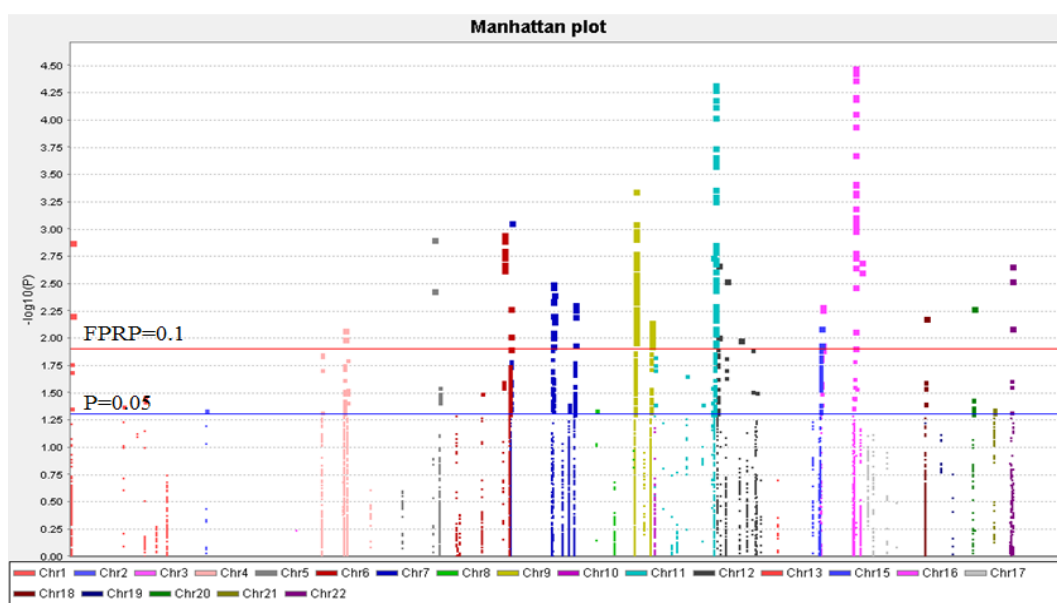
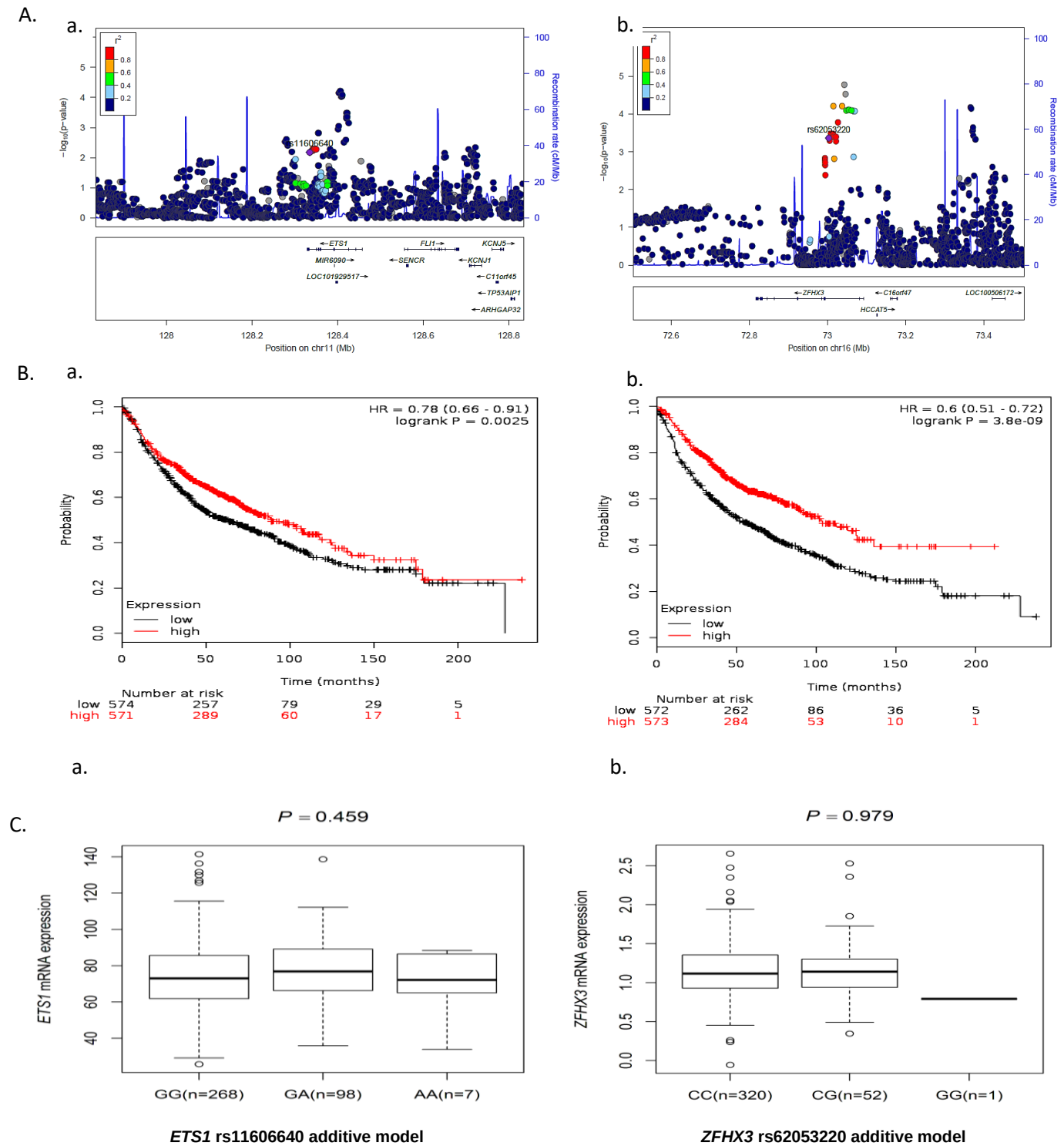




Supplementary Figure 1. Manhattan plot of 8587 SNPs of the c-Myb pathway genes in the PLCO trial. The statistical values across the autosomes for associations between 8587 SNPs and overall survival are plotted as $-\log_{10} P$ values. The blue horizontal line indicates $P = 0.05$ and the red line indicates FPRP = 0.10.



Supplementary Figure 2. A. Regional association plots. B. Kaplan-Meier analysis for patients with NSCLC by the two genes. C. Correlations between the two validated SNPs and mRNA expression levels of the associated genes by using the data of 373 European descents in the 1000 Genomes project.

A. The left-hand Y-axis shows the $-\log_{10}$ transformation of P -value of individual SNPs, which is plotted against the chromosomal base-pair position with an expansion of 500 KB in the flanks of the gene region. The right-hand Y-axis shows the recombination rate estimated for European populations from HapMap Data Rel 22/phase II. **a.** *ETS1* rs11606640; **b.** *ZFH3* rs62053220. **B.** Based on online survival analysis software (www.kmplot.com/analysis), **a.** low *ETS1* expression were associated with poorer survival of NSCLC; **b.** low *ZFH3* expression were associated with poorer survival of NSCLC. **C. a.** *ETS1* rs11606640 in an additive model, ($P = 0.459$); **b.** *ZFH3* rs62053220 in an additive model, ($P = 0.979$).