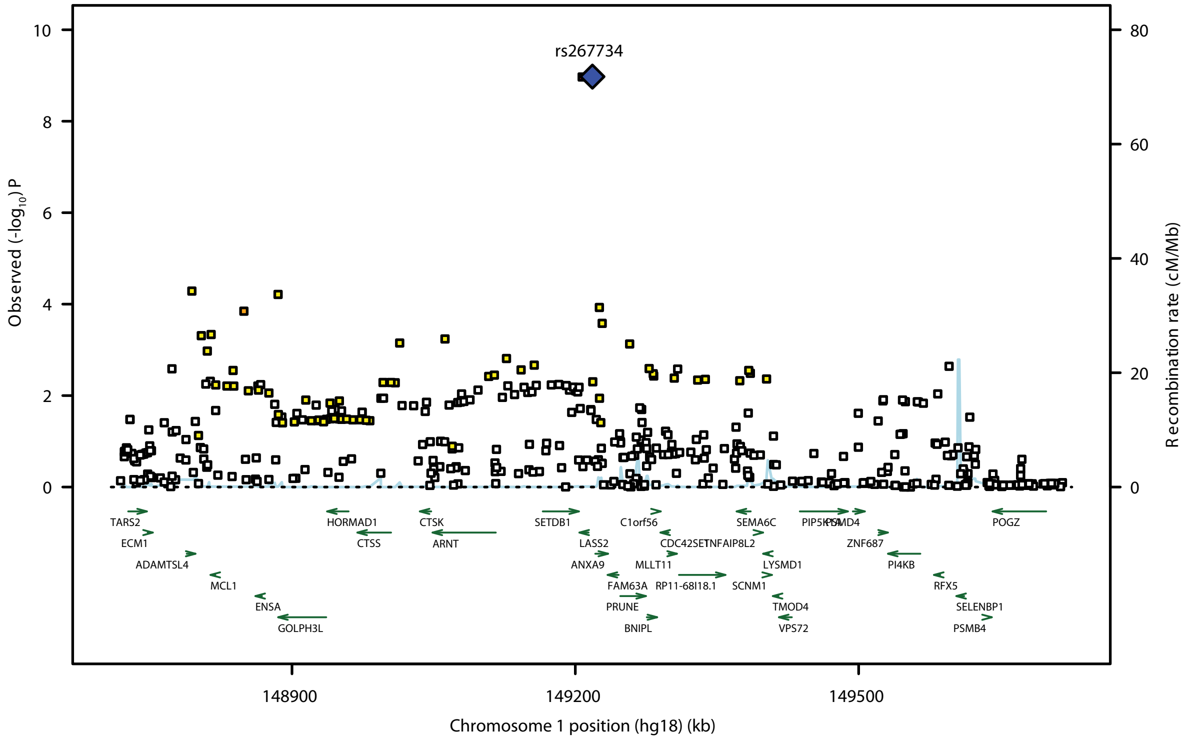
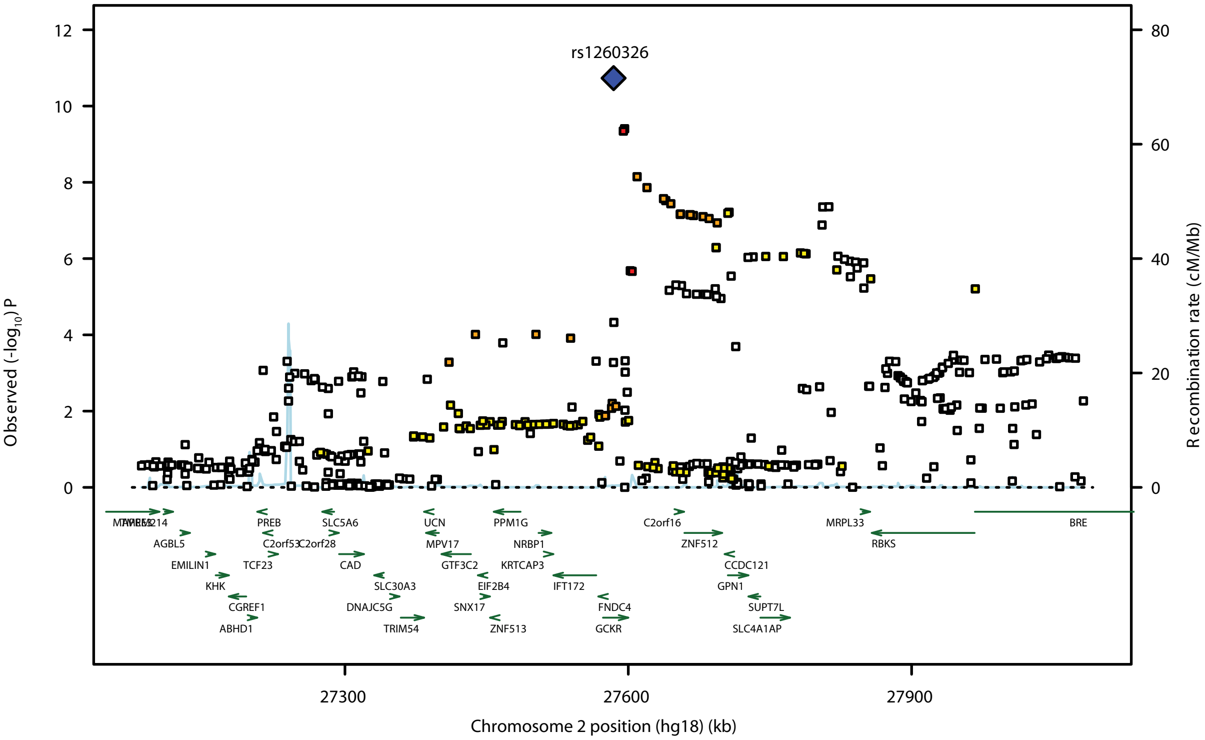
Supplementary Figure 2

