Table S1. Pairwise interaction of MBW components in Arabidopsis (*A. thaliana*)

ProtA fusion	Luciferase fusion	Pulldown/input ratio (%)		References
AtTTG1	AtTTG1	0.35±0.00	-	(Baudry, et al. 2004)
AtTTG1	AtGL3	27.43±0.02	+	(Payne, et al. 2000; Zhang, et al. 2003; Zhao, et al. 2008)
AtTTG1	AtEGL3	10.58±0.12	+	(Zhang, et al. 2003)
AtTTG1	AtTT8	4.79±0.03	+	(Baudry, et al. 2004; Baudry, et al. 2006)
AtTTG1	AtMYC1	59.70±1.09	+	(Symonds, et al. 2011; Pesch, et al. 2013)
AtTTG1	AtGL1	0.67±0.00	-	(Symonds, et al. 2011)
AtTTG1	AtWER	0.60±0.00	-	This work
AtTTG1	AtPAP1	0.31±0.00	-	This work
AtTTG1	AtPAP2	0.63±0.00	-	This work
AtTTG1	AtTT2	1.95±0.05	w	(Baudry, et al. 2004; Baudry, et al. 2006)
AtTTG1	AtMYB61	0.61±0.00	-	This work
AtTTG1	w/o	0.55±0.01	-	This work
AtGL3	AtTTG1	8.45±0.05	+	(Payne, et al. 2000; Zhang, et al. 2003; Zhao, et al. 2008)
AtGL3	AtGL3	5.44±0.04	+	(Payne, et al. 2000; Bernhardt, et al. 2003; Zhang, et al. 2003)
AtGL3	AtEGL3	2.70±0.01	+	(Zhang, et al. 2003)
AtGL3	AtTT8	2.71±0.00	+	This work
AtGL3	AtMYC1	2.59±0.03	+	(Zhao, et al. 2012)[1]
AtGL3	AtGL1	47.21±2.18	+	(Payne, et al. 2000; Zhang, et al. 2003; Morohashi, et al. 2007; Zhao, et al. 2008; Morohashi and Grotewold 2009; Pesch, et al. 2013)
AtGL3	AtWER	78.89±3.23	+	(Bernhardt, et al. 2003; Zimmermann, et al. 2004; Tominaga, et al. 2007)
AtGL3	AtPAP1	29.99±1.17	+	(Zhang, et al. 2003; Baudry, et al. 2006)
AtGL3	AtPAP2	22.59±2.14	+	(Zhang, et al. 2003)
AtGL3	AtTT2	33.40±3.09	+	(Baudry, et al. 2006)
AtGL3	AtMYB61	2.17±0.35	w	This work
AtGL3	w/o	0.48±0.04	-	This work
AtEGL3	AtTTG1	8.40±0.15	+	(Zhang, et al. 2003)
AtEGL3	AtGL3	3.21±0.06	+	(Zhang, et al. 2003)
AtEGL3	AtEGL3	2.89±0.02	+	(Bernhardt, et al. 2003; Zhang, et al. 2003)
AtEGL3	AtTT8	4.09±0.01	+	This work
AtEGL3	AtMYC1	2.25±0.02	w	This work
AtEGL3	AtGL1	10.44±0.10	+	(Zhang, et al. 2003; Zimmermann, et al. 2004; Morohashi, et al. 2007)
AtEGL3	AtWER	7.19±0.13	+	(Zimmermann, et al. 2004; Tominaga, et al. 2007)

AtEGL3	AtPAP1	7.85±0.06	+	(Zimmermann, et al. 2004; Baudry, et al. 2006)
AtEGL3	AtPAP2	6.25±0.04	+	(Zhang, et al. 2003; Zimmermann, et al. 2004)
AtEGL3	AtTT2	7.38±0.02	+	(Zimmermann, et al. 2004; Baudry, et al. 2006)
AtEGL3	AtMYB61	2.33±0.05	w	This work
AtEGL3	w/o	0.45±0.00	-	This work
AtTT8	AtTTG1	4.32±0.13	+	(Baudry, et al. 2004)
AtTT8	AtGL3	3.13±0.16	+	This work
AtTT8	AtEGL3	2.66±0.08	+	This work
AtTT8	AtTT8	2.94±0.04	+	(Baudry, et al. 2004)[2]
AtTT8	AtMYC1	2.23±0.01	w	This work
AtTT8	AtGL1	3.72±0.05	+	(Zimmermann, et al. 2004)
AtTT8	AtWER	2.28±0.01	w	(Zimmermann, et al. 2004)
AtTT8	AtPAP1	15.91±0.12	+	(Zimmermann, et al. 2004)
AtTT8	AtPAP2	15.69±0.11	+	(Zimmermann, et al. 2004)
AtTT8	AtTT2	18.99±0.12	+	(Baudry, et al. 2004; Zimmermann, et al. 2004; Baudry, et al. 2006)
AtTT8	AtMYB61	2.13±0.03	w	This work
AtTT8	w/o	0.55±0.00	-	This work
AtMYC1	AtTTG1	31.75±1.89	+	(Symonds, et al. 2011; Pesch, et al. 2013)
AtMYC1	AtGL3	2.39±0.30	+	(Zhao, et al. 2012)[1]
AtMYC1	AtEGL3	2.30±0.04	w	This work
AtMYC1	AtTT8	2.39±0.03	w	This work
AtMYC1	AtMYC1	3.06±0.04	+	(Zhao, et al. 2012)[3]
AtMYC1	AtGL1	21.17±0.12	+	(Zimmermann, et al. 2004; Zhao, et al. 2012; Pesch, et al. 2013)
AtMYC1	AtWER	11.54±0.19	+	(Zimmermann, et al. 2004; Zhao, et al. 2012)
AtMYC1	AtPAP1	17.20±0.60	+	(Zimmermann, et al. 2004)
AtMYC1	AtPAP2	15.34±0.31	+	(Zimmermann, et al. 2004)
AtMYC1	AtTT2	18.26±1.37	+	(Zimmermann, et al. 2004)
AtMYC1	AtMYB61	2.36±0.23	w	This work
AtMYC1	w/o	0.57±0.00	-	This work
AtGL1	AtTTG1	0.58±0.00	-	(Symonds, et al. 2011)
AtGL1	AtGL3	19.61±0.59	+	(Payne, et al. 2000; Zhang, et al. 2003; Morohashi, et al. 2007; Zhao, et al. 2008; Morohashi and Grotewold 2009; Pesch, et al. 2013)
AtGL1	AtEGL3	17.76±0.75	+	(Zhang, et al. 2003; Zimmermann, et al. 2004)

AtGL1	AtTT8	26.51±1.66	+	(Zimmermann, et al. 2004)
AtGL1	AtMYC1	22.61±0.30	+	(Zimmermann, et al. 2004; Zhao, et al. 2012; Pesch, et al. 2013)
AtGL1	AtGL1	1.81±0.05	w	(Liang, et al. 2014)
AtGL1	AtWER	0.61±0.01	-	This work
AtGL1	AtPAP1	0.63±0.00	-	This work
AtGL1	AtPAP2	0.59±0.03	-	This work
AtGL1	AtTT2	0.58±0.01	-	This work
AtGL1	AtMYB61	0.54±0.02	-	This work
AtGL1	w/o	0.57±0.02	-	This work
AtWER	AtTTG1	0.60±0.00	-	This work
AtWER	AtGL3	16.56±0.32	+	(Bernhardt, et al. 2003; Zimmermann, et al. 2004; Tominaga, et al. 2007)
AtWER	AtEGL3	19.88±0.74	+	(Zimmermann, et al. 2004; Tominaga, et al. 2007)
AtWER	AtTT8	2.44±0.98	w	(Zimmermann, et al. 2004)
AtWER	AtMYC1	14.42±0.29	+	(Zimmermann, et al. 2004; Zhao, et al. 2012)
AtWER	AtGL1	0.62±0.03	-	This work
AtWER	AtWER	0.61±0.04	-	This work
AtWER	AtPAP1	0.63±0.03	-	This work
AtWER	AtPAP2	0.60±0.02	-	This work
AtWER	AtTT2	0.58±0.00	-	This work
AtWER	AtMYB61	0.57±0.01	-	This work
AtWER	w/o	0.58±0.00	-	This work
AtPAP1	AtTTG1	0.61±0.01	-	This work
AtPAP1	AtGL3	19.93±0.23	+	(Zhang, et al. 2003; Baudry, et al. 2006)
AtPAP1	AtEGL3	22.60±0.79	+	(Zimmermann, et al. 2004; Baudry, et al. 2006)
AtPAP1	AtTT8	25.83±0.85	+	(Zimmermann, et al. 2004)
AtPAP1	AtMYC1	17.15±0.59	+	(Zimmermann, et al. 2004)
AtPAP1	AtGL1	0.65±0.01	-	This work
AtPAP1	AtWER	0.61±0.01	-	This work
AtPAP1	AtPAP1	0.63±0.02	-	This work
AtPAP1	AtPAP2	0.60±0.04	-	This work
AtPAP1	AtTT2	0.58±0.02	-	(Baudry, et al. 2006)
AtPAP1	AtMYB61	0.62±0.03	-	This work
AtPAP1	w/o	0.57±0.02	-	This work

AtPAP2	AtTTG1	0.94±0.08	-	This work
AtPAP2	AtGL3	19.56±0.41	+	(Zhang, et al. 2003)
AtPAP2	AtEGL3	12.44±0.17	+	(Zhang, et al. 2003; Zimmermann, et al. 2004)
AtPAP2	AtTT8	35.22±0.39	+	(Zimmermann, et al. 2004)
AtPAP2	AtMYC1	17.15±0.99	+	(Zimmermann, et al. 2004)
AtPAP2	AtGL1	0.65±0.01	-	This work
AtPAP2	AtWER	0.60±0.01	-	This work
AtPAP2	AtPAP1	0.65±0.02	-	This work
AtPAP2	AtPAP2	0.60±0.04	-	This work
AtPAP2	AtTT2	0.66±0.02	-	This work
AtPAP2	AtMYB61	0.62±0.03	-	This work
AtPAP2	w/o	0.55±0.02	-	This work
AtTT2	AtTTG1	0.82±0.02	-	(Baudry, et al. 2004)
AtTT2	AtGL3	20.33±0.59	+	(Baudry, et al. 2006)
AtTT2	AtEGL3	22.59±0.35	+	(Zimmermann, et al. 2004; Baudry, et al. 2006)
AtTT2	AtTT8	28.63±0.74	+	(Baudry, et al. 2004; Zimmermann, et al. 2004; Baudry, et al. 2006)
AtTT2	AtMYC1	19.59±0.99	+	(Zimmermann, et al. 2004)
AtTT2	AtGL1	0.65±0.00	-	This work
AtTT2	AtWER	0.61±0.03	-	This work
AtTT2	AtPAP1	0.63±0.00	-	(Baudry, et al. 2006)
AtTT2	AtPAP2	0.60±0.00	-	This work
AtTT2	AtTT2	1.87±0.02	w	(Baudry, et al. 2004)
AtTT2	AtMYB61	0.62±0.01	-	This work
AtTT2	w/o	0.57±0.00	-	This work
AtMYB61	AtTTG1	0.60±0.01	-	This work
AtMYB61	AtGL3	0.85±0.04	-	This work
AtMYB61	AtEGL3	0.89±0.02	-	This work
AtMYB61	AtTT8	1.19±0.06	-	This work
AtMYB61	AtMYC1	0.88±0.01	-	This work
AtMYB61	AtGL1	0.64±0.04	-	This work
AtMYB61	AtWER	0.60±0.02	-	This work
AtMYB61	AtPAP1	0.63±0.02	-	This work
AtMYB61	AtPAP2	0.60±0.00	-	This work
AtMYB61	AtTT2	0.58±0.02	-	This work

AtMYB61	AtMYB61	0.62±0.02	-	This work
AtMYB61	w/o	0.57±0.00	-	This work
w/o	AtTTG1	0.54±0.01	-	This work
w/o	AtGL3	0.69±0.07	-	This work
w/o	AtEGL3	0.71±0.05	-	This work
w/o	AtTT8	0.70±0.09	-	This work
w/o	AtMYC1	0.68±0.01	-	This work
w/o	AtGL1	0.69±0.01	-	This work
w/o	AtWER	0.58±0.08	-	This work
w/o	AtPAP1	0.60±0.02	-	This work
w/o	AtPAP2	0.62±0.04	-	This work
w/o	AtTT2	0.57±0.03	-	This work
w/o	AtMYB61	0.65±0.01	-	This work
w/o	w/o	0.54±0.00	-	This work

The proteins were single-expressed in human cells (HEK293TN) and immunoprecipitated with IgG Dynabeads. Data are mean ± s.d. (n = 3).

w/o: Empty vector without CDS fusion.

+: Positive interaction (Luciferase activity ≥ 2.5%)

w: Weak interaction (Luciferase activity = 1.5% ~ 2.5%)

-: No interaction (Luciferase activity < 1.5%)

[1] In the reference (Zhao, et al. 2012), no interaction was found between AtMYC1 and AtGL3CT in yeast two hybrid.

[2] In the reference (Baudry, et al. 2004), AtTT8 homodimerization was not clearly supported in yeast two hybrid.

[3] In the reference (Zhao, et al. 2012), AtMYC1 homodimerization was not clearly supported in yeast two hybrid.

Table S2: Protein sequence identity matrix WD40 proteins

Pairwise	Identities	Similarities
AtTTG1 - GhTTG1	78.0	90.7
AtTTG1 - GhTTG2	61.4	80.8
AtTTG1 - GhTTG3	78.1	90.5
AtTTG1 - GhTTG4	60.6	79.4
AtTTG1 - PhAN11	78.1	92.4
AtTTG1 - ZmPAC1	60.9	81.2
AtTTG1 - ZmMP1	47.8	65.5

Table S3: Protein sequence identity matrix bHLH proteins

AtGL3 - AtEGL3	74.5	79.3
AtGL3 - AtMYC1	37.8	48.0
AtGL3 - AtTT8	32.9	43.5
AtGL3 - AaGL3	88.7	90.7
AtGL3 - AaEGL3	72.1	77.7
AtGL3 - AaTT8	32.7	44.0
AtGL3 - AaMYC1	36.1	46.4
AtGL3 - GhDEL61	49.2	60.1
AtGL3 - GhDEL65	52.3	60.4
AtGL3 - PhAN1	34.7	44.9
AtGL3 - PhJAF13	45.5	56.5
AtGL3 - ZmR(Lc)	34.8	43.8
AtGL3 - ZmR(S)	35.5	44.7
AtGL3 - ZmB	33.4	42.2
AtEGL3 - AtMYC1	34.4	44.3
AtEGL3 - AtTT8	33.8	44.7
AtEGL3 - AaGL3	74.2	78.4
AtEGL3 - AaEGL3	84.6	88.5
AtEGL3 - AaTT8	34.3	45.6
AtEGL3 - AaMYC1	37.1	47.5
AtEGL3 - GhDEL61	50.1	60.1
AtEGL3 - GhDEL65	53.4	62.3
AtEGL3 - PhAN1	35.1	43.9
AtEGL3 - PhJAF13	45.1	55.4
AtEGL3 - ZmR(Lc)	35.2	44.5
AtEGL3 - ZmR(S)	35.1	44.4
AtEGL3 - ZmB	34.2	43.0
AtTT8 - AtMYC1	30.9	40.2
AtTT8- AaGL3	32.4	43.0
AtTT8 - AaEGL3	33.8	43.0
AtTT8 - AaTT8	80.3	85.8
AtTT8 - AaMYC1	34.2	42.5
AtTT8 - GhDEL61	33.8	43.4
AtTT8 - GhDEL65	33.8	44.2
AtTT8 - PhAN1	43.9	52.4
AtTT8 - PhJAF13	31.7	43.7
AtTT8 - ZmR(Lc)	36.4	48.5
AtTT8 - ZmR(S)	36.5	48.6
AtTT8 - ZmB	36.0	47.8
AtMYC1- AaGL3	33.5	43,6
AtMYC1 - AaEGL3	34.0	42,7
AtMYC1 - AaTT8	31.8	40,3
AtMYC1 - AaMYC1	74.4	77,1
AtMYC1 - GhDEL61	34.6	42,5
AtMYC1 - GhDEL65	33.6	42,6
AtMYC1- PhAN1	27.2	35,4
AtMYC1 - PhJAF13	31.1	40,7
AtMYC1 - ZmR(Lc)	30,0	38,9
AtMYC1 - ZmR(S)	29,8	39,2
AtMYC1 - ZmB	29,8	36,5

Table S4: Protein sequence identity matrix R2R3 MYB proteins

AtGL1 - AtWER	55,9	64,0
AtGL1 - AtPAP1	37,2	45,1
AtGL1 - AtPAP2	37,2	42,9
AtGL1 - AtTT2	36,2	45,3
AtGL1 - AtMYB61	27,1	36,6
AtGL1 - AaGL1	79,7	84,1
AtGL1 - AaWER	55,2	64,0
AtGL1 - AaPAPL	36,3	36,3
AtGL1 - GhMYB2	38,4	49,2
AtGL1 - GhMYB25	32,2	39,0
AtGL1 - GhRLC1	33,9	40,8
AtGL1 - PhAN2	36,6	48,0
AtGL1 - PhAN4	35,2	43,8
AtGL1 - PhPH4	36,6	47,0
AtGL1 - ZmC1	35,4	44,7
AtGL1 - ZmPL	35,2	42,9
AtGL1 - ZmP1	30,2	37,6
AtWER - AtPAP1	35,4	42,4
AtWER - AtPAP2	35,9	42,3
AtWER - AtTT2	37,0	46,5
AtWER - AtMYB61	27,1	34,5
AtWER - AaGL1	58,4	66,5
AtWER - AaWER	93,7	94,6
AtWER - AaPAPL	36,2	42,5
AtWER - GhMYB2	45,6	56,2
AtWER - GhMYB25	33,1	39,6
AtWER - GhRLC1	38,6	45,1
AtWER - PhAN2	37,3	46,3
AtWER - PhAN4	34,9	42,8
AtWER - PhPH4	41,6	48,6
AtWER - ZmC1	34,1	43,4
AtWER - ZmPL	36,2	42,5
AtWER - ZmP1	29,8	35,8
AtPAP1 - AtPAP2	78,8	83,2
AtPAP1 - AtTT2	36,4	44,0
AtPAP1 - AtMYB61	31,5	36,4
AtPAP1 - AaGL1	35,9	44,8
AtPAP1 - AaWER	36,9	41,8
AtPAP1 - AaPAPL	76,3	83,1
AtPAP1 - GhMYB2	37,0	45,3
AtPAP1 - GhMYB25	34,5	40,8
AtPAP1 - GhRLC1	49,0	54,1
AtPAP1 - PhAN2	46,7	55,4
AtPAP1 - PhAN4	38,2	45,2
AtPAP1 - PhPH4	38,2	45,2
AtPAP1 - ZmC1	34,1	41,5
AtPAP1 - ZmPL	33,6	41,0
AtPAP1 - ZmP1	32,7	39,5
AtPAP2 - AtTT2	36,3	43,9
AtPAP2 - AtMYB61	30,9	37,1
AtPAP2 - AaGL1	37,5	44,9
AtPAP2 - AaWER	35,6	42,7
AtPAP2 - AaPAPL	78,4	83,6
AtPAP2 - GhMYB2	37,1	47,1
AtPAP2 - GhMYB25	35,1	40,2
AtPAP2 - GhRLC1	48,3	54,2
AtPAP2 - PhAN2	47,3	54,1
AtPAP2 - PhAN4	44,5	49,7
AtPAP2 - PhPH4	36,7	45,7
AtPAP2 - ZmC1	34,3	43,2
AtPAP2 - ZmPL	35,4	44,0

AtPAP2 - ZmP1	31,8	38,8
AtTT2 - AtMYB61	32,2	39,0
AtTT2 - AaGL1	36,4	45,5
AtTT2 - AaWER	38,4	47,6
AtTT2 - AaPAPL	38,8	45,2
AtTT2 - GhMYB2	40,0	47,4
AtTT2- GhMYB25	36,3	44,7
AtTT2 - GhRLC1	37,8	45,8
AtTT2 - PhAN2	39,9	49,7
AtTT2- PhAN4	38,0	47,1
AtTT2- PhPH4	36,8	45,7
AtTT2 - ZmC1	39,6	46,0
AtTT2 - ZmPL	39,5	46,9
AtTT2 - ZmP1	35,8	41,5
AtMYB61 - AaGL1	28,8	36,1
AtMYB61 - AaWER	26,8	34,0
AtMYB61 - AaPAPL	32,7	39,5
AtMYB61 - GhMYB2	27,3	32,5
AtMYB61 - GhMYB25	38,8	45,5
AtMYB61 - GhRLC1	30,3	37,9
AtMYB61 - PhAN2	31,9	39,1
AtMYB61 - PhAN4	30,8	39,5
AtMYB61 - PhPH4	34,9	41,6
AtMYB61 - ZmC1	30,2	38,1
AtMYB61 - ZmPL	33,1	39,2
AtMYB61 - ZmP1	33,9	40,9

Table S5. Pairwise interaction of MBW components in Arabis (*A. alpine*)

