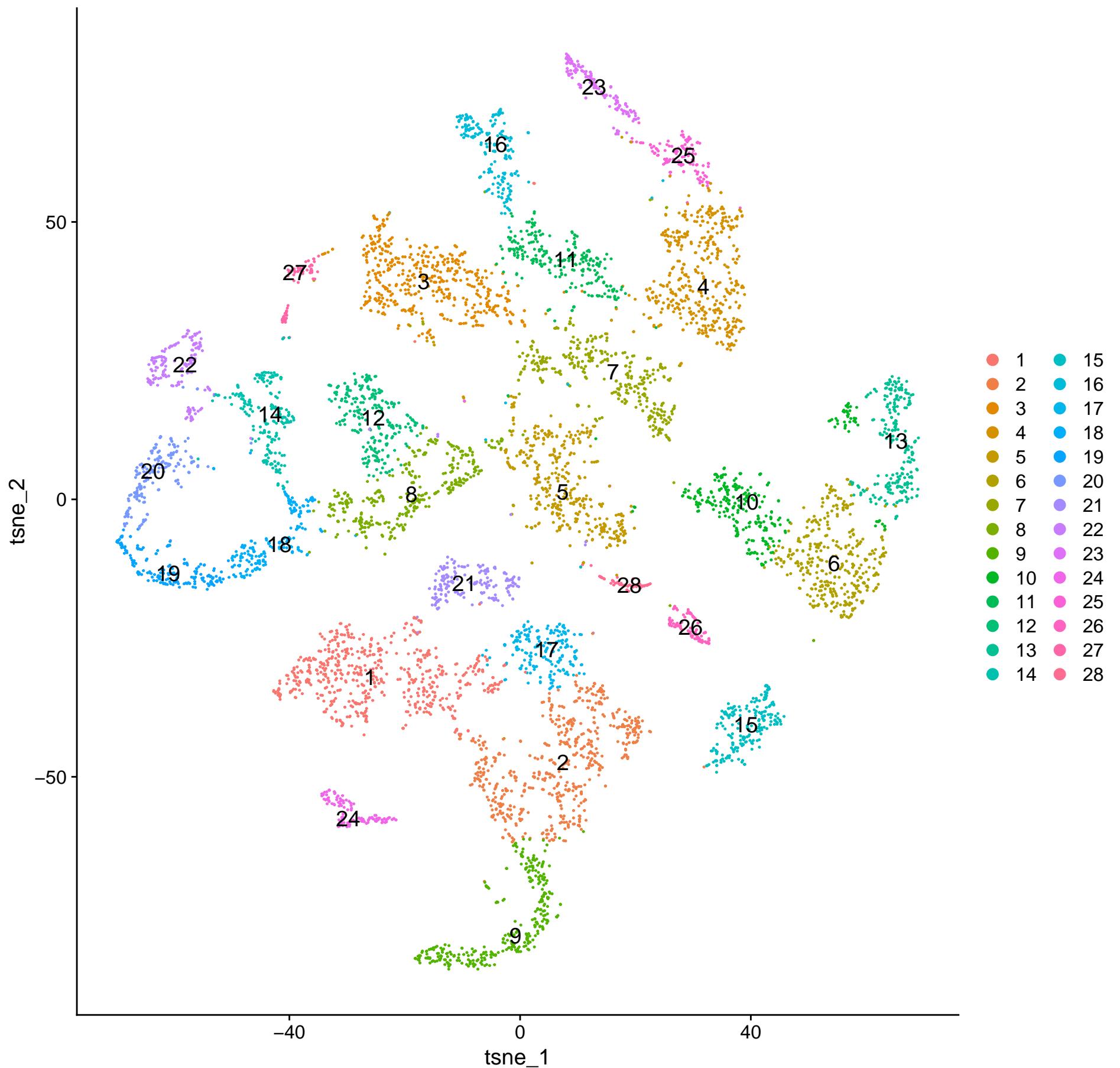
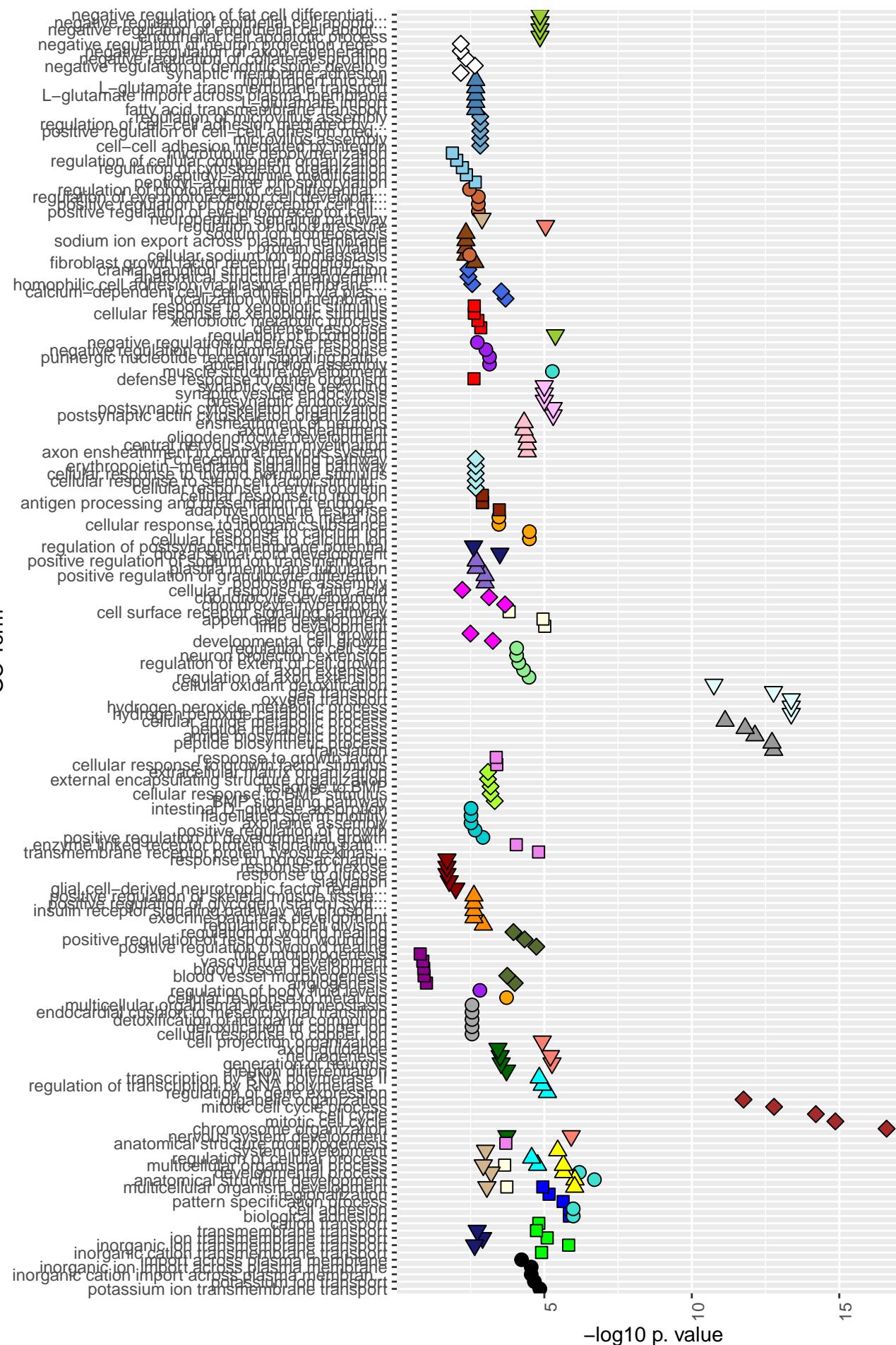


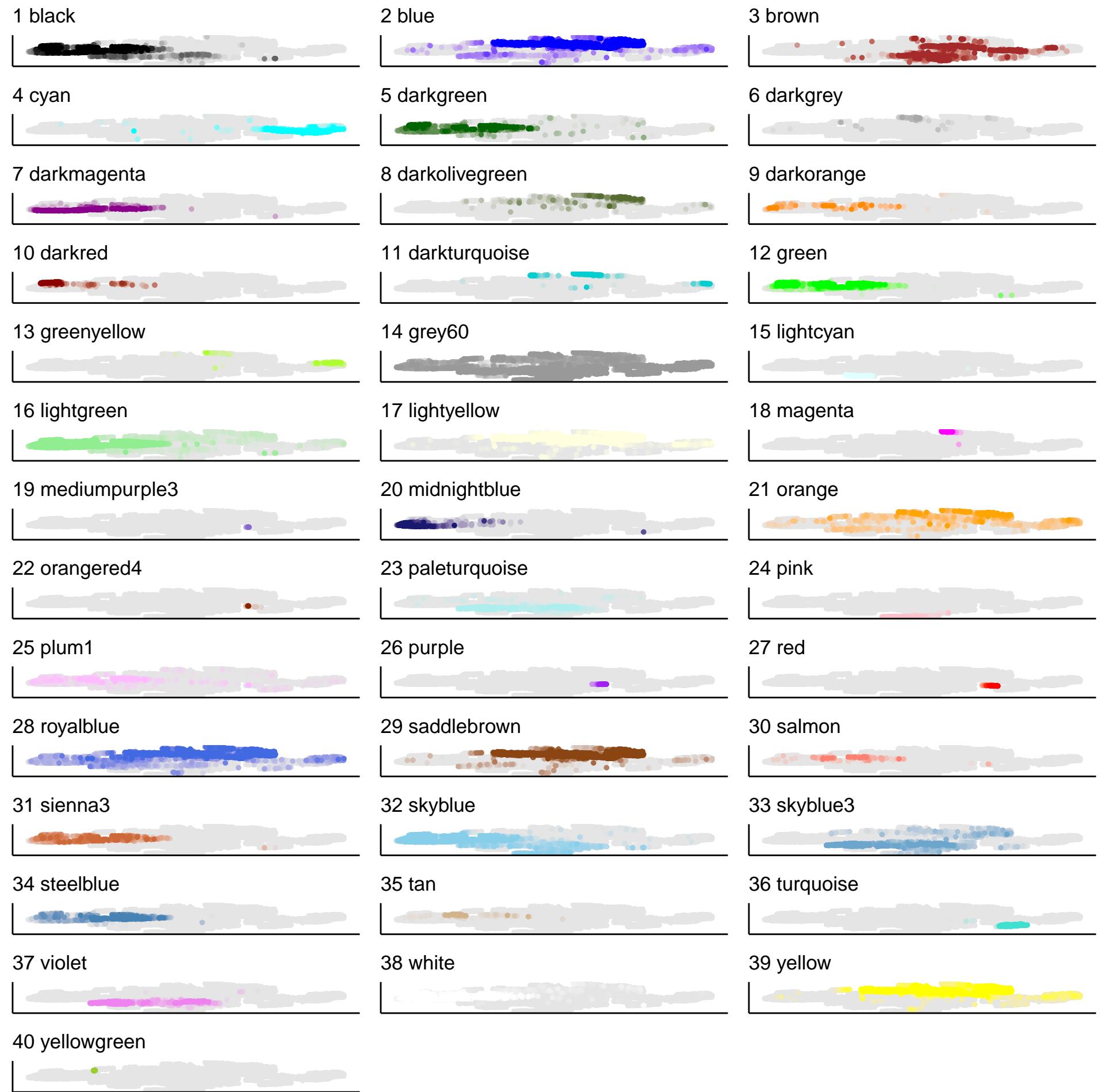
Gg_lumb_int scWGCNA modules

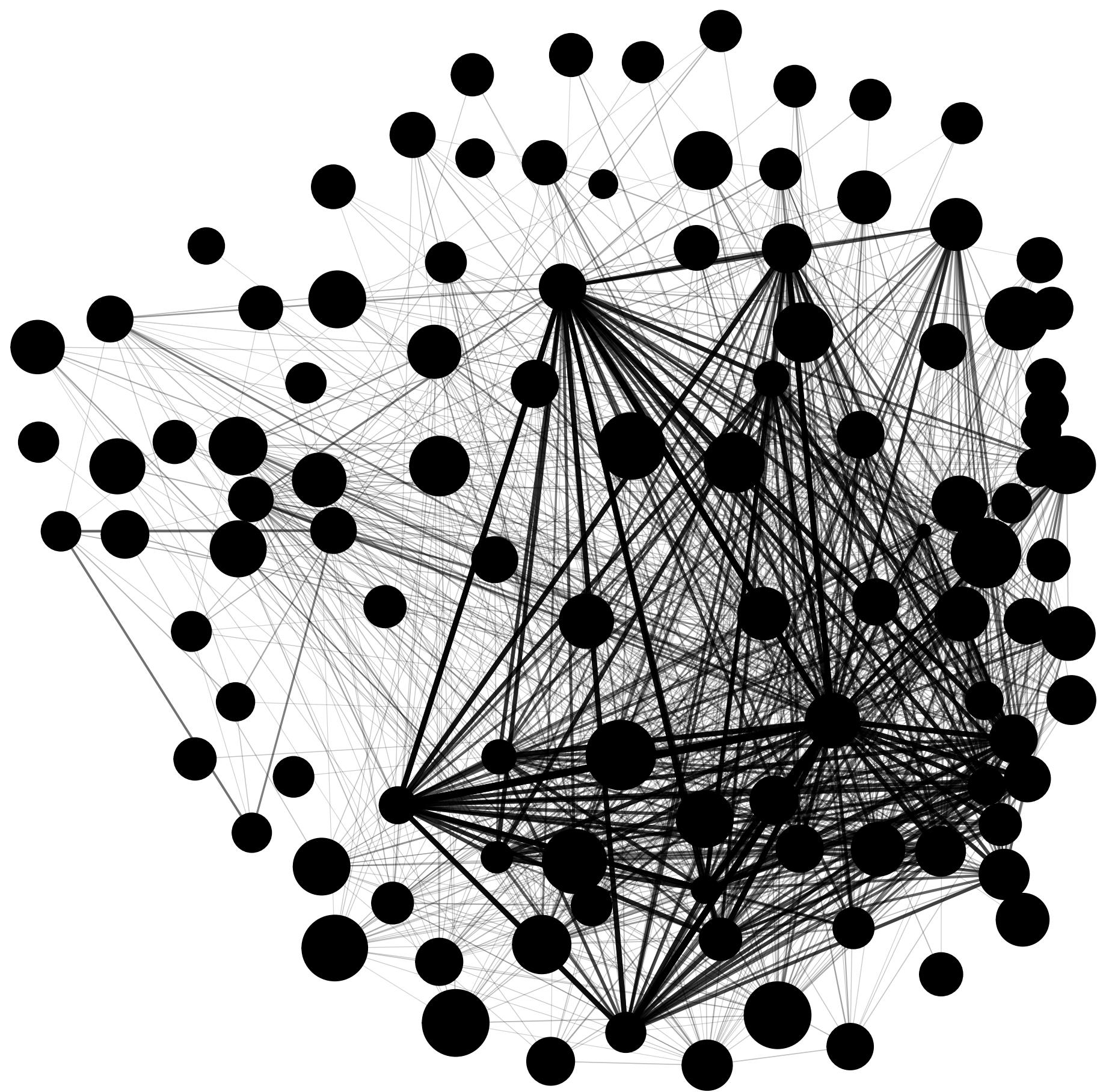




KEGG pathway



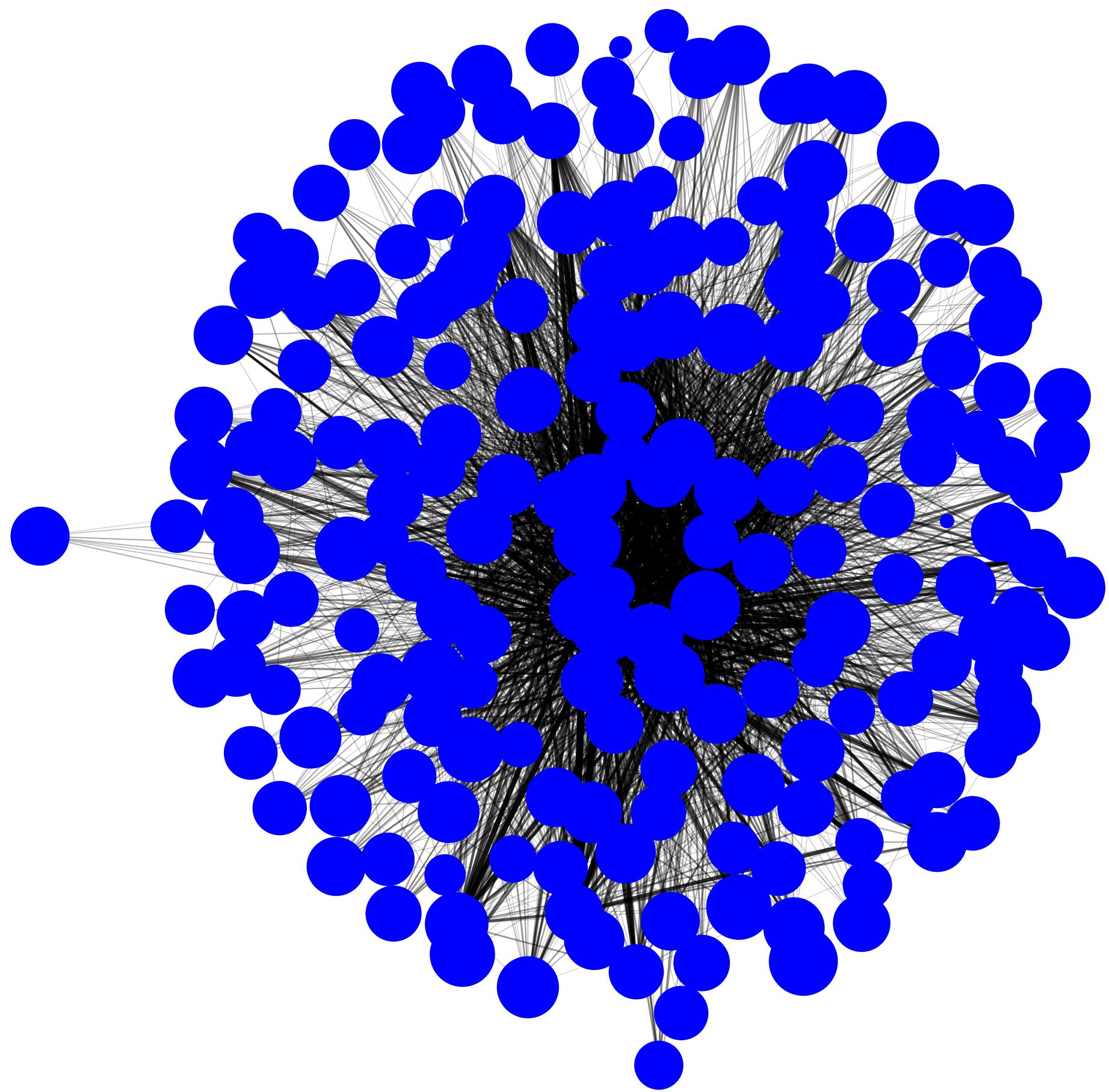




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	Term	Ont	N	n	Adj. p-value
GO:0071805	potassium ion transmembrane transport	BP	19	4	1.422e-05
GO:0006813	potassium ion transport	BP	21	4	2.168e-05
GO:0098659	inorganic cation import across plasma membrane	BP	8	3	2.789e-05
GO:0099587	inorganic ion import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

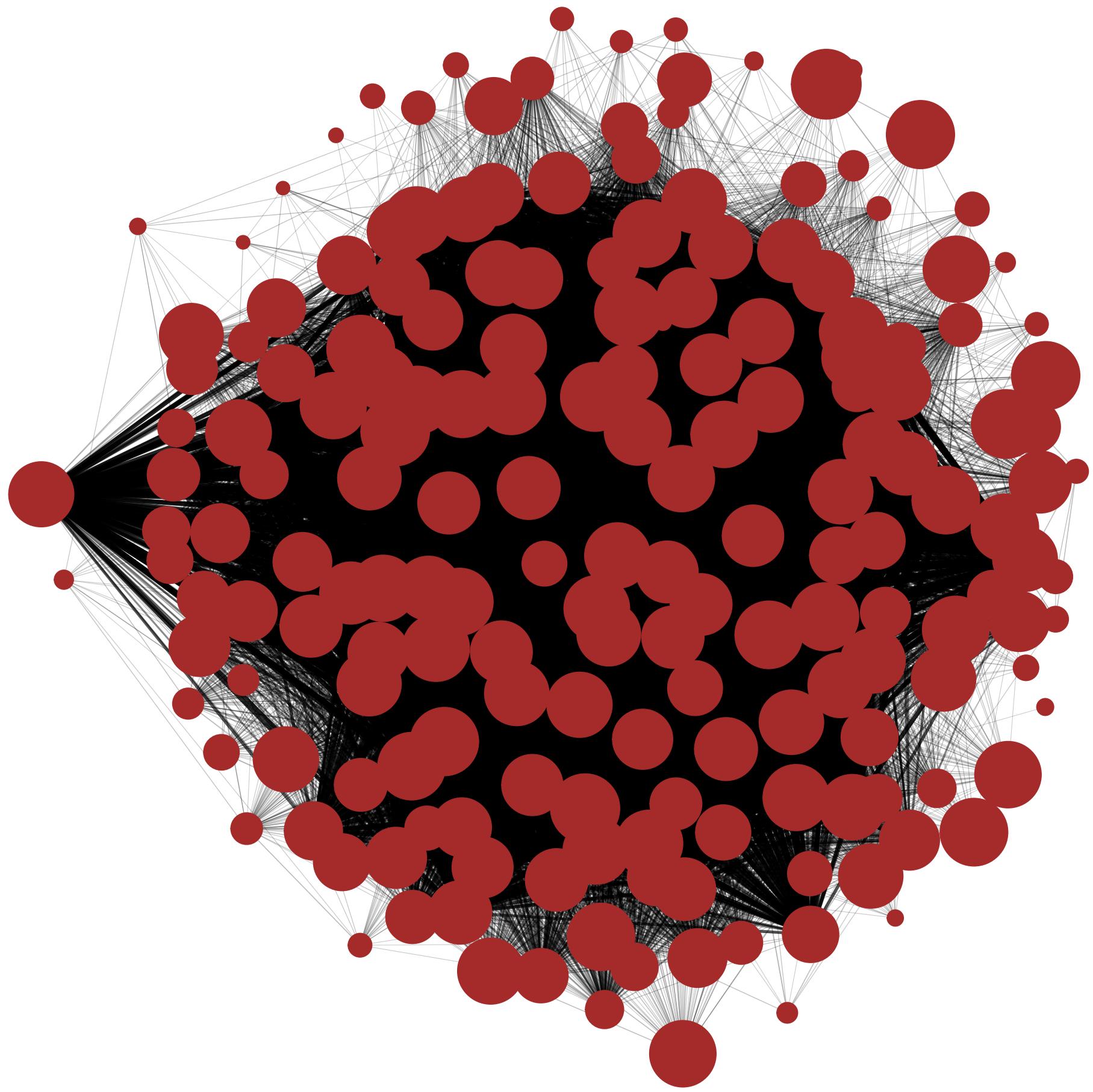
	Pathway	N	DE	P.DE
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.03195
<i>path:gga04114</i>	Oocyte meiosis	92	3	0.0384
<i>path:gga04514</i>	Cell adhesion molecules	98	3	0.04495
<i>path:gga04270</i>	Vascular smooth muscle contraction	101	3	0.04841
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes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



