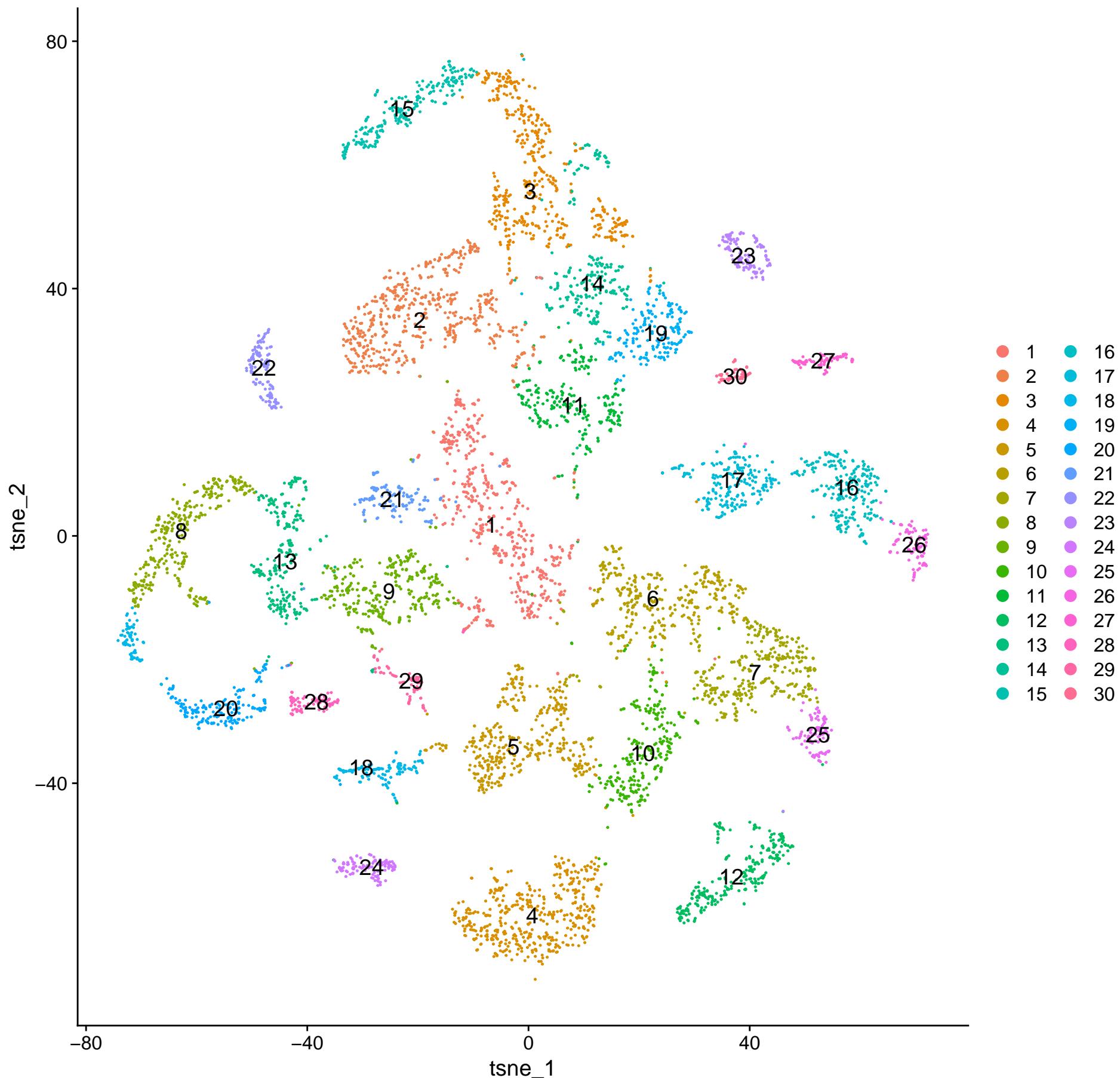
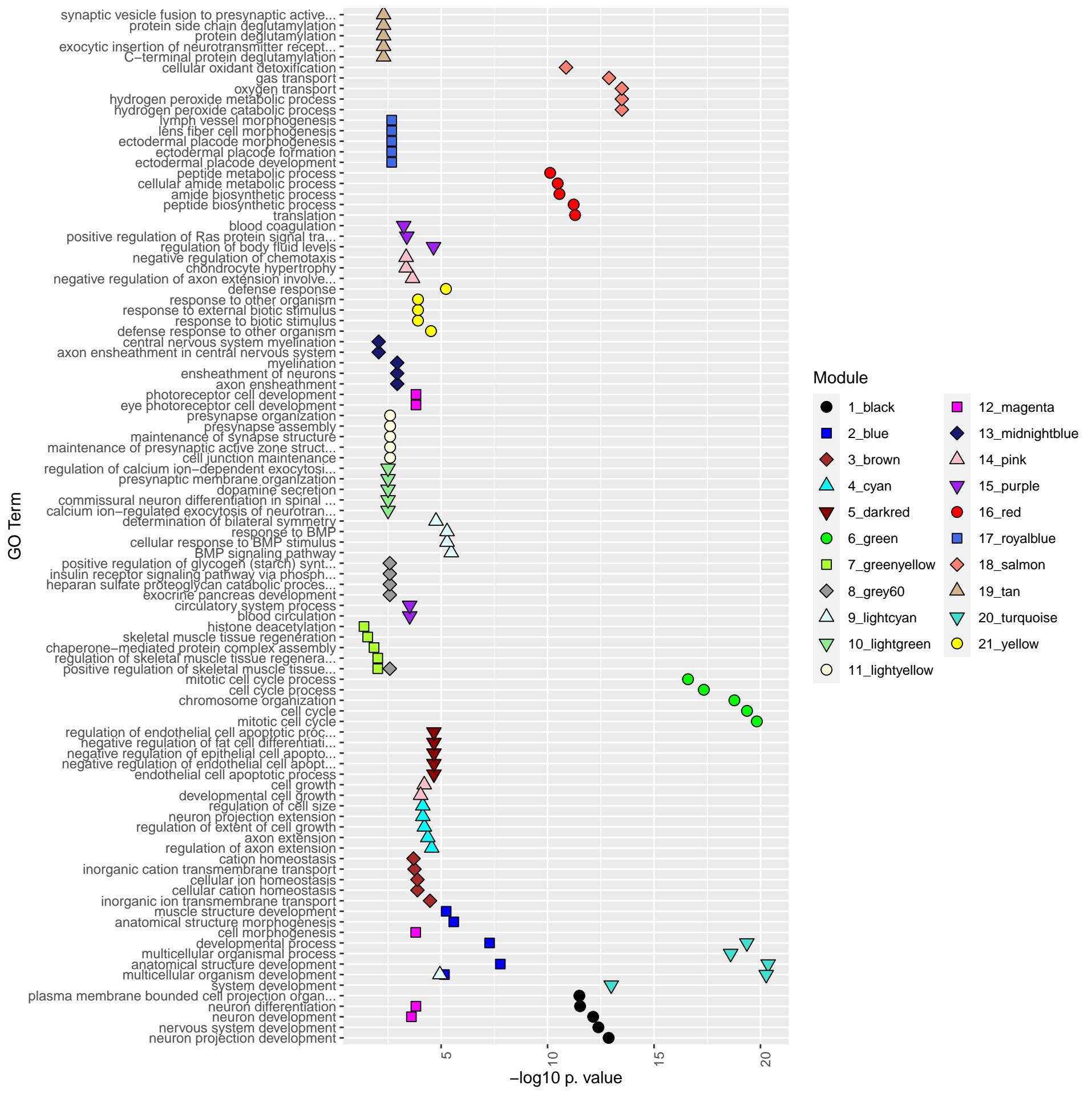
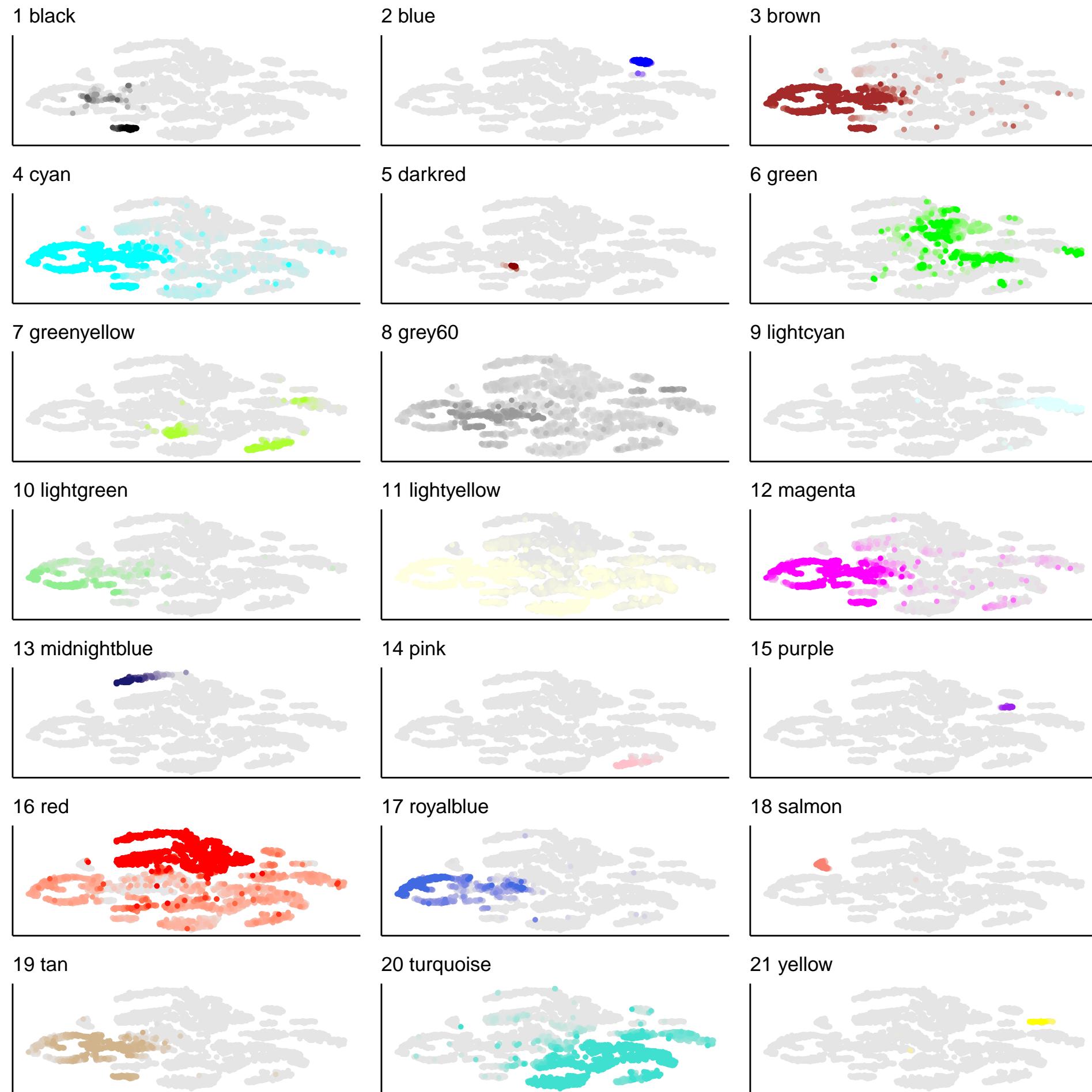


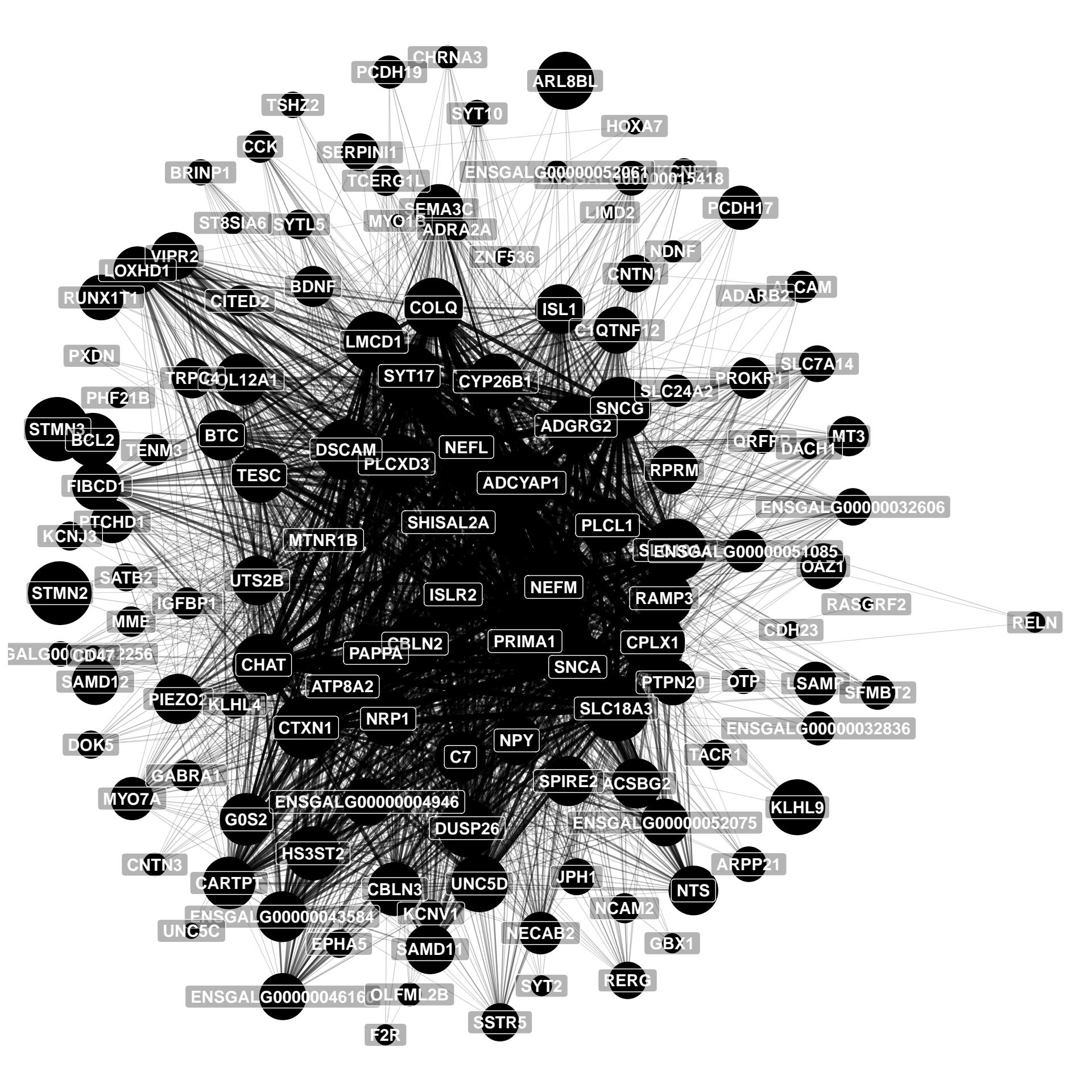
Gg_poly_int scWGCNA modules







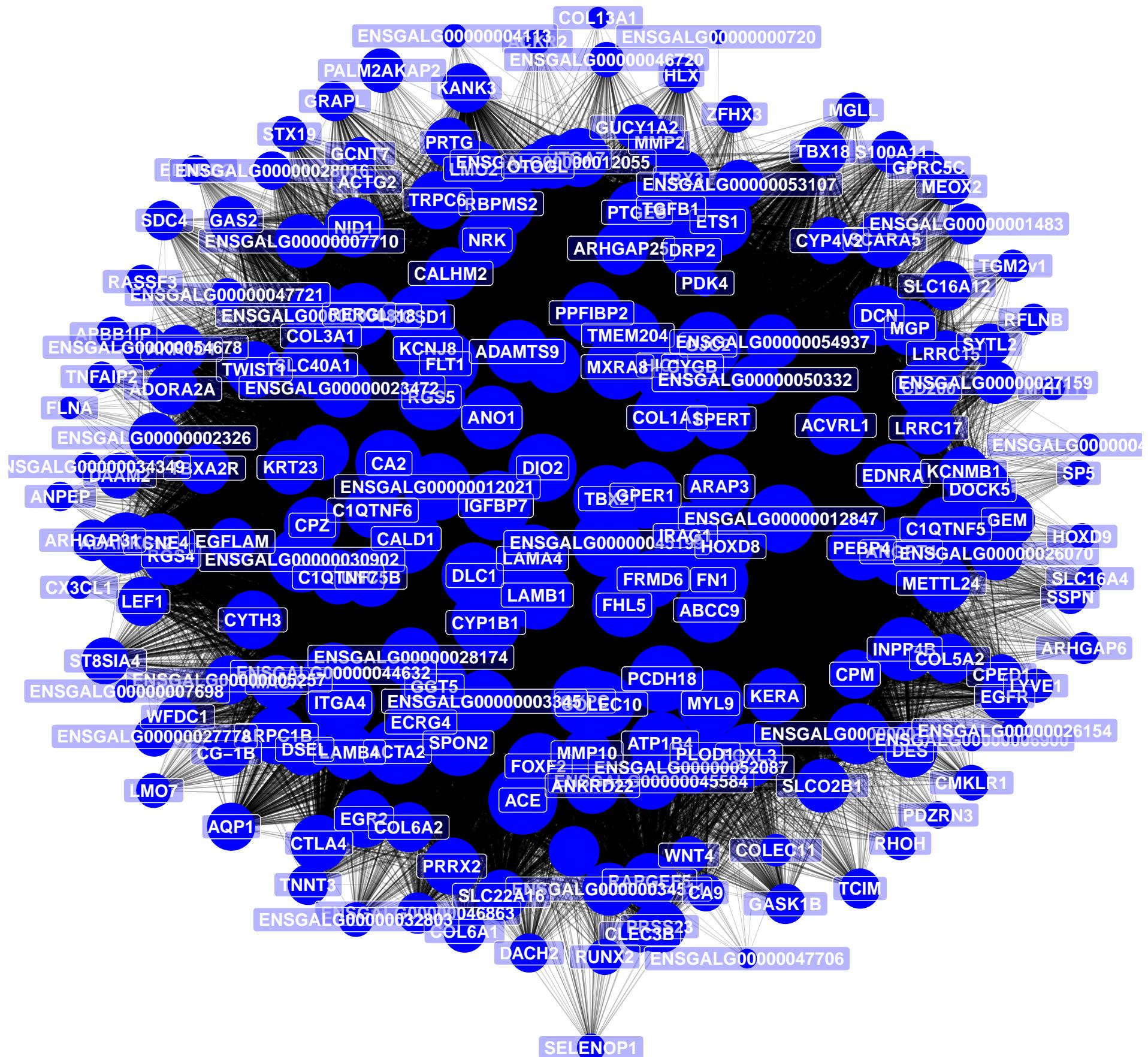




1	NEFM	SNCA	SLC18A3	NEFL	ADCYAP1	STMN2	STMN3	CPLX1
2	ISLR2	DSCAM	SLC10A4	SYT17	CHAT	COLQ	HS3ST2	CBLN2
3	ADGRG2	LMCD1	CTXN1	SNCG	PLCXD3	RUNX1T1	G0S2	TESC
4	ATP8A2	DUSP26	NRP1	UTS2B	CYP26B1	NTS	ISL1	PRIMA1
5	PLCL1	RAMP3	CARTPT	SAMD12	UNC5D	PAPPA	C7	COL12A1
6	RPRM	SPIRE2	ARL8BL	NPY	CBLN3	KLHL9	PIEZO2	SEMA3C
7	MYO7A	SERPINI1	ACSBG2	ENSGALG00000046160	BCL2	BTC	VIPR2	ENSGALG00000032836
8	MT3	OAZ1	ENSGALG00000032606	PTCHD1	SAMD11	ENSGALG00000043584	NECAB2	ARPP21
9	ENSGALG0000051085	PTPN20	FIBCD1	TRPC4	LOXHD1	PROKR1	CNTN1	PCDH17
10	BDNF	TENM3	RERG	JPH1	CITED2	ENSGALG0000004946	CCK	PCDH19
11	SLC24A2	ENSGALG00000052075	LSAMP	GABRA1	SFMBT2	C1QTNF12	KLHL4	SSTR5
12	SLC7A14	KCNJ3	BRINP1	EPHA5	SHISAL2A	ZNF536	ENSGALG00000015418	TCERG1L
13	TACR1	DOK5	CD47	MME	SYT10	SYTL5	KCNF1	PHF21B
14	ENSGALG0000042256	ADRA2A	OLFML2B	IGFBP1	OTP	F2R	TSHZ2	ENSGALG00000052061
15	MTNR1B	ST8SIA6	CHRNA3	UNC5C	MYO1B	RELN	ALCAM	QRFPR
16	PXDN	NDNF	LIMD2	NCAM2	DACH1	CNTN3	SYT2	KCNV1
17	SATB2	CDH23	GBX1	RASGRF2	ADARB2	HOXA7		