BD or ProtA fusion	AD or Luciferase fusion	Yeast two hybrid	Pulldown/input ratio (%)		References
AaTTG1	AaTTG1	-	0.63±0.01	-	This work
AaTTG1	AaGL3	+	4.06±0.39	+	This work
AaTTG1	AaEGL3	+	4.54±0.27	+	This work
AaTTG1	AaTT8	+	5.53±0.11	+	This work
AaTTG1	AaMYC1	+	4.33±0.19	+	This work
AaTTG1	AaGL1	-	0.61±0.02	-	This work
AaTTG1	AaWER	-	0.62±0.02	-	This work
AaTTG1	AaPAPL	-	0.65±0.01	-	This work
AaTTG1	w/o	-	0.55±0.01	-	This work
AaGL3	AaTTG1	+	7.74±0.29	+	This work
AaGL3	AaGL3	+	3.87±0.04	+	This work
AaGL3	AaEGL3	+	2.69±0.03	+	This work
AaGL3	AaTT8	w	4.77±0.07	+	This work
AaGL3	AaMYC1	w	3.76±0.09	+	This work
AaGL3	AaGL1	+	15.74±1.63	+	This work
AaGL3	AaWER	+	14.84±1.00	+	This work
AaGL3	AaPAPL	+	10.38±0.35	+	This work
AaGL3	w/o	-	0.58±0.01	-	This work
AaEGL3	AaTTG1	+	8.12±0.54	+	This work
AaEGL3	AaGL3	w	3.83±0.20	+	This work
AaEGL3	AaEGL3	w	3.09±0.05	+	This work
AaEGL3	AaTT8	w	5.01±0.17	+	This work
AaEGL3	AaMYC1	-	2.23±0.04	w	This work
AaEGL3	AaGL1	+	5.74±1.19	+	This work
AaEGL3	AaWER	+	6.84±1.06	+	This work
AaEGL3	AaPAPL	+	5.38±0.61	+	This work
AaEGL3	w/o	-	0.57±0.01	-	This work
AaTT8	AaTTG1	+	8.51±1.31	+	This work
AaTT8	AaGL3	-	2.96±0.12	+	This work
AaTT8	AaEGL3	-	1.91±0.02	w	This work

AaTT8	AaTT8	w	3.62±0.17	+	This work
AaTT8	AaMYC1	-	2.83±0.04	+	This work
AaTT8	AaGL1	+	4.74±0.36	+	This work
AaTT8	AaWER	+	3.97±0.19	+	This work
AaTT8	AaPAPL	+	4.25±0.08	+	This work
AaTT8	w/o	-	0.58±0.01	-	This work
AaMYC1	AaTTG1	+	6.93±0.16	+	This work
AaMYC1	AaGL3	-	3.31±0.07	+	This work[1]
AaMYC1	AaEGL3	-	1.97±0.04	w	This work[1]
AaMYC1	AaTT8	-	3.62±0.17	+	This work[1]
AaMYC1	AaMYC1	-	2.83±0.04	+	This work[1]
AaMYC1	AaGL1	+	4.74±0.36	+	This work
AaMYC1	AaWER	+	3.97±0.19	+	This work
AaMYC1	AaPAPL	+	4.25±0.08	+	This work
AaMYC1	w/o	-	0.58±0.01	-	This work
AaGL1	AaTTG1	-	0.60±0.02	-	This work
AaGL1	AaGL3	+	9.56±0.14	+	This work
AaGL1	AaEGL3	+	8.22±0.47	+	This work
AaGL1	AaTT8	+	8.80±0.17	+	This work
AaGL1	AaMYC1	+	11.28±0.38	+	This work
AaGL1	AaGL1	-	0.64±0.01	-	This work
AaGL1	AaWER	-	0.62±0.02	-	This work
AaGL1	AaPAPL	-	0.62±0.00	-	This work
AaGL1	w/o	-	0.57±0.00	-	This work
AaWER	AaTTG1	A	0.62±0.02	-	This work
AaWER	AaGL3	A	14.37±0.69	+	This work
AaWER	AaEGL3	A	14.44±0.64	+	This work
AaWER	AaTT8	A	15.52±1.38	+	This work
AaWER	AaMYC1	A	13.59±1.00	+	This work
AaWER	AaGL1	A	0.66±0.02	-	This work
AaWER	AaWER	A	0.60±0.01	-	This work
AaWER	AaPAPL	A	0.61±0.00	-	This work
AaWER	w/o	A	0.57±0.00	-	This work

AaPAPL	AaTTG1	A	0.61±0.02	-	This work
AaPAPL	AaGL3	A	13.90±0.52	+	This work
AaPAPL	AaEGL3	A	8.59±0.29	+	This work
AaPAPL	AaTT8	A	35.31±3.17	+	This work
AaPAPL	AaMYC1	A	20.96±2.38	+	This work
AaPAPL	AaGL1	A	0.61±0.01	-	This work
AaPAPL	AaWER	A	0.63±0.02	-	This work
AaPAPL	AaPAPL	A	0.63±0.01	-	This work
AaPAPL	w/o	A	0.59±0.01	-	This work
w/o	AaTTG1	-	0.61±0.03	-	This work
w/o	AaGL3	-	0.65±0.02	-	This work
w/o	AaEGL3	-	0.60±0.01	-	This work
w/o	AaTT8	-	0.58±0.02	-	This work
w/o	AaMYC1	-	0.59±0.03	-	This work
w/o	AaGL1	-	0.64±0.01	-	This work
w/o	AaWER	-	0.63±0.02	-	This work
w/o	AaPAPL	-	0.66±0.01	-	This work
w/o	w/o	-	0.57±0.01	-	This work

The proteins were single-expressed in human cells (HEK293TN) and immunoprecipitated with IgG Dynabeads. Data are mean ± s.d. (n = 3).

w/o: Empty vector without CDS fusion.

+: Positive interaction (Luciferase activity ≥ 2.5%)

w: Weak interaction (Few colonies grew on SD-L/W/H with 3-AT or Luciferase activity = 1.5% ~ 2.5%)

-: No interaction (Luciferase activity < 1.5%)

Table S6. Pairwise interaction of MBW components in Cotton (*G.hirsutum*)

BD or ProtA fusion	AD or Luciferase fusion	Yeast two hybrid	Pulldown/input ratio (%)		References
GhTTG1	GhTTG1	-	0.45±0.06	-	This work
GhTTG1	GhTTG2	-	0.47±0.05	-	This work
GhTTG1	GhTTG3	-	0.59±0.05	-	This work
GhTTG1	GhTTG4	-	0.57±0.05	-	This work
GhTTG1	GhDEL61	+	6.18±0.89	+	This work
GhTTG1	GhDEL65	+	13.86±2.80	+	This work
GhTTG1	GhMYB2	-	0.55±0.07	-	This work
GhTTG1	GhMYB25	-	0.61±0.04	-	This work
GhTTG1	GhRLC1	-	0.61±0.06	-	This work
GhTTG1	w/o	-	0.50±0.03	-	This work
GhTTG2	GhTTG1	-	0.52±0.08	-	This work
GhTTG2	GhTTG2	-	0.57±0.02	-	This work
GhTTG2	GhTTG3	-	0.59±0.04	-	This work
GhTTG2	GhTTG4	-	0.56±0.05	-	This work
GhTTG2	GhDEL61	-	0.58±0.05	-	This work
GhTTG2	GhDEL65	-	0.61±0.04	-	This work
GhTTG2	GhMYB2	-	0.59±0.04	-	This work
GhTTG2	GhMYB25	-	0.61±0.04	-	This work
GhTTG2	GhRLC1	-	0.59±0.07	-	This work
GhTTG2	w/o	-	0.49±0.03	-	This work
GhTTG3	GhTTG1	-	0.48±0.08	-	This work
GhTTG3	GhTTG2	-	0.57±0.04	-	This work
GhTTG3	GhTTG3	-	0.59±0.05	-	This work
GhTTG3	GhTTG4	-	0.56±0.05	-	This work
GhTTG3	GhDEL61	+	6.90±0.11	+	(Shangguan, et al. 2016)
GhTTG3	GhDEL65	+	14.83±3.27	+	(Shangguan, et al. 2016)
GhTTG3	GhMYB2	-	0.57±0.03	-	This work
GhTTG3	GhMYB25	-	0.63±0.06	-	This work
GhTTG3	GhRLC1	-	0.61±0.07	-	This work
GhTTG3	w/o	-	0.49±0.04	-	This work

GhTTG4	GhTTG1	-	0.53±0.09	-	This work
GhTTG4	GhTTG2	-	0.51±0.05	-	This work
GhTTG4	GhTTG3	-	0.58±0.05	-	This work
GhTTG4	GhTTG4	-	0.56±0.05	-	This work
GhTTG4	GhDEL61	-	0.58±0.03	-	This work
GhTTG4	GhDEL65	-	0.65±0.05	-	This work
GhTTG4	GhMYB2	-	0.57±0.06	-	This work
GhTTG4	GhMYB25	-	0.64±0.05	-	This work
GhTTG4	GhRLC1	-	0.60±0.07	-	This work
GhTTG4	w/o	-	0.49±0.03	-	This work
GhDEL61	GhTTG1	A	8.86±0.40	+	This work
GhDEL61	GhTTG2	A	0.56±0.05	-	This work
GhDEL61	GhTTG3	A	7.59±0.27	+	(Shangguan, et al. 2016)
GhDEL61	GhTTG4	A	0.57±0.06	-	This work
GhDEL61	GhDEL61	A	3.60±0.11	+	(Shangguan, et al. 2016)
GhDEL61	GhDEL65	A	4.86±3.27	+	(Shangguan, et al. 2016)
GhDEL61	GhMYB2	A	39.53±8.13	+	(Wan, et al. 2014; Shangguan, et al. 2016)
GhDEL61	GhMYB25	A	5.84±0.12	+	(Wan, et al. 2014)
GhDEL61	GhRLC1	A	42.22±5.83	+	This work
GhDEL61	w/o	A	0.49±0.04	-	This work
GhDEL65	GhTTG1	+	20.93±5.04	+	(Wang, et al. 2013)
GhDEL65	GhTTG2	-	0.56±0.03	-	This work
GhDEL65	GhTTG3	+	15.54±2.20	+	(Shangguan, et al. 2016)
GhDEL65	GhTTG4	-	0.56±0.03	-	This work
GhDEL65	GhDEL61	+	3.74±0.11	+	(Shangguan, et al. 2016)
GhDEL65	GhDEL65	+	3.86±3.27	+	(Shangguan, et al. 2016)
GhDEL65	GhMYB2	+	43.67±6.25	+	(Wan, et al. 2014; Shangguan, et al. 2016)
GhDEL65	GhMYB25	+	4.83±0.38	+	(Wan, et al. 2014)
GhDEL65	GhRLC1	+	40.60±3.77	+	This work
GhDEL65	w/o	-	0.50±0.03	-	This work
GhMYB2	GhTTG1	A	0.63±0.04	-	This work
GhMYB2	GhTTG2	A	0.58±0.04	-	This work

GhMYB2	GhTTG3	A	0.61±0.03	-	This work
GhMYB2	GhTTG4	A	0.57±0.05	-	This work
GhMYB2	GhDEL61	A	13.72±0.41	+	(Wan, et al. 2014; Shangguan, et al. 2016)
GhMYB2	GhDEL65	A	17.80±1.71	+	(Wan, et al. 2014; Shangguan, et al. 2016)
GhMYB2	GhMYB2	A	0.66±0.06	-	This work
GhMYB2	GhMYB25	A	0.59±0.06	-	This work
GhMYB2	GhRLC1	A	0.63±0.07	-	This work
GhMYB2	w/o	A	0.51±0.02	-	This work
GhMYB25	GhTTG1	A	0.64±0.07	-	This work
GhMYB25	GhTTG2	A	0.53±0.04	-	This work
GhMYB25	GhTTG3	A	0.57±0.06	-	This work
GhMYB25	GhTTG4	A	0.51±0.04	-	This work
GhMYB25	GhDEL61	A	7.99±0.30	+	(Wan, et al. 2014)
GhMYB25	GhDEL65	A	9.48±0.85	+	(Wan, et al. 2014)
GhMYB25	GhMYB2	A	0.60±0.07	-	This work
GhMYB25	GhMYB25	A	0.62±0.04	-	This work
GhMYB25	GhRLC1	A	0.67±0.07	-	This work
GhMYB25	w/o	A	0.52±0.04	-	This work
GhRLC1	GhTTG1	A	0.65±0.06	-	This work
GhRLC1	GhTTG2	A	0.55±0.04	-	This work
GhRLC1	GhTTG3	A	0.60±0.06	-	This work
GhRLC1	GhTTG4	A	0.53±0.04	-	This work
GhRLC1	GhDEL61	A	9.64±0.26	+	This work
GhRLC1	GhDEL65	A	9.38±1.17	+	This work
GhRLC1	GhMYB2	A	0.60±0.05	-	This work
GhRLC1	GhMYB25	A	0.66±0.03	-	This work
GhRLC1	GhRLC1	A	0.68±0.06	-	This work
GhRLC1	w/o	A	0.49±0.03	-	This work
w/o	GhTTG1	-	0.67±0.06	-	This work
w/o	GhTTG2	-	0.55±0.03	-	This work
w/o	GhTTG3	-	0.62±0.05	-	This work
w/o	GhTTG4	-	0.56±0.03	-	This work

w/o	GhDEL61	-	0.53±0.02	-	This work
w/o	GhDEL65	-	0.61±0.03	-	This work
w/o	GhMYB2	-	0.64±0.05	-	This work
w/o	GhMYB25	-	0.64±0.03	-	This work
w/o	GhRLC1	-	0.67±0.07	-	This work
w/o	w/o	-	0.49±0.04	-	This work

The proteins were single-expressed in human cells (HEK293TN) and immunoprecipitated with IgG Dynabeads. Data are mean ± s.d. (n = 3).

w/o: Empty vector without CDS fusion.

+: Positive interaction (Luciferase activity ≥ 2.5%)

w: Weak interaction (Few colonies grew on SD-L/W/H with 3-AT or Luciferase activity = 1.5% ~ 2.5%)

-: No interaction (Luciferase activity < 1.5%)

A: Autoactivation

Table S7. Pairwise interaction of MBW components in Petunia (*P. hybrida*)

BD or ProtA fusion	AD or Luciferase fusion	Yeast two hybrid	Pulldown/input ratio (%)		References
PhAN11	PhAN11	-	0.58±0.08	-	(Albert, et al. 2014)
PhAN11	PhAN1	+	18.45±0.65	+	(Albert, et al. 2014)
PhAN11	PhJAF13	+	26.77±4.24	+	(Albert, et al. 2014)
PhAN11	PhAN2	+	0.59±0.02	-	(Albert, et al. 2014)[1]
PhAN11	PhAN4	+	0.55±0.02	-	This work
PhAN11	PhPH4	-	0.56±0.07	-	This work
PhAN11	w/o	-	0.48±0.03	-	(Albert, et al. 2014)
PhAN1	PhAN11	+	29.75±3.68	+	(Albert, et al. 2014)
PhAN1	PhAN1	w	9.19±2.91	+	(Spelt, et al. 2002; Albert, et al. 2014)[2]
PhAN1	PhJAF13	-	17.06±3.46	+	(Spelt, et al. 2002; Quattrocchio, et al. 2006; Albert, et al. 2014)[3]
PhAN1	PhAN2	+	47.21±5.22	+	(Albert, et al. 2014)
PhAN1	PhAN4	+	50.39±7.63	+	This work
PhAN1	PhPH4	w	51.89±8.89	+	(Quattrocchio, et al. 2006)
PhAN1	w/o	-	0.49±0.05	-	(Quattrocchio, et al. 2006)
PhJAF13	PhAN11	A	31.80±4.51	+	(Albert, et al. 2014)
PhJAF13	PhAN1	A	5.77±0.54	+	(Spelt, et al. 2002; Albert, et al. 2014)
PhJAF13	PhJAF13	A	8.99±1.26	+	(Spelt, et al. 2002; Quattrocchio, et al. 2006; Albert, et al. 2014)
PhJAF13	PhAN2	A	48.26±8.02	+	(Albert, et al. 2014)
PhJAF13	PhAN4	A	51.39±8.81	+	This work
PhJAF13	PhPH4	A	50.73±6.53	+	(Quattrocchio, et al. 2006)
PhJAF13	w/o	A	0.50±0.04	-	(Quattrocchio, et al. 2006)
PhAN2	PhAN11	A	0.59±0.00	-	This work
PhAN2	PhAN1	A	18.17±0.66	+	This work
PhAN2	PhJAF13	A	26.08±6.27	+	This work
PhAN2	PhAN2	A	0.55±0.03	-	This work
PhAN2	PhAN4	A	0.56±0.04	-	This work
PhAN2	PhPH4	A	0.59±0.03	-	This work
PhAN2	w/o	A	0.47±0.06	-	This work

PhAN4	PhAN11	A	0.55±0.02	-	This work
PhAN4	PhAN1	A	19.65±2.43	+	This work
PhAN4	PhJAF13	A	32.21±4.02	+	This work
PhAN4	PhAN2	A	0.58±0.02	-	This work
PhAN4	PhAN4	A	0.57±0.02	-	This work
PhAN4	PhPH4	A	0.58±0.01	-	This work
PhAN4	w/o	A	0.48±0.05	-	This work
PhPH4	PhAN11	A	0.57±0.04	-	This work
PhPH4	PhAN1	A	31.94±6.10	+	This work
PhPH4	PhJAF13	A	42.77±4.48	+	This work
PhPH4	PhAN2	A	0.58±0.03	-	This work
PhPH4	PhAN4	A	0.56±0.01	-	This work
PhPH4	PhPH4	A	0.59±0.03	-	This work
PhPH4	w/o	A	0.50±0.01	-	This work
					This work
w/o	PhAN11	-	0.55±0.03	-	This work
w/o	PhAN1	-	0.60±0.02	-	This work
w/o	PhJAF13	-	0.62±0.05	-	This work
w/o	PhAN2	-	0.59±0.03	-	This work
w/o	PhAN4	-	0.52±0.02	-	This work
w/o	PhPH4	-	0.58±0.01	-	This work
w/o	w/o	-	0.47±0.03	-	This work

The proteins were single-expressed in human cells (HEK293TN) and immunoprecipitated with IgG Dynabeads. Data are mean ± s.d. (n = 3).

w/o: Empty vector without CDS fusion.

+: Positive interaction (Luciferase activity ≥ 2.5%)

w: Weak interaction (Few colonies grew on SD-L/W/H with 3-AT or Luciferase activity = 1.5% ~ 2.5%)

-: No interaction (Luciferase activity < 1.5%)

A: Autoactivation

[1] In the references (Albert, et al. 2014), the interaction between PhAN11 and PhAN2 was not supported in the yeast experiment.

[2] In the references (Spelt, et al. 2002; Albert, et al. 2014), PhAN1 homodimerization was not clearly supported in yeast experiments.

[3] In the references (Spelt, et al. 2002; Quattrocchio, et al. 2006; Albert, et al. 2014), positive interaction was confirmed in yeast two hybrid.

