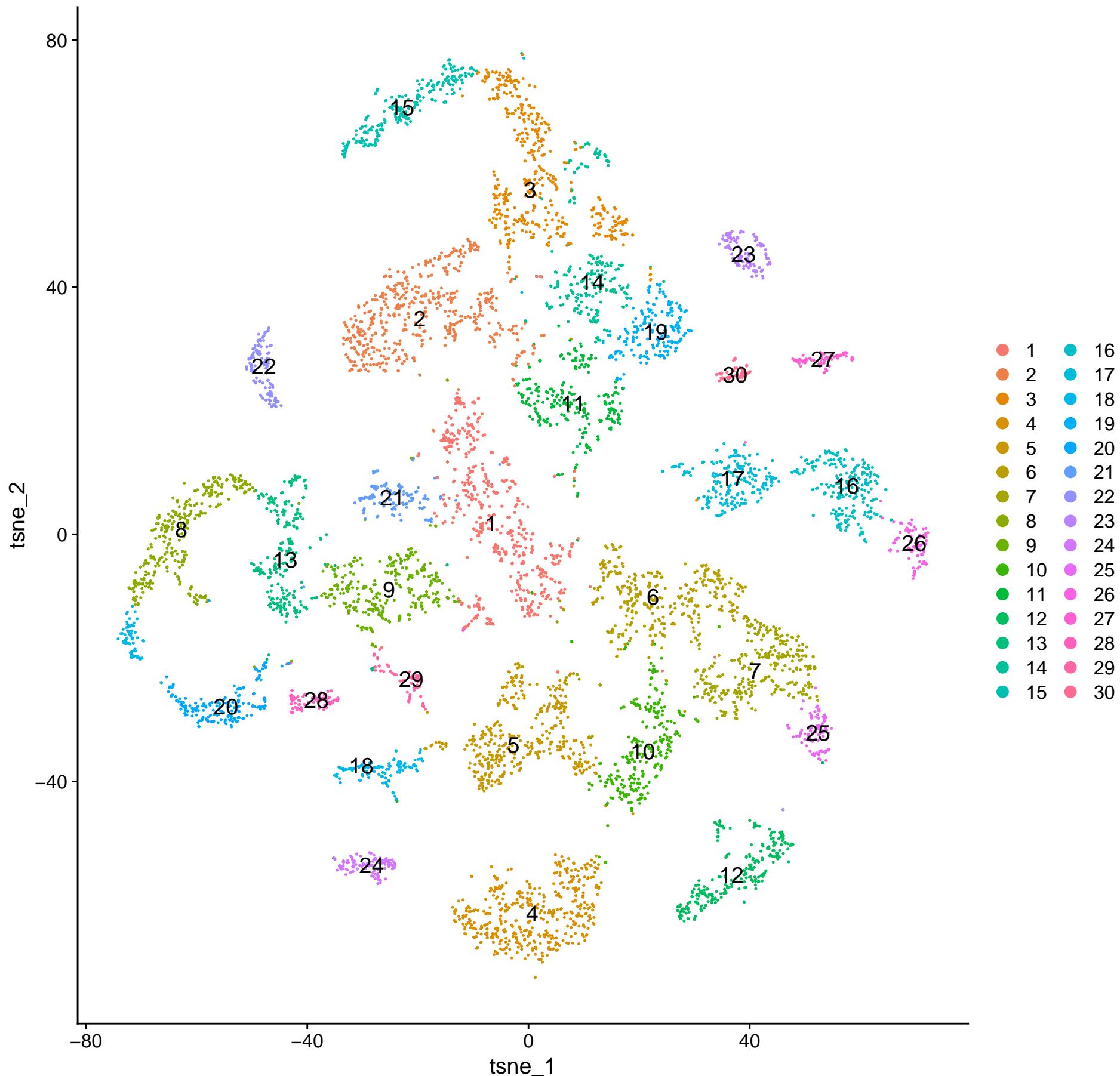
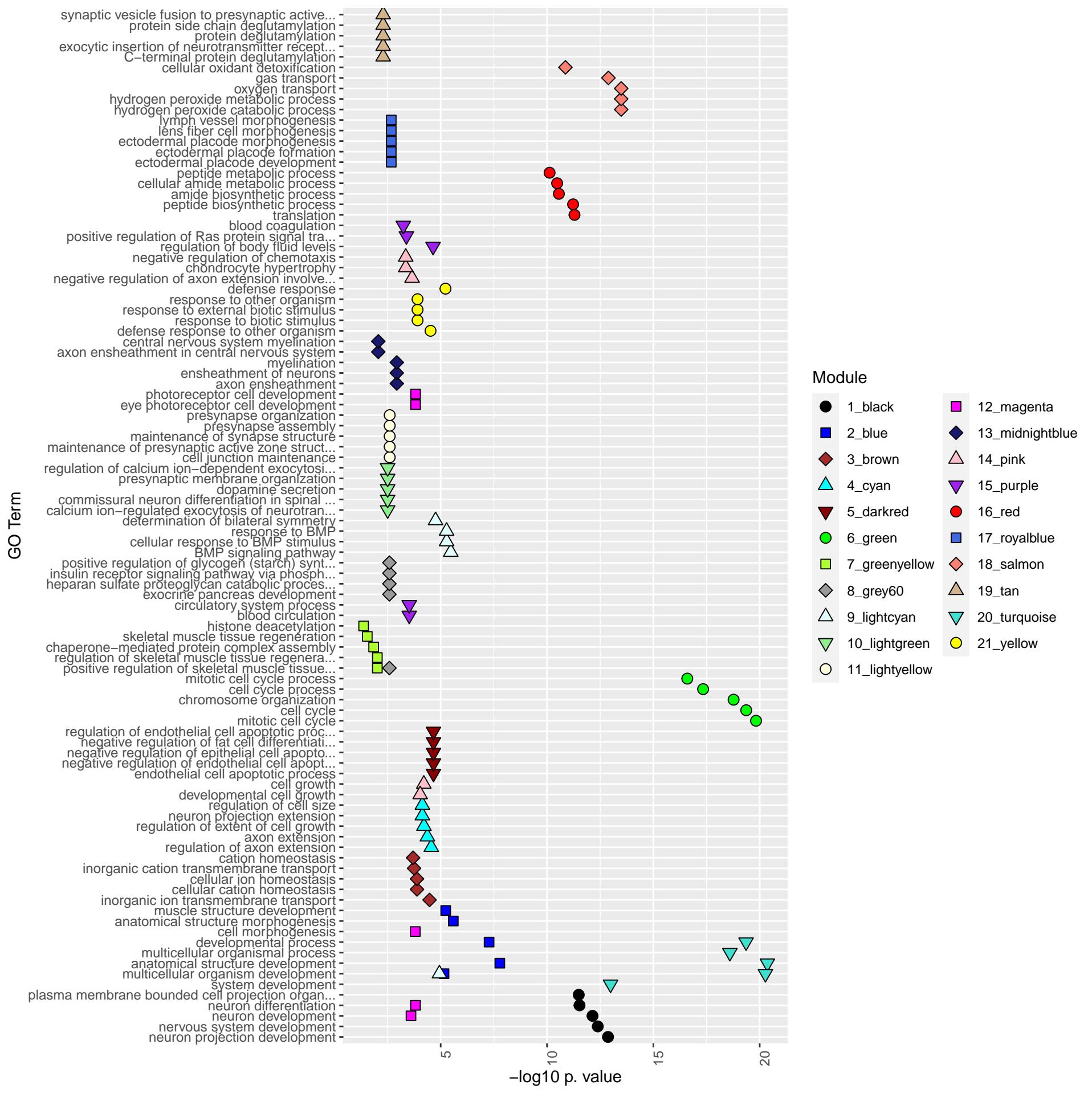
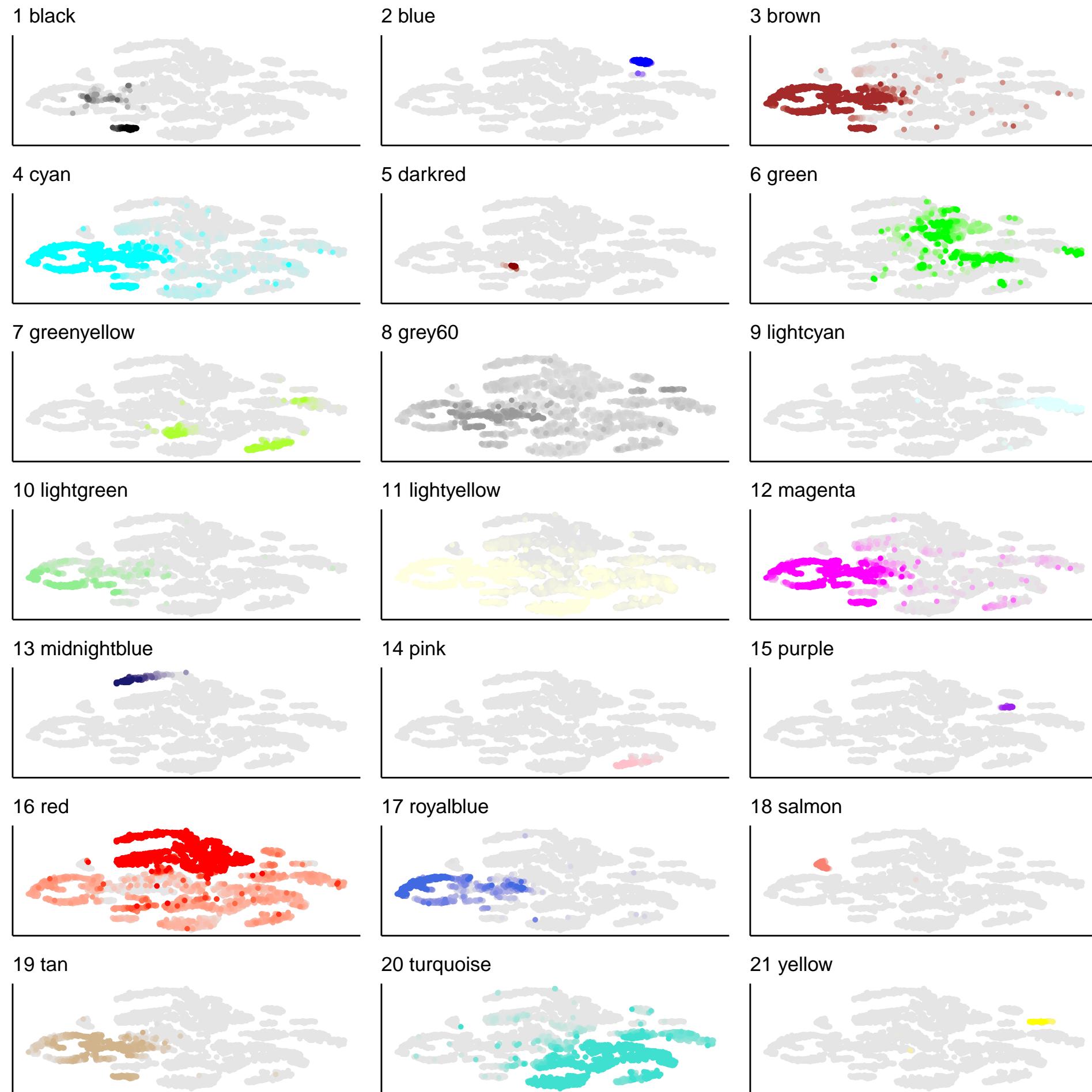


