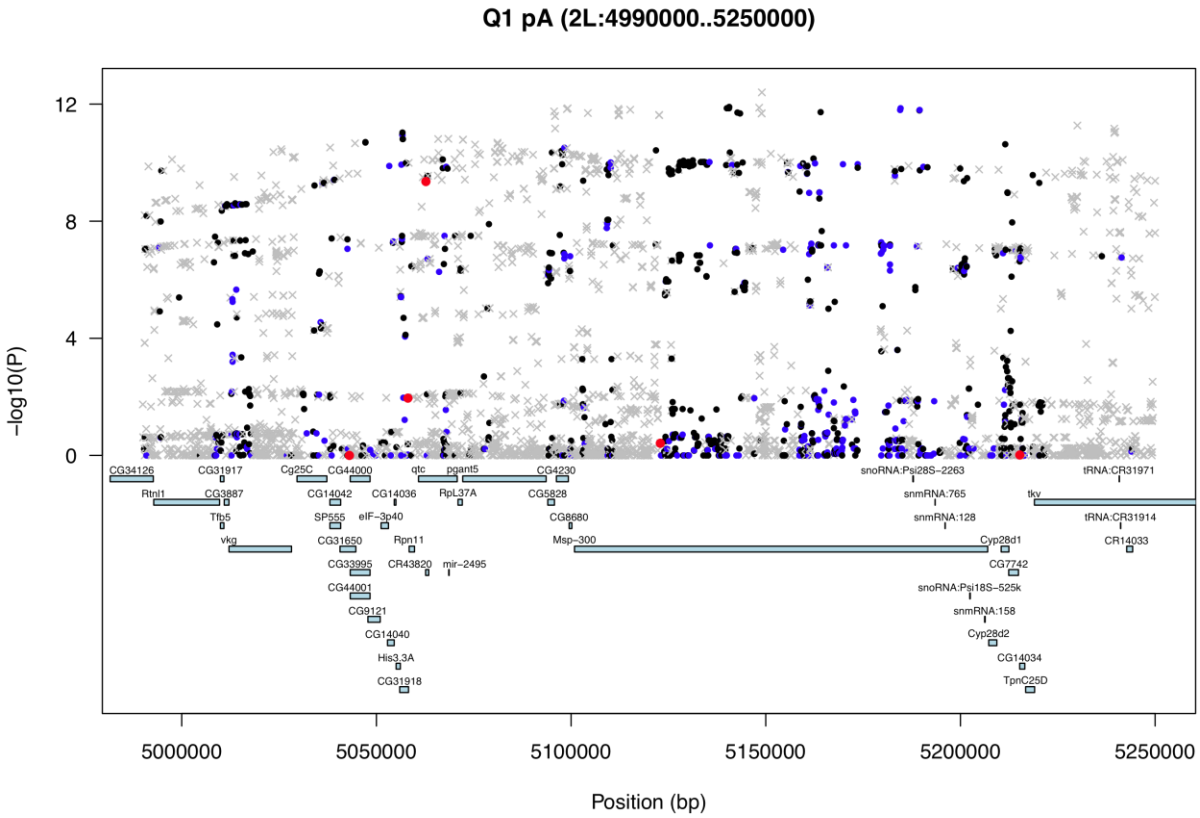

Figure S2 Association tests at SNPs residing beneath all four mapped QTL for nicotine resistance (Q1, Q2, Q3, and Q4 mapped in pA, and Q4 only mapped in pB). SNP genotypes in RILs were inferred from the mosaic founder haplotype structure of each RIL. The $-\log_{10}(p)$ value is plotted for each segregating site, with the plot symbol reflecting the impact of the variant: Red filled circles (loss of a start codon, loss or gain of a stop codon, changes in splice sites), blue filled circles (nonsynonymous changes), black filled circles (synonymous changes), and gray crosses (all other variants). The position of each gene within each QTL is shown as a light blue box, with the width of each box showing the distance from the start to the end of the gene model. Note that due to the number of genes under Q3, no gene names are provided for this plot. Note also the absence of tested variants at ~15,600-kb in the Q3 plot; This is due to a large array of 5S rRNA genes that likely precluded high-quality SNP identification in this region.

