SUPPLEMENTAL MATERIAL

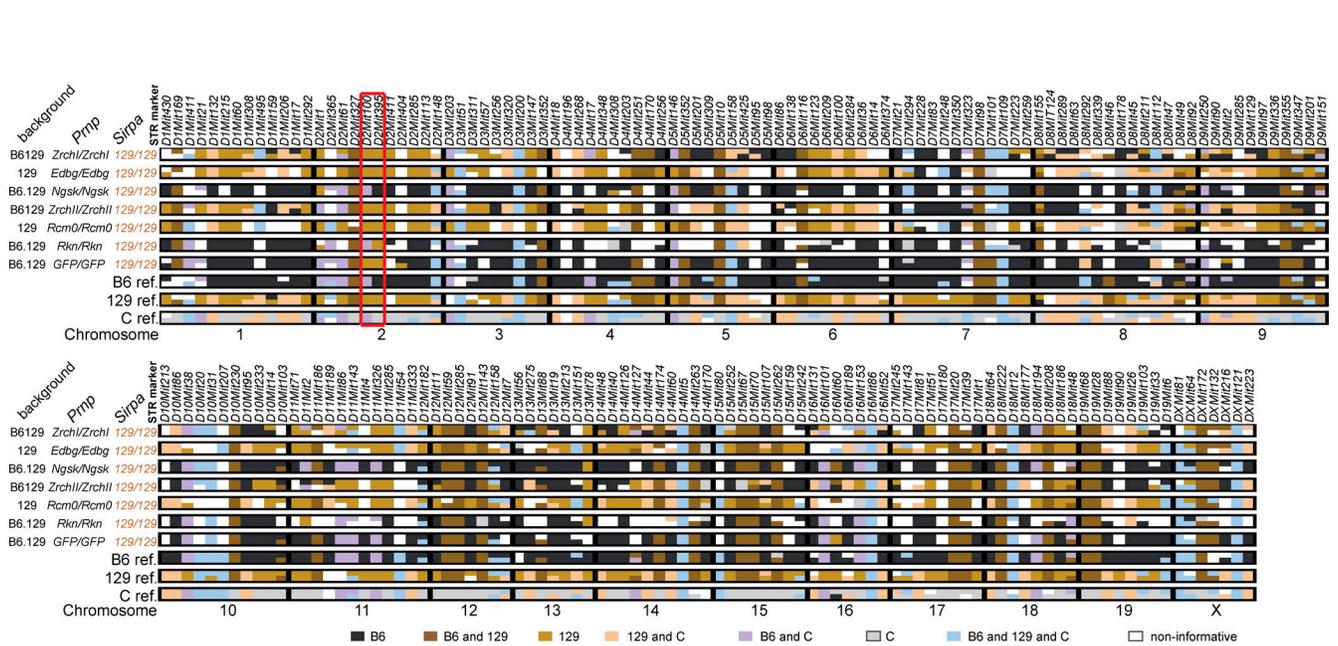**Nuvolone et al., http://www.jem.org/cgi/content/full/jem.20131274/DC1**

