Figure S3 Estimating the false discovery rate for SNP marker association with HTR: (a) A density histogram showing p-value distribution of 44,520 SNP markers following genome-wide association analysis. (b) The q-values plotted against their respective p-values. (c) The number of SNPs plotted against each of the respective q-value estimates. (d) The expected number of false positive SNPs versus the total number of significant SNPs given by the q-values.