

#114550 HEPATOCELLULAR CARCINOMA

OMIM Gene ID	HGNC	UniProtAC
116806	CTNNB1	P35222
147280	IGF2R	P11717
164860	MET	P08581
171834	PIK3CA	P42336
191170	TP53	P04637
601763	CASP8	Q14790
603816	AXIN1	O15169
604584	PDGFRL	Q15198
611731	APC	P25054

Table 1: OMIM - UniProtAC mapping

Legend

- N1: #input proteins associated to the significant GO term
- N2: #proteins associated to the significant GO term
- P-value: Bonferroni-corrected p-value of Fisher's exact test
- *red*: go terms not related to the input proteins
- *blue*: go terms related to the input proteins (enriched uniquely by network-based method)
- *green*: go terms ancestors of terms enriched with the standard method (enriched uniquely by network-based method)

1 Standard enrichment

GO Term	N1	N2	P-value	Description
GO:0007166	9	4368	4.65081e-06	cell surface receptor signaling pathway
GO:0051247	7	1526	7.34735e-06	positive regulation of protein metabolic process
GO:0043067	7	1982	4.4956e-05	regulation of programmed cell death
GO:0010941	7	2079	6.25475e-05	regulation of cell death
GO:0032268	7	2272	0.000115444	regulation of cellular protein metabolic process
GO:0048856	8	4289	0.00028145	anatomical structure development
GO:0006921	3	54	0.000290748	cellular component disassembly involved in execution phase of apoptosis
GO:0033077	3	60	0.000400833	T cell differentiation in thymus
GO:0048585	6	1639	0.000627196	negative regulation of response to stimulus
GO:0006915	5	805	0.000643604	apoptotic process
GO:0007165	9	7592	0.000675637	signal transduction
GO:0032880	5	819	0.000700819	regulation of protein localization
GO:0051246	7	2954	0.000702604	regulation of protein metabolic process
GO:0001775	5	825	0.000726542	cell activation
GO:0042110	4	319	0.000767711	T cell activation
GO:0012501	5	868	0.000933626	programmed cell death
GO:0042325	6	1770	0.000986368	regulation of phosphorylation
GO:0031399	6	1823	0.00117326	regulation of protein modification process
GO:1902531	6	1847	0.00126702	regulation of intracellular signal transduction
GO:0010604	7	3285	0.00145452	positive regulation of macromolecule metabolic process
GO:0002521	4	375	0.00146148	leukocyte differentiation
GO:0003002	4	380	0.00154051	regionalization
GO:0048513	6	1910	0.00154296	organ development
GO:0048732	4	391	0.00172552	gland development
GO:0042981	6	1970	0.00185013	regulation of apoptotic process
GO:1902533	5	1008	0.0019503	positive regulation of intracellular signal transduction
GO:0044336	2	10	0.00285848	canonical Wnt signaling pathway involved in negative regulation of apoptotic process
GO:0007167	5	1091	0.00287739	enzyme linked receptor protein signaling pathway
GO:0009893	7	3630	0.00287769	positive regulation of metabolic process
GO:0048522	8	5768	0.00289948	positive regulation of cellular process
GO:0060070	3	116	0.0029491	canonical Wnt signaling pathway
GO:0008219	5	1106	0.00307692	cell death
GO:0016265	5	1117	0.00323008	death
GO:0042327	5	1129	0.00340398	positive regulation of phosphorylation
GO:0060548	5	1147	0.00367866	negative regulation of cell death
GO:0046649	4	484	0.00402317	lymphocyte activation
GO:0009798	3	132	0.00435098	axis specification
GO:0048646	5	1201	0.00460931	anatomical structure formation involved in morphogenesis
GO:0048584	6	2308	0.00467537	positive regulation of response to stimulus
GO:0051716	9	9450	0.00485063	cellular response to stimulus
GO:0010562	5	1255	0.00571704	positive regulation of phosphorus metabolic process
GO:0045937	5	1255	0.00571704	positive regulation of phosphate metabolic process
GO:0043065	4	536	0.00602499	positive regulation of apoptotic process
GO:0002761	3	148	0.00613622	regulation of myeloid leukocyte differentiation
GO:0043068	4	543	0.00634212	positive regulation of programmed cell death
GO:0030217	3	154	0.00691374	T cell differentiation
GO:0007389	4	579	0.00817287	pattern specification process
GO:0010942	4	579	0.00817287	positive regulation of cell death
GO:0045321	4	579	0.00817287	leukocyte activation
GO:0051259	4	582	0.00834136	protein oligomerization
GO:0009968	5	1361	0.00849842	negative regulation of signal transduction
GO:0032270	5	1363	0.00855958	positive regulation of cellular protein metabolic process
GO:0060341	5	1363	0.00855958	regulation of cellular localization
GO:0048518	8	6624	0.00857238	positive regulation of biological process
GO:0006461	5	1365	0.0086211	protein complex assembly
GO:0001889	3	173	0.00980036	liver development
GO:0044767	8	6740	0.00981841	single-organism developmental process
GO:0044707	7	4361	0.0100237	single-multicellular organism process
GO:0023057	5	1420	0.0104543	negative regulation of signaling
GO:0010648	5	1424	0.0105987	negative regulation of cell communication

