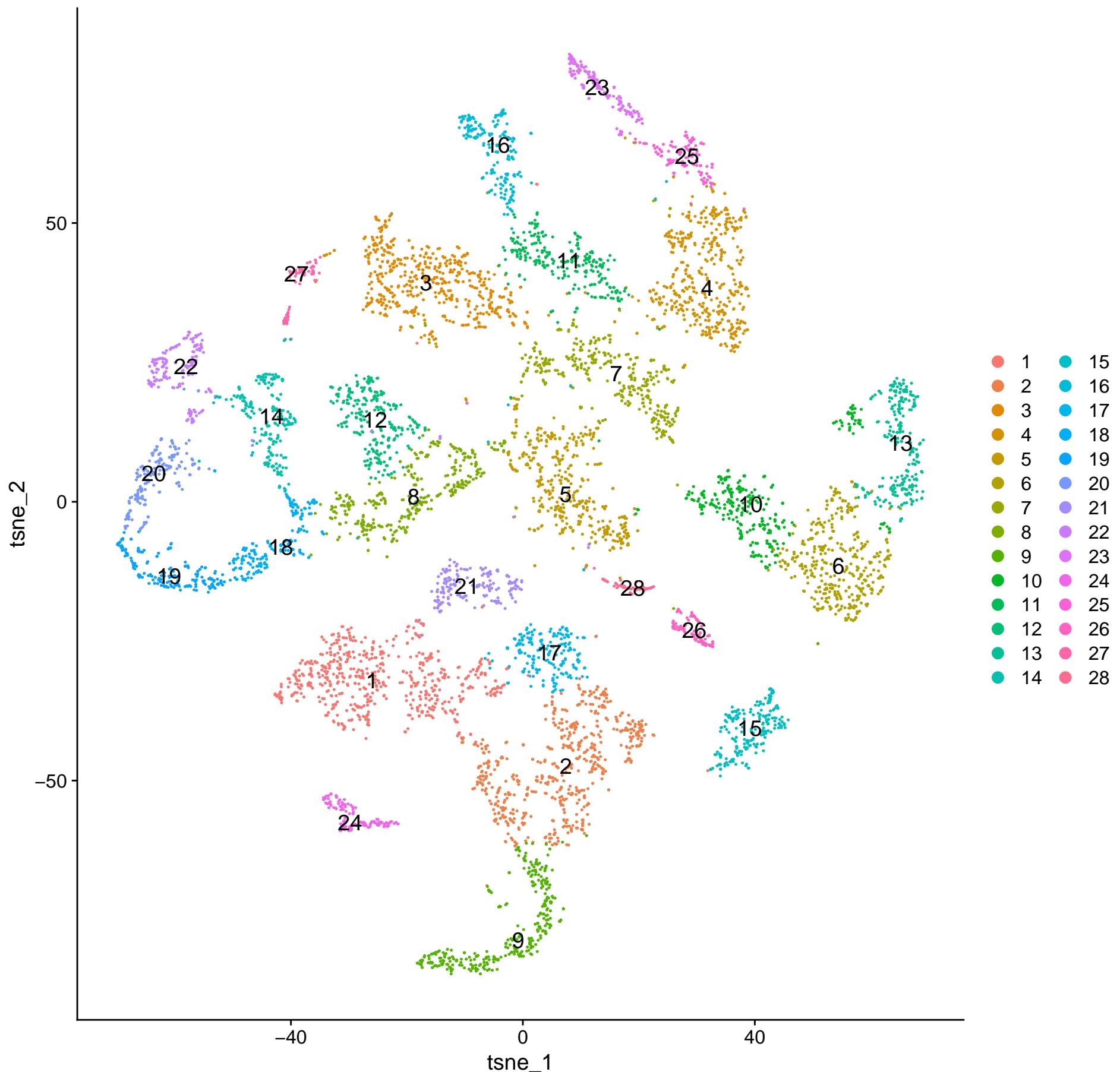
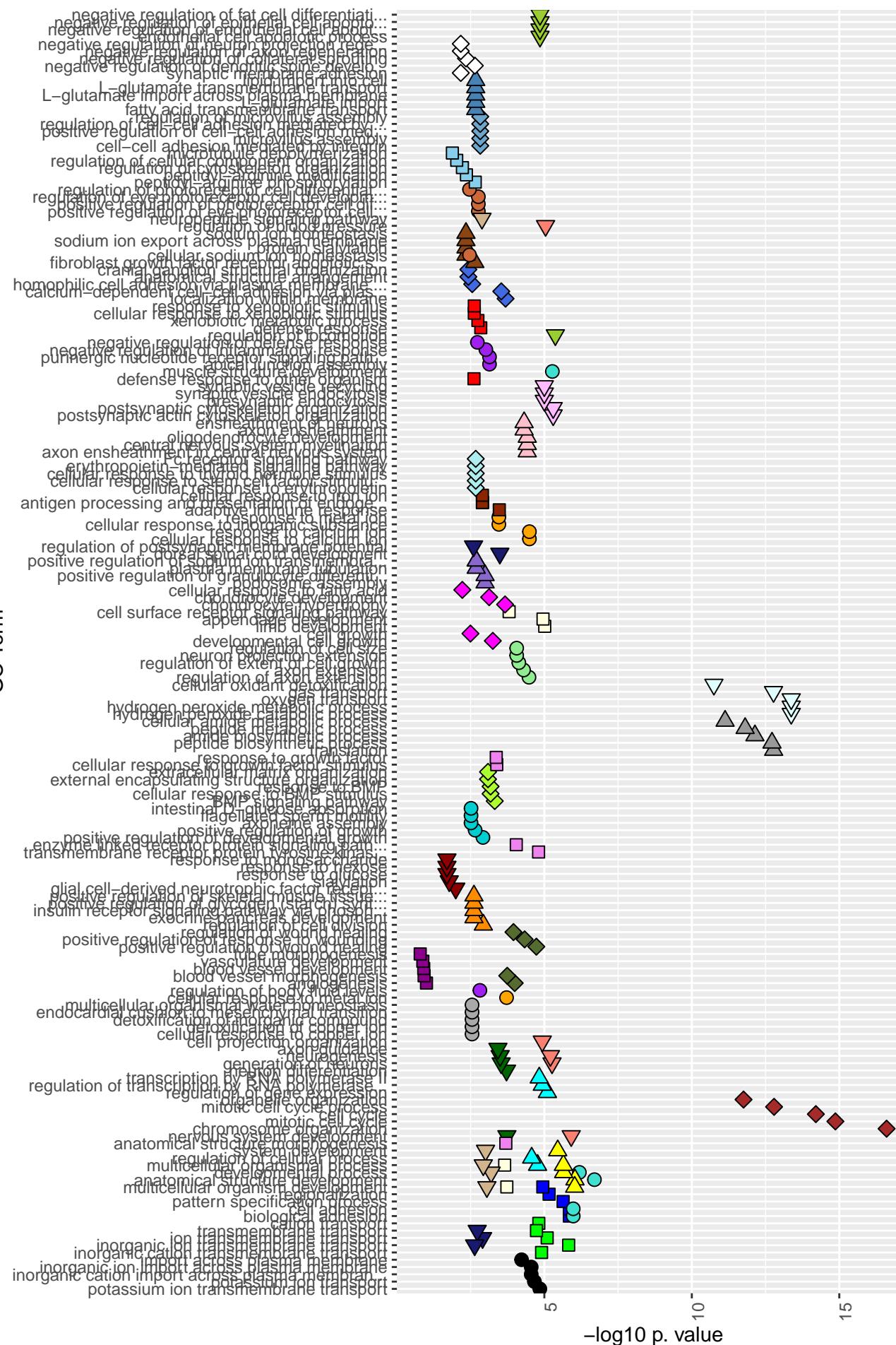
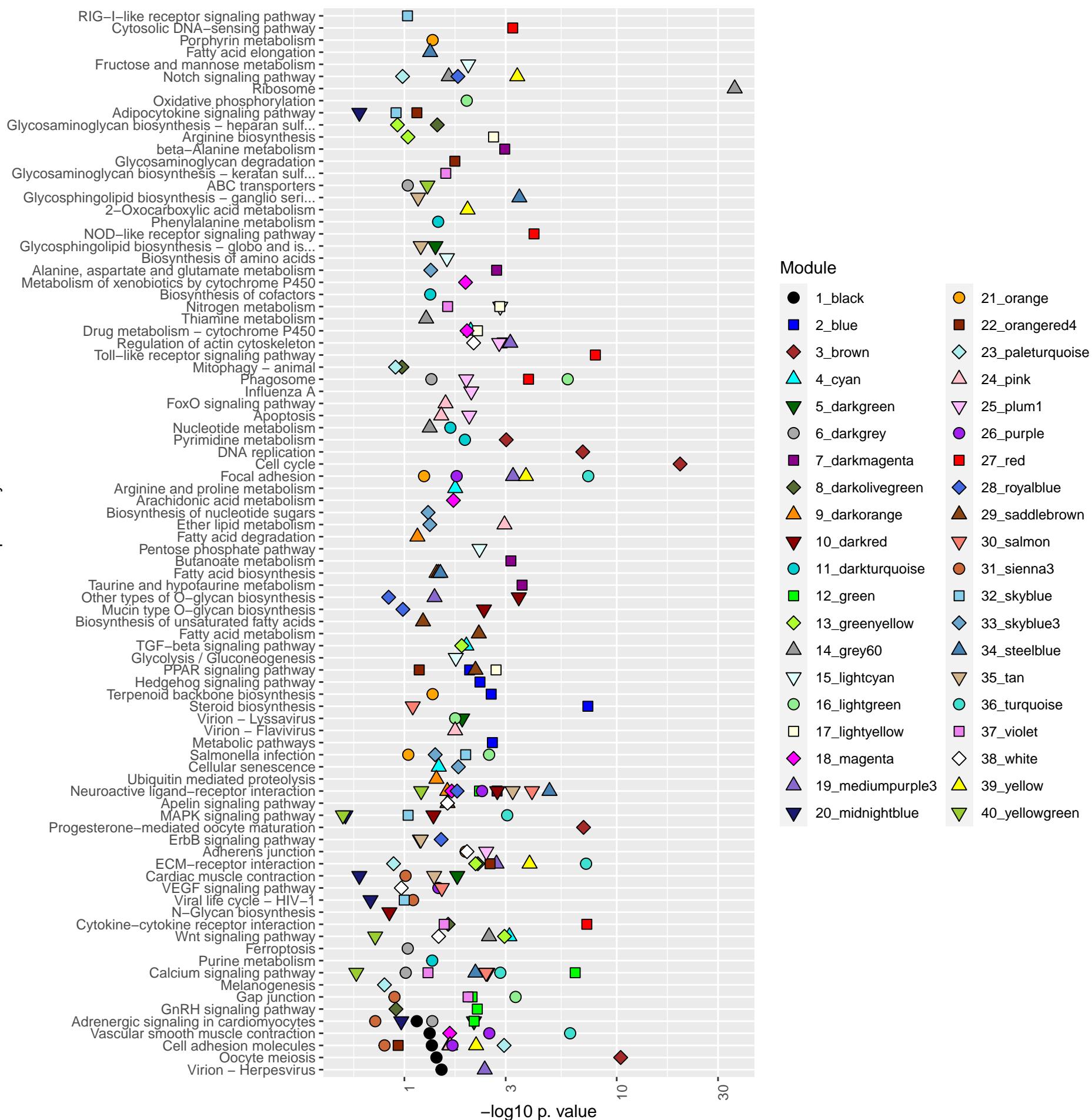


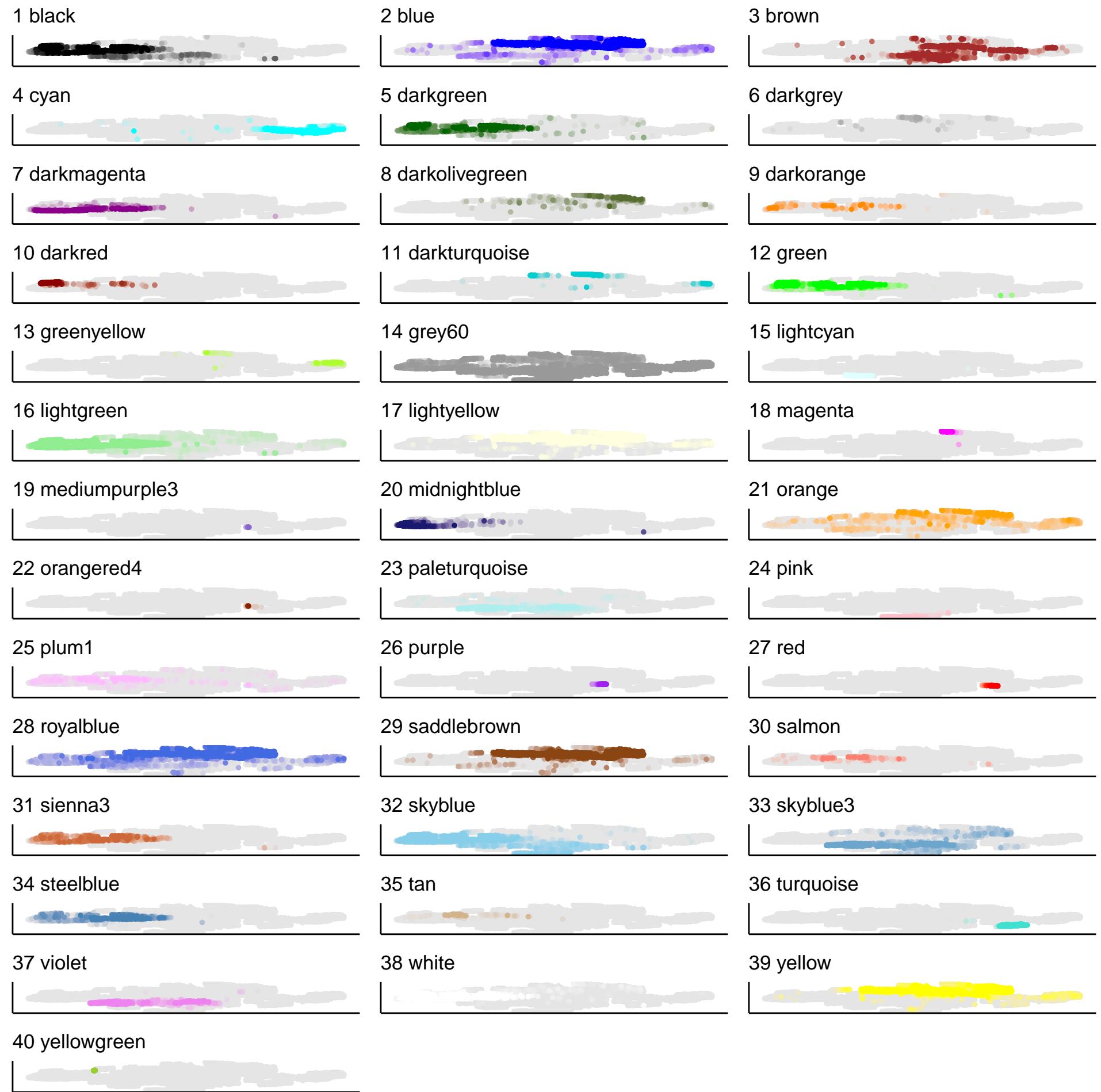
Gg_lumb_int scWGCNA modules

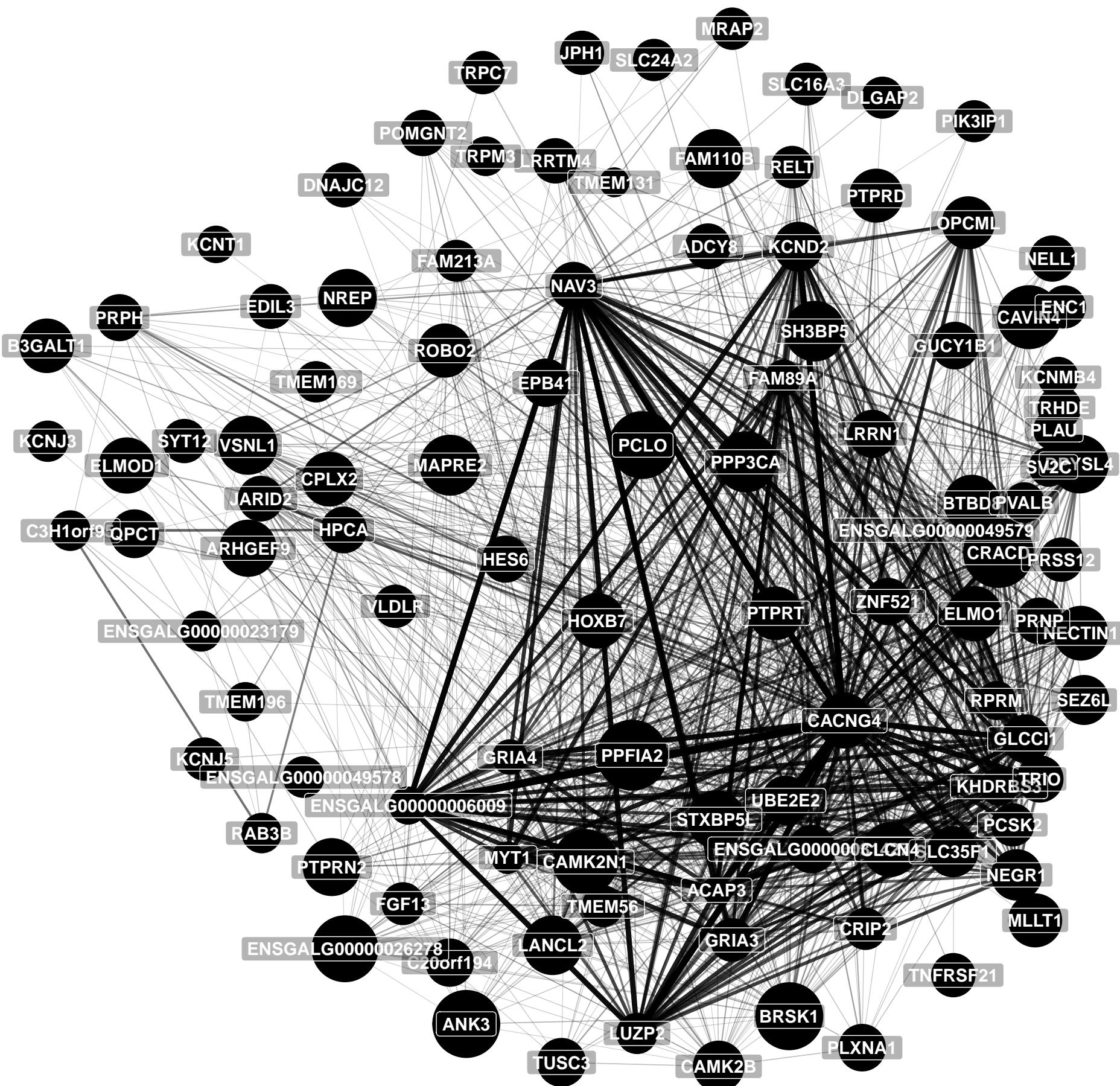




KEGG pathway



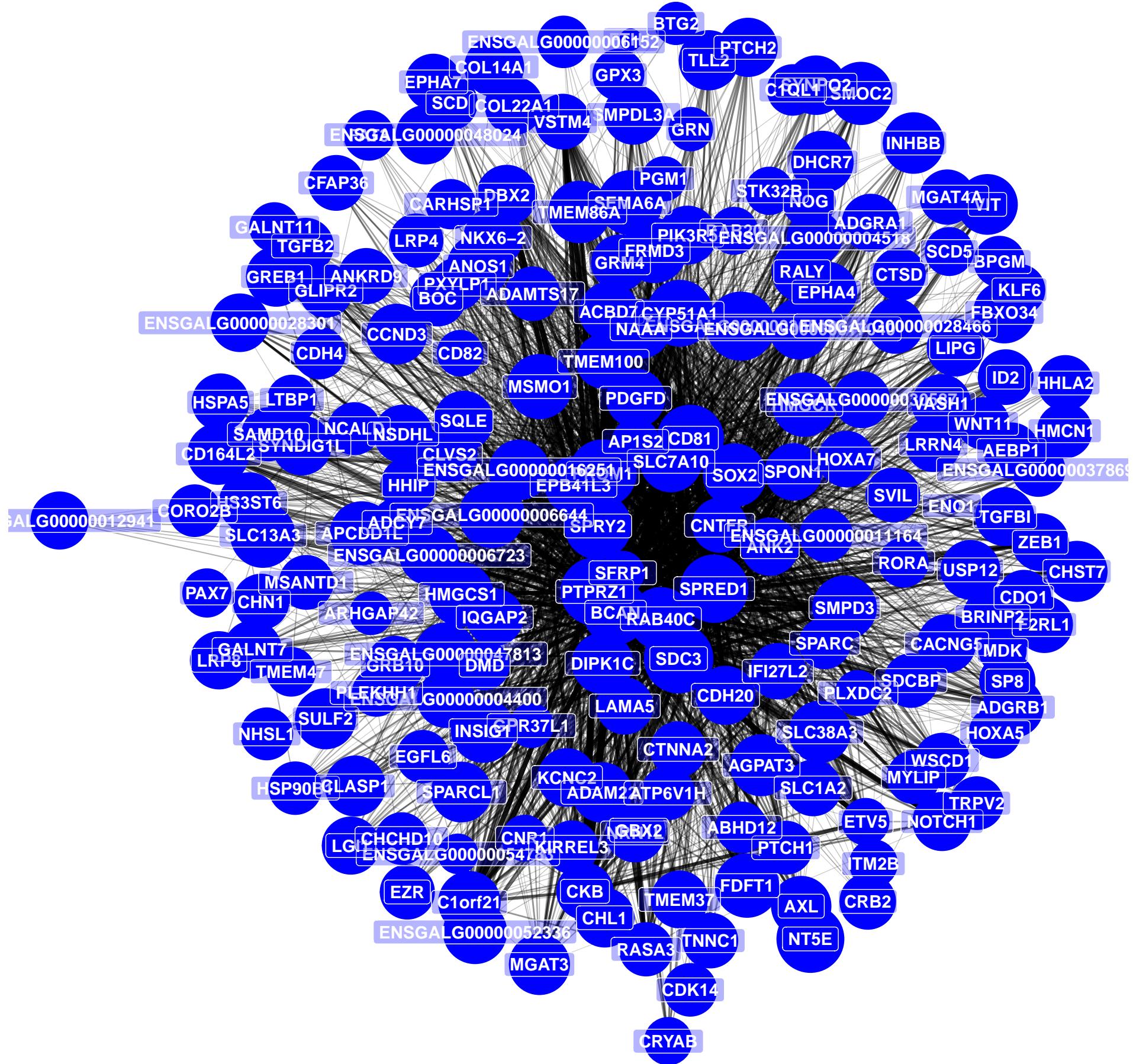




1	CRACD	BRSK1	PPFIA2	CAVIN4	CAMK2N1	ANK3	PCLO	ENSGALG00000026278
2	DPYSL4	CACNG4	SH3BP5	MAPRE2	PTPRD	PPP3CA	BTBD8	ELMO1
3	FAM110B	CPLX2	LANCL2	ELMOD1	VSNL1	NAV3	ARHGEF9	MYT1
4	CLCN4	TRIO	STXBP5L	PTPRN2	KCND2	OPCML	PTPRT	GLCCI1
5	HOXB7	HES6	NREP	LRRN1	FAM89A	ENSGALG00000031427	SLC35F1	MLLT1
6	NECTIN1	C20orf194	ACAP3	EPB41	KHDRBS3	ROBO2	NEGR1	ENSGALG0000006009
7	LUZP2	PCSK2	PRNP	GRIA3	GRIA4	CRIP2	B3GALT1	GUCY1B1
8	FGF13	QPCT	UBE2E2	SEZ6L	PRPH	CAMK2B	HPCA	TUSC3
9	RELT	ZNF521	JARID2	TMEM169	POMGNT2	NELL1	ENC1	LRRTM4
10	EDIL3	DNAJC12	PLXNA1	KCNJ5	SYT12	TNFRSF21	KCNJ3	FAM213A
11	RAB3B	ADCY8	TRHDE	PVALB	SLC16A3	PRSS12	TMEM56	VLDLR
12	KCNMB4	SLC24A2	RPRM	PLAU	ENSGALG00000023179	TRPC7	TMEM196	ENSGALG00000049578
13	DLGAP2	SV2C	C3H1orf95	PIK3IP1	JPH1	MRAP2	ENSGALG00000049579	TRPM3
14	KCNT1	TMEM131						

	Term	Ont	N	n	Adj. p-value
GO:0071805	potassium ion transmembrane transport	BP	19	4	1.422e-05
GO:0006813	potassium ion transport	BP	21	4	2.168e-05
GO:0098659	inorganic cation import across plasma membrane	BP	8	3	2.789e-05
GO:0099587	inorganic ion import across plasma membrane	BP	8	3	2.789e-05
GO:0098739	import across plasma membrane	BP	10	3	5.907e-05
GO:0098657	import into cell	BP	13	3	0.0001383
GO:0098703	calcium ion import across plasma membrane	BP	3	2	0.0001931
GO:1902656	calcium ion import into cytosol	BP	3	2	0.0001931
GO:0043954	cellular component maintenance	BP	3	2	0.0001931
GO:0098662	inorganic cation transmembrane transport	BP	51	4	0.0007517

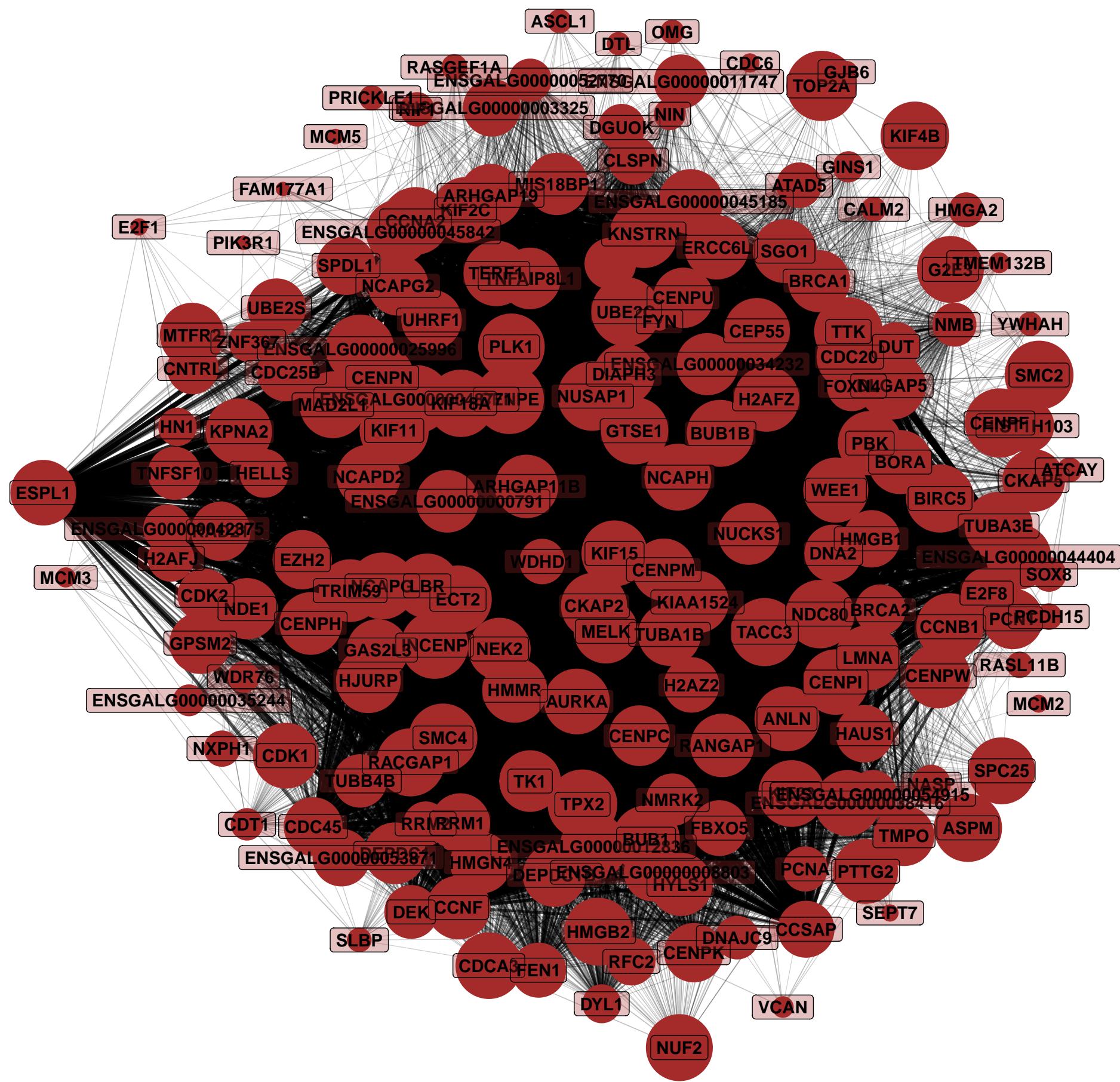
	Pathway	N	DE	P.DE
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.03195
<i>path:gga04114</i>	Oocyte meiosis	92	3	0.0384
<i>path:gga04514</i>	Cell adhesion molecules	98	3	0.04495
<i>path:gga04270</i>	Vascular smooth muscle contraction	101	3	0.04841
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	3	0.07182
<i>path:gga04912</i>	GnRH signaling pathway	72	2	0.1151
<i>path:gga04540</i>	Gap junction	78	2	0.1311
<i>path:gga04916</i>	Melanogenesis	80	2	0.1366
<i>path:gga00601</i>	Glycosphingolipid biosynthesis – lacto and neolacto series	21	1	0.1568
<i>path:gga00515</i>	Mannose type O–glycan biosynthesis	22	1	0.1636



1	ENSGALG00000030512	PTPRZ1	NT5E	BCAN	SDC3	SPRY2	SLC13A3	PROM1
2	SMOC2	APCDD1L	SPRED1	SPON1	ACBD7	CD81	SULF2	SOX2
3	CKB	CYP51A1	SPARC	COL14A1	SEMA6A	DBX2	ENSGALG0000006644	MSMO1
4	SPARCL1	ENSGALG00000052336	SLC7A10	SMPD3	SYNPO2	ANOS1	DIPK1C	HMGCR
5	FRMD3	NOTCH1	ANK2	INSIG1	CDH20	HMGCS1	ENSGALG00000016251	TGFB1
6	RAB40C	SLC38A3	C1orf21	VIT	CHST7	NKX6-2	CNTFR	CHL1
7	ENSGALG00000048024	ENSGALG00000047813	FDFT1	TLL2	EPB41L3	INHBB	ADGRB1	HS3ST6
8	ENSGALG00000017040	EPHA4	CD164L2	AGPAT3	PDGFD	FBXO34	BRINP2	TMEM86A
9	SYNDIG1L	ENSGALG00000012941	NRN1L	KCNC2	DHCR7	MGAT3	ADAM22	USP12
10	CHN1	CCND3	GALNT7	GRM4	CLASP1	PIK3R5	TGFB2	VSTM4
11	SMPDL3A	AXL	RALY	GREB1	ZEB1	F2RL1	PXYLP1	CACNG5
12	LGI1	ID2	COL22A1	IFI27L2	EZR	LRP8	PTCH2	ANKRD9
13	SQLE	ENSGALG00000004400	VASH1	ADGRA1	HSPA5	RASA3	NAAA	HOXA7
14	GRB10	CRYAB	NCALD	WSCD1	ENSGALG00000006723	CRB2	CTNNA2	TMEM37
15	TNNC1	EPHA7	AEBP1	BOC	SVIL	IQGAP2	CDO1	CFAP36
16	ENSGALG00000028301	CLVS2	NSDHL	KLF6	CDH4	CDK14	HHIP	ENSGALG00000004518
17	KIRREL3	LAMA5	ENSGALG00000011164	HSP90B1	HMCN1	LIPG	CTSD	SCD
18	SDCBP	ENSGALG00000030587	MGAT4A	SLC1A2	NOG	SP8	CNR1	LRP4
19	GBX2	MSANTD1	PTCH1	GPX3	ENSGALG00000037869	TMEM100	ATP6V1H	EGFL6
20	LRRN4	ITM2B	SAMD10	HOXA5	CORO2B	ADAMTS17	WNT11	ETV5
21	ENSGALG00000028466	RORA	BPGM	SCD5	LTBP1	ABHD12	MYLIP	TRPV2
22	HHLA2	NHSL1	GLIPR2	GPR37L1	TMEM47	DMD	AP1S2	ENSGALG0000006152
23	STK32B	CD82	C1QL1	MDK	GRN	ENSGALG00000054783	FAT3	CHCHD10
24	PLEKHH1	GALNT11	RAB20	ADCY7	PGM1	CARHSP1	PLXDC2	PAX7
25	ARHGAP42	BTG2	SFRP1	FTH1	ENO1			

