

Supplemental Figure 1. Morphology of Podostemaceae.

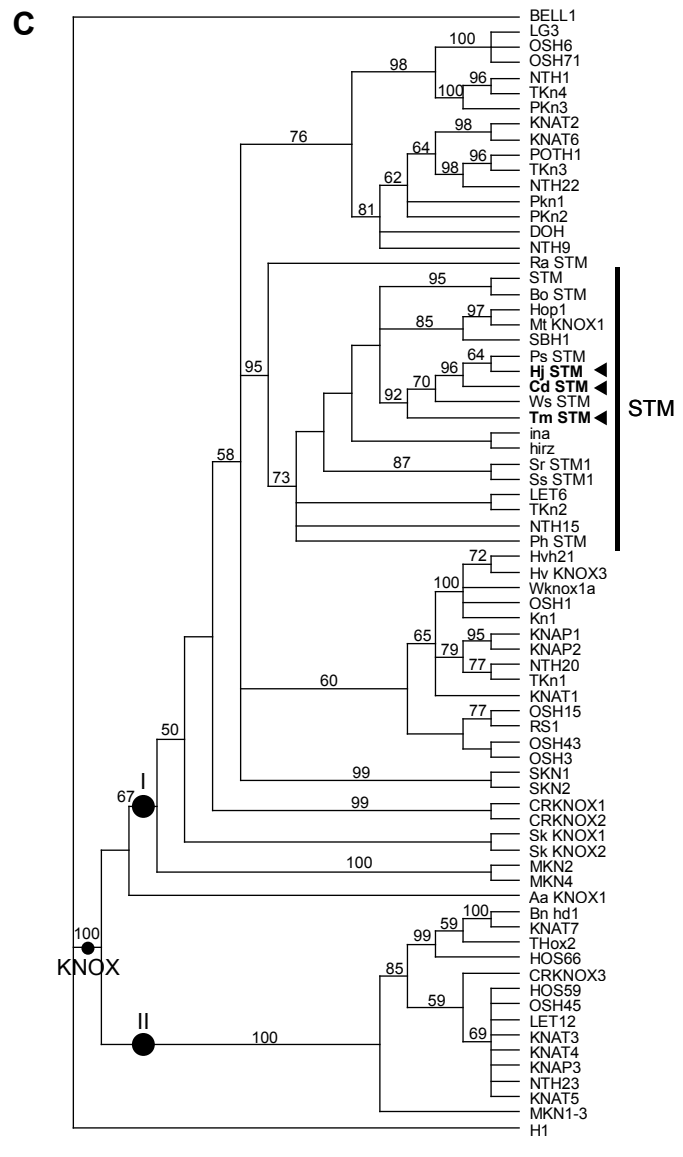
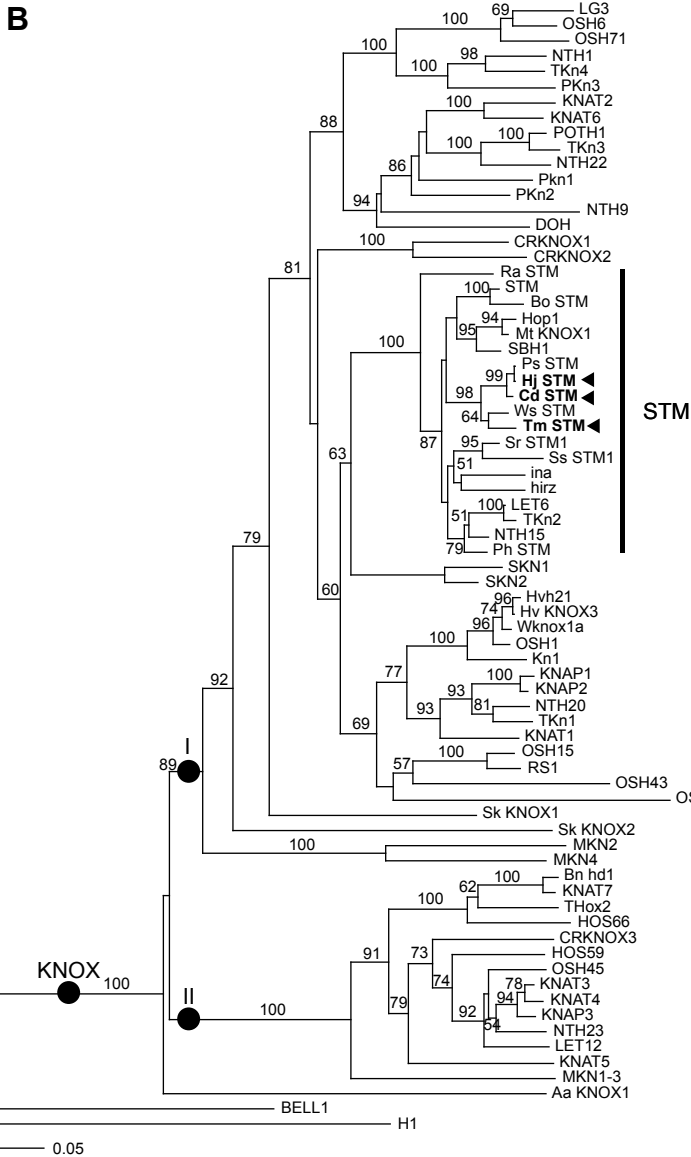
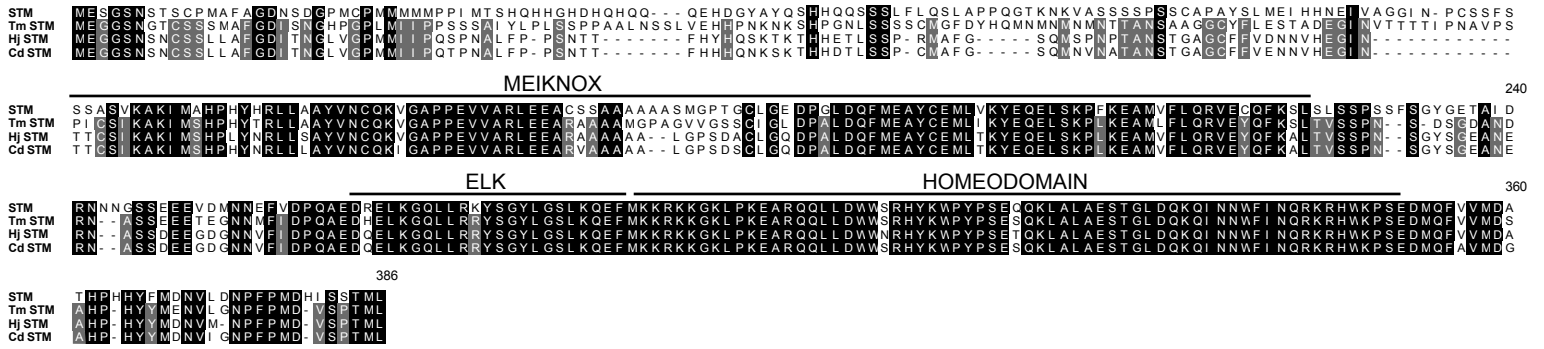
(A–C) Light micrographs of *Terniopsis brevis* (A), *Cladopus doianus* (B), and *Hydrobryum japonicum* (C).