Table 2: Overrepresented GO terms with the standard enrichment

GO Term	N1	N2	P-value	Description
GO:0001932	5	1440	0.0111922	regulation of protein phosphorylation
GO:0032501	7	4447	0.0114422	multicellular organismal process
GO:0048583	7	4515	0.0126809	regulation of response to stimulus
GO:0070243	2	22	0.0146518	regulation of thymocyte apoptotic process
GO:0032879	6	2827	0.015227	regulation of localization
GO:0009967	5	1548	0.0159184	positive regulation of signal transduction
GO:0060272	2	23	0.0160452	embryonic skeletal joint morphogenesis
GO:0060768	2	23	0.0160452	regulation of epithelial cell proliferation involved in prostate gland development
GO:0042221	7	4712	0.016929	response to chemical
GO:0050793	6	2884	0.0170952	regulation of developmental process
GO:0032502	8	7299	0.0182877	developmental process
GO:0065003	5	1623	0.0200353	macromolecular complex assembly
GO:0023056	5	1630	0.0204586	positive regulation of signaling
GO:0019220	6	2977	0.0205452	regulation of phosphate metabolic process
GO:0009950	2	26	0.0206038	dorsal/ventral axis specification
GO:0010647	5	1637	0.0208888	positive regulation of cell communication
GO:0051174	6	2996	0.0213157	regulation of phosphorus metabolic process
GO:0045637	3	225	0.0215133	regulation of myeloid cell differentiation
GO:2000027	3	225	0.0215133	regulation of organ morphogenesis
GO:1900739	2	27	0.0222492	regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway
GO:1900740	2	27	0.0222492	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway
GO:0009952	3	235	0.0244958	anterior/posterior pattern specification
GO:0090287	3	237	0.0251233	regulation of cellular response to growth factor stimulus
GO:0043408	4	794	0.0283236	regulation of MAPK cascade
GO:0007169	4	798	0.0288873	transmembrane receptor protein tyrosine kinase signaling pathway
GO:0050896	9	11721	0.0337221	response to stimulus
GO:0030098	3	263	0.0342685	lymphocyte differentiation
GO:0045596	4	834	0.0343416	negative regulation of cell differentiation
GO:0009966	6	3261	0.0347792	regulation of signal transduction
GO:0048523	7	5279	0.0364236	negative regulation of cellular process
GO:0071496	3	275	0.0391399	cellular response to external stimulus
GO:0001838	2	36	0.0398902	embryonic epithelial tube formation
GO:0050790	6	3371	0.0421041	regulation of catalytic activity
GO:0072175	2	37	0.0421644	epithelial tube formation
GO:0031325	6	3418	0.0455963	positive regulation of cellular metabolic process
GO:0051239	6	3432	0.0466812	regulation of multicellular organismal process
GO:0071822	5	1933	0.0467155	protein complex subunit organization
GO:0031122	2	40	0.0493634	cytoplasmic microtubule organization

