```
TA2893     1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTT-GTGTG
Tim01      1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTTTGTGTG
TA39       1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTT-GTGTG
TA2804     1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTT-GTGTG
TA808      1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTT-GTGTG
TA763      1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTT-GTGTG
TA2894     1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTT-GTGTG
TA2892     1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTT-GTGTG

TA2893    60 CTTCCAAAGTAACTTTGATTGGTATCCAACTAATCTTTTAAGCATTAGCTGAAGCAACAC
Tim01     61 CTTCCAAAGTAACTTTGATTGGTATCCAACTAATCTTTTAAGCATTAGCTGAAGCAACAC
TA39      60 CTTCCAAAGTAACTTTGATTGGTATCCAACTAATCTTTTAAGCATTAGCTGAAGCAACAC
TA2804    60 CTTCCAAAGTAACTTTGATTGGTATCCAACTAATCTTTTAAGCATTAGCTGAAGCAACAC
TA808     60 CTTCCAAAGTAACTTTGATTGGTATCCAACTAATCTTTTAAGCATTAGCTGAAGCAACAC
TA763     60 CTTCCAAAGTAACTTTGATTGGTATCCAACTAATCTTTTAAGCATTAGCTGAAGCAACAC
TA2894    60 CTTCCAAAGTAACTTTGATTGGTATCCAACTAATCTTTTAAGCATTAGCTGAAGCAACAC
TA2892    60 CTTCCAAAGTAACTTTGATTGGTATCCAACTAATCTTTTAAGCATTAGCTGAAGCAACAC

TA2893   120 ACAACTGCACACAGAAATCGTGCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCAT
Tim01    121 ACAACTGCACACAGAAATCGTGCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCAT
TA39     120 ACAACTGCACACAGAAATCGTGCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCAT
TA2804   120 ACAACTGCACACAGAAATCGTGCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCAT
TA808    120 ACAACTGCACACAGAAATCGTGCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCAT
TA763    120 ACAACTGCACACAGAAATCGTGCCACCTCATTTATAAATAAAGGTGTGGCCTCATATCAT
TA2894   120 ACAACTGCACACAGAAATCGTGCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCAT
TA2892   120 ACAACTGCACACAGAAATCGTGCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCAT

                                                 *
TA2893   180 CTATTCATCTCCACCTGCACGAAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGG
Tim01    181 CTATTCATCTCCACCTGCACGAAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGG
TA39     180 CTATTCATCTCCACCTGCACGAAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGG
TA2804   180 CTATTCATCTCCACCTGCACGAAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGG
TA808    180 CTATTCATCTCCACCTGCACGAAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGG
TA763    180 CTATTCATCTCCACCTGCACGAAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGG
TA2894   180 CTATTCATCTCCACCTGCACGAAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGG
TA2892   180 CTATTCATCTCCACCTGCACGAAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGG

TA2893   240 CCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAATATAGCGAAATTGTTGGCAGTTA
Tim01    241 CCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAATATAGCGAAATTGTTGGCAGTTA
TA39     240 CCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAATATAGCGAAATTGTTGGCAGTTA
TA2804   240 CCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAATATAGCGAAATTGTTGGCAGTTA
TA808    240 CCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAATATAGCGAAATTGTTGGCAGTTA
TA763    240 CCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAATATAGCGAAATTGTTGGCAGTTA
TA2894   240 CCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAATATAGCGAAATTGTTGGCAGTTA
TA2892   240 CCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAATATAGCGAAATTGTTGGCAGTTA

TA2893   300 CGATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATG
Tim01    301 CGATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATG
TA39     300 CGATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATG
TA2804   300 CGATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATG
TA808    300 CGATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATG
TA763    300 CGATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATG
TA2894   300 CGATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATG
TA2892   300 CGATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATG

TA2893   360 CAGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTG
Tim01    361 CAGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTG
TA39     360 CAGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTG
TA2804   360 CAGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTG
TA808    360 CAGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTG
TA763    360 CAGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTG
TA2894   360 CAGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTG
TA2892   360 CAGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTG
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TA2893   420 GTGGAAATGGTGGAAGGGAGGTTGTCTAGAGCTCCTTGGGGAGTGTTGCAGTCAGCTCGG
Tim01    421 GTGGAAATGGTGGAAGGGAGGTTGTCTAGAGCTCCTTGGGGAGTGTTGCAGTCAGCTCGG
TA39     420 GTGGAAATGGTGGAAGGGAGGTTGTCTAGAGCTCCTTGGGGAGTGTTGCAGTCAGCTCGG
TA2804   420 GTGGAAATGGTGGAAGGGAGGTTGTCTAGAGCTCCTTGGGGAGTGTTGCAGTCAGCTCGG
TA808    420 GTGGAAATGGTGGAAGGGAGGTTGTCTAGAGCTCCTTGGGGAGTGTTGCAGTCAGCTCGG
TA763    420 GTGGAAATGGTGGAAGGGAGGTTGTCTAGAGCTCCTTGGGGAGTGTTGCAGTCAGCTCGG
TA2894   420 GTGGAAATGGTGGAAGGGAGGTTGTCTAGAGCTCCTTGGGGAGTGTTGCAGTCAGCTCGG
TA2892   420 GTGGAAATGGTGGAAGGGAGGTTGTCTAGAGCTCCTTGGGGAGTGTTGCAGTCAGCTCGG

TA2893   480 CCAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGACCTCAG
Tim01    481 CCAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGACCTCAG
TA39     480 CCAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGACCTCAG
TA2804   480 CCAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGACCTCAG
TA808    480 CCAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGACCTCAG
TA763    480 CCAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGACCTCAG
TA2894   480 CCAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGACCTCAG
TA2892   480 CCAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGACCTCAG

TA2893   540 TGGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCT
Tim01    541 TGGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCT
TA39     540 TGGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCT
TA2804   540 TGGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCT
TA808    540 TGGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCT
TA763    540 TGGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCT
TA2894   540 TGGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCT
TA2892   540 TGGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCT

TA2893   600 GCCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTAT-GGCTATTA
Tim01    601 GCCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTATTGGCTATTA
TA39     600 GCCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTATTGGCTATTA
TA2804   600 GCCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTAT-GGCT-TTA
TA808    600 GCCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTATTGGCTATTA
TA763    600 GCCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTATTGGCTATTA
TA2894   600 GCCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTATTGGCTATTA
TA2892   600 GCCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTAT-GGCTATTA
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Supplementary Fig. 1s. Alignment of *Pina* sequences from *T. timopheevii* and *T. urartu*. * indicates position of the start codon. Accessions TA39, TA2804, TA2892, TA2893, TA2894 and Tim01 are *T. timopheevii*. TA763 and TA808 are *T. urartu* and their sequences were retrieved from GenBank under accession numbers AJ302094 and AJ302095, respectively.

