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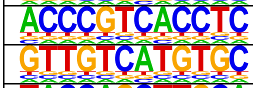
Supplementary information

TFEB induces mitochondrial itaconate synthesis to suppress bacterial growth in macrophages

Supplementary Information

Motif	Transcription Factor	p-value
	Zfp691	1e-4
	Homeobox protein Nkx-6.1	1e-4
	FOXH1	1e-4
	Mlxip	1e-4
	Homeobox protein Nkx-2.1	1e-4
	Hmx1	1e-4
	ZNF354C	1e-4
	Spz1	1e-4
	Homeobox protein Six1	1e-4
	RAR:RXR (NR)	1e-4
	at_AC_acceptor	1e-4
	SREBF2	1e-4
	Irf3	1e-4
	Mybl1	1e-4
	GATA	1e-4
	Cux1	1e-4
	Zbtb3	1e-4
	RUNX	1e-4
	TBX15	1e-4
	PRDM1	1e-4
	Eomes-2	1e-4
	TFEB	1e-4
	Tcf21	1e-4
	Eomes-1	1e-4
	Homeobox protein Pknox1	1e-4
	Mnx1	1e-4
	SMAD3	1e-4
	HIF-1A	1e-3
	Nkx-2.2	1e-3
	TATA-Box	1e-3
	BMYB (HTH)	1e-3
	NRL	1e-3
	KLF10	1e-3

Supplementary Table 1. Potential Irg1 regulators upon TFEB activation.

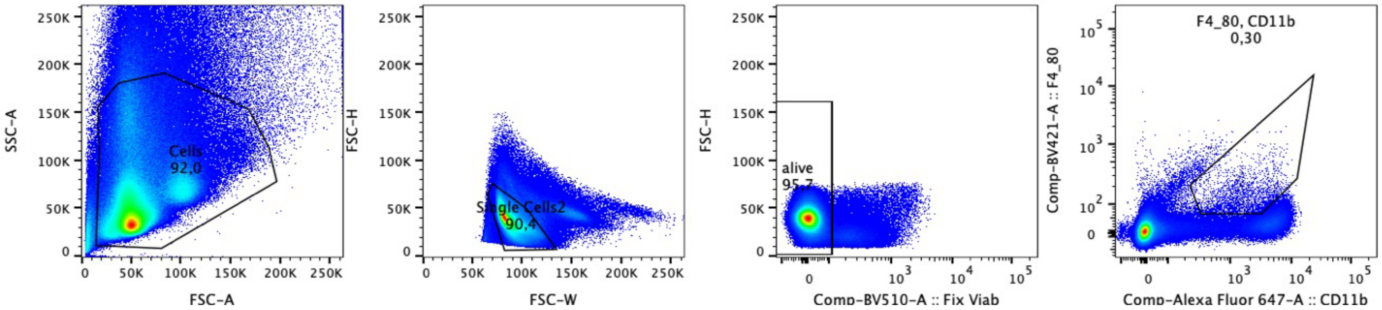
List of identified transcription factor binding motifs in significantly opened chromatin regions of the *Irg1* locus from ATAC-seq analysis (shown in Figure 4h) in TFEB-GFP- versus GFP-expressing BMDMs. Identified motifs are shown in column 1. Column 2 indicates the respective transcription factor. Column 3 represents the significance of enrichment of the binding motifs in the gained *Irg1* peaks calculated via the HOMER motif analysis software.

Supplementary Table 2
Oligonucleotide sequences

Cloning primers	
Irg1-forw	TTCAAGCTTGCCACCATGATGCTCAAGTCTGTCACAGAG
Irg1-rev	GGCCCGCGGTACCTTGATATTGGTAAACCTGGGCAACG
BFP-forw	CCACCGGTCGCCACCATGAGCGAGCTGATTAAGGAG
BFP-rev	TGTGCTGGCGGCCGCTCAATTAAGCTTGTGCCCCAG
RT-qPCR primers	
Irg1-forw	GCAACATGATGCTCAAGTCTG
Irg1-rev	TGCTCCTCCGAATGATACCA
Tfeb-forw	TGATCCCCAAGGCCAATGAC
Tfeb-forw	TCCCTGGACTTTTGCAGGTC
b2m fw	CTGCTACGTAACACAGTTCCACCC
b2m rev	CATGATGCTTGATCACATGTCTCG
Actin fw	TCGTTGCCGGTCCACACCCG
Actin rev	CTTTGCACATGCCGGAGCCGT
ChIP-qPCR primer	
-800bp_FW	GGCCACCATTCCTCACAAAT
-800bp_RV	ACGAGTAAGTGAGCATGGGT
-200bp_FW	GTCTTCAAGAGTGGGATGCC
-200bp_RV	ATAATTACAGAGGGATGGCCTG
negative-control_FW	TGCTCCACAGTGTCCATGTACA
negative-control_RV	AGCAATTTCATGGGTGAGAGAAG

Supplementary Figure

Flow cytometry gating strategy



Supplementary Figure 1: Flow cytometry gating strategy to identify splenic macrophages.
Relvant for Figure 4d, g and Extended Data Figure 4 c,h. From splenic cells suspensions (SSC-A to FSC-A), doublets (FSC-W to FCH-H) and dead cells (viable to FSC-H) were excluded. Macrophages were identified as double positive F4/80+ and CD11b+ population.