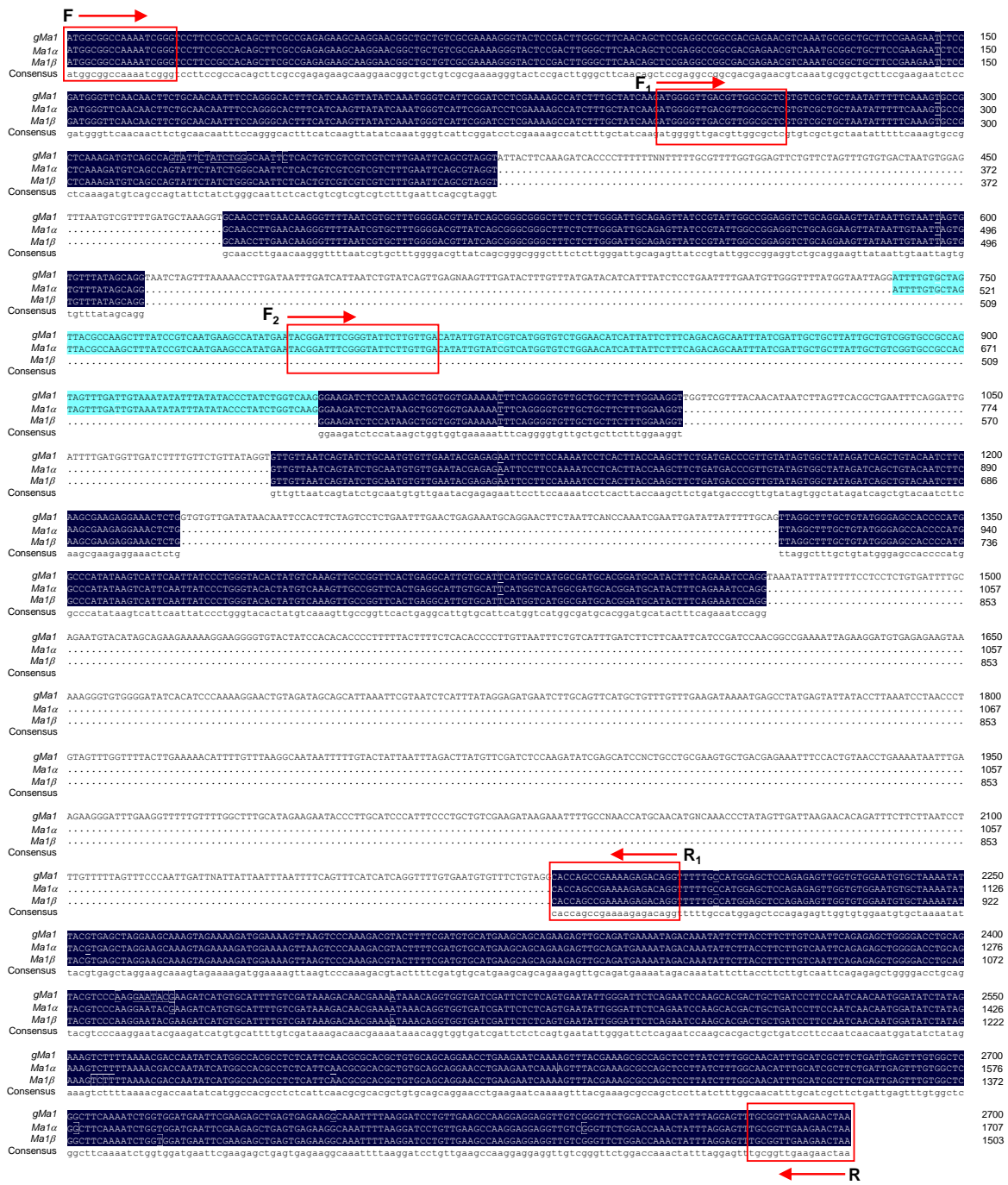


Supporting Information

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Alternative Splicing Underpins the ALMT9 Transporter Function for Vacuolar Malic Acid Accumulation in Apple

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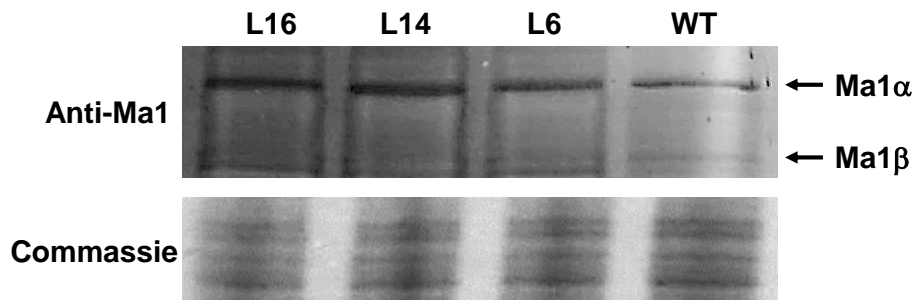
Supplemental Figure 1. Nucleotide sequence alignment of genomic *Ma1* (*gMa1*), *Ma1α* CDS and *Ma1β* CDS using DNAMAN software.

The primers used for the PCR assay of Figure 2A-C are highlighted in the red box.

