

Fig. S1. Phylogenetic analysis of Poaceae *Btr1* and *Btr1-like* genes including those likely non-translated. Members of the *Btr1* clade are colored orange. The truncated *Btr1* copies in *Ae. tauschii* (chromosome 3D: 59424083-59424248) and *Ae. longissima* (un: 73407949-73408115) are shown underlined. Numbers given at a branch node indicate bootstrap probabilities (only those >50% are shown). The number refer to the accession / scaffold / contig and the start location of each gene is given in Table S3.

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T_boeoticum_Btr1-like-A-1 ATGGCGCAGCCGCCGCATGGAAGGCGATGTACCTGCCTGTGACGAGCGACGCGATCCGA 60
T_boeoticum_Btr1-like-A-2 ATGGCGCAGCCGCCGCATGGAGGACGATGTACCTGTCTGTGACGAGCGAGGCGATCCGA 60
***** * *****
T_boeoticum_Btr1-like-A-1 TCCGCCGCCCGCTCAAGCGAAGCGTCCGCCGCCGCGGTACCGAGCTGGCGTCCCGCGAG 120
T_boeoticum_Btr1-like-A-2 TCCGCCGCCCGCTCAAGCAAAGCGTCCGCCGCCGCGGTACCGAGCTGGCGTCCCGCGC-- 118
***** *****
T_boeoticum_Btr1-like-A-1 GTGGTGTGACACCCGCGACGCCAGGGGCGGTACACCTTGCTGGAGTCCGCGCTGACC 180
T_boeoticum_Btr1-like-A-2 -TGGTGTGACACCCGCGACTCCGAGGGGCGGTACACCTTGCTGGAGTCCGCGCTGACA 177
*****
T_boeoticum_Btr1-like-A-1 CACATCGACCACGCATCCGGTCCCTCTCCGCTTTCATCATCAACATGGTGGTGGCCGAG 240
T_boeoticum_Btr1-like-A-2 CACATCGACCACGCATCCGGTCCCTCTCCGCTTTCATCATCAACACGGTGGTGGCCGAG 237
*****
T_boeoticum_Btr1-like-A-1 CGCCTGACGCTCCACGGCTGCGGGCGCGTCCCGTCCGAGCCGGTGGCCCGCTCGGCGAC 300
T_boeoticum_Btr1-like-A-2 CGCCTGACGCTCCACGGCTGCGGGCGCGTCCCATCGGAGCCGGTGGCCCGCATCGGCGAC 297
*****
T_boeoticum_Btr1-like-A-1 CTCCGCGACGGCCACGGGCGCCACGACGAGTGGCTTGCTCTGATCAGGCTCCAGGCCGCC 360
T_boeoticum_Btr1-like-A-2 CTCCGCGACGGCCACGGGCGCCACGACGAGTGGCTTGCTCTCGTCCAGGCTCCAGGCCGCC 357
*****
T_boeoticum_Btr1-like-A-1 AGGGAGCACGCCAGGACGCGCTCCGCCGAGTGGAGGGGGCCTACACCTCTGGCCACC 420
T_boeoticum_Btr1-like-A-2 AGGGAGCACGCCAGGACGCGCTCCGCCGAGTGGAGGGGGCCTACACCTCTGGGCTCC 417
***** * **
T_boeoticum_Btr1-like-A-1 GTCGGGTTTCATGCTTCACAGCCAGAACCCCGACGCTCCAGGGCGCCGGCAAGCCATGGAA 480
T_boeoticum_Btr1-like-A-2 GTCGGGTTTCATGCTTCACAGCCAGAACCCCGACGCTCCAGGGCGCCGGCAAGCCATGGAA 477
*** *****
T_boeoticum_Btr1-like-A-1 GGGCAGCTCCACGCCCTCGACCTCCAGCCCGTGGTGGTTCGGCGTGGCGAGCATGTCCGCG 540
T_boeoticum_Btr1-like-A-2 GGGCAGCTCCACGCCCTCGATCTCCAGCCCGTGGTGGTTCGGCGTGGCGAGCATGTCCGCG 537
*****
T_boeoticum_Btr1-like-A-1 CTGGCCTCCTTGGCCACCCAGCCCCCATCCGCTACCGCATCCAGTGA 588
T_boeoticum_Btr1-like-A-2 CTGGCCTCCTTGGCCACCCAGCCCCCATCCGCTACCGCATCCAGTGA 585
*****

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a

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T_boeoticum_BTR1-LIKE-A-1 MAQPPPWKAMYLPVTSDAIRSAAVKRSVAAARTELASPVVLDTRDAEGRYTLLESALT 60
T_boeoticum_BTR1-LIKE-A-2 MAQPPPWRTMYLSVTSEAIRSAARVKQSVAAARRDLASP-LVLDTRDSEGRYTLLESALT 59
*****:***.***:***** **:***** :**** :*****:*****
T_boeoticum_BTR1-LIKE-A-1 HIDHASGSLSAFIINMVVAERLTLHGCGAVPSEPVARVGDRLRDGHRHDEWLALIRLQAA 120
T_boeoticum_BTR1-LIKE-A-2 HIDHASGSLSAFIINTVVAERLTLHGCGAVPSEPVARIGDLRDGHRHDEWLALVRLQAA 119
***** *****:*****:*****
T_boeoticum_BTR1-LIKE-A-1 REHAQDALRRVEGAYTLLATVGFMLHSQNPDPGRRQAMEGQLHALDLQPVVVGVASMSA 180
T_boeoticum_BTR1-LIKE-A-2 REHAEDALRRVEGAYTLLGSVRFMLHSQNPDPGRRQAMEGQLHALDLQPVVVGVASMSA 179
***:*****.* *****
T_boeoticum_BTR1-LIKE-A-1 LASLATQPPPIRYRIQ 195
T_boeoticum_BTR1-LIKE-A-2 LASLATQPPPIRYRIQ 194
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b

Fig. S2. Alignment of the products of the *T. boeoticum* genes *Btr1-like-A-1* and *Btr1-like-A-2*.