Table S8. Pairwise interaction of MBW components in Maize (*Z.mays*)

BD or ProtA fusion	AD or Luciferase fusion	Yeast two hybrid	Pulldown/input ratio (%)		References
ZmPAC1	ZmPAC1	-	0.67±0.00	-	This work
ZmPAC1	ZmMP1	-	0.65±0.02	-	This work
ZmPAC1	ZmR(Lc)	+	10.97±1.33	+	This work
ZmPAC1	ZmR(S)	+	10.34±0.71	+	This work
ZmPAC1	ZmB	+	10.84±0.49	+	This work
ZmPAC1	ZmC1	+	0.61±0.07	-	This work
ZmPAC1	ZmPL	+	0.52±0.05	-	This work
ZmPAC1	ZmP1	+	0.51±0.04	-	This work
ZmPAC1	w/o	-	0.49±0.07	-	This work
ZmMP1	ZmPAC1	-	0.62±0.08	-	This work
ZmMP1	ZmMP1	-	0.65±0.02	-	This work
ZmMP1	ZmR(Lc)	-	0.70±0.12	-	This work
ZmMP1	ZmR(S)	-	0.63±0.03	-	This work
ZmMP1	ZmB	-	0.64±0.09	-	This work
ZmMP1	ZmC1	-	0.66±0.07	-	This work
ZmMP1	ZmPL	-	0.56±0.15	-	This work
ZmMP1	ZmP1	-	0.51±0.08	-	This work
ZmMP1	w/o	-	0.47±0.05	-	This work
ZmR(Lc)	ZmPAC1	A	18.38±0.75	+	This work
ZmR(Lc)	ZmMP1	A	0.67±0.04	-	This work
ZmR(Lc)	ZmR(Lc)	A	9.63±0.84	+	This work
ZmR(Lc)	ZmR(S)	A	9.36±1.09	+	This work
ZmR(Lc)	ZmB	A	2.22±0.19	w	This work
ZmR(Lc)	ZmC1	A	48.68±2.07	+	This work
ZmR(Lc)	ZmPL	A	59.56±3.95	+	This work
ZmR(Lc)	ZmP1	A	0.52±0.09	-	This work
ZmR(Lc)	w/o	A	0.49±0.06	-	This work
ZmR(S)	ZmPAC1	A	19.86±1.81	+	This work
ZmR(S)	ZmMP1	A	0.64±0.07	-	This work
ZmR(S)	ZmR(Lc)	A	8.44±0.84	+	This work

ZmR(S)	ZmR(S)	A	10.29±1.40	+	(Feller, et al. 2006; Kong, et al. 2012)
ZmR(S)	ZmB	A	2.16±0.15	w	This work
ZmR(S)	ZmC1	A	56.41±8.36	+	(Grotewold, et al. 2000; Hernandez, et al. 2004; Kong, et al. 2012)
ZmR(S)	ZmPL	A	39.57±4.51	+	(Grotewold, et al. 2000; Hernandez, et al. 2004)
ZmR(S)	ZmP1	A	0.53±0.10	-	(Grotewold, et al. 2000; Hernandez, et al. 2004)
ZmR(S)	w/o	A	0.50±0.05	-	This work
ZmB	ZmPAC1	+	12.51±1.20	+	This work
ZmB	ZmMP1	-	0.63±0.12	-	This work
ZmB	ZmR(Lc)	w	3.56±0.06	+	This work
ZmB	ZmR(S)	-	3.39±0.06	+	This work
ZmB	ZmB	-	3.90±0.09	+	This work
ZmB	ZmC1	-	0.66±0.16	-	(Goff, et al. 1992; Hernandez, et al. 2004)[1]
ZmB	ZmPL	-	0.58±0.14	-	(Goff, et al. 1992)[1]
ZmB	ZmP1	-	0.49±0.06	-	This work
ZmB	w/o	-	0.51±0.05	-	This work
ZmC1	ZmPAC1	w	0.61±0.05	-	This work
ZmC1	ZmMP1	-	0.63±0.02	-	This work
ZmC1	ZmR(Lc)	+	35.56±3.66	+	This work
ZmC1	ZmR(S)	-	44.54±5.60	+	(Grotewold, et al. 2000; Hernandez, et al. 2004; Kong, et al. 2012)
ZmC1	ZmB	-	1.73±0.19	-	(Goff, et al. 1992; Hernandez, et al. 2004)[1]
ZmC1	ZmC1	+	0.52±0.16	-	This work
ZmC1	ZmPL	+	0.52±0.14	-	This work
ZmC1	ZmP1	-	0.53±0.06	-	This work
ZmC1	w/o	-	0.53±0.01	-	This work
ZmPL	ZmPAC1	A	0.65±0.02	-	This work
ZmPL	ZmMP1	A	0.60±0.05	-	This work
ZmPL	ZmR(Lc)	A	47.19±3.91	+	This work
ZmPL	ZmR(S)	A	46.37±4.45	+	(Grotewold, et al. 2000; Hernandez, et al. 2004; Kong, et al. 2012)
ZmPL	ZmB	A	0.63.±0.18	-	(Goff, et al. 1992; Hernandez, et al. 2004) [1]
ZmPL	ZmC1	A	0.57±0.14	-	This work
ZmPL	ZmPL	A	0.53±0.10	-	This work
ZmPL	ZmP1	A	0.53±0.12	-	This work

ZmPL	w/o	A	0.52±0.05	-	This work
ZmP1	ZmPAC1	-	0.63±0.05	-	This work
ZmP1	ZmMP1	-	0.57±0.09	-	This work
ZmP1	ZmR(Lc)	-	0.59±0.11	-	This work
ZmP1	ZmR(S)	-	0.65±0.09	-	(Grotewold, et al. 2000; Hernandez, et al. 2004)
ZmP1	ZmB	-	0.63±0.08	-	This work
ZmP1	ZmC1	-	0.66±0.16	-	This work
ZmP1	ZmPL	+	0.55±0.12	-	This work
ZmP1	ZmP1	-	0.49±0.06	-	This work
ZmP1	w/o	-	0.50±0.05	-	This work
w/o	ZmPAC1	-	0.61±0.09	-	This work
w/o	ZmMP1	-	0.56±0.05	-	This work
w/o	ZmR(Lc)	-	0.62±0.10	-	This work
w/o	ZmR(S)	-	0.60±0.08	-	This work
w/o	ZmB	-	0.62.±0.02	-	This work
w/o	ZmC1	-	0.65±0.08	-	This work
w/o	ZmPL	-	0.55±0.06	-	This work
w/o	ZmP1	-	0.53±0.04	-	This work
w/o	w/o	-	0.51±0.02	-	This work

The proteins were single-expressed in human cells (HEK293TN) and immunoprecipitated with IgG Dynabeads.

Data are mean ± s.d. (n = 3).

w/o: Empty vector without CDS fusion.

+: Positive interaction (Luciferase activity ≥ 2.5%)

w: Weak interaction (Few colonies grew on SD-L/W/H with 3-AT or Luciferase activity = 1.5% ~ 2.5%)

-: No interaction (Luciferase activity < 1.5%)

A: Autoactivation

[1] In the references (Goff, et al. 1992; Hernandez, et al. 2004), positive interaction was confirmed in yeast two hybrid.

Table S9. MBW CDS sequence information

Gene Name	Sequence
AtTTG1	ATGGATAATTCAGCTCCAGATTCGTTATCCAGATCGGAAACCGCCGTCACATACGACTCACCATATCC ACTCTACGCCATGGCTTTCTCTTCTCTCCGCTCATCCTCCGGTCACAGAATCGCCGTCGGAAGCTTCCT CGAAGATTACAACAACCGCATCGACATTCTCTCTTTCGATTCCGATTCAATGACCGTTAAGCCTCTCCC GAATCTCTCCTTCGAGCATCCTTATCCTCCAACAAAGCTAATGTTCAGTCCTCCTTCTCTCCGTCGTCC TTCCTCCGGAGATCTCCTCGCTTCCTCCGGCGATTTCCTCCGTCTTTGGGAAATTAACGAAGATTCATC AACCGTCGAGCCAATCTCGGTTCTCAACAACAGCAAAACGAGCGAGTTTTGTGCGCCGTTGACTTCCT TCGATTGGAACGATGTAGAGCCGAAACGTCTCGGAACTTGTAGTATTGATACGACGTGTACGATTTGG GATATTGAGAAGTCTGTTGTTGAGACTCAGCTTATAGCTCATGATAAAGAGGTTCATGACATTGCTTG GGGAGAAGCTAGGGTTTTCGCATCAGTCTCTGCTGATGGATCCGTTAGGATCTTTGATTTACGTGATA AGGAACATTCTACAATCATTTACGAGAGTCCTCAGCCTGATACGCCTTTGTTAAGACTTGCTTGGAAC AAACAAGATCTTAGATATATGGCTACGATTTTGATGGATTCTAATAAGGTTGTGATTCTCGATATTCG TTCGCCGACTATGCCTGTTGCTGAGCTTGAAAGACATCAGGCTAGTGTGAATGCTATAGCTTGGGCGC CTCAGAGCTGTAAACATATTTGTTCTGGTGGTGATGATACACAGGCTCTTATTTGGGAGCTTCCTACTG TTGCTGGACCCAATGGGATTGATCCGATGTCGGTTTATTCGGCTGGTTCGGAGATTAATCAGTTGCAG TGGTCTTCTTCGCAGCCTGATTGGATTGGTATTGCTTTTGCTAACAAAATGCAGCTCCTTAGAGTTTGA
AaTTG1	ATGGATAACTCAGCTCCAGATTCGTTATCCAGATCGGAAACCGCCGTGACCTACGAGTCTCCTTATCC ACTCTACGCAATGGCTTTCTCTTCTTCACGCGCCGGTACATCTTCCGGTCACAGAATCGCCGTCGGTAG CTTCTTAGAAGATTACAACAACCGTATCGATATTCTCACCTTCGATTCCGATTCCATGACTATCAAATC TCTCCCGAATCTATCCGTCGATCATCCTTATCCTCCAACAAAGCTAATGTTCAGTCCTCCTTCTCTCCG TCGTCCTTCCGCCGGAGATCTACTCGCTTCCTCCGGTGATTTCCTCCGTTTATGGGAGGTTAACGAAGA TTCATCCACCGTTGAGCCTGTTGCGGTGCTTAACAATAGTAAGACGAGTGAGTTTTGTGCGCCGTTGA CTTCCTTTGATTGGAACGATGTTGAGCCGAAACGACTCGGGACTTGTAGTATTGATACGACTTGTACG ATTTGGGATATTGAGAAATCTGTGGTGGAGACTCAGCTTATAGCTCATGATAAAGAAGTACATGACAT TGCTTGGGGAGAAGCTAGGGTTTTCGCTTCGGTTTCTGCTGATGGATCAGTGAGAATCTTTGATTTAC GTGATAAGGAACATTCAACAATCATATACGAGAGTCCTCAGCCTGATACGCCTCTCTTAAGACTAGCT TGGAACAAGCAAGATTTGAGATACATGGCTACGATTCTTATGGATTCTAATAAGGTTGTGATTCTTGA TATTCGTTCACCGACTATGCCTGTTGCGGAGTTAGAAAGGCATCAGGCTAGTGTTAATGCTATAGCTT GGGCTCCACAGAGCTGTAAACATATTTGCTCTGGTGGTGATGATACACAGGCTTTGATTTGGGAGTTA CCGACTGTGGCTGGACCTAATGGGATTGATCCTATGTCGGTTTACTCGGCTGGCTCGGAGATTAATCA GTTGCAGTGGTCTTCTTCACAGCCTGATTGGATTGGCATTGCTTTTGCTAACAAAATGCAGCTCCTTAG AGTTTGA
GhTTG1	ATGGAGAATTCAACTCAGGAATCCCACCTCCGATCCGATAACGCCGTAACCTACGAATCACCCTACCC ACTCTACGCCATGGCCTTATCTTCCACGCCCGCCGTCACCCATCTCAACTACCAACGCATCGCTCTCGG CAGTTTCATCGAGGATTACACTAACAGAGTCCACATAATCTCTTTCGACCCTGAATCACTTACCCTCAT AACCCACCCATCTTTGTCGTTCGACCACCCTTACCCACCCACCAAACTTATGTTCCAACCCCCACCGGA AATCCCCTTTCTCTTCCTCCTCCGACCTCCTCGCTTCATCCGGTGACTACCTCCGTCTCTGGGAAGTTG GGCACTCTTCTATCGAACTTATCTCCGTTCTCGACAACAGCAAAACCAGCGAGTTTTCTGCTCCCTTAA CTTCCTTCGATTGGAACGACGTTGAACCCAATAGAATCGGAACATCCAGCATCGACACCACCTGCACC ATTTGGGACATTGAAAAAGGCGTTGTGGAAACCCAATTGATTGCTCACGACAAGGAGGTTTACGACA TCGCTTGGGGTGAAGGTAGAGTTTTCGGTTCCGTTTCCGCTGATGGGTCCGTAAGGATTTTCGATTTAA GGGACAAAGAACACTCAACTATCATCTACGAAAGCCCTCAACCGGACACCCCTTTGCTAAGATTAGC TTGGAACAAACAAGATTTGAGGTATATGGCTACGACACTAATGGATAGCAATAAAGTTGTGATTTTG GACATAAGGTCGCCTACTACGCCGGTGGCTGAGTTGGATAGACATGGAGCCAGTGTCAATGCGATTG CTTGGGCTCCCCAGAGCTGTAAGCACATTTGCTCTGCAGGGGATGATACGCATGCCCTTATTTGGGAG TTACCAACTGTAGCTGGGCCTAACGGAATCGATCCTTTGTCTATGTACTCGGCTAGTTCCGAAATTAA TCAGTTGCAGTGGTCTGCTGCTCAGCCTGATTGGATTGCCATTGCCTTCTCCAACAAAATGCAGCTTCT CAAAGTTTGA
GhTTG2	ATGGCCGCTAGCAGCGATCCTAACCCGGAGGGTTCCGATGAGCAGCAGAAACGATCCGAGATATACA CTTACGAGGCCCCTTGGCATATCTACGCCATGAACTGGAGTGTCCGCCGCGACAAGAAATACCGTCTC GCCATCGCCAGCTTGCTCGAGCATTACAACAACCGCCTTGAGATTGTCCAGCTCGATGACTCCAATGG CGAGATCCGATCGGACCCAAATCTCTCCTTCGATCATCCTTATCCCCCGACCAAGACCATCTTCATCCC CGACAAGGAGTGCCAGAAACCCGACCTTCTCGCCACGTCCTCCGACTTCCTCCGCATTTGGCGCATCT CCGATGACCACTCCCGCGTCGACCTCAAGTCTCTCCTTAATGGCAATAAGAACAGTGAATTCTGCGGT CCTCTTACCTCCTTCGACTGGAATGAGGCGGAGCCCAAGCGAATCGGCACCTCCTCCATTGATACGAC TTGTACTATATGGGATATCGAGAGGGAGACGGTGGATACCCAGCTTATCGCCCACGATAAGGAGGTT TATGATATTGCCTGGGGCGGCGTCGGTGTTTTTGCTTCCGTCTCTGCTGATGGGTCCGTTAGGGTTTTC GACCTGCGCGACAAGGAGCACTCCACTATCATTTATGAAAGTTCGGAGCCCGATACTCCGCTTGTACG GTTGGGGTGGAACAAGCAGGACCCGAGATATATGGCTACTATAATTATGGACAGTGCTAAGGTTGTT GTTTTGGATATCCGCTTCCCGACACTGCCGGTAGTTGAGCTGCAGAGGCACCAGGCTAGCGTCAATGC CATCGCATGGGCACCCCACAGCTCTTGCCACATTTGCACCGCCGGGGATGATTCCCAGGCCTTGATTT GGGACTTGTCCTCCATGAGTCAGCCTGTGGAGGGTGGGCTTGACCCCATCCTTGCCTACACCGCTGGG GCTGAAATCGAGCAGTTACAGTGGTCATCTTCCCAGCCTGATTGGGTTGCCATCGCCTTCTCCACCAA GCTTCAGATTCTCAGGGTATGA

GhTTG3	ATGGAGAATTCAACTCAAGAATCCCACCTGAGATCCGATAATTCGGTAACCTACGAATCAGCTTACAC AGTTTATGCCATGGCCTTATCTTCCACGCCTTCCTCCACCAATATCAACCATCAACGCATCGCTCTCGG CAGCTTCCTCGAAGATTACACTAACAGAGTCGACATAATCTCATTTGATCCAGAAACCCTCTCCTTCA AGACCCACCCAAAGCTTGCCTTCGACCACCCTTATCCACCCACCAAGCTCATGTTCCAACCCAATCGA AAATCCGCTTCATCCTCTTCTTCTTGTTCCGATCTTCTCGCTTCAACCGGCGATTTCCTGCGTCTCTGGG AAGTTCGAGAATCTTCCATTGAACCTGTCACTGTTCTAAACAATAGCAAAACCAGCGAGTTTTGTGCC CCGTTAACTTCCTTCGATTGGAACGATGTTGAACCCAAGAGAATTGGGACTTCCAGCATCGACACAAC TTGCACCATTTGGGACATCGAGAAATGCGTCGTTGAAACCCAATTGATCGCTCATGATAAAGAGGTTT ACGACATTGCTTGGGGTGAAGCTAGAGTTTTTGCTTCCGTTTCCGCTGATGGGTCCGTTAGGATTTTCG ATTTGAGAGACAAAGAACATTCCACCATCATTTATGAAAGTCCCCAACCCGACACCCCTTTATTAAGA TTGGCTTGGAACAAGCAAGATTTGAAGTATATGGCTACCATTCAAATGGATAGCAATAAAGTTGTGAT TTTGGATATAAGGTCACCCACAACCCCCGTTGCTGAGTTGGAGCGGCATCACGCTAGTGTCAATGCCA TTGCCTGGGCTCCTCAGAGTTGTAAGCATATTTGTTCCGCTGGGGATGATACCCAGGCTCTTATTTGGG AGTTGCCTACGGTGGCGGGACCTAATGGTATCGATCCTCTGTGTGTTTACTCTGCTGGCTACGAAATT AATCAATTACAGTGGTCTGCTGCGCAACCTGATTGGATTGCCATTGCCTTTTCCAACAAATTGCAGCTT CTCAAAGTTTGA
GhTTG4	ATGACGGCCACCAGCGATCCGAACCCCGAAGTTTCCGACGAGCAGCAAAAACGATCGGAGATATACA CATATGAAGCTCCCTGGTACATCTACGCTATGAATTGGAGCGTCCGCCGCGACAAAAAGTACCGACTC GCCATCGCCAGCCTCCTCGAGCAATACCCTAACCGTCTCCAGATTGTTCAACTCGACGACTCCAATGG TGAGATCCGGTCGGATCCCAACCTCTCCTTCGACCATCCCTATCCCGCTACTAAGACCATCTTCATTCC CGACAAGGATTGCCAGAAACCCGATCTTCTCGCTACCTCCTCCGATTTTCTTCGCATATGGCGGATCTC GGATGACGGTTCCCGCGTTGACCTCAAATCGCTCCTTAATGGCAATAAGAACAGTGAATTTTGCGGTC CTCTCACGTCTTTCGACTGGAACGAGGCGGAGCCGAAGCGAATCGGGACTTCCTCCATTGATACGACT TGCACTATTTGGGATATCGAGAAGGAAACAGTGGATACCCAGTTAATTGCCCACGATAAGGAGGTTT ACGACATCGCTTGGGGTGGAGTTGGGGTTTTCGCTTCCGTCTCCGCCGACGGTTCCGTTAGGGTTTTCG ATTTACGCGACAAGGAACATTCGACGATCATCTACGAGAGTTCGGAGCCGGACGCGCCGCTGGTGCG GTTGGGGTGGAACAAGCAGGACCCCAGATATATGGCGACCATTATAATGGATAGTGCCAAGGTGGTT GTTTTGGATATCCGTTTCCCGACGTTGCCGGTGGTTGAGTTGCGGAGACACCAGGCGAGCGTCAATGC CGTCGCTTGGGCTCCCCATAGTTCCTGCCACATTTGCACCGCCGGCGATGATTCTCAGGCGTTGATTTG GGATTTGTCTTCGATGGGTCAGCCTGTTAAAGGTGGGCTTGACCCCATTCTTGCATACACGGCTGGGG CTGAAATTGAACAGTTGCAATGGTCGTCGTCTCAGCCTGATTGGGTGGCCATTGCCTTCTCCACTAAG CTTCAGATTCTAAGGGTATGA
PhAN11	ATGGAAAATTCAAGTCAAGAATCACAACATCTCCGATCTGAAAACTCCGTTACATATGATTCCACTTA CCCAATTTACTCCATGGCATTTTCCTCTTTCCCCACCCCCCGCCGCCGCATTGCCGTGGGTAGCTTTAT TGAAGAATTAAACAACCGGGTCGAACTCCTTTCATTTAATGAAGAAACCCTAACCCTAAACCCAATCC CAAATCTTTCTTTTGATCATCCATACCCCCCAACTAAATTAATGTTCCATCCTAACCCCATAAAATCCA ATAATGACATTCTTGCTTCTTCAGGTGATTATTTGCGTTTATGGGAAGTTAAAGAAAGTTCAATTGAA CCCCTTTTTACTTTAAATAATAGTAAAACTAGTGAATATTGTGCCCCTTTAACTTCTTTTGATTGGAAT GAAGTTGAGCCTAAAAGAATTGGTACTTCTAGTATTGATACTACTTGTACTATTTGGGATGTCGAAAA GGGCGTCGTTGAAACTCAGTTAATTGCTCATGATAAAGAGGTTTATGATATTGCTTGGGGTGAAGCTG GTGTTTTTGCATCTGTTTCTGCTGATGGATCGGTTAGGATTTTCGATTTAAGAGATAAGGAGCATTCGA CGATTATTTATGAGAGTCCAACGCCTGATACTCCGTTGTTGAGGTTGGCGTGGAATAAGCAAGATTTG AGATATATGGCTACTATATTGATGGATAGTAATAAGGTTGTGATTTTAGATATTAGGTCGCCTGCTAT GCCTGTGGCGGAGTTGGAAAGGCATCAGGCGAGTGTGAATGCCATTGCTTGGGCTCCCCAGAGTTGT AGACATATTTGTTCAGGTGGAGATGATGGGCAGGCGTTGATTTGGGAGTTGCCTACTGTTGCTGGGCC TAATGGGATTGATCCCATGTCGATGTACTCTGCTGGTGCTGAGATTAATCAGCTTCAGTGGTCTCCTGC GCAGCGTGATTGGATTGCTATTGCATTTTCTAACAAGTTGCAATTGCTTAAAGTATAG
ZmPAC1	ATGGACCCACCCAAGCCGCCGTCCTCGGTCGCCTCGTCGTCGGGGCCGGAGACGCCGAACCCGCACG CCTTCACCTGCGAGCTCCCGCACTCGATCTACGCGCTCGCCTTCTCCCCCGTCGCGCCCGTCCTCGCCT CCGGCAGCTTCCTCGAGGACCTCCACAACCGCGTCTCCCTGCTCTCCTTCGACCCCGTCCGCCCCTCCG CCGCCTCCTTCCGCGCCCTCCCGGCGCTCTCCTTCGACCACCCTTACCCACCCACCAAGCTCCAGTTCA ACCCCCGCGCCGCCGCGCCGTCCCTCCTCGCCTCCTCCGCCGACACGCTCCGCATCTGGCACACCCCG CTCGACGACCTCTCCGACACCGCCCCCGCGCCCGAGCTCCGCTCCGTTCTCGACAACCGCAAGGCCTC CTCCGAGTTCTGCGCACCCCTCACCTCCTTCGATTGGAACGAGGTCGAGCCCCGCCGTATCGGGACCG CCTCCATCGACACCACCTGCACCGTCTGGGACATCGATCGCGGGGTCGTGGAGACGCAGCTCATCGC GCACGACAAGGCCGTGCACGACATCGCCTGGGGGGAGGCCGGGGTCTTCGCCTCCGTATCGGCCGAC GGCTCCGTCCGCGTCTTCGACCTTCGGGACAAGGAGCACTCCACCATCGTCTACGAGAGCCCCCGCCC CGACACGCCGCTACTAAGGCTGGCGTGGAACCGCTCTGACCTCCGCTATATGGCCGCGCTGCTCATGG ACAGCAGCGCCGTCGTCGTGCTCGACATACGTGCGCCCGGGGTGCCGGTGGCCGAGCTGCACCGGCA CCGGGCGTGCGCCAACGCAGTCGCGTGGGCGCCGCAAGCCACTAGGCACCTCTGTTCGGCTGGGGAC GACGGGCAAGCATTGATCTGGGAACTGCCTGAGACGGCGGCGGCTGTACCCGCCGAGGGGATTGATC CTGTGCTAGTGTACGATGCAGGCGCCGAAATAAACCAACTTCAGTGGGCGGCCGCGCACCCGGACTG GATGGCCATCGCCTTTGAGAACAAGGTCCAGCTTCTTAGGGTCTAG

