

Figure S1. Alignment of translated protein sequences from known orthologues of five trichome regulatory genes (GL1, GL2, EGL3, TTG1, TRY) in the *Brassic*s and *Arabidopsis*



GL2

	(1)	1	10	20	30	40	58	Section 1
A.thaliana	(1)	M	KSIDGCQCCSWPCFKLLNSKKLARDR	I	C	SMAVD	MSSKQPTKDFEFSSPALSLSLAGI	
B.napus-1	(1)	-	-	-	-	MMAVEM	MSSKQPTKDFEFSSPALSLSLAGI	
B.napus-2	(1)	-	-	-	-	MMAVEM	MSSKQPTKDFEFSSPALSLSLAGI	
B.oleracea	(1)	-	-	-	-	MSMETAVEM	MSSKQPTKDFEFSSPALSLSLAGI	
B.rapa	(1)	-	-	-	-	MMAVEM	MSSKQPTKDFEFSSPALSLSLAGI	
B.villosa	(1)	-	-	-	-	MMAVEM	MSSKQPTKDFEFSSPALSLSLAGI	
Consensus	(1)	-	-	-	-	MMAVEM	MSSKQPTKDFEFSSPALSLSLAGI	

	(59)	59	70	80	90	100	116	Section 2
A.thaliana	(59)	FRNASSSGSTNPEEDFLGRRV	V	DD	EDRTVEMSSSENSG	ETRSRS	EEEDLEGEDHDD	EEEEE
B.napus-1	(30)	FRNASSSGSTNPEEDFLGRRV	A	DD	EDRTVEMSSSENSG	ETRSRS	EDNLEGEEDDQ	EE---
B.napus-2	(30)	FRNASSSGSTNPEEDFLGRRV	A	DD	EDRTVEMSSSENSG	ETRSRS	KDNLEGEEDDQ	EE---
B.oleracea	(32)	FRNASSSGSTNPEEDFLGRRV	A	DD	EDRTVEMSSSENSG	ETRSRS	EDNLEGEEDDQ	EE---
B.rapa	(30)	FRNASSSGSTNPEEDFLGRRV	A	DD	EDRTVEMSSSENSG	ETRSRS	EDNLEGEEDDQ	EE---
B.villosa	(30)	FRNASSSGSTNPEEDFLGRRV	A	DD	EDRTVEMSSSENSG	ETRSRS	EDNLEGEEDDQ	EE---
Consensus	(59)	FRNASSSGSTNPEEDFLGRRV	A	DD	EDRTVEMSSSENSG	ETRSRS	EDNLEGEEDDQ	EEEEE

Homeobox Domain (96-151)

	(117)	117	130	140	150	160	174	Section 3
A.thaliana	(117)	EDGA	AGNKG	TN	KRKRKKYHRHTTDQIRHMEALFKE	TPHPDEKQRQQLSKQLGLAPRQV		
B.napus-1	(85)	---	DGAGNKG	N	KRKRKKYHRHTTDQIRHMEALFKE	TPHPDEKQRQQLSKQLGLAPRQV		
B.napus-2	(85)	---	DGAGNKG	N	KRKRKKYHRHTTDQIRHMEALFKE	TPHPDEKQRQQLSKQLGLAPRQV		
B.oleracea	(87)	---	DGAGNKG	N	KRKRKKYHRHTTDQIRHMEALFKE	TPHPDEKQRQQLSKQLGLAPRQV		
B.rapa	(86)	---	DGAGNKG	N	KRKRKKYHRHTTDQIRHMEALFKE	TPHPDEKQRQQLSKQLGLAPRQV		
B.villosa	(85)	---	DGAGNKG	N	KRKRKKYHRHTTDQIRHMEALFKE	TPHPDEKQRQQLSKQLGLAPRQV		
Consensus	(117)	DGAGNKG	N	KRKRKKYHRHTTDQIRHMEALFKE	TPHPDEKQRQQLSKQLGLAPRQV			

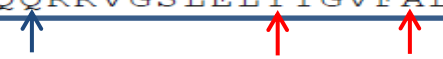
Homeobox Domain (96-151)

	(175)	175	180	190	200	210	220	232	Section 4
A.thaliana	(175)	KFWFQNRRTQIKAIQERHENSLLKAELEKLR	ENK	AMRESFSKAN	-	SSCP	PNCGGG	---	
B.napus-1	(140)	KFWFQNRRTQIKAIQERHENSLLKAELEKLR	ENK	AMRESFSKAN	S	SSCP	PNCGGGG	GGG	
B.napus-2	(140)	KFWFQNRRTQIKAIQERHENSLLKAELEKLR	ENK	AMRESFSKAN	S	SSCP	PNCGGGG	GGG	
B.oleracea	(142)	KFWFQNRRTQIKAIQERHENSLLKAELEKLR	ENK	AMRESFSKAN	S	SSCP	PNCGGGG	GGG	
B.rapa	(141)	KFWFQNRRTQIKAIQERHENSLLKAELEKLR	ENK	AMRESFSKAN	S	SSCP	PNCGGGG	GGG	
B.villosa	(140)	KFWFQNRRTQIKAIQERHENSLLKAELEKLR	ENK	AMRESFSKAN	S	SSCP	PNCGGGG	GGG	
Consensus	(175)	KFWFQNRRTQIKAIQERHENSLLKAELEKLR	ENK	AMRESFSKAN	S	SSCP	PNCGGGG	GGG	

