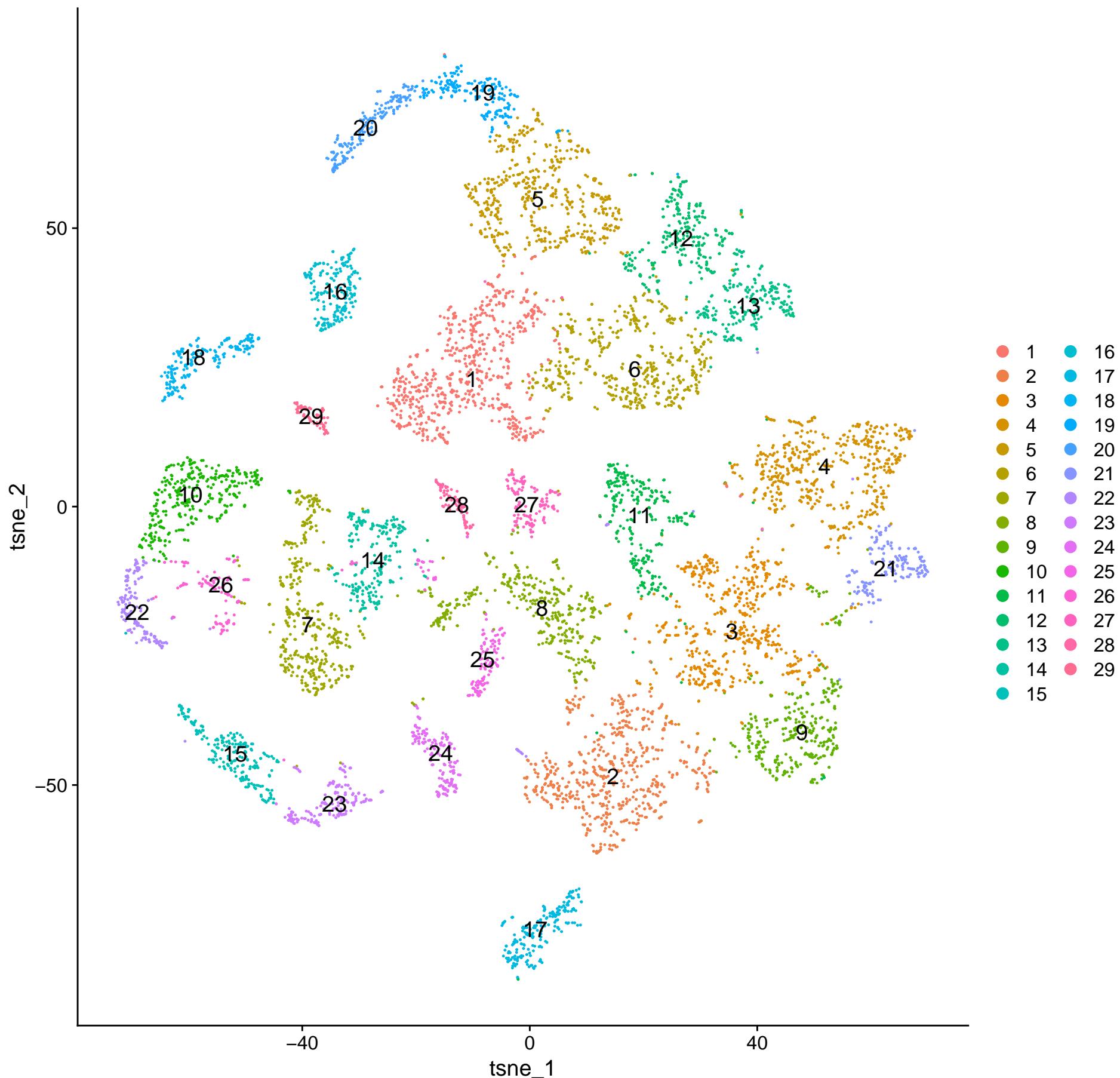
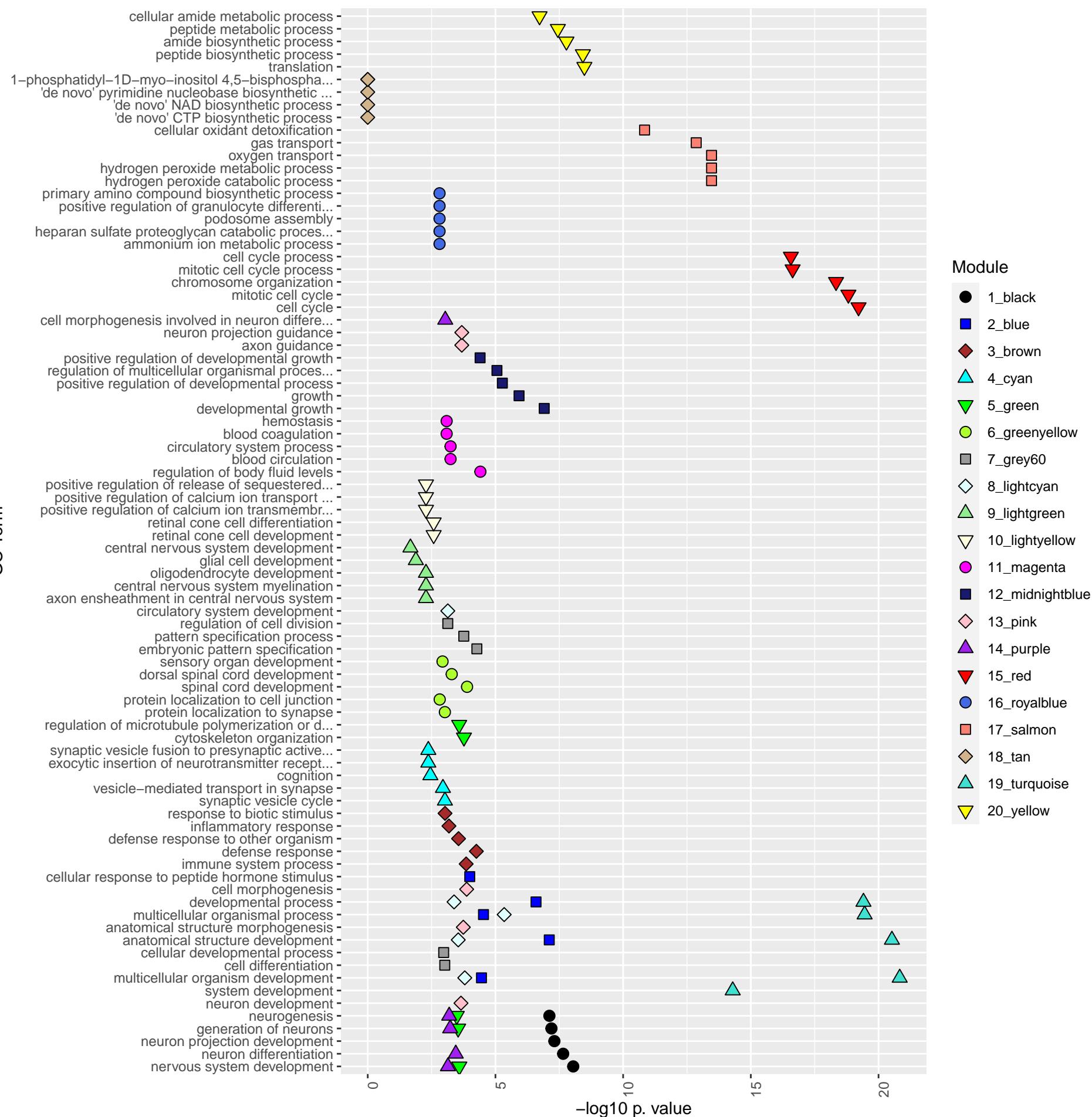
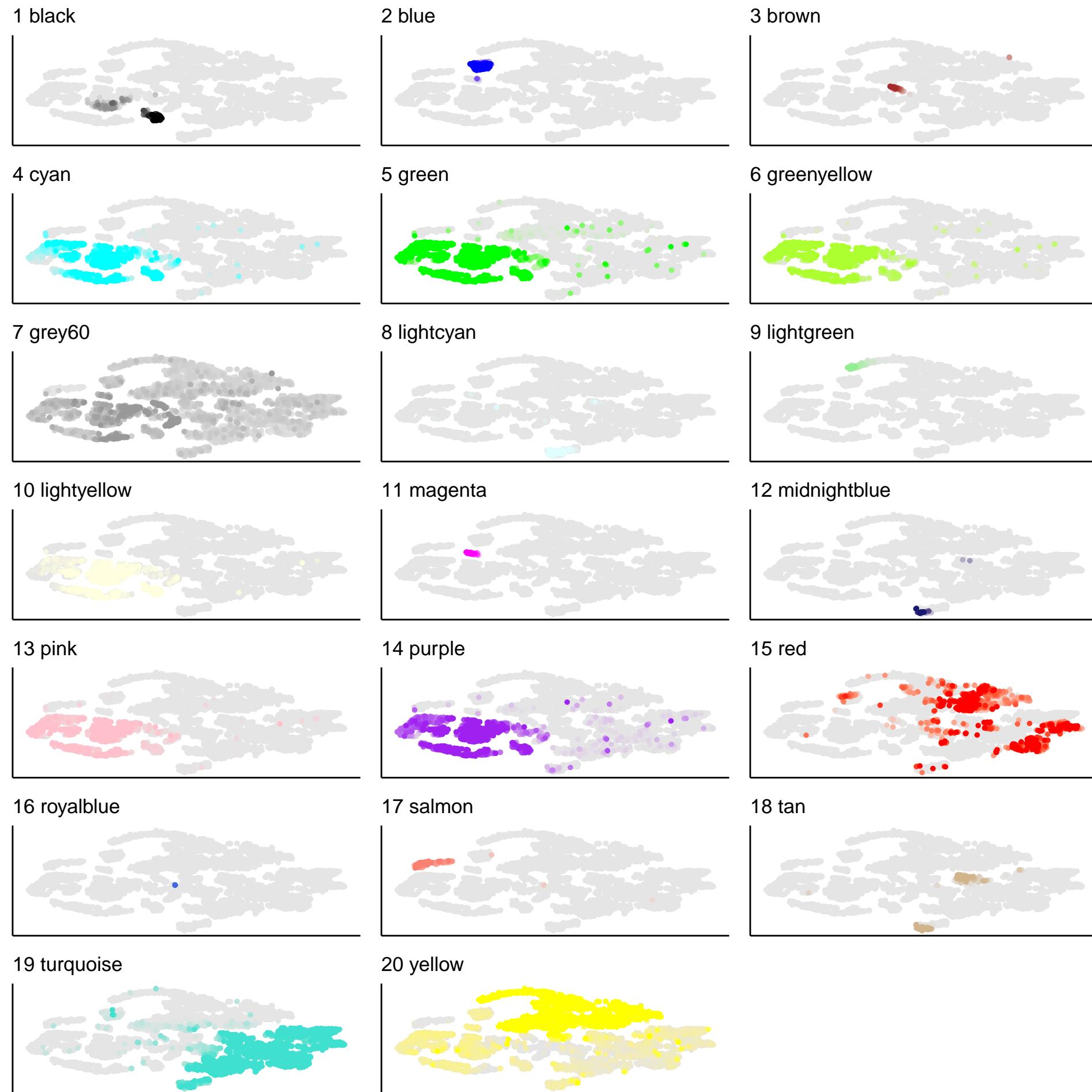


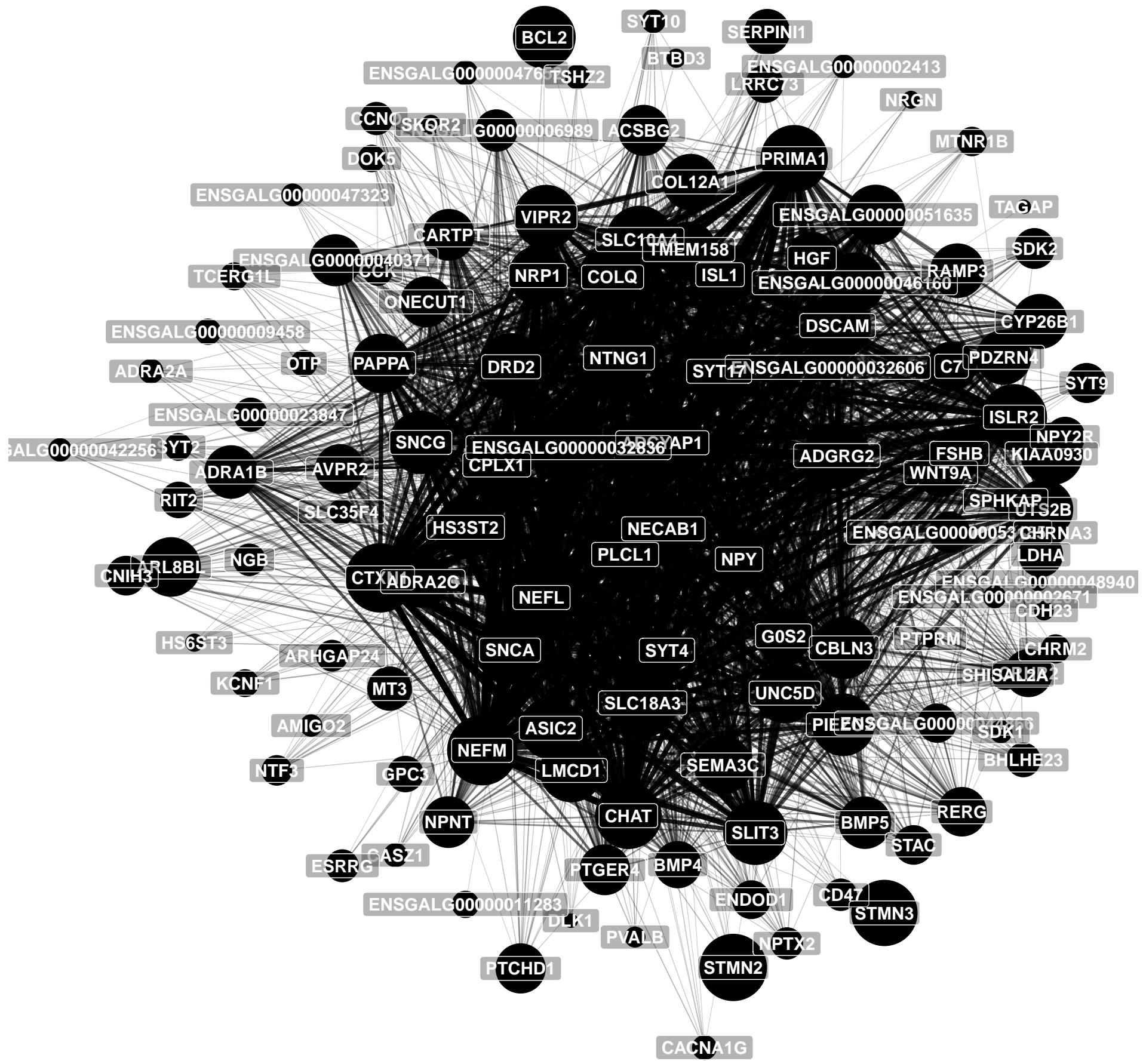
# Gg\_ctrl\_int scWGCNA modules







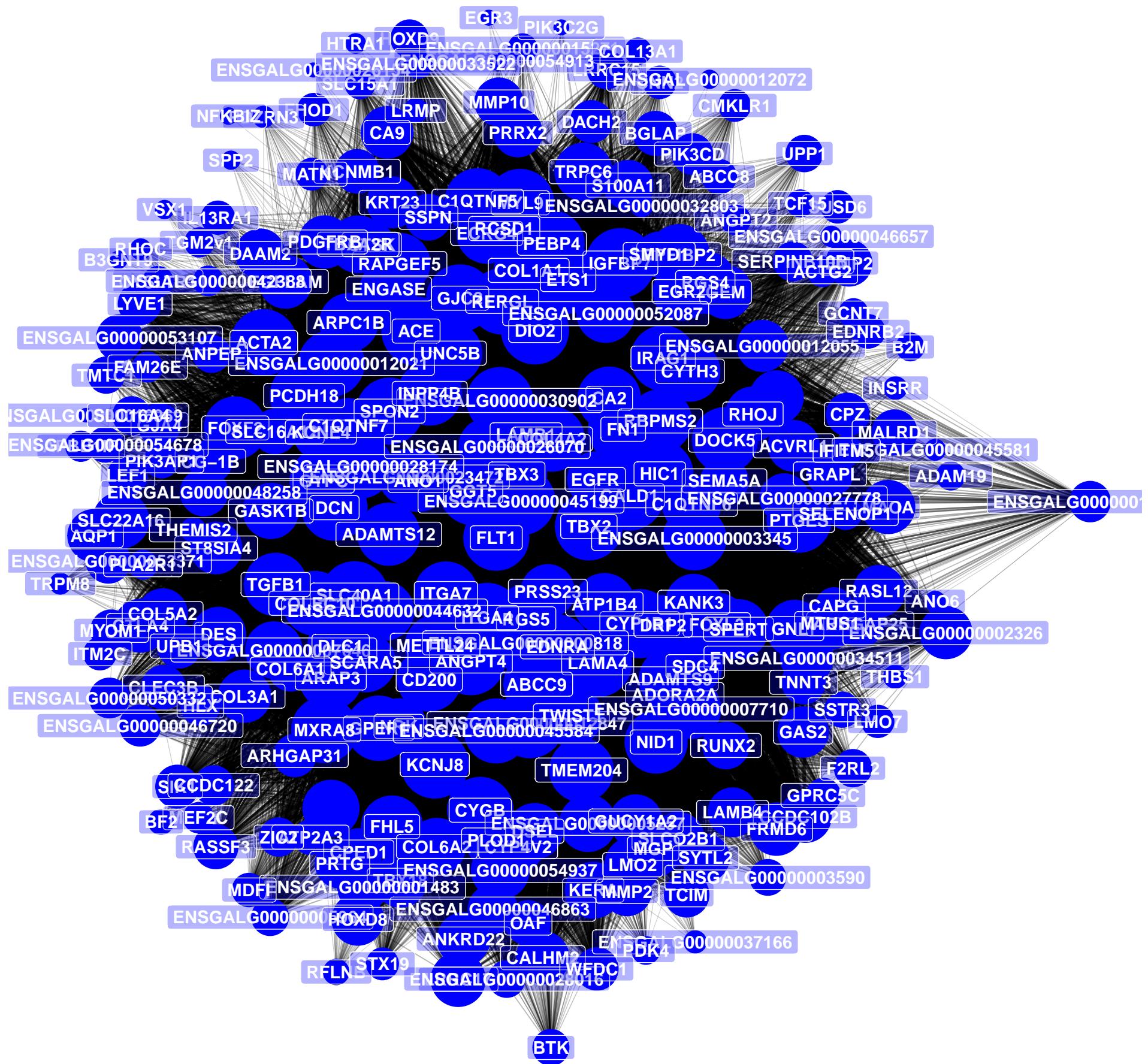






	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0007399	nervous system development	BP	255	15	9.001e-09
GO:0030182	neuron differentiation	BP	161	12	2.233e-08
GO:0031175	neuron projection development	BP	109	10	4.92e-08
GO:0048699	generation of neurons	BP	177	12	6.414e-08
GO:0022008	neurogenesis	BP	180	12	7.722e-08
GO:0048666	neuron development	BP	123	10	1.558e-07
GO:0120036	plasma membrane bounded cell projection organization	BP	135	10	3.736e-07
GO:0030030	cell projection organization	BP	139	10	4.903e-07
GO:0048731	system development	BP	472	17	1.089e-06
GO:0009887	animal organ morphogenesis	BP	122	9	1.521e-06