Table 3: Overrepresented GO terms with the standard enrichment

2 Network-based enrichment

GO Term	N1	N2	P-value	Description
GO:0030111	7	814	4.70478e-07	regulation of Wnt signaling pathway
GO:0045786	7	824	5.12345e-07	negative regulation of cell cycle
GO:0008544	6	418	8.24269e-07	epidermis development
GO:0035412	4	50	1.51324e-06	regulation of catenin import into nucleus
GO:0001933	7	963	1.5199e-06	negative regulation of protein phosphorylation
GO:0060828	6	550	4.27051e-06	regulation of canonical Wnt signaling pathway
GO:0070302	6	569	5.23273e-06	regulation of stress-activated protein kinase signaling cascade
GO:0042326	7	1164	5.68891e-06	negative regulation of phosphorylation
GO:0070613	6	609	7.85516e-06	regulation of protein processing
GO:1903317	6	609	7.85516e-06	regulation of protein maturation
GO:0060627	7	1229	8.30055e-06	regulation of vesicle-mediated transport
GO:0007346	7	1240	8.83084e-06	regulation of mitotic cell cycle
GO:0051249	7	1264	1.00892e-05	regulation of lymphocyte activation
GO:0002684	8	2287	1.10907e-05	positive regulation of immune system process
GO:1902532	7	1289	1.15597e-05	negative regulation of intracellular signal transduction
GO:2001233	7	1313	1.31399e-05	regulation of apoptotic signaling pathway
GO:0010563	7	1353	1.61839e-05	negative regulation of phosphorus metabolic process
GO:0045936	7	1353	1.61839e-05	negative regulation of phosphate metabolic process
GO:1901990	6	692	1.68481e-05	regulation of mitotic cell cycle phase transition
GO:0031400	7	1368	1.74712e-05	negative regulation of protein modification process
GO:0080135	7	1388	1.93227e-05	regulation of cellular response to stress
GO:0007257	4	95	2.08054e-05	activation of JUN kinase activity
GO:0090090	5	307	2.11602e-05	negative regulation of canonical Wnt signaling pathway
GO:0038179	6	720	2.13462e-05	neurotrophin signaling pathway
GO:1901987	6	721	2.15237e-05	regulation of cell cycle phase transition
GO:0002694	7	1443	2.5302e-05	regulation of leukocyte activation
GO:0032386	7	1443	2.5302e-05	regulation of intracellular transport
GO:0071900	7	1492	3.18948e-05	regulation of protein serine/threonine kinase activity
GO:0009896	6	786	3.60056e-05	positive regulation of catabolic process
GO:0050865	7	1568	4.5004e-05	regulation of cell activation
GO:0042176	6	816	4.50046e-05	regulation of protein catabolic process
GO:0033043	8	2759	4.91912e-05	regulation of organelle organization
GO:0032147	6	832	5.052e-05	activation of protein kinase activity
GO:0051130	8	2782	5.25388e-05	positive regulation of cellular component organization
GO:0045860	7	1636	6.0386e-05	positive regulation of protein kinase activity
GO:0072310	3	23	6.47901e-05	glomerular epithelial cell development
GO:0031647	5	386	6.64088e-05	regulation of protein stability
GO:0043254	6	874	6.77222e-05	regulation of protein complex assembly
GO:0033157	6	878	6.95868e-05	regulation of intracellular protein transport
GO:0071902	6	897	7.90352e-05	positive regulation of protein serine/threonine kinase activity
GO:0033674	7	1706	8.06988e-05	positive regulation of kinase activity
GO:0051052	6	905	8.33195e-05	regulation of DNA metabolic process
GO:0043405	6	930	9.79694e-05	regulation of MAP kinase activity
GO:0000187	5	421	0.000102354	activation of MAPK activity
GO:0097193	5	421	0.000102354	intrinsic apoptotic signaling pathway
GO:0030162	7	1768	0.000103299	regulation of proteolysis
GO:0043409	5	424	0.000106039	negative regulation of MAPK cascade
GO:0043547	7	1783	0.000109513	positive regulation of GTPase activity
GO:0080134	8	3072	0.000115282	regulation of response to stress
GO:0030178	5	432	0.000116385	negative regulation of Wnt signaling pathway
GO:0032269	7	1804	0.000118746	negative regulation of cellular protein metabolic process
GO:0044087	7	1812	0.000122434	regulation of cellular component biogenesis
GO:0070201	7	1849	0.000140789	regulation of establishment of protein localization
GO:1901991	5	457	0.000153998	negative regulation of mitotic cell cycle phase transition
GO:0060429	6	1006	0.000156207	epithelium development
GO:0071363	7	1903	0.000171762	cellular response to growth factor stimulus
GO:0030335	6	1024	0.000173544	positive regulation of cell migration
GO:0051129	7	1913	0.000178092	negative regulation of cellular component organization
GO:0043087	7	1921	0.000183299	regulation of GTPase activity
GO:0030334	7	1926	0.000186618	regulation of cell migration

