

Supplementary Figure 1. a, Blimp1 expression in *L. monocytogenes*-infected BMDM and Neutrophils.

RNA was isolated from untreated or Lm-infected BMDM 2, 4, 8 or 24 hpi and Blimp1 gene expression was quantified by qPCR. Data were normalized with β -Actin and are representative of 3 independent experiments.

b, Blimp1 transcription in different myeloid cell types. Blimp1 gene expression was monitored in freshly isolated FLT3-L DC, GMCSF DC, BMDM, PEC and neutrophils by qPCR. Data were normalized with β -Actin.

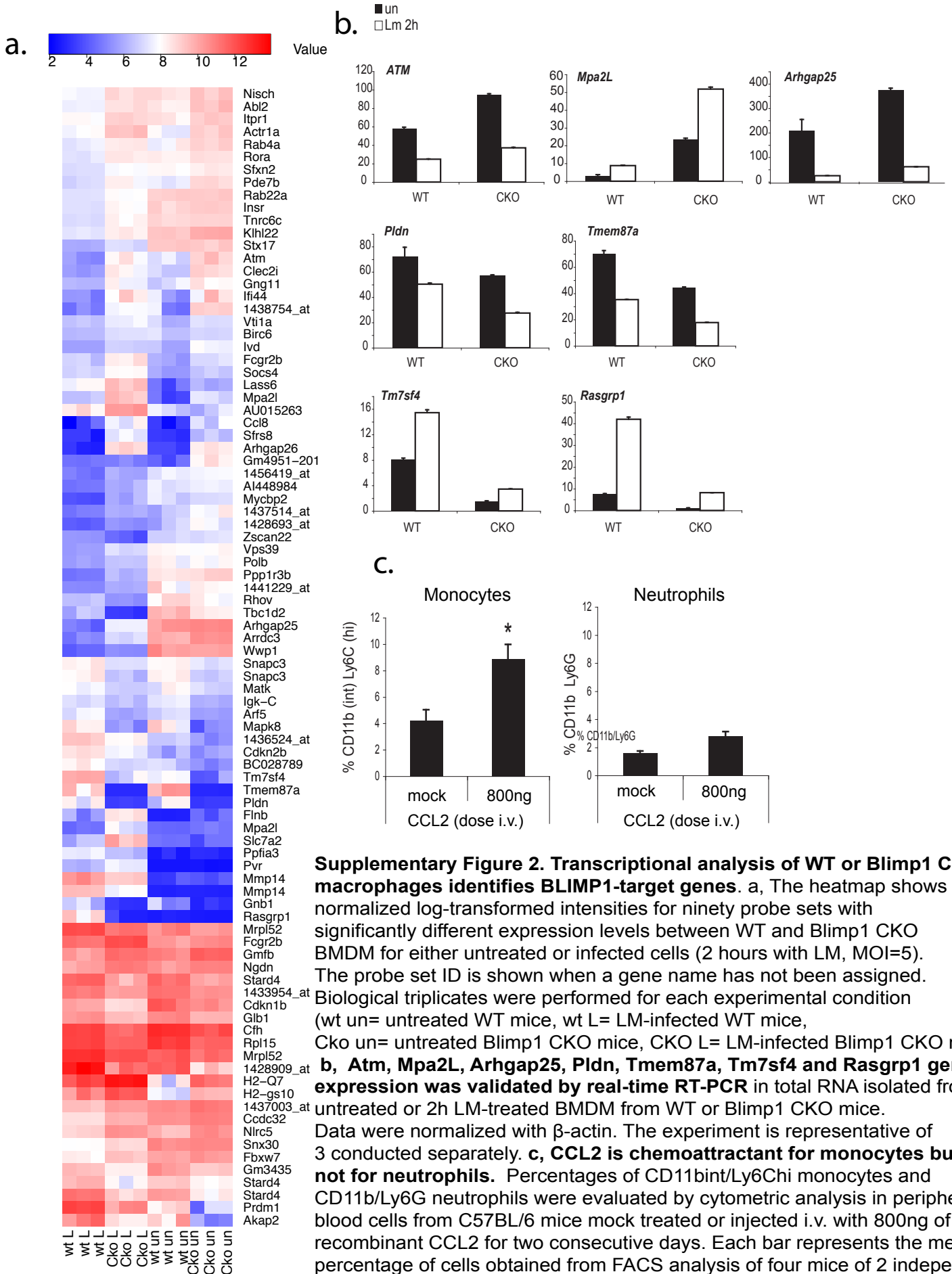
c, Deletion of Blimp1 in neutrophils derived from Blimp1 CKO mice. Lysozyme M-driven cre-mediated deletion of Blimp1 was confirmed by PCR in genomic DNA of freshly isolated neutrophils from WT or Blimp1 CKO mice.

d, Blimp1 expression was monitored by qPCR in neutrophils from bone marrow or peripheral blood left untreated or treated for 4h with LPS or *L. monocytogenes*. Enhanced protection of myeloid-specific Blimp1-deficient mice to infection with *L. monocytogenes*.

e, WT or Blimp1 CKO mice were infected i.v. with 3×10^4 cfu of *L. monocytogenes* and bacterial loads from livers and spleens were calculated 20, 48 and 72hpi. Counts from 2 mice per condition are depicted and are representative of two experiments conducted independently. * $p < 0.05$ (two-tailed Student's t-test).

f, WT (n=19) or Blimp1 CKO mice (n=17) were infected i.v. with *L. monocytogenes* and survival monitored as indicated.

g, C57BL/6 mice and C57BL/6 Mlyz Cre mice (n=10/each genotype) were infected as stated above and bacterial burdens were monitored in infected spleens and livers.