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

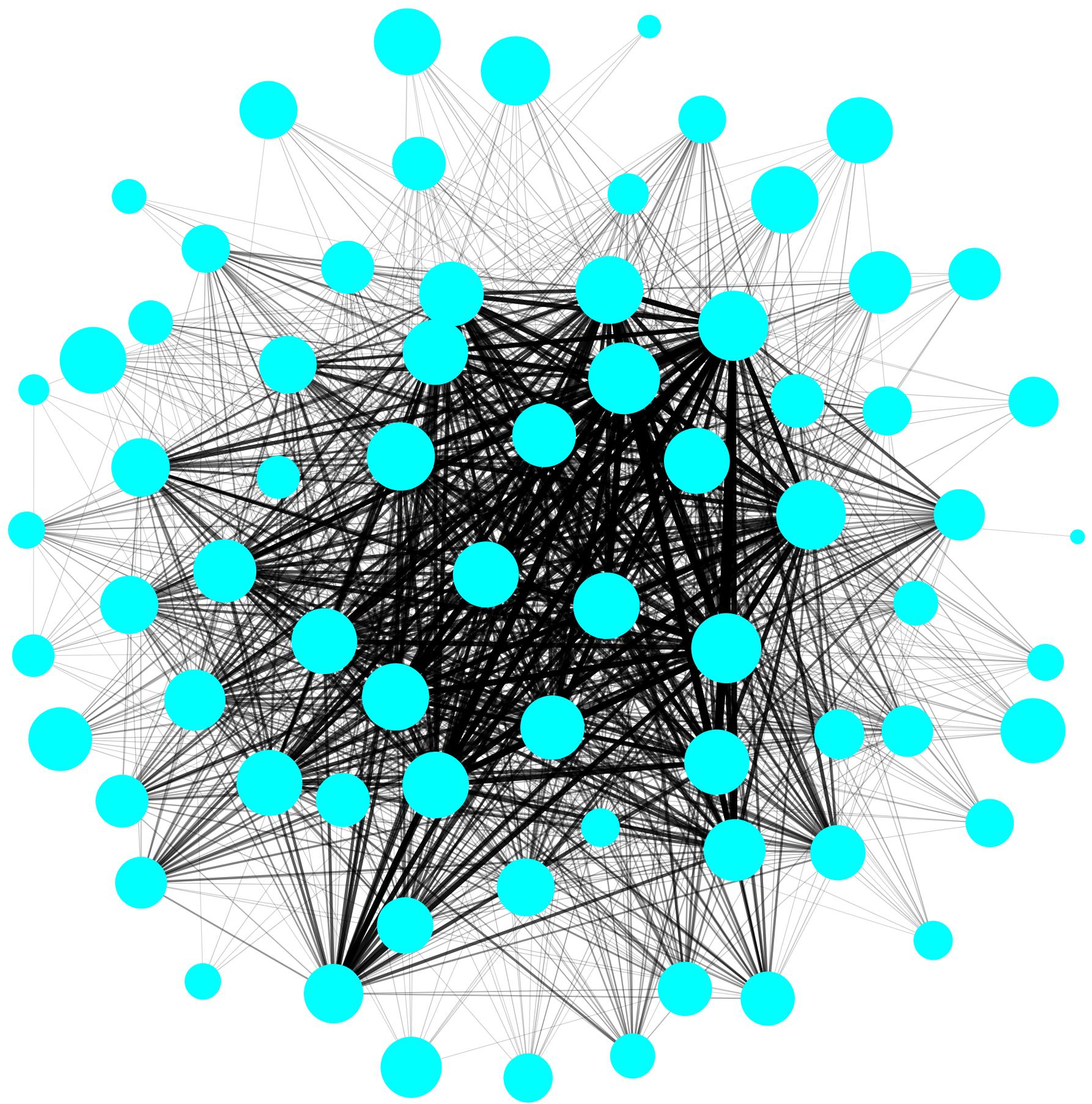
	Pathway	N	DE	P.DE
<i>path:gga00100</i>	Steroid biosynthesis	15	6	4.84e-08
<i>path:gga01100</i>	Metabolic pathways	1218	31	0.002531
<i>path:gga00900</i>	Terpenoid backbone biosynthesis	19	3	0.002732
<i>path:gga04340</i>	Hedgehog signaling pathway	47	4	0.005376
<i>path:gga03320</i>	PPAR signaling pathway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



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

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



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

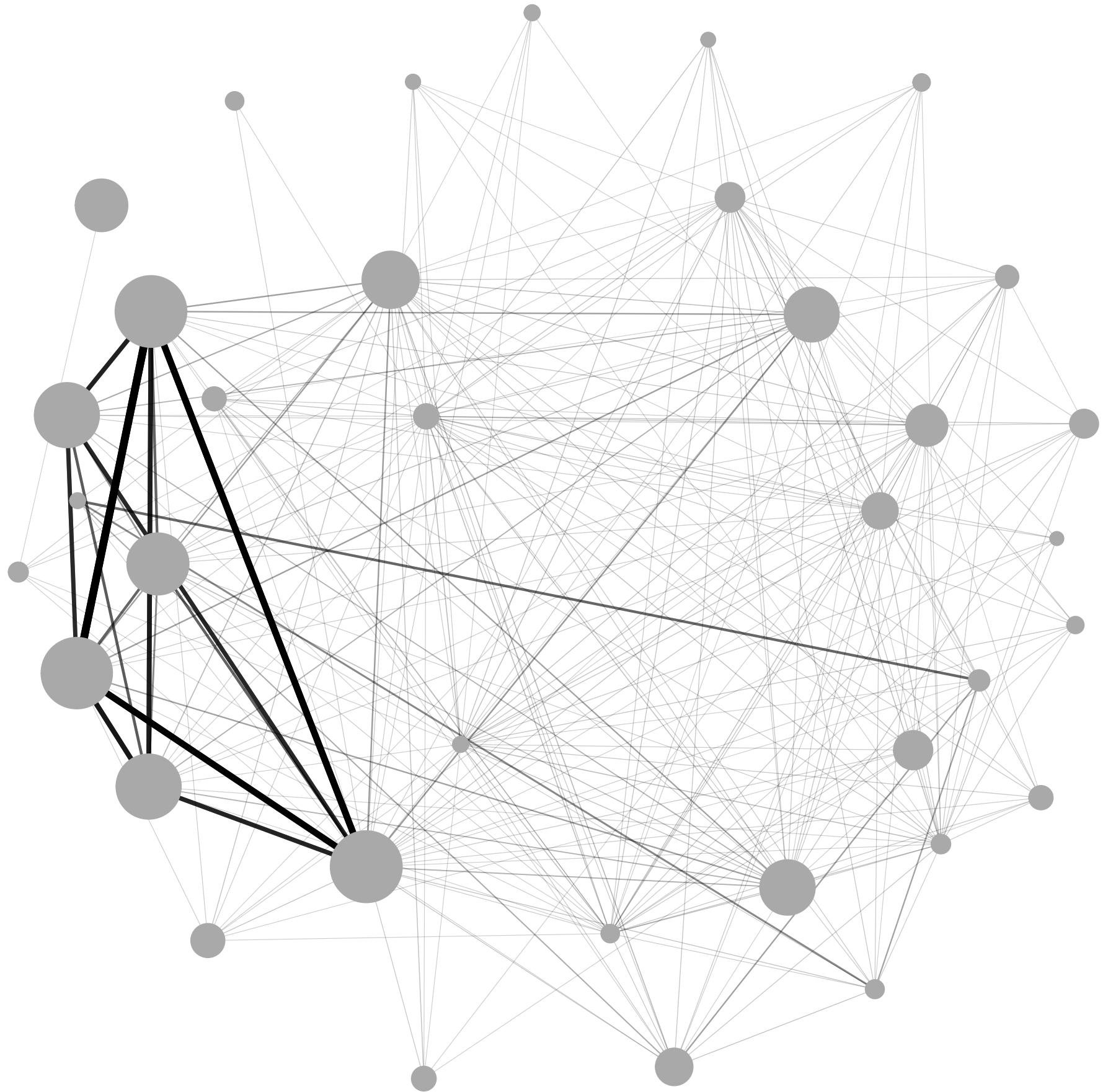
	Pathway	N	DE	P.DE
<i>path:gga04310</i>	Wnt signaling pathway	131	5	0.0007543
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	26	2	0.00888
<i>path:gga04350</i>	TGF–beta signaling pathway	84	3	0.01102
<i>path:gga00330</i>	Arginine and proline metabolism	38	2	0.01841
<i>path:gga04218</i>	Cellular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



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

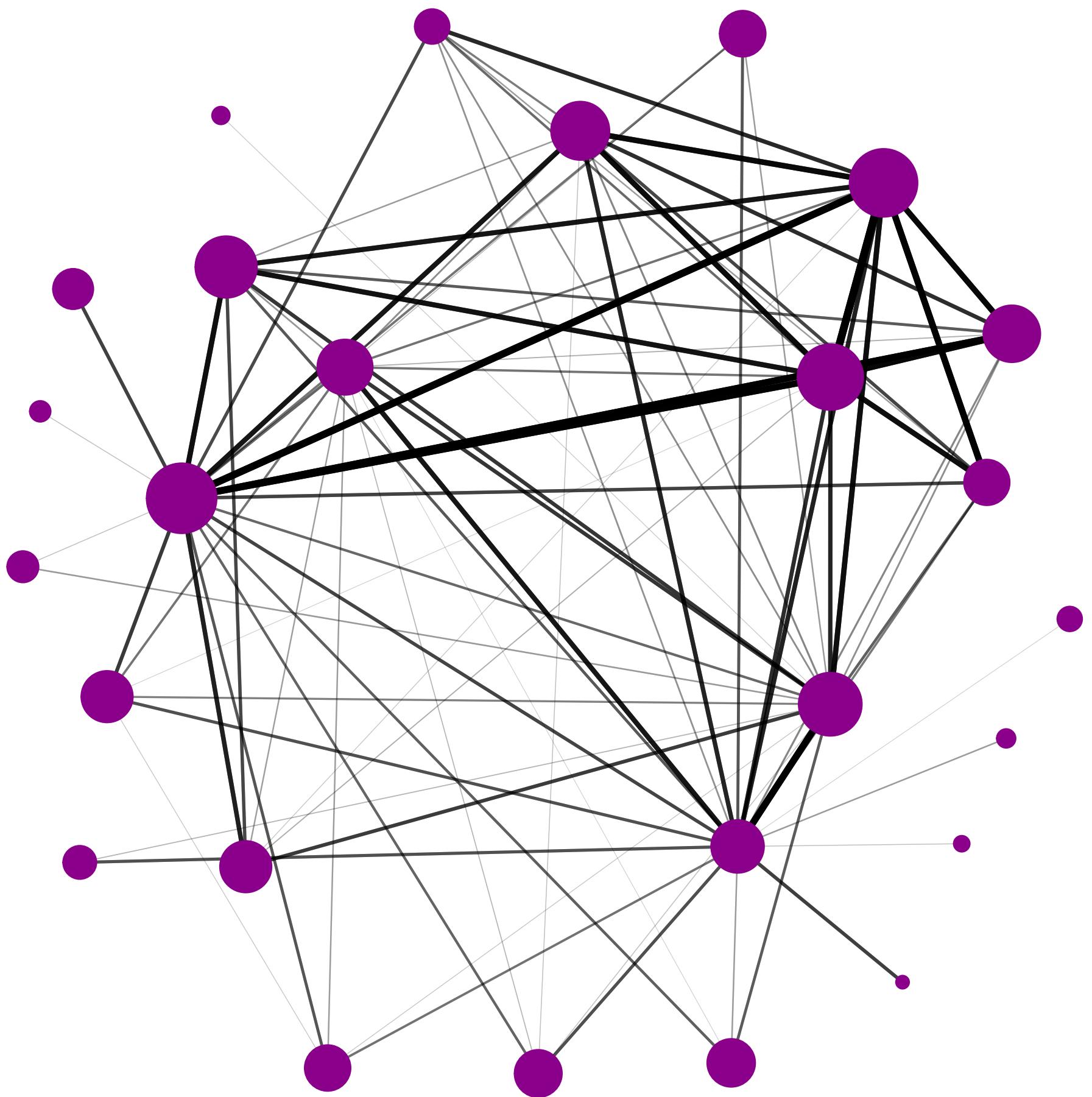
	Pathway	N	DE	P.DE
<i>path:gga04020</i>	Calcium signaling pathway	186	4	0.003479
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	3	0.007469
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.01343
<i>path:gga04260</i>	Cardiac muscle contraction	59	2	0.01685
<i>path:gga00603</i>	Glycosphingolipid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



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

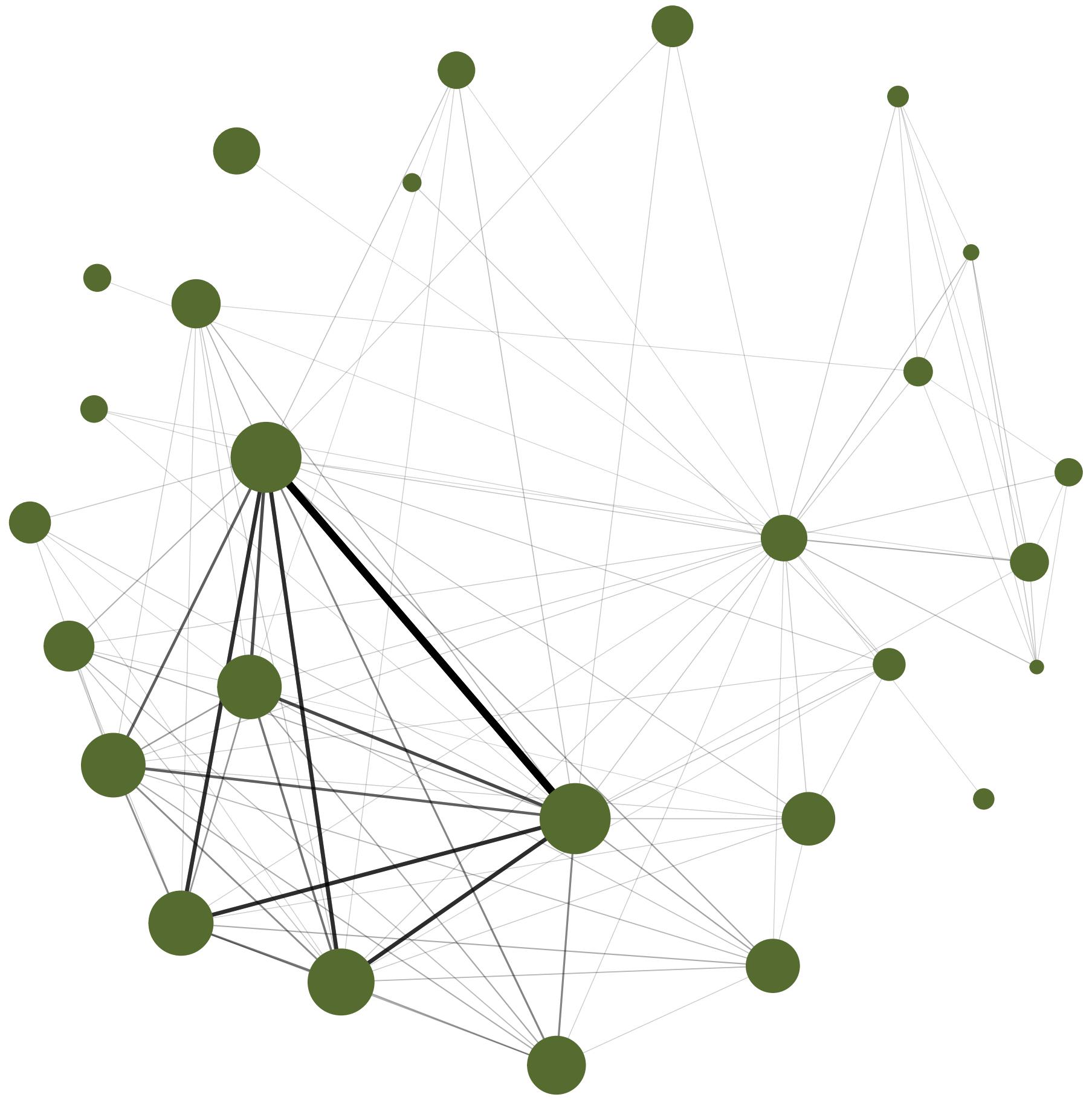
	Pathway	N	DE	P.DE
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	2	0.04433
<i>path:gga04145</i>	Phagosome	121	2	0.04568
<i>path:gga02010</i>	ABC transporters	34	1	0.09183
<i>path:gga04216</i>	Ferroptosis	34	1	0.09183
<i>path:gga04020</i>	Calcium signaling pathway	186	2	0.09672
<i>path:gga04512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



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

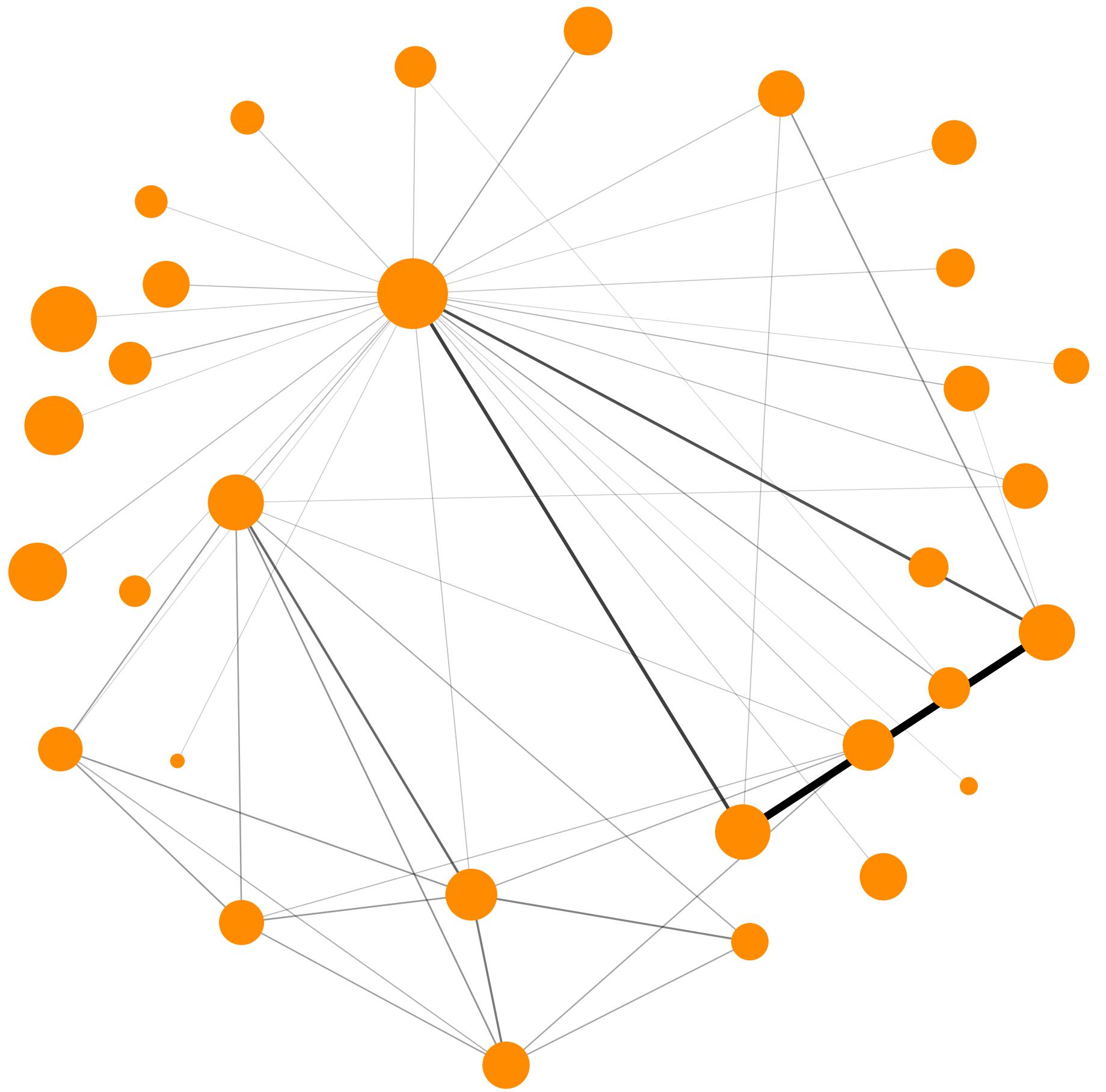
	Pathway	N	DE	P.DE
<i>path:gga00430</i>	Taurine and hypotaurine metabolism	12	2	0.000261
<i>path:gga00650</i>	Butanoate metabolism	19	2	0.0006702
<i>path:gga00410</i>	beta–Alanine metabolism	24	2	0.001075
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	4	0.001854
<i>path:gga00250</i>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



