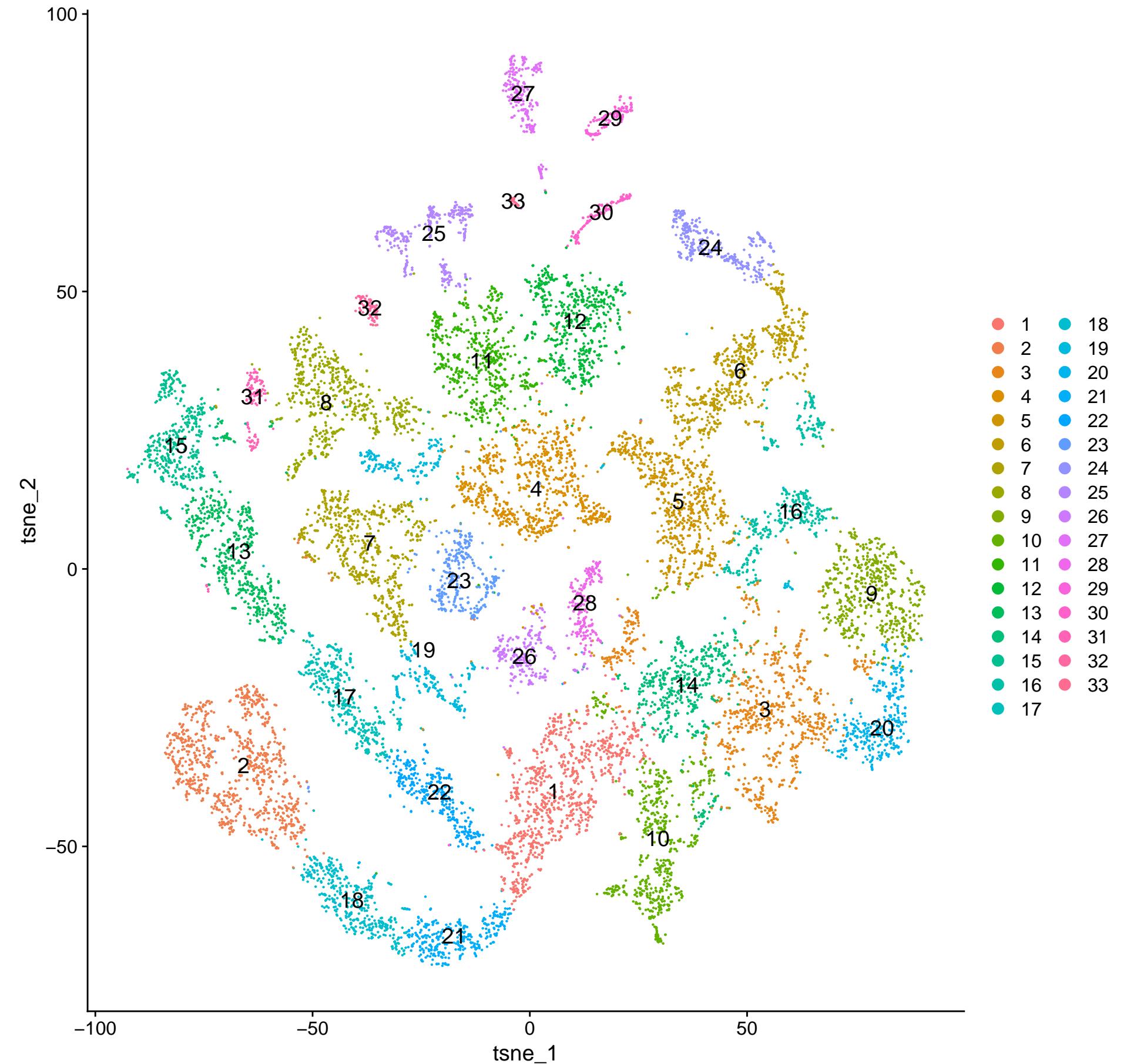
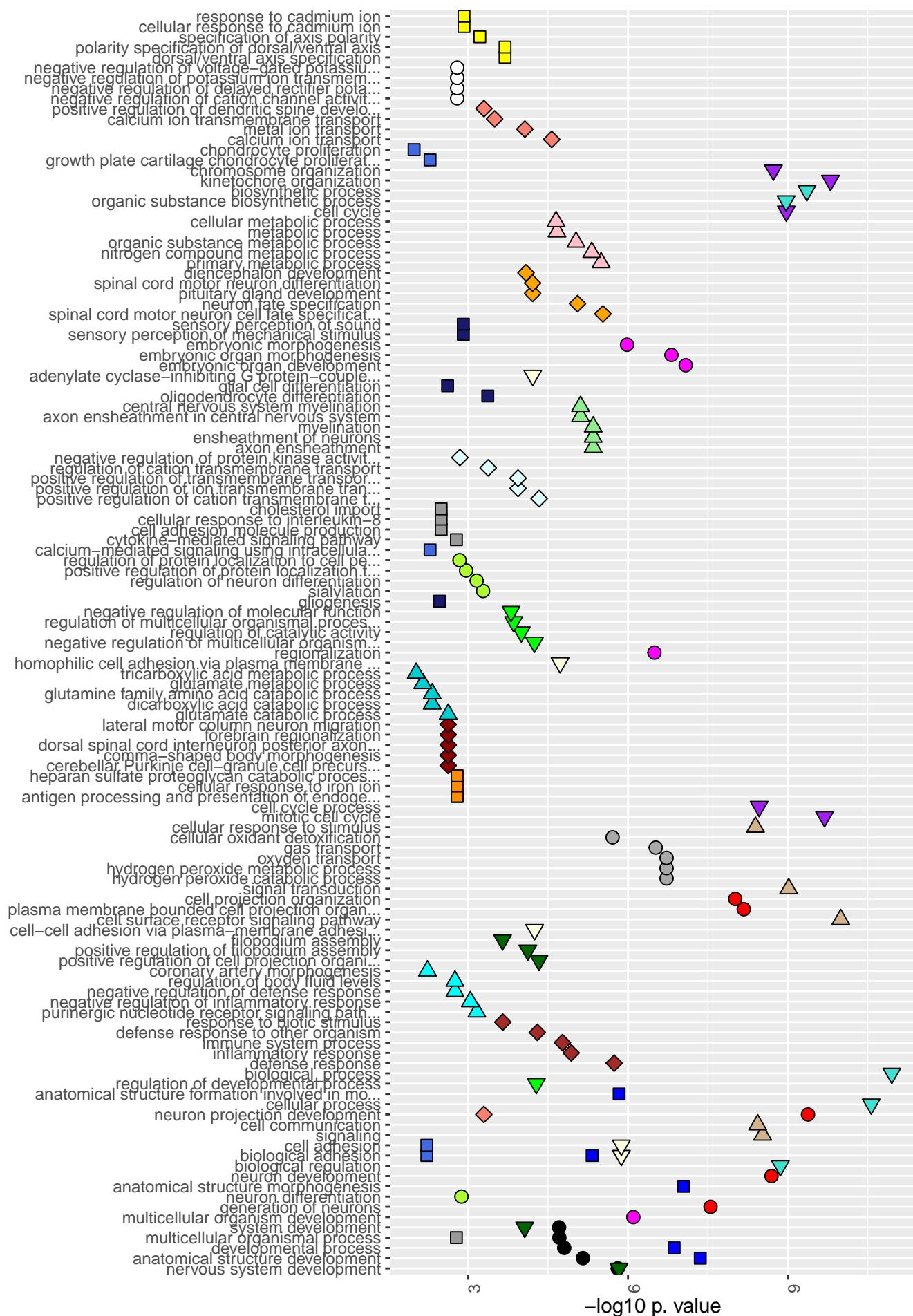
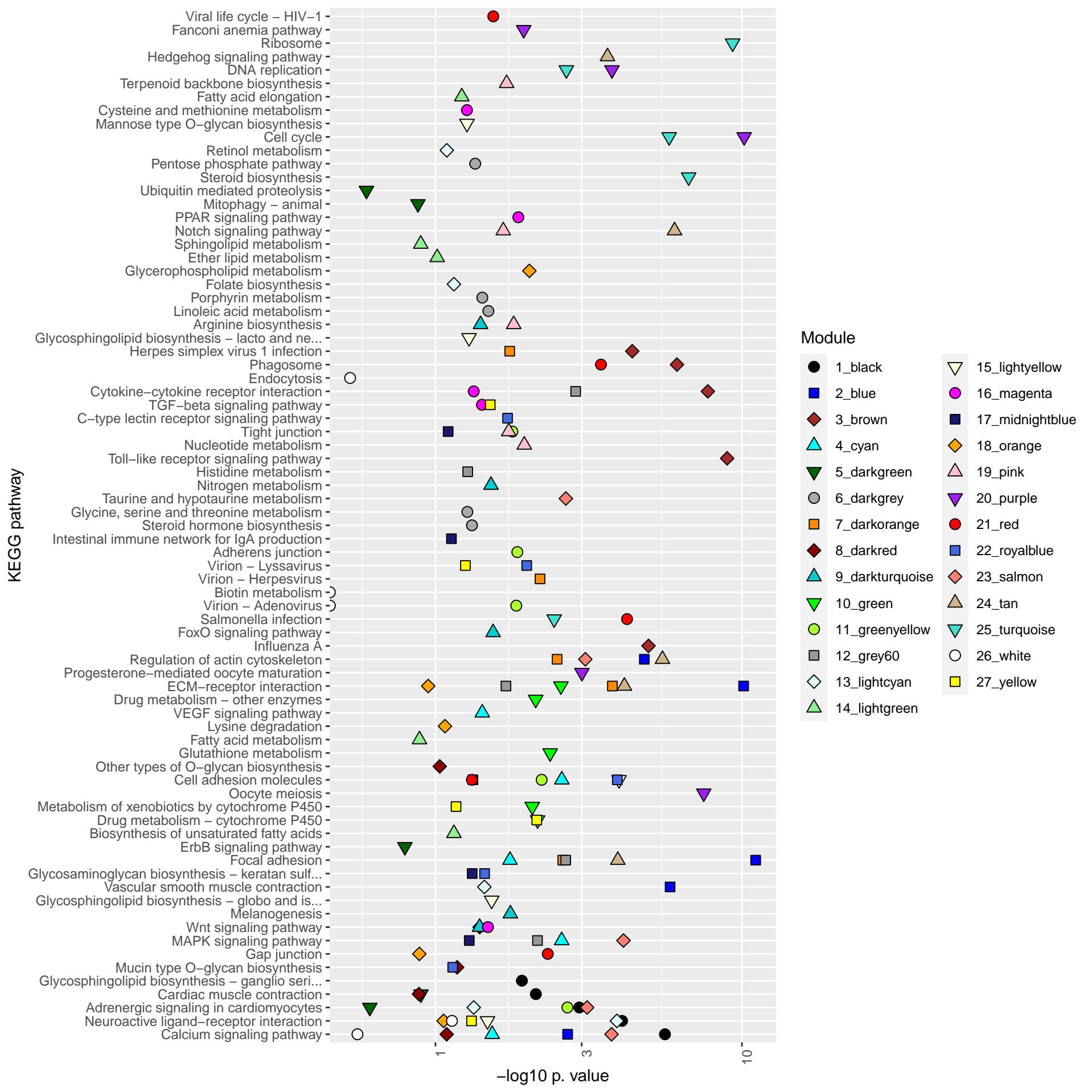