Regional Association Plots - Susceptibility Loci for Reduced Renal Function and Chronic Kidney Disease

chromosome 1, rs267734, *LASS2* region

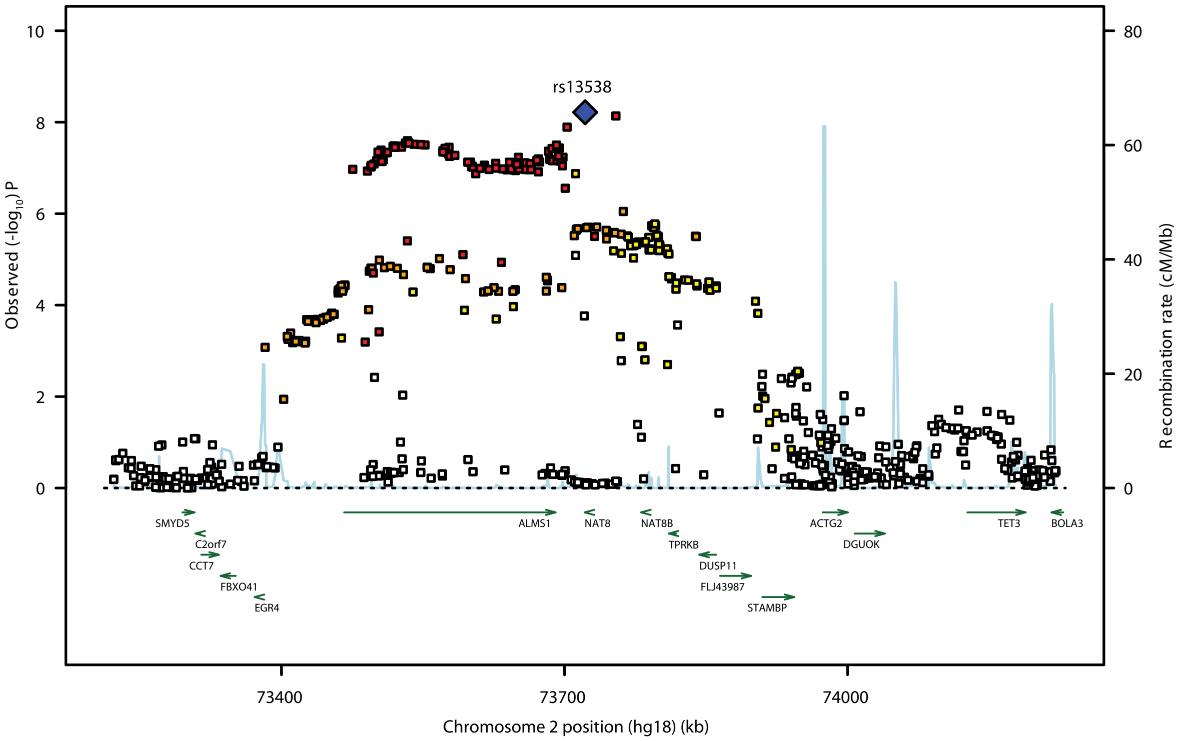


chromosome 2, rs1260326, *GCKR* region

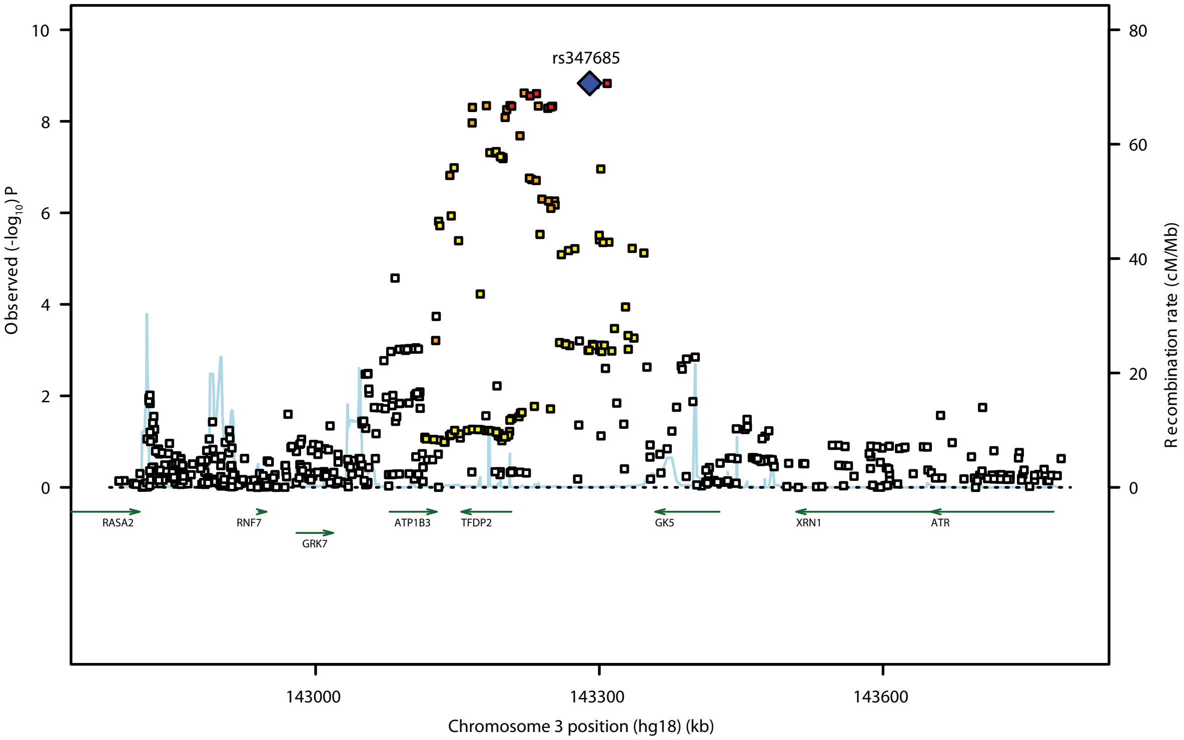


-log$_{10}$ p-values are plotted versus genomic position (build 36). The lead SNP in each region is plotted in blue. Other SNPs in each region are color-coded based on their LD to the lead SNP (LD based on the HapMap CEU): red (r2 to lead SNP 0.8–1.0), orange (0.5–0.8), yellow (0.2–0.5) and white (<0.2), unless indicated otherwise. Gene annotations are based on UCSC Genome Browser (RefSeq Genes, b36) and arrows present direction of transcription. Graphs were generated using the software SNAP (http://www.broadinstitute.org/mpg/snap/index.php).

