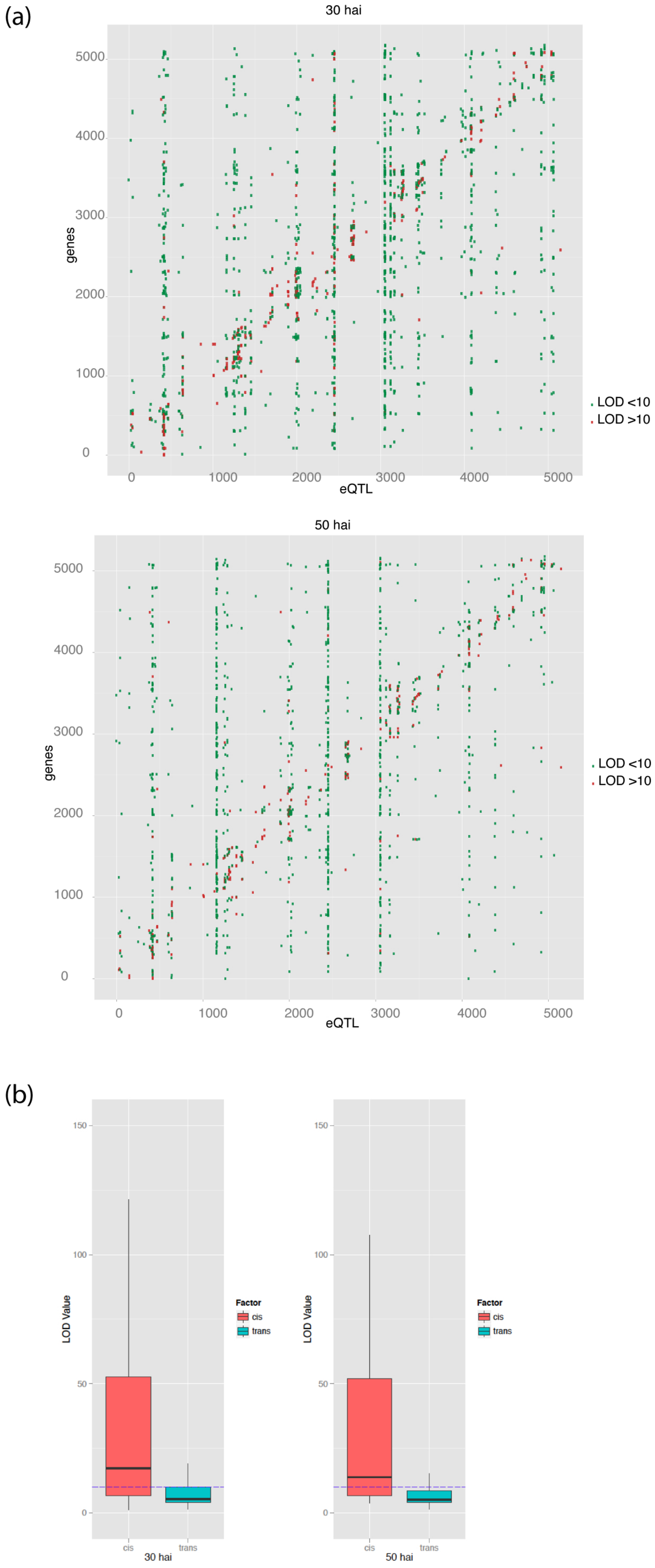

Figure S2 (a) Genome Zipper mapped eQTL position at 30 hai and 50 hai. x-axis indicates genetic positions of eQTL sorted along the transformed marker intervals from the transposed CM-82036 x Remus map to the Chinese Spring consensus map. Chinese Spring mapped genes are plotted Green and red dots represent eQTL with LOD score under or above 10, respectively.

(b) Boxplot with LOD distributions of cis and trans mapped eQTL. The dashed indicates a LOD of 10, which was chosen as a cut-off to distinguish cis and trans eQTL in the complete eQTL dataset.