

Fig. S1. Clustering analysis of expression array and ChIP-PCR assay in the ARF3 locus. (A) Typical examples of the transgenic plants used for ChIP-chip and ChIP-PCR assays. The presence of pAS1:T7:AS1 complemented the *as1-1* mutant phenotype, and the presence of pAS2:AS2:FLAG complemented the *as2-1* mutant phenotype. Schematics of the construction of pAS1:T7:AS1 and pAS2:AS2:FLAG are shown. The green and blue boxes indicate T7-tag and FLAG-tag, respectively. Black and white boxes indicate coding and non-coding exons, respectively. (B) Clustering analysis by KB-FuzzyART. Levels of gene expression in comparison with those of Col-0 (WT) are shown. Clusters 3 and 6 contained genes having elevated transcription levels in *as1-1* and *as2-1*. (C) Enrichment of genes for transcription factors among 35 selected genes, and heatmap and hierarchical clustering. The ratio of genes for transcription factors to all genes in *Arabidopsis* is 6.20% (2061/33,239) in the TAIR9 database (<http://www.arabidopsis.org/>). The ratio was 34.3% (12/35) in the case of the 35 selected genes. Therefore, the enrichment rate was estimated as 5.53 ($P=6.83 \times 10^{-7}$, as calculated by Fisher's exact test). For the signal log2 ratio of 12 transcription factors, hierarchical clustering was performed by using Euclidean distance and average linkage. In the present study, we merged three databases for transcription factors: namely, the *Arabidopsis* transcription factor database (AtTFDB; <http://arabidopsis.med.ohio-state.edu/AtTFDB/>), the *Arabidopsis thaliana* Regulatory Network (AtRegNet; <http://arabidopsis.med.ohio-state.edu/REIN/>), and the transcription factors portion of the Gene Ontology database (<http://www.geneontology.org/>). In all, 2374 transcription factors were identified as the products of independent genes. (D) Schematic of the ARF3 genomic region. Boxes indicate exons. Relative positions of primer pairs used in ChIP-PCR assays are shown. (E) Results of ChIP-PCR assays of plants harboring p35S:AS1:GFP with GFP- and AS1-specific antibodies, as indicated. (F) Expression analysis of *BP*, *KAN2* and *YAB5* genes in 35S:AS2:GR plants. Relative expression levels of the *BP*, *KAN2* and *YAB5* genes in 7-day-old 35S:AS2:GR plants after treatment with DEX (gray bars) or DEX and CHX (white bars) for the times indicated.

