

**Supplementary Table 3: Gene Ontology analysis of SOM patterns**

Cluster	GO category	PValue	Bonferroni	Benjamini	FDR
<b>A</b>	GO:0006953~acute-phase response	1.58E-06	1.24E-04	1.24E-04	0.00167495
	GO:0002526~acute inflammatory response	3.25E-05	0.00253446	0.00126803	0.03440818
	GO:0006952~defense response	3.20E-04	0.02465078	0.00828538	0.33791341
	GO:0006954~inflammatory response	6.70E-04	0.05093971	0.01298569	0.70651655
	GO:0009611~response to wounding	0.00233891	0.16693894	0.03587051	2.44652206
	GO:0033209~tumor necrosis factor-mediated signaling pathway	0.00323458	0.2233038	0.04124304	3.36896172
<b>B</b>	GO:0055085~transmembrane transport	1.32E-04	0.11524319	0.11524319	0.20665382
	GO:0055066~di-, tri-valent inorganic cation homeostasis	0.00220131	0.87005715	0.63952413	3.38895782
	GO:0006461~protein complex assembly	0.00296841	0.93625292	0.60052762	4.54443584
	GO:0070271~protein complex biogenesis	0.00296841	0.93625292	0.60052762	4.54443584
	GO:0032101~regulation of response to external stimulus	0.00394095	0.97417802	0.59913568	5.99078609
	GO:0055065~metal ion homeostasis	0.00436589	0.98260657	0.55528985	6.61628447
	GO:0065003~macromolecular complex assembly	0.00520051	0.99199942	0.55278102	7.83351037
	GO:0055080~cation homeostasis	0.00590572	0.99585107	0.54322198	8.85038871
	GO:0045444~fat cell differentiation	0.00654814	0.99771985	0.53253904	9.76759295
	GO:0048878~chemical homeostasis	0.00782144	0.99930467	0.55420815	11.5600474
	GO:0043933~macromolecular complex subunit organization	0.00804847	0.99943746	0.52683167	11.8761213
	GO:0050729~positive regulation of inflammatory response	0.00976166	0.9998865	0.56211168	14.2273517
	GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	0.00989459	0.99989977	0.53575142	14.4073143
	<b>C</b>	GO:0002274~myeloid leukocyte activation	0.00343368	0.81903955	0.81903955
GO:0007049~cell cycle		0.01708181	0.99980896	0.98617813	21.956233
GO:0055114~oxidation reduction		0.02469342	0.99999599	0.98411267	30.2152692
GO:0042116~macrophage activation		0.02475031	0.9999961	0.95557363	30.2738096
GO:0051301~cell division		0.03266343	0.99999993	0.963152	37.9863551
GO:0001817~regulation of cytokine production		0.04709859	1	0.98161458	50.0497802
<b>D</b>	GO:0022613~ribonucleoprotein complex biogenesis	2.30E-05	0.03904446	0.03904446	0.03894293
	GO:0042254~ribosome biogenesis	7.15E-05	0.11623301	0.05991118	0.1207692
	GO:0006259~DNA metabolic process	4.73E-04	0.5581783	0.23836128	0.79568719
	GO:0006396~RNA processing	7.81E-04	0.74058583	0.28632838	1.31096113
	GO:0046907~intracellular transport	0.00153269	0.92938492	0.41145525	2.55886437
	GO:0030036~actin cytoskeleton organization	0.0019722	0.96700275	0.4336569	3.28120744
	GO:0007010~cytoskeleton organization	0.00209184	0.97317661	0.40364901	3.47695212
	GO:0031532~actin cytoskeleton reorganization	0.00249615	0.98668322	0.41715927	4.13571911
	GO:0009967~positive regulation of signal transduction	0.00273007	0.99112053	0.40837975	4.51493643
	GO:0030029~actin filament-based process	0.00325904	0.99645004	0.43111776	5.36725376
	GO:0006974~response to DNA damage stimulus	0.00366657	0.99824882	0.43844331	6.01900224
	GO:0010647~positive regulation of cell communication	0.00555722	0.99993425	0.55177993	8.98783302
	GO:0007049~cell cycle	0.00586708	0.99996163	0.54258641	9.46590707
	GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid	0.00823304	0.99999938	0.63954863	13.0390865
	<b>E</b>	GO:0055114~oxidation reduction	1.03E-09	9.38E-07	9.38E-07
GO:0008202~steroid metabolic process		1.43E-05	0.01297239	0.00650737	0.02235257
GO:0006694~steroid biosynthetic process		4.36E-04	0.32811686	0.12414695	0.67853137
<b>F</b>	GO:0000097~sulfur amino acid biosynthetic process	0.0153517	0.85086494	0.85086494	16.33818
	GO:0000096~sulfur amino acid metabolic process	0.02510419	0.95616115	0.79062272	25.4098969
	GO:0044271~nitrogen compound biosynthetic process	0.04272496	0.9953493	0.83308088	39.5575984
	GO:0044272~sulfur compound biosynthetic process	0.0443393	0.99622116	0.75206403	40.7225295
	GO:0008652~cellular amino acid biosynthetic process	0.04751051	0.99748925	0.69803212	42.9514196
<b>G</b>	GO:0006955~immune response	2.03E-16	3.74E-13	3.74E-13	3.77E-13
	GO:0006952~defense response	9.07E-08	1.53E-04	7.63E-05	1.53E-04
	GO:0042110~T cell activation	4.35E-07	7.32E-04	2.44E-04	7.33E-04
	GO:0050865~regulation of cell activation	1.74E-06	0.00292082	7.31E-04	0.00292794
	GO:0001775~cell activation	3.01E-06	0.00505593	0.00101324	0.00507364

