



Figure S1. Distribution of chromatin features over all chromosomes. Whole genome distribution of the euchromatin-associated histone modification H3K4me2 (green line), the constitutive heterochromatin-associated histone modification H3K9me3 (red line), the facultative heterochromatin-associated histone modification H3K27me3 (yellow line) and chromatin accessibility (blue line) as determined by ATAC-seq. Genes are indicated in light blue, transposons are indicated in red, centromere is indicated in dark blue and adaptive genomic regions are indicated in yellow.