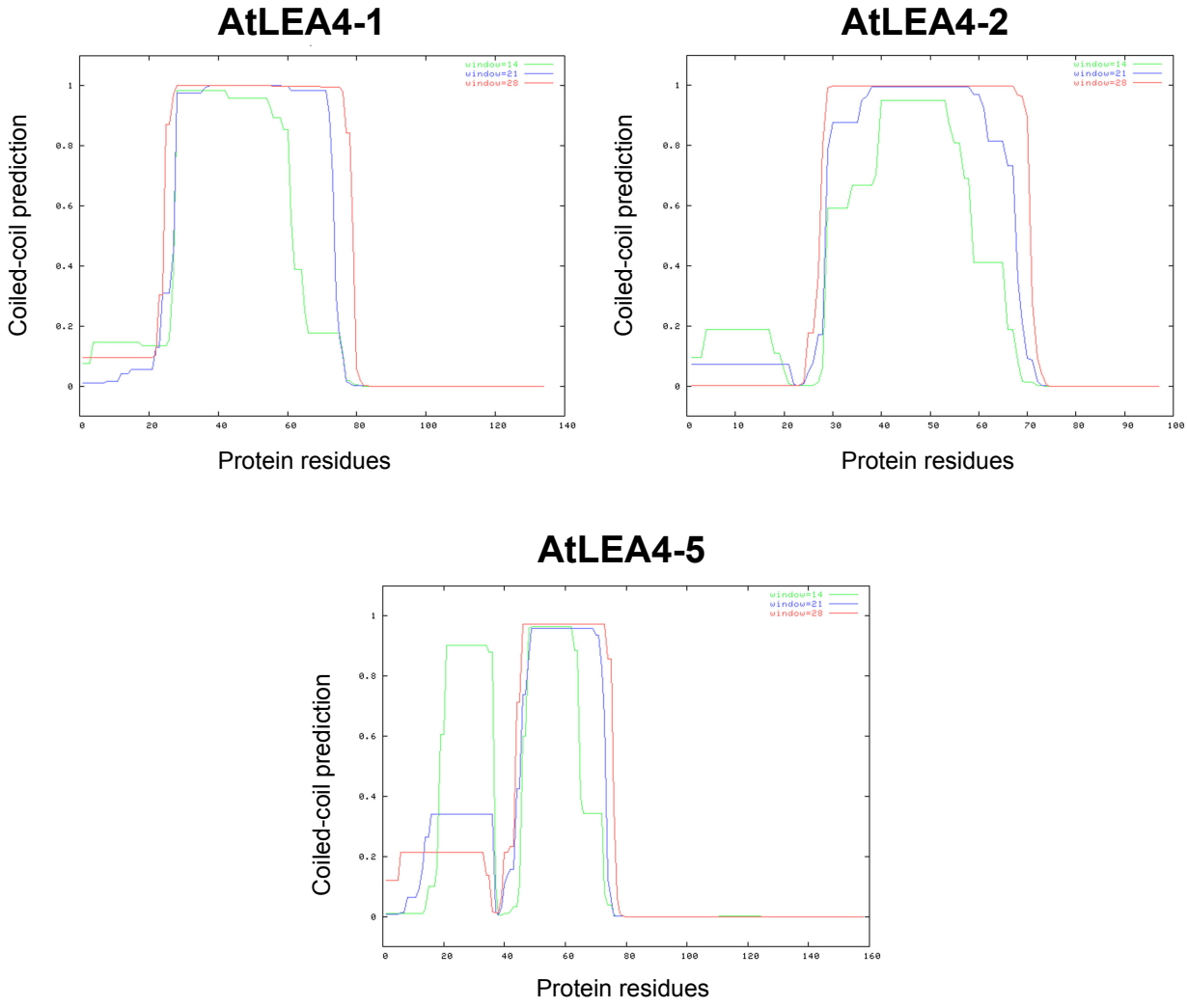
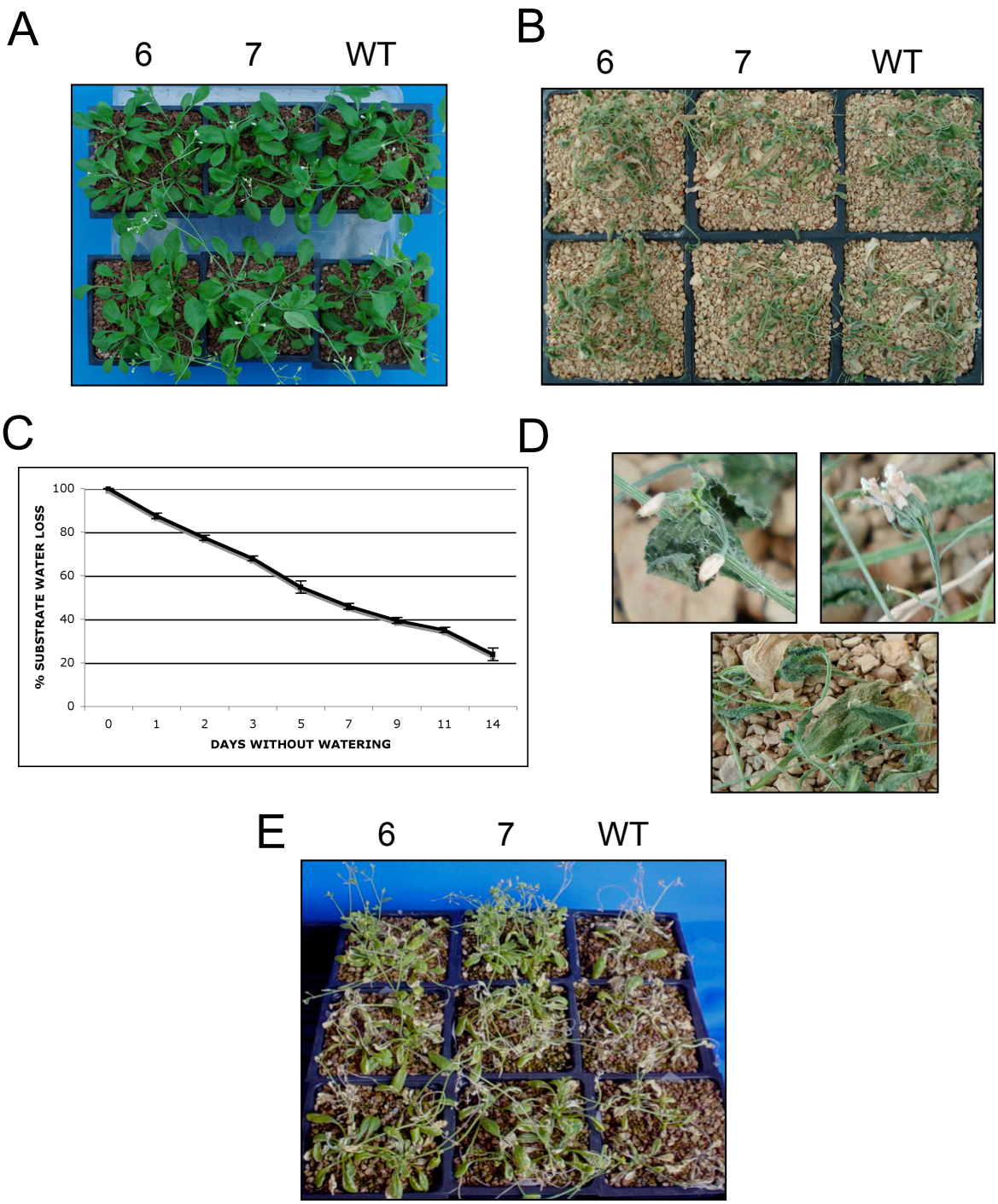
A

```
AtLEA4-1   MQSAKQKISDMASTAKEKMVICQAKADEKAERAMARTKEEKEIAHQRRKAKEAEANMDMH
AtLEA4-2   MQSAKEKISDMASTAKEKLNIGGAKAQGHAEKTMARTKKEKKLAQEREKSKEAQAKADLH
AtLEA4-5   MQSMKETASNIAASAKSGMDKTKATLEEKAEKMKTRDPVQKQMATQVKEDKINQAEMHKR
           *** *:. *::*::**. :    *. : :**:  :*   :*::* : .: *  :*: . :

AtLEA4-1   MAKAAHAEDKLMA-----------KQSHYHVTDHGPHVPQQAPVPAPAPVMGHGYGHNPT
AtLEA4-2   QSKAEHAADAQV----------------------HGHHLPGHSTYPTRA-----------T
AtLEA4-5   ETRQHNAAMKEAAGAGTGLGLGTGTHSTTGQVGHGTGTHQMSALP------GHGTGQLTD
           ::  :*                            **      :. *

AtLEA4-1   GV-------------TSVPPQTYHPTY----PPTGHHNHHHY--
AtLEA4-2   GA-------------NYPPGQI----------------------
AtLEA4-5   RVVEGTAVTDPIGRNTGTGRTTAHNTHVGGGGATGYGTGGGYTG
```

