

Supplementary Materials

Table S1. Genes encoding for transcription factors participating in anthocyanin biosynthesis regulation in different plant species.

	MYC (bHLH)	MYB	WD40
<i>Arabidopsis thaliana</i>	<i>TT8</i> (Nesi <i>et al.</i> , 2000) <i>GL3/EGL3</i> (Bernhardt <i>et al.</i> , 2003; Heim <i>et al.</i> , 2003; Zhang <i>et al.</i> , 2003)	<i>TT2, CPC</i> (Borevitz <i>et al.</i> , 2000; Gonzalez <i>et al.</i> , 2008) <i>MYBL2</i> (Dubos <i>et al.</i> , 2008; Matsui <i>et al.</i> , 2008) <i>PAP1, PAP2</i> (Borevitz <i>et al.</i> , 2000)	<i>TTG1</i> (Walker <i>et al.</i> , 1999)
<i>Petunia hybrida</i>	<i>ANI, JAF13</i> (Llyod <i>et al.</i> , 1992; Quattrocchio <i>et al.</i> , 1998; Spelt <i>et al.</i> , 2000, 2002)	<i>AN2, AN4</i> (Quattrocchio <i>et al.</i> , 1999, 2006)	<i>AN11</i> (de Vetten <i>et al.</i> , 1997)
<i>Antirrhinum majus</i>	<i>Delila</i> (Gong <i>et al.</i> , 1999)	<i>Rosea1, Rosea2, Venosa, MYB308, MYB330</i> (Schwinn <i>et al.</i> , 2006)	not defined
<i>Vitis vinifera</i>	<i>MYC1, MYCA1</i> (Hichri <i>et al.</i> , 2010; Matus <i>et al.</i> , 2010)	<i>MYBA1, MYBA2, MYB5a</i> (Kobayashi <i>et al.</i> , 2002; Deluc <i>et al.</i> , 2006, 2008; Walker <i>et al.</i> , 2007; Cutanda-Perez <i>et al.</i> , 2009)	<i>WDR1, WDR2</i> (Matus <i>et al.</i> , 2010)
<i>Zea mays</i>	<i>B, R, Lc, Sn, In1</i> (Burr <i>et al.</i> , 1996; Chandler <i>et al.</i> , 1989; Ludwig <i>et al.</i> , 1989; Consonni <i>et al.</i> , 1993; Petroni <i>et al.</i> , 2000)	<i>CI, P11, P1</i> (Paz-Ares <i>et al.</i> , 1987; Chandler <i>et al.</i> , 1989; Goff <i>et al.</i> , 1990; Petroni <i>et al.</i> , 2000)	<i>PAC1</i> (Selinger and Chandler, 1999)
<i>Oryza sativa</i>	<i>R, Pl, Ra, Pb</i> (Hu <i>et al.</i> , 1996; 2000; Sakamoto <i>et al.</i> , 2001; Wang and Shu, 2007)	<i>OsCI</i> (Reddy <i>et al.</i> , 1998; Saitoh <i>et al.</i> , 2004)	not defined
<i>Hordeum vulgare</i>	<i>ANT2</i> (Cockram <i>et al.</i> , 2010)	not defined	not defined
<i>Triticum aestivum</i>	<i>TaMyc1</i> (current study)	<i>Mpc1</i> (Li <i>et al.</i> , 1999)	not defined

Table S2. PCR primers amplifying *Myc*-like gene sequences of wheat. e: exon, i: intron, UTR: untranslated region, TDN: touchdown, TDN ext: touchdown extended, *: primers designed from *T. aestivum* contigs 32064, 42144, 65805, 248535, 249890, 302985, 445995, 467773, 1280203, 1475001, 1815797, 1821237 and 4203206 found in www.cerealsdb.uk.net. Primer pairs used for cDNA sequencing are shown in gray color.

