

## **Gene Deletion in Barley Mediated by LTR-retrotransposon *BARE***

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**Supplementary Table 1.** List of primers used for genetic mapping and identification of the deletion.

**Supplementary Table 2.** The Alignment Hit Table of each target sequence found by 15345-16193 as query hitting maize genome.

**Supplementary Table 3.** The Alignment Hit Table of each target sequence found by 16423-18000 as query hitting maize genome.

**Supplementary Table 4.** The Alignment Hit Table of each target sequence found by 18046-18087 as query hitting maize genome.

**Supplementary Table 5.** The Alignment Hit Table of each target sequence found by 27390-27543 as query hitting maize genome.

**Supplementary Table 6.** The Alignment Hit Table of each target sequence found by 25868-26648 as query hitting maize genome.

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**Supplementary Figure 1.** Linkage map of the *prbs* gene on chromosome 3H.

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**Supplementary Figure 3.** Hits diagram of 15345-16193 on maize chromosomes.

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**Supplementary Figure 6.** Hits diagram of 27390-27543 on maize chromosomes.

**Supplementary Figure 7.** Hits diagram of 25868-26648 on maize chromosomes.

**Supplementary Table 1.** List of primers used for genetic mapping and identification of the deletion.

Primer Name	Forward sequence (5'-3')	Reverse sequence (5'-3')	Tm (°C)	size (bp)
Cbic43	ATCCAAAGCTCCCAAATATC	TTTCTTCCGAATGCTAACTA	55	115
Cbic44	GATACAGCTATTTCCCCCAT	GGTTAGTCATTTTCCCGAGA	55	174
Cbic45	AGGTATTTGTCCCGCTTCATAG	CAGAGTAATCATGCACACTTGC	55	799
Cbic46	CATTCGGTATGTCGTTTTGTCC	GGAGTGGAGGGGAGATATAGAG	55	639
Cbic47	GATTAATCGATCCGTTTTCGCAG	GAATAGTGCCGAGAATACTGCT	55	412
Cbic48	CGACACAGTACAAACGAATGTC	CACATCAGCTCACCAAGTAAGA	55	589
Cbic49	GGCATAACATGCATGGGTTTAG	GGATGAAGATTGGGGAAAGTGA	55	656
Cbic50	CCTAGAAAACAACAAGGGGGAT	ATCAATACTACTAGCAACCGCC	55	274
Cbic76	GAATGGTAGGGGCGATGGAG	CTCCATGCATCGTCCAGGTT	60	766
Cbic77	GTCAGCTAACGGTCAAAGGC	TCCAGCAGTTATGCCCAAGG	60	949
Cbic82	ACACATGCCCAATCAAGAGC	CGAACAATTCCACGCGATGA	60	898
Cbic83	CCGGTGCTAAGGTGTTGTTC	ATCTTGGGGCAGGCTTCTAG	60	775
Cbic85	TGAGGGAGGACCAATCTTCA	ACGGGTGATTTGGTGATGTT	58	1185
Cbic86	AGAATCGTCACTAAACGCC	TGCTACTCAGATTCGTTGCC	58	581
Cbic87	AGATGGAGGCGATGAAGGTA	AGGTTATAACGGACGTTGCC	58	308
Cbic93	TCATTCGTCATGCACACACA	GGCTGTATAGTTCTCGCTG	58	1663
Cbic94	AACCAATGCAACTAGGGAGC	CTGGGCTGTATAGTTCTCGC	58	1099
Cbic95	ATCGGTTGCGAGTTTCCC	CCGGTTTACCAATCGGGAC	58	906
Cbic110	AGGAGGGTGTGTGGATGAAG	GCATTCCTTCGGTGCTAGTG	60	740
Cbic111	TCCACGTGCAACTCAGATCT	CCATCCAATCACAACTGGC	60	654
Cbic112	TACAGAAAACCCAGCCCAT	CTCACTTTTCCCCACTCCCT	60	702
Cbic113	TTGTTCTCGTGGACATGGGA	CCAACGACGAGCAAAAGGAA	60	766
Cbic116	AGTCCCTAGCTACTTCCCCA	AGAGAGATATCCCACGTGCG	60	608
Cbic117	CGGGAATGACGAATGGGTTT	TGAGCAACGGACTTACTCGT	60	968
Cbic118	CTGCCGCCAAGCTATAAAGG	ACGCTCCATTGTTCTGAGA	60	966
Cbic119	TCGACAGTCACACCCTGTTG	CCATGTCTTCTATGTGTCCGA	60	707
Cbic120	AGTAAGACTCAGTGCCAGC	TAGTCGCGGATGAGGTTGAA	60	596
Cbic121	ATGCACCCAATGTGAGAGGA	TTTTCCGCTTTGGGTTCCAG	60	850
Cbic122	TAAAGATGACTGGCGGGTGT	ACCTTAGGATGCTACCGTGC	60	602
Cbic123	CCGGGGCAATAATAGGGTCT	TGCACACAAGGCATTTCTCC	60	890
Cbic131	CAAGTCTCTAATGTCCTCCATA GTCACC	CGACACCTCTCTCAAATTA TGTCGTC	68	42919
Cbic132	CGTCTTCAGAGGGAAAGATCTA ACATGGTG	AATCCCATGTCTTCTATGTGT CCGATG	68	42820

