



Figure S5. The number of distant eQTL along the genome. The grey bars are identical in A and B and indicate the average number of distant eQTL per 2cM window based on a sliding window analysis. The width of the window was 18 cM, corresponding to the median size of the eQTL confidence intervals. A, The 99th quantile of the expected eQTL density from 1,000 randomizations of eQTL positions per chromosome is shown as a blue line. B, Light red rectangles: Confidence intervals for tameness QTL locations.