# *HvEXPB7*, a Novel β-Expansin Gene Revealed by Root Hair Transcriptome of Tibetan Wild Barley Improves Root Hair Growth under Drought Stress

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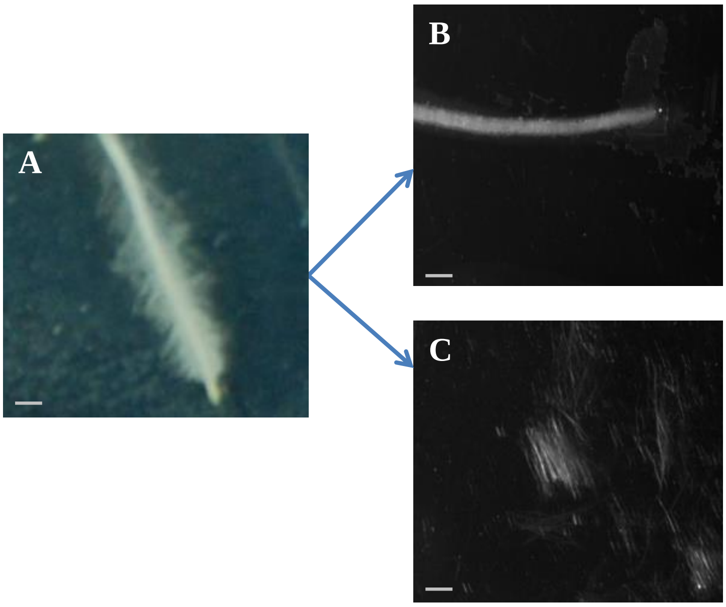

**Fig. S1. Root hair isolation.** (a) Root. (b) Stripped root. (c) Isolated root hair. Scale bars=1 mm.

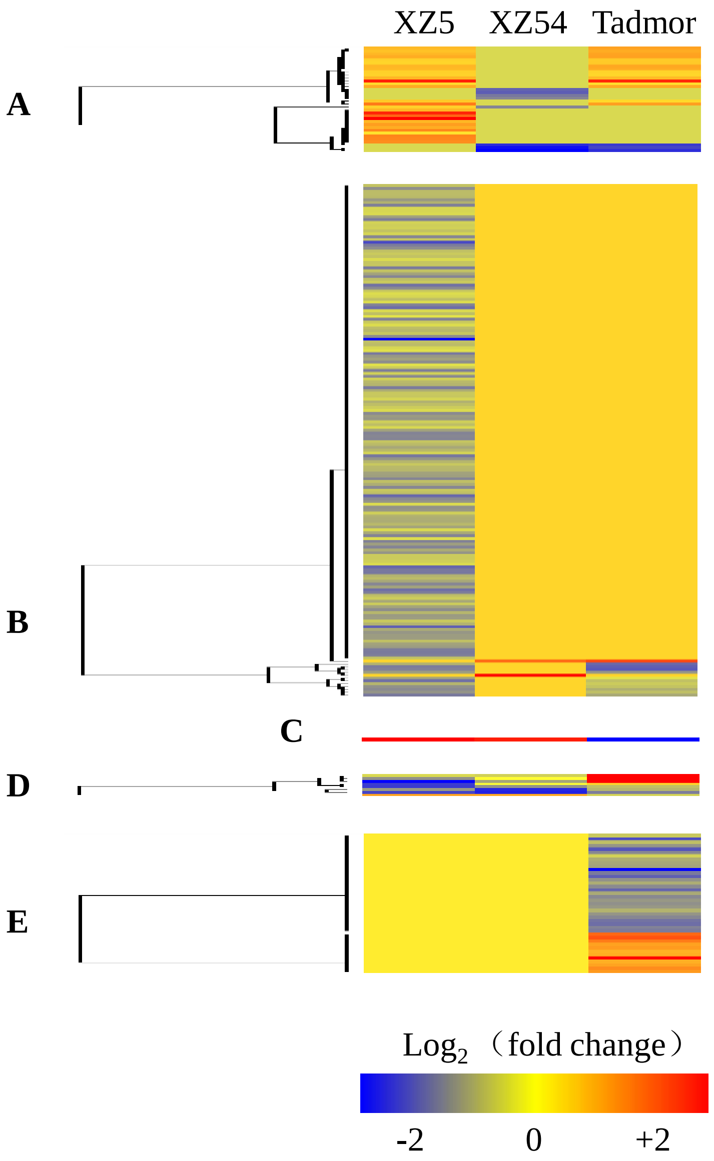

**Fig. S2. Hierarchical cluster analysis of all 266 DEGs of root hairs of XZ5, XZ54 and Tadmor according to their relative expression levels in response to drought stress.** (A) 36 DEGs up-regulated in XZ5 but down-regulated or unchanged in XZ54, or no change in XZ5 but down-regulated in XZ54. (B) 180 DEGs up-regulated in XZ54 but down-regulated or unchanged in XZ5, or unchanged in XZ54 but down-regulated in XZ5. (C) 1 DEG up-regulated in both of XZ5 and XZ54. (D) 8 DEGs down-regulated in both of XZ5 and XZ54. (E) 41 DEGs only up- or down-regulated in Tadmor. The relative expression levels and functions of these DEGs were listed in Supplementary Table S4-S8. Hierarchical clustering of DEGs was displayed by pearson correlation and pairwise average-linkage as a measurement of similarity.

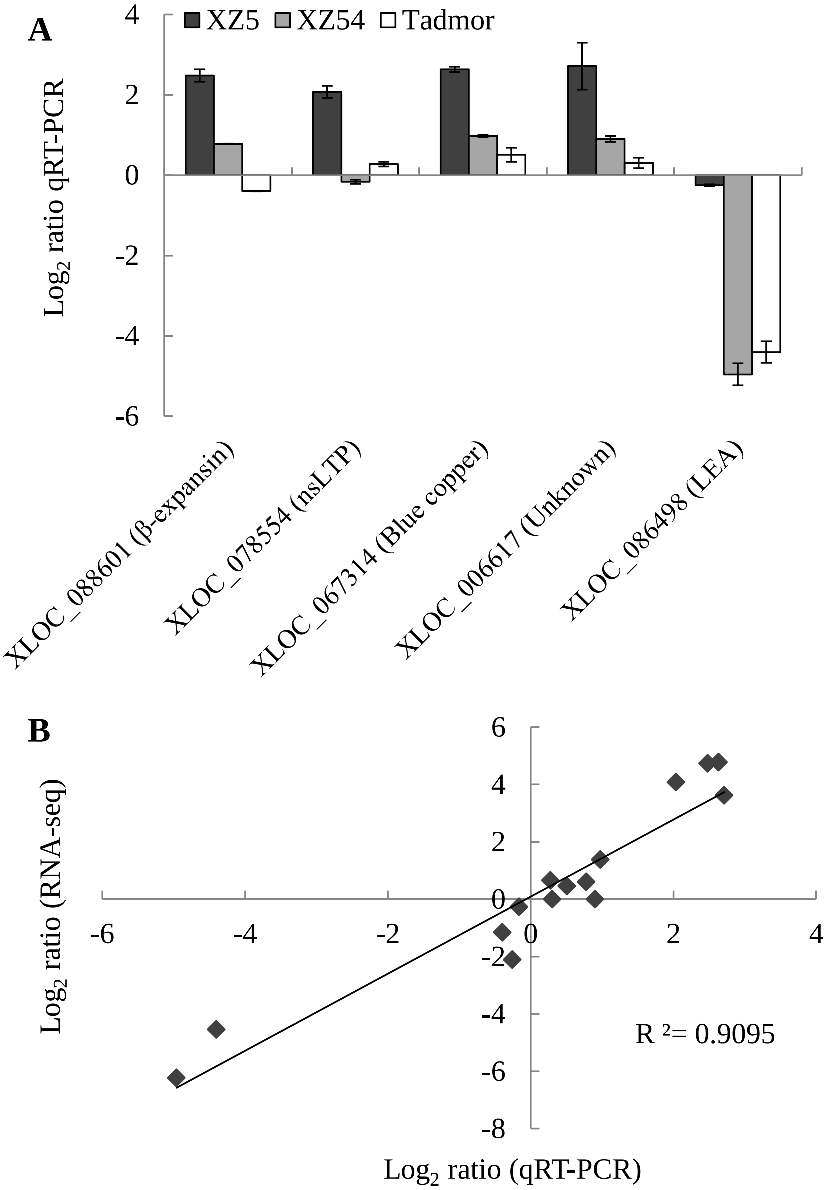

**Fig. S3. Expression profiles confirmation of five root hair genes by qRT-PCR in three barely genotypes.** (A) qRT-PCR of five genes in XZ5, XZ54 and Tadmor. The fold changes in gene expression were transformed to $\log_2$ scale (with three biological replications and three technology replications). (B) The qRT-PCR data log2-values (X-axis) were plotted against the RNA-seq log2 values (Y-axis) ($R^2 = 0.9095$; $P < 0.001$).

```
1       aatctccccaacggcattaaccaccagagtagggtcatcgatcagtaaccaacgagaccagcaagcgagccatggcagcggccttttcct
                                                                              M  A  A  A  F  S  S
91      cctactccgtcgcggccgctttcctctgcctgctcgccgccaacggctgctgcggctgcccctggtttctccctgctacattctgccctg
         Y  S  V  A  A  A  F  L  C  L  L  A  A  N  G  C  C  G  C  P  W  F  L  P  A  T  F  C  P  E
181     aaccgacacccgaccccatacctacacctgaccccgctccagctacacctccgcctgctctggctacccccagcccaggctccggctctg
         P  T  P  D  P  I  P  T  P  D  P  A  P  A  T  P  P  P  A  L  A  T  P  S  P  G  S  G  S  G
271     gcagcgccaacggttccatgggcggctggctggacgccagggccacatggtacggcgctccggatggcgccgggccgttggacaacggtg
         S  A  N  G  S  M  G  G  W  L  D  A  R  A  T  W  Y  G  A  P  D  G  A  G  P  L  D  N  G  G
361     gcgcgtgcgggttcaagaacgtgaacctgccgcccttcaacgccatgacgtcgtgcggcaacgagccgatcttcaaggacggcaagggat
         A  C  G  F  K  N  V  N  L  P  P  F  N  A  M  T  S  C  G  N  E  P  I  F  K  D  G  K  G  C
451     gcggctcctgctaccagataaggtgcgtgggcaaggttcacccagcgtgctccggcgaccccgagacggtgatcatcaccgacatgaact
         G  S  C  Y  Q  I  R  C  V  G  K  V  H  P  A  C  S  G  D  P  E  T  V  I  I  T  D  M  N  Y
541     actacccggtcgcccgctaccacttcgacctcagcggcactgccttcggcgccatggccaaggacggccgcaacgacgagctccgccacg
         Y  P  V  A  R  Y  H  F  D  L  S  G  T  A  F  G  A  M  A  K  D  G  R  N  D  E  L  R  H  A
631     ccggcatcatcgacatgcagttcaagagggtgccgtgccagtacacagggctgtccgtgacgtttcacgtggagaaggggtcgaacccga
         G  I  I  D  M  Q  F  K  R  V  P  C  Q  Y  T  G  L  S  V  T  F  H  V  E  K  G  S  N  P  N
721     attacctggcgatcctggtggagtacgggaacggcgacggcgacgtggcgcaggtggacctcatggacggcggcgagccaacggtgtcct
         Y  L  A  I  L  V  E  Y  G  N  G  D  G  D  V  A  Q  V  D  L  M  D  G  G  E  P  T  V  S  W
811     ggaggccgatgagggagtcctggggctccatctggcgcctggacacgcggcgcccgcttcgggggcccttctcgctgcgggtcaccaacg
         R  P  M  R  E  S  W  G  S  I  W  R  L  D  T  R  R  P  L  R  G  P  F  S  L  R  V  T  N  G
901     ggtccggcaggtcgctcgtcgcggaccaggtcatccccgccgactggcagcccgacaccgtgtacagctccgacgtccagttcgatgaat
         S  G  R  S  L  V  A  D  Q  V  I  P  A  D  W  Q  P  D  T  V  Y  S  S  D  V  Q  F  D  E  *
991     gatcccgtccgatgatccatggaaggcatgcacgtacgtccatgcctgcatggatttttttgtgccaagctatatagctgagacgtcgcct
1081    gtgacttccggtgcaagtcctcgtcgtgtgctacctatgctacatatgtacacgtagtacataacatacgtggcagctttaattagtttg
1171    tgggatctggagtaggcagcgagtagtatatattgctcgcagctataaatttacgtttgtaatttctcctgtattacacaagtttattat
1261    gtcactggtgtgtataaa
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**Fig. S4. The nucleotide and amino acid sequences of *HvEXPB7*.**

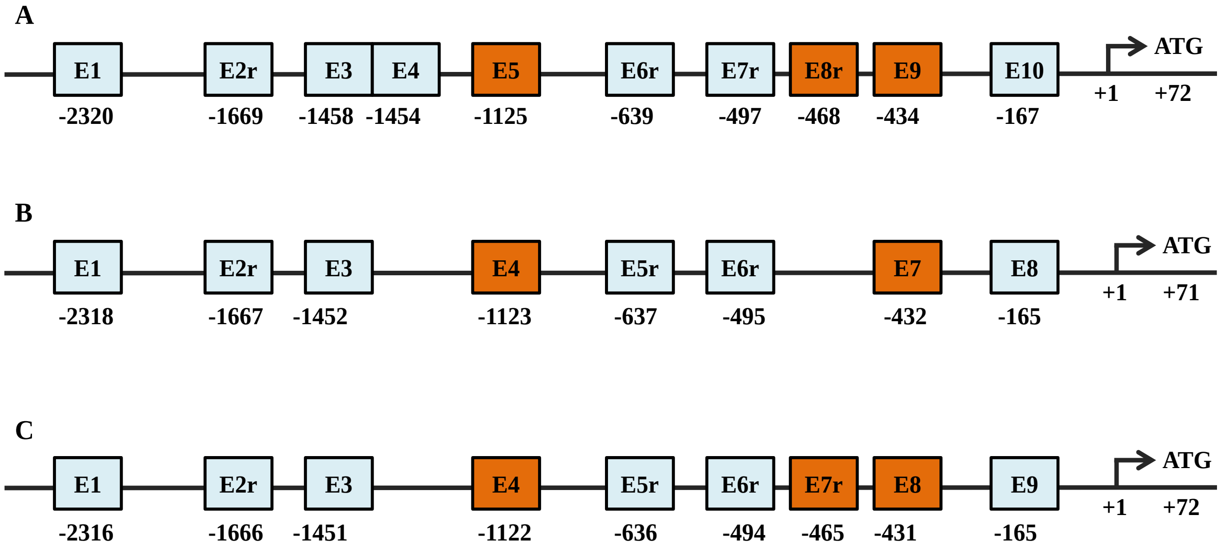

**Fig. S5. Relative positions of RHEs in the *HvEXPB7* promoter regions of XZ5, XZ54 and Tadmor.** (A) XZ5. (B) XZ54. (C) Tadmor. Numbers below the sequence represent the nucleotide positions of the RHE motifs (light blue and orange red boxes) relative to the putative transcription initiation site (+1). 'r' indicates that the RHE is in the reverse direction. RHEs with major- and minor-type consensus sequences are boxed in orange red and light blue, respectively.

