

Table 1 Suppl. Materials used in this study and comparisons of their sequences with *Wx* of hexaploid wheat.

Gene	Species	Accession /Cultivar	Nucleotides (bps)											Amino acid residues											GenBank accession number									
			Exons											Introns												Mature protein			Transit peptide					
			Total											Total												Total								
			1	2	3	4	5	6	7	8	9	10	11	Total	1	2	3	4	5	6	7	8	9	10		Total	No	Mr	PI	No	Mr	PI		
<i>Wx-A1</i>	<i>T. aestivum</i>	Chinese spring	2781	321	81	99	153	102	354	180	192	87	129	117	1815	82	84	108	123	99	91	95	90	97	93	962	604	534	58.95	5.57	70	7.62	12.08	AB019622
<i>Wx-B1</i>	<i>T. aestivum</i>	Chinese spring	2794	324	81	99	153	102	354	180	192	87	129	117	1818	99	88	113	133	69	92	86	84	97	115	976	605	535	58.80	5.44	71	7.57	12.25	AB019623
<i>Wx-D1</i>	<i>T. aestivum</i>	Chinese spring	2862	321	81	99	153	102	354	180	192	87	129	117	1815	90	85	104	152	141	85	82	84	98	116	1047	604	534	58.90	5.60	70	7.38	12.24	AB019624
<i>Wx-Ta1</i>	<i>Ta. crinitum</i>	PI 204577	2808	321	81	99	153	102	354	180	192	87	129	117	1815	83	87	112	145	101	88	82	84	96	115	993	604	534	58.69	5.16	70	7.32	12.18	KT878862
<i>Wx-Ta2</i>	<i>Ta. crinitum</i>	PI 220590	2808	321	81	99	153	102	354	180	192	87	129	117	1815	83	87	112	145	101	88	82	84	96	115	993	604	534	58.69	5.16	70	7.32	12.18	KT878863
<i>Wx-Ta3</i>	<i>Ta. asperum</i>	PI 561091	2777	324	81	99	153	102	354	180	192	87	129	117	1818	77	86	95	141	98	88	82	84	96	112	959	605	535	58.6	5.20	71	7.51	12.25	KT878864
<i>Wx-Ta4</i>	<i>Ta. asperum</i>	PI 561092	2777	324	81	99	153	102	354	180	192	87	129	117	1818	77	86	95	141	98	88	82	84	96	112	959	605	535	58.68	5.20	71	7.51	12.25	KT878865
<i>Wx-Ta5</i>	<i>Ta. crinitum</i>	PI 561094	2808	321	81	99	153	102	354	180	192	87	129	117	1815	83	87	112	145	101	88	82	84	96	115	993	604	534	58.66	5.16	70	7.32	12.18	KT878866
<i>Wx-Ta6</i>	<i>Ta. caput-medusae</i>	PI 577708	2777	324	81	99	153	102	354	180	192	87	129	117	1818	77	86	95	141	98	88	82	84	96	112	959	605	535	58.64	5.20	71	7.51	12.25	KT878867
<i>Wx-Ta7</i>	<i>Ta. caput-medusae</i>	PI 577710	2806	321	81	99	153	102	354	180	192	87	129	117	1815	83	87	112	145	102	88	82	84	96	112	991	604	534	58.65	5.16	70	7.35	12.25	KT878868
<i>Wx-Ta8</i>	<i>Ta. caput-medusae</i>	PI 598389	2777	324	81	99	153	102	354	180	192	87	129	117	1818	77	86	95	141	98	88	82	84	96	112	959	605	535	58.65	5.25	71	7.51	12.25	KT878869

Table 2 Suppl. A comparison of amino acid compositions among *Wx* alleles from *Taeniatherum* and *Wx-D1* from wheat (* -substitutions with probable deleterious effects showed a probability of 0.00).

