Fig. S1. Distribution of fruit size (FS), shape (FSI) and weight (FW) QTL across 7 cucumber chromosomes from 17 QTL mapping studies. The vertical bars are 1.5- or 2.0-LOD support intervals from those studies. QTL detected by the same study have the same color. Dashed rectangles delimit consensus QTL from multiple studies with the consensus QTL name as indicated. FS QTL with asterisks indicate that only FL or FD QTL but not both have been detected in associated studies.
Fig. S2. Distribution of fruit size (FS), shape (FSI) and weight (FW) QTL across 12 melon chromosomes from 19 QTL mapping studies. The vertical bars are 1.5- or 2.0-LOD support intervals from those studies. QTL detected by the same study have the same color. Dashed rectangles delimit consensus QTL from multiple studies with the consensus QTL name as indicated. FS QTL with asterisks indicate that only FL or FD QTL but not both have bee...
Fig. S3. Distribution of fruit size (FS), shape (FSI) and weight (FW) QTL across 10 of 11 watermelon chromosomes from 7 QTL mapping studies. The vertical bars are 1.5- or 2.0-LOD support intervals from those studies. QTL detected by the same study have the same color. Dashed rectangles delimit consensus QTL from multiple studies with the consensus QTL name as indicated. FS QTL with asterisks indicate that only FL or FD QTL but not both have been detected in associated studies.
Fig. S4. Syntenic relationships of cucumber and melon consensus FS and/or FSI QTL. Each of the seven cucumber chromosomes (Gy14 V2.0) is aligned against the melon genome (DHL92 V3.6.1) using annotated genes. Syntenic regions harboring QTL pairs are indicated with different colors. The Python version of MCscan (Tang et al., 2008) is used for scanning the cucumber and melon genomes to align syntenic blocks.
Fig. S5. Phylogenetic trees of seven fruit size-related gene homologs from cucumber, melon, and watermelon. The seed genes for fruit/grain size or weight in tomato, rice and Arabidopsis are also included as references in clustering analysis. All cloned genes or their homologs are in red. The neighbor-joining trees for homologs of SUN, OFP, TRM, CYP78A, CNR, and YABBY, and WOX are shown in A thru G, respectively. The phylograms are constructed with protein sequences in MEGA V7.0. (https://www.megasoftware.net/) with 1000 bootstrap replications.