85A	EHD4	MEOX2	TM4SF18	ENSGALG00000021092
8	TEK	APCDD1	JCAD	ELK3	ENSGALG0000004113	EMP1	CHMP4C	PTPRB
9	C1orf115	KLHL6	DLL4	STAB1	F10	PTGS2	KCNE3	GJA5
10	TM6SF1	ATF3	ENSGALG00000041296	NEURL2	ENSGALG00000036680	ENSGALG00000047761	HMOX1	CX3CL1
11	MT-CO1	COX3	PIK3R6	ND3	ENSGALG00000054913	SIK1	ND6	ND5
12	CYTB	ND1	ND4	HPCAL1	ATP6	ENSGALG00000051500		

	Term	Ont	N	n	Adj. p-value
GO:0050878	regulation of body fluid levels	BP	11	3	3.397e-05
GO:0008015	blood circulation	BP	28	3	0.0006262
GO:0003013	circulatory system process	BP	28	3	0.0006262
GO:0007596	blood coagulation	BP	7	2	0.000744
GO:0007599	hemostasis	BP	7	2	0.000744
GO:0035590	purinergic nucleotide receptor signaling pathway	BP	7	2	0.000744
GO:0050817	coagulation	BP	8	2	0.0009881
GO:0008217	regulation of blood pressure	BP	8	2	0.0009881
GO:0050728	negative regulation of inflammatory response	BP	10	2	0.001576
GO:0031348	negative regulation of defense response	BP	13	2	0.002699

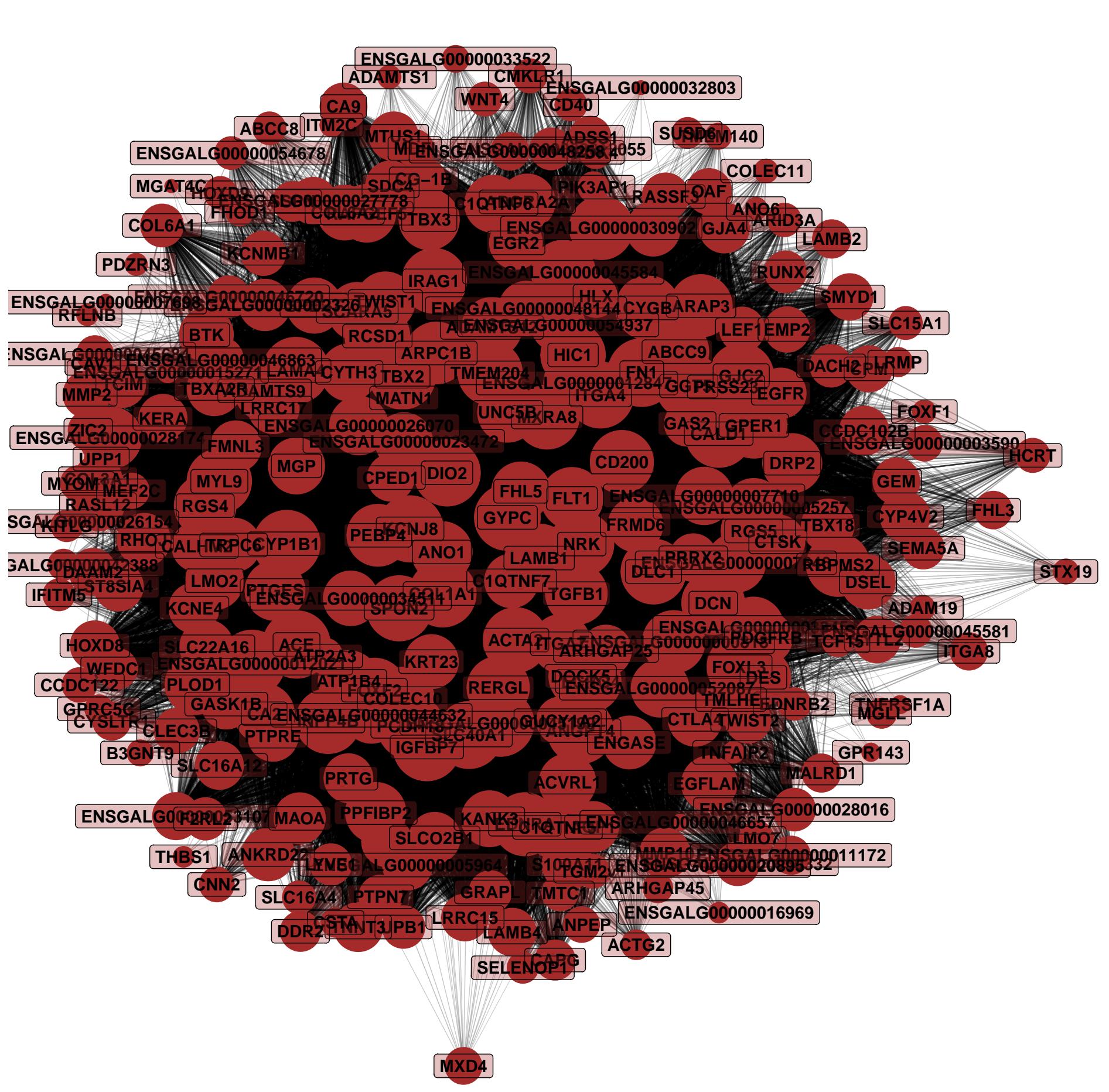
	Pathway	N	DE	P.DE
<i>path:gga04370</i>	VEGF signaling pathway	55	3	0.00446
<i>path:gga04510</i>	Focal adhesion	176	4	0.02192
<i>path:gga04514</i>	Cell adhesion molecules	105	3	0.02571
<i>path:gga04371</i>	Apelin signaling pathway	114	3	0.03174
<i>path:gga04010</i>	MAPK signaling pathway	241	4	0.05819
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.09805
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	305	4	0.1132
<i>path:gga00860</i>	Porphyrin metabolism	21	1	0.1197
<i>path:gga04020</i>	Calcium signaling pathway	204	3	0.1261
<i>path:gga04270</i>	Vascular smooth muscle contraction	111	2	0.1451



1	UGT8	RPL13	RPS3A	RPS10	RPL15	RPS26	RPL32	SOX8
2	RPL14	RPL27A	RPL35	RPL18A	RPL17	SOX10	RPL11	RPL7A
3	OLIG2	RPS2	RPL26L1	RPL23	RPS19	RPL9	RPS15A	RPS27A
4	RPL35A	RPS11	RPS6	RPS3	GNB2L1	RPS17	RPL39L	RPS8
5	RPS15	RPL19	BCAS1	RPS12	RPL8	RPL23A	NKX2–2	RPL7
6	RPL12	RPLP1	YBX1	ATCAY	RPS16	LRATD1	FAM177A1	ENSGALG00000037441
7	EEF1A1	TSPAN2	NPM1	ZNF488	ENSGALG00000035769	ITGB1BP3	ENSGALG00000047664	AFAP1L2
8	EEF1D	FYN	ANTXRL	EEF1B2	PLP1	GLRA4	NXPH1	EIF5A2
9	DLL1	OMG	SOX6	COLEC12	TCF7L2	LMO4	PTPRJ	PCDH15
10	MTSS1	ACAP3	MBP	DOCK10	C1orf198	TPT1	VCAN	CHD7
11	CTBP2	GAL3ST1	CYFIP2	B3GNT7	PDGFRA	ENSGALG00000043329	BMPER	DLK2
12	KHDRBS3	CNP	NAV3	ENSGALG0000007131	INKA2	FA2H	GSN	TTYH2
13	HMGB1	PTPN13	MAP7D3	KANK1	ITGA9	ENSGALG00000023546	H2AZ2	GAB1
14	LUZP2	MYT1	ENSGALG00000014897	PIK3R1	IFNAR2	ENSGALG0000006009	GLCCI1	COBL
15	ENSGALG00000053371	CLTA	SYNE2	HDGF	ENSGALG00000034050	MCM2	ENSGALG00000031604	NA
16	CCND1	GRIA4	SUSD5	REEP6	MAP3K1	ENSGALG00000034218	ENSGALG00000049579	SH3BP4
17	BAMBI	ZEB2	SASH1	USP53	DYL1	CCNY	ETS2	SLC44A5
18	PAPSS1	MYRF	MYCN	PSIP1	ENSGALG00000047717	AHR	MAPK10	BMP2
19	ASCL1	FAM129A	FRZB	ENSGALG00000020999	ENSGALG00000048883	PDLM5	TRIO	ANKRD11
20	FAM89A	GPR1	RGCC	HAVCR1	ITPR2	TPPP	GRIA3	ASB5
21	CACNG4	HMGN4	NUCKS1	PTCH1	IGFBP5	TENM1	LIMA1	ETS1
22	PCSK2	LBR	ELFN1	SCRG1	SMTN	SHROOM4	TUBB	PHACTR3
23	GADD45B	UHRF1	KIT	CDC14B	ENSGALG00000045350	STXBP6	FANCL	NOTCH1
24	EPN2	SGK1	ENSGALG00000050460	AKAP9	LMNA	EPS8	PDE5A	RPL22L1
25	ARHGEF3	TSPAN12	MARCHF3	NEGR1	TOX3	H2AFZ	NRCAM	ENSGALG00000039468
26	BRINP1	ENSGALG00000030179	ENSGALG00000016908	SOX5	PHLDA2	YBX3	PODXL	CRIP2
27	PRICKLE1	ADARB2	TMEM132B	ENSGALG0000007193	BRINP3	REPS2	GRIK3	MARCH8
28	FLRT3	ELMO1	TENM2	AOX2	BCL11B	MYCL	YPEL1	ENSGALG00000028749
29	CA8	NLGN4Y	KCND2	JAG2	FHL2	OPCML	TSKU	TUB
30	TPD52L1	AK2	TIMD4	FEN1	ADAM12	HMGA2	ENSGALG00000031427	RRM1
31	METTL24	ENSGALG00000047143	MDGA2	RBIS	SLC38A2	NPL	MYL6	CPNE4
32	CLDN20	NREP	LRP1B	STC2	NLGN1	ENSGALG00000015297	B3GAT1L	ROR2
33	NRIP1	GADD45A	SPRY4	SHTN1	LRRTM1	ENSGALG00000042797		

	Term	Ont	N	n	Adj. p-value
GO:0006412	translation	BP	87	16	5.872e-12
GO:0043043	peptide biosynthetic process	BP	88	16	7.057e-12
GO:0043604	amide biosynthetic process	BP	101	16	6.264e-11
GO:0006518	peptide metabolic process	BP	107	16	1.535e-10
GO:0043603	cellular amide metabolic process	BP	125	17	1.884e-10
GO:0010467	gene expression	BP	616	36	1.406e-09
GO:0034645	cellular macromolecule biosynthetic process	BP	554	33	4.585e-09
GO:0009059	macromolecule biosynthetic process	BP	556	33	5.013e-09
GO:0044271	cellular nitrogen compound biosynthetic process	BP	538	32	8.329e-09
GO:0034641	cellular nitrogen compound metabolic process	BP	732	37	3.938e-08

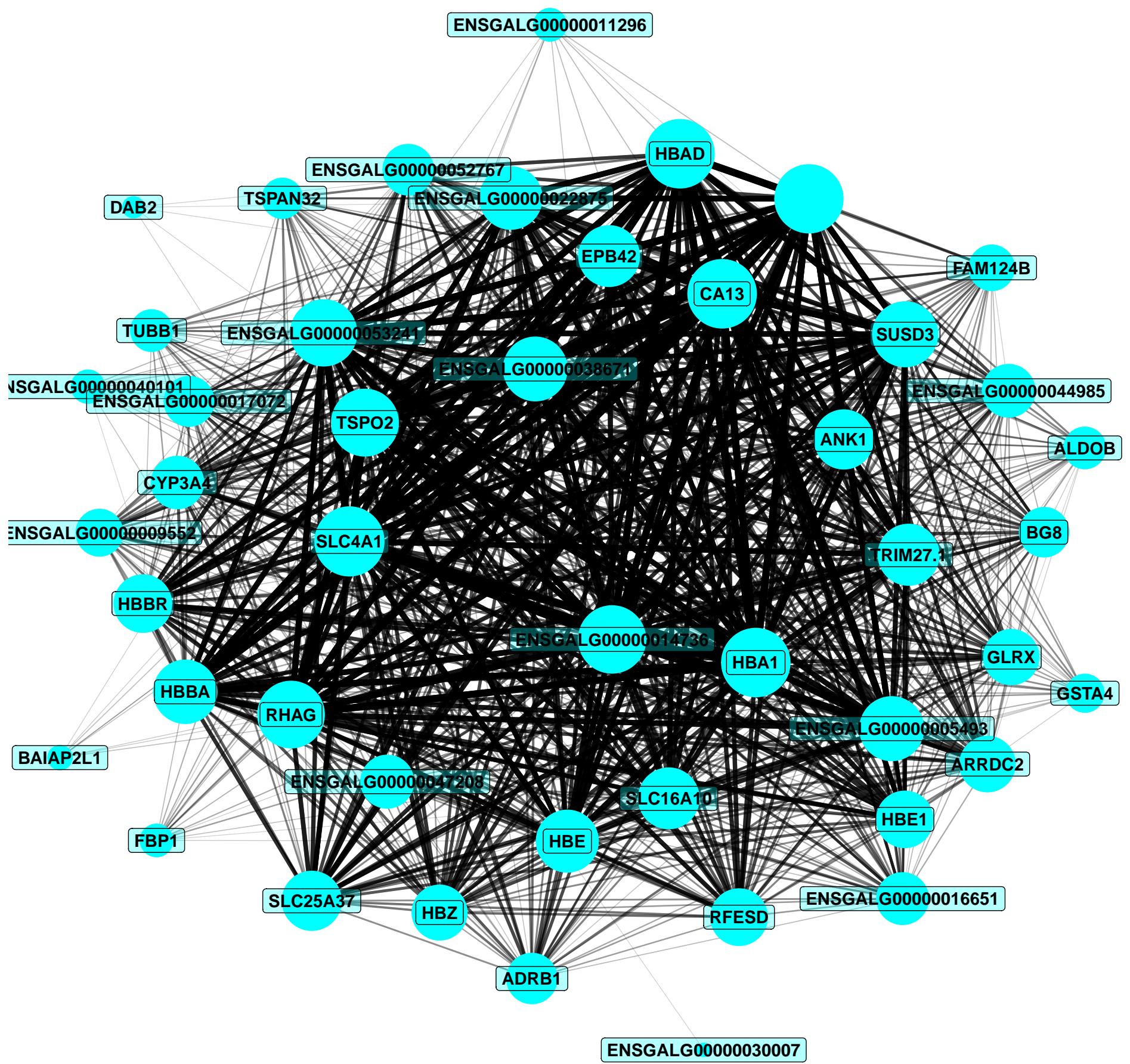
	Pathway	N	DE	P.DE
<i>path:gga03010</i>	Ribosome	116	38	2.959e-37
<i>path:gga04514</i>	Cell adhesion molecules	105	8	0.0008359
<i>path:gga04210</i>	Apoptosis	116	8	0.001595
<i>path:gga04310</i>	Wnt signaling pathway	137	8	0.00448
<i>path:gga04068</i>	FoxO signaling pathway	113	7	0.005592
<i>path:gga05132</i>	Salmonella infection	221	10	0.009365
<i>path:gga04218</i>	Cellular senescence	133	7	0.01315
<i>path:gga04530</i>	Tight junction	136	7	0.01471
<i>path:gga04330</i>	Notch signaling pathway	52	4	0.01657
<i>path:gga04520</i>	Adherens junction	69	4	0.04139



