

[illegible]

		cov	pid	1041	:	.	.	.	.	1	.	1120
1	AB714574.1[genA_ex1-3]	100.0%	100.0%		CGGCGACAACCCCGCGTCCTCAAAGCCGTCACGtaagtcgccgtcatttc	catgaacc	cagctg	acccgct	aggcacc			
2	TsABA8'OH-A	77.9%	99.9%		CGGCGACAACCCCGCGTCCTCAAAGCCGTCACGtaagtcgccgtcatttc	catgaacc	cagctg	acccgct	aggcacc			
3	TsABA8'OH-B	76.2%	94.3%		CGGCGACAACCCCGCGTGCTCAAAGCCGTCACGtaagtcgcca	ca-----	ccagctg	acccgctt	ggtaccc			
4	TsABA8'OH-R	77.0%	92.3%		CGGCGACAACCCCGCGTCCTCAAAGCCGTCACGtaagtcgcca	catatttc	catgaacca	-gctg	acccgctt	ggtgccc		
		cov	pid	1121	.	.	:	.	.	.	.	2 1200
1	AB714574.1[genA_ex1-3]	100.0%	100.0%		gatcga	aaagcagcgactg	accc---	gttc	atcata	caatca	acagGAAGAGCACGCCGAGATCGCGAGGGAGAAGGCGT	
2	TsABA8'OH-A	77.9%	99.9%		gatcga	aaagcagcgactg	accc---	gttc	atcata	caatca	acagGAAGAGCACGCCGAGATCGCGAGGGAGAAGGCGT	
3	TsABA8'OH-B	76.2%	94.3%		gatcga	aaagcagcgactg	accc---	gtg	catc	caaca	atcaacagGAAGAGCATGCCGAGATCGCGAGGGAGAAGGCGT	
4	TsABA8'OH-R	77.0%	92.3%		gatcga	aaagcagcgactg	accc---	gtg	catc	caaca	atcaacagGAAGAGCATGCCGAGATCGCGAGGGAGAAGGCGT	
		cov	pid	1201	.	.	:	.	.	.	.	1280
1	AB714574.1[genA_ex1-3]	100.0%	100.0%		TGTCCGGCGAGGCGCTGTCGTGGGCCGACACGCGCGGATGCGGTTGACGGGCCGGGTGATCCAGGAGACGATGCGGGTG							
2	TsABA8'OH-A	77.9%	99.9%		TGTCCGGCGAGGCGCTGTCGTGGGCCGACACGCGCGGATGCGGTTGACGGGCCGGGTGATCCAGGAGACGATGCGGGTG							
3	TsABA8'OH-B	76.2%	94.3%		TGTCCGGCGAGCCGCTGTCGTGGGCCGACACGCGCGGATGCGGATGACGGGCCGGGTGATCCAGGAGACGATGCGGGTG							
4	TsABA8'OH-R	77.0%	92.3%		TGTCCGGCGAGCCGCTGTCGTGGGCCGACACGCGCGGATGCGGGTGACGGGGCGGGGTGATCCAGGAGACGATGCGGGTG							
		cov	pid	1281	.	3	.	.	.	.	.	] 1335
1	AB714574.1[genA_ex1-3]	100.0%	100.0%		GCGTCCATCCTCTCCTTCACCTTCAGGGAGGCCGTGGAGGACGTGGAGTACCAAG							
2	TsABA8'OH-A	77.9%	99.9%		G-----	ABA uR	-----					
3	TsABA8'OH-B	76.2%	94.3%		G-----		-----					
4	TsABA8'OH-R	77.0%	92.3%		G-----		-----					

**Figure S1.** TsABA8'OH partial sequences of Triticale cv. Bogo (NCBI MW538321-MW538323) generated with Clustal Omega and visualized with MView on-line tools [47-48]. Sequences were aligned to common wheat genome A reference sequence of ABA 8'-hydroxylase. Primers and gRNAs used in this study were marked with black boxes. Notice NSP in R genome sequence of ABA/1/364 and site for introduced mismatches in genome specific primers Aex3R, Bex3R and Rex3R (marked with red boxes, compare to Table S1).