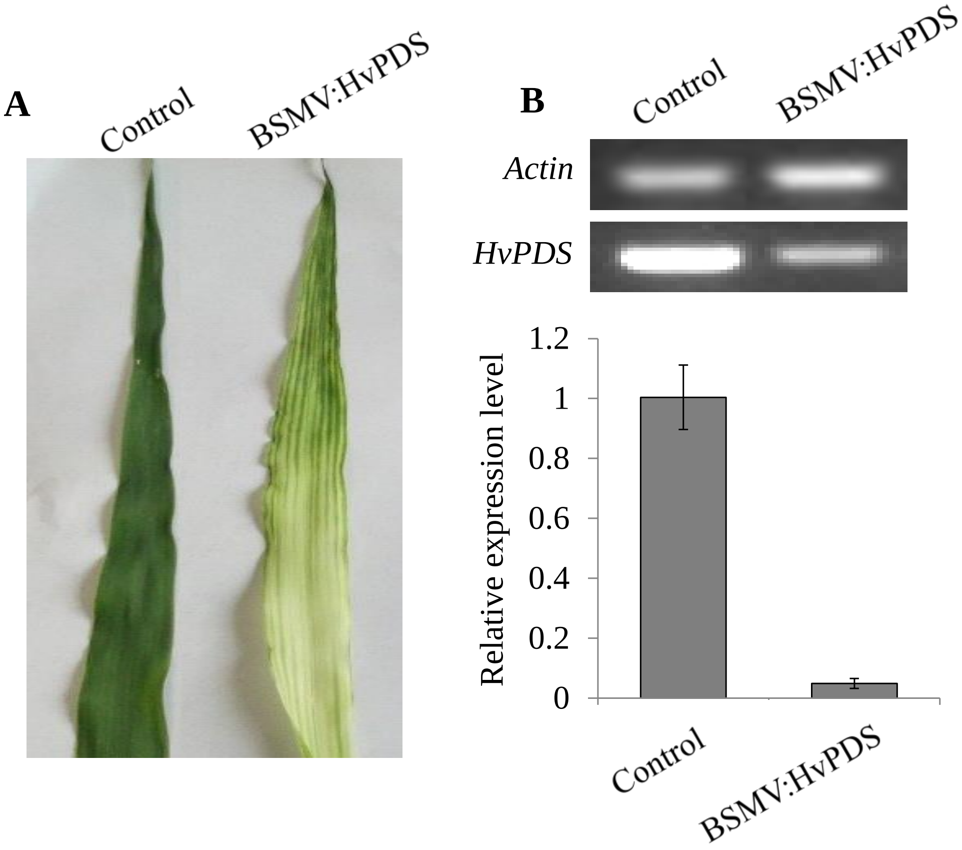

**Fig. S6. Silencing of the phytoene desaturase (*PDS*) gene in wild barley XZ5 using BSMV-VIGS.** (A) Photobleaching symptom of BSMV:HvPDS inoculated plants in contrast to those treated with empty vectors. Photograph was taken 21 dpi. (B) RT-PCR analysis of *HvPDS* transcript abundance in leaves of XZ5 21 dpi.

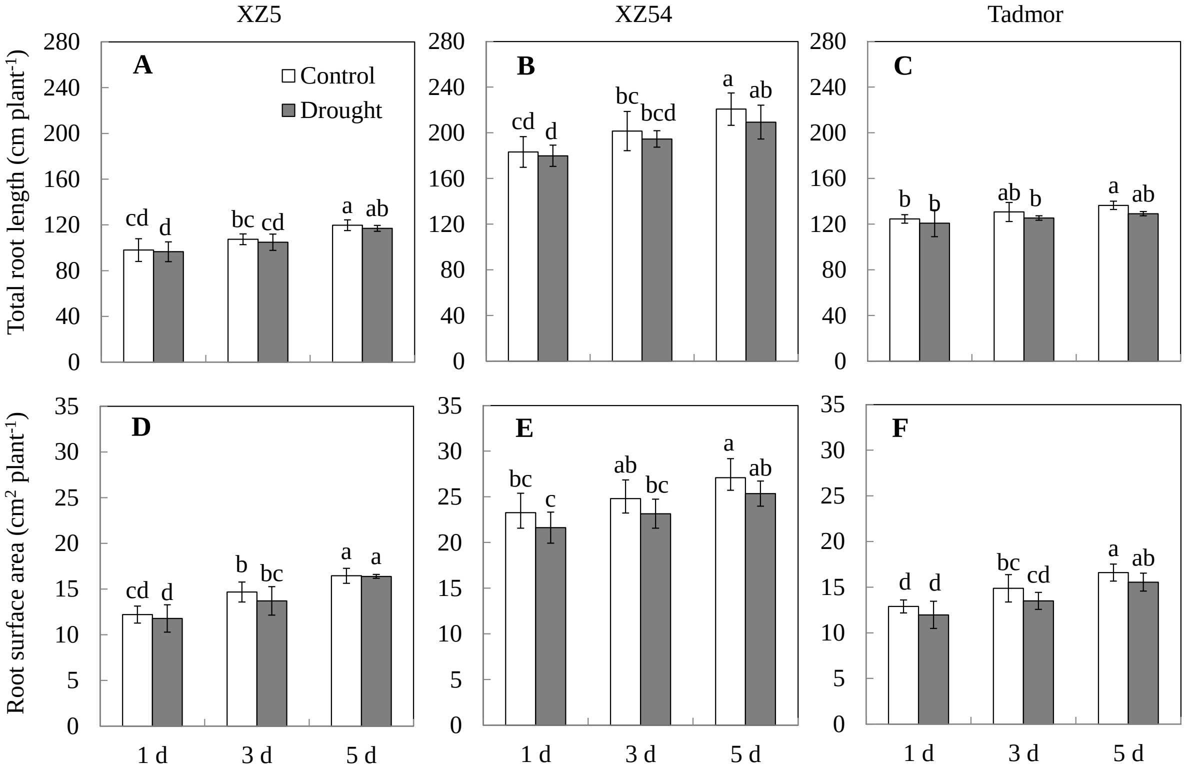

**Fig. S7. Root scanning of the root length (A, B, C) and root surface area (D, E, F) of Tibetan wild barley XZ5 (left panel), XZ54 (middle panel) and *cv.* Tadmor (right panel) grown under control or drought conditions.** Error bars represent SD values (n=6). Different letters indicate significant differences (*P*<0.05) among the treatments within each genotype.

**Table S1** List of real-time PCR primers for confirmation of RNA-Seq

| **Gene Id** | **Description** | **Forward primer（5′ → 3′）** |
|---|---|---|
| XLOC_088601 | Beta-expansin 1a expressed | Forward primer: GCCTTGATGCCAATCACCAG |
| | | Reverse primer: TGGTTAATGCCGTTGGGGAG |
| XLOC_078554 | Non-specific lipid-transfer protein precursor | Forward primer: ATCTCACCCCCTAACACCCA |
| | | Reverse primer: ATGGCGTCTCTGGAACTCTG |
| XLOC_067314 | Blue copper | Forward primer: ACGCGGAATCCAGTTACTAGC |
| | | Reverse primer: CACAAGCAGCGTGATCAGAG |
| XLOC_006617 | Unknown | Forward primer: GCACCGCCAGGAAGAAAAAG |
| | | Reverse primer: ATGTAGCGCACAAGGAACGA |
| XLOC_086498 | Similarity to late embryogenesis abundant protein (LEA) | Forward primer: ACCCATCCTTCTCCACCAGT |
| | | Reverse primer: CGTACGGCCAGTACAACACT |
| Actin | | Forward primer: TGGCTGACGGTGAGGACA |
| | | Reverse primer: CGAGGGCGACCAACTATG |

**Table S2** List of PCR primers for HvEXPB7 cloning and function verification

| **Primer name** | **Primer sequence (5' → 3')** |
|---|---|
| GSPF | TTCAAGGACGGCAAGGGATG |
| GSPR | GTTCGACCCCTTCTCCACGT |
| UPM-S | CTAATACGACTCACTATAGGGC |
| UPM -L | CTAATACGACTCACTATAGGGCAAGCAGTGGTATCAACGCAGAGT |
| EXPB7F | CAATCTCCCCAACGGCATTAAC |
| EXPB7R | TTTATACACACCAGTGACATAAT |
| EXPB7-promoter-F | TTCGCAAGTTTAAATCATCACAAG |
| EXPB7-promoter R | CAACGAGACCAGCAAGCGAGCC |
| EXPB7-CDS-F | ATGGCAGCGGCCTTTTCCTC |
| EXPB7-CDS-R | TCATTCATCGAACTGGACGT |
| EXPB7-35S:sGFP-F | CTCAGGTACCATGGCAGCGGCCTTTTCC |
| EXPB7-35S:sGFP-R | CTAGTCTAGATTCATCGAACTGGACGTC |
| EXPB7-γ-F | GTACGCTAGCACCCCATACCTACACCTG |
| EXPB7-γ-R | GTACGCTAGCATCCCTTGCCGTCCTTG |
| PDS-γ-F | GTACGCTAGCCGACGAGGTTTTTATTGC |
| PDS-γ-R | GTACGCTAGCAGTTATTTGAGTCCCGTC |
| EXPB7-RT-PCR-F | TCAAGAACGTGAACCTGCCG |
| EXPB7-RT-PCR-R | CTTGCCCACGCACCTTATCT |
| PDS- RT-PCR -F | AGTCTTTGGGTGGTGAGGTC |
| PDS- RT-PCR -R | CTTGAAGATATCGACTGGTG |
| γ-stain-F | CAACTGCCAATCGTGAGTAGG |
| ActinF | TGGCTGACGGTGAGGACA |
| ActinR | CGAGGGCGACCAACTATG |

**Table S3** Summary of root hair reads numbers of XZ5, XZ54 and Tadmor, and their mapped results to barely genome

| **Sample** | **Genotype** | | | | | |
|---|---|---|---|---|---|---|
| | **XZ5** | | **XZ54** | | **Tadmor** | |
| | **Control** | **Drought** | **Control** | **Drought** | **Control** | **Drought** |
| Raw reads | 29476018 | 26423412 | 27690596 | 27698298 | 29397348 | 24862762 |
| Clean reads | 29433186 | 26415212 | 27682280 | 27689364 | 29385518 | 24854408 |
| Clean data rate | 96.00% | 97.43% | 97.42% | 97.38% | 97.30% | 97.32% |
| Total mapped reads | 29433186 | 26415212 | 27682280 | 27689364 | 29385518 | 24854408 |
| Uniquely mapped | 20547478 | 15475014 | 19158705 | 21098069 | 21871926 | 14753813 |
| Multiple mapped reads | 3832360 | 7075850 | 4007429 | 3256107 | 3656852 | 6376676 |
| Unmapped reads | 5048859 | 3862596 | 4515124 | 3333126 | 3855525 | 3722213 |
| Exp_gene_number | 46383 | 43005 | 45318 | 45145 | 45247 | 42570 |

**Table S4** DEGs up-regulated in XZ5 but down-regulated or unchanged in XZ54, or no change in XZ5 but down-regulated in XZ54

| **GeneId** | **$Log_2$(fold change）** | | | **Description** |
|---|---|---|---|---|
| | **XZ5** | **XZ54** | **Tadmor** | |
| **Energy** | | | | |
| XLOC_004739 | 3.24 | — | 3.95 | ATP synthase subunit beta |
| XLOC_006853 | 2.58 | — | 2.48 | ATP synthase subunit beta |
| XLOC_012447 | 3.66 | — | 3.99 | ATP synthase subunit beta |
| XLOC_013896 | 3.69 | — | 3.68 | ATP sulfurylase |
| XLOC_016879 | 3.33 | — | 3.92 | ATP synthase subunit beta |
| XLOC_013018 | 3.40 | — | 3.24 | Plastid glutamine synthetase 2 |
| **Cell wall modification and root hair development** | | | | |
| XLOC_024622 | 3.35 | — | — | Cell wall-associated hydrolase |
| XLOC_031639 | 5.79 | — | — | Xyloglucan endotransglycosylase hydrolase protein 8 |
| XLOC_012543 | 2.42 | — | 2.75 | Cell wall-associated hydrolase |
| XLOC_088601 | 4.74 | — | — | Beta-expansin 1a expressed |
| **Transcription** | | | | |
| XLOC_004913 | 3.00 | — | 3.65 | rRNA intron-encoded homing endonuclease |
| XLOC_006324 | 2.50 | — | 2.39 | rRNA intron-encoded homing endonuclease |
| **Metabolism** | | | | |
| XLOC_094366 | 2.06 | — | — | Serine acetyltransferase |
| XLOC_012656 | 2.50 | — | 2.72 | Aldolase-type TIM barrel family protein isoform 1 |
| XLOC_018005 | 2.75 | — | 2.29 | Leucine rich protein |
| XLOC_020158 | 8.83 | — | — | Small glutamine-rich tetratricopeptide repeat-containing protein beta |
| **Stress defense** | | | | |
| XLOC_014532 | 7.86 | — | 7.60 | Cytochrome p450 liketbp |
| XLOC_019100 | 4.86 | — | — | Peroxidase 52 |
| XLOC_032107 | 3.32 | — | — | Cold-regulated protein blt14 |
| XLOC_085743 | — | -3.61 | — | Peroxidase 12 |
| XLOC_086498 | — | -6.23 | -4.55 | Similarity to late embryogenesis abundant protein |
| XLOC_088358 | — | -5.31 | -4.90 | Similarity to late embryogenesis abundant protein |
| **Unknown** | | | | |
| XLOC_040065 | 2.58 | -2.59 | — | Conserved domain partial |
| XLOC_049979 | 2.31 | — | 2.18 | Conserved protein |
| XLOC_057865 | — | -3.00 | — | ORF16-lacz fusion protein |
| XLOC_062616 | 3.36 | — | 3.82 | Hypothetical protein |
| XLOC_088641 | — | -6.68 | -5.28 | Predicted protein |
| XLOC_003324 | — | -3.80 | — | Predicted protein |
| XLOC_006617 | 3.63 | — | — | ---NA--- |
| XLOC_064342 | — | -2.55 | — | Conserved protein |
| XLOC_060028 | 5.14 | — | 4.03 | Conserved hypothetical protein |
| XLOC_028401 | 4.57 | — | — | Hypothetical protein ZEAMMB73_284819 |
| XLOC_025502 | 3.29 | — | 3.68 | ORF16-lacz fusion protein |

— represents no change.

