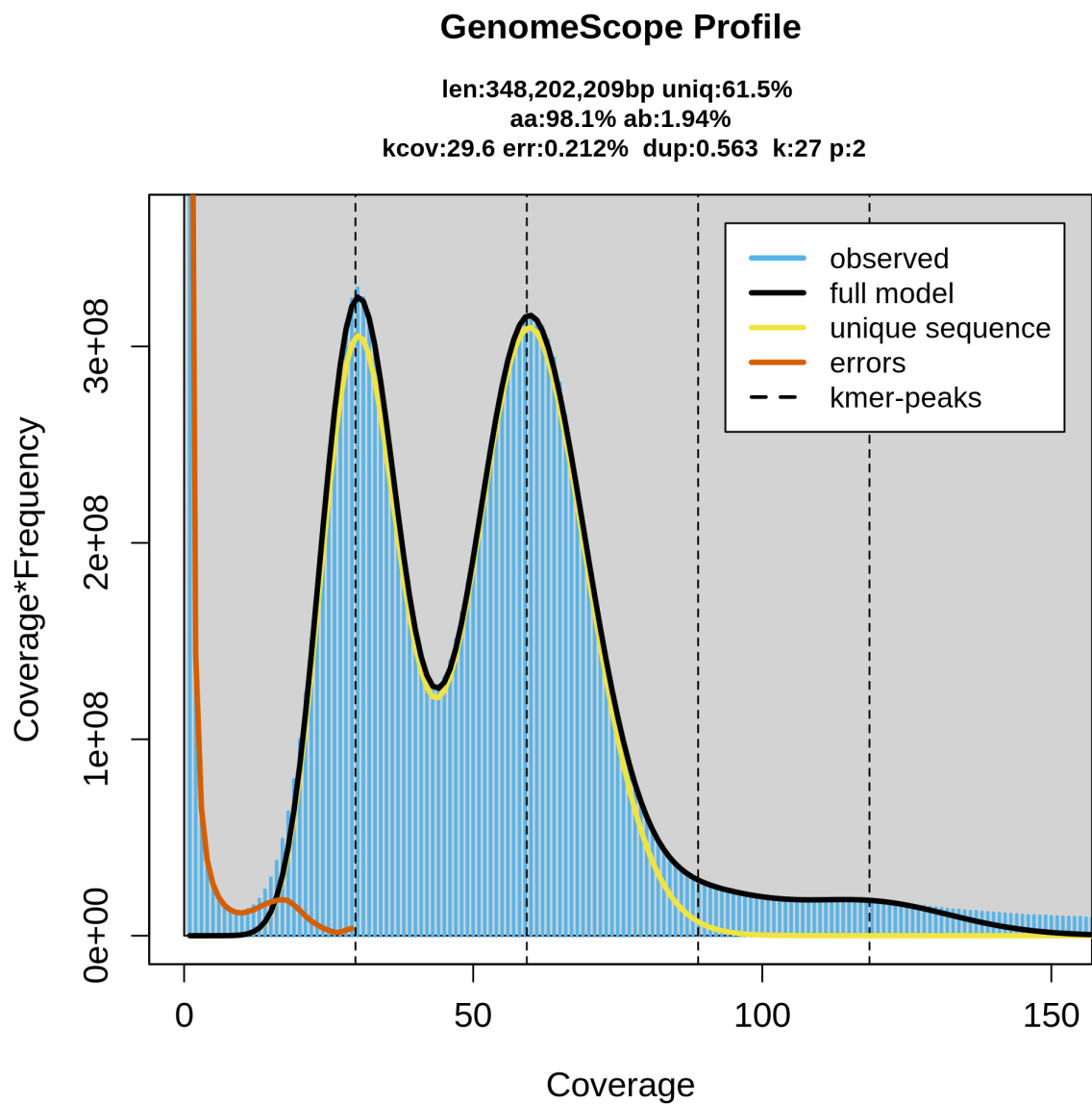
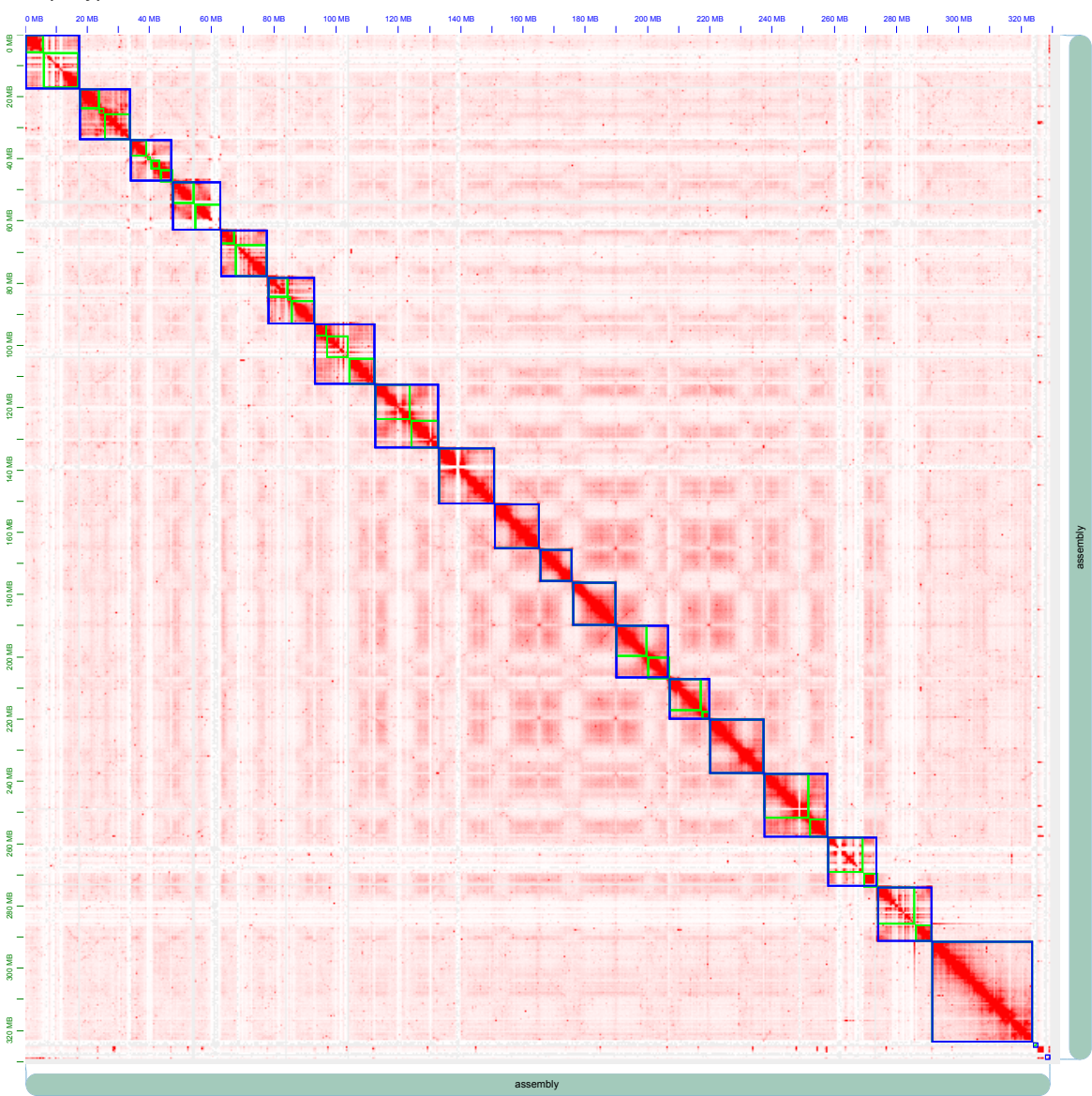