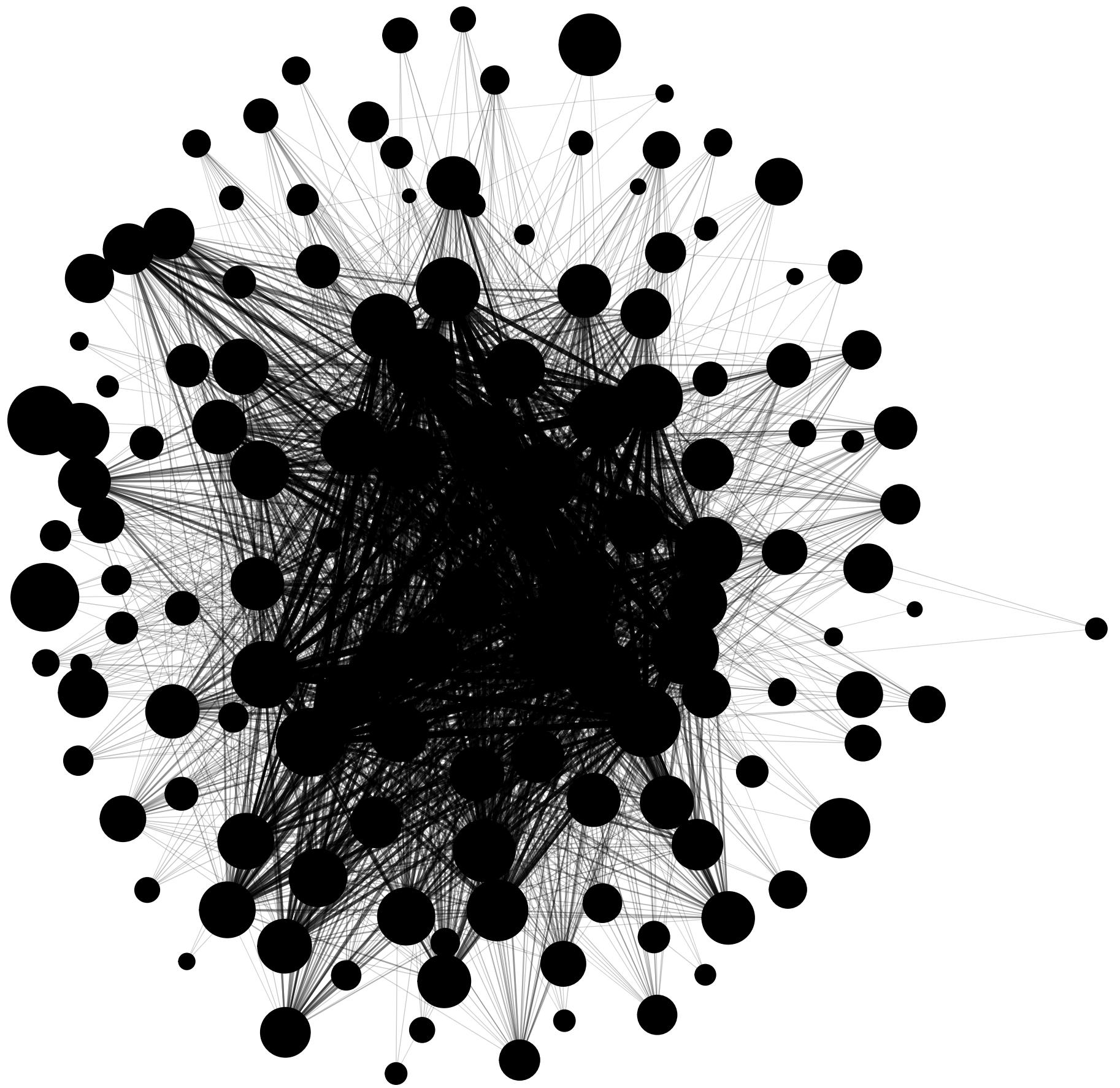
Gg_poly_int scWGCNA modules





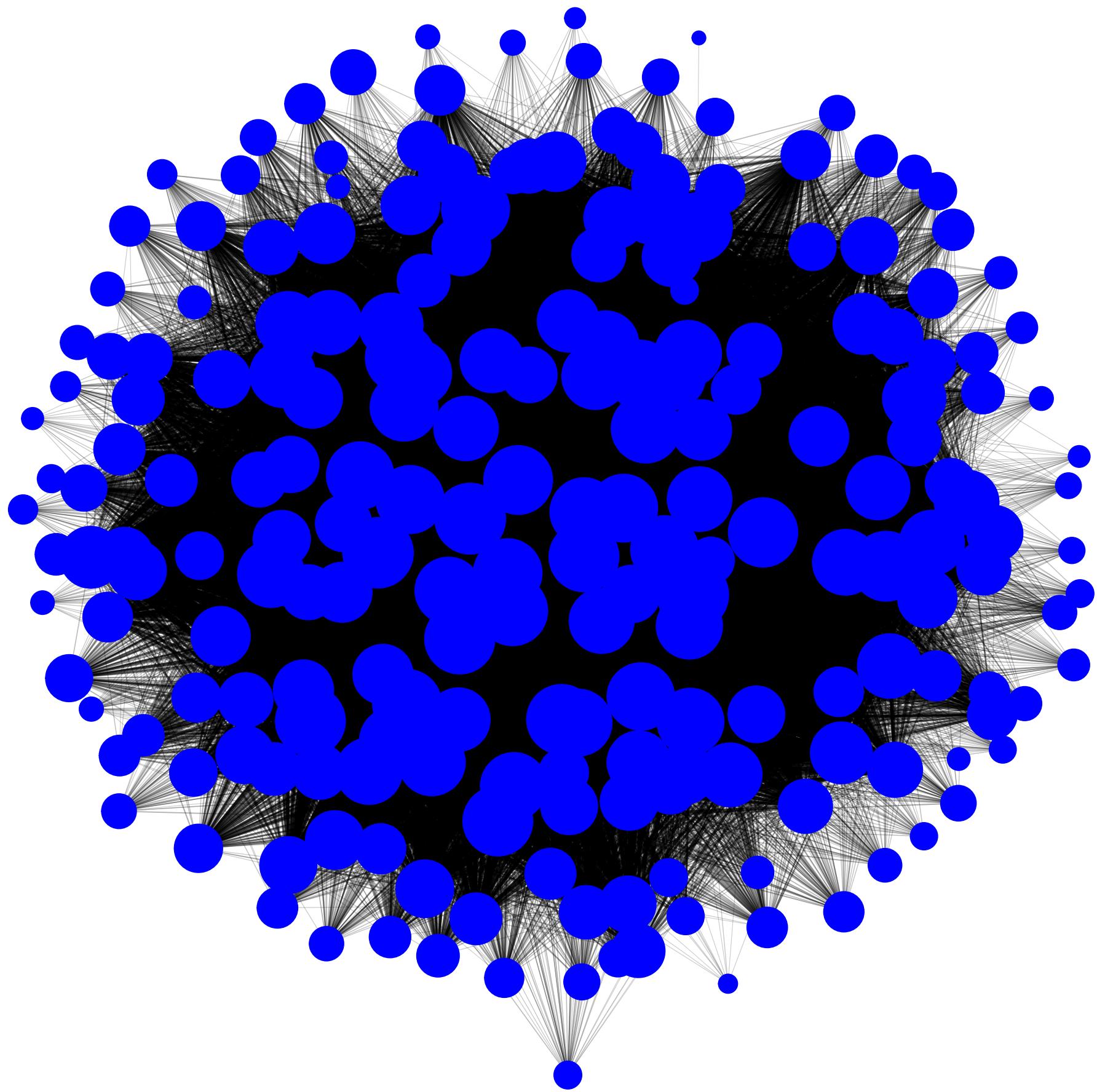






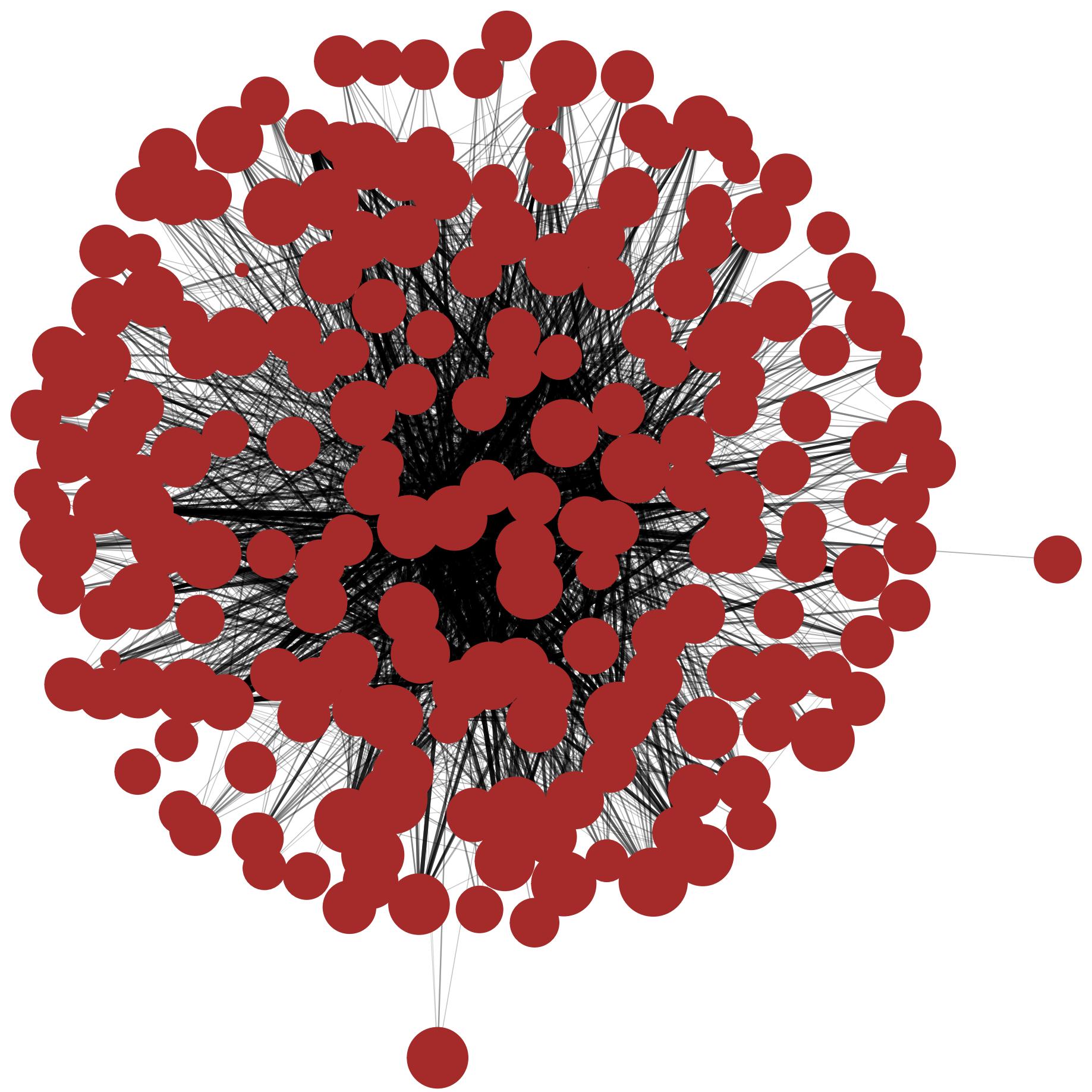
	Term	Ont	N	n	Adj. p-value
GO:0031175	neuron projection development	BP	110	15	1.351e-13
GO:0007399	nervous system development	BP	255	20	4.101e-13
GO:0048666	neuron development	BP	123	15	7.258e-13
GO:0030182	neuron differentiation	BP	161	16	2.961e-12
GO:0120036	plasma membrane bounded cell projection organization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

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



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

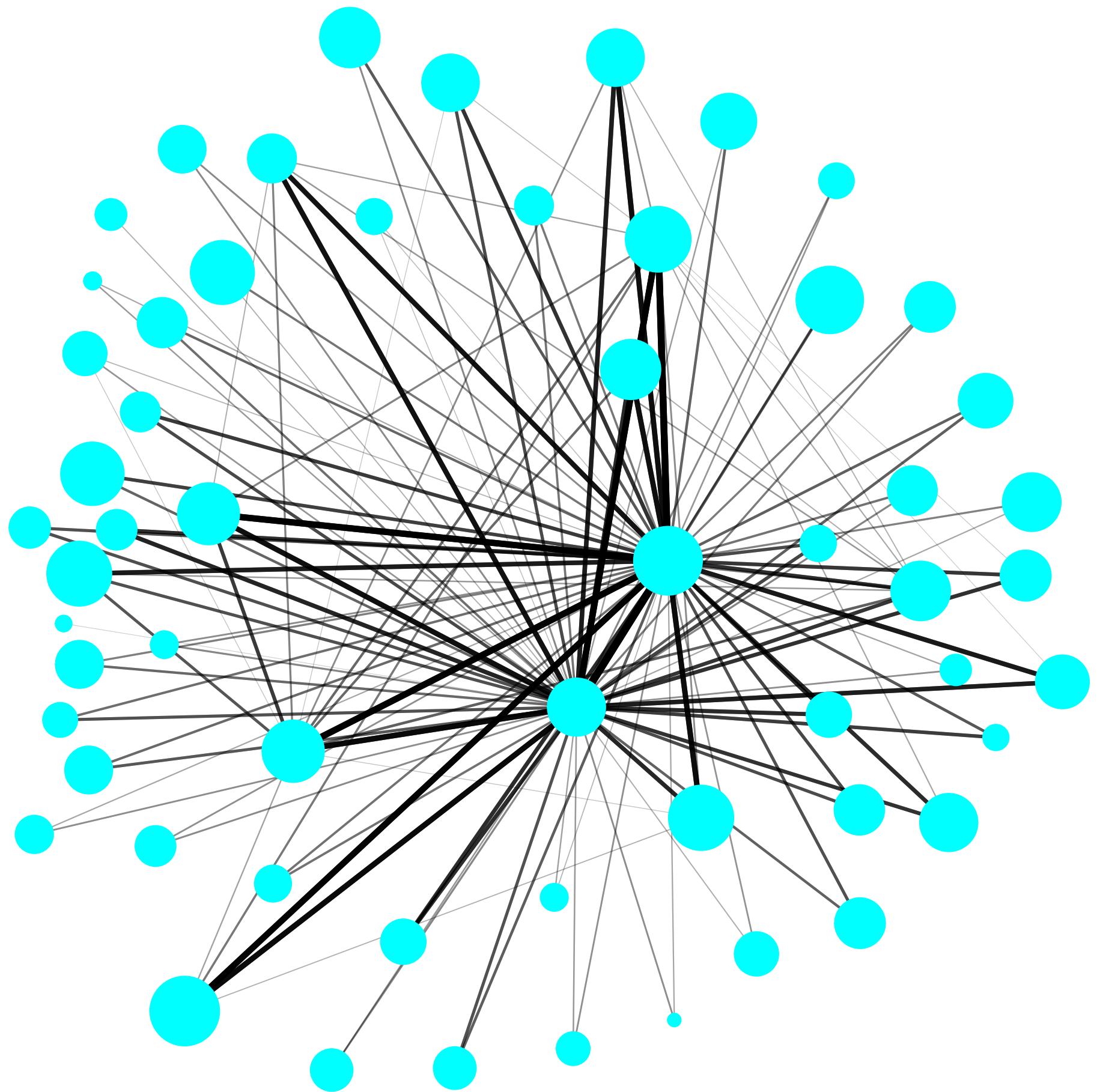
	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	66	10	6.93e–08
<i>path:gga04510</i>	Focal adhesion	169	14	4.09e–07
<i>path:gga04270</i>	Vascular smooth muscle contraction	102	10	4.293e–06
<i>path:gga04520</i>	Adherens junction	69	5	0.004461
<i>path:gga00120</i>	Primary bile acid biosynthesis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