Primer Pair Number	Purpose	Gene (Copy)	PCR Product Length (DNA/cDNA)	Forward Primer (FP), 5'→3'	Reverse Primer (RP), 5'→3'	PCR Conditions (Amplification Program/MgCl ₂ Concentration, mM)	Gene Region Containing Primer Annealing Site	
							Forward	Reverse
1	cloning	<i>TaMyc1-4</i>	373, 379, 382	gtggacaaggcatccatcctagc	tcttgagagcgaggaggccg	60 grad ¹ /1.5	e8	e8
2	sequencing	<i>TaMyc1</i>	453/-	ataattgcatcggcaggc *	gaactaagaagtaagctagccatgac *	TDNext ² /1.8	5' region	i1
3	sequencing	<i>TaMyc1</i>	640/228	gctccatcttctccccg	cgccgtttagaaccctg	TDN ² /1.0	e1	e3
4	sequencing	<i>TaMyc1</i>	491/-	gtcatggctagcttacttcttagtc *	cacaacaacggccggt *	55 grad ¹ /1.8	i1	i2
5	sequencing	<i>TaMyc1</i>	296/-	taccggccgtttgtgt *	tgttcttgagatacatacccttg *	TDNext ² /1.8	i2	e3i3
6	sequencing	<i>TaMyc1</i>	393/262	tcaccagctcggcggaca *	gcgactgagcattgcacaa *	TDN ² /1.8	e3	e4
7	sequencing	<i>TaMyc1</i>	600/-	gagcaacgagcatggtttgt *	atcgggtgcagattagagagt *	TDNext ² /1.8	e4	i4
8	sequencing	<i>TaMyc1</i>	147/-	acgtgtagccgcatccttg *	ccggcagaggtagcatgcat *	TDN ² /1.8	i4	i4
9	sequencing	<i>TaMyc1</i>	245/-	atggcgcccatgcatgc *	aaggagaacatcgtgtcctcgc *	TDN ² /1.8	i4	i6
10	sequencing	<i>TaMyc1</i>	802/-	tgagtttcgtccatgatga *	catgagattgcccctgtaag *	TDNext ² /1.8	i6	i6
11	sequencing	<i>TaMyc1</i>	687/-	cttacaggggcaaatctcatg *	gagaactggaaaaactcatggac *	TDNext ² /1.8	i6	i6
12	sequencing	<i>TaMyc1</i>	492/-	aaatcagtcgatgagttttcca *	cgtgattcgtcaaggtgt *	TDN ² /1.8	i6	e7
13	sequencing	<i>TaMyc1</i>	534/-	gataccggggaactgagctag *	ttacttttggtggtgcgtgt *	TDNext ² /1.8	e7	i7
14	sequencing	<i>TaMyc1</i>	283/177	aaccatgtcatttcggagagga *	ggccgcctgttgatc	TDN ² /1.8	e7	e8

Table S2. Cont.

Primer Pair Number	Purpose	Gene (Copy)	PCR Product Length (DNA/cDNA)	Forward Primer (FP), 5'→3'	Reverse Primer (RP), 5'→3'	PCR Conditions (Amplification Program/MgCl ₂ Concentration, mM)	Gene Region Containing Primer Annealing Site	
							Forward	Forward
15	sequencing	<i>TaMyc1</i>	422/331	acgacggcctgagcagtg	atgaagggttccgatagcc *	TDN ² /1.8	e8	3UTR
16	5'RACE	<i>TaMyc1</i>	466/332	agtagtctgctcatgccag	ggctctcaggcgacag	MINTa ³ , 55°C, 29 cycles	e2	e3
17		<i>TaMyc1</i>	-/151	(primer for control)	ccacgtcagaacccc	MINTa ³ , 53°C, 26 cycles		e2e3
18	3'RACE	<i>TaMyc1</i>	531/440	1FP	agtgtctcgctaatcatc	MINTa ³ , 60°C, 24 cycles	e8	e9
19		<i>TaMyc1</i>	407/316	gcggggaagaaggtgtag	(primer for control)	MINTa ³ , 55°C, 20 cycles	e8	
20	mapping expression	<i>TaMyc1</i>	283/177	13F	13R	TDN ² /1.8	e7	e8
21	mapping expression	<i>TaMyc2</i>	330/220	13F	tcttcccgccgacttcatga	TDN ² /1.5	e7	e8
22	mapping expression	<i>TaMyc3</i>	347/198	13F	gagtttccggacggctgttg	TDN ² /1.8	e7	e8
23	mapping expression	<i>TaMyc4</i>	341/188	13F	acggctgttccggcca	TDN ² /1.8	e7	e8

¹ The amplification was initiated by a denaturing step (94 °C/2 min), followed by 45 cycles (35 cycles in **55 grad** program) of 94 °C/15 s, 60 °C (55 °C in **55 grad** program)/30 s, 72 °C/60 s, and completed with a final extension step of 72 °C/5 min; ² The amplification was initiated by a denaturing step (94 °C/2 min), followed by 13 cycles of 94 °C/15 s, 65 °C/30 s (decreasing by 0.7 °C/cycle), 72 °C/45 s (2 min in **TDNext** program), 24 cycles of 94 °C/15 s, 56 °C/30 s, 72 °C/45 s (2 min in **TDNext** program); and a final extension of 72 °C/5 min; ³ The amplification program was as in a manual to a Mint RACE primer set (Evrogen, Moscow, Russia) with annealing temperature and numbers of cycles, established empirically (pointed in column “PCR Conditions”).

Table S3. Sequence similarity between *TaMyc1* and its three related copies.

