

Table S2. ClueGO analysis of the RNA-Seq analysis in tissue isolated from *HBUS* polyps compared with unaffected proximal cecum

GO ID	GO term	GO groups	Number of genes	% associated genes	Term p-value	Term p-value corrected with Benjamini and Hochberg
GO:0000165	MAPK cascade	[Group15]	35	6.836	0.000	0.000
GO:0000902	cell morphogenesis	[Group31]	53	6.280	0.000	0.000
GO:0000904	cell morphogenesis involved in differentiation	[Group31]	40	7.299	0.000	0.000
GO:0001501	skeletal system development	[None]	33	8.505	0.000	0.000
GO:0001503	ossification	[None]	31	10.438	0.000	0.000
GO:0001525	angiogenesis	[Group5]	50	13.369	0.000	0.000
GO:0001568	blood vessel development	[Group35, Group5]	63	11.864	0.000	0.000
GO:0001654	eye development	[Group16]	25	7.962	0.000	0.000
GO:0001655	urogenital system development	[None]	26	8.307	0.000	0.000
GO:0001775	cell activation	[Group30]	35	5.401	0.000	0.001
GO:0001816	cytokine production	[Group0, Group30]	28	6.437	0.000	0.000
GO:0001932	regulation of protein phosphorylation	[Group15]	42	5.924	0.000	0.000
GO:0001944	vasculature development	[Group20, Group35, Group5]	66	11.828	0.000	0.000
GO:0002009	morphogenesis of an epithelium	[Group18, Group34]	31	7.243	0.000	0.000
GO:0002237	response to molecule of bacterial origin	[Group21, Group37]	28	11.155	0.000	0.000
GO:0002520	immune system development	[Group2]	31	4.704	0.006	0.008
GO:0002682	regulation of immune system process	[Group30]	48	6.358	0.000	0.000
GO:0002684	positive regulation of immune system process	[Group0, Group30, Group4]	31	6.568	0.000	0.000
GO:0003006	developmental process involved in reproduction	[Group17]	30	6.508	0.000	0.000
GO:0005975	carbohydrate metabolic process	[Group13]	32	4.969	0.003	0.003
GO:0006082	organic acid metabolic process	[Group12]	54	6.767	0.000	0.000
GO:0006464	cellular protein	[Group1, Group15]	100	4.505	0.000	0.000

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GO ID	GO term	GO groups	Number of genes	% associated genes	Term p-value	Term p-value corrected with Benjamini and Hochberg
	modification process					
GO:0006468	protein phosphorylation	[Group15]	50	5.061	0.000	0.000
GO:0006508	proteolysis	[None]	48	4.762	0.001	0.001
GO:0006629	lipid metabolic process	[Group12]	66	6.647	0.000	0.000
GO:0006793	phosphorus metabolic process	[Group15]	89	4.190	0.000	0.001
GO:0006796	phosphate-containing compound metabolic process	[Group15]	85	4.089	0.001	0.002
GO:0006810	transport	[Group14, Group28]	124	4.193	0.000	0.000
GO:0006811	ion transport	[Group14, Group28]	49	5.506	0.000	0.000
GO:0006812	cation transport	[Group28]	27	4.397	0.022	0.028
GO:0006873	cellular ion homeostasis	[Group10]	37	5.958	0.000	0.000
GO:0006915	apoptotic process	[Group11]	85	6.102	0.000	0.000
GO:0006928	cellular component movement	[Group6]	86	7.956	0.000	0.000
GO:0006950	response to stress	[Group29, Group33]	154	6.247	0.000	0.000
GO:0006952	defense response	[Group21, Group29, Group30, Group33, Group4]	68	7.320	0.000	0.000
GO:0006954	inflammatory response	[Group29, Group33, Group4]	40	8.969	0.000	0.000
GO:0006955	immune response	[Group29, Group30]	55	6.748	0.000	0.000
GO:0006979	response to oxidative stress	[None]	29	11.197	0.000	0.000
GO:0007010	cytoskeleton organization	[None]	34	4.282	0.017	0.022
GO:0007154	cell communication	[Group15]	184	3.767	0.000	0.000
GO:0007155	cell adhesion	[Group3]	81	9.310	0.000	0.000
GO:0007165	signal transduction	[Group15]	168	3.859	0.000	0.000
GO:0007166	cell surface receptor signaling pathway	[Group15, Group25]	106	3.747	0.005	0.007
GO:0007167	enzyme linked receptor protein signaling pathway	[Group15, Group25]	47	7.860	0.000	0.000
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	[Group25]	33	8.824	0.000	0.000
GO:0007243	intracellular protein kinase cascade	[Group15]	52	6.089	0.000	0.000

