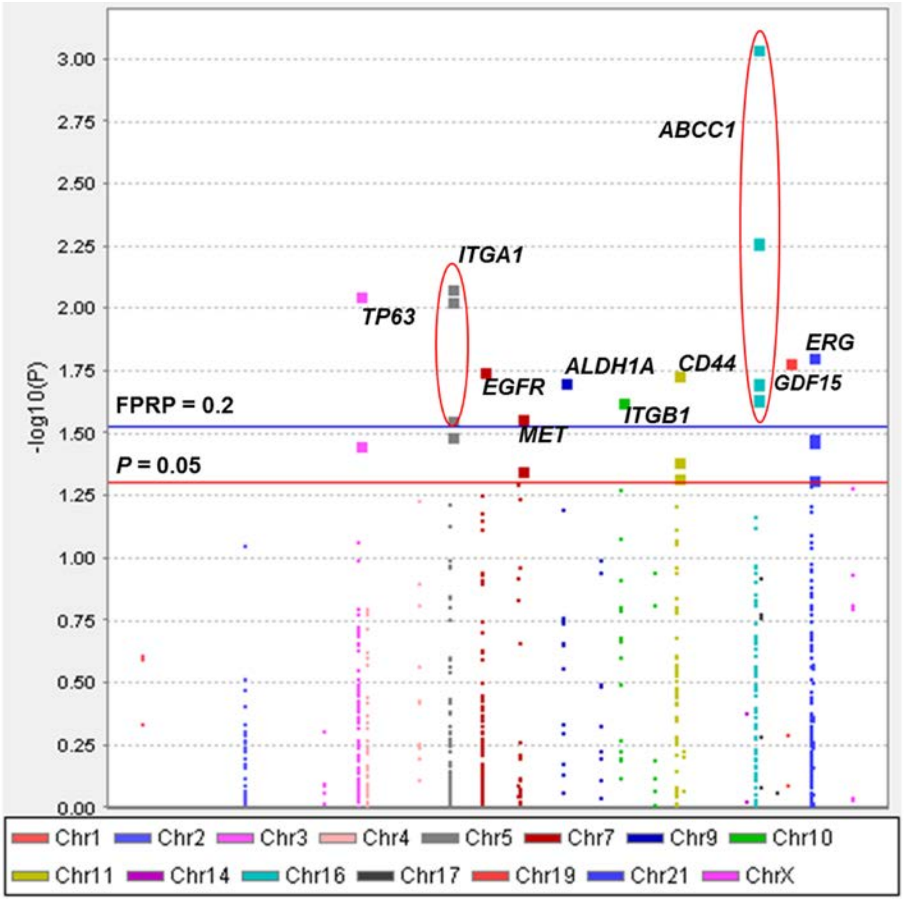
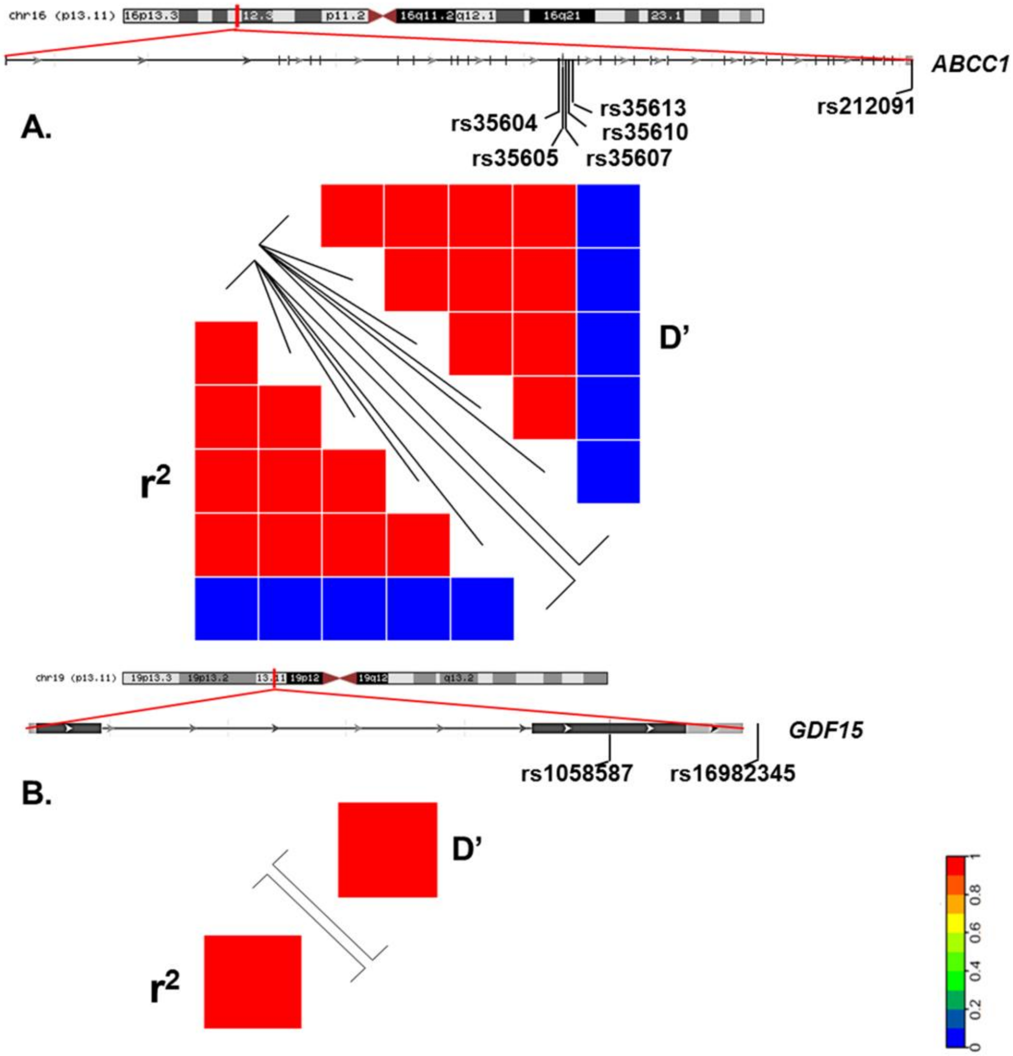
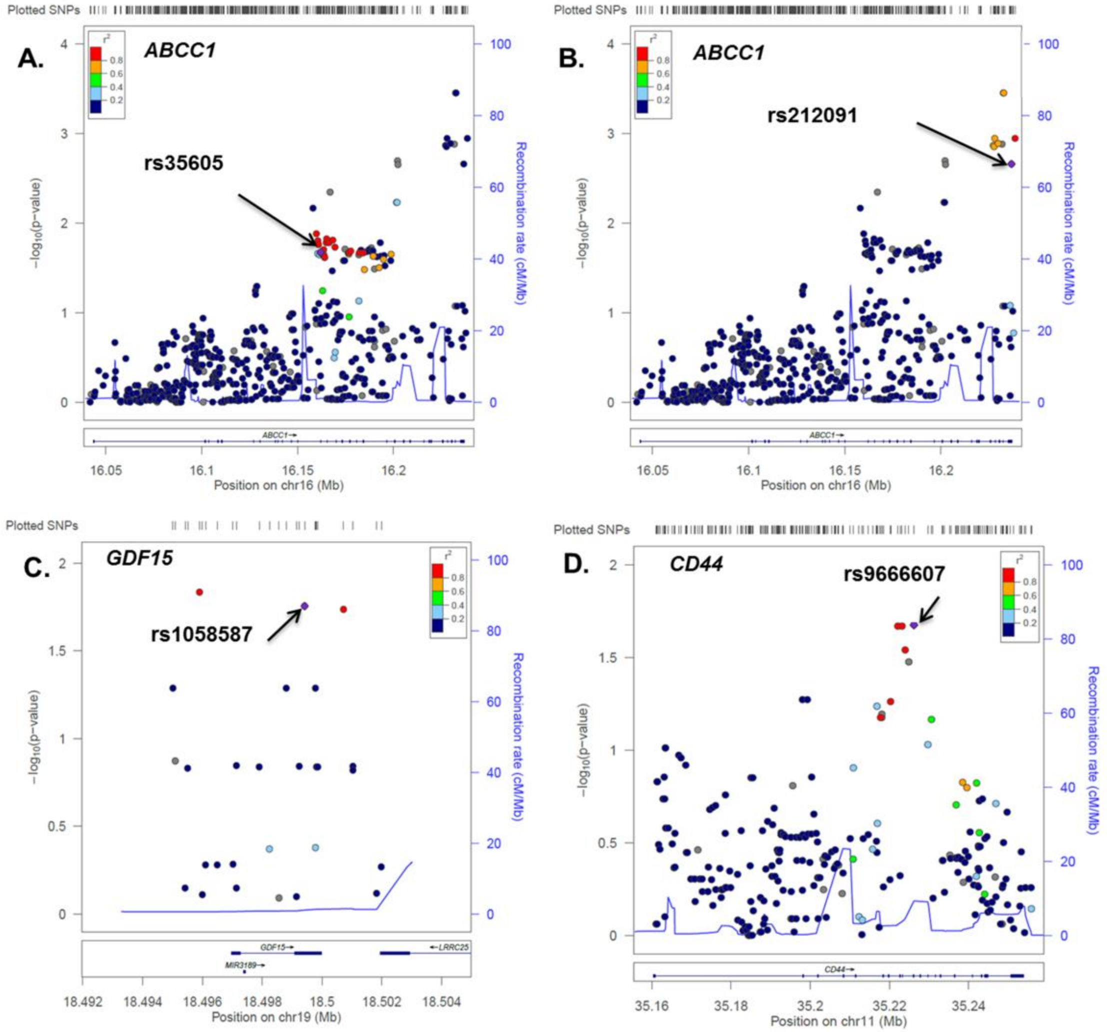
Supplementary Figure S1: Manhattan plot of the genotyped data from the PLCO study. The statistical values across the chromosomes of association between 635 SNPs in 25 genes and prostate cancer overall survival are plotted as −log10 *P* values. The red horizontal line indicates *P* = 0.05 and the blue line indicates false positive report probability (FPRP) = 0.2.