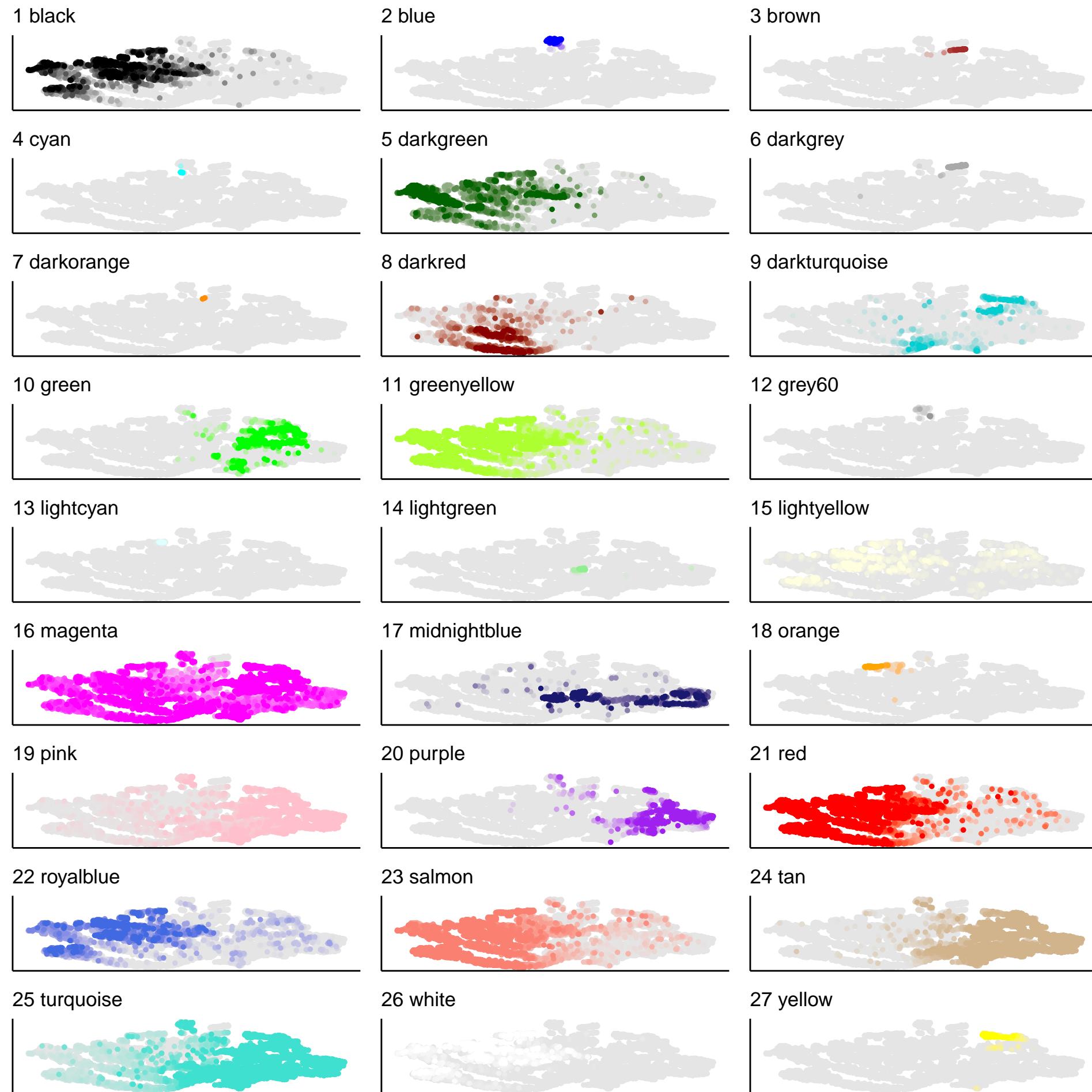
Gg-devel_int scWGCNA modules

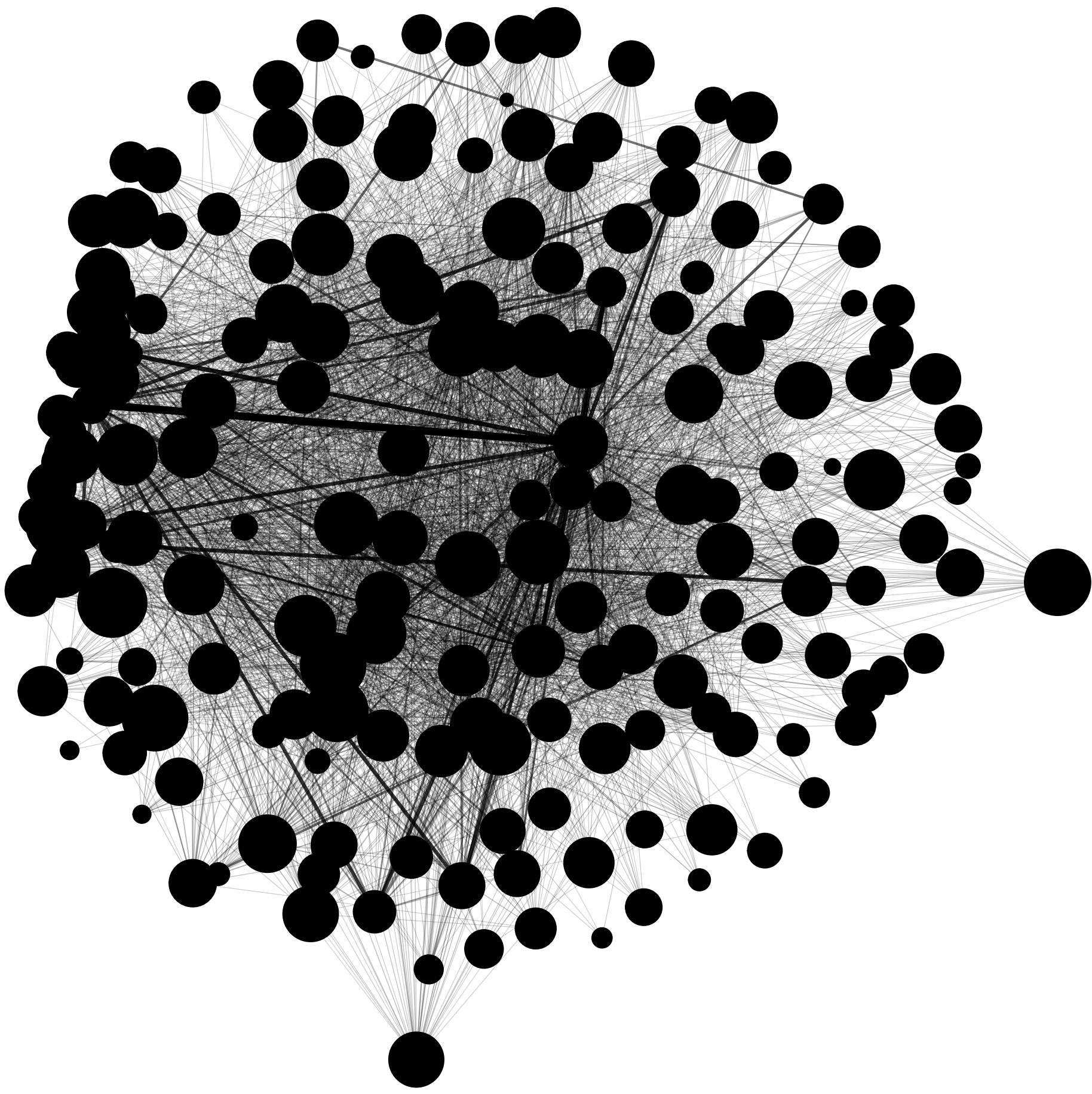




Module



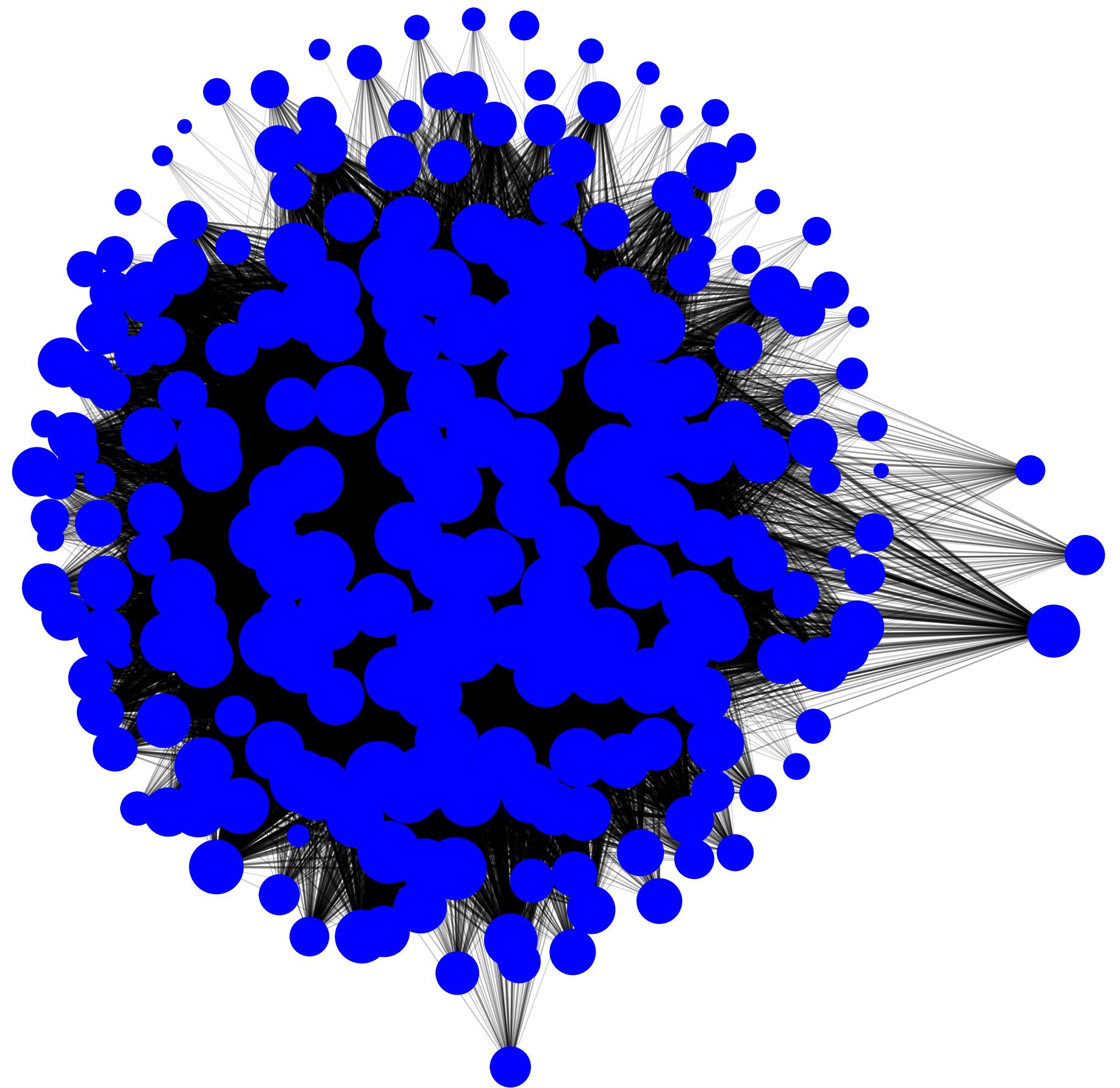




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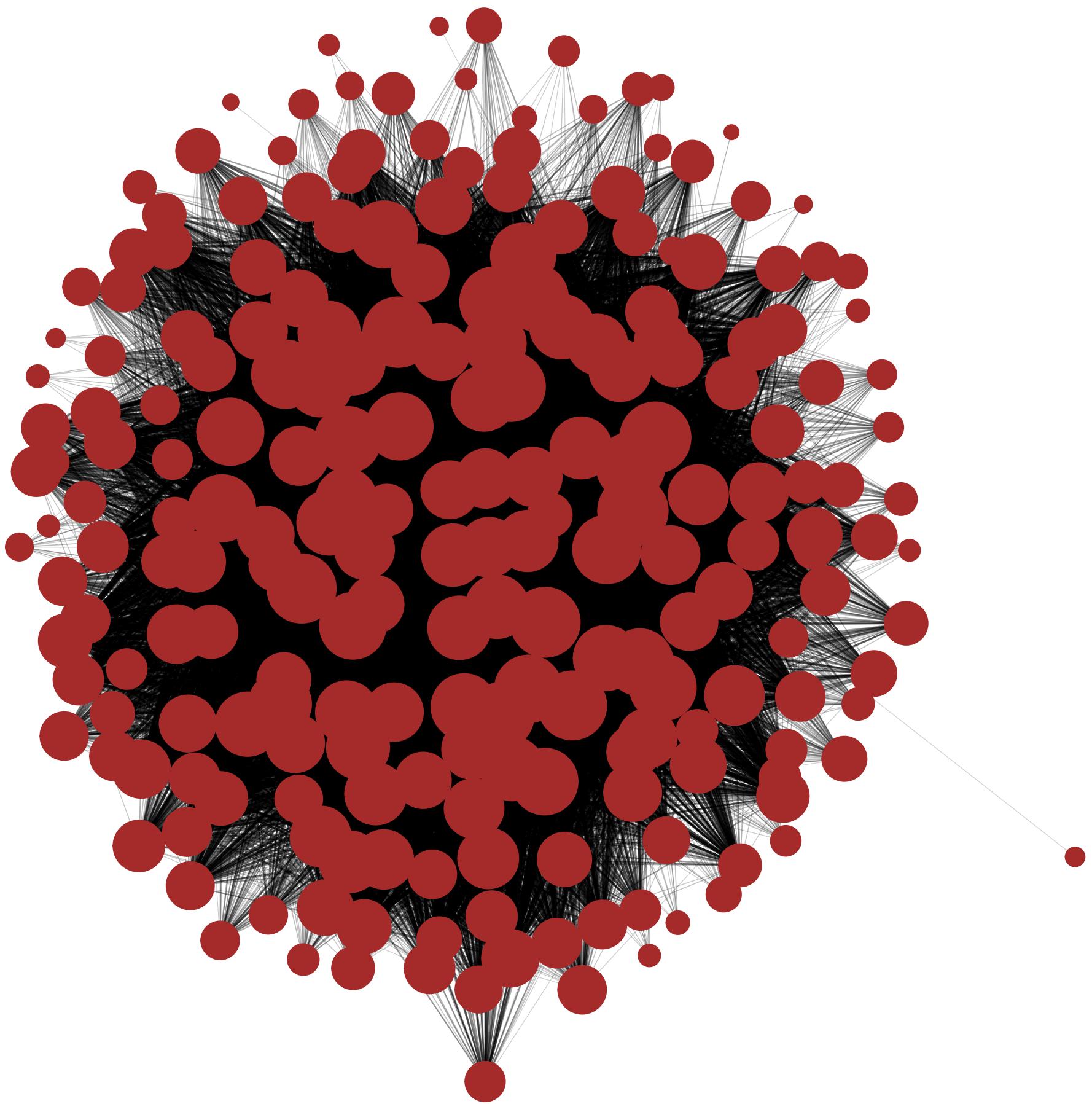
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GO:0007399	nervous system development	BP	258	15	1.553e-06
GO:0048856	anatomical structure development	BP	623	23	7.007e-06
GO:0032502	developmental process	BP	655	23	1.575e-05
GO:0032501	multicellular organismal process	BP	711	24	1.94e-05
GO:0048731	system development	BP	483	19	1.965e-05
GO:0007275	multicellular organism development	BP	577	21	2.248e-05
GO:0048699	generation of neurons	BP	180	11	2.546e-05
GO:0022008	neurogenesis	BP	183	11	2.967e-05
GO:0030182	neuron differentiation	BP	165	9	0.0003294
GO:0009653	anatomical structure morphogenesis	BP	292	12	0.0004805

	Pathway	N	DE	P.DE
<i>path:gga04020</i>	Calcium signaling pathway	201	13	2.464e-06
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	281	13	8.677e-05
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	7	0.001132
<i>path:gga04260</i>	Cardiac muscle contraction	59	4	0.007482
<i>path:gga00604</i>	Glycosphingolipid biosynthesis – ganglio series	13	2	0.01218
<i>path:gga04912</i>	GnRH signaling pathway	76	4	0.01777
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis – heparan sulfate / heparin	21	2	0.03063
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	2	0.05532
<i>path:gga04371</i>	Apelin signaling pathway	111	4	0.05859
<i>path:gga04540</i>	Gap junction	79	3	0.08572



	Term	Ont	N	n	Adj. p-value
GO:0048856	anatomical structure development	BP	623	31	4.403e-08
GO:0009653	anatomical structure morphogenesis	BP	292	20	9.046e-08
GO:0032502	developmental process	BP	655	31	1.36e-07
GO:0048646	anatomical structure formation involved in morphogenesis	BP	128	12	1.468e-06
GO:0022610	biological adhesion	BP	143	12	4.72e-06
GO:0007155	cell adhesion	BP	143	12	4.72e-06
GO:0030154	cell differentiation	BP	417	21	6.465e-06
GO:0032501	multicellular organismal process	BP	711	29	7.074e-06
GO:0048869	cellular developmental process	BP	426	21	8.968e-06
GO:0007275	multicellular organism development	BP	577	25	1.16e-05

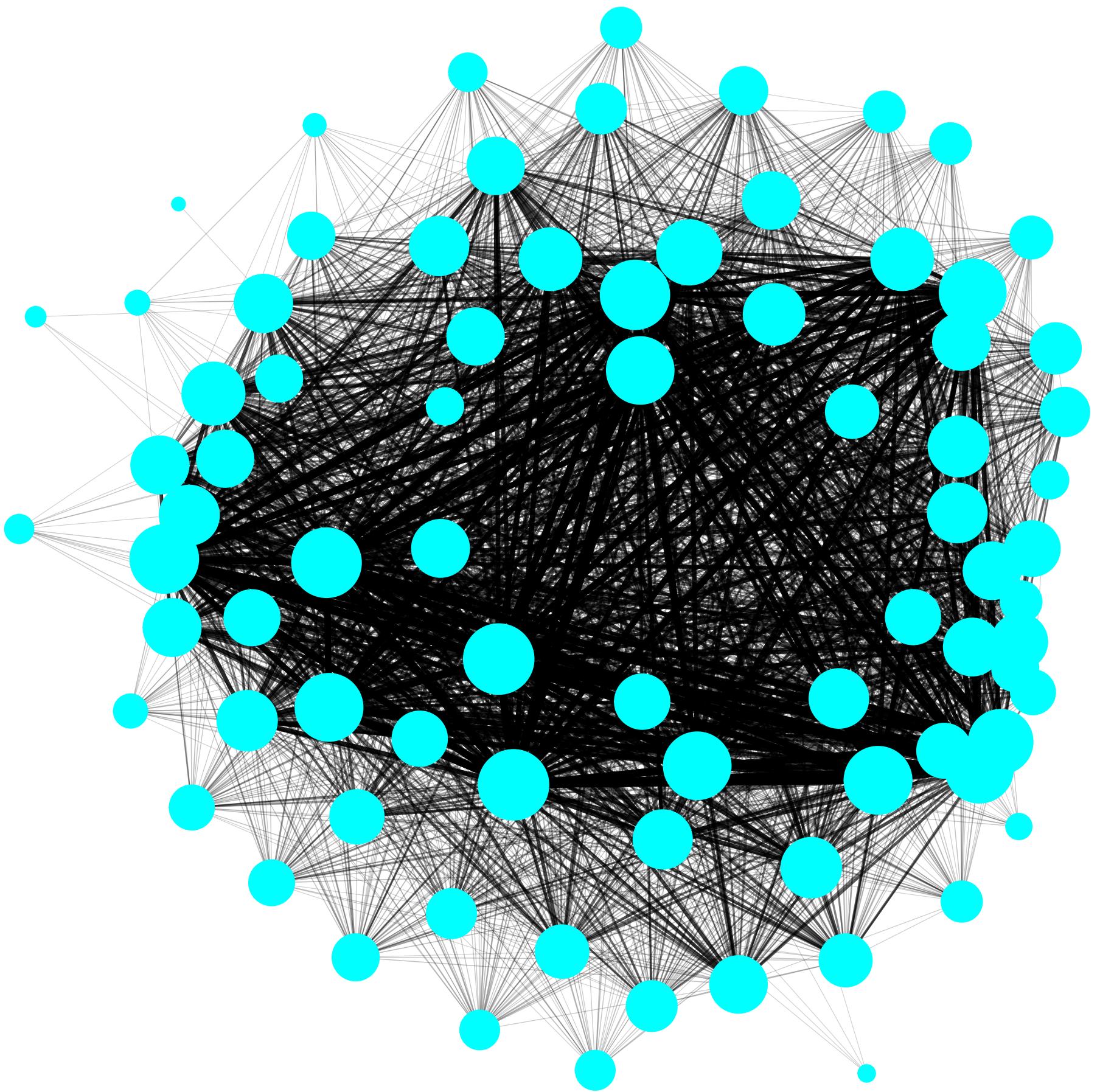
	Pathway	N	DE	P.DE
<i>path:gga04510</i>	Focal adhesion	172	20	8.178e-12
<i>path:gga04512</i>	ECM–receptor interaction	68	13	7.451e-11
<i>path:gga04270</i>	Vascular smooth muscle contraction	106	11	1.482e-06
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	13	1.577e-05
<i>path:gga04020</i>	Calcium signaling pathway	201	10	0.001999
<i>path:gga04520</i>	Adherens junction	69	5	0.005806
<i>path:gga00360</i>	Phenylalanine metabolism	12	2	0.01634
<i>path:gga04010</i>	MAPK signaling pathway	239	9	0.01881
<i>path:gga04514</i>	Cell adhesion molecules	99	5	0.02483
<i>path:gga00310</i>	Lysine degradation	50	3	0.05046



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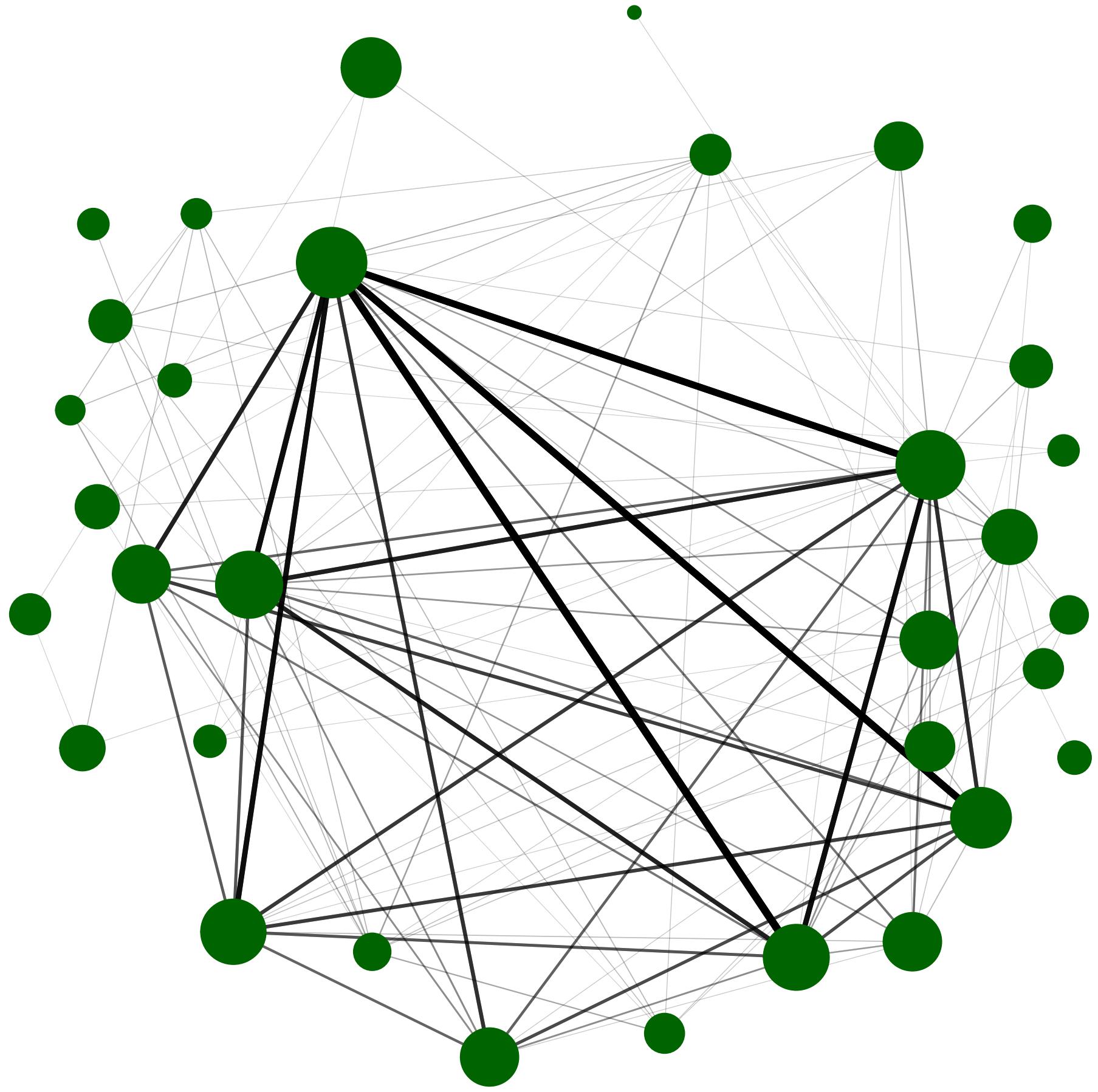
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GO:0006952	defense response	BP	91	10	1.816e–06
GO:0006954	inflammatory response	BP	49	7	1.166e–05
GO:0002376	immune system process	BP	169	12	1.699e–05
GO:0098542	defense response to other organism	BP	61	7	5.037e–05
GO:0009607	response to biotic stimulus	BP	77	7	0.0002239
GO:0043207	response to external biotic stimulus	BP	77	7	0.0002239
GO:0051707	response to other organism	BP	77	7	0.0002239
GO:0044419	biological process involved in interspecies interaction between organisms	BP	88	7	0.0005098
GO:0009605	response to external stimulus	BP	192	10	0.001036
GO:0006950	response to stress	BP	319	13	0.001863

	Pathway	N	DE	P.DE
<i>path:gga04620</i>	Toll-like receptor signaling pathway	71	12	1.126e-09
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	151	15	1.813e-08
<i>path:gga04145</i>	Phagosome	125	12	7.281e-07
<i>path:gga05164</i>	Influenza A	111	10	1.104e-05
<i>path:gga05168</i>	Herpes simplex virus 1 infection	129	10	4.106e-05
<i>path:gga04623</i>	Cytosolic DNA–sensing pathway	42	6	5.018e-05
<i>path:gga04621</i>	NOD–like receptor signaling pathway	116	9	9.923e-05
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	82	7	0.0003309
<i>path:gga04672</i>	Intestinal immune network for IgA production	22	4	0.0003691
<i>path:gga04210</i>	Apoptosis	115	8	0.0005079



	Term	Ont	N	n	Adj. p-value
GO:0035590	purinergic nucleotide receptor signaling pathway	BP	7	2	0.0006861
GO:0050728	negative regulation of inflammatory response	BP	8	2	0.0009113
GO:0031348	negative regulation of defense response	BP	11	2	0.00177
GO:0050878	regulation of body fluid levels	BP	11	2	0.00177
GO:0060982	coronary artery morphogenesis	BP	1	1	0.005808
GO:0001712	ectodermal cell fate commitment	BP	1	1	0.005808
GO:0003094	glomerular filtration	BP	1	1	0.005808
GO:0070254	mucus secretion	BP	1	1	0.005808
GO:1900453	negative regulation of long-term synaptic depression	BP	1	1	0.005808
GO:0070256	negative regulation of mucus secretion	BP	1	1	0.005808