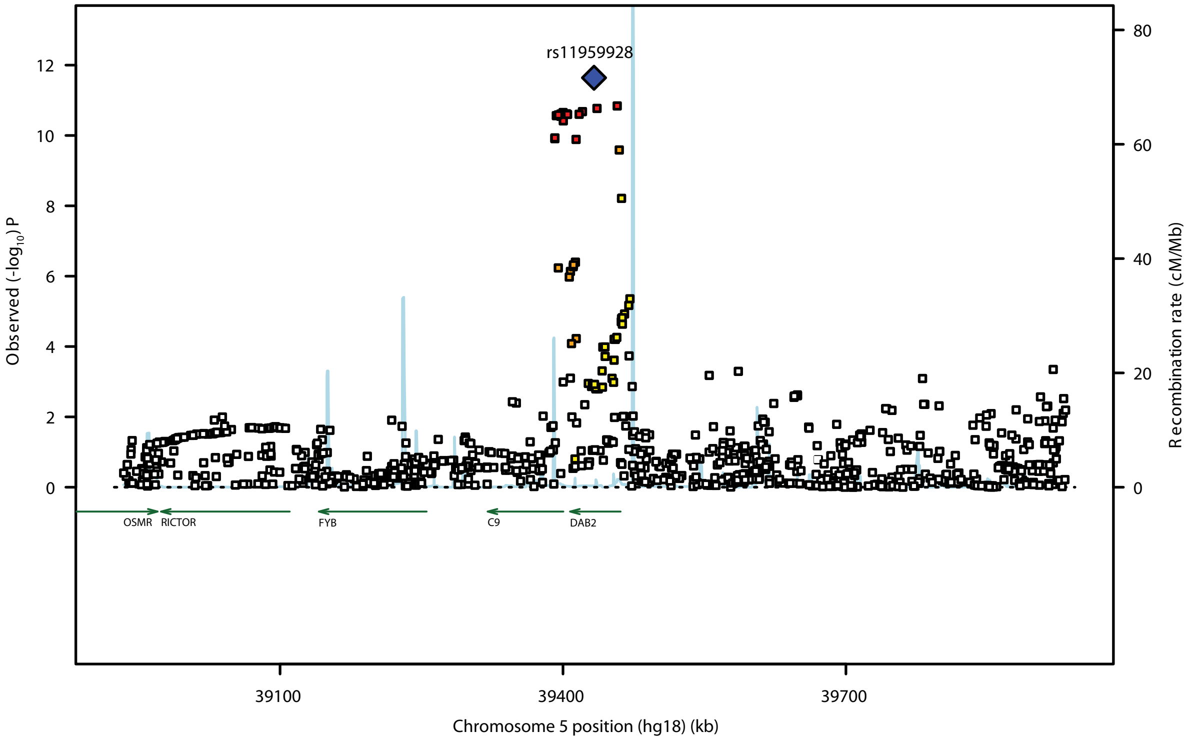
chromosome 2, rs13538, *ALMS1* region



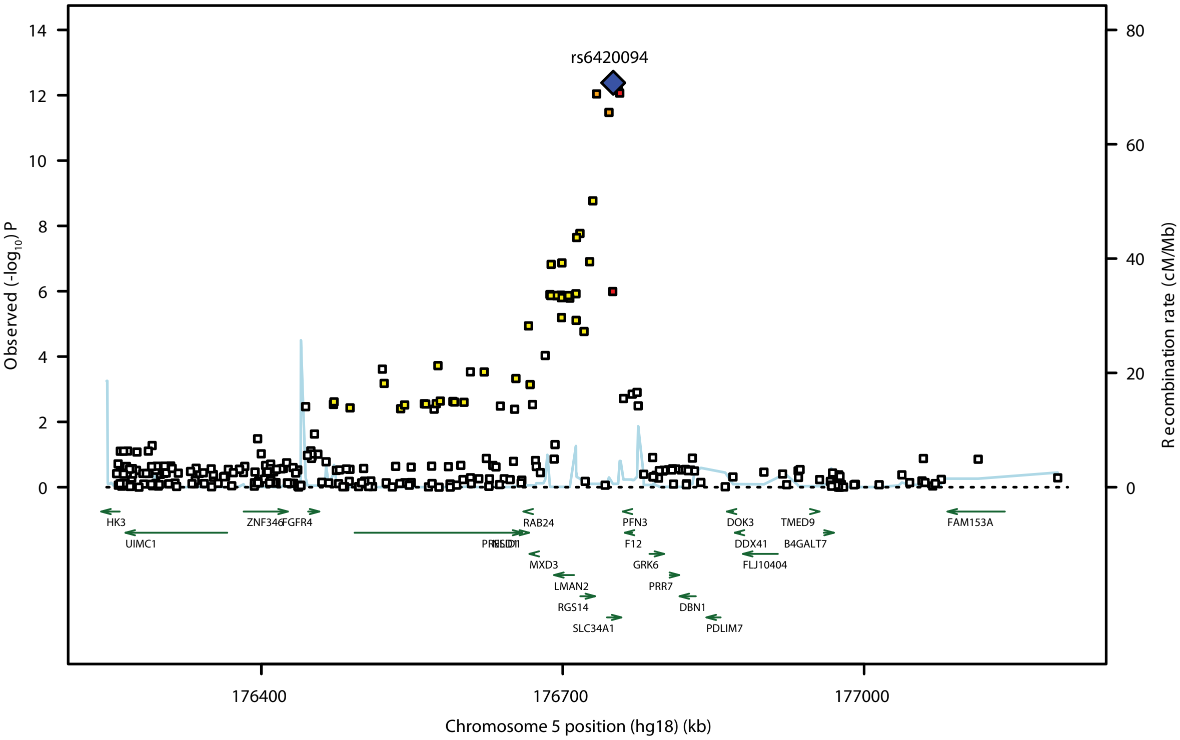
