

**Additional file 13: Full set of annexin sequences from wheat (*T. aestivum*), barely (*H.vulgare*), *T.urartu* and *A.tauschii*.**

The sequences below are the complete collection of full length cDNA/mRNA sequences for annexin genes from barely (*H.vulgare*), *T.urartu* and *A.tauschii*. Sequences derived solely from GB ESTs may not be eligible for submission to GB as third party annotations. Sequences derived from Triticale hiseq2000 EST libraries which are identical to *T. aestivum* annexin are eligible for submission and this is in progress.

**(1). Wheat (*T. aestivum*)**

>TaAnn1-A

MASLSVPPVLTTPRDDAVALHKAFKFGGCDSTTVTNILAHRDSAQRALILHEYKAIYHQDLYHRLATELSG  
NHKCSRNEPAWLWLQNAMLLWVLDPVGRDATILNQALNSDITDLRAATEVICSRTPSQLQIMKQTYRARF  
GCYLEHDITERTYGDHQKLLLAYLGLYQAGEKRVGTDERAFIRIFERSWAHMVSVANAYQHMYARSLEK  
AVKSETTGNFQFGLLTILRCADTPAKYFAKVLHKAMKGLGTSNAALTRVAVTRTEVDMKYIKAETHNKYK  
GSLAEAIHSETSGNYRTFLLSLVGWDR

>TaAnn1-D

MASLSVPPVLTTPRDDAVALHKAFKFGGCDSTTVTNILAHRDSAQRALILHEYKAMYHQDLYHRLATELS  
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YGDHQKILLAYLGVPRNEGPEVDPSAVTDDARELYRAGEKRVGTDERAFIRIFTESSRAHLVSIANAYQHM  
YARSLEKTLKSETTGNFQFGLLTILRCADTPAKYFAKVLHKAMKGLGTSNAALIRVAVTRTEVDMKYIKAE  
YHNKYKGSLEAIHSETSGNYRTFLLSLVGRDR

>TaAnn2-A

MCGWCGCLECIHNIPPLNLLFLHFSSAARTGREGGEGARTLSPMASISVPDPAPSPTEDAESIRKAVQGWGT  
DENALIEILGHRATAQRAEIAVAYEGLYDKPLLRTLQDELSSHFKGAMTLWAMPAAARDAKLAYKALRKK  
GGDRHAWVLIEVACASSPDHLVAVRKAYCSAYDSSLEEDVAACPLYKDPLKQFLVRLVSSYRHGGEHVDG  
ELARAEAAELHGAVAACKQPLHGDVVRIVSSRSKPQLKATFQHYKREHGKAIDEVLEGNRNDKLSAMLK  
TAVWCLTSPEKHFAEVIRSSIIGLGTDEESLTRAIVSRAEVDLKKVKEEYKVRYKTTVTKDVGDTSGYYQ  
GILLTLIGAE

>TaAnn2-B

MCGWCCCLECIHNIPPLNLLFLHFSSAPRTGRDGEGARTLSPMASISVPDPASSPTEDAENIRKAVQGWGT  
DENALIEILGHRATAQRAEIAVAYEGLYDKPLLRTLQDELSSHFKGAMTLWTMDPAARDAKLAYKALRKK  
GGDRHAWVLIEVACASSPDHLVAVRKAYCSAYDSSLEEDVAACPLYKEPLKQFLVRLVSSYRDGGDHVDG  
ELARAEAAELHGAVAACKQPLHGDVVRIVSSRSKPQLKATFQHYKREHGKAIDEVLEGNRNDKLSAMLK  
TAVWCLTSPEKHFAEVIRSSIIGLGTDEESLTRAIVSRAEVDLKKVKEEYKVRYKTTVTKDVGDTSGYYQ  
GILLTLIGAE

>TaAnn3-A

MADEVQALTKAFSGLGGLGVDEPTMVAALANWRKQPEKRSFGRKSFPLFKEHGVIERCEDEYMLHLA  
AEFSRFKNMLVWAMHPWERDARLAHHVLHQAHPAAILVEVACTRSAEELGARKAYMALFHHSLEEDV  
AYRAKDKPYCSLLVGLVSAYRYEGPKVSDDTAKAEAKALGAAVKSAAAGGKLVENDEVVRILTTRSKPHLV  
QTFKYKELHGKHIQEDLGSEEALREAVQCLATPERYFSQVMAAALREGADHHGKEALARVAVTRSDVD  
MDGIRAAEQEFGAKLEDAVAGSAHGFKDALVSLIVGK