ZmMP1	ATGGGCGGAGTCGGCGAAGGTGACGCGTGGGCGGATCAGGAGCAGGGCAACGGCGGGGGCAGCCGT GGTGTTGGCGGTGGCGGCGGCGAGGCGAAGCGGTCGGAGATCTACACGTACGAGGCCGCCTGGCACA TCTACGCGATGAACTGGAGCGTGCGGCGCGATAAGAAATACCGCCTTGCCATCGCCAGCCTTCTCGA GCAGGTCACCAACCGCGTCGAGGTCGTCCAGCTCGATGAGGCCTCGGGTGACATCGCCCCCGTCCTCA CCTTCGACCATCAGTACCCGCCCACCAAGACCATGTTCATGCCGGACCCGCACGCGCTCCGCCCCGAC CTGCTCGCCACCTCCGCCGACCACCTGCGCATCTGGCGCATCCCGTCCTCCGACGACGCCGAGGACGG CGCCGCCTCCGCCAACAACAACAACGGCTCCGTCCGCTGCAACGGCACCCAGCAGCCGGGCATCGAG CTACGCTCCGAGCTCAACGGCAACCGCAACAGCGACTACTGCGGGCCGCTCACCTCCTTCGACTGGA ACGACGCCGATCCGCGCCGCATCGGTACCTCCTCCATCGACACCACCTGCACAATCTGGGACGTCGAG CGCGAGGCCGTTGACACCCAGCTCATCGCCCACGACAAGGAGGTCTACGACATCGCCTGGGGCGGCG CGGGGGTCTTTGCCTCCGTCTCCGCCGACGGCTCTGTTCGCGTCTTTGATTTACGGGACAAGGAGCAC TCCACAATCATTTATGAGTCTGGTTCAGGTGGCAGCAGCGGCGGCGGTTCCAACTCTGGCGCCGGAGA TGGTGGGACTGCGTCCCCGACACCACTCGTGAGGTTGGGCTGGAACAAGCAGGACCCAAGGTACATG GCCACCATCATCATGGACAGCCCCAAGGTGGTTGTGCTTGATATCCGCTACCCAACACTGCCAGTGGT AGAGCTACACCGTCACCATGCCCCTGTCAATGCCATTGCGTGGGCACCTCACTCTTCTTGCCACATCT GCACAGCTGGGGATGACATGCAGGCACTGATATGGGATTTGTCGTCTATGGGAACTGGTAGCAATGG CAGTGGCAATGGGAATGGTAACACAGCCGCTGGAGCAGCAGCAGAGGGCGGTCTTGATCCCATTTTG GCATATACAGCAGGGGCAGAGATTGAGCAGTTGCAGTGGTCGGCGACCCAGCCTGACTGGGTTGCAA TCGCATTCGCCAATAAGCTTCAGATTCTCAGGGTCTGA
AtGL3	ATGGCTACCGGACAAAACAGAACAACTGTGCCAGAGAATCTGAAGAAACACCTCGCAGTTTCAGTTC GAAACATTCAATGGAGTTATGGTATCTTTTGGTCTGTCTCTGCTTCTCAGTCTGGAGTTTTAGAATGGG GAGATGGATACTATAATGGAGATATCAAAACGAGGAAGACGATTCAAGCTTCGGAGATCAAAGCTGA TCAGCTTGGTCTACGGAGGAGCGAGCAGCTTAGCGAGCTTTACGAGTCTCTCTCCGTCGCTGAATCTT CTTCTTCAGGCGTTGCTGCCGGATCTCAAGTCACCAGACGAGCTTCCGCCGCCGCACTTTCACCGGAA GATCTCGCCGACACCGAGTGGTACTATTTGGTTTGTATGTCTTTCGTCTTCAACATTGGTGAAGGAATG CCTGGACGGACGTTTGCAAACGGTGAACCGATATGGTTGTGCAACGCTCATACGGCGGATAGTAAAG TGTTTAGCCGTTCTCTTCTAGCAAAAAGTGCTGCGGTTAAGACAGTGGTTTGCTTCCCGTTCCTTGGAG GAGTCGTTGAGATTGGTACCACAGAACATATTACGGAAGACATGAATGTAATACAATGCGTGAAGAC ATCATTCCTCGAAGCCCCTGATCCGTACGCTACAATATTACCAGCAAGATCCGATTATCACATCGACA ACGTTCTTGATCCGCAACAGATTCTAGGCGACGAGATTTACGCGCCTATGTTCAGTACGGAGCCTTTT CCAACAGCTTCTCCGAGCAGAACTACCAACGGTTTCGATCAAGAACATGAACAAGTAGCAGATGATC ATGATTCTTTCATGACCGAAAGAATCACTGGAGGAGCTTCTCAGGTGCAAAGCTGGCAGCTCATGGA CGACGAGCTTAGTAACTGCGTTCACCAGTCGCTAAATTCCAGCGATTGCGTCTCTCAAACGTTTGTTG AAGGGGCGGCTGGACGGGTTGCTTACGGTGCAAGAAAGAGTAGAGTTCAAAGACTAGGGCAAATTC AAGAGCAACAGAGAAATGTGAAGACATTGTCATTTGATCCAAGAAACGACGACGTTCATTACCAAAG TGTGATCTCAACGATTTTTAAGACCAACCATCAGTTAATTCTCGGACCGCAGTTTCGAAACTGCGATA AACAGTCAAGCTTCACTAGGTGGAAGAAATCATCGTCATCATCATCAGGAACCGCCACGGTCACGGC ACCATCACAAGGAATGTTAAAGAAAATTATTTTCGATGTTCCGCGAGTGCACCAGAAAGAGAAGTTA ATGTTGGACTCACCAGAAGCCAGAGATGAAACTGGGAACCATGCGGTTTTAGAGAAGAAGCGCCGCG AGAAATTGAACGAACGGTTCATGACCTTGAGAAAAATCATTCCGTCAATCAACAAGATCGATAAAGT ATCGATTCTTGACGATACGATAGAGTATCTTCAAGAACTCGAGAGACGGGTTCAAGAACTAGAATCTT GCAGAGAATCAACCGATACAGAGACTCGTGGGACGATGACGATGAAGAGGAAGAAACCATGCGACG CAGGAGAAAGAACATCAGCTAATTGCGCAAATAATGAAACAGGAAATGGGAAGAAGGTGTCGGTTA ACAATGTTGGTGAAGCCGAGCCAGCAGATACCGGTTTTACTGGTTTAACCGATAATTTAAGGATCGGT TCGTTTGGTAATGAGGTGGTTATTGAGCTTAGATGTGCTTGGAGAGAAGGAGTATTGCTTGAGATAAT GGATGTGATTAGTGATCTCCATTTGGATTCTCATTCGGTTCAATCCTCGACCGGAGACGGTTTGCTCTG CTTAACCGTCAATTGCAAGCACAAGGGGTCAAAAATAGCGACACCAGGAATGATCAAAGAAGCACTT CAAAGGGTTGCATGGATCTGTTGA
AtEGL3	ATGGCAACCGGAGAAAACAGAACGGTGCCGGACAATCTAAAGAAACAGCTCGCAGTTTCAGTTCGAA ACATTCAATGGAGTTATGGAATCTTCTGGTCTGTCTCTGCTTCTCAACCAGGAGTGTTGGAGTGGGGA GATGGATATTACAATGGAGACATAAAGACAAGGAAGACGATTCAAGCAGCAGAAGTCAAAATTGAC CAGTTAGGTCTTGAGAGAAGTGAGCAGCTTAGAGAGCTTTATGAATCTCTCTCCCTCGCTGAATCCTC AGCTTCCGGTAGCTCTCAGGTCACTAGACGAGCTTCCGCCGCCGCTCTCTCACCGGAGGACCTCACCG ACACCGAGTGGTACTACTTAGTATGCATGTCTTTCGTCTTCAACATCGGTGAAGGAATCCCCGGAGGA GCGTTATCCAATGGAGAACCAATATGGCTTTGTAACGCTGAAACCGCCGATAGCAAAGTCTTCACTCG TTCTCTTCTAGCTAAAAGTGCTTCGCTTCAGACAGTGGTTTGCTTCCCGTTTCTTGGAGGAGTCCTTGA GATTGGCACGACCGAACATATTAAAGAGGACATGAACGTGATACAAAGTGTTAAGACGTTGTTCCTT GAAGCTCCTCCATATACTACAATATCGACAAGATCAGACTATCAAGAAATTTTTGATCCCTTAAGTGA CGATAAATACACTCCGGTGTTTATAACCGAAGCTTTTCCAACAACTTCTACTAGCGGGTTTGAGCAAG AACCTGAGGATCATGATTCGTTCATCAACGATGGTGGTGCGTCTCAGGTACAAAGCTGGCAGTTTGTG GGTGAAGAAATCAGTAACTGCATTCACCAATCGTTAAATTCAAGCGATTGCGTTTCCCAAACGTTTGT TGGAACAACCGGGAGACTTGCTTGCGATCCAAGGAAGAGTAGGATTCAACGGTTAGGTCAGATTCAA GAACAGAGTAACCATGTAAATATGGACGACGATGTTCATTACCAAGGCGTGATATCGACGATTTTCA AAACAACGCATCAGCTAATACTCGGACCGCAGTTTCAGAACTTCGATAAGCGGTCTAGCTTCACAAG GTGGAAGCGATCATCATCTGTGAAAACATTGGGAGAGAAATCGCAGAAGATGATAAAGAAGATACTC TTCGAGGTTCCTTTGATGAACAAGAAAGAAGAGTTGTTACCGGACACACCAGAGGAAACCGGGAACC ATGCCTTGTCCGAGAAGAAACGCCGCGAGAAATTGAATGAACGGTTTATGACATTGAGATCAATCAT TCCCTCAATTAGTAAGATTGATAAAGTGTCGATTCTTGATGATACAATTGAGTATCTTCAAGATTTAC AGAAACGGGTTCAAGAGTTGGAATCTTGTAGAGAATCTGCTGATACAGAGACACGGATAACGATGAT GAAGAGGAAGAAACCGGATGATGAGGAGGAAAGAGCATCAGCGAATTGTATGAACAGCAAAAGGA AGGGGAGTGATGTGAATGTAGGAGAAGATGAACCAGCTGATATCGGTTATGCTGGTCTAACGGATAA CTTAAGGATCAGTTCATTAGGTAACGAGGTGGTTATTGAGCTTAGATGCGCTTGGAGAGAAGGGATA TTGCTTGAGATAATGGATGTGATTAGTGATCTCAACTTGGATTCTCACTCGGTTCAGTCGTCAACCGG AGACGGTTTACTCTGCTTAACTGTCAATTGCAAGCATAAAGGGACAAAAATAGCAACAACAGGAATG ATCCAAGAGGCACTTCAAAGGGTTGCATGGATATGTTAA

AtMYC1	ATGTCTTTGACAATGGCTGATGGTGTAGAAGCTGCAGCAGGAAGAAGTAAAAGACAAAACAGCTTAT TAAGAAAACAACTTGCTTTAGCTGTAAGAAGTGTTCAATGGAGCTACGCAATCTTCTGGTCGTCTTCA CTTACTCAACCTGGGGTTTTGGAGTGGGGAGAAGGATGTTACAATGGAGATATGAAGAAGAGGAAGA AGAGTTATGAATCTCATTATAAATATGGGTTGCAAAAAAGCAAGGAGCTTCGGAAACTTTATTTGTCT ATGCTTGAAGGAGACAGTGGTACTACTGTTAGTACTACTCATGATAATCTCAATGATGATGATGATAA TTGTCACAGTACAAGTATGATGCTGTCACCAGATGACCTCTCTGATGAAGAGTGGTACTATTTAGTCT CCATGTCCTATGTCTTCTCTCCTTCACAATGTTTGCCTGGAAGAGCTTCAGCGACGGGTGAGACCATAT GGCTCTGCAACGCTCAATATGCGGAGAACAAGCTCTTCTCTCGTTCTTTGTTAGCAAGAAGCGCATCA ATTCAGACTGTTGTGTGTTTCCCTTACTTGGGCGGAGTCATTGAGCTGGGCGTCACTGAATTGATTTCA GAAGACCATAACCTGCTTCGAAACATCAAATCTTGCTTGATGGAAATATCTGCACACCAAGACAACG ATGACGAGAAGAAGATGGAGATTAAGATCAGTGAAGAGAAGCATCAGCTTCCATTAGGTATTTCTGA TGAAGACTTGCATTACAAAAGAACCATTTCAACAGTACTCAACTACTCCGCAGATAGATCAGGTAAG AACGATAAGAACATTCGTCATCGTCAGCCAAATATTGTTACTTCTGAACCTGGCTCAAGTTTCTTGCG GTGGAAGCAATGTGAGCAGCAAGTCTCGGGTTTTGTTCAGAAAAAAAAGTCACAGAATGTGTTGCGG AAGATATTGCATGATGTCCCTTTGATGCACACAAAGAGAATGTTCCCAAGTCAGAACTCTGGTCTGAA TCAAGATGATCCTTCAGATAGAAGAAAAGAGAACGAAAAGTTCAGTGTCCTTAGAACTATGGTTCCC ACTGTCAACGAGGTTGATAAAGAATCGATACTAAACAACACAATCAAGTACCTGCAAGAACTGGAGG CAAGAGTAGAAGAGCTAGAATCTTGTATGGGATCAGTTAATTTTGTAGAAAGACAAAGAAAGACGAC AGAGAACCTTAACGACTCTGTGTTGATCGAAGAGACATCAGGGAACTACGATGATAGCACGAAGATC GATGACAATTCAGGAGAAACCGAACAAGTCACTGTTTTCAGAGATAAGACACATTTGAGAGTTAAAC TCAAAGAAACAGAAGTTGTGATCGAAGTAAGATGTTCTTACAGAGACTACATAGTTGCGGACATCAT GGAAACTCTGAGCAATCTTCACATGGATGCTTTCTCTGTTAGATCTCACACGCTCAATAAGTTCCTCAC ATTGAATCTCAAGGCCAAGTTTCGCGGGGCTGCAGTTGCGTCCGTAGGAATGATTAAGCGAGAGCTG AGAAGAGTCATTGACTTTCGTGAACCGATATGCGATGTGCCATTATCTTTACATCAAGTTTTCAGGGT TTTTGTATGTAAAGTTTGCCAAAGTTTGGTTGGAATTTTCGACAACGTTGTCTCTTCCTCTTCTACAAA ACCAAGATCTATACTTATTCATAATTCATGGGCGATTTGTATCTTTCATTAA
AtTT8	ATGGATGAATCAAGTATTATTCCGGCAGAGAAAGTGGCCGGAGCTGAGAAAAAAGAGCTTCAAGGG CTGCTTAAGACGGCGGTTCAATCTGTGGACTGGACTTATAGTGTCTTCTGGCAATTTTGTCCTCAACAA CGGGTCTTGGTGTGGGGGAATGGATACTACAACGGTGCAATAAAGACGAGGAAGACAACTCAACCA GCGGAGGTGACGGCAGAAGAGGCGGCGTTAGAGAGGAGCCAACAGCTCAGGGAGCTTTATGAGACA CTTTTAGCCGGAGAGTCAACGTCAGAAGCAAGAGCATGCACCGCATTGTCACCGGAGGATTTGACGG AGACAGAATGGTTTTATCTAATGTGCGTCTCTTTCTCTTTTCCTCCTCCATCTGGGATGCCAGGAAAAG CGTATGCAAGGAGGAAGCACGTATGGCTAAGTGGTGCAAATGAAGTTGACAGTAAAACTTTTTCTAG AGCTATTCTCGCTAAGAGTGCTAAAATTCAGACAGTGGTTTGCATTCCAATGCTTGATGGTGTTGTGG AACTAGGCACAACGAAAAAGGTAAGAGAAGATGTAGAGTTTGTTGAGCTCACAAAGAGTTTCTTCTA TGACCACTGCAAGACGAACCCAAAGCCGGCTCTTTCTGAACACTCCACCTACGAAGTGCATGAAGAA GCCGAAGACGAAGAAGAAGTAGAAGAAGAGATGACAATGTCAGAGGAAATGAGGCTTGGCTCTCCT GATGATGAAGATGTTTCCAATCAAAATCTACACTCTGATCTTCATATTGAATCAACCCATACGTTAGA CACACATATGGACATGATGAATCTAATGGAGGAAGGTGGAAACTATTCTCAGACAGTAACAACACTT CTCATGTCACACCCCACAAGTCTTCTTTCAGATTCAGTTTCCACATCTTCTTACATCCAATCATCGTTT GCCACGTGGAGGGTTGAGAATGGCAAAGAGCATCAGCAAGTGAAAACGGCGCCGTCGTCACAATGG GTGCTCAAACAAATGATCTTCAGAGTTCCTTTCCTCCATGACAACACTAAAGATAAGAGGCTACCGCG GGAAGATCTGAGCCACGTAGTAGCAGAGCGACGCAGGAGGGAGAAGCTGAACGAGAAATTCATAAC GTTGAGATCAATGGTTCCATTTGTGACCAAGATGGATAAAGTCTCAATCCTTGGAGACACCATTGCGT ACGTAAATCATCTTCGAAAGAGGGTCCATGAGCTTGAGAATACTCATCATGAGCAACAGCATAAGCG GACGCGTACTTGTAAGAGAAAAACATCGGAGGAGGTGGAGGTTTCCATCATAGAGAATGATGTTTTG TTAGAGATGAGATGTGAGTACCGAGATGGTTTGTTGCTTGACATTCTTCAGGTTCTTCATGAGCTTGGT ATAGAGACTACGGCAGTTCATACCTCGGTGAACGACCATGATTTCGAGGCGGAGATAAGGGCGAAAG TAAGAGGGAAGAAAGCAAGCATCGCTGAGGTCAAAAGAGCCATCCACCAAGTCATAATACATGATA CTAATCTATAG
AaGL3	ATGGCTTCCGGACAAAACAGAGCATCTGTACCGGAGAATCTAAAGAAACAGCTTGCAGTTTCAGTTC GAAGTATTCAATGGAGTTATGCAATTTTTTGGTCTGTTTCTGCTTCTCAATCAGGGGTATTAGAGTGGG GAGATGGATACTATAATGGAGATATCAAAACGAGGAAGACGATTCAAGCTTCGGAGATCAAAGCTGA TCAGCTTGGTTTACGGAGGAGTGAGCAACTTAGAGAGCTTTACGAGTCTCTCAACATCGCTGAATCTT CTTCCTCCGGTTCTCAGGTCACTAGACGAGCTTCCGCCGCCGCACTATCGCCTGAAGATCTCGCCGAC ACCGAGTGGTATTACTTGGTTTGTATGTCTTTCGTCTTCAACATTGGTGAAGGAATGCCTGGACGAAC GTTTACGAATGGTGAACCGATATGGTTGTGTAACGCTCATACCGCGGATAGTAAAGTCTTTAGCCGCT CTCTTTTGGCAAAAAGTGCTGCCGTTAAGACAGTGATTTGTTTCCCGTTTCTTGGAGGAGTCGTTGAG ATCGGTACTACAGAACATATTCAAGAAGACATGAACCTTATACAATGCGTGAAGACATCATTCCTAG AAGCTCCTGATCCATACGCTACAATATTACCAACAAGATCCGACTATCACATGGATCTCGATCCGCAA CAGATTCTAGGCGATGAGATTTACGCTCCTATGTTCGGTACTGAGCCTTTTCCAACAACTTCTCCTAGC AGAACTACAAATGGTTTCGATACCGAACACGAACAAGTAGCCGAAGATTCATTCATGGCTGATGGAA TGAATGGAGGAGCTTCTCAAGTGCAAAGTTGGCAGCTTATGGACGACGAGCTTAGTAATTGCGTTCAT CAATCGCTAAATTCCAGCGATTGCGTCTCTCAAACGTTTGTTGAAGCAGCGGGTGGCCGAGTTTCTTG CGGTGCAAGAAAAGGTAGGGCTCAAAGATTAGGGCAAATTCAAGAGCAACAGAGAAACGTGAAGAT GTTGTCTTTTGATCCAAGAAACGATGATGTTCATTACCAAGGTGTTATCTCCACGATTTTTAAGACCAA CCATCAGTTAATTCTTGGACCGCAATTTCGAAACTGCGATAAGCAGTCAAGCTTCACAAGGTGGAAG AAATCATCAACCTCATCATCATCAGGAACCGCCGTGGTTGCACCATCATCACAAAGAATGATAAAGA AGATTCTTTTCGATGTTCCGCGAGCTCATCTAAAAGAGAAAATGTTGTTGGATTCACCAGAGCTCGGG GATGAAACCGCGAACCACGCGGGTTTAGATAAGAAACGGCGTGAGAAATTGAACGAACGGTTCATG ACCCTTAGATCTATCATTCCTTCAATCAATAAGATCGACAAAGTATCGATTCTTGATGATACAATAGA GTATCTTCAAGAACTCGAAAGACGGGTTCAAGAACTAGAATCTTGCAGAGAATCAACCGATACAGAA ACTCGCGGGACAATGGCAATGAAGAGGAAGAAACAGCACGATGCAGGAGAAAGAACGTCAGCTAAT TGCACAAATAATGAAACCGATAATGGGAAGAAAGTTCCGGTTGGAGAAGCCGAACCAGCTGAAACC GGTTATACTGGTCTAACCGATAATTTAAGGATCGGTTCGTTTGGTAACGAGGTGGTTATTGAGCTTAG