chromosome 3, rs347685, *TFDP2* region



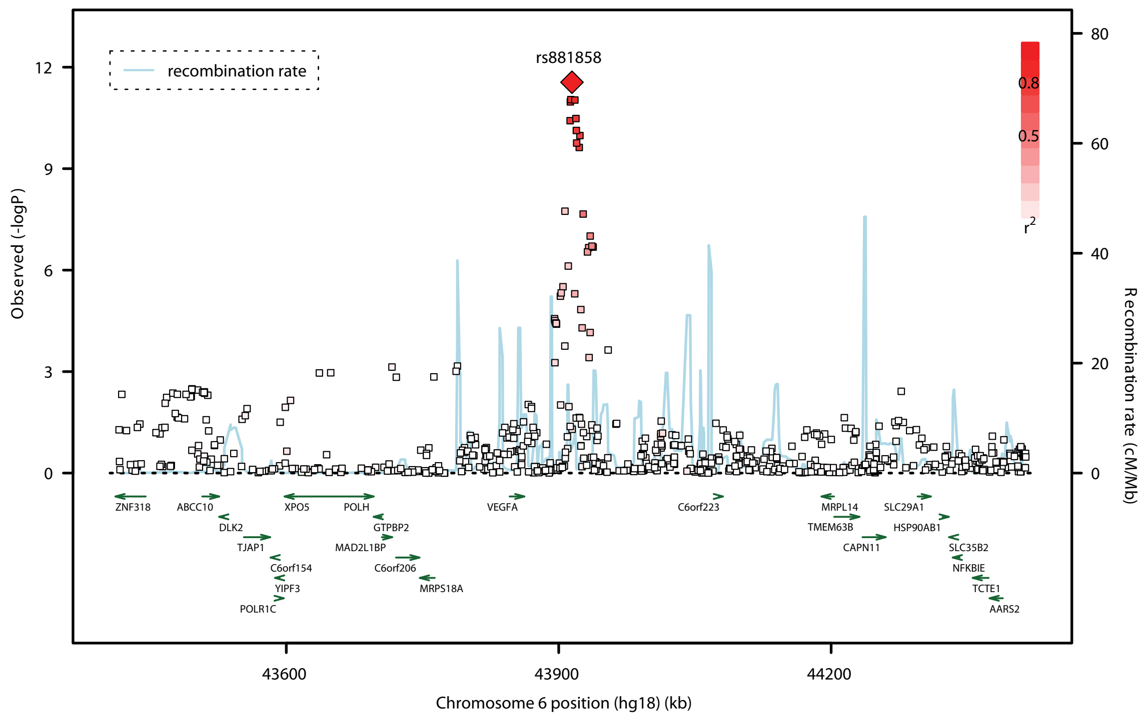
chromosome 