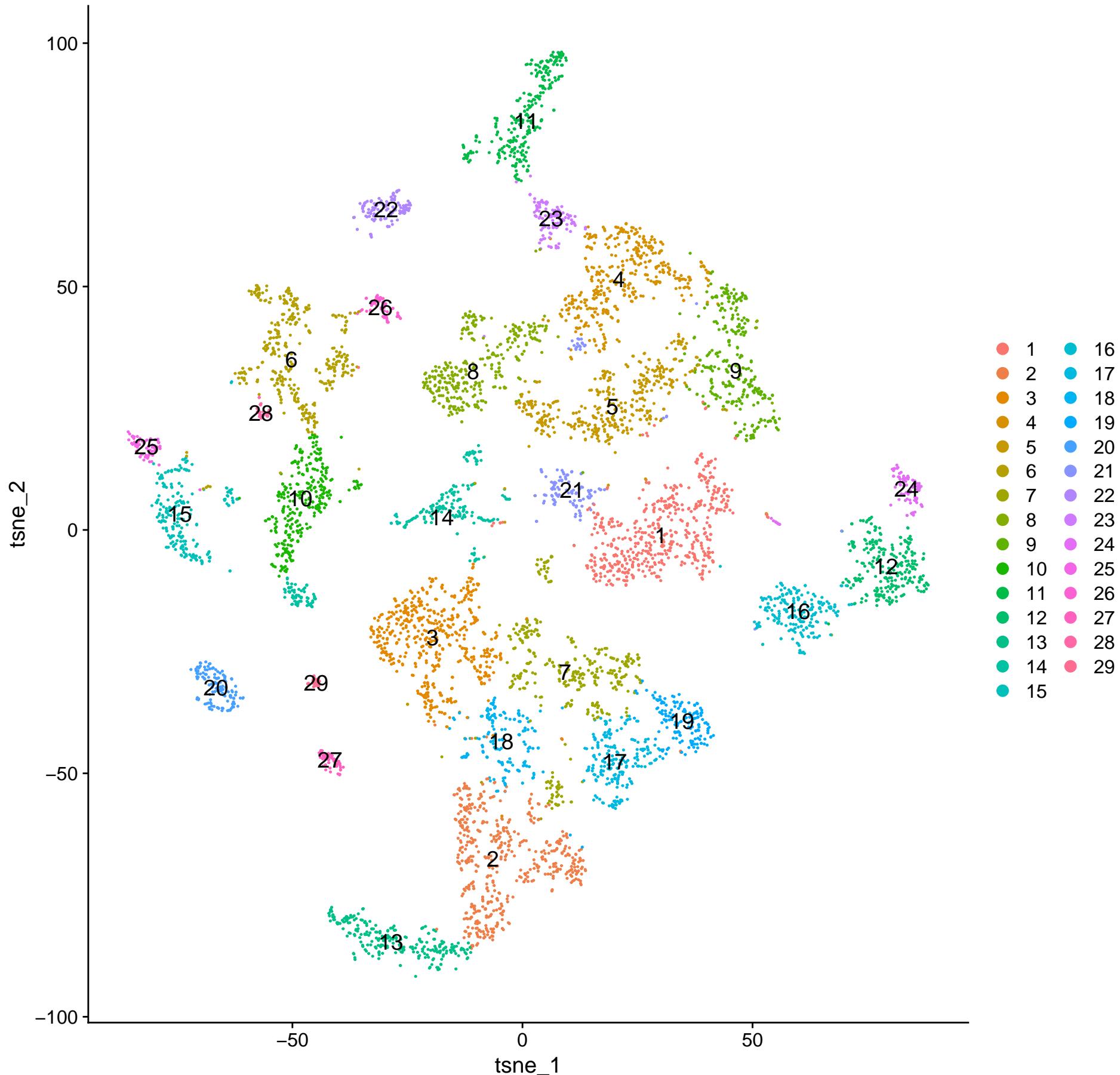
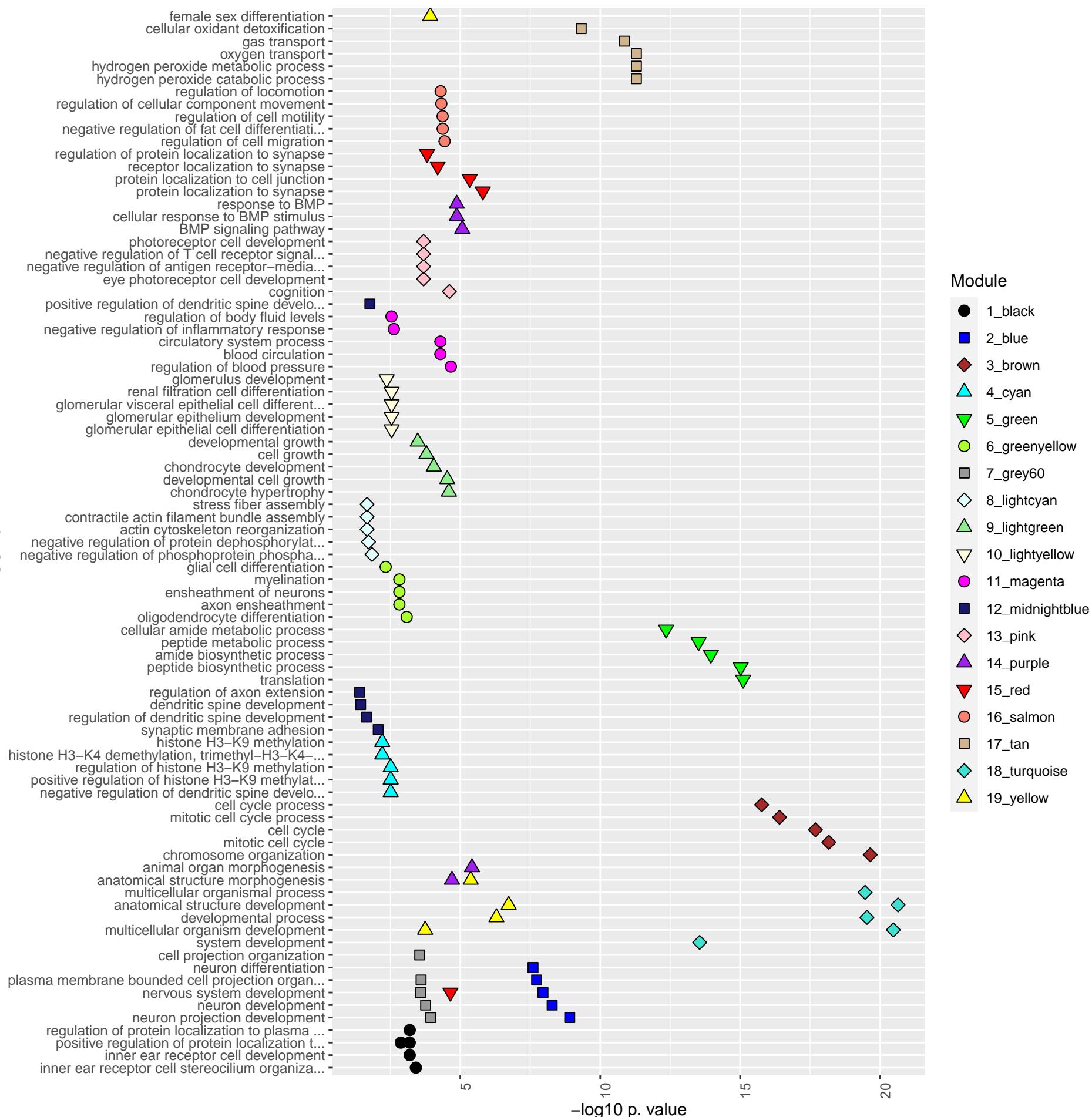
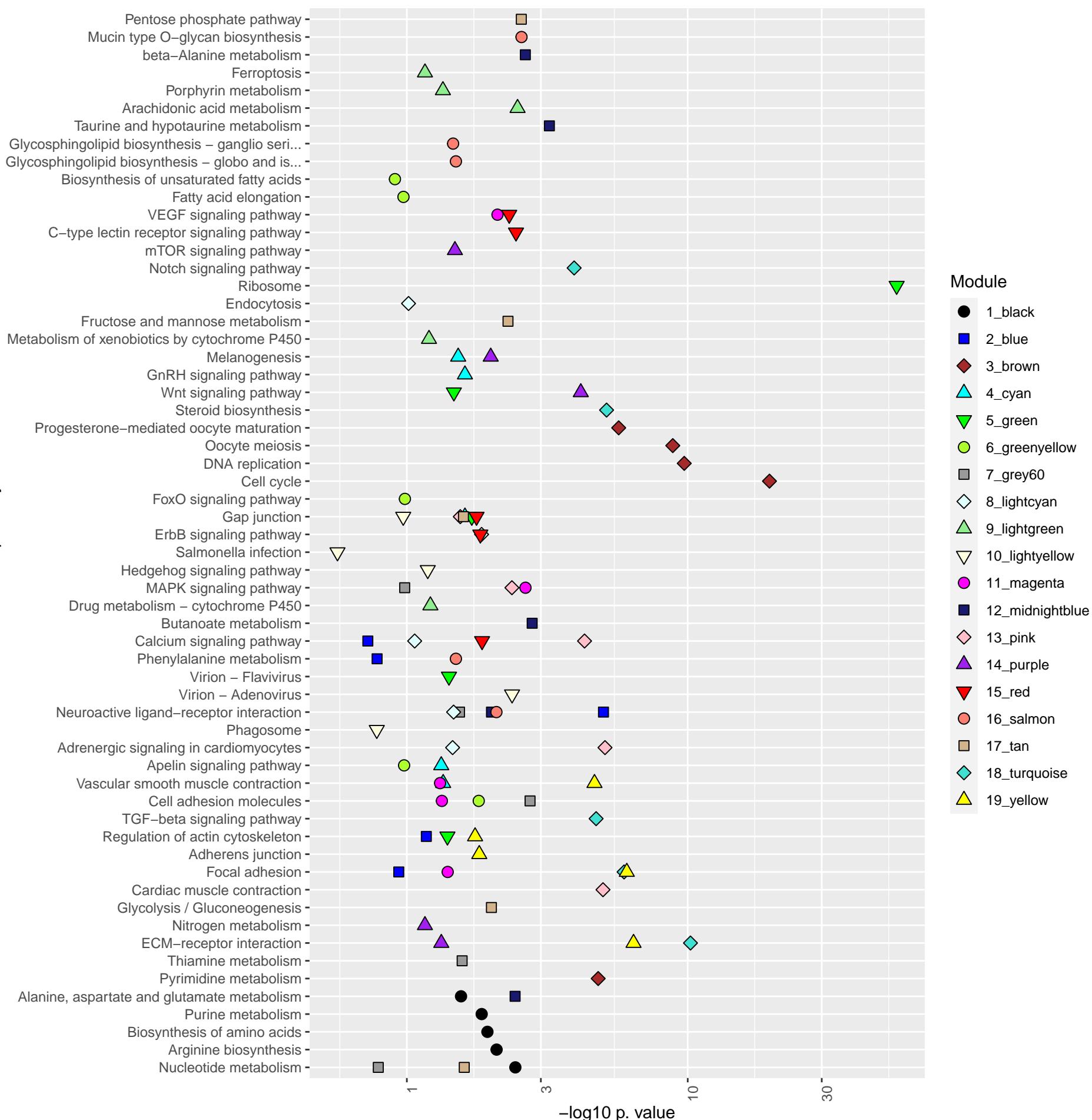
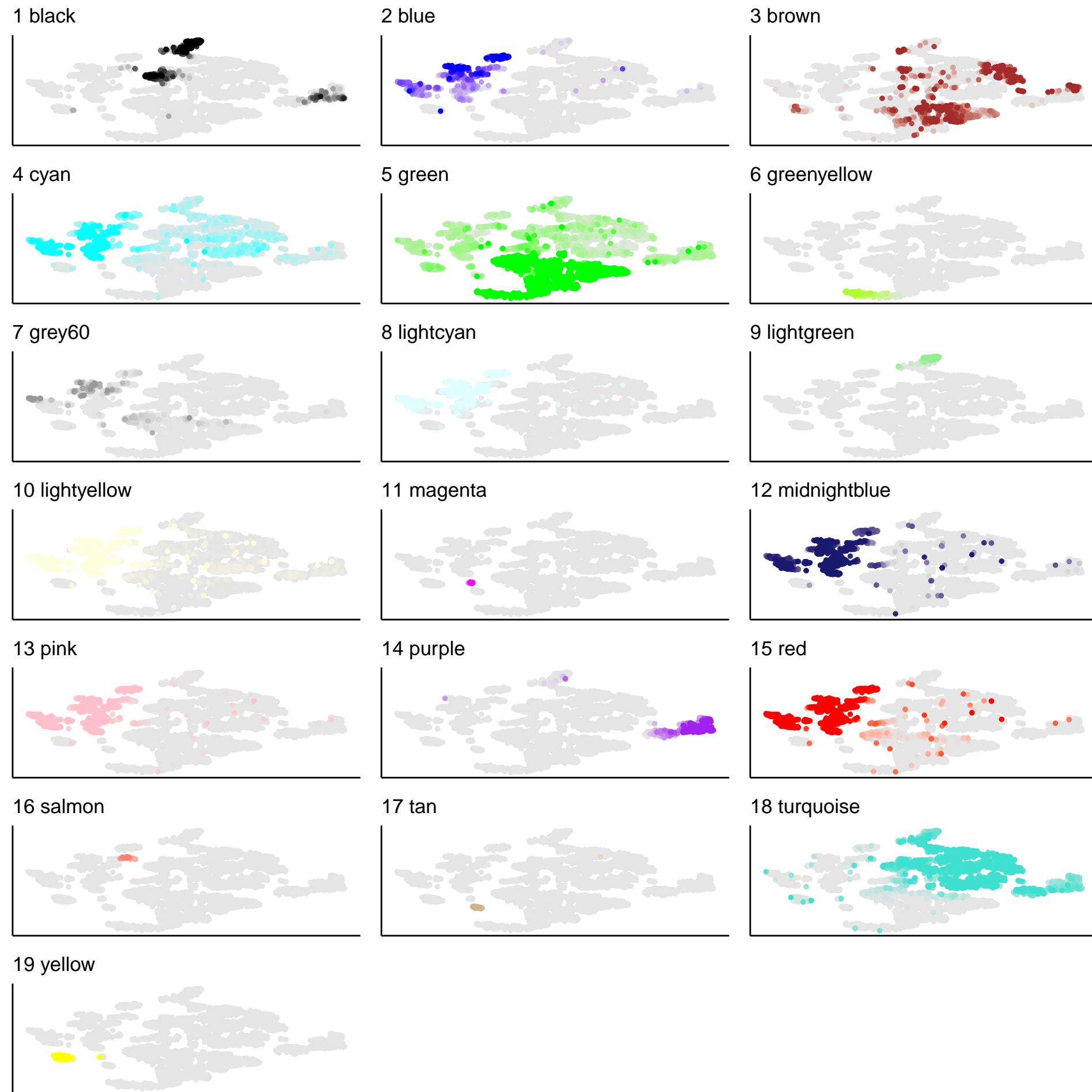