(A) Shoot (S) arising from the lateral side of the subcylindrical root (R) of *T. brevis*.

(B) Leaves (L) arising near the lateral side of the ribbonlike root (R) of *C. doianus*.

(C) Leaves (L) arising from the dorsal surface of the crustose root (R) of *H. japonicum*.

L, leaf; R, root; S, shoot. Bars = 1 mm.

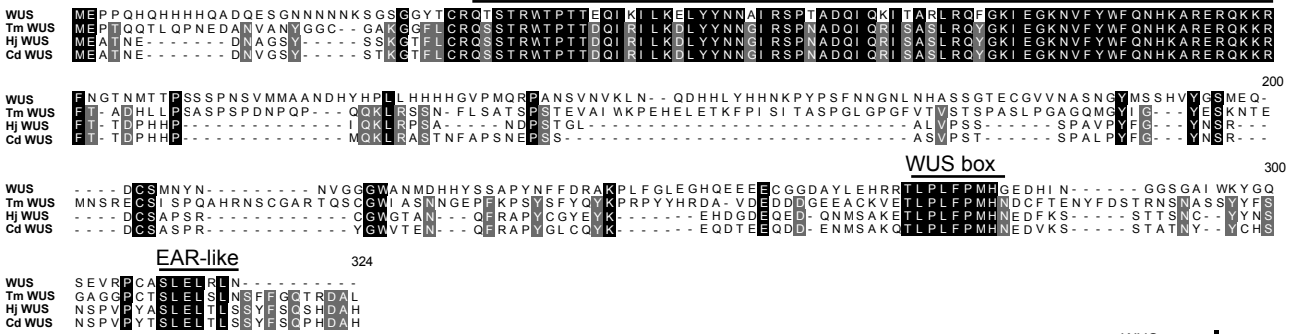


Supplemental Figure 2. Structure and Phylogeny of Podostemaceae STM Genes.

