

Table S1 linkage analysis in 23 backcrossed lines with large flower phenotype.

locus	backcrossed lines with large flower phenotype																						
	1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
AT2G46400 ^X	W/H	W/H	M	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H	W/H
AT4G04920 ^Y	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M	M
AT4G08430 ^Z	M	M	M	M	M	H	M	M	M	H	M	H	H	M	W	M	M	M	M	M	M	M	M

^XDeletion at AT2G46400 was detected by PCR with primer sets: forward primer 5′ -CAGCAGCAGGTGCAGATAAA-3′ and reverse primer 5′ -TTCTAAAAACGTCTTCAAAAAGAGG-3′ . The reverse primer was designed on the deletion.

^YMutations at AT4G04920 were detected by high resolution melting curve analysis with primer sets: forward primer 5′ -AAGGAGCCTGATTCTGGTGA-3′ and reverse primer 5′ -AGCAGCATCATGCCATACAG-3′ .

^ZRegion including base change at AT4G08430 was amplified with primer sets: forward primer 5′ -TGGCAGCTTCATTGCATACT-3′ and reverse primer 5′ -GTGCGTGTGAGCCATATGAT-3′ . The amplified fragment was sequenced.

W/H : homozygous of WT allele or hetelozygous of WT allele and mutant allele, H: hetelozygous of WT allele and mutant allele, M: homozygous of mutant allele.

Table S2 Absolute values of phenotypic data in the large flower mutants and the double mutant lines created through a cross with *ohb1*

	petal					sepal		seed weight (mg)
	length (mm)	width (mm)	area (mm ²)	cell area (μm ²)	Total number of epidermal cells	length (mm)	width (mm)	
WT	2.36 ± 0.05	0.723 ± 0.021	1.08 ± 0.05	151.5 ± 3.8	5359 ± 275	1.65 ± 0.05	0.575 ± 0.020	2.12 ± 0.04
<i>ohb1</i>	2.75 ± 0.06	0.860 ± 0.026	1.54 ± 0.09	220.1 ± 3.7	5787 ± 326	1.98 ± 0.06	0.720 ± 0.025	2.36 ± 0.04
<i>sfr6-2</i>	3.01 ± 0.04	0.892 ± 0.017	1.72 ± 0.05	238.8 ± 3.6	6319 ± 234	2.03 ± 0.04	0.701 ± 0.035	-
<i>ohb1 sfr6-2</i>	2.83 ± 0.05	0.864 ± 0.018	1.53 ± 0.05	220.0 ± 5.4	5693 ± 183	2.03 ± 0.05	0.717 ± 0.016	-
<i>arf8-2</i>	2.72 ± 0.03	0.895 ± 0.016	1.53 ± 0.04	177.4 ± 2.8	-	1.81 ± 0.03	0.685 ± 0.030	2.18 ± 0.02
<i>ohb1 arf8-2</i>	3.17 ± 0.04	1.127 ± 0.017	2.26 ± 0.06	223.5 ± 2.3	-	2.11 ± 0.05	0.863 ± 0.027	-
<i>bpe-2</i>	2.66 ± 0.04	0.754 ± 0.012	1.27 ± 0.03	179.8 ± 3.0	-	1.78 ± 0.04	0.595 ± 0.026	2.08 ± 0.06
<i>ohb1 bpe-2</i>	3.16 ± 0.04	0.926 ± 0.010	1.86 ± 0.04	255.4 ± 4.0	-	2.20 ± 0.03	0.716 ± 0.020	2.74 ± 0.02
<i>ein2-7</i>	2.99 ± 0.04	0.928 ± 0.014	1.63 ± 0.05	237.5 ± 5.9	-	1.87 ± 0.03	0.694 ± 0.027	2.40 ± 0.04
<i>ohb1 ein2-7</i>	3.50 ± 0.04	1.190 ± 0.019	2.35 ± 0.05	349.6 ± 7.6	-	2.15 ± 0.03	0.771 ± 0.023	2.80 ± 0.11
<i>med25-2</i>	3.03 ± 0.04	0.980 ± 0.017	1.82 ± 0.04	242.9 ± 3.0	6196 ± 180	2.05 ± 0.05	0.765 ± 0.021	2.24 ± 0.05
<i>ohb1 med25-2</i>	3.15 ± 0.04	0.975 ± 0.014	1.90 ± 0.05	252.5 ± 2.9	6376 ± 210	2.10 ± 0.05	0.755 ± 0.021	2.32 ± 0.02
<i>opr3-1</i>	2.67 ± 0.03	0.856 ± 0.008	1.37 ± 0.03	202.0 ± 3.1	-	1.75 ± 0.03	0.671 ± 0.019	2.38 ± 0.04
<i>ohb1 opr3-1</i>	2.99 ± 0.04	0.994 ± 0.015	1.83 ± 0.05	240.3 ± 3.2	-	2.06 ± 0.03	0.782 ± 0.022	2.48 ± 0.06
<i>bb-3</i>	2.69 ± 0.04	0.970 ± 0.016	1.53 ± 0.04	156.6 ± 4.0	-	1.87 ± 0.04	0.803 ± 0.020	2.34 ± 0.02
<i>ohb1 bb-3</i>	3.41 ± 0.06	1.231 ± 0.030	2.56 ± 0.10	211.7 ± 4.2	-	2.34 ± 0.07	0.945 ± 0.032	2.76 ± 0.10
<i>dal-kol</i>	2.74 ± 0.04	0.849 ± 0.016	1.43 ± 0.04	156.8 ± 2.7	-	1.86 ± 0.04	0.730 ± 0.026	2.22 ± 0.04
<i>ohb1 dal-kol</i>	3.42 ± 0.04	1.148 ± 0.022	2.40 ± 0.06	219.3 ± 3.8	-	2.22 ± 0.04	0.878 ± 0.026	2.48 ± 0.04

Each value is expressed as the mean ± SE.