# Methods for isolation of *PpEXPA5* and *PpEXPA6* sequence

## Plant material

*Physcomitrella patens* was grown on solid BCD minimal moss medium (1 mM $MgSO_4$, 10 mM $KNO_3$, 45 µM $FeSO_4$, 1.8 mM $KH_2PO_4$ pH 6.5) supplemented with 1 mM $CaCl_2$ and 5 mM ammonium tartrate, overlaid with cellophane disks from Leeds Innovations Ltd. (Leeds, West Yorkshire, UK) at 25 °C, under a photoperiod of 16 h light/8 h dark.

## Isolation of *PpEXPA5* and *PpEXPA6* genomic DNA sequences

*PpEXPA5* and *PpEXPA6* gene sequences were first amplified with the degenerate PCR primers 5'–GGNGCNTGYGGNTAYGGNAAYYTNTAY–3' and 5'–RTTNSWYTGCCARTTYTGNCCCCA–3' (designed to conserved amino acid motifs from EXPA sequences) using genomic DNA extracted by a modified CTAB protocol (Murray and Thompson, 1980). $^{32}$P-labelled cDNA probes (labelled with the Rediprime II random labeling kit from Amersham, Little Chalfont, Buckinghamshire, UK) corresponding to the *Arabidopsis* expansin genes *AtEXPA4*, *AtEXPA8*, *AtEXPA11* and *AtEXPA12*, were used on a DNA gel blot to identify products with a high sequence similarity to expansin genes.

Products hybridizing to this mixed probe were isolated with the Qiagen (Valencia, CA) gel extraction kit and cloned with the TOPO TA cloning kit from Invitrogen (Carlsbad, CA). To obtain the full-length genomic sequences, thermal asymmetric interlaced (TAIL)-PCR was performed according to a protocol adapted from Liu and Whittier (1995). The three nested specific primers 5'–CCAACAGAGCAGAAAATCAGATTC–3', 5'–CCCAAAGCATCTCAAAGAGAGTC–3', and 5'–GGCTGGATTGTCAAGGTCTACC–3' and the random degenerate primer AD1 (Liu and Whittier, 1995) 5'–TGWGNAGWANCASAGA–3' were used to obtain the complete 5'-end coding sequence of *PpEXPA5*. The three nested specific primers 5'–CAGCCCTTCGTTCAAACG–3', 5'–TGACTCTCTTTGAGATGCTTTGG–3', and 5'–CGTTTCTGAATCTGATTTTCTGCTC–3' and the random degenerate primer AD2 (Liu and Whittier, 1995) 5'–AGWGNAGWANCAWAGG–3' were used to obtain the complete 3'-end coding sequence of *PpEXPA5*. DNA gel blots and *PpEXPA5* genomic sequence probes were used to identify the desired products. TAIL-PCR products corresponding to *PpEXPA5* sequence were purified with the Qiagen gel extraction kit (Qiagen, Valencia, CA) and cloned with the TOPO-TA cloning kit (Invitrogen, Carlsbad, CA).

The TAIL-PCR sequence was then assembled into a contig with the original degenerate PCR sequence by means of the SeqMan program from the DNASTAR software package version 5.01 (DNASTAR, Madison, WI). Based on this sequence, the specific primers 5'–GGAGAAGCACAGACAGACAGAATC–3' and 5'–GTGGAGAAGCAAAGGTGGTC–3' were designed and used to amplify 1944 bp of *PpEXPA5* with Acupol proofreading polymerase from Gene Choice. The three nested specific primers 5'–TGAATGCAGACACATCGGATAC–3', 5'–CATTGCATCTACTTCCAGGTGAG–3', and 5'–GCAAATAGCACGAACCTTCG–3' and the random degenerate primer AD4 (Liu & Whittier 1995) 5'–TCSTICGNACITWGGA–3' were used to obtain the complete 5'-end coding sequence of *PpEXPA6*. DNA gel blots and *PpEXPA6* genomic sequence probes were used to identify the desired TAIL-PCR products. TAIL-PCR products corresponding to the *PpEXPA6* sequence were isolated with the Qiagen gel extraction kit and cloned with the TOPO-TA cloning kit (Invitrogen).

The complete 3'-end coding sequence for *PpEXPA6* was obtained by screening a lambda phage cDNA library (provided by Dr R. Quatrano, Washington University, St. Louis, MO). A 3' partial cDNA was obtained from this screen and used together with the TAIL-PCR product and degenerate PCR products to generate a contig with the SeqMan program. This sequence and the specific primers 5'–GGATGTACCAAACACTAGCATGTC–3' and 5'–GTGAGAGAAACCCATCCGAG–3' were used to amplify 2399 bp of *PpEXPA6* with Acupol proofreading polymerase (GeneChoice, PGC Scientifics).

## Isolation of *PpEXPA5* and *PpEXPA6* cDNA sequence by RT-PCR

For RT-PCR, total RNA from 14- or 28-d-old *Physcomitrella patens* was isolated with the RNeasy Plant Mini Kit (Qiagen). RT-PCR was performed with the Titan One-Step

RT-PCR System (Roche Diagnostics, Mannheim, Germany). Each 10-µL reaction mixture was composed of 0.4 mM of each deoxynucleotide phosphate, 5 mM DTT, 0.3 µM of each primer, and ~10 ng of RNA template. The primers (designed to the signal peptide and 3' UTR regions of the gene) used for *PpEXPA5* cDNA amplification were 5'–TAGCGTGTTGGTGACTC–3' and 5'–AGGTGGTCACGTGCAGATC–3', yielding a product of 925 bp with RNA from 28-d-old tissue (largely gametophyte tissue). Primers (designed to the signal peptide and 3' untranslated regions of the gene) used for *PpEXPA6* cDNA amplification were 5' – AAAGAACGCAGATTTCAAGG–3' and 5'–GTCAACTCTCCGCTACTGTCTAC–3', yielding a product of 1006 bp with RNA from either 14- or 28-d-old tissue.

## Degenerate PCR

For degenerate PCR, each 10-µL reaction mixture was composed of 0.2 mM of each deoxynucleotide phosphate, 1 µM of each primer, 0.1 µL Taq polymerase (GeneChoice, PGC Scientifics), and between 100 and 200 ng genomic DNA. Annealing temperature was ‘stepped down’ from 65 °C to 45 °C by 1 °C per cycle. Twenty additional cycles were then run with an annealing temperature of 45 °C.

## Discussion of partial expansin sequences and other potential pseudogenes

It should be noted that there were several partial expansin sequences found in the EXPA and EXPB trace searches as well. Six partial *Physcomitrella* EXPA and three partial *Physcomitrella* EXPB sequences were found that could not be assembled into contigs with any of the other sequences found. *PpEXPB7* is lacking some 3' coding sequence and appears to be a pseudogene. In the case of the other three partial EXPB sequences, a gene encoding a protein highly similar to a ‘putative retrotransposon nucleocapsid protein’ is found less than 100 bp away from the gene fragment. All three of these gene fragments lack introns and contain one or more premature stop codons, suggesting that they are pseudogenes created by a retrotransposition event. Phylogenies using partial sequences (data not shown) seem to indicate that all of these partial EXPB genes are related to *PpEXPB5*, which is intronless. Two of these EXPB fragments are represented by multiple traces while one is represented by only a single trace. In the case of three of the six partial EXPA sequences, between 400 bp and 2400 bp of sequence on either side of the fragment does not reveal additional expansin sequence. One of these sequences contains a frameshift and two contain multiple stop codons. Five of these partial EXPA sequences are represented by multiple traces while one is represented by only a single trace. These data would seem to indicate that these are pseudogenes. In the case of the other three EXPA partial sequences, the partial sequence is due to the end of a contig and the inability to find another trace with which to continue the sequence.

There are also two full-length EXPA sequences (*PpEXPA20* and *PpEXPA21*) and one full-length EXPB sequence (*PpEXPB6*) that contain one or more stop codons. However, because the coding regions of these genes seem to contain no other instances of sequence degradation, these stop codons are being treated as potential sequencing errors at present and not as evidence of pseudogenes.

## Literature Cited

**Liu YG, Whittier RF. 1995.** Thermal asymmetric interlaced PCR: automatable amplifi-cation and sequencing of insert end fragments from P1 and YAC clones for chromosome walking. *Genomics* **25**: 674–681.

**Murray YHG, Thompson WF. 1980.** Rapid isolation of highmolecular weight plant DNA. *Nucleic Acids Research* **8**: 4321– 4325.

SUPPLEMENTAL TABLE 1. The smallest Poisson-corrected amino acid distance of each *Physcomitrella* gene to an *Arabidopsis* and rice expansin . The clades from which each of these *Arabidopsis* and rice genes come from is also given. The clade highlighted in yellow has its smallest distance to members of clades other than EXPA I-IV.

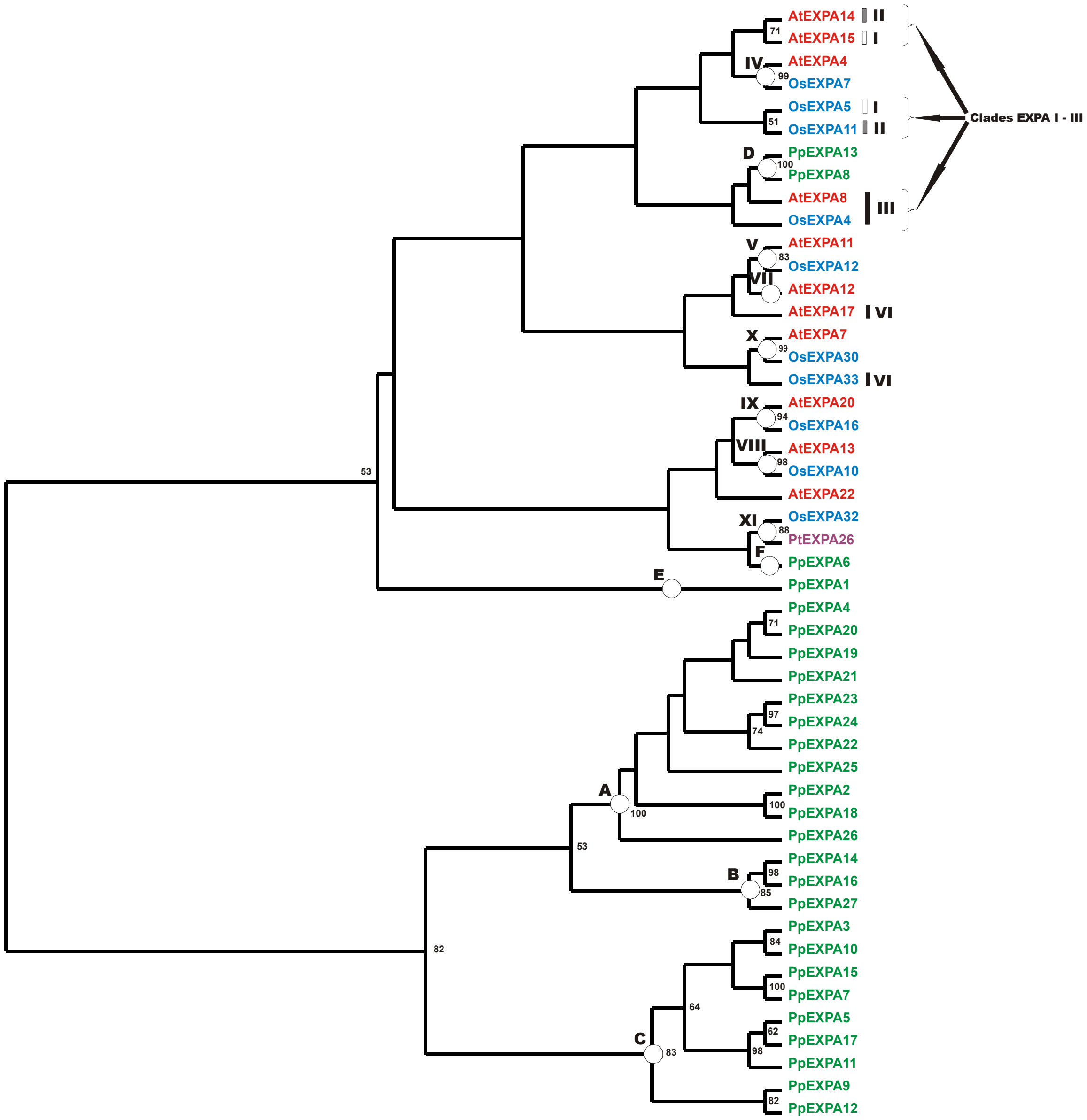
| **PC distance** | ***Arabidopsis thaliana*** | **Clade** | ***Oryza sativa*** | **Clade** |
|---|---|---|---|---|
| **PpEXPA1** | 0.344 AtEXPA10 | EXPA - I | 0.365 OsEXPA7 | EXPA - IV |
| **PpEXPA2** | 0.580 AtEXPA14 | EXPA - II | 0.621 OsEXPA4 and OsEXPA7 | EXPA - III/IV |
| **PpEXPA3** | 0.443 AtEXPA15 | EXPA - I | 0.491 OsEXPA7 | EXPA - IV |
| **PpEXPA4** | 0.607 AtEXPA14 | EXPA - II | 0.594 OsEXPA4 | EXPA - III |
| **PpEXPA5** | 0.432 AtEXPA1 and AtEXPA16 | EXPA - I/IV | 0.467 OsEXPA7 | EXPA - IV |
| **PpEXPA6** | 0.541 AtEXPA1 and AtEXPA4 | EXPA - I/IV | 0.528 OsEXPA5 | EXPA - I |
| **PpEXPA7** | 0.491 AtEXPA9 and AtEXPA10 | EXPA - IV/I | 0.479 OsEXPA6 | EXPA - III |
| **PpEXPA8** | 0.409 AtEXPA8 | EXPA - III | 0.421 OsEXPA4 | EXPA - III |
| **PpEXPA9** | 0.409 AtEXPA1 | EXPA - I | 0.421 OsEXPA5 | EXPA - I |
| **PpEXPA10** | 0.409 AtEXPA15 | EXPA - I | 0.409 OsEXPA7 | EXPA - IV |
| **PpEXPA11** | 0.443 AtEXPA1 and AtEXPA15 | EXPA - I | 0.491 OsEXPA5 | EXPA - I |
| **PpEXPA12** | 0.387 AtEXPA1 | EXPA - I | 0.443 OsEXPA5 | EXPA - I |
| **PpEXPA13** | 0.479 AtEXPA8 | EXPA - III | 0.503 OsEXPA4 | EXPA - III |
| **PpEXPA14** | 0.503 AtEXPA15 | EXPA - I | 0.528 OsEXPA4 | EXPA - III |

| | | | | |
|---|---|---|---|---|
| **PpEXPA15** | 0.491 AtEXPA8 and AtEXPA9 | EXPA - III/IV | 0.467 OsEXPA6 | EXPA - III |
| **PpEXPA16** | 0.491 AtEXPA6 | EXPA - IV | 0.503 OsEXPA7 | EXPA - IV |
| **PpEXPA17** | 0.479 AtEXPA16 | EXPA - IV | 0.528 OsEXPA5 | EXPA - I |
| **PpEXPA18** | 0.635 AtEXPA14 | EXPA - II | 0.594 OsEXPA4 | EXPA - III |
| **PpEXPA19** | 0.649 AtEXPA14 | EXPA - II | 0.635 OsEXPA2 and OsEXPA4 | EXPA - III |
| **PpEXPA20** | 0.767 AtEXPA10 | EXPA - I | 0.750 OsEXPA21 | EXPA - I |
| **PpEXPA21** | 0.649 AtEXPA14 | EXPA - II | 0.708 OsEXPA6 and OsEXPA7 | EXPA - III/IV |
| **PpEXPA22** | 0.649 AtEXPA4 | EXPA - IV | 0.594 OsEXPA21 | EXPA - I |
| **PpEXPA23** | 0.554 AtEXPA14 | EXPA - II | 0.580 OsEXPA4 | EXPA - III |
| **PpEXPA24** | 0.607 AtEXPA14 | EXPA - II | 0.594 OsEXPA4 | EXPA - III |
| **PpEXPA25** | 0.678 AtEXPA4,AtEXPA14,AtEXPA25 | EXPA - IV/II/XII | 0.635 OsEXPA4 | EXPA - III |
| **PpEXPA26** | 0.635 AtEXPA14 | EXPA - II | 0.649 OsEXPA4,OsEXPA5,OsEXPA6 | EXPA - III/I |
| **PpEXPA27** | 0.516 AtEXPA14 | EXPA - II | 0.541 OsEXPA5 | EXPA - I |
| | | | | |
| **PpEXPB1** | 0.794 AtEXPB2 | EXPB - I | 0.763 OsEXPB5 and OsEXPB14 | EXPB - I |
| **PpEXPB2** | 0.827 AtEXPB3 | EXPB - II | 0.805 OsEXPB5 | EXPB - I |
| **PpEXPB3** | 0.794 AtEXPB1 and AtEXPB3 | EXPB - II | 0.827 OsEXPB5 | EXPB - I |
| **PpEXPB4** | 0.816 AtEXPB3 | EXPB - II | 0.773 OsEXPB14 | EXPB - I |
| **PpEXPB5** | 0.753 AtEXPB3 | EXPB - II | 0.794 OsEXPB1 | EXPB - I |
| **PpEXPB6** | 0.838 AtEXPB1 | EXPB - II | 0.849 OsEXPB5 and OsEXPB14 | EXPB - I |