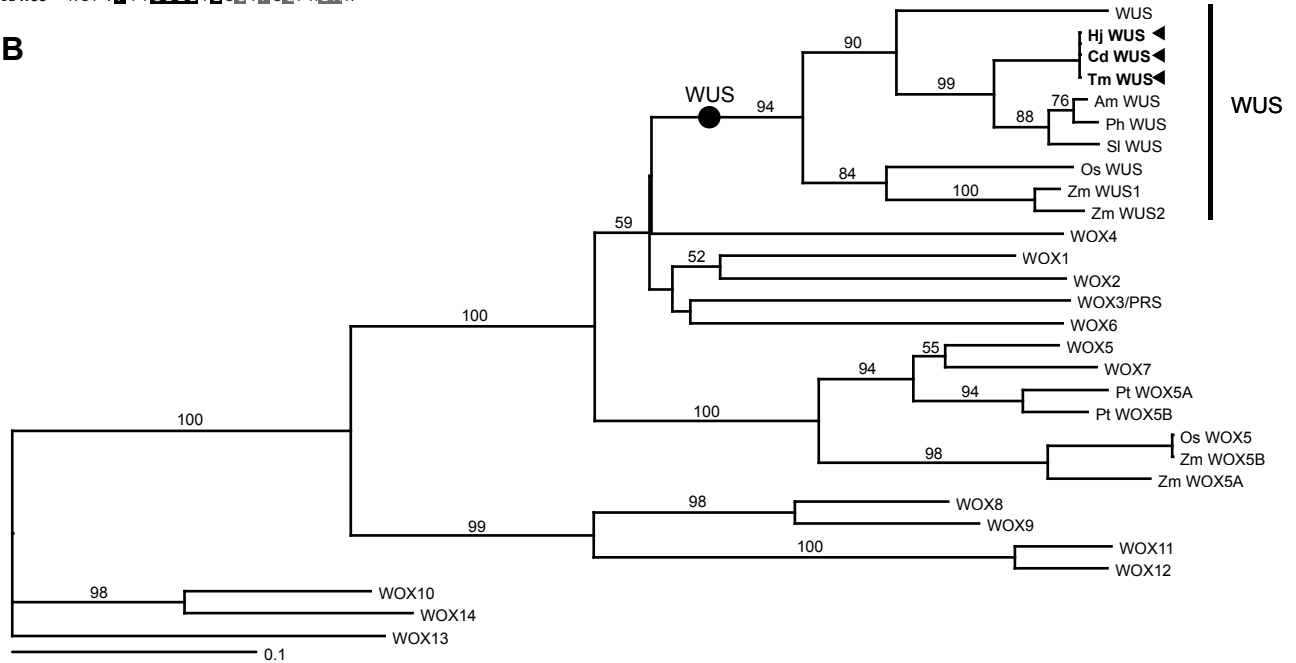
(A) Alignment of inferred amino acids of Tm STM, HJ STM and Cd STM to those of *Arabidopsis thaliana* STM. Identical residues are shaded (black boxes highlight invariant amino acids, and gray boxes show conserved amino acids among Podostemaceae STMs), and dashed lines are added to maximize alignment. Horizontal lines show conserved domains, i.e., MEINOX domain, ELK domain and homeodomain.

(B) Neighbor Joining tree of KNOX genes using amino acid sequences of three conserved domains (Supplemental Dataset 1). Podostemaceae STM genes are marked by arrowheads. Bootstrap values (>50%) are indicated above branches. Bar indicates 0.05 amino acid substitutions per site.

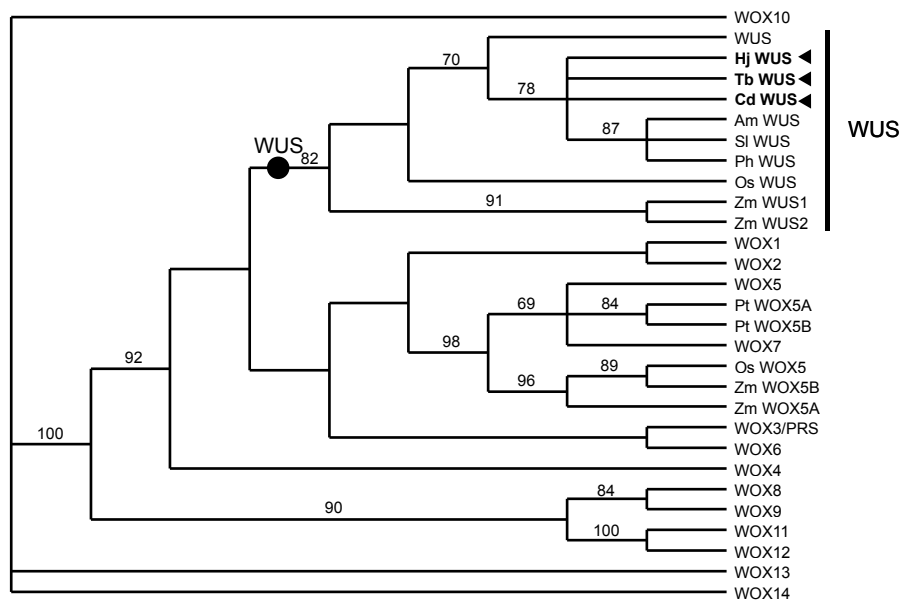
(C) Strict consensus of the 4611 Most Parsimonious trees using amino acid sequences of three conserved domains (Supplemental Dataset 1). Podostemaceae STM genes are marked by arrowheads. Bootstrap values (>50%) are indicated above branches.



