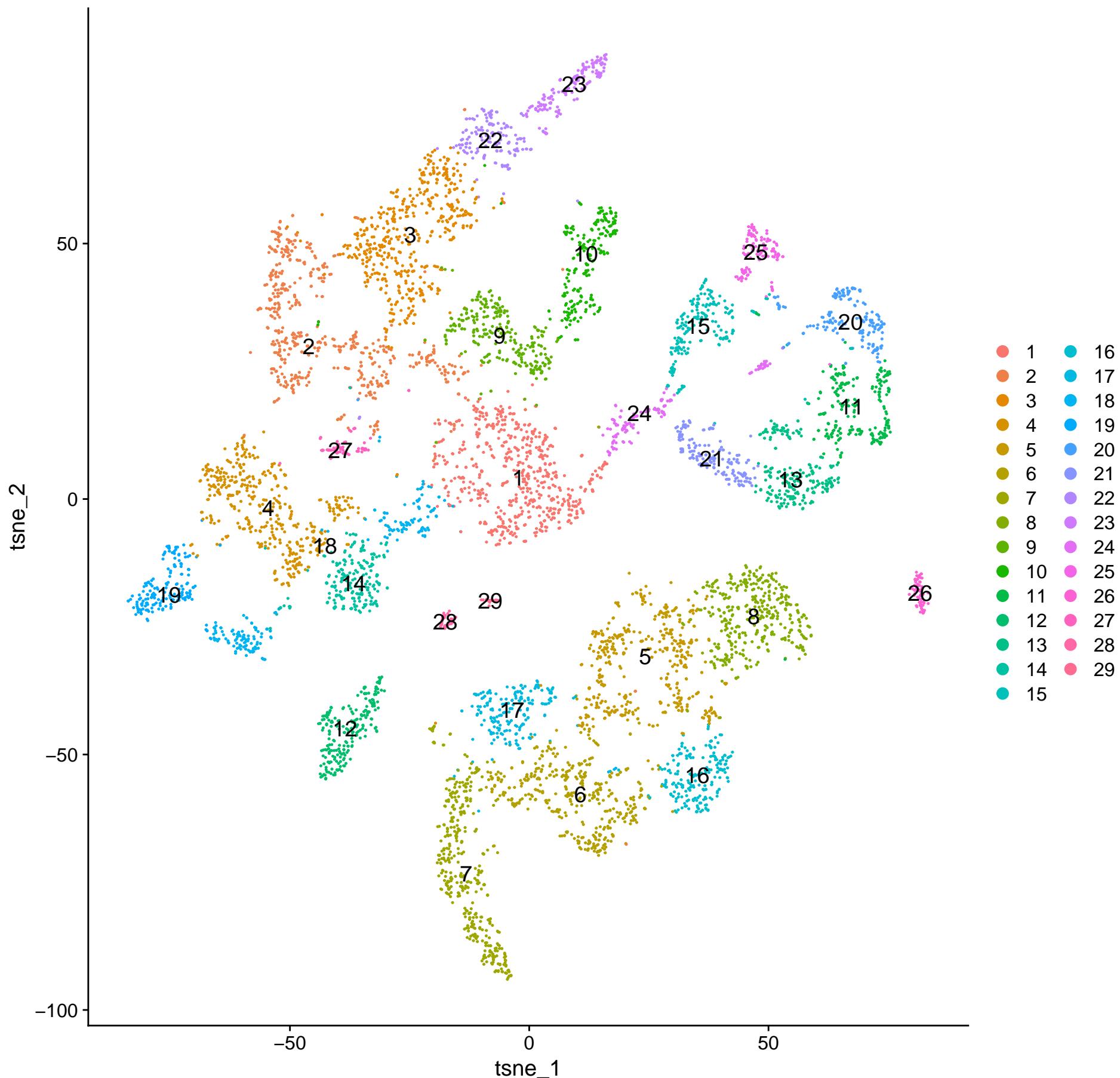
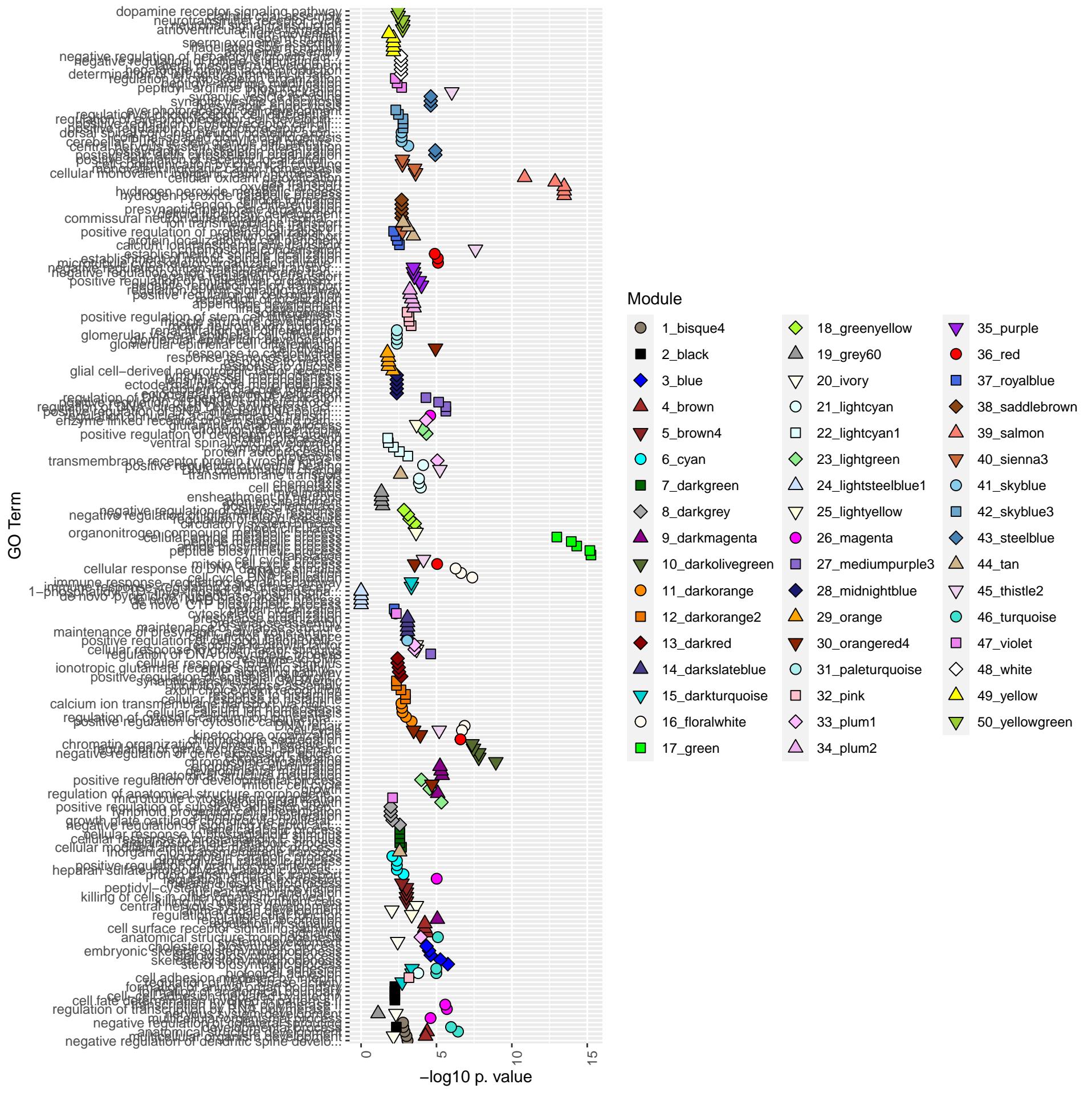
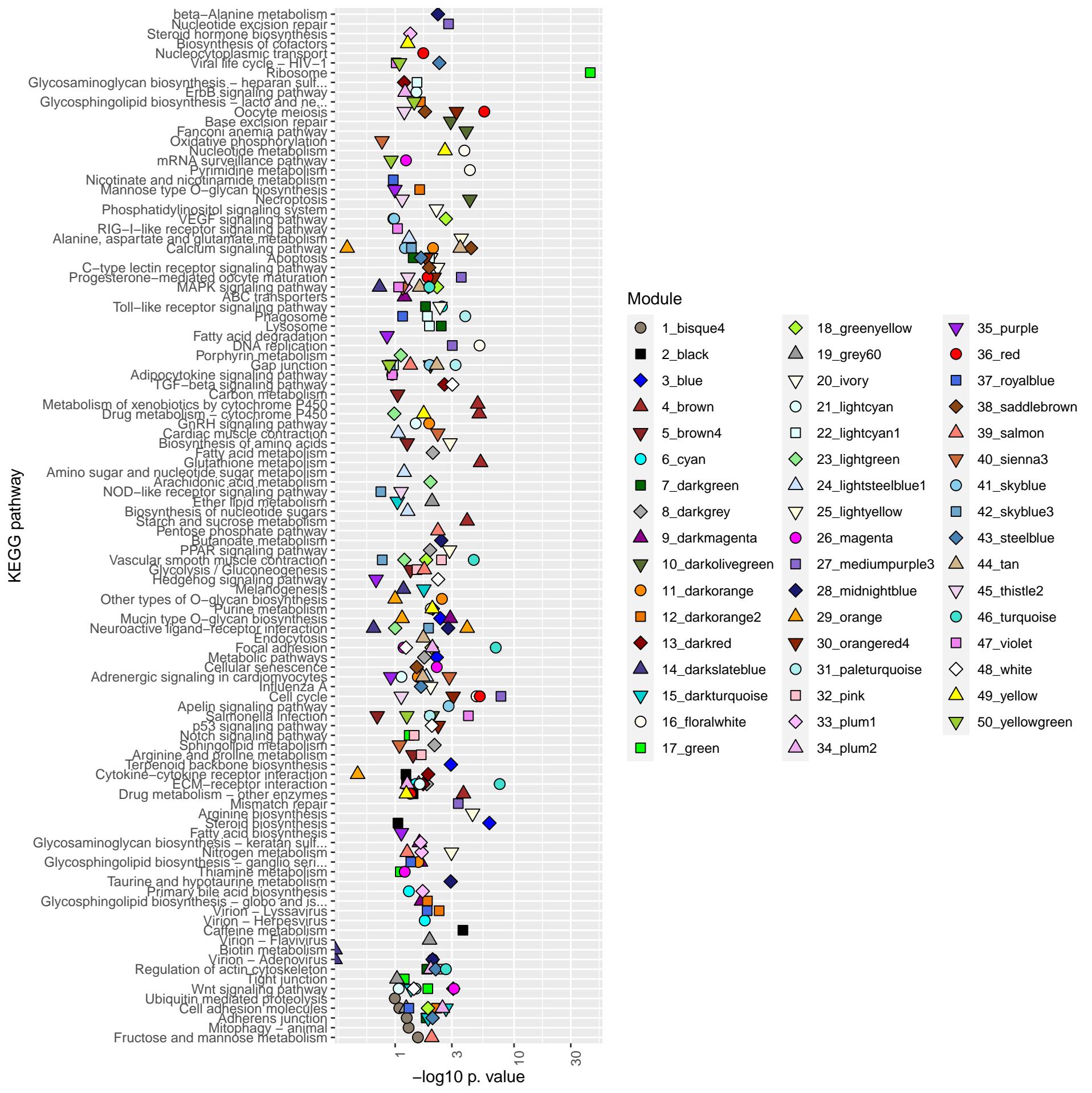
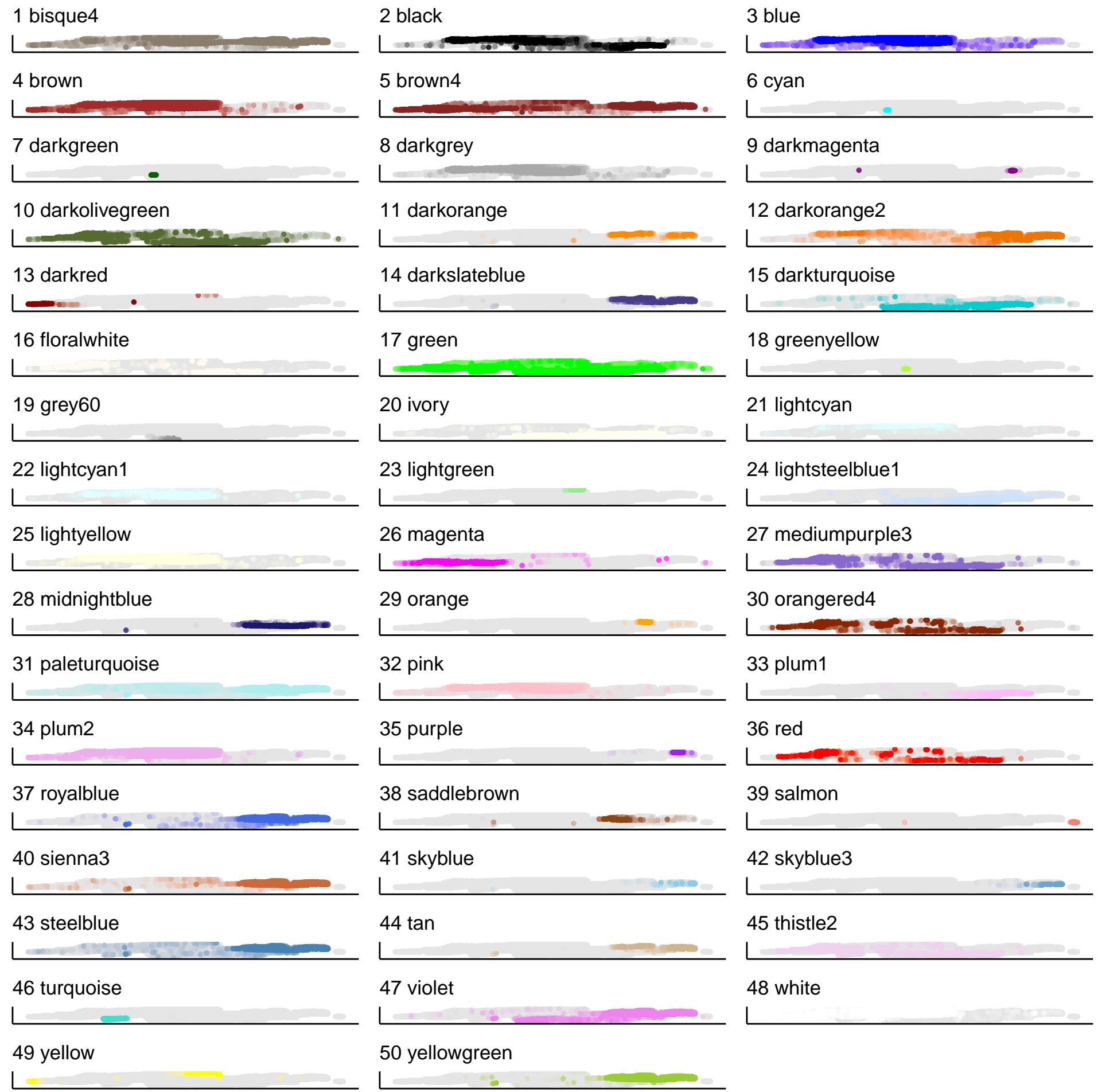


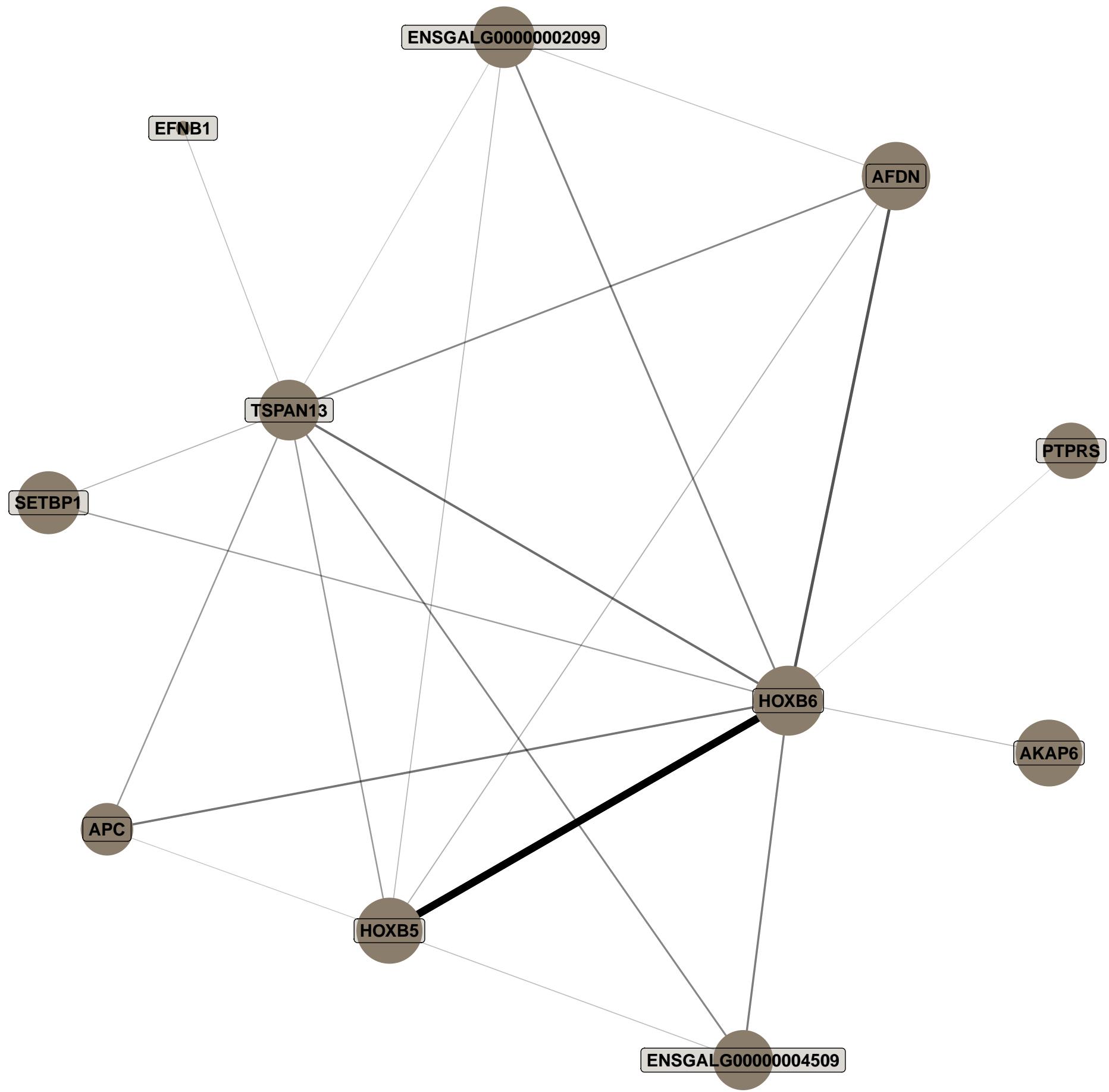
Gg_lumb_int scWGCNA modules







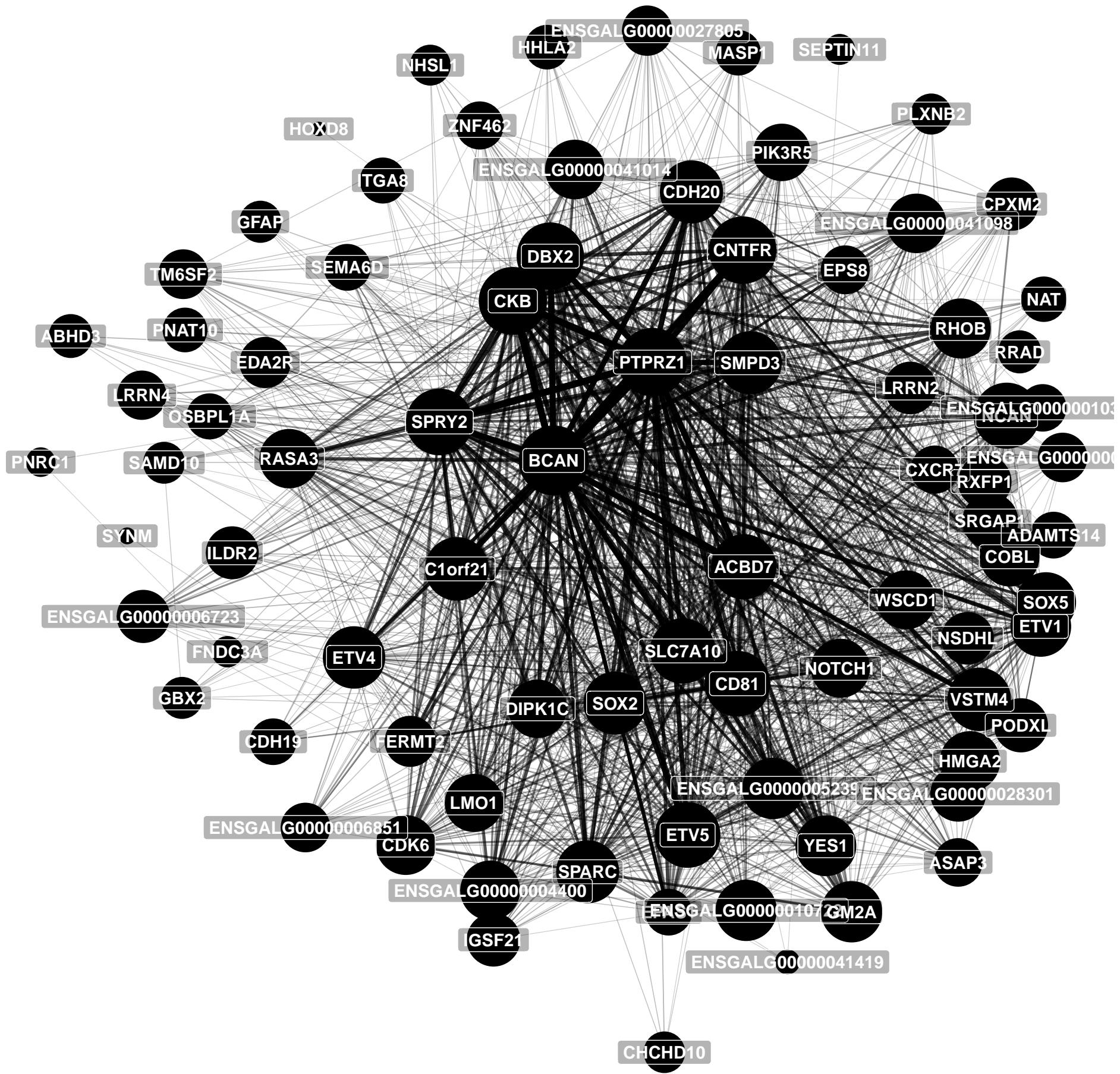




1	HOXB6	TSPAN13	HOXB5	AFDN	AKAP6	SETBP1	ENSGALG00000004509	APC
2	ENSGALG00000002099	PTPRS	EFNB1					

	Term	Ont	N	n	Adj. p-value
GO:0061000	negative regulation of dendritic spine development	BP	1	1	0.0008304
GO:0007275	multicellular organism development	BP	586	4	0.0009754
GO:0048856	anatomical structure development	BP	634	4	0.00131
GO:0032502	developmental process	BP	666	4	0.001574
GO:0048671	negative regulation of collateral sprouting	BP	2	1	0.00166
GO:0032501	multicellular organismal process	BP	724	4	0.002144
GO:0048681	negative regulation of axon regeneration	BP	3	1	0.002489
GO:0070571	negative regulation of neuron projection regeneration	BP	3	1	0.002489
GO:0099560	synaptic membrane adhesion	BP	3	1	0.002489
GO:0048668	collateral sprouting	BP	5	1	0.004146

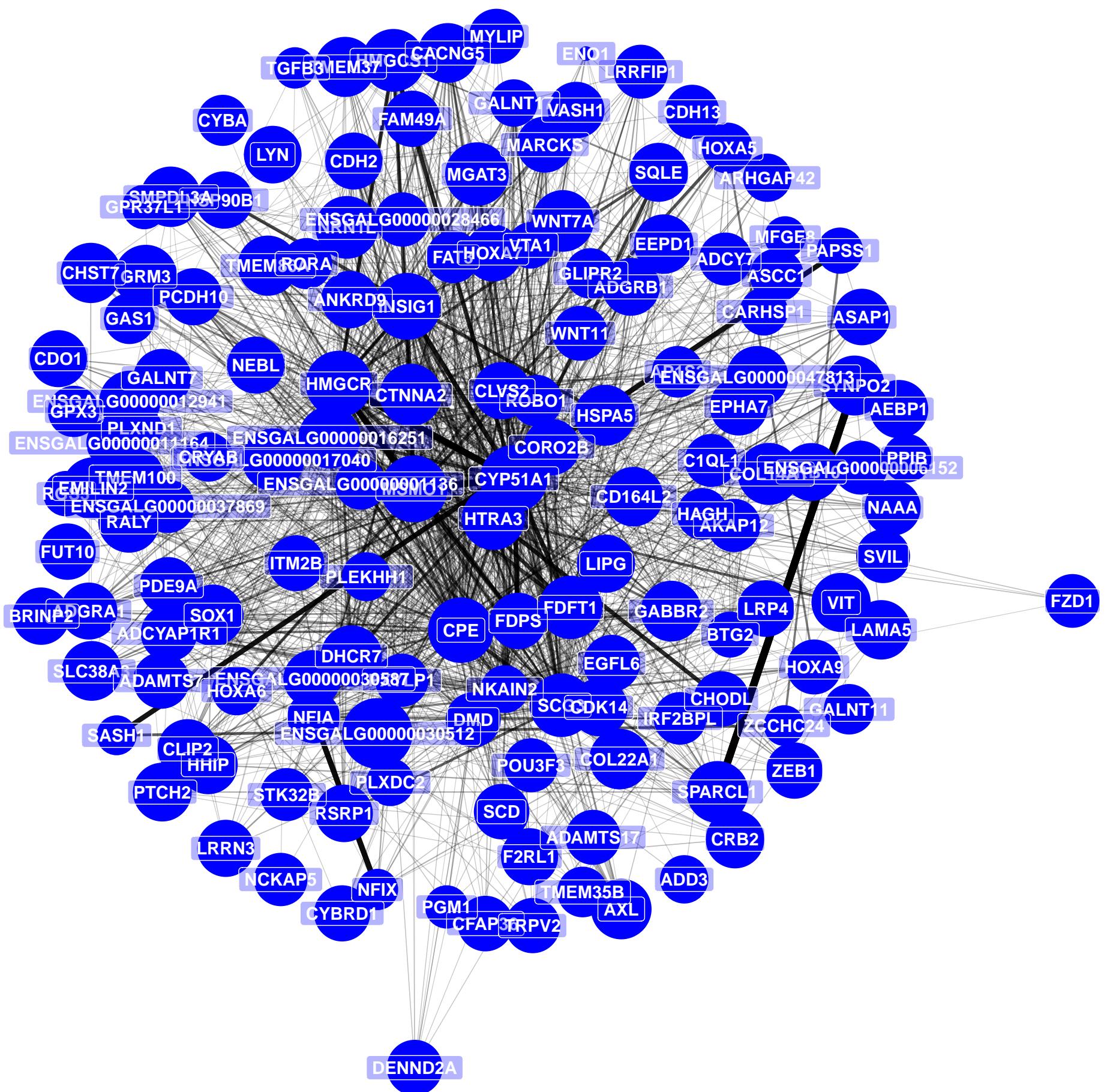
	Pathway	N	DE	P.DE
<i>path:gga00051</i>	Fructose and mannose metabolism	34	1	0.02789
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.05032
<i>path:gga04520</i>	Adherens junction	69	1	0.05585
<i>path:gga04514</i>	Cell adhesion molecules	103	1	0.08232
<i>path:gga04120</i>	Ubiquitin mediated proteolysis	128	1	0.1013
<i>path:gga04310</i>	Wnt signaling pathway	134	1	0.1059
<i>path:gga04530</i>	Tight junction	135	1	0.1066
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	1	0.1456
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1



1	PTPRZ1	BCAN	DBX2	CKB	CNTFR	ETV5	SPRY2	CD81
2	ACBD7	NCAN	SPARC	ENSGALG00000010722	CDH20	SOX2	SLC7A10	NOTCH1
3	VSTM4	SMPD3	ETV1	C1orf21	DIPK1C	RHOB	YES1	ETV4
4	COBL	RASA3	ENSGALG00000052396	GM2A	SOX5	CDK6	PODXL	HMGA2
5	LMO1	WSCD1	ENSGALG00000004400	ENSGALG00000041014	PIK3R5	ENSGALG00000041098	FERMT2	EPAS1
6	SRGAP1	IGSF21	LRRN2	ENSGALG00000028301	EPS8	NSDHL	CPXM2	ENSGALG00000006723
7	RXFP1	ILDR2	ASAP3	CXCR7	EDA2R	ENSGALG0000006851	ZNF462	ENSGALG00000004518
8	ENSGALG00000027805	OSBPL1A	SEMA6D	TM6SF2	ENSGALG00000010316	LRRN4	ADAMTS14	CDH19
9	NAT	GBX2	PLXNB2	MASP1	ITGA8	HHLA2	PNAT10	ABHD3
10	GFAP	RRAD	SAMD10	NHSL1	CHCHD10	FNDC3A	PNRC1	SEPTIN11
11	ENSGALG00000041419	SYNM	HOXD8					

	Term	Ont	N	n	Adj. p-value
GO:0032502	developmental process	BP	666	10	0.004585
GO:0060582	cell fate determination involved in pattern specification	BP	1	1	0.005738
GO:0033631	cell–cell adhesion mediated by integrin	BP	1	1	0.005738
GO:0048859	formation of anatomical boundary	BP	1	1	0.005738
GO:0010160	formation of animal organ boundary	BP	1	1	0.005738
GO:0030033	microvillus assembly	BP	1	1	0.005738
GO:0033634	positive regulation of cell–cell adhesion mediated by integrin	BP	1	1	0.005738
GO:0033632	regulation of cell–cell adhesion mediated by integrin	BP	1	1	0.005738
GO:0032534	regulation of microvillus assembly	BP	1	1	0.005738
GO:0008052	sensory organ boundary specification	BP	1	1	0.005738

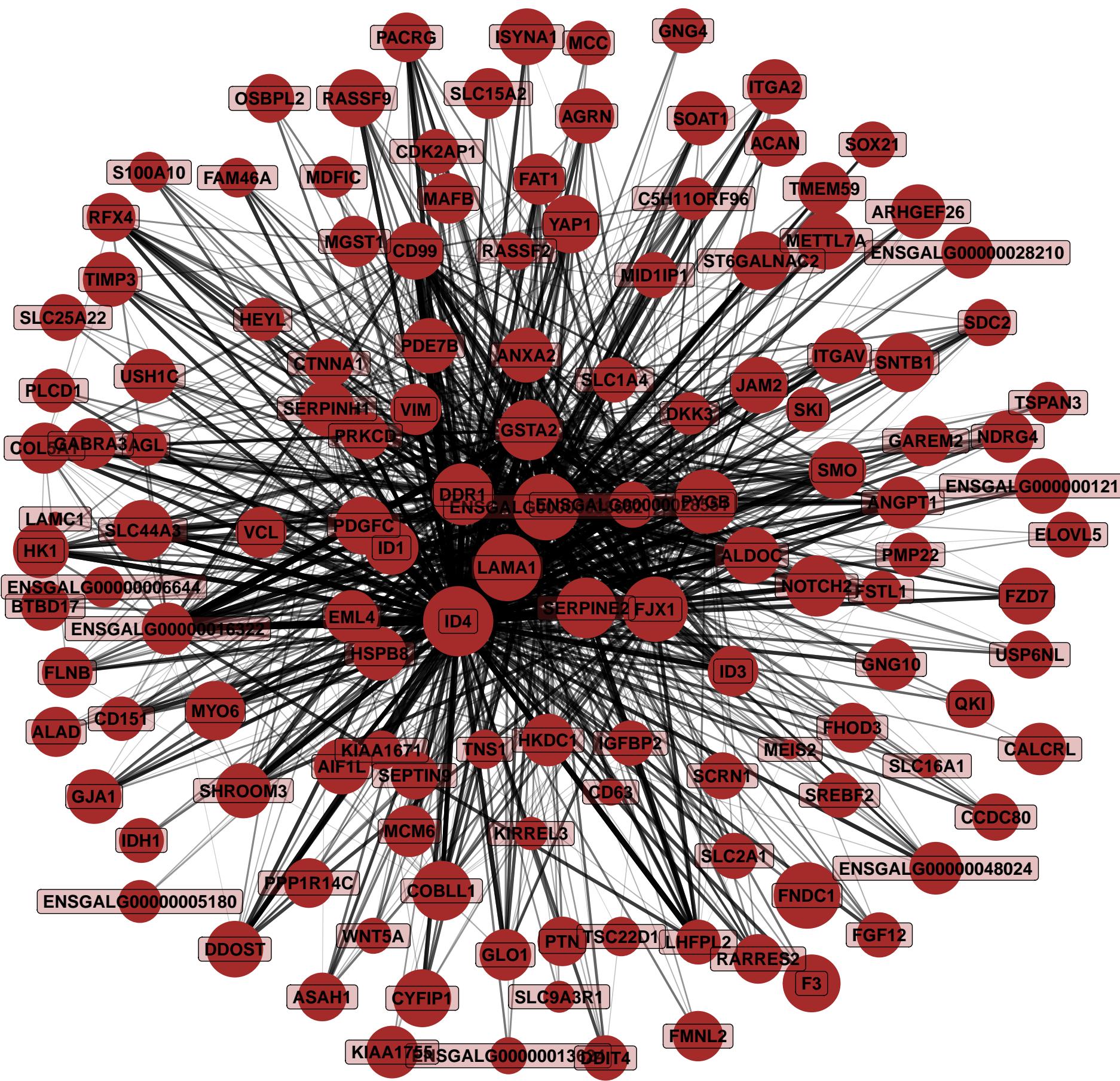
	Pathway	N	DE	P.DE
<i>path:gga00232</i>	Caffeine metabolism	4	2	0.0001935
<i>path:gga00983</i>	Drug metabolism – other enzymes	54	2	0.03837
<i>path:gga04512</i>	ECM–receptor interaction	67	2	0.05655
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	154	3	0.0586
<i>path:gga00100</i>	Steroid biosynthesis	16	1	0.088
<i>path:gga00900</i>	Terpenoid backbone biosynthesis	19	1	0.1036
<i>path:gga00260</i>	Glycine, serine and threonine metabolism	32	1	0.1684
<i>path:gga00330</i>	Arginine and proline metabolism	40	1	0.2059
<i>path:gga00270</i>	Cysteine and methionine metabolism	42	1	0.215
<i>path:gga00600</i>	Sphingolipid metabolism	47	1	0.2373



1	ENSGALG00000030512	COL14A1	MSMO1	HTRA3	CYP51A1	INSIG1	HMGCR	CPE
2	GRM3	SCG3	SOX1	SPARCL1	SYNPO2	ENSGALG0000016251	NRN1L	ENSGALG0000012941
3	CDH2	CTNNA2	FDFT1	GABBR2	ENSGALG0000017040	HMGCS1	MGAT3	VIT
4	ENSGALG0000047813	NFIA	CDK14	EMILIN2	ENSGALG0000001136	CHST7	DHCR7	CACNG5
5	WNT7A	BRINP2	SLC38A3	HSPA5	ADCYAP1R1	ANKRD9	PXYLP1	CLVS2
6	ROBO1	SMPDL3A	CD164L2	CRB2	AKAP12	RSRP1	COL22A1	TMEM86A
7	EPHA7	ITM2B	PTCH2	F2RL1	ADGRB1	HHIP	NKAIN2	RALY
8	GALNT7	AEBP1	SCD	CHODL	LAMA5	LRP4	CLIP2	AXL
9	EEPD1	CORO2B	CDO1	SQLE	TMEM37	HOXA7	SVIL	PCDH10
10	DMD	NEBL	GRB10	CDH13	ADGRA1	AP1S2	HSP90B1	LYN
11	TMEM100	HOXA9	PDE9A	MARCKS	LIPG	IRF2BPL	ASAP1	LRRN3
12	EGFL6	ZEB1	ADAMTS7	VASH1	WNT11	STK32B	DENND2A	CRYAB
13	POU3F3	ENSGALG00000030587	MYLIP	FDPS	FAM49A	HOXA5	GALNT17	RORA
14	LRRFIP1	ASCC1	CFAP36	TRPV2	RGS3	FUT10	NAAA	FZD1
15	ENSGALG0000006152	CYBRD1	ENSGALG0000037869	FAT3	HAGH	ADAMTS17	GPX3	ENSGALG0000011164
16	ENSGALG0000028466	GAS1	PLEKHH1	HOXA6	ADCY7	NCKAP5	C1QL1	GALNT11
17	NFIX	BTG2	PLXDC2	CYBA	TMEM35B	ARHGAP42	ADD3	TGFB3
18	PPIB	GLIPR2	CARHSP1	PAPSS1	PGM1	VTA1	GPR37L1	PLXND1
19	MFGE8	SASH1	ZCCHC24	ENO1				

	Term	Ont	N	n	Adj. p-value
GO:0016126	sterol biosynthetic process	BP	9	4	1.757e-06
GO:0048705	skeletal system morphogenesis	BP	41	6	5.505e-06
GO:0006694	steroid biosynthetic process	BP	16	4	2.389e-05
GO:0048704	embryonic skeletal system morphogenesis	BP	17	4	3.097e-05
GO:0006695	cholesterol biosynthetic process	BP	7	3	4.537e-05
GO:1902653	secondary alcohol biosynthetic process	BP	7	3	4.537e-05
GO:1901362	organic cyclic compound biosynthetic process	BP	456	16	4.625e-05
GO:0016125	sterol metabolic process	BP	19	4	4.957e-05
GO:1901576	organic substance biosynthetic process	BP	673	20	5.346e-05
GO:0009058	biosynthetic process	BP	682	20	6.429e-05

