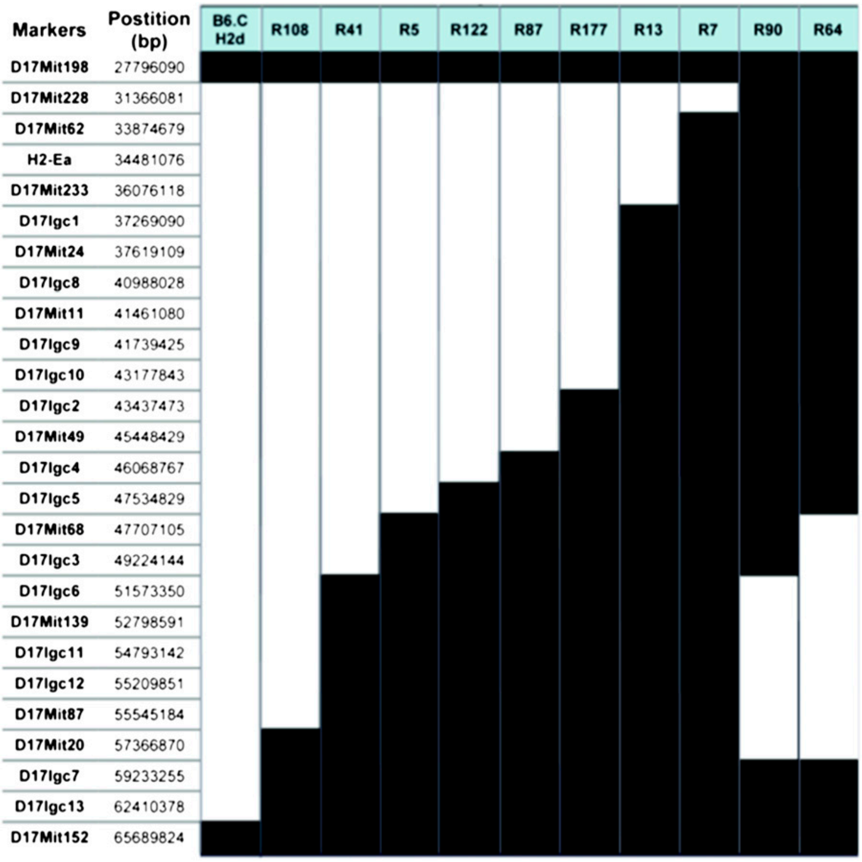
Supporting Information

Gonçalves et al. 10.1073/pnas.1306873110

SI Materials and Methods

Gene Expression Quantification. mRNAs from isolated nonparenchymal cells (NPCs) were similarly purified as described in *Materials and Methods*. cDNA specific to *Bysl*, *Ccnd3*, *Frs3*, *Foxp4*, *Med20*, *Mocs1*, *Mdfi*, *Nfya*, *Plcl2*, *Rftn1*, *Taf8*, *Tbc1d5*, *Tfeb*, and *Tomm6* expression was quantified using TaqMan Gene Expression Assays (Mm00479473_m1, Mm01612362_m1, Mm00460745_m1, Mm00466364_m1, Mm00498409_m1, Mm01273749_m1, Mm00521984_m1, Mm00477820_m1, Mm01277344_m1, Mm01281622_m1, Mm01273585_m1, Mm00813934_m1, Mm00448968_m1, and Mm00481240_m1, respectively; Applied Biosystems). Endogenous control GAPDH (Mouse GAPD Endogenous Control; Applied Biosystems) was used in multiplex PCR reactions (Prism 7900HT; Applied Biosystems), and relative quantification was calculated using the $\Delta\Delta C_t$ method.



