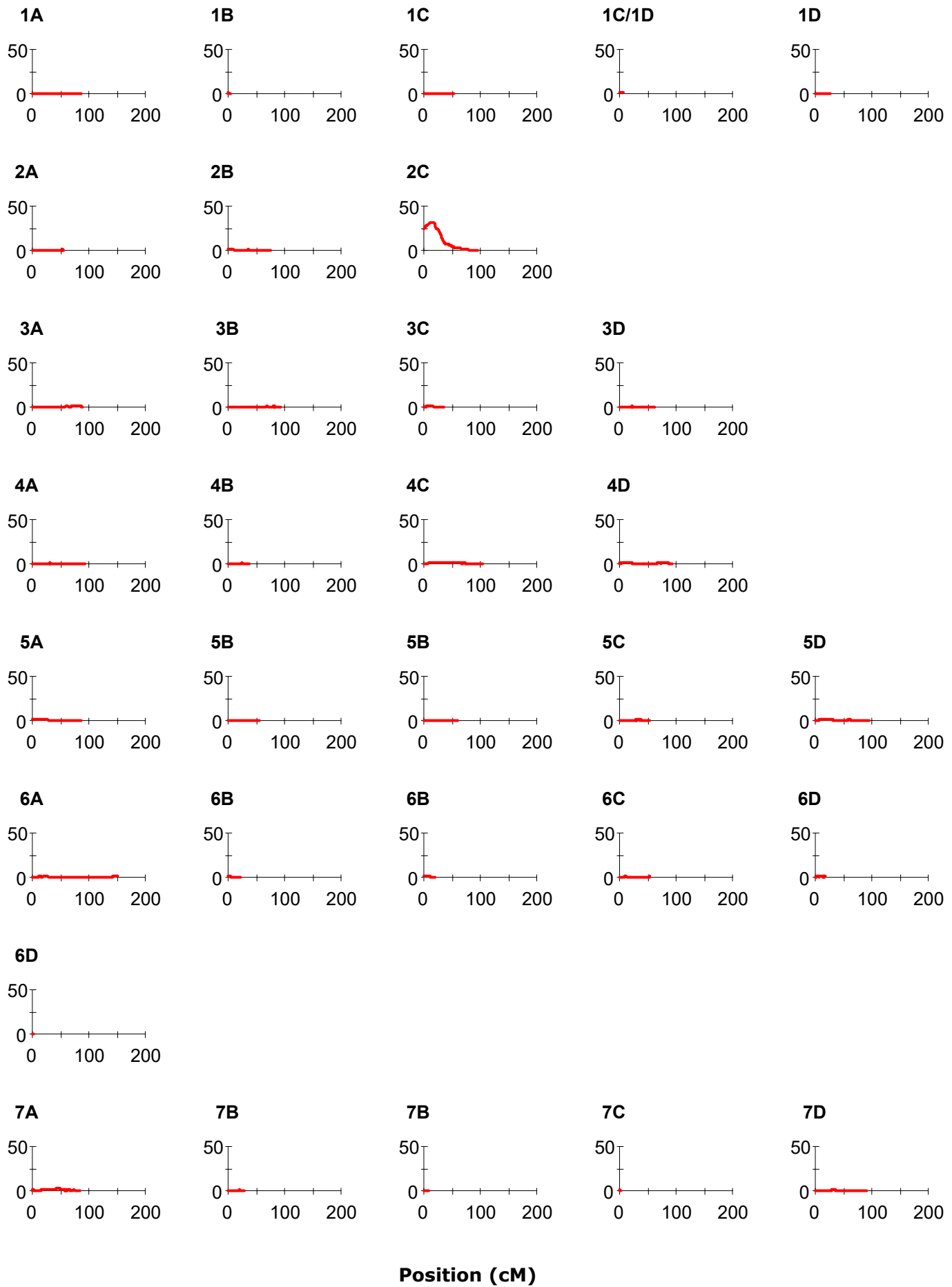


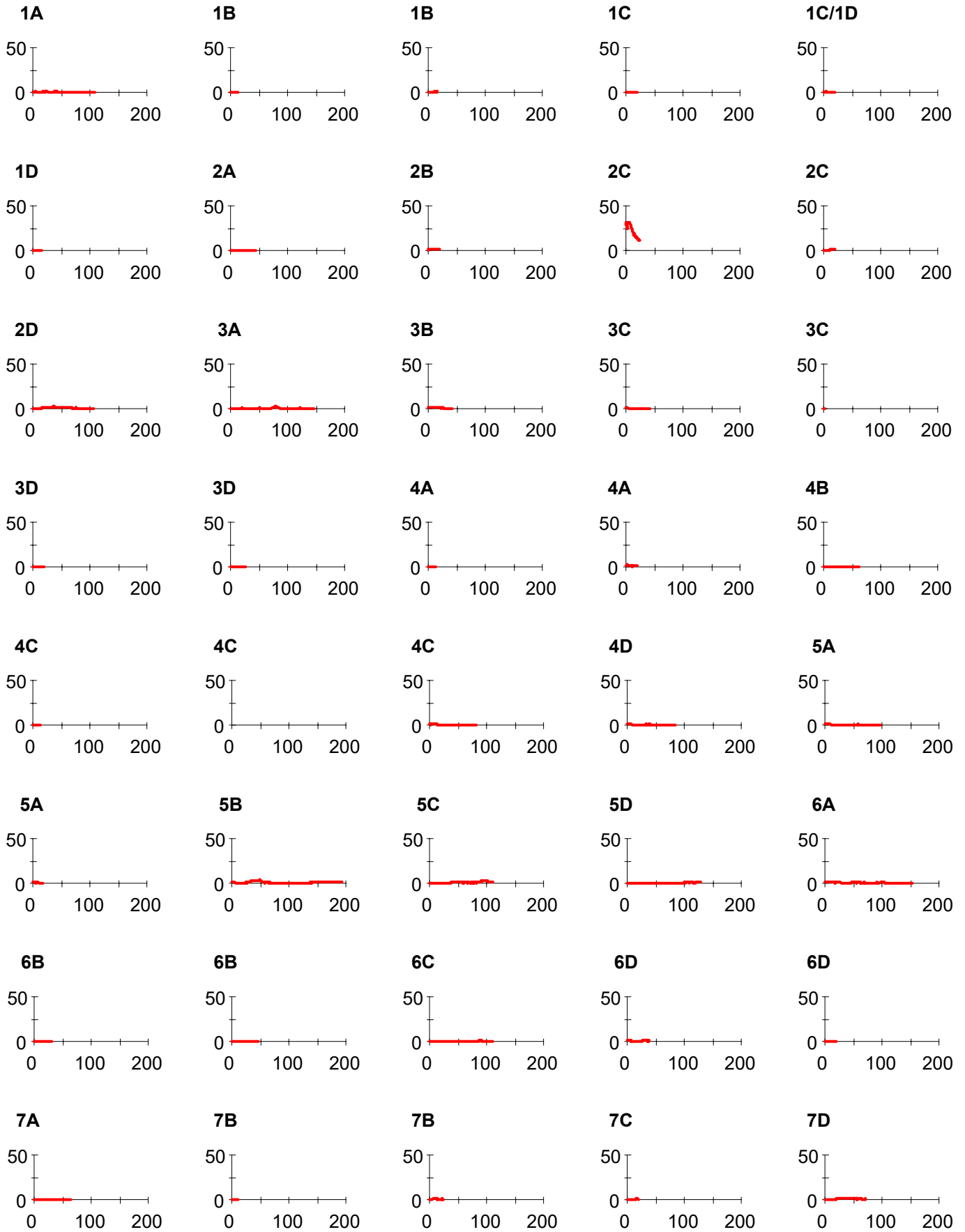
# Fronteras

LOD



# Portola

LOD



Position (cM)

**Supplemental File 4.** QTL mapping statistics for resistance to Fusarium wilt in two *F. x ananassa* S1 mapping populations genotyped with the Affymetrix iStraw35 SNP array. Collectively, 5,673 co-dominant SNP markers were genetically mapped in Fronteras S1 mapping population ( $n=93$ ) and assembled into 40 linkage groups, where  $n$  = number of S1 progeny. Similarly, 7,345 co-dominant SNP markers were genetically mapped in the Portola S1 population ( $n=93$ ) and assembled into 50 linkage groups. Linkage groups were numbered and aligned with 28 linkage groups previously described by van Dijk et al. (2014) and Mangandi et al. (2017) and are hypothesized to correspond to the 28 chromosomes in the haploid genome of *F. x ananassa*. Likelihood-odds (LOD) statistics and linkage group positions (cM) are shown for QTL interval mapping across linkage groups. Linkage groups that did not align to the reference or had fewer than 10 SNPs are excluded from the figure, but were included in the mapping and did not show significant LOD scores.