

Supplementary materials



Figure S1. Trait for flesh color and cream-colored spots on the pericarp. Flesh color of mature fruits at harvest (ca. three months after transplanting) in the parental lines, **(A)** 'Bí Hồ Lô TN 6 (TN 6)' and **(B)** 'Shishigatani'-K. **(C)** Presence/absence of cream-colored spots on the pericarp of immature fruits. A single F₂ individual is shown as a representative of fruit with (left) or without spots (right). Scale bar, 5 cm.

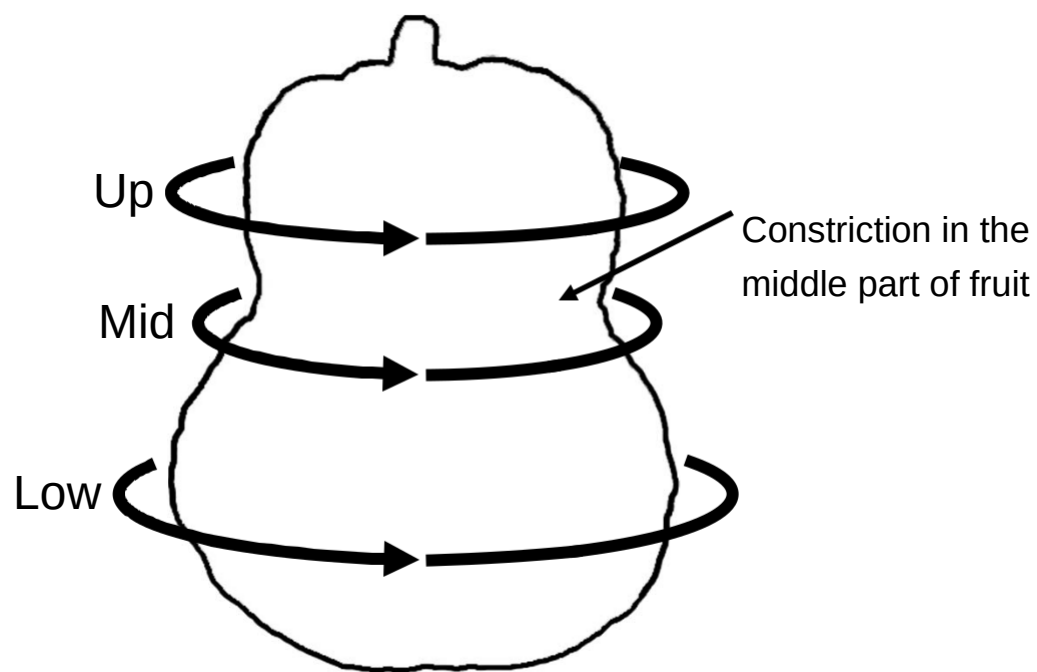
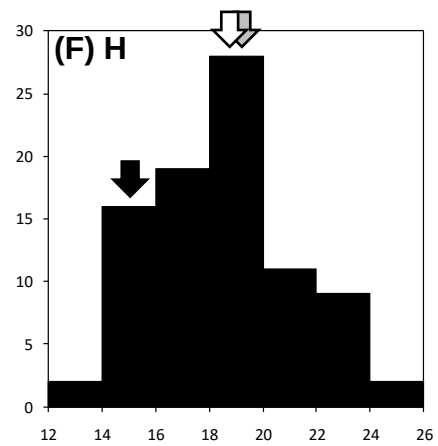
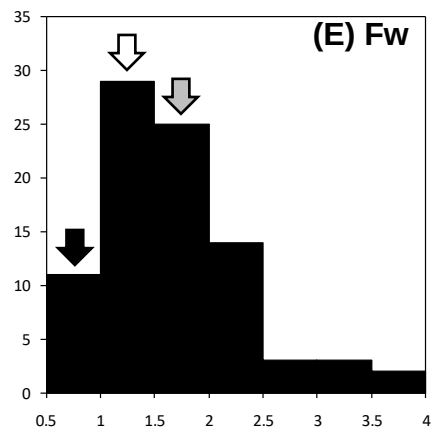
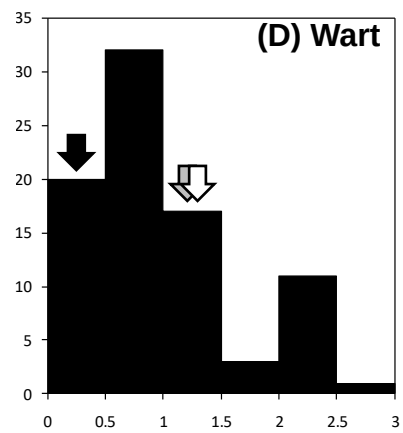
