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Expression patterns of Class I *KNOX* and *YABBY* genes in *Ruscus aculeatus*

(Asparagaceae) with implications for phylloclade homology

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**Abstract** *STM* (*RaSTM*) and *YAB2* (*RaYAB2*) homologues were isolated from *Ruscus aculeatus* (Asparagaceae, monocots) and their expressions were analyzed by real-time PCR to assess hypotheses on the evolutionary origin of the phylloclade in the Asparagaceae. In young shoot buds, *RaSTM* is expressed in the shoot apex, while *RaYAB2* is expressed in the scale leaf subtending the shoot bud. This expression pattern is shared by other angiosperms, suggesting that the expression patterns of *RaSTM* and *RaYAB2* are useful as molecular markers to identify the shoot and leaf, respectively. *RaSTM* and *RaYAB2* are expressed concomitantly in phylloclade primordia. These results suggest that the phylloclade is not homologous to either the shoot or leaf, but that it has a double organ identity.

**Keywords** Asparagaceae    phylloclade    *Ruscus aculeatus*    *STM*    *YABBY*

## Introduction

The body plan of vascular plants is quite uniform in that they consist of three major vegetative organs: root, stem and leaf (e.g. Gifford and Forster, 1989). Contrary to this uniform body plan, some plants produce novel organs that are not strictly homologous or identical to one of the three major vegetative organs; such innovations contribute to morphological diversification of vascular plants. Phylloclades are a unique organ with a compressed, leaf-like appearance despite being located in the axillary position where a lateral shoot should arise generally (Bell, 1991). A typical phylloclade is seen in the coniferous genus *Phyllocladus* (Podocarpaceae) where it is interpreted as a laterally compressed shoot system (Tomlinson et al., 1987).

In the Asparagaceae family of basal monocots (Rudall et al., 2000; Chase, 2004), a compressed, elliptic organ with a pointed apex is formed in the axil of the scale leaf (Figs. 1a-c). It also has been designated as a phylloclade, but the organ identity and evolutionary process are not fully understood. Some studies have considered the Asparagaceae phylloclade to be a compressed stem (caulome) because of its axial position and ability to generate floral buds (e.g., Turpin, 1820 cited in Hirsch, 1977;

Zweigelt, 1913; Hirsch, 1977). Others have compared it to a leaf borne on an aborted shoot, because it grows determinately and has a venation pattern similar to that of the leaf (de Candolle, 1827 cited in Hirsch, 1977; Schlittler, 1960; Cusset and Tran, 1966).

In addition to these simple interpretations, the Asparagaceae phylloclade was also considered to be a *de novo* organ with stem and leaf identities (Croizat-Chaley, 1973; Sattler, 1984; Cooney-Sovetts and Sattler, 1986). Furthermore, some authors have postulated that the phylloclade is a congenital-fusion product of an axillary branch and its prophylls (Van Tieghen, 1884 cited in Cooney-Sovetts and Sattler, 1986; Arber, 1924).

The expression patterns of transcription factor genes would be helpful in clarifying the identity of the Asparagaceae phylloclade. In some model plants with simple leaves, Class I *KNOTTED*-like homeobox (*KNOX*) genes are expressed in the shoot apical meristem (SAM), while they are down-regulated in lateral organ primordia (Vollbrecht et al., 1990; Barton and Poethig, 1993). This expression pattern is plesiomorphic for Class I *KNOX* genes (Bharathan et al., 2002; Harrison et al., 2005; Sano et al., 2005). On the other hand, some genes, such as *ASYMMETRIC LEAVES 1*, *ASYMMETRIC LEAVES 2*, Class III *HOMEODOMAIN-LEUCIN ZIPPER* genes, *KANADI* genes, and

*YABBY* genes, are expressed in lateral organ primordia and promote their asymmetric growth (Eshed et al., 2001; Bowman et al., 2002; Emery et al., 2003; Engstrom et al., 2004). Among them, expression of *YABBY* genes is specific to lateral organs in diverse lineages of angiosperms (Bowman, 2000; Kim et al., 2001; Yamaguchi et al., 2003; Yamada et al., 2004; Jang et al., 2004; Juarez et al., 2004; Fourquin et al., 2005).

Based on these previous studies, it is probable that the expression patterns of Class I *KNOX* genes and *YABBY* genes could be markers for assessing the SAM and lateral organ identities, respectively, in most angiosperm lineages.

In this study, we isolated *SHOOTMERISTEMLESS (STM)* and *YABBY2 (YAB2)* homologues from *Ruscus aculeatus* L. (Asparagaceae), which are members of Class I *KNOX* and *YABBY* genes, respectively. Their expressions were analyzed by real-time PCR to assess the proposed hypotheses on phylloclade evolution.

## **Materials and Methods**

Plant materials and phenology of *Ruscus aculeatus*

Plants of *R. aculeatus* cultivated in the Tokyo campus of Japan Women's University were used in this study. Dormant buds enclosed by several scale leaves (bud scales) formed at the base of the current shoots became enlarged during February and March (stage 0, Figs. 1d, 2a; see also Hirsch, 1977). At stage 0, the shoot apex was round without its own scale leaves. The shoot apex formed four to six lateral shoot axes subtended by scale leaves from April to June (stage I, Fig. 2b). In stage II lasting about 5 months from July to November, phylloclade primordia emerged acropetally in the axils of scale leaf primordia on the main or lateral axes (Fig. 2c). In the subsequent 3 months (December to early February), floral buds subtended by bracts developed on the adaxial surface of the phylloclade primordia (stage III, Fig. 2d). The basal-most phylloclades on each axis were devoid of floral buds. The phylloclade primordia became flattened at stage IV (mid-February to mid-March) while the main and lateral shoot apices ceased indeterminate growth and also flattened (Fig. 2e). At this stage, the next main shoot system (stage 0) was initiated in the axil of the scale leaf remaining on the base of the current shoot. The shoot system grew above ground and the floral buds began differentiation in late March (stage V, Fig. 2f). Anthesis began in April (stage VI, Fig. 1e).



### Cloning *STM* homologue and *YABBY* gene

Samples collected for cloning were frozen in liquid N<sub>2</sub>. Total RNA was extracted from floral buds and first-strand cDNA for 3' RACE was synthesized following Shindo et al. (1999). The partial cDNA sequence of an *STM* homologue was amplified by STM-ELK1 and UAP. Nested PCR was performed by KN4-1 and UAP (Table1). The remaining 5' end sequence was determined by 5' RACE following Shindo et al. (1999). Similarity between the obtained *STM* homologue and other *KNOX* genes was estimated by BLAST (<http://www.ncbi.nlm.nih.gov/BLAST>). A *YABBY* gene was isolated following Yamada et al. (2003). The obtained sequences were registered in DDBJ/EMBL/GenBank as AB000000 (*RaSTM*) and AB168115 (*RaYAB2*).

### Phylogenetic analyses of *KNOX* and *YABBY* genes

The deduced amino acid sequences of *KNOX* genes and *BELLI* were obtained from the NCBI DNA Database. (See S1 for the accession numbers.) They were aligned with

the predicted amino acid sequence of the obtained *STM* homologue of *R. aculeatus* using CLUSTAL X ver. 1.64b (Thompson et al., 1997) and the alignment was revised manually. Phylogenetic analysis was performed with CLUSTAL X ver. 1.64b based on amino acid sequences of MEIKNOX, ELK, and Homeodomains (Fig. 2, S2). Bootstrap supports with 1000 replicates were also calculated by CLUSTAL X ver. 1.64b for each cluster. The obtained tree was rooted by choosing *BELLI* as an outgroup. Alignment and phylogenetic analysis of *YABBY* genes (see S3 for their accession numbers) were conducted following Yamada et al. (2003).

#### Real-time PCR

Collected samples were soaked in RNAlater (Ambion Inc., Austin, TX, USA) after dissection under a binocular microscope. We extracted total RNA from: shoot apices and bud scales subtending the shoot apices at stage 0; the basal-most phylloclade primordia on each axis at stage IV; scale leaves on main and lateral axes at stage IV; floral buds at stage V; and mature basal-most vegetative phylloclades at stage VI. The sample stages and contained organ type(s) are summarized in Table 2. First-strand

cDNAs were synthesized for each sample by the methods described above and were used as a template for real-time PCR. To eliminate possibly-contaminated genomic DNA, we treated total RNAs with DNase I before cDNA synthesis. TaqMan® probes and primers (Table 1) were designed by Primer Express ver. 1.5 (Applied Biosystems, Foster City, CA, USA). Mixtures for PCR were prepared using Platinum® Quantitative PCR SuperMIX-UDG (Invitrogen Co. Ltd, Carlsbad, CA, USA). As an internal control, the expression level of 18S rRNA was quantified for each sample using Pre-Developed TaqMan® Assay Reagents (Applied Biosystems). Three independent reactions were prepared for each amplification set. Threshold cycle (Ct) values were measured by PTC-200 DNA Engine Cycler (Bio-Rad Laboratories, Inc., Waltham, MA, USA). The obtained Ct values were compared with Ct values of standard templates with the known number of initial templates for estimating the initial target and control cDNA molecules in each reaction. The number of target cDNA molecules was divided by that of 18S rRNA and standard deviations among the three reactions were calculated. Experiments were replicated five times to verify the results.

## **Results**

### Isolation of *STM* homologue

We isolated one *STM* homologue (*RaSTM*) from *R. aculeatus*. The determined partial mRNA was 1114 bp, including a complete coding sequence. The predicted amino acid sequence consists of 321 residues and includes the MEIKNOX, ELK, and Homeodomains (Fig. 3, S2). BLAST X search clearly suggested a close similarity to Class I *KNOX* genes such as *STM* and *NTH15* (data not shown).

Phylogenetic analysis robustly supported a sister relationship of *RaSTM* to dicot *STM* homologues (100% bootstrap support), showing that *RaSTM* is distantly related to *Kn1* and *RS1* homologues, which are Class I *KNOX* genes of Poaceae (Fig. 4).

### Isolation of *YAB2* homologue

The obtained putative *YABBY2* homologue (*RaYAB2*) was 793 bp long. We could not obtain a complete coding sequence, but recognized Zinc finger-like and YABBY domains in the deduced amino acid sequence (Fig. 5). *RaYAB2* shares a motif located

just downstream of the Zn finger-like domain with other *YAB2* homologues (Fig. 5), suggesting homology of *RaYAB2* and *YAB2*.

Phylogenetic analysis showed that *RaYAB2* is nested in a clade consisting of *YAB2* homologues and clade monophyly is suggested by 64% bootstrap support (Fig. 6).

Expression analyses of *RaSTM* and *RaYAB2* by real-time PCR

Expression of *RaSTM* was detected in the shoot apex, phylloclade primordial, and floral buds (Fig. 7). Among them, the strongest transcription was observed in the shoot apex, and the expression level in the phylloclade primordia was higher than that in the floral buds. No significant amplification of *RaSTM* was detected in the stage-VI phylloclade and scale leaves (Fig. 7).

The *RaYAB2* expression was highest in the scale leaves, while an expression intensity of less than half the highest expression was also detected in the shoot apex, phylloclade primordia, and floral buds (Fig. 7). Expression in the stage-VI phylloclade was very weak.

Experiments were replicated five times and resulted in identical patterns (data not

shown).

## **Discussion**

*STM* homologue lost during monocots diversification

*RaSTM* is clearly identified as an *STM* homologue by the phylogenetic analysis. This is the first isolation of an *STM* homologue in the monocots despite extensive genomic research into the Poaceae, including rice and maize. In Poaceae, *Kn1*, a Class I *KNOX* gene, participates in maintenance of the shoot apical meristem instead of *STM* (Jackson et al., 1994; Bharathan et al., 1999; Reiser et al., 2000). Taking into account the phylogeny in which the Asparagaceae diverged earlier than the Poaceae (Chase, 2004), the occurrence of the *STM* homologue in *R. aculeatus* suggests that an *STM* homologue was lost during diversification of the monocots while its function was taken over by the *Kn1* homologue.