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GO ID	GO term	GO groups	Number of genes	% associated genes	Term p-value	Term p-value corrected with Benjamini and Hochberg
GO:0007267	cell-cell signaling	[Group7]	36	5.021	0.001	0.002
GO:0007275	multicellular organismal development	[Group35]	215	5.492	0.000	0.000
GO:0007399	nervous system development	[Group31, Group35]	80	5.016	0.000	0.000
GO:0007417	central nervous system development	[Group31]	40	5.495	0.000	0.000
GO:0007420	brain development	[Group31]	35	6.206	0.000	0.000
GO:0007423	sensory organ development	[Group16, Group34]	36	7.214	0.000	0.000
GO:0007507	heart development	[Group23, Group32, Group5]	30	6.897	0.000	0.000
GO:0007517	muscle organ development	[Group23]	34	9.043	0.000	0.000
GO:0008219	cell death	[Group11]	87	5.859	0.000	0.000
GO:0008283	cell proliferation	[Group9]	84	6.105	0.000	0.000
GO:0008284	positive regulation of cell proliferation	[Group15, Group9]	46	7.256	0.000	0.000
GO:0008285	negative regulation of cell proliferation	[Group9]	29	6.105	0.000	0.000
GO:0008610	lipid biosynthetic process	[Group12]	31	6.499	0.000	0.000
GO:0009056	catabolic process	[Group27]	78	4.827	0.000	0.000
GO:0009058	biosynthetic process	[Group1, Group15]	173	3.591	0.002	0.003
GO:0009605	response to external stimulus	[Group4]	70	6.487	0.000	0.000
GO:0009611	response to wounding	[Group29, Group33, Group8]	77	10.322	0.000	0.000
GO:0009617	response to bacterium	[Group21]	36	8.491	0.000	0.000
GO:0009628	response to abiotic stimulus	[Group24]	50	6.477	0.000	0.000
GO:0009653	anatomical structure morphogenesis	[Group20, Group31, Group34, Group35, Group5]	136	6.557	0.000	0.000
GO:0009719	response to endogenous stimulus	[Group37]	85	8.449	0.000	0.000
GO:0009725	response to hormone stimulus	[Group37]	53	8.775	0.000	0.000
GO:0009790	embryo development	[Group16, Group34, Group5]	54	5.238	0.000	0.000
GO:0009792	embryo development	[Group16]	28	4.361	0.022	0.028