**Table S5** DEGs up-regulated in XZ54 but down-regulated/unchanged in XZ5, or unchanged in XZ54 but down-regulated in XZ5

| **Gene Id** | **Log$_2$(fold change）** | | | **Description** |
|---|---|---|---|---|
| | **XZ5** | **XZ54** | **Tadmor** | |
| **Protein synthesis** | | | | |
| XLOC_075318 | -2.74 | — | — | 40s ribosomal protein s10 |
| XLOC_079203 | -3.26 | — | — | 40s ribosomal protein s11 |
| XLOC_020875 | -2.47 | — | — | 40s ribosomal protein s12 |
| XLOC_070718 | -3.36 | — | — | 40s ribosomal protein s13 |
| XLOC_039539 | -2.70 | — | — | 40s ribosomal protein s14 |
| XLOC_046148 | -3.90 | — | — | 40s ribosomal protein s14 |
| XLOC_081223 | -3.64 | — | — | 40s ribosomal protein s15 |
| XLOC_054162 | -3.55 | — | — | 40s ribosomal protein s15a-1-like |
| XLOC_082918 | -3.75 | — | — | 40s ribosomal protein s18 |
| XLOC_032123 | -2.85 | — | — | 40s ribosomal protein s19 |
| XLOC_040402 | -3.23 | — | — | 40s ribosomal protein s23 |
| XLOC_092443 | -3.71 | — | — | 40s ribosomal protein s23 |
| XLOC_007060 | -3.32 | — | — | 40s ribosomal protein s24 |
| XLOC_054218 | -3.73 | — | — | 40s ribosomal protein s24 |
| XLOC_015079 | -3.39 | — | — | 40s ribosomal protein s25-1 |
| XLOC_083823 | -2.34 | — | — | 40s ribosomal protein s26 |
| XLOC_052949 | -3.47 | — | — | 40s ribosomal protein s27 |
| XLOC_000608 | -3.77 | — | — | 40s ribosomal protein s27a |
| XLOC_069430 | -3.56 | — | — | 40s ribosomal protein s28 |
| XLOC_013012 | -3.64 | — | — | 40s ribosomal protein s30 |
| XLOC_008838 | -7.72 | — | — | 40s ribosomal protein s3a |
| XLOC_073619 | -3.86 | — | — | 40s ribosomal protein s3a-like |
| XLOC_048775 | -3.87 | — | — | 40s ribosomal protein s4 |
| XLOC_000670 | -3.27 | — | — | 40s ribosomal protein s5 |
| XLOC_094261 | -2.91 | — | — | 40s ribosomal protein s6 |
| XLOC_070590 | -3.81 | — | — | 40s ribosomal protein s6 |
| XLOC_077626 | -2.74 | — | — | 40s ribosomal protein s9 |
| XLOC_069897 | -3.28 | — | — | 40s ribosomal protein sa |
| XLOC_086164 | -4.07 | — | — | 60s acidic ribosomal protein p2a |
| XLOC_074236 | -2.55 | — | — | 60s acidic ribosomal protein p3 |
| XLOC_050223 | -4.04 | — | — | 60s ribosomal protein l10a-1 |
| XLOC_089139 | -5.33 | — | — | 60s ribosomal protein l10a-1 |
| XLOC_052453 | -3.18 | — | — | 60s ribosomal protein l11-1 |
| XLOC_085384 | -2.72 | — | — | 60s ribosomal protein l12 |
| XLOC_024978 | -3.21 | — | — | 60s ribosomal protein l12 |
| XLOC_000238 | -3.97 | — | — | 60s ribosomal protein l13-2 |
| XLOC_072997 | -3.00 | — | — | 60s ribosomal protein l13a |
| XLOC_074061 | -3.24 | — | — | 60s ribosomal protein l13a |
| XLOC_059199 | -4.13 | — | — | 60s ribosomal protein l14-1 |
| XLOC_070829 | -3.95 | — | — | 60s ribosomal protein l15 |
| XLOC_087363 | -3.05 | — | — | 60s ribosomal protein l17 |
| XLOC_027406 | -2.97 | — | — | 60s ribosomal protein l18 |
| XLOC_069091 | -3.72 | — | — | 60s ribosomal protein l18a |

| **Gene Id** | **Log$_2$(fold change）** | | | **Description** |
|---|---|---|---|---|
| | **XZ5** | **XZ54** | **Tadmor** | |
| XLOC_068657 | -3.40 | — | — | 60s ribosomal protein l21 |
| XLOC_081378 | -3.60 | — | — | 60s ribosomal protein l22-2 |
| XLOC_052029 | -2.50 | — | — | 60s ribosomal protein l23 |
| XLOC_073457 | -4.11 | — | — | 60s ribosomal protein l23 |
| XLOC_087786 | -2.90 | — | — | 60s ribosomal protein l24 |
| XLOC_088045 | -4.68 | — | -2.44 | 60s ribosomal protein l27 |
| XLOC_073413 | -3.29 | — | — | 60s ribosomal protein l28 |
| XLOC_044358 | -3.48 | — | — | 60s ribosomal protein l28 |
| XLOC_054228 | -2.78 | — | — | 60s ribosomal protein l29 |
| XLOC_079130 | -2.73 | — | — | 60s ribosomal protein l31 |
| XLOC_030675 | -3.17 | — | — | 60s ribosomal protein l32-1 |
| XLOC_023616 | -2.59 | — | — | 60s ribosomal protein l34 |
| XLOC_022235 | -2.90 | — | — | 60s ribosomal protein l35 |
| XLOC_086081 | -3.08 | — | — | 60s ribosomal protein l36 |
| XLOC_048731 | -3.74 | — | — | 60s ribosomal protein l37 |
| XLOC_071115 | -3.72 | — | — | 60s ribosomal protein l37a |
| XLOC_076961 | -4.29 | — | — | 60s ribosomal protein l37a |
| XLOC_000488 | -3.29 | — | — | 60s ribosomal protein l39 |
| XLOC_005927 | -3.37 | — | — | 60s ribosomal protein l39 |
| XLOC_064561 | -2.74 | — | — | 60s ribosomal protein l4 |
| XLOC_050541 | -3.67 | — | — | 60s ribosomal protein l4 |
| XLOC_071105 | -4.67 | — | — | 60s ribosomal protein l44 |
| XLOC_018594 | -4.97 | — | — | 60s ribosomal protein l44 |
| XLOC_052973 | -3.37 | — | — | 60s ribosomal protein l5 |
| XLOC_077183 | -2.90 | — | — | 60s ribosomal protein l6 |
| XLOC_034007 | -3.72 | — | — | 60s ribosomal protein l7-1 |
| XLOC_038379 | -3.43 | — | — | 60s ribosomal protein l7-2 |
| XLOC_048797 | -3.44 | — | — | 60s ribosomal protein l7a |
| XLOC_072252 | -3.38 | — | — | 60s ribosomal protein l7a-like |
| XLOC_077210 | -2.83 | — | — | 60s ribosomal protein l8 |
| XLOC_039836 | -3.88 | — | — | 60s ribosomal protein l9 |
| XLOC_070264 | -3.09 | — | — | ribosomal protein l3 |
| XLOC_053311 | -3.88 | — | — | ribosomal protein l3 |
| XLOC_014690 | -5.68 | — | — | ribosomal protein l35a |
| XLOC_077690 | -2.62 | — | — | ribosomal protein s8e family protein |
| XLOC_089142 | -3.53 | — | — | ubiquitin-60s ribosomal protein l40-like |
| XLOC_067175 | -3.57 | — | — | h aca ribonucleoprotein complex subunit 1-like protein 1 |
| **Metabolism** | | | | |
| XLOC_067835 | -4.15 | — | -6.62 | n- acetylneuraminyllactose-wheat germ agglutinin isolectin complexes |
| XLOC_023275 | -4.81 | — | -5.02 | bowman-birk type trypsin inhibitor |
| XLOC_084419 | -4.85 | — | — | btb poz domain-containing protein npy2-like |
| XLOC_082237 | -4.45 | — | — | enoyl |
| XLOC_059664 | -5.82 | — | — | floral organ regulator partial |
| XLOC_072581 | -4.00 | — | -3.28 | fructan:fructan 1-fructosyltransferase |
| XLOC_066763 | -5.69 | — | — | glucan endo- -beta-glucosidase-like protein 3-like |
| XLOC_066593 | -4.71 | — | — | glycine-rich rna-binding protein 2 |

| **Gene Id** | **Log$_2$(fold change）** | | | **Description** |
|---|---|---|---|---|
| | **XZ5** | **XZ54** | **Tadmor** | |
| XLOC_084315 | -3.75 | — | — | pescadillo homolog |
| XLOC_088471 | -3.14 | — | — | plasminogen activator inhibitor 1 rna-binding protein |
| XLOC_020421 | -5.96 | — | -6.91 | polygalacturonase precursor |
| XLOC_049760 | -3.78 | — | — | nucleolar protein 56-like |
| XLOC_058943 | -2.71 | — | — | nucleoside diphosphate kinase 1 |
| XLOC_023030 | -5.52 | — | — | nucleotide-diphospho-sugar transferase |
| XLOC_059652 | -3.52 | — | — | probable nucleolar protein 5-2-like |
| XLOC_037868 | -6.12 | — | — | probable xyloglucan glycosyltransferase 3-like |
| XLOC_019557 | -5.78 | — | — | proliferating cell nuclear antigen |
| XLOC_080710 | -5.03 | — | — | xylanase inhibitor |
| XLOC_035315 | -5.91 | — | — | xyloglucan endotransglycosylase |
| XLOC_021898 | -4.94 | — | — | rrna 2 -o-methyltransferase fibrillarin 2-like |
| XLOC_032762 | -10.20 | — | — | soluble starch synthase ii-1 |
| XLOC_072428 | -3.29 | — | — | sucrose:sucrose 1-fructosyltransferase |
| **Transcription** | | | | |
| XLOC_088407 | -4.42 | — | — | iq calmodulin-binding motif family protein |
| XLOC_077254 | -5.07 | — | — | transcription factor |
| XLOC_002612 | -4.90 | — | — | histone |
| XLOC_030128 | -5.07 | — | — | histone |
| XLOC_004416 | -5.10 | — | — | histone |
| XLOC_004357 | -6.06 | — | — | histone |
| XLOC_091211 | -6.49 | — | — | histone |
| XLOC_056012 | -4.81 | — | — | histone h2a |
| XLOC_035520 | -5.67 | — | — | histone h2a |
| XLOC_002279 | -4.67 | — | — | histone |
| XLOC_050837 | -6.96 | — | — | histone h2ax |
| XLOC_090463 | -3.87 | — | — | histone h2b |
| XLOC_091768 | -5.65 | — | — | histone h2b |
| XLOC_000527 | -4.46 | — | — | histone h3 |
| XLOC_079769 | -4.49 | — | — | histone h3 |
| XLOC_004411 | -4.84 | — | — | histone h3 |
| XLOC_004571 | -5.24 | — | — | histone h3 |
| XLOC_037264 | -5.51 | — | — | histone h3 |
| XLOC_044200 | -5.93 | — | — | histone h3 |
| XLOC_031968 | -6.72 | — | — | histone h3 |
| XLOC_017764 | -5.48 | — | — | histone H3.2 |
| XLOC_000112 | -4.30 | — | — | histone h4 |