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	GO:0030097~hemopoiesis	3.90E-06	0.00654528	0.00109387	0.00657308
	GO:0051249~regulation of lymphocyte activation	4.38E-06	0.00734654	0.00105283	0.00738069
	GO:0045619~regulation of lymphocyte differentiation	4.39E-06	0.00736451	9.24E-04	0.0073988
	GO:0002694~regulation of leukocyte activation	8.76E-06	0.01463978	0.00163733	0.01476151
	GO:0050863~regulation of T cell activation	1.10E-05	0.01839036	0.00185444	0.01857821
	GO:0045582~positive regulation of T cell differentiation	1.16E-05	0.01930859	0.00177092	0.01951483
	GO:0045580~regulation of T cell differentiation	1.21E-05	0.02020353	0.00169942	0.02042852
	GO:0019882~antigen processing and presentation	1.24E-05	0.02069267	0.00160715	0.02092827
	GO:0045321~leukocyte activation	1.54E-05	0.02551378	0.00184436	0.02586713
	GO:0046649~lymphocyte activation	1.60E-05	0.0265876	0.00179488	0.02697048
<b>H</b>	GO:0010565~regulation of cellular ketone metabolic process	6.79E-04	0.20339696	0.20339696	0.91809586
	GO:0042304~regulation of fatty acid biosynthetic process	0.01513572	0.99395927	0.92227784	18.716886
	GO:0010907~positive regulation of glucose metabolic process	0.01513572	0.99395927	0.92227784	18.716886
	GO:0010676~positive regulation of cellular carbohydrate metabo	0.01680387	0.99657663	0.84928686	20.5677827
	GO:0045913~positive regulation of carbohydrate metabolic proce	0.01680387	0.99657663	0.84928686	20.5677827
	GO:0043467~regulation of generation of precursor metabolites a	0.02179214	0.99937708	0.84201759	25.8721648
	GO:0010906~regulation of glucose metabolic process	0.02344951	0.99964704	0.79603993	27.5606209
	GO:0006109~regulation of carbohydrate metabolic process	0.02510419	0.99980002	0.75817581	29.2107382
	GO:0010675~regulation of cellular carbohydrate metabolic proce	0.02510419	0.99980002	0.75817581	29.2107382
	GO:0019217~regulation of fatty acid metabolic process	0.03169614	0.9999794	0.78592885	35.4448849
	GO:0046890~regulation of lipid biosynthetic process	0.0366121	0.99999626	0.79026318	39.7585572
	GO:0008624~induction of apoptosis by extracellular signals	0.04150419	0.99999932	0.79358223	43.7848438
<b>I</b>	GO:0055114~oxidation reduction	1.49E-15	1.56E-12	1.56E-12	2.30E-12
	GO:0008202~steroid metabolic process	2.62E-06	0.00283067	0.00141634	0.00418754
	GO:0006631~fatty acid metabolic process	8.64E-06	0.00928285	0.00310391	0.01377649
	GO:0055092~sterol homeostasis	9.28E-05	0.09534576	0.02473945	0.14791792
	GO:0042632~cholesterol homeostasis	9.28E-05	0.09534576	0.02473945	0.14791792
	GO:0055088~lipid homeostasis	2.72E-04	0.25428201	0.05699299	0.4325084
	GO:0046395~carboxylic acid catabolic process	9.57E-04	0.64459466	0.15837107	1.51662579