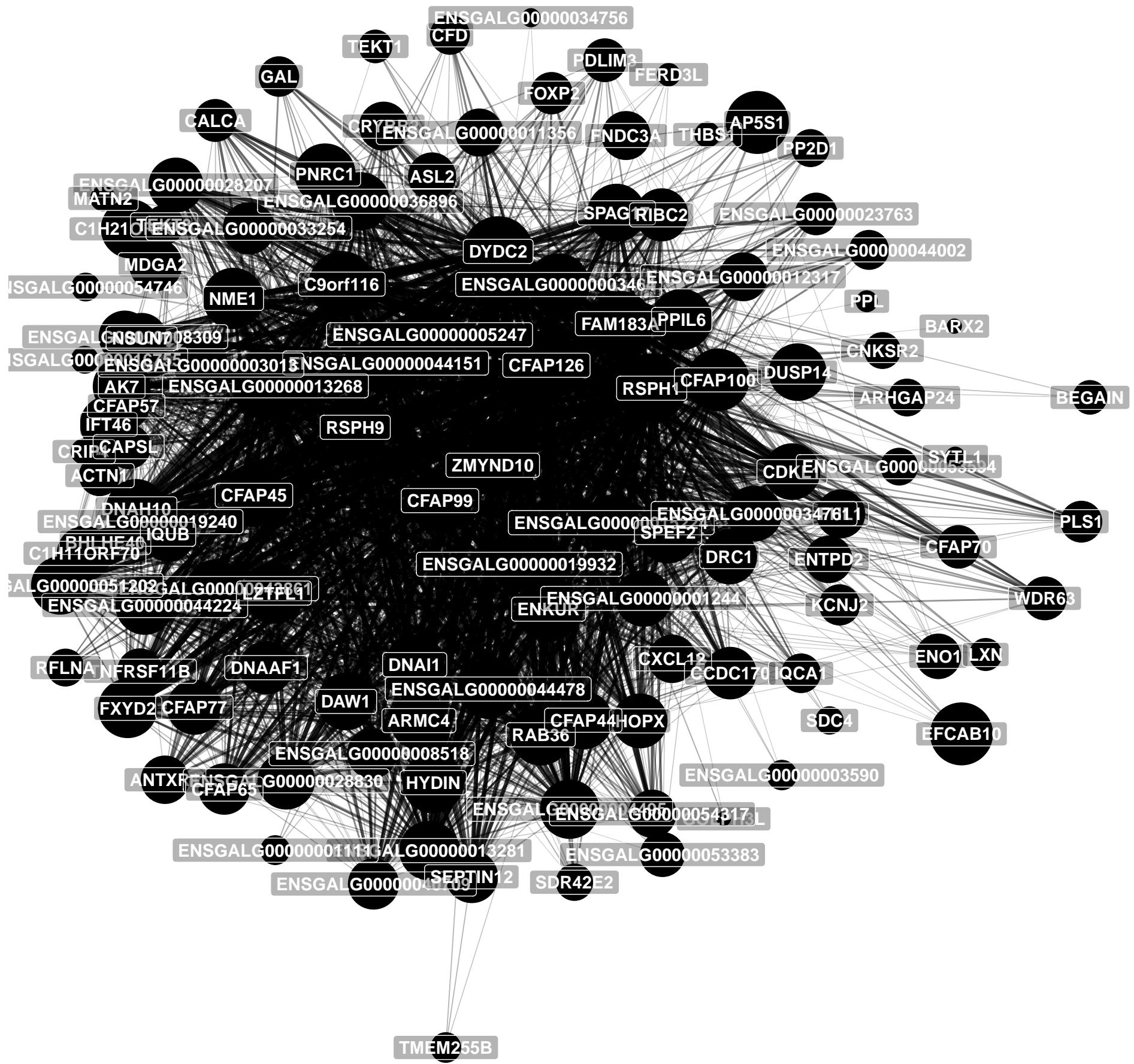
# Gg\_poly\_int scWGCNA modules







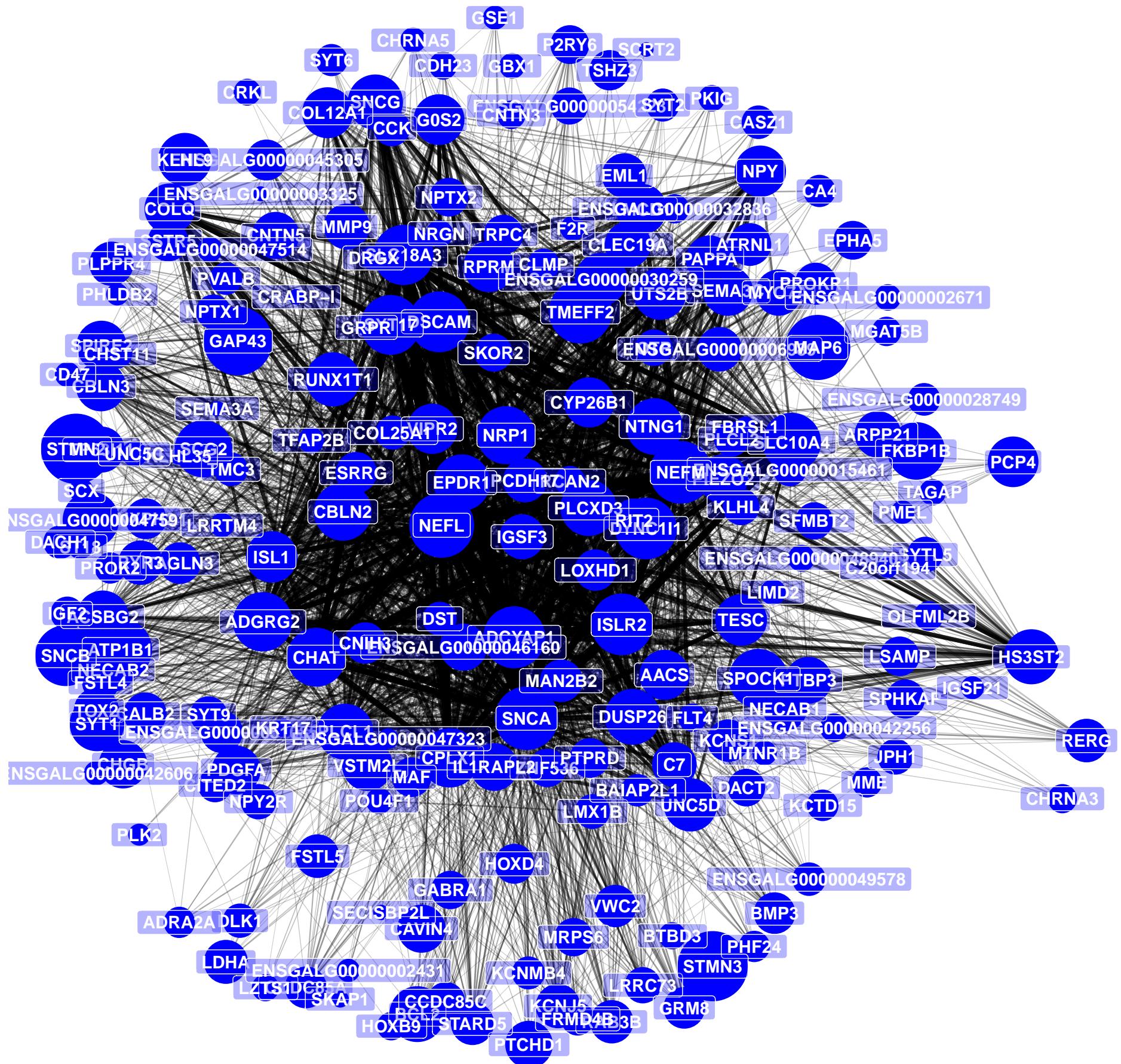




1	CFAP126	DYDC2	RSPH1	ENSGALG00000013268	FAM183A	RSPH9	ENKUR	RAB36
2	C9orf116	CFAP99	CFAP45	CFAP100	PPIL6	EFCAB10	ENSGALG00000044151	ENSGALG0000003464
3	SPEF2	ENSGALG00000044478	HYDIN	ZMYND10	ENSGALG00000013281	ENSGALG00000044224	AP5S1	FXYD2
4	ENSGALG00000043861	LZTFL1	DNAI1	NME1	ENSGALG0000004495	PNRC1	ARMC4	DNAH10
5	C1H21ORF59	DAW1	CFAP44	ENSGALG00000036896	AK7	HOPX	SPAG17	ENSGALG00000019932
6	IFT46	CDKL1	ENSGALG0000005247	ENSGALG00000051202	IQUB	ENSGALG0000001244	ENSGALG00000003013	ENSGALG00000034761
7	DUSP14	ENSGALG00000028830	ENSGALG00000015224	CFAP77	FHL1	CCDC170	RIBC2	DRC1
8	ENSGALG00000028207	ENSGALG00000012317	TNFRSF11B	DNAAF1	ENSGALG00000019240	ENSGALG00000033254	C1H11ORF70	CRYBB2
9	ENSGALG00000054317	ANTXR1	ENSGALG0000008518	ENSGALG0000008309	KCNJ2	GAL	ASL2	CXCL12
10	ENSGALG00000011356	CFAP65	NSUN7	ENSGALG00000040709	ENO1	SEPTIN12	PDLIM3	MDGA2
11	CALCA	FOXP2	CFD	ENTPD2	ACTN1	PLS1	FNDC3A	ENSGALG00000023763
12	CAPSL	CFAP57	CFAP70	ENSGALG00000044002	WDR63	ENSGALG00000053383	ARHGAP24	IQCA1
13	ENSGALG0000003590	TMEM255B	ENSGALG00000053594	TEKT3	PP2D1	SDR42E2	RFLNA	BEGAIN
14	TEKT1	CNKS2R	SDC4	ENSGALG0000001111	ENSGALG00000016755	LXN	THBS1	ENSGALG00000054746
15	PPL	BHLHE40	BARX2	FERD3L	MATN2	SYTL1	ENSGALG00000034756	CRIP1
16	GOLPH3L							

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0060122	inner ear receptor cell stereocilium organization	BP	4	2	0.0003869
GO:0060119	inner ear receptor cell development	BP	5	2	0.0006415
GO:1903078	positive regulation of protein localization to plasma membrane	BP	5	2	0.0006415
GO:1903076	regulation of protein localization to plasma membrane	BP	5	2	0.0006415
GO:1904377	positive regulation of protein localization to cell periphery	BP	7	2	0.001333
GO:1905477	positive regulation of protein localization to membrane	BP	7	2	0.001333
GO:1904375	regulation of protein localization to cell periphery	BP	8	2	0.001768
GO:0060113	inner ear receptor cell differentiation	BP	9	2	0.002261
GO:1905475	regulation of protein localization to membrane	BP	9	2	0.002261
GO:0061061	muscle structure development	BP	72	4	0.002757

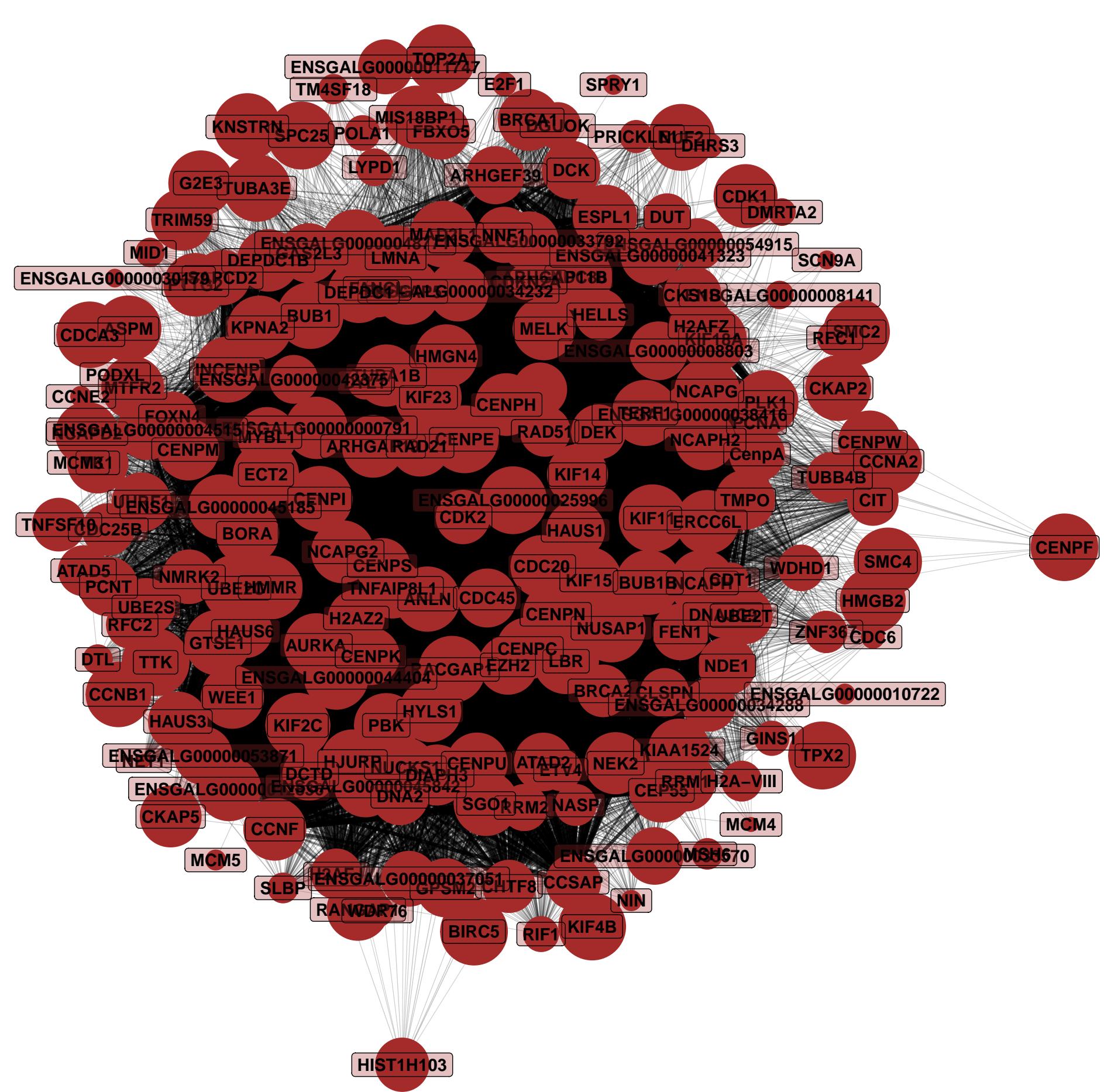
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga01232</i>	Nucleotide metabolism	78	4	0.003684
<i>path:gga00220</i>	Arginine biosynthesis	17	2	0.008187
<i>path:gga01230</i>	Biosynthesis of amino acids	58	3	0.01159
<i>path:gga00230</i>	Purine metabolism	115	4	0.01422
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	2	0.0276
<i>path:gga01240</i>	Biosynthesis of cofactors	118	3	0.071
<i>path:gga00240</i>	Pyrimidine metabolism	56	2	0.07566
<i>path:gga00730</i>	Thiamine metabolism	12	1	0.09314
<i>path:gga04512</i>	ECM–receptor interaction	68	2	0.1053
<i>path:gga00910</i>	Nitrogen metabolism	14	1	0.1078



1	STMN2	STMN3	MAP6	NEFM	NEFL	SYT1	SCG2	GAP43
2	SNCA	TMEFF2	ENSGALG00000047591	SNCB	CHGB	ATP1B1	CPLX1	ADCYAP1
3	SPOCK1	RUNX1T1	CAVIN4	DYNC1I1	ISLR2	CBLN2	DSCAM	SLC18A3
4	TAGLN3	PCP4	HS3ST2	NRP1	ADGRG2	PLCXD3	SYT17	FKBP1B
5	SLC10A4	NTNG1	CHAT	IGSF3	PLCL1	VSTM2L	COLQ	G0S2
6	SNCG	DUSP26	UNC5D	PDGFA	RPRM	ENSGALG00000030259	EPDR1	SPIRE2
7	LMCD1	MYO7A	ACSBG2	RAB3B	ARPP21	TESC	KLHL9	COL12A1
8	CALB2	TP53I11	NPY	ZNF536	UTS2B	BCL2	ISL1	CBLN3
9	AACS	PTBP3	FSTL5	KCNJ5	PLPPR4	CYP26B1	MAN2B2	RYR3
10	CNTN5	IL1RAPL2	VIPR2	LDHA	PIEZ02	PTCHD1	ENSGALG00000032836	NECAB1
11	ENSGALG00000045305	CCDC85A	PTPRD	SEMA3C	NECAB2	TOX2	NXPH2	EML1
12	PAPPA	STARD5	TSHZ3	CCDC85C	NPTX2	CLEC19A	MRPS6	ENSGALG00000046160
13	C7	CITED2	GRM8	RIT2	SPHKAP	ENSGALG00000054223	MMP9	PROKR1
14	EPHA5	LRRC73	BMP3	KLHL4	MAF	ENSGALG0000006989	ENSGALG00000051085	RERG
15	JPH1	ESRRG	HOXD4	NPTX1	PVALB	ATRNL1	GABRA1	DACT2
16	KCNS1	P2RY6	TRPC4	FRMD4B	VWC2	COL25A1	SYT9	CNIH3
17	FSTL4	DST	ENSGALG00000028749	RCAN2	LMX1B	NPY2R	SKOR2	TMC3
18	SYT5	ENSGALG00000042256	ADRA2A	PCDH17	CCK	SFMBT2	OTP	SYT6
19	SSTR5	LOXHD1	CRABP-I	CASZ1	ST18	PLCL2	PHF24	OLFML2B
20	FLT4	DLK1	CD47	TAGAP	ENSGALG00000049578	KCNMB4	UNC5C	LSAMP
21	BTBD3	DACH1	CHST11	IGF2	CRKL	KCTD15	TFAP2B	NRGN
22	PKIG	F2R	CA4	POU4F1	ENSGALG00000047323	ENSGALG00000015461	PHLDB2	MTNR1B
23	SEMA3A	CHRNA5	CDH23	LIMD2	MME	SCX	CHRNA3	HOXB9
24	PROK2	CLMP	GSE1	ENSGALG00000047514	CNTN3	SYT2	LRRTM4	ENSGALG0000002671
25	C20orf194	IGSF21	KLHL35	BAIAP2L1	SECISBP2L	ENSGALG00000042606	MGAT5B	FBRSL1
26	ENSGALG0000003325	PLK2	ENSGALG0000002431	ENSGALG00000048940	GRPR	LZTS1	GBX1	DRGX
27	PMEL	SKAP1	SCRT2	KRT17				

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0031175	neuron projection development	BP	113	14	1.23e-09
GO:0048666	neuron development	BP	126	14	5.22e-09
GO:0007399	nervous system development	BP	260	19	1.111e-08
GO:0120036	plasma membrane bounded cell projection organization	BP	139	14	1.874e-08
GO:0030182	neuron differentiation	BP	166	15	2.52e-08
GO:0030030	cell projection organization	BP	143	14	2.699e-08
GO:0048731	system development	BP	490	25	7.084e-08
GO:0030154	cell differentiation	BP	425	23	8.579e-08
GO:0048699	generation of neurons	BP	182	15	8.63e-08
GO:0022008	neurogenesis	BP	185	15	1.071e-07