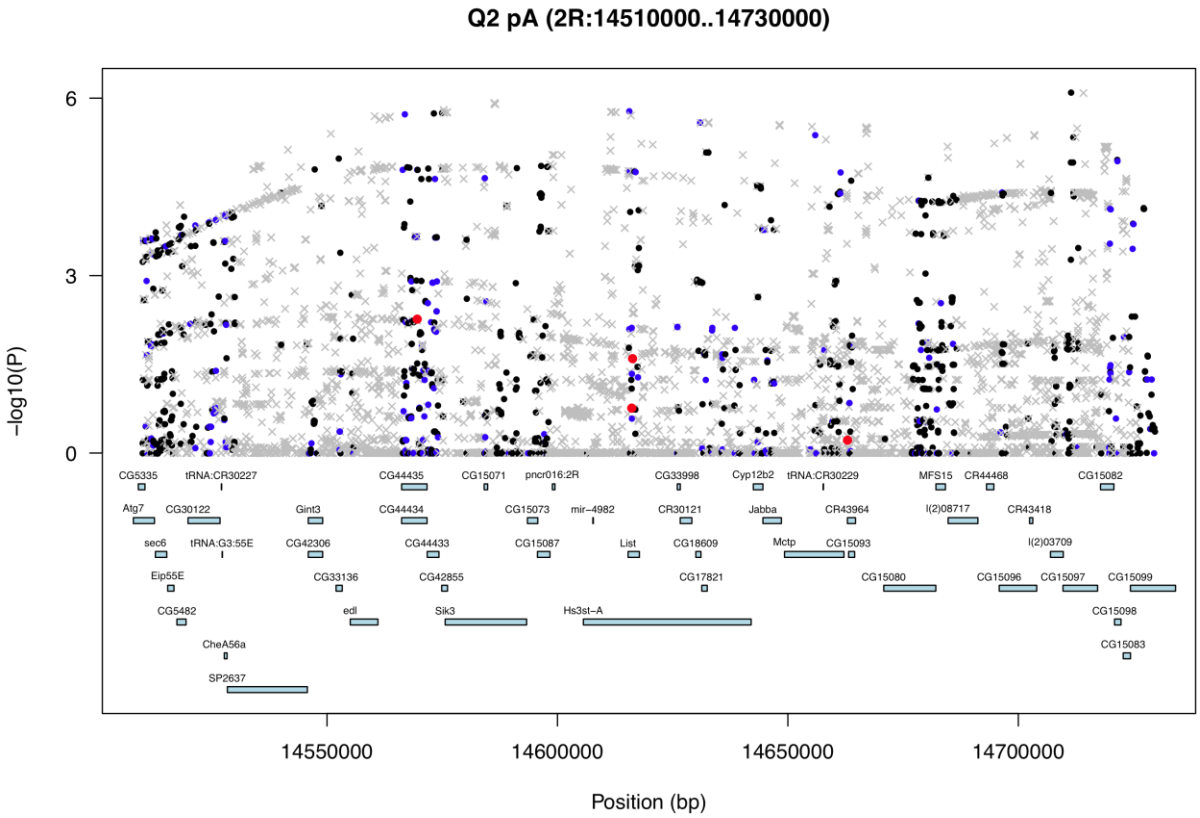

Figure S2 Continued.