	Term	Ont	N	n	Adj. p-value
GO:0031175	neuron projection development	BP	110	15	1.351e-13
GO:0007399	nervous system development	BP	255	20	4.101e-13
GO:0048666	neuron development	BP	123	15	7.258e-13
GO:0030182	neuron differentiation	BP	161	16	2.961e-12
GO:0120036	plasma membrane bounded cell projection organization	BP	136	15	3.223e-12
GO:0030030	cell projection organization	BP	140	15	4.938e-12
GO:0048699	generation of neurons	BP	177	16	1.275e-11
GO:0022008	neurogenesis	BP	180	16	1.648e-11
GO:0048468	cell development	BP	207	16	1.362e-10
GO:0007409	axonogenesis	BP	66	10	6.511e-10

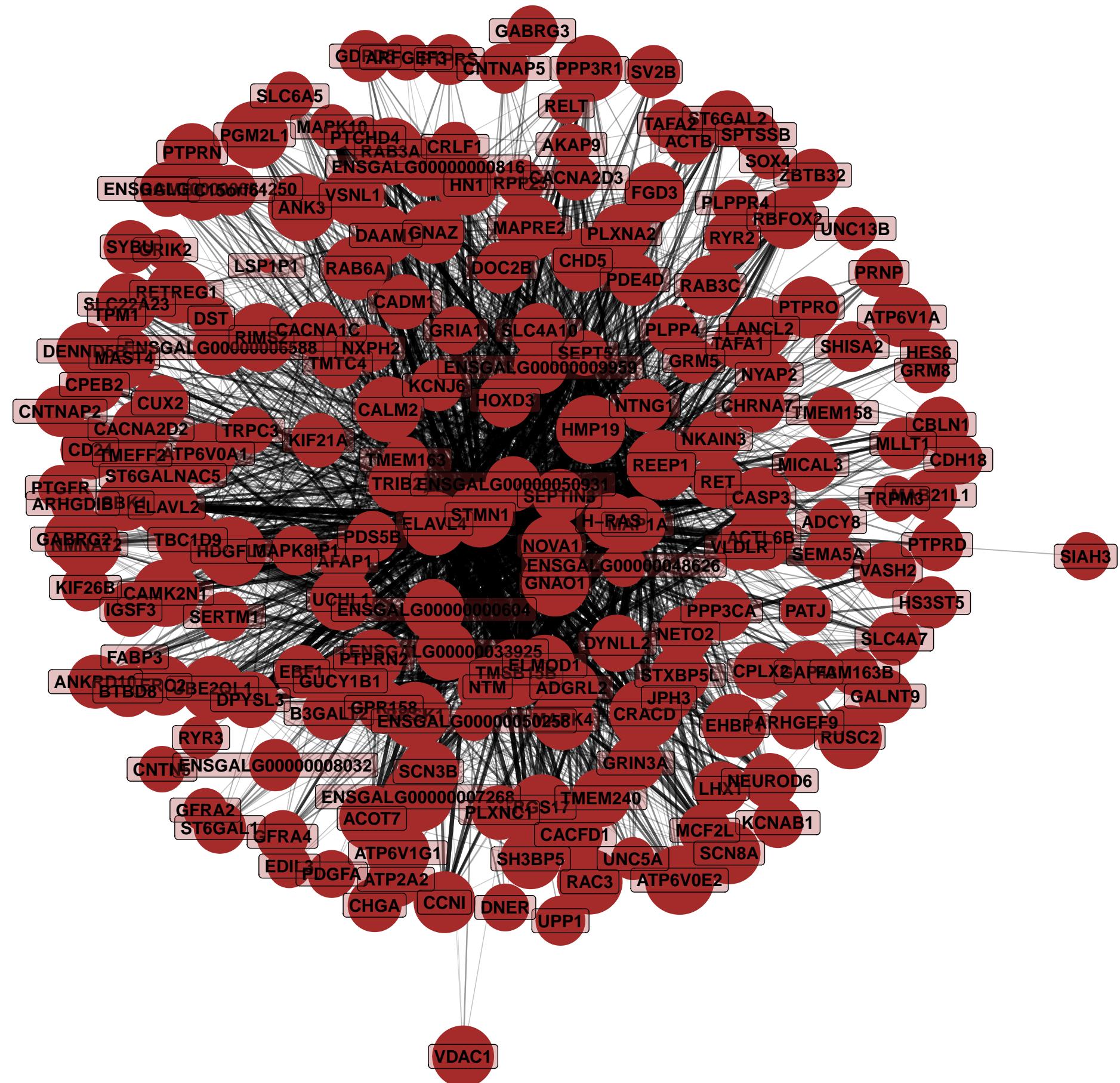
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<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	275	15	6.138e–08
<i>path:gga04512</i>	ECM–receptor interaction	66	3	0.02586
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.03806
<i>path:gga04514</i>	Cell adhesion molecules	99	3	0.07073
<i>path:gga00360</i>	Phenylalanine metabolism	11	1	0.1012
<i>path:gga04920</i>	Adipocytokine signaling pathway	58	2	0.1079
<i>path:gga00061</i>	Fatty acid biosynthesis	16	1	0.1438
<i>path:gga00340</i>	Histidine metabolism	17	1	0.1521
<i>path:gga00350</i>	Tyrosine metabolism	23	1	0.2001
<i>path:gga04510</i>	Focal adhesion	169	3	0.2237



1	DIO2	ANGPT4	ACE	HIC1	FN1	GYPC	COL1A1	RGS5
2	KCNJ8	ACTA2	TBX2	GGT5	SPON2	GPER1	ITGA4	LAMB1
3	CYP1B1	IGFBP7	ENSGALG00000012847	ENSGALG00000012021	MXRA8	FOXF2	CA2	ENSGALG00000030902
4	LAMA4	MYL9	FLT1	ENSGALG0000007646	COLEC10	ARAP3	RBPM2	TMEM204
5	SLC40A1	ENSGALG0000000818	CALD1	RCSD1	ABCC9	ENSGALG0000045199	DOCK5	IRAG1
6	GJC2	CD200	ECRG4	ATP1B4	C1QTNF5	FHL5	PCDH18	CYGB
7	PEBP4	ETS1	FOXL3	ANO1	ACVRL1	INPP4B	ENSGALG00000023472	SPERT
8	DLC1	PTGES	NRK	ITGA7	RERGL	DCN	ADAMTS12	ARPC1B
9	ENSGALG0000045584	TBX3	EDNRA	PPFIBP2	SCARA5	NA	SLCO2B1	ADAMTS9
10	ENSGALG0000028174	ENSGALG0000034511	RGS4	UNC5B	EGR2	GEM	ENSGALG0000044632	ENSGALG0000003345
11	ANKRD22	TWIST1	PRRX2	KERA	CTLA4	DRP2	FRMD6	LMO2
12	RAPGEF5	ENSGALG0000026070	PLOD1	ADORA2A	CYTH3	DES	KCNE4	NID1
13	LRRC17	TGFB1	MGP	KRT23	AQP1	MMP10	NA	PRSS23
14	C1QTNF6	METTL24	ENSGALG0000046863	CPZ	ENSGALG0000012055	LAMB4	AKR1D1	MAOA
15	KANK3	ENSGALG0000052087	NA	DSEL	ENSGALG0000005257	KCNMB1	ENSGALG0000007710	SLC22A16
16	C1QTNF7	ENSGALG0000054937	CG-1B	COL5A2	TRPC6	ENSGALG0000050332	TBXA2R	EGFR
17	ENSGALG0000002326	CALHM2	COL6A2	CPED1	LEF1	TBX18	LRRC15	GASK1B
18	GAS2	ARHGAP25	EGFLAM	ARHGAP31	COL3A1	ZFHX3	MMP2	ST8SIA4
19	PRTG	S100A11	SLC16A12	CPM	HOXD8	ENSGALG0000028016	ENSGALG0000054678	TNNT3
20	WFDC1	OTOGL	CYP4V2	COL6A1	ENSGALG0000001483	TCIM	DAAM2	GUCY1A2
21	GRAPL	RUNX2	ENSGALG0000027778	ENSGALG0000027159	PALM2AKAP2	SYTL2	SDC4	ENSGALG0000053107
22	HLX	HOXD9	ARHGAP6	CLEC3B	STX19	RASSF3	WNT4	COLEC11
23	LMO7	CA9	RFLNB	DACH2	LYVE1	CMKLR1	RHOH	MGLL
24	GPRC5C	ENSGALG0000032803	TGM2v1	GCNT7	SLC16A4	EDNRB2	ANPEP	ENSGALG0000006900
25	ENSGALG0000046720	ENSGALG0000034349	ENSGALG0000047721	SSPN	APBB1IP	PDZRN3	SP5	COL13A1
26	ENSGALG0000026154	SELENOP1	MEOX2	TNFAIP2	ACTG2	ACKR2	ENSGALG0000007698	CX3CL1
27	ENSGALG0000041909	ENSGALG0000000720	PDK4	ENSGALG0000004113	MYH11	FLNA	ENSGALG00000047706	

	Term	Ont	N	n	Adj. p-value
GO:0048856	anatomical structure development	BP	602	30	1.657e-08
GO:0032502	developmental process	BP	634	30	5.293e-08
GO:0009653	anatomical structure morphogenesis	BP	286	17	2.547e-06
GO:0061061	muscle structure development	BP	63	8	5.794e-06
GO:0007275	multicellular organism development	BP	559	24	6.958e-06
GO:0032501	multicellular organismal process	BP	686	27	8.863e-06
GO:0048513	animal organ development	BP	311	16	3.07e-05
GO:0033002	muscle cell proliferation	BP	15	4	6.939e-05
GO:0022610	biological adhesion	BP	142	10	7.792e-05
GO:0007155	cell adhesion	BP	142	10	7.792e-05

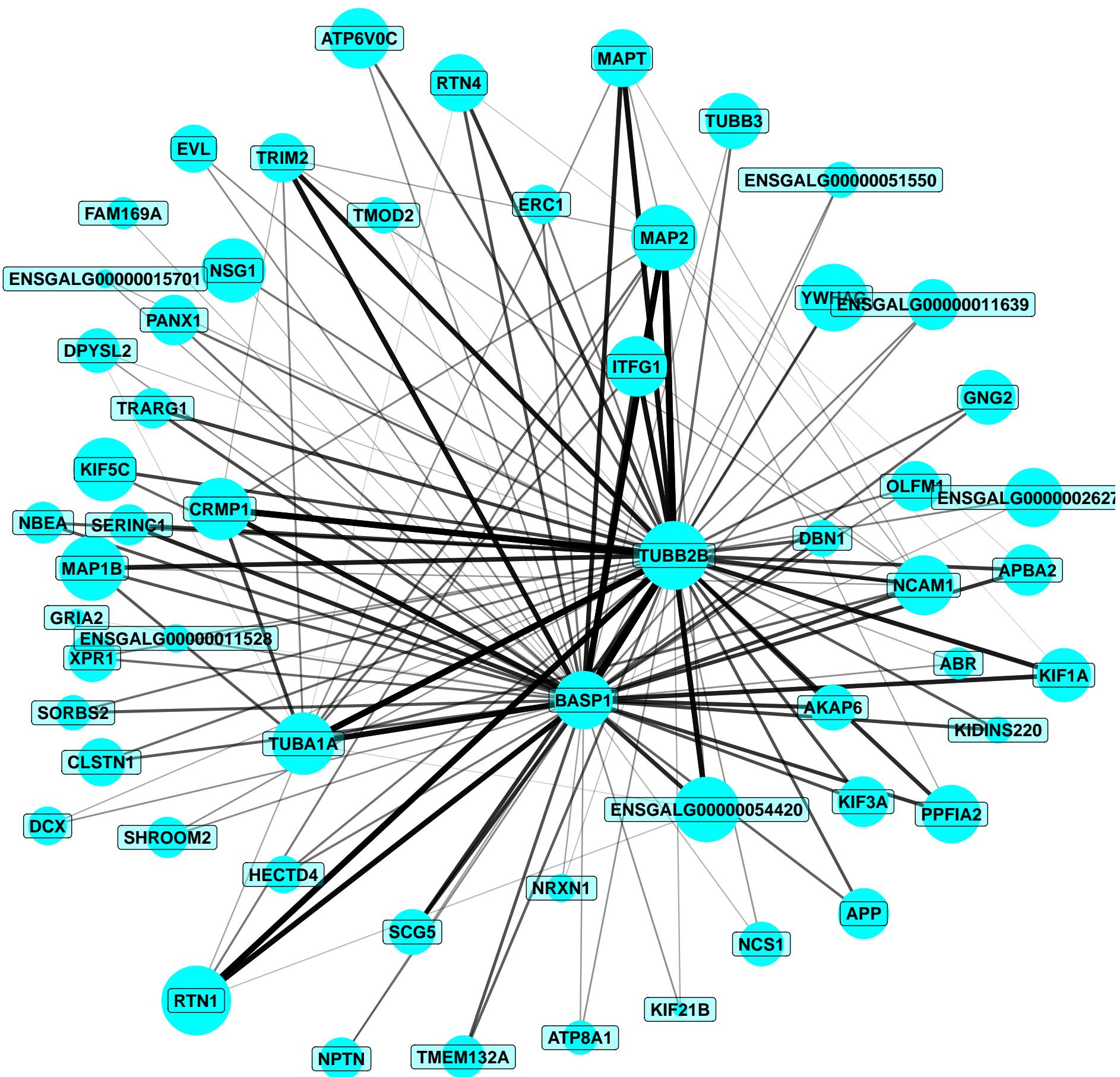
	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	66	10	6.93e–08
<i>path:gga04510</i>	Focal adhesion	169	14	4.09e–07
<i>path:gga04270</i>	Vascular smooth muscle contraction	102	10	4.293e–06
<i>path:gga04520</i>	Adherens junction	69	5	0.004461
<i>path:gga00120</i>	Primary bile acid biosynthesis	11	2	0.01221
<i>path:gga00910</i>	Nitrogen metabolism	13	2	0.01697
<i>path:gga04810</i>	Regulation of actin cytoskeleton	180	7	0.02316
<i>path:gga04020</i>	Calcium signaling pathway	191	7	0.03067
<i>path:gga04010</i>	MAPK signaling pathway	236	8	0.03233
<i>path:gga04672</i>	Intestinal immune network for IgA production	22	2	0.04585



1	HMP19	BRSK1	ENSGALG00000007268	CRACD	ANK3	ELAVL4	ATP6V0E2	RAB3C
2	RIMS2	NMNAT2	CAMK2N1	RAB3A	ACTL6B	PGM2L1	CHGA	GAP43
3	REEP1	DPYSL3	GNAO1	ACOT7	HDGFL3	TMSB15B	ENSGALG00000054250	RUSC2
4	MAST4	TMEFF2	CD24	EHBP1	UBE2QL1	ELAVL2	RGS17	CALM2
5	MAPRE2	ELMOD1	RGMB	UCHL1	STMN1	SEPT5	RETREG1	PTPRO
6	NEUROD6	PPP3R1	TBC1D9	PLXNA2	SH3BP5	GALNT9	MAP1A	SCN8A
7	MAPK4	VDAC1	NOVA1	GNAZ	RBFOX2	SLC22A23	RAC3	ENSGALG0000000816
8	LANCL2	IGSF3	RAB6A	SCN3B	LHX1	ENSGALG0000000604	VSNL1	CACNA2D2
9	CHD5	ATP6V0A1	DYNLL2	FABP3	PTPRN2	TMEM240	HN1	CCNI
10	NTM	GABRG2	CPEB2	PTPRN	CACFD1	PLXNC1	FGD3	CPLX2
11	CBLN1	ERC2	PPP3CA	TRIB2	CASP3	ST6GAL2	ATP6V1A	PTPRD
12	ZBTB32	CACNA1C	DENND5B	SEPTIN3	GRIN3A	ATP6V1G1	MAB21L1	ENSGALG00000033925
13	AFAP1	RET	BTBD8	EBF1	VASH2	DAAM1	SYBU	SBK1
14	ENSGALG0000009959	STXBP5L	ENSGALG0000006588	KIF21A	GDPD5	HOXD3	CUX2	ANKRD10
15	SLC4A10	ENSGALG00000050931	B3GALT2	GUCY1B1	SV2B	MICAL3	ACTB	MAPK10
16	KCNAB1	RYR2	GFRA4	PDE4D	SLC4A7	NETO2	NKAIN3	ARHGEF9
17	MAPK8IP1	NTNG1	GRIA1	SERTM1	DOC2B	ST6GAL1	MCF2L	GRM5
18	MLLT1	H-RAS	ATP2A2	CADM1	ADGRL2	CHRNA7	GPR158	TAFA1
19	KCNJ6	SHISA2	TMTC4	C15orf61	ENSGALG0000008032	CRLF1	GABRG3	TMEM158
20	HES6	RPP25	UNC13B	PATJ	PRNP	HS3ST5	ST6GALNAC5	PTPRS
21	CNTNAP2	SEMA5A	JPH3	NYAP2	SLC6A5	NXPH2	ARHGDI	PDS5B
22	CNTNAP5	DNER	PDGFA	DST	CDH18	PTGFR	LSP1P1	UPP1
23	CACNA2D3	TAFA2	KIF26B	PLPP4	GFRA2	SPTSSB	VLDLR	GRIK2
24	CNTN5	PLPPR4	TMEM163	AKAP9	PTCHD4	ARFGEF3	FAM163B	RYR3
25	UNC5A	ENSGALG00000050258	TPM1	SIAH3	TRPC3	TRPM3	EDIL3	SOX4
26	RELT	GRM8	ADCY8	ENSGALG00000048626				

	Term	Ont	N	n	Adj. p-value
GO:0098660	inorganic ion transmembrane transport	BP	59	7	3.325e–05
GO:0030003	cellular cation homeostasis	BP	51	6	0.0001293
GO:0006873	cellular ion homeostasis	BP	51	6	0.0001293
GO:0098662	inorganic cation transmembrane transport	BP	54	6	0.0001784
GO:0055080	cation homeostasis	BP	55	6	0.0001976
GO:0098771	inorganic ion homeostasis	BP	55	6	0.0001976
GO:0050801	ion homeostasis	BP	55	6	0.0001976
GO:0055082	cellular chemical homeostasis	BP	56	6	0.0002185
GO:0034220	ion transmembrane transport	BP	105	8	0.0002226
GO:0006812	cation transport	BP	81	7	0.0002544