>TaAnn3-B

MADEVQALTKAFSGLGGLGVDEPTMVAALANWRKQPEKRSQFRKSPGLFKEHGVIERCEDEYMLHLA  
AEFSRFKNLMVLWAMHPWERDARLAHHVLHQAHPSAIVVEIACTRS AEELLGARKAYMALFHHSLEEDV  
AYRAKDPKPYCSLLVGLVSAYRYEGPKVSDDTAKAEAKALGAAVKSAAAGKLVENDEVVRILTTRSKPHLV  
QTFKYYKELHGKHIEEDLGSEEALRETVQCLATPERYFSQVMAAALREGADHHGKEALSRAVAVTRSDVD  
MDGIRAAYQE QFGAKLEDAVAGSAHGHEFKDALVSLIVGK

>TaAnn4-A

MTTITVPQVVPSPVEDAEALMKAFQGWGTDEQAVIYILAHRDAAQRKLIRQAYEKEYNELLDRLQSELS  
GDLQTAMGYWVLDPTERQAVIANAATKCIDEYYPVIVEIACANSPAELEVKQAYHAIYKRSLEEDVAAGA  
TGNLRNLLVALVSTYRYDGDEVNGGLARSEAKIIQADVKNVGTADHGELIRVLGTRSRAQLGATFNCFRD  
EHGTTVTKVLNRNAMHKSQGTDEESLLRVVVMHAEKDLRAIKDEFHRRASVALEQAIKETSQDFKTFIMAL  
VGTSQ

>TaAnn4-D

MATIKVPQVVPSPVEDAEALMKAFQGWGTDEQAVIYILAHRDAAQRKLIRLAYEKEYDER  
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SLEEDVAAGATGNLRNLLVALVSAYRYDGDEVNGGLARSEAKIIQADVKNVGTADHGELIRVLGTRSRAQ  
LGATFNCFRDEHGTTVTKALLHAPDTTGYARALRTAARCIADTDKYFAKVLNRNAMHKSQGTDEESLLRVV  
VMRAEKDLRGKDEFHKKRASVALEQAIKE  
ASGDFKTFITALVGT

>TaAnn5-B

MSAIVVPSPVSPSDDAEGIRKALQGW RADKEALVRILAGPLLNSFRQLSRQYCPVTVDFWKAILWTM  
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LVSLVSSYRYGGDRVDADVAKLEASQLSEAVRKKQPHHDEVVQILGTRSKPQLRATLRRYREDHGT DIVE  
DIDSRCSSQFARTLKS AVWCLTSPEKHFAEMIRESV VGLGT YEDMLTRVVVSRAEIDMKQIKEEYRARFKT  
TVTCDVVDDTSFGYKDILLALVGCEEE

>TaAnn6-A

MASLSVPPVLTSPRHDAIALHRAFKGFGCDSTTVINILAHRDAVQRGLIMQEYRAIYHQDLYHRLSTELSG  
NHKKAMLLWVLDPVGRDATILNQLNGDITDLRAATEVICSRTPSQLQIMKQTYRARFGCYLEQDITERTY  
GDHHKLLLAYLGIPRYEGPEVDPAAAARDARELYRAGEKRLGTDERAFIRVFTERS WAHLAAVAGAYHHL  
YARSLEKAVKSETSGTFEFGLLTILRCAESPARYFAKALHKAMKGLGTS DTTLIRVVVTRAEVDMQYIKAE  
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>TaAnn6-A

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YGDHQKLLLAYLG VRRNEGPEVDPSAVTDDARELYQAGEKRVGTDERAFIRIFSERSWAHMVSVANAYQ  
HMYARSLEKAVKSETTG NFQFGLL TILRCADTPAKYFAKVLHKAMKGLGTSNAALTRVAVTRTEVDMKYI  
KAEYHNKYKGLAEAIHSETSGNYRTFLLSLVGRDR