	<i>TaMyc1</i>	<i>TaMyc2</i>	<i>TaMyc3</i>
<i>TaMyc2</i>	87.61% 2 in/dels (6+3bp)	-	-
<i>TaMyc3</i>	89.97% 1 in/del (3bp)	86.73% 3 in/del (3+6+3 bp)	-
<i>TaMyc4</i>	91.45% 1 in/del (3bp)	87.32% 3 in/del (3+6+3 bp)	95.83% 0 in/del

Table S4. Fold differences in transcript *TaMyc1* abundance between test genotypes in various parts of the wheat plant. *: differences statistically significant at $p \leq 0.05$.

Comparable Genotypes	Pericarp	Culm	Leaf	Coleoptile	Root
“i:S29Pp-A1Pp-D1Pp3 ^P ”/“Saratovskaya 29”	1446.31 *	18.79 *	35.54 *	61.12 *	47.87 *
“i:S29Pp-A1Pp-D1Pp3 ^{PF} ”/“Saratovskaya 29”	1492.27 *	6.81 *	2.59 *	100.82 *	30.79 *
“i:S29Pp-A1Pp-D1Pp3 ^P ”/“i:S29Pp-A1Pp-D1Pp3 ^{PF} ”	0.97	2.76 *	13.70 *	0.61	1.55 *

Table S5. Fold differences in transcript *TaMyc1* abundance between genotypes marked in the table line to the genotypes marked in the table row. *: differences significant at $p \leq 0.05$.

	Saratovskaya29 i:S29Pp-A1pp-D1pp3	i:S29Pp-A1Pp-D1Pp3 ^P	i:S29Pp-A1pp-D1Pp3 ^P	i:S29Pp-A1Pp-D1pp3 ^P
i:S29pp-A1pp-D1pp3	3.31 *	197.82 *	476.45 *	1.67 *
Saratovskaya29 i:S29Pp-A1pp-D1pp3	-	59.76 *	143.93 *	-
i:S29Pp-A1Pp-D1pp3 ^P	1.98 *	118.63 *	285.71 *	-
i:S29Pp-A1Pp-D1Pp3 ^P	-	-	2.41 *	-

Table S6. Fold differences in transcript *TaMyc1* abundance between genotypes marked in the table line to the genotypes marked in the table row. * differences significant at $p \leq 0.05$.

	Saratovskaya29 i:S29Pp-A1pp-D1pp3	i:S29Pp-A1Pp-D1Pp3 ^{PF}	i:S29Pp-A1pp-D1Pp3 ^{PF}	i:S29Pp-A1Pp-D1pp3 ^{PF}
i:S29pp-A1pp-D1pp3	3.31 *	80.55 *	150.01 *	3.04 *
Saratovskaya29 i:S29Pp-A1pp-D1pp3	-	24.33 *	45.32 *	-
i:S29Pp-A1Pp-D1pp3 ^{PF}	1.09	26.46 *	49.28 *	-
i:S29Pp-A1Pp-D1Pp3 ^{PF}	-	-	1.86	-

Figure S1. Multiple alignment of the coding regions of maize *Lc*, rice *Ra* and the *T. urartu* *Myc*-like gene. Intron positions are marked by triangles, its localizations were predicted by comparison of the mRNA sequences with the corresponding rice (AL60682) and maize (DQ414252) genomic sequences with determined gene structures. The sites of the primers forming primer pair 1 (Table S2) are underlined.

