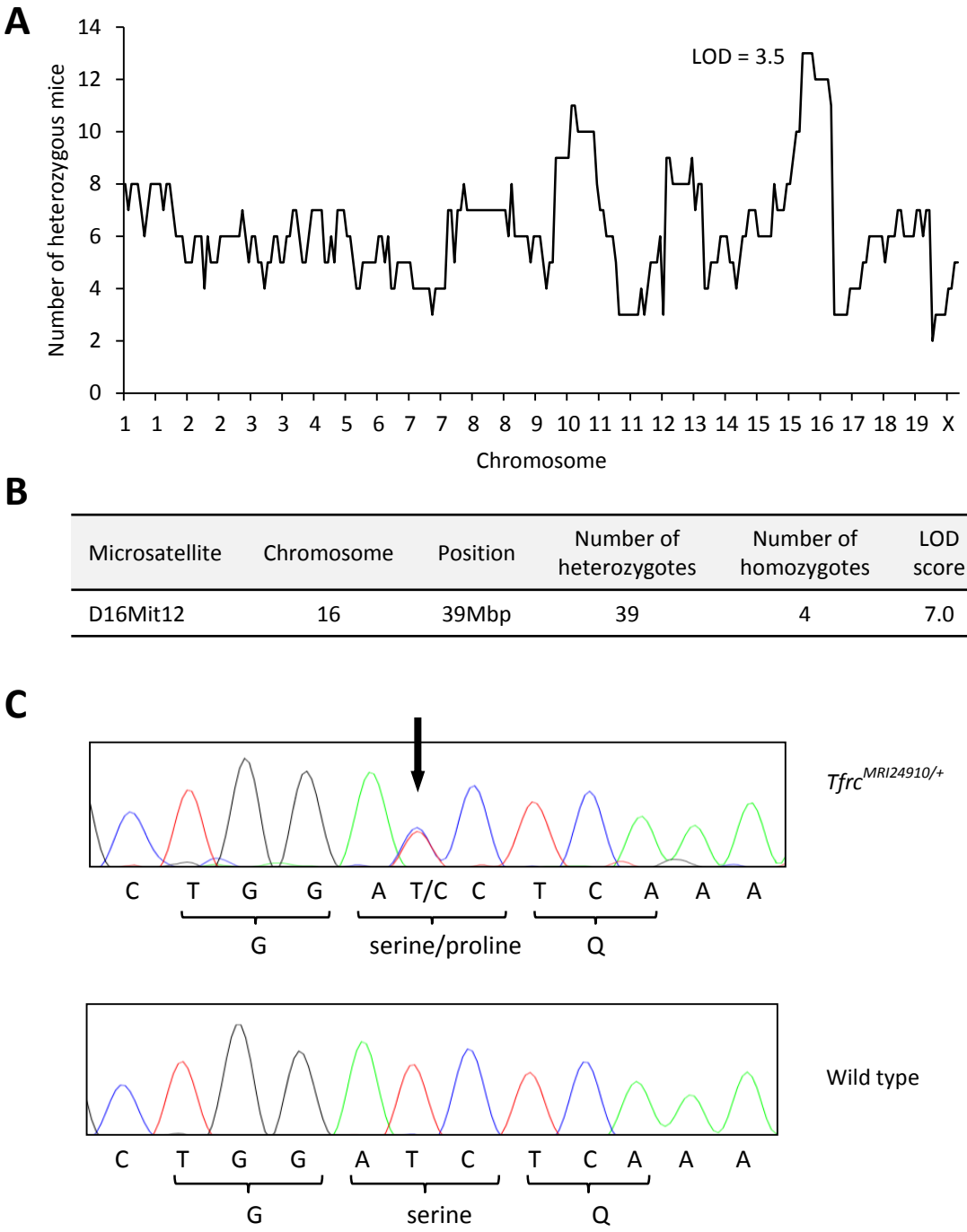


Microsatellite	Chromosome	Position	Number of heterozygotes	Number of homozygotes	LOD score
D16Mit12	16	39Mbp	39	4	7.0

Figure S1. Mapping of the MRI24910 mutation causing microcytosis. Heterozygosity of 13 microcytic N2 mice (MCV < 48 fL) indicates a linkage peak on chromosome 16 between 7Mbp and 67Mbp (A). The interval was confirmed in 43 additional microcytic N2 mice using the microsatellite marker D16Mit12 (B). *Tfrc* was selected as a candidate gene within this interval as it is known to cause a phenotype similar to that reported here. Sanger sequencing of all *Tfrc* exons revealed a T to C heterozygous mutation in exon 5, indicated with an arrow, resulting in a serine to proline amino acid substitution (C). LOD score was calculated using a chi squared test based on the expected number of heterozygotes.