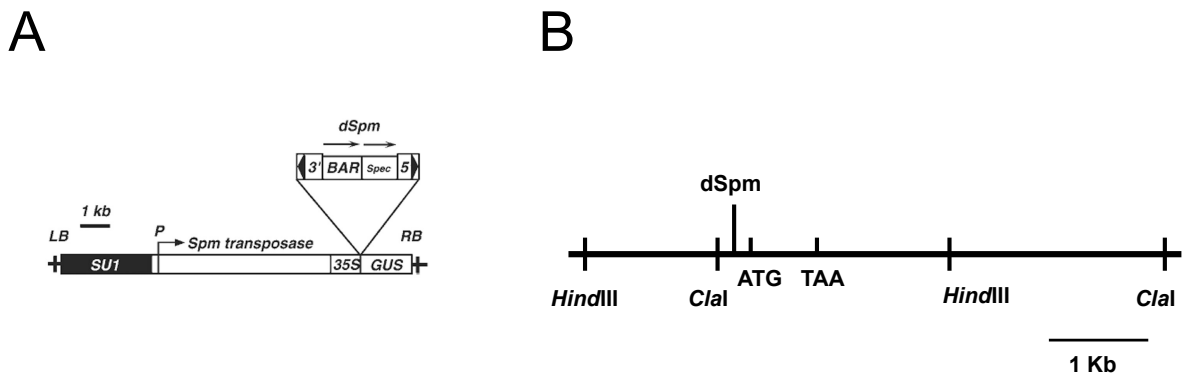
B

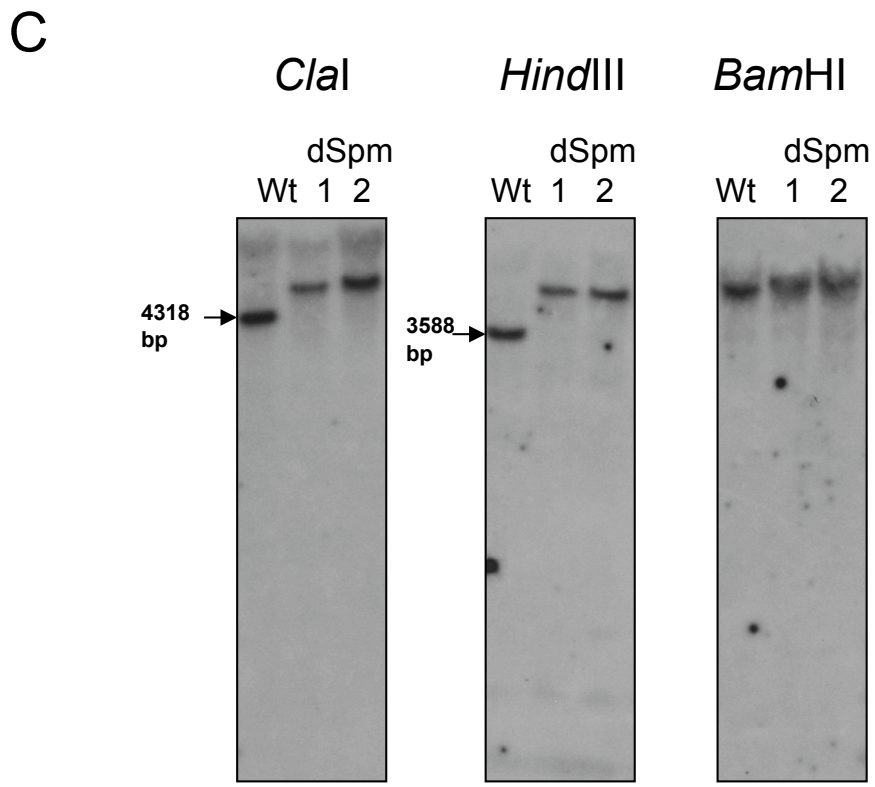


Supplemental Figure S1. Sequence similarity between group 4 LEA proteins in Arabidopsis and prediction of coiled-coil regions in these proteins. A) Sequence alignment of group 4 LEA proteins showing the high conservation among the three members at their amino portion. The highest similarity was found between AtLEA4-1 and AtLEA4-2 proteins. Identities are marked with asterisks (*) and similarities with dots (.) (:). Sequences were obtained from the Swissprot database for previously reported LEA4 proteins (listed as LEA_1, PFAM 03760) B) Predicted coiled-coil regions of group 4 LEA proteins are present in the conserved N-terminal region, while the predicted C-terminal (which varies in length 20-70 residues) is predicted to be unstructured or "random-coil" (Lupas et al., 1991). The "y" axis represents the confidence on the coiled-coil prediction, using different lengths of the coiled-coil (14, 21, 28 residues).



Supplemental Figure S2. Phenotypic analysis of plants overexpressing AtLEA4-5 protein. A) Wild type (WT) plants and five homozygous transgenic lines were germinated *in vitro* and transplanted to a low-water-retention substrate, kept under optimal irrigation conditions with nutrient solution until they reached the flowering stage; watering was stopped at this point. B) A representative image of Arabidopsis plants after 14 days of dehydration ($\Psi_{substrate}$ = - 6.45 (± 0.57) MPa). C) Graph showing the water loss rate from the substrate (±SD) as a percentage of the initial water content in each pot during the course of the drought experiment. D) Detail of floral buds, inflorescences and leaves to denote severe dehydration in all the aerial tissues and senescence of some rosette leaves. Plants were rehydrated with nutrient solution at this point. E) Arabidopsis plants after 10 days of rehydration showing that transgenic plants were capable not only of leaf recovery, but also bud maintenance and recovery, while WT plants were only able to recover some rosette leaves but the floral axis became senescent and could not maintain their reproductive tissues.