Table 4: Overrepresented terms with the network-based enrichment. Only terms not detected with the standard method.

GO Term	N1	N2	P-value	Description
GO:0033124	7	1931	0.000189989	regulation of GTP catabolic process
GO:2000147	6	1042	0.000192445	positive regulation of cell motility
GO:1901988	5	482	0.000200709	negative regulation of cell cycle phase transition
GO:0051272	6	1060	0.000213021	positive regulation of cellular component movement
GO:0048608	6	1062	0.000215416	reproductive structure development
GO:0070848	7	1987	0.000231433	response to growth factor
GO:0051090	6	1091	0.000252723	regulation of sequence-specific DNA binding transcription factor activity
GO:0046328	5	505	0.000253041	regulation of JNK cascade
GO:2000145	7	2039	0.000276584	regulation of cell motility
GO:1903320	5	520	0.000292644	regulation of protein modification by small protein conjugation or removal
GO:0040017	6	1124	0.000301532	positive regulation of locomotion
GO:0042306	5	527	0.000312737	regulation of protein import into nucleus
GO:0071260	4	187	0.000318849	cellular response to mechanical stimulus
GO:0033233	3	39	0.000333619	regulation of protein sumoylation
GO:0071407	6	1148	0.000341727	cellular response to organic cyclic compound
GO:0033121	7	2107	0.000346786	regulation of purine nucleotide catabolic process
GO:0048609	7	2109	0.000349063	multicellular organismal reproductive process
GO:0030811	7	2111	0.00035135	regulation of nucleotide catabolic process
GO:0048754	5	542	0.000359496	branching morphogenesis of an epithelial tube
GO:0009118	7	2125	0.000367728	regulation of nucleoside metabolic process
GO:0001101	6	1170	0.000382378	response to acid chemical
GO:0032101	7	2173	0.00042891	regulation of response to external stimulus
GO:0051270	7	2182	0.000441297	regulation of cellular component movement
GO:0051248	7	2189	0.000451143	negative regulation of protein metabolic process
GO:0032872	5	568	0.00045359	regulation of stress-activated MAPK cascade
GO:0030155	6	1217	0.000482738	regulation of cell adhesion
GO:0040012	7	2224	0.000503217	regulation of locomotion
GO:0048320	2	3	0.00052365	axial mesoderm formation
GO:0010638	6	1260	0.000592773	positive regulation of organelle organization
GO:1900180	5	602	0.00060512	regulation of protein localization to nucleus
GO:0043410	6	1269	0.000618244	positive regulation of MAPK cascade
GO:0050670	5	605	0.000620211	regulation of lymphocyte proliferation
GO:0032944	5	609	0.000640794	regulation of mononuclear cell proliferation
GO:0000122	7	2314	0.000661203	negative regulation of transcription from RNA polymerase II promoter
GO:0051101	4	227	0.000692965	regulation of DNA binding
GO:0043434	6	1303	0.000722792	response to peptide hormone
GO:0061138	5	624	0.000722881	morphogenesis of a branching epithelium
GO:0008285	7	2354	0.00074393	negative regulation of cell proliferation
GO:0070304	4	232	0.000756047	positive regulation of stress-activated protein kinase signaling cascade
GO:0045862	4	233	0.00076916	positive regulation of proteolysis
GO:0001934	7	2371	0.000781668	positive regulation of protein phosphorylation
GO:0051493	6	1336	0.000837851	regulation of cytoskeleton organization
GO:0030278	5	644	0.0008451	regulation of ossification
GO:0045859	7	2438	0.000946702	regulation of protein kinase activity
GO:0006259	7	2443	0.000960125	DNA metabolic process
GO:0043406	5	661	0.000961416	positive regulation of MAP kinase activity
GO:0007093	4	247	0.000971152	mitotic cell cycle checkpoint
GO:0043506	4	247	0.000971152	regulation of JUN kinase activity
GO:1901652	6	1373	0.000984465	response to peptide
GO:0010608	6	1385	0.00103633	posttranscriptional regulation of gene expression
GO:1901320	2	4	0.00104715	negative regulation of heart induction
GO:2000044	2	4	0.00104715	negative regulation of cardiac cell fate specification
GO:0046822	5	675	0.00106645	regulation of nucleocytoplasmic transport
GO:1900542	7	2485	0.00107941	regulation of purine nucleotide metabolic process
GO:0006140	7	2500	0.00112497	regulation of nucleotide metabolic process
GO:0045597	7	2514	0.00116895	positive regulation of cell differentiation
GO:0001763	5	690	0.0011889	morphogenesis of a branching structure
GO:0048011	5	692	0.00120604	neurotrophin TRK receptor signaling pathway
GO:0008283	7	2526	0.0012078	cell proliferation
GO:0043549	7	2576	0.00138176	regulation of kinase activity

