**Genome-wide association analysis reveals a novel QTL *CsFS1* for fruit skin color in cucumber**

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**Supplementary Information**

**Additional file 1: Figure S1.** Eight categories of fruit skin colors were defined to evaluate phenotypes of 289 cucumber accessions. **a** White, **b** Yellow-white, **c** White-green, **d** Yellow-green, **e** Light-green, **f** Green, **g** Dark-green, **h** Black-green.

**Additional file 2: Figure S2.** Relative expression of three candidate genes in fruit pericarp of the light-green near isogenic line NIL-1334 and the dark-green near isogenic line NIL-1325 at 0 days post-anthesis (DPA), 5 DPA, and 10 DPA. The relative expression is shown as the mean ± standard deviation, and statistical significance was determined using Student’s *t*-tests (\**P* < 0.05).

**Additional file 3: Table S1.** QTL analysis of fruit skin color in the cucumber F2 population.

**Additional file 4: Table S2.** Information on 15 candidate genes between 39,531,980 and 39,626,163 bp on chromosome 3.

**Additional file 5: Table S3.** Information on 35 KASP SNP markers for QTL analysis.

**Additional file 6: Table S4.** Primers used in qRT-PCR.