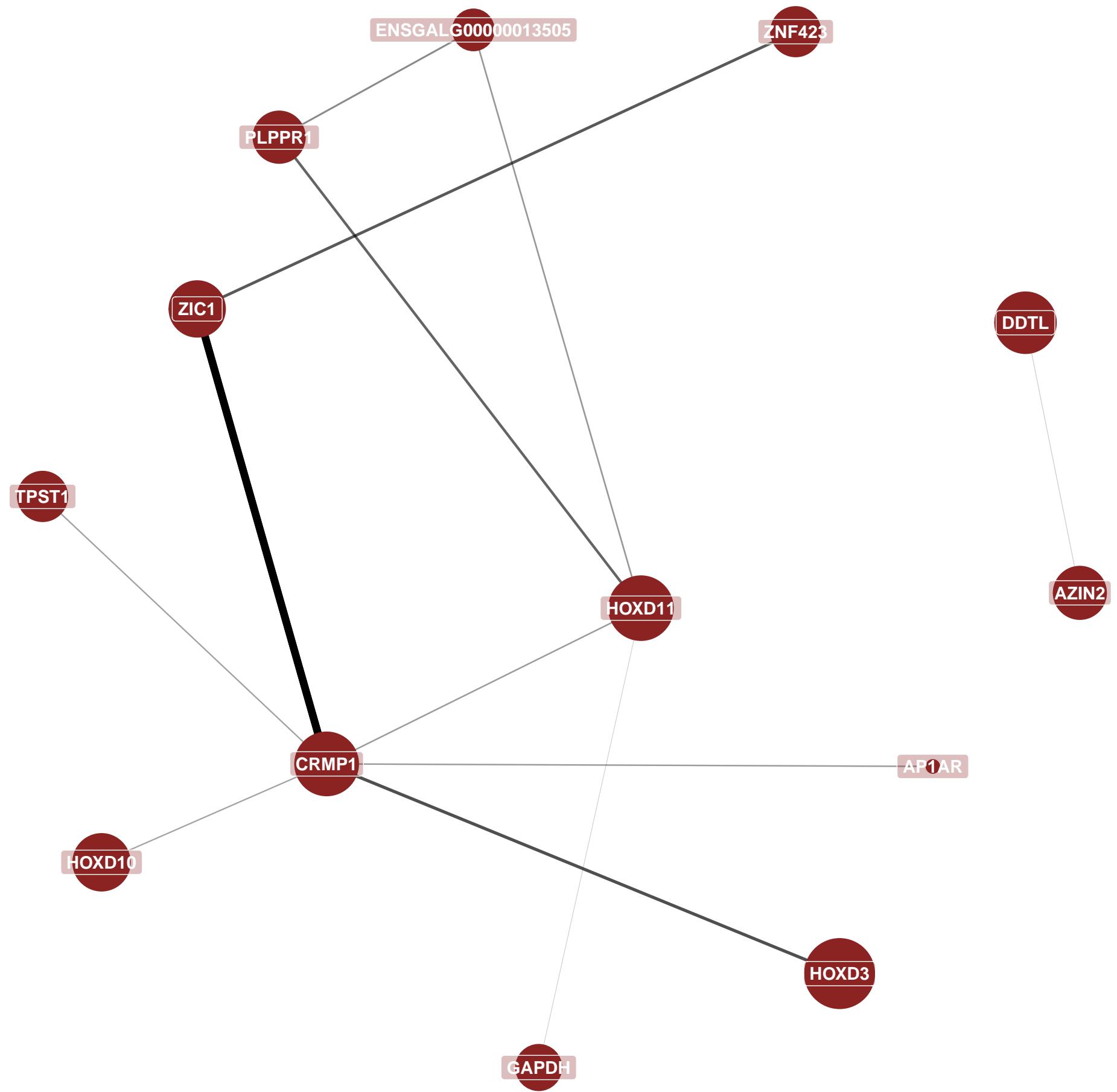
	Pathway	N	DE	P.DE
<i>path:gga00100</i>	Steroid biosynthesis	16	5	6.224e-07
<i>path:gga00900</i>	Terpenoid backbone biosynthesis	19	3	0.001139
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	3	0.003961
<i>path:gga01100</i>	Metabolic pathways	1256	24	0.005772
<i>path:gga00230</i>	Purine metabolism	113	5	0.008466
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	3	0.01049
<i>path:gga04916</i>	Melanogenesis	83	4	0.0136
<i>path:gga04340</i>	Hedgehog signaling pathway	47	3	0.01521
<i>path:gga03264</i>	Virion – Flavivirus	3	1	0.03293
<i>path:gga04150</i>	mTOR signaling pathway	134	4	0.06203



1	ID4	GSTA2	FNDC1	DDR1	ENSGALG00000038652	FJX1	LAMA1	ENSGALG00000016322
2	CD99	GJA1	SERPINE2	VIM	COL5A1	PTN	AGRN	ID1
3	TIMP3	PYGB	ENSGALG00000028551	COBLL1	SERPINH1	SNTB1	ANXA2	AIF1L
4	YAP1	NOTCH2	F3	ANGPT1	LHFPL2	GNG10	SHROOM3	MYO6
5	ENSGALG00000048024	SLC44A3	PDGFC	MAFB	SDC2	ID3	ISYNA1	SMO
6	METTL7A	RFX4	DKK3	FZD7	PMP22	PDE7B	JAM2	HSPB8
7	ST6GALNAC2	FAT1	RASSF9	HKDC1	CYFIP1	ALDOC	VCL	CTNNNA1
8	HK1	ITGAV	PACRG	ENSGALG00000028210	C5H11ORF96	ITGA2	FLNB	NDRG4
9	DDOST	FSTL1	USH1C	ENSGALG00000012121	SLC2A1	HEYL	CALCRL	RARRES2
10	MCM6	SOAT1	KIAA1755	GAREM2	ASAHI	ACAN	PRKCD	TMEM59
11	PPP1R14C	WNT5A	ARHGEF26	GNG4	EML4	SLC1A4	KIAA1671	MEIS2
12	MID1IP1	QKI	SLC15A2	TNS1	MGST1	CDK2AP1	IDH1	CD151
13	FAM46A	SOX21	BTBD17	FHOD3	GLO1	S100A10	FMNL2	CCDC80
14	GABRA3	FGF12	SLC25A22	SCRN1	AGL	IGFBP2	SEPTIN9	ALAD
15	USP6NL	DDIT4	LAMC1	OSBPL2	PLCD1	MDFIC	ELOVL5	TSPAN3
16	MCC	SKI	CD63	TSC22D1	SLC9A3R1	ENSGALG00000013624	KIRREL3	ENSGALG00000005180
17	RASSF2	SREBF2	ENSGALG00000006644	SLC16A1				

	Term	Ont	N	n	Adj. p-value
GO:0048856	anatomical structure development	BP	634	18	4.153e-05
GO:0023052	signaling	BP	519	16	4.358e-05
GO:0007275	multicellular organism development	BP	586	17	5.299e-05
GO:0007166	cell surface receptor signaling pathway	BP	267	11	5.913e-05
GO:0023051	regulation of signaling	BP	267	11	5.913e-05
GO:0032501	multicellular organismal process	BP	724	19	7.22e-05
GO:0032502	developmental process	BP	666	18	7.844e-05
GO:0009653	anatomical structure morphogenesis	BP	300	11	0.0001663
GO:0007154	cell communication	BP	526	15	0.0001817
GO:0048583	regulation of response to stimulus	BP	306	11	0.0001976

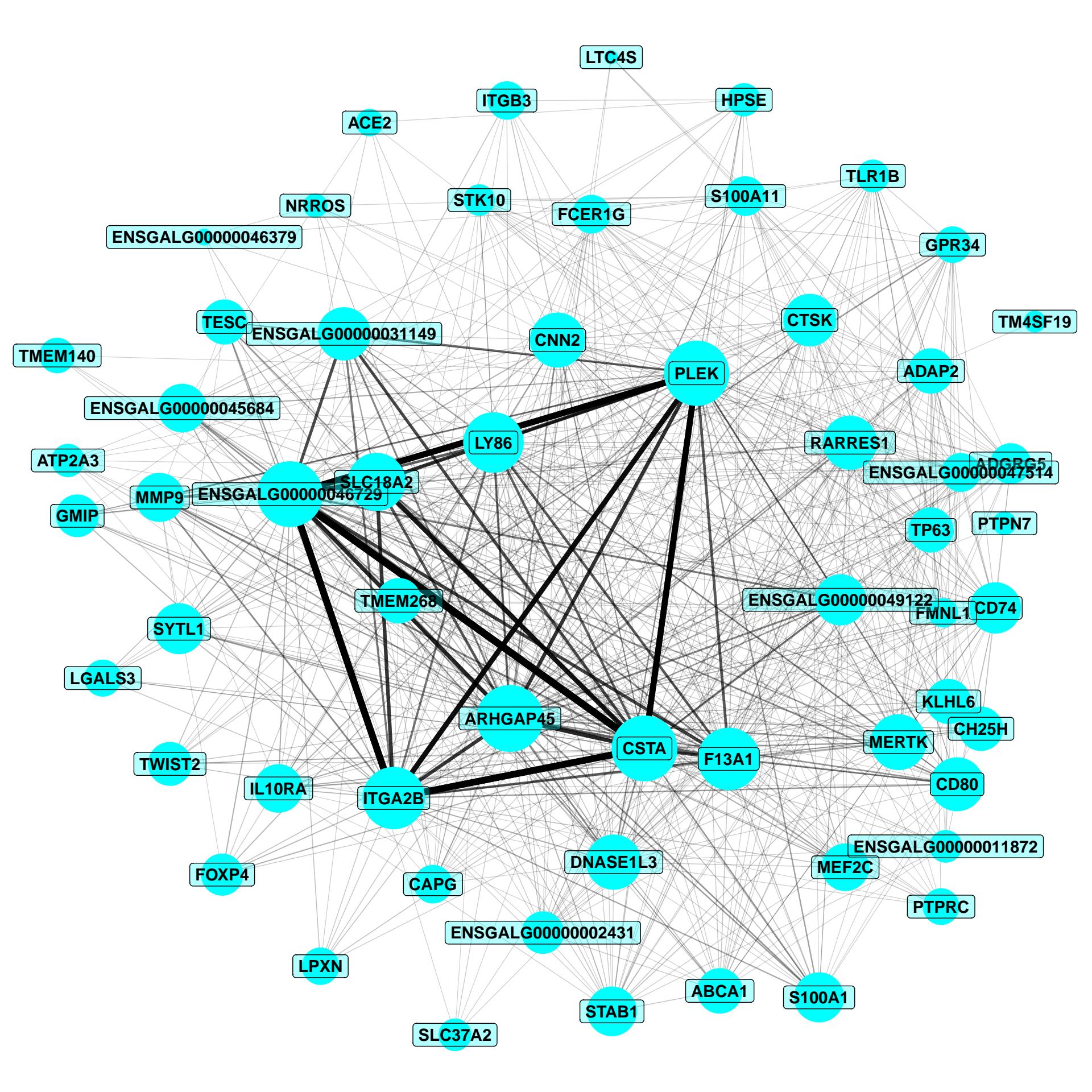
	Pathway	N	DE	P.DE
<i>path:gga00480</i>	Glutathione metabolism	47	6	5.877e-06
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	5	7.979e-06
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	31	5	1.124e-05
<i>path:gga00500</i>	Starch and sucrose metabolism	25	4	9.268e-05
<i>path:gga00983</i>	Drug metabolism – other enzymes	54	5	0.0001749
<i>path:gga04512</i>	ECM–receptor interaction	67	5	0.0004828
<i>path:gga00524</i>	Neomycin, kanamycin and gentamicin biosynthesis	5	2	0.0009232
<i>path:gga04510</i>	Focal adhesion	174	7	0.00156
<i>path:gga00051</i>	Fructose and mannose metabolism	34	3	0.004332
<i>path:gga01100</i>	Metabolic pathways	1256	21	0.009721



1	ZIC1	HOXD3	CRMP1	PLPPR1	DDTL	GAPDH	HOXD11	ZNF423
2	HOXD10	AZIN2	ENSGALG00000013505	TPST1	AP1AR			

	Term	Ont	N	n	Adj. p-value
GO:0051873	killing by host of symbiont cells	BP	1	1	0.0009814
GO:0051883	killing of cells in other organism involved in symbiotic interaction	BP	1	1	0.0009814
GO:0000740	nuclear membrane fusion	BP	1	1	0.0009814
GO:0035606	peptidyl-cysteine S-trans-nitrosylation	BP	1	1	0.0009814
GO:0042438	melanin biosynthetic process	BP	2	1	0.001962
GO:0044550	secondary metabolite biosynthetic process	BP	2	1	0.001962
GO:0051702	biological process involved in interaction with symbiont	BP	3	1	0.002942
GO:0006582	melanin metabolic process	BP	3	1	0.002942
GO:0018119	peptidyl-cysteine S-nitrosylation	BP	3	1	0.002942
GO:0017014	protein nitrosylation	BP	3	1	0.002942

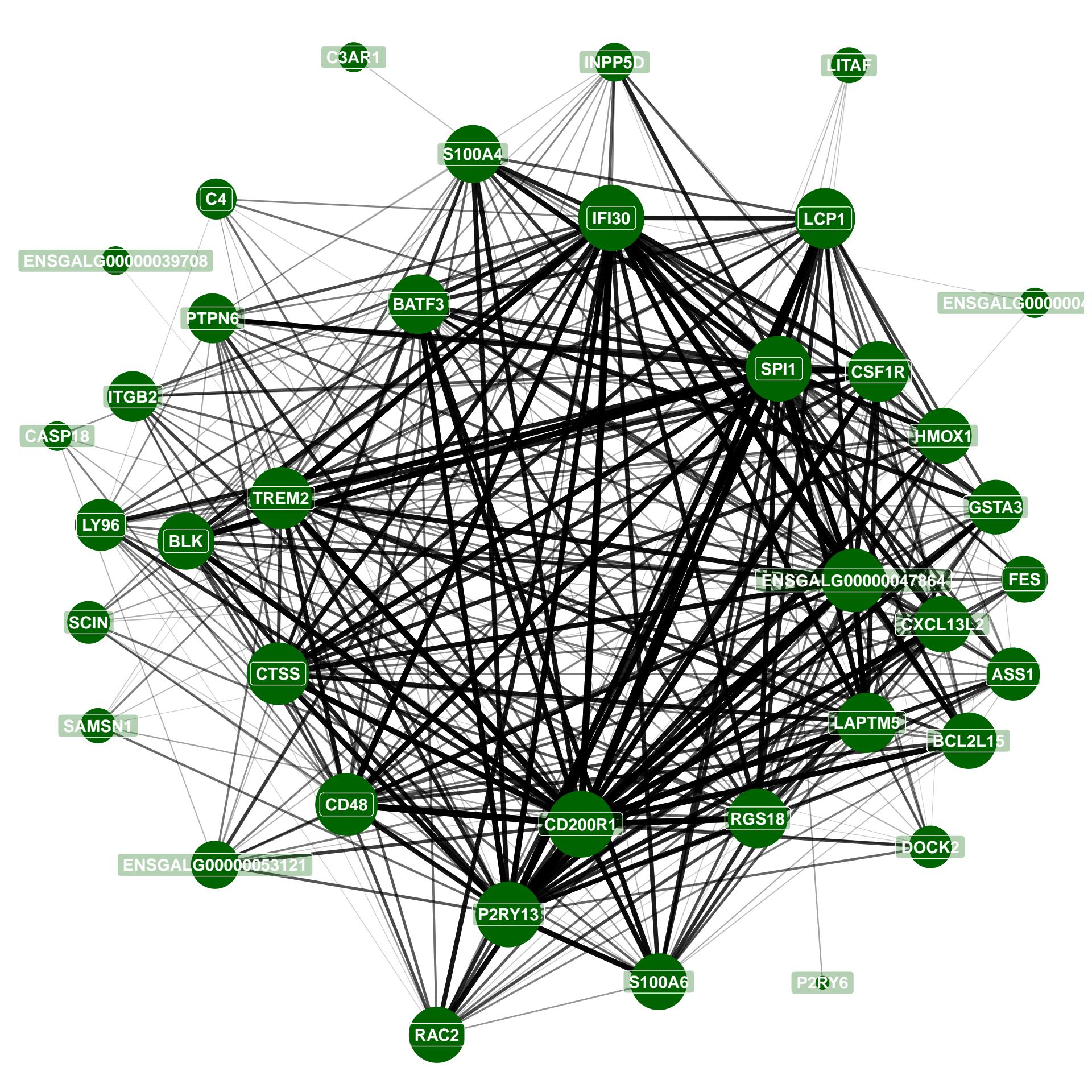
	Pathway	N	DE	P.DE
<i>path:gga00330</i>	Arginine and proline metabolism	40	1	0.03857
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	47	1	0.04518
<i>path:gga01230</i>	Biosynthesis of amino acids	57	1	0.05454
<i>path:gga01200</i>	Carbon metabolism	95	1	0.08937
<i>path:gga05132</i>	Salmonella infection	221	1	0.1965
<i>path:gga01100</i>	Metabolic pathways	1256	2	0.3532
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1
<i>path:gga00785</i>	Lipoic acid metabolism	3	0	1
<i>path:gga00290</i>	Valine, leucine and isoleucine biosynthesis	3	0	1



1	ARHGAP45	F13A1	CSTA	LY86	ENSGALG00000046729	DNASE1L3	TMEM268	ITGA2B
2	CNN2	PLEK	PTPRC	ENSGALG00000011872	ENSGALG0000002431	SYTL1	GPR34	ENSGALG00000047514
3	ENSGALG00000031149	ENSGALG00000045684	TP63	CD74	KLHL6	CTSK	STAB1	SLC18A2
4	RARRES1	LPXN	MEF2C	S100A11	CD80	MERTK	FMNL1	FCER1G
5	ATP2A3	TESC	ABCA1	CAPG	ITGB3	ENSGALG00000049122	PTPN7	TLR1B
6	STK10	IL10RA	HPSE	NRROS	ADAP2	TWIST2	S100A1	SLC37A2
7	CH25H	TMEM140	ADGRG5	LTC4S	MMP9	ENSGALG00000046379	LGALS3	TM4SF19
8	FOXP4	GMIP	ACE2					

	Term	Ont	N	n	Adj. p-value
GO:1902600	proton transmembrane transport	BP	14	2	0.001546
GO:0030200	heparan sulfate proteoglycan catabolic process	BP	1	1	0.004228
GO:0030854	positive regulation of granulocyte differentiation	BP	1	1	0.004228
GO:0030167	proteoglycan catabolic process	BP	1	1	0.004228
GO:0006516	glycoprotein catabolic process	BP	2	1	0.008438
GO:1902307	positive regulation of sodium ion transmembrane transport	BP	2	1	0.008438
GO:2000651	positive regulation of sodium ion transmembrane transporter activity	BP	2	1	0.008438
GO:0010765	positive regulation of sodium ion transport	BP	2	1	0.008438
GO:0032417	positive regulation of sodium:proton antiporter activity	BP	2	1	0.008438
GO:0030852	regulation of granulocyte differentiation	BP	2	1	0.008438

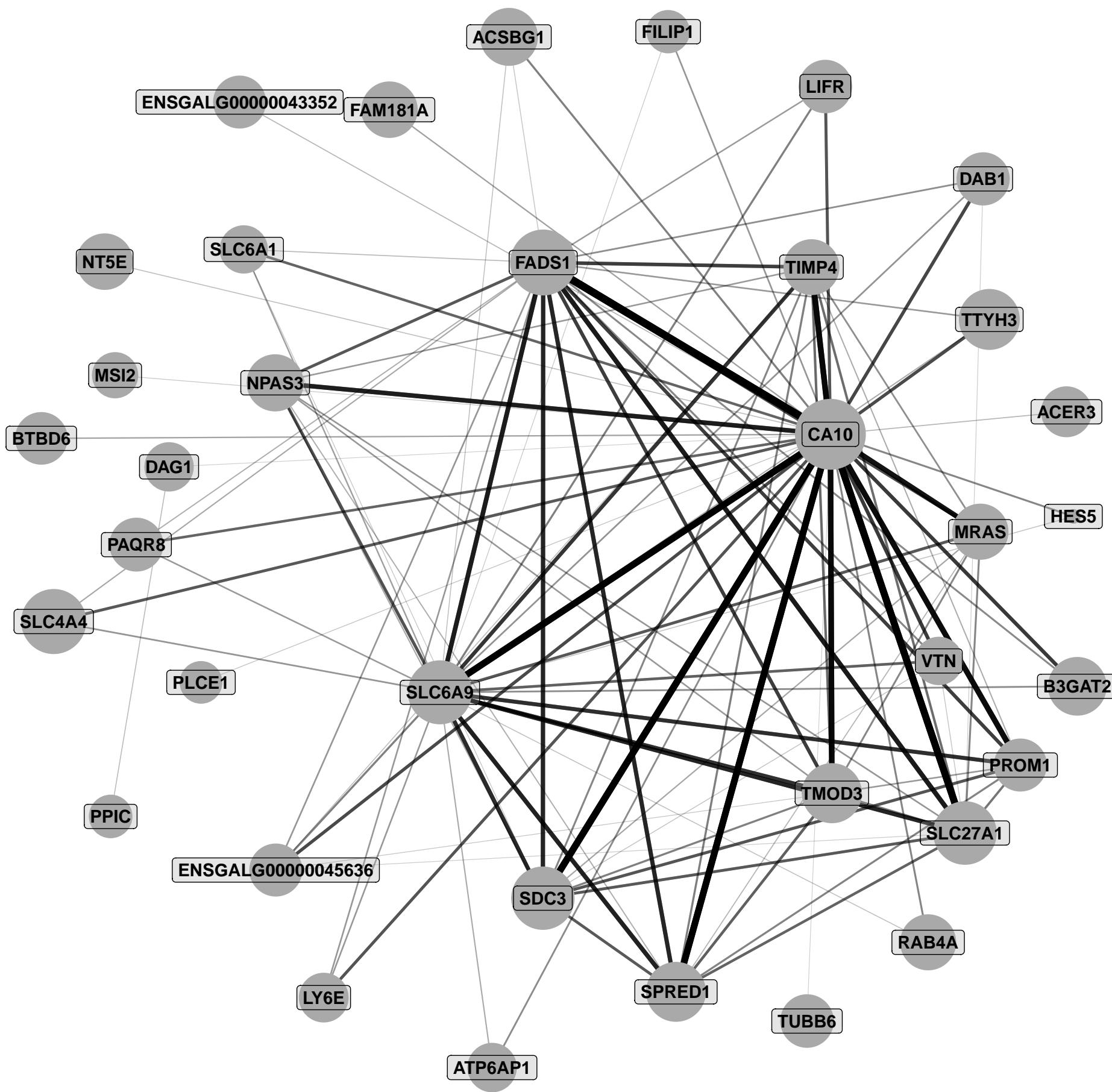
	Pathway	N	DE	P.DE
<i>path:gga04620</i>	Toll-like receptor signaling pathway	71	3	0.003338
<i>path:gga03267</i>	Virion – Adenovirus	2	1	0.008438
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.01681
<i>path:gga04512</i>	ECM–receptor interaction	67	2	0.03257
<i>path:gga00120</i>	Primary bile acid biosynthesis	12	1	0.04959
<i>path:gga00531</i>	Glycosaminoglycan degradation	16	1	0.06558
<i>path:gga04514</i>	Cell adhesion molecules	103	2	0.07034
<i>path:gga04672</i>	Intestinal immune network for IgA production	22	1	0.08906
<i>path:gga05168</i>	Herpes simplex virus 1 infection	130	2	0.1046
<i>path:gga02010</i>	ABC transporters	36	1	0.1416



1	SPI1	IFI30	RGS18	LAPTM5	S100A4	ENSGALG00000047864	P2RY13	TREM2
2	LCP1	CTSS	CSF1R	CD200R1	BATF3	CD48	GSTA3	ENSGALG00000053121
3	BLK	HMOX1	CXCL13L2	SAMSN1	LY96	PTPN6	ASS1	S100A6
4	INPP5D	ITGB2	P2RY6	FES	LITAF	BCL2L15	C4	C3AR1
5	RAC2	DOCK2	CASP18	SCIN	ENSGALG00000039708	ENSGALG00000044313		

	Term	Ont	N	n	Adj. p-value
GO:0006575	cellular modified amino acid metabolic process	BP	25	2	0.002071
GO:0000053	argininosuccinate metabolic process	BP	1	1	0.002718
GO:0071380	cellular response to prostaglandin E stimulus	BP	1	1	0.002718
GO:0071379	cellular response to prostaglandin stimulus	BP	1	1	0.002718
GO:0042167	heme catabolic process	BP	1	1	0.002718
GO:0006788	heme oxidation	BP	1	1	0.002718
GO:0046149	pigment catabolic process	BP	1	1	0.002718
GO:0006787	porphyrin-containing compound catabolic process	BP	1	1	0.002718
GO:0034694	response to prostaglandin	BP	1	1	0.002718
GO:0034695	response to prostaglandin E	BP	1	1	0.002718

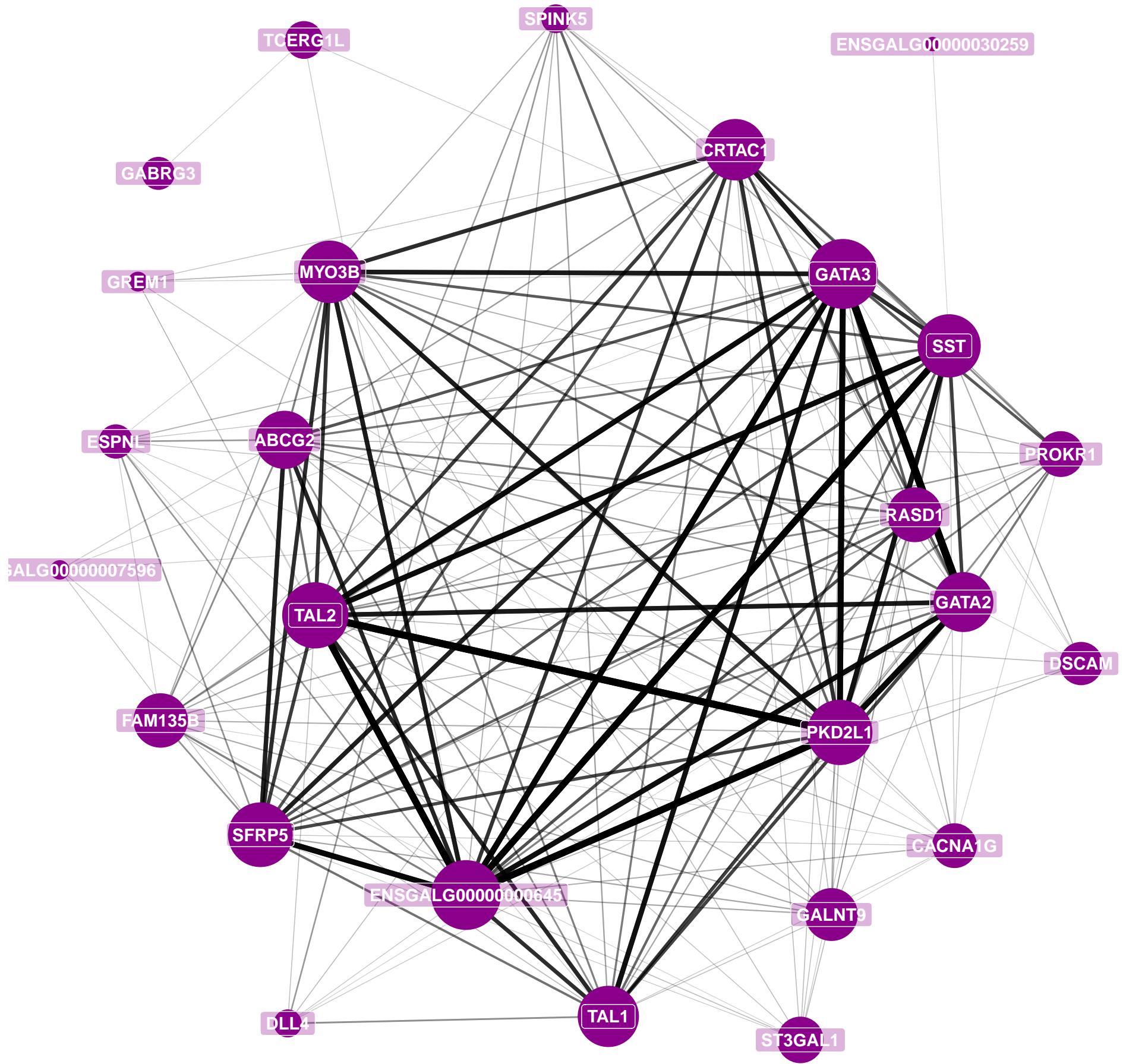
	Pathway	N	DE	P.DE
<i>path:gga04142</i>	Lysosome	114	3	0.003605
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	3	0.01425
<i>path:gga04520</i>	Adherens junction	69	2	0.01503
<i>path:gga04620</i>	Toll-like receptor signaling pathway	71	2	0.01587
<i>path:gga04210</i>	Apoptosis	114	2	0.03825
<i>path:gga04145</i>	Phagosome	125	2	0.04518
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.04524
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	295	3	0.04548
<i>path:gga00860</i>	Porphyrin metabolism	21	1	0.05559
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	154	2	0.06542



1	CA10	B3GAT2	SLC27A1	FADS1	SLC6A9	SLC4A4	TIMP4	ACSBG1
2	NT5E	SDC3	DAB1	TTYH3	TUBB6	TMOD3	MRAS	SLC6A1
3	SPRED1	HES5	VTN	FAM181A	PROM1	FILIP1	NPAS3	PAQR8
4	BTBD6	RAB4A	ENSGALG00000045636	ACER3	LIFR	LY6E	ENSGALG00000043352	DAG1
5	ATP6AP1	MSI2	PPIC	PLCE1				

	Term	Ont	N	n	Adj. p-value
GO:2000272	negative regulation of signaling receptor activity	BP	1	1	0.002718
GO:0003419	growth plate cartilage chondrocyte proliferation	BP	3	1	0.008132
GO:0035988	chondrocyte proliferation	BP	4	1	0.01083
GO:0002320	lymphoid progenitor cell differentiation	BP	4	1	0.01083
GO:1900026	positive regulation of substrate adhesion–dependent cell spreading	BP	4	1	0.01083
GO:1900024	regulation of substrate adhesion–dependent cell spreading	BP	4	1	0.01083
GO:0010770	positive regulation of cell morphogenesis involved in differentiation	BP	6	1	0.0162
GO:0010769	regulation of cell morphogenesis involved in differentiation	BP	6	1	0.0162
GO:0010469	regulation of signaling receptor activity	BP	7	1	0.01887
GO:0034446	substrate adhesion–dependent cell spreading	BP	9	1	0.0242

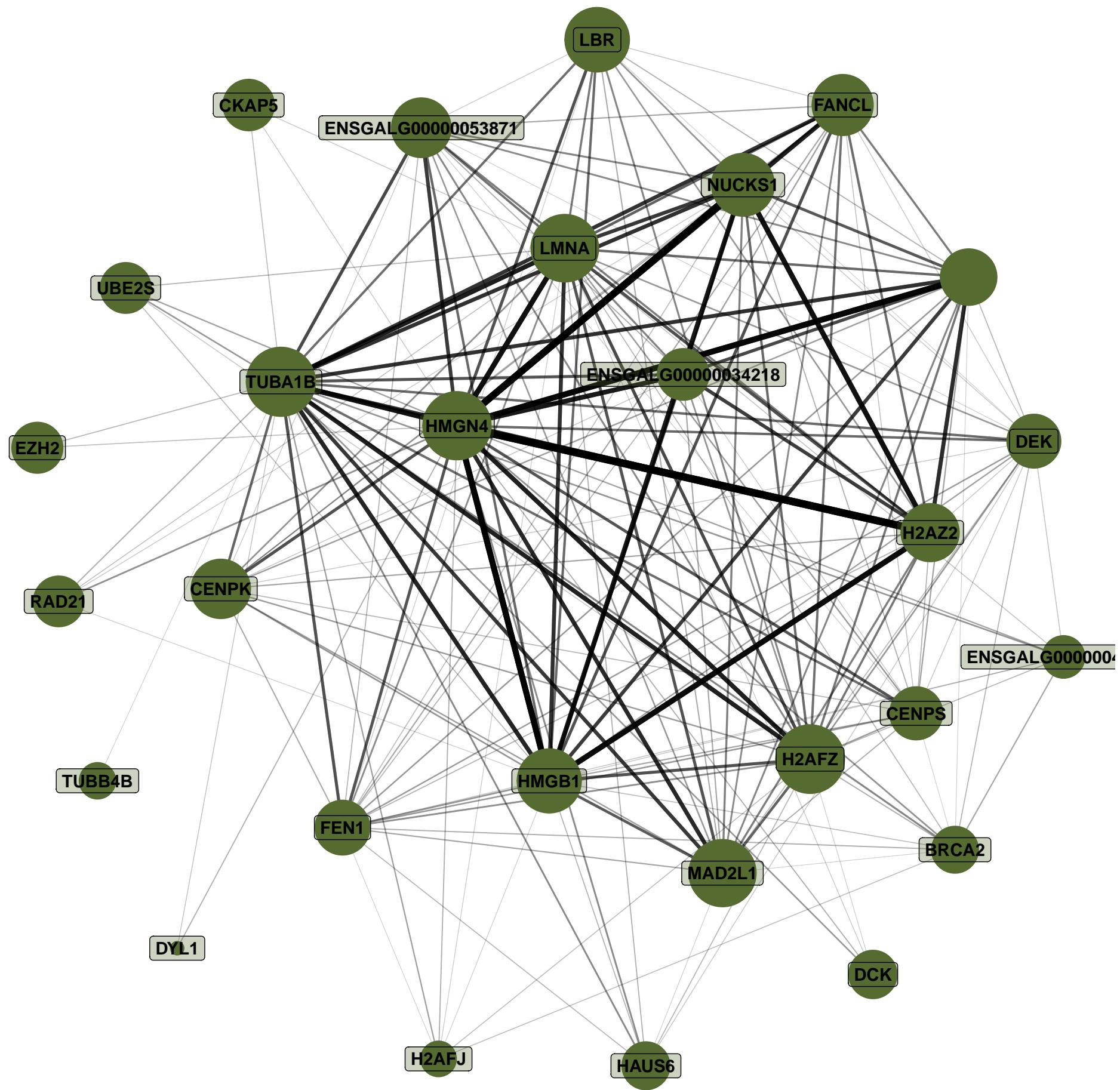
	Pathway	N	DE	P.DE
<i>path:gga00600</i>	Sphingolipid metabolism	47	2	0.00719
<i>path:gga01212</i>	Fatty acid metabolism	51	2	0.008422
<i>path:gga03320</i>	PPAR signaling pathway	58	2	0.01079
<i>path:gga04512</i>	ECM–receptor interaction	67	2	0.01421
<i>path:gga01100</i>	Metabolic pathways	1256	8	0.01744
<i>path:gga00061</i>	Fatty acid biosynthesis	16	1	0.04263
<i>path:gga04145</i>	Phagosome	125	2	0.04518
<i>path:gga00515</i>	Mannose type O–glycan biosynthesis	22	1	0.05816
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	28	1	0.07344
<i>path:gga00071</i>	Fatty acid degradation	31	1	0.08099



1	GATA3	PKD2L1	TAL2	TAL1	CRTAC1	GATA2	SFRP5	ENSGALG00000000645
2	MYO3B	ABCG2	ST3GAL1	FAM135B	GALNT9	DSCAM	PROKR1	SPINK5
3	SST	DLL4	CACNA1G	RASD1	ENSGALG00000007596	GABRG3	TCERG1L	ENSGALG00000030259
4	ESPNL	GREM1						

	Term	Ont	N	n	Adj. p-value
GO:0071695	anatomical structure maturation	BP	18	3	4.189e–06
GO:0021700	developmental maturation	BP	19	3	4.969e–06
GO:0043542	endothelial cell migration	BP	20	3	5.839e–06
GO:0022603	regulation of anatomical structure morphogenesis	BP	73	4	8.298e–06
GO:0040012	regulation of locomotion	BP	74	4	8.762e–06
GO:0060231	mesenchymal to epithelial transition	BP	3	2	9.428e–06
GO:0072172	mesonephric tubule formation	BP	3	2	9.428e–06
GO:0060676	ureteric bud formation	BP	3	2	9.428e–06
GO:0040011	locomotion	BP	166	5	1.02e–05
GO:0043066	negative regulation of apoptotic process	BP	81	4	1.256e–05

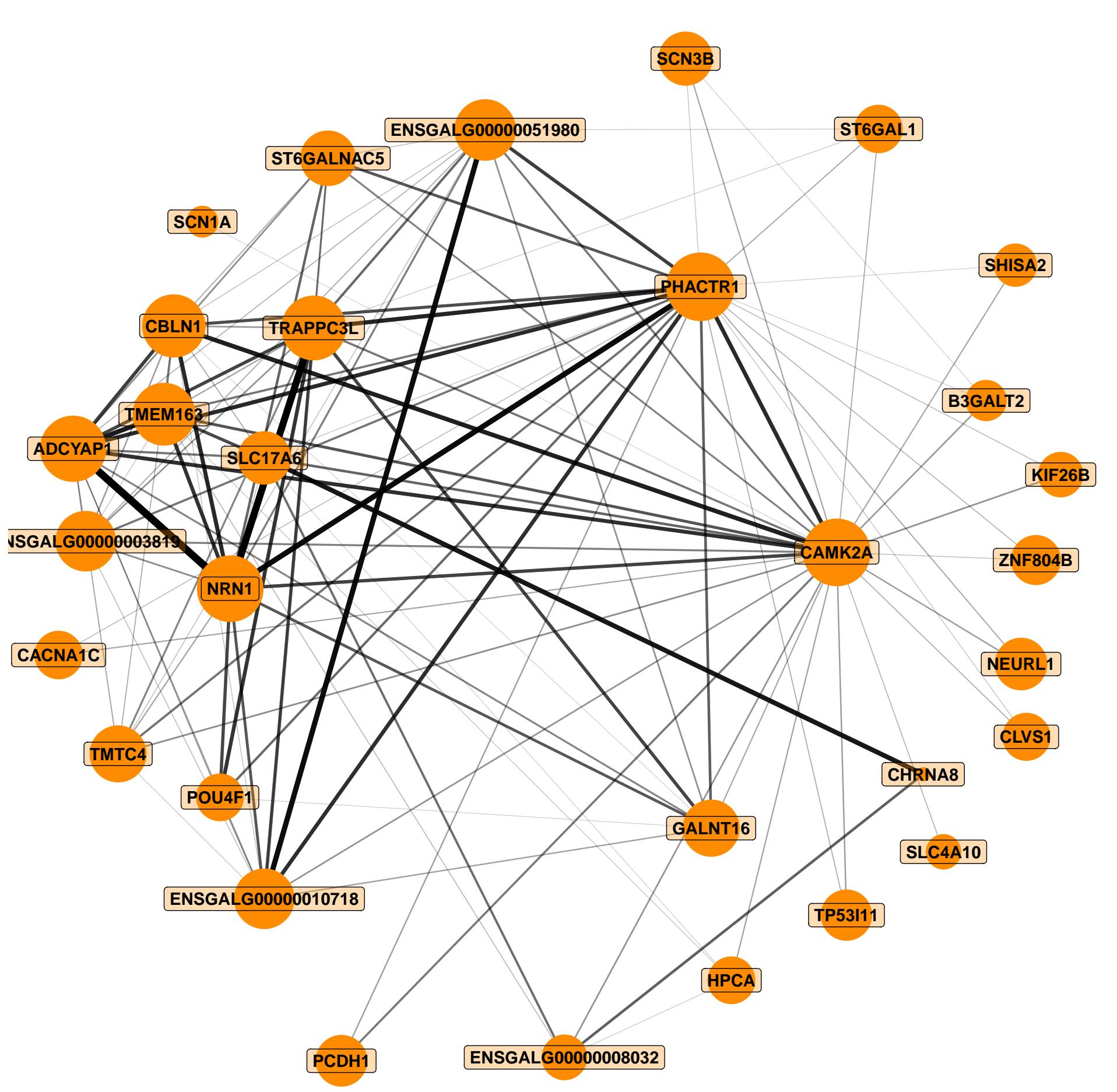
	Pathway	N	DE	P.DE
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	2	0.00124
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	1	0.02154
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	1	0.02331
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.02508
<i>path:gga02010</i>	ABC transporters	36	1	0.06328
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	1	0.07176
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.09016
<i>path:gga04350</i>	TGF-beta signaling pathway	86	1	0.14448
<i>path:gga04310</i>	Wnt signaling pathway	134	1	0.2167
<i>path:gga04020</i>	Calcium signaling pathway	199	1	0.3048