Position/Change	<i>Wx-Ta1</i>	<i>Wx-Ta2</i>	<i>Wx-Ta3</i>	<i>Wx-Ta4</i>	<i>Wx-Ta5</i>	<i>Wx-Ta6</i>	<i>Wx-Ta7</i>	<i>Wx-Ta8</i>
18 Ile/Val	+	+			+		+	
45/46 -/Leu			+	+		+		+
52 Thr/Lys	+	+	+	+	+	+	+	+
55 Arg/Gln	+	+			+			
61 Thr/Ser	+	+	+	+	+	+	+	+
67 Met/Val	+	+			+		+	
71 Ala/Thr				+				
124 Lys/Asn	+	+	+	+	+	+	+	+
138 Val/Ala	+	+	+	+	+	+	+	+
140 Lys/Glu	+	+	+	+	+	+	+	+
190 Gln/Glu	+	+			+		+	
190 Gln/Leu			+	+		+		+
202 Val/Ala	+	+	+	+	+	+	+	+
249 Arg/Ser	+	+			+		+	
249 Arg/Thr			+	+		+		+
279 Arg/Lys	+	+	+	+	+	+	+	+
291 Asp/Asn								+
308 Gln/Glu	+	+	+	+	+	+	+	+
330 Gly/Ser*	+							
364 Val/Ala	+		+		+			+
378 Asn/Ser				+				
444 Ile/Thr*			+	+		+	+	+
467 Met/Val						+	+	
517 Met/Ile			+					
525 Asn/Thr	+	+	+	+	+	+	+	+
536 Val/Ala	+	+	+	+	+	+	+	+
552 His/Gln	+	+	+	+	+	+	+	
555 Val/Ala			+					

Table 3 Suppl. Sequence similarity coefficients among *Wx* sequences of *Taeniatherum* (a, b, c, and d indicate complete nucleotide, exon, intron, and amino acid sequences, respectively).

<i>Wx</i> genes		Group I <i>Wx-Ta1</i>	<i>Wx-Ta2</i>	<i>Wx-Ta5</i>	<i>Wx-Ta7</i>	Group II <i>Wx-Ta3</i>	<i>Wx-Ta4</i>	<i>Wx-Ta6</i>	<i>Wx-Ta8</i>
Group I	<i>Wx-Ta1</i>		99.7 % ^a	99.8 %	98.2 %	94.8 %	94.8 %	94.8 %	94.8 %
	<i>Wx-Ta2</i>	99.8 % ^b		99.7 %	98.3 %	94.8 %	94.8 %	94.9 %	94.8 %
	<i>Wx-Ta5</i>	99.8 %	99.8 %		98.2 %	94.8 %	94.8 %	94.8 %	94.8 %
	<i>Wx-Ta7</i>	98.8 %	99.1 %	98.9 %		96.3 %	96.4 %	96.6 %	96.4 %
Group II	<i>Wx-Ta3</i>	97.4 %	97.5 %	97.4 %	98.2 %		99.7 %	99.7 %	99.6 %
	<i>Wx-Ta4</i>	97.3 %	97.5 %	97.4 %	98.2 %	99.7 %		99.7 %	99.6 %
	<i>Wx-Ta6</i>	97.4 %	97.6 %	97.4 %	98.4 %	99.7 %	99.7 %		99.7 %
	<i>Wx-Ta8</i>	97.4 %	97.5 %	97.5 %	98.2 %	99.6 %	99.6 %	99.7 %	