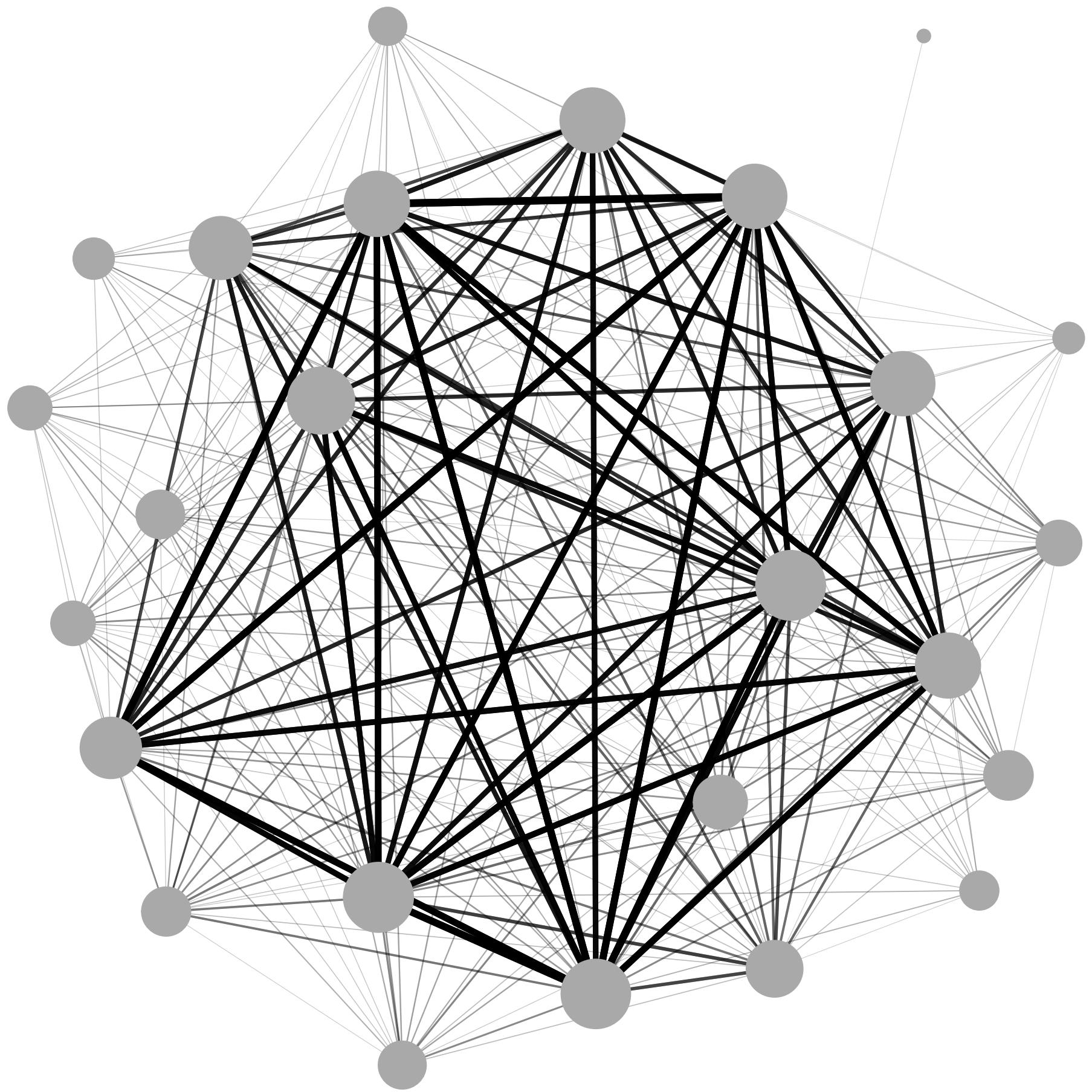
	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	99	4	0.002608
<i>path:gga04010</i>	MAPK signaling pathway	239	6	0.002626
<i>path:gga04510</i>	Focal adhesion	172	4	0.01777
<i>path:gga04020</i>	Calcium signaling pathway	201	4	0.02941
<i>path:gga04370</i>	VEGF signaling pathway	53	2	0.03792
<i>path:gga04520</i>	Adherens junction	69	2	0.06086
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	4	0.08062
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.09434
<i>path:gga04270</i>	Vascular smooth muscle contraction	106	2	0.1262
<i>path:gga04371</i>	Apelin signaling pathway	111	2	0.136



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	Term	Ont	N	n	Adj. p-value
GO:0007399	nervous system development	BP	258	7	1.475e-06
GO:0031346	positive regulation of cell projection organization	BP	31	3	4.681e-05
GO:0051491	positive regulation of filopodium assembly	BP	6	2	7.579e-05
GO:0048731	system development	BP	483	7	8.692e-05
GO:0046847	filopodium assembly	BP	10	2	0.0002261
GO:0051489	regulation of filopodium assembly	BP	10	2	0.0002261
GO:0007275	multicellular organism development	BP	577	7	0.0002622
GO:0120035	regulation of plasma membrane bounded cell projection organization	BP	56	3	0.0002777
GO:0031344	regulation of cell projection organization	BP	57	3	0.0002927
GO:0120034	positive regulation of plasma membrane bounded cell projection assembly	BP	12	2	0.0003306

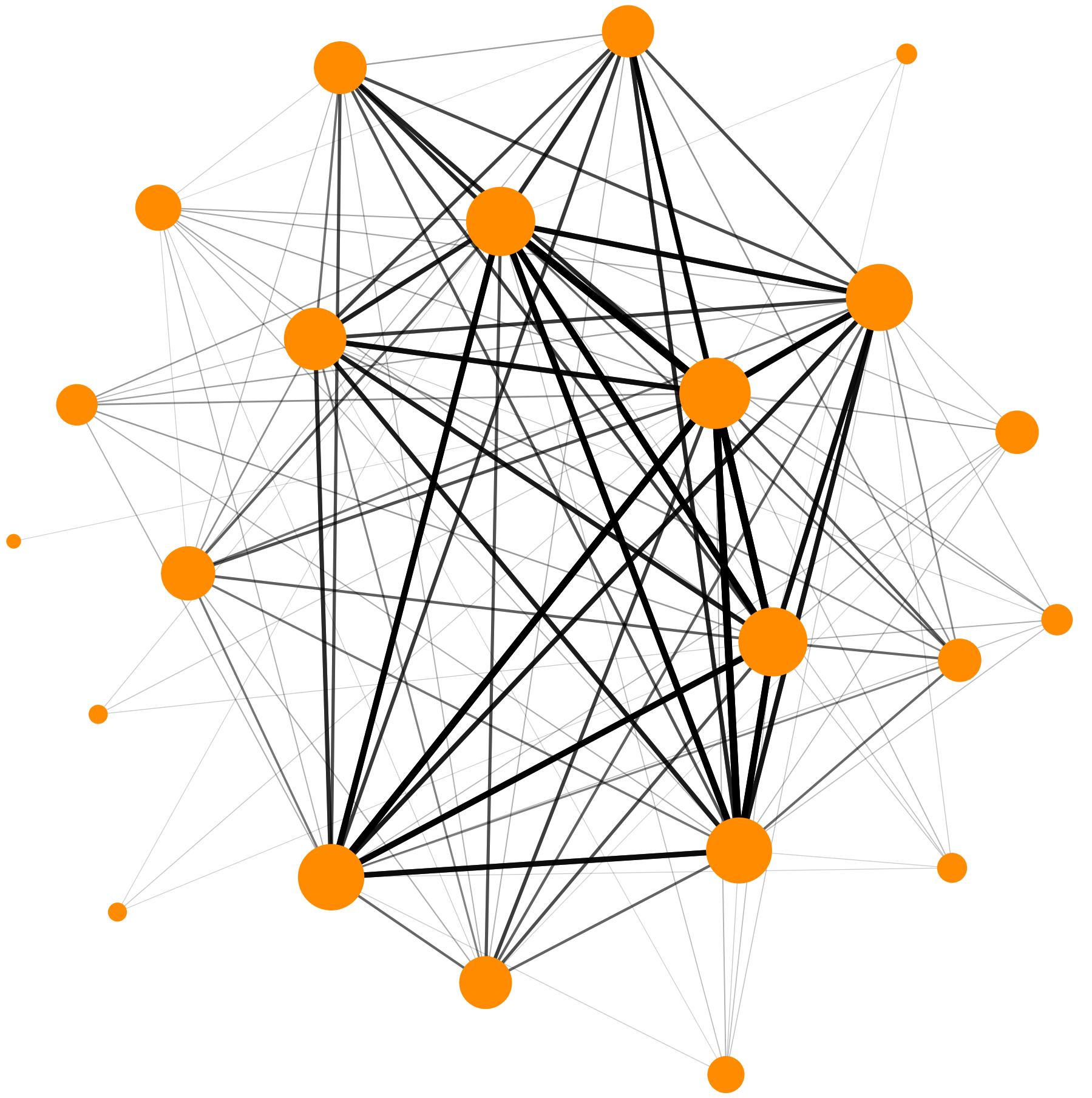
	Pathway	N	DE	P.DE
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.1269
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.1329
<i>path:gga04012</i>	ErbB signaling pathway	76	1	0.1605
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	1	0.2452
<i>path:gga04120</i>	Ubiquitin mediated proteolysis	127	1	0.2539
<i>path:gga04144</i>	Endocytosis	218	1	0.3962
<i>path:gga04010</i>	MAPK signaling pathway	239	1	0.4251
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	1	0.479
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1



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	Term	Ont	N	n	Adj. p-value
GO:0042744	hydrogen peroxide catabolic process	BP	7	3	1.888e-07
GO:0042743	hydrogen peroxide metabolic process	BP	7	3	1.888e-07
GO:0015671	oxygen transport	BP	7	3	1.888e-07
GO:0015669	gas transport	BP	8	3	3.018e-07
GO:0098869	cellular oxidant detoxification	BP	14	3	1.948e-06
GO:1990748	cellular detoxification	BP	16	3	2.989e-06
GO:0097237	cellular response to toxic substance	BP	16	3	2.989e-06
GO:0098754	detoxification	BP	17	3	3.625e-06
GO:0072593	reactive oxygen species metabolic process	BP	18	3	4.345e-06
GO:0009636	response to toxic substance	BP	20	3	6.056e-06

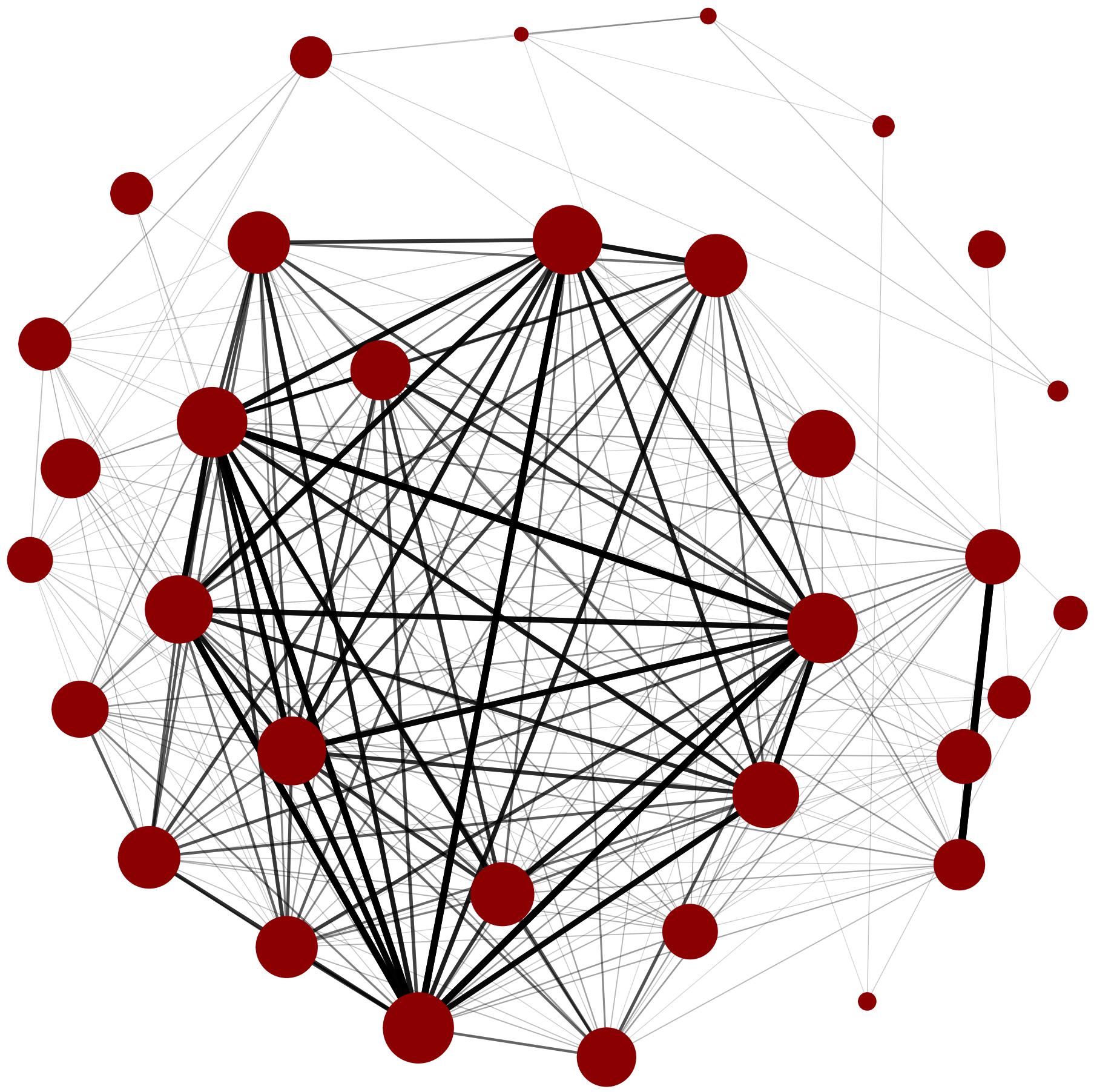
	Pathway	N	DE	P.DE
<i>path:gga00591</i>	Linoleic acid metabolism	18	1	0.03253
<i>path:gga00860</i>	Porphyrin metabolism	21	1	0.03785
<i>path:gga00030</i>	Pentose phosphate pathway	25	1	0.0449
<i>path:gga00140</i>	Steroid hormone biosynthesis	27	1	0.04841
<i>path:gga00260</i>	Glycine, serine and threonine metabolism	30	1	0.05364
<i>path:gga00830</i>	Retinol metabolism	30	1	0.05364
<i>path:gga00051</i>	Fructose and mannose metabolism	34	1	0.06058
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	46	1	0.08112
<i>path:gga04540</i>	Gap junction	79	1	0.1354
<i>path:gga01200</i>	Carbon metabolism	95	1	0.1606



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	Term	Ont	N	n	Adj. p-value
GO:0019883	antigen processing and presentation of endogenous antigen	BP	1	1	0.001605
GO:0002483	antigen processing and presentation of endogenous peptide antigen	BP	1	1	0.001605
GO:0019885	antigen processing and presentation of endogenous peptide antigen via MHC class I	BP	1	1	0.001605
GO:0071281	cellular response to iron ion	BP	1	1	0.001605
GO:0030200	heparan sulfate proteoglycan catabolic process	BP	1	1	0.001605
GO:2000978	negative regulation of forebrain neuron differentiation	BP	1	1	0.001605
GO:1900121	negative regulation of receptor binding	BP	1	1	0.001605
GO:0071800	podosome assembly	BP	1	1	0.001605
GO:0090343	positive regulation of cell aging	BP	1	1	0.001605
GO:2000774	positive regulation of cellular senescence	BP	1	1	0.001605

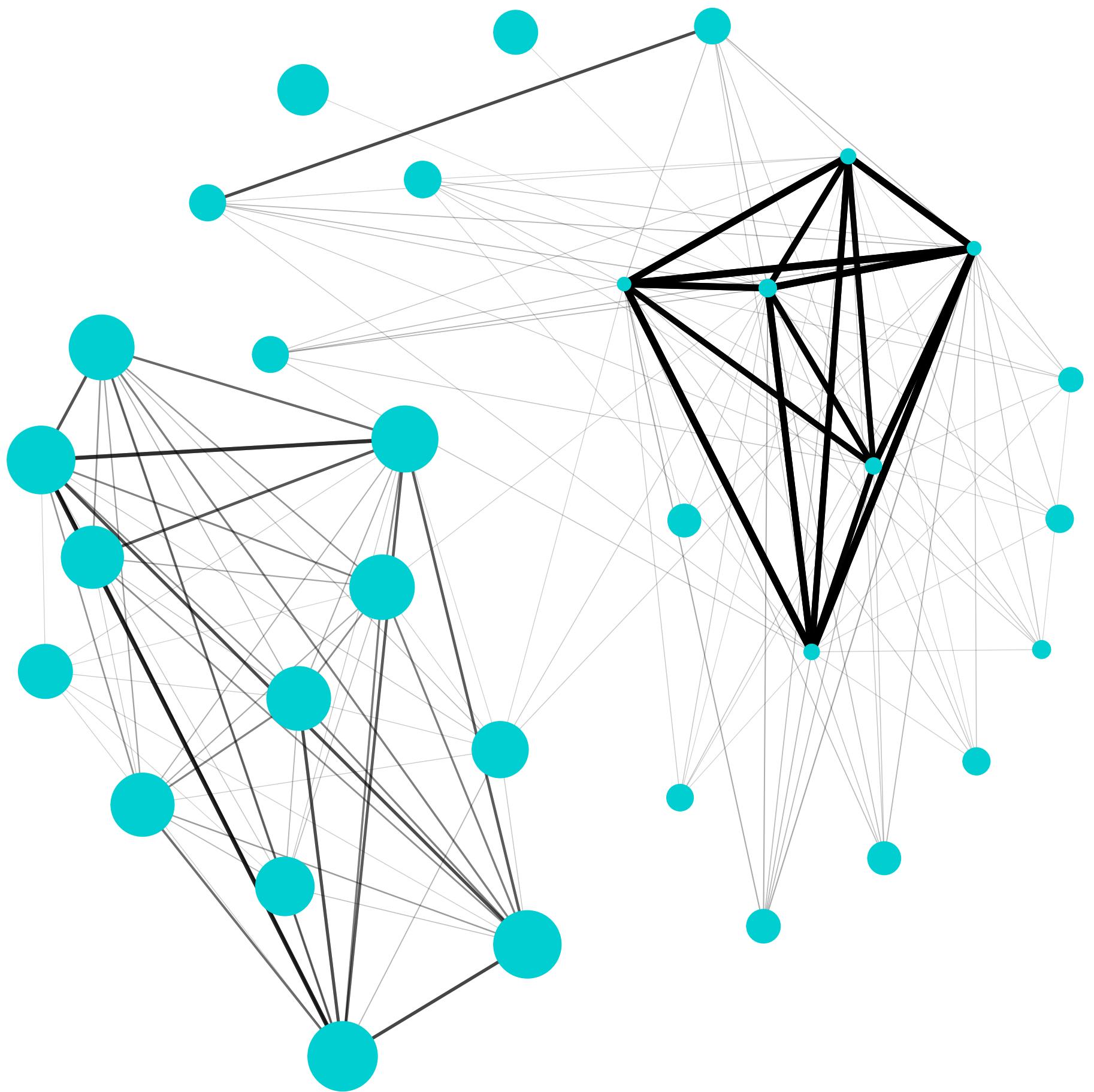
	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	68	3	0.000167
<i>path:gga04510</i>	Focal adhesion	172	3	0.002494
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	3	0.003208
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.006405
<i>path:gga05168</i>	Herpes simplex virus 1 infection	129	2	0.01792
<i>path:gga00531</i>	Glycosaminoglycan degradation	15	1	0.02382
<i>path:gga04130</i>	SNARE interactions in vesicular transport	28	1	0.04402
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.0906
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	1	0.1787
<i>path:gga04145</i>	Phagosome	125	1	0.1827



