

Additional file 6: Table S11. Biological processes enriched from differentially expressed genes in MØ1H-MØC, MØ7-MØC, and MØHK-MØC comparisons.

MØ1H versus MØC						
GO term ID	Description	padj	Count	Frequency _a	Uniqueness _b	Dispensability _c
GO:0002376	Immune system process	5.16E-04	128	10.27 %	0.97	0.00
GO:0002684	PR of immune system process	3.01E-02	60	3.65 %	0.72	0.00
GO:0051249	<i>Regulation of lymphocyte activation</i>	2.07E-02	25	1.77 %	0.73	0.83
GO:0006955	<i>Immune response</i>	2.39E-05	88	6.05 %	0.75	0.67
^d GO:0045321	<i>Leukocyte activation</i>	1.36E-02	41	3.51 %	0.77	0.61
GO:0002521	<i>Leukocyte differentiation</i>	4.16E-03	33	2.47 %	0.76	0.74
^d GO:1903708	<i>PR of hemopoiesis</i>	2.88E-03	41	0.80 %	0.70	0.69
GO:0006732	Coenzyme metabolic process	1.67E-02	33	1.38 %	0.94	0.00
GO:0006954	Inflammatory response	5.74E-05	58	2.67 %	0.87	0.00
GO:0050729	<i>PR of inflammatory response</i>	5.74E-05	18	0.41 %	0.76	0.76
GO:0031349	<i>PR of defense response</i>	1.35E-04	32	1.29 %	0.77	0.66
GO:0007159	Leukocyte cell-cell adhesion	1.23E-03	35	2.37 %	0.88	0.00
^d GO:0046634	<i>Regulation of alfa-beta T cell-activation</i>	9.40E-03	10	0.33 %	0.72	0.69
GO:1903039	<i>PR of leukocyte cell-cell adhesion</i>	1.02E-02	18	0.82 %	0.81	0.82
^d GO:0002286	<i>T cell activation involved in immune response</i>	1.36E-03	12	0.57 %	0.72	0.73
^d GO:0016032	Viral process	3.20E-02	43	1.24 %	0.91	0.00
^d GO:0044419	<i>Interspecies interaction between organisms</i>	3.92E-02	44	1.46 %	0.92	0.65
^d GO:0044403	<i>Symbiosis, mutualism through parasitism</i>	3.92E-02	44	1.44 %	0.91	0.96
GO:0050663	Cytokine secretion	1.23E-03	20	0.85 %	0.78	0.02
^d GO:0042990	<i>Regulation of TF import into nucleus</i>	1.40E-02	10	0.40 %	0.78	0.68
^d GO:0042991	<i>TF import into nucleus</i>	1.40E-02	10	0.41 %	0.83	0.78
GO:0001817	<i>Regulation of cytokine production</i>	1.12E-02	38	3.51 %	0.83	0.81
^d GO:0070201	<i>Regulation of protein localization</i>	1.40E-02	50	3.44 %	0.78	0.55
GO:0046822	<i>Regulation of nucleocytoplasmic transport</i>	3.93E-02	17	0.98 %	0.80	0.75
^d GO:0051046	<i>Regulation of secretion</i>	4.45E-03	46	2.86 %	0.78	0.72
GO:0050707	<i>Regulation of cytokine secretion</i>	2.87E-03	16	0.72 %	0.73	0.79
GO:0032943	Mononuclear cell proliferation	1.92E-02	21	1.42 %	0.89	0.02
GO:0032944	<i>Regulation of mononuclear cell proliferation</i>	4.59E-02	17	0.93 %	0.85	0.93
GO:0043067	Regulation of programmed cell death	1.19E-03	87	6.47 %	0.88	0.09
GO:0050793	Regulation of developmental process	3.92E-02	107	10.36 %	0.89	0.09
^d GO:0051707	Response to other organism	1.23E-03	61	3.57 %	0.87	0.14
^d GO:0043207	<i>Response to external biotic stimulus</i>	1.23E-03	61	3.58 %	0.87	0.95
GO:0043408	Regulation of MAPK cascade	1.80E-03	52	2.97 %	0.65	0.14
GO:1902531	<i>Regulation of intracellular signal transduction</i>	2.20E-04	104	7.58 %	0.74	0.62
GO:0023057	<i>NR of signaling</i>	9.40E-03	70	5.32 %	0.85	0.62
GO:0042325	<i>Regulation of phosphorylation</i>	6.28E-03	87	6.87 %	0.82	0.75
GO:0016310	<i>Phosphorylation</i>	1.22E-02	128	11.27 %	0.89	0.55
GO:0010648	<i>NR of cell communication</i>	9.40E-03	70	5.30 %	0.84	0.63
GO:0006468	<i>Protein phosphorylation</i>	2.00E-02	101	9.30 %	0.87	0.77
^d GO:0010647	<i>PR of cell communication</i>	4.94E-02	80	6.61 %	0.81	0.65
GO:0071345	Cellular response to cytokine stimulus	3.80E-03	41	2.93 %	0.88	0.18
GO:0034097	<i>Response to cytokine</i>	1.11E-02	44	3.27 %	0.88	0.55
GO:0006509	Membrane protein ectodomain proteolysis	1.55E-02	8	0.25 %	0.94	0.18
GO:0001816	Cytokine production	1.23E-02	43	3.03 %	0.91	0.23