H_vulgare_Btr1_KR813335:434572-435162 ATGGCGCAGCCGCCCAATGGAAGGCGATGTACCAGTATGTCGCGCAGCGGGCGCACGAC 60
S_vavilovii_Btr1-R-1 ATGGCGCAGCCGCCCAATGGAAGGCGATGTACCAGTACGTGGCGATACGGGCGCACGAC 60
S_vavilovii_contig_160742:842-1852 ATGGCGCAGCCACCSCAATGGAAGGCGATGTACCAGTACGTGGCGATACGGGCGCACGA 60
S_vavilovii_Btr1-R-2 ATGGCGCAGCCACCSCAATGGAAGGCGATGTACCAGTACGTGGCGATACGGGCGCACGA 60

H_vulgare_Btr1_KR813335:434572-435162 GGCTGCGCCCGCGTCCAGGAAAGTGTCCGCGACGCGCGCAGGGCGCTGGCGTCCACCGCTG 120
S_vavilovii_Btr1-R-1 GGCTGCGCCCGCGTCCAGGAAAGTGTCCGCGACGCGCGCAGGGCGCTGGCGTCCACCGCTG 120
S_vavilovii_contig_160742:842-1852 GGCTGCGCCCGCGTCCAGGAAAGTGTCCGCGACGCGCGCAGGGCGCTGGCGTCCACCGCTG 120
S_vavilovii_Btr1-R-2 GGCTGCGCCCGCGTCCAGGAAAGTGTCCGCGACGCGCGCAGGGCGCTGGCGTCCACCGCTG 120

H_vulgare_Btr1_KR813335:434572-435162 GTGCTGGACACCCCGCAGCCGCGGGGCGGTGCACGTTGCTGCATCCCGGCTGACCCAC 180
S_vavilovii_Btr1-R-1 GTGCTGGACACCCCGCAGCCGCGGGGCGGTGCACCTCCTTGCATCCCGGATGACCCAC 180
S_vavilovii_contig_160742:842-1852 GTGCTGGACACCCCGCAGCCGCGGGGCGGTGCACCTCCTTGCATCCCGGATGACCCAC 180
S_vavilovii_Btr1-R-2 GTGCTGGACACCCCGCAGCCGCGGGGCGGTGCACCTCCTTGCATCCCGGATGACCCAC 180

H_vulgare_Btr1_KR813335:434572-435162 GTCGAGCACGCATCCGACTGCCCTCCGGTTTCATAGTCAGCGTGGTGGTGGCGGAGCTC 240
S_vavilovii_Btr1-R-1 GTCGAGCACGCATCCGACTGCCCTCCGGTTTCATATTCAGCATGGTGGTGGCGGAGCTC 240
S_vavilovii_contig_160742:842-1852 GTCGAGCACGCATCCGACTGCCCTCCGGTTTCATATTCAGCATGGTGGTGGCGGAGCTC 240
S_vavilovii_Btr1-R-2 GTCGAGCACGCATCCGACTGCCCTCCGGTTTCATATTCAGCATGGTGGTGGCGGAGCTC 240

H_vulgare_Btr1_KR813335:434572-435162 CTGGTGCTCCATGGCTGCGGGGCGCTCCCTTCGAGGCCGTTGGCCAGCATCGCGGCCTC 300
S_vavilovii_Btr1-R-1 CTGGTGCTCCATGGCTGCGGGGCGCTCCCGTTCGAGGCCGTTGGCCAGCATCGCGGCCTC 300
S_vavilovii_contig_160742:842-1852 CTGGTGCTCCATGGCTGCGGGGCGCTCCCGTTCGAGGCCGTTGGCCAGCATCGCGGCCTC 300
S_vavilovii_Btr1-R-2 CTGGTGCTCCATGGCTGCGGGGCGCTCCCGTTCGAGGCCGTTGGCCAGCATCGCGGCCTC 300

H_vulgare_Btr1_KR813335:434572-435162 CGCCGCAACCGCAGCAGCAGCAGGAGTGGCTCGCTCTGAGCAGGCTCGAGGCCGCCAGG 360
S_vavilovii_Btr1-R-1 CGCCGCGACCGCAGCAGCAGCAGGAGTGGCTCGCTCTGAGCAGGCTCGAGGCCGCCAGG 360
S_vavilovii_contig_160742:842-1852 CGCCGCGACCGCAGCAGCAGCAGGAGTGGCTCGCTCTGAGCAGGCTCGAGGCCGCCAGG 360
S_vavilovii_Btr1-R-2 CGCCGCGACCGCAGCAGCAGCAGGAGTGGCTCGCTCTGAGCAGGCTCGAGGCCGCCAGG 360

H_vulgare_Btr1_KR813335:434572-435162 GAGCAGCGCCAGGACGCGCTCCGCGGAGTGGAGGGGCGCTTACCCTCCTGGCCTCCGTC 420
S_vavilovii_Btr1-R-1 GAGCAGCGCCAGGATGCGCTCCGCGGGGTGGAGGGGCGCTTACCCTCCTGGCCTCCGTC 420
S_vavilovii_contig_160742:842-1852 GAGCAGCGCCAGGACGCGCTCCGCGGGGTGGAGGGGCGCTTACCCTCCTGGCCTCCGTC 420
S_vavilovii_Btr1-R-2 GAGCAGCGCCAGGACGCGCTCCGCGGGGTGGAGGGGCGCTTACCCTCCTGGCCTCCGTC 420