Phylloclade SAM and leaf identities

The validity of homology assessment based only on gene expression has been questioned because the same gene is co-opted for similar functions among non-homologous organs (e.g., Abouheif et al., 1997; Nielsen and Martinez, 2003; Theissen, 2005). Such functional co-option of a gene would cause expressional commonality (homocracy) among non-homologous organs (Nielsen and Martinez, 2003). Thus, a homocracy among organs does not necessarily ensure their homology, but it could be a tool to assess their organ identity (Rutishauser and Isler, 2001; Nielsen and Martinez, 2003).

In *Arabidopsis* and other eudicots, *STM* maintains proper growth of the SAM by expression in both vegetative and reproductive SAMs, while it is down-regulated in leaf primordia (Barton and Poethig, 1993; Long et al., 1996). Although we could not specify the exact function of *RaSTM*, we infer that monocot *RaSTM*, like other dicot *STM* homologues, is involved in maintenance of the SAM, because it is expressed strongly in the vegetative and reproductive shoot apices, but expression is not detected in the scale leaves as is usual in dicots. Notably, *RaSTM* is expressed in the phylloclade primordia, suggesting that young phylloclades are functionally comparable to the SAM.

Strong expression of *RaYAB2* in the scale leaves suggests that it may be involved in leaf formation. The expression detected in shoot apices might be attributed to the scale leaves (bud scales) covering them. *RaYAB2* is also transcribed in the phylloclade primordia, so the phylloclade is also partly comparable to a leaf.

The concomitant expression of *RaSTM* and *RaYAB2* in the phylloclade suggests that both SAM and leaf developmental pathways may be partly incorporated into the phylloclade developmental pathway. Similar incorporation of SAM and leaf developmental pathways confers continuous identity between SAM and leaf in a tomato compound leaf of (Sinha, 1999; Kim et al., 2003). The phylloclade twofold pattern could explain the apparently contradictory characteristics of leaf-like appearance and shoot-like axillary position.

Traditional plant morphological studies emphasize the positional criterion (homotopy) to assess organ homology and do not permit coexistence of multiple identities in a single organ (Rutishauser and Isler, 2001). Such an approach is called Classical Morphology (ClAM) (Rutishauser and Isler, 2001), and the ClAM approach has been applied to homology assessments of the phylloclade, interpreting it as either a compressed stem (Turpin, 1820 cited in Hirsch, 1977; Zweigelt, 1913; Hirsch, 1977) or



a leaf borne on an aborted shoot (de Candolle, 1827 cited in Hirsch, 1977; Schlittler, 1960; Cusset and Tran, 1966).

There are many studies of organ heterotopy whereby organs with different identities are formed in an equivalent position (e.g., Rutishauser and Grubert, 1999; Rutishauser and Isler, 2001). Furthermore, developmental genetic studies clarify that amalgamation of different developmental pathways obscures the boundary between the three major vegetative organs (root, stem, leaf) (Hofer, 1998; Sinha, 1999). These findings have led to recent re-evaluation of the importance of the Fuzzy Arberian Morphology (FAM) approach named after Agnes Arber (Rutishauser and Isler, 2001), such as the Leaf–Shoot Continuum Hypothesis (Arber, 1950). The FAM approach emphasizes estimation of organ identities over homology, and accepts heterotopy and continuum identity between organs (Rutishauser and Isler, 2001). Arber (1924) explained the contradictory characteristics of the phylloclade as a fusion/coexistence of leaf and SAM and this interpretation is subsumed into later FAM approaches interpreting the phylloclade as having a double identity (Croizat-Chaley, 1973; Sattler, 1984; Cooney-Sovetts and Sattler, 1986).

The FAM interpretation of the phylloclade matches the results of our expression

analyses, although it is not shown here whether the *STM* and *YABBY* genes are expressed in the same or different parts (tissues) of the phylloclade. We still need to clarify how the developmental pathways of the SAM and leaf are incorporated into phylloclade development to assess phylloclade evolution. Expression analyses of other genes involved in SAM and leaf developmental pathways, as well as *in situ* hybridization experiments, which are ongoing, will shed light on this.

### **Acknowledgements**

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### Figure legends

**Fig. 1.** Morphology of *Ruscus aculeatus*. **a** Mature shoot system. **b** Close-up of mature phylloclade formed at main shoot apex and lateral phylloclades. **c** Phylloclade subtended by scale leaf. **d** Young bud at stage 0 covered by scale leaves (arrowhead). **e** Flower on adaxial surface of phylloclade. *p* phylloclade, *l* scale leaf. Bars: 1 cm (a, b, e), 5 mm (c, d)

**Fig. 2.** Phenology of *Ruscus aculeatus*. The main shoot system of the previous year is omitted in stage 0 and I. Stage VI is not shown. The dashed line in stage II illustrates the disintegrated main shoot system of the previous year.

**Fig. 3.** Alignment of deduced amino acid sequences of selected *KNOX* genes. Amino acid positions used for phylogenetic analysis are shaded. MEIKNOX, ELK, and Homeodomains are indicated by clumps. Asterisks indicate identical amino acids. See S1 for the full alignment.

**Fig. 4.** Neighbor joining tree of *KNOX* genes. Bootstrap supports (>50%) are shown above branches. Bar: 0.05 amino acid substitutions per site

**Fig. 5.** Alignment of deduced amino acid sequences of *YABBY* genes. Amino acid positions used for phylogenetic analysis are shaded. Zinc finger-like and *YABBY* domains are marked by clumps. Asterisks indicate identical amino acids. Note a motif shared by *YAB2* homologues (boxed).

**Fig. 6.** Neighbor joining tree of *YABBY* genes. Bootstrap supports (>50%) are shown above branches. Bar: 0.01 amino acid substitutions per site

**Fig. 7.** Relative expression levels of *RaSTM* (open) and *RaYAB2* (shaded) in phylloclade primordia (PP), shoot apices and bud scales subtending them (S), floral buds (F), scale leaves (L) and mature phylloclades (PM). The expression level in shoot apices is set to 100%. Double-ended bars indicate standard deviations among three independent reactions.

**Table 1.** Primers used in this study. I, N, R, S, W, and Y follow the IUPAC code.

**Table 2.** Organs in each sample. + present, - absent

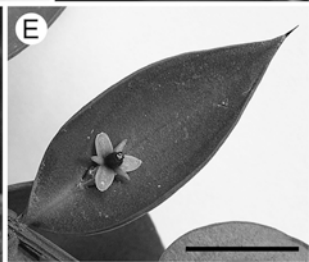
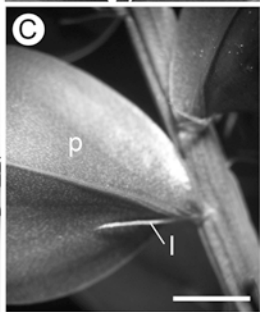
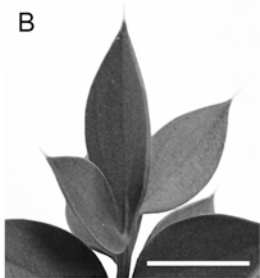
Footnote. \*Abbreviations in parentheses correspond to those in Fig. 7.

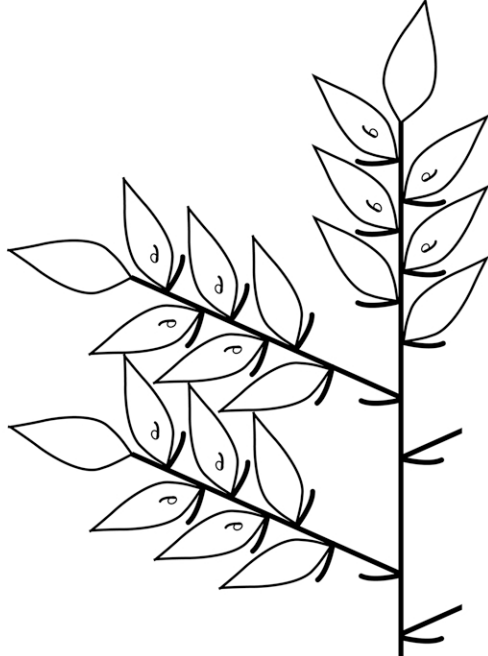
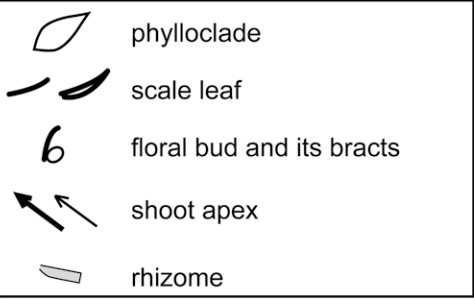
**S1.** *KNOX* genes and *BELLI* used in phylogenetic analysis and their

DDBJ/EMBL/GenBank accession numbers. Data published only in the database are indicated by asterisks.

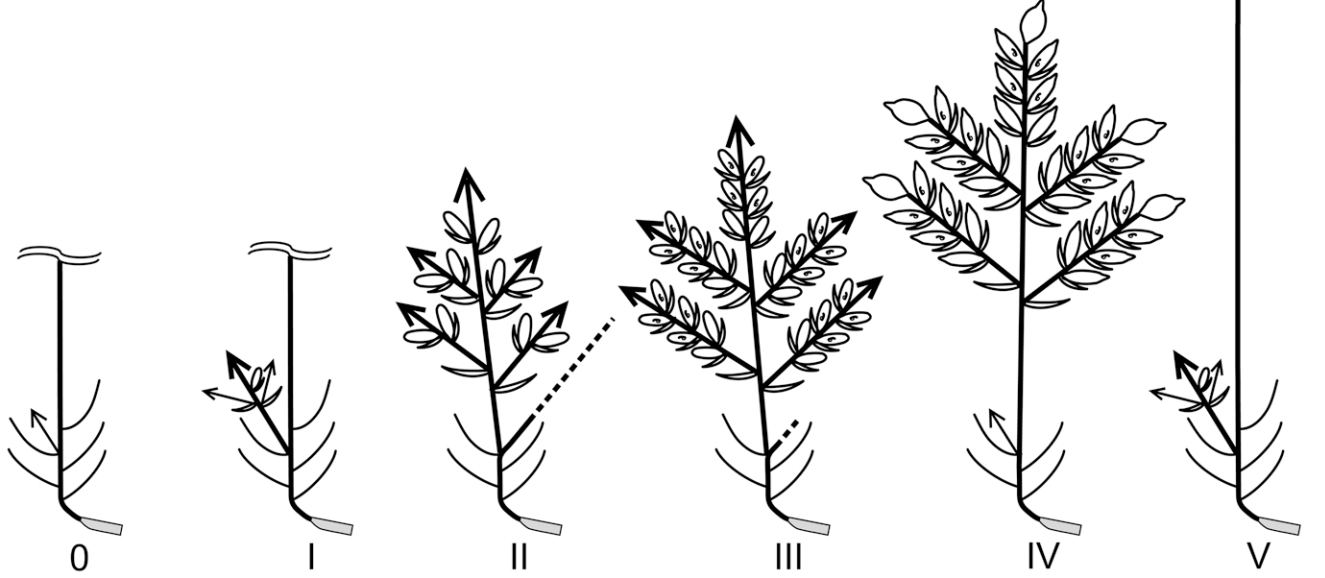
**S2.** Alignment of deduced amino acid sequences of *KNOX* genes and *BELLI*. Amino acid positions used for phylogenetic analysis are shaded. MEIKNOX, ELK, and Homeodomains are indicated by clumps. Asterisks indicate identical amino acids.