5, rs11959928, *DAB2* region



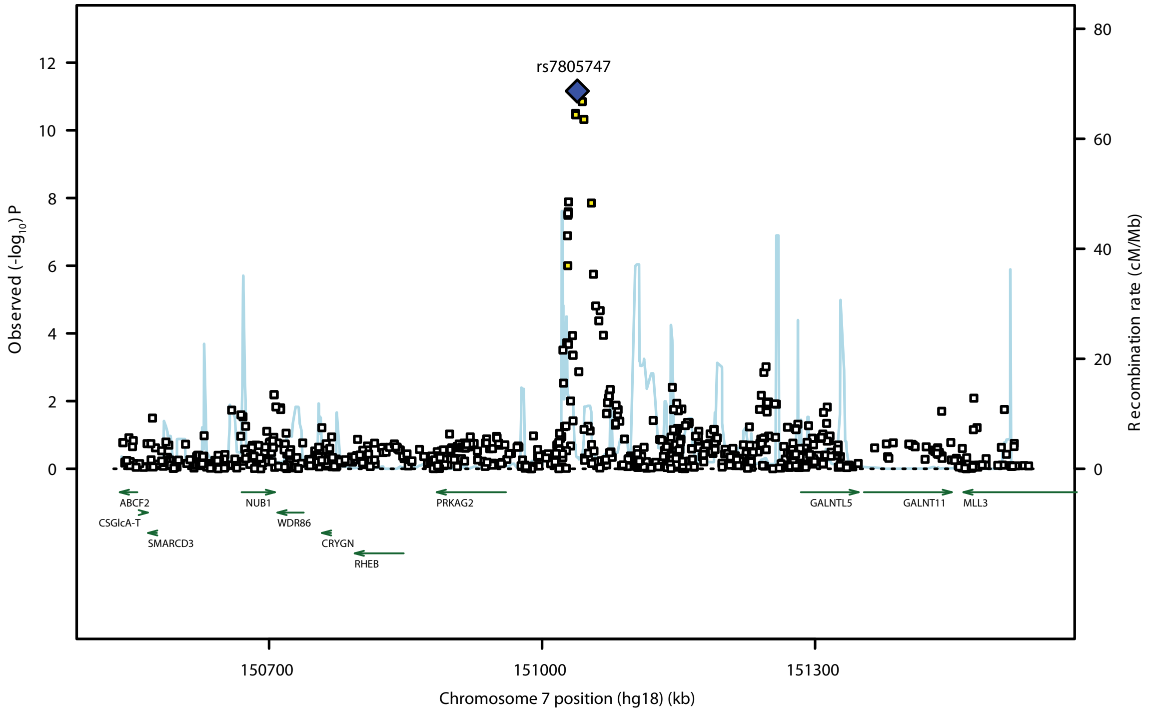
chromosome 5, rs6420094, *SLC34A1* region



