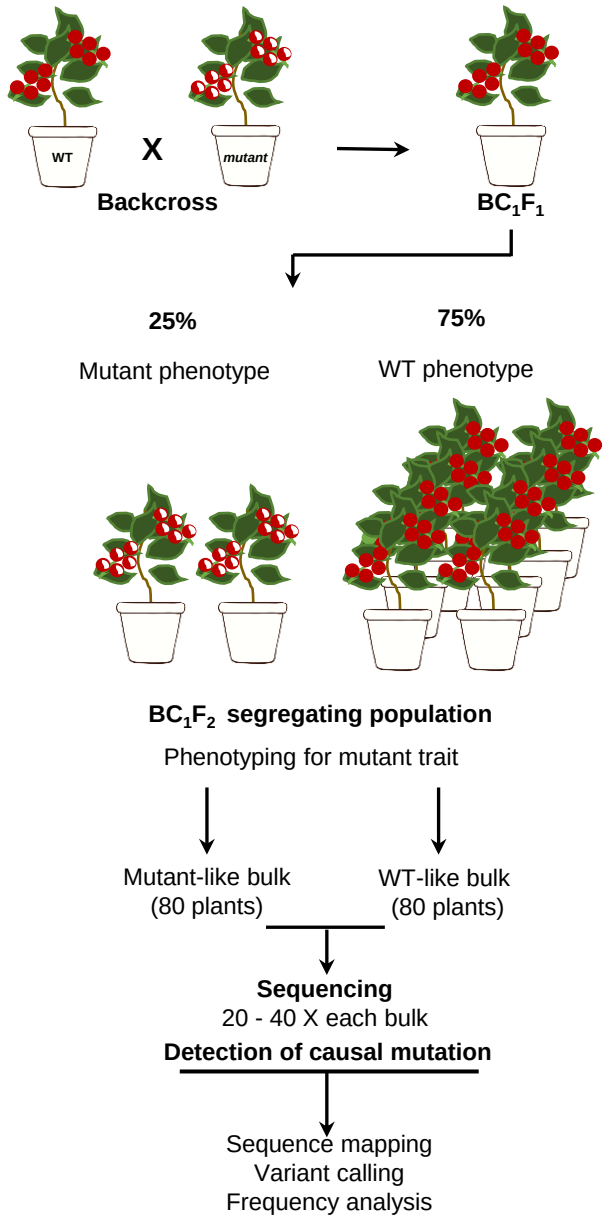

Supplemental Figure S1. Mapping-by-sequencing strategy for the identification of mutations underlying fruit cuticle phenotypic changes in Micro-Tom EMS mutants. The homozygous mutant line carrying a recessive mutation is first back-crossed (BC_1) with the WT parental line used for generating the EMS mutant collection. The BC_1F_1 hybrid plant displaying a WT-like phenotype is self-crossed. The resulting BC_1F_2 population segregating for the mutant trait is phenotyped and two bulks (80 plants each) are then constituted by pooling plants displaying either the WT or the mutant phenotype. Each bulk is then sequenced using Next Generation Sequencing (Illumina) to a depth of 20 to 40X coverage of the tomato genome. Trimmed sequences are mapped onto the tomato reference genome and EMS mutation variants are filtered. Comparison of the allelic mutation frequencies in the two bulks then allows the identification of the causal mutation, which shows very high frequency in the mutant-like bulk (~100% of mutant allele) and lower than average frequency in the WT-like bulk (~33% of mutant allele).