>TaAnn6-B

MASLSVPPVLTSPRHDAIALHRAFKGFGCDSTTVINILAHRDAVQRALIMQEYRAMYRQDLYHRLSTELSG  
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GDHQKLLLAYLGIPRYEGPEVDPAAAARDARELYRAGERRLGTDERAFIRVFTERS WAHLAAVAGAYHHL  
YARSLEKAVKSETSGTFELGLLTILRCAESPARYFAKALHKAMKGLGTS DTTLIRVVVTRAEVDMQYIKAE  
YHKKYKRS LADAIHSETSGNYRTFLLSLVGRDR

>TaAnn7-B

MATIAVPTPLPSAADAESLRNAVQGWGTDEKALVEILGRRTAAQRAEIRRAYASLYKESLLTRLHDELSGH

FQKAMVLLATDPAERDAKLVREALGRRGDDRDWVLEAACAATPEHLVAVRRAYRSLHGSSLEEDVAA  
CSAFQEPLRKLKLVSLVRSYRCAEESVDMVAKLEAAQLAEAVRRKKQPHGGEVVVRIVSTRSKSQAATFR  
CYKEQHGS DIEEDMKQYSSSQFARMLKIAVWCLTSPEKHAEVIRYSILGLGTDEDLTLTRAIVSRADIDME  
KIKQEYRVRFKTTVTDDVVGDTSRYYMDILLALVGKE

>TaAnn7-D

MATIDVPTPVPSAADADSLRNAVQGWGTDEKALVEILGRRRTAAQRAEIRRAYASLYKESLLTRLHGELSG  
HFQKAMVLLATDPAERDAKLAREALGRRGDDRDWVLEAACAAPDHLVAVRRAYRSLHGSSLEEDVA  
ACSAFQEPLRKLKLVSLVRSYRCAEESVDMVAKLEAAQLAEAIRRKKQPHAGEVVVRIVSTRSKPQLAATF  
RCYKEQHGS DIEEDMKQYSSSQFARMLKIAVWCLTSPEKHFAEVIRYSILGLGTDEDALTRAIVSRADIDM  
KKIKQEYRVRFKTTVTDDVVGDTSGYYMDILLALVGKE

>TaAnn8-A

MQQFLAAQPSSNGSTAAAAAAPPSPSPLSRPPRRRQQQSIVKEATMADEHQELTKAFSGMGGLGV  
EETALVSALGRWRKQPEKRAQFRRGFPGFFAPAAAGAGAGAIERCSDDYVRHLKTEFARFKTLMVLWAM  
HPWERDARWAHRALHKKHHPVAVLVELACTRAADELLGARRAYHALYHRSLEEDVAYRVKDAAAANRLL  
LGLVTAYRYEGPRVDEELAKEEAAALSAGAGAKAAQSELVVRVLATRSKPQLRATFRLYRELHGKPLEEEFG  
GEAPCLREAVRCLESPARYFGEVIDGAFKEGADKQAKAALTRVVVSRSDADMEEIKEAYLKQHGDKLVD  
VAKNTHGHYRDALLAMIGK

>TaAnn8-D

MQQFLAAQPSSNGSTAAAAAPPSPSPLSRPPRRRQQQSIKEATMADEHQELTKAFSGMGGLGVEETA  
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WAHRALHKKHHPASVVELACTRAADELLGARRAYHALYHRSLEEDVAYRVKDAAAANRLLGLVTAYRY  
EGPRVDEELAREEAAALSAGPGAGAKAQSQSELVVRVLATRSKPQLRATFRLYRELHGKPLEEEFGDAP  
CLREAVRCLESPAKYFGEVIDGAFKEGADKQAKAALTRVVVSRSDADMEEIKEAYLKQHGAKLVD  
VAKNTHGHYRDALLAMIGK

>TaAnn9-B

MASLTLPAPPNPRQDAIDLHKAFKGFCDSTTVSNILHRDSMQRGYIQQEYKTMYSSELSRRISSELSG  
NHKKAMSLWILDPAGRDATVLKEALS AESLDLKAATDIICSRTPSQLQIMKQTYAKFGTYLEHDISQQAS  
GDHQKILLAYVGIPRYEGPEVDPTIVTHDAKDLYKAGEKKLGTDEKTFIRIFTERS WAHMAAVASAYHHM  
YDRSLQKVVKNETSGNFEVALLTILRCAENPAKYFAKVLKSMKGLGTDDKTLVRVVVTRTEIDMQYIKA  
EYKYYKKPLADAIHSETSGGYRTFLLSLVGSH

