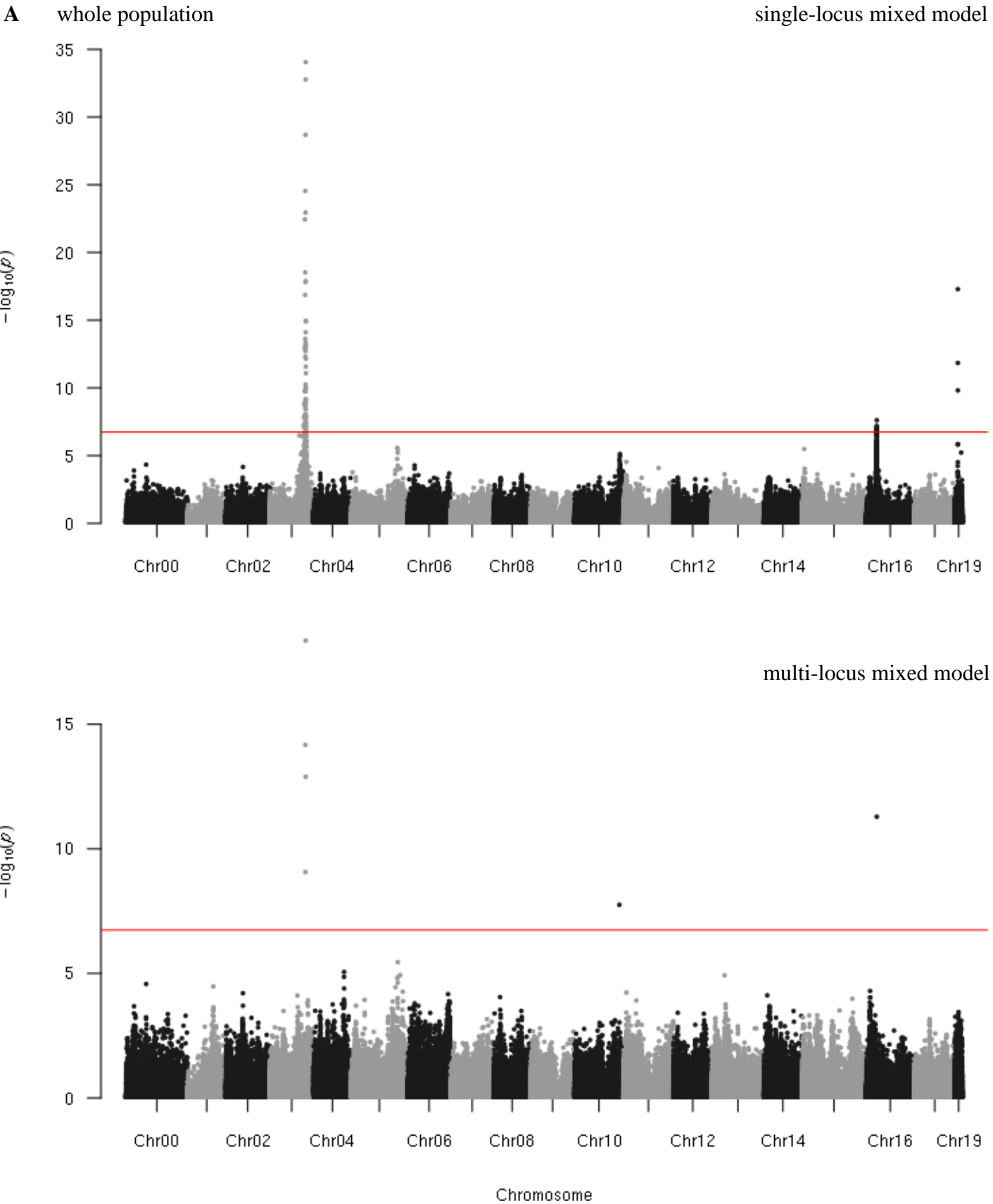


Figure S4. Manhattan plots for ripening period in the whole population (A) based on a single-locus mixed model (upper part) and on a multi-locus mixed model (lower part) at a Bonferroni-corrected threshold of 0.05 (dashed horizontal line). Manhattan plots for ripening period in each of the six collections (B - G) based on a single-locus mixed model (upper part) and on a multi-locus mixed model (lower part) at a Bonferroni-corrected threshold of 0.05 (dashed horizontal line): INRA (B), UNIBO (C), CRA-W (D), RBIPH (E), NFC (F) and SLU (G). The fictive chromosome 0 contained the SNPs in all unassigned scaffolds and the fictive chromosome 19 contained SNPs with no position after blasting on the GDDH13 genome.