Figure S1. **Whole–genome STR analysis of the seven *Prnp*^{−/−} lines analyzed in this study.** The red border marks the region on Chr 2 containing *Prnp* and *Sirpa*. For each line, a representative mouse is shown. For heterozygous markers, the strain-defining color is arbitrary and not intended to designate a specific haplotype. Data show representative mice of at least three animals analyzed per group, except for *Prnp*^{Rcm0/Rcm0} and *Prnp*^{Rkn/Rkn}, for which one mouse was analyzed.
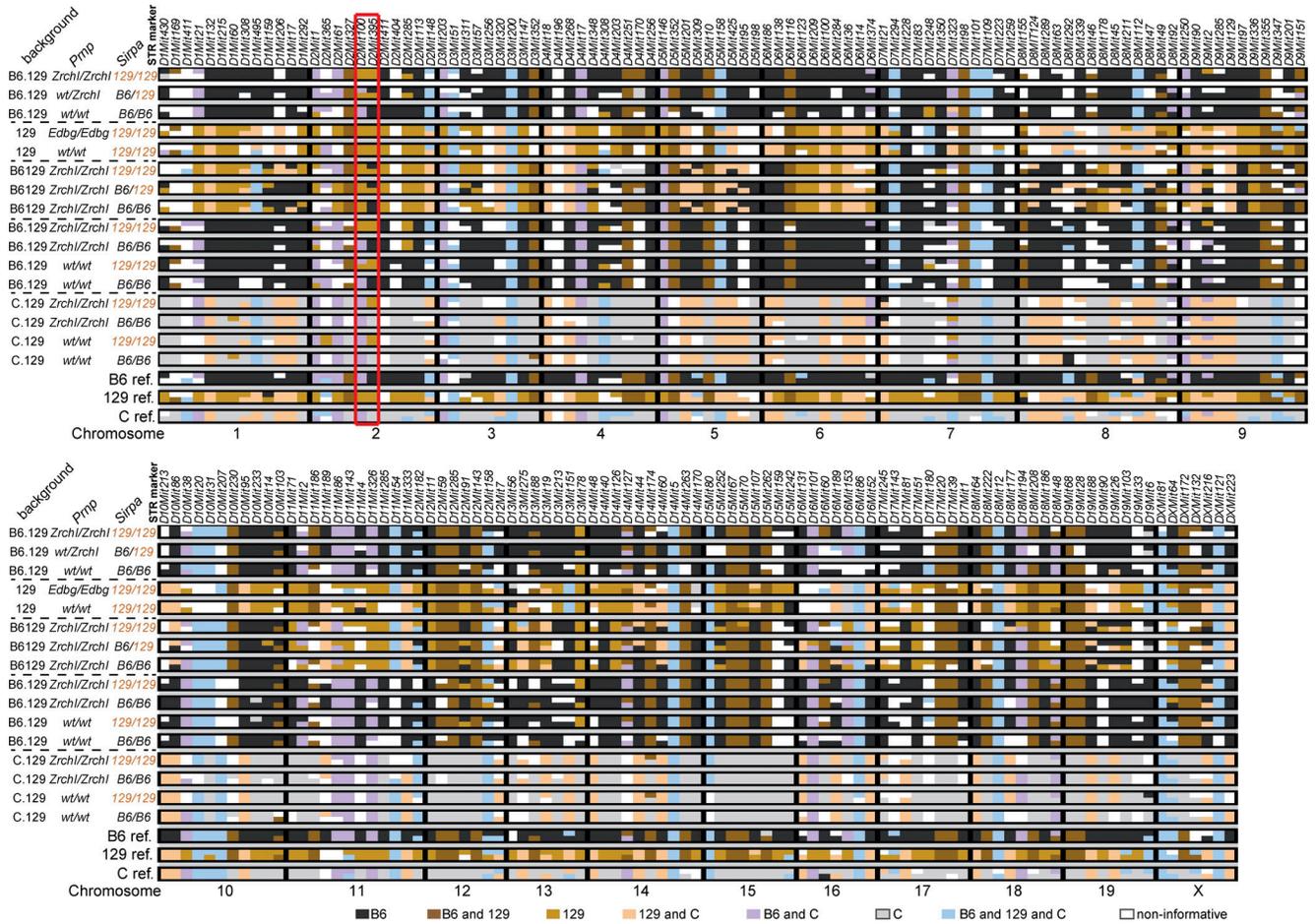
Figure S2. Whole–genome STR analysis of *Prnp^Zrchl/Zrchl*, *Prnp^Edbg/Edbg*, and control mice. The red box denotes the region on Chr 2 containing *Prnp* and *Sirpa*. Each line represents one mouse of strain shown at left. For heterozygous markers, the strain-defining color is arbitrary and not intended to designate a specific haplotype. Reference B6, 129, and C samples and 129-*Prnp^Edbg/Edbg* are the same as in Fig. S1. Data show representative mice of at least three animals analyzed per group.