```
TA2893    1 CGTCACCTGTCTCAACAACGCACCATTTCTGTTGGCTCGCAAAGTAACTTTAATTTGTGA
TA2894    1 CGTCACCTGTCTCAACAACGCACCATTTCTGTTGGCTCGCAAAGTAACTTTAATTTGTGA
Tim01     1 CGTCACCTGTCTCAACAACGCACCATTTCTGTTGGCTCGCAAAGTAACTTTAATTTGTGA
TA2804    1 CGTCACCTGTCTCAACAACGCACCATTTCTGTTGGCTCGCAAAGTAACTTTAATTTGTGA
TA2892    1 CGTCACCTGTCTCAACAACGCACCATTTCTGTTGGCTCGCAAAGTAACTTTAATTTGTGA
TA39      1 CGTCACCTGTCTCAACAACGCACCATTTCTGTTGGCTCGCAAAGTAACTTTAATTTGTGA
TA763     1 CGTCACCTGTCTCAACAACGCACCATTTCTGTTGGCTCGCAAAGTAACTTTAATTTGTGA
TA808     1 CGTCACCTGTCTCAACAACGCACCATTTCTGTTGGCTCGCAAAGTAACTTTAATTTGTGA

TA2893   1 GCATTAGCCAAAGCAACACACAATGGTAGGCAAAAACCATGTCACTAAGCAATAAATAAA
TA2894   61 GCATTAGCCAAAGCAACACACAATGGTAGGCAAAAACCATGTCACTAAGCAATAAATAAA
Tim01    61 GCATTAGCCAAAGCAACACACAATGGTAGGCAAAAACCATGTCACTAAGCAATAAATAAA
TA2804   61 GCATTAGCCAAAGCAACACACAATGGTAGGCAAAAACCATGTCACTAAGCAATAAATAAA
TA2892   61 GCATTAGCCAAAGCAACACACAATGGTAGGCAAAAACCATGTCACTAAGCAATAAATAAA
TA39     61 GCATTAGCCAAAGCAACACACAATGGTAGGCAAAAACCATGTCACTAAGCAATAAATAAA
TA763    61 GCATTAGCCAAAGCAACACACAATGGTAGGCAAAAACCATGTCACTAAGCAATAAATAAA
TA808    61 GCATTAGCCAAAGCAACACACAATGGTAGGCAAAAACCATGTCACTAAGCAATAAATAAA

                                                                      *
TA2893  121 GGGGAGCCTCAACCCATCTATTCATCTCCACCACCACCACCAAAACAACATTGAAAACAT
TA2894  121 GGGGAGCCTCAACCCATCTATTCATCTCCACCACCACCACCAAAACAACATTGAAAACAT
Tim01   121 GGGGAGCCTCAACCCATCTATTCATCTCCACCACCACCACCAAAACAACATTGAAAACAT
TA2804  121 GGGGAGCCTCAACCCATCTATTCATCTCCACCACCACCACCAAAACAACATTGAAAACAT
TA2892  121 GGGGAGCCTCAACCCATCTATTCATCTCCACCACCACCACCAAAACAACATTGAAAACAT
TA39    121 GGGGAGCCTCAACCCATCTATTCATCTCCACCACCACCACCAAAACAACATTGAAAACAT
TA763   121 GGGGAGCCTCAACCCATCTATTCATCTCCACCACCACCACCAAAACAACATTGAAAACAT
TA808   121 GGGGAGCCTCAACCCATCTATTCATCTCCACCACCACCACCAAAACAACATTGAAAACAT

TA2893  181 GAAGACCTTATTCCTCCTAGCCCTCCTTGCTCTTGTAGCGAGCACAACCTTCGCGCAATA
TA2894  181 GAAGACCTTATTCCTCCTAGCCCTCCTTGCTCTTGTAGCGAGCACAACCTTCGCGCAATA
Tim01   181 GAAGACCTTATTCCTCCTAGCCCTCCTTGCTCTTGTAGCGAGCACAACCTTCGCGCAATA
TA2804  181 GAAGACCTTATTCCTCCTAGCCCTCCTTGCTCTTGTAGCGAGCACAACCTTCGCGCAATA
TA2892  181 GAAGACCTTATTCCTCCTAGCCCTCCTTGCTCTTGTAGCGAGCACAACCTTCGCGCAATA
TA39    181 GAAGACCTTATTCCTCCTAGCCCTCCTTGCTCTTGTAGCGAGCACAACCTTCGCGCAATA
TA763   181 GAAGACCTTATTCCTCCTAGCCCTCCTTGCTCTTGTAGCGAGCACAACCTTCGCGCAATA
TA808   181 GAAGACCTTATTCCTCCTAGCCCTCCTTGCTCTTGTAGCGAGCACAACCTTCGCGCAATA

TA2893  241 CTCAGAAGTTGGTGGCTGGTACAATGAAGTTGGTGCAGGAGGTGGTTCTCAACAATGCCC
TA2894  241 CTCAGAAGTTGGTGGCTGGTACAATGAAGTTGGTGCAGGAGGTGGTTCTCAACAATGCCC
Tim01   241 CTCAGAAGTTGGTGGCTGGTACAATGAAGTTGGTGCAGGAGGTGGTTCTCAACAATGCCC
TA2804  241 CTCAGAAGTTGGTGGCTGGTACAATGAAGTTGGTGCAGGAGGTGGTTCTCAACAATGCCC
TA2892  241 CTCAGAAGTTGGTGGCTGGTACAATGAAGTTGGTGCAGGAGGTGGTTCTCAACAATGCCC
TA39    241 CTCAGAAGTTGGTGGCTGGTACAATGAAGTTGGTGCAGGAGGTGGTTCTCAACAATGCCC
TA763   241 CTCAGAAGTTGGTGGCTGGTACAATGAAGTTGGTGCAGGAGGTGGTTCTCAACAATGCCC
TA808   241 CTCAGAAGTTGGTGGCTGGTACAATGAAGTTGGTGCAGGAGGTGGTTCTCAACAATGCCC

TA2893  301 GCTGGAGCGGCCGAAGCTAAGCTCTTGCAAGGATTACGTGATGGAGCGGTGTTTCACAAT
TA2894  301 GCTGGAGCGGCCGAAGCTAAGCTCTTGCAAGGATTACGTGATGGAGCGGTGTTTCACAAT
Tim01   301 GCTGGAGCGGCCGAAGCTAAGCTCTTGCAAGGATTACGTGATGGAGCGGTGTTTCACACT
TA2804  301 GCTGGAGCGGCCGAAGCTAAGCTCTTGCAAGGATTACGTGATGGAGCGGTGTTTCACACT
TA2892  301 GCTGGAGCGGCCGAAGCTAAGCTCTTGCAAGGATTACGTGATGGAGCGGTGTTTCACAAT
TA39    301 GCTGGAGCGGCCGAAGCTAAGCTCTTGCAAGGATTACGTGATGGAGCGGTGTTTCACAAT
TA763   301 GCTGGAGCGGCCGAAGCTAAGCTCTTGCAAGGATTACGTGATGGAGCGGTGTTTCACAAT
TA808   301 GCTGGAGCGGCCGAAGCTAAGCTCTTGCAAGGATTACGTGATGGAGCGGTGTTTCACAAT