**Supplementary Table 2.** The Alignment Hit Table of each target sequence found by 15345-16193 as query hitting maize genome.

<b>Target ID</b>	<b>definition</b>	<b>e-value</b>	<b>percent identity</b>	<b>#</b>
chr5	chr5	1.484e-75	73.01	99
chr9	chr9	6.905e-74	72.87	69
chr7	chr7	6.905e-74	72.87	74
chr6	chr6	6.905e-74	72.90	79
chr3	chr3	6.905e-74	72.90	76
chr1	chr1	6.905e-74	72.87	137
chr8	chr8	3.213e-72	72.78	92
chr4	chr4	3.213e-72	72.78	96
chr2	chr2	3.213e-72	72.75	133
chr10	chr10	3.213e-72	72.72	69
scaffold_495	scaffold_495 dna:scaffold scaffold:AGPv3:scaffold_495:1:380467:1	1.505e-65	72.38	1
scaffold_509	scaffold_509 dna:scaffold scaffold:AGPv3:scaffold_509:1:487110:1	3.282e-57	71.92	1

**Supplementary Table 3.** The Alignment Hit Table of each target sequence found by 16423-18000 as query hitting maize genome.

<b>Target ID</b>	<b>definition</b>	<b>e-value</b>	<b>percent identity</b>	<b>#</b>
chr3	chr3	2.035e-121	72.61	90
chr8	chr8	9.467e-120	72.52	106
chr4	chr4	9.467e-120	72.52	93
chr7	chr7	4.405e-118	72.45	89
chr6	chr6	4.405e-118	72.47	93
chr5	chr5	4.405e-118	72.47	110
chr2	chr2	4.405e-118	72.49	134
chr10	chr10	4.405e-118	72.45	77
chr9	chr9	2.049e-116	72.38	79
chr1	chr1	2.049e-116	72.38	146
scaffold_495	scaffold_495 dna:scaffold scaffold:AGPv3:scaffold_495:1:380467:1	9.602e-110	72.26	1
scaffold_509	scaffold_509 dna:scaffold scaffold:AGPv3:scaffold_509:1:487110:1	4.467e-108	75.59	1

**Supplementary Table 4.** The Alignment Hit Table of each target sequence found by 18046-18087 as query hitting maize genome.

<b>Target ID</b>	<b>definition</b>	<b>e-value</b>	<b>percent identity</b>	<b>#</b>
chr2	chr2	3.378e-12	97.62	122
chr1	chr1	3.378e-12	97.62	128
scaffold_509	scaffold_509 dna:scaffold scaffold:AGPv3:scaffold_509:1:487110:1	1.571e-10	95.24	1
scaffold_495	scaffold_495 dna:scaffold scaffold:AGPv3:scaffold_495:1:380467:1	1.571e-10	95.24	1
chr9	chr9	1.571e-10	95.24	65
chr8	chr8	1.571e-10	95.24	84
chr7	chr7	1.571e-10	95.24	74
chr6	chr6	1.571e-10	95.24	77
chr5	chr5	1.571e-10	95.24	88
chr4	chr4	1.571e-10	95.24	84
chr3	chr3	1.571e-10	95.24	79
chr10	chr10	1.571e-10	95.24	76

**Supplementary Table 5.** The Alignment Hit Table of each target sequence found by 27390-27543 as query hitting maize genome.

<b>Target ID</b>	<b>definition</b>	<b>e-value</b>	<b>percent identity</b>	<b>#</b>
chr3	chr3	3.106e-45	88.20	1

**Supplementary Table 6.** The Alignment Hit Table of each target sequence found by 25868-26648as query hitting maize genome.