Table S1, included as a separate PDF file, shows a list of 305 differentially expressed genes identified by RNA-Seq (P < 0.05), sorted by Log$_2$ fold change.

Table S2, included as a separate PDF file, shows genes containing nonsynonymous SNPs between B6.129-*Prnp*$^{wt/wt}$ and B6.129-*Prnp*$^{ZrchI/ZrchI}$ pMΦs sorted by chromosome location.

Table S3. Overview of allelotypes of the four candidate genes on Chr 2 linked to *Prnp* (*Sirpa*, *Mertk*, *Tyro3*, and *Thbs1*) in five *Prnp*-KO strains and congenic B6.129 mice with different combinations of *Prnp* and *Sirpa* alleles

Strain	*Prnp* chr2:131,909,927– 131,938,431	*Sirpa* chr2:129,592,838– 129,632,228	*Mertk* chr2:128,698,996– 128,802,188	*Tyro3* chr2:119,799,513– 119,818,103	*Thbs1* chr2:118,111,921– 118,127,133
Prnp$^{ZrchI/ZrchI}$	KO	129/129	129/129	129/129	129/129
Prnp$^{Ngsk/Ngsk}$	KO	129/129	129/129	B6/B6	B6/B6
Prnp$^{Edbg/Edbg}$	KO	129/129	129/129	129/129	129/129
Prnp$^{GFP/GFP}$	KO	129/129	129/129	129/129	129/129
Prnp$^{ZrchII/ZrchII}$	KO	129/129	129/129	129/129	129/129
B6.129-*Prnp*$^{ZrchI/ZrchI}$ *Sirpa*$^{129/129}$	KO	129/129	129/129	129/129	129/129
B6.129-*Prnp*$^{ZrchI/ZrchI}$ *Sirpa*$^{B6/B6}$	KO	B6/B6	B6/B6	B6/B6	B6/B6
B6.129-*Prnp*$^{wt/wt}$ *Sirpa*$^{129/129}$	WT	129/129	129/129	129/129	129/129
B6.129-*Prnp*$^{wt/wt}$ *Sirpa*$^{B6/B6}$	WT	B6/B6	B6/B6	B6/B6	B6/B6

