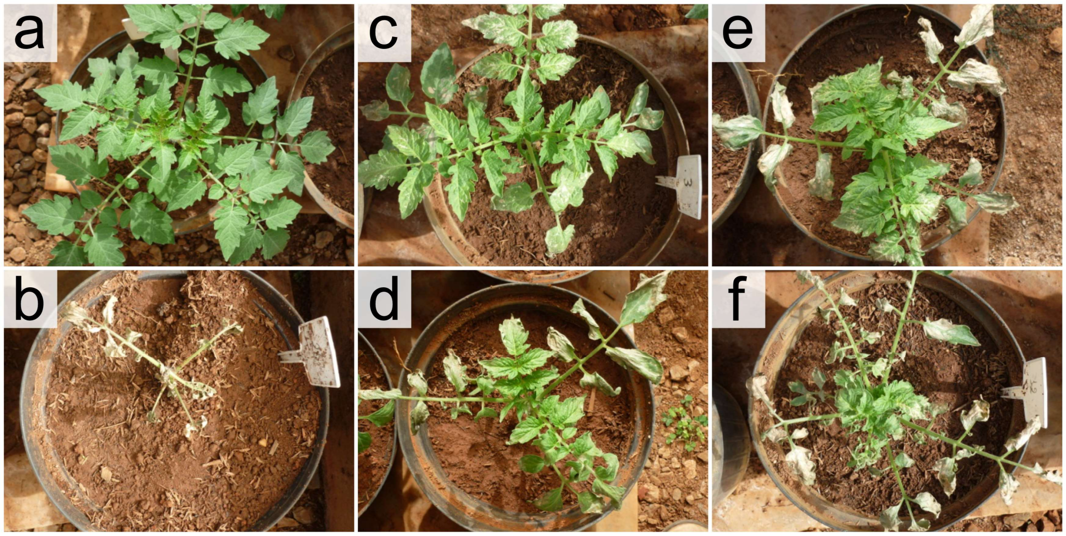
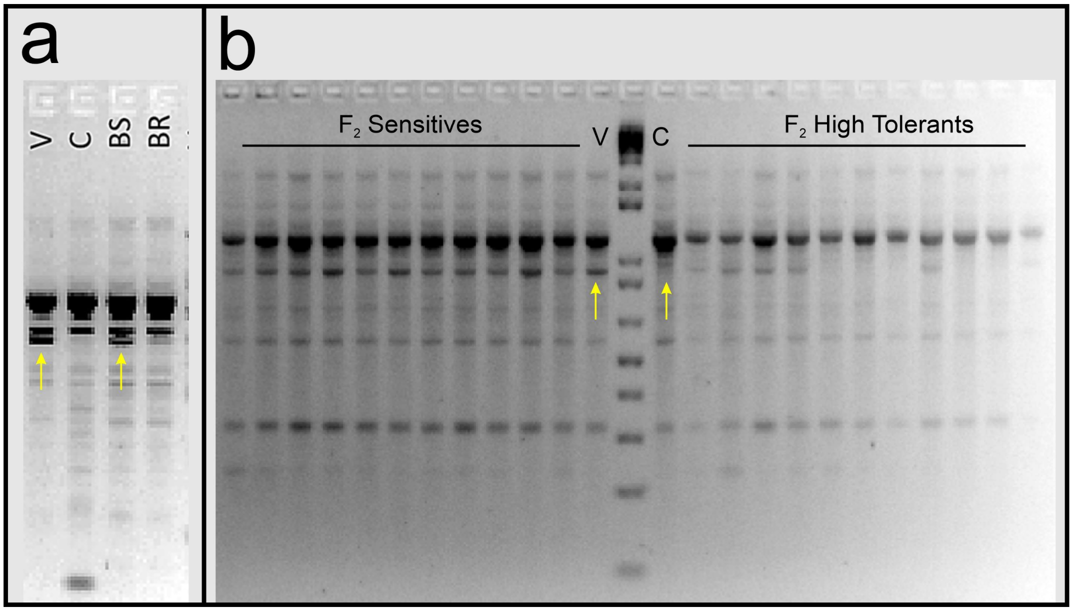
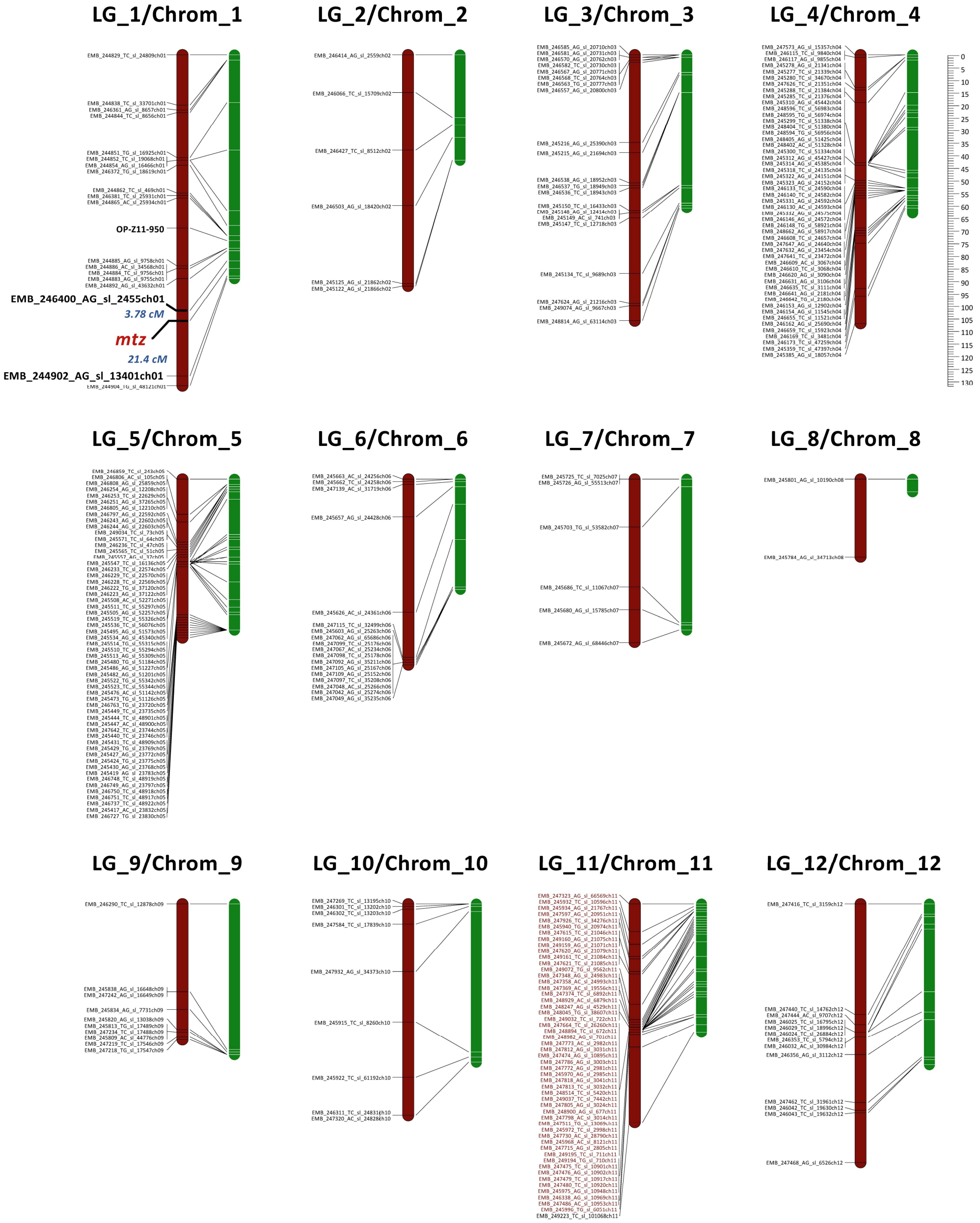


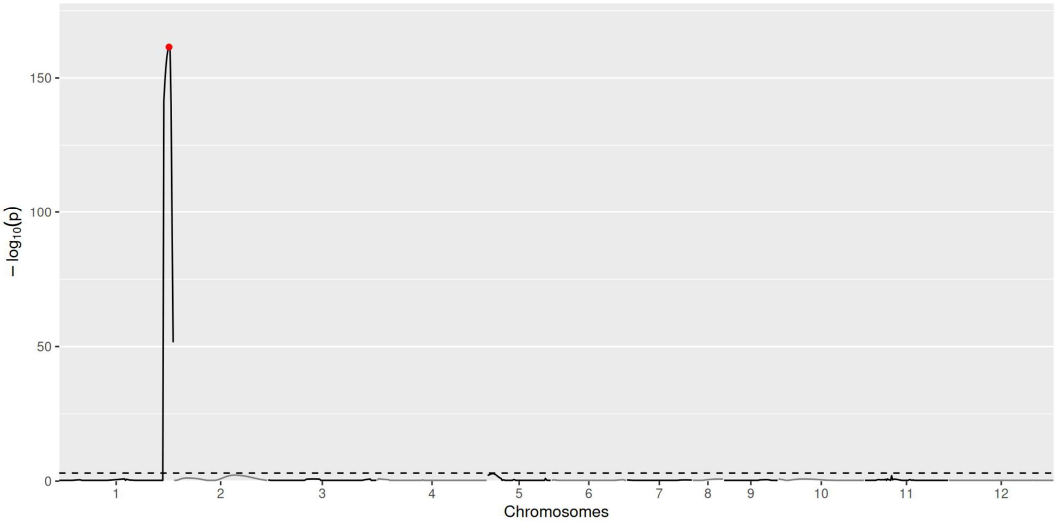
Online Resource 1 Responses of a subgroup of F_2 tomato (*Solanum lycopersicum* L.) individuals derived from the cross of the tomato cultivar 'Viradoro' × 'CNPH–0498' at five days after application of 0.96 Kg per hectare of metribuzin**. a)** Plant with complete absence of metribuzin-induced foliar toxicity symptoms (= high tolerant F_2 individual); **b)** to **f)** distinct levels of foliar toxicity in F_2 individuals classified as sensitives.