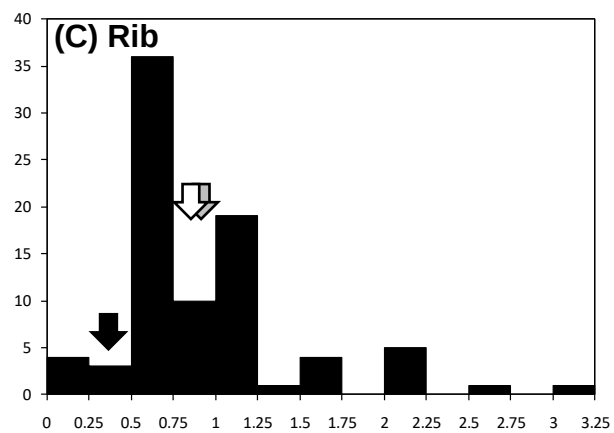
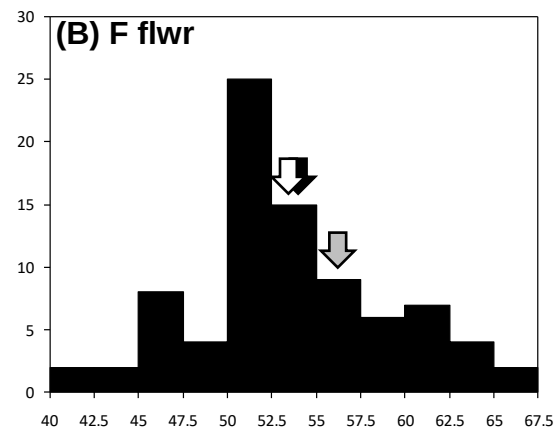
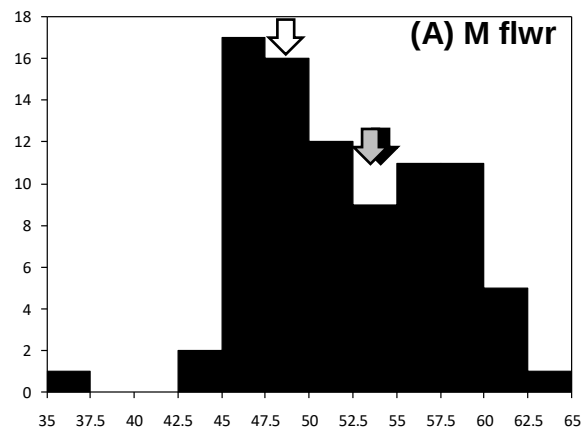
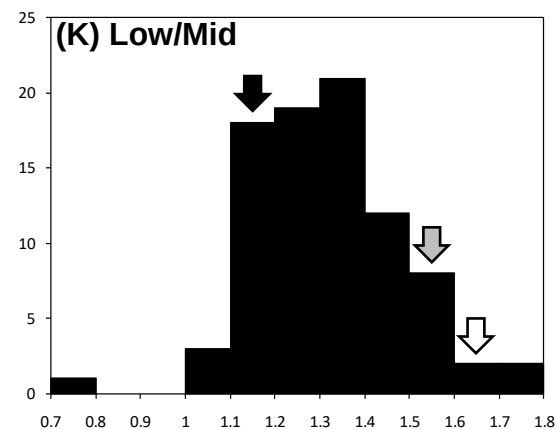
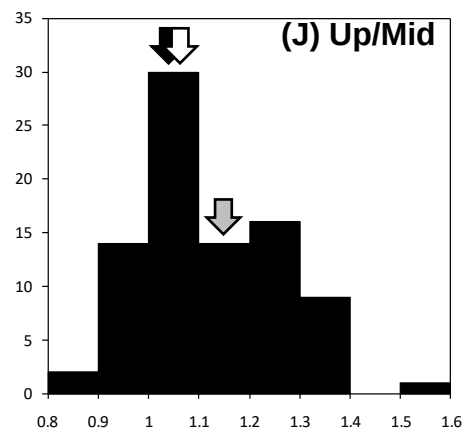
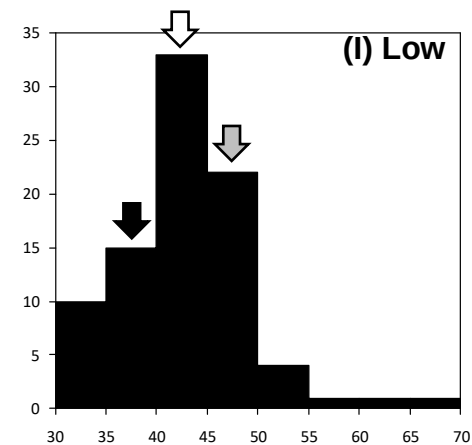
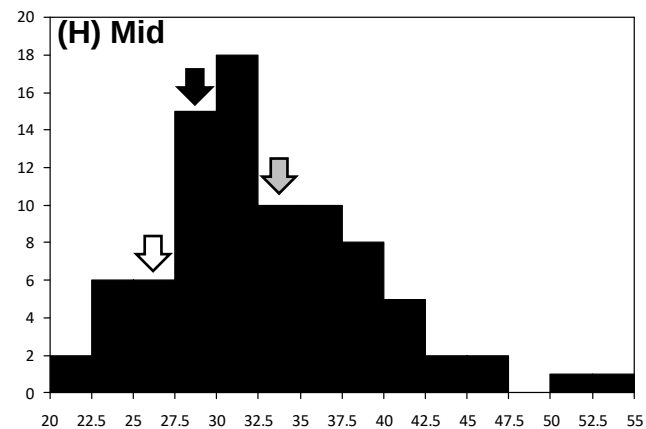
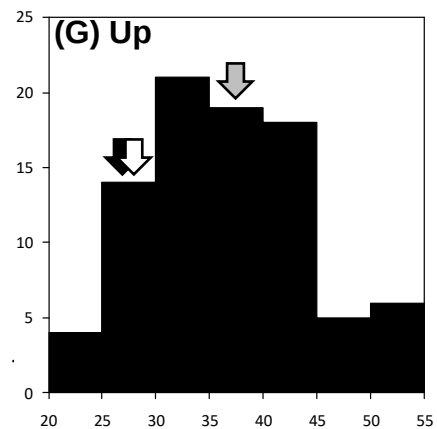