	(233)	233	240	250	260	270	280	290	Section 5	
A.thaliana	(229)	---	PDDL	HLENT	SKLKAELDKLRAAI	GRT	PHYPLQASCSD	DDQ	EHRLGSLDFY	TGVFALEK
B.napus-1	(198)	---	GGSPDDL	HLENT	TKLKAELDKLRAAI	GRT	PHYPLQASCSD	DDQ	HRRVGSLELY	TGVFALEK
B.napus-2	(198)	---	GGSPDDL	HLENT	TKLKAELDKLRAAI	GRT	PHYPLQASCSD	DDQ	QRRVGSLELY	TGVFALEK
B.oleracea	(199)	---	GSPDDL	HLENT	TKLKAELDKLRAAI	GRT	PHYPLQASCSD	DDQ	HRRVGSLELY	TGVFALEK
B.rapa	(198)	---	AGSPDDL	LLENT	TKLKAELDKLRAAI	GRT	PHYPLQASCSD	DDQ	QRRVGSLELY	TGVFALEK
B.villosa	(197)	---	GGSPDDL	HLENT	TKLKAELDKLRAAI	GRT	PHYPLQASCSD	DDQ	QRRVGSLELY	TGVFALEK
Consensus	(233)	---	GGSPDDL	HLENT	TKLKAELDKLRAAI	GRT	PHYPLQASCSD	DDQ	QRRVGSLELY	TGVFALEK

START Domain (258-487)

GL2 orthologues and gene copies



GL2 (291) Section 6

START Domain (258-487)

	291	300	310	320	330	348
A.thaliana (284)	SRIAEISNRATLELQKMATSGEPLWLRSLVETGREILNYDEYLKEFPQAQASSFPGRKT					
B.napus-1 (256)	SRIVEIANRATLEVQKMATSGEPLWLRSLLETGREILNYDEYLKEFPQAQASSFHGRKT					
B.napus-2 (256)	SRIVEIANRATLEVQKMATSGEPLWLRSLLETGREILNYDEYLKEFPQAQASSFHGRKT					
B.oleracea (256)	SRIVEIANRATLEVQKMATSGEPLWLRSLLETGREILNYDEYLKEFPQAQASSFHGRKT					
B.rapa (256)	SRIVEIANRATLEVQKMATSGEPLWLRSLLETGREILNYDEYLKEFPQDQTSSFHGRKT					
B.villosa (254)	SRIVEIANRATLEVQKMATSGEPLWLRSLLETGREILNYDEYLKEFPQAQASSFHGRKT					
Consensus (291)	SRIVEIANRATLEVQKMATSGEPLWLRSLLETGREILNYDEYLKEFPQAQASSFHGRKT					

START Domain (258-487)

Section 7

	349	360	370	380	390	406
A.thaliana (342)	IEASRDAGIVFMDAHKLAQSFMDVGGQWKEVTFACLISKAATVVDVIRQEGEGPSRIDGAIQ					
B.napus-1 (314)	IEASRDVGVIVFMDAHKLAQSFMDVEQWKEVTFACLISKAATVVDVIRQEGEGPSRIDGAIQ					
B.napus-2 (314)	IEASRDVGVIVFMDAHKLAQSFMDVEQWKEVTFACLISKAATVVDVIRQEGEGPSRIDGAIQ					
B.oleracea (314)	IEASRDVGVIVFMDAHKLAQSFMDVEQWKEVTFACLISKAATVVDVIRQEGEGPSRIDGAIQ					
B.rapa (314)	IEASRDVGVIVFMDAHKLAQSFMDVEQWKEVTFACLISKAATVVDVIRQEGEGPSRIDGAIQ					
B.villosa (312)	IEASRDVGVIVFMDAHKLAQSFMDVEQWKEVTFACLISKAATVVDVIRQEGEGPSRIDGAIQ					
Consensus (349)	IEASRDVGVIVFMDAHKLAQSFMDVEQWKEVTFACLISKAATVVDVIRQEGEGPSRIDGAIQ					

START Domain (258-487)

Section 8

	407	420	430	440	450	464
A.thaliana (400)	LMFGEMQLLTPVVPVPTREVYFVRSRQLSPEKWAVIVDVSVSVEDSNTEK--EASLLKCR					
B.napus-1 (372)	LMFGEMQLLTPVVPVPTREVYFVRSRQLSPEKWAVIVDVSVSVEEDNNSTEKKEGSLRLCR					
B.napus-2 (372)	LMFGEMQLLTPVVPVPTREVYFVRSRQLSPEKWAVIVDVSVSMEEDNNNAE-KEGSLRLCR					
B.oleracea (372)	LMFGEMQLLTPVVPVPTREVYFVRSRQLSPEKWAVIVDVSVSVEEDNNSTEKKEGSLRLCR					
B.rapa (372)	LMFGEMQLLTPVVPVPTREVYFVRSRQLSPEKWAVIVDVSVSMEEDNNNAE-KEGSLRLCR					
B.villosa (370)	LMFGEMQLLTPVVPVPTREVYFVRSRQLSPEKWAVIVDVSVSVEEDNNSTEKKEGSLRLCR					
Consensus (407)	LMFGEMQLLTPVVPVPTREVYFVRSRQLSPEKWAVIVDVSVSVEEDNNSTEKKEGSLRLCR					