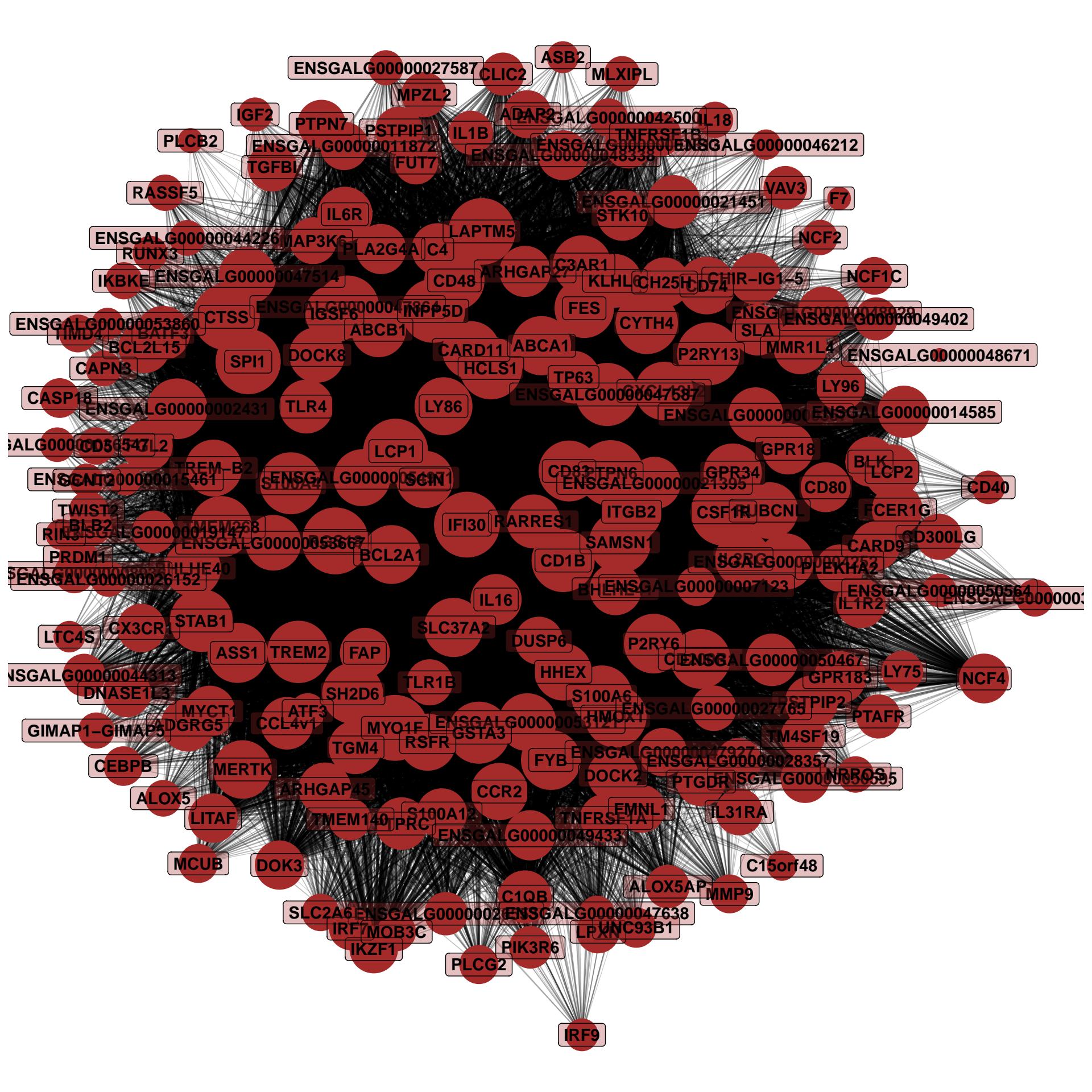
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	272	18	3.692e–11
<i>path:gga04920</i>	Adipocytokine signaling pathway	58	2	0.09647
<i>path:gga04020</i>	Calcium signaling pathway	196	4	0.1015
<i>path:gga00360</i>	Phenylalanine metabolism	12	1	0.1032
<i>path:gga04512</i>	ECM–receptor interaction	67	2	0.1226
<i>path:gga00061</i>	Fatty acid biosynthesis	16	1	0.1352
<i>path:gga00340</i>	Histidine metabolism	17	1	0.143
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis – heparan sulfate / heparin	21	1	0.1736
<i>path:gga04350</i>	TGF–beta signaling pathway	84	2	0.1757
<i>path:gga00350</i>	Tyrosine metabolism	25	1	0.2031



1	LAMB1	RGS5	FN1	ACE	DIO2	ANGPT4	GYPC	HIC1
2	COL1A1	IGFBP7	KCNJ8	ITGA4	LAMA4	ACTA2	MYL9	TBX2
3	GGT5	SPON2	CYP1B1	ENSGALG00000012847	ENSGALG00000012021	CALD1	GJC2	ENSGALG00000045199
4	GPER1	FLT1	ENSGALG0000007646	MXRA8	FOXF2	ABCC9	CA2	ENSGALG00000030902
5	COLEC10	RCSD1	SLC40A1	ARAP3	IRAG1	PCDH18	ENSGALG00000000818	DOCK5
6	C1QTNF5	TMEM204	RBPMS2	DCN	FOXL3	CYGB	PEBP4	CD200
7	ANO1	DLC1	RERGL	ECRG4	ATP1B4	ETS1	ENSGALG00000045584	INPP4B
8	PTGES	NRK	ENSGALG00000023472	ITGA7	FHL5	ARPC1B	SPERT	RGS4
9	TBX3	COL4A2	EDNRA	ACVRL1	ADAMTS12	ENSGALG00000028174	TGFB1	PPFIBP2
10	EGR2	UNC5B	SCARA5	ENSGALG0000003345	ADAMTS9	RHOJ	TWIST1	NA
11	AQP1	MGP	ENSGALG0000007710	ADORA2A	ENSGALG0000005257	RAPGEF5	PLOD1	PRSS23
12	ENSGALG00000044632	ENSGALG00000052087	KANK3	ENSGALG00000026070	NID1	DES	SLCO2B1	TRPC6
13	ANKRD22	GNLY	DRP2	ENSGALG00000054937	KCNE4	LMO2	CYTH3	ENSGALG00000034511
14	METTL24	C1QTNF6	TBXA2R	CG-1B	GEM	CTLA4	CALHM2	NA
15	COL6A2	ENSGALG0000012055	TBX18	LRRC17	EGFR	MAOA	PRRX2	KERA
16	KRT23	EGFLAM	FRMD6	ENSGALG0000002326	MMP10	ENGASE	DSEL	SLC22A16
17	RUNX2	PDGFRB	LAMB4	GASK1B	RASL12	HOXD8	CPED1	SDC4
18	C1QTNF7	ENSGALG0000046863	CTSK	ARHGAP25	COL5A2	CPZ	ST8SIA4	TCIM
19	KCNMB1	SLC16A12	CCDC102B	S100A11	CYP4V2	CA9	MTUS1	COL3A1
20	GJA4	ENSGALG0000027778	COL6A1	RASSF3	MMP2	ENSGALG0000003590	DAAM2	ENSGALG0000001483
21	TNNT3	PRTG	GAS2	GUCY1A2	SYTL2	LRRC15	EMP2	ARHGAP31
22	BTK	CLEC3B	ENSGALG0000050332	LEF1	OAF	F2RL2	ENSGALG00000053371	SIK1
23	SEMA5A	GRAPL	WFDC1	HLX	ENSGALG0000005964	LYVE1	ENSGALG00000053107	ZIC2
24	SMYD1	ATP2A3	PIK3CD	SSPN	UPB1	DACH2	ENSGALG00000028016	ENSGALG00000048258
25	CCDC122	HOXD9	LMO7	TGM2v1	ENSGALG0000011172	ANPEP	SLC16A4	ENSGALG00000046720
26	CNN2	TMTC1	MALRD1	SERPINB10B	ENSGALG0000054678	CMKLR1	CAPG	FHOD1
27	CYSLTR1	IL13RA1	BGLAP	UPP1	SUSD6	STX19	ITM2C	SLC15A1
28	RFLNB	MDFI	EDNRB2	PLA2R1	IFITM5	ACTG2	TCF15	PIK3AP1
29	INSRR	MYOM1	FAM26E	SSTR3	GCNT7	SELENOP1	B2M	APBB1IP
30	GPRC5C	PDK4	BF2	ANGPT2	LRMP	MEF2C	MATN1	HTRA1
31	RHOC	ABCC8	ENSGALG0000015271	ENSGALG0000032803	ENSGALG0000016969	PDZRN3	ENSGALG00000033522	ENSGALG00000026154
32	ANO6	ENSGALG0000037166	ENSGALG0000042388	ENSGALG0000045581	B3GNT9	VSX1	COL13A1	THBS1
33	TRPM8	SPP2	THEMIS2	NFKBIZ	EGR3	ENSGALG0000012072	ENSGALG00000054913	ENSGALG00000046657
34	ADAM19	PIK3C2G						

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0048856	anatomical structure development	BP	608	33	7.816e-08
GO:0032502	developmental process	BP	640	33	2.574e-07
GO:0032501	multicellular organismal process	BP	692	30	2.938e-05
GO:0007275	multicellular organism development	BP	562	26	3.521e-05
GO:0071375	cellular response to peptide hormone stimulus	BP	25	5	0.0001014
GO:0048513	animal organ development	BP	312	17	0.0001239
GO:0009653	anatomical structure morphogenesis	BP	287	16	0.0001508
GO:0008150	biological_process	BP	1879	58	0.0001608
GO:1901653	cellular response to peptide	BP	29	5	0.0002128
GO:0043434	response to peptide hormone	BP	30	5	0.0002513

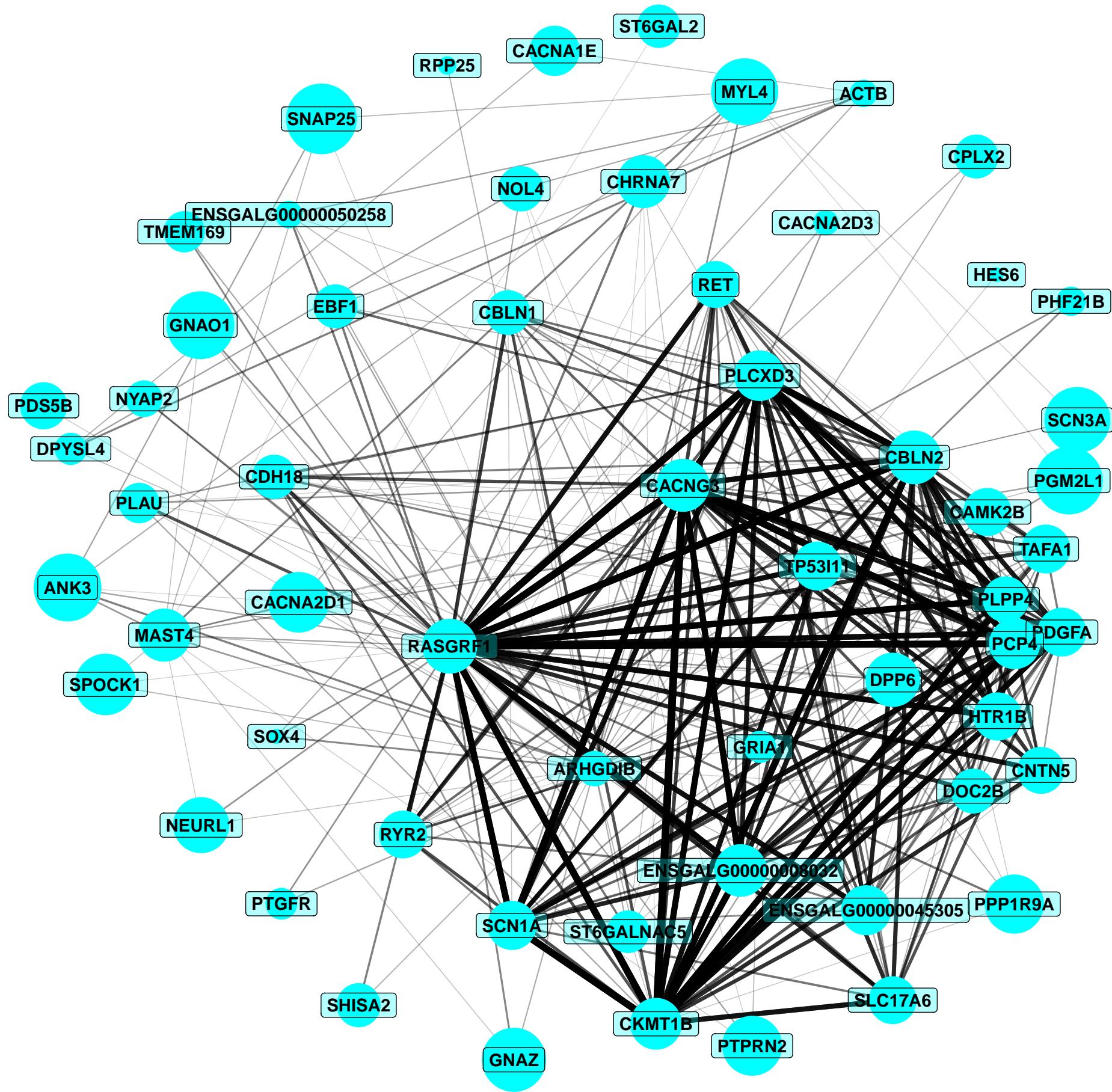
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04512</i>	ECM–receptor interaction	67	12	5.012e–09
<i>path:gga04510</i>	Focal adhesion	170	18	5.037e–09
<i>path:gga04270</i>	Vascular smooth muscle contraction	104	9	0.0001844
<i>path:gga04020</i>	Calcium signaling pathway	196	10	0.004898
<i>path:gga04810</i>	Regulation of actin cytoskeleton	182	9	0.009051
<i>path:gga04520</i>	Adherens junction	69	5	0.01077
<i>path:gga04010</i>	MAPK signaling pathway	236	10	0.01679
<i>path:gga00360</i>	Phenylalanine metabolism	12	2	0.02171
<i>path:gga00910</i>	Nitrogen metabolism	14	2	0.02918
<i>path:gga04514</i>	Cell adhesion molecules	95	5	0.0372



1	CSF1R	CTSS	RGS18	IFI30	LAPTM5	SPI1	MYO1F	PTPN6
2	S100A4	ENSGALG00000053121	LCP1	ENSGALG0000047864	P2RY13	ITGB2	S100A6	CCL4v1
3	TREM2	CD200R1	CD83	HCLS1	HMOX1	CD48	INPP5D	TMEM268
4	GSTA3	CD1B	SAMSN1	HHEX	ENSGALG0000002431	ENSGALG0000053667	CYTH4	ASS1
5	LY86	ENSGALG0000047587	ENSGALG0000004252	STAB1	C3AR1	SH2D6	ENSGALG0000000357	FYB
6	BCL2A1	FES	ARHGAP27	ENSGALG0000054971	S100A12	ENSGALG0000047514	CCR2	TLR4
7	IGSF6	LITAF	BHLHE40	P2RY6	ARHGAP45	GPR34	CXCL13L2	ENSGALG0000014585
8	PTPRC	DOCK8	RSFR	IL2RG	CARD11	CD74	ABCB1	MERTK
9	SLA	ENSGALG0000048929	GPR183	BLK	LCP2	LY96	FGL2	ENSGALG0000021395
10	CHIR-IG1-5	SLC37A2	CX3CR1	RARRES1	ENSGALG0000050467	ABCA1	TREM-B2	NCF4
11	ENSGALG0000011872	C1QB	ENSGALG0000021451	KLHL6	ENSGALG0000048338	ENSGALG0000049433	BATF3	DNASE1L3
12	MYCT1	TGM4	PSTPIP2	CD80	ENSGALG0000047927	C4	ADAP2	STK10
13	IL1R2	IL16	BCL2L15	ENSGALG0000050595	ENSGALG0000019147	SCIN	BHLHE41	RUBCNL
14	FAP	MMR1L4	DOCK2	IL1B	PTGDR	IL6R	LPXN	PTAFR
15	CLIC2	TP63	MAP3K6	PSTPIP1	GPR18	DOK3	FMNL1	ADGRG5
16	CARD9	ENSGALG0000042500	FCER1G	CD300LG	ENSGALG0000027765	TLR1B	IKZF1	TGFBI
17	CEBPB	CASP18	DUSP6	TWIST2	ENSGALG0000003313	PTPN7	TM4SF19	SLC2A6
18	TNFRSF1A	CH25H	FUT7	ENSGALG0000026553	IL31RA	ENSGALG0000027587	NRROS	ENSGALG0000049402
19	ENSGALG0000039708	MMP9	PLA2G4A	ENSGALG0000044313	ENSGALG0000028357	LY75	PLEKHA2	MPZL2
20	CAPN3	NCF2	PIK3R6	TNFRSF1B	TIMD4	BLB2	ENSGALG0000015461	MLXIPL
21	VAV3	ENSGALG0000047638	RUNX3	ENSGALG0000036547	IRF7	UNC93B1	ALOX5AP	MOB3C
22	NCF1C	LTC4S	TMEM140	ENSGALG0000007123	IGF2	ENSGALG0000050564	IL18	PRDM1
23	ALOX5	MCUB	ENSGALG0000046212	CD40	ASB2	ENSGALG0000044226	ENSGALG0000008936	ATF3
24	RIN3	ENSGALG0000053860	IKBKE	CD5	RASSF5	PLCG2	GIMAP1-GIMAP5	GCNT2
25	ENSGALG0000026152	PLCB2	IRF9	C15orf48	ENSGALG0000048671	F7		