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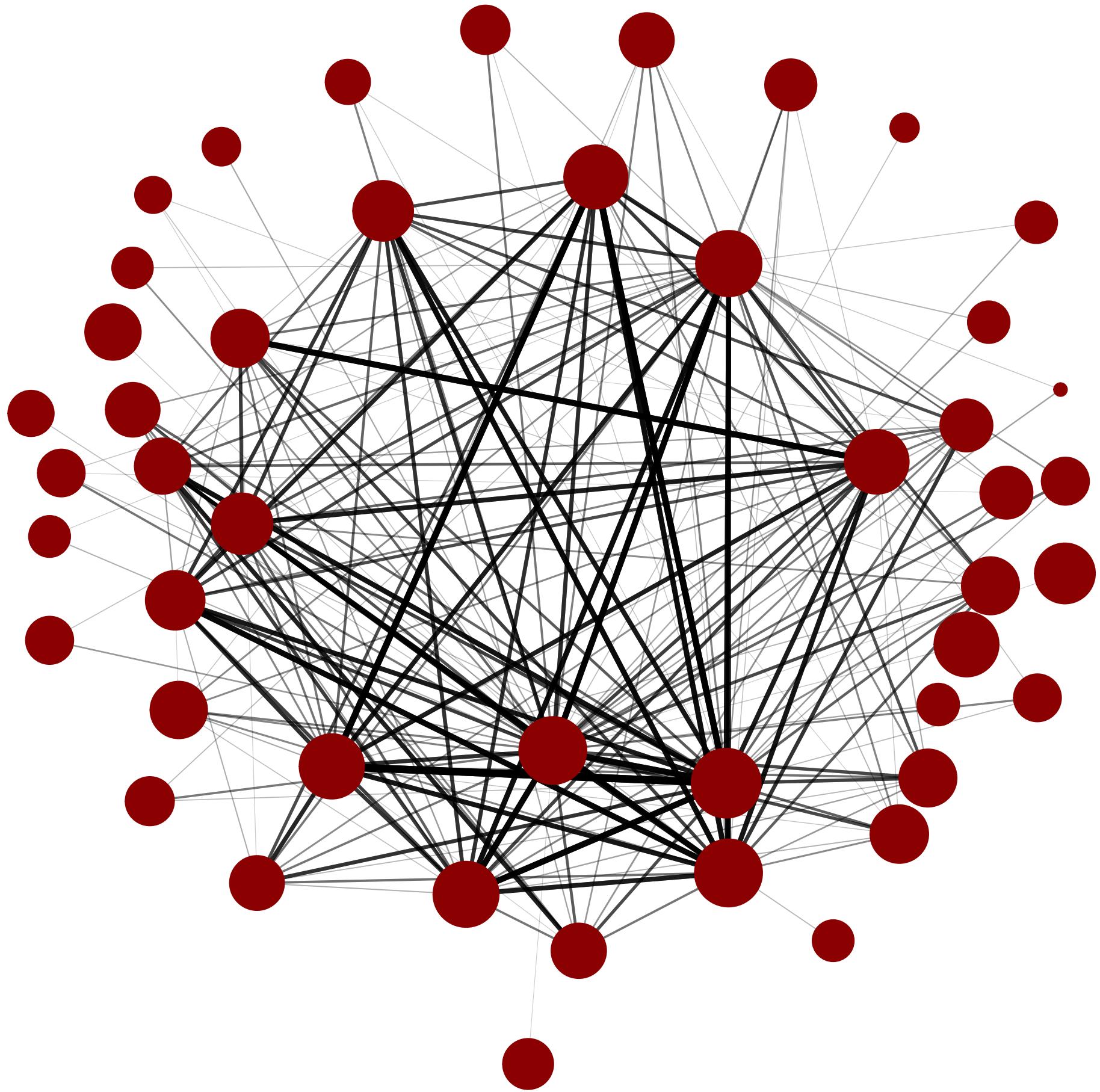
	Term	Ont	N	n	Adj. p-value
GO:0090303	positive regulation of wound healing	BP	4	2	1.866e-05
GO:1903036	positive regulation of response to wounding	BP	6	2	4.655e-05
GO:0001525	angiogenesis	BP	51	3	0.0001011
GO:0061041	regulation of wound healing	BP	9	2	0.0001113
GO:0048514	blood vessel morphogenesis	BP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

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



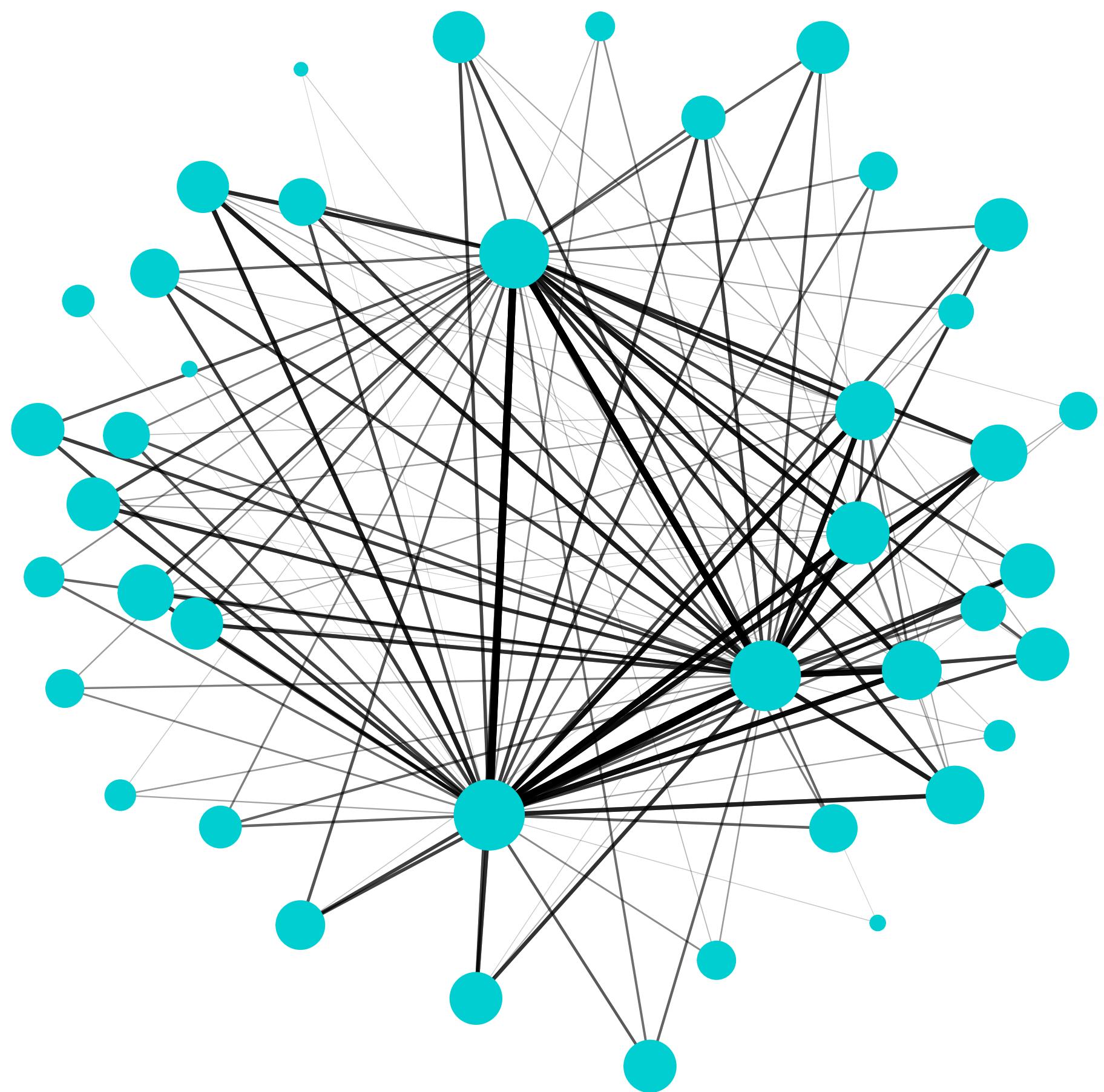
	Term	Ont	N	n	Adj. p-value
GO:0051302	regulation of cell division	BP	21	2	0.001169
GO:0031017	exocrine pancreas development	BP	1	1	0.002433
GO:0038028	insulin receptor signaling pathway via phosphatidylinositol 3-kinase	BP	1	1	0.002433
GO:2000467	positive regulation of glycogen (starch) synthase activity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

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



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

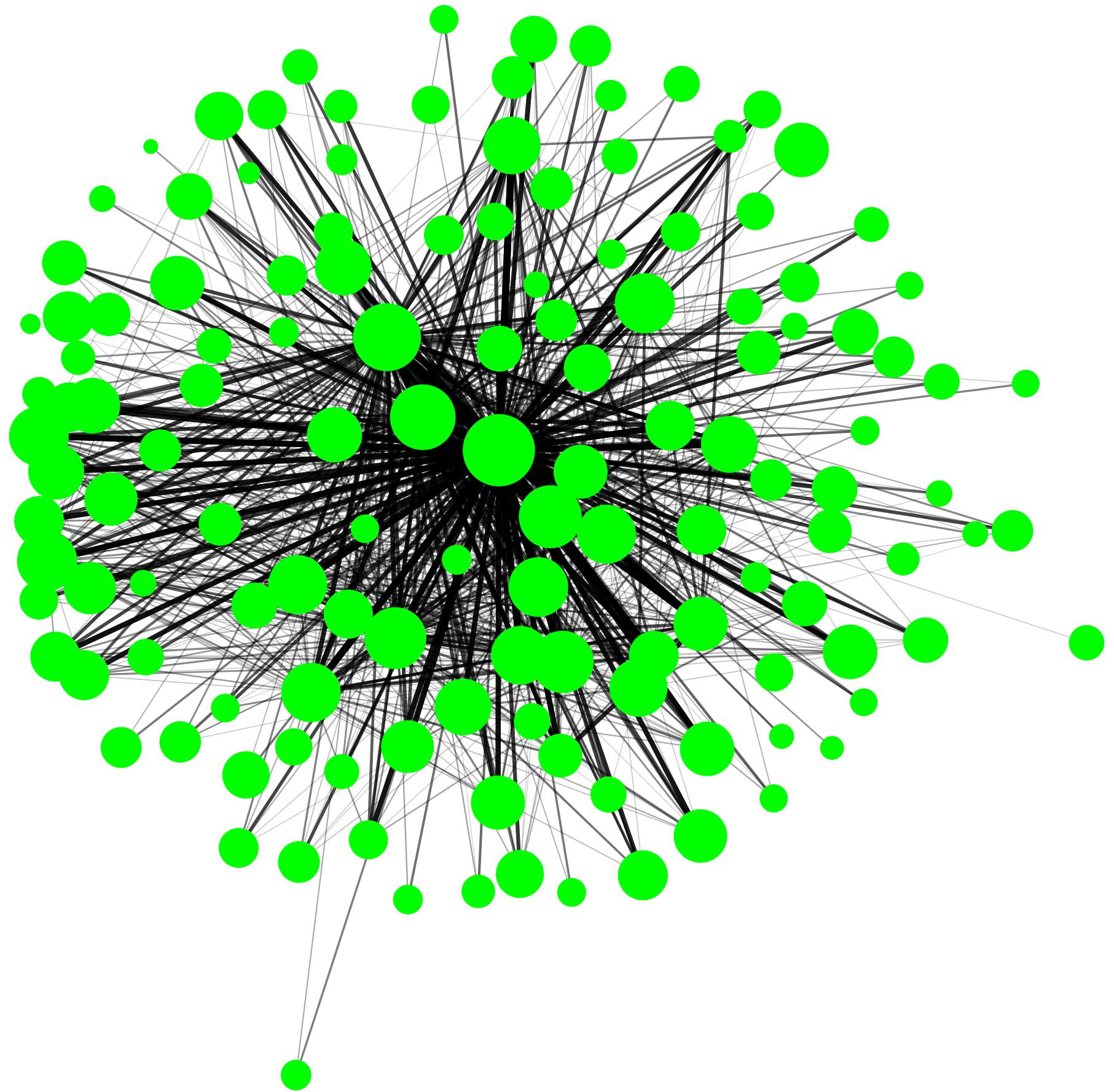
	Pathway	N	DE	P.DE
<i>path:gga00514</i>	Other types of O-glycan biosynthesis	41	3	0.000349
<i>path:gga04080</i>	Neuroactive ligand-receptor interaction	263	5	0.001829
<i>path:gga00512</i>	Mucin type O-glycan biosynthesis	29	2	0.004263
<i>path:gga04010</i>	MAPK signaling pathway	231	3	0.04268
<i>path:gga00510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



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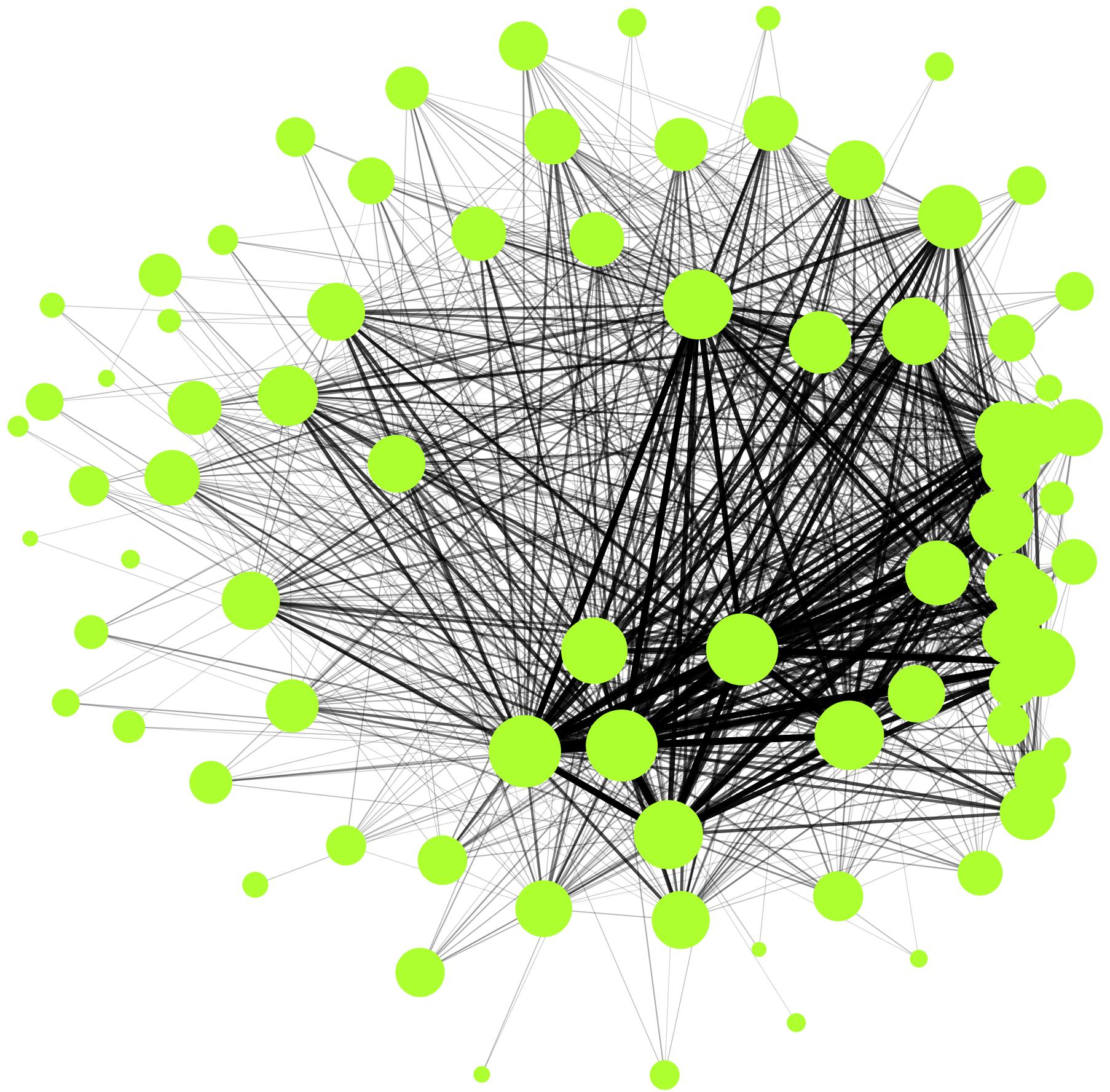
	Term	Ont	N	n	Adj. p-value
GO:0048639	positive regulation of developmental growth	BP	17	2	0.001206
GO:0045927	positive regulation of growth	BP	23	2	0.002218
GO:0035082	axoneme assembly	BP	1	1	0.003061
GO:0030317	flagellated sperm motility	BP	1	1	0.003061
GO:0001951	intestinal D–glucose absorption	BP	1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

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



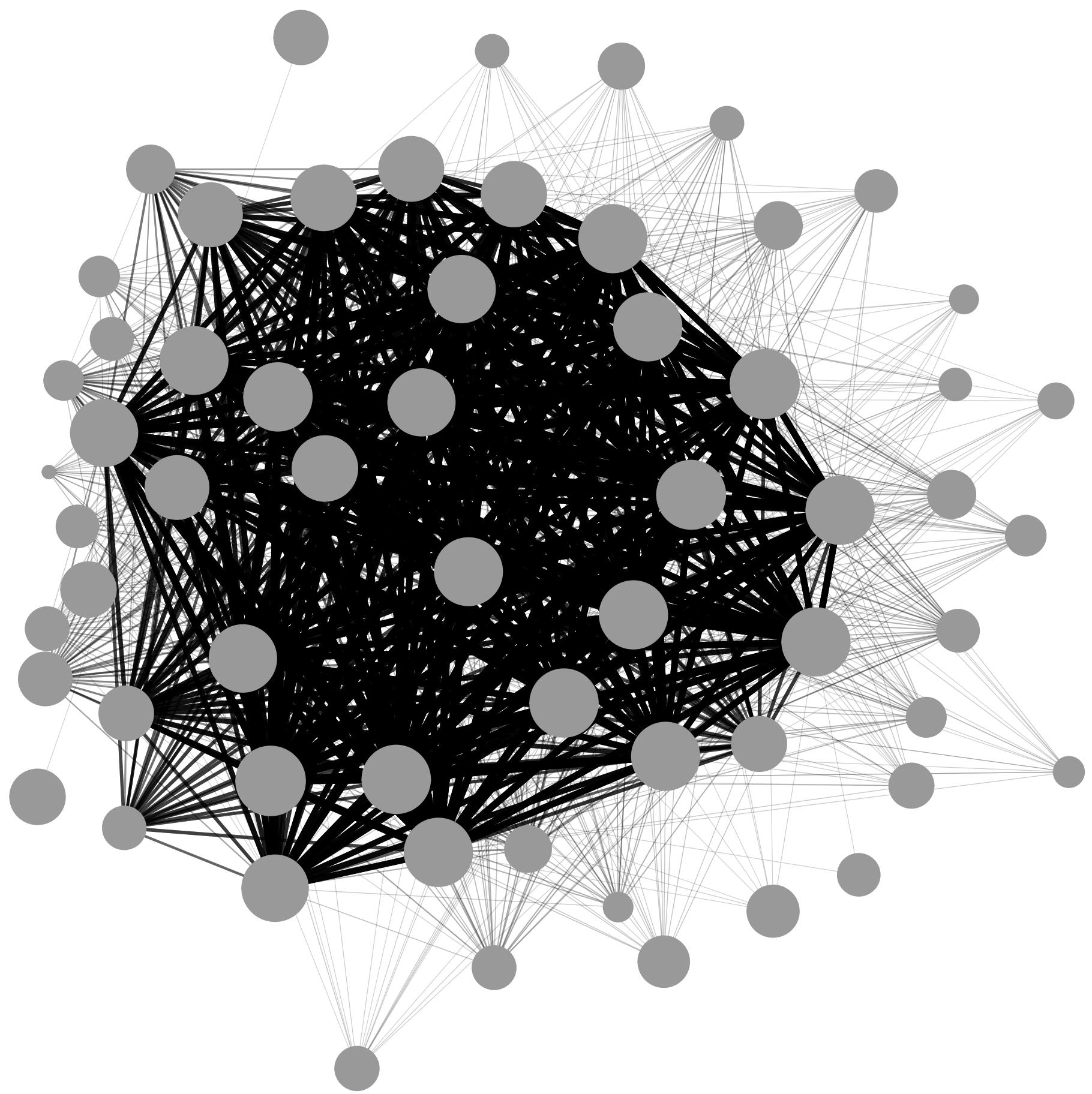
	Term	Ont	N	n	Adj. p-value
GO:0098660	inorganic ion transmembrane transport	BP	56	7	1.497e–06
GO:0034220	ion transmembrane transport	BP	100	8	8.014e–06
GO:0098662	inorganic cation transmembrane transport	BP	51	6	1.242e–05
GO:0006812	cation transport	BP	79	7	1.541e–05
GO:0055085	transmembrane transport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