TA2893  361 GAAGGATTTTCCAGTCACTTGGCCCACGAAATGGTGGAAGGGAGGTTGTGAGCACGAGGT
TA2894  361 GAAGGATTTTCCAGTCACTTGGCCCACGAAATGGTGGAAGGGAGGTTGTGAGCACGAGGT
Tim01   361 GAAGGATTTTCCAGTCACTTGGCCCACGAAATGGTGGAAGGGAGGTTGTGAGCACGAGGT
TA2804  361 GAAGGATTTTCCAGTCACTTGGCCCACGAAATGGTGGAAGGGAGGTTGTGAGCACGAGGT
TA2892  361 GAAGGATTTTCCAGTCACTTGGCCCACGAAATGGTGGAAGGGAGGTTGTGAGCACGAGGT
TA39    361 GAAGGATTTTCCAGTCACTTGGCCCACGAAATGGTGGAAGGGAGGTTGTGAGCACGAGGT
TA763   361 GAAGGATTTTCCAGTCACTTGGCCCACAAAATGGTGGAAGGGCGGTTGTGAGCACGAGGT
TA808   361 GAAGGATTTTCCAGTCACTTGGCCCACGAAATGGTGGAAGGGCGGTTGTGAGCACGAGGT
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TA2893   421 TCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCTAT
TA2894   421 TCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCTAT
Tim01    421 TCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCTAT
TA2804   421 TCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCTAT
TA2892   421 TCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCTAT
TA39     421 TCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCTAT
TA763    421 TCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCTAT
TA808    421 TCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCTCTGCGATTCTAT

TA2893   481 CCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTATT
TA2894   481 CCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTATT
Tim01    481 CCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTATT
TA2804   481 CCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTATT
TA2892   481 CCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTATT
TA39     481 CCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTATT
TA763    481 CCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTATT
TA808    481 CCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTATT

TA2893   541 CAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGCAA
TA2894   541 CAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGCAA
Tim01    541 CAAACAAATTCAGAGGGCCCAGAGCCCCCCCTCAAAGTGCAACATGGGAGCCGACTGCAA
TA2804   541 CAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGCAA
TA2892   541 CAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGCAA
TA39     541 CAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGCAA
TA763    541 CAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGCAA
TA808    541 CAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGCAA

TA2893   601 ATTACCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCA
TA2894   601 ATTACCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCA
Tim01    601 ATTACCTAGTGGCTATTACTGGTGATGATATAGCCTCTACTCGTGACCAATAAAATGTCA
TA2804   601 ATTACCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCA
TA2892   601 ATTACCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCA
TA39     601 ATTACCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCA
TA763    601 ATTACCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCA
TA808    601 ATTACCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCA

TA2893   661 CATACCACAACATGGGAGCCGACTGCAAATTACCTAGTGGCTATTACTGGTGATGATATA
TA2894   661 CATACCACAACATGGGAGCCGACTGCAAATTACCTAGTGGCTATTACTGGTGATGATATA
Tim01    661 CATACCACAACATGGGAGCCGACTGCAAATTACCTAGTGGCTATTACTGGTGATGATATA
TA2804   661 CATACCACAACATGGGAGCCGACTGCAAATTACCTAGTGGCTATTACTGGTGATGATATA
TA2892   661 CATACCACAACATGGGAGCCGACTGCAAATTACCTAGTGGCTATTACTGGTGATGATATA
TA39     661 CATACCACAACATGGGAGCCGACTGCAAATTACCTAGTGGCTATTACTGGTGATGATATA
TA763    661 CATACCA-----------------------------------------------------
TA808    661 CATACCA-----------------------------------------------------

TA2893   721 GCCTCTATTCGTGACCAATAAAATGTCACATACCACAACATGGGAGCCGACTGCAAATTA
TA2894   721 GCCTCTATTCGTGACCAATAAAATGTCACATACCACAACATGGGAGCCGACTGCAAATTA
Tim01    721 GCCTCTATTCGTGACCAATAAAATGTCACATACCACAACATGGGAGCCGACTGCAAATTA
TA2804   721 GCCTCTATTCGTGACCAATAAAATGTCACATACCACAACATGGGAGCCGACTGCAAATTA
TA2892   721 GCCTCTATTCGTGACCAATAAAATGTCACATACCACAACATGGGAGCCGACTGCAAATTA
TA39     721 GCCTCTATTCGTGACCAATAAAATGTCACATACCACAACATGGGAGCCGACTGCAAATTA
TA763        ------------------------------------------------------------
TA808        ------------------------------------------------------------

TA2893   781 CCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCACATA
TA2894   781 CCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCACATA
Tim01    781 CCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCACATA
TA2804   781 CCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCACATA
TA2892   781 CCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCACATA
TA39     781 CCTAGTGGCTATTACTGGTGATGATATAGCCTCTATTCGTGACCAATAAAATGTCACATA
TA763        ------------------------------------------------------------
TA808        ------------------------------------------------------------

TA2893   841 CCACAACATGTGACAAATAAGTGTGCTCCTATGATAATCTATGAATAAAATCACCCTTGT
TA2894   841 CCACAACATGTGACAAATAAGTGTGCTCCTATGATAATCTATGAATAAAATCACCCTTGT
Tim01    841 CCACAACATGTGACAAATAAGTGTGCTCGTATGATAATCTATGAATAAAATCACCCTTGT
TA2804   841 CCACAACATGTGACAAATAAGTGTGCTCGTATGATAATCTATGAATAAAATCACCCTTGT
TA2892   841 CCACAACATGTGACAAATAAGTGTGCTCGTATGATAATCTATGAATAAAATTACCCTTGT
TA39     841 CCACAACATGTGACAAATAAGTGTGCTCCTATGATAATCTATGAATAAAATCACCCTTGT
TA763    668 ---CAACATGTGACAAATAAGTGTGCTCGTATGATAATCTATGAATAAAATCACCCTTGT
TA808    668 ---CAACATGTGACAAATAAGTGTGCTCGTATGATAATCTATGAATAAAATCACCCTTGT
```

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TA2893   901 ATATTGATTTGTGTTGGAGA
TA2894   901 ATATTGATTTGTGTTGGAGA
Tim01    901 ATATTGATTTGTGTTGGAGA
TA2804   901 ATATTGATTTGTGTTGGAGA
TA2892   901 ATATTGATTTGTGTTGGAGA
TA39     901 ATATTGATTTGTGTTGGAGA
TA763    725 ATATTGATTTGTGTTGGAGA
TA808    725 ATATTGATTTGTGTTGGAGA
```