1	MAD2L1	TUBA1B	HMGN4	LMNA	H2AFZ	HMGB1	CENPK	LBR
2	NUCKS1	H2AZ2	FANCL	ENSGALG00000053871	NA	FEN1	ENSGALG00000034218	CENPS
3	DEK	RAD21	BRCA2	UBE2S	HAUS6	DCK	CKAP5	EZH2
4	ENSGALG00000042375	DYL1	TUBB4B	H2AFJ				

	Term	Ont	N	n	Adj. p-value
GO:0051276	chromosome organization	BP	178	8	1.154e-09
GO:0006342	chromatin silencing	BP	15	4	1.569e-08
GO:0045814	negative regulation of gene expression, epigenetic	BP	15	4	1.569e-08
GO:0040029	regulation of gene expression, epigenetic	BP	18	4	3.502e-08
GO:0097549	chromatin organization involved in negative regulation of transcription	BP	19	4	4.43e-08
GO:0034401	chromatin organization involved in regulation of transcription	BP	19	4	4.43e-08
GO:0006996	organelle organization	BP	437	9	8.089e-08
GO:0016458	gene silencing	BP	31	4	3.539e-07
GO:0006325	chromatin organization	BP	110	5	2.063e-06
GO:0016043	cellular component organization	BP	668	9	2.88e-06

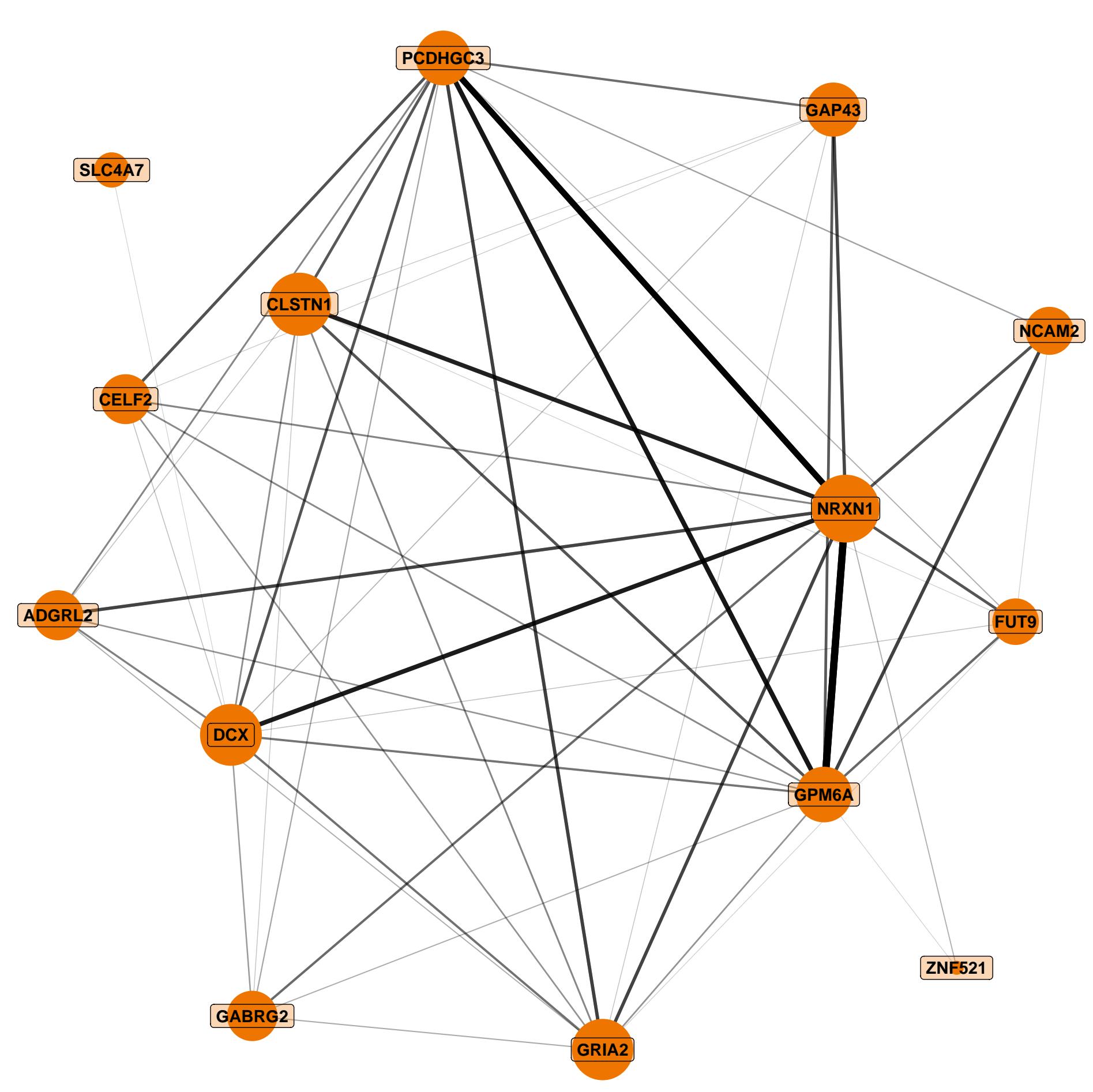
	Pathway	N	DE	P.DE
<i>path:gga04217</i>	Necroptosis	109	4	5.641e–05
<i>path:gga03460</i>	Fanconi anemia pathway	48	3	0.0001095
<i>path:gga03410</i>	Base excision repair	26	2	0.00117
<i>path:gga05132</i>	Salmonella infection	221	3	0.008976
<i>path:gga04540</i>	Gap junction	79	2	0.0104
<i>path:gga04210</i>	Apoptosis	114	2	0.02086
<i>path:gga04110</i>	Cell cycle	114	2	0.02086
<i>path:gga03450</i>	Non–homologous end–joining	12	1	0.02331
<i>path:gga04145</i>	Phagosome	125	2	0.02477
<i>path:gga04120</i>	Ubiquitin mediated proteolysis	128	2	0.02588



1	NRN1	CBLN1	ADCYAP1	PHACTR1	TRAPP C3L	CAMK2A	ENSGALG00000010718	ENSGALG00000051980
2	TMEM163	SLC17A6	ENSGALG00000003819	ST6GALNAC5	GALNT16	NEURL1	TMTC4	TP53I11
3	SCN3B	POU4F1	PCDH1	CLVS1	CACNA1C	ST6GAL1	ZNF804B	HPCA
4	SHISA2	ENSGALG00000008032	B3GALT2	KIF26B	SCN1A	SLC4A10	CHRNA8	

	Term	Ont	N	n	Adj. p-value
O:0007204	positive regulation of cytosolic calcium ion concentration	BP	15	2	0.0004448
O:0051480	regulation of cytosolic calcium ion concentration	BP	23	2	0.001061
O:0006874	cellular calcium ion homeostasis	BP	30	2	0.001807
O:0055074	calcium ion homeostasis	BP	31	2	0.001929
O:0061577	calcium ion transmembrane transport via high voltage-gated calcium channel	BP	1	1	0.002114
O:0010881	regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	BP	1	1	0.002114
O:0010880	regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	BP	1	1	0.002114
O:1903514	release of sequestered calcium ion into cytosol by endoplasmic reticulum	BP	1	1	0.002114
O:0014808	release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	BP	1	1	0.002114
O:0070296	sarcoplasmic reticulum calcium ion transport	BP	1	1	0.002114

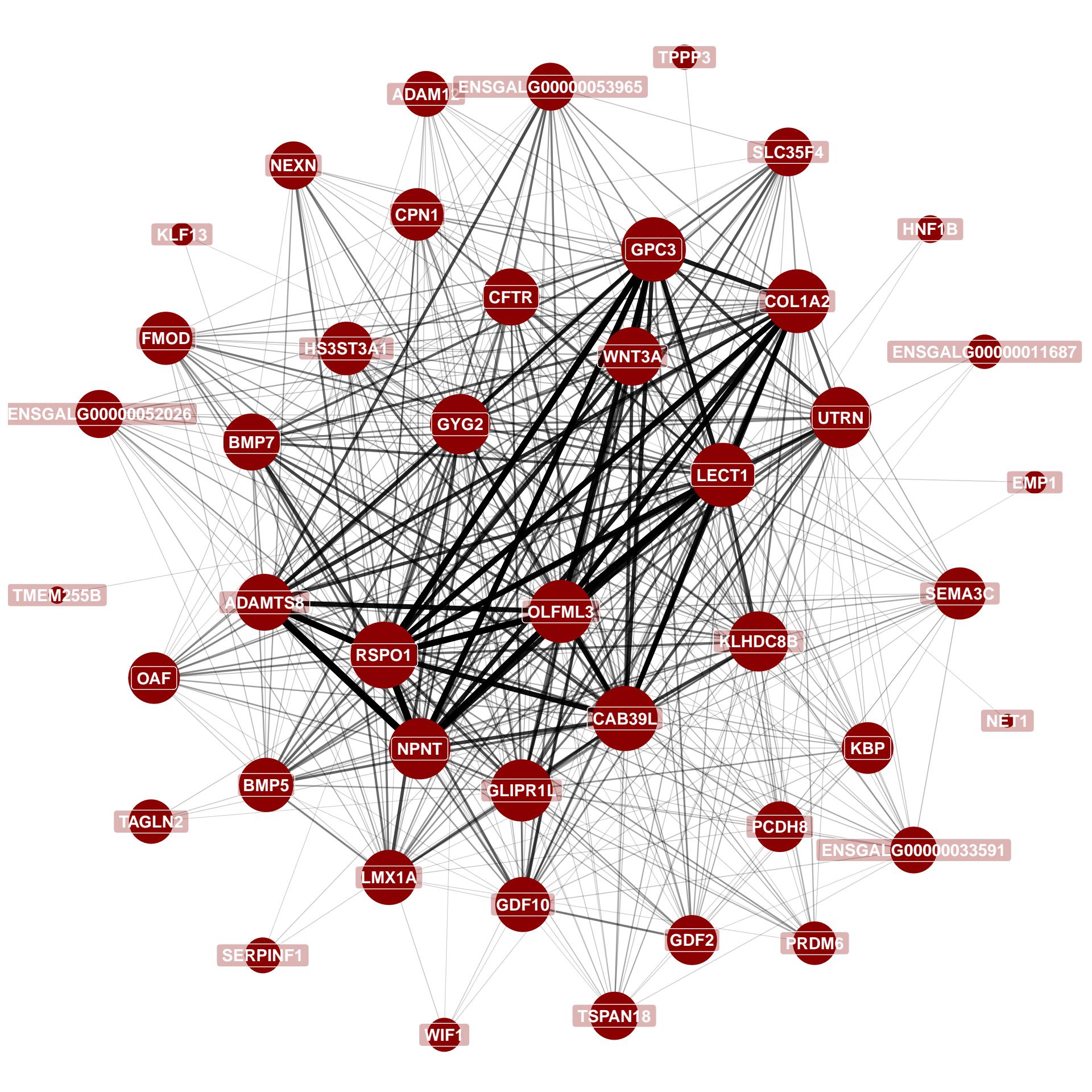
	Pathway	N	DE	P.DE
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	2	0.003358
<i>path:gga04020</i>	Calcium signaling pathway	199	3	0.008299
<i>path:gga04912</i>	GnRH signaling pathway	78	2	0.01172
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	1	0.02715
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	124	2	0.02804
<i>path:gga00601</i>	Glycosphingolipid biosynthesis – lacto and neolacto series	21	1	0.0435
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	1	0.05958
<i>path:gga00510</i>	N-Glycan biosynthesis	45	1	0.09097
<i>path:gga04260</i>	Cardiac muscle contraction	60	1	0.1195
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	295	2	0.1281



1	NRXN1	GPM6A	PCDHGC3	GAP43	CLSTN1	GRIA2	DCX	ADGRL2
2	NCAM2	CELF2	GABRG2	FUT9	ZNF521	SLC4A7		

	Term	Ont	N	n	Adj. p-value
GO:0071420	cellular response to histamine	BP	1	1	0.001132
GO:0034776	response to histamine	BP	1	1	0.001132
GO:0016198	axon choice point recognition	BP	2	1	0.002264
GO:1904862	inhibitory synapse assembly	BP	4	1	0.004522
GO:0051932	synaptic transmission, GABAergic	BP	4	1	0.004522
GO:1902476	chloride transmembrane transport	BP	5	1	0.00565
GO:0007214	gamma-aminobutyric acid signaling pathway	BP	5	1	0.00565
GO:0098661	inorganic anion transmembrane transport	BP	5	1	0.00565
GO:0006376	mRNA splice site selection	BP	5	1	0.00565
GO:0009791	post-embryonic development	BP	6	1	0.006777

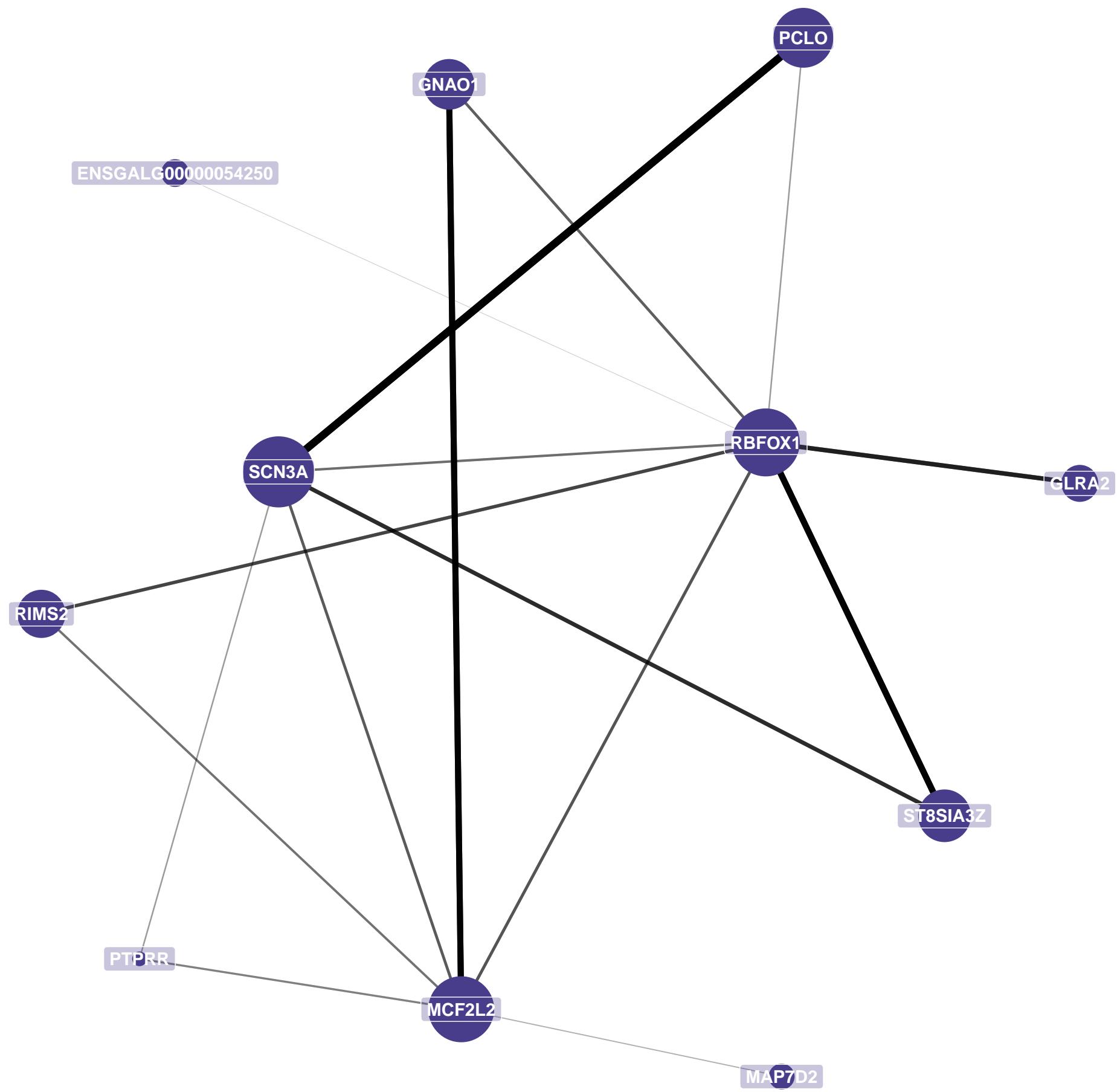
	Pathway	N	DE	P.DE
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.004522
<i>path:gga04514</i>	Cell adhesion molecules	103	2	0.005886
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	1	0.01351
<i>path:gga00601</i>	Glycosphingolipid biosynthesis – lacto and neolacto series	21	1	0.02353
<i>path:gga00515</i>	Mannose type O-glycan biosynthesis	22	1	0.02464
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	295	2	0.04288
<i>path:gga01100</i>	Metabolic pathways	1256	1	0.7758
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1
<i>path:gga00785</i>	Lipoic acid metabolism	3	0	1



1	RSPO1	CAB39L	LECT1	GPC3	OLFML3	COL1A2	GYG2	KLHDC8B
2	GLIPR1L	UTRN	LMX1A	WNT3A	CFTR	BMP5	NPNT	HS3ST3A1
3	PCDH8	SEMA3C	BMP7	KBP	GDF10	NEXN	ADAMTS8	ENSGALG00000052026
4	FMOD	CPN1	GDF2	TSPAN18	OAF	ENSGALG00000033591	TAGLN2	ADAM12
5	WIF1	ENSGALG00000053965	SLC35F4	PRDM6	SERPINF1	ENSGALG00000011687	HNF1B	KLF13
6	TMEM255B	TPPP3	NET1	EMP1				

	Term	Ont	N	n	Adj. p-value
GO:0050679	positive regulation of epithelial cell proliferation	BP	22	2	0.002178
GO:0030509	BMP signaling pathway	BP	26	2	0.00304
GO:0035235	ionotropic glutamate receptor signaling pathway	BP	1	1	0.003171
GO:0071773	cellular response to BMP stimulus	BP	29	2	0.003774
GO:0071772	response to BMP	BP	29	2	0.003774
GO:0090287	regulation of cellular response to growth factor stimulus	BP	32	2	0.004583
GO:0050678	regulation of epithelial cell proliferation	BP	33	2	0.004869
GO:0007215	glutamate receptor signaling pathway	BP	2	1	0.006332
GO:2000279	negative regulation of DNA biosynthetic process	BP	2	1	0.006332
GO:0045603	positive regulation of endothelial cell differentiation	BP	2	1	0.006332

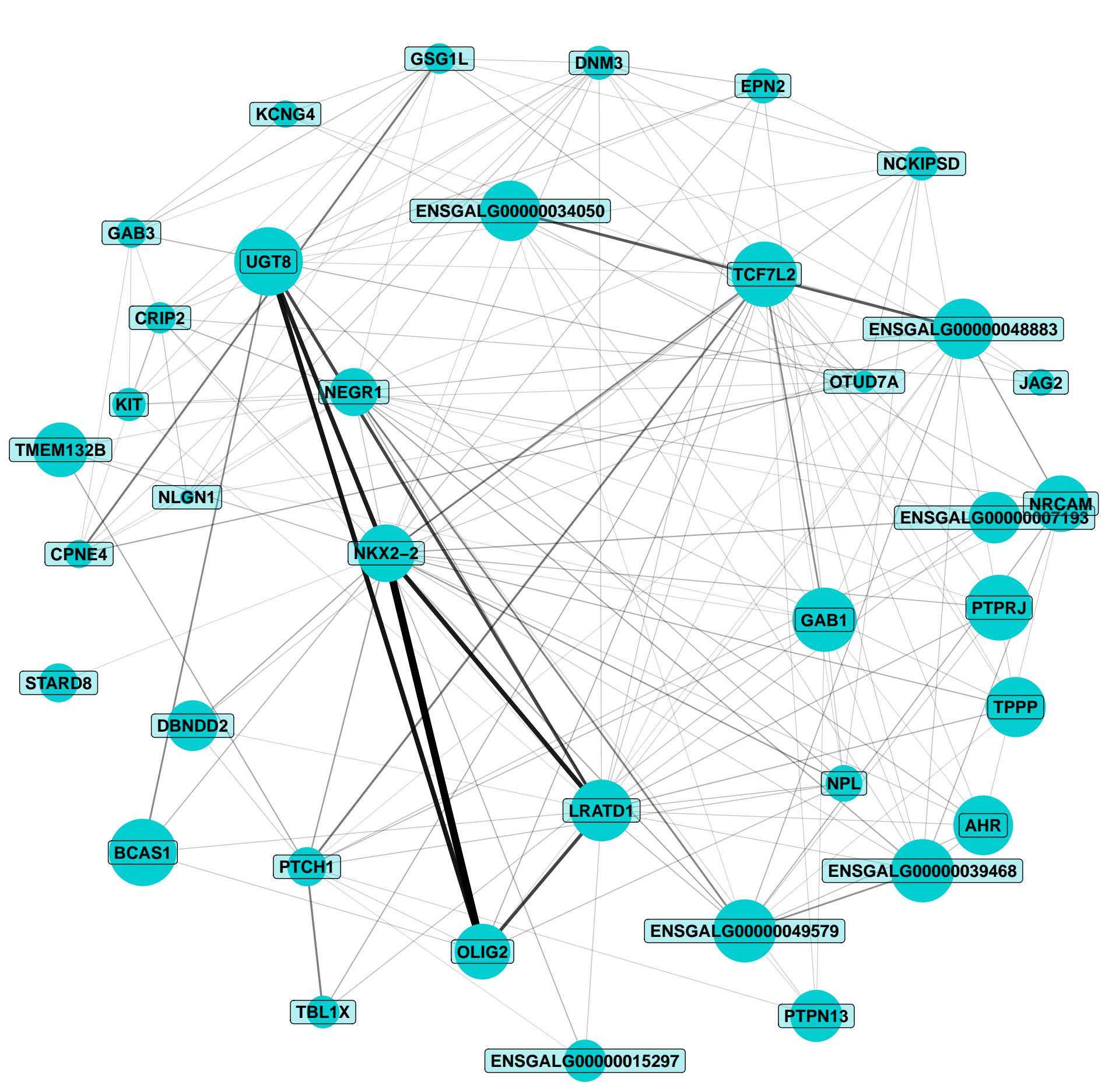
	Pathway	N	DE	P.DE
<i>path:gga04310</i>	Wnt signaling pathway	134	4	0.000832
<i>path:gga04350</i>	TGF–beta signaling pathway	86	3	0.002527
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	154	3	0.0127
<i>path:gga04512</i>	ECM–receptor interaction	67	2	0.01905
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis – heparan sulfate / heparin	21	1	0.06456
<i>path:gga04150</i>	mTOR signaling pathway	134	2	0.06727
<i>path:gga00500</i>	Starch and sucrose metabolism	25	1	0.07639
<i>path:gga04510</i>	Focal adhesion	174	2	0.1051
<i>path:gga02010</i>	ABC transporters	36	1	0.1082
<i>path:gga00310</i>	Lysine degradation	51	1	0.1498



1	RBFOX1	MCF2L2	SCN3A	PCLO	GLRA2	RIMS2	MAP7D2	ST8SIA3Z
2	PTPRR	GNAO1	ENSGALG00000054250					

	Term	Ont	N	n	Adj. p-value
GO:0034331	cell junction maintenance	BP	1	1	0.0008304
GO:0048790	maintenance of presynaptic active zone structure	BP	1	1	0.0008304
GO:0099558	maintenance of synapse structure	BP	1	1	0.0008304
GO:0099054	presynapse assembly	BP	1	1	0.0008304
GO:0099172	presynapse organization	BP	1	1	0.0008304
GO:1904071	presynaptic active zone assembly	BP	1	1	0.0008304
GO:1990709	presynaptic active zone organization	BP	1	1	0.0008304
GO:0043954	cellular component maintenance	BP	3	1	0.002489
GO:0035418	protein localization to synapse	BP	8	1	0.006626
GO:1902414	protein localization to cell junction	BP	10	1	0.008276

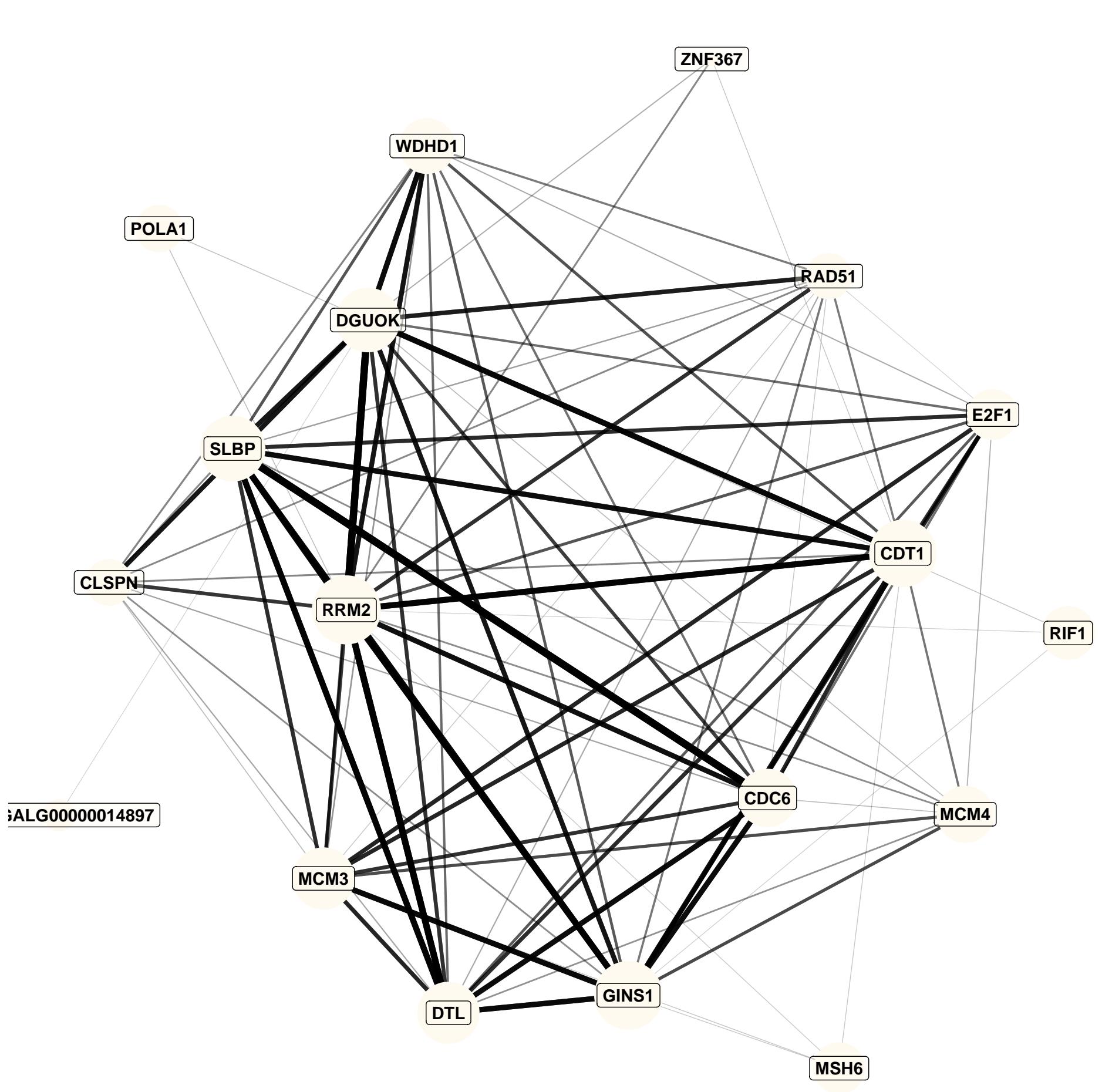
	Pathway	N	DE	P.DE
<i>path:gga04916</i>	Melanogenesis	83	1	0.06683
<i>path:gga04010</i>	MAPK signaling pathway	240	1	0.1823
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	295	1	0.2195
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1
<i>path:gga00785</i>	Lipoic acid metabolism	3	0	1
<i>path:gga00290</i>	Valine, leucine and isoleucine biosynthesis	3	0	1
<i>path:gga03264</i>	Virion – Flavivirus	3	0	1
<i>path:gga00232</i>	Caffeine metabolism	4	0	1
<i>path:gga03266</i>	Virion – Herpesvirus	4	0	1



1	UGT8	BCAS1	OLIG2	LRATD1	NKX2-2	PTPRJ	TCF7L2	TPPP
2	ENSGALG00000039468	GAB1	ENSGALG00000049579	ENSGALG00000048883	ENSGALG00000034050	AHR	NRCAM	PTPN13
3	NEGR1	TMEM132B	ENSGALG0000007193	EPN2	DBNDD2	PTCH1	NPL	ENSGALG00000015297
4	STARD8	DNM3	NCKIPSD	KIT	JAG2	CRIP2	CPNE4	TBL1X
5	GSG1L	GAB3	NLGN1	KCNG4	OTUD7A			

	Term	Ont	N	n	Adj. p-value
GO:0022610	biological adhesion	BP	143	4	0.0004178
GO:0007155	cell adhesion	BP	143	4	0.0004178
GO:0002768	immune response-regulating cell surface receptor signaling pathway	BP	13	2	0.0004615
GO:0002764	immune response-regulating signaling pathway	BP	13	2	0.0004615
GO:0043405	regulation of MAP kinase activity	BP	26	2	0.001884
GO:0046348	amino sugar catabolic process	BP	1	1	0.002491
GO:0016338	calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules	BP	1	1	0.002491
GO:0036018	cellular response to erythropoietin	BP	1	1	0.002491
GO:0036216	cellular response to stem cell factor stimulus	BP	1	1	0.002491
GO:0097067	cellular response to thyroid hormone stimulus	BP	1	1	0.002491

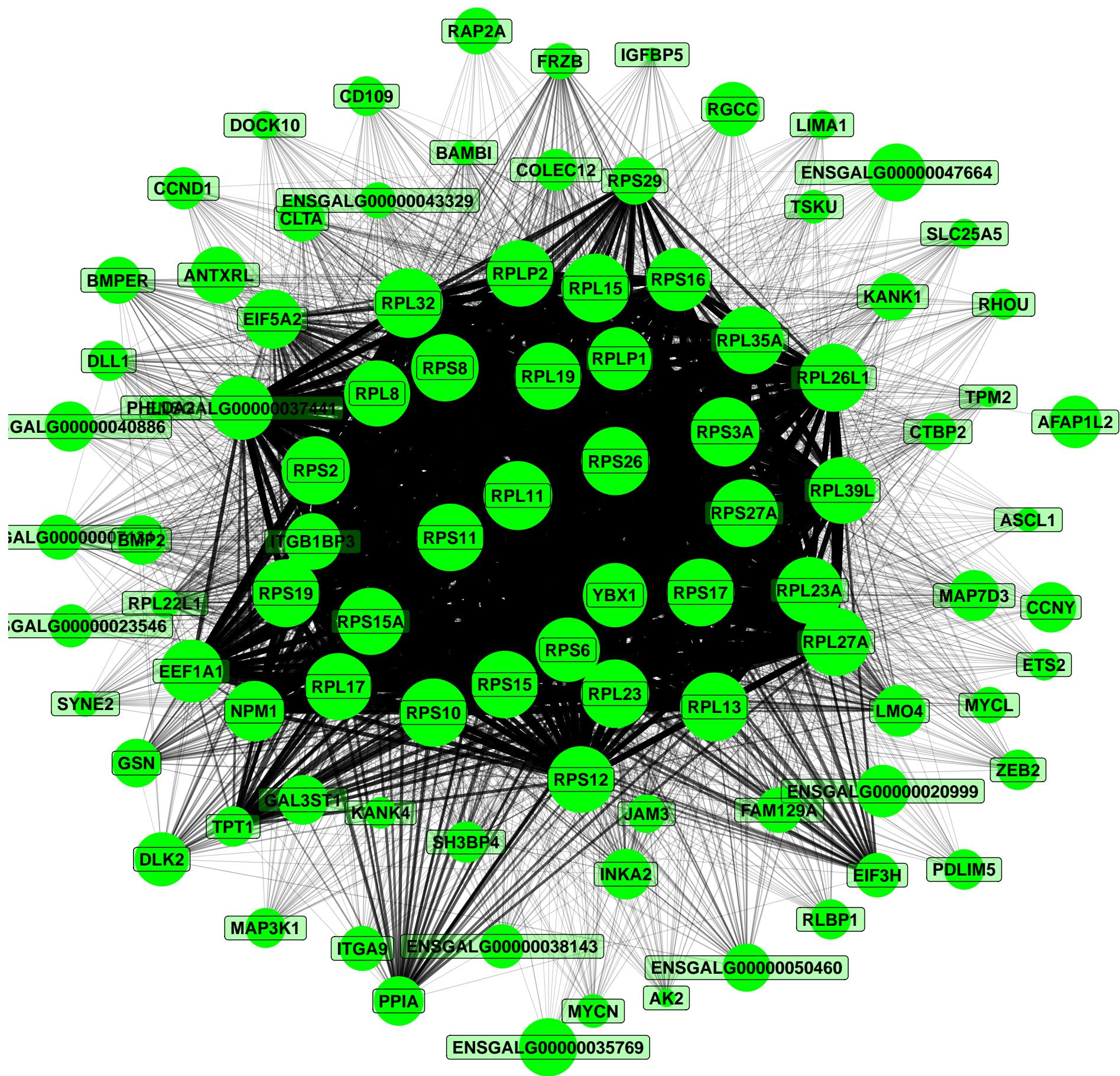
	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	103	3	0.002103
<i>path:gga04520</i>	Adherens junction	69	2	0.01272
<i>path:gga04916</i>	Melanogenesis	83	2	0.01806
<i>path:gga04310</i>	Wnt signaling pathway	134	2	0.04373
<i>path:gga00565</i>	Ether lipid metabolism	38	1	0.09056
<i>path:gga00520</i>	Amino sugar and nucleotide sugar metabolism	44	1	0.1041
<i>path:gga04340</i>	Hedgehog signaling pathway	47	1	0.1108
<i>path:gga00600</i>	Sphingolipid metabolism	47	1	0.1108
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.1219
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.1436



1	RRM2	DGUOK	GINS1	SLBP	DTL	CDT1	MCM3	CDC6
2	WDHD1	E2F1	MCM4	RAD51	RIF1	MSH6	CLSPN	POLA1
3	ZNF367	ENSGALG00000014897						

	Term	Ont	N	n	Adj. p-value
GO:0044786	cell cycle DNA replication	BP	6	3	4.203e–08
GO:0006281	DNA repair	BP	95	5	1.358e–07
GO:0007049	cell cycle	BP	205	6	2.031e–07
GO:0006260	DNA replication	BP	41	4	2.342e–07
GO:0006974	cellular response to DNA damage stimulus	BP	125	5	5.363e–07
GO:0006259	DNA metabolic process	BP	127	5	5.804e–07
GO:0006310	DNA recombination	BP	55	4	7.796e–07
GO:0000018	regulation of DNA recombination	BP	19	3	2.014e–06
GO:1903047	mitotic cell cycle process	BP	78	4	3.198e–06
GO:0006261	DNA–dependent DNA replication	BP	24	3	4.189e–06

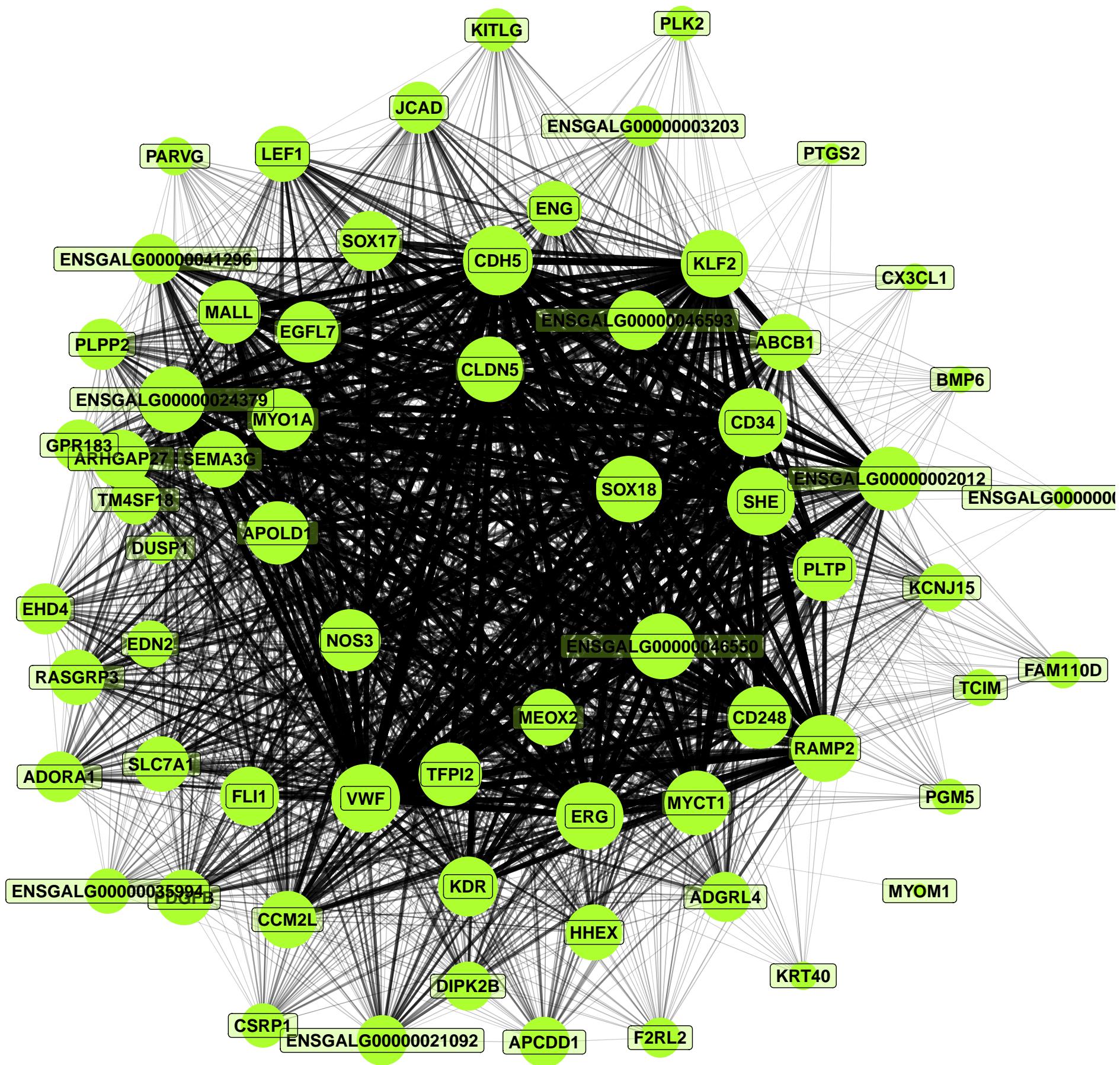
	Pathway	N	DE	P.DE
<i>path:gga03030</i>	DNA replication	29	3	7.531e-06
<i>path:gga04110</i>	Cell cycle	114	4	1.451e-05
<i>path:gga00240</i>	Pyrimidine metabolism	56	3	5.584e-05
<i>path:gga01232</i>	Nucleotide metabolism	78	3	0.0001504
<i>path:gga00230</i>	Purine metabolism	113	2	0.0101
<i>path:gga00670</i>	One carbon pool by folate	15	1	0.0202
<i>path:gga03430</i>	Mismatch repair	19	1	0.02552
<i>path:gga03440</i>	Homologous recombination	36	1	0.04784
<i>path:gga00480</i>	Glutathione metabolism	47	1	0.06202
<i>path:gga03460</i>	Fanconi anemia pathway	48	1	0.0633