Markers	Postition (bp)	B6.C H2d	R108	R41	R5	R122	R87	R177	R13	R7	R90	R64
D17Mit198	27796090	■	■	■	■	■	■	■	■	■	■	■
D17Mit228	31366081	□	□	□	□	□	□	□	□	□	■	■
D17Mit62	33874679	□	□	□	□	□	□	□	□	■	■	■
H2-Ea	34481076	□	□	□	□	□	□	□	□	■	■	■
D17Mit233	36076118	□	□	□	□	□	□	□	□	■	■	■
D17Igc1	37269090	□	□	□	□	□	□	□	■	■	■	■
D17Mit24	37619109	□	□	□	□	□	□	□	■	■	■	■
D17Igc8	40988028	□	□	□	□	□	□	□	■	■	■	■
D17Mit11	41461080	□	□	□	□	□	□	□	■	■	■	■
D17Igc9	41739425	□	□	□	□	□	□	□	■	■	■	■
D17Igc10	43177843	□	□	□	□	□	□	□	■	■	■	■
D17Igc2	43437473	□	□	□	□	□	□	■	■	■	■	■
D17Mit49	45448429	□	□	□	□	□	□	■	■	■	■	■
D17Igc4	46068767	□	□	□	□	□	■	■	■	■	■	■
D17Igc5	47534829	□	□	□	□	■	■	■	■	■	■	■
D17Mit68	47707105	□	□	□	■	■	■	■	■	■	■	□
D17Igc3	49224144	□	□	□	■	■	■	■	■	■	■	□
D17Igc6	51573350	□	□	■	■	■	■	■	■	■	□	□
D17Mit139	52798591	□	□	■	■	■	■	■	■	■	□	□
D17Igc11	54793142	□	□	■	■	■	■	■	■	■	□	□
D17Igc12	55209851	□	□	■	■	■	■	■	■	■	□	□
D17Mit87	55545184	□	□	■	■	■	■	■	■	■	□	□
D17Mit20	57366870	□	■	■	■	■	■	■	■	■	□	□
D17Igc7	59233255	□	■	■	■	■	■	■	■	■	■	■
D17Igc13	62410378	□	■	■	■	■	■	■	■	■	■	■
D17Mit152	65689824	■	■	■	■	■	■	■	■	■	■	■

Fig. S1. Chromosome 17 genotype maps of 10 subcongenic lines selected from the B6.C-H2d × C57BL/6 backcross progeny using 24 polymorphic microsatellites. Genotypes of BALB/c origin are in white, and those of C57BL/6 are in black.

