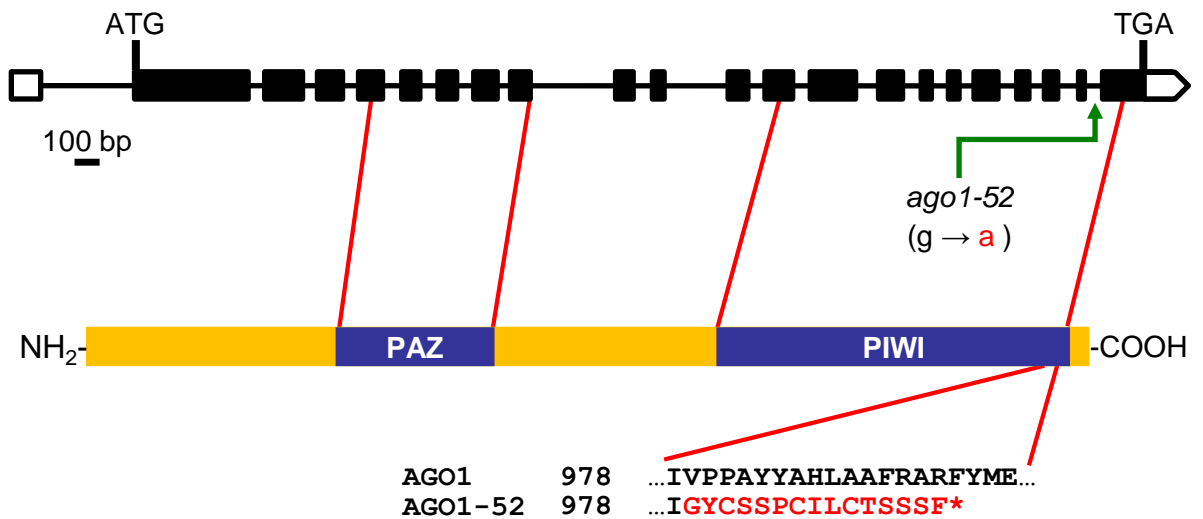


**A genetic screen for suppressors of a hypomorphic  
allele of *Arabidopsis ARGONAUTE1***

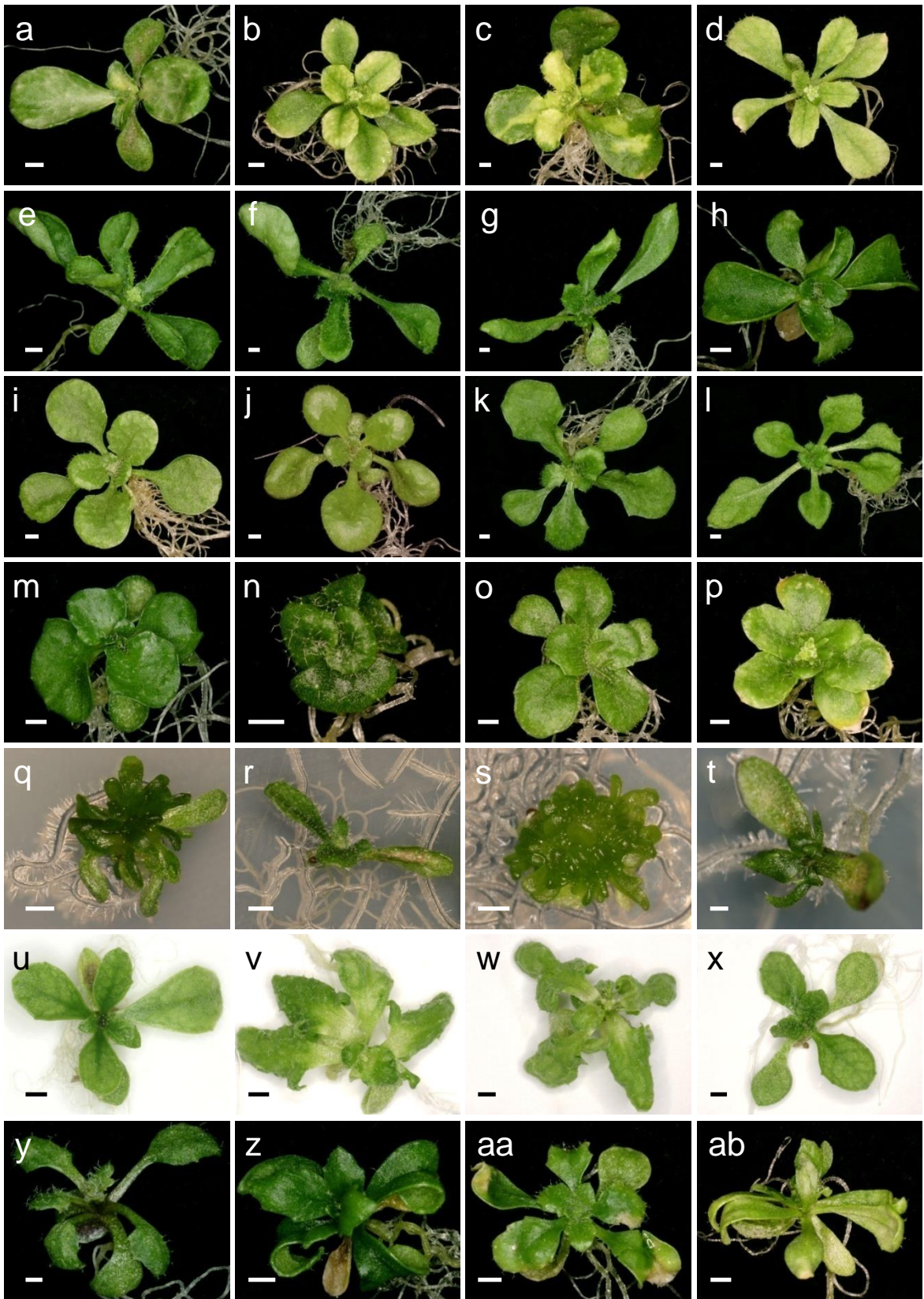
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**Supplementary Information**



AGO1 DNA            ...ATTGgt...gggatattgtagTTCCCCCTGCATATTATGCACATCTAGCAGCTTTTAG...  
 ago1-52 DNA        ...ATTGgt...aGATATTGTAGTTCCCCCTGCATATTATGCACATCTAGCAGCTTTTAG...

**Figure S1 Schematic representation of the structure of the *AGO1* gene and the *AGO1* protein, with indication of the nature of the *ago1-52* mutation and its impact on the mRNA and protein products of the mutated gene.** Boxes and lines between boxes represent exons and introns, respectively. White boxes represent untranslated 5' and 3' regions. The PAZ and PIWI domains of the *AGO1* protein are shown in blue. Lower case letters