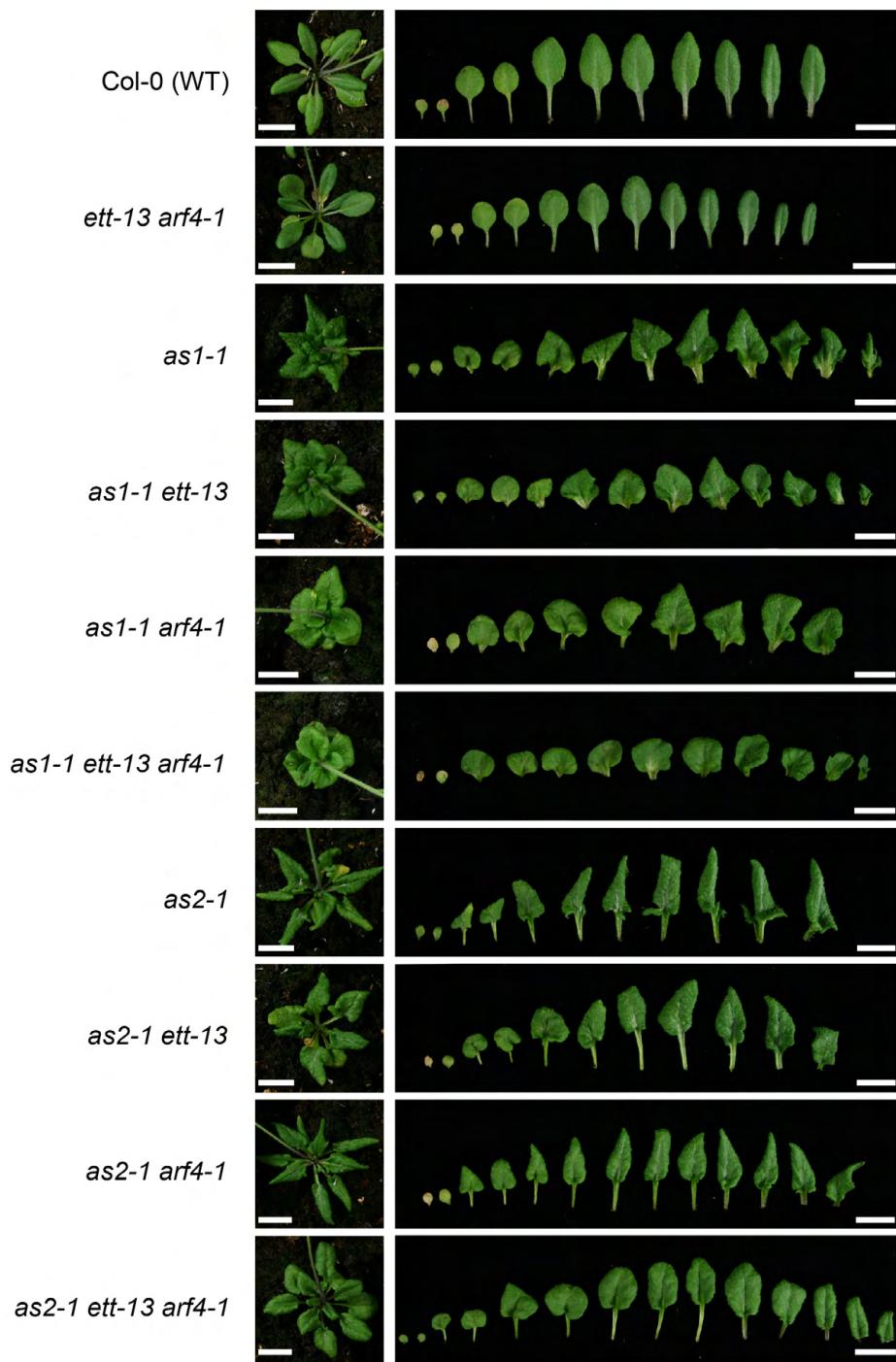


Fig. S2. Mutations in *ARF3* and *ARF4* suppressed major phenotypes of *as1* and *as2*. Representative gross morphology of 40-day-old plants and their leaves are shown. The genotype of each plant is indicated. Scale bars: 5 mm.