START Domain (258-487)

Section 9

	465	470	480	490	500	510	522
A.thaliana (456)	KLPSGCIIEDTSTNGHSHKVTWVEHLDVLSASTVQPLFRSLVNTGLAFGARHFWATLQLHC						
B.napus-1 (430)	KRPSGCIIEDTSTNGHSHKVTWVEHLDLSASTVQPLFRSFVNTGLAFGARHFWATLQLHC						
B.napus-2 (429)	KRPSGCIIEDTSTNGHSHKVTWVEHLDLSASTVQPLFRSFVNTGLAFGARHFWATLQLHC						
B.oleracea (430)	KRPSGCIIEDTSTNGHSHKVTWVEHLDLSASTVQPLFRSFVNTGLAFGARHFWATLQLHC						
B.rapa (429)	KRPSGCIIEDTSTNGHSHKVTWVEHLDLSASTVQPLFRSFVNTGLAFGARHFWATLQLHC						
B.villosa (428)	KRPSGCIIEDTSTNGHSHKVTWVEHLDLSASTVQPLFRSFVNTGLAFGARHFWATLQLHC						
Consensus (465)	KRPSGCIIEDTSTNGHSHKVTWVEHLDLSASTVQPLFRSFVNTGLAFGARHFWATLQLHC						