Table 5: Overrepresented terms with the network-based enrichment. Only terms not detected with the standard method.

GO Term	N1	N2	P-value	Description
GO:0010954	4	271	0.00140625	positive regulation of protein processing
GO:1903319	4	271	0.00140625	positive regulation of protein maturation
GO:0010948	5	717	0.00143728	negative regulation of cell cycle process
GO:0033993	7	2604	0.00148817	response to lipid
GO:0048731	7	2612	0.00151982	system development
GO:0043086	7	2637	0.00162246	negative regulation of catalytic activity
GO:0032102	5	737	0.00164651	negative regulation of response to external stimulus
GO:1901028	3	66	0.00166438	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway
GO:0051291	4	286	0.00174329	protein heterooligomerization
GO:0051093	7	2690	0.00185968	negative regulation of developmental process
GO:0033135	4	294	0.00194592	regulation of peptidyl-serine phosphorylation
GO:0008584	4	300	0.00210904	male gonad development
GO:0070507	4	300	0.00210904	regulation of microtubule cytoskeleton organization
GO:0051726	7	2760	0.00221771	regulation of cell cycle
GO:0022402	7	2771	0.00227897	cell cycle process
GO:0043269	6	1590	0.002337	regulation of ion transport
GO:2001020	4	308	0.00234213	regulation of response to DNA damage stimulus
GO:0060706	3	75	0.00245302	cell differentiation involved in embryonic placenta development
GO:0000902	5	800	0.00246807	cell morphogenesis
GO:0010564	6	1606	0.00247874	regulation of cell cycle process
GO:0022604	6	1615	0.00256154	regulation of cell morphogenesis
GO:0051338	7	2819	0.00256345	regulation of transferase activity
GO:0030177	4	316	0.00259389	positive regulation of Wnt signaling pathway
GO:0009725	7	2824	0.00259475	response to hormone
GO:0030910	2	6	0.00261714	olfactory placode formation
GO:0022603	7	2832	0.0026455	regulation of anatomical structure morphogenesis
GO:0016055	5	814	0.00268846	Wnt signaling pathway
GO:0051223	6	1645	0.00285424	regulation of protein transport
GO:0051098	5	826	0.00288954	regulation of binding
GO:0048008	3	80	0.00298265	platelet-derived growth factor receptor signaling pathway
GO:1902105	5	834	0.00303007	regulation of leukocyte differentiation
GO:0010959	5	835	0.00304801	regulation of metal ion transport
GO:0016032	6	1665	0.00306427	viral process
GO:0044403	6	1665	0.00306427	symbiosis, encompassing mutualism through parasitism
GO:2000045	4	334	0.00323364	regulation of G1/S transition of mitotic cell cycle
GO:0044764	6	1682	0.00325269	multi-organism cellular process
GO:1902806	4	336	0.00331136	regulation of cell cycle G1/S phase transition
GO:0031401	7	2947	0.00347381	positive regulation of protein modification process
GO:0051345	7	2953	0.00352247	positive regulation of hydrolase activity
GO:0071901	4	342	0.00355285	negative regulation of protein serine/threonine kinase activity
GO:0051251	5	874	0.00381635	positive regulation of lymphocyte activation
GO:0045944	7	2989	0.00382676	positive regulation of transcription from RNA polymerase II promoter
GO:0045667	4	360	0.0043563	regulation of osteoblast differentiation
GO:1903047	6	1769	0.0043732	mitotic cell cycle process
GO:0016337	5	900	0.00440853	single organismal cell-cell adhesion
GO:0001817	6	1774	0.0044462	regulation of cytokine production
GO:0032886	4	362	0.00445326	regulation of microtubule-based process
GO:0006955	7	3063	0.00452295	immune response
GO:0043124	3	93	0.00470263	negative regulation of I-kappaB kinase/NF-kappaB signaling
GO:0050863	5	912	0.00470529	regulation of T cell activation
GO:0031329	7	3094	0.00484504	regulation of cellular catabolic process
GO:0060596	2	8	0.00488398	mammary placode formation
GO:0045732	4	374	0.00506912	positive regulation of protein catabolic process
GO:0050878	6	1837	0.00545555	regulation of body fluid levels
GO:0002696	5	941	0.00548808	positive regulation of leukocyte activation
GO:0010038	5	951	0.00578067	response to metal ion
GO:0051094	7	3200	0.00609775	positive regulation of developmental process
GO:0048858	5	963	0.00614797	cell projection morphogenesis
GO:0032989	6	1879	0.006228	cellular component morphogenesis
GO:0045664	6	1894	0.00652479	regulation of neuron differentiation