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



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

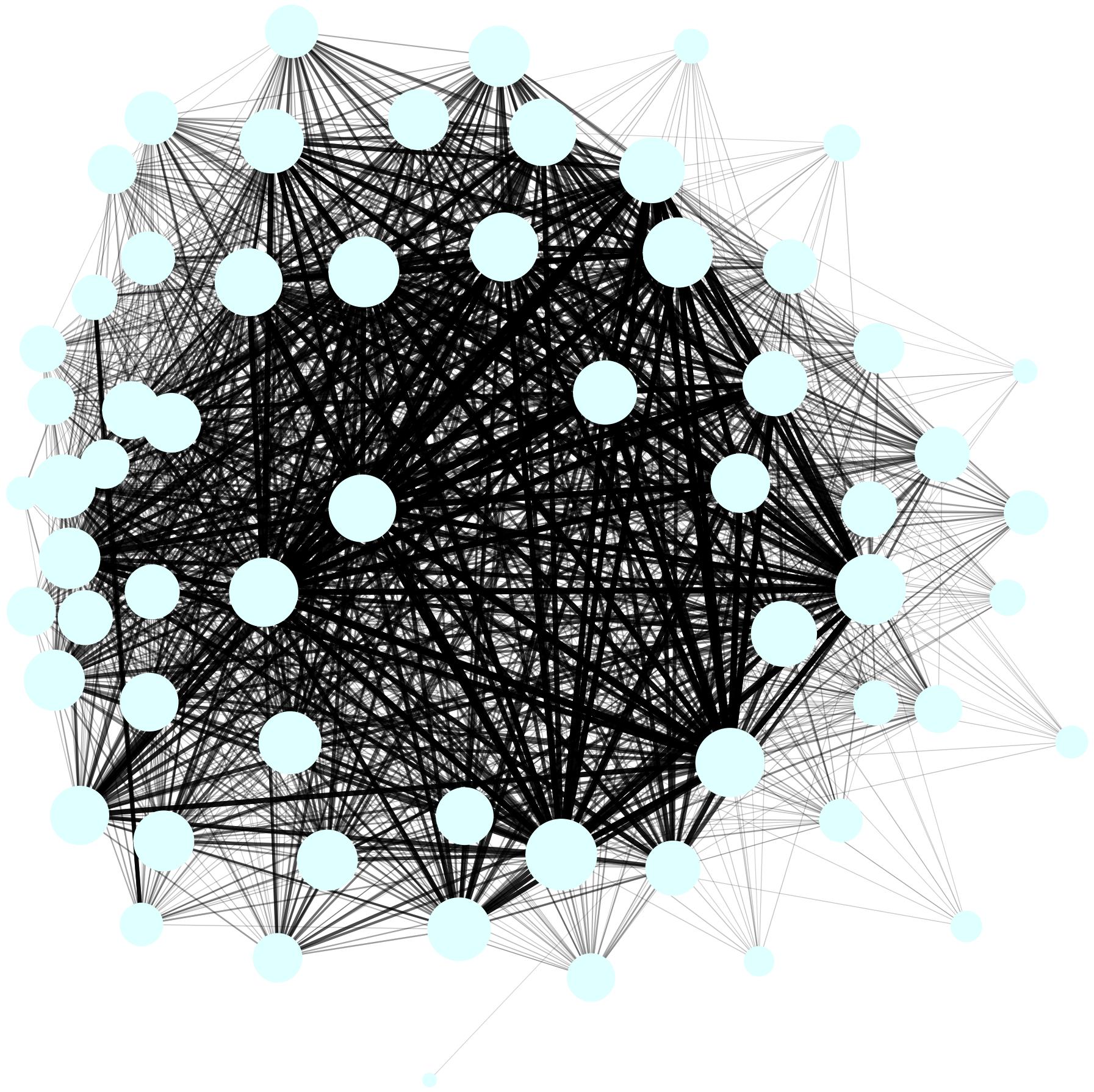
	Pathway	N	DE	P.DE
<i>path:gga04310</i>	Wnt signaling pathway	131	5	0.001096
<i>path:gga04512</i>	ECM–receptor interaction	65	3	0.006833
<i>path:gga04350</i>	TGF–beta signaling pathway	84	3	0.01375
<i>path:gga00220</i>	Arginine biosynthesis	16	1	0.09133
<i>path:gga00534</i>	Glycosaminoglycan biosynthesis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



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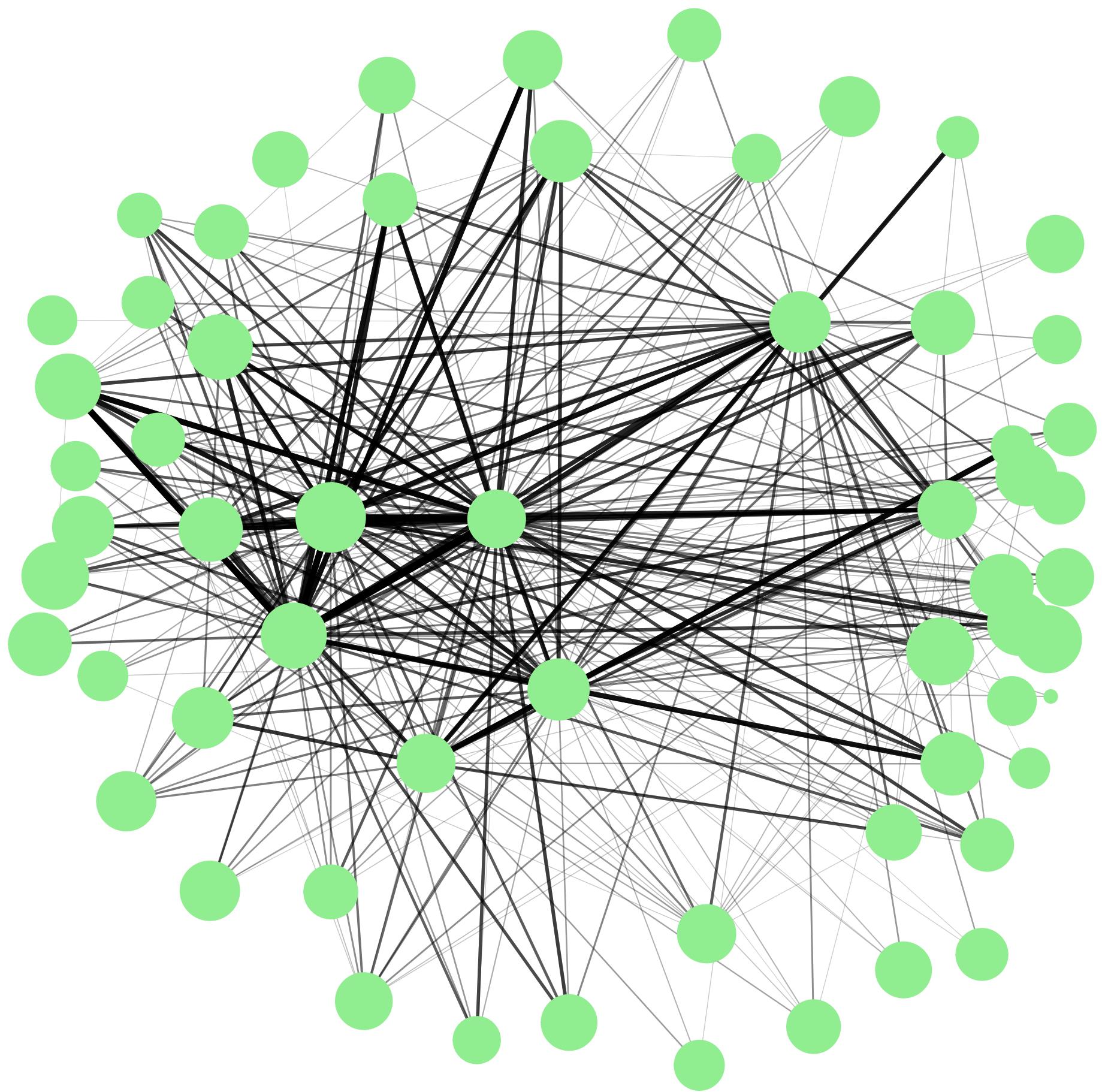
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GO:0006412	translation	BP	87	11	1.679e-13
GO:0043043	peptide biosynthetic process	BP	88	11	1.913e-13
GO:0043604	amide biosynthetic process	BP	99	11	7.25e-13
GO:0006518	peptide metabolic process	BP	106	11	1.56e-12
GO:0043603	cellular amide metabolic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

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



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

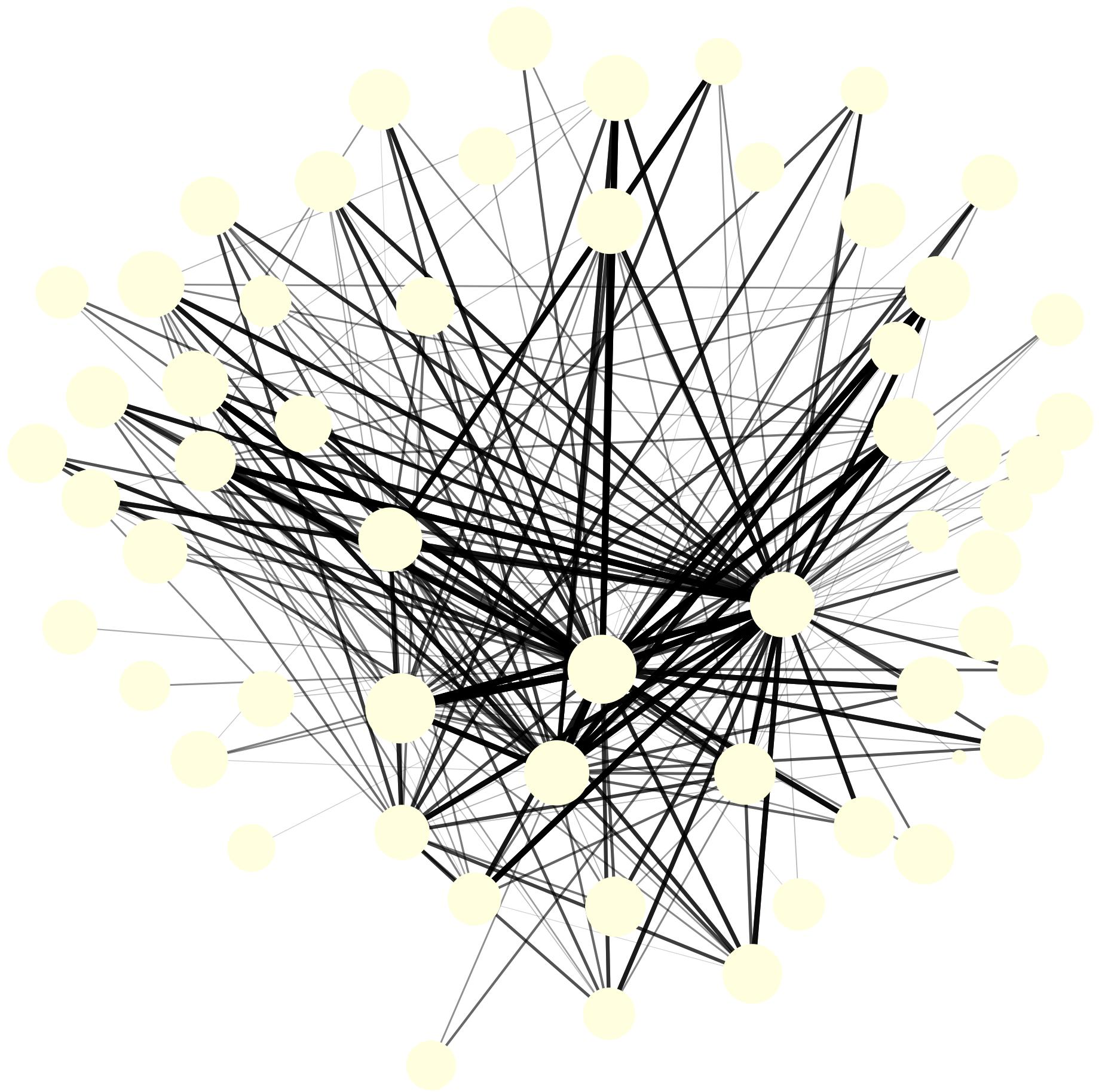
	Pathway	N	DE	P.DE
<i>path:gga00910</i>	Nitrogen metabolism	13	2	0.001486
<i>path:gga00030</i>	Pentose phosphate pathway	25	2	0.005521
<i>path:gga00051</i>	Fructose and mannose metabolism	34	2	0.01006
<i>path:gga00010</i>	Glycolysis / Gluconeogenesis	46	2	0.01794
<i>path:gga01230</i>	Biosynthesis of amino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



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

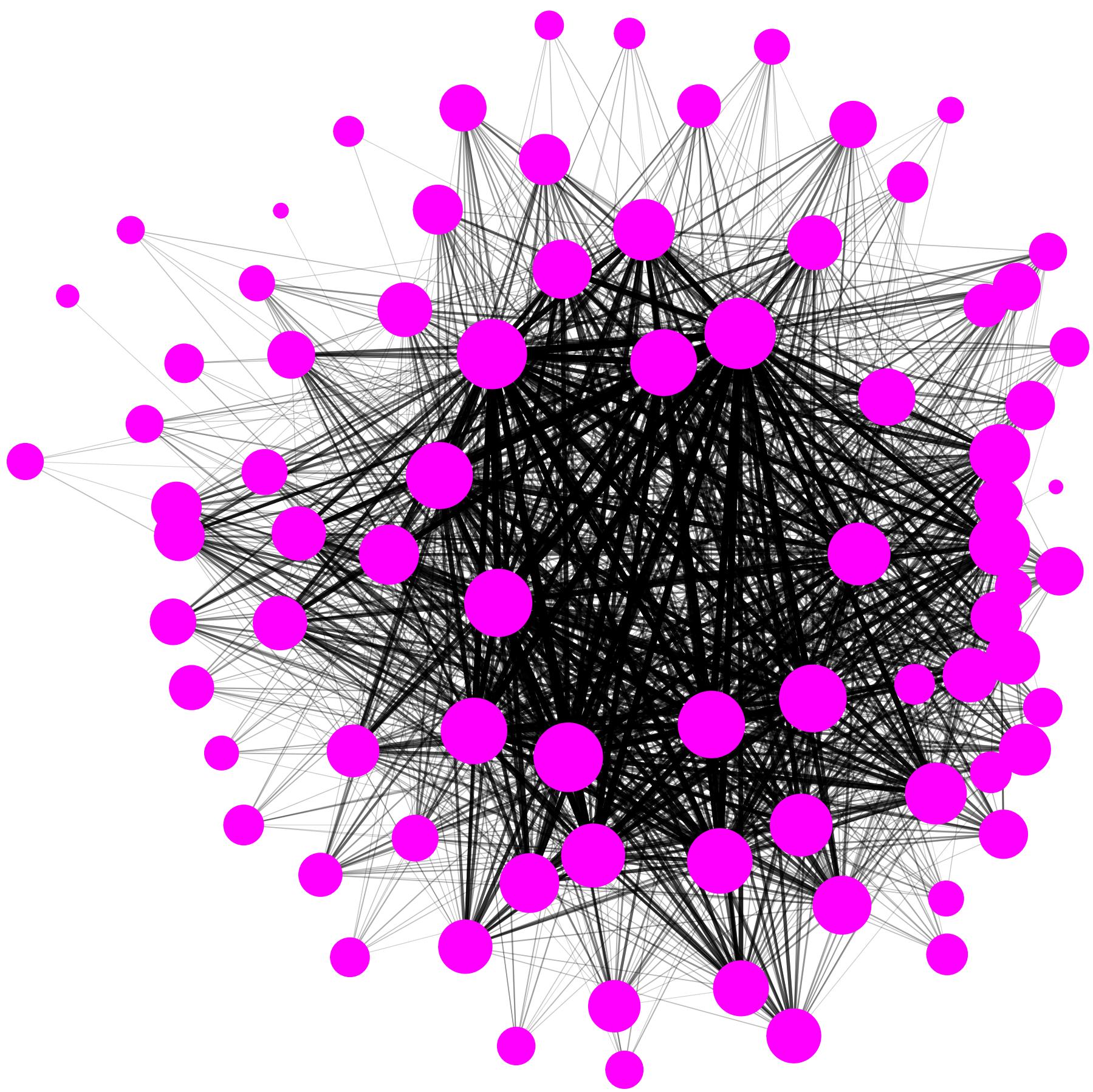
	Pathway	N	DE	P.DE
<i>path:gga04145</i>	Phagosome	121	7	1.326e-06
<i>path:gga04540</i>	Gap junction	78	4	0.0004581
<i>path:gga05132</i>	Salmonella infection	215	5	0.00312
<i>path:gga00190</i>	Oxidative phosphorylation	99	3	0.0108
<i>path:gga03265</i>	Virion – Lyssavirus	4	1	0.0184
<i>path:gga04514</i>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



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

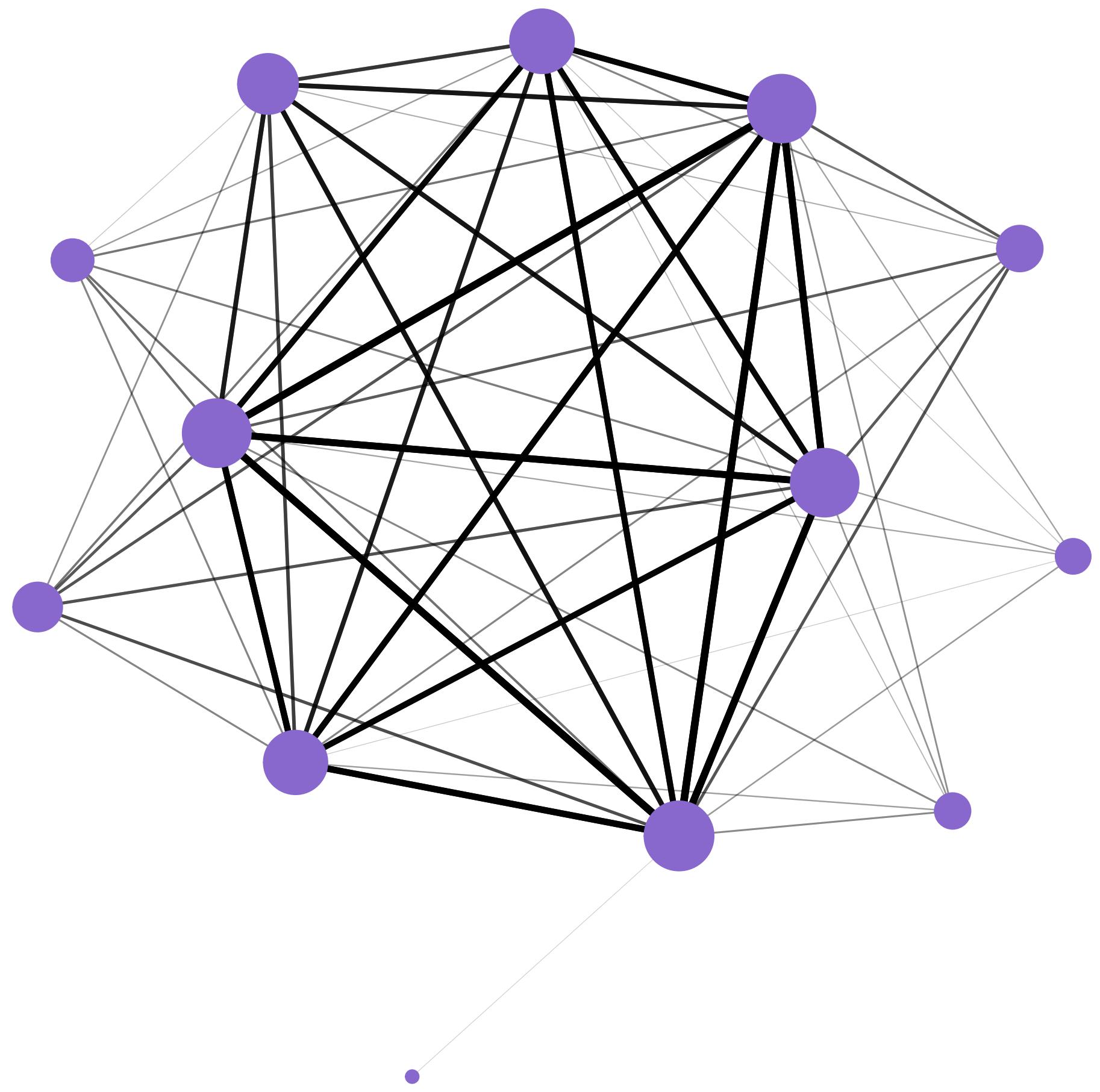
	Pathway	N	DE	P.DE
<i>path:gga04810</i>	Regulation of actin cytoskeleton	179	5	0.001298
<i>path:gga00910</i>	Nitrogen metabolism	13	2	0.001538
<i>path:gga03320</i>	PPAR signaling pathway	55	3	0.001985
<i>path:gga00220</i>	Arginine biosynthesis	16	2	0.002346
<i>path:gga00982</i>	Drug metabolism – cytochrome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