<b>Target ID</b>	<b>definition</b>	<b>e-value</b>	<b>percent identity</b>	<b>#</b>
chr3	chr3	5.543e-169	81.10	3
chr8	chr8	6.569e-49	80.86	5
chr9	chr9	8.618e-38	78.14	4
chr5	chr5	8.618e-38	78.29	3
chr1	chr1	1.115e-36	78.12	9
chr6	chr6	1.452e-30	75.69	5
chr4	chr4	4.096e-21	74.65	3
chr10	chr10	1.919e-14	79.69	2
chr2	chr2	5.412e-5	85.19	1

**Supplementary Table 7.** Genetic variations induced by introduction of exogenous genomic DNA.

DNA donor	Recipient	Method	Trait	Reference
Sorghum	Wheat	Pollen tube	Glutenin, tolerance	Zhou et al. 1992 <sup>1</sup> , Pei et al. 1999 <sup>2</sup> , Wang et al. 2000 <sup>3</sup> , Ni et al. 2005a <sup>4</sup> , Ni et al. 2005b <sup>5</sup> .
Sorghum	Wheat	Pollen tube	Stripe-rust resistance, quality indicators	Wang et al. 1995 <sup>6</sup> , Ou et al. 2013 <sup>7</sup>
Barley	Wheat	Pollen tube	Stable immunity and high-resistance to powdery mildew	Yan et al. 1994a <sup>8</sup> , Yan et al. 1994b <sup>9</sup> .
Wheat (white seed)	Wheat (red seed)	Pollen tube	Seed colour	Liu et al. 1994 <sup>10</sup> .
Wheat (Fuzhuang 30 and Xiaobaidongmai)	Wheat (beinong 6)	Pollen tube	High-resistance to powdery mildew	Wang et al. 2003 <sup>11</sup> .
<i>Elytrigia elongata</i>	Wheat	Pollen tube	Rust resistance	Wang et al. 1995 <sup>6</sup> , Qin et al. 1997 <sup>12</sup> .
<i>Elytrigia elongata</i>	Wheat	Pollen tube	Stripe rust resistance	Ou et al. 2005 <sup>13</sup> .
Reed	Wheat	Pollen tube	The awn property, grain color, plant height, ear length, grain number of each ear and sharp or dull of grain husk point,	Liu et al. 1998 <sup>14</sup> .

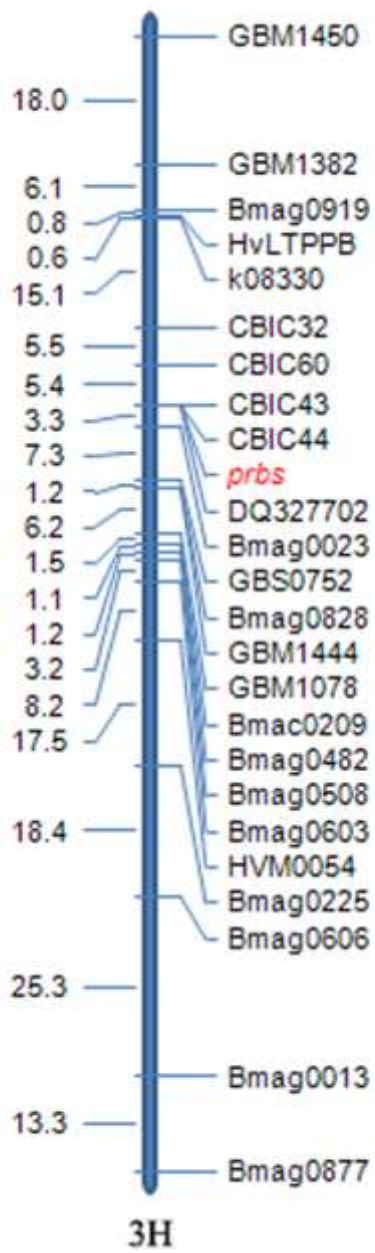
			especially salt resistance	
Maize	Wheat	embryo soaking	Plant height, protein content , lysine content, earlier matured,	Bai et al. 1999 <sup>15</sup> .
Maize	Wheat	Pollen tube	Length and square of the flag leaf, ear shape and disease resistance	Hu et al. 2007 <sup>16</sup> .
<i>Leymus racemosus</i>	Wheat	Pollen tube	Exogenous DNA fragment	Miao et al. 2000 <sup>17</sup> , Zhang et al. 2000 <sup>18</sup> .
<i>Agropyron elongatum</i>	Wheat	Pollen tube	Plant height, plant type, spike type, disease resistance and stress tolerance, lower saline damage index, higher saline tolerance, high ratio of SOD activity of flag leaves to the top second leaves, high saline and drought tolerance	Huang et al. 2000 <sup>19</sup> .
Soybean	Wheat	Pollen tube	Protein content and amino acid content, gene of wild soybean	Wang et al. 2003 <sup>20</sup> .
Oat ( <i>Avena sativa</i> L.)	Wheat	Pollen tube	Flag leaf area, spike length, grain number of main spike, grain weight of main spike and weight of thousand grains	Liu et al. 2006 <sup>21</sup> .
<i>T. Aegilopoides</i> Bal, <i>T. Dicoccoides</i> korn, <i>Timopheevi</i> zhuk, and <i>T. Polonicum</i> L.	Wheat	injection to ovule or transduction through pollen tube path	Protein content, auricles color etc.	Kong et al. 1992 <sup>22</sup> .
<i>Spartina angelica</i>	Rice	injection to ovule	Plant shape with broad, short, stiff and erect leaves, contents of the	Duan et al. 1985 <sup>23</sup> .