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0006952	defense response	BP	93	8	5.58e-05
GO:0002376	immune system process	BP	166	10	0.0001401
GO:0098542	defense response to other organism	BP	63	6	0.0002782
GO:0006954	inflammatory response	BP	49	5	0.0006602
GO:0009607	response to biotic stimulus	BP	79	6	0.0009418
GO:0043207	response to external biotic stimulus	BP	79	6	0.0009418
GO:0051707	response to other organism	BP	79	6	0.0009418
GO:0050865	regulation of cell activation	BP	35	4	0.00152
GO:0044419	biological process involved in interspecies interaction between organisms	BP	90	6	0.001853
GO:0072676	lymphocyte migration	BP	5	2	0.001992

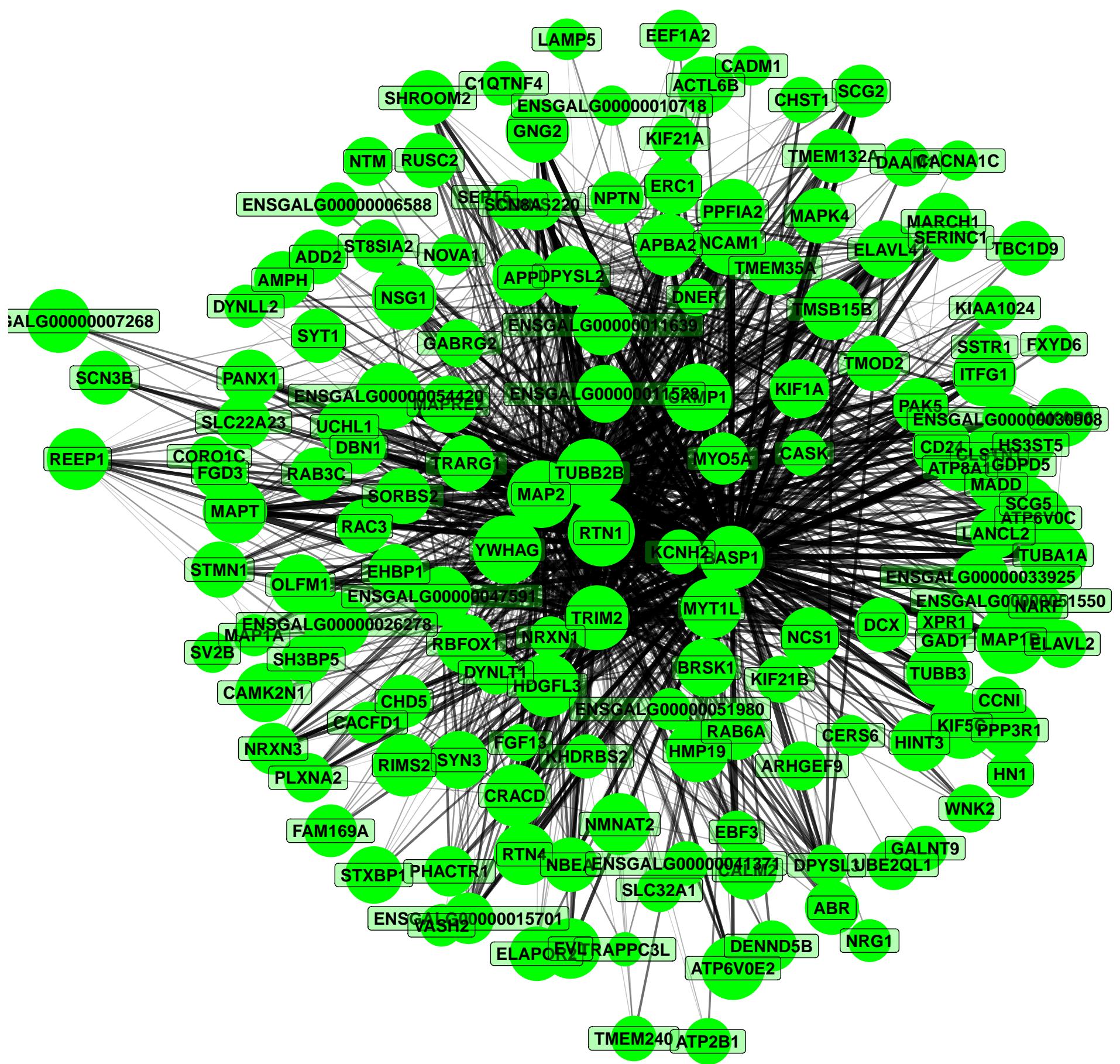
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	146	15	2.645e–09
<i>path:gga04620</i>	Toll–like receptor signaling pathway	70	10	5.489e–08
<i>path:gga04145</i>	Phagosome	123	11	1.514e–06
<i>path:gga04621</i>	NOD–like receptor signaling pathway	115	10	5.905e–06
<i>path:gga04623</i>	Cytosolic DNA–sensing pathway	41	6	2.39e–05
<i>path:gga05164</i>	Influenza A	109	8	0.0001713
<i>path:gga05168</i>	Herpes simplex virus 1 infection	127	8	0.0004857
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	81	6	0.001074
<i>path:gga04672</i>	Intestinal immune network for IgA production	18	3	0.002026
<i>path:gga04514</i>	Cell adhesion molecules	95	6	0.002439



1	SNAP25	ANK3	MYL4	SCN3A	PGM2L1	SPOCK1	GNAO1	CACNA1E
2	GNAZ	PCP4	MAST4	DPP6	CACNA2D1	PTPRN2	CBLN2	PPP1R9A
3	HTR1B	NEURL1	CBLN1	CKMT1B	RASGRF1	NOL4	RYR2	SCN1A
4	SLC17A6	PLCXD3	CACNG3	ENSGALG00000045305	TAFA1	CHRNA7	CPLX2	TP53I11
5	ENSGALG00000008032	RET	PDGFA	ARHGDIB	EBF1	PLPP4	CAMK2B	DPYSL4
6	DOC2B	SHISA2	CDH18	TMEM169	PDS5B	ST6GAL2	CNTN5	GRIA1
7	ACTB	NYAP2	PTGFR	ST6GALNAC5	ENSGALG00000050258	PLAU	HES6	PHF21B
8	RPP25	CACNA2D3	SOX4					

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0099504	synaptic vesicle cycle	BP	11	2	0.0009495
GO:0099003	vesicle-mediated transport in synapse	BP	12	2	0.001136
GO:0050890	cognition	BP	21	2	0.003528
GO:0098967	exocytic insertion of neurotransmitter receptor to postsynaptic membrane	BP	1	1	0.004245
GO:0031629	synaptic vesicle fusion to presynaptic active zone membrane	BP	1	1	0.004245
GO:0016082	synaptic vesicle priming	BP	1	1	0.004245
GO:0099500	vesicle fusion to plasma membrane	BP	1	1	0.004245
GO:0099590	neurotransmitter receptor internalization	BP	2	1	0.008472
GO:0042396	phosphagen biosynthetic process	BP	2	1	0.008472
GO:0006599	phosphagen metabolic process	BP	2	1	0.008472

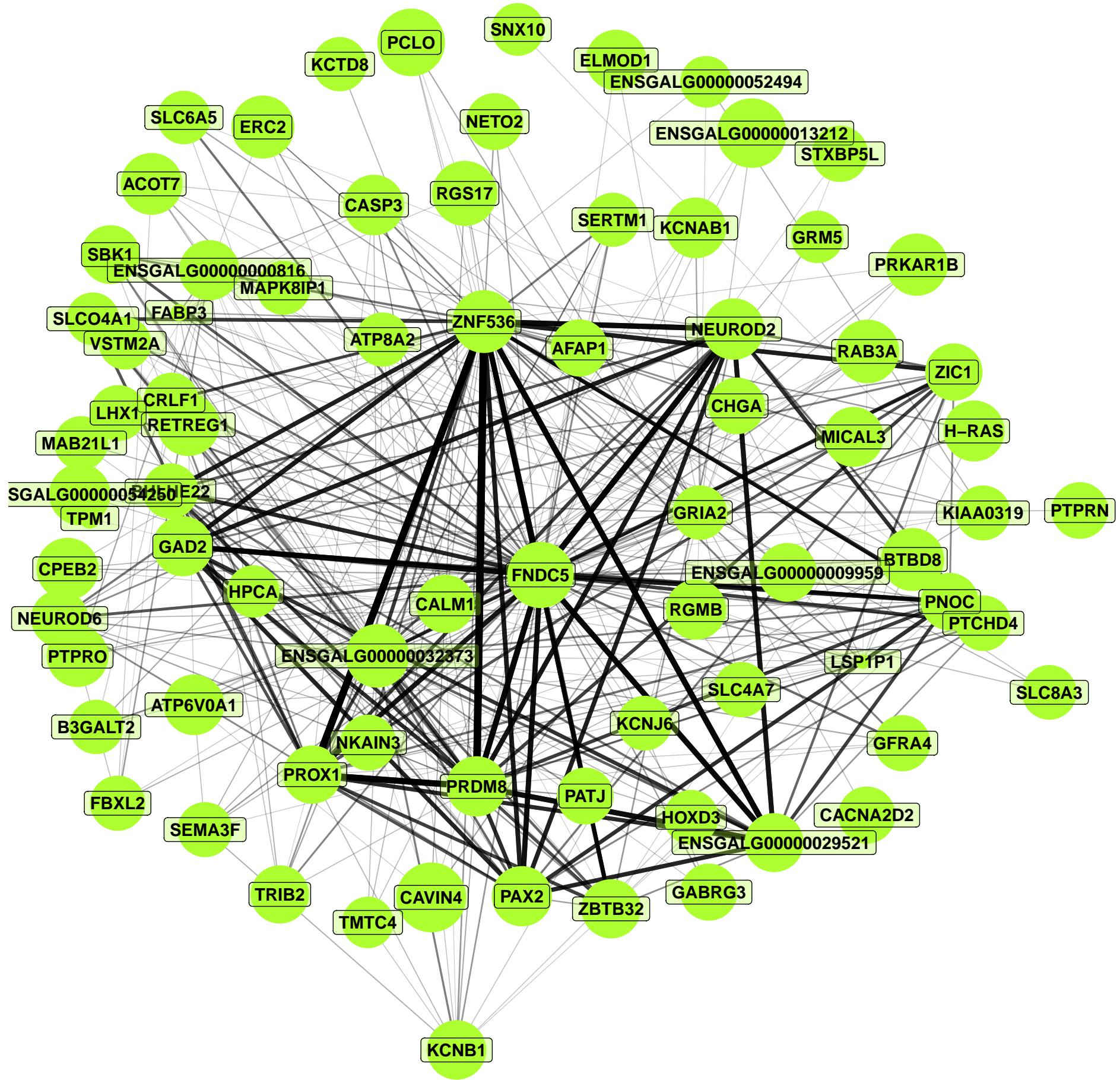
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04260</i>	Cardiac muscle contraction	59	5	4.813e-06
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	6	1.225e-05
<i>path:gga04020</i>	Calcium signaling pathway	196	7	1.787e-05
<i>path:gga04010</i>	MAPK signaling pathway	236	6	0.0004711
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	272	4	0.02808
<i>path:gga04510</i>	Focal adhesion	170	3	0.03541
<i>path:gga04916</i>	Melanogenesis	84	2	0.04943
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	1	0.05382
<i>path:gga04371</i>	Apelin signaling pathway	111	2	0.08058
<i>path:gga00500</i>	Starch and sucrose metabolism	27	1	0.1086





	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0007010	cytoskeleton organization	BP	165	9	0.0001708
GO:0007399	nervous system development	BP	255	11	0.0002605
GO:0031110	regulation of microtubule polymerization or depolymerization	BP	11	3	0.0002631
GO:0048699	generation of neurons	BP	177	9	0.0002887
GO:0022008	neurogenesis	BP	180	9	0.0003269
GO:0031175	neuron projection development	BP	109	7	0.000342
GO:0031109	microtubule polymerization or depolymerization	BP	14	3	0.0005653
GO:0030516	regulation of axon extension	BP	14	3	0.0005653
GO:0048666	neuron development	BP	123	7	0.0007088
GO:0030182	neuron differentiation	BP	161	8	0.0007316

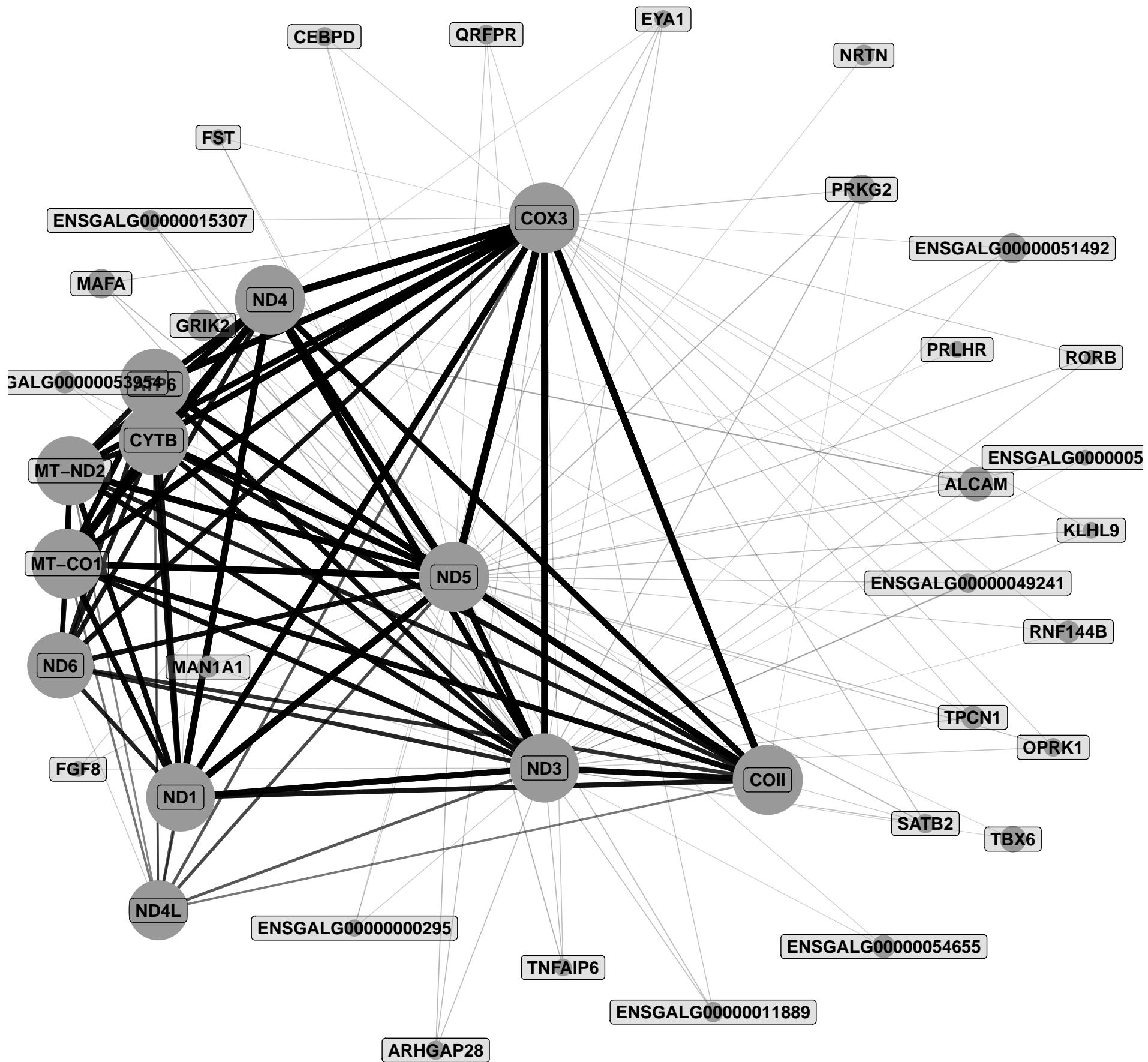
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04145</i>	Phagosome	123	6	0.003699
<i>path:gga05132</i>	Salmonella infection	221	8	0.005296
<i>path:gga04540</i>	Gap junction	79	4	0.01512
<i>path:gga03267</i>	Virion – Adenovirus	2	1	0.02394
<i>path:gga04514</i>	Cell adhesion molecules	95	4	0.02767
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.0473
<i>path:gga04261</i>	Adrenergic signalling in cardiomyocytes	122	4	0.05979
<i>path:gga04020</i>	Calcium signalling pathway	196	5	0.08815
<i>path:gga04114</i>	Oocyte meiosis	96	3	0.1093
<i>path:gga03250</i>	Viral life cycle – HIV-1	48	2	0.1136



1	CAVIN4	ENSGALG00000013212	FNDC5	CHGA	PCLO	PRDM8	NEUROD2	ZNF536
2	PAX2	PNOC	RAB3A	PROX1	NEUROD6	ELMOD1	GAD2	ENSGALG00000029521
3	RGMB	RETREG1	ACOT7	BTBD8	RGS17	LHX1	ENSGALG00000032373	ENSGALG00000054250
4	PTPRO	BHLHE22	KCNB1	CPEB2	ZBTB32	ERC2	ATP6V0A1	SERTM1
5	PRKAR1B	CACNA2D2	KCNAB1	ZIC1	ENSGALG0000009959	AFAP1	SEMA3F	FABP3
6	VSTM2A	ENSGALG0000000816	GFRA4	CALM1	CASP3	TRIB2	HOXD3	NETO2
7	GABRG3	ATP8A2	MICAL3	NKAIN3	SBK1	GRIA2	PTPRN	H-RAS
8	STXBP5L	PATJ	SLC8A3	KIAA0319	TMTC4	SLCO4A1	GRM5	FBXL2
9	MAB21L1	SLC6A5	KCTD8	PTCHD4	SLC4A7	MAPK8IP1	CRLF1	SNX10
10	B3GALT2	KCNJ6	HPCA	ENSGALG00000052494	LSP1P1	TPM1		