B



C

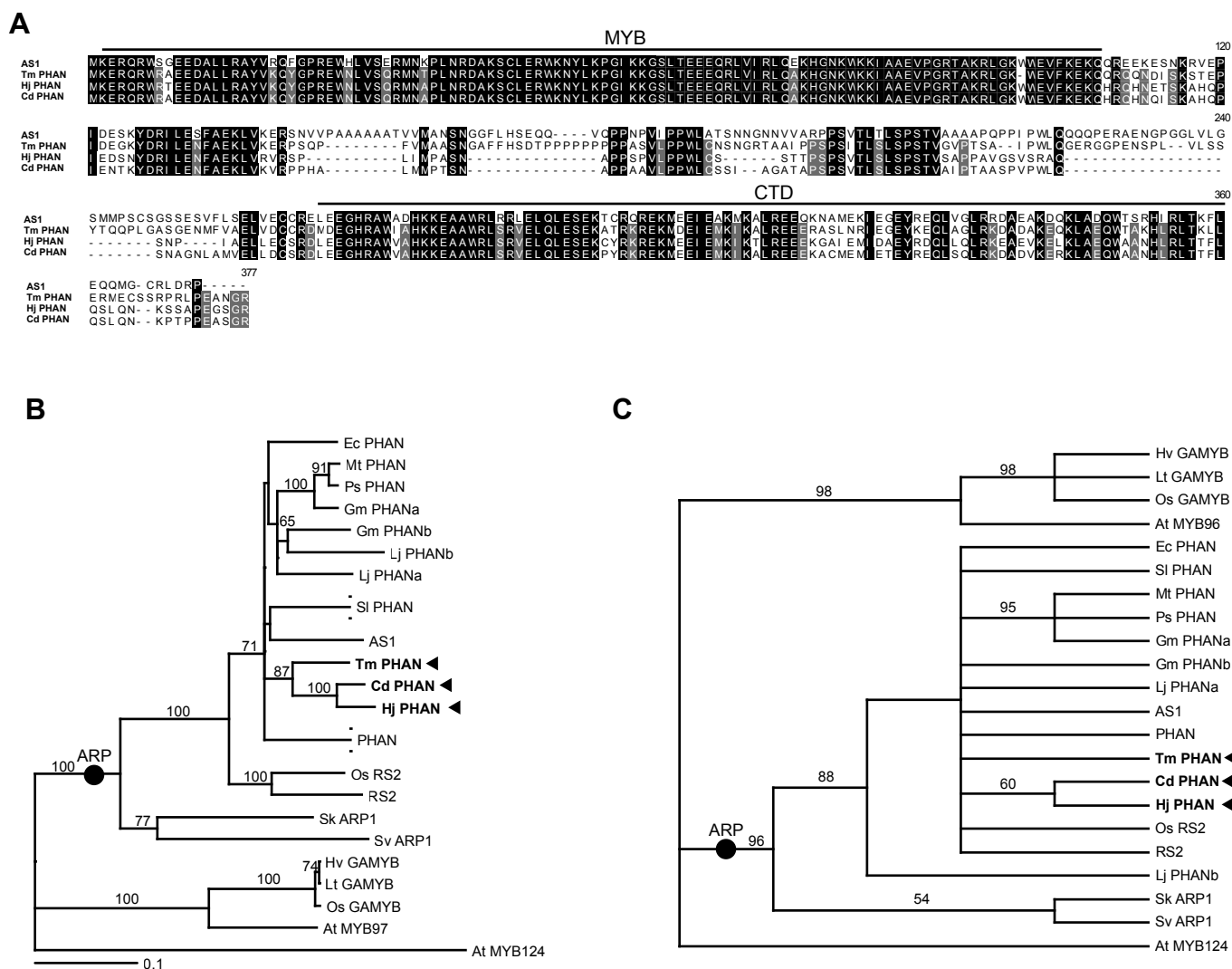


Supplemental Figure 3. Structure and Phylogeny of Podostemaceae WUS Genes.

(A) Alignment of inferred amino acids of Tm *WUS*, Hj *WUS* and Cd *WUS* to those of *Arabidopsis thaliana* *WUS*. Black boxes highlight invariant amino acids and gray boxes show conserved amino acids among Podostemaceae *WUS* genes. Dashed lines are added to maximize alignment. Horizontal lines show conserved domains, homeodomain, WUS box and EAR-like domain, which characterize *WUS* genes.

(B) Neighbor Joining tree of *WOX* family genes based on amino acid sequences of Homeodomain (Supplemental Dataset 2). Podostemaceae *WUS* genes are marked by arrowheads. Bootstrap values (>50%) are indicated above branches. Bar indicates 0.1 amino acid substitutions per site.