1	RPL32	RPS3A	RPL23	RPL13	RPS19	RPS27A	RPL27A	RPL26L1
2	RPL15	RPL35A	RPS17	RPS26	RPS11	RPL11	RPS15A	RPS15
3	RPS2	RPS10	RPS8	RPL39L	RPLP1	RPLP2	RPL17	RPL23A
4	RPL8	RPL19	RPS12	ENSGALG0000037441	RPS16	RPS6	YBX1	EEF1A1
5	ITGB1BP3	NPM1	RPS29	TPT1	ENSGALG0000047664	ENSGALG0000035769	EIF5A2	ANTXRL
6	AFAP1L2	PPIA	LMO4	RGCC	EIF3H	DLK2	COLEC12	ENSGALG0000043329
7	DLL1	ENSGALG0000020999	ENSGALG0000007131	GSN	BMPER	CCNY	GAL3ST1	INKA2
8	CLTA	RPL22L1	BMP2	FRZB	ENSGALG0000040886	KANK1	ZEB2	MAP7D3
9	ENSGALG0000050460	CTBP2	ITGA9	CCND1	SH3BP4	ENSGALG0000023546	FAM129A	PDLIM5
10	RAP2A	ENSGALG0000038143	MAP3K1	CD109	RLBP1	PHLDA2	BAMBI	DOCK10
11	TPM2	SYNE2	RHOU	ETS2	MYCL	JAM3	ASCL1	SLC25A5
12	MYCN	TSKU	IGFBP5	LIMA1	AK2	KANK4		

	Term	Ont	N	n	Adj. p-value
GO:0006412	translation	BP	87	14	5.659e-16
GO:0043043	peptide biosynthetic process	BP	88	14	6.693e-16
GO:0043604	amide biosynthetic process	BP	101	14	4.976e-15
GO:0006518	peptide metabolic process	BP	107	14	1.142e-14
GO:0043603	cellular amide metabolic process	BP	125	14	1.044e-13
GO:1901566	organonitrogen compound biosynthetic process	BP	208	14	1.131e-10
GO:0044271	cellular nitrogen compound biosynthetic process	BP	537	19	2.542e-09
GO:0010467	gene expression	BP	615	20	3.841e-09
GO:0034645	cellular macromolecule biosynthetic process	BP	552	19	3.999e-09
GO:0009059	macromolecule biosynthetic process	BP	554	19	4.243e-09

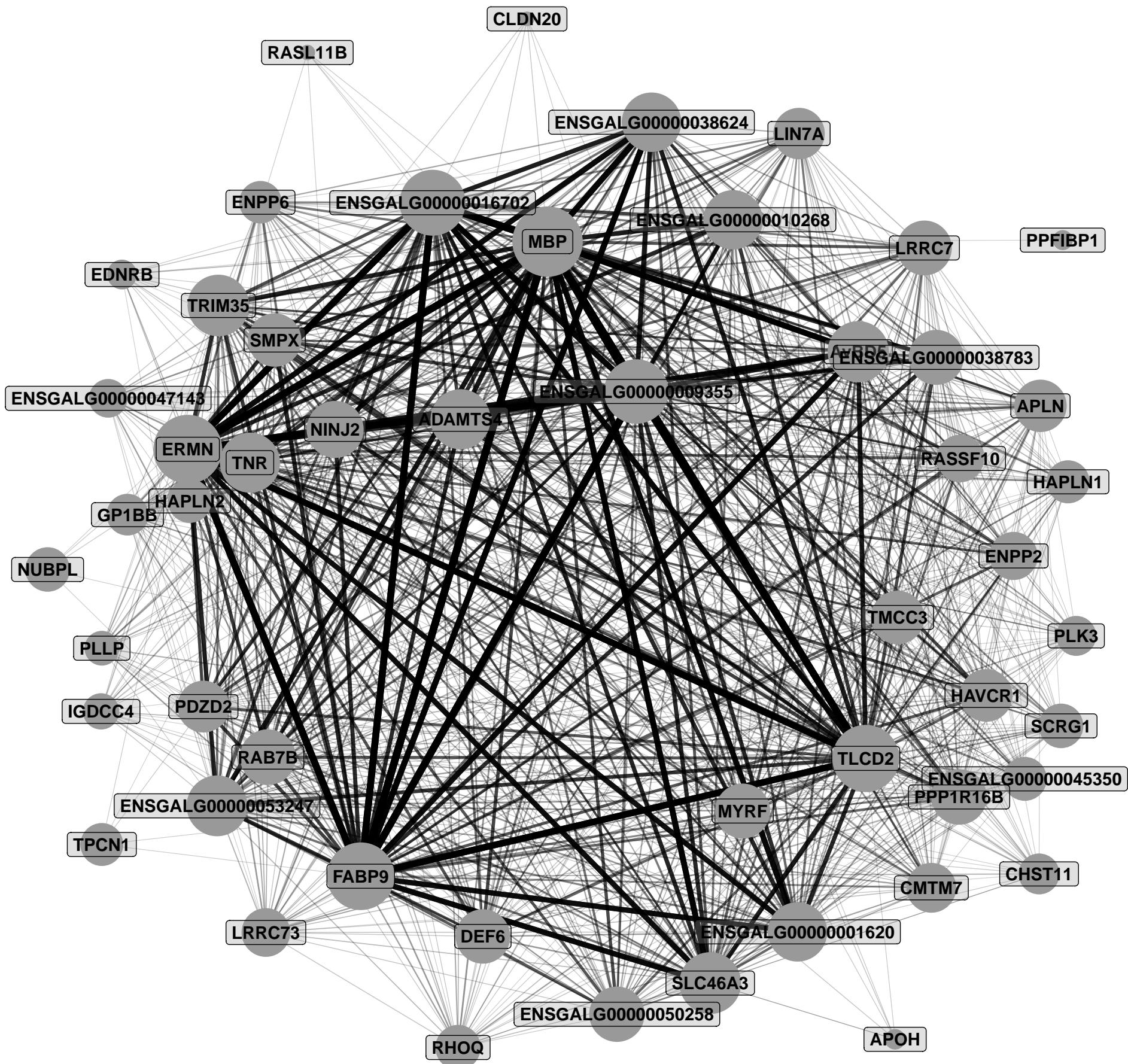
	Pathway	N	DE	P.DE
<i>path:gga03010</i>	Ribosome	115	32	1.607e-44
<i>path:gga04310</i>	Wnt signaling pathway	134	4	0.0131
<i>path:gga04330</i>	Notch signaling pathway	52	2	0.04862
<i>path:gga04530</i>	Tight junction	135	3	0.06417
<i>path:gga00730</i>	Thiamine metabolism	12	1	0.07859
<i>path:gga04350</i>	TGF-beta signaling pathway	86	2	0.1159
<i>path:gga00900</i>	Terpenoid backbone biosynthesis	19	1	0.1216
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	3	0.136
<i>path:gga04514</i>	Cell adhesion molecules	103	2	0.155
<i>path:gga04217</i>	Necroptosis	109	2	0.1693



1	CDH5	VWF	CD34	MYO1A	MYCT1	NOS3	ENSGALG00000046550	RAMP2
2	ERG	SOX18	SHE	APOLD1	KLF2	ENSGALG00000002012	SOX17	ENSGALG00000024379
3	CD248	ARHGAP27	ENSGALG00000046593	CLDN5	MALL	CCM2L	HHEX	KDR
4	ABCB1	MEOX2	ENSGALG00000021092	EGFL7	PDGFB	SEMA3G	FLI1	RASGRP3
5	GPR183	ADORA1	TFPI2	DIPK2B	LEF1	ENG	ADGRL4	PLTP
6	EHD4	KCNJ15	TM4SF18	ENSGALG00000041296	PLPP2	APCDD1	SLC7A1	FAM110D
7	JCAD	ENSGALG0000003203	F2RL2	ENSGALG00000035994	CSRP1	EDN2	PARVG	TCIM
8	KITLG	PLK2	ENSGALG0000006407	PGM5	KRT40	DUSP1	CX3CL1	BMP6
9	PTGS2	MYOM1						

	Term	Ont	N	n	Adj. p-value
GO:0008015	blood circulation	BP	27	3	0.0002765
GO:0003013	circulatory system process	BP	27	3	0.0002765
GO:0008217	regulation of blood pressure	BP	8	2	0.000612
GO:0050728	negative regulation of inflammatory response	BP	9	2	0.0007844
GO:0031348	negative regulation of defense response	BP	12	2	0.001425
GO:0006954	inflammatory response	BP	49	3	0.001616
GO:0002685	regulation of leukocyte migration	BP	13	2	0.001679
GO:0030334	regulation of cell migration	BP	68	3	0.004124
GO:0050900	leukocyte migration	BP	21	2	0.004411
GO:2000145	regulation of cell motility	BP	71	3	0.004656

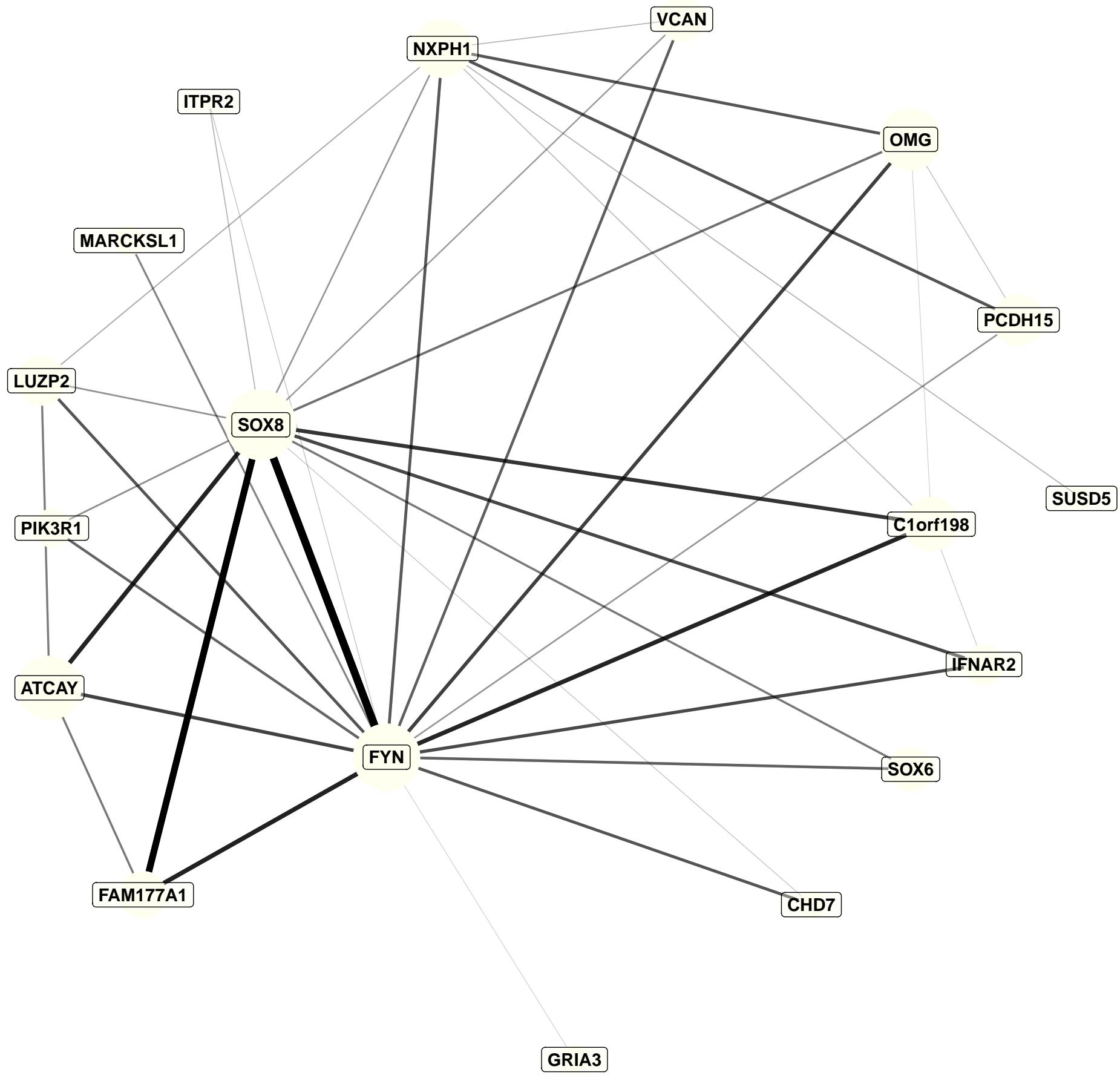
	Pathway	N	DE	P.DE
<i>path:gga04370</i>	VEGF signaling pathway	54	3	0.00214
<i>path:gga04010</i>	MAPK signaling pathway	240	5	0.005604
<i>path:gga04510</i>	Focal adhesion	174	4	0.009386
<i>path:gga04514</i>	Cell adhesion molecules	103	3	0.01294
<i>path:gga04270</i>	Vascular smooth muscle contraction	109	3	0.01506
<i>path:gga04310</i>	Wnt signaling pathway	134	3	0.02587
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	295	4	0.0516
<i>path:gga04916</i>	Melanogenesis	83	2	0.05926
<i>path:gga04020</i>	Calcium signaling pathway	199	3	0.06889
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.0779



1	FABP9	ERMN	MBP	TLCD2	ENSGALG0000009355	ENSGALG00000053247	ENSGALG00000016702	TNR
2	SLC46A3	ADAMTS4	AVBD5	TRIM35	ENSGALG00000010268	PPP1R16B	MYRF	ENSGALG00000001620
3	SMPX	CMTM7	DEF6	TMCC3	ENSGALG00000038624	RAB7B	HAVCR1	LRRC73
4	ENSGALG00000050258	NINJ2	LRRC7	APLN	LIN7A	PDZD2	HAPLN1	RHOQ
5	RASSF10	GP1BB	ENSGALG00000038783	NUBPL	TPCN1	ENSGALG00000045350	ENPP2	SCRG1
6	CHST11	IGDCC4	HAPLN2	ENSGALG00000047143	PLK3	ENPP6	PLLP	PPFIBP1
7	EDNRB	RASL11B	CLDN20	APOH				

	Term	Ont	N	n	Adj. p-value
GO:0050918	positive chemotaxis	BP	10	1	0.03712
GO:0008366	axon ensheathment	BP	12	1	0.04439
GO:0007272	ensheathment of neurons	BP	12	1	0.04439
GO:0042552	myelination	BP	12	1	0.04439
GO:0007399	nervous system development	BP	260	3	0.07473
GO:0042742	defense response to bacterium	BP	25	1	0.09029
GO:0060326	cell chemotaxis	BP	26	1	0.09373
GO:0022610	biological adhesion	BP	143	2	0.1014
GO:0007155	cell adhesion	BP	143	2	0.1014
GO:0050767	regulation of neurogenesis	BP	32	1	0.1141

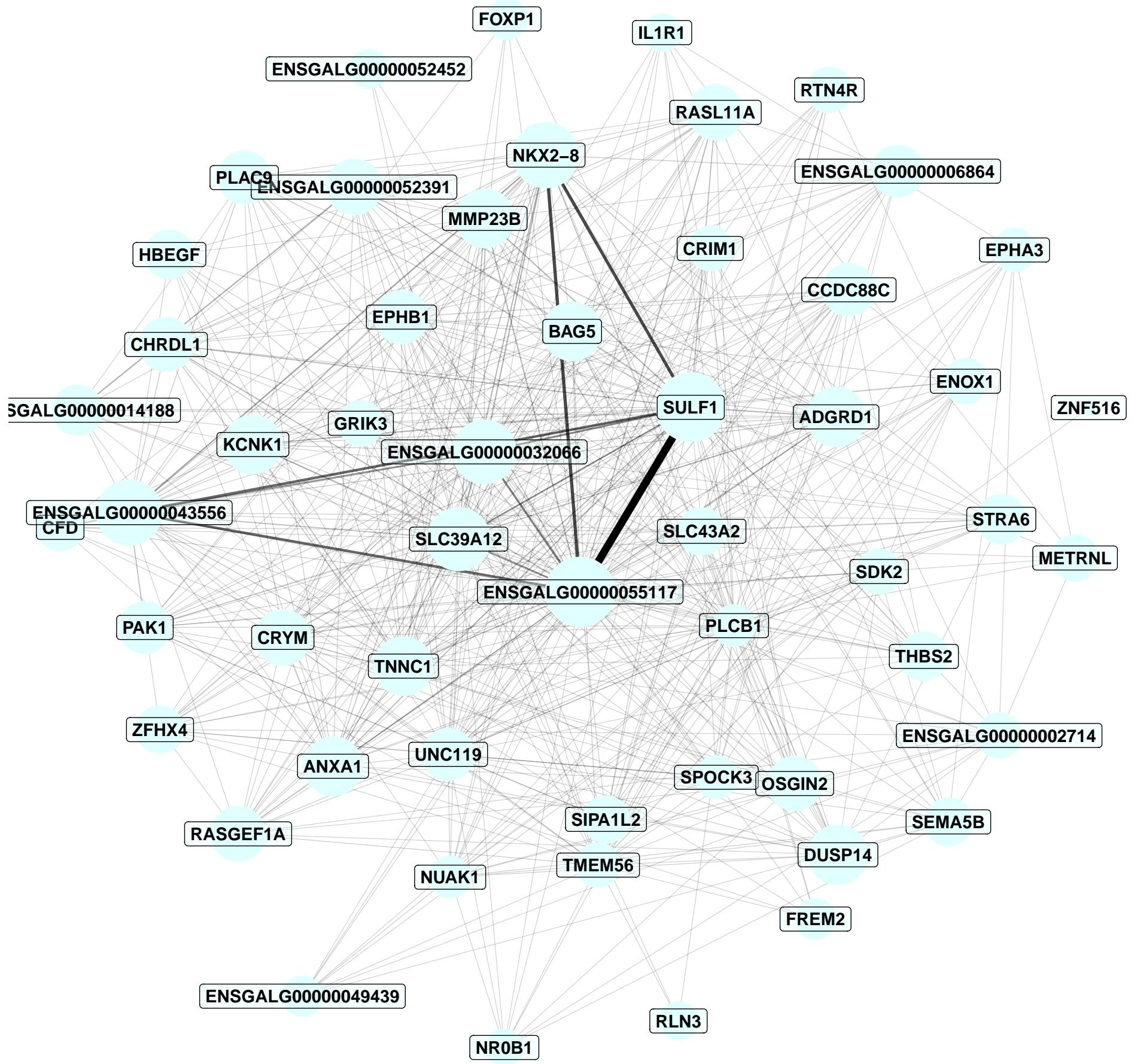
	Pathway	N	DE	P.DE
<i>path:gga00565</i>	Ether lipid metabolism	38	2	0.009002
<i>path:gga03264</i>	Virion – Flavivirus	3	1	0.01128
<i>path:gga04512</i>	ECM–receptor interaction	67	2	0.02642
<i>path:gga04514</i>	Cell adhesion molecules	103	2	0.05763
<i>path:gga04530</i>	Tight junction	135	2	0.09206
<i>path:gga04020</i>	Calcium signaling pathway	199	2	0.1729
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.2094
<i>path:gga03015</i>	mRNA surveillance pathway	73	1	0.2418
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	81	1	0.2645
<i>path:gga04916</i>	Melanogenesis	83	1	0.2701



1	SOX8	ATCAY	FYN	NXPH1	OMG	FAM177A1	LUZP2	PCDH15
2	VCAN	C1orf198	SOX6	IFNAR2	CHD7	GRIA3	PIK3R1	MARCKSL1
3	ITPR2	SUSD5						

	Term	Ont	N	n	Adj. p-value
GO:0007417	central nervous system development	BP	88	3	0.0002151
GO:0048731	system development	BP	490	4	0.003744
GO:0007399	nervous system development	BP	260	3	0.004904
GO:0007275	multicellular organism development	BP	586	4	0.007067
GO:0048513	animal organ development	BP	326	3	0.009161
GO:0048856	anatomical structure development	BP	634	4	0.009299
GO:0032502	developmental process	BP	666	4	0.01102
GO:0003170	heart valve development	BP	9	1	0.01217
GO:0048709	oligodendrocyte differentiation	BP	9	1	0.01217
GO:0050852	T cell receptor signaling pathway	BP	9	1	0.01217

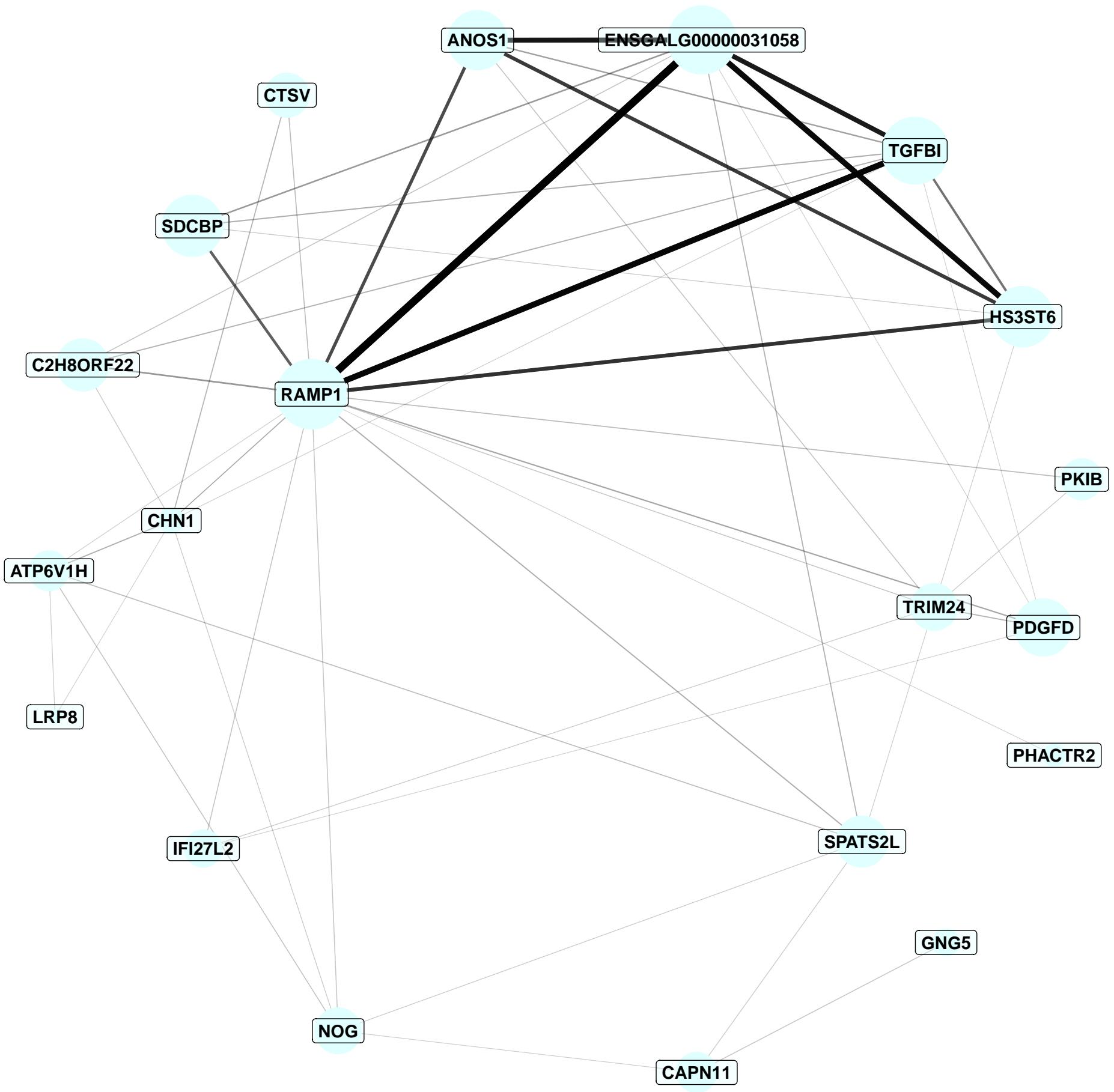
	Pathway	N	DE	P.DE
<i>path:gga04620</i>	Toll-like receptor signaling pathway	71	2	0.0041
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	81	2	0.005303
<i>path:gga04070</i>	Phosphatidylinositol signaling system	86	2	0.005958
<i>path:gga04210</i>	Apoptosis	114	2	0.01027
<i>path:gga05164</i>	Influenza A	114	2	0.01027
<i>path:gga04621</i>	NOD-like receptor signaling pathway	115	2	0.01044
<i>path:gga05168</i>	Herpes simplex virus 1 infection	130	2	0.0132
<i>path:gga04218</i>	Cellular senescence	134	2	0.01398
<i>path:gga04510</i>	Focal adhesion	174	2	0.02287
<i>path:gga04370</i>	VEGF signaling pathway	54	1	0.07094



1	ENSGALG00000055117	SULF1	NKX2-8	ENSGALG00000043556	ENSGALG00000032066	SLC39A12	ADGRD1	TNNC1
2	ENSGALG00000052391	RASL11A	KCNK1	MMP23B	BAG5	ANXA1	CRYM	DUSP14
3	EPHB1	RASGEF1A	CHRDL1	ENSGALG00000014188	UNC119	OSGIN2	PLAC9	CCDC88C
4	PAK1	ENSGALG0000006864	ZFHX4	CFD	THBS2	GRIK3	SIPA1L2	HBEGF
5	CRIM1	SEMA5B	PLCB1	ENOX1	SLC43A2	METRNL	TMEM56	STRA6
6	EPHA3	SPOCK3	SDK2	RTN4R	FOXP1	RLN3	NUAK1	ENSGALG0000002714
7	ENSGALG00000049439	ENSGALG00000052452	IL1R1	NR0B1	FREM2	ZNF516		

	Term	Ont	N	n	Adj. p-value
GO:0090303	positive regulation of wound healing	BP	4	2	7.68e-05
GO:0060326	cell chemotaxis	BP	26	3	0.0001095
GO:0006935	chemotaxis	BP	74	4	0.000145
GO:0042330	taxis	BP	74	4	0.000145
GO:0022610	biological adhesion	BP	143	5	0.0001612
GO:0007155	cell adhesion	BP	143	5	0.0001612
GO:0050790	regulation of catalytic activity	BP	231	6	0.0001753
GO:1903036	positive regulation of response to wounding	BP	6	2	0.0001911
GO:0040011	locomotion	BP	166	5	0.0003224
GO:0007399	nervous system development	BP	260	6	0.0003318

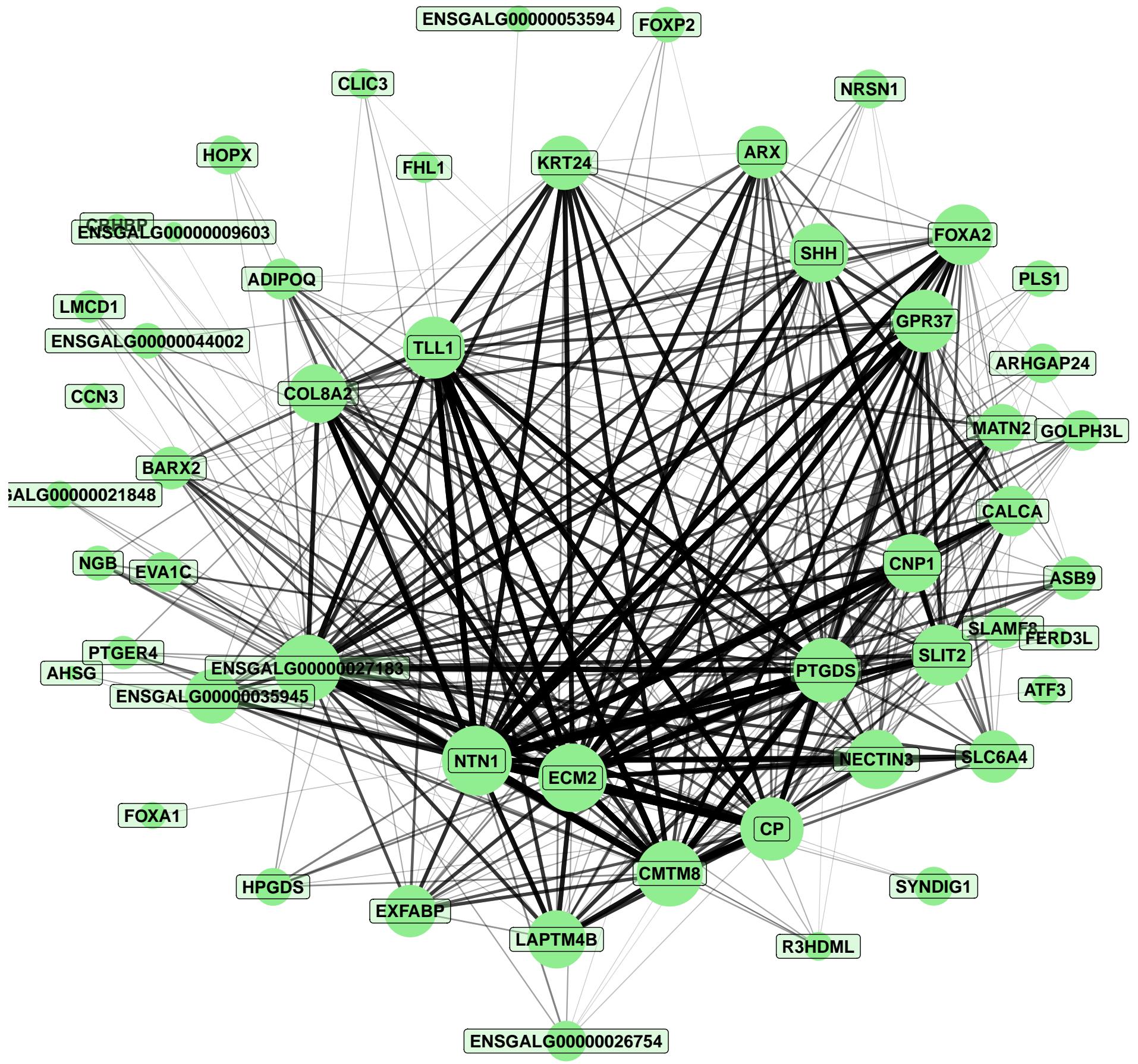
	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	67	2	0.02448
<i>path:gga04012</i>	ErbB signaling pathway	76	2	0.03092
<i>path:gga04912</i>	GnRH signaling pathway	78	2	0.03243
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	124	2	0.07421
<i>path:gga04310</i>	Wnt signaling pathway	134	2	0.08479
<i>path:gga04510</i>	Focal adhesion	174	2	0.131
<i>path:gga04020</i>	Calcium signaling pathway	199	2	0.1622
<i>path:gga04260</i>	Cardiac muscle contraction	60	1	0.1961
<i>path:gga04010</i>	MAPK signaling pathway	240	2	0.2159
<i>path:gga00562</i>	Inositol phosphate metabolism	68	1	0.2192



1	RAMP1	ENSGALG00000031058	TGFBI	ANOS1	HS3ST6	PDGFD	C2H8ORF22	SDCBP
2	SPATS2L	PKIB	NOG	TRIM24	IFI27L2	CTSV	CHN1	CAPN11
3	ATP6V1H	GNG5	PHACTR2	LRP8				

	Term	Ont	N	n	Adj. p-value
GO:0006508	proteolysis	BP	130	3	0.0007978
GO:0016540	protein autoprocessing	BP	2	1	0.002867
GO:0031638	zymogen activation	BP	5	1	0.007153
GO:0021517	ventral spinal cord development	BP	11	1	0.01567
GO:0016485	protein processing	BP	12	1	0.01708
GO:0021510	spinal cord development	BP	17	1	0.02412
GO:0051604	protein maturation	BP	20	1	0.02832
GO:0010951	negative regulation of endopeptidase activity	BP	21	1	0.02972
GO:0010466	negative regulation of peptidase activity	BP	22	1	0.03111
GO:0045861	negative regulation of proteolysis	BP	26	1	0.03667

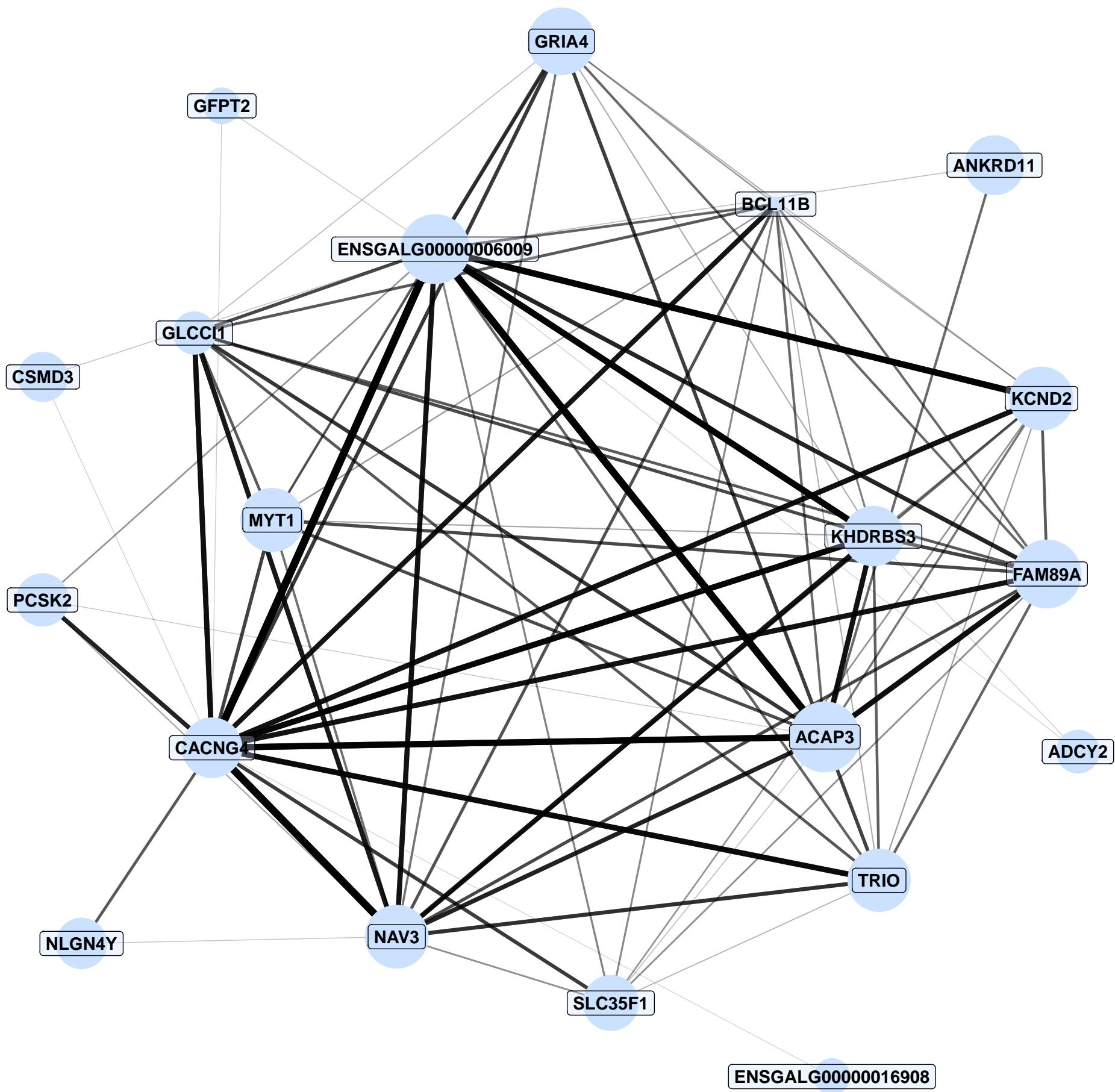
	Pathway	N	DE	P.DE
<i>path:gga04210</i>	Apoptosis	114	2	0.01141
<i>path:gga04142</i>	Lysosome	114	2	0.01141
<i>path:gga04145</i>	Phagosome	125	2	0.0136
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis – heparan sulfate / heparin	21	1	0.02972
<i>path:gga04540</i>	Gap junction	79	1	0.1075
<i>path:gga00190</i>	Oxidative phosphorylation	101	1	0.1354
<i>path:gga04217</i>	Necroptosis	109	1	0.1454
<i>path:gga04270</i>	Vascular smooth muscle contraction	109	1	0.1454
<i>path:gga04371</i>	Apelin signaling pathway	113	1	0.1503
<i>path:gga04140</i>	Autophagy – animal	125	1	0.165



1	PTGDS	ECM2	SHH	FOXA2	CNP1	CMTM8	NTN1	SLIT2
2	TLL1	ENSGALG00000027183	COL8A2	CALCA	GPR37	CP	ENSGALG00000035945	ARX
3	KRT24	HPGDS	LAPTM4B	FOXA1	EXFABP	SLC6A4	NECTIN3	ADIPOQ
4	MATN2	ASB9	HOPX	FHL1	ENSGALG00000026754	ARHGAP24	SLAMF8	EVA1C
5	AHSG	SYNDIG1	R3HDM1	FOXP2	GOLPH3L	LMCD1	CLIC3	ENSGALG00000021848
6	BARX2	PTGER4	CCN3	NRSN1	ENSGALG00000044002	PLS1	ENSGALG00000053594	ENSGALG00000009603
7	FERD3L	ATF3	NGB	CRHBP				

	Term	Ont	N	n	Adj. p-value
GO:0048589	developmental growth	BP	66	5	4.691e-06
GO:0040007	growth	BP	95	5	2.801e-05
GO:0048639	positive regulation of developmental growth	BP	19	3	4.7e-05
GO:0003415	chondrocyte hypertrophy	BP	4	2	8.338e-05
GO:0051094	positive regulation of developmental process	BP	124	5	0.0001003
GO:0045927	positive regulation of growth	BP	25	3	0.0001098
GO:0051239	regulation of multicellular organismal process	BP	205	6	0.0001151
GO:0048588	developmental cell growth	BP	29	3	0.0001726
GO:0048638	regulation of developmental growth	BP	32	3	0.0002324
GO:0002063	chondrocyte development	BP	7	2	0.0002897

