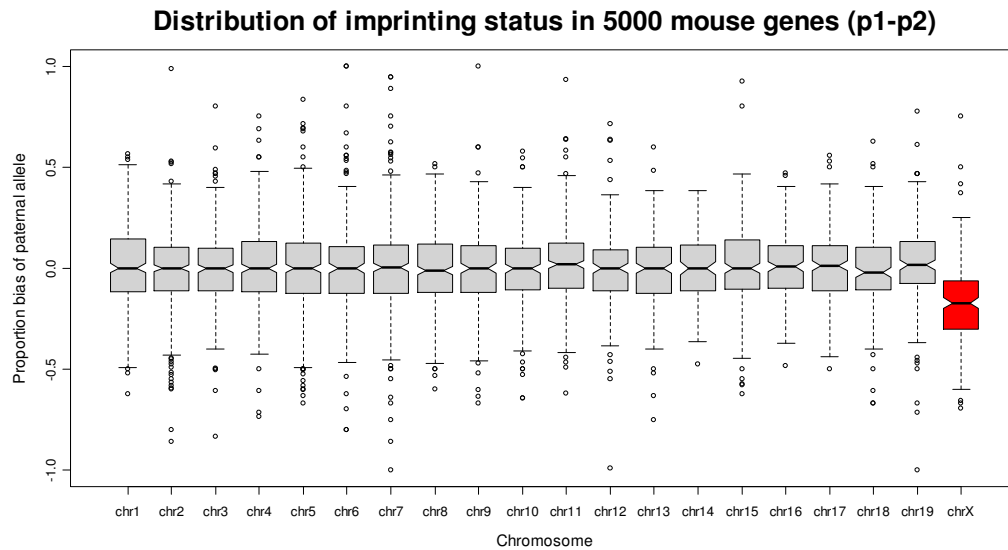
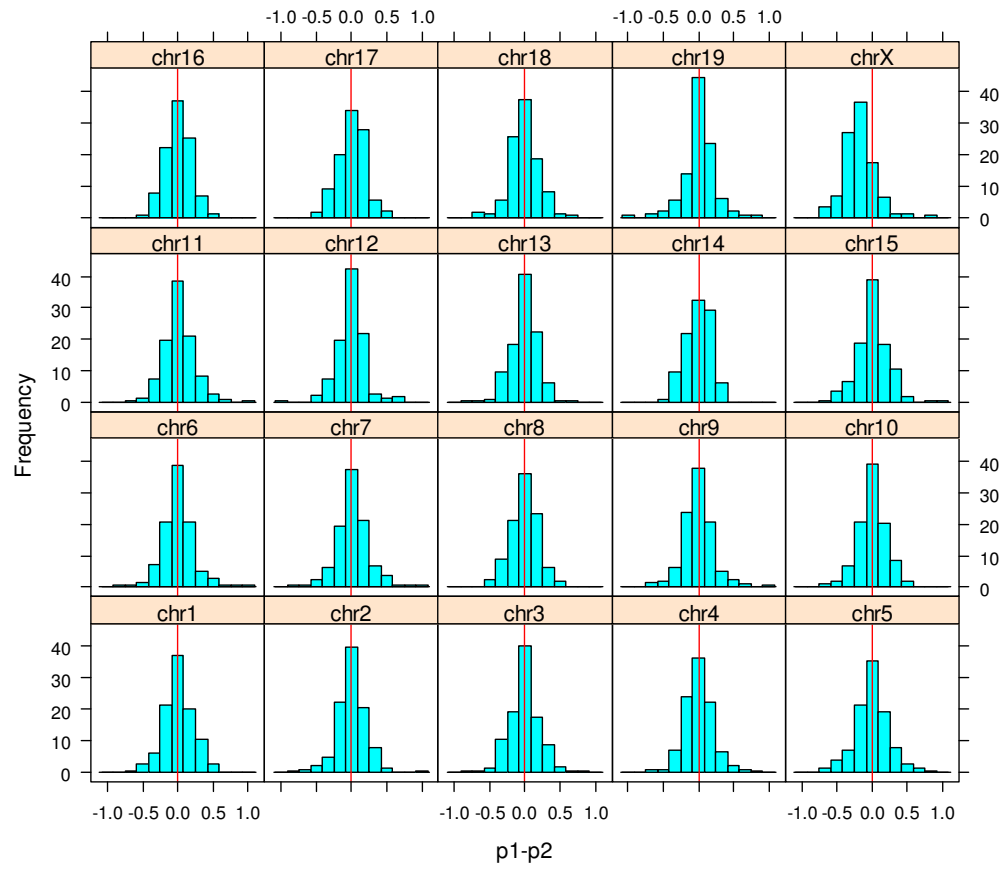


Figure S1. Distribution of imprinting status of 5000 genes covered by the RNA-seq study.



A. Boxplot of the imprinting status for autosomes and the X chromosome. The Y axis is proportion bias from the paternal allele (p1-p2). From the plot, for all autosomes, the mean is very close to zero. However, the mean for X chromosome is -0.17, which indicate a 17% maternal bias in allele-specific expression. The difference between X and autosome is extremely significant from non-parametric statistical test of distributions. So this is a chromosome-wide effect, rather than effect of single imprinted genes.

**Distribution of imprinting status in 5000 mouse genes (p1-p2)**



**B. Histogram of the imprinting status for autosomes and the X chromosome.**