1	NA								
2	NA								
3	NA								
4	NA								
5	NA								
6	NA								
7	NA								
8	NA								
9	NA								
10	NA								
11	NA								
12	NA								
13	NA								
14	NA								
15	NA								
16	NA								
17	NA								
18	NA								
19	NA								
20	NA								
21	NA								
22	NA								
23	NA								
24	NA								
25	NA								
26	NA	NA	NA	NA					

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

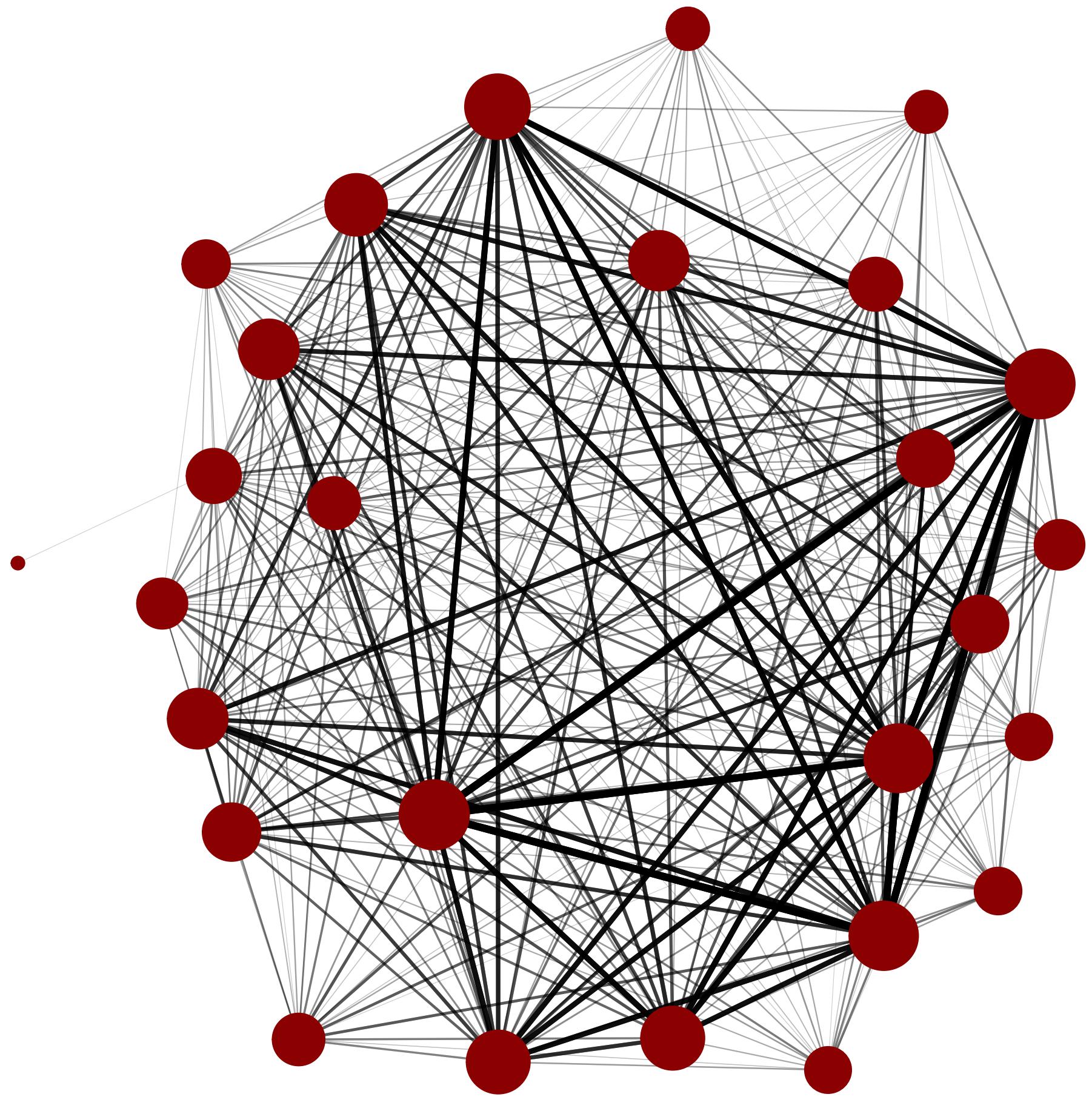
	Pathway	N	DE	P.DE
<i>path:gga04020</i>	Calcium signaling pathway	191	14	1.591e-06
<i>path:gga04260</i>	Cardiac muscle contraction	58	6	0.0002655
<i>path:gga04010</i>	MAPK signaling pathway	236	12	0.0003117
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	118	8	0.0004922
<i>path:gga04625</i>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



1	NA							
2	NA							
3	NA							
4	NA							
5	NA							
6	NA							
7	NA							
8	NA							

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

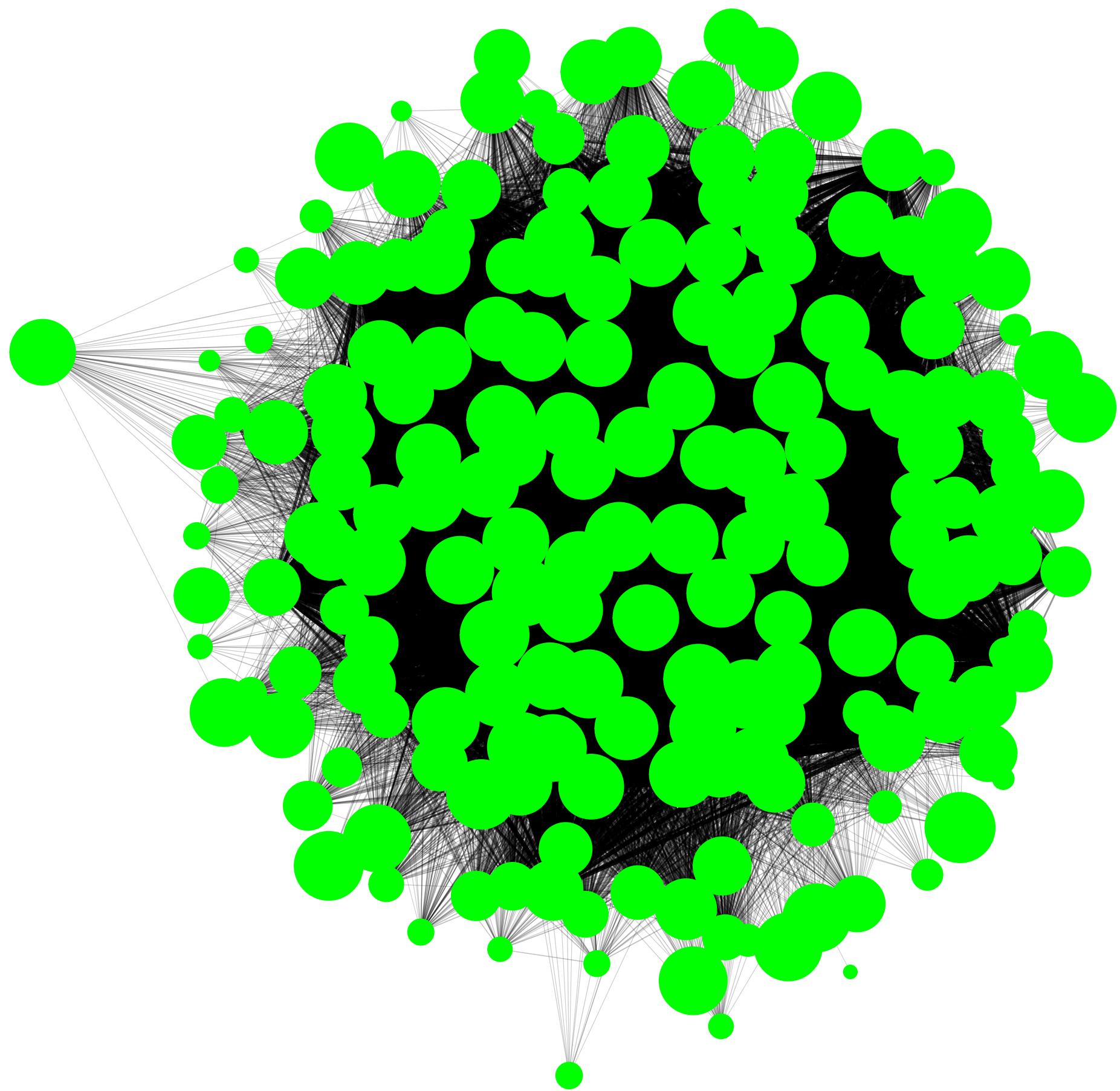
	Pathway	N	DE	P.DE
<i>path:gga04145</i>	Phagosome	121	5	0.0001777
<i>path:gga05132</i>	Salmonella infection	218	6	0.0003569
<i>path:gga04540</i>	Gap junction	78	4	0.0003637
<i>path:gga03267</i>	Virion – Adenovirus	3	1	0.01302
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.01733
<i>path:gga04514</i>	Cell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