**S3.** *YABBY* genes used in phylogenetic analysis and their DDBJ/EMBL/GenBank accession numbers





ground



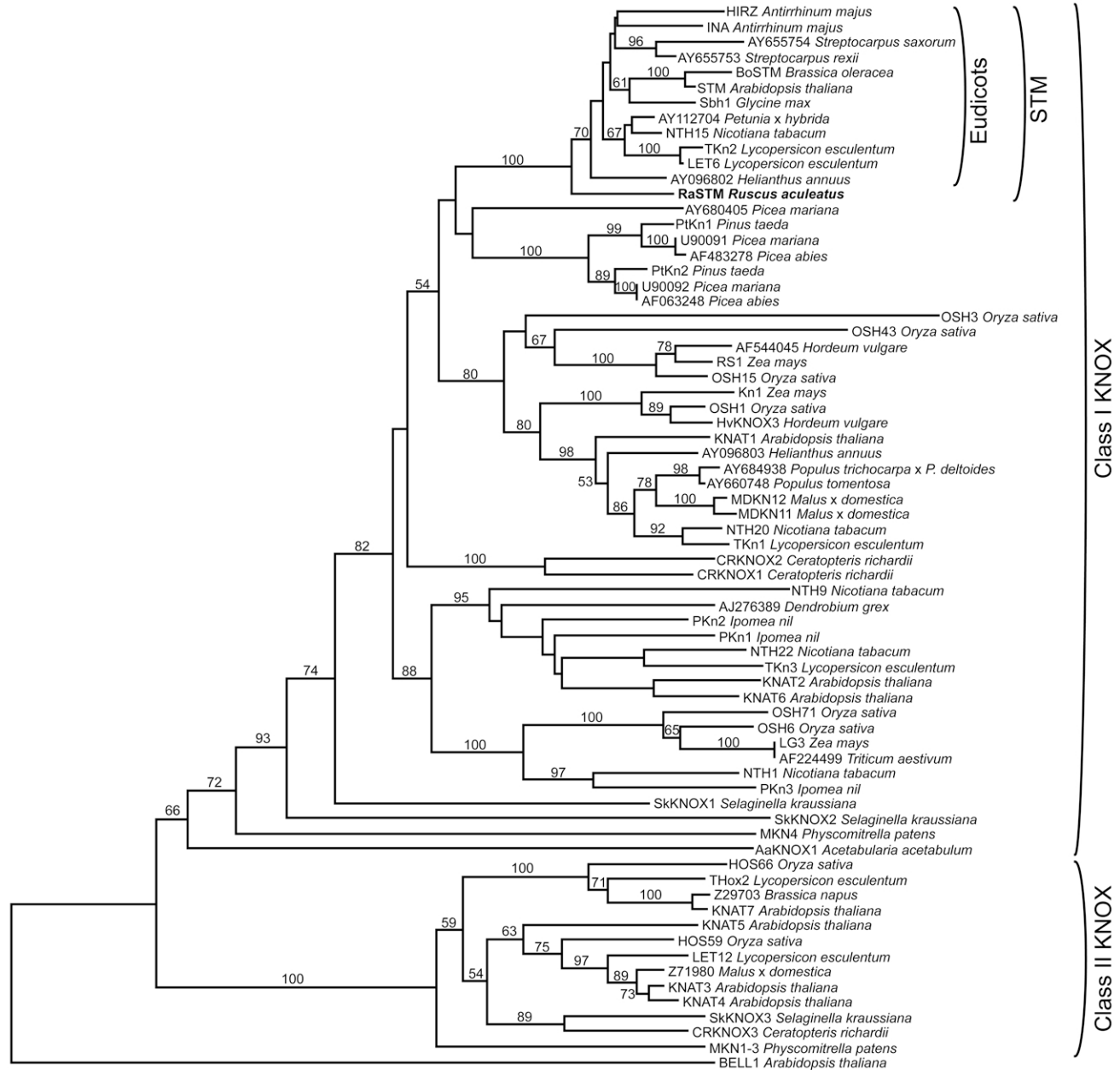
# MEIKNOX

RaSTM	ILKAKIMSHPIHYKLLSAYINCOQ	VGAPPEVVARLEEA	GSSSLMI	GRAASSSSSS	-----	AVGGDPALDOFMEAYCEML	TKYEQELSKPFEAMVFLSR	IDAQFKLS	NSSEEDVDVSENY						
STM	SVKAKIMAHPIHYHRLLAAYVNCQK	VGAPPEVVARLEEAC	-----	SSAAAAAAS	-----	MGPTGCLG	GEDPGLDQFMEAYCEML	VKYEQELSKPFEAMVFLQR	VECFQFKLSGSSEEDVDMNNEF						
BoSTM	LVKAKIMAHPIHYHRLLLAYVNCQK	VGAPPEVQARLEEC	-----	SSAAAAAAS	-----	MGPTGSL	GEDPGLDQFMEAYCEML	VKYEQELSKPFEAMVFLQHV	ECFQFKLSGSSEEDVDMNNEF						
INA	SVKAKIMAHPIHYHRLLAAYINCOQ	VGAPPEVAVKLEEAC	-----	ASAAATMG	-----	RNSVSR	I	GEDPALDOFMEAYCEML	SKYEQELSKPFEAMVFLSR	IECFQFKLSGSSEEDVDVNSL					
AY655753	SVKSKIIMAHPIHYPRLLAAAYVNCQK	IGAPPEVVALLEAAC	-----	ASTITIGG	-----	RNERSCV	GEDPALDOFMEAYCEML	TKYEQELSKPFEAMVFLSR	IECFQFKLSGSSEEDVDVNSF						
AY655754	SVKSKIIMAHPIHYPRLLAAAYVSCQK	IGAPPEVVALLEEV	-----	ASATSTGC	-----	RNERSCV	GEDPALDOFMEAYCEML	TKYEQELSKPFEAMVFLSR	IECFQFKLSGSSEEDVDVNSF						
HIRZ	SLKAKIMAHPIHYHRLLAAYVNCQK	IGAPPEVVSRLLEEA	-----	AAMARHG	-----	TI	SVGEDPGLDQFMEAYCEML	SKYEQELSKPFEAMVFLSR	IESQFKLSGSSEEDVDVNSF						
Sbh1	AVKAKIMAHPIHYHRLLAAYVNCQK	VGAPPEVVARLEEAC	-----	ASATIMAGG	-----	DAAAGSSC	I	GEDPALDOFMEAYCEML	TKYEQELSKPFEAMVFLSR	IECFQFKLSGSSEEDVDLHN-M					
LET6	SIKSKIIMAHPIHYHRLLTAYLNCQK	IGAPPEVVARLEEC	-----	ATSATMGRSSSSSSGGG	-----	I	GEDPALDOFMEAYCEML	TKYEQELSKPFEAMVFLSR	IECFQFKLSGSSEEDVDVNSF						
Tkr2	SIKSKIMLNPHYHRLLTAYLNCQK	IGAPPEVVARLEEC	-----	ATSATMGRSSSSSSGGG	-----	I	GEDPALDOFMEAYCEML	TKYEQELSKPFEAMVFLSR	IECFQFKLSGSSEEDVDVNSF						
NTH15	SIKSKIIMAHPIHYPRLLSAYVNCQK	IGAPPEVVARLEEV	-----	ATSATIGRN	-----	SGG	-----	I	GEDPALDOFMEAYCEML	TKYEQELSKPFEAMVFLSR	IECFQFKLSGSSEEDVDVNSG				
AY112704	N1KAKIMAHPIHYPRLLAAAYINCOQ	IGAPPEVVARLEEV	-----	ATSAMGRSSSSSSGGG	-----	NNV	I	GEDPALDOFMEAYCEML	TKYEQELSKPFEAMVFLSR	IECFQFKLSGSSEEDVDVNSL					
AY096802	SVKAKIMSHPIHYPRLLSAYLNCQK	IGAPPEVVERLEEAC	-----	RASVVAAMSSCSGGAGTSDGSGGGGMMNI	-----	I	GODPALDOFMEAYCEML	KYEQELSKPFEAMVFLSR	IESQFKLSGSSEEDVDVNSL						
KNAT6	V1KAKIACHPSYRLLQAYIDCQK	GVGAPPEIA	-----	IACLEELIE	-----	RDSDVYKQEV	-----	VPSSCF	GADPELDFEMETYCDILVKYKSDL	ARPFDEATFLNKL	EMQLRNL	DHEVAE	-----	D	
KNAT2	V1KSKIASHPLYRLLQTYIDCQK	VGAPFMEI	-----	IACILEE10	-----	RENHYKQDV	-----	APLSCF	GADPELDFEMETYCDILVKYKSDL	ARPFDEATFLNKL	EMQLRNL	DD1AAD	-----	D	
KNAT1	AMKAKIIMAHPIHYSTLLQAYLDCQK	IGAPPDVDRIT	-----	AAR	-----	QDFEARQ	-----	RSTPSVAS	ASSRDPEDOFMEAYCEML	VKYEQELTRP	IQEAMF	IRRE	ESQLSML	-----	SGGETELPE
Kn1	A1KAKIIMSHPIHYSTLLTAYLECNK	VGAPPEVSARLE	-----	TEIA	-----	QVEEARQ	-----	RTALGGL	AAATEPELDOFMEAYCEML	VKYEQELTRP	IQEAMF	MRRVES	QNSLNS	-----	SGGETELPE
RS1	A1KAKIIMAHPIHYQSALLAAYLDCQK	VGAPPDVLRL	-----	TAMA	-----	AKLDASA	-----	AGR	HPREDPELDOFMEAYCEML	VKYEQELTRP	IQEAMF	KRVEAQ	LDCI	-----	NGRENDPPE

## ELK

## Homeodomain

RaSTM	VDPQAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WWTTRHYKWPYPSE	SQKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	SEEI	QTYVWMDGGER	I				
STM	VDPQAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WWSRHYKWPYPSE	QKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DATHP				
BoSTM	VDPQAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WWSRHYKWPYPSE	QKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DATHP				
INA	IDPOAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WWSRHYKWPYPSE	SQKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DAHP				
AY655753	IDPOAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WWSRHYKWPYPSE	SQKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DATHP				
AY655754	IDPOAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WWSRHYKWPYPSE	SQKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DAHP				
HIRZ	IDPOAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WWSRHYKWPYPSE	SQKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DAHP				
Sbh1	IDPOAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WWSRHYKWPYPSE	SQKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DPSPH				
LET6	IDPOAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WVWLRH	I	KNWPYPSE	SQKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DAHP		
Tkr2	IDPOAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WVWLRH	I	KNWPYPSE	SQKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DAHP		
NTH15	IDPOAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WWTTRHYKWPYPSE	SQKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DAHP				
AY112704	VDPQAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WWTTRHYKWPYPSE	SQKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DAHP				
AY096802	IDPOAEDELKGGQLLRKYSYGL	GSLKQEF	MKKRKKGKLPKEARQQLD	WWTTRHYKWPYPSE	AQKMLA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DAHP				
KNAT6	GRQRCEDRDLKDRLLRKF	GSRISTL	KLEFSK	KKKGGKLPREARQQLD	WVWLRH	I	KNWPYPTE	GDKL	ALADAT	GLDQKQ	INWFI	I	NQRKRHWKPS	ENMP	FMM	DDS
KNAT2	SQQRSDRDLKDRLLRKF	GSHISSL	KLEFSK	KKKGGKLPREARQQLD	WVWLRH	I	KNWPYPTE	GDKL	SLAET	GLDQKQ	INWFI	I	NQRKRHWKPS	ENMP	FMM	DDS
KNAT1	IDPRAEDELKQHLKYSYGL	SSLKQEL	SKKKKGGKLPKEARQQL	L	INWELHYKWPYPSE	SEKVALA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	DG			
Kn1	VDAHGDQELKHLKYSYGL	SSLKQEL	SKKKKGGKLPKEARQQL	SWWDG	HYKWPYPSE	TQKVALA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EEMH	HLMM	DG			
RS1	IDPRAEDELKQHLKYSYGL	SSLKQEL	SKKKKGGKLPKEARQQL	L	INWELHYKWPYPSE	TEKIALA	AESTGLDQKQ	INWFI	I	NQRKRHWKPS	EDMQ	FVVM	EG			