Supplementary Fig. 2s. Alignment of *Pinb* sequences from *T. timopheevii* and *T. urartu*. Accessions TA39, TA2804, TA2892, TA2893, TA2894 and Tim01 are *T. timopheevii*. TA763 and TA808 and *T. urartu* and their sequences were retrieved from GenBank under accession numbers AJ302103 and AJ302104, respectively. * indicates the start codon. The 88-bp tandem repeats are highlighted in yellow, green and blue. The 7-mer CAACATG flanking the triplication is underlined.

```
TA39      1 MKALFLIGLLALVASTAFAQYSEIVGSYDVAGGGGAQQCPLETKLNSCRNYLLDRCSTMK
Tim01     1 MKALFLIGLLALVASTAFAQYSEIVGSYDVAGGGGAQQCPLETKLNSCRNYLLDRCSTMK
TA763     1 MKALFLIGLLALVASTAFAQYSEIVGSYDVAGGGGAQQCPLETKLNSCRNYLLDRCSTMK
TA808     1 MKALFLIGLLALVASTAFAQYSEIVGSYDVAGGGGAQQCPLETKLNSCRNYLLDRCSTMK
TA2894    1 MKALFLIGLLALVASTAFAQYSEIVGSYDVAGGGGAQQCPLETKLNSCRNYLLDRCSTMK
TA2892    1 MKALFLIGLLALVASTAFAQYSEIVGSYDVAGGGGAQQCPLETKLNSCRNYLLDRCSTMK
TA2893    1 MKALFLIGLLALVASTAFAQYSEIVGSYDVAGGGGAQQCPLETKLNSCRNYLLDRCSTMK
TA2804    1 MKALFLIGLLALVASTAFAQYSEIVGSYDVAGGGGAQQCPLETKLNSCRNYLLDRCSTMK


TA39     61 DFPVTWRWWKWWKGGCLELLGECCSQLGQMPPQCRCNIIQGSIQGDLSGIFGFQRDRASK
Tim01    61 DFPVTWRWWKWWKGGCLELLGECCSQLGQMPPQCRCNIIQGSIQGDLSGIFGFQRDRASK
TA763    61 DFPVTWRWWKWWKGGCLELLGECCSQLGQMPPQCRCNIIQGSIQGDLSGIFGFQRDRASK
TA808    61 DFPVTWRWWKWWKGGCLELLGECCSQLGQMPPQCRCNIIQGSIQGDLSGIFGFQRDRASK
TA2894   61 DFPVTWRWWKWWKGGCLELLGECCSQLGQMPPQCRCNIIQGSIQGDLSGIFGFQRDRASK
TA2892   61 DFPVTWRWWKWWKGGCLELLGECCSQLGQMPPQCRCNIIQGSIQGDLSGIFGFQRDRASK
TA2893   61 DFPVTWRWWKWWKGGCLELLGECCSQLGQMPPQCRCNIIQGSIQGDLSGIFGFQRDRASK
TA2804   61 DFPVTWRWWKWWKGGCLELLGECCSQLGQMPPQCRCNIIQGSIQGDLSGIFGFQRDRASK


TA39    121 VIQEAKNLPPRCNQGPPCNIPGTIGY
Tim01   121 VIQEAKNLPPRCNQGPPCNIPGTIGY
TA763   121 VIQEAKNLPPRCNQGPPCNIPGTIGY
TA808   121 VIQEAKNLPPRCNQGPPCNIPGTIGY
TA2894  121 VIQEAKNLPPRCNQGPPCNIPGTIGY
TA2892  121 VIQEAKNLPPRCNQGPPCNIPGTMAI
TA2893  121 VIQEAKNLPPRCNQGPPCNIPGTMAI
TA2804  121 VIQEAKNLPPRCNQGPPCNIPGTMAL
```

Supplementary Fig. 3s. Alignment of PINA protein sequences of *T. timopheevii* and *T. urartu*. Accessions TA39, TA2804, TA2892, TA2893, TA2894 and Tim01 are *T. timopheevii*. TA763 and TA808 and *T. urartu* and their sequences were retrieved from GenBank under accession numbers CAC33797 and CAC33798.

```
Tim01      1 MKTLFLLALLALVASTTFAQYSEVGGWYNEVGAGGGSQQCPLERPKLSSCKDYVMERCFT
TA2804     1 MKTLFLLALLALVASTTFAQYSEVGGWYNEVGAGGGSQQCPLERPKLSSCKDYVMERCFT
TA39       1 MKTLFLLALLALVASTTFAQYSEVGGWYNEVGAGGGSQQCPLERPKLSSCKDYVMERCFT
TA2892     1 MKTLFLLALLALVASTTFAQYSEVGGWYNEVGAGGGSQQCPLERPKLSSCKDYVMERCFT
TA2893     1 MKTLFLLALLALVASTTFAQYSEVGGWYNEVGAGGGSQQCPLERPKLSSCKDYVMERCFT
TA2894     1 MKTLFLLALLALVASTTFAQYSEVGGWYNEVGAGGGSQQCPLERPKLSSCKDYVMERCFT
TA808      1 MKTLFLLALLALVASTTFAQYSEVGGWYNEVGAGGGSQQCPLERPKLSSCKDYVMERCFT
TA763      1 MKTLFLLALLALVASTTFAQYSEVGGWYNEVGAGGGSQQCPLERPKLSSCKDYVMERCFT


Tim01     61 LKDFPVTWPTKWWKGGCEHEVREKCCQQLSQIAPQCRCDSIRGMIQGKLGGFFGIWRGDV
TA2804    61 LKDFPVTWPTKWWKGGCEHEVREKCCQQLSQIAPQCRCDSIRGMIQGKLGGFFGIWRGDV
TA39      61 MKDFPVTWPTKWWKGGCEHEVREKCCQQLSQIAPQCRCDSIRGMIQGKLGGFFGIWRGDV
TA2892    61 MKDFPVTWPTKWWKGGCEHEVREKCCQQLSQIAPQCRCDSIRGMIQGKLGGFFGIWRGDV
TA2893    61 MKDFPVTWPTKWWKGGCEHEVREKCCQQLSQIAPQCRCDSIRGMIQGKLGGFFGIWRGDV
TA2894    61 MKDFPVTWPTKWWKGGCEHEVREKCCQQLSQIAPQCRCDSIRGMIQGKLGGFFGIWRGDV
TA808     61 MKDFPVTWPTKWWKGGCEHEVREKCCQQLSQIAPQCRCDSIRGMIQGKLGGFFGIWRGDV
TA763     61 MKDFPVTWPTKWWKGGCEHEVREKCCQQLSQIAPQCLCDSIRGMIQGKLGGFFGIWRGDV


Tim01    121 FKQIQRAQSLPSKCNMGADCKLPSGYYW
TA2804   121 FKQIQRAQSLPSKCNMGADCKLPSGYYW
TA39     121 FKQIQRAQSLPSKCNMGADCKLPSGYYW
TA2892   121 FKQIQRAQSLPSKCNMGADCKLPSGYYW
TA2893   121 FKQIQRAQSLPSKCNMGADCKLPSGYYW
TA2894   121 FKQIQRAQSLPSKCNMGADCKLPSGYYW
TA808    121 FKQIQRAQSLPSKCNMGADCKLPSGYYW
TA763    121 FKQIQRAQSLPSKCNMGADCKLPSGYYW
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Supplementary Fig. 4s. Alignment of PINB protein sequences of *T. timopheevii* and *T. urartu*. Accessions TA39, TA2804, TA2892, TA2893, TA2894 and Tim01 are *T. timopheevii*. TA763 and TA808 and *T. urartu* and their sequences were retrieved from GenBank under accession numbers CAC33799 and CAC33800.

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AJ249933m    1 ATGAAGGCCCTCTTCCTCATAGGCCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAA
AJ242715m    1 ATGAAGGCCCTCTTCCTCATAGGCCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAA
AJ302093m    1 ATGAAGGCCCTCTTCCTCATAGGCCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAA
Timopheev    1 ATGAAGGCCCTCTTCCTCATAGGCCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAA
DQ269826u    1 ATGAAGGCCCTCTTCCTCATAGGCCTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAA
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AJ242715m   61 TATAGCGAAATTGTTGGCAGTTACGATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCT
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Timopheev  241 GGGGAGTGTTGCAGTCAGCTCGGCCAAATGCCACCGCAATGCCGCTGCAACATCATCCAG
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TA2610     361 GTGATACAAGAAGCCAAGAACCTACCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATC
AJ249933m  361 GTGATACAAGAAGCCAAGAACCTACCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATC
AJ242715m  361 GTGATACAAGAAGCCAAGAACCTACCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATC
AJ302093m  361 GTGATACAAGAAGCCAAGAACCTACCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATC
Timopheev  361 GTGATACAAGAAGCCAAGAACCTGCCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATC
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Supplementary Fig. 5s. Alignment of DNA sequences of *Pina*. PI355352, PI355353 and TA2610 are *T. zhukovskyi*. Letters affixed to the GenBank accessions are abbreviations for the species or subspecies, a for *T. monococcum* subsp. *agilopoides*, m for *T. monococcum* subsp. *monococcum* and u for *T. urartu*. Timopheev is the consensus sequence of *Pina-A* of *T. timopheevii*. * indicates the single nucleotide polymorphism (SNP) at position 384 where A is present in *T. monococcum* but not in *T. urartu*.

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TA2610      1 ATGAAGACCTTATTCCTCCTAGCCCTCCTTGCTCTTGTAGCGAGCACAACCTTCGCGCAA
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DQ269855a   241 GTCCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCT
DQ269854a   241 GTCCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCT
DQ269853a   241 GTCCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCT
DQ269852a   241 GTCCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCT
AJ302101m   241 GTTCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCT
DQ269860u   241 GTTCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCT
DQ269859u   241 GTTCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCT
DQ269861u   241 GTTCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCT
Timopheev   241 GTTCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCT
DQ269858u   241 GTTCGGGAGAAGTGCTGCCAGCAGCTGAGCCAGATAGCACCACAGTGTCTCTGCGATTCT
AJ249934m   241 GTTCGGGAGAACTGCTGCAAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCGATTCT

DQ269857m   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTA
DQ269856m   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTA
PI355352    301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTA
PI355353    301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTA
TA2610      301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTA
DV92BACm    301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTA
AJ302102m   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTA
DQ269855a   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGCA
DQ269854a   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGCA
DQ269853a   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGCA
DQ269852a   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGCA
AJ302101m   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGCA
DQ269860u   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTA
DQ269859u   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTA
DQ269861u   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTA
Timopheev   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTA
DQ269858u   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTCGGAATTTGGCGAGGTGATGTA
AJ249934m   301 ATCCGAGGAATGATCCAAGGCAAGCTCGGTGGCTTCTTTGGAATTTGGCGAGGTGATGTA
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```
DQ269857m  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
DQ269856m  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
PI355352   361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
PI355353   361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
TA2610     361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
DV92BACm   361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
AJ302102m  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
DQ269855a  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
DQ269854a  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
DQ269853a  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
DQ269852a  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
AJ302101m  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
DQ269860u  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
DQ269859u  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
DQ269861u  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
Timopheev  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
DQ269858u  361 TTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
AJ249934m  361 TTCAAAAAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGAGCCGACTGC
```