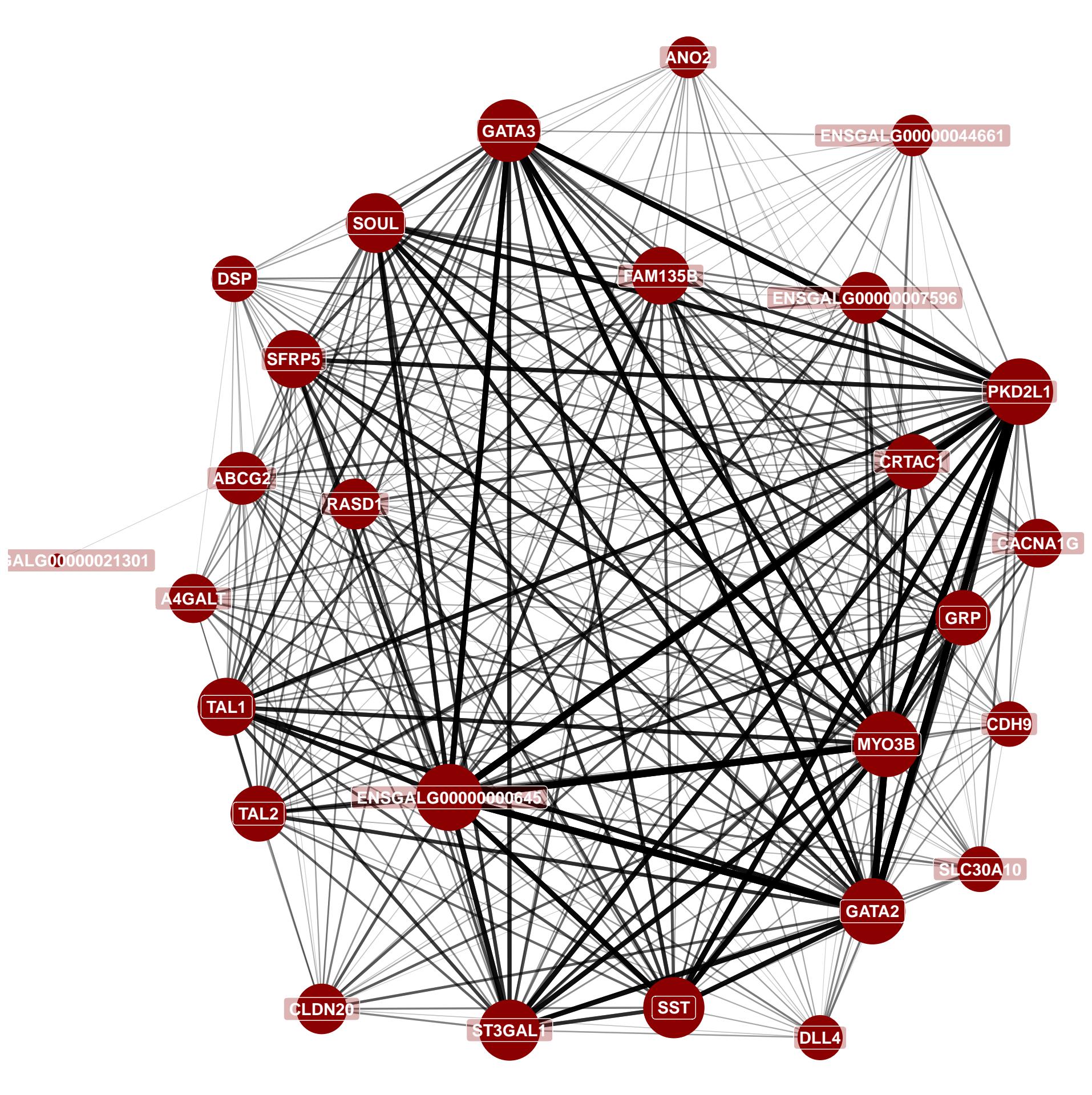
	Pathway	N	DE	P.DE
<i>path:gga04020</i>	Calcium signaling pathway	191	14	1.591e-06
<i>path:gga04260</i>	Cardiac muscle contraction	58	6	0.0002655
<i>path:gga04010</i>	MAPK signaling pathway	236	12	0.0003117
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	118	8	0.0004922
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	80	6	0.001488
<i>path:gga04912</i>	GnRH signaling pathway	73	5	0.005439
<i>path:gga04540</i>	Gap junction	78	5	0.007185
<i>path:gga04370</i>	VEGF signaling pathway	52	4	0.008474
<i>path:gga04114</i>	Oocyte meiosis	94	5	0.01534
<i>path:gga04514</i>	Cell adhesion molecules	99	5	0.0188



1	RTN1	YWHAG	TUBB3	TUBB2B	KIF5C	NSG1	MAP2	ENSGALG00000054420
2	TUBA1A	TRARG1	MAP1B	OLFM1	ATP6V0C	BASP1	ITFG1	PPFIA2
3	CRMP1	APP	ENSGALG00000026278	NCAM1	GNG2	MAPT	TRIM2	KIF1A
4	DPYSL2	RTN4	AKAP6	SCG5	EVL	CLSTN1	ENSGALG00000011639	XPR1
5	APBA2	PANX1	NPTN	KIDINS220	NCS1	DBN1	ATP8A1	SERINC1
6	SHROOM2	KIF3A	TMEM132A	NRXN1	DCX	NBEA	SORBS2	TMOD2
7	GRIA2	ENSGALG00000051550	ENSGALG00000015701	ABR	KIF21B	HECTD4	ERC1	FAM169A
8	ENSGALG00000011528							

	Term	Ont	N	n	Adj. p-value
GO:0030516	regulation of axon extension	BP	14	3	2.762e-05
GO:0048675	axon extension	BP	16	3	4.222e-05
GO:0061387	regulation of extent of cell growth	BP	18	3	6.114e-05
GO:1990138	neuron projection extension	BP	19	3	7.239e-05
GO:0008361	regulation of cell size	BP	19	3	7.239e-05
GO:0031175	neuron projection development	BP	110	5	0.0001134
GO:0048699	generation of neurons	BP	177	6	0.0001153
GO:0022008	neurogenesis	BP	180	6	0.0001265
GO:0060560	developmental growth involved in morphogenesis	BP	26	3	0.0001901
GO:0007409	axonogenesis	BP	66	4	0.000191

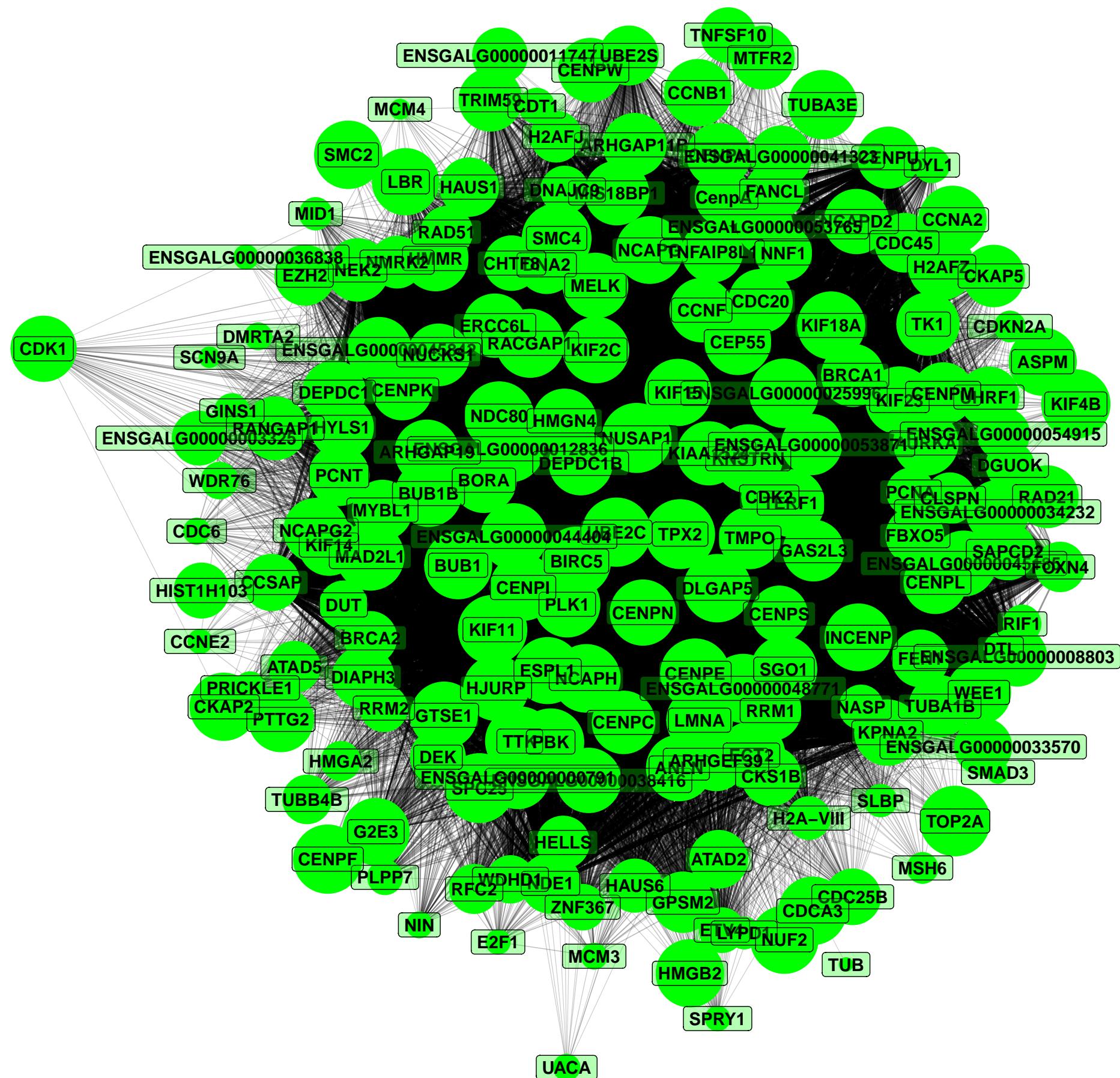
	Pathway	N	DE	P.DE
<i>path:gga04145</i>	Phagosome	121	5	0.0001777
<i>path:gga05132</i>	Salmonella infection	218	6	0.0003569
<i>path:gga04540</i>	Gap junction	78	4	0.0003637
<i>path:gga03267</i>	Virion – Adenovirus	3	1	0.01302
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.01733
<i>path:gga04514</i>	Cell adhesion molecules	99	2	0.06925
<i>path:gga04340</i>	Hedgehog signaling pathway	47	1	0.1859
<i>path:gga03250</i>	Viral life cycle – HIV-1	47	1	0.1859
<i>path:gga04114</i>	Oocyte meiosis	94	1	0.3378
<i>path:gga00190</i>	Oxidative phosphorylation	100	1	0.3551



1	PKD2L1	GATA2	GATA3	MYO3B	ENSGALG0000000645	GRP	SFRP5	TAL1
2	TAL2	CRTAC1	ST3GAL1	SOUL	FAM135B	ABCG2	ENSGALG0000007596	SST
3	CLDN20	CACNA1G	A4GALT	ENSGALG0000044661	RASD1	DLL4	SLC30A10	ANO2
4	CDH9	DSP	ENSGALG0000021301					

	Term	Ont	N	n	Adj. p-value
GO:0072577	endothelial cell apoptotic process	BP	4	2	2.177e-05
GO:2000352	negative regulation of endothelial cell apoptotic process	BP	4	2	2.177e-05
GO:1904036	negative regulation of epithelial cell apoptotic process	BP	4	2	2.177e-05
GO:0045599	negative regulation of fat cell differentiation	BP	4	2	2.177e-05
GO:2000351	regulation of endothelial cell apoptotic process	BP	4	2	2.177e-05
GO:1904035	regulation of epithelial cell apoptotic process	BP	4	2	2.177e-05
GO:0035162	embryonic hemopoiesis	BP	5	2	3.624e-05
GO:1902895	positive regulation of pri-miRNA transcription by RNA polymerase II	BP	5	2	3.624e-05
GO:0035065	regulation of histone acetylation	BP	5	2	3.624e-05
GO:2000756	regulation of peptidyl-lysine acetylation	BP	5	2	3.624e-05

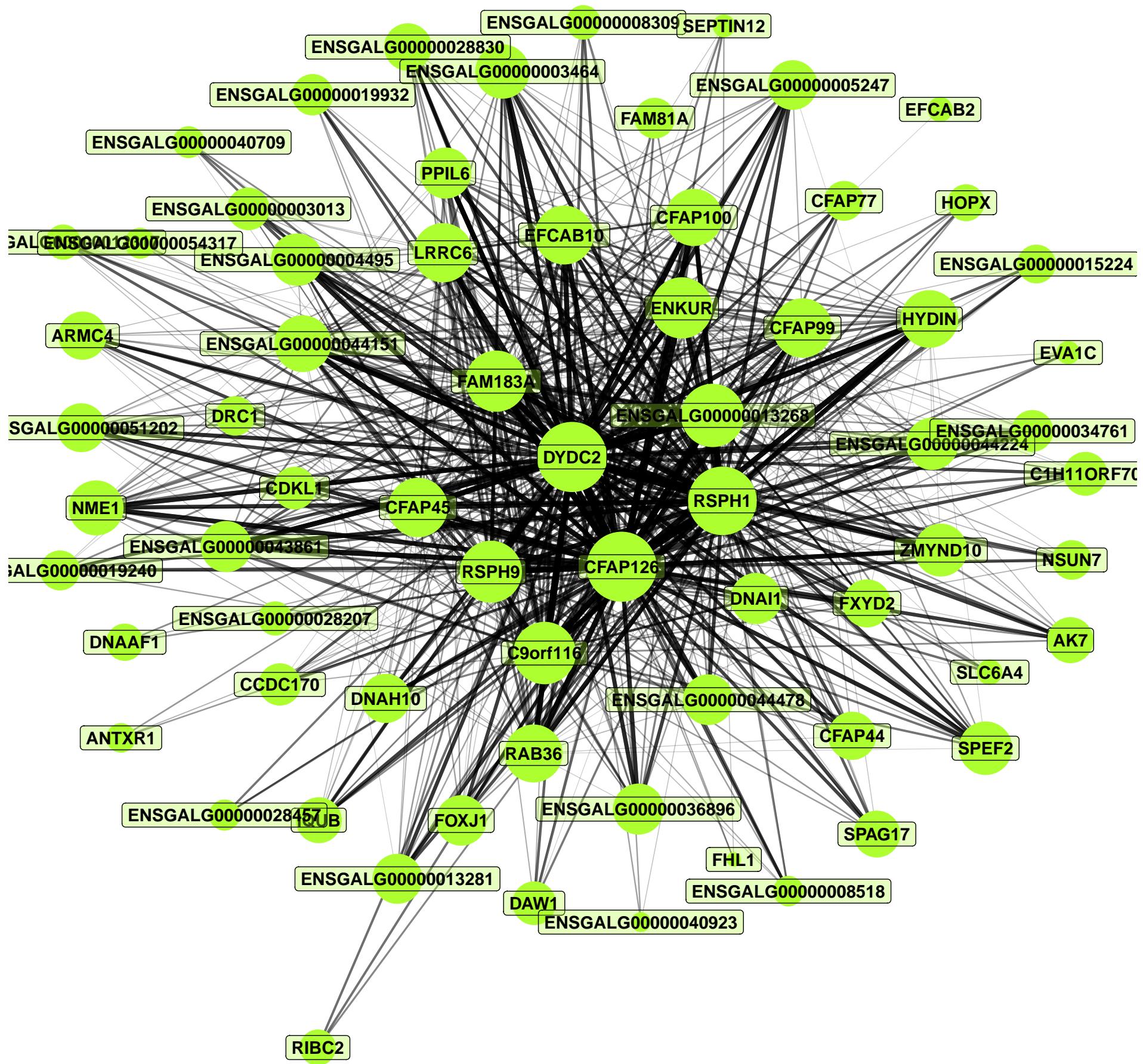
	Pathway	N	DE	P.DE
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	2	0.0002372
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	275	3	0.01576
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	1	0.02502
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.02692
<i>path:gga00601</i>	Glycosphingolipid biosynthesis – lacto and neolacto series	21	1	0.04012
<i>path:gga00512</i>	Mucin type O–glycan biosynthesis	29	1	0.05499
<i>path:gga02010</i>	ABC transporters	34	1	0.06417
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.09653
<i>path:gga04514</i>	Cell adhesion molecules	99	1	0.176
<i>path:gga04142</i>	Lysosome	113	1	0.1984



1	NUSAP1	TOP2A	CENPE	TPX2	SMC2	CENPF	ENSGALG00000025996	UBE2C
2	KIF11	SMC4	NDC80	KIF4B	RACGAP1	BIRC5	SPC25	ENSGALG00000048771
3	KNSTRN	TTK	ASPM	INCENP	KIF15	KPNA2	DLGAP5	NUF2
4	BUB1	KIF23	CDCA3	TUBA3E	ECT2	GTSE1	ENSGALG00000012836	PLK1
5	CKAP2	AURKA	KIF18A	NCAPG	NCAPH	ANLN	BUB1B	CDK1
6	MAD2L1	PBK	CCNB1	CENPI	CCNA2	CENPW	KIF2C	HMGB2
7	SGO1	TK1	ENSGALG00000044404	TERF1	ENSGALG00000045185	CEP55	BRCA1	ENSGALG00000038416
8	HMMR	PTTG2	CDC20	G2E3	ESPL1	UHRF1	HJURP	BORA
9	ARHGAP11B	CENPH	CENPN	ENSGALG00000045842	NCAPD2	LBR	ERCC6L	CENPL
10	NCAPG2	MIS18BP1	MELK	KIAA1524	LMNA	NEK2	CCNF	WEE1
11	H2AFZ	ENSGALG0000000791	HMGN4	CENPC	DEPDC1	DEPDC1B	DIAPH3	ARHGAP19
12	CENPK	CENPM	RRM1	ENSGALG00000034232	MTFR2	HAUS1	CDC45	ENSGALG00000011747
13	KIF14	HYLS1	TRIM59	ENSGALG00000053871	GAS2L3	FANCL	CENPU	TUBA1B
14	DNA2	TNFAIP8L1	ENSGALG00000041323	MYBL1	TMPO	CDK2	HIST1H103	RANGAP1
15	NUCKS1	GPSM2	CKS1B	FEN1	ATAD2	NDE1	CHTF8	ARHGEF39
16	NMRK2	RRM2	HELLS	DGUOK	RAD21	EZH2	CENPS	FBXO5
17	ENSGALG00000008803	CenpA	UBE2S	PCNT	SAPCD2	RAD51	NNF1	BRCA2
18	CKAP5	DEK	ENSGALG00000033570	PCNA	ATAD5	ENSGALG00000053765	HAUS6	ENSGALG00000054915
19	WDHD1	RFC2	CLSPN	DUT	CDC25B	CCSAP	TNFSF10	H2AFJ
20	NASP	DNAJC9	ENSGALG0000003325	TUBB4B	ZNF367	DYL1	FOXN4	ETV4
21	GINS1	H2A-VIII	RIF1	CDT1	WDR76	SLBP	HMGA2	DTL
22	LYPD1	MSH6	PLPP7	MCM3	CDC6	NIN	E2F1	MID1
23	DMRTA2	PRICKLE1	SPRY1	CCNE2	MCM4	SCN9A	SMAD3	UACA
24	CDKN2A	TUB	ENSGALG00000036838					

	Term	Ont	N	n	Adj. p-value
GO:0000278	mitotic cell cycle	BP	99	22	1.483e-20
GO:0007049	cell cycle	BP	201	28	4.292e-20
GO:0051276	chromosome organization	BP	174	26	1.685e-19
GO:0022402	cell cycle process	BP	127	22	4.574e-18
GO:1903047	mitotic cell cycle process	BP	78	18	2.538e-17
GO:0051383	kinetochore organization	BP	10	8	6.396e-14
GO:0006996	organelle organization	BP	430	31	6.658e-14
GO:0007059	chromosome segregation	BP	43	12	5.081e-13
GO:0065004	protein-DNA complex assembly	BP	36	10	4.966e-11
GO:0034508	centromere complex assembly	BP	12	7	7.922e-11