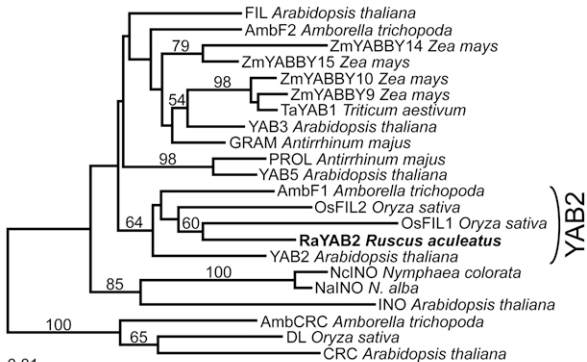
## Zinc finger-like

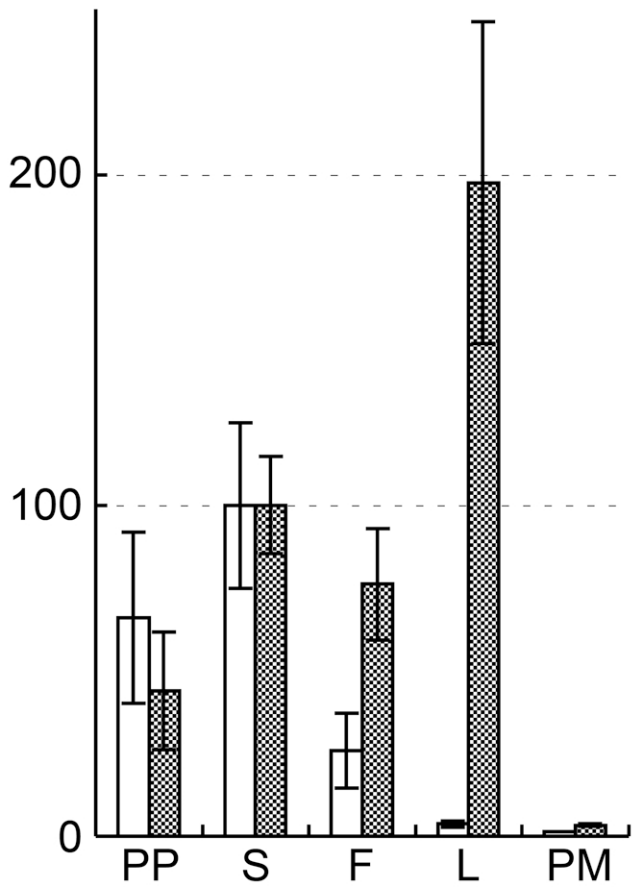
RaYAB2	PEHVCYVHCNFCNTILVNVVPGNNLFNIVTIRCGHCANLLSVN	MGAL	LQALP	LQDFQNH	QVASQDNRG	D-CSSSS	NCNRTALM	FTQE	HD										
YAB2	SERVCYVHCSFCTTILAVSVPYASLFTLVTRCGCHTLLSLN	IGV	SLHQTASAPP	IHDLOPH	ROHTTSLVTRK	D-CASSRS	TN	NLSENID	RE										
OsFIL1	SEHVCYVNCYCNITILVNVVPPNCSYNIIVTRCGCHTMVLSMD	LAPF	HQARTV	QDH	QN	RGFOG	NW	FGSYDIA	RNORTSTAMYPMP	TS									
OsFIL2	PEHVCYVHCNFCNTIFAVSVPNSMLNIVTRCGCHTSLSVN	LRGL	VOALPA	EDHL	QDN	LKMH	MSFRE	N	YSEYGS	RYGRVPM	FSK	ND							
AmbF1	SEHVCYVQCNCNTILAVSVPGSCFLGIVTTRCGCHTNLLSMN	MGAL	LQT	IP	FHDL	QNGS	VAPQER	M	E	DGSS	KSJKSET	IPSEN	EE						
YAB5	TEQLCYIPCNFCNIIILAVNVPCCSLFDIVTRCGCHTNLWSVN	MAAA	LQSLSRPN		FQATN		YAVP	EYV		GSSS	RSHTK1PSRIS	T	RT						
PROL	LEQLCYISCNFCIVLAVSVPCCSLFDVVTRCGCHTNLWSVN	MAAAAT	FQSLQP		HWODAVVHOAP		NHAST	EYNV		D-LGSSS	RWNKMAVQPS		LD						
GRAM	TEQLCYVHCNFCDTVLAVSVPCTSLIKVTVTRCGCHTNLWSN	MRGLLLP	AANG	LH	LGH	SFFSP	QNLLE	ERN		S	N	LLMNQ	NPND	SMPVP	LD				
YAB3	TDQLCYVHCSFCDTILAVSVPSSLFKTVTRCGCHSNLLSVTSMRALLLPVS		NLGH	SF	LPP	PPPPPP	NLLEEMRS	GGONINM		N	MMSHHA	SAHH	PNEH	VMAT	RNG				
FIL	SDHLCYVQCNCQITILAVNVPYTLSTFKTVTRCGCHTNLLSVN	MRSYVLP	AS	NQLQL	LGP	HSYFNP	QD	LEELRD	APSNMNP		MMMNQHP	TMND	IP	SMFDLQ	QH				
TaYAB1	SEQLCYVHCNFCDTVLAVSVPSSLFKTVTRCGCHSNLLTVD	MRGLL	FPTTTTT	VAEASA		SAVTTTTSPPPA	AAAHH	GOFH	YVSSLN	LAPGNPPR	HSLL	DEISS	AN	PSLQL	LEQ	HG			
ZmYABBY9	AEQLCYVHCYCDTILVSVPTSSLFKTVTRCGHCSLLTVD	MRGLL	FPGTDT	VAGAAPP		AADTSTTTTTITAPP	ANSVN	GOFH	LPHSLN		HPYH	QSL	LVDEISS	AAN	PSLQL	LEQ	HG		
ZmYABBY10	SEQLCYVHCNFCDTVLAVSVPSSLFKTVTRCGHCSLLTYN	MRGLL	FPGPANT	AAAAAAPP	PPPAAV	STTATMTAPP	PATSVNNNGOFH	IPHSLDLALPIPH	QSL	LD	DEISS	AAN	PSLQL	LEQ	HG				
AmbF2	TEQLCYVHCNFCDTVLAVSVPSSLFKTVTRCGCHTNLSDV	TRGLLHPT	AATQLH				LGH	AFSPT	PHNLLDE		CS	PPS		SLLHD					
ZmYABBY15	TEQLCYVHCNCCDTILAVGVPCCSLFKTVTRCGHCANLLSVN	LRGLL	LPPA	APAPNH	LN		FAH	SLLSPTS	PHGLLDE		LALQQA		PSFL	MEQ	ASANL	SSTM	TRSS	NS	
ZmYABBY14	QEQICVYHCSYCDTILAVGVPSSLFTQVTRCGHCANLLYVN	LRALL	PPAT	APAA	NHLLP		F	GQALLSPTS	PHGLLDA		ETMSSSS	FQA	PSL	SPAEP	SAACV	SGT	ISNN	TA	
INO	PGQICHVQCFCCTILAVSVPSSLTSMVVTRCGCHTNLWSN	LRGLLHPT	AATQLH				LGH	AFSPT	PHNLLDE		CS	PPS		SLLHD					
Na1NO	TEQLCYVQCFCDTILVSVVPCCSLKVVVTRCGCHSNLFSVN	MLKASFLP	LQLLAS				INN		E	AKQD			SFENAP		VK	IGD	TFMES		
Nc1NO	TEQLCYVQCFCDTILVSVVPCCSLKVVVTRCGCHSNLFSVN	MLKASFLP	LQLLAS				INN		E	TKQE			NFGNAP		AK	IGD	TFMES		
CRC	AEHLVYVRCISCNITILAVGIPKRLMDITVTKCGHCGNLSFLT	TTTP		LOG			H	VSL	TLMQ		SF	GS	D	Y	KG	SSSSSSST	SSD		
AmbCRC	TDHLCYVRCNFCDTILAVGVPQRLLMDITVTKCGHCSHLSFL	ARPL	LQNGS				LEL	LSTQ					NFCGDNK		K	SQ	SSSSSPLT	NO	
DL	SEHLCYVRCYQNTVLAVGVPCKRLMDITVTKCGHCGNLSFLS	PRPP	MVQPLSPT				D	HPL	GPFO				GP	CTD	C	RRNQ	PLP	LVSP	TSN

## YABBY

RaYAB2		QQR	LPIRSPEKQRVPSAYNRF	IKEE	IQRIKANNPDI	SHREAF	SAAK	NWAHF	PHIH	FGLT	LDG	NK	QSTL	DEA	IAAA	HGGG	QK									
YAB2		APRM	PIRPPEKQRVPSAYNRF	IKEE	IQRIKACNPEI	SHREAF	STA	AKNWAHF	PHIH	FGLK	LDG	NK	KGK	QLD		QSV	AGK									
OsFIL1		QQOV	SPIRPEKQRVPSAYNRF	IKEE	IQRIKTSNPEI	SHREAF	SAAK	NWAHL	PRLH	FGLN	VADGGG		GGNS	RRR	GL	PAGHR										
OsFIL2		TEHM	LHVRPEKQRVPSAYNRF	IKEE	IQRIKANNPDI	SHREAF	STA	AKNWAHF	PHIH	FGLG	SHSSSK		L	DEA	GAP	SPQK										
AmbF1		PRT	IPNRPPEKQRVPSAYNRF	IKEE	IQRIKARNPEI	THREAF	STA	AKNWAHF	PHI	H	YGLS	LERN		QVT	LE	V	LVN	GSQSDP								
YAB5		ITE	QR	IVNRPPEKQRVPSAYNQ	IKEE	IQRIKANNPDI	SHREAF	STA	AKNWAHF	PHIH	FGLM	LES	NK	QAK	I											
PROL		KPE	QR	IVNRPPEKQRVPSAYNQ	IKEE	IQRIKANNPEI	SHREAF	STA	AKNWAHF	PHIH	FGLM	LET	N	QAK	V	NEG	SEK	HRSHAK								
GRAM		ELMPK		VANRPPEKQRVPSAYNRF	IKDE	IQRIKAGNPD	SHREAF	SAAK	NWAHF	PHIH	FGLMPD	QPVK		KPN	V	CRHGD										
YAB3	RS	VDHL	EMPRPP	PANRPPEKQRVPSAYNRF	IKEE	IQRIKAGNPD	SHREAF	SAAK	NWAHF	PHIH	FGLMAD	PTTK		ANV	RQ	EDG	MMG									
FIL		EIPKAP		PVNRPPEKQRVPSAYNRF	IKEE	IQRIKAGNPD	SHREAF	SAAK	NWAHF	PHIH	FGLV	PD	NQ	V	PKK	TM	PQ	QEG	EDN	MVM						
TaYAB1		LGGL	IAAG	GRNAAAPALPPPPVA	GGKGG	KE	PSPRTN	PVNRPPEKQRVPSAYNRF	IKDE	IQRIKAGNPD	SHREAF	SAAK	NWAHF	PHIH	FGLMPD	HQGLR		TSL	POD	HQRK	DGHGL					
ZmYABBY9		GLGL	ILGGS	RNAATAP	PPP	PPAAGKA	KE	PSPRN	PVNRPPEKQRVPSAYNRF	IKDE	IQRIKAGNPN	SHREAF	SAAK	NWAHF	PHIH	FGLMPD	HQGLR		TSL	POD	HQRK	DL				
ZmYABBY10		LGGM	ITSG	RNAAAPHPPQ	QAPAA	AGKA	KE	PSPRAN	SAINRPPEKQRVPSAYNRF	IKDE	IQRIKAGNPD	SHREAF	SAAK	NWAHF	PHIH	FGLMPD	HQGP		TSL	POD	HRS	DGGGL				
AmbF2		PLMT	PSNTG	SAS	TRLQ		ENE	LHSP	VSRPPEKQRVPSAYNRF	IKEE	IQRIKAGNPD	I	THREAF	STA	AKNWAHF	PHIH	FGLM	Q	IKK	TM	Q	DD	VL			
ZmYABBY15		SAN	SL	NSLPPAPMPAAQ	VQQA	ELPKTA	P	VNRPPEKQRVPSAYNRF	IKDE	IQRIKAGNPD	I	THREAF	STA	AKNWAHF	PHIH	FGLMPD	QGLK		TFK	TH	GDG	AE	MDLL			
ZmYABBY14		CGN	NAASAMA	PPP	KAL	HEPPQL	PRSA	A	SANKT	SEKQRVPSAYNRF	IKDE	IQRIKASNPDI	THREAF	SAAK	NWAHF	PHIH	FGLMPD	QGLK		HPM	Q	TQEG	AE	CMFL		
INO		EDE	YSR	YOVN	PKPEKQRVPSAYNRF	IKEE	IRL	KAGNPSMAK	HEFSL	AAKNWAHF	PPAHKR		AA	SQ	Q	CE	ED	NAL	IP	ON	V	F	EDHEES			
Na1NO		YEE	ERRP	AF	TVN	PKRH	RAPSAYNRF	IKEE	IQRL	KTSEPN	I	SHREAF	STA	AKNWAHF	PHIH	FGL	Q	DAES	GS	RSQ	SNK	GK	D	KHVDRE		
Nc1NO		FCE	ERKP	AF	TVN	PKPEK	RHAPSAYNRF	IKEE	IQRL	KTSEPS	I	SHREAF	STA	AKNWAHF	PHIH	FGL	Q	DAES	GS	RSQ	SNK	GK	D	KHVDRE		
CRC		QVP	PSPP	FV	PKPEK	QRL	PSAYNRF	MRDE	IQRIK	SANPEI	I	PHREAF	SAAK	NWAKY	I	PN	ST	I	SG	H	M	I	H	GL	GF	EKK
AmbCRC		QV	PKVP	NV	PKPEK	HRL	PSAYNRF	MKEE	IKRIK	AGNPEI	I	PHREAF	SAAK	NWAKY	I	PN	ST	I	SG	H	M	I	H	GL	GF	EKK
DL		EGS	PRAP	FV	PKPEK	HRL	PSAYNRF	MRDE	IQRIK	AGNPD	I	PHREAF	SAAK	NWAKY	I	PN	ST	I	SG	H	M	I	H	GL	GF	EKK