Table 3 Suppl. Continued

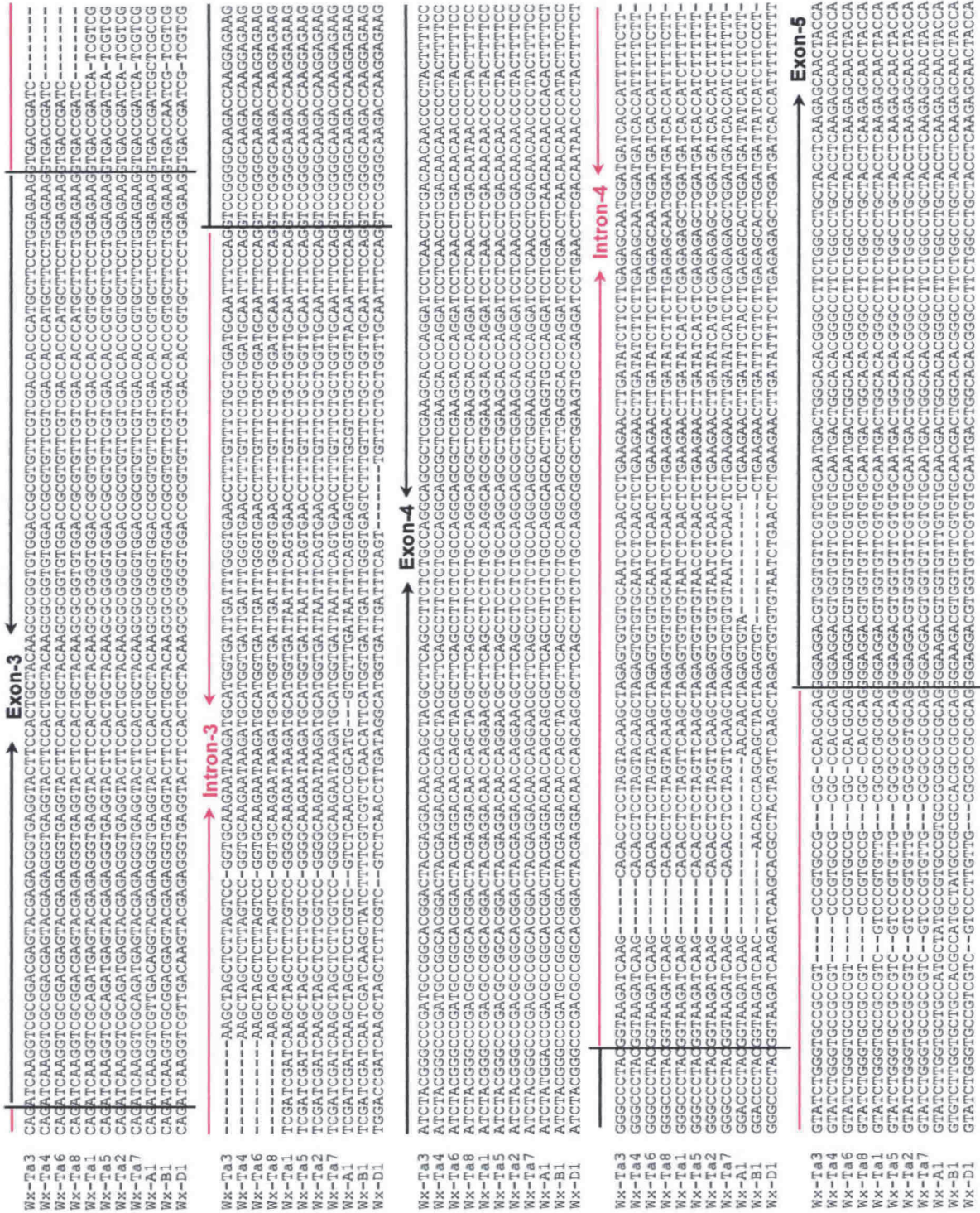
<i>Wx</i> genes		Group I <i>Wx-Ta1</i>	<i>Wx-Ta2</i>	<i>Wx-Ta5</i>	<i>Wx-Ta7</i>	Group II <i>Wx-Ta3</i>	<i>Wx-Ta4</i>	<i>Wx-Ta6</i>	<i>Wx-Ta8</i>
Group I	<i>Wx-Ta1</i>		99.6% ^c	99.9%	97.0%	89.4%	89.5%	89.5%	89.4%
	<i>Wx-Ta2</i>	99.7% ^d		99.5%	96.8%	89.2%	89.3%	89.3%	89.2%
	<i>Wx-Ta5</i>	99.8%	99.8%		96.9%	89.3%	89.4%	89.4%	89.3%
	<i>Wx-Ta7</i>	99.2%	99.5%	99.3%		92.4%	92.5%	92.7%	92.4%
Group II	<i>Wx-Ta3</i>	98.5%	98.5%	98.7%	98.7%		99.7%	99.7%	99.6%
	<i>Wx-Ta4</i>	98.3%	98.7%	98.5%	98.8%	99.2%		99.8%	99.7%
	<i>Wx-Ta6</i>	98.5%	98.8%	98.7%	99.3%	99.3%	99.5%		99.7%
	<i>Wx-Ta8</i>	98.7%	98.7%	98.8%	98.8%	99.5%	99.3%	99.5%	