Supplemental Figure S3. Description of the transposon insertion mutant (dSpm 4-5) in the *AtLEA4-5* gene. A) Construct used to select stable dSpm transpositions in the SLAT mutant collection from the John Innes Centre (image reproduced from Tissier et al. Plant Cell **11**:1841-1852, 1999). An Enhancer/Suppressor-mutator (En/Spm) element was introduced into Arabidopsis in a single T-DNA construct, which carried a non-autonomous defective Spm (dSpm) element with a phosphinothricin herbicide resistance (BAR) gene, a transposase expression cassette, and a counter-selectable gene. B) Location of the stable dSpm insertion in the promoter region of *AtLEA4-5* gene (208 bp from the ATG codon) and restriction sites used for Southern blot analysis. Mutant seeds were obtained from the NASC European Arabidopsis Stock Centre (N122943). Plants were grown from each seed and its progeny was collected separately from each plant. C) Southern blot analysis using a specific probe to detect the insertion of dSpm in the expected region of *AtLEA4-5* gene promoter and genomic DNA (40 μg) extracted from wild type (WT) and mutant plants from two T_4 lines (dSpm 1, 2). Genomic DNA was digested with *Cla*I or HindIII, which gave a restriction fragment in the expected size for WT plants and a higher fragment in the mutant lines, in agreement to the transposon size and orientation. Digestion with *Bam*HI was used as negative control.

A

1) Search for a region of 22 nucleotides with maximal identity between *AtLEA4-1* and *AtLEA4-2* transcripts.

```
AtLEA4-1  AUGCAAUCGGCGAAACAGAAGAUAAGCGAUAUGGCUAGUACAGCCAAGGA
          ||||| ||||||||  | ||||| || || ||||| ||||| ||||||||
AtLEA4-2  AUGCAGUCGGCGAAGGAAAAGAUCAGUGACAUGGCCAGUACGGCCAAGGA
```

2) Search for a region with the least number of unpairings with the microRNA template (*ath-miR159a*).

```
AtLEA4-1/2 mRNA      5′ GACAUGGCCAGUACAGCCAAG 3′
                          | |   ||  |  | ||||
  ath-miR159a        3′ AUCUCGAGGGAAGUUAGGUUU 5′
```

3) Introduce point mutations in the microRNA template (*ath-miR159a*) to eliminate unpaired sites.

```
AtLEA4-1/2 mRNA      5′ GACAUGGCCAGUACAGCCAAG 3′
                        ||||||||||||||||||||
  a-miRLEA4-1/2      3′ CUGUACCGGUCAUGUCGGUUU5′
```

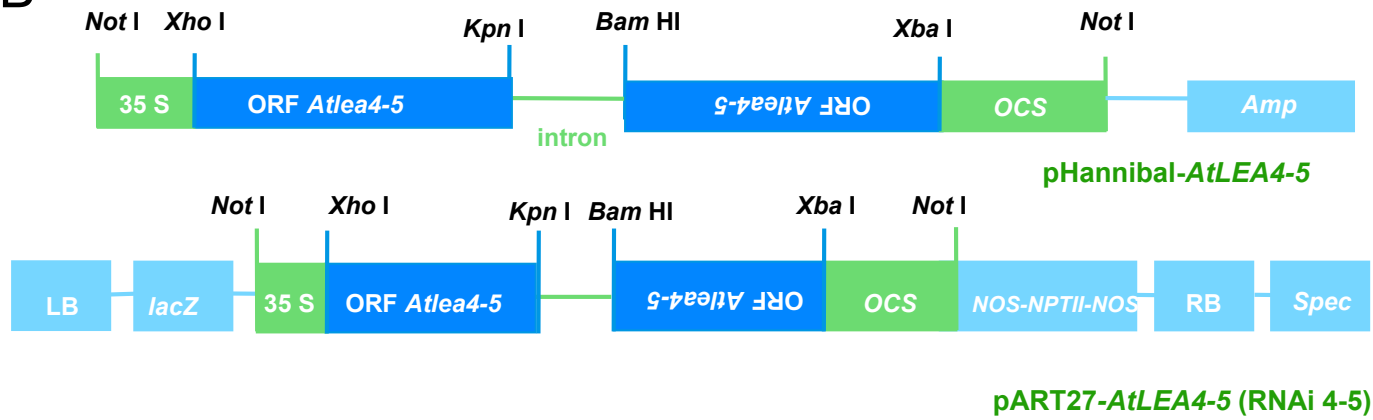
4) From the original stem-loop precursor sequence in *ath-miR159*,

```
                                  AA
ath-miR159a*   5′-- UAGAGCUCCUU     AGUUCAAA----------
                   ||||||||||||     ||||||||
ath-miR159a    3′-- AUCUCGAGGGA     UUAGGUUU----------
                                  AG

                    U  G  GCU     UUA  A  U
ath-miR159a*   5′--   A  A      CC      A  G UCAAA------------
                      |  |      ||      |  |
a-miRLEA4-1/2  3′--   U  U      GG      U  U GGUUU-----------
                    C  G  ACC     UCA  G C
```

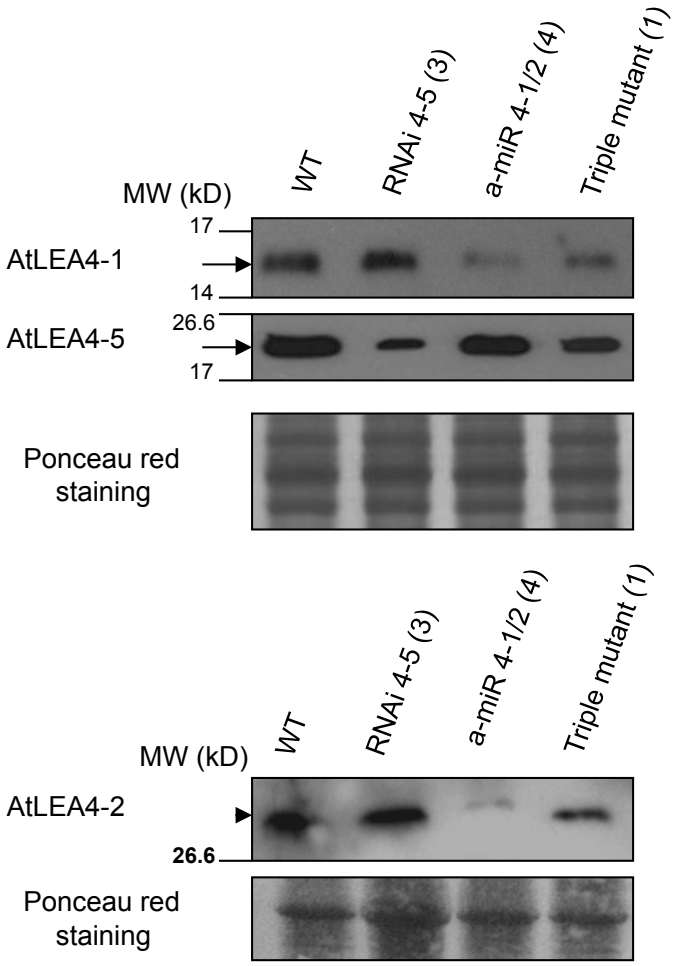
5) restore the secondary structure with the corresponding changes in the sequence of *ath-miR159**.

```
                                  AA
ath-miR159a*   5′-- GACAUGGCCAG     CGGUCAAA----------
                   ||||||||||||     ||||||||
a-miRLEA4-1/2  3′-- CUGUACCGGUC     GUCGGUUU----------
                                  AU
```