1	NA							
2	NA							
3	NA							
4	NA	NA	NA					

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

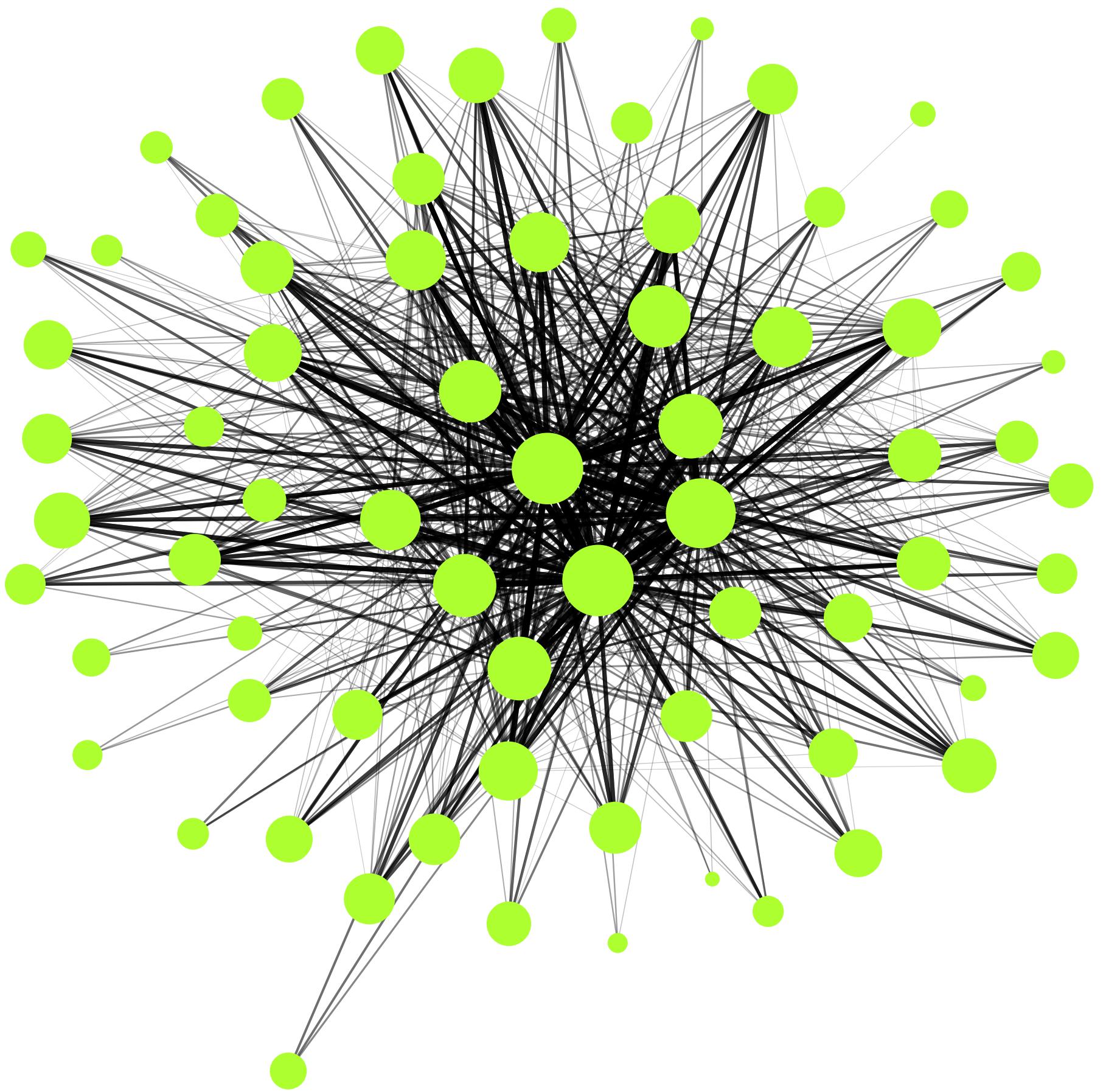
	Pathway	N	DE	P.DE
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	2	0.0002372
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	275	3	0.01576
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	1	0.02502
<i>path:gga00533</i>	Glycosaminoglycan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



1	NA								
2	NA								
3	NA								
4	NA								
5	NA								
6	NA								
7	NA								
8	NA								
9	NA								
10	NA								
11	NA								
12	NA								
13	NA								
14	NA								
15	NA								
16	NA								
17	NA								
18	NA								
19	NA								
20	NA								
21	NA								
22	NA								
23	NA								
24	NA	NA	NA						

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

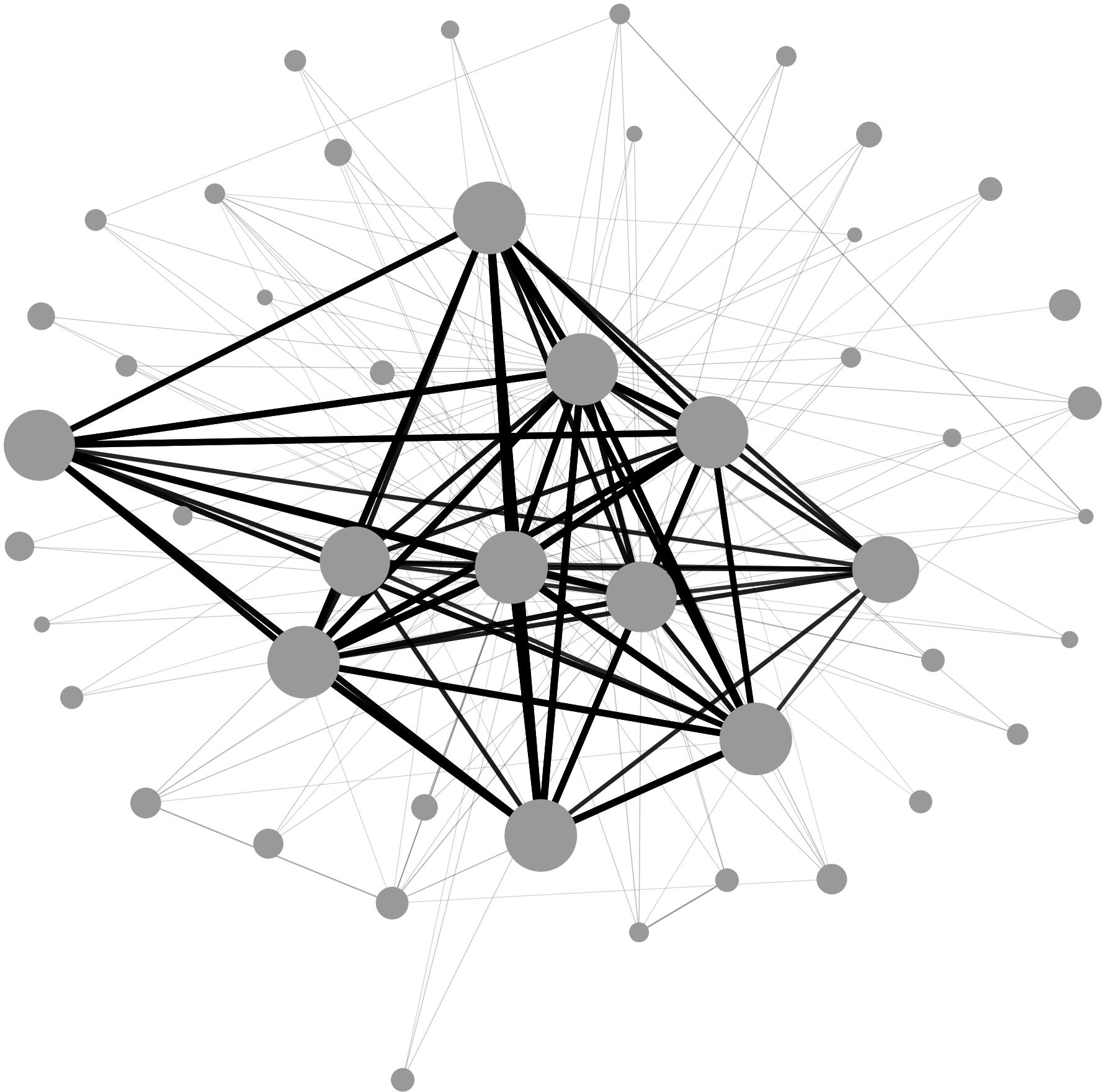
	Pathway	N	DE	P.DE
<i>path:gga04110</i>	Cell cycle	113	23	1.622e-20
<i>path:gga04114</i>	Oocyte meiosis	94	13	7.159e-10
<i>path:gga04914</i>	Progesterone-mediated oocyte maturation	78	9	1.555e-06
<i>path:gga03030</i>	DNA replication	29	6	2.787e-06
<i>path:gga04115</i>	p53 signaling pathway	63	6	0.0002669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



1	NA							
2	NA							
3	NA							
4	NA							
5	NA							
6	NA							
7	NA							
8	NA							
9	NA	NA	NA	NA	NA			

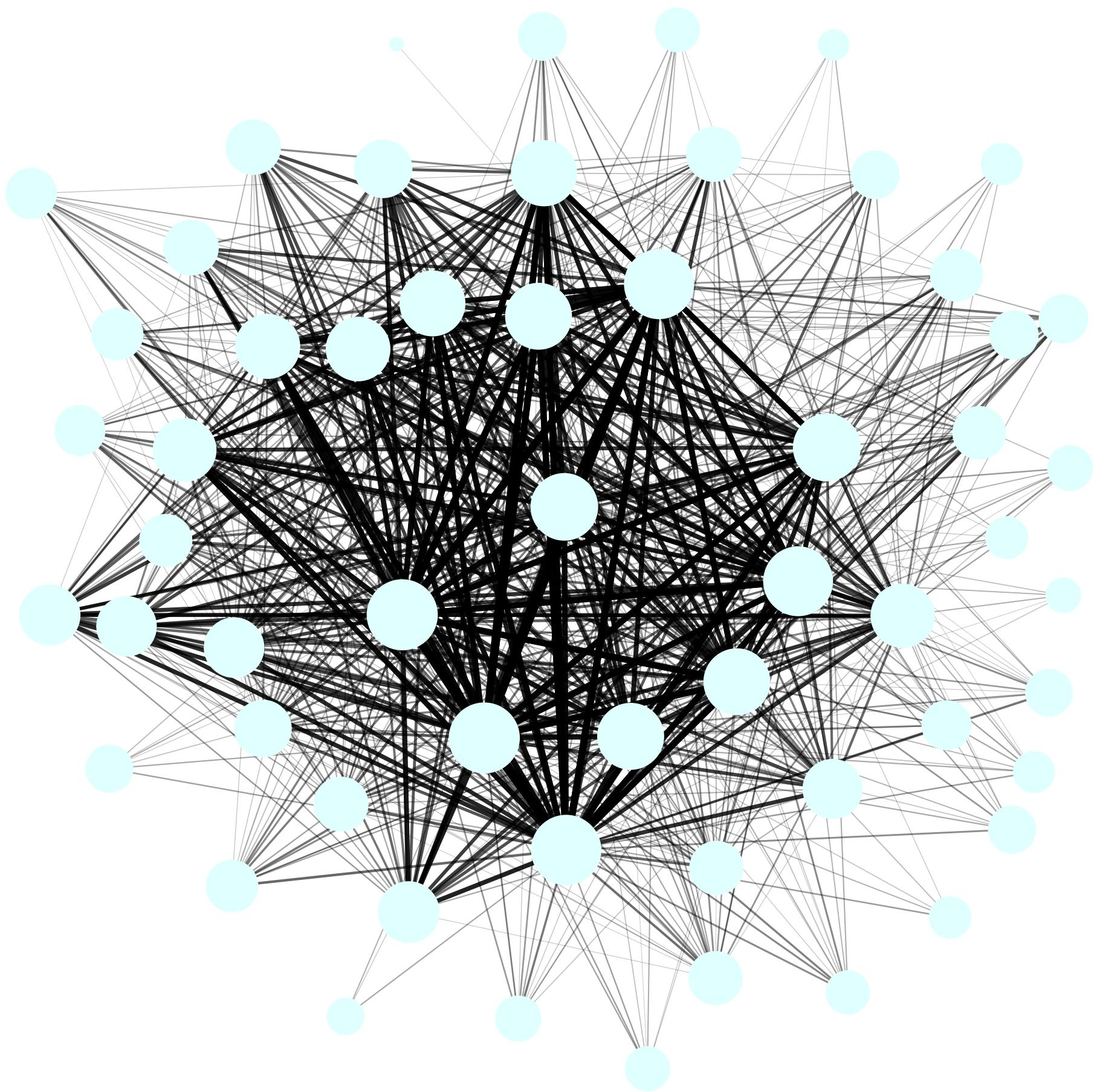
	Term	Ont	N	n	Adj. p-value
GO:0043415	positive regulation of skeletal muscle tissue regeneration	BP	2	1	0.009476
GO:0043416	regulation of skeletal muscle tissue regeneration	BP	2	1	0.009476
GO:0051131	chaperone-mediated protein complex assembly	BP	3	1	0.01418
GO:0043403	skeletal muscle tissue regeneration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

