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

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

			log10 p-				
term_ID	description	Frequency	value	Uniqueness ^b	Dispensability	Eliminated ^d	Ontology
_	regulation of				,		<u> </u>
	response to						
GO:0032101	external stimulus	0.32%	-4.8447	0.473	0	0	BP
	monocarboxylic						
	acid metabolic						
GO:0032787	process	2.31%	-4.0141	0.769	0	0	BP
	osteoblast						
GO:0001649	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
	regulation of						
	leukocyte						
GO:0070663	proliferation	0.01%	-4.2733	0.426	0.222	0	BP
	regulation of						
	lymphocyte						
GO:0051249	activation	0.02%	-4.0205	0.51	0.23	0	BP
	regulation of cell						
GO:0010646	communication	0.38%	-3.752	0.566	0.292	0	BP
	regulation of						
GO:0023051	signaling	0.38%	-3.6799	0.581	0.297	0	BP
	cellular response						
	to endogenous						
GO:0071495	stimulus	0.09%	-3.3507	0.736	0.347	0	BP
	response to						
	endogenous						
GO:0009719	stimulus	0.11%	-3.6615	0.734	0.353	0	BP
	regulation of						
00 00 40 500	response to	0.600/	2.0260	0.534	0.440		
GO:0048583	stimulus	0.69%	-3.8268	0.524	0.413	0	BP
	regulation of						
CO.0050004	synaptic	0.010/	2 (770	0.000	0.434		DD
GO:0050804	transmission	0.01%	-3.6778	0.606	0.431	0	BP
	monocarboxylic						
60,0073330	acid biosynthetic	0.930/	2.4472	0.774	0.51		DD.
GO:0072330	process	0.82%	-3.4473	0.774	0.51	0	BP

	proteinaceous						
	extracellular						
GO:0005578	matrix	0.11%	-5.4597	0.22	0	0	СС
20.0003370	anchored	0.1170	31.1337	0.22	<u> </u>		
	component of						
GO:0031225	membrane	0.02%	-4.0867	0.575	0	0	СС
	integral						
	component of						
GO:0005887	plasma membrane	1.25%	-4.011	0.392	0.104	0	CC
	endopeptidase						
GO:0004866	inhibitor activity	0.08%	-3.5686	0.617	0	0	MF
GO:0004872	receptor activity	1.87%	-5.2984	0.794	0	0	MF
	signaling receptor						
GO:0038023	activity	1.49%	-4.399	0.487	0	0	MF
	molecular						
GO:0060089	transducer activity	2.04%	-3.7852	0.794	0	0	MF
	sulfur compound				_	_	
GO:1901681	binding	0.62%	-4.3595	0.777	0	0	MF
GO:0008201	heparin binding	0.01%	-4.6402	0.75	0.037	0	MF
	glycosaminoglycan						
GO:0005539	binding	0.02%	-3.6517	0.75	0.17	0	MF
	regulation of						
CO-1002024	response to	0.000/	-3.8041	0.503	0.771	1	ВР
GO:1903034	wounding regulation of	0.09%	-3.8041	0.502	0.771	1	ВР
GO:0080134	response to stress	0.37%	-3.8069	0.47	0.87	1	BP
30.0000134	regulation of	0.5770	3.0003	0.47	0.07	1	ы
	mononuclear cell						
GO:0032944	proliferation	0.01%	-4.1739	0.424	0.997	1	BP
	regulation of						
	lymphocyte						
GO:0050670	proliferation	0.01%	-3.8416	0.32	0.965	1	BP
	leukocyte						
GO:0070661	proliferation	0.01%	-3.5031	0.588	0.761	1	BP
	negative						
	regulation of cell					_	
GO:0008285	proliferation	0.03%	-3.5498	0.43	0.831	1	BP
	regulation of						
60,0003604	leukocyte	0.030/	2 5 400	0.500	0.002	4	DD
GO:0002694	activation extracellular	0.02%	-3.5498	0.508	0.983	1	BP
GO:0044420	matrix part	0.02%	-3.9914	0.237	0.834	1	сс
30.0044420	basement	0.02/0	-3.3314	0.237	0.034	1	
GO:0005604	membrane	0.01%	-3.3179	0.239	0.82	1	СС
30.00004	intrinsic	0.01/0	3.3173	0.233	0.02		
	component of						
GO:0031226	plasma membrane	1.34%	-3.9666	0.392	0.778	1	СС
					_		<u> </u>

