



Figure S5 (A) LD heatmap above showing LD measure (r^2) calculated (for each pairwise comparison of SNPs (colors red to white correspond to 1 to 0 r^2 values, while black diagonal compares the same SNP to itself) within a chromosome 10 genomic region (21 – 22 mbp) containing 3 significantly associated SNPs indicated by dashed lines (21,693,685 bp, 21,722,883 bp and 21,823,409 bp). (B) Chart with markers indicating $-\log_{10}$ of p-values of SNPs following genome-wide association analysis with HTR (mutant-to-wildtype height ratio).