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0021510	spinal cord development	BP	17	3	0.0001292
GO:0021516	dorsal spinal cord development	BP	6	2	0.0005149
GO:0035418	protein localization to synapse	BP	8	2	0.0009537
GO:0007423	sensory organ development	BP	78	4	0.001179
GO:1902414	protein localization to cell junction	BP	10	2	0.001521
GO:0090596	sensory organ morphogenesis	BP	43	3	0.002099
GO:0048562	embryonic organ morphogenesis	BP	45	3	0.002393
GO:0043010	camera-type eye development	BP	46	3	0.002549
GO:0072175	epithelial tube formation	BP	13	2	0.002606
GO:0035148	tube formation	BP	14	2	0.003029

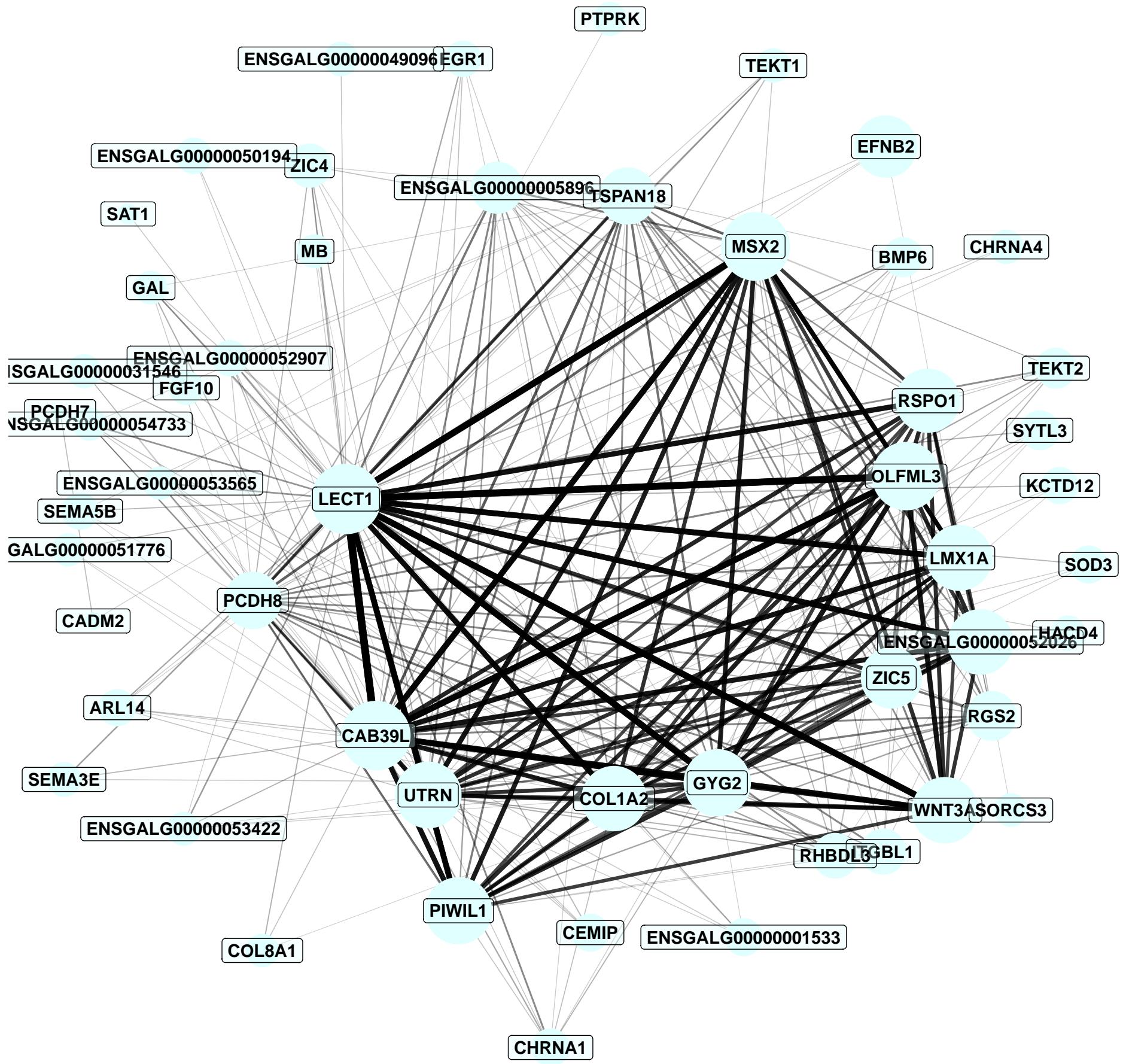
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04260</i>	Cardiac muscle contraction	59	3	0.005167
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	4	0.005966
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	81	3	0.01236
<i>path:gga04910</i>	Insulin signaling pathway	108	3	0.0264
<i>path:gga04371</i>	Apelin signaling pathway	111	3	0.02832
<i>path:gga04010</i>	MAPK signaling pathway	236	4	0.05181
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	1	0.06906
<i>path:gga04912</i>	GnRH signaling pathway	73	2	0.06991
<i>path:gga04744</i>	Phototransduction	13	1	0.07459
<i>path:gga04540</i>	Gap junction	79	2	0.08014



1	COX3	MT-CO1	ATP6	CYTB	COII	ND5	ND4	ND1
2	ND6	MT-ND2	ND3	ND4L	ALCAM	GRIK2	KLHL9	TPCN1
3	PRKG2	MAFA	TNFAIP6	OPRK1	ARHGAP28	EYA1	ENSGALG00000051492	ENSGALG00000011889
4	ENSGALG00000000295	ENSGALG00000015307	ENSGALG00000049241	SATB2	FGF8	MAN1A1	CEBD	RNF144B
5	TBX6	ENSGALG00000054655	ENSGALG00000053954	FST	PRLHR	RORB	ENSGALG00000052227	QRFPR
6	NRTN							

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0009880	embryonic pattern specification	BP	6	2	5.336e-05
GO:0007389	pattern specification process	BP	57	3	0.0001733
GO:0051302	regulation of cell division	BP	21	2	0.0007339
GO:0030154	cell differentiation	BP	409	5	0.0009637
GO:0048869	cellular developmental process	BP	418	5	0.001063
GO:0009790	embryo development	BP	118	3	0.001463
GO:0060684	epithelial–mesenchymal cell signaling	BP	1	1	0.001929
GO:0035852	horizontal cell localization	BP	1	1	0.001929
GO:1902870	negative regulation of amacrine cell differentiation	BP	1	1	0.001929
GO:1902864	negative regulation of embryonic camera-type eye development	BP	1	1	0.001929

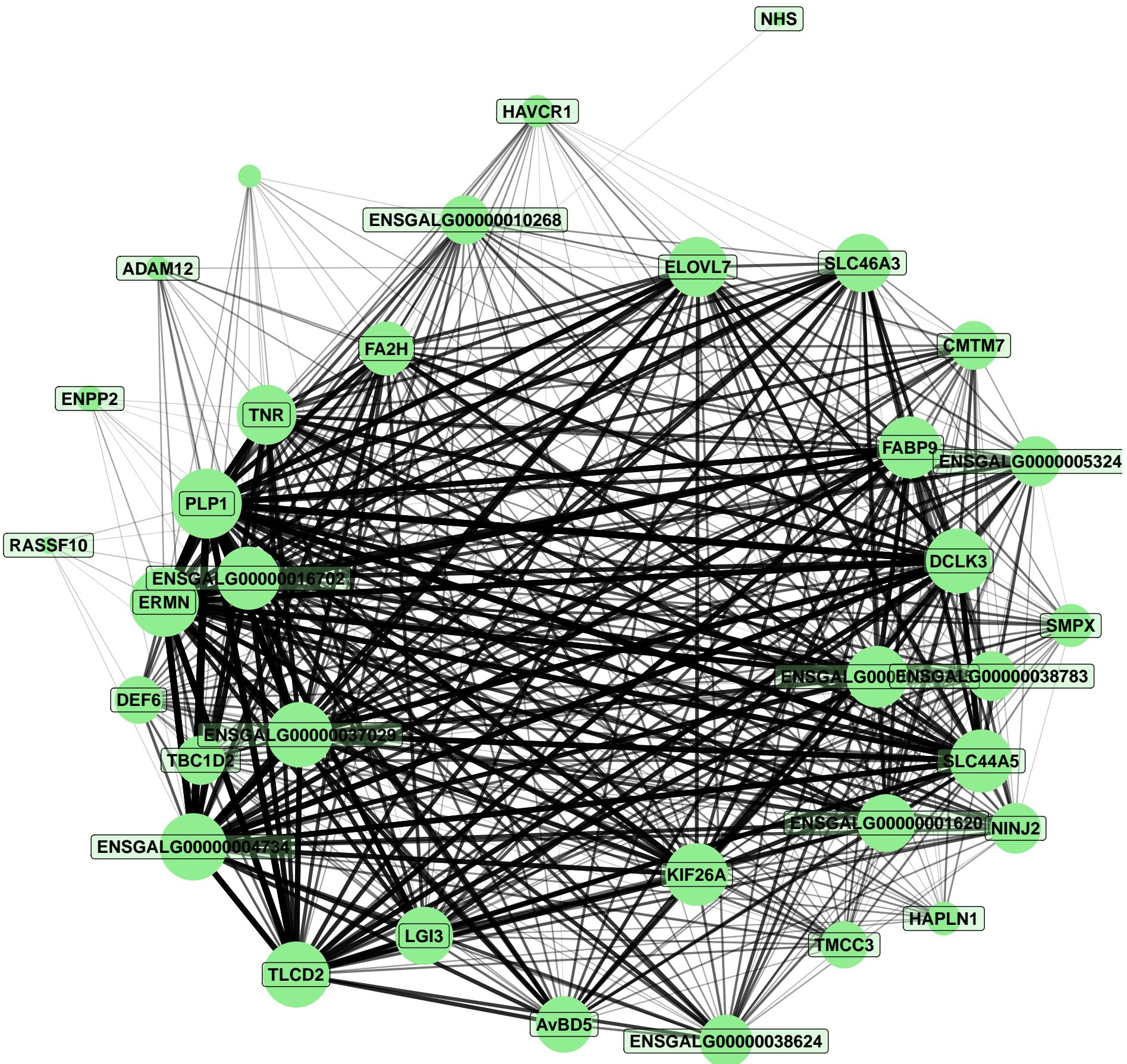
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	272	4	0.001697
<i>path:gga04020</i>	Calcium signaling pathway	196	2	0.0544
<i>path:gga00513</i>	Various types of N–glycan biosynthesis	38	1	0.07086
<i>path:gga00510</i>	N–Glycan biosynthesis	45	1	0.08338
<i>path:gga04540</i>	Gap junction	79	1	0.1419
<i>path:gga04350</i>	TGF–beta signaling pathway	84	1	0.1502
<i>path:gga04514</i>	Cell adhesion molecules	95	1	0.1682
<i>path:gga04270</i>	Vascular smooth muscle contraction	104	1	0.1826
<i>path:gga04120</i>	Ubiquitin mediated proteolysis	128	1	0.22
<i>path:gga04141</i>	Protein processing in endoplasmic reticulum	146	1	0.2469



1	MSX2	LECT1	CAB39L	PIWIL1	LMX1A	GYG2	ZIC5	OLFML3
2	UTRN	WNT3A	EFNB2	COL1A2	TSPAN18	ENSGALG00000052026	PCDH8	ENSGALG00000005896
3	RSPO1	RGS2	ZIC4	RHBDL3	CEMIP	ITGBL1	EGR1	SORCS3
4	BMP6	GAL	ENSGALG00000051776	SEMA3E	FGF10	ENSGALG00000052907	SEMA5B	TEKT2
5	CHRNA1	PTPRK	ARL14	SYTL3	ENSGALG00000031546	SOD3	TEKT1	ENSGALG00000001533
6	CHRNA4	ENSGALG00000054733	KCTD12	ENSGALG00000053565	HACD4	ENSGALG00000050194	ENSGALG00000053422	COL8A1
7	ENSGALG00000049096	MB	SAT1	CADM2	PCDH7			

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0032501	multicellular organismal process	BP	692	12	4.547e-06
GO:0007275	multicellular organism development	BP	562	9	0.0001586
GO:0048856	anatomical structure development	BP	608	9	0.0002857
GO:0032502	developmental process	BP	640	9	0.0004169
GO:0072359	circulatory system development	BP	113	4	0.0007328
GO:0001525	angiogenesis	BP	51	3	0.0008245
GO:0099565	chemical synaptic transmission, postsynaptic	BP	14	2	0.00114
GO:0060079	excitatory postsynaptic potential	BP	14	2	0.00114
GO:0048514	blood vessel morphogenesis	BP	62	3	0.001456
GO:0001568	blood vessel development	BP	64	3	0.001596

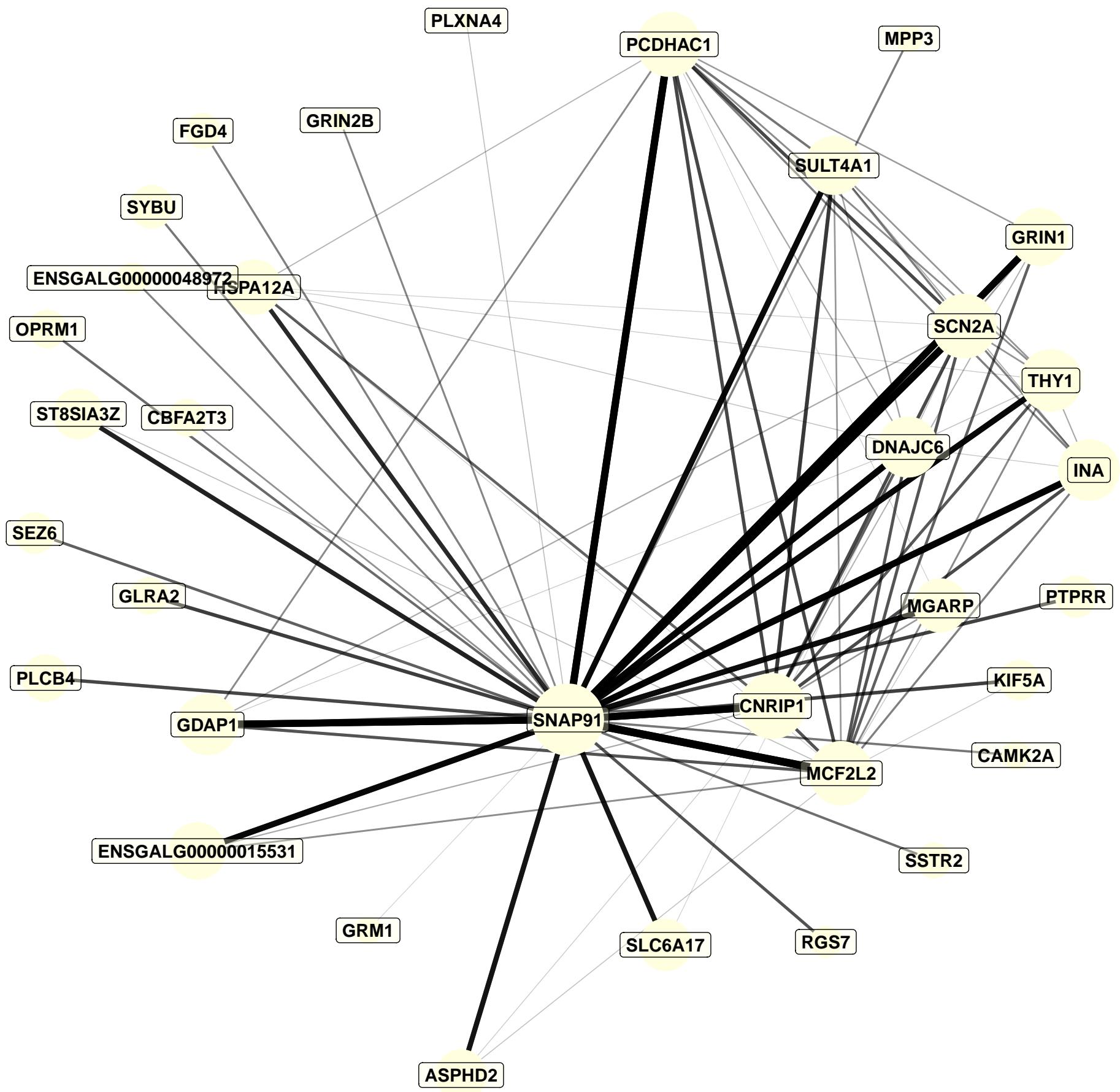
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.01443
<i>path:gga00910</i>	Nitrogen metabolism	14	1	0.04963
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	272	3	0.07556
<i>path:gga00062</i>	Fatty acid elongation	22	1	0.0769
<i>path:gga04150</i>	mTOR signaling pathway	133	2	0.08384
<i>path:gga04310</i>	Wnt signaling pathway	134	2	0.08492
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	26	1	0.09024
<i>path:gga00500</i>	Starch and sucrose metabolism	27	1	0.09355
<i>path:gga04216</i>	Ferroptosis	34	1	0.1164
<i>path:gga00330</i>	Arginine and proline metabolism	39	1	0.1323



1	FABP9	ERMN	PLP1	ENSGALG00000037029	ENSGALG00000004734	DCLK3	TLCD2	KIF26A
2	TNR	SLC44A5	ELOVL7	ENSGALG00000016702	LGI3	ENSGALG00000009355	FA2H	ENSGALG0000001620
3	SLC46A3	ENSGALG00000053247	AvBD5	CMTM7	TBC1D2	HAVCR1	NINJ2	ENSGALG00000010268
4	TMCC3	DEF6	HAPLN1	ENSGALG00000038624	ADAM12	SMPX	ENSGALG00000038783	NA
5	RASSF10	ENPP2	NHS					

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0032291	axon ensheathment in central nervous system	BP	2	1	0.005241
GO:0022010	central nervous system myelination	BP	2	1	0.005241
GO:0014003	oligodendrocyte development	BP	2	1	0.005241
GO:0021782	glial cell development	BP	5	1	0.01305
GO:0007417	central nervous system development	BP	86	2	0.02129
GO:0048709	oligodendrocyte differentiation	BP	9	1	0.02338
GO:0050918	positive chemotaxis	BP	9	1	0.02338
GO:0007399	nervous system development	BP	255	3	0.02878
GO:0008366	axon ensheathment	BP	12	1	0.03105
GO:0007272	ensheathment of neurons	BP	12	1	0.03105