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Primer name	Reaction used	Oligonucleotide sequence
KN4-1	Isolation of <i>STM</i> homologue	5'-CAUCAUCAUCAUARAARGGIAARYTNCC-3'
STM-ELK1	Isolation of <i>STM</i> homologue	5'-GGNWSYYTNAARCARGARTTYAT-3'
RaSTM-RTF	Real-time PCR	5'-GCGCATCACCAGCATTATTTC-3'
RaSTM-RTR	Real-time PCR	5'-CAGATAAGGGCTGGAGTGACATC-3'
RaSTM-TaqMan® Probe	Real-time PCR	5'-GGCGTAGGGATTGCCGAAGCCATT-3'
RaYAB2-RTF	Isolation of <i>YAB2</i> homologue	5'-TGGGCACATTTCCACACAT-3'
RaYAB2-RTR	Isolation of <i>YAB2</i> homologue	5'-CGTCCAGCGTTGATTGCTTA-3'
RaYAB2-TaqMan® Probe	Real-time PCR	5'-CCCGTCAAGAGTGAGCCCCGAAATG-3'
UAP	Isolation of <i>STM</i> homologue	5'-CUACUACUACUAGGCCACGCGTCGACTAGTAC-3'

Sample*	Stage	Shoot apex	Phylloclade	Scale leaf	Floral organs
Phylloclade primordium (PP)	IV	-	+	-	-
Shoot apex (S)	0	+	-	+	-
Floral bud (F)	V	-	-	-	+
Scale leaf (L)	IV	-	-	+	-
Mature phylloclade (PM)	VI	-	+	-	-