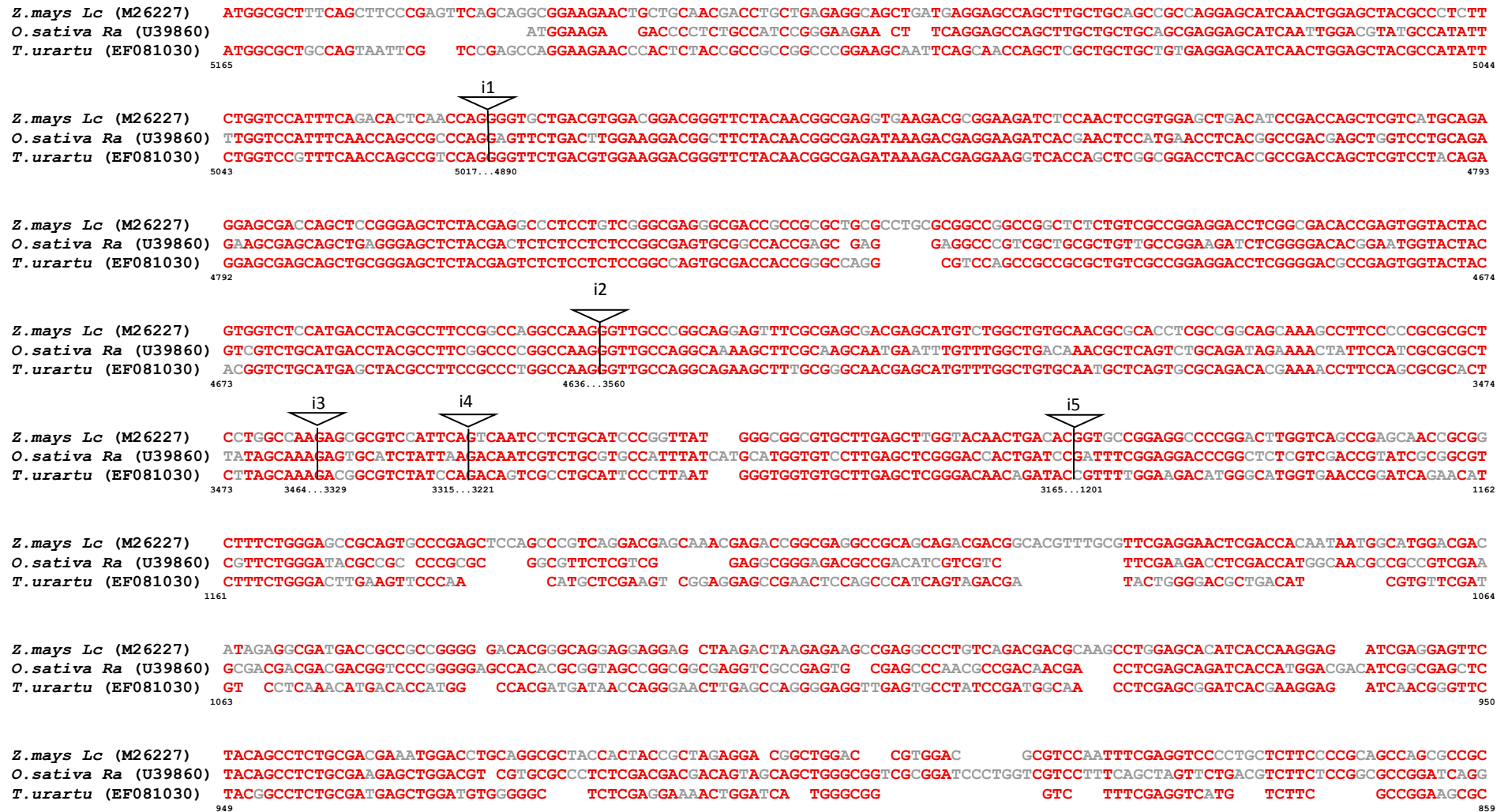


Figure S1. Cont.

Z.mays Lc (M26227) CTCCGGTGGACAGGGCTAC CGCTAACGTCGCCGCCGACGCCTC AAGGGCAC CCGTCTACGGCTCTCGCGCCGACGAGTTTCATGGCTTGACGAGGTCCTCGCAGCAGTCGTCGTGC
O.sativa Ra (U39860) CGCCGGCGGCAGAGCTACTGACGTCGACGACGTCGTCGTCGCCGCTTACACGGTAGCTCCATTGATGGATCTTGCAGGCCG TCGCCGTCGAGTTTTGTGGCGTGGAAAGAGACGGCGGAC
T.urartu (EF081030) CGCCAGCGCCTGTCCGCCACGGACGGGTCACACTAGTGGTGTGTTGCTTT TAGTTCGGTTGGACCTCTCAC CCATCGTGCTTTGCGGCTTGGAAAGATCATGGCAC 858 752

Z.mays Lc (M26227) TCCGACGACGGCGCCCGCAGCAGTAGTGCCGGCCATCGAGGAGCCGAGAGATTGCTGAAGAAAGTGGTGGCCGGCGCGTGCTTGGGAGAGCTGTGGCGGC GCGACGGGAGCAGCACAGG
O.sativa Ra (U39860) TCGGACGAGGTGCAGGCCG TGCCGCTCATCAG CGGAGAGCCGCCACAGAAATTGCTGAAGAAAGCTGTCGCCGGAGCCGGTGCTGGATGAACAATGGTGACAGCAGCCG GCGGCCATGA
T.urartu (EF081030) TCGGCCAAGACGTG GTTGTGCCGGTCGCCGGGAGTCGCAGAAATTGCTAAGAAAGCTTTGGCCGGTG GGCATGGGCAATAATGATGACGACGGCA CCGCTAGAG 751 643

Z.mays Lc (M26227) AAATGAGTGGCACTGGCACCAAGAACCACGTCATGTCGGAGCGAAAGCGACGAGAGAAGCTCAACGAGATGTTCTCGTCTCAAGTCACTGCTTCCGTCCATTACAGGTTGACAAAGCGTCC
O.sativa Ra (U39860) CGACTCAAGAAAGCAGCATCAAGAACCATGTCATGTCAGAGAGAAGCCGGGAGAAGCTCAACGAGATGTTCTGATTTCTCAAATCAGTTGTCCCGTCCATTACAAAGTTGGACAAAGCATCC
T.urartu (EF081030) CTCAGCAAAGTACCAACACCAAAACCATGTCATTCGGAGAGAGGCCGCCGGGAGAAGCTCAACGAGATGTTCTGATTTCTAAGTCTTGGTCCCGTCCATTACAAAGTTGGACAAAGCATCC 642 533...420 406
i6
1FP