	GO:0016054~organic acid catabolic process	9.57E-04	0.64459466	0.15837107	1.51662579
	GO:0019318~hexose metabolic process	0.00104055	0.6751444	0.14838857	1.64730082
	GO:0008610~lipid biosynthetic process	0.00141742	0.78387512	0.17426994	2.23763383
	GO:0019319~hexose biosynthetic process	0.00157794	0.81832164	0.17262889	2.48805712
	GO:0016053~organic acid biosynthetic process	0.00207659	0.8940781	0.20108868	3.26218421
	GO:0046394~carboxylic acid biosynthetic process	0.00207659	0.8940781	0.20108868	3.26218421
	GO:0005996~monosaccharide metabolic process	0.00210133	0.89687619	0.18659777	3.30043594
	GO:0046364~monosaccharide biosynthetic process	0.00296055	0.95932473	0.23420793	4.62031798
<b>J</b>	GO:0048193~Golgi vesicle transport	0.00188304	0.25755046	0.25755046	2.24540445
	GO:0006888~ER to Golgi vesicle-mediated transport	0.03568976	0.99679188	0.9433597	35.459986
	GO:0006886~intracellular protein transport	0.04574646	0.99938782	0.91508997	43.1186003
<b>K</b>	GO:0007049~cell cycle	0.00159644	0.24512046	0.24512046	1.94149541
	GO:0022402~cell cycle process	0.00231148	0.33454984	0.18424871	2.79981588
	GO:0000910~cytokinesis	0.03902641	0.99909382	0.90323048	38.6452764
<b>L</b>	GO:0007067~mitosis	0.0230449	0.98309343	0.98309343	24.8606348
	GO:0000280~nuclear division	0.0230449	0.98309343	0.98309343	24.8606348
	GO:0000087~M phase of mitotic cell cycle	0.02395792	0.98564527	0.88018877	25.7170027
	GO:0048285~organelle fission	0.02465247	0.9873266	0.76685232	26.362446
	GO:0000278~mitotic cell cycle	0.03657942	0.99852841	0.80413964	36.6726958
	GO:0007422~peripheral nervous system development	0.03689879	0.99861137	0.73176376	36.9295823
	GO:0051301~cell division	0.04724974	0.99979043	0.75628081	44.7549182
	GO:0000279~M phase	0.04785623	0.99981253	0.70653027	45.1845071
	GO:0010810~regulation of cell-substrate adhesion	0.04891091	0.99984558	0.66612124	45.9242634
<b>P</b>	GO:0055114~oxidation reduction	5.99E-05	0.02583107	0.02583107	0.08456959

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	GO:0006732~coenzyme metabolic process	0.0068268	0.94989042	0.7761483	9.22412616
	GO:0051186~cofactor metabolic process	0.01315056	0.99692643	0.85460565	17.0570745
	GO:0016054~organic acid catabolic process	0.02042539	0.99987883	0.89508218	25.2893961
	GO:0046395~carboxylic acid catabolic process	0.02042539	0.99987883	0.89508218	25.2893961
	GO:0009225~nucleotide-sugar metabolic process	0.02690746	0.99999334	0.90781251	31.9783456

The analysis was performed using the Database for Annotation, Visualization and Integrated Discovery (DAVID ) v6.7 and gene ontology categories with multiple test (Holm–Bonferroni method) corrected P value <0.05 were considered significant.