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

^a Proportion of the GO term in the protein annotation database (UniProt)

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

ID		£	log10 p-		dia	.	0
term_ID	description	frequency	value	uniqueness	dispensability	eliminated	Ontology
60 0002276	immune system	0.630/	2.5607	0.054			
GO:0002376	process	0.63%	-3.5607	0.951	0	0	BP
	cellular						
60.0006030	component	0.400/	4.0500	0.002			
GO:0006928	movement	0.49%	-4.9508	0.882	0	0	BP
GO:0009987	cellular process	65.99%	-4.4056	0.983	0	0	BP
	positive						
	regulation of						
	cellular						
	component						
GO:0051130	organization	0.05%	-6.7645	0.68	0	0	BP
	branching						
	morphogenesis						
	of an epithelial						
GO:0048754	tube	0.01%	-4.2581	0.495	0.04	0	BP
	single						
	organismal cell-						
GO:0016337	cell adhesion	0.04%	-4.1107	0.807	0.041	0	BP
	regulation of						
	osteoblast						
GO:0033688	proliferation	0.02%	-3.9706	0.737	0.177	0	BP
	regulation of						
	ERK1 and ERK2						
GO:0070372	cascade	0.01%	-4.9208	0.654	0.197	0	BP
	regulation of						
	protein						
	metabolic						
GO:0051246	process	0.88%	-3.3665	0.735	0.294	0	BP

^b Measures whether the term is an outlier when compared semantically to the whole list

^cThe semantic similarity threshold at which the term was removed from the list

^d 1: GO term is redundant; 0: GO term is non-redundant

	regulation of						
	transcription						
	from RNA						
	polymerase II						
GO:0006357	promoter	0.21%	-3.3546	0.741	0.389	0	BP
	collagen						
	biosynthetic					_	
GO:0032964	process	0.02%	-3.2933	0.575	0.482	0	BP
	vascular						
	endothelial						
GO:0010573	growth factor production	0.00%	-3.7399	0.59	0.484	0	ВР
GO.0010373	regulation of	0.00%	-3.7333	0.39	0.464	U	DF
	cellular						
	component						
GO:0051128	organization	1.02%	-4.0701	0.742	0.497	0	ВР
	developmental						
	process						
	involved in						
GO:0003006	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
	positive						
	regulation of						
	endothelial cell						
GO:0010595	migration	0.03%	-4.7696	0.362	0.553	0	BP
	glomerulus						
GO:0032835	development	0.00%	-4.1244	0.5	0.556	0	BP
60,0000015	blood	0.020/	2 5512	0.522	0.563	0	DD
GO:0008015	circulation	0.03%	-3.5513	0.532	0.563	0	BP
	positive regulation of						
	cell-substrate						
GO:0010811	adhesion	0.01%	-4.7352	0.612	0.57	0	ВР
00.0010011	positive	0.0170	1.7552	0.012	0.37	0	, Di
	regulation of						
GO:0045766	angiogenesis	0.01%	-4.7375	0.365	0.59	0	ВР
	single organism						
GO:0098602	cell adhesion	0.02%	-3.5186	0.806	0.608	0	BP
	osteoblast						
GO:0033687	proliferation	0.00%	-3.5935	0.855	0.617	0	BP
	regulation of						
	cellular						
00.0071075	component	0.044	0 = 0=		2.25	_	
GO:0051270	movement	0.04%	-3.767	0.662	0.664	0	BP
GO:0022008	neurogenesis	0.08%	-3.6676	0.456	0.667	0	BP
60 000001	renal system	0.000/	2 5 4 2 5	0 = 00	0.00	_	
GO:0003014	process	0.00%	-3.5406	0.563	0.681	0	BP