Figure S2. Schematic representation of the measurement of fruit-size related traits. Up: largest circumference on the upper part; Mid: smallest circumference on the middle part; and Low: largest circumference on the lower part.





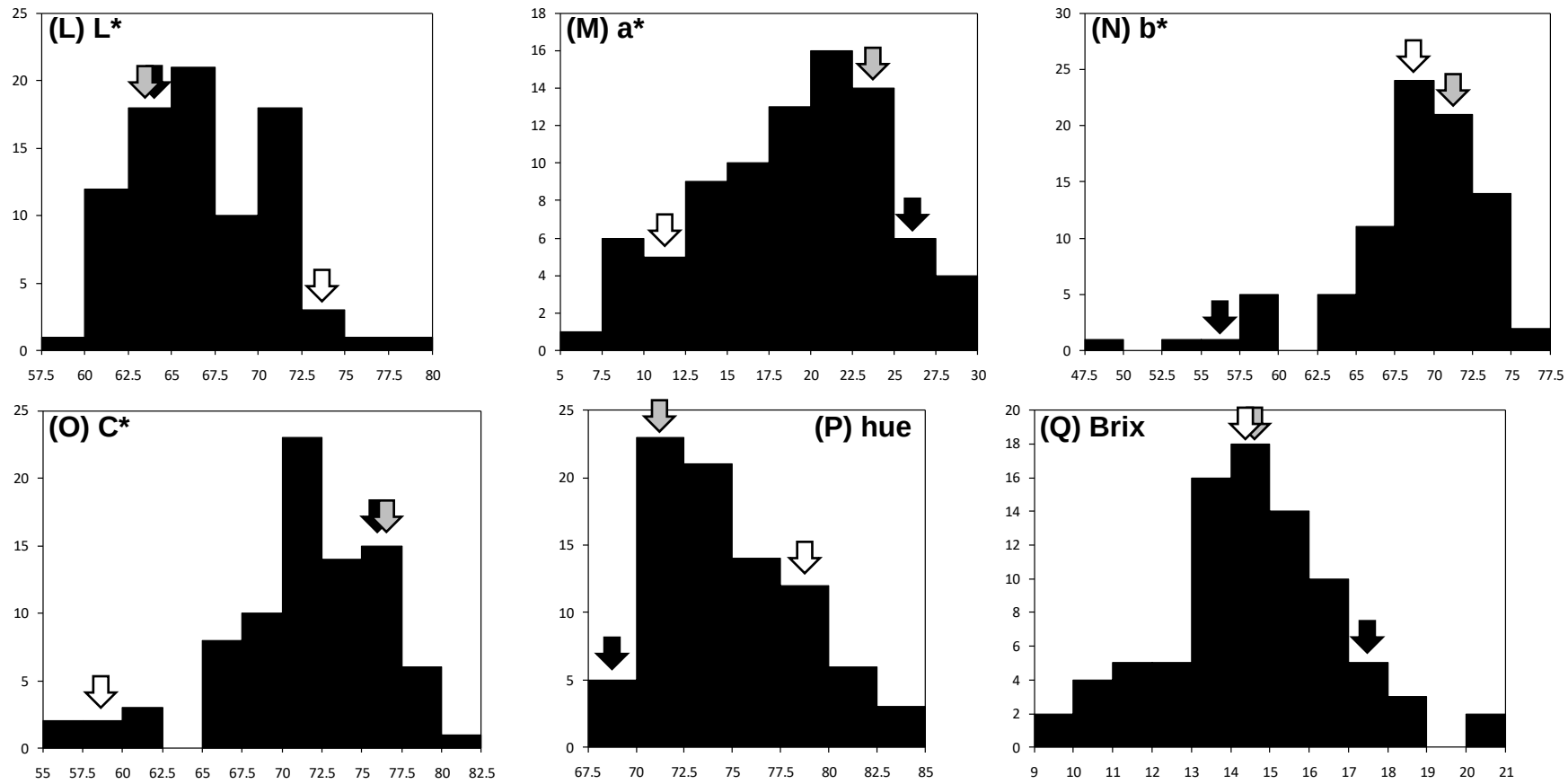
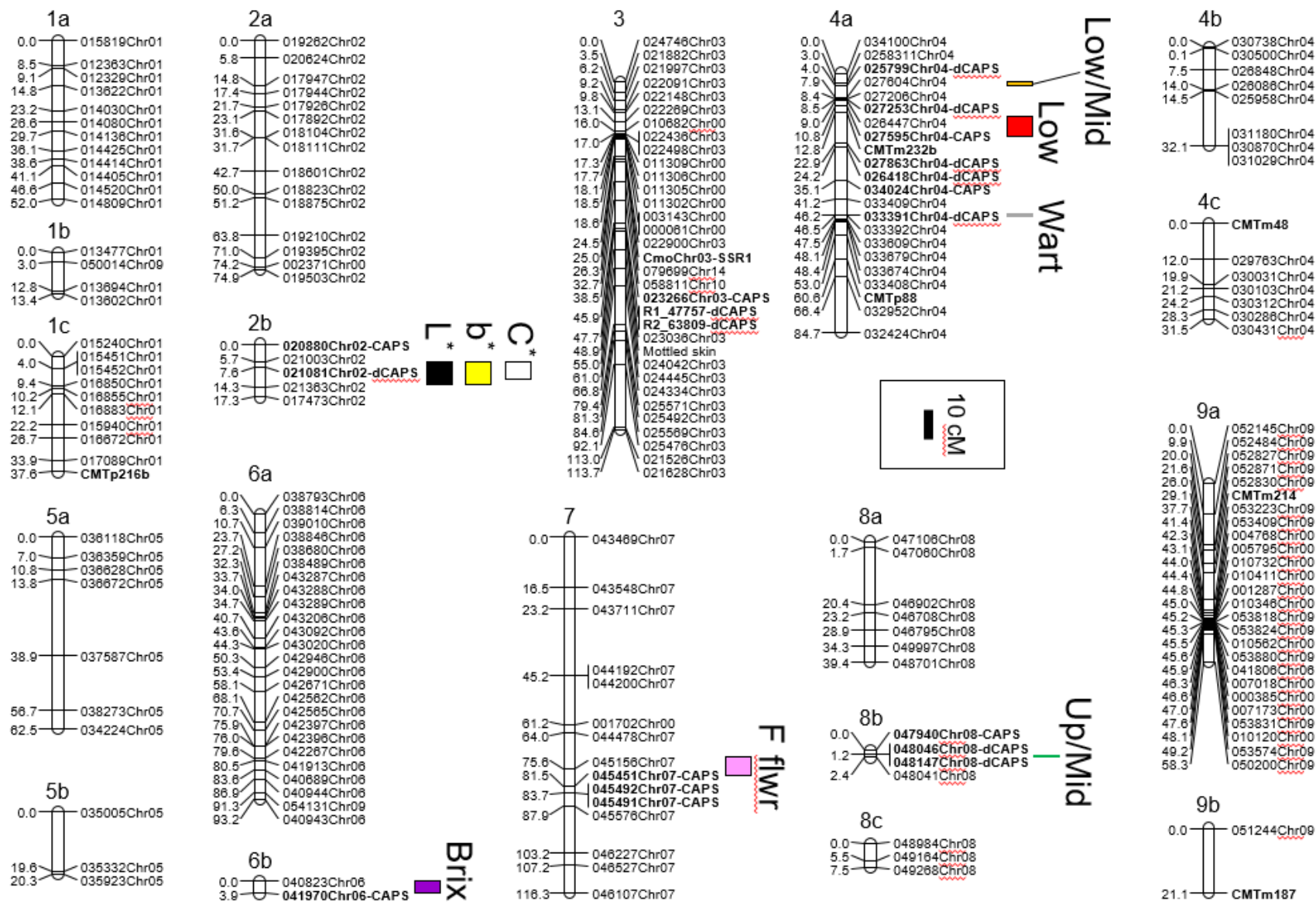