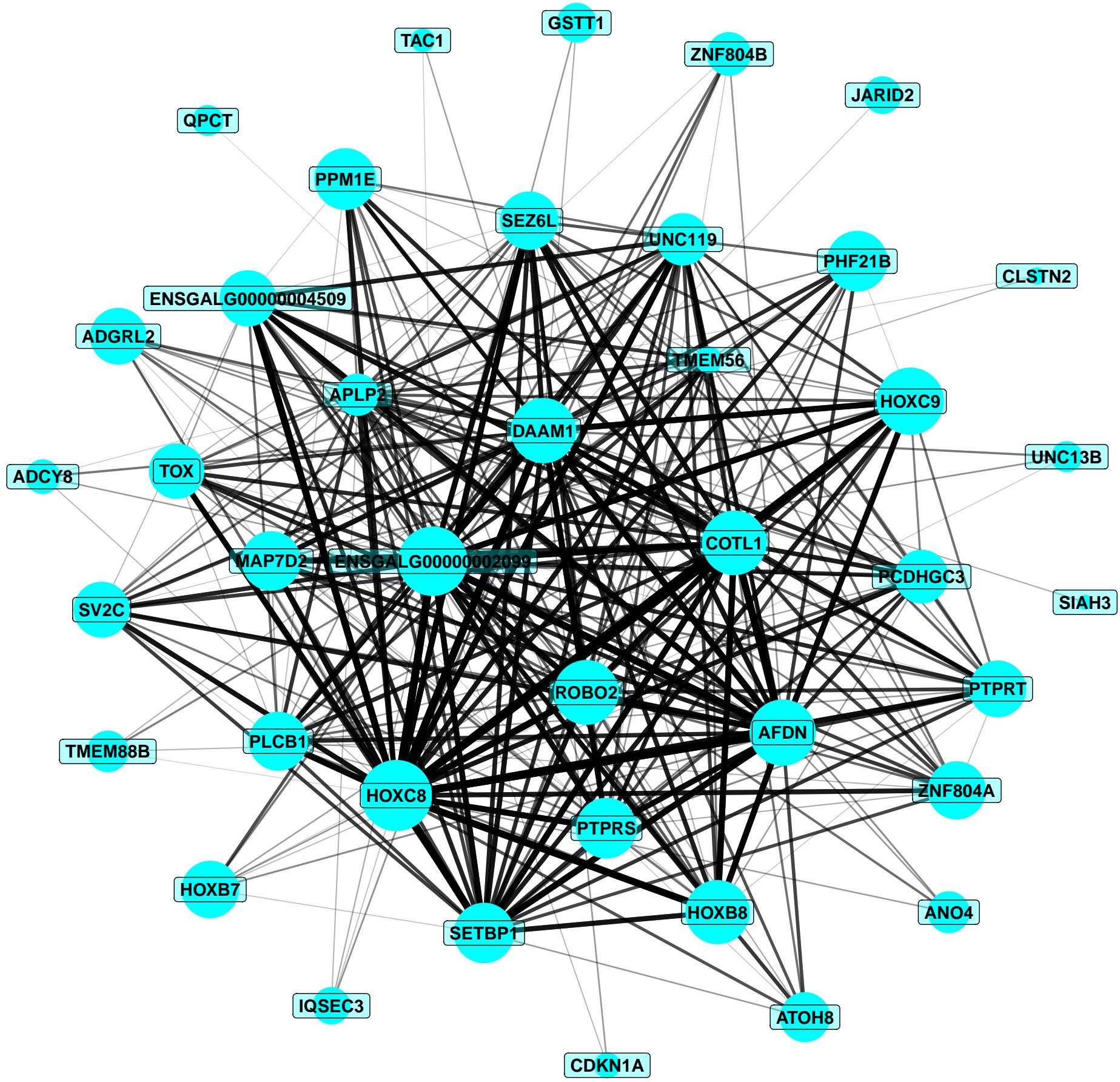
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	298	16	9.713e–06
<i>path:gga04810</i>	Regulation of actin cytoskeleton	192	6	0.06713
<i>path:gga04510</i>	Focal adhesion	173	5	0.1159
<i>path:gga00360</i>	Phenylalanine metabolism	12	1	0.1646
<i>path:gga04020</i>	Calcium signaling pathway	204	5	0.1878
<i>path:gga00910</i>	Nitrogen metabolism	14	1	0.1893
<i>path:gga00061</i>	Fatty acid biosynthesis	16	1	0.2132
<i>path:gga04920</i>	Adipocytokine signaling pathway	60	2	0.2242
<i>path:gga00511</i>	Other glycan degradation	17	1	0.225
<i>path:gga00340</i>	Histidine metabolism	18	1	0.2365



1	NUSAP1	TOP2A	ENSGALG00000025996	CENPF	SMC2	CENPE	TPX2	KIF11
2	UBE2C	KIF4B	SMC4	NDC80	BIRC5	SPC25	KNSTRN	RACGAP1
3	TTK	ENSGALG00000048771	ASPM	INCENP	KIF15	NUF2	DLGAP5	KPNA2
4	BUB1	KIF23	TUBA3E	CDCA3	ECT2	GTSE1	KIF18A	CKAP2
5	ENSGALG00000012836	PLK1	AURKA	CDK1	NCAPG	NCAPH	ANLN	BUB1B
6	MAD2L1	CENPI	PBK	CCNB1	CCNA2	TK1	CENPW	KIF2C
7	SGO1	ENSGALG00000045185	HMGB2	BRCA1	ENSGALG00000044404	TERF1	CEP55	ENSGALG00000038416
8	HMMR	PTTG2	CDC20	UHRF1	G2E3	ESPL1	HJURP	CENPH
9	CENPN	BORA	ERCC6L	ENSGALG00000045842	LBR	NCAPD2	ARHGAP11B	LMNA
10	NCAPG2	MIS18BP1	KIAA1524	MELK	NEK2	H2AFZ	HMGN4	CCNF
11	WEE1	ENSGALG00000000791	CENPC	TUBA1B	ENSGALG00000011747	CENPK	DIAPH3	DEPDC1
12	DEPDC1B	NCAPH2	RRM1	ARHGAP19	CENPM	CDC45	ENSGALG0000004515	MTFR2
13	HAUS1	KIF14	ENSGALG00000034232	HYLS1	FANCL	DNA2	CENPU	TRIM59
14	HAUS3	ENSGALG00000053871	GAS2L3	CDK2	ENSGALG00000033792	TMPO	MYBL1	TNFAIP8L1
15	ENSGALG00000041323	HIST1H103	NUCKS1	FEN1	RANGAP1	NMRK2	CKS1B	H2AZ2
16	ATAD2	RRM2	GPSM2	DGUOK	CHTF8	UBE2T	HELLS	NA
17	NDE1	ARHGEF39	ENSGALG00000037051	CENPS	RAD21	FBXO5	ENSGALG00000034288	EZH2
18	ENSGALG0000008803	DCK	CenpA	RAD51	PCNT	CKAP5	NNF1	BRCA2
19	DEK	PCNA	UBE2S	DCTD	SAPCD2	ATAD5	HAUS6	ENSGALG00000054915
20	WDHD1	ENSGALG00000033570	DUT	RFC2	CLSPN	H2AFJ	ENSGALG00000042375	CDC25B
21	TNFSF10	CCSAP	DNAJC9	NASP	CIT	TUBB4B	ZNF367	FOXN4
22	GIN51	DYL1	CDT1	RIF1	H2A-VIII	ETV4	SLBP	WDR76
23	DTL	POLA1	ENSGALG00000010722	RFC1	LYPD1	MSH6	E2F1	CDC6
24	MCM3	MCM5	PRICKLE1	ENSGALG0000008141	DMRTA2	MID1	NIN	NET1
25	PODXL	TM4SF18	ENSGALG00000030179	CCNE2	SPRY1	MCM4	DHRS3	SCN9A
26	CDKN2A							

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0051276	chromosome organization	BP	174	27	2.248e-20
GO:0000278	mitotic cell cycle	BP	100	21	6.787e-19
GO:0007049	cell cycle	BP	206	27	2.045e-18
GO:1903047	mitotic cell cycle process	BP	78	18	3.906e-17
GO:0022402	cell cycle process	BP	129	21	1.698e-16
GO:0006996	organelle organization	BP	435	32	2.923e-14
GO:0051383	kinetochore organization	BP	10	8	7.712e-14
GO:0007059	chromosome segregation	BP	43	12	6.718e-13
GO:0065004	protein-DNA complex assembly	BP	36	10	6.247e-11
GO:0034508	centromere complex assembly	BP	12	7	9.311e-11

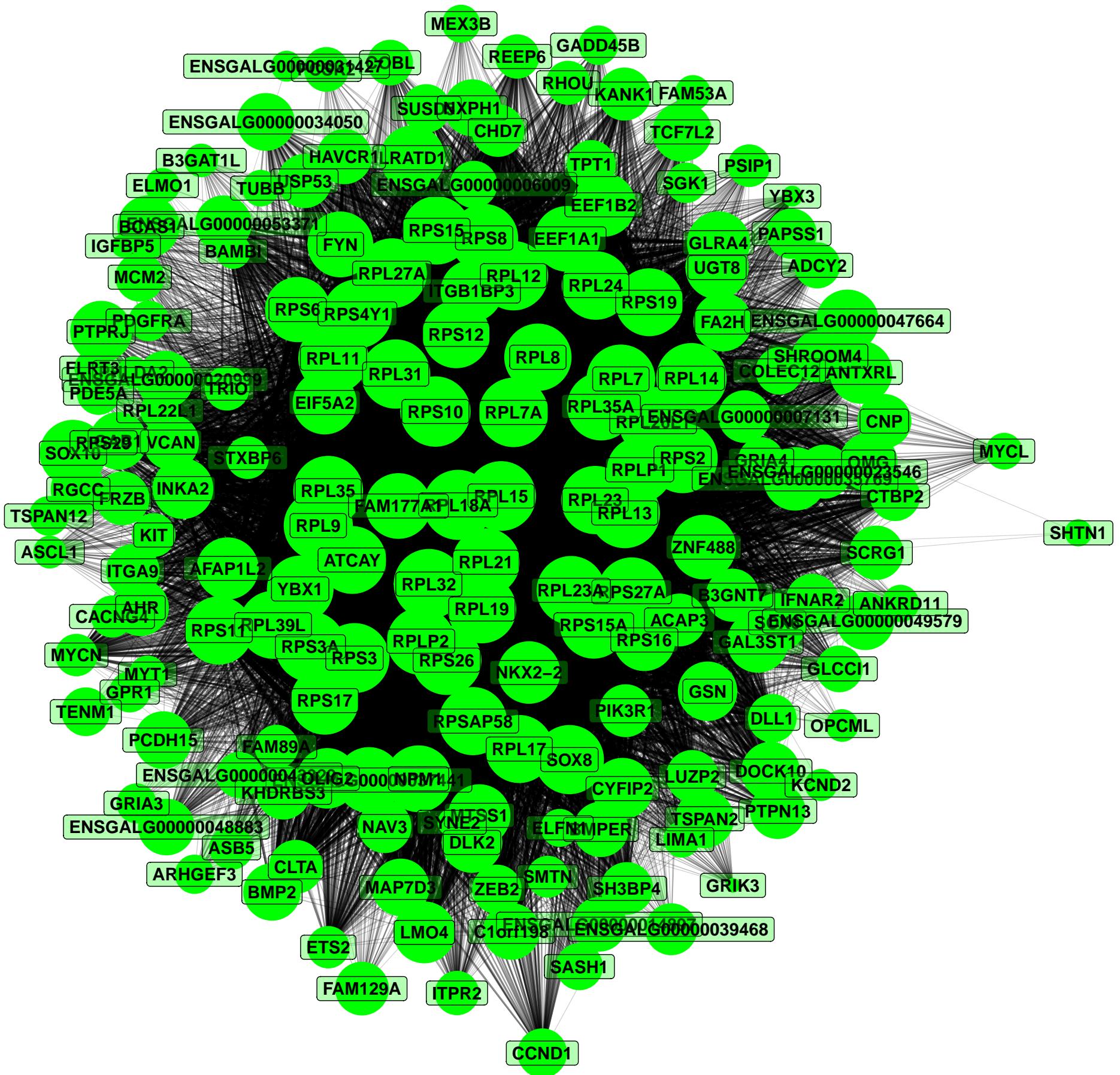
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04110</i>	Cell cycle	113	23	2.855e-20
<i>path:gga03030</i>	DNA replication	29	9	1.912e-10
<i>path:gga04114</i>	Oocyte meiosis	97	13	1.423e-09
<i>path:gga04914</i>	Progesterone-mediated oocyte maturation	79	9	2.098e-06
<i>path:gga00240</i>	Pyrimidine metabolism	56	7	1.585e-05
<i>path:gga03460</i>	Fanconi anemia pathway	48	6	6.528e-05
<i>path:gga01232</i>	Nucleotide metabolism	78	7	0.0001379
<i>path:gga03430</i>	Mismatch repair	19	4	0.0001426
<i>path:gga04115</i>	p53 signaling pathway	63	6	0.0003016
<i>path:gga04217</i>	Necroptosis	109	6	0.005184





	Term	Ont	N	n	Adj. p-value
GO:0061000	negative regulation of dendritic spine development	BP	1	1	0.003079
GO:0051574	positive regulation of histone H3–K9 methylation	BP	1	1	0.003079
GO:0051570	regulation of histone H3–K9 methylation	BP	1	1	0.003079
GO:0034721	histone H3–K4 demethylation, trimethyl–H3–K4–specific	BP	2	1	0.006149
GO:0051567	histone H3–K9 methylation	BP	2	1	0.006149
GO:0048671	negative regulation of collateral sprouting	BP	2	1	0.006149
GO:0031061	negative regulation of histone methylation	BP	2	1	0.006149
GO:0031057	negative regulation of histone modification	BP	2	1	0.006149
GO:0031062	positive regulation of histone methylation	BP	2	1	0.006149
GO:0034720	histone H3–K4 demethylation	BP	3	1	0.009209

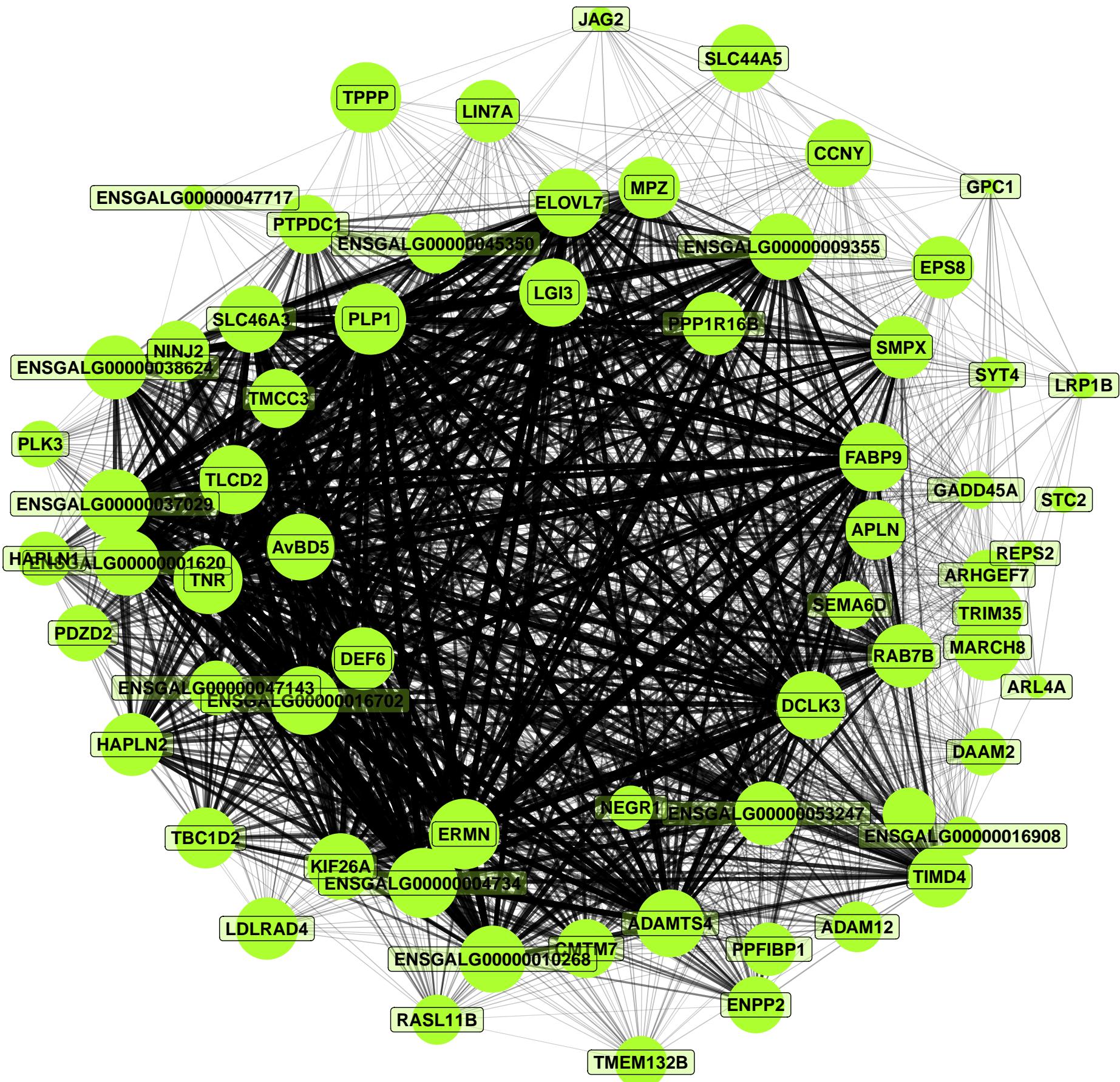
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04540</i>	Gap junction	79	2	0.02454
<i>path:gga04912</i>	GnRH signaling pathway	79	2	0.02454
<i>path:gga04916</i>	Melanogenesis	88	2	0.02997
<i>path:gga04270</i>	Vascular smooth muscle contraction	110	2	0.045
<i>path:gga04371</i>	Apelin signaling pathway	113	2	0.04722
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	123	2	0.05493
<i>path:gga04310</i>	Wnt signaling pathway	137	2	0.06641
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	30	1	0.08845
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	31	1	0.09127
<i>path:gga00051</i>	Fructose and mannose metabolism	34	1	0.09966