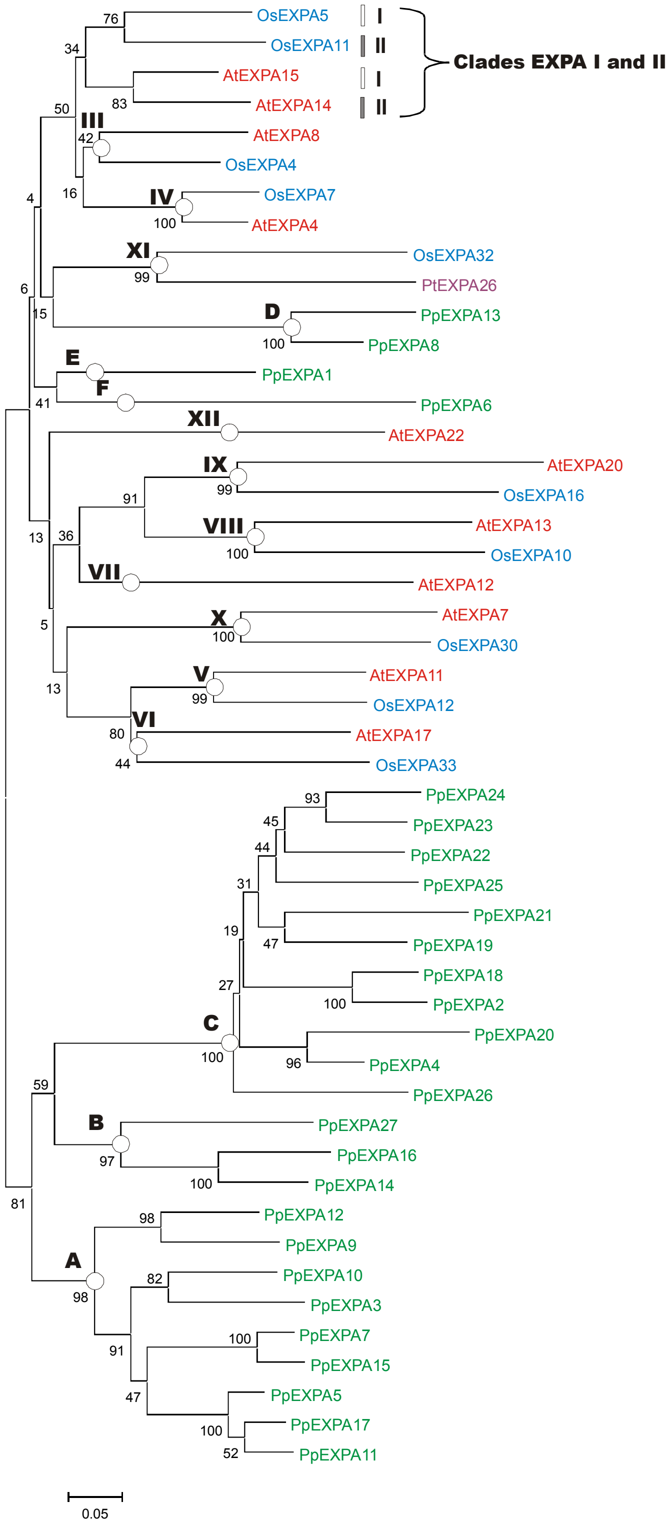
| | | | | |
|---|---|---|---|---|
| **PpEXPB7** | 0.872 AtEXPB3 | EXPB - **II** | 0.895 OsEXPB11 | EXPB - **I** |

SUPPLEMENTAL TABLE 2. Average nucleotide compostion of *Arabidopsis*, rice and *Physcomitrella* EXPA genes. Values given are a percentage of all nucleotides in a dataset trimmed as was done for the phylogenies presented here.

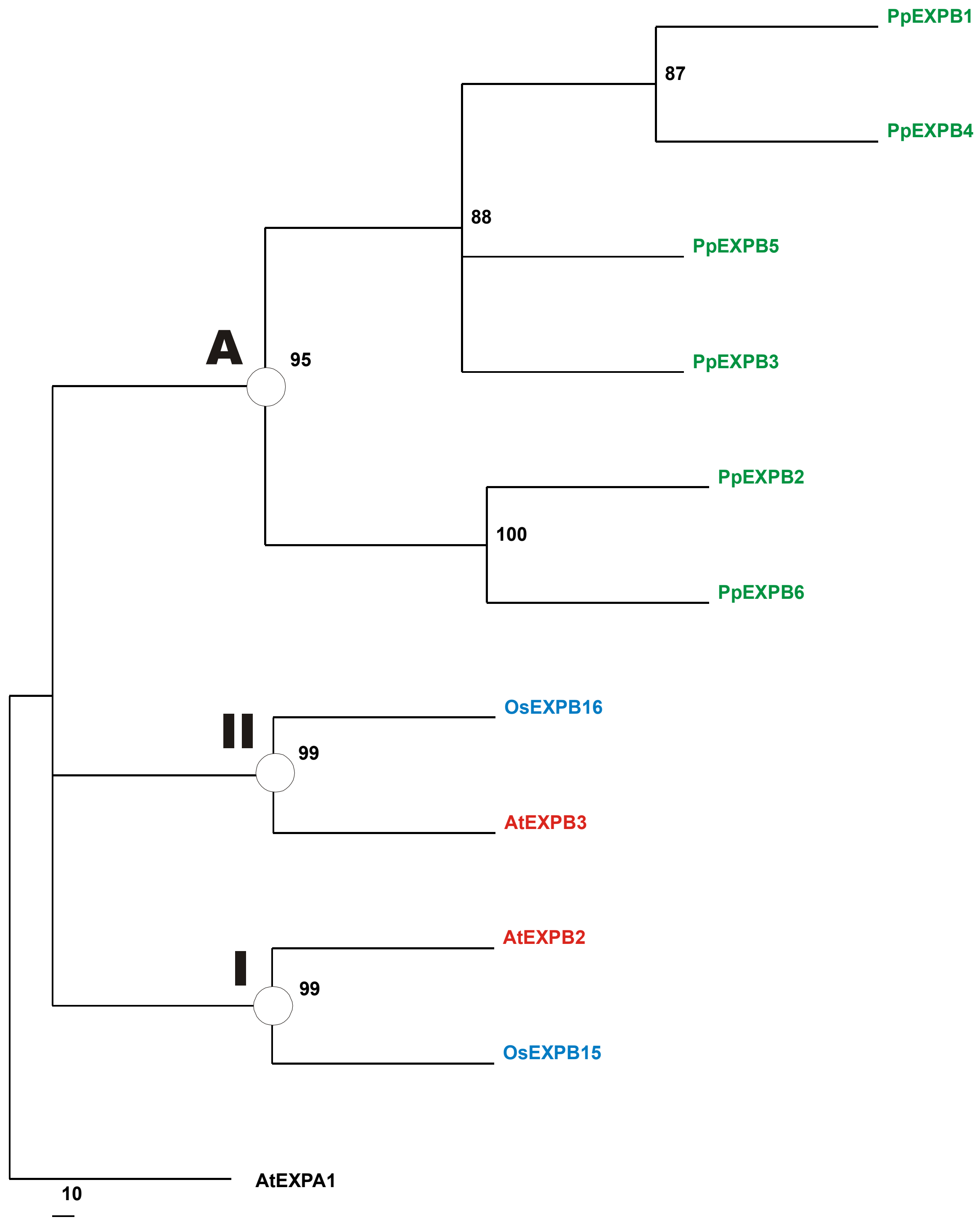
| Species | Ave % T | Ave % C | Ave % A | Ave % G |
|---|---|---|---|---|
| *Arabidopsis thaliana* | 25.3 | 22.8 | 26.1 | 25.9 |
| *Oryza sativa* | 15.4 | 32.9 | 17.3 | 34.5 |
| *Physcomitrella patens* | 22.2 | 26.4 | 22.1 | 29.4 |



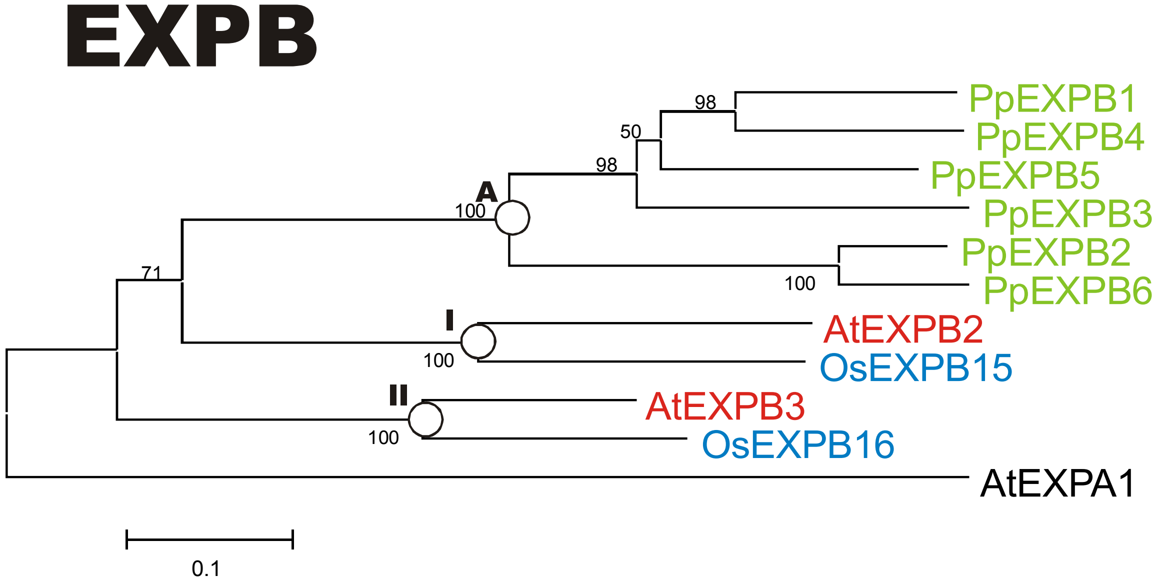
SUPPLEMENTAL FIG. 1. One of two maximum-parsimony EXPA trees of length 2282. Significant bootstrap values from the bootstrap consensus tree are indicated. The tree was rooted manually at groups A, B and C. Clade and groupings are marked with circles (or bars when they are poorly resolved as in the case of clades EXPA-I, EXPA-II and EXPA-III). *Physcomitrella patens* sequences are labelled in green, rice sequences in blue, *Arabidopsis* sequences in red and a *Populus* sequence in violet.


76
OsEXPA5
I
34
OsEXPA11
II
Clades EXPA I and II
AtEXPA15
I
83
AtEXPA14
II
50
III
42
AtEXPA8
OsEXPA4
16
IV
OsEXPA7
4
100
AtEXPA4
XI
OsEXPA32
99
PtEXPA26
6
15
D
PpEXPA13
100
PpEXPA8
E
PpEXPA1
F
41
PpEXPA6
XII
AtEXPA22
IX
AtEXPA20
91
99
OsEXPA16
VIII
AtEXPA13
13
36
100
OsEXPA10
VII
AtEXPA12
X
AtEXPA7
5
100
OsEXPA30
V
AtEXPA11
13
99
OsEXPA12
VI
AtEXPA17
80
44
OsEXPA33
93
PpEXPA24
45
PpEXPA23
44
PpEXPA22
31
PpEXPA25
PpEXPA21
19
47
PpEXPA19
PpEXPA18
27
100
PpEXPA2
C
PpEXPA20
100
96
PpEXPA4
59
PpEXPA26
B
PpEXPA27
PpEXPA16
97
100
PpEXPA14
81
98
PpEXPA12
PpEXPA9
A
82
PpEXPA10
98
PpEXPA3
100
PpEXPA7
91
PpEXPA15
47
PpEXPA5
100
PpEXPA17
52
PpEXPA11
0.05

SUPPLEMENTAL FIG. 2. Neighbour-joining tree for EXPA family. The tree was rooted manually at groups A, B and C. Clade and groupings are marked with circles (or bars when they are poorly resolved as in the case of clades EXPA-I and EXPA-II). *Physcomitrella patens* sequences are labelled in green, rice sequences in blue, *Arabidopsis* sequences in red and a *Populus* sequence in purple.



SUPPLEMENTAL FIG. 3. Bootstrap consensus parsimony tree obtained for the EXPB family. The tree was rooted manually at *AtEXPA1*. Clade and groupings are marked with circles. *Physcomitrella patens* sequences are labelled in green, rice sequences in blue and *Arabidopsis* sequences in red.



SUPPLEMENTAL FIG. 4. Neighbour-joining tree for EXPB family. The tree was rooted manually at AtEXPA1. Clade and groupings are marked with circles. *Physcomitrella patens* sequences are labelled in green, rice sequences in bluel, and *Arabidopsis* sequences in red.

SUPPLEMENTAL FIG. 5. *Physcomitrella* expansins assembled from trace data. Named genes and their intron patterns are followed by their amino acid and nucleotide sequence. Introns in the nucleotide sequence are marked in red.

