

## Tables of unique enriched GO terms identified by the regular and integrated methods

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Table 1: Uniquely identified enriched GO terms by regular edgeR.

term_ID	description	Frequency <sup>a</sup>	log10 p-value	Uniqueness <sup>b</sup>	Dispensability <sup>c</sup>	Eliminated <sup>d</sup>	Ontology
GO:0032101	regulation of response to external stimulus	0.32%	-4.8447	0.473	0	0	BP
GO:0032787	monocarboxylic acid metabolic process	2.31%	-4.0141	0.769	0	0	BP
GO:0001649	osteoblast differentiation	0.01%	-3.399	0.831	0.079	0	BP
GO:0006915	apoptotic process	0.25%	-3.3675	0.817	0.103	0	BP
GO:0070663	regulation of leukocyte proliferation	0.01%	-4.2733	0.426	0.222	0	BP
GO:0051249	regulation of lymphocyte activation	0.02%	-4.0205	0.51	0.23	0	BP
GO:0010646	regulation of cell communication	0.38%	-3.752	0.566	0.292	0	BP
GO:0023051	regulation of signaling	0.38%	-3.6799	0.581	0.297	0	BP
GO:0071495	cellular response to endogenous stimulus	0.09%	-3.3507	0.736	0.347	0	BP
GO:0009719	response to endogenous stimulus	0.11%	-3.6615	0.734	0.353	0	BP
GO:0048583	regulation of response to stimulus	0.69%	-3.8268	0.524	0.413	0	BP
GO:0050804	regulation of synaptic transmission	0.01%	-3.6778	0.606	0.431	0	BP
GO:0072330	monocarboxylic acid biosynthetic process	0.82%	-3.4473	0.774	0.51	0	BP

GO:0005578	proteinaceous extracellular matrix	0.11%	-5.4597	0.22	0	0	CC
GO:0031225	anchored component of membrane	0.02%	-4.0867	0.575	0	0	CC
GO:0005887	integral component of plasma membrane	1.25%	-4.011	0.392	0.104	0	CC
GO:0004866	endopeptidase inhibitor activity	0.08%	-3.5686	0.617	0	0	MF
GO:0004872	receptor activity	1.87%	-5.2984	0.794	0	0	MF
GO:0038023	signaling receptor activity	1.49%	-4.399	0.487	0	0	MF
GO:0060089	molecular transducer activity	2.04%	-3.7852	0.794	0	0	MF
GO:1901681	sulfur compound binding	0.62%	-4.3595	0.777	0	0	MF
GO:0008201	heparin binding	0.01%	-4.6402	0.75	0.037	0	MF
GO:0005539	glycosaminoglycan binding	0.02%	-3.6517	0.75	0.17	0	MF
GO:1903034	regulation of response to wounding	0.09%	-3.8041	0.502	0.771	1	BP
GO:0080134	regulation of response to stress	0.37%	-3.8069	0.47	0.87	1	BP
GO:0032944	regulation of mononuclear cell proliferation	0.01%	-4.1739	0.424	0.997	1	BP
GO:0050670	regulation of lymphocyte proliferation	0.01%	-3.8416	0.32	0.965	1	BP
GO:0070661	leukocyte proliferation	0.01%	-3.5031	0.588	0.761	1	BP
GO:0008285	negative regulation of cell proliferation	0.03%	-3.5498	0.43	0.831	1	BP
GO:0002694	regulation of leukocyte activation	0.02%	-3.5498	0.508	0.983	1	BP
GO:0044420	extracellular matrix part	0.02%	-3.9914	0.237	0.834	1	CC
GO:0005604	basement membrane	0.01%	-3.3179	0.239	0.82	1	CC
GO:0031226	intrinsic component of plasma membrane	1.34%	-3.9666	0.392	0.778	1	CC

GO:0004867	serine-type endopeptidase inhibitor activity	0.03%	-3.71	0.617	0.932	1	MF
GO:0004888	transmembrane signaling receptor activity	0.37%	-4.5317	0.506	0.797	1	MF
GO:0004871	signal transducer activity	2.03%	-3.7852	0.487	0.94	1	MF

<sup>a</sup> Proportion of the GO term in the protein annotation database (UniProt)

<sup>b</sup> Measures whether the term is an outlier when compared semantically to the whole list

<sup>c</sup> The semantic similarity threshold at which the term was removed from the list

<sup>d</sup> 1: GO term is redundant; 0: GO term is non-redundant

Table 2: Uniquely identified enriched GO terms by integrated edgeR.