>TaAnn9-D

MASLTLPAPPNPRQDAIDLHKAFKGFCDSTTVSNILSHRDSMQRGYIQQEYKTMYSSELSHRISSELSGN  
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DHQKILLAYVGIPRYEGPEVDPTIVTHDAKDLYKAGEKKLGTDEKTFIRIFTERS WAHMAAVASAYRHM  
YDRSLQKVVKNETSGNFEVALLTILRCAENPAKYFAKVLKSMKGLGTDDKTLVRVVVTRTEIDMQYIKAE  
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>TaAnn10-A

MAARSPAAAGFENE CREIHGACDEPRRLSRLLAHRSASERQQIKATYRAMFGEDLAGRLHKTTLANQDNE  
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DPSPHYQRLLVALATSHKSHHDEPSQHIAKCDARRLYDAKNGGGTGSVDEAAILEMFSKRSIPQLRLALCS  
YKHIYGHDFTKALKKNLARDFEESLRVVVKCIYTPSKYYCKLLQRSMQRPEADKRLVTRAILGSDDVGIN  
EIKLAFKSNFGKNLADFIHESLPQSDYREFLWLWQGGQCLVAS

>TaAnn10-B

MAARSPAAAGFENE CREIHGACDEPRRLSRLLAHRSASERQQIKATYRAMFGEDLAGRLHKTTLANQDNE  
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LEQDMVTDPSHPYQRLLIATSHKSHHDEPSQHIAKCDARRLYDAKNGGGTGSVDEAAVLEMFSKRSIP  
QLRLALCSYKHIYGHDFTKALKKNLARDFEESLRVVVKCIYTPSKYYCKLLQRSMQRPEADKRLVTRAIL  
GSGDVGINEIKLAFKSNFGKNLADFIHESLPQSDYREFLWLWQGGQCPVAS

>TaAnn10-D

MAARSPAAAGFENEHREIHGACDEPRRLSRLLAHRSASERQQIKATYRAMFGEDLAGRLHKTTLANQDNE  
SQHGLPLQLCNLLYLWMLDLAERDAIMARDAIESGAAADYRALVEVFTRRKQDQLFFTKQAYLARFKKN  
LEQDMVTDPSHPYQRLLVALATSHKSHHDEPSRHIKCDARRLYDAKNGGGTGSVDEAAILEMFSKRSIP  
QLRLALCSYKHIYGHDFTKALKKNLAGDFEESLRVVVKCIYTPSKYYCKLLQRSMQRPEADKRLVTRAIL  
GSSDVGINEIKLAFKSNFGKNLADFIHESLPQSDYREFLWLWQGGQCLVAS

>TaAnn11-A

MATLSVPAAVPAVAEDCEQLRKAFAGWGTNERLIVSILAHRDAAQRRAIRRAYAEAYGEELLRAIGDEIHG  
KFERAVIQWTLDPAPERDAELANEEAKKWQPGGRALVEIACARTPAQLFAAKQAYHDFRFRSLEEDVAAH  
VTGDFRKLPLVPLVSAYRYDGPEVNTSLAHSEAKLLNGKINEKAYSDDDEVVRLITRTRSKAQLLATFNNSYNDQ  
FSPITKDLKEDPKNEFLSTLRAIIRCFTCPDRYFEKVRLALGGVGTDEDTLTRVITTRAEVDLKVIKEAY  
QKRNSVPLEKAVSKETSRYEDMMLALLGAEY

>TaAnn11-B

MATLSVPAAVPAVAEDCEQLRKAFAGWGTNERLIVSILAHRDAAQRRAIRRAYAEAYGEELLRAIGDEIHG  
KFERAVAQWTLDPAPERDAELAGEEAKKWQPGGRALVEIACARTPAQLFAARQAYHDFRFRSLEEDVAAH  
VTGEFRKLLVPLVSAYRYDGPEVNTSLAHSEAKILNGKINEKAYSDDDEIIRILTTRSKAQLLATFNNSYNDQFS  
HPITKDLKEDPKNEFLSTLRAIIRCFTCPDRYFEKIIRLALGGVGTDETLTRVITTRAEVDLKVIKEAYQKR  
NSVPLDKAVSKETSRYEDMMLALLGAEY