1	UGT8	RPS3A	RPL13	RPL32	RPS10	RPS2	RPL27A	RPS26
2	RPL14	RPL15	RPL35	RPL11	RPL18A	RPL26L1	RPS27A	RPS3
3	RPL7A	RPL31	RPL9	RPL39L	RPL12	SOX10	RPL23	RPS11
4	RPS4Y1	RPL17	RPS19	RPS15	RPL19	RPL7	RPS17	RPL35A
5	OLIG2	RPL24	RPS15A	RPS8	RPL23A	RPL8	RPL21	RPS12
6	SOX8	BCAS1	RPLP2	RPLP1	RPSAP58	YBX1	RPS6	ATCAY
7	ENSGALG00000037441	ITGB1BP3	NKX2-2	TSPAN2	FAM177A1	ZNF488	EEF1A1	RPS16
8	LRATD1	NPM1	ENSGALG00000047664	ENSGALG00000035769	AFAP1L2	GLRA4	EEF1B2	EIF5A2
9	FYN	ANTXRL	OMG	NXPH1	LMO4	B3GNT7	TCF7L2	TPT1
10	PTPRJ	DLL1	CNP	PCDH15	MTSS1	CYFIP2	DOCK10	GAL3ST1
11	VCAN	INKA2	ACAP3	DLK2	FA2H	SOX6	PDGFRA	C1orf198
12	COLEC12	KHDRBS3	GSN	BMPER	CHD7	ENSGALG00000053371	ENSGALG00000043329	ENSGALG00000007131
13	RGCC	CTBP2	MYT1	SUSD5	GAB1	ENSGALG00000014897	RPS29	PIK3R1
14	ENSGALG00000049579	ENSGALG00000023546	ENSGALG00000020999	BMP2	MAP7D3	ITGA9	ZEB2	IFNAR2
15	ENSGALG0000006009	AHR	NAV3	LUZP2	ENSGALG00000034050	SH3BP4	PTPN13	GLCCI1
16	HAVCR1	MCM2	KANK1	CLTA	SCRG1	CCND1	USP53	GRIA4
17	ETS2	FAM129A	FAM89A	SGK1	FRZB	ENSGALG00000048883	PAPSS1	COBL
18	SASH1	SMTN	SHROOM4	ITPR2	RPL22L1	ASB5	CACNG4	GPR1
19	RHOU	PHLDA2	REEP6	PSIP1	KIT	ENSGALG00000039468	ADCY2	TENM1
20	ASCL1	PCSK2	BAMBI	TRIO	MYCN	STXBP6	LIMA1	GRIA3
21	TSPAN12	TUBB	SYNE2	PDE5A	ARHGEF3	ANKRD11	ELFN1	ELMO1
22	YBX3	IGFBP5	KCND2	FLRT3	FAM53A	GRIK3	MYCL	GADD45B
23	OPCML	MEX3B	ENSGALG00000031427	B3GAT1L	SHTN1			

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0006412	translation	BP	86	17	7.803e-16
GO:0043043	peptide biosynthetic process	BP	87	17	9.589e-16
GO:0043604	amide biosynthetic process	BP	100	17	1.114e-14
GO:0006518	peptide metabolic process	BP	106	17	3.056e-14
GO:0043603	cellular amide metabolic process	BP	124	17	4.414e-13
GO:0010467	gene expression	BP	611	31	6.446e-11
GO:0044271	cellular nitrogen compound biosynthetic process	BP	532	28	2.666e-10
GO:0034645	cellular macromolecule biosynthetic process	BP	547	28	5.025e-10
GO:0009059	macromolecule biosynthetic process	BP	549	28	5.459e-10
GO:1901566	organonitrogen compound biosynthetic process	BP	207	17	1.69e-09

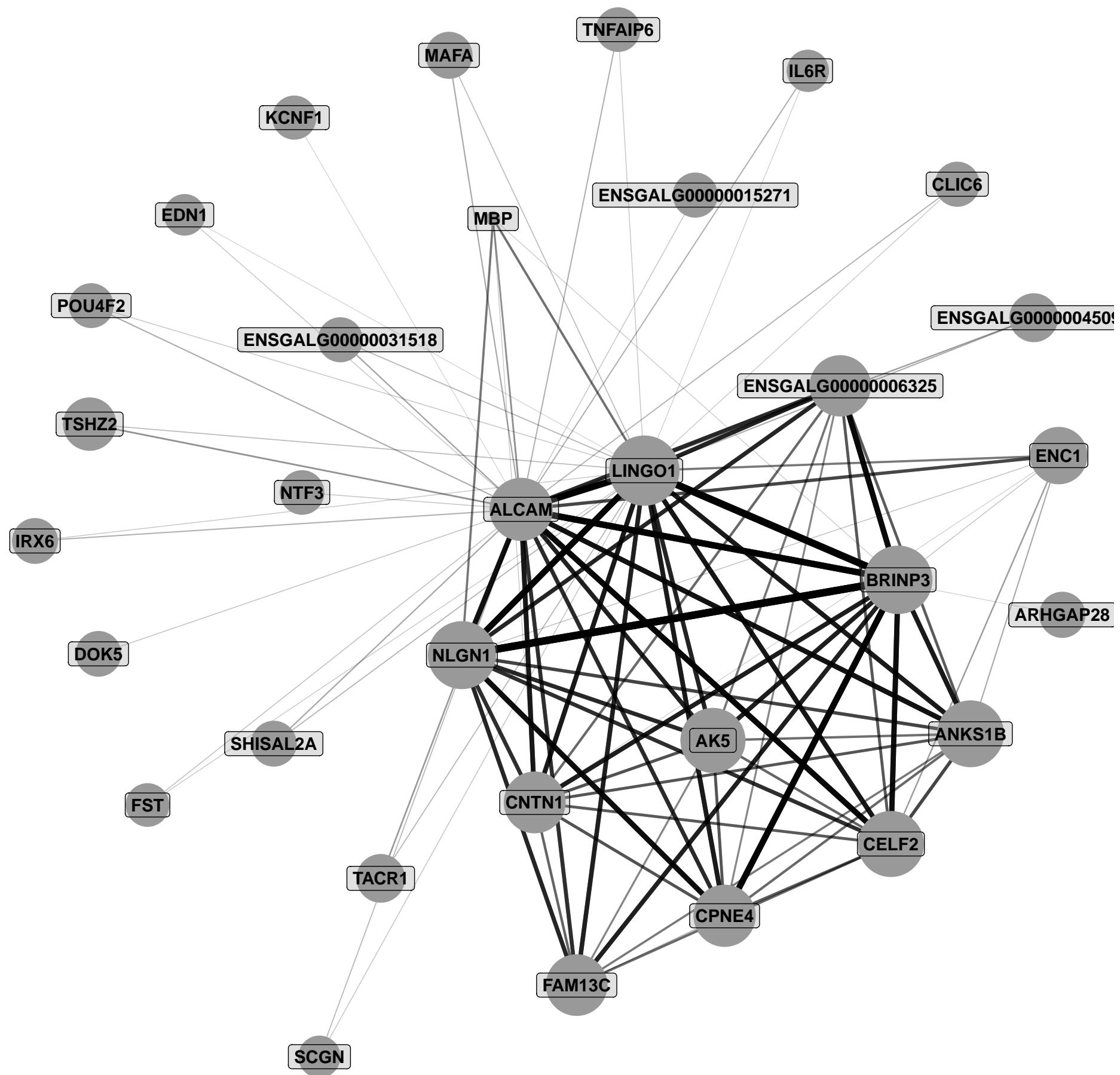
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga03010</i>	Ribosome	115	45	3.676e-56
<i>path:gga04540</i>	Gap junction	79	4	0.01982
<i>path:gga04310</i>	Wnt signaling pathway	137	5	0.03386
<i>path:gga03264</i>	Virion – Flavivirus	3	1	0.03869
<i>path:gga04810</i>	Regulation of actin cytoskeleton	192	6	0.04031
<i>path:gga04068</i>	FoxO signaling pathway	112	4	0.05914
<i>path:gga04371</i>	Apelin signaling pathway	113	4	0.06071
<i>path:gga04520</i>	Adherens junction	69	3	0.06145
<i>path:gga04210</i>	Apoptosis	116	4	0.06556
<i>path:gga05132</i>	Salmonella infection	220	6	0.0689



1	FABP9	ERMN	PLP1	ENSGALG0000004734	DCLK3	ENSGALG0000037029	TLCD2	ELOVL7
2	TNR	TPPP	LGI3	ENSGALG0000009355	ADAMTS4	ENSGALG0000016702	SLC4A5	AvBD5
3	CCNY	KIF26A	TRIM35	SLC46A3	ENSGALG0000010268	ENSGALG0000053247	PPP1R16B	ENSGALG0000001620
4	MARCH8	ENSGALG0000038624	DEF6	RAB7B	NINJ2	LIN7A	LDLRAD4	TMCC3
5	SMPX	TIMD4	HAPLN2	MPZ	EPS8	APLN	TBC1D2	CMTM7
6	ENSGALG0000045350	ENPP2	ENSGALG0000047143	HAPLN1	PTPDC1	PDZD2	PPFIBP1	ADAM12
7	TMEM132B	ARHGEF7	PLK3	SEMA6D	DAAM2	NA	NEGR1	RASL11B
8	SYT4	GADD45A	ENSGALG0000016908	STC2	JAG2	LRP1B	REPS2	ENSGALG0000047717
9	ARL4A	GPC1						

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0048709	oligodendrocyte differentiation	BP	9	2	0.0008262
GO:0008366	axon ensheathment	BP	12	2	0.0015
GO:0007272	ensheathment of neurons	BP	12	2	0.0015
GO:0042552	myelination	BP	12	2	0.0015
GO:0010001	glial cell differentiation	BP	21	2	0.004641
GO:0048715	negative regulation of oligodendrocyte differentiation	BP	1	1	0.004881
GO:1902726	positive regulation of skeletal muscle satellite cell differentiation	BP	1	1	0.004881
GO:1902724	positive regulation of skeletal muscle satellite cell proliferation	BP	1	1	0.004881
GO:0022610	biological adhesion	BP	144	4	0.00533
GO:0007155	cell adhesion	BP	144	4	0.00533

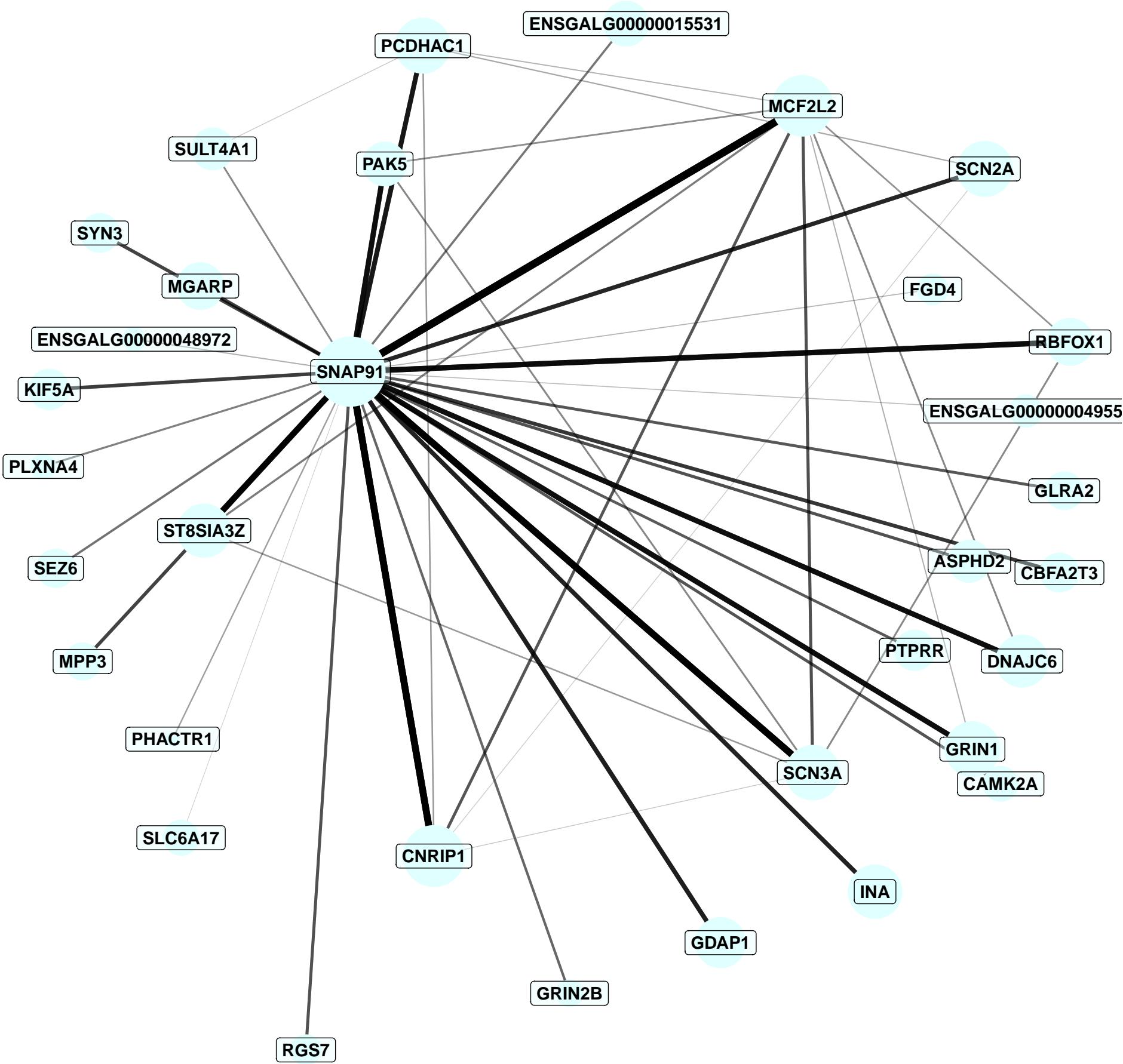
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04514</i>	Cell adhesion molecules	108	3	0.01575
<i>path:gga04068</i>	FoxO signaling pathway	112	2	0.1037
<i>path:gga04371</i>	Apelin signaling pathway	113	2	0.1053
<i>path:gga00062</i>	Fatty acid elongation	23	1	0.1065
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	27	1	0.1239
<i>path:gga00565</i>	Ether lipid metabolism	38	1	0.1699
<i>path:gga01212</i>	Fatty acid metabolism	50	1	0.2174
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.225
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.2622
<i>path:gga04115</i>	p53 signaling pathway	63	1	0.2658



1	LINGO1	BRINP3	NLGN1	CELF2	ANKS1B	AK5	ALCAM	CNTN1
2	CPNE4	ENSGALG00000006325	FAM13C	ENC1	TSHZ2	MAFA	TACR1	ENSGALG00000045096
3	SHISAL2A	ENSGALG00000031518	ARHGAP28	DOK5	TNFAIP6	ENSGALG00000015271	FST	POU4F2
4	CLIC6	KCNF1	IRX6	NTF3	IL6R	EDN1	SCGN	MBP
5								

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0031175	neuron projection development	BP	113	4	0.0001136
GO:0048666	neuron development	BP	126	4	0.0001731
GO:0120036	plasma membrane bounded cell projection organization	BP	139	4	0.0002524
GO:0007399	nervous system development	BP	260	5	0.0002609
GO:0030030	cell projection organization	BP	143	4	0.0002813
GO:0030182	neuron differentiation	BP	166	4	0.0004957
GO:0048699	generation of neurons	BP	182	4	0.0007008
GO:0022008	neurogenesis	BP	185	4	0.000745
GO:0048468	cell development	BP	219	4	0.001394
GO:0045664	regulation of neuron differentiation	BP	25	2	0.001425

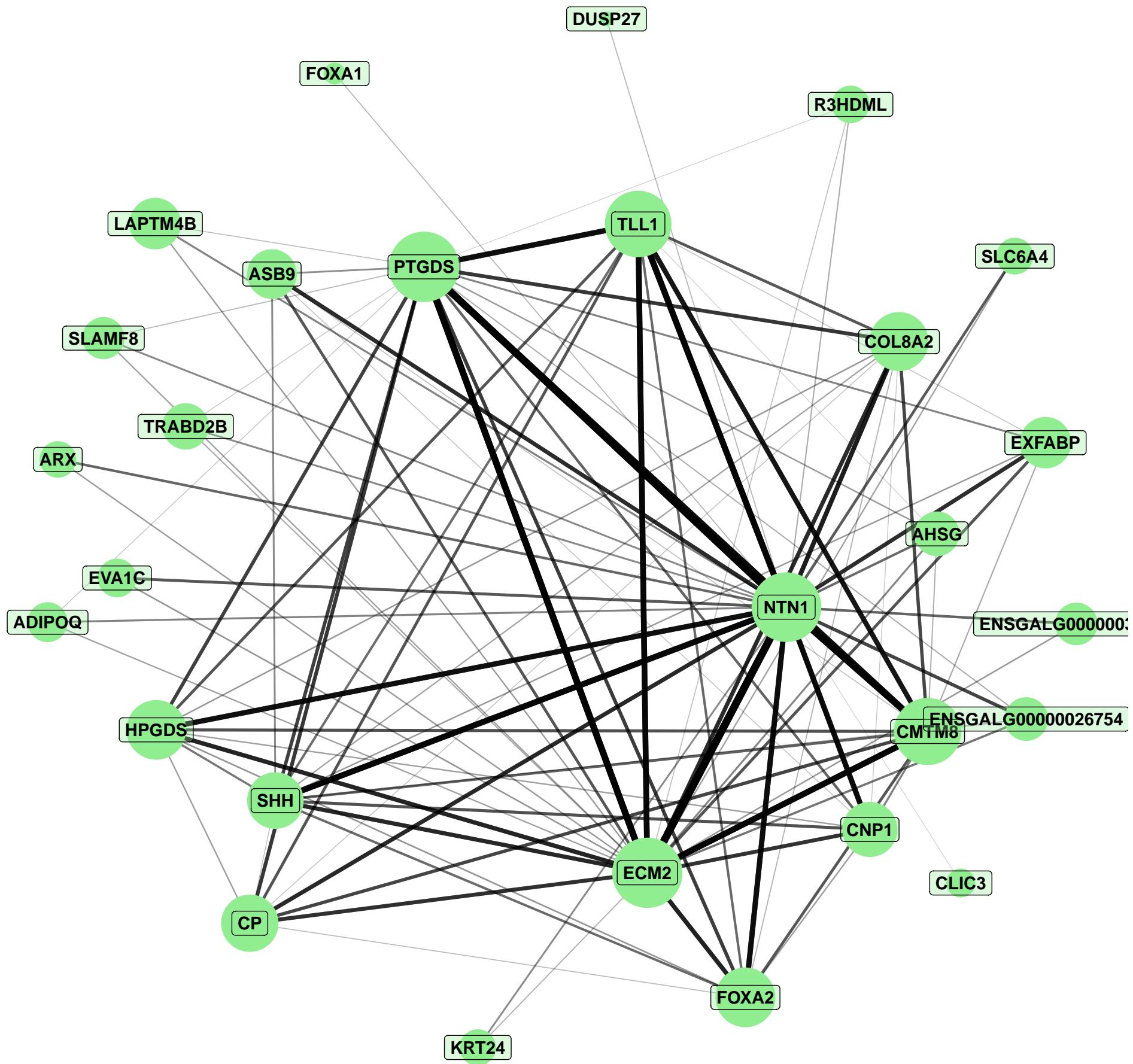
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04514</i>	Cell adhesion molecules	108	3	0.001796
<i>path:gga00730</i>	Thiamine metabolism	12	1	0.02671
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	298	3	0.02885
<i>path:gga04010</i>	MAPK signaling pathway	244	2	0.1041
<i>path:gga01232</i>	Nucleotide metabolism	78	1	0.1617
<i>path:gga04350</i>	TGF–beta signaling pathway	86	1	0.1768
<i>path:gga04916</i>	Melanogenesis	88	1	0.1806
<i>path:gga04270</i>	Vascular smooth muscle contraction	110	1	0.2205
<i>path:gga00230</i>	Purine metabolism	115	1	0.2293
<i>path:gga04210</i>	Apoptosis	116	1	0.2311



