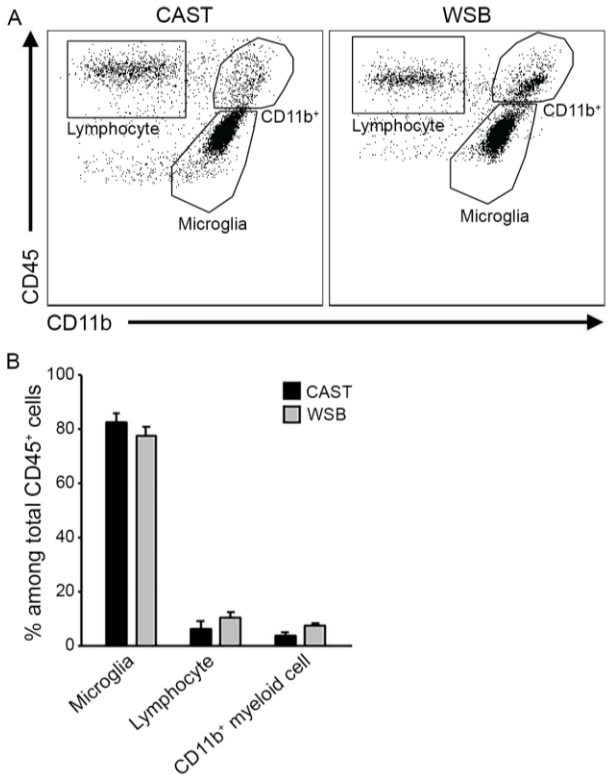
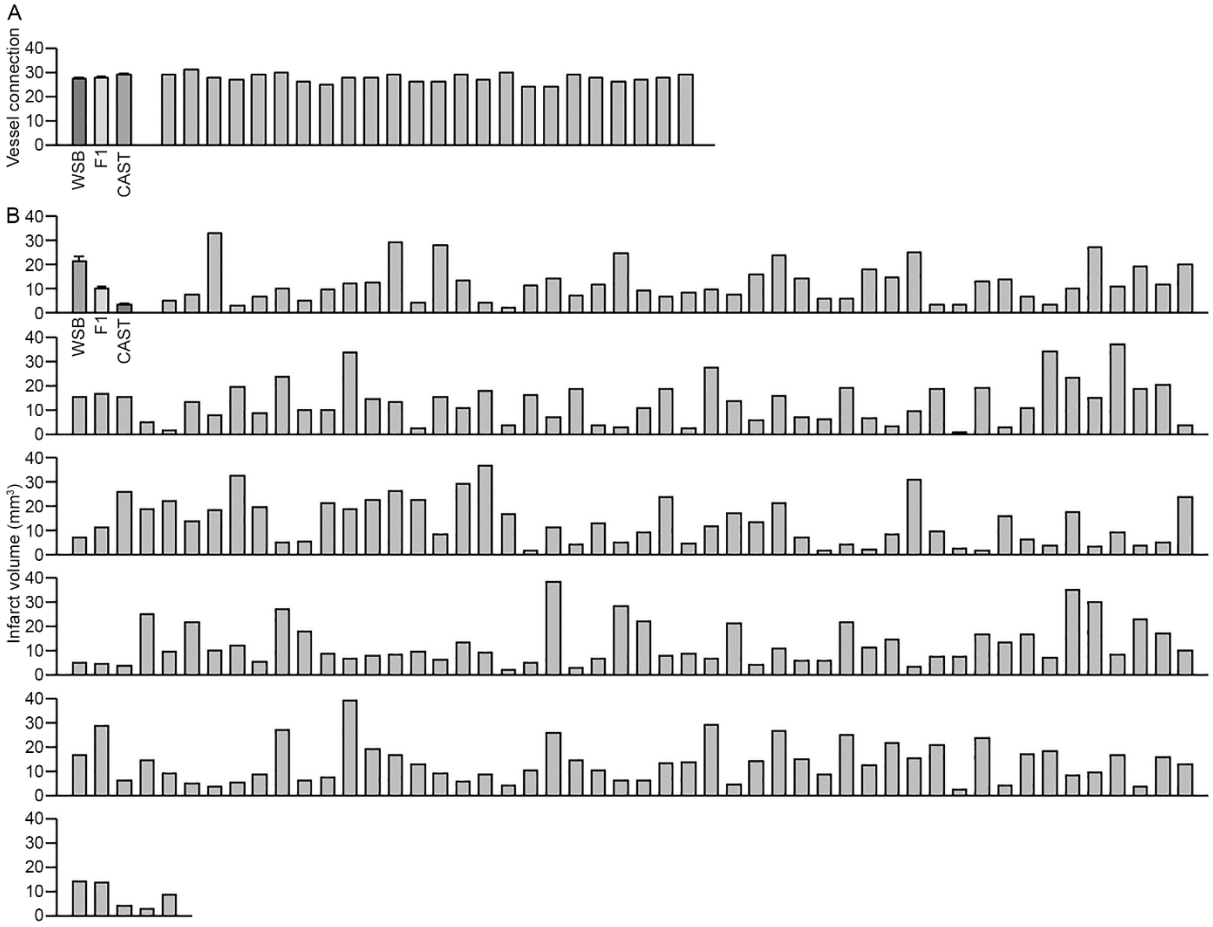
Figure S1



Flow cytometric analysis of CD45$^+$ hematopoietic cells in the cerebral cortex of CAST and WSB mice. (A) The representative dot plots show the major cell types among CD45$^+$ hematopoietic cells in the brain cortex. **(B)** The graph shows levels of CD45$^+$ hematopoietic cells from the brain cortex of CAST and WSB mice. Data represent the mean ± SEM. No statistical significance was found in any cell type between CAST (n=3) and WSB (n=6), using 2-way ANOVA followed by Bonferroni's test.

Figure S2



Difference in phenotype distribution for collateral vessel density and infarct volume phenotypes for F2 (CAST x WSB) intercross progeny. (A) The graph displays the average number of collateral vessel connection between the ACA and MCA for two parental strains, WSB and CAST, and for individual F1 and intercross progeny. The total number of animals for WSB, F1, and CAST were 13, 18, and 32, respectively, and 24 representative F2 individual mice are shown. Data represent the mean ± SEM. **(B)** The graph shows the average infarct volume for the two parental strains, WSB and CAST, as well as for F1 animals. The total number of animals for WSB, F1, and CAST was 18, 14,

and 32, respectively. Data represent the mean ± SEM. Infarct volume for 251 individual F2 animals is shown.

Table S1

Genotype and phenotype information of 251 F2 (CAST x WSB) animals used for QTL mapping.

Table S2

Genes mapping within one of the four loci that harbor coding SNP differences between CAST and WSB. The table shows all non-synonymous coding SNPs between CAST and WSB for 191 genes mapping within each of the four loci. The functional consequences on protein function for each coding SNP was predicted using 3 independents *in silico* algorithms, SIFT, PolyPhen-2, and Provean. Coding SNP predicted to be “damaging” are highlighted in red.

Table S3

Genes mapping within one of the four loci that show strain-specific differential gene expression between CAST and WSB. For each of the 220 genes, the table displays the fold change, with either a negative value or positive value for higher expression for the CAST or WSB allele, respectively.