Supplementary Fig. 6s. Alignment of DNA sequences of *Pinb*. PI355352, PI355353 and TA2610 are *T. zhukovskyi*. Letters affixed to the GenBank accessions are abbreviations for the species or subspecies, a for *T. monococcum* subsp. *agilopoides*, m for *T. monococcum* subsp. *monococcum* and u for *T. urartu*. Timopheev is the consensus sequence of *Pinb-A* of *T. timopheevii*. * indicates the single nucleotide polymorphism (SNP) at position 75 which distinguishes *T. monococcum* and *T. urartu*.

```
TMB02          1 AGGTCGGATTCAGTACACGGAACATCGCATATCTCAACAACTTCCACCAGTTTGGTGTGC
TH02/TMB02     1 AGGTCGGATTCAGTACACGGAACATCGCATATCTCAACAACTTCCACCAGTTTGGTGTGC

TMB02         61 TTCCAAAGTAACTTTGATTGGTATCCAACTAATCTTTTAAGCATTAGCTGAAGCAACACA
TH02/TMB02    61 TTCCAAAGTAACTTTGATTGGTATCCAACTAATCTTTTAAGCATTAGCTGAAGCAACACA

TMB02        121 CAACTGCACACAGAAATCGTGCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCATC
TH02/TMB02   121 CAACTGCACACAGAAATCGTGCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCATC

TMB02        181 TATTCATCTCCACCTGCACCAAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGGC
TH02/TMB02   181 TATTCATCTCCACCTGCACCAAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGGC

TMB02        241 CTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAATATAGCGAAATTGTTGGCAGCTAC
TH02/TMB02   241 CTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAATATAGCGAAATTGTTGGCAGCTAC

TMB02        301 GATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATGC
TH02/TMB02   301 GATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATGC

TMB02        361 AGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTGG
TH02/TMB02   361 AGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTGG

TMB02        421 TGGAAATGGTGGAAGGGAGGTTGTCTAGAGCTCCTTGGGGAGTGCTGCAGTCAGCTCGGC
TH02/TMB02   421 TGGAAATGGTGGAAGGGAGGTTGTCTAGAGCTCCTTGGGGAGTGCTGCAGTCAGCTCGGC

TMB02        481 CAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGATCTCGGT
TH02/TMB02   481 CAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGATCTCGGT

TMB02        541 GGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCTG
TH02/TMB02   541 GGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCTG

TMB02        601 CCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTATTGGCTATTA
TH02/TMB02   601 CCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTATTGGCTATTA
```