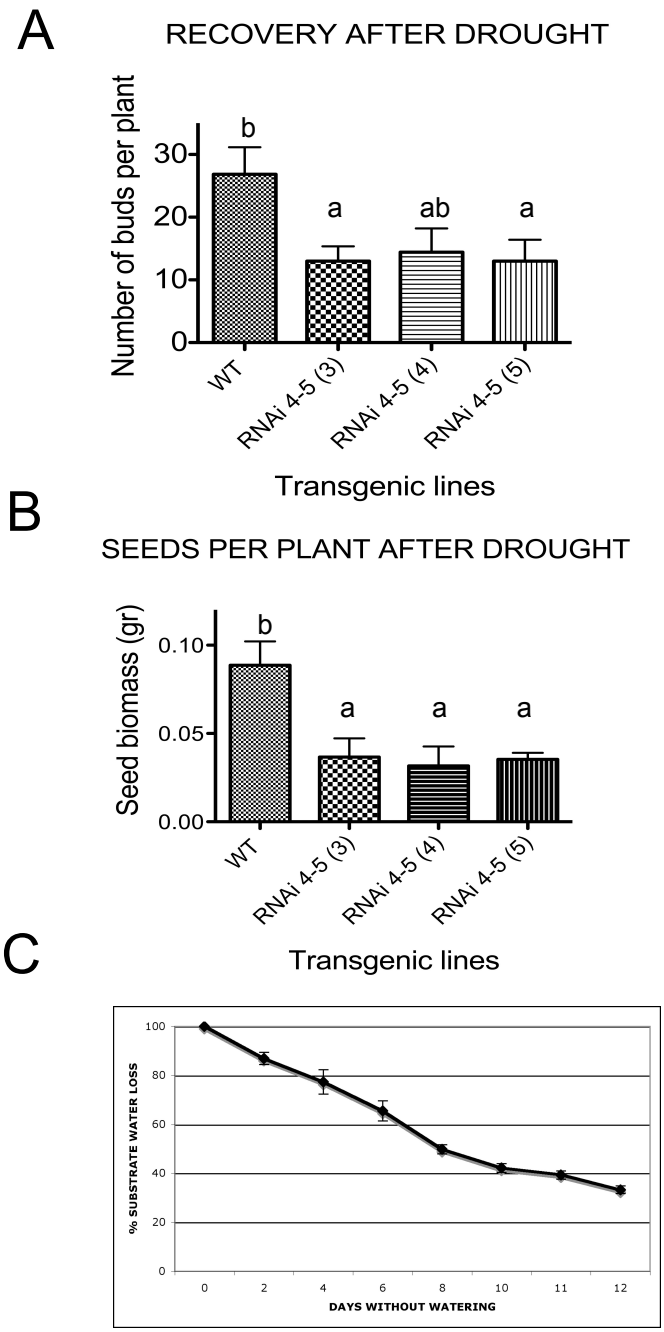
B



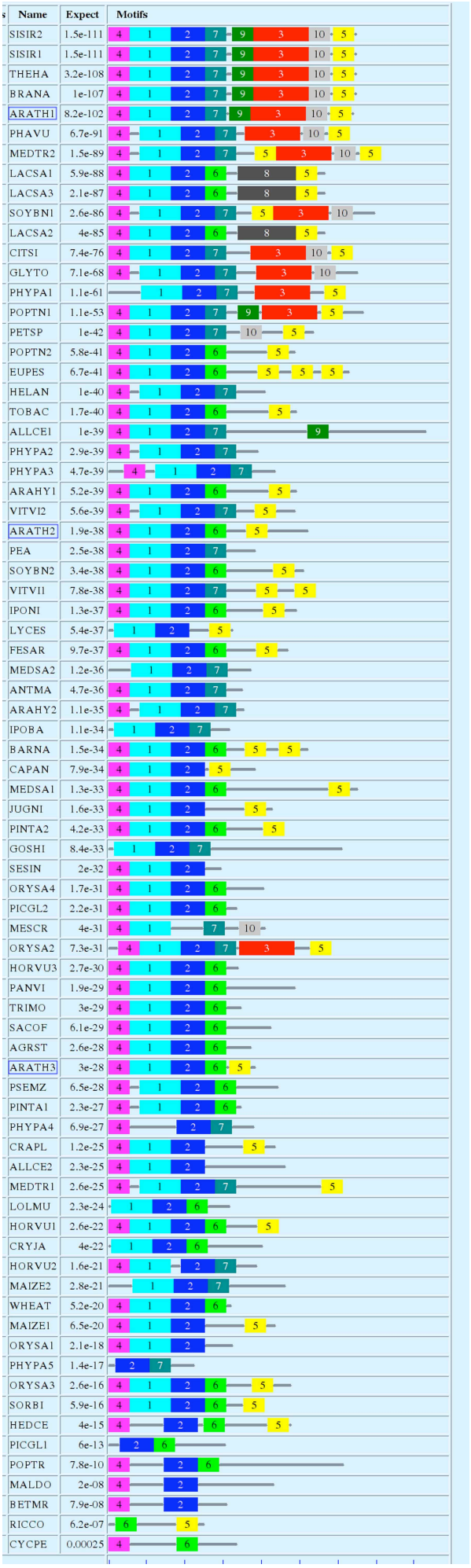
Supplemental Figure S4. Design of artificial microRNA to silence *AtLEA4-1* and *AtLEA4-2* genes and construction of RNAi-triggered silencing for *AtLEA4-5* gene. A) Point mutations were inserted into *ath-miR159a* precursor by PCR in order to target *AtLEA4-1* and *AtLEA4-2* genes as silencing targets of artificial microRNA (*a-miR 4-1/2*) as depicted in the diagram. B) RNAi silencing of *AtLEA4-5* gene was achieved by constitutively expressing the ORF as inverted repeats to trigger the specific silencing of the endogenous gene by siRNAs.



Supplemental Figure S5. Protein reduction levels in PTGS single, double and triple mutants of *AtLEA4* gene family subjected to drought. Western blot analysis using specific antibodies against each member of AtLEA4 protein family and total protein extracts (10 μg) from adult plants under dehydration treatments to show the reduction in the accumulation levels of silenced mutants compared to wild type plants (WT). The homozygous transgenic lines used were: RNAi-directed silencing mutant for *AtLEA4-5* gene (RNAi 4-5), artificial microRNA-directed silencing double mutant for *AtLEA4-1* and *AtLEA4-2* transcripts (a-miR 4-1/2), triple silencing mutant resulting from the cross between the single and double mutant described above (Triple mutant). Reversible stain after transfer is shown as loading reference. The arrowhead indicates the protein band (≈ 30 kD) specifically detected by the antibodies against AtLEA4-2 protein.



