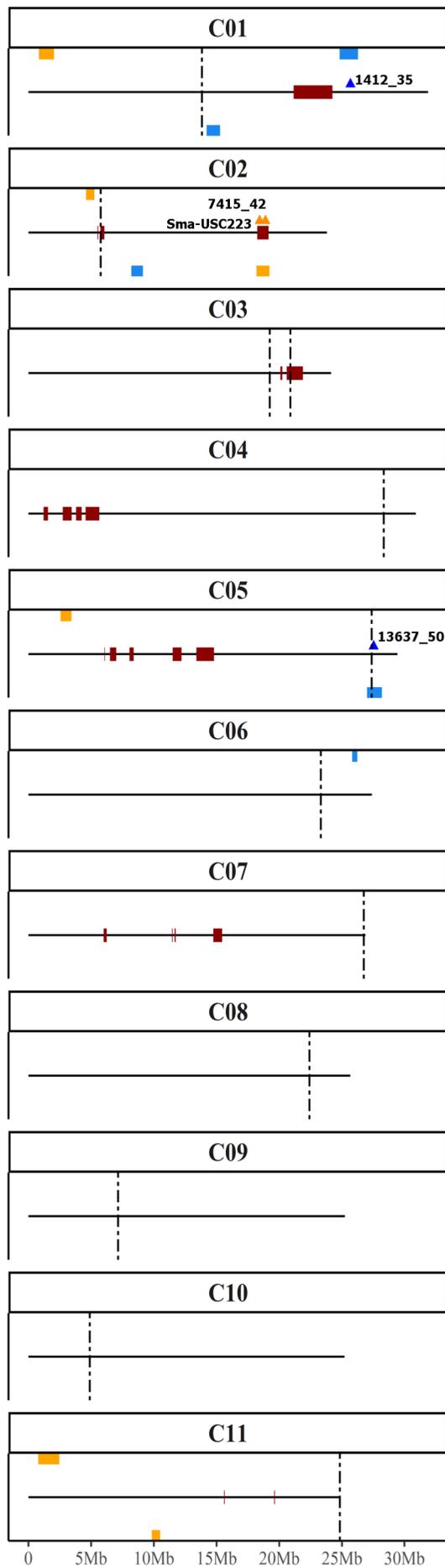
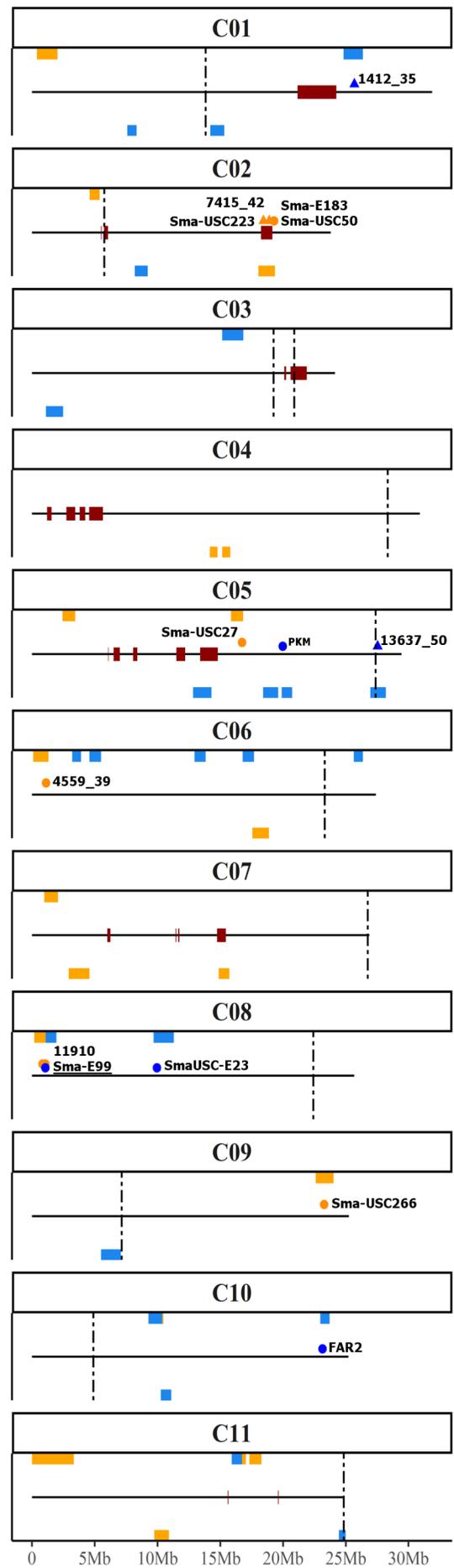


A Strict ZHp threshold (ZHp > 3.0; ZHp < -3.0)