Supplementary Fig. 7s Alignment of *Pina-A*^{m} between the amphiploid TH02/TMB02 (2n==4x=28, $A^mA^mS^{sh}S^{sh}$) and its parent TMB02 (*T. monococcum*, 2n=2x=14, A^mA^m).

```
TH02           1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTTGTGTGC
TH02/TMB02     1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTTGTGTGC

TH02          61 TTTCAAAGTAACTTTGATTGGTATCCAGCTATACAACACACAACCGCACACAGAAATCGT
TH02/TMB02    61 TTTCAAAGTAACTTTGATTGGTATCCAGCTATACAACACACAACCGCACACAGAAATCGT

TH02         121 GCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCATCTACTCATCTCCACCTGCACC
TH02/TMB02   121 GCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCATCTATTCATCTCCACCTGCACC

TH02         181 AAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGGCCTGCTTGCTCTGGTAGCGAG
TH02/TMB02   181 AAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGGCCTGCTTGCTCTGGTAGCGAG

TH02         241 CACCGCCTTTGCGCAATATAGCGAAGTTGTTGGCAGTTACGATGCTGCTGGCGGGGGTGG
TH02/TMB02   241 CACCGCCTTTGCGCAATATAGCGAAGTTGTTGGCAGTTACGATGCTGCTGGCGGGGGTGG

TH02         301 TGCTCAACAATGCCCTCTAGAGACAAAGCTAAATGCATGCAGGAATTACTTGCTAGATCG
TH02/TMB02   301 TGCTCAACAATGCCCTCTAGAGACAAAGCTAAATGCATGCAGGAATTACTTGCTAGATCG

TH02         361 ATGCTCAACGATGAAGGATTTCCCAGTCACCTGGCGTTGGTGGAGATGGTGGAAGGGAGG
TH02/TMB02   361 ATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTGGTGGAGATGGTGGAAGGGAGG

TH02         421 TTGTCAAGAGCTCCTTGGGGAGTGTTGCAGTCGGCTCGGCCAACTGCCACCGCAATGCCG
TH02/TMB02   421 TTGTCAAGAGCTCCTTGGGGAGTGTTGCAGTCGGCTCGGCCAACTGCCACCGCAATGCCG

TH02         481 CTGCAACATCATCCAGGGGTCAATCCAAGGCAATCTCGGTGGCATCTTCGGATTTCAGCG
TH02/TMB02   481 CTGCAACATCATCCAGGGGTCAATCCAAGGCAATCTCGGTGGCATCTTCGGATTTCAGCG

TH02         541 TGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCTGCCGCCCAGGTGCAACCAGGG
TH02/TMB02   541 TGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCTGCCGCCCAGGTGCAACCAGGG

TH02         601 CCCTCCCTGCGACATCCGCAGCACCAGTGGCTATTACT
TH02/TMB02   601 CCCTCCCTGCGACATCCGCAGCACCAGTGGCTATTACT
```

Supplementary Fig. 8s. Alignment of *Pina*-S^{sh} between the amphiploid TH02/TMB02 (2n==4x=28, $A^mA^mS^{sh}S^{sh}$) and its parent TH02 (*Ae. sharonensis*, 2n=2x=14, $S^{sh}S^{sh}$).

```
TMB02          1 AGGTAATTTGCAGTCGGCTCCCATGTTGCACTTTGAGGGGAGGCTCTGGGCCCTCTGAAT
TH02/TMB02     1 AGGTAATTTGCAGTCGGCTCCCATGTTGCACTTTGAGGGGAGGCTCTGGGCCCTCTGAAT

TMB02         61 TTGTTTGAATGCATCACCTCGCCAAATTCCGAAGAAGCCACCGAGCTTGCCTTGGATCAT
TH02/TMB02    61 TTGTTTGAATGCATCACCTCGCCAAATTCCGAAGAAGCCACCGAGCTTGCCTTGGATCAT

TMB02        121 TCCTCGGATAGAATCGCAGCGACACTGTGGTGCTATCTGGCTCAGCTGCTGGCAGCACTT
TH02/TMB02   121 TCCTCGGATAGAATCGCAGCGACACTGTGGTGCTATCTGGCTCAGCTGCTGGCAGCACTT

TMB02        181 CTCCCGGACCTCGTGCTCACAACCGCCCTTCCACCATTTCGTGGGCCAAGTGACTGGAAA
TH02/TMB02   181 CTCCCGGACCTCGTGCTCACAACCGCCCTTCCACCATTTCGTGGGCCAAGTGACTGGAAA

TMB02        241 ATCCTTCATTGTGAAACACCGCTCCATCACGTAATCCTTGCAAGAGCTTAGCTTCGGCCG
TH02/TMB02   241 ATCCTTCATTGTGAAACACCGCTCCATCACGTAATCCTTGCAAGAGCTTAGCTTCGGCCG

TMB02        301 CTCCAGCGGGCATTGTTGAGAACCACCTCCTGCACCAACTTCATTGTACCAGCCGCCAAC
TH02/TMB02   301 CTCCAGCGGGCATTGTTGAGAACCACCTCCTGCACCAACTTCATTGTACCAGCCGCCAAC

TMB02        361 TTCTGAGTATTGCGCGAAGGTTGTGCTCGCTACAAGAGCAAGGAGAGCTAGGAGGAATAA
TH02/TMB02   361 TTCTGAGTATTGCGCGAAGGTTGTGCTCGCTACAAGAGCAAGGAGAGCTAGGAGGAATAA

TMB02        421 GGTCTTCATGTTTTCAATGTTGTTTTGGTGGTGGTGGTGGAGATGAATAGATGGGTTGAG
TH02/TMB02   421 GGTCTTCATGTTTTCAATGTTGTTTTGGTGGTGGTGGTGGAGATGAATAGATGGGTTGAG

TMB02        481 ACTCCCCTTTATTTATTGCTTAGTGACATGGTTTTTGCCTACCATTGTGTGTTGCTTTGG
TH02/TMB02   481 ACTCCCCTTTATTTATTGCTTAGTGACATGGTTTTTGCCTACCATTGTGTGTTGCTTTGG

TMB02        541 CTAATGCTCACGAATTAAAGTTACTTTGCGAGCCAACAGAAATGGTGCGTTGTTGAGACA
TH02/TMB02   541 CTAATGCTCACGAATTAAAGTTACTTTGCGAGCCAACAGAAATGGTGCGTTGTTGAGACA

TMB02        601 GGTGACG
TH02/TMB02   601 GGTGACG
```

