

Table S2 Significant QTLs detected for fruit length when the 39 lines with the erecta phenotype were removed from the analysis. “Chr” indicates the chromosome location, and “Peak Kb” the position in the chromosome of the QTL peak. Significance of QTL is indicated by LogP and Genome wide P. r^2 indicates the amount of variation explained by the QTL.

Chr.	Peak bp	Marker	-logP	Genome-wide P	r^2
1	9516363	MASC00393	3.95	0.02	0.04
1	16874541	MN1_16874540	4.07	0.02	0.02
2	16893586	MASC06022	3.80	0.03	0.06
5	16446291	NMSNP5_16446291	7.22	0.00	0.04
5	23815655	MN5_23815654	3.88	0.03	0.05