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



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

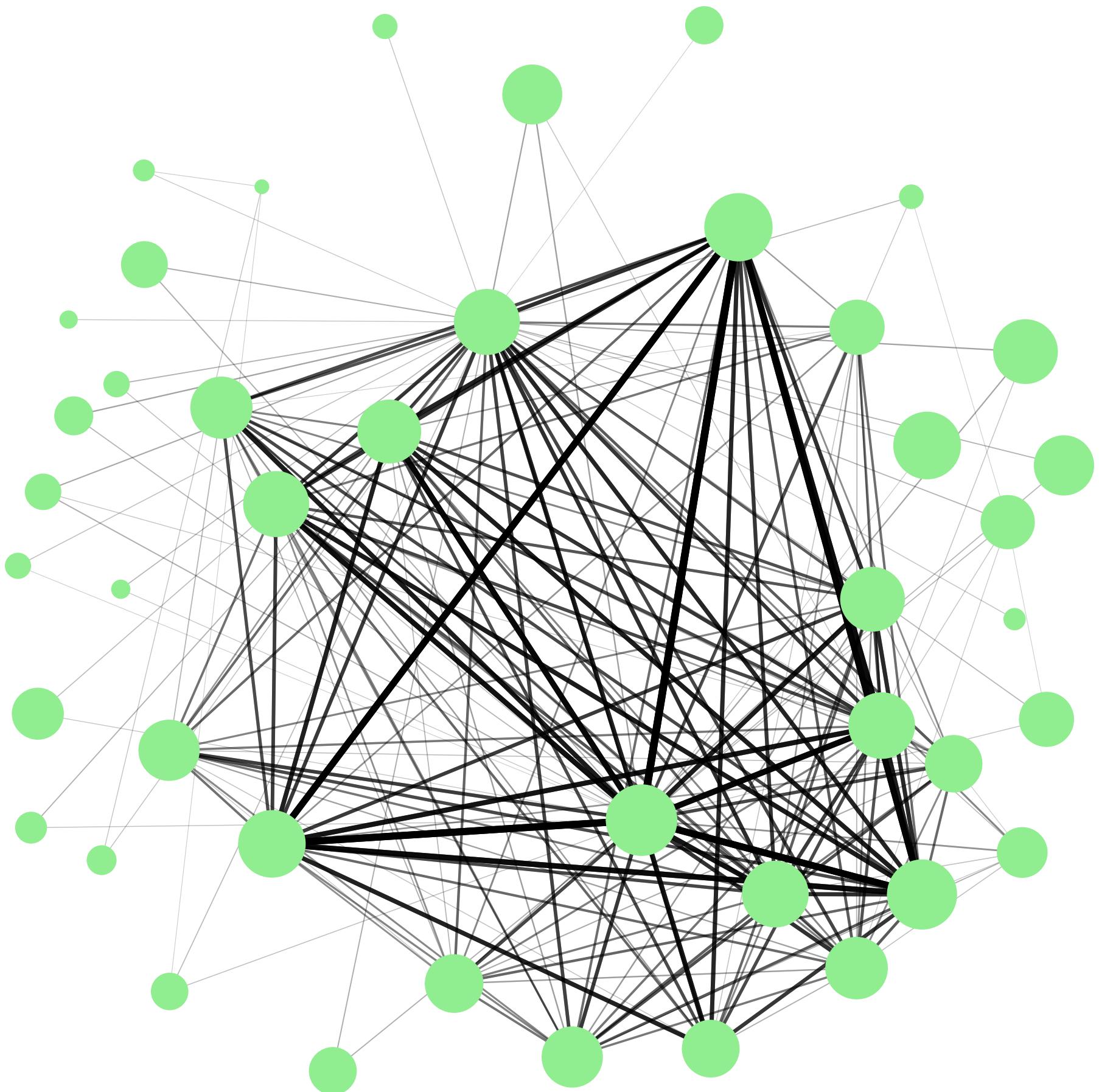
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	275	4	0.00516
<i>path:gga00531</i>	Glycosaminoglycan degradation	16	1	0.04035
<i>path:gga00640</i>	Propanoate metabolism	28	1	0.06957
<i>path:gga00620</i>	Pyruvate metabolism	33	1	0.08148
<i>path:gga00590</i>	Arachidonic acid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



1	NA							
2	NA							
3	NA							
4	NA							
5	NA							
6	NA							
7	NA							
8	NA							

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

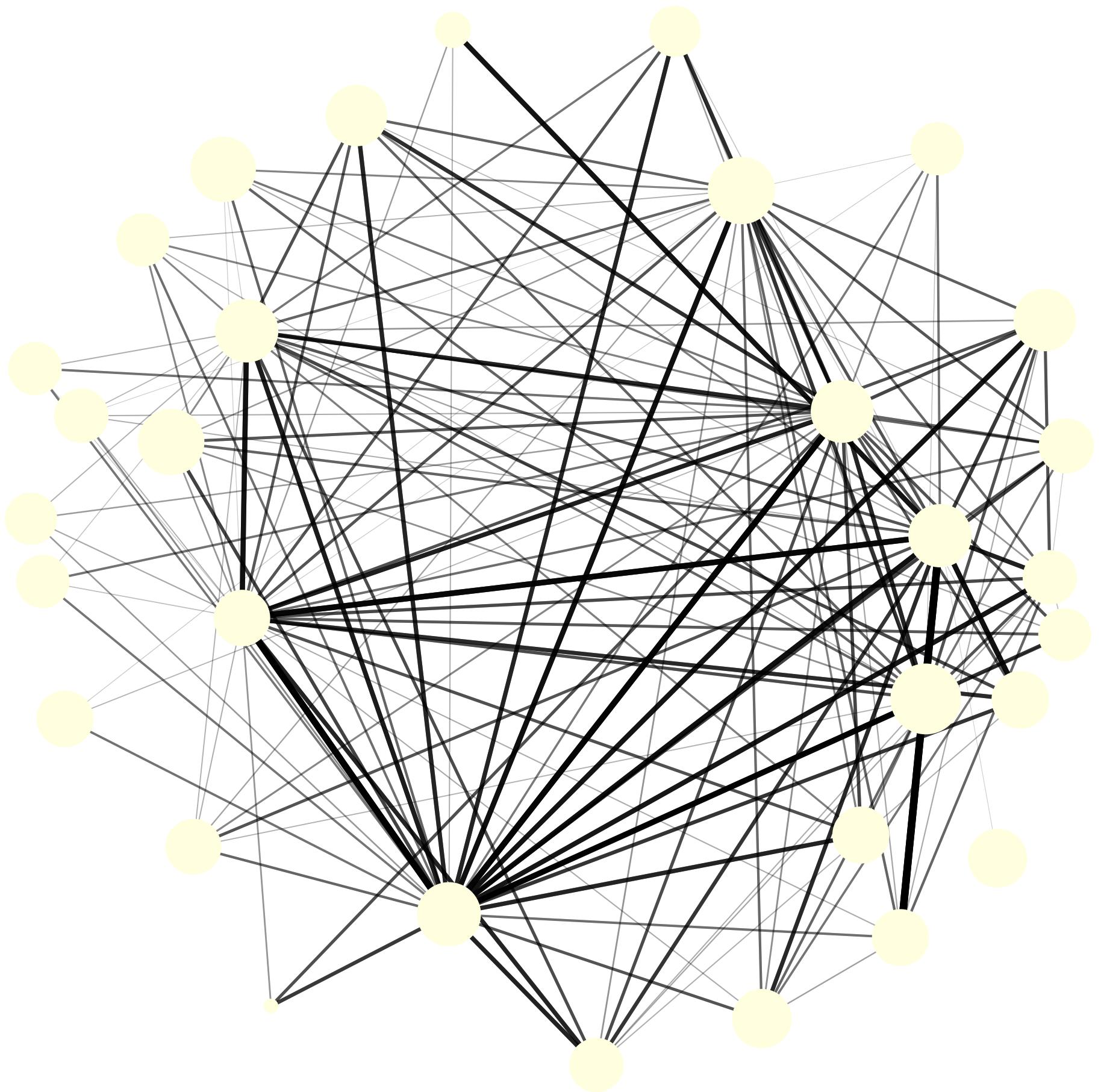
	Pathway	N	DE	P.DE
<i>path:gga04310</i>	Wnt signaling pathway	133	6	1.516e-05
<i>path:gga04150</i>	mTOR signaling pathway	133	4	0.002025
<i>path:gga04916</i>	Melanogenesis	82	3	0.004425
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	136	3	0.01759
<i>path:gga04512</i>	ECM–receptor interaction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



1	NA							
2	NA							
3	NA							
4	NA							
5	NA							
6	NA	NA	NA					

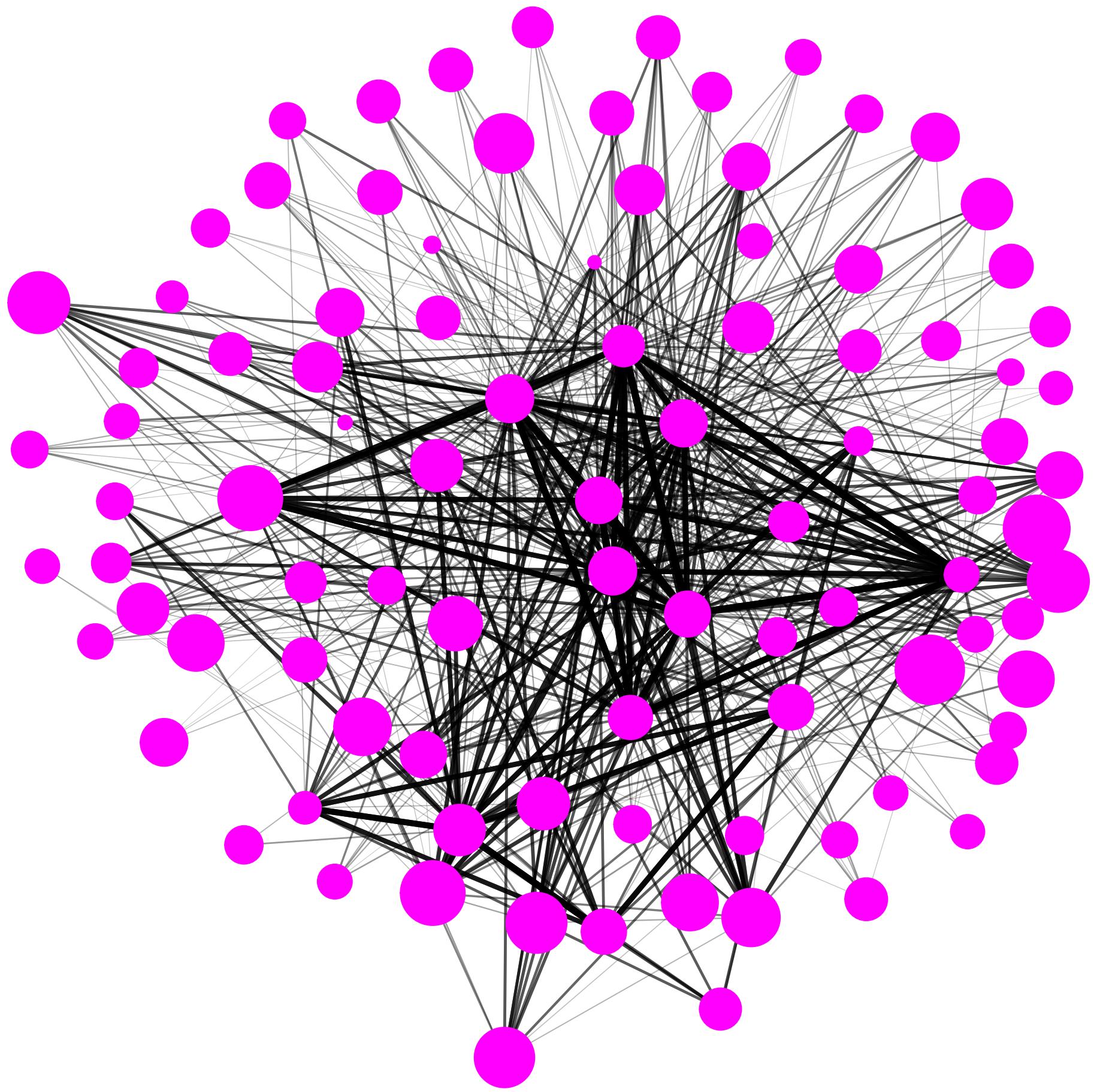
	Term	Ont	N	n	Adj. p-value
GO:0048791	calcium ion-regulated exocytosis of neurotransmitter	BP	1	1	0.003114
GO:0021528	commissural neuron differentiation in spinal cord	BP	1	1	0.003114
GO:0014046	dopamine secretion	BP	1	1	0.003114
GO:0097090	presynaptic membrane organization	BP	1	1	0.003114
GO:0017158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