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

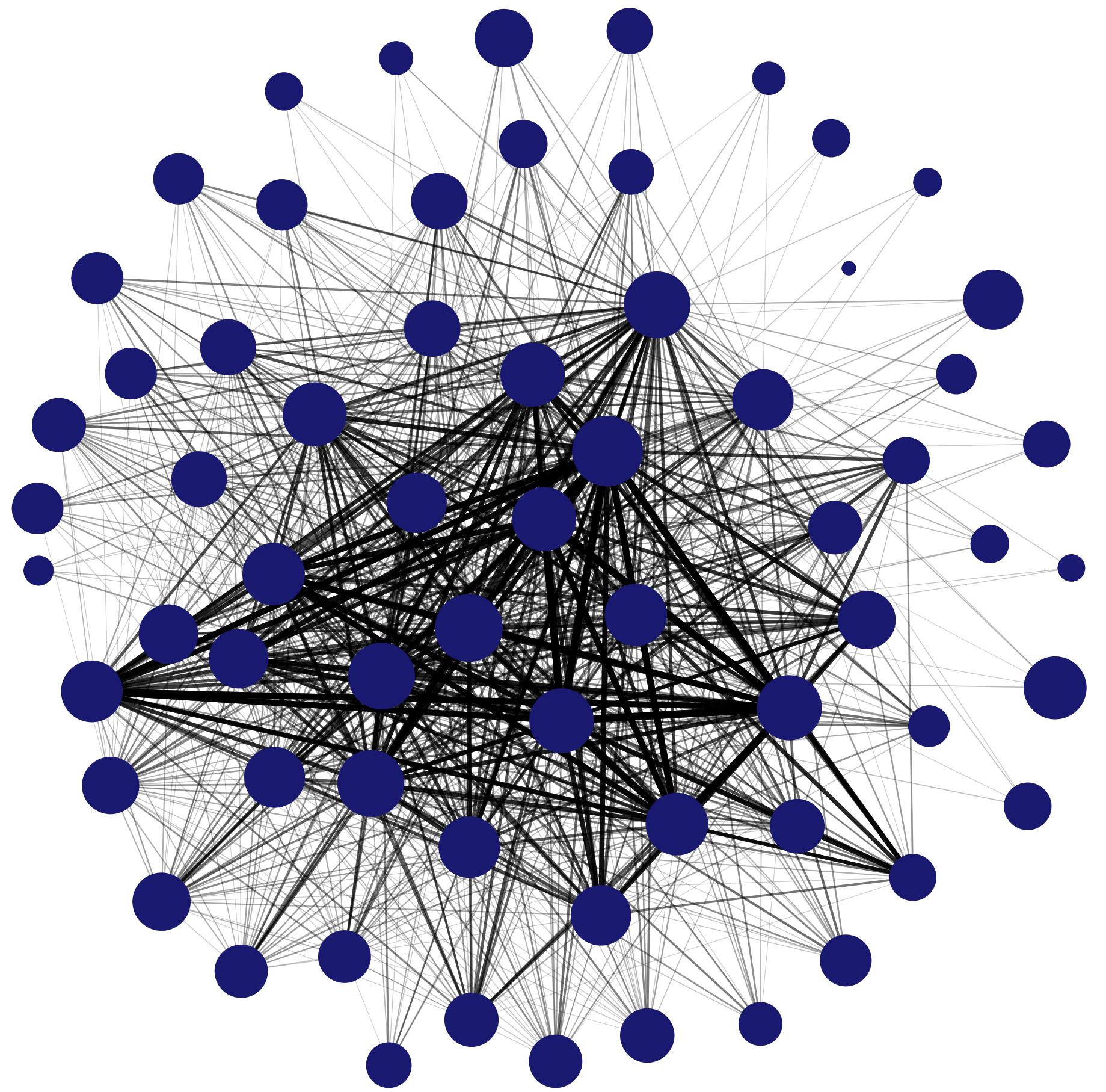
	Pathway	N	DE	P.DE
<i>path:gga00982</i>	Drug metabolism – cytochrome P450	26	2	0.01067
<i>path:gga00980</i>	Metabolism of xenobiotics by cytochrome P450	27	2	0.01147
<i>path:gga00590</i>	Arachidonic acid metabolism	36	2	0.01989
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	5	0.02136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



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

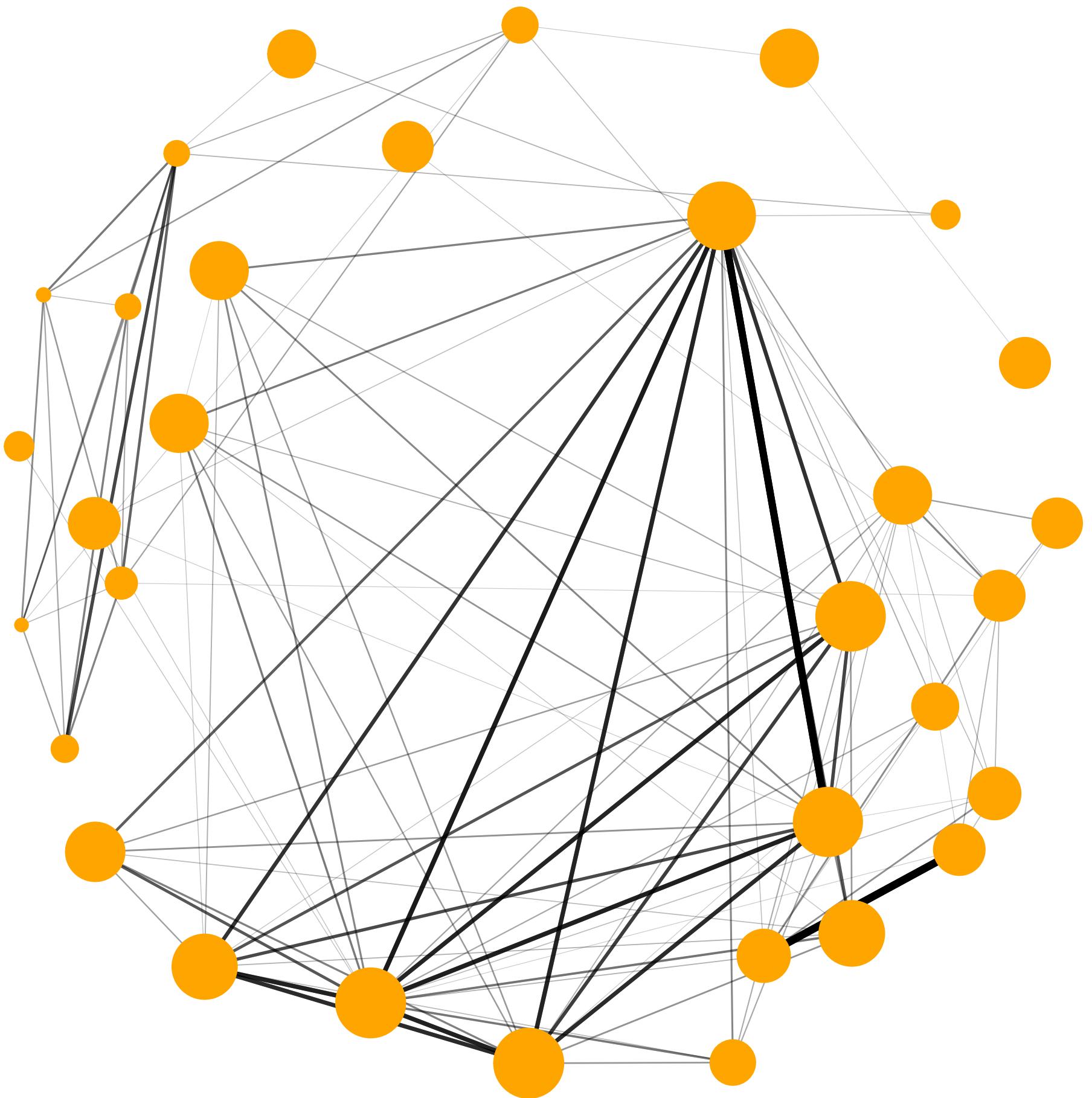
	Pathway	N	DE	P.DE
<i>path:gga04510</i>	Focal adhesion	166	3	0.0005642
<i>path:gga04810</i>	Regulation of actin cytoskeleton	179	3	0.0007029
<i>path:gga04512</i>	ECM–receptor interaction	65	2	0.001928
<i>path:gga03266</i>	Virion – Herpesvirus	4	1	0.004075
<i>path:gga00514</i>	Other types of O–glycan biosynthesis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



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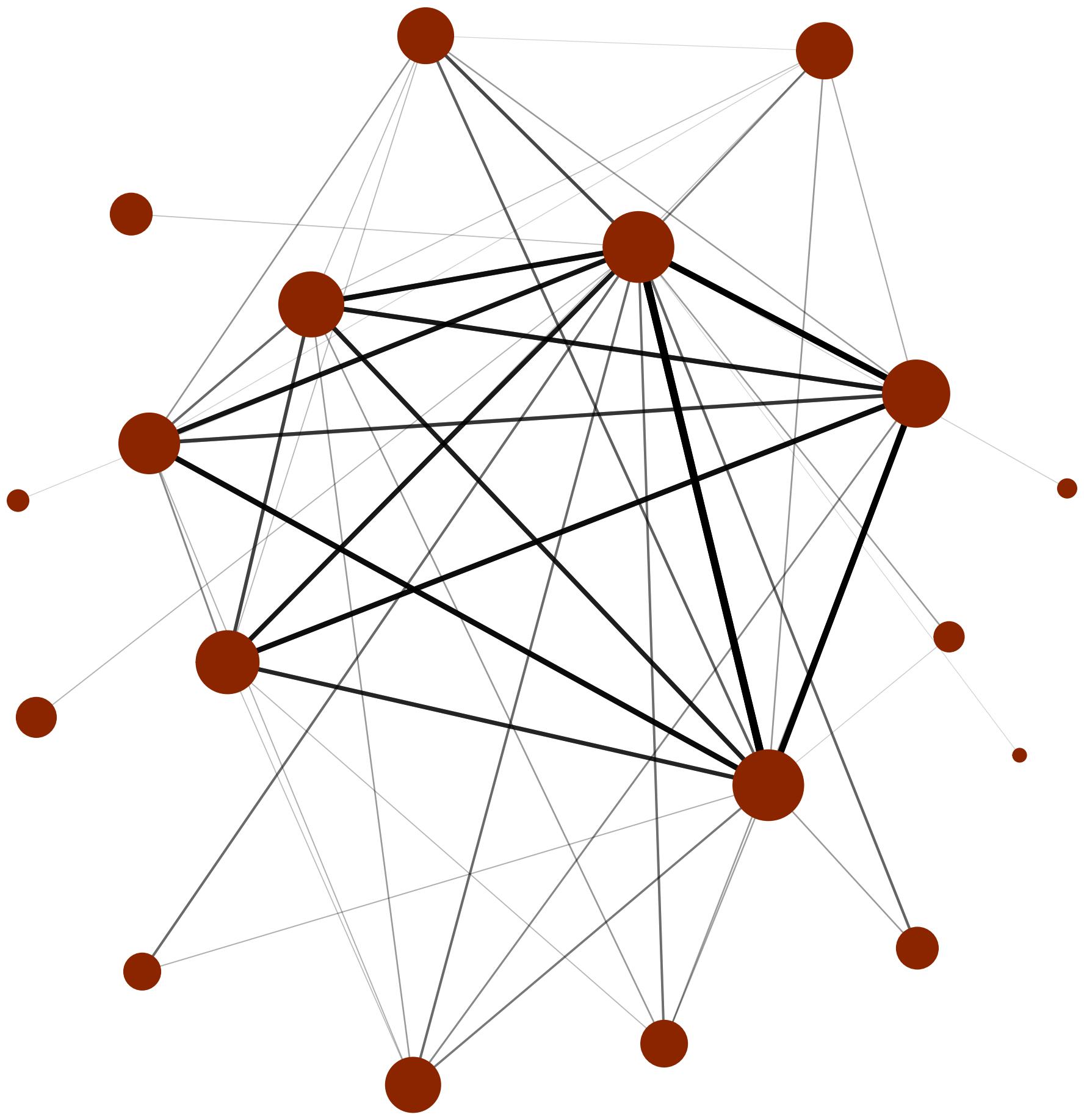
	Term	Ont	N	n	Adj. p-value
GO:0021516	dorsal spinal cord development	BP	6	2	0.0003231
GO:0034220	ion transmembrane transport	BP	100	4	0.001244
GO:0055085	transmembrane transport	BP	112	4	0.001889
GO:0098660	inorganic ion transmembrane transport	BP	56	3	0.002304
GO:0060078	regulation of postsynaptic membrane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

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



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

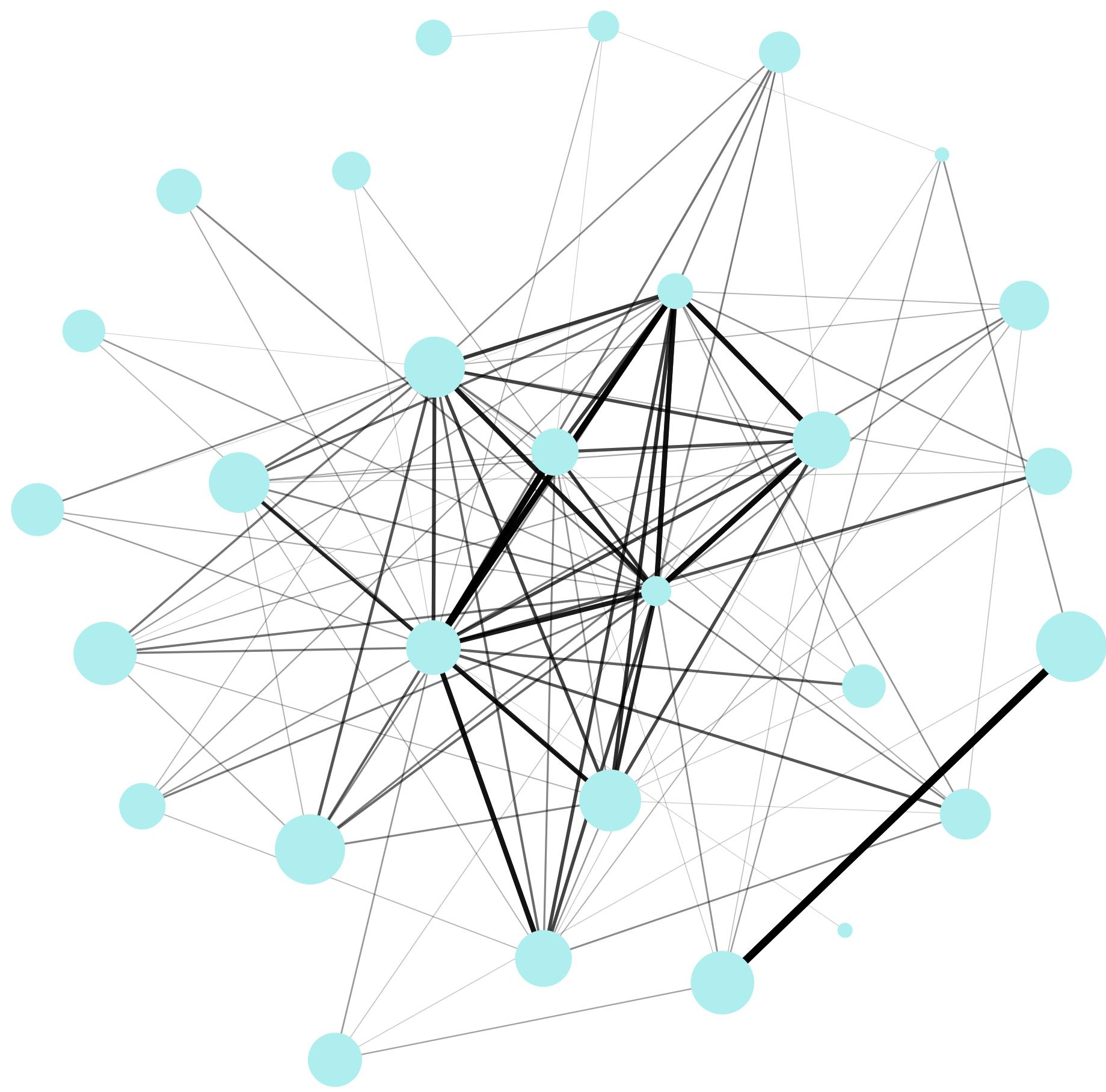
	Pathway	N	DE	P.DE
<i>path:gga04520</i>	Adherens junction	69	2	0.0114
<i>path:gga00860</i>	Porphyrin metabolism	19	1	0.04383
<i>path:gga00900</i>	Terpenoid backbone biosynthesis	19	1	0.04383
<i>path:gga04510</i>	Focal adhesion	166	2	0.05785
<i>path:gga05132</i>	Salmonella infection	215	2	0.09061
<i>path:gga04010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



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2	NA								
3	NA	NA							

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

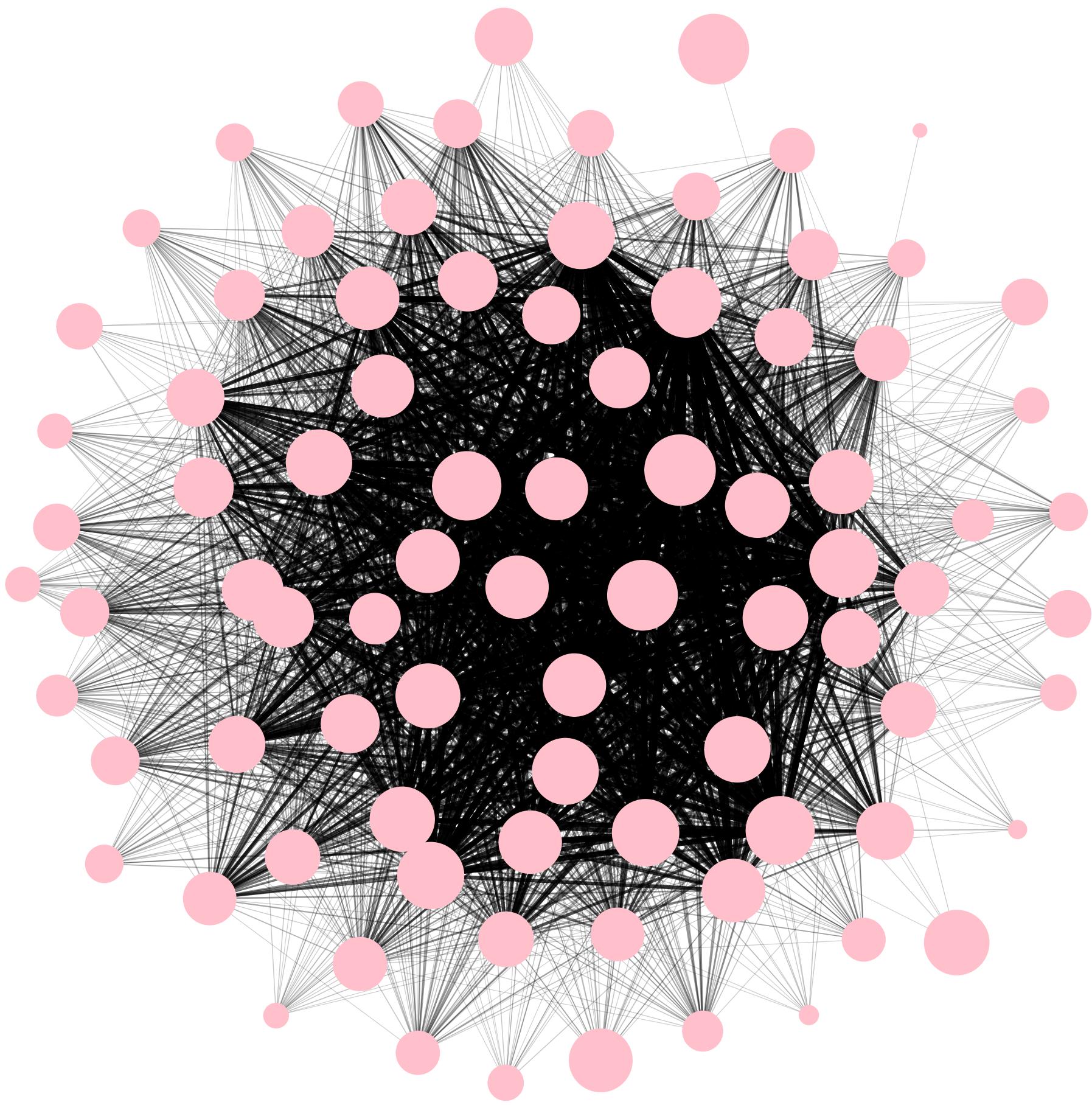
	Pathway	N	DE	P.DE
<i>path:gga04512</i>	ECM–receptor interaction	65	2	0.002936
<i>path:gga00531</i>	Glycosaminoglycan degradation	15	1	0.01868
<i>path:gga03320</i>	PPAR signaling pathway	55	1	0.06691
<i>path:gga04920</i>	Adipocytokine signaling pathway	59	1	0.07161
<i>path:gga04514</i>	Cell adhesion molecules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



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4	NA	NA	NA	NA				

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

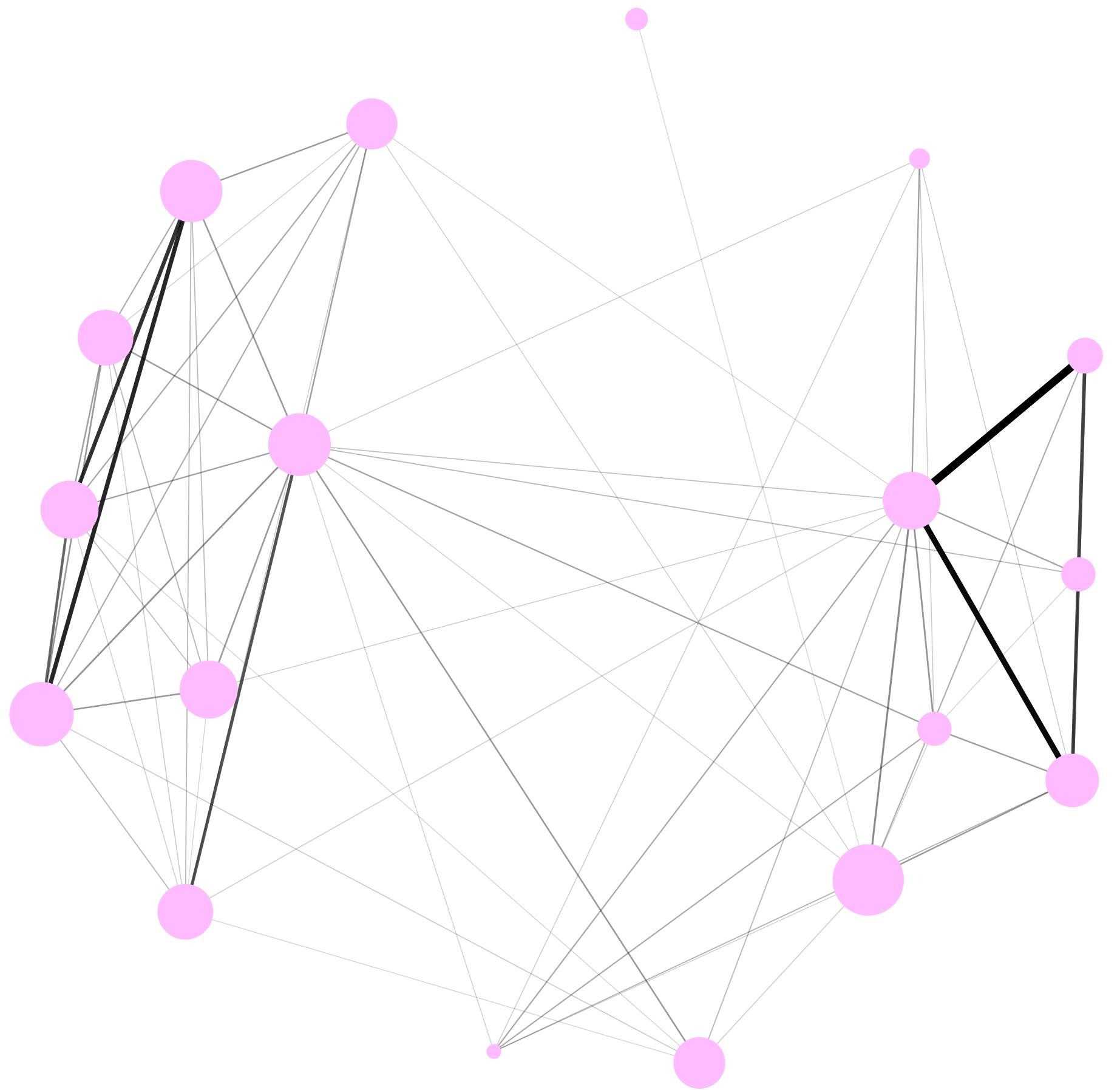
	Pathway	N	DE	P.DE
<i>path:gga04514</i>	Cell adhesion molecules	98	3	0.001129
<i>path:gga04330</i>	Notch signaling pathway	52	1	0.1046
<i>path:gga04137</i>	Mitophagy – animal	62	1	0.1235
<i>path:gga04512</i>	ECM–receptor interaction	65	1	0.1291
<i>path:gga04916</i>	Melanogenesis	80	1	0.1565
<i>path:gga04068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