Supplemental Figure S6. Phenotypic analysis of T_2 homozygous plants expressing an RNAi to silence *AtLEA4-5* transcript after recovery from dehydration. Wild type (WT) and three silenced lines (transgenic lines 3 - 5 as in Fig. 8), which showed significant reduction of AtLEA4-5 protein levels under drought were used. Plants were grown in a greenhouse, watered until flowering and subjected to dehydration during a 12 d period ($\Psi_{substrate}$ = - 4.62 (± 0.62) MPa). A) Average number of floral and axillary buds per plant were counted after 6 d of recovery. Bars indicate means (±SE, n=7), significant differences between groups were found with P = 0.0273, using one-way ANOVA. B) Rehydrated plants were kept under optimum irrigation with nutrient solution and seeds were harvested from each plant until senescence. Bars indicate means (±SE, n=3). Significant differences were found between groups with P = 0.0133, using one-way ANOVA. Different letters show significant differences between groups as indicated by Duncan's post-tests (P<0.05). C) Water loss rate from the substrate (±SD) during dehydration for mutant lines with reduced levels of AtLEA4 family members, shown as a percentage of the initial water content in each pot during the course of the drought experiment.



Supplemental Figure S7. Conserved motifs and their arrangement in the LEA4 protein sequences from plants. Motifs were found using MEME from 77 protein sequences obtained from protein and EST databases (Bailey and Gribskov, 1998). Based on the low e-value, the two last sequences (RICCO and CYCPE) were not used for further analysis.

Supplemental Table S1. Phenotypic analysis of T_3 homozygous adult plants overexpressing AtLEA4-5 protein (*35S::AtLEA4-5::NOS)* during drought and after recovery from stress. Plants were grown in greenhouse environment, watered with nutrient solution until flowering and subjected to severe dehydration ($\Psi_{substrate}$ = - 6.447 (± 0.574) MPa). At this point plants were rehydrated and recovered during 10-days. The number of floral and axillary buds per plant were counted after 10-days of recovery; dry weight of whole plants was also recorded. In separate experiments, the relative water content (RWC) was calculated in control (well-irrigated) plants and in dehydrated plants ($\Psi_{substrate}$ = - 3.851 (± 0.704) MPa).

Genotype	Dry biomass of whole plants kept under optimum irrigation (gr)[ς]	Dry biomass of whole plants after recovery from severe drought[δ] (gr)	Number of buds per plant under optimum irrigation[ς]	Number of buds per plant after recovery from severe drought[δ]	RWC of plants kept under optimum irrigation[ς]	RWC of plants after 10 days of withholding irrigation[ξ]
WT (±SD) (lower 95% CI, upper 95% CI)	**0.1457** (±0.00153) (0.1419, 0.1495)	**0.03528** (±0.00435) (0.02448, 0.04608)	**48.33** (±3.215) (40.35, 56.32)	**0**	**0.936** (±0.01669) (0.8946, 0.9775)	**0.2771** (±0.01034) (0.2514, 0.3027)
OE 4-5 (2) (±SD) (lower 95% CI, upper 95% CI)	**0.1433** (±0.01901) (0.0961, 0.1906)	**0.04278** (±0.002999) (0.03534, 0.05021)	**55.67** (±3.786) (46.26, 65.07)	**4.375** (±4.658) (0.4808, 8.269)	**0.9237** (±0.02077) (0.8721, 0.9753)	**0.3856** (±0.02945) (0.3125, 0.4588)
OE 4-5 (3) (±SD) (lower 95% CI, upper 95% CI)	**0.156** (±0.00361) (0.147, 0.165)	**0.05233** (±0.00808) (0.03226, 0.0724)	**37** (±11.27) (9.005, 64.99)	**5.875** (±5.643) (1.158, 10.59)	**0.948** (±0.02254) (0.892, 1.004)	**0.3987** (±0.03116) (0.3213, 0.4761)
OE 4-5 (4) (±SD) (lower 95% CI, upper 95% CI)	**0.1332** (±0.03435) (0.04783, 0.2185)	**0.05233** (±0.00351) (0.04361, 0.06106)	**75.33** (±6.028) (60.36, 90.31)	**8.375** (±8.331) (1.41, 15.34)	**0.9454** (±0.00055) (0.9441, 0.9468)	**0.3689** (±0.03419) (0.284, 0.4539)
OE 4-5 (6) (±SD) (lower 95% CI, upper 95% CI)	**0.1565** (±0.00769) (0.1374, 0.1756)	**0.04767** (±0.00298) (0.04026, 0.05508)	**66.33** (±8.737) (44.63, 88.04)	**6** (±2.878) (3.593, 8.407)	**0.9477** (±0.02026) (0.8974, 0.998)	**0.3629** (±0.04513) (0.2508, 0.475)
OE 4-5 (7) (±SD) (lower 95% CI, upper 95% CI)	**0.1793** (±0.00635) (0.1636, 0.1951)	**0.04414** (±0.00768) (0.02505, 0.06323)	**30** (±7) (12.61, 47.39)	**5.125** (±5.276) (0.7139, 9.536)	**0.9363** (±0.01563) (0.8975, 0.9751)	**0.3315** (±0.03201) (0.252, 0.4111)

[ς]Equivalent to $\Psi_{substrate}$ = - 0.451 (± 0.212) MPa

[δ]Equivalent to $\Psi_{substrate}$ = - 6.447 (± 0.574) MPa

[ξ]Equivalent to $\Psi_{substrate}$ = - 3.851 (± 0.704) MPa

Supplemental Table S2. Phenotypic analysis of T_4 homozygous transposon insertion mutant in *AtLEA4-5* gene and of homozygous T_2 PTGS mutants in *AtLEA4* gene family during drought and after recovery from stress. Plants were grown in greenhouse environment and watered until flowering, subjected to dehydration ($\Psi_{substrate}$ = - 4.617 (± 0.619) MPa). At this point plants were rehydrated and recovered during 6-days. The number of floral and axillary buds per plant were counted after 6d of recovery; dry weight of whole plants was also recorded. In separate experiments, the relative water content (RWC) was calculated in control (well irrigated) plants and in dehydrated plants ($\Psi_{substrate}$ = - 5.415 (± 0.543) MPa).