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Format:
>Sequence name [intron pattern]

Amino acid sequence

>Sequence name
Nucleic acid sequence (introns in red)

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>PpEXPA1 [AB]

MARHNATKPVTLILAALMVLSATDNVEGRHHVRDGKNWRKAHATFYGGADASGTMGGACGYGNLYSTGYGVD

STALSTALFNNGAKCGACFAIQCYRSQYCVPGSPVITVTATNFCPPNHKGDGTPGWCNPPMRHFDLAQPSFT

KIAKYRAGIVPVLFRRVPCEKKGGVRFTINGNKYFNLVLVHNVGGKGDVHAVDIKGSNTEWIPMKRNWGMNW

QTDAVMTGQALSFRVTTSDGKTIVSMNATPSHWSFGQTFEGGQFAMN

>PpEXPA1

ATGGCGAGGCATAATGCAACAAAGCCTGTGACACTCATTCTTGCTGCACTGATGGTTCTTTCAGCCACCGAC

AACGTCGAAGGTCGTCATCACGTCAGAGATGGAAAAAACTGGCGCAAAGCTCATGCAACTTTCTACGGGGGT

GCTGATGCTTCAGGAACTATGGGTAACTTTTTTCAACCTCTTGTTCAACTTCGGAGGCGTCCCATGAATCCT

TACAAGTAGTAATTAAAACTTAAGTTTCTTGACAATGTGTATGCTTCCTATCTATTTGGAACTAAACCATTC

CTCTGCTCTGATCAGAAACTTGAATCAGCTGCAAAGAGAATAAGACGCCAATATACATGTATCAGAAAACTA

ACGAAGAGGACTACAAATTTTGGATCTCTTCCATGTAGCTCTTGTCCATAAGGCACCACCTTATGGAGAAAT

TTTTTTTCGAAAGTTTTGAATTCAGAGATCGGTTGACTAAATAGTAACCTTCGAATGTGCAGACGGTGCATG

CGGTGCATGCGGTTACGGAAACCTCTACAGCACTGGCTATGGAGTCGATTCGACAGCTTTGAGTACAGCTCT

TTTCAACAATGGGGCAAAATGCGGAGCTTGTTTTGCGATCCAATGCTATCGTTCACAGTATTGCGTTCCAGG

TTCACCTGTAATCACTGTCACAGCTACAAACTTCTGCCCTCCTAACCACAAAGGTGATGGCACGCCAGGATG

GTGTAATCCGCCAATGCGTCACTTCGACCTTGCGCAGCCTAGCTTCACCAAAATCGCTAAGTATAGAGCCGG

CATCGTCCCCGTTCTCTTCAGAAGGTGTGCATTGCGTTGAAGACTGATTTGTAAATTGTGACTTTAAGCCTT

AATTACTGAGGATGGAGACAGCTGTGCAATCACTTCGCAAATTAAACCATGCATGTTTTTAAGAAAACAGAA
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ACGGCAGAACAAACCGTCAGCCAATTGAAAGAGATGTTCTGAAACTTAGTAAAAGAGGTTGTCTTAGTCCTG
TTTGGATTGGTAGTTTGATATTACGAAGTCCGTACTGACCAAAACTTTGTTATATGCCTTGCACAATGCAGG
GTACCATGCGAGAAAAAAGGTGGCGTCAGGTTCACTATCAATGGAAATAAGTATTTCAATCTCGTCCTAGTT
CACAATGTTGGTGGAAAAGGCGATGTGCACGCAGTAGACATCAAGGGATCCAATACAGAATGGATTCCCATG
AAGCGAAACTGGGGAATGAACTGGCAGACAGATGCTGTTATGACTGGCCAGGCACTCTCCTTCCGAGTGACA
ACCAGTGATGGTAAGACCATAGTCTCTATGAACGCAACGCCATCTCACTGGAGCTTCGGCCAGACCTTCGAG
GGAGGTCAGTTCGCTATGAATTG

>PpEXPA2 [none]
GTRKLAVCIAAVAILALNSLPSVLGAPYGWKEAHITYYGTANGGGTQGGACGYPNTFAMGYGVMTAALSYPL
FQGGKSCGACYQLKCKWLAPTRTVHNWCWSYSRTITITATNSCPPGSHGGWCDWKPHFDLPMPAFMTLARRE
GGVAPVYYRKVRCAKRGGIRFTLGGNPYFMMILIHNVGGAGDLRAVKIKGRNGYWVPMWQNWGALWTCKTKL
SGALSFQITTGDGRTVTVNRAVGDYWKFGQTWEGSQFR

>PpEXPA2
GGCACGAGGAAACTCGCAGTTTGCATTGCCGCAGTCGCTATTTTGGCACTGAACTCCCTGCCTTCGGTGCTT
GGAGCACCATACGGATGGAAGGAGGCGCATATCACGTACTATGGAACAGCTAATGGCGGTGGCACACAGGGA
GGCGCATGCGGATATCCGAACACCTTTGCGATGGGATACGGGGTGATGACCGCAGCATTGAGTTATCCTTTG
TTCCAGGGCGGAAAGTCTTGCGGGGCGTGTTACCAGCTGAAGTGCAAATGGCTGGCGCCCACTCGCACCGTT
CACAACTGGTGCTGGAGCTACAGTCGCACCATCACTATCACTGCAACAAACTCGTGCCCTCCAGGATCGCAC
GGAGGTTGGTGCGACTGGAAGCCTCACTTCGACTTGCCCATGCCTGCTTTCATGACATTGGCGCGGCGTGAA
GGAGGAGTGGCCCCCGTGTACTACAGAAAGGTTCGGTGTGCGAAGCGCGGCGGAATTCGGTTTACCCTTGGC
GGCAACCCATACTTCATGATGATCTTGATTCACAACGTGGGAGGTGCAGGCGATTTGAGGGCAGTGAAGATC
AAGGGGCGGACGGATATTGGGTACCAATGTGGCAGAACTGGGGTGCGCTGTGGACATGCAAAACGAAGTTGA
GCGGAGCATTGTCTTTCCAGATCACGACGGGCGACGGGCGCACTGTGACGGTTAACAGAGCAGTTGGAGACT
ACTGGAAGTTTGGACAAACGTGGGAGGGCTCTCAGTTCCGATAG

>PpEXPA3 [AB]
MAMATHVALLLVSALALVTSVQSGYAGSDWISGVAHATFYGGVDAQGTQGGACGYGNLYSTGYGTSTTALSS
ALFNAGLSCGACFELKCDSANSKYCLPGDKSITVTATNYCPQGSDGGWCDSPKQHFDLSHPMFTSLAQEVGG
VIPVTYRRAPCAKKGGMRFTINGNPWFVMILVTNCGGAGDVQQLQIRGSDTPWYPCVRNWGQMWQMTSDPNL
PGKALSFRATLSDGSVAESLNAAPSNWGWGQTFEGVATY

>PpEXPA3
ATGGCGATGGCTACCCATGTTGCGCTCTTGCTCGTATCTGCTCTAGCGTTGGTGACTTCGGTGCAGTCTGGG
TATGCTGGCAGCGACTGGATCAGCGGCGTTGCTCATGCGACGTTCTACGGTGGCGTGGACGCACAGGGAACT

CAAGGTGTGAATCTAATGCAGCTCCTCTAGAGGGTAGCGGGGTCTTTGAACTGGGAAGTTTTCTAGCTCGGC
AATGTCGAGGATTGGATGGATGCGTTGATAGATACATCGATAGATGAATTACTGAAGGTGTCCACAGGTCCA
TGTTCTTGAAGACGCCTGAGCATGTTCGACATAGCAGTTCTCAATGGGTATGTGCAGGTGGAGCTTGCGGTT
ACGGAAACCTCTACTCAACCGGATATGGCACCAGTACCACCGCACTCAGTAGTGCTTTGTTTAATGCGGGCC
TTAGCTGCGGAGCCTGCTTCGAACTCAAGTGCGACAGCGCCAACTCCAAGTACTGTCTTCCAGGGGACAAGT
CCATCACAGTTACAGCAACGAACTACTGTCCTCAGGGCTCAGATGGCGGGTGGTGCGATTCCCCGAAGCAGC
ACTTCGACCTCTCGCACCCCATGTTCACCAGCCTTGCTCAAGAGGTTGGGGGTGTCATTCCCGTCACGTATC
GGAGGTCAGTCATTCAATCTACTCTCCTTCTTCACACGCGTTCTTTGAATTGCATCAATACTACATCGTGAG
TCGCCCAATTGATACGTCACCGCTCACTCTCTTTTTCGCTGCCTGTGCTTCTTCAGAGCTCCTTGTGCAAAG
AAAGGCGGCATGAGGTTCACAATTAACGGCAACCCATGGTTCGTGATGATACTAGTCACCAATTGCGGTGGT
GCAGGAGATGTGCAGCAACTTCAGATCAGGGGCAGCGACACCCCGTGGTACCCTTGCGTCCGCAACTGGGGA
CAGATGTGGCAGATGACCTCGGACCCAAATCTGCCTGGGAAGGCACTCTCCTTCAGAGCTACCCTGAGTGAC
GGCAGCGTGGCCGAGTCTCTGAACGCCGCGCCCTCCAACTGGGGCTGGGGTCAAACGTTCGAGGGCGTCGCT
ACCTACTAG

>PpEXPA4 [B]

MGSICSMKFPILMVAFLALGLPSVLGAPYGWKDAHITYYGSPNGGGTQGGACGYQNTYALGYGSFTAALSAP
LFQGGAACGGCYQLKCAPVRETRTVHNWCWSYSRSIVVTATNLCPPGSHGGWCAWRPHFDLPMPAFTSLAKQ
VGGVAPVFYRRVRCAKRGGVRFTIGGNPYFLMVLIHNVGGAGDIRSVRIKGQYSGWVTMFRNWGSLWTCRTK
LSGPLSFMITTSDGRTLVSNRAVGSWWKFGQTWEGSQFR

>PpEXPA4

ATGGGTTCCATATGCAGCATGAAGTTTCCCATTCTCATGGTCGCCTTTTTAGCGCTGGGCTTACCTTCGGTG
CTTGGAGCACCTTATGGATGGAAGGATGCGCACATTACCTACTACGGATCTCCCAACGGCGGAGGGACGCAG
GGAGGTGCTTGCGGATATCAGAATACTTATGCCCTCGGATACGGATCTTTCACTGCGGCATTGAGTGCCCCG
TTGTTTCAAGGAGGAGCCGCTTGCGGGGGATGCTACCAGCTTAAGTGTGCACCAGTGAGAGAAACCAGAACC
GTGCATAACTGGTGCTGGAGTTACTCTCGCTCTATCGTTGTCACCGCTACGAACCTGTGCCCGCCAGGATCT
CACGGAGGGTGGTGCGCATGGCGCCCCCACTTCGACTTACCAATGCCTGCTTTCACCTCTCTCGCAAAGCAA
GTAGGAGGTGTTGCTCCTGTCTTCTACAGAAGGTGTGTGACCTGGTGTATATGGTCCTTATTATTTATTCAA
ATCCGCTTCAAATGTCACTGCTGTTTGGGTTGAATACTAATCTTGTTGAGAAATGTTTGATATCCAGGGTAA
GATGCGCTAAGCGCGGTGGAGTTCGCTTCACGATCGGAGGAAATCCATACTTCTTGATGGTTCTGATCCACA
ACGTCGGGGGAGCAGGCGACATCAGGTCTGTGAGGATCAAAGGGCAATACTCAGGATGGGTGACCATGTTCC
GTAACTGGGGTTCACTGTGGACTTGCCGGACTAAGTTGAGTGGACCCCTGTCCTTCATGATTACCACCAGCG

ACGGACGCACTCTAGTGTCCAACAGAGCCGTGGGATCGTGGTGGAAATTCGGACAAACCTGGGAGGGTAGCC
AGTTCAGATAG

>PpEXPA5 [AB]

MAIPWSSVVLVTLVSLMACAEAKGSSFMGSDWGRAHATFYGGADASGTQGGACGYGNLYSTGYGTNTAALSS
SLFNSGLSCGACYELTCDPSCSQYCLPGGSAIITATNFCPTGSNGGWCNPPKQHFDLAQPVFSKIARTVGGV
IPINYRRVPCSKSGGMRFTVNGNPYFLLVLVTNVGGAGDVQQLYIKGASTGWLPLKRNWGQMWQFTGNSGMH
GQAISFKAVTSDGAEAISPNVAPANWGFGQTFEGSNF

>PpEXPA5

For nucleotide sequence see Figure S6

>PpEXPA6 [AB]

MPSISSFEKNADFKGSSFSTETTLSTDDQPDEVFARKAGYAPVPRSYGGVWRNARSTFYGGMDAAGTMSGAC
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>PpEXPA6

For nucleotide sequence see Figure S6

>PpEXPA7 [AB]

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>PpEXPA8 [AB]

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>PpEXPB2 [A]