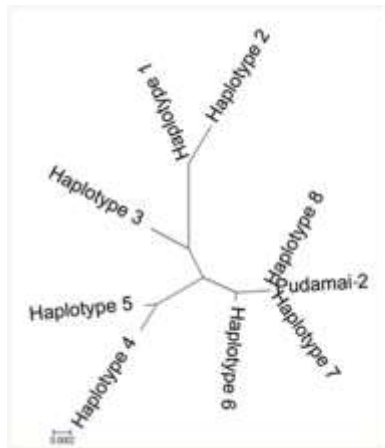
			protein and 16 amino acids	
Maize	Rice	imbibing rice seed with corn DNA solution.	Amylase content, the percentage of albumin, globulin and glutelin in the seeds	Chen et al. 1997 <sup>24</sup> .
Sorghum	Rice	Pollen tube	Net photosynthesis rates, exogenous DNA fragment	Hong et al. 1999 <sup>25</sup> , Lou et al. 2004 <sup>26</sup> , Lou et al. 2005 <sup>27</sup> .
Sorghum	Rice	spike-stalk injection	Exogenous DNA fragment	Zhao et al. 2001 <sup>28</sup> , Zhao et al. 2004 <sup>29</sup>
Wild rice	Rice	Pollen tube and stem injecting	Exogenous DNA fragment	Li et al. 2006 <sup>30</sup> .
Wild rice	Rice	spike-stalk injection	Plant type, grain quality and grain yield, exogenous DNA, specific SNPs and InDels.	Zhao et al. 2001 <sup>28</sup> , Wang et al. 2006 <sup>31</sup> . Sun et al. 2013 <sup>32</sup> .
Yunnan <i>O. Officinalis</i> and oats	Rice	pollen tube or by injecting exogenous DNA into the stem of rice in boot stage	Growth period, shape of plant, content of protein and amino acid, resistance to rice blast and isoenzymes of esterase and peroxidase, rice blast resistance	Song et al. 1993 <sup>33</sup> .
Kidney bean	Maize	pollen grain introduction	Progenies have characteristic type of donor, and most of traits can stable in D4 generation	Qi et al. 1995 <sup>34</sup> .
Soybean	Maize	Pollen tube	High-protein, plant pattern and anther color	Qi. 2000 <sup>35</sup> Ding et al. 2001 <sup>36</sup> .
<i>Tripsacum</i> and	Maize	Pollen tube	High combining ability	Yang et al.

<i>Teosinte</i>			of yield	2005 <sup>37</sup> .
Sugarcane	Maize	seed-immersion	The height of plant, the height of fruit, the number of leaf, the color and morphology of leaf, the length and width of leaf, the area of leaf, the weight of 1000 grain and the period of growth, photosynthetic pigment contents and quality	Zhang et al.2006 <sup>38</sup> , Zhang et al. 2008 <sup>39</sup> .
Waxy corn	Sweet maize	Pollen tube	Height of plant, the height of fruit, the area of leaf, sugar, protein and starch content	Zhang et al. 2006 <sup>40</sup> .
Island Cotton ( <i>Gossypium barbadense</i> L.)	Upland Cotton ( <i>Gossypium hirsutum</i> L.)	Injection donor DNA into ovaries	Morphological characters, growing period, vegetative organs, reproductive organs and other characters of economic importance	Huang et al. 1981 <sup>41</sup> .
Island cotton	Upland cotton	Pollen tube	Highly resistance to <i>Fusarium</i> wilt	Zhou et al. 1983 <sup>42</sup> .
Island cotton	Upland cotton	Pollen tube	High quality of fiber, morphology, exogenous DNA fragments	Wang et al. 2005 <sup>43</sup> , Wang et al. 2006 <sup>44</sup> .
Fusarium wilt-resistant cotton cultivar	Susceptible cotton cultivars	Injection donor DNA into ovaries	Disease resistance and yields	Huang et al. 1986 <sup>45</sup> .
Wild soybean	Cultivated soybean	Pollen tube	Protein content, globin content, fat content, yield	Lei et al. 1995 <sup>46</sup> , Lei et al. 2000 <sup>47</sup> .
Soybean	Soybean	Pollen tube	Exogenous DNA fragments (RAPD)	Lei et al. 1996 <sup>48</sup> .
Soybean landrace, wild soybean and	Cultivated soybean	Pollen tube	Yield, SMV resistance	Liu et al. 1997 <sup>49</sup> .