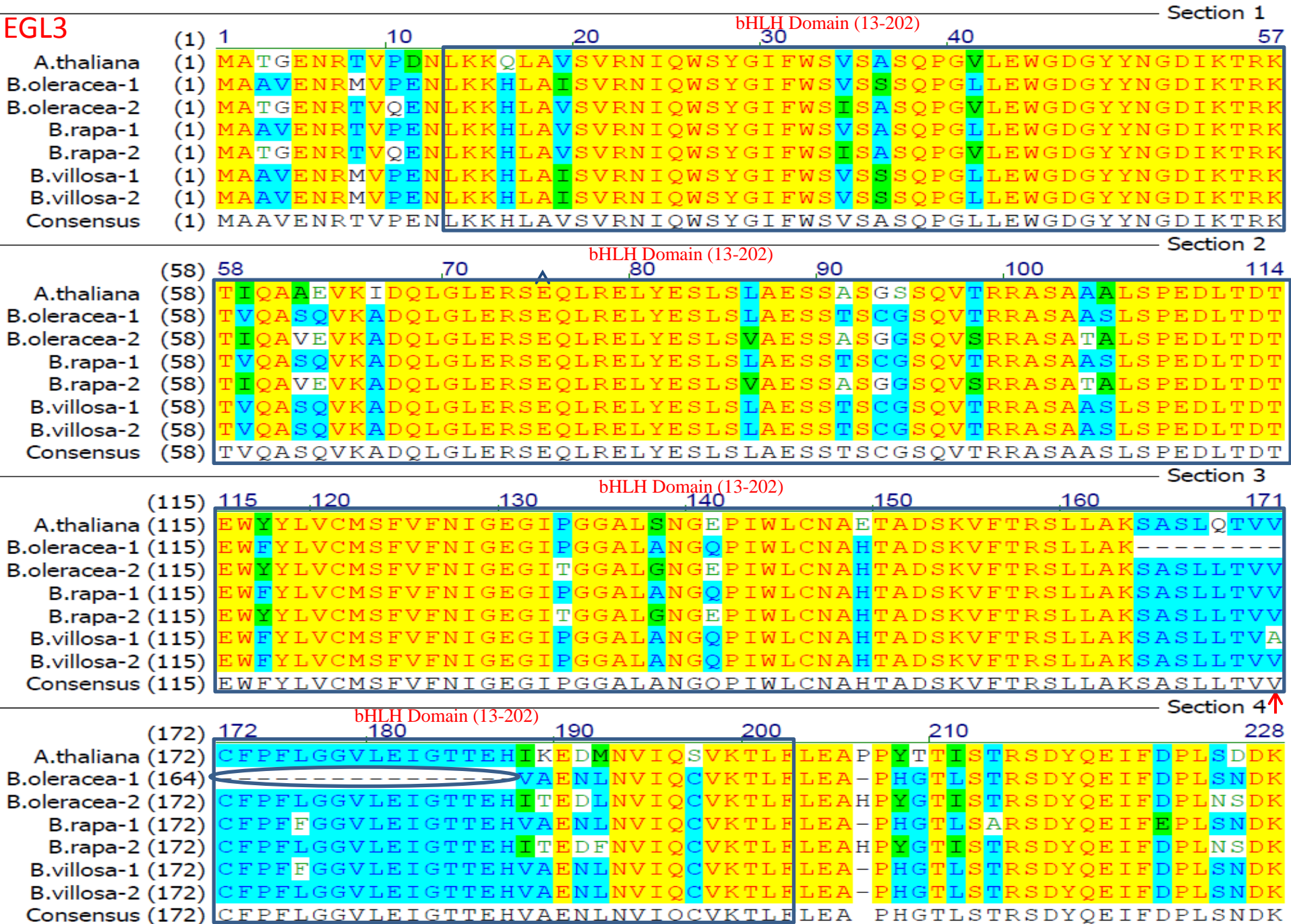
Section 10

	523	530	540	550	560	570	580
A.thaliana (514)	ERLVFFMATNVPTKDSLGVTTLAGRKSVLKMAQRMTQSFYRAIAASSYHQWTKITTKT						
B.napus-1 (488)	ERLVFFMATNVPTKDSLGVTTLAGRKSVLKMAQRMTQSFYRAIAASSYHQWVTKITTKT						
B.napus-2 (487)	ERLVFFMATNVPTKDSLGVTTLAGRKSVLKMAQRMTQSFYRAIAASSYHQWVTKITTKT						
B.oleracea (488)	ERLVFFMATNVPTKDSLGVTTLAGRKSVLKMAQRMTQSFYRAIAASSYHQWVTKITTKT						
B.rapa (487)	ERLVFFMATNVPTKDSLGVTTLAGRKSVLKMAQRMTQSFYRAIAASSYHQWVTKITTKT						
B.villosa (486)	ERLVFFMATNVPTKDSLGVTTLAGRKSVLKMAQRMTQSFYRAIAASSYHQWVTKITTKT						
Consensus (523)	ERLVFFMATNVPTKDSLGVTTLAGRKSVLKMAQRMTQSFYRAIAASSYHQWVTKITTKT						

GL2 orthologues and gene copies

GL2		Section 11																												
	(581)	581	590	600	610	620	630	640	650	660	638																			
A.thaliana	(572)	GQDMRVSSRKNLHDPGEPTGVIVCASSSLWLPVSP	A	LLFDFFRDE	A	RRHEWDALSNGA																								
B.napus-1	(546)	GQDMRVSSRKNLHDPGEPTGVIVCASSSLWLPVSP	T	LLFDFFRDE	T	RRHEWDALSNGA																								
B.napus-2	(545)	GQDMRVSSRKNLHDPGEPTGVIVCASSSLWLPVSP	T	LLFDFFRDE	T	RRHEWDALSNGA																								
B.oleracea	(546)	GQDMRVSSRKNLHDPGEPTGVIVCASSSLWLPVSP	T	LLFDFFRDE	T	RRHEWDALSNGA																								
B.rapa	(545)	GQDMRVSSRKNLHDPGEPTGVIVCASSSLWLPVSP	T	LLFDFFRDE	T	RRHEWDALSNGA																								
B.villosa	(544)	GQDMRVSSRKNLHDPGEPTGVIVCASSSLWLPVSP	T	LLFDFFRDE	T	RRHEWDALSNGA																								
Consensus	(581)	GQDMRVSSRKNLHDPGEPTGVIVCASSSLWLPVSP	T	LLFDFFRDE	T	RRHEWDALSNGA																								
		Section 12																												
	(639)	639	650	660	670	680	690	700	710	720	696																			
A.thaliana	(630)	HVQSI	AN	LSKGQDRGNSV	A	IQTVKSREKS	I	WVLQDS	S	TNSYESVVVYAPVDINTTQ	LV																			
B.napus-1	(604)	HVQSI	VS	LSKGQDRGNSV	S	IQTVKSREKS	T	WVLQDS	C	TNSYESVVVYAPVDINTTQ	LV																			
B.napus-2	(603)	HVQSI	VS	LSKGQDRGNSV	S	IQTVKSREKS	T	WVLQDS	C	TNSYESVVVYAPVDINTTQ	MV																			
