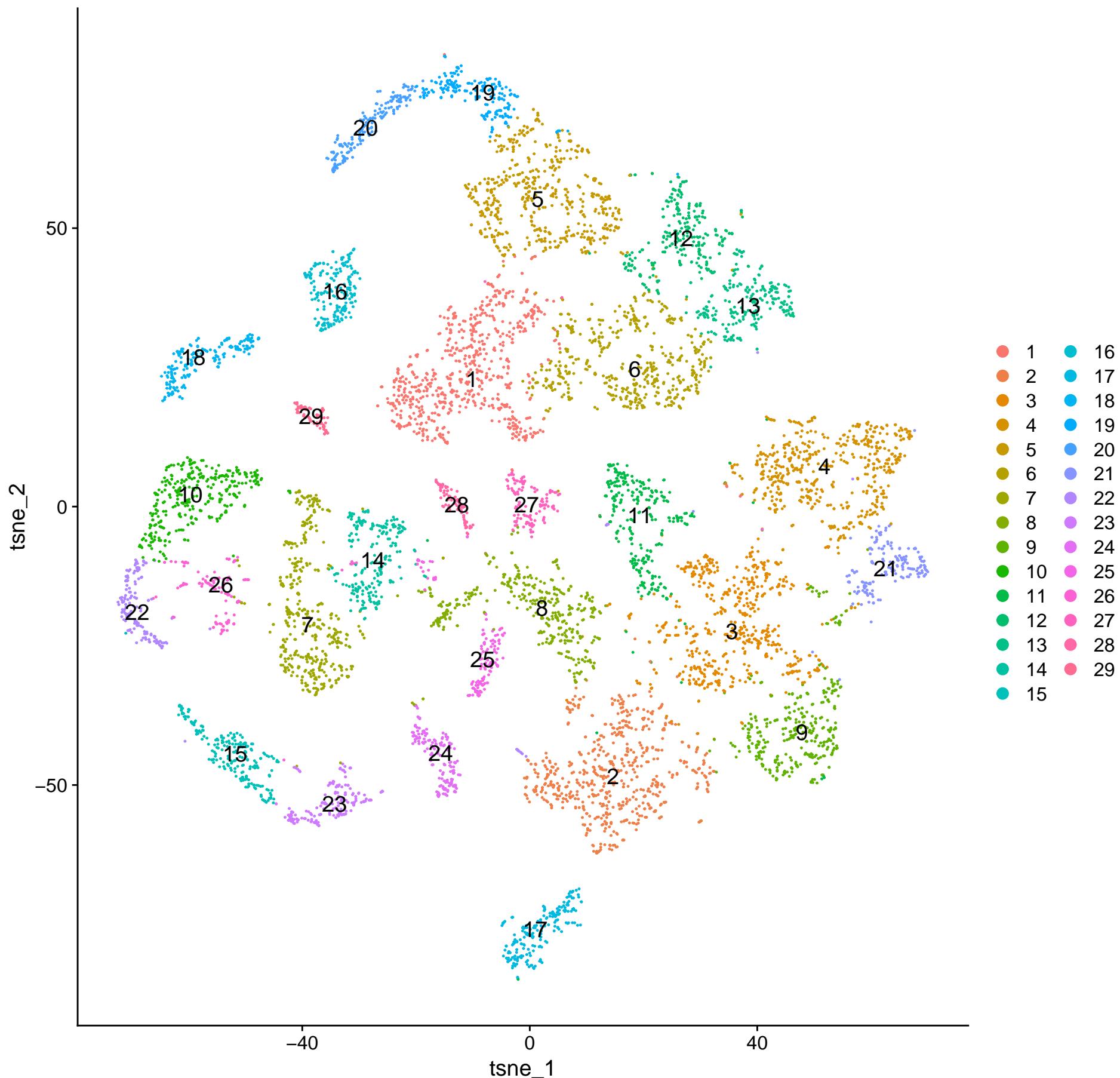
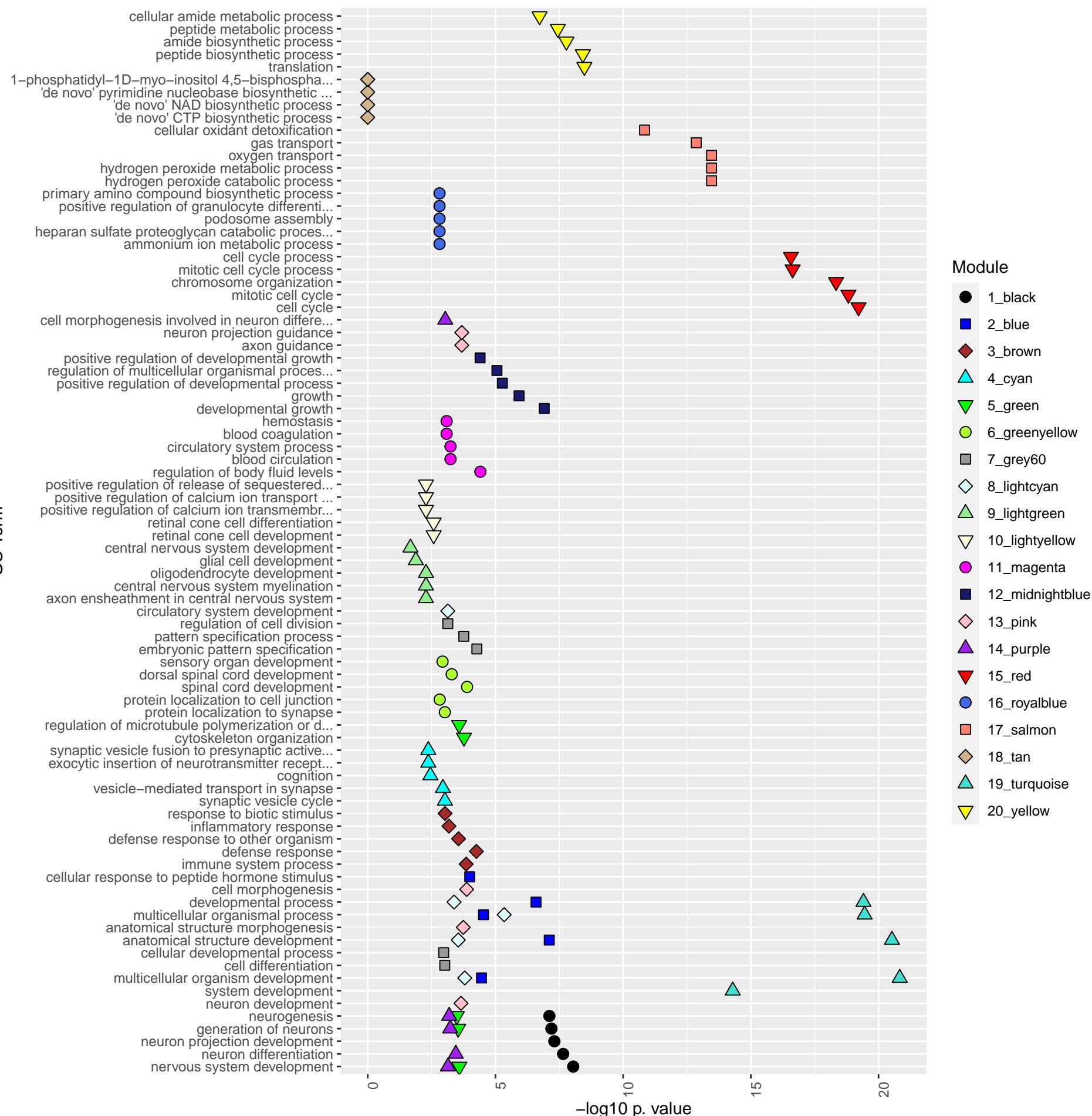
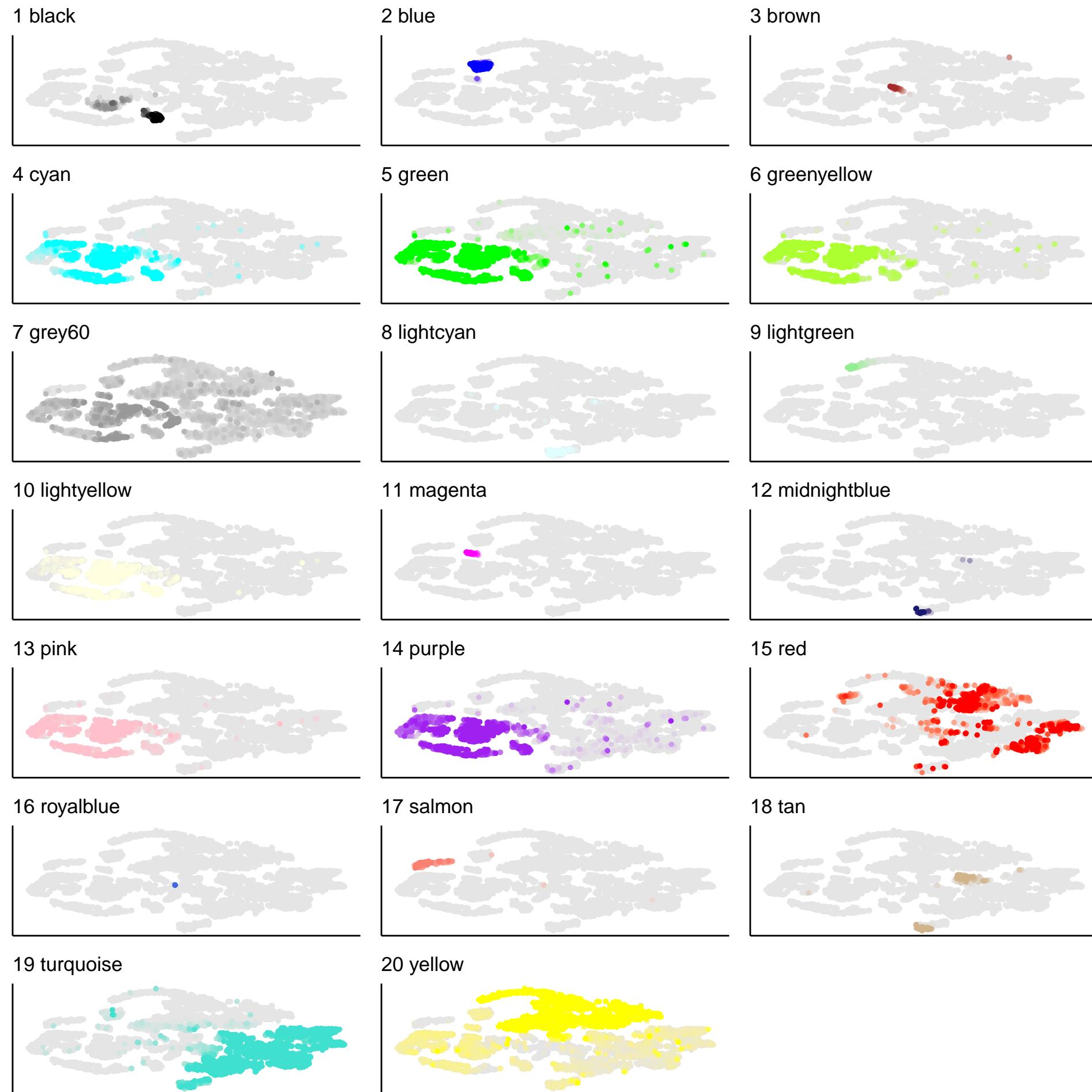