Supplementary Fig. 9s. Alignment of *Pinb-A^m* between the amphiploid TH02/TMB02 (2n==4x=28, $A^mA^mS^{sh}S^{sh}$) and its parent TMB02 (*T. monococcum*, 2n=2x=14, A^mA^m).

```
TH02          1 TTTCTCAACAACTTGCACCGTTTCTGTTTGCTCGCAAAGTAACTTTAATTAGTACCAACT
TH02/TMB02    1 TTTCTCAACAACTTGCACCGTTTCTGTTTGCTCGCAAAGTAACTTTAATTAGTACCAACT


TH02         61 AAATTTGTAAGCATTAGCCAAAGCGACACACAATGGTAGGCAAAAACCATGTCCCGTAGC
TH02/TMB02   61 AAATTTGTAAGCATTAGCCAAAGCGACACACAATGGTAGGCAAAAACCATGTCTCGTAGC


TH02        121 AATAAATAAAGGGGAGCCTCAACCCATCTATTCATCTCCAACACCACCAAAACAACATTG
TH02/TMB02  121 AATAAATAAAGGGGAGCCTCAACCCATCTATTCATCTCCAACACCACCAAAACAACATTG

                     *
TH02        181 AAAGCATGAAGTCCTTATTCCTCCTAGGTCTCCTTGCTCTTGTAGCGAGCACAACCTTCG
TH02/TMB02  181 AAAGCATGAAGTCCTTATTCCTCCTAGGTCTCCTTGCTCTTGTAGCGAGCACAACCTTCG


TH02        241 CGCAATACTCAGAAGTTGGCGGCTGGTACAATGAAGTTGGCGGAGGAGGTGGTTCTCAAC
TH02/TMB02  241 CGCAATACTCA---------------------GAAGTTGGCGGAGGAGGTGGTTCTCAAC


TH02        301 AATGCCCACAGGAGCGACCGAAGCTAGGCTCTTGCAAGGATTACGCGTTGGAGCGGTGCT
TH02/TMB02  280 AATGCCCACAGGAGCGACCGAAGCTAGGCTCTTGCAAGGATTACGCGTTGGAGCGGTGCT


TH02        361 TCACAATGAAGGATTTTCCAGTCACCTGGCCCACAAAATGGTGGAAGGGTGGATGTGAGC
TH02/TMB02  340 TCACAATGAAGGATTTTCCAGTCACCTGGCCCACAAAATGGTGGAAGGGTGGATGTGAGC


TH02        421 ATGAGGTTCGGGAGAAGTGCTGCAAGCAACTGAGCGAGATAGCACCACAGTGTCGATGCG
TH02/TMB02  400 ATGAGGTTCGGGAGAAGTGCTGCAAGCAGCTGAGCGAGATAGCACCACAGTGTCGATGCG


TH02        481 ATTCTCTCCATAGAGTGATCCAAGGCAAGCTCGGTGGTTTCTTTGGCATTTGGCGAGGTG
TH02/TMB02  460 ATTCTCTCCATAGAGTGATCCAAGGCAAGCTCGGTGGTTTCTTTGGCATTTGGCGAGGTG


TH02        541 AGGTATTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGCGCTG
TH02/TMB02  520 AGGTATTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGCGCTG


TH02        601 ACTGCAAGTTTCCTA
TH02/TMB02  580 ACTGCAAGTTTCCTA
```

Supplementary Fig. 10s. Alignment of *Pinb-S*^{sh} between the amphiploid TH02/TMB02 (2n==4x=28, $A^mA^mS^{sh}S^{sh}$) and its parent TH02 (*Ae. sharonensis*, 2n=2x=14, $S^{sh}S^{sh}$). The 11-mer direct repeat (GAAGTTGGCGG) is underlined. * indicates the start codon.

```
TA831     1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTTGTGTGC
TA3438    1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTTGTGTGC

TA831    61 TTCCAAAGTAACTTTGATTGGTATCCAACTAATCTTTTAAGCATTAGCTGAAGCAACACA
TA3438   61 TTCCAAAGTAACTTTGATTGGTATCCAACTAATCTTTTAAGCATTAGCTGAAGCAACACA

TA831   121 CAACTGCACACAGAAATCGTGCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCATC
TA3438  121 CAACTGCACACAGAAATCGTGCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCATC

TA831   181 TATTCATCTCCACCTGCACGAAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGGC
TA3438  181 TATTCATCTCCACCTGCACGAAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGGC

TA831   241 CTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAATATAGCGAAATTGTTGGCAGTTAC
TA3438  241 CTGCTTGCTCTGGTAGCGAGCACCGCCTTTGCGCAATATAGCGAAATTGTTGGCAGTTAC

TA831   301 GATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATGC
TA3438  301 GATGTTGCTGGCGGGGGTGGTGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATGC

TA831   361 AGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTGG
TA3438  361 AGGAATTACCTGCTAGATCGATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTGG

TA831   421 TGGAAATGGTGGAAGGGAGGTTGTCTAGAGCTCCTTGGGGAGTGTTGCAGTCAGCTCGGC
TA3438  421 TGGAAATGGTGGAAGGGAGGTTGTCTAGAGCTCCTTGGGGAGTGTTGCAGTCAGCTCGGC

TA831   481 CAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGACCTCAGT
TA3438  481 CAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGGTCAATCCAAGGCGACCTCAGT

TA831   541 GGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCTG
TA3438  541 GGCATCTTCGGATTTCAGCGTGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCTG

TA831   601 CCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTATTGGCTATT
TA3438  601 CCGCCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTATTGGCTATT
```

Supplementary Fig. 11s. Alignment of *Pina-A* between the amphiploid TA3438 (2n=4x=28, AASS) and its parent TA831 (*T. urartu*, 2n=2x=14, AA).

```
TA1785     1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTCGTGTGC
TA3438     1 AGGTCGGATTCAGTACACGGAACATCACATATCTCAACAACTTCCACCAGTTTTGTGTGC

TA1785    61 TTTCAAAGTAACTTTGATTGGTATCCAGCTATACAACACACAACCGCACACAGAAATCGT
TA3438    61 TTTCAAAGTAACTTTGATTGGTATCCAGCTATACAACACATAACCGCACACAGAAATCGT

TA1785   121 GCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCATCTATTCATCTCCACCTGTACC
TA3438   121 GCCACCTCATTTATAAATAAAGGTGTGGCCTCATCTCATCTATTCATCTCCACCTGCACC

TA1785   181 AAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGGCCTGCTTGCTCTGGTAGCGAG
TA3438   181 AAAACACACTGACAACATGAAGGCCCTCTTCCTCATAGGCCTGCTTGCTCTGGTAGCGAG

TA1785   241 CACCGCCTTTGCGCAATATAGCGAAGTTGTTGGCAGTTACGATGTTGCTGGCGGGGGTGG
TA3438   241 CACCGCCTTTGCGCAATATAGCGAAGTTGTTGGCAGTTACGATGTTGCTGGCGGGGGTGG

TA1785   301 TGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATGCAGGAATTACTTGCTAGATCG
TA3438   301 TGCTCAACAATGCCCTCTAGAGACAAAGCTAAATTCATGCAGGAATTACTTGCTAGATCG

TA1785   361 ATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTGGTGGAGATGGTGGAAGGGAGG
TA3438   361 ATGCTCAACGATGAAGGATTTCCCGGTCACCTGGCGTTGGTGGAGATGGTGGAAGGGAGG

TA1785   421 TTGTCTAGAGCTCCTTGGGGAGTGTTGCAGTCGGCTCGGCCAACTACCACCGCAATGCCG
TA3438   421 TTGTCTAGAGCTCCTTGGGGAGTGTTGCAGTCGGCTCGGCCAACTACCACCGCAATGCCG

TA1785   481 CTGCAACATCATCCAGGGGTCAATCCAAGGCGATCTCGGTGGCATCTTCGGATTTCAGCG
TA3438   481 CTGCAACATCATCCAGGGGTCAATCCAAGGCGATCTCGGTGGCATCTTCGGATTTCAGCG

TA1785   541 TGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCTGCCGCCCAGGTGCAACCAGGG
TA3438   541 TGATCGGGCAAGCAAAGTGATACAAGAAGCCAAGAACCTGCCGCCCAGGTGCAACCAGGG

TA1785   601 CCCTCCCTGCGACATCCGCAGCACCAGTGGCTATTACT
TA3438   601 CCCTCCCTGCGACATCCGCAGCACCAGTGGCTATTACT
```