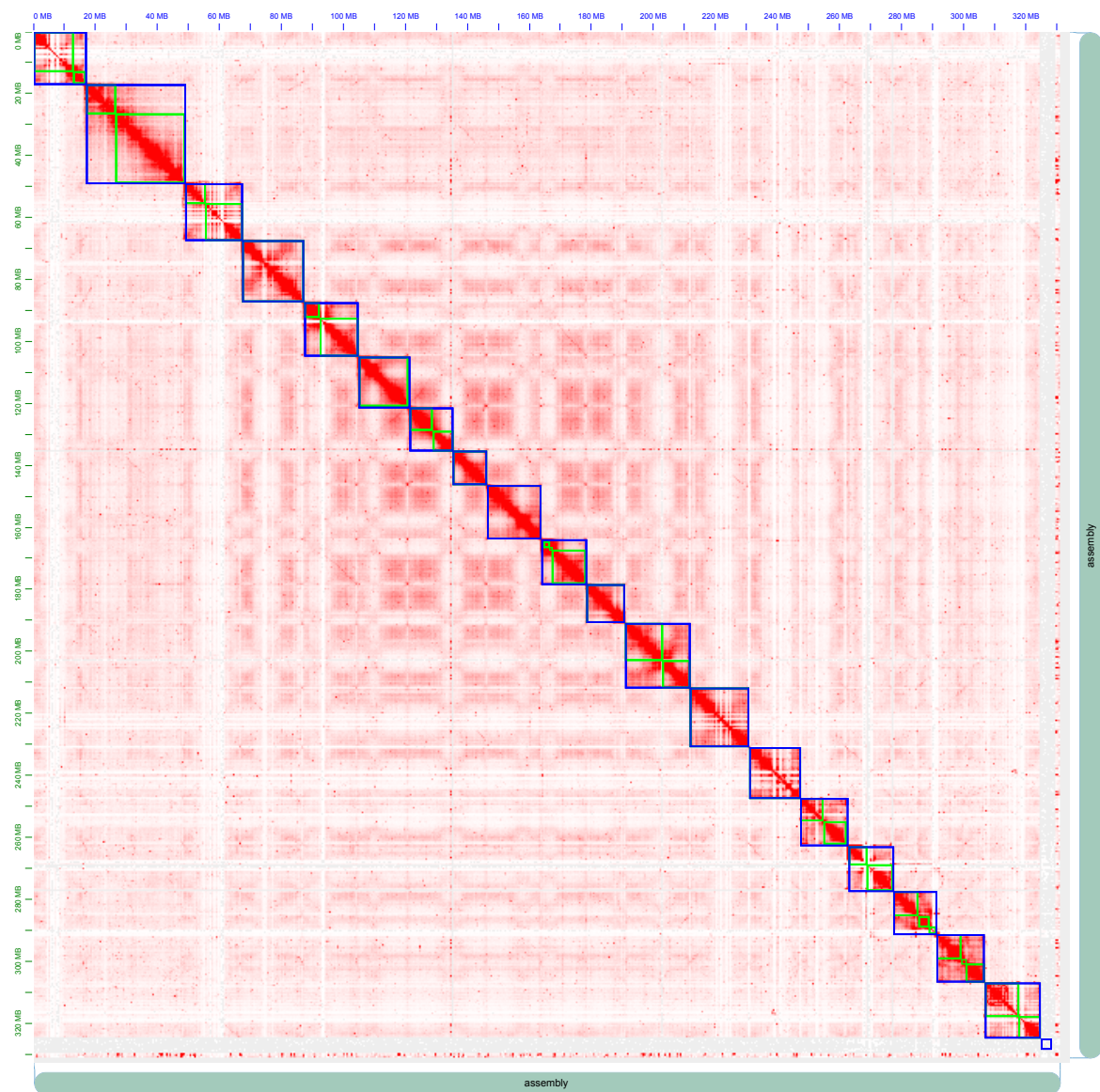


**Supplementary Figure S1.** The 27-mer distribution of the PacBio HiFi reads of *Salix herbacea*.

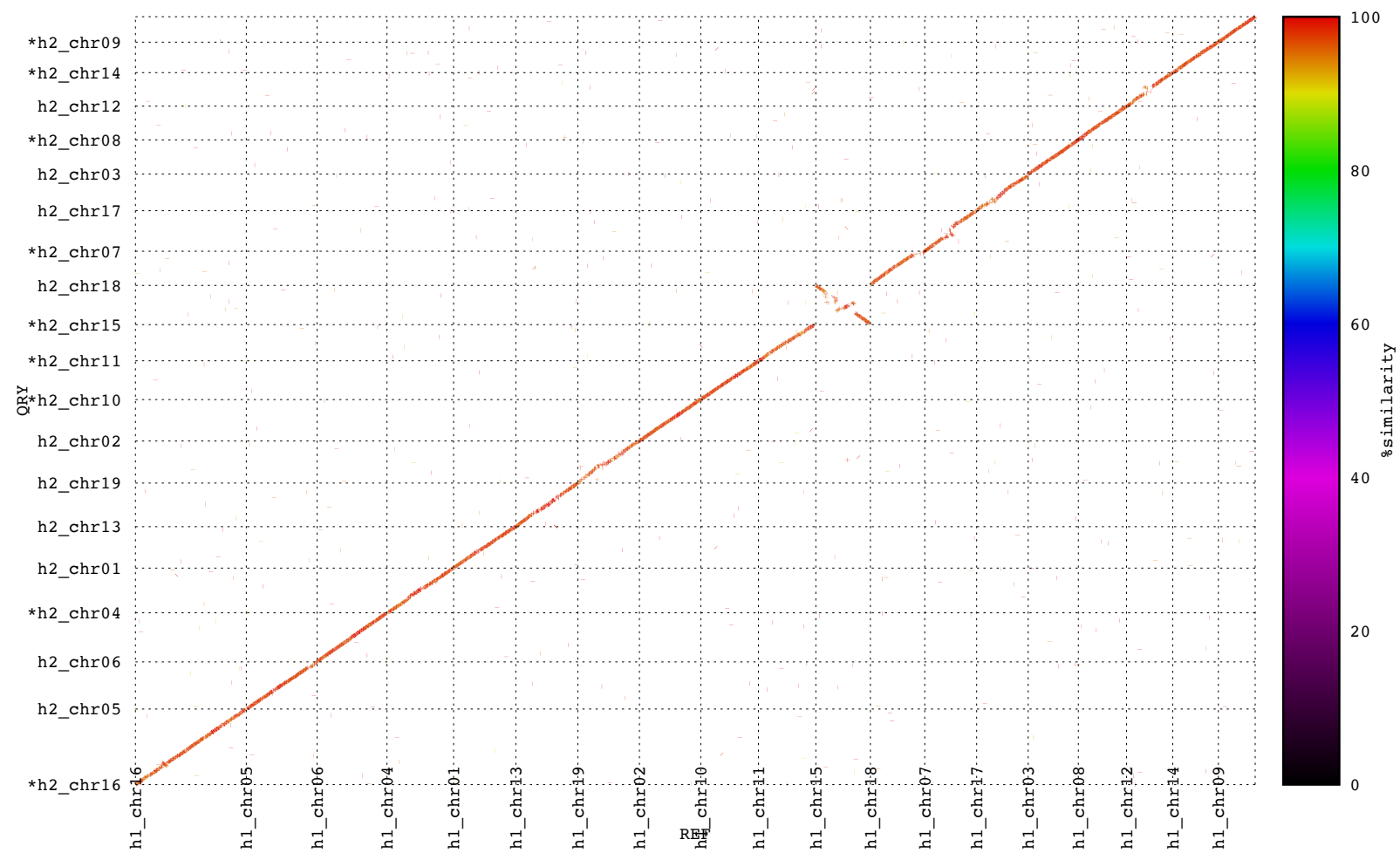
a. haplotype 1 of *Salix herbacea*