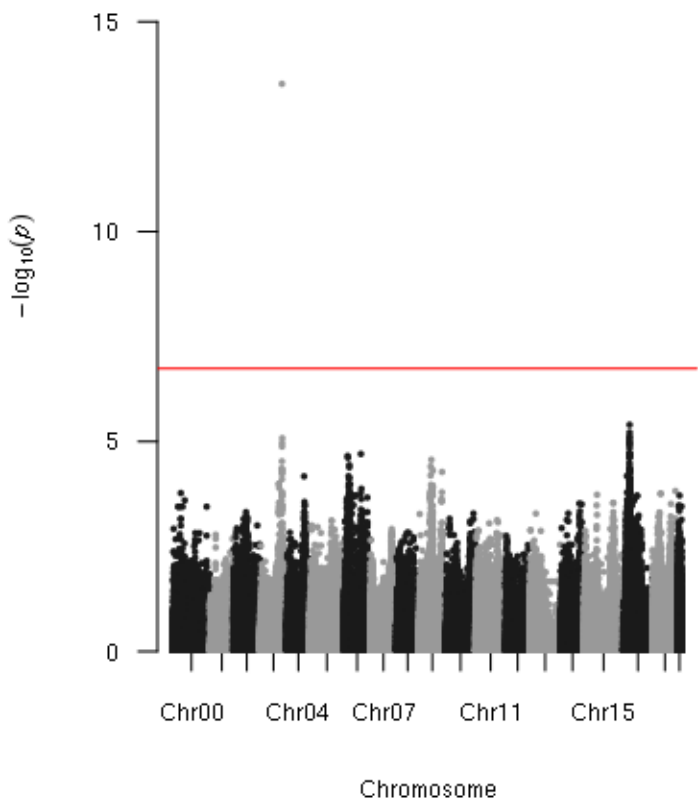
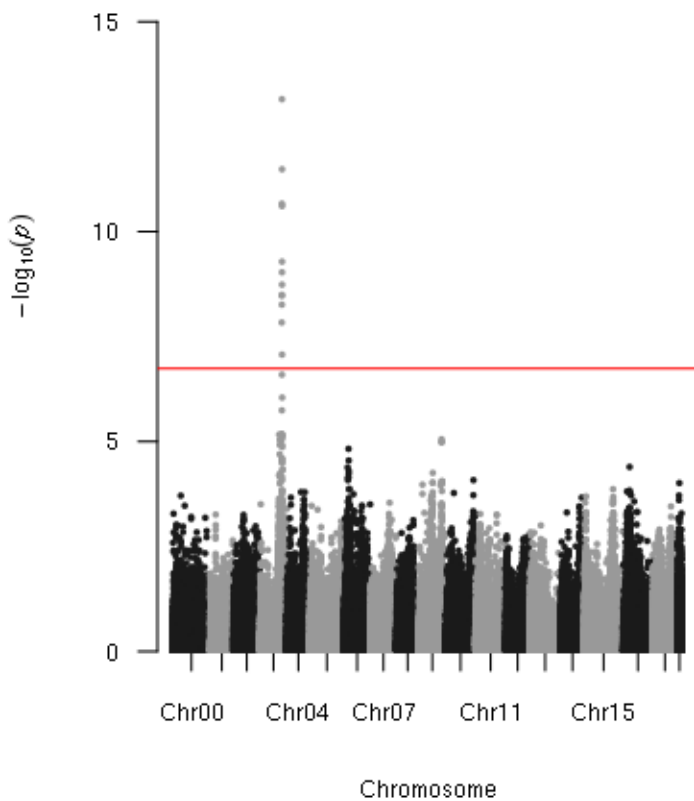


