

Supplementary. Figure 3 - Manhattan plots for physiological traits using (A) haplotype-based or (B) SNP-based mixed models. The x-axis shows genomic position and y-axis the significance as negative log 10 of the p-value of the test of association. Thresholds are shown as red horizontal lines and indicate the genome-wide 10% thresholds as determined by permutation in haplotype and bootstraps in SNP-based method.