GO:0030054	cell junction	0.15%	-4.4437	0.563	0	0	СС
	intrinsic						
	component of						
GO:0031224	membrane	35.35%	-3.7825	0.703	0	0	CC
	extracellular						
	vesicular					_	
GO:0070062	exosome	0.30%	-3.52	0.125	0	0	CC
GO:0043230	extracellular	0.30%	-3.4685	0.206	0.594	0	СС
GU:0043230	organelle cell adhesion	0.30%	-3.4085	0.206	0.594	U	CC
	molecule						
GO:0050839	binding	0.01%	-3.7959	0.011	0	0	MF
GO:0005178	integrin binding	0.00%	-4.0991	0	0.374	0	MF
30.0003170	growth factor	0.0070	110331	0	0.07		.,,,,
GO:0008083	activity	0.03%	-3.3645	0	0.6	0	MF
	connective						
	tissue						
GO:0061448	development	0.02%	-4.2464	0.754	0.746	1	BP
	regulation of						
	epithelial cell					_	
GO:0050678	proliferation	0.02%	-3.3261	0.713	0.716	1	BP
CO.0042225	regulation of	0.100/	4 2054	0.686	0.860	1	DD
GO:0042325	phosphorylation regulation of	0.18%	-4.3054	0.080	0.869	1	BP
	protein						
GO:0001932	phosphorylation	0.17%	-4.5528	0.676	0.805	1	ВР
	ERK1 and ERK2						
GO:0070371	cascade	0.01%	-4.1232	0.7	0.819	1	BP
	positive						
	regulation of						
	ERK1 and ERK2						
GO:0070374	cascade	0.01%	-4.0443	0.572	0.976	1	BP
GO:0001541	ovarian follicle development	0.00%	2 6615	0.509	0.704	4	ВР
30.0001541	endothelial cell	0.00%	-3.6615	0.509	0.781	1	DY
GO:0043542	migration	0.01%	-3.5114	0.473	0.98	1	ВР
33.0043342	epithelium	0.01/0	3.3114	0.773	0.50		51
GO:0090132	migration	0.01%	-3.3716	0.494	0.996	1	ВР
	positive						
	regulation of						
	epithelial cell						
GO:0010634	migration	0.01%	-4.2182	0.353	0.933	1	BP
	epithelial cell			_			
GO:0010631	migration	0.01%	-3.3716	0.466	0.951	1	BP
	glomerulus						
GO:0072012	vasculature development	0.00%	-3.6345	0.507	0.889	1	ВР
90:00/2012	uevelopment	0.00%	-3.0345	0.507	0.889	1	אם

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

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

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

	nucleic acid						
	binding						
60.0001071	transcription	4.000/	4 (402	0.656	0		N 4 F
GO:0001071	factor activity	4.98%	-4.6402	0.656	0	0	MF
	sequence-						
	specific DNA binding						
	transcription						
GO:0003700	factor activity	4.96%	-4.6402	0.509	0	0	MF
30.0003700	sulfur	4.5070	7.0702	0.505	0		1411
	compound						
GO:1901681	binding	0.62%	-5.4023	0.614	0	0	MF
	receptor						
GO:0005102	binding	0.42%	-3.5935	0.47	0.049	0	MF
	RNA						
	polymerase II						
	core promoter						
	proximal region						
	sequence-						
	specific DNA						
	binding						
	transcription						
GO:0000982	factor activity	0.02%	-4.0453	0.495	0.483	0	MF
60.000000	growth factor	0.030/	2 0207	0.473	0.527		N 4 F
GO:0008083	activity regulation of	0.03%	-3.8297	0.472	0.527	0	MF
	cell-substrate						
GO:0010810	adhesion	0.01%	-3.9914	0.547	0.915	1	ВР
30.0010010	regulation of	0.0170	3.3314	0.547	0.515	1	ы
	lymphocyte						
GO:0051249	activation	0.02%	-3.8153	0.207	0.947	1	BP
	regulation of T						
GO:0050863	cell activation	0.01%	-4.1273	0.21	0.967	1	ВР
	regulation of						
GO:0050865	cell activation	0.02%	-3.8894	0.224	0.911	1	BP
	regulation of						
	leukocyte						
GO:0070663	proliferation	0.01%	-3.5686	0.354	0.761	1	BP
	positive						
	regulation of						
	alpha-beta T						
60:0046644	cell	0.000/	2 0007	0 121	0.050	4	DD
GO:0046641	proliferation T cell	0.00%	-3.8097	0.131	0.858	1	BP
GO:0042098	proliferation	0.01%	-3.5229	0.151	0.962	1	ВР
30.0042036	intrinsic	0.01/0	-3.3443	0.131	0.302	1	וט
GO:0031226	component of	1.34%	-4.1568	0.01	0.778	1	сс
33.3031220	Jon porterit of	1.57/0	500	3.01	3.770		