	ATGTGCTTGGAGAGAAGGAGTATTACTTGAGATAATGGATGTGATTAGTGATCTCAACTTGGATTCTC ATTCAGTACAATCATCGACCGGAGACGGTTTACTCTGCTTAACCGTCAATTGCAAGCATAAAGGATCA AAAATAGCTACACAAGGAATGATCAAAGAGGCACTTCAAAGGGTTGCATGGATCTGTTGA
AaEGL3	ATGGCTGCCGGAGAAAACAGAACGGTACCACCAGAGAATCTAAAGAAACAACTCGCAGTTTCAGTTC GAAATATTCAATGGAGTTATGGAATCTTTTGGTCTGTCTCTACTTCTCAACCAGGAATGTTGGAGTGG GGAGATGGATACTACAATGGAGACATTAAGACAAGGAAGACGATTCAAGCAGCTGAAGTAAAAGTC GACAAGTTAGGTCTTGAGAGAAGTGAACAGCTTAGAGAGCTTTATGAATCTCTCTCCATCGCTGAATC TTCAACTTCCGGTGGCTCTCAGGTCAGTAGACGAGTTTCCGCCGCCGCTCTATCCCCGGAGGACCTCA CCGACACTGAGTGGTATTACTTAGTCTGCATGTCATTCATCTTCAACATTGGTGAAGGAATCCCCGGA GGAGTGTTGGCAAACGGAGAACCAATATGGCTTTGTAACGCTCAAACCGCTGATAGCAAAGTCTTCA CTCGCTCTCTTCTCGCTAAAAGTGCTTCGCTTCAGACAGTTGTTTGCTTCCCATTTCTTGGAGGAGTCC TTGAGATCGGCACTACCGAACATATTAAAGAGGACTTAAACGTGATACAATGCATAAAGACATTGTT TCTTGAAGCTCCACCTTATCCTACAATATCATCAAGATCCGATTATCAAGAAATCTTCGATCCATTAA GCGACGATAAATACATTCCCGTGTTTGGATCTGAACCCTTTCCGACACCTTCCACGAGCGGGTTTGAG CAAGAACAAGAGGATCATGATTCGTTTATCAATGGTGGTGGTGCGTCTCAGGTCCAAAGCTGGCAGTT TGTTGGTGAAGAACTCAGTAATTGCGTTCATCAATCGCTTAATTCTAGCGACCGCGTTTCGCAGACGC TTGTTGGGAGAGTAGCTTGCGATCCAAGAATAAGTAGGGTTCAAAAATTAGGTCAGACACAAGAACA GTGTAACCGTGTAAATATGGATGATGATGATCATTACCAAAGCGTGATCTCGACGATTTTTAAAACGA CGCATCAGCTTATTCTTGGACCGCAGTTTCAGAATTTCGATAAGCGGTCAAGTTTTACGCGGTGGAAA CGCTCATCATTTGCAAGAACAATGGGAGAGAAACCGCAGAATATGTTAAAGAAGATTATTTTTGAGG TTCCTCTGATGAACCAAAAGAAGTTGTTGTTACTTGACACACCCGAAGATAGCGGGATTAAGGTCGG GGATGAAACGGCGAACCATGCCTTGTCTGAGAAGAAACGTCGTGAGAAATTGAATGATCGGTTCATG ACTTTGAGATCTATCATTCCTTCGACTAGTAAGATTGATAAAGTGTCGATTCTTGATGATACAATTGA GTATCTTCAAGAACTGCAAAGACGGGTTCAAGAATTGGAATCTTGCAAAGAATCTACTCATATAGAG ACGCGAATGACGACAATGAAGAGGAAGAAACCAGAGGATGAAGATGAAAGAGCCTCAGCTAATTGT ATGAACAAGAGGAAGGAGAGTGATGTGAATGTAGGACAAGATGAACCGGCTGATACCGGTTTTGCTG GTTTAACCGATAATTTAAGGATTGGTTCGTTTGGTAATGAGGTGGTTATTGAGCTTAGATGTGCTTGG AGAGAAGGGATATTGCTTGAGATCATGGATGTTATAAGTAACCTCAACTTGGATTCTCACTCGGTACA GTCCTCAACCGGGGACGGTTTACTATGCTTAACCGTCAATTGCAAGCATAAAGGGACAAAAGTAGCT ACAACAGGAATGATCCAAGAGGCACTTCAAAGAGTTGCATGGATATGTTAA
AaMYC1	ATGTCTTTGACAATGGATGATAGTGTAGAAGTAGGAAGAGGAGGAAGAAGTAAAGCACAAAACAGC TTATTAAGAAAACAACTTGCTTTAGCTGTAAGAAGTGTTCAATGGAGCTATGCAATCTTCTGGTCTTCT TCACCAACTCAATCCGGGGTTTTGGAGTGGGGTGAAGGATCTTATAATGGAGACATAAAGAAGAGGA AGAAGATATATGAAGCTCATTGTAAATATGGATTGCAAAGAAGCAAGCAACTTAGGAAACTTTATCT GTGTATGCTTGAAGGAGATACTAGTAGTACTACTCATCATGATGATTATGATGATGGTGATGATGATG GTGGTCGTAATAGTACAACTATGATGCTTTCACCAGATGATCTCTCTGATGAAGAGTGGTACTATTTA GTCTCCATGTCCTATGTCTTCTCTCCTTCTCAATGTTTGCCAGGAAGAGCTTTGGCAACTGGTGAGACC ATATGGCTATGCAACGCTCAGTACGCGGAGACCAAACTCTTTTCTCGTTCTTTGTTAGCAAGAAGTGC ATCAATCCAGACCGTTGTGTGTTTCCCTTTATTGGGTGGTGTGATTGAGCTAGGCGTCACAGAATTGA TATCAGAAGATCCTAATGTGCTTCAACACATCAAATCTTGCTTGTTGGAGACCTCGAAACCCGATTGC TCTTTAAACCACTTCTCTGTTCACCAAGACAACGATGAAGAGAAGAATCAAATGAGGATTAAGACTA GTGAAGGAAACTCAATGCTCGAAGAGAACCATGAGATTCTATTAGGTCTATCTGATGAAGACTTGCA TTACAAAAGAACCATCACAACGGTACTCAAACACGCTGCGAATAGATCGAGAAGGAACGACAAAAA CATTCATCATCGTCGACCTAATGTTGATTCTGGCTCAAGTTTCTTCCGGTGGAAGCGACATGAGCAGC CAAAGTCAAATGTGTTGCAGCCACCTTCACAGAATGTGTTGCGGAAAATACTTCATGATGTCCCTTTG ATGCACTCTACAGACACAAAGAGAATGTTCCCAAGTCAAAGATTTGGTCTGAATCAAGATGATCCTA ATTCGGACAGAAGAAGAGAGAACGAAAAGTTCAGTGTCCTTAGAACAATGGTTCCTACTGTCAACGA GGTTGATAAAGAATCGATATTGAACAATACAATCAAGTACTTGCAAGAACTTGAGGCAAGAGTAGAG GAGCTAGAATCTTGTATGGGATCAGTTAATTTCACTGAAAGACAAAAAATGACTACGAAGAACCTTA ACGACTCTGTGTTGATCGAAGAGACATCAGGGAACTATGATGACAGTACAAAGATCGATGGGAACTC AGGAGAAACCGAACAAGTCTTTAGAGACCAGACACATTTGAGTGTCAAACTTGAAGAAACAGAAGTT GTGATCGAAGTAAGATGTTCTTACAGAGACTATATAGTTGCAGACATCATGGAAACTCTGAGTAATCT TCACATGGATGCTTTCTCTGTTAGATCTCACACACTTAATGGGTTTCTCACATTGAATCTCAAGGCCAA GTTCCGCGGGGCTGCAGTTGCGTCAGTAGGAATGATCAAGCGAGAGCTGAGAAGAGTTATTGACTTT CTTGAATCTATATGGGATGTTTCATTACCTTCTGCATCAAGTTTTCCGAGTGTTTTGATGTAA
AaTT8	ATGGATGAATCAAGTACGATTCCGGCAGAGAAACTGGTCGTCGGAGTTGAAAGAAGGGAGTTGCAAG AGCTGCTTAAGGCGGCGGTGCAATCTGTAGAGTGGACTTATAGTCTCTTCTGGCAATTATGTCCTCAA CAAAGGGTTTTAGTATGGGGGAATGGATACTACAACGGTGCAATAAAGACAAGGAAGACAACTCAG CCAAAGGAAGTGACAACGGAAGAGGCTGCTCTAGAGAGGAGTCAACAGATCAGGGAGCTTTACGAA ACACTTTTGGCCGGAGAGTCATCCACTGAAGCGAGAGCATGCACCGCATTGTCGCCGGAAGATTTAA CGGAGACTGAATGGTTTTATCTAATGTGTGCCTCCTTTACTTTCTCTCCTCCTTCAGGGATGCCGGGAA AAGCGTATGCGAGGAGTAAACACGTATGGCTAAGTGGTGCAAATGATGCTGACAGTAAAATCTTTTC CAGGGCTATTCTTGCTAAGAGTGCCAAAATTCAGACCGTGGTTTGTATTCCCATGCTTGATGGCGTCG TGGAACTTGGTACAACGGCCAAGGTAAAAGAAGATTTAGAGTTTGTTGAGCTCATAAAAAGTTTCTTC CATGACCACACCAAGTCAAACCCAAAGCCTGTTCTTTCTGAACACTCCACATACGAATTAGAGCACGA AGATGAAGACGAAGAAGAAGAAGTAGAAGCAGAGGTAGAAATGACAATGTCAGAGGAAGTAAGGC TTGGTTCTCCTGATGATGACGAAGCCTCTATTCAAAATCTACGCTCTGATTTACATATAGAATCAACCC GCTCGTTAGATATAGACACACACATGGACATGATGAATCTAGTGGAGGAAGGTGGAAACTATTCTCA GACAGTATCAACACTTCTCTTGTCACAACCAACGAGTCTTCTTTCAGATTCAGTTTCCACATCTTCCTA CATCCAATCATCGTTTACCACGTGGAGGATTGAGGCTTTGAAAGAGCATGACCATCAGCGAATGGAC AATGTGTCATCGTCCTCCTCGTCGCAACGGATGCTCAAATACATTCTCTTGAGAGCTCCTTTCCTCCAC GAAGACACTAAAGATCATAAGACACTACCGCGAGAAGAGATTAACCACGTTGTGGCAGAGCGACGC AGAAGAGAGAAGTTAAACGAGAGATTCATAACATTGAGATCAATTGTTCCATTTGTGACCAAGATGG ATAAAGTCTCAATCCTTGGAGATACCATCGATTACTTAAACCATCTTCGAAAGAGGATTGTTGAGCTT

	GAGACTACTCAACACGAGCAACAACATAAGCGGATGCGTACTTGTAAGGGAAAAACATCGGAAGAA GTGGAGGTTTCCATCATAGAAAGAGATGTTTTGTTAGAGATGAGATGTGAGTATCGAGATGGTGTATT GCTCGAAATTCTTCAGGTTCTTAAGGGCCTCGGTATAGAGACTACCACAGTTCATACCGCGGTGAAGG ACAATGATTTCGAGGCCGAGATAAGGGCTAAGGTGAGAGGGAAGAAAGCAAGTATCGCTGAGGTCA AAAGAGCTATCCATCAAATCATATCCAATACTATACTATAG
GhDEL61	ATGGCTACTACTGGGGTTCAAAATCAAGAGAAGGTCCCAATGAACTTGAAGCAACAACTTGCTCTTG CTGTTAGAAACATTCAATGGAGCTATGGGATTTTCTGGTCCATTTCAGCTAAACAACCAGGGGTCTTG GAATGGGGTGATGGTTATTACAATGGAGATATAAAGACAAGGAAAACAGTTCAATCTTTTGAACCTA AAGCTGATGACCAACTAGGTTTACAAAGAAGTGAGCAATTAAGAGAACTATTTGAATCACTTTCAGC TGGTGAAACTAGTCCTCATACTAAAAGACCTTCAGTTGCATTATCCCCTGAAGATCTCACTGCTACTG AATGGTATTATTTGGTCTGTATGTCATTTGTATTCAACATTGACCAAGGATTGCCTGGAAGAACATTAT CAATTGGTCAACCTATTTGGCTATGTAATGCTCAATATGCAGATAGTAAAGTGTTTAGTCGTTCACTG GTTGCTAAGAGCGCGTCTATTCAGACAGTAGTATGCTTTCCATATGCAGGAGGTGTGATTGAGCTTGG TGTGACTGATTTGGTATCGAAAGACCCCGGTCTTATTCATCGTGTTAAAAGTTTGTTGTTGGATGCTCC GGAGACGATAACAGGGAACATCAATGATGTTGCTTGTCCAGGTCTTGGTCCGAACGAAATTGAGTCC GAATTGAGTCCGTTTTTAGGCTGTGAACAACTAGAAAGAGGTTCTCCAAACGAGATTTCGGATGGTTT TGAGCCTAACCAACCAGCAGAAGATCCGTTCGTGAATGGTGGGGCTTCTCAGGTGCAAAGTTGGCAA TTCATGGATGACCACCATTCTTTGAATACAAGTGACTGCATATCTCAAACCTTTTCTGATCATGAAGAT GTTGTTCCTCTGTGCCAGGGTGAAAATGATAATGACAATGATTTCCGAGATGTCGAAGAGTGTGATCG TATAAACCGGGCTGCTTTTGATCCTATAAGCGATGATATGCACTACCGAACCGTCGTGTCGGTCCTAT TAAAGAGCTCGCACCAGTTTATTCTGGGACCGCATTTTGGAAACTCGAACAAGGAATCCGGGTTCATT AGCTGGAAGATGAATAGCTCAGTGAAATATCGGAAAGCAAAGGTTGAAATCCCTCAAAAGTTATTGA AGAAGATGTTGTTTGAAGTCCCTCGGATGCATGATAAAGGATTGCTTAAATCTCCACAAGGCGGTGAT GGTGTTGGAGATGCGGTTTGGAGACCAGAAGCGGATGAACTTTGTAAAAGCCACGTCTTATCAGAGA GGAGGCGTCGGGAAAAAATAAACGAACGACTTATGATCCTCAAATCATTGGTCCCTACGAATAGCAA GGCTGATAAAGTTTCTATCTTAGATGATACAATAGAGTACCTACAAGACCTCGAAAGAAGAGTTGAA GAATTGGAATGTTGCAGAGAATTAACCGAGTCTGAGACTAAAACGAAACAGAAACATCATCGGGATC GTGCTGAGCGAACATCCAGTAACAAAGTCACCAACGGAAACAAATCGGCTTCCTCAAATAAAAGGAA AGCGTACGATATTGAGGAAACAAAACAGGATATCGACCATGTTGCATCTAAAGACGGCTCGACCGAA AATCTAACCGTTAGTACGAACAACAAGGATTTAACAATCGAGTTTAAGTGTCGATGGCGGGATGGAA TTCTGTTCGAGATAATGGATGCTCTAAGCGTACTTGATTTGGATTGCCACTCTGTTCAATCGTCTACCA TCGAAGGGATTCTTTCTGTGACTATAAAATCAAAGTACAAAGGATCAAGTGTTGCAAAACCAGGGAC AATCAAGCAAGCATTATTACAAAAGGTTCAATCTTTAACCTTTGTGTAA
GhDEL65	ATGTCTACTGGAGTTCAACATCAAGAGAGAGTACCAATGAACCTGAAGAAACAACTTGCTCTTGCTGT GAGGAACATTCAATGGAGTTATGCAATTTTCTGGTCCATATCAACTAGACAACCAGGGGTGTTAGAAT GGGGAGAAGGTTATTACAATGGAGATATAAAGACAAGGAAAACAGTTCAATCTGTAGAACTCAACAC TGACCAATTGAGTTTACAGAGAAGTGAGCAACTGAGACAGCTTTATGAGTCTCTTTCAGCTGGTGAAA GCAGTCCTCAAGCTAAACGACCTTCAGCAGCATTATCTCCTGAAGATCTTACTGATACTGAATGGTAT TACTTGGTTTGTATGTCATTTGTATTCAACATTGGCCAAGGATTACCTGGAAGAACATTGTCTAGTGGT CAACCTGTTTGGCTTTGTAATGCTCATTGTGCTGACAGTAAAGTGTTTGGTCGTTCACTACTAGCTAAG AGTGCATCGATTCAGACTGCAGTATGCTTTCCGTTTTCAGGAGGTGTGGTTGAGCTCGGTGTGACTGA TTTGGTATTTGAAGATTTGAGCCTCATTCAGCGCGTTAAAACTTTGCTCTTGGATGATCCACAGCCGAT TGTTTCTAAGAGATCGATTCAAGTCGATGGGATGAACAACGATCTTGCTTGTCCAGCTCTTGATCCTTT GATCCTTGCCACCAAATTGAGTCCAATATTAGGCTGTGAACAACTAGAAACGGTTTCTCCTGATGATA GTCCGGACGGCTTGGAGCCTAAGCAATCAAGAGAAGATTCATTATTGATTGAAGGGATAAATGGTGG AGCTTCTCAAGTACAAAGTTGGCAATTCATGGATGAAGAGTTCAGCAATTGTGTTCACCATTCCTTGA ATTCAAGTGACTGCATATCTCAAACCATTGCGGATCATCGAAAGGTCGTTCCTCTTTGCCGGGGAGAA AATGATAATGGTTTGCAAGATGTTGAAGAGTGCAATCAGACTAAACTAACATCTTTTGATCGTCAAAA CGATGATCGGCACTTCCATGAAGTTCTCTCGGCCTTATTCAAGAGCTCACACCCGTTGATTTTAGGAC CACAGTTTCGAAACTCTAACAAGGAATCGAGCTTTATCAGATGGCAGAAAAATGGCTTGAAGCCTCA AAAAGAAAGAGATGAAACCCCTCAAAAGTTACTGAAGAAGATATTGTTCTTGGTTCCTCATATGCAT GATAGAGGATTGATTGAATCTCCTGAAACTAATGCTGTTCGAGATGCAGCTTGGAGACCCGAAGCTG ATGAAATTTGCGGAAACCATGTGTTATCGGAGAGGAAGCGGAGGGAAAAAATAAACGAACGACTTA TGATGTTGAAATCACTTGTCCCTGCAAATAACAAGGCTGACAAGGTTTCTATACTAGATGTCACGATA GAATACTTACAAACCCTCGAAAGAAGGGTTGCGGAATTGGAATCTTGCAGAAAGTCAGAAGCAAGAA CGAAAATCGAGCGAACATCAGATAACAACGGAAAGAAATCGTCCCTAAGTAAAAGGAAAGCCTATG ATGTTGTTGATGAAGCTGATCAAGAGATCGGCTATGTTGCATCTAAAGACGGTTCAACAGATAAAGTT ACTCTCAGTATGAACAACAAGGAGCTTCTAATCGAGTTCAAGTGTCCATGGCGAGAAGGAATTTTGCT TGAGGTAATGGATGCATTAAGCATTCTCAATTTGGATTGCCACTCAGTTCAGTCATCTACCACTGAGG GGATTCTCTCCCTGACCATAAAATCCAAGTACAAAGGATCAAGTGTTGCAAAAGCAGGACCAATCGA GCAAGCATTGCAAAGAATTGCTAGCAAGTGTTGA