	Term	Ont	N	n	Adj. p-value
GO:0022610	biological adhesion	BP	141	12	1.421e-06
GO:0007155	cell adhesion	BP	141	12	1.421e-06
GO:0007389	pattern specification process	BP	58	8	2.311e-06
GO:0003002	regionalization	BP	48	7	6.903e-06
GO:0007275	multicellular organism development	BP	558	23	1.128e-05
GO:0048856	anatomical structure development	BP	603	24	1.285e-05
GO:0032502	developmental process	BP	635	24	2.99e-05
GO:0032501	multicellular organismal process	BP	684	25	3.514e-05
GO:0072176	nephric duct development	BP	6	3	6.515e-05
GO:0045216	cell–cell junction organization	BP	17	4	0.000102

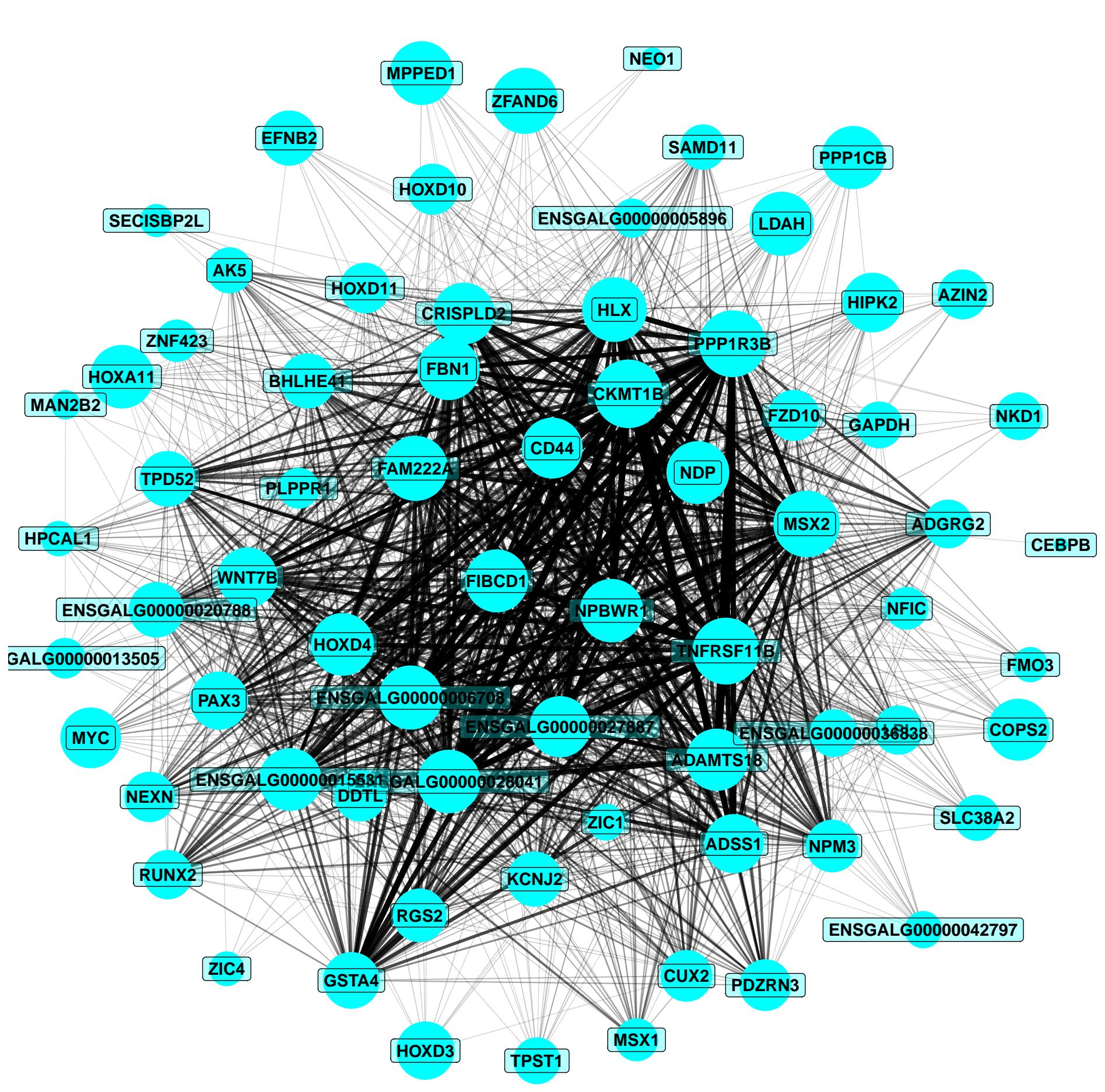
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<i>path:gga00100</i>	Steroid biosynthesis	15	6	4.84e-08
<i>path:gga01100</i>	Metabolic pathways	1218	31	0.002531
<i>path:gga00900</i>	Terpenoid backbone biosynthesis	19	3	0.002732
<i>path:gga04340</i>	Hedgehog signaling pathway	47	4	0.005376
<i>path:gga03320</i>	PPAR signaling pathway	55	4	0.009366
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	46	3	0.03184
<i>path:gga04350</i>	TGF-beta signaling pathway	84	4	0.03796
<i>path:gga01212</i>	Fatty acid metabolism	50	3	0.03937
<i>path:gga03264</i>	Virion – Flavivirus	3	1	0.04453
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	27	2	0.06199



1	CENPF	CENPE	NUSAP1	TOP2A	TPX2	ENSGALG0000025996	UBE2C	KIF11
2	SMC2	KIF4B	ASPM	SMC4	INCENP	ENSGALG0000048771	KPNA2	NDC80
3	TTK	KNSTRN	RACGAP1	BIRC5	BUB1	AURKA	DLGAP5	ENSGALG0000012836
4	SPC25	TACC3	TUBA3E	GTSE1	KIF23	KIF15	ECT2	BUB1B
5	NUF2	CCNB1	KIF18A	PLK1	ANLN	HMGB2	CCNA2	NCAPH
6	NCAPG	CDC20	CDCA3	CKAP2	ENSGALG0000038416	MAD2L1	CENPI	CDK1
7	ENSGALG0000044404	ENSGALG0000045185	TK1	CEP55	KIF2C	TERF1	CENPW	BRCA1
8	G2E3	SGO1	ESPL1	HMMR	PTTG2	PBK	UHRF1	HJURP
9	ENSGALG0000045842	BORA	H2AFZ	MELK	NCAPD2	ARHGAP11B	NEK2	WEE1
10	ERCC6L	CENPN	DEPDC1B	LMNA	TUBA1B	CCNF	ENSGALG0000000791	ARHGAP19
11	HMGN4	LBR	MIS18BP1	KIAA1524	HYLS1	CENPH	MTFR2	CENPM
12	CENPK	RRM1	NCAPG2	DEPDC1	ENSGALG0000011747	GAS2L3	TRIM59	CENPC
13	ENSGALG0000034232	DIAPH3	TNFAIP8L1	RANGAP1	HAUS1	CENPU	DNA2	CDC45
14	NUCKS1	TMPO	HIST1H103	ENSGALG0000053871	NDE1	HMGB1	GPSM2	FEN1
15	CDK2	RAD21	H2AZ2	ENSGALG0000008803	NMRK2	DGUOK	RRM2	SPDL1
16	UBE2S	CKAP5	PCNT	EZH2	NA	FBXO5	DEK	PCNA
17	HELLS	E2F8	DUT	BRCA2	RFC2	CCSAP	CDC25B	TUBB4B
18	ATAD5	ENSGALG0000003325	CLSPN	WDHD1	TNFSF10	ENSGALG0000042375	DNAJC9	ENSGALG0000054915
19	H2AFJ	DYL1	NASP	FOXN4	ENSGALG0000052770	NMB	CNTRL	ZNF367
20	NXPH1	GINS1	SOX8	RIF1	WDR76	CDT1	CALM2	HN1
21	SLBP	HMGAA2	DTL	NIN	MCM2	MCM3	MCM5	SEPT7
22	CDC6	ASCL1	PCDH15	YWHAH	OMG	FAM177A1	VCAN	E2F1
23	ATCAY	ENSGALG0000035244	PRICKLE1	RASGEF1A	RASL11B	FYN	TMEM132B	PIK3R1
24	GJB6							

	Term	Ont	N	n	Adj. p-value
GO:0051276	chromosome organization	BP	174	24	2.493e-17
GO:0000278	mitotic cell cycle	BP	97	18	1.356e-15
GO:0007049	cell cycle	BP	199	23	6.236e-15
GO:1903047	mitotic cell cycle process	BP	77	15	1.628e-13
GO:0006996	organelle organization	BP	428	29	1.765e-12
GO:0022402	cell cycle process	BP	126	17	2.013e-12
GO:0007059	chromosome segregation	BP	43	11	1.278e-11
GO:0051383	kinetochore organization	BP	10	6	1.465e-09
GO:0071103	DNA conformation change	BP	56	10	5.001e-09
GO:0006259	DNA metabolic process	BP	125	13	2.234e-08

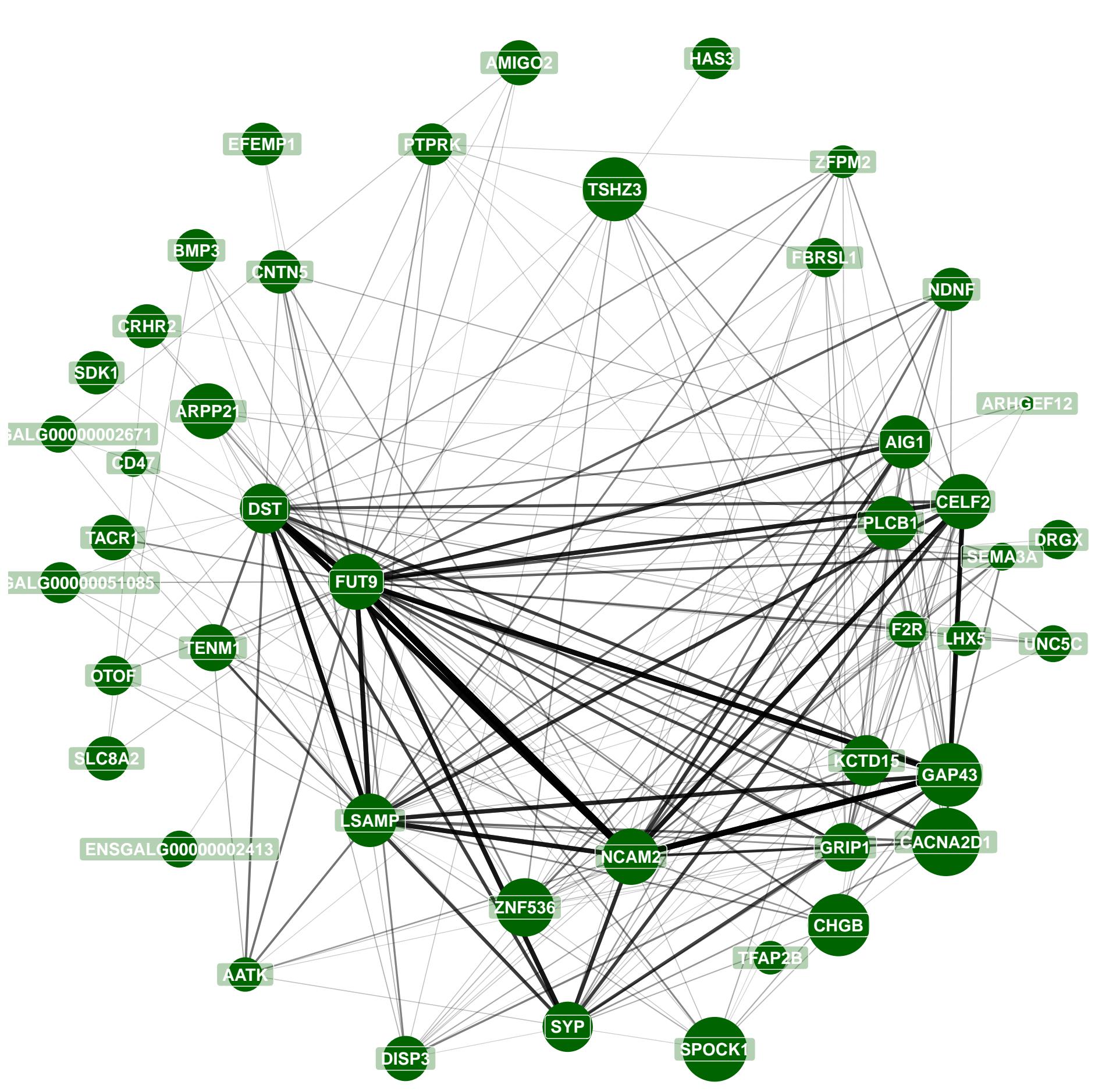
	Pathway	N	DE	P.DE
<i>path:gga04110</i>	Cell cycle	113	23	1.317e–20
<i>path:gga04114</i>	Oocyte meiosis	92	14	3.66e–11
<i>path:gga04914</i>	Progesterone–mediated oocyte maturation	76	10	1.051e–07
<i>path:gga03030</i>	DNA replication	29	7	1.199e–07
<i>path:gga00240</i>	Pyrimidine metabolism	54	5	0.0009612
<i>path:gga04115</i>	p53 signaling pathway	62	5	0.001796
<i>path:gga04218</i>	Cellular senescence	131	7	0.002565
<i>path:gga01232</i>	Nucleotide metabolism	76	5	0.004378
<i>path:gga03410</i>	Base excision repair	25	3	0.005073
<i>path:gga04210</i>	Apoptosis	112	6	0.005087



1	MSX2	PPP1R3B	TNFRSF11B	CKMT1B	ENSGALG00000028041	HLX	FAM22A	NPBWR1
2	NDP	FIBCD1	ENSGALG00000027887	ENSGALG0000006708	ENSGALG00000015531	MPPED1	ADAMTS18	ZFAND6
3	GSTA4	HOXD4	CRISPLD2	FBN1	CD44	HOXA11	LDAH	PAX3
4	EFNB2	WNT7B	ADSS1	RGS2	FZD10	KCNJ2	HOXD3	MYC
5	PPP1CB	BHLHE41	COPS2	TPD52	ENSGALG00000020788	HIPK2	ZIC1	DDTL
6	HOXD10	NPM3	NKD1	AZIN2	NEXN	PDZRN3	CUX2	MSX1
7	SLC38A2	RUNX2	LPL	ADGRG2	GAPDH	PLPPR1	HOXD11	ZNF423
8	SAMD11	AK5	TPST1	NFIC	HPCAL1	ENSGALG00000036838	ENSGALG00000013505	ENSGALG00000042797
9	ZIC4	ENSGALG0000005896	MAN2B2	SECISBP2L	NEO1	FMO3	CEPB	

	Term	Ont	N	n	Adj. p-value
GO:0010468	regulation of gene expression	BP	467	12	7.848e-06
GO:0006357	regulation of transcription by RNA polymerase II	BP	260	9	1.171e-05
GO:0006366	transcription by RNA polymerase II	BP	268	9	1.492e-05
GO:0032501	multicellular organismal process	BP	684	14	1.697e-05
GO:0050794	regulation of cellular process	BP	1020	17	2.689e-05
GO:0045600	positive regulation of fat cell differentiation	BP	2	2	2.975e-05
GO:0032502	developmental process	BP	635	13	3.551e-05
GO:0065007	biological regulation	BP	1156	18	3.668e-05
GO:1901576	organic substance biosynthetic process	BP	650	13	4.523e-05
GO:0050789	regulation of biological process	BP	1069	17	4.893e-05

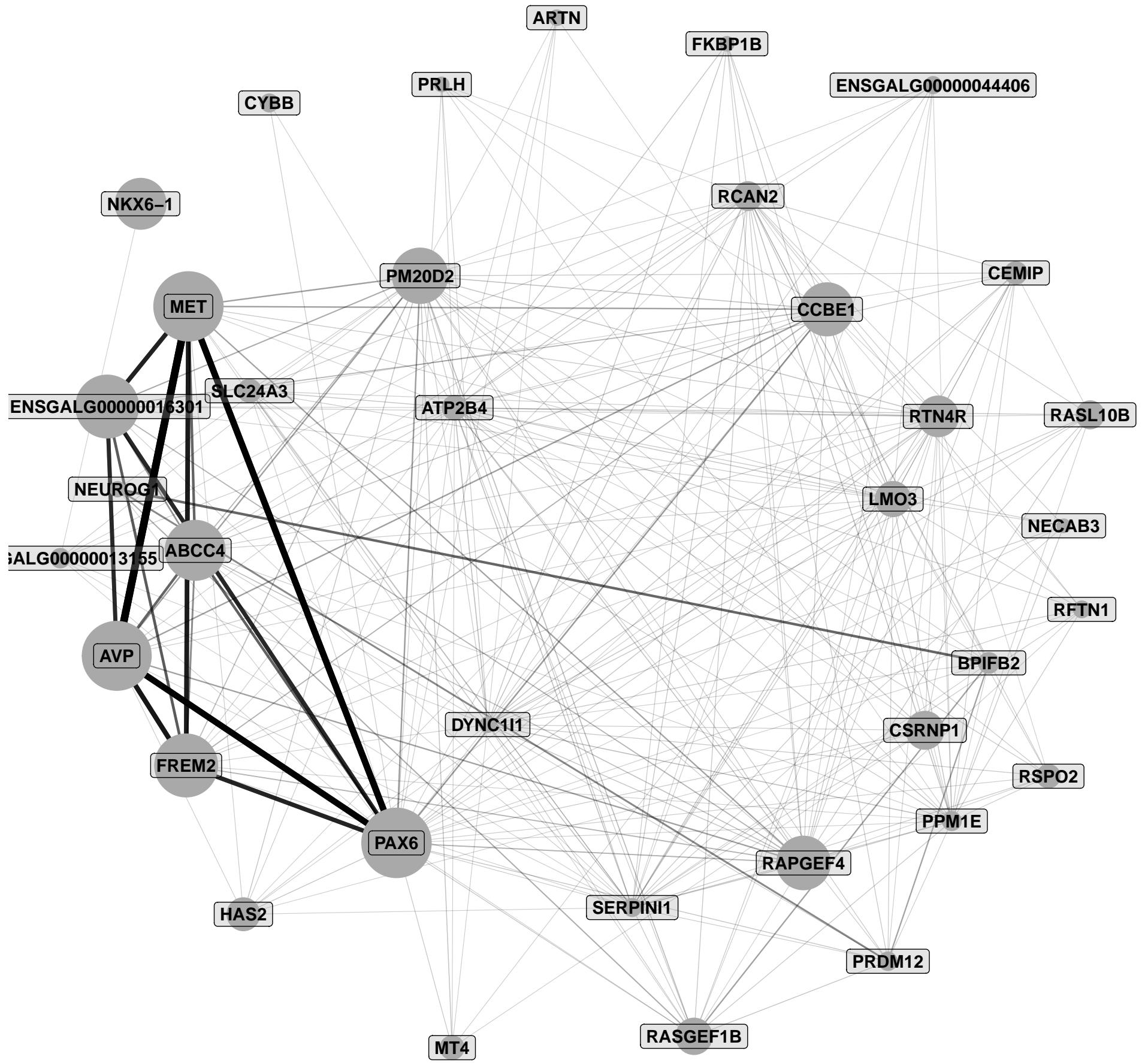
	Pathway	N	DE	P.DE
<i>path:gga04310</i>	Wnt signaling pathway	131	5	0.0007543
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	26	2	0.00888
<i>path:gga04350</i>	TGF–beta signaling pathway	84	3	0.01102
<i>path:gga00330</i>	Arginine and proline metabolism	38	2	0.01841
<i>path:gga04218</i>	Cellular senescence	131	3	0.0353
<i>path:gga03015</i>	mRNA surveillance pathway	72	2	0.05945
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	1	0.06399
<i>path:gga00730</i>	Thiamine metabolism	12	1	0.06399
<i>path:gga01232</i>	Nucleotide metabolism	76	2	0.06538
<i>path:gga00910</i>	Nitrogen metabolism	13	1	0.06914



1	CHGB	SPOCK1	GAP43	CACNA2D1	ZNF536	TSHZ3	ARPP21	PLCB1
2	FUT9	SYP	NCAM2	LSAMP	CELF2	DST	AIG1	GRIP1
3	KCTD15	CNTN5	SEMA3A	TENM1	DISP3	BMP3	AMIGO2	NDNF
4	TACR1	PTPRK	SDK1	F2R	FBRSL1	ENSGALG0000002671	ZFPM2	SLC8A2
5	EFEMP1	ENSGALG00000051085	CD47	AATK	CRHR2	OTOF	TFAP2B	ENSGALG0000002413
6	DRGX	ARHGEF12	HAS3	LHX5	UNC5C			

	Term	Ont	N	n	Adj. p-value
GO:0007399	nervous system development	BP	252	6	0.0001861
GO:0030182	neuron differentiation	BP	160	5	0.000192
GO:0048699	generation of neurons	BP	175	5	0.0002911
GO:0022008	neurogenesis	BP	178	5	0.0003149
GO:0007411	axon guidance	BP	42	3	0.0003749
GO:0097485	neuron projection guidance	BP	42	3	0.0003749
GO:0008038	neuron recognition	BP	10	2	0.0004921
GO:0008037	cell recognition	BP	12	2	0.0007186
GO:0048666	neuron development	BP	122	4	0.0007398
GO:0120036	plasma membrane bounded cell projection organization	BP	135	4	0.00108

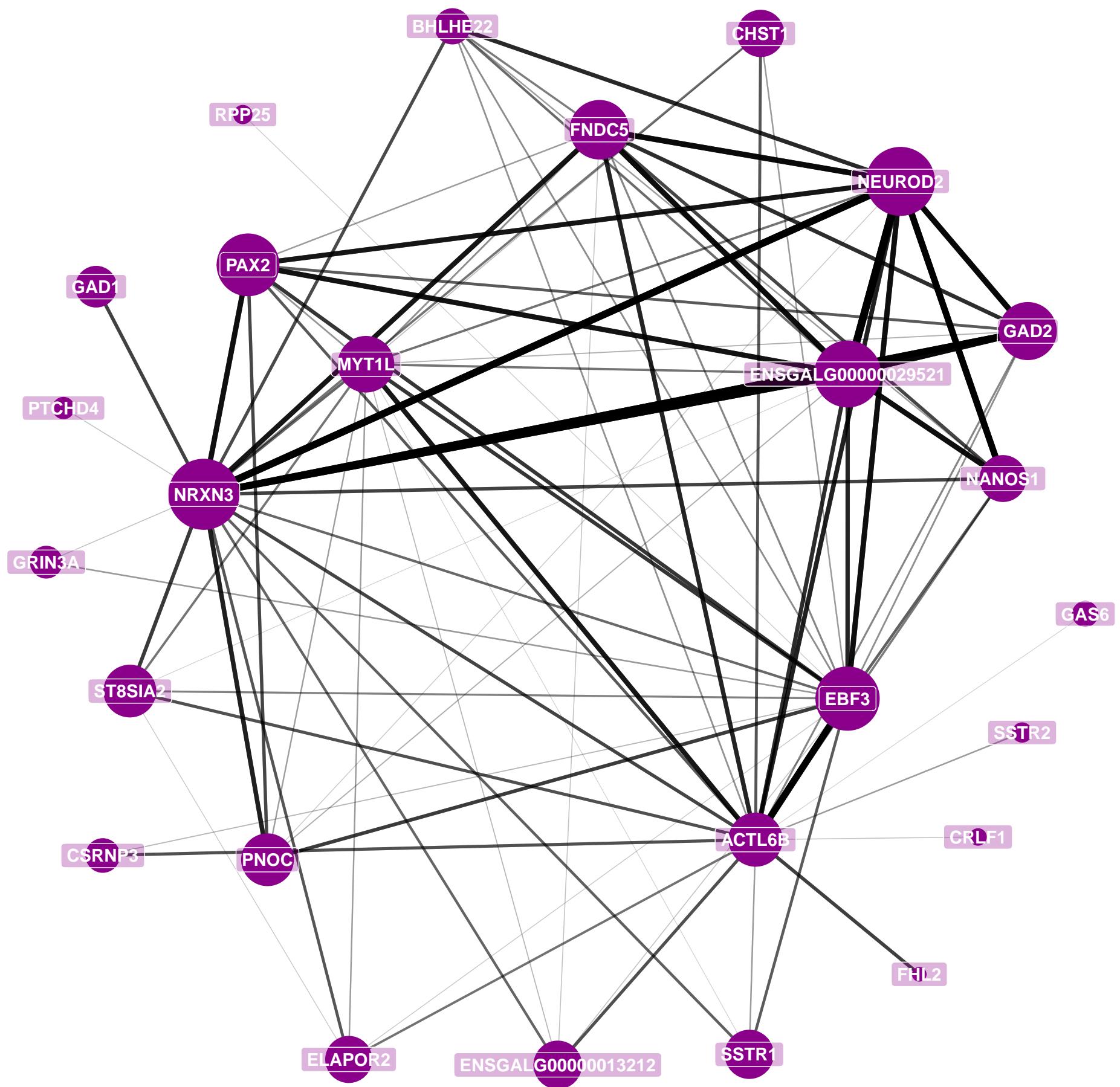
	Pathway	N	DE	P.DE
<i>path:gga04020</i>	Calcium signaling pathway	186	4	0.003479
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	3	0.007469
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.01343
<i>path:gga04260</i>	Cardiac muscle contraction	59	2	0.01685
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	1	0.03977
<i>path:gga04270</i>	Vascular smooth muscle contraction	101	2	0.04552
<i>path:gga04371</i>	Apelin signaling pathway	109	2	0.05217
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	3	0.05862
<i>path:gga00601</i>	Glycosphingolipid biosynthesis – lacto and neolacto series	21	1	0.06858
<i>path:gga00515</i>	Mannose type O–glycan biosynthesis	22	1	0.07173



1	AVP	MET	PAX6	PM20D2	FREM2	NKX6-1	ENSGALG00000016301	ABCC4
2	RAPGEF4	RASGEF1B	CCBE1	RTN4R	LMO3	CSRNP1	RCAN2	ATP2B4
3	RASL10B	SERPINI1	HAS2	PPM1E	CEMIP	SLC24A3	DYNC1I1	PRDM12
4	RSPO2	ARTN	BPIFB2	NECAB3	ENSGALG00000013155	RFTN1	MT4	NEUROG1
5	FKBP1B	PRLH	CYBB	ENSGALG00000044406				

	Term	Ont	N	n	Adj. p-value
GO:0071280	cellular response to copper ion	BP	1	1	0.002825
GO:0010273	detoxification of copper ion	BP	1	1	0.002825
GO:0061687	detoxification of inorganic compound	BP	1	1	0.002825
GO:0090500	endocardial cushion to mesenchymal transition	BP	1	1	0.002825
GO:0050891	multicellular organismal water homeostasis	BP	1	1	0.002825
GO:0035810	positive regulation of urine volume	BP	1	1	0.002825
GO:0035809	regulation of urine volume	BP	1	1	0.002825
GO:0070295	renal water absorption	BP	1	1	0.002825
GO:0003091	renal water homeostasis	BP	1	1	0.002825
GO:0003097	renal water transport	BP	1	1	0.002825

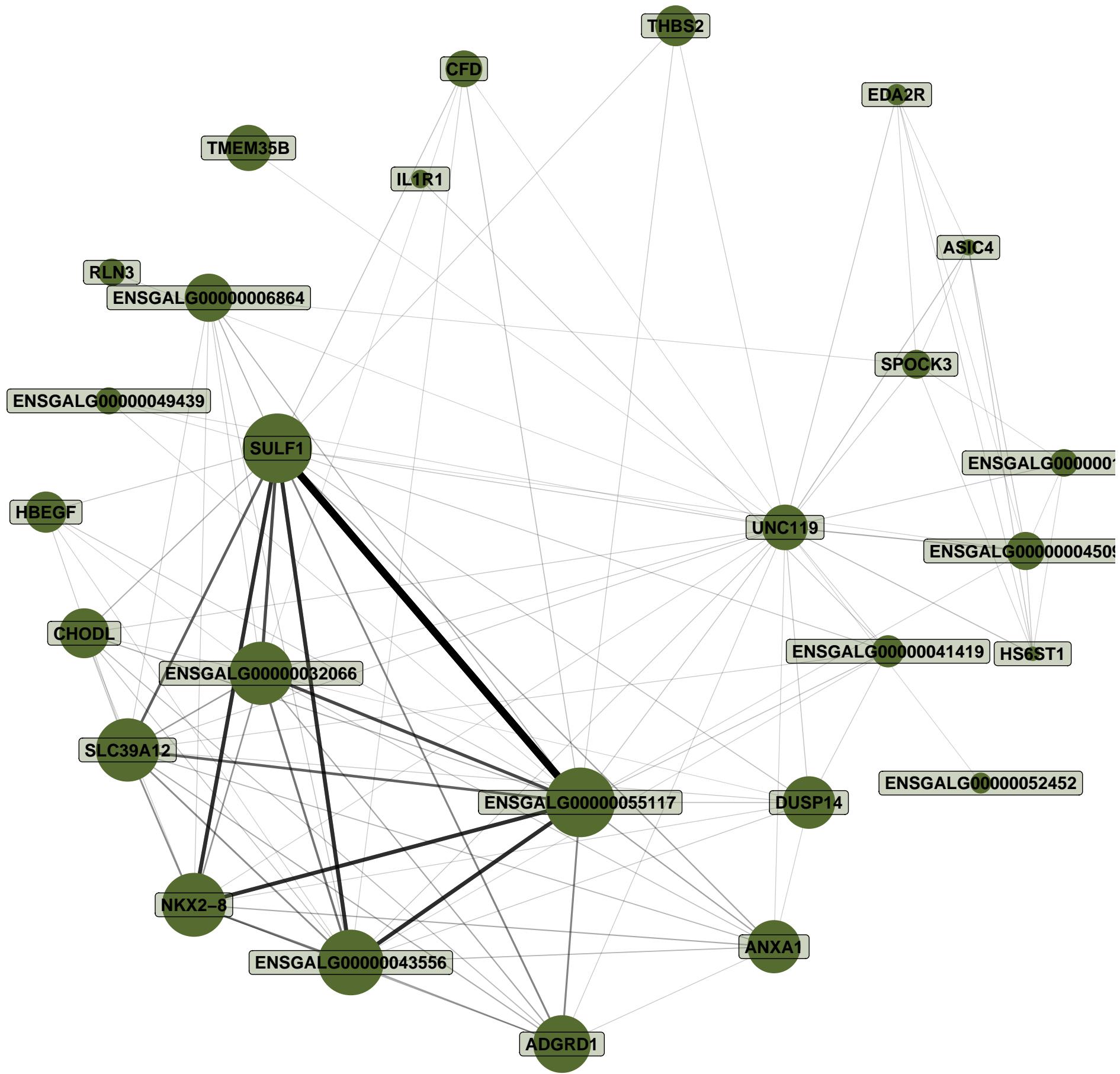
	Pathway	N	DE	P.DE
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	2	0.04433
<i>path:gga04145</i>	Phagosome	121	2	0.04568
<i>path:gga02010</i>	ABC transporters	34	1	0.09183
<i>path:gga04216</i>	Ferroptosis	34	1	0.09183
<i>path:gga04020</i>	Calcium signaling pathway	186	2	0.09672
<i>path:gga04512</i>	ECM–receptor interaction	65	1	0.1684
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	2	0.1698
<i>path:gga04520</i>	Adherens junction	69	1	0.1778
<i>path:gga04270</i>	Vascular smooth muscle contraction	101	1	0.2494
<i>path:gga04217</i>	Necroptosis	104	1	0.2558



1	NRXN3	NEUROD2	PAX2	EBF3	PNOC	ENSGALG00000029521	GAD2	GAD1
2	FNDC5	MYT1L	SSTR1	ST8SIA2	ELAPOR2	BHLHE22	ACTL6B	NANOS1
3	ENSGALG0000013212	CHST1	GRIN3A	PTCHD4	FHL2	CSRNP3	SSTR2	RPP25
4	GAS6	CRLF1						

	Term	Ont	N	n	Adj. p-value
GO:0001525	angiogenesis	BP	51	1	0.09911
GO:0048514	blood vessel morphogenesis	BP	62	1	0.1192
GO:0001568	blood vessel development	BP	64	1	0.1228
GO:0001944	vasculature development	BP	69	1	0.1318
GO:0035239	tube morphogenesis	BP	86	1	0.1616
GO:0035295	tube development	BP	104	1	0.1921
GO:0072359	circulatory system development	BP	111	1	0.2036
GO:0048646	anatomical structure formation involved in morphogenesis	BP	125	1	0.2263
GO:0048731	system development	BP	467	2	0.2465
GO:0022610	biological adhesion	BP	141	1	0.2514