Ma1 α	MAAKIGSFRHSFAERSKERLLSRKGYSDLGFNSSEAGDENVKCGCFRRISDGFNNFCNNFQGTFFIKLYQMGHSDPRKAIFAIKMGLTLALVSLLIFFKVP	100
Ma1 β	MAAKIGSFRHSFAERSKERLLSRKGYSDLGFNSSEAGDENVKCGCFRRISDGFNNFCNNFQGTFFIKLYQMGHSDPRKAIFAIKMGLTLALVSLLIFFKVP	100
Consensus	maakigsfrhsfaerskerllsrkgySDLGFNSSEAGDENVKCGCFRRISDGFNNFCNNFQGTFFIKLYQMGHSDPRKAIFAIKMGLTLALVSLLIFFKVP	
Ma1 α	LKDVSQYSIWAILTIVVVVFEFSVGTATLNKGFNRALGTLGAGGLSLGIAELSVLAGGLQEVIIIVISVFIAGFCASYAKLYPSMKPYEYGFVFLTYCIVM	200
Ma1 β	LKDVSQYSIWAILTIVVVVFEFSVGTATLNKGFNRALGTLGAGGLSLGIAELSVLAGGLQEVIIIVISVFIAG.....	170
Consensus	lkdvSQYSIWAILTIVVVVFEFSVGTATLNKGFNRALGTLGAGGLSLGIAELSVLAGGLQEVIIIVISVFIAG.....	
Ma1 α	VSGTSLFFQTAIYRLLLIAGAAATSLIVNIFIYPIWNSR.....EDLHKLWVKNFRGVAASLEGVVMQYVLCQVEYERIPSKILTYQASDDPLYSGYRSVAVQSSSEE	300
Ma1 βEDLHKLWVKNFRGVAASLEGVVMQYVLCQVEYERIPSKILTYQASDDPLYSGYRSVAVQSSSEE	232
ConsensusedlhklwvknfrgvaaslegvvmqyVLCQVEYERIPSKILTYQASDDPLYSGYRSVAVQSSSEE	
Ma1 α	ETLLGFVWPEPPHGPYKSFNYPWVHYVKVAGSLRHCAFVMVMAMHGCILSEIQAPAEKRQVFAMELQRVGVCEAKILRELGSKVEKMEKLSPKDVLFDVHE	400
Ma1 β	ETLLGFVWPEPPHGPYKSFNYPWVHYVKVAGSLRHCAFVMVMAMHGCILSEIQAPAEKRQVFAMELQRVGVCEAKILRELGSKVEKMEKLSPKDVLFDVHE	332
Consensus	etllgfavwpepphgpYKSFNYPWVHYVKVAGSLRHCAFVMVMAMHGCILSEIQAPAEKRQVFAMELQRVGVCEAKILRELGSKVEKMEKLSPKDVLFDVHE	
Ma1 α	AAEELQMKIDKYSYLLVNSESWGPAVRPKEYEDHVHFVDKDNENKQVVIDSLSEYWDSQNPSTADPSNQOWISIESLLKRPISWPRLSFNHNAVQQEPE	500
Ma1 β	AAEELQMKIDKYSYLLVNSESWGPAVRPKEYEDHVHFVDKDNENKQVVIDSLSEYWDSQNPSTADPSNQOWISIESLLKRPISWPRLSFNHNAVQQEPE	432
Consensus	aaeelqmkidkysyllvnseSWGPAVRPKEYEDHVHFVDKDNENKQVVIDSLSEYWDSQNPSTADPSNQOWISIESllkrpISWPRLSFNHNAVQQEPE	
Ma1 α	ESKVYESASSLSLATFASLLIEFVARLQNLVDEFELSEKANFKDPVEAKEEVVGFWTKLFRSLRLKN	568
Ma1 β	ESKVYESASSLSLATFASLLIEFVARLQNLVDEFELSEKANFKDPVEAKEEVVGFWTKLFRSLRLKN	500
Consensus	eskvyesasslsLATFASllIEFVARLqnlVDEFELSEKANFKDPVEAKEEVVGFWTKLFRslrLkn	

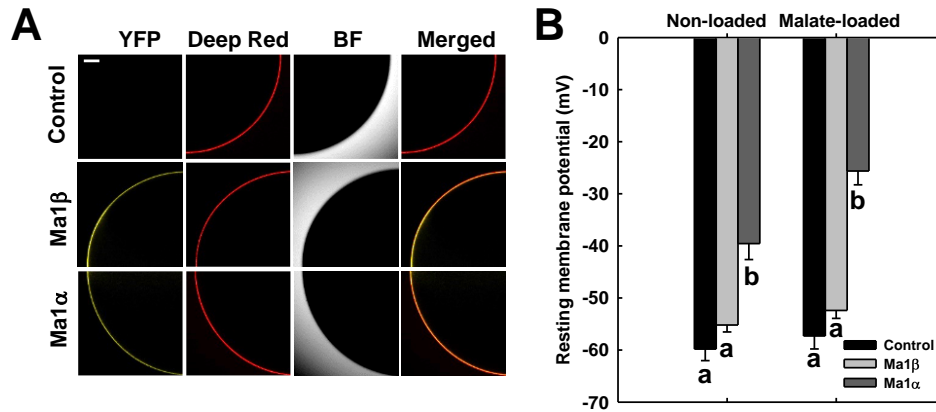
Supplemental Figure 2. Protein sequence alignment of Ma1 α and Ma1 β using DNAMAN software.

The peptide sequence ELSEKANFKDPVEA used to generate the antibody against Ma1 is highlighted in the red box.



Supplemental Figure 3. Detection of Ma1 α and Ma1 β proteins by immunoblotting at the peak of malic acid accumulation (31 days after bloom) during fruit development in wild type (WT) and *cMa1*-OE lines (L6, L14, L16) of 'Royal Gala' apple.

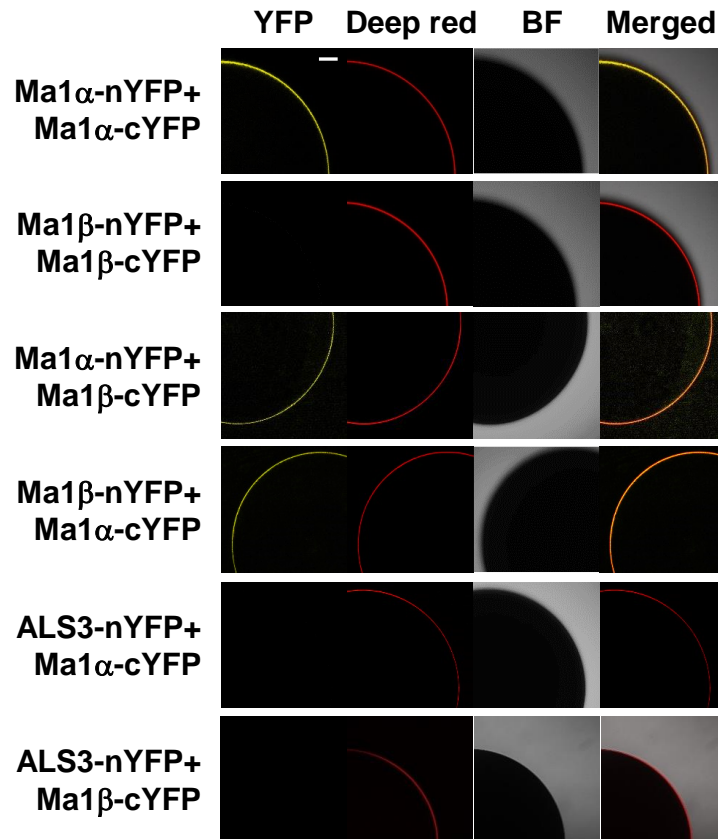
The antibody was generated against peptide ELSEKANFKDPVEA in rabbit, which recognizes both Ma1 α and Ma1 β .