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



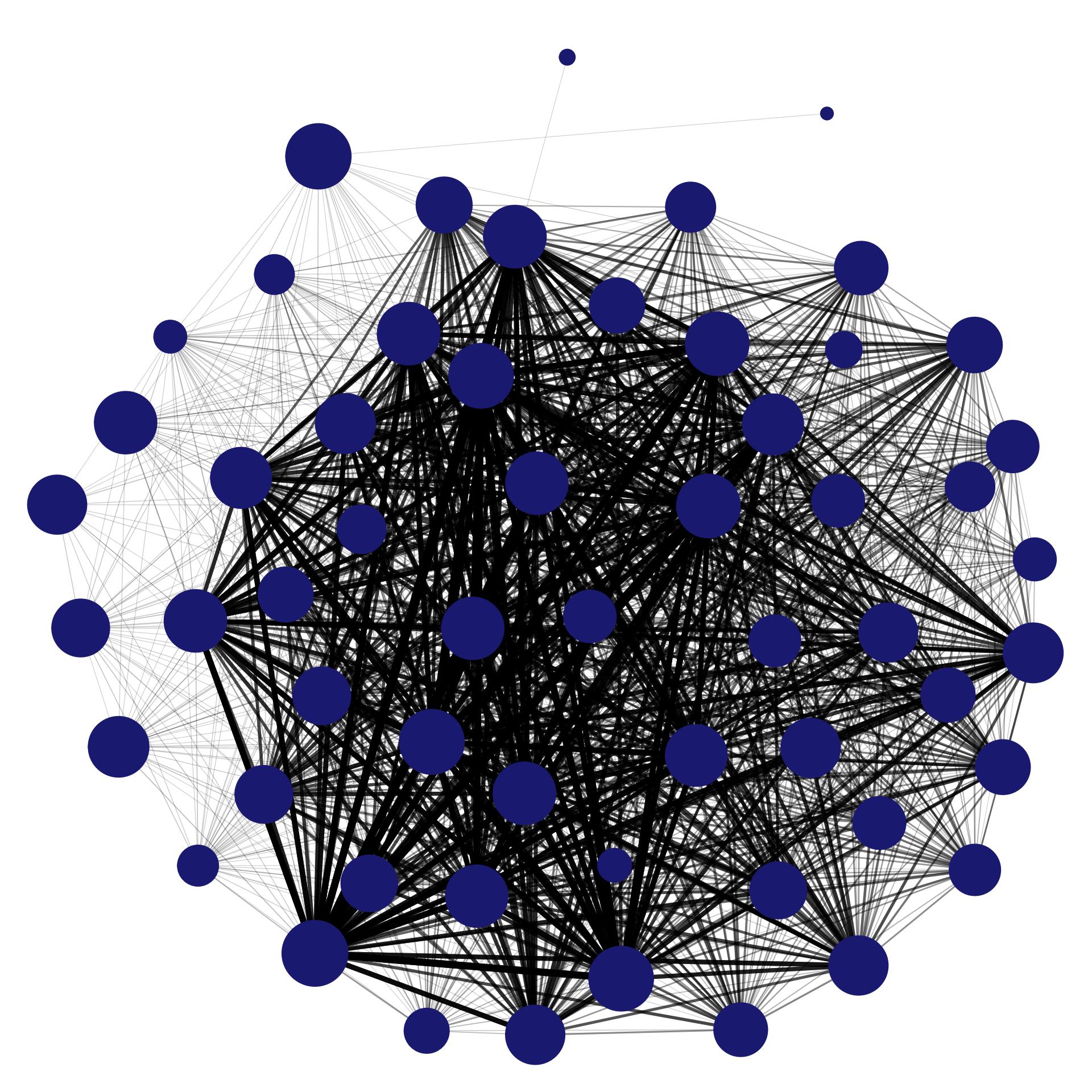
	Term	Ont	N	n	Adj. p-value
GO:0034331	cell junction maintenance	BP	1	1	0.002491
GO:0048790	maintenance of presynaptic active zone structure	BP	1	1	0.002491
GO:0099558	maintenance of synapse structure	BP	1	1	0.002491
GO:0099054	presynapse assembly	BP	1	1	0.002491
GO:0099172	presynapse organization	BP	1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

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



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

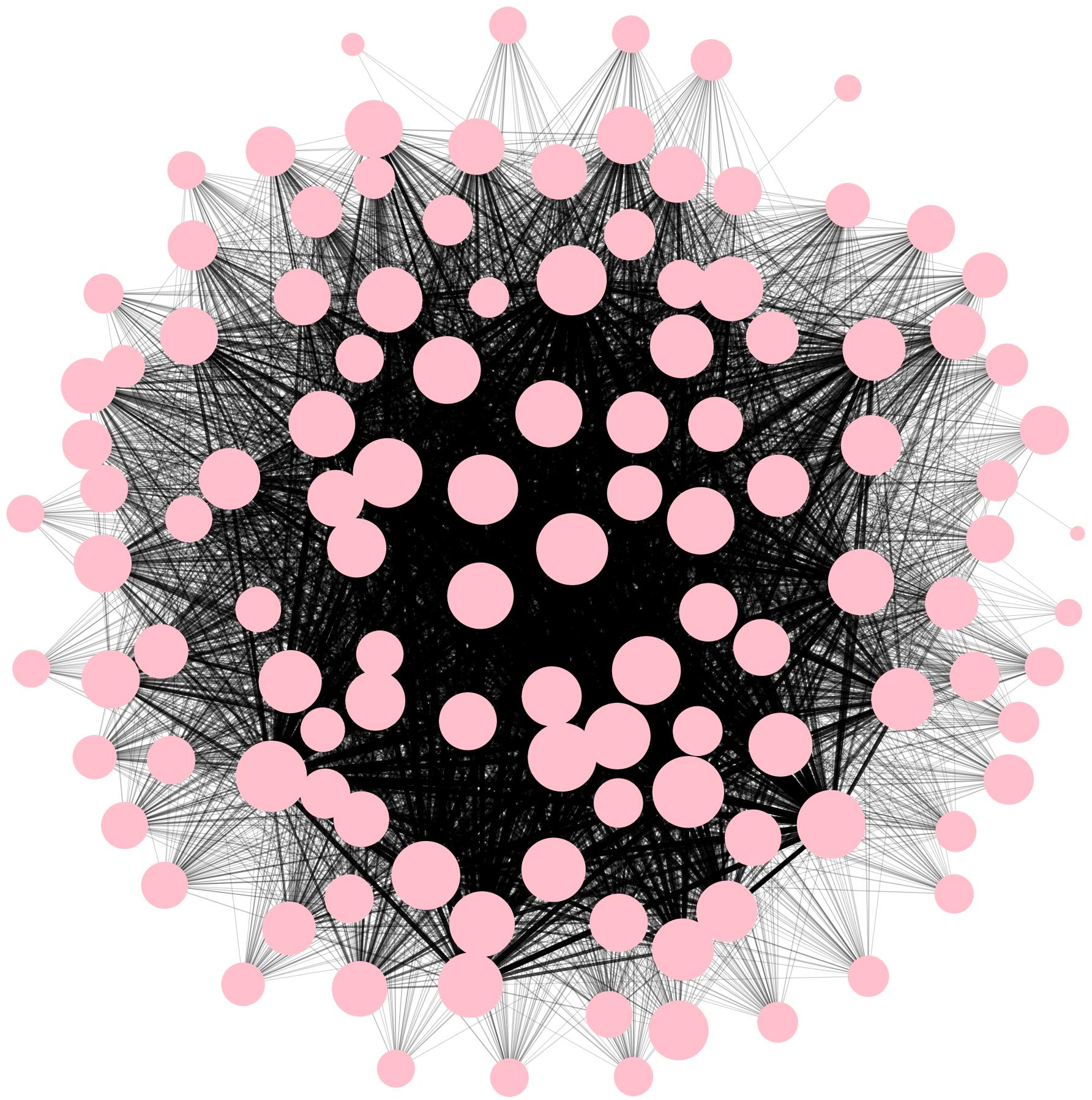
	Pathway	N	DE	P.DE
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	118	5	0.001564
<i>path:gga04260</i>	Cardiac muscle contraction	58	3	0.008257
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.02835
<i>path:gga04514</i>	Cell adhesion molecules	99	3	0.03406
<i>path:gga05132</i>	Salmonella infection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



1	NA							
2	NA							
3	NA							
4	NA							
5	NA							
6	NA							
7	NA							
8	NA							

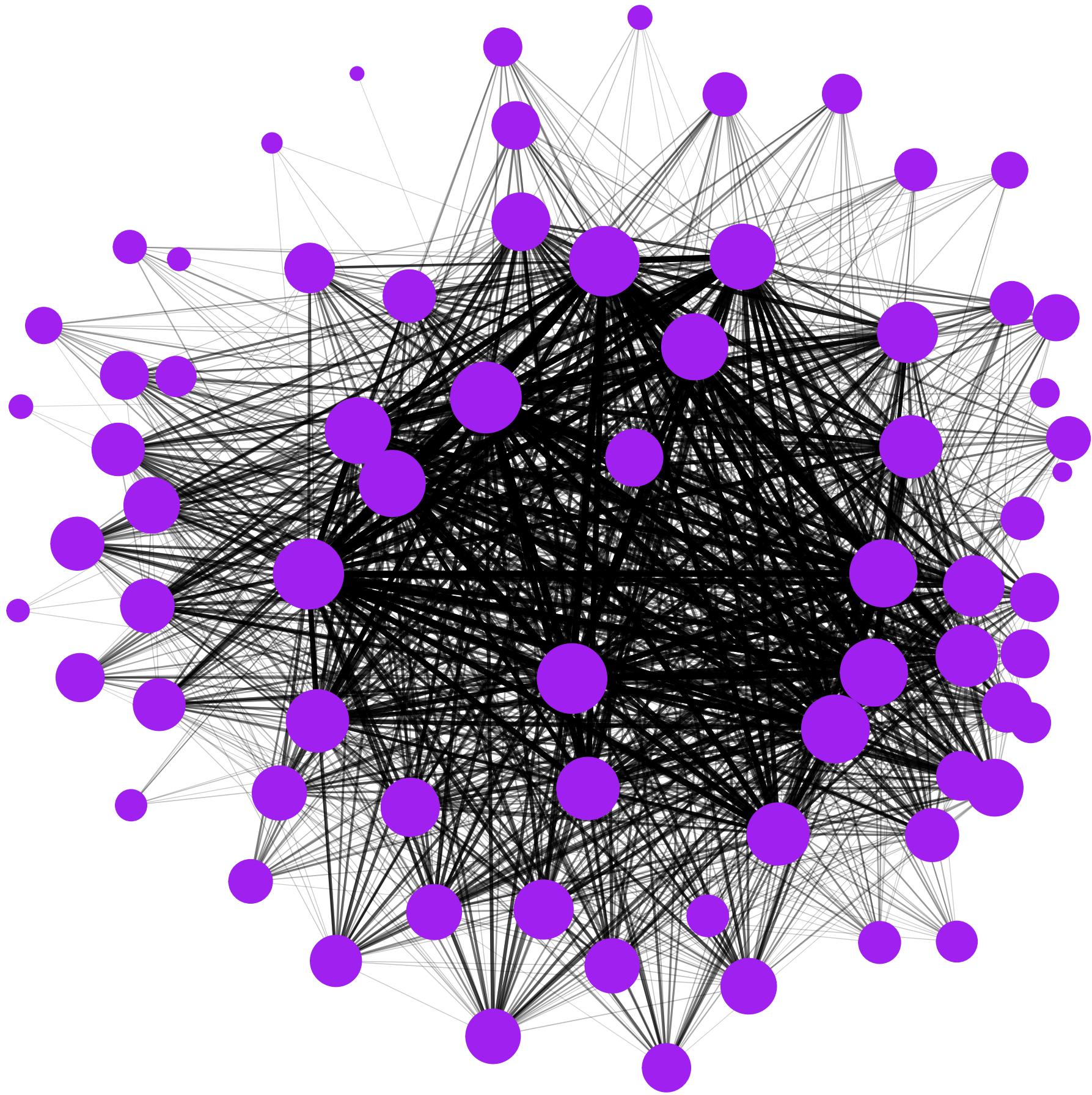
	Term	Ont	N	n	Adj. p-value
GO:0008366	axon ensheathment	BP	12	2	0.001156
GO:0007272	ensheathment of neurons	BP	12	2	0.001156
GO:0042552	myelination	BP	12	2	0.001156
GO:0032291	axon ensheathment in central nervous system	BP	2	1	0.008546
GO:0022010	central nervous system myelination	BP	2	1	0.008546
GO:0014003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