term_ID	description	frequency	log10 p-value	uniqueness	dispensability	eliminated	Ontology
GO:0002376	immune system process	0.63%	-3.5607	0.951	0	0	BP
GO:0006928	cellular component movement	0.49%	-4.9508	0.882	0	0	BP
GO:0009987	cellular process	65.99%	-4.4056	0.983	0	0	BP
GO:0051130	positive regulation of cellular component organization	0.05%	-6.7645	0.68	0	0	BP
GO:0048754	branching morphogenesis of an epithelial tube	0.01%	-4.2581	0.495	0.04	0	BP
GO:0016337	single organismal cell-cell adhesion	0.04%	-4.1107	0.807	0.041	0	BP
GO:0033688	regulation of osteoblast proliferation	0.02%	-3.9706	0.737	0.177	0	BP
GO:0070372	regulation of ERK1 and ERK2 cascade	0.01%	-4.9208	0.654	0.197	0	BP
GO:0051246	regulation of protein metabolic process	0.88%	-3.3665	0.735	0.294	0	BP

GO:0006357	regulation of transcription from RNA polymerase II promoter	0.21%	-3.3546	0.741	0.389	0	BP
GO:0032964	collagen biosynthetic process	0.02%	-3.2933	0.575	0.482	0	BP
GO:0010573	vascular endothelial growth factor production	0.00%	-3.7399	0.59	0.484	0	BP
GO:0051128	regulation of cellular component organization	1.02%	-4.0701	0.742	0.497	0	BP
GO:0003006	developmental process involved in reproduction	0.08%	-3.4815	0.752	0.524	0	BP
GO:0090130	tissue migration	0.01%	-3.3716	0.558	0.538	0	BP
GO:0010595	positive regulation of endothelial cell migration	0.03%	-4.7696	0.362	0.553	0	BP
GO:0032835	glomerulus development	0.00%	-4.1244	0.5	0.556	0	BP
GO:0008015	blood circulation	0.03%	-3.5513	0.532	0.563	0	BP
GO:0010811	positive regulation of cell-substrate adhesion	0.01%	-4.7352	0.612	0.57	0	BP
GO:0045766	positive regulation of angiogenesis	0.01%	-4.7375	0.365	0.59	0	BP
GO:0098602	single organism cell adhesion	0.02%	-3.5186	0.806	0.608	0	BP
GO:0033687	osteoblast proliferation	0.00%	-3.5935	0.855	0.617	0	BP
GO:0051270	regulation of cellular component movement	0.04%	-3.767	0.662	0.664	0	BP
GO:0022008	neurogenesis	0.08%	-3.6676	0.456	0.667	0	BP
GO:0003014	renal system process	0.00%	-3.5406	0.563	0.681	0	BP

GO:0030054	cell junction	0.15%	-4.4437	0.563	0	0	CC
GO:0031224	intrinsic component of membrane	35.35%	-3.7825	0.703	0	0	CC
GO:0070062	extracellular vesicular exosome	0.30%	-3.52	0.125	0	0	CC
GO:0043230	extracellular organelle	0.30%	-3.4685	0.206	0.594	0	CC
GO:0050839	cell adhesion molecule binding	0.01%	-3.7959	0.011	0	0	MF
GO:0005178	integrin binding	0.00%	-4.0991	0	0.374	0	MF
GO:0008083	growth factor activity	0.03%	-3.3645	0	0.6	0	MF
GO:0061448	connective tissue development	0.02%	-4.2464	0.754	0.746	1	BP
GO:0050678	regulation of epithelial cell proliferation	0.02%	-3.3261	0.713	0.716	1	BP
GO:0042325	regulation of phosphorylation	0.18%	-4.3054	0.686	0.869	1	BP
GO:0001932	regulation of protein phosphorylation	0.17%	-4.5528	0.676	0.805	1	BP
GO:0070371	ERK1 and ERK2 cascade	0.01%	-4.1232	0.7	0.819	1	BP
GO:0070374	positive regulation of ERK1 and ERK2 cascade	0.01%	-4.0443	0.572	0.976	1	BP
GO:0001541	ovarian follicle development	0.00%	-3.6615	0.509	0.781	1	BP
GO:0043542	endothelial cell migration	0.01%	-3.5114	0.473	0.98	1	BP
GO:0090132	epithelium migration	0.01%	-3.3716	0.494	0.996	1	BP
GO:0010634	positive regulation of epithelial cell migration	0.01%	-4.2182	0.353	0.933	1	BP
GO:0010631	epithelial cell migration	0.01%	-3.3716	0.466	0.951	1	BP
GO:0072012	glomerulus vasculature development	0.00%	-3.6345	0.507	0.889	1	BP