1	SNAP91	GRIN1	MCF2L2	CNRIP1	PCDHAC1	SCN2A	RBFOX1	SCN3A
2	MGARP	ST8SIA3Z	INA	DNAJC6	GDAP1	ENSGALG00000015531	SEZ6	SULT4A1
3	PAK5	GLRA2	SLC6A17	PTPRR	PLXNA4	CBFA2T3	SYN3	CAMK2A
4	RGS7	PHACTR1	ASPHD2	KIF5A	ENSGALG0000004955	ENSGALG00000048972	MPP3	FGD4
5	GRIN2B							

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0032515	negative regulation of phosphoprotein phosphatase activity	BP	6	1	0.01434
GO:0035308	negative regulation of protein dephosphorylation	BP	8	1	0.01907
GO:0031532	actin cytoskeleton reorganization	BP	9	1	0.02143
GO:0030038	contractile actin filament bundle assembly	BP	9	1	0.02143
GO:0043149	stress fiber assembly	BP	9	1	0.02143
GO:0010923	negative regulation of phosphatase activity	BP	11	1	0.02613
GO:0051017	actin filament bundle assembly	BP	13	1	0.03081
GO:0061572	actin filament bundle organization	BP	13	1	0.03081
GO:0035305	negative regulation of dephosphorylation	BP	13	1	0.03081
GO:0043666	regulation of phosphoprotein phosphatase activity	BP	13	1	0.03081

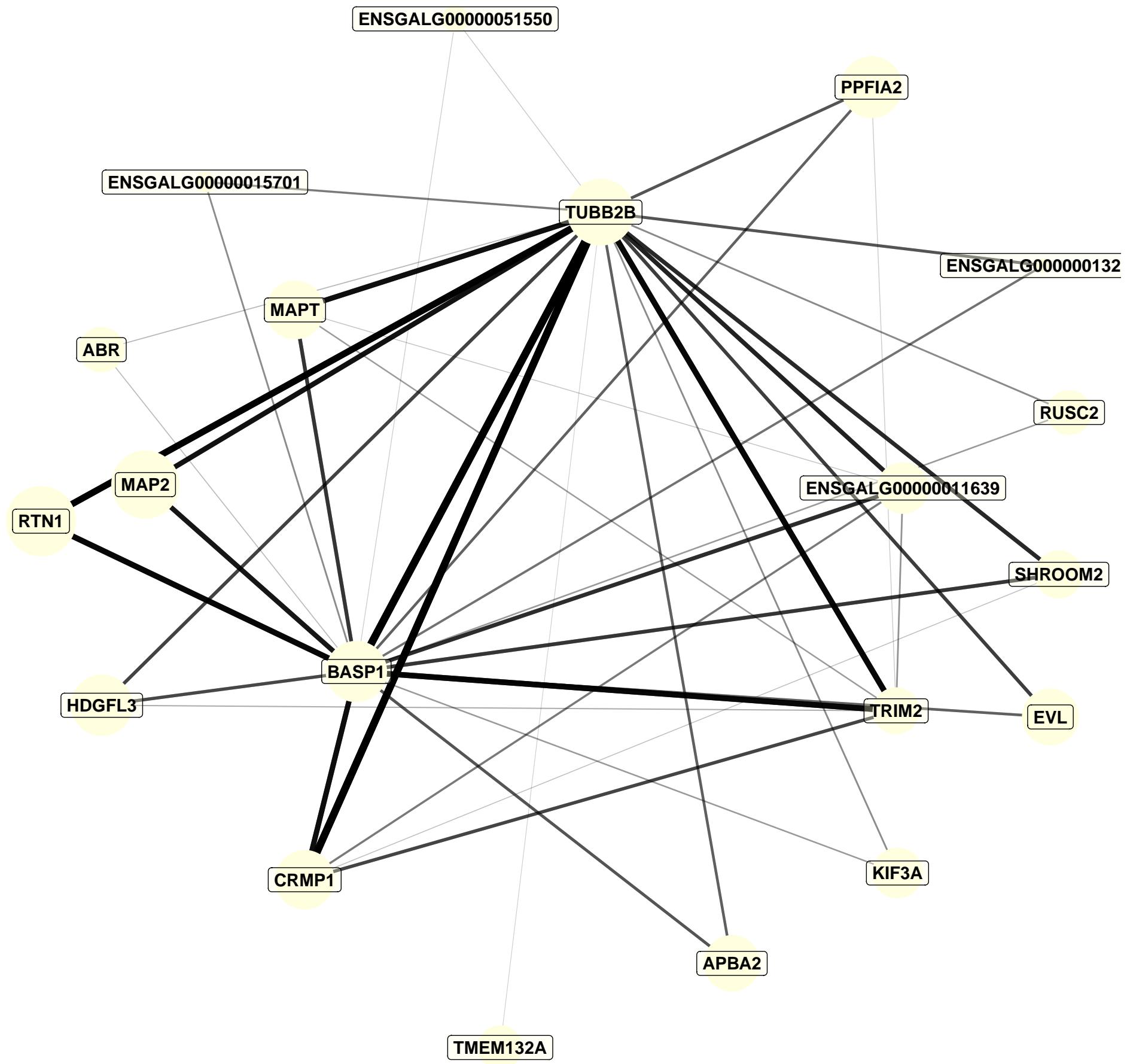
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04012</i>	ErbB signaling pathway	76	2	0.01427
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	298	3	0.03412
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	123	2	0.03505
<i>path:gga04020</i>	Calcium signaling pathway	204	2	0.08587
<i>path:gga04144</i>	Endocytosis	219	2	0.09685
<i>path:gga03015</i>	mRNA surveillance pathway	73	1	0.1615
<i>path:gga04912</i>	GnRH signaling pathway	79	1	0.1736
<i>path:gga04916</i>	Melanogenesis	88	1	0.1914
<i>path:gga04114</i>	Oocyte meiosis	97	1	0.2088
<i>path:gga04217</i>	Necroptosis	109	1	0.2315



1	PTGDS	ECM2	SHH	CMTM8	FOXA2	TLL1	HPGDS	CNP1
2	NTN1	EXFABP	ENSGALG00000026754	COL8A2	FOXA1	ARX	ASB9	KRT24
3	LAPTM4B	CP	ENSGALG00000035945	ADIPOQ	TRABD2B	AHSG	EVA1C	CLIC3
4	SLC6A4	R3HDM1	SLAMF8	DUSP27				

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0003415	chondrocyte hypertrophy	BP	4	2	2.552e-05
GO:0048588	developmental cell growth	BP	29	3	2.933e-05
GO:0002063	chondrocyte development	BP	7	2	8.896e-05
GO:0016049	cell growth	BP	51	3	0.0001621
GO:0048589	developmental growth	BP	65	3	0.0003333
GO:0008283	cell population proliferation	BP	176	4	0.0004712
GO:0051239	regulation of multicellular organismal process	BP	207	4	0.0008667
GO:0040007	growth	BP	95	3	0.001013
GO:0002062	chondrocyte differentiation	BP	23	2	0.00105
GO:0060560	developmental growth involved in morphogenesis	BP	26	2	0.001343

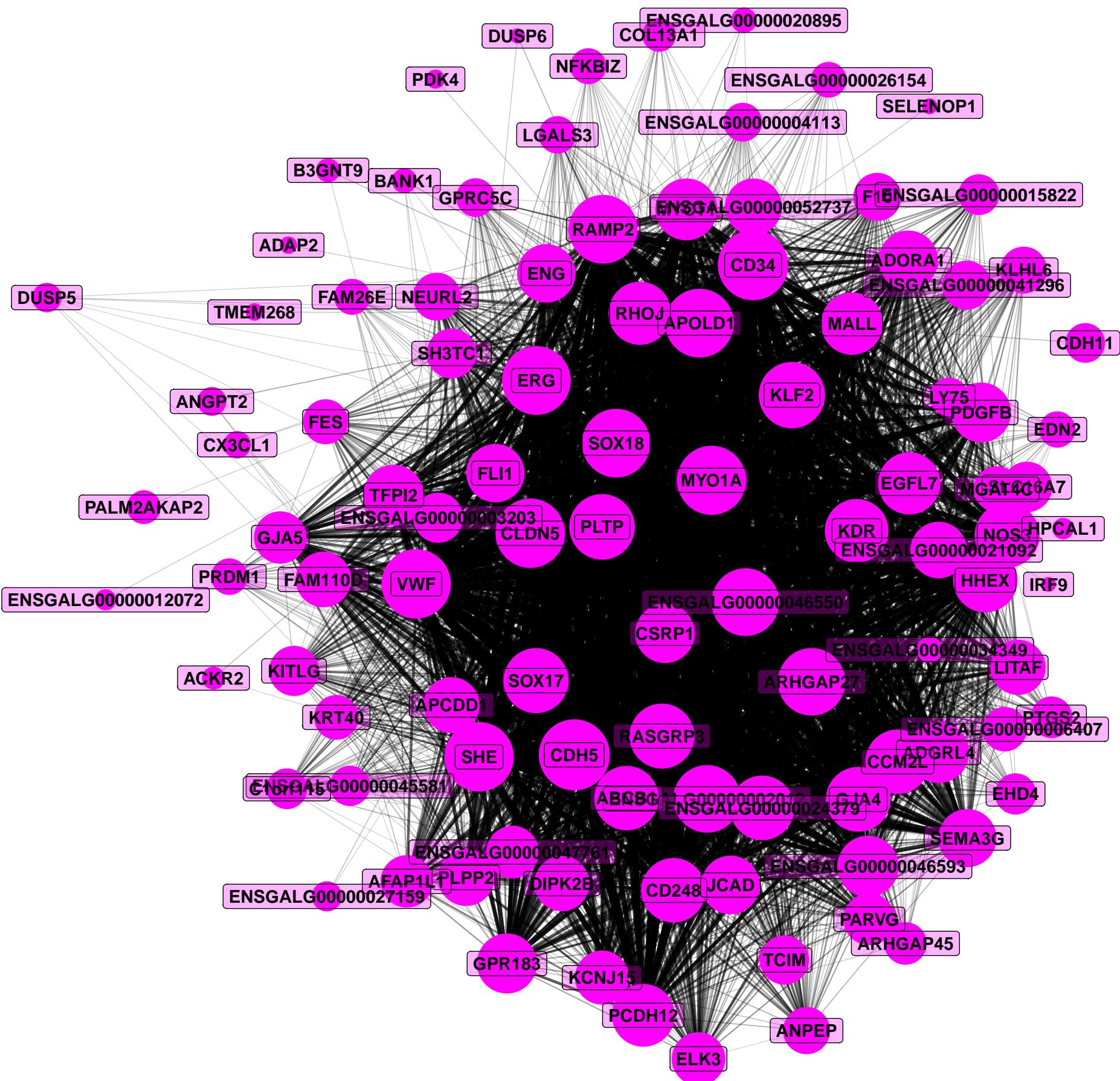
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga00590</i>	Arachidonic acid metabolism	41	2	0.003324
<i>path:gga00860</i>	Porphyrin metabolism	22	1	0.04529
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	30	1	0.06126
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	31	1	0.06324
<i>path:gga04216</i>	Ferroptosis	34	1	0.06915
<i>path:gga00480</i>	Glutathione metabolism	47	1	0.09435
<i>path:gga04340</i>	Hedgehog signaling pathway	47	1	0.09435
<i>path:gga03320</i>	PPAR signaling pathway	57	1	0.1133
<i>path:gga04920</i>	Adipocytokine signaling pathway	60	1	0.1189
<i>path:gga04270</i>	Vascular smooth muscle contraction	110	1	0.2074



1	RTN1	TUBB2B	MAP2	PPFIA2	MAPT	BASP1	TRIM2	CRMP1
2	EVL	ENSGALG00000011639	HDGFL3	APBA2	SHROOM2	RUSC2	ABR	TMEM132A
3	ENSGALG00000013212	KIF3A	ENSGALG00000015701	ENSGALG00000051550				

	Term	Ont	N	n	Adj. p-value
GO:0072311	glomerular epithelial cell differentiation	BP	2	1	0.002852
GO:0072010	glomerular epithelium development	BP	2	1	0.002852
GO:0072112	glomerular visceral epithelial cell differentiation	BP	2	1	0.002852
GO:0061318	renal filtration cell differentiation	BP	2	1	0.002852
GO:0032835	glomerulus development	BP	3	1	0.004275
GO:0061005	cell differentiation involved in kidney development	BP	5	1	0.007115
GO:0035850	epithelial cell differentiation involved in kidney development	BP	5	1	0.007115
GO:0031115	negative regulation of microtubule polymerization	BP	5	1	0.007115
GO:0031111	negative regulation of microtubule polymerization or depolymerization	BP	6	1	0.008532
GO:0031113	regulation of microtubule polymerization	BP	6	1	0.008532

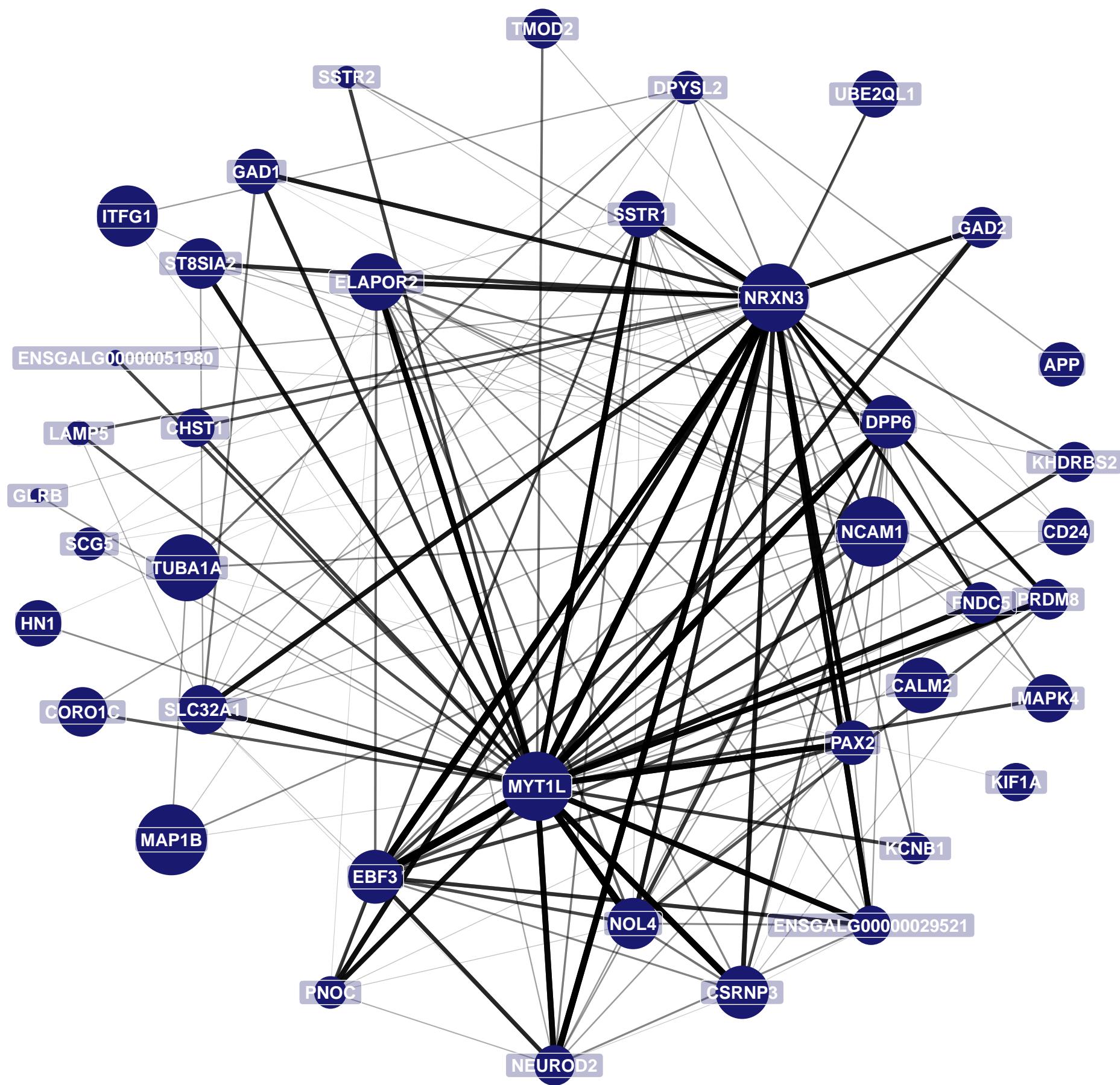
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga03267</i>	Virion – Adenovirus	3	1	0.004275
<i>path:gga04340</i>	Hedgehog signaling pathway	47	1	0.06502
<i>path:gga04540</i>	Gap junction	79	1	0.107
<i>path:gga04145</i>	Phagosome	126	1	0.1654
<i>path:gga05132</i>	Salmonella infection	220	1	0.2715
<i>path:gga04010</i>	MAPK signaling pathway	244	1	0.2965
<i>path:gga00780</i>	Biotin metabolism	3	0	1
<i>path:gga00785</i>	Lipoic acid metabolism	3	0	1
<i>path:gga00290</i>	Valine, leucine and isoleucine biosynthesis	3	0	1
<i>path:gga03264</i>	Virion – Flavivirus	3	0	1



