

**Table S1. Molecular lesions and phenotypic strength of *amp1* alleles****A. Molecular lesions of *amp1* alleles**

Mutant	Origin	Ecotype	Position*	Sequence change	Mutagen <sup>†</sup>
<i>amp1-1</i>	Chaudhury et al., 1993	Col	2225 bp	G to A (Stop)	EMS
<i>amp1-8</i>	This work	Ler	976 bp	C to T (Stop)	EMS
<i>amp1-9</i>	This work	Ler	1434 bp	G to A (3' acceptor splice site)	EMS
<i>amp1-10</i>	This work	Col	1112 bp	SALK_021406	T-DNA
<i>amp1-11</i>	This work	Col	1129 bp	SALK_038402	T-DNA
<i>amp1-12</i>	This work	Col	1133 bp	SALK_044086	T-DNA
<i>amp1-13</i>	This work	Col	2461 bp	SALK_022988	T-DNA

\*The origin of mutation was mapped by PCR. The full-length *AMP1* genomic sequence is 2964 bp in length and comprises 10 exons.

<sup>†</sup>EMS, ethylmethanesulfonate; T-DNA, insertion of T-DNA.

**B. Phenotypic strength of *amp1* alleles**

Genotype	<i>n</i>	Monocot %	Fused <sup>‡</sup> %	Dicot %	Tricot %	Tetracot %	Pentacot %	Collar <sup>§</sup> %	Twin <sup>¶</sup> %
Col-0	169			100					
<i>amp1-1</i>	172		1.7	76.1	21.5	0.6			
<i>amp1-12</i>	167	0.6	6.0	50.3	37.7	3.0		1.8	0.6
<i>amp1-13</i>	154	0.6	10.4	46.1	39.6	1.9		0.6	0.6
<i>amp1-10</i>	130	0.7	14.6	44.6	36.1	0.7		3.1	
<i>amp1-11</i>	147	2.7	10.2	41.5	44.2	0.7			0.7
Ler	167			100					
<i>amp1-8</i>	189		3.1	60.8	34.9	1.1			
<i>amp1-9</i>	213	0.5	5.1	48.3	39.2	6.1		0.5	
<i>pt</i>	198	0.5	2.5	48.4	45.5	2.5	0.5	0.5	

The phenotypic spectrum of cotyledon number indicates which *amp1* alleles are considered weak and strong, increasing in severity as the number of cotyledons increase. Seedlings were classified at 5 DAG. The *amp1-1* allele displays milder defects, which is consistent with the residual *AMP1* gene activity in this allele.

*pt*, Primordia timing.

<sup>‡</sup>Fused cotyledons have one or more fused cotyledons.

<sup>§</sup>Collar seedlings form a continuous ring of tissue surrounding the SAM.

<sup>¶</sup>Twin seedlings develop more than one embryo from a single seed coat.