B.oleracea	(604)	HVQSI	VS	LSKGQDRGNSV	S	IQTVKSREKS	T	WVLQDS	C	TNSYESVVVYAPVDINTTQ	LV																			
B.rapa	(603)	HVQSI	VS	LSKGQDRGNSV	S	IQTVKSREKS	T	WVLQDS	C	TNSYESVVVYAPVDINTTQ	MV																			
B.villosa	(602)	HVQSI	VS	LSKGQDRGNSV	S	IQTVKSREKS	T	WVLQDS	C	TNSYESVVVYAPVDINTTQ	LV																			
Consensus	(639)	HVQSI	VS	LSKGQDRGNSV	S	IQTVKSREK	S	TWVLQDS	C	TNSYESVVVYAPVDINTTQ	LV																			
		Section 13																												
	(697)	697	710	720	730	740	750	760	770	780	754																			
A.thaliana	(688)	L	AGHDPSNIQILP	S	GFSIIPDGVESR	P	LVI	T	S	T	Q	D	-	DRNS	S	QGGSLLT	L	L	A	L	Q	T	L	I	N	P	S	P		
B.napus-1	(662)	I	AGHDPSNIQILP	C	GFSIIPDGVESR	Q	LVI	S	S	A	Q	E	-	DRNT	T	QGGSLLT	L	L	A	L	Q	T	L	V	N	Q	S	P		
B.napus-2	(661)	I	AGHDPSNIQILP	C	GFSIIPDGVESR	Q	LVI	S	S	A	Q	E	A	DRNT	T	QGGSLLT	M	L	A	L	Q	T	L	V	N	Q	S	P		
B.oleracea	(662)	I	AGHDPSNIQILP	C	GFSIIPDGVESR	Q	LVI	S	S	A	Q	E	-	D	K	N	T	QGGSLLT	L	L	A	L	Q	T	L	V	N	Q	S	P
B.rapa	(661)	I	AGHDPSNIQILP	C	GFSIIPDGVESR	Q	LVI	S	S	A	Q	E	A	DRNT	T	QGGSLLT	M	L	A	L	Q	T	L	V	N	Q	S	P		
B.villosa	(660)	I	AGHDPSNIQILP	C	GFSIIPDGVESR	Q	LVI	S	S	A	Q	E	-	DRNT	T	QGGSLLT	L	L	A	L	Q	T	L	V	N	Q	S	P		
Consensus	(697)	I	AGHDPSNIQILP	C	GFSIIPDGVESR	Q	LVI	S	S	A	Q	E	-	DRNT	T	QGGSLLT	L	L	A	L	Q	T	L	V	N	Q	S	P		
		Section 14																												
	(755)	755	760	770	786																									
A.thaliana	(745)	AAKLNMESVESVTNLVSVTLHNIKR	S	LQIEDC																										
B.napus-1	(719)	AAKLNMESVESVTNLVSVTLHNIKR	S	LQIEDC																										
B.napus-2	(719)	AAKLNMESVESVTNLVSVTLHNIKR	C	LQIEDC																										
B.oleracea	(719)	AAKLNMESVESVTNLVSVTLHNIKR	S	LQIEDC																										
B.rapa	(719)	AAKLNMESVESVTNLVSVTLHNIKR	C	LQIEDC																										
B.villosa	(717)	AAKLNMESVESVTNLVSVTLHNIKR	S	LQIEDC																										
Consensus	(755)	AAKLNMESVESVTNLVSVTLHNIKR	S	LQIEDC																										