MSTAFQAVWLVCVGLLSLQAAEAGYLAQNGYHERWVRARGTWYGDPYGEGSSGGNCGYTKLWGTPIGPKIVA

GSRSIYANGQGCGQCYQIRCVDPNGGPRLCNPQGTNVVVTDFCPGGTYCSTGENAFDMSGAAINAMALRGRE

```
GQLRNRGLYNLLYKRVPCRYRGTNIEFRVDNGSSPFWLSILIKYVGGPGDIGQVYIRMANWYKFQPMRHAWG
ANWMIPNYDGKPFRGPMDIRIVSRLNRHTVLARGVIPAYFRPGTSYRSRVQMAF
>PpEXPB2
ATGTCGACGGCTTTCCAAGCGGTGTGGCTGGTGTGTGTGGGCCTTTTGAGCCTGCAAGCAGCCGAAGCGGGC
TATTTGGCCCAGAATGGATACCACGAGCGATGGGTCCGCGCTCGCGGCACCTGGTACGGGGATCCTTATGGC
GAAGGCTCTAGCGGTACGTTTCCAGCTAAGAATATGTTCAGCAATTCCTTGTCCAAACTAATTAATCTGAAA
GAATTATATGTATCGTTGTCATTTTTCTGACGGTTGCTCTTGCGTTTTCAGGAGGAAACTGCGGATACACTA
AGCTTTGGGGCACACCCATCGGGCCTAAAATTGTTGCCGGAAGCAGGTCAATCTATGCTAATGGGCAGGGTT
GCGGCCAATGCTATCAAATCAGGTGTGTTGATCCAAACGGAGGACCCAGGCTCTGCAATCCTCAAGGCACGA
ACGTCGTCGTGACTGATTTCTGTCCCGGTGGAACTTACTGCAGCACCGGGGAAAATGCCTTCGACATGAGCG
GGGCCGCGATAAATGCAATGGCGTTGCGTGGGAGAGAAGGCCAGCTCCGCAACCGTGGTTTGTACAACCTGC
TCTACAAGAGAGTCCCTTGTCGATACAGGGGTACCAATATAGAATTCCGTGTTGATAACGGCTCCAGTCCCT
TCTGGCTCAGTATTTTGATAAAGTACGTGGGAGGGCCTGGTGACATTGGTCAGGTGTACATTAGGATGGCGA
ACTGGTATAAGTTCCAGCCGATGAGGCATGCGTGGGGCGCTAACTGGATGATTCCCAACTACGACGGGAAGC
CGTTCAGGGGCCCCATGGATATTAGAATTGTATCGAGATTGAACCGTCACACAGTGCTTGCTAGAGGAGTCA
TTCCCGCCTACTTCAGACCTGGAACGTCTTACAGGTCTAGAGTGCAAATGGCTTTTTAG
>PpEXPB3 [ACnFn]
MGSSVVLRQPTVLLWIALASVLPVAHCSGSLEASGYTASWLPGHATWYGDPYGEGSSGGACGYTELAGTPYG
LSVGAGSAVIYQNGQGCGECYEVKCTYPSCKPTPSRIVITDFCPGGTFCSTGEPAFDLSGMAMTNMALPGRD
QELRNLGLYEIQYRRVPCYYPNQNVAFKVDPGSTPFWLSFTIEYQGGPGDIESVAIRQAGSSEFQQMQHNWG
ANYMLICYSGKPFKGPYDVMITAKLNGHVLIAQDAIPEYFQPGGIYESNVQLGY
>PpEXPB3
ATGGGAGTTGTACAAAAGCAGTTATTGCGGTTAGTAGGAGACTGGTCCTGCATTGCATGGGGATGCTTGGAC
TGGTCGAATAGACGTTGCGGTCTGTGTGGAGCTACCCACATTTTCTGCAGCACTTGTGACCAAGGATGGGAT
CCTCAGTGGTTCTTCGCCAACCCACTGTGCTGCTGTGGATAGCCCTTGCGAGTGTGCTTCCAGTTGCTCACT
GCAGCGGCTCCCTGGAGGCCAGCGGGTACACCGCTTCCTGGCTCCCTGGACATGCAACTTGGTATGGGGATC
CATATGGAGAGGGCTCAAGCGGTACCACACTCGATAATCACTCATTCTTGCATTGAAATTGCCTGTAACTCT
AAATTGTCTGTATTATCTAAATTGCATAAATATAGATATATATGTATATATATATATATCATCTGCTAGACA
ATTCTGATAGTACATATCGTGCTTCCGCATATCAGTTGATAGGGATAAGTGAAACCAAGAGTAGTAACCAGT
AGCTTTCAACAATGTCTATTGGTGTGGTTACCGTAGAGAATCTTCTTTCTTTGGACTTATTCACTTGATGAC
TGTTGACATTGTTCAGGAGGAGCTTGTGGCTACACAGAGCTCGCAGGTACTCCGTATGGTTTGAGTGTGGGT
GCGGGAAGTGCTGTCATCTACCAGAATGGCCAAGGGTGCGGCGAATGCTACGAAGTAAGTGGTCTGTGTAGA
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ACGCCATACCTTGCAAAATAGAAAACACACACAGATCCTCAAGACATTAATCTCCATAGAGATATTCAAGCA
CATAATTCATATTCTTTTGCTTTTTCTCCGGTGTATGATTCACAATGCAGGCCAACTTTTACGAAGAGGAGA
ATTAAAATACTTGTCAAAACTGTTGCCACAGGTTAAGTGCACGTACCCATCTTGCAAGCCGACGCCCAGTAG
AATTGTTATTACTGATTTTTGTCCAGGTTTGTGCACTTGGCTCATTCGTTCAATTTTCTAACACATTATCAC
AGTCACGATGTCAGTTTATAACGATAATGTCTTTTGTACTCAAATACGCATTACTTGACAGATTAGTCCGTG
TTTTCACAGGAGGAACGTTTTGCAGCACAGGCGAACCAGCATTTGATCTCAGTGGCATGGCCATGACAAACA
TGGCTCTTCCTGGCAGGGACCAGGAGTTACGTAACTTGGGCTTGTACGAGATTCAATACAGAAGAGTGCCCT
GTTATTATCCAAACCAGAACGTCGCTTTTAAAGTAGACCCCGGGTCCACCCCGTTTTGGCTTTCGTTCACCA
TTGAATACCAAGGAGGACCAGGAGACATTGAAAGCGTCGCTATAAGACAGGTAATGAATTTGGCCTTCTCGT
TCACGGTCTCCAGGCTTAAACTTGGAGTATTGCATGAAGTTTCTGTCATAGAGTTGCATGTATCTCCCAAAA
TCAGATCAAGAAACTTTGCTTTAAGGGATGCTCTACTTTTAACAAGCACACAGATCATTCTATGTCCTCAAC
TCTCTTTTAAACTTTTTGGATGTTTGTCTCCAGGCTGGTAGCTCTGAGTTCCAGCAGATGCAACACAACTGG
TAATGCCACTCAGAATCACGCACTAGTACTACATCTGCTTCACTTGGAGTGAAGAATATTCAGTCGCATGCT
GTTAGACTAAATGGTCATGTGTTGATGTTTTTTCTGCAGGGGTGCTAATTACATGTTAATCTGCTACTCCGG
AAAGCCATTCAAGGGACCCTACGACGTGATGATCACTGCCAAATTGAACGGCCATGTCCTTATTGCCCAGGA
TGCCATTCCGGAATACTTCCAACCAGGAGGTATCTACGAGTCCAATGTGCAGCTAGGGTAC
>PpEXPB4 [A]
MAAIQVVLLLVGLVGLPAAMGLASSSMAANGYNENWVPGHATWYGDPYGEGSSGG?CGYLQLTGTPIGNKIA
AGNEAIFQKGKG??QCYEVKCNYPVCRPEGTRIVITDLCPG?QFCSGGNPAFDLSGAAISAMAKDGQDGALR
NIGLYDIQYKRVPCEYPGQNIVFKVDAGSSPFWLSFTVKYMGGPGDIESVSISQRDGSFIPAQHSWGANWML
INYSGAPFQGPYSVKINCMLNGHTVVAKDVIPAGFAPGQEYESNVQIGF
>PpEXPB4
ATGGCAGCTATCCAAGTTGTGTTGCTACTGGTGGGTCTGGTGGGATTGCCGGCAGCCATGGGATTGGCAAGC
TCCAGCATGGCTGCAAATGGATACAACGAGAACTGGGTCCCTGGACACGCTACATGGTACGGCGATCCCTAT
GGCGAAGGATCCAGCGGTAAGTGCATCTAGTTCATTCTCAACTCTTCCACAAAACTGTGGATTAAACCAAGC
CACGTTGCTAAGATTACCATGTTGCTGACAATGTGAGATTCATCATGGCCAGTCTAGACTCATGTGGGTGTT
GTAACCCTTTGTGCAGGAgGASMATGTGGCTACCTCCAGCTCACTGGAACGCCCATTGGCAACAAGATTGCT
GCCGGAAACGAAGCCATCTTtCCAAAAAGGCAAGGGTKGCGSCCAATGCTACGAGGTGAAGTGCAATTATCCA
GTGTGCAGACCTGAGGGGACGAGGATTGTCATCACAGACTTGTGCCCAGGAGSCCAGTTCTGCAgTGGTGGC
AACCCCGCCTTTGACCTGAGCGGCGCAGCCATCAGCGCCATGGCGAAGGATGGTCAAGACGGAGCCTTACGG
AACATTGGCTTATACGACATTCAGTACAAGAGGGTGCCGTGCGAGTACCCGGGCCAGAACATTGTCTTCAAA
GTAGACGCTGGCTCTAGCCCTTTCTGGCTCTCATTCACCGTGAAGTACATGGGAGGCCCAGGTGACATTGAA
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AGCGTTTCAATCAGTCAGCGTGATGGCTCTTTCATCCCGGCTCAACACAGCTGGGGAGCCAATTGGATGCTC

ATCAACTACTCCGGAGCACCATTCCAGGGTCCCTACTCCGTGAAAATCAACTGCATGCTGAACGGCCACACC

GTTGTTGCCAAGGACGTTATTCCAGCTGGTTTTGCACCCGGTCAGGAATACGAGAGCAATGTGCAGATTGGG

TTC

>PpEXPB5 [none]

MKMSTLAFCAVLLLFLELLGLPVAFCGTLALSGYNEQWMAGHATWYGEPLGEGSSGGACGYTKLADTPYGPK

IAAGNDPIFQGGSGCGACFEVKCNYPSCKSEPTRIIITDQCPGGTYCSTSQPAFDLSGAAISDMAVSGKDGE

LRNIGLYDILYKRVPCEYPNQNIAFQVDAGSSAFWLSLLVKYMGGPGDIESVEIRTTGSSSFQPAKHNWGAS

WMLINTSGQPFKGPYDVKIVSKLNGHTVIAEKAIPEFFEPGKLYESNVQMAY

>PpEXPB5

ATGAAAATGTCGACACTGGCGTTCTGTGCGGTACTGCTGTTGTTCCTAGAGCTACTGGGTCTCCCAGTTGCT

TTCTGCGGCACCTTGGCTCTAAGCGGGTACAATGAACAGTGGATGGCCGGACATGCCACATGGTACGGGGAA

CCTCTTGGTGAAGGATCCAGTGGTGGCGCTTGTGGCTACACAAAGCTTGCGGATACACCATATGGACCCAAA

ATTGCAGCGGGAAACGATCCAATTTTCCAAGGAGGTAGCGGATGCGGCGCATGCTTCGAGGTGAAGTGCAAC

TATCCATCTTGCAAGTCCGAGCCAACCCGGATTATCATCACAGACCAATGTCCTGGAGGAACTTACTGCAGC

ACATCTCAGCCTGCATTCGACCTGAGTGGCGCTGCTATCAGCGACATGGCTGTTTCGGGTAAGGACGGAGAA

CTGCGCAACATTGGGTTATACGACATCCTGTACAAGAGAGTGCCATGCGAGTACCCGAATCAGAATATTGCC

TTCCAGGTCGACGCAGGCTCATCTGCTTTCTGGTTGTCGCTCCTGGTGAAGTATATGGGAGGGCCTGGCGAT

ATTGAAAGTGTCGAAATTCGTACAACGGGGAGCTCATCTTTCCAACCAGCAAAGCACAACTGGGGTGCCAGC

TGGATGCTCATCAACACGTCCGGCCAGCCATTCAAAGGCCCTTACGACGTCAAGATTGTGTCCAAGTTAAAC

GGTCATACTGTCATCGCCGAGAAAGCGATTCCTGAGTTTTTTGAACCAGGGAAGCTTTACGAGAGCAACGTG

CAGATGGCGTAC

>PpEXPB6 [A]

MATMAQVVWLVVLGLMSLLLCAEAGWLGNQGYHEQWVRARGTWYGDPYGEGSSGGNCGYTRL*GTPIGPKIV

AGSRSIY?NGLGCGQCYQNQCVDP??G?KL?NSF?TQ???TDFCPGG?YCSTGENAFDMSGAAINAMALPSR

EGQLRNRGLYNLLYKRVPCRYRGT?I??RVD??SSAYWLSILIKYVGGPGDIGQVYIKMANWFAFQPMKHAW

GANWMMPSYDGKPFKGPMDIKIVSKLNRHSVVARGVIPGYFRPGTTYNSRVQMAF

>PpEXPB6

ATGGCGTCACAGGCGCGGTTCCCAAAAGCTTTACCTCCCAAATTCGATATACCGACGCCGGGTCTATTTTCG

GACCCCAGTTACTTGTTTCTCTGGAGGTCAGCGCTAAGAACTAGCGTTGAATTACGCATCGGATCCCTCCGA

AACAACCTCTCGGCTGTTAGCTATAATCGAACTATTGCTAATTGAATACACAGAAAGAAGTCGGTTATTCGT

CACCTGTCAATCTCGTCGCGACACGAACTCCGATTCCCCTCCTCCCCACCCACTCCCCGGCCCCACCAGCAT

CATCGTCGATTAAGTGCTGCCGGTGGGACGGTCTACTTCCGTGCAACTTGTTGAATTCGGTGCAAGTGTGGT

AGCAGCAGTGGTGCAGCTGAGGAAGAGCAGTGTTCGTGATTGAGAGAGTTAGCTGGGACTGCACCATGGCGA

CGATGGCTCAGGTGGTGTGGCTGGTTGTGTTGGGCCTCATGAGCCTGCTGCTTTGTGCCGAAGCGGGTTGGT

TGGGTAACCAGGGGTATCATGAGCAGTGGGTCCGCGCTCGCGGCACGTGGTACGGAGATCCTTACGGCGAAG

GGTCAAGCGGTGAGTTGATGCTACTCACGCTCCTGCAGCAATACTGTGTTGATCTGCACTGTGTCGATGAGT

AAATGGCAGCACTAGTCTTCTGACTTTCTTACTGATTTCTTTGTCCAGGTGGGAACTGCGGTTACACGAGGC

TCTAGGGCACTCCCATCGGTCCCAAGATTGTTGCCGGCAGTCGCTCGATCTACGCMAACGGGCTTGGTTGTG

GCCAATGCTACCAGAaTCAGTGCGTTGATCCCAGSCAMGGAMCCAAGCTCKGCAATtCCTTCRGSACaCAAK

TTGYCKTGaCCGATTTCTGCCCCGGTGGAaCWTACTGTAGCACTGGGGAGAATGCATTTGACATGAGCGGAG

CTGCCATCAATGCCATGGCGCTTCCGAGCAGAGAGGGCCAACTTCGCAACCGGGGCTTGTACAACCTCCTCT

ACAAGAGAGTGCCGTGCCGGTACAGAGGCACCARCATCCWATTSCGCGTCGACARMGGMTCCagcgCCTATT

GGCTGAGCaTTTTGATCAAGTACGTCGGGGGACCAGGCGACATTGGTCAGGTTTATATTAAGATGGCCAACT

GGTTTGCGTTTCAGCCAATGAAACATGCTTGGGGAGCCAACTGGATGATGCCTAGCTACGACGGGAAGCCGT

TCAAGGGCCCCATGGACATCAAGATTGTGTCGAAGCTGAACAGGCACTCCGTTGTTGCTAGAGGAGTCATTC

CCGGTTACTTCCGGCCCGGAACGACCTACAATTCTAGGGTGCAGATGGCTTTC

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SUPPLEMENTAL FIG. 6. *Physcomitrella* expansins isolated by degenerate PCR/TAIL-PCR. Nucleotide and amino acid sequence are given. Introns are marked in blue with their phase noted in red.

## *Physcomitrella patens* expansin *PpEXP5*

```
+1   M  A  I   P  W  S  S   V  V  L   V  T  L   V  S  L  M   A  C  A   E  A  K   G  S  S  F   M  G  S   D  W  G

  1 ATGGCCATTC CGTGGAGTAG CGTGGTGTTG GTGACTCTTG TTTCATTGAT GGCCTGCGCT GAGGCCAAGG GGAGCAGCTT CATGGGCAGC GACTGGGGGA

    TACCGGTAAG GCACCTCATC GCACCACAAC CACTGAGAAC AAAGTAACTA CCGGACGCGA CTCCGGTTCC CCTCGTCGAA GTACCCGTCG CTGACCCCCT


+1  R  A  H  A   T  F  Y  G   G  A   D  A  S  G   T  Q      INTRON #1 = 381 bp Phase = 1

101 GAGCCCATGC CACTTTCTAT GGTGGAGCTG ACGCTTCTGG TACTCAAGGT GGGTGCCAAG GCCGGTTACT TCGATCTTTG TGGCCACTGA CTTGAATGAG

    CTCGGGTACG GTGAAAGATA CCACCTCGAC TGCGAAGACC ATGAGTTCCA CCCACGGTTC CGGCCAATGA AGCTAGAAAC ACCGGTGACT GAACTTACTC


201 CGTGGTTGGC TCCAGCTACG GTGAAAGCGT TCGCGAGGTG TCCCGGTTGT GACTGTAGTT AACAGGAACG TATGTCATAA ATGTCTGTTA CCCTCATTGT

    GCACCAACCG AGGTCGATGC CACTTTCGCA AGCGCTCCAC AGGGCCAACA CTGACATCAA TTGTCCTTGC ATACAGTATT TACAGACAAT GGGAGTAACA


301 TGCGTGGTTG TCCGTGGCTA GCAAAGAATT CTTCTACTCT CCTGTAACGC CGTTTAGAAG CTCTGGCGCA GTTCTCGTTT TCAAGATTAG GTCCTCTGTA

    ACGCACCAAC AGGCACCGAT CGTTTCTTAA GAAGATGAGA GGACATTGCG GCAAATCTTC GAGACCGCGT CAAGAGCAAA AGTTCTAATC CAGGAGACAT


401 ATGCGAGTGT GACAGTACGA GTTTTCTGGT TAATATCGCT GATTTTCCTC TTTGTAGACA CGTACGTGCC CAACCCTACT CATGAGAGTG GTCGATTTCT

    TACGCTCACA CTGTCATGCT CAAAAGACCA ATTATAGCGA CTAAAAGGAG AAACATCTGT GCATGCACGG GTTGGGATGA GTACTCTCAC CAGCTAAAGA


+1                                 G   G  A  C   G  Y  G   N  L  Y  S   T  G  Y   G  T  N   T  A  A  L   S  S  S

501 GAGGTTGTGC ATTGTTAATG CTTCTGTAGG TGGAGCTTGT GGATACGGAA ATCTCTACAG CACTGGCTAC GGAACAAACA CAGCCGCACT GAGTTCTTCG

    CTCCAACACG TAACAATTAC GAAGACATCC ACCTCGAACA CCTATGCCTT TAGAGATGTC GTGACCGATG CCTTGTTTGT GTCGGCGTGA CTCAAGAAGC


+1   L  F  N   S  G  L  S   C  G  A   C  Y  E   L  T  C  D   P  S  G   S  Q  Y   C  L  P  G   G  S  A   I  I  T

601 TTGTTCAACT CCGGCCTCAG CTGCGGAGCC TGTTACGAGC TCACGTGCGA TCCATCCGGT TCTCAGTACT GCCTCCCAGG TGGTTCCGCT ATCATCACTG

    AACAAGTTGA GGCCGGAGTC GACGCCTCGG ACAATGCTCG AGTGCACGCT AGGTAGGCCA AGAGTCATGA CGGAGGGTCC ACCAAGGCGA TAGTAGTGAC
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```
  +1 A  T  N  F   C  P  T   G  S  N   G  G  W  C   N  P  P   K  Q  H   F  D  L  A   Q  P  V   F  S  K   I  A  R  T
 701 CAACAAACTT CTGTCCTACC GGTTCTAACG GAGGCTGGTG CAATCCACCC AAGCAGCACT TTGATTTGGC ACAACCTGTC TTTAGCAAGA TAGCTCGCAC
     GTTGTTTGAA GACAGGATGG CCAAGATTGC CTCCGACCAC GTTAGGTGGG TTCGTCGTGA AACTAAACCG TGTTGGACAG AAATCGTTCT ATCGAGCGTG