Figure S3. Frequency distributions of the traits scored for the F₂ population of 'TN 6' × 'Shishigatani'-K. Trait code names are shown on the top of each histogram (A–Q). The x- and y-axes indicate trait value and individual number, respectively. The black bars represent data of the F₂ population. Filled, gray, and open arrows indicate average values of 'TN 6', F₁, and 'Shishigatani'-K, respectively.



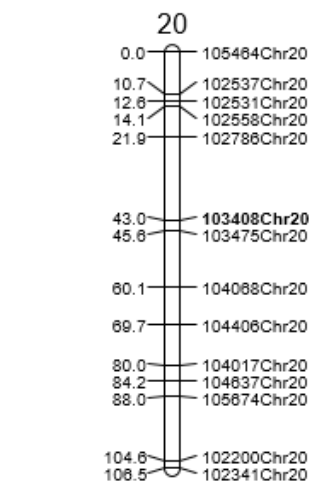
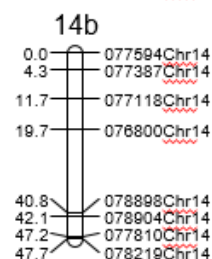
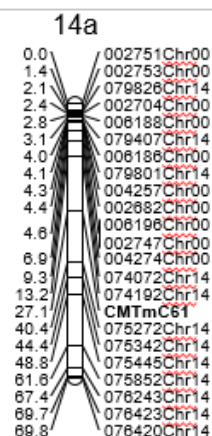
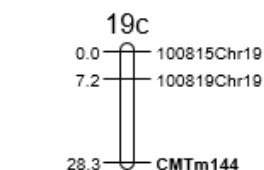
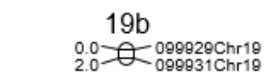
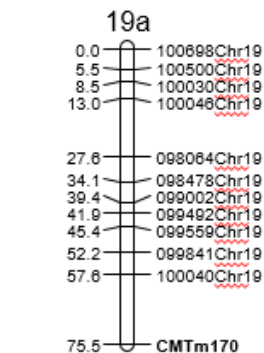
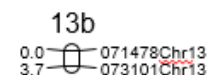
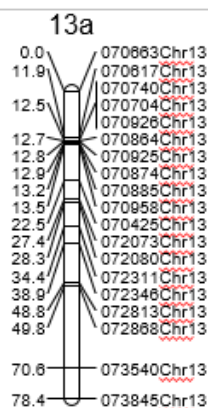
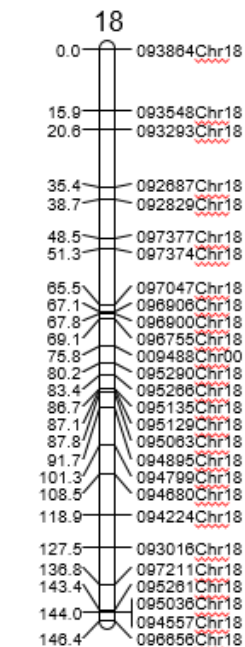
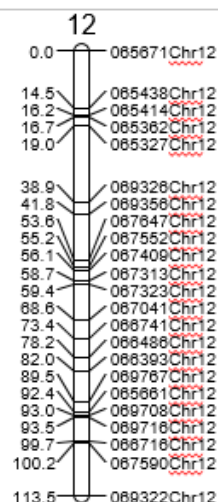
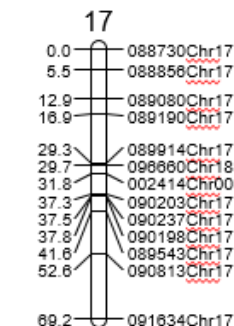
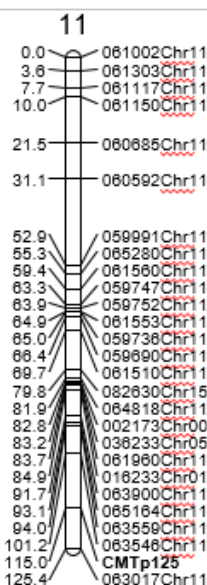
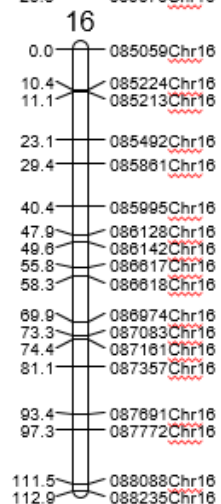
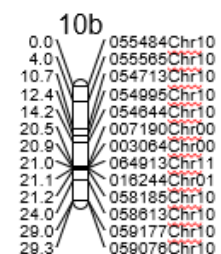
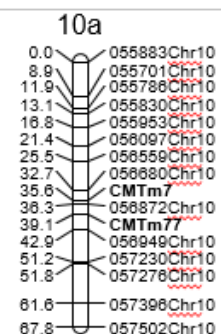


