Supporting Figures

Figure S1. Venn diagram depicting the overlap between genes with differential expression in parental accessions pairs (Cvi vs. Col and Bur vs. Col).

Figure S2. Histograms of the explained phenotypic variance ($R^2$; %) for the eQTLs in the a.CviCol and b. BurCol populations.

Figure S3. Number of eQTLs per trait. The percentage and number of traits explained by 1 to 5 eQTLs are indicated along the y-axis and on top of each bar, respectively. a. CviCol b. BurCol at a FDR of 5%.

Figure S4. Venn diagram depicting the overlap between probes with local eQTLs in the CviCol and BurCol populations.

Figure S5. Histogram of the number of probes with a significant eQTL for different numbers of hidden factors tested with VBQTL in CviCol.

Figure S6. Genetic landscape for transcript accumulation variation in BaySha. a. eQTL heatmap for BaySha population significant at a 5% FDR. Each horizontal bar represents an eQTL mapped on the x-axis and controlling the accumulation of a transcript expressed from the locus indicated on the y-axis. The colour of the bar indicates the direction and strength of the eQTL additive effect, and its length along the x axis encompasses the eQTL support interval. Local eQTLs form the diagonal, while distant eQTLs fall elsewhere in the map. b. Bar plot indicating the proportion of local and distant eQTLs for increasing LOD value intervals.

Figure S7. Histogram of the explained phenotypic variance ($R^2$) for the eQTLs in the BaySha population

Figure S8. Number of eQTLs per trait in BaySha. The percentage and number of traits explained by 1 to 5 eQTLs are indicated along the y-axis and on top of each bar, respectively.

Figure S9. Distribution of distant-eQTLs along the genome in BaySha. The number of eQTLs (y-axis) is plotted against the physical position of the 1Mb-window where they peak (x-axis). Intervals with an excess of eQTLs relative to the threshold estimated by permutation (red dashed line) were classified as hotspots.
Figure S1
Figure S2

(a) Frequency distribution of CviCol explained phenotypic variance (%)

(b) Frequency distribution of BurCol explained phenotypic variance (%)

The histograms show the distribution of explained phenotypic variance for CviCol and BurCol, indicating a skew towards lower variance values for both traits.
Figure S3

(a) Percentage of eQTLs/trait for CviCol.

(b) Percentage of eQTLs/trait for BurCol.
Figure S4
Figure S5

Probes with eQTLs

Number of Hidden Factors
Figure S6
Figure S7
Figure S8
Figure S9