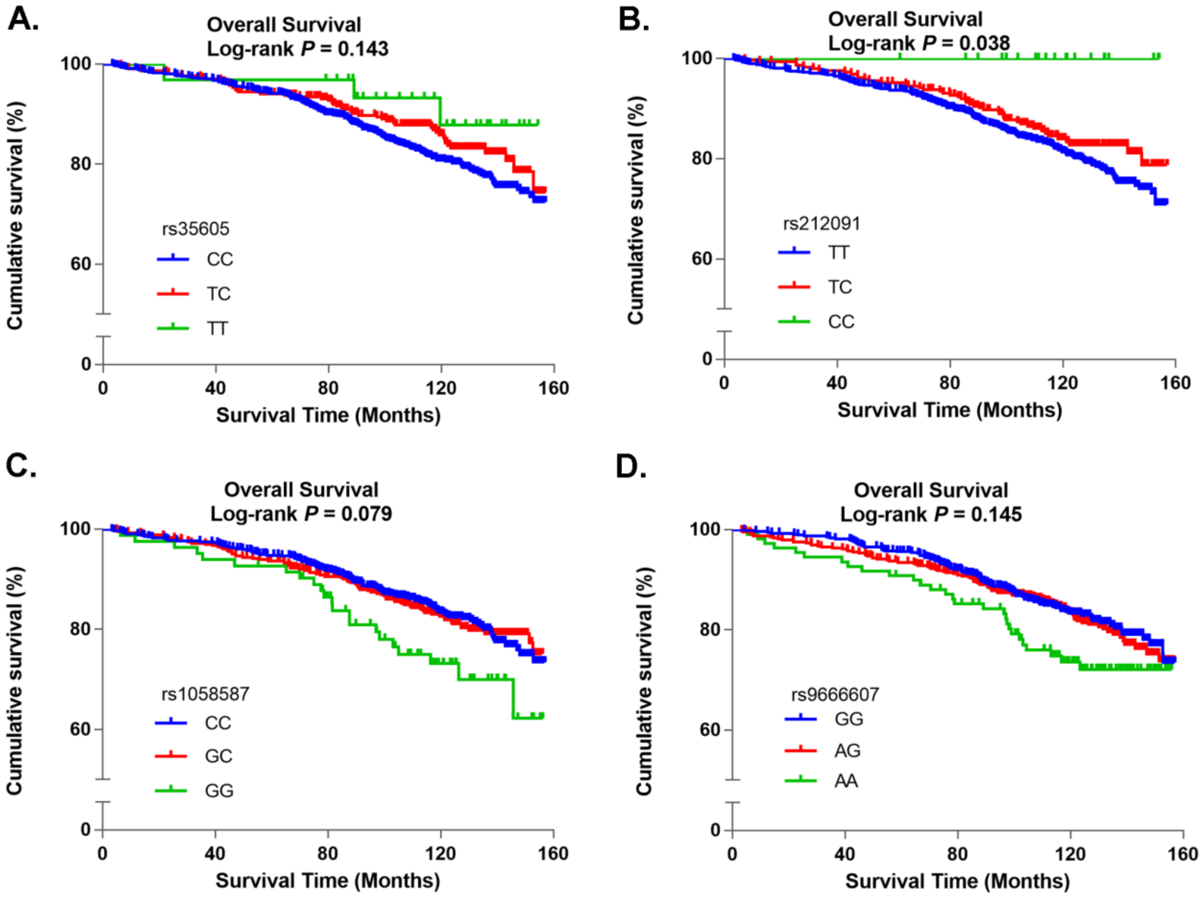
Supplementary Figure S2: Linkage disequilibrium plots of the selected SNPs on *ABCC1* and *GDF15* by using data from European individuals of the 1000 Genomes Project.



Supplementary Figure S3: Regional association plots of the the five independent and significant SNPs based on imputation data from the PLCO study. The left-hand Y-axis shows the -log10 *P*-value of each SNP, which is plotted according to the chromosomal base-pair position. The genome build and linkage population were plotted according to the hg19/1000 Genomes European. The right-hand Y-axis shows the recombination rate estimated from the recombination rate estimated for European populations from the HapMap Data Rel 22/phase II.



Supplementary Figure S4: Kaplan-Meier survival curves of prostate cancer patients according to genotypes of the five independent and significant SNPs, (A) rs35605 and (B) rs212091 in *ABCC1,* (C) rs1058587 in *GDF15* and (D) rs9666607 in *CD44*.



Supplementary Figure S5: Kaplan-Meier survival curves of prostate cancer patients according to combined risk alleles of the four independent and significant SNPs.