1	LAMB1	RGS5	ACE	DIO2	FN1	ANGPT4	GPC	HIC1
2	ITGA4	KCNJ8	IGFBP7	GGT5	ACTA2	ENSGALG00000012021	COL1A1	TBX2
3	MYL9	LAMA4	SPON2	RCSD1	CYP1B1	CALD1	ENSGALG00000007646	GJC2
4	FOXF2	ENSGALG00000012847	ARAP3	GPER1	FLT1	ABCC9	SLC40A1	ENSGALG00000045199
5	CA2	MXRA8	COLEC10	ENSGALG00000030902	IRAG1	ENSGALG0000000818	TMEM204	PCDH18
6	RBPMS2	DOCK5	C1QTNF5	FOXL3	NRK	CYGB	PEBP4	ANO1
7	CD200	DCN	ECRG4	INPP4B	RERGL	DLC1	ATP1B4	ENSGALG00000045584
8	ENSGALG00000023472	ARPC1B	ACVRL1	PTGES	FHL5	ITGA7	TBX3	SPERT
9	RGS4	TGFB1	ENSGALG00000028174	EDNRA	ADAMTS12	NA	UNC5B	RHOJ
10	ENSGALG00000005257	PPFIBP2	SCARA5	SLCO2B1	EGR2	ENSGALG00000003345	ENSGALG00000007710	ADORA2A
11	TWIST1	MGP	ADAMTS9	RAPGEF5	AQP1	ENSGALG00000026070	PRSS23	ENSGALG00000052087
12	KANK3	PLOD1	ENSGALG00000044632	LMO2	TRPC6	DES	TBXA2R	DRP2
13	ENSGALG00000034511	ENSGALG00000054937	GEM	ANKRD22	KCNE4	CG-1B	KRT23	CYTH3
14	CALHM2	C1QTNF6	EGFLAM	CTLA4	COL6A2	ENSGALG00000002326	TBX18	FRMD6
15	ENSGALG00000012055	MAOA	BTK	LRRC17	KERA	NA	PRRX2	EGFR
16	DSEL	ARHGAP25	ENSGALG00000048144	CTSK	GASK1B	CPED1	MMP10	PDGFRB
17	ENGASE	RASL12	LAMB4	ST8SIA4	SLC22A16	HOXD8	RUNX2	GJA4
18	SDC4	TCIM	S100A11	KCNMB1	C1QTNF7	TMLHE	PTPRE	ENSGALG00000046863
19	FMNL3	ENSGALG00000027778	RASSF3	SLC16A12	CCDC102B	TNNT3	COL6A1	COL3A1
20	ENSGALG00000005964	MTUS1	SYTL2	GUCY1A2	MMP2	CA9	DAAM2	LRRC15
21	ENSGALG00000003590	CYP4V2	LEF1	PRTG	GAS2	ENSGALG00000050332	OAF	F2RL2
22	EMP2	SEMA5A	CLEC3B	HLX	GRAPL	TWIST2	WFDC1	LYVE1
23	SMYD1	ATP2A3	ENSGALG00000053107	CNN2	UPB1	CPM	ENSGALG00000045684	SSPN
24	TGM2v1	ENSGALG00000011172	DACH2	ZIC2	MALRD1	ADSS1	ARID3A	CAPG
25	ENSGALG00000054678	CMKLR1	FHOD1	MXD4	CCDC122	SLC16A4	LAMB2	ENSGALG00000028016
26	LMO7	ANPEP	FHL3	CYSLTR1	TMTC1	ENSGALG00000046720	ITGA8	SLC15A1
27	STX19	WNT4	HOXD9	IFITM5	KITLG	ENSGALG00000048258	HCRT	MDFI
28	PIK3AP1	MYOM1	UPP1	SUSD6	DDR2	TCF15	ARHGAP45	PTPN7
29	ITM2C	RFLNB	GPRC5C	MEF2C	SELENOP1	ACTG2	EDNRB2	LRMP
30	PDK4	CSTA	CD40	ENSGALG00000045581	TNFRSF1A	COLEC11	B3GNT9	ENSGALG00000033522
31	ABCC8	ENSGALG00000015271	ENSGALG00000032803	ENSGALG00000026154	MGLL	ENSGALG00000016969	ANO6	PDZRN3
32	MATN1	TMEM140	ENSGALG00000042388	ENSGALG00000007698	FOXF1	THBS1	ADAMTS1	MGAT4C
33	ENSGALG00000046657	TNFAIP2	CAV1	ADAM19	ENSGALG00000020895	GPR143		

	Term	Ont	N	n	Adj. p-value
GO:0022610	biological adhesion	BP	149	14	7.151e-07
GO:0007155	cell adhesion	BP	149	14	7.151e-07
GO:0032502	developmental process	BP	671	31	2.643e-06
GO:0048856	anatomical structure development	BP	639	30	2.815e-06
GO:0048608	reproductive structure development	BP	29	5	0.0001759
GO:0061458	reproductive system development	BP	29	5	0.0001759
GO:0007548	sex differentiation	BP	29	5	0.0001759
GO:0007275	multicellular organism development	BP	591	24	0.0002769
GO:0033002	muscle cell proliferation	BP	18	4	0.0002907
GO:0061061	muscle structure development	BP	70	7	0.0003122

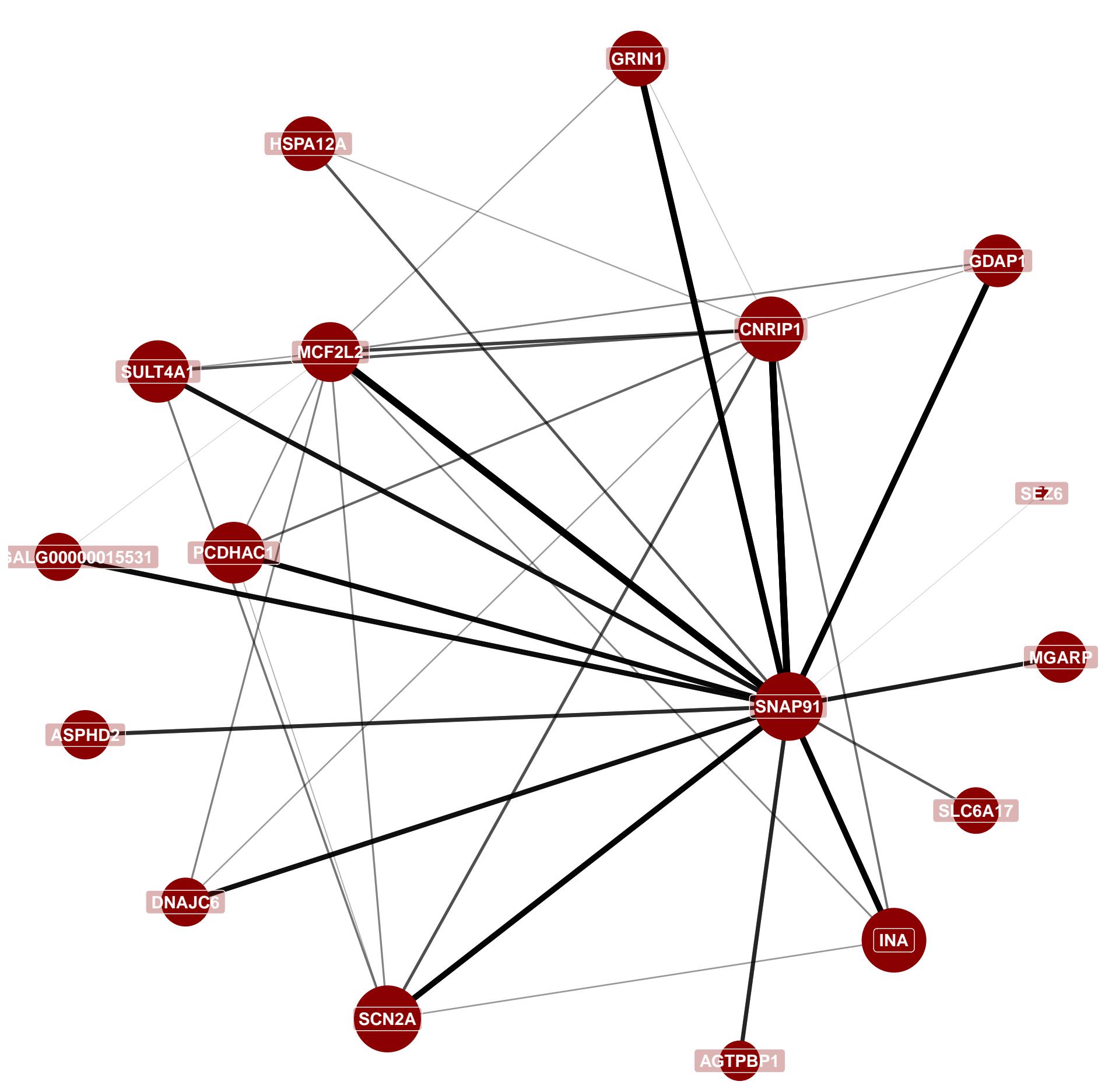
	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	70	13	4.301e–10
<i>path:gga04510</i>	Focal adhesion	176	19	6.822e–10
<i>path:gga04270</i>	Vascular smooth muscle contraction	111	9	0.0002232
<i>path:gga04010</i>	MAPK signaling pathway	241	12	0.001864
<i>path:gga04020</i>	Calcium signaling pathway	204	10	0.00488
<i>path:gga04520</i>	Adherens junction	69	5	0.009128
<i>path:gga04672</i>	Intestinal immune network for IgA production	24	3	0.009632
<i>path:gga04514</i>	Cell adhesion molecules	105	6	0.01357
<i>path:gga00360</i>	Phenylalanine metabolism	12	2	0.0201
<i>path:gga04810</i>	Regulation of actin cytoskeleton	189	8	0.02508



1	SLC4A1	NA	HBAD	HBA1	CA13	HBE	RHAG	ENSGALG00000053241
2	TSPO2	ENSGALG00000014736	ENSGALG00000022875	SUSD3	ENSGALG0000005493	HBE1	HBBA	HBBR
3	TRIM27.1	EPB42	HBZ	RFESD	ENSGALG00000038671	ANK1	ENSGALG00000047208	CYP3A4
4	ARRDC2	SLC25A37	SLC16A10	GLRX	ALDOB	ENSGALG00000016651	ENSGALG00000044985	GSTA4
5	BG8	ADRB1	ENSGALG00000017072	TUBB1	ENSGALG0000009552	ENSGALG00000052767	TSPAN32	FAM124B
6	FBP1	ENSGALG00000011296	ENSGALG00000040101	DAB2	BAIAP2L1	ENSGALG00000030007		

	Term	Ont	N	n	Adj. p-value
GO:0042744	hydrogen peroxide catabolic process	BP	7	6	4.578e-15
GO:0042743	hydrogen peroxide metabolic process	BP	7	6	4.578e-15
GO:0015671	oxygen transport	BP	7	6	4.578e-15
GO:0015669	gas transport	BP	8	6	1.827e-14
GO:0098869	cellular oxidant detoxification	BP	14	6	1.932e-12
GO:1990748	cellular detoxification	BP	16	6	5.129e-12
GO:0097237	cellular response to toxic substance	BP	16	6	5.129e-12
GO:0098754	detoxification	BP	17	6	7.909e-12
GO:0072593	reactive oxygen species metabolic process	BP	20	6	2.46e-11
GO:0009636	response to toxic substance	BP	20	6	2.46e-11

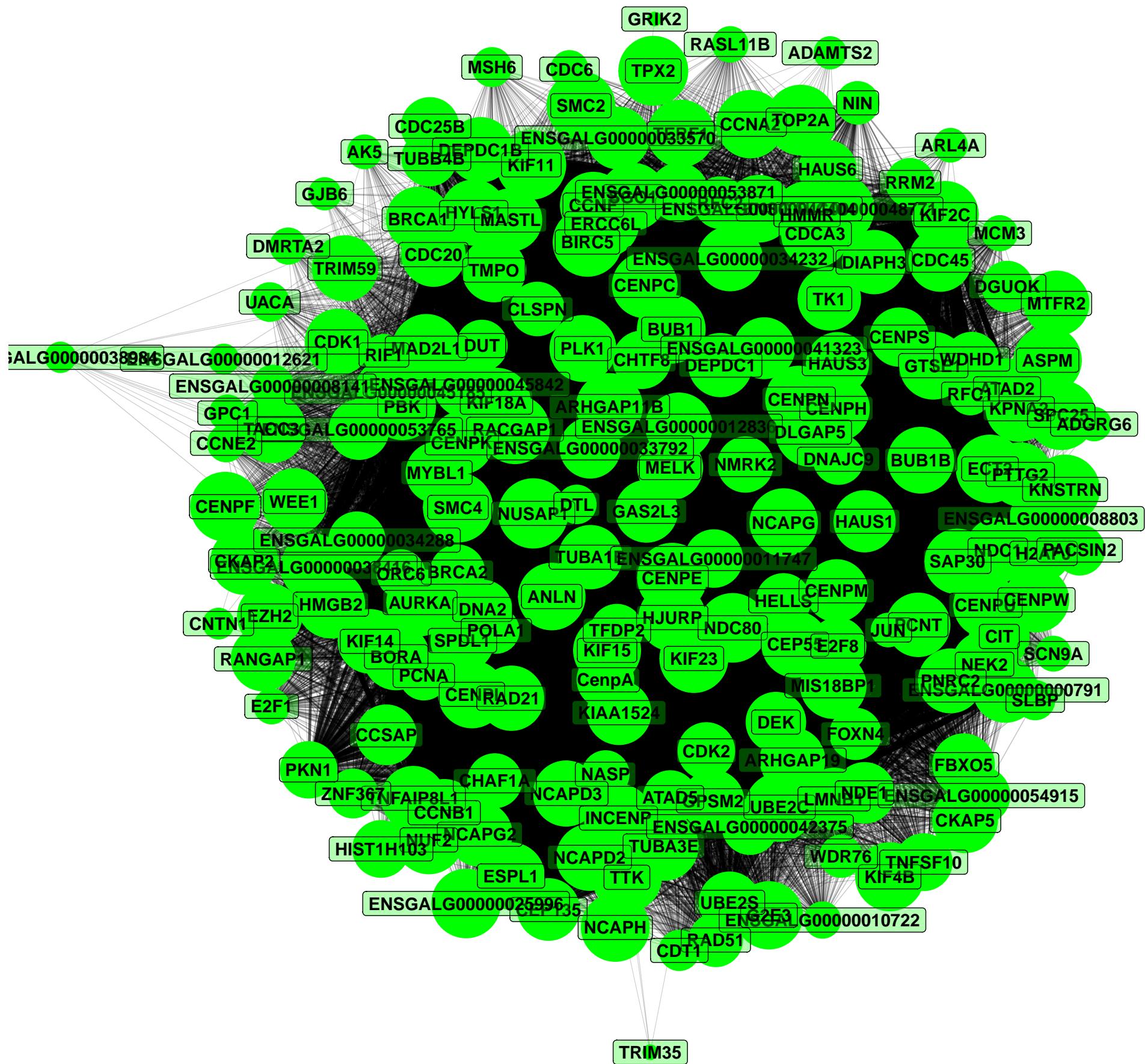
	Pathway	N	DE	P.DE
<i>path:gga00030</i>	Pentose phosphate pathway	25	2	0.002752
<i>path:gga00051</i>	Fructose and mannose metabolism	34	2	0.005055
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	48	2	0.009886
<i>path:gga04540</i>	Gap junction	79	2	0.0254
<i>path:gga01200</i>	Carbon metabolism	95	2	0.03568
<i>path:gga00910</i>	Nitrogen metabolism	14	1	0.04304
<i>path:gga00591</i>	Linoleic acid metabolism	21	1	0.06388
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	1	0.08715
<i>path:gga00140</i>	Steroid hormone biosynthesis	29	1	0.08715
<i>path:gga00260</i>	Glycine, serine and threonine metabolism	31	1	0.09288



1	SNAP91	GRIN1	SCN2A	PCDHAC1	CNRIP1	MCF2L2	INA	MGARP
2	SULT4A1	ENSGALG00000015531	HSPA12A	SLC6A17	GDAP1	DNAJC6	SEZ6	ASPHD2
3	AGTPBP1							

	Term	Ont	N	n	Adj. p-value
GO:0035609	C-terminal protein deglutamylation	BP	1	1	0.001419
GO:0035608	protein deglutamylation	BP	1	1	0.001419
GO:0035610	protein side chain deglutamylation	BP	1	1	0.001419
GO:0021702	cerebellar Purkinje cell differentiation	BP	2	1	0.002836
GO:0021680	cerebellar Purkinje cell layer development	BP	2	1	0.002836
GO:0021694	cerebellar Purkinje cell layer formation	BP	2	1	0.002836
GO:0021692	cerebellar Purkinje cell layer morphogenesis	BP	2	1	0.002836
GO:0050905	neuromuscular process	BP	2	1	0.002836
GO:0021772	olfactory bulb development	BP	2	1	0.002836
GO:0021988	olfactory lobe development	BP	2	1	0.002836