| XLOC_002050 | -4.33 | — | — | histone h4 |
| XLOC_020172 | -6.01 | — | — | histone h4 |
| XLOC_053550 | -6.64 | — | — | histone partial |
| XLOC_027882 | -5.73 | — | — | histone superfamily protein |
| XLOC_078906 | -3.99 | — | — | probable histone h2a variant 3-like |
| **Cell growth** | | | | |
| XLOC_079294 | -5.51 | — | -4.23 | alpha-expansin 11 precursor family protein |
| XLOC_023702 | -4.68 | — | — | expansin a14 |
| XLOC_081596 | -2.73 | — | — | elongation factor 1-beta |

| **Gene Id** | **Log$_2$(fold change）** | | | **Description** |
|---|---|---|---|---|
| | **XZ5** | **XZ54** | **Tadmor** | |
| XLOC_091348 | -5.93 | — | — | high mobility group b protein 7-like |
| XLOC_001013 | — | 7.54 | — | cuticle protein |
| XLOC_007466 | — | 3.93 | 5.02 | cortical cell-delineating protein |
| XLOC_058291 | -5.27 | — | -3.53 | cortical cell-delineating protein precursor |
| XLOC_073825 | -4.86 | — | — | tubulin beta-1 chain-like |
| **Stress defense** | | | | |
| XLOC_051168 | -5.14 | — | -3.68 | pathogenesis-related protein pr-1-like |
| XLOC_069149 | -4.35 | — | — | peroxidase 12 |
| XLOC_074244 | -4.14 | — | — | peroxidase 12-like |
| **Unknown** | | | | |
| XLOC_052824 | -5.11 | — | — | hypothetical protein F775_23023 |
| XLOC_086268 | -3.86 | — | — | hypothetical protein TRIUR3_19916 |
| XLOC_055368 | -3.11 | — | — | ---NA--- |
| XLOC_030033 | -4.39 | — | — | ---NA--- |
| XLOC_066162 | -4.59 | — | — | ---NA--- |
| XLOC_062550 | -4.59 | — | — | ---NA--- |
| XLOC_052773 | -4.64 | — | — | ---NA--- |
| XLOC_063492 | -4.64 | — | — | ---NA--- |
| XLOC_018595 | -4.77 | — | — | ---NA--- |
| XLOC_063388 | -5.07 | — | — | ---NA--- |
| XLOC_020560 | -5.33 | — | — | ---NA--- |
| XLOC_042487 | -5.42 | — | — | ---NA--- |
| XLOC_036694 | -5.42 | — | — | ---NA--- |
| XLOC_086267 | -5.48 | — | — | ---NA--- |
| XLOC_024947 | -5.60 | — | — | ---NA--- |
| XLOC_029127 | -5.66 | — | — | ---NA--- |
| XLOC_035662 | -5.70 | — | — | ---NA--- |
| XLOC_041302 | -5.71 | — | — | ---NA--- |
| XLOC_086452 | -5.79 | — | -7.15 | ---NA--- |
| XLOC_070581 | -5.79 | — | — | ---NA--- |
| XLOC_050650 | -5.89 | — | — | ---NA--- |
| XLOC_057217 | -6.03 | — | — | ---NA--- |
| XLOC_036913 | -6.09 | — | — | ---NA--- |
| XLOC_038742 | -6.19 | — | — | ---NA--- |
| XLOC_066253 | -6.37 | — | — | ---NA--- |
| XLOC_037637 | -6.44 | — | -3.62 | ---NA--- |
| XLOC_071146 | -3.54 | — | — | nucl1_orysj ame: full=nucleolin 1 ame: full=protein nucleolin like 1 |
| XLOC_039880 | -5.92 | — | — | predicted protein |
| XLOC_072929 | -5.97 | — | — | predicted protein |
| XLOC_071850 | -6.07 | — | -4.44 | predicted protein |
| XLOC_090738 | -6.14 | — | — | predicted protein |
| XLOC_056048 | -4.88 | — | — | PREDICTED: uncharacterized protein LOC100830818 |
| XLOC_002739 | -4.30 | — | — | protein |
| XLOC_094886 | -4.63 | — | — | protein |
| XLOC_049284 | -5.39 | — | — | protein |
| XLOC_041525 | -5.65 | — | — | protein |
| XLOC_045462 | -5.92 | — | — | protein |
| XLOC_040319 | -6.52 | — | — | protein |
| XLOC_024380 | -5.16 | — | — | Protein H2A.5 |

| **Gene Id** | **Log$_2$(fold change）** | | | **Description** |
|---|---|---|---|---|
| | **XZ5** | **XZ54** | **Tadmor** | |
| XLOC_053272 | -4.09 | — | — | protein set |

— represents no change. NA represents unknown.

**Table S6** DEG up-regulated in both of XZ5 and XZ54

| **Gene Id** | **Log$_2$(fold change）** | | | **Description** |
|---|---|---|---|---|
| | **XZ5** | **XZ54** | **Tadmor** | |
| XLOC_073621 | 3.94759 | 3.80 | — | cortical cell-delineating protein |

— represents no change.

**Table S7** DEGs down-regulated in both of XZ5 and XZ54

| **Gene Id** | **Log$_2$(fold change）** | | | **Description** |
|---|---|---|---|---|
| | **XZ5** | **XZ54** | **Tadmor** | |
| XLOC_089282 | -2.73 | -2.84 | -4.62 | caffeic acid o-methyltransferase |
| XLOC_036698 | -5.16 | -4.21 | — | histone h2a |
| XLOC_092820 | -4.58 | -4.65 | — | ---NA--- |
| XLOC_071561 | -5.07 | -6.02 | -4.86 | ---NA--- |
| XLOC_067168 | -5.83 | -4.31 | -3.51 | ---NA--- |
| XLOC_049544 | -6.32 | -5.01 | — | ---NA--- |
| XLOC_090528 | -5.85 | -5.15 | -4.77 | predicted protein |
| XLOC_093109 | -5.79 | -6.07 | -5.33 | predicted protein |

— represents no change. NA represents unknown.

**Table S8** DEGs only up- or down-regulated in Tadmor

| **Gene Id** | **Log$_2$(fold change）** | | | **Description** |
|---|---|---|---|---|
| | **XZ5** | **XZ54** | **Tadmor** | |
| **Metabolism** | | | | |
| XLOC_083676 | —— | — | -2.17 | s-adenosylmethionine decarboxylase |
| XLOC_095268 | — | — | -2.47 | stem 28 kda glycoprotein |
| XLOC_034864 | — | — | -2.80 | triacylglycerol lipase |
| XLOC_082307 | — | — | -3.21 | n- acetylneuraminyllactose-wheat germ agglutinin isolectin complexes |
| XLOC_054295 | — | — | -3.40 | gdsl esterase lipase at4g28780-like |
| XLOC_073045 | — | — | -4.18 | gdsl esterase lipase |
| XLOC_073015 | — | — | -4.22 | arginine decarboxylase |
| XLOC_074328 | — | — | -4.32 | rare lipoprotein a like double-psi beta-barrel containing expressed |
| XLOC_027571 | — | — | -6.38 | glycosyltransferase protein 2-like |
| XLOC_090724 | — | — | -6.68 | snare-interacting protein keule |
| XLOC_089757 | — | — | -9.17 | caffeic acid 3-o-methyltransferase |
| XLOC_037002 | — | — | -5.07 | low-molecular-weight cysteine-rich protein lcr69 precursor |
| **Stress defense** | | | | |
| XLOC_084723 | — | — | 4.89 | dhn4 |
| XLOC_051828 | — | — | 2.74 | dehydration responsive protein |
| XLOC_034696 | — | — | -3.41 | lipid-transfer protein dir1-like |
| XLOC_031430 | — | — | -4.57 | pathogenesis-related maize seed protein |
| XLOC_070385 | — | — | -5.83 | stress responsive protein |
| **Transcription** | | | | |
| XLOC_022317 | — | — | -3.60 | nuclease s1 |
| XLOC_041687 | — | — | -4.82 | transposon unclassified |
| XLOC_067227 | — | — | -3.50 | transposon protein precursor |
| XLOC_041304 | — | — | 3.03 | is1 transposase partial |
| **Protein synthesis** | | | | |
| XLOC_049399 | — | — | 2.14 | 23s ribosomal rna |
| **Cell growth** | | | | |
| XLOC_063970 | — | — | 2.31 | cell wall-associated hydrolase |
| XLOC_057886 | — | — | 3.56 | cell wall-associated partial |
| XLOC_062551 | — | — | -4.68 | cortical cell-delineating protein |
| XLOC_059960 | — | — | -6.00 | cortical cell-delineating protein precursor |
| XLOC_083214 | — | — | -5.34 | keratin-associated protein 5-4-like |
| XLOC_091007 | — | — | -4.63 | root cap protein 1 |
| XLOC_079375 | — | — | -4.66 | root cap protein 1 |
| XLOC_018231 | — | — | -4.11 | root cap protein 1 |
| XLOC_030829 | — | — | -3.75 | root cap protein 1 |
| XLOC_001464 | — | — | 5.72 | muscle actin |
| **Transporter** | | | | |
| XLOC_034972 | — | — | -5.50 | mate efflux family protein |
| XLOC_030052 | — | — | -5.06 | organic cation transporter |
| **Unknown** | | | | |
| XLOC_062789 | — | — | 8.72 | predicted protein |

| **Gene Id** | **Log$_2$(fold change）** | | | **Description** |
|---|---|---|---|---|
| | **XZ5** | **XZ54** | **Tadmor** | |
| XLOC_057872 | — | — | 4.23 | protein |
| XLOC_082234 | — | — | 3.06 | hypothetical protein POPTR_1605s00200g |
| XLOC_026478 | — | — | 2.67 | hypothetical protein |
| XLOC_023118 | — | — | -4.37 | hypothetical protein F775_03747 |
| XLOC_092659 | — | — | -4.10 | ---NA--- |
| XLOC_031190 | — | — | 2.27 | predicted protein |

— represents no change. NA represents unknown.

**Table S9** KEGG pathways of tolerance related root hair genes in response to drought stress

| **Gene Id** | **$Log_2$ (fold change)** | | | **Pathway** |
|---|---|---|---|---|
| | **XZ5** | **XZ54** | **Tadmor** | |
| XLOC_013018 | 3.39 | — | 3.23 | Arginine and proline metabolism<br>Nitrogen metabolism<br>Alanine, aspartate and glutamate metabolism<br>Glyoxylate and dicarboxylate metabolism<br>Glutathione metabolism |
| XLOC_013896 | 3.68 | — | 3.68 | Selenocompound metabolism<br>Sulfur metabolism<br>Purine metabolism |
| XLOC_019100 | 4.85 | — | -2.58 | Phenylpropanoid biosynthesis<br>Phenylalanine metabolism |
| XLOC_012656 | 2.5 | — | 2.72 | Glyoxylate and dicarboxylate metabolism |

— represents no change.