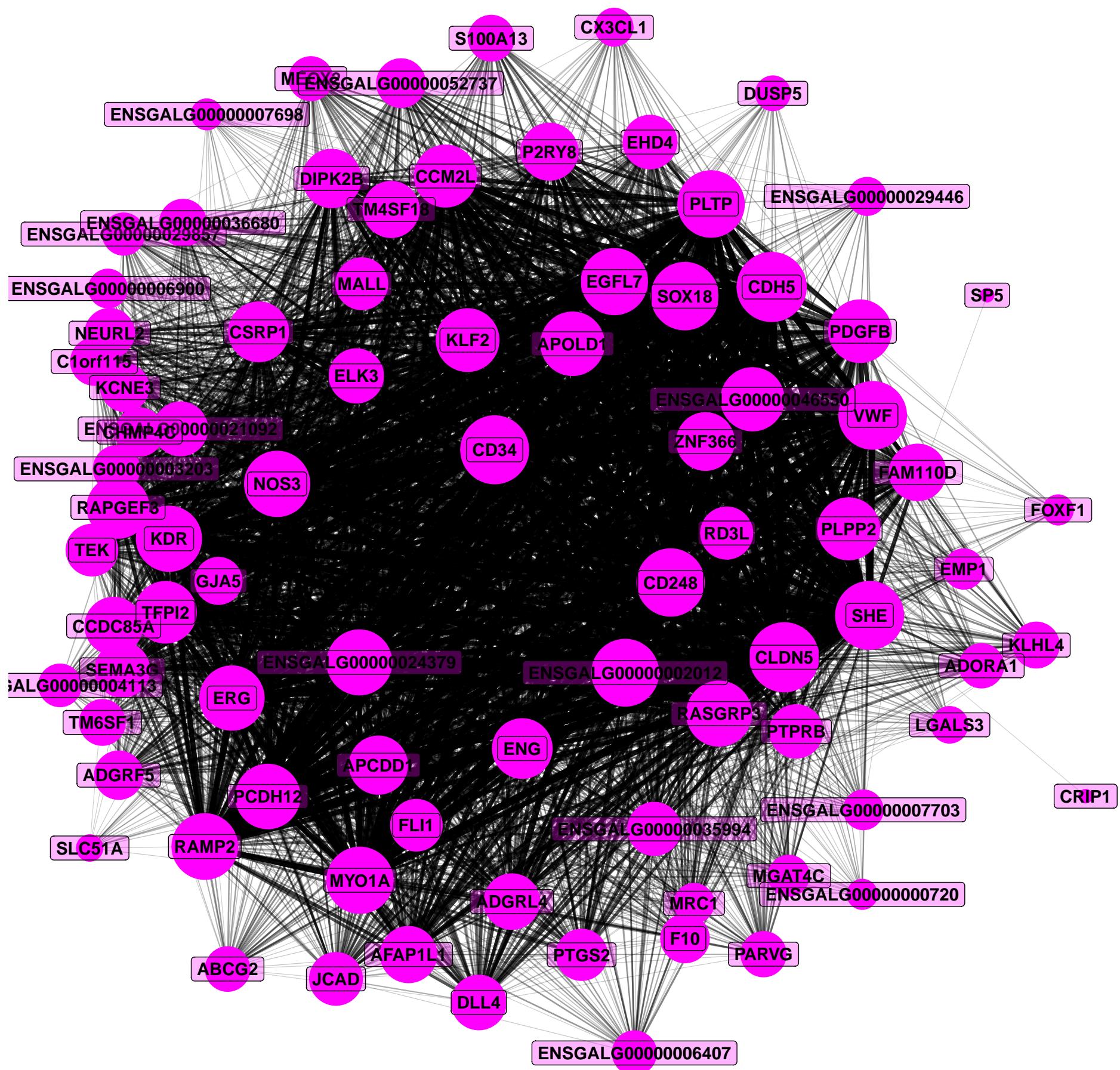
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga03264</i>	Virion – Flavivirus	3	1	0.007852
<i>path:gga00062</i>	Fatty acid elongation	22	1	0.05621
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	26	1	0.0661
<i>path:gga00565</i>	Ether lipid metabolism	34	1	0.08557
<i>path:gga01212</i>	Fatty acid metabolism	49	1	0.121
<i>path:gga04512</i>	ECM–receptor interaction	67	1	0.1618
<i>path:gga03015</i>	mRNA surveillance pathway	72	1	0.1728
<i>path:gga04514</i>	Cell adhesion molecules	95	1	0.2216
<i>path:gga00230</i>	Purine metabolism	113	1	0.2578
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	1	0.2753



1	SNAP91	GRIN1	SCN2A	CNRIP1	MCF2L2	PCDHAC1	THY1	MGARP
2	INA	ENSGALG00000015531	DNAJC6	SULT4A1	GDAP1	HSPA12A	SLC6A17	ST8SIA3Z
3	GLRA2	SEZ6	ASPHD2	SYBU	PLCB4	PTPRR	RGS7	KIF5A
4	OPRM1	PLXNA4	CBFA2T3	SSTR2	MPP3	CAMK2A	FGD4	ENSGALG0000048972
5	GRM1	GRIN2B						

	Term	Ont	N	n	Adj. p-value
GO:0046549	retinal cone cell development	BP	1	1	0.002624
GO:0042670	retinal cone cell differentiation	BP	1	1	0.002624
GO:1904427	positive regulation of calcium ion transmembrane transport	BP	2	1	0.005241
GO:0010524	positive regulation of calcium ion transport into cytosol	BP	2	1	0.005241
GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	BP	2	1	0.005241
GO:0042462	eye photoreceptor cell development	BP	3	1	0.007852
GO:0050858	negative regulation of antigen receptor-mediated signaling pathway	BP	3	1	0.007852
GO:0050860	negative regulation of T cell receptor signaling pathway	BP	3	1	0.007852
GO:0050854	regulation of antigen receptor-mediated signaling pathway	BP	3	1	0.007852
GO:0051279	regulation of release of sequestered calcium ion into cytosol	BP	3	1	0.007852

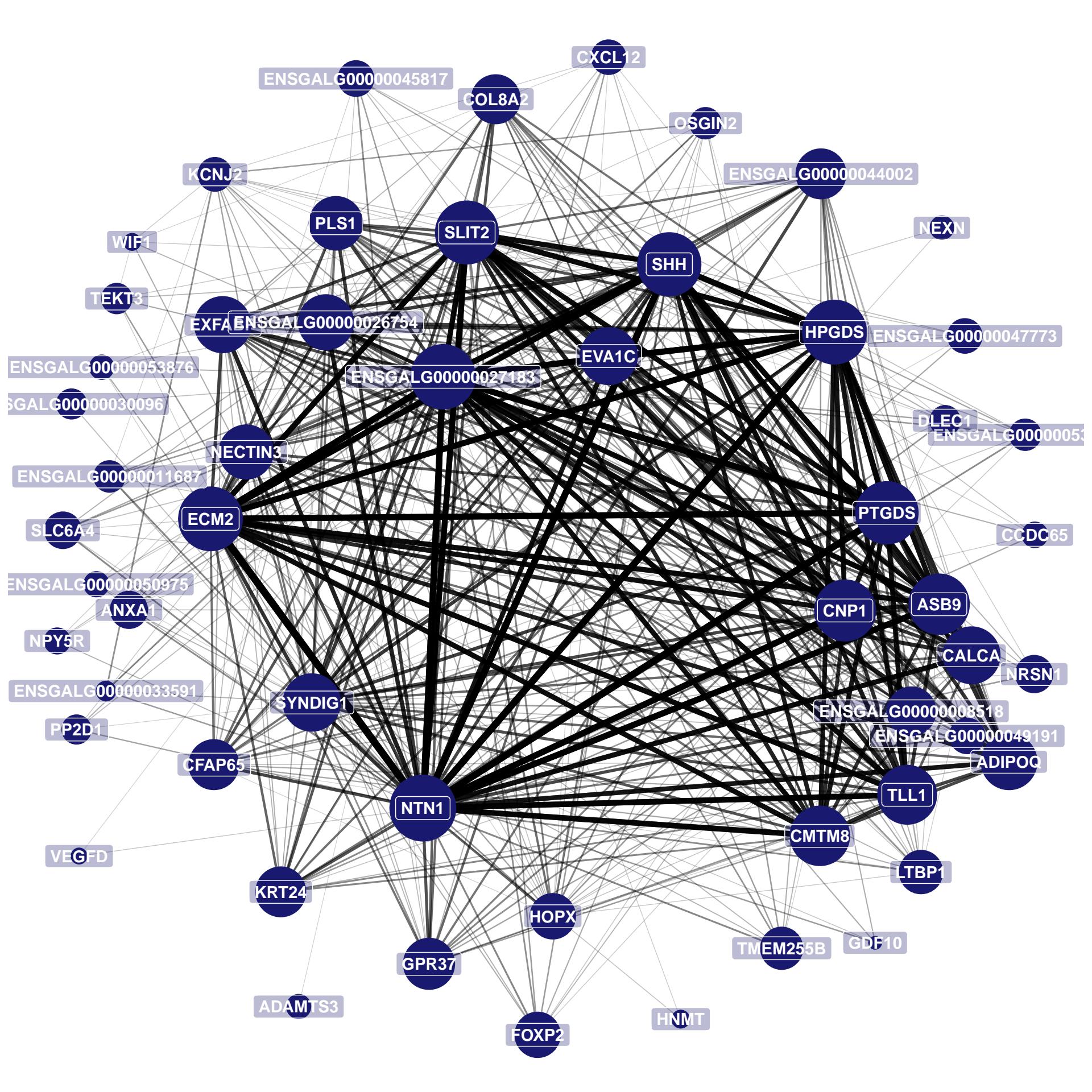
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	272	6	6.644e–05
<i>path:gga04020</i>	Calcium signaling pathway	196	4	0.001651
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	3	0.003939
<i>path:gga04912</i>	GnRH signaling pathway	73	2	0.01563
<i>path:gga04540</i>	Gap junction	79	2	0.01815
<i>path:gga04916</i>	Melanogenesis	84	2	0.02037
<i>path:gga04310</i>	Wnt signaling pathway	134	2	0.04802
<i>path:gga04144</i>	Endocytosis	217	2	0.1106
<i>path:gga00562</i>	Inositol phosphate metabolism	66	1	0.1596
<i>path:gga03015</i>	mRNA surveillance pathway	72	1	0.1728



1	CDH5	VWF	CD34	MYO1A	RAMP2	CLDN5	SOX18	CD248
2	SHE	ENSGALG00000002012	APOLD1	ERG	PCDH12	NOS3	ENSGALG00000024379	KLF2
3	EGFL7	ENSGALG00000046550	KDR	RASGRP3	TFPI2	PLPP2	MALL	PLTP
4	CCM2L	ENG	PDGFB	AFAP1L1	ZNF366	FAM110D	P2RY8	ADGRL4
5	RAPGEF3	FLI1	SEMA3G	CSRP1	CCDC85A	RD3L	DIPK2B	ADORA1
6	TEK	KLHL4	TM4SF18	ENSGALG0000003203	APCDD1	ENSGALG00000021092	ENSGALG00000035994	JCAD
7	EHD4	PTPRB	DLL4	S100A13	ENSGALG00000052737	ELK3	PTGS2	MEOX2
8	EMP1	ABCG2	CHMP4C	ENSGALG00000029857	ENSGALG0000004113	GJA5	F10	KCNE3
9	PARVG	NEURL2	C1orf115	LGALS3	ENSGALG0000007703	TM6SF1	ENSGALG0000006407	ADGRF5
10	ENSGALG00000036680	MGAT4C	MRC1	ENSGALG0000000720	ENSGALG00000029446	ENSGALG0000006900	CX3CL1	DUSP5
11	FOXF1	ENSGALG0000007698	SP5	CRIP1	SLC51A			

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0050878	regulation of body fluid levels	BP	11	3	3.886e-05
GO:0008015	blood circulation	BP	26	3	0.0005718
GO:0003013	circulatory system process	BP	26	3	0.0005718
GO:0007596	blood coagulation	BP	7	2	0.0008139
GO:0007599	hemostasis	BP	7	2	0.0008139
GO:0035590	purinergic nucleotide receptor signaling pathway	BP	7	2	0.0008139
GO:0050817	coagulation	BP	8	2	0.001081
GO:0008217	regulation of blood pressure	BP	8	2	0.001081
GO:0050728	negative regulation of inflammatory response	BP	9	2	0.001384
GO:0031348	negative regulation of defense response	BP	12	2	0.002506

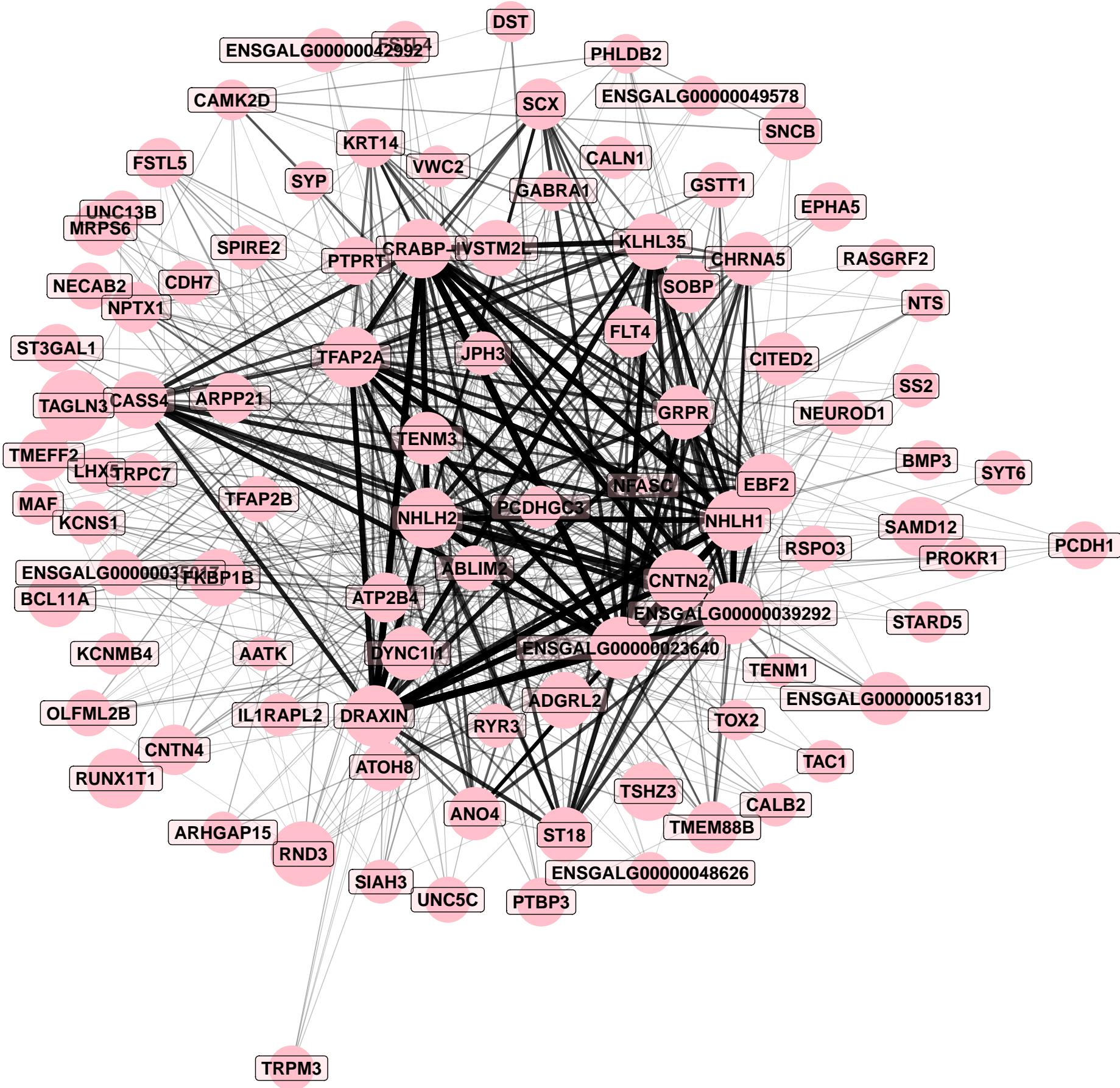
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04370</i>	VEGF signaling pathway	51	3	0.004088
<i>path:gga04510</i>	Focal adhesion	170	5	0.004435
<i>path:gga04010</i>	MAPK signaling pathway	236	5	0.01686
<i>path:gga04514</i>	Cell adhesion molecules	95	3	0.02229
<i>path:gga00220</i>	Arginine biosynthesis	16	1	0.09664
<i>path:gga04020</i>	Calcium signaling pathway	196	3	0.1275
<i>path:gga04371</i>	Apelin signaling pathway	111	2	0.1559
<i>path:gga04621</i>	NOD-like receptor signaling pathway	115	2	0.1648
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	1	0.1683
<i>path:gga00565</i>	Ether lipid metabolism	34	1	0.1944



1	ECM2	HPGDS	PTGDS	SHH	CNP1	ENSGALG00000027183	NTN1	SLIT2
2	EXFABP	ASB9	CMTM8	EVA1C	TLL1	SYNDIG1	ENSGALG00000026754	ADIPOQ
3	PLS1	HOPX	ENSGALG00000044002	KRT24	CFAP65	FOXP2	CALCA	GPR37
4	SLC6A4	ENSGALG0000008518	LTBP1	KCNJ2	COL8A2	NECTIN3	ENSGALG00000045817	TMEM255B
5	ANXA1	OSGIN2	NRSN1	ENSGALG00000033591	ENSGALG00000053594	ENSGALG00000049191	CXCL12	ENSGALG00000011687
6	TEKT3	DLEC1	ENSGALG00000050975	NPY5R	ENSGALG00000053876	CCDC65	ENSGALG00000047773	ADAMTS3
7	PP2D1	WIF1	NEXN	VEGFD	GDF10	ENSGALG00000030096	HNMT	