GO:0072109	glomerular mesangium development	0.00%	-3.7986	0.505	0.961	1	BP
GO:0003013	circulatory system process	0.03%	-3.8069	0.532	0.756	1	BP
GO:0033630	positive regulation of cell adhesion mediated by integrin	0.00%	-3.9208	0.638	0.86	1	BP
GO:0001952	regulation of cell-matrix adhesion	0.01%	-3.5214	0.69	0.945	1	BP
GO:0065010	extracellular membrane-bounded organelle	0.30%	-3.4685	0.125	0.996	1	CC

Table 3: Uniquely identified enriched GO terms by regular DESeq2.

term_ID	description	frequency	log10 p-value	uniqueness	dispensability	eliminated	Ontology
GO:0045785	positive regulation of cell adhesion	0.01%	-4.6968	0.502	0	0	BP
GO:0042110	T cell activation	0.02%	-3.9172	0.272	0.016	0	BP
GO:0070661	leukocyte proliferation	0.01%	-3.6308	0.514	0.033	0	BP
GO:0035914	skeletal muscle cell differentiation	0.00%	-3.6696	0.769	0.054	0	BP
GO:0032787	monocarboxylic acid metabolic process	2.31%	-3.6498	0.744	0.083	0	BP
GO:0032101	regulation of response to external stimulus	0.32%	-3.6289	0.621	0.221	0	BP
GO:0044459	plasma membrane part	3.06%	-6.266	0.007	0	0	CC
GO:0005887	integral component of plasma membrane	1.25%	-4.4449	0.01	0.431	0	CC

GO:0001071	nucleic acid binding transcription factor activity	4.98%	-4.6402	0.656	0	0	MF
GO:0003700	sequence- specific DNA binding transcription factor activity	4.96%	-4.6402	0.509	0	0	MF
GO:1901681	sulfur compound binding	0.62%	-5.4023	0.614	0	0	MF
GO:0005102	receptor binding	0.42%	-3.5935	0.47	0.049	0	MF
GO:0000982	RNA polymerase II core promoter proximal region sequence- specific DNA binding transcription factor activity	0.02%	-4.0453	0.495	0.483	0	MF
GO:0008083	growth factor activity	0.03%	-3.8297	0.472	0.527	0	MF
GO:0010810	regulation of cell-substrate adhesion	0.01%	-3.9914	0.547	0.915	1	BP
GO:0051249	regulation of lymphocyte activation	0.02%	-3.8153	0.207	0.947	1	BP
GO:0050863	regulation of T cell activation	0.01%	-4.1273	0.21	0.967	1	BP
GO:0050865	regulation of cell activation	0.02%	-3.8894	0.224	0.911	1	BP
GO:0070663	regulation of leukocyte proliferation	0.01%	-3.5686	0.354	0.761	1	BP
GO:0046641	positive regulation of alpha-beta T cell proliferation	0.00%	-3.8097	0.131	0.858	1	BP
GO:0042098	T cell proliferation	0.01%	-3.5229	0.151	0.962	1	BP
GO:0031226	intrinsic component of	1.34%	-4.1568	0.01	0.778	1	CC

	plasma membrane						
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Table 4: Uniquely identified enriched GO terms by integrated DESeq2.

term_ID	description	frequency	log10 p-value	uniqueness	dispensability	eliminated	Ontology
GO:0009611	response to wounding	0.11%	-5.1101	0.824	0	0	BP
GO:0009987	cellular process	65.99%	-7.4179	0.988	0	0	BP
GO:0044699	single-organism process	53.98%	-8.5114	0.984	0	0	BP
GO:0050673	epithelial cell proliferation	0.02%	-5.8962	0.869	0	0	BP
GO:0051130	positive regulation of cellular component organization	0.05%	-5.1612	0.614	0	0	BP
GO:0060429	epithelium development	0.08%	-6.3028	0.712	0	0	BP
GO:0003008	system process	0.20%	-5.7423	0.704	0.038	0	BP
GO:0015669	gas transport	0.07%	-3.8153	0.885	0.042	0	BP
GO:0046033	AMP metabolic process	0.13%	-4.2426	0.875	0.044	0	BP
GO:0044763	single-organism cellular process	42.00%	-8.3605	0.892	0.08	0	BP
GO:0016477	cell migration	0.07%	-3.6778	0.76	0.195	0	BP
GO:0006357	regulation of transcription from RNA polymerase II promoter	0.21%	-4.057	0.66	0.241	0	BP
GO:0042981	regulation of apoptotic process	0.13%	-3.7645	0.637	0.268	0	BP
GO:0007167	enzyme linked receptor protein signaling pathway	0.06%	-4.8928	0.586	0.312	0	BP
GO:0048583	regulation of response to stimulus	0.69%	-4.3307	0.605	0.376	0	BP
GO:0065008	regulation of biological quality	2.71%	-4.2958	0.649	0.377	0	BP
GO:0044087	regulation of cellular	0.13%	-3.3449	0.697	0.388	0	BP