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10	NA							
11	NA	NA	NA	NA				

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

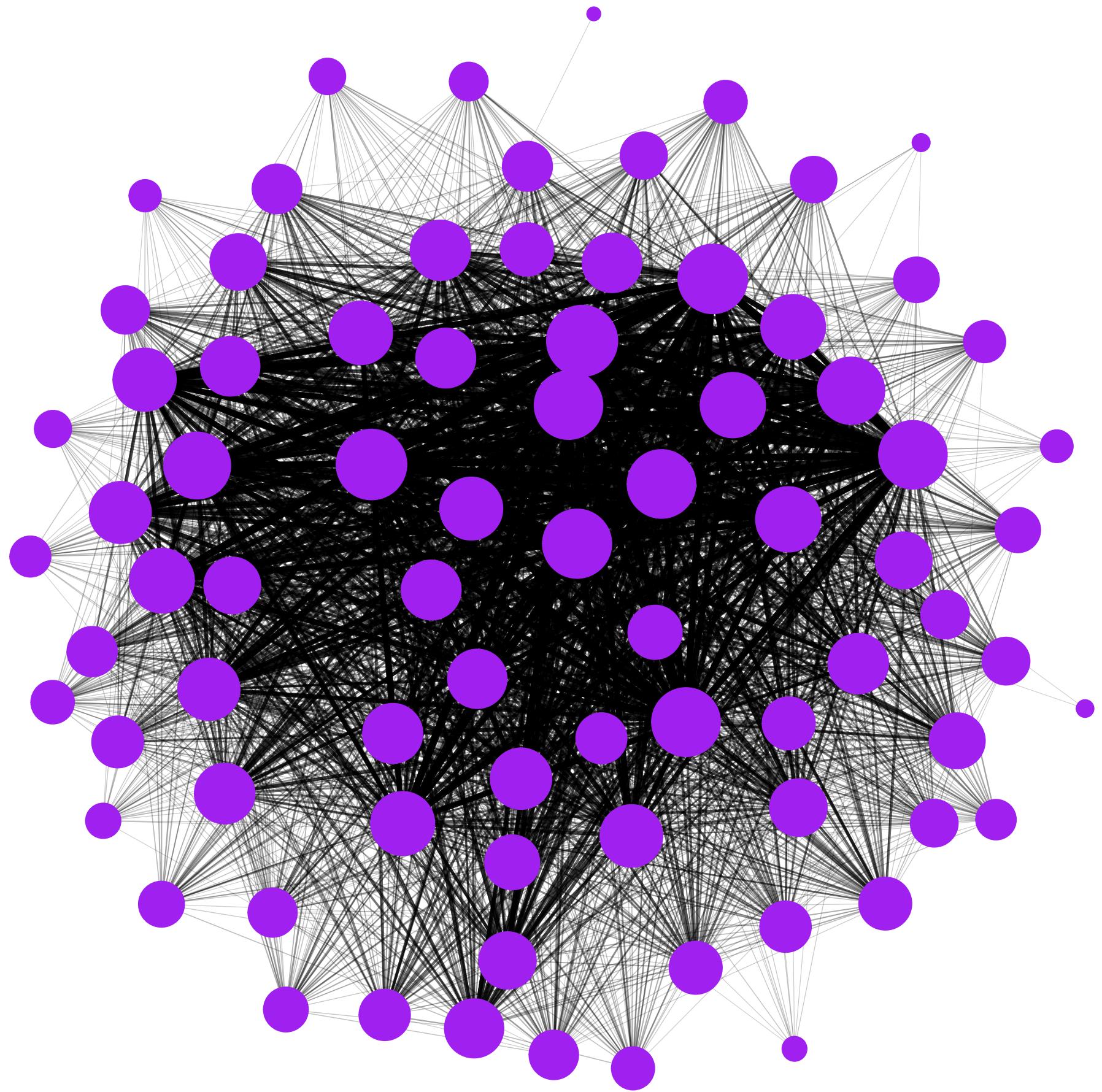
	Pathway	N	DE	P.DE
<i>path:gga00565</i>	Ether lipid metabolism	33	3	0.001095
<i>path:gga03264</i>	Virion – Flavivirus	3	1	0.01849
<i>path:gga04514</i>	Cell adhesion molecules	98	3	0.0229
<i>path:gga04068</i>	FoxO signaling pathway	105	3	0.02738
<i>path:gga04210</i>	Apoptosis	112	3	0.03228
<i>path:gga04530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



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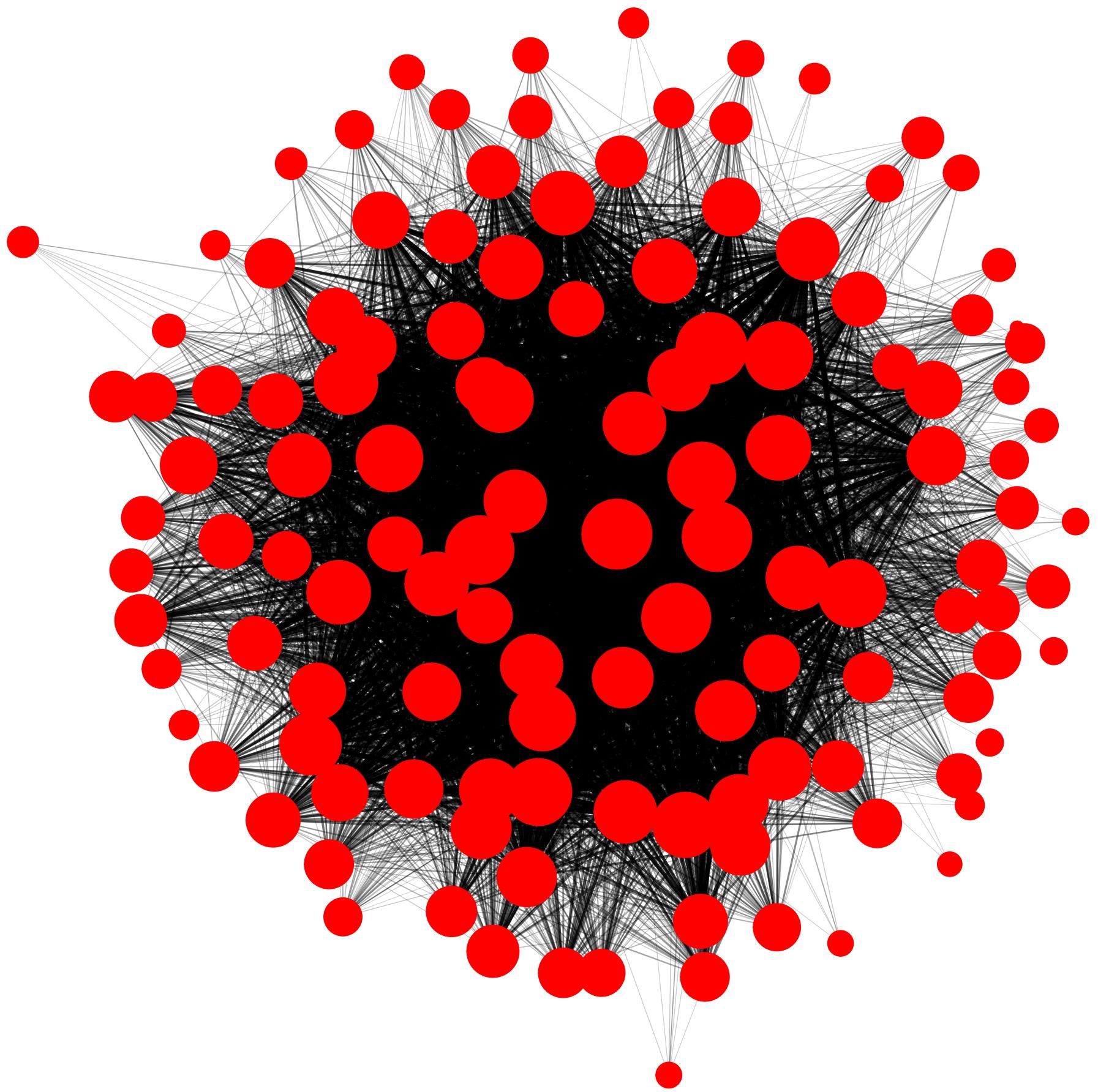
	Term	Ont	N	n	Adj. p-value
GO:0098974	postsynaptic actin cytoskeleton organization	BP	3	2	5.022e-06
GO:0099188	postsynaptic cytoskeleton organization	BP	3	2	5.022e-06
GO:0140238	presynaptic endocytosis	BP	4	2	1.004e-05
GO:0048488	synaptic vesicle endocytosis	BP	4	2	1.004e-05
GO:0036465	synaptic vesicle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

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



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

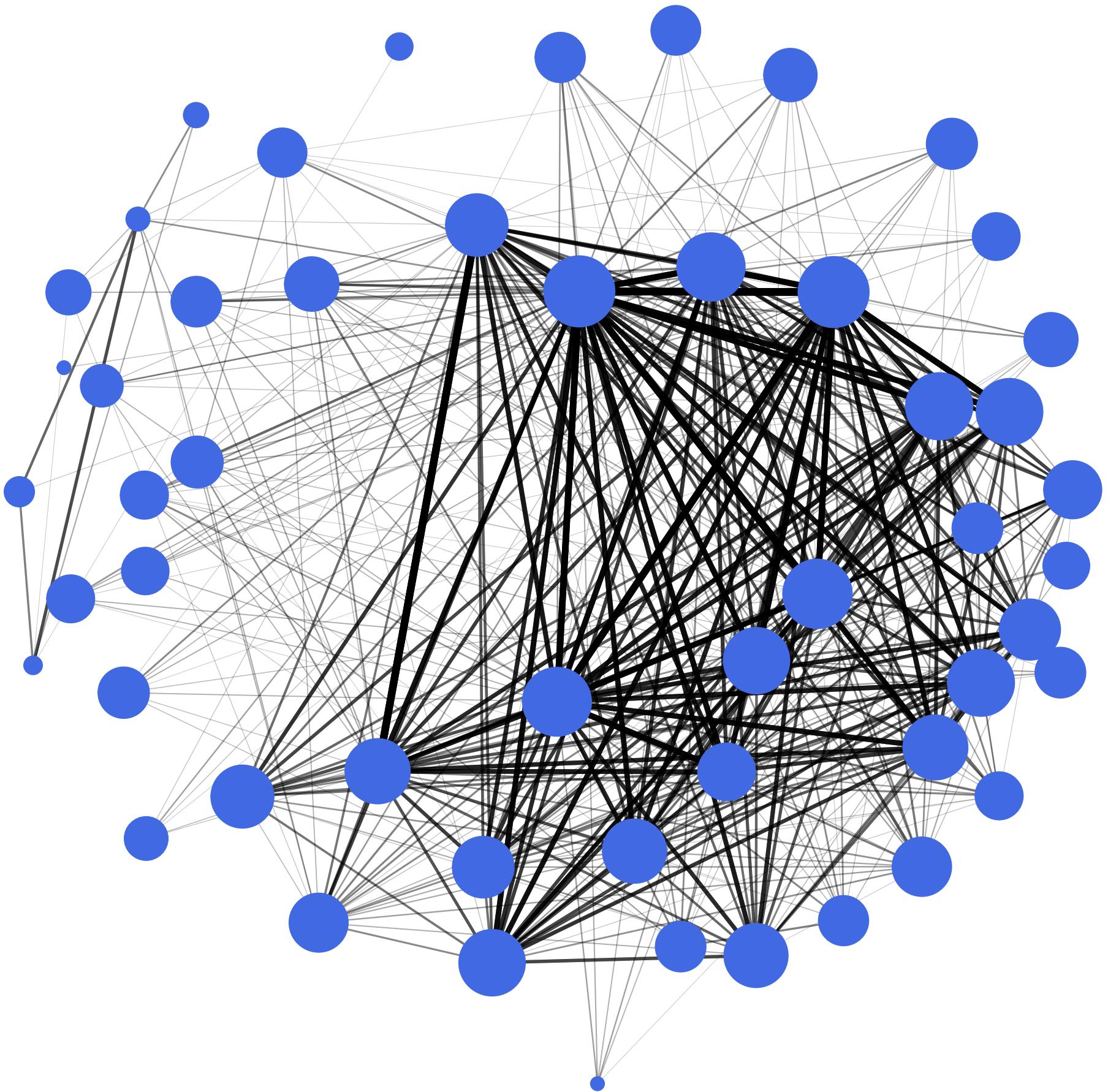
	Pathway	N	DE	P.DE
<i>path:gga04270</i>	Vascular smooth muscle contraction	101	4	0.003083
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	6	0.004778
<i>path:gga04510</i>	Focal adhesion	166	4	0.01725
<i>path:gga04514</i>	Cell adhesion molecules	98	3	0.0207
<i>path:gga04370</i>	VEGF signaling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



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14	NA								
15	NA								
16	NA	NA	NA	NA	NA				

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

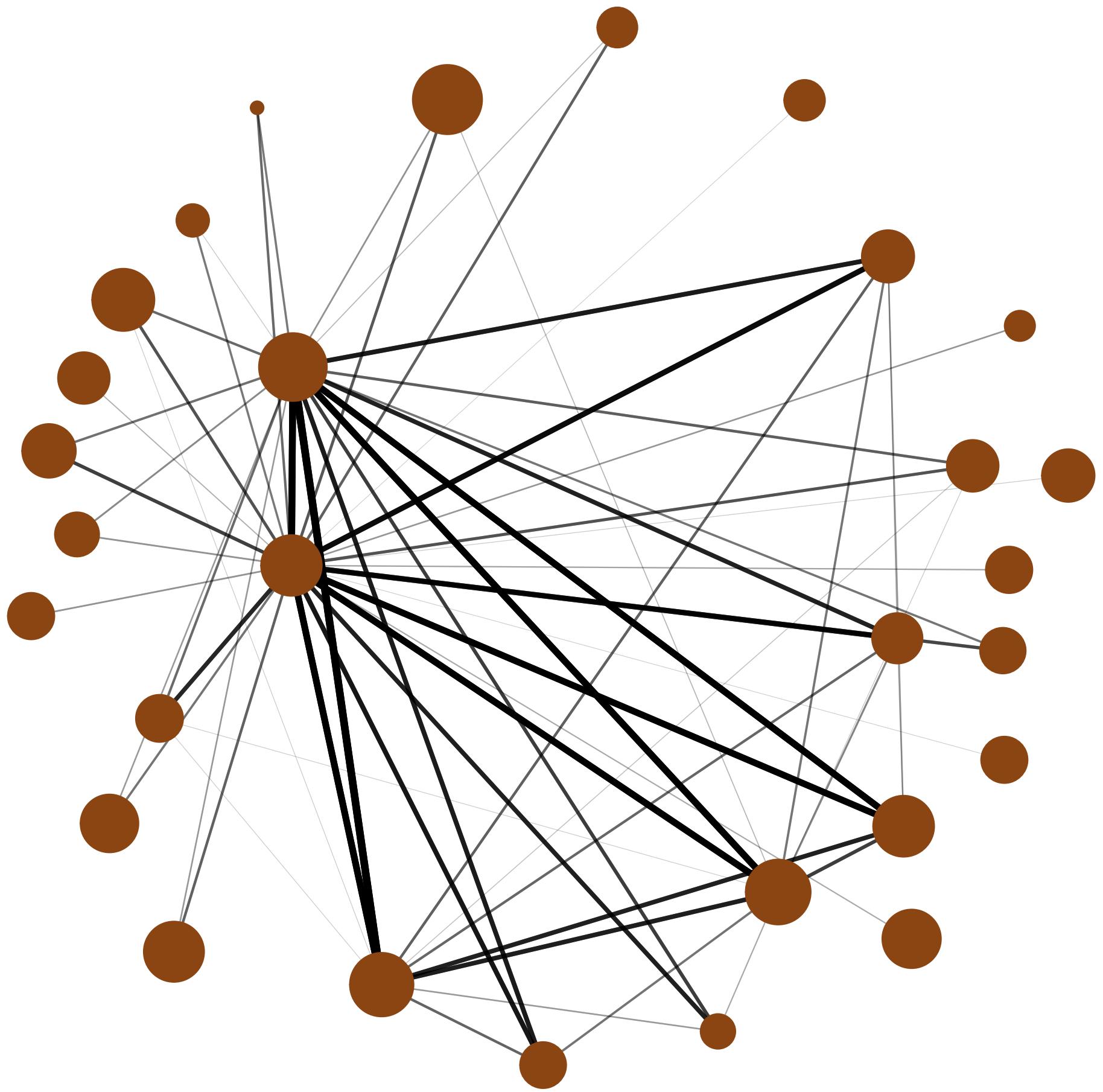
	Pathway	N	DE	P.DE
<i>path:gga04620</i>	Toll-like receptor signaling pathway	67	9	1.164e-08
<i>path:gga04060</i>	Cytokine–cytokine receptor interaction	136	11	5.881e-08
<i>path:gga04621</i>	NOD–like receptor signaling pathway	111	7	8.337e-05
<i>path:gga04145</i>	Phagosome	121	7	0.0001434
<i>path:gga04623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



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7	NA	NA	NA	NA				

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

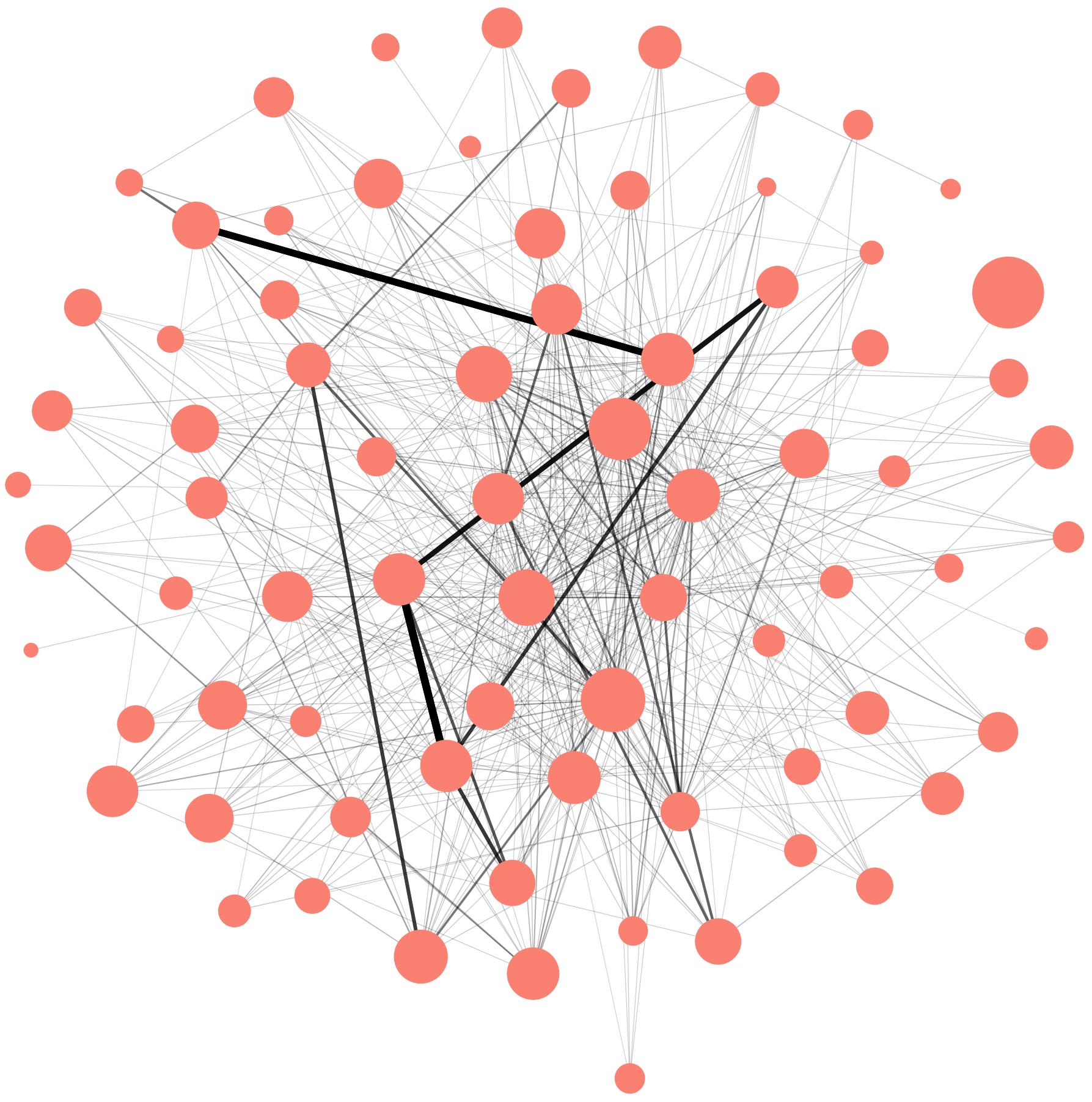
	Pathway	N	DE	P.DE
<i>path:gga04330</i>	Notch signaling pathway	52	2	0.01635
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	4	0.01696
<i>path:gga04012</i>	ErbB signaling pathway	75	2	0.03239
<i>path:gga00512</i>	Mucin type O–glycan biosynthesis	29	1	0.1038
<i>path:gga00514</i>	Other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