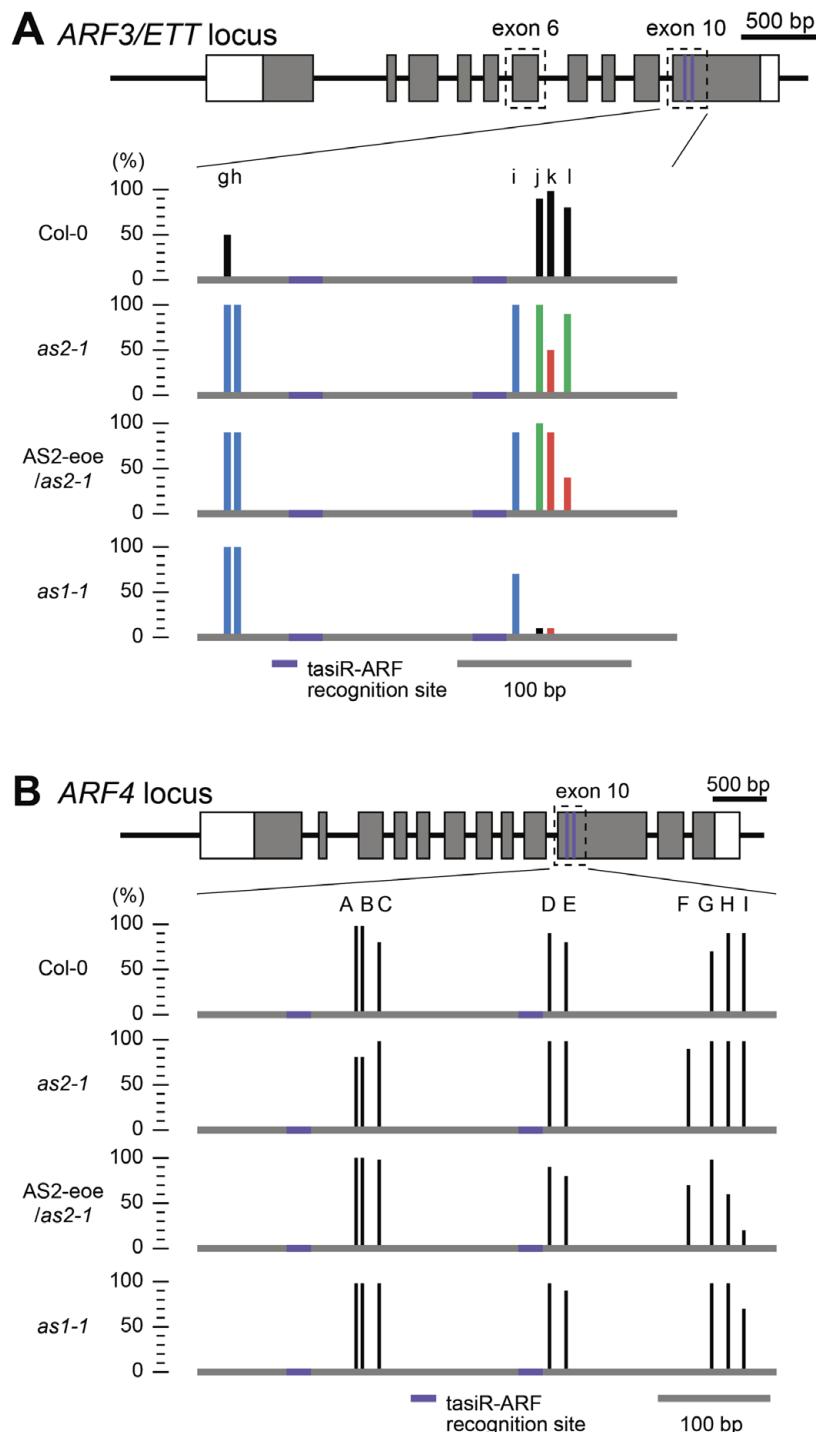


Fig. S3. Effect of 5-aza-2'-deoxycytidine on leaf polarity and levels of cytosine methylation of the *ARF3* and *ARF4* loci in *Col-0*, *as2-1*, *AS2-eoe/as2-1* and *as1-1* plants. (A) Schematic of the *ARF3* locus. Gray boxes indicate exons. The region delineated by a dashed line (exon 10) was examined for cytosine methylation. Vertical bars indicate percentages of methylated cytosines in CG pairs. Red and blue bars indicate cytosines with decreased and increased levels of methylation, respectively, in the *as1* and *as2* mutants. Green bars indicate a decreased level in the *as1* mutant and an increased level of methylation in the *as2* mutant. (B) Schematic of the *ARF4* gene. Gray boxes indicate exons. Exon 10 was examined for cytosine methylation. Vertical bars indicate percentages of methylated cytosines in CG pairs. The tasiR-ARF recognition sites are indicated as purple lines.

Table S1. Sequences of primers used for real-time RT-PCR, ChIP-PCR, Northern blotting of small RNA and bisulfite sequencing

Experiment	Primer	Sequence (5'-3')
Real-time RT-PCR	ETTIN-F	CGCCTACTCAATAACCGATCATC
	ETTIN-R	ACGGCCCACACCAAATGTT
	BP-F	TGTTGTTCCACATATGAGCTCT
	BP-R	TCATGATCAGATCGGAAGCAAT
	KAN2-F	AAGGAACTAGATGGAAAGTGCTCAA
	KAN2-R	GCTTGTCCCCGAGATGCTTG
	YAB5-F1	ACGCCCTAATTCCAGGCAAC
	YAB5-R1	GTTGCTCAGTTATGGTACGAG
	ARF4-F	CGCTTAAATCATTCCGCAAT
	ARF4-R	ACTTGTGGCTTGGTAAGCAAAG
	ACT2-F	TCGGTGGTTCCATTCTTGCT
	ACT2-R	GCTTTTAAGCCTTGATCTTGAGAG
ChIP-PCR assays	pETT-1F	CAAACCTAAACTAAACAATG
	pETT-1R	GTTTGAAACGAATAACAC
	pETT-2F	ATTCGTTCAAACATTGTC
	pETT-2R	CGAGGGTTCAACACAATT
	pETT-3F	TGTTGAACCCTCGAACATGA
	pETT-3R	AAGTCTCTCGAGCCTCAC
	pETT-4F	GCTCGAGAGACTTCCAA
	pETT-4R	AAATTTGATGAACACCGC
	pETT-5F2	ACTGTCTCGCGTGTTCATCA
	PETT-5R2	CAAGAACATGCAAGGGTAGAA
	pETT-6F	GCATGTTCTTGTATTAC
	PETT-6R	CTATCAAACCACAATTG
	pETT-7F	TGTGGTTGATAGTAAGT
	pETT-7R	TTGAATTAAAGTGCAGTG
	pETT-8F2	ATGCCGTTGGAAAAATCAAC
	pETT-8R2	ACACTGAACTAGTGATGATGCT
	pETT-9F	ATAGCATCATCACTAGTT
	pETT-9R	TTGGTAAGATGAGGTTT
	pETT-10F	CCAAAACATATATAATCTCTACC
	pETT-10R	AGAAATTGTCATGAAC
	pETT-11F	AAGATTGTTCTTCTTGCG
	pETT-11R	TTGTTGCCAATGTGTCCA
	pETT-12F	ACATTGGCAACAAATGT
	pETT-12R	TAATACGACCTATTGATC
	pETT-13F	ATAGTCGTATTAATCG