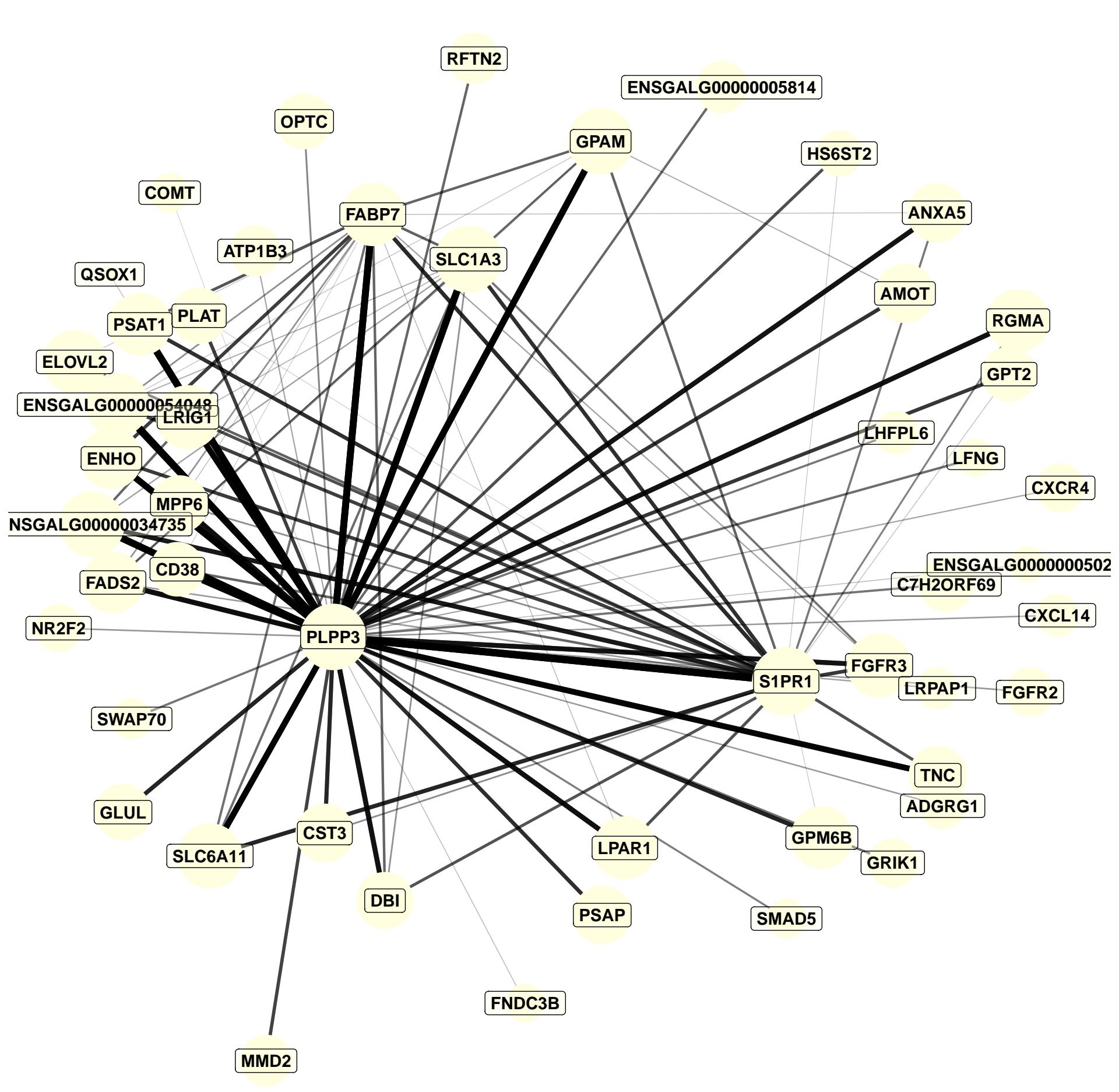
	Pathway	N	DE	P.DE
<i>path:gga00590</i>	Arachidonic acid metabolism	41	2	0.01042
<i>path:gga04270</i>	Vascular smooth muscle contraction	109	2	0.06367
<i>path:gga00860</i>	Porphyrin metabolism	21	1	0.0764
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	295	3	0.09992
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	1	0.104
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	31	1	0.1107
<i>path:gga04216</i>	Ferroptosis	34	1	0.1208
<i>path:gga00480</i>	Glutathione metabolism	47	1	0.1631
<i>path:gga04340</i>	Hedgehog signaling pathway	47	1	0.1631
<i>path:gga03320</i>	PPAR signaling pathway	58	1	0.1973



1	MYT1	ACAP3	GRIA4	FAM89A	ENSGALG00000006009	CACNG4	KCND2	NAV3
2	KHDRBS3	TRIO	PCSK2	GLCCI1	BCL11B	NLGN4Y	SLC35F1	ANKRD11
3	CSMD3	ENSGALG00000016908	ADCY2	GFPT2				

	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

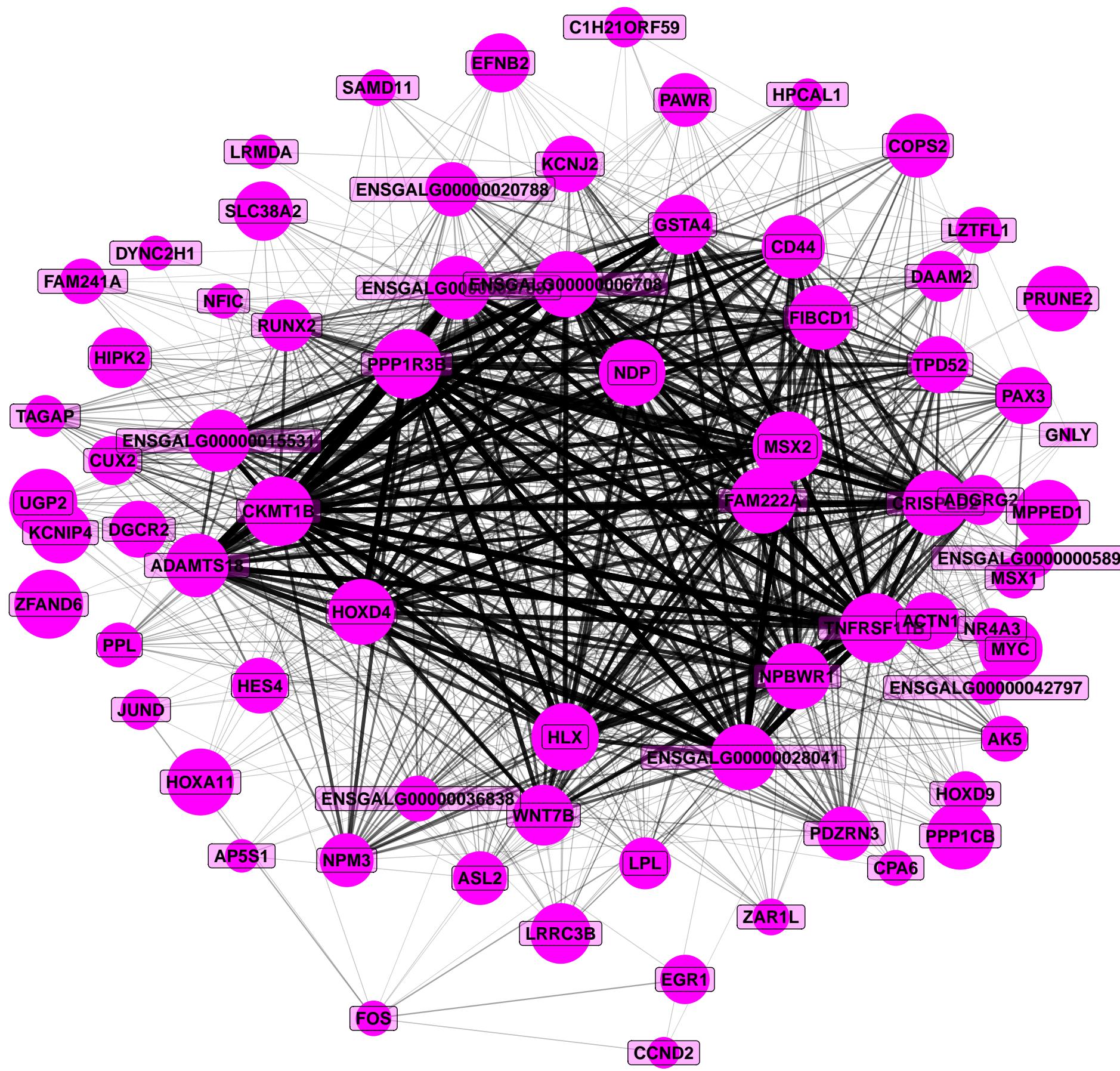
	Pathway	N	DE	P.DE
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	124	2	0.01479
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	33	1	0.0487
<i>path:gga01250</i>	Biosynthesis of nucleotide sugars	36	1	0.05301
<i>path:gga00520</i>	Amino sugar and nucleotide sugar metabolism	44	1	0.06442
<i>path:gga04260</i>	Cardiac muscle contraction	60	1	0.08686
<i>path:gga04912</i>	GnRH signaling pathway	78	1	0.1115
<i>path:gga04540</i>	Gap junction	79	1	0.1128
<i>path:gga04914</i>	Progesterone-mediated oocyte maturation	79	1	0.1128
<i>path:gga04916</i>	Melanogenesis	83	1	0.1182
<i>path:gga04114</i>	Oocyte meiosis	97	1	0.1368



1	SLC1A3	SLC6A11	S1PR1	PLPP3	TNC	ENSGALG00000054048	FGFR3	CST3
2	ENSGALG00000034735	LRIG1	RGMA	CXCL14	GPAM	DBI	LPAR1	FADS2
3	ELOVL2	PSAT1	ENHO	FABP7	OPTC	CD38	GPM6B	ANXA5
4	AMOT	GLUL	MPP6	MMD2	PSAP	PLAT	GRIK1	CXCR4
5	C7H2ORF69	GPT2	FGFR2	NR2F2	HS6ST2	LHFPL6	RFTN2	ENSGALG0000005814
6	LFNG	ENSGALG0000005024	SWAP70	ATP1B3	QSOX1	SMAD5	ADGRG1	COMT
7	FNDC3B	LRPAP1						

	Term	Ont	N	n	Adj. p-value
GO:0006541	glutamine metabolic process	BP	6	2	0.0002075
GO:0071363	cellular response to growth factor stimulus	BP	78	4	0.0002086
GO:0070848	response to growth factor	BP	79	4	0.0002191
GO:1901564	organonitrogen compound metabolic process	BP	695	10	0.0002255
GO:0065009	regulation of molecular function	BP	263	6	0.000442
GO:0009064	glutamine family amino acid metabolic process	BP	14	2	0.001234
GO:0007167	enzyme linked receptor protein signaling pathway	BP	125	4	0.001245
GO:0008150	biological_process	BP	1923	16	0.001345
GO:0032501	multicellular organismal process	BP	724	9	0.001378
GO:0065007	biological regulation	BP	1208	12	0.001446

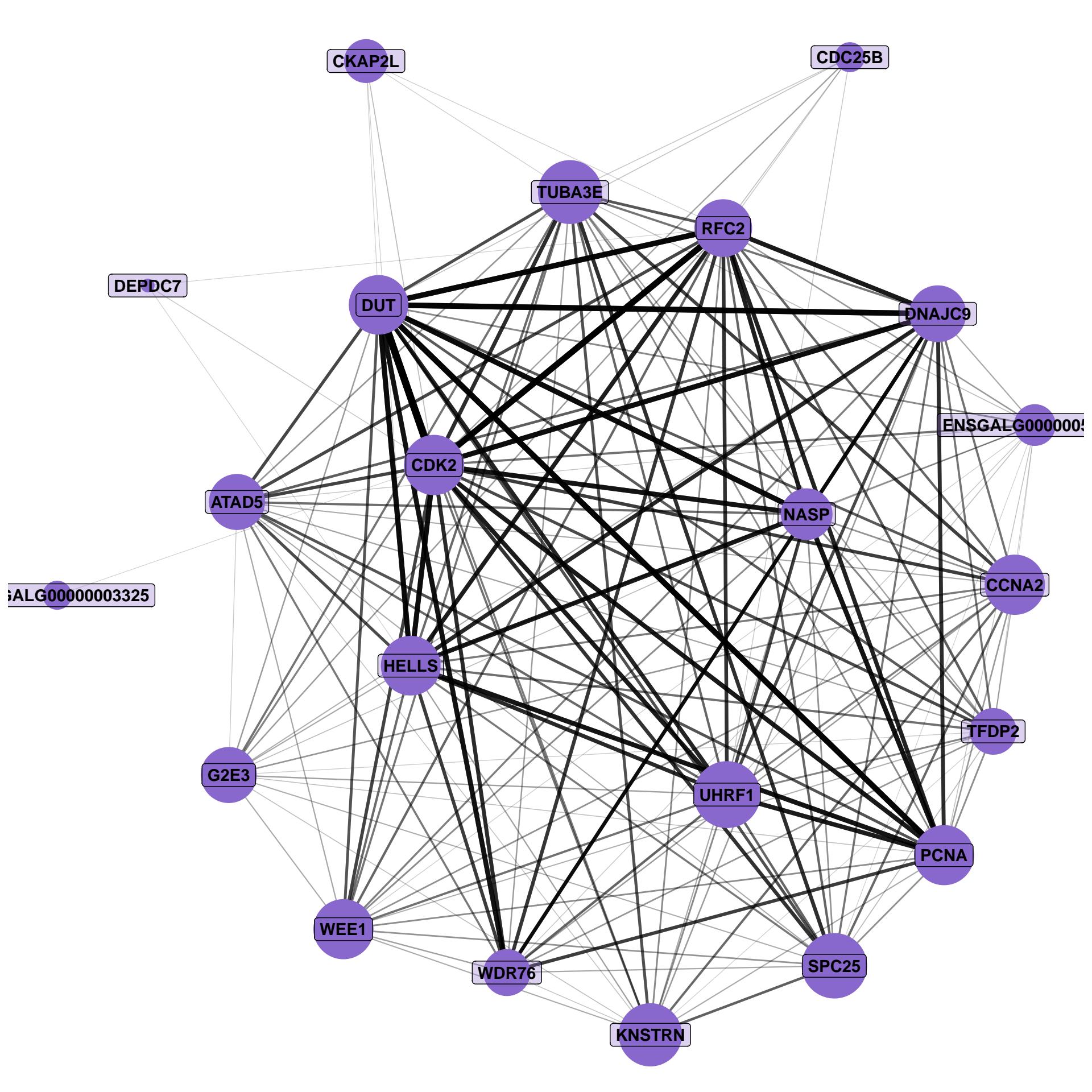
	Pathway	N	DE	P.DE
<i>path:gga00220</i>	Arginine biosynthesis	17	3	3.316e-05
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	33	3	0.000255
<i>path:gga00910</i>	Nitrogen metabolism	13	2	0.001061
<i>path:gga01230</i>	Biosynthesis of amino acids	57	3	0.001283
<i>path:gga03320</i>	PPAR signaling pathway	58	3	0.001349
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	28	2	0.004958
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	4	0.005441
<i>path:gga01200</i>	Carbon metabolism	95	3	0.00549
<i>path:gga04020</i>	Calcium signaling pathway	199	4	0.006639
<i>path:gga00600</i>	Sphingolipid metabolism	47	2	0.01355



1	MSX2	PPP1R3B	TNFRSF11B	CKMT1B	ENSGALG00000028041	HLX	FAM22A	NDP
2	NPBWR1	FIBCD1	KCNIP4	GSTA4	ENSGALG0000006708	ENSGALG00000027887	MPPED1	ZFAND6
3	PRUNE2	UGP2	ADAMTS18	ENSGALG00000015531	HOXA11	HOXD4	EFNB2	CRISPLD2
4	CD44	PAX3	WNT7B	KCNJ2	HES4	MYC	PPP1CB	COPS2
5	LRRC3B	HIPK2	TPD52	ACTN1	SLC38A2	ENSGALG00000020788	DGCR2	ASL2
6	NPM3	PAWR	EGR1	PDZRN3	LPL	MSX1	RUNX2	LZTFL1
7	CUX2	DAAM2	ADGRG2	FOS	AK5	FAM241A	HPCAL1	SAMD11
8	NFIC	ENSGALG00000036838	NR4A3	PPL	C1H21ORF59	TAGAP	JUND	AP5S1
9	ENSGALG00000042797	HOXD9	ENSGALG0000005896	CPA6	DYNC2H1	CCND2	GNLY	LRMDA
10	ZAR1L							

	Term	Ont	N	n	Adj. p-value
GO:0006357	regulation of transcription by RNA polymerase II	BP	277	10	2.04e-06
GO:0006366	transcription by RNA polymerase II	BP	285	10	2.633e-06
GO:0010468	regulation of gene expression	BP	488	12	9.661e-06
GO:0032501	multicellular organismal process	BP	724	14	2.466e-05
GO:1903506	regulation of nucleic acid-templated transcription	BP	370	10	2.592e-05
GO:2001141	regulation of RNA biosynthetic process	BP	370	10	2.592e-05
GO:0006355	regulation of transcription, DNA-templated	BP	370	10	2.592e-05
GO:0060255	regulation of macromolecule metabolic process	BP	634	13	2.735e-05
GO:0097659	nucleic acid-templated transcription	BP	381	10	3.328e-05
GO:0006351	transcription, DNA-templated	BP	381	10	3.328e-05

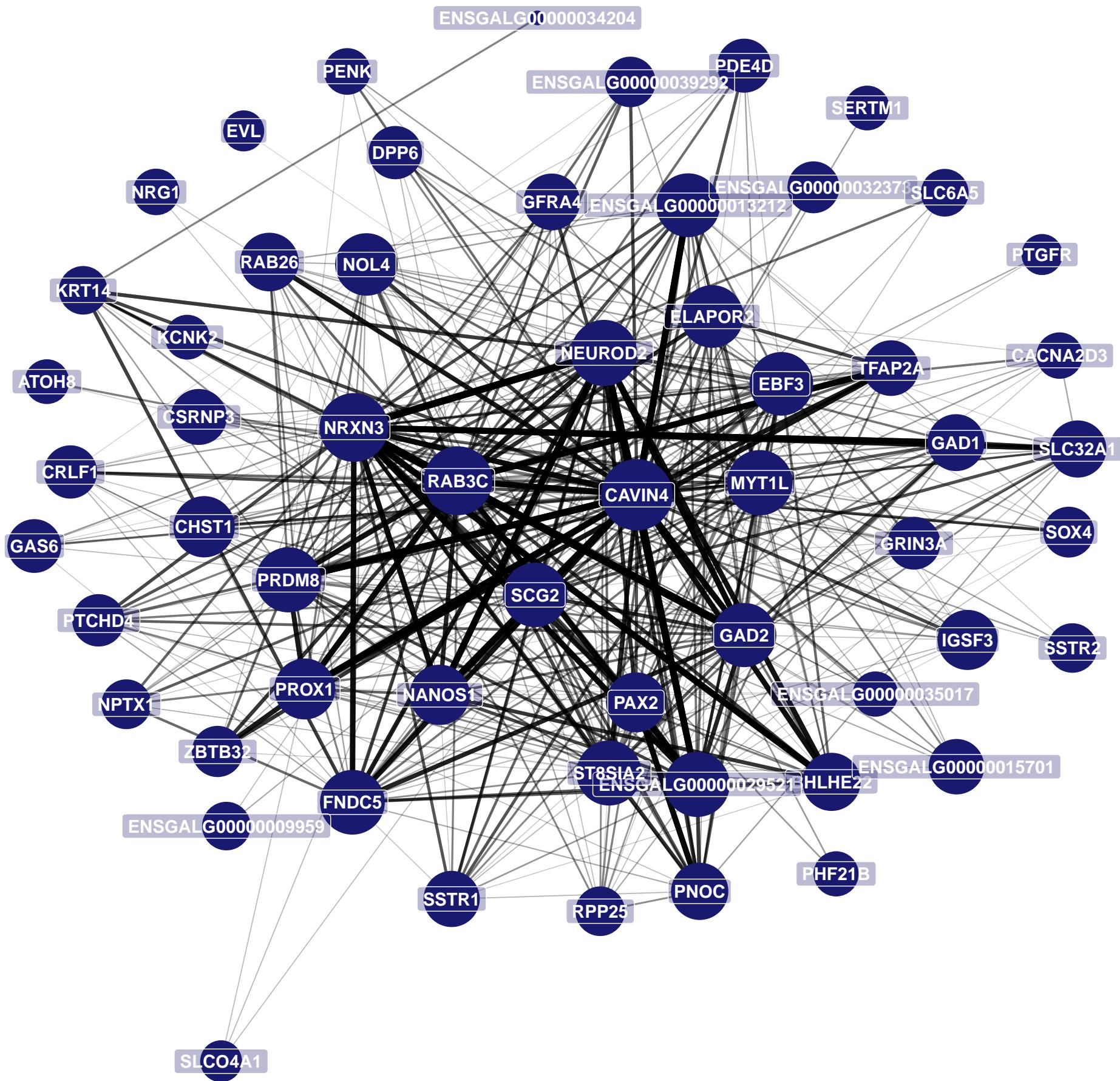
	Pathway	N	DE	P.DE
<i>path:gga04310</i>	Wnt signaling pathway	134	5	0.0007498
<i>path:gga04218</i>	Cellular senescence	134	4	0.005766
<i>path:gga03015</i>	mRNA surveillance pathway	73	2	0.05835
<i>path:gga00730</i>	Thiamine metabolism	12	1	0.06248
<i>path:gga04510</i>	Focal adhesion	174	3	0.06663
<i>path:gga00910</i>	Nitrogen metabolism	13	1	0.06751
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.08737
<i>path:gga00040</i>	Pentose and glucuronate interconversions	21	1	0.1068
<i>path:gga05132</i>	Salmonella infection	221	3	0.1152
<i>path:gga04910</i>	Insulin signaling pathway	110	2	0.1176



1	UHRF1	SPC25	KNSTRN	TUBA3E	CCNA2	PCNA	WEE1	CDK2
2	DUT	HELLS	RFC2	G2E3	ATAD5	DNAJC9	NASP	WDR76
3	TFDP2	ENSGALG00000052770	CKAP2L	CDC25B	ENSGALG0000003325	DEPDC7		

	Term	Ont	N	n	Adj. p-value
GO:1900264	positive regulation of DNA-directed DNA polymerase activity	BP	2	2	2.394e-06
GO:1900262	regulation of DNA-directed DNA polymerase activity	BP	2	2	2.394e-06
GO:2000573	positive regulation of DNA biosynthetic process	BP	3	2	7.175e-06
GO:2000278	regulation of DNA biosynthetic process	BP	5	2	2.387e-05
GO:0090329	regulation of DNA-dependent DNA replication	BP	7	2	5.003e-05
GO:0006275	regulation of DNA replication	BP	9	2	8.561e-05
GO:0051054	positive regulation of DNA metabolic process	BP	18	2	0.0003607
GO:0071897	DNA biosynthetic process	BP	19	2	0.0004028
GO:0000278	mitotic cell cycle	BP	100	3	0.000503
GO:0051338	regulation of transferase activity	BP	107	3	0.0006131

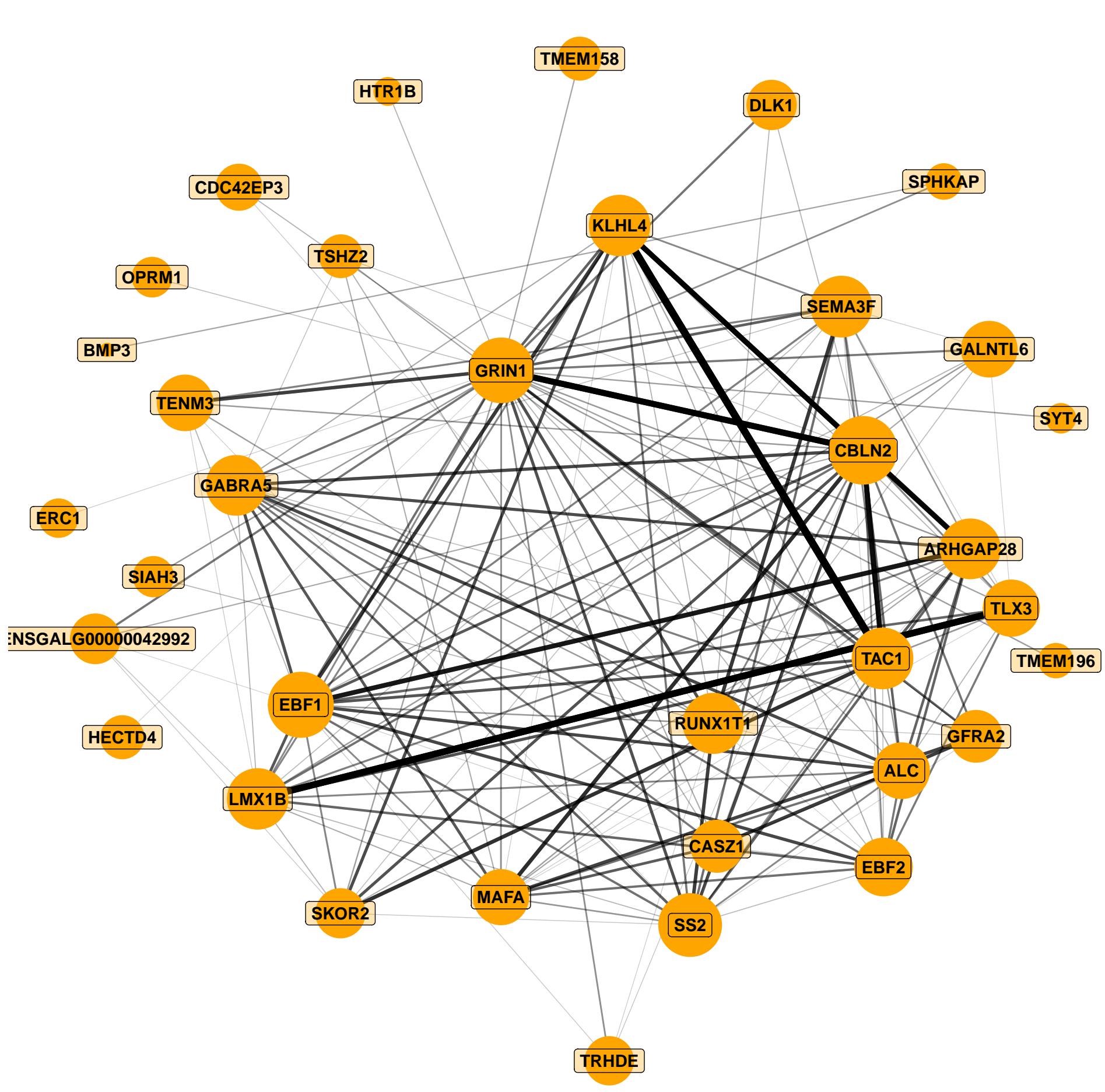
	Pathway	N	DE	P.DE
<i>path:gga04110</i>	Cell cycle	114	6	1.738e-08
<i>path:gga04914</i>	Progesterone-mediated oocyte maturation	79	3	0.0002513
<i>path:gga03430</i>	Mismatch repair	19	2	0.0004028
<i>path:gga03030</i>	DNA replication	29	2	0.0009472
<i>path:gga03420</i>	Nucleotide excision repair	37	2	0.001542
<i>path:gga04218</i>	Cellular senescence	134	2	0.01881
<i>path:gga04530</i>	Tight junction	135	2	0.01908
<i>path:gga03410</i>	Base excision repair	26	1	0.04045
<i>path:gga00310</i>	Lysine degradation	51	1	0.07787
<i>path:gga00983</i>	Drug metabolism – other enzymes	54	1	0.08227



1	CAVIN4	NRXN3	EBF3	RAB3C	PRDM8	SCG2	NEUROD2	ENSGALG00000029521
2	PAX2	PNOC	PROX1	MYT1L	SLC32A1	TFAP2A	ST8SIA2	FNDC5
3	GAD2	GAD1	BHLHE22	IGSF3	ELAPOR2	ENSGALG00000013212	NANOS1	SSTR1
4	GFRA4	CHST1	NOL4	ZBTB32	KRT14	PENK	GRIN3A	DPP6
5	RAB26	CSRNP3	EVL	SSTR2	ENSGALG00000015701	NPTX1	PTCHD4	GAS6
6	ENSGALG00000032373	CRLF1	ENSGALG00000039292	SERTM1	PDE4D	RPP25	SLC6A5	ENSGALG00000009959
7	CACNA2D3	NRG1	SLCO4A1	PTGFR	SOX4	PHF21B	KCNK2	ENSGALG00000035017
8	ATOH8	ENSGALG00000034204						

	Term	Ont	N	n	Adj. p-value
GO:0071696	ectodermal placode development	BP	1	1	0.004303
GO:0060788	ectodermal placode formation	BP	1	1	0.004303
GO:0071697	ectodermal placode morphogenesis	BP	1	1	0.004303
GO:0070309	lens fiber cell morphogenesis	BP	1	1	0.004303
GO:0036303	lymph vessel morphogenesis	BP	1	1	0.004303
GO:0001946	lymphangiogenesis	BP	1	1	0.004303
GO:0071698	olfactory placode development	BP	1	1	0.004303
GO:0030910	olfactory placode formation	BP	1	1	0.004303
GO:0071699	olfactory placode morphogenesis	BP	1	1	0.004303
GO:0043049	otic placode formation	BP	1	1	0.004303

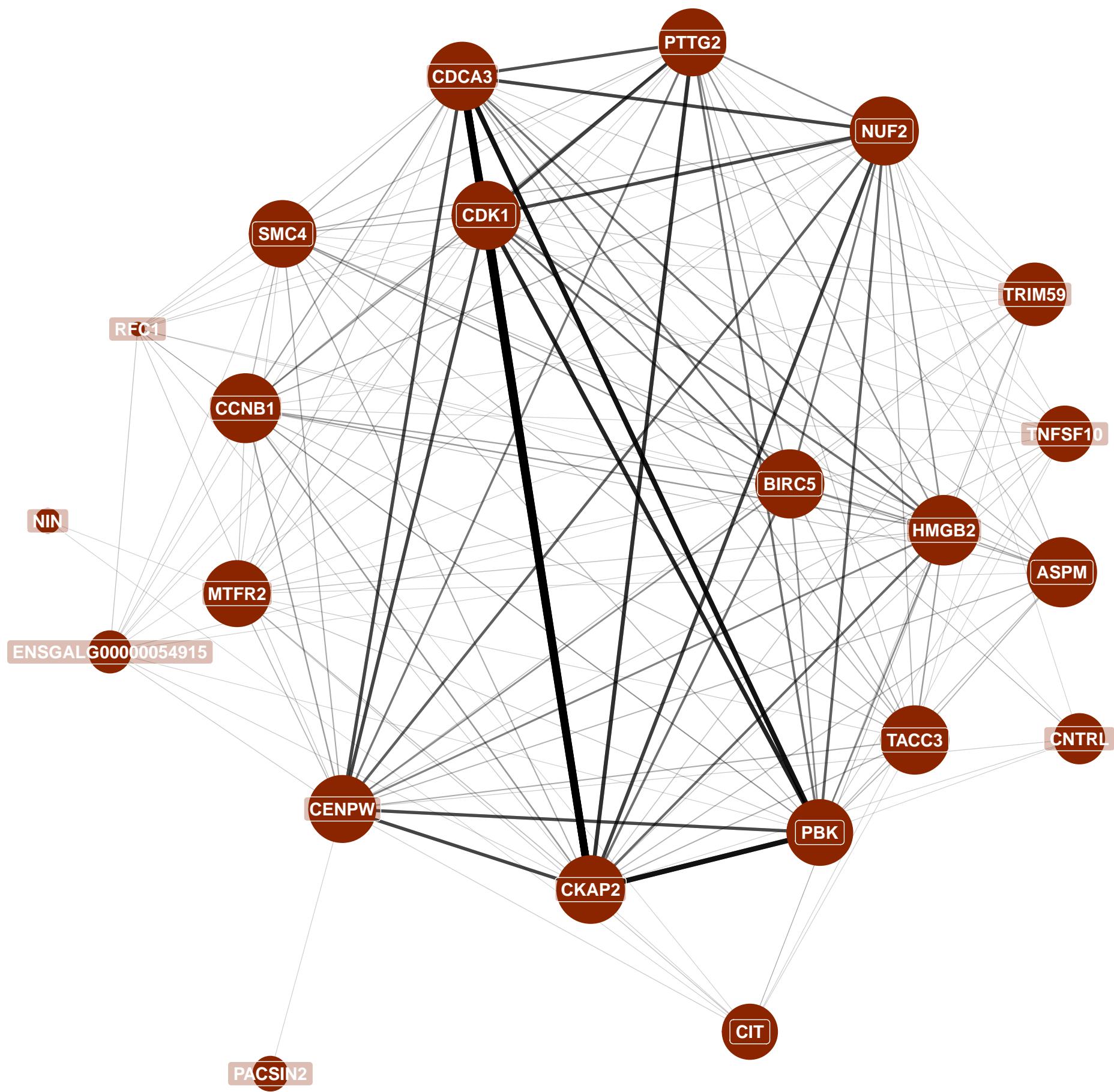
	Pathway	N	DE	P.DE
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	2	0.001168
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	295	6	0.001621
<i>path:gga00650</i>	Butanoate metabolism	21	2	0.003625
<i>path:gga00410</i>	beta–Alanine metabolism	25	2	0.005122
<i>path:gga03267</i>	Virion – Adenovirus	2	1	0.008588
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	33	2	0.008819
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.05862
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	124	2	0.09954
<i>path:gga04920</i>	Adipocytokine signaling pathway	59	1	0.2251
<i>path:gga04260</i>	Cardiac muscle contraction	60	1	0.2284



1	CBLN2	SS2	GRIN1	RUNX1T1	TAC1	EBF1	SEMA3F	LMX1B
2	TLX3	GABRA5	KLHL4	EBF2	GALNTL6	ARHGAP28	TENM3	ALC
3	SKOR2	MAFA	GFRA2	DLK1	CASZ1	ENSGALG00000042992	TRHDE	HECTD4
4	ERC1	CDC42EP3	SPHKAP	TMEM158	OPRM1	SYT4	SIAH3	HTR1B
5	TMEM196	TSHZ2	BMP3					

	Term	Ont	N	n	Adj. p-value
GO:0035860	glial cell–derived neurotrophic factor receptor signaling pathway	BP	3	1	0.007681
GO:0009749	response to glucose	BP	6	1	0.01531
GO:0009746	response to hexose	BP	6	1	0.01531
GO:0034284	response to monosaccharide	BP	6	1	0.01531
GO:0009743	response to carbohydrate	BP	7	1	0.01783
GO:0030073	insulin secretion	BP	16	1	0.04031
GO:0072163	mesonephric epithelium development	BP	18	1	0.04524
GO:0072164	mesonephric tubule development	BP	18	1	0.04524
GO:0001823	mesonephros development	BP	18	1	0.04524
GO:0030072	peptide hormone secretion	BP	19	1	0.04769

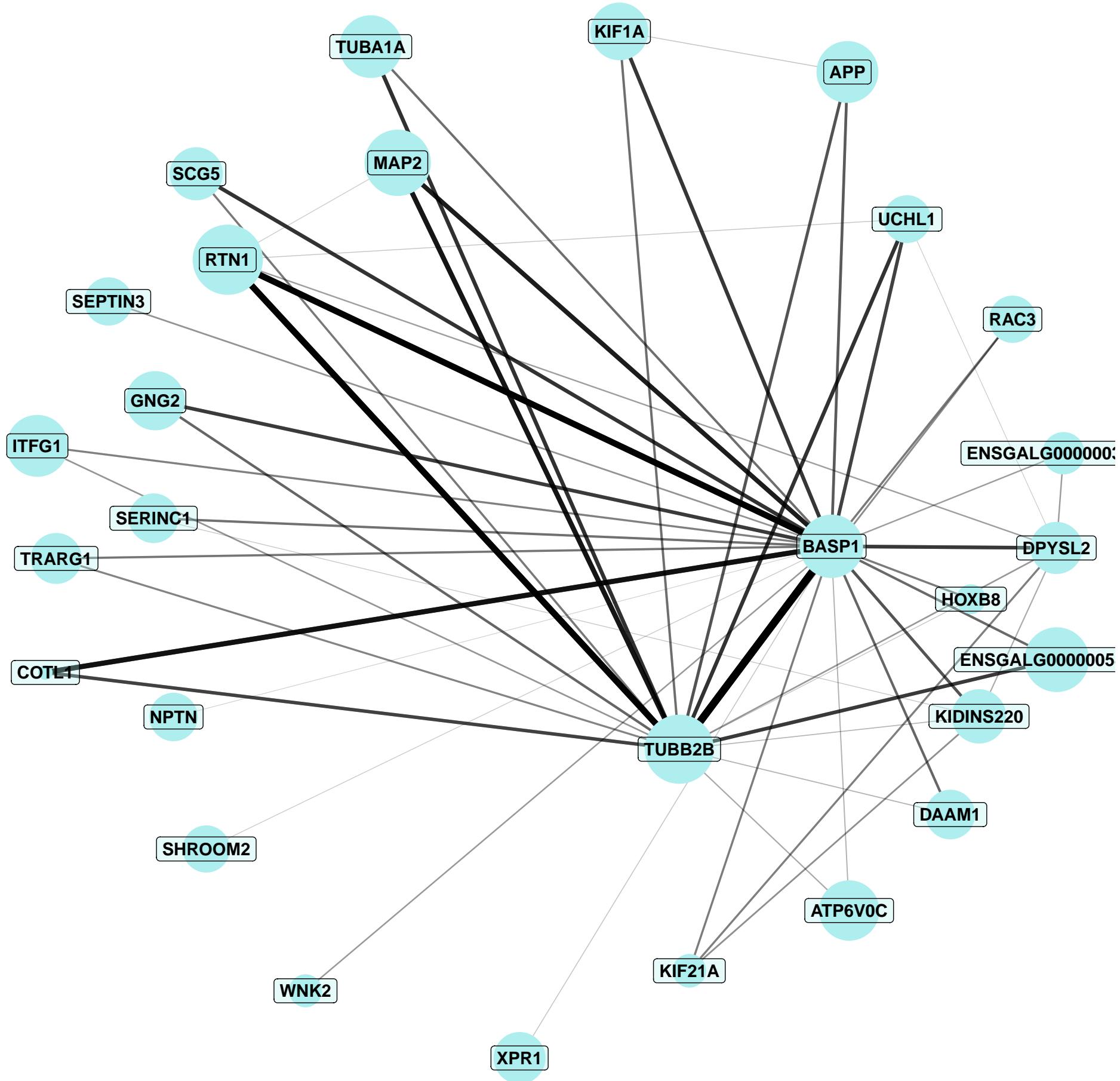
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	295	6	9.221e–05
<i>path:gga00512</i>	Mucin type O–glycan biosynthesis	29	1	0.0719
<i>path:gga00514</i>	Other types of O–glycan biosynthesis	41	1	0.1002
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	154	1	0.3284
<i>path:gga04020</i>	Calcium signaling pathway	199	1	0.4027
<i>path:gga01100</i>	Metabolic pathways	1256	1	0.9663
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1
<i>path:gga00785</i>	Lipoic acid metabolism	3	0	1
<i>path:gga00290</i>	Valine, leucine and isoleucine biosynthesis	3	0	1



1	ASPM	CDK1	CDCA3	NUF2	CKAP2	BIRC5	HMGB2	CCNB1
2	TACC3	CENPW	PTTG2	PBK	SMC4	MTFR2	TRIM59	TNFSF10
3	CIT	CNTRL	ENSGALG00000054915	PAC SIN2	NIN	RFC1		

	Term	Ont	N	n	Adj. p-value
GO:0051301	cell division	BP	87	4	1.16e-05
GO:0000278	mitotic cell cycle	BP	100	4	2.015e-05
GO:0051383	kinetochore organization	BP	10	2	0.0001175
GO:1903047	mitotic cell cycle process	BP	78	3	0.0002791
GO:0007049	cell cycle	BP	205	4	0.0003275
GO:0140013	meiotic nuclear division	BP	20	2	0.0004913
GO:1903046	meiotic cell cycle process	BP	22	2	0.0005962
GO:0006996	organelle organization	BP	437	5	0.0006318
GO:0044839	cell cycle G2/M phase transition	BP	25	2	0.0007719
GO:0007051	spindle organization	BP	25	2	0.0007719