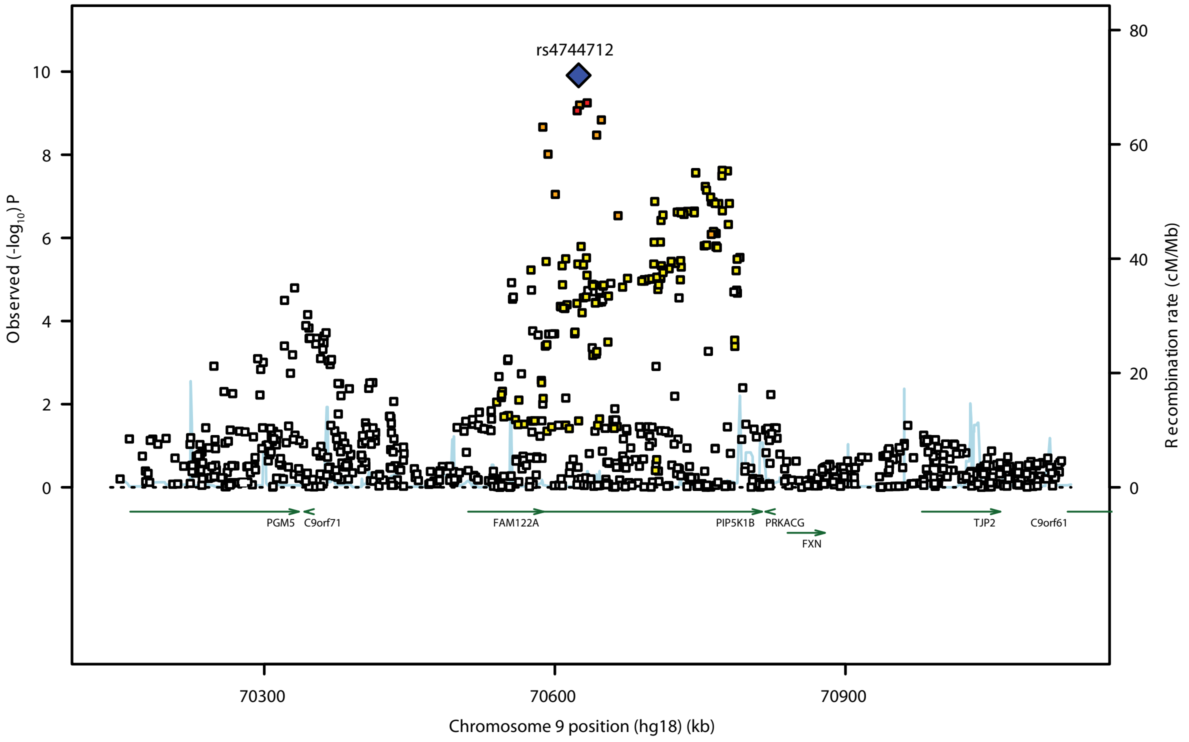
chromosome 6, rs881858, *VEGFA* region



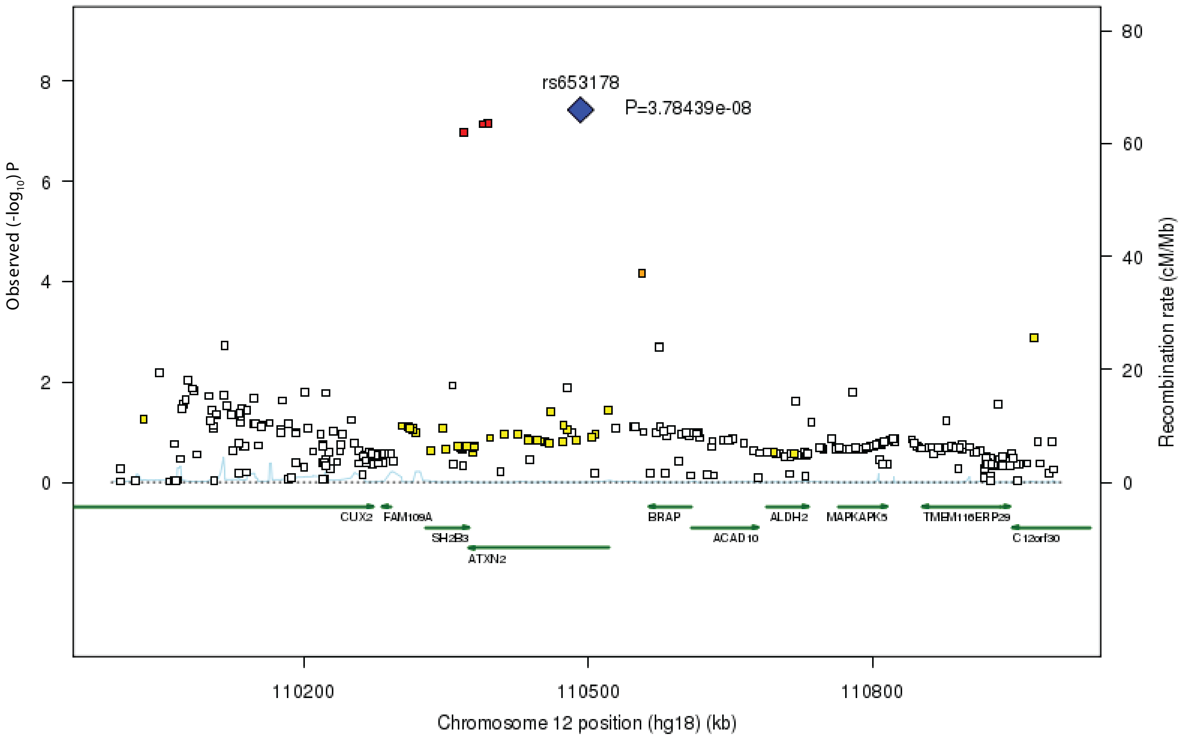