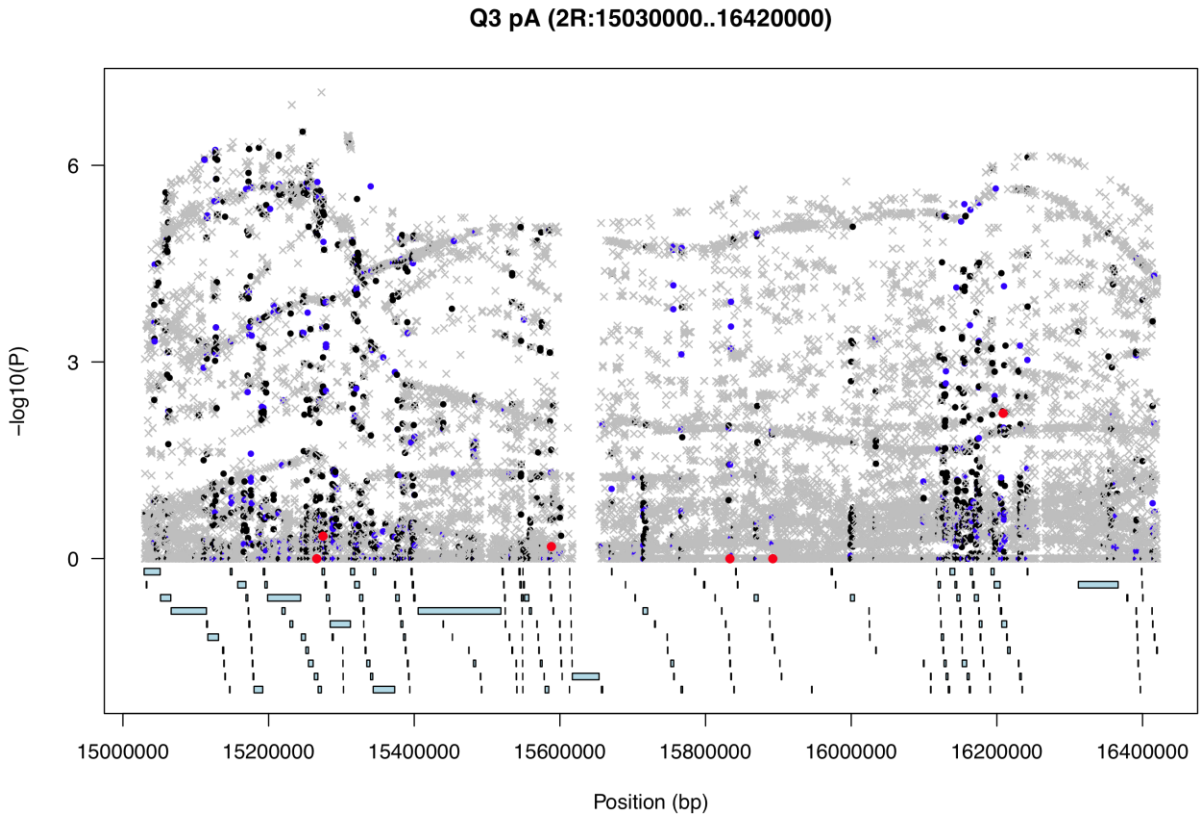

Figure S2 Continued.