Table 6: Overrepresented terms with the network-based enrichment. Only terms not detected with the standard method.

GO Term	N1	N2	P-value	Description
GO:0048662	3	104	0.00658951	negative regulation of smooth muscle cell proliferation
GO:0045892	7	3247	0.00673549	negative regulation of transcription, DNA-templated
GO:0044419	6	1908	0.00681224	interspecies interaction between organisms
GO:0007050	4	403	0.00681784	cell cycle arrest
GO:0044092	7	3258	0.00689265	negative regulation of molecular function
GO:0050867	5	996	0.00725405	positive regulation of cell activation
GO:0006974	6	1933	0.00735149	cellular response to DNA damage stimulus
GO:0051347	6	1933	0.00735149	positive regulation of transferase activity
GO:0031334	4	411	0.00737054	positive regulation of protein complex assembly
GO:0045087	6	1935	0.00739611	innate immune response
GO:1902679	7	3295	0.00744433	negative regulation of RNA biosynthetic process
GO:0045471	4	417	0.00780643	response to ethanol
GO:0010632	4	419	0.00795589	regulation of epithelial cell migration
GO:0009409	3	111	0.00801888	response to cold
GO:0070232	3	111	0.00801888	regulation of T cell apoptotic process
GO:0008406	4	424	0.00833887	gonad development
GO:0006508	7	3357	0.00845281	proteolysis
GO:0031345	4	428	0.00865498	negative regulation of cell projection organization
GO:0051253	7	3369	0.0086608	negative regulation of RNA metabolic process
GO:0043392	3	114	0.00868954	negative regulation of DNA binding
GO:0050707	4	430	0.00881633	regulation of cytokine secretion
GO:0043433	4	432	0.00897992	negative regulation of sequence-specific DNA binding transcription factor activity
GO:0000075	4	434	0.00914574	cell cycle checkpoint
GO:0009894	7	3408	0.00936707	regulation of catabolic process
GO:0097190	5	1052	0.00948645	apoptotic signaling pathway
GO:0042129	4	439	0.00957027	regulation of T cell proliferation
GO:0032990	5	1056	0.00966457	cell part morphogenesis
GO:0001569	3	119	0.00988816	patterning of blood vessels
GO:0009895	4	445	0.0100988	negative regulation of catabolic process
GO:0032320	5	1071	0.0103562	positive regulation of Ras GTPase activity
GO:0010595	3	122	0.0106574	positive regulation of endothelial cell migration
GO:0045668	3	122	0.0106574	negative regulation of osteoblast differentiation
GO:0003382	3	123	0.0109223	epithelial cell morphogenesis
GO:0097305	5	1084	0.0109867	response to alcohol
GO:0032526	4	457	0.0112207	response to retinoic acid
GO:0015031	7	3506	0.0113608	protein transport
GO:0035303	4	461	0.0116144	regulation of dephosphorylation
GO:0043393	4	465	0.0120183	regulation of protein binding
GO:0009266	4	469	0.0124326	response to temperature stimulus
GO:0030856	4	470	0.0125377	regulation of epithelial cell differentiation
GO:0010629	7	3561	0.0126296	negative regulation of gene expression
GO:0042592	7	3571	0.0128728	homeostatic process
GO:2000113	7	3633	0.0144706	negative regulation of cellular macromolecule biosynthetic process
GO:0002009	5	1159	0.0152424	morphogenesis of an epithelium
GO:0044702	7	3664	0.0153305	single organism reproductive process
GO:0090244	2	14	0.0158595	Wnt signaling pathway involved in somitogenesis
GO:0045934	7	3691	0.0161144	negative regulation of nucleobase-containing compound metabolic process
GO:0042098	3	140	0.0161172	T cell proliferation
GO:0018193	6	2224	0.0166707	peptidyl-amino acid modification
GO:0035914	3	143	0.0171765	skeletal muscle cell differentiation
GO:0045184	7	3728	0.0172436	establishment of protein localization
GO:0071396	5	1198	0.0179185	cellular response to lipid
GO:0045216	4	516	0.0181343	cell-cell junction organization
GO:0030282	3	146	0.0182809	bone mineralization
GO:0046434	6	2260	0.0183049	organophosphate catabolic process
GO:0042742	4	519	0.0185542	defense response to bacterium
GO:0010558	7	3771	0.0186395	negative regulation of macromolecule biosynthetic process
GO:0018108	4	523	0.0191253	peptidyl-tyrosine phosphorylation
GO:1901215	4	524	0.0192701	negative regulation of neuron death
GO:0051172	7	3798	0.019564	negative regulation of nitrogen compound metabolic process

Table 7: Overrepresented terms with the network-based enrichment. Only terms not detected with the standard method.