H_vulgare_Btr1_KR813335:434572-435162 CGGTTTCATGCTTCGACGCCGACCCCTGACGCGCGCGGGCGCGCAAGCCATGGAAGAG 480
S_vavilovii_Btr1-R-1 CGGTTTCATGCTTCACAGCCGACCCCGCAGCGTCCGCGGGCGCGCAAGCCATGGAAGAG 480
S_vavilovii_contig_160742:842-1852 CGGTTTCATGCTTCACAGCCGTACCCTGACGCTGCTGGGCGCGCAAGCCATGGAAGAG 480
S_vavilovii_Btr1-R-2 CGGTTTCATGCTTCACAGCCGTACCCTGACGCTGCTGGGCGCGCAAGCCATGGAAGAG 480

H_vulgare_Btr1_KR813335:434572-435162 CAGCTCCACGCCCGCCGTCGAATTCAGGCCGTTGGTGGGACGCTGGCGAACATGTTC 540
S_vavilovii_Btr1-R-1 CAGCTCCACGCCCGCCGTCGAATTCAGGCCGTTGGTGGGACGCTGGCGAACATGTTC 540
S_vavilovii_contig_160742:842-1852 CAGCTCCACGCCCGCCGTCGAATTCAGGCCGTTGGTGGGACGCTGGCC----TGTTC 536
S_vavilovii_Btr1-R-2 CAGCTCCACGCCCGCCGTCGAATTCAGGCCGTTGGTGGGACGCTGGCC----TGTTC 536

H_vulgare_Btr1_KR813335:434572-435162 GCGCTGGCTTCTTGGCCACTCAGCCTGCCATCCGCAACCGCATCCAGTGA----- 591
S_vavilovii_Btr1-R-1 GCGCTGGCTTCTTGGCCACCCAGCCTGCCATCCGCAACCGCTTCCAGTGA----- 591
S_vavilovii_contig_160742:842-1852 GCGCTGGCTTCTTGGCCACCCAGCCTGCCATCCGCAACCGAATCCAGTGAAGAGTCCCT 596
S_vavilovii_Btr1-R-2 GCGCTGGCTTCTTGGCCACCCAGCCTGCCATCCGCAACCGAATCCAGTGA----- 587

H_vulgare_Btr1_KR813335:434572-435162 ----- 591
S_vavilovii_Btr1-R-1 ----- 591
S_vavilovii_contig_160742:842-1852 TGACTTGCTCTGTCTGCACGATCTGCTTTGCTTGATATCGATGGTTCGCGTTGGCTAGGG 656
S_vavilovii_Btr1-R-2 ----- 587

H_vulgare_Btr1_KR813335:434572-435162 ----- 591
S_vavilovii_Btr1-R-1 ----- 591
S_vavilovii_contig_160742:842-1852 CTAGCCCATGCATGGTCTATGTGTCGTCGAATTCGAATACGTACTGTTTTCGGTTCTG 716
S_vavilovii_Btr1-R-2 ----- 587

H_vulgare_Btr1_KR813335:434572-435162 ----- 591
S_vavilovii_Btr1-R-1 ----- 591
S_vavilovii_contig_160742:842-1852 TTGTTGTTAACTGCAAGGATCTCTATATACCGGGACCTAATTAGATGTATACTTTGATG 776
S_vavilovii_Btr1-R-2 ----- 587

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H_vulgare_Btr1_KR813335:434572-435162 ----- 591
S_vavilovii_Btr1-R-1 ----- 591
S_vavilovii_contig_160742:842-1852 TTTGTCGATCTGAAATCCGAGAGATATTTGTTGGTAATTTGGCGTGGTTCATCACTTAAT 836
S_vavilovii_Btr1-R-2 ----- 587

H_vulgare_Btr1_KR813335:434572-435162 ----- 591
S_vavilovii_Btr1-R-1 ----- 591
S_vavilovii_contig_160742:842-1852 TACTGTCATGCATGATTGTATGATGATGATGCGTCGATCATGCATGCCTGGGTGGGTTCG 896
S_vavilovii_Btr1-R-2 ----- 587

H_vulgare_Btr1_KR813335:434572-435162 ----- 591
S_vavilovii_Btr1-R-1 ----- 591
S_vavilovii_contig_160742:842-1852 TACGTTAGTTGCAACTTGCAACGTACATTGGCAGTGCTGTTTTCTTTGTGGTGGCATTG 956
S_vavilovii_Btr1-R-2 ----- 587

H_vulgare_Btr1_KR813335:434572-435162 ----- 591
S_vavilovii_Btr1-R-1 ----- 591
S_vavilovii_contig_160742:842-1852 CACTTTGCAGTTGAGATTCAACTATGATCGATCAGCGAGCGATATCGTAGAATAA 1011
S_vavilovii_Btr1-R-2 ----- 587

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a

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H_vulgare_BTR1_KR813335:434572-435162 MAQPPQWKAMYQYVARRAHGDCARVEESVAAARGALATPMVLDRDAAGRCTLLHSAVTH 60
S_vavilovii_BTR1-R-1 MAQPPQWKAMYQYVAIRAHGDCARVEESVADARRALASPLVLDTRDAAGRYTSLHSAMTH 60
S_vavilovii_contig_160742:842-1852 MAQPPQWKAMYQYVAIRAHGDCARVQESVADARRALASPLVLDTRDAAGRYTSLHSAMTH 60
*****:***:* ** ***:***** * ***:**