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0048589	developmental growth	BP	63	6	1.23e-07
GO:0040007	growth	BP	92	6	1.189e-06
GO:0051094	positive regulation of developmental process	BP	119	6	5.356e-06
GO:0051239	regulation of multicellular organismal process	BP	198	7	8.73e-06
GO:0048639	positive regulation of developmental growth	BP	18	3	3.985e-05
GO:0051240	positive regulation of multicellular organismal process	BP	113	5	6.482e-05
GO:0009888	tissue development	BP	193	6	8.295e-05
GO:0003415	chondrocyte hypertrophy	BP	4	2	8.366e-05
GO:0015909	long-chain fatty acid transport	BP	4	2	8.366e-05
GO:0045927	positive regulation of growth	BP	24	3	9.728e-05

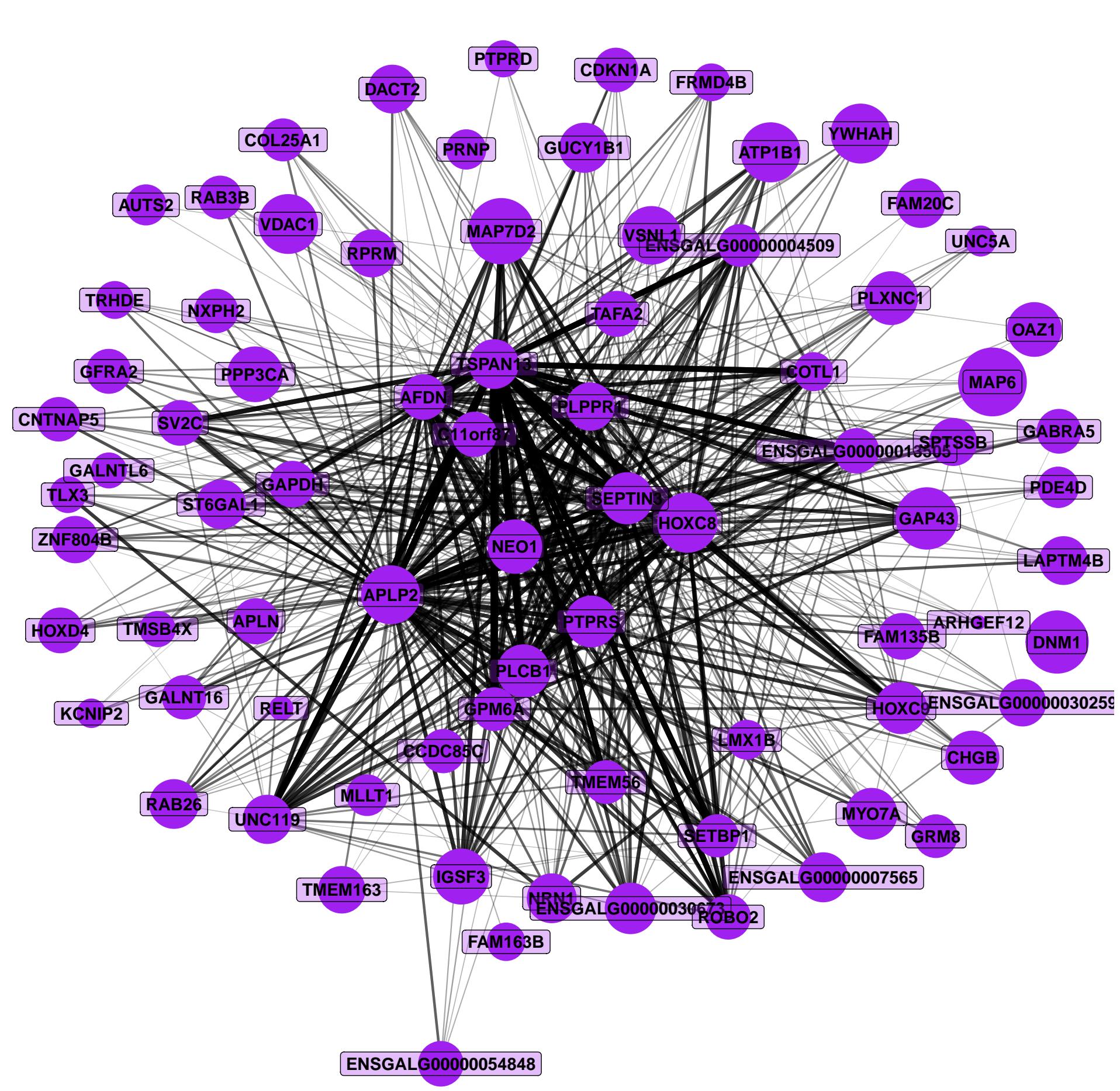
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga00590</i>	Arachidonic acid metabolism	37	2	0.008576
<i>path:gga00910</i>	Nitrogen metabolism	14	1	0.05169
<i>path:gga04270</i>	Vascular smooth muscle contraction	104	2	0.0588
<i>path:gga00220</i>	Arginine biosynthesis	16	1	0.05885
<i>path:gga00340</i>	Histidine metabolism	17	1	0.06242
<i>path:gga04672</i>	Intestinal immune network for IgA production	18	1	0.06597
<i>path:gga00630</i>	Glyoxylate and dicarboxylate metabolism	28	1	0.1008
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	1	0.1042
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	31	1	0.1109
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	1	0.1143



1	TAGLN3	DRAVIN	CRABP-I	NHLH1	ENSGALG00000023640	CNTN2	TFAP2A	RND3
2	RUNX1T1	SAMD12	SNCB	EBF2	ENSGALG00000039292	ST18	NHLH2	DYNC1I1
3	TSHZ3	TMEFF2	FKBP1B	VSTM2L	CITED2	CASS4	KRT14	FSTL5
4	GRPR	KLHL35	ADGRL2	ARPP21	FLT4	TAC1	TENM3	MRPS6
5	SCX	TMEM88B	ANO4	SOBP	NPTX1	CHRNA5	ENSGALG00000051831	PTPRT
6	ATOH8	GSTT1	BCL11A	EPHA5	PCDHGC3	ENSGALG00000035017	SPIRE2	PTBP3
7	ATP2B4	UNC13B	CNTN4	SS2	JPH3	UNC5C	TFAP2B	PCDH1
8	SYP	ST3GAL1	CALB2	OLFML2B	ARHGAP15	DST	ABLIM2	FSTL4
9	RSPO3	NFASC	SYT6	NEUROD1	NECAB2	CAMK2D	SIAH3	ENSGALG00000042992
10	CALN1	TRPM3	RYR3	PHLDB2	LHX5	KCNS1	IL1RAPL2	CDH7
11	GABRA1	ENSGALG00000048626	PROKR1	AATK	STARD5	TRPC7	KCNMB4	TOX2
12	MAF	NTS	RASGRF2	BMP3	ENSGALG00000049578	VWC2	TENM1	

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0000902	cell morphogenesis	BP	112	6	0.0001338
GO:0009653	anatomical structure morphogenesis	BP	287	9	0.0001812
GO:0007411	axon guidance	BP	42	4	0.0002078
GO:0097485	neuron projection guidance	BP	42	4	0.0002078
GO:0048666	neuron development	BP	123	6	0.0002235
GO:0048856	anatomical structure development	BP	608	13	0.0003097
GO:0007399	nervous system development	BP	255	8	0.000419
GO:0048731	system development	BP	472	11	0.0004549
GO:0032502	developmental process	BP	640	13	0.0005055
GO:0030154	cell differentiation	BP	409	10	0.0005781

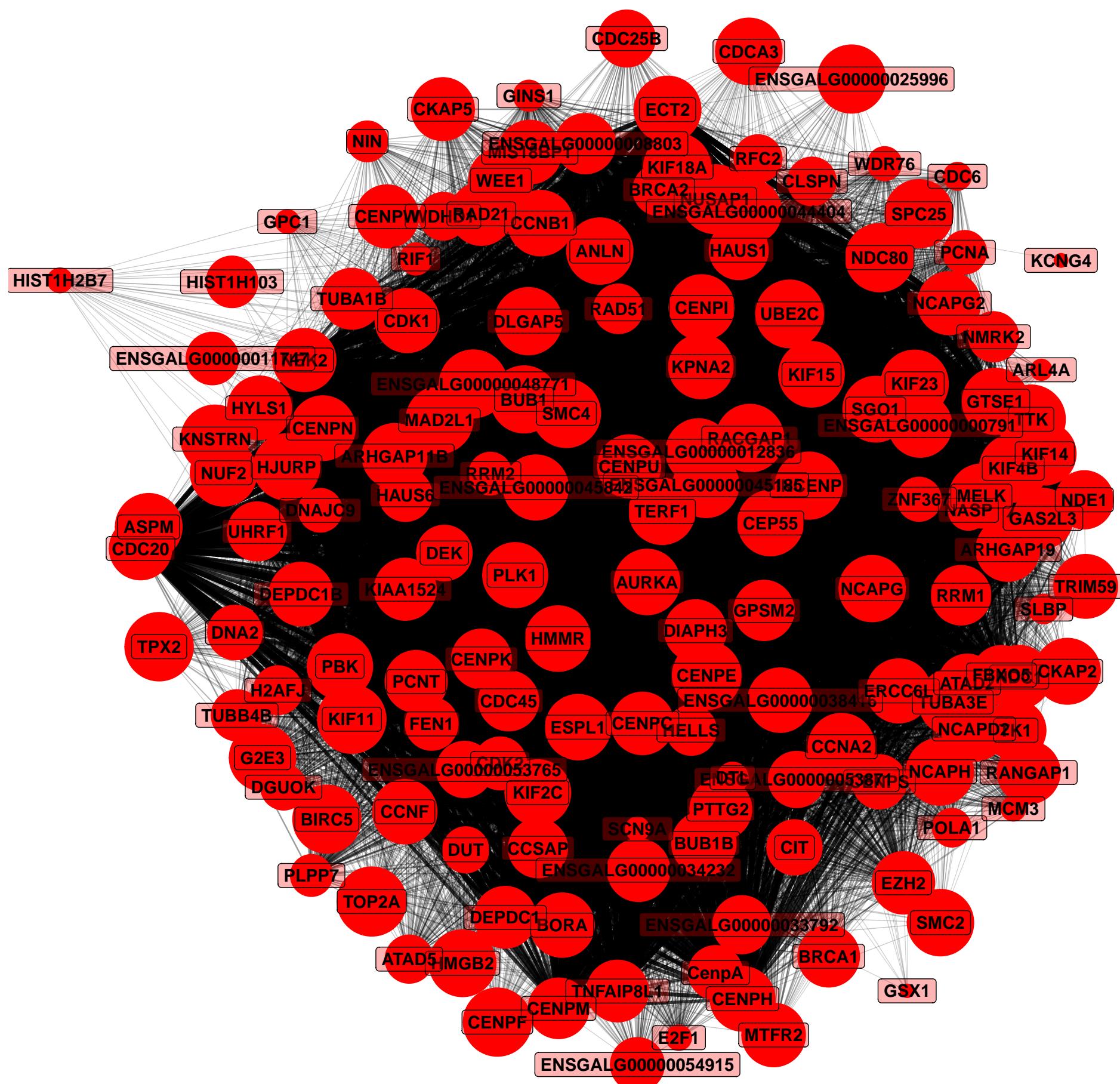
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	272	6	0.01221
<i>path:gga04020</i>	Calcium signaling pathway	196	5	0.01227
<i>path:gga04310</i>	Wnt signaling pathway	134	3	0.06819
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	1	0.08113
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	1	0.08759
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.09401
<i>path:gga04514</i>	Cell adhesion molecules	95	2	0.1437
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	1	0.185
<i>path:gga00512</i>	Mucin type O–glycan biosynthesis	29	1	0.185
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	31	1	0.1965





	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0030182	neuron differentiation	BP	161	6	0.0003576
GO:0048699	generation of neurons	BP	177	6	0.0005916
GO:0022008	neurogenesis	BP	180	6	0.0006463
GO:0007399	nervous system development	BP	255	7	0.0007245
GO:0048667	cell morphogenesis involved in neuron differentiation	BP	74	4	0.0009218
GO:0031103	axon regeneration	BP	8	2	0.0009292
GO:0098659	inorganic cation import across plasma membrane	BP	8	2	0.0009292
GO:0099587	inorganic ion import across plasma membrane	BP	8	2	0.0009292
GO:0048812	neuron projection morphogenesis	BP	77	4	0.00107
GO:0120039	plasma membrane bounded cell projection morphogenesis	BP	78	4	0.001123

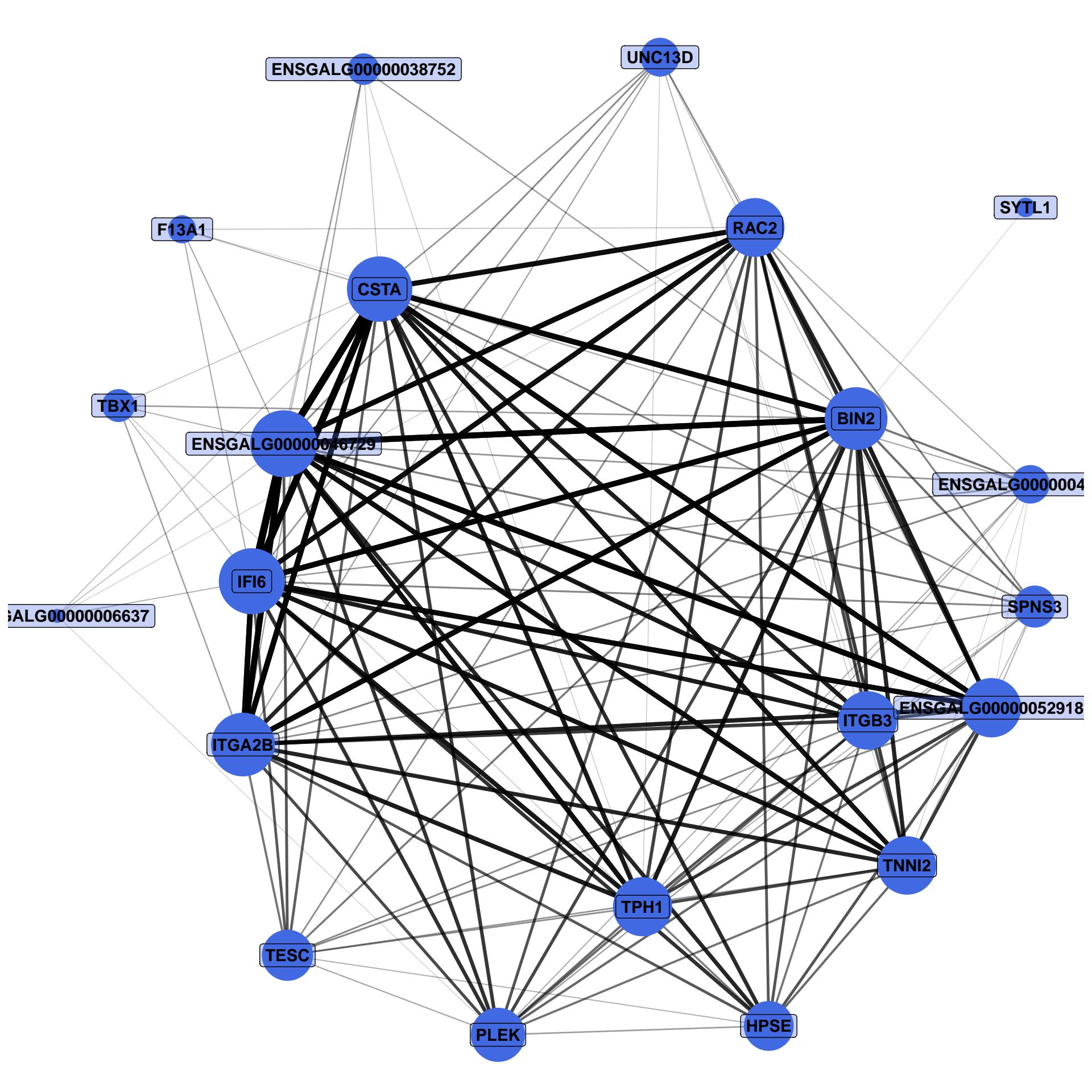
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	3	0.001761
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	2	0.01244
<i>path:gga04514</i>	Cell adhesion molecules	95	3	0.01826
<i>path:gga04270</i>	Vascular smooth muscle contraction	104	3	0.02314
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	3	0.03484
<i>path:gga04218</i>	Cellular senescence	133	3	0.04323
<i>path:gga04540</i>	Gap junction	79	2	0.07836
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	81	2	0.0818
<i>path:gga04020</i>	Calcium signaling pathway	196	3	0.1079
<i>path:gga04114</i>	Oocyte meiosis	96	2	0.109



1	NUSAP1	CENPE	TPX2	TOP2A	KIF11	CENPF	ENSGALG00000025996	SMC2
2	UBE2C	SMC4	BIRC5	KNSTRN	NDC80	KIF4B	SPC25	TTK
3	ASPM	INCENP	RACGAP1	ENSGALG00000048771	KPNA2	DLGAP5	KIF23	KIF15
4	NUF2	TUBA3E	BUB1	KIF18A	GTSE1	HMGB2	ANLN	CDCA3
5	AURKA	ECT2	PLK1	ENSGALG00000012836	KIF2C	NCAPG	CKAP2	CCNB1
6	BUB1B	CENPI	NCAPH	SGO1	PBK	CDK1	MAD2L1	CCNA2
7	HMMR	ENSGALG00000044404	CEP55	CENPW	ENSGALG00000038416	TERF1	TK1	G2E3
8	ENSGALG00000045185	HJURP	BRCA1	ESPL1	CENPH	CDC20	PTTG2	ARHGAP11B
9	ENSGALG00000045842	UHRF1	BORA	CCNF	ERCC6L	NCAPD2	CENPN	MELK
10	MIS18BP1	WEE1	NEK2	CENPC	DEPDC1B	DIAPH3	KIAA1524	NCAPG2
11	TRIM59	ARHGAP19	CENPK	HYLS1	ENSGALG0000000791	DEPDC1	CENPU	ENSGALG00000034232
12	CDC45	MTFR2	KIF14	ENSGALG00000011747	HAUS1	NDC1	CENPM	RRM1
13	TNFAIP8L1	TUBA1B	GAS2L3	DNA2	HIST1H103	NDE1	RANGAP1	RAD21
14	ENSGALG00000033792	GPSM2	EZH2	ATAD2	PCNT	CDK2	FBXO5	ENSGALG00000053871
15	ENSGALG00000008803	CKAP5	FEN1	CENPS	DEK	DGUOK	HELLS	ENSGALG00000053765
16	HAUS6	CenpA	BRCA2	RRM2	NMRK2	WDHD1	ENSGALG00000054915	CCSAP
17	H2AFJ	CDC25B	ATAD5	RAD51	CLSPN	RFC2	PCNA	CIT
18	DUT	TUBB4B	DNAJC9	NASP	ZNF367	POLA1	WDR76	GINS1
19	NIN	RIF1	SLBP	DTL	PLPP7	CDC6	MCM3	E2F1
20	SCN9A	GPC1	HIST1H2B7	ARL4A	GSX1	KCNG4		

