



Figure S1: Sanger chromatograms and HRM analysis of the targeted *StDMR6-1* locus of the potato cultivar Desiree. For chromatograms, guide and PAM sequences are indicated in black and red, respectively. A, T, C and G bases are represented in green, red, blue and dark, respectively. For HRM analysis, Desiree samples are depicted in blue while the mutant curve is depicted in red.



Figure S2: Sanger chromatograms and ICE analysis of the targeted *SlEIF4E2* locus for some tomato plants.

For chromatograms, guide and PAM sequences are indicated in black and red, respectively. A, T, C and G bases are represented in green, red, blue and black, respectively. For ICE analysis, outputs examples are depicted with the wild-type sequence indicated by a yellow cross. Contribution for each sequence (wild-type or mutated) is represented as a percentage, with the cut site indicated on the left (g1 and/or g2).