H_vulgare_BTR1_KR813335:434572-435162 VEHASDCLSGFIVSVVVAELLVLHGCGAVPSRPVASIGGLRRNRDDHDEWLALSRLAAR 120
S_vavilovii_BTR1-R-1 VEHASGCLSGVIFSMVVAELLLALHGCGAVPSRPVAGIGDLRRDRDDHDEWLALSRLAAR 120
S_vavilovii_contig_160742:842-1852 VEHASGYLSGVIFSMVVAELLLALHGCGAVPSRPVAGIGDLRRDRDDHDEWLAVSRLEAAR 120
*****.***.*.*:*****.*****.***.***:*****:*****

H_vulgare_BTR1_KR813335:434572-435162 EHQDALRGVEGAFTLLASVRFMLRSRTPDAAGRQAMEEQLHAAAVELQAVVGSVANMS 180
S_vavilovii_BTR1-R-1 EHAQDALRGVEGAFTLLASVRFMLHSRTPDAAGRQAMEEQLHAAAVELQAVVGSVANLS 180
S_vavilovii_contig_160742:842-1852 EHAQDALRGVEGAFTLLASVRFMLHSRTPDAAGRQAMEEQLHAAAVELQAVL-----R 174
**.*:*****.*****:*****:

H_vulgare_BTR1_KR813335:434572-435162 ALAFLATQPAIRNRIQ 196
S_vavilovii_BTR1-R-1 ALAFLATQPAIRNRFQ 196
S_vavilovii_contig_160742:842-1852 F-NYDRSASDIVE--- 186
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b

Fig. S3. The *Btr1* genes present in *S. vavilovii*. (a) Nucleotide alignment between *S_vavilovii_contig_160742*, *Btr1-R-1*, *Btr1-R-2* and barley *Btr1*. Exons in *S_vavilovii_contig_160742* and *Btr1-R-2* are shown boxed. (b) Polypeptide alignment between the products of the *S. vavilovii Btr1* genes and barley *Btr1*.



Fig. S4. The mature spike of *S. vavilovii*. Scale bar, 2cm.

H_vulgare_Btr1_KR813335:434572-435162 ATGGCGCAGCCGCGCAATGGAAGGCGATGTACCAGTATGTGCGCGACGGGCGCACGAC 60
Ae_sharonensis_98068:3518-2928 ATGGCGCAGCCGCGCAGTGGAAAGGCGATGTACCAGTATGTGGCGATACGGGCGCACGAC 60
Ae_longissima_3S:86738095-86738685 ATGGCGCAGCCGCGCAGTGGAAAGGCGATGTACCAGTATGTGGCGATACGAGCGCACGAC 60
Ae_sharonensis_1151931:2022-1843 ATGGCGCAGCCGCGCAATGCAAGGCGATGTACGTGTATGTGGCGAGACGGGCGCGCAA 60
Ae_longissima_un:73407949-73408128 ATGGCGCAGCCGCGCAATGCAAGGCGATGTACGTGTATGTGGCGAGACGGGCGCGCAA 60
Ae_tauschii_3D:59424083-59424261 A-GGCGCAGCCGCGCAATGGAAGGCGATGTACGTGTATGTGGCGCGACGGGCGCGCAA 59
* ***** ** ***** ***** ** * * * * *

H_vulgare_Btr1_KR813335:434572-435162 GGCTGCGCCCGCTCGAGGAAAGCGTTCGCGCGCGCGGAGCGCTGGCGACCCCGATG 120
Ae_sharonensis_98068:3518-2928 AGCTGCGCCCGAGTGGAGGAAAGTGTGCTGCGCGCGCTAGGGAGCTGGCGTCCCGCGG 120
Ae_longissima_3S:86738095-86738685 GGCTGACCCCGCTTGAGGAAAGTGTGCGCGCGCGCTAGGGAGCTGGCGTCCCGGAG 120
Ae_sharonensis_1151931:2022-1843 GGCTGCTCTCGCTCGAGCAAAGTGTGCGCGCGCGCTACGGTGTGGCGTCCCGGTG 120
Ae_longissima_un:73407949-73408128 GGCTGCTCTCGCTCGAGCAAAGTGTGCGCGCGCGCTACGGTGTGGCGTCCCGGTG 120
Ae_tauschii_3D:59424083-59424261 GGCTGCTCTCGCTCGAGCACAGTGTGCGCGCGCGCTACGGTGTGGCGTCCCGGTG 119
***** ** *

H_vulgare_Btr1_KR813335:434572-435162 GTGCTGGACACCCGCGACGCGCGGGGGCGGTGCACGTTGCTGCATTCCGCGGTGACCCAC 180
Ae_sharonensis_98068:3518-2928 GTGCTGGACACCCGCAACGCGCGGGGGCGGTATGCCTTGTTCGATTCCGCGATGACCCAC 180
Ae_longissima_3S:86738095-86738685 TTGCTGGACACCCGCGACGCGCGGGGGCGGTACACCTTGTTCGATTCCGCGATGACCCAC 180
Ae_sharonensis_1151931:2022-1843 GTGCTGGACACCCGCAACGCGCGGGGGCGGTACACCTTGTTCGATTCTACTTGGATATGA 180
Ae_longissima_un:73407949-73408128 GTGCTGGACACCCGCAACGCGCGGGGGCGGTACACCTTGTTCGATTCTACTTGGATATGA 180
Ae_tauschii_3D:59424083-59424261 GTGCTGGACACCCGCAACGCGCGGGGGCGGTACACCTTGTTCGATTCTACTTGGATATGA 179
***** ** *

