

Supplementary Table S1 Proteins used for the phylogenetic analysis

Name in phylogenetic trees	Annotated name in NCBI	Miscellaneous ^a
Proteins obtained from the BLASTp search using entire sequence of ATXR3 as a query ^b		
ATXR3	gi 186511821 ref NP_193253.4 SDG2 (SET DOMAIN-CONTAINING PROTEIN 2) [Arabidopsis thaliana]	
Arabidopsis lyrata-1	gi 297804746 ref XP_002870257.1 SET domain-containing protein [Arabidopsis lyrata subsp. lyrata]	
Arabidopsis thaliana-2	gi 2244876 emb CAB10297.1 hypothetical protein [Arabidopsis thaliana]	Old annotation of ATXR3
Vitis vinifera-1	gi 225447392 ref XP_002275342.1 PREDICTED: hypothetical protein [Vitis vinifera]	
Ricinus communis-1	gi 255549293 ref XP_002515700.1 huntingtin interacting protein, putative [Ricinus communis]	
Populus trichocarpa-1	gi 224132582 ref XP_002327831.1 SET domain protein [Populus trichocarpa]	
Populus trichocarpa-2	gi 224095776 ref XP_002310475.1 SET domain protein [Populus trichocarpa]	
Vitis vinifera-2	gi 297739332 emb CB128983.3 unnamed protein product [Vitis vinifera]	
Oryza sativa Indica-1	gi 218200574 gb EEC83001.1 hypothetical protein OsL_28046 [Oryza sativa Indica Group]	
Arabidopsis thaliana-3	gi 110741769 dbj BAE98829.1 hypothetical protein [Arabidopsis thaliana]	Partial sequence of ATXR3
Sorghum bicolor-1	gi 242078371 ref XP_002443954.1 hypothetical protein SORBIIDRAFT_07g005020 [Sorghum bicolor]	
Physcomitrella patens-1	gi 168035499 ref XP_001770247.1 predicted protein [Physcomitrella patens subsp. patens]	
Physcomitrella patens-2	gi 168059519 ref XP_001781749.1 predicted protein [Physcomitrella patens subsp. patens]	
Oryza sativa Japonica-1	gi 115475081 ref NP_001061137.1 Os08g0180100 [Oryza sativa Japonica Group]	
Selaginella moellendorffii-1	gi 302821685 ref XP_002992504.1 hypothetical protein SELMODRAFT_448778 [Selaginella moellendorffii]	
Selaginella moellendorffii-2	gi 302817012 ref XP_002990183.1 hypothetical protein SELMODRAFT_447947 [Selaginella moellendorffii]	
Selaginella moellendorffii-3	gi 302825692 ref XP_002994441.1 hypothetical protein SELMODRAFT_432361 [Selaginella moellendorffii]	
Zea mays-1	gi 212723442 ref NP_001132870.1 hypothetical protein LOC100194363 [Zea mays]	
Tragopogon dubius-1	gi 237506940 gb ACQ99221.1 hypothetical protein [Tragopogon dubius]	
Tragopogon pratensis-1	gi 237506942 gb ACQ99222.1 hypothetical protein [Tragopogon pratensis]	
Ostreococcus tauri-1	gi 116060411 emb CAL55747.1 SET domain-containing protein (ISS) [Ostreococcus tauri]	
Ostreococcus lucimarinus-1	gi 145351886 ref XP_001420292.1 predicted protein [Ostreococcus lucimarinus CCE9901]	
Ostreococcus tauri-2	gi 116058540 emb CAL53729.1 SET domain-containing protein (ISS) [Ostreococcus tauri]	
Ostreococcus lucimarinus-2	gi 145347753 ref XP_001418326.1 predicted protein [Ostreococcus lucimarinus CCE9901]	
Paramecium tetraurelia-1	gi 145494033 ref XP_001433011.1 hypothetical protein [Paramecium tetraurelia strain d4-2]	
Paramecium tetraurelia-2	gi 145532427 ref XP_001451969.1 hypothetical protein [Paramecium tetraurelia strain d4-2]	
Tetrahymena thermophila-1	gi 118383419 ref XP_001024864.1 SET domain containing protein [Tetrahymena thermophila]	
Chlamydomonas reinhardtii-1	gi 159486133 ref XP_001701098.1 histone methyltransferase [Chlamydomonas reinhardtii]	
Blastocystis hominis-1	gi 300175979 emb CBK22196.2 unnamed protein product [Blastocystis hominis]	
Micromonas sp. RCC299-1	gi 255073265 ref XP_002500307.1 set domain protein [Micromonas sp. RCC299]	
Tetrahymena thermophila-2	gi 146185998 ref XP_001032856.2 SET domain containing protein [Tetrahymena thermophila]	
Vitis vinifera-3	gi 147775274 emb CAN61590.1 hypothetical protein [Vitis vinifera]	
Ectocarpus siliculosus-1	gi 299473409 emb CBN77807.1 conserved unknown protein [Ectocarpus siliculosus]	
Phaeodactylum tricornutum-1	gi 219116062 ref XP_002178826.1 predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	
Micromonas sp. RCC299-2	gi 255084155 ref XP_002508652.1 set domain protein [Micromonas sp. RCC299]	
Micromonas pusilla-1	gi 303285194 ref XP_003061887.1 predicted protein [Micromonas pusilla CCMP1545]	
Thalassiosira pseudonana-1	gi 224002090 ref XP_002290717.1 predicted protein [Thalassiosira pseudonana CCMP1335]	