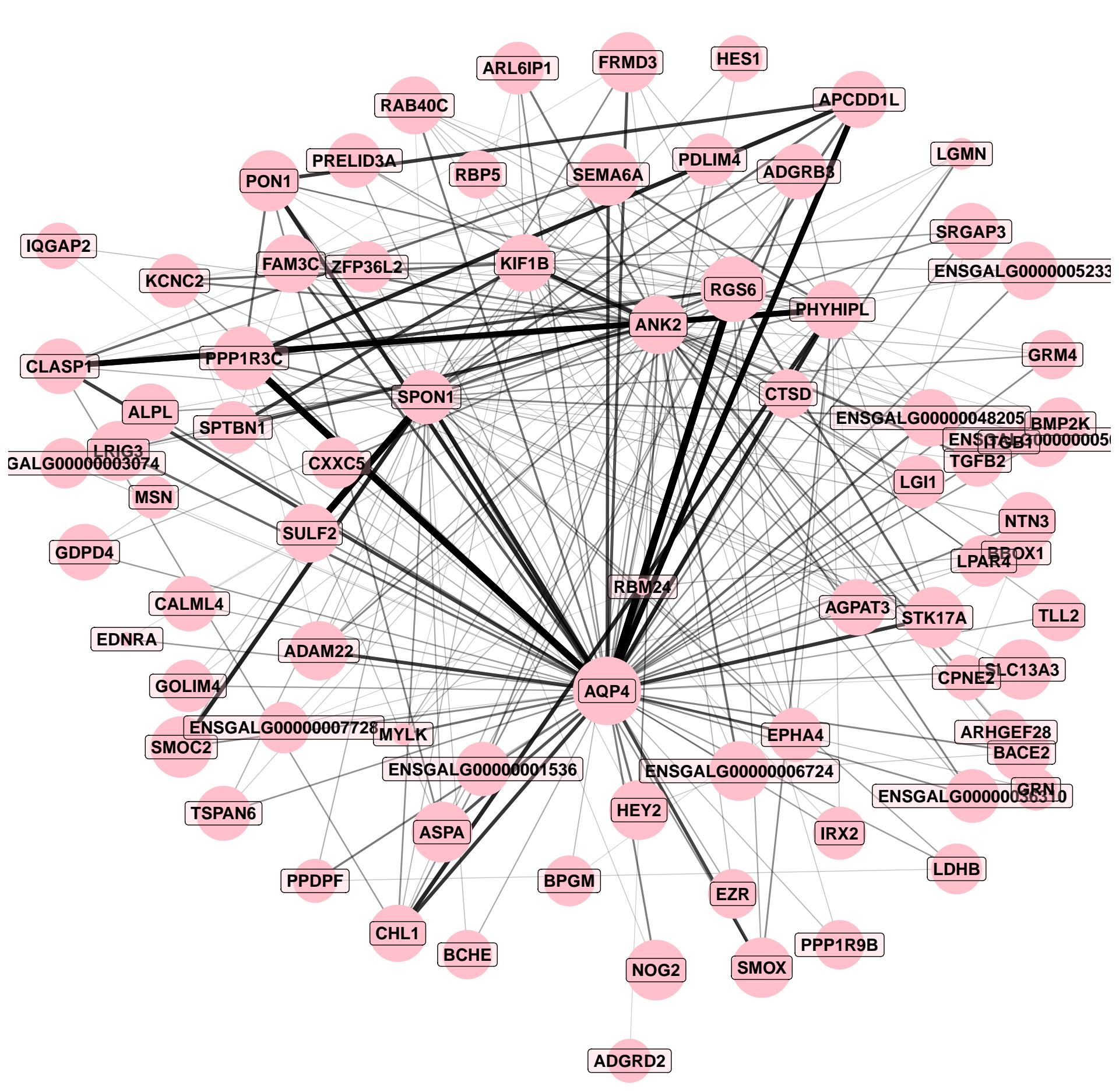
	Pathway	N	DE	P.DE
<i>path:gga04114</i>	Oocyte meiosis	97	3	0.0005299
<i>path:gga04110</i>	Cell cycle	114	3	0.0008486
<i>path:gga04115</i>	p53 signaling pathway	64	2	0.004988
<i>path:gga04914</i>	Progesterone–mediated oocyte maturation	79	2	0.007509
<i>path:gga04210</i>	Apoptosis	114	2	0.01516
<i>path:gga04068</i>	FoxO signaling pathway	114	2	0.01516
<i>path:gga04218</i>	Cellular senescence	134	2	0.02056
<i>path:gga03430</i>	Mismatch repair	19	1	0.03111
<i>path:gga03030</i>	DNA replication	29	1	0.04711
<i>path:gga03420</i>	Nucleotide excision repair	37	1	0.05973



1	TUBB2B	RTN1	BASP1	MAP2	TUBA1A	TRARG1	APP	ENSGALG00000054420
2	DPYSL2	GNG2	UCHL1	ITFG1	KIDINS220	KIF1A	SCG5	ATP6VOC
3	NPTN	SERINC1	XPR1	KIF21A	COTL1	ENSGALG00000033925	SEPTIN3	DAAM1
4	SHROOM2	HOXB8	RAC3	WNK2				

	Term	Ont	N	n	Adj. p-value
GO:0072311	glomerular epithelial cell differentiation	BP	2	1	0.004223
GO:0072010	glomerular epithelium development	BP	2	1	0.004223
GO:0072112	glomerular visceral epithelial cell differentiation	BP	2	1	0.004223
GO:0061318	renal filtration cell differentiation	BP	2	1	0.004223
GO:0007010	cytoskeleton organization	BP	167	3	0.005115
GO:0032835	glomerulus development	BP	3	1	0.006329
GO:0000226	microtubule cytoskeleton organization	BP	67	2	0.008753
GO:0061005	cell differentiation involved in kidney development	BP	5	1	0.01053
GO:0035850	epithelial cell differentiation involved in kidney development	BP	5	1	0.01053
GO:0031115	negative regulation of microtubule polymerization	BP	5	1	0.01053

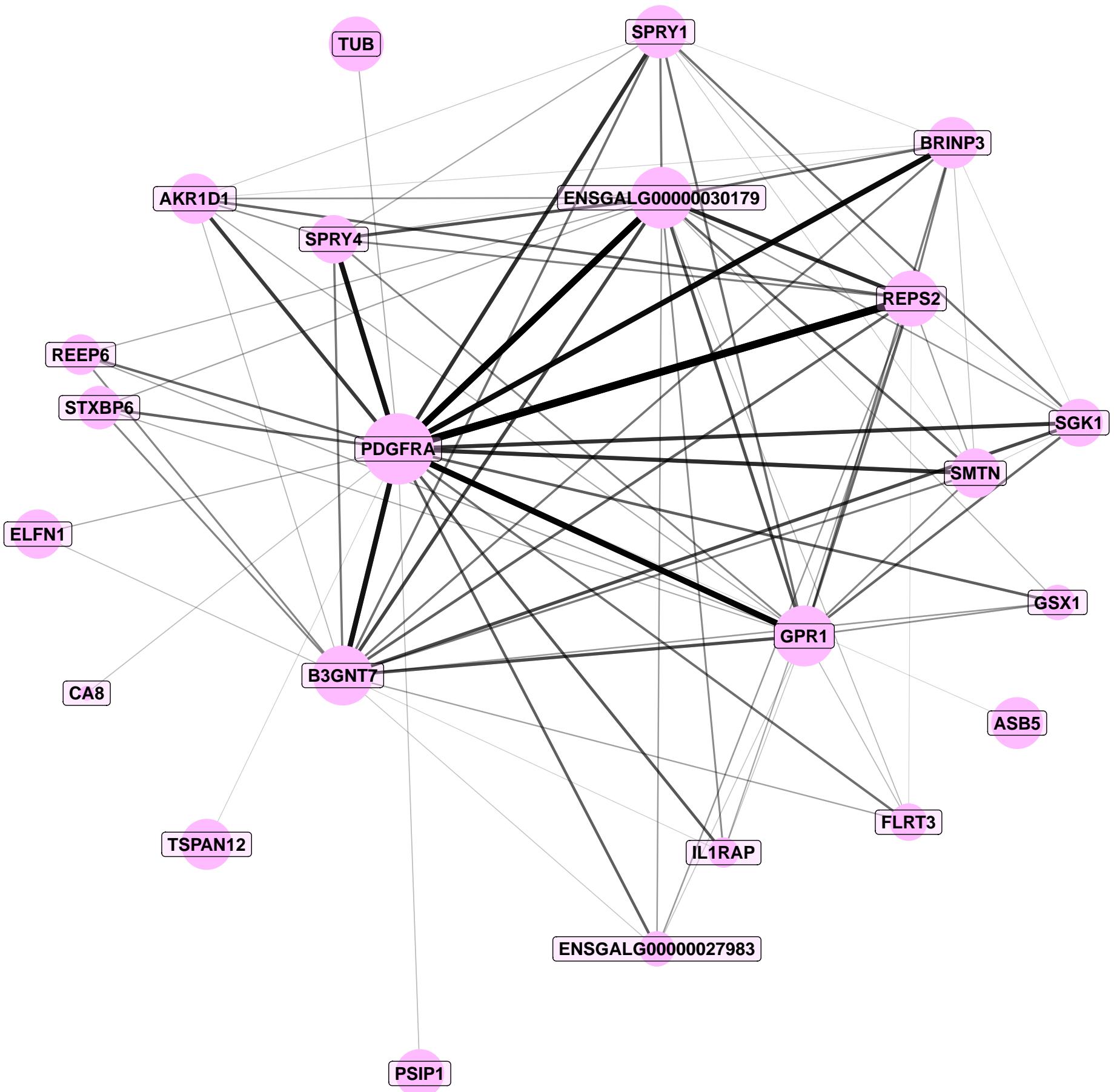
	Pathway	N	DE	P.DE
<i>path:gga04145</i>	Phagosome	125	4	0.0001298
<i>path:gga04540</i>	Gap junction	79	3	0.0006008
<i>path:gga05132</i>	Salmonella infection	221	3	0.01104
<i>path:gga04310</i>	Wnt signaling pathway	134	2	0.03234
<i>path:gga04370</i>	VEGF signaling pathway	54	1	0.1082
<i>path:gga04520</i>	Adherens junction	69	1	0.1362
<i>path:gga00190</i>	Oxidative phosphorylation	101	1	0.1931
<i>path:gga04371</i>	Apelin signaling pathway	113	1	0.2135
<i>path:gga04210</i>	Apoptosis	114	1	0.2152
<i>path:gga04142</i>	Lysosome	114	1	0.2152



1	AQP4	RGS6	SLC13A3	SMOC2	PON1	PPP1R3C	SPON1	ASPA
2	ANK2	SEMA6A	APCDD1L	SULF2	ENSGALG0000006724	NOG2	STK17A	SMOX
3	PHYHIPL	ENSGALG00000052336	HEY2	NTN3	KIF1B	FAM3C	FRMD3	CHL1
4	LRIG3	TLL2	BACE2	SRGAP3	EPHA4	ALPL	GDPD4	ADAM22
5	ADGRB3	AGPAT3	RAB40C	EZR	CALML4	KCNC2	TSPAN6	LDHB
6	PRELID3A	SPTBN1	TGFB2	ENSGALG00000036310	ENSGALG00000048205	PDLIM4	ENSGALG00000001536	CXXC5
7	ENSGALG00000005076	IRX2	GRM4	LGI1	ENSGALG0000007728	CLASP1	CTSD	LPAR4
8	ARL6IP1	ENSGALG00000003074	CPNE2	BMP2K	GOLIM4	ZFP36L2	RBP5	HES1
9	PPP1R9B	BBOX1	BCHE	BPGM	IQGAP2	MSN	ITGB1	LGNN
10	ARHGEF28	MYLK	ADGRD2	PPDPF	GRN	EDNRA	RBM24	

	Term	Ont	N	n	Adj. p-value
GO:0008045	motor neuron axon guidance	BP	6	2	0.0004801
GO:0061061	muscle structure development	BP	69	4	0.0006524
GO:0033627	cell adhesion mediated by integrin	BP	7	2	0.0006697
GO:2000738	positive regulation of stem cell differentiation	BP	7	2	0.0006697
GO:0001756	somitogenesis	BP	8	2	0.0008896
GO:2000736	regulation of stem cell differentiation	BP	10	2	0.001419
GO:0035282	segmentation	BP	10	2	0.001419
GO:0061053	somite development	BP	14	2	0.002827
GO:0045216	cell–cell junction organization	BP	17	2	0.004179
GO:0014902	myotube differentiation	BP	17	2	0.004179

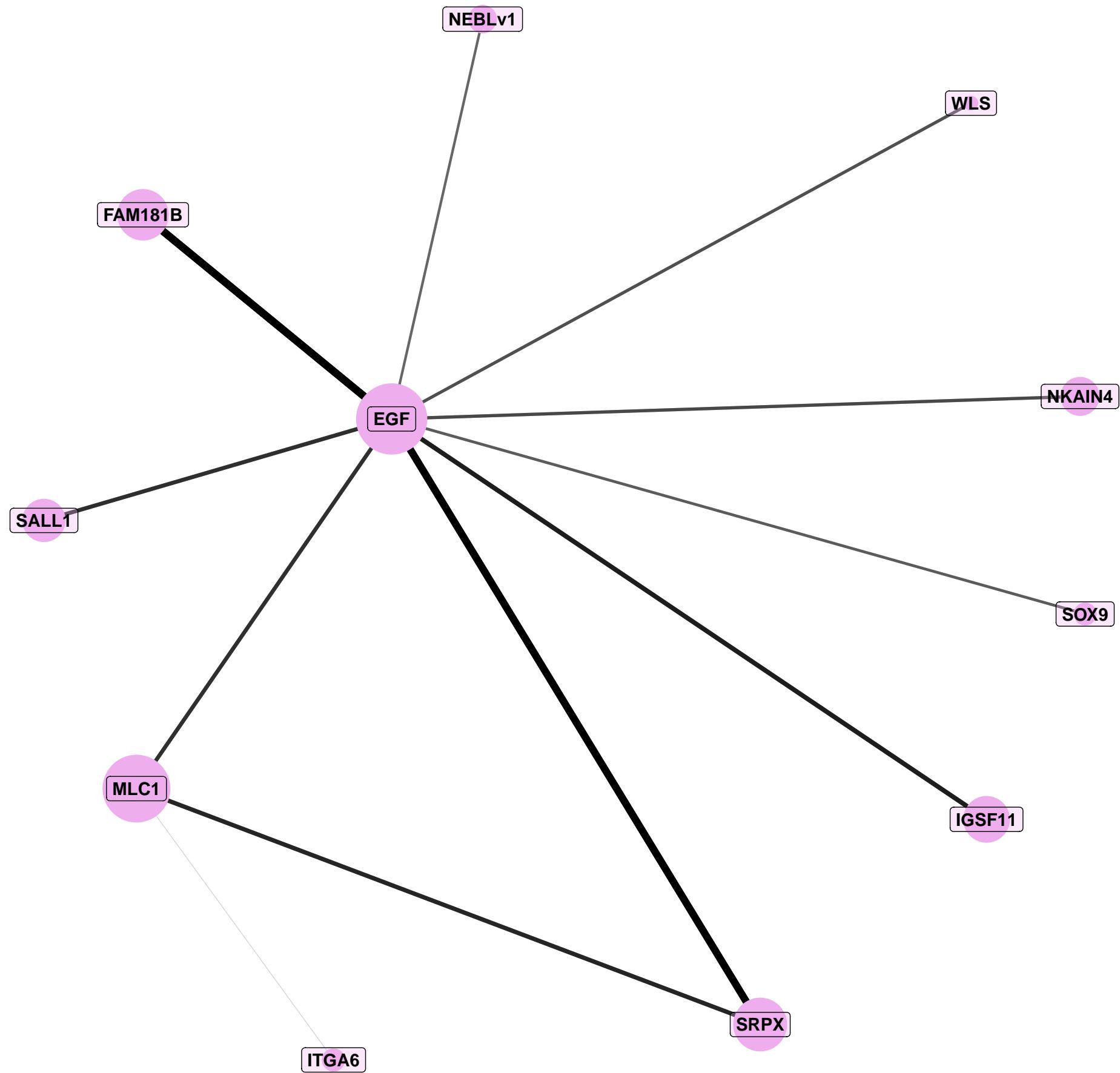
	Pathway	N	DE	P.DE
<i>path:gga04270</i>	Vascular smooth muscle contraction	109	4	0.003533
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	5	0.004471
<i>path:gga00330</i>	Arginine and proline metabolism	40	2	0.02202
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	47	2	0.02974
<i>path:gga04330</i>	Notch signaling pathway	52	2	0.03582
<i>path:gga04218</i>	Cellular senescence	134	3	0.0417
<i>path:gga00730</i>	Thiamine metabolism	12	1	0.06675
<i>path:gga04350</i>	TGF–beta signaling pathway	86	2	0.08727
<i>path:gga04744</i>	Phototransduction	16	1	0.088
<i>path:gga00100</i>	Steroid biosynthesis	16	1	0.088



1	PDGFRA	AKR1D1	B3GNT7	GPR1	ENSGALG00000030179	REPS2	SGK1	BRINP3
2	SPRY1	SMTN	ASB5	TUB	ELFN1	SPRY4	TSPAN12	STXBP6
3	REEP6	GSX1	FLRT3	PSIP1	ENSGALG00000027983	IL1RAP	CA8	

	Term	Ont	N	n	Adj. p-value
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	BP	81	4	8.729e-06
GO:0007167	enzyme linked receptor protein signaling pathway	BP	125	4	4.847e-05
GO:0009653	anatomical structure morphogenesis	BP	300	5	0.0001106
GO:0071363	cellular response to growth factor stimulus	BP	78	3	0.0002791
GO:0070848	response to growth factor	BP	79	3	0.0002898
GO:0008543	fibroblast growth factor receptor signaling pathway	BP	20	2	0.0004913
GO:0044344	cellular response to fibroblast growth factor stimulus	BP	21	2	0.0005425
GO:0071774	response to fibroblast growth factor	BP	22	2	0.0005962
GO:0007166	cell surface receptor signaling pathway	BP	267	4	0.0008867
GO:0007165	signal transduction	BP	483	5	0.0009935

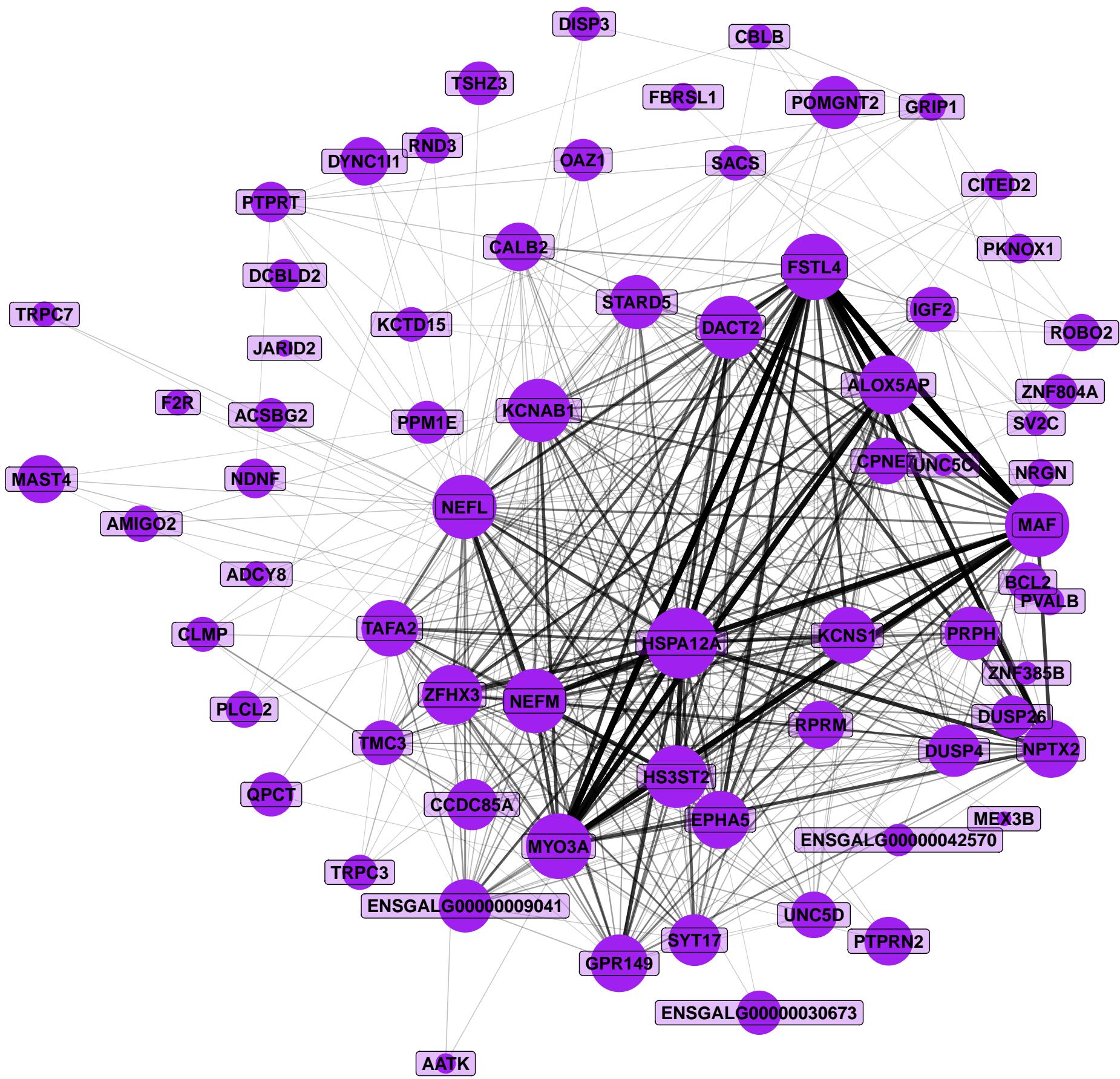
	Pathway	N	DE	P.DE
<i>path:gga00120</i>	Primary bile acid biosynthesis	12	1	0.01976
<i>path:gga00910</i>	Nitrogen metabolism	13	1	0.02139
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.02301
<i>path:gga00140</i>	Steroid hormone biosynthesis	28	1	0.04552
<i>path:gga04010</i>	MAPK signaling pathway	240	2	0.05955
<i>path:gga03250</i>	Viral life cycle – HIV-1	49	1	0.07836
<i>path:gga04540</i>	Gap junction	79	1	0.1234
<i>path:gga04514</i>	Cell adhesion molecules	103	1	0.1579
<i>path:gga04068</i>	FoxO signaling pathway	114	1	0.1733
<i>path:gga04150</i>	mTOR signaling pathway	134	1	0.2006



1	MLC1	EGF	SRPX	SOX9	ITGA6	NEBLv1	NKAIN4
2	SALL1	IGSF11	WLS				FAM181B

	Term	Ont	N	n	Adj. p-value
GO:0060173	limb development	BP	32	2	0.0003068
GO:0048736	appendage development	BP	33	2	0.0003264
GO:0032879	regulation of localization	BP	189	3	0.0004336
GO:0030335	positive regulation of cell migration	BP	43	2	0.0005557
GO:0030111	regulation of Wnt signaling pathway	BP	44	2	0.0005819
GO:2000147	positive regulation of cell motility	BP	45	2	0.0006087
GO:0051272	positive regulation of cellular component movement	BP	47	2	0.0006641
GO:0040017	positive regulation of locomotion	BP	47	2	0.0006641
GO:0060018	astrocyte fate commitment	BP	1	1	0.0008304
GO:1904837	beta–catenin–TCF complex assembly	BP	1	1	0.0008304

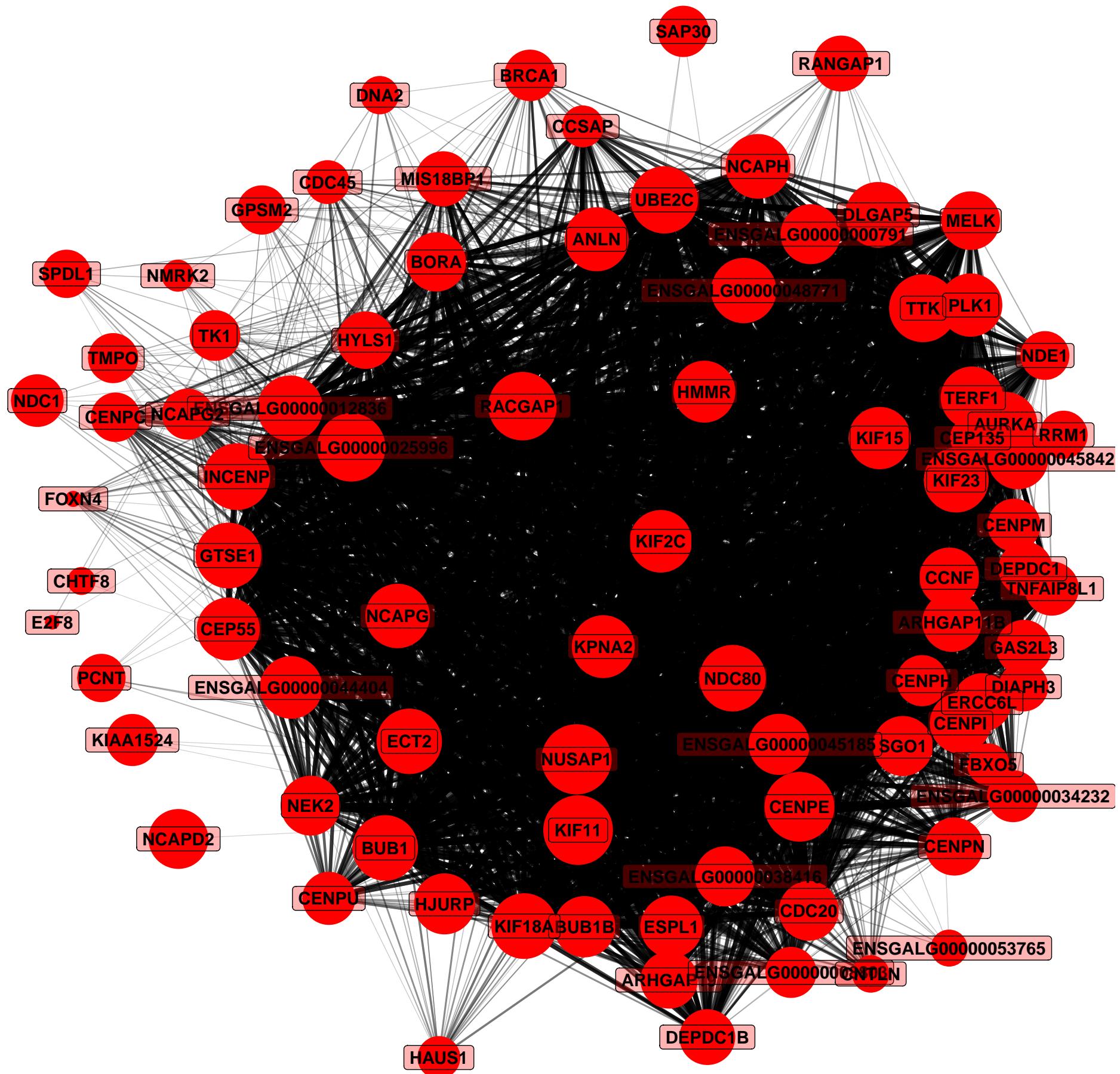
	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	103	2	0.003146
<i>path:gga04510</i>	Focal adhesion	174	2	0.008729
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	2	0.01013
<i>path:gga04512</i>	ECM–receptor interaction	67	1	0.05427
<i>path:gga04012</i>	ErbB signaling pathway	76	1	0.06136
<i>path:gga04540</i>	Gap junction	79	1	0.06371
<i>path:gga04068</i>	FoxO signaling pathway	114	1	0.09073
<i>path:gga04020</i>	Calcium signaling pathway	199	1	0.1534
<i>path:gga04010</i>	MAPK signaling pathway	240	1	0.1823
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1



1	HSPA12A	NEFL	FSTL4	NEFM	HS3ST2	KCNAB1	NPTX2	DACT2
2	ALOX5AP	MAF	MYO3A	MAST4	KCNS1	TAFA2	TMC3	STARD5
3	DYNC1I1	CALB2	ZFHX3	GPR149	EPHA5	ENSGALG0000009041	PTPRN2	POMGNT2
4	CCDC85A	TSHZ3	PRPH	ENSGALG00000030673	DUSP4	RPRM	RND3	SYT17
5	PPM1E	CPNE7	QPCT	PTPRT	IGF2	ROBO2	UNC5D	OAZ1
6	BCL2	NDNF	DUSP26	SACS	ZNF804A	DCBL2	DISP3	TRPC3
7	PLCL2	CITED2	PVALB	AMIGO2	SV2C	ACSBG2	NRGN	GRIP1
8	KCTD15	PKNOX1	AATK	F2R	TRPC7	ENSGALG0000042570	CBLB	FBRSL1
9	ADCY8	JARID2	UNC5C	CLMP	ZNF385B	MEX3B		

	Term	Ont	N	n	Adj. p-value
GO:0043271	negative regulation of ion transport	BP	19	3	9.864e-05
GO:0040018	positive regulation of multicellular organism growth	BP	4	2	0.000137
GO:0051051	negative regulation of transport	BP	27	3	0.0002897
GO:0034766	negative regulation of ion transmembrane transport	BP	6	2	0.0003404
GO:0034763	negative regulation of transmembrane transport	BP	6	2	0.0003404
GO:0048636	positive regulation of muscle organ development	BP	6	2	0.0003404
GO:1901863	positive regulation of muscle tissue development	BP	6	2	0.0003404
GO:0048643	positive regulation of skeletal muscle tissue development	BP	6	2	0.0003404
GO:0045844	positive regulation of striated muscle tissue development	BP	6	2	0.0003404
GO:0040014	regulation of multicellular organism growth	BP	6	2	0.0003404

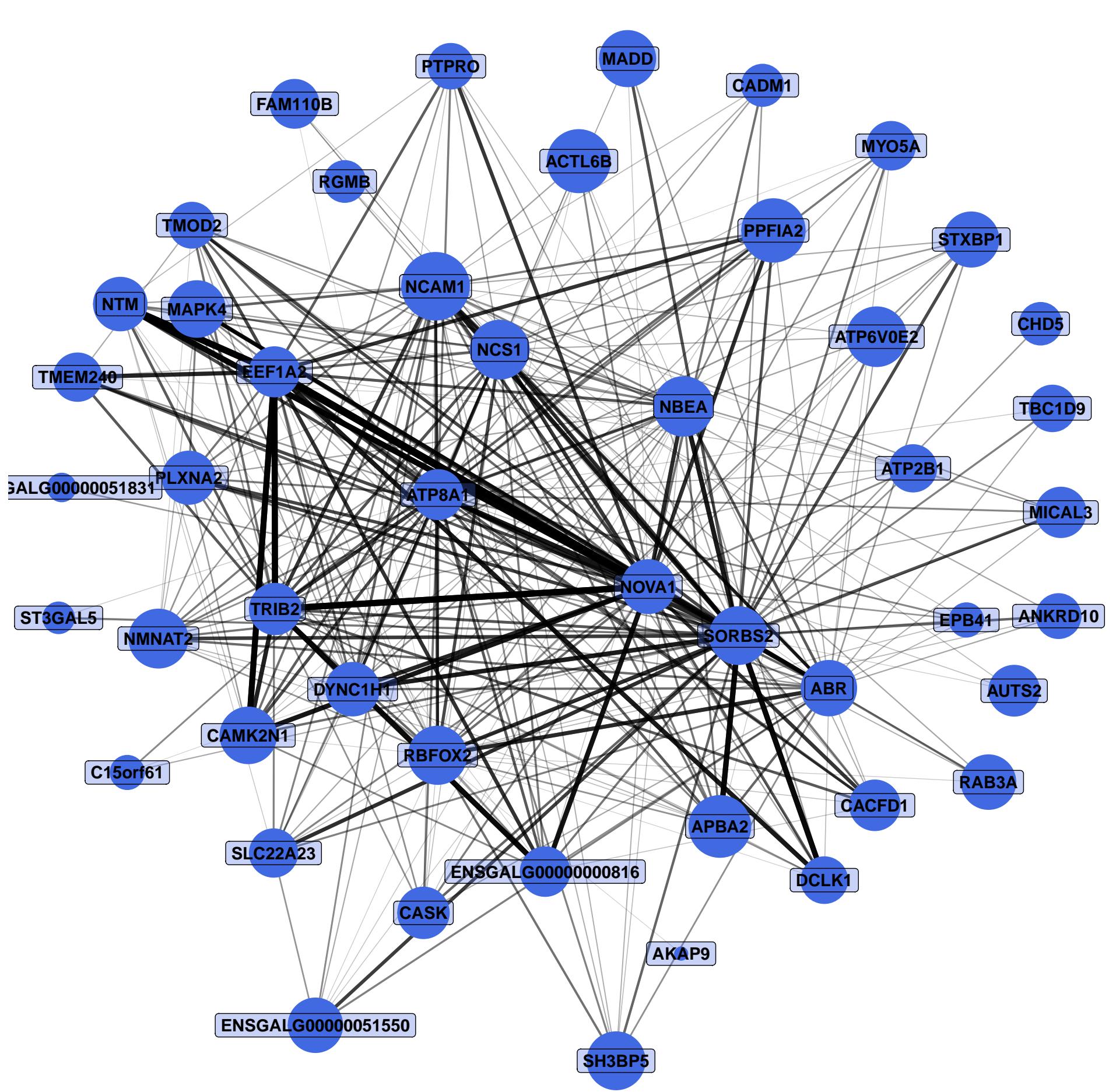
	Pathway	N	DE	P.DE
<i>path:gga00061</i>	Fatty acid biosynthesis	16	1	0.07461
<i>path:gga00515</i>	Mannose type O–glycan biosynthesis	22	1	0.1011
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	124	2	0.1207
<i>path:gga00071</i>	Fatty acid degradation	31	1	0.1396
<i>path:gga04340</i>	Hedgehog signaling pathway	47	1	0.2039
<i>path:gga01212</i>	Fatty acid metabolism	51	1	0.2192
<i>path:gga03320</i>	PPAR signaling pathway	58	1	0.2454
<i>path:gga04920</i>	Adipocytokine signaling pathway	59	1	0.249
<i>path:gga04020</i>	Calcium signaling pathway	199	2	0.2499
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.2599



1	NUSAP1	CENPE	KIF11	ENSGALG00000025996	UBE2C	KPNA2	RACGAP1	AURKA
2	INCENP	TTK	ENSGALG00000048771	NDC80	BUB1	ENSGALG0000012836	GTSE1	DLGAP5
3	KIF23	ECT2	KIF18A	ANLN	PLK1	BUB1B	CDC20	NCAPG
4	KIF15	NCAPH	CEP55	CENPI	ENSGALG00000038416	ENSGALG00000044404	KIF2C	ENSGALG00000045185
5	SGO1	HMMR	ESPL1	TERF1	HJURP	BORA	ENSGALG00000045842	NEK2
6	TK1	MELK	ARHGAP11B	BRCA1	ENSGALG0000000791	ERCC6L	CCNF	DEPDC1B
7	CENPN	NCAPD2	HYLS1	GAS2L3	ARHGAP19	MIS18BP1	CENPM	DEPDC1
8	NCAPG2	CENPH	TNFAIP8L1	KIAA1524	ENSGALG00000034232	RANGAP1	DIAPH3	CENPC
9	NDC1	CENPU	RRM1	CDC45	DNA2	NDE1	ENSGALG0000008803	HAUS1
10	SAP30	TMPO	GPSM2	CEP135	SPDL1	FBXO5	NMRK2	PCNT
11	CCSAP	CHTF8	CNTLN	E2F8	ENSGALG00000053765	FOXN4		

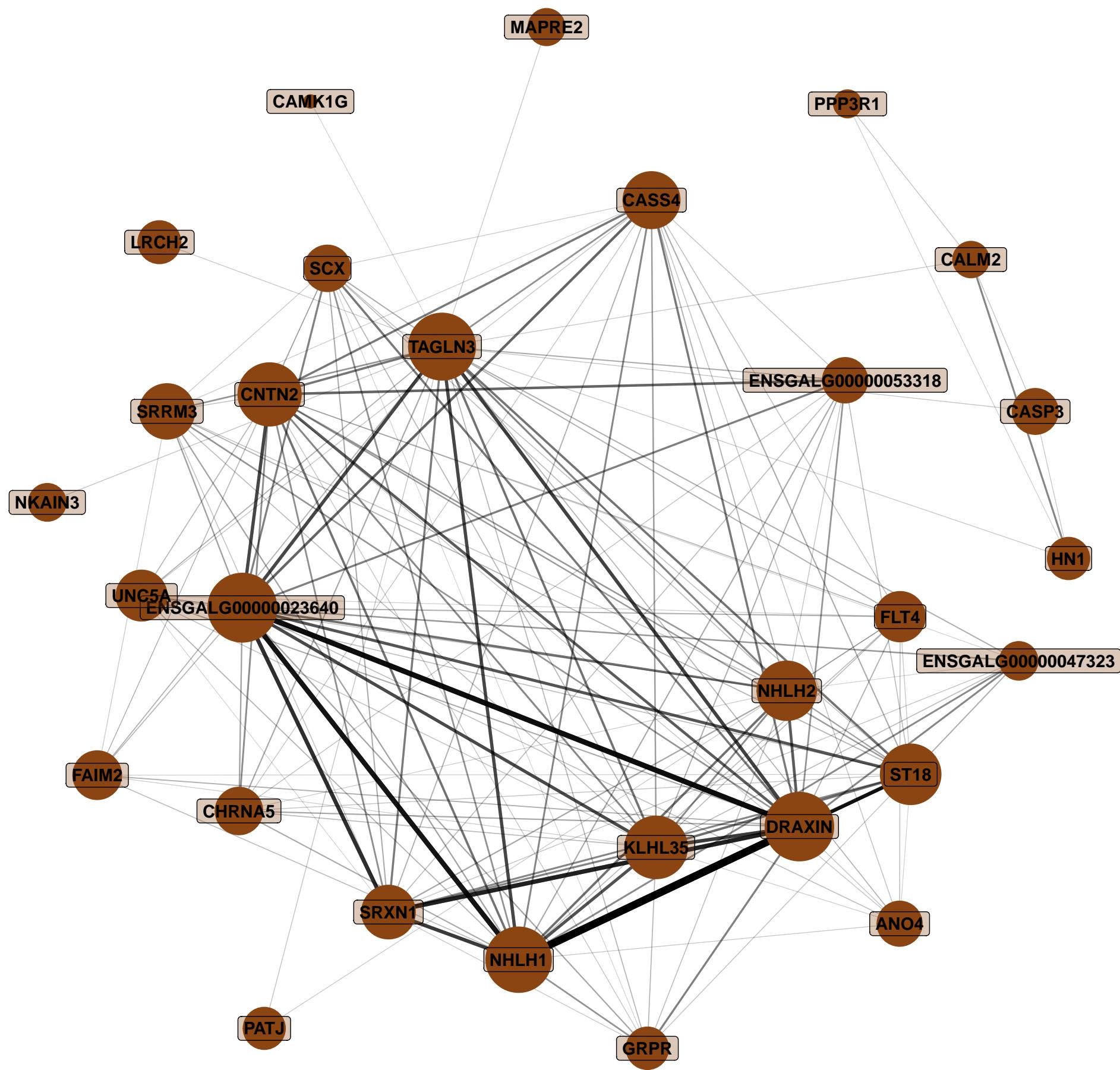
	Term	Ont	N	n	Adj. p-value
GO:0007059	chromosome segregation	BP	43	6	2.553e-07
GO:1902850	microtubule cytoskeleton organization involved in mitosis	BP	21	4	7.909e-06
GO:0040001	establishment of mitotic spindle localization	BP	7	3	8.155e-06
GO:1903047	mitotic cell cycle process	BP	78	6	9.033e-06
GO:0051293	establishment of spindle localization	BP	8	3	1.299e-05
GO:0051653	spindle localization	BP	9	3	1.939e-05
GO:0051383	kinetochore organization	BP	10	3	2.758e-05
GO:0140014	mitotic nuclear division	BP	29	4	3.021e-05
GO:0000278	mitotic cell cycle	BP	100	6	3.757e-05
GO:0050000	chromosome localization	BP	11	3	3.775e-05