Wx-Ta3	ATGGCGGCTCTGTGTACGTCCAGTTCGCACTCTCGGCACCGTCTCTGGGATCACCGACAGTTTCAGGGGTGAGGCCCCGAGGCCACGCGATCGGGGCTC
Wx-Ta4	ATGGCGGCTCTGTGTACGTCCAGTTCGCACTCTCGGCACCGTCTCTGGGATCACCGACAGTTTCAGGGGTGAGGCCCCGAGGCCACGCGATCGGGGCTC
Wx-Ta6	ATGGCGGCTCTGTGTACGTCCAGTTCGCACTCTCGGCACCGTCTCTGGGATCACCGACAGTTTCAGGGGTGAGGCCCCGAGGCCACGCGATCGGGGCTC
Wx-Ta8	ATGGCGGCTCTGTGTACGTCCAGTTCGCACTCTCGGCACCGTCTCTGGGATCACCGACAGTTTCAGGGGTGAGGCCCCGAGGCCACGCGATCGGGGCTC
Wx-Ta1	ATGGCGGCTCTGTGTACGTCCAGTTCGCACTCTCGGCACCGTCTCTGGGATCACCGACAGTTTCAGGGGTGAGGCCCCGAGGCCACGCGATCGGGGCTC
Wx-Ta5	ATGGCGGCTCTGTGTACGTCCAGTTCGCACTCTCGGCACCGTCTCTGGGATCACCGACAGTTTCAGGGGTGAGGCCCCGAGGCCACGCGATCGGGGCTC
Wx-Ta2	ATGGCGGCTCTGTGTACGTCCAGTTCGCACTCTCGGCACCGTCTCTGGGATCACCGACAGTTTCAGGGGTGAGGCCCCGAGGCCACGCGATCGGGGCTC
Wx-Ta7	ATGGCGGCTCTGTGTACGTCCAGTTCGCACTCTCGGCACCGTCTCTGGGATCACCGACAGTTTCAGGGGTGAGGCCCCGAGGCCACGCGATCGGGGCTC
Wx-A1	ATGGCGGCTCTGTGTACGTCCAGTTCGCACTCTCGGCACCGTCTCTGGGATCACCGACAGTTTCAGGGGTGAGGCCCCGAGGCCACGCGATCGGGGCTC
Wx-B1	ATGGCGGCTCTGTGTACGTCCAGTTCGCACTCTCGGCACCGTCTCTGGGATCACCGACAGTTTCAGGGGTGAGGCCCCGAGGCCACGCGATCGGGGCTC
Wx-D1	ATGGCGGCTCTGTGTACGTCCAGTTCGCACTCTCGGCACCGTCTCTGGGATCACCGACAGTTTCAGGGGTGAGGCCCCGAGGCCACGCGATCGGGGCTC

[illegible][illegible]