are used for intron sequences. Red letters indicate mutated nucleotides or amino acids. The asterisk indicates a stop codon<sup>17</sup>.



**Figure S2 Double mutants representative of the phenotypic classes defined in this work.** (a-d) Depigmented plants: (a) P5 25.1, (b) P6 9.2, (c) P6 9.3 and (d) P6 23.3. (e-h) Severe Ago1-52 mutant phenotype: (e) P2 3.4, (f) P3 39.1, (g) P3 40.3 and (h) P5 26.1. (i-l) Weak Ago1-52 mutant phenotype: (i) P6 3.2, (j) P6 29.1, (k) P8 6.2 and (l) P8 35.3. (m-p) Compact rosette: (m) P4 48.1, (n) P6 3.6, (o) P6 5.1 and (p) P6 8.1. (q-t) Synergistic phenotypes: (q) P1 6.3, (r) P1 10.13, (s) P1 15.11 and (t) P1 23.4. (u-x) Reticulate leaves: (u) P6 65.1, (v) P8 7.1, (w) P8 16.1 and (x) P8 21.1. (y-ab) Other phenotypes: (y) P3 3.5, (z) P3 28.1, (aa) P3 36.4 and (ab) P6 2.4. Pictures were taken at 21 das. Scale bars: 1 mm.