GL2 orthologues and gene copies



EGL3 orthologues and gene copies

EGL3 Section 9

Helix-Loop-Helix DNA binding Domain (403-487)

	(457)	457	470	480	490	500	513
A.thaliana (446)	YLQD	LQKRVQE	LESCRES	ADTETRI	TMMKR	RKKPD	DEEERASANCMNSKRKKGSDVNVG
B.oleracea-1 (426)	YLQE	LQRRVQE	LESCRES	IDTEMRMAMK	-RKKPD	GEDES	SASANCLNNKRKE--SDMG
B.oleracea-2 (455)	YLQE	LQRRVQE	LESCRE	YTDTEM	QMPMK	-RKKPE	DEDERASANCLNTKRKESDVNVG
B.rapa-1 (449)	YLQE	LQRRVQE	LESCRES	TDTEMRMAMK	-RKKPD	GEDES	SASANCLNNKRKE--SDIG
B.rapa-2 (456)	YLQE	LQRRVQE	LESCRE	YTDTEM	QMPMK	-RKKPE	DDERASANCLNTKRKESDVNVG
B.villosa-1 (450)	YLQE	LQRRVQE	LESCRES	IDTEMRMAMK	-RKKPD	GEDES	SASANCLNNKRKE--SDMG
B.villosa-2 (393)	LQTH	LKITCLR	LGMKPG	TMPCPRGNA	ER	-S	-----
Consensus (457)	YLQEL	LQRRVQE	LESCRES	DTEMRMAMK	RKKPD	EDE	ASANCLNKRKEVG

Section 10

	(514)	514	520	530	540	550	560	570
A.thaliana (503)	EDEPAD	-I	GYAGLTDNLRIS	SLGNEVVIELRC	AWREGILLE	IMDVIS	DLNLD	SHSVQ
B.oleracea-1 (480)	EDEPAD	-	TGYAGLTDNLRIGS	FGNEVVIELRC	AWREGILLE	IMDVIS	DLNLD	SHSVQ
B.oleracea-2 (511)	EDEPAD	-	TGYAGLTDNLRIGS	FGNEVVIELRC	AWREGILLE	IMDVIS	H	LNLD
B.rapa-1 (503)	EDEPAD	-	TGYAGLTDNLRIGS	FGNEGVIELRC	AWREGILLE	IMDVIS	DLNLD	SHSVQ
B.rapa-2 (512)	EDEPAD	D	TGYAGLTDNLS	IGSFGNEVVIELRC	AWREGILLE	IMDVIS	H	LNLD
B.villosa-1 (504)	EDEPAD	-	TGYAGLTDNLRIGS	FGNEVVIELRC	AWREGI	V	LEIMDVIS	DLNLD
B.villosa-2 (422)	-----	-----	-----	-----	-----	-----	-----	-----
Consensus (514)	EDEPAD		TGYAGLTDNLRIGS	FGNEVVIELRC	AWREGILLE	IMDVIS	DLNLD	SHSVQ