pETT-13R	TAGTATATGGTGAAAAGG
pETT-14F	CCATATACTAAACTACTG
pETT-14R	TTGTGGGAGAAATAAAAG
pETT-15F2	TGCAATTGTTGATAGAAC
pETT-15R2	CATGCCGACACATAGTTT
pETT-16F2	TCTCTCACGCACAAAAGGTC
pETT-16R2	TGACTTTACCCTCTCAGCCAA
pETT-17F2	TTTCTCCACGGCTAAAGACTC
pETT-17R2	CCTCCGTCTCCATCACGTT
pETT-18F	CTCTCTTTAATGGGTG
pETT-18R	TTGGTAGAGAGATAAGGG
pETT-19F	ATCTCTCTACCAAAAAGA
pETT-19R	GAGAGCAGAGGAGAAAAC
pETT-20F2	TGTTTCTCCTCTGCTCTCAA
pETT-20R2	AATGCCACGAGAAGAAATGC
pETT-21F2	TCCTCTTTGCTCCATTG
pETT-21R2	CAAAATCCCCCACATTGT
pETT-22F	TTTGATTCGTAGGCAGAGA
pETT-22R	ACCTCTTAAGCACTTCATAA
pETT-23F	TGGAGAGGAAGATTATGAAG
pETT-23R	ATGAGCTAATAAGAGAACTC
pETT-24F	CTCTTATTAGCTCATATTGAG
pETT-24R	AGGTTGCCCTAAAGTCACT
pETT-25F	TTGAATGGTTGAGTGACTT
pETT-25R	CCAGTCGCAGTTGCCATCA
pETT-26F	TACAGAGGAGATGATGGCAA
pETT-26R	GAAATTAAATGCTAAAACG
pETT-27F	CAGCATTAAAATTTCATTTCAG
pETT-27R	TCCCAATGCAAAAGGGATAG
pETT-28F	GAAGGTTGTTGACTATCCCT
pETT-28R	TTGAACCAGGCCACCTGATT
pETT-29F	TGGATCCAATCAGGTGGCCT
pETT-29R	ATGGCGAGACACGCTGTTGA
pETT-30F	ATCAACAGCGTGTCTGCCA
pETT-30R	CGCGAATCCCCTCTGCAATA
pETT-31F	TTTCTGCTATTATTGCAGAG
pETT-31R	TGATCGGTTATTGAGTAGGC
pETT-32F	GAAACAGTCCCCGCTACTC
pETT-32R	CGTCGGTTAATGGAAACCA
pETT-33F	ATGCAGGCTGTTGGTTCC

	pETT-33R pETT-34F pETT-34R	GAACTTACTTAAGCCACAA TGTGTTATTCGCTTGCTGGCT AACGATATCGGACTCCTTCC
Small RNA Northern blotting	miR390 tasiR-ARF miR165/166 miR173	GGcGCTaTCCcTCCtGAGcTT TgGGGtCTTaCAAgGTCAaGAA GGgGGAAtGAAgCCTgGTCCGA GTgATTtCTCtCTGcAAGcGAA
Bisulfite sequencing	pETT-4_top-F pETT-4_top-R ETT-exon6_top-F ETT-exon6_top-R ETT-exon6_top-F2 ETT-exon6_top-R2 ETT-exon10_top-F ETT-exon10_top-R ARF4-exon10_top-F ARF4-exon10_top-R2	AAGTAGAAGAAGAAGTAAGTGAA ARAATRAATCTCATCTCAACAACAA AGAGGTTTGTGATATATGGGT CAATCAACTARAACAATACACAACCTTA TGTGTTTTTTAGGTAGTTAAAAATG TTCCTAATATTATTAAAATTAACAAACTTCT TTTYTGYTATTATTGYAGAGGGGATT AAACCAAACARCCTRCATCT GGTTTTTGGAYTTTGAGGA ACCTTCATTTRRCATCAAACCT

Table S2 Summary of ChIP-chip and expression array analysis [Download Table S2](#)