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B INRA

single-locus mixed model

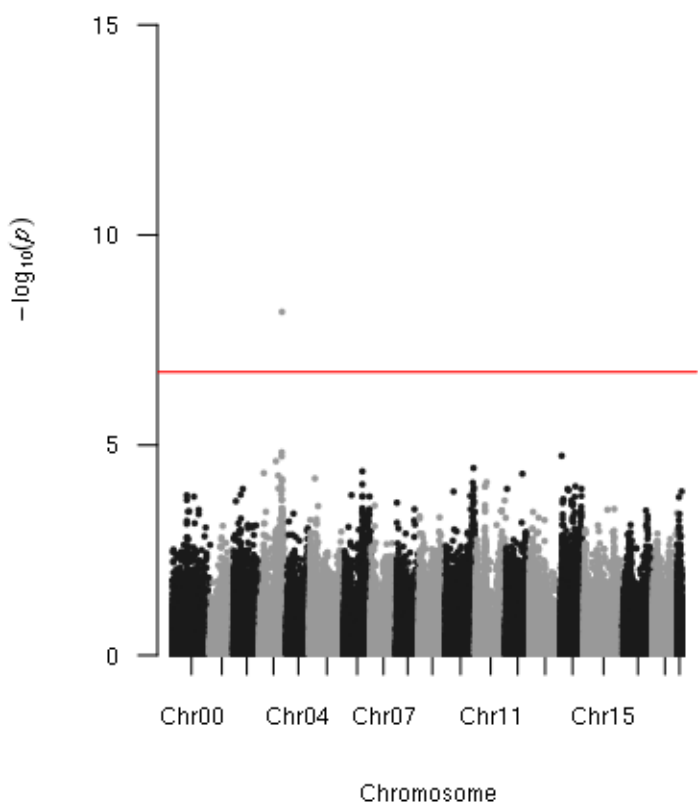
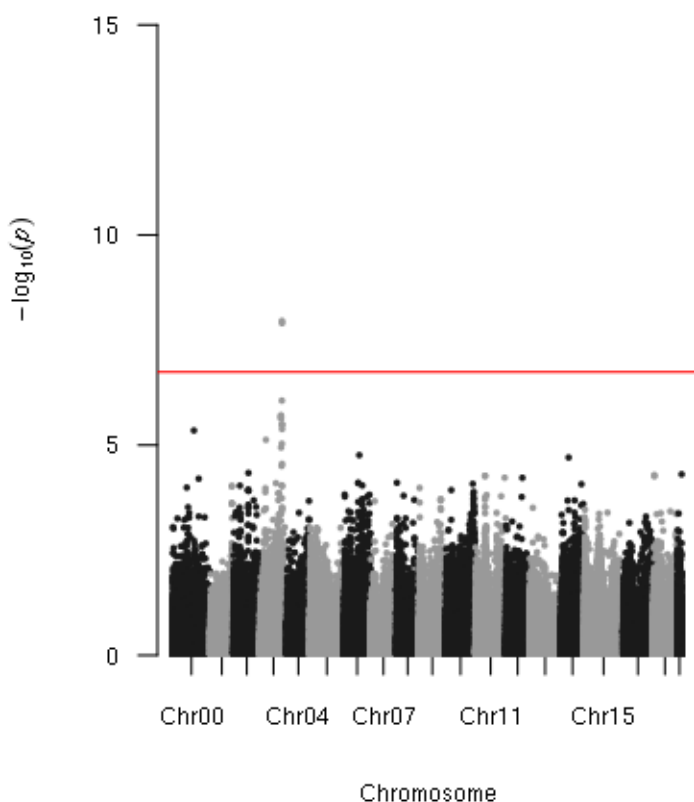
multi-locus mixed model