Volvox carteri-1	gi 302839886 ref XP_002951499.1 hypothetical protein VOLCADRAFT_117846 [Volvox carteri f. nagariensis]	
Micromonas pusilla-2	gi 303286928 ref XP_003062753.1 predicted protein [Micromonas pusilla CCMP1545]	
Vitis vinifera-4	gi 147823106 emb CAN66333.1 hypothetical protein [Vitis vinifera]	
Vitis vinifera-5	gi 147814949 emb CAN70304.1 hypothetical protein [Vitis vinifera]	
Vitis vinifera-6	gi 147855182 emb CAN83840.1 hypothetical protein [Vitis vinifera]	
Populus trichocarpa-3	gi 224095774 ref XP_002310474.1 hypothetical protein POPTRDRAFT_562330 [Populus trichocarpa]	
Paramecium tetraurelia-3	gi 145485412 ref XP_001428714.1 hypothetical protein [Paramecium tetraurelia strain d4-2]	
Micromonas sp. RCC299-3	gi 255086485 ref XP_002509209.1 set domain protein [Micromonas sp. RCC299]	
Paramecium tetraurelia-4	gi 145521184 ref XP_001446447.1 hypothetical protein [Paramecium tetraurelia strain d4-2]	
Vitis vinifera-7	gi 147866108 emb CAN83034.1 hypothetical protein [Vitis vinifera]	
Brugia malayi-1	gi 170573421 ref XP_001892464.1 SET domain containing protein [Brugia malayi]	
Schizosaccharomyces japonicus-1	gi 213402529 ref XP_002172037.1 histone-lysine N-methyltransferase [Schizosaccharomyces japonicus yFS275]	
Rattus norvegicus-1	gi 157818737 ref NP_001101159.1 probable histone-lysine N-methyltransferase ASH1L [Rattus norvegicus]	
Gallus gallus-1	gi 118102182 ref XP_422858.2 PREDICTED: similar to ash1 (absent, small, or homeotic)-like [Gallus gallus]	
Mus musculus-1	gi 73622271 ref NP_619620.3 probable histone-lysine N-methyltransferase ASH1L [Mus musculus]	
Mus musculus-2	gi 118572534 sp Q99MY8.2 ASH1L_MOUSE RecName: Full=Probable histone-lysine N-methyltransferase ASH1L; Alt=	Redundant to M. musculus-1
Equus caballus-1	gi 149751370 ref XP_001499134.1 PREDICTED: ash1 (absent, small, or homeotic)-like (Drosophila) isoform 1 [Equus]	
Ailurotopoda melanoleuca-1	gi 301785832 ref XP_002928328.1 PREDICTED: probable histone-lysine N-methyltransferase ASH1L-like [Ailurotopoda]	
Brugia malayi-2	gi 170591502 ref XP_001900509.1 SET domain containing protein [Brugia malayi]	
Equus caballus-2	gi 149751372 ref XP_001499144.1 PREDICTED: ash1 (absent, small, or homeotic)-like (Drosophila) isoform 2 [Equus]	Redundant to E. caballus-1
Ailurotopoda melanoleuca-2	gi 281338719 gb EFB14303.1 hypothetical protein PANDA_018255 [Ailurotopoda melanoleuca]	Redundant to A. melanoleuca-1
Mus musculus-3	gi 13442965 gb AAK26242.1 AF247132_1 putative chromatin remodeling factor [Mus musculus]	Redundant to M. musculus-1
Canis familiaris-1	gi 73960946 ref XP_537251.2 PREDICTED: similar to ash1 (absent, small, or homeotic)-like isoform 1 [Canis familiaris]	
Proteins obtained from the BLASTp search using SET domain sequence of ATXR3 as a query ^c		
Oryza sativa Japonica-2	gi 222640020 gb EEE68152.1 hypothetical protein OsJ_26262 [Oryza sativa Japonica Group]	
Chlorella variabilis-1	gi 307109213 gb EFN57451.1 hypothetical protein CHLNCRAFT_142939 [Chlorella variabilis]	
Xenopus tropicalis-1	gi 301629157 ref XP_002943714.1 PREDICTED: hypothetical protein LOC100496979 [Xenopus (Silurana) tropicalis]	
Bos taurus-1	gi 300795068 ref NP_001179672.1 probable histone-lysine N-methyltransferase ASH1L [Bos taurus]	
Callithrix jacchus-1	gi 296229115 ref XP_002760038.1 PREDICTED: probable histone-lysine N-methyltransferase ASH1L [Callithrix jacchu]	
Known SET-domain proteins from <i>D. melanogaster</i>		
TRX	gi 17136556 ref NP_476769.1 trithorax, isoform D [Drosophila melanogaster]	
DmSet1	gi 82862148 ref NP_001015221.1 CG40351, isoform A [Drosophila melanogaster]	
Ash1	gi 17737643 ref NP_524160.1 absent, small, or homeotic discs 1 [Drosophila melanogaster]	
E(z)	gi 404864 gb AAC46462.1 E(z) [Drosophila melanogaster]	
G9a	gi 18543183 ref NP_569834.1 G9a [Drosophila melanogaster]	
Bacterial SET proteins used for the roots		
Polynucleobacter necessarius-1	gi 171462836 ref YP_001796949.1 nuclear protein SET [Polynucleobacter necessarius subsp. necessarius STIR1]	
Polynucleobacter necessarius-2	gi 145588193 ref YP_001154790.1 nuclear protein SET [Polynucleobacter necessarius subsp. asymbioticus QLW-P1D]	