>TaAnn11-D

MATLSVPAAVPAVAEDCEQLRKAFAGWGTNERLIVSILAHRDAAQRRAIRRAYAEAYGEELLRAIGDEIHG  
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VTGDFRKLPLVPLVSAYRYDGPEVNTSLAHSEAKILNGKINEKAYSDDDEIVRILTTRSKAQLLATFNNSYNDQF  
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>TaAnn12-A

MATLKVPSNVPALADDCDNLKAFQGWGTNEALIISILGHRDASQRRAIRKHYADTYGEELRSITDEISGD  
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DFRKLPLVPLVSSHRYEGPEVNTRLAHSEAKLLHEKIEHKAYADDEVIRILTTRSKAQLLATFNNSYNDTFGHP  
ITKDLKADPKDEFKTLRAVIRCFTCPDRYFEKVARVAIAGNGTDENSLTRVITTRAEVDLKLIKEAYQKR  
NSVPLEKAVAGDTSGDYESMMLALLGKE

>TaAnn12-D

MATLKVPSNVPALADDCDNLKAFQGWGTNEALIISILGHRDAAQRRAIRKHYADTYGEELRSITDEISG  
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TGDFRKLPLVPLVSSHRYEGPEVNTRLAHSEAKLLHEKIEHKAYGDDEVIRILTTRSKAQLLATFNNSYNDTF  
GHPITKDLKADPKDEFKTLRAVIRCFTCPDRYFEKVARLAIAAGNGTDENSLTRVITTRAEVDLKLIKEAYQ  
KRNSVPLEKAVAGDTSGDYESMMLALLGKE

>TaAnn1-A

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CTTCAAAGGGTTCCGGCTGCGACAGCAGCAGCGGTGACTAACATACTTGCTCACCGCGACTCGGCGCAG  
CGCGCGCTCATCTGCACGAGTACAAAGCCATATACCATCAGGATCTCTACCATCGCCTAGCAACTGAA  
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TTGGGTCTCGACCCCGTGGGGCGTGACGCGACCATACTGAACCAGGCTCTCAACAGCGACATCACC  
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CCTACCGCGCGAGGTTTCGGTTGCTACCTCGAGCATGACATCACCGAACGCACCTACGGTGATCATCAG  
AAGCTTTTGGCTTGGCTACCTGGGACTGTATCAAGCCGGCGAGAAGAGGGTGGGCACCGATGAGCGGG  
CCTTCATCCGCATCTTCAGCGAACGCAGCTGGGCGCACATGGTGTCCGTGGCCAACGTTACCAGCAC  
ATGTACGCCCCGGTCCCTGGAGAAGGCCGTGAAGAGTGAGACGACAGGGAACCTCCAGTTCGGGCTGC  
TGACCATCTCAGGTGCGCCGACACTCCGGCAAAGTACTTTGCCAAGGTCCTGCACAAGGCGATGAA  
AGGCTGGGCACCAGCAACGCGGCGCTCACACGGGTGGCGGTGACGAGGACCGAGGTTGACATGAA  
GTACATCAAGGCAGAGTACCACAACAAGTACAAGGGTTCGCTGGCTGAAGCTATCCACTCCGAGACG  
TCGGGGAACCTACCGAACCTTCCTCCTCTCACTCGTCGGCTGGGACCGCTAA