# MEIKNOX

RaSTM	ILKAKIMSHPHYKLLSAYINCQK	VGAPP	EVVARLEEAC	SSSLMIGRAASSSSSS	AVGGDPA	LDQFMEAYCEMLKYQEQLSKPF	KEAMMFLSRIEIQAFKSL	NSSEEDVDVSENYDPOAE	
STM	SVKAKIMAHPHYHRLLAAYNCQK	VGAPP	EVVARLEEAC	SSAAAAAS	MGPTGSLGDEGP	LDQFMEAYCEMLKYQEQLSKPF	KEAMVFLGRVCEQFKSL	GSSEEEVDMMNEFVDPQAE	
BoSTM	LVKAKIMAHPHYHRLLAAYNCQK	VGAPP	EVVARLEETC	SSAAAAAS	MGPTGSLGDEGP	LDQFMEAYCEMLKYQEQLSKPF	KEAMVFLGRVCEQFKSL	GSSEEEVDMMNEFVDPQAE	
INA	SVKAKIMAHPHYHRLLAAYINCQK	IGAPP	EVAVKLEEAC	ASAATMG	RNSVSRIGEDPA	LDQFMEAYCEMLKYQEQLSKPF	REAMFLSRIEQCFKAL	GSSEEEIDVNSLIDPOAE	
AY655753	SVKSKIMAHPHYRLLAAYNCQK	IGAPP	EVVAKLEEAC	ASTITIGG	RNERSVGEDPA	LDQFMEAYCEMLKYQEQLSKPF	KEAMFLSRIEQCFKAL	GSSEEEVDVNSFIDPOAE	
AY655754	SVKSKIHAHPHYRLLAAYVSCQK	IGAPP	EVVAKLEEV	ASATSTGC	RNERSVGEDPA	LDQFMEAYCEMLKYQEQLSKPF	KDAMFLFSRFCEQFKAL	GSSEEEFDVNSFIDPOAE	
HIRZ	SLKAKIMAHPHYHRLLAAYVNCBK	IGAPP	EVVSRLEEAA	AMARHG	TVSIVGEDP	LDQFMEAYCEMLKYQEQLSKPF	KEAMFLSRIEQCFKAL	GSSEEEIDVNSFIDPOAE	
Sbh1	AVKAKIMAHPHYHRLLAAYNCQK	VGAPP	EVVARLEEAC	ASATMAGG	DAAGSSGIGEDPA	LDQFMEAYCEMLKYQEQLSKPL	KEAMFLGRIEQCFKAL	GSSEEDVDLHNMIDPOAE	
LET6	SISKSIMAHPHYHRLLAAYNCQK	IGAPP	EVVARLEEIC	ATSATMGRSSSSSSGGG	IIGEDPA	LDQFMEAYCEMLKYQEQLSKPF	KEAMVFLSRIEQCFKAL	GSSEEEVDVNSFIDPOAE	
Tkn2	SISKSIMLNPHYHRLLAAYNCQK	IGAPP	EVVARLEEIC	ATSATMGRSSSSSSGGG	IIGEDPA	LDQFMEAYCEMLKYQEQLSKPF	KEAMVFLSRIEQCFKAL	GSSEEDVDVNSFIDPOAE	
NTH15	SISKSIMAHPHYRLLSAYNCQK	IGAPP	EVVARLEEIC	ATSATIGRN	SGG	IIGEDPA	LDQFMEAYCEMLKYQEQLSKPF	KEAMVFLSRIEQCFKAL	GSSEEEVDVNSFIDPOAE
AY112704	NIKAKIMAHPHYRLLAAYINCQK	IGAPP	EVVARLEEV	ATSAHMGRSSSSSSGGG	NNVIGEDPA	LDQFMEAYCEMLKYQEQLSKPF	KEAMVFLSRIEQCFKAL	GSSEEEVDVNSLIDPOAE	
AY096802	SVKAKIMSHPHYRLLSAYLNCQK	IGAPP	EVVERLEEAC	RASVVAAMSSCSGGGAGTSDGSGGGMMI	IIGADPA	LDQFMEAYCEMLKYQEQLSKPF	KEAMFLSRIEQCFKAL	GSSEEEVDVNSLIDPOAE	
Pkn3	VVKQATIASHPLYRLLSAYVIGCRK	VGAAP	EMAALEELS	KVTPITIT	AEIIGADPE	LDDEFMSEYCEVLLKYKKEELSKPF	DEAKTFLSSIESQLSNL	EVEAASQWHLNNNSEG	
NTH1	LKIAQIANHPYRLLSAYLNCQK	VGAPG	EMASILEEIS	KENHLSISGH	NTEIGTDE	LDDEFMSEYCAVLLKYKKEELSKPF	DEATFLNLNIESQLSNL	EMEAASQWHLNNNSEG	
AF224499	LMKAQIASHPYRLLSAYIECRK	VGAPH	HVTSLLEEV	RERRPDA	AG	EIGVDPDE	LDDEFMAYCRVLLRYKKEELTRPF	DEAASFLSSIQALQSDL	
L63	LMKAQIASHPYRLLSAYIECRK	VGAPH	HVTSLLEEV	RERRPDA	AG	EIGVDPDE	LDDEFMAYCRVLLRYKKEELTRPF	DEAASFLSSIQALQSDL	
OSH6	LMKAQIAGHPRYRLLSAYIECRK	VGAPH	EVASLLEEIG	RERRA	GAG	QIGVDPDE	LDDEFMAYCRVLLRYKKEELSRPF	DEAASFLSSIQALQSDL	
OSH71	LMKAQIAGHPYRLLSAYIECRK	VGAPP	EVTLLLEEIG	REGR	GGGGGAT	AGGEIGLDPDE	LDDEFMAYCRVLLRYKKEELTRPF	DEAASFLTGHTIQLASL	
CRKNOX1	VRSKIMSHPTPYRLLVMAYVNCBK	IGAPP	EVAATLLEEIS	KYQFSRSS	PAPT	GADPE	LDNFMETYCIVLKYKDELMOY	KEAMTFMRKIELQNLAL	
CRKNOX2	LIRTKIVSHSPYRLLVMAYVNCBK	IGAPE	DVALLEEVS	RKYOEIRSSD	SEVIGADPE	LDNFMELYNCLORYHEELTHY	KEAMFAFKIELQDLA	DMSSGEVDFHDEMIDP	
KNAT6	VIKAKIACHSPYRLLQAYIDCQK	VGAPP	EIACLLEEIG	RESDVYKQEV	VPSSCFGADPE	LDDEFMAYCEMLKYKYSKDLARPF	DEATGFLNKLQNLNL	DHEVAE	
KNAT2	VIKSKIASHPLYRLLQAYIDCQK	VGAPG	EIACLLEEIG	RENHVYKRPD	APLSCFGADPE	LDDEFMAYCEMLKYKYSKDLARPF	DEATFLNKLQNLNL	DDIAD	
Tkn3	IKAKILSHPHYRLLQAYIDCQK	VGAPA	SIVNLEEIR	QOND	FRKPN	ATLCICGADPE	LDDEFMAYCEMLKYKYSKDLARPF	DEATFLNLNKLQNLNL	
NTH22	IKAKIVSHPHYRLLQAYIDCQK	VGAPP	EIATVLEEIR	QOND	FRKPN	ATSLICGADPE	LDDEFMAYCEMLKYKYSKDLARPF	DEATFLSKIELQNLNL	
Pkn1	LKAKIASHPYRLLQAYIDCQK	VGAPP	EIASFLDEIR	RENDFKHS	RVSTCGADPE	LDDEFMAYCEMLKYKYSKDLARPF	DEAKTFLNKLQNLNL	EAEQ	
Pkn2	MIKAKIASHPYRLLQAYIDCQK	VGAPP	EIASFLDEIR	REDELLRKG	AVSSCLGADPE	LDDEFMAYCEMLKYKYSKDLARPF	HEATFLNLNKLQNLNL	ETDIQOQ	
AJ276389	EMKARIASHPHYRLLQAYIDCQK	VGAPP	DIASLLEEIR	RENAGGERLA	SSSVILGSDPE	LDDEFMAYCEMLKYKYSKDLARPF	DEATAFLNTEVQLS	EGEAP	
NTH9	DIRAKISSHPLYRLLQAYIDCQK	VGAPSDPE	IVMDLNLINIV	HENDLRSSN	RLSDDE	LDDEFMAYCEMLKYKYSKDLARPF	NEATFLNLNKLQNLNL	DTSGGGG	
AF063248	AIKAKILAHPOQPSLLGAYIDCQK	IGAPP	EVVARLDALT	HEYENQOVRT	TVSIVGMDPE	LDQFMEAYCEMLKYHEELTKPF	KEAMFLLKIELQNLNL	ASSEEEVDGSGGTDQFQEV	
U90092	AIKAKILAHPOQPSLLGAYIDCQK	IGAPP	EVVARLDALT	HEYENQOVRT	TVSIVGMDPE	LDQFMEAYCEMLKYHEELTKPF	KEAMFLLKIELQNLNL	ASSEEEVDGSGGTDQFQEV	
PTkn2	AIKSKILAHPOQPSLLGAYIDCQK	IGAPP	EAVSRDLALS	HEYENQOVRT	SLSIGMDPE	LDQFMEAYCEMLKYHEELTKPF	KEAMFLLKIELQNLNL	ASSEEEVDGSGGTDQFQEV	
AF483278	AIKSKILAHPOQPSLLGAYIDCQK	IGAPP	EAVSRDLALS	REYONQRRS	TVSIGMDPE	LDQFMEAYCEMLKYHEELTKPF	KEAMTFLLKIELQNLNL	GSSEEEVDGSGGTDQFQEV	
U90091	AIKSKILAHPOQPSLLGAYIDCQK	IGAPP	EAVSRDLALS	HEYENQOVRT	TVSIVGMDPE	LDQFMEAYCEMLKYHEELTKPF	KEAMTFLLKIELQNLNL	GSSEEEVDGSGGTDQFQEV	
PTkn1	AIKSKILAHPOQPSLLGAYIDCQK	IGAPP	EAVSRDLALS	REHDDPRR	TVSIGMDPE	LDQFMEAYCEMLKYHEELTKPF	KEAMTFLLKIELQNLNL	GSSEEEVDGSGGTDQFQEV	
AY80405	TLKTKIACHPHYRLLAAYMDCQK	IGAPP	EVVTLDEIS	QENQLGRHLA	TMDIGVDPDE	LDQFMEAYCEMLKYHEELTKPF	KEARFTFLNKLQNLNL	GSSE	
Tkn1	ALKAKIHAHQPSLLDAYMDCQK	VGAPP	EVAARLSAVR	QEFEARQ	RRSLDRDVSKDPE	LDQFMEAYCEMLKYHEELTRPL	QEAMEFMKIELQNLNL	SGGETELPEIDPRAE	
NTH20	ALKAKIHAHQPSLLDAYMDCQK	VGAPP	EVVARLSAVR	QEFVYRQ	RRSDSTRDVSKDPE	LDQFMEAYCEMLKYHEELTRPL	HEAMDFMRKIELQNLNL	SGGETEIPIDPRAE	
MDKN11	AIKAKIHAHQPSYLLDAYMDCQK	VGAPP	DVVARLSAVR	QEFEARQ	RSSGTSRETSKDPE	LDQFMEAYCEMLKYHEELTRPI	QEAMDFMRRIETQLNML	SGGETEIPIDPRAE	
MDKN12	AIKAKIHAHQPSYLLDAYMDCQK	VGAPS	DVVARLSAVR	QEFEARQ	RSSGTSRETSKDPE	LDQFMEAYCEMLKYHEELTRPI	QEAMDFMRRIETQLNML	SGGETEIPIDPRAE	
AY660748	AIKAKIHAHQPSYLLDAYMDCQK	VGAPP	EVVARLSAVR	QEFESRQ	RSF	ITRONSKDPE	LDQFMEAYCEMLKYHEELTRPI	QEAMDFMRRIETQLNML	
AY684938	AIKAKIHAHQPSYLLDAYMDCQK	VGAPP	EVVARLSAVR	QEFESRQ	RSF	ITRONSKDPE	LDQFMEAYCEMLKYHEELTRPI	QEAMDFMRRIETQLNML	
AY096803	ALKAKIISHPHYRLLQAYMDCQK	VGAPP	EVVGRILTAVR	QEYEARQ	RANLGCYENYKDPDE	LDQFMEAYCEMLKYHEELTRPI	QEAMEFMRRIESQLSTL	SGGETEVAEIDPRAE	
KNAT1	AMKAKIISHPHYRLLQAYLDCQK	IGAPP	DVDRILTAVR	QDFEARQO	RSTPSVASRSDPE	LDQFMEAYCEMLKYHEELTRPI	QEAMEFMRRIESQLSTL	SGGETEPEIDPRAE	
HVKNOX3	AIKAKIISHPHYRLLQAYLDCQK	VGAPP	EVVARLSAVR	QDFEARQO	RTALGGLQATEPE	LDQFMEAYCEMLKYHEELTRPI	QEAMEFLRRVETQLNLSL	SGGETEPEIDAHGV	
OSH1	AIKAKIISHPHYRLLQAYLDCQK	VGAPP	EVVARLSAVR	QDFEARQO	RTALGVLGAATEPE	LDQFMEAYCEMLKYHEELTRPI	QEAMEFLRRVETQLNLSL	SGGETEPEIDAHGV	
Kn1	AIKAKIISHPHYRLLQAYLDCQK	VGAPP	EVVARLTAIA	QEYEARQ	RTALGVLGAATEPE	LDQFMEAYCEMLKYHEELTRPI	QEAMEFMRRVETQLNLSL	SGGETEPEIDAHGV	
OSH15	SIAKAKIHAHQPSYLLAAYLDCQK	VGAPP	EVVRLERTATA	AKLDARP	PGR	HADARDE	LDQFMEAYCEMLKYHEELTRPI	DEAMEFLKRVEAQLDQI	
RS1	AIKAKIHAHQPSYLLAAYLDCQK	VGAPP	DVLERLTAMA	AKLDASA	AGR	HEPRDPE	LDQFMEAYCEMLKYHEELTRPI	DEAMEFLKRVEAQLDQI	
AF544045	AIKTKIHAHQPSYLLAAYLDCQK	VGAPP	DVLERLTAMA	AKLDAHT	PGR	HEARDE	LDQFMEAYCEMLKYHEELTRPI	DEAMEFLKRVEAQLDQI	
OSH43	AVKAEIMSHPOYSALLAAYLGCKK	VGAPP	DVLTKLTAVPA	AQOLDEADGH	PRRRHEARDDDDQLDQFMDAYCSML	TYRREELTRPI	LEAAEFVSRVETQLDQI	S	
OSH3	PVKARIASHPHYRLLAAYLDCQK	VGCPA	EAAEIAAAAR	VREARQRAA	AAASRMPAPPEDE	LKLVTEYDQKLLVEGKEELSRPL	QEAEFLRTEVESELE	EMMEEADEDLGIDPRSD	
SKNNOX1	MLRAAIVSHPHYRLLAAYVHNCBK	VGAAS	VOSSDIEIQN	KDFQSP	VAAASLGAPE	LDQFMEAYCEMLKQEKVYKTF	KEAVAFQCKKLDQOQVPI	SEDESSGAEVEIDPMAK	
SKNNOX2	MKAAISGHPOYELVIAKHSIKK	VGAAS	QKVAINEVIRRM	HQDSQSSP	VHTNIGANPE	LDQFMEAYCEMLKQEKVYKTF	TGAI	EYCKQOQKQELKLV	
MKN4	LLRDAIVDHPYELVVAHISIFK	IGAPK	GLLKLDEMEKK	SFRQFYGESSWN	VLHVTKFGDPS	LDFFMRSYIDLTKFREDENPY	NKFAQYKDKVTKDLEL	NLMYTADIDESVIDPDA	
CRKNOX3	RLKADITMHPYDQLLAHAHVACL	IATVP	DQLPRIDQAQO	SQIVAKYVLLG	NLLVEGKDE	LDQFMAHYVLLGTFCEQLQHVHVHAMEAVMACWELQSLTL	WDTHSGAFGLPIPTESER		
SKNNOX3	KLKADIVTHPYDQLLAHAHVACL	IATVP	DQLPRIDQAQO	HQLIAKYLILAN	HQLLGCNSKE	LDQFMAHYVLLGTFCEQLQHVHVHAMEAVMACWELQSLTL	WDTHSGAFGLPIPTESER		
KNAT7	QLKGEIATHMPYDQLLAHAHVACL	VATPI	DQLPIEAQLSOS	HLLRSYAST	AVGY	HDRHRE	LDNFLAQYVMLGCSFEQLQHVHVHAMEAVMACREIENNLHSL	SGGHDMTGFGLLPTESER	
229703	QMKGEIATHMPYDQLLAHAHVACL	VATPI	DQLPIEAQLSOS	HLLRSYAST	AVGY	HDRHRE	LDNFLAQYVMLGCSFEQLQHVHVHAMEAVMACREIENNLHSL	SGGHDMTGFGLLPTESER	
Thox2	QLKSEIATHPYDQLLAHAHVACL	VRTPI	DQLPRIDQAQO	HLLRSYASSOQQO	QOHSLSHQRLQ	LDNFLAQYVMLGCSFEQLQHVHVHAMEAVMACREIENNLHSL	AHGLMGFGPLPTESER		
HOS66	LLKGEIATHPYDQLLAHAHVACL	VATPI	DHLPLIDQAQO	SGLLHSAHAH	RPF	SPHDKQE	LDLSFLAQMMLGCSFEQLQHVHVHAMEAVMACREIENNLHSL	GHDLMGFGPLMPTDSE	
KNAT4	RHKAEILSHPLYDQLLAHAHVACL	IATVP	DQLPRIDQAQO	QNVVAKYSLEA	AGQLLGDGKE	LDHFMTHYVLLGCSFEQLQHVHVHAMEAVMACREIENNLHSL	SLDGLGFGPLPTESER		
KNAT3	RHKAEILSHPLYDQLLAHAHVACL	IATVP	DQLPRIDQAQO	QNVVAKYSALGA	AAOGLVGDGKE	LDHFMTHYVLLGCSFEQLQHVHVHAMEAVMACREIENNLHSL	SLDGLGFGPLPTESER		
Z71980	RHKAEILSHPLYDQLLAHAHVACL	IATVP	DQLPRIDQAQO	QNVVAKYSALG	NGMVGDGKE	LDHFMRNYVLLGCSFEQLQHVHVHAMEAVMACREIENNLHSL	E	GHDMSGFGPLPTESER	
LET12	KCKADILNHPYDQLLAHAHVACL	IATVP	DQLPRIDQAQO	QNVVAKYSVLG	QGQPLDGDG	LDQFMTHYVLLGCSFEQLQHVHVHAMEAVMACWELQSLTL	D	GDMSGFGPLPTESER	
HOS59	KAATAAHPYDQLLAHAHVACL	VATVP	DQLPRIDQAQO	AAATAAAAAA	AGGAPSDGKE	LDHFMTHYVLLGCSFEQLQHVHVHAMEAVMACWELQSLTL	D	GDMSGFGPLMTEGER	
KNAT5	SYKAAILRHPMYDQLLAHAHVACL	VATVP	DQIPRIDQAQO	HTVAKYSTLG	VVDNKE	LDHFMSHYVLLGCSFEQLQHVHVHAMEAVMACREIENNLHSL	DGSDCLMGFGPLPTESER		
MKN1-3	RDKFLVAHPLYDQLLAHAHVACL	VGTPV	DQLPHIEAQLTOA	RHYTSKYVSLHP	DHLEI	TEDEKTE	LDQFMAYQIMLLGCSFKDLQHVHVHAMEAVMACWELQSLTL	DPQDS	
AAKNOX1	DMGEQVIMHPYDQLLAHAHVACL	VGMDG	ESRHQIIRTEQGLADLHRKREQYITG		RMPALDPE	LDQFLROYIQLVDELHQLNIN	READN	ILHMTTPIAIEV	
BELL1	NNGVGFYNNRYETSGFVSSVLRSLYKPTQQLLDEVVSRKDKLKL	GNKMKNDGQDFHN			GSSDN	ITEDKSSQSELSPSERQELGSKSKLLTMVDEVKRYNQYHQMAELASSF		KEQIQVIRGKLERETSD	

