

Figure 3: Genome-wide association mapping results from the analysis of the mouse data for the single-locus method FaST-LMM and the multiple-locus method Eagle. Eagle was run under two settings; its default setting (Eagle^{default}) and where the model selection criterion had been optimised for a false discovery rate of 5% (Eagle^{optimal}). The number of SNP-trait associations found are reported. The bar plots with boxes around them are for those traits where using Eagle^{default} and Eagle^{optimal} resulted in more findings than with single-locus analysis.