H_vulgare_Btr1_KR813335:434572-435162 GTCGAGCAGCATCCGACTGCCTCTCCGGTTTCATAGTCAGCGTGGTGGTGGCGGAGCTC 240
Ae_sharonensis_98068:3518-2928 GTCGAGCAGCATCCGGCTGCCTCTCCGGTGTATTCAGCATGGGGGTGGCCGAGCAA 240
Ae_longissima_3S:86738095-86738685 GTCGAGCAGCATCCGGCTGCCTCTCCGGTGGCGTATTCAGCATGGGGGTGGCCGAGCTC 240
Ae_sharonensis_1151931:2022-1843 ----- 180
Ae_longissima_un:73407949-73408128 ----- 180
Ae_tauschii_3D:59424083-59424261 ----- 179

H_vulgare_Btr1_KR813335:434572-435162 CTGGTGTCCATGGCTGCGGGGCGCTCCCTTCGAGGCCGGTGGCCAGCATCGCGGCCTC 300
Ae_sharonensis_98068:3518-2928 CTGGCGCTCTATGGCTGCGGGGCGCTCCCTTCGAGGCCGGTGGCCAGCATCGCGGCCTC 300
Ae_longissima_3S:86738095-86738685 CTGGCGCTCCATGGCTGCGGGGCGCTCCCTTCGAGGCCGGTGGCCAGCATCGCGGCCTC 300
Ae_sharonensis_1151931:2022-1843 ----- 180
Ae_longissima_un:73407949-73408128 ----- 180
Ae_tauschii_3D:59424083-59424261 ----- 179

H_vulgare_Btr1_KR813335:434572-435162 CGCCGCAACCCGCGACGACCACGACGAGTGGCTCGCTCTGAGCAGGCTCGAGGCCGCCAGG 360
Ae_sharonensis_98068:3518-2928 CGCCGCGACCCGCGGCGACCACGATGAGTGGCTCGCTCTGAGCAGGCTCGAGGCCGCCAGG 360
Ae_longissima_3S:86738095-86738685 CGCCGCGACCCGCGACGACCACGACGAGTGGCTCGCTCTGAGCAGGCTCGAGGCCGCCAGG 360
Ae_sharonensis_1151931:2022-1843 ----- 180
Ae_longissima_un:73407949-73408128 ----- 180
Ae_tauschii_3D:59424083-59424261 ----- 179

H_vulgare_Btr1_KR813335:434572-435162 GAGCACGCCAGGACGCGCTCCGCGGAGTGGAGGGGGCTTCACCCTCTGGCTCCGTC 420
Ae_sharonensis_98068:3518-2928 GAGCACGCCAGGACGCGCTCCCGGGTGGAGGGGGCTTCACCCTCTGGCTCCGTC 420
Ae_longissima_3S:86738095-86738685 GAGCACGCCAGGACGCGCTCCGCGGGTGGAGAGGGCTTCACCCTCTGGCATCCGTC 420
Ae_sharonensis_1151931:2022-1843 ----- 180
Ae_longissima_un:73407949-73408128 ----- 180
Ae_tauschii_3D:59424083-59424261 ----- 179

H_vulgare_Btr1_KR813335:434572-435162 CGGTTTCATGCTTCGAGCCGGACCCCTGACGCCGCGGGCGCCGCAAGCCATGGAAGAG 480
Ae_sharonensis_98068:3518-2928 CGGTTCTGCTTCACAGCCGAGCCCTGACGCTGCCGCGCCGCGCAAGCCATGGAAGAG 480
Ae_longissima_3S:86738095-86738685 CGGTTCTGCTTCACAGCCGACCCCGACGCTGCCGCGCGCCGCAAGCCATGGAAGAG 480
Ae_sharonensis_1151931:2022-1843 ----- 180
Ae_longissima_un:73407949-73408128 ----- 180
Ae_tauschii_3D:59424083-59424261 ----- 179

H_vulgare_Btr1_KR813335:434572-435162 CAGCTCCACGCCCGCCGCTCGAACTTCAGGCCGTGGTGGGCAGCGTGGCCAACATGTCC 540
Ae_sharonensis_98068:3518-2928 CAGCTCCACGCCCGCCACCGACGAACTTCAGGCCGTGGTGGGCAGCGTGGCCAACATGTCC 540
Ae_longissima_3S:86738095-86738685 CAGCTCCACGCCCGCCGCTCGAACTTCAGGCCCGGTAGGCAGCGTGGCCAACATGTCC 540
Ae_sharonensis_1151931:2022-1843 ----- 180
Ae_longissima_un:73407949-73408128 ----- 180
Ae_tauschii_3D:59424083-59424261 ----- 179

H_vulgare_Btr1_KR813335:434572-435162 GCGCTGGCTTCTTGCCACTCAGCCTGCCATCCGCAACCGCATCCAGTGA 591
Ae_sharonensis_98068:3518-2928 GCGCTGGCTTCTTGCCACCCAGCCTGCCATCCGCAACCGCATCCAGTGA 591
Ae_longissima_3S:86738095-86738685 GCGCTGGCTTCTTGCCACCCAGCCTGCCATCCGCAACCGCATCCAGTGA 591
Ae_sharonensis_1151931:2022-1843 ----- 180
Ae_longissima_un:73407949-73408128 ----- 180
Ae_tauschii_3D:59424083-59424261 ----- 179