Genotype	Dry biomass of whole plants kept under optimum irrigation (gr)$^{\varsigma}$	Dry biomass of whole plants after recovery from drought (gr)$^{\phi}$	Number of buds per plant after recovery from drought$^{\phi}$	RWC of leaf discs from plants kept under optimum irrigation$^{\varsigma}$	RWC of leaf discs from plants after 13 days of withholding irrigation$^{\zeta}$
WT 1	**0.1021**	**0.03505**	**13.75**	**0.9019**	**0.17**
(±SD)	(±0.02358)	(±0.008034)	(±2.486)	(±0.02323)	(±0.00674)
(lower 95% CI, upper 95% CI)	(0.07734, 0.1268)	(0.02833, 0.04177)	(12.42, 15.58)	(0.8775, 0.9263)	(0.1593, 0.1808)
dSpm 4-5 (1)	**0.1141**	**0.01826**	**7.58**	**0.8985**	**0.1552**
(±SD)	(±0.01072)	(±0.00529)	(±3.059)	(±0.03627)	(±0.01283)
(lower 95% CI, upper 95% CI)	(0.1028, 0.1253)	(0.01384, 0.02268)	(5.64, 9.527)	(0.8604, 0.9365)	(0.1347, 0.1756)
WT 2	**0.1078**	**0.03485**	**16.25**	**0.9147**	**0.2164**
(±SD)	(±0.0398)	(±0.00798)	(±3.991)	(±0.03054)	(±0.01408)
(lower 95% CI, upper 95% CI)	(0.06601, 0.1496)	(0.02818, 0.04152)	(12.91, 19.59)	(0.8826, 0.9467)	(0.194, 0.2388)
RNAi 4-5 (3)	**0.1224**	**0.01816**	**6.5**	**0.9135**	**0.1337**
(±SD)	(±0.03627)	(±0.00397)	(±2.39)	(±0.05177)	(±0.0368)
(lower 95% CI, upper 95% CI)	(0.08434, 0.1605)	(0.01485, 0.02148)	(4.502, 8.498)	(0.8591, 0.9678)	(0.07519, 0.1923)
WT 3	**0.106**	**0.03769**	**15.88**	**0.9255**	**0.1567**
(±SD)	(±0.0199)	(±0.00398)	(±5.276)	(±0.02639)	(±0.02432)
(lower 95% CI, upper 95% CI)	(0.08515, 0.1269)	(0.03436, 0.04102)	(11.46, 20.29)	(0.8978, 0.9532)	(0.118, 0.1954)
a-miR 4-1/2 (4)	**0.1088**	**0.02015**	**7.5**	**0.9138**	**0.1478**
(±SD)	(±0.02774)	(±0.00420)	(±2.507)	(±0.01799)	(±0.03539)
(lower 95% CI, upper 95% CI)	(0.07968, 0.1379)	(0.01664, 0.02366)	(5.404, 9.596)	(0.8949, 0.9327)	(0.09152, 0.2041)
WT 4	**0.1099**	**0.0342**	**16.38**	**0.9203**	**0.1883**
(±SD)	(±0.02415)	(±0.00649)	(±4.897)	(±0.02924)	(±0.00859)
(lower 95% CI, upper 95% CI)	(0.07155, 0.1484)	(0.02877, 0.03963)	(12.28, 20.47)	(0.8896, 0.951)	(0.1746, 0.202)
Triple mutant (1)	**0.1236**	**0.0207**	**7.875**	**0.9247**	**0.1279**
(±SD)	(±0.01129)	(±0.00538)	(±3.523)	(±0.01299)	(±0.01971)
(lower 95% CI, upper 95% CI)	(0.1056, 0.1415)	(0.0162, 0.0252)	(4.93, 10.82)	(0.911, 0.9383)	(0.0965, 0.1592)
WT 5	**0.0967**	**0.03986**	**12.88**	**0.9019**	**0.1932**
(±SD)	(±0.02718)	(±0.00759)	(±3.563)	(±0.02323)	(±0.01446)
(lower 95% CI, upper 95% CI)	(0.06813, 0.1252)	(0.03352, 0.04621)	(9.896, 15.85)	(0.8775, 0.9263)	(0.1702, 0.2162)
Compl dSpm (1)	**0.1143**	**0.04573**	**11.25**	**0.9083**	**0.1987**
(±SD)	(±0.03298)	(±0.00547)	(±5.97)	**(±0.02954)**	(±0.03705)
(lower 95% CI, upper 95% CI)	(0.08381, 0.1448)	(0.04115, 0.0503)	(6.259, 16.24)	**(0.8773, 0.9393)**	(0.1398, 0.2577)
WT 6	**0.1244**	**0.03721**	**11.88**	**0.9338**	**0.228**
(±SD)	(±0.01351)	(±0.00811)	(±4.824)	(±0.02097)	(±0.007428)
(lower 95% CI, upper 95% CI)	(0.08965, 0.1591)	(0.03044, 0.04399)	(7.842, 15.91)	(0.9117, 0.9558)	(0.2162, 0.2398)
OE 4-5 (4)	**0.1244**	**0.04755**	**14.38**	**0.9536**	**0.1971**
(±SD)	(±0.01947)	(±0.00674)	(±4.438)	(±0.02697)	(±0.03261)
(lower 95% CI, upper 95% CI)	(0.104, 0.1448)	(0.04191, 0.05319)	(10.66, 18.09)	(0.9253, 0.9819)	(0.1452, 0.249)

$^{\varsigma}$Equivalent to $\Psi_{substrate}$ = - 0.451 (± 0.212) MPa

$^{\phi}$Equivalent to $\Psi_{substrate}$ = - 4.617 (± 0.619) MPa

$^{\zeta}$Equivalent to $\Psi_{substrate}$ = - 5.415 (± 0.543) MPa

Supplemental Table S3. Taxonomic classification of the sequences used for motif search, sequence number and sequence name depicted in Figure 9. Motifs are shown in ascendant order by the number assigned; however, this order does not represent the motif arrangement within the protein sequence (to see that refer to Supplemental Fig. S7). Seq_25, Seq_46 and Seq_47 showed the worst e-value in MEME analysis and were therefore excluded from subsequent phylogenetic analysis.