GO Term	N1	N2	P-value	Description
GO:0014068	3	150	0.0198252	positive regulation of phosphatidylinositol 3-kinase signaling
GO:0006897	5	1228	0.0202189	endocytosis
GO:0018212	4	533	0.0206099	peptidyl-tyrosine modification
GO:0040008	6	2308	0.0206864	regulation of growth
GO:0052548	5	1238	0.0210354	regulation of endopeptidase activity
GO:0000165	4	537	0.0212271	MAPK cascade
GO:0048538	3	155	0.021874	thymus development
GO:0031331	4	542	0.0220177	positive regulation of cellular catabolic process
GO:0003006	6	2335	0.0221343	developmental process involved in reproduction
GO:0042308	3	157	0.0227312	negative regulation of protein import into nucleus
GO:0032091	3	160	0.0240583	negative regulation of protein binding
GO:0050767	6	2377	0.0245512	regulation of neurogenesis
GO:0050776	6	2377	0.0245512	regulation of immune response
GO:0032318	5	1285	0.0252283	regulation of Ras GTPase activity
GO:0035019	3	163	0.0254356	somatic stem cell maintenance
GO:0052547	5	1292	0.0259054	regulation of peptidase activity
GO:0007368	3	164	0.0259061	determination of left/right symmetry
GO:0009855	3	167	0.0273519	determination of bilateral symmetry
GO:0009799	3	168	0.0278454	specification of symmetry
GO:0006954	5	1314	0.0281271	inflammatory response
GO:0034330	4	577	0.0281791	cell junction organization
GO:0001764	4	578	0.028372	neuron migration
GO:2001236	4	581	0.0289565	regulation of extrinsic apoptotic signaling pathway
GO:0070228	3	172	0.0298784	regulation of lymphocyte apoptotic process
GO:0070646	3	174	0.0309309	protein modification by small protein removal
GO:0051346	5	1348	0.0318536	negative regulation of hydrolase activity
GO:0048729	5	1359	0.0331389	tissue morphogenesis
GO:0030030	6	2507	0.0334448	cell projection organization
GO:0051050	6	2507	0.0334448	positive regulation of transport
GO:0010243	6	2509	0.0336001	response to organonitrogen compound
GO:0009617	4	605	0.0339607	response to bacterium
GO:0007596	5	1367	0.0340993	blood coagulation
GO:0050817	5	1367	0.0340993	coagulation
GO:0051051	5	1375	0.0350812	negative regulation of transport
GO:0007599	5	1382	0.0359588	hemostasis
GO:0046823	3	183	0.0359698	negative regulation of nucleocytoplasmic transport
GO:1901701	6	2540	0.0360796	cellular response to oxygen-containing compound
GO:0001704	3	184	0.036561	formation of primary germ layer
GO:0001841	2	21	0.0365632	neural tube formation
GO:0001501	4	620	0.0373968	skeletal system development
GO:0070663	4	621	0.0376347	regulation of leukocyte proliferation
GO:0006497	3	186	0.0377628	protein lipidation
GO:0002252	5	1396	0.0377652	immune effector process