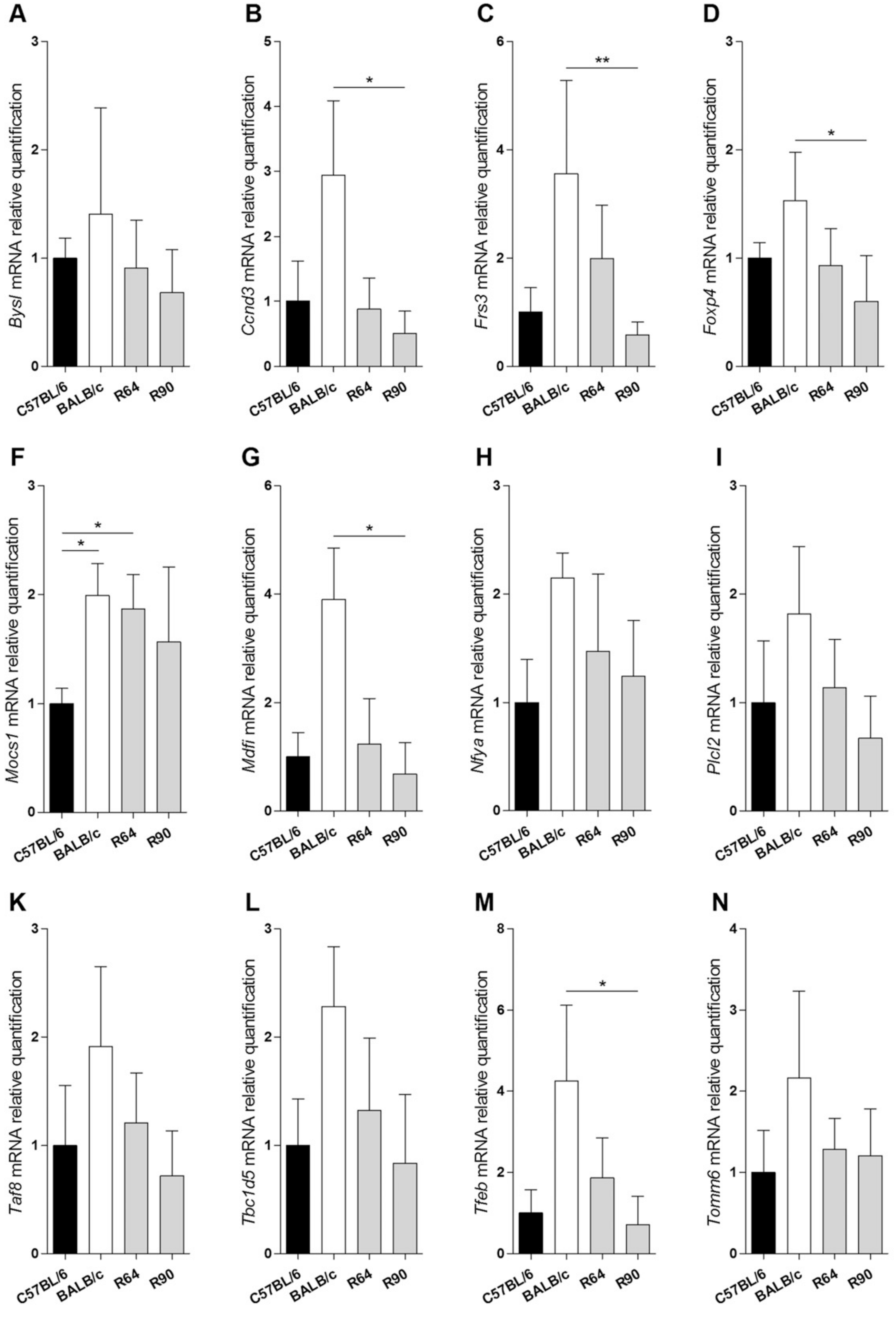


Fig. S2. NPC expression of non-TREM genes mapping within the *belr1* interval. mRNA of the indicated genes was quantified in NPCs isolated from non-infected R64, R90, and BALB/c mice relative to C57BL/6 mice (*A*, Bysl; *B*, Ccnd3; *C*, Frs3; *D*, Foxp4; *E*, Med20; *F*, Mocs1; *G*, Mdfi; *H*, Nfya; *I*, Plcl2; *J*, Rftn1; *K*, Taf8; *L*, Tbc1d5; *M*, Tfeb; *N*, Tomm6). Data are mean ± SD; $n > 6$. $*P < 0.05$; $**P < 0.01$. mRNA expression of indicated genes did not correlate with the liver stage resistance phenotype in the tested strains.