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0007049	cell cycle	BP	202	26	6.058e–20
GO:0000278	mitotic cell cycle	BP	99	20	1.515e–19
GO:0051276	chromosome organization	BP	176	24	4.601e–19
GO:1903047	mitotic cell cycle process	BP	78	17	2.311e–17
GO:0022402	cell cycle process	BP	127	20	2.704e–17
GO:0051383	kinetochore organization	BP	10	8	1.387e–14
GO:0006996	organelle organization	BP	433	29	2.065e–14
GO:0007059	chromosome segregation	BP	43	12	5.321e–14
GO:0065004	protein–DNA complex assembly	BP	36	11	2.019e–13
GO:0071824	protein–DNA complex subunit organization	BP	39	11	5.464e–13

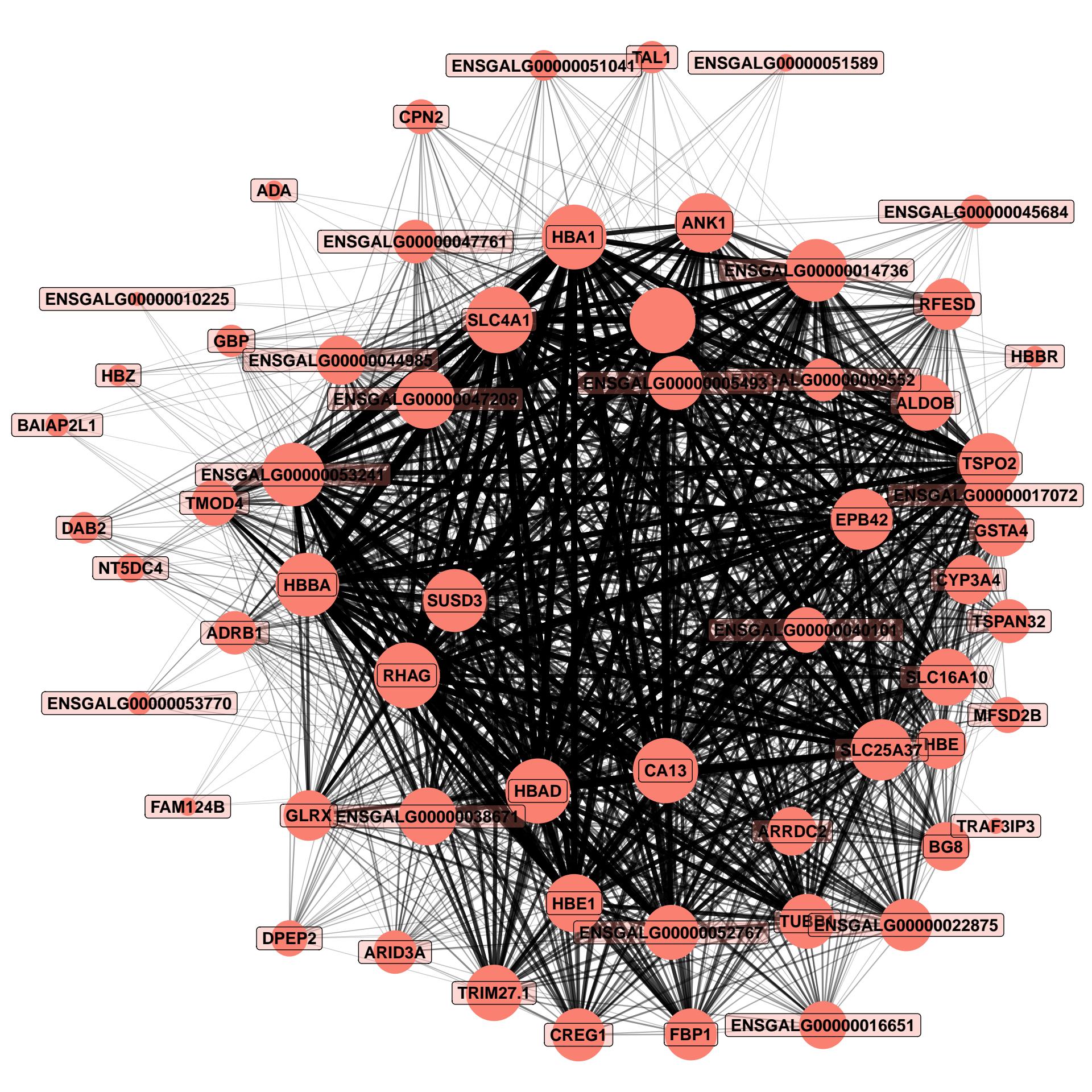
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04110</i>	Cell cycle	114	20	2.928e–18
<i>path:gga04114</i>	Oocyte meiosis	96	12	1.268e–09
<i>path:gga04914</i>	Progesterone–mediated oocyte maturation	78	9	3.211e–07
<i>path:gga03030</i>	DNA replication	29	6	9.327e–07
<i>path:gga00240</i>	Pyrimidine metabolism	55	5	0.0004649
<i>path:gga04115</i>	p53 signaling pathway	63	5	0.000871
<i>path:gga01232</i>	Nucleotide metabolism	77	5	0.002146
<i>path:gga03460</i>	Fanconi anemia pathway	48	4	0.002429
<i>path:gga00983</i>	Drug metabolism – other enzymes	55	4	0.003996
<i>path:gga03440</i>	Homologous recombination	36	3	0.008667



1	IFI6	CSTA	ENSGALG00000046729	ITGA2B	BIN2	ENSGALG00000052918	TNNI2	HPSE
2	TPH1	ITGB3	PLEK	RAC2	F13A1	ENSGALG0000006637	TESC	UNC13D
3	TBX1	SPNS3	ENSGALG00000038752	SYTL1	ENSGALG00000049122			

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0097164	ammonium ion metabolic process	BP	1	1	0.001544
GO:0030200	heparan sulfate proteoglycan catabolic process	BP	1	1	0.001544
GO:0071800	podosome assembly	BP	1	1	0.001544
GO:0030854	positive regulation of granulocyte differentiation	BP	1	1	0.001544
GO:1901162	primary amino compound biosynthetic process	BP	1	1	0.001544
GO:1901160	primary amino compound metabolic process	BP	1	1	0.001544
GO:0030167	proteoglycan catabolic process	BP	1	1	0.001544
GO:0042427	serotonin biosynthetic process	BP	1	1	0.001544
GO:0042428	serotonin metabolic process	BP	1	1	0.001544
GO:0009072	aromatic amino acid family metabolic process	BP	2	1	0.003085

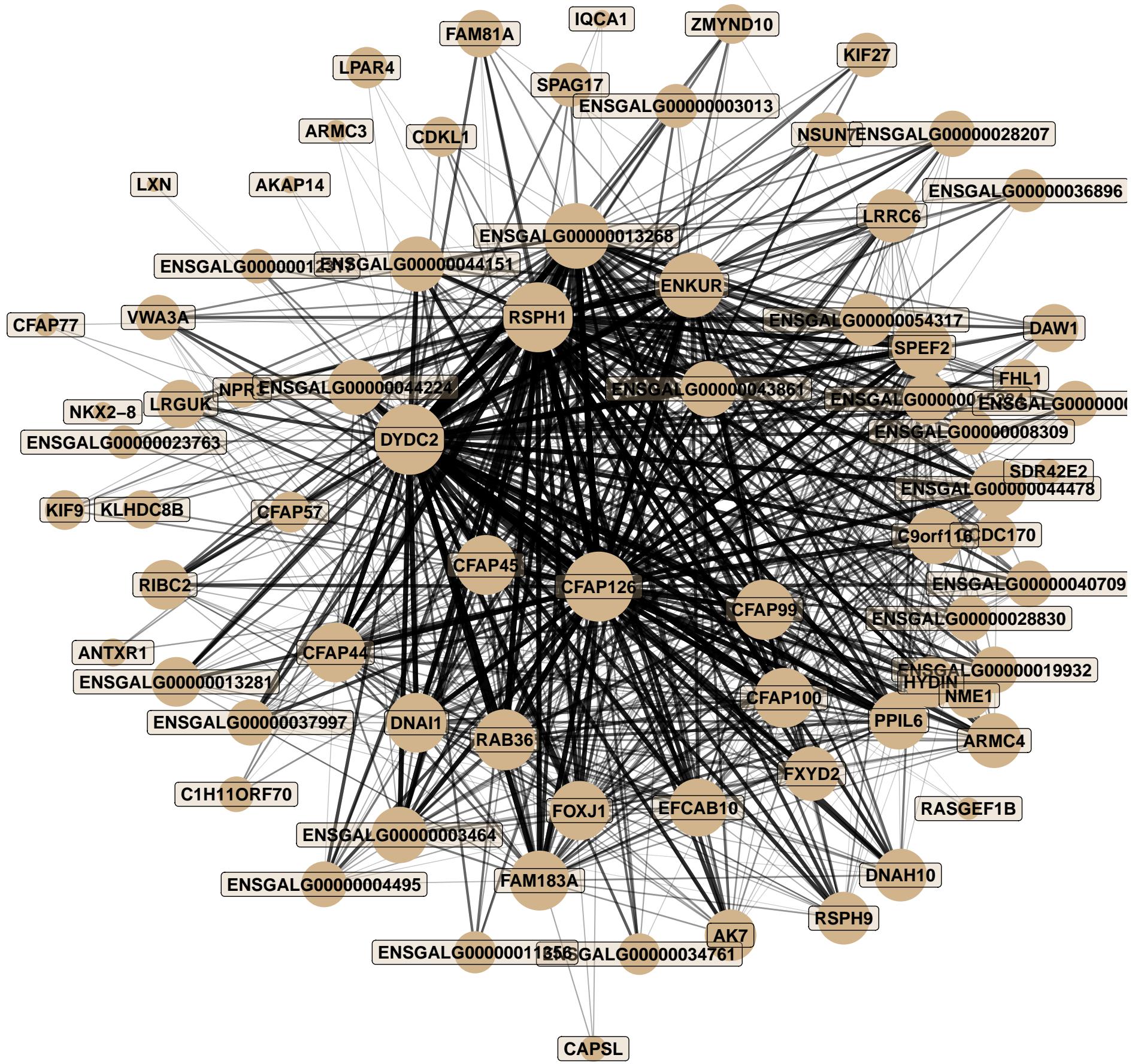
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04512</i>	ECM–receptor interaction	67	3	0.0001415
<i>path:gga04510</i>	Focal adhesion	170	3	0.002147
<i>path:gga04810</i>	Regulation of actin cytoskeleton	182	3	0.002606
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.006161
<i>path:gga00531</i>	Glycosaminoglycan degradation	15	1	0.02292
<i>path:gga00790</i>	Folate biosynthesis	26	1	0.03941
<i>path:gga00380</i>	Tryptophan metabolism	33	1	0.04976
<i>path:gga04370</i>	VEGF signaling pathway	51	1	0.0759
<i>path:gga04520</i>	Adherens junction	69	1	0.1014
<i>path:gga04145</i>	Phagosome	123	1	0.1738



1	HBAD	SLC4A1	HBA1	NA	CA13	RHAG	HBBA	TSPO2
2	HBE1	ENSGALG00000053241	SUSD3	HBE	ENSGALG00000014736	EPB42	SLC25A37	ENSGALG0000005493
3	ANK1	ENSGALG00000038671	TRIM27.1	ENSGALG00000047208	ENSGALG00000022875	ENSGALG00000052767	GSTA4	ALDOB
4	TUBB1	GLRX	FBP1	SLC16A10	RFESD	HBGR	TAL1	ENSGALG0000009552
5	CYP3A4	HBZ	ARRDC2	ENSGALG00000044985	ENSGALG00000016651	BG8	CREG1	TMOD4
6	ARID3A	CPN2	ENSGALG00000045684	ENSGALG00000047761	ADRB1	ENSGALG00000017072	ENSGALG00000040101	TSPAN32
7	DPEP2	FAM124B	MFSD2B	DAB2	BAIAP2L1	TRAF3IP3	ENSGALG00000010225	ENSGALG00000051041
8	NT5DC4	GBP	ADA	ENSGALG00000053770	ENSGALG00000051589			

	Term	Ont	N	n	Adj. p-value
GO:0042744	hydrogen peroxide catabolic process	BP	7	6	3.451e-14
GO:0042743	hydrogen peroxide metabolic process	BP	7	6	3.451e-14
GO:0015671	oxygen transport	BP	7	6	3.451e-14
GO:0015669	gas transport	BP	8	6	1.376e-13
GO:0098869	cellular oxidant detoxification	BP	14	6	1.446e-11
GO:1990748	cellular detoxification	BP	16	6	3.832e-11
GO:0097237	cellular response to toxic substance	BP	16	6	3.832e-11
GO:0098754	detoxification	BP	17	6	5.902e-11
GO:0072593	reactive oxygen species metabolic process	BP	18	6	8.824e-11
GO:0009636	response to toxic substance	BP	20	6	1.83e-10

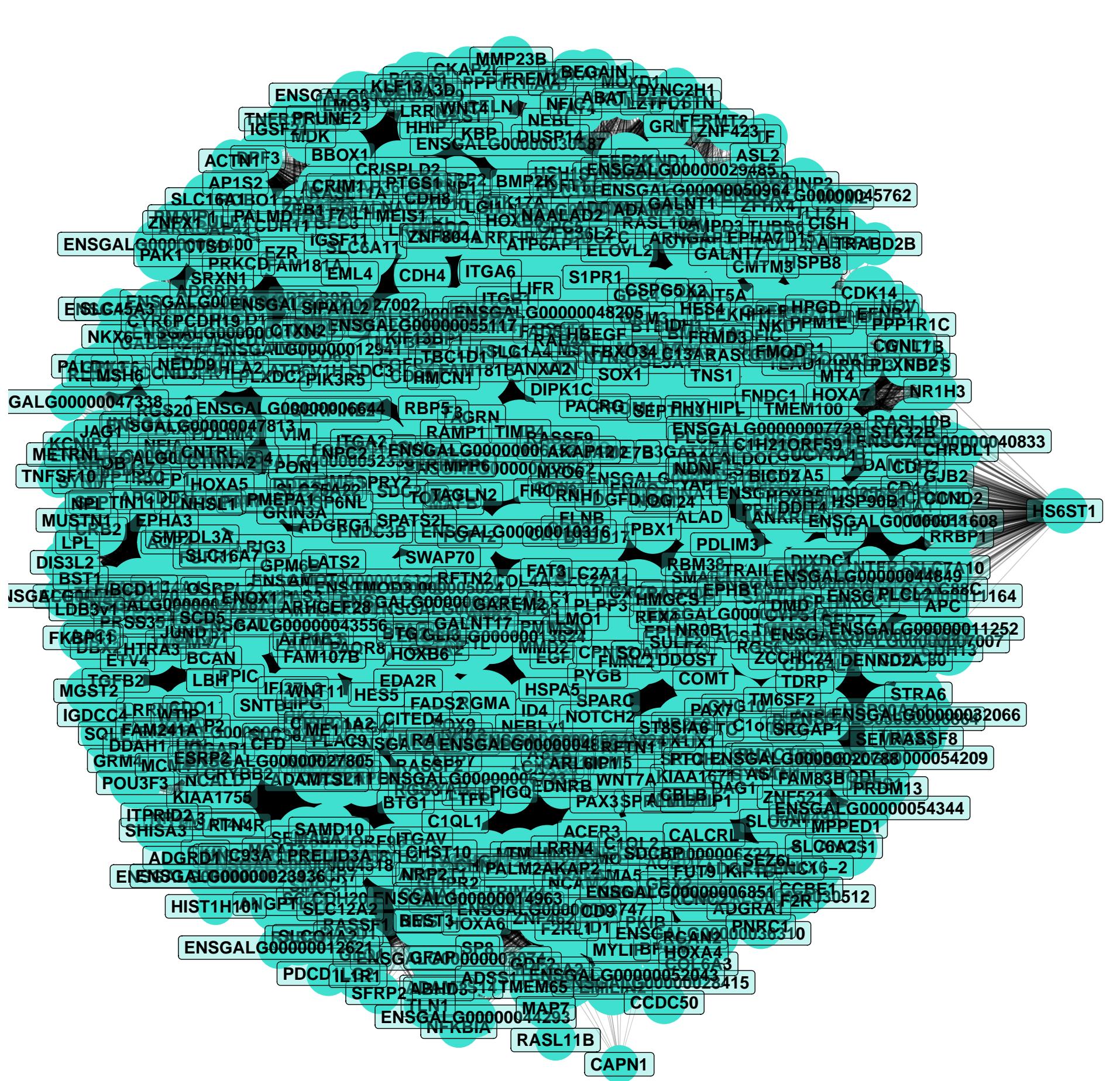
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	47	3	0.001084
<i>path:gga00030</i>	Pentose phosphate pathway	25	2	0.005164
<i>path:gga01200</i>	Carbon metabolism	94	3	0.007765
<i>path:gga00051</i>	Fructose and mannose metabolism	34	2	0.00942
<i>path:gga01232</i>	Nucleotide metabolism	77	2	0.04367
<i>path:gga04540</i>	Gap junction	79	2	0.04574
<i>path:gga00910</i>	Nitrogen metabolism	14	1	0.05887
<i>path:gga00591</i>	Linoleic acid metabolism	16	1	0.06699
<i>path:gga01100</i>	Metabolic pathways	1236	9	0.08174
<i>path:gga00230</i>	Purine metabolism	113	2	0.08569