Supplemental Figure 4. Localization of Ma1 β -YFP and Ma1 α -YFP fusion proteins in oocytes and Resting Membrane Potentials (RMPs) recorded in control and Ma1 β or Ma1 α -expressing cells

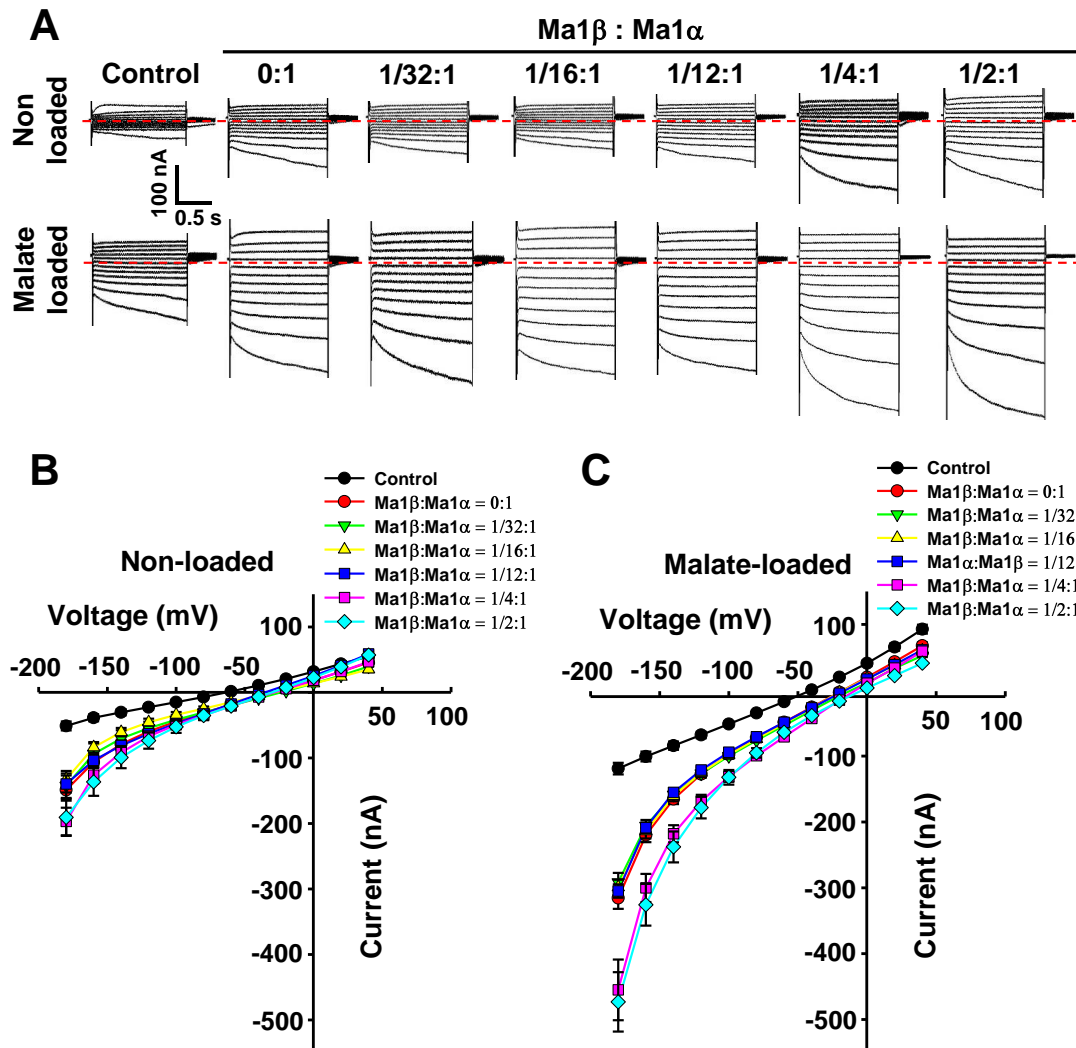
(A) Expression and localization of Ma1 β -YFP and Ma1 α -YFP fusion proteins in oocytes, with Deep Red as a plasma membrane marker (PM Marker). Each oocyte was injected with 25 ng cRNA. Bar = 100 μ m. BF: Bright Field.

(B) RMPs recorded in control and Ma1 β or Ma1 α -expressing cells. RMPs were recorded in cells non-loaded or loaded with malate by microinjecting cells with 50 nl of 100 mM Na-Malate (increasing cytosolic malate²⁻ concentration by 4.5 mM) 2 to 3 hours prior to the electrophysiological recordings. Data are mean \pm SE. The number of cells recorded: Control-non-loaded (n = 11), Ma1 β -non-loaded (n = 18), Ma1 α -non-loaded (n = 9), Control-malate-loaded (n = 10), Ma1 β -malate-loaded (n = 20), and Ma1 α -malate-loaded (n = 19). Different letters (a, b, c) indicate significant differences between groups using Tukey's HSD test at P < 0.05 after ANOVA.



Supplemental Figure 5. BiFC assays of Ma1 α and Ma1 β in *Xenopus laevis* oocytes.

BiFC assays of Ma1 α and Ma1 β in *X. laevis* oocytes co-expressing Ma1 α -nYFP/Ma1 α -cYFP, Ma1 β -nYFP/Ma1 β -cYFP, Ma1 α -nYFP/Ma1 β -cYFP, or Ma1 β -nYFP/Ma1 α -cYFP fusion constructs, with a tonoplast localized protein ALS3 and empty vector (nYFP) as negative controls. Deep Red was used as a plasma membrane marker (PM Marker). Bar = 100 μ m. BF: Bright Field.