b. haplotype 2 of *Salix herbacea*

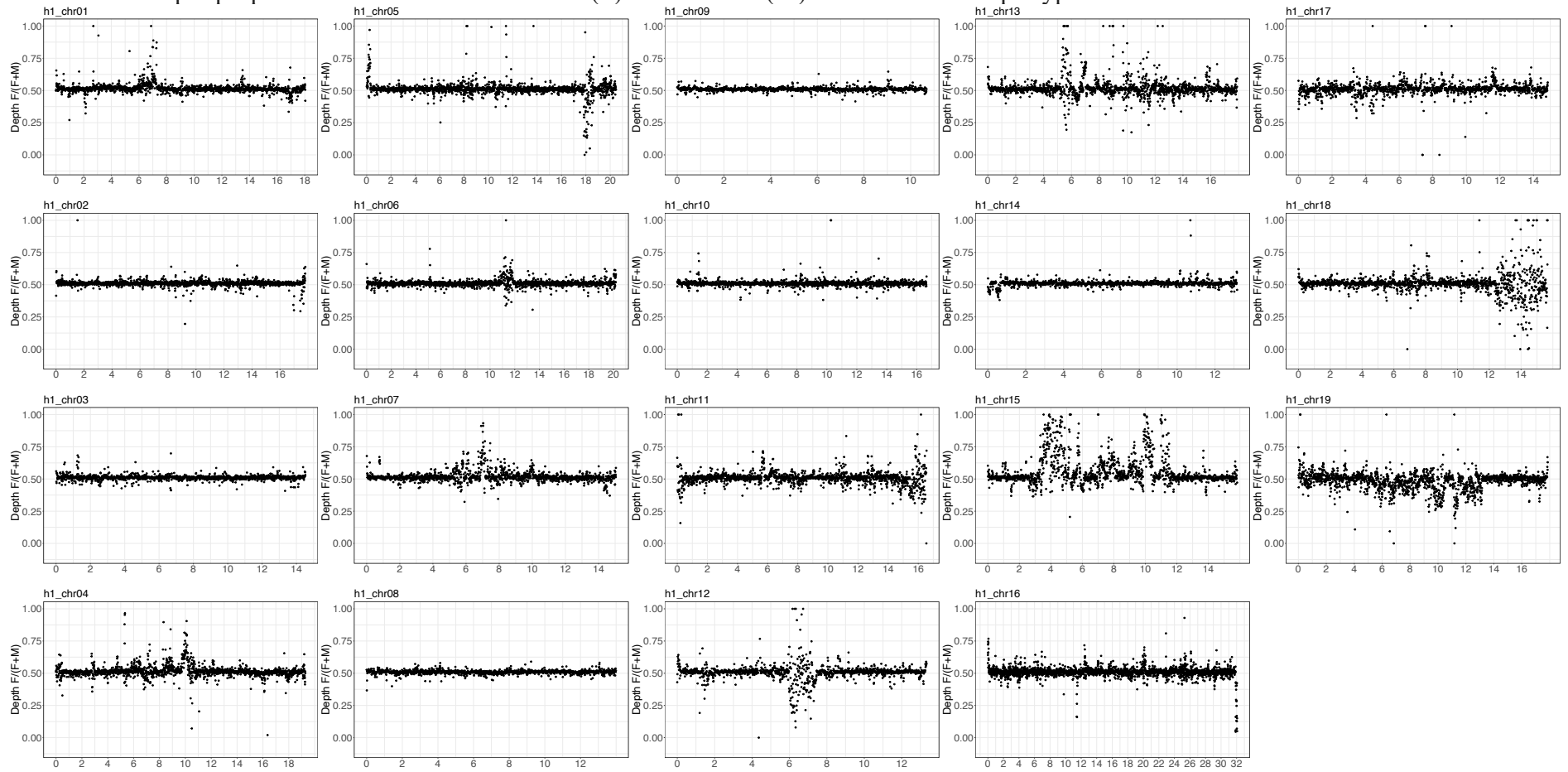


**Figure S2.** Genome-wide analysis of chromatin interactions at 1-Mb resolution in two haplotypes (a,b) of *Salix herbacea*.