H_vulgare_BTR1_KR813335:434572-435162	MAQPPQWKAMYQYVARRAHDGSCARVEESVAAAARGALATPMVLDTRDAAGRCTLLHSVAVTH	60
Ae_sharonensis_98068:3518-2928	MAQPPQWKAMYQYVAIRAHDSCARVEESVAAAARRELASPRVLDTRNAAGRYALLHSAMTH	60
Ae_longissima_3S:86738095-86738685	MAQPPQWKAMYQYVAIRAHDGCTRVEESVAAAARRVLASPELLDTRDAAGRYTLLHSAMTH	60
Ae_sharonensis_1151931:2022-1843	MAQPPQCKAMYVYVARRAREGCSRVEQSVAAARTVLASPLVLDTRNAAGRYTLLHST---	57
Ae_longissima_un:73407949-73408128	MAQPPQCKAMYVYVARRAREGCSRVEQSVAAARTVLASPLVLDTRNAAGRYTLLHST---	57
	***** ** ** ** *::.*:***:***** **:* :***:*** :***:	
H_vulgare_BTR1_KR813335:434572-435162	VEHASDCLSGFIVSVVVAEELLVLHGCGAVPSRPVASIGGLRRNRDDHDEWLALSRLEAAR	120
Ae_sharonensis_98068:3518-2928	VEHASGCLSGVIFSMGVAEQLALYGCAGVPSRPVAGIGDLRRDRGDHDEWLALSRLEAAR	120
Ae_longissima_3S:86738095-86738685	VEHASGCLSGGVFSGMVAEELLALHGCGAVPSRPVAGIGDLRRDRDDHDEWLALSRLEAAR	120
Ae_sharonensis_1151931:2022-1843	-----WI-----	59
Ae_longissima_un:73407949-73408128	-----WI-----	59
	*:	
H_vulgare_BTR1_KR813335:434572-435162	EHGQDALRGVEGAFTLLASVRFMLRSRTPDAAGRRQAMEEQLHAAAVELQAVVGSVANMS	180
Ae_sharonensis_98068:3518-2928	EHAQDALPGVEGAFTLLASVRFLLHSRSPDAAGRRQAIIEEQLHAATDELQAVVGSVANMS	180
Ae_longissima_3S:86738095-86738685	EHAQDALRGVERAFTLLASVRFLLHSRTPDAAGRRQAMEEQLHAAGVELQAAVGSVANMS	180
Ae_sharonensis_1151931:2022-1843	-----	59
Ae_longissima_un:73407949-73408128	-----	59
H_vulgare_BTR1_KR813335:434572-435162	ALAFLATQPAIRNRIQ	196
Ae_sharonensis_98068:3518-2928	ALAFLATQPAIRNRIQ	196
Ae_longissima_3S:86738095-86738685	ALAFMATQPAIRNRIQ	196
Ae_sharonensis_1151931:2022-1843	-----	59
Ae_longissima_un:73407949-73408128	-----	59

b

Fig. S6. The truncated *Btr1* genes present in *Ae. tauschii*, *Ae. longissima* and *Ae. sharonensis*. (a) Nucleotide alignment between the truncated *Ae. tauschii Btr1* (*Ae_tauschii_3D*: 59424083-59424261), *Ae. longissima Btr1* (*Ae_longissima_3S*: 86738095-86738685), a truncated *Ae. longissima Btr1* (*Ae_longissima_un*: 73407949-73408128), *Ae. sharonensis Btr1* (*Ae_sharonensis_98068*: 3518-2928), a truncated *Ae. sharonensis Btr1* (*Ae_sharonensis_1151931*: 2022-1843) and barley *Btr1*. The putative stop codon in the *Btr1* sequence is marked in bold. (b) Polypeptide alignment between the products of the *Aegilops* spp. *Btr1* genes and barley *Btr1*.