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GO ID	GO term	GO groups	Number of genes	% associated genes	Term p-value	Term p-value corrected with Benjamini and Hochberg
	ending in birth or egg hatching					
GO:0009887	organ morphogenesis	[Group16, Group18, Group34, Group35]	55	6.351	0.000	0.000
GO:0009888	tissue development	[Group18, Group34, Group35]	105	7.028	0.000	0.000
GO:0009892	negative regulation of metabolic process	[Group15]	55	3.798	0.030	0.037
GO:0009893	positive regulation of metabolic process	[Group15]	76	3.981	0.004	0.006
GO:0009894	regulation of catabolic process	[Group27]	26	5.190	0.003	0.004
GO:0009966	regulation of signal transduction	[Group15]	93	5.360	0.000	0.000
GO:0009967	positive regulation of signal transduction	[Group15]	51	6.100	0.000	0.000
GO:0009968	negative regulation of signal transduction	[Group15]	39	6.122	0.000	0.000
GO:0009991	response to extracellular stimulus	[None]	25	7.716	0.000	0.000
GO:0010033	response to organic substance	[Group37]	141	7.825	0.000	0.000
GO:0010035	response to inorganic substance	[Group36]	45	13.761	0.000	0.000
GO:0010038	response to metal ion	[Group36]	32	14.159	0.000	0.000
GO:0010243	response to organonitrogen compound	[Group37]	50	9.074	0.000	0.000
GO:0010604	positive regulation of macromolecule metabolic process	[Group15, Group9]	66	3.754	0.024	0.030
GO:0010605	negative regulation of macromolecule metabolic process	[Group15]	53	3.906	0.021	0.026
GO:0010627	regulation of intracellular protein kinase cascade	[Group15]	46	6.581	0.000	0.000
GO:0010646	regulation of cell communication	[Group15]	102	5.157	0.000	0.000
GO:0010647	positive regulation of cell communication	[Group15]	54	6.102	0.000	0.000
GO:0010648	negative regulation of	[Group15]	42	6.241	0.000	0.000

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GO ID	GO term	GO groups	Number of genes	% associated genes	Term p-value	Term p-value corrected with Benjamini and Hochberg
GO:0010740	cell communication positive regulation of intracellular protein kinase cascade	[Group15]	33	6.875	0.000	0.000
GO:0010817	regulation of hormone levels	[None]	28	7.778	0.000	0.000
GO:0010941	regulation of cell death	[Group11]	72	6.463	0.000	0.000
GO:0010942	positive regulation of cell death	[Group11]	37	8.605	0.000	0.000
GO:0014070	response to organic cyclic compound	[Group37]	59	9.768	0.000	0.000
GO:0016043	cellular component organization	[None]	185	4.954	0.000	0.000
GO:0016310	phosphorylation	[Group15]	53	4.840	0.000	0.000
GO:0016337	cell-cell adhesion	[None]	25	6.527	0.000	0.000
GO:0016477	cell migration	[Group6]	81	10.037	0.000	0.000
GO:0018193	peptidyl-amino acid modification	[None]	34	5.893	0.000	0.000
GO:0019222	regulation of metabolic process	[Group1, Group15]	155	3.404	0.026	0.031
GO:0019538	protein metabolic process	[Group1, Group15]	164	4.432	0.000	0.000
GO:0019725	cellular homeostasis	[Group10]	46	5.890	0.000	0.000
GO:0019752	carboxylic acid metabolic process	[Group12]	49	6.676	0.000	0.000
GO:0022008	neurogenesis	[Group31, Group35]	64	5.839	0.000	0.000
GO:0022414	reproductive process	[Group17]	66	5.259	0.000	0.000
GO:0022603	regulation of anatomical structure morphogenesis	[Group20]	48	7.453	0.000	0.000
GO:0022607	cellular component assembly	[Group26]	76	5.181	0.000	0.000
GO:0023051	regulation of signaling	[Group15]	103	5.226	0.000	0.000
GO:0023056	positive regulation of signaling	[Group15]	55	6.222	0.000	0.000
GO:0023057	negative regulation of signaling	[Group15]	42	6.278	0.000	0.000
GO:0030030	cell projection organization	[Group31]	49	5.833	0.000	0.000
GO:0030097	hemopoiesis	[Group2]	28	4.770	0.008	0.010
GO:0030154	cell differentiation	[Group20, Group31, Group35]	152	5.477	0.000	0.000