## Text S1 Protein sequences used for alignment analysis in Figure 6.

**>HvEXPB7 (NCBI accession number KR732966)**
MAAAFSSYSVAAAFLCLLAANGCCGCPWFLPATFCPEPTPDPIPTPDPAPATPPPALATPSPGSGSGSA
NGSMGGWLDARATWYGAPDGAGPLDNGGACGFKNVNLPPFNAMTSCGNEPIFKDGKGCGSCYQ
IRCVGKVHPACSGDPETVIITDMNYYPVARYHFDLSGTAFGAMAKDGRNDELRHAGIIDMQFKRVP
CQYTGLSVTFHVEKGSNPNYLAILVEYGNGDGDVAQVDLMDGGEPTVSWRPMRESWGSIWRLDT
RRPLRGPFSLRVTNGSGRSLVADQVIPADWQPDTVYSSDVQFDE
**>OsEXPB7 (UniProtKB accession number Q9LD07)**
MAGRSRRRSFWSVGVAAALLCLLAAHGCSAKHHKPKPTPGGISGNASSSSSNSSTPSIPPPVAPTPT
APTPPIPSPGTGSSNGSSGGGGGGWLNARATWYGAPNGAGPDDNGGACGFKNVNLPPFSAMTSC
GNEPLFKDGKGCGSCYQIRCVGHPACSGLPETVIITDMNYYPVSLYHFDLSGTAFGAMAKDNRND
ELRHAGIIDIQFRRVPCQYPGLTVTFHVEQGSNPVYMAILVEYENGDGDVVQVDLMESRYSTGGVD
GTPTGVWTPMRESWGSIWRLDTNHPLQGPFSLRITNESGKTLIADQVIPADWQPNTVYSSIVQFD
**>ZmEXPB7 (NCBI accession number AAK56130.1)**
MATTLSSTVVVALGAPLFLLLVTCGSCARPVSFNASDLTADPGWDAARATWYGAPTGAGPDDDGG
ACGFKNVNLPPFSAMTSCGNEPLFKDGKGCGSCYQIRCQNHPACSGNPETVIITDMNYYPVAKYHF
DLSGTAFGAMAKPGRNDELRHAGIIDIQFKRVPCNYPGQKVTFHVEEGSNPVYFAVLVEFEDGDGD
AVQVDLMEANSASWTPMRESWGSIWRLDSGHRLTAPFSLRITNESGKTLVADHVIPANWVPNTYY
RSIVQY
**>TaEXPB7 (NCBI accession number AAS48884.1)**
MAGLLSVKAFALAAVLAAAYVSCAAAEQPGAADLDASAVSYSSAWLPARATWYGAPNGAGPDD
NGGACGFKHVNQYPFSSMTSCGNQPLFKDGKGCGSCNQIRCSGDKSCSGKIETVMITDMNYYPVA
QYHFDLSGTAFGALAKSGLNEKLRHSGIIDIQFRRVPCNFPGLKINFHVVDGSNAVYLAVLVEYED
MDGDVIQVDMKEANSGSWTPMRESWGSIWRMDSNHRLQGPFSMRITSDSGKKLVANNVIPANWR
PNTDYRSFVQFS

## Text S2 Protein sequences used for phylogenetic tree analysis in Figure 7a.

**>HvEXPB7 (NCBI accession number KR732966)**
MAAAFSSYSVAAAFLCLLAANGCCGCPWFLPATFCPEPTPDPIPTPDPAPATPPPALATPSPGSGSGSA
NGSMGGWLDARATWYGAPDGAGPLDNGGACGFKNVNLPPFNAMTSCGNEPIFKDGKGCGSCYQ
IRCVGKVHPACSGDPETVIITDMNYYPVARYHFDLSGTAFGAMAKDGRNDELRHAGIIDMQFKRVP
CQYTGLSVTFHVEKGSNPNYLAILVEYGNGDGDVAQVDLMDGGEPTVSWRPMRESWGSIWRLDT
RRPLRGPFSLRVTNGSGRSLVADQVIPADWQPDTVYSSDVQFDE
**>TaEXPA1 (NCBI accession number AAR27327.1)**
MAAAGALFFLFSSFCLLARQAAAGGYGGWQSAHATFYDGGDASGTMGGACGYGNLYSTGYGTN
TAALSTALFNDGAACGSCYELRCDNAGSSCRPGSILVTATNFCPPNYGLPSDDGGWCNPPRPHFDM
AEPAFLHIAQHRAGIVPVPYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGAGDARSVSIKGTRTGW
QAMSRNWGMNWQSNTFLDGQCLSFRVTSSDGRTVTSNAAAPAGWHFGQTFEGAQF
**>TaEXPA2 (NCBI accession number AAS48871.1)**
METRRPAVSTVSVGAVVLILAWSPAAAVASGGWMDAHATFYGDETGAETMQGACGYGNLFQQGY
GLDTTALSVALFSDGWSCGGCYEIQCHGDPHCKPGGAQVTVTATNLCPANYSKPYENWCNPPLKH
FDLSKPMFLRLVTDFHVGIIPVQYRRVPCAKKGGIRIEMTGNQYWVGVLVFNVAGPGEVKVLAVK
GAKDGQWRNMKRNWGQIWDGHVQNLVGQGLSFRVVASDGRSVVLDGVVPASWTIGQSFEGKG
QF
**>TaEXPA3 (NCBI accession number AAS48872.1)**
MASANALLLLFSAAFCFLARRAAGGYGSWQSAHATFYGGGDASGTMGGACGYGNLYSSGYGTN
AAALSTALFNDGAACGSCYELKCQEVSSSCLPGSITITATNLCPPNYALPNDERGWCNPPRAHFDM
AEPAYLQIGIYRAGIVAVAYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGAGDVQSVAIKGYSTGW
QAMARIWGQNWQSNADLDGQSFSFRVTFSDGRTVTSNNAAPAGWSFGQTFEGAQF
**>TaEXPA4 (NCBI accession number AAS48873.1)**
METPSLLLFTTLLAFAFKASVAQWTPAFATFYGGSDASDTMGGACGYGNLYNAGYGVNSAALSTA
LFNNGASCGMCFTITCDASKTPSCKQGTSITITATNFCPPNYALASDNGGWCNPPRQHFDMSQPAW
ETIAVYQAGIVPVNYRRVPYQRSGGMRFTINGNDYFELVTVANVGGSGVVSQMWIKGFKTDWMV
MSRNWGASWQSNAYLNSQSISFRVQTDDGRVITADNVAPYNWWFGGTYTSWQQF
**>TaEXPA5 (NCBI accession number AAS48874.1)**
MAVIKMLLLPALFALLLRAASAAQWTPAHATFYGGGDASGTMGGACGYGNLYGAGYGTQTTALS
TALFNNGASCGACFTIACDTRKSRMCKPGTSITVTATNFCPPNYALAGDNGGWCNPPRQHFDMAQ
PAWETIAVYKAGIVPVNHRRVRCQRSGGIRFTINGHSYFELVLVTNVGGSGGVAQMWIKGSRTNW
MEMSRNWGANWQSNAKLDGQSLSFRVKSDDGRVVTANDVAPPGWWFGGTYTSGAQLY
**>TaEXPA6 (NCBI accession number AAS48875.1)**
MAAGMRFLQLFAAVLAFCFVQARSDYWHQAYATFYGGADGAETMGGACGYDNLYAAGYGLNN
AALSTVLFNNGLSCGQCYLITCDTSKSNMCKPGTSITVSATNLCPPNWALANDNGGWCNPPREHF
DMSQPAWENLAIYRAGIVPVLYQRVACQRQGGLRFTMSGFNYFELVLVTNIAMSGSIRSMSVKGTN
TAWITMSQNWGANWQCLAGLKGQALSFGITSSGGQYKVFQDVVPAWWLFGQTFSTWQQFDY
**>TaEXPA7 (NCBI accession number AAS48876.1)**
MAPPLILLVVFLLPALAAGHQHPSSYGSSALSEWRNAKSSYFAADPGDAIGGACGFGDLGKHGYG
MATVGLSTALFERGAACGGCYEVKCVEDLKYCLPGTSIVVTATNFCPPNYGFPADAGGVCNPPNH
HFLLPIQAFEKIALWKAGVMPIQYRRVKCLREGGVRFSVSGKSFFFTVLISNVGGAGDVRSVKIKGT
ESGWLDMGRNWGQIWHINLDLTGQPVSFELTSSDGTTMTNFNVVPKDWEFGKTYTGKQFLL

**>TaEXPA8 (NCBI accession number AAS48877.1)**

MEFLGLLALAIAAMVGVVAGDDSTWSNGRATFYGGNDASGTMGGACGYGNMFSAGYGTNTAALSTALFNNGQSCGACFEIRCAGSGSCLPGSAVVTATNLCPANYALPNNEGGWCNPPQSHFDLAEPMFTKIAQARAGVVPVQYRRVVCVKTSGIRFTITGHSYFNLVLITNVAGAGDLTAVYVKSPSTGWLTMSHNWGANWQNGAMLNGQPLSFRVTTSDGRTTTSNNVAPSGWSFGQTYAGSQF

**>TaEXPA9 (NCBI accession number AAS48878.1)**

MAAAMPPSLPALLAALLLLVTLSPAAARVPGVYTGGDWQSAHATFYGGTDASGTMGGACGYGNLYSQGYGVNNAALSTALFNEGQRCGACFEIRCVNQPGWAWCLPGRPSIVVTATNFCPPNYALPSDDGGWCKPPRPHFDLAMPMFLHMAQYRAGIVPVSYRRVACRKSGGVRFTINGFRYFNLVLITNVAGAGDLVRASVKGSSTGWMPMSRNWGQNWQSNAILVGQALSFRVTASDRRTSTSWNAAPQNWRFGRTFEGKNLRV

**>TaEXPB1 (NCBI accession number AAS48879.1)**

MAPLSSKAVALVALFSLLVTYAAGAGNFNDSAFTADPNWEDARATWYGAPTGAGPDDDGGACGFKNTNQYPFSSMTSCGNEPIFKDGKGCGSCYQMRCTNDQSCSGNPETVVITDMNYYPVAKYHFDLSSTAFGAMAKPGLSEKLRHSGIIDIQFKRVPCEFPGLKVTFHVEQGSNPVYFAVLVEYEDGDGDVVQVDLMEANSGTWTPMRESWGSIWRLDSGHRLQAPFSMRITNESGKTLVADKVIPANWAPSTFYRSIVQYS

**>TaEXPB2 (NCBI accession number AAS48880.1)**

MGSLPLAVLAALLCCFLAVGGGAVELNTTDPSPFDVDLNATDATKYWGPWTPARATWYGQPNGAGPDDNGGACGFKHTNQYPFASMTSCGNQPLFKDGKGCGSCYKIRCRKDMSCSGRTETVIITDMNYYPVAPFHFDLSGTAFGRLAKPGLNDRLRHSGIIDIEFTRVPCEFPGLKIGFHVEEYSNPVYFAVLVEYEDGDGDVVQVDLMESRGPGGGKWTRMRESWGSVWRLDSNHRLQAPFSIRIRNESGKTLVANKVIPANWRPNTFYRSFVQYS

**>TaEXPB3 (NCBI accession number AAS48881.1)**

MAPLSSKAVALVALFSLLVTYAAGAGNFNDSAFTADPNWEDARATWYGAPTGAGPDDDGGACGFKNTNQYPFSSMTSCGNEPIFKDGKGCGSCYQIRCTNDQSCSGNPETVVITDMNYYPVAKYHFDLSGTAFGAMAKPGLSEKLRHSGIIDIQFKRVPCEFPGLKVTFHVEQGSNPVYFAVLVEYEDGDGDVVQVDLMEANSGTWTPMRESWGSIWRLDSGHRLQAPFSMRITNESGKSLVADKVIPANWAPSTFYRSIVQYS

**>TaEXPB4 (NCBI accession number AAS48882.1)**

MASSSSSVLLVAAVLAAVVCGAHGIAKVPPGPNITASPTSYGNKWLDAKTTWYGKPTGAGPKDNGGACGYKEVDKAPFHGMTSCGNIPIFKDGRGCGSCFELKCTKPEACSGEPTMVTITDKNEEPIAPYHFDLSGHAFGSMAKKGEEQKLRDAGEVEIKFRRVKCKYPAGTKVNFHVEKSSNENYLALVIKFLQGDGDVVGVDIKQKGEDKWTELNESWGAVWRIDTPHKLIGPFSVRYTTEGGTKTVVDDVIPKGWKPDTSYEAKGGY

**>TaEXPB5 (NCBI accession number AAS48883.1)**

MGSVSYVPAAAVLAALVSGGACIPSVPPGPNITTNYNNQWLPAKATWYGKPTGSGPKDNGGACGIKDVNLAPYNGMIACGNVPIFKDGKGCGSCHEIKCQKPSPCSDKPVTIFITDKNYEPIAPYHIGLSGTAFGAMATPGKEQTLRSFGELELQFRRVRCKYAPGTKITFHVEKGSNPNYLAVLVKFVSDDGDVVQMDIQESKSPAWIPLTLSWGAIWRWDGAKPLKGPFSIRVTSEPGKKLIAKDVIPANWKADTVYTSNVQF

**>TaEXPB7 (NCBI accession number AAS48884.1)**

MAGLLSVKAFALAAVLAAAYVSCAAAEQPGAADLDASAVSYSSAWLPARATWYGAPNGAGPDDNGGACGFKHVNQYPFSSMTSCGNQPLFKDGKGCGSCNQIRCSGDKSCSGKIETVMITDMNYYPVAQYHFDLSGTAFGALAKSGLNEKLRHSGIIDIQFRRVPCNFPGLKINFHVVDGSNAVYLAVLVEYEDMDGDVIQVDMKEANSGSWTPMRESWGSIWRMDSNHRLQGPFSMRITSDSGKKLVANNVIPANWR

PNTDYRSFVQFS