Figure S4. A linkage map of the F₂ population ('TN 6' × 'Shishigatani'-K). The number of each linkage group (LG) refers to that of the *C. moschata* pseudochromosome [4]. Marker names and genetic distance (cM) are indicated on the right and left of each LG, respectively. SSR, CAPS, and dCAPS markers are indicated by bold type. The phenotype trait marker (*Mottled skin*) on LG 3 is italicized. Other markers are RAD markers, in which the number of pseudochromosomes assigned to the *C. moschata* genome [4] is presented as Chrxx. The positions of the QTLs detected in this study are indicated by colored boxes. Scale bar, 10 cM.

Table S1. List of traits analyzed, and the phenotypic values of the F₂ population and the parental lines.

Trait	Abbreviation	Scale	Range in F ₂ (<i>n</i> = 88) ⁴	Mean ± SD in F ₂ (<i>n</i> = 88) ⁴	Mean ± SD in F ₁ (<i>n</i> = 3) ⁴	Mean ± SD in 'TN 6' (<i>n</i> = 4) ⁴	Mean ± SD in 'Shishigatani'-K (<i>n</i> = 4) ⁴
<i>Flowering trait</i>							
Flowering time of male flower	M flwr	Days after transplant to the opening of the first male flower	36–63	51.9 ± 4.3	53.0 ± 0.0	55.0 ± 3.1	48.3 ± 0.8
Flowering time of female flower	F flwr	Days after transplant to the opening of the first female flower	42–67	53.2 ± 5.5	57.0 ± 5.6	55.0 ± 2.8	52.8 ± 2.0
<i>Fruit trait</i>							
Degree of rib on the surface	Rib	0–3 (no rib = 0, intermediate = 1–2, deep rib = 3)	0.00–3.00	0.823 ± 0.535	0.750 ± 0.000	0.286 ± 0.247	0.800 ± 0.245
Degree of wartiness on the surface	Wart	0–3 (no wart = 0, intermediate = 1–2, heavy wart = 3)	0.00–2.50	0.794 ± 0.630	1.042 ± 0.059	0.071 ± 0.175	1.200 ± 0.678
Fresh weight	Fw	kg	0.66–3.66	1.696 ± 0.662	1.826 ± 0.844	0.910 ± 0.252	1.311 ± 0.536
Height	H	cm	13.63–24.60	18.477 ± 2.591	18.356 ± 2.885	14.750 ± 0.726	19.043 ± 1.900
Circumference on upper part	Up	Largest circumference on the upper part (cm) ³	22.10–54.50	36.623 ± 7.650	36.406 ± 13.689	29.238 ± 4.147	29.943 ± 7.275
Circumference on middle part	Mid	Smallest circumference on the middle part (cm) ³	20.40–52.60	32.985 ± 6.263	32.506 ± 10.199	28.400 ± 4.155	27.386 ± 6.152
Circumference on lower part	Low	Largest circumference on the lower part (cm) ³	30.13–65.00	42.859 ± 6.356	46.317 ± 4.266	35.775 ± 5.353	43.457 ± 5.352
Ratio of circumferences on upper/middle parts	Up/Mid	-	0.879–1.512	1.1179 ± 0.1329	1.102 ± 0.130	1.0197 ± 0.0277	1.0938 ± 0.0213
Ratio of circumferences on lower/middle parts	Low/Mid	-	0.784–1.752	1.3190 ± 0.1703	1.510 ± 0.409	1.1624 ± 0.0509	1.6757 ± 0.3234
Lightness or darkness of flesh color	L *	-	57.753–79.693	66.8586 ± 4.0928	62.5939 ± 1.6696	63.0429 ± 1.5209	73.0713 ± 3.5161
Red/green coordinate of flesh color	a *	-	7.230–28.937	18.9036 ± 5.3388	23.4222 ± 4.4406	27.4225 ± 1.8181	12.2292 ± 7.0320
Yellow/blue coordinate of flesh color	b *	-	48.650–76.982	68.5265 ± 4.8773	72.3617 ± 1.3993	70.2913 ± 1.9495	57.4887 ± 8.0470
Chroma (color saturation or intensity) of flesh color	C *	-	55.617–80.141	71.4670 ± 5.0668	76.1053 ± 2.6971	75.4123 ± 0.9686	58.6977 ± 10.0104
¹ Hue angle (relative amounts of redness and yellowness) of flesh color ²	hue	0°–90°	68.340–84.404	74.7676 ± 3.7759	72.1148 ± 2.8586	68.4326 ± 0.9433	78.9385 ± 4.6124
Brix	Brix	%	9.39–20.73	14.508 ± 2.221	14.243 ± 21.221	18.940 ± 2.226	14.000 ± 3.006