GO Biological process	Number of genes observed	Expected number of genes	Total number of genes in category	P-value
regulation of macrophage activation	2	0.022854241	5	0.000203275
regulation of leukocyte activation	5	0.580497715	127	0.000275194
regulation of cell activation	5	0.585068563	128	0.000285395
regulation of cellular process	33	20.71965465	4533	0.000577988
myeloid leukocyte activation	3	0.182833926	40	0.000791349
macrophage activation	2	0.054850178	12	0.001314345
leukocyte activation	6	1.238699848	271	0.00141389
regulation of biological process	33	21.76180802	4761	0.001576146
protein ubiquitination	3	0.2468258	54	0.001899076
cell activation	6	1.316404266	288	0.001926118
negative regulation of apoptosis	5	0.923311326	202	0.002229077
cytoskeleton organization	6	1.357541899	297	0.002248813
biological regulation	34	23.15591671	5066	0.002285019
negative regulation of programmed cell death	5	0.941594718	206	0.002427475
negative regulation of cell death	5	0.941594718	206	0.002427475
signal transduction	19	9.918740477	2170	0.002468391
nitric oxide biosynthetic process	2	0.077704418	17	0.00266898
nitric oxide metabolic process	2	0.077704418	17	0.00266898
protein modification by small protein conjugation	3	0.283392585	62	0.002822068
cell communication	20	11.03402743	2414	0.003547852
protein modification by small protein conjugation or removal	3	0.315388522	69	0.003822625
immune system process	9	3.231589639	707	0.004396854
negative regulation of type I hypersensitivity	1	0.004570848	1	0.004570848
ornithine transport	1	0.004570848	1	0.004570848
branchiomotor neuron axon guidance	1	0.004570848	1	0.004570848
regulation of cytoskeleton organization	3	0.342813611	75	0.004832623
protein localization	9	3.359573388	735	0.005663125
regulation of cellular component organization	5	1.156424581	253	0.005824961
negative regulation of cell motion	2	0.118842052	26	0.006212534
regulation of immune system process	5	1.179278822	258	0.006319439
actin filament organization	3	0.383951244	84	0.00662539
actin cytoskeleton organization	4	0.767902489	168	0.00718126
macromolecule localization	9	3.524123921	771	0.007690774
antigen processing and presentation of peptide antigen	2	0.141696293	31	0.008760064
actin filament-based process	4	0.822752666	180	0.009113226
production of nitric oxide during acute inflammatory response	1	0.009141696	2	0.009121189
JUN phosphorylation	1	0.009141696	2	0.009121189
lysine transport	1	0.009141696	2	0.009121189
regulation of endocytosis	2	0.150837989	33	0.009889142

Supplementary Table1. List of probe set IDs and gene names corresponding to supplementary figure 2.

Probe set ID	Gene
1444128_at	Arhgap26
1443905_at	Sfrs8
1438676_at	Mpa2l
1424454_at	Tmem87a
1438754_at	
1437072_at	Arhgap25
1434295_at	Rasgrp1
1437176_at	Nlrc5
1429239_a_at	Stard4
1457088_at	Pldn
1416572_at	Mmp14
1422166_at	Clec2l
1456792_at	Tbc1d2
1457970_at	Actr1a
1425474_a_at	Vps39
1421205_at	Atm
1449001_at	Ivd
1460558_at	Ccdc32
1447150_at	Mycbp2
1436590_at	Ppp1r3b
1457936_at	Mapk8
1421275_s_at	Socs4
1454617_at	Arrdc3
1431007_at	Gm3435
1455682_at	Abl2
1434045_at	Cdkn1b
1425908_at	Gnb1
1424034_at	Rora
1440506_at	Slc7a2
1423555_a_at	Ifi44
1428693_at	
1447927_at	Mpa2l
1437514_at	
1426481_at	Klhl22
1442959_at	Birc6
1428917_at	Stx17
1430151_at	Nisch
1424976_at	Rhov
1428760_at	Snapc3
1439819_at	AU015263
1435719_at	AI448984
1436524_at	
1423903_at	Pvr
1460203_at	Itpr1
1456479_at	Snx30
1445534_at	Flnb
1441229_at	
1448942_at	Gng11
1453077_a_at	Snapc3
1416205_at	Glb1
1439840_at	Polb
1460363_at	Tnrc6c
1457449_at	Lass6
1415761_at	Mrpl52
1449048_s_at	Rab4a
1449168_a_at	Akap2
1422807_at	Arf5
1449152_at	Cdkn2b
1455332_x_at	Fcgr2b
1446365_at	Vti1a
1460701_a_at	Mrpl52
1443628_at	Wwp1
1419684_at	Ccl8
1442118_at	Fcgr2b
1417069_a_at	Gmfb
1431046_at	Ppfia3
1434328_at	Rpl15
1433954_at	
1420425_at	Prdm1
1437003_at	
1423153_x_at	Cfh
1438318_x_at	Ngdn
1434446_at	Insr
1455011_at	Stard4
1451558_at	Fbxw7
1432329_a_at	Matk
1428909_at	
1454988_s_at	Rab22a
1431970_at	Tm7sf4
1429240_at	Stard4
1436360_at	Zscan22
1418536_at	H2-Q7
1460064_at	BC028789
1435896_at	Sfxn2
1456419_at	
1448383_at	Mmp14
1439831_at	Gm4951-201
1427660_x_at	Igk-C
1445539_at	Pde7b
1451644_a_at	H2-gs10

Supplementary Table2. GO enrichment analysis for genes with significantly different expression levels ($p < 0.05$). A GO enrichment analysis was performed on the set of genes in supplementary Table 1. GO biological processes are ordered by P-values obtained from the hypergeometric test.