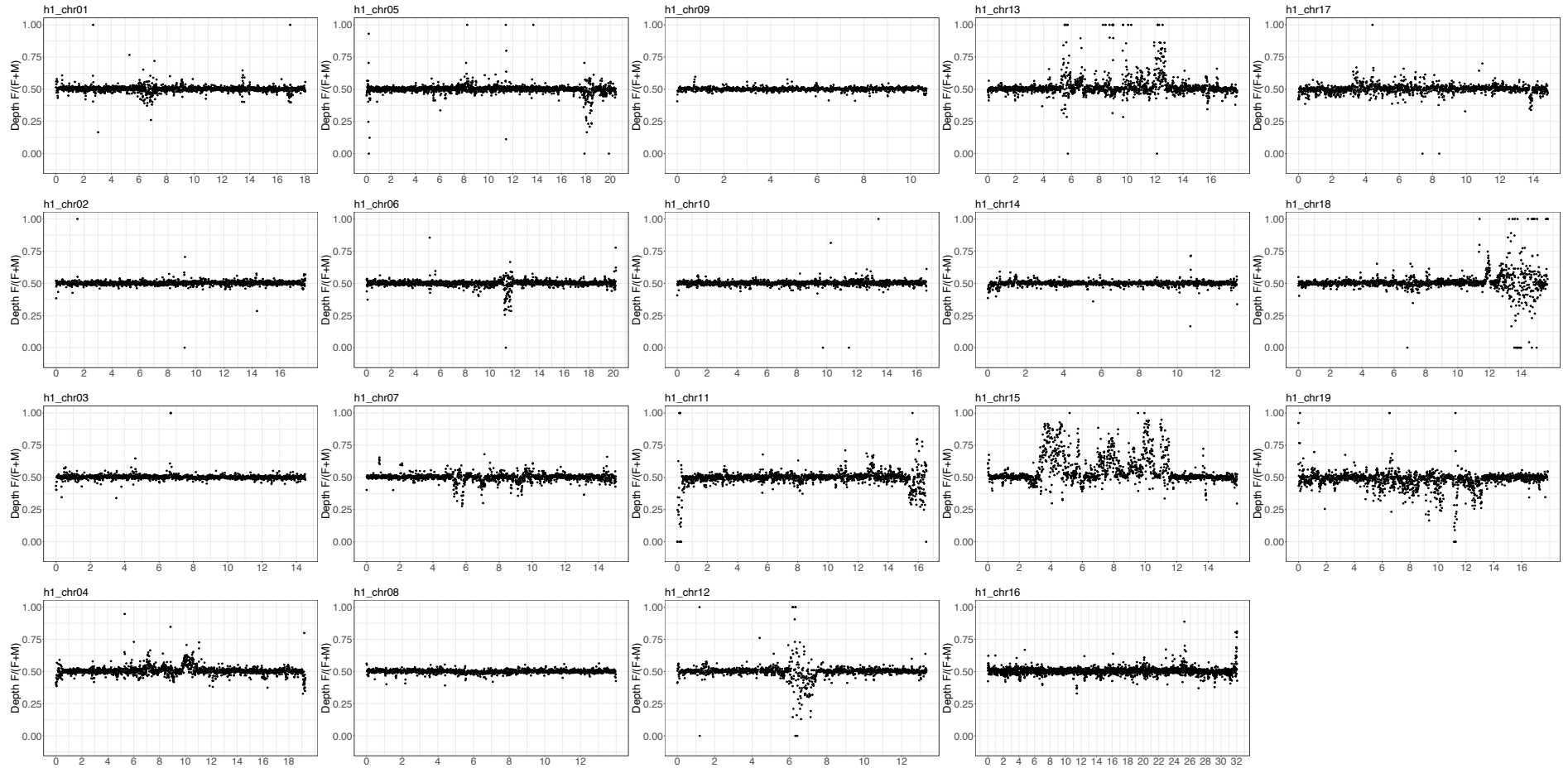


**Figure S3.** Alignment of the two haplotypes in a PacBio HiFi genome assembly of *Salix herbacea*.

a. Read depth proportion of females in 10 female (F) and 10 male (M) individuals for haplotype 1

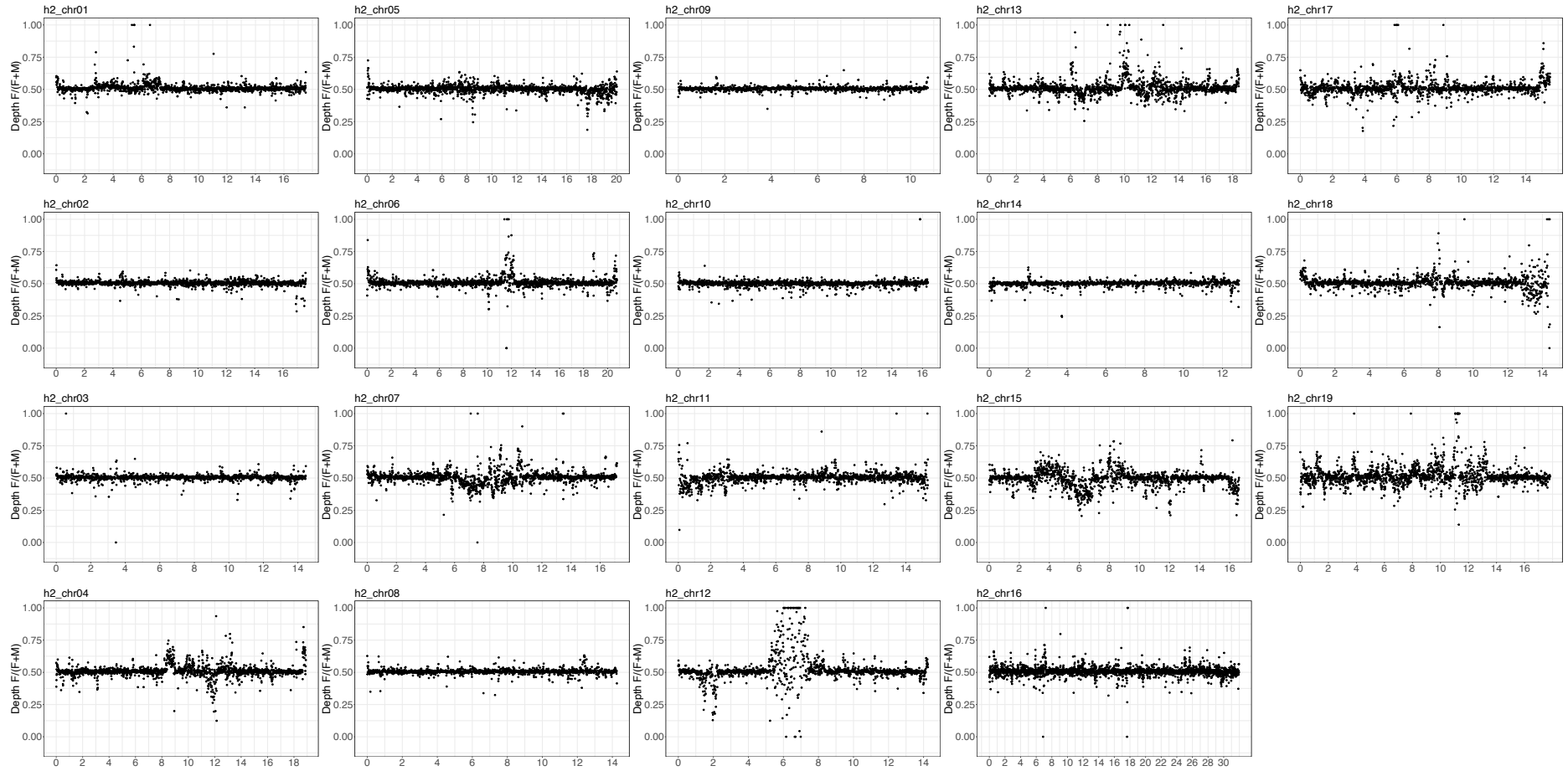


b. Read depth proportion of females in in pooled sequences of 50 females (F) and 50 males (M) for haplotype 1.