Wx-Ta3	TTGCAGC-----CAGCATTGCTGCCATTACAA-----CGGTGCTG-TGTCGTGCAGCCCAACGGTCAACGGGTCAATGTCATCCCGGCTATGACCCAGTACAAATGA
Wx-Ta4	TTGCAGC-----CAGCATGCTGCGCATTAACA-----CGGTGCTG-TGTCGTGCAGCCCAACGGTCAACGGGTCAATGTCATCCCGGCTATGACCCAGTACAAATGA
Wx-Ta6	TTGCAGC-----CAGCATGCTGCGCATTAACA-----CGGTGCTG-TGTCGTGCAGCCCAACGGTCAACGGGTCAATGTCATCCCGGCTATGACCCAGTACAAATGA
Wx-Ta8	TTGCAGC-----CAGCATGCTGCGCATTAACA-----CGGTGCTG-TGTCGTGCAGCCCAACGGTCAACGGGTCAATGTCATCCCGGCTATGACCCAGTACAAATGA
Wx-Ta5	TAATGTTCTTCT-----TGAGCAGCATGCC--CCATTACAA-----CTGATGGTG-TGTCGTGCAGCCCAACGGCCACGGGTCAATGTCATCCCGGCTACGACCCAGTACAAATGA
Wx-Ta1	TAATGTTCTTCT-----TGAGCAGCATGCC--CCATTACAA-----CTGATGGTG-TGTCGTGCAGCCCAACGGCCACGGGTCAATGTCATCCCGGCTACGACCCAGTACAAATGA
Wx-Ta2	TAATGTTCTTCT-----TGAGCAGCATGCC--CCATTACAA-----CTGATGGTG-TGTCGTGCAGCCCAACGGCCACGGGTCAATGTCATCCCGGCTACGACCCAGTACAAATGA
Wx-Ta7	TAATGTTCTTCT-----TGAGCAGCATGCC--CCATTACAA-----CTGATGGTG-TGTCGTGCAGCCCAACGGCCACGGGTCAATGTCATCCCGGCTACGACCCAGTACAAATGA
Wx-Al	TAATGTTCTTCT-----CTGAGCAGCATGCCGCTGCGGTTACAA-----CGGTGCGCC-TGTCGTGCAGCCCAACGGTCAACGGGTCAATGTCATCCCGGCTACGACCCAGTACAAATGA
Wx-B1	TAATGTTCTTCTTGAGC-CAGCATGCTGCGCATTAACAAGTTTAACTATGTCGTGTCAGCCCAACGGTCAACGGGTCAATGTCATCCCGGCTACGACCCAGTACAAATGA
Wx-D1	TAATGTTCTTCTTGAGCTGAGCATGCTGCGGTTACAA-----CGGTGCTG-TGTCGTGCAGCCCAACGGCCACGGGTCAATGTCATCCCGGCTACGACCCAGTACAAATGA

Wx-Ta3
 GCCTTGGGACACACAGCGTCGTCGCGAGTACTC-----TATCCGGACATGAGTGATCACAGCTCGCATGCTCTGCACATTTCTGGAAGATTCTACTCACTCACTCGAT
 Wx-Ta4
 GCCTTGGGACACACAGCGTCGTCGCGAGTACTC-----TATCCGGACATGAGTGATCACAGCTCGCATGCTCTGCACATTTCTGGAAGATTCTACTCACTCACTCGAT
 Wx-Ta6
 GCCTTGGGACACACAGCGTCGTCGCGAGTACTC-----TATCCGGACATGAGTGATCACAGCTCGCATGCTCTGCACATTTCTGGAAGATTCTACTCACTCACTCGAT
 Wx-Ta8
 GCCTTGGGACACACAGCGTCGTCGCGAGTACTC-----TATCCGGACATGAGTGATCACAGCTCGCATGCTCTGCACATTTCTGGAAGATTCTACTCACTCACTCGAT
 Wx-Ta1
 GCCTTGGGACACACAGCGTCGTCGCGAGTATACATA---TATCCGGACATGAATCATCAAAATTCACATGCTCTGCAGGTTCTTACTGACTCACTCGAT
 Wx-Ta5
 GCCTTGGGACACACAGCGTCGTCGCGAGTATACATA---TATCCGGACATGAATCATCAAAATTCACATGCTCTGCAGGTTCTTACTGACTCACTCGAT
 Wx-Ta2
 GCCTTGGGACACACAGCGTCGTCGCGAGTATACATA---TATCCGGACATGAATCATCAAAATTCACATGCTCTGCAGGTTCTTACTGACTCACTCGAT
 Wx-Ta7
 GCCTTGGGACACACAGCGTCGTCGCGAGTATACATA---TATCCGGACATGAATCATCAAAATTCACATGCTCTGCAGGTTCTTACTGACTCACTCGAT
 Wx-A1
 GCCTTGGGACACACAGCGTCGTCGCGAGTATAT-----TATCCGGACATGAATCATCAAAATTCACATGCTCTGCAGGTTCTTACTGACTGCTCGAT
 Wx-B1
 GCCTTGGGACACACAGCGTCGTCGCGAGTATACATA---TATCCGGACATGAATCATCAAAATTCACATGCTCTGCAGGTTCTTACTGACTCACTCGAT
 Wx-D1
 GCCTTGGGACACACAGCGTCGTCGCGAGTATGAACCTTAAAGCATCAAAATTCGATGCTCTGCAGGTTCTTACTGACTGACTCACTCACTCGAT



