

- 1 **Supplemental Table S4.** Significant QTLs from composite interval mapping of transformed
 2 flowering time phenotypes in the ABR6 x Bd21 F_{4:5} families (T1).

ENV ^a	Chr ^b	cM	EWT ^c	LOD	AEE ^d	PVE ^e
2	Bd1	297.6	3.14	7.50	0.95	19.2%
2	Bd2	409.0	3.14	3.35	0.56	6.6%
2	Bd3	93.2	3.14	5.61	0.82	13.5%
4	Bd3	60.8	3.20	5.12	4.13	16.9%
5	Bd1	297.6	3.35	5.52	8.88	48.0%

- 3 ^aEnvironment (see Supplemental Table S1)
 4 ^bChromosome
 5 ^cExperiment-wide permutation threshold
 6 ^dAdditive effect estimate for transformed phenotypes
 7 ^ePercent of phenotypic variance explained