GO:0098869	Cellular oxidant detoxification	4.46E-02	13	0.46 %	0.90	0.28
GO:0009636	Response to toxic substance	2.81E-02	16	0.73 %	0.90	0.30
GO:0010883	Regulation of lipid storage	3.92E-02	8	0.20 %	0.84	0.33
GO:0006082	Organic acid metabolic process	3.74E-03	82	4.72 %	0.86	0.38
GO:0044712	Single-organism catabolic process	2.81E-02	66	3.68 %	0.87	0.39
^d GO:1901575	<i>Organic substance catabolic process</i>	2.20E-02	127	8.73 %	0.92	0.76
GO:0050790	Regulation of catalytic activity	2.27E-02	124	10.94 %	0.88	0.46
GO:0044093	<i>PR of molecular function</i>	2.81E-02	90	7.90 %	0.89	0.72
GO:0048585	NR of response to stimulus	3.80E-03	83	6.25 %	0.79	0.49
^d GO:0006952	Defense response	5.74E-05	98	5.99 %	0.87	0.50
MØ7 versus MØC						
GO term ID	Description	padj	Count	Frequency _a	Uniqueness _b	Dispensability _c
GO:0002376	Immune system process	6.98E-04	109	10.27 %	0.97	0.00
GO:0007159	Leukocyte cell-cell adhesion	2.54E-03	30	2.37 %	0.89	0.00
^e GO:0042110	<i>T cell activation</i>	1.49E-02	25	2.18 %	0.73	0.86
GO:1903039	<i>PR of leukocyte cell-cell adhesion</i>	4.79E-02	14	0.82 %	0.82	0.76
^e GO:0022610	Biological adhesion	1.67E-02	68	6.66 %	0.97	0.00
GO:0031349	PR of defense response	9.10E-06	31	1.29 %	0.77	0.00
GO:0050729	<i>PR of inflammatory response</i>	5.69E-06	18	0.41 %	0.79	0.76
GO:0006954	<i>Inflammatory response</i>	7.59E-05	51	2.67 %	0.86	0.66
^e GO:0070661	Leukocyte proliferation	1.52E-02	20	1.48 %	0.89	0.02
GO:0001816	Cytokine production	4.20E-03	40	3.03 %	0.90	0.02
GO:0006082	Organic acid metabolic process	1.14E-02	68	7.72 %	0.86	0.03
GO:0050790	Regulation of catalytic activity	1.12E-02	109	10.94 %	0.87	0.05
^e GO:0044092	<i>NR of molecular function</i>	4.51E-02	54	5.20 %	0.87	0.66
GO:0044093	<i>PR of molecular function</i>	3.75E-02	76	7.90 %	0.87	0.72
GO:0006509	Membrane protein ectodomain proteolysis	2.57E-02	7	0.25 %	0.93	0.05
GO:0006732	Coenzyme metabolic process	1.69E-02	29	1.38 %	0.94	0.08
GO:0042981	Regulation of apoptotic process	4.70E-04	76	6.08 %	0.86	0.11
GO:0071345	Cellular response to cytokine stimulus	4.52E-03	36	2.93 %	0.87	0.12
GO:0034097	<i>Response to cytokine</i>	1.00E-02	39	3.27 %	0.88	0.55
^e GO:0009605	Response to external stimulus	1.13E-03	103	8.74 %	0.90	0.16
^e GO:0014033	Neural crest cell differentiation	3.74E-02	7	0.34 %	0.86	0.21
GO:0050707	Regulation of cytokine secretion	5.03E-03	14	0.72 %	0.70	0.23
GO:0050663	<i>Cytokine secretion</i>	3.63E-03	17	0.85 %	0.76	0.97
^e GO:1903531	<i>NR of secretion by cell</i>	5.64E-03	17	0.69 %	0.74	0.71
GO:0001817	<i>Regulation of cytokine production</i>	5.17E-03	35	2.72 %	0.81	0.81
^e GO:1904589	<i>Regulation of protein import</i>	6.64E-03	16	0.81 %	0.78	0.85
^e GO:1900180	<i>Regulation of protein localization to nucleus</i>	1.18E-02	18	1.04 %	0.78	0.85
GO:0046822	<i>Regulation of nucleocytoplasmic transport</i>	1.14E-02	17	0.98 %	0.80	0.81
^e GO:0042306	<i>Regulation of protein import into nucleus</i>	5.17E-03	16	0.80 %	0.76	0.69
GO:0050793	Regulation of developmental process	3.07E-02	92	10.36 %	0.86	0.25
^e GO:0046470	Phosphatidylcholine metabolic process	3.75E-02	6	0.18 %	0.86	0.27
GO:0002684	PR of immune system process	1.01E-03	52	3.65 %	0.74	0.27
^e GO:1902107	<i>PR of leukocyte differentiation</i>	1.89E-02	13	0.64 %	0.69	0.72
GO:0032943	<i>Mononuclear cell proliferation</i>	1.52E-02	19	1.42 %	0.66	0.97
GO:0032944	<i>Regulation of mononuclear cell proliferation</i>	4.68E-02	15	0.93 %	0.82	0.94
GO:0051249	<i>Regulation of lymphocyte activation</i>	3.83E-02	21	1.77 %	0.74	0.81
GO:0006955	<i>Immune response</i>	5.69E-06	78	6.05 %	0.77	0.67