  +1   V  G  G   V  I  P   I  N  Y   R  R     INTRON #2 = 150 bp Phase = 2
 801 AGTGGGCGGC GTAATCCCTA TCAATTACAG AAGGTAGACC TTGACAATCC AGCCCTTCGT TCAAACGTAC GGCGTTTCGC TCCACATTCA TGTTAATGAC
     TCACCCGCCG CATTAGGGAT AGTTAATGTC TTCCATCTGG AACTGTTAGG TCGGGAAGCA AGTTTGCATG CCGCAAAGCG AGGTGTAAGT ACAATTACTG

  +1                                                                                              V  P   C  S  K
 901 TCTCTTTGAG ATGCTTTGGG TTTCTGGTTA GCTTCAATTT TGACACGTTT CTGAATCTGA TTTTCTGCTC TGTTGGCTGC CAGAGTGCCC TGCTCCAAGT
     AGAGAAACTC TACGAAACCC AAAGACCAAT CGAAGTTAAA ACTGTGCAAA GACTTAGACT AAAAGACGAG ACAACCGACG GTCTCACGGG ACGAGGTTCA

  +1 S  G  G  M   R  F  T   V  N  G   N  P  Y  F   L  L  V   L  V  T   N  V  G  G   A  G  D   V  Q  Q   L  Y  I  K
1001 CTGGAGGCAT GAGGTTCACC GTGAATGGAA ACCCCTACTT TCTGCTGGTG CTCGTCACAA ACGTCGGAGG GGCTGGTGAT GTCCAGCAAT TGTACATCAA
     GACCTCCGTA CTCCAAGTGG CACTTACCTT TGGGGATGAA AGACGACCAC GAGCAGTGTT TGCAGCCTCC CCGACCACTA CAGGTCGTTA ACATGTAGTT

  +1   G  A  S   T  G  W   L  P  L  K   R  N  W   G  Q  M   W  Q  F  T   G  N  S   G  M  H   G  Q  A  I   S  F  K
1101 GGGTGCCAGC ACTGGCTGGC TACCCTTGAA GCGCAACTGG GGGCAGATGT GGCAGTTTAC CGGCAACAGT GGCATGCATG GCCAAGCCAT CTCCTTCAAG
     CCCACGGTCG TGACCGACCG ATGGGAACTT CGCGTTGACC CCCGTCTACA CCGTCAAATG GCCGTTGTCA CCGTACGTAC CGGTTCGGTA GAGGAAGTTC

  +1  A  V  T   S  D  G  A   E  A  I   S  P  N   V  A  P  A   N  W  G   F  G  Q   T  F  E  G   S  N  F
1201 GCTGTCACCA GCGATGGCGC TGAGGCCATA TCCCCAAATG TAGCTCCAGC CAACTGGGGC TTCGGACAGA CTTTCGAGGG CTCCAACTTT
     CGACAGTGGT CGCTACCGCG ACTCCGGTAT AGGGGTTTAC ATCGAGGTCG GTTGACCCCG AAGCCTGTCT GAAAGCTCCC GAGGTTGAAA
```

## *Physcomitrella patens* expansin *PpEXPA6*

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  +1  M  P  S   I  S  S  F   E  K  N   A  D  F   K  G  S  S   F  S  T   E  T  T   L  S  T  D   D  Q  P   D  E  V
   1 ATGCCATCCA TCTCGAGTTT CGAAAAGAAC GCAGATTTCA AGGGATCTTC TTTCAGCACG GAGACCACTC TGAGCACGGA TGACCAACCA GATGAGGTTT
     TACGGTAGGT AGAGCTCAAA GCTTTTCTTG CGTCTAAAGT TCCCTAGAAG AAAGTCGTGC CTCTGGTGAG ACTCGTGCCT ACTGGTTGGT CTACTCCAAA

  +1 F  A  R  K   A  G  Y   A  P  V   P  R  S  Y   G  G  V   W  R  N   A  R  S  T   F  Y  G   G  M  D   A  A  G  T
```

```
101 TTGCCAGAAA GGCCGGGTAT GCTCCAGTTC CTAGGAGCTA TGGTGGAGTG TGGAGGAACG CAAGGTCTAC CTTCTACGGT GGAATGGATG CTGCGGGAAC
    AACGGTCTTT CCGGCCCATA CGAGGTCAAG GATCCTCGAT ACCACCTCAC ACCTCCTTGC GTTCCAGATG GAAGATGCCA CCTTACCTAC GACGCCCTTG

 +1   M    INTRON #1 = 159 bp Phase = 1
201 CATGTGTAAG TTTTTATTTG GAATACGCCT GCAAGGATTC CATTGTCTTC GCCTTCATTA GTGTAAGGTT TGGATGTCGG CTTTCATTGT TTTCCCTTGT
    GTACACATTC AAAAATAAAC CTTATGCGGA CGTTCCTAAG GTAACAGAAG CGGAAGTAAT CACATTCCAA ACCTACAGCC GAAAGTAACA AAAGGGAACA

 +1                                                                       S  G   A  C  G  Y   G  N  L   Y  A  S
301 GGAGGTGTAG TTTTTTTAGT ACGTACTGCG TGCGATTATC TTACTATGGT GCATGTTGAT GCAGCGGGAG CTTGTGGATA TGGCAATTTG TACGCTTCTG
    CCTCCACATC AAAAAAATCA TGCATGACGC ACGCTAATAG AATGATACCA CGTACAACTA CGTCGCCCTC GAACACCTAT ACCGTTAAAC ATGCGAAGAC

 +1 G  Y  G  V   H  T  T   A  L  S   S  A  L  F   K  N  G   M  A  C   G  A  C  F   E  V  Q   C  G  G   K  G  K  P
401 GGTACGGTGT GCACACCACT GCGTTGTCCT CAGCGTTGTT CAAGAACGGA ATGGCTTGCG GCGCTTGTTT CGAGGTGCAG TGCGGTGGGA AGGGAAAGCC
    CCATGCCACA CGTGTGGTGA CGCAACAGGA GTCGCAACAA GTTCTTGCCT TACCGAACGC CGCGAACAAA GCTCCACGTC ACGCCACCCT TCCCTTTCGG

 +1   C  K  P   G  S  V   V  V  T  A   T  N  F   C  P  P   N  P  G  Q   S  A  N   N  G  G   W  C  N  P   P  N  E
501 CTGCAAACCT GGATCTGTGG TTGTGACCGC CACCAACTTC TGCCCACCCA ATCCAGGACA GAGTGCGAAC AATGGAGGAT GGTGCAATCC TCCTAATGAG
    GACGTTTGGA CCTAGACACC AACACTGGCG GTGGTTGAAG ACGGGTGGGT TAGGTCCTGT CTCACGCTTG TTACCTCCTA CCACGTTAGG AGGATTACTC

 +1  H  F  D   L  S  Y  P   A  F  V   K  I  A   D  P  K  A   G  A  V   P  L  Q   Y  R  R INTRON #2 = 138 bp Phase
= 2
601 CACTTTGACC TTTCCTACCC CGCTTTCGTT AAAATCGCCG ATCCCAAGGC TGGAGCTGTG CCCCTGCAAT ACCGAAGGTT CGTGCTATTT GCCTTTAAAA
    GTGAAACTGG AAAGGATGGG GCGAAAGCAA TTTTAGCGGC TAGGGTTCCG ACCTCGACAC GGGGACGTTA TGGCTTCCAA GCACGATAAA CGGAAATTTT

701 ACTTTGTTTG CTGGCTTTGA CTGCTCTTTT TTTCCATCGT TATATTTCTC ACCTGGAAGT AGATGCAATG TTTCTTCTCA TGAACTAAAG TGGTATCCGA
    TGAAACAAAC GACCGAAACT GACGAGAAAA AAAGGTAGCA ATATAAAGAG TGGACCTTCA TCTACGTTAC AAAGAAGAGT ACTTGATTTC ACCATAGGCT

 +1                   V   P  C  Q  K   Q  G  G   I  R  F   T  I  N  G   N  C  N   F  I  L   V  T  I  T   N  V  G
801 TGTGTCTGCA TTCAGAGTGC CGTGCCAGAA GCAAGGAGGG ATTCGATTTA CTATTAATGG CAACTGCAAC TTCATCCTCG TGACCATCAC CAACGTCGGC
    ACACAGACGT AAGTCTCACG GCACGGTCTT CGTTCCTCCC TAAGCTAAAT GATAATTACC GTTGACGTTG AAGTAGGAGC ACTGGTAGTG GTTGCAGCCG

 +1  G  S  G   V  V  T  A   A  Y  L   K  G  D   K  T  E  W   S  P  L   S  R  N   W  G  A  N   W  Q  C   R  R  N
```

```
 901 GGTTCGGGAG TGGTGACTGC GGCGTACTTG AAGGGCGACA AGACAGAGTG GTCTCCGTTG TCAAGAAACT GGGGCGCGAA CTGGCAGTGC AGGCGCAATT

     CCAAGCCCTC ACCACTGACG CCGCATGAAC TTCCCGCTGT TCTGTCTCAC CAGAGGCAAC AGTTCTTTGA CCCCGCGCTT GACCGTCACG TCCGCGTTAA


  +1 Y  C  G  Q   G  I  S   I  K  I   V  T  S  D   N  K  V   S  V  T   K  L  A  K   S  D  W   C  F  G   K  T  F   I

1001 ACTGCGGTCA AGGTATCTCC ATCAAGATCG TCACCAGTGA CAACAAGGTT TCAGTCACGA AGCTAGCCAA ATCTGACTGG TGTTTCGGGA AGACCTTCAT

     TGACGCCAGT TCCATAGAGG TAGTTCTAGC AGTGGTCACT GTTGTTCCAA AGTCAGTGCT TCGATCGGTT TAGACTGACC ACAAAGCCCT TCTGGAAGTA


  +1   G  K  Q   V

1101 CGGAAAGCAA GTC

     GCCTTTCGTT CAG
```

