

SUPPLEMENTAL MATERIAL

Nakamura et al., <http://www.jem.org/cgi/content/full/jem.20130028/DC1>**Table S1.** Sequences of the primers used for RT-PCR

Target	Forward primer	Reverse primer
β -Actin	5'-CGTTGACATCCGTAAAGACCTC-3'	5'-AGCCACCGATCCACACAGA-3'
SP-A	5'-GAGGAGCTCAGACTGCACTC-3'	5'-GAGTGCAGTCTGAAGCTCCTC-3'
SP-B	5'-CTGCTTCTACCTCTGC-3'	5'-CTTGGCACAGGTCATTAGCTC-3'
SP-C	5'-ATGGACATGAGTAGCAAAGAGGT-3'	5'-CACGATGAGAAGGCGTTTGAG-3'
SP-D	5'-CAAAGGGAGAACGTGGACTA-3'	5'-CTTTGCCCTGTAGATCCT-3'
Bach2	5'-AGTTCATCCACGACATCC-3'	5'-AGGTGATTCCTCTCCGAC-3'
Pparg1	5'-TGTGAGACCAACAGCCTGAC-3'	5'-TATCAGTGGTTCACCGTTC-3'
Lxr α	5'-TGGAGACGTACGGAGGTACA-3'	5'-CAGCTCATTATGGCTCTGGA-3'
Abca1	5'-CTCAGTTAAGGCTGCTGCTG-3'	5'-TCAGGCGTACAGAGATCAGG-3'
Abcg1	5'-GCCTACTACCTGGCAAAGACC-3'	5'-AGCAGCGAACAGCACAAAAC-3'
GM-CSF	5'-TTGAACATGACAGCCAGCTA-3'	5'-GCATTCAAAGGGGATATCAG-3'
GM-CSFR α	5'-GAGTGACGTGCAGGAGGTTT-3'	5'-TTCCTGTCAGTCACGTTGGG-3'
GM-CSFR β c	5'-AACATGACCCCTATCACCAG-3'	5'-GGAGTAGTAGTCTTCGTTTGA-3'
PU.1	5'-GATGCACGTCCTCGATACTC-3'	5'-TCATCTGAGCTCTGCTGGTG-3'
Ccl2	5'-CAGGTCCTGTCTGCTTC-3'	5'-TGAGTGGGGCGTAACTGC-3'
Ccl24	5'-CTCATCTTGCTGCACGTC-3'	5'-GGGGTCAGTACAGATCTTATGG-3'
Cxcl1	5'-ATGTGTGGGAGGCTGTGTTT-3'	5'-AGCGAGACGAGACCAGGAG-3'
Il-6	5'-GATGCTACAAACTGGATATATTC-3'	5'-GGTCCTTAGCCACTCCTTCTGTG-3'
Il-1b	5'-AAGGAGAACCAAGCAACGA-3'	5'-CTCCACTTTGCTCTTGACTTCTA-3'
Arg1	5'-GGAAAGTCCCAGATGTACC-3'	5'-CCCAGCTTGTCTACTTCAG-3'
Ym1	5'-TCAACGGTTTTCCACAG-3'	5'-GTACAGCAGACAAGACATCC-3'
Retlna	5'-GTGTCAAGACTATGAACAGATG-3'	5'-TGGTCCAGTCAACGAGTA-3'
Mrc1	5'-CATCTCGGGCCTTGGGAATA-3'	5'-TGACCACTCCTGCTGCTTTAG-3'
Blimp-1	5'-CCCTCATCGGTGAAGTCTA-3'	5'-ACGTAGCGCATCCAGTTG-3'
Irf4	5'-TGTGCTCTGAACAAGAGCAAT-3'	5'-TATGAACCTGCTGGGCTGG-3'