(C) Strict consensus of the 12 Most Parsimonious trees of *WOX* family genes based on amino acid sequences of Homeodomain (Supplemental Dataset 2). Podostemaceae *WOX* genes are marked by arrowheads. Bootstrap values (>50%) are indicated above branches.

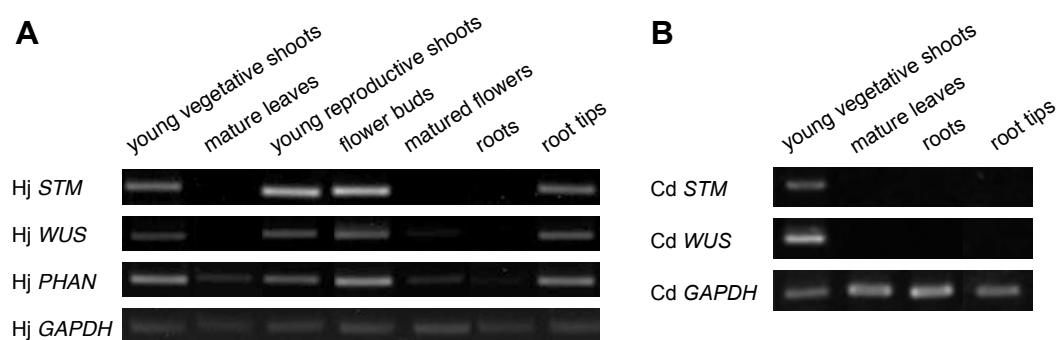


Supplemental Figure 4. Structure and Phylogeny of Podostemaceae *ARP* Genes.

(A) Alignment of inferred amino acids of *TmPHAN*, *HjPHAN* and *CdPHAN* to those of *A. thaliana ASI*. Black boxes highlight invariant amino acids, and gray boxes show conserved amino acids among Podostemaceae *ARP* genes. Dashed lines are added to maximize alignment. Horizontal lines show conserved MYB and CTD domains.

(B) Neighbor Joining tree of *ARP* genes based on amino acid sequences of conserved MYB domains (Supplemental Dataset 3). Podostemaceae *ARP* genes are marked by arrowheads. Bootstrap values (>50%) are indicated above branches. Bar indicates 0.1 amino acid substitutions per site.

(C) Strict consensus of the 195 Most Parsimonious trees of *ARP* genes based on amino acid sequences of conserved MYB domains (Supplemental Dataset 3). Podostemaceae *ARP* genes are marked by arrowheads. Bootstrap values (>50%) are indicated above branches.



Supplemental Figure 5. Results of RT-PCR analyses of gene expression in different organs of *Hydrobryum japonicum*, and *Cladopus doianus*.

(A) Hj *STM*, Hj *WUS*, and Hj *PHAN* expression in *H. japonicum*. Total RNA was extracted from several kinds of organs (young vegetative shoots, mature leaves, young reproductive shoots, flower buds, mature flowers, roots, and root tips). Transcripts were amplified by 32 cycles of PCR with gene-specific primers. Similar results were obtained from two biological replicates. The expression of Hj *GAPDH* was used as a control.

(B) Cd *STM* and Cd *WUS* expressions in *C. doianus*. Total RNA was extracted from several kinds of organs (young vegetative shoots, mature leaves, roots, and root tips). Transcripts were amplified by 40 cycles of PCR with gene-specific primers. Similar results were obtained from two biological replicates. The expression of Cd *STM* or Cd *WUS* was weakly detected from the root tips or mature leaves in replicated experiment. The expression of Cd *GAPDH* was used as a control.

Supplemental Table 1. Organs Contained in Samples Used in RT-PCR Analysis.

Sample	Contained organ	Leaf	Shoot apex	Bract	Floral organ	Root
Young vegetative shoots		+	+	-	-	+
Mature leaves		+	-	-	-	-
Young reproductive shoots		-	+	+	-	+
Floral buds		-	+	+	+	+
Mature flowers		-	+	+	+	-
Roots		-	-	-	-	+
Root tips		- or +*	- or +*	-	-	+

*Dessected samples of root tips may include leaf and shoot apex, because a new vegetative shoot arises in close proximity to the root meristem.

Supplemental Table 2. Sample Collection Sites.

Species	Collection site
<i>Hydrobryum japonicum</i>	Ogawa River, Kagoshima Prefecture, Japan
<i>Cladopus doianus</i>	Sendai River, Kagoshima Prefecture, Japan
<i>Cladopus doianus</i>	Amori River, Kagoshima Prefecture, Japan
<i>Terniopsis minor</i>	Pong Nam Ron stream, Chanthaburi, Thailand

Supplemental Table 3.
GenBank Accession Numbers for Genes Isolated in This Study.