**>TaEXPB8 (NCBI accession number AAS48885.1)**

MAGVSTNAIALVLVTLLSVLVTSVRSAANYDTAAARSYNSGWLPAKATWYGAPTGAGPMDNGGA
CGFKNVNKYPFSSMTSCGNEPLFDGGAGCGSCYEIRCIAANNPSCSGQPRTVVITDMNYYPVARYH
FELSGTAFGAMAKYGLNDKLRHAGIIDMQFRRVRCNFPGMKVTFHVQRGSNPNYLAVLVEYANID
GTVVRMELMQTRNGRPTGSWEPMRRSWGSIWRMDTSRPLQGPFSMRITSDSGKTLVANNVIPAY
WRPDNAYWSNVQFY

**>TaEXPB9 (NCBI accession number AAS48886.1)**

MAKTCTLALLGALLVLSLLVSPIACSRKLAKVGGHDKSAPVKGHKNQTTTNPSSSAAYGGGWLPA
GATYYGNPNGDGSDGGACGYQTAVGHRPFSSMIAAGSSPLFMAGKGCGACYDVKCTSNSACSGK
PVNIVITDLSPGNLYPGEPCHFDMSGTALGAMAKPGMADKLRAGGVIRMQYKRVPCKYPGVNIAF
RVDQGSNPFYFKTLIEFEDDDGDLKAVALKEAGSGAWTPMAQDWGALWRLNEGRQLRAPFSLRL
TSDSGRKLVVSNVIPANWKAGATYRSLVNYP

**>TaEXPB10 (NCBI accession number AAS48887.1)**

MAGVSSNAIAFVALLSVLFTGVRSAVNYDTAVARSYNSGWLPAKATWYGAPNGAGPDDNGGACG
FKNVNQYPISSMGACGNEPIFAGGEGCGMCYEIKCDYSNNPSCSGQPRRIVITDMNYYPVARYHLD
LSGTAFGSMARYGLNDRLRHAGIIDMQFRRVPCNFPGMKVTFHVQRGSNPNYLAVLVEYANVDGT
VVRMELMQTINGRPTGYYQDMRRSWGSIWRMDTNRPLQGPFAIRITSDTGKTLVANNAIPAYWQP
DHAYWSNLQFY

**>OsEXPA1 (UniProtKB accession number Q7XWU8)**

MGGACGYGDLYSTGYGTNTAALSTVLFNDGASCGQCYRIMCDYQADRRFCISGTSVTITATNLCPP
NYALPNDAGGWCNPPRQHFDMAEPAWLKIGVYVGGIVPVMYQRVPCAKQGGVRFTINGRDYFEL
VLVSNVGGVGSIQSVSIKGSRTGWMAMSRNWGVNWQSNAYLDGQSLSFKVTSSDGQTLTFLDVAP
AGWTFGQTFSTSQQFS

**>OsEXPA2 (UniProtKB accession number Q40636)**

MASRSSALLLLFSAFCFLARRAAADYGSWQSAHATFYGGGDASGTMGGACGYGNLYSTGYGTNT
AALSTVLFNDGAACGSCYELRCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFD
MAEPAFLQIGVYRAGIVPVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTG
WQPMSRNWGQNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF

**>OsEXPA3 (UniProtKB accession number Q40637)**

MLSGMEKQPAMLLVLVTLCAFACKXSVAQSAFATFYGGKDGSCTMGGACGYGNLYNAGYGLYN
AALSSALFNDGAMCGACYTITCDTSQTKWCKPGGNSITITATNLCPPNWALPSNSGGWCNPPLQHF
DMSQPAWENIAVYQAGIVPVNYKRVPCQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSN
TGWMAMSRNWGANWQSNAYLAGQSLSFIVQLDDGRKVTAWNVAPSNWFFGATYSTSWVQF

**>OsEXPA4 (UniProtKB accession number Q0DHB7)**

MAIAGVLFLLFLARQASAAGYGGWQSAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALS
TALFNDGAACGSCYELRCDNAGSSCLPGSITVTATNFCPPNYGLPSDDGGWCNPPRPHFDMAEPAF
LHIAQYRAGIVPVSFRRVPCVKKGGVRFTVNGHSYFNLVLVTNVAGAGDVRSVSIKGSRTGWQPM
SRNWGQNWQSNAFLDGQSLSFQVTASDGRTVTSNNVAHPGWQFGQTFEGGQF

**>OsEXPA5 (UniProtKB accession number Q6ZGU9)**

MSSRRDVLAVVLVAALLPPALSRGLWLGHHGLGHGHGRWRAPHVGGHGQGQGPQQHAPLGGGG
WSSAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEVRCDAGGG
GSHSCLPGSVVVTATNFCPPNNALPSDDGGWCNPPRAHFDMSQPVFQRIALFKAGIVPVSYRRVAC
QKKGGIRFTINGHSYFNLVLVTNVGGAGDVHAVAVKSERSAAWQALSRNWGQNWQSAALLDGQ
ALSFRVTTGDGRSVVSNNAVPRGWSFGQTFSGAQFN

**>OsEXPA6 (UniProtKB accession number Q9M4X7)**

MAPPLLLLLASLLLVAARRALGLGLGQWQPGHATFYGGGDASGTMGGACGYGNLYSQGYGTSTA
ALSTALFNRGLSCGSCYELRCAGDHRRSCLPGGATVTVTATNFCPPNYALPSDGGGWCNPPRRHFD
LAEPAFLRIARHAAGIVPVSFRRVACARKGGVRFTVNGHAYFNLVLVTNVGGAGDVRSLAVXGSGS
GSRVGGRWQPMSRNWGQNWQSNAYLDGKALSFRVTAGDGRSLTCADVAPAGWQFGQTFEGRQF

**>OsEXPA7 (UniProtKB accession number Q852A1)**

MSPAPRVLVLVVATVVALQVSPAAGRIPGAYGGGEWQSAHATFYGGSDASGTMGGACGYGNLYSQ
GYGVNNAALSTALFNSGQSCGACFEIKCVNQPGWEWCHPGSPSILITATNFCPPNYALPSDNGGWC
NPPRPHFDLAMPMFLHIAEYRAGIVPVSYRRVPCRKKGGVRFTINGFRYFNLVLITNVAGAGDIVRA
SVKGTSTGWMPMSRNWGQNWQSNSVLVGQALSFRVTGSDRRTSTSWNAAPAGWHFGQTFEGKN
FRV

**>OsEXPA8 (UniProtKB accession number Q9XHX0)**

MAAARMLVLLASLCALLLTASAAKWTPAFATFYGGSDASGTMGGACGYGDLYGAGYGTRTAALS
TALFNGGASCGACFTIACDTRKTQWCKPGTSITVTATNFCPPNYALSGDAGGWCNPPRRHFDMSQP
AWETIAVYRAGIVPVNYRRVPCQRSGGIRFAVNGHSYFELVLVTNVGGSGAVAQMWIKGSGTGWM
AMSRNWGANWQSNARLDGQALSFRVQADDGRVVTAADVAPAGWSFGATYTSSAQFY

**>OsEXPA9 (UniProtKB accession number Q4PR53)**

MEKKLLVVLFLSLCCASRLRGEAAQQWTSATATFYGGSDASGTMGGSCGYGNMYSAGYGTNTTA
LSSALYGDGASCGACYLVTCDASATRWCKNGTSVTVTATNYCPPNYSESGDAGGWCNPPRRHFD
MSQPAWEAIAVYSSGIVPVRYARTPCRRVGGIRFGIAGHDYYELVLVTNVAGSGAVAAAWVKGSGT
EWLSMSRNWGENWQSNAYLTGQALSFRVQADDGGVVTAYDVAPANWQFGSTYQSDVNFSY

**>OsEXPA10 (UniProtKB accession number Q7XUD0)**

MAPCLLLVLFLLPALATGHQHPSTLGSSALSEWRSAKASYYAADPEDAIGGACGFGDLGKHGYGM
ATVGLSTALFERGAACGGCYEVKCVDDLKYCLPGTSIVVTATNFCAPNFGLPADAGGVCNPPNHH
FLLPIQSFEKIALWKAGVMPIQYRRVNCLRDGGVRFAVAGRSFFLTVLISNVGGAGDVRSVKIKGTE
SGWLSMGRNWGQIWHINSDFRGQPLSFELTSSDGKTLTNYNVVPKEWDFGKTYTGKQFLL

**>OsEXPA11 (UniProtKB accession number Q4PNY1)**

MELLRLLAVAAVAAMAAEVAAGGDSGWSSGSATFYGGSDASGTMGGACGYGNLYSAGYGTSTAA
LSTALFNNGQSCGACFEVRCGGGGSCLAGTVAVTATNLCPPNYALAGDAGGWCNPPRPHFDMAEP
AFTRIAQARAGVVPVQYRRVACAKQGGIRFTITGHSYFNLVLVTNVGGAGDVTAVSVKGSRSGWQ
AMSHNWGANWQNGANLDGQPLSFRVTASDGRTVTSDNVAPSGWSFGQTFSGGQF

**>OsEXPA12 (UniProtKB accession number Q7G6Z2)**

MARSAFFFHCVAAVAACIAATAAALSGTATFYGGSDASGTMGGACGYGNLYSTGYGTNTAALSSA
LFNDGAACGECYQITCDQSNSKWCKAGTSVTITATNLCPPDYSKPSNDGGWCNPPRQHFDMAQPA
WEQIGVYRGGIVPVNFQRVSCTRKGGVRFTINGNSYFELVLITNVGGPGSIKSVQIKGTKTGWVTM
SRNWGANWQANNYLNNQAISFSVTSTAGKTLVFEDVAPSNWQFGQTFTSGVQFY

**>OsEXPA13 (UniProtKB accession number Q4PR52)**

MAGVARMLAAVVCAIMPAAAMAAGGVGALEPSGWVRAHATFYGGADASGTMGGACGYGNLYA
QGYGTRTAALSTALFNDGLACGQCYKLVCDRKTDRTWCKPGVSVTITATNFCPPNWDLPSDSGGW
CNPPRPHFDMAQPAWEKIGIYRGGIIPVIYQRVPCMKKGGVRFTINGHDYFQLVLLTNVGAAGSIKA
MDVKGSKSPDWMAMAHNWGAQWHSLAYLTGQGLSFRVTITDGQTLVFPNVVRPGWRFGQTFAS
NIQFK

**>OsEXPA14 (UniProtKB accession number Q4PR51)**

MASSPRAFALVFFAIAAVGCTQLTTADDAAPPVWQKAHATFYGGADASGTMGGGCGYGDLYSQG
YGTRNAALSTALFNDGASCGQCYKIACDRKRAPQWCKPGVTVTITATNFCPPNWDLPSDNGGWC
NPPRPHFDMAQPAWEKIGIYSAGIIPVIYQRVPCIKKGGVRFTINGHDYFNLVLVTNVATTGSIKSMD
IMGSNSTDWMPMVRNWGANWHSLSYLTGQTLSFRVTNMDGQTLVFKNIVPSGWKFGQTFTSKLQ

FK

**>OsEXPA15 (UniProtKB accession number Q4PR50)**

MAMWKKKKTPSILPLVVVIAAASLIAPTTAGWSSGTATFYGGSDASGTMGGACGYGNLYWSGYGTNTAALSSALFNDGASCGQCYQIACDHQAEPRWCLQGRTVTITGTNLCPPNYALSSNDGGWCNPPRTHFDMAEPAWLQIGIYKAGIVPVLYQRVPCVKQGGVRFTMGGFNYFELVLISNVAGSGSIQSVWVKGPNTDRMPLSRNWGANWQSHAGLVGQTLTFGVTSTGGQTLVFQNIVPAWWKFGQSFSSNLQFSY

**>OsEXPA16 (UniProtKB accession number Q69XV9)**

MSSVLLFLLLLLLSGVSLSGCIRLGSGGYEEWRMGSATYIKESLGHPLNDGGGACGYGDLDIFRYGRYTAGVSGALFGRGSACGGCYEVRCVNHVLWCLRGSPTVVVTATDFCAPNLGLSDDYGGWCNFPKEHFEMSEAAFLRVAKAKADIVPVQFRRVSCDRAGGMRFTITGGASFLQVLITNVAADGEVAAVKVKGSRTGWIPMGRNWGQNWQCDADLRGQPLSFEVTGGRGRTVVAYSVAPPDWMFAQTFEGKQFVE

**>OsEXPA17 (UniProtKB accession number Q4PR49)**

MASSWNNPAIFLAAALAVATAAQVVTAGFTTDLYWQQQPAPGAVTPYKTSDWHDGSATFYGDPSGMGDDFGGACGYVSNDIVSLYSTKTAALSTPLFADGNGCGQCYELRCVKSPWCNPGSPSVVITGTNLCPPNWYLPNDDGGWCNPPRHHFDMAPPSFLKLAQRVAGIVPVQYRRVPCQRTGGVRFCLQGNHYWLLLYVMNVGGAGDVSSLSVKTSGGGGAWIQAAHNWGITYQVFAALDNSDGLTVKLTTYSTPQQTIIVSDAISPWWITGLCYQGSNNFY

**>OsEXPA18 (UniProtKB accession number Q4PR48)**

MGNIVLQLLAILALCIAPARSGWLQGTATFYGGADGSGTMGGACGYGNLYDQGYGINNAALSTPLFNNGASCGQCYLIICNYDKAPSGCRMGTAITVTGTNFCPPNYDLPYGGWCNTTRPHFDMSQPAWENIGIYSAGIVPILYQQVKCWRSGGVRFTITGLNYFELVLVTNMAGSGSIASMSVKGSSTGWIQMSRNWGANWQCLAGLAGQALSFTVTSTGGQTIVFDSVVPAGWSFGQTFSTYQQFDY