nlacma			
Piasilia			
membrane			

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

		_	log10 p-	_			_
term_ID	description	frequency	value	uniqueness	dispensability	eliminated	Ontology
	response to				_	_	
GO:0009611	wounding	0.11%	-5.1101	0.824	0	0	BP
GO:0009987	cellular process	65.99%	-7.4179	0.988	0	0	BP
	single-organism						
GO:0044699	process	53.98%	-8.5114	0.984	0	0	BP
	epithelial cell						
GO:0050673	proliferation	0.02%	-5.8962	0.869	0	0	BP
	positive regulation of cellular						
GO:0051130	component organization	0.05%	-5.1612	0.614	0	0	ВР
30.0031130	epithelium	0.03/6	-3.1012	0.014	0	0	טר
GO:0060429	development	0.08%	-6.3028	0.712	0	0	BP
GO:0003008	·	0.20%	-5.7423	0.704	0.038	0	BP
	system process						
GO:0015669	gas transport	0.07%	-3.8153	0.885	0.042	0	BP
60.0046033	AMP metabolic	0.120/	4 2 4 2 6	0.075	0.044		D.D.
GO:0046033	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	·	0.07%	-3.6778	0.76	0.195	0	BP
	regulation of transcription from RNA polymerase II						
GO:0006357	promoter	0.21%	-4.057	0.66	0.241	0	BP
	regulation of					_	
GO:0042981	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
55.0007107	regulation of	0.0070	7.0520	0.500	0.512		51
	response to						
GO:0048583	stimulus	0.69%	-4.3307	0.605	0.376	0	ВР
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	ВР

	component						
	component biogenesis						
	regulation of						
	protein metabolic						
GO:0051246	process	0.88%	-3.3382	0.658	0.389	0	BP
GO:0031240	negative	0.8676	-3.3362	0.038	0.363	0	ы
	regulation of						
GO:0048523	cellular process	0.94%	-3.9788	0.59	0.391	0	BP
GO.0048323	cellular response	0.94/6	-3.3700	0.39	0.331	U	Dr
	to organic						
GO:0071310	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
	negative						
60.0040540	regulation of	1 240/	2 5022	0.663	0.405	0	D.D.
GO:0048519	biological process	1.24%	-3.5622	0.662	0.405	0	BP
	regulation of						
CO-00000CC	signal	0.26%	4.057	0.504	0.404	0	DD
GO:0009966	transduction	0.36%	-4.857	0.504	0.484	0	BP
	regulation of cellular						
CO:00E1139	component	1 020/	4 2200	0.654	0.407	0	DD
GO:0051128	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
	transmembrane						
	receptor protein						
	serine/threonine						
00 0007470	kinase signaling	0.020/	4.0045	0.6	0.544	•	
GO:0007178	pathway	0.02%	-4.0915	0.6	0.641	0	BP
	morphogenesis of						
60 0004763	a branching	0.030/	4.0257	0.676	0.647	0	0.0
GO:0001763	structure	0.02%	-4.0357	0.676	0.647	0	BP
00 0004655	urogenital system	0.020/	2 7222	0.657	0.55	•	
GO:0001655	development	0.02%	-3.7399	0.657	0.66	0	BP
	positive						
60.0030335	regulation of cell	0.030/	2 4045	0.524	0.000	0	DD
GO:0030335	migration	0.02%	-3.4815	0.524	0.689	0	BP
	leukocyte						
	migration						
	involved in						
GO:0002523	inflammatory	0.000/	-3.3458	0.704	0.695	^	BP
	response	0.00%		0.704		0	†
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
	extracellular						
GO:0070062	vesicular exosome	0.30%	-5.6144	0.328	0	0	CC