**Table S1** Expressivity of the mutant phenotypes in M<sub>3</sub> families, classified by phenotypic class

Phenotypic class	M <sub>2</sub> double mutants	Expressivity in the M <sub>3</sub> generation			
		constant	reduced	variable	null
Severe Ago1-52 phenotype	42	11	4	18	9
Weak Ago1-52 phenotype	93	21	6	39	27
Compact rosette	25	3	2	7	13
Depigmented plants	34	8	4	14	8
Reticulate leaves	48	45	0	2	1
Other phenotypes	60	4	5	24	27
Total	302	92	21	104	85

Values indicate the number of individuals of each type.

**Table S2** Phenotypic segregation in the F<sub>2</sub> progeny of several *mas ago1-52* × *Ler* backcrosses

<i>mas ago1-52</i> line backcrossed	Phenotypic classes in the F <sub>2</sub>						
	WT <sup>a</sup>	Putative <i>mas</i> single mutant <sup>b</sup>	Ago1-52	Putative double mutant <sup>c</sup>	Lethal		Other
					seeds <sup>d</sup>	seedlings <sup>e</sup>	phenotypes
P1 5.33 ( <i>mas1</i> ) <sup>h</sup>	122	0	16	27			
P2 11.1 ( <i>mas2</i> ) <sup>i</sup>	121	0	8	14			
P4 22.2 <sup>j</sup>	107	0	3	12	15		11 <sup>f</sup>
P5 11.1 <sup>k</sup>	113	0	28	3	3		17 <sup>f</sup>
P7 13.1 ( <i>mas7</i> ) <sup>l</sup>	160	26	13	27	62	22	
P7 23.1 <sup>m</sup>	284	14	13	77			18 <sup>g</sup>
P7 26.1 ( <i>mas4</i> ) <sup>n</sup>	125	20	31	22	20	18	9 <sup>g</sup>
P8 14.1 ( <i>mas3</i> ) <sup>o</sup>	308	0	49	101			
P8 25.1 ( <i>mas5</i> ) <sup>p</sup>	136	13	14	24		54	

Values indicate the number of plants from each phenotypic class. <sup>a</sup>Phenotypically wild type class, including *MAS/MAS;AGO1/-* plants. If the *mas* mutation was recessive or dominant but had no morphological phenotype on its own, the *MAS/mas;AGO1/-* plants would also be included in this class. The *mas/mas;AGO1/-* plants would also be included in this class if the *mas* mutation is recessive but has no phenotype on its own. <sup>b</sup>Plants that share some phenotypes with the putative double mutants but not with *ago1-52*. <sup>c</sup>Plants that show a partially suppressed Ago1-52 phenotype. <sup>d</sup>Seeds exhibiting no or abortive germination. <sup>e</sup>Seedlings in which only the cotyledons and the first pair of leaves expand. <sup>f</sup>Plants with mutant phenotypes different among themselves and from that of *ago1-52*. <sup>g</sup>Plants with a phenotype other than that observed in M<sub>2</sub> and M<sub>3</sub>. <sup>h-p</sup>See Figure <sup>h</sup>3d, <sup>i</sup>3e, <sup>j</sup>3f, <sup>k</sup>3g, <sup>l</sup>3j, <sup>m</sup>3l, <sup>n</sup>3n, <sup>o</sup>3q and <sup>p</sup>3r.