1	CDH5	CD34	VWF	ERG	RAMP2	MYO1A	SOX18	APOLD1
2	MYCT1	ENSGALG00000046550	ENSGALG0000002012	SHE	KLF2	CD248	SOX17	NOS3
3	ENSGALG0000024379	PCDH12	ARHGAP27	CLDN5	HHEX	ABCB1	KDR	CCM2L
4	MALL	EGFL7	GJA4	GPR183	FLI1	RASGRP3	ADGRL4	PLPP2
5	FAM110D	TFPI2	DIPK2B	ENG	PARVG	ENSGALG0000052737	ENSGALG0000021092	RHOJ
6	SEMA3G	ENSGALG0000046593	ADORA1	PLTP	PDGFB	LITAF	ENSGALG0000047761	KCNJ15
7	JCAD	AFAP1L1	APCDD1	SH3TC1	CSRP1	KRT40	ENSGALG0000041296	NEURL2
8	ENSGALG0000004113	EDN2	TCIM	ENSGALG0000015822	ENSGALG0000006407	ELK3	ENSGALG0000045581	SLC16A7
9	MGAT4C	EHD4	GJA5	KLHL6	KITLG	ANPEP	C1orf115	ENSGALG0000003203
10	F10	PTGS2	FES	LGALS3	ACKR2	TMEM268	ARHGAP45	LY75
11	NFKBIZ	GPRC5C	PRDM1	ENSGALG0000026154	CDH11	ANGPT2	CX3CL1	PALM2AKAP2
12	FAM26E	COL13A1	HPCAL1	ENSGALG0000012072	DUSP5	DUSP6	ENSGALG0000027159	IRF9
13	BANK1	PDK4	ENSGALG0000034349	B3GNT9	ADAP2	SELENOP1	ENSGALG0000020895	

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0008217	regulation of blood pressure	BP	8	3	2.173e-05
GO:0008015	blood circulation	BP	28	4	5.132e-05
GO:0003013	circulatory system process	BP	28	4	5.132e-05
GO:0050728	negative regulation of inflammatory response	BP	10	2	0.002369
GO:0050878	regulation of body fluid levels	BP	11	2	0.002881
GO:0031348	negative regulation of defense response	BP	13	2	0.004046
GO:0002685	regulation of leukocyte migration	BP	13	2	0.004046
GO:0003008	system process	BP	148	5	0.00491
GO:0006954	inflammatory response	BP	50	3	0.006067
GO:0019371	cyclooxygenase pathway	BP	1	1	0.007435

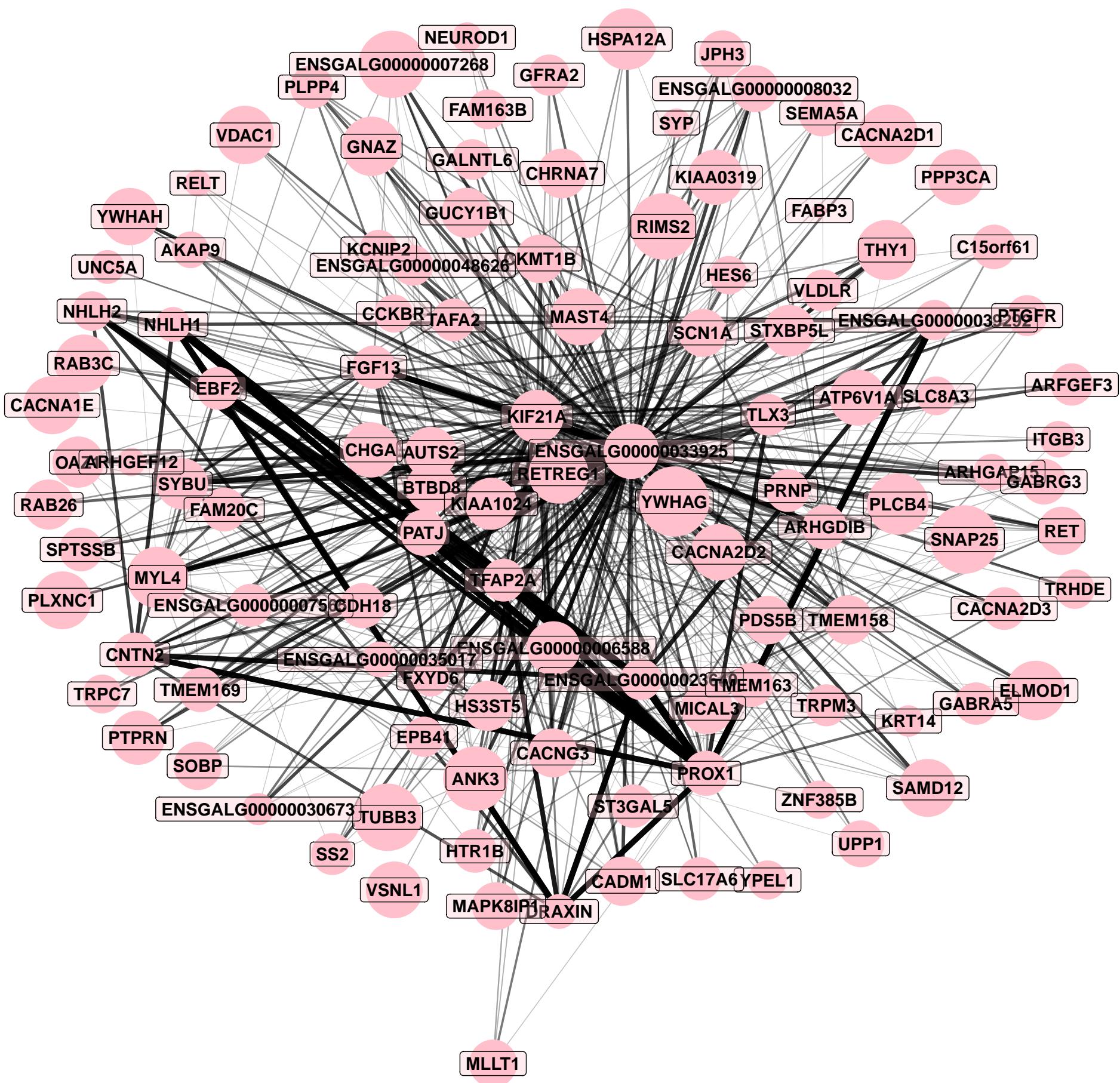
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04010</i>	MAPK signaling pathway	244	7	0.002267
<i>path:gga04370</i>	VEGF signaling pathway	55	3	0.007907
<i>path:gga04510</i>	Focal adhesion	173	4	0.04001
<i>path:gga04514</i>	Cell adhesion molecules	108	3	0.0465
<i>path:gga04270</i>	Vascular smooth muscle contraction	110	3	0.04864
<i>path:gga03320</i>	PPAR signaling pathway	57	2	0.06709
<i>path:gga00120</i>	Primary bile acid biosynthesis	11	1	0.07884
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.1192
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	298	4	0.1813
<i>path:gga04020</i>	Calcium signaling pathway	204	3	0.1939





	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0099560	synaptic membrane adhesion	BP	3	1	0.008537
GO:0060999	positive regulation of dendritic spine development	BP	6	1	0.017
GO:0060998	regulation of dendritic spine development	BP	8	1	0.02261
GO:0060996	dendritic spine development	BP	13	1	0.03649
GO:0030516	regulation of axon extension	BP	14	1	0.03924
GO:0031175	neuron projection development	BP	113	2	0.04115
GO:0048675	axon extension	BP	16	1	0.04472
GO:0048666	neuron development	BP	126	2	0.05005
GO:0061387	regulation of extent of cell growth	BP	18	1	0.05017
GO:1990138	neuron projection extension	BP	19	1	0.05289

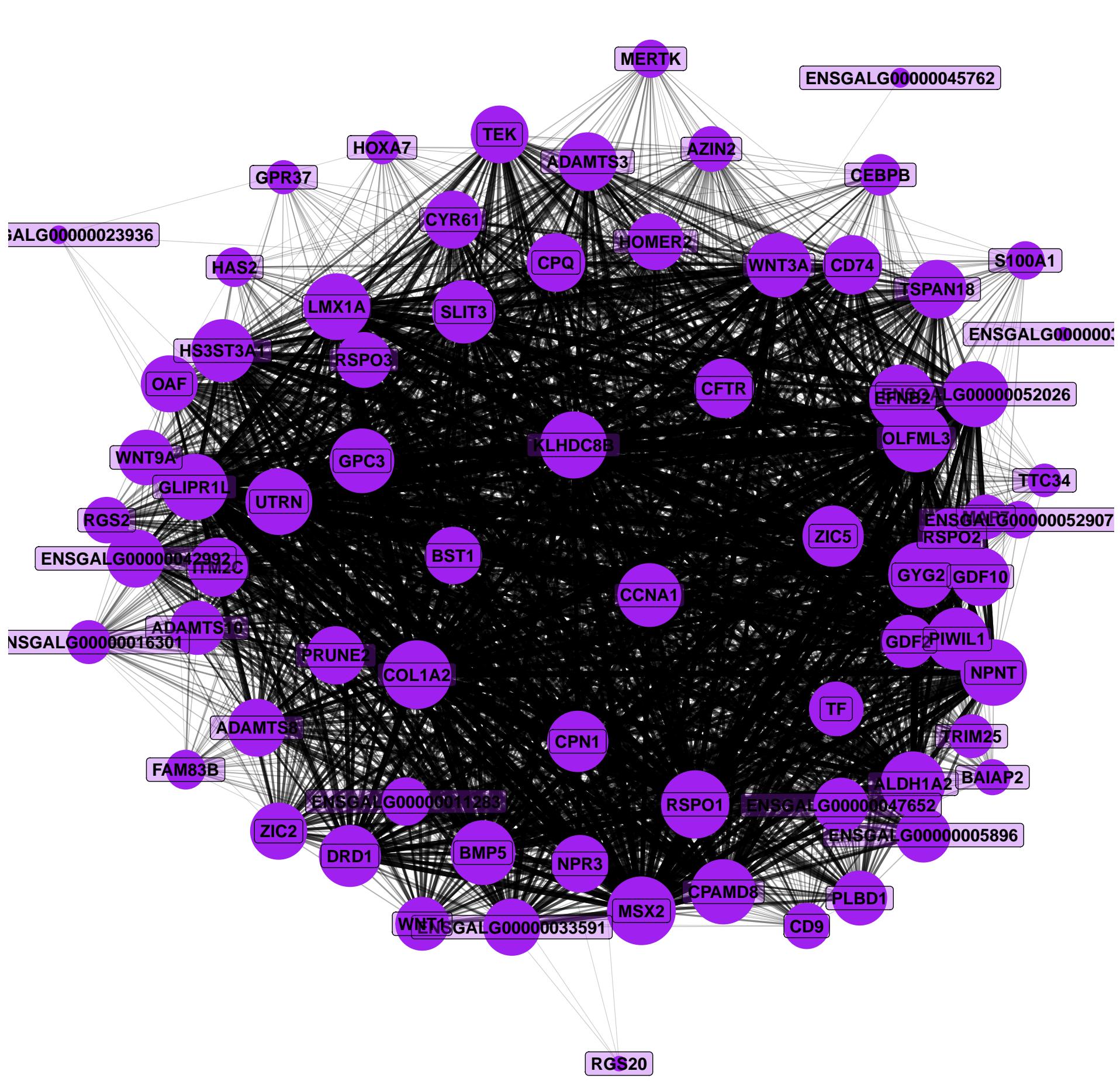
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	13	2	0.0006064
<i>path:gga00650</i>	Butanoate metabolism	21	2	0.001609
<i>path:gga00410</i>	beta-Alanine metabolism	25	2	0.002282
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	2	0.003727
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	298	4	0.009974
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.01137
<i>path:gga04514</i>	Cell adhesion molecules	108	2	0.03791
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.03924
<i>path:gga04744</i>	Phototransduction	15	1	0.04198
<i>path:gga03250</i>	Viral life cycle – HIV-1	48	1	0.1284



1	SNAP25	YWHAG	TUBB3	ENSGALG00000007268	ANK3	RAB3C	RIMS2	CHGA
2	HSPA12A	MYL4	CACNA1E	MAST4	THY1	ELMOD1	SAMD12	PLCB4
3	RETREG1	VDAC1	GNAZ	CACNA2D1	PLXNC1	FABP3	YWHAH	KIAA1024
4	CACNA2D2	CNTN2	ENSGALG00000033925	PTPRN	VSNL1	TFAP2A	BTBD8	KIF21A
5	ATP6V1A	SYBU	PROX1	DRAVIN	ENSGALG0000006588	RET	KIAA0319	AUTS2
6	RAB26	PPP3CA	ENSGALG00000023640	HTR1B	ENSGALG0000007565	OAZ1	MICAL3	STXBP5L
7	MAPK8IP1	CACNG3	SCN1A	GUCY1B1	NHLH1	ARHGDI	EBF2	FGF13
8	HS3ST5	GABRG3	CKMT1B	FXYD6	CHRNA7	MLLT1	ENSGALG0000008032	SS2
9	TMEM158	HES6	TMEM169	SLC8A3	PATJ	ENSGALG00000039292	SEMA5A	JPH3
10	SLC17A6	SOBP	C15orf61	FAM20C	UPP1	CADM1	ST3GAL5	PTGFR
11	TLX3	EPB41	CACNA2D3	CDH18	GFRA2	PDS5B	ARFGEF3	SPTSSB
12	TAFA2	NHLH2	ENSGALG00000030673	TMEM163	KRT14	GABRA5	YPEL1	PRNP
13	ARHGAP15	VLDLR	PLPP4	KCNIP2	TRPM3	SYP	ARHGEF12	CCKBR
14	FAM163B	TRPC7	GALNTL6	UNC5A	ENSGALG00000035017	ITGB3	ENSGALG00000048626	AKAP9
15	ZNF385B	RELT	TRHDE	NEUROD1				

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0050890	cognition	BP	21	4	2.453e-05
GO:0042462	eye photoreceptor cell development	BP	3	2	0.0002055
GO:0050858	negative regulation of antigen receptor-mediated signaling pathway	BP	3	2	0.0002055
GO:0050860	negative regulation of T cell receptor signaling pathway	BP	3	2	0.0002055
GO:0042461	photoreceptor cell development	BP	3	2	0.0002055
GO:0050854	regulation of antigen receptor-mediated signaling pathway	BP	3	2	0.0002055
GO:0050856	regulation of T cell receptor signaling pathway	BP	3	2	0.0002055
GO:0031345	negative regulation of cell projection organization	BP	16	3	0.0002917
GO:0034220	ion transmembrane transport	BP	111	6	0.0003261
GO:0021510	spinal cord development	BP	18	3	0.0004199

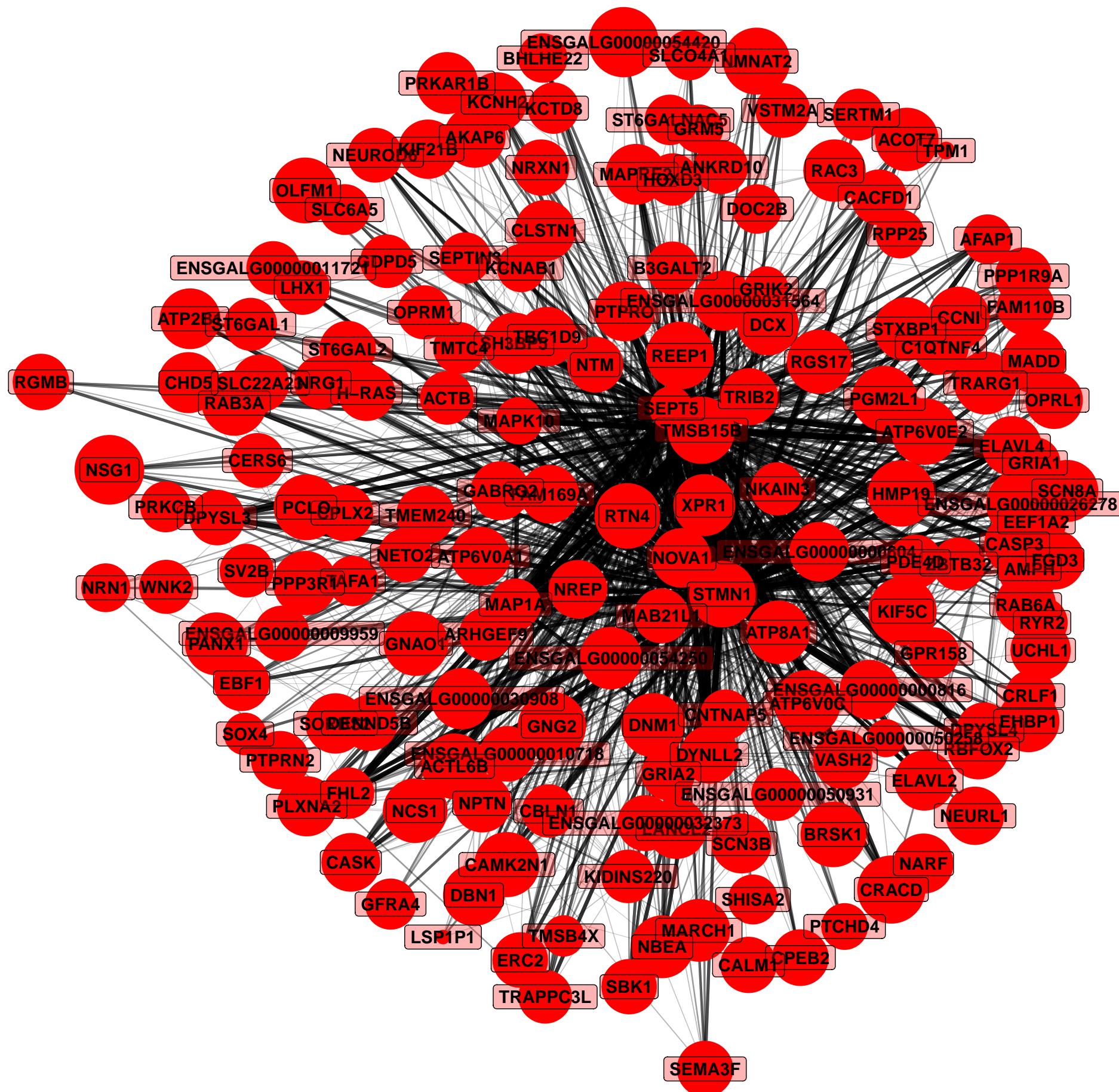
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	123	8	8.411e-06
<i>path:gga04260</i>	Cardiac muscle contraction	60	6	1.017e-05
<i>path:gga04020</i>	Calcium signaling pathway	204	9	5.111e-05
<i>path:gga04010</i>	MAPK signaling pathway	244	7	0.004301
<i>path:gga04540</i>	Gap junction	79	3	0.02822
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	82	3	0.03104
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.03293
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	298	6	0.03843
<i>path:gga04114</i>	Oocyte meiosis	97	3	0.0473
<i>path:gga04270</i>	Vascular smooth muscle contraction	110	3	0.06415