shortName	ncbiTax	CLASS	ORDER	FAMILY	GENUS	1	2	3	4	5	6	7	8	9	10	sequenceHeading
AGRST	15297	monocots	Poales	Poaceae	Agrostis	X	X		X		X					>gi|82773414|gb|DV866976.1| CRP6708 Creeping bentgrass EST Agrostis stolonifera cDNA clone CRP315T_G03 3', mRNA sequence Frame = +3
ALLCE1	4678	monocots	Asparagales	Alliaceae	Allium	X	X		X	X		X		X		>EST555884 BI935995 cTOD24L13 onion frame +1
ALLCE2	4678	monocots	Asparagales	Alliaceae	Allium	X	X	X	X							>EST686129 CF449784 ACACW17 onion frame +1
ANTMA	4150	dicots	Lamiales	Plantaginaceae	Antirrhinum	X	X		X			X				>Antirrhinum majus AJ560281 Frame = +3
ARAHY1	3817	dicots	Fabales	Fabaceae	Arachis	X	X		X	X	X					>Arachis hypogaea AAZ20279.1 GI:7104066 DQ097719.1
ARAHY2	3817	dicots	Fabales	Fabaceae	Arachis	X	X		X			X				>Gsi-22 Arachis hypogaea AAO33589.1 GI:28194655
ARATH1	3701	dicots	Brassicales	Brassicaceae	Arabidopsis	X	X	X	X	X		X		X	X	>Q96272|Q96272_ARATH LEA D113 homologue type1 At5g06760
ARATH2	3701	dicots	Brassicales	Brassicaceae	Arabidopsis	X	X		X	X	X					>Q39138|Q39138_ARATH LEA protein Le25 homolog At1g32560
ARATH3	3701	dicots	Brassicales	Brassicaceae	Arabidopsis	X	X		X	X	X					>Q96273|Q96273_ARATH LEA D113 homologue type2 At2g33500
BETMR	3554	dicots	Caryophyllales	Amaranthaceae	Beta		X		X							>gi|26114695|gb|BQ585113.1| E011827-024-002-P05-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris cDNA clone 024-002-P05 5-PRIME, Frame = +3
BRANA	3705	dicots	Brassicales	Brassicaceae	Brassica	X	X	X	X	X		X		X	X	>AAT77223.1 GI:50429308 Brassica napus Group I late embryogenesis abundant protein
BRANA	3705	dicots	Brassicales	Brassicaceae	Brassica	X	X		X	X	X					>83831777 CX280000.1 Brassica napus 16ACDHDS Frame = +3
CAPAN	4071	dicots	Solanales	Solanaceae	Capsicum	X	X		X	X						>TC6258 ORF 39..331 frame +3 pepper Capsicum annuum
CITSI	2706	dicots	Sapindales	Rutaceae	Citrus	X	X	X	X	X		X			X	>gi|38052736|gb|CF837084.1| Orange Shoot Meristem cDNA Library frame +2 Citrus sinensis
CRAPL	4152	dicots	Lamiales	Linderniaceae	Craterostigma	X	X		X	X						>O3YMR0|O3YMR0_CRAPL Group 4 LEA protein
CRYJA	3368	Coniferopsida	Coniferales	Cupressaceae	Cryptomeria	X	X				X					>gi|9962207|dbj|AU084224.1| AU084224 Cryptomeria japonica inner bark cDNA clone CC1106 5', mRNA sequence Frame = +3
CYCPE	59973	dicots	Ericales	Myrsinaceae	Cyclamen						X					>gi|81488050|emb|AJ886946.1| AJ886946 Cyclamen persicum induced calli and somatic embryos clone 33T7.E05, mRNA sequence Frame = +2
EUPES	3990	dicots	Malpighiales	Euphorbiaceae	Euphorbia	X	X		X	X	X					>gi|7662853|gb|DV153846.1| CV03093A1H12.f1 CV03-normalized library Euphorbia esula cDNA clone CV03093A1H12.f1 5, mRNA sequence Frame = +2
FESAR	4605	monocots	Poales	Poaceae	Festuca	X	X		X	X	X					>gi|74424198|gb|DT680373.1| s13dFA13B03DS029_78397 Tall fescue, Festuca arundinacea Schreb, Drought Stress frame = +2
GLYTO	3846	dicots	Fabales	Fabaceae	Glycine	X	X	X	X			X			X	>Q9FNW4|Q9FNW4_GLYTO Glycine tomentella Seed maturation protein LEA 4
GOSHI	3633	dicots	Malvales	Malvaceae	Gossypium	X	X			X		X				>P09441|LEA13_GOSHI Late embryogenesis abundant protein D-113
HEDCE	58416	dicots	Gentianales	Rubiaceae	Hedyotis		X		X	X	X					>gi|27911444|gb|CB087252.1| hj98b07.g1 Hedyotis centranthoides flower cDNA clone hj98b07, mRNA sequence Frame = +2
HELAN	4231	dicots	Asterales	Asteraceae	Helianthus	X	X		X			X				>P46515|LEA11_HELAN Helianthus annus 11 kDa
HORVU1	4512	monocots	Poales	Poaceae	Hordeum	X	X		X	X	X					>Hordeum1 vulgare BQ740127 var vulgare frame +3
HORVU2	4512	monocots	Poales	Poaceae	Hordeum	X	X		X			X				>TC141523 ORF 65..360 frame +2 Hordeum vulgare barley
HORVU3	4512	monocots	Poales	Poaceae	Hordeum	X	X		X		X					>gi|13084331|gb|BF624252.2| HVSMEa0013C05f Hordeum vulgare seedling shoot EST library HVcDNA0001 (Cold stress)HVSMEa0013C05f, frame = +2
IPOBA	4119	dicots	Solanales	Convolvulaceae	Ipomoea	X	X					X				>TC118882 ORF 422..163 frame -2 Potato
IPONI	4119	dicots	Solanales	Convolvulaceae	Ipomoea	X	X		X	X	X					>27260544|BJ578716 mixture of flower and flower bud Ipomoea nil cDNA clone jm39c17 3', mRNA sequence Frame = -2
JUGNI	16718	dicots	Fagales	Juglandaceae	Juglans	X	X		X	X						>gi|52125110|gb|CV196273.1| CGF1003499_A05 Seed coat from mid-season walnut embryos Juglans regia cDNA clone WSC0008_IF_A05 5' Frame = +3
LACSA1	4235	dicots	Asterales	Asteraceae	Lactuca	X	X		X	X	X		X			>gi|83876902|gb|DW078982.1| CLPX14950.b1_L18.ab1 CLP(XYZ)Lactuca perennis cDNA clone CLPX14950, mRNA sequence Frame = +1
LACSA2	4235	dicots	Asterales	Asteraceae	Lactuca	X	X		X	X	X		X			>gi|84018004|gb|DW155274.1| CLVX731.b1_F16.ab1 CLV(XYZ) Lactuca virosa cDNA clone CLVX731, mRNA sequence Frame = +3
LACSA3	4235	dicots	Asterales	Asteraceae	Lactuca	X	X		X	X	X		X			>gi|83989100|gb|DW135209.1| CLSY2723.b1_E09.ab1 CLS(XYZ)Lactuca sativa cDNA clone CLSY2723, mRNA sequence Frame = +2
LOLMU	4520	monocots	Poales	Poaceae	Lolium	X	X				X					>gi|46504283|dbj|AU247014.1| AU247014 CL Lolium multiflorum cDNA clone CL013G06-5, mRNA sequence Frame = +2
LYCES	4107	dicots	Solanales	Solanaceae	Solanum	X	X			X						>Q00747|LE25_LYCES Protein LE25 tomate
MAIZE1	4575	monocots	Poales	Poaceae	Zea	X	X		X	X						>Zea mays CD445945 Endosperm frame +1
