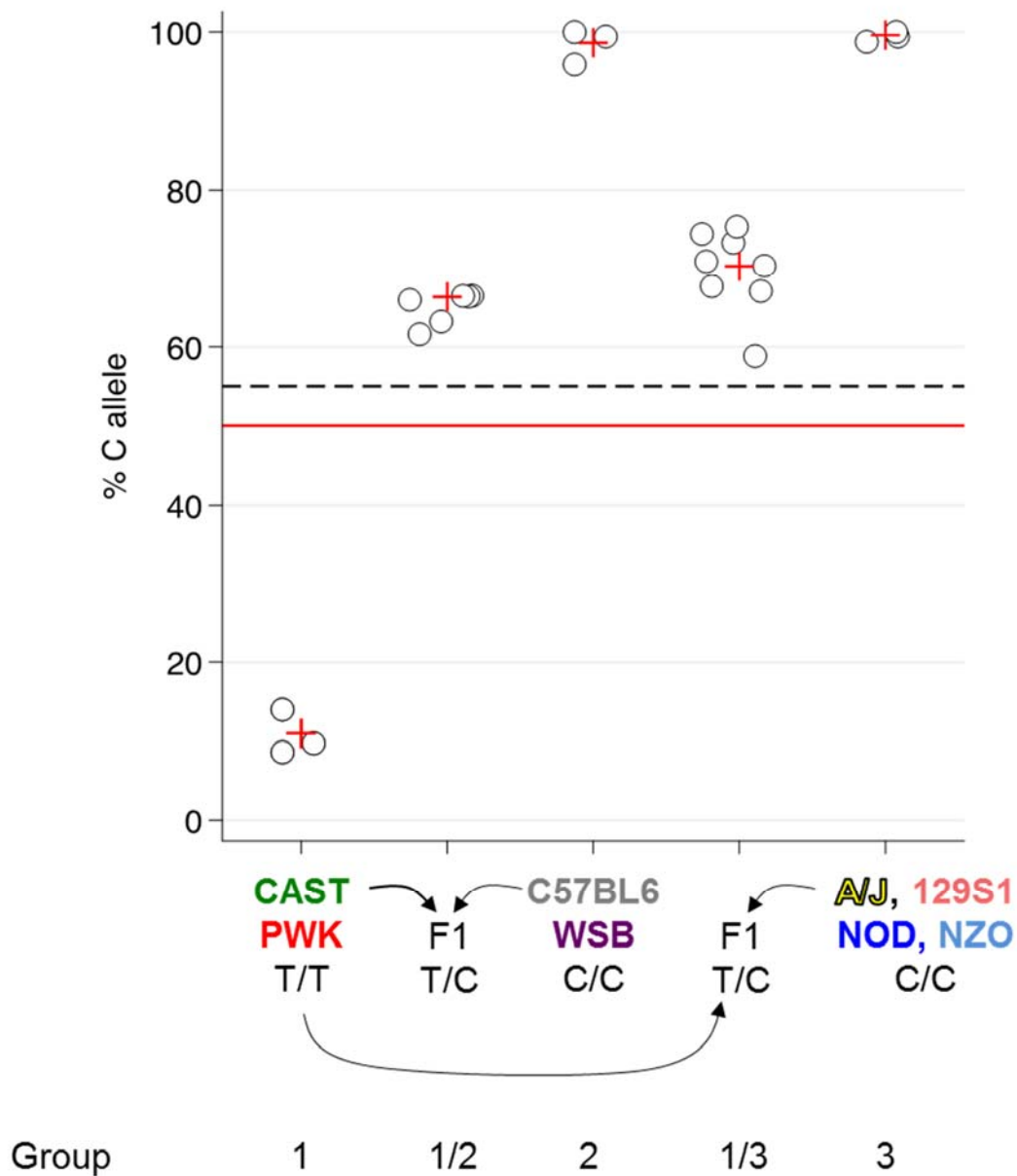**Figure S1** *Zfp30* **gene expression measured by microarray and qRT-PCR is strongly correlated.** Data points represent the mean of 2-4 mice per CC founder strain and are color coded as in Figure 1. Dashed red line represents linear fit of data. R^2 = 0.85 (p = 0.001).

Figure S2 Allele-specific gene expression of *Zfp30*. Expression of alternate alleles of rs45830063 (C/T) was measured using pyro-sequencing on whole lung cDNA samples from CC founder lines (n=3/group) and F1 heterozygotes from crosses of CC founder lines from each *Zfp30* expression group (n=6-8/group). Strain groups on X-axis correspond to gene expression groups identified in Figure 4. Plus symbols denote mean. Dashed black line indicates mean of T/T and C/C homozygotes (55%). Both groups of F1 heterozygotes (1/2 and 1/3) express significantly higher levels of the C allele than T allele (>55%, one sided t-test *p*-value < 1 x 10^-4) and Group 1/3 heterozygotes express higher levels of the C allele than Group 1/2 heterozygotes (70% vs. 66%, one sided t-test *p*-value = 0.04).