Species	Gene	Accession number
<i>Hydrobryum japonicum</i>	Hj <i>STM</i>	AB512740
	Hj <i>WUS</i>	AB512741
	Hj <i>PHAN</i>	AB512742
	Hj <i>GAPDH</i>	AB512750
<i>Cladopus doianus</i>	Cd <i>STM</i>	AB512743
	Cd <i>WUS</i>	AB512744
	Cd <i>PHAN</i>	AB512745
	Cd <i>GAPDH</i>	AB512751
<i>Terniopsis minor</i>	Tm <i>STM</i>	AB512752
	Tm <i>WUS</i>	AB512753
	Tm <i>PHAN</i>	AB512754
<i>Polyleurum stylosum</i>	Ps <i>STM</i>	AB512746
<i>Weddellina squamulosa</i>	Ws <i>STM</i>	AB512748

Supplemental Table 4. Gene Accession Numbers for *KNOX* Phylogeny.

Gene	Species	Accession Number
<i>Aa KNOX1</i>	<i>Acetabularia acetabulum</i>	AF170172
<i>BELL1</i>	<i>Arabidopsis thaliana</i>	U39944
<i>Bn hd1</i>	<i>Brassica napus</i>	Z29073
<i>Bo STM</i>	<i>Brassica oleracea</i>	AF193813
<i>CRKNOX1</i>	<i>Ceratopteris richardii</i>	AB043954
<i>CRKNOX2</i>	<i>Ceratopteris richardii</i>	AB043956
<i>CRKNOX3</i>	<i>Ceratopteris richardii</i>	AB043957
<i>DOH1</i>	<i>Dendrobium grex</i>	AJ276389
<i>H1</i>	<i>Arabidopsis thaliana</i>	X801227
<i>hirz</i>	<i>Antirrhinum majus</i>	AY072736
<i>Hop1</i>	<i>Pisum sativum</i>	AF063307
<i>HOS59</i>	<i>Oryza sativa</i>	AB061818
<i>HOS66</i>	<i>Oryza sativa</i>	BAB55660
<i>Hvh21</i>	<i>Hordeum vulgare</i>	AF022390
<i>Hv KNOX3</i>	<i>Hordeum vulgare</i>	X83518
<i>ina</i>	<i>Antirrhinum majus</i>	AY072735
<i>Kn1</i>	<i>Zea mays</i>	X61308
<i>KNAP1</i>	<i>Malus domestica</i>	Z71978
<i>KNAP2</i>	<i>Malus domestica</i>	Z71979
<i>KNAP3</i>	<i>Malus domestica</i>	Z71980
<i>KNAT1</i>	<i>Arabidopsis thaliana</i>	U14174
<i>KNAT2</i>	<i>Arabidopsis thaliana</i>	U14175
<i>KNAT3</i>	<i>Arabidopsis thaliana</i>	X92392
<i>KNAT4</i>	<i>Arabidopsis thaliana</i>	X92393
<i>KNAT5</i>	<i>Arabidopsis thaliana</i>	NM119356
<i>KNAT6S</i>	<i>Arabidopsis thaliana</i>	AB072361
<i>KNAT7</i>	<i>Arabidopsis thaliana</i>	AF308451
<i>LET12</i>	<i>Solanum lycopersicum</i>	AF000142
<i>LET6</i>	<i>Solanum lycopersicum</i>	AF000141
<i>LG3</i>	<i>Zea mays</i>	AF100455
<i>MKN1-3</i>	<i>Physcomitrella patens</i>	AF285148
<i>MKN2</i>	<i>Physcomitrella patens</i>	AF285147
<i>MKN4</i>	<i>Physcomitrella patens</i>	AF284817
<i>Mt KNOX1</i>	<i>Medicago trunculata</i>	AF308454
<i>NTH1</i>	<i>Nicotiana tabacum</i>	AB025573
<i>NTH15</i>	<i>Nicotiana tabacum</i>	AB004785

Supplemental Table 4. (Continued).