<i>Gleditsia japonica</i>				
Cotton	Ramie	soaking embryo	Exogenous DNA fragments (RAPD)	Zhang et al. 2000 <sup>50</sup> .
Squash	Watermelon	Injection donor DNA into ovaries	Wilt resistance	Chen et al. 1998 <sup>51</sup> .
Pumpkin	Watermelon	embryo injection	Resistance to <i>Fusarium oxysporum</i> sp. niveum, new special rind color and strip	Wang et al. 2002 <sup>52</sup> .
Pineapple	Cucumber	Pollen tube	Yield, the content of sugar	Chen et al. 1998 <sup>3</sup> . Chen et al. 2002 <sup>54</sup>
<i>Rhizophora apiculata</i>	<i>Capsicum annuum</i>	Pollen tube	Salt tolerance	Lin et al. 1999 <sup>55</sup> .
<i>Rhizophora apiculata</i>	<i>Solanum melongena</i>	Pollen tube	Salt tolerance, growth, rate of transpiration and photosynthesis, the activity of pepcase and the morphology of the blade stomas.	Lin et al. 2001 <sup>56</sup> .
<i>Rhizophora apiculata</i>	Alfalfa ( <i>Medicago sativa</i> )	Pollen tube	Salt tolerance, exogenous DNA fragments (RAPD)	Zhang et al. 2011 <sup>57</sup> .
<i>Suaeda salsa</i>	Tomato	Pollen tube	Salt tolerance	Xiao et al. 2008 <sup>58</sup> .



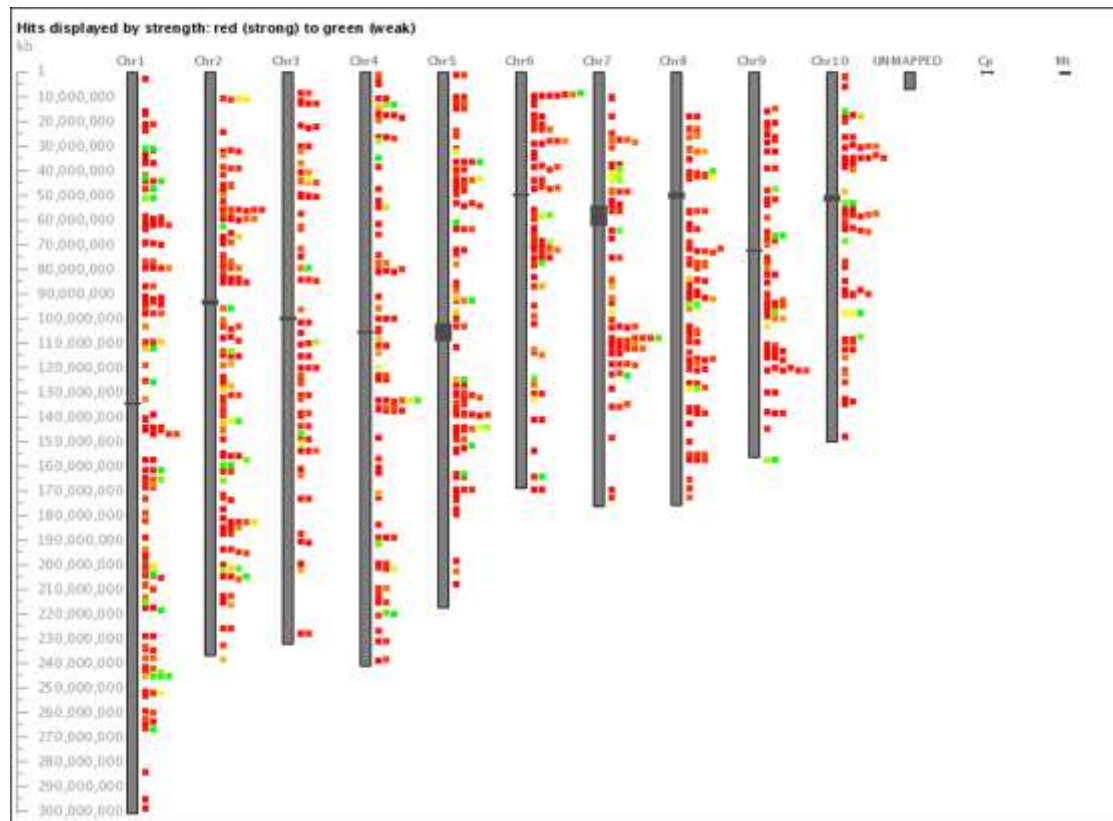
**Supplementary Figure 1.** Linkage map of the *prbs* gene on chromosome 3H.