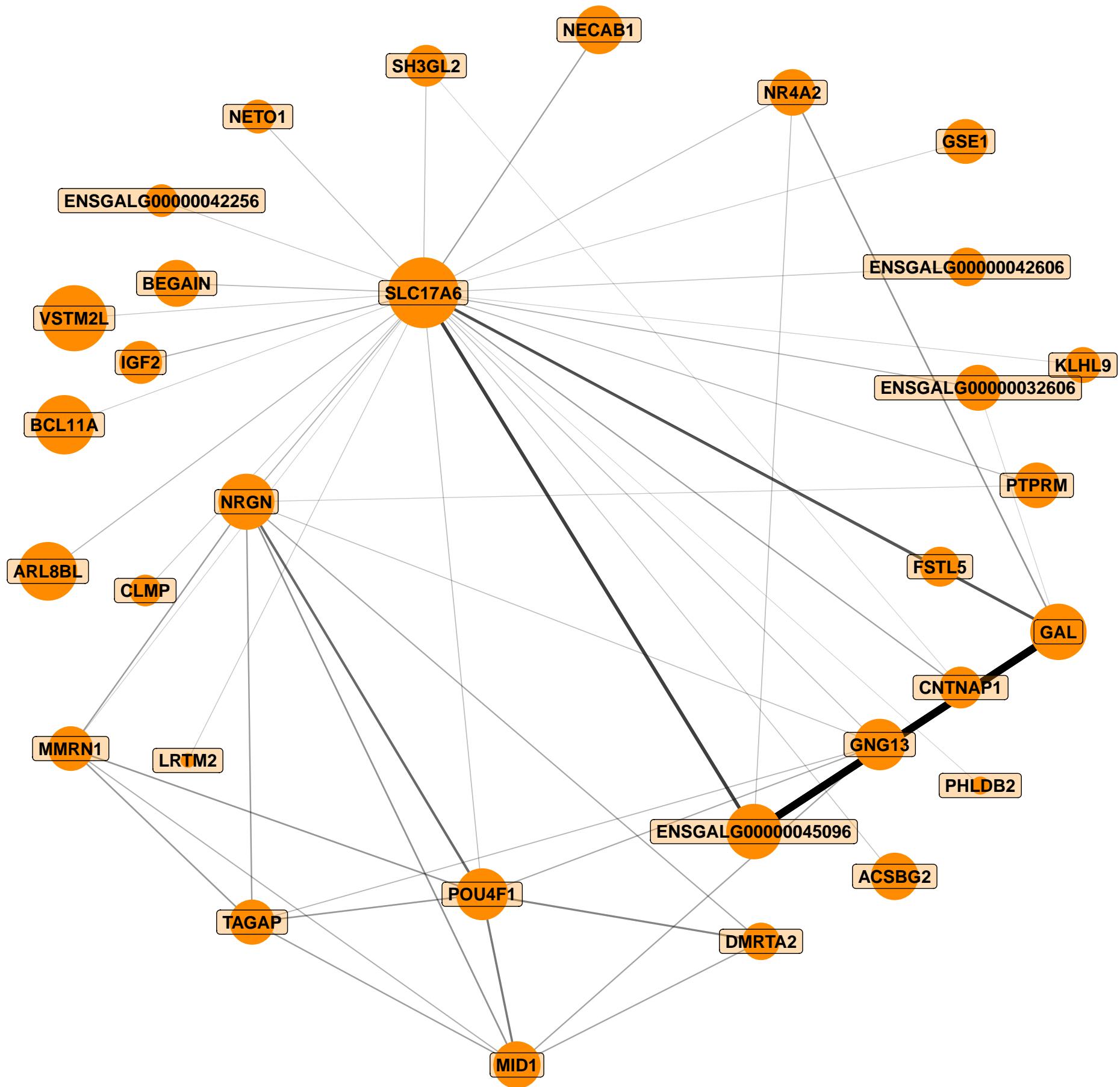
	Pathway	N	DE	P.DE
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	2	0.000261
<i>path:gga00650</i>	Butanoate metabolism	19	2	0.0006702
<i>path:gga00410</i>	beta–Alanine metabolism	24	2	0.001075
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	4	0.001854
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	2	0.001913
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.02821
<i>path:gga03008</i>	Ribosome biogenesis in eukaryotes	62	1	0.1192
<i>path:gga04514</i>	Cell adhesion molecules	98	1	0.182
<i>path:gga01100</i>	Metabolic pathways	1218	2	0.7253
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1



1	ENSGALG00000055117	SULF1	NKX2–8	ENSGALG00000043556	ENSGALG00000032066	SLC39A12	ADGRD1	CHODL
2	ANXA1	DUSP14	TMEM35B	UNC119	ENSGALG0000006864	ENSGALG0000004509	THBS2	CFD
3	HBEGF	ENSGALG00000041419	RLN3	ASIC4	SPOCK3	EDA2R	ENSGALG00000010316	ENSGALG00000052452
4	ENSGALG00000049439	IL1R1	HS6ST1					

	Term	Ont	N	n	Adj. p-value
GO:0090303	positive regulation of wound healing	BP	4	2	1.866e-05
GO:1903036	positive regulation of response to wounding	BP	6	2	4.655e-05
GO:0001525	angiogenesis	BP	51	3	0.0001011
GO:0061041	regulation of wound healing	BP	9	2	0.0001113
GO:0048514	blood vessel morphogenesis	BP	62	3	0.0001813
GO:0001568	blood vessel development	BP	64	3	0.0001992
GO:0001944	vasculature development	BP	69	3	0.0002491
GO:0010634	positive regulation of epithelial cell migration	BP	14	2	0.0002799
GO:1903034	regulation of response to wounding	BP	14	2	0.0002799
GO:0035239	tube morphogenesis	BP	86	3	0.0004768

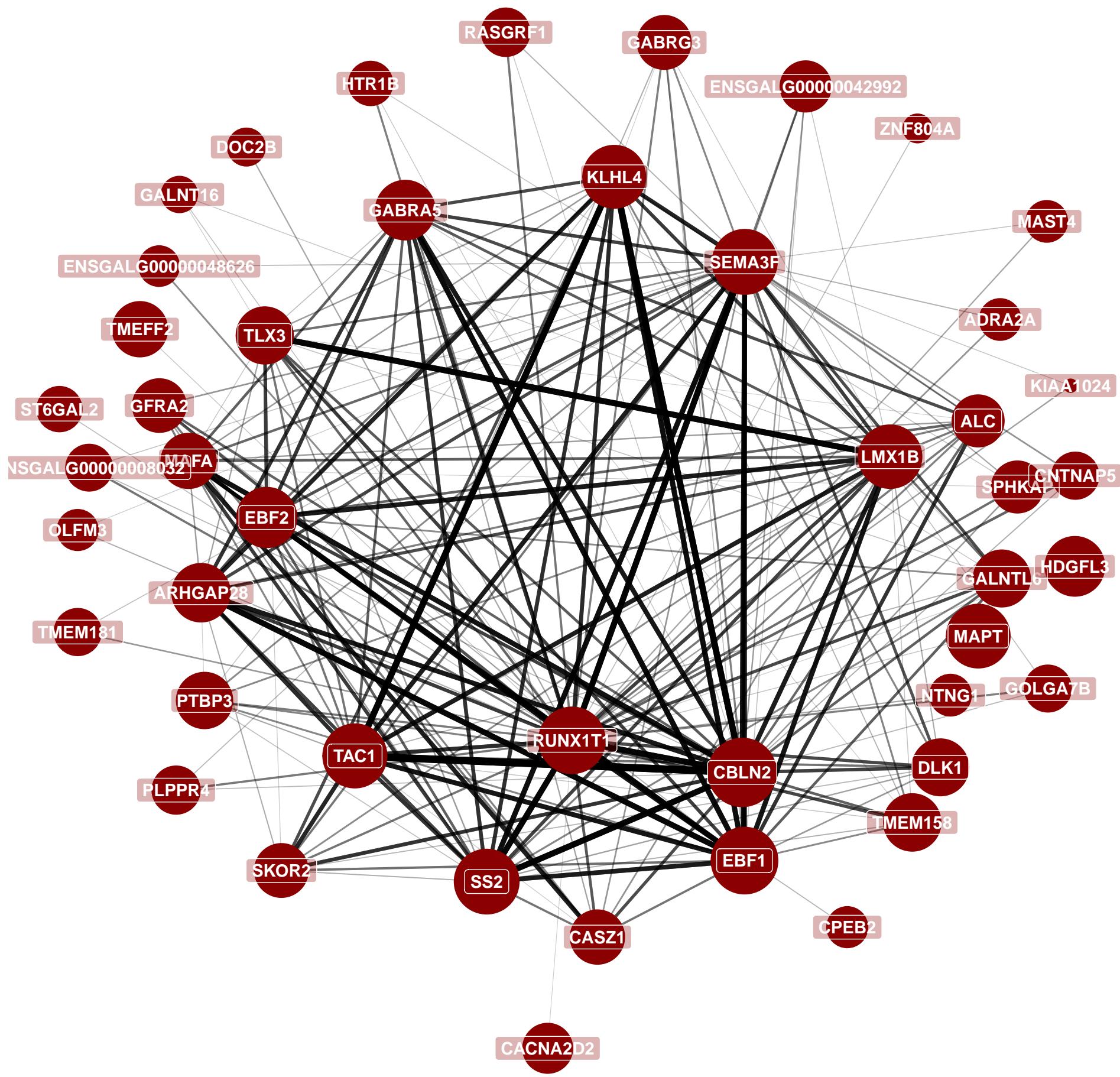
	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	65	2	0.00605
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	136	2	0.02471
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis – heparan sulfate / heparin	21	1	0.03726
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.1062
<i>path:gga04912</i>	GnRH signaling pathway	72	1	0.1223
<i>path:gga04012</i>	ErbB signaling pathway	75	1	0.1271
<i>path:gga04145</i>	Phagosome	121	1	0.1972
<i>path:gga04120</i>	Ubiquitin mediated proteolysis	128	1	0.2074
<i>path:gga04510</i>	Focal adhesion	166	1	0.2606
<i>path:gga04010</i>	MAPK signaling pathway	231	1	0.3437



1	SLC17A6	VSTM2L	NRGN	ARL8BL	POU4F1	ENSGALG00000045096	BCL11A	ACSBG2
2	GNG13	PTPRM	NECAB1	BEGAIN	GSE1	MID1	GAL	FSTL5
3	IGF2	SH3GL2	MMRN1	CNTNAP1	ENSGALG00000032606	TAGAP	NR4A2	KLHL9
4	ENSGALG00000042256	NETO1	DMRTA2	ENSGALG00000042606	PHLDB2	LRTM2	CLMP	

	Term	Ont	N	n	Adj. p-value
GO:0051302	regulation of cell division	BP	21	2	0.001169
GO:0031017	exocrine pancreas development	BP	1	1	0.002433
GO:0038028	insulin receptor signaling pathway via phosphatidylinositol 3-kinase	BP	1	1	0.002433
GO:2000467	positive regulation of glycogen (starch) synthase activity	BP	1	1	0.002433
GO:0048633	positive regulation of skeletal muscle tissue growth	BP	1	1	0.002433
GO:2000465	regulation of glycogen (starch) synthase activity	BP	1	1	0.002433
GO:0009250	glucan biosynthetic process	BP	2	1	0.00486
GO:0005978	glycogen biosynthetic process	BP	2	1	0.00486
GO:0042104	positive regulation of activated T cell proliferation	BP	2	1	0.00486
GO:1900078	positive regulation of cellular response to insulin stimulus	BP	2	1	0.00486

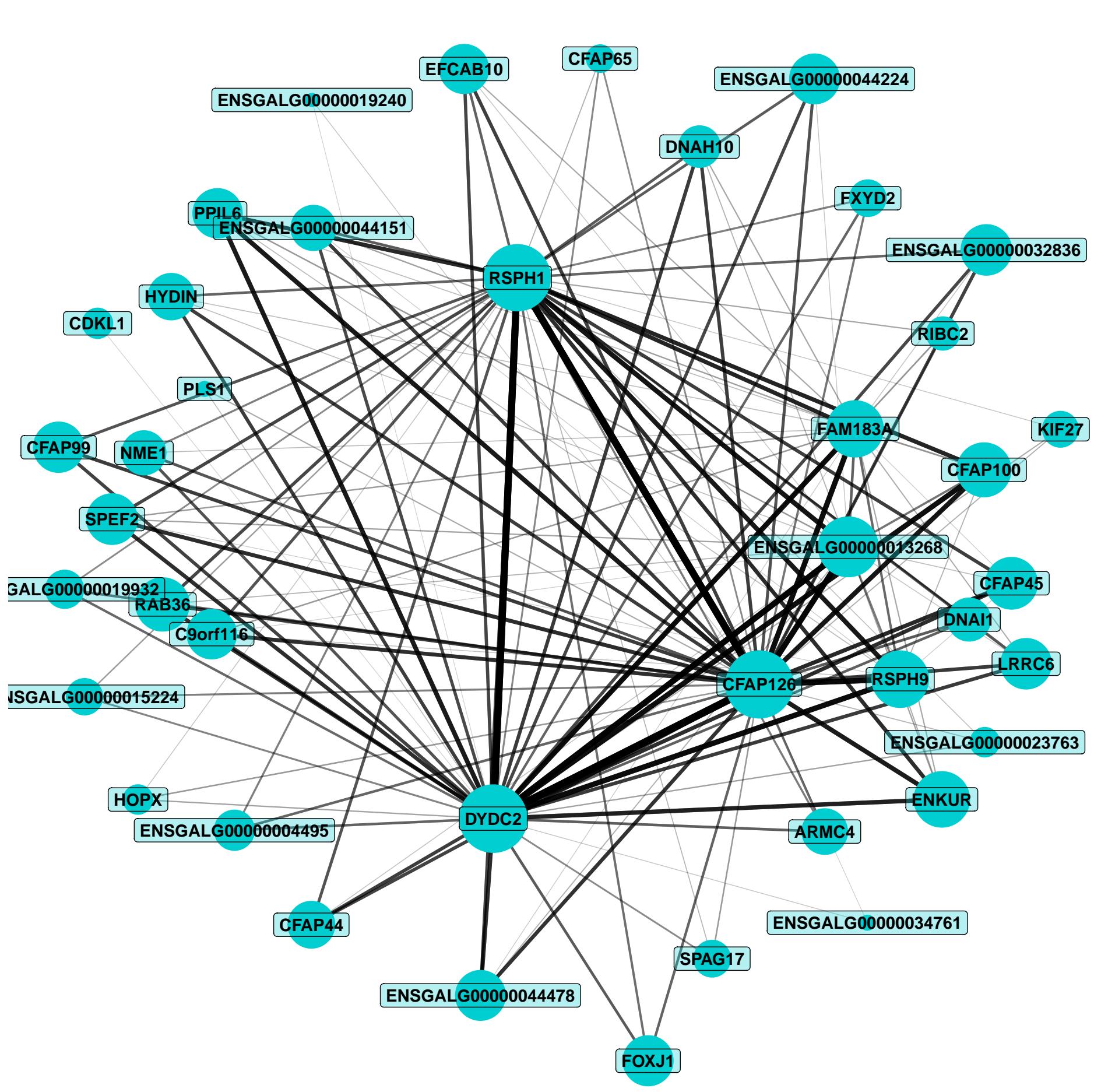
	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	98	2	0.02356
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	3	0.02553
<i>path:gga00061</i>	Fatty acid biosynthesis	16	1	0.03825
<i>path:gga04120</i>	Ubiquitin mediated proteolysis	128	2	0.03851
<i>path:gga00071</i>	Fatty acid degradation	30	1	0.07055
<i>path:gga01212</i>	Fatty acid metabolism	50	1	0.1149
<i>path:gga03320</i>	PPAR signaling pathway	55	1	0.1256
<i>path:gga04920</i>	Adipocytokine signaling pathway	59	1	0.1342
<i>path:gga04520</i>	Adherens junction	69	1	0.1551
<i>path:gga04371</i>	Apelin signaling pathway	109	1	0.2341



1	CBLN2	SS2	RUNX1T1	TAC1	EBF1	LMX1B	SEMA3F	EBF2
2	MAPT	TLX3	GABRA5	KLHL4	GALNTL6	HDGFL3	CACNA2D2	TMEFF2
3	MAFA	ARHGAP28	DLK1	GFRA2	PTBP3	SKOR2	CASZ1	ENSGALG00000042992
4	GABRG3	ALC	MAST4	SPHKAP	ENSGALG0000008032	RASGRF1	TMEM158	TMEM181
5	PLPPR4	ST6GAL2	GOLGA7B	HTR1B	CNTNAP5	ADRA2A	CPEB2	OLFM3
6	NTNG1	GALNT16	DOC2B	ENSGALG00000048626	KIAA1024	ZNF804A		

	Term	Ont	N	n	Adj. p-value
GO:0035860	glial cell-derived neurotrophic factor receptor signaling pathway	BP	3	1	0.01009
GO:0097503	sialylation	BP	5	1	0.01676
GO:0009749	response to glucose	BP	6	1	0.02008
GO:0009746	response to hexose	BP	6	1	0.02008
GO:0034284	response to monosaccharide	BP	6	1	0.02008
GO:0009743	response to carbohydrate	BP	7	1	0.02339
GO:0030073	insulin secretion	BP	13	1	0.04301
GO:0030072	peptide hormone secretion	BP	16	1	0.05268
GO:0072163	mesonephric epithelium development	BP	18	1	0.05907
GO:0072164	mesonephric tubule development	BP	18	1	0.05907

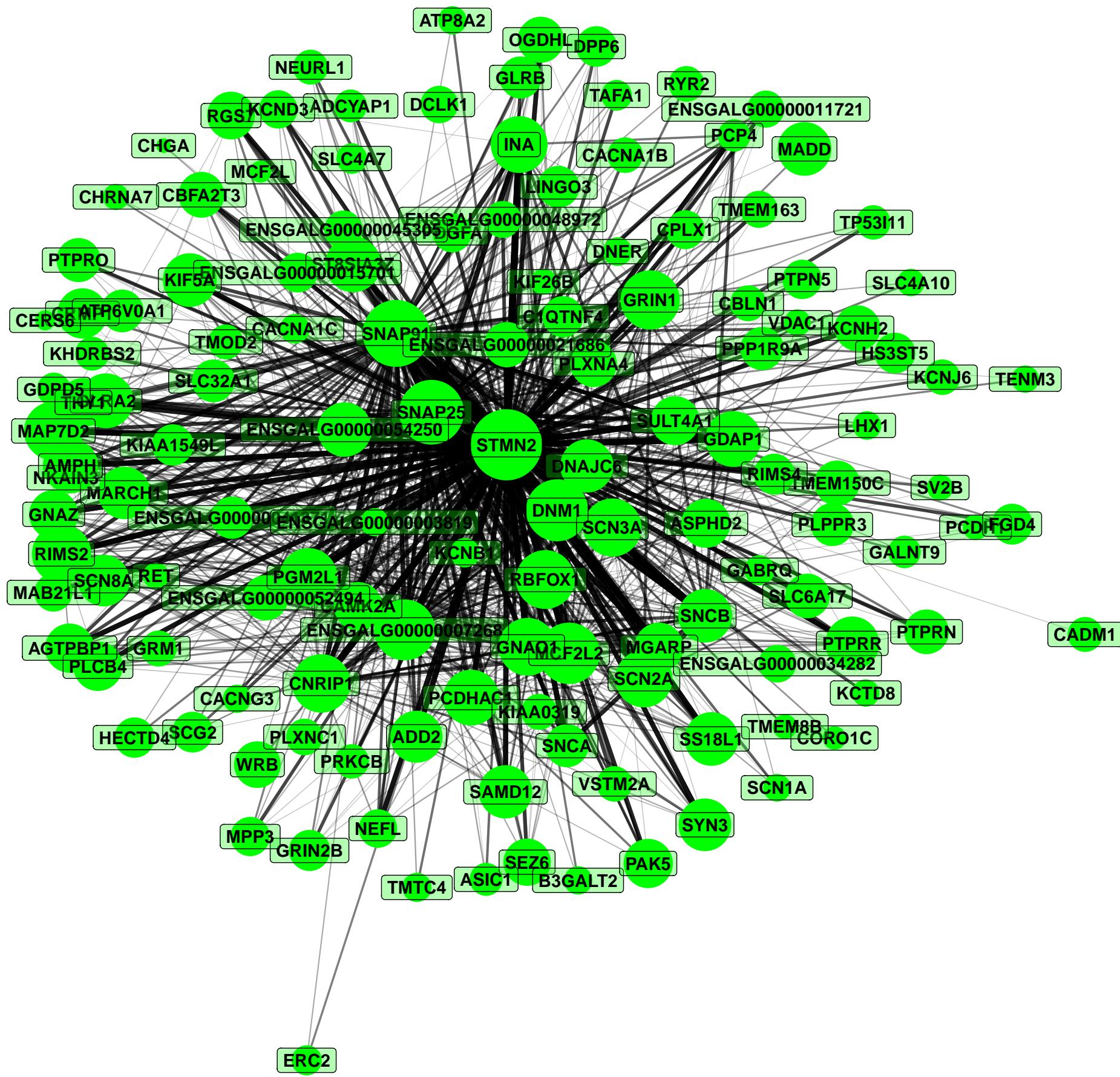
	Pathway	N	DE	P.DE
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	3	0.000349
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	263	5	0.001829
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	2	0.004263
<i>path:gga04010</i>	MAPK signaling pathway	231	3	0.04268
<i>path:gga00510</i>	N-Glycan biosynthesis	45	1	0.1413
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.1812
<i>path:gga04914</i>	Progesterone-mediated oocyte maturation	76	1	0.2271
<i>path:gga04114</i>	Oocyte meiosis	92	1	0.2681
<i>path:gga04514</i>	Cell adhesion molecules	98	1	0.2829
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	1	0.3325



1	CFAP126	DYDC2	RSPH1	ENSGALG00000013268	FAM183A	ENKUR	FOXJ1	RSPH9
2	RAB36	CFAP100	PPIL6	CFAP99	C9orf116	CFAP45	ENSGALG00000044224	ENSGALG00000044478
3	ENSGALG0000032836	ENSGALG00000044151	LRRC6	SPEF2	HYDIN	FXYD2	EFCAB10	CFAP44
4	ARMC4	DNAI1	ENSGALG0000004495	RIBC2	HOPX	ENSGALG0000019932	DNAH10	NME1
5	ENSGALG0000015224	CDKL1	KIF27	SPAG17	ENSGALG0000023763	ENSGALG0000034761	ENSGALG0000019240	CFAP65
6	PLS1							

	Term	Ont	N	n	Adj. p-value
GO:0048639	positive regulation of developmental growth	BP	17	2	0.001206
GO:0045927	positive regulation of growth	BP	23	2	0.002218
GO:0035082	axoneme assembly	BP	1	1	0.003061
GO:0030317	flagellated sperm motility	BP	1	1	0.003061
GO:0001951	intestinal D–glucose absorption	BP	1	1	0.003061
GO:0106001	intestinal hexose absorption	BP	1	1	0.003061
GO:0032536	regulation of cell projection size	BP	1	1	0.003061
GO:0032532	regulation of microvillus length	BP	1	1	0.003061
GO:0007288	sperm axoneme assembly	BP	1	1	0.003061
GO:0097722	sperm motility	BP	1	1	0.003061

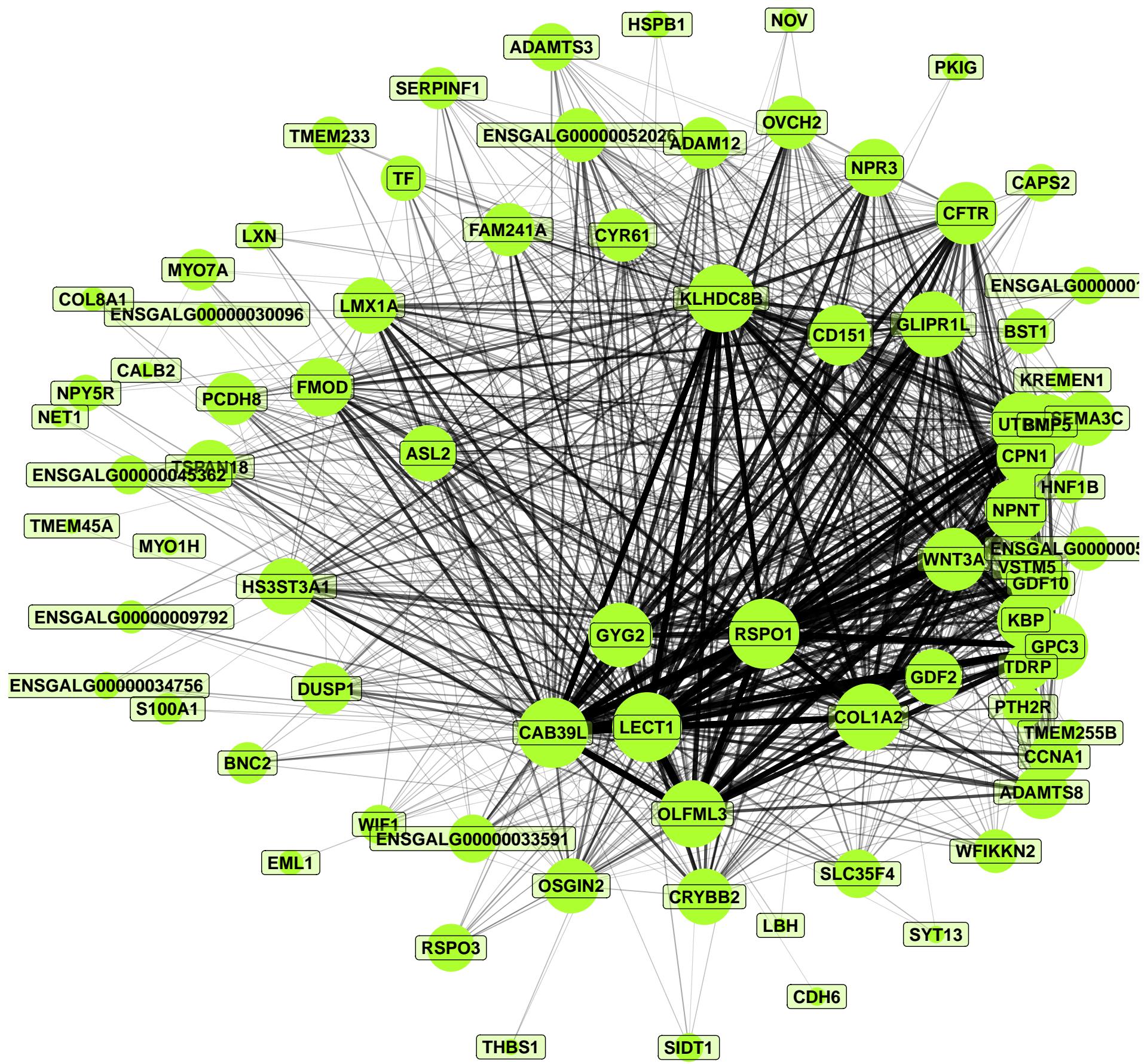
	Pathway	N	DE	P.DE
<i>path:gga00240</i>	Pyrimidine metabolism	54	2	0.01182
<i>path:gga01232</i>	Nucleotide metabolism	76	2	0.02256
<i>path:gga00360</i>	Phenylalanine metabolism	12	1	0.03613
<i>path:gga00230</i>	Purine metabolism	110	2	0.04449
<i>path:gga01240</i>	Biosynthesis of cofactors	114	2	0.04743
<i>path:gga00340</i>	Histidine metabolism	16	1	0.04789
<i>path:gga00350</i>	Tyrosine metabolism	23	1	0.06813
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	26	1	0.07668
<i>path:gga00260</i>	Glycine, serine and threonine metabolism	30	1	0.08796
<i>path:gga00380</i>	Tryptophan metabolism	32	1	0.09354



1	STMN2	SNAP25	SNAP91	GRIN1	RBFOX1	MCF2L2	ENSGALG00000007268	SCN3A
2	DNM1	SCG2	PCDHAC1	CNRIP1	SCN2A	SNCB	GLRA2	INA
3	MAP7D2	RIMS2	ST8SIA3Z	MARCH1	PGM2L1	ENSGALG00000054250	C1QTNF4	CHGA
4	GNAO1	PTPRR	PLXNA4	DNAJC6	KIF5A	SLC32A1	MGARP	SLC6A17
5	AMPH	SAMD12	GDAP1	PAK5	SS18L1	MADD	SYN3	THY1
6	CAMK2A	RGS7	SEZ6	PCP4	PLCB4	CPLX1	DPP6	SNCA
7	CBFA2T3	SCN8A	CBLN1	AGTPBP1	SULT4A1	CRMP1	ADD2	ASPHD2
8	ATP6V0A1	GALNT9	GNAZ	PTPRO	VSTM2A	MAB21L1	OGDHL	TMEM150C
9	ENSGALG0000048972	ENSGALG0000015701	KCNH2	NEFL	GRIN2B	WRB	PLXNC1	MPP3
10	LHX1	ENSGALG0000041371	PTPRN	HS3ST5	ADCYAP1	KCNJ6	KIAA0319	ENSGALG00000052494
11	GLRB	PPP1R9A	ENSGALG0000021686	KIAA1549L	FGD4	PLPPR3	HECTD4	LINGO3
12	CACNA1B	PDGFA	KHDRBS2	RET	TMOD2	RYR2	DCLK1	PTPN5
13	KCTD8	SV2B	KCNB1	GDPD5	GRM1	NEURL1	TMEM163	ENSGALG0000045305
14	ENSGALG0000011721	SCN1A	ENSGALG0000034282	CADM1	TP53I11	KCND3	CHRNA7	ERC2
15	RIMS4	GABRQ	VDAC1	CORO1C	TAFA1	NKAIN3	TENM3	ENSGALG0000003819
16	CACNA1C	SLC4A7	ASIC1	ATP8A2	CACNG3	DNER	PRKCB	SLC4A10
17	TMEM8B	TMTC4	CERS6	MCF2L	B3GALT2	PCDH1	KIF26B	

	Term	Ont	N	n	Adj. p-value
GO:0098660	inorganic ion transmembrane transport	BP	56	7	1.497e–06
GO:0034220	ion transmembrane transport	BP	100	8	8.014e–06
GO:0098662	inorganic cation transmembrane transport	BP	51	6	1.242e–05
GO:0006812	cation transport	BP	79	7	1.541e–05
GO:0055085	transmembrane transport	BP	112	8	1.849e–05
GO:0098655	cation transmembrane transport	BP	58	6	2.633e–05
GO:0021702	cerebellar Purkinje cell differentiation	BP	2	2	0.0001033
GO:0021680	cerebellar Purkinje cell layer development	BP	2	2	0.0001033
GO:0021694	cerebellar Purkinje cell layer formation	BP	2	2	0.0001033
GO:0021692	cerebellar Purkinje cell layer morphogenesis	BP	2	2	0.0001033

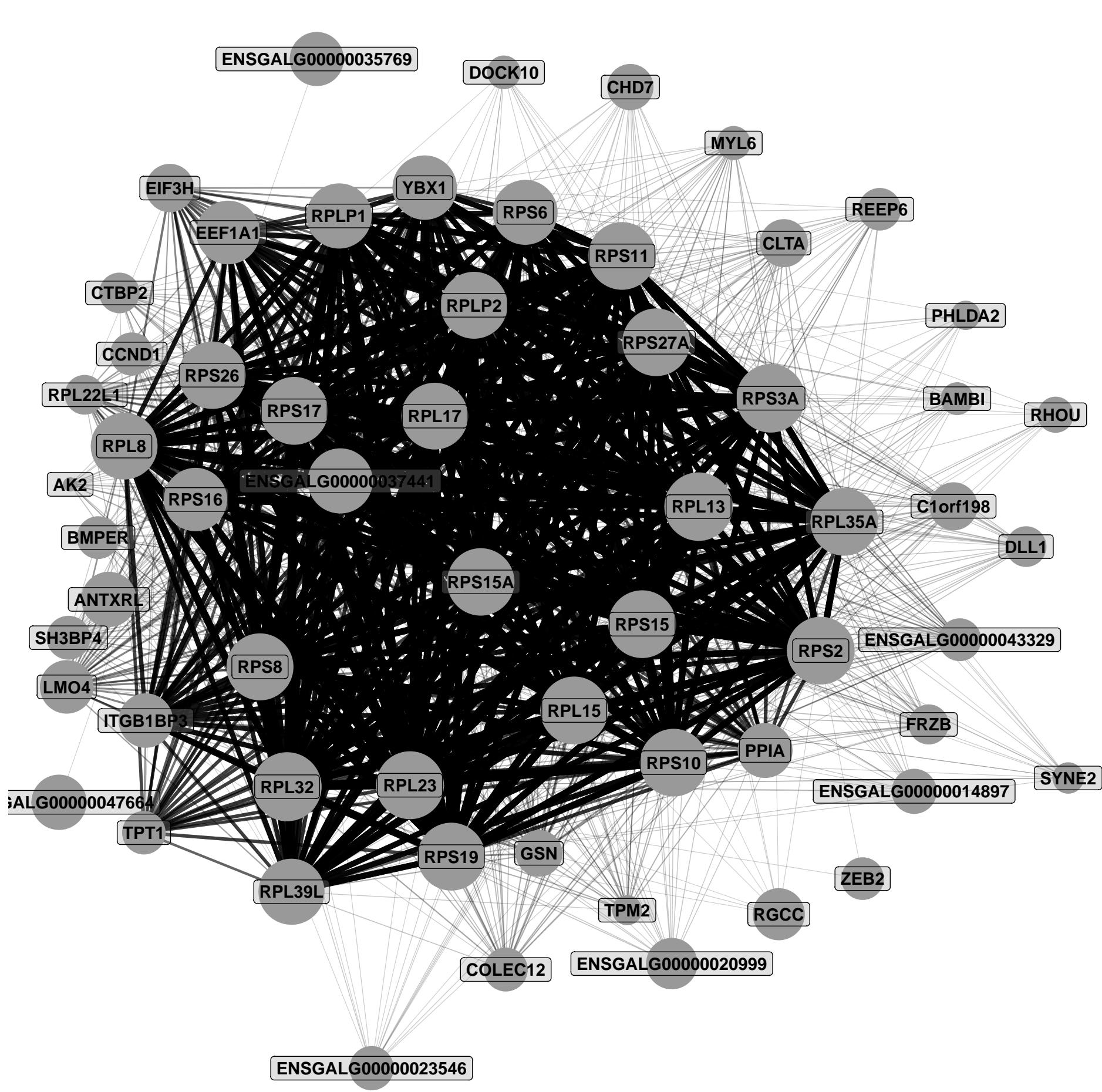
	Pathway	N	DE	P.DE
<i>path:gga04020</i>	Calcium signaling pathway	186	12	4.222e-07
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	8	0.005521
<i>path:gga04912</i>	GnRH signaling pathway	72	4	0.006233
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	5	0.007403
<i>path:gga04540</i>	Gap junction	78	4	0.008248
<i>path:gga04916</i>	Melanogenesis	80	4	0.009005
<i>path:gga04010</i>	MAPK signaling pathway	231	7	0.009452
<i>path:gga03267</i>	Virion – Adenovirus	2	1	0.0203
<i>path:gga04260</i>	Cardiac muscle contraction	59	3	0.02228
<i>path:gga04012</i>	ErbB signaling pathway	75	3	0.04119