**>OsEXPA19 (UniProtKB accession number Q7G6Z5)**

MGNIFLQLLAVVALCIAPARSDWLPGTATFYGGADGSGTMGGACGYGNLYDQGYGINNAALSTPLFNDGASCGQCYLIICDYSKAPDWCKLGKAITVTGTNYCPPNYDLPYGGWCNATRPHFDMSQPAWENIGIYNAGIIPILYQQVKCWRYGGVRFTINGFNYFELVLVTNMAGSGSIASMSVKGSCTGWIQMTRNWGANWQCLAGLAGQALSFNVTSTGGQTIVFDDAVPAGWSFGQTFSTYHQFDY

**>OsEXPA20 (UniProtKB accession number Q10RK1)**

MGNILLQLLAVVALCIAPARSDWLPGTATFYGGADGSGTMGGACGYGNLYDQRYGINNAALSTPLFNDGASCGQCYLIICDYGKAPDWCKLGKAITVTGTNYGGWCNATRPYFDMSQPAWENIGIYSAGIVPILYQQVKCWRYGGVRFIINGFNYFELVLVTNMPGSGSIVSMSVKGSCTGWIQMTRNWGANWQCLAGLAGQALSFNVTSTGGQTIVFDDAVPAGWSFGQTFSTYHQFDY

**>OsEXPA21 (UniProtKB accession number Q10KN4)**

MAPPSLPILLVLLSLSSSLSSSSAAAAGRWTDAHATFYGGADASGTMGGACGYGNTYGQGYGTDTAALSAVMFGDGLSCGACFELRCGGGGGGDRRGCLPPAAGKSIVVTATDLCPANHALPGDRGGWCNPPLHHFDLSQPAFLRIARFQSGIVPVSYRRVACRRKGGMRFTINGHSYFNLVLVSNVGGAGDVHAVAVKAGGGRKARWQAMARNWGQNWQSGALLDGQALSFTVTTGDRRSVVSYNVAPAGWAFGQTFTGRQFT

**>OsEXPA22 (UniProtKB accession number Q4PR44)**

MAPARPFALLFLAVTVGFVLLTAADDSANATATTTTAMAPSSSTDDAAPPVWLKAHATFYGGADASGTMGGACGYGDLYSQGYGTRNAALSTALFNDGASCGQCYKIACDRKRAPQWCRPGVTVTITATNFCPPNWDLPSDNGGWCNPPRPHFDMAQPAWEKIGIYRAGIIPVIYQRVPCVKKGGVRFTINGHDYFNLVLVTNVATTGLIKSMDVMGSNSTDWLPMVRNWGANWHSLSYLTGQMLSFRVTNMDGQTLVFRNIVPSGWKFGQTFASKLQFK

**>OsEXPA23 (UniProtKB accession number Q4PR43)**
MAPARAFVLVLLAVASASTAAANTATTTPTNPVAAPTQWQKAHATFYGGADASGTMGGACGYGN
LYSQGYGTRNAALSTALFNDGASCGQCYKIACDRKRAPQWCKPGVTVTITATNFCPPNWNLPSDN
GGWCNPPRPHFDMAQPAWEKIGVYSAGIIPVIYQRVPCVKKGGLRFTINGHDYFQLVLVTNVAAAG
SIKSMEVMGSNTADWMPMARNWGAQWHSLAYLTGQGLSFRVTNTDDQTLVFTNVVPPGWKFGQ
TFASKLQFK

**>OsEXPA24 (UniProtKB accession number Q4PR42)**
MADMAPARALALVLLAVAVGSALMAAAQDAPSPPTPMAPSPSTDETPPVWLKAHATFYGGADAS
GTMGGACGYVDLYSQGYGTRNAALSTALFNDGASCGQCYKIACDRKRAPQWCKPGVTVTVTAT
NFCPPNWNLPSDNGGWCNPPRPHFDMAQPAWEKIGIYRAGIIPVMYQRVPCVKKGGVRFTINGHD
YFNLVLVTNVATTGSIKSMDIMGSNSTDWMPMVRNWGANWHSLSYLTGQMLSFRVTNMDGQTL
VFRNIVPSGWKFGQTFASKLQFK

**>OsEXPA25 (UniProtKB accession number Q4PR41)**
MEYAILFATSLVITVLAASGFAPAHGWNKGTATFYGGADASGTMGGACGYGNLYTAGYGTNTAAL
SSVLFNDGWSCGQCYLIMCDAAATPQWCRAGAAVTITATNLCPPNWALPSNSGGWCNPPRPHFDM
AEPAWLQIGIYKAGIIPVLYQQVKCWRQGGIRFTMGGFNFFELVLVSNVAGSGSVRSVSVKGGSTG
WITLNRNWGANWQCNSGLVGQALSFAVTSTGGQTLYIYNVVPSWWSFGMTFTSNQQFSY

**>OsEXPA26 (UniProtKB accession number Q2QP13)**
MAPLPLLTTTSLLLFFFLASSFAADVVVAGGGGGGGGYDGGGDEGGGGGDEGGGGGGGAKM
PHVNHGRYKCGPWVDGHATFYGGRDASGTTEGGACGYKDADGYGAMTAAVSPALFDNGAGCG
ACYELKGDSGKTVVVTATNQAPPPVNGMKGEHFDLTMPAFLSIAEEKLGVVPVSYRKVACVRQGG
IKYTITGNPSYNMVMVKNVGGAGDVVKLTVKGTKRVKWTPLQRSWGQLWKTEANLTGESLTFRV
MTGDHRKATSWRVAPRDWTYDNTYQAKKNF

**>OsEXPA27 (UniProtKB accession number Q7XE35)**
MGAMAENLLVLCTILAARMALAAADDWIPATATFYGGNDGSGTMGGACGYGNLYDQGYGLENA
ALSTALFNDGAACGQCYLIVCDTDKAGRWCKPRGAVTVTATNLCPPNWALPSDGGGWCNPPRRH
FDMSQPAWERIGVYRAGIVPVLYRRVRCWRRGGVRFTVGGFDHFELVLVANVAGSGSVAAVSVRG
AGTGWLQMSRNWGANWQSLAGLAGQPLSFGVTTTGGQYILFQDVAPAGWKFGQTFSTSKQFDY

**>OsEXPA28 (UniProtKB accession number Q4PR40)**
MVIRFFAVLAAALCITSASAAAAGGWVSGTATFYGGKDASGTMGGACGYGNLYTQGYGVYNAAL
STALFNGGASCGQCYLIMCDASKTPEWCKAGTAVTITATNLCPPNWALANDDGGWCNPPRPHFDM
SQPAWETIGIYRAGIVPVLYQQVKCWRQGGVRFTVSGFNYFELVLITNVAGSGSVQAMSVKGSKTG
WIPLARNWGANWQCNSALVGQALSFRVTSTGGQTLQINSVVPEWWEFGTTFTSNQQFDY

**>OsEXPA29 (UniProtKB accession number Q4PR39)**
MARRGHVFAVVAFVSYALLAAASTTVEAFAASGWSKGTATFYGGSDASGTMGGACGYGNLYTQG
YGTRTAALSTALFDDGASCGQCYALTCDARADPRWCRAGASVTVTATNFCPPNYALPSDDGGWCN
PPRPHFDMAQPAWERIGVYRGGIVPVAFRRVPCRRRGGVRFTVAGRDYFELVLVTNVAAAGSVRS
MEVRGSRRGAGWMAMSRNWGANWQSLAYLDGQGLSFRVTATDGQTIVFAGVVPPSWRFGQTFA
STQQFM

**>OsEXPA30 (UniProtKB accession number Q8W2X8)**
MAAASSTTATTAILAAVIISLAGAATTVDAKFRAMQWTPAHATFYGDETASETMGGACGYGNLYAS
GYGTDTAALSTTLFKDGYGCGTCYQMRCVGTASCYRGSPAITVTATNLCPPNWAEDPDRGGGGW
CNPPRAHFDLSKPAFMRMADWRAGIVPVMYRRVPCARAGGLRFALQGNPYWLLAYVMNVAGAG
DVGDMWVKAGGGGGWVRMSHNWGASYQAFAQLGGQALSFKVTSYTTGQTILAAGVTPASWCF
GLTYQARVNFS

**>OsEXPA31 (UniProtKB accession number Q75I75)**

MAMSSRLALCLAVVAACAAGGAVADWSPATATFYGGSDGSGTMGGACGYGNLYDQGYGVDNAA
LSQALFNDGASCGQCYLIVCDTSRAPQWCKAGTAVTVTATNLCPPNWALPSDGGGWCNPPRPHFD
MSQPAWEQIGVYQAGIVPVLYQRVRCWRQGGVRFTVAGLNYFELVLITNVAGSGSVASAWIKGTN
TGWIQMSRNWGANWQSLAGLAGQALSFAVTTTGGQYLQFQDVAPAWWQFGQTFSTYQQFDY

**>OsEXPA32 (UniProtKB accession number Q6YYW5)**

MWCTWALGRVVLAVVFLVALAAGDAAPPKVHRNHGKFTAGPWKQAHATFYGGRDGSGTLDGAC
GYKDTSKEGYGVQTVAVSTPLFGAGAGCGACYEVKCVDSPDGCKVGAAPLVVTATNLCPPNPGQS
NDNGGWCNPPREHFDLSMPAFLQIAQEKAGIVPISYRRVPCVKVGGIRYTITGNPYFNLVMVSNVG
GAGDVAGLSVKGNKRVKWTPLKRNWGQEWQTSEVLTGESLTFRVMTGDHRKATSWHVLPPDWQ
FGVTYQATKNFN

**>OsEXPA33 (UniProtKB accession number POC1Y4)**

MAMPVVQVLLLCALAYQAVDAQWTPATATFYGGSDGAGTMGGACGYGNLYNAGYGLNNAALSS
ALFNDGAMCGACYTIACDTSQSTWCKPGTSITITATNLCPPNYAKKSDAGGWCNPPRKHFDMSQP
AWTSIAIYQAGIVPVNFKRVPCQKSXGIRFTISGRDYFELVTVFNVGGSGVVAQVSIKGSKTDWMA
MSRNWGQNWQSNAYLNTQSLSFKVKLDDAREVTVWNIAPSNWNFGTTYTSNINF

**>OsEXPB1 (UniProtKB accession number Q40638)**

MASSSLLLACVVVAAMVSAVSCGPPKVPPGPNITTSYGDKWLEAKATWYGAPKGAGPKDNGGAC
GYKDVDKAPFLGMNSCGNDPIFKDGKGCGSCFEIKCSKPEACSDKPALIHVTDMNDEPIAAYHFDL
SGLAFGAMAKDGKDEELRKAGIIDTQFRRVKCKYPADTKITFHIEKASNPNYLALLVKYVAGDGD
VVEVEIKEKGSEEWKALKESWGAIWRIDTPKPLKGPFSVRVTTEGGEKIIAEDAIPDGWKADSVYK
SNVQAK

**>OsEXPB2 (UniProtKB accession number O24230)**

MAGASAKVVAMLLSVLATYGFAAGVVYTNDWLPAKATWYGQPNGAGPDDNGGACGFKNTNQY
PFMSMTSCGNEPLFQDGKGCGACYQIRCTNNPSCSGQPRTVIITDMNYYPVARYHFDLSGTAFGAM
ARPGLNDQLRHAGIIDIQFRRVPCYHRGLYVNFHVEAGSNPVYLAVLVEFANKDGTVVQLDVMES
LPSGKPTRVWTPMRRSWGSIWRLDANHRLQGPFSLRMVSESGQTVIAHQVIPANWRANTNYGSK
VQFR

**>OsEXPB3 (UniProtKB accession number Q336T5)**

MAFSISKKAAVAALFSFLVVTCVAGARPGNFSASDFTADPNWEVARATWYGAPTGAGPDDDGGAC
GFKNTNQYPFSSMTSCGNEPIFKDGKGCGSCYQIRCVNHPACSGNPETVIITDMNYYPVSKYHFDL
SGTAFGAMAKPGQNDQLRHAGIIDIQFKRVPCNFPGLKVTFHVEEGSNPVYFAVLVEYEDGDGDV
VQVDLMEANSQSWTPMRESWGSIWRLDSNHRLTAPFSLRITNESGKQLVASQVIPANWAPMAVYR
SFVQYSS

**>OsEXPB4 (UniProtKB accession number Q94LR4)**

MGSLSSLAAAAVFLSLLAVGHCAAADFNATDADADFAGNGWDFNSSDAAVYWGPWTKARATWY
GQPNGAGPDDNGGACGFKHTNQYPFMSMTSCGNQPLFKDGKGCGSCYKIRCTKDQSCSGRSETV
IITDMNYYPVAPFHFDLSGTAFGRLAKPGLNDKLRHSGIIDIEFTRVPCEFPGLKIGFHVEEYSNPVYF
AVLVEYEDGDGDVVQVDLMESKTAHGPPTGKWTPMRESWGSIWRLDTNHRLQAPFSIRIRNESGK
TLVANNVIPANWRPNTFYRSFVQYS

**>OsEXPB5 (UniProtKB accession number Q7XT39)**

MVSRGTFVFAVLVALPILSLPVSGYEQNYTAGRRSTMSLGRGYGWSSGGATWYGGPQGDGSEGGA
CGYQSAVGQRPFSSMIAAGGPSLFKNGKGCGSCYQIKCTGNRACSGRPVTVVITDSCPGGVCLNEA
AHFDMSGTAFGAMANRGMGDRLRSAGVLKIQYKRVPCRFAMNVAFKVDAGSNPYYLAILVQYAN
GDGDLAAVHIMKARGGGGWKAMQQSWGATWRLNSNTGKPLSPPFSIRLTSGSGKVLVANNVIPSG
WQAGLTYRSTVNYAA

**>OsEXPB6 (UniProtKB accession number Q7XCA7)**

MAARMGSKVAAILAILSVLVVHGSCKGHPVNYNVSDASAYGSGWLPARATWYGAPTGAGPDDN
GGACGFKNVNQYPFSSMTSCGNEPIFKDGKGCGSCYQIRCNKDPSCSGNIETVIITDMNYYPVARY