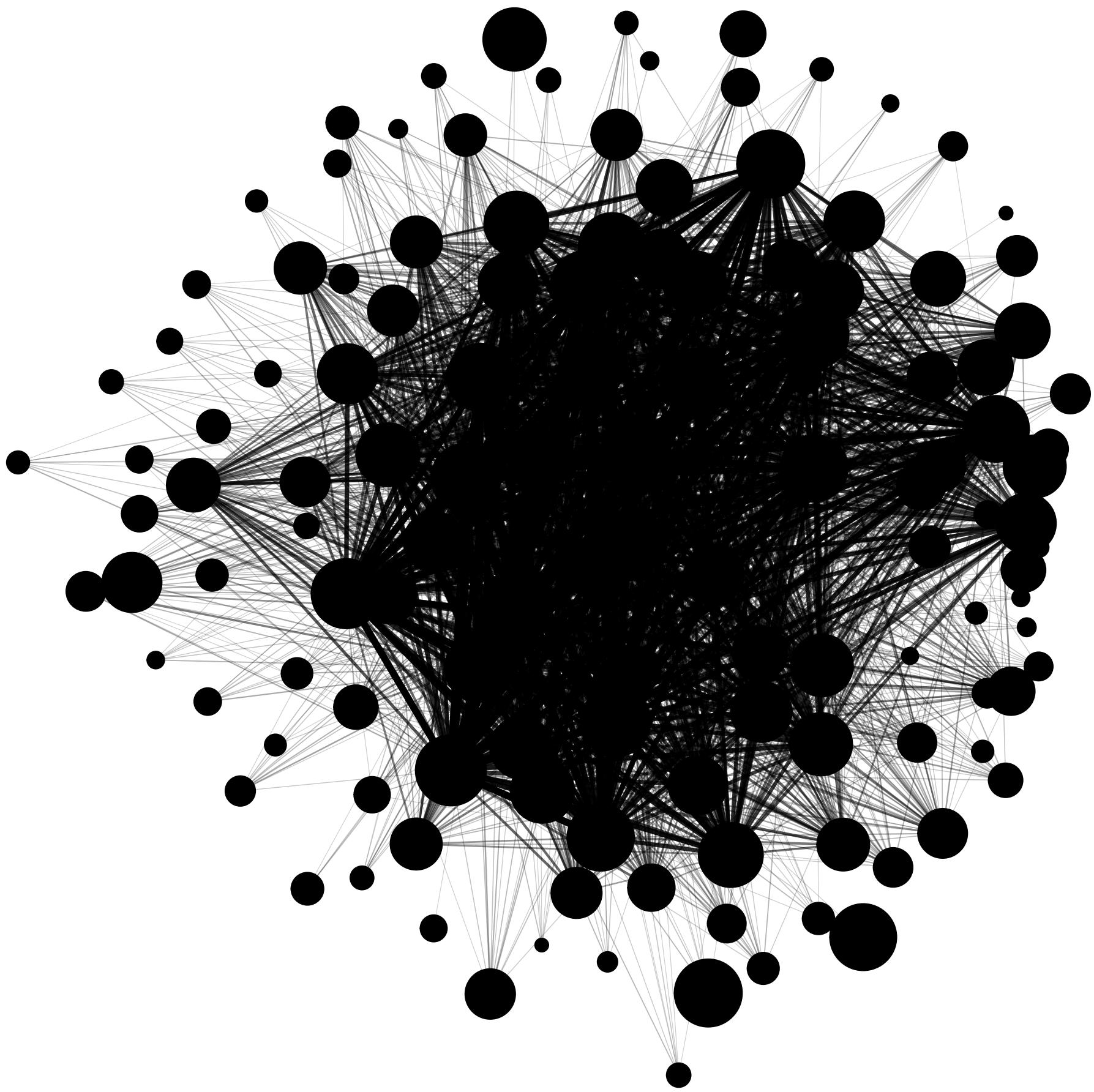
Gg_ctrl_int scWGCNA modules





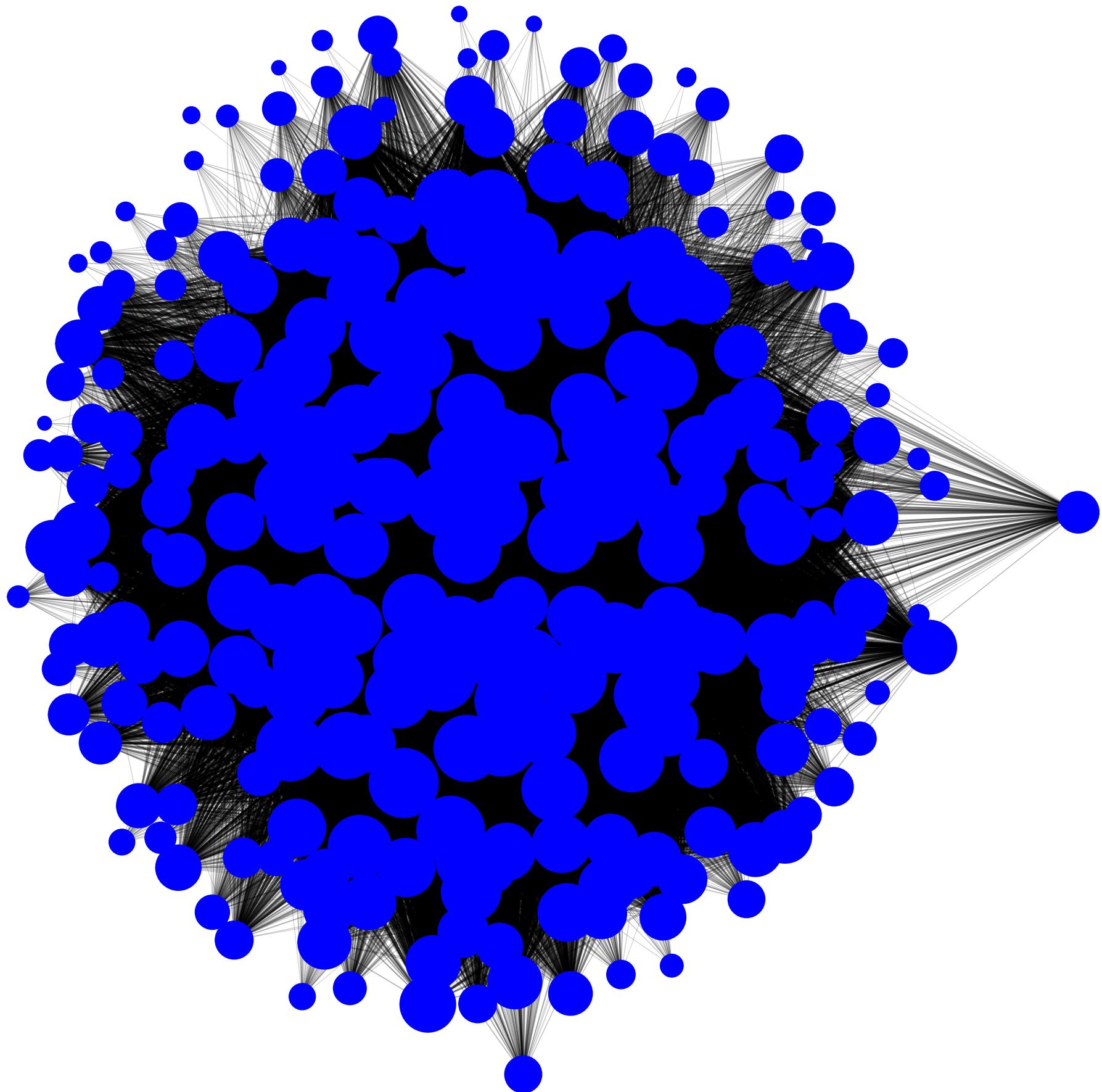






	Term	Ont	N	n	Adj. p-value
GO:0007399	nervous system development	BP	255	15	9.001e-09
GO:0030182	neuron differentiation	BP	161	12	2.233e-08
GO:0031175	neuron projection development	BP	109	10	4.92e-08
GO:0048699	generation of neurons	BP	177	12	6.414e-08
GO:0022008	neurogenesis	BP	180	12	7.722e-08
GO:0048666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

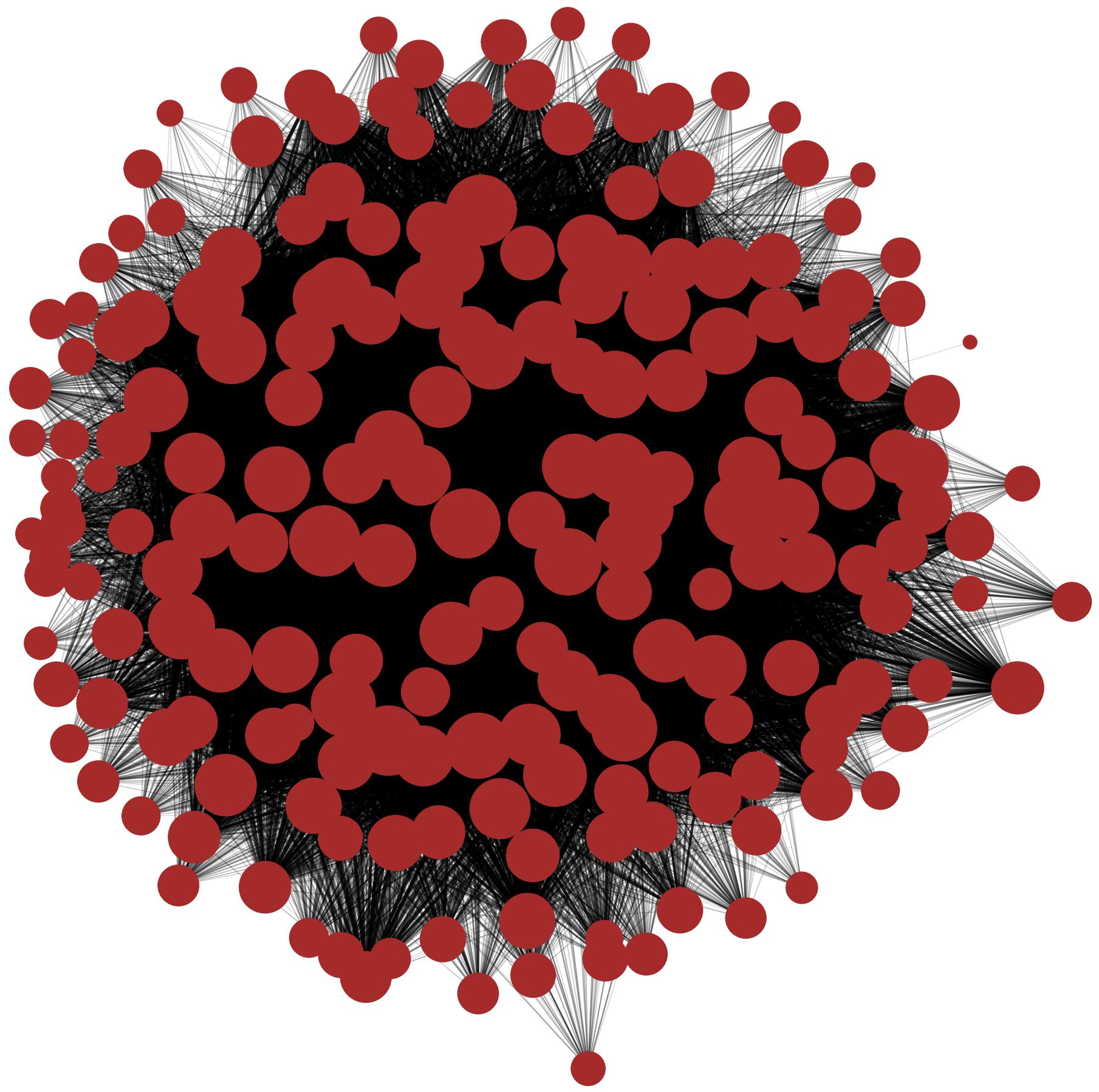
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<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	272	18	3.692e–11
<i>path:gga04920</i>	Adipocytokine signaling pathway	58	2	0.09647
<i>path:gga04020</i>	Calcium signaling pathway	196	4	0.1015
<i>path:gga00360</i>	Phenylalanine metabolism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