Z.mays Lc (M26227) ATCCTCGCCGAAACGATAGCCTACCTCAAGGAGCTTCAGAAAGGGTGCAGAGCTGGAGTCCAGTAGGGAACTCGCTCGCCCATCCGAAACGACGACAGGCTAAATA CAAGGCCCTCCC
O.sativa Ra (U39860) ATTCTCGCAGAAACGATAGCCTACCTCAAAGAGCTGGAGAAAAGAGTGGAAAGAGCTGGAATCCAGCAGCCAACATCGCCATGTCATTGAAACAAGAAAGCAGCCGAAAGTGCCTGAGATCAC
T.urartu (EF081030) ATCCTAGCTGAGACGATAGCAATCTCAGAGAGCTGGAACAGAGGTGGAGGAGCTAGAATCTAACAGGG CTGCCGGAACAAAAGTTGTTCAGGAAACGTCATGAAGTTGG 405 296
1FP

Z.mays Lc (M26227) GTGGCAATAA TGAGAGTGTGAGGAAGGAGGTCCTGCGCGGGCTCCAAAGGGAAGAGCCAGAGCTCGGCAGAGACGACGTGGAGGCCCCCGGTCCTCACCATGGACGCCGGCACCCAGCAACGT
O.sativa Ra (U39860) TGGGAAGAAGGTTTCTGCAGGAGCGAAGAGAAAGGCCCGGCGCC GGAGGTGGCCAGCGA CGACGACACCGACGGGAGCG GCGCCATTGT GTGAGCAACGTGAACGT
T.urartu (EF081030) CGGGAAGAAGGTGTTAGCTGGTTCTAAGAGAAAGCGTTGGAGCTCGGCGG GGAGGACA CGCTCTCCCCAAGGAGGAC GCC CGAGCAAC ATCGT 295 200

Z.mays Lc (M26227) CACCGTCACCGTCTCGGACAAGGACGTGCTCCTGGAGGTGCAAGTCCGGTGGGAGGAGCTCCTGATGACGGAGTGTTCGACGCCATCAAGAGCCTCCATTGGACGTCTCTCGGTTCCAGGCTT
O.sativa Ra (U39860) CACCATCATGACA ACAAGGAGGTTCTCCTCGAGCTGCAATGCCAGTGAAGGAATTCTGATGACGAGAGTGTTCGACGCCATCAAGGGAGTCTCCTGGATGTCCTCTCGGTCCAGGCAAT
T.urartu (EF081030) CAATGTCACCGTGACGGATAAAGAGGTGCTCCTTGAGGTGCAATGCCGGTGAAGGAGCTACTGATGACACGAGTGTTCGACGCCATCAAGAGCCTCCGCTGGACGTGTTGTCCTCGTCCGCGCT 199 75

Z.mays Lc (M26227) CAGCGCCAGATGGCTTCATGGGCTTAAGATACGAGCTCAATTTGCTGGCTCCGGTGGCGTCCCTGGATGATCAGCGAGGCTCTTCGCAAAGCTATAGGGAAGCGGTGA
O.sativa Ra (U39860) CAACATCGGATGGTCTCCTTGGACTCAAGATACAGCCAAATTTGCTCTCACTGTGCCGTCGAACTGGGATGATACAGAAGCTCTCCGAAAGCTATAGCAAGCTAG
T.urartu (EF081030) CCACGCTGACGGCTCCTCGCTCTCAAGATACGAGCTCA 74 34
i7
1RP

Figure S2. *TaMyc1* structure and the placement of the overlapping amplicons used to derive the gene's full sequence. Primers used for 5'- and 3'-RACE shown in red.