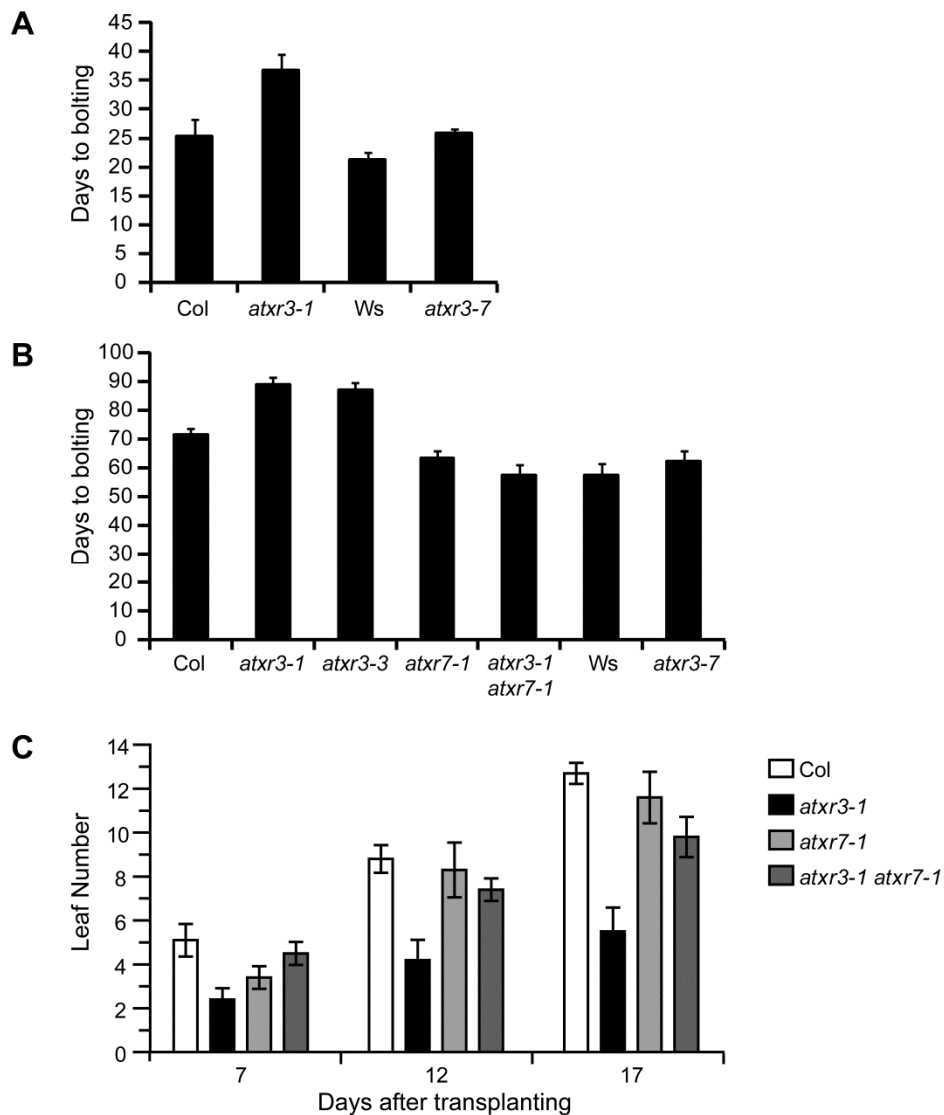
^aReasons why the proteins are omitted from the analyses are described. We also excluded the proteins that lack the SET domain and/or impair the quality of the phylogenetic analyses due to their short sequences.