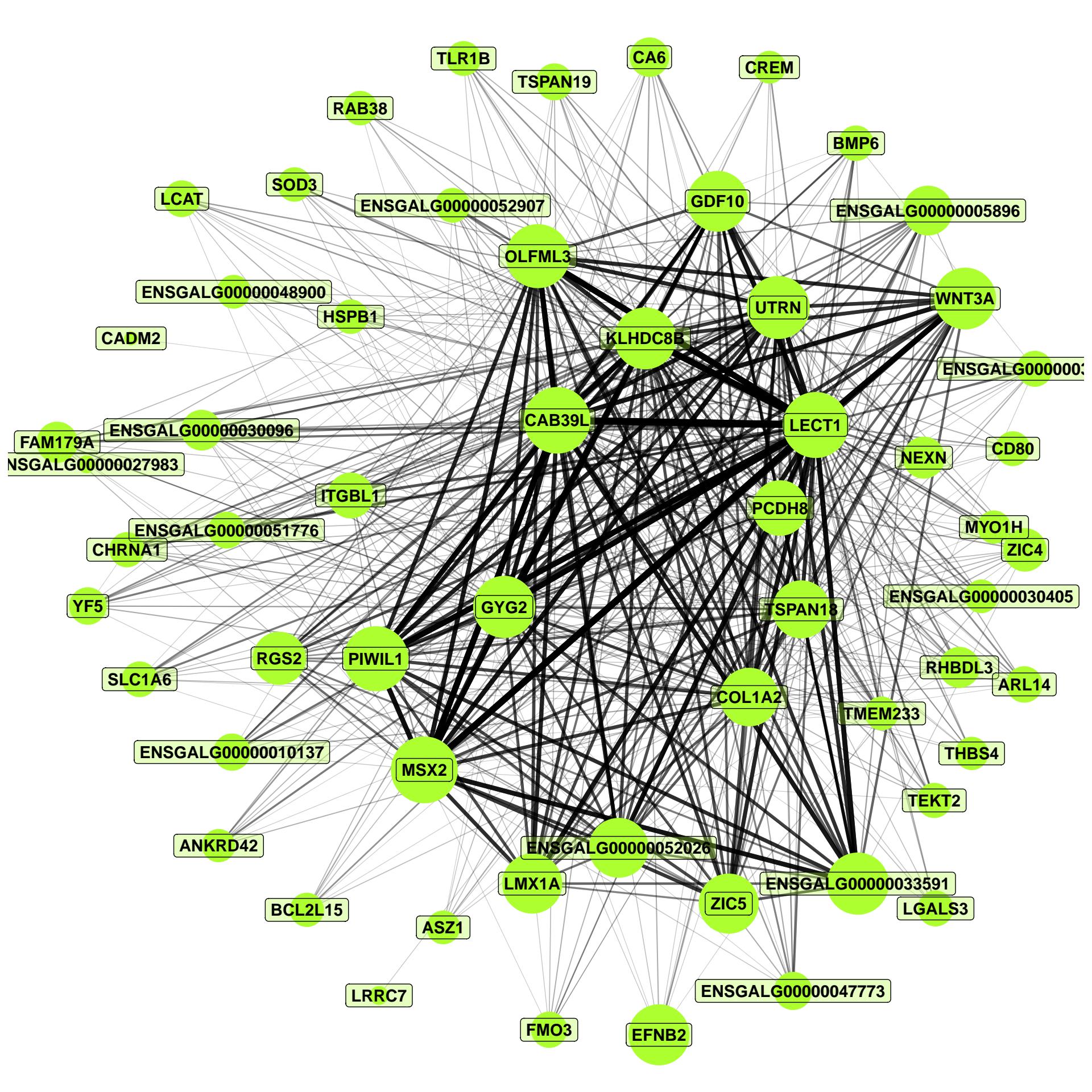
	Pathway	N	DE	P.DE
<i>path:gga03015</i>	mRNA surveillance pathway	73	1	0.0987
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	125	1	0.1633
<i>path:gga04530</i>	Tight junction	136	1	0.1764
<i>path:gga04020</i>	Calcium signaling pathway	204	1	0.2531
<i>path:gga04144</i>	Endocytosis	222	1	0.2723
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	305	1	0.3547
<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:gga03267</i>	Virion – Adenovirus	3	0	1



1	NUSAP1	CENPE	TOP2A	ENSGALG00000025996	TPX2	KIF11	CENPF	SMC2
2	UBE2C	SMC4	KIF4B	KNSTRN	NDC80	SPC25	BIRC5	INCENP
3	TTK	ASPM	RACGAP1	ENSGALG00000048771	KPNA2	DLGAP5	KIF23	TACC3
4	KIF15	NUF2	TUBA3E	BUB1	KIF18A	GTSE1	HMGB2	ANLN
5	AURKA	CDCA3	ECT2	ENSGALG00000012836	PLK1	KIF2C	CKAP2	NCAPG
6	CCNB1	NCAPH	BUB1B	CENPI	SGO1	CDK1	PBK	MAD2L1
7	CCNA2	HMMR	TK1	ENSGALG00000044404	CEP55	ENSGALG00000038416	G2E3	TERF1
8	CENPW	ENSGALG00000045185	BRCA1	HJURP	ESPL1	CENPH	CDC20	ARHGAP11B
9	PTTG2	ENSGALG00000045842	BORA	NCAPD2	ERCC6L	CCNF	CENPN	MIS18BP1
10	MELK	NEK2	WEE1	NCAPD3	CENPC	DEPDC1B	NCAPG2	DIAPH3
11	KIAA1524	TRIM59	ARHGAP19	CENPK	HYLS1	ENSGALG00000000791	DEPDC1	ENSGALG00000011747
12	CENPU	CDC45	KIF14	MTFR2	ENSGALG00000034232	NDC1	TUBA1B	HAUS1
13	TNFAIP8L1	HAUS3	CENPM	TMPO	GAS2L3	MASTL	HIST1H103	DNA2
14	CEP135	RANGAP1	SAP30	NDE1	RAD21	ENSGALG00000033792	MYBL1	EZH2
15	GPSM2	CHTF8	CKAP5	ENSGALG00000041323	ATAD2	PCNT	FBXO5	CDK2
16	ENSGALG0000008803	ENSGALG00000053871	PNRC2	SPDL1	CENPS	DEK	LMNB1	ENSGALG00000033570
17	DGUOK	RRM2	NMRK2	HELLS	UBE2S	E2F8	ENSGALG00000054915	BRCA2
18	ENSGALG00000034288	ENSGALG00000053765	HAUS6	CenpA	WDHD1	H2AFJ	CCSAP	ATAD5
19	CHAF1A	CDC25B	RAD51	CLSPN	CIT	RFC2	PCNA	DUT
20	ENSGALG00000042375	TNFSF10	TUBB4B	PKN1	TFDP2	DNAJC9	NASP	ZNF367
21	ORC6	FOXN4	POLA1	PAC SIN2	WDR76	CDT1	RIF1	SLBP
22	NIN	DTL	RFC1	ENSGALG00000010722	ENSGALG00000008141	MSH6	CDC6	DMRTA2
23	E2F1	MCM3	CCNE2	GPC1	SCN9A	UACA	JUN	RASL11B
24	AK5	ARL4A	ADAMTS2	CNTN1	ENSGALG00000012621	ADGRG6	GJB6	ENSGALG00000038984
25	TRIM35	GRIK2						

	Term	Ont	N	n	Adj. p-value
GO:0007049	cell cycle	BP	205	29	3.967e–21
GO:0000278	mitotic cell cycle	BP	100	22	1.422e–20
GO:1903047	mitotic cell cycle process	BP	78	19	8.182e–19
GO:0051276	chromosome organization	BP	178	24	3.937e–17
GO:0022402	cell cycle process	BP	128	21	6.715e–17
GO:0051383	kinetochore organization	BP	10	8	5.71e–14
GO:0006996	organelle organization	BP	438	30	4.858e–13
GO:0065004	protein–DNA complex assembly	BP	36	11	1.377e–12
GO:0071824	protein–DNA complex subunit organization	BP	39	11	3.704e–12
GO:0007059	chromosome segregation	BP	43	11	1.211e–11

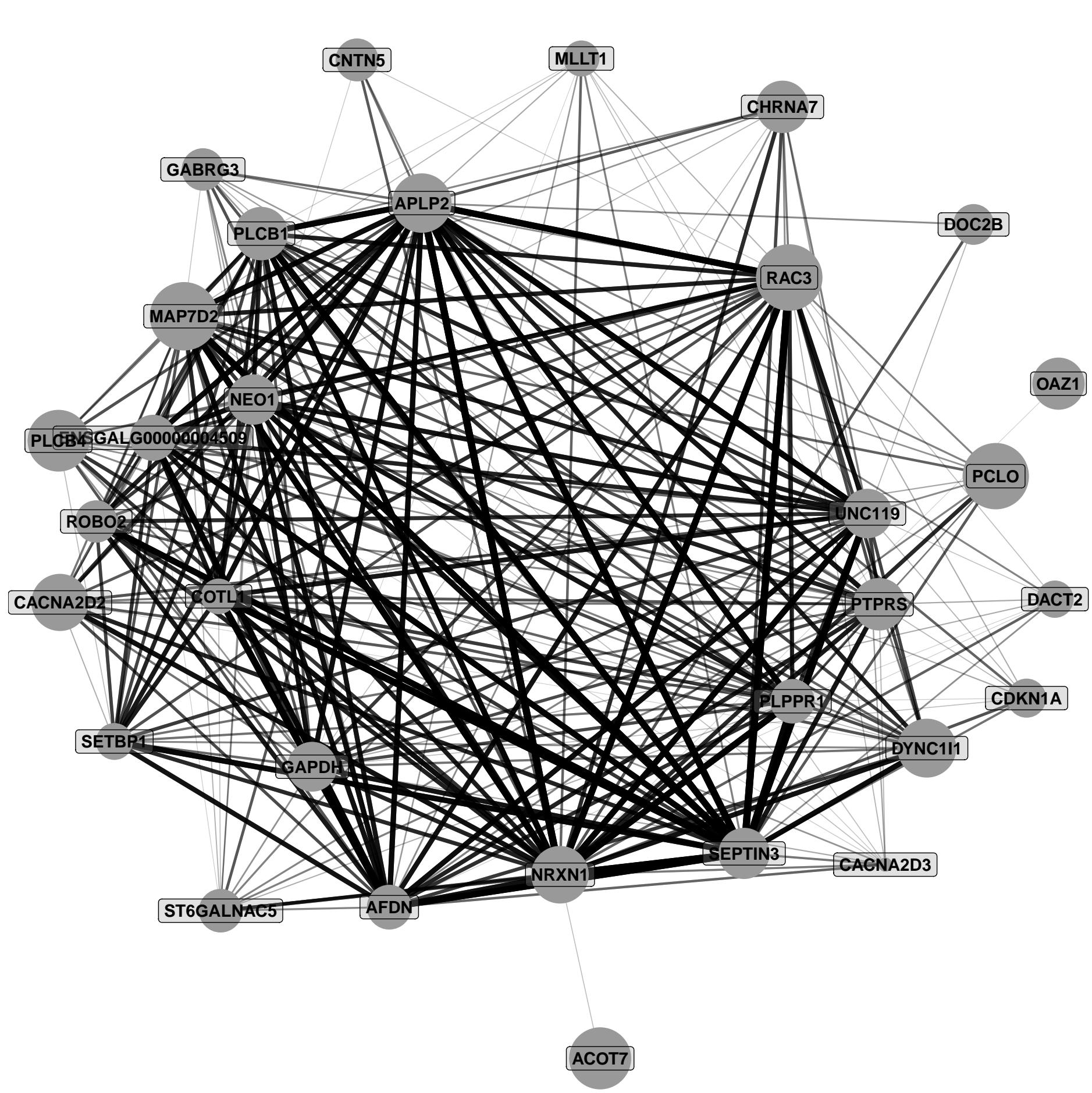
	Pathway	N	DE	P.DE
<i>path:gga04110</i>	Cell cycle	114	23	1.506e–20
<i>path:gga04114</i>	Oocyte meiosis	96	13	7.919e–10
<i>path:gga04914</i>	Progesterone–mediated oocyte maturation	78	9	1.385e–06
<i>path:gga03030</i>	DNA replication	29	6	2.566e–06
<i>path:gga03430</i>	Mismatch repair	19	4	0.0001236
<i>path:gga04115</i>	p53 signaling pathway	63	6	0.0002471
<i>path:gga03460</i>	Fanconi anemia pathway	48	4	0.004521
<i>path:gga01232</i>	Nucleotide metabolism	78	5	0.004771
<i>path:gga04210</i>	Apoptosis	116	6	0.005861
<i>path:gga00240</i>	Pyrimidine metabolism	55	4	0.007346



1	MSX2	LECT1	ENSGALG00000033591	CAB39L	PIWIL1	LMX1A	KLHDC8B	GDF10
2	ZIC5	GYG2	UTRN	OLFML3	WNT3A	EFNB2	COL1A2	TSPAN18
3	PCDH8	ENSGALG00000052026	ENSGALG0000005896	RGS2	ZIC4	NEXN	RHBDL3	ITGBL1
4	ENSGALG00000010137	ENSGALG00000047773	HSPB1	ENSGALG00000051776	ENSGALG00000052907	BMP6	TEKT2	YF5
5	ENSGALG00000030096	ARL14	CHRNA1	SOD3	ENSGALG00000031546	FMO3	ASZ1	CA6
6	LCAT	SLC1A6	TMEM233	CREM	FAM179A	TLR1B	THBS4	ENSGALG00000030405
7	TSPAN19	BCL2L15	ANKRD42	ENSGALG00000048900	MYO1H	CD80	LGALS3	RAB38
8	LRRC7	ENSGALG00000027983	CADM2					

	Term	Ont	N	n	Adj. p-value
GO:1902176	negative regulation of oxidative stress–induced intrinsic apoptotic signaling pathway	BP	1	1	0.004032
GO:0010529	negative regulation of transposition	BP	1	1	0.004032
GO:1902175	regulation of oxidative stress–induced intrinsic apoptotic signaling pathway	BP	1	1	0.004032
GO:0010528	regulation of transposition	BP	1	1	0.004032
GO:0035092	sperm chromatin condensation	BP	1	1	0.004032
GO:0035093	spermatogenesis, exchange of chromosomal proteins	BP	1	1	0.004032
GO:0032196	transposition	BP	1	1	0.004032
GO:0034587	piRNA metabolic process	BP	2	1	0.008049
GO:0007289	spermatid nucleus differentiation	BP	2	1	0.008049
GO:0034435	cholesterol esterification	BP	3	1	0.01205

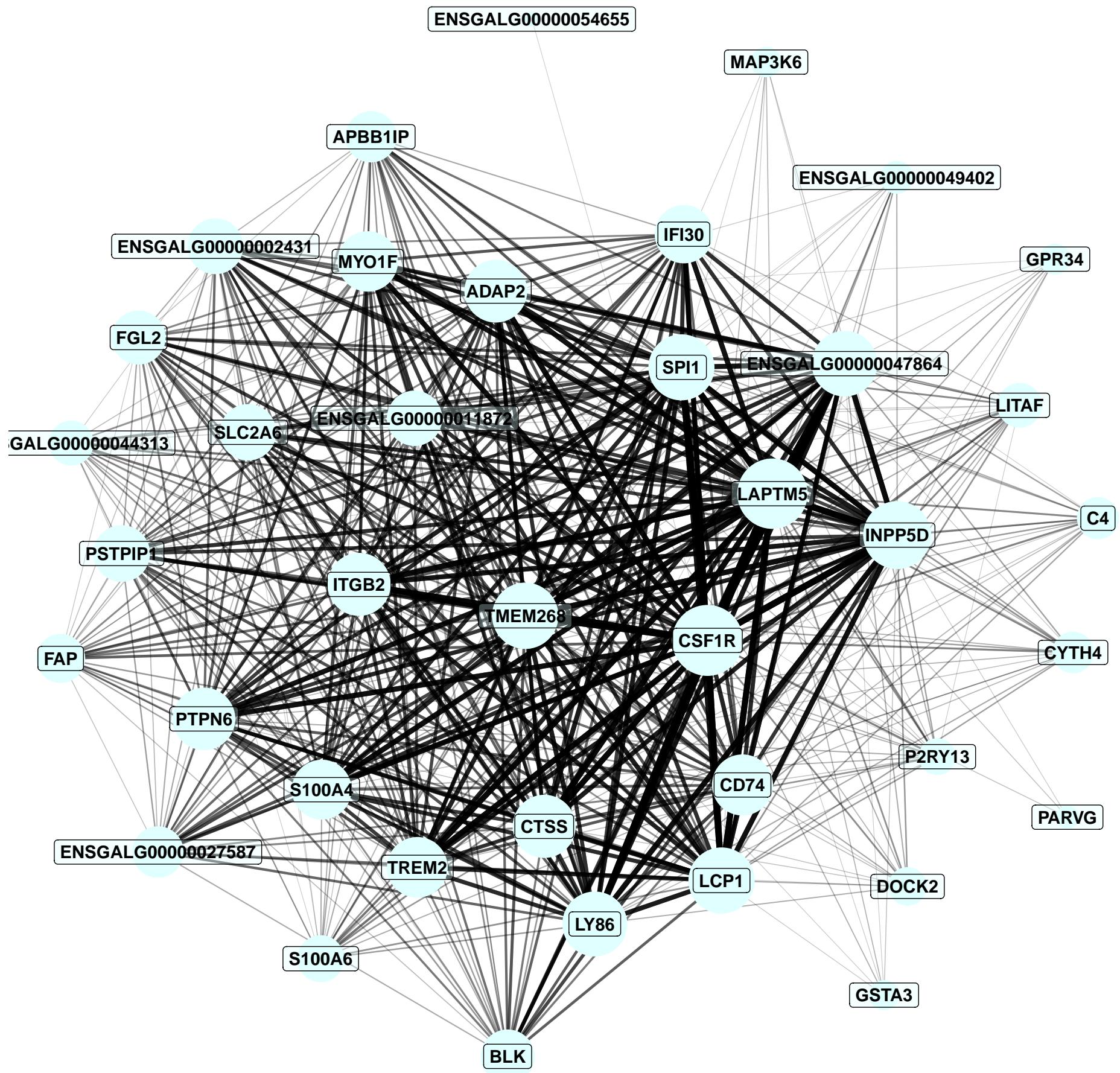
	Pathway	N	DE	P.DE
<i>path:gga00910</i>	Nitrogen metabolism	14	2	0.001408
<i>path:gga03267</i>	Virion – Adenovirus	3	1	0.01205
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.01603
<i>path:gga04512</i>	ECM–receptor interaction	70	2	0.03236
<i>path:gga04620</i>	Toll-like receptor signaling pathway	72	2	0.03408
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	1	0.04735
<i>path:gga04514</i>	Cell adhesion molecules	105	2	0.06697
<i>path:gga04145</i>	Phagosome	125	2	0.0904
<i>path:gga04672</i>	Intestinal immune network for IgA production	24	1	0.09249
<i>path:gga00500</i>	Starch and sucrose metabolism	27	1	0.1034



