

Revised Supplemental Table 3: Primer sequences used in RT-PCR analysis of gene expression

gene	forward (5'-3')	reverse (5'-3')	chromosome / nucleotide position ^(a)		comments
irf8-a	AAAGGATGTGGAGCCCTCTGACTG	GGAAACGCAGGAAAGGAATGC	chr8	120755243-266 120755377-397	3'-UTR
irf8-b	TTCCTGAGATGGAGTGTGGC	TGGGCTCCTCTTGGTCATAC	chr8	120745659-678 120747225-244	exon 4-5
pel1-a	AATCTGTTGTTGGTGACTTTTGTATG	GGAGTCCCAGGCAGTTATGAGC	chr11	21142700-725 21142889-910	"retained intron" transcript ^(b)
pel1-b	GCCCCAGTAAAATATGGCGAA	TTCCTCTATCACCGTTTGGGA	chr11	21136151-171 21140578-598	exon 2-3
malt1-a	AGCATATCCAGGAGGACCGC	CAGCTTGGGCAATGTTAAGATACC	chr18	65454165-184 65454328-351	"retained intron" transcript ^(c)
malt1-b	CTGATCCAGTCCAGGGAGC	AATGTGAACGCCACACTGAA	chr18	65470467-485 65473027-046	exon 15-16
ccl22-a	CCTCAGAAAATAGATGGTTGTGGG	CTGTTGTCTCCAGGGAAGCAAG	chr8	94750926-949 94751039-060	3'-UTR
ccl22-b	GGACTACATCCGTCACCCTC	AGTAGCTTCTTCACCCAGACC	chr8	94746942-961 94749850-870	exon 2-3
LIF	AACCAGATCAAGAATCAACTGGC	TGTTAGGCGCACATAGCTTTT	chr11	4268303-325 4268961-981	exon 4-5
ligp1	GAGCCTGTAGCAGTGAAGGT	GCTGACCCATGACTTCAAGC	chr18	60376057-076 60389802-821	exon 2-5
Gbp2	TGACTGAGAAGATGAAAGACGAAC	TTTTGCTCTATTCTCGAATCCTT	chr3	142635903-926 142637405-428	exon 10-11
Gbp3	GTGGTGGTGGCCATTGTTG	GGCACACACCACATCCAGA	chr3	142561860-878 142564148-166	exon 3-4
Gbp6	GAAGGAAGCTGGAGCAGGA	TCTCAGTTGCTGTATCTCTTTGTT	chr5	105274239-257 105273213-236	exon 12-13

(a) reference sequence GRCm38.p4 C57BL/6J

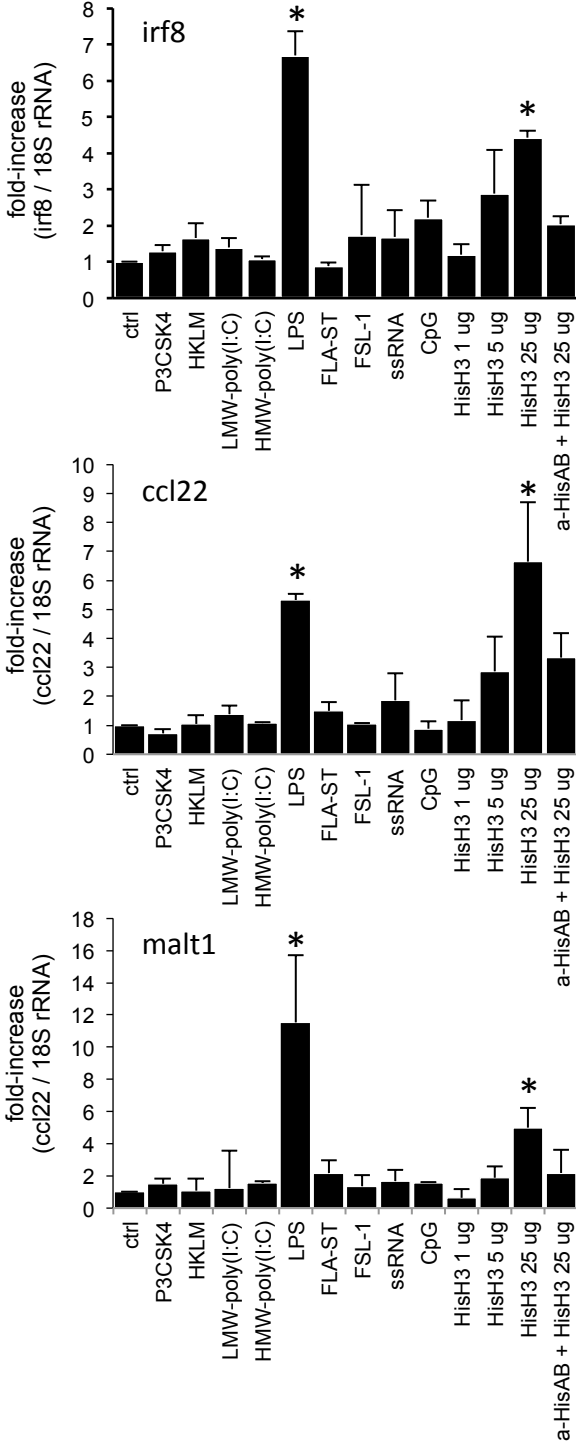
(b) Peli1 transcripts with "retained intron": ENSMUST00000156122.7; ENSMUST00000149675.1

(c) Malt1 transcripts with "retained intron": ENSMUST00000225085.1; ENSMUST00000224229.1

Supplemental Figure S2: **EPCR-dependent biomarker regulation in cultured RAW cells.**

RAW cells were treated for 3h with the indicated TLR ligands, and the abundance of *Irf8*, *Ccl22*, and *Malt1* mRNA relative to 18S rRNA was measured by RT-PCR. Data represent the average \pm standard deviation from 2 independent experiments with triplicate measurements of each sample. Ctrl: untreated sample. Asterisk indicates $P < 0.01$ by pairwise comparison to levels in the untreated sample (Student's 2-tailed T-test). HKLM: heat-killed *L.monocytogenes*; FLA-ST: Flagellin *S.typhimurium* (TLR5 agonist; RAW cells lack TLR5); FSL-1: Pam2CGDPKHPKSF.

Figure S2



Supplemental Figure S3: Biomarker induction by LPS in PAR-deficient BMDC

Irf8, *Ccl22*, and *Malt1* mRNA abundance relative to 18S rRNA was measured via RT-PCR in LPS-treated BMDC prepared from wildtype mice and mice lacking the indicated PARs. Data are expressed as the -fold increase over baseline levels in wildtype cells and represent the average \pm standard deviation of 4 culture experiments with triplicate measurements per sample. Asterisk indicates $P < 0.01$ for LPS-treated samples in comparison to wildtype cells via Student's t-test.

Figure S3