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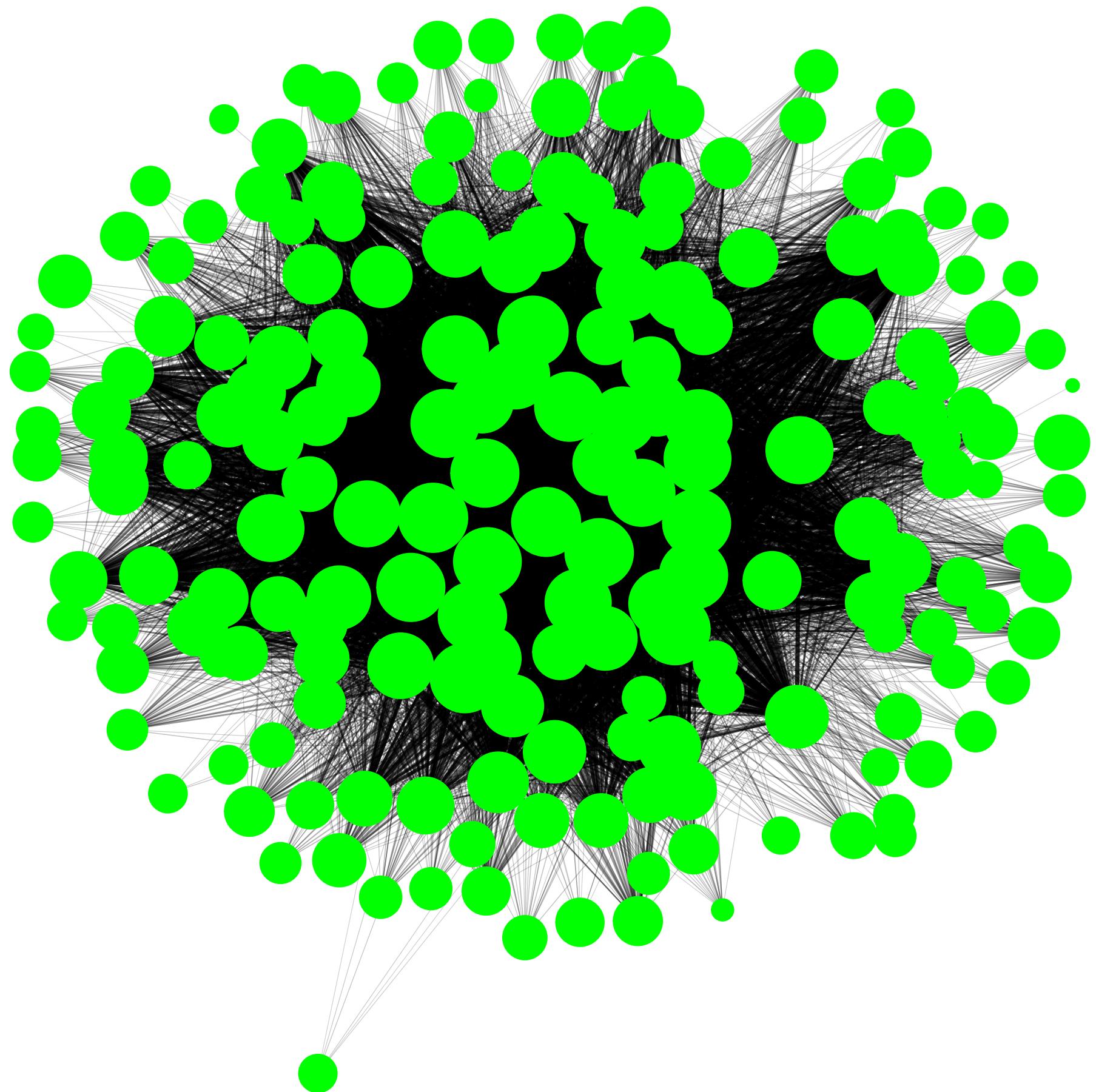
Term	Ont	N	n
cerebellar Purkinje cell–granule cell precursor cell signaling involved in regulation of granule cell precursor cell proliferation	BP	1	1
comma-shaped body morphogenesis	BP	1	1
dorsal spinal cord interneuron posterior axon guidance	BP	1	1
forebrain regionalization	BP	1	1
lateral motor column neuron migration	BP	1	1
motor neuron migration	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
positive regulation of nephron tubule epithelial cell differentiation	BP	1	1
presynaptic membrane organization	BP	1	1

	Pathway	N	DE	P.DE
<i>path:gga04310</i>	Wnt signaling pathway	135	2	0.04043
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	1	0.06654
<i>path:gga04020</i>	Calcium signaling pathway	201	2	0.08167
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	1	0.09281
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.1309
<i>path:gga04514</i>	Cell adhesion molecules	99	1	0.21
<i>path:gga04371</i>	Apelin signaling pathway	111	1	0.2323
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	1	0.2523
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	1	0.3618
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	281	1	0.4902



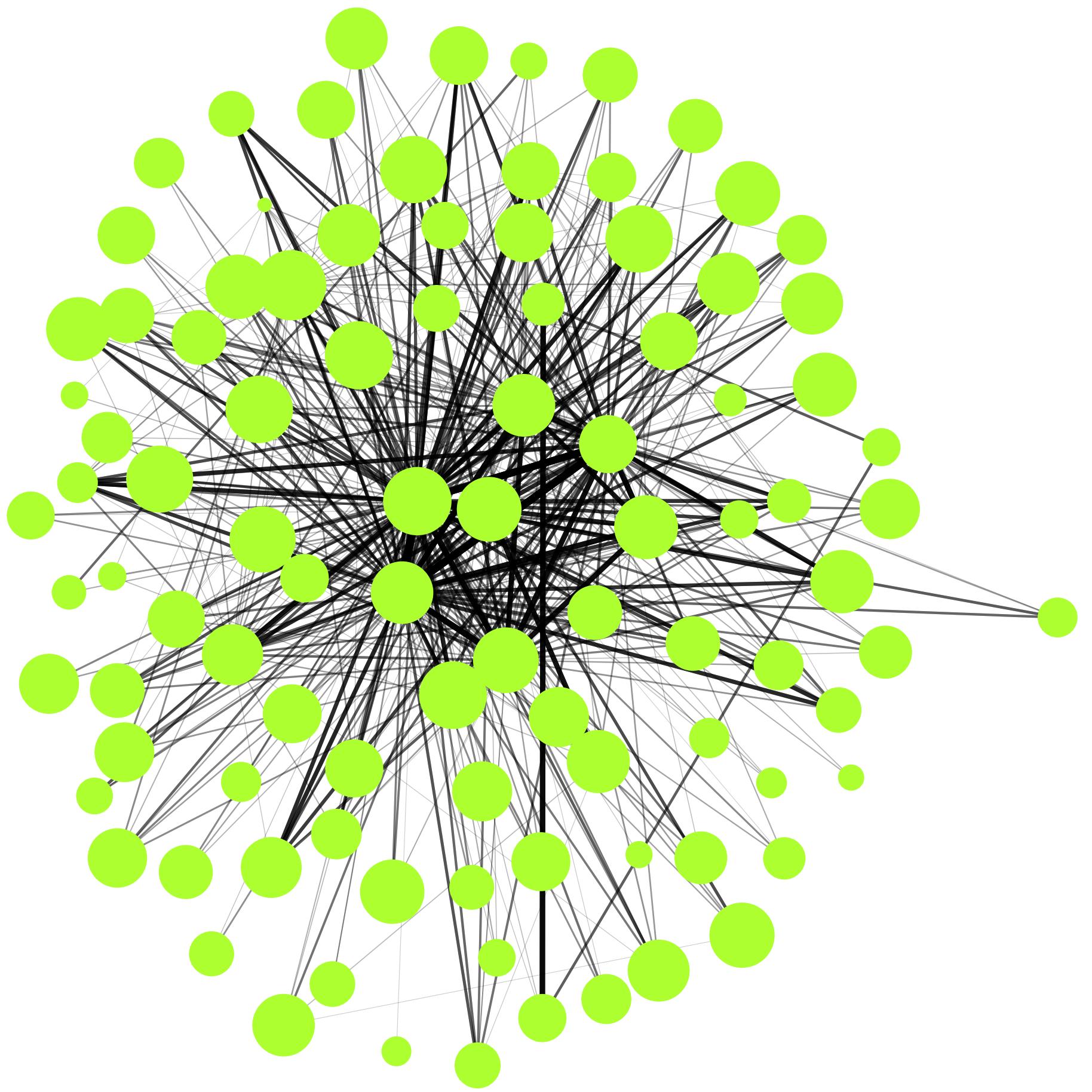
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GO:0006538	glutamate catabolic process	BP	1	1	0.002369
GO:0043649	dicarboxylic acid catabolic process	BP	2	1	0.004733
GO:0009065	glutamine family amino acid catabolic process	BP	2	1	0.004733
GO:0006536	glutamate metabolic process	BP	3	1	0.007091
GO:0072350	tricarboxylic acid metabolic process	BP	4	1	0.009444
GO:0048263	determination of dorsal identity	BP	5	1	0.01179
GO:0048262	determination of dorsal/ventral asymmetry	BP	5	1	0.01179
GO:0043648	dicarboxylic acid metabolic process	BP	5	1	0.01179
GO:1901606	alpha–amino acid catabolic process	BP	6	1	0.01413
GO:0006541	glutamine metabolic process	BP	6	1	0.01413

	Pathway	N	DE	P.DE
<i>path:gga04916</i>	Melanogenesis	86	2	0.01755
<i>path:gga04068</i>	FoxO signaling pathway	112	2	0.02873
<i>path:gga00910</i>	Nitrogen metabolism	13	1	0.03038
<i>path:gga00220</i>	Arginine biosynthesis	17	1	0.03954
<i>path:gga04310</i>	Wnt signaling pathway	135	2	0.04043
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	1	0.07318
<i>path:gga00565</i>	Ether lipid metabolism	36	1	0.08195
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.1163
<i>path:gga04115</i>	p53 signaling pathway	62	1	0.1371
<i>path:gga00562</i>	Inositol phosphate metabolism	66	1	0.1452



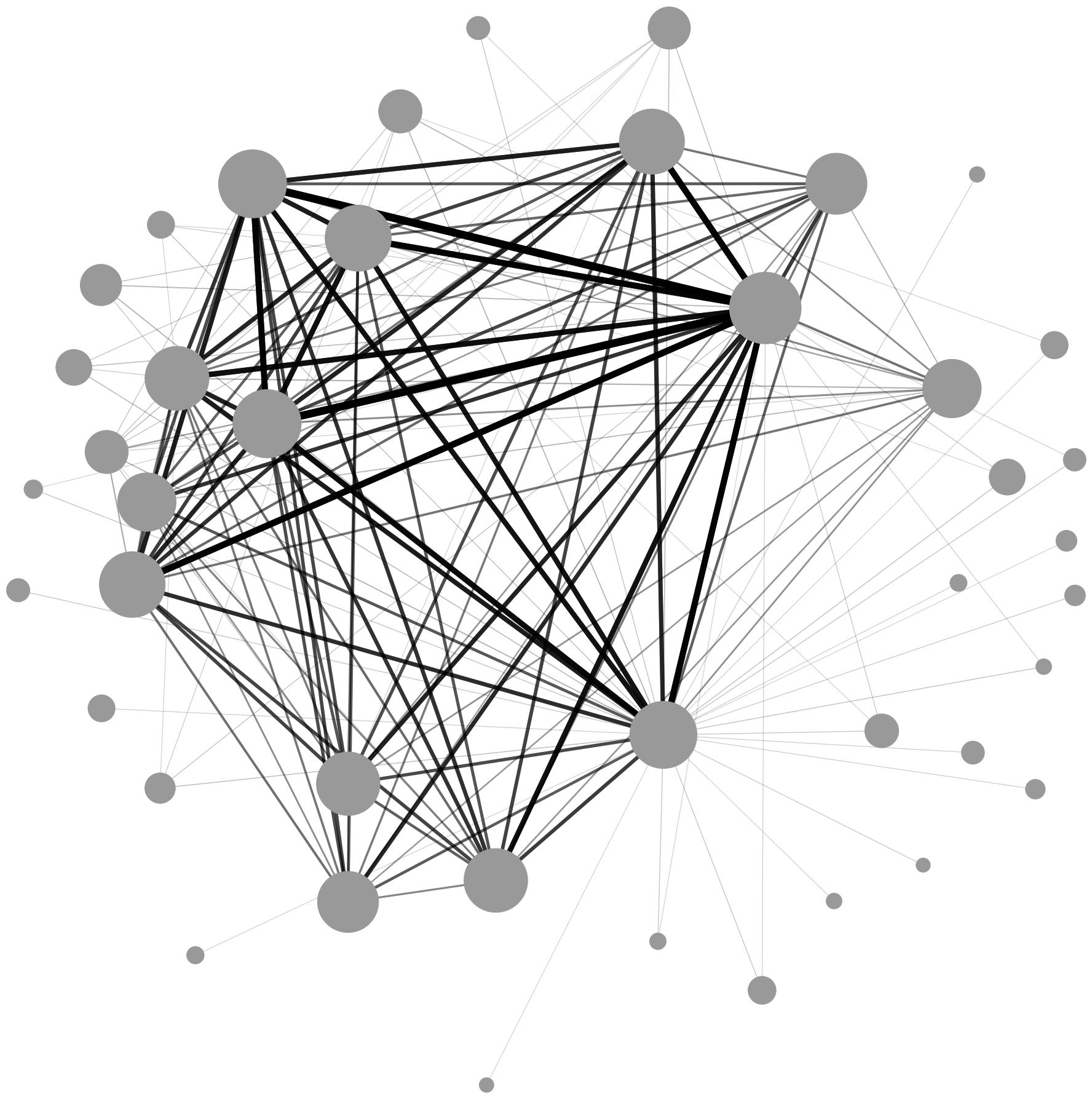
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GO:0050793	regulation of developmental process	BP	214	12	5.249e-05
GO:0051241	negative regulation of multicellular organismal process	BP	70	7	5.7e-05
GO:0050790	regulation of catalytic activity	BP	229	12	0.0001006
GO:0051239	regulation of multicellular organismal process	BP	202	11	0.0001401
GO:0044092	negative regulation of molecular function	BP	82	7	0.0001568
GO:0048731	system development	BP	483	18	0.0001695
GO:0048513	animal organ development	BP	321	14	0.0001887
GO:0045597	positive regulation of cell differentiation	BP	85	7	0.0001964
GO:0006928	movement of cell or subcellular component	BP	178	10	0.0002192
GO:0071621	granulocyte chemotaxis	BP	9	3	0.0002194

	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	68	5	0.002716
<i>path:gga00480</i>	Glutathione metabolism	47	4	0.004294
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	28	3	0.007024
<i>path:gga00983</i>	Drug metabolism – other enzymes	55	4	0.007525
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	30	3	0.008527
<i>path:gga00760</i>	Nicotinate and nicotinamide metabolism	32	3	0.01021
<i>path:gga00330</i>	Arginine and proline metabolism	39	3	0.0175
<i>path:gga00532</i>	Glycosaminoglycan biosynthesis – chondroitin sulfate / dermatan sulfate	17	2	0.02352
<i>path:gga04540</i>	Gap junction	79	4	0.02557
<i>path:gga04510</i>	Focal adhesion	172	6	0.03544



	Term	Ont	N	n	Adj. p-value
GO:0097503	sialylation	BP	5	2	0.0005251
GO:0045664	regulation of neuron differentiation	BP	24	3	0.0006926
GO:1904377	positive regulation of protein localization to cell periphery	BP	7	2	0.001092
GO:0030182	neuron differentiation	BP	165	6	0.001335
GO:1904375	regulation of protein localization to cell periphery	BP	8	2	0.001449
GO:0048699	generation of neurons	BP	180	6	0.002078
GO:0022008	neurogenesis	BP	183	6	0.002258
GO:1903829	positive regulation of cellular protein localization	BP	15	2	0.005256
GO:0007204	positive regulation of cytosolic calcium ion concentration	BP	15	2	0.005256
GO:0099173	postsynapse organization	BP	16	2	0.005978

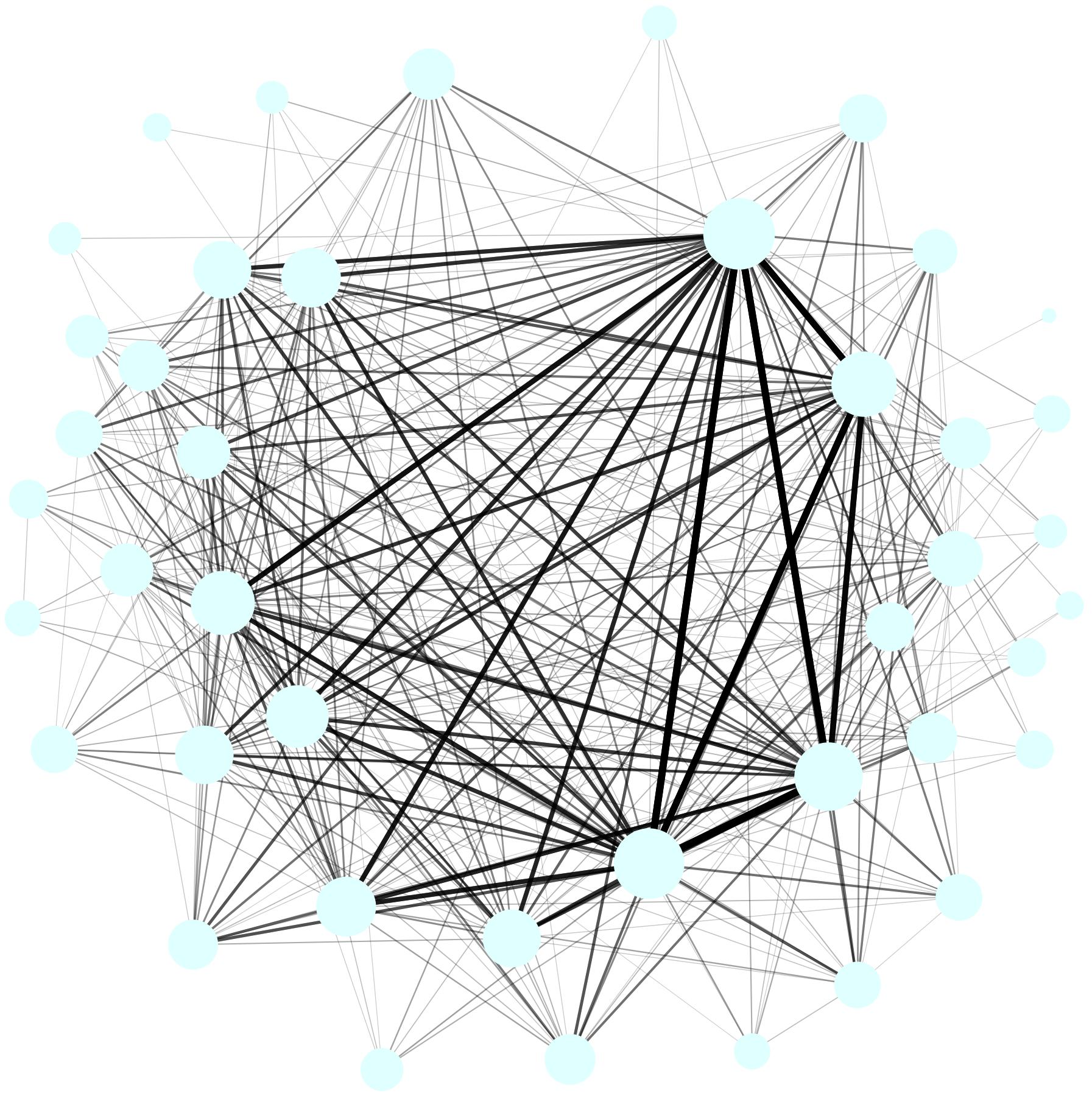
	Pathway	N	DE	P.DE
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	5	0.002018
<i>path:gga04514</i>	Cell adhesion molecules	99	4	0.00602
<i>path:gga04520</i>	Adherens junction	69	3	0.01414
<i>path:gga03267</i>	Virion – Adenovirus	2	1	0.01462
<i>path:gga04530</i>	Tight junction	133	4	0.01651
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.02903
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	2	0.03629
<i>path:gga00510</i>	N-Glycan biosynthesis	45	2	0.043
<i>path:gga04260</i>	Cardiac muscle contraction	59	2	0.06962
<i>path:gga00601</i>	Glycosphingolipid biosynthesis – lacto and neolacto series	21	1	0.1434