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



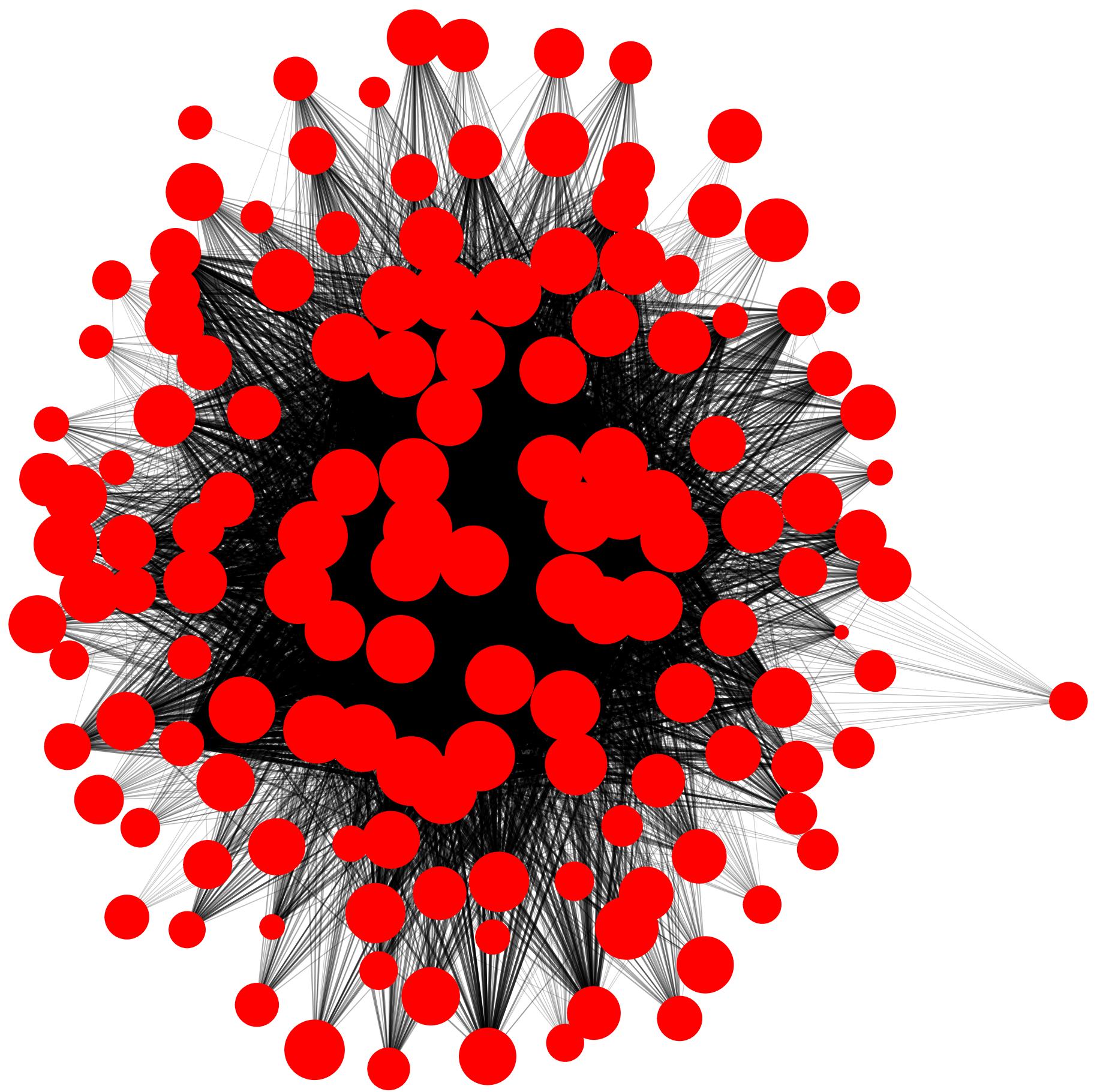
	Term	Ont	N	n	Adj. p-value
GO:0016049	cell growth	BP	49	5	6.2e-05
GO:0048588	developmental cell growth	BP	28	4	9.215e-05
GO:0048843	negative regulation of axon extension involved in axon guidance	BP	3	2	0.0002208
GO:0003415	chondrocyte hypertrophy	BP	4	2	0.000439
GO:0050922	negative regulation of chemotaxis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

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



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

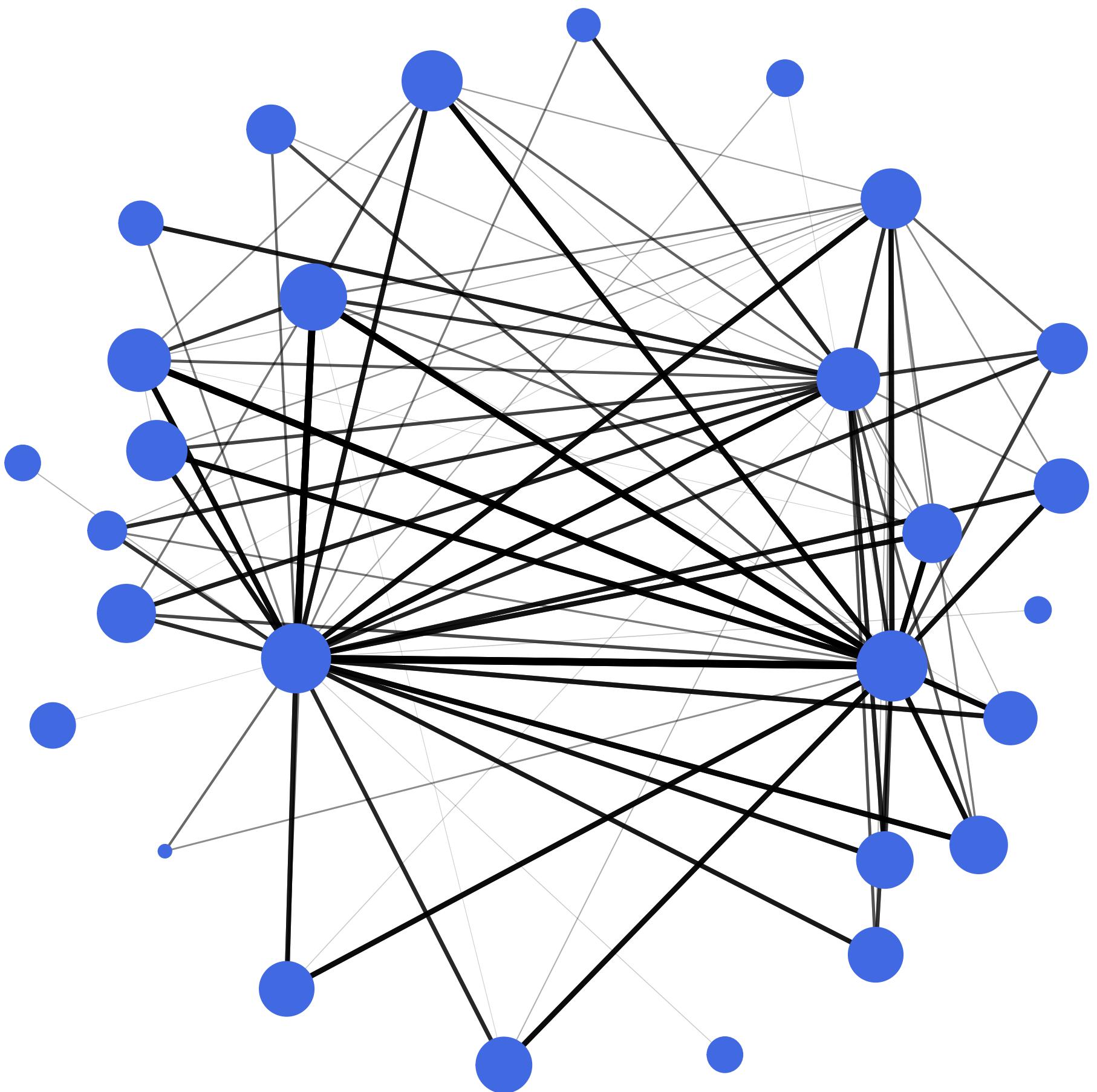
	Pathway	N	DE	P.DE
<i>path:gga04370</i>	VEGF signaling pathway	52	3	0.002605
<i>path:gga04510</i>	Focal adhesion	169	4	0.01226
<i>path:gga04514</i>	Cell adhesion molecules	99	3	0.0155
<i>path:gga04010</i>	MAPK signaling pathway	236	4	0.03627
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction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



1	NA							
2	NA							
3	NA							
4	NA							
5	NA							
6	NA							
7	NA							
8	NA							
9	NA							
10	NA							
11	NA							
12	NA							
13	NA							
14	NA							
15	NA							
16	NA							
17	NA							
18	NA	NA	NA	NA				

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

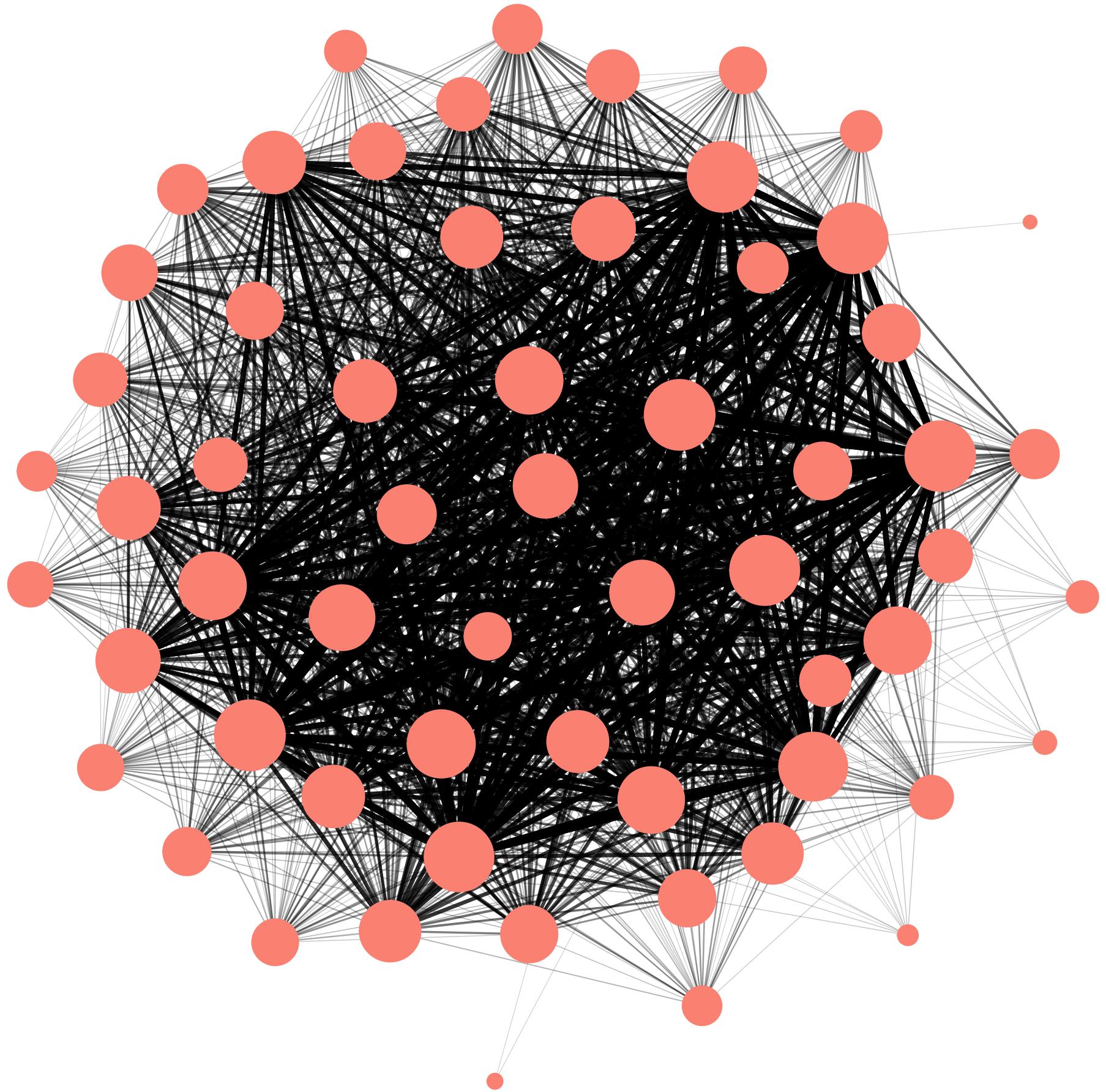
	Pathway	N	DE	P.DE
<i>path:gga03010</i>	Ribosome	115	32	1.056e-37
<i>path:gga04310</i>	Wnt signaling pathway	133	6	0.002679
<i>path:gga04810</i>	Regulation of actin cytoskeleton	180	7	0.002786
<i>path:gga04068</i>	FoxO signaling pathway	108	4	0.0264
<i>path:gga04210</i>	Apoptosis	113	4	0.03049
<i>path:gga04510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