>TaAnn1-D

ATGGCGAGCCTGAGCGTGCCTCCGGTGTACGCCCCCGCGGATGACGCCGTCGCTCTCCACAAGG  
CCTTCAAAGGTTTCGGCTGCGACAGCACGACGGTGACCAACATACTTGCTCACCGCGACTCGGCGCA  
GCGCGCGCTCATCTGCACGAGTACAAAGCCATGTACCATCAGGATCTCTACCATCGCCTAGCAACCG  
AGCTGAGTGAAACCACAAGAATGCTATGCTGCTTTGGGTCTCGACCCTGCTGGGCGTGATGCGACC  
ATACTGAACCAAGCTCTCAACGGCGACATCACCAGCTGAGAGCCGCCACCGAGGTTATCTGCTCCAG  
GACGCCGTGCGAGCTGCAGATCATGAAGCAAACCTACCGTGCAGGTTTCGGTTGCTACCTCGAGCATG  
ACATCACCGAACGCACCTATGGAGATCATCAGAAGATTTGCTTGCCTACCTGGGAGTCCCACGCAAC  
GAAGGCCCGGAAGTTGATCCTTCGGCGGTGACAGACGACGCGAGGGAGCTGTATAGGGCCGGCGAG  
AAGAGGGTGGGCACCGATGAGCGGGCCTTCATCCGCATCTTCACCGAAAGCAGCAGGGCACACCTGG  
TGTCATCGCCAACGCTTACCAGCACATGTACGCCCCGGTCCCTGGAGAAGACCCTGAAGAGTGAGAC  
GACAGGGAACCTCCAATTCGGGCTGCTGACCATCCTCAGGTGCGCCGACACTCCGGCAAAGTACTTTG  
CCAAGTCTCTGCACAAGGCGATGAAAGCCCTGGGCACCAGCAACGCGGCGCTCATAAGGGTGGCGG  
TGACGAGGACCGAGGTCGACATGAAGTACATC  
AAGGCAGAGTACCACAACAAGTACAAGGGTTCGCTGGCTGAAGCTATCCACTCCGAGACGTCAGGGA  
ACTACCGAACCTTCCTCCTCTCGCTCGTCGGCCGGGACCGCTAA

>TaAnn2-A

ATGTGTGGCTGGTGC GGCTGCCTCGAGTGCATCCATAACATCCCTCCCCTCAATCTCCTCTTCCCTCCAC  
TTCTCCTCGGCTGCACGGACGGGAAGGGAGGGAGAAGAAGGAGCGGAACGCTCAGCCCCATGGCC  
TCCATCTCGGTCCCGACCCCGCCCTTCCCCGACCGAGGATGCAGAGAGCATCAGAAAAGCAGTGC  
AAGGGTGGGGGACGGACGAGAACGCGCTGATCGAGATCCTGGGCCACCGGACGGCGGCGCAGCGCG  
CGGAGATCGCCGTCGCCTACGAGGGCCTTACGACAAGCCCTCCTCCGCACGCTCCAGGACGAGCT  
CTCCAGCCACTTCAAAGGGCGGATGACGCTGTGGGCGATGGACCCGGCGGCGGGACGCCAAGCTG  
GCCTACAAGGCCCTCAGGAAGAAGGGCGGCGACCGGCACGCCTGGGTGCTCATCGAGGTCGCCTGCG  
CGTCGTCGCCGGACCACCTCGTCGCCGTCAGGAAGGCCACTGCTCCGCTACGACTCGTCGCTCGAG  
GAGGACGTCGCCGCTGCCGCTTACAAGGACCCCTCAAGCAGTTCTTGGTGCGCCTGGTGAGCT  
CGTACCGCCACGGCGGCGAGCACGTCGACGGCGAGCTGGCGAGGGCCGAGGCGGCCGAGCTGCACG  
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AGCCGCAGCTCAAGGCGACGTTCCAGCACTACAAGCGAGAGCACGGCAAGGCCATCGACGAGGTTT  
TCGAGGGCAATCGCAACGACAAGCTGTGCGGATGCTGAAAACCTGCGGTCTGGTGCCTGACATCGCC  
GGAGAAGCACTTCGCAGAGGTGATCCGGAGCTCGATCATCGGGCTCGGCACCGACGAGGAATCCCTG  
ACCAGAGCGATTGTCTCGCGCGCCGAGGTGCACTTGAAGAAAGTGAAGGAGGAATACAAGGTGAGGT  
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CCTCATCGGGGCCGAGTAG

>TaAnn2-B

ATGTGTGGCTGGTGTCTGCTGCCTCGAGTGCATCCATAACATCCCTCCCCTCAATCTCCTCTTCCCTCCACT  
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CTCGGTCCCGGACCCTGCCTCTTCCCCAACCGAGGATGCAGAGAACATAAGGAAAGCAGTACAAGGG  
TGGGGGACGGACGAGAACCGCTGATCGAGATCCTGGGCCACCGGACGGCGGCAGCGCGCGGAG  
ATCGCCGTGGCCTACGAGGGCCTCTACGACAAGCCCCTCCTCCGCACGCTCCAAGACGAGCTCTCCAG  
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GCGACGGTGGCGACCACGTCGACGGCGAGCTGGCGAGGGCGGAGGCGGCCGAGCTGCACGGCGCGG  
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GCACTTCGACAGAGGTGATCCGGAGCTCAATCATCGGGCTCGGCACCGACGAGGAATCCCTGACCAGA  
GCGATCGTCTCGCGCGCCGAGGTCGACTTGAAGAAAGTCAAGGAGGAATAACAAGGTGAGGTACAAG  
ACGACGGTGACCAAGGATGTCGTCGGCGACACTTCCGGCTACTACCAGGGCATCCTGCTCACCCTCAT  
CGGGGCCGAGTAG