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

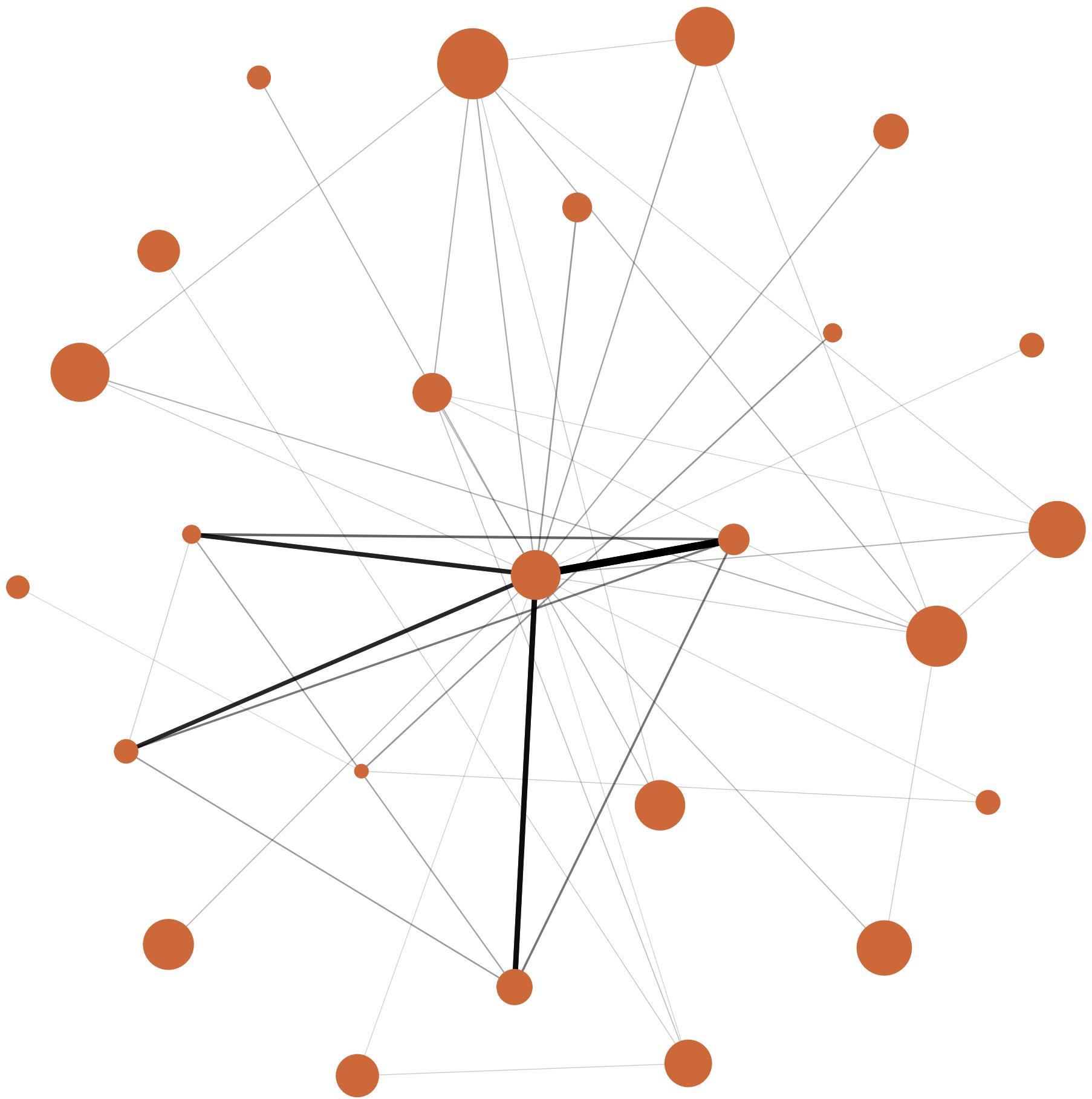
	Pathway	N	DE	P.DE
<i>path:gga01212</i>	Fatty acid metabolism	50	2	0.005726
<i>path:gga03320</i>	PPAR signaling pathway	55	2	0.006893
<i>path:gga04371</i>	Apelin signaling pathway	109	2	0.02533
<i>path:gga00061</i>	Fatty acid biosynthesis	16	1	0.03582
<i>path:gga01040</i>	Biosynthesis of unsaturated fatty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



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10	NA	NA	NA	NA					

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

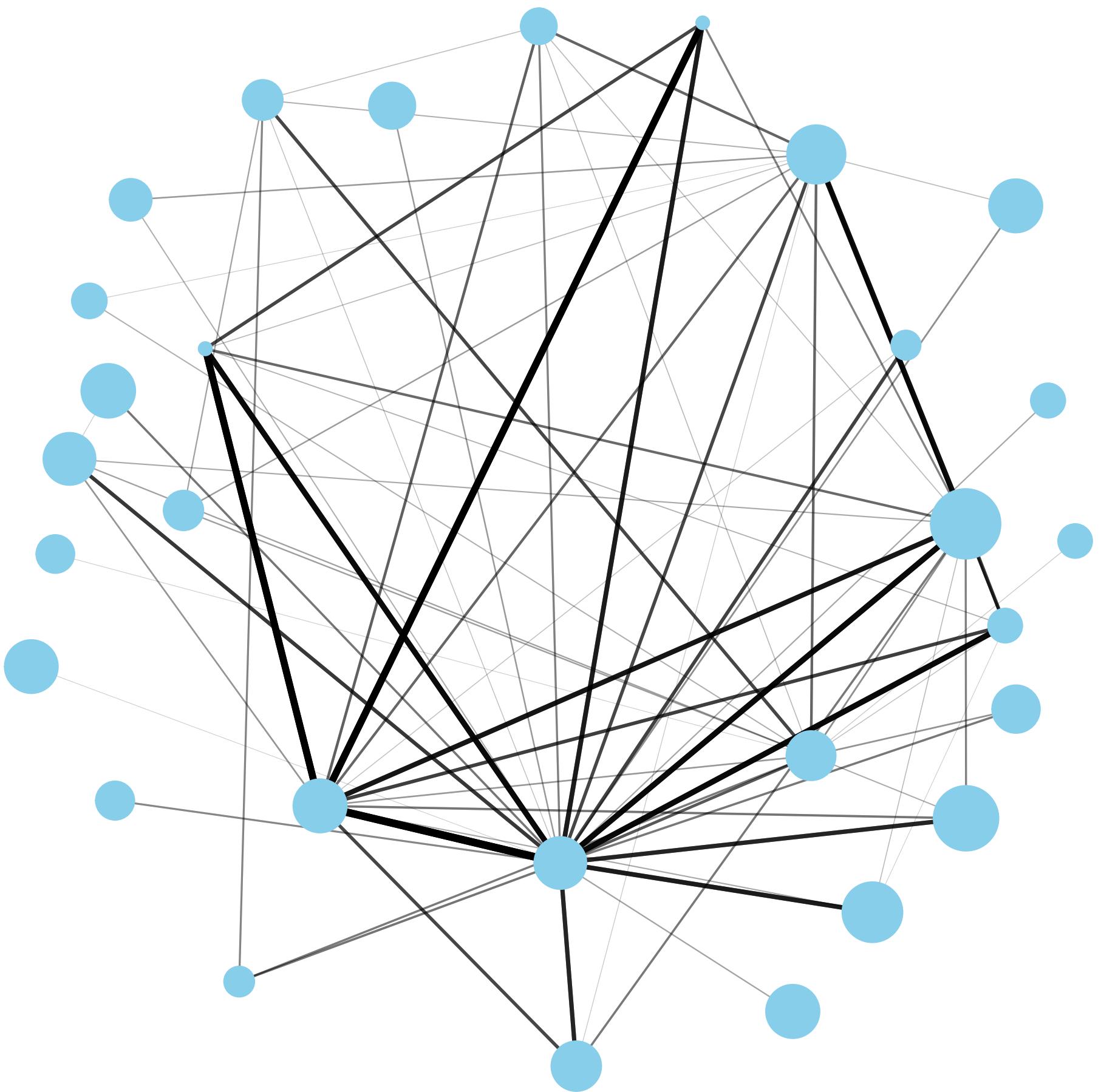
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	8	0.0001024
<i>path:gga04020</i>	Calcium signaling pathway	186	5	0.003755
<i>path:gga04370</i>	VEGF signaling pathway	50	2	0.03158
<i>path:gga04012</i>	ErbB signaling pathway	75	2	0.06549
<i>path:gga00100</i>	Steroid biosynthesis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



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

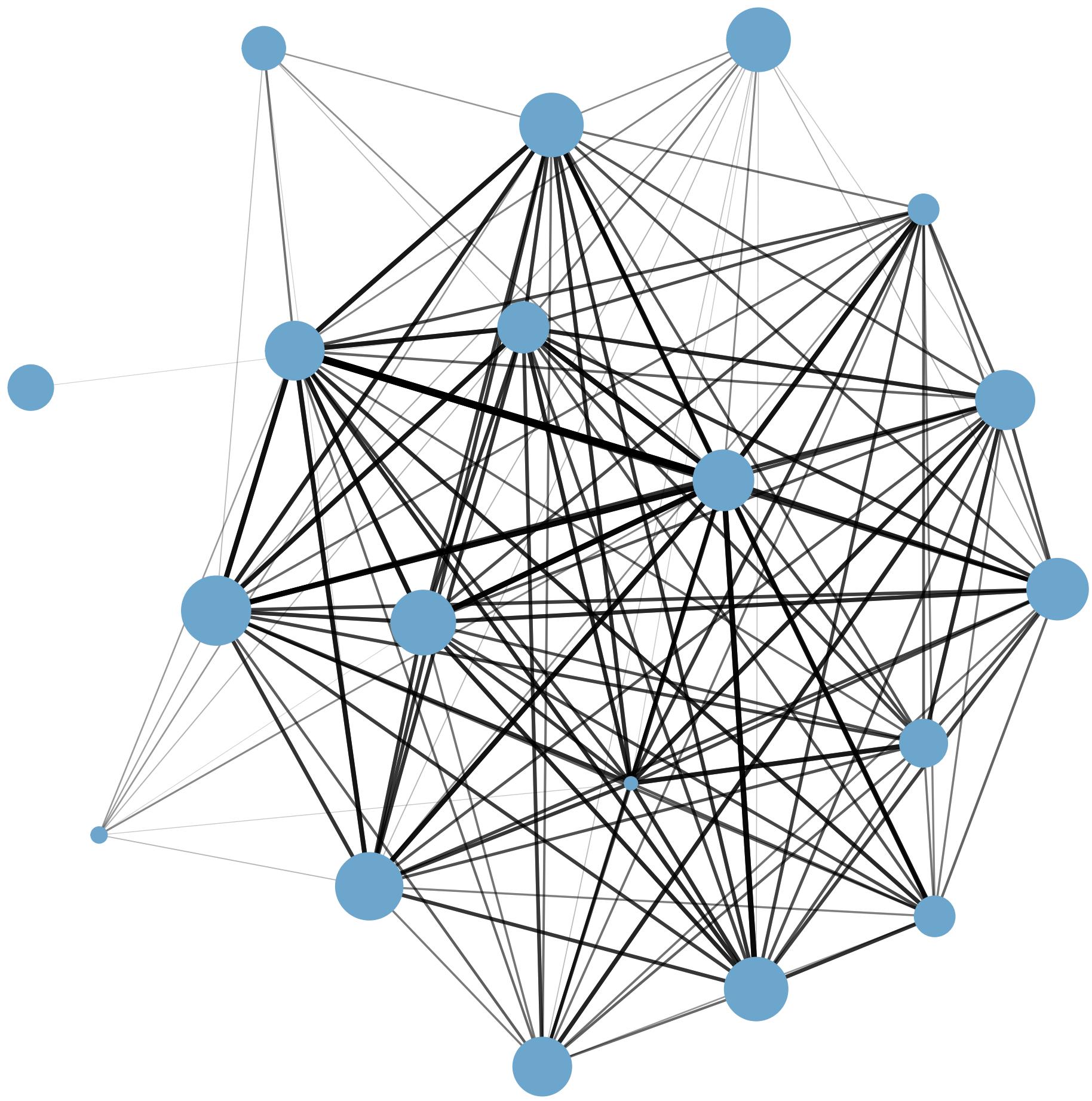
	Pathway	N	DE	P.DE
<i>path:gga03250</i>	Viral life cycle – HIV–1	48	1	0.07974
<i>path:gga04260</i>	Cardiac muscle contraction	59	1	0.09714
<i>path:gga04540</i>	Gap junction	78	1	0.1265
<i>path:gga04514</i>	Cell adhesion molecules	98	1	0.1563
<i>path:gga04261</i>	Adrenergic signaling in cardiomyocytes	119	1	0.1867
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1
<i>path:gga00232</i>	Caffeine metabolism	3	0	1
<i>path:gga00785</i>	Lipoic acid metabolism	3	0	1
<i>path:gga00290</i>	Valine, leucine and isoleucine biosynthesis	3	0	1



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3	NA							
4	NA	NA	NA	NA	NA			

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

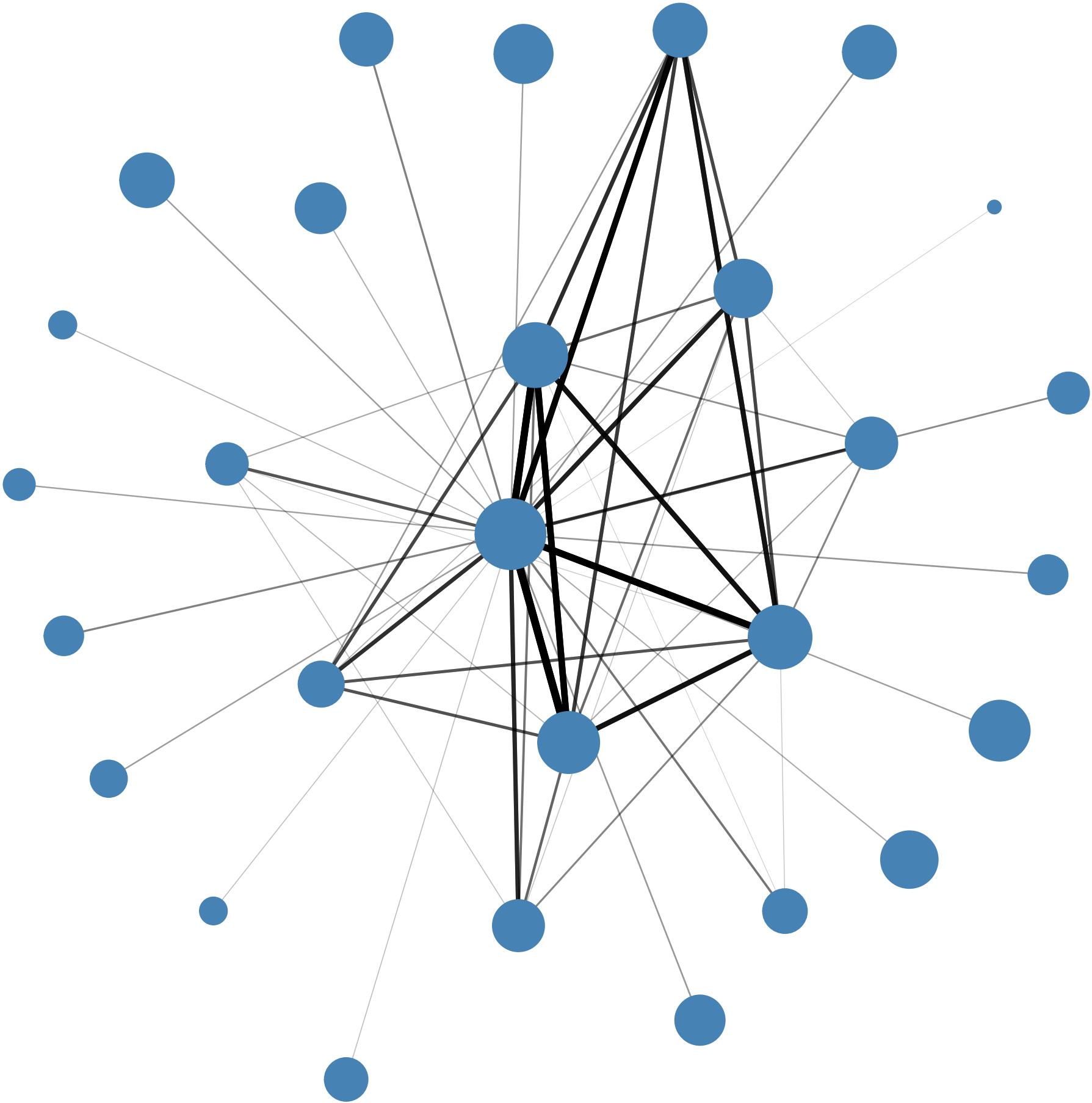
	Pathway	N	DE	P.DE
<i>path:gga05132</i>	Salmonella infection	215	3	0.01137
<i>path:gga04010</i>	MAPK signaling pathway	231	2	0.09095
<i>path:gga04622</i>	RIG-I-like receptor signaling pathway	44	1	0.09241
<i>path:gga03250</i>	Viral life cycle – HIV-1	48	1	0.1004
<i>path:gga04920</i>	Adipocytokine signaling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



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2	NA							
3	NA	NA	NA					

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

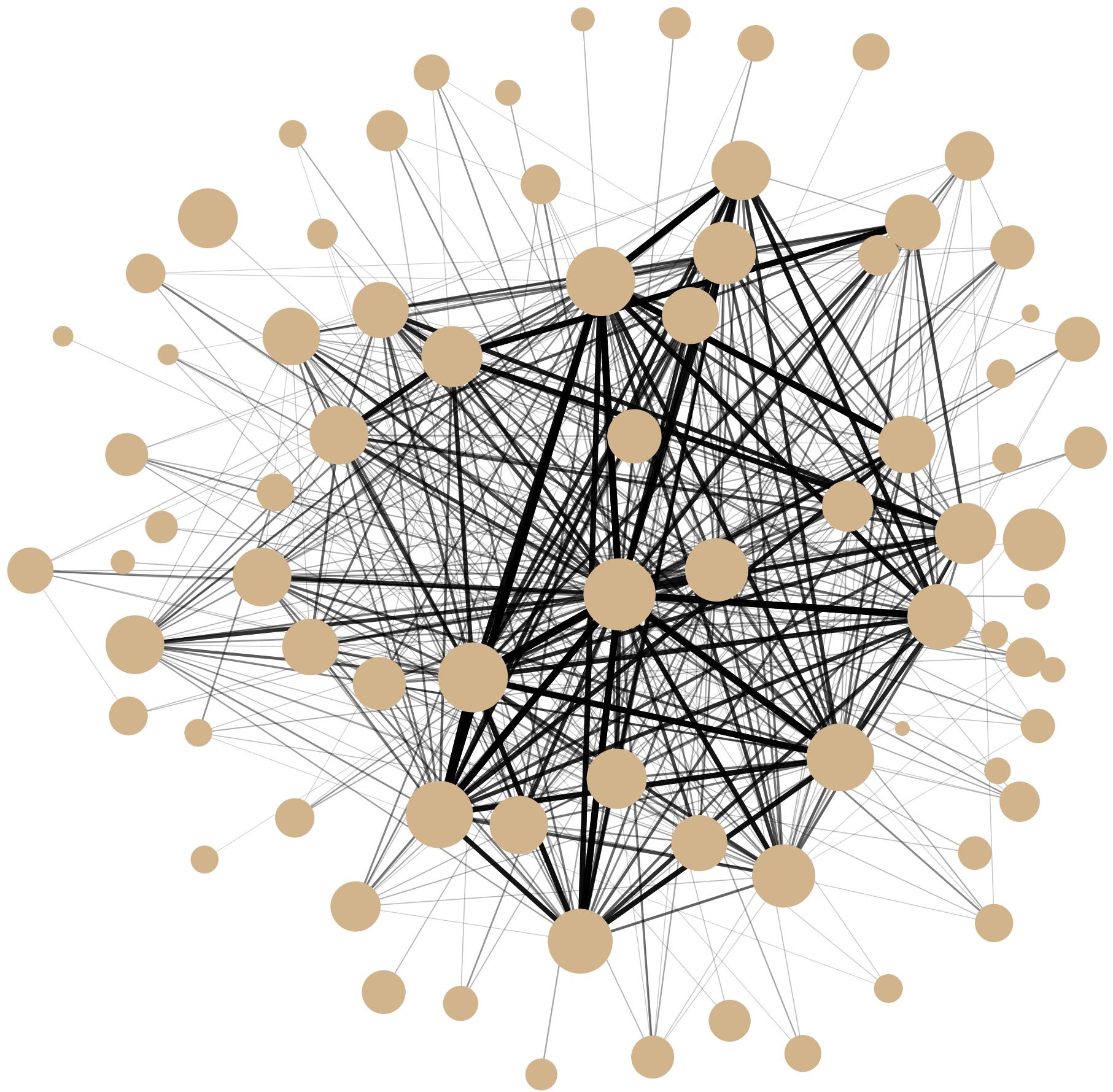
	Pathway	N	DE	P.DE
<i>path:gga04218</i>	Cellular senescence	131	2	0.016
<i>path:gga05132</i>	Salmonella infection	215	2	0.04014
<i>path:gga00250</i>	Alanine, aspartate and glutamate metabolism	32	1	0.04669
<i>path:gga00565</i>	Ether lipid metabolism	33	1	0.04811
<i>path:gga01250</i>	Biosynthesis of nucleotide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



