

Figure S1. Manhattan plots showing the genome-wide associations for UTW (untrimmed 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.