Table S2. GO analysis of genes with >10-fold up-regulation

GO accession number	GO term	Corrected p-value
GO:0044421	Extracellular region part	9.57 ⁻¹⁵
GO:0005576	Extracellular region	6.18 ⁻¹⁴
GO:0009611 GO:0002245	Response to wounding	9.36 ⁻¹³
GO:0005615	Extracellular space	5.45 ⁻¹²
GO:0040011	Locomotion	1.00 ⁻¹⁰
GO:0006954	Inflammatory response	2.33 ⁻⁸
GO:0032879	Regulation of localization	3.29 ⁻⁸
GO:0048518 GO:0043119	Positive regulation of biological process	3.88 ⁻⁸
GO:0009605	Response to external stimulus	4.36 ⁻⁸
GO:0048731	System development	2.04 ⁻⁷
GO:0048856	Anatomical structure development	3.50 ⁻⁷
GO:0032502	Developmental process	7.13 ⁻⁷
GO:0030334	Regulation of cell migration	7.13 ⁻⁷
GO:0030335	Positive regulation of cell migration	7.13 ⁻⁷
GO:0005102	Receptor binding	7.13 ⁻⁷
GO:0050896 GO:0051869	Response to stimulus	7.13 ⁻⁷
GO:2000147	Positive regulation of cell motility	7.13 ⁻⁷
GO:2000145	Regulation of cell motility	9.74 ⁻⁷
GO:0051272	Positive regulation of cellular component movement	1.02 ⁻⁶
GO:0048522 GO:0051242	Positive regulation of cellular process	1.03 ⁻⁶
GO:0040017	Positive regulation of locomotion	1.03 ⁻⁶
GO:0009653	Anatomical structure morphogenesis	2.24 ⁻⁶
GO:0006935	Chemotaxis	3.06 ⁻⁶
GO:0042330	Taxis	3.12 ⁻⁶
GO:0051270	Regulation of cellular component movement	3.13 ⁻⁶
GO:0007275	Multicellular organismal development	3.33 ⁻⁶
GO:0040012	Regulation of locomotion	3.33 ⁻⁶
GO:0042127	Regulation of cell proliferation	4.63 ⁻⁶
GO:0071944	Cell periphery	1.37 ⁻⁵
GO:0005886 GO:0005904	Plasma membrane	2.02 ⁻⁵
GO:0051239	Regulation of multicellular organismal process	2.15 ⁻⁵
GO:0048583	Regulation of response to stimulus	2.18 ⁻⁵
GO:0065009	Regulation of molecular function	2.31 ⁻⁵
GO:0065007	Biological regulation	3.77 ⁻⁵
GO:0016477	Cell migration	3.90 ⁻⁵
GO:0001936	Regulation of endothelial cell proliferation	4.54 ⁻⁵
GO:0044699	Single-organism process	4.54 ⁻⁵
GO:0048513	Organ development	4.54 ⁻⁵
GO:0051674	Localization of cell	5.03 ⁻⁵
GO:0048870	Cell motility	5.03 ⁻⁵
GO:0051049	Regulation of transport	7.48 ⁻⁵
GO:0002682	Regulation of immune system process	7.56 ⁻⁵
GO:0008284	Positive regulation of cell proliferation	1.14 ⁻⁴
GO:0006928	Cellular component movement	1.20 ⁻⁴
GO:0006952 GO:0002217 GO:0042829	Defense response	1.27 ⁻⁴
GO:0002376	Immune system process	1.87 ⁻⁴
GO:0051240	Positive regulation of multicellular organismal process	1.91 ⁻⁴
GO:0005178	Integrin binding	1.91 ⁻⁴
GO:0005515 GO:0045308	Protein binding	1.95 ⁻⁴

Table S2. GO analysis of genes with >10-fold up-regulation (*Continued*)