1	MAP7D2	PCLO	DYNC1I1	RAC3	NRXN1	APLP2	PLCB4	SEPTIN3
2	CACNA2D2	ACOT7	PLCB1	PLPPR1	NEO1	AFDN	GAPDH	UNC119
3	PTPRS	ENSGALG00000004509	GABRG3	COTL1	SETBP1	ROBO2	CHRNA7	ST6GALNAC5
4	DOC2B	CNTN5	OAZ1	MLLT1	CDKN1A	DACT2	CACNA2D3	

	Term	Ont	N	n	Adj. p-value
GO:0022610	biological adhesion	BP	149	4	0.000322
GO:0007155	cell adhesion	BP	149	4	0.000322
GO:0034331	cell junction maintenance	BP	1	1	0.00224
GO:0051873	killing by host of symbiont cells	BP	1	1	0.00224
GO:0051883	killing of cells in other organism involved in symbiotic interaction	BP	1	1	0.00224
GO:0048790	maintenance of presynaptic active zone structure	BP	1	1	0.00224
GO:0099558	maintenance of synapse structure	BP	1	1	0.00224
GO:0061000	negative regulation of dendritic spine development	BP	1	1	0.00224
GO:1902268	negative regulation of polyamine transmembrane transport	BP	1	1	0.00224
GO:0000740	nuclear membrane fusion	BP	1	1	0.00224

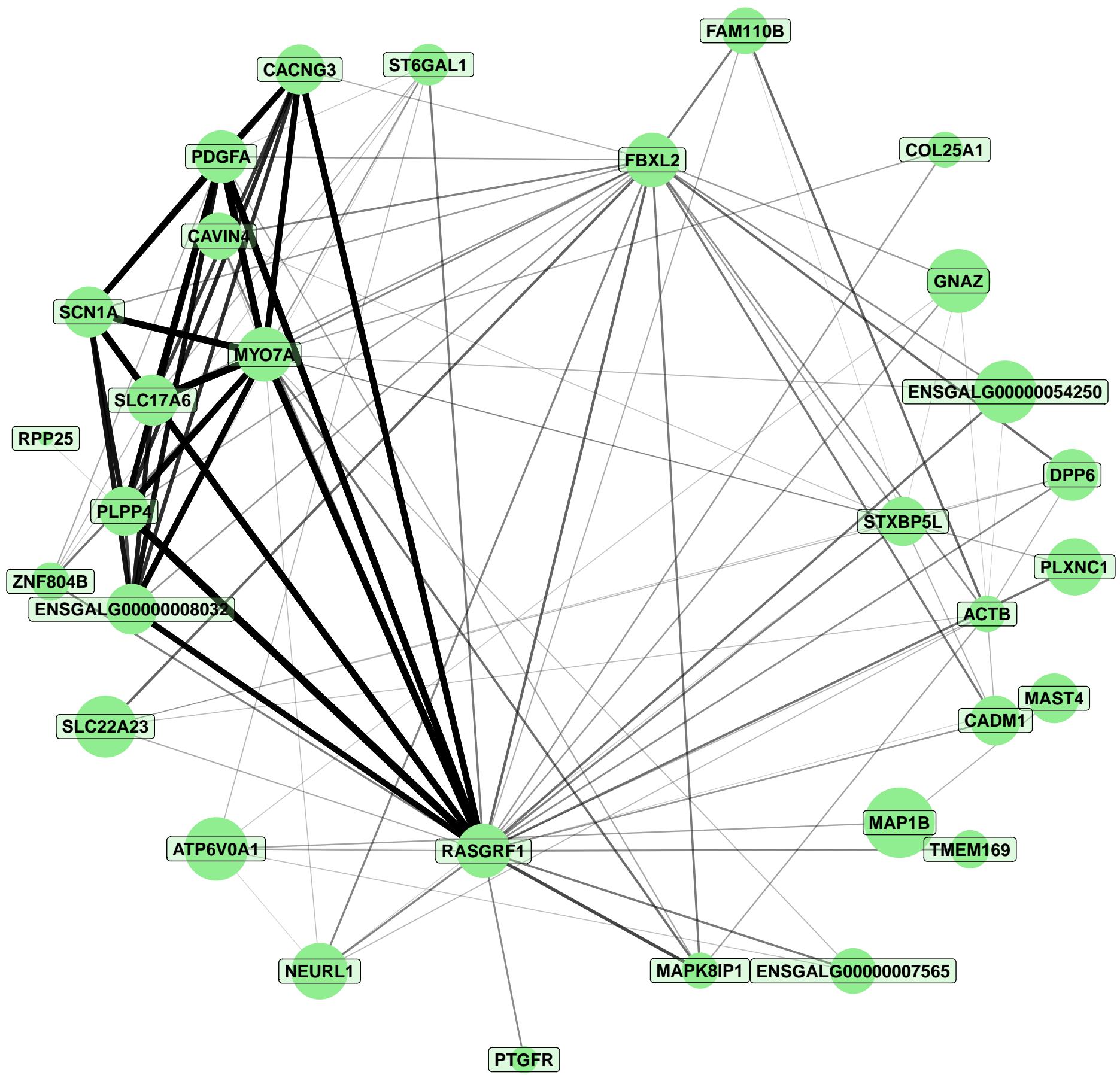
	Pathway	N	DE	P.DE
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	125	4	0.0001643
<i>path:gga04514</i>	Cell adhesion molecules	105	3	0.00163
<i>path:gga04310</i>	Wnt signaling pathway	137	3	0.003474
<i>path:gga04260</i>	Cardiac muscle contraction	61	2	0.008179
<i>path:gga00562</i>	Inositol phosphate metabolism	68	2	0.01008
<i>path:gga04520</i>	Adherens junction	69	2	0.01037
<i>path:gga04020</i>	Calcium signaling pathway	204	3	0.01045
<i>path:gga04912</i>	GnRH signaling pathway	77	2	0.01279
<i>path:gga04540</i>	Gap junction	79	2	0.01343
<i>path:gga04916</i>	Melanogenesis	87	2	0.01613



1	LAPTM5	CTSS	SPI1	S100A4	CSF1R	P2RY13	TREM2	ENSGALG00000047864
2	INPP5D	IFI30	LCP1	ITGB2	TMEM268	LY86	MYO1F	LITAF
3	GSTA3	PTPN6	S100A6	BLK	ENSGALG00000011872	FGL2	C4	PSTPIP1
4	ADAP2	SLC2A6	PARVG	ENSGALG0000002431	CYTH4	ENSGALG00000049402	ENSGALG00000027587	APBB1IP
5	GPR34	CD74	FAP	DOCK2	ENSGALG00000044313	MAP3K6	ENSGALG00000054655	

	Term	Ont	N	n	Adj. p-value
GO:0006749	glutathione metabolic process	BP	8	1	0.02131
GO:0006805	xenobiotic metabolic process	BP	8	1	0.02131
GO:0071466	cellular response to xenobiotic stimulus	BP	9	1	0.02394
GO:0009410	response to xenobiotic stimulus	BP	9	1	0.02394
GO:0051781	positive regulation of cell division	BP	14	1	0.037
GO:0051302	regulation of cell division	BP	21	1	0.055
GO:0006575	cellular modified amino acid metabolic process	BP	25	1	0.06514
GO:0006790	sulfur compound metabolic process	BP	26	1	0.06765
GO:0045087	innate immune response	BP	43	1	0.1095
GO:0001816	cytokine production	BP	50	1	0.1261

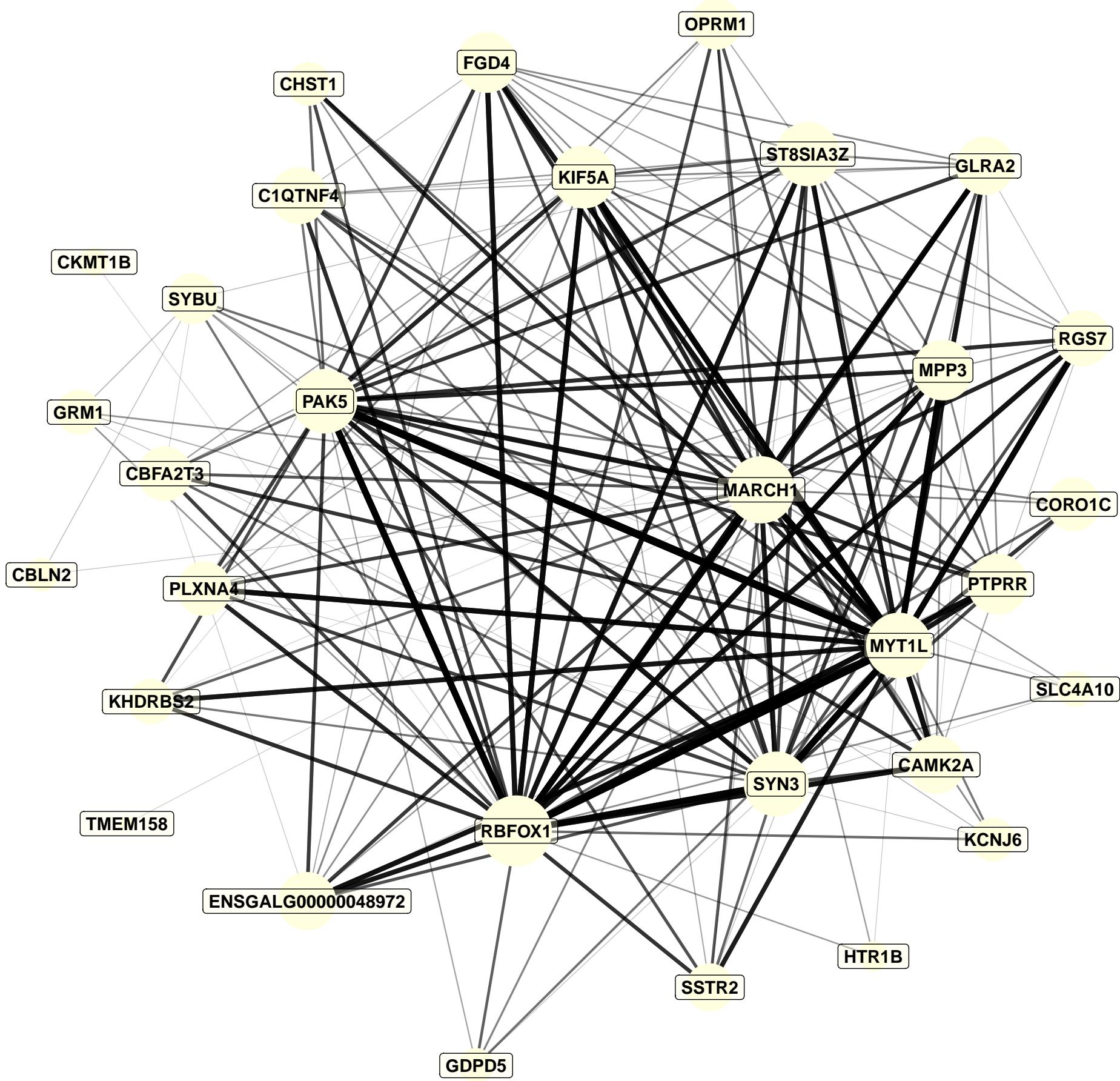
	Pathway	N	DE	P.DE
<i>path:gga04142</i>	Lysosome	116	3	0.003672
<i>path:gga04145</i>	Phagosome	125	2	0.0443
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	1	0.07517
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	31	1	0.08015
<i>path:gga00480</i>	Glutathione metabolism	47	1	0.119
<i>path:gga04010</i>	MAPK signaling pathway	241	2	0.1366
<i>path:gga00983</i>	Drug metabolism – other enzymes	56	1	0.1402
<i>path:gga00562</i>	Inositol phosphate metabolism	68	1	0.1676
<i>path:gga04520</i>	Adherens junction	69	1	0.1699
<i>path:gga04070</i>	Phosphatidylinositol signaling system	87	1	0.2094



1	MAP1B	CAVIN4	GNAZ	ENSGALG00000054250	ATP6V0A1	SLC22A23	MAST4	DPP6
2	PLXNC1	NEURL1	MYO7A	ENSGALG0000007565	SCN1A	FBXL2	RASGRF1	SLC17A6
3	CACNG3	FAM110B	STXBP5L	ENSGALG0000008032	PDGFA	ACTB	PLPP4	MAPK8IP1
4	ST6GAL1	CADM1	TMEM169	ZNF804B	PTGFR	COL25A1	RPP25	

	Term	Ont	N	n	Adj. p-value
GO:0006054	N-acetylneuraminate metabolic process	BP	3	1	0.006483
GO:0018196	peptidyl-asparagine modification	BP	3	1	0.006483
GO:0098974	postsynaptic actin cytoskeleton organization	BP	3	1	0.006483
GO:0099188	postsynaptic cytoskeleton organization	BP	3	1	0.006483
GO:0018279	protein N-linked glycosylation via asparagine	BP	3	1	0.006483
GO:0007035	vacuolar acidification	BP	3	1	0.006483
GO:0006040	amino sugar metabolic process	BP	4	1	0.008635
GO:0140238	presynaptic endocytosis	BP	4	1	0.008635
GO:0048488	synaptic vesicle endocytosis	BP	4	1	0.008635
GO:0036465	synaptic vesicle recycling	BP	4	1	0.008635

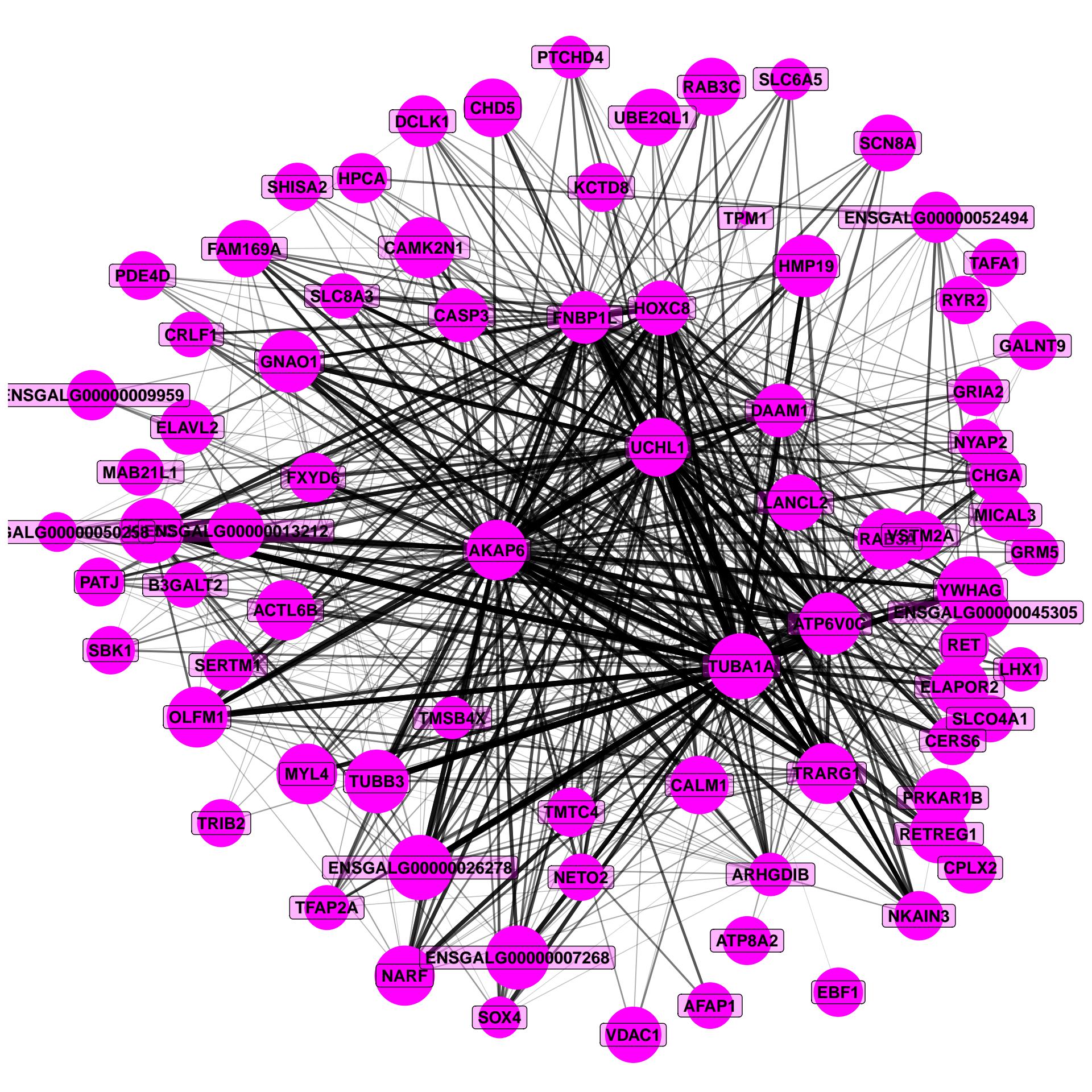
	Pathway	N	DE	P.DE
<i>path:gga04010</i>	MAPK signaling pathway	241	4	0.001706
<i>path:gga04510</i>	Focal adhesion	176	3	0.006343
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	125	2	0.02977
<i>path:gga04145</i>	Phagosome	125	2	0.02977
<i>path:gga04530</i>	Tight junction	136	2	0.03476
<i>path:gga04810</i>	Regulation of actin cytoskeleton	189	2	0.06272
<i>path:gga04020</i>	Calcium signaling pathway	204	2	0.07168
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	1	0.08517
<i>path:gga00510</i>	N-Glycan biosynthesis	45	1	0.09309
<i>path:gga03250</i>	Viral life cycle – HIV-1	49	1	0.1009