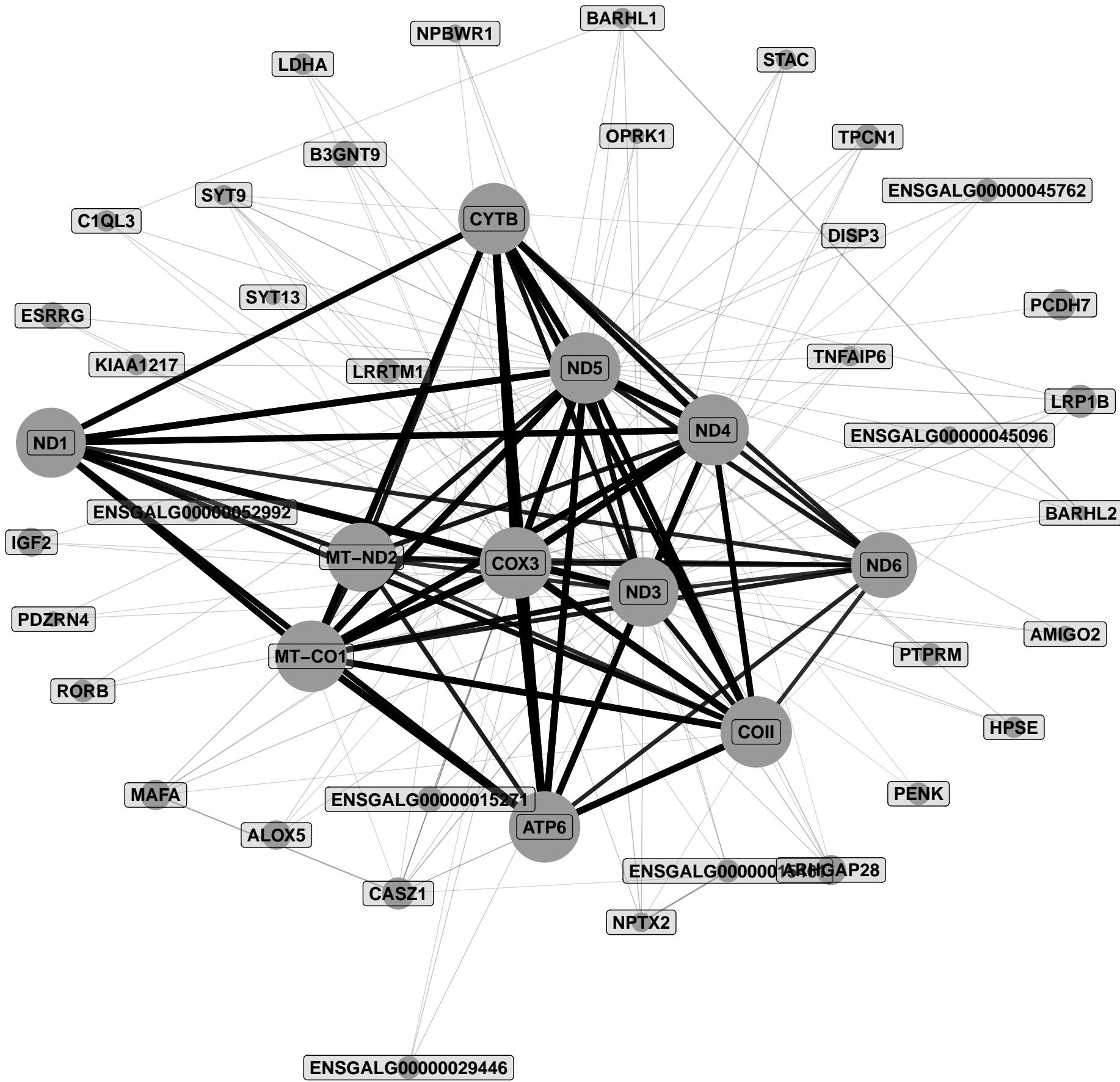
	Pathway	N	DE	P.DE
<i>path:gga04110</i>	Cell cycle	113	23	1.622e-20
<i>path:gga04114</i>	Oocyte meiosis	94	13	7.159e-10
<i>path:gga04914</i>	Progesterone-mediated oocyte maturation	78	9	1.555e-06
<i>path:gga03030</i>	DNA replication	29	6	2.787e-06
<i>path:gga04115</i>	p53 signaling pathway	63	6	0.0002669
<i>path:gga03460</i>	Fanconi anemia pathway	48	5	0.0005792
<i>path:gga00240</i>	Pyrimidine metabolism	55	5	0.001086
<i>path:gga03430</i>	Mismatch repair	19	3	0.00233
<i>path:gga04218</i>	Cellular senescence	132	7	0.002808
<i>path:gga01232</i>	Nucleotide metabolism	76	5	0.004539



1	CFAP126	DYDC2	RSPH1	ENSGALG00000013268	FAM183A	ENKUR	RSPH9	RAB36
2	C9orf116	CFAP99	FOXJ1	CFAP45	CFAP100	PPIL6	LRRC6	ENSGALG00000044151
3	EFCAB10	ENSGALG0000003464	HYDIN	ENSGALG00000044478	SPEF2	ENSGALG00000044224	ZMYND10	ENSGALG00000013281
4	FXYD2	ENSGALG00000043861	DNAI1	ENSGALG0000004495	NME1	DNAH10	ARMC4	CFAP44
5	DAW1	AK7	ENSGALG00000036896	SPAG17	ENSGALG00000051202	ENSGALG00000019932	ENSGALG00000005247	CDKL1
6	IQUB	HOPX	ENSGALG00000034761	ENSGALG0000003013	ENSGALG00000028830	CFAP77	ENSGALG00000015224	FAM81A
7	CCDC170	RIBC2	DRC1	ENSGALG00000028207	ENSGALG00000012317	FHL1	DNAAF1	ANTXR1
8	C1H11ORF70	ENSGALG0000008309	ENSGALG00000019240	ENSGALG00000054317	EFCAB2	ENSGALG0000008518	ENSGALG00000040709	NSUN7
9	ENSGALG00000028457	SEPTIN12	EVA1C	SLC6A4	ENSGALG00000040923			

	Term	Ont	N	n	Adj. p-value
GO:0043415	positive regulation of skeletal muscle tissue regeneration	BP	2	1	0.009476
GO:0043416	regulation of skeletal muscle tissue regeneration	BP	2	1	0.009476
GO:0051131	chaperone-mediated protein complex assembly	BP	3	1	0.01418
GO:0043403	skeletal muscle tissue regeneration	BP	6	1	0.02816
GO:0016575	histone deacetylation	BP	9	1	0.04195
GO:0006476	protein deacetylation	BP	9	1	0.04195
GO:0051155	positive regulation of striated muscle cell differentiation	BP	10	1	0.0465
GO:1903522	regulation of blood circulation	BP	10	1	0.0465
GO:0008016	regulation of heart contraction	BP	10	1	0.0465
GO:0051149	positive regulation of muscle cell differentiation	BP	11	1	0.05103

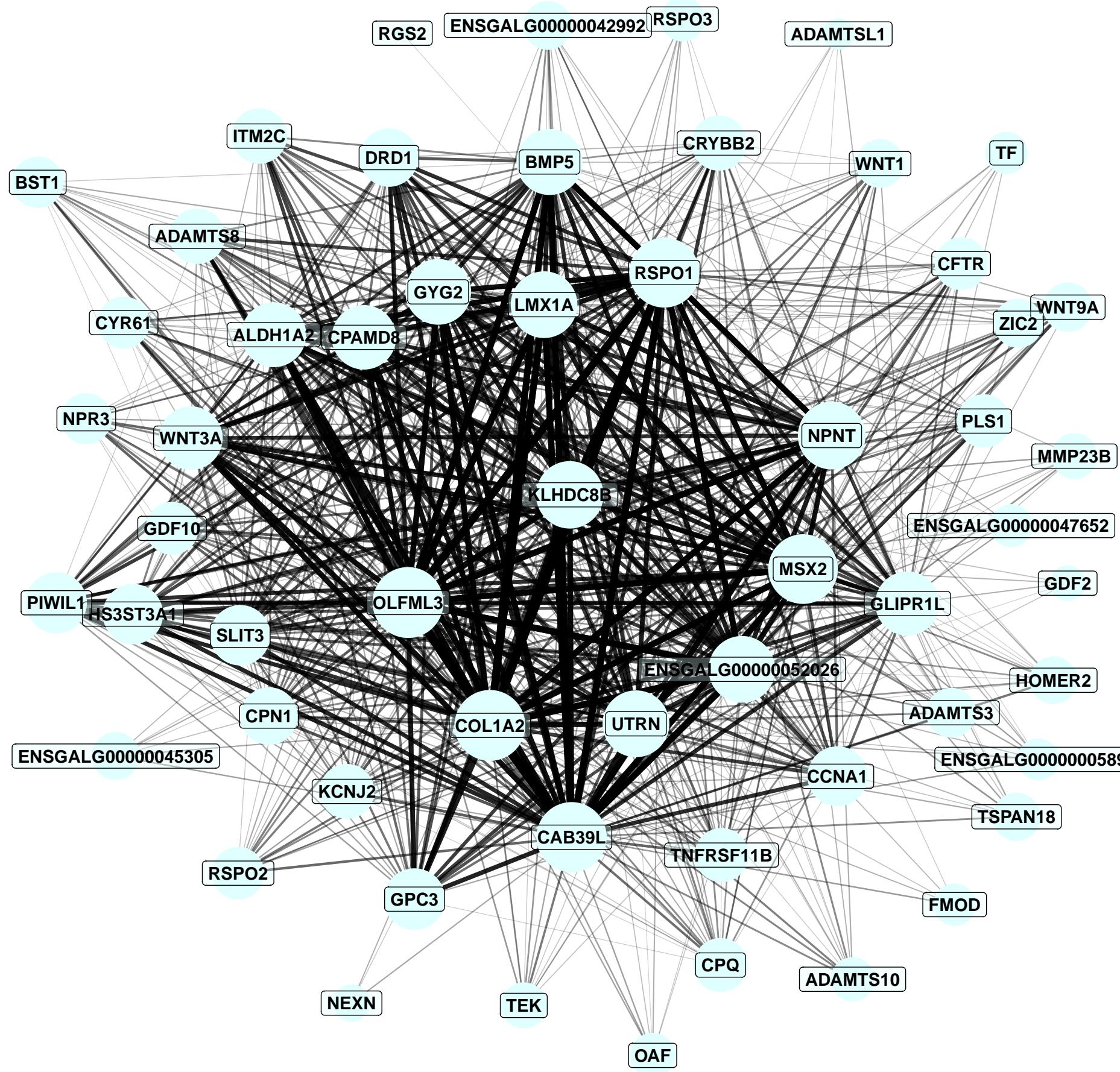
	Pathway	N	DE	P.DE
<i>path:gga01232</i>	Nucleotide metabolism	76	4	0.0004575
<i>path:gga00730</i>	Thiamine metabolism	12	2	0.00142
<i>path:gga00230</i>	Purine metabolism	111	4	0.001887
<i>path:gga01240</i>	Biosynthesis of cofactors	114	4	0.002081
<i>path:gga00240</i>	Pyrimidine metabolism	55	2	0.02804
<i>path:gga00910</i>	Nitrogen metabolism	13	1	0.06003
<i>path:gga00220</i>	Arginine biosynthesis	16	1	0.07338
<i>path:gga00630</i>	Glyoxylate and dicarboxylate metabolism	29	1	0.1291
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	1	0.1415
<i>path:gga00983</i>	Drug metabolism – other enzymes	52	1	0.2197



1	CYTB	COX3	MT-CO1	COII	ND5	ATP6	ND1	ND4
2	ND6	MT-ND2	ND3	LDHA	LRP1B	CASZ1	MAFA	LRRTM1
3	SYT9	TPCN1	STAC	DISP3	ESRRG	NPTX2	ENSGALG00000045762	B3GNT9
4	ENSGALG00000015461	PENK	PTPRM	C1QL3	ARHGAP28	IGF2	AMIGO2	ENSGALG00000045096
5	PCDH7	ENSGALG00000029446	ENSGALG00000015271	ALOX5	ENSGALG00000052992	PDZRN4	OPRK1	KIAA1217
6	TNFAIP6	SYT13	HPSE	BARHL1	BARHL2	NPBWR1	RORB	

	Term	Ont	N	n	Adj. p-value
GO:0031017	exocrine pancreas development	BP	1	1	0.002569
GO:0030200	heparan sulfate proteoglycan catabolic process	BP	1	1	0.002569
GO:0038028	insulin receptor signaling pathway via phosphatidylinositol 3-kinase	BP	1	1	0.002569
GO:2000467	positive regulation of glycogen (starch) synthase activity	BP	1	1	0.002569
GO:0048633	positive regulation of skeletal muscle tissue growth	BP	1	1	0.002569
GO:0030167	proteoglycan catabolic process	BP	1	1	0.002569
GO:2000465	regulation of glycogen (starch) synthase activity	BP	1	1	0.002569
GO:0006516	glycoprotein catabolic process	BP	2	1	0.005132
GO:1900078	positive regulation of cellular response to insulin stimulus	BP	2	1	0.005132
GO:0046628	positive regulation of insulin receptor signaling pathway	BP	2	1	0.005132

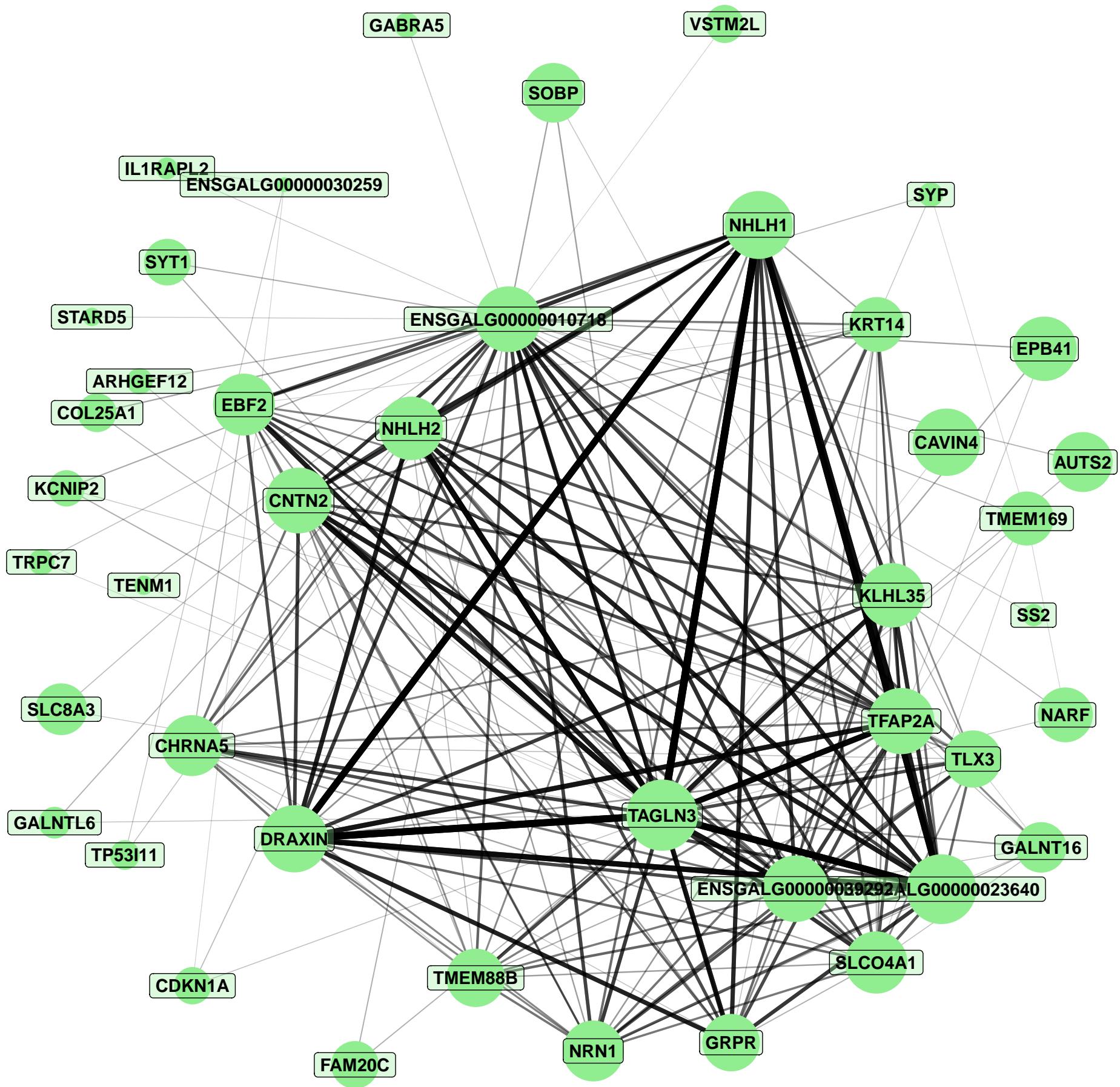
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	275	4	0.00516
<i>path:gga00531</i>	Glycosaminoglycan degradation	16	1	0.04035
<i>path:gga00640</i>	Propanoate metabolism	28	1	0.06957
<i>path:gga00620</i>	Pyruvate metabolism	33	1	0.08148
<i>path:gga00590</i>	Arachidonic acid metabolism	37	1	0.09091
<i>path:gga00270</i>	Cysteine and methionine metabolism	41	1	0.1002
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	47	1	0.1141
<i>path:gga04520</i>	Adherens junction	69	1	0.163
<i>path:gga04514</i>	Cell adhesion molecules	99	1	0.2256
<i>path:gga04020</i>	Calcium signaling pathway	191	1	0.3904



1	MSX2	OLFML3	COL1A2	RSPO1	CAB39L	LMX1A	ENSGALG00000052026	KLHDC8B
2	GLIPR1L	NPNT	UTRN	GYG2	BMP5	SLIT3	GPC3	ALDH1A2
3	WNT3A	CPAMD8	CCNA1	HS3ST3A1	PIWIL1	TNFRSF11B	GDF10	KCNJ2
4	ADAMTS8	NPR3	PLS1	CPN1	DRD1	CFTR	CRYBB2	TSPAN18
5	ENSGALG0000005896	CYR61	ZIC2	MMP23B	BST1	CPQ	TEK	ENSGALG00000045305
6	RSPO3	ADAMTSL1	ITM2C	RSPO2	ADAMTS3	ENSGALG00000042992	GDF2	TF
7	OAF	ADAMTS10	HOMER2	WNT9A	WNT1	ENSGALG00000047652	NEXN	RGS2
8	FMOD							

	Term	Ont	N	n	Adj. p-value
GO:0030509	BMP signaling pathway	BP	26	4	3.342e–06
GO:0071773	cellular response to BMP stimulus	BP	29	4	5.263e–06
GO:0071772	response to BMP	BP	29	4	5.263e–06
GO:0007275	multicellular organism development	BP	559	11	1.142e–05
GO:0009855	determination of bilateral symmetry	BP	13	3	1.739e–05
GO:0009799	specification of symmetry	BP	13	3	1.739e–05
GO:0048856	anatomical structure development	BP	602	11	2.284e–05
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	44	4	2.876e–05
GO:0032502	developmental process	BP	634	11	3.683e–05
GO:0032501	multicellular organismal process	BP	686	11	7.539e–05