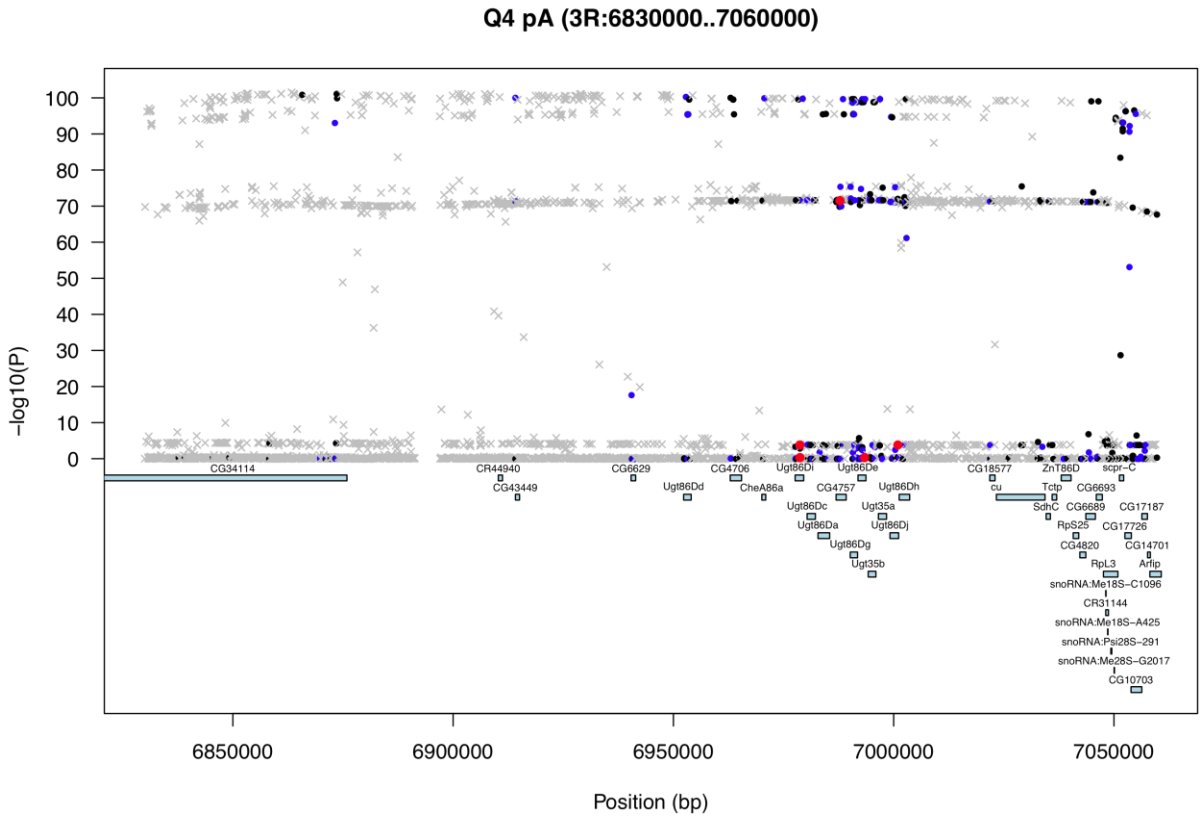

Figure S2 Continued.

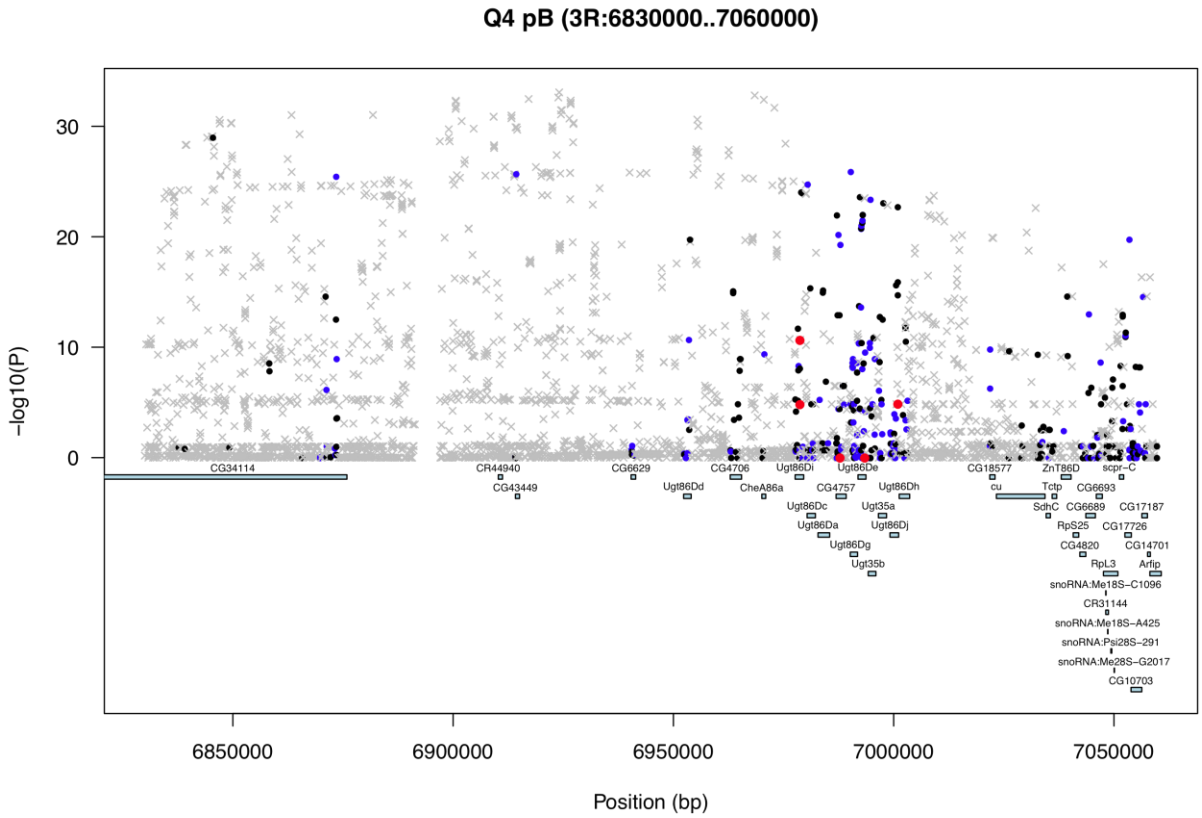

Figure S2 Continued.