SUPPLEMENTAL FIG. 7. Alignment of *Physcomitrella* EXPA sequences with selected *Arabidopsis*, rice and a *Populus* EXPA gene. Alignment made using the Clustal W algorithm as described in the Materials and Methods section.

```
  ------------------+-------------------+-------------------+-------------------+-------------------+-------------------+-

                    10                  20                  30                  40                  50                  60

  ------------------+-------------------+-------------------+-------------------+-------------------+-------------------+-

1 W K E A H A T F Y E G - - - - G S G T F - - - - G - - - G - A C N Y K D V A G Q G Y G M N T A A L S S V L F K N G Q A C  PtEXPA26

1 W K I A T A T L S R D R D G S S S V A T - - - - G - - - G - A C G Y G D L R Q S S F A G Y S A G L S G K L F N R G S S C  AtEXPA20

1 W R P A R A T Y Y A A T N - - P R D A V - - - - G - - - G - A C G Y G D L V K S G Y G M A T V G L S E T L F E R G Q I C  AtEXPA13

1 W I R A H A T Y Y G V N D - - S P A S L - - - - G - - - G - A C G Y D N P Y H A G F G A H T A A L S G E L F R S G E S C  AtEXPA12

1 W V N A R A T F Y G G A D - - A S G T M - - - - G - - - G - A C G Y G N L Y S Q G Y G T N T A A L S T A L F N G G Q S C  AtEXPA14

1 W V N A H A T F Y G G S D - - A S G T M - - - - G - - - G - A C G Y G N L Y S Q G Y G T N T A A L S T A L F N N G L S C  AtEXPA15

1 W Q G G H A T F Y G G E D - - A S G T M - - - - G - - - G - A C G Y G N L Y G Q G Y G T N T A A L S T A L F N N G L T C  AtEXPA8

1 W Y D A R A T F Y G D I H - - G G D T Q - - - - P - - - - - - C G Y G N L F R Q G Y G L A T A A L S T A L F N D G Y T C  AtEXPA22

1 W Q N A H A T F Y G G S D - - A S G T M - - - - G - - - G - A C G Y G N L Y S Q G Y G T N T A A L S T A L F N N G M S C  AtEXPA4

1 L T N G H A T F Y G G S D - - A S G T M - - - - G - - - G - A C G Y G D L Y S A G Y G T M T A A L S T A L F N D G A S C  AtEXPA11

1 W L Q A H A T F Y G G S D - - A S G T M - - - - G - - - G - A C G Y G N L Y T D G Y K T N T A A L S T A L F N D G K S C  AtEXPA17

1 W R Y A H A T F Y G D E T - - G G E T M - - - - G - - - G - A C G Y G N L F N S G Y G L S T A A L S T T L F N D G Y G C  AtEXPA7

1 W R M G S A T Y I K E S L G H P L N D G - - - - G - - - G - A C G Y G D L D I F R Y G R Y T A G V S G A L F G R G S A C  OsEXPA16

1 W R S A K A S Y Y A A D - - - P E D A I - - - - G - - - G - A C G F G D L G K H G Y G M A T V G L S T A L F E R G A A C  OsEXPA10
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1  W S S A H A T F Y G G G D - - A S G T M - - - - G - - - G - A C G Y G N L Y S Q G Y G T N T A A L S T A L F N N G L S C  OsEXPA5

1  W S S G S A T F Y G G S D - - A S G T M - - - - G - - - G - A C G Y G N L Y S A G Y G T S T A A L S T A L F N N G Q S C  OsEXPA11

1  W Q S A H A T F Y G G G D - - A S G T M - - - - G - - - G - A C G Y G N L Y S Q G Y G T N T A A L S T A L F N D G A A C  OsEXPA4

1  W K Q A H A T F Y G G R D - - G S G T L - - - - D - - - G - A C G Y K D T S K E G Y G V Q T V A V S T P L F G A G A G C  OsEXPA32

1  W Q S A H A T F Y G G S D - - A S G T M - - - - G - - - G - A C G Y G N L Y S Q G Y G V N N A A L S T A L F N S G Q S C  OsEXPA7

1  W T P A T A T F Y G G S D - - G A G T M - - - - G - - - G - A C G Y G N L Y N A G Y G L N N A A L S S A L F N D G A M C  OsEXPA33

1  W T P A H A T F Y G D E T - - A S E T M - - - - G - - - G - A C G Y G N L Y A S G Y G T D T A A L S T T L F K D G Y G C  OsEXPA30

1  - L S G T A T F Y G G S D - - A S G T M - - - - G - - - G - A C G Y G N L Y S T G Y G T N T A A L S S A L F N D G A A C  OsEXPA12

1  W R K A H A T F Y G G A D - - A S G T M - - - - G - - - G - A C G Y G N L Y S T G Y G V D S T A L S T A L F N N G A K C  PpEXPA1

1  W K E A H I T Y Y G T A N - - G G G T Q - - - - G - - - G - A C G Y P N T F A M G Y G V M T A A L S Y P L F Q G G K S C  PpEXPA2

1  S G V A H A T F Y G G V D - - A Q G T Q - - - - G - - - G - A C G Y G N L Y S T G Y G T S T T A L S S A L F N A G L S C  PpEXPA3

1  W K D A H I T Y Y G S P N - - G G G T Q - - - - G - - - G - A C G Y Q N T Y A L G Y G S F T A A L S A P L F Q G G A A C  PpEXPA4

1  W G R A H A T F Y G G A D - - A S G T Q - - - - G - - - G - A C G Y G N L Y S T G Y G T N T A A L S S S L F N S G L S C  PpEXPA5

1  W R N A R S T F Y G G M D - - A A G T M - - - - S - - - G - A C G Y G N L Y A S G Y G V H T T A L S S A L F K N G M A C  PpEXPA6

1  W T D A H A T F Y G G A D - - A S G T Q G G C A G - - - G - A C G F G N L Y S T G Y G T N T A A L S Q A L F N S G L T C  PpEXPA9

1  W G R A H A T Y Y G G A D - - A S G T Q - - - - G - - - G - A C G F G N L Y S S G Y G T D T A A L S S A L F N S G L S C  PpEXPA11

1  W N D A H A T Y Y G G A D - - A S - - - - - - - G - - - G - A C G F G N L Y S T G Y G T S T A A L S Q A L F N S G L T C  PpEXPA12

1  W N E A R A T F Y G G S D - - A G G T T - - - - G - - - G - A C G Y G D L Y S T G Y G T N T V A T S S A I F D R G L A C  PpEXPA13

1  W D K G H A T Y Y G E G D - - A R G T M - - - - G - - - G - A C G Y S N L Y S T G Y G V N T A A L S G P L F N G G A T C  PpEXPA14

1  W G Y A H A T Y Y G G A D - - A S G T Q - - - - G - - - G G A C G F G N L Y S T G Y G T N T A A L S A A L F N S G L S C  PpEXPA15

1  W D T A H A T Y Y G G R D - - A G G T M - - - - G - - - G - A C G Y G N L Y N T G Y G V K T A A L S A P L F K G G A T C  PpEXPA16
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1  W G R A H A T Y Y G G A D - - A S G T Q - - - - G - - - G - A C G F G N L Y S S G Y G T S T A A L S S S L F N S G L S C  PpEXPA17

1  W N E A H I T Y Y G T A N - - G G G T Q - - - - G - - - G - A C G Y P N T F A M G Y G A M T A A L S Y P L F Q G G K A C  PpEXPA18

1  W G D A H I T Y Y G S P N - - G A G T E - - - - G - - - G - A C G Y Q N T Y K L G Y G S M T A A L S S R L F Q G G K A C  PpEXPA19

1  W K D A H I T Y Y G S P N - - G G G T Q - - - - G - - - G - A - - Y Q N T Y A L G Y - P L T A A L S S P L F Q G G A A C  PpEXPA20

1  - R D A H I T Y Y G S P N - - G G G T E - - - - G - - - G - A C G Y Q N T Y S L G Y G F M T A A L S S S L F Q G G S S C  PpEXPA21

1  W Q D A H I T Y Y G S P N - - G G G T Q - - - - G - - - G - A C G Y Q N T V S L G Y G F M T A A L S S P L F Q G G K A C  PpEXPA22

1  W I N G R I T Y Y G S P N - - G G G T Q - - - - G - - - G - A C G Y Q N T V S L G Y G F M T A A L S T T L F K G G A A C  PpEXPA23

1  W S S G R I T Y Y G S P N - - G G G T Q - - - - G - - - G - A C G Y Q N T V S L G Y G F M T A A L S T P L F N G G A A C  PpEXPA24

1  W R D A H I T Y Y G S P N - - G G G T Q - - - - G - - - G - A C A Y Q N T F S L G Y G A M T A A L S S P L F E G G A A C  PpEXPA25

1  W N F G R I T Y Y G S P N - - G G G T Q - - - - G - - - G - A C G Y Q N T F A L G Y G T N T A A L S S R L F Q G G A A C  PpEXPA26

1  W A T A T A T F Y G G A D - - A G - - - - - - - G - - - G - A C G Y G N L Y S T G Y G A S T T A L S A P L V N G G S A C  PpEXPA27

1  W G Y A H A T Y Y A G A D - - A S G T Q - - - - G - - - G G A C G F G N L Y S T G Y G T N T A A L S A A L F N S G L S C  PpEXPA7

1  W N E A H A T F Y G G S D - - A G G T T - - - - G T R G G - A C G Y G D L Y S T G Y G T S T V A I S S A L F D R G L A C  PpEXPA8

1  S G R A H A T F Y G G A D - - A S G T Q - - - - G - - - G - A C G Y G N L Y S T G Y G T S T A A L S S A L F N S G L S C  PpEXPA10
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                     70                  80                  90                  100                 110                 120
   ------------------+-------------------+-------------------+-------------------+-------------------+-------------------+-
49 G A C F E I K C A D N P - - - - - - - - - Q W C K L G Q P S L I V T A T D H C P P N P S L P N D - - N G G W C N V P R E  PtEXPA26
53 G A C L E V R C V N H I - - - - - - - - - R W C L Q G S P S V V V T A T D F C P P N S G L S S D - - Y G G W C N F P K E  AtEXPA20
51 G A C F E L R C V D D L - - - - - - - - - R W C I P G T - S I I L T A T N F C A P N Y G F D P D - - G G G H C N P P N K  AtEXPA13
51 G G C Y Q V R C D F P A - D - - - - - - P K W C L R G A - A V T V T A T N F C P - - - - - T N N - - N N G W C N L P R H  AtEXPA12
51 G A C F Q I K C V D D P - - - - - - - - - K W C I G G - - T I T V T G T N F C P P N F A Q A N N - - A G G W C N P P Q H  AtEXPA14
51 G A C F E I K C Q S D G - - - - - - - - - A W C L P G - - A I I V T A T N F C P P N N A L P N N - - A G G W C N P P L H  AtEXPA15
51 G A C Y E M K C N D D P - - - - - - - - - R W C L G S - - T I T V T A T N F C P P N P G L S N D - - N G G W C N P P L Q  AtEXPA8
49 G A C Y E I M C T R D - - - - - - - - - P Q W C L P G S - - V K I T A T N F C P A N Y S K T T D - - - - L W C N P P Q K  AtEXPA22
51 G A C F E L K C A N D P - - - - - - - - - Q W C H S G S P S I L I T A T N F C P P N L A Q P S D - - N G G W C N P P R E  AtEXPA4
51 G E C Y R I T C D H A A - D - - - - - - S R W C L K G A - S V V I T A T N F C P P N F A L P N N - - N G G W C N P P L K  AtEXPA11
51 G G C Y Q I L C D A T K - V - - - - - - P Q W C L K G K - S I T I T A T N F C P P N F A Q A S D - - N G G W C N P P R P  AtEXPA17
51 G Q C F Q I T C S K S - - - - - - - - - P - H C Y S G K - S T V V T A T N L C P P N W Y Q D S N - - A G G W C N P P R T  AtEXPA7
53 G G C Y E V R C V N H V - - - - - - - - - L W C L R G S P T V V V T A T D F C A P N L G L S D D - - Y G G W C N F P K E  OsEXPA16
50 G G C Y E V K C V D D L - - - - - - - - - K Y C L P G T - S I V V T A T N F C A P N F G L P A D - - A G G V C N P P N H  OsEXPA10
51 G A C F E V R C D A G G G G - - - - - - S H S C L P G - - S V V V T A T N F C P P N N A L P S D - - D G G W C N P P R A  OsEXPA5
51 G A C F E V R C G G G G - - - - - - - - - - S C L A G - - T V A V T A T N L C P P N Y A L A G D - - A G G W C N P P R P  OsEXPA11
51 G S C Y E L R C D N A G - - - - - - - - S - S C L P G - - S I T V T A T N F C P P N Y G L P S D - - D G G W C N P P R P  OsEXPA4
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51  G A C Y E V K C V D S P - - - - - - - - - D G C K V G A A P L V V T A T N L C P P N P G Q S N D - - N G G W C N P P R E  OsEXPA32

51  G A C F E I K C V N Q P G - - - - - - - W E W C H P G S P S I L I T A T N F C P P N Y A L P S D - - N G G W C N P P R P  OsEXPA7

51  G A C Y T I A C D T S - - Q - - - - - - S T W C K P G T - S I T I T A T N L C P P N Y A K K S D - - A G G W C N P P R K  OsEXPA33

51  G T C Y Q M R C V G T - - - - - - - - - A - S C Y R G S P A I T V T A T N L C P P N W A E D P D R G G G G W C N P P R A  OsEXPA30

50  G E C Y Q I T C D Q S - - N - - - - - - S K W C K A G T - S V T I T A T N L C P P D Y S K P S N - - D G G W C N P P R Q  OsEXPA12

51  G A C F A I Q C Y R S Q - - - - - - - - - - Y C V P G S P V I T V T A T N F C P P N H K - G D G - - T P G W C N P P M R  PpEXPA1

51  G A C Y Q L K C K W L A P T R T - - - V H N W C W S Y S R T I T I T A T N S C P P G - - - - S H - - - G G W C D W - K P  PpEXPA2

51  G A C F E L K C D S A N - - - - - - - - S K Y C L P G D K S I T V T A T N Y C P Q G - - - - S D - - - G G W C D S P K Q  PpEXPA3

51  G G C Y Q L K C A P V R E T R T - - - V H N W C W S Y S R S I V V T A T N L C P P G - - - - S H - - - G G W C A W - R P  PpEXPA4

51  G A C Y E L T C D P S C - - - - - - - - S Q Y C L P G G - S A I I T A T N F C P T G - - - - S N - - - G G W C N P P K Q  PpEXPA5

51  G A C F E V Q C G G K G - - - - - - - - - K P C K P G S - - V V V T A T N F C P P N P G Q S A N - - N G G W C N P P N E  PpEXPA6

55  G A C F E L V C D S S G - - - - - - - - S R Y C V T S S - S V V V T A T N F C P T G - - - - S T - - - G G W C D Y P R Q  PpEXPA9

51  G A C Y E L T C D P S G - - - - - - - - S K F C I P G G - S A I I T V T N F C P T G - - - - S N - - - G G W C N P P K Q  PpEXPA11

48  G A C F E L A C D P S G - - - - - - - - S K Y C Y K G S - S I V V T A T N F C P S G - - - - S E - - - G G W C D S P K Q  PpEXPA12

51  G A C Y Q V K C A G S A - - - - - - - - - S E C Q P G T P A I Q V T V T N F C P P N P S L P E G - - N G G W C N L P L H  PpEXPA13

51  G A C Y E L T C I L N E - - - - - - - - S K W C Y R G K - N I I V T A T N F C P S G - - - - S T - - - G G W C N P P Q K  PpEXPA14

52  G S C Y E L A C D P N G - - - - - - - - S K Y C L P G G R T V T V T A T N F C P H G - - - - S L - - - G G W C D S P K Q  PpEXPA15

51  G A C Y E L T C I L S Q - - - - - - - - S K Y C Y Q N K - K I L I T A T N F C P T G - - - - S T - - - G G W C N P P R K  PpEXPA16

51  G A C Y E L T C D P S G - - - - - - - - S Q Y C L P G G - S A I I T V T N F C P T G - - - - S N - - - G G W C N P P R Q  PpEXPA17

51  G G C Y Q L R C K W V T P T R T - - - V H N W C W S Y S R T I T V T A T N S C P P G - - - - S H - - - G G W C N W - R P  PpEXPA18

51  G G C Y Q L R C A P N R G - - - - - - - R N W C W S Y A R A I V V T A T N L C P Q G - - - - S H - - - G G W C D Y P K S  PpEXPA19
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48  E S C Y Q L K C A L V R A S - I - - - A R N W C W N Y F R T I V V T A T N L C P R G - - - - S H - - - G G W C D Y - R P  PpEXPA20
50  G A C Y Q I R C E P I R V T R T - - - V K N W C W S Y S R T I T V T A I N L C P P R - - - - S S - - - G G C C N P P L Q  PpEXPA21
51  G A C F Q L Q C A R V Q E T R T - - - V K N W C H D Y S K A I T V T A T N L C P P G - - - - S E - - - G T W C D P P R H  PpEXPA22
51  G A C Y Q L Q C A P V S E T P S G L L K R N W C W Q V G R S I L V T A T N L C P P G - - - - S S - - - G G W C N P P Q H  PpEXPA23
51  G A C Y Q L Q C A P V H E T P K N L L Q R N W C W K V G R R I T I T A T N L C P P G - - - - S E - - - G G W C D P P Q H  PpEXPA24
51  G A C Y Q L Q C K R V Q E T R T - - - V K N W C W S Y S R T I T I T A T N L C P P G - - - - S A - - - G A W C D P P R H  PpEXPA25
51  G A C Y Q L R C I A P K W G - - - - - - K N W C W N Y A R S I V V T A T N L C P S G - - - - S N - - - G G W C P S - Q A  PpEXPA26
48  G A C Y Q L Q C A R - - - - - - - - - - S N H C Y A G R - S I T V T A T N F C P T G - - - - S E - - - G G W C N P P R K  PpEXPA27
52  G S C Y E L A C D P N G - - - - - - - - S K Y C L P G G P T V T V T A T N F C P H G - - - - S L - - - G G W C D A P K Q  PpEXPA7
54  G A C Y Q V K C A G S S - - - - - - - - - S E C R S D S P A I Q V T V T N F C P P N P S L P E D - - N G G W C N L P L H  PpEXPA8
51  G A C Y E L T C D T S G - - - - - - - - S K Y C L P G N P S I I L T A T N Y C P Q N - - - - S N - - - G G W C D A P K Q  PpEXPA10
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                      130                 140                 150                 160                 170                 180

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 98 H F D V A K P V F S Q L A E Y - E A G I I P I Q Y R R V P C Q K Q G G I R F T I L G N P W F Y Q V I V W N V G G A G D V  PtEXPA26

102 H L E L S H A A F T G I A E T - R A E M I P I Q Y R R V K C G R R G G L R F S L S G S S H F F Q V L I S N V G L D G E V  AtEXPA20

 99 H F V L P I E A F E K I A I W - K A G N M P V Q Y R R I N C R K E G S M R F T V D G G G I F I S V L I T N V A G S G D I  AtEXPA13

 96 H F D M S S P A F F R I A R R G N E G I V P V F Y R R V G C K R R G G V R F T M R G Q G N F N M V M I S N V G G G G S V  AtEXPA12

 98 H F D L A Q P I F L R I A Q Y - K A G V V P V Q Y R R V A C R R K G G I R F T I N G H S Y F N L V L I T N V A G A G D V  AtEXPA14

 98 H F D L S Q P V F Q R I A Q Y - K A G V V P V S Y R R V P C M R R G G I R F T I N G H S Y F N L V L V T N V G G A G D V  AtEXPA15

 98 H F D L A E P A F L Q I A Q Y - R A G I V P V S F R R V P C M K K G G I R F T I N G H S Y F N L V L I S N V G G A G D V  AtEXPA8

 94 H F D L S L A M F L K I A K Y - K A G V V P V R Y R R I P C S K T G G V K F E T K G N P Y F L M V L I Y N V G G A G D I  AtEXPA22

100 H F D L A M P V F L K I A Q Y - R A G I V P V S Y R R V P C R K R G G I R F T I N G H R Y F N L V L I T N V A G A G D I  AtEXPA4

101 H F D M A Q P A W E K I G I Y - R G G I V P V V F Q R V S C Y K K G G V R F R I N G R D Y F E L V N I Q N V G G A G S I  AtEXPA11

101 H F D M A Q P A F L T I A K Y - K A G I V P I L Y K K V G C R R S G G M R F T I N G R N Y F E L V L I S N V A G G G E I  AtEXPA17

 98 H F D M A K P A F M K L A Y W - R A G I I P V A Y R R V P C Q R S G G M R F Q F Q G N S Y W L L I F V M N V G G A G D I  AtEXPA7

102 H F E M S E A A F L R V A K A - K A D I V P V Q F R R V S C D R A G G M R F T I T G G A S F L Q V L I T N V A A D G E V  OsEXPA16

 98 H F L L P I Q S F E K I A L W - K A G V M P I Q Y R R V N C L R D G G V R F A V A G R S F F L T V L I S N V G G A G D V  OsEXPA10

101 H F D M S Q P V F Q R I A L F - K A G I V P V S Y R R V A C Q K K G G I R F T I N G H S Y F N L V L V T N V G G A G D V  OsEXPA5

 97 H F D M A E P A F T R I A Q A - R A G V V P V Q Y R R V A C A K Q G G I R F T I T G H S Y F N L V L V T N V G G A G D V  OsEXPA11

 98 H F D M A E P A F L H I A Q Y - R A G I V P V S F R R V P C V K K G G V R F T V N G H S Y F N L V L V T N V A G A G D V  OsEXPA4
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100  H F D L S M P A F L Q I A Q E - K A G I V P I S Y R R V P C V K V G G I R Y T I T G N P Y F N L V M V S N V G G A G D V  OsEXPA32
102  H F D L A M P M F L H I A E Y - R A G I V P V S Y R R V P C R K K G G V R F T I N G F R Y F N L V L I T N V A G A G D I  OsEXPA7
100  H F D M S Q P A W T S I A I Y - Q A G I V P V N F K R V P C Q K S G G I R F T I S G R D Y F E L V T V F N V G G S G V V  OsEXPA33
101  H F D L S K P A F M R M A D W - R A G I V P V M Y R R V P C A R A G G L R F A L Q G N P Y W L L A Y V M N V A G A G D V  OsEXPA30
 99  H F D M A Q P A W E Q I G V Y - R G G I V P V N F Q R V S C T R K G G V R F T I N G N S Y F E L V L I T N V G G P G S I  OsEXPA12