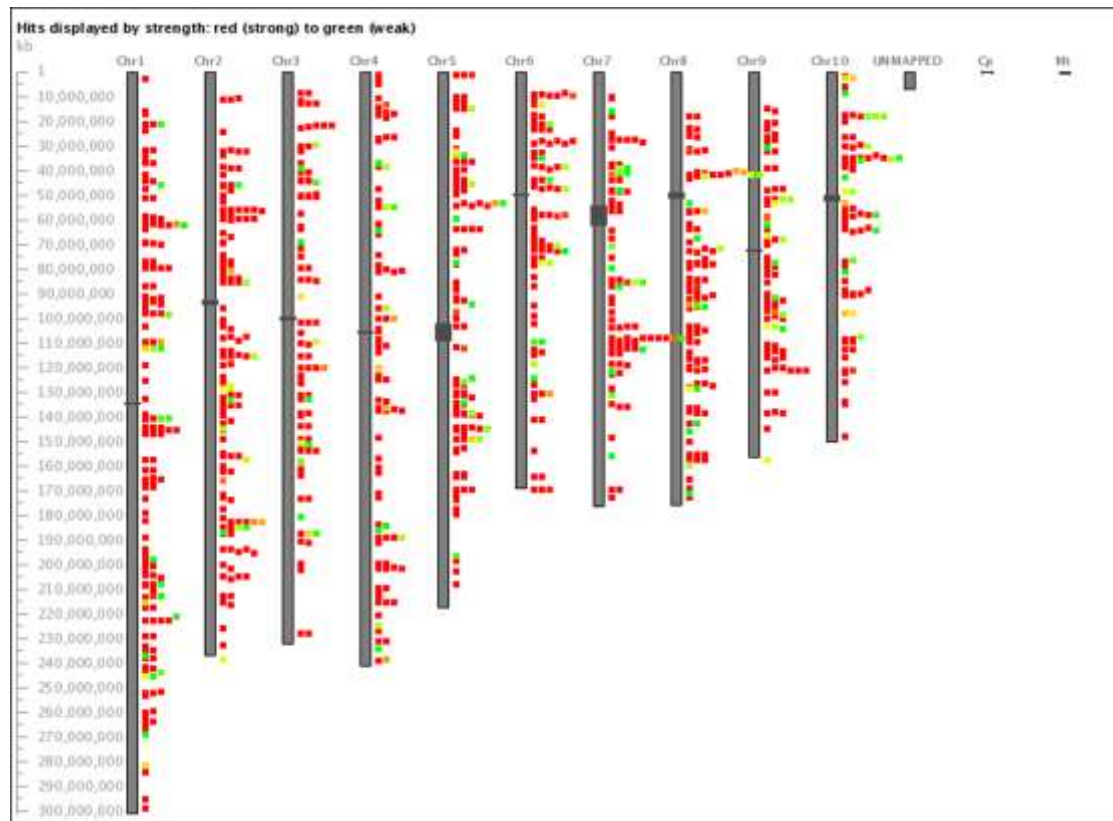
sequence name	SNP site																				
	1	2	8	8	8	8	8	8	8	8	8	9	9	9	0	1	4	5			
Haplotype 1	T	C	C	T	T	C	C	C	A	G	A	A	C	A	-	-	G	C	G	A	
Haplotype 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	-	
Haplotype 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	T	G	
Haplotype 4	-	T	T	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	
Haplotype 5	-	T	T	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	G	
Haplotype 6	-	T	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	-	G	
Haplotype 7	-	T	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	T	G	
Haplotype 8	-	T	T	-	-	-	-	-	-	-	-	-	-	-	-	-	T	A	A	T	G
Pudamai-2	-	T	T	-	-	-	-	-	-	-	-	-	-	-	-	-	T	A	A	T	G