¹ $\sqrt{(a^*)^2 + (b^*)^2}$. As chromaticity increases, a color becomes more vivid. As it decreases, a color becomes more dull

² $\tan^{-1}(b^*/a^*)$. An angular measurement, in which 0° = red and 90° = yellow.

³ See Figure S2 for representative phenotype of each scale

⁴ *n*: number of plants investigated.

Table S2. List of *Cucurbita* simple sequence repeat (SSR) markers localized on the linkage map in this study

SSR locus	Primer sequence (5'-to-3')	LG ¹	Chr ²
CMTm7	Forward: AACCAAACCTCCGGCAAGA Reverse: GTTCTCTCCGTTTCAGGATGG	p8	10
CMTm48	Forward: AAGCCTTTGGGGACCTTTAC Reverse: TTGAAACCTTCAAACAAGAAATTG	p2	4
CMTm77	Forward: AACACTCGGCCACAACATC Reverse: CTCCTTGTAACCGGGTTGC	p8	10
CMTm144	Forward: ACATGGGCATACCTCGAATC Reverse: CACCTGGCTGTTTTGTCTGA	p7	19
CMTm170	Forward: TCAGACCCACTCCCATGAAC Reverse: AGCGAACACGTGAAAACGTC	p7	19
CMTm187	Forward: ATCGGTGAGTCCCAAAAATG Reverse: ATCACAAAGCGGGAAAACAC	p18	9
CMTm214	Forward: TGCTTTGATCAGTGAGCAGT Reverse: GGATGTACTCTCCGGACTTTC	p18	9
CMTm232b	Forward: AGAAAGAAATAAGGAACCCACAG Reverse: CGTCTCGCAATTCTTCAACT	p10a	1
CMTmC61	Forward: TTATTGTCGTCGCTCTGCAC Reverse: TCCGGAACCTATTATAACAACGACA	p20	14
CMTp88	Forward: ACCTACCGTCACACCCACAT Reverse: CCACCTGAAAACAGGGCTAA	p5	4
CMTp125	Forward: CTTGTTCCGCAGCATCAG Reverse: AGTGAGAGGGAGACGCAAAG	p16	11
CMTp216b	Forward: CGTTGGCCATGGAAGTCT Reverse: CCCTATATGAGACCGCGAGA	p5	No hit

¹ Linkage group (LG), on which each SSR locus was localized in the previous report [8].

² Pseudochromosome (chr), from which each SSR locus was found in the *C. moschata* whole genome [4].



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