

The development and validation of new DNA markers linked to the thousand-grain weight QTL in bread wheat (*Triticum aestivum* L.)

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Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

Table S1. Genes within the target interval

Gene ID	Gene ID	Gene ID
Traes_2DL_0454E5C6F.1	Traes_2DL_1288645A4.1	Traes_2DL_00E4230F1.1
Traes_2DL_025DD4C90.1	Traes_2DL_099D4CA9B.1	Traes_2DL_0C7D603C2.1
Traes_2DL_04B442359.1	Traes_2DL_0D8943F9D.1	Traes_2DL_09AE5E1D5.1
Traes_2DL_039832D76.1	Traes_2DL_060519447.1	Traes_2DL_0F555772A.1
Traes_2DL_08ED30064.1	Traes_2DL_0BCB26B5D.1	Traes_2DL_0DD2BDF13.1
Traes_2DL_0367084B6.1	Traes_2DL_09CB3E4B8.1	Traes_2DL_09A84CB09.1
Traes_2DL_10A4DDD75.1	Traes_2DL_003F57666.1	Traes_2DL_0E27F3A5B.1
Traes_2DL_03E388B44.1	Traes_2DL_0858561A3.1	Traes_2DL_099F54442.1
Traes_2DL_0896D13AE.1	Traes_2DL_09E7EE3FE.1	Traes_2DL_1253EEAF6.1
Traes_2DL_0FC1C6597.1	Traes_2DL_07F08C844.1	Traes_2DL_04BB2BD07.1
Traes_2DL_09546CF83.1	Traes_2DL_0F859298B.1	Traes_2DL_0B1444B68.1
Traes_2DL_10E3118B4.1	Traes_2DL_0C5C34696.1	Traes_2DL_0ABA21628.1
Traes_2DL_0D1C8A54F.1	Traes_2DL_101480271.1	Traes_2DL_0C6C7C3A6.1
Traes_2DL_0F6CA6B24.1	Traes_2DL_09717E59F.1	Traes_2DL_0BE2C95D6.1
Traes_2DL_05D7DDA57.1	Traes_2DL_03C813801.1	Traes_2DL_0E831B777.1
Traes_2DL_06717449C.1	Traes_2DL_0A96AAC5B.1	Traes_2DL_1111EBF63.1
Traes_2DL_091F48866.1	Traes_2DL_0753011C3.1	Traes_2DL_0C238F673.1
Traes_2DL_04892661A.1	Traes_2DL_1089B6A48.1	Traes_2DL_11D80D68C.1
Traes_2DL_03CAA3B80.1	Traes_2DL_07C68D56E.1	Traes_2DL_128886711.1
Traes_2DL_04FB06EB3.1	Traes_2DL_0FD654C6C.1	Traes_2DL_128C9BA9E.1
Traes_2DL_068810069.1	Traes_2DL_06B9A730B.1	Traes_2DL_04714FD93.1
Traes_2DL_097D119DE.1	Traes_2DL_058C07200.1	Traes_2DL_06C373049.1
Traes_2DL_112D5E5F8.1	Traes_2DL_002CF6406.1	Traes_2DL_0F4374B82.1
Traes_2DL_09AEAA124.1	Traes_2DL_0F0A9C3B9.1	Traes_2DL_0977D942F.1
Traes_2DL_05C6D048C.1	Traes_2DL_07E54848B.1	Traes_2DL_08D815674.1
Traes_2DL_10E6885D8.1	Traes_2DL_0E2E3EC45.1	Traes_2DL_0165388EA.1
Traes_2DL_013F9616A.1	Traes_2DL_02C3FCCCE.1	Traes_2DL_01683813A.1
Traes_2DL_0DD946101.1	Traes_2DL_056AD859E.1	Traes_2DL_02C9FBBB4.1
Traes_2DL_11ADB71A2.1	Traes_2DL_1227A48DF.1	Traes_2DL_038DEB504.1
Traes_2DL_036F2A3FC.1	Traes_2DL_09D5984EF.1	Traes_2DL_03DA7F1ED.1
Traes_2DL_0D8A3DD95.1	Traes_2DL_0E9BE0271.1	Traes_2DL_05552C023.1
Traes_2DL_0E40A4BC4.1	Traes_2DL_0618793E2.1	Traes_2DL_10579A99E.1
Traes_2DL_109A64712.1	Traes_2DL_0C98E720C.1	Traes_2DL_117603113.1
Traes_2DL_0DFFD3CE2.1		