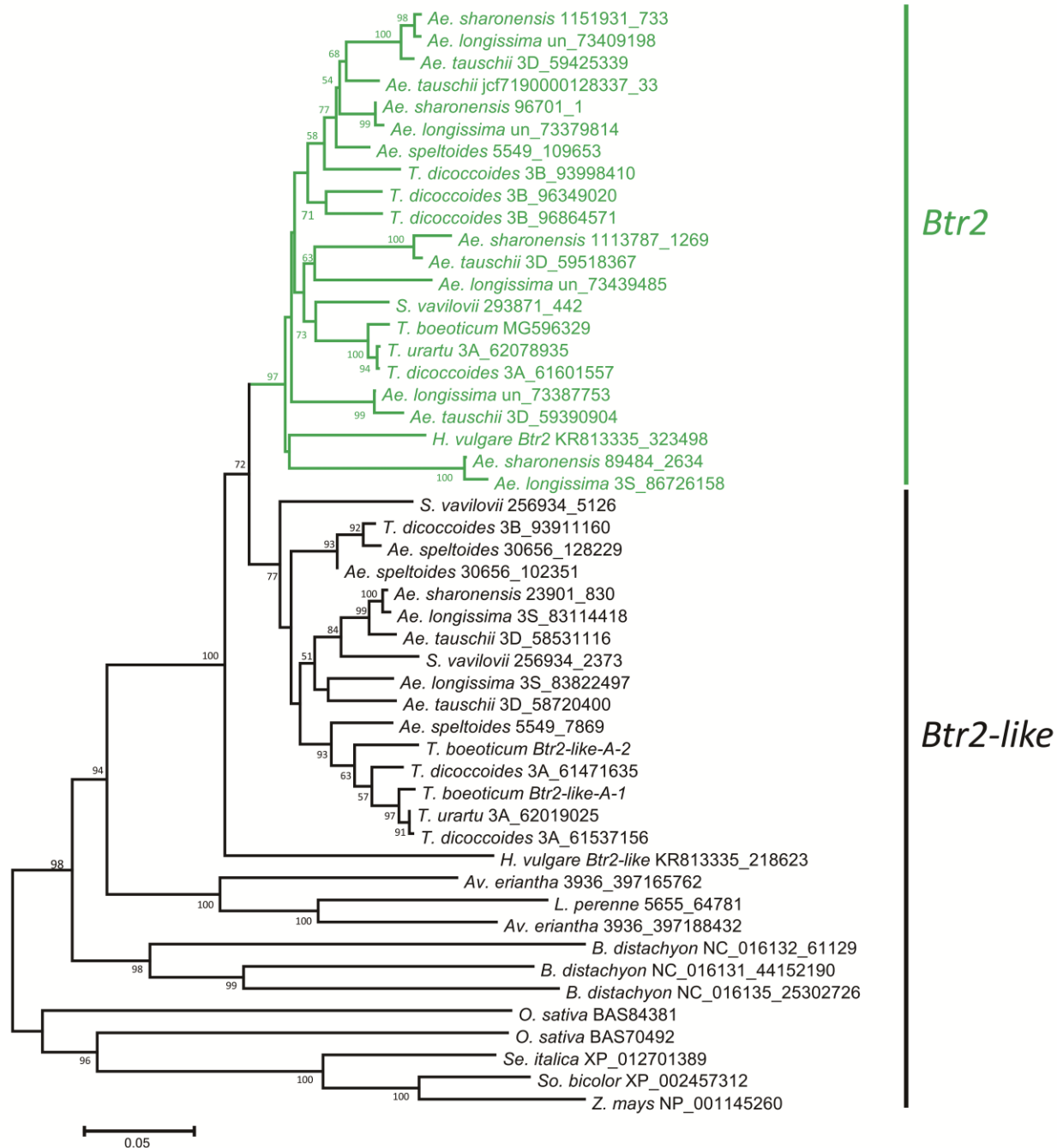


Fig. S7. Phylogenetic analysis of *Poaceae* *Btr2* and *Btr2-like* genes including those likely non-translated. Members of the *Btr2* clade are colored green. Numbers given at a branch node indicate bootstrap probabilities (only those >50% are shown). The number refer to the accession / scaffold / contig and the start location of each gene is given in Table S6.