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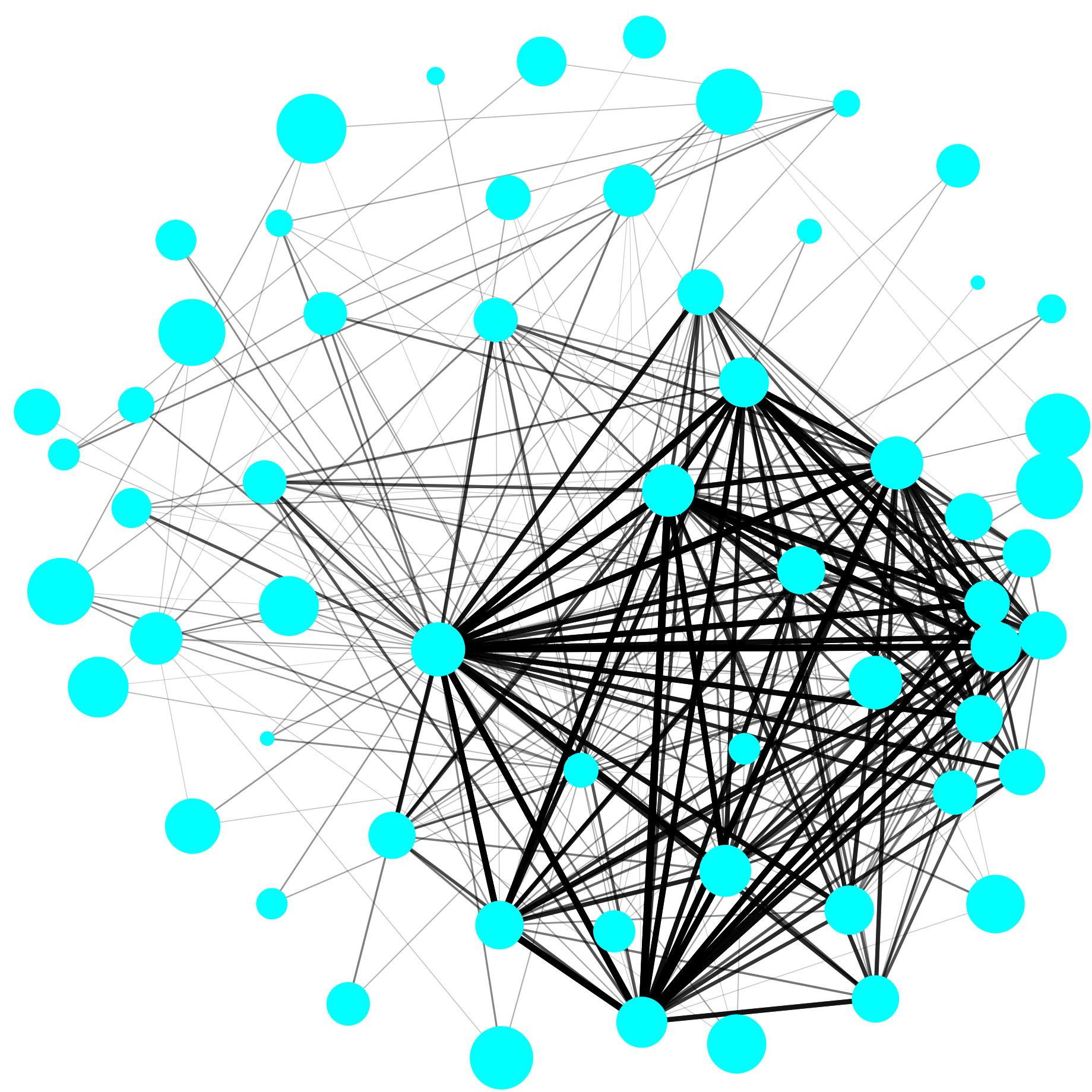
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GO:0048856	anatomical structure development	BP	608	33	7.816e-08
GO:0032502	developmental process	BP	640	33	2.574e-07
GO:0032501	multicellular organismal process	BP	692	30	2.938e-05
GO:0007275	multicellular organism development	BP	562	26	3.521e-05
GO:0071375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

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



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

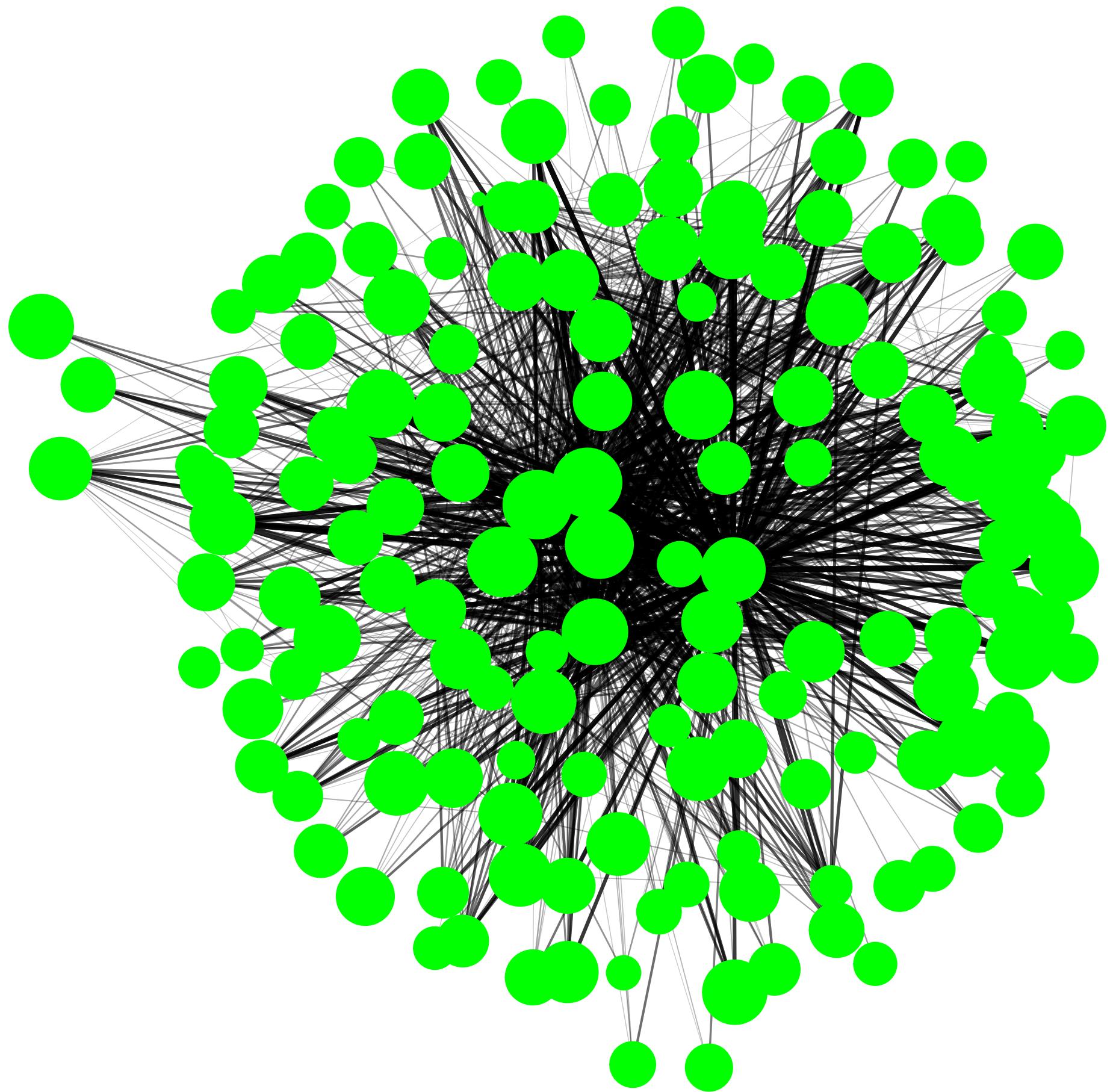
	Pathway	N	DE	P.DE
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	146	15	2.645e–09
<i>path:gga04620</i>	Toll–like receptor signaling pathway	70	10	5.489e–08
<i>path:gga04145</i>	Phagosome	123	11	1.514e–06
<i>path:gga04621</i>	NOD–like receptor signaling pathway	115	10	5.905e–06
<i>path:gga04623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



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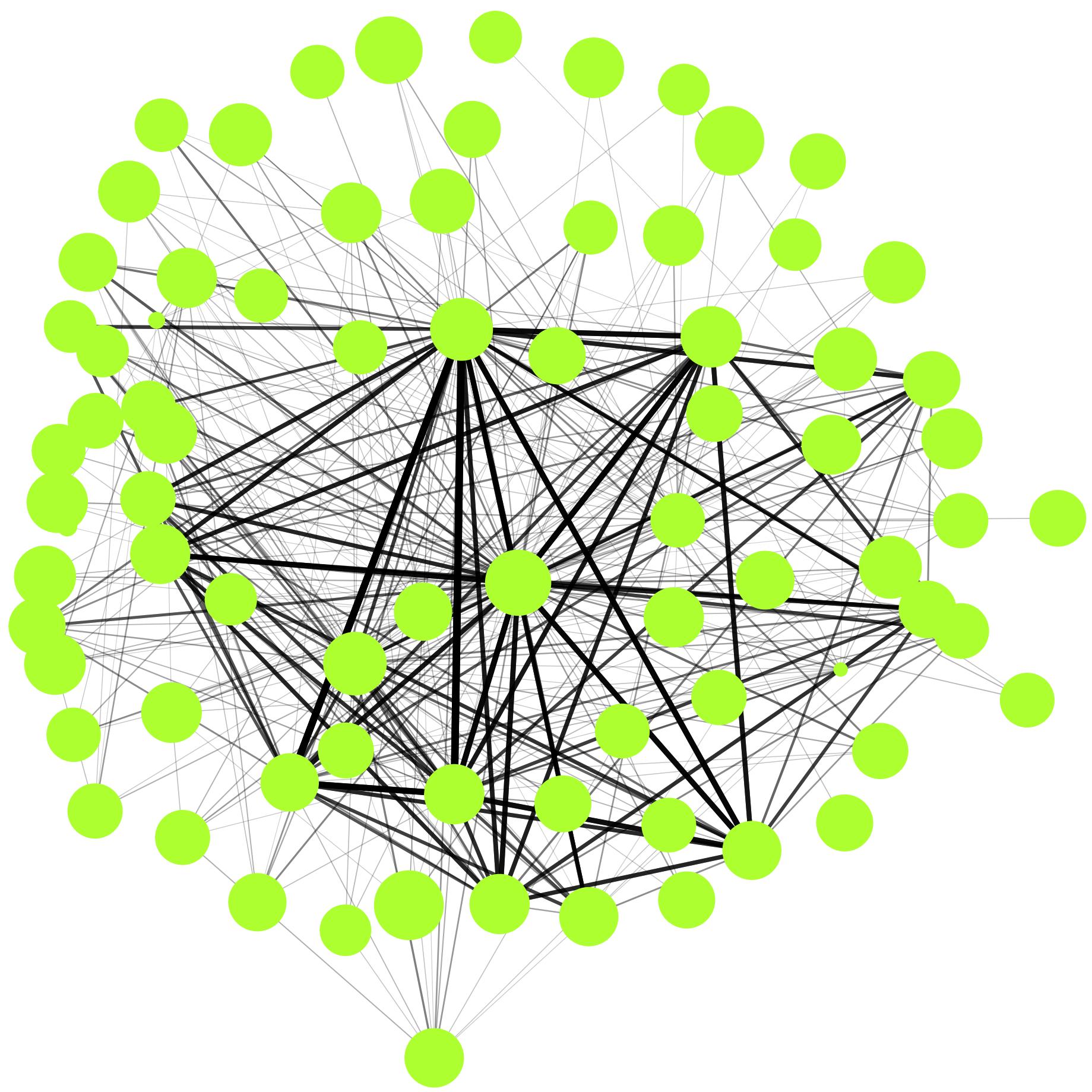
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GO:0099504	synaptic vesicle cycle	BP	11	2	0.0009495
GO:0099003	vesicle-mediated transport in synapse	BP	12	2	0.001136
GO:0050890	cognition	BP	21	2	0.003528
GO:0098967	exocytic insertion of neurotransmitter receptor to postsynaptic membrane	BP	1	1	0.004245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