 98  H F D L A Q P S F T K I A K Y - R A G I V P V L F R R V P C E K K G G V R F T I N G N K Y F N L V L V H N V G G K G D V  PpEXPA1
100  H F D L P M P A F M T L A R R - E G G V A P V Y Y R K V R C A K R G G I R F T L G G N P Y F M M I L I H N V G G A G D L  PpEXPA2
 96  H F D L S H P M F T S L A Q E - V G G V I P V T Y R R A P C A K K G G M R F T I N G N P W F V M I L V T N C G G A G D V  PpEXPA3
100  H F D L P M P A F T S L A K Q - V G G V A P V F Y R R V R C A K R G G V R F T I G G N P Y F L M V L I H N V G G A G D I  PpEXPA4
 95  H F D L A Q P V F S K I A R T - V G G V I P I N Y R R V P C S K S G G M R F T V N G N P Y F L L V L V T N V G G A G D V  PpEXPA5
 98  H F D L S Y P A F V K I A D P - K A G A V P L Q Y R R V P C Q K Q G G I R F T I N G N C N F I L V T I T N V G G S G V V  PpEXPA6
 99  H F D L S Q P V F T R I A Q P - V G G V V T L K Y R R V R C Q K S G G I R F T I T G N P Y F I L V L V T N V G G A G D V  PpEXPA9
 95  H F D L A Q P V F R K I A R T - V G G V V P I N Y R R V S C L K D G G M R F T V N G N P Y F L L V L V T N V G G A G D V  PpEXPA11
 92  H F D L S Q P V F N K I A Q Q - A G G V I P V K Y R R V P C R K S G G M R F T I N G N P Y F I L V L V T N V G G A G D V  PpEXPA12
100  H F D M A M P A F Q Q I A S Y - R V G I V P I L Y R R A S C V R T G G I R F T M S G H K F M N L V L V T N V G G M G D V  PpEXPA13
 95  H F D L S E P M F T T L A N R - V G G V I P V N F R R V A C Y K Q G G M R F T I N G N P Y F F I V L V Y N V A G A G D V  PpEXPA14
 97  H F D L A H P M F V T L A K E - V G G V I P I K F R R V P C V K S G G M H F T I N G N P W F L L V L V T N V A G A G D L  PpEXPA15
 95  H F D L S E P M F T T L A N R - V G G V I P V N F R R V H C Y K K G G M R F T I N G N P Y H M M V L V Y N V A G A G D V  PpEXPA16
 95  H F D L A Q P V F S K I A R T - V G G V I P I N Y R R V S C L K S G G M R F T V N G N P Y F L L V L V T N V G G A G D V  PpEXPA17
100  H F D L P M P A F L T L A R R - E G G V A P V Y Y R K V R C A K R G G I R F T I G G N P Y F L M I L I H N V G G A G D L  PpEXPA18
 97  H F D L P M P A F T S L A R R - E G G V A P V W Y R K V R C A K R G G V R F T I G G N P W F L M V L I H N V G G A G D V  PpEXPA19
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 96  H F D L P M P A F T A L A R R - E G G V A P V F Y R R V K C V K R G G V R F T I G G N P Y F T M I L I D N V G G A G D I  PpEXPA20
100  H F D L P M P A F L S L A R R - E G G V A P V Y T - K V R S E K R G G I R F T M G G N L W F L T I L I H N V G G A G D V  PpEXPA21
101  H F D L P M P A F L S L A R Q - E G G V A P V Y Y R R V Q C L K K G G I R F T M G G N P W F L M V L V H N V A G A G D V  PpEXPA22
104  H F D L P M P A F L A L A R R - E G G V V P V Y Y R K V N C A R K G G I R F T V G G N P W F L M I L I H N V G G A G D V  PpEXPA23
104  H F D L P M P A F T A L A K R - E G G V V P I Y Y R R V R C A K Q G G I R F T M G G N P W F L M I L I H N V A G A G D V  PpEXPA24
101  H F D L T M P A F L T L A R R - E G G V A P V L Y R R V K C V K R G G I R F T I G G N P W F L M I L I H N V A G A G D V  PpEXPA25
 97  H F D W P M P A F T S L A R K - E G G V T P I M Y R R V R C A R R G G I R F T I G G N P F F L M V L I H N V G G A G D V  PpEXPA26
 90  H F D L S M P M F T T L A R Q - V A G V V P V D Y R R V A C N K K G G Q R F L M T G N P Y F I M V L V Y N V A G A G D V  PpEXPA27
 97  H F D L A H P M F V S L A R E - V G G V I P I K Y R R V P C V K S G G M R F T I N G N P W F L L V L V T N V A G A G D V  PpEXPA7
103  H F D M S M P A F E Q I A T Y - K A G I V P V M Y R R T S C V R T G G I H F T M S G H N F M N L V L V T N V G G M G D V  PpEXPA8
 96  H F D L A H P M F V S L A E E - R G G V I P V N Y R R V P C A K K G G M R F Q M N G N P W F L L V L V T N V G G A G D V  PpEXPA10
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                       190                 200                 210                 220                 230                 240

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157  V G V Q V K - G D D K L K W T Q M E R D W G T T W K T S A I - - - L L G E S L S F R V S A - S D D R D S T S W H V T P K  PtEXPA26

161  V G V K V K - G H - T T A W I P M A R N W G Q N W H S S L D - - - L I G Q S L S F E V T L - K G G K T I A S Y D V A P P  AtEXPA20

158  A A V K I K - G S - R T G W L P M G R N W G Q N W H I N A D - - - L R N Q A L S F E V T S - S D R S T V T S Y N V S P K  AtEXPA13

156  R S V A V R - G S K G K T W L Q M T R N W G A N W Q S S G D - - - L R G Q R L S F K V T L - T D S K T Q T F L N V V P S  AtEXPA12

157  I S V S I K - G T N T R - W Q S M S R N W G Q N W Q S N A K - - - L D G Q A L S F K V T T - S D G R T V I S N N A T P R  AtEXPA14

157  H S V A V K - G S R T R - W Q Q M S R N W G Q N W Q S N N L - - - L N G Q A L S F K V T A - S D G R T V V S N N I A P A  AtEXPA15

157  H A V S I K - G S K T Q S W Q A M S R N W G Q N W Q S N S Y - - - M N D Q S L S F Q V T T - S D G R T L V S N D V A P S  AtEXPA8

153  K Y V Q V K - G N K T G - W I T M K K N W G Q N W T T I T V - - - L T G Q G L S F R V T T - S D G I T K D F W N V M P K  AtEXPA22

159  V R A S V K - G S R - T G W M S L S R N W G Q N W Q S N A V - - - L V G Q A L S F R V T G - S D R R T S T S W N M V P S  AtEXPA4

160  K S V S I K - G S K T G - W L A M S R N W G A N W Q S N A Y - - - L D G Q A L S F S I T T - T D G A T R V F L N V V P S  AtEXPA11

160  S K V W I K - G S K S N K W E T M S R N W G A N Y Q S N T Y - - - L N G Q S L S F K V Q L - S D G S I K A A L N V V P S  AtEXPA17

157  K S M A V K - G S R T N - W I S M S H N W G A S Y Q A F S S - - - L Y G Q S L S F R V T S Y T T G E T I Y A W N V A P A  AtEXPA7

161  A A V K V K - G S - R T G W I P M G R N W G Q N W Q C D A D - - - L R G Q P L S F E V T G - G R G R T V V A Y S V A P P  OsEXPA16

157  R S V K I K - G T - E S G W L S M G R N W G Q I W H I N S D - - - F R G Q P L S F E L T S - S D G K T L T N Y N V V P K  OsEXPA10

160  H A V A V K - S E R S A A W Q A L S R N W G Q N W Q S A A L - - - L D G Q A L S F R V T T - G D G R S V V S N N A V P R  OsEXPA5

156  T A V S V K - G S R - S G W Q A M S H N W G A N W Q N G A N - - - L D G Q P L S F R V T A - S D G R T V T S D N V A P S  OsEXPA11

157  R S V S I K - G S R - T G W Q P M S R N W G Q N W Q S N A F - - - L D G Q S L S F Q V T A - S D G R T V T S N N V A H P  OsEXPA4
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159  A G L S V K - G N K R V K W T P L K R N W G Q E W Q T S E V - - - L T G E S L T F R V M T - G D H R K A T S W H V L P P  OsEXPA32

161  V R A S V K - G T S - T G W M P M S R N W G Q N W Q S N S V - - - L V G Q A L S F R V T G - S D R R T S T S W N A A P A  OsEXPA7

159  A Q V S I K - G S K T D - W M A M S R N W G Q N W Q S N A Y - - - L N T Q S L S F K V K L - D D A R E V T V W N I A P S  OsEXPA33

160  G D M W V K A G G G G G - W V R M S H N W G A S Y Q A F A Q - - - L G G Q A L S F K V T S Y T T G Q T I L A A G V T P A  OsEXPA30

158  K S V Q I K - G T K T G - W V T M S R N W G A N W Q A N N Y - - - L N N Q A I S F S V T S - T A G K T L V F E D V A P S  OsEXPA12

157  H A V D I K - G S N - T E W I P M K R N W G M N W Q T D A V - - - M T G Q A L S F R V T T - S D G K T I V S M N A T P S  PpEXPA1

159  R A V K I K - G R - N G Y W V P M W Q N W G A L W T C K T K - - - L S G - A L S F Q I T T - G D G R T V T V N R A - - V  PpEXPA2

155  Q Q L Q I R - G S - D T P W Y P C V R N W G Q M W Q M T S D P N - L P G K A L S F R A T L - S D G S V A E S L N A A P S  PpEXPA3

159  R S V R I K - G Q - Y S G W V T M F R N W G S L W T C R T K - - - L S G - P L S F M I T T - S D G R T L V S N R A - - V  PpEXPA4

154  Q Q L Y I K - G A - S T G W L P L K R N W G Q M W Q F T G N S G - M H G Q A I S F K A V T - S D G A E A I S P N V A P A  PpEXPA5

157  T A A Y L K - G D - K T E W S P L S R N W G A N W Q C R R N - - - Y C G Q G I S I K I V T - S D N K - V S V T K L A K S  PpEXPA6

158  Q Q L Y I K - G S - S T G W N A M S R N W G Q L W E I R - N A A - L M G Q A L S F R V V T - S D R A E V A S F D A V P A  PpEXPA9

154  Q Q L Y M K - G S - S T N W Q P L K R N W G Q M W Q F T G N S R - M H G Q A I S F K A V T - S D G S V A V S N N V A P P  PpEXPA11

151  Q Q L S L K - G S - S T G W Y T M S R N W G Q Q W E F R G N S A - L V G Q A L S F R V V T - S D G A E A V S Y D A A S E  PpEXPA12

159  Q T V F I Q - G S - K T K L V A M I R N F G Q I W Q S S V N - - - V S G Q R L S F M V M T - S D G E S V V S R N V A P S  PpEXPA13

154  Q Q V Y I K - G P - K T Q W L Q M Y R N W G S Q W T F N G G P N N I V G S A L S F R V H T - S D G R Q V I S Y N A A P A  PpEXPA14

156  Q Q V Y I K - G S - N T P W E P M S R N W G S M W Q F T G N S K - M K G Q A L S F K T I T - S D G A V A I S Y D A A P N  PpEXPA15

154  Q Q M F I K - S P - T T G W L Q M S R N W G Q I W T Y K G G P R N I V G F A L S F R V Y T - S D R R Q V V S Y N A A P A  PpEXPA16

154  Q Q L Y I K - G S - S T A W L P L K R N W G Q M W Q F T G N S G - M H G Q A I S F K A V T - S D G A E A I S N N V A S S  PpEXPA17

159  K A V K V R - G G - N G Y W V P M W R N W G A L W T C K T R - - - M S G - A L S F Q I T T - G D G R T L T T Y K A - - V  PpEXPA18

156  V S V K V K - C P - Y T G W V S A Y R N W G C L W T V R T K - - - M T G - P L S F T L V T - S D G R T L Y S M N A V R N  PpEXPA19
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155  R S M R V K - G Q - Y G G W V N I F R N W G S I R T C R T K - - - V A G - A L S F M I T T - T D G R S I V S N R A A N V  PpEXPA20

158  R S V R I K - S P - H S G L I S M Y R N W G S L W T V R A R - - - M S G - A L F F M I T T - S H G R V L I T R N A - - V  PpEXPA21

160  V P V K V K - C P - S S G W Y D M Y R N W G A L W T V Q K K - - - M V G - P L S F L L T T - G D G R R L T A Y N A - - V  PpEXPA22

163  V A V K V K - C P - T S G W Y D M Y R N W G A L W T V Q K K - - - M N G - P L S F A I T T - S D G R T V T T Y N A - - V  PpEXPA23

163  V A V K I K - C P - T S D W C D M Y R N W G A F W T V Q K K - - - M E G - P L S F Q I T T - S D R R K V T T H N A - - V  PpEXPA24

160  R A V R I K - T P - S T D W I P M Y R N W G A L W T V Q R K - - - L S G - P L S F Q I T A - G D R R Q I T I N S A - - V  PpEXPA25

156  R A V S I K - G Q - Y T G W V G M Y R N W G S L W T C T T K - - - I D G - A L T F R I T T - G D G K T L I L Y N A V R K  PpEXPA26

149  Q R F F V K - G S - M T G W Y E L R R N W G Q I W T C T A D S R - L K G Q A L S F R T Q T - S D G R Q V V S I D A A P A  PpEXPA27

156  Q H M Y I K - G S - N T P W E P M S R N W G S M W Q F T G D S K - M K G Q A L S F K A V T - S D G S V A V S M D A A P G  PpEXPA7

162  Q S V S I R - G S - K T S W V T M T R N F G Q I W Q S T V N - - - M S G Q S L S F M V T T - S D G K T V V S N N V A P P  PpEXPA8

155  Q Q L S I K - G S - N S G W Y Q M K R N W G Q M W Q L T G N S N - M P G Q A L S F R A V L - S D G T T V E S L D A A P A  PpEXPA10
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                       250                 260                 270                 280                 290

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212  N - - - - - - - - - - - - - - - - - W Q F G - - - - - - - - - - - - - - - - Q T Y - - - - - E G                          PtEXPA26

215  Y - - - - - - - - - - - - - - - - - W R F G - - - - - - - - - - - - - - - - M T Y - - - - - Q G K Q                      AtEXPA20

212  N - - - - - - - - - - - - - - - - - W N Y G - - - - - - - - - - - - - - - - Q T F - - - - - E G K Q                      AtEXPA13

211  S - - - - - - - - - - - - - - - - - W W F G - - - - - - - - - - - - - - - - Q T F - - - - - S S R G R Q                  AtEXPA12

211  N - - - - - - - - - - - - - - - - - W S F G - - - - - - - - - - - - - - - - Q T Y - - - - - T G K Q                      AtEXPA14

211  S - - - - - - - - - - - - - - - - - W S F G - - - - - - - - - - - - - - - - Q T F - - - - - T G R Q                      AtEXPA15

212  N - - - - - - - - - - - - - - - - - W Q F G - - - - - - - - - - - - - - - - Q T Y - - - - - Q G G Q                      AtEXPA8

207  N - - - - - - - - - - - - - - - - - W G F G - - - - - - - - - - - - - - - - Q T F - - - - - D G R I N                    AtEXPA22

213  N - - - - - - - - - - - - - - - - - W Q F G - - - - - - - - - - - - - - - - Q T F - - - - - V G K N                      AtEXPA4

214  S - - - - - - - - - - - - - - - - - W S F G - - - - - - - - - - - - - - - - Q I Y - - - - - S S N V Q                    AtEXPA11

215  N - - - - - - - - - - - - - - - - - W R F G - - - - - - - - - - - - - - - - Q S F - - - - - K S N V N                    AtEXPA17

212  N - - - - - - - - - - - - - - - - - W S G G - - - - - - - - - - - - - - - - K T Y - - - - - K S T A N                    AtEXPA7

215  D - - - - - - - - - - - - - - - - - W M F A - - - - - - - - - - - - - - - - Q T F - - - - - E G K Q                      OsEXPA16

211  E - - - - - - - - - - - - - - - - - W D F G - - - - - - - - - - - - - - - - K T Y - - - - - T G K Q                      OsEXPA10

215  G - - - - - - - - - - - - - - - - - W S F G - - - - - - - - - - - - - - - - Q T F - - - - - S G A Q                      OsEXPA5

210  G - - - - - - - - - - - - - - - - - W S F G - - - - - - - - - - - - - - - - Q T F - - - - - S G G Q                      OsEXPA11

211  G - - - - - - - - - - - - - - - - - W Q F G - - - - - - - - - - - - - - - - Q T F - - - - - E G G Q                      OsEXPA4
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214  D - - - - - - - - - - - - - - - - - W Q F G - - - - - - - - - - - - - - - - V T Y - - - - - Q A T K N          OsEXPA32
215  G - - - - - - - - - - - - - - - - - W H F G - - - - - - - - - - - - - - - - Q T F - - - - - E G K N            OsEXPA7
213  N - - - - - - - - - - - - - - - - - W N F G - - - - - - - - - - - - - - - - T T Y - - - - - T S N I N          OsEXPA33
216  S - - - - - - - - - - - - - - - - - W C F G - - - - - - - - - - - - - - - - L T Y - - - - - Q A R V N          OsEXPA30
212  N - - - - - - - - - - - - - - - - - W Q F G - - - - - - - - - - - - - - - - Q T F - - - - - T S G V Q          OsEXPA12
211  H - - - - - - - - - - - - - - - - - W S F G - - - - - - - - - - - - - - - - Q T F - - - - - E G G Q            PpEXPA1
210  G - - - - - - - - - - - - - - - D Y W K F G - - - - - - - - - - - - - - - - Q T W - - - - - E G S Q            PpEXPA2
211  N - - - - - - - - - - - - - - - - - W G W G - - - - - - - - - - - - - - - - Q T F - - - - - E G V A            PpEXPA3
210  G - - - - - - - - - - - - - - - S W W K F G - - - - - - - - - - - - - - - - Q T W - - - - - E G S Q            PpEXPA4
210  N - - - - - - - - - - - - - - - - - W G F G - - - - - - - - - - - - - - - - Q T F - - - - - E G S N            PpEXPA5
210  D - - - - - - - - - - - - - - - - - W C F G - - - - - - - - - - - - - - - - K T F - - - - - I G K Q            PpEXPA6
213  N - - - - - - - - - - - - - - - - - W A F S - - - - - - - - - - - - - - - - Q T F - - - - - E G S N            PpEXPA9
210  N - - - - - - - - - - - - - - - - - W G F G - - - - - - - - - - - - - - - - Q T F - - - - - E G T L            PpEXPA11
207  N - - - - - - - - - - - - - - - - - W S F S - - - - - - - - - - - - - - - - Q T F - - - - - E G I N            PpEXPA12
213  D - - - - - - - - - - - - - - - - - W A Y G - - - - - - - - - - - - - - - - Q T Y - - - - - E G S Q            PpEXPA13
211  N - - - - - - - - - - - - - - - - - W W F G - - - - - - - - - - - - - - - - Q T F - - - - - S S G A            PpEXPA14
212  N - - - - - - - - - - - - - - - - - W Q F G - - - - - - - - - - - - - - - - Q T F - - - - - E G V N            PpEXPA15
211  N - - - - - - - - - - - - - - - - - W R F G - - - - - - - - - - - - - - - - Q T F - - - - - S S G A            PpEXPA16
210  N - - - - - - - - - - - - - - - - - W G F G - - - - - - - - - - - - - - - - Q T F - - - - - E G S N            PpEXPA17
210  G - - - - - - - - - - - - - - - G Y W R F G - - - - - - - - - - - - - - - - Q T W - - - - - E G S Q            PpEXPA18
209  G - - - - - - - - - - - - - - - - - W K F G - - - - - - - - - - - - - - - - Q T W - - - - - E G S Q            PpEXPA19
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208  G G L P V Q I V P L G P I A I L S L S R K G P F R S K L N D A P R T L M C L Q E W P V R P R E A D R S P R        PpEXPA20
209  G - - - - - - - - - - - - - - - S G W R F G - - - - - - - - - - - - - - - - Q T W - - - - - E G N                  PpEXPA21
211  G - - - - - - - - - - - - - - - N G W T F G - - - - - - - - - - - - - - - - Q T W - - - - - E G A Q                PpEXPA22
214  G - - - - - - - - - - - - - - - N G W K F G - - - - - - - - - - - - - - - - Q T W - - - - - E G A Q                PpEXPA23
214  G - - - - - - - - - - - - - - - H G W Q F G - - - - - - - - - - - - - - - - Q T W - - - - - E G A Q                PpEXPA24
211  G - - - - - - - - - - - - - - - N A W K F G - - - - - - - - - - - - - - - - Q T W - - - - - E G H N                PpEXPA25
209  G - - - - - - - - - - - - - - - - - W R F G - - - - - - - - - - - - - - - - Q T W - - - - - E G S Q                PpEXPA26
205  N - - - - - - - - - - - - - - - - - W N F G - - - - - - - - - - - - - - - - Q T F - - - - - S S G V                PpEXPA27
212  N - - - - - - - - - - - - - - - - - W Q F G - - - - - - - - - - - - - - - - Q T F - - - - - E G V N                PpEXPA7
216  D - - - - - - - - - - - - - - - - - W A F G - - - - - - - - - - - - - - - - Q T Y - - - - - E G S Q                PpEXPA8
211  N - - - - - - - - - - - - - - - - - W H F G - - - - - - - - - - - - - - - - Q M F - - - - - E G S Q                PpEXPA10
```