1	RBFOX1	MYT1L	C1QTNF4	GLRA2	PAK5	MARCH1	ST8SIA3Z	PLXNA4
2	PTPRR	SYN3	RGS7	CBFA2T3	SYBU	CAMK2A	KIF5A	OPRM1
3	MPP3	SSTR2	FGD4	ENSGALG00000048972	CBLN2	HTR1B	CORO1C	KHDRBS2
4	CHST1	GRM1	CKMT1B	KCNJ6	SLC4A10	GDPD5	TMEM158	

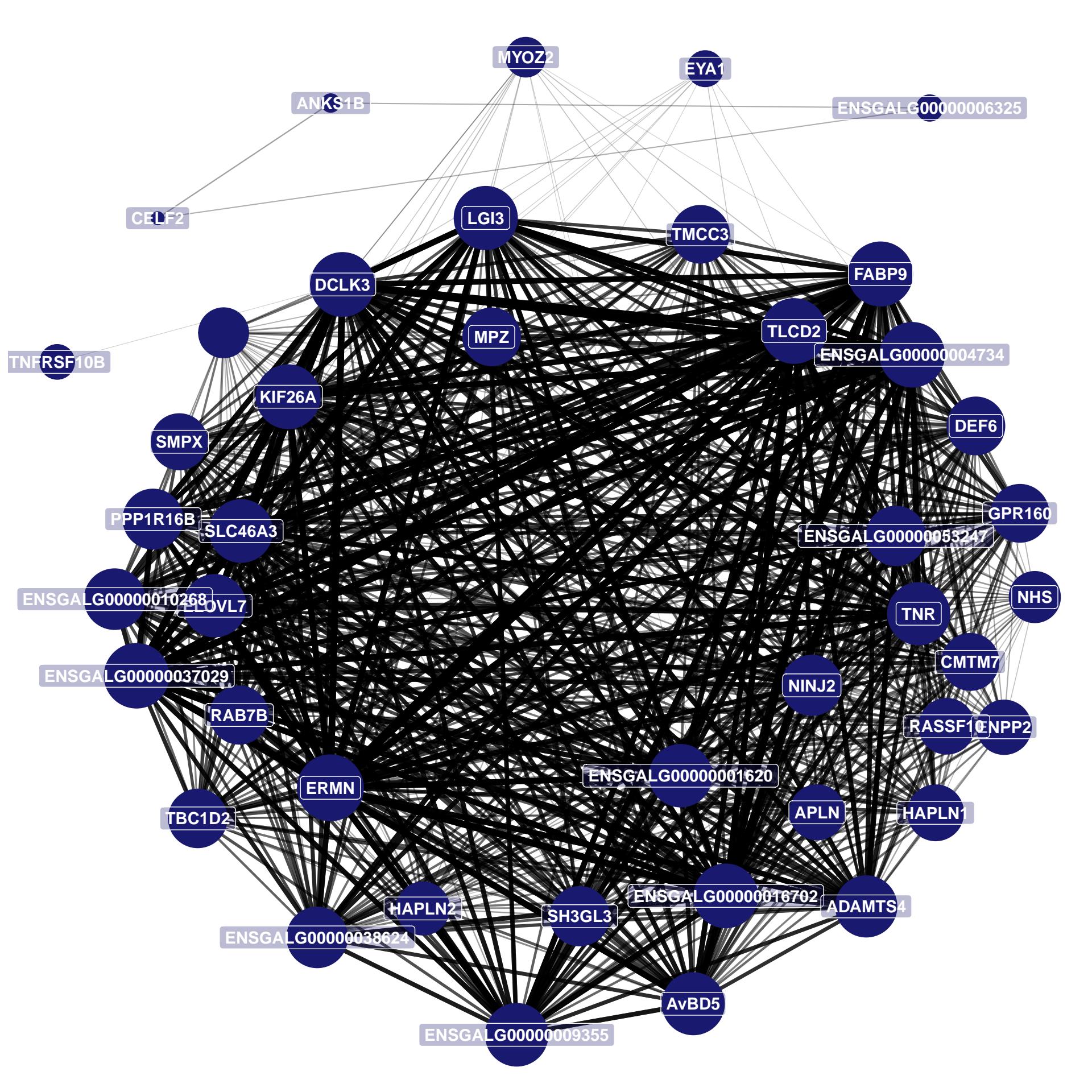
	Term	Ont	N	n	Adj. p-value
GO:0042396	phosphagen biosynthetic process	BP	3	1	0.006483
GO:0006599	phosphagen metabolic process	BP	3	1	0.006483
GO:0046314	phosphocreatine biosynthetic process	BP	3	1	0.006483
GO:0006603	phosphocreatine metabolic process	BP	3	1	0.006483
GO:0045666	positive regulation of neuron differentiation	BP	8	1	0.0172
GO:0042398	cellular modified amino acid biosynthetic process	BP	9	1	0.01933
GO:0006575	cellular modified amino acid metabolic process	BP	25	1	0.0528
GO:0045664	regulation of neuron differentiation	BP	25	1	0.0528
GO:0090407	organophosphate biosynthetic process	BP	55	1	0.1126
GO:0045597	positive regulation of cell differentiation	BP	89	1	0.176

	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	305	5	0.0004493
<i>path:gga04012</i>	ErbB signaling pathway	76	2	0.01169
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.02991
<i>path:gga04020</i>	Calcium signaling pathway	204	2	0.07168
<i>path:gga00330</i>	Arginine and proline metabolism	40	1	0.08318
<i>path:gga04912</i>	GnRH signaling pathway	77	1	0.1541
<i>path:gga04540</i>	Gap junction	79	1	0.1578
<i>path:gga04916</i>	Melanogenesis	87	1	0.1724
<i>path:gga04114</i>	Oocyte meiosis	96	1	0.1885
<i>path:gga04217</i>	Necroptosis	110	1	0.2129



Term	Ont	N	n
atrioventricular valve formation	BP	1	1
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
lateral motor column neuron migration	BP	1	1
motor neuron migration	BP	1	1
neuronal signal transduction	BP	1	1
peptidyl–arginine phosphorylation	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

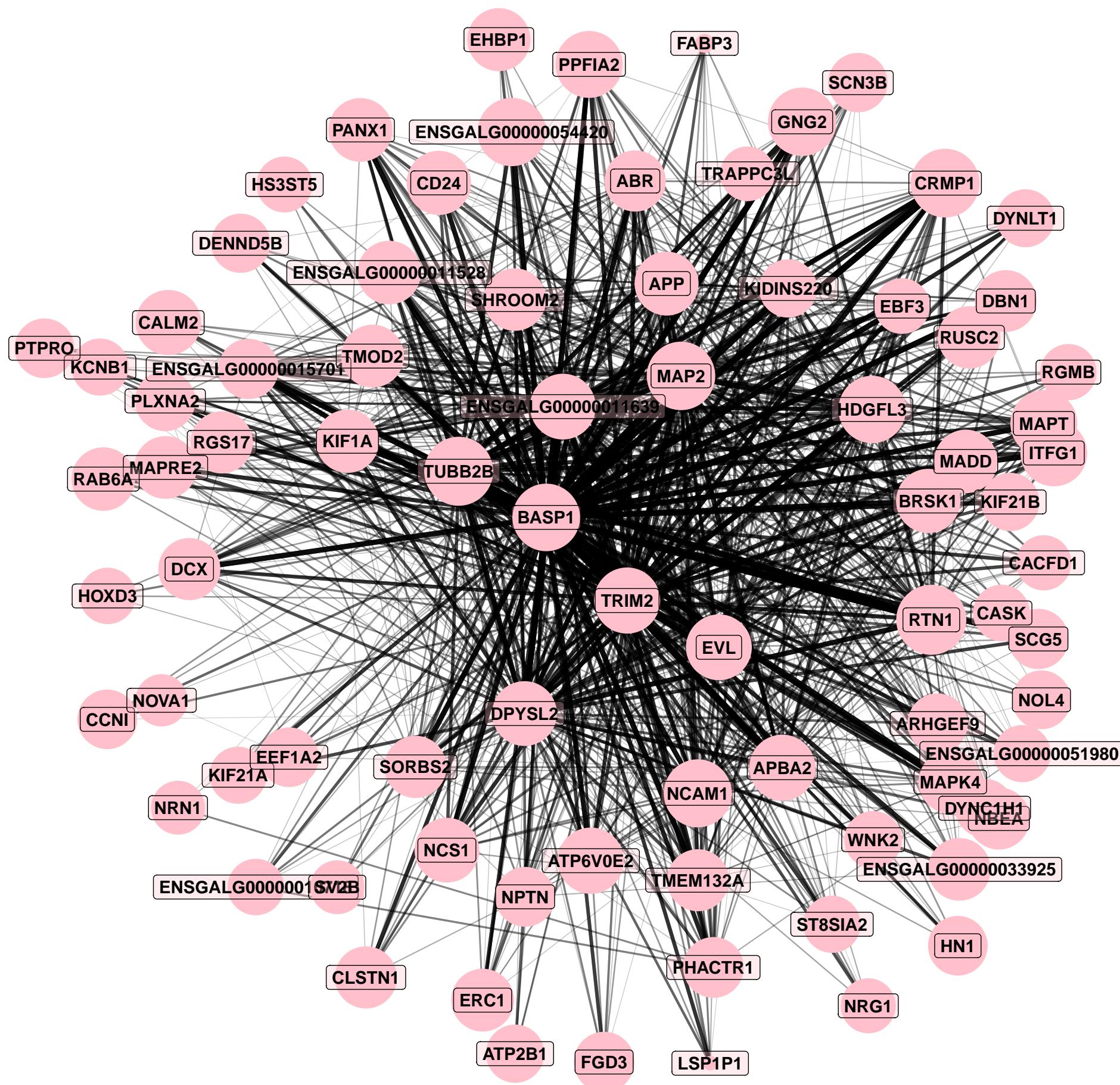
	Pathway	N	DE	P.DE
<i>path:gga04260</i>	Cardiac muscle contraction	61	4	0.0004113
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	125	5	0.0007553
<i>path:gga04020</i>	Calcium signaling pathway	204	6	0.001121
<i>path:gga04371</i>	Apelin signaling pathway	114	4	0.004182
<i>path:gga04540</i>	Gap junction	79	3	0.01057
<i>path:gga04145</i>	Phagosome	125	3	0.03524
<i>path:gga05132</i>	Salmonella infection	221	4	0.03837
<i>path:gga04744</i>	Phototransduction	15	1	0.0829
<i>path:gga04916</i>	Melanogenesis	87	2	0.08933
<i>path:gga04114</i>	Oocyte meiosis	96	2	0.1054



1	FABP9	ERMN	ENSGALG00000004734	DCLK3	ENSGALG00000037029	TLCD2	KIF26A	TNR
2	ELOVL7	LGI3	ENSGALG00000009355	ENSGALG00000016702	SLC46A3	ENSGALG00000001620	PPP1R16B	ENSGALG00000053247
3	CMTM7	ADAMTS4	AvBD5	GPR160	ENSGALG00000010268	TBC1D2	NINJ2	TMCC3
4	ENSGALG00000038624	SH3GL3	DEF6	HAPLN1	MPZ	RAB7B	SMPX	APLN
5	ENPP2	HAPLN2	RASSF10	NA	NHS	MYOZ2	EYA1	TNFRSF10B
6	ENSGALG00000006325	ANKS1B	CELF2					

	Term	Ont	N	n	Adj. p-value
GO:0016576	histone dephosphorylation	BP	3	1	0.00938
GO:0022610	biological adhesion	BP	149	3	0.01129
GO:0007155	cell adhesion	BP	149	3	0.01129
GO:2001240	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	BP	4	1	0.01249
GO:1901099	negative regulation of signal transduction in absence of ligand	BP	4	1	0.01249
GO:0006376	mRNA splice site selection	BP	5	1	0.01559
GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	BP	5	1	0.01559
GO:0000245	spliceosomal complex assembly	BP	6	1	0.01867
GO:0098743	cell aggregation	BP	8	1	0.02482
GO:0016925	protein sumoylation	BP	8	1	0.02482

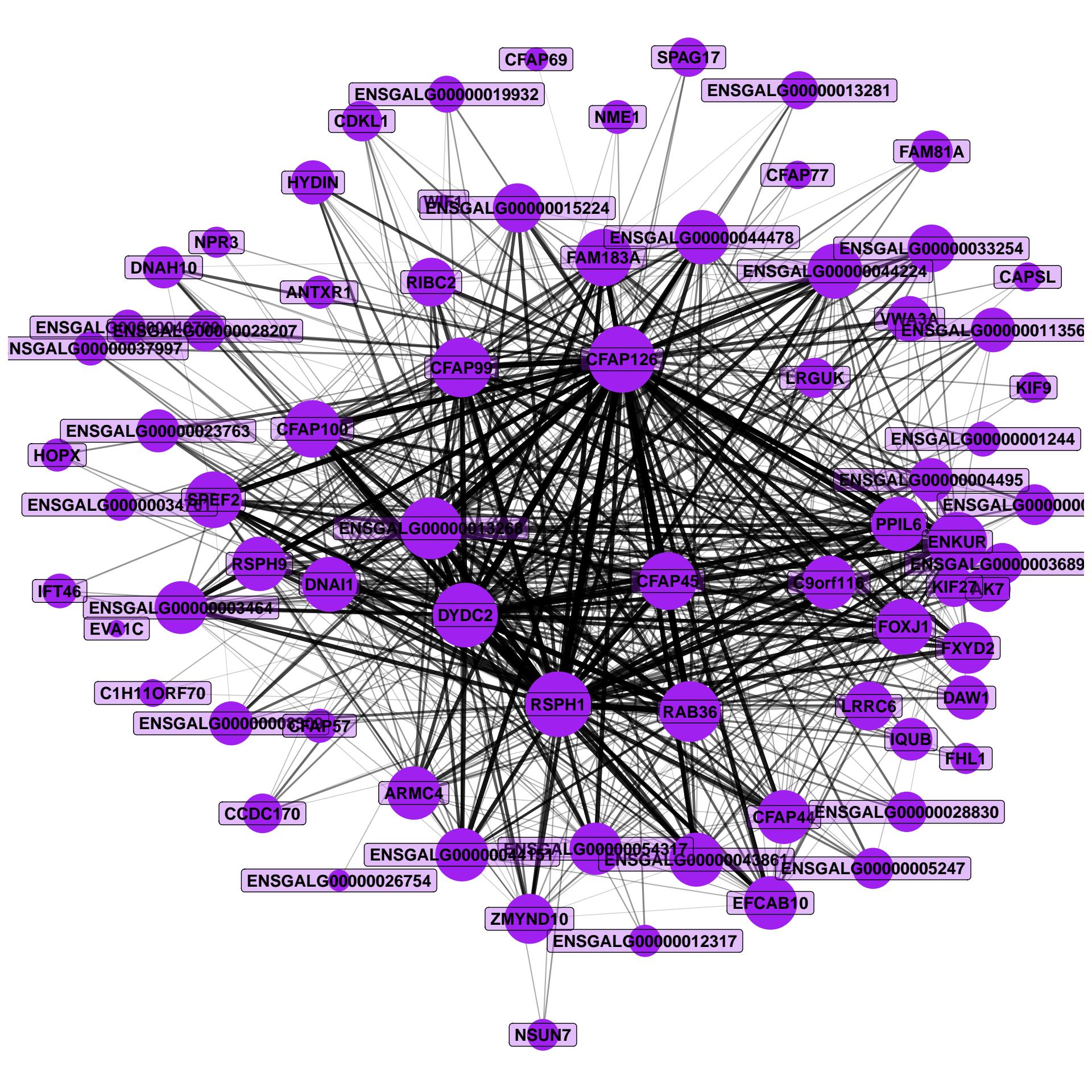
	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	105	2	0.04279
<i>path:gga00062</i>	Fatty acid elongation	23	1	0.06975
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	27	1	0.08139
<i>path:gga00565</i>	Ether lipid metabolism	39	1	0.1155
<i>path:gga01212</i>	Fatty acid metabolism	50	1	0.1456
<i>path:gga05132</i>	Salmonella infection	221	2	0.1523
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.1773
<i>path:gga04115</i>	p53 signaling pathway	63	1	0.1799
<i>path:gga04512</i>	ECM–receptor interaction	70	1	0.1978
<i>path:gga03015</i>	mRNA surveillance pathway	73	1	0.2054