PhAN1	ATGCAGCTGCAAACCATGTTACGGAACGCTGTGCAATCTGTTCAGTGGACATATAGTCTTTTCTGGCA ATTATGTCCTCAACAAGGGGTGTTAGTGTGGAGAGATGGATATTACAATGGAGCTATAAAGACTAGG AAAACAGTGCAACCAATGGAAGTTAGTGCTGAGGAGGCTTCTCTTCACAGAAGCCAGCAACTTAGAG AACTTTATGAATCACTTTCTGCCGGCGAATCAAATCAACCGACGAGAAGGCCATCAGCAGCTTTATCA CCGGAGGACTTGACTGAATCAGAGTGGTTTTATCTCATGTGTGTTTCTTTCTCTTTTCCTGCTGGAATC GGATTACCAGGCAAGGCTTATTCAAAGAAACATCACATATGGATAACTGGTGCAAACGAGGTTGAAA GCAAAGTCTTTTGTAGAGCTATTCTTGCTAAGAGTGCCCGCGTACAGACTGTCGTCTGTATTCCTCTAT TGGATGGTGTAGTGGAACTGGGGACTACACAACGGATTCAAGAAGACATTGGATTCATAAACCATGT CAAGACTTTCTTCATTGAGCAACAACCACCTCTGCCGCCAAAGCCAGCCTTATCTGAGCACTCCACTT CCAATCCCACCACATTTTCAGAACTAAACTTTTACTCCAGCAATACTCCACCATCCGCTGGCACTACTC CTGCGGATGAACACGGTGGAGTAGCCGGAGATGAAGACGAAGAAGATGAGGATGAGGAGGACGAAG ACGAGGAACAAGAGGATGATGAAGAAGCCGAGTTGGACTCGGATAAGATAGCGGCTCAGGTTGGCC CGGCTGATGTTATAGCCGCGGCTGAGGCCAGTGAACTTATGCAGCTTGATATGTCTGAGGCAATACGG TTTGGGTCACCGGATGACGGCTCCAATACAAATATGGACTCTGATTTCCATATGGTTGGAGTTAGCCA AGCCGAAAACCCAGCTGACTACCAGCGCCAAGCTGAGTCATTCAAAGCTGACACTTCCATTAGCTGG GCTCATTTCCAAGACCTTCCACATTTACCAGGCGGCCCTAGTTATGATGAATTATCACAAGAAGACAC ACATTACTCTCAAACAGTGTCGACCATTCTTGAACACCTCTCAAACCAAAGCTCCAAATTTTCCTCTAC CATAATGGGCTGTATTTCCCAAACAACCCAATCTGCCTTCACAAGGTGGCCCAGCCCCAGCACCACCG TCTCCAGCCCATTTCTTGACGGCGGCGCCACCTCCGGCCAGTGGCTGCTCAAAAGCATACTATTCTCT GTTCCATTTCTTCACACTAAATACCAAACTGCAGCTGAAGTTTCTCCAAAGTCACGTGACGCTACCAC TGTTGATTCCTCCACTGCATCTCGCTTTCGAAAAGGGTGTAGTATAACACAAGAAGAGCCTAGTGGAA ACCATGTACTTGCTGAACGACGGCGTAGAGAAAAGCTCAACGAACGGTTTATCATTTTGAGGTCACTT GTTCCTTTTGTTACGAAAATGGATAAAGCCTCCATTCTTGGTGACACCATAGAATATGTCAAGCAGTT ACGTAAGAAAGTTCAGGATCTTGAAGCTAGAGCCAATCAGACGGAGGCTACGCTGCAGACAAAGGAT ACAGGTACTGTGAAGGTGTTGCAAGGAAGGGGTAAGAGGAGAATGAAGATAGTGGAAGGAAGTGTT GGTGGAGGACAGGCAAAGATCACGGCATCCTCGCCCTCAACGACACATGAAGAGGAGATAGTGCAA GTAGAAGTATCAATTATCGAGAGTGATGCACTGGTGGAGCTCAGGTGTCCATACAAAGAAGGGTTGT TGTTAGATGTAATGCAAATGCTAAGGGAACTTAAAGTGGAGGTTGTAACCATTCAATCATCTCTTAAT AATGGCAGCTTCTTTGCTGAGCTGAGAGCTAAGGTAAAAGAGAATATATATGGAAGGAAAGCAAGCA TTCTGGAAGTCAAGAAGTCAATACACCAGTTAATCCCTAGAGTTTAA
PhJAF13	ATGGCTATGGGATGCAAAGACCATAATGGAGTCCCTGACAACTTGAGAAAACAACTTGCTTTTGCTGT TAGAGGCATTCAATGGAGTTATGCAATTTTCTGGTCAACTACAGTTTCACAACCAGGGGAGTTGGAAT GGAGTGATGGTTACTATAATGGAGATATTAAGACCAGGAAGACAGTTCAGGCAGGGGAAGTCGATGA AGACCAGCTGGGATTGCAAAGAACTGAGCAGTTGAGAGAACTTTATAGTTCCCTCTTAATAGGTGAA GGTGAGGAAGACCTCCAACCACAGGCTAAAAGGCCCTCGGCTGCATTATCTCCTGAAGATCTCACTG ATACAGAGTGGTATTTCTTAGTATGCATGTCGTTCGTCTTCAATGTTGGCCAAGGGTTGCCAGGAAAG AGCTTAGCAAGGAACGAAACAATCTGGCTATGTAATGCTCACCAAGCAGAGAGTAGAGTATTTTCTC GGTCTCTTCTAGCAAAGAGTGCATCTATCCAGACTGTTGTATGCTTTCCGTATCTTGGAGGAGTAATTG AGCTGGGAGTCACTGAGCTTGTTGTAGAAGATCCCAACCTCATTCAGCAAATAAAAATTTCAATACTA AAGGTTGATCACTCCATTATTCCGAAGAGGCCTAATTATGTCTCTAGTGATGCAAAAAATGACGCCAT TGGCGTTTGCCCAAAGCCTGATCATAATGTTCTTGAAAATGATGCTTATCCAGTTGAAATAAACAATA GTTCACCTCATGATAGTTCAAATGGTTTTGGTGCCAATCAGGAGGTAGAAGATTCACTAATGGTGGTA GGTGTTATAGGTGAAACTTCACAAGCTCAAAGCTGGAAATTCACGGATGATAATATGAGTAACGGTG TGCATAATTCTTTGAATTCCAGTGACTGTACCTCTCAAAATTATGCAAATTGTGAAAAGTTGTCCCCTC TTTCTAGTGGAGAAAAAGAAACAAAGCCTGCCCCACTAGACCATCAAGAGCACAATCAGAGGAAGCT ACATTTGTTGGATCACCAAGGAGATGAAACTCAGTATCAATCTGTCCTTTCAACCCTTCTAAAGAGCT CTGACCAATTAACTTTGGGACCATATTTTAGAAATACTAATAAAAGGTCATGTTTTTCTGGTTGGAAA AACGATGCTCATATTCCAAGTAGAGGAACTGCTCAAAAACTATTGAAGAAGGTACTTGTTGAAGTTCC TAGAATGCATGGTAGTGTTATACATAAATTCAGCAGAGAGAATCGTAAAAGGAACGGTCTTTGGAGA CCAGAGGTTGATGACACTGATAGAAGCCGTGTTATTTCTGAGAGAAGGCGAAGAGAAAAGATAAATG AGAGATTTATGCTTCTTGCATCAATGCTTCCAGCTGGTGGCAAGGTTGACAAAATATCACTTCTTGAT GAGACAATAGAATACCTGAAAGAGCTTGAAAGGAGAGTTCAAGATCTTGAGGCTAAATCAGGAAGA AGACCAAATGACGTAGCAGAGCAGACATCTGATAATTGTGGCACTAGTAAATTCAATGACATCGAGG AATCACTACCGAACAAGAGGAAGGCATGTGAAATGGATGAACTGGAACCTGAAAGTCGTAATGGATT AATGAAAGGTAGTTCAGCTGATAGTATTGTCATCAATATGATCGATAAGGAAGTTTCAATCAAGATG AGGTGTCTTTCGAGTGAGGGCTTGTTGTTTAAGATTATGGAAGCACTGACCGGCCTACAGATGGATTG CCATACAGTTCAATCTTCCAACATTGATGGGATTCTATCCATTTCTATTGAATCTAAGTCAAATGTATC GAAAACTGTATCAGTTGGAACGATTAGAGAAGCACTTCAGCGAGTAGTCTGGAAATCT
ZmR(Lc)	ATGGCGCTTTCAGCTTCCCGAGTTCAGCAGGCGGAAGAACTGCTGCAACGACCTGCTGAGAGGCAGC TGATGAGGAGCCAGCTTGCTGCAGCCGCCAGGAGCATCAACTGGAGCTACGCCCTCTTCTGGTCCATT TCAGACACTCAACCAAGGGTGCTGACGTGGACGGACGGGTTCTACAACGGCGAGGTGAAGACGCGG AAGATCTCCAACTCCGTGGAGCTGACATCCGACCAGCTCGTCATGCAGAGGAGCGACCAGCTCCGGG AGCTCTACGAGGCCCTCCTGTCGGGCGAGGGCGACCGCCGCGCTGCGCCTGCGCGGCCGGCCGGCTC TCTGTCGCCGGAGGACCTCGGCGACACCGAGTGGTACTACGTGGTCTCCATGACCTACGCCTTCCGGC CAGGCCAAGGGTTGCCCGGCAGGAGTTTCGCGAGCGACGAGCATGTCTGGCTGTGCAACGCGCACCT CGCCGGCAGCAAAGCCTTCCCCCGCGCGCTCCTGGCCAAGAGCGCGTCCATTCAGTCAATCCTCTGCA TCCCGGTTATGGGCGGCGTGCTTGAGCTTGGTACAACTGACACGGTGCCGGAGGCCCCGGACTTGGTC AGCCGAGCAACCGCGGCTTTCTGGGAGCCGCAGTGCCCGAGCTCCAGCCCGTCAGGACGAGCAAACG AGACCGGCGAGGCCGCAGCAGACGACGGCACGTTTGCGTTCGAGGAACTCGACCACAATAATGGCAT GGACGACATAGAGGCGATGACCGCCGCCGGGGGACACGGGCAGGAGGAGGAGCTAAGACTAAGAGA AGCCGAGGCCCTGTCAGACGACGCAAGCCTGGAGCACATCACCAAGGAGATCGAGGAGTTCTACAGC CTCTGCGACGAAATGGACCTGCAGGCGCTACCACTACCGCTAGAGGACGGCTGGACCGTGGACGCGT CCAATTTCGAGGTCCCCTGCTCTTCCCCGCAGCCAGCGCCGCCTCCGGTGGACAGGGCTACCGCTAAC GTCGCCGCCGACGCCTCAAGGGCACCCGTCTACGGCTCTCGCGCGACGAGTTTCATGGCTTGGACGAG GTCCTCGCAGCAGTCGTCGTGCTCCGACGACGCGGCGCCCGCAGCAGTAGTGCCGGCCATCGAGGAG

	CCGCAGAGATTGCTGAAGAAAGTGGTGGCCGGCGGCGGTGCTTGGGAGAGCTGTGGCGGCGCGACG GGAGCAGCACAGGAAATGAGTGGCACTGGCACCAAGAACCACGTCATGTCGGAGCGAAAGCGACGA GAGAAGCTCAACGAGATGTTCCTCGTCCTCAAGTCACTGCTTCCGTCCATTCACAGGGTGAACAAAGC GTCGATCCTCGCCGAAACGATAGTCTACCTCAAGGAGCTTCAGAGAAGGGTGCAAGAGCTGGAGTCC AGTAGGGAACCTGCGTCGCGCCCATCCGAAACGACGACAAGGCTAATAACAAGGCCCTCCCGTGGCA ATAATGAGAGTGTGAGGAAGGAGGTCTGCGCGGGCTCCAAGAGGAAGAGCCCAGAGCTCGGCAGAG ACGACGTGGAGCGCCCCCCGGTCCTCACCATGGACGCCGGCACCAGCAACGTCACCGTCACCGTCTC GGACAAGGACGTGCTCCTGGAGGTGCAGTGCCGGTGGGAGGAGCTCCTGATGACGCGAGTGTTCGAC GCCATCAAGAGCCTCCATTTGGACGTCCTCTCGGTTCAGGCTTCAGCGCCAGATGGCTTCATGGGGCT TAAGATACGAGCTCAGTTTGCTGGCTCCGGTGCCGTCGTGCCCTGGATGATCAGCGAGGCTCTTCGCA AAGCTATAGGGAAGCGGTGA
ZmR(S)	ATGGCGCTTTCAGCTTCCCGAGTTCAGCAGGCGGAAGAACTGCTGCAACGACCTGCTGAGAGGCAGC TGATGAGGAGCCAGCTTGCTGCAGCCGCCAGGAGCATCAACTGGAGCTACGCCCTCTTCTGGTCCATT TCAGACACTCAACCAGGGGTGCTGACGTGGACGGACGGGTTCTACAACGGCGAGGTGAAGACGCGG AAGATCTCCAACTCCGTGGAGCTGACATCCGACCAGCTCGTCATGCAGAGGAGCGACCAGCTCCGGG AGCTCTACGAGGCCCTCCTGTCGGGCGAGGGCGACCGCCGCGCTGCGCCTGCGCGGCCGGCCGGCTC TCTGTCGCCGGAGGACCTCGGCGACACCGAGTGGTACTACGTGGTCTCCATGACCTACGCCTTCCGGC CAGGCCAAGGGTTGCCCGGCAGGAGTTTCGCGAGCGACGAGCATGTCTGGCTGTGCAACGCGCACCT CGCCGGCAGCAAGGCCTTCCCCCGCGCGCTCCTGGCCAAGAGCGCGTCCATTCAGTCAATCCTCTGCA TCCCGGTTATGGGCGGCGTGCTTGAGCTTGGTACAACTGACACGGTGCCGGAGGCCCCGGACTTGGTC AGCCGAGCAACCGCGGCTTTCTGGGAGCCGCAGTGCCCGACGTACTCGGAAGAGCCGAGCTCCAGCC CGTCAGGACGAGCAAACGAGACCGGCGAGGCCGCAGCAGACGACGGCACGTTTGCGTTCGAGGAAC TCGACCACAATAATGGCATGGACATAGAGGCGATGACCGCCGCCGGGGGACACGGGCAGGAGGAGG AGCTAAGACTAAGAGAAGCCGAGGCCCTGTCAGACGACGCAAGCCTGGAGCACATCACCAAGGAGA TCGAGGAGTTCTACAGCCTCTGCGACGAAATGGACCTGCAGGCGCTACCACTACCGCTAGAGGACGG CTGGACCGTGGACGCGTCCAATTTCGAGGTCCCCTGCTCTTCCCCGCAGCCAGCGCCGCCTCCGGTGG ACAGGGCTACCGCTAACGTCGCCGCCGACGCCTCAAGGGCACCCGTCTACGGCTCTCGCGCGACGAG TTTCATGGCTTGGACGAGGTCCTCGCAGCAGTCGTCGTGCTCCGACGACGCGGCGCCCGCAGCAGTAG TGCCGGCCATCGAGGAGCCGCAGAGATTGCTGAAGAAAGTGGTGGCCGGCGGCGGTGCTTGGGAGA GCTGTGGCGGCGCGACGGGAGCAGCACAGGAAATGAGTGGCACTGGCACCAAGAACCACGTCATGT CGGAGCGAAAGCGACGAGAGAAGCTCAACGAGATGTTCCTCGTCCTCAAGTCACTGCTTCCGTCCATT CACAGGGTGAACAAAGCGTCGATCCTCGCCGAAACGATAGCCTACCTCAAGGAGCTTCAGAGAAGGG TGCAAGAGCTGGAGTCCAGTAGGGAACCTGCGTCGCGCCCATCCGAAACGACGACAAGGCTAATAAC AAGGCCCTCCCGTGGCAATAATGAGAGTGTGAGGAAGGAGGTCTGCGCGGGCTCCAAGAGGAAGAG CCCAGAGCTCGGCAGAGACGACGTGGAGCGCCCCCCGGTCCTCATCATGGACGCCGGCACCAGCAAC GTCACCGTCACCGTCTCGGACAAGGACGTGCTCCTGGAGGTGCAGTGCCGGTGGGAGGAGCTCCTGA TGACGCGAGTGTTCGACGCCATCAAGAGCCTCCATTTGGACGTCCTCTCGGTTCAGGCTTCAGCGCCA GATGGCTTCATGGGGCTTAAGATACGAGCTCAGTTTGCTGGCTCCGGTGCCGTCGTGCCCTGGATGAT CAGCGAGGCTCTTCGCAAAGCTATAGGGAAGCGGTGA
ZmB	ATGGCCCTGTCTGCTTGTCCAGCTCAAGAGGAACTTCTGCAACCTGCTGGTAGGCCACTGAGGAAGCA ACTTGCAGCTGCTGCTCGCAGCATCAACTGGTCCTACTCACTGTTCTGGTCCATCAGCTCTACCCAGA GGCCAAGGGTTCTGACTTGGACCGATGGCTTCTACAACGGCGAGGTTAAGACCCGCAAGATCAGCCA CTCTGTTGAGCTGACCGCTGACCAGCTTCTGATGCAGAGGTCTGAGCAGCTGAGAGAGCTTTACGAGG CTCTGCAATCTGGTGAATGCGATAGAAGGGCTGCTAGGCCAGTTGGCTCACTGTCTCCAGAGGATCTT GGCGATACCGAGTGGTACTACGTGATCTGTATGACCTACGCCTTCTTGCCAGGTCAGGGACTTCCTGG TAGAAGCTCTGCTTCTAACGAGCACGTGTGGCTGTGCAACGCTCATCTTGCTGGCTCTAAGGACTTCC CAAGGGCTCTGTTGGCTAAGGTTCCCGAGGATCCAGACCTGATCAACAGGGCTACTGCCGCTTTCAGG GAACCACAGTGCCCAATCTACTCCGAGCAGCCAAGCTCTAACCCAAGCGCTGATGAGACTGGTGAGG CCGCTGATATCGCTGTTTTCGAGGGCCTGGATCACAACGCCATGGACATGGAAACTGCCGGCATTGCT GTGTTTGAAGGCCTCGACCATAACGCTATGGATATGGAGACAGTTACCGCCGCTGCAGGCAGACATG GTACTGGTCAAGAACTTGGCGAGGCTGACAGCCCATCTAACGCTTCTCTCGAGCATATCACCAAGGGC ATCGACGAGTTCTACAATCTGTGCGAAGAGATGGACGTGCAGCCACTTGAGGACGCCTGGATTATGG ACGGCTCTAACTTCGAGGTGCCAAGCAGTGCACTTCCAGTGGACGGTTCTTCTGCTCCTGCTGATGGT TCTAGGGCCACCTCTTTCGTTGCTTGGACTAGGTCTAGCCAGTCCTGCTCAGGTGAAGCTGCCGCTGTT CCAGTTATTGAGGAACCGCAGAAGCTCCTGAAGAAGGCTGTTGCTGGCGGCGGTGCTTGGGCTAACA CTAATTGCGGAGGTGGCGGCACTACCGTTACTGCACAAGAGAACGGCGCTAAGAACCACGTGATGTT GGAGAGAAAGAGGCGCGAGAAGCTGAACGAGATGTTCCTGGTGCTGAAGTCTCTGGTGCCGAGCATC CATAAGGTGGACAAGGCTAGCATCCTGGCCGAGACTATCGCCTACCTTAAGGAACTGCAGCGCAGGG TGCAAGAGCTTGAATCTAGAAGGCAAGGCGGTTCTGGCTGCGTGTCAAAGAAGGTTTGCGTTGGCAG CAACTCCAAGCGCAAGTCACCAGAGTTTGCCGGGGGTGCTAAGGAACACCCTTGGGTTTTGCCAATG GATGGCACCAGCAACGTGACCGTGACTGTGTCTGATAGGGATGTGCTGCTTGAGGTGCAGTGCCTGTG GGAAAAGCTGCTTATGACCAGGGTTTTCGACGCCATCAAGAGCCTGCATCTGGACGCTCTGTCTGTGC AAGCTTCAGCTCTTGACGGCTTCATGAGGCTGAAGATCGGCGCTCAATTCGCTGGATCTGGCGCTGTT GTTCCAGGCATGATCTCTCAGAGCCTTAGGAAGGCTATCGGCAAGAGGTGA
AtGL1	ATGAGAATAAGGAGAAGAGATGAAAAAGAGAATCAAGAATACAAGAAAGGTTTATGGACAGTTGAA GAAGACAACATCCTTATGGACTATGTTCTTAATCATGGCACTGGCCAATGGAACCGCATCGTCAGAAA AACTGGGCTAAAGAGATGTGGGAAAAGTTGTAGACTGAGATGGATGAATTATTTGAGCCCTAATGTG AACAAAGGCAATTTCACTGAACAAGAAGAAGACCTCATTATTCGTCTCCACAAGCTCCTCGGCAATA GATGGTCTTTGATAGCTAAAAGAGTACCGGGAAGAACAGATAACCAAGTCAAGAACTACTGGAACAC TCATCTCAGCAAAAAACTCGTCGGAGATTACTCCTCCGCCGTCAAAACCACCGGAGAAGACGACGAC TCTCCACCGTCATTGTTCATCACTGCCGCCACACCTTCTTCTTGTCATCATCAACAAGAAAATATCTAC GAGAATATAGCCAAGAGCTTTAACGGCGTCGTATCAGCTTCGTACGAGGATAAACCAAAACAAGAAC TGGCTCAAAAAGATGTCCTAATGGCAACTACTAATGATCCAAGTCACTATTATGGCAATAACGCTTTA TGGGTTCATGACGACGATTTTGAGCTTAGTTCACTCGTAATGATGAATTTTGCTTCTGGTGATGTTGAG