1	LECT1	CAB39L	RSPO1	KLHDC8B	OLFML3	COL1A2	GYG2	GPC3
2	GLIPR1L	UTRN	WNT3A	LMX1A	CFTR	CD151	BMP5	NPR3
3	KBP	ASL2	PCDH8	NPNT	SEMA3C	HS3ST3A1	OSGIN2	ADAMTS8
4	GDF10	CPN1	CCNA1	FMOD	GDF2	ENSGALG00000052026	CRYBB2	TSPAN18
5	FAM241A	ENSGALG00000033591	CYR61	VSTM5	OVCH2	TF	ADAM12	WIF1
6	DUSP1	TDRP	RSPO3	ENSGALG00000053965	BST1	ADAMTS3	SLC35F4	SERPINF1
7	NPY5R	MYO7A	BNC2	WF1KK2	ENSGALG00000011687	TMEM233	PTH2R	HSPB1
8	PKIG	CAPS2	ENSGALG0000009792	LXN	HNF1B	TMEM255B	ENSGALG00000034756	NOV
9	ENSGALG00000045362	SIDT1	EML1	S100A1	KREMEN1	NET1	ENSGALG00000030096	THBS1
10	COL8A1	CDH6	MYO1H	TMEM45A	SYT13	LBH	CALB2	

	Term	Ont	N	n	Adj. p-value
GO:0030509	BMP signaling pathway	BP	26	3	0.0004803
GO:0071773	cellular response to BMP stimulus	BP	29	3	0.0006665
GO:0071772	response to BMP	BP	29	3	0.0006665
GO:0045229	external encapsulating structure organization	BP	31	3	0.0008129
GO:0030198	extracellular matrix organization	BP	31	3	0.0008129
GO:0043062	extracellular structure organization	BP	31	3	0.0008129
GO:0090287	regulation of cellular response to growth factor stimulus	BP	32	3	0.0008931
GO:0030513	positive regulation of BMP signaling pathway	BP	8	2	0.0009605
GO:0051216	cartilage development	BP	44	3	0.002266
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	BP	44	3	0.002266

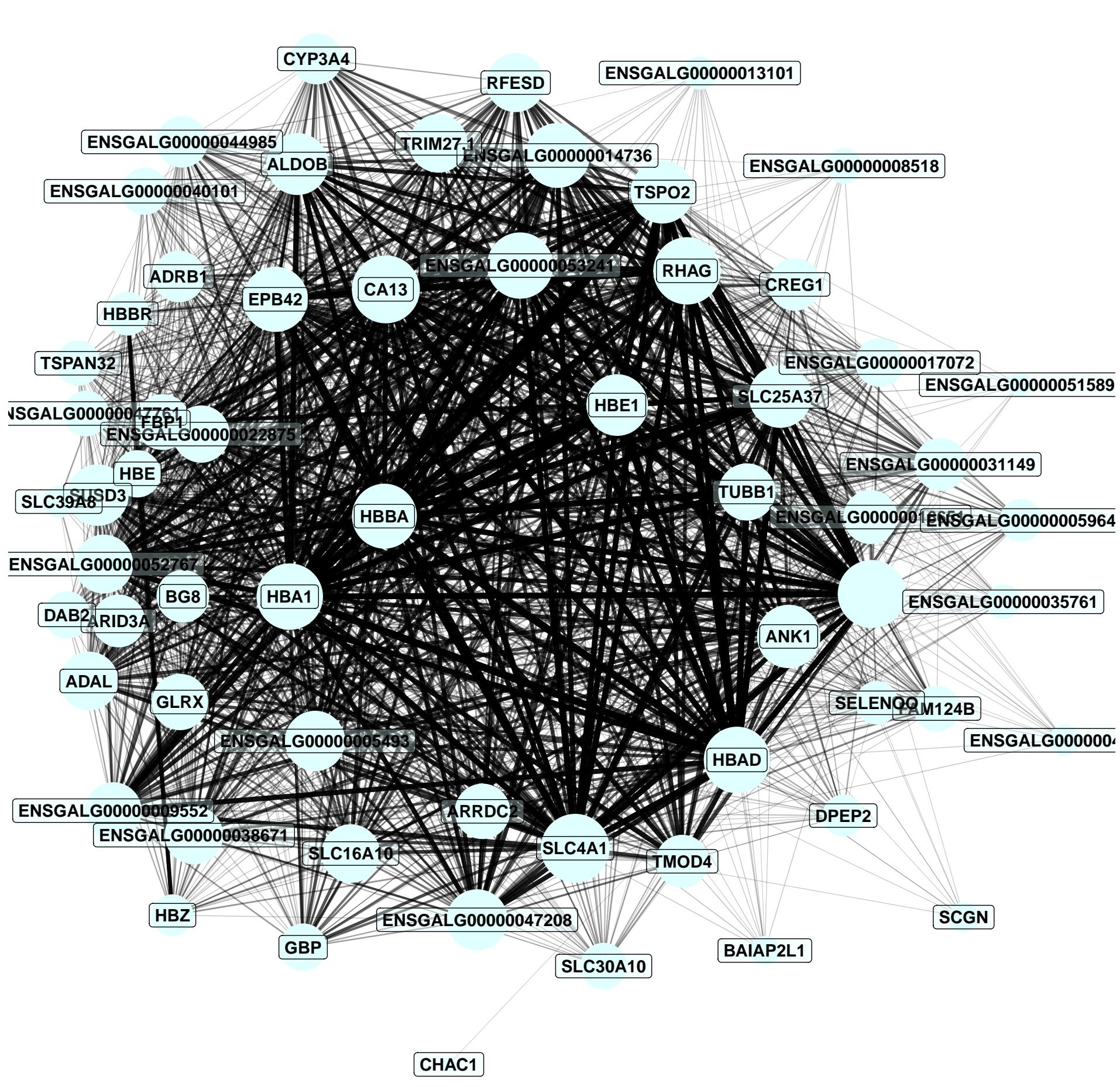
	Pathway	N	DE	P.DE
<i>path:gga04310</i>	Wnt signaling pathway	131	5	0.001096
<i>path:gga04512</i>	ECM–receptor interaction	65	3	0.006833
<i>path:gga04350</i>	TGF–beta signaling pathway	84	3	0.01375
<i>path:gga00220</i>	Arginine biosynthesis	16	1	0.09133
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis – heparan sulfate / heparin	21	1	0.1181
<i>path:gga00500</i>	Starch and sucrose metabolism	24	1	0.1339
<i>path:gga04371</i>	Apelin signaling pathway	109	2	0.1378
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	1	0.1744
<i>path:gga00760</i>	Nicotinate and nicotinamide metabolism	32	1	0.1744
<i>path:gga04150</i>	mTOR signaling pathway	130	2	0.1817



1	RPL32	RPS27A	RPL15	RPS17	RPL23	RPL13	RPS15	RPS19
2	RPS15A	RPL35A	RPS11	RPS10	RPS3A	RPS8	RPS2	RPLP2
3	RPS26	RPLP1	RPL39L	ENSGALG00000037441	RPL17	RPL8	RPS16	YBX1
4	RPS6	EEF1A1	ITGB1BP3	PPIA	TPT1	ENSGALG00000043329	ANTXRL	ENSGALG00000047664
5	EIF3H	LMO4	ENSGALG00000035769	COLEC12	RPL22L1	RGCC	ENSGALG00000020999	C1orf198
6	DLL1	CLTA	GSN	CHD7	CTBP2	MYL6	ENSGALG00000014897	FRZB
7	CCND1	SH3BP4	REEP6	ZEB2	BMPER	TPM2	ENSGALG00000023546	BAMBI
8	SYNE2	PHLDA2	RHOU	DOCK10	AK2			

	Term	Ont	N	n	Adj. p-value
GO:0006412	translation	BP	87	11	1.679e-13
GO:0043043	peptide biosynthetic process	BP	88	11	1.913e-13
GO:0043604	amide biosynthetic process	BP	99	11	7.25e-13
GO:0006518	peptide metabolic process	BP	106	11	1.56e-12
GO:0043603	cellular amide metabolic process	BP	122	11	7.45e-12
GO:1901566	organonitrogen compound biosynthetic process	BP	204	11	1.934e-09
GO:0010467	gene expression	BP	593	13	2.364e-06
GO:0044271	cellular nitrogen compound biosynthetic process	BP	515	12	3.301e-06
GO:0002181	cytoplasmic translation	BP	23	4	3.438e-06
GO:0044267	cellular protein metabolic process	BP	523	12	3.87e-06

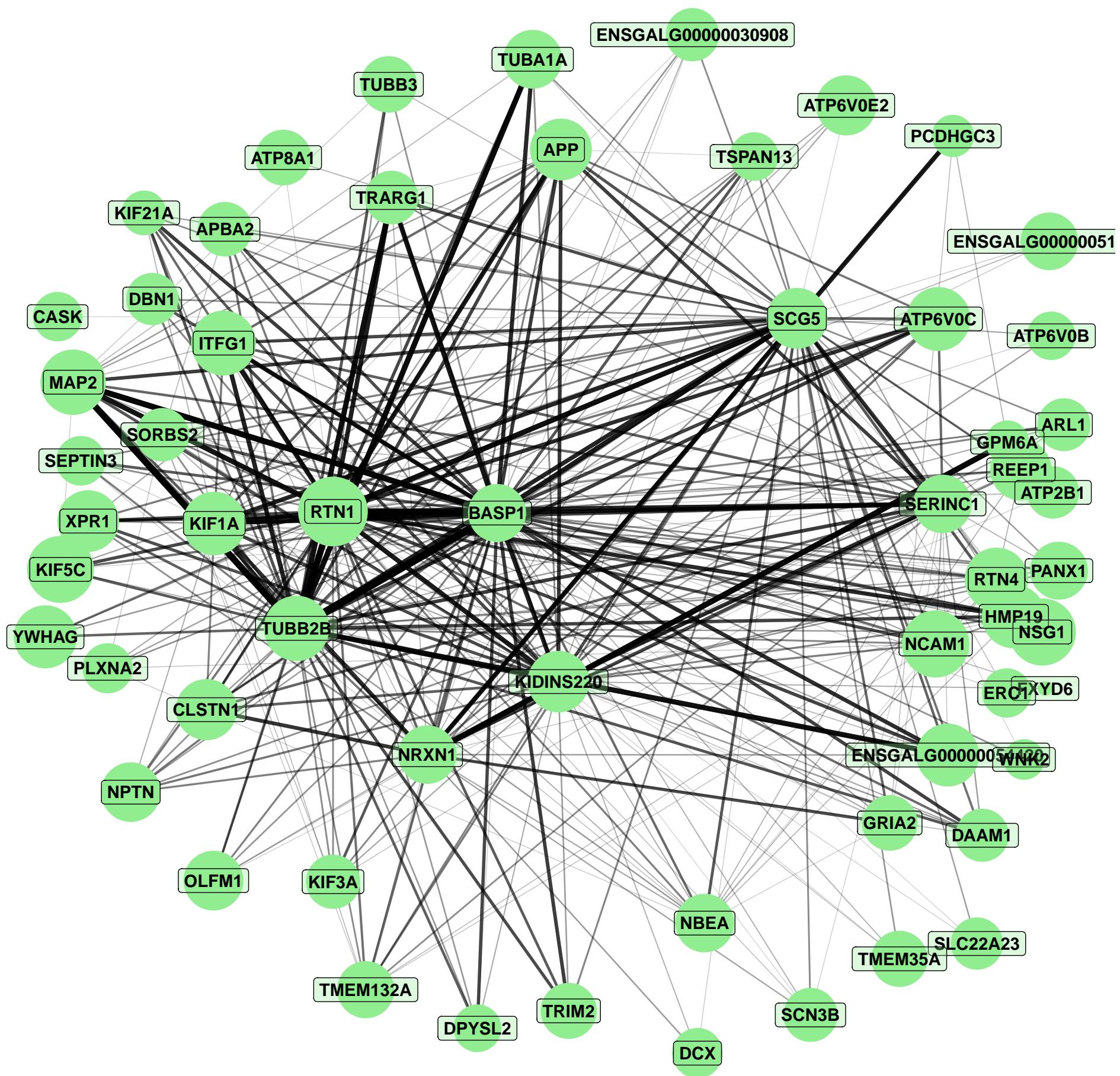
	Pathway	N	DE	P.DE
<i>path:gga03010</i>	Ribosome	115	25	1.132e-36
<i>path:gga04310</i>	Wnt signaling pathway	131	4	0.003137
<i>path:gga04330</i>	Notch signaling pathway	52	2	0.0241
<i>path:gga01232</i>	Nucleotide metabolism	76	2	0.04829
<i>path:gga00730</i>	Thiamine metabolism	12	1	0.05419
<i>path:gga00670</i>	One carbon pool by folate	15	1	0.06728
<i>path:gga04371</i>	Apelin signaling pathway	109	2	0.09063
<i>path:gga04530</i>	Tight junction	133	2	0.1262
<i>path:gga00760</i>	Nicotinate and nicotinamide metabolism	32	1	0.1382
<i>path:gga04340</i>	Hedgehog signaling pathway	47	1	0.1963



1	HBAD	SLC4A1	HBA1	NA	CA13	HBBA	HBE1	RHAG
2	TSPO2	ENSGALG00000053241	EPB42	SUSD3	HBE	ENSGALG0000014736	ANK1	ENSGALG0000047208
3	SLC25A37	ENSGALG0000052767	ENSGALG0000005493	ENSGALG0000022875	ALDOB	ENSGALG0000038671	TRIM27.1	TUBB1
4	RFESD	HBZ	FBP1	ENSGALG0000009552	SLC16A10	GLRX	HBBR	ADAL
5	ENSGALG0000016651	TMOD4	ENSGALG000004985	CYP3A4	ARID3A	ADRB1	ARRDC2	ENSGALG0000031149
6	TSPAN32	CREG1	BG8	ENSGALG0000047761	DPEP2	FAM124B	ENSGALG0000017072	ENSGALG0000040101
7	ENSGALG0000008518	ENSGALG0000005964	GBP	DAB2	SLC30A10	SCGN	SELENOO	BAIAP2L1
8	ENSGALG0000013101	ENSGALG0000048671	ENSGALG0000035761	SLC39A8	ENSGALG0000051589	CHAC1		

	Term	Ont	N	n	Adj. p-value
GO:0042744	hydrogen peroxide catabolic process	BP	7	6	4.264e-14
GO:0042743	hydrogen peroxide metabolic process	BP	7	6	4.264e-14
GO:0015671	oxygen transport	BP	7	6	4.264e-14
GO:0015669	gas transport	BP	8	6	1.7e-13
GO:0098869	cellular oxidant detoxification	BP	14	6	1.786e-11
GO:1990748	cellular detoxification	BP	16	6	4.729e-11
GO:0097237	cellular response to toxic substance	BP	16	6	4.729e-11
GO:0098754	detoxification	BP	17	6	7.283e-11
GO:0072593	reactive oxygen species metabolic process	BP	18	6	1.089e-10
GO:0009636	response to toxic substance	BP	20	6	2.258e-10

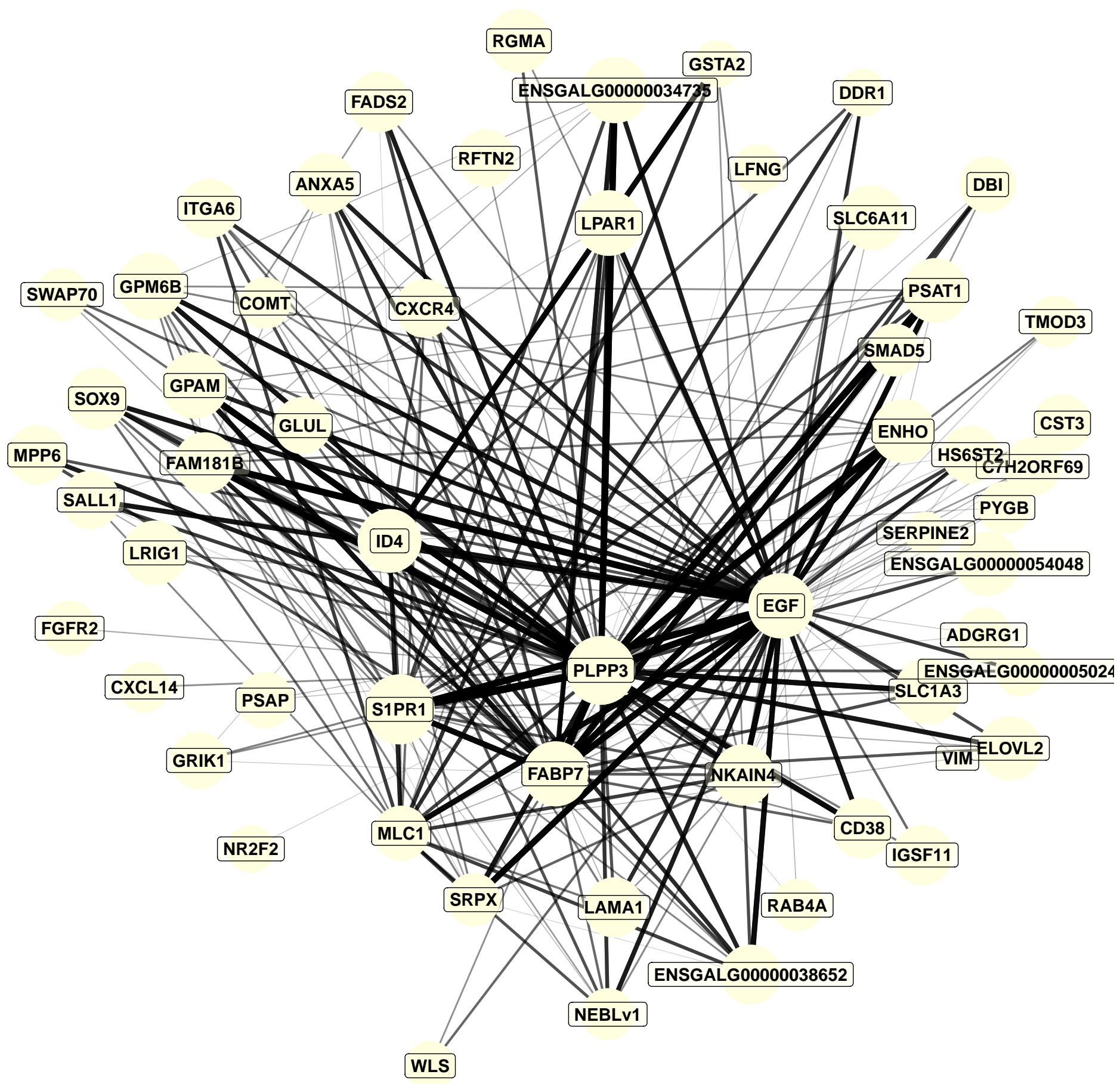
	Pathway	N	DE	P.DE
<i>path:gga00910</i>	Nitrogen metabolism	13	2	0.001486
<i>path:gga00030</i>	Pentose phosphate pathway	25	2	0.005521
<i>path:gga00051</i>	Fructose and mannose metabolism	34	2	0.01006
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	46	2	0.01794
<i>path:gga01230</i>	Biosynthesis of amino acids	56	2	0.02595
<i>path:gga04540</i>	Gap junction	78	2	0.04755
<i>path:gga00591</i>	Linoleic acid metabolism	15	1	0.06507
<i>path:gga01200</i>	Carbon metabolism	94	2	0.06617
<i>path:gga00220</i>	Arginine biosynthesis	16	1	0.06926
<i>path:gga00140</i>	Steroid hormone biosynthesis	22	1	0.094



1	RTN1	NSG1	HMP19	TUBB2B	KIF5C	YWHAG	OLFM1	APP
2	TUBB3	MAP2	NCAM1	ITFG1	ENSGALG00000054420	KIDINS220	TUBA1A	KIF1A
3	TRARG1	SCG5	CLSTN1	BASP1	NRXN1	ATP6V0C	SERINC1	XPR1
4	NPTN	RTN4	TRIM2	ATP8A1	REEP1	ATP6V0E2	GRIA2	APBA2
5	DPYSL2	TSPAN13	PCDHGC3	DBN1	TMEM132A	NBEA	GPM6A	ENSGALG00000051550
6	TMEM35A	PANX1	SORBS2	DAAM1	ENSGALG00000030908	KIF21A	SLC22A23	SCN3B
7	ATP2B1	DCX	PLXNA2	SEPTIN3	KIF3A	ARL1	ATP6V0B	FXYD6
8	CASK	ERC1	WNK2					

	Term	Ont	N	n	Adj. p-value
GO:0030516	regulation of axon extension	BP	14	3	3.31e-05
GO:0048675	axon extension	BP	16	3	5.059e-05
GO:0061387	regulation of extent of cell growth	BP	18	3	7.324e-05
GO:1990138	neuron projection extension	BP	19	3	8.669e-05
GO:0008361	regulation of cell size	BP	19	3	8.669e-05
GO:0060560	developmental growth involved in morphogenesis	BP	26	3	0.0002273
GO:0007409	axonogenesis	BP	65	4	0.0002274
GO:0048588	developmental cell growth	BP	27	3	0.0002549
GO:0061564	axon development	BP	70	4	0.0003027
GO:0048638	regulation of developmental growth	BP	29	3	0.0003163

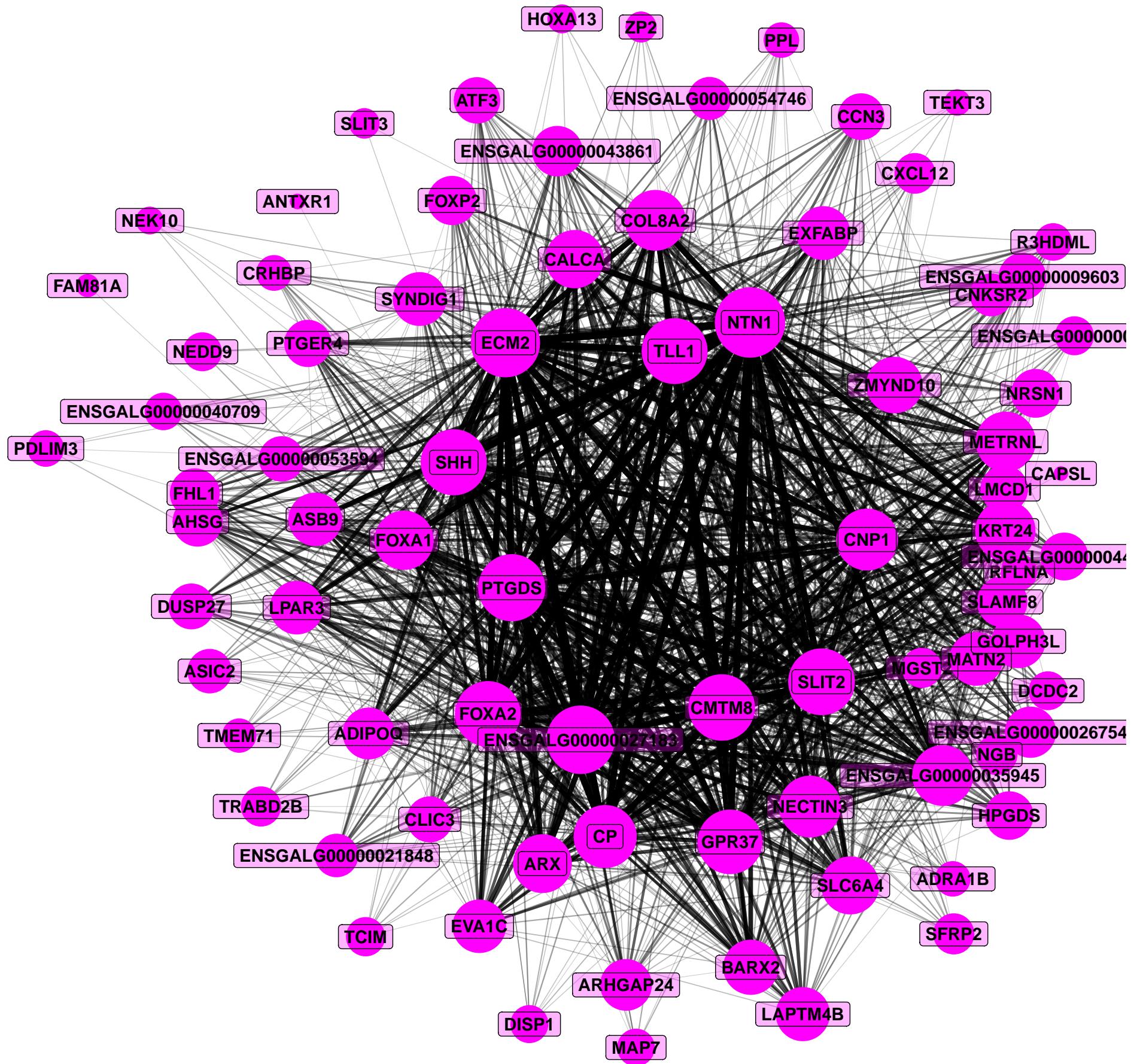
	Pathway	N	DE	P.DE
<i>path:gga04145</i>	Phagosome	121	7	1.326e-06
<i>path:gga04540</i>	Gap junction	78	4	0.0004581
<i>path:gga05132</i>	Salmonella infection	215	5	0.00312
<i>path:gga00190</i>	Oxidative phosphorylation	99	3	0.0108
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.0184
<i>path:gga04514</i>	Cell adhesion molecules	98	2	0.07554
<i>path:gga04142</i>	Lysosome	112	2	0.09488
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	2	0.105
<i>path:gga04340</i>	Hedgehog signaling pathway	47	1	0.1963
<i>path:gga04020</i>	Calcium signaling pathway	186	2	0.2129



1	SLC1A3	S1PR1	SLC6A11	PLPP3	EGF	MLC1	SOX9	ID4
2	ENSGALG00000054048	CST3	LPAR1	ENSGALG00000034735	LRIG1	CXCL14	SRPX	FAM181B
3	NKAIN4	RGMA	PSAT1	ENHO	FABP7	GPAM	CD38	DBI
4	NEBLv1	GPM6B	ELOVL2	GSTA2	ITGA6	ANXA5	FADS2	CXCR4
5	SALL1	ENSGALG00000038652	DDR1	IGSF11	GLUL	GRIK1	MPP6	LAMA1
6	C7H2ORF69	FGFR2	HS6ST2	PSAP	WLS	ENSGALG0000005024	SERPINE2	NR2F2
7	LFNG	VIM	RFTN2	SWAP70	TMOD3	PYGB	SMAD5	COMT
8	ADGRG1	RAB4A						

	Term	Ont	N	n	Adj. p-value
GO:0060173	limb development	BP	30	4	9.696e-06
GO:0048736	appendage development	BP	31	4	1.11e-05
GO:0007166	cell surface receptor signaling pathway	BP	257	7	0.0001564
GO:0007275	multicellular organism development	BP	558	10	0.000187
GO:0032501	multicellular organismal process	BP	684	11	0.0002218
GO:0007165	signal transduction	BP	464	9	0.0002267
GO:0071773	cellular response to BMP stimulus	BP	29	3	0.0003007
GO:0071772	response to BMP	BP	29	3	0.0003007
GO:0006541	glutamine metabolic process	BP	6	2	0.0003019
GO:0048856	anatomical structure development	BP	603	10	0.0003489

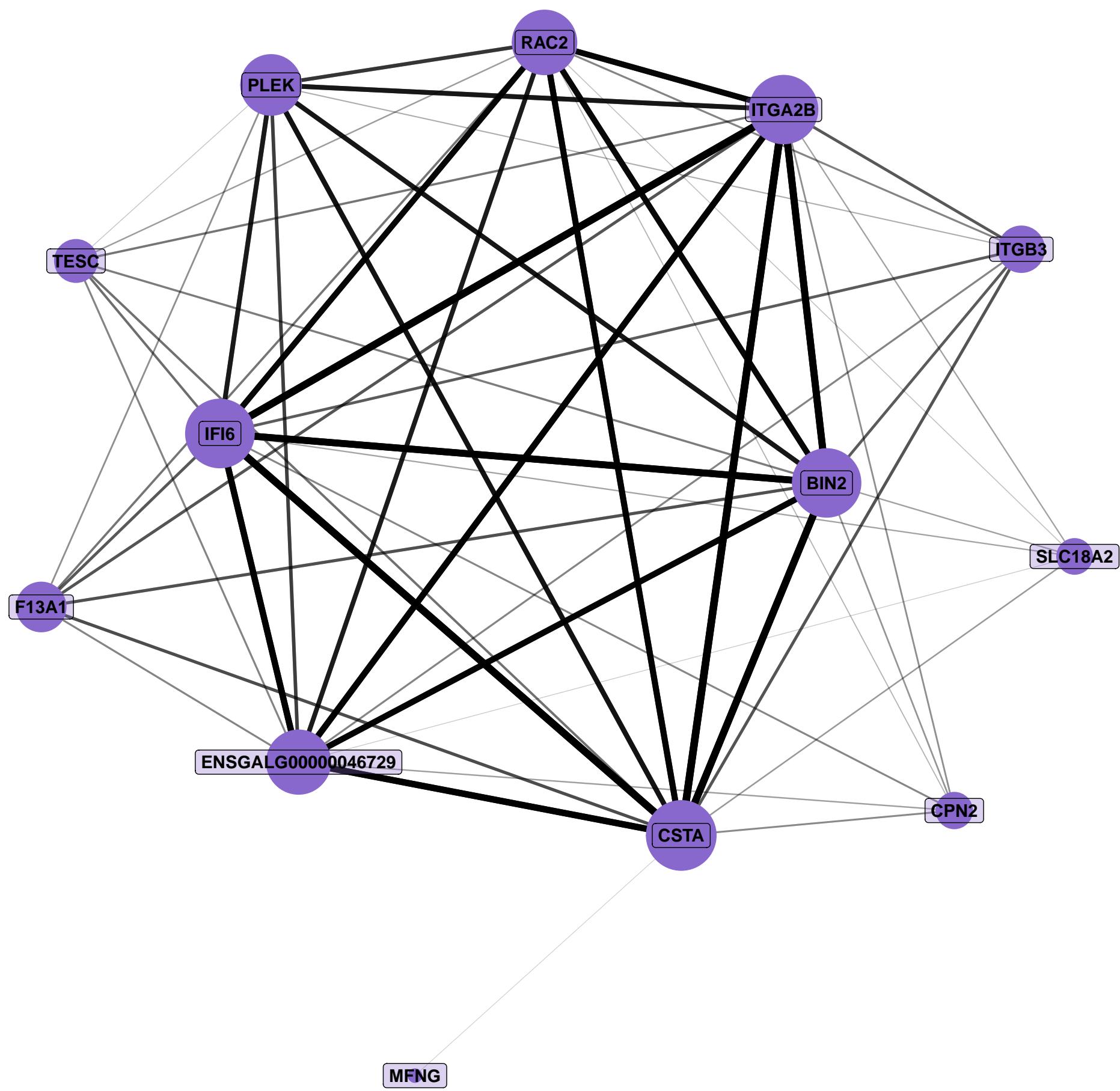
	Pathway	N	DE	P.DE
<i>path:gga04810</i>	Regulation of actin cytoskeleton	179	5	0.001298
<i>path:gga00910</i>	Nitrogen metabolism	13	2	0.001538
<i>path:gga03320</i>	PPAR signaling pathway	55	3	0.001985
<i>path:gga00220</i>	Arginine biosynthesis	16	2	0.002346
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	26	2	0.00617
<i>path:gga04350</i>	TGF–beta signaling pathway	84	3	0.00657
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	27	2	0.006644
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	27	2	0.006644
<i>path:gga01100</i>	Metabolic pathways	1218	12	0.007801
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	2	0.009253



