Supplementary Figure 5: Overview of the results for the 5p13.1 locus. (A) Plot of the negative common logarithm of the p-values of the different tiers across the 650 kb region. The red line shows the significance threshold of p = 0.05. Results of the two lead SNPs rs1992662 and rs1992660 are highlighted in pink color. The broad replicated peak between 40.29 Mb and 40.66 Mb localizes to a gene desert upstream of PTGER4. (B) Recombination rate in cM/Mb shows that the peak region is delineated by two sites of increased recombination. (C) Linkage-disequilibrium (LD) plot from HapMap, using the metrics D’ and (D) r^2. Genotypes of trios with northern and western European ancestry for 633 SNPs (CR ≥ 90%, MAF ≥ 1%, pHWE ≥ 0.01, Mendel errors ≤ 3) were retrieved from HapMap. Positions are from NCBI build 35.