

**Table S1 Significant QTLs detected for total number of healthy seeds per fruit.** “Chr.”

indicates the chromosome location, and “Peak (Kb)” the position in the chromosome of the QTL peak in kilobases. Statistical significance of each QTL is indicated by LogP and Genome wide P.  $r^2$  indicates the amount of variation explained by the QTL. Positions highlighted in bolt are the same as when QTL for total seed number was mapped (see Table 1 in the main text).

Chr.	Peak (kb)	-logP	Genome-wide P	$r^2$
1	<b>20,175</b>	4.691553	0.006	0.06
1	<b>24,795</b>	4.287234	0.01	0.04
3	<b>15,233</b>	4.885016	0.005	0.05
3	<b>18,512</b>	4.951098	0.004	0.07
4	<b>269</b>	5.615617	0.002	0.09
4	2,588	4.288144	0.01	0.03
4	<b>5,290</b>	4.408708	0.009	0.06
4	<b>7,177</b>	5.41221	0.002	0.07
4	9,198	3.70522	0.032	0.02
4	13,180	3.822907	0.026	0.03
4	14,787	3.556139	0.043	0.03
5	3,696	3.497428	0.048	0.03
5	<b>16,446</b>	3.918824	0.024	0.03
5	<b>21,039</b>	5.1142	0.003	0.08