1	RTN1	TUBB2B	ENSGALG00000054420	BRSK1	GNG2	MAPT	ATP6V0E2	MAP2
2	PPFIA2	BASP1	TRIM2	CRMP1	NCAM1	ITFG1	CD24	DPYSL2
3	EVL	NCS1	HDGFL3	EBF3	ENSGALG00000011639	APP	CALM2	ST8SIA2
4	APBA2	PANX1	PHACTR1	EHBP1	MADD	KIF1A	DCX	MAPRE2
5	RUSC2	ENSGALG00000033925	MAPK4	CLSTN1	KIDINS220	ABR	PLXNA2	ENSGALG00000011528
6	SHROOM2	SORBS2	DBN1	TMOD2	TMEM132A	RGMB	RGS17	SCG5
7	ENSGALG00000015701	NPTN	KIF21A	RAB6A	ENSGALG00000010718	TRAPPC3L	PTPRO	ERC1
8	SCN3B	HN1	NOL4	NBEA	NRN1	ENSGALG00000051980	KCNB1	ARHGEF9
9	EEF1A2	FGD3	KIF21B	DENND5B	CCNI	WNK2	DYNLT1	ATP2B1
10	CACFD1	HS3ST5	CASK	HOXD3	FABP3	NRG1	DYNC1H1	SV2B
11	NOVA1	LSP1P1						

	Term	Ont	N	n	Adj. p-value
GO:0060999	positive regulation of dendritic spine development	BP	6	2	0.0005205
GO:0060998	regulation of dendritic spine development	BP	8	2	0.000964
GO:0031110	regulation of microtubule polymerization or depolymerization	BP	11	2	0.001872
GO:0060996	dendritic spine development	BP	13	2	0.002634
GO:0031109	microtubule polymerization or depolymerization	BP	14	2	0.003061
GO:0030516	regulation of axon extension	BP	14	2	0.003061
GO:0007010	cytoskeleton organization	BP	168	5	0.003299
GO:0048675	axon extension	BP	16	2	0.004005
GO:0051493	regulation of cytoskeleton organization	BP	54	3	0.00409
GO:0070507	regulation of microtubule cytoskeleton organization	BP	17	2	0.004522

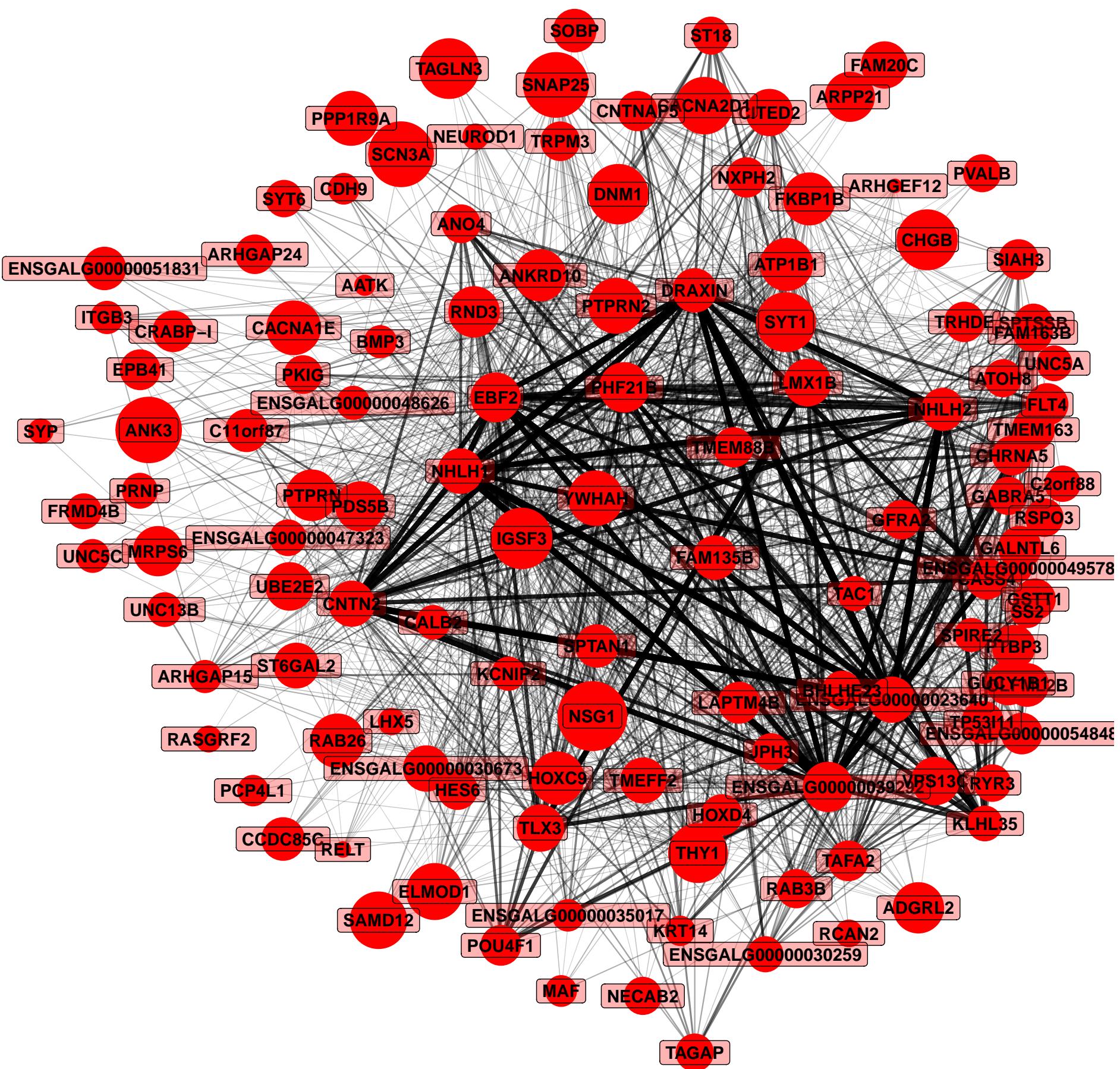
	Pathway	N	DE	P.DE
<i>path:gga04145</i>	Phagosome	125	4	0.006627
<i>path:gga05132</i>	Salmonella infection	221	5	0.01033
<i>path:gga03267</i>	Virion – Adenovirus	3	1	0.01782
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.02368
<i>path:gga04540</i>	Gap junction	79	2	0.08088
<i>path:gga04744</i>	Phototransduction	15	1	0.086
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	83	2	0.088
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis – heparan sulfate / heparin	21	1	0.1183
<i>path:gga04371</i>	Apelin signaling pathway	114	2	0.1484
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	125	2	0.1715



1	CFAP126	DYDC2	RSPH1	ENSGALG00000013268	RAB36	CFAP100	ENKUR	CFAP99
2	PPIL6	SPEF2	FOXJ1	FAM183A	CFAP45	ENSGALG00000043861	ENSGALG00000044478	RSPH9
3	CFAP44	DNAI1	ENSGALG0000003464	FXYD2	RIBC2	ENSGALG00000044224	ARMC4	HYDIN
4	C9orf116	ENSGALG00000015224	ENSGALG00000054317	ENSGALG00000044151	AK7	ZMYND10	LRRC6	ENSGALG00000013281
5	EFCAB10	ENSGALG0000005247	DNAH10	ENSGALG00000019932	DAW1	ENSGALG0000004495	ENSGALG00000028207	VWA3A
6	ENSGALG00000003013	ENSGALG00000008309	IQUB	CCDC170	ENSGALG00000033254	LRGUK	ENSGALG00000023763	ENSGALG00000011356
7	ENSGALG00000037997	ENSGALG00000034761	ENSGALG00000040709	CDKL1	FAM81A	SPAG17	ENSGALG00000001244	ENSGALG00000036896
8	ENSGALG00000012317	HOPX	KIF27	NSUN7	FHL1	CFAP57	NPR3	ENSGALG00000028830
9	NME1	ANTXR1	C1H11ORF70	CFAP77	KIF9	CAPSL	EVA1C	WIF1
10	ENSGALG00000026754	IFT46	CFAP69					

	Term	Ont	N	n	Adj. p-value
GO:0043415	positive regulation of skeletal muscle tissue regeneration	BP	2	1	0.01028
GO:0043416	regulation of skeletal muscle tissue regeneration	BP	2	1	0.01028
GO:0051131	chaperone-mediated protein complex assembly	BP	3	1	0.01538
GO:0043403	skeletal muscle tissue regeneration	BP	6	1	0.03052
GO:0016575	histone deacetylation	BP	9	1	0.04544
GO:0006476	protein deacetylation	BP	9	1	0.04544
GO:0008016	regulation of heart contraction	BP	10	1	0.05036
GO:0051155	positive regulation of striated muscle cell differentiation	BP	11	1	0.05526
GO:1903522	regulation of blood circulation	BP	11	1	0.05526
GO:0042246	tissue regeneration	BP	11	1	0.05526

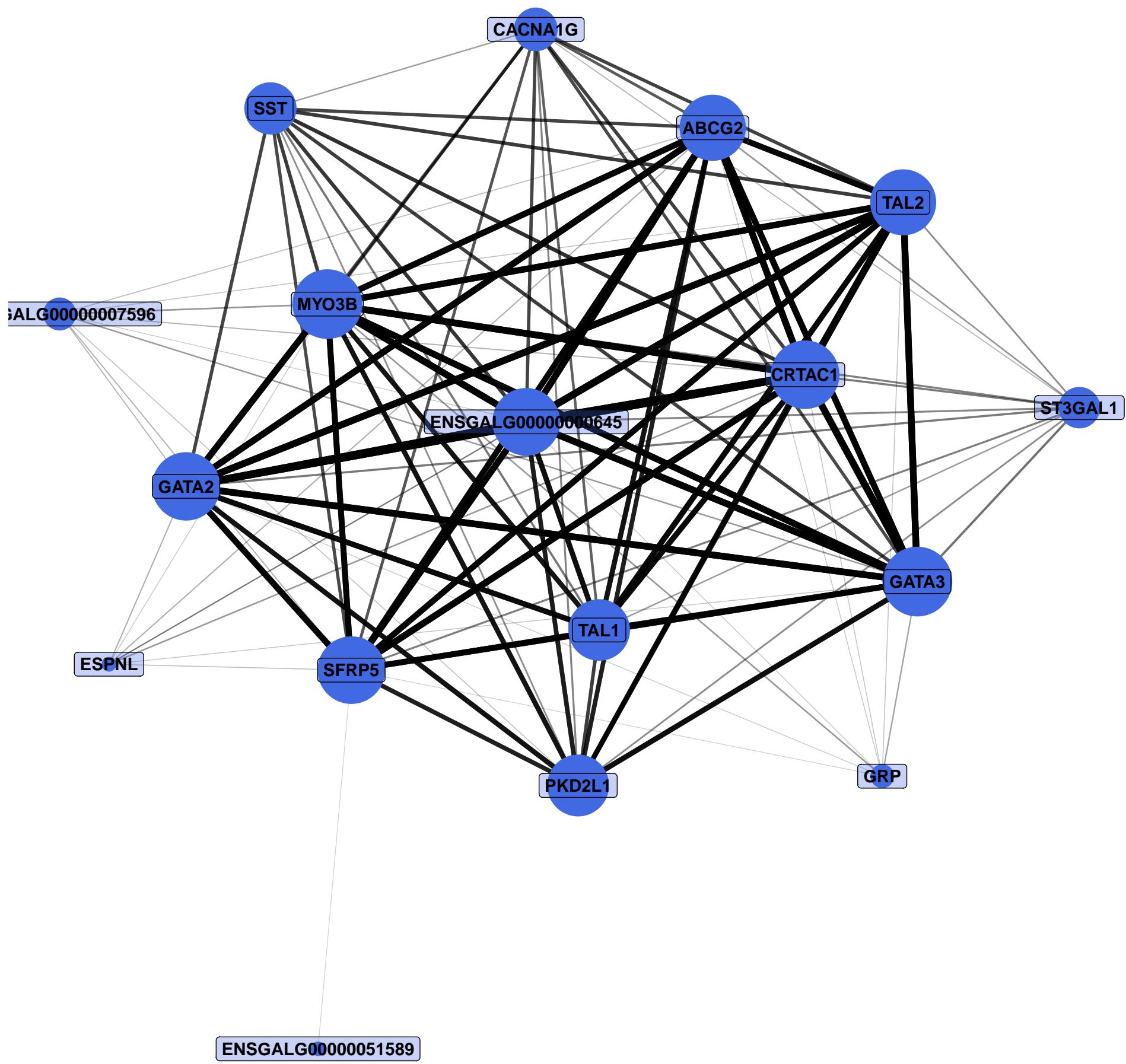
	Pathway	N	DE	P.DE
<i>path:gga01232</i>	Nucleotide metabolism	78	3	0.007559
<i>path:gga00230</i>	Purine metabolism	116	3	0.02194
<i>path:gga01240</i>	Biosynthesis of cofactors	117	3	0.02243
<i>path:gga00240</i>	Pyrimidine metabolism	55	2	0.0326
<i>path:gga00730</i>	Thiamine metabolism	12	1	0.06013
<i>path:gga00983</i>	Drug metabolism – other enzymes	56	1	0.2516
<i>path:gga04260</i>	Cardiac muscle contraction	61	1	0.2708
<i>path:gga04621</i>	NOD–like receptor signaling pathway	115	1	0.4493
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	125	1	0.4773
<i>path:gga04310</i>	Wnt signaling pathway	137	1	0.509



1	SNAP25	NSG1	CHGB	ANK3	SYT1	TAGLN3	SCN3A	THY1
2	IGSF3	DNM1	SAMD12	CACNA1E	ATP1B1	DRAVIN	ELMOD1	CACNA2D1
3	TMEFF2	CRABP-I	YWHAH	PTPRN2	FKBP1B	ENSGALG00000023640	RAB26	CNTN2
4	NHLH1	RND3	PTPRN	PPP1R9A	EBF2	ANKRD10	TLX3	ENSGALG00000039292
5	LMX1B	ENSGALG00000030673	ARPP21	CITED2	HES6	TAC1	PHF21B	LAPTM4B
6	ST18	ADGRL2	MRPS6	GUCY1B1	TP53I11	ST6GAL2	NHLH2	PDS5B
7	FAM20C	HOXC9	TMEM163	UBE2E2	FRMD4B	KRT14	FAM135B	VPS13C
8	CCDC85C	C11orf87	EPB41	PTBP3	SPTSSB	SPTAN1	KCNIP2	ENSGALG00000051831
9	GFRA2	SS2	SOBP	CASS4	FLT4	TAFA2	PKIG	TMEM88B
10	UNC13B	CALB2	NXPH2	SPIRE2	HOXD4	GABRA5	JPH3	RAB3B
11	CNTNAP5	ENSGALG00000030259	POU4F1	UNC5A	ARHGAP24	GSTT1	ANO4	GALNTL6
12	ENSGALG00000054848	ATOH8	PVALB	OLFML2B	RYR3	ENSGALG00000047323	TRHDE	SYP
13	PRNP	ARHGAP15	CHRNA5	ITGB3	FAM163B	TAGAP	NECAB2	SIAH3
14	TRPM3	ARHGEF12	KLHL35	ENSGALG00000035017	C2orf88	UNC5C	SYT6	RSPO3
15	RELT	RCAN2	CDH9	NEUROD1	ENSGALG00000048626	BMP3	BHLHE23	PCP4L1
16	MAF	AATK	LHX5	ENSGALG00000049578	RASGRF2			

	Term	Ont	N	n	Adj. p-value
GO:0065008	regulation of biological quality	BP	363	12	8.462e-05
GO:1990778	protein localization to cell periphery	BP	27	4	8.594e-05
GO:0099003	vesicle-mediated transport in synapse	BP	12	3	0.0001384
GO:0090150	establishment of protein localization to membrane	BP	13	3	0.0001788
GO:0098657	import into cell	BP	13	3	0.0001788
GO:0042462	eye photoreceptor cell development	BP	3	2	0.0002296
GO:0050858	negative regulation of antigen receptor-mediated signaling pathway	BP	3	2	0.0002296
GO:0050860	negative regulation of T cell receptor signaling pathway	BP	3	2	0.0002296
GO:0050854	regulation of antigen receptor-mediated signaling pathway	BP	3	2	0.0002296
GO:0050856	regulation of T cell receptor signaling pathway	BP	3	2	0.0002296