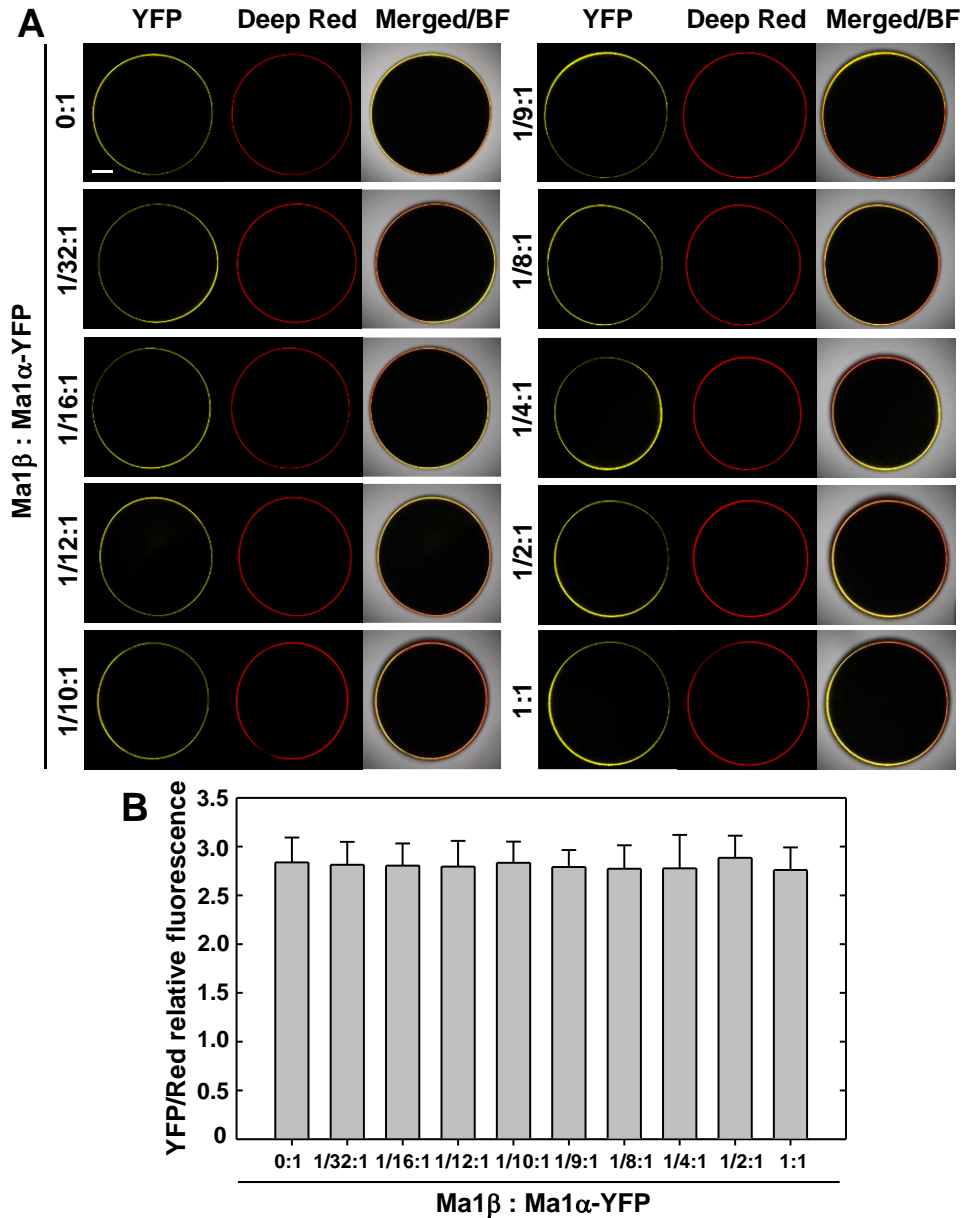


Supplemental Figure 6. Malate transport activity in *Xenopus laevis* oocytes co-expressing *Ma1 α* and *Ma1 β* genes in various ratios.

(A) Examples of currents elicited in response to holding potentials ranging from +40 to -180 mV (in 20 mV steps) recorded in control, *Ma1 β* /*Ma1 α* co-expressing cells, either non-loaded or loaded with malate. *Ma1 β* : *Ma1 α* = 0:1, 1/32:1, 1/16:1, 1/12:1, 1/4:1, 1/2:1 at a fixed amount (25 ng) of *Ma1 α* cRNA. The zero-current level is indicated by the red dotted line.

(B) Current-voltage (*I/V*) relationships constructed from steady-state current recordings with non-loaded cells such as those shown in **A**. Data are mean \pm SE. The number of cells recorded: Control ($n = 18$), 0:1 ($n = 15$), 1/32:1 ($n = 10$), 1/16:1 ($n = 10$), 1/12:1 ($n = 10$), 1/4:1 ($n = 10$), and 1/2:1 ($n = 10$).

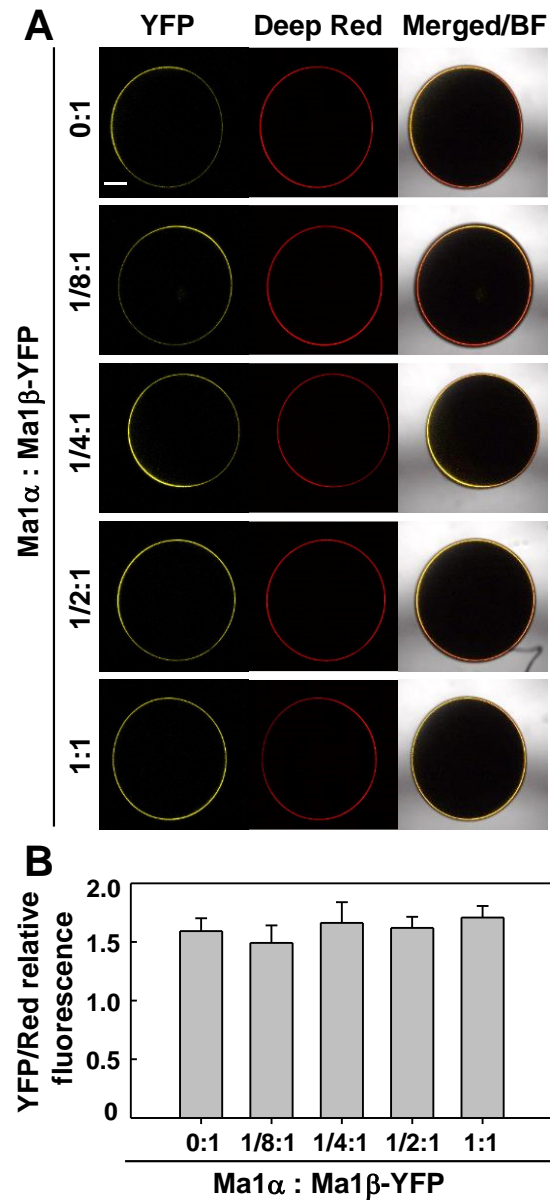
(C) Current-voltage (*I/V*) relationships constructed from steady-state current recordings with malate-loaded cells such as those shown in **A**. Data are mean \pm SE. The number of cells recorded: Control ($n = 16$), 0:1 ($n = 17$), 1/32:1 ($n = 10$), 1/16:1 ($n = 24$), 1/12:1 ($n = 22$), 1/4:1 ($n = 22$), and 1/2:1 ($n = 15$).



Supplemental Figure 7. Ma1 α protein expression is not affected by injection of Ma1 β cRNA at different ratios in *Xenopus laevis* oocytes.

(A) Representative images of the Ma1 α -YFP fluorescence signals in oocytes co-injected with Ma1 β at the indicated ratios, at a fixed amount of Ma1 α cRNA (25 ng) per oocyte. Deep red was used as a plasma membrane marker and a reference fluorescence signal. Bar = 200 μ m. BF: Bright Field.