Table S2. Single copy genes within the target interval

Gene ID	Gene ID	Gene ID	Gene ID
Traes_2DL_06717449C.1	Traes_2DL_05D7DDA57.1	Traes_2DL_0F6CA6B24.1	Traes_2DL_07F08C844.1
Traes_2DL_0E9BE0271.1	Traes_2DL_03E388B44.1	Traes_2DL_091F48866.1	Traes_2DL_0F555772A.1
Traes_2DL_128C9BA9E.1	Traes_2DL_128886711.1	Traes_2DL_099F54442.1	Traes_2DL_0DFFD3CE2.1
Traes_2DL_002CF6406.1	Traes_2DL_10E6885D8.1	Traes_2DL_1089B6A48.1	Traes_2DL_02C3FCCCE.1
Traes_2DL_112D5E5F8.1	Traes_2DL_09D5984EF.1	Traes_2DL_09E7EE3FE.1	Traes_2DL_0E2E3EC45.1
Traes_2DL_0D8943F9D.1	Traes_2DL_1227A48DF.1	Traes_2DL_0896D13AE.1	Traes_2DL_09A84CB09.1
Traes_2DL_04892661A.1	Traes_2DL_0A96AAC5B.1	Traes_2DL_0C98E720C.1	Traes_2DL_09AE5E1D5.1
Traes_2DL_0C6C7C3A6.1	Traes_2DL_0FD654C6C.1	Traes_2DL_1111EBF63.1	Traes_2DL_0BE2C95D6.1

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Table S3. Primer details for the 11 selected genes