Section 11

	(571)	571	580	590	608
A.thaliana (559)	SSTGDGLLCLTVNCKHKG	TKIATTGMIQ	EALQ	RVAWIC	
B.oleracea-1 (536)	SSTGDGLLCLTVNCKHKG	TKIATTGMIQ	DALQ	RVAWIC	
B.oleracea-2 (567)	SSTGDGLLCLTVNCKHKG	TNIATAGMIQ	EALQ	RVAWIC	
B.rapa-1 (559)	SSTGDGLLCLTVNCKHKG	TKIATTGMIQ	DALQ	RVAWIC	
B.rapa-2 (569)	SSTGDGLLCLTVNCKHKG	TNIATAGMIQ	EALQ	RVAWIC	
B.villosa-1 (560)	SSTGDGLLCLTVNCKHKG	TKIATTGMIQ	DALQ	RVAWIC	
B.villosa-2 (422)	-----	-----	-----	-----	-----
Consensus (571)	SSTGDGLLCLTVNCKHKG	TKIATTGMIQ	DALQ	RVAWIC	

EGL3 orthologues and gene copies

		Section 1																																																								
TTG-1		(1)	1	10	20	30	40	57																																																		
A.thaliana	(1)	MDNSAPDSL	S	RSETAVTYDSPYPLYAM	A	FSS	LRSSSG	GHRIAVG	SFLEDYNNRIDILS																																																	
B.napus-1	(1)	MDNSAPDSL	LRSETAVTYDSPYPLYAM	S	FSS	---	---	THRIAVG	SFLEDYNNRIDILS																																																	
B.napus-2	(1)	MDNSAPDSL	LRSETAVTYDSPYPLYAM	S	FSS	---	---	THRIAVG	SFLEDYNNRIDILS																																																	
B.napus-3	(1)	MDNSAPDSL	LRSETAVTYDSPYPLYAM	S	FSS	---	---	THRIAVG	SFLEDYNNRIDILS																																																	
B.napus-4	(1)	MDNSAPDSL	LRSETAVTYDSPYPLYAM	S	FSS	---	---	THRIAVG	SFLEDYNNRIDILS																																																	
B.napus-5	(1)	MDNSAPDSL	LRSETAVTYDSPYPLYAM	S	FSS	---	---	THRIAVG	SFLEDYNNRIDILS																																																	
B.napus-6	(1)	MDNSAPDSL	LRSETAVTYDSPYPLYAM	S	FSS	---	---	THRIAVG	SFLEDYNNRIDILS																																																	
B.oleracea-1	(1)	MDNSAPDSL	LRSETAVTYDSPYPLYAM	S	FSS	---	---	THRIAVG	SFLEDYNNRIDILS																																																	
B.oleracea-2	(1)	---	---	---	---	---	---	---	---																																																	
B.rapa	(1)	MDNSAPDSL	LRSETAVTYDSPYPLYAM	S	FSS	---	---	THRIAVG	SFLEDYNNRIDILS																																																	
B.villosa	(1)	MDN	A	APDSL	LRSETAVTYDSPYPLYAM	S	FSS	---	---	THRIAVG	SFLEDYNNRIDILS																																															
Consensus	(1)	MDNS	A	APDSL	LRSETAVTYDSPYPLYAM	S	FSS	---	---	THRIAVG	SFLEDYNNRIDILS																																															
		Section 2																																																								
		(58)	58	70	80	90	100	114																																																		
A.thaliana	(58)	FDS	DSM	T	V	KPLP	N	LSFEHPYPPTKL	M	F	S	PPSLR	R	PSS	S	G	DLLASSG	G	D	FLR	L	W	E	I	N	E	D	S																														
B.napus-1	(54)	FDS	DSM	S	L	KPLP	S	LSFEHPYPPTKL	M	F	S	PPSLR	R	R	S	G	G	DLLASSG	G	D	FLR	L	W	E	V	N	E	D	S																													
B.napus-2	(54)	FDS	DSM	S	L	KPLP	S	LSFEHPYPPTKL	M	F	S	PPSLR	R	R	S	G	G	DLLASSG	G	D	FLR	L	W	E	V	N	E	D	S																													
B.napus-3	(54)	FDS	DSM	S	L	KPLP	S	LSFEHPYPPTKL	M	F	S	PPSLR	R	R	S	G	G	DLLASSG	G	D	FLR	L	W	E	V	N	E	D	S																													
B.napus-4	(54)	FDS	DSM	S	L	KPLP	S	LSFEHPYPPTKL	M	F	S	PPSLR	R	R	S	G	G	DLLASSG	G	D	FLR	L	W	E	V	N	E	D	S																													
B.napus-5	(54)	FDS	DSM	S	L	KPLP	S	LSFEHPYPPTKL	M	F	S	PPSLR	R	R	S	G	G	DLLASSG	G	D	FLR	L	W	E	V	N	E	D	S																													
B.napus-6	(54)	FDS	DSM	S	L	KPLP	S	LSFEHPYPPTKL	M	F	S	PPSLR	R	R	S	G	G	DLLASSG	G	D	FLR	L	W	E	V	N	E	D	S																													
B.oleracea-1	(54)	FDS	DSM	S	L	KPLP	S	LSFEHPYPPTKL	M	F	S	PPSLR	R	R	S	G	G	DLLASSG	G	D	FLR	L	W	E	V	N	E	D	S																													
B.oleracea-2	(1)	---	---	---	---	---	---	---	M	F	I	PPSLR	L	P	S	G	-	DLLASSG	G	D	FLR	F	L	E	I	K	R	L	H																													
B.rapa	(54)	FDS	DSM	S	L	KPLP	S	LSFEHPYPPTKL	M	F	S	PPSLR	R	R	S	G	G	DLLASSG	G	D	FLR	L	W	E	V	N	E	D	S																													
B.villosa	(54)	FDS	DSM	S	L	KPLP	S	LSFEHPYPPTKL	M	F	S	PPSLR	R	R	S	G	G	DLLASSG	G	D	FLR	L	W	E	V	N	E	D	S																													
Consensus	(58)	FDS	DSM	S	L	KPLP	S	LSFEHPYPPTKL	M	F	S	PPSLR	R	R	S	G	G	DLLASSG	G	D	FLR	L	W	E	V	N	E	D	S																													
		Section 3																																																								
		(115)	115	120	130	140	150	160	171																																																	
A.thaliana	(115)	S	T	V	E	P	I	S	V	L	N	N	S	K	T	S	E	F	C	A	P	L	T	S	F	D	W	N	D	V	E	P	K	R	L	G	T	C	S	I	D	T	T	C	T	I	W	D	I	E	K	S	V	V	E	T	Q	L
B.napus-1	(111)	S	S	A	E	P	V	S	V	L	N	N	S	K	T	S	E	F	C	A	P	L	T	S	F	D	W	N	D	V	E	P	K	R	L	G	T	C	S	I	D	T	T	C	T	I	W	D	V	E	R	S	V	V	E	T	Q	L
B.napus-2	(111)	S	S	A	E	P	V	S	V	L	N	N	S	K	T	S	E	F	C	A	P	L	T	S	F	D	W	N	D	V	E	P	K	R	L	G	T	C	S	I	D	T	T	C	T	I	W	D	V	E	R	S	V	V	E	T	Q	L
B.napus-3	(111)	S	S	A	E	P	V	S	V	L	N	N	S	K	T	S	E	F	C	A	P	L	T	S	F	D	W	N	D	V	E	P	K	R	L	G	T	C	S	I	D	T	T	C	T	I	W	D	V	E	R	S	V	V	E	T	Q	L
B.napus-4	(111)	S	S	A	E	P	V	S	V	L	N	N	S	K	T	S	E	F	C	A	P	L	T	S	F	D	W	N	D	V	E	P	K	R	L	G	T	C	S	I	D	T	T	C	T	I	W	D	V	E	R	S	V	V	E	T	Q	L
B.napus-5	(111)	S	S	A	E	P	V	S	V	L	N	N	S	K	T	S	E	F	C	A	P	L	T	S	F	D	W	N	D	V	E	P	K	R	L	G	T	C	S	I	D	T	T	C	T	I	W	D	V	E	R	S	V	V	E	T	Q	L
B.napus-6	(111)	S	S	A	E	P	V	S	V	L	N	N	S	K	T	S	E	F	C	A	P	L	T	S	F	D	W	N	D	V	E	P	K	R	L	G	T	C	S	I	D	T	T	C	T	I	W	D	V	E	R	S	V	V	E	T	Q	L
B.oleracea-1	(111)	S	S	A	E	P	V	S	V	L	N	N	S	K	T	S	E	F	C	A	P	L	T	S	F	D	W	N	D	V	E	P	K	R	L	G	T	C	S	I	D	T	T	C	T	I	W	D	V	E	R	S	V	V	E	T	Q	L
B.oleracea-2	(32)	H	R	Q	-	P	-	-	-	-	-	-	R	E	C	P	Q	Q	V	R	A	V	N	L	L	R	L	E	R	H	R	R	K	R	L	R	T	C	N	I	H	T	T	C	T	I	W	D	V	E	K	A	V	V	E	A	Q	L
B.rapa	(111)	S	S	A	E	P	V	S	V	L	N	N	S	K	T	S	E	F	C	A	P	L	T	S	F	D	W	N	D	V	E	P	K	R	L	G	T	C	S	I	D	T	T	C	T	I	W	D	V	E	R	S	V	V	E	T	Q	L
B.villosa	(111)	S	S	A	E	P	V	S	V	L	N	N	S	K	T	S	E	F	C	A	P	L	T	S	F	D	W	N	D	V	E	P	K	R	L	G	T	C	S	I	D	T	T	C	T	I	W	D	V	E	R	S	V	V	E	T	Q	L
Consensus	(115)	S	S	A	E	P	V	S	V	L	N	N	S	K	T	S	E	F	C	A	P	L	T	S	F	D	W	N	D	V	E	P	K	R	L	G	T	C	S	I	D	T	T	C	T	I	W	D	V	E	R	S	V	V	E	T	Q	L