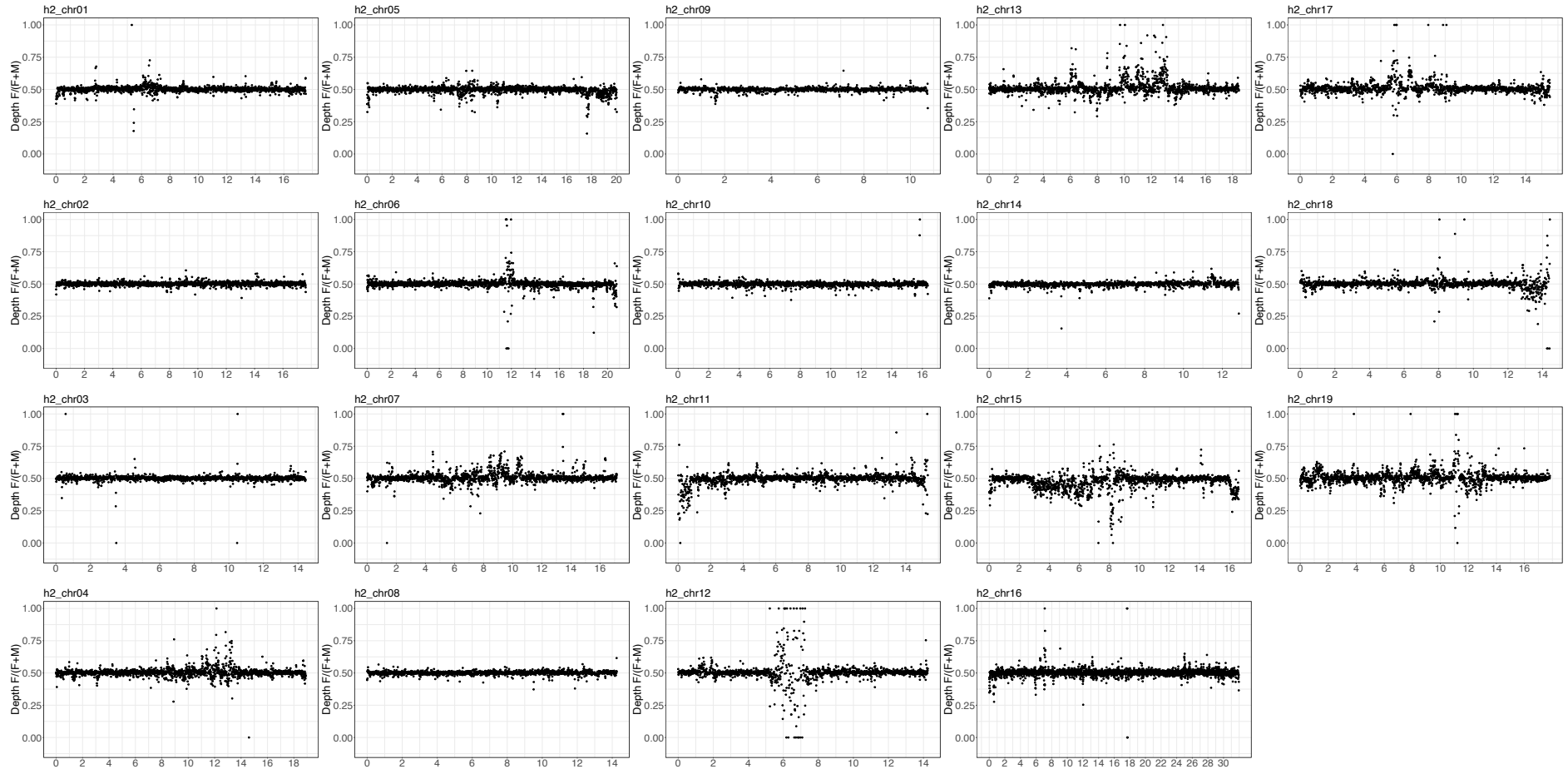


**Figure S4.** Read depth proportion of females in individual sequences of 10 females and 10 males (a) and pooled sequences of 50 females and 50 males (b) of *Salix herbacea*, calculated as  $F/(F+M)$  in 10 Kb windows mapped to **haplotype 1**.

a. Read depth proportion of females in 10 female (F) and 10 male (M) individuals for haplotype 2

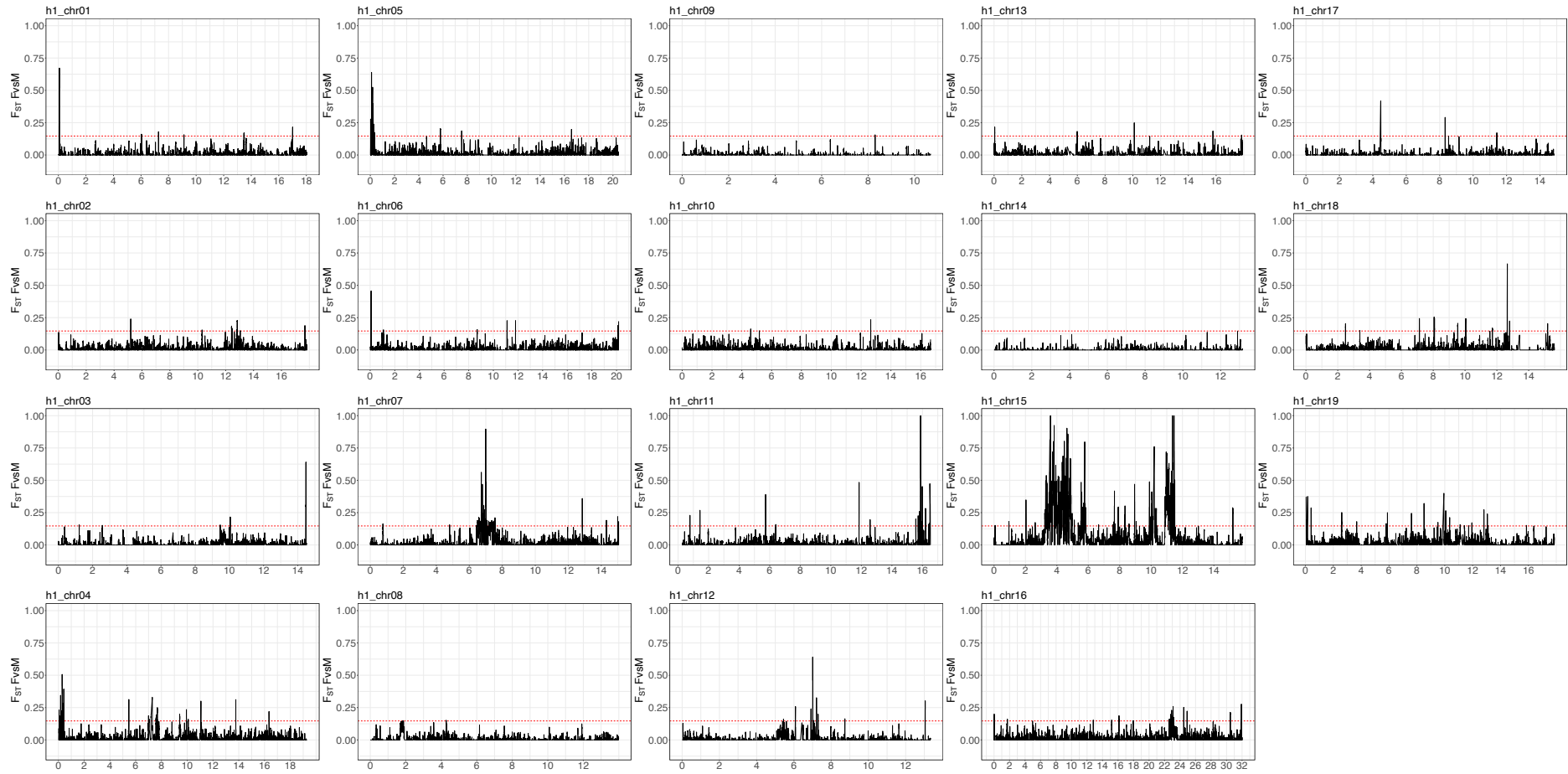


b. Read depth proportion of females in in pooled sequences of 50 females (F) and 50 males (M) for haplotype 2.