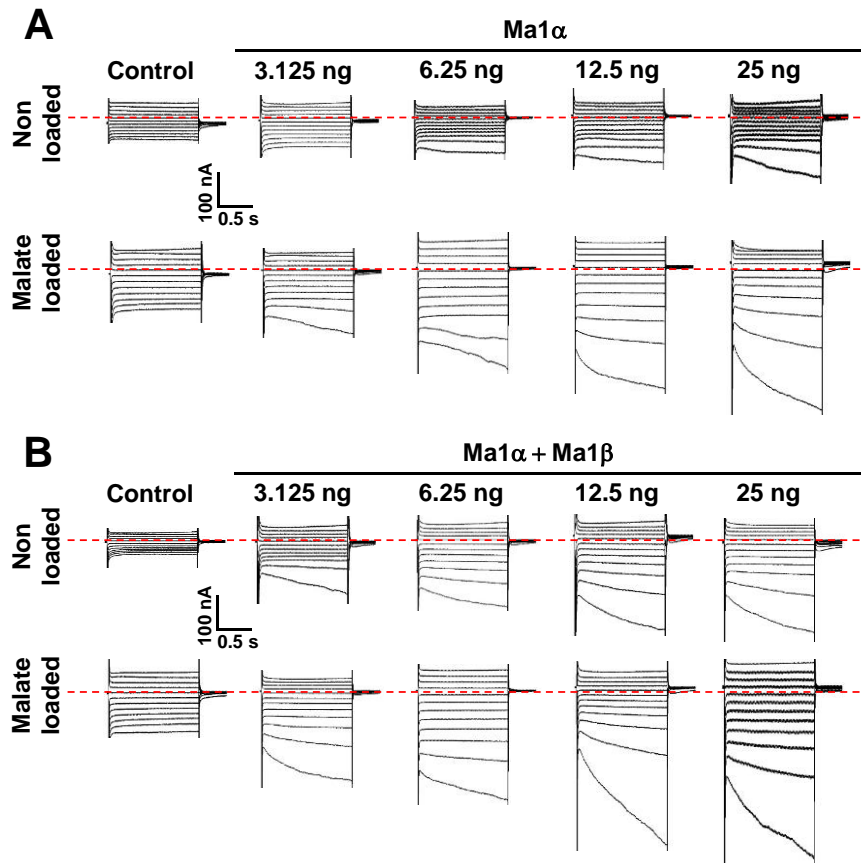
(B) The expression of Ma1 α protein indicated by the YFP/Red relative fluorescence in response to the addition of Ma1 β . Data are mean \pm SE of 20 cells recorded.



Supplemental Figure 8. Ma1 β protein expression is not affected by co-injection of *Ma1 α* cRNA at different ratios in *Xenopus laevis* oocytes.

(A) Representative images of the Ma1 β -YFP fluorescence signals in oocytes co-injected with *Ma1 α* at the indicated ratios, at a fixed amount of Ma1 β cRNA (25 ng) per oocyte. Deep red was used as a plasma membrane marker and a reference fluorescence signal. Bar = 200 μ m. BF: Bright Field.

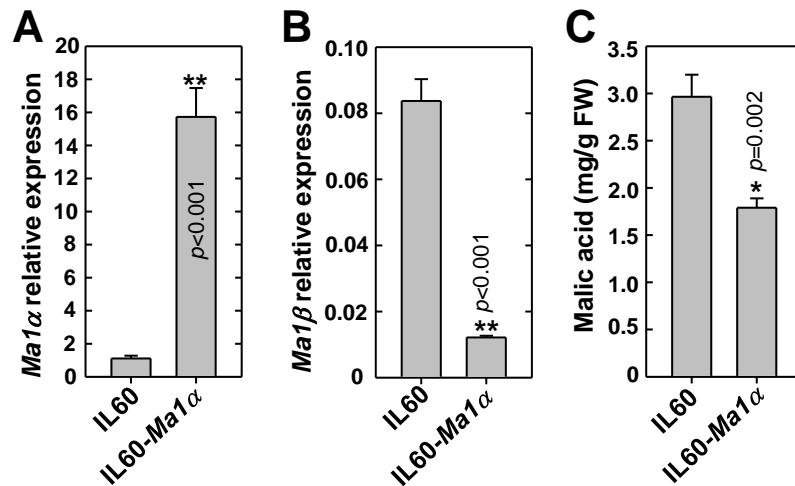
(B) The expression of Ma1 β protein indicated by the YFP/Red relative fluorescence in response to the addition of *Ma1 α* . Data are mean \pm SE of 20 cells recorded.



Supplemental Figure 9. Traces of currents elicited in *Xenopus laevis* oocytes in response to increasing amounts of *Ma1 α* cRNA alone or co-expressed at a constant ratio with *Ma1 β* .

(A) Examples of currents elicited in response to holding potentials ranging from +40 to -180 mV (in 20 mV steps) recorded in non-loaded and malate-loaded oocyte cells injected with various amounts of *Ma1 α* cRNA (0 to 25 ng). The red dotted line indicates the zero-current level.

(B) Examples of currents elicited in response to holding potentials ranging from +40 to -180 mV (in 20 mV steps) recorded in non-loaded and malate-loaded oocyte cells injected with *Ma1 α* and *Ma1 β* cRNA in a constant ratio of 1 to 1/8 at various amounts of *Ma1 α* cRNA (0 to 25 ng). The red dotted line indicates the zero-current level.



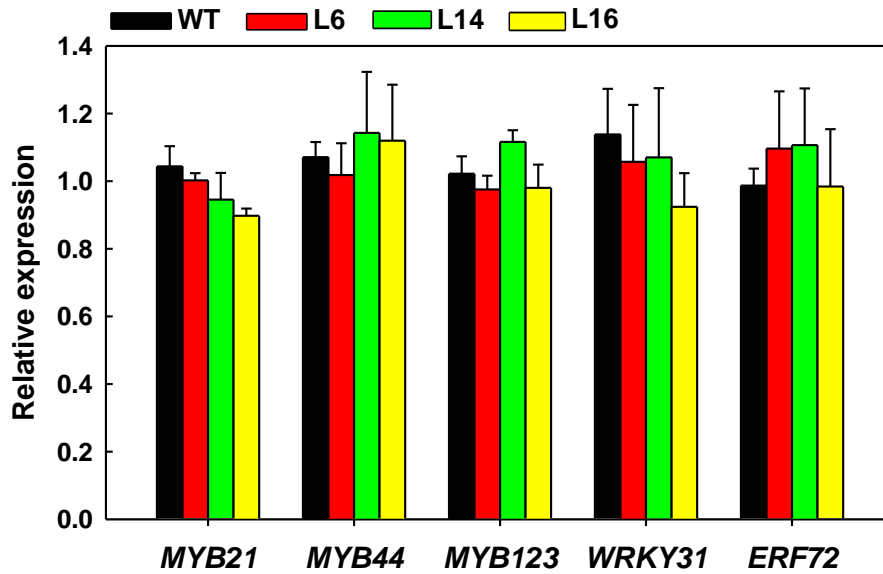
Supplemental Figure 10. Virus-based gene-overexpression of *Ma1α* decreases malic acid concentrations in wild-type 'Royal Gala' mature fruit.

(A) The expression of *Ma1α* after rattle virus-based gene-overexpression of *Ma1α*.

(B) The expression of *Ma1β* after rattle virus-based gene-overexpression of *Ma1α*.