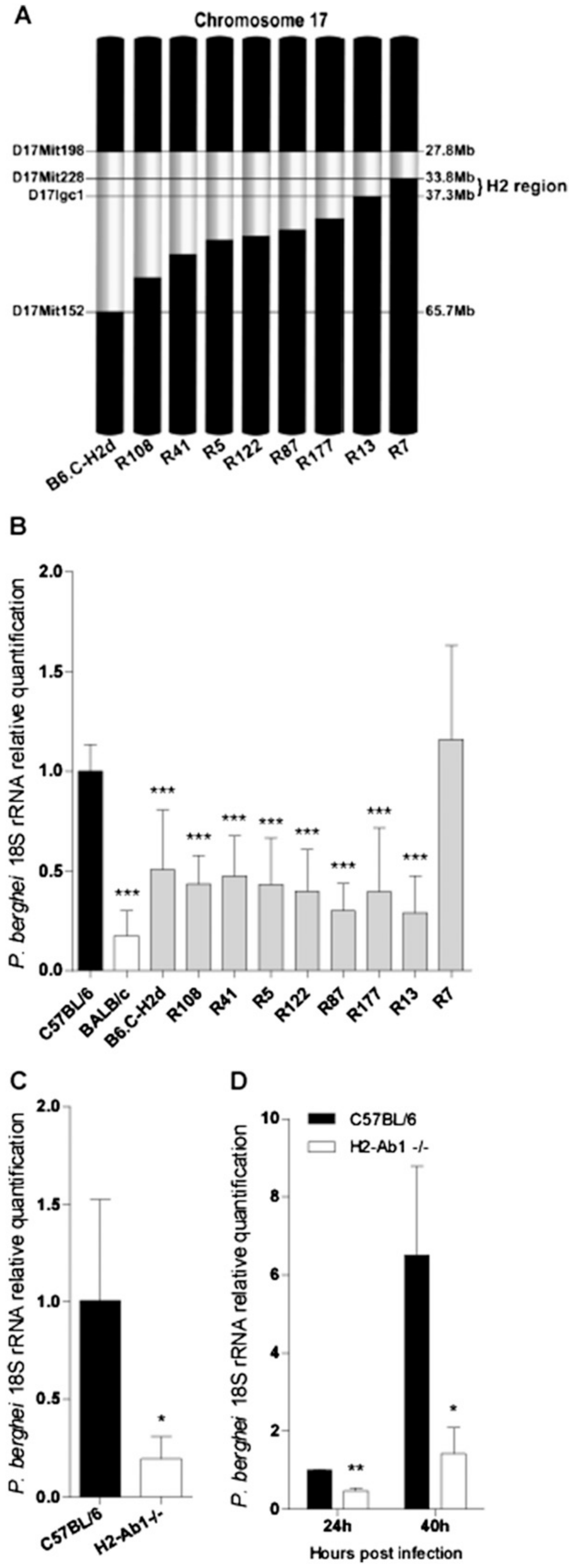


Fig. S3. The H2 region and class II genes contribute to malaria liver stage resistance. (*A*) Diagram representing the relative size of BALB/c-derived congenic regions (in white) in the B6.C-H2d strain and eight single recombinant subcongenic lines in the C57BL/6 background (in black). The R13 congenic region encompasses the H2 locus within 5.9 Mb. (*B*) Liver parasite burden in subcongenic lines at 40 h postinfection (p.i.) was ascertained as described in Fig. 1. Data are mean ± SD; n = 10. (*C*) Liver parasite burden in *H2-Ab1*$^{-/-}$ mice at 40 h p.i. Data are mean ± SD. (*D*) Parasite yield in infected primary cultures of *H2-Ab1*–deficient and C57BL/6 hepatocytes measured at 24 h and 40 h p.i. Data are mean ± SD of triplicate cultures. *$P < 0.05$; **$P \leq 0.001$; ***$P < 0.0001$.

Table S1. ***belr1*** **gene content: Protein-coding genes encompassed in the interval D17Igc5-D17Igc6 on mouse chromosome 17**