	call division sita						
GO:0032155	cell division site part	0.01%	-4.2366	0.823	0.02	0	СС
GO:0032133	vesicle	0.45%	-4.3665	0.659	0.266	0	CC
GO.0031982	basement	0.4376	-4.3003	0.039	0.200	0	CC
GO:0005604	membrane	0.01%	-3.4123	0.49	0.468	0	СС
30.0003001	extracellular	0.0170	3.1123	0.13	0.100		
GO:0043230	organelle	0.30%	-5.5654	0.452	0.594	0	СС
	endopeptidase	010071					
GO:0004866	inhibitor activity	0.08%	-3.5017	0.695	0	0	MF
	extracellular						
	matrix structural						
GO:0005201	constituent	0.01%	-3.7282	0.694	0	0	MF
GO:0005515	protein binding	2.48%	-5.5376	0.662	0	0	MF
	oxidoreductase						
	activity, acting on						
	paired donors,						
	with oxidation of						
	a pair of donors						
	resulting in the						
	reduction of						
	molecular oxygen						
	to two molecules	/			_		
GO:0016717	of water	0.03%	-3.4473	0.695	0	0	MF
	protein						
GO:0042803	homodimerization	0.130/	4 0770	0.434	0.05	0	MF
GU:0042803	activity cell adhesion	0.12%	-4.0778	0.434	0.05	0	IVIF
GO:0050839	molecule binding	0.01%	-3.4763	0.456	0.451	0	MF
<u>do.0030833</u>	identical protein	0.0170	-3.4703	0.430	0.431	0	IVII
GO:0042802	binding	0.15%	-3.3161	0.432	0.547	0	MF
30.0012002	negative	0.1370	3.3101	0.132	0.5 17		
	regulation of cell						
GO:0008285	proliferation	0.03%	-3.567	0.607	0.853	1	ВР
	regulation of						
	epithelial cell						
GO:0050678	proliferation	0.02%	-3.6234	0.674	0.793	1	BP
	positive						
	regulation of						
	macromolecule						
GO:0010604	metabolic process	0.31%	-3.4179	0.578	0.743	1	BP
	positive						
	regulation of			_			
GO:0009893	metabolic process	0.33%	-3.4535	0.579	0.86	1	BP
00 00 10 70 7	tissue	0.040	4.00=5	2 22-	2 22 2		
GO:0048729	morphogenesis	0.04%	-4.8356	0.687	0.886	1	BP