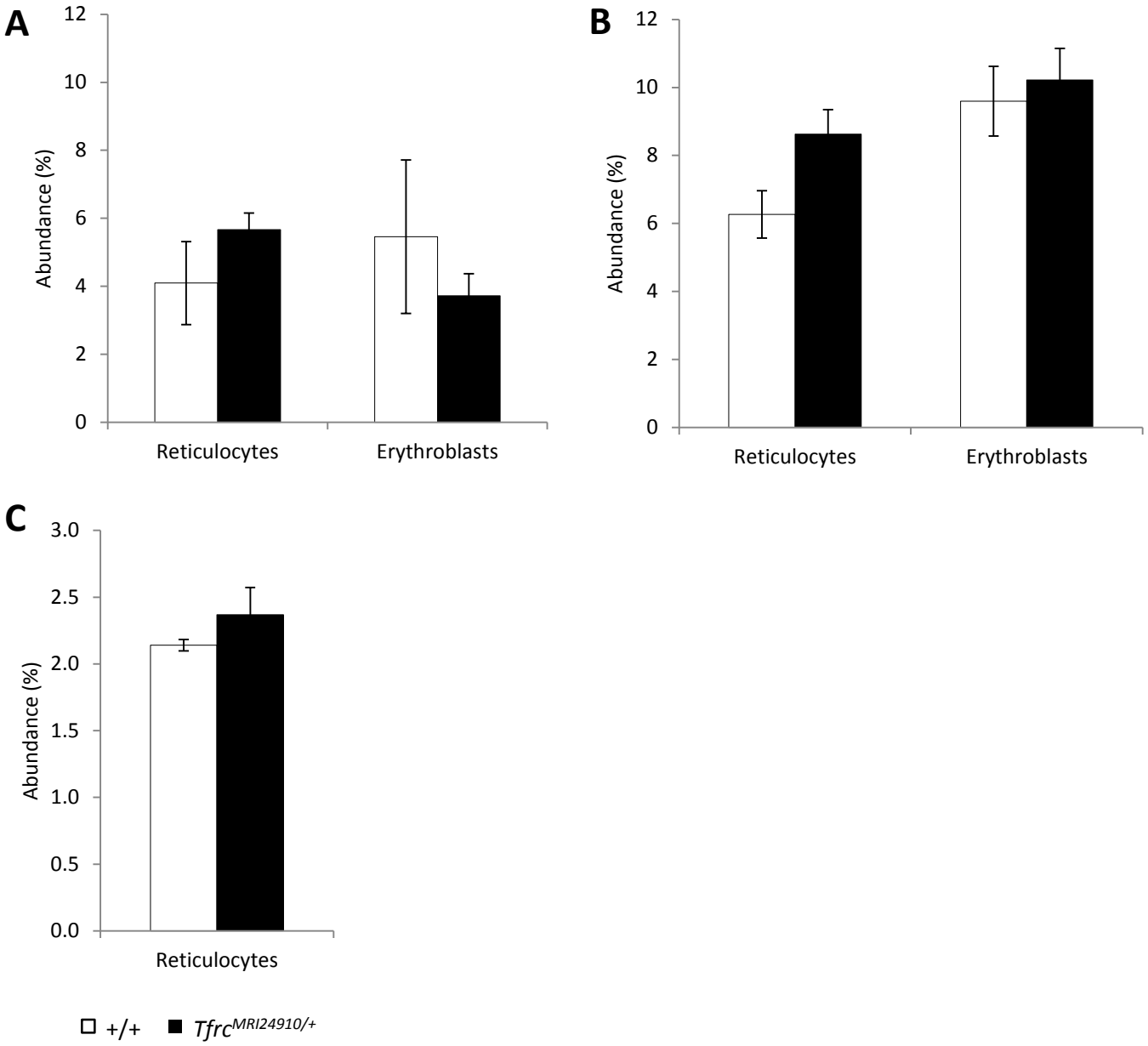
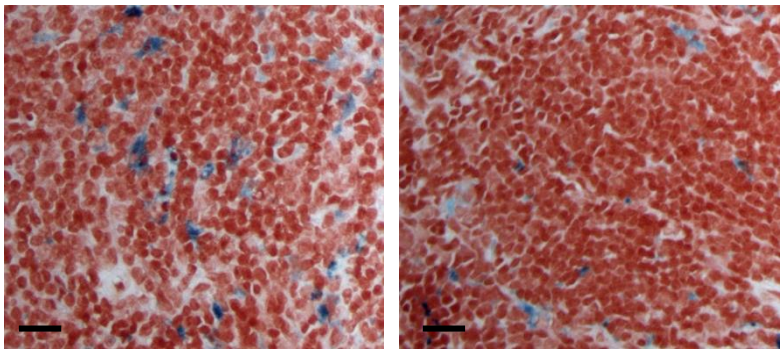


Figure S2. Erythroblast and reticulocyte levels in *Tfrc*$^{MRI24910/+}$. Reticulocytes and erythroblasts in the spleen, identified as in Figure 2, in uninfected (A), and day 10 infected mice (B). Reticulocytes in the peripheral blood of uninfected mice as determined by positive staining with anti-CD71(Tfr1) using flow cytometry (C). Error bars indicate SEM, data is from 4 mice per group for spleen reticulocyte and erythroblast abundance, and 7-8 mice per group for peripheral blood reticulocyte abundance.



+/+ *Tfrc*$^{MRI24910/+}$

Figure S3. Spleen histological sections. Spleen sections from uninfected wild type and *Tfrc*$^{MRI24910/+}$ mice stained with Perls' Prussian blue. 200 x magnification, scale bar is 10µM