Gene	Species	Accession Number
<i>NTH20</i>	<i>Nicotiana tabacum</i>	AB025714
<i>NTH22</i>	<i>Nicotiana tabacum</i>	AB025715
<i>NTH23</i>	<i>Nicotiana tabacum</i>	AB004797
<i>NTH9</i>	<i>Nicotiana tabacum</i>	AB025713
<i>OSH1</i>	<i>Oryza sativa</i>	D16507
<i>OSH15</i>	<i>Oryza sativa</i>	AB016071
<i>OSH3</i>	<i>Oryza sativa</i>	AB028882
<i>OSH43</i>	<i>Oryza sativa</i>	AB028884
<i>OSH45</i>	<i>Oryza sativa</i>	D49704
<i>OSH6</i>	<i>Oryza sativa</i>	AB028883
<i>OSH71</i>	<i>Oryza sativa</i>	AB028885
<i>Ph STM</i>	<i>Petunia hybrida</i>	AY112704
<i>PKn1</i>	<i>Ipomoea nil</i>	AB015999
<i>PKn2</i>	<i>Ipomoea nil</i>	AB016000
<i>PKn3</i>	<i>Ipomoea nil</i>	AB016002
<i>POTH1</i>	<i>Solanum tuberosum</i>	U65648
<i>Ra STM</i>	<i>Ruscus aculeatus</i>	AB300055
<i>RS1</i>	<i>Zea mays</i>	L44133
<i>SBH1</i>	<i>Glycine max</i>	L13663
<i>Sk KNOX1</i>	<i>Selaginella kraussiana</i>	AY667449
<i>Sk KNOX2</i>	<i>Selaginella kraussiana</i>	AY667450
<i>SKN1</i>	<i>Picea mariana</i>	U90091
<i>SKN2</i>	<i>Picea mariana</i>	U90092
<i>Sr STM1</i>	<i>Streptocarpus rexii</i>	AY655753
<i>Ss STM1</i>	<i>Streptocarpus saxorum</i>	AY655754
<i>STM</i>	<i>Arabidopsis thaliana</i>	U32344
<i>THox2</i>	<i>Solanum lycopersicum</i>	U76410
<i>TKn1</i>	<i>Solanum lycopersicum</i>	U32247
<i>TKn2</i>	<i>Solanum lycopersicum</i>	U76407
<i>TKn3</i>	<i>Solanum lycopersicum</i>	U76408
<i>TKn4</i>	<i>Solanum lycopersicum</i>	AF533597
<i>Wknox1</i>	<i>Triticum aestivum</i>	AB182943

Supplemental Table 5. Gene Accession Numbers for *WOX* Phylogeny.

Gene	Species	Accession Number
Am <i>WUS</i>	<i>Antirrhinum majus</i>	AY162209
Sl <i>WUS</i>	<i>Solanum lycopersicum</i>	AJ538329
Os <i>WOX5A</i>	<i>Oryza sativa</i>	AM234751
Os <i>WUS</i>	<i>Oryza sativa</i>	AM234746
Ph <i>WUS</i>	<i>Petunia x hybrida</i>	AF481951
Pt <i>WOX5A</i>	<i>Populus trichocarpa</i>	AM234765
Pt <i>WOX5B</i>	<i>Populus trichocarpa</i>	AM234766
<i>WOX1</i>	<i>Arabidopsis thaliana</i>	NM112682
<i>WOX10</i>	<i>Arabidopsis thaliana</i>	NM101923
<i>WOX11</i>	<i>Arabidopsis thaliana</i>	AY251402
<i>WOX12</i>	<i>Arabidopsis thaliana</i>	NM121787
<i>WOX13</i>	<i>Arabidopsis thaliana</i>	NM119720
<i>WOX14</i>	<i>Arabidopsis thaliana</i>	NM101922
<i>WOX2</i>	<i>Arabidopsis thaliana</i>	NM125325
<i>WOX3/PRS</i>	<i>Arabidopsis thaliana</i>	NM128422
<i>WOX4</i>	<i>Arabidopsis thaliana</i>	AY251396
<i>WOX5</i>	<i>Arabidopsis thaliana</i>	NM111961
<i>WOX6</i>	<i>Arabidopsis thaliana</i>	AY251399
<i>WOX7</i>	<i>Arabidopsis thaliana</i>	NM120659
<i>WOX8</i>	<i>Arabidopsis thaliana</i>	NM123966
<i>WOX9</i>	<i>Arabidopsis thaliana</i>	NM128948
<i>WUS</i>	<i>Arabidopsis thaliana</i>	NM127349
Zm <i>WOX5A</i>	<i>Zea mays</i>	AM234769
Zm <i>WOX5B</i>	<i>Zea mays</i>	AM234770
Zm <i>WUS1</i>	<i>Zea mays</i>	AM234744
Zm <i>WUS2</i>	<i>Zea mays</i>	AM234745

Supplemental Table 6. Gene Accession Numbers for *ARP* Phylogeny.

Gene	Species	Accession Number
<i>AS1</i>	<i>Arabidopsis thaliana</i>	AF175996
<i>At MYB124</i>	<i>Arabidopsis thaliana</i>	AF371982
<i>At MYB97</i>	<i>Arabidopsis thaliana</i>	AF176002
<i>Ec PHAN</i>	<i>Eschscholzia californica</i> subsp. <i>californica</i>	AY228766
<i>Gm PHANa</i>	<i>Glycine max</i>	AY790252
<i>Gm PHANb</i>	<i>Glycine max</i>	AY790253
<i>Hv GAMYB</i>	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	X87690
<i>Sl PHAN</i>	<i>Solanum lycopersicum</i>	AF148934
<i>Lj PHANa</i>	<i>Lotus japonicus</i>	AY790244
<i>Lj PHANb</i>	<i>Lotus japonicus</i>	AY790245
<i>Lt GAMYB</i>	<i>Lolium temulentum</i>	AF114162
<i>Mt PHAN</i>	<i>Medicago trunculata</i>	AF308453
<i>Os GAMYB</i>	<i>Oriza sativa</i>	X98355
<i>Os RS2</i>	<i>Oriza sativa</i>	AB064519
<i>PHAN</i>	<i>Antirrhinum majus</i>	AJ005586
<i>Ps PHAN</i>	<i>Pisum sativum</i>	AF299140
<i>RS2</i>	<i>Zea mays</i>	AF126489
<i>Sk ARP</i>	<i>Selaginella kraussiana</i>	AY667452
<i>Sv ARP</i>	<i>Selaginella viticulosa</i>	AY667453

Supplemental Table 7. Primers Used in This Study.

