

Discovery of mitochondrial DNA variants associated with
genome-wide blood cell gene expression: a
population-based mtDNA sequencing study

Supplementary figures

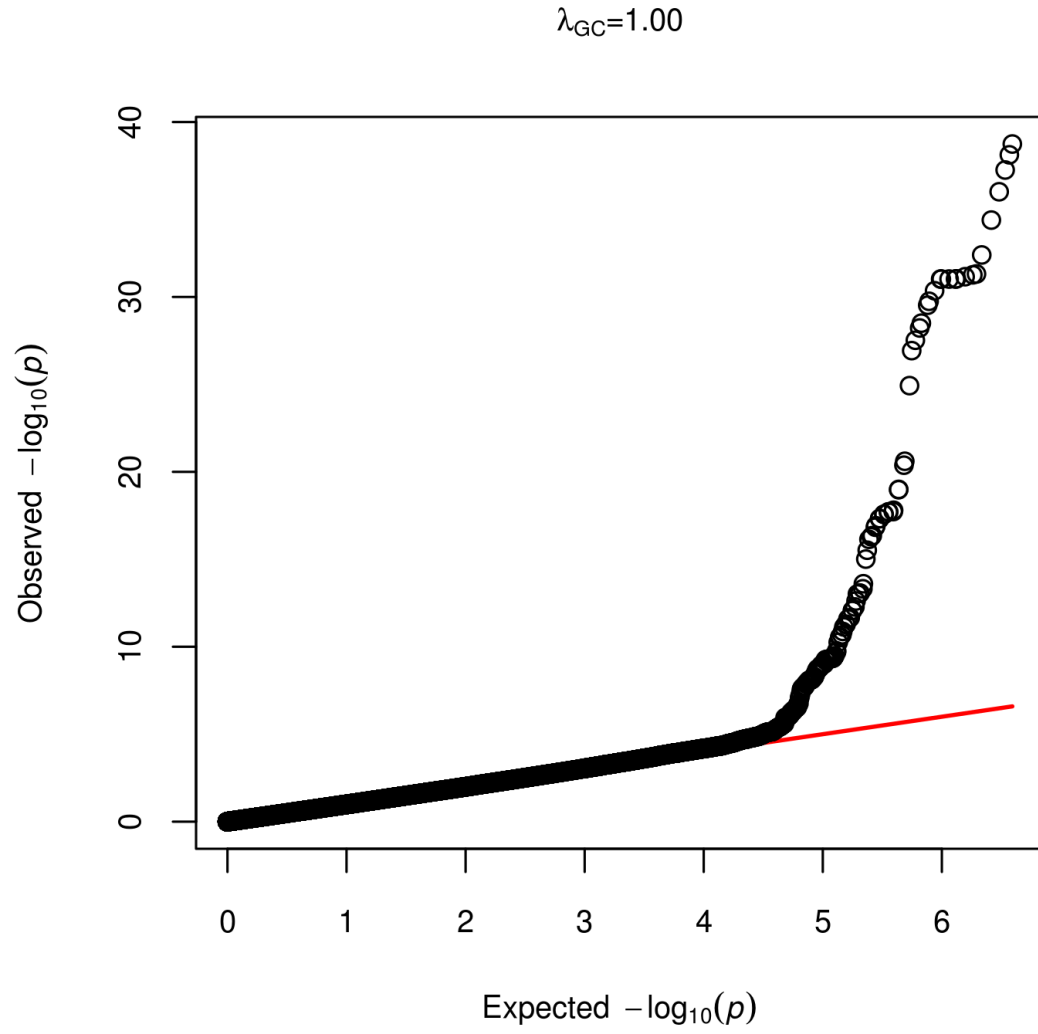


Figure S1: Quantile-quantile plot for expected versus observed p-values of 3,907,763 probe-mtSNP associations. A strong deviation from the expected is observed for large $-\log_{10}(p)$.