TTG1 orthologues and gene copies

TRY

Section 1

	(1)	1	10	20	30	40	57
A.thaliana	(1)	-----	-----	-----	-----	-----	MDNT
B.napus	(1)	-----	-----	-----	-----	-----	MDNT
B.oleracea-1	(1)	-----	-----	-----	-----	-----	MDNT
B.oleracea-2	(1)	-----	-----	-----	-----	-----	MDNT
B.oleracea-3	(1)	MDNTDRRCRRKQHKATLHDSEGPLSIPYIILTWYFTCLHNCSWVAHLGSSICERPQI					
B.rapa-1	(1)	-----	-----	-----	-----	-----	-----
B.rapa-2	(1)	-----	-----	-----	-----	-----	-----
B.rapa-3	(1)	-----	-----	-----	-----	-----	MDNT
B.villosa-1	(1)	-----	-----	-----	-----	-----	MDNT
B.villosa-2	(1)	-----	-----	-----	-----	-----	-----
Consensus	(1)	-----	-----	-----	-----	-----	MDNT

Section 2

R3 MYB_DNA binding Domain (86-125)

	(58)	58	70	80	90	100	114
A.thaliana	(5)	DRRRRRKQHKIA	LHDSEEVS	SIIEWEFIN	MTEQEEDLI	FRMYRLVGDR	WDLIAGRVP
B.napus	(5)	DRRRRRKQHKVT	LHDSEEVS	SIIEWEFIN	MTEQEEDLI	FRMHRLVGDR	WDLIAGRVP
B.oleracea-1	(5)	NRRRRSKQHKT	LEDSEEVS	SIIEWKFIN	MTEQEEDLI	LRMYRLVGDR	WDLIAGRVP
B.oleracea-2	(5)	DRRRRRKQQKVS	LHDSEEVS	SIIEWEFIN	MTEQEEDLI	CRMYRLVGDR	WDLIAGRVP
B.oleracea-3	(58)	LPLRALVENNANEH	AVLKVSS	SIIEWEFIN	MTEQEEDLI	FRMHRLVGDR	WDLIAGRVP
B.rapa-1	(1)	-----	-----	-----	MTEQEEDI	LRMYRLVGDR	WDLIAGRVP
B.rapa-2	(1)	-----	-----	-----	MSQQEEDLI	LRMYRLVGDR	WEIAGRVP
B.rapa-3	(5)	DRRRRRKQQKVT	LHDSEEVS	SIIEWEFIN	MTEQEEDLI	CRMYRLVGDR	-----
B.villosa-1	(5)	DRRRRRKQHKT	LHDSEEVS	SIIEWEFIN	MTEQEEDLI	FRMHRLVGDR	WDLIAGRVP
B.villosa-2	(1)	-----	-----	-----	MTEQEEDLI	FRMHRLVGDR	WDLIAGRVP
Consensus	(58)	DRRRRRKQ KVT	LHDSEEVS	SIIEWEFIN	MTEQEEDLI	FRMYRLVGDR	WDLIAGRVP

Section 3

R3 MYB_DNA binding Domain (86-125)

	(115)	115	120	130	140	150	160
A.thaliana	(62)	RQPEEIERYWIMRNS	EGFADKRR	-QLHSSSHK	H	TKPHRPRFSIYPS	
B.napus	(62)	RQPEEIERYWIMRNS	DGFAEKRRQL	LHSSSHKS	S	TKPHRPRFSIYPS	
B.oleracea-1	(62)	RQPEEIERFWIMRNS	DSFAEKRLQL	LHSSSHKNN	NKLHRPRPSIYPS		
B.oleracea-2	(62)	RQPEEIERYWIMRNS	DGFAEKRR	-QLHSSSHKN	TKPYRPRFSVYPS		
B.oleracea-3	(115)	RQPEEIERYWIMRNS	DGFAEKRRQL	LHSSSHKS	S	TKPHRPRFSIYPS	
B.rapa-1	(30)	RQPEEIERYWIMRNS	DSFAEKRLQL	LHSSSHKNN	NKLHRPRPSIYPS		
B.rapa-2	(30)	RKAVEIERYWIMRNS	THEIPSSK	F	-----		
B.rapa-3	(52)	-----	-----	-----	-----		
B.villosa-1	(62)	RQPEEIERYWIMRNS	DGFAEKRRQL	LHSSSHKS	S	TKPHRPSFSIYPS	
B.villosa-2	(30)	RQPEEIERYWIMRNS	DGFAEKRRQL	LHSSSHKS	S	TKPHRPSFSIYPS	
Consensus	(115)	RQPEEIERYWIMRNS	DGFAEKRRQL	LHSSSHK	TKPHRPRFSIYPS		

TRY orthologues and gene copies