Gene	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')	Length (bp)	Locations of primers
Traes_2DL_458CEA548.1	CATCCAGCATCCTTGCCGTC	CATCTGACACATGTGGTCA	755	Coding region
	TGAAGAGGAAAAGTAAGGAGAT	GACCTGAGGTCGAAAACCGA	761	Coding region
	TAGGAGCTGAAGTACTGCTCAG	CTGTCCC GCCAATCATGCCA	780	Coding region
Traes_2DL_B0BBBEE64.1	TCTAACGCTGCTCTGACTT	CTCTAGGGTGTATCAGGCCG	812	Coding region
	TGACCAGCTTTGCCCCGAAC	ACACGTTGCCAACGTCATG	745	Coding region
	TGACCAGCTTTGCCCCGAAC	CCATTGGCTTTGTCGCGTCGA	733	Coding region
Traes_2DL_E301FB6B9.1	TAGTACCACCTGGGTTGT	ATGGTGTATGCGTGTGGA	756	Coding region
	TGGGTTTCAGAGTGGTGAAC	CCTTGTTCAGTCGGATTCGCA	774	Coding region
	TAGTACCACCTGGGTTGT	CGACGTCCTTGTTCAGTCGGA	732	Coding region
Traes_2DL_0C98E720C.1	TACCTCTGAGCTCAGAGTGC	ACGCTCGAAGTACATGCGA	786	Promoter region
	CGATGCGCACCGTCGTCTCT	GCGCGACATAGAGACGCAGT	767	Promoter region
Traes_2DL_0DFFD3CE2.1	CATAAAGTTCACCTTGATAGGC	TTCGGATCACACAGATTGA	746	Promoter region
Traes_2DL_0F6CA6B24.1	TGACAACCTAACCGATGTGCC	TTTCAGGAGTGAGATTTTCTA	777	Promoter region
	TCACAAGCGACGAAGAAGTAA	AAAATGTTTGTGAATGTG	784	Promoter region
	TCACAAGCGACGAAGAAGTAA	ACCTTGTTCATGCGTGACACA	871	Promoter region
	TGAAGTTGCTCAGCGCGCCC	ACCAAATTTGCTTGTAGAA	782	Promoter region
	CGATGCTACAACCTTTGTAT	GATGCTTGGTTACATGGCAGA	711	Promoter region
Traes_2DL_0F555772A.1	GAAACAACCTTCTGAATCCA	ACTTGCCTTCCTCAAGCGTGA	703	Promoter region
	CGAACAGCGACGACACCCTG	TCGTGCTCTGCGGGCAGACCG	798	Promoter region
	CGAACAGCGACGACACCCTG	TCTGCGGGCAGACCGTGGC	781	Promoter region
Traes_2DL_07F08C844.1	TCTCAGTTCTGGAAGTCGATTC	CGAGTTTCGAGAACTTAGCCA	688	Promoter region
	TGAAGATCAAGATCTTTGT	GAGGGTTGATATTGCTACGA	694	Promoter region
	TTCTTGAAGAGAGAGAACA	ATGTTCTTCTGTCGGAGCA	706	Promoter region
	GCTCCATGATCCTAGCGAT	CTATGGTCGTAGTAGTAGGCA	788	Promoter region
	TGGGGTCTGGAACATCCCA	ACCAGGAATTTGAAGACATG	718	Promoter region
Traes_2DL_09AE5E1D5.1	TCTGCAAAACCCACATATCCAT	GAAAATATATCAACAAAT	766	Promoter region
	TCAACATCTGCTAGGATCCTT	AACTGGTGTATTATCACGAG	789	Promoter region
	AGGAGGCGGAGAGACCCCTT	GTCCTTGCTCTCTTGTCTT	744	Promoter region
	AGGAGGCGGAGAGACCCCTT	CGTGCTGCCGGATCAGAA	821	Promoter region
	TAGTCTGTGTCACTCCTTGAT	CCGGGTGAAGGCATACAGGTG	855	Promoter region
	AAGCAGACAGCAGACTTTG	GTCTTCAATCTCTGCCTGC	1482	Promoter region
Traes_2DL_0896D13AE.1	TAACACTGAGCTCGAAATCTA	CCTGGCCTGCGTCCTCGTCCT	756	Promoter region
	GCAAGTTTTTCTTGCTACCC	AGAGCCGTCGGGCGATGCA	777	Promoter region
	GTTGAAAGGAGCAGGTAAAC	TAGATCTAAAAATGTTGGTC	710	Promoter region
Traes_2DL_04892661A.1	GGTTCCTCCTGCCGGCAAC	GACTTTTTTGTGAGGGTTC	755	Promoter region
	GGTTCCTCCTGCCGGCAAC	GGGAGGCAATCAGCTGCTG	712	Promoter region
	CACGGGCGTCAGGTGCTTCA	CAGTCAGCGACGTACATAA	798	Promoter region
	TGAGGAGGTTACTCAGACGC	CTGTGTTACTACATCGTCA	763	Promoter region
Traes_2DL_1111EBF63.1	TCTGTGTAATTAAGTTATTTTC	ACAGCTAGTTTGACAGAGA	723	Promoter region
	GATCAAACTCATTCTTCTGG	TTCAAAGCCGCCAACTCCTG	754	Promoter region
Traes_2DL_10E6885D8.1	GAACGTATTTCTGACTTCTTTG	GTACTGTTCAAAGAACATG	731	Promoter region
	TTCTCCTGATTAACAGTA	CAGGGTCAGCTCTCCGCTA	803	Promoter region
	TATCACATGCTTGCAATACCA	ATGACAGAGATGTTTTTCTCA	861	Promoter region
	CTGAATGATTAGATGAATC	ATTGCTTTTGAGAAGGCTGA	804	Promoter region
	TTGTTAATGCCTAGGCACC	CTCTCTTCGCGCTATAACGA	741	Promoter region
Traes_2DL_1089B6A48.1	CAGCTCCCTCCCTCTATCTTC	ACGCAAAGAAGAAGAAAACGGA	750	Promoter region
	CAGGGTCAGCTCTCCGCTA	CCAAGTGGCACAGTGGTGGTG	755	Promoter region
	TCGATCTCAATTTGTTGTTC	GTGGCTTAAGCTAAGTCTG	764	Promoter region