	Pathway	N	DE	P.DE
<i>path:gga04114</i>	Oocyte meiosis	97	7	2.393e–06
<i>path:gga04110</i>	Cell cycle	114	7	7.036e–06
<i>path:gga04914</i>	Progesterone–mediated oocyte maturation	79	3	0.01333
<i>path:gga03013</i>	Nucleocytoplasmic transport	90	3	0.01886
<i>path:gga00983</i>	Drug metabolism – other enzymes	54	2	0.045
<i>path:gga04120</i>	Ubiquitin mediated proteolysis	128	3	0.04634
<i>path:gga00240</i>	Pyrimidine metabolism	56	2	0.04804
<i>path:gga01232</i>	Nucleotide metabolism	78	2	0.08587
<i>path:gga03030</i>	DNA replication	29	1	0.1668
<i>path:gga00760</i>	Nicotinate and nicotinamide metabolism	33	1	0.1875



	Term	Ont	N	n	Adj. p-value
GO:0070588	calcium ion transmembrane transport	BP	23	2	0.00285
GO:1990778	protein localization to cell periphery	BP	27	2	0.003919
GO:0006816	calcium ion transport	BP	30	2	0.004824
GO:0008104	protein localization	BP	214	4	0.00636
GO:1904778	positive regulation of protein localization to cell cortex	BP	2	1	0.006934
GO:0072697	protein localization to cell cortex	BP	2	1	0.006934
GO:1904776	regulation of protein localization to cell cortex	BP	2	1	0.006934
GO:0030001	metal ion transport	BP	40	2	0.008462
GO:0051179	localization	BP	539	6	0.01038
GO:0099560	synaptic membrane adhesion	BP	3	1	0.01038

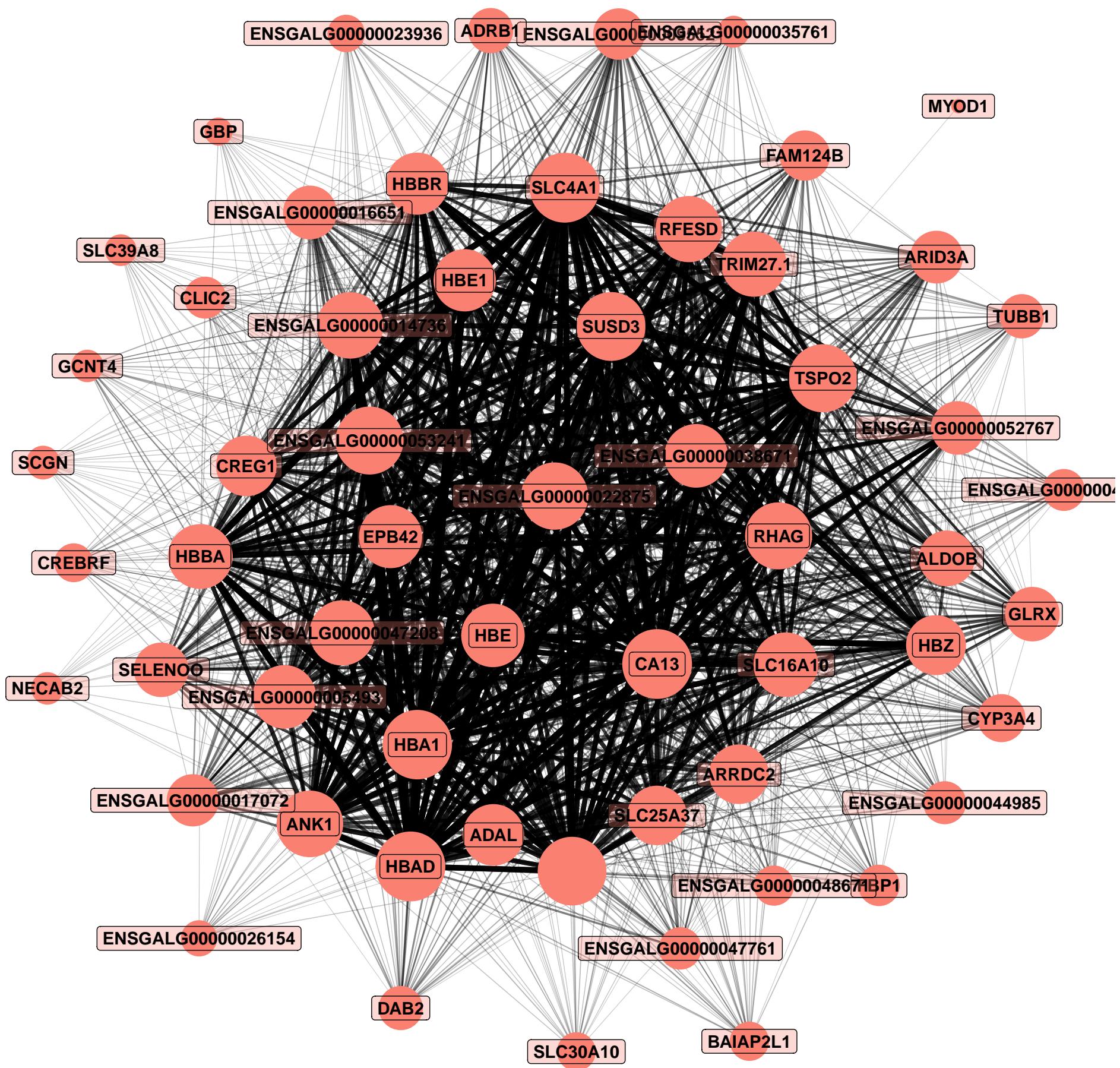
	Pathway	N	DE	P.DE
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.01382
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	1	0.04424
<i>path:gga04514</i>	Cell adhesion molecules	103	2	0.04967
<i>path:gga04145</i>	Phagosome	125	2	0.06988
<i>path:gga00760</i>	Nicotinate and nicotinamide metabolism	33	1	0.1086
<i>path:gga04350</i>	TGF–beta signaling pathway	86	1	0.2593
<i>path:gga03013</i>	Nucleocytoplasmic transport	90	1	0.2696
<i>path:gga00190</i>	Oxidative phosphorylation	101	1	0.2972
<i>path:gga01240</i>	Biosynthesis of cofactors	118	1	0.3379
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	124	1	0.3517



1	DRAVIN	NHLH1	TAGLN3	ENSGALG00000023640	CNTN2	ST18	KLHL35	NHLH2
2	CASS4	FLT4	SRRM3	ANO4	UNC5A	SCX	CALM2	CHRNA5
3	HN1	SRXN1	MAPRE2	NKAIN3	LRCH2	PATJ	FAIM2	CASP3
4	ENSGALG00000053318	ENSGALG00000047323	GRPR	PPP3R1	CAMK1G			

	Term	Ont	N	n	Adj. p-value
GO:0021528	commissural neuron differentiation in spinal cord	BP	1	1	0.002038
GO:0035993	deltoid tuberosity development	BP	1	1	0.002038
GO:0097090	presynaptic membrane organization	BP	1	1	0.002038
GO:0035990	tendon cell differentiation	BP	1	1	0.002038
GO:0035992	tendon formation	BP	1	1	0.002038
GO:0001958	endochondral ossification	BP	2	1	0.004073
GO:1905725	protein localization to microtubule end	BP	2	1	0.004073
GO:1904825	protein localization to microtubule plus-end	BP	2	1	0.004073
GO:0036075	replacement ossification	BP	2	1	0.004073
GO:0035989	tendon development	BP	2	1	0.004073

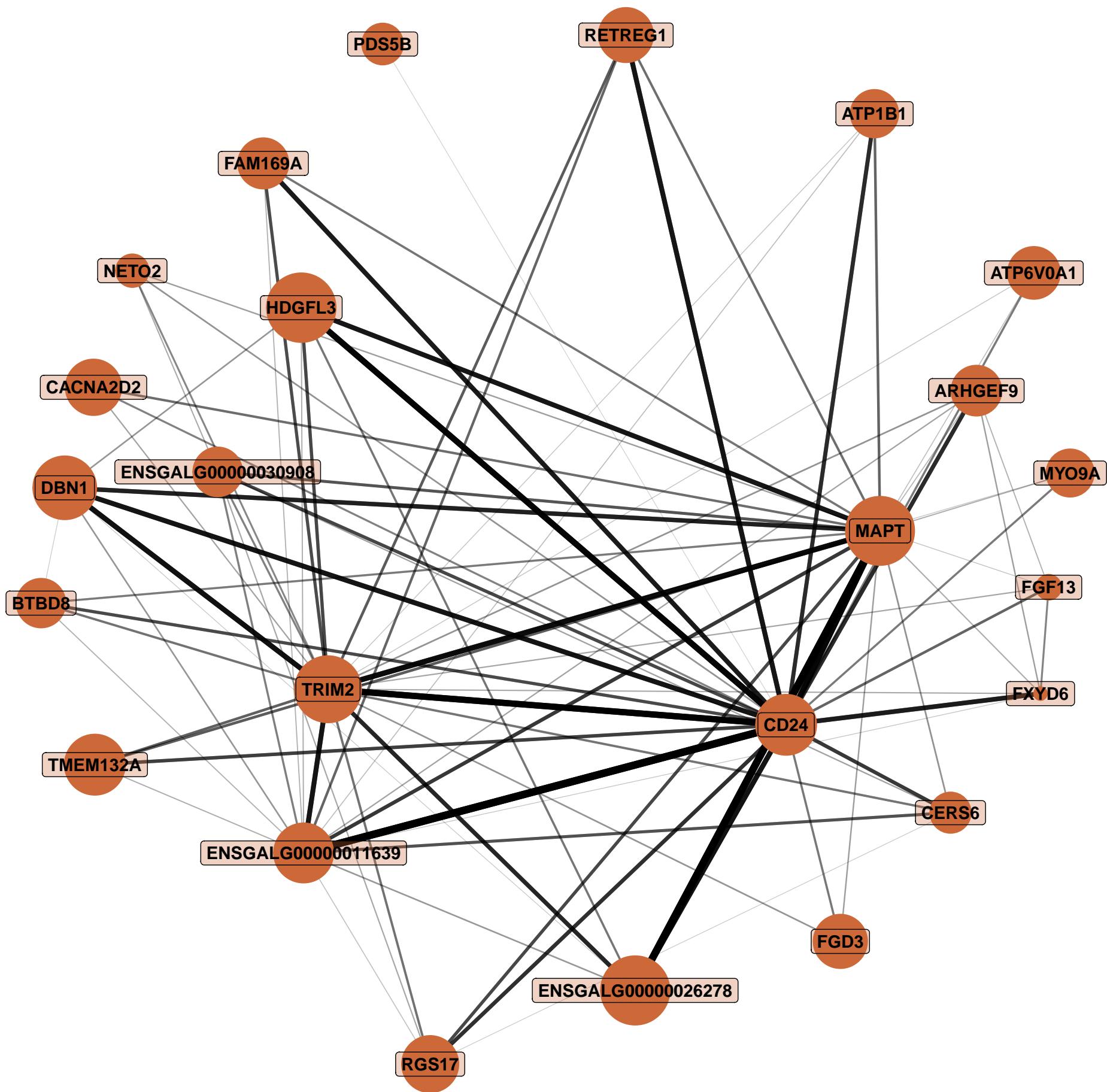
	Pathway	N	DE	P.DE
<i>path:gga04020</i>	Calcium signaling pathway	199	5	4.49e-05
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	81	2	0.01174
<i>path:gga04010</i>	MAPK signaling pathway	240	3	0.01247
<i>path:gga04114</i>	Oocyte meiosis	97	2	0.01654
<i>path:gga04218</i>	Cellular senescence	134	2	0.03023
<i>path:gga04310</i>	Wnt signaling pathway	134	2	0.03023
<i>path:gga04744</i>	Phototransduction	16	1	0.03214
<i>path:gga04623</i>	Cytosolic DNA-sensing pathway	43	1	0.08413
<i>path:gga04370</i>	VEGF signaling pathway	54	1	0.1045
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	295	2	0.1207



1	SLC4A1	NA	HBAD	HBA1	CA13	HBE	TSPO2	ENSGALG00000053241
2	RHAG	HBBA	HBE1	SUSD3	ENSGALG00000022875	ENSGALG00000014736	HBZ	HBBR
3	TRIM27.1	ENSGALG0000005493	ANK1	EPB42	RFESD	ENSGALG00000047208	ENSGALG00000038671	SLC16A10
4	ALDOB	ENSGALG00000052767	SLC25A37	ARRDC2	ADAL	FAM124B	GLRX	CREG1
5	ENSGALG0000016651	ENSGALG0000009552	CYP3A4	ARID3A	ENSGALG00000044985	ENSGALG00000017072	ADRB1	TUBB1
6	SELENOO	CLIC2	FBP1	ENSGALG00000040101	SLC30A10	ENSGALG00000047761	CREBRF	ENSGALG00000023936
7	ENSGALG0000026154	SCGN	ENSGALG00000048671	ENSGALG00000035761	DAB2	NECAB2	BAIAP2L1	SLC39A8
8	GCNT4	GBP	MYOD1					

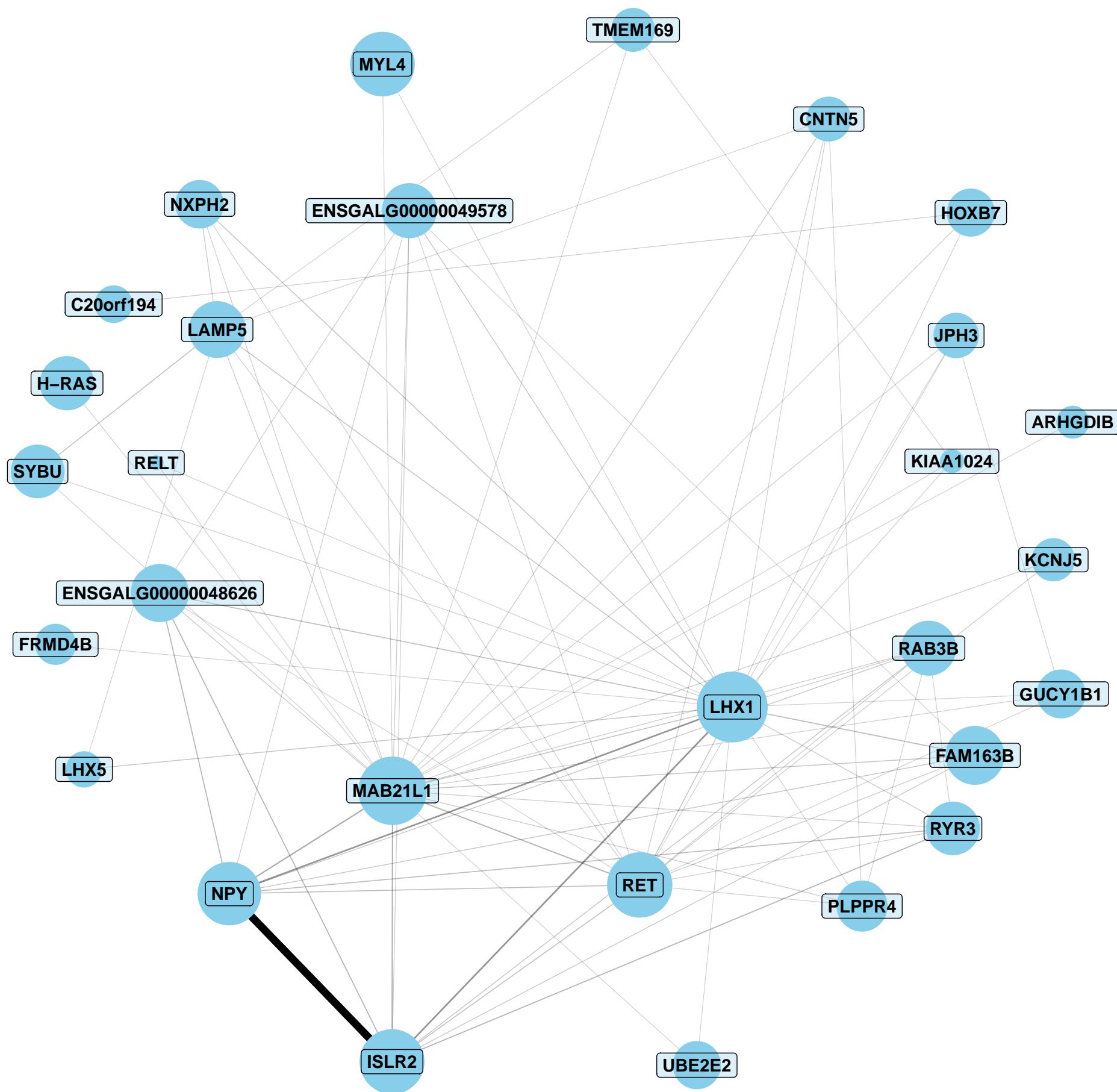
	Term	Ont	N	n	Adj. p-value
GO:0042744	hydrogen peroxide catabolic process	BP	7	6	3.379e-14
GO:0042743	hydrogen peroxide metabolic process	BP	7	6	3.379e-14
GO:0015671	oxygen transport	BP	7	6	3.379e-14
GO:0015669	gas transport	BP	8	6	1.347e-13
GO:0098869	cellular oxidant detoxification	BP	14	6	1.416e-11
GO:1990748	cellular detoxification	BP	16	6	3.752e-11
GO:0097237	cellular response to toxic substance	BP	16	6	3.752e-11
GO:0098754	detoxification	BP	17	6	5.779e-11
GO:0072593	reactive oxygen species metabolic process	BP	19	6	1.259e-10
GO:0009636	response to toxic substance	BP	20	6	1.792e-10

	Pathway	N	DE	P.DE
<i>path:gga00030</i>	Pentose phosphate pathway	25	2	0.005122
<i>path:gga00051</i>	Fructose and mannose metabolism	34	2	0.009344
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	47	2	0.01737
<i>path:gga04540</i>	Gap junction	79	2	0.04539
<i>path:gga00910</i>	Nitrogen metabolism	13	1	0.05454
<i>path:gga01200</i>	Carbon metabolism	95	2	0.063
<i>path:gga00591</i>	Linoleic acid metabolism	21	1	0.08664
<i>path:gga00140</i>	Steroid hormone biosynthesis	28	1	0.1139
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	1	0.1177
<i>path:gga00260</i>	Glycine, serine and threonine metabolism	32	1	0.129



	Term	Ont	N	n	Adj. p-value
GO:0030004	cellular monovalent inorganic cation homeostasis	BP	13	2	0.0002424
GO:0055067	monovalent inorganic cation homeostasis	BP	14	2	0.0002825
GO:0010643	cell communication by chemical coupling	BP	1	1	0.001812
GO:1902474	positive regulation of protein localization to synapse	BP	1	1	0.001812
GO:1902685	positive regulation of receptor localization to synapse	BP	1	1	0.001812
GO:0031915	positive regulation of synaptic plasticity	BP	1	1	0.001812
GO:0010644	cell communication by electrical coupling	BP	2	1	0.003621
GO:0006883	cellular sodium ion homeostasis	BP	2	1	0.003621
GO:0051220	cytoplasmic sequestering of protein	BP	2	1	0.003621
GO:0050775	positive regulation of dendrite morphogenesis	BP	2	1	0.003621

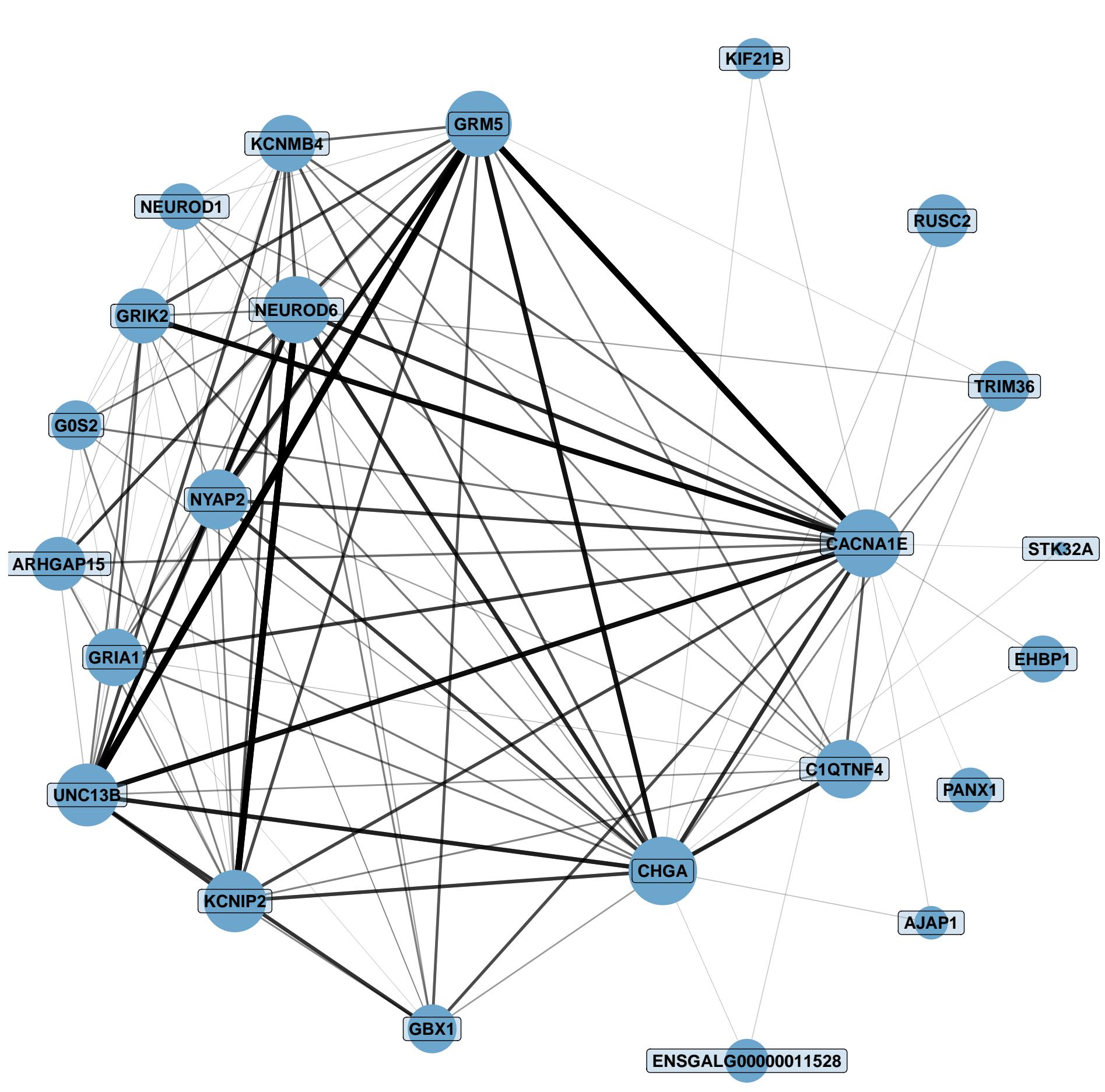
	Pathway	N	DE	P.DE
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	124	3	0.001404
<i>path:gga04260</i>	Cardiac muscle contraction	60	2	0.005223
<i>path:gga04010</i>	MAPK signaling pathway	240	2	0.06951
<i>path:gga00600</i>	Sphingolipid metabolism	47	1	0.08184
<i>path:gga00190</i>	Oxidative phosphorylation	101	1	0.1679
<i>path:gga04142</i>	Lysosome	114	1	0.1875
<i>path:gga04145</i>	Phagosome	125	1	0.2037
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	1	0.2906
<i>path:gga04020</i>	Calcium signaling pathway	199	1	0.3048
<i>path:gga01100</i>	Metabolic pathways	1256	2	0.6786



1	LHX1	MYL4	MAB21L1	ISLR2	RET	LAMP5	NPY	SYBU
2	ENSGALG00000048626	RYR3	FAM163B	ENSGALG00000049578	RAB3B	TMEM169	H-RAS	GUCY1B1
3	PLPPR4	JPH3	UBE2E2	NXPH2	KIAA1024	ARHGDI	CNTN5	KCNJ5
4	HOXB7	FRMD4B	C20orf194	LHX5	RELT			

Term	Ont	N	n
central nervous system neuron differentiation	BP	20	20
positive regulation of cell population proliferation	BP	93	33
cerebellar Purkinje cell–granule cell precursor cell signaling involved in regulation of granule cell precursor cell proliferation	BP	1	1
comma-shaped body morphogenesis	BP	1	1
dorsal spinal cord interneuron posterior axon guidance	BP	1	1
lateral motor column neuron migration	BP	1	1
motor neuron migration	BP	1	1
negative regulation of GTPase activity	BP	1	1
positive regulation of anterior head development	BP	1	1
positive regulation of epithelial cell differentiation involved in kidney development	BP	1	1

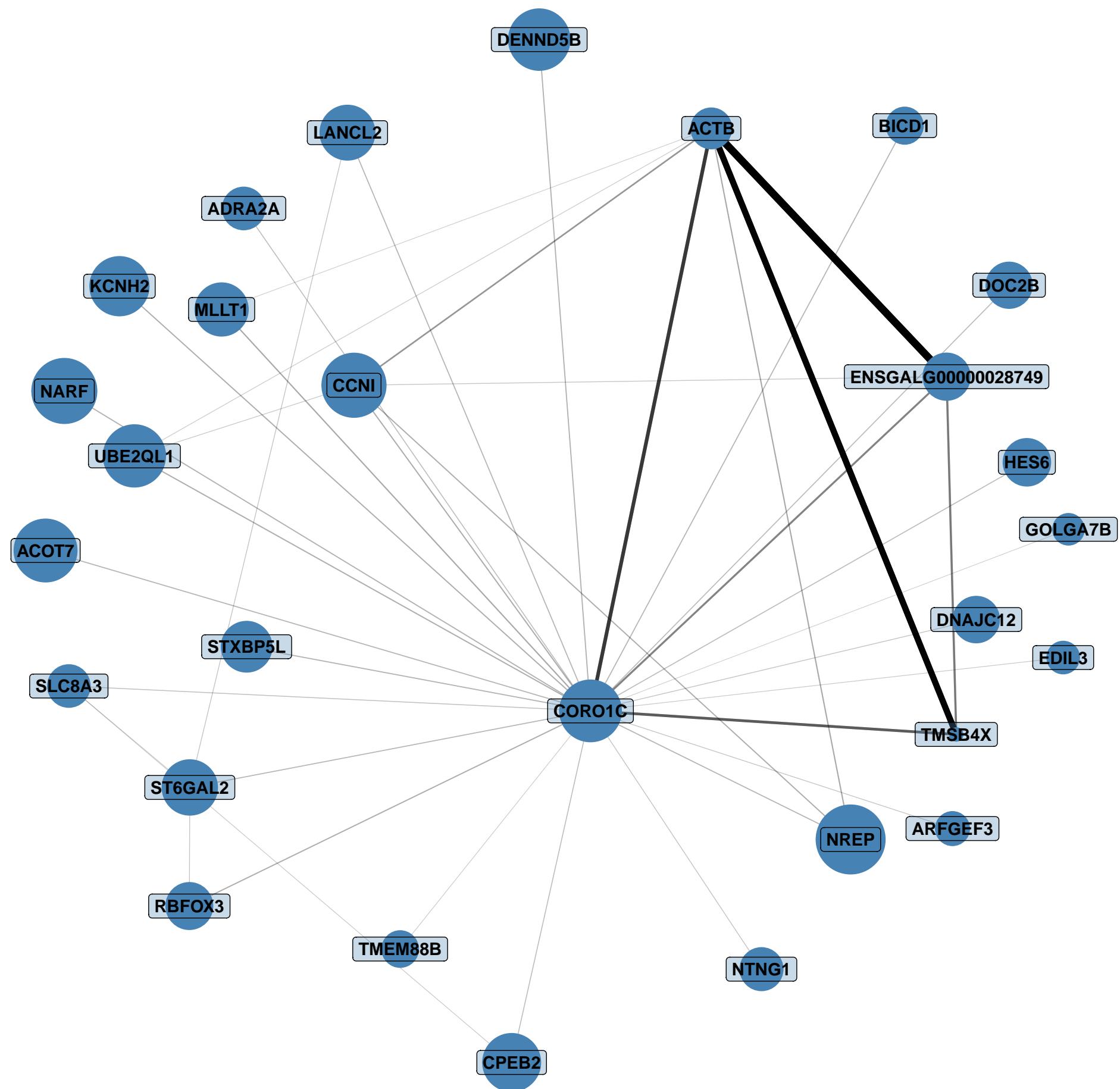
	Pathway	N	DE	P.DE
<i>path:gga04371</i>	Apelin signaling pathway	113	3	0.001523
<i>path:gga04540</i>	Gap junction	79	2	0.01119
<i>path:gga04020</i>	Calcium signaling pathway	199	2	0.06167
<i>path:gga04370</i>	VEGF signaling pathway	54	1	0.1045
<i>path:gga04920</i>	Adipocytokine signaling pathway	59	1	0.1137
<i>path:gga04260</i>	Cardiac muscle contraction	60	1	0.1155
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.1191
<i>path:gga04012</i>	ErbB signaling pathway	76	1	0.144
<i>path:gga04912</i>	GnRH signaling pathway	78	1	0.1475
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	81	1	0.1528



1	CACNA1E	CHGA	NEUROD6	GRM5	UNC13B	C1QTNF4	KCNIP2	ARHGAP15
2	RUSC2	NYAP2	GRIK2	GRIA1	EHBP1	G0S2	PANX1	TRIM36
3	KCNMB4	ENSGALG00000011528	NEUROD1	KIF21B	GBX1	AJAP1	STK32A	

	Term	Ont	N	n	Adj. p-value
GO:0042479	positive regulation of eye photoreceptor cell development	BP	1	1	0.001661
GO:0046534	positive regulation of photoreceptor cell differentiation	BP	1	1	0.001661
GO:0042478	regulation of eye photoreceptor cell development	BP	1	1	0.001661
GO:0046532	regulation of photoreceptor cell differentiation	BP	2	1	0.003319
GO:0042462	eye photoreceptor cell development	BP	3	1	0.004975
GO:0042461	photoreceptor cell development	BP	3	1	0.004975
GO:0050793	regulation of developmental process	BP	219	3	0.005444
GO:0045666	positive regulation of neuron differentiation	BP	8	1	0.01321
GO:0001754	eye photoreceptor cell differentiation	BP	10	1	0.01649
GO:0046530	photoreceptor cell differentiation	BP	10	1	0.01649

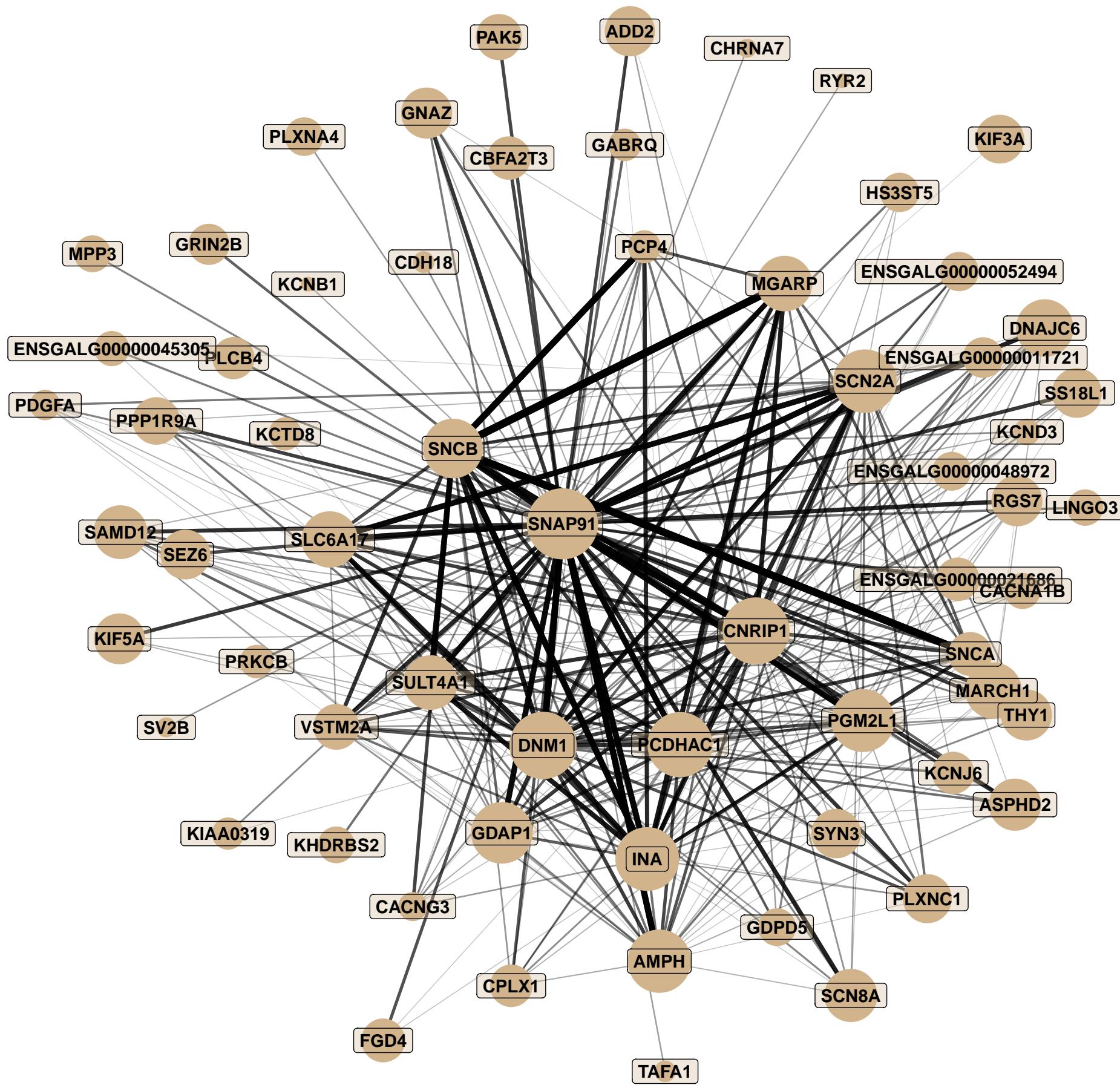
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	295	3	0.01231
<i>path:gga04020</i>	Calcium signaling pathway	199	2	0.0426
<i>path:gga04540</i>	Gap junction	79	1	0.1234
<i>path:gga04270</i>	Vascular smooth muscle contraction	109	1	0.1663
<i>path:gga04621</i>	NOD–like receptor signaling pathway	115	1	0.1747
<i>path:gga05132</i>	Salmonella infection	221	1	0.3096
<i>path:gga04010</i>	MAPK signaling pathway	240	1	0.3314
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1
<i>path:gga00785</i>	Lipoic acid metabolism	3	0	1



1	ACOT7	NREP	UBE2QL1	NARF	CORO1C	DENND5B	HES6	CPEB2
2	CCNI	KCNH2	ACTB	LANCL2	ST6GAL2	MLLT1	STXBP5L	SLC8A3
3	ENSGALG00000028749	TMSB4X	DOC2B	RBFOX3	ADRA2A	BICD1	DNAJC12	NTNG1
4	TMEM88B	GOLGA7B	ARFGEF3	EDIL3				

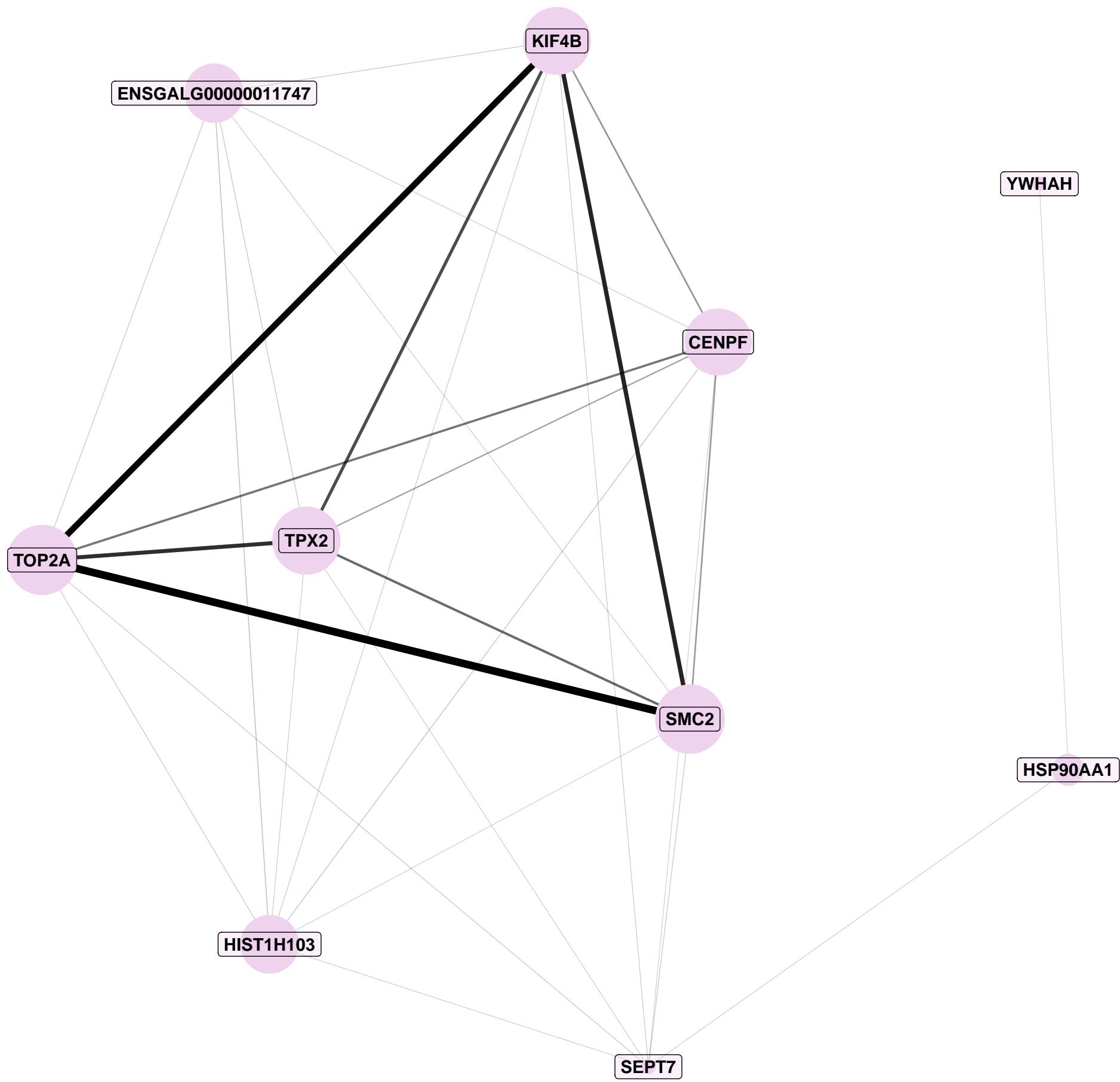
	Term	Ont	N	n	Adj. p-value
GO:0098974	postsynaptic actin cytoskeleton organization	BP	3	2	1.199e-05
GO:0099188	postsynaptic cytoskeleton organization	BP	3	2	1.199e-05
GO:0140238	presynaptic endocytosis	BP	4	2	2.395e-05
GO:0048488	synaptic vesicle endocytosis	BP	4	2	2.395e-05
GO:0036465	synaptic vesicle recycling	BP	4	2	2.395e-05
GO:0099504	synaptic vesicle cycle	BP	11	2	0.0002176
GO:0099003	vesicle-mediated transport in synapse	BP	12	2	0.0002608
GO:0099173	postsynapse organization	BP	16	2	0.0004718
GO:0050808	synapse organization	BP	37	2	0.00255
GO:0006897	endocytosis	BP	40	2	0.002975