1	ECM2	PTGDS	SHH	FOXA2	CNP1	CMTM8	NTN1	ENSGALG00000027183
2	SLIT2	TLL1	COL8A2	CALCA	GPR37	ENSGALG00000035945	CP	ARX
3	HPGDS	ZMYND10	KRT24	FOXA1	SLC6A4	FHL1	NECTIN3	ENSGALG00000043861
4	EXFABP	ADIPOQ	MATN2	METRNL	ENSGALG00000026754	ASB9	LAPTM4B	SYNDIG1
5	MGST2	ARHGAP24	SLAMF8	EVA1C	FOXP2	AHSG	LMCD1	GOLPH3L
6	LPAR3	R3HDML	SFRP2	NEDD9	BARX2	NRSN1	ENSGALG00000044002	CCN3
7	ENSGALG00000054746	PTGER4	CLIC3	DUSP27	CXCL12	TCIM	ENSGALG00000021848	PDLIM3
8	ENSGALG0000008309	DCDC2	ENSGALG00000053594	ASIC2	SLIT3	ATF3	CNKS2	ENSGALG0000009603
9	MAP7	FAM81A	TRABD2B	ENSGALG00000040709	NGB	NEK10	RFLNA	DISP1
10	CAPSL	CRHBP	HOXA13	TMEM71	PPL	TEKT3	ANTXR1	ZP2
11	ADRA1B							

	Term	Ont	N	n	Adj. p-value
GO:0003415	chondrocyte hypertrophy	BP	4	2	0.0002146
GO:0048588	developmental cell growth	BP	27	3	0.0005591
GO:0002063	chondrocyte development	BP	7	2	0.0007423
GO:0016049	cell growth	BP	49	3	0.003202
GO:0071398	cellular response to fatty acid	BP	1	1	0.006043
GO:0071399	cellular response to linoleic acid	BP	1	1	0.006043
GO:0055089	fatty acid homeostasis	BP	1	1	0.006043
GO:0033504	floor plate development	BP	1	1	0.006043
GO:0021508	floor plate formation	BP	1	1	0.006043
GO:0033505	floor plate morphogenesis	BP	1	1	0.006043

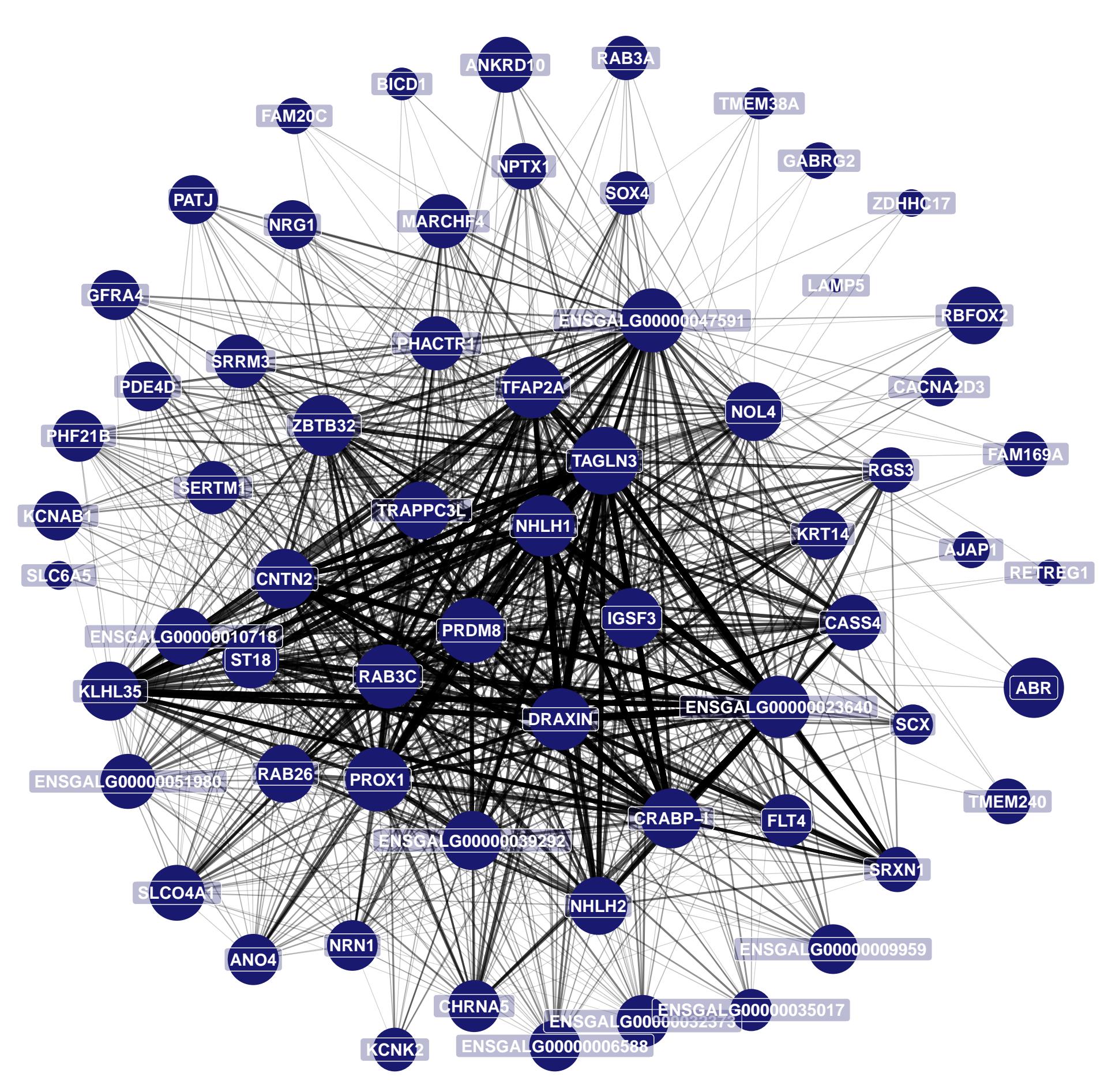
	Pathway	N	DE	P.DE
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	26	2	0.01067
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	27	2	0.01147
<i>path:gga00590</i>	Arachidonic acid metabolism	36	2	0.01989
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	5	0.02136
<i>path:gga04270</i>	Vascular smooth muscle contraction	101	3	0.02317
<i>path:gga00480</i>	Glutathione metabolism	47	2	0.0327
<i>path:gga04340</i>	Hedgehog signaling pathway	47	2	0.0327
<i>path:gga04672</i>	Intestinal immune network for IgA production	18	1	0.1034
<i>path:gga00860</i>	Porphyrin metabolism	19	1	0.1089
<i>path:gga04216</i>	Ferroptosis	34	1	0.1865



1	CSTA	ENSGALG00000046729	IFI6	ITGA2B	BIN2	RAC2	PLEK	TESC
2	CPN2	ITGB3	F13A1	SLC18A2	MFNG			

	Term	Ont	N	n	Adj. p-value
GO:0071800	podosome assembly	BP	1	1	0.00102
GO:0030854	positive regulation of granulocyte differentiation	BP	1	1	0.00102
GO:0097320	plasma membrane tubulation	BP	2	1	0.00204
GO:1902307	positive regulation of sodium ion transmembrane transport	BP	2	1	0.00204
GO:2000651	positive regulation of sodium ion transmembrane transporter activity	BP	2	1	0.00204
GO:0010765	positive regulation of sodium ion transport	BP	2	1	0.00204
GO:0032417	positive regulation of sodium:proton antiporter activity	BP	2	1	0.00204
GO:0030852	regulation of granulocyte differentiation	BP	2	1	0.00204
GO:1902305	regulation of sodium ion transmembrane transport	BP	2	1	0.00204
GO:2000649	regulation of sodium ion transmembrane transporter activity	BP	2	1	0.00204

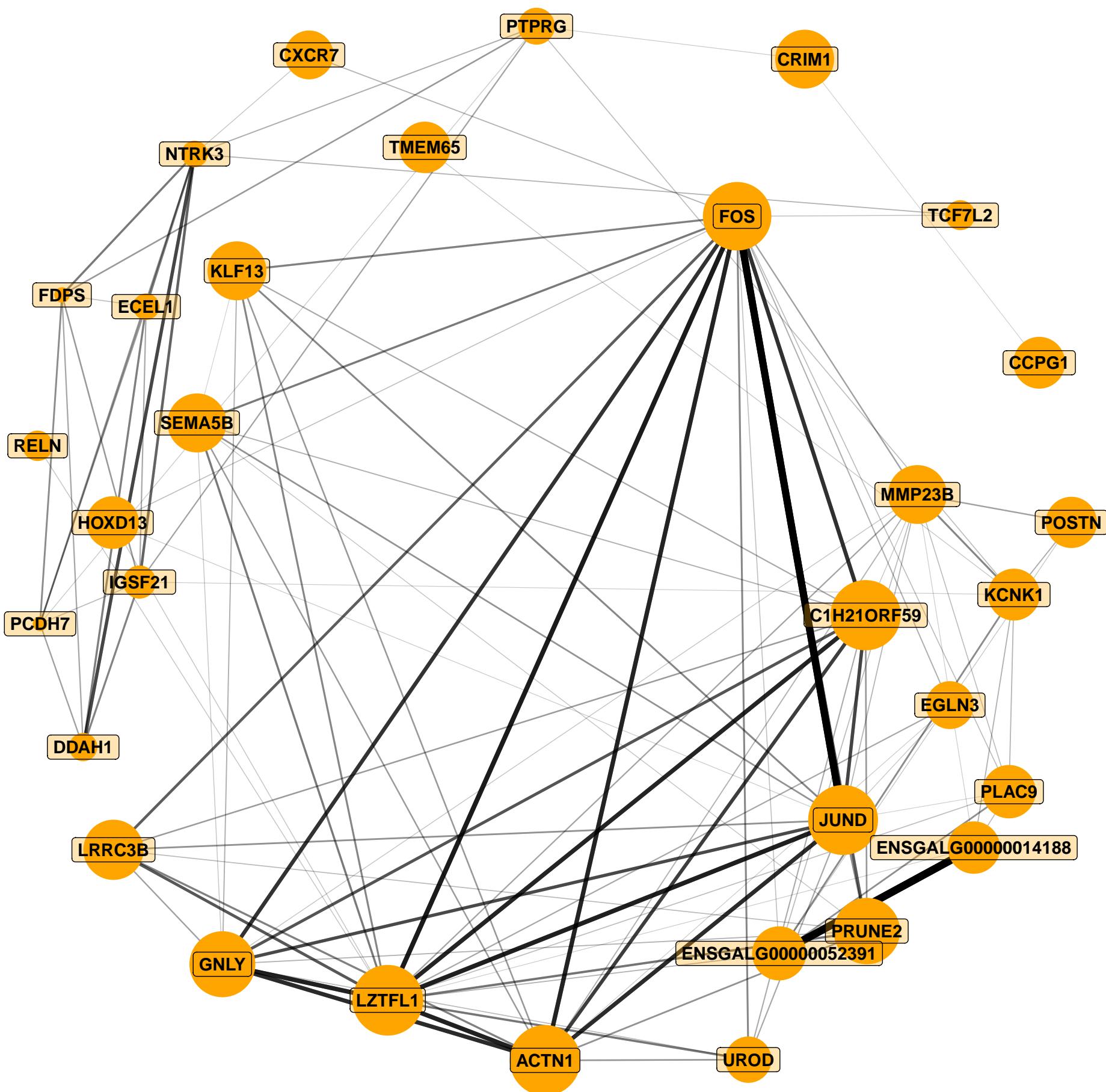
	Pathway	N	DE	P.DE
<i>path:gga04510</i>	Focal adhesion	166	3	0.0005642
<i>path:gga04810</i>	Regulation of actin cytoskeleton	179	3	0.0007029
<i>path:gga04512</i>	ECM–receptor interaction	65	2	0.001928
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.004075
<i>path:gga00514</i>	Other types of O–glycan biosynthesis	41	1	0.04105
<i>path:gga04370</i>	VEGF signaling pathway	50	1	0.04985
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.0518
<i>path:gga04520</i>	Adherens junction	69	1	0.06819
<i>path:gga04145</i>	Phagosome	121	1	0.1167
<i>path:gga05168</i>	Herpes simplex virus 1 infection	127	1	0.1222



1	TAGLN3	DRAKIN	PRDM8	NHLH1	PROX1	ENSGALG00000047591	RAB3C	TFAP2A
2	ENSGALG00000023640	CRABP-I	CNTN2	ZBTB32	ST18	IGSF3	TRAPPC3L	NOL4
3	GFRA4	ABR	ENSGALG00000010718	KLHL35	SERTM1	ENSGALG00000039292	NRN1	KRT14
4	PHACTR1	RBFOX2	NHLH2	RAB26	ENSGALG00000051980	SLCO4A1	ENSGALG00000032373	ANKRD10
5	CASS4	FLT4	KCNAB1	MARCHF4	NPTX1	SRRM3	RAB3A	ANO4
6	NRG1	PDE4D	ENSGALG00000009959	PHF21B	TMEM240	PATJ	CHRNA5	ENSGALG0000006588
7	FAM169A	CACNA2D3	KCNK2	SCX	ENSGALG00000035017	SOX4	RGS3	FAM20C
8	GABRG2	RETREG1	SRXN1	LAMP5	TMEM38A	AJAP1	ZDHHC17	BICD1
9	SLC6A5							

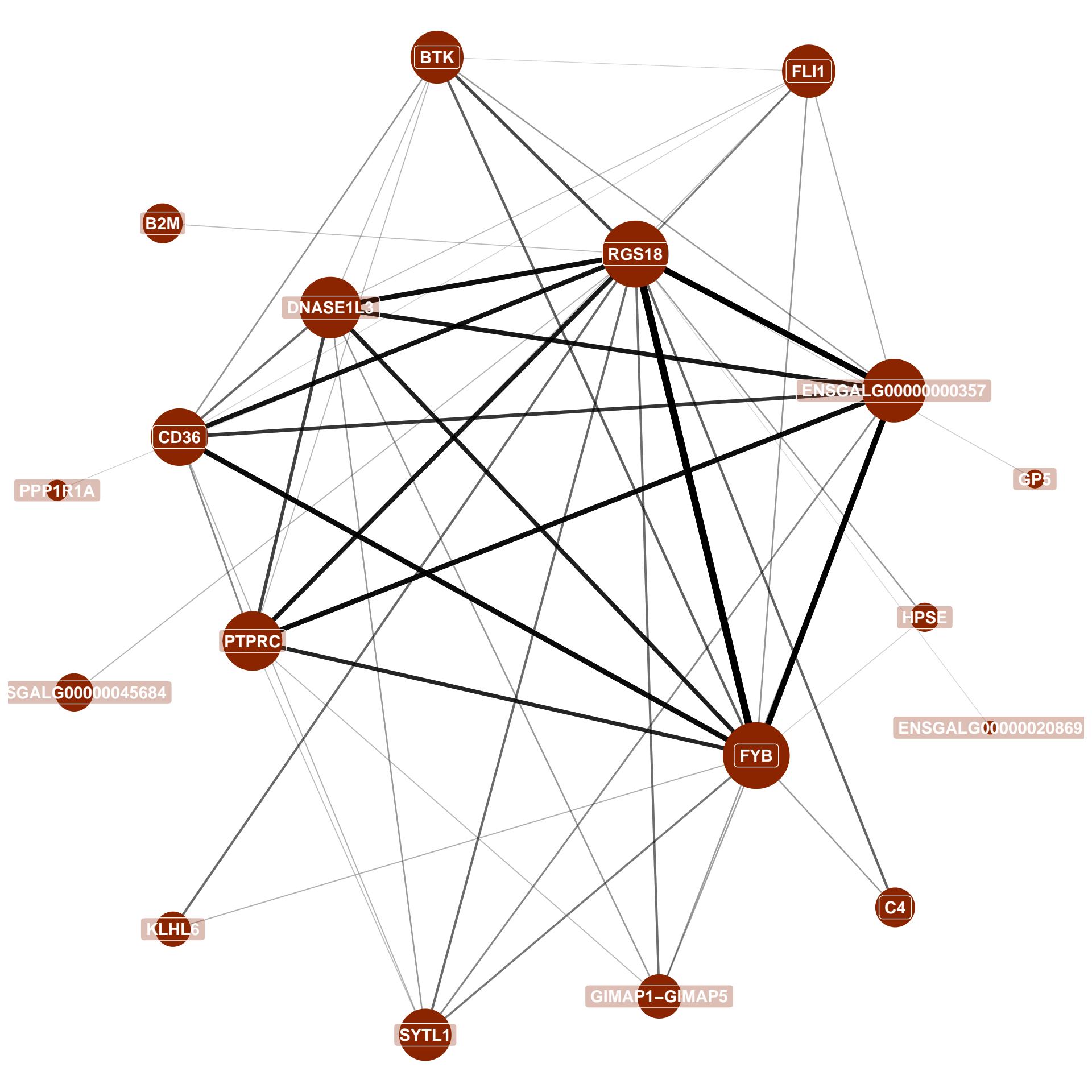
	Term	Ont	N	n	Adj. p-value
GO:0021516	dorsal spinal cord development	BP	6	2	0.0003231
GO:0034220	ion transmembrane transport	BP	100	4	0.001244
GO:0055085	transmembrane transport	BP	112	4	0.001889
GO:0098660	inorganic ion transmembrane transport	BP	56	3	0.002304
GO:0060078	regulation of postsynaptic membrane potential	BP	16	2	0.002508
GO:0021510	spinal cord development	BP	17	2	0.002834
GO:0071805	potassium ion transmembrane transport	BP	19	2	0.003541
GO:0006813	potassium ion transport	BP	21	2	0.004323
GO:0071420	cellular response to histamine	BP	1	1	0.004709
GO:0021528	commissural neuron differentiation in spinal cord	BP	1	1	0.004709

	Pathway	N	DE	P.DE
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	2	0.108
<i>path:gga03250</i>	Viral life cycle – HIV–1	48	1	0.2031
<i>path:gga04920</i>	Adipocytokine signaling pathway	59	1	0.2435
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.2435
<i>path:gga04010</i>	MAPK signaling pathway	231	2	0.2968
<i>path:gga04012</i>	ErbB signaling pathway	75	1	0.2988
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	78	1	0.3088
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	2	0.3523
<i>path:gga04514</i>	Cell adhesion molecules	98	1	0.3714
<i>path:gga00230</i>	Purine metabolism	110	1	0.4063



	Term	Ont	N	n	Adj. p-value
GO:0071277	cellular response to calcium ion	BP	4	2	3.206e-05
GO:0051592	response to calcium ion	BP	4	2	3.206e-05
GO:0071248	cellular response to metal ion	BP	9	2	0.000191
GO:0071241	cellular response to inorganic substance	BP	12	2	0.0003485
GO:0010038	response to metal ion	BP	12	2	0.0003485
GO:0031325	positive regulation of cellular metabolic process	BP	305	5	0.0006627
GO:0009893	positive regulation of metabolic process	BP	333	5	0.0009845
GO:0007519	skeletal muscle tissue development	BP	21	2	0.001094
GO:0060538	skeletal muscle organ development	BP	22	2	0.001202
GO:0048468	cell development	BP	209	4	0.001379

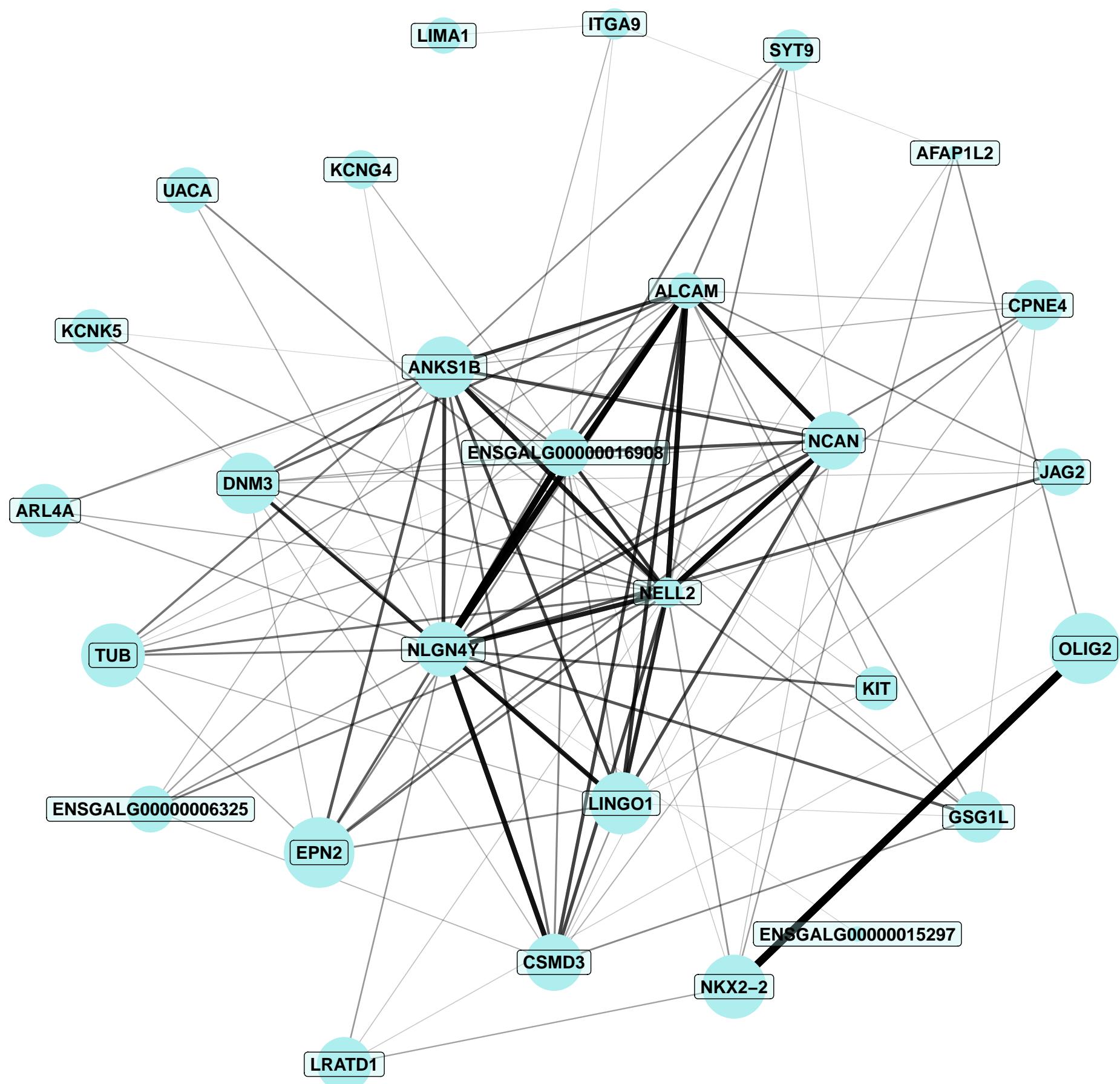
	Pathway	N	DE	P.DE
<i>path:gga04520</i>	Adherens junction	69	2	0.0114
<i>path:gga00860</i>	Porphyrin metabolism	19	1	0.04383
<i>path:gga00900</i>	Terpenoid backbone biosynthesis	19	1	0.04383
<i>path:gga04510</i>	Focal adhesion	166	2	0.05785
<i>path:gga05132</i>	Salmonella infection	215	2	0.09061
<i>path:gga04010</i>	MAPK signaling pathway	231	2	0.1023
<i>path:gga04512</i>	ECM–receptor interaction	65	1	0.1424
<i>path:gga04620</i>	Toll-like receptor signaling pathway	67	1	0.1464
<i>path:gga04916</i>	Melanogenesis	80	1	0.1723
<i>path:gga05164</i>	Influenza A	106	1	0.2219



1	RGS18	FYB	DNASE1L3	CD36	PTPRC	BTK	ENSGALG0000000357	FLI1
2	C4	KLHL6	SYTL1	ENSGALG00000045684	GIMAP1–GIMAP5	B2M	HPSE	GP5
3	PPP1R1A	ENSGALG00000020869						

	Term	Ont	N	n	Adj. p-value
GO:0002250	adaptive immune response	BP	22	2	0.0003365
GO:0019883	antigen processing and presentation of endogenous antigen	BP	1	1	0.001256
GO:0002483	antigen processing and presentation of endogenous peptide antigen	BP	1	1	0.001256
GO:0019885	antigen processing and presentation of endogenous peptide antigen via MHC class I	BP	1	1	0.001256
GO:0071281	cellular response to iron ion	BP	1	1	0.001256
GO:0030200	heparan sulfate proteoglycan catabolic process	BP	1	1	0.001256
GO:2000978	negative regulation of forebrain neuron differentiation	BP	1	1	0.001256
GO:1900121	negative regulation of receptor binding	BP	1	1	0.001256
GO:0090343	positive regulation of cell aging	BP	1	1	0.001256
GO:2000774	positive regulation of cellular senescence	BP	1	1	0.001256

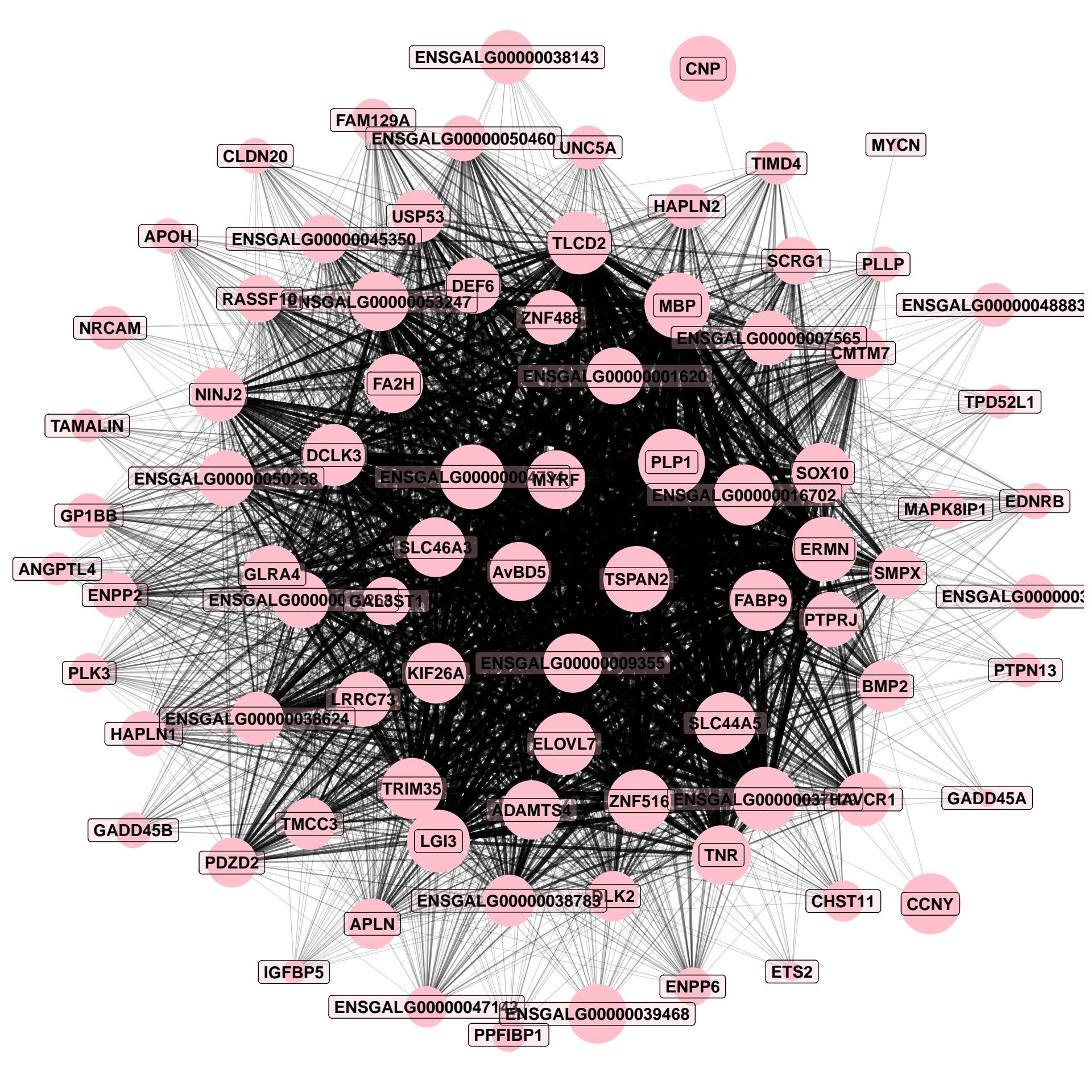
	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	65	2	0.002936
<i>path:gga00531</i>	Glycosaminoglycan degradation	15	1	0.01868
<i>path:gga03320</i>	PPAR signaling pathway	55	1	0.06691
<i>path:gga04920</i>	Adipocytokine signaling pathway	59	1	0.07161
<i>path:gga04514</i>	Cell adhesion molecules	98	1	0.1163
<i>path:gga04145</i>	Phagosome	121	1	0.1417
<i>path:gga05168</i>	Herpes simplex virus 1 infection	127	1	0.1482
<i>path:gga05132</i>	Salmonella infection	215	1	0.2385
<i>path:gga01100</i>	Metabolic pathways	1218	1	0.7998
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1



1	OLIG2	NKX2–2	EPN2	LRATD1	LINGO1	TUB	NCAN	NLGN4Y
2	DNM3	ANKS1B	NELL2	CSMD3	ENSGALG00000016908	ALCAM	JAG2	CPNE4
3	ARL4A	GSG1L	AFAP1L2	KIT	ITGA9	SYT9	UACA	LIMA1
4	KCNK5	ENSGALG0000006325	KCNG4	ENSGALG00000015297				

	Term	Ont	N	n	Adj. p-value
GO:0036018	cellular response to erythropoietin	BP	1	1	0.002119
GO:0036216	cellular response to stem cell factor stimulus	BP	1	1	0.002119
GO:0097067	cellular response to thyroid hormone stimulus	BP	1	1	0.002119
GO:0038162	erythropoietin-mediated signaling pathway	BP	1	1	0.002119
GO:0038093	Fc receptor signaling pathway	BP	1	1	0.002119
GO:0021780	glial cell fate specification	BP	1	1	0.002119
GO:0035701	hematopoietic stem cell migration	BP	1	1	0.002119
GO:0038109	Kit signaling pathway	BP	1	1	0.002119
GO:0097326	melanocyte adhesion	BP	1	1	0.002119
GO:0097324	melanocyte migration	BP	1	1	0.002119

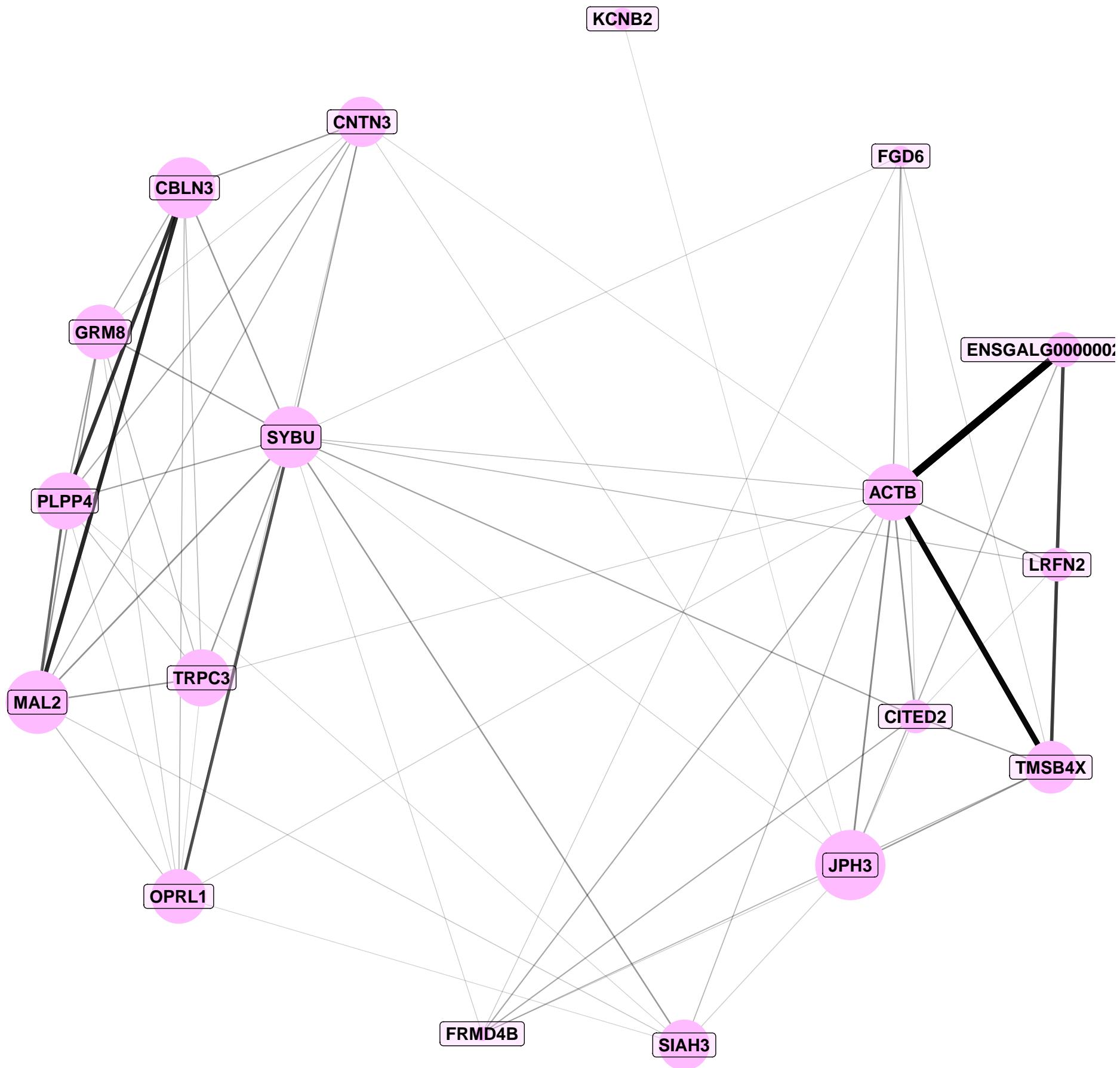
	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	98	3	0.001129
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.1046
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.1235
<i>path:gga04512</i>	ECM–receptor interaction	65	1	0.1291
<i>path:gga04916</i>	Melanogenesis	80	1	0.1565
<i>path:gga04068</i>	FoxO signaling pathway	105	1	0.2004
<i>path:gga04218</i>	Cellular senescence	131	1	0.2437
<i>path:gga04510</i>	Focal adhesion	166	1	0.2984
<i>path:gga04810</i>	Regulation of actin cytoskeleton	179	1	0.3178
<i>path:gga04144</i>	Endocytosis	218	1	0.3728