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GO:0030155	regulation of cell adhesion	[Group3]	31	11.877	0.000	0.000
GO:0030182	neuron differentiation	[Group22, Group31]	50	5.464	0.000	0.000
GO:0030198	extracellular matrix organization	[None]	28	16.766	0.000	0.000
GO:0030334	regulation of cell migration	[Group6]	58	14.078	0.000	0.000
GO:0030335	positive regulation of cell migration	[Group6]	36	15.126	0.000	0.000
GO:0030855	epithelial cell differentiation	[Group18]	38	7.024	0.000	0.000
GO:0031175	neuron projection development	[Group31]	35	6.206	0.000	0.000
GO:0031324	negative regulation of cellular metabolic process	[Group15]	50	3.782	0.040	0.048
GO:0031325	positive regulation of cellular metabolic process	[Group15]	68	3.797	0.018	0.023
GO:0031347	regulation of defense response	[Group29, Group30, Group4]	25	7.813	0.000	0.000
GO:0031399	regulation of protein modification process	[Group15]	47	5.353	0.000	0.000
GO:0031589	cell-substrate adhesion	[Group3]	31	15.500	0.000	0.000
GO:0032101	regulation of response to external stimulus	[Group4]	30	7.833	0.000	0.000
GO:0032268	regulation of cellular protein metabolic process	[Group15]	56	4.934	0.000	0.000
GO:0032270	positive regulation of cellular protein metabolic process	[Group15]	33	5.069	0.002	0.002
GO:0032496	response to lipopolysaccharide	[Group21, Group37]	25	10.638	0.000	0.000
GO:0032504	multicellular organism reproduction	[Group17]	36	4.472	0.008	0.010
GO:0032787	monocarboxylic acid metabolic process	[Group12]	28	7.198	0.000	0.000
GO:0032879	regulation of localization	[Group14, Group6]	95	6.899	0.000	0.000
GO:0032940	secretion by cell	[Group14]	27	4.478	0.018	0.023
GO:0032989	cellular component	[Group31, Group35]	60	6.438	0.000	0.000

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GO ID	GO term	GO groups	Number of genes	% associated genes	Term p-value	Term p-value corrected with Benjamini and Hochberg
GO:0033036	morphogenesis macromolecule localization	[Group14]	68	3.972	0.007	0.009
GO:0033554	cellular response to stress	[None]	44	4.026	0.021	0.026
GO:0033993	response to lipid	[Group21, Group37]	62	10.248	0.000	0.000
GO:0034097	response to cytokine stimulus	[None]	35	8.883	0.000	0.000
GO:0035239	tube morphogenesis	[Group18]	27	7.826	0.000	0.000
GO:0035295	tube development	[Group18]	36	7.258	0.000	0.000
GO:0035556	intracellular signal transduction	[Group15]	96	5.295	0.000	0.000
GO:0035637	multicellular organismal signaling	[Group7]	26	4.586	0.015	0.020
GO:0040008	regulation of growth	[None]	29	5.631	0.001	0.001
GO:0040012	regulation of locomotion	[Group6]	59	12.661	0.000	0.000
GO:0042060	wound healing	[Group33, Group8]	42	15.498	0.000	0.000
GO:0042127	regulation of cell proliferation	[Group9]	73	6.612	0.000	0.000
GO:0042221	response to chemical stimulus	[Group37]	183	5.345	0.000	0.000
GO:0042325	regulation of phosphorylation	[Group15]	46	5.982	0.000	0.000
GO:0042327	positive regulation of phosphorylation	[Group15]	29	5.979	0.000	0.000
GO:0042493	response to drug	[None]	36	10.141	0.000	0.000
GO:0042592	homeostatic process	[Group10]	80	6.231	0.000	0.000
GO:0042692	muscle cell differentiation	[Group23]	29	8.056	0.000	0.000
GO:0042981	regulation of apoptotic process	[Group11]	70	6.585	0.000	0.000
GO:0043065	positive regulation of apoptotic process	[Group11]	35	8.495	0.000	0.000
GO:0043066	negative regulation of apoptotic process	[Group11]	34	5.986	0.000	0.000
GO:0043085	positive regulation of catalytic activity	[Group15]	35	5.287	0.001	0.001
GO:0043170	macromolecule metabolic process	[Group1, Group15]	228	3.309	0.021	0.026
GO:0043408	regulation of MAPK cascade	[Group15]	31	6.843	0.000	0.000