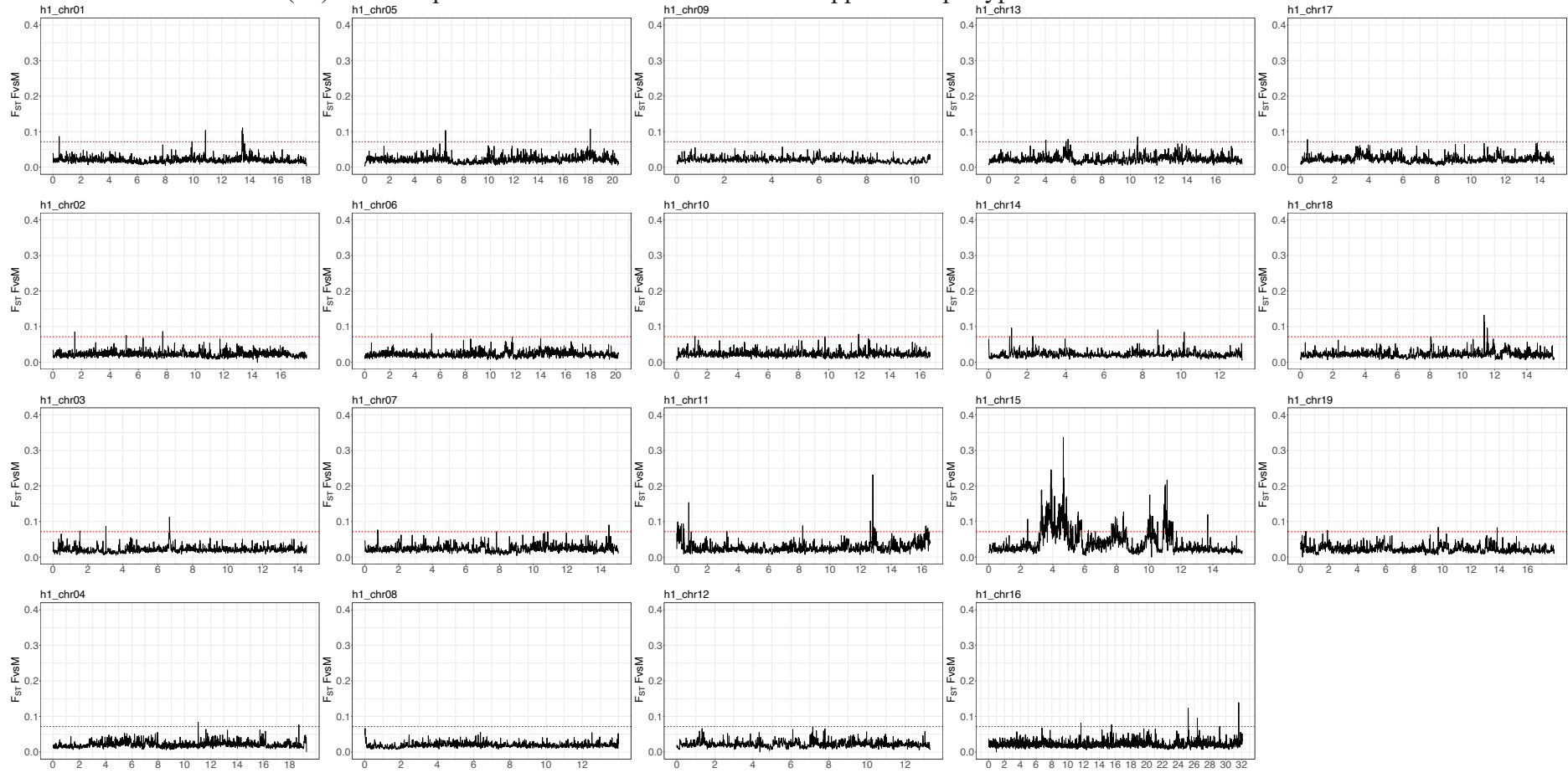


**Figure S5.** Read depth proportion of females in individual sequences of 10 females and 10 males (a) and pooled sequences of 50 females and 50 males (b) of *Salix herbacea*, calculated as  $F/(F+M)$  in 10 Kb windows mapped to **haplotype 2**.

a. Genetic differentiation ( $F_{ST}$ ) between 10 female (F) and 10 male (M) individuals mapped to haplotype 1