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4	NA	NA	NA	NA				

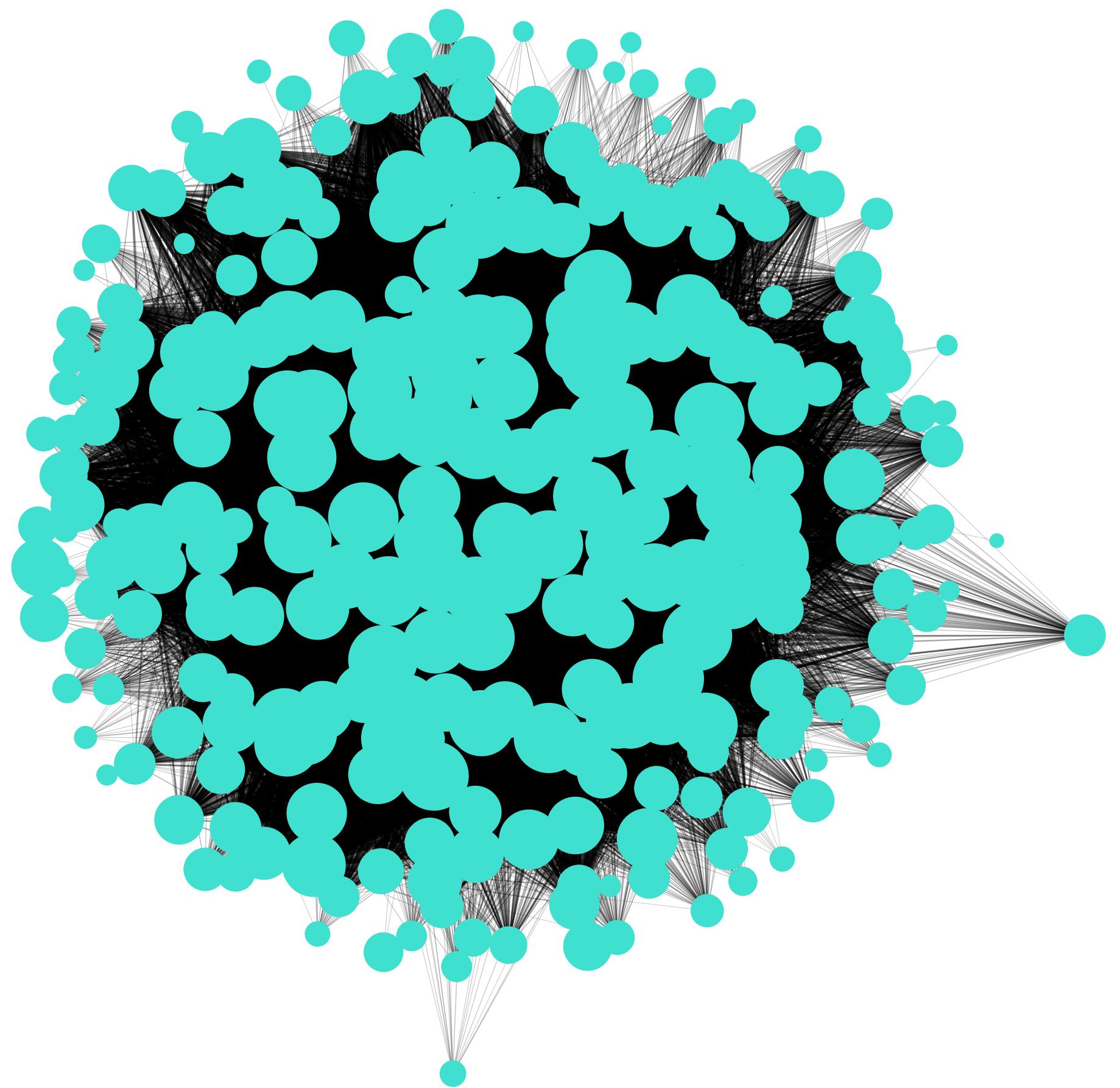
	Term	Ont	N	n	Adj. p-value
GO:1902001	fatty acid transmembrane transport	BP	1	1	0.002119
GO:0051938	L-glutamate import	BP	1	1	0.002119
GO:0098712	L-glutamate import across plasma membrane	BP	1	1	0.002119
GO:0015813	L-glutamate transmembrane transport	BP	1	1	0.002119
GO:0140354	lipid import into cell	BP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

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



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

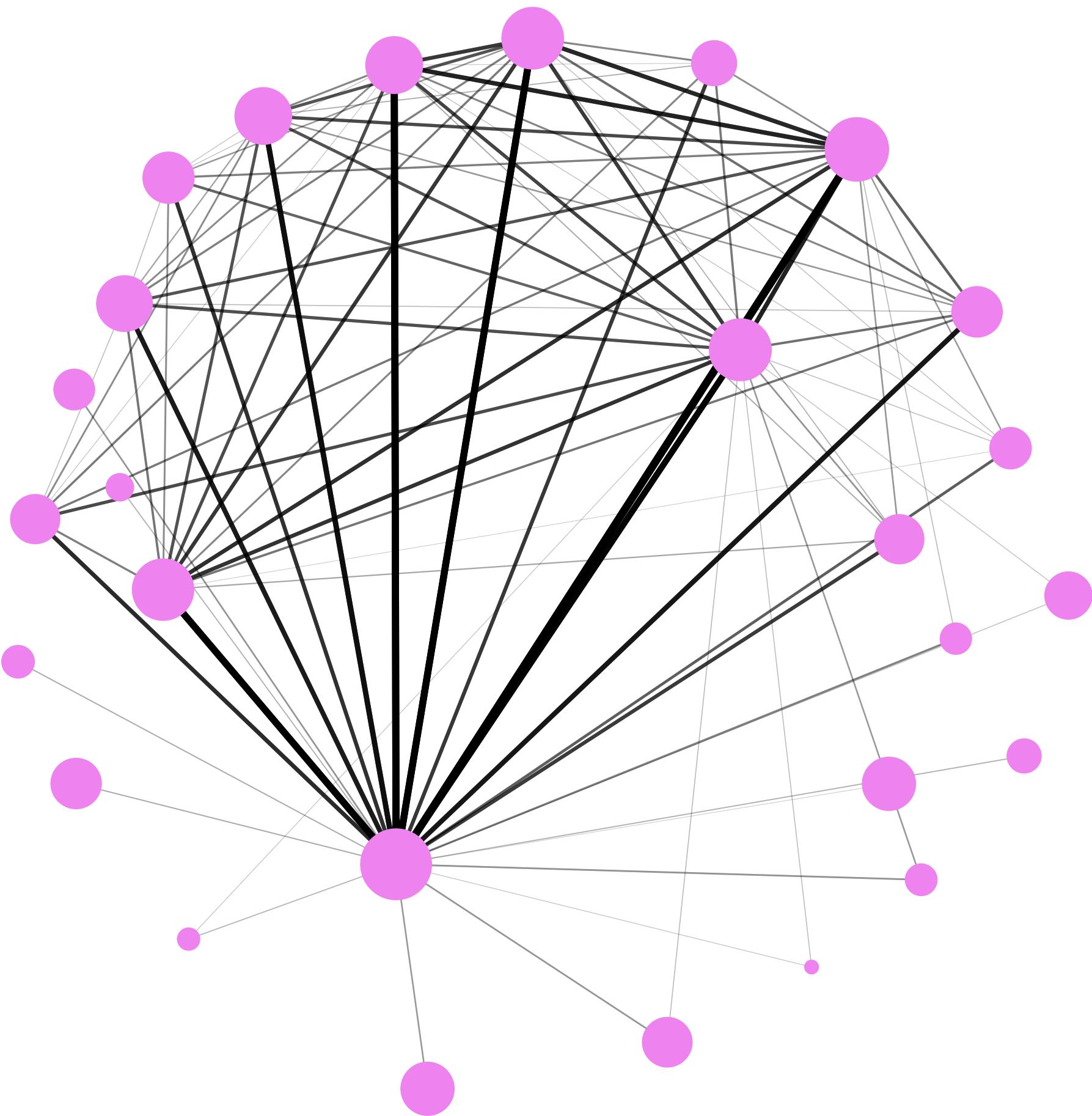
	Pathway	N	DE	P.DE
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	7	0.0005828
<i>path:gga04260</i>	Cardiac muscle contraction	59	2	0.04164
<i>path:gga04012</i>	ErbB signaling pathway	75	2	0.06388
<i>path:gga00603</i>	Glycosphingolipid biosynthesis – globo and isoglobo series	12	1	0.06399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



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

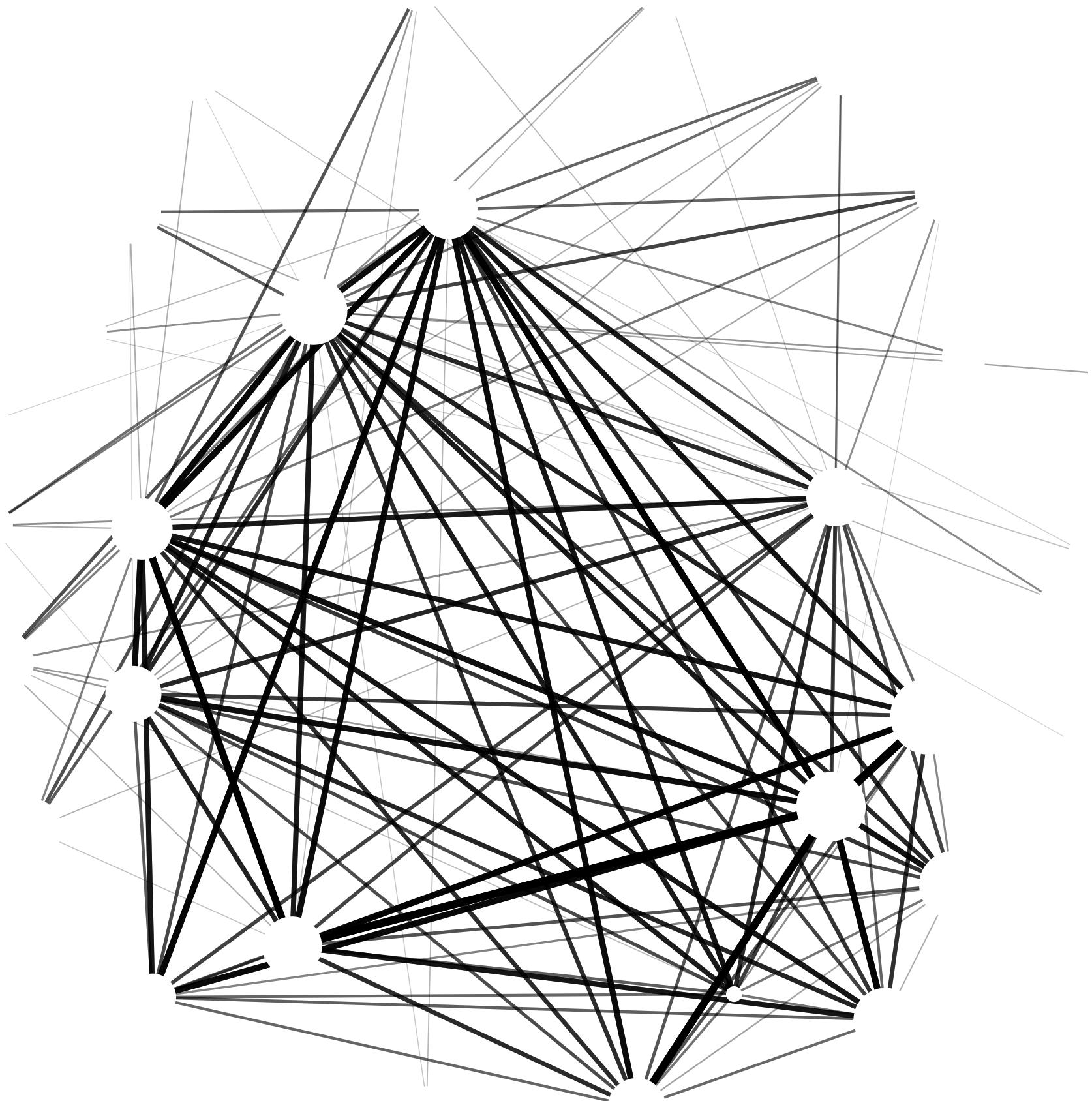
	Pathway	N	DE	P.DE
<i>path:gga04510</i>	Focal adhesion	166	17	4.543e-08
<i>path:gga04512</i>	ECM–receptor interaction	65	11	6.715e-08
<i>path:gga04270</i>	Vascular smooth muscle contraction	101	12	9.242e-07
<i>path:gga04010</i>	MAPK signaling pathway	231	13	0.000893
<i>path:gga04020</i>	Calcium signaling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



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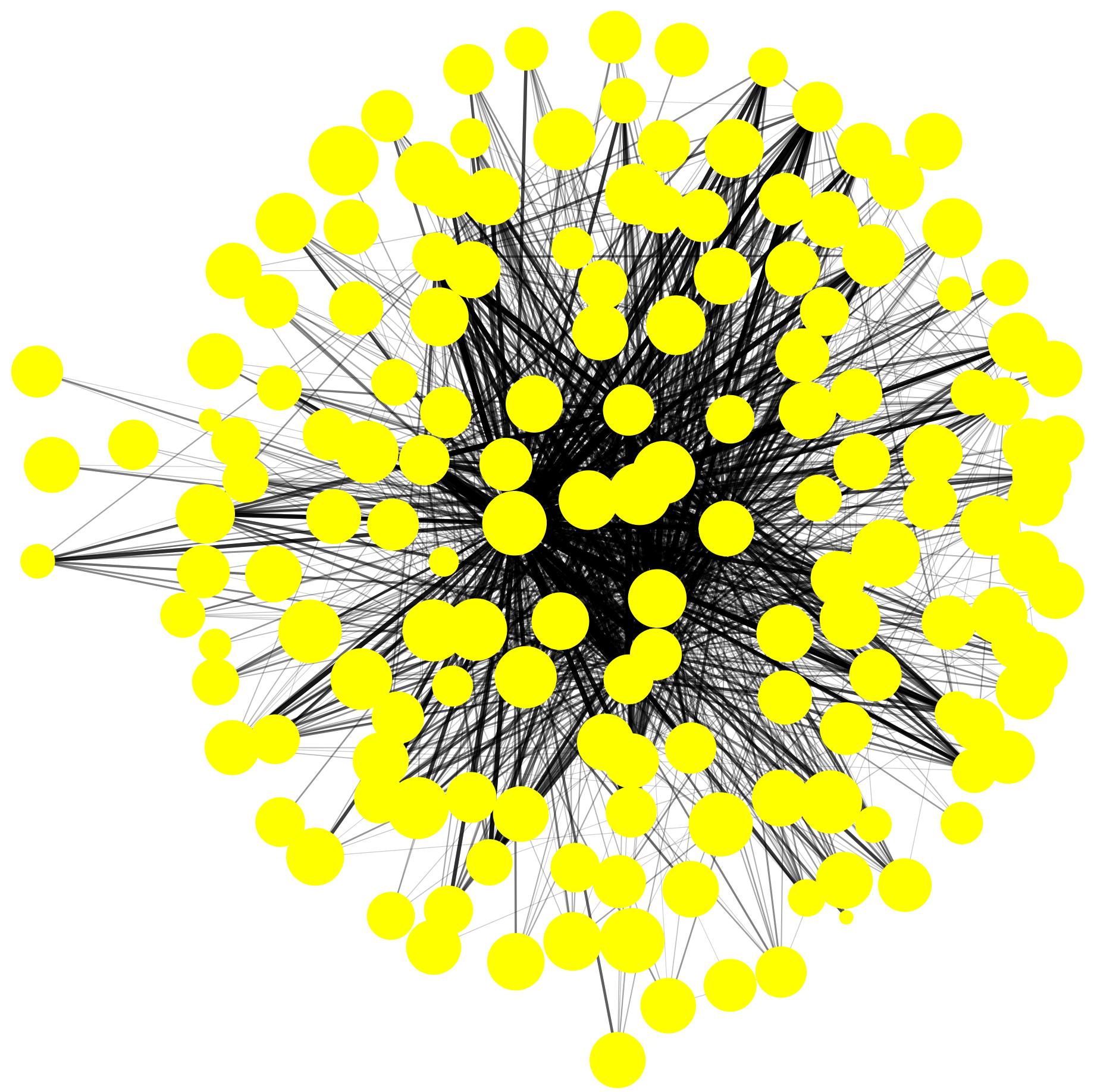
	Term	Ont	N	n	Adj. p-value
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	BP	79	4	1.568e-05
GO:0007167	enzyme linked receptor protein signaling pathway	BP	123	4	8.94e-05
GO:0009653	anatomical structure morphogenesis	BP	286	5	0.0002021
GO:0071363	cellular response to growth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

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



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

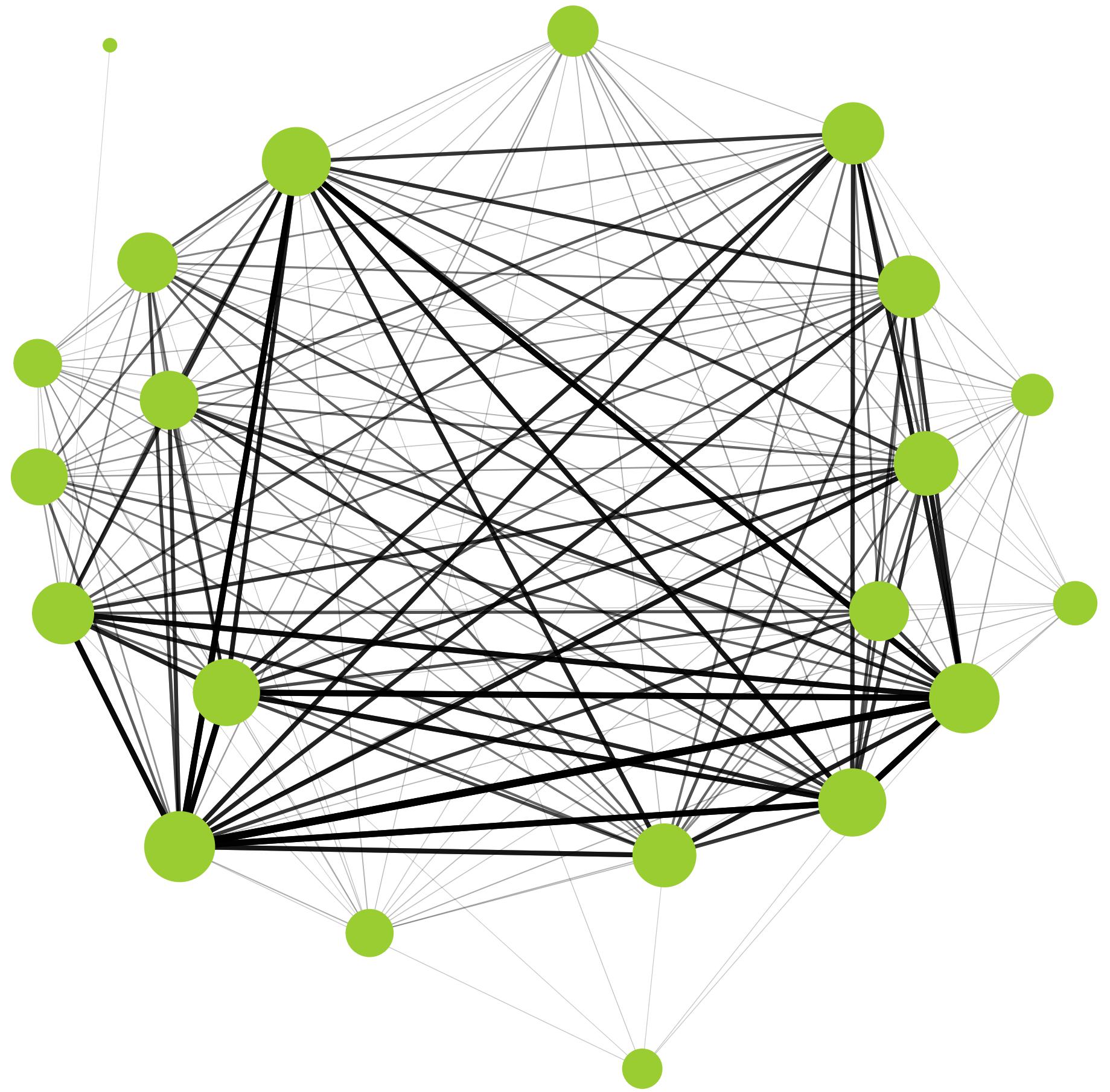
	Pathway	N	DE	P.DE
<i>path:gga04810</i>	Regulation of actin cytoskeleton	179	3	0.007616
<i>path:gga04520</i>	Adherens junction	69	2	0.01068
<i>path:gga04371</i>	Apelin signaling pathway	109	2	0.02533
<i>path:gga04310</i>	Wnt signaling pathway	131	2	0.03554
<i>path:gga04370</i>	VEGF signaling pathway	50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



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18	NA							
19	NA							
20	NA	NA	NA	NA				

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

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



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3	NA	NA	NA	NA	NA			

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

	Pathway	N	DE	P.DE
<i>path:gga02010</i>	ABC transporters	34	1	0.05207
<i>path:gga04080</i>	Neuroactive ligand–receptor interaction	263	2	0.06319
<i>path:gga04310</i>	Wnt signaling pathway	131	1	0.1868
<i>path:gga04020</i>	Calcium signaling pathway	186	1	0.255
<i>path:gga04010</i>	MAPK signaling pathway	231	1	0.3066
<i>path:gga03267</i>	Virion – Adenovirus	2	0	1
<i>path:gga00780</i>	Biotin metabolism	3	0	1
<i>path:gga00232</i>	Caffeine metabolism	3	0	1
<i>path:gga00785</i>	Lipoic acid metabolism	3	0	1
<i>path:gga00290</i>	Valine, leucine and isoleucine biosynthesis	3	0	1