	component biogenesis						
GO:0051246	regulation of protein metabolic process	0.88%	-3.3382	0.658	0.389	0	BP
GO:0048523	negative regulation of cellular process	0.94%	-3.9788	0.59	0.391	0	BP
GO:0071310	cellular response to organic substance	0.21%	-3.6108	0.784	0.398	0	BP
GO:0042060	wound healing	0.03%	-3.7932	0.836	0.405	0	BP
GO:0048519	negative regulation of biological process	1.24%	-3.5622	0.662	0.405	0	BP
GO:0009966	regulation of signal transduction	0.36%	-4.857	0.504	0.484	0	BP
GO:0051128	regulation of cellular component organization	1.02%	-4.2388	0.654	0.497	0	BP
GO:0048468	cell development	0.13%	-4.1158	0.684	0.63	0	BP
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	0.02%	-4.0915	0.6	0.641	0	BP
GO:0001763	morphogenesis of a branching structure	0.02%	-4.0357	0.676	0.647	0	BP
GO:0001655	urogenital system development	0.02%	-3.7399	0.657	0.66	0	BP
GO:0030335	positive regulation of cell migration	0.02%	-3.4815	0.524	0.689	0	BP
GO:0002523	leukocyte migration involved in inflammatory response	0.00%	-3.3458	0.704	0.695	0	BP
GO:0005912	adherens junction	0.03%	-3.4609	0.701	0	0	CC
GO:0030054	cell junction	0.15%	-3.8697	0.827	0	0	CC
GO:0032153	cell division site	0.26%	-4.2366	0.824	0	0	CC
GO:0070062	extracellular vesicular exosome	0.30%	-5.6144	0.328	0	0	CC

GO:0032155	cell division site part	0.01%	-4.2366	0.823	0.02	0	CC
GO:0031982	vesicle	0.45%	-4.3665	0.659	0.266	0	CC
GO:0005604	basement membrane	0.01%	-3.4123	0.49	0.468	0	CC
GO:0043230	extracellular organelle	0.30%	-5.5654	0.452	0.594	0	CC
GO:0004866	endopeptidase inhibitor activity	0.08%	-3.5017	0.695	0	0	MF
GO:0005201	extracellular matrix structural constituent	0.01%	-3.7282	0.694	0	0	MF
GO:0005515	protein binding	2.48%	-5.5376	0.662	0	0	MF
GO:0016717	oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	0.03%	-3.4473	0.695	0	0	MF
GO:0042803	protein homodimerization activity	0.12%	-4.0778	0.434	0.05	0	MF
GO:0050839	cell adhesion molecule binding	0.01%	-3.4763	0.456	0.451	0	MF
GO:0042802	identical protein binding	0.15%	-3.3161	0.432	0.547	0	MF
GO:0008285	negative regulation of cell proliferation	0.03%	-3.567	0.607	0.853	1	BP
GO:0050678	regulation of epithelial cell proliferation	0.02%	-3.6234	0.674	0.793	1	BP
GO:0010604	positive regulation of macromolecule metabolic process	0.31%	-3.4179	0.578	0.743	1	BP
GO:0009893	positive regulation of metabolic process	0.33%	-3.4535	0.579	0.86	1	BP
GO:0048729	tissue morphogenesis	0.04%	-4.8356	0.687	0.886	1	BP