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



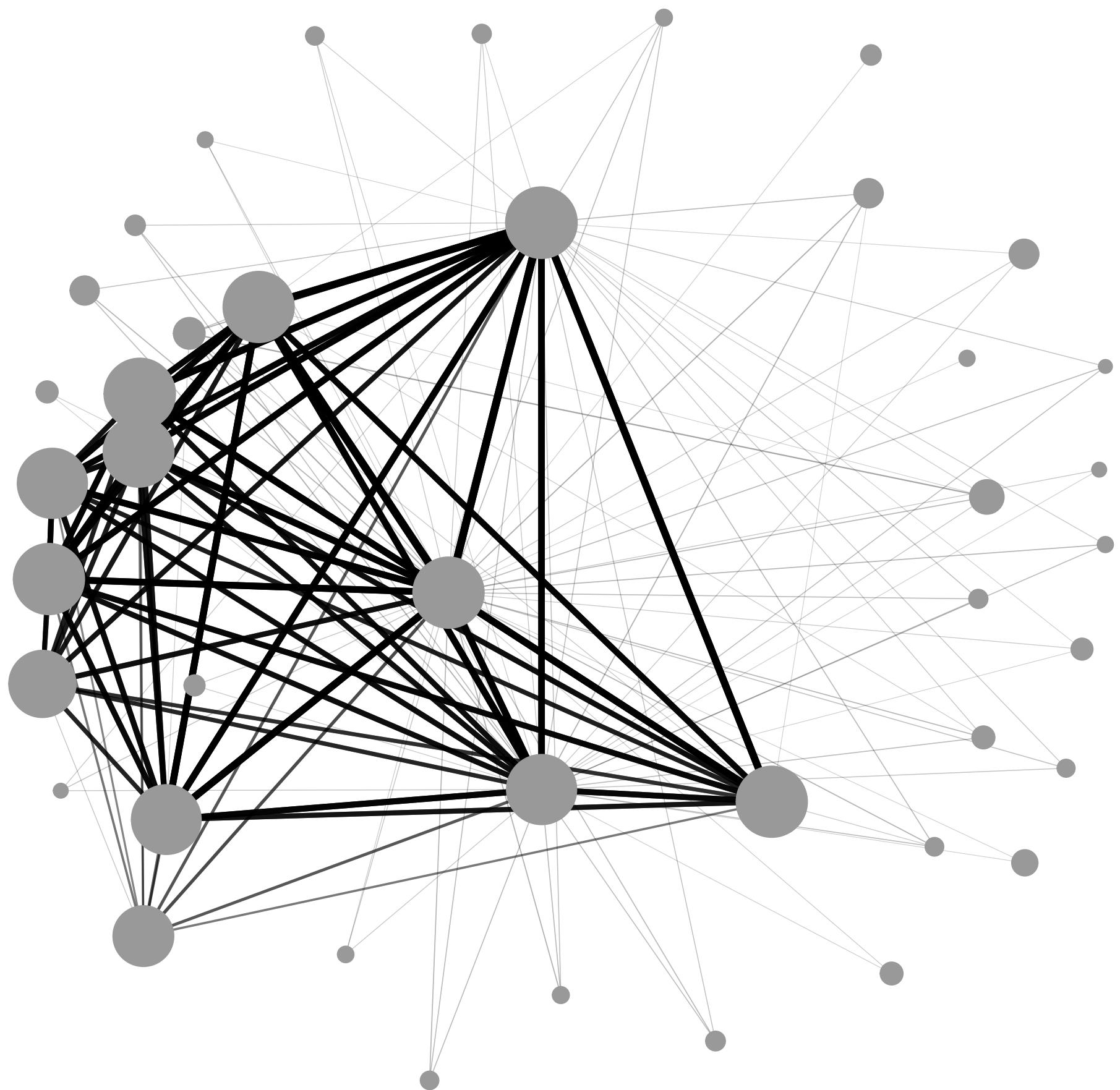
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GO:0007010	cytoskeleton organization	BP	165	9	0.0001708
GO:0007399	nervous system development	BP	255	11	0.0002605
GO:0031110	regulation of microtubule polymerization or depolymerization	BP	11	3	0.0002631
GO:0048699	generation of neurons	BP	177	9	0.0002887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

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



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

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



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

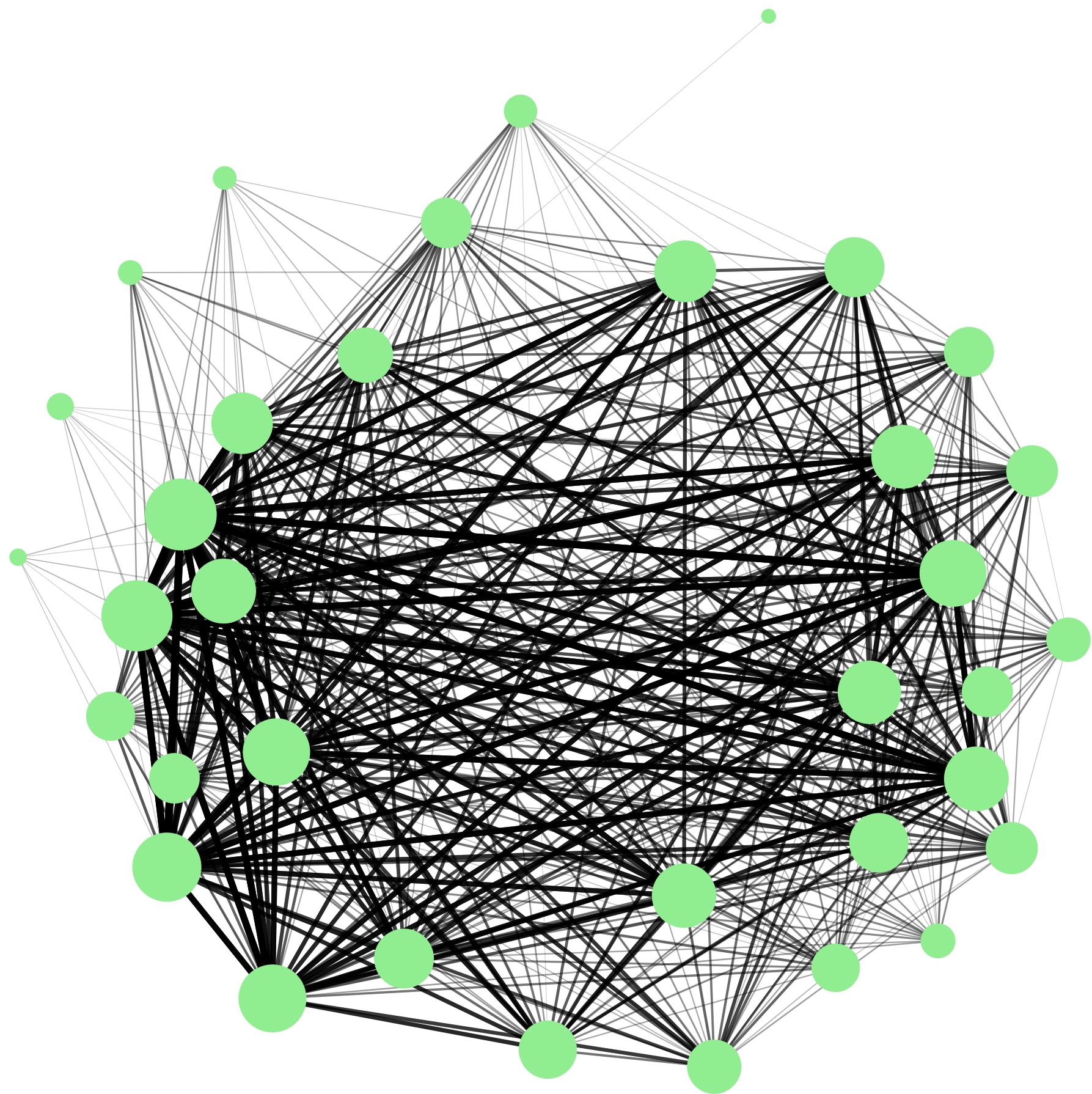
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	272	4	0.001697
<i>path:gga04020</i>	Calcium signaling pathway	196	2	0.0544
<i>path:gga00513</i>	Various types of N–glycan biosynthesis	38	1	0.07086
<i>path:gga00510</i>	N–Glycan biosynthesis	45	1	0.08338
<i>path:gga04540</i>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