A pranching epithellum O.02% -4.3063 O.639 O.829 1 BP							<u> </u>	1
GO:0061138 epithelium		morphogenesis of						
Branching morphogenesis of an epithelial tube 0.01% -3.5171 0.632 0.982 1 BP		_	/					
Morphogenesis of an epithelial tube	GO:0061138	•	0.02%	-4.3063	0.639	0.829	1	ВР
GO:0048754 an epithelial tube epithelial cell								
Epithelial cell GO:0030855 differentiation GO:004% -3.8697 O.666 O.878 1 BP								
GO:0030855 differentiation D.04% -3.8697 D.666 D.878 1 BP	GO:0048754		0.01%	-3.5171	0.632	0.982	1	BP
Docitive Progression Pro		'						
Regulation of angiogenesis 0.01% -3.9172 0.441 0.957 1 BP	GO:0030855	differentiation	0.04%	-3.8697	0.666	0.878	1	BP
GO:0045766 angiogenesis 0.01% -3.9172 0.441 0.957 1 BP GO:0045765 angiogenesis 0.01% -4.9872 0.491 0.925 1 BP regulation of organ regulation of organ morphogenesis 0.01% -4.3028 0.501 0.746 1 BP GO:00009887 morphogenesis 0.08% -5.1979 0.634 0.722 1 BP GO:0001525 angiogenesis 0.03% -4.7144 0.638 0.728 1 BP regulation of programmed cell death 0.13% -3.8962 0.636 0.992 1 BP GO:0010941 death 0.14% -3.5331 0.639 0.886 1 BP GO:1901701 compound 0.23% -3.3925 0.783 0.864 1 BP Regulation of signaling 0.18% -4.3925 0.562 0.93 1 BP Regulation of signaling 0.18% -3.7852 0.502 0.929 1 BP Regulation of regulation of regulation of response to megative regulation of signal transduction 0.18% -3.7852 0.502 0.929 1 BP GO:0048585 stimulus 0.36% -4.1337 0.538 0.88 1 BP Regative regulation of cell communication 0.18% -4.1785 0.555 0.93 1 BP Regulation of cell communication 0.18% -4.1785 0.555 0.93 1 BP Regulation of cell communication 0.18% -4.1785 0.555 0.93 1 BP		positive						
Regulation of angiogenesis 0.01% -4.9872 0.491 0.925 1 BP		regulation of						
GO:0045765 angiogenesis O.01% -4.9872 O.491 O.925 1 BP	GO:0045766	angiogenesis	0.01%	-3.9172	0.441	0.957	1	BP
Tegulation of organ Colored Co		regulation of						
Organ Orga	GO:0045765	angiogenesis	0.01%	-4.9872	0.491	0.925	1	BP
GO:2000027 morphogenesis O.01% -4.3028 O.501 O.746 1 BP		regulation of						
GO:2000027 morphogenesis		organ						
Organ morphogenesis O.08% -5.1979 O.634 O.722 1 BP	GO:2000027	_	0.01%	-4.3028	0.501	0.746	1	BP
GO:0009887 morphogenesis O.08% -5.1979 O.634 O.722 1 BP								
GO:0001525 angiogenesis O.03% -4.7144 O.638 O.728 1 BP	GO:0009887	_	0.08%	-5.1979	0.634	0.722	1	ВР
Pegulation of programmed cell O.13% -3.8962 O.636 O.992 1 BP			0.03%			0.728	1	RP
Programmed cell GO:0043067 death GO:013% -3.8962 GO:0636 GO:0992 1 BP	00.0001323		0.0370	11.7 ± 1 1	0.030	0.720		<i>D</i> 1
GO:0043067 death		_						
Tegulation of cell death 0.14% -3.5331 0.639 0.886 1 BP	GO:00/3067	. •	0.13%	-3 8962	0.636	0 992	1	RD
GO:0010941 death	GO:0043007		0.1370	-3.0302	0.030	0.552	<u> </u>	ы
Cellular response to oxygen-containing Compound C	GO:0010941	_	0 14%	_2 5221	0.630	0.886	1	RD.
to oxygen- containing GO:1901701 compound 0.23% -3.3925 0.783 0.864 1 BP negative regulation of signal GO:00023057 signaling 0.18% -4.3925 0.562 0.93 1 BP negative regulation of signal GO:0009968 transduction 0.18% -3.7852 0.502 0.929 1 BP negative regulation of response to stimulus 0.36% -4.1337 0.538 0.88 1 BP negative regulation of cell communication 0.18% -4.1785 0.555 0.93 1 BP	00.0010341		0.14/6	-3.3331	0.039	0.880		БГ
Containing Compound Compoun		· ·						
GO:1901701 compound 0.23% -3.3925 0.783 0.864 1 BP negative regulation of		, -						
negative regulation of GO:0023057 signaling O.18% -4.3925 O.562 O.93 1 BP	GO:1001701	_	0.22%	2 2025	0.792	0.964	1	DD.
Tegulation of signaling 0.18% -4.3925 0.562 0.93 1 BP	00.1901/01	·	0.25%	-5.5925	0.765	0.804	1	DP
GO:0023057 signaling 0.18% -4.3925 0.562 0.93 1 BP negative regulation of signal GO:0009968 transduction 0.18% -3.7852 0.502 0.929 1 BP negative regulation of response to GO:0048585 stimulus 0.36% -4.1337 0.538 0.88 1 BP GO:0010648 communication 0.18% -4.1785 0.555 0.93 1 BP		•						
negative regulation of signal	CO.00220F7	_	0.100/	4 2025	0.563	0.02	_	DD
regulation of signal	GO:0023057		0.18%	-4.3925	0.562	0.93	1	ВР
Signal		_						
GO:0009968 transduction 0.18% -3.7852 0.502 0.929 1 BP negative regulation of response to GO:0048585 stimulus 0.36% -4.1337 0.538 0.88 1 BP negative regulation of cell regulation of cell communication 0.18% -4.1785 0.555 0.93 1 BP regulation of ERK1 and ERK2		_						
negative regulation of response to	00 000000	_	0.400/	2 7052	0.503	0.000		
regulation of response to Stimulus 0.36% -4.1337 0.538 0.88 1 BP negative regulation of cell Communication 0.18% -4.1785 0.555 0.93 1 BP regulation of ERK1 and ERK2	GO:0009968		0.18%	-3./852	0.502	0.929	1	Bb
Tesponse to Stimulus 0.36% -4.1337 0.538 0.88 1 BP		-						
GO:0048585 stimulus 0.36% -4.1337 0.538 0.88 1 BP negative regulation of cell communication 0.18% -4.1785 0.555 0.93 1 BP regulation of ERK1 and ERK2		•						
negative regulation of cell GO:0010648 communication 0.18% -4.1785 0.555 0.93 1 BP regulation of ERK1 and ERK2		•			_			
regulation of cell	GO:0048585		0.36%	-4.1337	0.538	0.88	1	ВР
GO:0010648 communication 0.18% -4.1785 0.555 0.93 1 BP regulation of ERK1 and ERK2		•						
regulation of ERK1 and ERK2		_						
ERK1 and ERK2	GO:0010648		0.18%	-4.1785	0.555	0.93	1	BP
GO:0070372 cascade 0.01% -4.0186 0.569 0.748 1 BP	GO:0070372	cascade	0.01%	-4.0186	0.569	0.748	1	BP
ERK1 and ERK2		ERK1 and ERK2						
GO:0070371 cascade 0.01% -3.4353 0.618 0.819 1 BP	GO:0070371	cascade	0.01%	-3.4353	0.618	0.819	1	BP