Online Resource 2 Agarose gels (1.5%) used for the bulked segregant analysis (BSA) with the RAPD marker OPZ-11-950 associated with metribuzin tolerance in tomato (*Solanum lycopersicum* L.). V = Sensitive parental cultivar 'Viradoro'. C = tolerant parental line 'CNPH–0498'), BS = Bulk sensitive: an equimolar DNA mix of seven F_2 individuals with the metribuzin sensitive phenotype), BR = bulk tolerant: an equimolar DNA mixture of seven F_2 individuals with the metribuzin tolerant phenotype). Yellow arrows indicate the presence of a polymorphic amplicon in V and BS. **b)** Marker evaluation of 11 sensitive F_2 individuals and 11 high tolerant F_2 individuals. Black arrows indicate the 950 bp position in the molecular weight marker (MM) lane, with the presence of the amplicon OP-Z11-950.



Online Resource 3 SNP linkage map built from segregation data of the ‘CNPH-0498’ (UGA-1113-MT) (tolerant) × ‘Viradoro’ (sensitive) F_2 (*n* = 501) population (red bars) aligned to the SL 4.0 version of the tomato genome sequence of cultivar ‘Heinz 1706’ (green bars). Distances among the 302 mapped SNPs are scaled in Kosambi centiMorgans for the linkage map and in Mbp for the genome sequence following the ruler on the right. The SCAR marker OP-Z11-950 is indicated. SNP markers displaying segregation distortion on chromosome 11 are highlighted in red.



Online Resource 4 Genome scan for independent tolerance loci. The only locus significantly associated with metribuzin tolerance is highlighted in red.