Purpose	Primer set (F and R)
RT-PCR of Hj <i>STM</i>	HjSTM-F2 (5'-GGAAGGCGGTTCCAATAGC-3') and HjSTM-R (5'-GTCGGCGACACGTCCATAGG-3')
probe for <i>in situ</i> hybridization of Hj <i>STM</i>	HjSTM-F2 (5'-GGAAGGCGGTTCCAATAGC-3') and HjSTM-R2 (5'-CCAGCTCCGGTTGAGTTAG-3')
RT-PCR of Hj <i>WUS</i>	HjWUS-F2 (5'-GCGATTCACCACCGATCCGC-3') and HjWUS-R (5'-GAGCGTCGTGTGACTGAGAG-3')
probe for <i>in situ</i> hybridization of Hj <i>WUS</i>	HjWUS-F1 (5'-GGCCACAAATGAAGACAACG-3') and HjWUS-R (5'-GAGCGTCGTGTGACTGAGAG-3')
RT-PCR of Hj <i>PHAN</i>	HjARP-F1 (5'-GAGAAGCAACACCGGCAGCA-3') and HjARP-R1 (5'-ATCCCGGCTGCATTCCAACA-3')
probe for <i>in situ</i> hybridization of Hj <i>PHAN</i>	HjARP-F (5'-GAGAGGCAGCGGTGGAGAAC-3') and HjARPR (5'-CACTGCCTTCGGGAGCTGATG-3')
RT-PCR of Hj <i>GAPDH</i>	HjGAPDH-F (5'-CCATCGCTGAATGGGAAGCTC-3') and HjGAPDH-R (5'-CTGAGCAGACGCCATGTGGAC-3')
RT-PCR of Cd <i>STM</i>	CdSTM-2F (5'-ATGGAAGGCGGTTCCAATAG-3') and CdSTM-2R (5'-ACTTCCCAGGTAGCCACTGT-3')
probe for <i>in situ</i> hybridization of Cd <i>STM</i>	CdSTM-2F (5'-ATGGAAGGCGGTTCCAATAG-3') and CdSTM-2R (5'-ACTTCCCAGGTAGCCACTGT-3')
RT-PCR of Cd <i>WUS</i>	CdWUS-2F (5'-GGCAAAAATGTGTTCTACTG-3') and CdWUS-2R (5'-CTTTTGACATCTTCGTTGTG-3')
RT-PCR of Cd <i>GAP</i>	Cd13GAP-2F (5'-GAAAGGGGGAGCGAAAAAGG-3') and Cd13GAP-R (5'-CTGGGTAGAGGCCATGTGGA-3')
probe for <i>in situ</i> hybridization of Tm <i>STM</i>	GR 5' Nested Primer (5'-GGACTGACATGGACTGAAGGAGTA-3') and Podo-STM-Pn (5'-GACATGATCTTGGCYTTRAT-3')
probe for <i>in situ</i> hybridization of Tm <i>WUS</i>	WUS-1-R (5'-GCATDGGRAADARDGGAAGHGT-3') and WUS-HD-Fn (5'-GGTTYCARAAYCAYAARGCNCG-3')

Supplemental Table 7. (Continued).

Purpose	Primer
1stPCR for isolating 3' ends of <i>STM</i>	5'- GGNWSYYTNAARCARGARTTYAT -3'
2nd PCR for isolating of 3' ends of <i>STM</i>	5'- (CAU)4AARAARGGIAARYTNCC -3'
1stPCR for isolating 3'ends of <i>WUS</i>	5'- GGNAARATHGARGGNAARAAYGT -3'
2ndPCR for isolating 3'ends of <i>WUS</i>	5'- GGTTYCARAAYCAYAARGCNCG -3'
1st PCR for isolating 5'ends of <i>ARP</i>	5'- CAYAARAARGARGCNGCNTGG -3'
2nd PCR for isolating 5'ends of <i>ARP</i>	5'- GARAARATGGARGARATHGARGC -3'
1st PCR for isolating 3' ends of <i>GAPDH</i>	5'- ACNGAYAARGAYAARGCNGC -3'
2nd PCR for isolating 3' ends of <i>GAPDH</i>	5'- (CUA)4 AAYGAYGCNCCNATGTTYGT -3'