1	MBP	PLP1	ERMN	ENSGALG00000004734	TSPAN2	CNP	FABP9	ENSGALG00000037029
2	DCLK3	TLCD2	SOX10	LGI3	ZNF488	ELOVL7	FA2H	ZNF516
3	SLC44A5	ENSGALG00000053247	TNR	GLRA4	CCNY	KIF26A	ENSGALG00000009355	ENSGALG00000016702
4	ADAMTS4	PTPRJ	TRIM35	MYRF	SLC46A3	AvBD5	ENSGALG00000039468	DLK2
5	LRRC73	CMTM7	ENSGALG00000010268	USP53	BMP2	DEF6	TMCC3	ENSGALG00000001620
6	NINJ2	ENSGALG00000050258	GAL3ST1	HAVCR1	SMPX	ENSGALG00000007565	ENSGALG00000050460	ENSGALG00000038624
7	HAPLN1	APLN	ENSGALG00000038143	SCRG1	ENSGALG00000034050	ENSGALG00000048883	ENSGALG00000045350	NRCAM
8	FAM129A	GP1BB	UNC5A	PDZD2	RASSF10	ENSGALG00000038783	IGFBP5	CHST11
9	HAPLN2	ENSGALG00000047143	TIMD4	ANGPTL4	PTPN13	PPFIBP1	ENPP2	MAPK8IP1
10	PLK3	TPD52L1	GADD45B	ETS2	ENPP6	PLLP	EDNRB	CLDN20
11	GADD45A	APOH	TAMALIN	MYCN				

	Term	Ont	N	n	Adj. p-value
GO:0032291	axon ensheathment in central nervous system	BP	2	2	3.796e-05
GO:0022010	central nervous system myelination	BP	2	2	3.796e-05
GO:0014003	oligodendrocyte development	BP	2	2	3.796e-05
GO:0008366	axon ensheathment	BP	12	3	4.847e-05
GO:0007272	ensheathment of neurons	BP	12	3	4.847e-05
GO:0042552	myelination	BP	12	3	4.847e-05
GO:0021782	glial cell development	BP	5	2	0.000375
GO:0048469	cell maturation	BP	8	2	0.001037
GO:0048709	oligodendrocyte differentiation	BP	9	2	0.001328
GO:0061138	morphogenesis of a branching epithelium	BP	12	2	0.002406

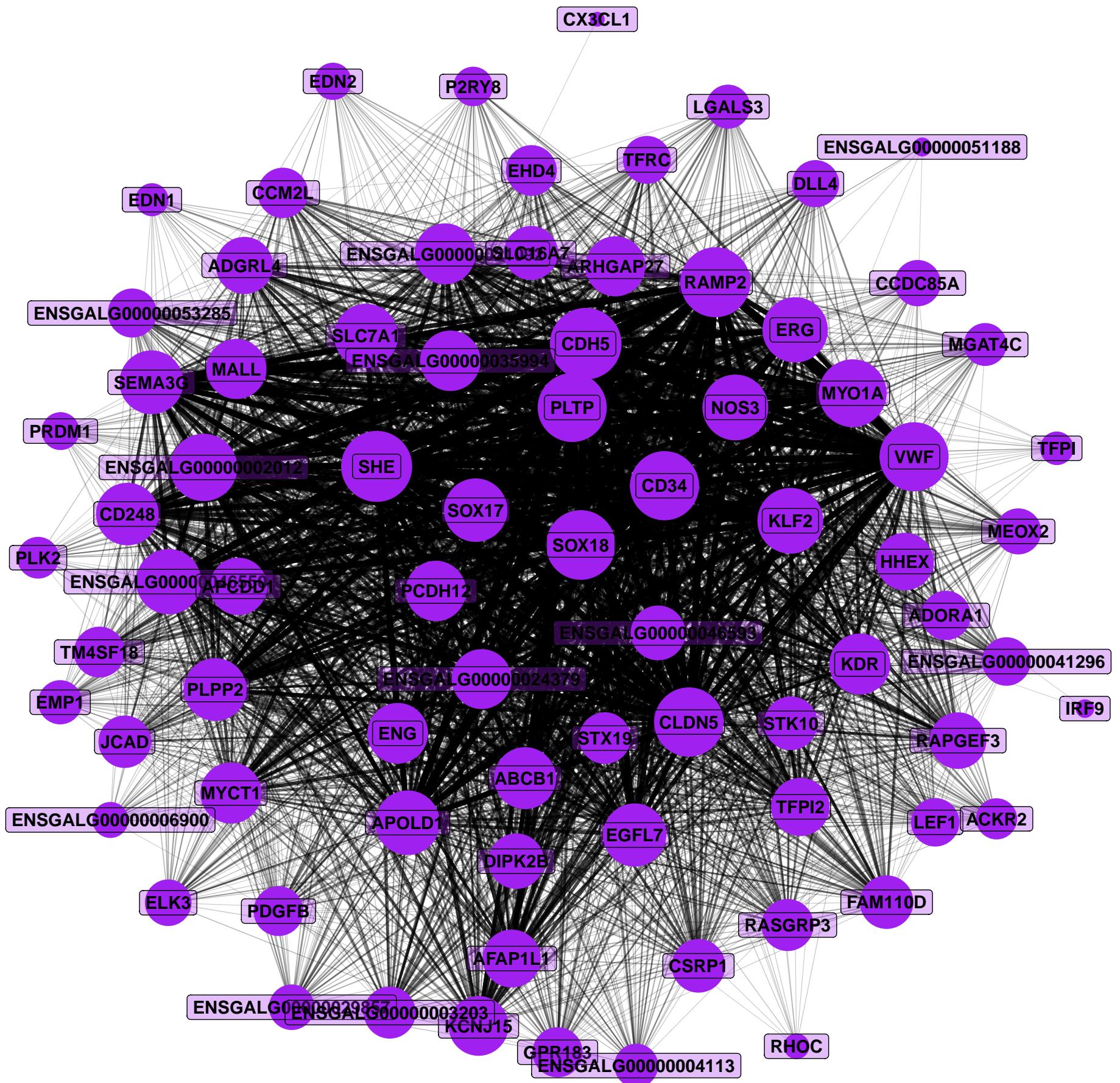
	Pathway	N	DE	P.DE
<i>path:gga00565</i>	Ether lipid metabolism	33	3	0.001095
<i>path:gga03264</i>	Virion – Flavivirus	3	1	0.01849
<i>path:gga04514</i>	Cell adhesion molecules	98	3	0.0229
<i>path:gga04068</i>	FoxO signaling pathway	105	3	0.02738
<i>path:gga04210</i>	Apoptosis	112	3	0.03228
<i>path:gga04530</i>	Tight junction	133	3	0.04956
<i>path:gga04115</i>	p53 signaling pathway	62	2	0.05652
<i>path:gga04512</i>	ECM–receptor interaction	65	2	0.06144
<i>path:gga03015</i>	mRNA surveillance pathway	72	2	0.07346
<i>path:gga00900</i>	Terpenoid backbone biosynthesis	19	1	0.1115



1	ACTB	TMSB4X	ENSGALG00000028749	JPH3	SYBU	OPRL1	TRPC3	SIAH3
2	CITED2	MAL2	FRMD4B	LRFN2	CNTN3	GRM8	CBLN3	FGD6
3	PLPP4	KCNB2						

	Term	Ont	N	n	Adj. p-value
GO:0098974	postsynaptic actin cytoskeleton organization	BP	3	2	5.022e-06
GO:0099188	postsynaptic cytoskeleton organization	BP	3	2	5.022e-06
GO:0140238	presynaptic endocytosis	BP	4	2	1.004e-05
GO:0048488	synaptic vesicle endocytosis	BP	4	2	1.004e-05
GO:0036465	synaptic vesicle recycling	BP	4	2	1.004e-05
GO:0099504	synaptic vesicle cycle	BP	11	2	9.15e-05
GO:0099003	vesicle-mediated transport in synapse	BP	12	2	0.0001097
GO:0099173	postsynapse organization	BP	16	2	0.0001989
GO:0050808	synapse organization	BP	36	2	0.001028
GO:0006897	endocytosis	BP	40	2	0.001268

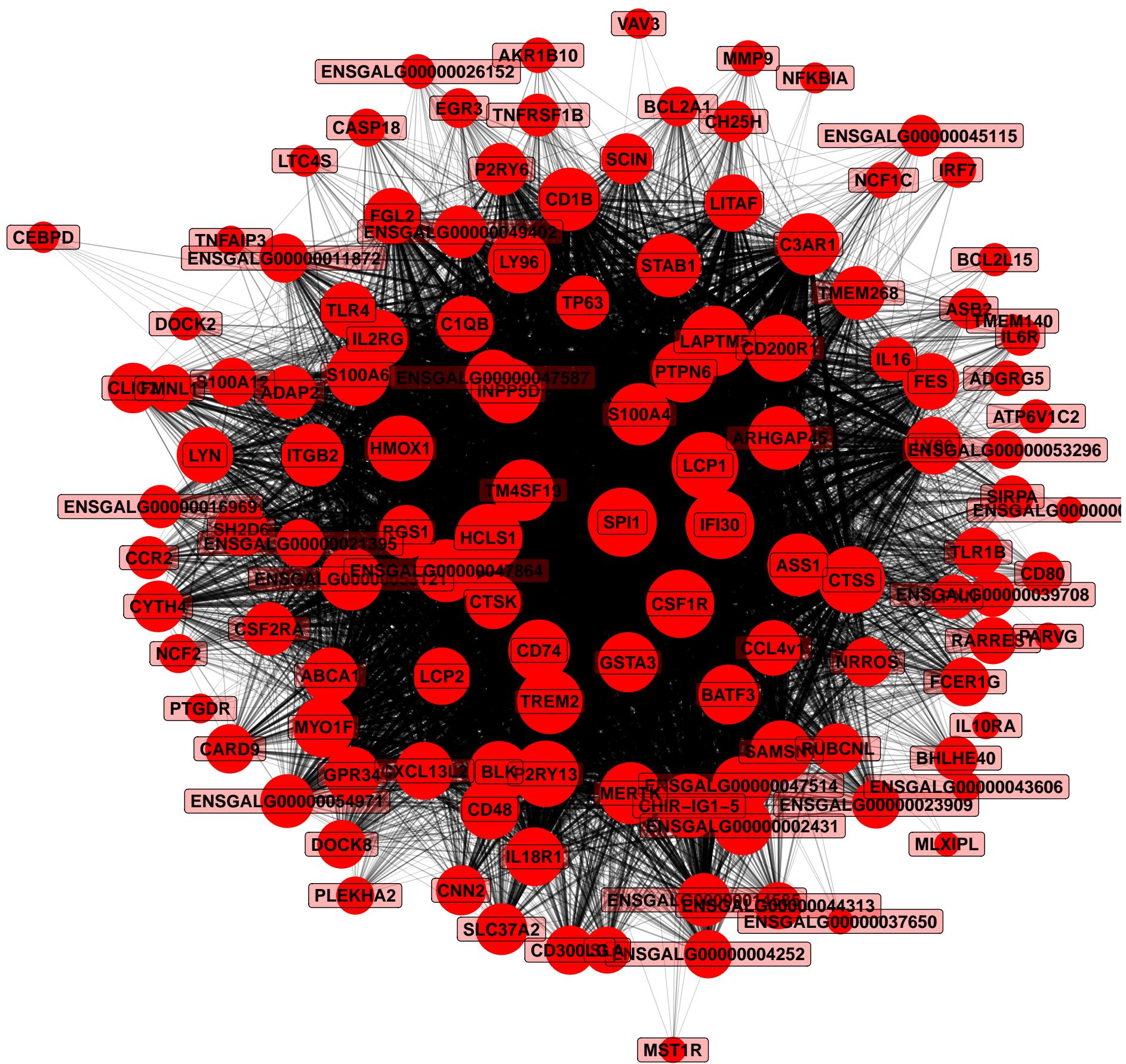
	Pathway	N	DE	P.DE
<i>path:gga04810</i>	Regulation of actin cytoskeleton	179	3	0.001604
<i>path:gga04520</i>	Adherens junction	69	2	0.003729
<i>path:gga05164</i>	Influenza A	106	2	0.008594
<i>path:gga04210</i>	Apoptosis	112	2	0.009555
<i>path:gga04145</i>	Phagosome	121	2	0.01108
<i>path:gga04530</i>	Tight junction	133	2	0.01327
<i>path:gga04510</i>	Focal adhesion	166	2	0.02018
<i>path:gga05132</i>	Salmonella infection	215	2	0.03263
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	2	0.04708
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.07962



1	CDH5	VWF	CD34	MYO1A	SHE	SOX18	NOS3	RAMP2
2	CLDN5	ENSGALG00000046550	ERG	KLF2	PCDH12	APOLD1	ENSGALG00000002012	SOX17
3	CD248	MYCT1	ENSGALG00000024379	EGFL7	SEMA3G	MALL	ENSGALG00000046593	ENSGALG00000021092
4	KDR	HHEX	CCM2L	PLTP	ARHGAP27	ABCB1	ENG	TFPI2
5	AFAP1L1	MEOX2	PDGFB	RASGRP3	GPR183	KCNJ15	PLPP2	FAM110D
6	LEF1	EHD4	APCDD1	TM4SF18	DIPK2B	ADGRL4	SLC7A1	ENSGALG0000003203
7	JCAD	ENSGALG00000041296	ENSGALG00000035994	RAPGEF3	P2RY8	DLL4	CSRP1	ADORA1
8	CCDC85A	ENSGALG00000053285	EDN2	STK10	SLC16A7	TFRC	ELK3	ENSGALG0000004113
9	ENSGALG00000029857	PLK2	PRDM1	LGALS3	EMP1	ENSGALG0000006900	MGAT4C	EDN1
10	TFPI	STX19	IRF9	ACKR2	CX3CL1	RHOC	ENSGALG00000051188	

	Term	Ont	N	n	Adj. p-value
GO:0043297	apical junction assembly	BP	7	2	0.0007232
GO:0035590	purinergic nucleotide receptor signaling pathway	BP	7	2	0.0007232
GO:0050728	negative regulation of inflammatory response	BP	8	2	0.0009605
GO:0050878	regulation of body fluid levels	BP	10	2	0.001532
GO:0031348	negative regulation of defense response	BP	11	2	0.001865
GO:0006875	cellular metal ion homeostasis	BP	43	3	0.00212
GO:0007043	cell–cell junction assembly	BP	12	2	0.002229
GO:0055065	metal ion homeostasis	BP	46	3	0.002575
GO:0002685	regulation of leukocyte migration	BP	13	2	0.002624
GO:0097435	supramolecular fiber organization	BP	102	4	0.003194

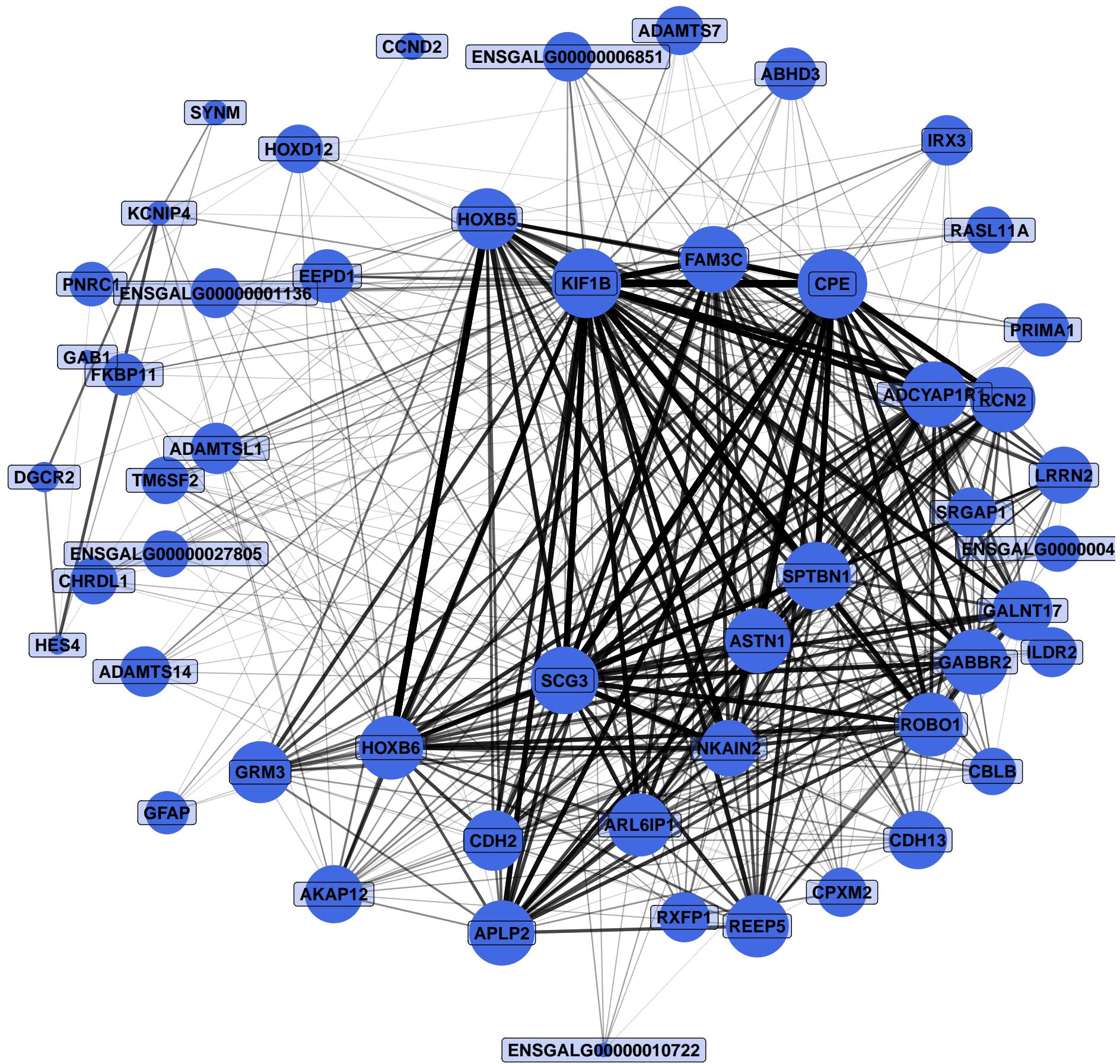
	Pathway	N	DE	P.DE
<i>path:gga04270</i>	Vascular smooth muscle contraction	101	4	0.003083
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	6	0.004778
<i>path:gga04510</i>	Focal adhesion	166	4	0.01725
<i>path:gga04514</i>	Cell adhesion molecules	98	3	0.0207
<i>path:gga04370</i>	VEGF signaling pathway	50	2	0.03577
<i>path:gga03320</i>	PPAR signaling pathway	55	2	0.04255
<i>path:gga04310</i>	Wnt signaling pathway	131	3	0.04339
<i>path:gga00120</i>	Primary bile acid biosynthesis	11	1	0.06371
<i>path:gga04916</i>	Melanogenesis	80	2	0.0824
<i>path:gga00220</i>	Arginine biosynthesis	16	1	0.09133



1	LAPTM5	CSF1R	SPI1	IFI30	LCP1	CTSS	ENSGALG00000047864	P2RY13
2	S100A4	CD200R1	HMOX1	MYO1F	ENSGALG00000053121	TREM2	PTPN6	BATF3
3	LY86	S100A6	ITGB2	HCLS1	ASS1	INPP5D	GSTA3	CXCL13L2
4	P2RY6	C1QB	S100A12	CHIR-IG1-5	CD48	ARHGAP45	ENSGALG00000014585	CD1B
5	BLK	RGS1	SAMSN1	ENSGALG00000047514	CCL4v1	TMEM268	STAB1	IL18R1
6	FES	IL2RG	LY96	C3AR1	ENSGALG0000002431	CSF2RA	ENSGALG00000047587	ENSGALG00000049402
7	TLR4	MERTK	CCR2	CD74	CTSK	SLA	RARRES1	TP63
8	CYTH4	LCP2	ENSGALG00000054971	GPR34	LITAF	ENSGALG00000011872	BCL2A1	ABCA1
9	NCF2	SH2D6	CLIC2	CARD9	FMNL1	SCIN	CNN2	ENSGALG00000021395
10	TM4SF19	LYN	FCER1G	TLR1B	FGL2	ENSGALG00000044313	CD300LG	CD80
11	IL6R	ENSGALG0000004252	DOCK8	BCL2L15	SLC37A2	NRROS	ENSGALG00000039708	ENSGALG00000053296
12	ASB2	CASP18	BHLHE40	PTGDR	NCF1C	TNFRSF1B	DOCK2	ADAP2
13	CH25H	ENSGALG00000016969	PLEKHA2	SIRPA	ADGRG5	IL16	ENSGALG00000045115	LPXN
14	RUBCNL	ENSGALG00000023909	MMP9	IL10RA	IRF7	CEBDP	PARVG	VAV3
15	AKR1B10	ENSGALG0000003313	ATP6V1C2	TMEM140	ENSGALG00000037650	LTC4S	EGR3	ENSGALG00000043606
16	ENSGALG00000026152	NFKBIA	MLXIPL	TNFAIP3	MST1R			

	Term	Ont	N	n	Adj. p-value
GO:0006952	defense response	BP	88	5	0.001432
GO:0006805	xenobiotic metabolic process	BP	7	2	0.001791
GO:0071466	cellular response to xenobiotic stimulus	BP	8	2	0.002373
GO:0009410	response to xenobiotic stimulus	BP	8	2	0.002373
GO:0098542	defense response to other organism	BP	60	4	0.00243
GO:0009607	response to biotic stimulus	BP	75	4	0.005437
GO:0043207	response to external biotic stimulus	BP	75	4	0.005437
GO:0051707	response to other organism	BP	75	4	0.005437
GO:0044419	biological process involved in interspecies interaction between organisms	BP	86	4	0.008779
GO:0007202	activation of phospholipase C activity	BP	1	1	0.009418

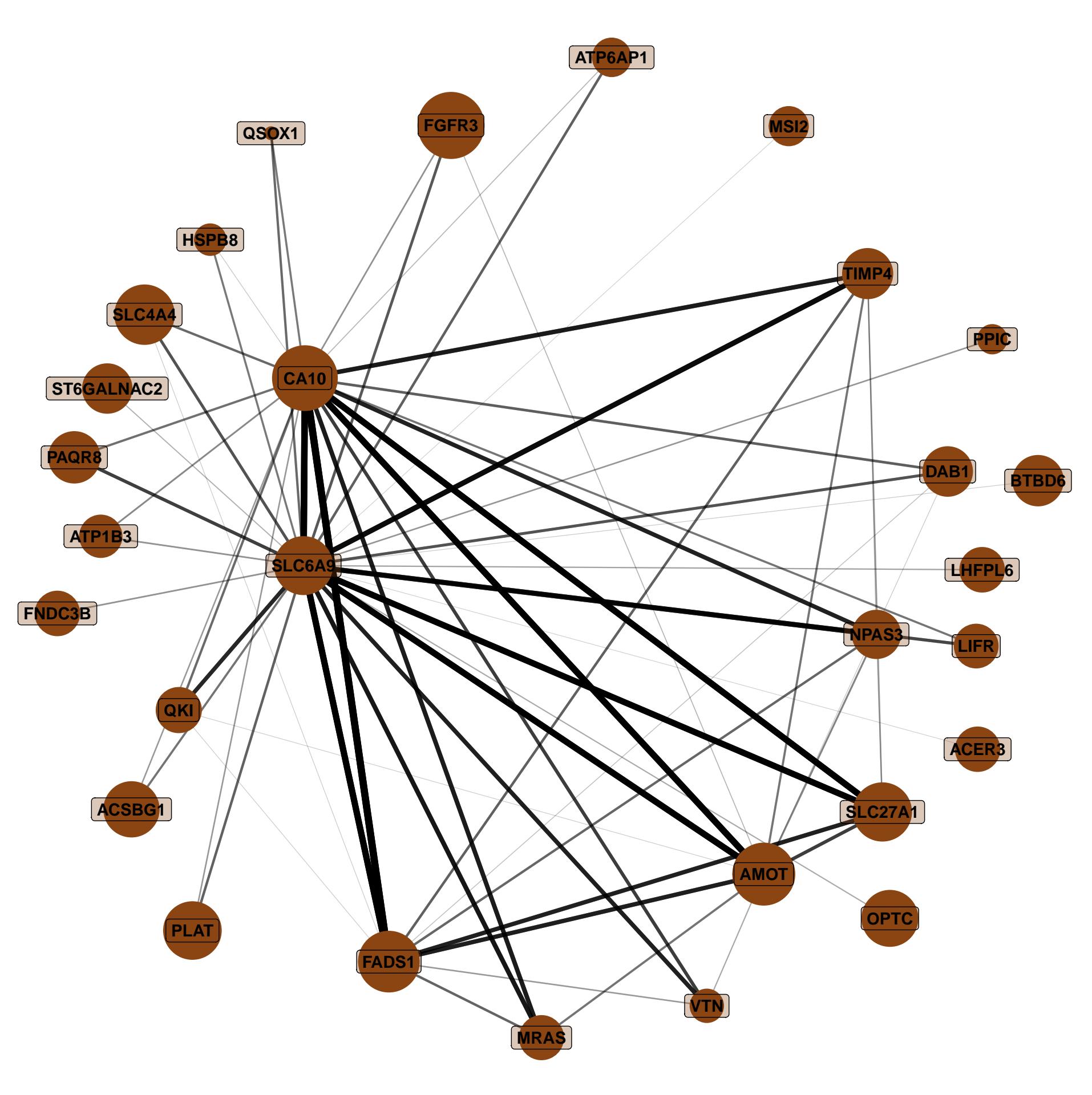
	Pathway	N	DE	P.DE
<i>path:gga04620</i>	Toll-like receptor signaling pathway	67	9	1.164e-08
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	136	11	5.881e-08
<i>path:gga04621</i>	NOD–like receptor signaling pathway	111	7	8.337e-05
<i>path:gga04145</i>	Phagosome	121	7	0.0001434
<i>path:gga04623</i>	Cytosolic DNA–sensing pathway	41	4	0.0005788
<i>path:gga04210</i>	Apoptosis	112	6	0.0006535
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	78	5	0.0008315
<i>path:gga04142</i>	Lysosome	112	5	0.004103
<i>path:gga05168</i>	Herpes simplex virus 1 infection	127	5	0.006958
<i>path:gga04622</i>	RIG-I–like receptor signaling pathway	44	3	0.008146



1	CPE	KIF1B	SCG3	SPTBN1	HOXB6	APLP2	FAM3C	CDH2
2	ASTN1	GRM3	HOXB5	ADCYAP1R1	ROBO1	GABBR2	NKAIN2	RCN2
3	ARL6IP1	GALNT17	AKAP12	REEP5	LRRN2	CDH13	SRGAP1	ENSGALG00000001136
4	ADAMTSL1	EEPD1	HOXD12	PRIMA1	IRX3	ABHD3	CBLB	ADAMTS7
5	CPXM2	RXFP1	ADAMTS14	ILDR2	ENSGALG0000006851	RASL11A	ENSGALG00000027805	TM6SF2
6	ENSGALG0000041014	PNRC1	FKBP11	GFAP	CHRDL1	DGCR2	KCNIP4	CCND2
7	HES4	ENSGALG0000010722	SYNM	GAB1				

	Term	Ont	N	n	Adj. p-value
GO:0051668	localization within membrane	BP	6	2	0.0002064
GO:0016339	calcium–dependent cell–cell adhesion via plasma membrane cell adhesion molecules	BP	7	2	0.0002883
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	BP	21	2	0.002788
GO:0048532	anatomical structure arrangement	BP	1	1	0.003767
GO:0061562	cranial ganglion structural organization	BP	1	1	0.003767
GO:0021604	cranial nerve structural organization	BP	1	1	0.003767
GO:0061555	ganglion structural organization	BP	1	1	0.003767
GO:0043616	keratinocyte proliferation	BP	1	1	0.003767
GO:0090497	mesenchymal cell migration	BP	1	1	0.003767
GO:0097118	neuroligin clustering involved in postsynaptic membrane assembly	BP	1	1	0.003767

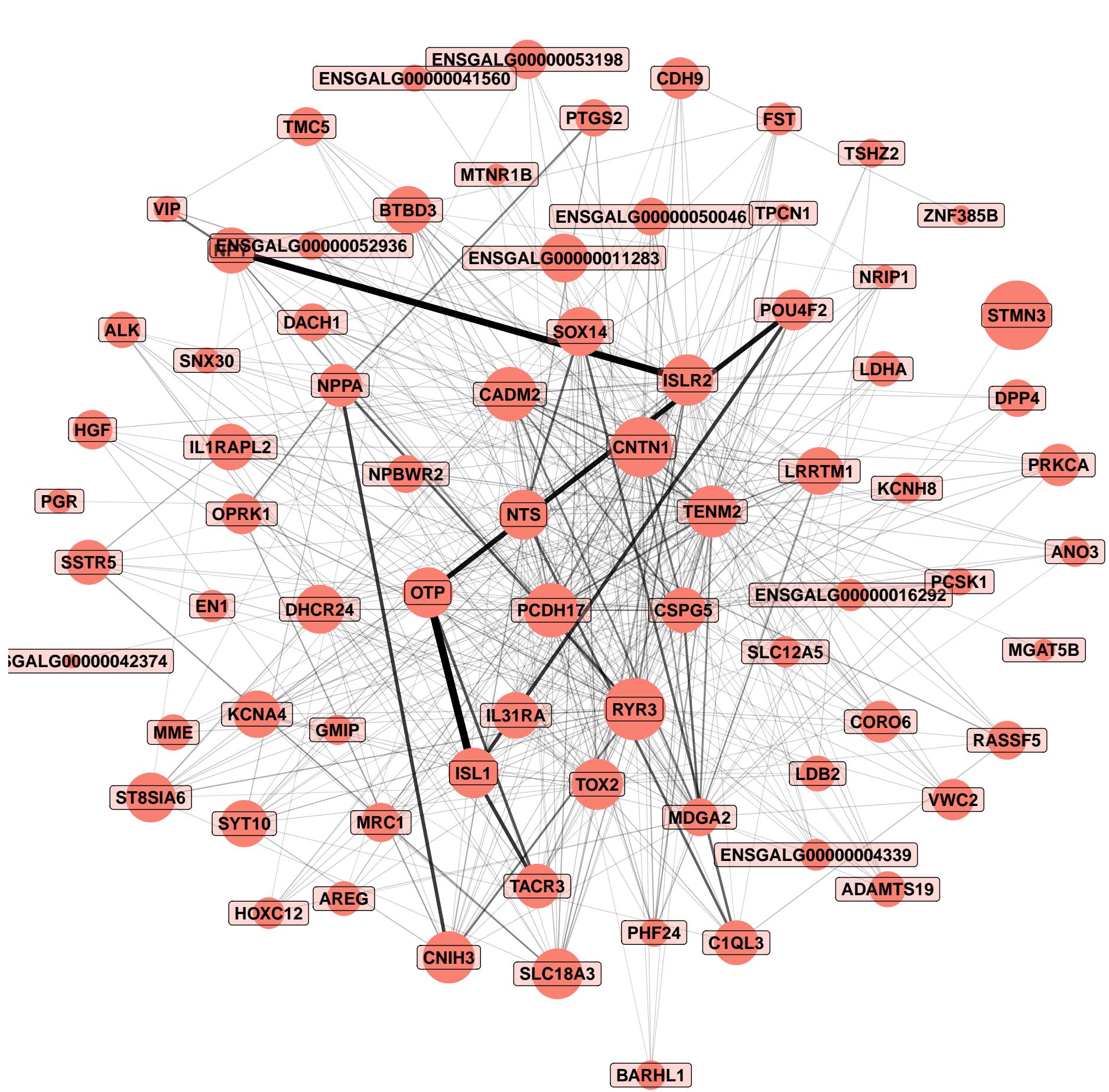
	Pathway	N	DE	P.DE
<i>path:gga04330</i>	Notch signaling pathway	52	2	0.01635
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	4	0.01696
<i>path:gga04012</i>	ErbB signaling pathway	75	2	0.03239
<i>path:gga00512</i>	Mucin type O–glycan biosynthesis	29	1	0.1038
<i>path:gga00514</i>	Other types of O–glycan biosynthesis	41	1	0.1436
<i>path:gga04340</i>	Hedgehog signaling pathway	47	1	0.1628
<i>path:gga03460</i>	Fanconi anemia pathway	48	1	0.166
<i>path:gga04115</i>	p53 signaling pathway	62	1	0.2091
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	78	1	0.2557
<i>path:gga04514</i>	Cell adhesion molecules	98	1	0.3102