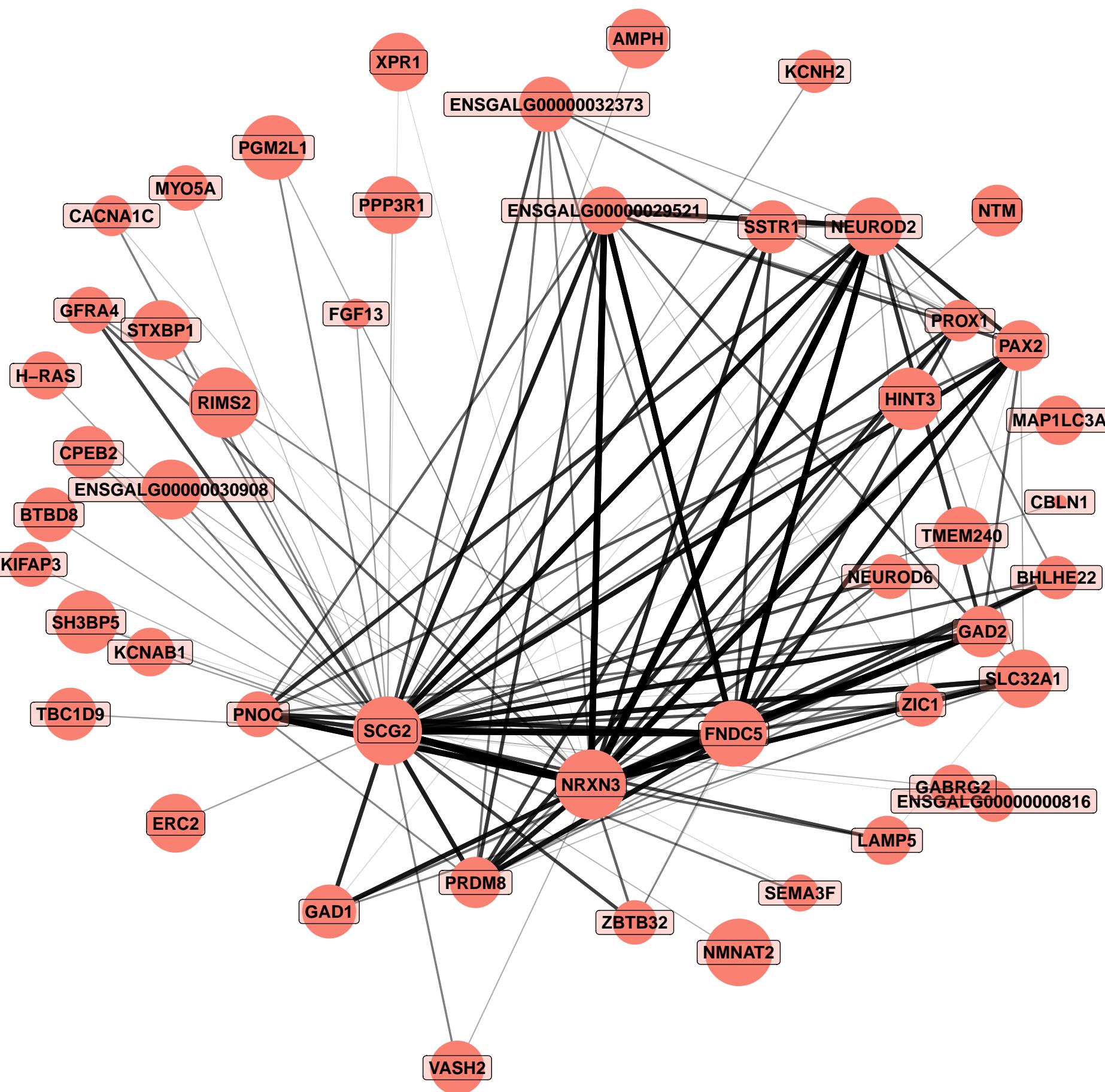
	Pathway	N	DE	P.DE
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.03479
<i>path:gga00514</i>	Other types of O–glycan biosynthesis	41	2	0.05051
<i>path:gga04260</i>	Cardiac muscle contraction	61	2	0.1008
<i>path:gga04010</i>	MAPK signaling pathway	241	4	0.1635
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	83	2	0.166
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	1	0.2266
<i>path:gga00512</i>	Mucin type O–glycan biosynthesis	29	1	0.2266
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	31	1	0.2402
<i>path:gga04270</i>	Vascular smooth muscle contraction	111	2	0.2561
<i>path:gga04216</i>	Ferroptosis	34	1	0.2601



1	PKD2L1	GATA2	GATA3	TAL2	CRTAC1	TAL1	SFRP5	ENSGALG0000000645
2	MYO3B	GRP	ABCG2	ENSGALG0000007596	ST3GAL1	CACNA1G	ENSGALG00000051589	SST
3	ESPNL							

	Term	Ont	N	n	Adj. p-value
GO:0045599	negative regulation of fat cell differentiation	BP	4	2	7.017e-06
GO:0035162	embryonic hemopoiesis	BP	5	2	1.169e-05
GO:0072577	endothelial cell apoptotic process	BP	5	2	1.169e-05
GO:2000352	negative regulation of endothelial cell apoptotic process	BP	5	2	1.169e-05
GO:1904036	negative regulation of epithelial cell apoptotic process	BP	5	2	1.169e-05
GO:2000351	regulation of endothelial cell apoptotic process	BP	5	2	1.169e-05
GO:1904035	regulation of epithelial cell apoptotic process	BP	5	2	1.169e-05
GO:0035065	regulation of histone acetylation	BP	5	2	1.169e-05
GO:2000756	regulation of peptidyl-lysine acetylation	BP	5	2	1.169e-05
GO:1902895	positive regulation of pri-miRNA transcription by RNA polymerase II	BP	6	2	1.752e-05

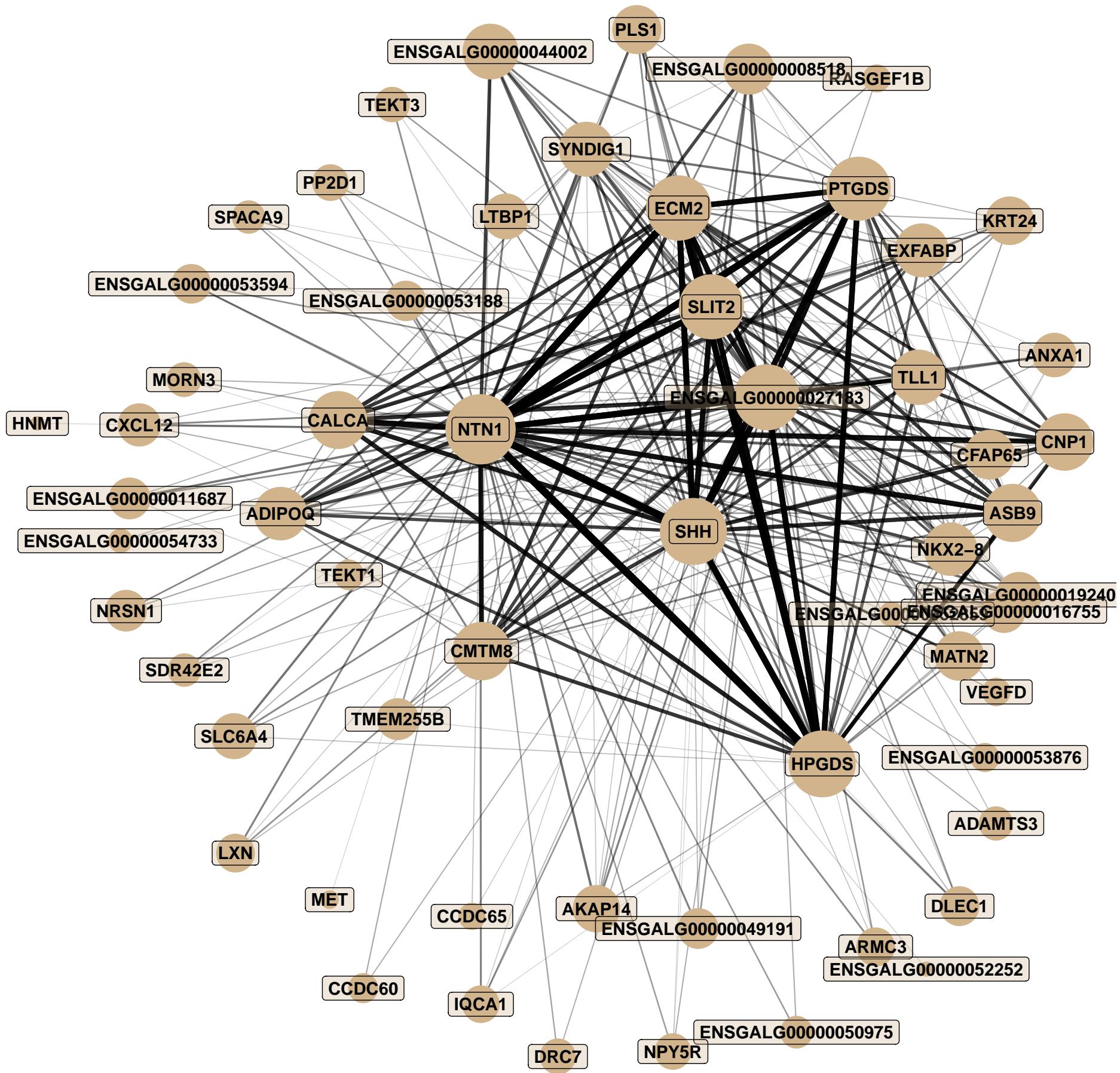
	Pathway	N	DE	P.DE
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	1	0.01336
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	1	0.01447
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.01557
<i>path:gga00512</i>	Mucin type O–glycan biosynthesis	29	1	0.03201
<i>path:gga02010</i>	ABC transporters	37	1	0.04067
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	305	2	0.04465
<i>path:gga04310</i>	Wnt signaling pathway	137	1	0.143
<i>path:gga04020</i>	Calcium signaling pathway	204	1	0.2058
<i>path:gga04010</i>	MAPK signaling pathway	241	1	0.2386
<i>path:gga01100</i>	Metabolic pathways	1272	1	0.7764



1	SCG2	NRXN3	NEUROD2	SLC32A1	FNDC5	PAX2	SSTR1	PNOC
2	PRDM8	GAD1	RIMS2	GAD2	PGM2L1	NMNAT2	LAMP5	ENSGALG00000029521
3	NEUROD6	PROX1	BHLHE22	SH3BP5	XPR1	HINT3	AMPH	BTBD8
4	TMEM240	ENSGALG00000030908	ENSGALG00000032373	STXBP1	VASH2	PPP3R1	TBC1D9	ZBTB32
5	CPEB2	ERC2	ZIC1	FGF13	KCNAB1	MAP1LC3A	GFRA4	SEMA3F
6	KCNH2	NTM	GABRG2	ENSGALG00000000816	MYO5A	CACNA1C	KIFAP3	H-RAS
7	CBLN1							

	Term	Ont	N	n	Adj. p-value
GO:1904062	regulation of cation transmembrane transport	BP	12	2	0.0008456
GO:0098916	anterograde trans-synaptic signaling	BP	58	3	0.001233
GO:0007268	chemical synaptic transmission	BP	58	3	0.001233
GO:0099537	trans-synaptic signaling	BP	58	3	0.001233
GO:0099536	synaptic signaling	BP	62	3	0.001496
GO:0098660	inorganic ion transmembrane transport	BP	63	3	0.001567
GO:0021510	spinal cord development	BP	18	2	0.001933
GO:0042472	inner ear morphogenesis	BP	19	2	0.002155
GO:0042471	ear morphogenesis	BP	20	2	0.002389
GO:0007399	nervous system development	BP	265	5	0.002737

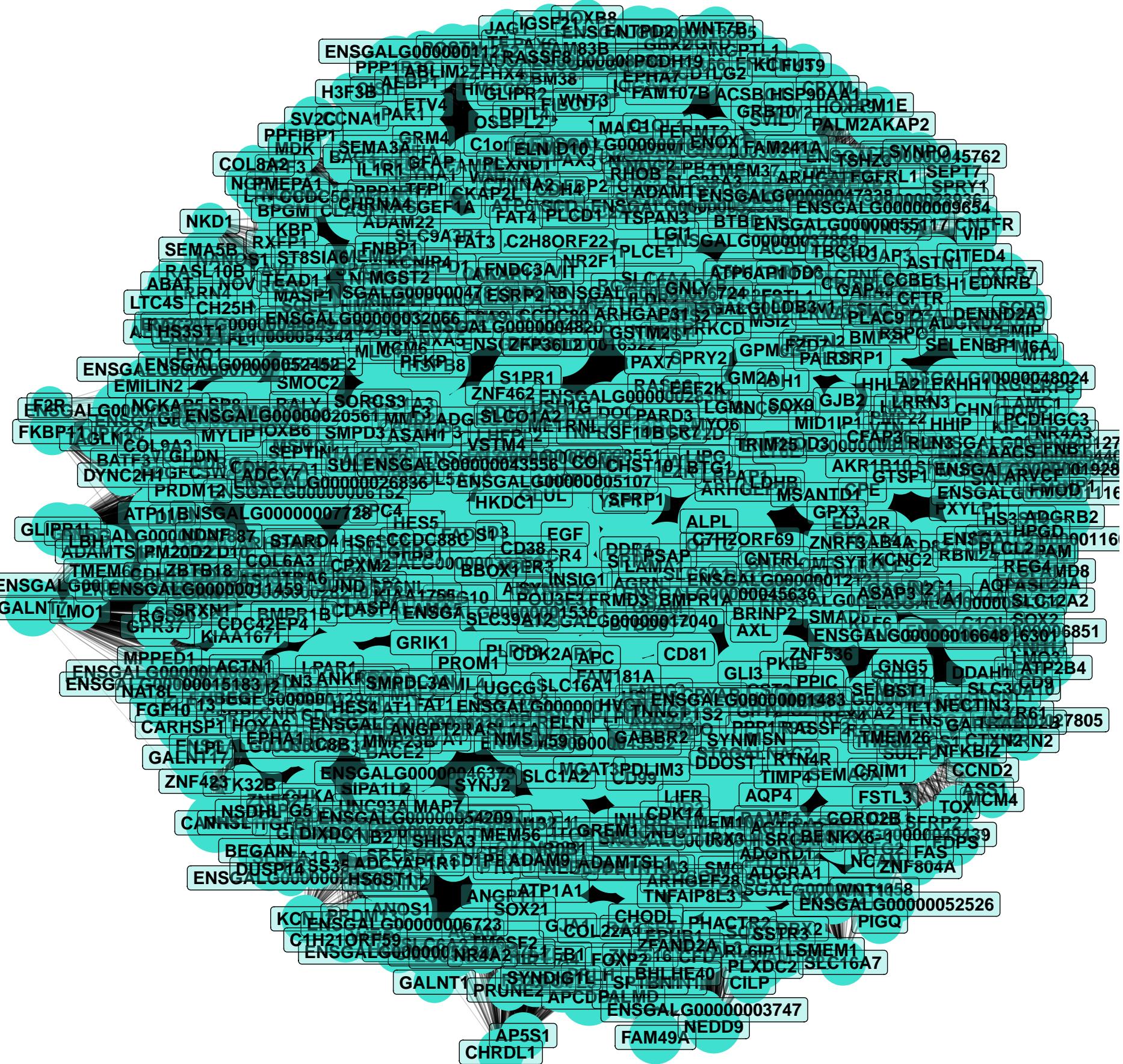
	Pathway	N	DE	P.DE
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	2	0.0008456
<i>path:gga00650</i>	Butanoate metabolism	21	2	0.002635
<i>path:gga00410</i>	beta-Alanine metabolism	25	2	0.003729
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	2	0.006065
<i>path:gga04370</i>	VEGF signaling pathway	55	2	0.01722
<i>path:gga04137</i>	Mitophagy – animal	62	2	0.02157
<i>path:gga04912</i>	GnRH signaling pathway	77	2	0.03224
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	83	2	0.03699
<i>path:gga04020</i>	Calcium signaling pathway	204	3	0.03846
<i>path:gga04114</i>	Oocyte meiosis	96	2	0.0481



1	ECM2	HPGDS	PTGDS	SHH	NTN1	CNP1	ENSGALG00000027183	EXFABP
2	SLIT2	ASB9	NKX2–8	CMTM8	ENSGALG0000044002	AKAP14	TLL1	ADIPOQ
3	SYNDIG1	PLS1	CFAP65	KRT24	SLC6A4	ENSGALG0000008518	CALCA	MATN2
4	ENSGALG0000019240	LTBP1	ANXA1	IQCA1	TMEM255B	NRSN1	DRC7	ENSGALG0000011687
5	ENSGALG0000049191	MORN3	ENSGALG0000053594	CXCL12	ENSGALG0000016755	LXN	ARMC3	DLEC1
6	ENSGALG0000050975	SDR42E2	TEKT3	ENSGALG0000053188	ENSGALG0000053876	NPY5R	RASGEF1B	CCDC60
7	SPACA9	ADAMTS3	PP2D1	CCDC65	ENSGALG0000052859	VEGFD	ENSGALG0000052252	TEKT1
8	ENSGALG0000054733	HNMT	MET					