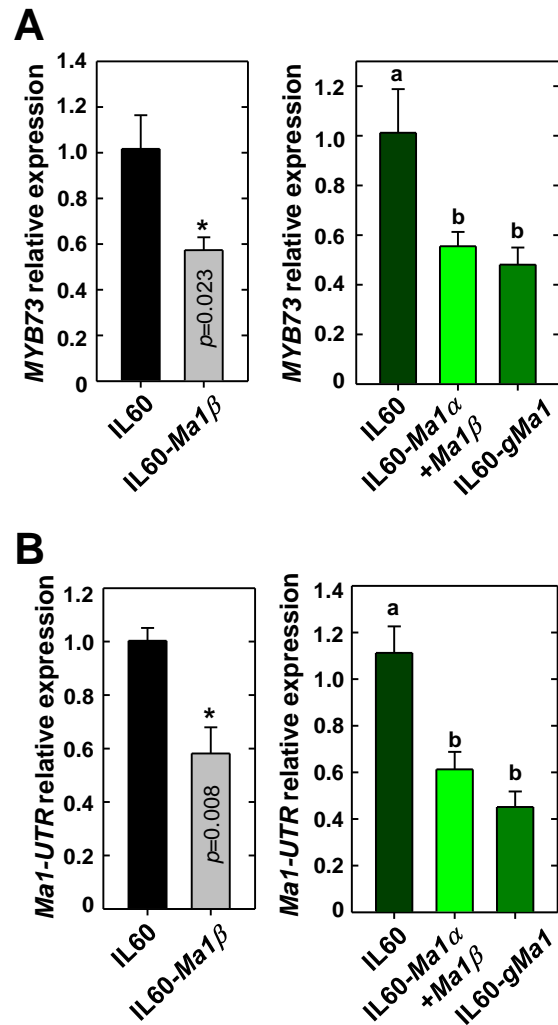
(C) Fruit malic acid concentrations in response to rattle virus-based gene-overexpression of *Ma1α*.

Virus vector IL60-*Ma1α* was infiltrated into fruit for overexpression of *Ma1α*, with empty vector (IL60) as a control. Data are mean \pm SE of 5 biological replicates with 3 fruits per replicate (3 injection sites per fruit). * Represents significant differences using Student's *t* test at $P < 0.05$, ** Represents significant differences using Student's *t* test at $P < 0.01$.



Supplemental Figure 11. Expression levels of several transcription factors at the peak of malic acid accumulation (31 days after bloom) during fruit development in wild type (WT) and *cMa1*-OE lines (L6, L14, L16) of 'Royal Gala' apple.

Quantitative RT-PCR was performed using gene-specific primers (Supplemental Table 1), with *actin* as the internal reference gene, and the relative expression level of each gene was obtained using the ddCT method. Data are mean \pm SE of 5 biological replicates, with 6 fruits pooled from 2 trees per replicate.



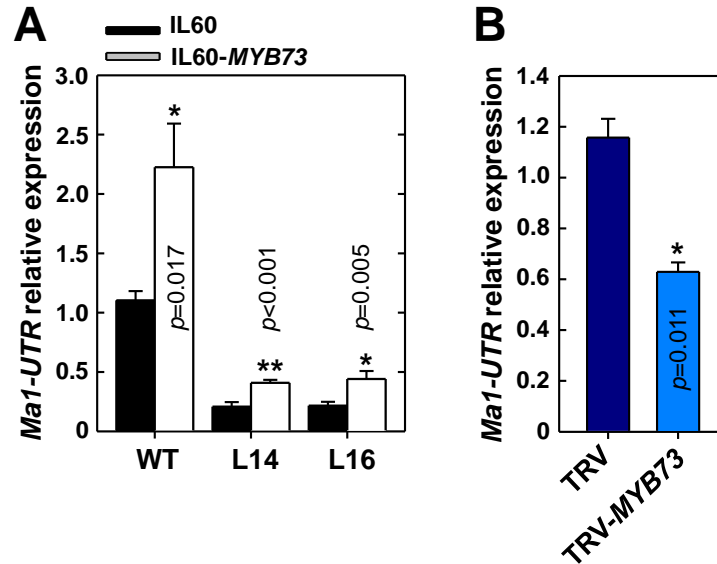
Supplemental Figure 12. Transcript levels of *MYB73* and the native *Ma1* gene in response to overexpression of *Ma1 β* , *Ma1 α* and *Ma1 β* , or *gMa1* in wild-type ‘Royal Gala’ apple.

(A) The expression level of *MYB73* after rattle virus-based gene-overexpression of *Ma1 β* , both *Ma1 α* and *Ma1 β* or genomic sequence of *Ma1* (*gMa1*) in WT mature fruits. Fruit was infiltrated with virus vector IL60-*Ma1 β* for overexpression of *Ma1 β* . IL60-*Ma1 α* and IL60-*Ma1 β* were co-infiltrated, or IL60-*gMa1* was infiltrated into fruits for overexpression of *Ma1 α* and *Ma1 β* . Fruit infiltrated with empty vector (IL60) was used as control.

(B) The expression level of native *Ma1* gene after rattle virus-based gene-overexpression of *Ma1 β* , both *Ma1 α* and *Ma1 β* or genomic sequence of *Ma1* (*gMa1*) in WT mature fruits. Fruit was infiltrated with virus vector IL60-*Ma1 β* for overexpression of *Ma1 β* . IL60-*Ma1 α* and IL60-*Ma1 β* were co-infiltrated, or IL60-*gMa1* was infiltrated into fruits for overexpression of *Ma1 α* and *Ma1 β* . Fruit infiltrated with empty vector (IL60) was used as control.

Quantitative RT-PCR was performed using gene-specific primers (Supplemental Table 1), with *actin* as the internal reference gene, and the relative expression level of each gene was obtained using the ddCT method. Data are mean \pm SE of 5 biological replicates with 3 fruits

per replicate (3 injection sites per fruit). * Represents significant differences using Student's *t* test at $P < 0.05$. Different letters (a, b) indicate significant difference between groups using Tukey's HSD test at $P < 0.05$ after ANOVA.



Supplemental Figure 13. The native *Ma1* transcript levels in response to virus-based gene-overexpression or silencing of *MdMYB73* in mature fruits of wild-type and *cMa1*-OE lines of 'Royal Gala' apple.

(A) The expression of native *Ma1* in response to rattle virus-based gene-overexpression of *MdMYB73* in mature fruits of WT and *cMa1*-OE lines (L14 and L16).

(B) The expression of native *Ma1* in response to rattle virus-induced gene-silencing of *MdMYB73* in WT mature fruit.

Virus vectors IL60-MYB73 and TRV-MYB73 were infiltrated into fruit for overexpression and silencing of MYB73, with empty vectors (IL60 or TRV) as control, respectively. Data are mean \pm SE of 5 biological replicates with 3 fruits per replicate (3 injection sites per fruit). * Represents significant differences using Student's *t* test at $P < 0.05$, ** Represents significant differences using Student's *t* test at $P < 0.01$.

Supplemental Table 1. Statistical analysis of transmembrane current (nA) at various ratios of Ma1 β /Ma1 α under malate-loaded conditions in oocytes.