1	FGFR3	CA10	OPTC	AMOT	PLAT	SLC4A4	SLC27A1	SLC6A9
2	ACSBG1	FADS1	TIMP4	DAB1	MRAS	LHFPL6	VTN	PAQR8
3	NPAS3	BTBD6	QSOX1	FNDC3B	ACER3	QKI	ATP1B3	LIFR
4	ST6GALNAC2	HSPB8	ATP6AP1	MSI2	PPIC			

	Term	Ont	N	n	Adj. p-value
GO:1902178	fibroblast growth factor receptor apoptotic signaling pathway	BP	1	1	0.002276
GO:0006883	cellular sodium ion homeostasis	BP	2	1	0.004547
GO:1990743	protein sialylation	BP	2	1	0.004547
GO:0036376	sodium ion export across plasma membrane	BP	2	1	0.004547
GO:0055078	sodium ion homeostasis	BP	2	1	0.004547
GO:0051345	positive regulation of hydrolase activity	BP	53	2	0.006414
GO:0030007	cellular potassium ion homeostasis	BP	3	1	0.006813
GO:0010248	establishment or maintenance of transmembrane electrochemical gradient	BP	3	1	0.006813
GO:0140115	export across plasma membrane	BP	3	1	0.006813
GO:0016242	negative regulation of macroautophagy	BP	3	1	0.006813

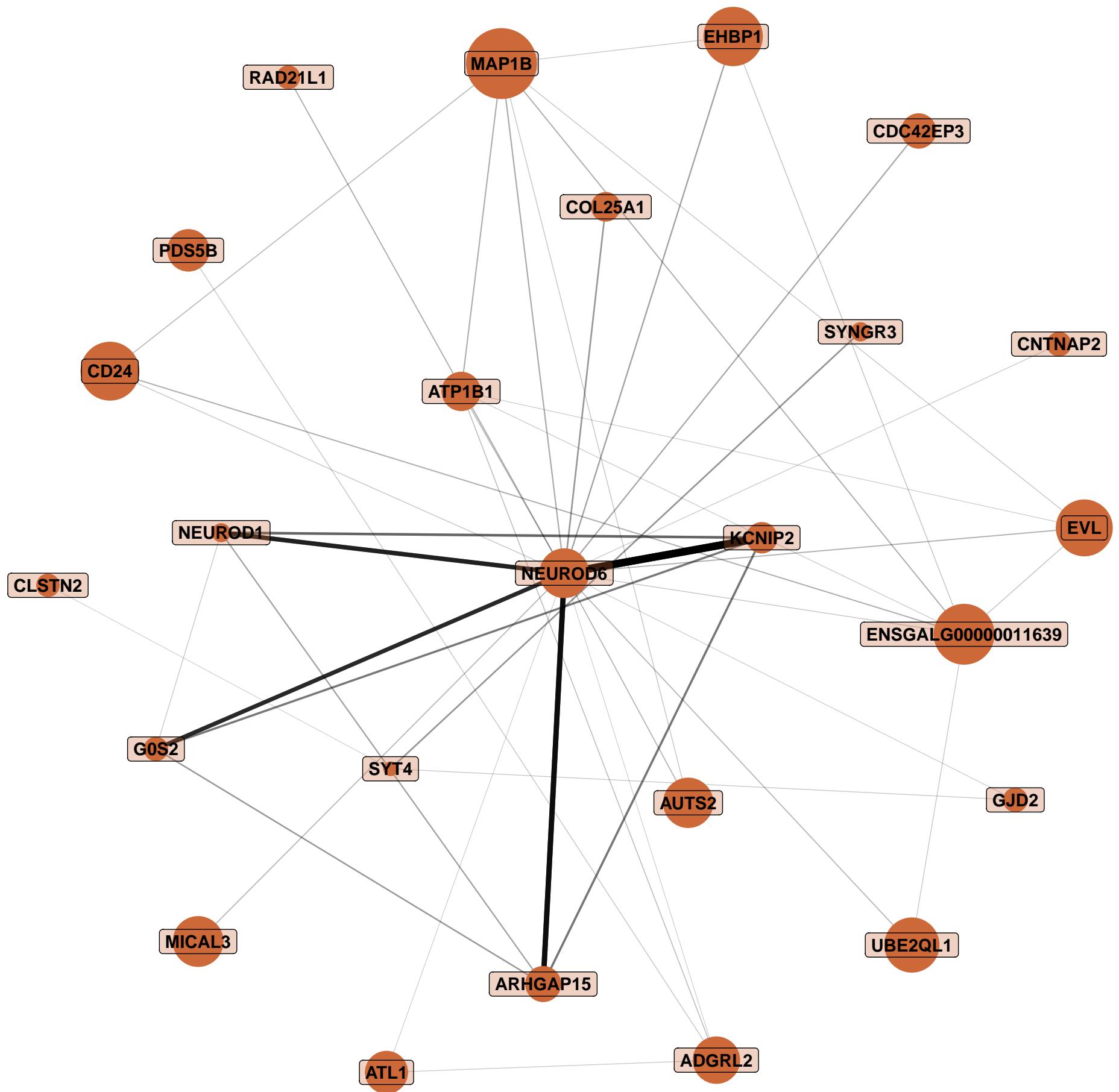
	Pathway	N	DE	P.DE
<i>path:gga01212</i>	Fatty acid metabolism	50	2	0.005726
<i>path:gga03320</i>	PPAR signaling pathway	55	2	0.006893
<i>path:gga04371</i>	Apelin signaling pathway	109	2	0.02533
<i>path:gga00061</i>	Fatty acid biosynthesis	16	1	0.03582
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	27	1	0.05973
<i>path:gga04810</i>	Regulation of actin cytoskeleton	179	2	0.06221
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	1	0.06401
<i>path:gga00071</i>	Fatty acid degradation	30	1	0.06614
<i>path:gga04010</i>	MAPK signaling pathway	231	2	0.09656
<i>path:gga00600</i>	Sphingolipid metabolism	46	1	0.09967



1	STMN3	RYR3	ISLR2	CNTN1	NPY	SLC18A3	CADM2	TENM2
2	PCDH17	CSPG5	ST8SIA6	SSTR5	LRRTM1	ENSGALG00000011283	OTP	CNIH3
3	DHCR24	CDH9	PRKCA	BTBD3	VWC2	KCNA4	IL1RAPL2	MDGA2
4	FST	SYT10	TOX2	ENSGALG00000050046	SLC12A5	ENSGALG00000053198	LDHA	ALK
5	IL31RA	NTS	DACH1	SNX30	ISL1	PHF24	SOX14	HGF
6	ADAMTS19	CORO6	ENSGALG00000016292	POU4F2	NPPA	ANO3	TMC5	C1QL3
7	RASSF5	GMIP	BARHL1	MME	DPP4	PCSK1	MRC1	EN1
8	MTNR1B	OPRK1	HOXC12	NPBWR2	AREG	ENSGALG00000052936	NRIP1	ENSGALG00000041560
9	KCNH8	TACR3	ZNF385B	ENSGALG0000004339	PTGS2	PGR	LDB2	TPCN1
10	TSHZ2	MGAT5B	ENSGALG00000042374	VIP				

	Term	Ont	N	n	Adj. p-value
GO:0007399	nervous system development	BP	252	10	1.226e–06
GO:0048699	generation of neurons	BP	175	8	5.493e–06
GO:0022008	neurogenesis	BP	178	8	6.227e–06
GO:0008217	regulation of blood pressure	BP	8	3	9.101e–06
GO:0030030	cell projection organization	BP	139	7	1.174e–05
GO:0008015	blood circulation	BP	27	4	1.41e–05
GO:0003013	circulatory system process	BP	27	4	1.41e–05
GO:0030182	neuron differentiation	BP	160	7	2.925e–05
GO:0031175	neuron projection development	BP	109	6	3.112e–05
GO:0048666	neuron development	BP	122	6	5.868e–05

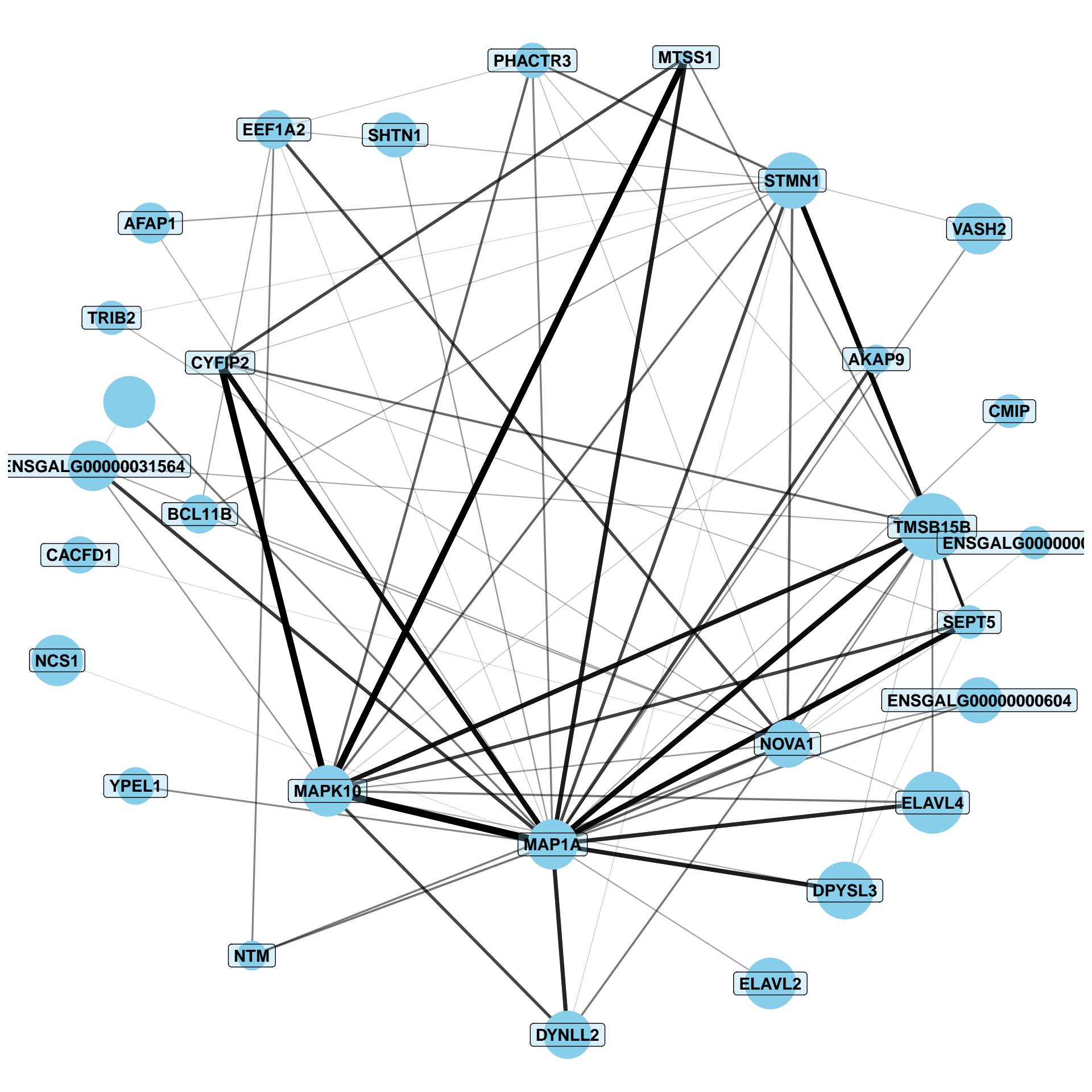
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	8	0.0001024
<i>path:gga04020</i>	Calcium signaling pathway	186	5	0.003755
<i>path:gga04370</i>	VEGF signaling pathway	50	2	0.03158
<i>path:gga04012</i>	ErbB signaling pathway	75	2	0.06549
<i>path:gga00100</i>	Steroid biosynthesis	15	1	0.08044
<i>path:gga04270</i>	Vascular smooth muscle contraction	101	2	0.1088
<i>path:gga00230</i>	Purine metabolism	110	2	0.1252
<i>path:gga04010</i>	MAPK signaling pathway	231	3	0.138
<i>path:gga00640</i>	Propanoate metabolism	28	1	0.145
<i>path:gga00620</i>	Pyruvate metabolism	32	1	0.1639



1	MAP1B	CD24	EVL	ATP1B1	EHBP1	ENSGALG00000011639	NEUROD6	AUTS2
2	UBE2QL1	MICAL3	ADGRL2	KCNIP2	ARHGAP15	ATL1	SYT4	PDS5B
3	G0S2	CDC42EP3	COL25A1	SYNGR3	RAD21L1	GJD2	CLSTN2	CNTNAP2
4	NEUROD1							

	Term	Ont	N	n	Adj. p-value
GO:0042479	positive regulation of eye photoreceptor cell development	BP	1	1	0.001727
GO:0046534	positive regulation of photoreceptor cell differentiation	BP	1	1	0.001727
GO:0042478	regulation of eye photoreceptor cell development	BP	1	1	0.001727
GO:0006883	cellular sodium ion homeostasis	BP	2	1	0.00345
GO:0046532	regulation of photoreceptor cell differentiation	BP	2	1	0.00345
GO:0036376	sodium ion export across plasma membrane	BP	2	1	0.00345
GO:0055078	sodium ion homeostasis	BP	2	1	0.00345
GO:0051345	positive regulation of hydrolase activity	BP	53	2	0.003718
GO:0030007	cellular potassium ion homeostasis	BP	3	1	0.005171
GO:0010248	establishment or maintenance of transmembrane electrochemical gradient	BP	3	1	0.005171

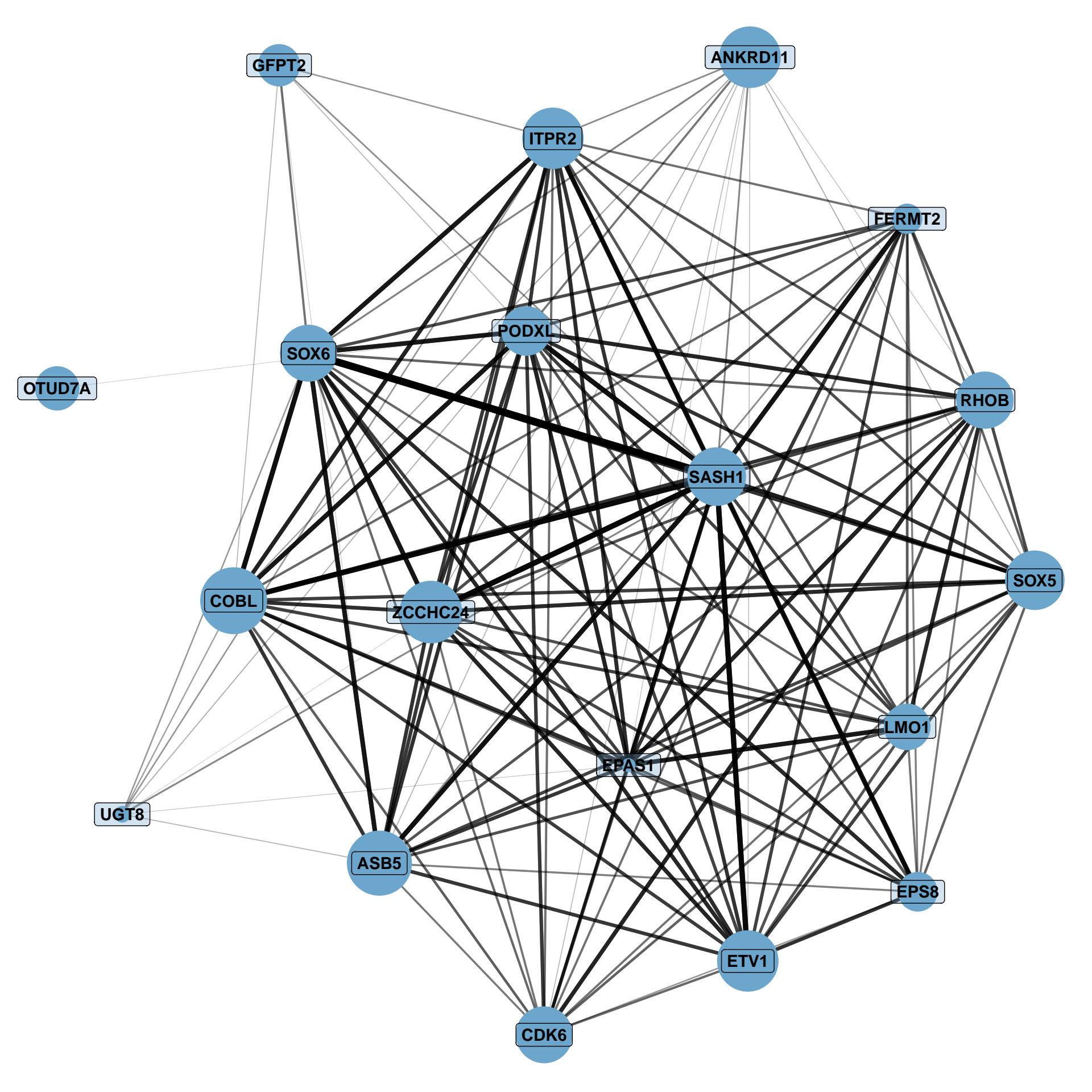
	Pathway	N	DE	P.DE
<i>path:gga03250</i>	Viral life cycle – HIV–1	48	1	0.07974
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.09714
<i>path:gga04540</i>	Gap junction	78	1	0.1265
<i>path:gga04514</i>	Cell adhesion molecules	98	1	0.1563
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	1	0.1867
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1
<i>path:gga00232</i>	Caffeine 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



1	ELAVL4	TMSB15B	DPYSL3	MAP1A	SEPT5	STMN1	MAPK10	CYFIP2
2	BCL11B	DYNLL2	NOVA1	NCS1	ENSGALG00000031564	ELAVL2	NA	VASH2
3	EEF1A2	MTSS1	NTM	PHACTR3	AFAP1	TRIB2	SHTN1	CACFD1
4	YPEL1	ENSGALG0000000604	CMIP	ENSGALG0000000816	AKAP9			

	Term	Ont	N	n	Adj. p-value
GO:0018109	peptidyl–arginine phosphorylation	BP	1	1	0.002197
GO:0018195	peptidyl–arginine modification	BP	2	1	0.00439
GO:0051493	regulation of cytoskeleton organization	BP	53	2	0.005988
GO:0051128	regulation of cellular component organization	BP	200	3	0.009349
GO:0007019	microtubule depolymerization	BP	6	1	0.01312
GO:0033043	regulation of organelle organization	BP	94	2	0.01797
GO:0031175	neuron projection development	BP	109	2	0.02371
GO:0031110	regulation of microtubule polymerization or depolymerization	BP	11	1	0.02392
GO:0048666	neuron development	BP	122	2	0.02922
GO:0031109	microtubule polymerization or depolymerization	BP	14	1	0.03034

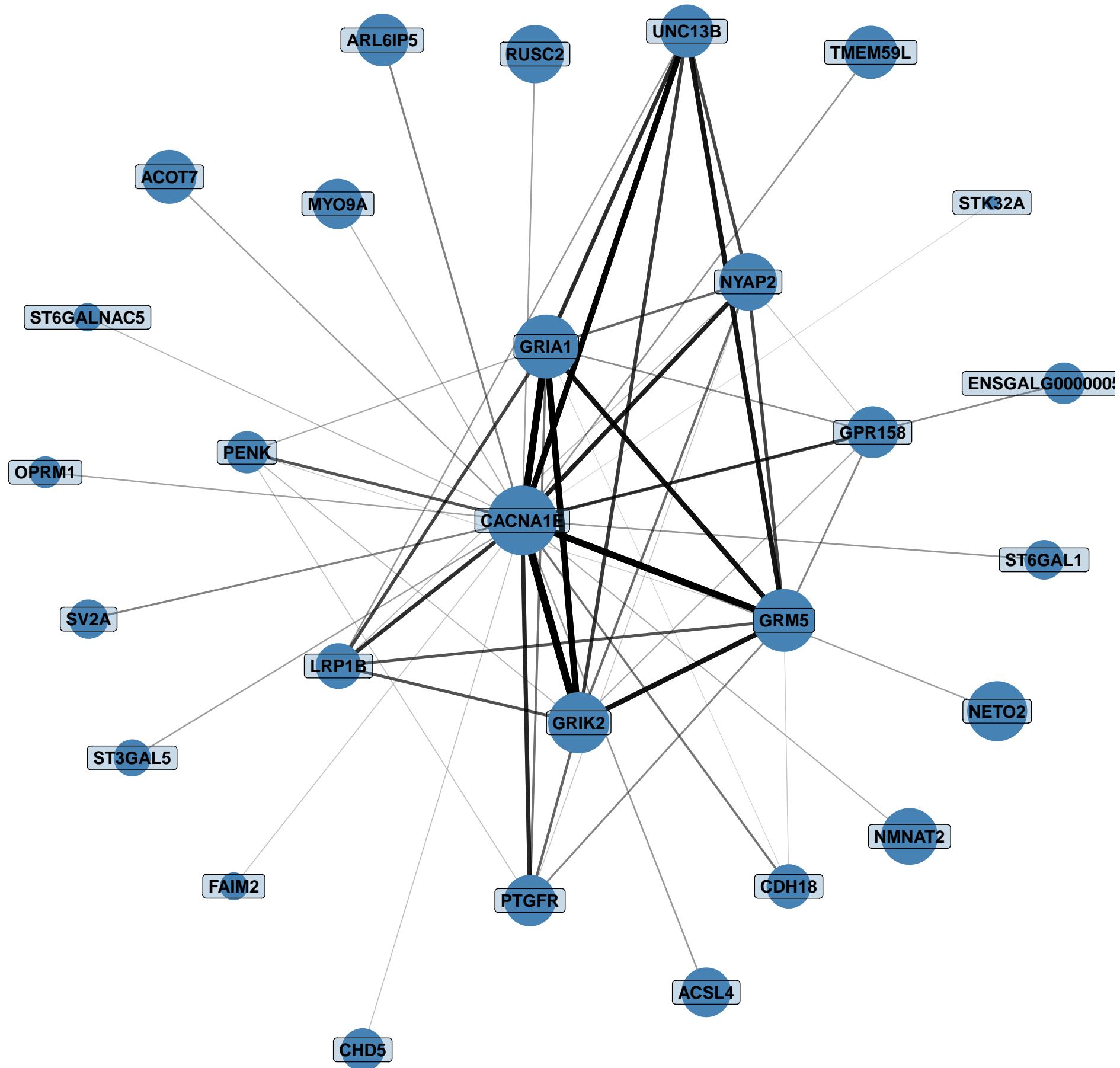
	Pathway	N	DE	P.DE
<i>path:gga05132</i>	Salmonella infection	215	3	0.01137
<i>path:gga04010</i>	MAPK signaling pathway	231	2	0.09095
<i>path:gga04622</i>	RIG-I-like receptor signaling pathway	44	1	0.09241
<i>path:gga03250</i>	Viral life cycle – HIV-1	48	1	0.1004
<i>path:gga04920</i>	Adipocytokine signaling pathway	59	1	0.122
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.1278
<i>path:gga04620</i>	Toll-like receptor signaling pathway	67	1	0.1374
<i>path:gga04912</i>	GnRH signaling pathway	72	1	0.1469
<i>path:gga04012</i>	ErbB signaling pathway	75	1	0.1525
<i>path:gga04914</i>	Progesterone-mediated oocyte maturation	76	1	0.1544



1	COBL	ITPR2	SASH1	ETV1	ZCCHC24	ASB5	SOX6	UGT8
2	SOX5	PODXL	ANKRD11	RHOB	CDK6	LMO1	EPS8	FERMT2
3	EPAS1	GFPT2	OTUD7A					

	Term	Ont	N	n	Adj. p-value
GO:0033631	cell–cell adhesion mediated by integrin	BP	1	1	0.001491
GO:0030033	microvillus assembly	BP	1	1	0.001491
GO:0033634	positive regulation of cell–cell adhesion mediated by integrin	BP	1	1	0.001491
GO:0033632	regulation of cell–cell adhesion mediated by integrin	BP	1	1	0.001491
GO:0032534	regulation of microvillus assembly	BP	1	1	0.001491
GO:0032530	regulation of microvillus organization	BP	2	1	0.00298
GO:0032528	microvillus organization	BP	3	1	0.004467
GO:0033630	positive regulation of cell adhesion mediated by integrin	BP	3	1	0.004467
GO:0033628	regulation of cell adhesion mediated by integrin	BP	5	1	0.007435
GO:0033627	cell adhesion mediated by integrin	BP	7	1	0.01039

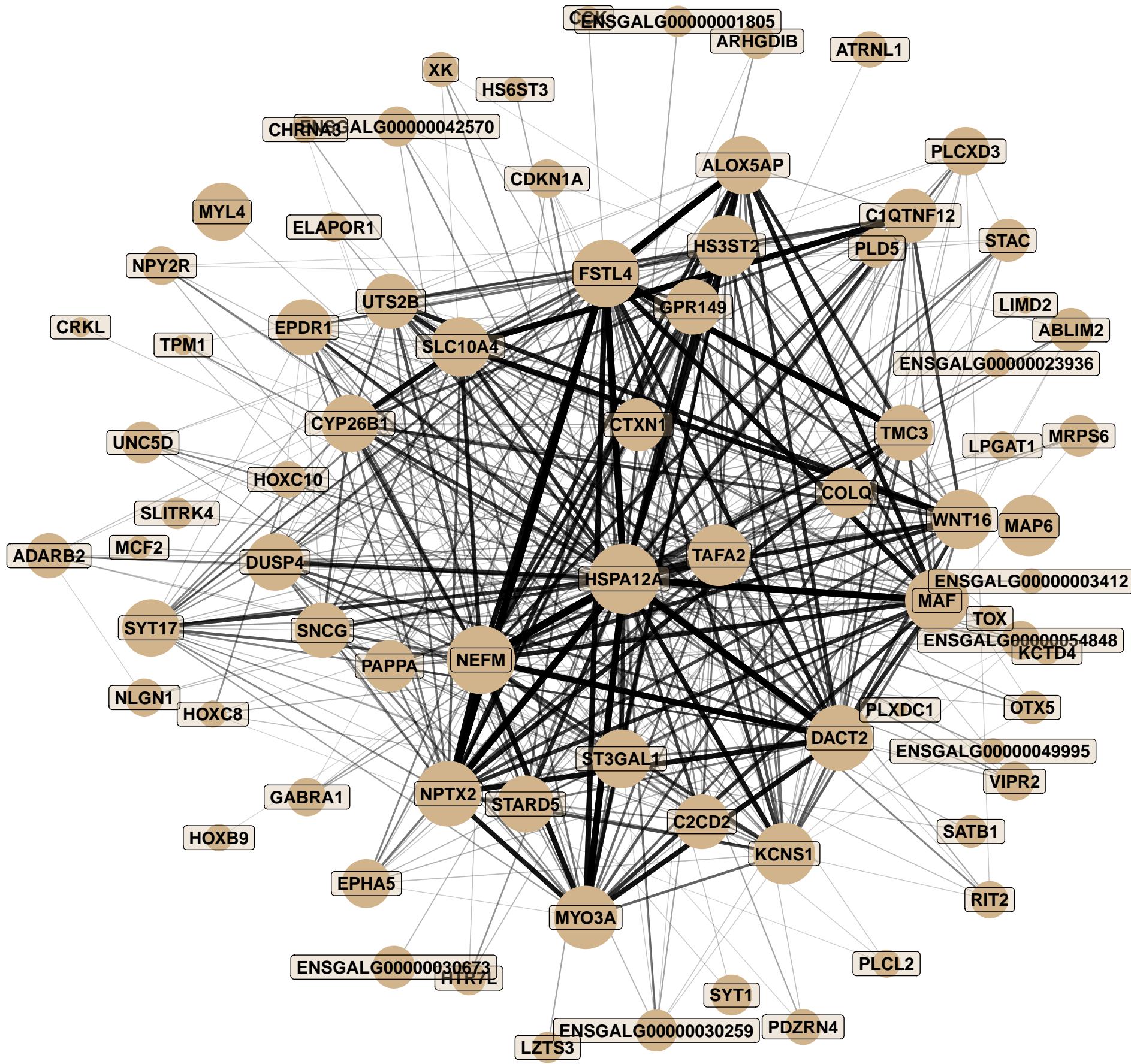
	Pathway	N	DE	P.DE
<i>path:gga04218</i>	Cellular senescence	131	2	0.016
<i>path:gga05132</i>	Salmonella infection	215	2	0.04014
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	1	0.04669
<i>path:gga00565</i>	Ether lipid metabolism	33	1	0.04811
<i>path:gga01250</i>	Biosynthesis of nucleotide sugars	35	1	0.05095
<i>path:gga00520</i>	Amino sugar and nucleotide sugar metabolism	44	1	0.06365
<i>path:gga00600</i>	Sphingolipid metabolism	46	1	0.06645
<i>path:gga04115</i>	p53 signaling pathway	62	1	0.08857
<i>path:gga04912</i>	GnRH signaling pathway	72	1	0.1021
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	78	1	0.1102



1	CACNA1E	GRM5	GRIK2	GRIA1	NMNAT2	RUSC2	UNC13B	NETO2
2	PENK	ACOT7	PTGFR	NYAP2	TMEM59L	ARL6IP5	GPR158	ACSL4
3	MYO9A	LRP1B	OPRM1	ST3GAL5	CHD5	CDH18	ST6GAL1	FAIM2
4	ENSGALG00000051831	SV2A	ST6GALNAC5	STK32A				

	Term	Ont	N	n	Adj. p-value
GO:1902001	fatty acid transmembrane transport	BP	1	1	0.002119
GO:0051938	L-glutamate import	BP	1	1	0.002119
GO:0098712	L-glutamate import across plasma membrane	BP	1	1	0.002119
GO:0015813	L-glutamate transmembrane transport	BP	1	1	0.002119
GO:0140354	lipid import into cell	BP	1	1	0.002119
GO:0002037	negative regulation of L-glutamate import across plasma membrane	BP	1	1	0.002119
GO:2001024	negative regulation of response to drug	BP	1	1	0.002119
GO:0010958	regulation of amino acid import across plasma membrane	BP	1	1	0.002119
GO:1903789	regulation of amino acid transmembrane transport	BP	1	1	0.002119
GO:0002036	regulation of L-glutamate import across plasma membrane	BP	1	1	0.002119