	Pathway	N	DE	P.DE
<i>path:gga03250</i>	Viral life cycle – HIV–1	49	2	0.004436
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	3	0.006405
<i>path:gga04520</i>	Adherens junction	69	2	0.00863
<i>path:gga04210</i>	Apoptosis	114	2	0.0224
<i>path:gga05164</i>	Influenza A	114	2	0.0224
<i>path:gga04145</i>	Phagosome	125	2	0.02659
<i>path:gga04530</i>	Tight junction	135	2	0.03065
<i>path:gga00062</i>	Fatty acid elongation	23	1	0.04588
<i>path:gga04510</i>	Focal adhesion	174	2	0.04859
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	28	1	0.05559



	Term	Ont	N	n	Adj. p-value
GO:0006816	calcium ion transport	BP	30	3	0.0003453
GO:0030001	metal ion transport	BP	40	3	0.0008132
GO:0034220	ion transmembrane transport	BP	110	4	0.001633
GO:0055085	transmembrane transport	BP	122	4	0.002385
GO:0098660	inorganic ion transmembrane transport	BP	61	3	0.002766
GO:0046549	retinal cone cell development	BP	1	1	0.004605
GO:0042670	retinal cone cell differentiation	BP	1	1	0.004605
GO:0070588	calcium ion transmembrane transport	BP	23	2	0.004959
GO:0006812	cation transport	BP	85	3	0.007021
GO:0042391	regulation of membrane potential	BP	29	2	0.007819

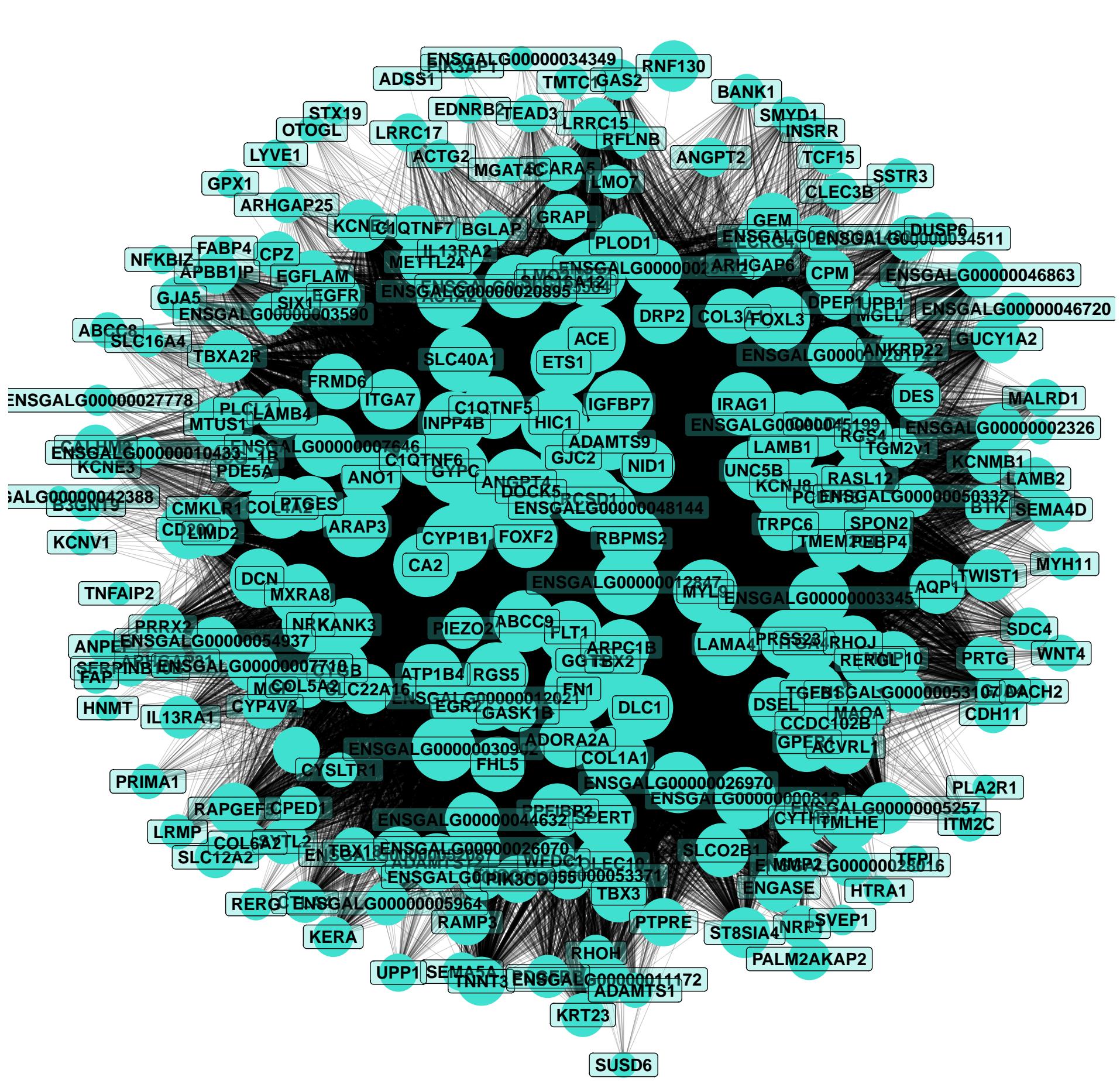
	Pathway	N	DE	P.DE
<i>path:gga04020</i>	Calcium signaling pathway	199	6	0.0002978
<i>path:gga04540</i>	Gap junction	79	3	0.005732
<i>path:gga04144</i>	Endocytosis	221	4	0.01876
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	124	3	0.01943
<i>path:gga04010</i>	MAPK signaling pathway	240	4	0.02453
<i>path:gga04260</i>	Cardiac muscle contraction	60	2	0.03112
<i>path:gga04510</i>	Focal adhesion	174	3	0.04607
<i>path:gga04012</i>	ErbB signaling pathway	76	2	0.04783
<i>path:gga04912</i>	GnRH signaling pathway	78	2	0.05011
<i>path:gga04916</i>	Melanogenesis	83	2	0.05597



1	TOP2A	SMC2	CENPF	TPX2	KIF4B	ENSGALG00000011747	HIST1H103	HSP90AA1
2	SEPT7	YWHAH						

	Term	Ont	N	n	Adj. p-value
GO:0030261	chromosome condensation	BP	10	3	2.597e-08
GO:0006323	DNA packaging	BP	31	3	9.658e-07
GO:0071103	DNA conformation change	BP	56	3	5.905e-06
GO:0007049	cell cycle	BP	205	4	6.606e-06
GO:0022402	cell cycle process	BP	129	3	7.262e-05
GO:0006996	organelle organization	BP	437	4	0.000129
GO:0051276	chromosome organization	BP	178	3	0.0001888
GO:0006310	DNA recombination	BP	55	2	0.0005981
GO:0016043	cellular component organization	BP	668	4	0.0006589
GO:0030263	apoptotic chromosome condensation	BP	1	1	0.0006795

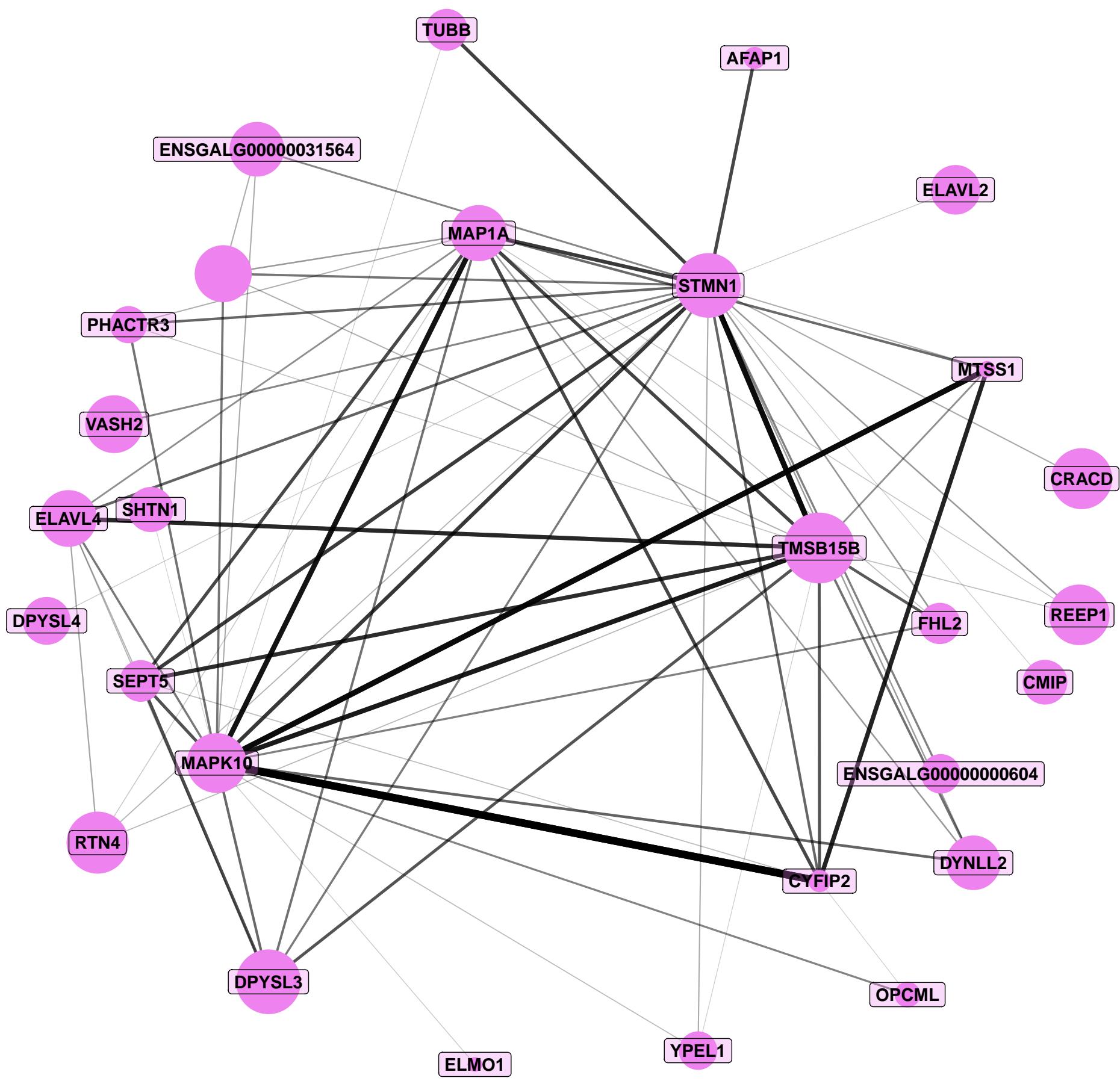
	Pathway	N	DE	P.DE
<i>path:gga04914</i>	Progesterone–mediated oocyte maturation	79	1	0.05243
<i>path:gga04114</i>	Oocyte meiosis	97	1	0.06403
<i>path:gga04217</i>	Necroptosis	109	1	0.07169
<i>path:gga04110</i>	Cell cycle	114	1	0.07487
<i>path:gga04621</i>	NOD–like receptor signaling pathway	115	1	0.0755
<i>path:gga04141</i>	Protein processing in endoplasmic reticulum	147	1	0.09559
<i>path:gga05132</i>	Salmonella infection	221	1	0.1406
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1
<i>path:gga00785</i>	Lipoic acid metabolism	3	0	1



1	DIO2	ACE	LAMB1	GYPC	FN1	ANGPT4	HIC1	ACTA2
2	RGS5	ITGA4	IGFBP7	GGT5	KCNJ8	COL1A1	CYP1B1	ENSGALG00000012021
3	TBX2	ENSGALG00000012847	RCSD1	ENSGALG00000045199	SLC40A1	ENSGALG0000007646	FOXF2	ENSGALG00000030902
4	GJC2	MYL9	LAMA4	CA2	SPON2	FLT1	MXRA8	PCDH18
5	IRAG1	ARAP3	DCN	GPER1	RBPM52	TMEM204	ETS1	ANO1
6	DLC1	ECRG4	CYGB	C1QTNF5	ENSGALG0000000818	ABCC9	FOXL3	ENSGALG00000045584
7	DOCK5	CD200	COLEC10	INPP4B	CALD1	PEBP4	ITGA7	COL4A2
8	ACVRL1	SPERT	NRK	RERGL	NA	ATP1B4	TBX3	ENSGALG00000023472
9	COL3A1	ARPC1B	ENSGALG00000003345	PRSS23	UNC5B	FHL5	ADAMTS12	AQP1
10	ENSGALG00000026970	TGFB1	RGS4	ADORA2A	ENSGALG00000028174	PPFIBP2	EGR2	PTGES
11	PLOD1	SLCO2B1	GEM	DRP2	RHOJ	KCNE4	ENSGALG00000026070	FRMD6
12	CYTH3	MAOA	ADAMTS9	ENSGALG00000044632	RAPGEF5	METTL24	ENSGALG00000052087	TWIST1
13	ENSGALG00000005257	EGFLAM	TRPC6	GJA4	NID1	DES	TBXA2R	LMO2
14	IL13RA2	DSEL	MMP10	C1QTNF6	CG-1B	ENSGALG00000034511	GUCY1A2	KANK3
15	ENSGALG00000048144	NA	RASL12	ANKRD22	SCARA5	TMLHE	EGFR	MGP
16	ENSGALG00000003590	ST8SIA4	SLC22A16	MTUS1	CTLA4	CCDC102B	ENSGALG00000054937	CALHM2
17	LAMB4	ENSGALG00000007710	LRRC15	ENGASE	TBX18	MMP2	ENSGALG00000046863	GRAPL
18	CYP4V2	CPM	ENSGALG00000053371	CPZ	NRP1	ENSGALG0000002326	PDGFRB	PRRX2
19	COL5A2	GJA5	KCNMB1	RAMP3	RNF130	ENSGALG00000012055	WFDC1	KRT23
20	PTPRE	TNNT3	LIMD2	KERA	CPED1	ENSGALG0000001483	PRTG	SYTL2
21	SEMA5A	BTK	COL6A2	ENSGALG00000053107	C1QTNF7	PIK3CD	ENSGALG00000005964	IL13RA1
22	ENSGALG00000050332	SEMA4D	PIEZ02	APBB1IP	ARHGAP31	SDC4	ARHGAP25	LRRC17
23	ENSGALG00000011172	PALM2AKAP2	MALRD1	ENSGALG00000028016	UPB1	SMYD1	CLEC3B	GASK1B
24	SLC16A12	RFLNB	WNT4	SLC12A2	LAMB2	LRMP	PDE5A	PLCL1
25	TGM2v1	ANGPT2	DUSP6	UPP1	ITM2C	GAS2	BANK1	TEAD3
26	RHOH	MGLL	TMTC1	SVEP1	SERPINB10B	ENSGALG00000027778	ENSGALG00000046720	TCF15
27	SSTR3	SUSD6	PLA2R1	CDH11	CMKLR1	B3GNT9	STX19	RERG
28	DACH2	HTRA1	FAP	PRIMA1	SLC16A4	ADAMTS1	ENSGALG00000010433	CYSLTR1
29	BGLAP	FABP4	DPEP1	LMO7	ARHGAP6	ADSS1	ACTG2	OTOGL
30	ANPEP	EDNRB2	ABCC8	INSRR	TFPI	GPX1	ENSGALG00000042388	NFKBIZ
31	SIX1	LYVE1	PIK3AP1	TNFAIP2	KCNV1	NA	HNMT	MGAT4C
32	MYH11	ENSGALG00000034349	KCNE3	ENSGALG00000020895				

	Term	Ont	N	n	Adj. p-value
GO:0048856	anatomical structure development	BP	634	31	3.729e-07
GO:0032502	developmental process	BP	666	31	1.073e-06
GO:0009653	anatomical structure morphogenesis	BP	300	18	8.039e-06
GO:0022610	biological adhesion	BP	143	12	1.022e-05
GO:0007155	cell adhesion	BP	143	12	1.022e-05
GO:0048513	animal organ development	BP	326	18	2.473e-05
GO:0061061	muscle structure development	BP	69	8	3.14e-05
GO:0007275	multicellular organism development	BP	586	25	5.45e-05
GO:0030154	cell differentiation	BP	425	20	8.43e-05
GO:0032501	multicellular organismal process	BP	724	28	0.0001063

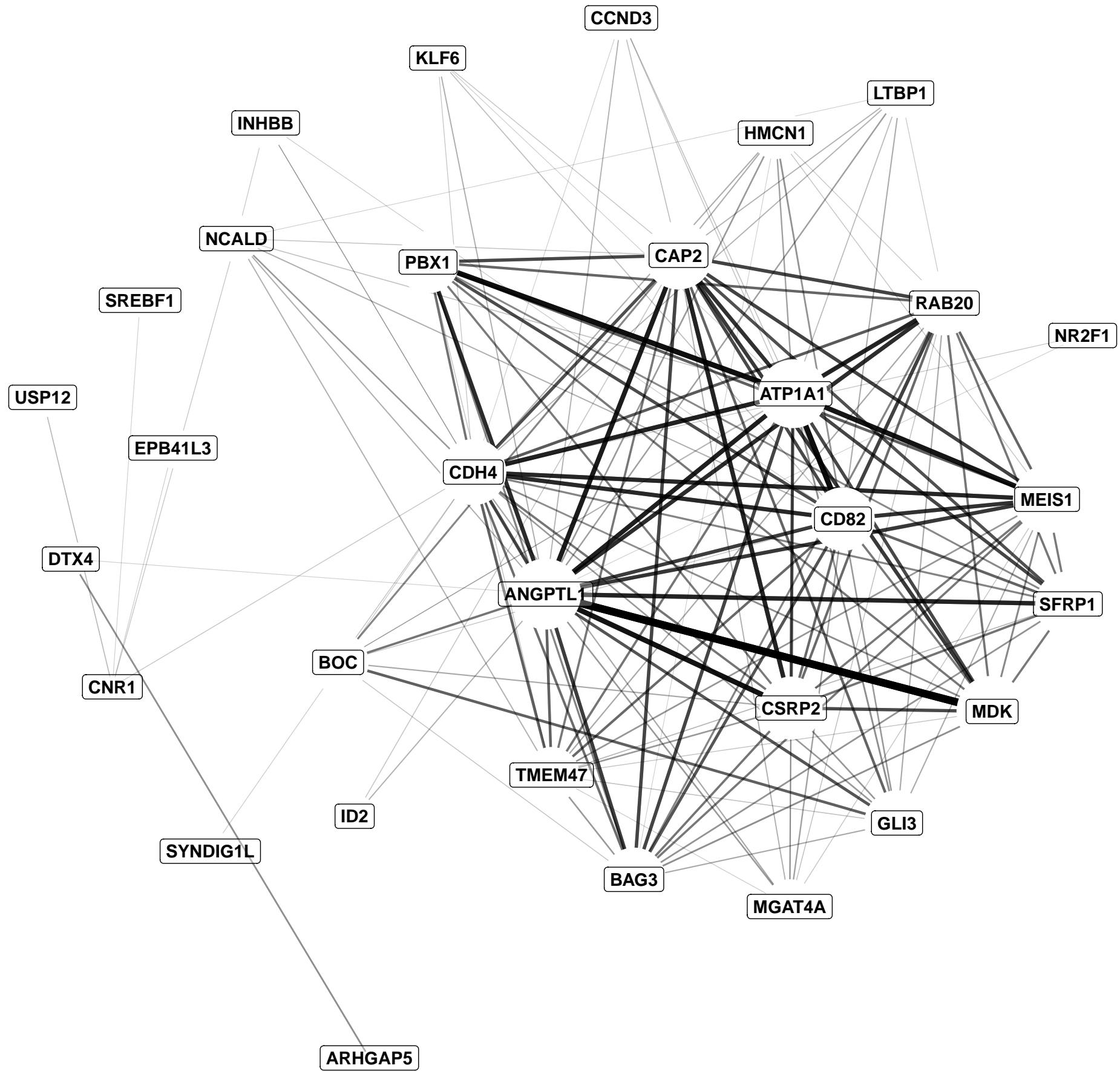
	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	67	11	2.651e–08
<i>path:gga04510</i>	Focal adhesion	174	16	9.508e–08
<i>path:gga04270</i>	Vascular smooth muscle contraction	109	10	2.611e–05
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	10	0.00213
<i>path:gga04010</i>	MAPK signaling pathway	240	10	0.01157
<i>path:gga04020</i>	Calcium signaling pathway	199	8	0.02744
<i>path:gga04520</i>	Adherens junction	69	4	0.03544
<i>path:gga00340</i>	Histidine metabolism	17	2	0.03662
<i>path:gga00480</i>	Glutathione metabolism	47	3	0.0521
<i>path:gga04672</i>	Intestinal immune network for IgA production	22	2	0.05868



1	ELAVL4	DPYSL3	TMSB15B	SEPT5	MAP1A	MAPK10	STMN1	CRACD
2	CYFIP2	REEP1	RTN4	FHL2	DYNLL2	DPYSL4	MTSS1	NA
3	VASH2	ENSGALG00000031564	ELAVL2	PHACTR3	TUBB	YPEL1	SHTN1	AFAP1
4	CMIP	ELMO1	ENSGALG00000000604	OPCML				

	Term	Ont	N	n	Adj. p-value
GO:0018109	peptidyl–arginine phosphorylation	BP	1	1	0.002038
GO:0018195	peptidyl–arginine modification	BP	2	1	0.004073
GO:0007010	cytoskeleton organization	BP	167	3	0.00461
GO:0051493	regulation of cytoskeleton organization	BP	54	2	0.005364
GO:0000226	microtubule cytoskeleton organization	BP	67	2	0.008154
GO:0007017	microtubule–based process	BP	78	2	0.01092
GO:0007019	microtubule depolymerization	BP	6	1	0.01217
GO:0033043	regulation of organelle organization	BP	96	2	0.01622
GO:0031110	regulation of microtubule polymerization or depolymerization	BP	11	1	0.0222
GO:0031109	microtubule polymerization or depolymerization	BP	14	1	0.02818

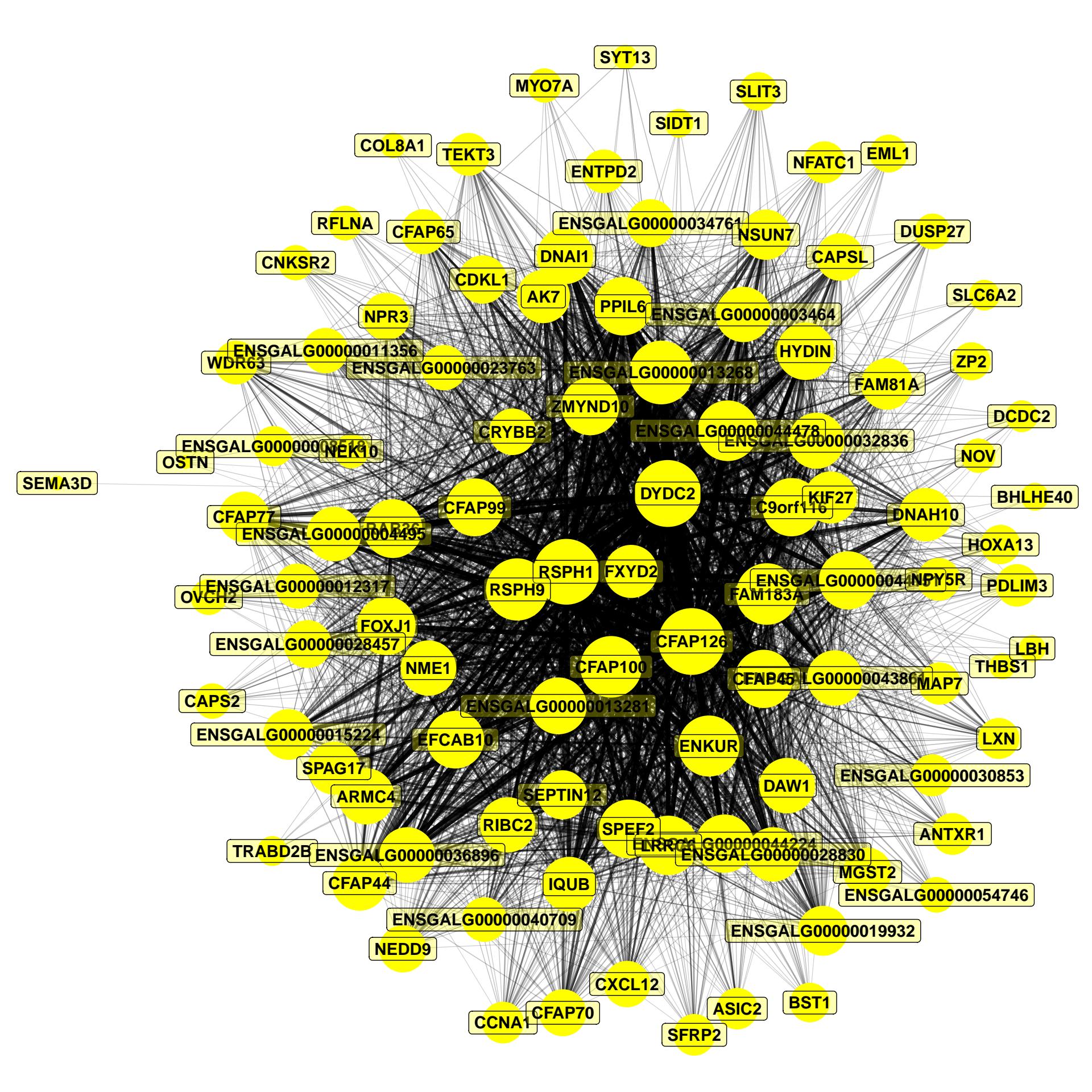
	Pathway	N	DE	P.DE
<i>path:gga05132</i>	Salmonella infection	221	5	7.393e-05
<i>path:gga04010</i>	MAPK signaling pathway	240	2	0.08536
<i>path:gga04622</i>	RIG-I-like receptor signaling pathway	46	1	0.08974
<i>path:gga03250</i>	Viral life cycle – HIV-1	49	1	0.09531
<i>path:gga04920</i>	Adipocytokine signaling pathway	59	1	0.1137
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.1191
<i>path:gga04620</i>	Toll-like receptor signaling pathway	71	1	0.1352
<i>path:gga04012</i>	ErbB signaling pathway	76	1	0.144
<i>path:gga04912</i>	GnRH signaling pathway	78	1	0.1475
<i>path:gga04540</i>	Gap junction	79	1	0.1493



1	ANGPTL1	MDK	CSRP2	ATP1A1	CDH4	CAP2	SFRP1	GLI3
2	MEIS1	CD82	BAG3	RAB20	BOC	PBX1	TMEM47	NCALD
3	MGAT4A	ID2	INHBB	LTBP1	HMCN1	KLF6	CCND3	SYNDIG1L
4	EPB41L3	NR2F1	USP12	DTX4	CNR1	ARHGAP5	SREBF1	

	Term	Ont	N	n	Adj. p
03140	determination of left/right asymmetry in lateral mesoderm	BP	1	1	0.00
32605	hepatocyte growth factor production	BP	1	1	0.00
48368	lateral mesoderm development	BP	1	1	0.00
46882	negative regulation of follicle-stimulating hormone secretion	BP	1	1	0.00
32686	negative regulation of hepatocyte growth factor production	BP	1	1	0.00
00164	nodal signaling pathway involved in determination of lateral mesoderm left/right asymmetry	BP	1	1	0.00
38107	nodal signaling pathway involved in determination of left/right asymmetry	BP	1	1	0.00
60279	positive regulation of ovulation	BP	1	1	0.00
32646	regulation of hepatocyte growth factor production	BP	1	1	0.00
00094	regulation of transcription from RNA polymerase II promoter involved in determination of left/right symmetry	BP	1	1	0.00

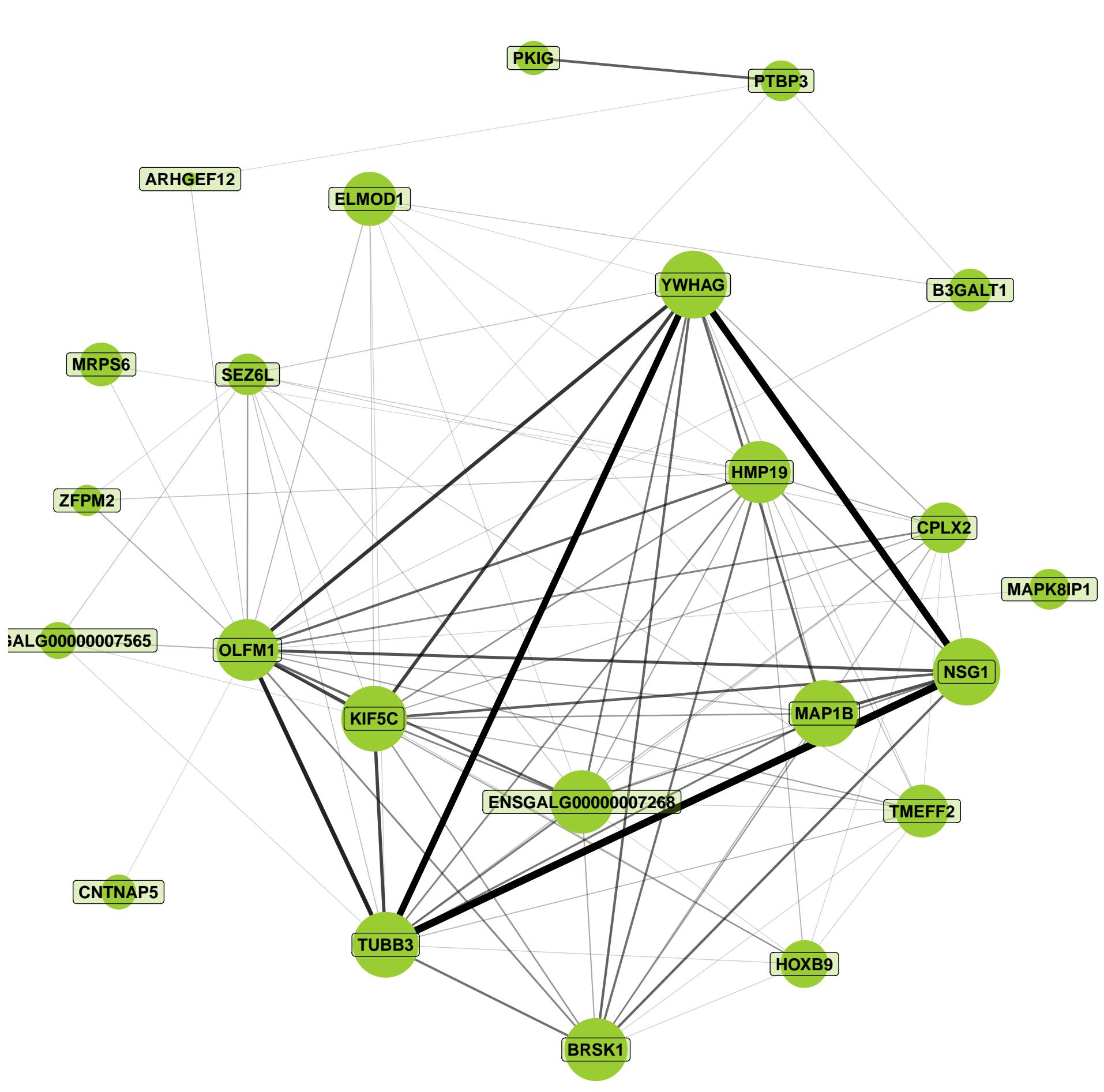
	Pathway	N	DE	P.DE
<i>path:gga04350</i>	TGF–beta signaling pathway	86	3	0.0009452
<i>path:gga04340</i>	Hedgehog signaling pathway	47	2	0.005032
<i>path:gga04115</i>	p53 signaling pathway	64	2	0.009163
<i>path:gga04310</i>	Wnt signaling pathway	134	2	0.03674
<i>path:gga04510</i>	Focal adhesion	174	2	0.05871
<i>path:gga00513</i>	Various types of N–glycan biosynthesis	38	1	0.08266
<i>path:gga00510</i>	N–Glycan biosynthesis	45	1	0.09715
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.1114
<i>path:gga04260</i>	Cardiac muscle contraction	60	1	0.1275
<i>path:gga04514</i>	Cell adhesion molecules	103	1	0.209



1	CFAP126	DYDC2	RSPH1	ENSGALG00000013268	FAM183A	CFAP100	FOXJ1	ENKUR
2	RSPH9	RAB36	PPIL6	CFAP99	ENSGALG00000032836	C9orf116	ENSGALG00000044224	CFAP45
3	ENSGALG00000044478	LRRC6	SPEF2	ZMYND10	ENSGALG00000044151	FXYD2	HYDIN	EFCAB10
4	CFAP44	ENSGALG00000043861	ENSGALG0000003464	DAW1	ARMC4	ENSGALG00000013281	ENSGALG00000036896	DNAI1
5	RIBC2	ENSGALG0000004495	DNAH10	ENSGALG00000019932	AK7	NME1	IQUB	ENSGALG00000015224
6	NPR3	SPAG17	CDKL1	KIF27	CFAP77	FAM81A	CXCL12	ENSGALG00000028830
7	SEPTIN12	CRYBB2	MGST2	ENSGALG00000023763	ENSGALG00000028457	ENSGALG00000034761	NSUN7	NEDD9
8	CCNA1	ENSGALG00000011356	ENSGALG00000012317	PDLM3	CAPSL	CFAP70	CFAP65	SLIT3
9	NPY5R	ASIC2	SFRP2	ENTPD2	WDR63	MAP7	ANTXR1	TEKT3
10	ENSGALG0000008518	ENSGALG00000040709	NFATC1	BST1	NOV	OVCH2	ENSGALG00000030853	ENSGALG00000054746
11	HOXA13	MYO7A	DUSP27	NEK10	LXN	SLC6A2	CNKS2	CAPS2
12	EML1	DCDC2	ZP2	RFLNA	BHLHE40	THBS1	TRABD2B	SIDT1
13	LBH	SYT13	COL8A1	OSTN	SEMA3D			

	Term	Ont	N	n	Adj. p-value
GO:0035082	axoneme assembly	BP	1	1	0.007172
GO:0030317	flagellated sperm motility	BP	1	1	0.007172
GO:0007288	sperm axoneme assembly	BP	1	1	0.007172
GO:0097722	sperm motility	BP	1	1	0.007172
GO:0003341	cilium movement	BP	2	1	0.01429
GO:0060294	cilium movement involved in cell motility	BP	2	1	0.01429
GO:0001539	cilium or flagellum-dependent cell motility	BP	3	1	0.02136
GO:0060285	cilium-dependent cell motility	BP	3	1	0.02136
GO:0048843	negative regulation of axon extension involved in axon guidance	BP	3	1	0.02136
GO:0009134	nucleoside diphosphate catabolic process	BP	3	1	0.02136

	Pathway	N	DE	P.DE
<i>path:gga01232</i>	Nucleotide metabolism	78	4	0.002362
<i>path:gga00230</i>	Purine metabolism	113	4	0.008818
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	29	2	0.01822
<i>path:gga01240</i>	Biosynthesis of cofactors	118	3	0.05287
<i>path:gga00983</i>	Drug metabolism – other enzymes	54	2	0.05726
<i>path:gga00240</i>	Pyrimidine metabolism	56	2	0.06106
<i>path:gga00360</i>	Phenylalanine metabolism	12	1	0.08278
<i>path:gga00730</i>	Thiamine metabolism	12	1	0.08278
<i>path:gga00910</i>	Nitrogen metabolism	13	1	0.08937
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.1152



1	NSG1	TUBB3	YWHAG	BRSK1	KIF5C	MAP1B	HMP19	ENSGALG00000007268
2	OLFM1	TMEFF2	CPLX2	ELMOD1	HOXB9	ENSGALG00000007565	MAPK8IP1	B3GALT1
3	SEZ6L	MRPS6	PTBP3	CNTNAP5	PKIG	ZFPM2	ARHGEF12	

	Term	Ont	N	n	Adj. p-value
GO:0003190	atrioventricular valve formation	BP	1	1	0.001736
GO:0023041	neuronal signal transduction	BP	1	1	0.001736
GO:0099627	neurotransmitter receptor cycle	BP	1	1	0.001736
GO:0048268	clathrin coat assembly	BP	2	1	0.00347
GO:0007212	dopamine receptor signaling pathway	BP	2	1	0.00347
GO:0099638	endosome to plasma membrane protein transport	BP	2	1	0.00347
GO:0099639	neurotransmitter receptor transport, endosome to plasma membrane	BP	2	1	0.00347
GO:0098887	neurotransmitter receptor transport, endosome to postsynaptic membrane	BP	2	1	0.00347
GO:0071870	cellular response to catecholamine stimulus	BP	3	1	0.0052
GO:1903351	cellular response to dopamine	BP	3	1	0.0052

	Pathway	N	DE	P.DE
<i>path:gga00601</i>	Glycosphingolipid biosynthesis – lacto and neolacto series	21	1	0.03586
<i>path:gga05132</i>	Salmonella infection	221	2	0.05573
<i>path:gga03250</i>	Viral life cycle – HIV–1	49	1	0.08177
<i>path:gga03015</i>	mRNA surveillance pathway	73	1	0.1195
<i>path:gga04540</i>	Gap junction	79	1	0.1286
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	81	1	0.1317
<i>path:gga04114</i>	Oocyte meiosis	97	1	0.1557
<i>path:gga04270</i>	Vascular smooth muscle contraction	109	1	0.1732
<i>path:gga04110</i>	Cell cycle	114	1	0.1804
<i>path:gga03010</i>	Ribosome	115	1	0.1819