	TACTGCCTTTAG
AtWER	ATGAGAAAGAAAGTAAGTAGTAGTGGTGACGAAGGAAACAATGAGTACAAGAAAGGTTTGTGGACA GTAGAAGAAGACAAAATCCTCATGGATTATGTCAAAGCTCATGGCAAAGGTCACTGGAATCGTATTG CCAAAAAGACTGGTTTAAAGAGATGTGGAAAGAGTTGTAGATTGAGGTGGATGAATTATCTCAGCCC TAATGTGAAAAGAGGCAATTTCACCGAGCAAGAAGAGGATCTTATCATTAGGCTCCACAAGTTGCTT GGTAATAGGTGGTCTTTAATTGCTAAAAGAGTGCCGGGTCGAACGGATAATCAAGTGAAGAACTATT GGAACACGCATCTTAGTAAGAAACTCGGAATCAAAGATCAGAAAACCAAACAGAGCAATGGTGATA TTGTTTATCAAATCAATCTCCCGAATCCTACCGAAACATCAGAAGAAACGAAAATCTCGAATATTGTC GATAACAATAATATCCTCGGAGATGAAATTCAAGAAGATCATCAAGGAAGTAACTACTTGAGTTCAC TTTGGGTTCATGAGGATGAGTTTGAGCTTAGCACACTCACCAACATGATGGACTTTATAGATGGACAC TGTTTTTGA
AtPAP1	ATGGAGGGTTCGTCCAAAGGGCTGCGAAAAGGTGCTTGGACTACTGAAGAAGATAGTCTCTTGAGAC AGTGCATTAATAAGTATGGAGAAGGCAAATGGCACCAAGTTCCTGTAAGAGCTGGGCTAAACCGGTG CAGGAAAAGTTGTAGATTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGAGGAAAACTTAGC TCTGATGAAGTCGATCTTCTTCTTCGCCTTCATAGGCTTCTAGGGAATAGGTGGTCTTTAATTGCTGGA AGATTACCTGGTCGGACCGCAAATGACGTCAAGAATTACTGGAACACTCATCTGAGTAAGAAACATG AACCGTGTTGTAAGATAAAGATGAAAAAGAGAGACATTACGCCCATTCCTACAACACCGGCACTAAA AAACAATGTTTATAAGCCTCGACCTCGATCCTTCACAGTTAACAACGACTGCAACCATCTCAATGCCC CACCAAAAGTTGACGTTAATCCTCCATGCCTTGGACTTAACATCAATAATGTTTGTGACAATAGTATC ATATACAACAAAGATAAGAAGAAAGACCAACTAGTGAATAATTTGATTGATGGAGATAATATGTGGT TAGAGAAATTCCTAGAGGAAAGCCAAGAGGTAGATATTTTGGTTCCTGAAGCGACGACAACAGAAAA GGGGGACACCTTGGCTTTTGACGTTGATCAACTTTGGAGTCTTTTCGATGGAGAGACTGTGAAATTTG ATTAG
AtPAP2	ATGGAGGGTTCGTCCAAAGGGTTGAGGAAAGGTGCATGGACTGCTGAAGAAGATAGTCTCTTGAGGC TATGTATTGATAAGTATGGAGAAGGCAAATGGCATCAAGTTCCTTTGAGAGCTGGGCTAAATCGATG CAGAAAGAGTTGTAGACTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGAGGAAGACTTAGC AATGATGAAGTTGATCTTCTTCTTCGCCTTCATAAGCTTCTAGGAAATAGGTGGTCCTTGATTGCTGGT CGATTGCCTGGTCGGACCGCTAATGATGTCAAAAATTACTGGAACACCCATCTGAGTAAAAAACATG AGTCTTCGTGTTGTAAGTCTAAAATGAAAAAGAAAAACATTATTTCCCCTCCTACAACACCGGTCCAA AAAATCGGTGTTTTTAAGCCTCGACCTCGATCCTTCTCTGTTAACAATGGTTGCAGCCATCTCAATGGT CTGCCAGAAGTTGATTTAATTCCTTCATGCCTTGGACTCAAGAAAAATAATGTTTGTGAAAATAGTAT CACATGTAACAAAGATGATGAGAAAGATGATTTTGTGAATAATCTAATGAATGGAGATAATATGTGG TTGGAGAATTTACTGGGGGAAAACCAAGAAGCTGATGCGATTGTTCCTGAAGCGACGACAGCTGAAC ATGGGGCCACTTTGGCGTTTGACGTTGAGCAACTTTGGAGTCTGTTTGATGGAGAGACTGTTGAACTT GATTAG
AtTT2	ATGGGAAAGAGAGCAACTACTAGTGTGAGGAGAGAAGAGTTAAACAGAGGAGCTTGGACTGATCAT GAAGACAAGATCCTTAGAGATTACATCACCACTCACGGCGAAGGCAAATGGAGCACTCTCCCTAACC AAGCTGGTCTCAAGAGGTGTGGCAAAAGCTGTAGACTTCGGTGGAAGAACTACCTAAGACCGGGGAT AAAGCGCGGTAACATCTCATCTGATGAAGAAGAACTCATAATCCGTCTCCATAATCTTCTTGGAAACA GATGGTCGTTGATAGCTGGGAGGCTTCCAGGCCGAACAGACAATGAAATAAAGAATCATTGGAACTC AAACCTCCGCAAAAGACTTCCCAAAACTCAAACCAAGCAACCAAAACGTATAAAACATTCGACGAAC AACGAGAATAATGTATGTGTTATACGTACAAAGGCGATTAGGTGCTCAAAGACTCTTCTCTTCTCGGA TCTCTCTCTTCAGAAGAAGAGTAGTACTAGTCCACTACCTCTGAAAGAACAAGAGATGGATCAAGGT GGATCTTCGTTGATGGGAGATCTCGAATTCGATTTCGATAGGATCCATTCGGAGTTTCACTTCCCGGA TTTGATGGATTTTGATGGTTTGGACTGTGGAAACGTTACATCTCTTGTTTCATCTAACGAGATTTTGGG AGAGTTGGTTCCTGCTCAAGGTAATCTCGATCTCAATAGACCTTTCACTTCTTGTCATCATCGTGGCGA CGATGAAGATTGGCTCCGAGACTTCACTTGTTGA
AtMYB61	ATGGGGAGACATTCTTGCTGTTACAAACAAAAGCTGAGGAAAGGGCTTTGGTCTCCTGAAGAAGACG AGAAGCTTCTTACTCACATCACCAATCACGGCCATGGCTGCTGGAGCTCTGTCCCTAAACTCGCTGGT TTGCAGAGATGTGGGAAGAGTTGTCGACTAAGATGGATCAATTACTTGAGACCTGATTTAAAGAGAG GAGCTTTTTCTCCTGAAGAAGAGAATCTCATCGTCGAACTTCATGCCGTCCTTGGAAACAGATGGTCA CAGATTGCGTCAAGGCTTCCGGGTAGAACCGACAACGAGATCAAGAATCTATGGAACTCAAGCATCA AGAAGAAACTGAAACAAAGAGGCATTGACCCAAACACACACAAGCCCATCTCTGAAGTTGAGAGTTT TAGCGACAAAGACAAACCAACAACAAGCAACAACAAAAGAAGCGGTAACGATCACAAGTCTCCTAG TTCCTCTTCTGCGACTAACCAAGACTTCTTCCTCGAAAGGCCATCTGATTTATCCGACTACTTCGGATT TCAGAAGCTTAACTTCAACTCCAATCTAGGACTCTCTGTTACAACTGATTCTTCACTCTGCTCGATGAT TCCGCCGCAGTTTAGCCCCGGGAACATGGTTGGTTCTGTCCTTCAGACACCAGTATGCGTAAAGCCCT CGATTAGTCTTCCTCCCGACAACAACAGTTCGAGTCCTATCTCCGGAGGAGATCATGTGAAATTGGCT GCACCAAACTGGGAATTTCAGACAAACAACAATAATACCTCAAATTTCTTCGACAATGGCGGATTCTC ATGGTCTATCCCAAATTCTTCTACTTCTTCTTCACAAGTCAAACCAAATCATAACTTCGAAGAAATAA AATGGTCAGAGTATTTGAACACACCGTTCTTCATAGGGAGTACTGTACAGAGTCAAACCTCTCAACCA ATCTACATCAAATCAGAAACAGATTACTTAGCCAATGTTTCAAACATGACAGATCCTTGGAGCCAAA ACGAGAACTTGGGCACAACTGAAACTAGTGACGTGTTCTCCAAGGATCTTCAGAGAATGGCCGTCTCT TTTGGTCAGTCCCTTTAG

AaGL1	ATGAGAATAAGGAGAAGATCAGAGAAAGAGGAGAATCAAAAAGAGTACAAGAAAGGTTTATGGACA GCTGAAGAAGACAACATCCTTATGGACTATGTCCTTACTCACGGCAAAGGTCAATGGAACCGCATCG TCAGAAAAACTGGGCTAAAGAGGTGTGGGAAAAGTTGTAGACTGAGATGGATGAATTATTTGAGCCC TAATGTGAAGAAAGGCAATTTCACTGAACAAGAAGAAGACCTCATTATCCGTCTCCACAAGCTCCTA GGCAATAGATGGTCTTTGATAGCTAAAAGAGTACCAGGAAGAACAGATAACCAAGTCAAGAACTACT GGAACACTCATCTCAGCAAAAAACTCGTCGGAGATTACTCCTCCGTCGTCAAAACCACCGGAGACGA CGACTCTCCACCGTCTATGTTCATCAACGTCGACACAACTTCCTCTCGTCATCACCAACAAAACAATA TTACAGGCAAGAACTTCGTATCAGCTTCGTACGAGAATAAACCGAAACTGGATTTGACGCAAAGCAA CGTCATTTTCGCAACTACTAATGATGATCATCCAAACCACTGTTATAGCAGTAATGCTTTTTGGGTTAA TGAAGATGAGTTCGATCTGAGTTCACTCGTGATGATGGATTTTGCTTCTGGTGATATTGGTTACTGCCT CTAG
AaWER	ATGAGAAAGAAAGTAAGTAGTAGTGGAGAAGAAGGAAACAATGAGTACAAGAAAGGTTTGTGGACA GTAGAAGAAGACAAGATCCTTATGGATTATGTCAAAGCTCATGGCAAAGGCCATTGGAATCGTATTG CCAAAAAGACAGGTCTAAAGAGATGTGGAAAGAGTTGTAGATTGAGGTGGATGAATTACCTCAGCCC AAATGTAAAAAGAGGCAATTTCACTGAGCAAGAAGAAGATCTTATCATTAGGCTCCACAAGCTGCTT GGTAATAGGTGGTCTTTGATTGCTAAACGAGTGCCGGGTCGGACGGATAATCAAGTGAAGAATTATT GGAACACACATCTTAGTAAGAAACTCGGAATCAAAGATCCAAAAACCAAACCAAGCAATAATGGTG AAATTGTTTATCAGATCAATCTCACGAATCCTACCGAAACATTAGAAGAAGAAACAAAAATCTCGAA TATTCACGATGCCAATAATATTCATAGAGATGAAATTCAAGAAGATCGTCAAGGAAGTAACTACTTG AGTTCACTTTGGGTTCATGAGGATGAGTTTGAGCTTAGTACACTCACCAACATGATGGATTTTATAGA CGGACACTGTTTTTAA
AaPAPL	ATGGAGGGTACATCCAAAGGTTTAAGGAAAGGTGCATGGACAGCTGAAGAAGATAGTCTCTTGAGGC AATGTATTGATGCGTATGGAGAAGGCAAATGGCACCAAGTTCCTTTAAGAGCTGGGCTAAATCGGTG CAGGAAGAGTTGTAGACTAAGATGGTTGAACTATTTGAAGCCAAGTATCAAGAGAGGAAGACTTAGC TCTGATGAAGTTGATCTTCTTCTCCGCCTTCATAAACTTCTAGGAAATAGGTGGTCCTTGATTGCTGGT AGATTGCCTGGCCGAACCGCTAACGACGTCAAGAACTACTGGAACACCCATTTGAGTAAGAAACATG AACCTTGTTGTAAAACCAAGATGAATAAGAGAAAAATTACTTGCTTTCCTACAACTCCAGCCCAAAA AATCGATGTTTTTAAGCCTCGACCTCGATCCTTCACTAGTAACAACGGCTGCAGCCGTCACAATGGCC TGACAAAAGTTGACGTCAGTCCTCCAATATGCCATGGACTCAACAACGATACTATTTGTGAAAACAGT ATCAAATGTAACAAAGATGAGGAGAAAGATGAGCTAGTGAATAGTCTAATGGATGGAGAGAATATG TGGTGGGAGAGTTTGCTACAAGAGAGCCAAGAGACAGAAGTGTTGGATCCAGTAACAGAAAAGGGG GCCACCTCGGCGTTTGACATTGAGCAACTTTGGAGTCTCTTTGATGGAGAAACAGTGGAACTTGATTA G
GhMYB2	ATGGCTCCAAAGAAGGCTGGAGTGAGCAAAAGGGTTTTTAACAAAGGTTCATGGACAGCTGAGGAAG ATAGAAGATTGGCTAAATATATTGAGATTCATGGTGCAAAGAGATGGAAAACAATCGCCATTAAATC AGGTTTGAATCGATGCGGCAAGAGTTGCAGGTTGAGATGGTTGAACTACTTGAGACCTAACATTAAG AGAGGCAACATATCAGATGAAGAAGAGGACTTAATTATTAGGCTTCATAAACTGCTGGGAAACAGGT GGTCTTTGATTGCTGGGAGACTTCCAGGGCGAACAGACAATGAAATTAAGAACTACTGGAATTCCCA TTTGAGCAAGAAAATGATAAACCATGATGTCAGAACAGAACAAACTTCCTCCTCGGAACAAATTGTG CCTCACAAAGCATGGGAAACTGTCCAGATGGAAGAAGAAGAGGTAGTAAAAGGAAGTGATGAAATT GAAAACTCTGAATTCAGCATTGATGTGGACGAATTCTTTGACTTCTCAACGGAAGGTTGCTTTGGTTT GGATTGGGTGAATAAGTTCCTTGAACTTGATGACCAACAGGATCCATTAGCAATGGTATAA
GhMYB25	ATGCAGCAGTCTCCATGTAGCGACAAGGTGGGGTTGAAGAAAGGGCCATGGACTCCAGAAGAAGAC CAAAAACTCTTGTCTTATATTCAAGAACACGGCGGTGGAAGCTGGCGAGGCTTGCCCGCAAAAGCTG GACTTCAAAGATGTGGCAAGAGTTGTAGACTTAGGTGGATTAACTACTTAAGACCAGATATCAAAAG AGGAAAGTTCAGTTCGCAGGAAGAACGAACCATCATTCAACTCCACGCCCTTCTTGGAAACAGGTGG TCGGCTATTGCGGCTCATTTGCCAAAAAGAACAGACAATGAGATCAAGAACTACTGGAATACACAGT TGAAGAAAAGGTTGACGACGATAGGGATCGACCCTGCAACTCACAGGCCTAAAACCGATACCCTCGG TTCAACTCCCAAGGATGCCGCTAACCTTAGCCACATGGCTCAATGGGAGAGTGCTCGGTTAGAAGCTG AAGCTAGATTGGTGAGAGAGTCGAAACGAGTTTCAAACCCTCCGCAAAACCAATTTAGGTTCACGTC TTCATCGGCTCCTCCACTGGTAAGCAAAATTGATGTTGGTTTGGCTCATGCTACTAAACCGCAATGCC TCGATGTACTCAAAGCTTGGCAACGTGTAGTCACTGGATTGTTCACTTTCAACACTGACAACCTCCAA TCTCCAACATCGACGTCGAGCTTCACGGAAAACACGTTACCAATCTCATCTGTCGGGTTCATTGACAG CTTTGTGGGGAACTCAAATAACAGCTGTTGCGGAAATAATTGGGAATGTGTGGAGAAATCGAGCCAA GTTGCTGAATTACAGGAAATATTGGATAACTCAATGGGGTTGCATGACATATTGGATCTCTCCTCAGA AGATGTATGGTTTCAAGGCTCATACAGGGCGGAAAATATGATGGAAGGGTATTCGGACACGTTAATG GTTTGTGATTCTGGGGATCATCCGAAGAGTTTGTCAATGGAGCCTAGACAAAACTTTAATGTTGGAAC AAGTAATGCTAGTAGTTTCGAAGAAAACAAGAATTACTGGAACAACATCCTTAATTTTGCGAATGCTT CCCCTTCTGGTTCTTCTGTCTTTTGA
GhRLC1	ATGGAGGGCTCATCTTTAAGAGTTAGAAAAGGTGCATGGACTGAAGAAGAAGACCTTCTTCTTAAGA AATGTATTGAGAAATATGGTGAAGGGAAATGGCATCAAGTGCCTGCTAGAGCTGGCTTGAATCGTTG CCGGAAAAGCTGTAGACTGCGGTGGCTAAATTATTTGAAGCCAAATATCAAGAGAGGACATTTTGCT GCTGATGAAGTTGACCTCATTATTCGCCTCCATAACCTCCTAGGTAATAGATGGTCACTGATTGCTGG TAGACTACCAGGAAGAACAGCAAACGATGTGAAAAACTATTGGAACACCCACTTGCTTAAAAAAAAT ATAGATACTTTCATTAAAACCTCGAACCCGAAATCTCATCAACTAAAACCTAATACTAAGCAACAAGC AACAACGTGGTATTGGCTAACTGCGGTGACAACCACGATGGATACTGTTTCCCTGACCATGATGAGAT CATGTGGTGGGAAAATATGATGATGAATGAAAAGGAGGTTGATGGCCATCAGCTACAATGTTCAGCC AATGACATTGATGAAAGTGTGTTGGACCAAATTATGAATGAAGACAATTTTGGCAATACTATGGATG AGCTTTTTCTTGATGAGGAACCGTGGAATGTGTTCAACCCATAG