^e GO:0046651	<i>Lymphocyte proliferation</i>	1.52E-02	19	1.41 %	0.71	0.54
GO:0002521	<i>Leukocyte differentiation</i>	1.04E-02	28	2.47 %	0.74	0.58
GO:0098869	Cellular oxidant detoxification	3.26E-02	12	0.46 %	0.90	0.28
GO:0009636	Response to toxic substance	1.69E-02	15	0.73 %	0.90	0.30
GO:0010883	Regulation of lipid storage	1.74E-02	8	0.20 %	0.84	0.34
GO:0009611	Response to wounding	4.94E-02	26	1.96 %	0.88	0.38
GO:0044712	Single-organism catabolic process	4.80E-02	55	3.68 %	0.90	0.39
GO:0043408	Regulation of MAPK cascade	2.37E-04	49	2.97 %	0.63	0.40
GO:1902531	<i>Regulation of intracellular signal transduction</i>	2.37E-04	90	7.58 %	0.73	0.62
GO:0023057	<i>NR of signaling</i>	4.05E-03	63	5.32 %	0.81	0.62
GO:0051248	<i>NR of protein metabolic process</i>	2.19E-02	58	5.29 %	0.81	0.56
GO:0042325	<i>Regulation of phosphorylation</i>	1.49E-02	73	6.87 %	0.80	0.75
GO:0010648	<i>NR of cell communication</i>	4.05E-03	63	5.30 %	0.80	0.63
GO:0006468	<i>Protein phosphorylation</i>	2.95E-02	85	9.30 %	0.85	0.77
GO:0048585	NR of response to stimulus	9.28E-04	75	6.25 %	0.76	0.49