1	MSX2	OLFML3	COL1A2	RSPO1	LMX1A	ENSGALG00000052026	NPNT	KLHDC8B
2	GLIPR1L	UTRN	GYG2	EFNB2	BMP5	SLIT3	GPC3	ALDH1A2
3	WNT3A	CPAMD8	CCNA1	HS3ST3A1	ENSGALG00000033591	PIWIL1	ZIC5	GDF10
4	ADAMTS8	DRD1	NPR3	CPN1	CFTR	ENSGALG0000005896	TSPAN18	ZIC2
5	CD74	CYR61	TEK	BST1	PRUNE2	RSPO3	GDF2	ENSGALG00000042992
6	ADAMTS3	ITM2C	CPQ	RSPO2	TF	ADAMTS10	OAF	HOMER2
7	WNT9A	ENSGALG00000047652	WNT1	PLBD1	RGS2	ENSGALG00000011283	AZIN2	MAP7
8	CD9	TRIM25	FAM83B	CEBPB	ENSGALG00000016301	GPR37	HAS2	S100A1
9	HOXA7	TTC34	MERTK	ENSGALG00000052907	BAIAP2	ENSGALG00000045762	ENSGALG00000023936	RGS20
10	ENSGALG00000036838							

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0009887	animal organ morphogenesis	BP	128	7	3.832e-06
GO:0030509	BMP signaling pathway	BP	26	4	8.543e-06
GO:0071773	cellular response to BMP stimulus	BP	29	4	1.342e-05
GO:0071772	response to BMP	BP	29	4	1.342e-05
GO:0009653	anatomical structure morphogenesis	BP	299	9	1.983e-05
GO:0007275	multicellular organism development	BP	584	12	3.469e-05
GO:0030154	cell differentiation	BP	425	10	5.475e-05
GO:0009855	determination of bilateral symmetry	BP	15	3	5.546e-05
GO:0009799	specification of symmetry	BP	15	3	5.546e-05
GO:0048869	cellular developmental process	BP	434	10	6.526e-05

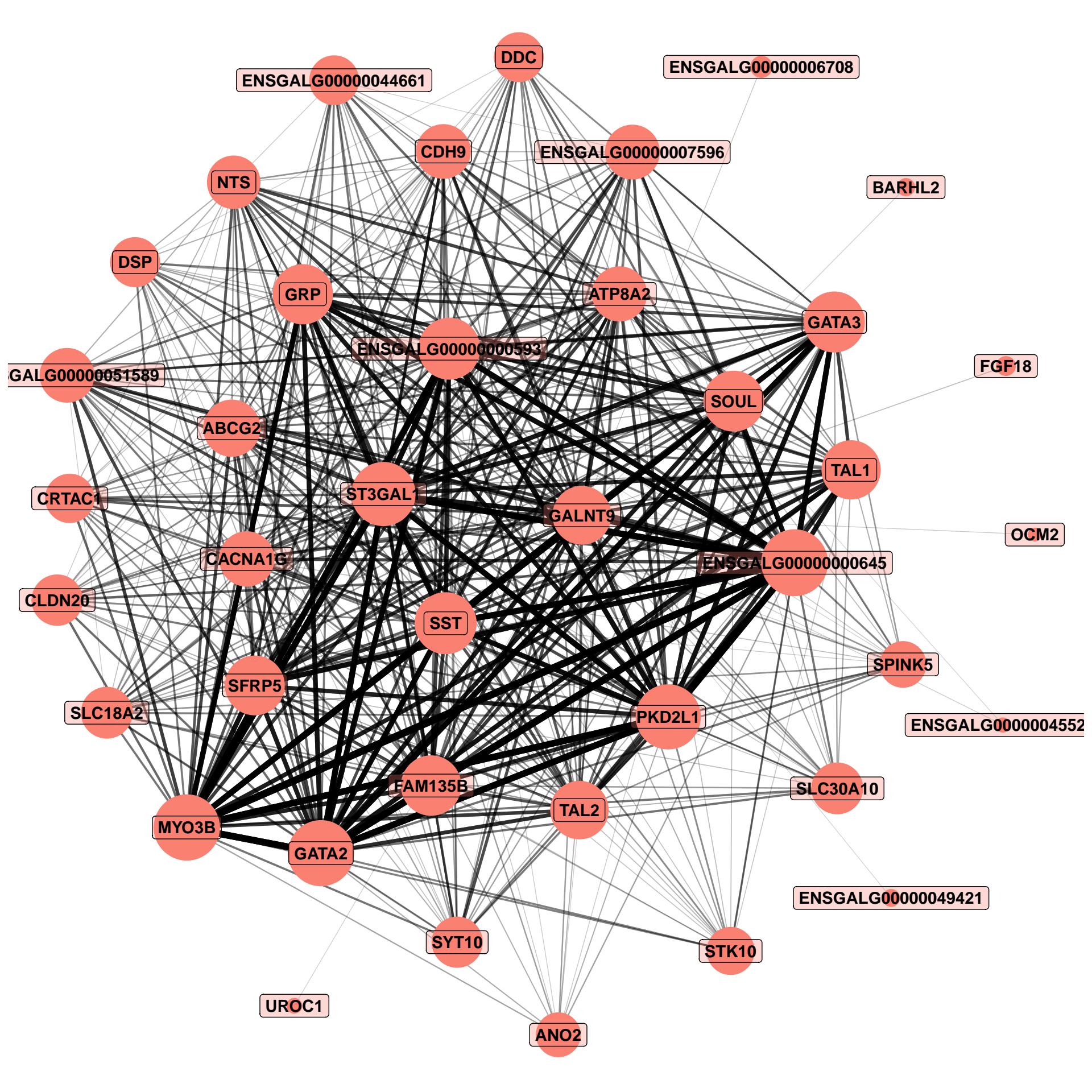
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04310</i>	Wnt signaling pathway	137	6	6.891e-05
<i>path:gga04916</i>	Melanogenesis	88	3	0.01026
<i>path:gga04150</i>	mTOR signaling pathway	137	3	0.03287
<i>path:gga04512</i>	ECM–receptor interaction	68	2	0.04717
<i>path:gga00910</i>	Nitrogen metabolism	14	1	0.0692
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis – heparan sulfate / heparin	21	1	0.102
<i>path:gga00500</i>	Starch and sucrose metabolism	27	1	0.1292
<i>path:gga00830</i>	Retinol metabolism	31	1	0.1469
<i>path:gga00760</i>	Nicotinate and nicotinamide metabolism	33	1	0.1556
<i>path:gga04216</i>	Ferroptosis	34	1	0.1599





	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0035418	protein localization to synapse	BP	8	4	1.568e-06
GO:1902414	protein localization to cell junction	BP	10	4	4.614e-06
GO:0007399	nervous system development	BP	260	13	2.253e-05
GO:0097120	receptor localization to synapse	BP	7	3	6.419e-05
GO:1902473	regulation of protein localization to synapse	BP	2	2	0.0001545
GO:1902683	regulation of receptor localization to synapse	BP	2	2	0.0001545
GO:0030182	neuron differentiation	BP	166	9	0.000233
GO:0120036	plasma membrane bounded cell projection organization	BP	139	8	0.0003478
GO:0030030	cell projection organization	BP	143	8	0.000421
GO:0048699	generation of neurons	BP	182	9	0.0004594

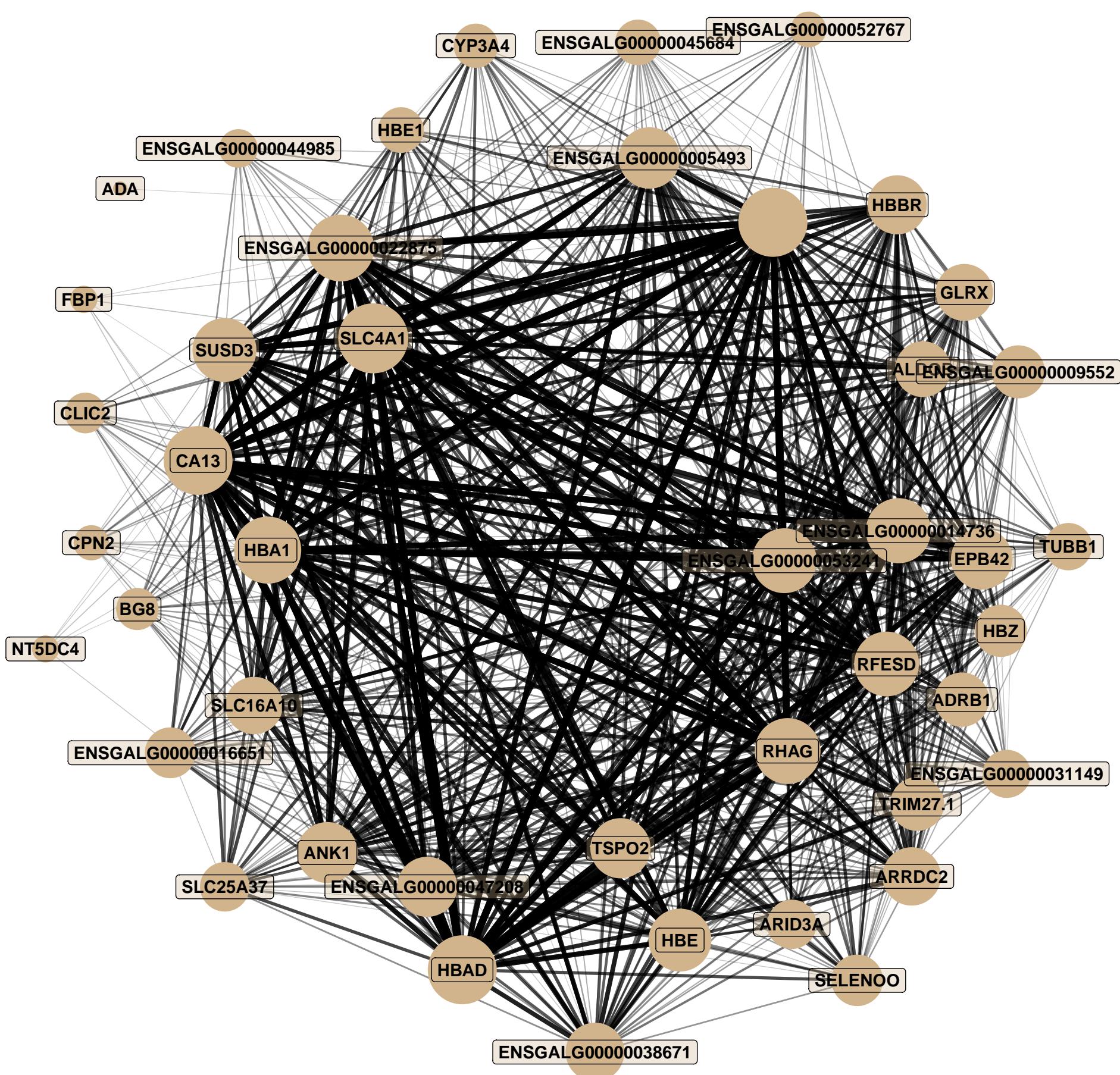
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	82	5	0.003572
<i>path:gga04370</i>	VEGF signaling pathway	55	4	0.004847
<i>path:gga04020</i>	Calcium signaling pathway	204	7	0.01403
<i>path:gga04012</i>	ErbB signaling pathway	76	4	0.01492
<i>path:gga04540</i>	Gap junction	79	4	0.01698
<i>path:gga04912</i>	GnRH signaling pathway	79	4	0.01698
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	123	5	0.01887
<i>path:gga05132</i>	Salmonella infection	220	7	0.02038
<i>path:gga04145</i>	Phagosome	126	5	0.02071
<i>path:gga04916</i>	Melanogenesis	88	4	0.02419





	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0030334	regulation of cell migration	BP	70	4	3.633e-05
GO:0045599	negative regulation of fat cell differentiation	BP	4	2	4.249e-05
GO:2000145	regulation of cell motility	BP	73	4	4.288e-05
GO:0051270	regulation of cellular component movement	BP	75	4	4.77e-05
GO:0040012	regulation of locomotion	BP	76	4	5.025e-05
GO:0035162	embryonic hemopoiesis	BP	5	2	7.07e-05
GO:0072577	endothelial cell apoptotic process	BP	5	2	7.07e-05
GO:0072676	lymphocyte migration	BP	5	2	7.07e-05
GO:2000352	negative regulation of endothelial cell apoptotic process	BP	5	2	7.07e-05
GO:1904036	negative regulation of epithelial cell apoptotic process	BP	5	2	7.07e-05

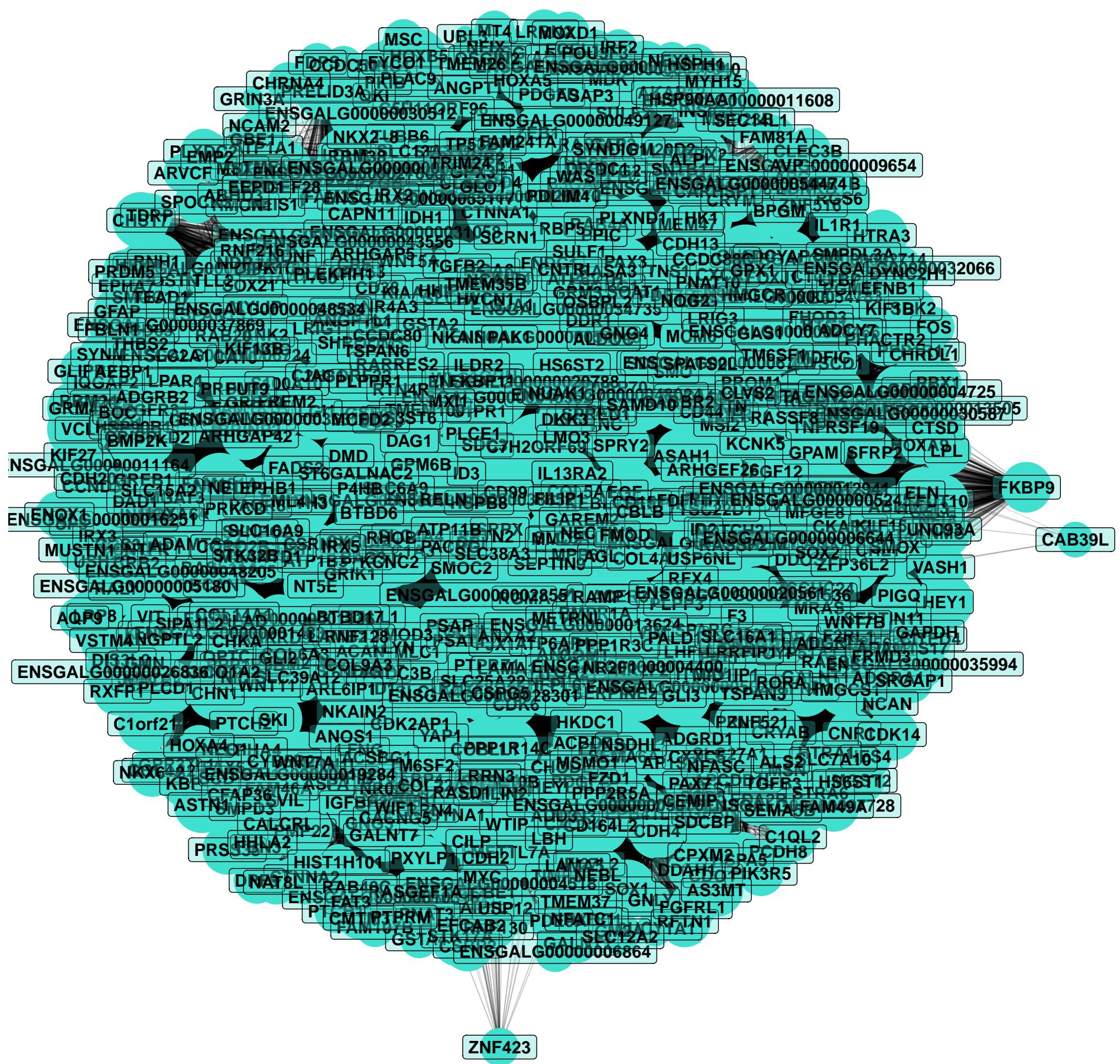
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga00512</i>	Mucin type O–glycan biosynthesis	29	2	0.002756
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	298	4	0.008241
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	1	0.03198
<i>path:gga00360</i>	Phenylalanine metabolism	12	1	0.03198
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	1	0.0346
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.03721
<i>path:gga00340</i>	Histidine metabolism	18	1	0.04759
<i>path:gga00350</i>	Tyrosine metabolism	28	1	0.07307
<i>path:gga02010</i>	ABC transporters	36	1	0.09298
<i>path:gga00380</i>	Tryptophan metabolism	36	1	0.09298



