

Figure S2. Manhattan plots showing the genome-wide associations for TTW (trimmed tight weight) trait obtained with single-SNP regression approach. Negative \log_{10} p-values of all SNPs that passed quality control are plotted against their genomic positions. Different chromosomes are distinguished with grey and black colours. The dashed lines indicate the nominal p-value of $5.0E-05$ and $5.0E-04$, respectively.