GO:0061138	morphogenesis of a branching epithelium	0.02%	-4.3063	0.639	0.829	1	BP
GO:0048754	branching morphogenesis of an epithelial tube	0.01%	-3.5171	0.632	0.982	1	BP
GO:0030855	epithelial cell differentiation	0.04%	-3.8697	0.666	0.878	1	BP
GO:0045766	positive regulation of angiogenesis	0.01%	-3.9172	0.441	0.957	1	BP
GO:0045765	regulation of angiogenesis	0.01%	-4.9872	0.491	0.925	1	BP
GO:2000027	regulation of organ morphogenesis	0.01%	-4.3028	0.501	0.746	1	BP
GO:0009887	organ morphogenesis	0.08%	-5.1979	0.634	0.722	1	BP
GO:0001525	angiogenesis	0.03%	-4.7144	0.638	0.728	1	BP
GO:0043067	regulation of programmed cell death	0.13%	-3.8962	0.636	0.992	1	BP
GO:0010941	regulation of cell death	0.14%	-3.5331	0.639	0.886	1	BP
GO:1901701	cellular response to oxygen-containing compound	0.23%	-3.3925	0.783	0.864	1	BP
GO:0023057	negative regulation of signaling	0.18%	-4.3925	0.562	0.93	1	BP
GO:0009968	negative regulation of signal transduction	0.18%	-3.7852	0.502	0.929	1	BP
GO:0048585	negative regulation of response to stimulus	0.36%	-4.1337	0.538	0.88	1	BP
GO:0010648	negative regulation of cell communication	0.18%	-4.1785	0.555	0.93	1	BP
GO:0070372	regulation of ERK1 and ERK2 cascade	0.01%	-4.0186	0.569	0.748	1	BP
GO:0070371	ERK1 and ERK2 cascade	0.01%	-3.4353	0.618	0.819	1	BP

GO:0030509	BMP signaling pathway	0.01%	-3.3595	0.598	0.829	1	BP
GO:2000147	positive regulation of cell motility	0.02%	-3.4012	0.533	0.995	1	BP
GO:0040017	positive regulation of locomotion	0.02%	-3.3152	0.582	0.871	1	BP
GO:0043542	endothelial cell migration	0.01%	-3.3143	0.61	0.933	1	BP
GO:0051272	positive regulation of cellular component movement	0.02%	-3.3507	0.547	0.893	1	BP
GO:0010634	positive regulation of epithelial cell migration	0.01%	-3.4962	0.435	0.927	1	BP
GO:0070161	anchoring junction	0.03%	-3.8125	0.701	0.788	1	CC
GO:0065010	extracellular membrane-bounded organelle	0.30%	-5.5654	0.404	0.996	1	CC
GO:0031988	membrane-bounded vesicle	0.42%	-4.4737	0.562	0.953	1	CC
GO:0043256	laminin complex	0.00%	-3.3363	0.508	0.892	1	CC

Table 5: Uniquely identified enriched GO terms by regular DSS.

term_ID	description	frequency	log10 p-value	uniqueness	dispensability	eliminated	Ontology
GO:0071944	cell periphery	17.51%	-8.6716	0.008	0.086	0	CC
GO:0005886	plasma membrane	13.93%	-8.8761	0.003	0	0	CC
GO:0016021	integral component of membrane	35.23%	-8.3507	0.047	0.606	0	CC
GO:0004930	G-protein coupled receptor activity	0.26%	-6.3179	0.497	0	0	MF
GO:0022838	substrate-specific channel activity	0.27%	-5.9431	0.205	0	0	MF

GO:0060089	molecular transducer activity	2.04%	-5.2262	0.7	0	0	MF
GO:0022803	passive transmembrane transporter activity	0.41%	-5.224	0.399	0.4	0	MF
GO:0004871	signal transducer activity	2.03%	-5.2262	0.501	0.774	1	MF
GO:0005216	ion channel activity	0.26%	-4.8894	0.206	0.923	1	MF
GO:0015267	channel activity	0.41%	-5.224	0.198	0.96	1	MF

Table 6: Uniquely identified enriched GO terms by integrated DSS.

term_ID	description	frequency	log10 p-value	uniqueness	dispensability	eliminated	Ontology
GO:0007154	cell communication	4.36%	-7.7878	0.617	0	0	BP
GO:0023052	signaling	3.84%	-7.6402	0.744	0	0	BP
GO:0051094	positive regulation of developmental process	0.05%	-5.4522	0.428	0	0	BP
GO:0044700	single organism signaling	3.84%	-7.6402	0.349	0.089	0	BP
GO:0050865	regulation of cell activation	0.02%	-4.3206	0.489	0.208	0	BP
GO:0045597	positive regulation of cell differentiation	0.04%	-4.4935	0.4	0.643	0	BP
GO:0044425	membrane part	36.83%	-4.5768	0.138	0.312	0	CC
GO:0031224	intrinsic component of membrane	35.35%	-9.5361	0.047	0	0	CC
GO:0001071	nucleic acid binding transcription factor activity	4.98%	-4.7496	0.276	0	0	MF
GO:0003700	sequence-specific DNA binding	4.96%	-4.7496	0.275	0	0	MF

	transcription factor activity						
GO:0004896	cytokine receptor activity	0.01%	-4.5884	0.25	0	0	MF
GO:0007166	cell surface receptor signaling pathway	0.62%	-4.4711	0.264	0.752	1	BP
GO:0007165	signal transduction	3.80%	-5.0575	0.217	0.96	1	BP