Supporting Information

Han et al. 10.1073/pnas.0904833106

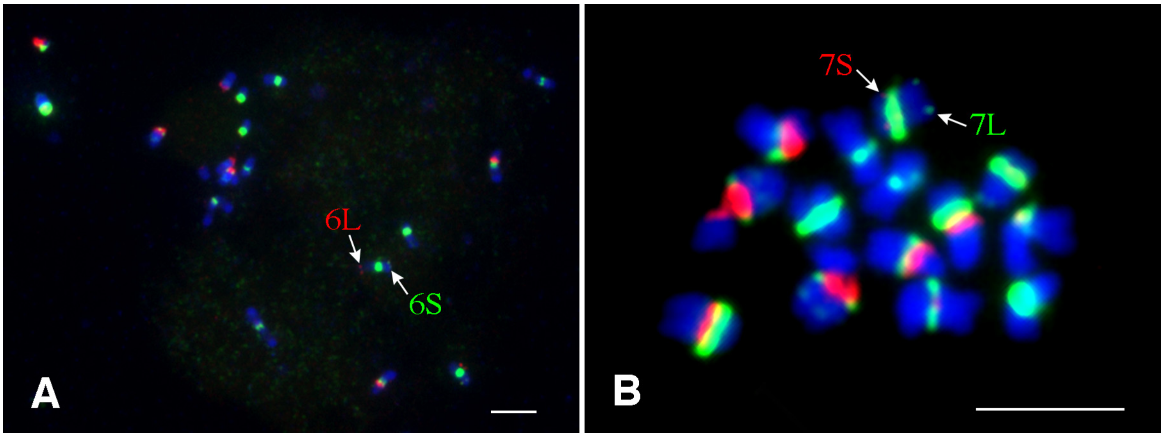

Fig. S1. Identification of cucumber chromosome 6 and 7. (*A*) Fosmid clones 6S and 6L, which were isolated using SSR markers mapped to cucumber linkage group 7, hybridized to cucumber chromosome 6 together with the centromere-specific Type III repeat (green) and 45S rDNA (red). (*B*) Fosmid clones 7S and 7L, which were isolated using SSR markers mapped to cucumber linkage group 3, hybridized to cucumber chromosome 7 together with the centromere-specific Type III repeat (green) and 45S rDNA (red). Chromosome nomenclature followed Han et al. (1). (Scale bars, 5 μm.)

1. Han YH, et al. (2008) Distribution of the tandem repeat sequences and karyotyping in cucumber (*Cucumis sativus L.*) by fluorescence in situ hybridization *Cytogenet Genome Res* 122:80–88.

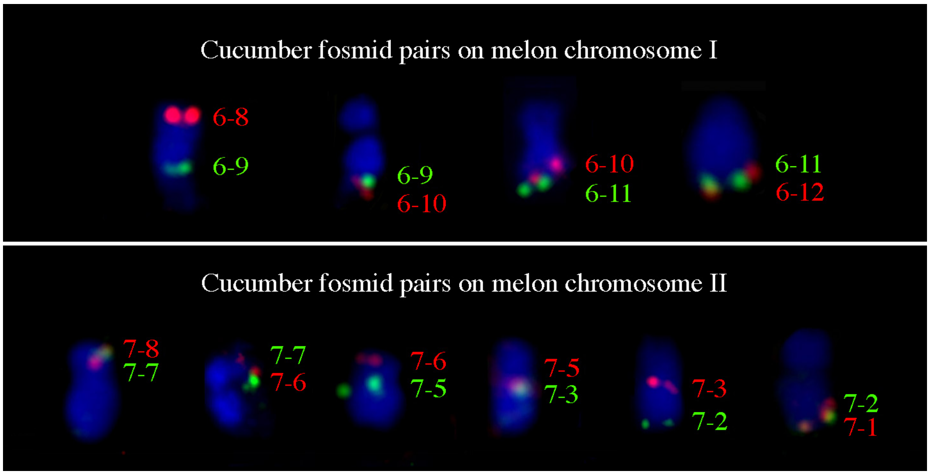

Fig. S2. FISH mapping of pairs of adjacent fosmid clones on specific melon chromosomes. The FISH results show the linkage of these pairs of cucumber fosmids on the same melon chromosomes.