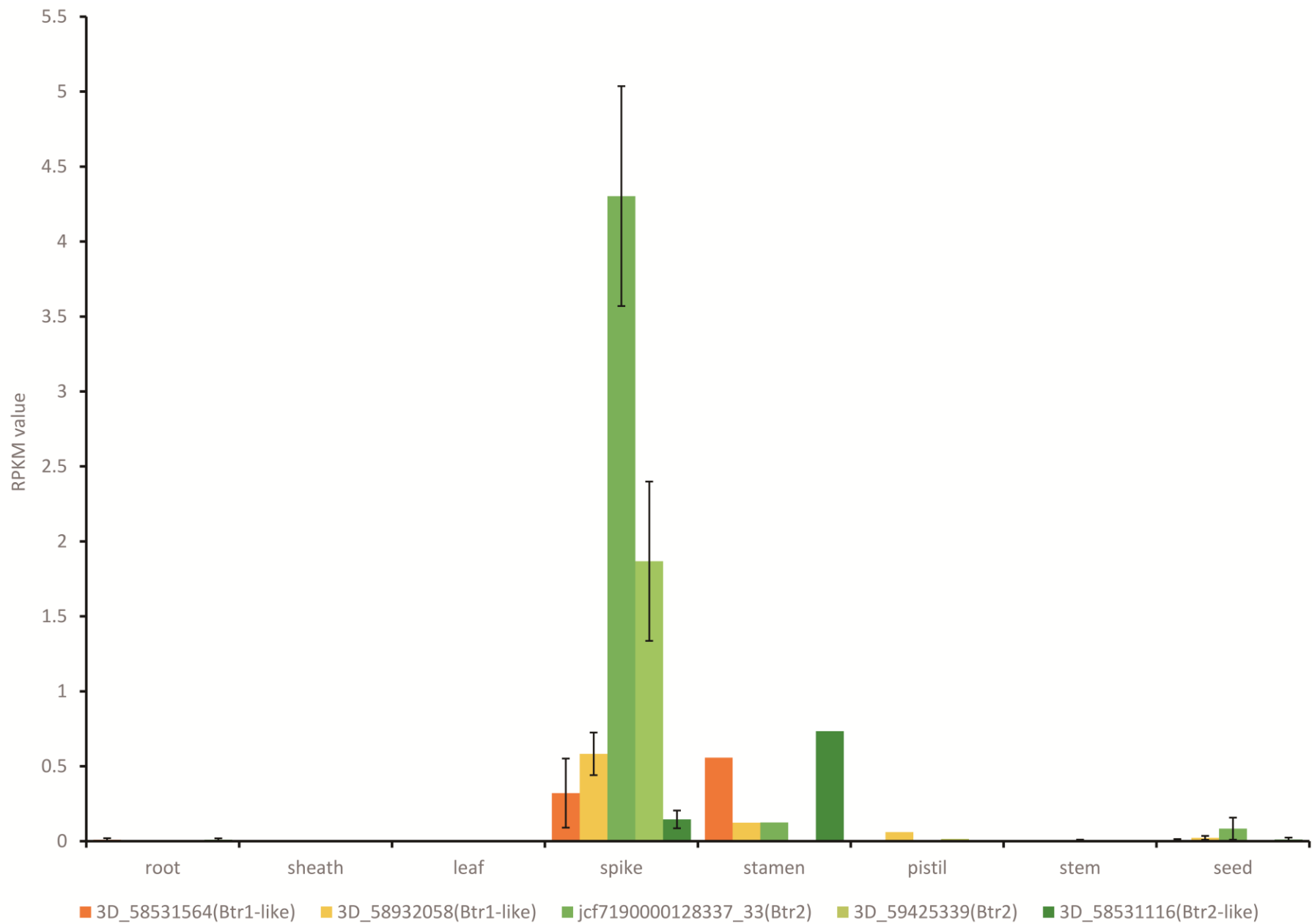


Fig. S8. RNA-seq derived transcript abundances (expressed as RPKM) of the *Ae. tauschii* *Btr* genes across various parts of the plant. The error bar indicates the SE ($n=2$ or 3).

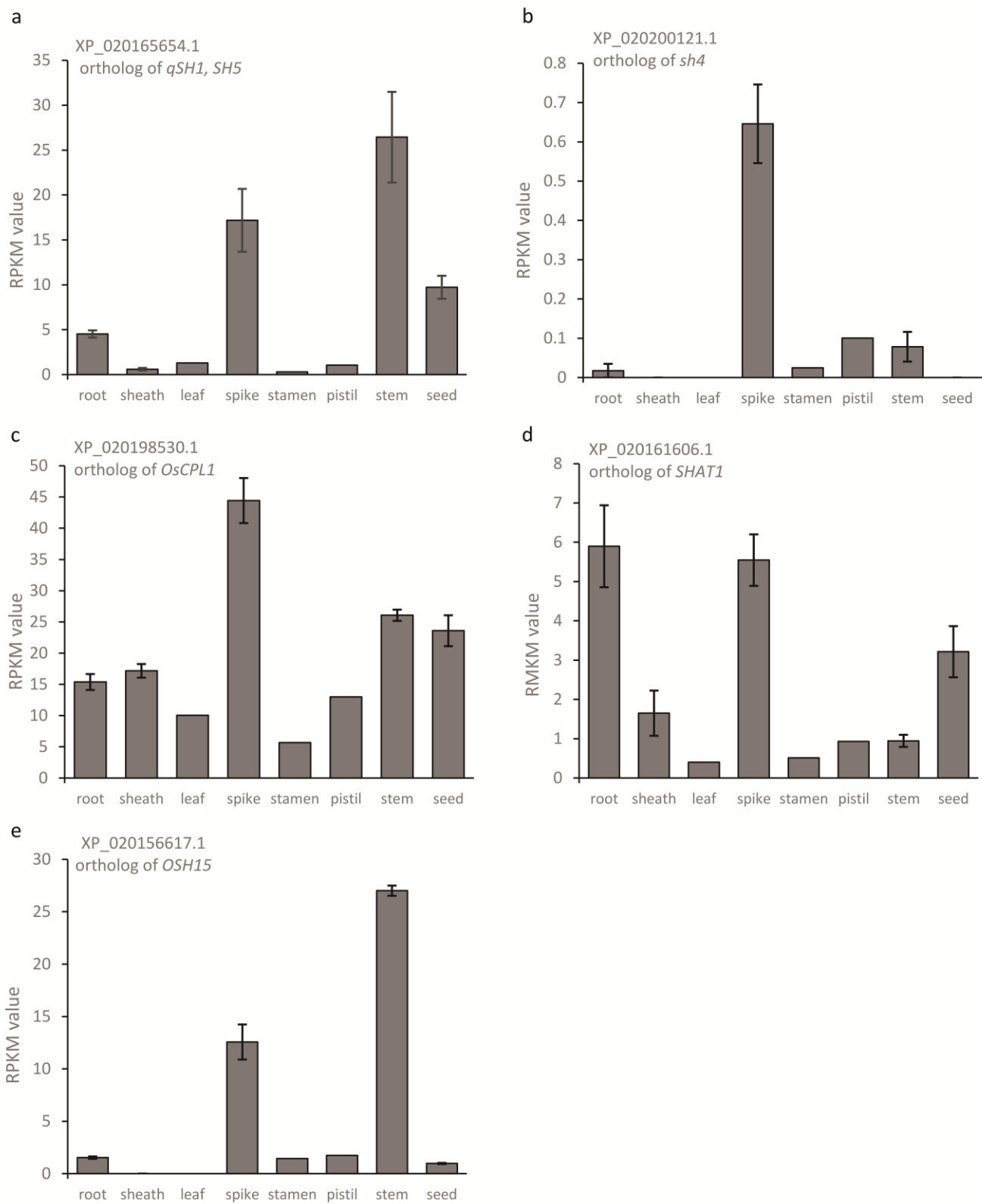


Fig. S9. RNA-seq derived transcript abundances (expressed as RPKM) of the *Ae. tauschii* orthologs of genes implicated in shattering in rice across various parts of the plant. (a) XP_020165654.1, the ortholog of *qSH1* and *SH5*, (b) XP_020200121.1, the ortholog of *sh4*, (c) XP_020198530.1, the ortholog of *OsCPL1*, (d) XP_020161606.1, the ortholog of *SHAT1*, (e) XP_020156617.1, the ortholog of *OSH15*. The error bar indicates the SE ($n=2$ or 3).