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	Term	Ont	N	n	Adj. p-value
GO:0019221	cytokine-mediated signaling pathway	BP	19	2	0.001661
GO:0032501	multicellular organismal process	BP	711	8	0.001664
GO:0060352	cell adhesion molecule production	BP	1	1	0.00321
GO:0098759	cellular response to interleukin-8	BP	1	1	0.00321
GO:0070508	cholesterol import	BP	1	1	0.00321
GO:0034113	heterotypic cell–cell adhesion	BP	1	1	0.00321
GO:0034380	high-density lipoprotein particle assembly	BP	1	1	0.00321
GO:0060354	negative regulation of cell adhesion molecule production	BP	1	1	0.00321
GO:0034115	negative regulation of heterotypic cell–cell adhesion	BP	1	1	0.00321
GO:0032691	negative regulation of interleukin-1 beta production	BP	1	1	0.00321

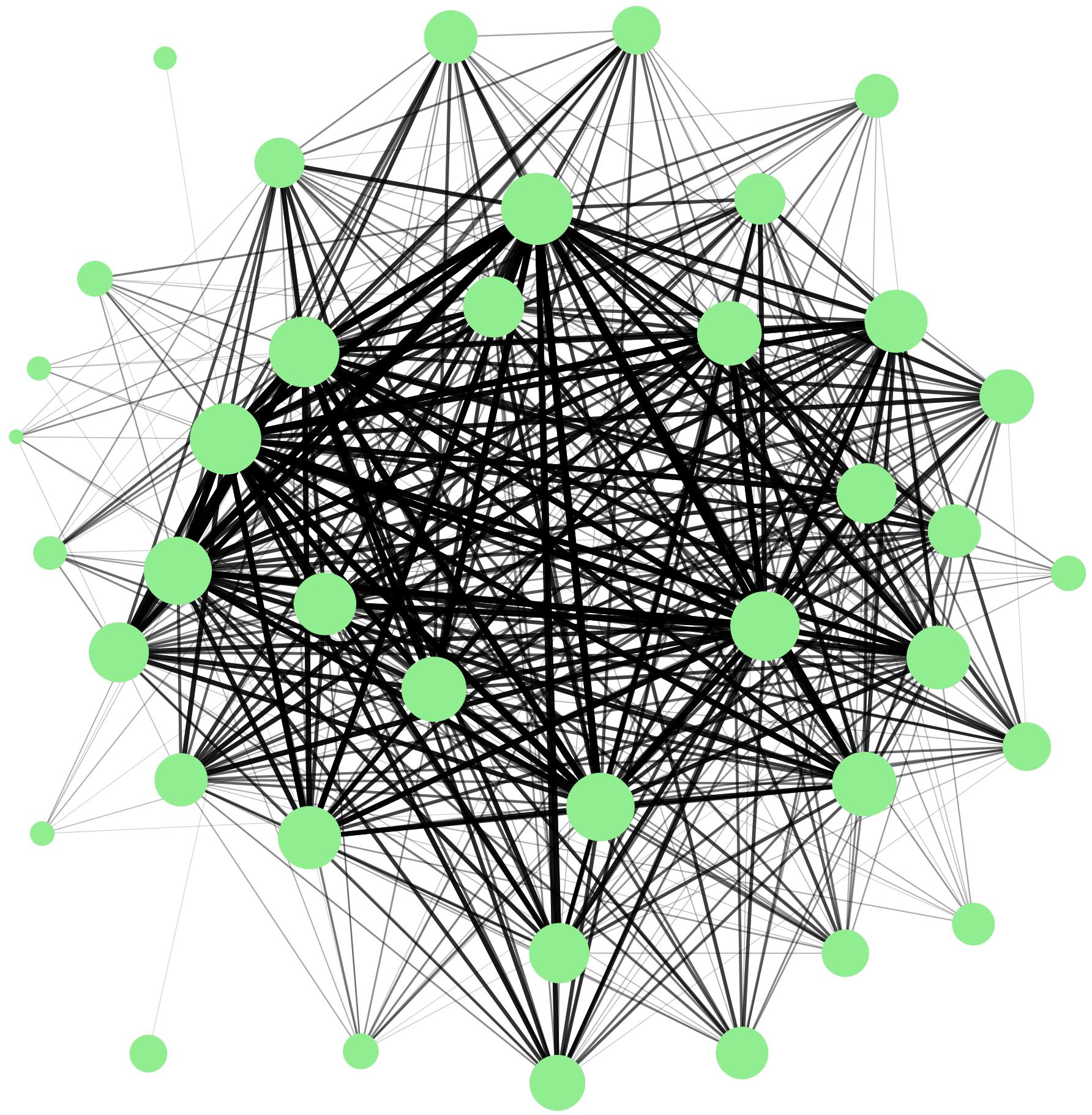
	Pathway	N	DE	P.DE
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	151	4	0.001357
<i>path:gga04510</i>	Focal adhesion	172	4	0.002186
<i>path:gga04010</i>	MAPK signaling pathway	239	4	0.007052
<i>path:gga04512</i>	ECM–receptor interaction	68	2	0.02004
<i>path:gga00340</i>	Histidine metabolism	17	1	0.05322
<i>path:gga04672</i>	Intestinal immune network for IgA production	22	1	0.06834
<i>path:gga04020</i>	Calcium signaling pathway	201	2	0.1358
<i>path:gga00561</i>	Glycerolipid metabolism	53	1	0.157
<i>path:gga00240</i>	Pyrimidine metabolism	54	1	0.1597
<i>path:gga00983</i>	Drug metabolism – other enzymes	55	1	0.1624



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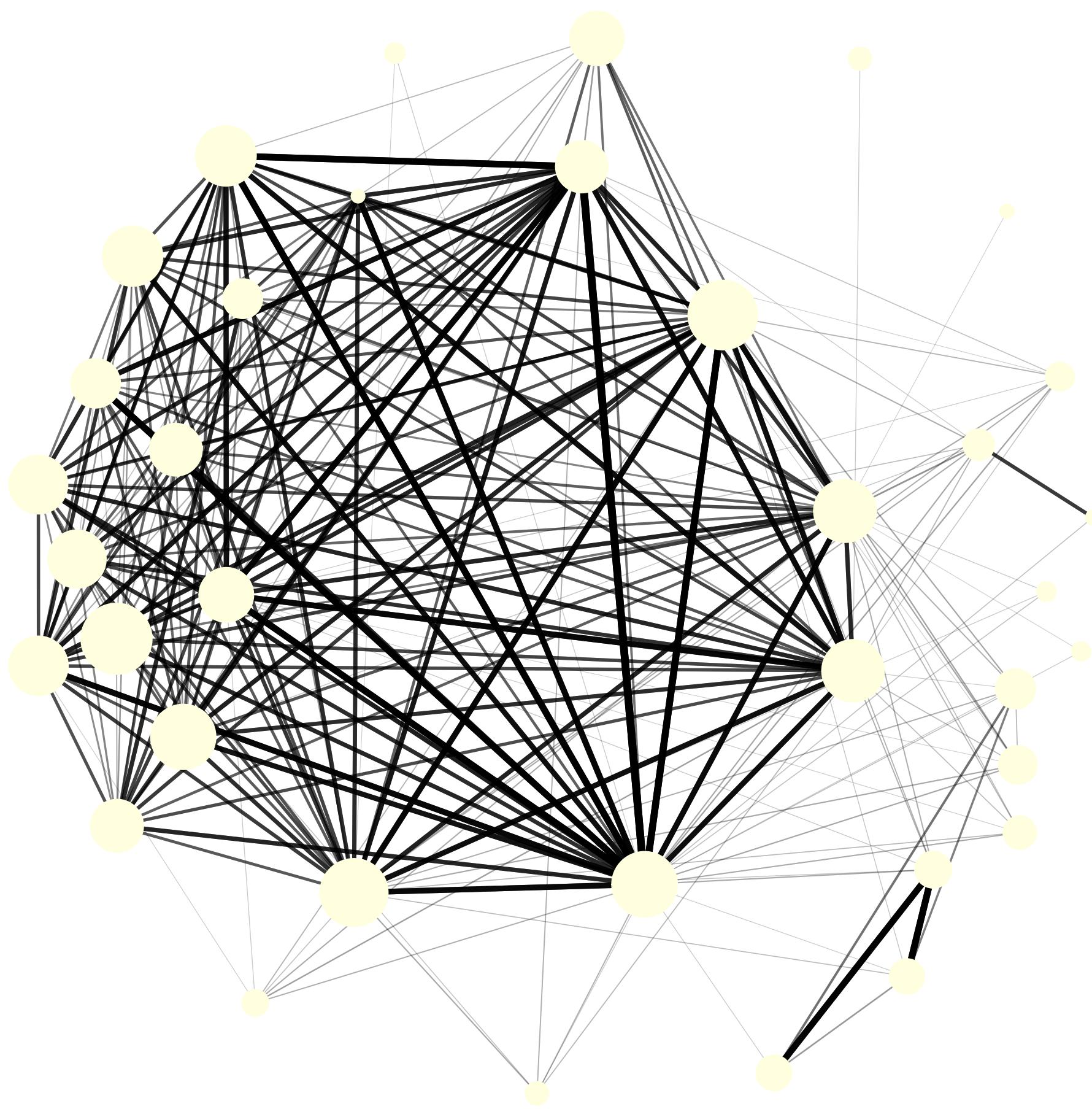
	Term	Ont	N	n	Adj. p-value
GO:1904064	positive regulation of cation transmembrane transport	BP	4	2	4.651e-05
GO:0034767	positive regulation of ion transmembrane transport	BP	6	2	0.0001159
GO:0034764	positive regulation of transmembrane transport	BP	6	2	0.0001159
GO:1904062	regulation of cation transmembrane transport	BP	11	2	0.0004211
GO:0006469	negative regulation of protein kinase activity	BP	20	2	0.001432
GO:0033673	negative regulation of kinase activity	BP	21	2	0.001579
GO:0051348	negative regulation of transferase activity	BP	24	2	0.002065
GO:0001933	negative regulation of protein phosphorylation	BP	26	2	0.002423
GO:0034765	regulation of ion transmembrane transport	BP	28	2	0.002808
GO:0030854	positive regulation of granulocyte differentiation	BP	1	1	0.002828

	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	6	0.0001235
<i>path:gga04270</i>	Vascular smooth muscle contraction	106	2	0.03602
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	2	0.04645
<i>path:gga00790</i>	Folate biosynthesis	26	1	0.07104
<i>path:gga00830</i>	Retinol metabolism	30	1	0.08153
<i>path:gga00380</i>	Tryptophan metabolism	33	1	0.08932
<i>path:gga04020</i>	Calcium signaling pathway	201	2	0.1103
<i>path:gga04920</i>	Adipocytokine signaling pathway	58	1	0.1518
<i>path:gga04540</i>	Gap junction	79	1	0.201
<i>path:gga00230</i>	Purine metabolism	113	1	0.2748



	Term	Ont	N	n	Adj. p-value
GO:0008366	axon ensheathment	BP	12	3	4.499e-06
GO:0007272	ensheathment of neurons	BP	12	3	4.499e-06
GO:0042552	myelination	BP	12	3	4.499e-06
GO:0032291	axon ensheathment in central nervous system	BP	2	2	7.78e-06
GO:0022010	central nervous system myelination	BP	2	2	7.78e-06
GO:0014003	oligodendrocyte development	BP	2	2	7.78e-06
GO:0021782	glial cell development	BP	5	2	7.739e-05
GO:0048709	oligodendrocyte differentiation	BP	9	2	0.0002766
GO:0010001	glial cell differentiation	BP	21	2	0.001579
GO:0042063	gliogenesis	BP	25	2	0.00224

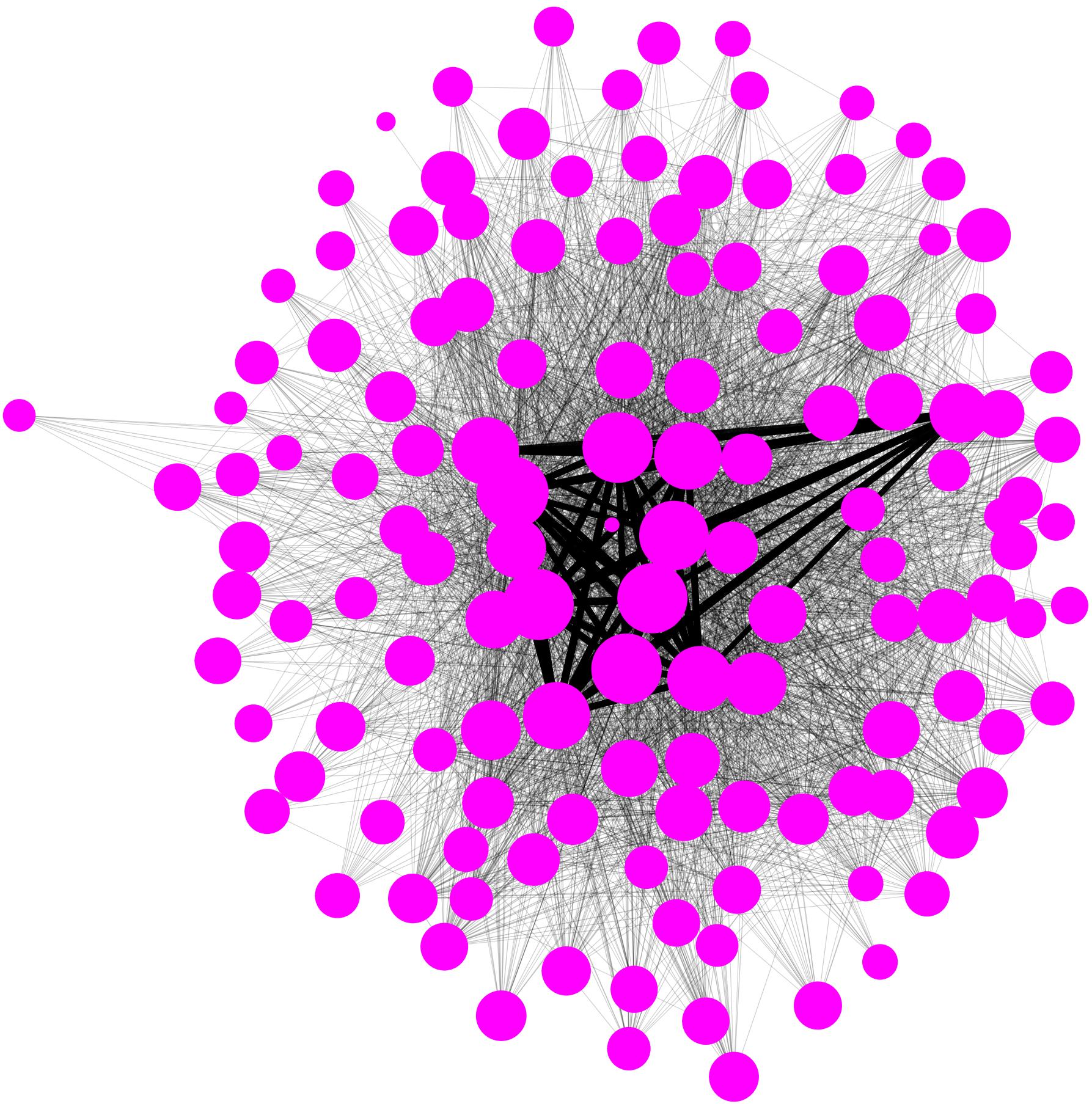
	Pathway	N	DE	P.DE
<i>path:gga00062</i>	Fatty acid elongation	22	1	0.06044
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	26	1	0.07104
<i>path:gga00565</i>	Ether lipid metabolism	36	1	0.09704
<i>path:gga00600</i>	Sphingolipid metabolism	48	1	0.1273
<i>path:gga01212</i>	Fatty acid metabolism	49	1	0.1298
<i>path:gga04512</i>	ECM–receptor interaction	68	1	0.1756
<i>path:gga04520</i>	Adherens junction	69	1	0.1779
<i>path:gga03015</i>	mRNA surveillance pathway	72	1	0.1849
<i>path:gga04350</i>	TGF–beta signaling pathway	83	1	0.21
<i>path:gga04514</i>	Cell adhesion molecules	99	1	0.2453



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	Term	Ont	N	n	Adj. p-value
GO:0022610	biological adhesion	BP	143	6	1.332e-06
GO:0007155	cell adhesion	BP	143	6	1.332e-06
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	BP	21	3	1.885e-05
GO:0098742	cell–cell adhesion via plasma–membrane adhesion molecules	BP	30	3	5.664e-05
GO:0007193	adenylate cyclase–inhibiting G protein–coupled receptor signaling pathway	BP	5	2	6.139e-05
GO:0098609	cell–cell adhesion	BP	66	3	0.0006002
GO:0007188	adenylate cyclase–modulating G protein–coupled receptor signaling pathway	BP	19	2	0.001027
GO:0007197	adenylate cyclase–inhibiting G protein–coupled acetylcholine receptor signaling pathway	BP	1	1	0.002522
GO:0098664	G protein–coupled serotonin receptor signaling pathway	BP	1	1	0.002522
GO:0007210	serotonin receptor signaling pathway	BP	1	1	0.002522