GO accession number	GO term	Corrected p-value
GO:0050789 GO:0050791	Regulation of biological process	2.26 ⁻⁴
GO:0001944	Vasculature development	2.50 ⁻⁴
GO:0001568	Blood vessel development	3.48 ⁻⁴
GO:0001938	Positive regulation of endothelial cell proliferation	4.75 ⁻⁴
GO:0045785	Positive regulation of cell adhesion	5.07 ⁻⁴
GO:0050678	Regulation of epithelial cell proliferation	6.55 ⁻⁴
GO:0006950	Response to stress	6.55 ⁻⁴
GO:0072359	Circulatory system development	6.76 ⁻⁴
GO:0072358	Cardiovascular system development	6.76 ⁻⁴
GO:0008289	Lipid binding	7.88 ⁻⁴
GO:0050790	Regulation of catalytic activity	7.88 ⁻⁴
GO:0030155	Regulation of cell adhesion	9.02 ⁻⁴
GO:0010646	Regulation of cell communication	9.45 ⁻⁴
GO:0044093	Positive regulation of molecular function	9.51 ⁻⁴
GO:0023051	Regulation of signaling	0.001032084
GO:0030324	Lung development	0.001047604
GO:0030323	Respiratory tube development	0.001107489
GO:0050793	Regulation of developmental process	0.001242768
GO:0046852	Positive regulation of bone remodeling	0.00143183
GO:0000050 GO:0006594 GO:0006871	Urea cycle	0.00143183
GO:0019627	Urea metabolic process	0.00143183
GO:0033993	Response to lipid	0.00143183
GO:0045860	Positive regulation of protein kinase activity	0.00143183
GO:0045780	Positive regulation of bone resorption	0.00143183
GO:0005488	Binding	0.00143183
GO:0071941	Nitrogen cycle metabolic process	0.00143183
GO:0050679	Positive regulation of epithelial cell proliferation	0.00143183
GO:0048646	Anatomical structure formation involved in morphogenesis	0.001574635
GO:0009966 GO:0035466	Regulation of signal transduction	0.001574635
GO:0008009	Chemokine activity	0.001581875
GO:0051897	Positive regulation of protein kinase B signaling cascade	0.001876034
GO:2000026	Regulation of multicellular organismal development	0.001876731
GO:0042060	Wound healing	0.002262661
GO:0009986 GO:0009928 GO:0009929	Cell surface	0.002267849
GO:0033674	Positive regulation of kinase activity	0.002267849
GO:0060541	Respiratory system development	0.002629323
GO:0048286	Lung alveolus development	0.002918511
GO:0051347	Positive regulation of transferase activity	0.003309521
GO:0005125	Cytokine activity	0.004327569
GO:0016020	Membrane	0.004495516
GO:0034105	Positive regulation of tissue remodeling	0.00455367
GO:0006525	Arginine metabolic process	0.00455367
GO:0048519 GO:0043118	Negative regulation of biological process	0.004751381
GO:0009888	Tissue development	0.004872057
GO:0031012	Extracellular matrix	0.005179694
GO:0010033	Response to organic substance	0.005179694
GO:0065008	Regulation of biological quality	0.005311207
GO:0042221	Response to chemical stimulus	0.005469468
GO:0042379	Chemokine receptor binding	0.005469468
GO:0010941	Regulation of cell death	0.005718335
GO:0010562	Positive regulation of phosphorus metabolic process	0.006022319
GO:0045937	Positive regulation of phosphate metabolic process	0.006022319

Table S2. GO analysis of genes with >10-fold up-regulation (*Continued*)

GO accession number	GO term	Corrected p-value
GO:0048869	Cellular developmental process	0.006868979
GO:0051056	Regulation of small GTPase mediated signal transduction	0.007710023
GO:0044707	Single-multicellular organism process	0.008118006
GO:0001934	Positive regulation of protein phosphorylation	0.008670883
GO:0051896	Regulation of protein kinase B signaling cascade	0.008670883
GO:0032501 GO:0050874	Multicellular organismal process	0.00879704

Table S3. GO analysis of genes with more than fourfold down-regulation

GO accession number	GO term	Corrected p-value
GO:0071944	Cell periphery	8.42 ⁻⁵
GO:0005886 GO:0005904	Plasma membrane	8.42 ⁻⁵
GO:0042613	MHC class II protein complex	0.003423147
GO:0071695	Anatomical structure maturation	0.004906325
GO:0042611	MHC protein complex	0.004906325
GO:0002478	Antigen processing and presentation of exogenous peptide antigen	0.005406083
GO:0048820	Hair follicle maturation	0.006303758
GO:0019886 GO:0042591 GO:0048005	Antigen processing and presentation of exogenous peptide antigen via MHC class II	0.009633509
GO:0019884	Antigen processing and presentation of exogenous antigen	0.01421624
GO:0002495	Antigen processing and presentation of peptide antigen via MHC class II	0.01634329
GO:0005488	Binding	0.018125836
GO:0050870	Positive regulation of T cell activation	0.02396895
GO:0002504	Antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	0.02396895
GO:0042638	Exogen	0.03296325
GO:0048002	Antigen processing and presentation of peptide antigen	0.036329534
GO:0019882 GO:0030333	Antigen processing and presentation	0.036329534
GO:0045621	Positive regulation of lymphocyte differentiation	0.03917532
GO:0048518 GO:0043119	Positive regulation of biological process	0.03919307
GO:0048583	Regulation of response to stimulus	0.049198814
GO:0051251	Positive regulation of lymphocyte activation	0.049198814
GO:0044459	Plasma membrane part	0.049198814