**Supplementary Figure 2.** *Vrs4* Haplotype analysis.

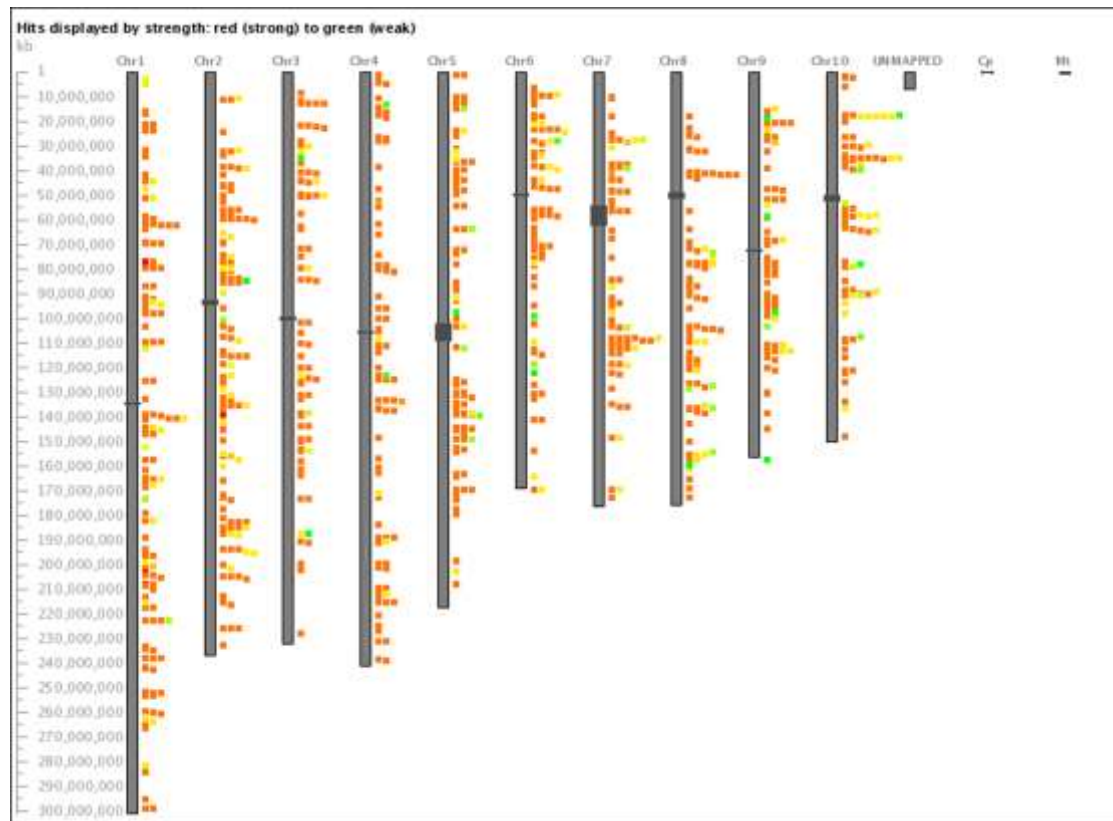
The primer pairs specific to *Vrs4* with overlapping fragments covering 2046 bp (Koppolu R et al. 2013) were amplified for direct PCR sequencing from wild barley cultivars Pudamai-2. Haplotypes of *Vrs4* were from GenBank (accession nos: KC854546 to KC854553) (Koppolu R et al. 2013). A phylogenetic tree was constructed using the MEGA6 program (Tamura K et al. 2013) with the minimum evolution method. The result showed that haplotype of *Vrs4* from Pudamai-2 was same as haplotype 8, which was characteristic of a inset of ‘TA’ bases in 5’ UTR of *Vrs4*.



Supplementary Figure 3. Hits diagram of 15345-16193 on maize chromosomes.