	Term	Ont	N	n	Adj. p-value
GO:0048589	developmental growth	BP	69	5	5.013e-06
GO:0040007	growth	BP	99	5	2.939e-05
GO:0051240	positive regulation of multicellular organismal process	BP	121	5	7.691e-05
GO:0015909	long-chain fatty acid transport	BP	4	2	7.832e-05
GO:0051094	positive regulation of developmental process	BP	127	5	9.675e-05
GO:0051239	regulation of multicellular organismal process	BP	210	6	0.0001103
GO:0003415	chondrocyte hypertrophy	BP	5	2	0.0001302
GO:0046456	icosanoid biosynthetic process	BP	5	2	0.0001302
GO:0001516	prostaglandin biosynthetic process	BP	5	2	0.0001302
GO:0006693	prostaglandin metabolic process	BP	5	2	0.0001302

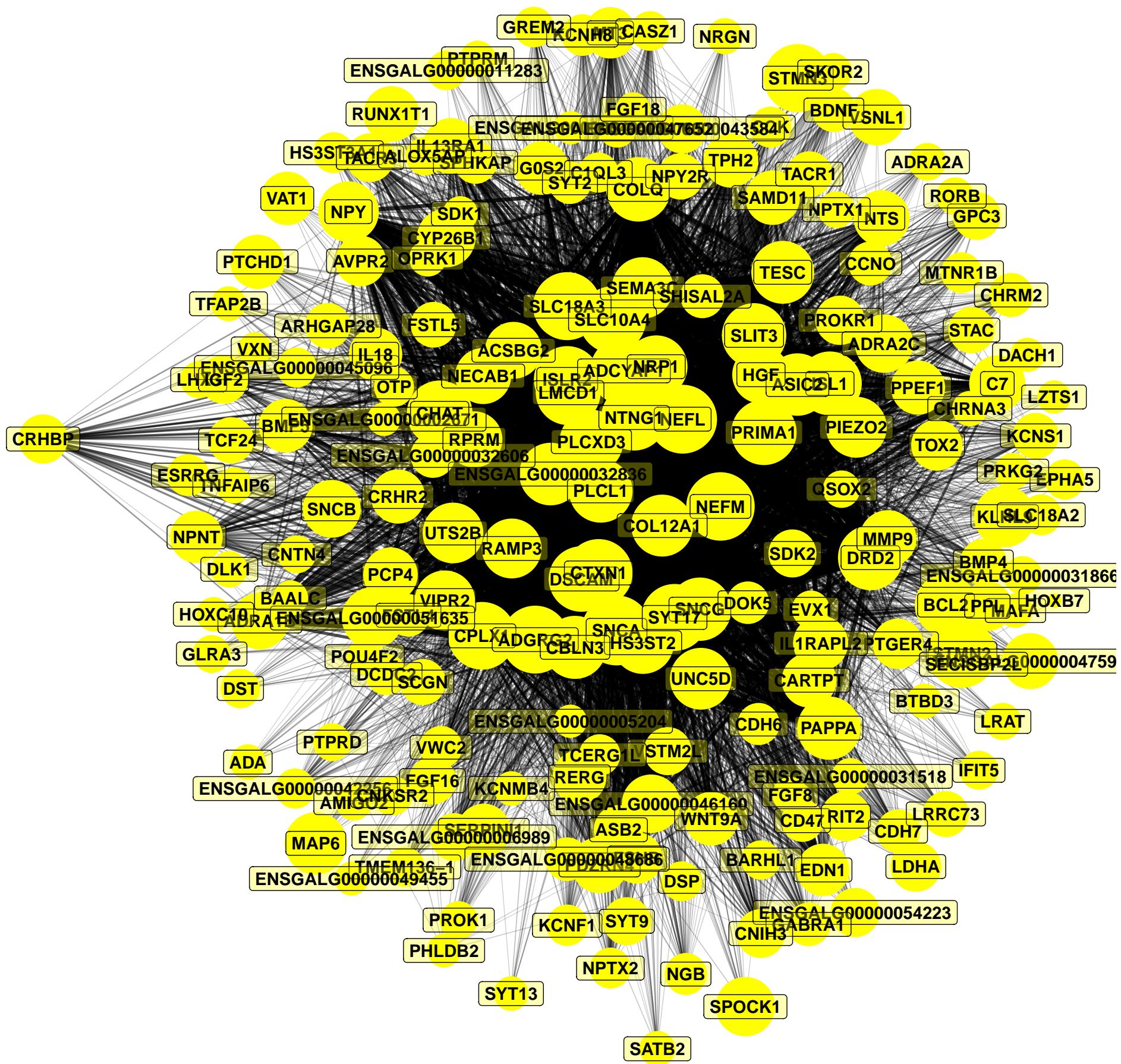
	Pathway	N	DE	P.DE
<i>path:gga00590</i>	Arachidonic acid metabolism	42	2	0.01029
<i>path:gga00910</i>	Nitrogen metabolism	14	1	0.05005
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.06045
<i>path:gga00340</i>	Histidine metabolism	17	1	0.06045
<i>path:gga04270</i>	Vascular smooth muscle contraction	111	2	0.06223
<i>path:gga04672</i>	Intestinal immune network for IgA production	24	1	0.08429
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	1	0.1009
<i>path:gga00630</i>	Glyoxylate and dicarboxylate metabolism	29	1	0.1009
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	31	1	0.1075
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	1	0.1108



32	BTBD17	BAG3	HSS316	SRGAP3	POLES	MDR	SOU21	CHNT
33	FAM3C	CAP2	ENSGALG00000048024	DMD	NOG	HOXB5	PFKP	ENSGALG0000007728
34	CDH4	BMP2K	ITGB1	BBOX1	ANGPTL1	APCDD1L	FAT4	FLNB
35	NTN3	IGFBP2	EPB41L3	NOG2	RBP5	DIPK1C	LAMC1	CYP51A1
36	TSPAN6	GPC4	ALPL	USP12	MYLK	CCND3	MSMO1	LDHB
37	BPGM	MGAT3	TSPAN13	KLF15	ELOVL5	KIF1B	TRIM24	EZR
38	LAMA5	MEIS2	GNG5	SFRP1	FRMD3	SPATS2L	BOC	ZNRF3
39	MDFIC	SMOX	SREBF2	MSN	CCDC80	SYT11	RBM24	CD82
40	FAM46A	ENSGALG00000001536	GREB1	SPARC	CHST7	LRP8	S100A10	COL22A1
41	SPARCL1	ENSGALG00000006644	CAPN11	CHST10	AGPAT3	NKAIN2	FAT3	CPNE2
42	TSPAN3	TMEM47	TBC1D1	HVCN1	TMEM37	WNT5A	FZD10	SMPDL3A
43	PHYHIPL	ENSGALG00000017040	CNR1	ENSGALG00000005180	ENSGALG00000013624	SLC15A2	CRISPLD2	SKI
44	ADAM22	C1QL2	SCRN1	MEIS1	HMGCR	RAB20	ARHGEF28	TGFB2
45	CD164L2	IQGAP2	C1orf21	RNH1	PDGFD	SLC1A2	PDLIM4	ENSGALG00000030587
46	SCG3	GBE1	CLASP1	ATP1A1	MID1IP1	ENSGALG00000012941	SMPD3	AP1S2
47	NEBL	ENSGALG00000048205	ENSGALG00000006152	SOX2	ADGRB2	HHIP	ARHGAP5	PLCD1
48	F2RL1	INHBB	CD63	RALY	BMPR1B	AXL	CDK14	GLIPR1L
49	C2H8ORF22	GAREM2	PKIB	LPAR4	ENSGALG00000034354	PRELID3A	EEPD1	ENSGALG00000010316
50	PXYLP1	LATS2	INSIG1	SLC38A3	GRB10	ACAN	ADAMTS17	GLO1
51	CDH2	CDH20	ZFP36L2	TLL2	GPM6A	ENSGALG00000036310	AEBP1	CRYAB
52	ABHD3	MSX1	ENSGALG00000049127	ENSGALG00000048534	EMILIN2	CTNNA2	PARD3	GSTM2
53	NHSL1	KIF13B	ENSGALG00000047813	LGI1	ZEB1	ADAMTS7	ENSGALG00000028301	TGFB3
54	ASTN1	ENSGALG00000055117	DDIT4	KIRREL3	PHACTR2	GABBR2	RFTN1	ARHGAP31
55	EDA2R	SULF1	CDO1	SEMA3A	ENSGALG0000005076	MYLIP	CSRP2	C1QL1
56	EFHD1	MGAT4A	ROBO1	GALNT7	ENSGALG00000026836	COL4A1	LRP4	NCALD
57	DBX2	TGFBI	KCNC2	HMGCS1	ADCYAP1R1	HSPA5	RSPO1	ATP11B
58	SDCBP	PTCH2	AKAP12	PAX3	TNNC1	CDH13	KLF6	MSANTD1
59	IQGAP1	FDFT1	NDP	PDLIM3	EEF2K	CDC42EP4	ARAP2	CRB2
60	ARL6IP1	ADCY7	ADD3	ADAMTS14	PDE9A	ASL2	CHL1	SLC7A10
61	RGS3	ENSGALG00000028466	SLC16A1	TNFRSF11B	NR2F1	RBM38	DHCR7	PLEKHH1
62	SP8	HTRA3	CORO2B	BRINP2	NKX6-2	ENSGALG00000016251	RELN	SYNDIG1L
63	ADGRD2	STEAP3	PAX7	IRX5	CFAP36	ENSGALG00000054209	NFIX	VASH1
64	CARHSP1	FNBP1	HES1	ENSGALG00000043556	TMEM86A	FAM49A	FNDC3A	RASA3
65	SLC39A12	VIT	CD44	ENSGALG0000002714	CKB	WTIP	COL4A2	KCNIP4
66	PRDM12	HSP90B1	WNT11	EPHA7	RASL11A	IRX3	GRM4	LGMN
67	SQLE	NRN1L	SVIL	CHKA	ILDR2	SPTBN1	TEAD1	ELN
68	MASP1	EPHB1	SAMD10	NCKAP5	ENO1	SEPTIN11	LRRC8B	APC
69	ARHGAP42	GLIPR2	KBP	CHODL	FBXO34	NEDD9	THBS2	ENSGALG00000020561
70	SCD5	SYNM	LIPG	NKX6-1	ENSGALG00000027805	BTG2	POU3F3	ENSGALG00000032066
71	PBX1	PAK1	RXFP1	ADAMTSL1	ENSGALG00000013505	LRRN3	GBX2	HOXA6
72	ZNF462	GAS1	NMS	HHLA2	WSCD1	RSRP1	METRNL	LRRN4
73	NECTIN3	BST1	ENSGALG0000006723	LPL	HOXA5	ENOX1	SCD	ENSGALG0000004518
74	PAM	FMOD	EDNRB	NR4A3	TMEM26	CFD	NSDHL	ENTPD2
75	NDNF	HS6ST1	RLN3	CCDC88C	MFGE8	CRYM	ENSGALG00000020788	VSTM4
76	EPHA1	FCER1A	CPY3	PRLH	HES4	TM6SF2	CRIM1	RASECFF1A

	Term	Ont	N	n	Adj. p-value
GO:0007275	multicellular organism development	BP	591	96	9.137e-19
GO:0048856	anatomical structure development	BP	639	100	2.362e-18
GO:0032501	multicellular organismal process	BP	730	107	1.794e-17
GO:0032502	developmental process	BP	671	101	2.516e-17
GO:0048731	system development	BP	496	75	3.533e-13
GO:0007166	cell surface receptor signaling pathway	BP	270	51	5.528e-13
GO:0009653	anatomical structure morphogenesis	BP	302	52	1.327e-11
GO:0023052	signaling	BP	524	73	4.134e-11
GO:0050789	regulation of biological process	BP	1118	124	5.684e-11
GO:0050794	regulation of cellular process	BP	1067	119	1.045e-10

	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	70	21	7.161e–10
<i>path:gga00100</i>	Steroid biosynthesis	16	8	1.734e–06
<i>path:gga04510</i>	Focal adhesion	176	27	1.098e–05
<i>path:gga04810</i>	Regulation of actin cytoskeleton	189	26	0.0001061
<i>path:gga04310</i>	Wnt signaling pathway	137	20	0.0002919
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	8	0.0005831
<i>path:gga04350</i>	TGF–beta signaling pathway	86	14	0.0007713
<i>path:gga00480</i>	Glutathione metabolism	47	9	0.002089
<i>path:gga00220</i>	Arginine biosynthesis	17	5	0.002988
<i>path:gga03320</i>	PPAR signaling pathway	59	10	0.003116



1	NEFM	NEFL	SLC18A3	SNCA	STMN2	STMN3	CPLX1	ADCYAP1
2	ISLR2	DSCAM	SLC10A4	ADGRG2	SYT17	MAP6	ENSGALG00000032836	CHAT
3	DRD2	CTXN1	COLQ	SNCB	SLIT3	NPY	ENSGALG00000047591	SPOCK1
4	PCP4	HS3ST2	PLCXD3	NTNG1	LMCD1	RUNX1T1	SNCG	ISL1
5	UTS2B	NRP1	PLCL1	SERPINI1	VIPR2	PRIMA1	ENSGALG00000046160	VSNL1
6	ASIC2	PIEZ02	SEMA3C	UNC5D	TESC	COL12A1	RAMP3	G0S2
7	NECAB1	CBLN3	PAPPA	NTS	BCL2	KLHL9	VSTM2L	BMP5
8	ENSGALG00000051635	ACSBG2	EDN1	CYP26B1	IL13RA1	RPRM	ADRA2C	LDHA
9	MT3	NPNT	PPEF1	CRHR2	PROKR1	RERG	ADRA1B	C7
10	HGF	IL1RAPL2	PTCHD1	FSTL5	ENSGALG00000032606	MMP9	PDZRN4	TOX2
11	ASB2	CARTPT	IL18	LRRC73	WNT9A	PPL	FGF16	VAT1
12	FSHB	IGF2	ENSGALG0000006989	BMP4	PTGER4	KCNS1	ENSGALG00000045096	NPTX2
13	STAC	ENSGALG00000054223	RIT2	CCNO	GPC3	SYT9	SAMD11	TACR1
14	AVPR2	SDK2	CNIH3	ENSGALG00000043584	TACR3	GABRA1	CD47	ESRRG
15	BDNF	BAALC	NGB	CDH7	VWC2	ENSGALG00000042256	SHISAL2A	CCK
16	FSTL4	SPHKAP	KCNF1	NPY2R	CDH6	OTP	CRHBP	ARHGAP28
17	EPHA5	QSOX2	ENSGALG00000031518	SCGN	CNKS2	TPH2	CHRM2	TCERG1L
18	CASZ1	PTPRD	DST	SYT2	DSP	HS3ST3A1	ADRA2A	TCF24
19	ENSGALG0000011283	MTNR1B	NPTX1	BARHL1	DOK5	SLC18A2	KCNH8	DCDC2
20	PRKG2	ENSGALG0000047652	SKOR2	SYT13	BTBD3	PHLDB2	AMIGO2	GREM2
21	C1QL3	LRAT	TMEM136-1	SECISBP2L	DLK1	SDK1	CNTN4	NRGN
22	ALOX5AP	PTPRM	PROK1	ENSGALG00000049529	TFAP2B	ENSGALG0000002671	LHX3	POU4F2
23	CHRNA3	KCNMB4	ENSGALG0000048686	EVX1	OPRK1	VXN	SATB2	DACH1
24	IFIT5	RORB	FGF8	LZTS1	TNFAIP6	FGF18	GLRA3	MAFA
25	ENSGALG0000049455	HOXC10	ENSGALG0000005204	ENSGALG00000031866	ADA	HOXB7		

	Term	Ont	N	n	Adj. p-value
GO:0007399	nervous system development	BP	265	20	5.768e-10
GO:0031175	neuron projection development	BP	113	13	4.412e-09
GO:0030182	neuron differentiation	BP	168	15	9.48e-09
GO:0048666	neuron development	BP	128	13	2.036e-08
GO:0009653	anatomical structure morphogenesis	BP	302	19	3.145e-08
GO:0048699	generation of neurons	BP	184	15	3.25e-08
GO:0007275	multicellular organism development	BP	591	27	3.266e-08
GO:0022008	neurogenesis	BP	187	15	4.036e-08
GO:0120036	plasma membrane bounded cell projection organization	BP	139	13	5.493e-08
GO:0048731	system development	BP	496	24	7.07e-08

	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	305	26	7.036e–14
<i>path:gga04020</i>	Calcium signaling pathway	204	8	0.00699
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis – heparan sulfate / heparin	21	2	0.03289
<i>path:gga04810</i>	Regulation of actin cytoskeleton	189	6	0.04534
<i>path:gga04010</i>	MAPK signaling pathway	241	7	0.0477
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	2	0.05926
<i>path:gga04270</i>	Vascular smooth muscle contraction	111	4	0.06568
<i>path:gga00830</i>	Retinol metabolism	31	2	0.06669
<i>path:gga00380</i>	Tryptophan metabolism	34	2	0.07838
<i>path:gga04350</i>	TGF–beta signaling pathway	86	3	0.1134