MAIZE2	4575	monocots	Poales	Poaceae	Zea	X	X					X				>zmrws48_0B20-011-e12.s3 CF633097 maiz frame -1
MALDO	3749	dicots	Rosales	Rosaceae	Malus		X		X							>gi|46614169|gb|CN493697.1| Mdfw2007i24.y1 Mdfw Malus x domestica cDNA clone Mdfw2007i24 5', mRNA sequence Frame = +3
MEDSA1	3877	dicots	Fabales	Fabaceae	Medicago	X	X		X	X	X					>BF633170 NF046G12DT Alfalfa frame +2 similar a pm29
MEDSA2	3877	dicots	Fabales	Fabaceae	Medicago	X	X				X					>TC94509 ORF 83..387 Alfalfa frame +2
MEDTR1	3877	dicots	Fabales	Fabaceae	Medicago	X	X	X	X	X		X				>TC94296 ORF 122..597 ? frame +2
MEDTR2	3877	dicots	Fabales	Fabaceae	Medicago	X	X	X	X	X		X			X	>TC96465 ORF 91..623 frame +1 Medicago truncatula alfalfa
MESCR	3543	dicots	Caryophyllales	Aizoaceae	Mesembryanthemum	X			X	X		X				>TC7047 Mesembryanthemum ORF 512..220 frame -3
ORYSA1	4527	monocots	Poales	Poaceae	Oryza	X	X		X							>Q5Z771|Q5Z771_ORYSA Os06g0324400 Hypothetical protein P0421H01.27
ORYSA2	4527	monocots	Poales	Poaceae	Oryza	X	X	X	X	X		X				>Q6Z0I0|Q6Z0I0_ORYSA Os08g0327700 Putative seed maturation protein
ORYSA3	4527	monocots	Poales	Poaceae	Oryza	X	X		X	X	X					>Q7XLZ7|Q7XLZ7_ORYSA Os04g0589800 OSJNBa0086O06.12 protein
ORYSA4	4527	monocots	Poales	Poaceae	Oryza	X	X		X		X					>Q8H683|Q8H683_ORYSA Hypothetical protein Os06g0110200 OSJNBa0004I20.22
PANVI	4539	monocots	Poales	Poaceae	Panicum	X	X		X		X					>gi|59873285|gb|DN152434.1| 5229_G10_M19 Switchgrass callus cDNA library Panicum virgatum cDNA clone 5229_G10_M19 5' Frame = +3
PEA	3887	dicots	Fabales	Fabaceae	Pisum	X	X					X				>Pisum sativum CD859796 Frame +2
PETSP	4101	dicots	Solanales	Solanaceae	Petunia	X	X		X	X		X			X	>EST888206 CV300863 PetuniaRF-5-C02 frame +3
PHAVU	3883	dicots	Fabales	Fabaceae	Phaseolus	X	X	X	X	X		X			X	>Phaseolus vulgaris EC911272 negro jamapa drought root frame +3
PHYPA1	3217	Bryopsida	Funariales	Funariaceae	Physcomitrella	X	X	X		X		X				>PP014005026R FrameD:1:504:1
PHYPA2	3217	Bryopsida	Funariales	Funariaceae	Physcomitrella	X	X		X			X				>PP013003013R FrameD:49:348:1 PP_cl.22605.singlet
PHYPA3	3217	Bryopsida	Funariales	Funariaceae	Physcomitrella	X	X		X			X				>PP_22646_C1 FrameD:1:336:1 nseq=2
PHYPA4	3217	Bryopsida	Funariales	Funariaceae	Physcomitrella		X		X			X				>PP_22605_C1 FrameD:196:486:-2 nseq=3
PHYPA5	3217	Bryopsida	Funariales	Funariaceae	Physcomitrella		X					X				>PP014002079R FrameD:208:393:-2 PP_cl.22646.singlet
PICGL1	3328	Coniferopsida	Coniferales	Pinaceae	Picea		X			X	X					>Q40841|Q40841_PICGL Lea-like protein EMb14
PICGL2	3328	Coniferopsida	Coniferales	Pinaceae	Picea	X	X		X		X					>TC8884 ORF 141..394 Picea frame +3
PINTA1	3337	Coniferopsida	Coniferales	Pinaceae	Pinus	X	X		X		X					>Pinus2 taeda DT629371 frame +2
PINTA2	3337	Coniferopsida	Coniferales	Pinaceae	Pinus	X	X		X	X	X					>TC65044 ORF 134..486 frame +2 Pinus
POPTN1	3689	dicots	Malpighiales	Salicaceae	Populus	X	X	X	X	X		X		X		>TC19988 ORF 54..571 frame +3 Populus
POPTN2	3689	dicots	Malpighiales	Salicaceae	Populus	X	X		X	X	X					>gi|60708624|gb|DN498434.1| S026H08.5pR imbibed seed cDNA library Populus tremula cDNA Frame = +2
POPTR	3689	dicots	Malpighiales	Salicaceae	Populus		X		X		X					>gi|60711848|gb|DN501658.1| V013B10.5pR male catkins cDNA library Populus trichocarpa cDNA clone V013B10 5', mRNA sequence Frame = +3
PSEMZ	3356	Coniferopsida	Coniferales	Pinaceae	Pseudotsuga	X	X		X		X					>Q40928|Q40928_PSEMZ Pseudotsuga menziesii (douglas-fir)
RICCO	4107	dicots	Solanales	Solanaceae	Solanum					X	X					>gi|688714|gb|T15059.1| Ricinus communis cDNA clone pcrs596 similar to Lycopersicon esculentum gene le25 protein, Frame = +2
SACOF	4546	monocots	Poales	Poaceae	Saccharum	X	X		X		X					>gi|35002515|gb|CA125027.1| SCQSLR1089F10.g LR1 Saccharum officinarum cDNA clone SCQSLR1089F10 5',Frame = +3
SESIN	4181	dicots	Lamiales	Pedaliaceae	Sesamum	X	X		X							>Sesamum indicum BU668967 frame+2
SISIR1	3729	dicots	Brassicales	Brassicaceae	Sisymbrium	X	X	X	X	X		X		X	X	>Sisymbrium irio AAY26119.1 GI:63020472
SISIR2	3729	dicots	Brassicales	Brassicaceae	Sisymbrium	X	X	X	X	X		X		X	X	>Sisymbrium irio AAY26119.1 GI:63020472
SORBI	4557	monocots	Poales	Poaceae	Sorghum	X	X		X	X	X					>Sorghum bicolor BG411045 EM1 frame +1
SOYBN1	3846	dicots	Fabales	Fabaceae	Glycine	X	X	X	X	X		X			X	>Q541U1|Q541U1_SOYBN Glycine max Seed maturation protein LEA 4
SOYBN2	3846	dicots	Fabales	Fabaceae	Glycine	X	X		X	X	X					>Q9XES9|Q9XES9_SOYBN Glycine max Seed maturation protein PM29
THEHA	72663	dicots	Brassicales	Brassicaceae	Thellungiella	X	X	X	X	X		X		X	X	>Thellungiella halophila ABY86896.1 GI:166359608
TOBAC	4085	dicots	Solanales	Solanaceae	Nicotiana	X	X		X	X	X					>gi|76866494|gb|DV157487.1| KG9B.001A12F.05062BT7 KG9B Nicotiana tabacum cDNA clone KG9B.001A12 Frame = +3
TRIMO	4564	monocots	Poales	Poaceae	Triticum	X	X		X		X					>gi|22016470|gb|BQ801501.1| WHE2815_B02_D03ZS Triticum monococcum vernalized apex cDNA library Frame = +2
VITVI1	3603	dicots	Vitales	Vitaceae	Vitis	X	X		X	X		X				>AN63334.1 GI:147806171 Vitis vinifera
VITVI2	3603	dicots	Vitales	Vitaceae	Vitis	X	X		X	X		X				>TC45434 ORF 39..415 frame +3 Vitis vinifera
WHEAT	4564	monocots	Poales	Poaceae	Triticum	X	X		X		X					>Triticum2 aestivum CJ641147 dormant embryo frame +1