PhAN2	ATGAGTACTTCTAATGCATCAACATCAGGAGTAAGAAAAGGTGCATGGACCGAGGAAGAAGATCTTT TATTGAGAGAATGCATTGAGAAGTATGGAGAAGGAAAGTGGCATCTAGTTCCAGTTAGAGCTGGTCT GAATAGATGCAGGAAAAGTTGCAGACTTAGGTGGTTGAATTATCTAAGGCCACATATAAAAAGAGGG GACTTCTCTTTGGATGAAGTAGATCTCATTTTGAGGCTTCATAAGCTTCTAGGCAACAGATGGTCACTT GTAGCTGGTAGACTTCCTGGAAGAACAGCAAACGATGTCAAAAACTATTGGAACACCCACCTTCGAA AGAAGTTAATTGCTCCTCATGATCAGAAACAAGAGAGCAAGAACAAAGCCATGAAAATTACCGAGA ACAACATAATAAAACCTCGTCCTCAGACCTTCTCAAGGCCGGCAATGAATCATGTTTCTTGTTGGAAC GGCAAAAGTTGTAGTAAAAACACTATAGACAAGAATGAAGGTGACACCGAAATAATAAAGTTTAGTG ATGAGAAGCAAAAACCGGAAGAATCGATAGATGATGGACTTCAATGGTGGGCAAATTTATTAGCCAA CAACATTGAGATTGAGGAATTAGTTAGTTGTAATTCACCAACATTGTTGCATGAGGAAACAGCACCAT CGGTAAATGCTGAAAGCAGCCTTACTCAAGGAGGAGGAAGTGGCTTAAGTGACTTTTCAGTTGATATT GATGACATATGGGATTTAGTTAGTTAG
PhAN4	ATGAAAACTTCTGTTTTTACGTCGTCGGGGGTACTGAGAAAAGGTTCATGGACTGAAGAAGAAGATA TTCTTTTGAGGAAATGTATTGAGAAGTACGGGGAAGGAAAGTGGCATCAAGTTCCTGTTAGAGCTGG TTTGAATAGATGCAGGAAGAGTTGCAGACTAAGGTGGATGAATTATCTAAGGCCACATATAAAGAGA GGTGACTTCTCTCCAGATGAAGTGGATCTTATTTTGAGGCTTCATAAGCTTCTTGGCAACAGGTGGTC ACTTATTGCTGGGAGACTTCCGGGAAGAACAGCAAACGATGTGAAAAACTACTGGAACACTAACCTT CTAAGGAGGTCAAAGTTTGCTCCTCCTCAGCAACACGATAGGAAATGTCCTAAAGCAATTAAGACCA TGGCCAAGAATGCCATAATAAGACCTCAACCTCGGAACCTCTCAAAATTAGCAAAGAATAACGTCAG TACTATACACAAGGATGAACATAGCAAACAGGAAATTATCATCGAGAAGCCAACGACGGCCGAAGTC GTGTCCAGAGACGAGAACGTTGAATGGTGGACGAATTTATTACTGGATAACTGCAACGGATTTGAGA AGGCAGCAACTGAAAGCACTTCAGCATTTAAGAACATAGAAAGTTTGTTAAACGAAGAACTATTATC ACCATCGATAAATGGTGGAACCTACTATCCCATGCAAGAAACTAGAGACATGGGTTGGAGTGACCTT TCTATTGATGCTGACCTCTGGGAATTACTATAG
PhPH4	ATGAGAACCCCATCATCATCATCAACAACAAGCAACAAAGTAACACCATGTTGTAGCAAGGTAGGGT TAAAAAGAGGTCCATGGACACCAGAAGAAGATGAAATATTGACAAATTATATAAATAAAGAAGGAG AAGGACGGTGGCGAACGTTGCCAAAGAAGGCGGGGCTCCTCCGTTGTGGAAAAAGCTGCCGCCTTCG GTGGATGAATTACCTCCGTCCTTCAGTTAAACGTGGCCATATTGCACCTGATGAAGAAGATCTCATTC TTCGCCTCCATCGTCTCCTTGGCAACAGGTGGTCCTTGATAGCTGGGAGAATTCCAGGGAGAACAGAT AATGAGATAAAGAATTATTGGAACACTCACCTTAGCAAGAAGTTAATCAGTCACGGAATAGATCCTA GAACTCACAAGCCATTGAAAAACTCTAATTCCTCAAGTGATGATATTACCAACAAATTAGCTTCTTCT TCTCCTCCTTCATCTTCAAAAGCAAATGATCTCAATCCAATTCTAAGCCCCACTTACATTTCTAGTTTT CAAATGGAAGAACCATTAGGAAAAATCAATACTCACCCGGGAGAAATTACTAGTCTTGATGATCAAT ATCAAAGTAACGCGATTCTTGCCGAGTATGGTGATGATCTGAATATTGCGGTTACTATTGAGGAAGAT GTTGAAATGAATTGTTGCACGGATGATGTTTTCTCCTCTTTCTTGAATTCTTTGATCAATGAAGATATG TTCGCTTGCCAAAACCAACAAACCAACGGGACGTTCCAAGATTTTGATCCTTTCATGGCTTCATCATC TACACCTTCATCTGATCAATATAATCCCAGTTAG
ZmC1	ATGGGGAGGAGGGCGTGCTGCGCGAAGGAAGGCGTTAAGAGAGGGGCGTGGACGAGCAAGGAGGA CGATGCCTTGGCCGCCTACGTCAAGGCCCATGGCGAAGGCAAATGGAGGGAAGTGCCCCAGAAAGCC GGTTTGCGTCGGTGCGGCAAGAGCTGCCGGCTGCGGTGGCTGAACTACCTCCGGCCCAACATCAGGC GCGGCAACATCTCCTACGACGAGGAGGATCTCATGATCATCCGCCTCCACAGGCTCCTCGGCAACAG GTGGTCGCTGATTGCAGGCAGGCTGCCTGGCCGAACAGACAATGAAATCAAGAACTACTGGAACAGC ACGCTGGGCCGGAGGGCAGGCGCCGGCGCCGGCGCTGGCGGCAGCAGGGTCGTCATCGCGCCGGAC ACCGGCTCGCACGCCACCCCGGCCGCGACGTCGGGCAGCGGCGAGACCGGCCAGAAGGGCGCCGCTC CTCGCGCGGACCCTGACTCAGCCGGGACGACGACGACCTCGGCGGCGGCGGTGTGGGCGCCCAAGGC CGTGCGGTGCACGGGCGGACTCTTCTTCTTCCACCGGGACACGACGCCGGCGCACGCGGGCGAGACG GCGACGCCAATGGCCGGAGGAGGATTAGGAGGAGAAGCAGGGTCGTCGGAAGATTGCAGCTCAGCG GCGTCGGTATCGCCTCTCGTCGGAAGCCAGGACGAGCCGTGCTTCTCCGGCGACGGTGACTGCGACTG GATGGACGACGTGAGGGCCCTGGCGTCGTTTCTCGAGTCCGACGAGGACTGGCTCCGCTGTCAGACG GCCGGGCAGCTTGCGTAG
ZmPL	ATGGGCCGCAGGGCTTGCTGTGCTAAGGAAGGTGTTAAGAGGGGCGCCTGGACCGCCAAGGAAGATG ATACTCTGGCCGCCTACGTGAAGGCTCATGGTGAAGGCAAGTGGCGCGAGGTGCCACAAAAGGCTGG TCTTAGAAGGTGCGGCAAGAGCTGCAGGCTGCGCTGGCTTAACTACCTGAGGCCGAACATCAAGAGG GGCAACATCAGCTACGACGAAGAGGACCTGATCGTGAGGCTGCACAAGCTGCTTGGCAACAGGTGGT CACTGATCGCTGGCAGACTTCCAGGCAGGACCGACAACGAGATCAAGAACTACTGGAACAGCACCCT CGGCAGACGCGCTGGCGCTGGTGCAGGCGCTGGTGGTTCTAGAGTTGTGTTCGCTCCAGACACCGGC AGCCATGCTACTCCAGCTGCTGCTGGCAGCAGAGAGATGACTGGCGGTCAAAAGGGTGCCGCTCCAA GGGCTGATCTTGGCTCTCCAGGTTCTGCTGCTGTGGTGTGGGCTCCAAAGGCTGCTAGATGCACTGGC GGCTTGTTCTTCCACAGGCGCGATACCCATACCCCACATGCTGGCGGTACTGAGACTCCGACCCCAAT GATGGCTGGCGGTGCTGGTGGTGAAGCTAGGTCTAGCGACGACTGCAGCTCTGCTGCTTCTGTGTCTG TGTCTCCACTGGTGGGCAGCTCTCAGCACGACCCATGCTTCTCTGGTGACGGCAACGGCGACTGGATG GACGATGTTAGGGCTCTGGCTAGCTTCCTCGAGAGCGACGAGGAATGGCTGAGGTGCCATACTGCTG AGCAGCTGGTT
ZmP1	ATGGGGAGGGCGCCGTGCTGCGAGAAGGTGGGGCTCAAGCGAGGGAGGTGGACGGCGGAAGAGGAC

CAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAGGTCGCTGCCCAAGAATGCAG
GCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTACCTTCGGGCGGACGTCAAGAG
GGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAGCTCCACGCCACCCTCGGCAACAGGTGG
TCCCTGATCGCCAGCCACCTCCCCGGCCGAACAGACAACGAGATCAAGAACTACTGGAACTCGCACC
TCAGCCGGCAGATCCACACGTACCGCCGGAAATACACCGCCGGGCCTGACGACACCGCCATCGCCAT
CGACATGAGCAAGCTGCAGAGCGCCGACAGGCGGCGCGGCGGCAGGACCCCGGGCCGGCCGCCGAA
GGCTAGCGCCAGCAGGACCAAGCAGGCGGACGCCGATCAGCCCGGCGGCGAGGCGAAAGGCCCGGC
CGCGGCGGCGTCGAGCCCGCGGCACAGCGACGTGGTGAACCCGGGCCCGAACCAGCCCAACAGCAG
CAGCGGCAGCACGGGCACGGCCGAGGAGGAGGGGCCCAGCAGCGAGGACGCGAGCGGGCCGTGGGT
GCTGGAGCCGATAGAGCTCGGGGACCTAGTCTGGGGGGAGGCCGACAGCGAGATGGACGCCCTGAT
GCCTATCGGGCCCGGCGGCCACGACTCGGCTGCCCTCGAAGGGCTTGGCGCGGTCGGCTGCGAGGCC
CAGGTGGACGACCTGTTCGACATGGACTGGGATGGCTTCGCGGCCCATCTGTGGGGCGGGCCGGAGC
AGGACGAGCACAGCGCGCAGCTGCGGCAGGCCGCCGAGCCGCTGGAAGTTGCTGCTGCTGCTGCTGC
TGCGACGGCGGCCCGCACCCCGGACGATCGCGAGCTGGAGGCGTTCGAGACTTGGCTCCTGTCCGAC
TCGTTC

Table S10. Plasmids

Stock No.	Gene name	TF family	TF name	Vector
UT6678	PAC1	WD40	ZmWD40	pENTR/SD/D-TOPO
UT3027	R(Lc)	bHLH	ZmbHLH1	pENTR/SD/D-TOPO
UT4953	B1	bHLH	ZmbHLH2	pENTR/SD/D-TOPO
UT6677	C1	R2R3MYB	ZmMYB1	pENTR/SD/D-TOPO
UT4632	PL1	R2R3MYB	ZmMYB2	pENTR/SD/D-TOPO
UT6679	P1	R2R3MYB	ZmMYB3	pENTR/SD/D-TOPO
468	AN2	R2R3MYB	PhMYB	pC-ACT2-attR (AD)
452	AN4	R2R3MYB	PhMYB	pC-ACT2-attR (AD)
517	PH4	R2R3MYB	PhMYB	pC-ACT2-attR (AD)
477	AN1	bHLH	PhbHLH	pC-ACT2-attR (AD)
484	JAF13	bHLH	PhbHLH	pC-ACT2-attR (AD)
930	AN11	WD40	PhWD40	pENTR1A

Table S11. Primers

Name	Sequence information
attB-AtTTG1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGATAATTCAGCTCCAGA
attB-AtTTG1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAAACTCTAAGGAGCTGCA
attB-AtGL3-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCTACCGGACAAAACAG
attB-AtGL3-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTAACTAAGTAGTCTTCAACAG
attB-AtEGL3-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCAACCGGAGAAAACAG
attB-AtEGL3-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTTAACATATCCATGCAACCC
attB-AtTT8-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGATGAATCAAGTATTAT
attB-AtTT8-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTATAGATTAGTATCATGTA
attB-AtMYC1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGTCTTTGACAATGGCTGA
attB-AtMYC1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTTAATGAAAGATACAAATCG
attB-AtGL1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAGAATAAGGAGAAGAGA
attB-AtGL1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTAAAGGCAGTACTCAACAT
attB-AtWER-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAGAAAGAAAGTAAGTAG
attB-AtWER-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAAAAACAGTGTCCATCTA
attB-AtPAP1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGAGGGTTCGTCCAAAGG
attB-AtPAP1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTAATCAAATTTCACAGTCT
attB-AtPAP2-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGAGGGTTCGTCCAAAGG
attB-AtPAP2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTAATCAAGTTCAACAGTCT
attB-AtTT2-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGGAAAGAGAGCAACTAC
attB-AtTT2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAACAAGTGAAGTCTCGGA
attB-AtMYB61-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGGGAGACATTCTTGCTG
attB-AtMYB61-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTAAAGGGACTGACCAAAAG
attB-AaTTG1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGATAACTCAGCTCCAGA
attB-AaTTG1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAAACTCTAAGGAGCTGCA
attB-AaGL3-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCTTCCGGACAAAACAG
attB-AaGL3-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAACAGATCCATGCAACCC

attB-AaEGL3-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCTGCCGGAGAAAACAG
attB-AaEGL3-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTTAACATATCCATGCAACTC
attB-AaTT8-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGATGAATCAAGTACGAT
attB-AaTT8-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTATAGTATAGTATTGGATA
attB-AaMYC1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGTCTTTGACAATGGATGA
attB-AaMYC1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCATCAAAACACTCGGAAAAC
attB-AaGL1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAGAATAAGGAGAAGATC
attB-AaGL1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTAGAGGCAGTAACCAATAT
attB-AaWER-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAGAAAGAAAGTAAGTAG
attB-AaWER-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTTAAAAACAGTGTCCGTCTA
ANS655 AaPAP-s	AACCCACAACATATACCCTCTTCC
ANS656 AaPAP-as	CAAAAGTACTCGCACACAAACAC
ANS657 AaPAP-attB1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGAGGGTACATCCAAAGG
ANS658 AaPAP-attB2	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTAATCAAGTTCCACTGTTTC
attB-GhTTG1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGAGAATTCAACTCAGGA
attB-GhTTG1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAAACTTTGAGAAGCTGCA
attB-GhTTG2-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCCGCTAGCAGCGATCC
attB-GhTTG2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCATACCCTGAGAATCTGAA
attB-GhTTG3-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGAGAATTCAACTCAAGA
attB-GhTTG3-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAAACTTTGAGAAGCTGCA
attB-GhTTG4-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGACGGCCACCAGCGATCC
attB-GhTTG4-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCATACCCTTAGAATCTGAA
attB-GhDEL61-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCTACTACTGGGGTTCA
attB-GhDEL61-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTTACACAAAGGTTAAAGATT
attB-GhDEL65-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGTCTACTGGAGTTCAACA
attB-GhDEL65-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAACACTTGCTAGCAATTC
attB-GhMYB2-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCTCCAAAGAAGGCTGG

attB-GhMYB2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTTATACCATTGCTAATGGAT
attB-GhMYB25-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGCAGCAGTCTCCATGTAG
attB-GhMYB25-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAAAAGACAGAAGAACCAG
attB-GhRLC1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGAGGGCTCATCTTTAAG
attB-GhRLC1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTATGGGTTGAACACATTCC
attB-PhAN11-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGAAAATTCAAGTCAAGA
attB-PhAN11-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTACTTTAAGCAATTGCAACT
attB-PhJAF13-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCTATGGGATGCAAAGA
attB-PhJAF13-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTAGATTTCCAGACTACTCGCT
attB-PhAN1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGCAGCTGCAAACCATGTT
attB-PhAN1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTTAAACTCTAGGGATTAACT
attB-PhAN2-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAGTACTTCTAATGCATC
attB-PhAN2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTAACTAACTAAATCCCATA
attB-PhAN4-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAAAACTTCTGTTTTTAC
attB-PhAN4-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTATAGTAATTCCCAGAGGT
attB-PhPH4-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAGAACCCCATCATCATC
attB-PhPH4-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCTAACTGGGATTATATTGAT
attB-ZmPAC1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGACCCACCCAAGCCGCC
attB-ZmPAC1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTGACCCTAAGAAGCTGGACCT
attB-ZmMP1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGGCGGAGTCGGCGAAGG
attB-ZmMP1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAGACCCTGAGAATCTGAA
attB-ZmR-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCGCTTTCAGCTTCCCG
attB-ZmR-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCACCGCTTCCCTATAGCTT
attB-ZmB-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCCCTGTCTGCTTGTCC
attB-ZmB-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCCTCTTGCCGATAGCCTTCC
attB-ZmPL-F	GGGGACAAGTTTGUACAAAAAAGCAGGCTTAATGGGCCGCAGGGCTTGCTG
attB-ZmPL-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTAACCAGCUTGCTCAGCAGTAT
attB-ZmC1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGGGAGGAGGGCGTGTTG

attB-ZmC1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCACGCAAGCTGCCCGGCCG
attB-ZmP1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGGGAGGGCGCCGTGCTG
attB-ZmP1-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTGAACGAGTCGGACAGGAGCC
PrimerF (F177I)	GTTAAGACAGTGGTTTGCATTCCGTTCCTTGGAGGAGTC
PrimerR (F177I)	GACTCCTCCAAGGAACGGAATGCAAACCACTGTCTTAAC
PrimerF (P377D)	TCAGTTAATTCTCGGAGATCAGTTTCGAAACTGCGAT
PrimerR (P377D)	ATCGCAGTTTCGAAACTGATCTCCGAGAATTAACTGA
PrimerF(D477G)	CGATAAAGTATCGATTCTTGGAGATACGATAGAGTATCTTC
PrimerR(D477G)	GAAGATACTCTATCGTATCTCCAAGAATCGATACTTTATCG
PrimerF(S589H)	GAGATAATGGATGTGATTCATGATCTCCATTTGGATTC
PrimerR(S589H)	GAATCCAAATGGAGATCATGAATCACATCCATTATCTC

Please note: The AaPAPL CDS was cloned by amplifying the respective region with ANS655 and ANS656 followed by amplification using Gateway® specific primers (ANS657,658).

References:

Albert NW, Davies KM, Lewis DH, Zhang H, Montefiori M, Brendolise C, Boase MR, Ngo H, Jameson PE, Schwinn KE. 2014. A Conserved Network of Transcriptional Activators and Repressors Regulates Anthocyanin Pigmentation in Eudicots. The Plant Cell Online.

Baudry A, Caboche M, Lepiniec L. 2006. TT8 controls its own expression in a feedback regulation involving TTG1 and homologous MYB and bHLH factors, allowing a strong and cell-specific accumulation of flavonoids in Arabidopsis thaliana. The Plant Journal 46:768-779.

Baudry A, Heim MA, Dubreucq B, Caboche M, Weisshaar B, Lepiniec L. 2004. TT2, TT8, and TTG1 synergistically specify the expression of BANYULS and proanthocyanidin biosynthesis in Arabidopsis thaliana. The Plant Journal 39:366-380.

Bernhardt C, Lee MM, Gonzalez A, Zhang F, Lloyd A, Schiefelbein J. 2003. The bHLH genes GLABRA3 (GL3) and ENHANCER OF GLABRA3 (EGL3) specify epidermal cell fate in the Arabidopsis root. Development 130:6431-6439.

Feller A, Hernandez JM, Grotewold E. 2006. An ACT-like Domain Participates in the Dimerization of Several Plant Basic-helix-loop-helix Transcription Factors. Journal of Biological Chemistry 281:28964-28974.

Goff SA, Cone KC, Chandler VL. 1992. Functional analysis of the transcriptional activator encoded by the maize B gene: evidence for a direct functional interaction between two classes of regulatory proteins. Genes & Development 6:864-875.

Grotewold E, Sainz MB, Tagliani L, Hernandez JM, Bowen B, Chandler VL. 2000. Identification of the residues in the Myb domain of maize C1 that specify the interaction with the bHLH cofactor R. Proceedings of the National Academy of Sciences 97:13579-13584.

Hernandez JM, Heine GF, Irani NG, Feller A, Kim M-G, Matulnik T, Chandler VL, Grotewold E. 2004. Different Mechanisms Participate in the R-dependent Activity of the R2R3 MYB Transcription Factor C1. Journal of Biological Chemistry 279:48205-48213.

Kong Q, Pattanaik S, Feller A, Werkman JR, Chai C, Wang Y, Grotewold E, Yuan L. 2012. Regulatory switch enforced by basic helix-loop-helix and ACT-domain mediated dimerizations of the maize transcription factor R. Proceedings of the National Academy of Sciences of the United States of America 109:E2091-E2097.

Liang G, He H, Li Y, Ai Q, Yu D. 2014. MYB82 functions in regulation of trichome development in Arabidopsis. Journal of Experimental Botany 65:3215-3223.

Morohashi K, Grotewold E. 2009. A Systems Approach Reveals Regulatory Circuitry for Arabidopsis Trichome Initiation by the GL3 and GL1 Selectors. PLOS Genetics 5:e1000396.

Morohashi K, Zhao M, Yang M, Read B, Lloyd A, Lamb R, Grotewold E. 2007. Participation of the Arabidopsis bHLH Factor GL3 in Trichome Initiation Regulatory Events. Plant Physiology 145:736-746.

Payne CT, Zhang F, Lloyd AM. 2000. GL3 encodes a bHLH protein that regulates trichome development in arabidopsis through interaction with GL1 and TTG1. Genetics 156:1349-1362.

Pesch M, Schultheiß I, Digiuni S, Uhrig JF, Hülskamp M. 2013. Mutual control of intracellular localisation of the patterning proteins AtMYC1, GL1 and TRY/CPC in Arabidopsis. Development 140:3456-3467.

Quattrocchio F, Verweij W, Kroon A, Spelt C, Mol J, Koes R. 2006. PH4 of Petunia Is an R2R3 MYB Protein That Activates Vacuolar Acidification through Interactions with Basic-Helix-Loop-Helix Transcription Factors of the Anthocyanin Pathway. The Plant Cell 18:1274-1291.

Shangguan X-X, Yang C-Q, Zhang X-F, Wang L-J. 2016. Functional characterization of a basic helix-loop-helix (bHLH) transcription factor GhDEL65 from cotton (Gossypium hirsutum). Physiologia Plantarum 158:200-212.

Spelt C, Quattrocchio F, Mol J, Koes R. 2002. ANTHOCYANIN1 of Petunia Controls Pigment Synthesis, Vacuolar pH, and Seed Coat Development by Genetically Distinct Mechanisms. The Plant Cell 14:2121-2135.

Symonds VV, Hatlestad G, Lloyd AM. 2011. Natural Allelic Variation Defines a Role for ATMYC1: Trichome Cell Fate Determination. PLOS Genetics 7:e1002069.

Tominaga R, Iwata M, Okada K, Wada T. 2007. Functional Analysis of the Epidermal-Specific MYB Genes CAPRICE and WEREWOLF in Arabidopsis. The Plant Cell 19:2264-2277.
Wan Q, Zhang H, Ye W, Wu H, Zhang T. 2014. Genome-Wide Transcriptome Profiling Revealed Cotton Fuzz Fiber Development Having a Similar Molecular Model as Arabidopsis Trichome. PLOS ONE 9:e97313.
Wang G, Zhao G-H, Jia Y-H, Du X-M. 2013. Identification and Characterization of Cotton Genes Involved in Fuzz-Fiber Development. Journal of Integrative Plant Biology 55:619-630.
Zhang F, Gonzalez A, Zhao M, Payne CT, Lloyd A. 2003. A network of redundant bHLH proteins functions in all TTG1-dependent pathways of Arabidopsis. Development.
Zhao H, Wang X, Zhu D, Cui S, Li X, Cao Y, Ma L. 2012. A Single Amino Acid Substitution in IIIf Subfamily of Basic Helix-Loop-Helix Transcription Factor AtMYC1 Leads to Trichome and Root Hair Patterning Defects by Abolishing Its Interaction with Partner Proteins in Arabidopsis. Journal of Biological Chemistry 287:14109-14121.
Zhao M, Morohashi K, Hatlestad G, Grotewold E, Lloyd A. 2008. The TTG1-bHLH-MYB complex controls trichome cell fate and patterning through direct targeting of regulatory loci. Development 135:1991-1999.
Zimmermann IM, Heim MA, Weisshaar B, Uhrig JF. 2004. Comprehensive identification of Arabidopsis thaliana MYB transcription factors interacting with R/B-like BHLH proteins. The Plant Journal 40:22-34.