Gene symbol	Gene start, bp	Gene name
Apobec2	48,558,556	Apolipoprotein B mRNA editing enzyme, catalytic polypeptide 2
Bysl	47,736,280	Bystin-like
Ccnd3	47,642,000	Cyclin D3
Dazl	50,418,719	Deleted in azoospermia-like
Daam2	49,595,347	Dishevelled associated activator of morphogenesis 2
Frs3	47,825,979	Fibroblast growth factor receptor substrate 3
Foxp4	48,004,082	Forkhead box P4
Guca1a	47,531,509	Guanylate cyclase activator 1a (retina)
Kif6	49,754,461	Kinesin family member 6
Lrfn2	49,071,704	Leucine-rich repeat and fibronectin type III domain containing 2
Med20	47,748,531	Mediator complex subunit 20
Mocs1	49,567,687	Molybdenum cofactor synthesis 1
Mdfi	47,952,277	MyoD family inhibitor
Nfya	48,526,210	Nuclear transcription factor-Y alpha
Plcl2	50,648,872	Phospholipase C-like 2
Prickle4	47,823,688	Prickle homolog 4 (*Drosophila*)
Pgc	47,863,791	Progastricsin (pepsinogen C)
Rftn1	50,131,582	Raftlin lipid raft linker 1
Trem5	48,262,555	Triggering receptor expressed on myeloid cells 5
Trem4	48,288,846	Triggering receptor expressed on myeloid cells 4
Treml6	48,455,466	Triggering receptor expressed on myeloid cells-like 6
Taf8	47,624,999	TAF8 RNA polymerase II, TATA box binding protein-associated factor 8
Tbc1d5	50,872,452	TBC1 domain family, member 5
Tfeb	47,873,979	Transcription factor EB
Tomm6	47,823,595	Translocase of outer mitochondrial membrane 6 homolog (yeast)
Tspo2	48,587,281	Translocator protein 2
Trem1	48,371,903	Triggering receptor expressed on myeloid cells 1
Trem2	48,485,726	Triggering receptor expressed on myeloid cells 2
Trem3	48,386,944	Triggering receptor expressed on myeloid cells 3
Treml1	48,499,241	Triggering receptor expressed on myeloid cells-like 1
Treml2	48,438,864	Triggering receptor expressed on myeloid cells-like 2
Treml4	48,403,659	Triggering receptor expressed on myeloid cells-like 4
Usp49	47,767,639	Ubiquitin specific peptidase 49
Unc5cl	48,594,226	Unc-5 homolog C (*C. elegans*)-like

Table S2. ***belr1*** **fine mapping: Polymorphic microsatellite markers**

Marker	Start position, bp	Fragment size*	Forward	Reverse
D17Igc1	37,269,090	132	GGGAGTGGGAATTCTTTTATTTTA	TGCTTTCTTCTGGTGTCTCTGAA
D17Igc2	43,437,473	135	GCTCACTTTTTCCTAGCATCATC	GCCATGGGAAGAAGTTATATGTC
D17Igc3	49,224,144	146	GATAAGTTTGGAGTCAGGCCTAA	ACTTATTCACTCCTGAGCCTTGT
D17Igc4	46,068,767	158	TAGGGCCTTTGCCTGTTTAA	AGCTCACAATCACCTGTAACTCTT
D17Igc5	47,534,829	120	TGAGATGTGAAATGGATTCCC	TCAACCTGGGCTGTATAATGAGA
D17Igc6	51,573,350	139	ATACCCCACACACAATTCCAT	GGGAAAGTATTTGGTGATCAGAGA
D17Igc7	59,233,255	301	TATTTTGCCAGCCTCCAAGA	ACATGCCTATTTTTGTGGGC
D17Igc8	40,988,028	134	CCAAAGCATGTTAGAGGTAAGACA	TGAAGCCAATAAACATCCTAGGTT
D17Igc9	41,739,425	116	TGTACAGTGTTTTTGTTTGTGCA	TGAAGGTATGAACACTCAAGCAA
D17Igc10	43,177,843	115	GAATCTTGCTTTTGGCTTTGT	GGATTGGGTGAGATTCTAAACATT
D17Igc11	54,793,142	137	CTCAAAGTTTGTTTGGGTGTGT	AGGGTGAATGAAATAAAGTTCCA
D17Igc12	55,209,851	128	CTAATTCTAAGGCGGGTTTCTATC	TAAAGCACAAGGCAGGTATAGGA
D17Igc13	62,410,378	313	AAGTTTGAGAGACTGGCTTCAGA	TTCTTGGTACTTTAGGTTGGGAG

*Referred to the C57BL/6 allele.