^bProteins whose e-values are $8e^{-12}$ or below are shown.

^cProteins whose e-values are $6e^{-13}$ or below, and that are not already listed, are shown.

Supplementary Table S2 Primers for Realtime PCR

Gene	Locus	Forward primer (5' to 3')	Reverse primer (5' to 3')
1, RT-PCR			
<i>FLC</i>		CCGAACTCATGTTGAAGCTTGTTGAG	CGGAGATTTGTCCAGCAGGTG
<i>FLM</i>		GGAAAGAATACGTTGCTGGCAACA	CCGTTGATGATGGTGGCTAATTGA
<i>MAF2</i>		CGAAATACATCATGCTGATGAACTTG	GCTTTGGACTATTTCTAGTAACTCTTTGA
<i>MAF3</i>		GGAAATAAAGGTAAAACAAAACGAAGCTCTT	GA ACTCTGATATTTGTCTACTAAGGTACA
<i>MAF4</i>		GATGGGGAAGATGAAAGAAGTCTGT	AGTCTCCGGTGGCTTGTGT
<i>MAF5</i>		GAAACAGGGGATGAAAGAGCAGTA	TGGGCTGTGGCCAGAGCTAT
<i>ACT7</i>		GGTAACATTGTGCTCAGTGGTGG	AACGACCTTAATCTTCATGCTGC
2, ChIP			
<i>FLC</i>	F1	AGCAGTGGCGGATCCAAGAA	CCCCACATCAATCCAAGTTCA
<i>FLC</i>	F2	GCTGATACAAGCATTTACCAAAA	CTTAAATGTCCACACATATGGCAAT
<i>FLC</i>	F3	GAAAGAAATAAAGCGAGAAAAGGAA	GGCTTTGTGCCCTAATTTGAT
<i>FLC</i>	F4	GTTGTTTCTCGGTTCTGTGTT	GCTAAAAAGCTTCTTCACGACAT
<i>FLC</i>	F5	CAATCTTTTGTGTTGAAAATCGACAA	ACAAGGCTGTGTGAATGACAA
<i>FLC</i>	F6	GAGGCTTATGTTTAGGGTTCTT	GAAAAGTCATACAAAGGCATACAGAT
<i>FLC</i>	F7	CGGTTGTTGGACATAACTAGGTT	CAAACCCAGACTTAACCAGACT
<i>FLC</i>	F8	CTTAAGTAGACGGA ACTAAGTCAA	TACTCAAGATCTCGATGCAA
<i>ACT7</i>		CGTTTCGCTTTCCTTAGTGTTAGCT	AGCGAACGGATCTAGAGACTCACCTTG
<i>AG</i>		CAATCGGAGCTAGGAGGAGA	ACCACGGCTAGAGAAGACGA



Supplementary Fig. S1 Flowering and primary leaf initiation rate of *atxr3* mutants. (A, B) Days to flowering from sowing of Col, *atxr3-1*, Ws and *atxr3-7* grown in long days (A) or Col, *atxr3-1*, *atxr3-3*, *atxr7-1*, *atxr3-1 atxr7-1*, Ws and *atxr3-7* in short days (B). The averages of the results from at least twelve plants are shown. Error bars indicate SE. (C) Numbers of visible leaves in Col, *atxr3-1*, *atxr7-1* and *atxr3-1 atxr7-1* plants grown in short days were scored at 7, 12, and 17 days after transplanting. The averages of the results from at least twelve plants are shown. Error bars indicate SE.