1	NA							
2	NA							
3	NA							
4	NA	NA	NA	NA				

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

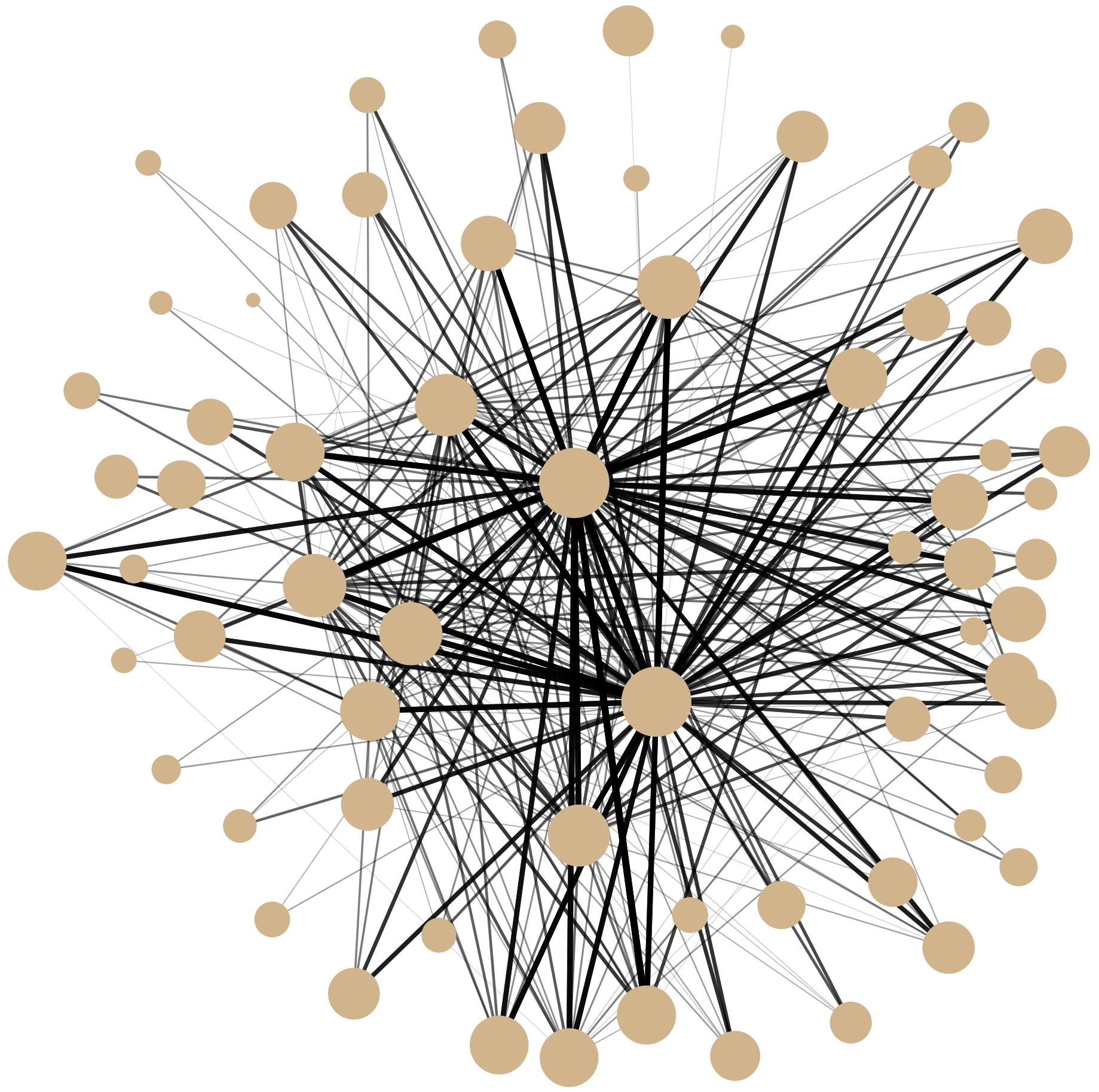
	Pathway	N	DE	P.DE
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	1	0.02494
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	118	2	0.02529
<i>path:gga00650</i>	Butanoate metabolism	21	1	0.04326
<i>path:gga00410</i>	beta-Alanine metabolism	25	1	0.05129
<i>path:gga04020</i>	Calcium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



1	NA							
2	NA							
3	NA							
4	NA							
5	NA							
6	NA							
7	NA							
8	NA	NA	NA	NA				

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

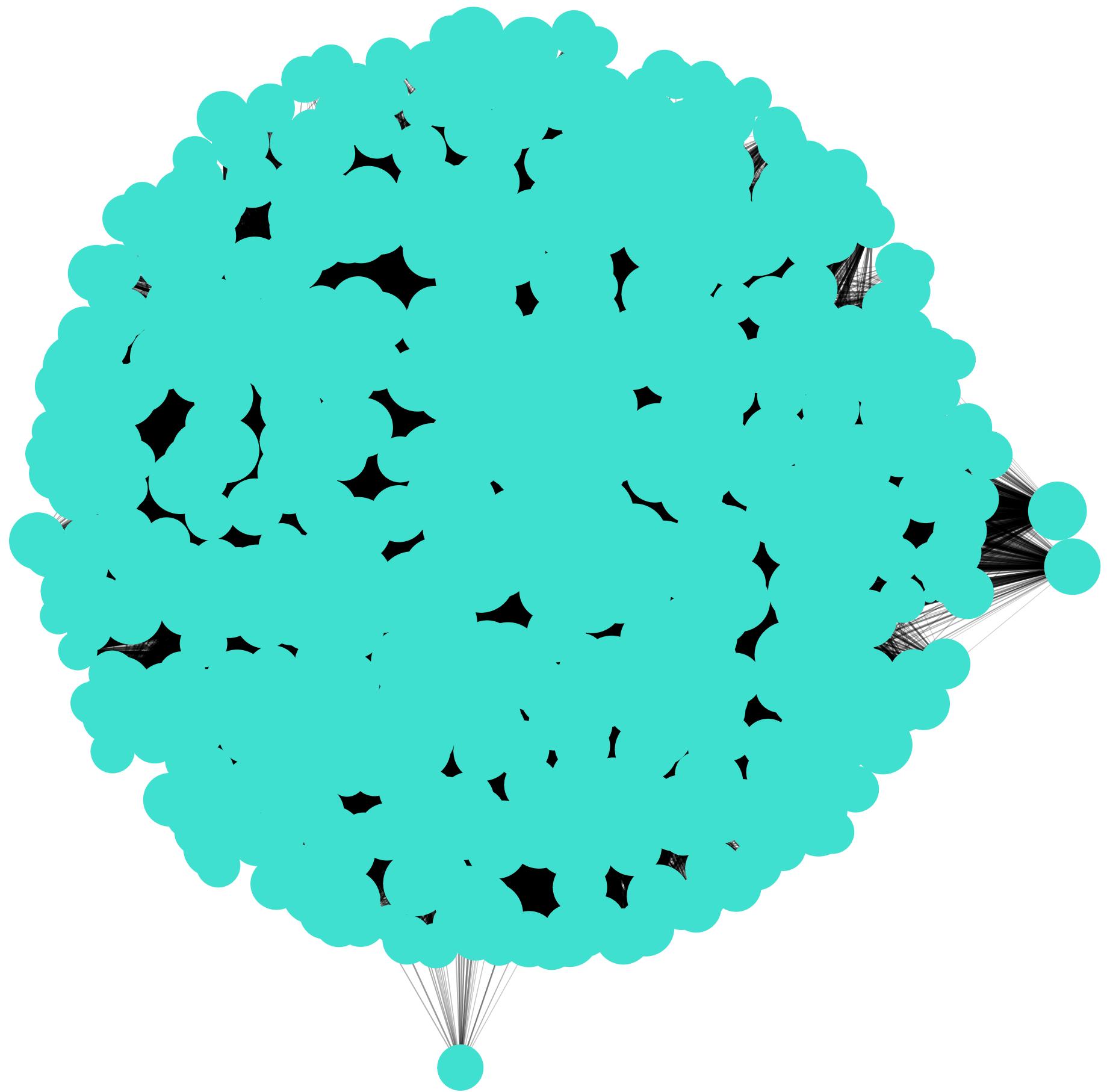
	Pathway	N	DE	P.DE
<i>path:gga00030</i>	Pentose phosphate pathway	25	2	0.00507
<i>path:gga00051</i>	Fructose and mannose metabolism	34	2	0.009251
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	47	2	0.0172
<i>path:gga04540</i>	Gap junction	78	2	0.04395
<i>path:gga00910</i>	Nitrogen metabolism	13	1	0.05428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



1	NA							
2	NA							
3	NA							
4	NA							
5	NA							
6	NA							
7	NA							
8	NA							
9	NA	NA	NA					

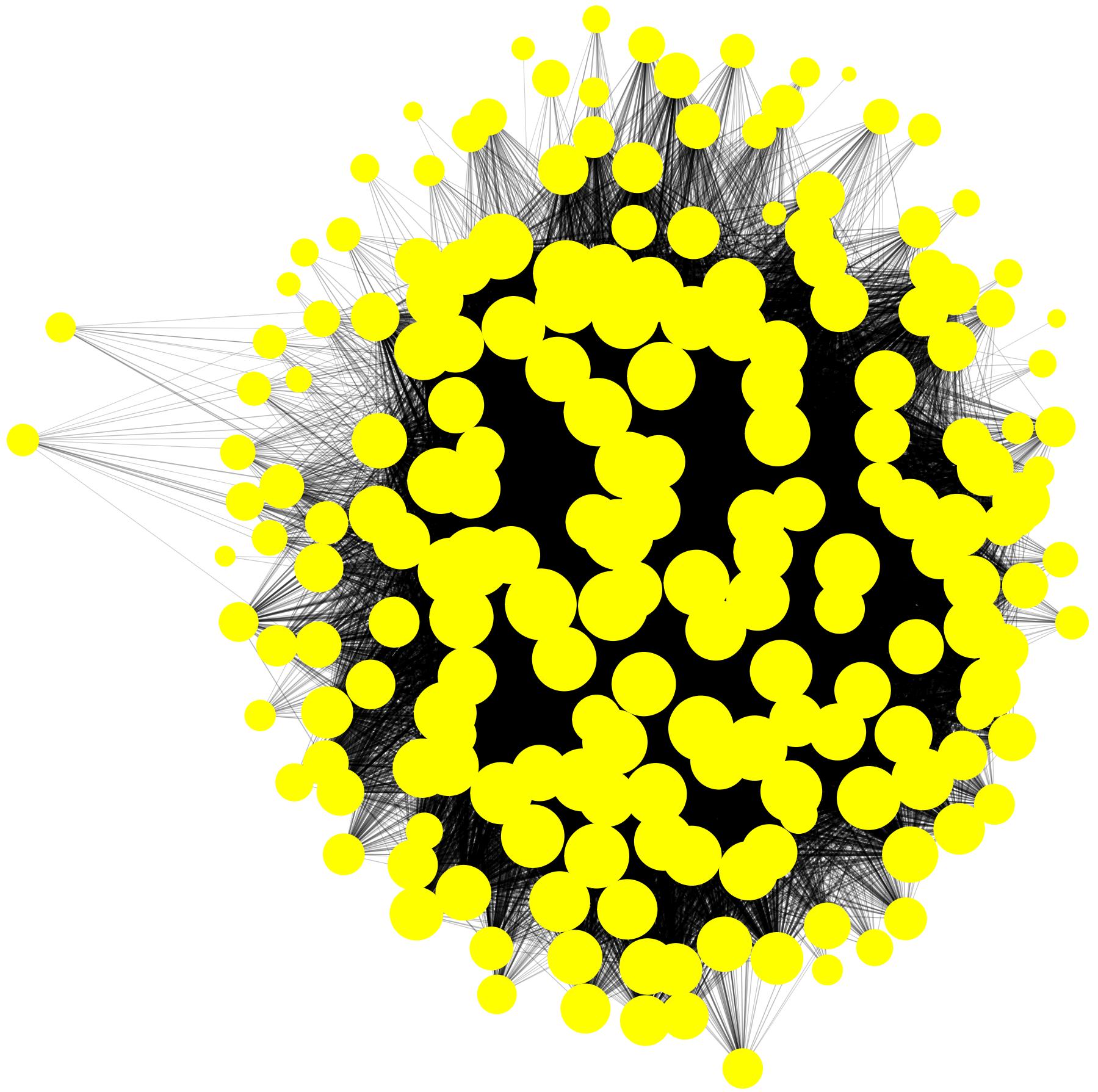
	Term	Ont	N	n	Adj. p-value
GO:0035609	C-terminal protein deglutamylation	BP	1	1	0.00506
GO:0098967	exocytic insertion of neurotransmitter receptor to postsynaptic membrane	BP	1	1	0.00506
GO:0035608	protein deglutamylation	BP	1	1	0.00506
GO:0035610	protein side chain deglutamylation	BP	1	1	0.00506
GO:0031629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

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



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

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



1	NA								
2	NA								
3	NA								
4	NA								
5	NA								
6	NA								
7	NA								
8	NA								
9	NA								
10	NA								
11	NA								
12	NA								
13	NA								
14	NA								
15	NA								
16	NA								
17	NA								
18	NA								
19	NA								
20	NA								
21	NA								
22	NA								
23	NA								
24	NA								
25	NA	NA	NA	NA					

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

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