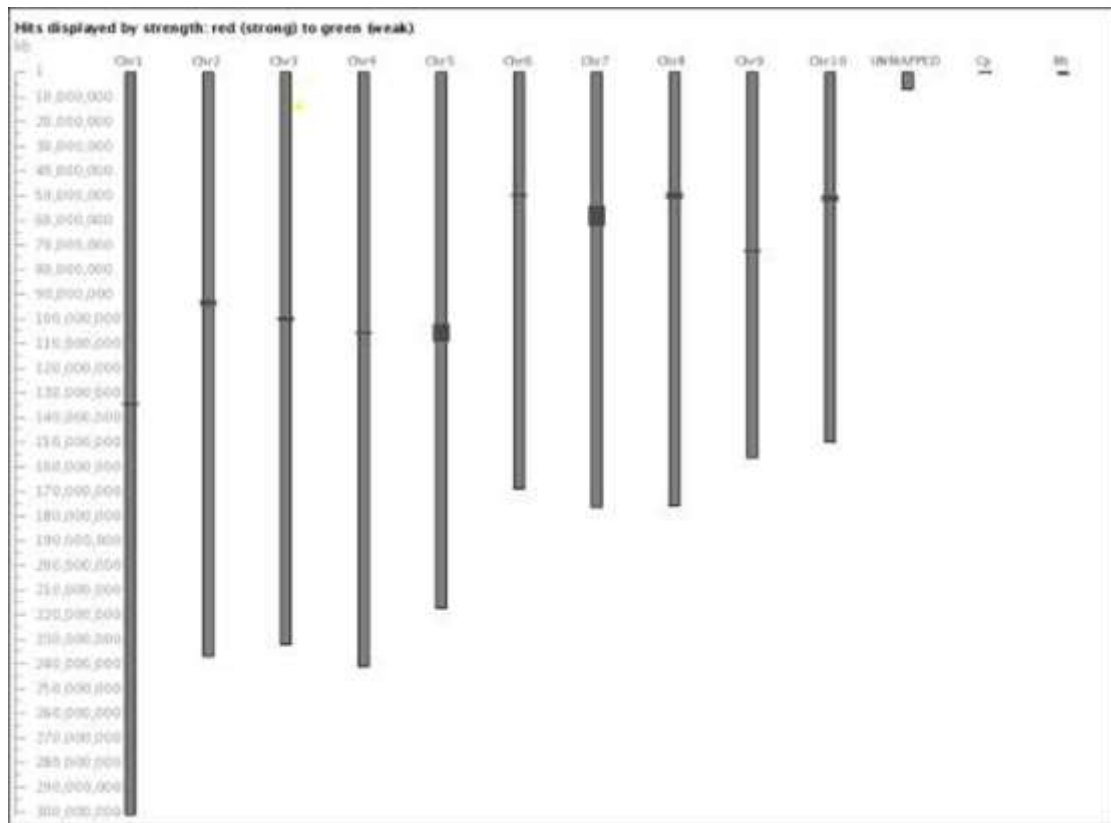


**Supplementary Figure 4.** Hits diagram of 16423-18000 on maize chromosomes.

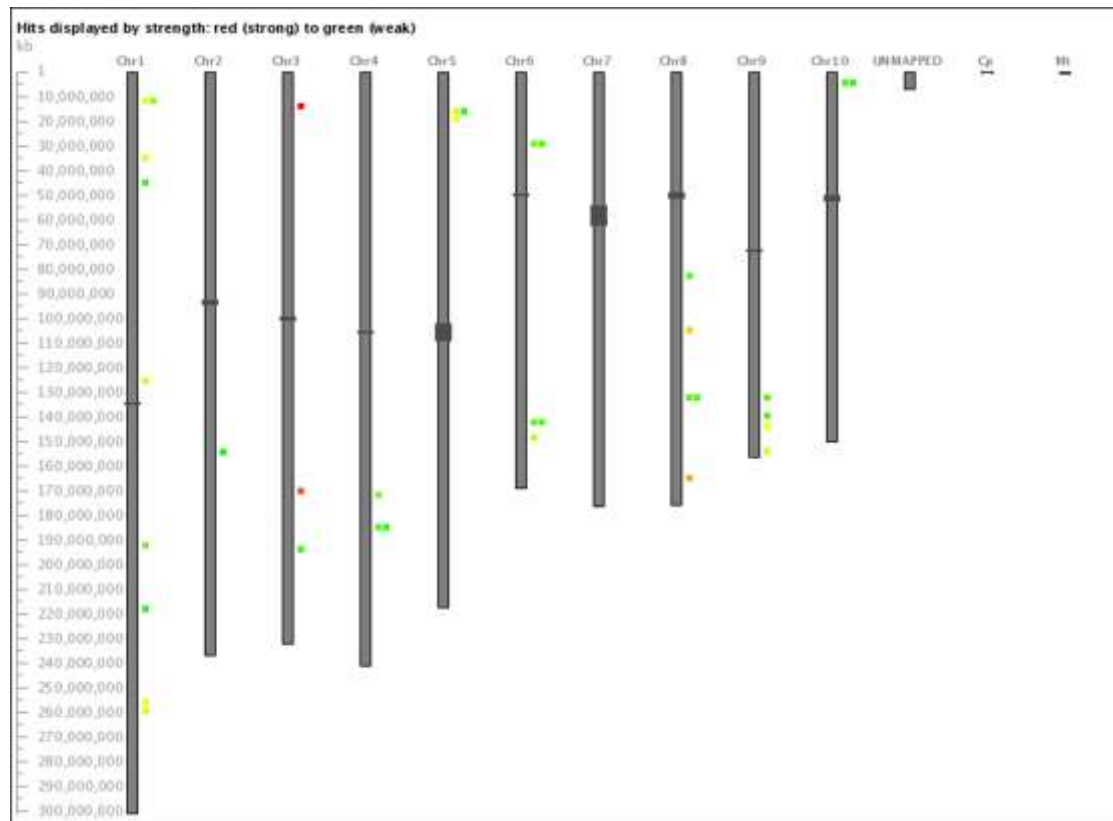


Supplementary Figure 5. Hits diagram of 18046-18087 on maize chromosomes.





**Supplementary Figure 6.** Hits diagram of 27390-27543 on maize chromosomes.



Supplementary Figure 7. Hits diagram of 25868-26648 on maize chromosomes.

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