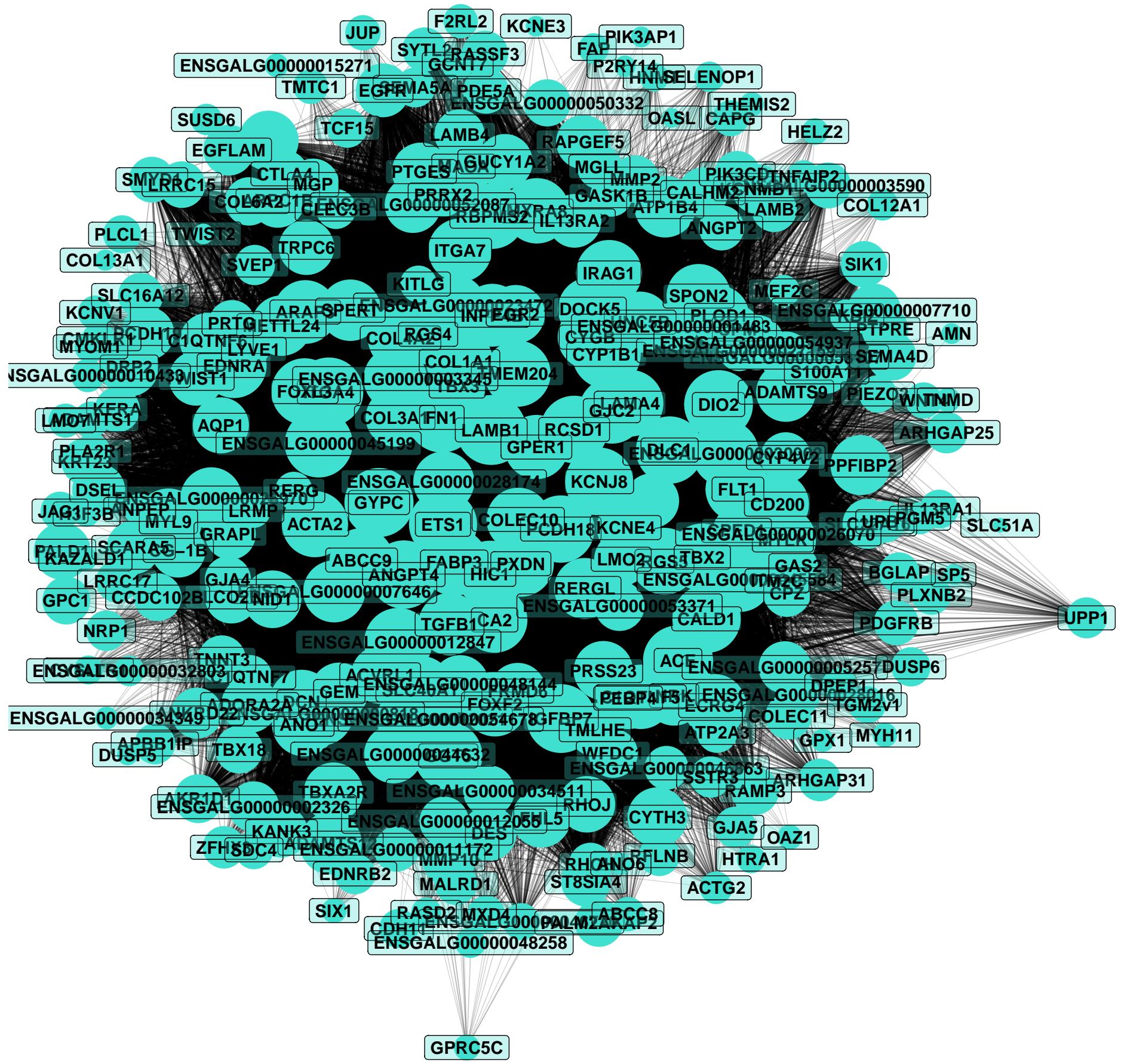
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	6	1.502e–05
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	2	0.0003325
<i>path:gga04020</i>	Calcium signaling pathway	186	3	0.006918
<i>path:gga00061</i>	Fatty acid biosynthesis	16	1	0.03339
<i>path:gga00062</i>	Fatty acid elongation	23	1	0.04766
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	27	1	0.05572
<i>path:gga00071</i>	Fatty acid degradation	30	1	0.06172
<i>path:gga00760</i>	Nicotinate and nicotinamide metabolism	32	1	0.0657
<i>path:gga04216</i>	Ferroptosis	34	1	0.06967
<i>path:gga00514</i>	Other types of O–glycan biosynthesis	41	1	0.08342



1	MAP6	HSPA12A	MYL4	NEFM	HS3ST2	FSTL4	DACT2	SYT1
2	KCNS1	NPTX2	TAFA2	MAF	ALOX5AP	MYO3A	ST3GAL1	STARD5
3	TMC3	C2CD2	EPHA5	SYT17	GPR149	ENSGALG00000030673	DUSP4	MRPS6
4	ADARB2	ARHGDIB	EPDR1	ABLIM2	UNC5D	ATRNL1	HOXC10	ENSGALG00000054848
5	NLGN1	SATB1	PLCXD3	SNCG	GABRA1	ENSGALG00000030259	STAC	SLC10A4
6	TPM1	CYP26B1	RIT2	PDZRN4	HOXB9	CTXN1	PLD5	PLCL2
7	NPY2R	VIPR2	C1QTNF12	HOXC8	WNT16	SLITRK4	CDKN1A	OTX5
8	CHRNA3	TOX	COLQ	LPGAT1	LIMD2	HTR7L	CCK	ENSGALG00000042570
9	ENSGALG00000003412	ENSGALG00000001805	UTS2B	CRKL	ELAPOR1	PAPPA	XK	MCF2
10	ENSGALG00000023936	LZTS3	ENSGALG00000049995	HS6ST3	PLXDC1	KCTD4		

	Term	Ont	N	n	Adj. p-value
GO:0032502	developmental process	BP	635	11	0.000638
GO:0007275	multicellular organism development	BP	558	10	0.000888
GO:0048731	system development	BP	467	9	0.0009856
GO:0032501	multicellular organismal process	BP	684	11	0.001175
GO:0007218	neuropeptide signaling pathway	BP	10	2	0.001301
GO:0048856	anatomical structure development	BP	603	10	0.001595
GO:0007399	nervous system development	BP	252	6	0.002568
GO:0098916	anterograde trans-synaptic signaling	BP	53	3	0.003056
GO:0007268	chemical synaptic transmission	BP	53	3	0.003056
GO:0099537	trans-synaptic signaling	BP	53	3	0.003056

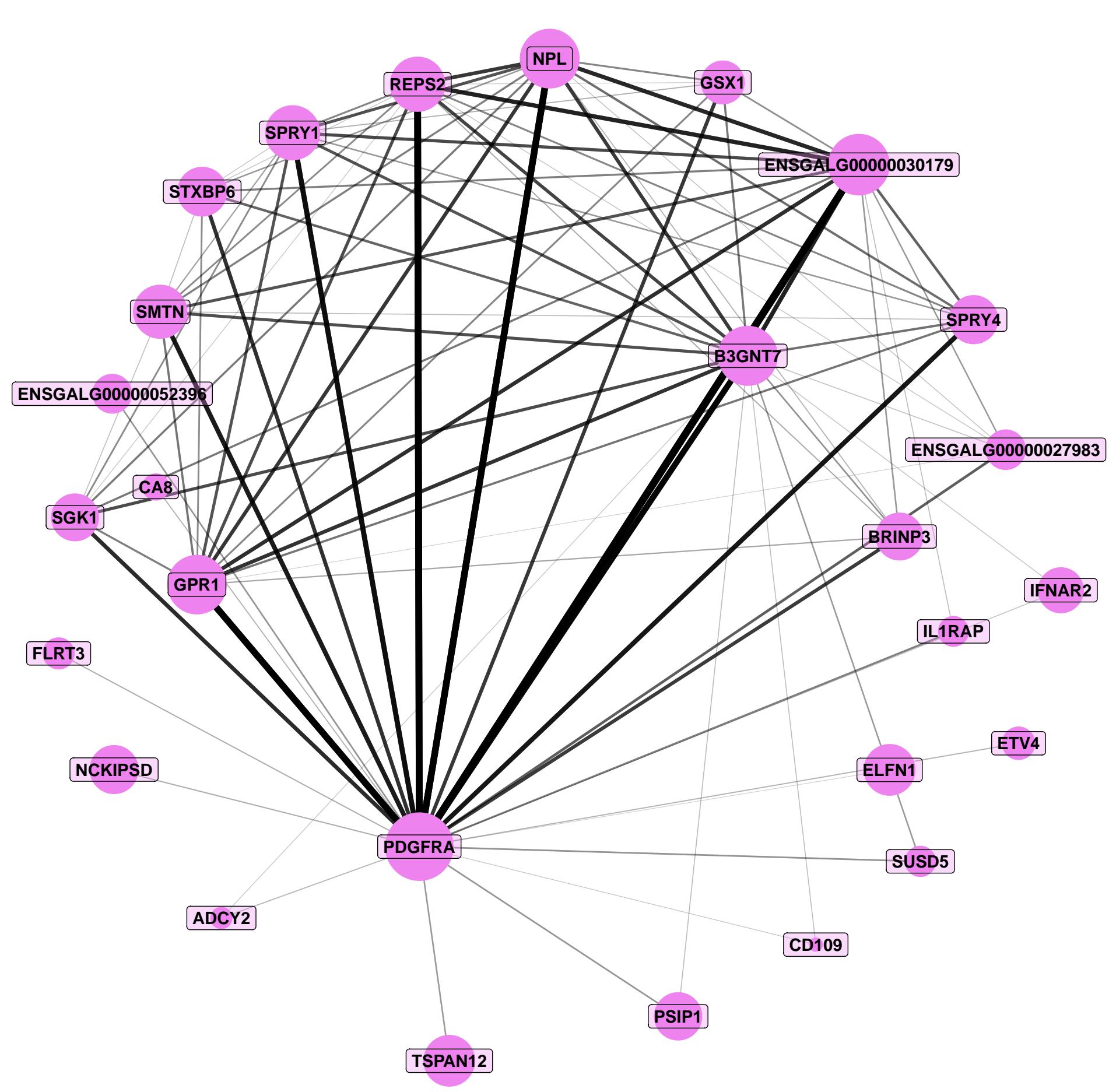
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	7	0.0005828
<i>path:gga04260</i>	Cardiac muscle contraction	59	2	0.04164
<i>path:gga04012</i>	ErbB signaling pathway	75	2	0.06388
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	1	0.06399
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	1	0.06914
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.07426
<i>path:gga04514</i>	Cell adhesion molecules	98	2	0.1011
<i>path:gga00830</i>	Retinol metabolism	26	1	0.1336
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	2	0.139
<i>path:gga00512</i>	Mucin type O–glycan biosynthesis	29	1	0.1478



1	ACE	DIO2	FN1	LAMB1	ANGPT4	GYPc	HIC1	RGS5
2	ACTA2	COL1A1	KCNJ8	CYP1B1	IGFBP7	ITGA4	GGT5	TBX2
3	ENSGALG00000012847	ENSGALG00000012021	ENSGALG00000045199	ENSGALG00000030902	SLC40A1	RCSD1	LAMA4	MYL9
4	GJC2	FOXF2	CA2	ENSGALG0000007646	DCN	SPON2	PCDH18	MXRA8
5	GPER1	FLT1	IRAG1	ECRG4	ETS1	ANO1	ARAP3	TMEM204
6	DLC1	RBPMS2	ABCC9	C1QTNF5	CYGB	ENSGALG0000000818	FOXL3	DOCK5
7	COLEC10	CALD1	CD200	ENSGALG00000045584	PEBP4	COL4A2	INPP4B	FABP3
8	ITGA7	SPERT	ATP1B4	MYLK	EDNRA	PXDN	RERGL	NRK
9	ACVRL1	ENSGALG00000023472	ENSGALG0000003345	COL3A1	TBX3	NA	FHL5	UNC5B
10	ENSGALG00000026970	AQP1	ADAMTS12	PRSS23	TGFB1	ARPC1B	RGS4	ENSGALG00000028174
11	PPFIBP2	PTGES	EGR2	ADORA2A	PLOD1	GEM	DRP2	KCNE4
12	FRMD6	RHOJ	TWIST1	ADAMTS9	ENSGALG00000044632	CYTH3	MAOA	METTL24
13	RAPGEF5	ENSGALG00000026070	ENSGALG00000052087	DES	NID1	SLCO2B1	TBXA2R	TRPC6
14	IL13RA2	AKR1D1	GJA4	LMO2	ENSGALG0000005257	EGFLAM	CG-1B	MMP10
15	C1QTNF6	GUCY1A2	NA	PALD1	ENSGALG00000048144	ANKRD22	EGFR	KANK3
16	ENSGALG0000003590	ENSGALG00000034511	CTLA4	SLC22A16	SCARA5	DSEL	CALHM2	TMLHE
17	PCDH19	MGP	ENSGALG00000054937	CCDC102B	ENSGALG0000007710	LAMB4	ENSGALG00000053371	MMP2
18	TBX18	CPM	PDGFRB	LRRC15	CPZ	ST8SIA4	ENSGALG00000002326	CYP4V2
19	GRAPL	KCNMB1	ZFHX3	PRRX2	WFDC1	KRT23	ENSGALG00000046863	CPED1
20	KERA	RASSF3	RAMP3	ENSGALG00000012055	S100A11	SIK1	GJA5	SYTL2
21	ENSGALG0000001483	NRP1	PRTG	COL6A2	PTPRE	C1QTNF7	ENSGALG00000053107	TNNT3
22	ENSGALG00000050332	ARHGAP31	PIK3CD	SMYD1	GPC1	SEMA4D	F2RL2	SDC4
23	PALM2AKAP2	ENSGALG0000011172	SEMA5A	CLEC3B	ENSGALG0000028016	GASK1B	UPB1	LRRC17
24	RFLNB	ARHGAP25	APBB1IP	SLC16A12	MALRD1	PDE5A	ENSGALG0000027159	LAMB2
25	PIEZ02	ANGPT2	UPP1	DUSP6	WNT4	GAS2	IL13RA1	ATP2A3
26	LRMP	PLCL1	ITM2C	TMTC1	COLEC11	TGM2v1	MGLL	KITLG
27	SVEP1	JUP	PLXNB2	RHOH	SSTR3	ENSGALG0000046720	TCF15	GPRC5C
28	SUSD6	CDH11	JAG1	MXD4	CAPG	MEF2C	CMKLR1	RERG
29	PLA2R1	TWIST2	COL12A1	ADAMTS1	DPEP1	ENSGALG0000054678	ACTG2	HTRA1
30	BGLAP	LMO7	ENSGALG0000048258	EDNRB2	CYSLTR1	H3F3B	FAP	ANPEP
31	ENSGALG0000010433	NFKBIZ	RASD2	SIX1	ABCC8	ENSGALG0000032803	HELZ2	GPX1
32	LYVE1	SELENOP1	GCNT7	MYOM1	PIK3AP1	TNFAIP2	OAZ1	KCNV1
33	PGM5	DUSP5	ENSGALG0000015271	THEMIS2	ANO6	HNMT	SP5	MYH11
34	ENSGALG0000034349	COL13A1	KAZALD1	KCNE3	TNMD	OASL	SLC51A	P2RY14
35	AMN							

	Term	Ont	N	n	Adj. p-value
GO:0048856	anatomical structure development	BP	603	33	2.003e-07
GO:0032502	developmental process	BP	635	33	6.496e-07
GO:0022610	biological adhesion	BP	141	14	1.049e-06
GO:0007155	cell adhesion	BP	141	14	1.049e-06
GO:0061061	muscle structure development	BP	64	9	5.349e-06
GO:0033002	muscle cell proliferation	BP	14	5	5.753e-06
GO:0009653	anatomical structure morphogenesis	BP	286	19	6.068e-06
GO:0009888	tissue development	BP	192	15	8.734e-06
GO:0040011	locomotion	BP	159	13	2.158e-05
GO:0016477	cell migration	BP	115	11	2.179e-05

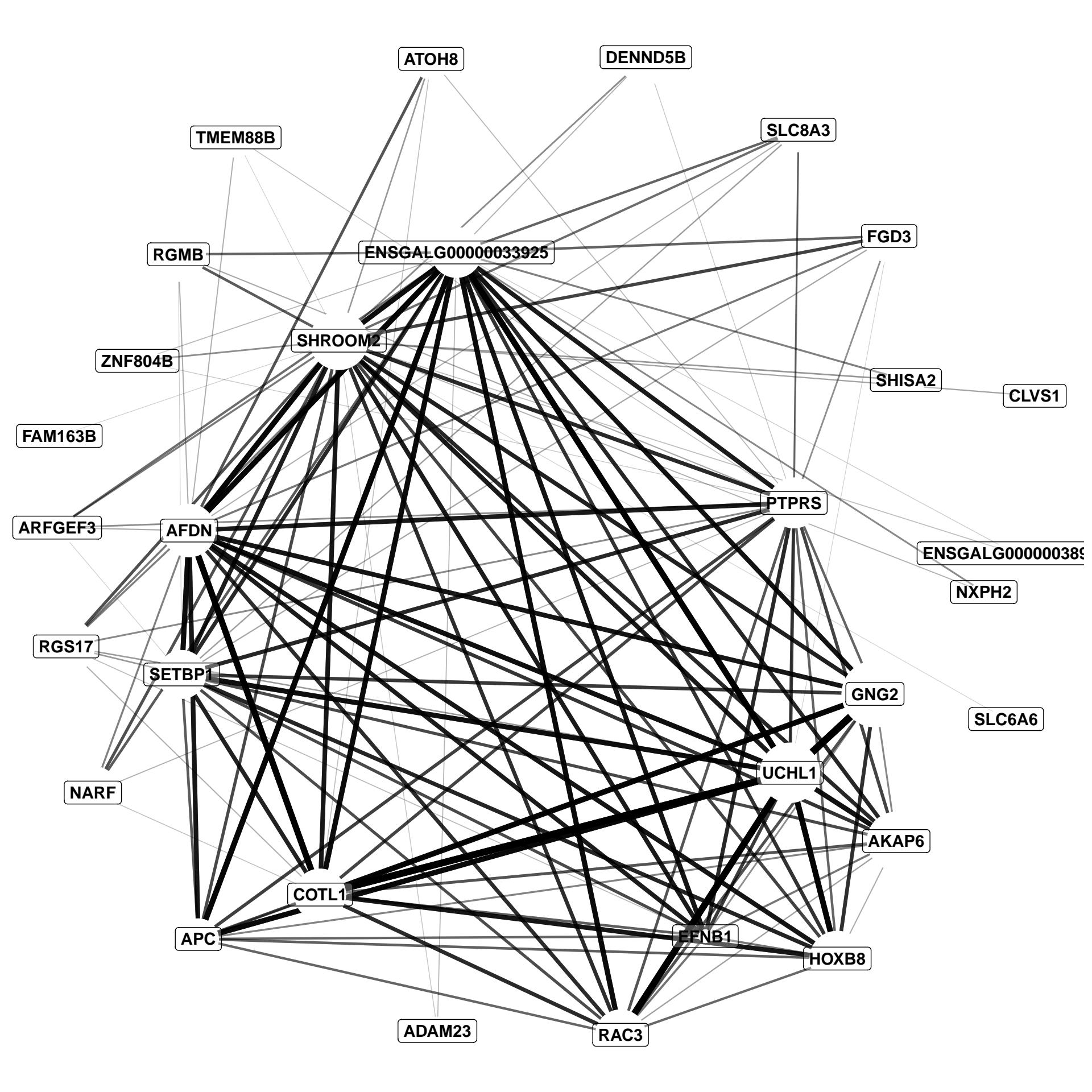
	Pathway	N	DE	P.DE
<i>path:gga04510</i>	Focal adhesion	166	17	4.543e-08
<i>path:gga04512</i>	ECM–receptor interaction	65	11	6.715e-08
<i>path:gga04270</i>	Vascular smooth muscle contraction	101	12	9.242e-07
<i>path:gga04010</i>	MAPK signaling pathway	231	13	0.000893
<i>path:gga04020</i>	Calcium signaling pathway	186	11	0.001478
<i>path:gga04810</i>	Regulation of actin cytoskeleton	179	10	0.003619
<i>path:gga00340</i>	Histidine metabolism	16	2	0.04095
<i>path:gga04672</i>	Intestinal immune network for IgA production	18	2	0.05085
<i>path:gga04520</i>	Adherens junction	69	4	0.05166
<i>path:gga00480</i>	Glutathione metabolism	47	3	0.07003



1	PDGFRA	B3GNT7	GPR1	ENSGALG00000030179	REPS2	SGK1	NPL	SPRY1
2	SMTN	BRINP3	ELFN1	SPRY4	TSPAN12	STXBP6	GSX1	IFNAR2
3	NCKIPSD	PSIP1	FLRT3	ENSGALG00000027983	ETV4	SUSD5	ENSGALG00000052396	CA8
4	IL1RAP	CD109	ADCY2					

	Term	Ont	N	n	Adj. p-value
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	BP	79	4	1.568e-05
GO:0007167	enzyme linked receptor protein signaling pathway	BP	123	4	8.94e-05
GO:0009653	anatomical structure morphogenesis	BP	286	5	0.0002021
GO:0071363	cellular response to growth factor stimulus	BP	75	3	0.0004104
GO:0070848	response to growth factor	BP	76	3	0.0004267
GO:0008543	fibroblast growth factor receptor signaling pathway	BP	20	2	0.0006872
GO:0044344	cellular response to fibroblast growth factor stimulus	BP	21	2	0.0007586
GO:0071774	response to fibroblast growth factor	BP	22	2	0.0008334
GO:0007166	cell surface receptor signaling pathway	BP	257	4	0.001465
GO:0009887	animal organ morphogenesis	BP	120	3	0.001611

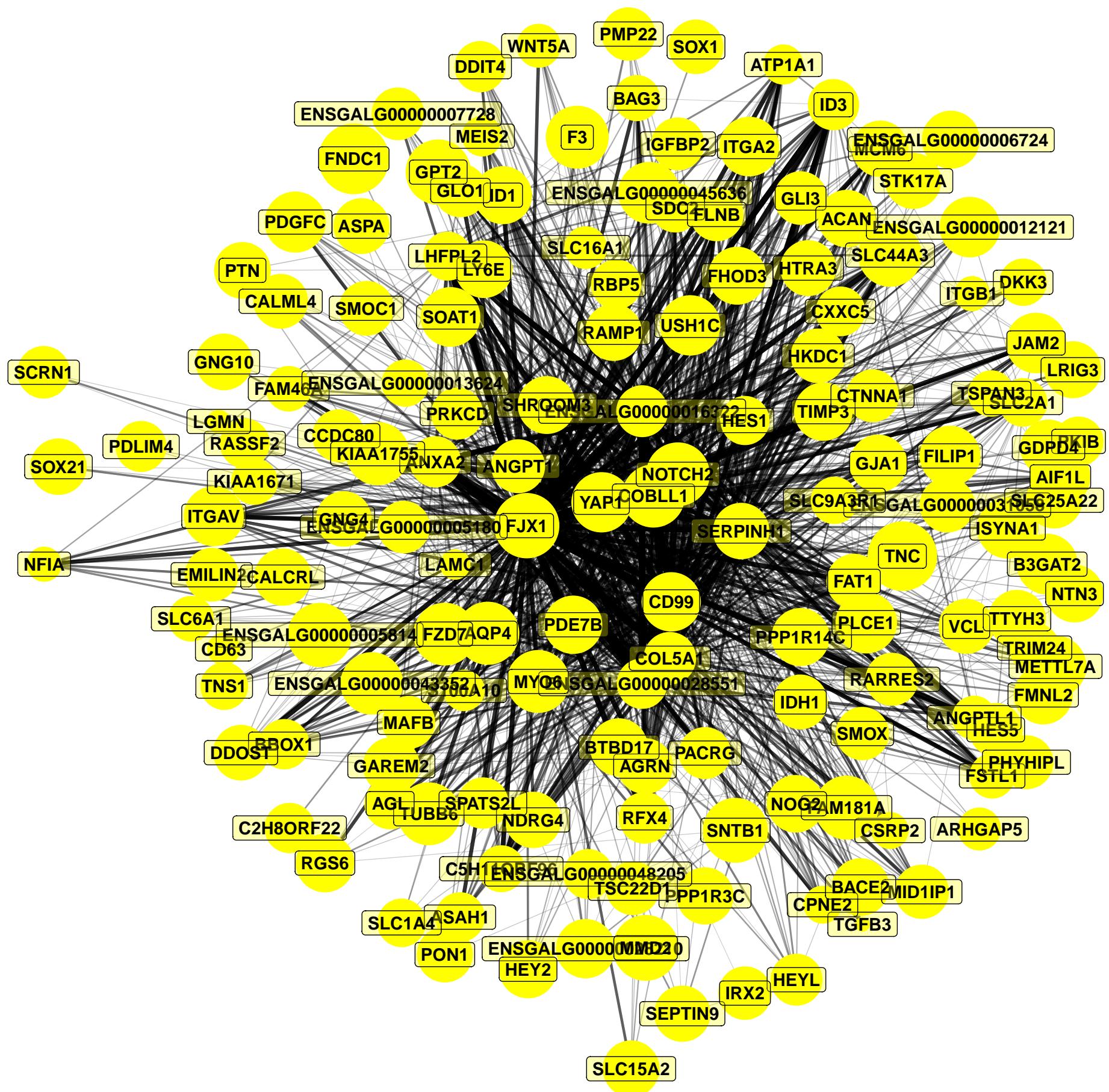
	Pathway	N	DE	P.DE
<i>path:gga04540</i>	Gap junction	78	2	0.01013
<i>path:gga00910</i>	Nitrogen metabolism	13	1	0.02522
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.02713
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	136	2	0.0289
<i>path:gga04020</i>	Calcium signaling pathway	186	2	0.05105
<i>path:gga04010</i>	MAPK signaling pathway	231	2	0.07474
<i>path:gga00520</i>	Amino sugar and nucleotide sugar metabolism	44	1	0.08292
<i>path:gga03250</i>	Viral life cycle – HIV-1	48	1	0.09012
<i>path:gga04620</i>	Toll-like receptor signaling pathway	67	1	0.1236
<i>path:gga04912</i>	GnRH signaling pathway	72	1	0.1322



1	GNG2	UCHL1	AKAP6	RGMB	COTL1	SHROOM2	HOXB8	ENSGALG00000033925
2	RGS17	AFDN	RAC3	PTPRS	NARF	SETBP1	FGD3	SLC8A3
3	DENND5B	APC	EFNB1	ATOH8	ZNF804B	ARFGEF3	CLVS1	SHISA2
4	TMEM88B	ADAM23	ENSGALG00000038930	SLC6A6	NXPH2	FAM163B		

	Term	Ont	N	n	Adj. p-value
GO:0061000	negative regulation of dendritic spine development	BP	1	1	0.002276
GO:0048671	negative regulation of collateral sprouting	BP	2	1	0.004547
GO:0048681	negative regulation of axon regeneration	BP	3	1	0.006813
GO:0070571	negative regulation of neuron projection regeneration	BP	3	1	0.006813
GO:0099560	synaptic membrane adhesion	BP	3	1	0.006813
GO:0048668	collateral sprouting	BP	5	1	0.01133
GO:0030517	negative regulation of axon extension	BP	5	1	0.01133
GO:0048679	regulation of axon regeneration	BP	5	1	0.01133
GO:0048670	regulation of collateral sprouting	BP	5	1	0.01133
GO:0070570	regulation of neuron projection regeneration	BP	6	1	0.01358

	Pathway	N	DE	P.DE
<i>path:gga04810</i>	Regulation of actin cytoskeleton	179	3	0.007616
<i>path:gga04520</i>	Adherens junction	69	2	0.01068
<i>path:gga04371</i>	Apelin signaling pathway	109	2	0.02533
<i>path:gga04310</i>	Wnt signaling pathway	131	2	0.03554
<i>path:gga04370</i>	VEGF signaling pathway	50	1	0.1079
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.1261
<i>path:gga04350</i>	TGF-beta signaling pathway	84	1	0.1747
<i>path:gga04514</i>	Cell adhesion molecules	98	1	0.2008
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	1	0.2385
<i>path:gga04530</i>	Tight junction	133	1	0.2626



1	TNC	FNDC1	PTN	MMD2	FJX1	GJA1	AQP4	HES5
2	TUBB6	SNTB1	ID1	CD99	ENSGALG00000016322	GPT2	F3	B3GAT2
3	AGRN	TIMP3	COL5A1	FILIP1	FAM181A	AIF1L	ENSGALG0000005814	COBLL1
4	SERPINH1	ENSGALG00000028551	GNG10	MYO6	HTRA3	YAP1	PDGFC	NOTCH2
5	ISYNA1	RAMP1	SLC44A3	SHROOM3	FZD7	MAFB	PMP22	ENSGALG00000028210
6	ANGPT1	METTL7A	ENSGALG00000043352	SMOC1	ANXA2	RGS6	TTYH3	JAM2
7	ENSGALG00000045636	LHFPL2	PLCE1	PDE7B	VCL	USH1C	SDC2	ENSGALG00000012121
8	ITGA2	ID3	PPP1R14C	CALCRL	PON1	ACAN	ASPA	GNG4
9	ITGAV	KIAA1755	ENSGALG0000006724	FAT1	PACRG	HKDC1	PPP1R3C	RFX4
10	CTNNA1	DKK3	ANGPTL1	SOAT1	HEYL	FLNB	NDRG4	SLC6A1
11	SLC2A1	SOX1	MCM6	C5H11ORF96	FSTL1	GAREM2	IDH1	ENSGALG00000031058
12	LY6E	HEY2	RARRES2	SOX21	BACE2	DDOST	SLC1A4	SLC15A2
13	GLI3	MID1IP1	BTBD17	FMNL2	TNS1	WNT5A	FHOD3	PRKCD
14	SEPTIN9	NFIA	CXXC5	NOG2	LRIG3	NTN3	TSC22D1	MEIS2
15	ASAH1	SLC25A22	CALML4	RBP5	GDPD4	KIAA1671	CCDC80	C2H8ORF22
16	FAM46A	GLO1	SMOX	ENSGALG0000007728	STK17A	SLC9A3R1	LAMC1	RASSF2
17	DDIT4	SCRN1	ENSGALG00000013624	AGL	BBOX1	S100A10	CSRP2	IRX2
18	EMILIN2	BAG3	PKIB	PHYHIPL	PDLIM4	IGFBP2	ENSGALG0000005180	CPNE2
19	SPATS2L	TRIM24	HES1	ITGB1	TSPAN3	ARHGAP5	ATP1A1	CD63
20	SLC16A1	ENSGALG00000048205	TGFB3	LGMN				

	Term	Ont	N	n	Adj. p-value
GO:0048856	anatomical structure development	BP	603	23	9.149e-07
GO:0007275	multicellular organism development	BP	558	22	9.365e-07
GO:0032502	developmental process	BP	635	23	2.213e-06
GO:0032501	multicellular organismal process	BP	684	24	2.26e-06
GO:0048731	system development	BP	467	19	3.516e-06
GO:0048513	animal organ development	BP	306	15	4.405e-06
GO:0023052	signaling	BP	498	19	8.86e-06
GO:0007154	cell communication	BP	505	18	3.832e-05
GO:0009653	anatomical structure morphogenesis	BP	286	13	4.331e-05
GO:0006928	movement of cell or subcellular component	BP	176	10	5.413e-05

	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	65	6	0.0001297
<i>path:gga04510</i>	Focal adhesion	166	9	0.0001835
<i>path:gga04330</i>	Notch signaling pathway	52	5	0.0003973
<i>path:gga04514</i>	Cell adhesion molecules	98	5	0.006666
<i>path:gga01210</i>	2–Oxocarboxylic acid metabolism	13	2	0.01037
<i>path:gga00100</i>	Steroid biosynthesis	15	2	0.01374
<i>path:gga04350</i>	TGF–beta signaling pathway	84	4	0.01877
<i>path:gga00480</i>	Glutathione metabolism	47	3	0.01904
<i>path:gga00500</i>	Starch and sucrose metabolism	24	2	0.03366
<i>path:gga04270</i>	Vascular smooth muscle contraction	101	4	0.034

ENSGALG00000046353

DSCAM

TAL1

NRP2

ABCG2

CRTAC1

GRP

GATA2

RASD1

PKD2L1

TAL2

PROKR1

SFRP5

GATA3

CACNA1G

ENSGALG00000007596

ENSGALG00000000645

MYO3B

FAM135B

TCERG1L

1	PKD2L1	GATA3	TAL2	SFRP5	ENSGALG0000000645	MYO3B	GATA2	TAL1
2	CRTAC1	GRP	NRP2	ABCG2	DSCAM	FAM135B	PROKR1	SST
3	RASD1	ENSGALG00000007596	CACNA1G	TCERG1L	ENSGALG00000046353			

	Term	Ont	N	n	Adj. p-value
GO:0040012	regulation of locomotion	BP	72	4	4.24e–06
GO:0072577	endothelial cell apoptotic process	BP	4	2	1.402e–05
GO:2000352	negative regulation of endothelial cell apoptotic process	BP	4	2	1.402e–05
GO:1904036	negative regulation of epithelial cell apoptotic process	BP	4	2	1.402e–05
GO:0045599	negative regulation of fat cell differentiation	BP	4	2	1.402e–05
GO:2000351	regulation of endothelial cell apoptotic process	BP	4	2	1.402e–05
GO:1904035	regulation of epithelial cell apoptotic process	BP	4	2	1.402e–05
GO:0035162	embryonic hemopoiesis	BP	5	2	2.334e–05
GO:1902895	positive regulation of pri–miRNA transcription by RNA polymerase II	BP	5	2	2.334e–05
GO:0009791	post–embryonic development	BP	5	2	2.334e–05

	Pathway	N	DE	P.DE
<i>path:gga02010</i>	ABC transporters	34	1	0.05207
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	2	0.06319
<i>path:gga04310</i>	Wnt signaling pathway	131	1	0.1868
<i>path:gga04020</i>	Calcium signaling pathway	186	1	0.255
<i>path:gga04010</i>	MAPK signaling pathway	231	1	0.3066
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1
<i>path:gga00232</i>	Caffeine 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