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GO:0043549	regulation of kinase activity	[Group15]	30	6.024	0.000	0.000
GO:0043588	skin development	[None]	26	9.701	0.000	0.000
GO:0043933	macromolecular complex subunit organization	[Group26]	51	4.282	0.004	0.006
GO:0044085	cellular component biogenesis	[Group26]	78	4.812	0.000	0.000
GO:0044093	positive regulation of molecular function	[Group15]	47	5.459	0.000	0.000
GO:0044237	cellular metabolic process	[Group1]	283	3.589	0.000	0.000
GO:0044238	primary metabolic process	[Group1]	292	3.583	0.000	0.000
GO:0044248	cellular catabolic process	[Group27]	56	4.201	0.004	0.006
GO:0044249	cellular biosynthetic process	[Group1, Group15]	159	3.403	0.024	0.030
GO:0044255	cellular lipid metabolic process	[Group12]	42	6.096	0.000	0.000
GO:0044267	cellular protein metabolic process	[Group1, Group15]	118	4.026	0.000	0.000
GO:0044281	small molecule metabolic process	[Group12]	94	5.412	0.000	0.000
GO:0044283	small molecule biosynthetic process	[Group12]	26	6.599	0.000	0.000
GO:0044700	single organism signaling	[Group15]	182	3.816	0.000	0.000
GO:0044702	single organism reproductive process	[Group17]	42	4.773	0.001	0.002
GO:0044707	single-multicellular organism process	[Group35]	265	4.418	0.000	0.000
GO:0044710	single-organism metabolic process	[Group12]	140	5.707	0.000	0.000
GO:0044723	single-organism carbohydrate metabolic process	[Group13]	30	5.871	0.000	0.000
GO:0044763	single-organism cellular process	[None]	369	3.812	0.000	0.000
GO:0044765	single-organism transport	[Group14, Group28]	109	4.640	0.000	0.000
GO:0044767	single-organism	[Group35]	215	5.827	0.000	0.000

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GO:0045087	developmental process innate immune response	[Group29, Group30]	25	7.289	0.000	0.000
GO:0045321	leukocyte activation	[Group30]	28	4.895	0.005	0.007
GO:0045595	regulation of cell differentiation	[Group20, Group22, Group35]	70	6.428	0.000	0.000
GO:0045597	positive regulation of cell differentiation	[Group20]	40	7.692	0.000	0.000
GO:0045859	regulation of protein kinase activity	[Group15]	27	5.782	0.001	0.001
GO:0046903	secretion	[Group14]	32	4.565	0.009	0.011
GO:0048468	cell development	[Group31, Group35]	92	6.041	0.000	0.000
GO:0048513	organ development	[Group35]	155	5.966	0.000	0.000
GO:0048514	blood vessel morphogenesis	[Group35, Group5]	55	11.931	0.000	0.000
GO:0048518	positive regulation of biological process	[Group15, Group20]	171	5.077	0.000	0.000
GO:0048519	negative regulation of biological process	[Group15, Group20]	145	4.753	0.000	0.000
GO:0048522	positive regulation of cellular process	[Group15, Group20]	147	4.892	0.000	0.000
GO:0048523	negative regulation of cellular process	[Group15]	127	4.591	0.000	0.000
GO:0048545	response to steroid hormone stimulus	[Group37]	32	10.667	0.000	0.000
GO:0048568	embryonic organ development	[Group16]	25	5.896	0.001	0.001
GO:0048583	regulation of response to stimulus	[Group15]	115	5.201	0.000	0.000
GO:0048584	positive regulation of response to stimulus	[Group15, Group4]	64	5.639	0.000	0.000
GO:0048585	negative regulation of response to stimulus	[Group15]	46	5.793	0.000	0.000
GO:0048598	embryonic morphogenesis	[Group16, Group18]	31	5.626	0.000	0.001
GO:0048609	multicellular organismal reproductive process	[Group17]	33	4.161	0.027	0.032
GO:0048646	anatomical structure formation involved in morphogenesis	[Group16, Group35, Group5]	79	8.476	0.000	0.000
GO:0048666	neuron development	[Group31]	39	5.652	0.000	0.000