	-180 mV	-160 mV	-140 mV	-120 mV	-100 mV	-80 mV	-60 mV	-40 mV	-20 mV	0 mV	20 mV	40 mV
Control	-112.60±4.64 a	-89.10±4.17 a	-72.26±3.73 a	-57.16±3.21 a	-42.62±2.67 a	-28.19±2.17 a	-13.91±1.75 a	0.68±1.55 a	16.19±1.69 a	33.16±2.26 a	53.26±3.15 a	76.80±3.95 a
Ma1 β :Ma1 α = 0:1	-300.86±8.23 b	-206.86±6.33 b	-154.49±4.93 b	-118.55±3.91 b	-90.69±3.18 b	-66.87±2.59 b	-45.23±2.11 b	-24.88±1.73 b	-5.11±1.63 b	14.50±2.03 b	34.80±2.83 b	56.31±3.80 b
Ma1 β :Ma1 α = 1/32:1	-291.76±14.43 b	-205.90±8.96 b	-158.61±6.59 b	-126.41±5.21 b	-99.90±3.75 b	-76.18±2.57 b	-53.61±1.66 b	-30.64±2.16 b	-8.47±2.89 b	11.02±1.99 b	33.39±2.65 b	52.54±2.19 b
Ma1 β :Ma1 α = 1/16:1	-299.25±11.57 b	-214.14±11.03 b	-160.57±8.02 b	-125.22±6.52 b	-98.08±5.78 b	-73.88±4.97 b	-50.72±4.27 b	-27.22±3.71 b	-3.19±3.33 b	17.88±2.39 b	37.77±2.02 b	60.14±2.03 b
Ma1 β :Ma1 α = 1/12:1	-304.83±10.14 b	-208.80±7.94 b	-155.19±6.27 b	-121.16±5.08 b	-94.08±4.07 b	-70.78±3.35 b	-48.69±2.96 b	-26.84±2.58 b	-4.69±2.43 b	16.98±2.68 b	38.81±3.19 b	61.26±3.83 b
Ma1 β :Ma1 α = 1/10:1	-308.66±13.21 b	-219.93±9.68 b	-163.19±6.71 b	-128.11±5.08 b	-100.29±4.13 b	-76.57±3.42 b	-54.83±2.77 b	-33.86±2.18 b	-12.49±1.85 c	9.64±2.07 b	33.19±2.96 b	58.49±4.35 b
Ma1 β :Ma1 α = 1/9:1	-329.18±18.99 b	-231.59±11.88 b	-172.16±9.53 b	-133.91±7.08 b	-103.68±5.42 b	-77.66±4.19 b	-53.96±3.23 b	-30.95±2.48 b	-8.56±2.03 b	13.48±2.42 b	35.77±3.63 b	59.20±5.36 b
Ma1 β :Ma1 α = 1/8:1	-454.62±10.30 c	-296.18±7.21 c	-212.51±5.64 c	-160.70±4.20 c	-123.52±3.07 c	-93.38±2.22 c	-67.47±1.60 c	-43.60±1.20 c	-20.55±1.06 c	1.89±1.22 c	24.08±1.61 b	46.62±2.16 b
Ma1 β :Ma1 α = 1/4:1	-454.96±46.06 c	-300.20±21.36 c	-217.95±13.02 c	-168.72±10.00 c	-131.27±7.69 c	-99.52±6.15 c	-70.84±4.60 c	-43.02±3.30 c	-15.08±3.05 c	10.61±3.92 b	33.55±5.27 b	59.20±6.47 b
Ma1 β :Ma1 α = 1/2:1	-473.26±45.09 c	-325.74±31.69 c	-237.94±23.49 c	-178.20±16.39 c	-132.23±11.16 c	-95.11±7.24 c	-63.83±4.42 c	-38.56±2.50 c	-16.58±1.49 c	3.48±1.12 c	22.15±1.22 b	41.09±1.87 b
Ma1 β :Ma1 α = 1:1	-466.60±19.21 c	-314.89±13.73 c	-230.52±11.39 c	-173.52±9.24 c	-131.01±7.27 c	-95.80±5.49 c	-66.61±4.13 c	-41.02±3.05 c	-18.14±2.19 c	4.44±1.80 c	28.12±2.32 b	54.21±3.92 b

Note: Different letters (a, b, c) indicate significant difference between groups using Tukey's Honest Significant Difference test at $P < 0.05$ after one-way ANOVA.

Supplemental Table 2. Statistical analysis of transmembrane current (nA) at different amounts of Ma1 α alone or co-expressed with Ma1 β (at 1/8 Ma1 α) under malate-loaded conditions in oocytes.

		-180 mV	-160 mV	-140 mV	-120 mV	-100 mV	-80 mV	-60 mV	-40 mV	-20 mV	0 mV	20 mV	40 mV
0 ng Ma1 α	Control-1	-103.35±7.74	-84.17±6.13	-69.36±5.19	-54.15±3.97	-37.88±2.93	-21.27±2.17	-4.63±1.66	11.51±1.57	26.57±1.68	41.90±2.24	58.99±3.10	71.36±2.83
	Control-2	-101.59±12.10	-75.78±10.71	-59.47±9.14	-45.32±7.67	-30.68±6.28	-15.74±4.99	-0.82±3.73	13.66±2.59	26.92±1.76	40.13±1.39	56.36±1.87	69.68±2.45
	<i>P</i> vaule	0.904	0.904	0.372	0.334	0.328	0.339	0.379	0.499	0.889	0.503	0.468	0.658
3.125 ng Ma1 α	Ma1 α	-170.83±10.10	-125.77±7.89	-99.35±6.83	-76.99±5.72	-55.85±4.72	-35.29±3.61	-15.01±2.50	4.62±1.61	22.74±1.32	40.67±1.76	59.29±2.63	78.34±4.12
	Ma1 α +Ma1 β	-280.47±17.93*	-193.56±17.63*	-149.42±15.52*	-114.37±13.42*	-83.15±10.89*	-54.57±8.25*	-27.78±5.62*	-2.30±3.11*	20.46±1.64	41.28±3.14	62.18±5.71	85.34±8.95
	<i>P</i> vaule	<0.001	0.001	0.004	0.011	0.021	0.030	0.035	0.047	0.287	0.860	0.624	0.451
6.25 ng Ma1 α	Ma1 α	-235.34±29.88	-150.91±10.12	-111.26±5.76	-84.85±4.80	-61.65±3.89	-40.51±2.91	-19.83±2.13	0.19±1.59	18.19±1.36	35.18±1.78	52.65±2.76	72.05±4.15
	Ma1 α +Ma1 β	-432.63±35.16*	-255.76±19.55*	-178.87±17.30*	-132.97±14.79*	-97.84±12.35*	-68.23±10.07*	-40.59±7.68*	-14.45±5.34*	9.56±1.95*	30.70±1.72	50.10±2.35	74.24±4.98
	<i>P</i> vaule	<0.001	<0.001	0.003	0.011	0.020	0.027	0.029	0.028	0.003	0.090	0.490	0.747
12.5 ng Ma1 α	Ma1 α	-340.73±19.45	-197.47±10.15	-130.87±8.05	-92.93±6.35	-64.69±4.96	-41.06±3.80	-20.14±2.84	-1.08±1.98	15.31±1.91	30.48±2.57	46.24±3.67	63.64±5.04
	Ma1 α +Ma1 β	-526.67±58.45*	-285.59±24.10*	-182.37±12.74*	-125.27±8.76*	-79.63±4.38*	-55.98±1.96*	-29.07±2.67*	-8.66±2.85*	9.99±2.32	26.74±2.07	43.81±2.23	64.84±2.79
	<i>P</i> vaule	0.006	0.003	0.003	0.008	0.039	0.008	0.036	0.041	0.093	0.282	0.590	0.843
25 ng Ma1 α	Ma1 α	-333.37±34.87	-188.46±16.19	-122.49±9.59	-85.39±6.31	-59.46±4.53	-38.87±3.36	-21.14±2.57	-4.60±1.92	9.73±1.52	24.63±2.17	40.73±5.31	45.69±4.01
	Ma1 α +Ma1 β	-568.68±69.48*	-311.58±36.61*	-206.52±37.36*	-153.95±21.45*	-117.68±12.38*	-85.20±12.12*	-52.51±12.60*	-22.42±7.96*	8.88±4.41	30.61±2.01	55.37±5.31	65.32±7.46*
	<i>P</i> vaule	0.008	0.007	0.045	0.007	<0.001	0.002	0.027	0.045	0.858	0.061	0.069	0.034