## ELK

## Homeodomain

RaSTM	---	DRELKQGLLRKYSGYLSSLKQEFLLKRRKKGKGLPKPEARQQLLDWVTRHYKYWPPYSESQKMLAESTGLDQKQINNWFINQRKRHWKPS	EE1QTIVYMGDGERI
STM	---	DRELKQGLLRKYSGYLGSLKQEFMKKRRKKGKGLPKPEARQQLLDWVSRHYKYWPPYSEQKLLAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FVVM-DATHP
BoSTM	---	DRELKQGLLRKYSGYLGSLKQEFMKKRRKKGKGLPKPEARQQLLDWVSRHYKYWPPYSEQKLLAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FVVM-DATHP
INA	---	DRELKQGLLRKYSGYLGSLKQEFMKKRRKKGKGLPKPEARQQLLDWVSRHYKYWPPYSEQKLLAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FVVM-DAAPH
AY655753	---	DRELKQGLLRKYSGYLGNLKQEFMKKRRKKGKGLPKPEARQQLLDWVSRHYKYWPPYSEQKLLAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FVVM-DATHP
AY655754	---	DHELKQGLLRKYSGYLGNLKQEFMKKRRKKGKGLPKPEARQQLLDWVSRHYKYWPPYSEQKLLAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FVVM-DAAPH
HIRZ	---	DIELKQGLLRKYSGYLGSLKQEFMKKRRKKGKGLPKPEARQQLLEWVSRHYKYWPPYSEQKLLAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FVVM-DAANP
Sbh1	---	DRELKQGLLRKYSGYLGSLKQEFMKKRRKKGKGLPKPEARQQLLEWVSRHYKYWPPYSEQKLLAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FVVM-DPSHP
LET6	---	DRELKQGLLRKYSGYLGSLKQEFMKKRRKKGKGLPKPEARQQLLDWVSRHYKYWPPYSEQKLLAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FVVM-DAAPH
Tkn2	---	DRELKQGLLRKYSGYLGSLKQEFMKKRRKKGKGLPKPEARQQLLDWVSRHYKYWPPYSEQKLLAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FVVM-DAAPH
NTH15	---	DQELKQGLLRKYSGYLGSLKQEFMKKRRKKGKGLPKPEARQQLLDWVTRHYKYWPPYSEQKLLAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FVVM-DAAPH
AY112704	---	DRELKQGLLRKYSGYLGSLKQEFMKKRRKKGKGLPKPEARQQLLDWVSRHYKYWPPYSEQKLLAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FVVM-DAAPH
AY096802	---	DRELKQGLLRKYSGYLGSLKQEFMKKRRKKGKGLPKPEARQQLLDWVTRHYKYWPPYSEQKLLAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FVVM-DAAPH
Pkn3	---	DQQIKEMLMRKYSGYLSSLRKEFLKRRKKGKGLPKDARVALLDWNVSHYRWPPYTEEKNLSEATGLDQKQINNWFINQRKRHWKPS	EDMR-FALM-EGVSS
NTH1	---	DNELKELLMRKYSGYLSSLRKEFLKRRKKGKGLPKDARTALLEWVSHYRWPPYTEEKNLSEITGLDQKQINNWFINQRKRHWKPS	EDMR-FALM-EGVSS
AF224499	---	DHELKEMLLKYSYSGLSRSEFLKRRKKGKGLPKDARTVLEWVSHYRWPPYTEEDKRLAAMTGLDQKQINNWFINQRKRHWKPS	EDMR-FALM-EGVAG
LG3	---	DHELKEMLLKYSYSGLSRSEFLKRRKKGKGLPKDARTVLEWVSHYRWPPYTEEDKRLAAMTGLDQKQINNWFINQRKRHWKPS	EDMR-FALM-EGVAG
OSH6	---	DHELKEMLLKYSYSGLSRSEFLKRRKKGKGLPKDARSALLEWVSHYRWPPYTEEDKRLAARTGLDQKQINNWFINQRKRHWKPS	DGMR-FAFM-EGVAG
OSH71	---	DHELKEMLLKYSYSGLSRSEFLKRRKKGKGLPKDARSALLDWNVSHYRWPPYTEEDKRLAAMTGLDQKQINNWFINQRKRHWKPS	EDMR-FALM-EGVGT
CRKNOX1	D---	DQKVKQGLLRKYSGYLYKLKQEFLLKRRKKGKGLPKPEARQQLLDWVSHYKYWPPYSEAEKALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-YVMV-DSPTA
CRKNOX2	E---	DQKLEKQGLLRKYSGYLIFKLEKFLKRRKKGKGLPKPEARQQLLDWVTHQYKYWPPYSEAEKALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-YVMV-DSPAG
KNAT6	---	DRDLKDRLLRKFGRSITLKLKFLSKRRKKGKGLPKPEARQQLLDWVLLHYKYWPPYTEGDKIALADATGLDQKQINNWFINQRKRHWKPS	ENMP-FAMM-DDS---
KNAT2	---	DRDLKQGLLRKFGSHISLKLKFLSKRRKKGKGLPKPEARQQLLDWVSHYKYWPPYTEGDKIALAESTGLDQKQINNWFINQRKRHWKPS	ENMP-FDMM-DDS---
Tkn3	---	DNELKDRLLRKFGRSHISLKLKFLSKRRKKGKGLPKPEARQQLLDWVSHYKYWPPYTEADKNSLAESTGLDQKQINNWFINQRKRHWKPS	ENMQ-LAVM-DNL---
NTH22	---	DNELKDRLLRKFGRSHISLKLKFLSKRRKKGKGLPKPEARQQLLDWVSHYKYWPPYTEADKNSLAESTGLDQKQINNWFINQRKRHWKPS	ENMQ-LAVM-DNL---
Pkn1	---	DRELKSRLLKYGGHISLKLKFLSKRRKKGKGLPKDARQILLEWVSHYKYWPPYTEEDKIALAESTGLDQKQINNWFINQRKRHWKPS	EHMQ-LAVM-DNL---
Pkn2	---	EROLKNTLRKYGSHISLKLKFLSKRRKKGKGLPKDARQILLDWVSHYKYWPPYTEADKIALAESTGLDQKQINNWFINQRKRHWKPS	ESMO-LAVM-ENL---
AJ276389	---	ERDLKELLRKYSGYLSSLKQEFSSKRRKKGKGLPKPEARQLFVEWVTHYKYWPPYTEADKIALAESTGLDQKQINNWFINQRKRHWKPS	ENMH-FVMV-DNSSL
NTH9	---	ENEIKDMLMRKYSGYLSSLKQEFSSKRRKKGKGLPREARQILLDWVTHYKYWPPYTEEKICLAESTGLDQKQINNWFINQRKRHWKPS	ENMO-YAVM-ESI---
AF632248	DHHA	VEDRELKDHLLRKYSGYLSSLKQEFMKKRRKKGKGLPKDARQQLLDWVTHYKYWPPYTEEKIALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-LMAM-DGGSP
U90092	DHHA	VEDRELKDHLLRKYSGYLSSLKQEFMKKRRKKGKGLPKDARQQLLDWVTHYKYWPPYTEEKIALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-LMAM-DGGSP
AF48322	DHHA	VEDRELKDHLLRKYSGYLSSLKQEFMKKRRKKGKGLPKDARQQLLDWVTHYKYWPPYTEEKIALAESTGLDQKQINNWFINQRKRHWKPS	EDMH-FMVM-NHSPH
AF63278	DHHA	VEDRELKDHLLRKYSGYLSSLKQEFMKKRRKKGKGLPKDARQQLLDWVSHLDKYWPPYTEEKIALAESTGLDQKQINNWFINQRKRHWKPS	EDMH-FMVM-NHSPH
U90091	DHHA	VEDRELKDHLLRKYSGYLSSLKQEFMKKRRKKGKGLPKDARQQLLDWVSHLDKYWPPYTEEKIALAESTGLDQKQINNWFINQRKRHWKPS	EDMH-FMVM-NHSPH
PtKn1	DHHA	VEDRELKDHLLRKYSGYLSSLKQEFMKKRRKKGKGLPKDARQQLLDWVSHLDKYWPPYTEEKIALAESTGLDQKQINNWFINQRKRHWKPS	EDMH-FMVM-NHSPH
AY680405	DPRA	EDRELKQGLLRKYSGYLSSLKQEFLLKRRKKGKGLPKPEARQQLLDWVSLHDKWPPYSETEKIALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FMVM-DG---
Tkn1	---	DRELKWHLLRKYSGYLSSLKQELSKRRKKGKGLPKDARQQLITWVLLHYKYWPPYSESEKVALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FMVM-DG---
NTH20	---	DRELKWHLLRKYSGYLSSLKQELSKRRKKGKGLPKDARQQLISWVLLHYKYWPPYSESEKVALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FMVM-DG---
MDKN11	---	DRELKWHLLRKYSGYLSSLKQELSKRRKKGKGLPKDARQQLISWVLLHYKYWPPYSESEKVALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FMVM-DG---
MDKN12	---	DRELKWHLLRKYSGYLSSLKQELSKRRKKGKGLPKDARQQLISWVLLHYKYWPPYSESEKVALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FMVM-DG---
AY660748	---	DRELKWHLLRKYSGYLSSLKQELSKRRKKGKGLPKPEARQQLISWVLLHYKYWPPYSETEKVALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FMVM-DG---
AY64938	---	DRELKWHLLRKYSGYLSSLKQELSKRRKKGKGLPKPEARQQLISWVLLHYKYWPPYSETEKVALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FMVM-DG---
AY096803	---	DRELKWHLLRKYSGYLSSLKQELSKRRKKGKGLPKPEARQQLISWVLLHYKYWPPYSESEKVALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FMVM-DG---
KNAT1	---	DRELKWHLLKYSYGYLSSLKQELSKRRKKGKGLPKPEARQQLITWVLLHYKYWPPYSESEKVALAESTGLDQKQINNWFINQRKRHWKPS	EDMO-FMVM-DG---
HvKNOX3	---	DQELKHILLKYSYGYLSSLKQELSKRRKKGKGLPKPEARQQLISWVEMHYKYWPPYSESQKVALAESTGLDQKQINNWFINQRKRHWKPT	DEMO-FVVM-DA---
OSH1	---	DQELKHILLKYSYGYLSSLKQELSKRRKKGKGLPKDARQQLISWVLLHYKYWPPYSESQKVALAESTGLDQKQINNWFINQRKRHWKPS	DEMO-FVVM-DG---
Kn1	---	DQELKHILLKYSYGYLSSLKQELSKRRKKGKGLPKPEARQQLISWVQHYKYWPPYSEKVALAESTGLDQKQINNWFINQRKRHWKPS	EEMH-HLMM-DG---
OSH15	---	DKELKQGLLRKYSGYLSSLRQEFSSKRRKKGKGLPKPEARQQLISWVLLHYKYWPPYSETEKIALAESTGLDQKQINNWFINQRKRHWKPS	EDMP-FVVM-EG---
RS1	---	DKELKQGLLRKYSGYLSSLRQEFSSKRRKKGKGLPKPEARQQLISWVLLHYKYWPPYSETEKIALAESTGLDQKQINNWFINQRKRHWKPS	EDMP-FVVM-EG---
AF544045	---	DKDLKQGLLRKYSGYLSSLRQEFSSKRRKKGKGLPKPEARQQLISWVLLHYKYWPPYSETEKIALAESTGLDQKQINNWFINQRKRHWKPS	EDMP-FVVM-EG---
OSH43	---	DQGLKQGLLRKYGGSGLDQVRFVSKTKKRRKKGKGLPKPEARQQLISWVLLHYKYWPPYSEMEKMTLAAETGLDQKQINNWFINQRKRHWKPTPVAGTA	FPTM-EAAGG
OSH3	---	DKALKRHLRKYSGYLGGRLKELSKRRKKGKGLPKPEARQQLITWVLLHYRWPNPSEMEKIALAESTGLEQKQINNWFINQRKRHWKPT	EEME-FAVM-EAYHH
SKKNOX1	---	DKELKQGLLRKYSGYLSSLKQEFLLKRRKKGKGLPKDQSRQILLDWVSHYKYWPPYSEKASLAESTGLDQKQINNWFINQRKRHWKPS	DEL-TALSGQ-PSGST
SKKNOX2	---	DKELKRALMKYSGYGLGKQHEFLKRRKKGKGLPKDQSRQILLDWVSHYKYWPPYSEKASLAESTGLDQKQINNWFINQRKRHWKPS	AAAASARGE-SLQOO
MKN4	---	DEELKMLRLKYGKGIAGLKAEFNRVRRKKGKGLPNTARQILDKDFVSRHSYKYWPPYSEMEKAYLQRLCGLNLKQINNWFINERKRHWISCK	GKCMYPNTK-FYPRD
CRKNOX3	---	TLMERVROELKHELKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKARLQVETGLQLKQINNWFINQRKRHWNSPSSSTA	MKT-KRR---
SKKNOX3	---	TLMERVROELKHELKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKARLQVETGLQLKQINNWFINQRKRHWNSPSSSTA	TTSK-LKCKS
KNAT7	---	SLMERVROELKHELKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKAKLVEETGLQLKQINNWFINQRKRHWNSHLSLTS	LKSK-RKH---
Z29703	---	SLMERVROELKHELKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKAKLVEETGLQLKQINNWFINQRKRHWNSHLSLTS	LKSK-RKH---
Thox2	---	SLMERVROELKELKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKAKLVEETGLQLKQINNWFINQRKRHWNSPSSSTA	LKSK-RKR---
HOS66	---	SLMERVROELKELKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKAKLVEETGLQLKQINNWFINQRKRHWNSPSSSTA	LKSK-RKR---
KNAT4	---	SLMERVROELKHELKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKARLQVETGLQLKQINNWFINQRKRHWNSPSSSTA	SKNK-RRSNA
KNAT3	---	SLMERVROELKHELKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKARLQVETGLQLKQINNWFINQRKRHWNSPSSSTA	LTKN-RKNSA
Z71980	---	SLMERVROELKHELKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKARLQVETGLQLKQINNWFINQRKRHWNSPSSSTA	LKSK-RKR---
LET12	---	SLMERVROELKHELKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKARLQVETGLQLKQINNWFINQRKRHWNSPSSSTA	QKSO-QOECR
HOS59	---	SLVVRVROELKHELKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKARLQVETGLQLKQINNWFINQRKRHWNSPSSSTA	DKSK-KRRRY
KNAT5	---	SLMERVROELKHELKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKAKLVEETGLQLKQINNWFINQRKRHWNSPSSSTA	LTKN-KRRRT
MKN1-3	---	WFEIRNEQEVRLKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKARLQVETGLQLKQINNWFINQRKRHWNSPSSSTA	LKSK-RKK---
AaKNOX1	---	WFEIRNEQEVRLKQYKREIVDVEEILRKRRAAGLPGDITVSLKAWWHAHSKWPPYTEEDKARLQVETGLQLKQINNWFINQRKRHWNSPSSSTA	DEAL-SARG-SLQOO
BELL1	---	OGERIPRLRYLDQRLRQGRALHQQLGMVRAWRPQRGLPENSVISLRAWLFELHLPYKPESEKIMLSKQTLGSKNOVANWFINARVRLIKPIMIEEYKE	ESAEELSNS-NODTK