MØHK versus MØC

GO term ID	Description	padj	Count	Frequency _a	Uniqueness _b	Dispensability _c
GO:0002376	Immune system process	2,01E-02	62	10.27 %	0.96	0.00
GO:0006954	Inflammatory response	8,37E-04	34	2.67 %	0.78	0.00
GO:0050729	<i>PR of inflammatory response</i>	9,35E-04	12	0.41 %	0.69	0.58
GO:0031349	<i>PR of defense response</i>	3,17E-02	15	1.29 %	0.70	0.76
^f GO:0032103	<i>PR of response to external stimulus</i>	2,03E-02	15	1.15 %	0.72	0.68
GO:0009611	<i>Response to wounding</i>	3,28E-03	23	1.96 %	0.81	0.42
^f GO:0007155	Cell adhesion	2,91E-02	42	6.62 %	0.96	0.00
^f GO:0040011	Locomotion	3,22E-02	42	7.12 %	0.96	0.00
^f GO:0050817	Coagulation	9,93E-03	15	0.92 %	0.92	0.00
^f GO:0050878	Regulation of body fluid levels	5,15E-03	22	1.52 %	0.90	0.00
GO:0050900	Leukocyte migration	2,25E-02	16	1.42 %	0.82	0.02
GO:0006955	<i>Immune response</i>	2,77E-02	39	6.05 %	0.81	0.58
^f GO:0030335	<i>PR of cell migration</i>	3,59E-02	17	1.82 %	0.76	0.66
^f GO:0008283	Cell proliferation	5,66E-03	54	8.54 %	0.94	0.02
GO:0048660	Regulation of smooth muscle cell proliferation	2,91E-02	7	0.33%	0.87	0.04
GO:0048659	<i>Smooth muscle cell proliferation</i>	2,91E-02	7	0.34 %	0.91	0.90
^f GO:0051348	NR of transferase activity	1,69E-02	17	1.40 %	0.87	0.04
^f GO:0043547	<i>PR of GTPase activity</i>	3,62E-02	19	2.67 %	0.88	0.50
^f GO:0006928	Movement of cell or subcellular component	3,68E-02	45	7.97 %	0.92	0.10
GO:0043408	Regulation of MAPK cascade	9,93E-03	29	2.97 %	0.55	0.14
GO:0016310	<i>Phosphorylation</i>	3,36E-02	65	11.27 %	0.83	0.68
GO:0048585	<i>NR of response to stimulus</i>	9,62E-03	46	6.26 %	0.67	0.49
^f GO:0080134	Regulation of response to stress	4,31E-02	38	5.11 %	0.71	0.54
GO:1902531	<i>Regulation of intracellular signal transduction</i>	1,09E-03	57	7.58 %	0.67	0.62
^f GO:0033673	<i>NR of kinase activity</i>	1,69E-02	16	1.29 %	0.68	0.88
GO:0006468	<i>Protein phosphorylation</i>	4,31E-02	52	9.30 %	0.81	0.66
GO:0023057	<i>NR of signaling</i>	2,94E-02	37	5.32 %	0.77	0.62
GO:0010648	<i>NR of cell communication</i>	2,94E-02	37	5.30 %	0.78	0.63
^f GO:0045936	<i>NR of phosphate metabolic process</i>	1,69E-02	24	2.70 %	0.72	0.65
GO:0051248	<i>NR of protein metabolic process</i>	2,91E-02	37	5.29 %	0.76	0.56
^f GO:0010563	<i>NR of phosphorus metabolic process</i>	1,69E-02	24	2.70 %	0.73	0.65

GO:0034097	Response to cytokine	1,69E-02	26	3.27 %	0.79	0.14
^f GO:0002237	<i>Response to molecule of bacterial origin</i>	4,31E-02	14	1.30 %	0.77	0.49
^f GO:0034612	<i>Response to tumor necrosis factor</i>	1,69E-02	10	0.81 %	0.80	0.47
GO:0071345	<i>Cellular response to cytokine stimulus</i>	1,70E-02	23	2.93 %	0.77	0.79
GO:0050707	Regulation of cytokine secretion	1,69E-02	10	0.72 %	0.79	0.20
GO:0050663	<i>Cytokine secretion</i>	4,62E-02	10	0.852%	0.84	0.79
^f GO:0051049	<i>Regulation of transport</i>	3,36E-02	50	7.79 %	0.81	0.51
GO:0098869	Cellular oxidant detoxification	3,46E-02	9	0.46 %	0.84	0.28
^f GO:0006694	Steroid biosynthetic process	3,95E-02	10	0.66 %	0.89	0.29
^f GO:0044283	<i>Small molecule biosynthetic process</i>	4,31E-02	26	2.35 %	0.89	0.59
GO:0009636	Response to toxic substance	2,22E-02	11	0.73 %	0.83	0.30

^aProportion of the GO term in the underlying protein annotation database (UniProt). Higher frequency implies more general terms and lower frequency more specific ones.

^bMeasures whether the term is an outlier when compared semantically to the whole list. Calculated as 1- (average semantic similarity of a term to all other terms). More unique terms tend to be less dispensable.

^cSemantic similarity threshold at which the term was removed from the list and assigned to a cluster.

^dGO terms not enriched from DEG in MØ7-MØC or MØHK-MØC comparisons.

^eGO terms not enriched from DEG in MØ1H-MØC or MØHK-MØC comparisons.

^fGO terms not enriched from DEG in MØ7-MØC or MØ1H-MØC comparisons.

MØ1H, macrophages inoculated with Nc-Spain1H; MØ7, macrophages inoculated with Nc-Spain7; MØHK, macrophages inoculated with heat-killed tachyzoites; MØC, non-infected macrophages; PR, positive regulation; NR negative regulation; TF transcription factor. Representative GO terms for each of the clusters are shown in bold and GO terms included within the clusters are italicized.