chromosome 7, rs7805747, *PRKAG2* region



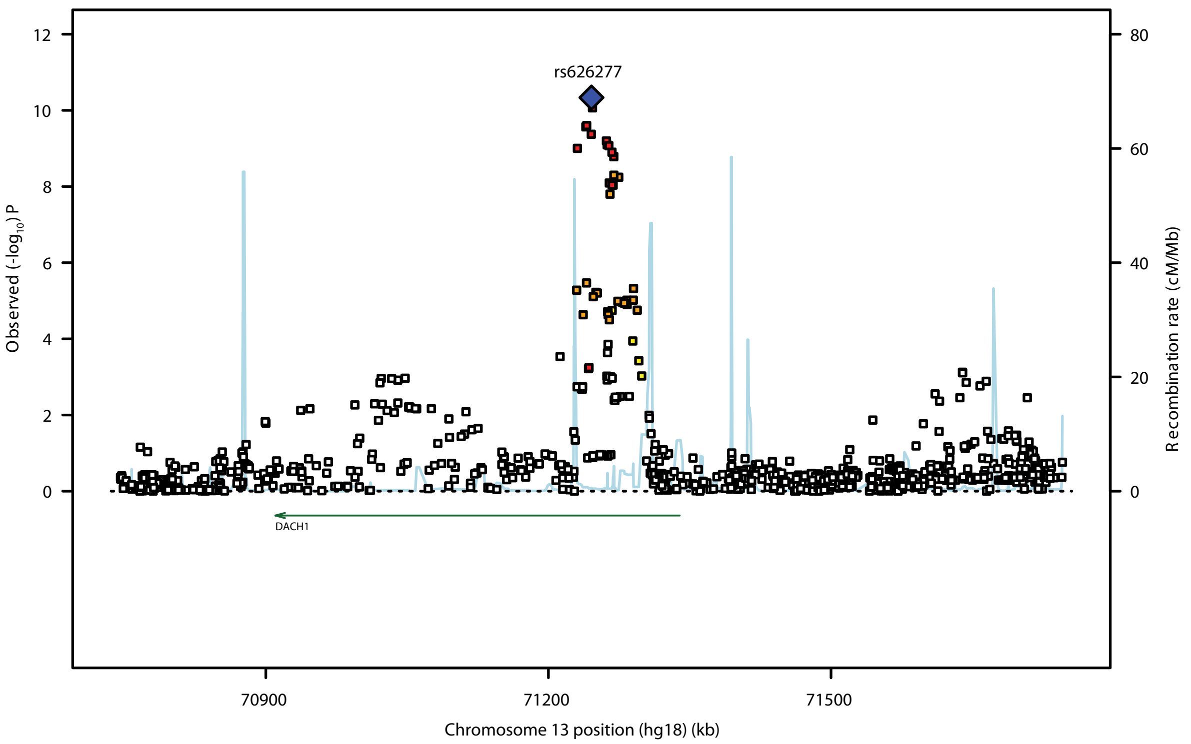
chromosome 9, rs4744712, *PIP5K1B* region