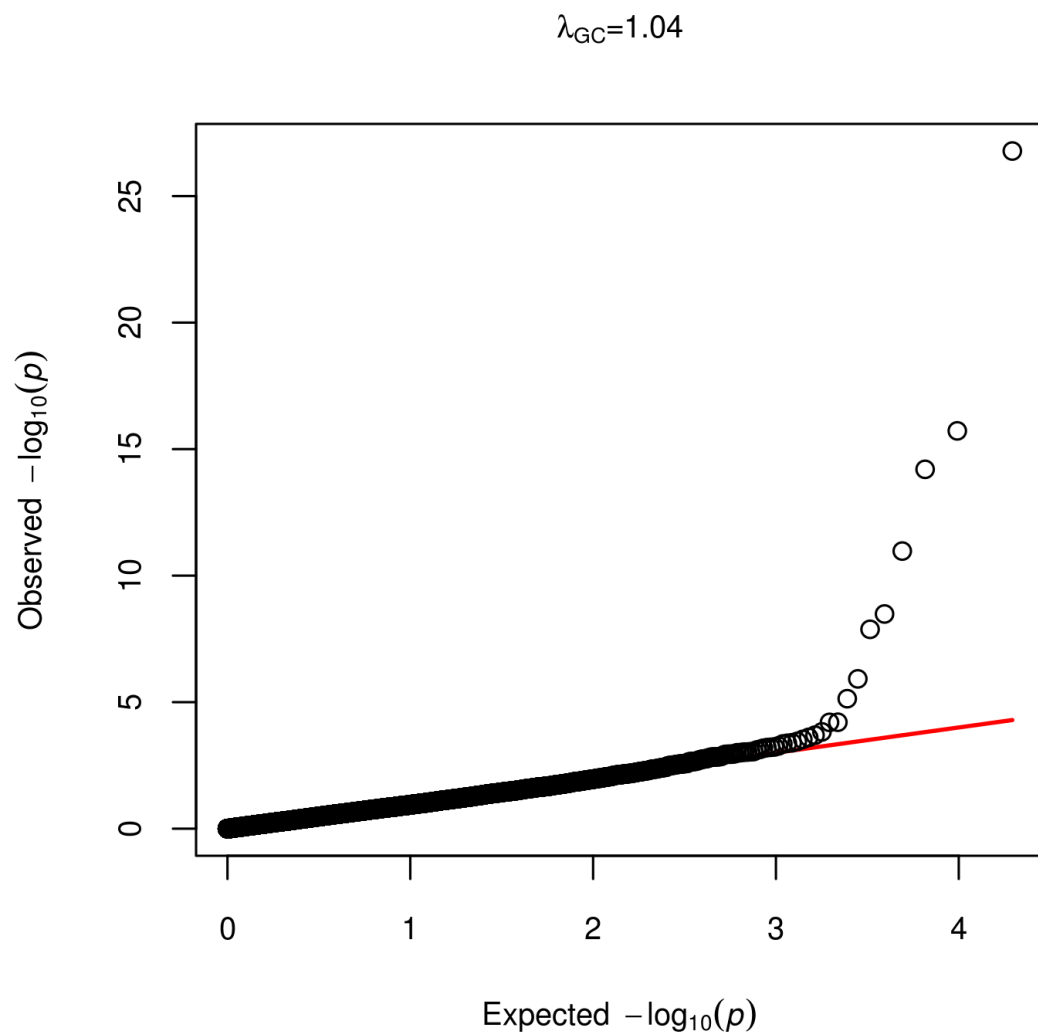


Figure S2: Quantile-quantile plot for expected versus observed p-values of 19,637 probe-haplogroup ANCOVA analysis.