1	CFAP126	DYDC2	RSPH1	ENSGALG00000013268	CFAP100	ENKUR	RAB36	PPI6
2	CFAP99	FOXJ1	SPEF2	FAM183A	CFAP45	CFAP44	ENSGALG00000043861	ENSGALG00000044478
3	RSPH9	DNAI1	FXYD2	RIBC2	ENSGALG0000003464	ENSGALG00000044224	HYDIN	ARMC4
4	C9orf116	ENSGALG00000015224	ENSGALG00000054317	LRRC6	EFCAB10	ENSGALG00000044151	AK7	ENSGALG00000013281
5	ZMYND10	DNAH10	ENSGALG0000005247	ENSGALG00000019932	ENSGALG0000004495	DAW1	VWA3A	ENSGALG00000028207
6	ENSGALG00000003013	ENSGALG00000008309	KLHDC8B	LRGUK	CCDC170	ENSGALG00000040709	ENSGALG00000023763	ENSGALG00000034761
7	CDKL1	ENSGALG00000011356	ENSGALG00000037997	SPAG17	FAM81A	KIF27	NSUN7	ENSGALG00000036896
8	ENSGALG00000012317	LPAR4	FHL1	NME1	NPR3	C1H11ORF70	ENSGALG00000028830	ANTXR1
9	CFAP57	CAPSL	KIF9	CFAP77	AKAP14	NKX2-8	RASGEF1B	SDR4E2
10	LXN	IQCA1	ARMC3					

	Term	Ont	N	n	Adj. p-value
GO:0044210	'de novo' CTP biosynthetic process	BP	1	0	1
GO:0034627	'de novo' NAD biosynthetic process	BP	1	0	1
GO:0006207	'de novo' pyrimidine nucleobase biosynthetic process	BP	1	0	1
GO:1902635	1-phosphatidyl-1D-myo-inositol 4,5-bisphosphate biosynthetic process	BP	1	0	1
GO:1902633	1-phosphatidyl-1D-myo-inositol 4,5-bisphosphate metabolic process	BP	1	0	1
GO:0061158	3'-UTR-mediated mRNA destabilization	BP	1	0	1
GO:0035998	7,8-dihydronopterin 3'-triphosphate biosynthetic process	BP	1	0	1
GO:0021560	abducens nerve development	BP	1	0	1
GO:0021599	abducens nerve formation	BP	1	0	1
GO:0021598	abducens nerve morphogenesis	BP	1	0	1

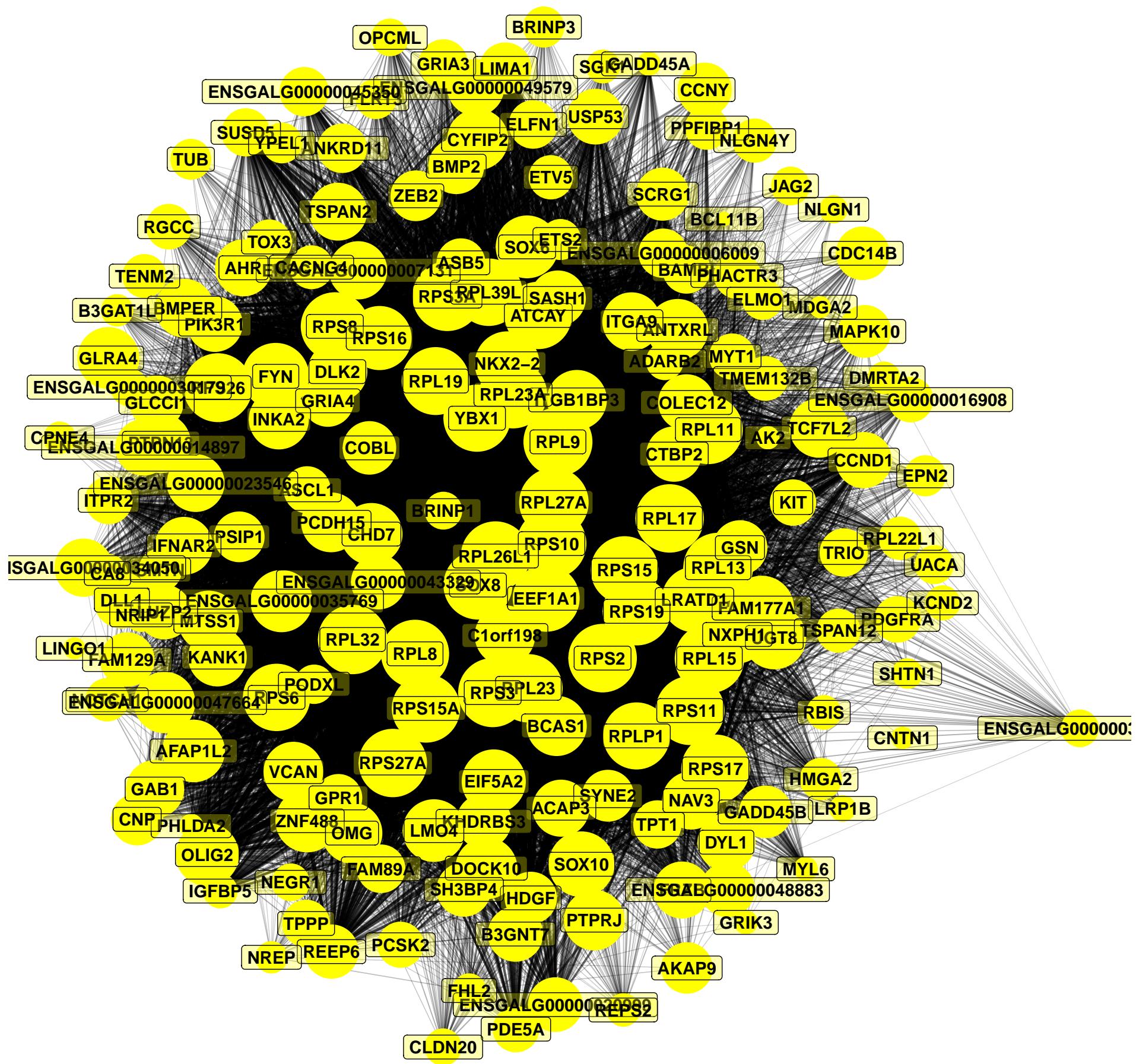
	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga01232</i>	Nucleotide metabolism	77	3	0.007982
<i>path:gga00230</i>	Purine metabolism	113	3	0.02232
<i>path:gga01240</i>	Biosynthesis of cofactors	116	3	0.02389
<i>path:gga00240</i>	Pyrimidine metabolism	55	2	0.03463
<i>path:gga00730</i>	Thiamine metabolism	12	1	0.06209
<i>path:gga00983</i>	Drug metabolism – other enzymes	55	1	0.2549
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.2708
<i>path:gga04621</i>	NOD–like receptor signaling pathway	115	1	0.4603
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	1	0.4803
<i>path:gga04810</i>	Regulation of actin cytoskeleton	182	1	0.6242



27	PACRG	NFIA	FHOD3	DKK3	ENSGALG0000001136	FGFR1	LRIG3	OSBPL2
28	ARHGEF26	WNT7A	PPP1R9B	RAB40C	BACE2	KIAA1755	ENSGALG00000045636	GNG4
29	TMEM100	ENSGALG00000052336	KIAA1671	PAX6	USP6NL	ASPA	RASSF2	SOX21
30	C5H11ORF96	BTBD17	BAG3	ANKRD9	LRRFIP1	MDK	FGF12	HS3ST6
31	CHN1	EPHA4	DIPK1C	NTN3	ATP6V1H	HK1	HMCN1	RARRES2
32	LAMC1	ANGPTL1	GRM3	BBOX1	CAP2	ENSGALG00000048024	TMEM59	RBP5
33	NOG	CALCRL	APCDD1L	FLNB	PRKCD	IGFBP2	NOG2	ITGB1
34	TSPAN6	ALPL	SLC2A1	LYN	HOXB5	GPC4	BMP2K	GPC5
35	MSN	CDH4	FAM3C	EPB41L3	USP12	SPARC	DMD	TRIM24
36	PHYHIPL	CCND3	CYP51A1	SMOX	FAT4	ENSGALG00000007728	CCDC80	MEIS2
37	SPATS2L	KLF15	BOC	EZR	MGAT3	MYLK	SPARCL1	SFRP1
38	FRMD3	SOX2	TBC1D1	FAM46A	GREB1	COL22A1	ENSGALG00000001536	LAMA5
39	ARHGAP5	CHST7	S100A10	CD82	CHST10	PDLM4	MSMO1	MDFIC
40	KIF1B	CPNE2	ENSGALG0000006644	SMPDL3A	WNT5A	C1orf21	TMEM37	CAPN11
41	RBM24	IQGAP2	NKAIN2	CRISPLD2	TSPAN3	CLASP1	PDGFD	ENSGALG00000013624
42	MID1IP1	LRP8	ENSGALG00000017040	GAREM2	CD164L2	RNH1	GBE1	ARHGEF28
43	FZD10	ENSGALG00000030587	SCRN1	GLO1	BPGM	SMPD3	TGFB2	C1QL2
44	PLCD1	HMGCR	MEIS1	ATP1A1	ENSGALG00000003074	FAT3	NEBL	F2RL1
45	ENSGALG00000048205	CDH20	RAB20	HHIP	TMEM47	GLDC	SCG3	GRB10
46	PRELID3A	PXYLP1	PKIB	AP1S2	C2H8ORF22	RALY	INHBB	CNR1
47	GLIPR1L	ZFP36L2	ACAN	TGFB3	SLC38A3	ENSGALG00000012941	CD63	ENSGALG00000036310
48	CRYAB	ZEB1	CDK14	ENSGALG0000006152	ADGRB2	NPC2	CDH2	SLC1A2
49	DDIT4	EEPDP1	MSX1	AEBP1	LATS2	ENSGALG00000048534	KIF13B	TLL2
50	EMILIN2	ENSGALG00000010316	ENSGALG00000047813	NHSL1	ADAMTS7	ABHD3	INSIG1	ENSGALG00000049127
51	ENSGALG00000055117	PHACTR2	DBX2	CDO1	SDCBP	MYLIP	EDA2R	SULF1
52	LGI1	GALNT7	CTNNA2	MGAT4A	ASTN1	TNNC1	SEMA3A	C1QL1
53	HMGCS1	PTCH2	ATP11B	LRP4	PAX3	AS3MT	HSPA5	COL4A1
54	CSRP2	RFTN1	KCNC2	CKB	GRN	NDP	IQGAP1	NCALD
55	GABBR2	KLF6	EEF2K	SLC7A10	CHL1	PDLM3	CDH13	CRB2
56	CTSD	NKX6-2	ADAMTS14	HES1	FDFT1	NFIX	RGS3	ASL2
57	KIRREL3	ADGRD2	CFAP36	AKAP12	CORO2B	RASA3	PAX7	ADCYAP1R1
58	TNFRSF11B	TMEM86A	PLEKHH1	ENO1	CARHSP1	HTRA3	ENSGALG00000028466	SP8
59	SYNDIG1L	WTIP	BRINP2	ROBO1	ARL6IP1	ENSGALG00000043556	ENSGALG00000054209	SLC16A1
60	ENSGALG00000002714	TEAD1	RELN	FAM49A	HSP90B1	LGMN	WNT11	VIT
61	TRAIL-LIKE	SEPTIN11	SVIL	POU3F3	FBXO34	PRDM12	CD44	RASL11A
62	NKX6-1	KCNIP4	SQLE	NRN1L	IRX3	EPHA7	GLIPR2	RBM38
63	ARHGAP42	SCD5	SAMD10	GRM4	PBX1	ENSGALG00000014963	ZNF462	EPHB1
64	KBP	APC	NEDD9	LIPG	WSCD1	ENSGALG00000032066	HOXA6	GAS1
65	THBS2	TLN1	RXFP1	VSTM4	PAK1	ENSGALG0000006723	ENSGALG00000004518	BTG2
66	METRNL	GBX2	ADAMTSL1	NMS	LRRN4	ENSGALG00000027805	ENOX1	HHLA2
67	CRYM	CHODL	NR4A3	BST1	CFD	LRRN3	DPF3	HSP90AA1
68	CCDC88C	MFGE8	GPX3	ENSGALG00000020788	FMOD	PRLH	SCD	ENSGALG00000011164
69	ENSGALG00000009654	NCAN	ME1	HOXA5	IFI27L2	HES4	SEPT7	RLN3
70	SYNM	ENSGALG0000004400	BTG1	ENSGALG00000037869	EDNRB	ADGRA1	RASD1	TM6SF2

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0007275	multicellular organism development	BP	562	94	1.481e-21
GO:0048856	anatomical structure development	BP	608	98	2.988e-21
GO:0032501	multicellular organismal process	BP	692	104	3.506e-20
GO:0032502	developmental process	BP	640	99	3.89e-20
GO:0048731	system development	BP	472	73	5.119e-15
GO:0050789	regulation of biological process	BP	1082	122	1.487e-13
GO:0050794	regulation of cellular process	BP	1032	118	1.522e-13
GO:0065007	biological regulation	BP	1175	128	4.252e-13
GO:0048513	animal organ development	BP	312	53	8.067e-13
GO:0009653	anatomical structure morphogenesis	BP	287	50	1.378e-12

	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga04512</i>	ECM–receptor interaction	67	18	2.56e–08
<i>path:gga04510</i>	Focal adhesion	170	25	1.386e–05
<i>path:gga03320</i>	PPAR signaling pathway	57	12	7.805e–05
<i>path:gga00100</i>	Steroid biosynthesis	15	6	0.0001141
<i>path:gga04810</i>	Regulation of actin cytoskeleton	182	23	0.0003154
<i>path:gga04330</i>	Notch signaling pathway	52	10	0.0006573
<i>path:gga04310</i>	Wnt signaling pathway	134	17	0.001757
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	7	0.001935
<i>path:gga04350</i>	TGF–beta signaling pathway	84	12	0.003007
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	146	17	0.004355



1	UGT8	RPL13	SOX8	OLIG2	RPS3A	RPS10	RPL27A	RPL15
2	RPS26	RPL32	RPL17	SOX10	RPL11	RPS3	RPL26L1	RPL9
3	NKX2-2	RPS2	RPS11	RPS6	RPL23	RPS15A	RPS19	RPS17
4	RPS27A	RPL19	RPL8	RPL39L	RPS8	RPS15	RPL23A	LRATD1
5	BCAS1	RPLP1	YBX1	FAM177A1	RPS16	ATCAY	EEF1A1	TSPAN2
6	ZNF488	AFAP1L2	FYN	DLL1	ENSGALG00000035769	NXPH1	ENSGALG00000047664	OMG
7	COLEC12	ITGB1BP3	ANTXRL	SOX6	GLRA4	EIF5A2	ACAP3	PCDH15
8	TCF7L2	LMO4	PDGFRA	B3GNT7	C1orf198	CHD7	ENSGALG00000043329	PTPRJ
9	ENSGALG00000007131	CTBP2	DOCK10	VCAN	KHDRBS3	MTSS1	BMPER	INKA2
10	TPT1	MYT1	COBL	NAV3	CNP	CYFIP2	ENSGALG00000014897	DLK2
11	KANK1	ITGA9	GSN	PIK3R1	PTPN13	IFNAR2	ENSGALG00000023546	BAMBI
12	SYNE2	GRIA4	GLCCI1	CCND1	GAB1	SUSD5	REEP6	ENSGALG0000006009
13	SH3BP4	ASCL1	SASH1	ENSGALG00000049579	LUZP2	DYL1	PSIP1	ENSGALG00000034050
14	FAM89A	ANKRD11	ASB5	GPR1	ZEB2	HDGF	ENSGALG00000020999	ITPR2
15	USP53	LIMA1	AHR	CCNY	FRZB	ETS2	BMP2	ELFN1
16	MAPK10	FAM129A	RGCC	TRIO	TPPP	SMTN	ETV5	RPL22L1
17	IGFBP5	NOTCH1	CACNG4	ENSGALG00000048883	PHACTR3	GRIA3	EPN2	PCSK2
18	KIT	SCRG1	TSPAN12	TOX3	GADD45B	ENSGALG00000045350	PODXL	SGK1
19	ENSGALG00000030179	CDC14B	PDE5A	REPS2	TUB	BRINP1	ELMO1	ENSGALG00000016908
20	PHLDA2	TMEM132B	AKAP9	ADARB2	BRINP3	HMGAA2	ENSGALG00000031427	CA8
21	FLRT3	PPFIBP1	KCND2	NEGR1	NLGN4Y	JAG2	YPEL1	MYL6
22	TENM2	GRIK3	FHL2	OPCML	CPNE4	NREP	BCL11B	CLDN20
23	UACA	MDGA2	NRIP1	RBIS	NLGN1	DMRTA2	GADD45A	LRP1B
24	AK2	B3GAT1L	SHTN1	LINGO1	CNTN1			

	<b>Term</b>	<b>Ont</b>	<b>N</b>	<b>n</b>	<b>Adj. p-value</b>
GO:0006412	translation	BP	87	12	3.295e-09
GO:0043043	peptide biosynthetic process	BP	88	12	3.768e-09
GO:0043604	amide biosynthetic process	BP	100	12	1.662e-08
GO:0006518	peptide metabolic process	BP	107	12	3.598e-08
GO:0043603	cellular amide metabolic process	BP	124	12	1.875e-07
GO:0048856	anatomical structure development	BP	608	24	5.36e-06
GO:0032502	developmental process	BP	640	24	1.268e-05
GO:0044271	cellular nitrogen compound biosynthetic process	BP	517	21	1.419e-05
GO:0007275	multicellular organism development	BP	562	22	1.555e-05
GO:0034645	cellular macromolecule biosynthetic process	BP	534	21	2.299e-05

	<b>Pathway</b>	<b>N</b>	<b>DE</b>	<b>P.DE</b>
<i>path:gga03010</i>	Ribosome	116	29	1.727e-28
<i>path:gga04514</i>	Cell adhesion molecules	95	8	6.023e-05
<i>path:gga04068</i>	FoxO signaling pathway	107	6	0.00418
<i>path:gga04210</i>	Apoptosis	115	6	0.005931
<i>path:gga04330</i>	Notch signaling pathway	52	4	0.006266
<i>path:gga04310</i>	Wnt signaling pathway	134	6	0.01215
<i>path:gga05132</i>	Salmonella infection	221	8	0.01366
<i>path:gga04510</i>	Focal adhesion	170	6	0.03438
<i>path:gga04218</i>	Cellular senescence	133	5	0.0411
<i>path:gga04810</i>	Regulation of actin cytoskeleton	182	6	0.04543