C UNIBO

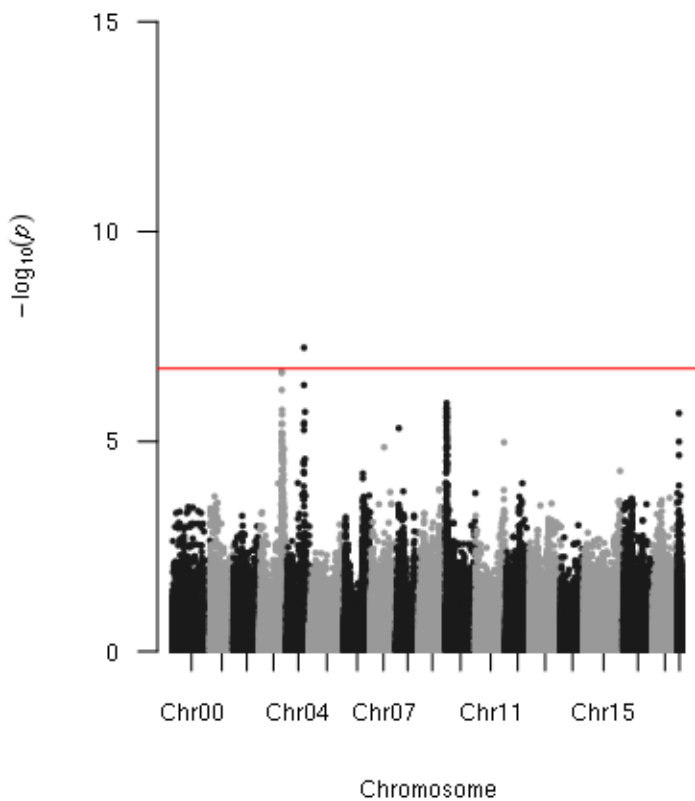
single-locus mixed model

multi-locus mixed model

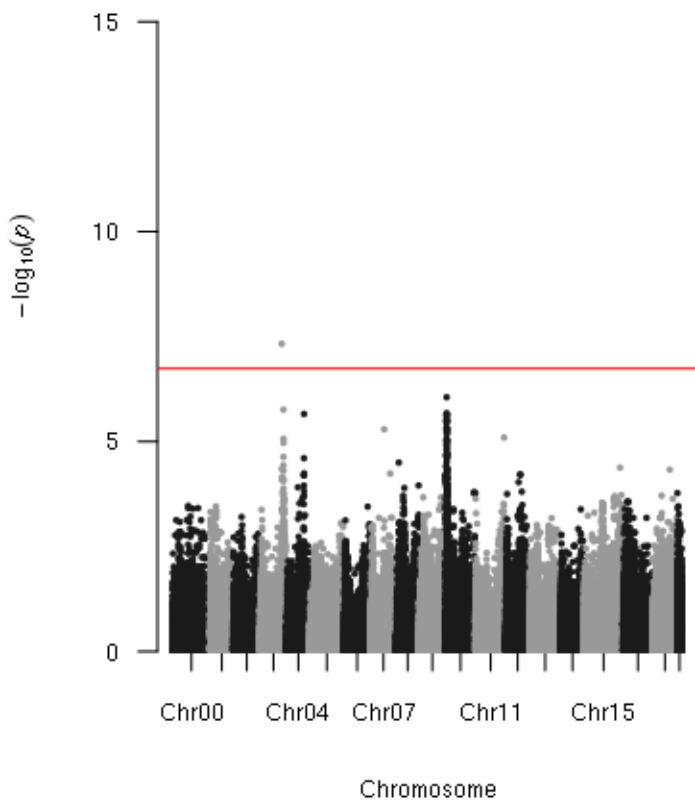


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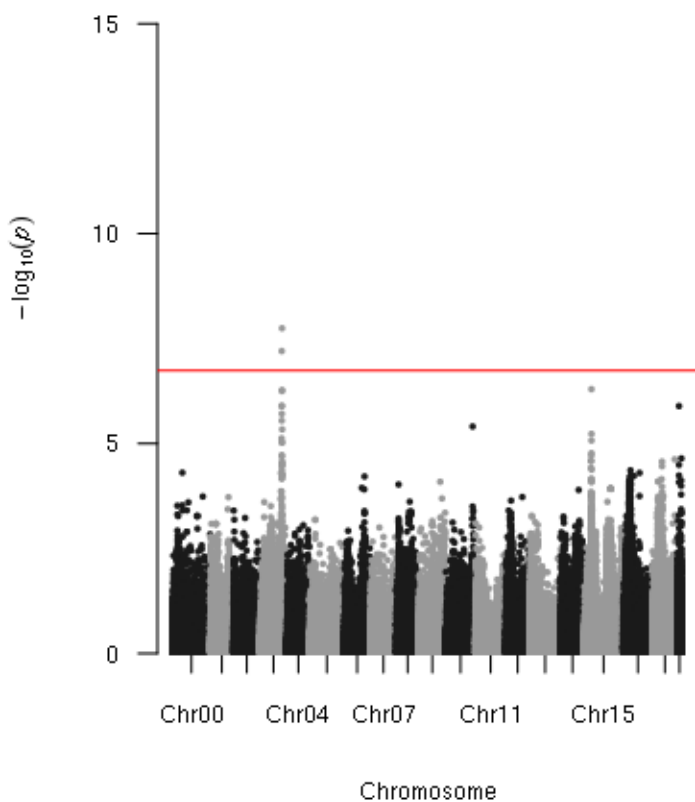
D CRA-W single-locus mixed model



multi-locus mixed model



E RBIPH single-locus mixed model



multi-locus mixed model