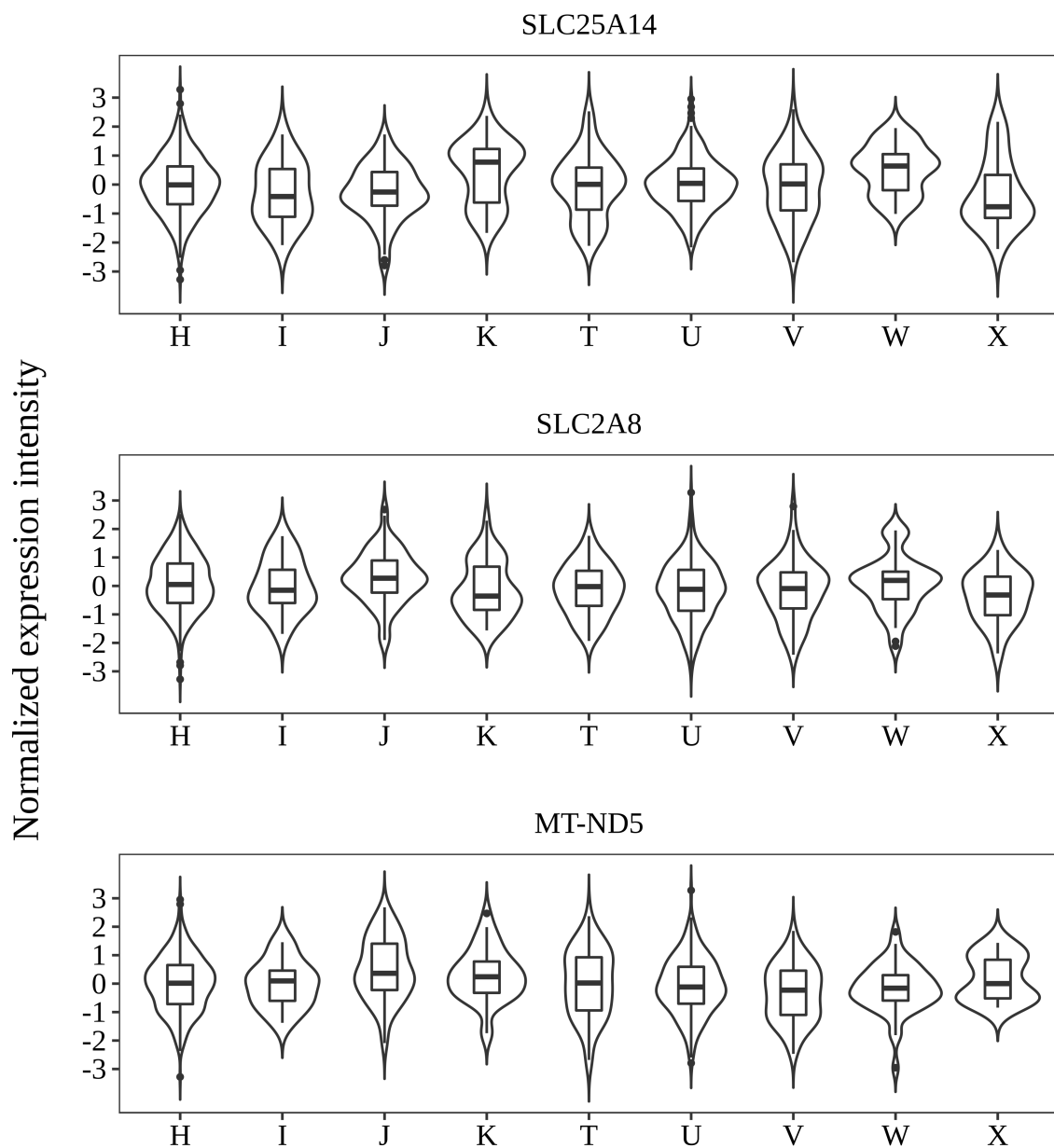


Figure S3: Combined boxplot and violin plot of the normalized expression intensities of SLC25A14, SLC2A8 and MT-ND5 across the haplogroups.