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

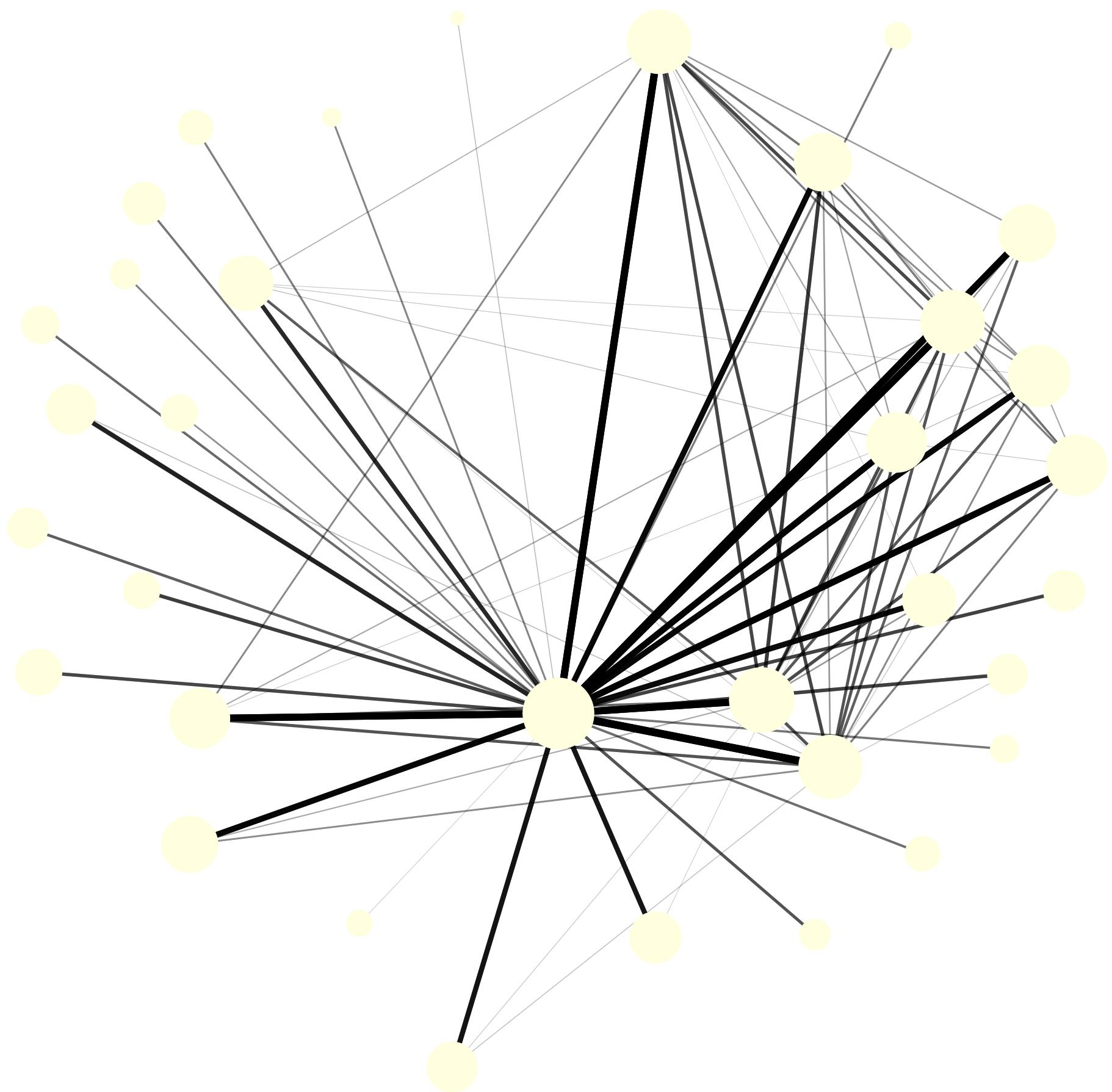
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<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.01443
<i>path:gga00910</i>	Nitrogen metabolism	14	1	0.04963
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	272	3	0.07556
<i>path:gga00062</i>	Fatty acid elongation	22	1	0.0769
<i>path:gga04150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



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

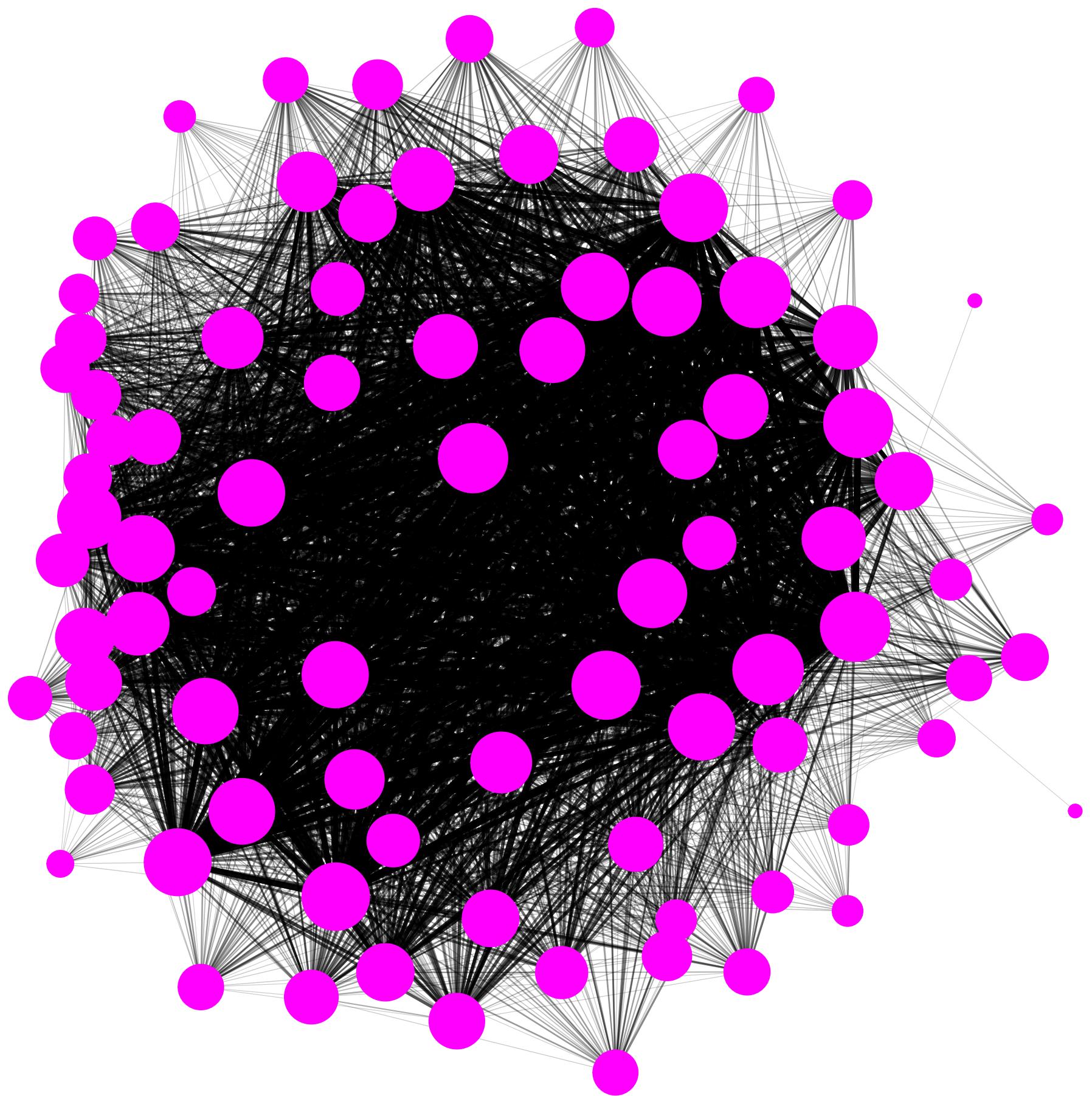
	Pathway	N	DE	P.DE
<i>path:gga03264</i>	Virion – Flavivirus	3	1	0.007852
<i>path:gga00062</i>	Fatty acid elongation	22	1	0.05621
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	26	1	0.0661
<i>path:gga00565</i>	Ether lipid metabolism	34	1	0.08557
<i>path:gga01212</i>	Fatty acid metabolism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



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

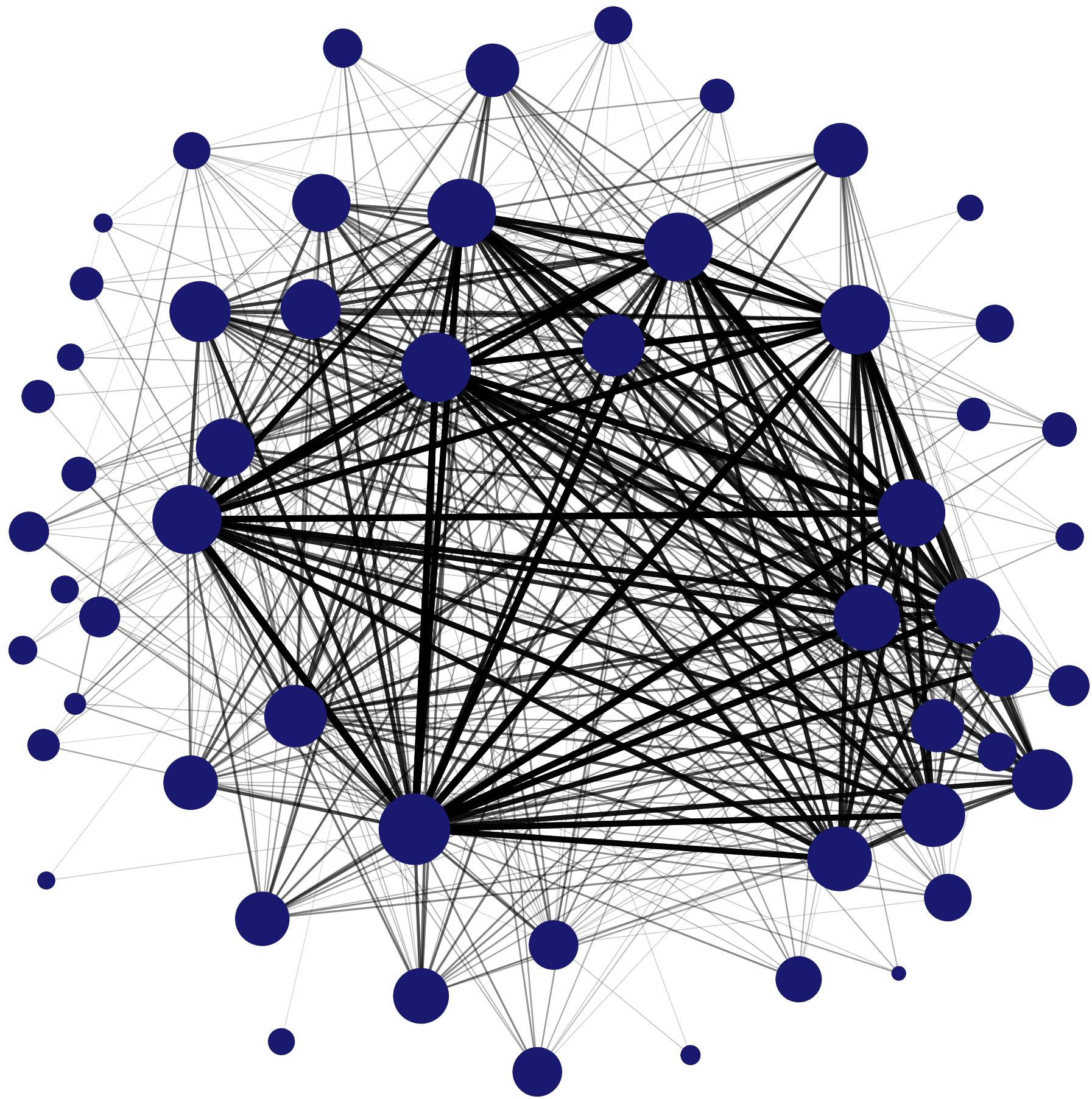
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	272	6	6.644e–05
<i>path:gga04020</i>	Calcium signaling pathway	196	4	0.001651
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	3	0.003939
<i>path:gga04912</i>	GnRH signaling pathway	73	2	0.01563
<i>path:gga04540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