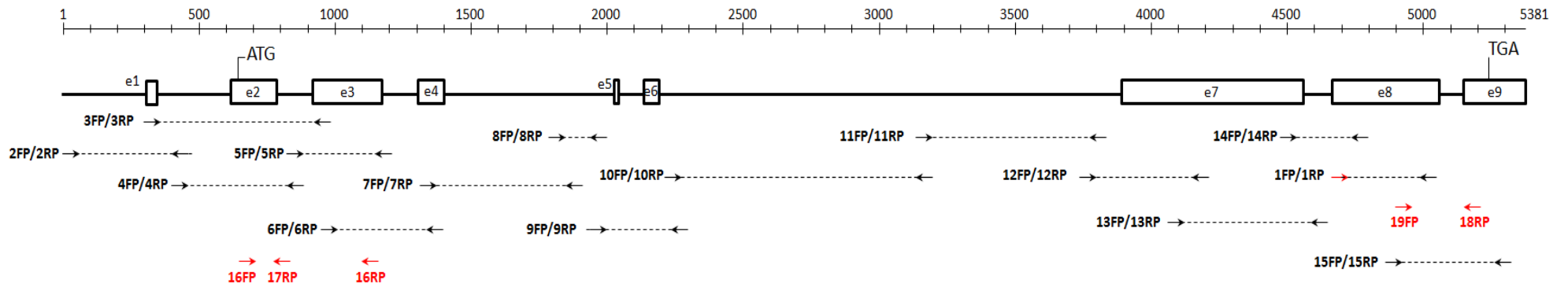


Figure S3. Alignment of wheat *Myc*-like sequences obtained by amplification with primer pair 1 (Table S2).



Figure S4. Physical mapping of the *TaMyc1-4* gene copies using “Chinese Spring” (CS) nulli-tetrasomic (a) and ditelosomic and deletion lines (b).

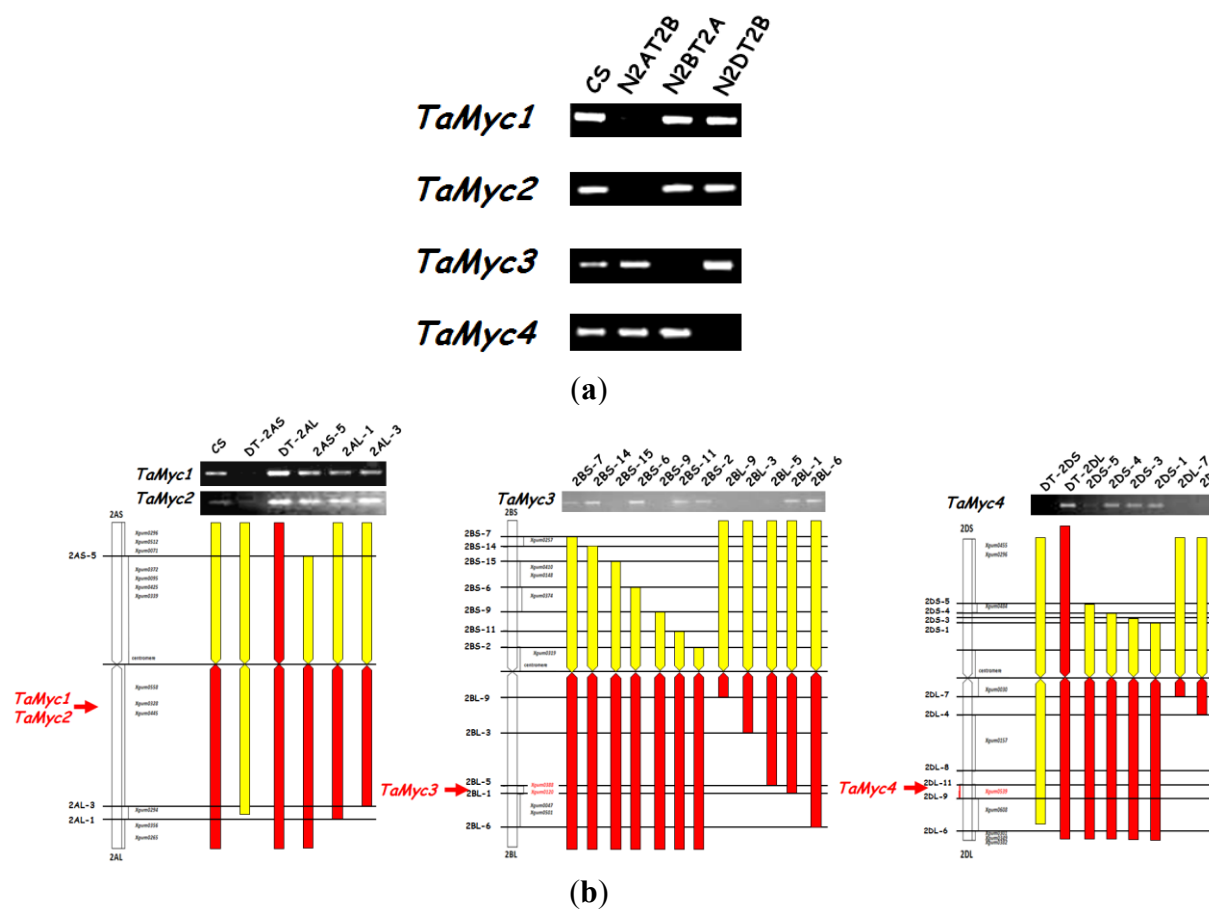


Figure S5. Alignment of maize, rice, wheat, barley, and *Arabidopsis* proteins participating in anthocyanin synthesis.