Table S4. Primer sequences and restriction enzymes for RFLP analysis

Name/marker ID	Forward primer/primer 1	Reverse primer/primer 2	Restriction enzyme
For RFLP analysis of *Sirpa*			
RFLP *Sirpa* B6vs129	5′-CCGTTCTGAACTGCACTTTG-3′	5′-GGGGTGACATTACTGATACGG-3′	AvaI
RFLP *Sirpa* Cvs129	5′-ACAGAGGAGTAGGGCAAAGC-3′	5′-TAGGTACCGGCATCTTCTGG-3′	XmnI
For RFLP analysis of *Tyro3*			
RFLP *Tyro3* B6vs129	5′-GGGATTAAAGGATCCGGCCC-3′	5′-CACCTTCGACAGTGAGCCAT-3′	HpyCH4III
For RFLP analysis of *Thbs1*			
RFLP *Thbs1* B6vs129	5′-CTTGGGGGAAACTCCACACT-3′	5′-AAATCTTTCCAGCCGATGTG-3′	BseRI
For *Mertk* sequencing			
Mertk	5′-TGGTCTGCAGTAAGCCCTTG-3′	5′-AAGGTAAGCTCGATGGCTCG-3′	
For *Sirpa* ORF sequencing			
Sirpa-1	5′-AGTCCACCTTAAGAGGACCAAGTAGC-3′	5′-TGTACAGAAACAGGACGCGGA-3′	
Sirpa-2	5′-TCTCCCTCCTTGCTCTGCAG-3′	5′-TACCTCGCAGATGACCTTAGAATTAA-3′	
Sirpa-3	5′-CCTAGTGGAAAGAATGTCTCCTACAACA-3′	5′-CATATTCTGTGTGGTTGTTAGGCTCA-3′	
Sirpa-4	5′-CCAGGTACAGTCTTTGATCCAGGA-3′	5′-CCAGGGAGTCTCTGCTGGTCTA-3′	
Sirpa-5	5′-ACCCCAGGTTGCGTCCTTGA-3′	5′-GTGGGTGGTTTGCCCTGGCT-3′	
Sirpa-6	5′-CCAATGCTGACCTAATGTTGGC-3′	5′-CATCTATACACCCGTGTGTGTATACACA-3′	
Sirpa-7	5′-AACTTGTCTTTGTCCGGGCC-3′	5′-GGCACAGTTCATCCTCACCC-3′	
For high-resolution microsatellite genotyping on Chr 2			
D2Jyh582	5′-ACTAAGCCCAACACAGCCTT-3′	5′-GCCTACCATATGCAAGACCC-3′	
D2Jyh1192	5′-TCTCTTTGACTTTCACACATGC-3′	5′-CCCTGTGAGTGACAGAGGTATC-3′	
D2Gul161	5′-GTGGCTCTTTCTCCTGTTCC-3′	5′-GTATGCATGTATGTTTATGTGTGGT-3′	
D2Gul169	5′-TGCCTGAAGCTAACTACAGTGTAC-3′	5′-CATCATCATTATCAGAAGCATGTT-3′	
D2Ngul1543	5′-GATGTACAGAGGGCACTGCA-3′	5′-AGTCACCTATGTTGGATGTACCAC-3′	
D2Ngul1586	5′-ATGGGCTGATGATGTCACA-3′	5′-AGGTCCACATCCATACAGCA-3′	
D2Gul289	5′-GGGAACTGACTTAGATCCTAAAAGT-3′	5′-CTGGCACACAACCCCC-3′	
D2Ngul1677	5′-ACCTCCAAAGCAGAATCCTC-3′	5′-TCCACACTCTAAAGGGATCAAG-3′	
D2Ngul1686	5′-CTCGAGAGTACATACGCATGC-3′	5′-AGCAAGACACCTGATAGTACGTG-3′	
D2Ngul1761	5′-TGTGGAGCAGGTGACGTC-3′	5′-AGCCTCACCTCATGAAAGCT-3′	
D2Ngul1797	5′-TTTCCCCAAAACCAGCAT-3′	5′-GATTTCTTTCCATTCCCCAA-3′	
D2Ngul1816	5′-ACTGTTGTGGCCAAAATGG-3′	5′-CCTGCACAGTCTTTGTTGTTG-3′	
D2Ngul1849	5′-AGGTGAAGGGTTATTTCTGGAC-3′	5′-CCAGGACAGCTTCTAGTAGTGTCT-3′	
D2Ngul1865	5′-TTAAACAGGAATTCTTTCAACATTT-3′	5′-ATAAGCTGTGCTCTGGCCTT-3′	
D2Ngul1888	5′-ACCACTTCGATATCATTGGGA-3′	5′-GCCCTGCAAACACTAAATCA-3′	
D2Ngul1937	5′-GCTCATGTCCTTCCAAGAATG-3′	5′-GGGAAGAAGAGGAAGGAATTG-3′	
D2Jyh2400	5′-GCAATACCTCCAGCAATTTGT-3′	5′-CCATCCTACCAAAAGTAATCCA-3′	
D2Jyh2407	5′-CAGTGAGACCCTGTCTCAAAA-3′	5′-CTGCCTTCCTAGAGCTGTCTT-3′	
D2Gul374	5′-ATGACTTAAGCATTTTAAGCCAAA-3′	5′-CCCCCCAACTTTAAACACA-3′	
D2Gul399	5′-CAGCAGGTAAGAGCCCTTG-3′	5′-TGAAATTATTTTTGTCCTTTTTTGT-3′	
D2Gul498	5′-GACCCTGCAGATCTCAGCA-3′	5′-CATTTTTCTAATCATTTATGTCTTATGTG-3′	