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GO:0048699	generation of neurons	[Group22, Group31]	56	5.506	0.000	0.000
GO:0048729	tissue morphogenesis	[Group18, Group34]	40	7.449	0.000	0.000
GO:0048731	system development	[Group35]	198	5.832	0.000	0.000
GO:0048732	gland development	[Group18]	27	9.000	0.000	0.000
GO:0048812	neuron projection morphogenesis	[Group31]	26	6.341	0.000	0.000
GO:0048856	anatomical structure development	[Group35]	225	5.679	0.000	0.000
GO:0048858	cell projection morphogenesis	[Group31]	30	5.576	0.001	0.001
GO:0048869	cellular developmental process	[Group20, Group31, Group35]	158	5.309	0.000	0.000
GO:0048870	cell motility	[Group6]	83	9.336	0.000	0.000
GO:0048878	chemical homeostasis	[Group10]	58	6.437	0.000	0.000
GO:0050776	regulation of immune response	[Group30, Group4]	25	6.313	0.000	0.000
GO:0050789	regulation of biological process	[Group15]	293	3.444	0.000	0.001
GO:0050790	regulation of catalytic activity	[Group15]	53	4.605	0.001	0.001
GO:0050793	regulation of developmental process	[Group15, Group20, Group35]	108	7.004	0.000	0.000
GO:0050794	regulation of cellular process	[Group15]	270	3.356	0.004	0.006
GO:0050801	ion homeostasis	[Group10]	43	6.117	0.000	0.000
GO:0050878	regulation of body fluid levels	[Group8]	26	11.017	0.000	0.000
GO:0051049	regulation of transport	[Group14, Group6]	49	5.036	0.000	0.000
GO:0051050	positive regulation of transport	[Group14]	29	5.847	0.000	0.000
GO:0051093	negative regulation of developmental process	[None]	37	6.379	0.000	0.000
GO:0051094	positive regulation of developmental process	[Group20]	59	8.082	0.000	0.000
GO:0051128	regulation of cellular component organization	[Group19]	66	5.148	0.000	0.000
GO:0051130	positive regulation of cellular component organization	[Group19]	34	6.227	0.000	0.000
GO:0051146	striated muscle cell differentiation	[Group23]	26	8.997	0.000	0.000

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GO:0051174	regulation of phosphorus metabolic process	[Group15]	52	4.626	0.001	0.001
GO:0051234	establishment of localization	[Group14]	126	4.175	0.000	0.000
GO:0051239	regulation of multicellular organismal process	[Group15, Group20]	122	6.260	0.000	0.000
GO:0051240	positive regulation of multicellular organismal process	[Group0]	44	7.971	0.000	0.000
GO:0051241	negative regulation of multicellular organismal process	[Group0]	25	7.331	0.000	0.000
GO:0051246	regulation of protein metabolic process	[Group15]	66	4.896	0.000	0.000
GO:0051247	positive regulation of protein metabolic process	[Group15]	36	4.871	0.002	0.003
GO:0051248	negative regulation of protein metabolic process	[Group15]	26	5.991	0.000	0.001
GO:0051259	protein oligomerization	[Group26]	27	7.895	0.000	0.000
GO:0051270	regulation of cellular component movement	[Group6]	60	12.552	0.000	0.000
GO:0051641	cellular localization	[Group14, Group6]	65	3.687	0.035	0.042
GO:0051649	establishment of localization in cell	[Group14]	58	3.811	0.025	0.031
GO:0051707	response to other organism	[Group21, Group29]	50	7.962	0.000	0.000
GO:0051716	cellular response to stimulus	[Group15, Group37]	212	4.024	0.000	0.000
GO:0051960	regulation of nervous system development	[Group22, Group31]	27	5.455	0.001	0.002
GO:0055080	cation homeostasis	[Group10]	26	6.311	0.000	0.000
GO:0055082	cellular chemical homeostasis	[Group10]	42	6.017	0.000	0.000
GO:0060284	regulation of cell development	[Group20, Group22, Group31]	27	4.770	0.009	0.011
GO:0060341	regulation of cellular localization	[Group14, Group6]	36	5.255	0.001	0.001
GO:0060429	epithelium	[Group18, Group35]	56	6.573	0.000	0.000