HFDLSGTAFGAMAKPGLNDKLRHSGIIDIQFRRVPCNYPGLKINFHVEEGSNPVYFAVLVEYEDLDG
DVVQVDLMESKSAYGGATGVWTPMRESWGSIWRLDSNHRLQAPFSLRIRSDSGKTLVANNVIPAN
WSPNSNYRSIVQFS

**>OsEXPB7 (UniProtKB accession number Q9LD07)**

MAGRSRRRSFWSVGVAAALLCLLAAHGCSAKHHKPKPTPGGISGNASSSSSNSSTPSIPPPVAPTPT
APTPPIPSPGTGSSNGSSGGGGGGWLNARATWYGAPNGAGPDDNGGACGFKNVNLPPFSAMTSC
GNEPLFKDGKGCGSCYQIRCVGHPACSGLPETVIITDMNYYPVSLYHFDLSGTAFGAMAKDNRND
ELRHAGIIDIQFRRVPCQYPGLTVTFHVEQGSNPVYMAILVEYENGDGDVVQVDLMESRYSTGGVD
GTPTGVWTPMRESWGSIWRLDTNHPLQGPFSLRITNESGKTLIADQVIPADWQPNTVYSSIVQFD

**>OsEXPB8 (UniProtKB accession number Q10T32)**

MVSGDVGVVVYYLLLVLVVVQGCKGSSAVQGEGRWYNESEAIGGAAAWGNAKATWYGQPNGA
GAADNGGACGFKKVNQYPFMGMTSCGNQPLYKGGKGCGSCYRVRCNRNPACSGNAQTVAITDM
NYFPLSQYHFDLSGIAFGRLAKPGRADDLRRAGIIDVQFARVPCEFPGLKVGFHVEEGSSPVYLAVL
VEYENGDGDVAQVDLKEAGAGGGRWTPMRESWGSVWRLDSNHRLRAPFSIRIRSDSGKTLVAPD
VIPLNWTPNTFYRSFVQYSS

**>OsEXPB9 (UniProtKB accession number Q7XCG7)**

MGSLTTNIVLAVAVVAALVGGGSCGPPKVPPGPNITTNYNAPWLPARATWYGQPYGSGSTDNGGA
CGIKNVNLPPYNGMISCGNVPIFKDGRGCGSCYEVKCEQPAACSKQPVTVFITDMNYEPISAYHFD
FSGKAFGAMACPGKETELRKAGIIDMQFRRVRCKYPGGQKVTFHVEKGSNPNYLAVLVKFVADDG
DVIQMDLQEAGLPAWRPMKLSWGAIWRMDTATPLKAPFSIRVTTESGKSLIAKDVIPVNWMPDAI
YVSNVQFY

**>OsEXPB10 (UniProtKB accession number Q8H7T4)**

MASSCLLLACVVAAAMVSAVSCGPPKVPPGPNITAAYGKQWLEARGTWYGKPKGAGPDDNGGA
CGYKDIDKAPFLGMNSCGNDPIFKDGKGCGSCFEVKCSKPEACSDKPVIIHITDMNTEPIAAYHFDL
SGHAFGAMAKEGKDEELRKAGIIDMQFRRVRCKYPGETKVTFHVEKGSNPNYFAVLVKYVGGDG
DVVKVELKEKGSEEWKPLNESWGAIWRIDTPKPLKGPFSLRVTTESDQKLVANDVIPDNWKANAL
YKSEIQVD

**>OsEXPB11 (UniProtKB accession number Q6H676)**

MAKSCTLVLLLVALVGLSLLVSPIACSRKLSKPKPKPKPSMKKPVVRAHNNYTGSPSVTVTTGWAA
AGATYYGAPNGDGSDGGACGYQTAVGQRPFSSMIAAGSPSLYKGGKGCGACYEVKCTTNAACSG
QPATVVITDECPGGICLAGAAHFDMSGTSMGAMAKPGMADKLRAAGILQVQYRRVPCKYSGVNI
AFRVDQGANPFYFEVLIEFEDGDGDLNAVDLMEAGCGWTPMVQNWGALWRYNSNTGKALKAPF
SLRLTSDSGKVLVANNVIPASWKPGVTYRSLVNYS

**>OsEXPB12 (UniProtKB accession number Q10G40)**

MAAFEPHRLQLLYFIAITVLASVFQPCTSIELHRELSGWSNGIATWYGDPNGAGSEGGACGYQYAV
DQPPFSSRIAAGSPYIYDSGKGCGSCYRVVCAGNEACSGIPVTVVITDQGPGGPCLEELVDGQCMN
EAAHFDMSGTAFGAMARPGQADQLRGAGLLQIQYTRVECEWTGVGLTFVVDSGSNPNYLALLVE
YDDNDSDLAAVDIMPIGAGASGSWIPMQQSWGAVWRLNSGSALQGPFSVRLTFSSGQMFVASNAI
PAGWNPGMAYQPGGVAMRVRGRNGGRRGYEAVGMLGGLCHLLLLLLLMLFEL

**>OsEXPB13 (UniProtKB accession number Q946J4)**

MASSSLLLASVVVAAMVSAVSCGPPKVPPGPNITASYGDKWLEARATWYGAAKGAGRKDNSGAC
GYKDVDKAPFLGMNSCGNDPIFKDGKGCGSCFEIKCSKPKACSDKPVLIHVTDMNDEPIAAYHFD
LFGLAFGAMAKDGKDEELRKAGIIDT*FRRFKCKYPADTKITFHIEKASNPNYLALLVKYVAGDGD
VVEVEIKEKGSEEWKALKESWGAIWRIDTPKPLKGPFSVRVTTEGGEKIIAEDAIPDGWKADSVYK

SNVQAK*

**>OsEXPB14 (UniProtKB accession number Q6H677)**

MALAAKLLPSIVAFVALACCVLRSSVASVDHHRKLSGWSIGGATWYGPANGSGTDGGACGYQGD
VGQPPFNSMIAAGSPSIYESGKGCGSCYQVKCSGNPSCSGKPVTVVLTDLCPGGACLEEPVHFDLS
GTAFGAMAKPGQDDQLRNAGKLPVQYARVPCKWQGVDIAFRVDAGSNQYYLAVLVEDEDGDGD
LSAVDLMQSGGSGGGGSWAAMQQSWGAVWKYNSGPAPLQAPMSIRLTSGSGRTLVASNVIPAGW
QPGGTYRSIVNFRRED

**>OsEXPB15 (UniProtKB accession number Q7XT40)**

MASRFQLILSTFVVIAAVTMLPRPCASIEFHRKLSSWSNGGATWYGAANGAGSDGGACGYQGAVF
QAPFSSMIAAGSPSIYKSGLGCGSCYQVKCTGNSACSGNPVTVVLTDECPGGPCLSEPVHFDLSGTA
FGAMANPGQADQLRAAGVLQIQYNRVPCNWGGVKLTFVVDVGSNPNYFAVLVKYENGDGDLSG
VELMQTGAGAAWTQMQQSWGAVWKLNAGSALQAPFSIRLTSSSGKTLVASNVIPSGWKPGMSYIS
TVNF

**>OsEXPB16 (UniProtKB accession number Q0DZ85)**

MLIRSVLFVSLLSAAFVFDSGEAGAAHRVVDPEWHPATATWYGSADGDGSDGGACGYGTLVDVV
PMKTRVGAVSPVLFKGGEGCGACYKVRCLDASICSRRAVTVIVTDECPGGVCAFGRTHFDLSGAAF
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KQANSAQWQDMKHIWGATWSLTPGPLVGPFSVRLTTLTTRQTLSAQDVIPKNWTPKATYTSRLNF
A

**>OsEXPB17 (UniProtKB accession number Q7X6J9)**

MAAASSRSFSLCVLLLLLLLAPPISASFLFDGGKSKSAAAAAAVDMEWRPATATWYGDAEGDGST
GGACGYGSLVDVVPMKARVGSVSPVLFKDGEGCGACYKVKCLDHGICSRRAVTVIVTDECPGGL
CAFGRTHFDLSGAAFSRMAVAGAGGHLRDRGQLSVVYRRTACKYGGKNIAFRVNEGSTNFWLSLL
VEFEDGQGDIGSMQIKQANSVEWLDMKHVWGATWCLVRGPLVGPFSVRLTTLSAQKALTARDVIP
RNWKPTATYTSRLNFEAAL

**>OsEXPB18 (UniProtKB accession number Q5W6Z9)**

MNSKFQLILSTFVVIAAFTLLPRPCASIEFHRKLSSWSNGGATWYGAANGAGSDGGACGYQAAVD
QAPFSSMIAAGSPSIYKSGLGCGSCYQVKCSGNSACSGNPVTVVLTDECPGGPCLSEPVHFDLSGTA
FGAMANPGQADQLRAAGVLQIQYNRVPCNWGGVMLTFAVDAGSNPSYFAVLVKYENGDGDLSG
MDLMQTGAGAAWTPMQQSWGAVWKLSAGAALQAPLSIRLTSSSGKTLVASNVIPSGWKPGASYT
STVNY

**>OsEXLA1 (UniProtKB accession number Q10S70)**

MAVSVRCCFGSSSLSHHARLLLVIVALLAPRLASGCDRCVRRSRAAYYTSSLTLTAGSCGYGTAAAT
FNGGGFLAAAGPALYRGGVGCGACYQVRCKDKKLCSNAGARVVVTDRARTNRTGLVLSSPAFAA
MARPGMAASLTELAAVDVEYKRVPCEYRHRSLSVRVDERSRGPNELTISFLYQGGQTDIVAVDVAQ
VGSSSWKFMTREHGPSWSMANAPPGPLQMRLVVTGGYDGKWVWADREVLPRRWRAGEVYDTG
VQITDIAQEGCFPCDTHEWK

**>OsEXLA2 (UniProtKB accession number Q7XCL0)**

MAVRCCSSMASASVVLFFVVVGMSASMVSGCDRCVRRSKAGFRDSSIALNAGSCGYGSLAASFN
GGHLAAASPALFRGGVGCGACFQVRCKDGKLCSTAGAKVVVTDEARSTNRTDLVLSAAAYAAMA
RPGMAAQLRTRRAVDVEYKRVPCEYAAGRNLSIRVEEKSRPPRELSIRFLYQGGQTDIVAVDVATVG
SSNWKFMTRDYGPAWSTAQAPAGPLQFRVVVTGGYDGKWVWADGEVLPRRWTAGRVYDAGVQI
ADVAQEGCYPCDTQEWK

**>OsEXLA3 (UniProtKB accession number Q8H274)**

MAVLLSILSSSFLLLLAASSSSTPRASACERCVRNGKAAYSPSLSPLPPGGGGGCGYGAMAMEMEL
NGGFLAAGGPRQHRGGLGCGRCFQMRCRNAEVCSNAGVRVVLTDFHRSNSTDFLLGGPAFAGLA

KPGMAHKLKKLDALSVEYRRIPCDYKDKNLSILVEEQSKRPNNLVIKFLYQGGQTDILAVDVAQVGSSDWRFMTRVYGPVWSIDRAPNGPLQFRAVVTGGYDGKWVWADREVLPANWQPGQVYDTGARIADVARESCLDCATLDWK

**>OsEXLA4 (UniProtKB accession number Q5Z980)**

MDDNGDVHFCHRATAVVALLLLHLVVVANAAAHSCDWCTPRHSTVSILPTPTHAAHLTGGACGFGAAPMELNVAAVTADLFRHGHACGACYQLRCRDRRLCGEDGVKVVVADMAKQPEQEGEMNRTAGGSLQFRITEDAFAAMAKQGVSAHELTRQRTLEVDFRRIPCEYRESRRLAVRVEEASRNPTHLAIRFLYQGGQTDIAAVEIAQANATPPSSSYYSSWRYMTRRDGAPGVWTTSRAPVGPLRLRVVVTAGSGGKWLRSDGEVLPADWRPGEVYDTGLRVTDVAVRSCSLSCAIQDMDSDDGEEEELR

**>OsEXLB1 (UniProtKB accession number Q850K7)**

MAQLLRRHLPVILSLILFLSKATADANFTVSRAAYYPNSDIKGTENGACEYGAFGATLNNGDVSASASLYRDGVGCGACYQVRCTNPYYCSPNGVTIVITDSGASDGTDFILSQHAFTRMAQSTDAGTALLTLGVVGIEYRRVSCTYPNKNIVFKITESSNFPNYLEFEIWYQQGNQDIIAVQLCETVNLTCQLLSRTHGAVWAAVSPPSGPLSIRMLFSSGAPRGGDTWLVPTNIVPQNWTAGATYDSGVQVQLQ

**Text S3 Promoter and gene sequence of *HvEXPB7* in XZ5, XZ54 and Tadmor.** Yellow represents RHEs in promoter; Red represents SNPs in CDS; green represents intron; pink represents start and stop codons.

**XZ5 (GeneBank accession number KT000616)**

TTCGCAAGTTTAAATCATCACAAGTTCAACATCACAACAAAAGTATCATCATAACAAGAAAAGC
AACAAGTCATGTAAAAGGCATAGAAGACCGTCAAGTTTGTCATCGCAAAGGC**T**TAAGC**CACG**T
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**XZ54 (GeneBank accession number KT000617)**

TTCGCAAGTTTAACATCATCACAAGTTCAACATCACAACAAAAGTATCATCATAACAAGAAAAG
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**Tadmor (GeneBank accession number KT000618)**

TTCGCAAGTTTAACATCATCACAAGTTCAACATCACAACAAAAGTATCATCATAACAAGAAAAG
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