[illegible]

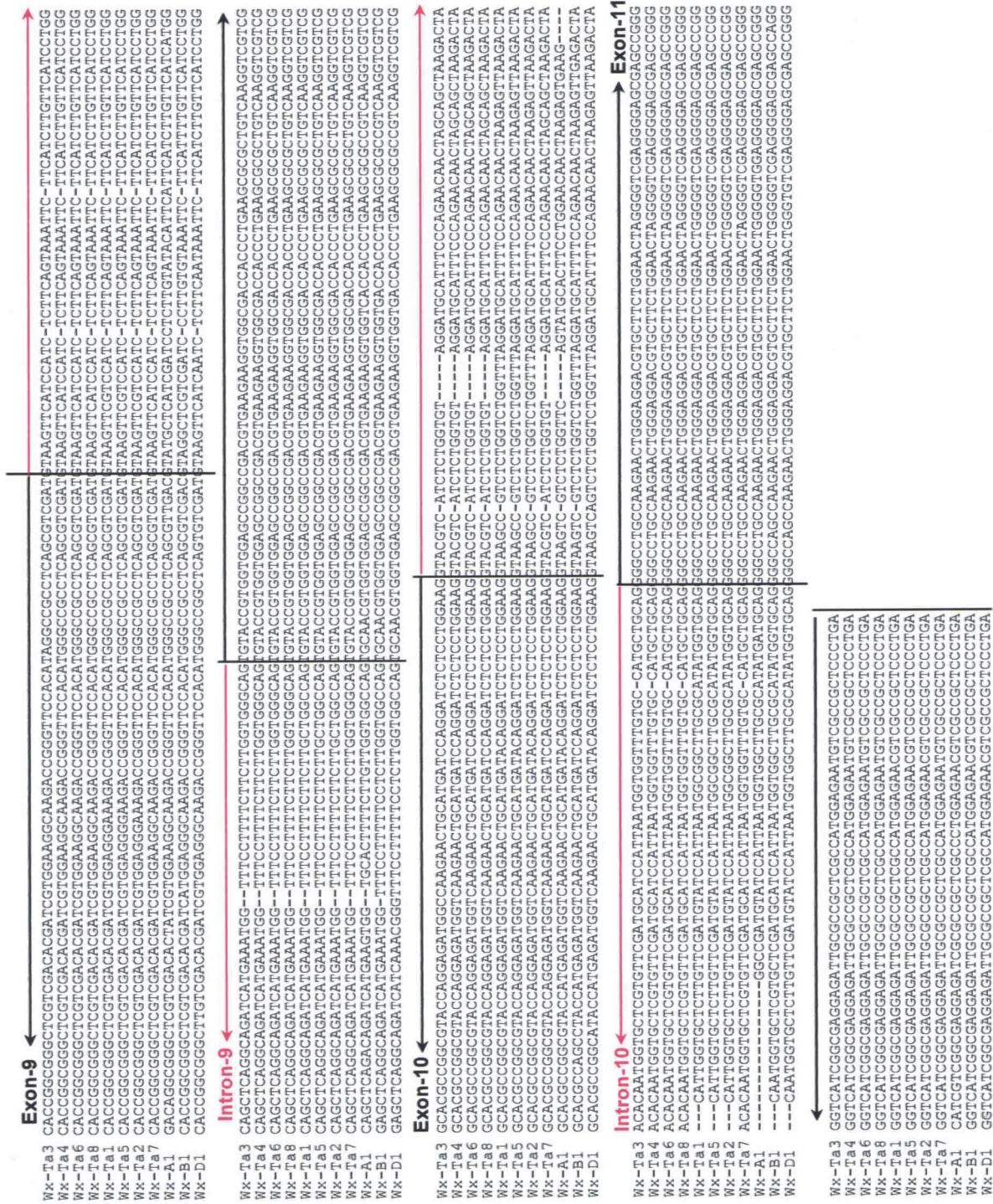


Fig. 1 Suppl. Multiple sequence alignments of *Wx* alleles from *Taeniattherum* species and *Wx* alleles from the hexaploid wheat cultivar 'Chinese Spring'.