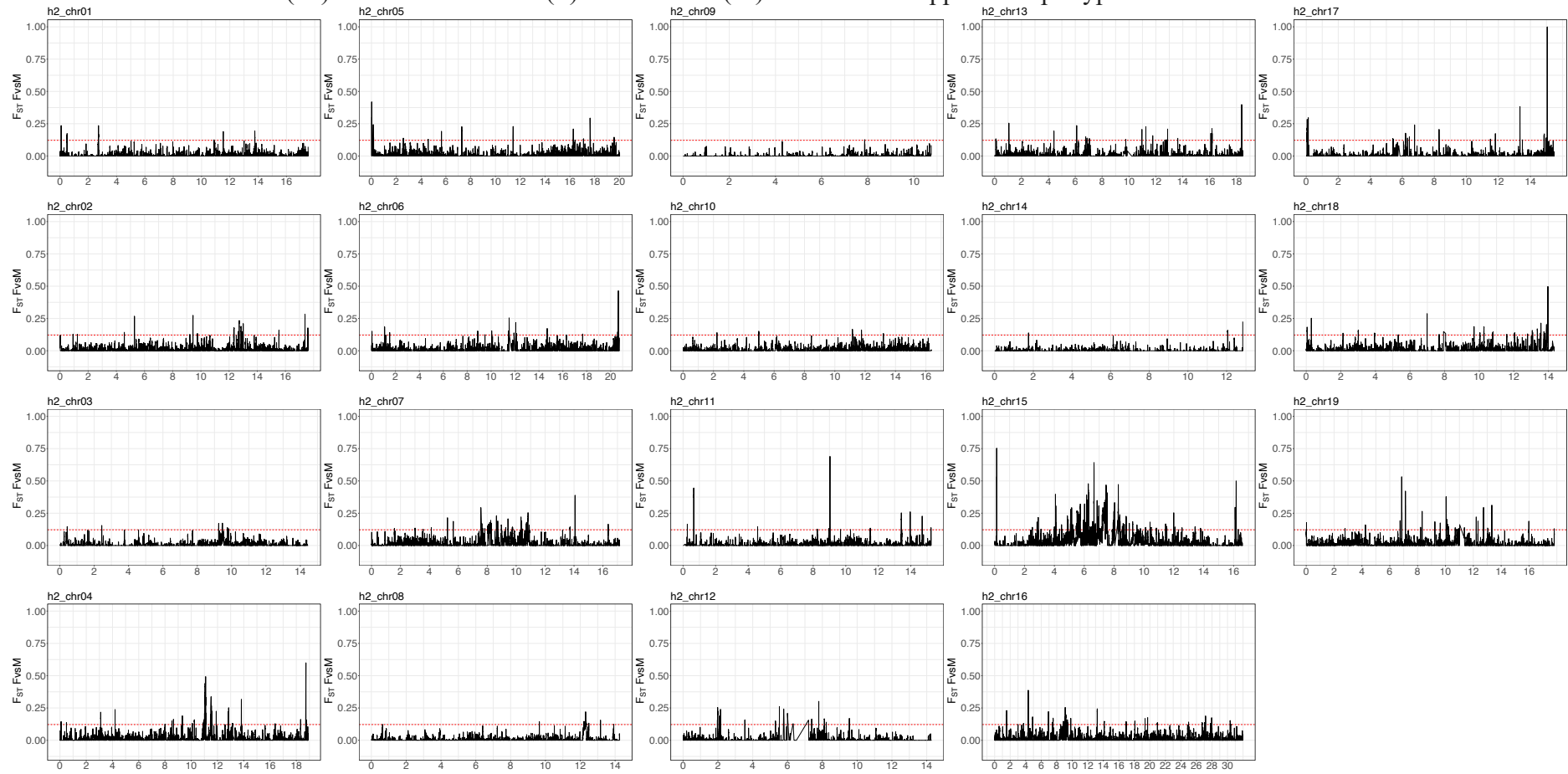


b. Genetic differentiation ( $F_{ST}$ ) between pools of 50 females and 50 males mapped to haplotype 1

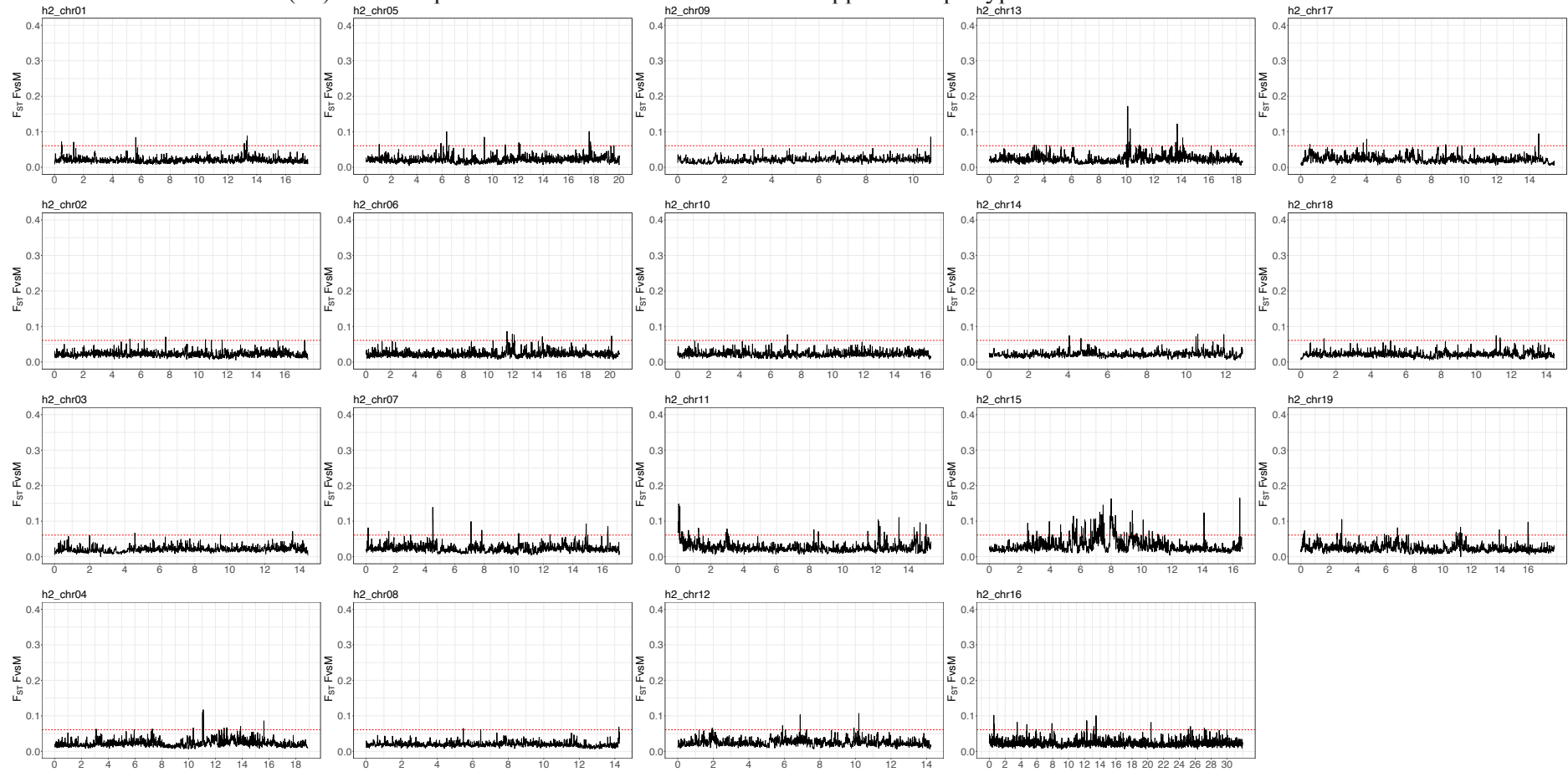


**Figure S6.** Between-sex genetic differentiation ( $F_{ST}$ ) in *Salix herbacea* in 10 Kb windows mapped to **haplotype 1**: (a)  $F_{ST}$  between individual sequences of 10 females and 10 males and (b)  $F_{ST}$  between pools of 50 females and 50 males. The genome-wide 99th percentile indicated as a red dashed line