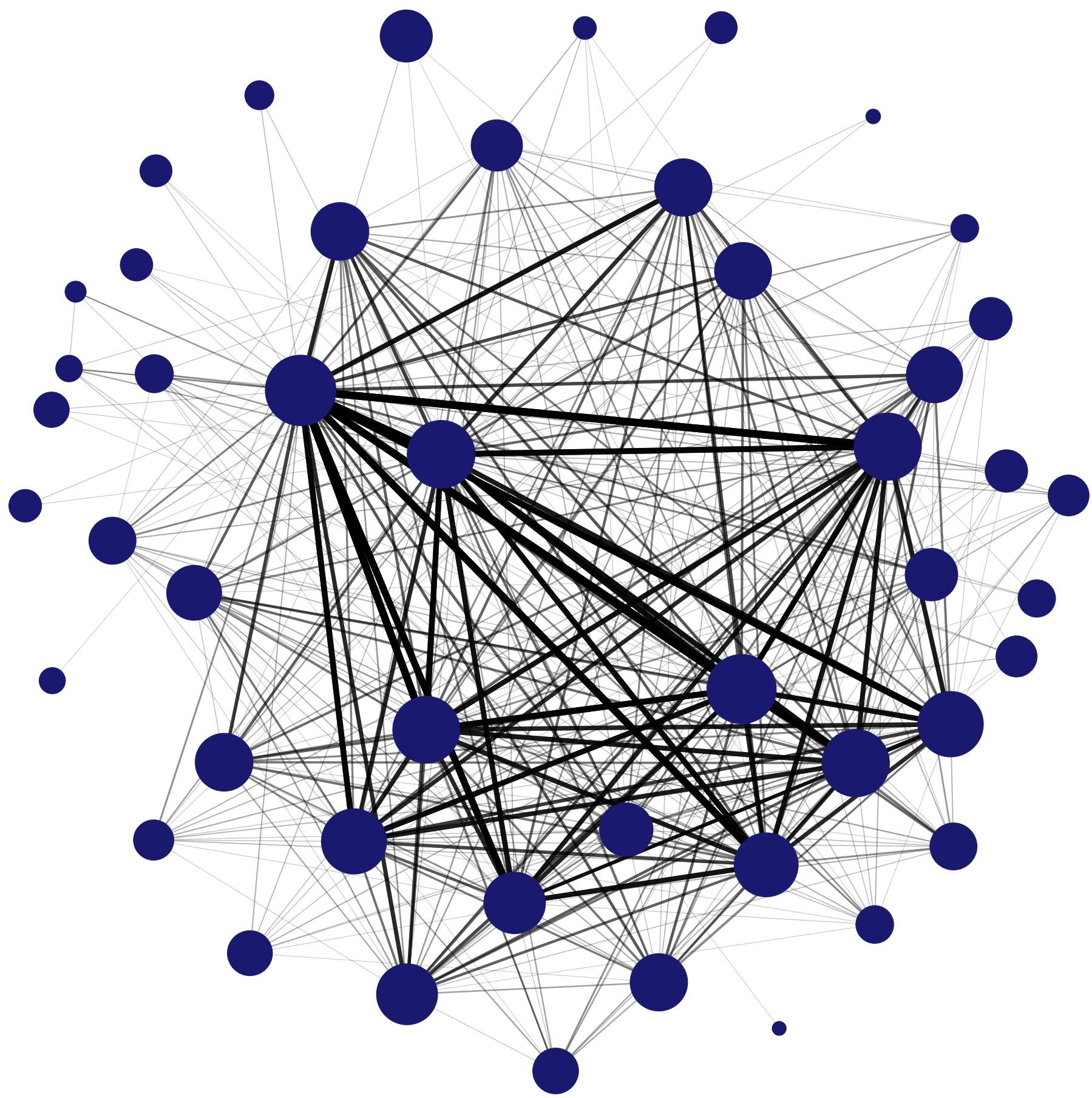
	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	99	4	0.0001066
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	1	0.02986
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	3	0.03327
<i>path:gga00601</i>	Glycosphingolipid biosynthesis – lacto and neolacto series	21	1	0.05169
<i>path:gga00515</i>	Mannose type O-glycan biosynthesis	22	1	0.05408
<i>path:gga00600</i>	Sphingolipid metabolism	48	1	0.1143
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.1387
<i>path:gga04142</i>	Lysosome	113	1	0.2492
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	1	0.2662
<i>path:gga04150</i>	mTOR signaling pathway	135	1	0.2901



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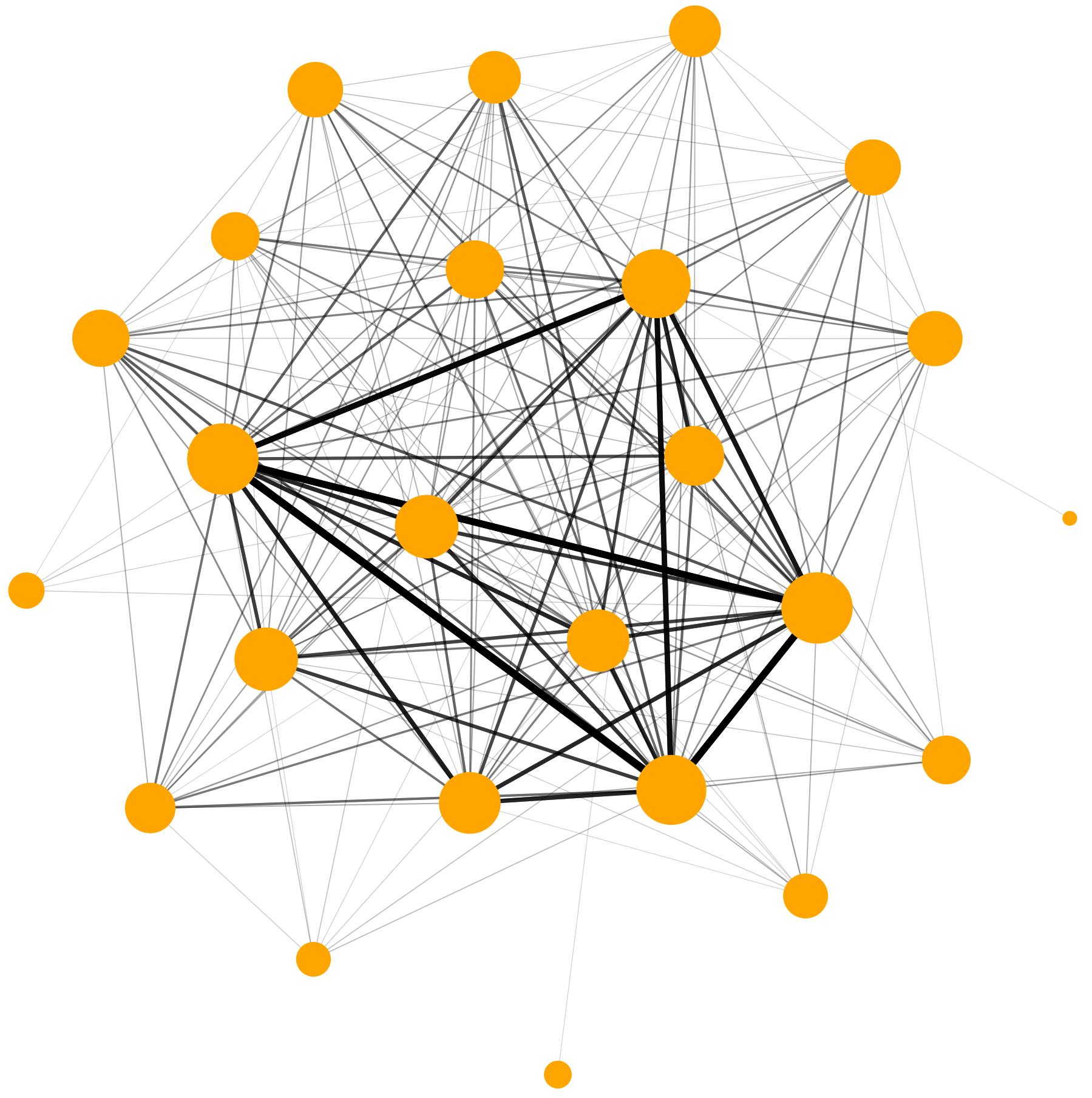
	Term	Ont	N	n	Adj. p-value
GO:0048568	embryonic organ development	BP	63	8	8.251e-08
GO:0048562	embryonic organ morphogenesis	BP	46	7	1.53e-07
GO:0003002	regionalization	BP	51	7	3.19e-07
GO:0007275	multicellular organism development	BP	577	19	7.944e-07
GO:0048598	embryonic morphogenesis	BP	87	8	1.042e-06
GO:0007389	pattern specification process	BP	61	7	1.117e-06
GO:0032501	multicellular organismal process	BP	711	21	1.142e-06
GO:0032502	developmental process	BP	655	20	1.279e-06
GO:0048731	system development	BP	483	17	1.307e-06
GO:0009790	embryo development	BP	121	9	1.31e-06

	Pathway	N	DE	P.DE
<i>path:gga03320</i>	PPAR signaling pathway	56	3	0.01369
<i>path:gga04310</i>	Wnt signaling pathway	135	4	0.03288
<i>path:gga04350</i>	TGF–beta signaling pathway	83	3	0.0382
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	151	4	0.04646
<i>path:gga00270</i>	Cysteine and methionine metabolism	42	2	0.05413
<i>path:gga04010</i>	MAPK signaling pathway	239	5	0.06324
<i>path:gga00480</i>	Glutathione metabolism	47	2	0.06605
<i>path:gga00600</i>	Sphingolipid metabolism	48	2	0.06853
<i>path:gga04270</i>	Vascular smooth muscle contraction	106	3	0.06938
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	3	0.09607



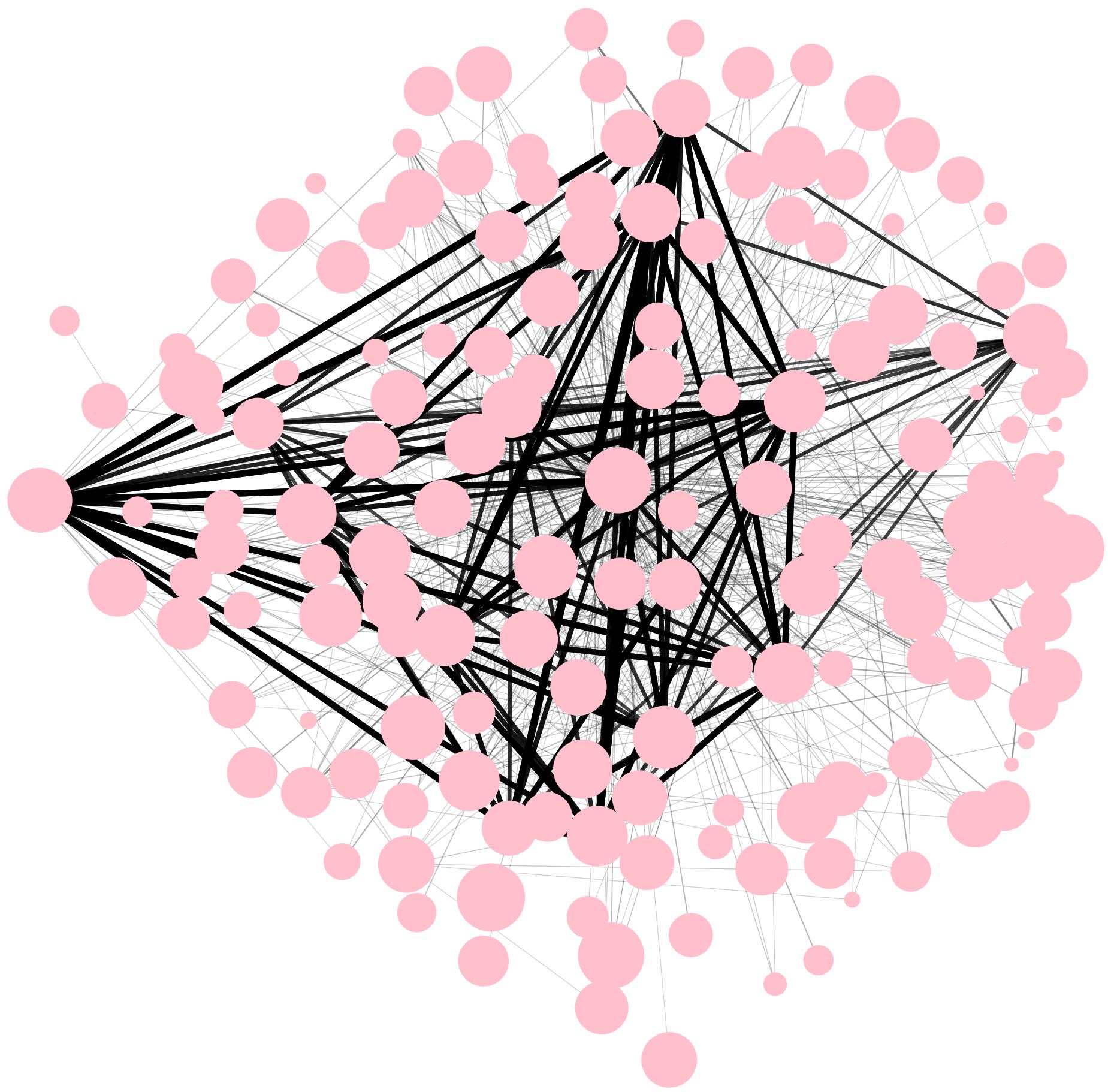
	Term	Ont	N	n	Adj. p-value
GO:0048709	oligodendrocyte differentiation	BP	9	2	0.0004285
GO:0050954	sensory perception of mechanical stimulus	BP	15	2	0.001233
GO:0007605	sensory perception of sound	BP	15	2	0.001233
GO:0010001	glial cell differentiation	BP	21	2	0.002433
GO:0042063	gliogenesis	BP	25	2	0.003445
GO:0036018	cellular response to erythropoietin	BP	1	1	0.003515
GO:0036216	cellular response to stem cell factor stimulus	BP	1	1	0.003515
GO:0097067	cellular response to thyroid hormone stimulus	BP	1	1	0.003515
GO:0038162	erythropoietin-mediated signaling pathway	BP	1	1	0.003515
GO:0038093	Fc receptor signaling pathway	BP	1	1	0.003515

	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	99	2	0.04729
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.04813
<i>path:gga04010</i>	MAPK signaling pathway	239	3	0.05143
<i>path:gga04672</i>	Intestinal immune network for IgA production	22	1	0.07461
<i>path:gga04530</i>	Tight junction	133	2	0.07945
<i>path:gga04310</i>	Wnt signaling pathway	135	2	0.08151
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.1676
<i>path:gga04115</i>	p53 signaling pathway	62	1	0.1966
<i>path:gga04512</i>	ECM–receptor interaction	68	1	0.2134
<i>path:gga03015</i>	mRNA surveillance pathway	72	1	0.2245



	Term	Ont	N	n	Adj. p-value
GO:0021520	spinal cord motor neuron cell fate specification	BP	2	2	2.956e-06
GO:0048665	neuron fate specification	BP	3	2	8.857e-06
GO:0021983	pituitary gland development	BP	7	2	6.173e-05
GO:0021522	spinal cord motor neuron differentiation	BP	7	2	6.173e-05
GO:0021536	diencephalon development	BP	8	2	8.223e-05
GO:0048663	neuron fate commitment	BP	8	2	8.223e-05
GO:0021515	cell differentiation in spinal cord	BP	10	2	0.0001319
GO:0021517	ventral spinal cord development	BP	12	2	0.000193
GO:0001708	cell fate specification	BP	13	2	0.0002278
GO:0035270	endocrine system development	BP	17	2	0.0003956

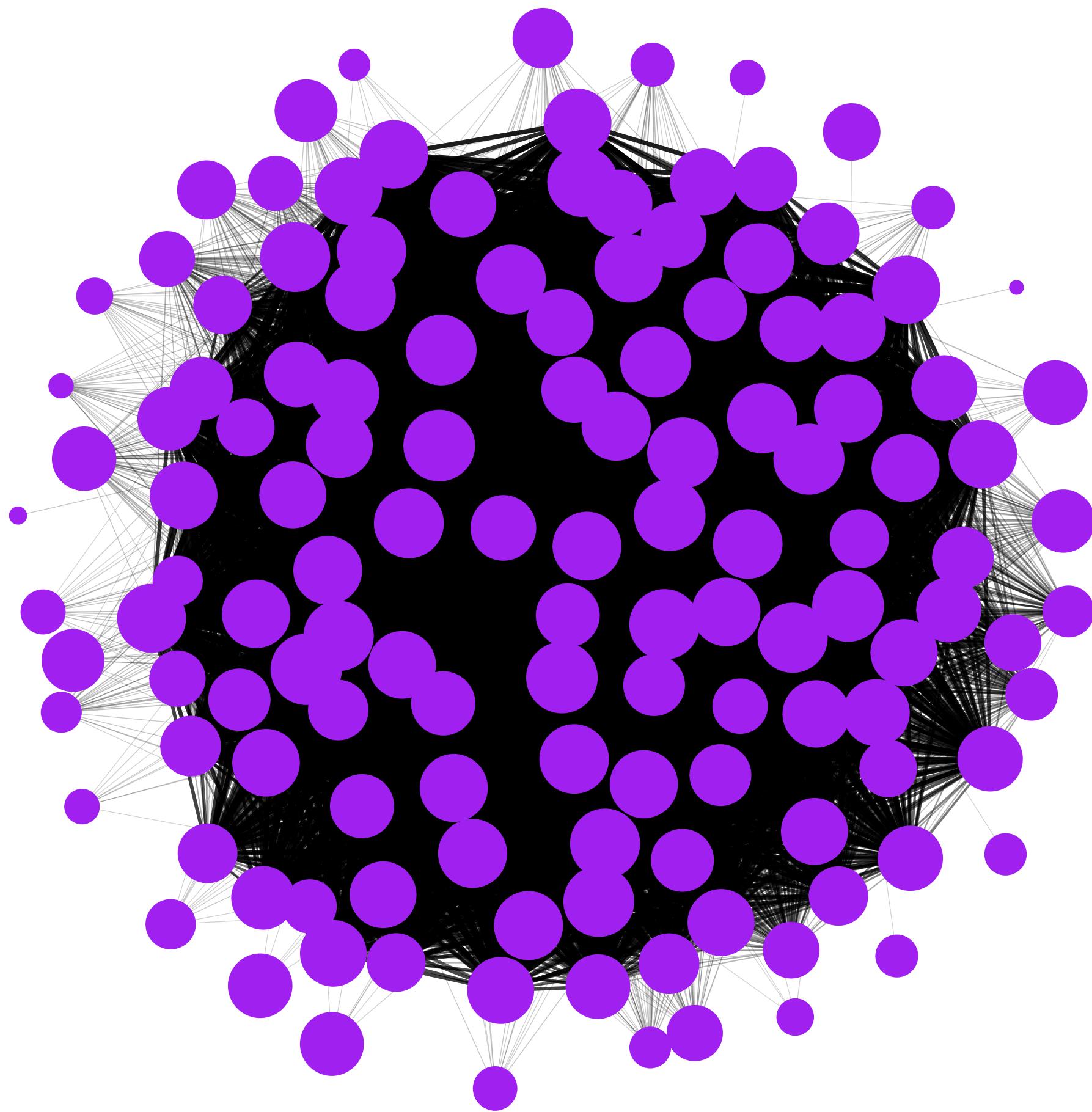
	Pathway	N	DE	P.DE
<i>path:gga00564</i>	Glycerophospholipid metabolism	84	2	0.00944
<i>path:gga00310</i>	Lysine degradation	50	1	0.08436
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	2	0.08654
<i>path:gga04512</i>	ECM–receptor interaction	68	1	0.113
<i>path:gga04540</i>	Gap junction	79	1	0.1301
<i>path:gga04020</i>	Calcium signaling pathway	201	1	0.2998
<i>path:gga04010</i>	MAPK signaling pathway	239	1	0.3458
<i>path:gga01100</i>	Metabolic pathways	1247	1	0.9003
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1



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	Term	Ont	N	n	Adj. p-value
GO:0044238	primary metabolic process	BP	1122	31	3.2e-06
GO:0006807	nitrogen compound metabolic process	BP	1086	30	4.79e-06
GO:0071704	organic substance metabolic process	BP	1183	31	9.444e-06
GO:0008152	metabolic process	BP	1233	31	2.149e-05
GO:0044237	cellular metabolic process	BP	1175	30	2.24e-05
GO:0060255	regulation of macromolecule metabolic process	BP	625	20	3.004e-05
GO:0051171	regulation of nitrogen compound metabolic process	BP	578	19	3.354e-05
GO:0051345	positive regulation of hydrolase activity	BP	55	6	3.746e-05
GO:0080090	regulation of primary metabolic process	BP	587	19	4.138e-05
GO:0065009	regulation of molecular function	BP	260	12	4.467e-05