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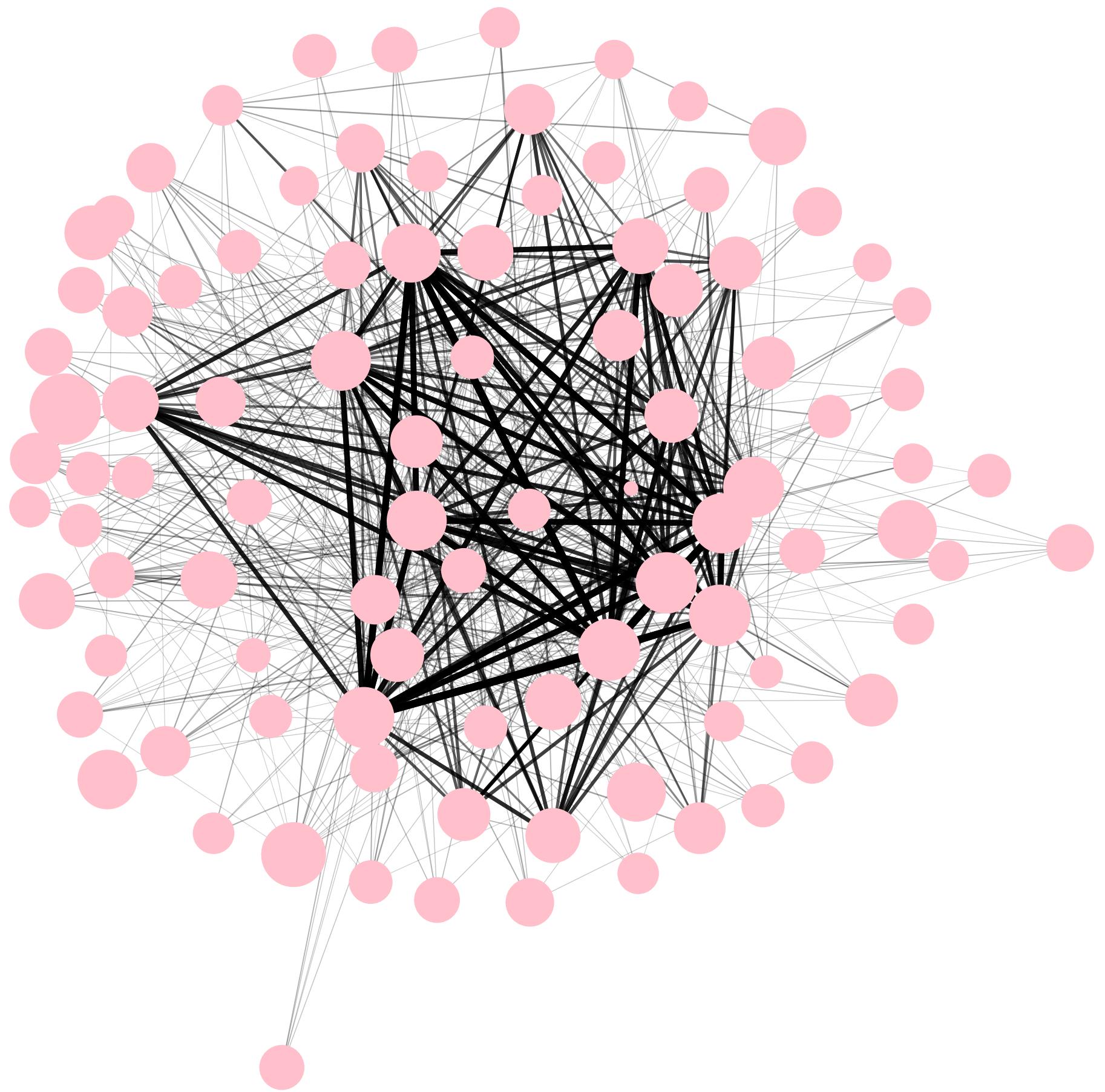
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GO:0050878	regulation of body fluid levels	BP	11	3	3.886e-05
GO:0008015	blood circulation	BP	26	3	0.0005718
GO:0003013	circulatory system process	BP	26	3	0.0005718
GO:0007596	blood coagulation	BP	7	2	0.0008139
GO:0007599	hemostasis	BP	7	2	0.0008139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

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



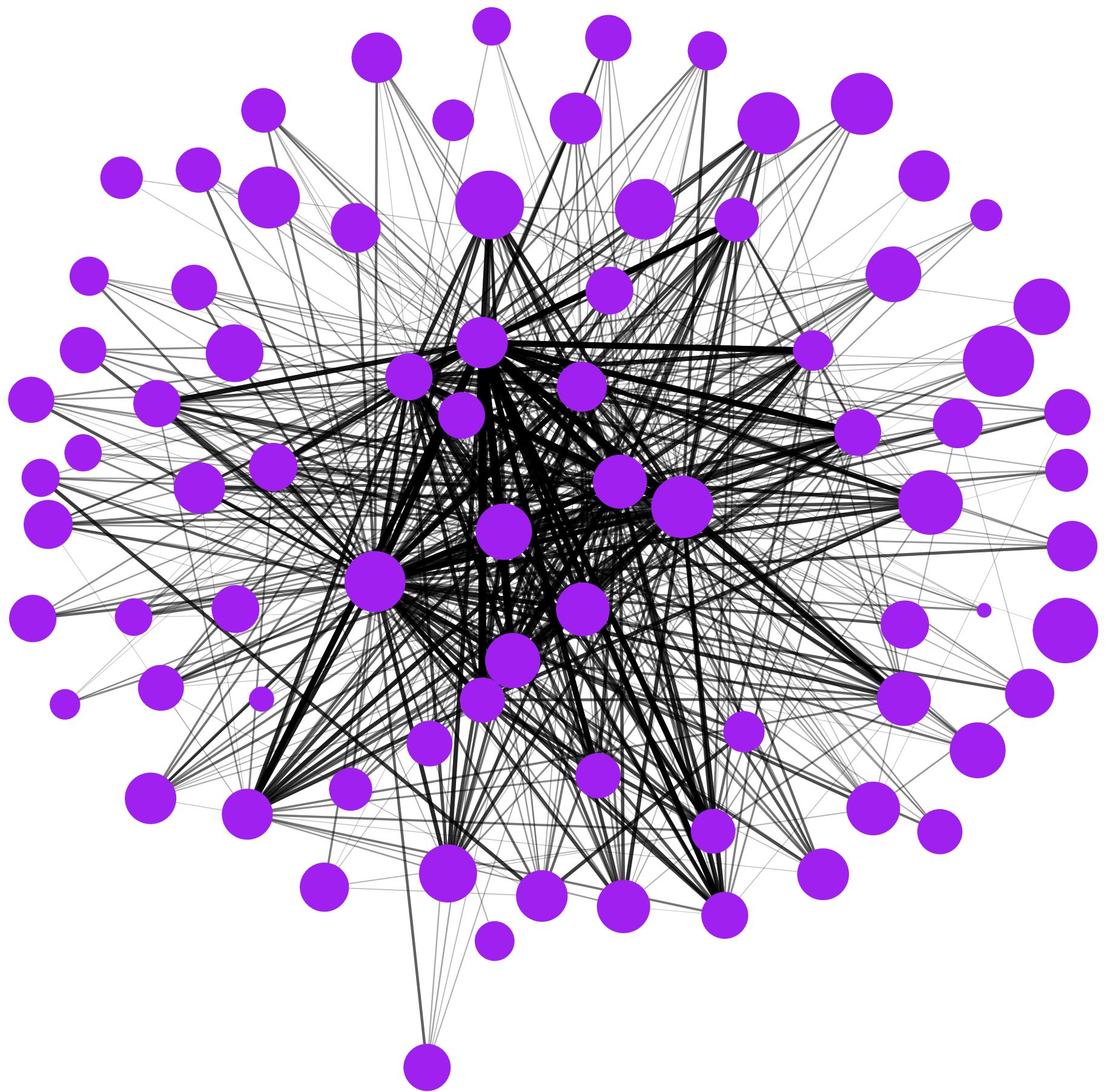
	Term	Ont	N	n	Adj. p-value
GO:0048589	developmental growth	BP	63	6	1.23e-07
GO:0040007	growth	BP	92	6	1.189e-06
GO:0051094	positive regulation of developmental process	BP	119	6	5.356e-06
GO:0051239	regulation of multicellular organismal process	BP	198	7	8.73e-06
GO:0048639	positive regulation of developmental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

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



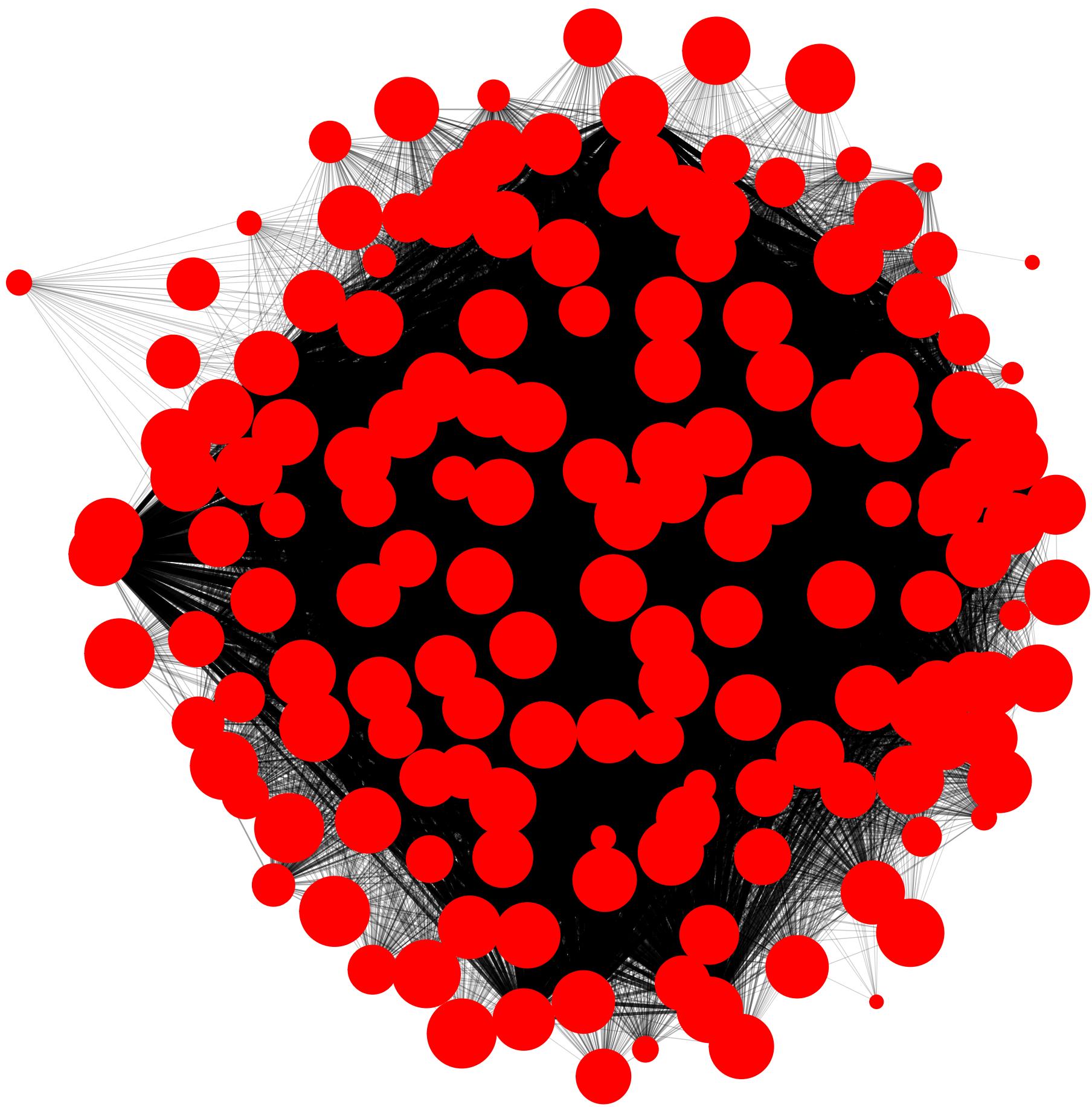
	Term	Ont	N	n	Adj. p-value
GO:0000902	cell morphogenesis	BP	112	6	0.0001338
GO:0009653	anatomical structure morphogenesis	BP	287	9	0.0001812
GO:0007411	axon guidance	BP	42	4	0.0002078
GO:0097485	neuron projection guidance	BP	42	4	0.0002078
GO:0048666	neuron development	BP	123	6	0.0002235
GO:0048856	anatomical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