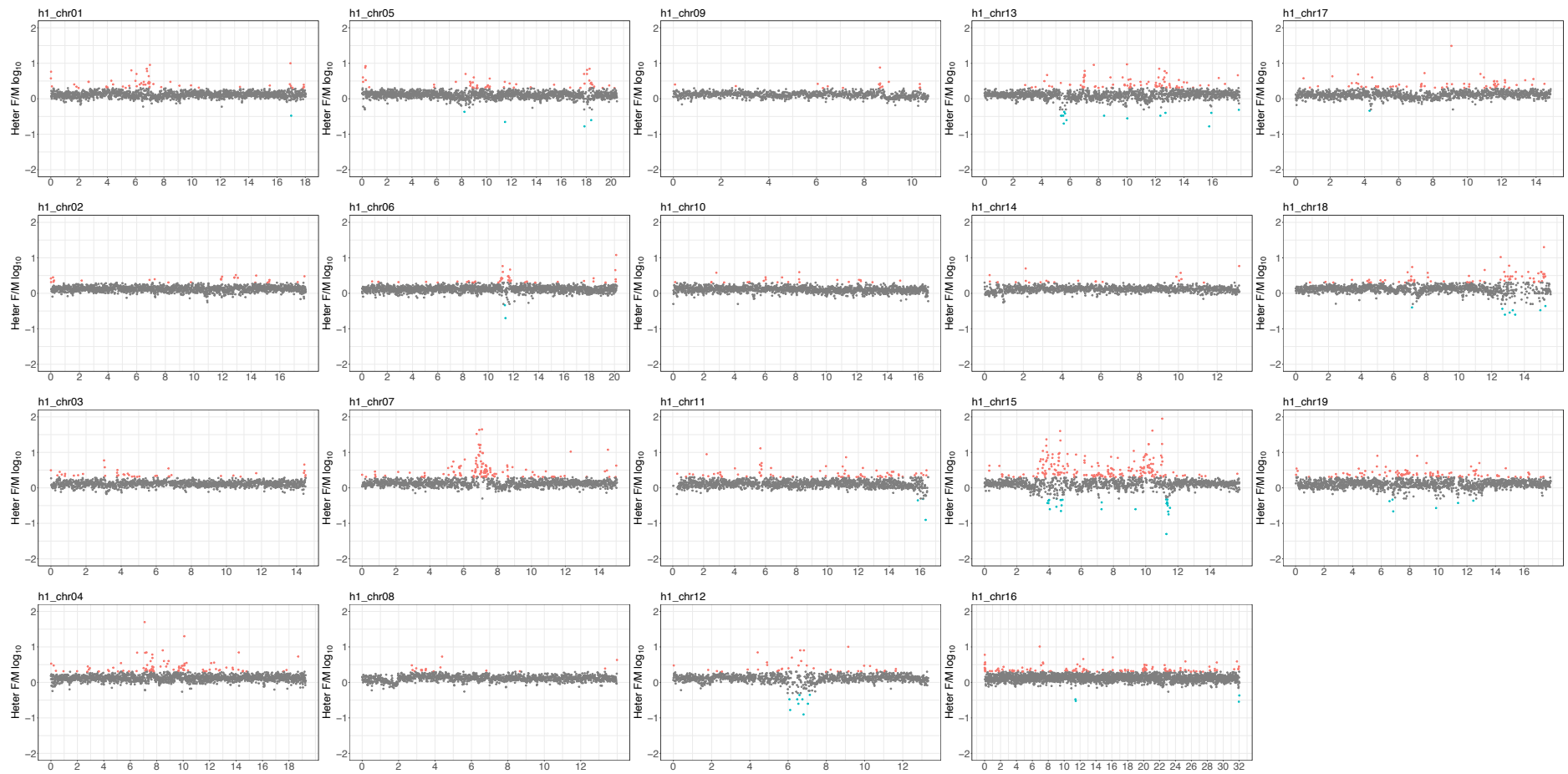
a. Genetic differentiation ( $F_{ST}$ ) between 10 female (F) and 10 male (M) individuals mapped to haplotype 2



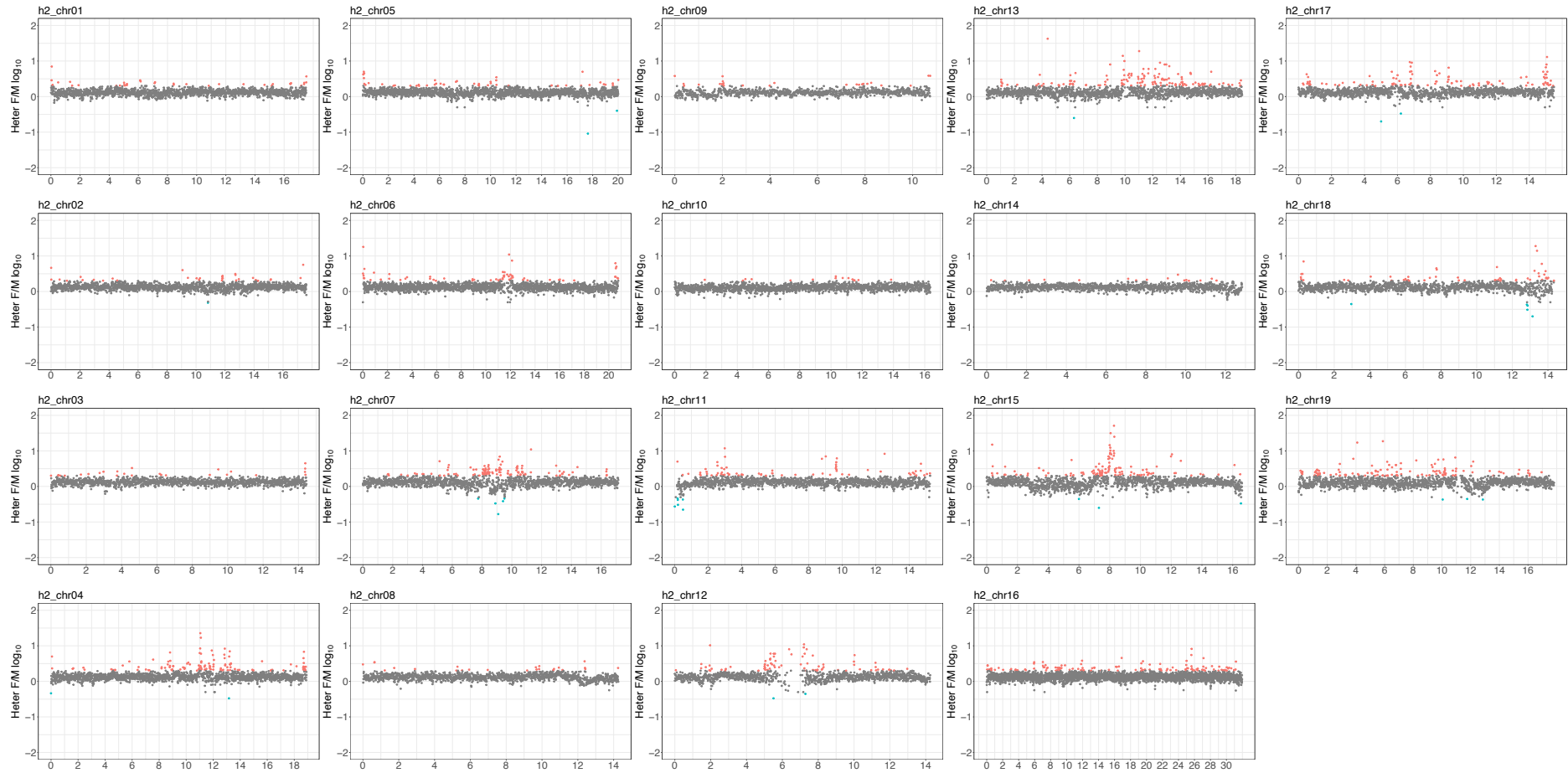
b. Genetic differentiation ( $F_{ST}$ ) between pools of 50 females and 50 males mapped to haplotype 2



**Figure S7.** Between-sex genetic differentiation ( $F_{ST}$ ) in *Salix herbacea* in 10 Kb windows mapped to **haplotype 2**: (a)  $F_{ST}$  between individual sequences of 10 females and 10 males and (b)  $F_{ST}$  between pools of 50 females and 50 males. The genome-wide 99th percentile indicated as a red dashed line.



**Figure S8.** Ratio of the number of heterozygous sites between 10 females (F) and 10 males (M) in 10 Kb windows (F/ M), mapped to **haplotype 1**; a twofold excess of female or male heterozygous sites is indicated in red and blue colour, respectively.



**Figure S9.** Ratio of the number of heterozygous sites between 10 females (F) and 10 males (M) of *Salix herbacea* in 10 Kb windows (F/ M), mapped to **haplotype 2**; a twofold excess of female or male heterozygous sites is indicated in red and blue colour, respectively.