	BMP signaling						
GO:0030509	pathway	0.01%	-3.3595	0.598	0.829	1	BP
	positive						
	regulation of cell						
GO:2000147	motility	0.02%	-3.4012	0.533	0.995	1	BP
	positive						
	regulation of						
GO:0040017	locomotion	0.02%	-3.3152	0.582	0.871	1	BP
	endothelial cell						
GO:0043542	migration	0.01%	-3.3143	0.61	0.933	1	BP
	positive						
	regulation of						
	cellular						
	component						
GO:0051272	movement	0.02%	-3.3507	0.547	0.893	1	BP
	positive						
	regulation of						
	epithelial cell					_	
GO:0010634	migration	0.01%	-3.4962	0.435	0.927	1	BP
	anchoring	/					
GO:0070161	junction	0.03%	-3.8125	0.701	0.788	1	CC
	extracellular						
	membrane-						
00 0005010	bounded	0.000/		0.404	0.000		
GO:0065010	organelle	0.30%	-5.5654	0.404	0.996	1	CC
00 0004000	membrane-	0.400/	4 4707	0.555	0.070		
GO:0031988	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.

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

	molecular transducer						
GO:0060089	activity	2.04%	-5.2262	0.7	0	0	MF
	passive						
	transmembrane						
	transporter						
GO:0022803	activity	0.41%	-5.224	0.399	0.4	0	MF
	signal						
	transducer						
GO:0004871	activity	2.03%	-5.2262	0.501	0.774	1	MF
	ion channel						
GO:0005216	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.

			log10 p-				
term_ID	description	frequency	value	uniqueness	dispensability	eliminated	Ontology
	cell						
GO:0007154	communication	4.36%	-7.7878	0.617	0	0	BP
GO:0023052	signaling	3.84%	-7.6402	0.744	0	0	BP
	positive						
	regulation of						
	developmental						
GO:0051094	process	0.05%	-5.4522	0.428	0	0	BP
	single organism						
GO:0044700	signaling	3.84%	-7.6402	0.349	0.089	0	BP
	regulation of						
GO:0050865	cell activation	0.02%	-4.3206	0.489	0.208	0	BP
	positive						
	regulation of						
60 0045507	cell	0.040/	4 4025	0.4	0.642		
GO:0045597	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
	intrinsic						
	component of						
GO:0031224	membrane	35.35%	-9.5361	0.047	0	0	CC
	nucleic acid						
	binding						
	transcription	4.000/	. =	0.0=0			
GO:0001071	factor activity	4.98%	-4.7496	0.276	0	0	MF
	sequence-						
60.0003700	specific DNA	4.000/	4 7400	0.375			NAT
GO:0003700	binding	4.96%	-4.7496	0.275	0	0	MF

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