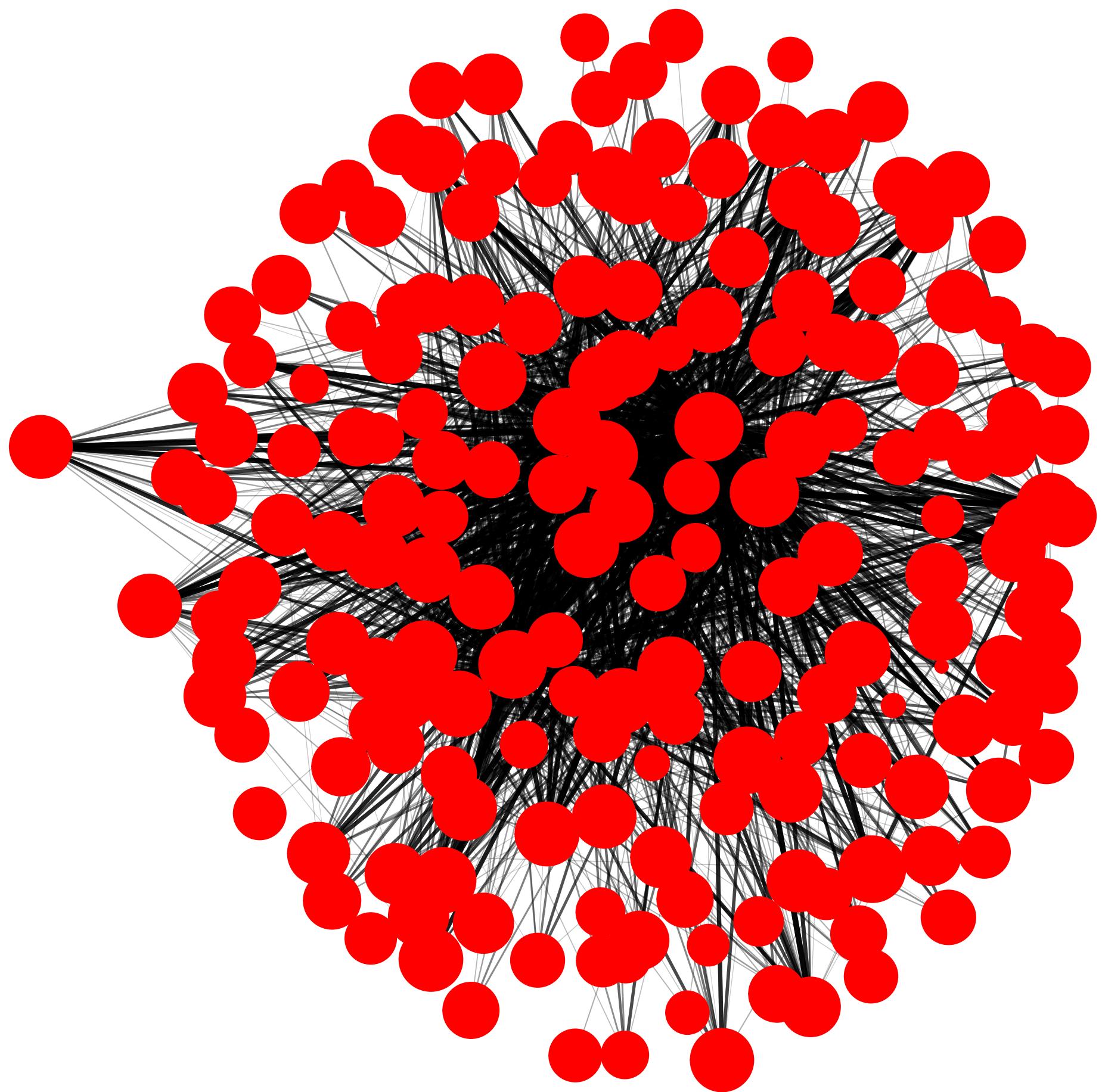
	Pathway	N	DE	P.DE
<i>path:gga01232</i>	Nucleotide metabolism	76	4	0.01125
<i>path:gga00220</i>	Arginine biosynthesis	17	2	0.01586
<i>path:gga04530</i>	Tight junction	133	5	0.01846
<i>path:gga00900</i>	Terpenoid backbone biosynthesis	19	2	0.01965
<i>path:gga04330</i>	Notch signaling pathway	52	3	0.02167
<i>path:gga00240</i>	Pyrimidine metabolism	54	3	0.02393
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty acids	26	2	0.03545
<i>path:gga04371</i>	Apelin signaling pathway	111	4	0.03874
<i>path:gga04110</i>	Cell cycle	113	4	0.04093
<i>path:gga04512</i>	ECM–receptor interaction	68	3	0.0431



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	Term	Ont	N	n	Adj. p-value
GO:0051383	kinetochore organization	BP	10	6	1.584e–10
GO:0000278	mitotic cell cycle	BP	99	12	2.048e–10
GO:0007049	cell cycle	BP	201	15	1.068e–09
GO:0051276	chromosome organization	BP	177	14	1.865e–09
GO:0022402	cell cycle process	BP	126	12	3.453e–09
GO:1903047	mitotic cell cycle process	BP	77	10	3.546e–09
GO:0007059	chromosome segregation	BP	43	8	7.319e–09
GO:1902850	microtubule cytoskeleton organization involved in mitosis	BP	21	6	3.747e–08
GO:0034508	centromere complex assembly	BP	12	5	6.209e–08
GO:0051301	cell division	BP	87	9	1.667e–07

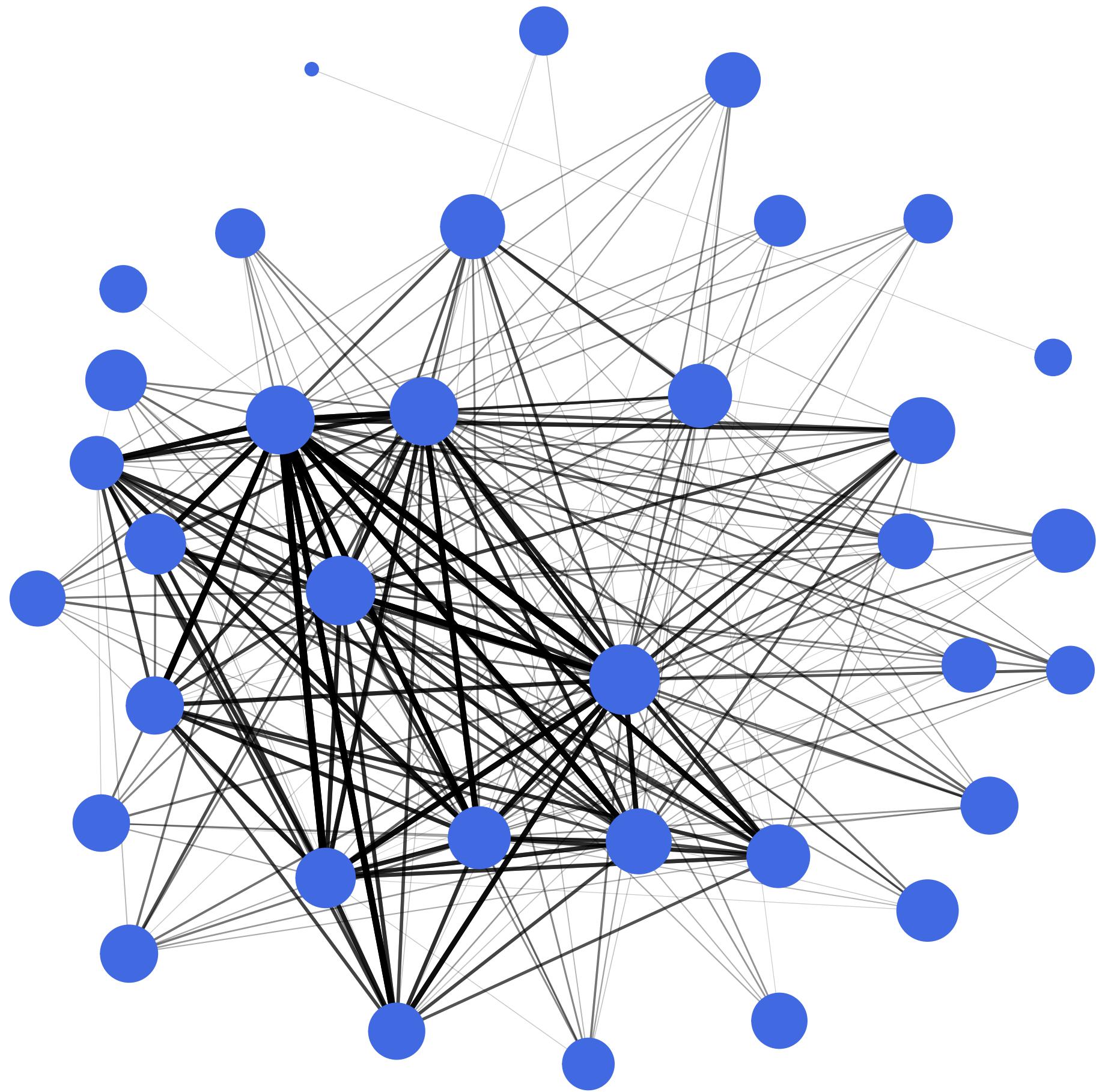
	Pathway	N	DE	P.DE
<i>path:gga04110</i>	Cell cycle	113	13	6.793e–11
<i>path:gga04114</i>	Oocyte meiosis	96	10	3.118e–08
<i>path:gga03030</i>	DNA replication	29	4	0.0001717
<i>path:gga04914</i>	Progesterone–mediated oocyte maturation	78	5	0.0009881
<i>path:gga03460</i>	Fanconi anemia pathway	48	3	0.01148
<i>path:gga03430</i>	Mismatch repair	19	2	0.01456
<i>path:gga04120</i>	Ubiquitin mediated proteolysis	127	4	0.03598
<i>path:gga03440</i>	Homologous recombination	36	2	0.04819
<i>path:gga03013</i>	Nucleocytoplasmic transport	89	3	0.05661
<i>path:gga04068</i>	FoxO signaling pathway	112	3	0.09702



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	Term	Ont	N	n	Adj. p-value
GO:0031175	neuron projection development	BP	112	14	4.183e-10
GO:0048666	neuron development	BP	126	14	2.028e-09
GO:0120036	plasma membrane bounded cell projection organization	BP	138	14	6.711e-09
GO:0030030	cell projection organization	BP	142	14	9.734e-09
GO:0048699	generation of neurons	BP	180	15	2.821e-08
GO:0022008	neurogenesis	BP	183	15	3.523e-08
GO:0030182	neuron differentiation	BP	165	14	6.641e-08
GO:0048667	cell morphogenesis involved in neuron differentiation	BP	77	10	9.845e-08
GO:0007399	nervous system development	BP	258	17	1.054e-07
GO:0048812	neuron projection morphogenesis	BP	80	10	1.426e-07

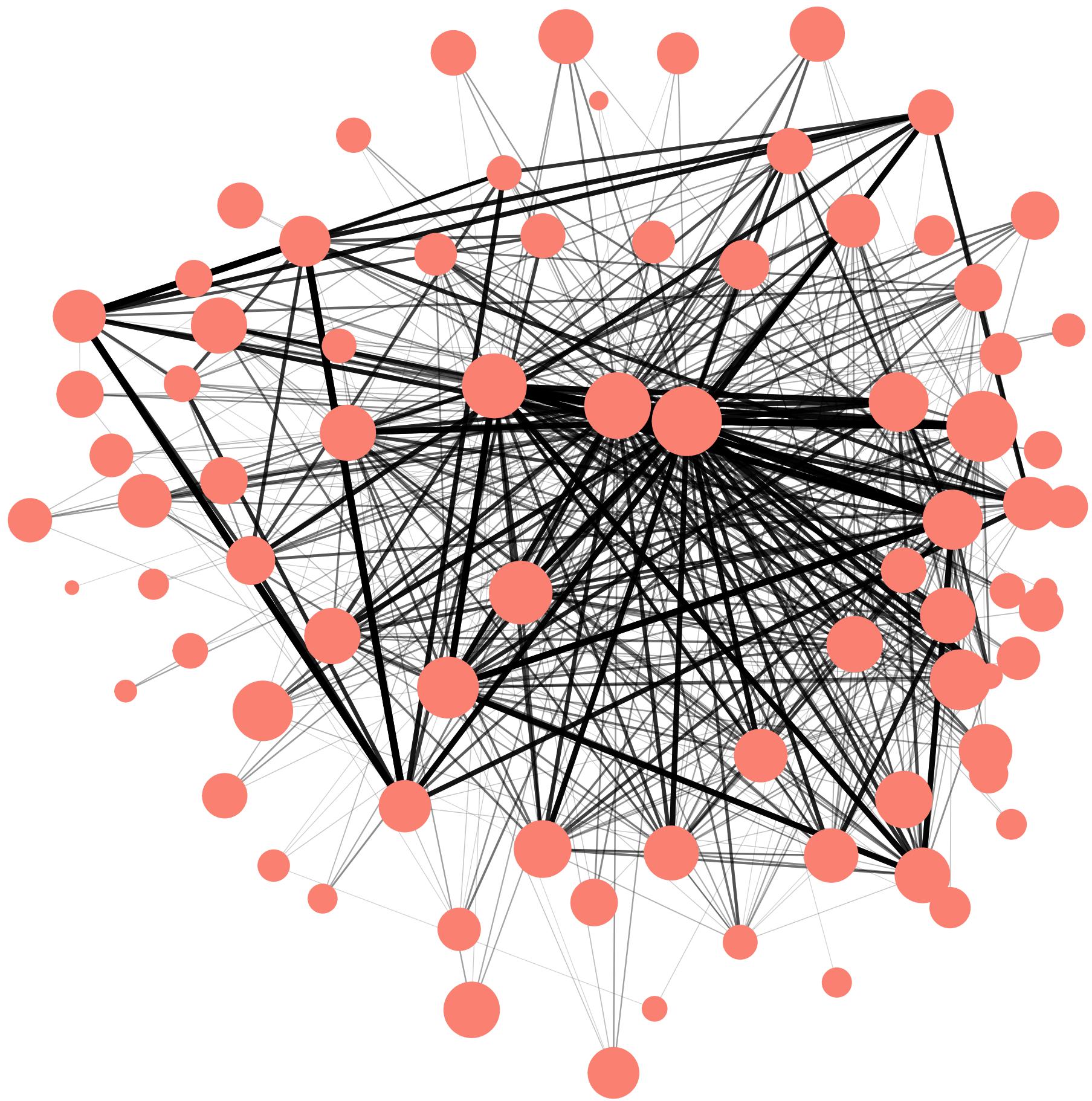
	Pathway	N	DE	P.DE
<i>path:gga05132</i>	Salmonella infection	222	12	6.055e-05
<i>path:gga04145</i>	Phagosome	125	8	0.000341
<i>path:gga04540</i>	Gap junction	79	5	0.00473
<i>path:gga03250</i>	Viral life cycle – HIV-1	48	3	0.02857
<i>path:gga04514</i>	Cell adhesion molecules	99	4	0.04843
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.0542
<i>path:gga04912</i>	GnRH signaling pathway	76	3	0.08815
<i>path:gga04070</i>	Phosphatidylinositol signaling system	85	3	0.1135
<i>path:gga04114</i>	Oocyte meiosis	96	3	0.1477
<i>path:gga00190</i>	Oxidative phosphorylation	100	3	0.1608



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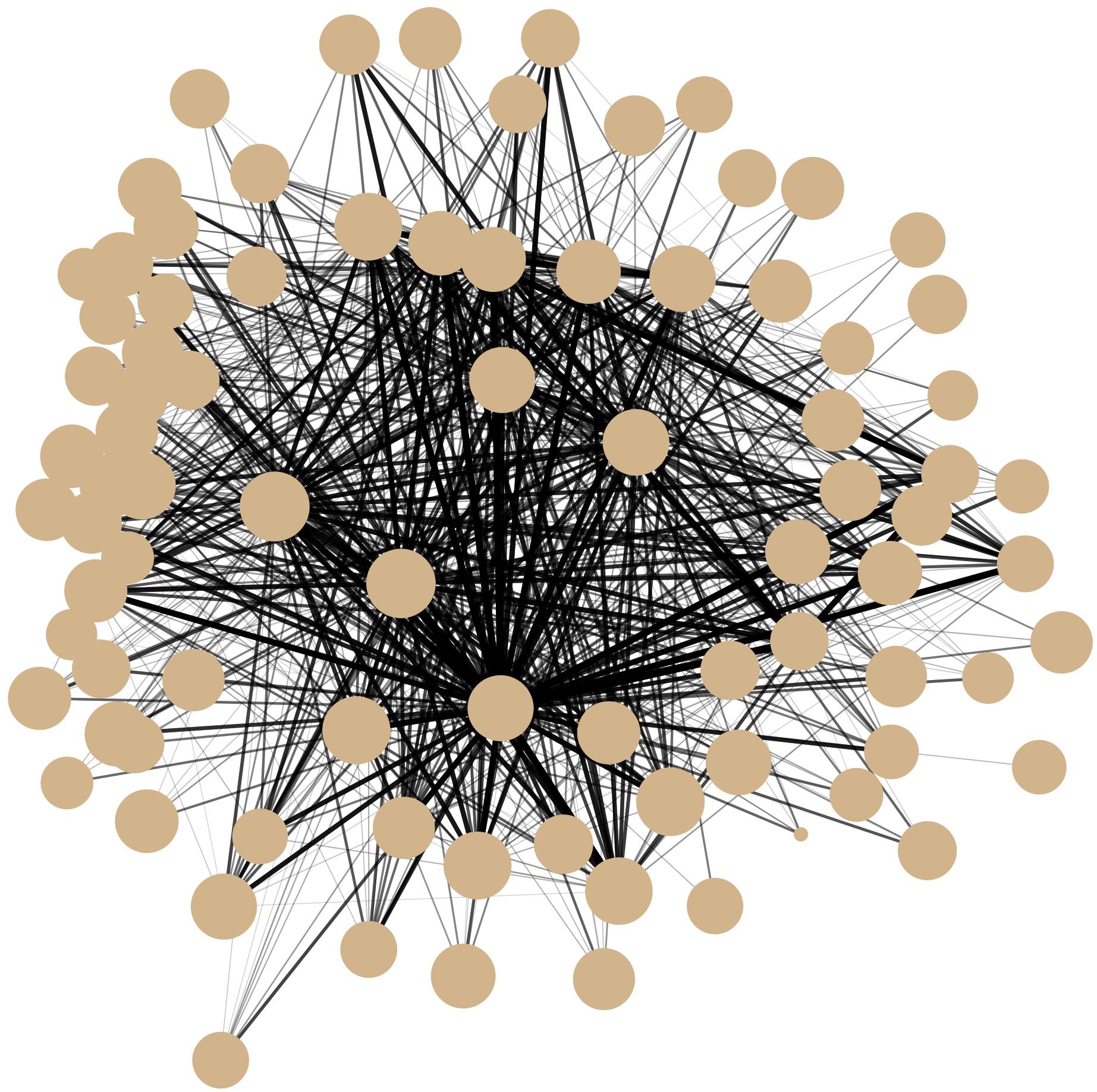
	Term	Ont	N	n	Adj. p-value
GO:0035584	calcium–mediated signaling using intracellular calcium source	BP	2	1	0.00519
GO:0003419	growth plate cartilage chondrocyte proliferation	BP	2	1	0.00519
GO:0022610	biological adhesion	BP	143	3	0.005969
GO:0007155	cell adhesion	BP	143	3	0.005969
GO:0035988	chondrocyte proliferation	BP	4	1	0.01035
GO:0007157	heterophilic cell–cell adhesion via plasma membrane cell adhesion molecules	BP	4	1	0.01035
GO:1900026	positive regulation of substrate adhesion–dependent cell spreading	BP	4	1	0.01035
GO:1900024	regulation of substrate adhesion–dependent cell spreading	BP	4	1	0.01035
GO:0010770	positive regulation of cell morphogenesis involved in differentiation	BP	6	1	0.01549
GO:0051491	positive regulation of filopodium assembly	BP	6	1	0.01549