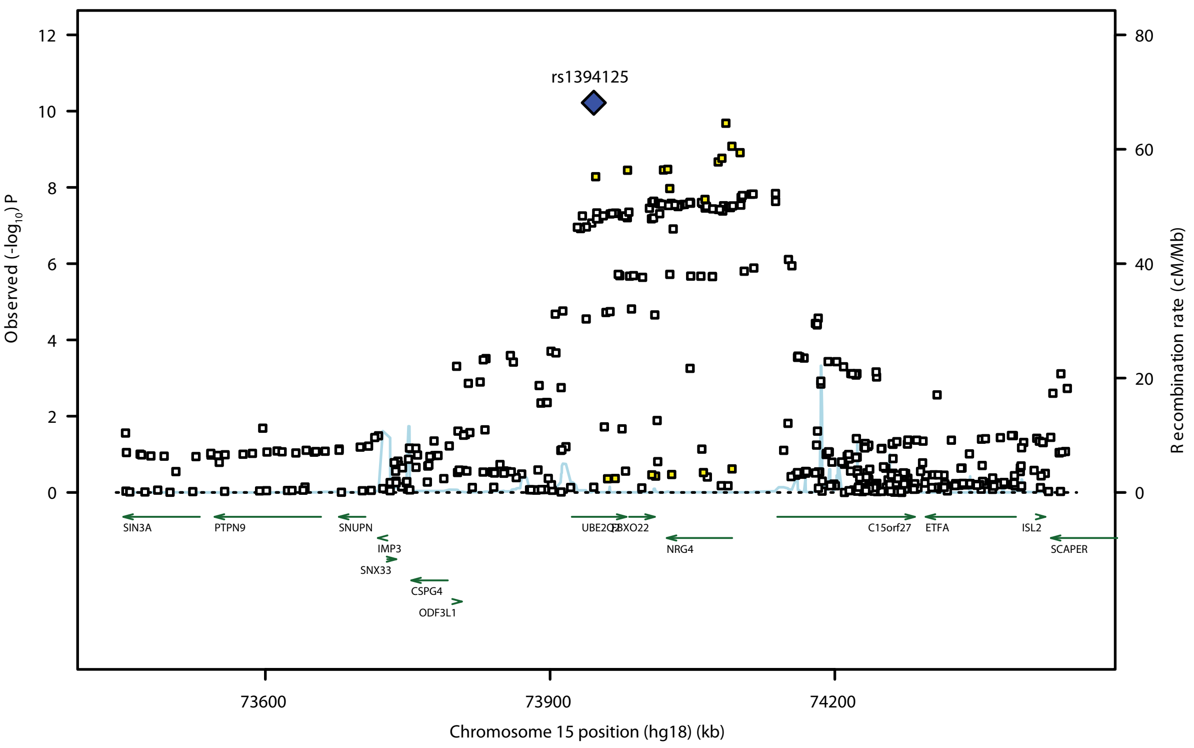
chromosome 12, rs653178, *ATXN2* region



chromosome 13, rs626277, *DACH1* region



chromosome 15, rs1394125, *UBE2Q2* region



chromosome 19, rs12460876, *SLC7A9* region