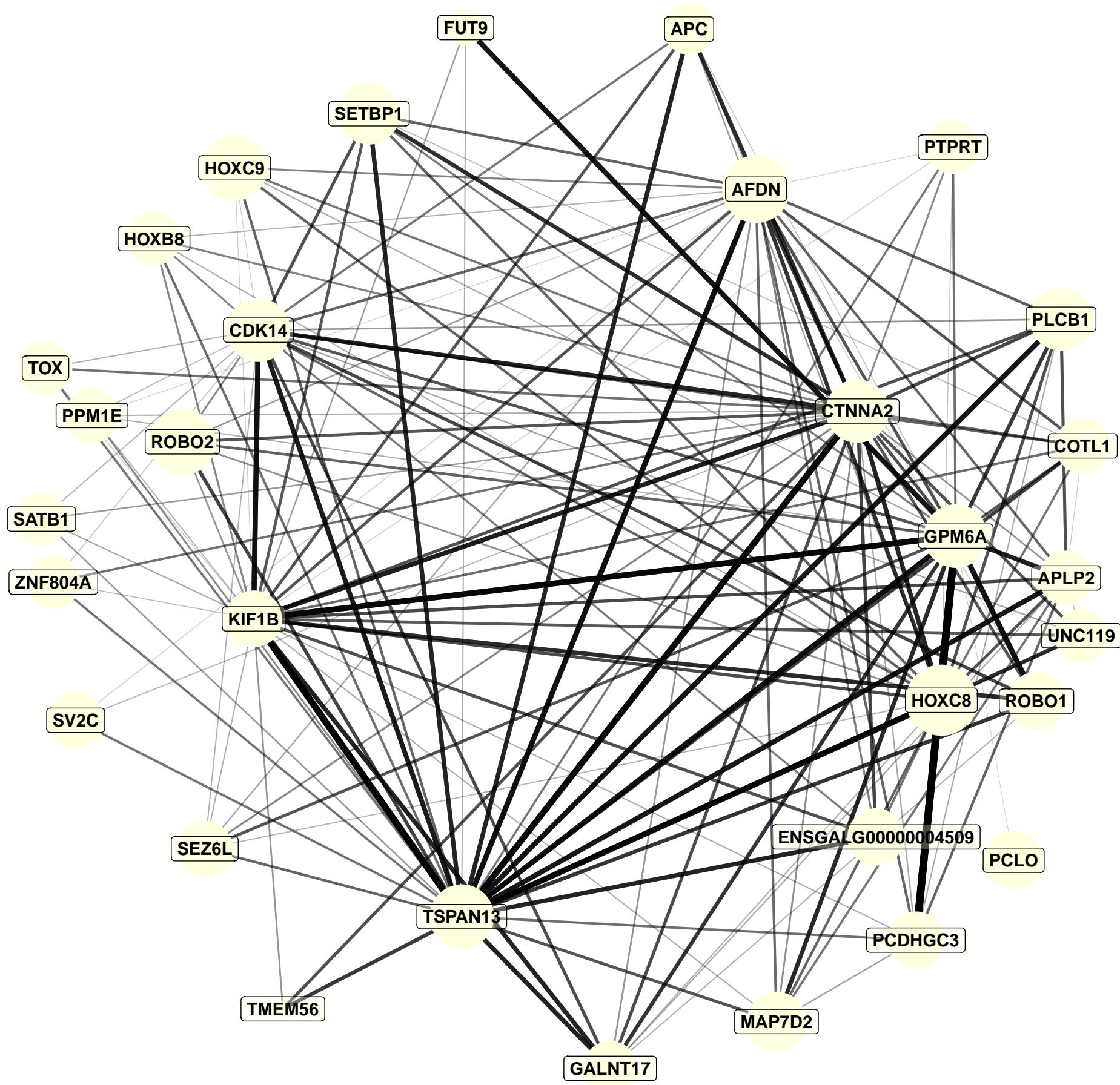
	Pathway	N	DE	P.DE
<i>path:gga04310</i>	Wnt signaling pathway	133	6	1.516e-05
<i>path:gga04150</i>	mTOR signaling pathway	133	4	0.002025
<i>path:gga04916</i>	Melanogenesis	82	3	0.004425
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	136	3	0.01759
<i>path:gga04512</i>	ECM–receptor interaction	66	2	0.02924
<i>path:gga04350</i>	TGF–beta signaling pathway	84	2	0.04539
<i>path:gga00910</i>	Nitrogen metabolism	13	1	0.05139
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis – heparan sulfate / heparin	21	1	0.08172
<i>path:gga00500</i>	Starch and sucrose metabolism	25	1	0.09653
<i>path:gga00830</i>	Retinol metabolism	27	1	0.1038



1	TAGLN3	NHLH1	CAVIN4	ENSGALG00000023640	DRAXIN	TFAP2A	CNTN2	ENSGALG0000010718
2	EBF2	NRN1	ENSGALG0000039292	SYT1	SLCO4A1	NHLH2	TLX3	AUTS2
3	EPB41	KLHL35	NARF	GRPR	KRT14	SOBP	SLC8A3	TMEM88B
4	TMEM169	CHRNA5	GALNT16	FAM20C	VSTM2L	COL25A1	SYP	KCNIP2
5	GALNTL6	CDKN1A	TP53I11	SS2	ARHGEF12	GABRA5	TENM1	TRPC7
6	ENSGALG0000030259	IL1RAPL2	STARD5					

	Term	Ont	N	n	Adj. p-value
GO:0048791	calcium ion-regulated exocytosis of neurotransmitter	BP	1	1	0.003114
GO:0021528	commissural neuron differentiation in spinal cord	BP	1	1	0.003114
GO:0014046	dopamine secretion	BP	1	1	0.003114
GO:0097090	presynaptic membrane organization	BP	1	1	0.003114
GO:0017158	regulation of calcium ion-dependent exocytosis	BP	1	1	0.003114
GO:0014059	regulation of dopamine secretion	BP	1	1	0.003114
GO:0006359	regulation of transcription by RNA polymerase III	BP	1	1	0.003114
GO:1903827	regulation of cellular protein localization	BP	37	2	0.005878
GO:0050432	catecholamine secretion	BP	2	1	0.006219
GO:0015872	dopamine transport	BP	2	1	0.006219

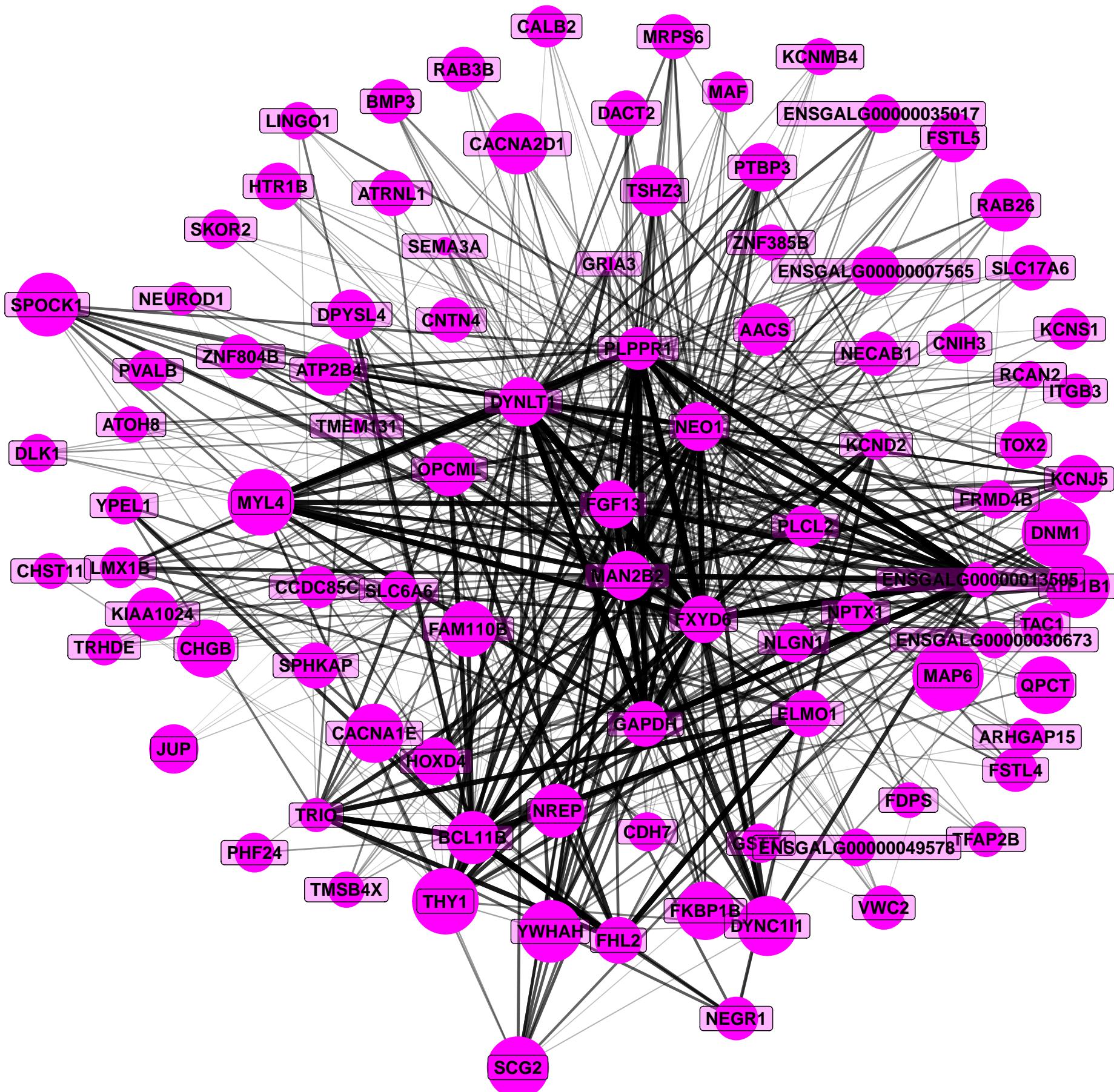
	Pathway	N	DE	P.DE
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	2	0.00364
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	2	0.007181
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	275	4	0.01026
<i>path:gga04020</i>	Calcium signaling pathway	191	2	0.119
<i>path:gga04260</i>	Cardiac muscle contraction	58	1	0.1658
<i>path:gga04115</i>	p53 signaling pathway	63	1	0.1788
<i>path:gga04012</i>	ErbB signaling pathway	76	1	0.2116
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	80	1	0.2214
<i>path:gga04514</i>	Cell adhesion molecules	99	1	0.2665
<i>path:gga04270</i>	Vascular smooth muscle contraction	102	1	0.2734



1	HOXC8	TSPAN13	GPM6A	CTNNA2	KIF1B	PCDHGC3	AFDN	COTL1
2	CDK14	SETBP1	PLCB1	APLP2	APC	MAP7D2	GALNT17	PTPRT
3	HOXC9	ROBO2	ENSGALG00000004509	ROBO1	UNC119	PCLO	SV2C	HOXB8
4	PPM1E	TOX	SEZ6L	ZNF804A	SATB1	TMEM56	FUT9	

	Term	Ont	N	n	Adj. p-value
GO:0034331	cell junction maintenance	BP	1	1	0.002491
GO:0048790	maintenance of presynaptic active zone structure	BP	1	1	0.002491
GO:0099558	maintenance of synapse structure	BP	1	1	0.002491
GO:0099054	presynapse assembly	BP	1	1	0.002491
GO:0099172	presynapse organization	BP	1	1	0.002491
GO:1904071	presynaptic active zone assembly	BP	1	1	0.002491
GO:1990709	presynaptic active zone organization	BP	1	1	0.002491
GO:0051823	regulation of synapse structural plasticity	BP	1	1	0.002491
GO:0050808	synapse organization	BP	36	2	0.003593
GO:0061551	trigeminal ganglion development	BP	2	1	0.004976

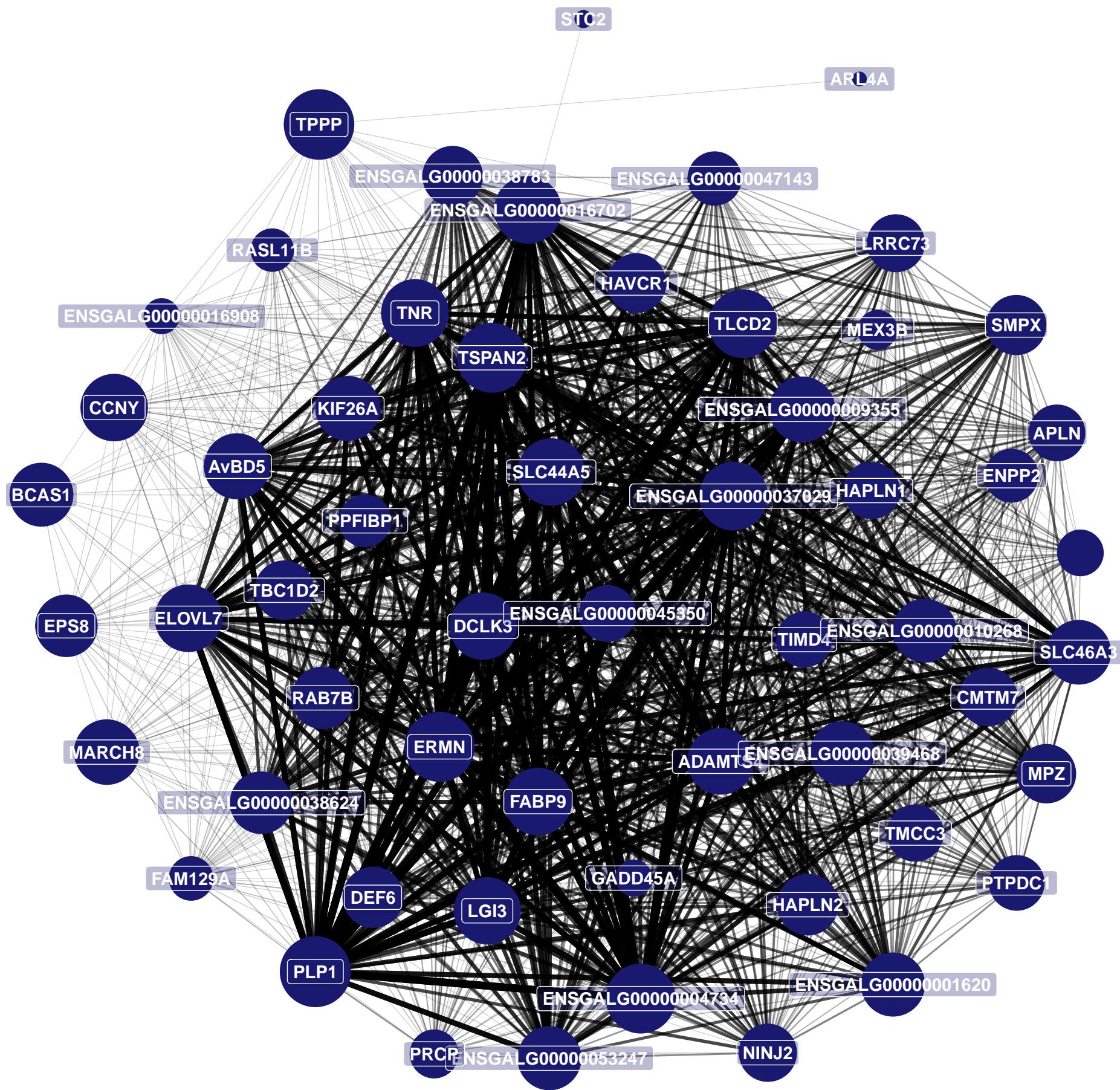
	Pathway	N	DE	P.DE
<i>path:gga04520</i>	Adherens junction	69	2	0.01271
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	1	0.0295
<i>path:gga04310</i>	Wnt signaling pathway	133	2	0.04311
<i>path:gga00601</i>	Glycosphingolipid biosynthesis – lacto and neolacto series	21	1	0.05107
<i>path:gga00515</i>	Mannose type O–glycan biosynthesis	22	1	0.05344
<i>path:gga00512</i>	Mucin type O–glycan biosynthesis	29	1	0.06986
<i>path:gga00514</i>	Other types of O–glycan biosynthesis	41	1	0.09736
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.1436
<i>path:gga04512</i>	ECM–receptor interaction	66	1	0.1521
<i>path:gga00562</i>	Inositol phosphate metabolism	66	1	0.1521



1	MAP6	CHGB	SCG2	MYL4	DNM1	SPOCK1	THY1	CACNA1E
2	ATP1B1	DYNC1I1	CACNA2D1	YWHAH	KIAA1024	FKBP1B	FXYD6	HTR1B
3	DPYSL4	FGF13	NREP	FAM110B	FSTL5	RAB26	QPCT	TSHZ3
4	ENSGALG00000007565	MAN2B2	FHL2	DYNLT1	PLPPR1	BCL11B	NEO1	CALB2
5	JUP	GAPDH	ENSGALG00000030673	SLC17A6	AACS	ATP2B4	KCNJ5	PTBP3
6	MRPS6	ELMO1	RAB3B	TAC1	OPCML	CNTN4	ARHGAP15	CCDC85C
7	SLC6A6	FRMD4B	NPTX1	ZNF804B	HOXD4	LINGO1	PVALB	SPHKAP
8	DACT2	LMX1B	ATRNL1	NLGN1	YPEL1	FSTL4	PLCL2	TRIO
9	TOX2	ENSGALG00000013505	ITGB3	TMSB4X	NEGR1	MAF	NECAB1	ATOH8
10	VWC2	PHF24	ENSGALG00000035017	BMP3	KCNS1	TRHDE	NEUROD1	SKOR2
11	KCNMB4	ZNF385B	GSTT1	KCND2	CDH7	SEMA3A	FDPS	ENSGALG00000049578
12	DLK1	TFAP2B	RCAN2	CNIH3	TMEM131	CHST11	GRIA3	

	Term	Ont	N	n	Adj. p-value
GO:0042462	eye photoreceptor cell development	BP	3	2	0.0001515
GO:0042461	photoreceptor cell development	BP	3	2	0.0001515
GO:0030182	neuron differentiation	BP	161	7	0.000153
GO:0000902	cell morphogenesis	BP	113	6	0.0001564
GO:0048666	neuron development	BP	123	6	0.0002485
GO:0048699	generation of neurons	BP	177	7	0.0002741
GO:0022008	neurogenesis	BP	180	7	0.0003036
GO:0055065	metal ion homeostasis	BP	47	4	0.0003473
GO:0007399	nervous system development	BP	255	8	0.0004777
GO:0055080	cation homeostasis	BP	55	4	0.0006358

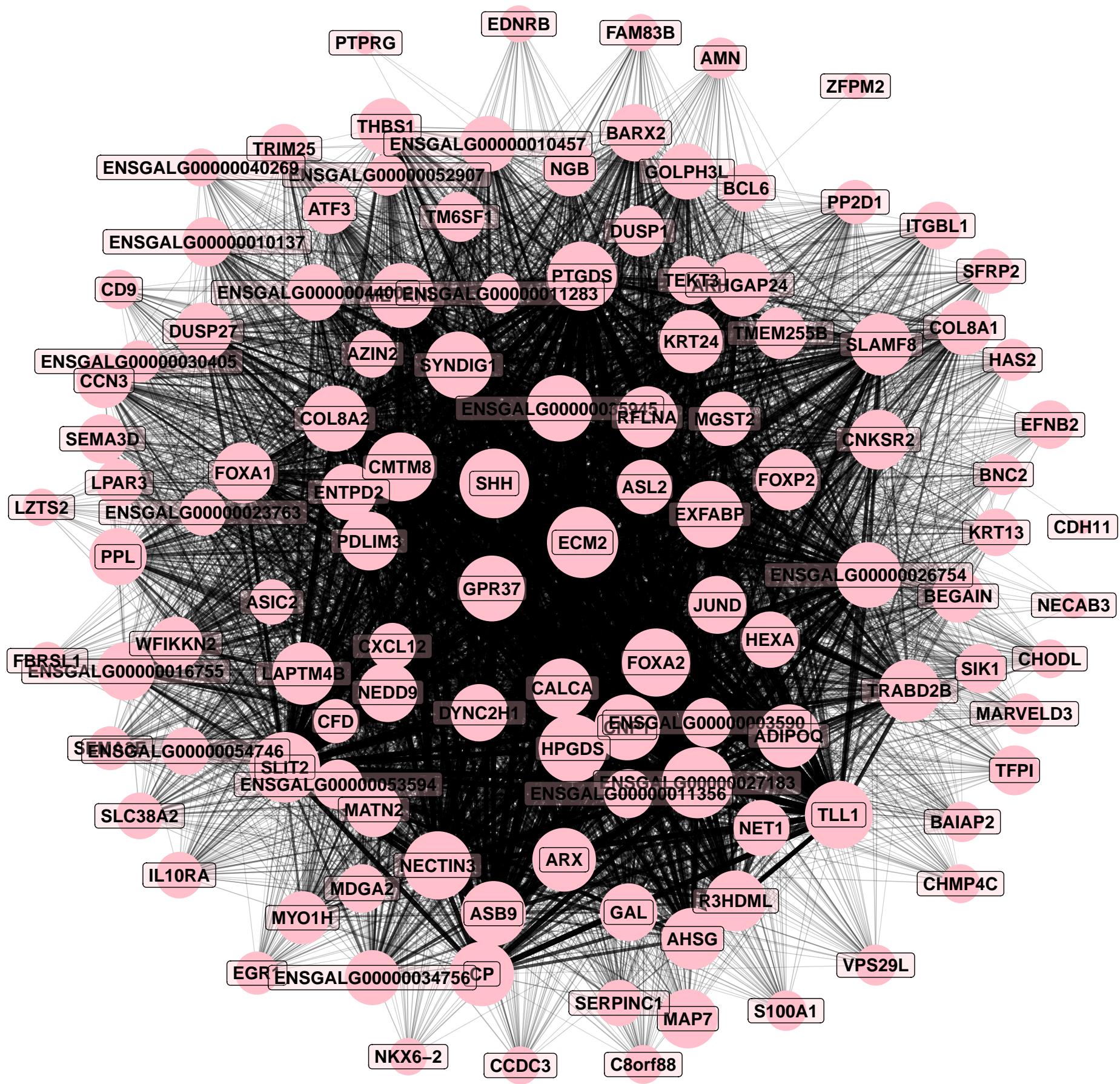
	Pathway	N	DE	P.DE
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	118	5	0.001564
<i>path:gga04260</i>	Cardiac muscle contraction	58	3	0.008257
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.02835
<i>path:gga04514</i>	Cell adhesion molecules	99	3	0.03406
<i>path:gga05132</i>	Salmonella infection	218	4	0.07125
<i>path:gga00511</i>	Other glycan degradation	17	1	0.1151
<i>path:gga00900</i>	Terpenoid backbone biosynthesis	19	1	0.1277
<i>path:gga00650</i>	Butanoate metabolism	21	1	0.1402
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	27	1	0.1766
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	28	1	0.1825