Supplementary Fig. 12s. Alignment of *Pina-S* between the amphiploid TA3438 (2n=4x=28, AASS) and its parent TA1785 (*Ae. speltoides*, 2n=2x=14, SS).

```
TA831      1 AGGTAATTTGCAGTCGGCTCCCATGTTGCACTTTGAGGGGAGGCTCTGGGCCCTCTGAAT
TA3438     1 AGGTAATTTGCAGTCGGCTCCCATGTTGCACTTTGAGGGGAGGCTCTGGGCCCTCTGAAT

TA831     61 TTGTTTGAATACATCACCTCGCCAAATTCCGAAGAAGCCACCGAGCTTGCCTTGGATCAT
TA3438    61 TTGTTTGAATACATCACCTCGCCAAATTCCGAAGAAGCCACCGAGCTTGCCTTGGATCAT

TA831    121 TCCTCGGATAGAATCGCAGCGACACTGTGGTGCTATCTGGCTCAGCTGCTGGCAGCACTT
TA3438   121 TCCTCGGATAGAATCGCAGCGACACTGTGGTGCTATCTGGCTCAGCTGCTGGCAGCACTT

TA831    181 CTCCCGAACCTCGTGCTCACAACCGCCCTTCCACCATTTTGTGGGCCAAGTGACTGGAAA
TA3438   181 CTCCCGAACCTCGTGCTCACAACCGCCCTTCCACCATTTTGTGGGCCAAGTGACTGGAAA

TA831    241 ATCCTTCATTGTGAAACACCGCTCCATCACGTAATCCTTGCAAGAGCTTAGCTTCGGCCG
TA3438   241 ATCCTTCATTGTGAAACACCGCTCCATCACGTAATCCTTGCAAGAGCTTAGCTTCGGCCG

TA831    301 CTCCAGCGGGCATTGTTGAGAACCACCTCCTGCACCAACTTCATTGTACCAGCCACCAAC
TA3438   301 CTCCAGCGGGCATTGTTGAGAACCACCTCCTGCACCAACTTCATTGTACCAGCCACCAAC

TA831    361 TTCTGAGTATTGCGCGAAGGTTGTGCTCGCTACAAGAGCAAGGAGGGCTAGGAGGAATAA
TA3438   361 TTCTGAGTATTGCGCGAAGGTTGTGCTCGCTACAAGAGCAAGGAGGGCTAGGAGGAATAA

TA831    421 GGTCTTCATGTTTTCAATGTTGTTTTGGTGGTGGTGGTGGAGATGAATAGATGGGTTGAG
TA3438   421 GGTCTTCATGTTTTCAATGTTGTTTTGGTGGTGGTGGTGGAGATGAATAGATGGGTTGAG

TA831    481 GCTCCCCTTTATTTATTGCTTAGTGACATGGTTTTTGCCTACCATTGTGTGTTGCTTTGG
TA3438   481 GCTCCCCTTTATTTATTGCTTAGTGACATGGTTTTTGCCTACCATTGTGTGTTGCTTTGG

TA831    541 CTAATGCTCACAAATTAAAGTTACTTTGCGAGCCAACAGAAATGGTGCGTTGTTGAGACA
TA3438   541 CTAATGCTCACAAATTAAAGTTACTTTGCGAGCCAACAGAAATGGTGCGTTGTTGAGACA

TA831    601 GGTGACG
TA3438   601 GGTGACG
```

Supplementary Fig. 13s. Alignment of *Pinb-A* between the amphiploid TA3438 (2n=4x=28, AASS) and its parent TA831 (*T. urartu*, 2n=2x=14, AA).

```
TA1785    1 TTTCTCAACAACTTGCACCGTTTCTGTTTGCTCGCAAAGTAACTTTAATTAGTACCAACT
TA3438    1 TTTCTCAACAACTTGCACCGTTTCTGTTTGCTCGCAAAGTAACTTTAGTTAGTACCAACT

TA1785   61 AGATTTGTAAGCATTAGCCAAAGCGACACACTATGGTAGGCAAAAACCATGTCTCGTAGC
TA3438   61 AGATTTGTAAGCATTAGCCAAAGCGACACACTATGGTAGGCAAAAACCATGTCTCGTAGC

TA1785  121 AATAAATAAAGGGGAGCCTCAACCCATCTATTCATCTCCAACACCACCAAAACAACATTG
TA3438  121 AATAAATAAAGGGGAGCCTCAACCCATCTATTCATCTCCAACACCACCAAAACAACATTG

TA1785  181 AAAACATGAAGTCCTTATTCCTCCTAGGTCTCCTTGCTCTTGTAGCGAGCACAACCTTCG
TA3438  181 AAAACATGAAGTCCTTATTCCTCCTAGGTCTCCTTGCTCTTGTAGCGAGCACAACCTTCG

TA1785  241 CGCAATACTCAGAAGTTGGCGGCTGGTACAATGAAGTTGGCGGAGGAAGTGGTTCTCAAC
TA3438  241 CGCAATACTCAGAAGTTGGCGGCTGGTACAATGAAGTTGGCGGAGGAAGTGGTTCTCAAC

TA1785  301 AATGCCCACAGGAGCGACCGAAGCTAGGCTCTTGCAAGGATTACGTGTTGGAGCGGTGCT
TA3438  301 AATGCCCACAGGAGCGACCGAAGCTAGGCTCTTGCAAGGATTACGTGTTGGAGCGGTGCT

TA1785  361 TCACAATGAAGGATTTTCCAGTCACCTGGCCCACAAAATGGTGGAAGGGTGGATGTGAGC
TA3438  361 TCACAATGAAGGATTTTCCAGTCACCTGGCCCACAAAATGGTGGAAGGGTGGATGTGAGC

TA1785  421 ATGAGGTTCGGGAGAAGTGCTGCAAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCG
TA3438  421 ATGAGGTTCGGGAGAAGTGCTGCAAGCAGCTGAGCCAGATAGCACCACAGTGTCGCTGCG

TA1785  481 ATTCTCTCCATAGAGTGATCCAAGGCAAGCTCGGCGGTTTCTTTGGCATTTGGCGAGGTG
TA3438  481 ATTCTCTCCATAGAGTGATTCAAGGCAAGCTCGGTGGTTTCTTGGGCATTTGGCGAGGTG

TA1785  541 AGGTATTCAAACAAATTCAGAGGGCCCAGAGCCTCCCCTCAAAGTGCAACATGGGCGCTG
TA3438  541 AGGTATTCAAACAAATTCAAAGGGCACAGAGCCTCCCCTCAAAGTGCAACATGGGCGCTG

TA1785  601 ACTGCAAGTTTCCTA
TA3438  601 ACTGCAAGTTTCCTA
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Supplementary Fig. 14s. Alignment of *Pina-S* between the amphiploid TA3438 (2n=4x=28, AASS) and its parent TA1785 (*Ae. speltoides*, 2n=2x=14, SS).