**Table S3** Low-resolution mapping of *MAS1*, *MAS2* and *MAS3*

Marker	Chromosome - Physical map position (bp)	Chromosomes studied			Recombination frequency ( $r \pm S$ ) <sup>a</sup>		
		<i>MAS1</i>	<i>MAS2</i>	<i>MAS3</i>	<i>MAS1</i>	<i>MAS2</i>	<i>MAS3</i>
nga59	1 - 2,768,000	116	84	76	35.34±4.44	50.00±5.46	32.89±5.39
JV18/19	1 - 5,160,595	116	84	54	<b>24.14±3.97</b>	31.71±5.14	38.89±6.63
AthZFPG	1 - 8,727,056	104	84	50	<b>16.35±3.63</b>	<b>21.43±4.48</b>	38.00±6.86
SNP10026	1 - 11,562,061	100	74	74	<b>11.00±3.13</b>	<b>20.27±4.67</b>	36.49±5.60
F1L21	1 - 15,993,202	116	84	74	<b>6.03±2.21</b>	<b>8.33±3.02</b>	<b>27.03±5.16</b>
nga128	1 - 20,695,113	116	84	76	<b>15.52±3.36</b>	<b>8.33±3.02</b>	31.58±5.33
SNP10490	1 - 24,344,448	116	84	76	23.28±3.92	20.24±4.38	30.26±5.27
nga111	1 - 27,418,736	116	84	76	34.48±4.41	42.86±5.40	25.00±4.97
nga1145	2 - 682,624	116	84	74	30.17±4.26	47.62±5.45	48.65±5.81
SNP8895	2 - 7,860,251	116	84	74	<b>12.93±3.12</b>	46.43±5.44	51.35±5.81
nga1126	2 - 11,670,000	110			<b>3.64±1.78</b>		
nga168	2 - 16,240,385	116	84	74	<b>18.10±3.58</b>	44.05±5.42	64.86±5.55
nga126	3 - 3,713,432	112	76	74	48.21±4.72	55.26±5.70	47.30±5.80
MYF24	3 - 6,466,772	98	50	74	43.88±5.00	56.00±7.02	43.24±5.76
AthGAPab	3 - 9,796,450	116	84	76	46.55±4.63	58.33±5.38	46.05±5.72
T32N15	3 - 16,986,906	108	84	74	41.67±4.74	47.62±5.45	50.00±5.81
F28P10	3 - 21,398,175	96	82	62	51.04±5.10	47.56±5.52	50.00±6.35
nga6	3 - 23,040,009	114	84	74	42.11±4.62	44.05±5.42	48.65±5.81
nga1111	4 - 5,074,681	116	84	76	40.52±4.56	<b>14.29±3.82</b>	<b>11.84±3.71</b>
AthF28J12.3	4 - 9,166,451	112	84	76	40.18±4.63	30.95±5.04	<b>6.58±2.84</b>
nga1139	4 - 15,408,641	116	84	76	43.10±4.60	42.86±5.40	<b>18.42±4.45</b>
AthCTR1	5 - 979,763	104			49.04±4.90		
nga151	5 - 4,669,932	106	76	76	48.11±4.85	46.05±5.72	43.42±5.69
nga76	5 - 10,375,531	104		74	50.96±4.90		39.19±5.67
AthPHYC	5 - 13,721,807	104	84	56	46.15±4.89	50.00±5.46	46.43±6.66
MNF13	5 - 17,908,612	116	84	52	49.14±4.64	50.00±5.46	40.38±6.80
MNB8	5 - 23,120,770	114	84	76	51.75±4.68	52.38±5.45	42.11±5.66
MUA2	5 - 23,956,127	106	84	74	53.77±4.84	50.00±5.46	54.05±5.79
K8K14	5 - 28,518,213	114	84	74	53.51±4.67	48.81±5.45	56.76±5.76

Genotyping results obtained for mapping populations of F<sub>2</sub> plants derived from crosses involving the wild type Col-0 and a *mas ago1-52* double mutant with a *Ler* genetic background. *r*: recombination frequency. *S*: Standard error of recombination frequency. Physical map positions of the markers were obtained from the Munich Information Center for Protein Sequences (MIPS) Arabidopsis database. Data corresponding to  $r < 30\%$  are highlighted in bold and were considered unequivocal evidence of linkage. The linkage found for chromosome 1 corresponds to the *ago1-52* mutation, whose physical map position is 17,885,633 bp.