1	FABP9	ERMN	PLP1	ENSGALG00000004734	ENSGALG00000037029	TSPAN2	DCLK3	TLCD2
2	TPPP	ELOVL7	TNR	ADAMTS4	ENSGALG00000016702	ENSGALG0000009355	LGI3	SLC44A5
3	BCAS1	AvBD5	CCNY	KIF26A	SLC46A3	ENSGALG00000053247	ENSGALG00000010268	ENSGALG00000001620
4	HAVCR1	MARCH8	DEF6	ENSGALG00000038624	NINJ2	RAB7B	ENSGALG00000039468	SMPX
5	TMCC3	EPS8	LRRK73	MPZ	HAPLN2	TIMD4	TBC1D2	APLN
6	CMTM7	ENSGALG00000045350	ENSGALG00000038783	HAPLN1	ENSGALG00000047143	ENPP2	PTPDC1	PPFIBP1
7	PRCP	FAM129A	NA	RASL11B	GADD45A	MEX3B	ENSGALG00000016908	STC2
8	ARL4A							

	Term	Ont	N	n	Adj. p-value
GO:0008366	axon ensheathment	BP	12	2	0.001156
GO:0007272	ensheathment of neurons	BP	12	2	0.001156
GO:0042552	myelination	BP	12	2	0.001156
GO:0032291	axon ensheathment in central nervous system	BP	2	1	0.008546
GO:0022010	central nervous system myelination	BP	2	1	0.008546
GO:0014003	oligodendrocyte development	BP	2	1	0.008546
GO:0021782	glial cell development	BP	5	1	0.02123
GO:0022610	biological adhesion	BP	142	3	0.02284
GO:0007155	cell adhesion	BP	142	3	0.02284
GO:0007399	nervous system development	BP	255	4	0.02347

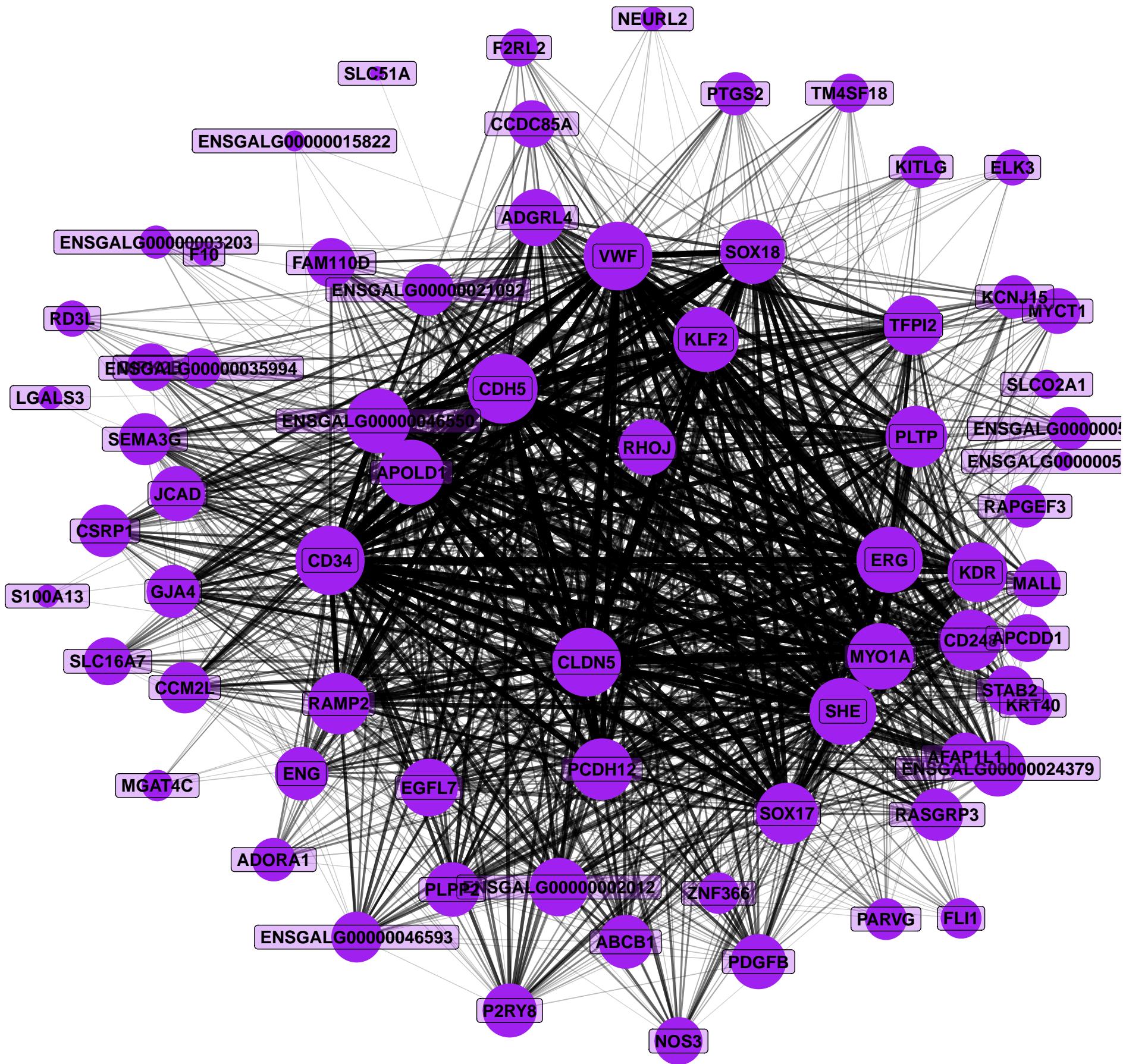
	Pathway	N	DE	P.DE
<i>path:gga03264</i>	Virion – Flavivirus	3	1	0.01279
<i>path:gga04514</i>	Cell adhesion molecules	99	2	0.0671
<i>path:gga00062</i>	Fatty acid elongation	23	1	0.09406
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	27	1	0.1095
<i>path:gga00565</i>	Ether lipid metabolism	34	1	0.1359
<i>path:gga01212</i>	Fatty acid metabolism	50	1	0.1934
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.2341
<i>path:gga04115</i>	p53 signaling pathway	63	1	0.2374
<i>path:gga04512</i>	ECM–receptor interaction	66	1	0.2472
<i>path:gga03015</i>	mRNA surveillance pathway	72	1	0.2664



1	ECM2	PTGDS	SHH	CMTM8	ENSGALG00000027183	CNP1	SLIT2	FOXA2
2	HPGDS	TLL1	EXFABP	ENSGALG00000026754	SYNDIG1	COL8A2	NECTIN3	CALCA
3	FOXA1	ARX	GPR37	KRT24	ENSGALG00000035945	ASB9	FOXP2	GAL
4	METRNL	LAPTM4B	ARHGAP24	CP	AHSG	ADIPOQ	TRABD2B	NEDD9
5	PDLIM3	MAP7	DUSP27	SLAMF8	ENTPD2	CNKS2R	RFLNA	DYNC2H1
6	HEXA	THBS1	BARX2	PPL	TMEM255B	ENSGALG00000044002	ASL2	MGST2
7	NET1	R3HDM1	JUND	ENSGALG00000016755	COL8A1	MATN2	GOLPH3L	BEGAIN
8	NGB	ENSGALG0000003590	EFNB2	ATF3	ASIC2	ENSGALG00000010457	TFPI	ENSGALG00000011356
9	ENSGALG00000034756	TM6SF1	SFRP2	CXCL12	ENSGALG00000023763	AZIN2	MDGA2	SIK1
10	ITGBL1	MYO1H	WFIKKN2	CFD	ENSGALG00000053594	DUSP1	ENSGALG00000054746	SLC38A2
11	CCN3	TRIM25	SEMA3D	LPAR3	BCL6	ENSGALG00000010137	EGR1	IL10RA
12	BNC2	KRT13	CHODL	PP2D1	TEKT3	SERPIN1C	SEMA3E	NKX6-2
13	ENSGALG00000011283	CD9	HAS2	S100A1	BAIAP2	MARVELD3	ENSGALG00000030405	ENSGALG00000052907
14	EDNRB	VPS29L	ENSGALG00000040269	FBRSL1	CHMP4C	C8orf88	AMN	FAM83B
15	CCDC3	LZTS2	NECAB3	ZFPM2	PTPRG	CDH11		

	Term	Ont	N	n	Adj. p-value
GO:0016049	cell growth	BP	49	5	6.2e-05
GO:0048588	developmental cell growth	BP	28	4	9.215e-05
GO:0048843	negative regulation of axon extension involved in axon guidance	BP	3	2	0.0002208
GO:0003415	chondrocyte hypertrophy	BP	4	2	0.000439
GO:0050922	negative regulation of chemotaxis	BP	4	2	0.000439
GO:0048841	regulation of axon extension involved in axon guidance	BP	4	2	0.000439
GO:0071526	semaphorin–plexin signaling pathway	BP	4	2	0.000439
GO:0030308	negative regulation of cell growth	BP	18	3	0.0004662
GO:0045926	negative regulation of growth	BP	20	3	0.0006432
GO:0048846	axon extension involved in axon guidance	BP	5	2	0.0007276

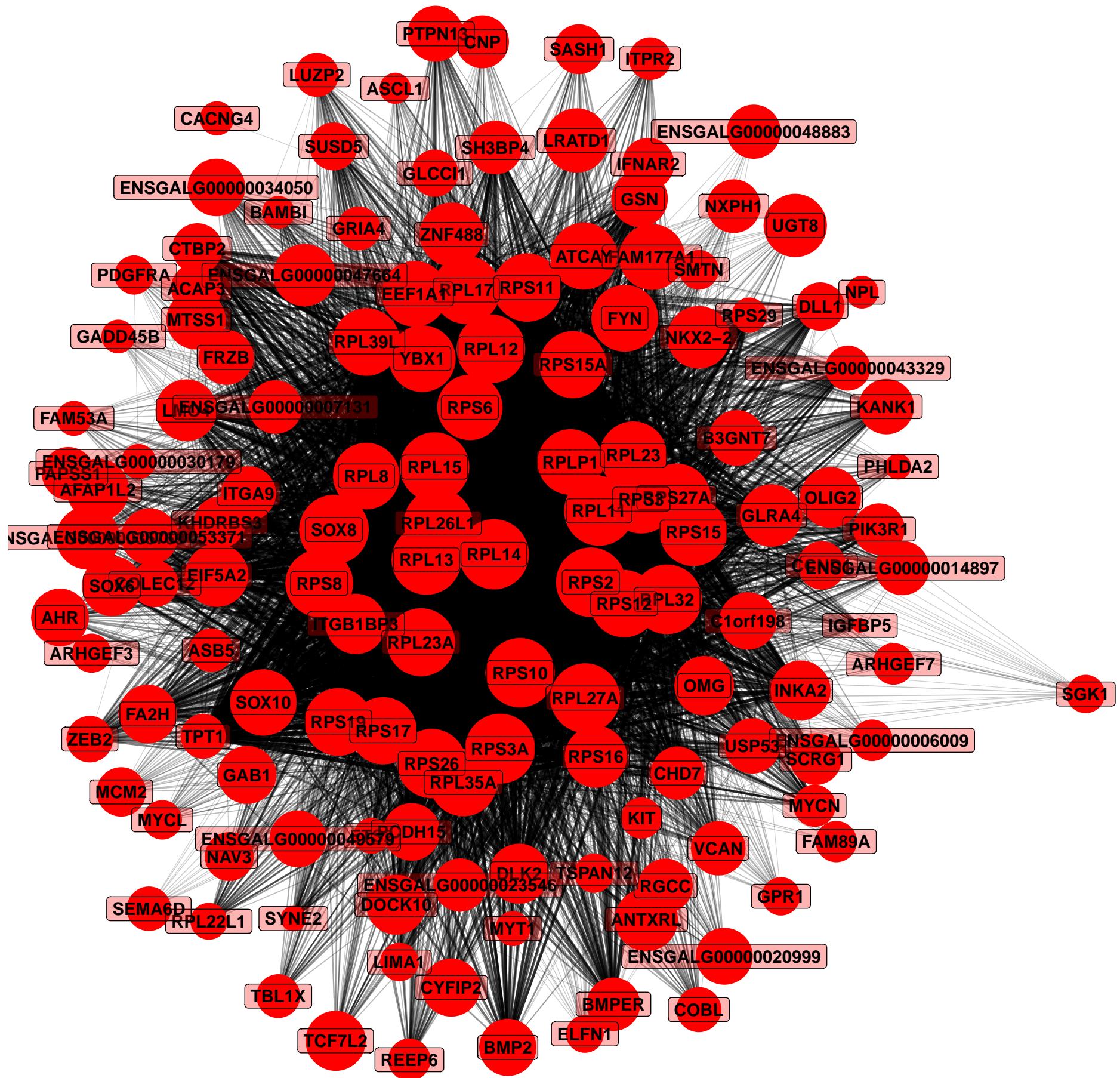
	Pathway	N	DE	P.DE
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	27	2	0.02257
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	28	2	0.02417
<i>path:gga00590</i>	Arachidonic acid metabolism	37	2	0.0405
<i>path:gga00480</i>	Glutathione metabolism	47	2	0.06221
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	1	0.09895
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	1	0.1067
<i>path:gga04520</i>	Adherens junction	69	2	0.1197
<i>path:gga00220</i>	Arginine biosynthesis	16	1	0.1297
<i>path:gga00531</i>	Glycosaminoglycan degradation	16	1	0.1297
<i>path:gga00511</i>	Other glycan degradation	17	1	0.1373



1	CDH5	CD34	VWF	SOX18	SHE	ERG	CLDN5	APOLD1
2	RAMP2	MYO1A	ENSGALG00000046550	KLF2	CD248	SOX17	ENSGALG00000024379	ENSGALG00000002012
3	PCDH12	NOS3	KDR	EGFL7	TFPI2	P2RY8	MYCT1	MALL
4	STAB2	ABCB1	PLPP2	RHOJ	ENG	PLTP	GJA4	CCM2L
5	RASGRP3	SEMA3G	FAM110D	ADGRL4	ENSGALG00000052737	FLI1	ZNF366	ADORA1
6	DIPK2B	ENSGALG00000021092	JCAD	PARVG	PDGFB	ENSGALG00000046593	CSRP1	AFAP1L1
7	APCDD1	CCDC85A	RAPGEF3	TM4SF18	S100A13	KCNJ15	ENSGALG00000035994	SLC16A7
8	RD3L	SLCO2A1	ELK3	F2RL2	KRT40	KITLG	MGAT4C	PTGS2
9	NEURL2	LGALS3	ENSGALG00000003203	ENSGALG00000015822	F10	ENSGALG00000053285	SLC51A	

	Term	Ont	N	n	Adj. p-value
GO:0050878	regulation of body fluid levels	BP	11	3	2.271e-05
GO:0008015	blood circulation	BP	25	3	0.0003003
GO:0003013	circulatory system process	BP	25	3	0.0003003
GO:0046579	positive regulation of Ras protein signal transduction	BP	6	2	0.0004086
GO:0007596	blood coagulation	BP	7	2	0.0005701
GO:0007599	hemostasis	BP	7	2	0.0005701
GO:0051057	positive regulation of small GTPase mediated signal transduction	BP	7	2	0.0005701
GO:0035590	purinergic nucleotide receptor signaling pathway	BP	7	2	0.0005701
GO:0050817	coagulation	BP	8	2	0.0007575
GO:0008217	regulation of blood pressure	BP	8	2	0.0007575

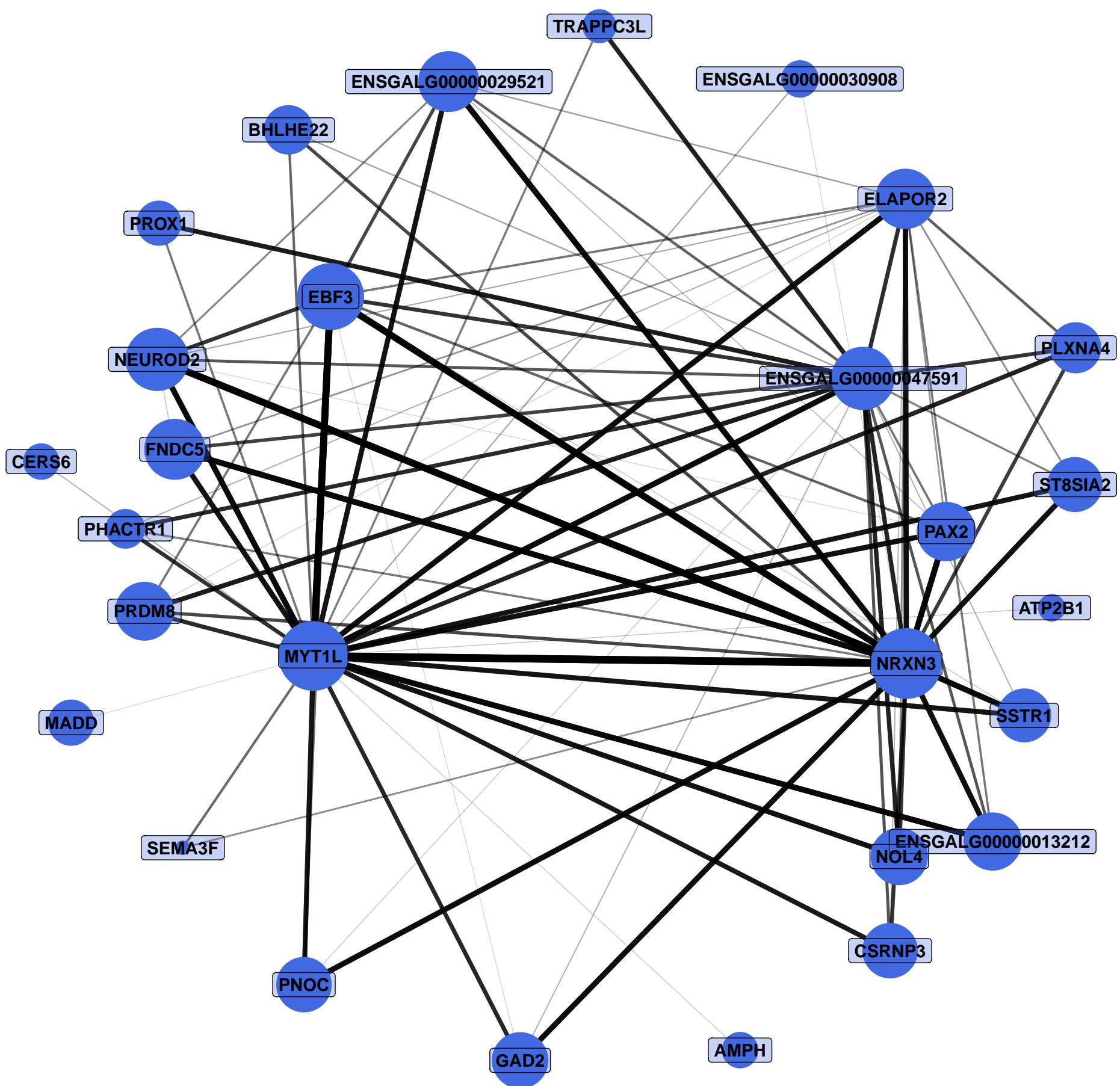
	Pathway	N	DE	P.DE
<i>path:gga04370</i>	VEGF signaling pathway	52	3	0.002605
<i>path:gga04510</i>	Focal adhesion	169	4	0.01226
<i>path:gga04514</i>	Cell adhesion molecules	99	3	0.0155
<i>path:gga04010</i>	MAPK signaling pathway	236	4	0.03627
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	275	4	0.05772
<i>path:gga04020</i>	Calcium signaling pathway	191	3	0.08048
<i>path:gga00220</i>	Arginine biosynthesis	16	1	0.08147
<i>path:gga04270</i>	Vascular smooth muscle contraction	102	2	0.1016
<i>path:gga04371</i>	Apelin signaling pathway	106	2	0.1083
<i>path:gga04310</i>	Wnt signaling pathway	133	2	0.1564