	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	99	4	0.0001201
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.01035
<i>path:gga04625</i>	C-type lectin receptor signaling pathway	82	2	0.01912
<i>path:gga00533</i>	Glycosaminoglycan biosynthesis – keratan sulfate	14	1	0.03579
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	1	0.07275
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	2	0.08541
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	1	0.1013
<i>path:gga00510</i>	N-Glycan biosynthesis	45	1	0.1107
<i>path:gga04370</i>	VEGF signaling pathway	53	1	0.129
<i>path:gga04114</i>	Oocyte meiosis	96	1	0.2217



	Term	Ont	N	n	Adj. p-value
GO:0006816	calcium ion transport	BP	30	4	2.704e-05
GO:0030001	metal ion transport	BP	40	4	8.626e-05
GO:0070588	calcium ion transmembrane transport	BP	23	3	0.0003188
GO:0060999	positive regulation of dendritic spine development	BP	6	2	0.0005049
GO:0031175	neuron projection development	BP	112	5	0.0005083
GO:0034762	regulation of transmembrane transport	BP	29	3	0.0006413
GO:0048666	neuron development	BP	126	5	0.0008682
GO:0070509	calcium ion import	BP	8	2	0.0009354
GO:0060998	regulation of dendritic spine development	BP	8	2	0.0009354
GO:0120036	plasma membrane bounded cell projection organization	BP	138	5	0.001305

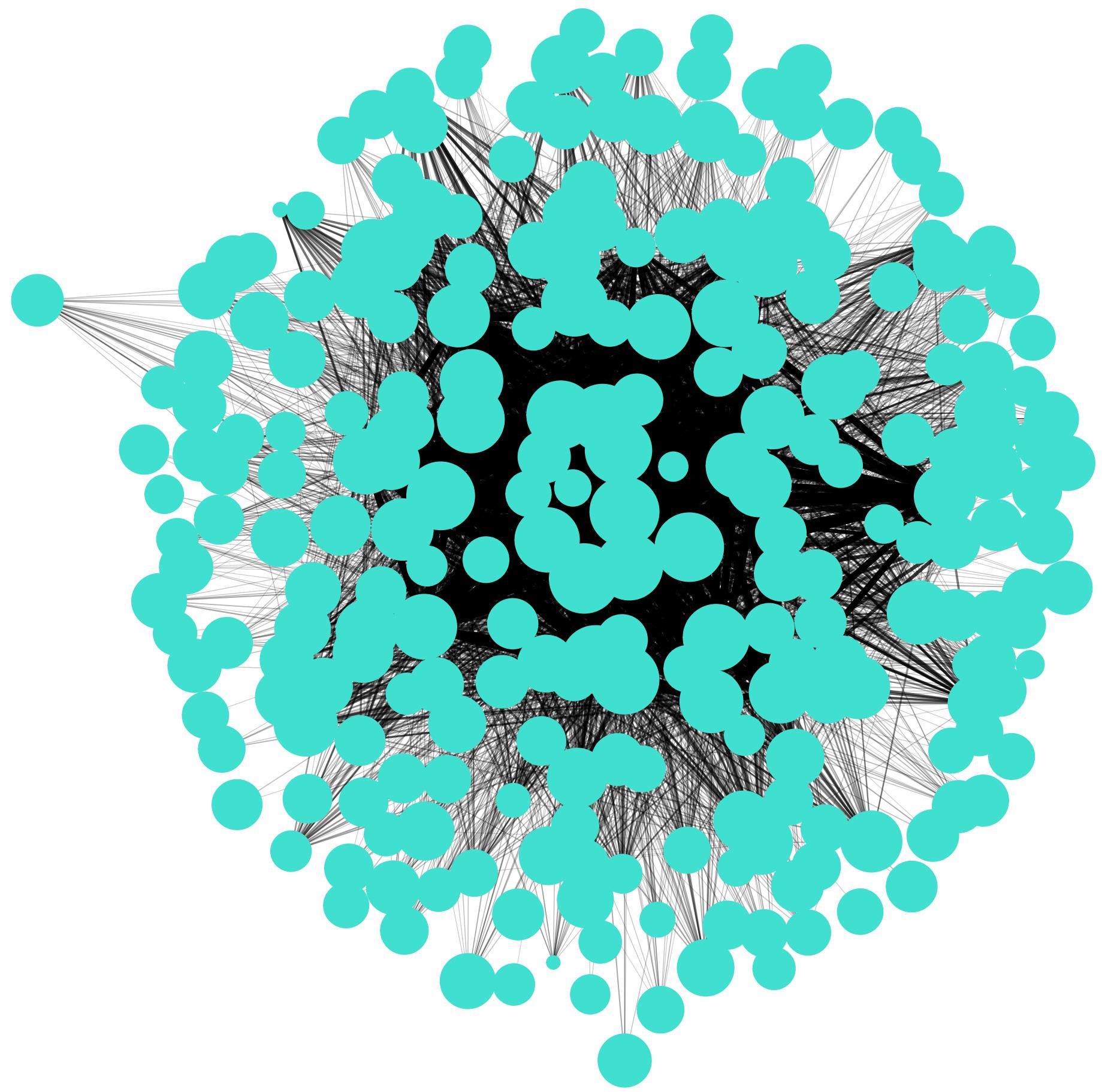
	Pathway	N	DE	P.DE
<i>path:gga04010</i>	MAPK signaling pathway	239	8	7.828e-05
<i>path:gga04020</i>	Calcium signaling pathway	201	7	0.0001761
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	122	5	0.0007504
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	6	0.0008267
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	2	0.002171
<i>path:gga04260</i>	Cardiac muscle contraction	59	3	0.005028
<i>path:gga00650</i>	Butanoate metabolism	21	2	0.006676
<i>path:gga00410</i>	beta-Alanine metabolism	25	2	0.009394
<i>path:gga05132</i>	Salmonella infection	222	5	0.009877
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	2	0.01512



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	Term	Ont	N	n	Adj. p-value
GO:0007166	cell surface receptor signaling pathway	BP	263	15	1.017e-10
GO:0007165	signal transduction	BP	477	18	9.649e-10
GO:0023052	signaling	BP	512	18	2.971e-09
GO:0007154	cell communication	BP	519	18	3.679e-09
GO:0051716	cellular response to stimulus	BP	657	20	4.042e-09
GO:0050896	response to stimulus	BP	779	21	1.312e-08
GO:0050789	regulation of biological process	BP	1098	24	5.513e-08
GO:0050794	regulation of cellular process	BP	1048	23	1.053e-07
GO:0007275	multicellular organism development	BP	577	17	1.159e-07
GO:0032502	developmental process	BP	655	18	1.317e-07

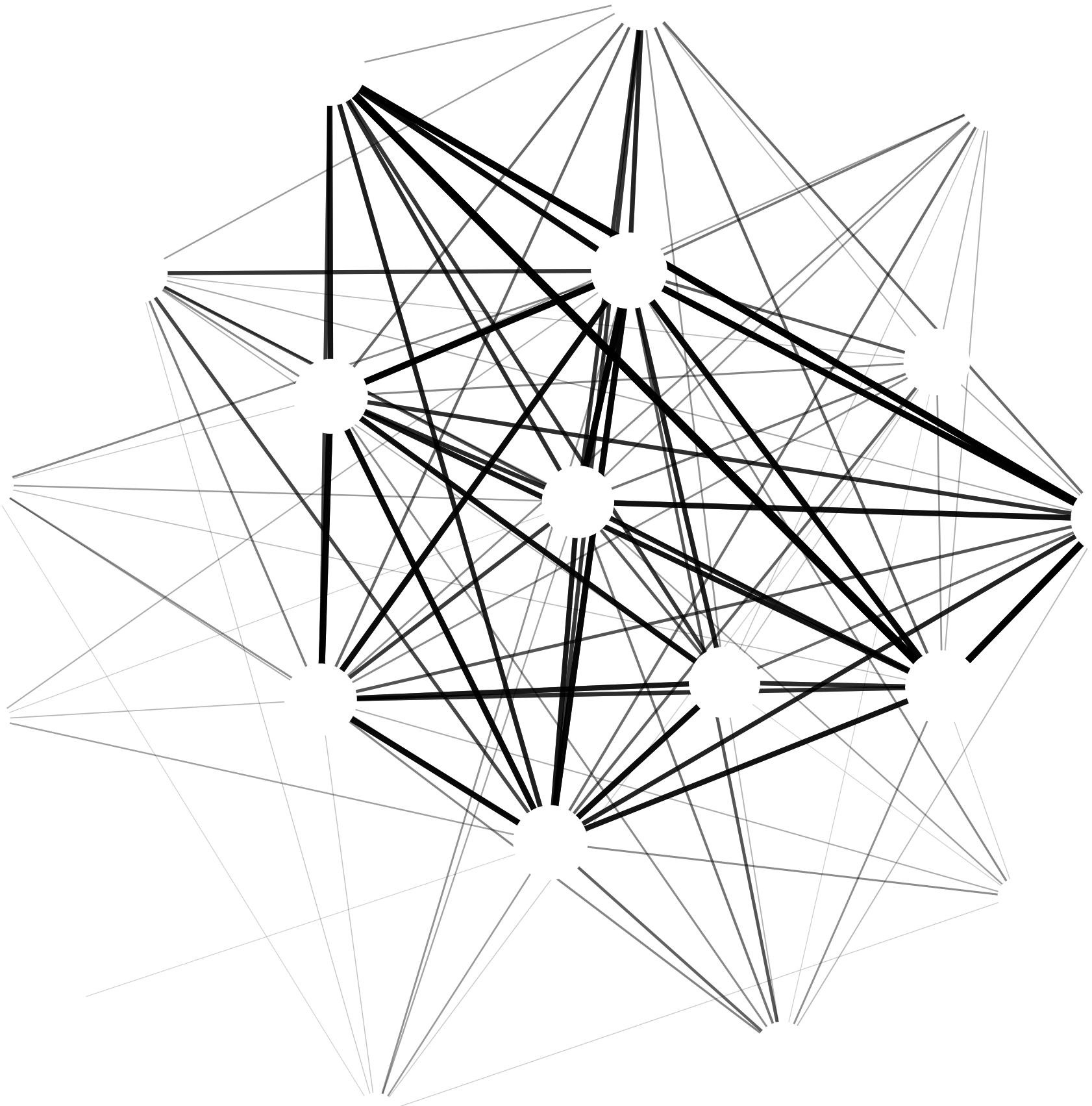
	Pathway	N	DE	P.DE
<i>path:gga04330</i>	Notch signaling pathway	52	6	9.391e-07
<i>path:gga04810</i>	Regulation of actin cytoskeleton	188	9	3.136e-06
<i>path:gga04512</i>	ECM–receptor interaction	68	5	7.338e-05
<i>path:gga04510</i>	Focal adhesion	172	7	0.0001161
<i>path:gga04340</i>	Hedgehog signaling pathway	47	4	0.0002284
<i>path:gga04520</i>	Adherens junction	69	4	0.0009948
<i>path:gga04020</i>	Calcium signaling pathway	201	6	0.001834
<i>path:gga04350</i>	TGF–beta signaling pathway	83	3	0.01622
<i>path:gga03260</i>	Virion – Human immunodeficiency virus	4	1	0.02543
<i>path:gga04514</i>	Cell adhesion molecules	99	3	0.02575



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	Term	Ont	N	n	Adj. p-value
GO:0008150	biological_process	BP	1904	78	1.119e-11
GO:0009987	cellular process	BP	1823	75	2.722e-11
GO:0009058	biosynthetic process	BP	672	39	4.385e-10
GO:1901576	organic substance biosynthetic process	BP	663	38	1.077e-09
GO:0065007	biological regulation	BP	1194	54	1.38e-09
GO:0016043	cellular component organization	BP	662	37	3.641e-09
GO:0050789	regulation of biological process	BP	1098	50	5.18e-09
GO:0032501	multicellular organismal process	BP	711	38	7.441e-09
GO:0071840	cellular component organization or biogenesis	BP	683	37	8.417e-09
GO:0048856	anatomical structure development	BP	623	35	8.895e-09

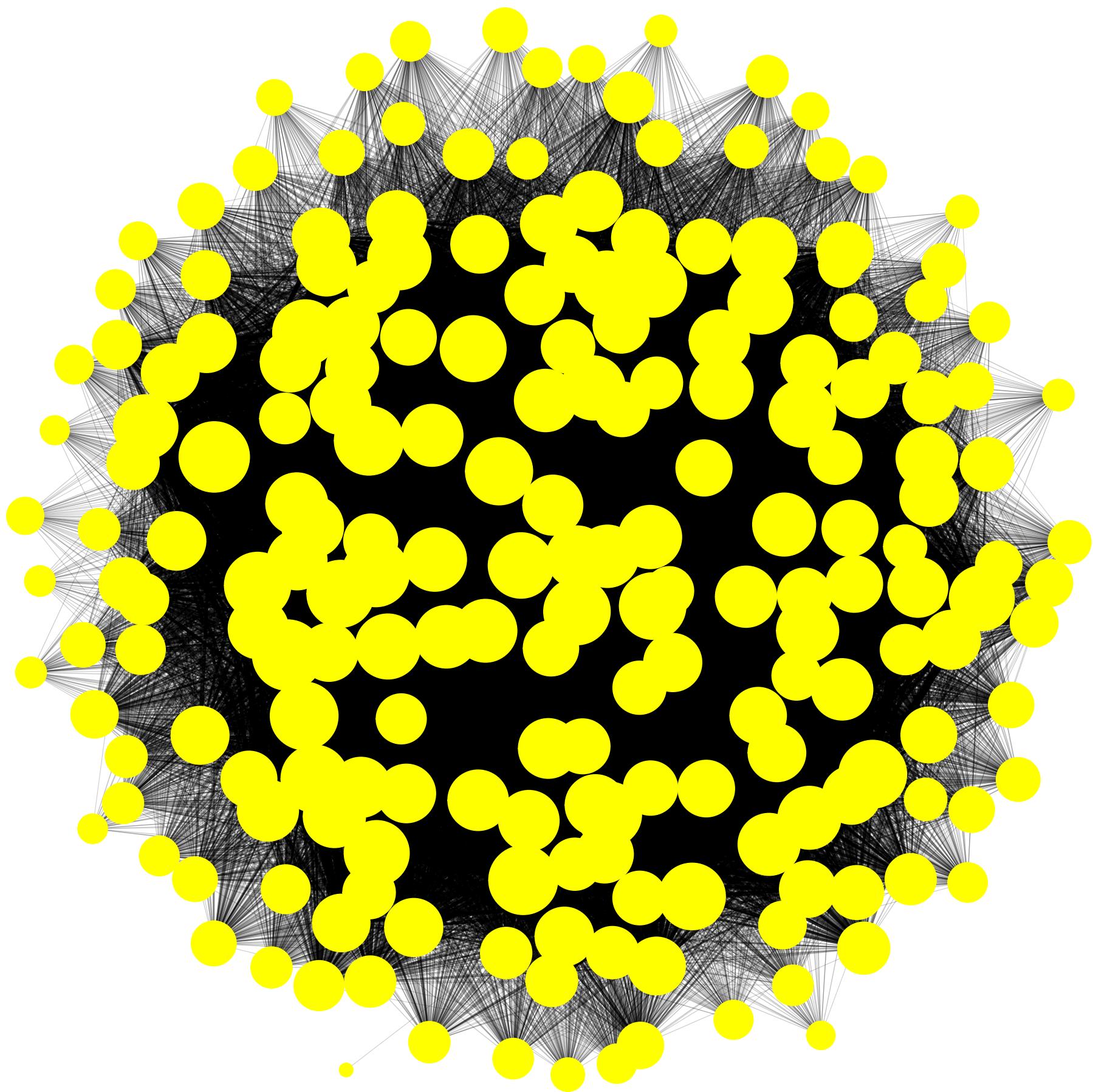
	Pathway	N	DE	P.DE
<i>path:gga03010</i>	Ribosome	114	16	4.748e–10
<i>path:gga00100</i>	Steroid biosynthesis	15	6	1.985e–07
<i>path:gga04110</i>	Cell cycle	113	12	1.628e–06
<i>path:gga03030</i>	DNA replication	29	4	0.002122
<i>path:gga05132</i>	Salmonella infection	222	11	0.003636
<i>path:gga04914</i>	Progesterone–mediated oocyte maturation	78	6	0.003735
<i>path:gga03430</i>	Mismatch repair	19	3	0.005324
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	46	4	0.01132
<i>path:gga04218</i>	Cellular senescence	134	7	0.01444
<i>path:gga04310</i>	Wnt signaling pathway	135	7	0.01499



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	Term	Ont	N	n	Adj. p-value
GO:2001258	negative regulation of cation channel activity	BP	1	1	0.001605
GO:1902260	negative regulation of delayed rectifier potassium channel activity	BP	1	1	0.001605
GO:1901380	negative regulation of potassium ion transmembrane transport	BP	1	1	0.001605
GO:1901017	negative regulation of potassium ion transmembrane transporter activity	BP	1	1	0.001605
GO:1903817	negative regulation of voltage-gated potassium channel activity	BP	1	1	0.001605
GO:2001257	regulation of cation channel activity	BP	1	1	0.001605
GO:1902259	regulation of delayed rectifier potassium channel activity	BP	1	1	0.001605
GO:1904063	negative regulation of cation transmembrane transport	BP	2	1	0.003207
GO:0032413	negative regulation of ion transmembrane transporter activity	BP	2	1	0.003207
GO:0043267	negative regulation of potassium ion transport	BP	2	1	0.003207

	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	2	0.07384
<i>path:gga04020</i>	Calcium signaling pathway	201	1	0.2777
<i>path:gga04144</i>	Endocytosis	218	1	0.2975
<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



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	Term	Ont	N	n	Adj. p-value
GO:0009950	dorsal/ventral axis specification	BP	2	2	0.0002032
GO:0009951	polarity specification of dorsal/ventral axis	BP	2	2	0.0002032
GO:0065001	specification of axis polarity	BP	3	2	0.0006037
GO:0071276	cellular response to cadmium ion	BP	4	2	0.001196
GO:0046686	response to cadmium ion	BP	4	2	0.001196
GO:0032501	multicellular organismal process	BP	711	21	0.001264
GO:0048856	anatomical structure development	BP	623	19	0.001499
GO:0007275	multicellular organism development	BP	577	18	0.001556
GO:0048513	animal organ development	BP	321	12	0.002241
GO:0048639	positive regulation of developmental growth	BP	19	3	0.002351

	Pathway	N	DE	P.DE
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	28	3	0.007235
<i>path:gga04350</i>	TGF–beta signaling pathway	83	4	0.03099
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	281	8	0.04886
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.05596
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	30	2	0.06807
<i>path:gga04512</i>	ECM–receptor interaction	68	3	0.07338
<i>path:gga04216</i>	Ferroptosis	34	2	0.08463
<i>path:gga00920</i>	Sulfur metabolism	7	1	0.09587
<i>path:gga00590</i>	Arachidonic acid metabolism	39	2	0.1068
<i>path:gga00480</i>	Glutathione metabolism	47	2	0.145