Table S2

GO ID	GO term	GO groups	Number of genes	% associated genes	Term p-value	Term p-value corrected with Benjamini and Hochberg
GO:0060537	development muscle tissue development	[Group23, Group32]	36	9.000	0.000	0.000
GO:0060562	epithelial tube morphogenesis	[Group16, Group18]	25	7.692	0.000	0.000
GO:0061061	muscle structure development	[Group23]	45	8.824	0.000	0.000
GO:0065003	macromolecular complex assembly	[Group26]	41	4.209	0.013	0.017
GO:0065008	regulation of biological quality	[Group10]	153	6.623	0.000	0.000
GO:0065009	regulation of molecular function	[Group15]	72	4.678	0.000	0.000
GO:0070482	response to oxygen levels	[Group24]	26	10.656	0.000	0.000
GO:0070848	response to growth factor stimulus	[Group25, Group37]	34	9.632	0.000	0.000
GO:0070887	cellular response to chemical stimulus	[Group15, Group37]	115	8.519	0.000	0.000
GO:0071310	cellular response to organic substance	[Group37]	92	8.526	0.000	0.000
GO:0071363	cellular response to growth factor stimulus	[Group25, Group37]	32	9.524	0.000	0.000
GO:0071396	cellular response to lipid	[Group21, Group37]	25	10.417	0.000	0.000
GO:0071495	cellular response to endogenous stimulus	[Group25, Group37]	51	8.778	0.000	0.000
GO:0071702	organic substance transport	[Group14]	71	4.181	0.002	0.002
GO:0071704	organic substance metabolic process	[Group1]	310	3.673	0.000	0.000
GO:0071822	protein complex subunit organization	[Group26]	49	5.094	0.000	0.000
GO:0072358	cardiovascular system development	[Group32, Group35, Group5]	78	9.466	0.000	0.000
GO:0080134	regulation of response to stress	[Group15, Group29, Group4]	40	6.144	0.000	0.000
GO:1901135	carbohydrate derivative metabolic process	[None]	44	4.147	0.013	0.017
GO:1901564	organonitrogen compound metabolic process	[Group12]	58	4.351	0.002	0.002

Table S2

GO ID	GO term	GO groups	Number of genes	% associated genes	Term p-value	Term p-value corrected with Benjamini and Hochberg
GO:1901575	organic substance catabolic process	[Group27]	64	4.414	0.001	0.001
GO:1901576	organic substance biosynthetic process	[Group1, Group15]	166	3.501	0.007	0.010
GO:1901615	organic hydroxy compound metabolic process	[None]	29	8.056	0.000	0.000
GO:1901698	response to nitrogen compound	[Group37]	52	8.739	0.000	0.000
GO:1901699	cellular response to nitrogen compound	[Group37]	27	9.184	0.000	0.000
GO:1901700	response to oxygen-containing compound	[Group37]	89	9.082	0.000	0.000
GO:1901701	cellular response to oxygen-containing compound	[Group21, Group37]	55	10.242	0.000	0.000
GO:2000026	regulation of multicellular organismal development	[Group20, Group5]	81	6.650	0.000	0.000