1	UGT8	RPL13	RPS10	RPL14	RPS2	RPS26	RPL27A	RPS3A
2	OLIG2	RPL15	RPL32	RPL11	SOX8	SOX10	RPL26L1	RPS27A
3	RPL39L	RPL12	RPS3	RPL17	RPL23	RPS11	RPS19	RPL35A
4	RPS15	RPS15A	RPS17	RPS8	RPL23A	RPS12	RPL8	YBX1
5	RPLP1	RPS6	NKX2-2	FAM177A1	RPS16	LRATD1	ATCAY	ZNF488
6	EEF1A1	ITGB1BP3	ENSGALG00000047664	AFAP1L2	ENSGALG00000035769	FYN	GLRA4	ANTXRL
7	EIF5A2	OMG	B3GNT7	LMO4	NXPH1	TCF7L2	DLL1	PCDH15
8	DOCK10	SOX6	PDGFRA	C1orf198	INKA2	CNP	ACAP3	COLEC12
9	ENSGALG0000007131	CHD7	ENSGALG00000043329	TPT1	DLK2	FA2H	RPS29	VCAN
10	GSN	ENSGALG00000053371	KHDRBS3	ENSGALG00000014897	CTBP2	BMPER	MYT1	CYFIP2
11	SUSD5	GAB1	MTSS1	IFNAR2	ITGA9	PIK3R1	RGCC	ENSGALG00000020999
12	ENSGALG00000049579	SH3BP4	ENSGALG00000023546	CCND1	MCM2	AHR	KANK1	BMP2
13	PTPN13	ZEB2	GLCCI1	PAPSS1	COBL	SASH1	ENSGALG00000034050	FAM89A
14	SCRG1	NAV3	FRZB	USP53	GRIA4	ASB5	SGK1	ITPR2
15	SMTN	ENSGALG0000006009	RPL22L1	GPR1	ETS2	LUZP2	REEP6	TBL1X
16	BAMBI	ASCL1	LIMA1	ENSGALG00000048883	PHLDA2	KIT	TSPAN12	ENSGALG00000030179
17	MYCN	ELFN1	SYNE2	ARHGEF3	CACNG4	NPL	SEMA6D	IGFBP5
18	ARHGEF7	FAM53A	MYCL	GADD45B				

	Term	Ont	N	n	Adj. p-value
GO:0006412	translation	BP	87	13	5.099e-12
GO:0043043	peptide biosynthetic process	BP	88	13	5.93e-12
GO:0043604	amide biosynthetic process	BP	99	13	2.773e-11
GO:0043603	cellular amide metabolic process	BP	123	14	3.339e-11
GO:0006518	peptide metabolic process	BP	107	13	7.568e-11
GO:0044271	cellular nitrogen compound biosynthetic process	BP	512	21	7.158e-08
GO:0034645	cellular macromolecule biosynthetic process	BP	530	21	1.283e-07
GO:0009059	macromolecule biosynthetic process	BP	532	21	1.367e-07
GO:0010467	gene expression	BP	590	22	1.788e-07
GO:1901566	organonitrogen compound biosynthetic process	BP	205	13	2.164e-07

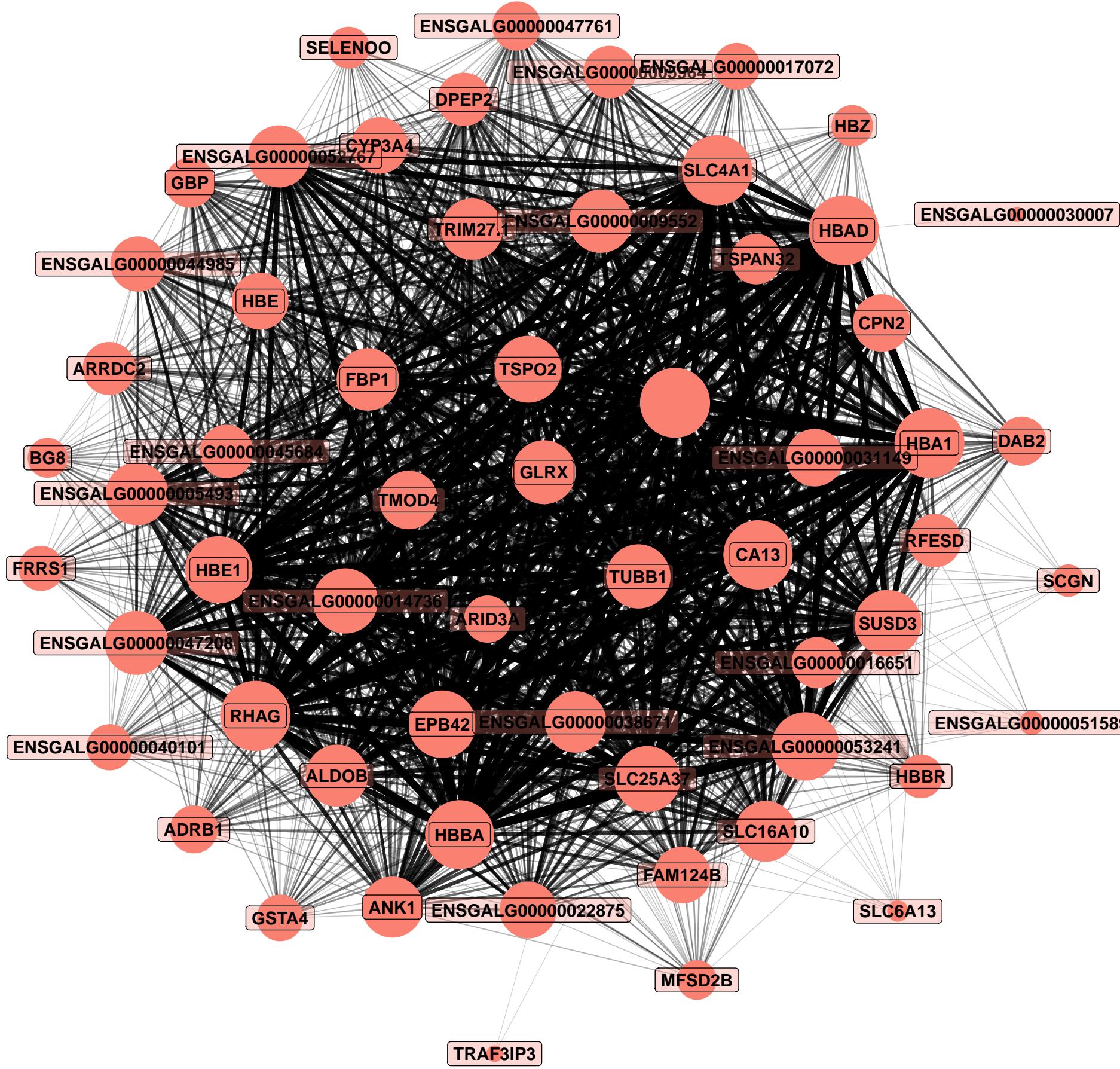
	Pathway	N	DE	P.DE
<i>path:gga03010</i>	Ribosome	115	32	1.056e-37
<i>path:gga04310</i>	Wnt signaling pathway	133	6	0.002679
<i>path:gga04810</i>	Regulation of actin cytoskeleton	180	7	0.002786
<i>path:gga04068</i>	FoxO signaling pathway	108	4	0.0264
<i>path:gga04210</i>	Apoptosis	113	4	0.03049
<i>path:gga04510</i>	Focal adhesion	169	5	0.03198
<i>path:gga04218</i>	Cellular senescence	132	4	0.04932
<i>path:gga00920</i>	Sulfur metabolism	7	1	0.07079
<i>path:gga04514</i>	Cell adhesion molecules	99	3	0.08474
<i>path:gga04371</i>	Apelin signaling pathway	106	3	0.09904



1	EBF3	NRXN3	NEUROD2	MYT1L	PRDM8	PAX2	ENSGALG00000047591	PNOC
2	ENSGALG00000029521	SSTR1	ELAPOR2	FNDC5	ST8SIA2	GAD2	BHLHE22	ENSGALG00000013212
3	PROX1	NOL4	PLXNA4	CSRNP3	TRAPPCL	PHACTR1	MADD	ENSGALG00000030908
4	AMPH	SEMA3F	CERS6	ATP2B1				

	Term	Ont	N	n	Adj. p-value
GO:0071696	ectodermal placode development	BP	1	1	0.002102
GO:0060788	ectodermal placode formation	BP	1	1	0.002102
GO:0071697	ectodermal placode morphogenesis	BP	1	1	0.002102
GO:0070309	lens fiber cell morphogenesis	BP	1	1	0.002102
GO:0036303	lymph vessel morphogenesis	BP	1	1	0.002102
GO:0001946	lymphangiogenesis	BP	1	1	0.002102
GO:0071698	olfactory placode development	BP	1	1	0.002102
GO:0030910	olfactory placode formation	BP	1	1	0.002102
GO:0071699	olfactory placode morphogenesis	BP	1	1	0.002102
GO:0043049	otic placode formation	BP	1	1	0.002102

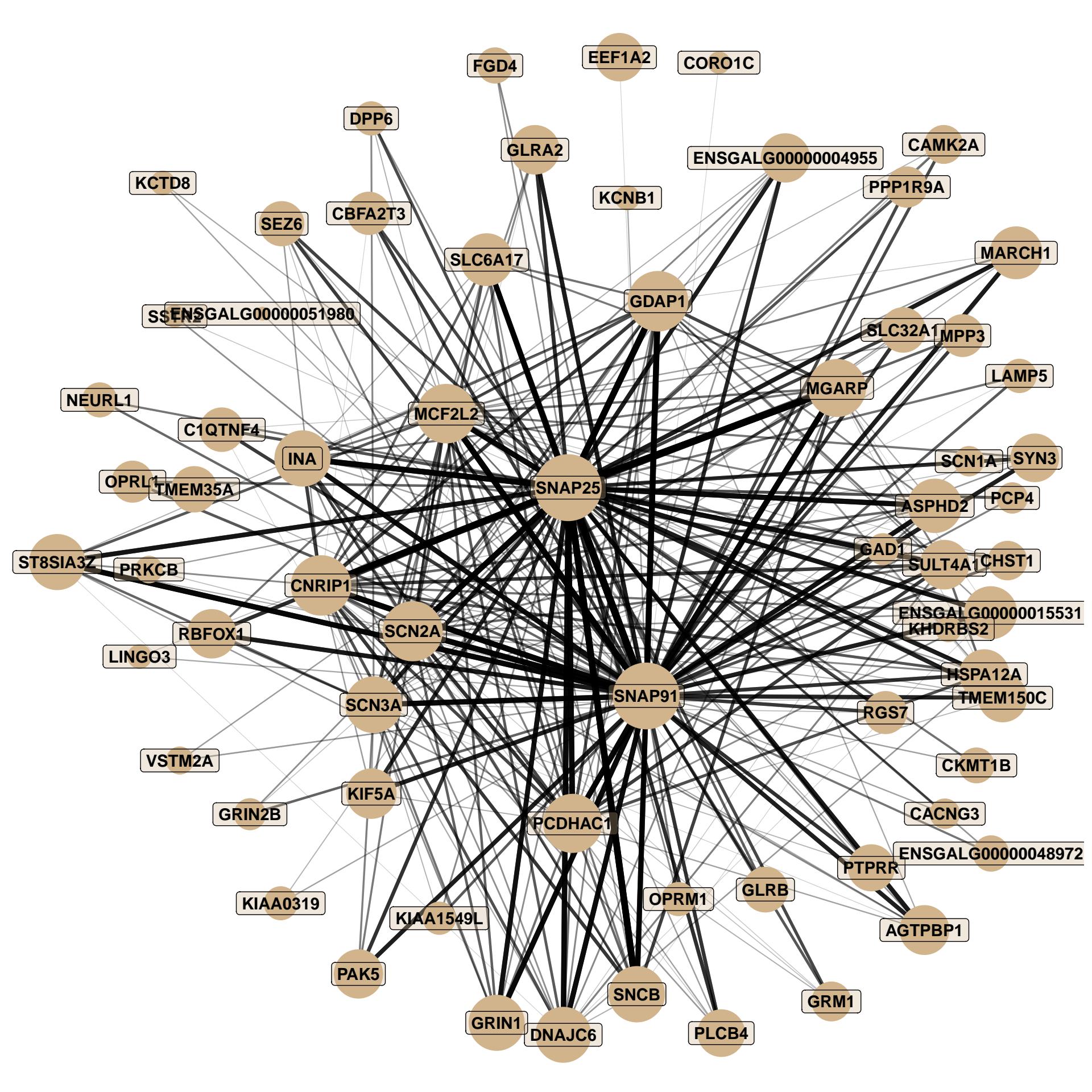
	Pathway	N	DE	P.DE
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	1	0.02494
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	118	2	0.02529
<i>path:gga00650</i>	Butanoate metabolism	21	1	0.04326
<i>path:gga00410</i>	beta-Alanine metabolism	25	1	0.05129
<i>path:gga04020</i>	Calcium signaling pathway	191	2	0.06056
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	1	0.06519
<i>path:gga00600</i>	Sphingolipid metabolism	47	1	0.09433
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	275	2	0.1131
<i>path:gga04514</i>	Cell adhesion molecules	99	1	0.1887
<i>path:gga04810</i>	Regulation of actin cytoskeleton	180	1	0.3171



1	HBAD	NA	SLC4A1	HBA1	CA13	RHAG	TSPO2	HBBA
2	HBE1	ENSGALG00000053241	EPB42	SUSD3	ENSGALG00000014736	HBE	ENSGALG00000047208	SLC25A37
3	ENSGALG00000052767	ALDOB	TUBB1	ENSGALG0000009552	ENSGALG0000005493	ANK1	TRIM27.1	ENSGALG00000022875
4	FBP1	ENSGALG00000038671	GLRX	CYP3A4	HBZ	HBBR	RFESD	SLC16A10
5	ENSGALG00000044985	CPN2	GSTA4	TMOD4	ENSGALG00000045684	ENSGALG00000031149	FAM124B	ADRB1
6	ENSGALG0000005964	DPEP2	ENSGALG00000016651	ARID3A	TSPAN32	ARRDC2	GBP	BG8
7	ENSGALG00000017072	ENSGALG00000047761	MFSD2B	SELENOO	FRRS1	ENSGALG00000040101	TRAF3IP3	SCGN
8	DAB2	ENSGALG00000030007	SLC6A13	ENSGALG00000051589				

	Term	Ont	N	n	Adj. p-value
GO:0042744	hydrogen peroxide catabolic process	BP	7	6	3.246e-14
GO:0042743	hydrogen peroxide metabolic process	BP	7	6	3.246e-14
GO:0015671	oxygen transport	BP	7	6	3.246e-14
GO:0015669	gas transport	BP	8	6	1.294e-13
GO:0098869	cellular oxidant detoxification	BP	14	6	1.361e-11
GO:1990748	cellular detoxification	BP	16	6	3.606e-11
GO:0097237	cellular response to toxic substance	BP	16	6	3.606e-11
GO:0098754	detoxification	BP	17	6	5.554e-11
GO:0072593	reactive oxygen species metabolic process	BP	18	6	8.304e-11
GO:0009636	response to toxic substance	BP	20	6	1.722e-10

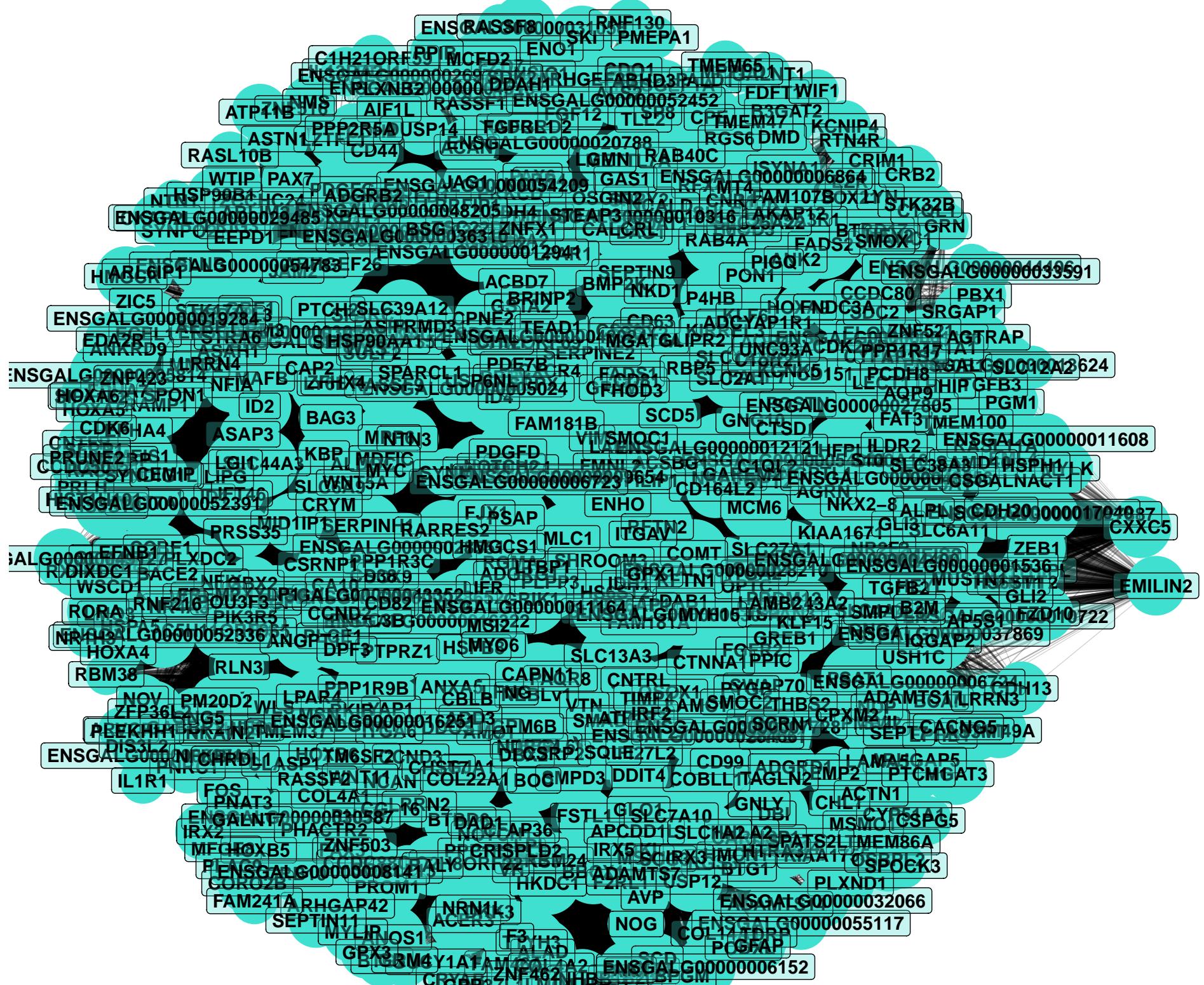
	Pathway	N	DE	P.DE
<i>path:gga00030</i>	Pentose phosphate pathway	25	2	0.00507
<i>path:gga00051</i>	Fructose and mannose metabolism	34	2	0.009251
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	47	2	0.0172
<i>path:gga04540</i>	Gap junction	78	2	0.04395
<i>path:gga00910</i>	Nitrogen metabolism	13	1	0.05428
<i>path:gga01200</i>	Carbon metabolism	95	2	0.06243
<i>path:gga00591</i>	Linoleic acid metabolism	16	1	0.06639
<i>path:gga00140</i>	Steroid hormone biosynthesis	24	1	0.09794
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	27	1	0.1095
<i>path:gga00830</i>	Retinol metabolism	27	1	0.1095