Length (bp) by chromosome

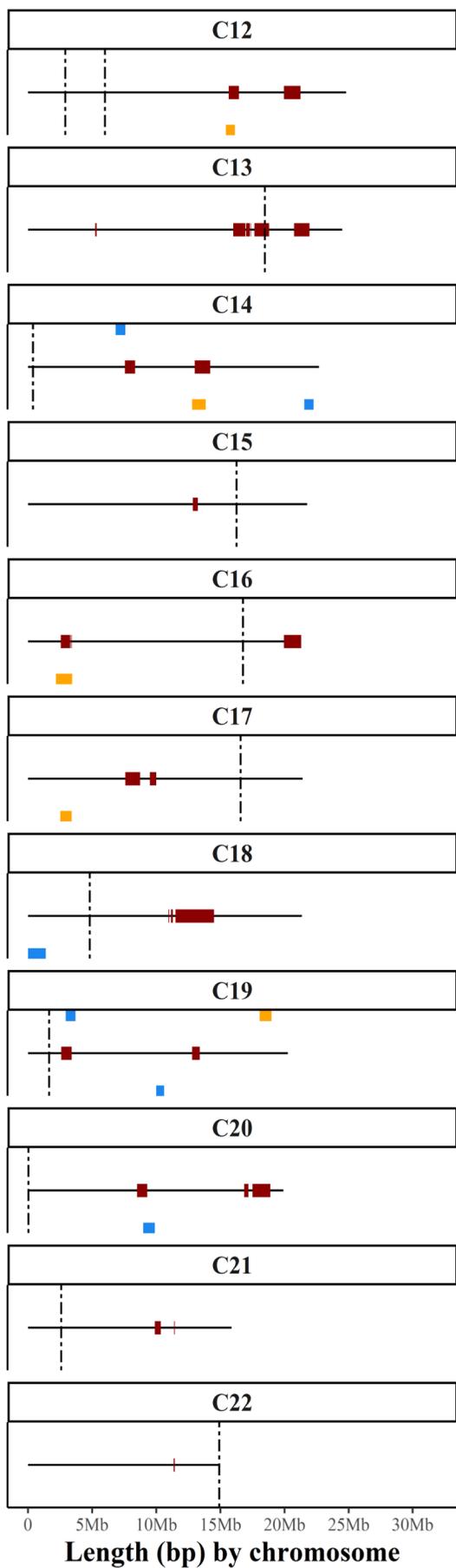
B Suggestive ZHp threshold (ZHp > 2.5; ZHp < -2.5)



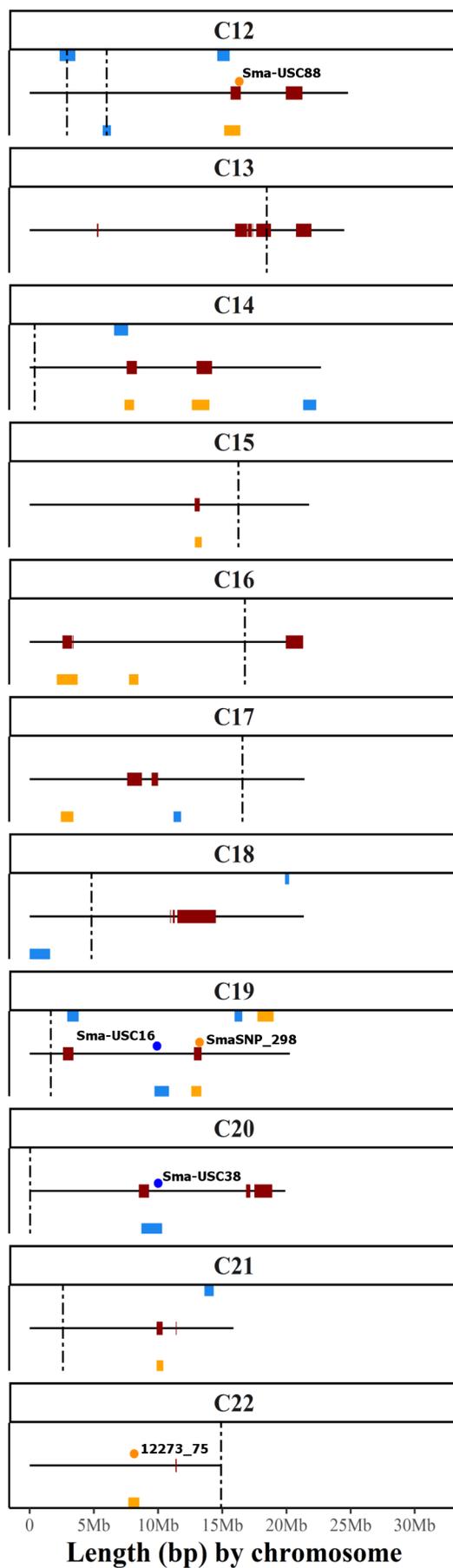
Length (bp) by chromosome

Supplementary Figure 7. Genome-wide distribution of ROHi and low-/high-GD windows in the broodstock population and low-/high-GD windows in the wild population, according to both strict (A) and suggestive (B) ZHp thresholds. Different SNP panels were used for each population. Broodstock ROHi are shown as red segments; high-/low-genetic diversity (GD) regions are drawn as orange segments for broodstock and blue segments for wild; in both cases, high-GD regions are represented above the horizontal black line, while low-GD windows are located below. Relevant suggestive markers included inside low-GD and/or high-GD regions in broodstock (orange) and wild (blue) had their positions graphed.

A Strict ZHp threshold (ZHp > 3.0; ZHp < -3.0)



B Suggestive ZHp threshold (ZHp > 2.5; ZHp < -2.5)



Supplementary Figure 7. Genome-wide distribution of ROHi and low-/high-GD windows in the broodstock population and low-/high-GD windows in the wild population, according to both strict (A) and suggestive (B) ZHp thresholds. Different SNP panels were used for each population. Broodstock ROHi are shown as red segments; high-/low-genetic diversity (GD) regions are drawn as orange segments for broodstock and blue segments for wild; in both cases, high-GD regions are represented above the horizontal black line, while low-GD windows are located below. Relevant suggestive markers included inside low-GD and/or high-GD regions in broodstock (orange) and wild (blue) had their positions graphed.