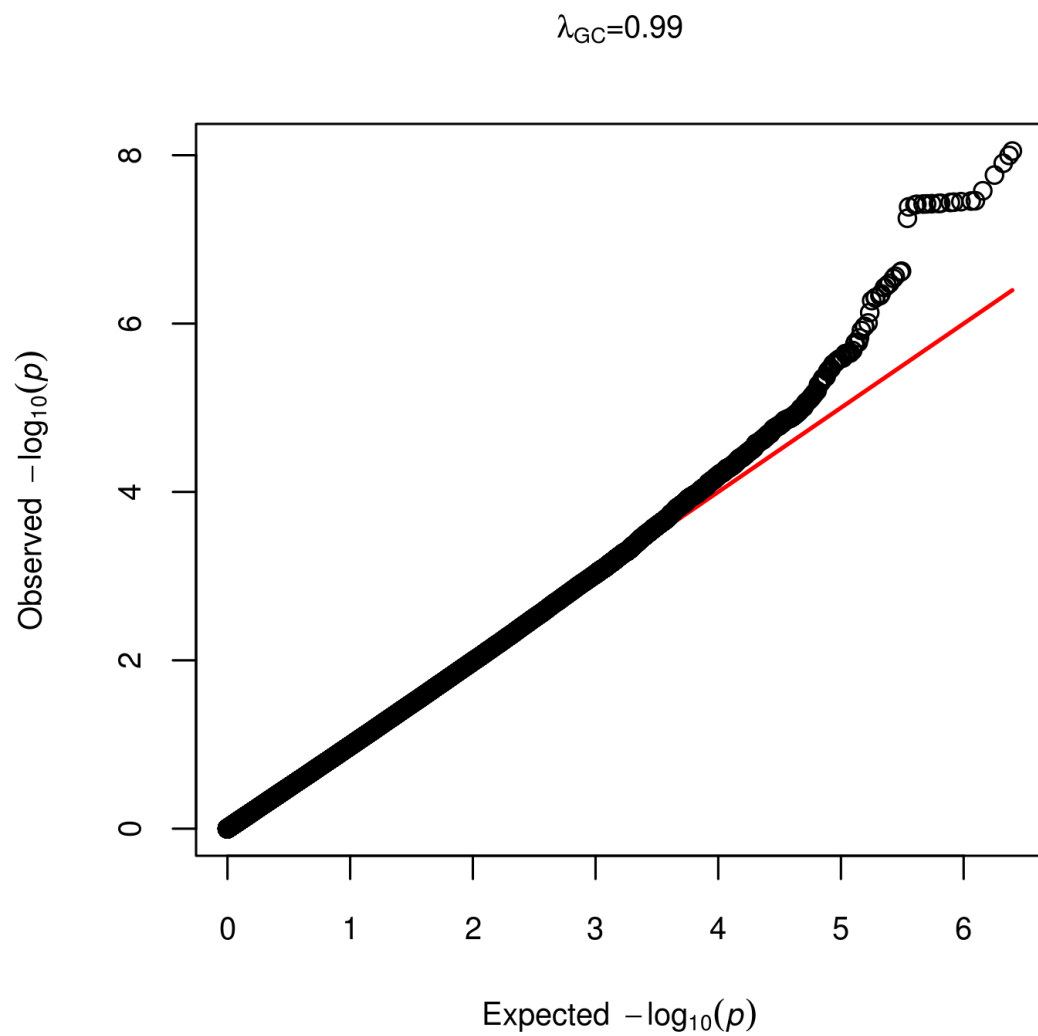


Figure S4: Quantile-quantile plot for expected versus observed p-values from random-effect meta-analysis between subjects with and without prediabetes.