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



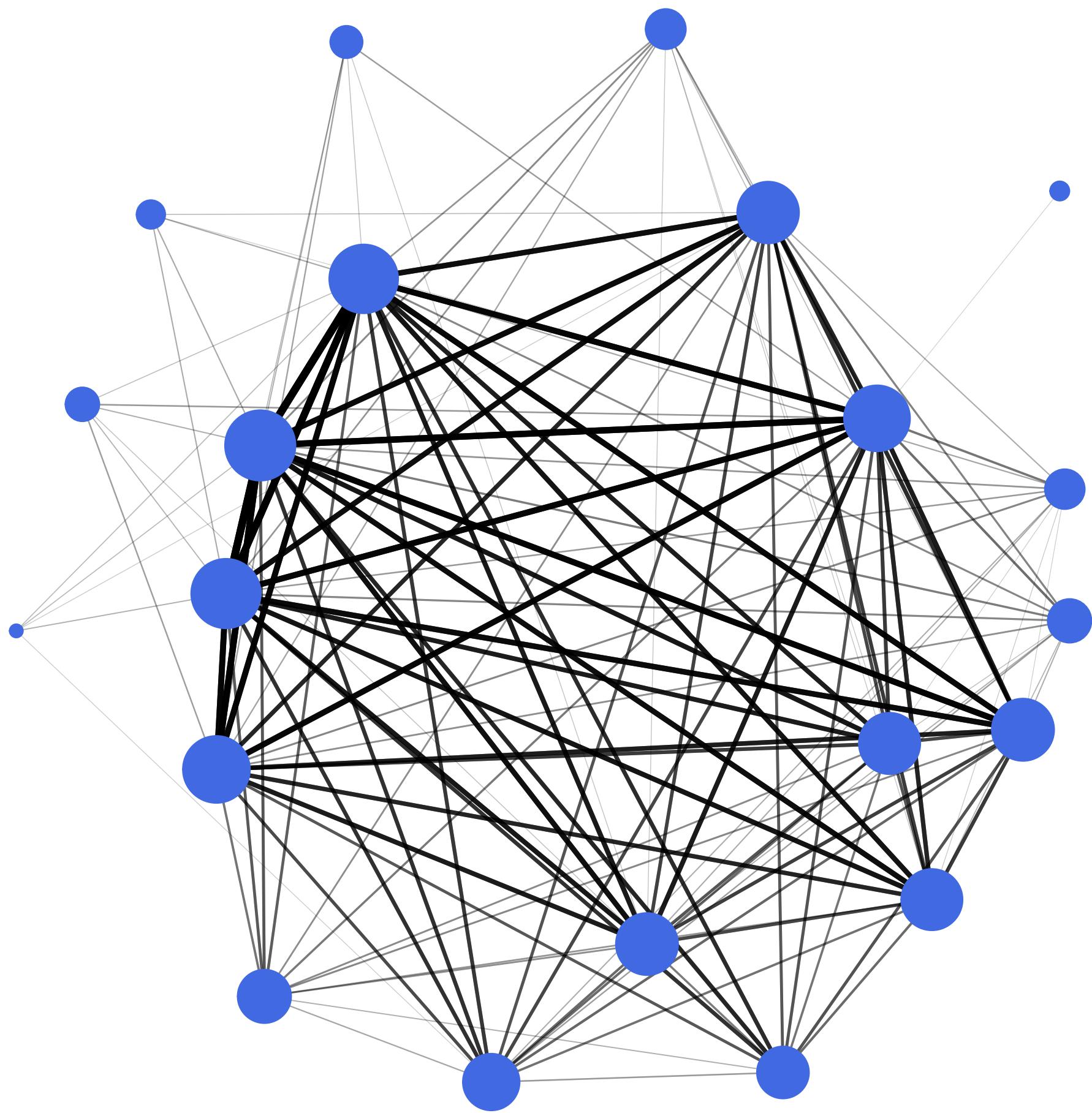
	Term	Ont	N	n	Adj. p-value
GO:0030182	neuron differentiation	BP	161	6	0.0003576
GO:0048699	generation of neurons	BP	177	6	0.0005916
GO:0022008	neurogenesis	BP	180	6	0.0006463
GO:0007399	nervous system development	BP	255	7	0.0007245
GO:0048667	cell morphogenesis involved in neuron differentiation	BP	74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

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



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

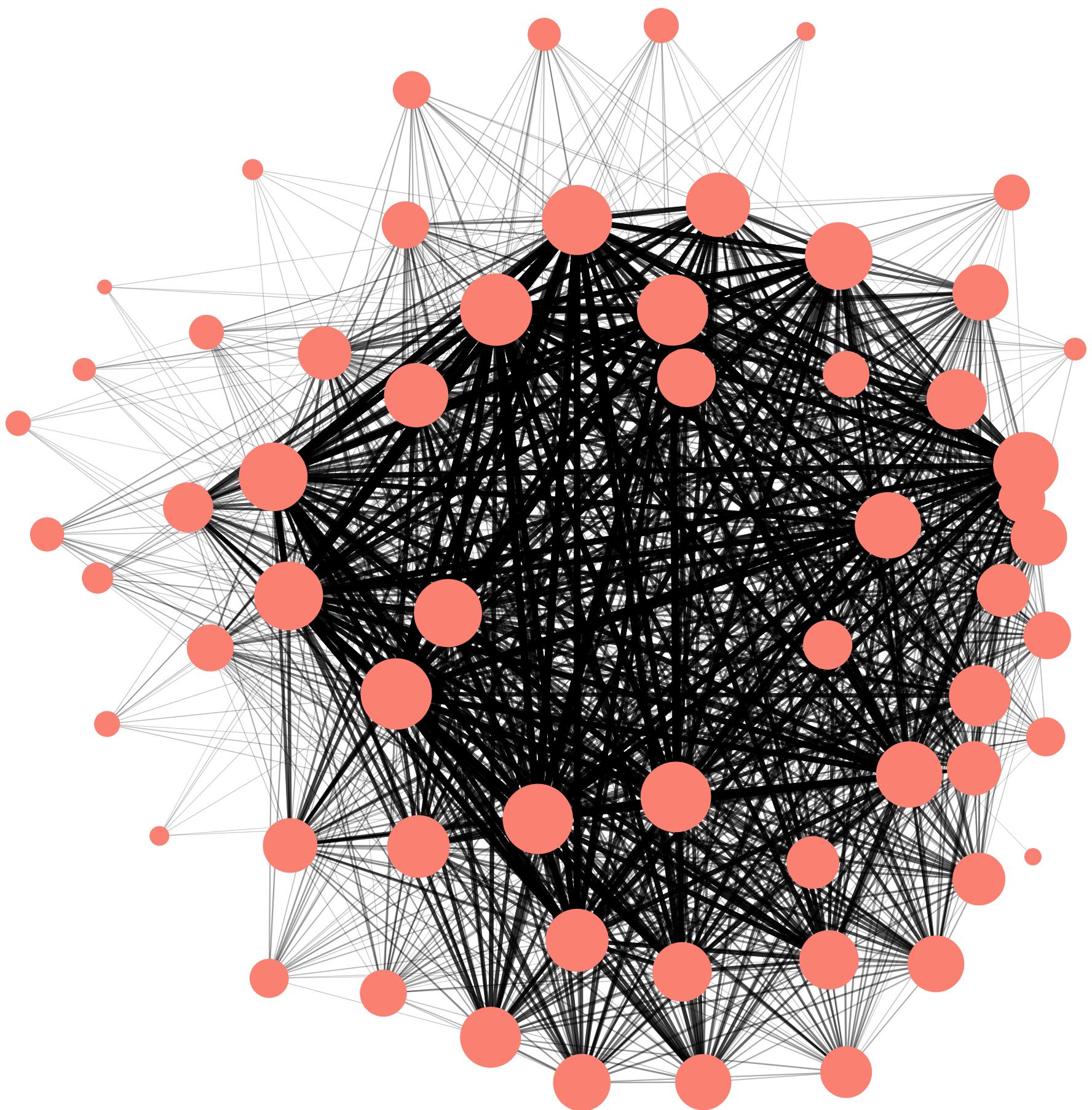
	Pathway	N	DE	P.DE
<i>path:gga04110</i>	Cell cycle	114	20	2.928e–18
<i>path:gga04114</i>	Oocyte meiosis	96	12	1.268e–09
<i>path:gga04914</i>	Progesterone–mediated oocyte maturation	78	9	3.211e–07
<i>path:gga03030</i>	DNA replication	29	6	9.327e–07
<i>path:gga00240</i>	Pyrimidine metabolism	55	5	0.0004649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