GO:0046330	3	187	0.0383731	positive regulation of JNK cascade
GO:0009888	6	2570	0.0386202	tissue development
GO:0016477	6	2574	0.0389697	cell migration
GO:0030858	3	188	0.0389902	positive regulation of epithelial cell differentiation
GO:0045682	3	189	0.0396137	regulation of epidermis development
GO:0043122	4	630	0.0398263	regulation of I-kappaB kinase/NF-kappaB signaling
GO:0050795	4	630	0.0398263	regulation of behavior
GO:0051960	6	2584	0.0398551	regulation of nervous system development
GO:2001239	3	190	0.0402439	regulation of extrinsic apoptotic signaling pathway in absence of ligand
GO:0045785	4	632	0.0403257	positive regulation of cell adhesion
GO:0042108	3	191	0.0408803	positive regulation of cytokine biosynthetic process
GO:0010035	5	1420	0.0410283	response to inorganic substance
GO:1903321	3	192	0.0415237	negative regulation of protein modification by small protein conjugation or removal
GO:0007507	4	638	0.0418523	heart development
GO:0051707	5	1426	0.0418776	response to other organism
GO:0043507	3	193	0.0421736	positive regulation of JUN kinase activity
GO:0034244	2	23	0.0440374	negative regulation of transcription elongation from RNA polymerase II promoter

Table 8: Overrepresented terms with the network-based enrichment. Only terms not detected with the standard method.

GO Term	N1	N2	P-value	Description
GO:0048332	2	23	0.0440374	mesoderm morphogenesis
GO:0032434	3	196	0.0441636	regulation of proteasomal ubiquitin-dependent protein catabolic process
GO:0050870	4	647	0.0442215	positive regulation of T cell activation
GO:0090263	3	197	0.0448407	positive regulation of canonical Wnt signaling pathway
GO:0023014	4	653	0.0458554	signal transduction by phosphorylation
GO:0009612	4	658	0.0472505	response to mechanical stimulus
GO:0030336	4	660	0.0478175	negative regulation of cell migration
GO:0032785	2	24	0.0480341	negative regulation of DNA-templated transcription, elongation
GO:0060638	2	24	0.0480341	mesenchymal-epithelial cell signaling
GO:0016485	4	661	0.0481027	protein processing
GO:0042493	5	1473	0.0490211	response to drug
GO:0021700	4	666	0.049548	developmental maturation
GO:2001234	4	666	0.049548	negative regulation of apoptotic signaling pathway
GO:1902807	3	204	0.0497714	negative regulation of cell cycle G1/S phase transition
GO:2000134	3	204	0.0497714	negative regulation of G1/S transition of mitotic cell cycle
GO:0030100	4	667	0.0498408	regulation of endocytosis

Table 9: Overrepresented terms with the network-based enrichment. Only terms not detected with the standard method.