Wheat TaMYC1 (KJ747954) MALPVVVRPCQEEPTLPPPTGTQF SNQLAAAVRSINWSYALFWSIS TSRPGVLTWKDGFYNGEIKTRKV
Rice RA (U39860) MEETPLPSGKNF RSQLAAAARSINWTYALFWSIS TSRPGVLTWKDGFYNGEIKTRKI
Maize B (X57276) MALSASPAQ EELLQ PAGRPL RKQLAAAARSINWSYALFWSISSTQRPRVLTWTDGFYNGEVKTRKI
Maize LC (M26227) MALSASRVQQAELLQRPAERQLMRSQLAAAARSINWSYALFWSISDTQ PGVLTWTDGFYNGEVKTRKI
Barley ANT2 (HM370319) MALPIVVRPSQEEP PTGKQF SYQLAAAVRSINWSYALFWSIS TSRPGVLTWKDGFYNGEIKTRKV
Arabidopsis TT8 (AJ277509) MDESSIIPAEKVAGAEKKELQGLLKTAVQSVDWTYSVFWQFCPQQR VLVWNGGYNGAIKTRKT

Wheat TaMYC1 (KJ747954) TSSADITADQLVLRSEQLRELYESLLSGQCDHRAR RPAALSPEDLDGAEWYYTVMCGYAFRPGQGL
Rice RA (U39860) TNSMNLTADELVLQRSEQLRELYDSLSSGECGHRAR RPVAALLPEDLDGETEYVYVCMFYAFPGQGL
Maize B (X57276) SHSVELTADQLLMQRSEQLRELYEALRSGECDRRGA RPVGSLSPEDLDGETEYVYVICMIFYAFRPGQGL
Maize LC (M26227) SNSVELTSDQLVQRSDQLREYFALLSGEGDRRAAPARPAAGSLSPEDLDGETEYVYVSMIFYAFRPGQGL
Barley ANT2 (HM370319) TSSADLTADQLLQRSEQLRELYQSLSSGQCDHRGR RPAALSPEDLDGAEWYYAVCMSYAFRPGQGL
Arabidopsis TT8 (AJ277509) TQPAEVTAEAAALERSQQLRELYETLLAGESTSEA RACTALSPEDLTFETEWYFLMCSVFSFPPPSGM

Wheat TaMYC1 (KJ747954) PGRSFASNEHVWLCNAQCADTKTFORALLAKTASIQTVACIP LMGVLELGTNTVLEDKGMVNWIGTS
Rice RA (U39860) PGKSFASNEFVWLTNAQSDRKLFRALAKSASIKTIVCVFIMHGVLELGTDP ISEDPALVDRIAAS
Maize B (X57276) PGRSSASNEHVWLCNAHLAGSKDFRALLAKSASIQTVACIP LMGVLELGTTDKVPEDPDLVSRATVA
Maize LC (M26227) PGRSFASDEHVWLCNAHLAGSKAFPRALLAKSASIQSILCIP VMGGVLELGTDTVPEAPDLVSRATAA
Barley ANT2 (HM370319) PGRSFASNEFVWLCNAQCADTKTFORSLLAKTTSIQTVACIP LMGVLELGTDTVLEDKGMVNRISTS
Arabidopsis TT8 (AJ277509) PGKAYARRKHVWLSGANVDSKTFRAILAKSAKIQTVCIP MLDGVVLELGTTKVREDVEFVELTKSF

Wheat TaMYC1 (KJ747954) FWECLKFPCTCSKEEPSNISIPSVDDTGDADIVFDVNLNHTM AMMIPG ELELGEVECLS DDN
Rice RA (U39860) FWDTP PRAAFSSEAGDADI VVFEGLDHGNAAVEATTTVPGEHAVAGGEVAECPNADND
Maize B (X57276) FWEFPQCPPTYSKEPSSNPSAYETGEAAIYVLEDLDHNAMDMEETVAAAAGRHGTGQELGEVESPS NAS
Maize LC (M26227) FWEFPQCPSSSPSGRANETGEAAADDGTFEELDHNGMDIEAMTAAGGHGQEEELRLREAEALSDAS
Barley ANT2 (HM370319) FWDLKIPTSSKPKPESS PSADDAGEADIVFDLDHNTM AAMIPG ELELGEVECLS DDN
Arabidopsis TT8 (AJ277509) FVDHC KTNPKPALSEHSTYEVHEAEDEEEVEEEMTME EMLRGSPPDEDEDVSNQL