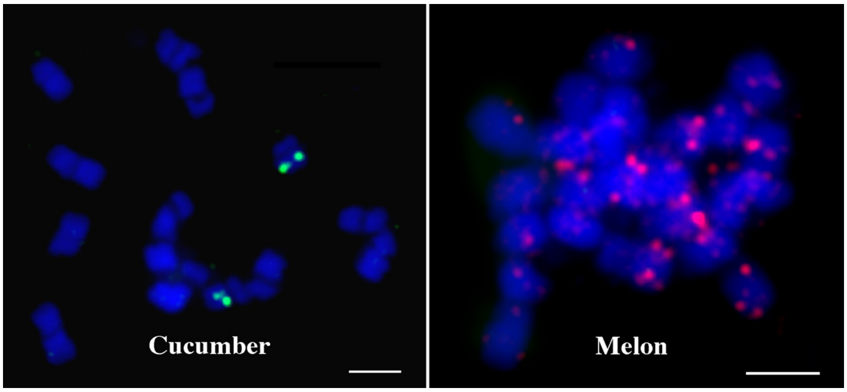

Fig. S3. FISH mapping of fosmid clone 7–4 on the somatic metaphase chromosomes of cucumber and melon, respectively. (Scale bars, 5 μm.)

Table S1. Genetic positions of SSR markers and chromosomal locations of fosmid clones anchored by the SSR markers in cucumber and melon

				Physical location	
SSR marker	Genetic position (CM)	Fosmid code	Fosmid Name	Cucumber Chro. 6	Melon Chro. I
SSR00158	1.8	6–1	gcfbe0_0620_F09.ab1	5.1	–
SSR11219	6.2	6–2	gcfbe0_0187_G09.ab1	10.2	–
SSR01903	10.8	6–3	gcfbe0_0459_C08.ab1	17.0	–
SSR02385	21.0	6–4	gcfbe0_0380_E04.ab1	27.8	–
SSR00647	30.4	6–5	rgcfbe0_0199_B05.ab1	38.5	–
SSR02086	39.6	6–6	gcfbd0_0868_F07.ab1	38.5/49.6	–
SSR00300	51.6	6–7	gcfbb0_0020_B11.ab1	62.9	–
SSR15199	62.4	6–8	rgcfbd0_0502_G07.ab1	71.9	10.2
SSR13741	72.3	6–9	gcfbe0_0325_A08.ab1	77.3	56.8
SSR02906	84.5	6–10	rgcfbe0_0257_E12.ab1	84.8	77.2
SSR22498	95.8	6–11	gcfbd0_0199_C06.ab1	94.9	87.1
SSR06271	106.5	6–12	gcfbd0_0131_G09.ab1	99.4	99.4
				Cucumber Chro. 7	Melon Chro. II
SSR15477	0.0	7–1	gcfbe0_0624_A03.ab1	20.8	2.5
SSR06585	7.0	7–2	rgcfba0_0055_H02.ab1	21.5	4.1
SSR04584	14.7	7–3	rgcfbe0_0058_F08.ab1	47.3	38.5
SSR11665	26.2	7–4	gcfbd0_0393_E02.ab1	59.0	–
SSR22097	36.5	7–5	gcfbd0_0214_B02.ab1	66.7	54.6
SSR01898	51.8	7–6	gcfbd0_0343_F07.ab1	77.7	80.1
SSR20122	61.0	7–7	rgcfbe0_0480_A04.ab1	95.9	99.4
SSR17062	66.5	7–8	gcfbd0_0556_D09.ab1	94.3	97.1

Physical location measured by (S/T) × 100, where S = the distance (in micrometers) from the FISH signal to the end of the short arm of the chromosome, and T = the total length of the chromosome (in micrometers).