Gene	Accession No.	Species	Family	Reference
AaKNOX1	AF170172	<i>Acetabularia acetabulum</i>	Dasycladaceae	Serikawa and Mandoli 1999
AF063248	AF063248	<i>Picea abies</i>	Pinaceae	*
AF224499	AF224499	<i>Triticum aestivum</i>	Poaceae	Takumi 2000
AF483278	AF483278	<i>Picea abies</i>	Pinaceae	Hjortswang et al. 2002
AF544045	AF544045	<i>Hordeum vulgare</i>	Poaceae	Lin and Muller 2002
AJ276389	AJ276389	<i>Dendrobium grex</i>	Orchidaceae	*
AY096802	AY096802	<i>Helianthus annuus</i>	Asteraceae	*
AY096803	AY096803	<i>Helianthus annuus</i>	Asteraceae	*
AY112704	AY112704	<i>Petunia x hybrida</i>	Solanaceae	*
AY655753	AY655753	<i>Streptocarpus rexii</i>	Gesneriaceae	Harrison et al. 2005
AY655754	AY655754	<i>Streptocarpus saxorum</i>	Gesneriaceae	Harrison et al. 2005
AY660748	AY660748	<i>Populus tomentosa</i>	Salicaceae	*
AY680405	AY680405	<i>Picea mariana</i>	Pinaceae	Guillet-Claude et al. 2004
AY684938	AY684938	<i>Populus trichocarpa x P. deltoides</i>	Salicaceae	Guillet-Claude et al. 2004
BELL1	AY085278	<i>Arabidopsis thaliana</i>	Brassicaceae	Haas et al. 2002
BoSTM	AF193813	<i>Brassica oleracea</i>	Brassicaceae	Zheng et al. 2002
CRKNOX1	AB043954	<i>Ceratopteris richardii</i>	Adiantaceae	Sano et al. 2005
CRKNOX2	AB043956	<i>Ceratopteris richardii</i>	Adiantaceae	Sano et al. 2005
CRKNOX3	AB043957	<i>Ceratopteris richardii</i>	Adiantaceae	Sano et al. 2005
HIRZ	AY072736	<i>Antirrhinum majus</i>	Scrophulariaceae	Golz et al. 2002
HvKNOX3	X83518	<i>Hordeum vulgare</i>	Poaceae	Mueller et al. 1995
HOS59	AB061818	<i>Oryza sativa</i>	Poaceae	Ito et al. 2002
HOS66	AB061819	<i>Oryza sativa</i>	Poaceae	Ito et al. 2002
INA	AY072735	<i>Antirrhinum majus</i>	Scrophulariaceae	Golz et al. 2002
Kn1	X61308	<i>Zea mays</i>	Poaceae	Vollbrecht et al. 1991
KNAT1	AF482995	<i>Arabidopsis thaliana</i>	Brassicaceae	Venglat et al. 2004
KNAT2	NM_105719	<i>Arabidopsis thaliana</i>	Brassicaceae	*
KNAT3	NM_122431	<i>Arabidopsis thaliana</i>	Brassicaceae	*
KNAT4	NM_121144	<i>Arabidopsis thaliana</i>	Brassicaceae	*
KNAT5	NM_119356	<i>Arabidopsis thaliana</i>	Brassicaceae	*
KNAT6	NM_102187	<i>Arabidopsis thaliana</i>	Brassicaceae	*
KNAT7	NM_104977	<i>Arabidopsis thaliana</i>	Brassicaceae	*
LET6	AF000141	<i>Lycopersicon esculentum</i>	Solanaceae	Janssen et al. 1998
LET12	AF000142	<i>Lycopersicon esculentum</i>	Solanaceae	Janssen et al. 1998
LG3	AF100455	<i>Zea mays</i>	Poaceae	Muehlbauer et al. 1999
MDKN11	Z71978	<i>Malus x domestica</i>	Rosaceae	Watillon et al. 1996
MDKN12	Z71979	<i>Malus x domestica</i>	Rosaceae	Watillon et al. 1996
MKN4	AF284817	<i>Physcomitrella patens</i>	Funariaceae	Champagne et al. 2001
MKN1-3	AF285148	<i>Physcomitrella patens</i>	Funariaceae	Champagne et al. 2001
NTH1	AB025573	<i>Nicotiana tabacum</i>	Solanaceae	*
NTH9	AB025713	<i>Nicotiana tabacum</i>	Solanaceae	Nishimura et al. 1999
NTH15	AB004785	<i>Nicotiana tabacum</i>	Solanaceae	Tamaoki et al. 1997
NTH20	AB025714	<i>Nicotiana tabacum</i>	Solanaceae	Nishimura et al. 1999



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NTH22	AB025715	<i>Nicotiana tabacum</i>	Solanaceae	Nishimura et al. 1999
OSH1	D16507	<i>Oryza sativa</i>	Poaceae	Matsuoka, 1993
OSH3	AB028882	<i>Oryza sativa</i>	Poaceae	Sentoku et al. 1999
OSH6	AB028883	<i>Oryza sativa</i>	Poaceae	Sentoku et al. 1999
OSH15	AB016071	<i>Oryza sativa</i>	Poaceae	Sato et al. 1998
OSH43	AB028884	<i>Oryza sativa</i>	Poaceae	Sentoku et al. 1999
OSH71	AB028885	<i>Oryza sativa</i>	Poaceae	Sentoku et al. 1999
PKn1	AB015999	<i>Ipomoea nil</i>	Convolvulaceae	*
PKn2	AB016000	<i>Ipomoea nil</i>	Convolvulaceae	*
PKn3	AB016002	<i>Ipomoea nil</i>	Convolvulaceae	*
PtKn1	AY680402	<i>Pinus taeda</i>	Pinaceae	Guillet-Claude et al. 2004
PtKn2	AY680403	<i>Pinus taeda</i>	Pinaceae	Guillet-Claude et al. 2004
RaSTM	AB000000	<i>Ruscus aculeatus</i>	Asparagaceae	This study
RS1	L44133	<i>Zea mays</i>	Poaceae	Schneeberger et al. 1995
Sbh1	L13663	<i>Glycine max</i>	Fabaceae	Ma et al. 1994
SkKNOX1	AY667449	<i>Selaginella kraussiana</i>	Selaginellaceae	Harrison et al. 2005
SkKNOX2	AY667450	<i>Selaginella kraussiana</i>	Selaginellaceae	Harrison et al. 2005
SkKNOX3	AY667451	<i>Selaginella kraussiana</i>	Selaginellaceae	Harrison et al. 2005
STM	NM_104916	<i>Arabidopsis thaliana</i>	Brassicaceae	Long et al. 1996
THox2	U76410	<i>Lycopersicon esculentum</i>	Solanaceae	*
TKn1	U32247	<i>Lycopersicon esculentum</i>	Solanaceae	Hareven et al. 1996
TKn2	U76407	<i>Lycopersicon esculentum</i>	Solanaceae	*
TKn3	U76408	<i>Lycopersicon esculentum</i>	Solanaceae	*
U90091	U90091	<i>Picea mariana</i>	Pinaceae	Rustledge et al. 1997
U90092	U90092	<i>Picea mariana</i>	Pinaceae	Rustledge et al. 1997
Z29073	Z29073	<i>Brassica napus</i>	Brassicaceae	Boivin et al. 1994
Z71980	Z71980	<i>Malus x domestica</i>	Rosaceae	Watillon et al. 1996