



**ESM Figure 7 Quantile-quantile plots of 16,192 SNPs for 12 metabolic traits in up to 15,989 Danish individuals (stage 2).**

For each of the traits the observed T statistics were plotted against the expected T statistics under the null hypothesis. In light blue colours are all SNPs passing quality control. Dark blue dots show results where SNPs that have been established as known genome-wide associated signals for each trait have been removed. All *P*-values were corrected by genomic control. The inflation factors ( $\lambda$ ) are shown for each analysis and were estimated by dividing observed median statistics by the expected median statistics.