1	SNAP25	SNAP91	GRIN1	PCDHAC1	CNRIP1	MGARP	SNCB	SCN2A
2	MCF2L2	SCN3A	RBFOX1	INA	C1QTNF4	ST8SIA3Z	GDAP1	SLC6A17
3	SEZ6	ENSGALG00000015531	DNAJC6	HSPA12A	SLC32A1	PAK5	MARCH1	SULT4A1
4	GLRA2	PCP4	RGS7	ASPHD2	PTPRR	LAMP5	CBFA2T3	SYN3
5	KIF5A	TMEM150C	OPRM1	DPP6	GAD1	ENSGALG0000004955	CAMK2A	PLCB4
6	AGTPBP1	VSTM2A	MPP3	ENSGALG00000048972	GLRB	NEURL1	OPRL1	CHST1
7	FGD4	GRIN2B	PPP1R9A	TMEM35A	KCNB1	EEF1A2	CACNG3	SCN1A
8	KIAA1549L	SSTR2	KIAA0319	CORO1C	ENSGALG00000051980	GRM1	CKMT1B	KCTD8
9	KHDRBS2	PRKCB	LINGO3					

	Term	Ont	N	n	Adj. p-value
GO:0035609	C-terminal protein deglutamylation	BP	1	1	0.00506
GO:0098967	exocytic insertion of neurotransmitter receptor to postsynaptic membrane	BP	1	1	0.00506
GO:0035608	protein deglutamylation	BP	1	1	0.00506
GO:0035610	protein side chain deglutamylation	BP	1	1	0.00506
GO:0031629	synaptic vesicle fusion to presynaptic active zone membrane	BP	1	1	0.00506
GO:0016082	synaptic vesicle priming	BP	1	1	0.00506
GO:0099500	vesicle fusion to plasma membrane	BP	1	1	0.00506
GO:0021702	cerebellar Purkinje cell differentiation	BP	2	1	0.0101
GO:0021680	cerebellar Purkinje cell layer development	BP	2	1	0.0101
GO:0021694	cerebellar Purkinje cell layer formation	BP	2	1	0.0101

	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	275	8	6.992e–05
<i>path:gga04020</i>	Calcium signaling pathway	191	5	0.002769
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	118	4	0.002976
<i>path:gga04912</i>	GnRH signaling pathway	73	3	0.005978
<i>path:gga04012</i>	ErbB signaling pathway	76	3	0.006684
<i>path:gga04540</i>	Gap junction	78	3	0.007182
<i>path:gga04916</i>	Melanogenesis	82	3	0.008242
<i>path:gga04310</i>	Wnt signaling pathway	133	3	0.02976
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	1	0.05909
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.06859

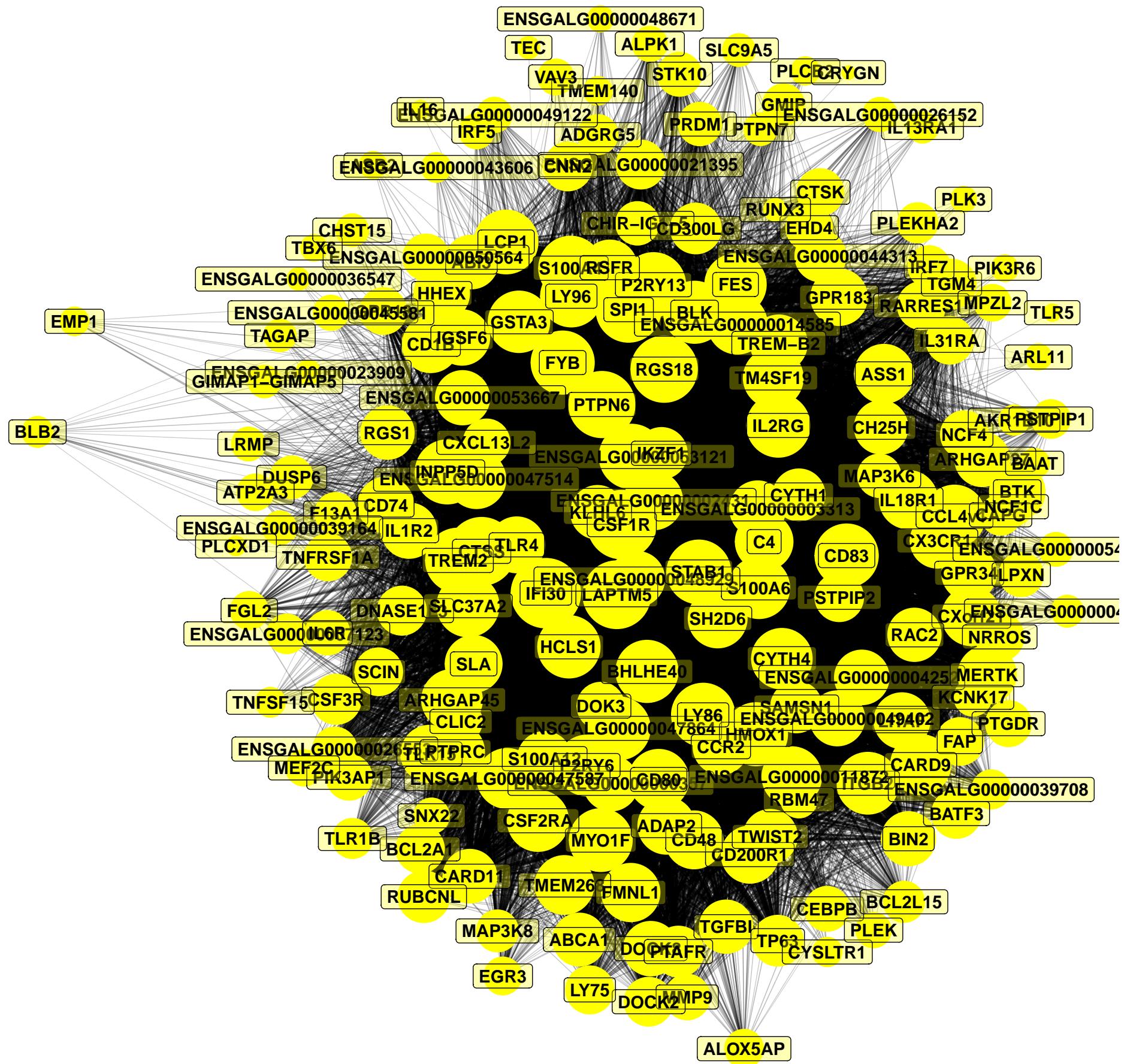


ENSGALG00000049439

21	CD81	HEY2	ENSGALG00000031058	CPE	PROM1	PLCE1	PPP1R14C	ATP6AP1
22	CDK2AP1	NFIA	ALDOC	HKDC1	ENSGALG0000006724	GLI3	NPAS3	MRAS
23	EML4	PPIC	GNG4	LIFR	SOX1	KIAA1755	ASA1H1	USH1C
24	SPARC	SOX21	SMOC2	ANGPTL1	ID2	ENSGALG0000001136	LAMC1	MDK
25	ENSGALG0000048024	SPRED1	SPON1	QKI	ENSGALG00000043352	PACRG	ENSGALG0000028210	BTBD17
26	SDC2	KIAA1671	ENSGALG0000045636	BACE2	ALAD	SPRY2	GBE1	IGFBP2
27	SDC3	RARRES2	C5H11ORF96	SEMA6A	SLC9A3R1	FHOD3	SLC25A22	ARHGEF26
28	STK17A	P4HB	SOX2	FLNB	ENSGALG0000052336	PRKCD	SULF2	SLC1A4
29	BBOX1	LRIG3	CXXC5	CD151	TSPAN6	SLC2A1	PDLIM4	ANKRD9
30	IDH1	BAG3	ANOS1	GNG5	TSC22D1	CDH4	HOXB5	FGF12
31	TMEM100	GAREM2	BCAN	CHN1	CCDC80	S100A10	SKI	ASPA
32	ALPL	ENSGALG0000054783	MSN	C2H8ORF22	ENSGALG0000007728	RBP5	PPP1R9B	BOC
33	GLO1	HS3ST6	SFRP1	NTN3	DMD	USP6NL	WNT7A	PPP1R3C
34	CAP2	BPGM	NOG	WNT5A	HMCN1	SYNPO2	RASSF2	ZFP36L2
35	MEIS1	KLF15	CD63	RAB40C	ENSGALG0000013624	ITGB1	PDGFD	DIPK1C
36	FZD10	CPNE2	LRP8	IQGAP2	EPB41L3	PAX6	ENSGALG0000003074	SMPDL3A
37	CD82	FAM46A	RAB20	SCRN1	ENSGALG0000001536	CDH2	COL22A1	OSBPL2
38	ATP1A1	LRRKIP1	BMP2K	LYN	MEIS2	CRISPLD2	CALCRL	AEBP1
39	GRM3	CAPN11	LAMA5	CDH20	MDFIC	TGFB2	EPHA4	KLF6
40	LPAR4	CRB2	F2RL1	USP12	MID1IP1	ZNF503	INHBB	HHIP
41	SCG3	ASTN1	AP1S2	ARHGAP5	TMEM47	MYLK	TSPAN3	RBM24
42	NCALD	CCND3	NOG2	SPARCL1	NKAIN2	ADAMTS7	APCDD1L	DDIT4
43	MSX1	ENSGALG0000012941	TMEM37	MSMO1	PXYLP1	CYP51A1	CD164L2	FRMD3
44	SMOX	CRYAB	GALNT7	SLC38A3	AKAP12	ENSGALG0000030587	LGI1	ENSGALG0000036310
45	C1QL1	ARHGEF28	SPATS2L	NDP	FAT3	MYLIP	ENSGALG0000055117	COL4A1
46	ENSGALG0000006152	CHST7	CTSD	ENO1	CORO2B	LRP4	NOTCH1	ENSGALG0000017040
47	PTCH2	HMGCR	ENSGALG0000048205	C1QL2	INSIG1	ADD3	KCNIP4	SMPD3
48	ADAMTS14	RALY	ABHD3	ZEB1	HSPA5	ADCYAP1R1	CDO1	BSG
49	CNR1	ADGRB2	PAX3	SULF1	GREB1	FOS	ENSGALG0000049127	ATP11B
50	EMILIN2	EZR	SCD5	PRDM12	PHACTR2	SLC7A10	TLL2	WNT11
51	C1orf21	LECT1	MGAT4A	MGAT3	GLI2	ADAMTS17	ACAN	PHYHIPL
52	FNDC3A	PKIB	SDCBP	TNNC1	ADGRD2	BRINP2	GRN	CDH13
53	PNRC1	AS3MT	GABBR2	CKB	PGM1	GAS1	WSCD1	SLC39A12
54	NR4A3	BTG2	SYNDIG1L	GRM4	ZNF462	LIPG	CSRP2	MCFD2
55	ENSGALG0000002714	KIRREL3	PPIB	SLC1A2	CLASP1	HTRA3	PAX7	EEPD1
56	GBX2	ARHGAP42	HES4	TGFB3	NFIX	KBP	DUSP14	HMGCS1
57	CFAP36	PLEKHH1	SAMD10	ENSGALG0000043556	NTN1	PAK1	TMEM86A	FDFT1
58	DBX2	COL4A2	GRB10	EPHA7	SP8	CHL1	TEAD1	POU3F3
59	FAM49A	RORA	SEPTIN11	HES1	CRYM	EDA2R	ILDR2	HSP90B1
60	GPX3	WTIP	ENSGALG0000010316	LAMB2	IRX2	GPR37L1	LGMD	CRIM1
61	ENSGALG0000028466	OSGIN2	MFGE8	CARHSP1	ANXA1	ENSGALG0000020788	PBX1	NRN1L
62	ENSGALG0000054209	LPL	ENSGALG0000032066	ARL6IP1	RGS3	CACNG5	ENSGALG0000019284	RBM38
63	TAGLN2	HOXA5	EMP2	RASGEF1A	HOXA6	RFTN1	EPHB1	RASA3
64	PNAT3	AP5S1	SCD	VIT	ALS2	LRRN3	SVIL	THBS2

	Term	Ont	N	n	Adj. p-value
GO:0048856	anatomical structure development	BP	602	90	4.363e-21
GO:0007275	multicellular organism development	BP	559	86	5.382e-21
GO:0032502	developmental process	BP	634	91	4.367e-20
GO:0032501	multicellular organismal process	BP	686	94	2.521e-19
GO:0048731	system development	BP	471	65	1.026e-13
GO:0009653	anatomical structure morphogenesis	BP	286	47	6.048e-13
GO:0050789	regulation of biological process	BP	1067	108	1.188e-12
GO:0050794	regulation of cellular process	BP	1019	104	2.021e-12
GO:0065007	biological regulation	BP	1158	113	3.606e-12
GO:0048513	animal organ development	BP	311	48	3.632e-12

	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	66	18	2.683e–09
<i>path:gga04510</i>	Focal adhesion	169	25	1.317e–06
<i>path:gga00100</i>	Steroid biosynthesis	15	6	5.592e–05
<i>path:gga04330</i>	Notch signaling pathway	52	10	0.0002388
<i>path:gga03320</i>	PPAR signaling pathway	57	10	0.0005188
<i>path:gga04810</i>	Regulation of actin cytoskeleton	180	20	0.0008001
<i>path:gga04350</i>	TGF–beta signaling pathway	84	12	0.001028
<i>path:gga04340</i>	Hedgehog signaling pathway	47	8	0.002268
<i>path:gga00480</i>	Glutathione metabolism	47	7	0.008932
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	27	5	0.0105



1	CSF1R	CTSS	LAPTM5	SPI1	IFI30	RGS18	S100A4	PTPN6
2	LCP1	ENSGALG00000053121	MYO1F	P2RY13	ENSGALG00000047864	INPP5D	CCL4v1	LY96
3	S100A6	FES	CD48	CD200R1	ENSGALG0000002431	BLK	HMOX1	HCLS1
4	TREM2	ITGB2	LY86	CD83	GSTA3	HHEX	TMEM268	ENSGALG0000000357
5	ENSGALG00000047514	SLA	ENSGALG00000014585	FYB	ASS1	IL2RG	CD1B	IL18R1
6	RGS1	ENSGALG00000011872	ARHGAP27	S100A12	ARHGAP45	GPR34	TM4SF19	CSF2RA
7	P2RY6	GPR183	CCR2	CD80	ENSGALG00000049402	TREM-B2	BIN2	CARD9
8	CX3CR1	BHLHE40	SLC37A2	SAMSN1	IGSF6	ENSGALG00000053667	MERTK	CYTH4
9	STAB1	TLR15	BTK	ENSGALG00000048929	ENSGALG00000047587	PTPRC	LITAF	CXorf21
10	C4	SH2D6	ENSGALG0000004252	ABI3	RSFR	TLR4	CARD11	CD300LG
11	IL1R2	CXCL13L2	CD74	CHIR-IG1-5	BATF3	KLHL6	ADAP2	FAP
12	BCL2A1	ENSGALG00000021395	ENSGALG00000026553	FMNL1	ENSGALG00000044313	GPR18	CSF3R	CAPG
13	LPXN	ABCA1	RUBCNL	DNASE1L3	TGFBI	DOCK8	DOCK2	IKZF1
14	MMP9	RARRES1	RAC2	NCF4	ENSGALG00000003313	SCIN	TP63	TWIST2
15	TGM4	IL6R	PTAFR	CTSK	ENSGALG00000039708	IL31RA	CLIC2	CEBPB
16	EHD4	PSTPIP2	TNFRSF1A	NCF1C	NRROS	FGL2	CH25H	BCL2L15
17	GMIP	CNN2	STK10	PTGDR	ENSGALG00000050564	PSTPIP1	ADGRG5	TLR1B
18	MAP3K6	CYTH1	DUSP6	PLEKHA2	TAGAP	IRF7	ENSGALG0000007123	MAP3K8
19	DOK3	PRDM1	LY75	ENSGALG00000049122	PIK3AP1	AKR1B10	TMEM140	ASB2
20	EGR3	F13A1	GIMAP1-GIMAP5	ENSGALG00000039164	BLB2	ALOX5AP	CHST15	RBM47
21	ENSGALG00000047638	KCNK17	ENSGALG00000054978	LRMP	VAV3	ENSGALG00000036547	ENSGALG00000048671	MPZL2
22	IL13RA1	MEF2C	PLEK	PLCB2	ENSGALG00000026152	IRF5	ENSGALG00000023909	BAAT
23	RUNX3	ATP2A3	TLR5	SNX22	ENSGALG00000045581	CYSLTR1	ALPK1	PIK3R6
24	PLK3	TNFSF15	TEC	ENSGALG00000043606	TBX6	SLC9A5	EMP1	PTPN7
25	CRYGN	PLCXD1	IL16	ARL11				

	Term	Ont	N	n	Adj. p-value
GO:0006952	defense response	BP	90	9	5.938e-06
GO:0098542	defense response to other organism	BP	62	7	2.994e-05
GO:0009607	response to biotic stimulus	BP	77	7	0.000122
GO:0043207	response to external biotic stimulus	BP	77	7	0.000122
GO:0051707	response to other organism	BP	77	7	0.000122
GO:0044419	biological process involved in interspecies interaction between organisms	BP	88	7	0.0002817
GO:0006954	inflammatory response	BP	47	5	0.0005652
GO:0002376	immune system process	BP	166	9	0.0006943
GO:0009605	response to external stimulus	BP	187	9	0.001606
GO:0072676	lymphocyte migration	BP	5	2	0.002027

	Pathway	N	DE	P.DE
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	136	16	1.123e–10
<i>path:gga04620</i>	Toll–like receptor signaling pathway	69	10	5.162e–08
<i>path:gga04145</i>	Phagosome	121	7	0.00188
<i>path:gga04621</i>	NOD–like receptor signaling pathway	114	6	0.00624
<i>path:gga00120</i>	Primary bile acid biosynthesis	11	2	0.01053
<i>path:gga04514</i>	Cell adhesion molecules	99	5	0.01444
<i>path:gga04010</i>	MAPK signaling pathway	236	8	0.02163
<i>path:gga04210</i>	Apoptosis	113	5	0.02415
<i>path:gga04142</i>	Lysosome	113	5	0.02415
<i>path:gga04625</i>	C–type lectin receptor signaling pathway	80	4	0.02873