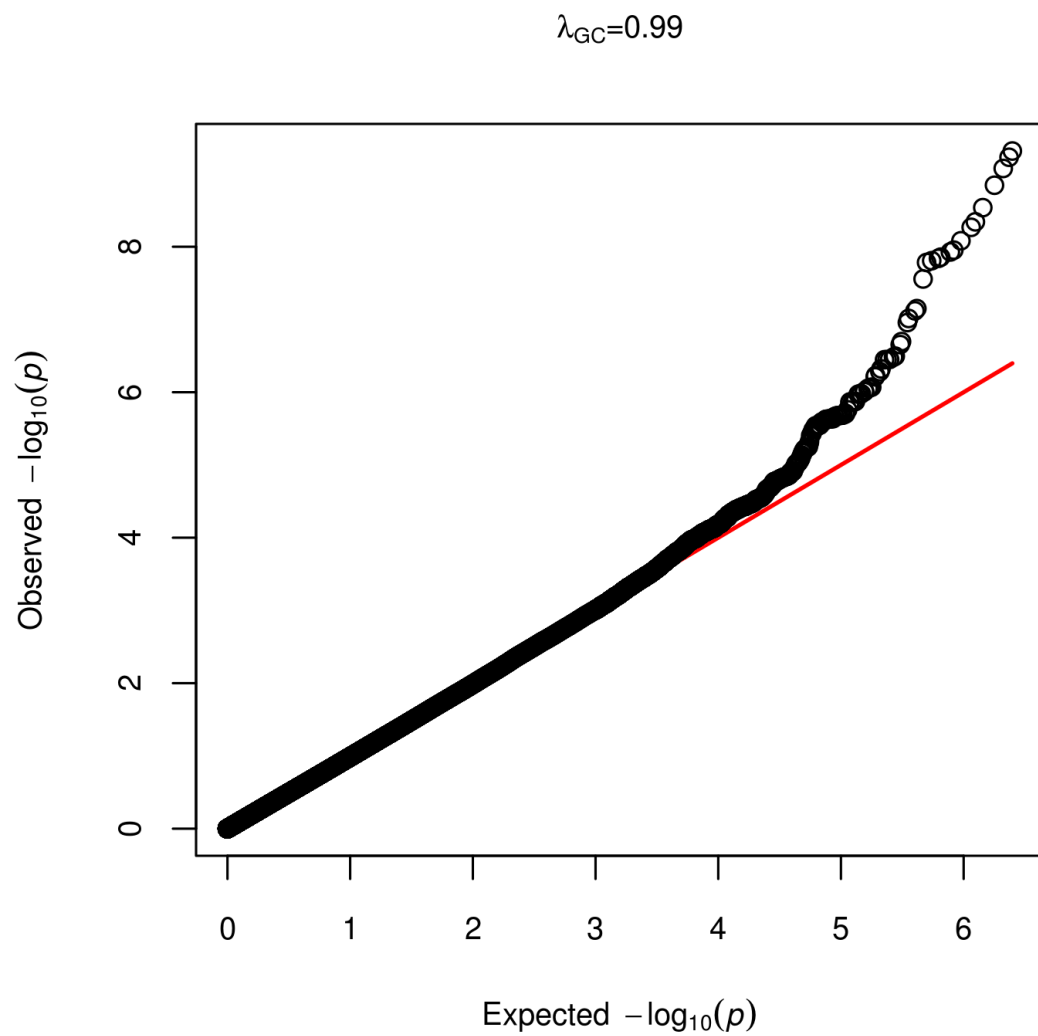


Figure S5: Quantile-quantile plot for expected versus observed p-values of 2,493,899 probe-mtSNP associations in subjects with prediabetes.

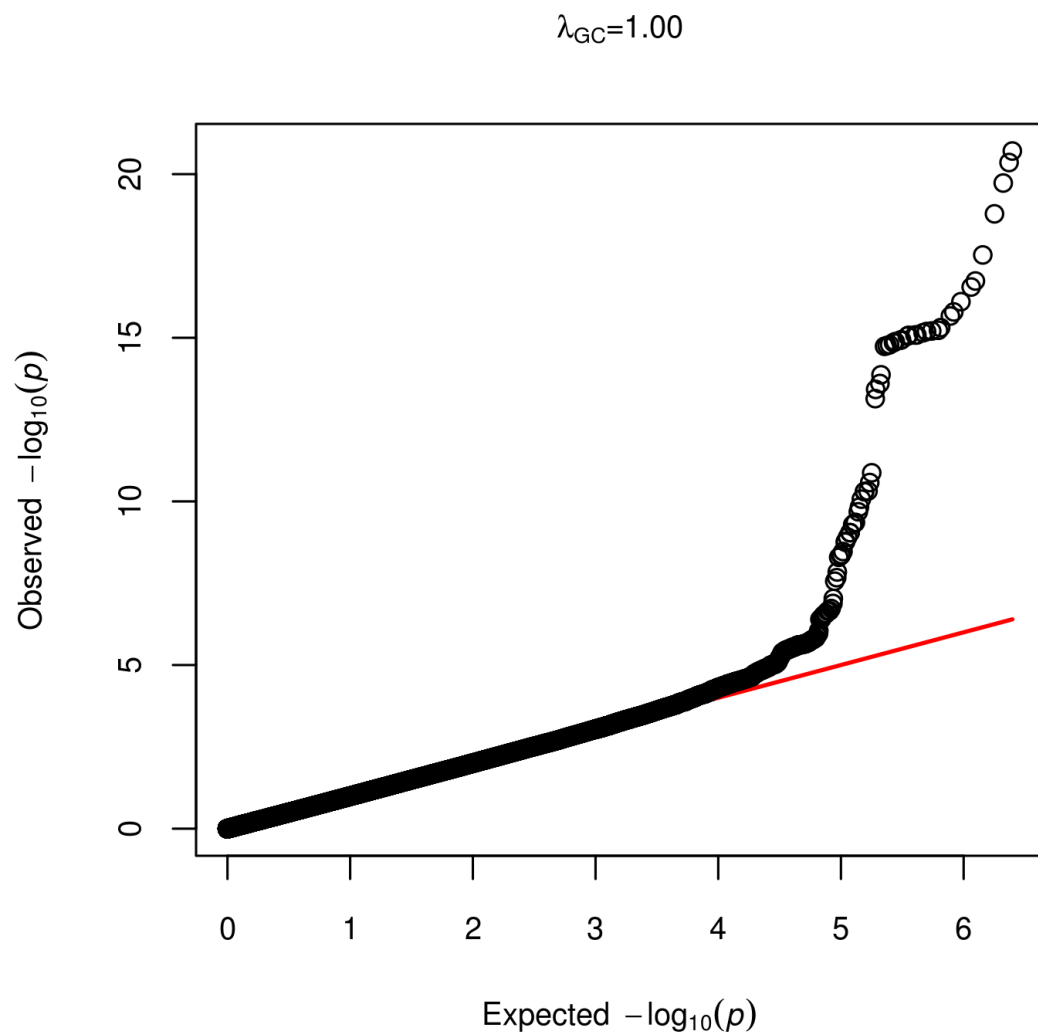


Figure S6: Quantile-quantile plot for expected versus observed p-values of 2,493,899 probe-mtSNP associations in subjects without prediabetes.