Note: Student *t*-test was used to detect the difference between Ma1 α alone and co-expression of Ma1 α and Ma1 β at each level of Ma1 α . An asterisk indicates a significant difference at $P < 0.05$.

Supplemental Table 3. List of primers used in this paper.

Name	Sequence (5'-3')
Gateway primers	
Ma1-GW-F	GGGGACAAGTTTGTACAAAAAGCAGGCTTCATGGCGGCCAAAATCGG
Ma1-GW-R	GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAGTTCTTCAACCGCA
Ma1-GW-R-W/O	GGGGACCACTTTGTACAAGAAAGCTGGGTCTTCTTCAACCGCAAAC
MYB73-GW-F	GGGGACAAGTTTGTACAAAAAGCAGGCTTCATGGAAGCGATGAATATGTGC
MYB73-GW-R	GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAATTTAATCTATGAAGCTCCG
MYB73-GW-R-W/O	GGGGACCACTTTGTACAAGAAAGCTGGGTCAATTTAATCTATGAAGCTCCGAAG
AtALS3-GW-F	GGGGACAAGTTTGTACAAAAAGCAGGCTTCATGGATCTGAAATGGGATGAT
AtALS3-GW-R	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCAATCTGAGGAGAAGACATG
Alternative splicing primers	
AS-F	ATGGCGGCCAAAATCGG
AS-R	TTAGTTCTTCAACCGCA
AS-F1	ATGGGGTTGACGTTGGCGCTC
AS-R1	CCTGTCTCTTTTCGGCTGGTG
AS-F2	TACGGATTTCCGGTATTCTTGTTGA
RT-qPCR	
qMa1-UTR-F	TTCAAATCCTTCTTCTCCGACG
qMa1-UTR-R	CTGTTGAAGCCCAAGTCGGAG
qMYB73-F	CCAACAAGCCCGAACGAA
qMYB73-R	ACCACCTGAGCCTGCACGAC
qMa1 β -F	GTGTGTTTATAGCAGGGGAAGATC
qMa1 β -R	CAACGGGTCATCAGAAGCTTGG
qMa1 α -F	CAGGATTTTGTGCTAGTTACGCC
qMa1 α -R	CAGCAATAAGCAGCAATCGATA

qMa1-F	GCGGCTGCTTCCGAAGAATCTC
qMa1-R	TATTAGCAGCGACACGAGCGCC
qRT-MdMYB21-F	CCTTCCGTGCCACTCTCAAC
qRT-MdMYB21-R	TAAGCTGCTGTAGCCAAGTCG
qRT-MdMYB44-F	ATCGCTCAGCCTTCCCTTC
qRT-MdMYB44-R	TCTCGCTGTTCTGGTTGCTC
qRT-MdMYB123-F	AGGAAACAAATGCAGGGGGA
qRT-MdMYB123-R	AGTCGTCGTGGTTAATCTCCG
qRT-MdWRKY31-F	ACCAACAACACTACAGTGCCTGC
qRT-MdWRKY31-R	CAATCCTTGCTTCTTTTCTTGATC
qRT-MdERF72-F	AGAGGGCTCTTTTTTCTC
qRT-MdERF72-R	ACCTTGTGATTCTCCGG
qActin-F	TGACCGAATGAGCAAGGAAATTACT
qActin-R	TACTCAGCTTTGGCAATCCACATC
User primers	
Ma1-USER-F	GGCTTAAUATGGCGGCCAAAATCGG
Ma1-USER-R	GGTTTAAUCCTTAGTTCTTCAACCGCAAAC
Ma1-USER-R-W/O	GGTTTAAUCCGTTCTTCAACCGCAAACCTCC
IL60 expression	
Ma1-IL60-F	CCGTCGACATGGCGGCCAAAATCGG
Ma1-IL60-R	GCTCTAGATTAGTTCTTCAACCGCAAACCTCC
MYB73-IL60-F	CCGTCGACATGGAAGCGATGAATATGTGC
MYB73-IL60-R	GCTCTAGATTAATTTAATCTATGAAGCTCCG
TRV2 expression	
Ma1-TRV2-F	GCTCTAGAATGGCGGCCAAAATCGG
Ma1-TRV2-R	GGGGTACCAACTTGATGAAAGTGCCCTGG
MYB73-TRV2-F	GCTCTAGAATGGAAGCGATGAATATGTGC
MYB73-TRV2-R	GGGGTACCCGACCTTTTATGTACCGGC

Y1H assay	
pGADT7-MdMYB73-F	TGGAATTCATGGAAGCGATGAATATGTGC
pGADT7-MdMYB73-R	TAGGATCCTTAATTTAATCTATGAAGCTCCG
pHis2-Ma1-Pro-F	TAGAATTCGTATAAATCATGTAAGCCAGGTG
pHis2-Ma1-Pro-R	TTGAGCTCTTCGTCGGAGAAGAAGGATTTG
ChIP-PCR	
Ma1-ChIP-F	CCAAAATAGTATAACCACATGTCTCC
Ma1-ChIP-R	GAGGGAAAGTGGAAAGCAGAG
Dual LUC assay	
MYB73-SK-F	GAATTCTGGAAGCGATGAATATGTG
MYB73-SK-R	GTCGAGATTTAATCTATGAAGCTCCG
Ma1-Pro-LUC-F	GTCGACAGAGAGAGTTATAAGCTTAG
Ma1-Pro-LUC-R	GGATCCTTGTTGGAAGAGGGAAAGTG
LCI assay	
Ma1-JW771-F	ACGGGGGACGAGCTCGGTACCATGGCGGCCAAAATCGG
Ma1-JW771-R	CGCGTACGAGATCTGGTCGACGTTCTTCAACCGCAAAC
Ma1-JW772-F	TACGCGTCCCAGGGCGGTACCATGGCGGCCAAAATCGG
Ma1-JW772-R	ACGAAAGCTCTGCAGGTCGACTTAGTTCTTCAACCGCAA