Wheat TaMYC1 (KJ747954) LERITKE INRFYGLYDELVDVGA LEENWTMGG C FE IMSSPEVP PAPAATNGITNGAVTL
Rice RA (U39860) LEQITMDDIGELYSLCEELDVVRPLDDSSWAVADPWSSFQVLVLTSSPAPDQAPAAEATDVDDVVVAAL
Maize B (X57276) LEHITKG IDEFYSICEEMDVQ PLEDAWIMDG SNFE VPSSA LPVDG
Maize LC (M26227) LEHITKE IEEFYSICEEMDLQALPLPLLEDGWTVDA SNFE VPCSSPQP APPVDRATANVAADA
Barley ANT2 (HM370319) LERITKE INGFYGLCELDVGA LDENWITGG S FE VMSSPEAP PAPAATGGITGIVTL
Arabidopsis TT8 (AJ277509) HSDLH IESTHTLDTHMDDMNL MEEGGNYS QVTVTLMSHP TSLSDSVSTY

Wheat TaMYC1 (KJ747954) SSVEP S RSSCFTAWKRSWD SAEDMAT LVARETQKLLKALAGG AWANNGDD TAR
Rice RA (U39860) DGSSIDGSCRPSPSFFVAWKRTAD SDEVQAVP LISGEPQKLLKAVAGAGAWMNG DSSAAM
Maize B (X57276) SSAPADGS RATSFVWTRSSH SCSGEEA VPVIEEPQKLLKALAGGAWANTCGGGGTTV
Maize LC (M26227) SRAPVYGS RATSFMAWTRSSQSSCSDDAAPAAVVPAAIEEPQRLKLVVAGGAWESC GATGAAQ
Barley ANT2 (HM370319) SAAAS S LSSCFTAWKRSWD SAEDMAA PVAGQSQKLLKALAGG VWAINGGGGTAR
Arabidopsis TT8 (AJ277509) SYIQ SSFATWRVENGKEHQVKTAP SSQVWLKQMFVFPFLHDN TKD

Wheat TaMYC1 (KJ747954) AQESTNTKNHVISERRRREKLNEMFLILKSLVPSIHKVKASILAETIYTLRELEQKVEELGNSRAART
Rice RA (U39860) TTQESSIKNHVMSERRRREKLNEMFLILKSLVPSIHKVKASILAETIAYLKELEKRVEELESSSQSPSC
Maize B (X57276) TAQENGAKNHVMSEKRRRREKLNEMFLVLKSLVPSIHKVKASILAETIAYLKELEKRVVELESSRQ
Maize LC (M26227) EMSGTGKNHVMSEKRRRREKLNEMFLVLKSLVPSIHRVKNASILAETIAYLKELEKRVVELESSREPASR
Barley ANT2 (HM370319) AQESSNTKNHVISERRRREKLNEMFLILKSLVPSIHKVKASILAETIAYLRELEQKVEELESNRAPSRP
Arabidopsis TT8 (AJ277509) KRLPREDLSHVVAERRRREKLNEMFLITLRSMPVFTKMDKVSILGDTIAYVNHLLKRVHELENT

Wheat TaMYC1 (KJ747954) TAV RKRHEVGGKKVLARS KRKASELGGDDTER VLPKDDGLSSVINVTVDNEVLELLE
Rice RA (U39860) PLETRSR RRCREITGKKSAGAKRKAPAEVASDDTDG ERRHCVSNVNTIMDNKEVLELLE
Maize B (X57276) GGSGCVSKKVCVGSNSKRKSEFAGGAKHEHPVLPMD GTSNV TVTVSDTNVLELLE
Maize LC (M26227) PSETTTRLITRPSRGNNEVSRKEVCAGS KRKSPLEGRDDVERPVLTM DAGTSNV TVTVSDKDVLELLE
Barley ANT2 (HM370319) AGAAV RRHDAAAKMLAGS KRKASELGGDD GPNSVNVTVTEKEVLELLE
Arabidopsis TT8 (AJ277509) HHEQQHKRTRTC KRKTSE EVEVSIENDVLELLE

Wheat TaMYC1 (KJ747954) VQCRWKELLMTQVFDAIKSLRLDVLVSRVASTPDDLLALKIRAQFAGPGVETGMISEALQRAIRRP
Rice RA (U39860) LQCQWKELLMTRVFDIAIKVSLDVLVSVQASTSDGLLGLKIQAFASSAAVEPGMI TEALRKAIAS
Maize B (X57276) VQCRWKELLMTRVFDIAIKSLHLDALSVQASAPDGFMLRKTGAQFAGSGAVVPGMISQSLRKAIGKR
Maize LC (M26227) VQCRWEE LLMTRVFDIAIKSLHLDVLVSVQASAPDGFMLKIRAQFAGSGAVVPMI SEALRKAIGKR
Barley ANT2 (HM370319) VQCRWKE LLMTQVFDAIKSLRLDVLVSRVASTPDGLLALKIRAQFAGPGVETGMISEALQRAIRRP
Arabidopsis TT8 (AJ277509) MRC EYRDGLLLDILQVLHELGIETAVHTSVNDHDFEAEIRAKVRGKASIAEVKRAIHQVIHDTNLT