>TaAnn3-A

ATGGCCGACGAAGTTCAGGCGCTCACCAAGGCCTTCTCAGGTCTGGGAGGTCTGGGCGTGGACGAGC  
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GCTTCCCGGGGCTGTTCAAGGAGCACGGCGTGATCGAGCGGTGCGAGGACGAGTACATGCTGCACCT  
GGCCGCCGAGTTCTCCCGTTCAAGAACCTCATGGTGTGTGGGCGATGCACCCGTGGGAGCGCGAC  
GCCCCGCTCGCGCACACGTCCTCCACCAGGCCACCCGCGCCATCGTCGTGGAGGTCGCCTGCA  
CCCCTCCGCCGAGGAGCTCCTCGGCGCGCGCAAGGCCTACATGGCGCTCTTCCACCACTCCCTCGAG  
GAGGACGTCGCCTACCGCGCCAAGGACAAGCCATACTGCAGCCTGCTGGTGGGGCTGGTGGAGCGCGT  
ACCGGTACGAAGGGCCCAAGGTGAGCGACGACACGGCCAAGGCGGAGGCCAAGGCGCTGGGCGCG  
GCGGTGAAGAGCGCCCGCGGCAAGCTGGTGGAGAACGACGAGGTGGTCAGGATCCTCACCACC  
AGGAGCAAGCCTCACCTCGTCCAGACCTTCAAGTACTACAAGGAGCTGCACGGCAAGCACATCGAGG  
AGGATCTGGGAAGCGAGGAGGCTCTGAGGGAGACCGTGCAGTGCTGGCGACGCCGAGAGGTA  
TCAGCCAGGTGATGGCGGCGGCGCTGAGGGAGGGCGCGGACCACCACGGGAAGGAGCCCTGTTCG  
GGGTGGCGGTGACGCGGTGCGACGTGGACATGGACGGCATCAGGGCGGCCTACCAGGAGCAGTTCTG  
GGCCAAGCTCGAGGACGCCGTCGCCGCGACGCGCACGGGCACTTCAAGGACGCGCTCGTCTCGCT  
CATCGTCGGCAAGTAA

>TaAnn3-B

ATGGCCGACGAAGTTCAGGCGCTCACCAAGGCCTTCTCAGGTCTGGGAGGTCTGGGCGTGGACGAGC  
CGACGATGGTGGCGGCGCTGGCGAACTGGCGAAGCAGCCGGAAGCGGTCCGGGTCCGAAAGA  
GCTTCCCGGGGCTGTTCAAGGAGCACGGCGTGATCGAGCGGTGCGAGGACGAGTACATGCTGCACCT  
GGCCGCCGAGTTCTCCCGTTCAAGAACCTCATGGTGTGTGGGCGATGCACCCGTGGGAGCGCGAC  
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>TaAnn12-A

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>TaAnn12-D

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(2). barely (*H.vulgare*)

>HvAnn1 MLOC\_15770.2

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>HvAnn2 MLOC\_54933.3

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>HvAnn3 MLOC\_54932.1

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>HvAnn5 MLOC\_15543.3

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>HvAnn6 MLOC\_55134.1

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>HvAnn7 MLOC\_3056.1

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>HvAnn10 MLOC\_54650.4

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>HvAnn1 MLOC\_15770.2

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>HvAnn2 MLOC\_54933.3

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>HvAnn3 MLOC\_54932.1

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>HvAnn5 MLOC\_15543.3

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>HvAnn6 MLOC\_55134.1





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>HvAnn10 MLOC\_54650.4

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3). *Turartu*

>TuAnn1 TRIUR3\_22191

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>TuAnn2 TRIUR3\_11010

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>TuAnn3 TRIUR3\_11009

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>TuAnn11 TRIUR3\_16577

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4). *A. tauschii*

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