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3	NA	NA	NA	NA	NA			

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

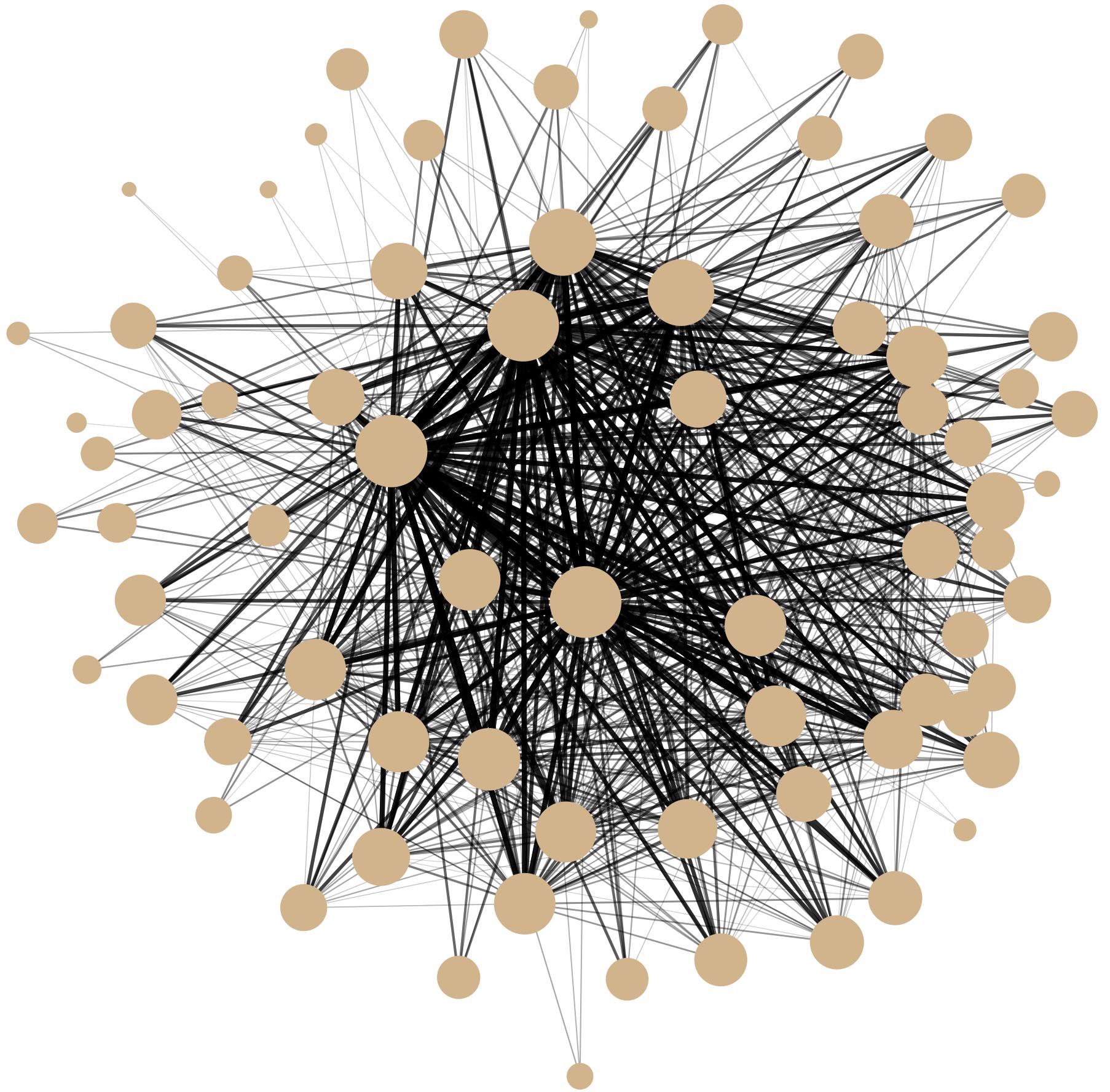
	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	67	3	0.0001415
<i>path:gga04510</i>	Focal adhesion	170	3	0.002147
<i>path:gga04810</i>	Regulation of actin cytoskeleton	182	3	0.002606
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.006161
<i>path:gga00531</i>	Glycosaminoglycan degradation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



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8	NA	NA	NA	NA	NA			

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

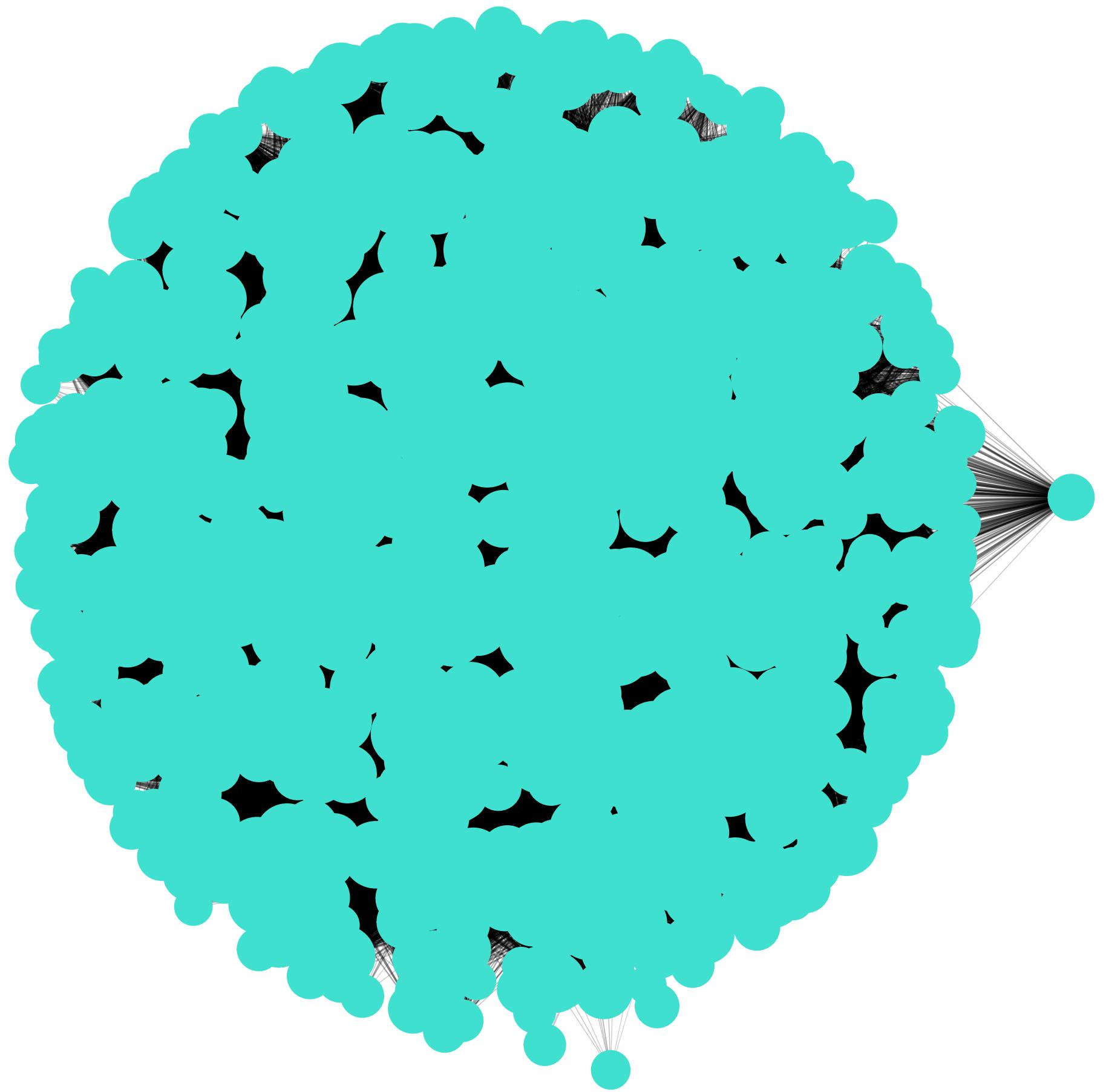
	Pathway	N	DE	P.DE
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	47	3	0.001084
<i>path:gga00030</i>	Pentose phosphate pathway	25	2	0.005164
<i>path:gga01200</i>	Carbon metabolism	94	3	0.007765
<i>path:gga00051</i>	Fructose and mannose metabolism	34	2	0.00942
<i>path:gga01232</i>	Nucleotide metabolism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



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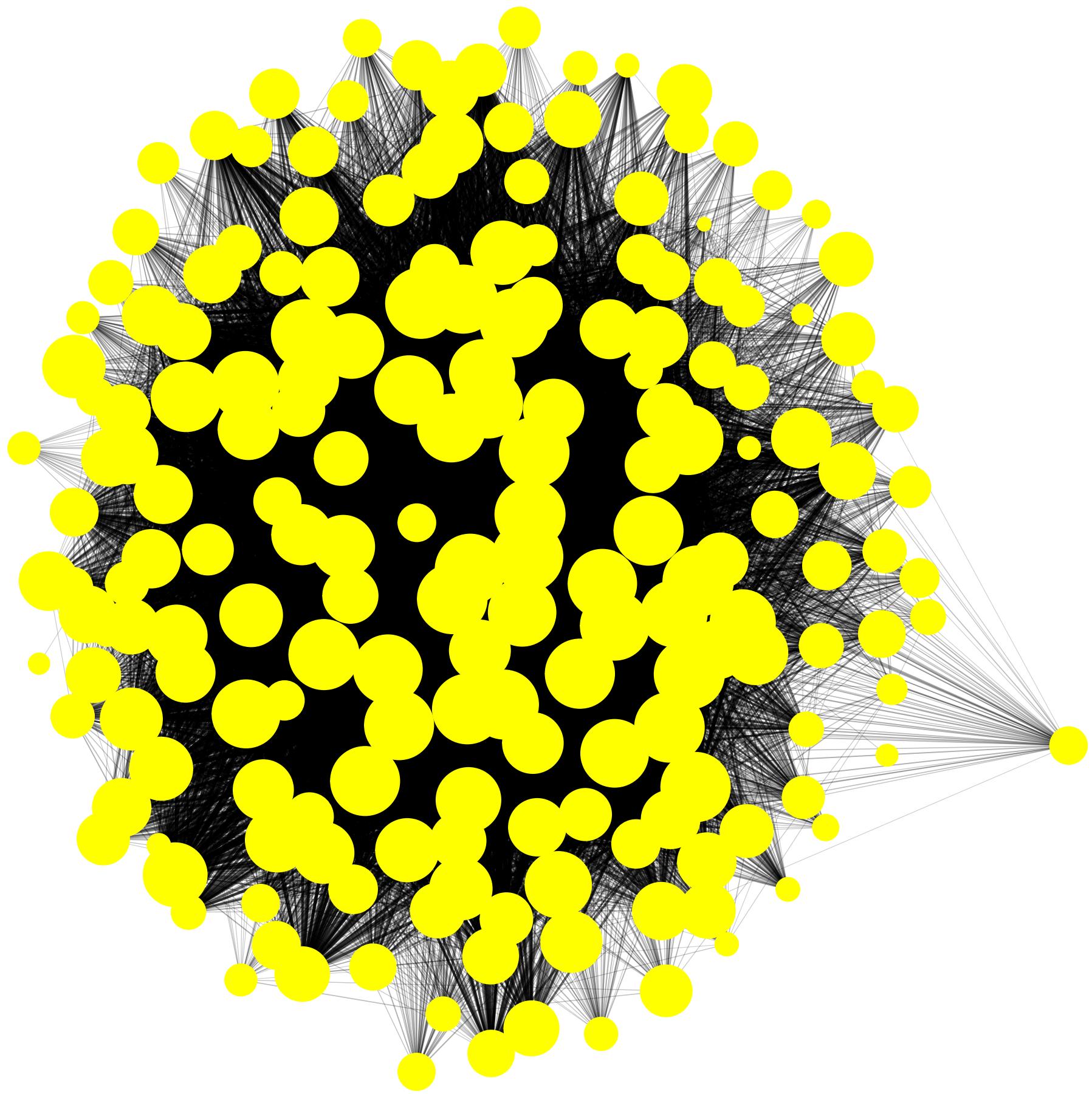
	Term	Ont	N	n	Adj. p-value
GO:0044210	'de novo' CTP biosynthetic process	BP	1	0	1
GO:0034627	'de novo' NAD biosynthetic process	BP	1	0	1
GO:0006207	'de novo' pyrimidine nucleobase biosynthetic process	BP	1	0	1
GO:1902635	1-phosphatidyl-1D-myo-inositol 4,5-bisphosphate biosynthetic process	BP	1	0	1
GO:1902633	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:gga01232</i>	Nucleotide metabolism	77	3	0.007982
<i>path:gga00230</i>	Purine metabolism	113	3	0.02232
<i>path:gga01240</i>	Biosynthesis of cofactors	116	3	0.02389
<i>path:gga00240</i>	Pyrimidine metabolism	55	2	0.03463
<i>path:gga00730</i>	Thiamine metabolism	12	1	0.06209
<i>path:gga00983</i>	Drug metabolism – other enzymes	55	1	0.2549
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.2708
<i>path:gga04621</i>	NOD–like receptor signaling pathway	115	1	0.4603
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	1	0.4803
<i>path:gga04810</i>	Regulation of actin cytoskeleton	182	1	0.6242



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

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



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

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