1	NA	SLC4A1	CA13	HBAD	HBE	HBA1	RHAG	ENSGALG00000022875
2	TSPO2	ENSGALG00000053241	ENSGALG0000014736	HBBR	HBZ	EPB42	SUSD3	RFESD
3	HBE1	TRIM27.1	ENSGALG0000005493	ENSGALG0000047208	ANK1	ALDOB	ENSGALG00000038671	ENSGALG0000009552
4	GLRX	CYP3A4	SLC25A37	ADRB1	ARRDC2	SLC16A10	ENSGALG0000045684	ENSGALG0000052767
5	CPN2	TUBB1	ENSGALG0000044985	ARID3A	ENSGALG0000031149	ENSGALG0000016651	SELENOO	CLIC2
6	FBP1	BG8	NT5DC4	ADA				

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0042744	hydrogen peroxide catabolic process	BP	7	5	5.1e-12
GO:0042743	hydrogen peroxide metabolic process	BP	7	5	5.1e-12
GO:0015671	oxygen transport	BP	7	5	5.1e-12
GO:0015669	gas transport	BP	8	5	1.357e-11
GO:0098869	cellular oxidant detoxification	BP	14	5	4.784e-10
GO:1990748	cellular detoxification	BP	16	5	1.039e-09
GO:0097237	cellular response to toxic substance	BP	16	5	1.039e-09
GO:0098754	detoxification	BP	17	5	1.468e-09
GO:0072593	reactive oxygen species metabolic process	BP	20	5	3.654e-09
GO:0009636	response to toxic substance	BP	20	5	3.654e-09

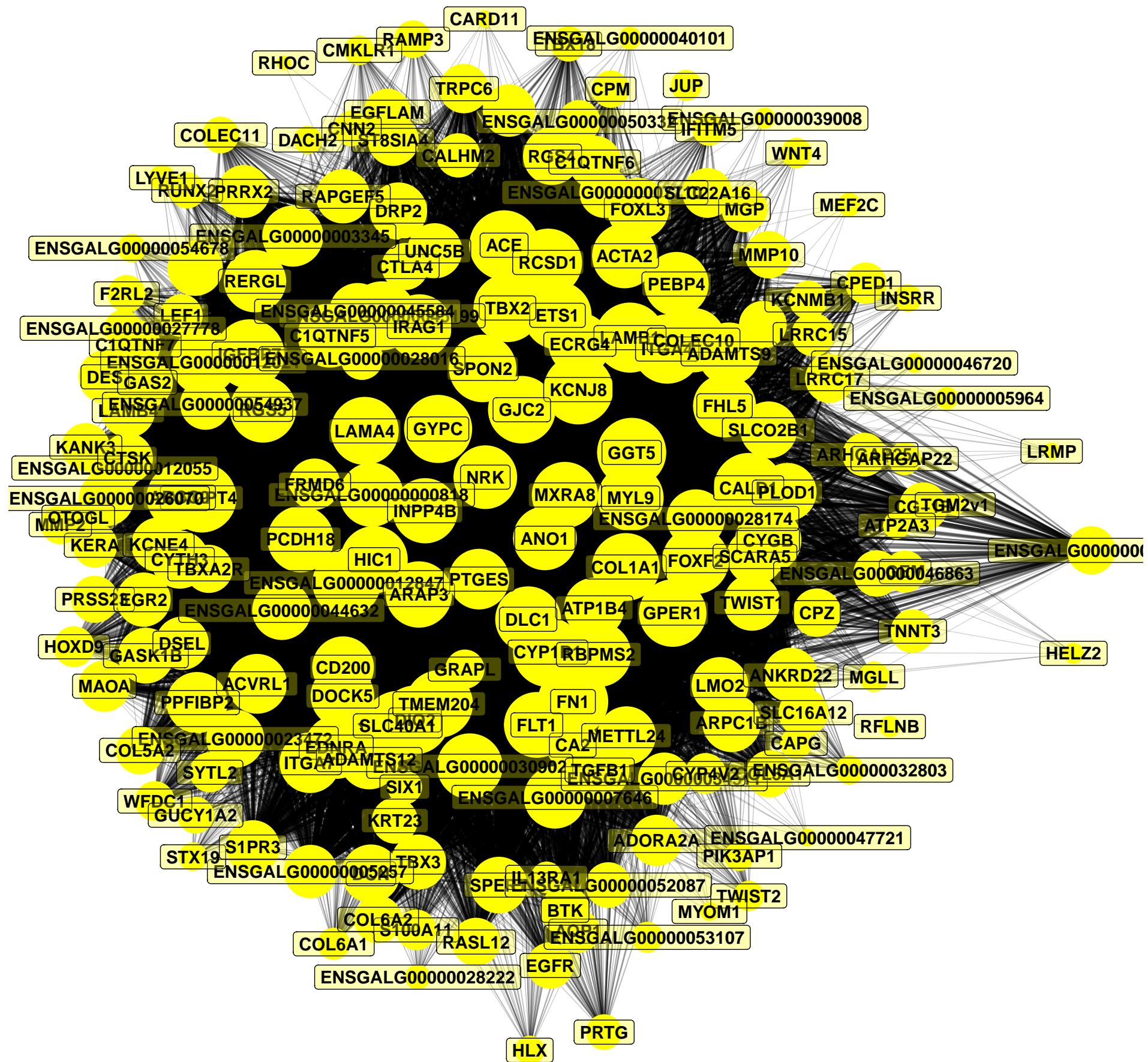
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga00030</i>	Pentose phosphate pathway	25	2	0.002783
<i>path:gga00051</i>	Fructose and mannose metabolism	34	2	0.005111
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	48	2	0.009994
<i>path:gga01232</i>	Nucleotide metabolism	78	2	0.02507
<i>path:gga04540</i>	Gap junction	79	2	0.02567
<i>path:gga01200</i>	Carbon metabolism	95	2	0.03605
<i>path:gga00910</i>	Nitrogen metabolism	14	1	0.04328
<i>path:gga00230</i>	Purine metabolism	115	2	0.05089
<i>path:gga00591</i>	Linoleic acid metabolism	20	1	0.06127
<i>path:gga00140</i>	Steroid hormone biosynthesis	27	1	0.08184



26	ID2	CDR4	SPRED1	SEMA6A	ENSGALG0000001136	STR7A	ENSGALG0000045332	ENSGALG0000045368
27	PACRG	SPON1	IGFBP2	SPARC	ANKRD9	C5H11ORF96	BMPR1A	ANOS1
28	BACE2	GDPD4	QKI	LAMC1	ENSGALG0000052336	BTBD17	ALAD	P4HB
29	RARRES2	GBE1	SLC2A1	FLNB	ARHGEF26	SPRY2	LDHB	BAG3
30	IDH1	SULF2	FGF12	TSC22D1	SLC9A3R1	BPGM	BBOX1	PFKP
31	CD151	AGL	HOXB5	DMD	LRIG3	ENSGALG0000007728	TMEM100	TSPAN6
32	CXXC5	ATP6V1H	HS3ST6	ASPA	PDLIM4	SFRP1	C2H8ORF22	CHN1
33	SKI	GAREM2	PPP1R9B	WNT7A	CAP2	CCDC80	HMCN1	USP6NL
34	ALPL	WNT5A	TSPAN13	SOX2	BOC	NTN3	GNG5	EPB41L3
35	LRP8	ENSGALG0000054783	BCAN	GRM3	PPP1R3C	NOG	S100A10	LYN
36	MSN	KIF1B	CD63	ENSGALG0000013624	CDH2	FZD10	RBP5	KLF15
37	SYNPO2	SCRN1	CALCRL	MEIS1	DIPK1C	ENSGALG0000003074	PDGFD	EPHA4
38	ITGB1	FAM3C	ZFP36L2	RAB40C	RASSF2	GLO1	LRRFIP1	SMPDL3A
39	CPNE2	ASTN1	SLC15A2	CD82	COL22A1	TMEM47	RAB20	OSBPL2
40	IQGAP2	PAX6	SCG3	LAMA5	ATP1A1	HEY1	FAM46A	ENSGALG0000001536
41	MEIS2	BMP2K	CAPN11	MSMO1	RBM24	TSPAN3	CRISPLD2	MDFIC
42	KLF6	ENSGALG0000006644	CYP51A1	TGFB2	AKAP12	USP12	AEBP1	NCALD
43	AP1S2	ENSGALG0000012941	MYLK	TRIM24	CCND3	HVCN1	LGI1	CDH20
44	NKAIN2	F2RL1	NOG2	ENSGALG0000005180	CRB2	FAT3	TGFBI	HHIP
45	FRMD3	MID1IP1	LPAR4	CTSD	INHBB	AXL	ZNF503	ENSGALG00000048534
46	BSG	TMEM37	ENSGALG0000006152	MSX1	CTNNA2	CNR1	PRELID3A	ADAMTS7
47	CHST7	PLCD1	BMPR1B	ADCYAP1R1	SPARCL1	PXYLP1	HMGCR	APCDD1L
48	ARHGAP5	NEBL	SLC16A9	SMOX	GALNT7	LRP4	CRYAB	GABBR2
49	SPATS2L	CD164L2	TNFRSF19	MYLIP	ENSGALG0000017040	INSIG1	ENSGALG00000030587	ARHGEF28
50	RNH1	DDIT4	HSPA5	KCNC2	SLC38A3	C1QL1	PDE9A	ENSGALG0000005076
51	CDK14	ENSGALG0000055117	ENSGALG0000036310	C1QL2	ENSGALG0000048205	ADGRB2	NDP	KCNIP4
52	CORO2B	COL4A1	ADD3	SCD5	KIRREL3	SMPD3	MGAT3	ABHD3
53	MSANTD1	EZR	RALY	CDH13	GPM6A	FOXJ1	PTCH2	GREB1
54	GRN	PRDM12	ADAMTS14	ATP11B	SULF1	ENSGALG0000049127	PAX3	NR2F1
55	CSRP2	ENSGALG0000026836	WNT11	PHACTR2	ANGPTL2	GRM4	CDO1	ACAN
56	EMILIN2	ADCY7	ADAMTS17	TP53BP2	NOTCH1	PKIB	BRINP2	FOS
57	ZEB1	LECT1	FUT10	TLL2	EEPD1	MGAT4A	SLC7A10	ENSGALG0000013505
58	GLI2	AS3MT	C1orf21	GBX2	SLC16A1	FZD1	ADGRD2	GAS1
59	ENSGALG0000027183	SDCBP	BTG2	PHYHIPL	ARHGAP31	KIF13B	TNNC1	ELN
60	CRIM1	LIPG	SLC39A12	HTRA3	ARL6IP1	SYNDIG1L	NR4A3	PAX7
61	ENSGALG0000028301	EPHA7	FYCO1	PGM1	APC	CHL1	SAMD10	WSCD1
62	PLEKHH1	ENSGALG000004725	HSP90B1	ARHGAP42	ENSGALG0000010316	CLASP1	ENSGALG0000002714	RORA
63	KBP	CHKA	FDFT1	EDA2R	TMEM86A	CKB	CHODL	HES4
64	COL4A2	RFTN1	SP8	ENSGALG0000043556	FAM49A	CLVS2	LRRN3	MCFD2
65	NKX6-2	HMGCS1	NEO1	LPL	RBM38	PPIB	PAK1	LGMN
66	TGFB3	GRB10	NFIX	ADAMTSL1	IRX2	TEAD1	CACNG5	ILDR2
67	ENSGALG0000020561	NRN1L	PNAT10	ENSGALG0000028466	CFAP36	ANXA1	LAMB2	HOXA5
68	HES1	TMEM35B	GPX3	CRYM	NEDD9	WTIP	RASGEF1A	POU3F3
69	ENSGALG0000020788	PXDC1	FKBP9	CARHSP1	OSGIN2	DBX2	EPHB1	PNAT3
70	SEPTIN11	TMEM26	CBP2ZL1	PRY1	THRS2	FMRP	MECE8	SCD

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0048856	anatomical structure development	BP	633	99	2.28e-21
GO:0007275	multicellular organism development	BP	584	94	3.362e-21
GO:0032502	developmental process	BP	666	100	2.95e-20
GO:0032501	multicellular organismal process	BP	722	105	3.436e-20
GO:0048731	system development	BP	490	72	2.797e-14
GO:0007166	cell surface receptor signaling pathway	BP	268	50	3.039e-14
GO:0022610	biological adhesion	BP	144	34	4.263e-13
GO:0007155	cell adhesion	BP	144	34	4.263e-13
GO:0050789	regulation of biological process	BP	1109	120	6.213e-13
GO:0050794	regulation of cellular process	BP	1058	116	6.682e-13

	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04512</i>	ECM–receptor interaction	68	21	5.914e–11
<i>path:gga04510</i>	Focal adhesion	173	27	1.163e–06
<i>path:gga00100</i>	Steroid biosynthesis	15	7	7.229e–06
<i>path:gga04350</i>	TGF–beta signaling pathway	86	16	1.912e–05
<i>path:gga04330</i>	Notch signaling pathway	52	11	0.0001145
<i>path:gga04310</i>	Wnt signaling pathway	137	18	0.0006224
<i>path:gga04514</i>	Cell adhesion molecules	108	15	0.0009691
<i>path:gga00480</i>	Glutathione metabolism	47	9	0.001024
<i>path:gga04340</i>	Hedgehog signaling pathway	47	9	0.001024
<i>path:gga03320</i>	PPAR signaling pathway	57	10	0.001115



1	DIO2	ANGPT4	ACE	GYPC	HIC1	FN1	RGS5	GGT5
2	COL1A1	ACTA2	KCNJ8	ITGA4	SPON2	GPER1	ENSGALG00000012021	FOXF2
3	LAMB1	TBX2	CYP1B1	ENSGALG00000012847	IGFBP7	ENSGALG00000030902	MXRA8	RCSD1
4	ENSGALG0000007646	SLC40A1	ARAP3	LAMA4	MYL9	FLT1	CA2	TMEM204
5	RBPMS2	COLEC10	ENSGALG00000045199	GJC2	ENSGALG0000000818	CALD1	ABCC9	IRAG1
6	DOCK5	ACVRL1	CD200	C1QTNF5	CYGB	ATP1B4	ECRG4	FHL5
7	PCDH18	FOXL3	NRK	PEBP4	INPP4B	ETS1	ANO1	DLC1
8	ITGA7	SPERT	ENSGALG00000023472	PTGES	RERGL	ARPC1B	DCN	ADAMTS12
9	SLCO2B1	TBX3	SCARA5	PPFIBP2	EDNRA	NA	ENSGALG00000045584	ADAMTS9
10	ENSGALG0000026070	ENSGALG0000028174	ENSGALG00000034511	EGR2	RGS4	ENSGALG0000003345	TWIST1	GEM
11	ENSGALG0000005257	UNC5B	RAPGEF5	PRRX2	DRP2	ENSGALG00000044632	LMO2	ADORA2A
12	KRT23	PLOD1	ANKRD22	KERA	DES	FRMD6	ENSGALG00000012055	CTLA4
13	LRRC17	CYTH3	TGFB1	KCNE4	NA	METTL24	BTK	KCNMB1
14	LAMB4	S1PR3	MMP10	AQP1	PRSS23	C1QTNF6	ENSGALG00000052087	ENSGALG00000046863
15	KANK3	GASK1B	DSEL	MGP	MAOA	CPZ	CG-1B	CTSK
16	TBXA2R	SLC22A16	ENSGALG0000007710	NA	ENSGALG0000002326	ENSGALG00000050332	C1QTNF7	ENSGALG00000054937
17	COL6A2	EGFR	TRPC6	LRRC15	CPED1	COL5A2	CALHM2	TBX18
18	ARHGAP25	ST8SIA4	EGFLAM	LEF1	GAS2	TNNT3	ENSGALG00000028016	S100A11
19	COL3A1	MMP2	ENSGALG00000054678	ENSGALG0000005964	SLC16A12	RASL12	WFDC1	CPM
20	PRTG	OTOGL	CYP4V2	GRAPL	COL6A1	RUNX2	RAMP3	GUCY1A2
21	SIX1	F2RL2	TWIST2	ENSGALG00000027778	SYTL2	CNN2	HOXD9	ARHGAP22
22	ENSGALG00000053107	JUP	CAPG	IFITM5	HLX	LYVE1	STX19	WNT4
23	COLEC11	ATP2A3	HELZ2	CMKLR1	DACH2	RFLNB	IL13RA1	INSRR
24	MGLL	ENSGALG00000032803	TGM2v1	MYOM1	MEF2C	ENSGALG00000039008	PIK3AP1	LRMP
25	ENSGALG00000046720	CARD11	ENSGALG00000047721	ENSGALG00000028222	ENSGALG00000040101	RHOC		

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0048856	anatomical structure development	BP	633	27	1.867e-07
GO:0032502	developmental process	BP	666	27	5.11e-07
GO:0009653	anatomical structure morphogenesis	BP	299	16	4.246e-06
GO:0046660	female sex differentiation	BP	19	4	0.0001187
GO:0007275	multicellular organism development	BP	584	20	0.0001802
GO:0022610	biological adhesion	BP	144	9	0.0001804
GO:0007155	cell adhesion	BP	144	9	0.0001804
GO:0008150	biological_process	BP	1925	45	0.0002367
GO:0032501	multicellular organismal process	BP	722	22	0.0004374
GO:0061061	muscle structure development	BP	72	6	0.0004844

	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04512</i>	ECM–receptor interaction	68	9	3.863e–07
<i>path:gga04510</i>	Focal adhesion	173	13	8.545e–07
<i>path:gga04270</i>	Vascular smooth muscle contraction	110	9	2.207e–05
<i>path:gga04520</i>	Adherens junction	69	4	0.01547
<i>path:gga04810</i>	Regulation of actin cytoskeleton	192	7	0.0178
<i>path:gga04010</i>	MAPK signaling pathway	244	8	0.02075
<i>path:gga04020</i>	Calcium signaling pathway	204	7	0.02389
<i>path:gga04672</i>	Intestinal immune network for IgA production	27	2	0.0537
<i>path:gga04216</i>	Ferroptosis	34	2	0.08064
<i>path:gga00380</i>	Tryptophan metabolism	36	2	0.08897