4 Table S4. Detected polymorphsim between Q1028 and ZM9023

Gene	Maeker name	Marker sequence(5'-3')	Parent	Sequence close to the SNPs
Traes_2DL_09AE5E1D5.1	09AE-149 F1	AGGAGAAGGTGACAAGGT	Q1028	ATGTCCTTTTGGT.TCTGCC
	09AE-149 R1	CCACTGTTGAGTCCATCTG	ZM9023	ATGTCCTTTTGGTTTCTGCC
	09AE-149 F2	AGGAGAAGGTGACAAGGT	Q1028	ATGTCCTTTTGGTTTCTGCC
	09AE-149 R2	ACAGCAGCATAACAGAGC	ZM9023	ATGTCCTTTTAGTTTCTGCC
	09AE-393 F	CACGCTGGTTACTGATTGC	Q1028	CGAATAATGAACGGATGCTT
	09AE-393 R	TTCCTGGATAATATTGTCCTAGCA	ZM9023	CGAATAATGAGCGGATGCTT
	09AE-374 F	GCACCGAAACGAAACGCCTTTACA	Q1028	ATTGTCTGTTTACCTCTTTC
	09AE-374 R	AATCACCGAGGTCAAGAGCACGAA	ZM9023	ATTGTCTGGTTACCTCTTTC
	09AE-431 F	CCTCGGTGATTATCTCCT	Q1028	GAGGTGGGGGAGGTATGTAC
	09AE-431 R	CTCAGGGTGAAGGTATCC	ZM9023	GAGGTGGGGGAAGTATGTAC
	09AE-490 F	CACCTGTATGCCTTCACC	Q1028	GAACAAAAGGGGGGTACTTG
	09AE-490 R	GTCTGCTGTCTGCTTATATTAGT	ZM9023	GAACAAAAGGTGGGTACTTG
	09AE-520 F	CACCTGTATGCCTTCACC	Q1028	TATTCTTCCTTGGAAGTGA
	09AE-520 R	CTGCTGTCTGCTTATATTAGTCA	ZM9023	TATTCTTCCTTGTAAGTGA
	09AE-550 F	CACCTGTATGCCTTCACC	Q1028	TCAGGACATGAATGACTAAT
	09AE-550 R	AAGTCTGCTGTCTGCTTAT	ZM9023	TCAGGACATGAGTGAAGTGA
	09AE-590 F	AAGCAGACAGCAGACTTTG	Q1028	TGCTTGATATGAAACACCCA
	09AE-590 R	GTCTTCAATCTCTGCCTGC	ZM9023	TGCTTGATATGAGACACCCA
Traes_2DL_0C98E720C.1	0C98-411 F1	CTCTTTCGTGCTCTTGAC	Q1028	GGTATGTACTCGACGTGCCT
	0C98-411 R1	GGATACCTTCACCCTGAG	ZM9023	GGTATGTACTCAACGTGCCT
	0C98-411 F2	CCTCGGTGATTATCTCCT	Q1028	GGTATGTACTCGACGTGCCT
	0C98-411 R2	CTCAGGGTGAAGGTATCC	ZM9023	GGTATGTACTCAACGTGCCT
Traes_2DL_0896D13AE.1	0896-400 F	AGAAGTGCTATACCATAA	Q1028	TATACCATAAA.CCAATGATA
	0896-400 R	CCTACCTTACTAGTAGTATGA	ZM9023	TATACCATAAACCCAATGATA

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Table S5. primers for isolation of genes flanking *QTgw.sau-2D*

Gene	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')	Length (bp)	Locations of primers
Traes_2DL_458CEA548.1	CATCCAGCATCCTTGCCGTC	CATCTGACACATGTGGTCA	755	Coding region
	TGAAGAGGAAAGTAAGGAGAT	GACCTGAGGTCGAAAACCGA	761	Coding region
	TAGGAGCTGAAGTACTGCTCAG	CTGTCCCGCCAATCATGCCA	780	Coding region
Traes_2DL_B0BBBEE64.1	TCTAACGCTGCTCTGACTT	CTCTAGGGTGTATCAGGCCG	812	Coding region
	TGACCAGCTTTGCCCCGGAAC	ACACGTTGCCAACGTCATG	745	Coding region
	TGACCAGCTTTGCCCCGGAAC	CCATTGGCTTTGTCGCGTCGA	733	Coding region
Traes_2DL_E301FB6B9.1	TAGTACCACCTGGGTTGTT	ATGGTGTATGCGTGTGGA	756	Coding region
	TGGGTTTCAGAGTGGTGAAC	CCTTGTCAGTCGGATTCGCA	774	Coding region
	TAGTACCACCTGGGTTGTTTA	CGACGTCCTTGTCAGTCGGA	732	Coding region