

**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).

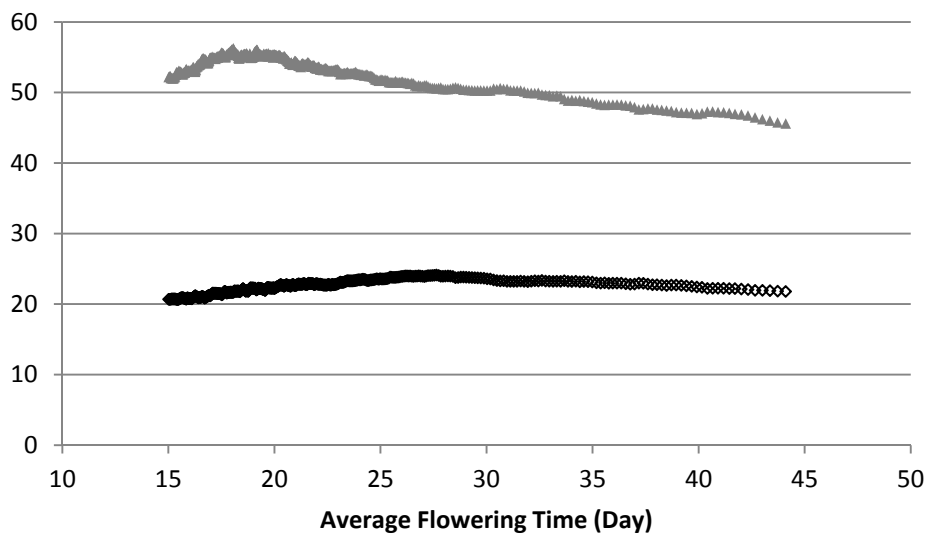
Chr.	Peak (kb)	-logP	Genome-wide P	$r^2$
1	<b>20,175</b>	4.691553	0.006	0.06
1	<b>24,795</b>	4.287234	0.01	0.04
3	<b>15,233</b>	4.885016	0.005	0.05
3	<b>18,512</b>	4.951098	0.004	0.07
4	<b>269</b>	5.615617	0.002	0.09
4	2,588	4.288144	0.01	0.03
4	<b>5,290</b>	4.408708	0.009	0.06
4	<b>7,177</b>	5.41221	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

**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.

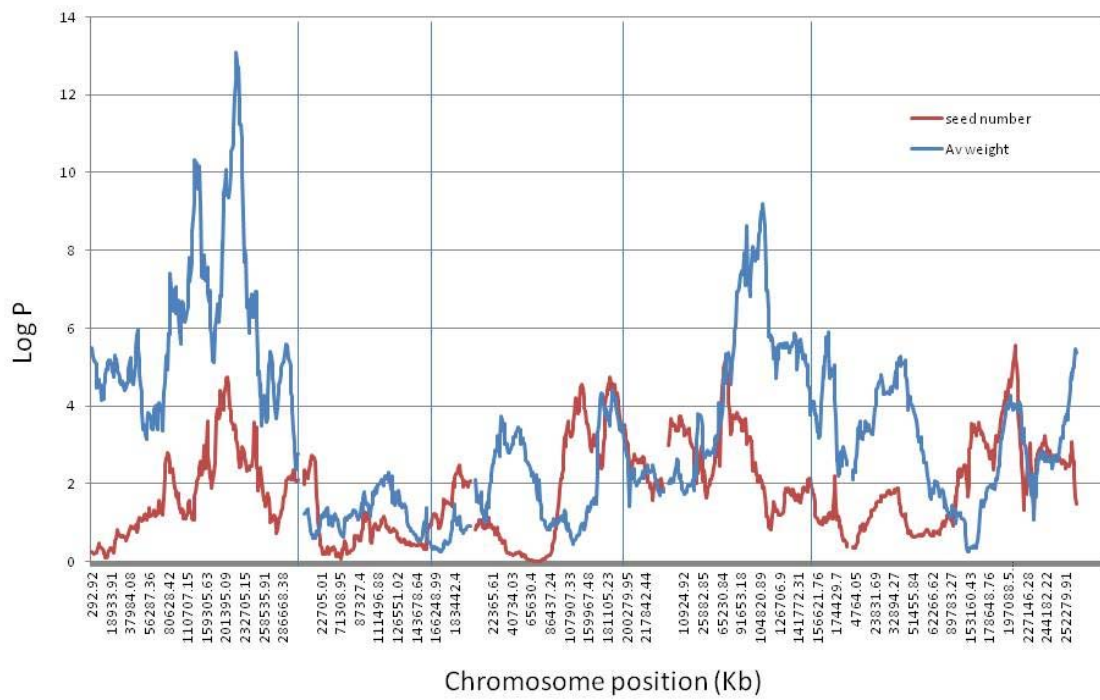
Chr.	Peak bp	Marker	-logP	Genome-wide P	$r^2$
1	9516363	MASC00393	3.95	0.02	0.04
1	16874541	MN1_16874540	4.07	0.02	0.02
2	16893586	MASC06022	3.80	0.03	0.06
5	16446291	NMSNP5_16446291	7.22	0.00	0.04
5	23815655	MN5_23815654	3.88	0.03	0.05

**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



**Figure S1** Changes in average of seed weight and seed number across flowering time. Average seed weight and seed number were calculated for 100 lines in a sliding window across increasing flowering time. The open black diamonds represent the seed weight averages in  $\mu\text{g}$ , and the grey triangles represent the average seed number/fruit for each window; plotted against the average flowering time for the same window.



**Figure S2** QTL scan for seed number per fruit (red) and seed weight (blue) for MAGIC lines ( $-\text{Log}P$  of 3.51 corresponds to a genome-wide  $p$ -value  $< 0.05$ ).

## Files S1-S2

Available for download as Excel files at  
<http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.170746/-/DC1>

**File S1** Genotypes for all MAGIC lines

**File S2** All phenotypic data