

**Table S3 The estimated values of 19 parent alleles on fruit length (mm) for each significant QTL detected by QTL mapping.** Alleles having the largest effect in increasing and decreasing the trait are underlined and bolded, respectively.

Chr.	Marker	Parental accession																		
		Bur-0	Can-0	Col-0	Ct-1	Edi-0	Hi-0	Kn-0	Ler-0	Mt-0	No-0	Oy-0	Po-0	Rsch-4	Sf-2	Tsu-0	Wil-2	Ws-0	Wu-0	Zu-0
1	MASC00393	14.8	15.6	15.3	<u>15.7</u>	<b>14.3</b>	15	14.9	15.3	15.1	15.4	15.2	15.3	15.6	15.2	15	15.1	15.3	14.5	15.6
	MN1_16874540	15	15.2	14.9	<u>15.8</u>	14.8	15.2	15.1	15.1	15	15	15.1	15.3	15.5	<b>14.8</b>	15	15	15	15.1	15.4
2	MASC06022	15.3	14.9	15.3	15	15.1	<u>16.5</u>	15.4	14.7	15.2	15.2	15.4	15.8	14.8	14.9	14.8	15.1	15.1	14.8	<b>14.6</b>
5	NMSNP5_14661352	14.9	15	15.6	15.1	<b>14.4</b>	14.9	14.9	<u>15.7</u>	15.1	15.6	15.1	14.9	15.6	14.5	15.7	14.9	14.8	15.1	15.4
	NMSNP5_16446291	14.7	15.4	15.4	15.2	14.9	14.9	14.9	<u>15.9</u>	15.2	15.1	15.1	15.2	15.6	<b>14.6</b>	15.6	14.6	14.7	15	15.1
	MN5_23815654	<b>14.2</b>	15.2	15.3	<u>15.9</u>	15.3	15	15.1	15.3	15.2	14.9	15.2	15.2	15.5	14.3	15.8	14.8	15	15	15.3