Concordant and Discordant SNPs in *Ztp30* (ENSMUST00000032803)
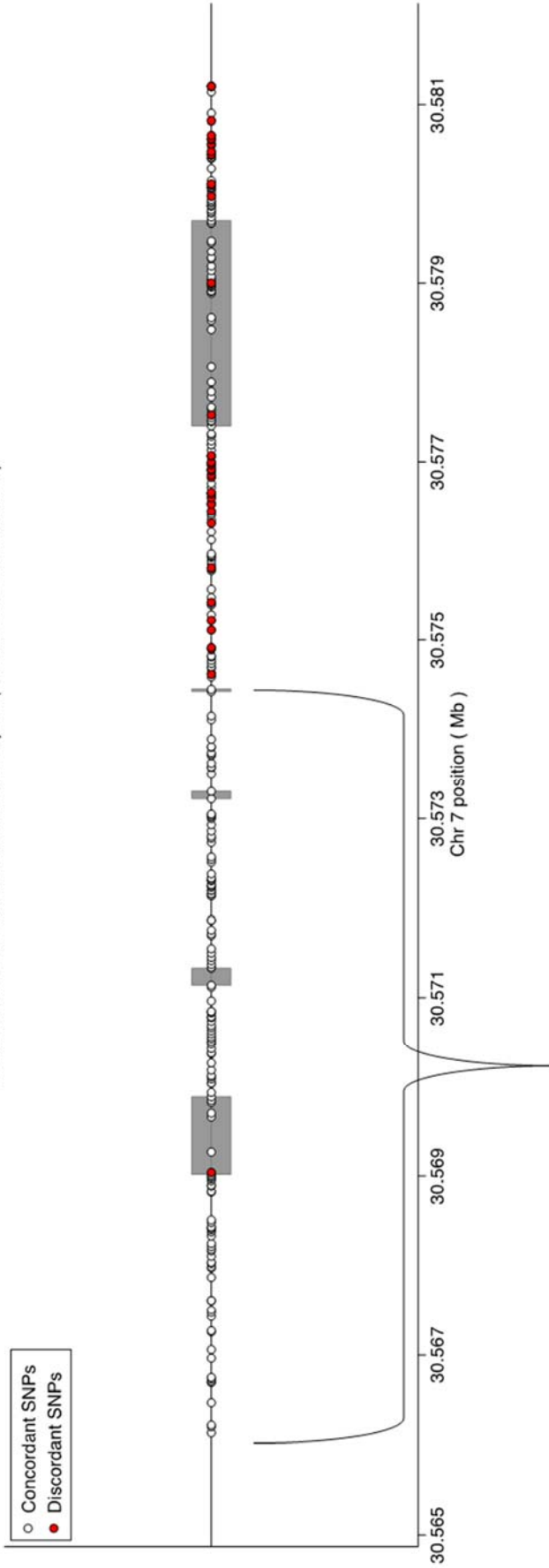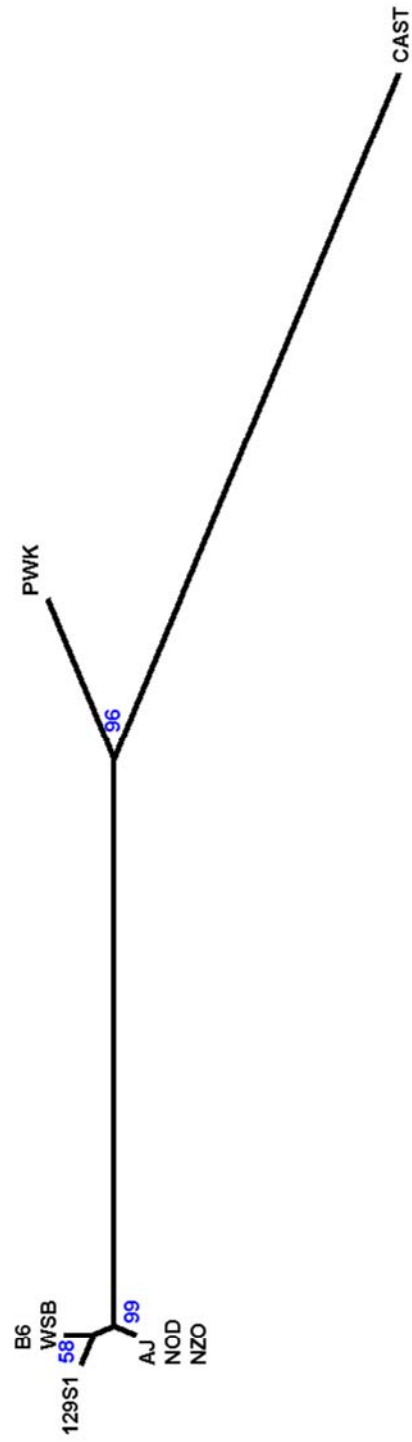
Figure S3 SNPs and haplotypes among CC founder strains at the *Zfp30* locus. A. SNPs (n = 242 SNPs) in *Zfp30* including 3kb of upstream and 1.5 kb of downstream sequence (30,566,017-30,581,221 bp) that are concordant (white circles) or discordant (red circles) with the pattern of gene expression shown in Figure 4. Gray boxes denote exons. **B.** Phylogeny of CC founder haplotypes for *Zfp30* sequence up to exon 4. Blue numbers indicate bootstrap support values.

File S1

Genotype Data. Genotype calls for preCC mice.

Available for download as a .gz file at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.168138/-/DC1

Tables S1-S4

Available for download at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.168138/-/DC1

Table S1   Phenotype data for CC founder strains and preCC mice

Table S2   Chr 7 Genotypes, *Zfp30* Expression Groups and Frequencies Used in Narrow Sense Heritability Regression Models and Structural Equation Models

Table S3   Genes with local eQTL in the PMN/CXCL1 QTL confidence interval on Chr 7.

Table S4   Potential Causal Variants for the *Zfp30* eQTL.