Supporting Information

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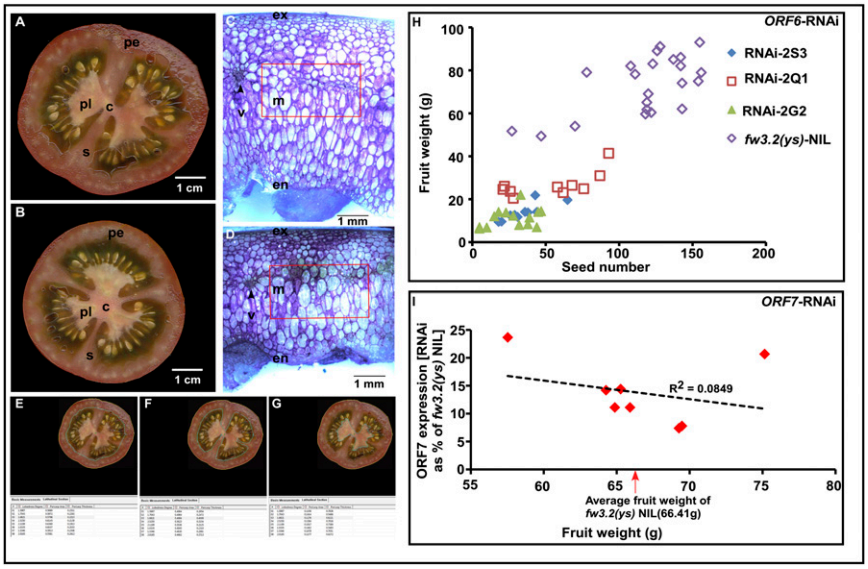

Fig. S1. Effect of *fruit weight 3.2* (*fw3.2*) on mature fruit structure, screenshots of different parts of fruits measured by TOMATO ANALYZER; fruit weight and seed number correlations in the nearly isogenic line (NIL) *fw3.2(ys)* and *ORF6* RNAi lines; fruit weight and *ORF7* transcript level in *ORF7* amiRNA lines. (*A* and *B*) Transverse section of the fruit from *fw3.2(ys)* and *fw3.2(wt)* NILs, respectively. (*C* and *D*) Pericarp cells of a transverse section of mature fruits from *fw3.2(ys)* and *fw3.2(wt)* NILs, respectively. Six large cells in the red box were used for cell measurements. Ten plants per genotype, two fruits per line, and two sections per fruit were used for the analysis. (*E*) Pericarp area surrounded by inner and outer pericarp boundaries. (*F*) Pericarp and septum area demarcated by outer pericarp boundary and inner pericarp boundary and septum. (*G*) Area covered by columella and placenta. (*H*) Fruit weight and total number of seeds per fruit were recorded for 10, 10, 14, and 22 fruits for RNAi-2S3, RNAi-2Q1, RNAi-2G2, and *fw3.2(ys)*, respectively. (*I*) Correlation of *ORF7* transcript accumulation and fruit size in *ORF7* amiRNA lines. Transcript level of *ORF7* in *ORF7* amiRNA lines were expressed as percentage of *ORF7* expression in *fw3.2(ys)* NIL. c, columella; en, endocarp; ex, exocarp; m, mesocarp; pe, pericarp; pl, placenta; s, septum; v, vascular bundle.

Other Supporting Information Files

Table S1 (DOCX)
Table S2 (DOCX)
Table S3 (DOCX)
Table S4 (DOCX)
Table S5 (DOCX)
Table S6 (DOCX)
Table S7 (DOCX)
Dataset S1 (XLSX)