Supplemental Fig. 8. Alignment of *Physcomitrella* EXPB sequences with selected *Arabidopsis* and rice EXPB genes. AtEXPA1 is included as a root. Alignment made using the Clustal W algorithm as described in the Materials and Methods section.

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  ------------------+-------------------+-------------------+-------------------+-------------------+-------------------+-

                    10                  20                  30                  40                  50                  60

  ------------------+-------------------+-------------------+-------------------+-------------------+-------------------+-

1 W L P A V A T W Y G S P N G D G S D G G A C G Y G T L V D V K P L H A R V G A V N P I L F K N G E G C G A C Y K V R C L AtEXPB3

1 W S I A G S T W Y G N P T G Y G S D G G A C G Y G N A V A Q P P F S K M V S A G G P S L F K S G K G C G A C Y Q V K C T AtEXPB2

1 W S N G G A T W Y G A A N G A G S D G G A C G Y Q G A V F Q A P F S S M I A A G S P S I Y K S G L G C G S C Y Q V K C T OsEXPB15

1 W H P A T A T W Y G S A D G D G S D G G A C G Y G T L V D V V P M K T R V G A V S P V L F K G G E G C G A C Y K V R C L OsEXPB16

1 W L G G H A T W Y G D P Y G E G S S G G A C G Y - T Q L T G T P I G S K I A A G N A P I F Q E G K G C G Q C Y E V K C N PpEXPB1

1 W V R A R G T W Y G D P Y G E G S S G G N C G Y - T K L W G T P I G P K I V A G S R S I Y A N G Q G C G Q C Y Q I R C V PpEXPB2

1 W V R A R G T W Y G D P Y G E G S S G G N C G Y - T R L - G T P I G P K I V A G S R S I Y A N G L G C G Q C Y Q N Q C V PpEXPB6

1 W V P G H A T W Y G D P Y G E G S S G G Q C G Y - L Q L T G T P I G N K I A A G N E A I F Q K G K G G A Q C Y E V K C N PpEXPB4

1 W M A G H A T W Y G E P L G E G S S G G A C G Y - T K L A D T P Y G P K I A A G N D P I F Q G G S G C G A C F E V K C N PpEXPB5

1 W L P G H A T W Y G D P Y G E G S S G G A C G Y - T E L A G T P Y G L S V G A G S A V I Y Q N G Q G C G E C Y E V K C T PpEXPB3

1 W V N A H A T F Y G G G D A S G T M G G A C G Y - G N L Y S Q G Y G T N T A A L S T A L F N N G L S C G A C F E I R C Q AtEXPA1
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    ------------------+-------------------+-------------------+-------------------+-------------------+-------------------+-
                      70                  80                  90                  100                 110                 120
    ------------------+-------------------+-------------------+-------------------+-------------------+-------------------+-
 61 D K S - - - - I C S R R A V T V I I T D E C P - - - - - - - - - G - - - C S K T S T H F D L S G A V F G R L A I A G E S  AtEXPB3
 61 S K S - - - - A C S K N P V T V V I T D E C P - - - - - - - - - G - - - C V K E S V H F D L S G T A F G A M A I S G Q D  AtEXPB2
 61 G N S - - - - A C S G N P V T V V L T D E C P - - - - - - - - - G G - P C L S E P V H F D L S G T A F G A M A N P G Q A  OsEXPB15
 61 D A S - - - - I C S R R A V T V I V T D E C P - - - - - - - - - G G - V C A F G R T H F D L S G A A F A R L A V A G H G  OsEXPB16
 60 Y P S - - - - - C S P Q G T R I V I T D L C P - - - - - - - - - G G Q Y C S T D Q P A F D F S G A A I T A M A L P G R D  PpEXPB1
 60 D P N G G P R L C N P Q G T N V V V T D F C P - - - - - - - - - G G T Y C S T G E N A F D M S G A A I N A M A L R G R E  PpEXPB2
 59 D P S Q G T K L G N S F S T Q V A V T D F C P - - - - - - - - - G G T Y C S T G E N A F D M S G A A I N A M A L P S R E  PpEXPB6
 60 Y P V - - - - - C R P E G T R I V I T D L C P - - - - - - - - - G A Q F C S G G N P A F D L S G A A I S A M A K D G Q D  PpEXPB4
 60 Y P S - - - - - C K S E P T R I I I T D Q C P - - - - - - - - - G G T Y C S T S Q P A F D L S G A A I S D M A V S G K D  PpEXPB5
 60 Y P S - - - - - C K P T P S R I V I T D F C P - - - - - - - - - G G T F C S T G E P A F D L S G M A M T N M A L P G R D  PpEXPB3
 60 N D G - - - K W C L P G S I V V T A T N F C P P N N A L P N N A G G - W C N P P Q Q H F D L S Q P V F Q R I A - - - - -  AtEXPA1

    ------------------+-------------------+-------------------+-------------------+-------------------+-------------------+-
                      130                 140                 150                 160                 170                 180
    ------------------+-------------------+-------------------+-------------------+-------------------+-------------------+-
105 G P L R N R G L I P V I Y R R T A C K Y R G K N I A F H V N E G S T D F W L S L L V E F E D G E G D I G S M H I R Q A G  AtEXPB3
105 S Q L R N V G E L Q I L Y K K V E C N Y I G K T V T F Q V D K G S N A N S F A V L V A Y V N G D G E I G R I E L K Q A L  AtEXPB2
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107  D Q L R A A G V L Q I Q Y N R V P C N W G G V K L T F V V D V G S N P N Y F A V L V K Y E N G D G D L S G V E L M Q T G  OsEXPB15
107  G Q L Q N R G E I S V V Y R R T A C K Y G G K N I A F H V N E G S T T F W L S L L V E F E D G D G D I G S M Q L K Q A N  OsEXPB16
106  G E L R N I G L Y D I Q Y K R V P C E Y P N Q N I A F K V D A G S S K Y W F S F T V K Y L G G P G D I N T V E V K C G K  PpEXPB1
111  G Q L R N R G L Y N L L Y K R V P C R Y R G T N I E F R V D N G S S P F W L S I L I K Y V G G P G D I G Q V Y I R M A N  PpEXPB2
110  G Q L R N R G L Y N L L Y K R V P C R Y R G T N I Q F R V D K G S S A Y W L S I L I K Y V G G P G D I G Q V Y I K M A N  PpEXPB6
106  G A L R N I G L Y D I Q Y K R V P C E Y P G Q N I V F K V D A G S S P F W L S F T V K Y M G G P G D I E S V S I S Q - R  PpEXPB4
106  G E L R N I G L Y D I L Y K R V P C E Y P N Q N I A F Q V D A G S S A F W L S L L V K Y M G G P G D I E S V E I R T T G  PpEXPB5
106  Q E L R N L G L Y E I Q Y R R V P C Y Y P N Q N V A F K V D P G S T P F W L S F T I E Y Q G G P G D I E S V A I R Q A G  PpEXPB3
111  - Q Y R - A G I V P V A Y R R V P C V R R G - G I R F T I N - - G H S Y F N L V L I T N V G G A G D V H S A M V K G S R  AtEXPA1
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    ------------------+-------------------+-------------------+-------------------+-------------------+-------------------+-
                      190                 200                 210                 220                 230                 240
    ------------------+-------------------+-------------------+-------------------+-------------------+-------------------+-
165 - A R E W L E M K H V W G A N W C I I - - G G - P L K G - P F S I K L T T L S A G K T L S A T D V V P R N W A P K A T Y  AtEXPB3
165 D S D K W L S M S Q S W G A V W K L D - - V S S P L R A - P L S L R V T S L E S G K T V V A S N V I P A N W Q P G A I Y  AtEXPB2
167 A G A A W T Q M Q Q S W G A V W K L N - - A G S A L Q A - P F S I R L T S S - S G K T L V A S N V I P S G W K P G M S Y  OsEXPB15
167 - S A Q W Q D M K H I W G A T W S L T - - P G - P L V G - P F S V R L T T L T T R Q T L S A Q D V I P K N W T P K A T Y  OsEXPB16
166 - N G Y F Q Y A Q H S W G A N W M L I N Y S G V P F Q F - P L T I K I T T K L N D H T V V A E D V I P D W F G P G V Q Y  PpEXPB1
171 - W Y K F Q P M R H A W G A N W M I P N Y D G K P F R G - P M D I R I V S R L N R H T V L A R G V I P A Y F R P G T S Y  PpEXPB2
170 - W F A F Q P M K H A W G A N W M M P S Y D G K P F K G - P M D I K I V S K L N R H S V V A R G V I P G Y F R P G T T Y  PpEXPB6
165 - D G S F I P A Q H S W G A N W M L I N Y S G A P F Q G - P Y S V K I N C M L N G H T V V A K D V I P A G F A P G Q E Y  PpEXPB4
166 - S S S F Q P A K H N W G A S W M L I N T S G Q P F K G - P Y D V K I V S K L N G H T V I A E K A I P E F F E P G K L Y  PpEXPB5
166 - S S E F Q Q M Q H N W G A N Y M L I C Y S G K P F K G - P Y D V M I T A K L N G H V L I A Q D A I P E Y F Q P G G I Y  PpEXPB3
166 - - T G W Q A M S R N W G Q N W Q S N - - S - - Y L N G Q S L S F K V T T S - D G Q T I V S N N V A N A G W S F G Q T F  AtEXPA1

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220 S S R L N F                                                                                                                AtEXPB3
222 K S N V N F                                                                                                                AtEXPB2
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| | | |
|---|---|---|
| **223** | **I S T V N F** | **OsEXPB15** |
| **222** | **T S R L N F** | **OsEXPB16** |
| **224** | **E S N V Q I** | **PpEXPB1** |
| **229** | **R S R V Q M** | **PpEXPB2** |
| **228** | **N S R V Q M** | **PpEXPB6** |
| **223** | **E S N V Q I** | **PpEXPB4** |
| **224** | **E S N V Q M** | **PpEXPB5** |
| **224** | **E S N V Q L** | **PpEXPB3** |
| **219** | **T G - A Q L** | **AtEXPA1** |