

Supplementary Tables

Supplementary Table 1. Vectors used in this study.

Name	Description
V113	pGTR; Amplification of gRNA cassettes; Addgene: 63143
V117	pTC217; Geminiviral expression vector; Addgene: 70018
V118	pTC217 without homologous region and gRNAs, with multiple cloning site
V181	pICH47761 with napinA::turboGFP; Addgene: 48003
V182	pICH47742 with egg-cell specific Cas9 cassette; Addgene: 48001
V183	pICH47732 with phosphinotricin acetyltransferase expression cassette; Addgene: 48000
V184	pDI1; Shuttle vector modified from Addgene: 79461
V186	pDI2; Shuttle vector modified from Addgene: 79462
V187	pDI2E; Shuttle vector modified from Addgene: 79463
V188	pDI3; Shuttle vector modified from Addgene: 79465
V189	pDI4E; Shuttle vector modified from Addgene: 79466
H386	Tomato transformation vector based on V118 with gRNA 3 and 4
H387	Tomato transformation vector based on V118 with gRNA 1 and 2
H668	pDI1 with <i>AtMAR1</i> gRNA
H669	pDI2 with <i>AtMAR1</i> gRNA
H672	pDI3 with <i>At</i> target gRNA
H673	pDI4E with <i>At</i> target gRNA
H675	pICH47751 with the four <i>At</i> gRNA cassettes from H668, H669, H672 and H673; Addgene: 48002
H677	pAGM4723 with expression cassettes from V181, V182, V183 and H675; for Arabidopsis transformation; Addgene: 48015
H749	pDI1 with <i>AtMAR1</i> gRNA
H753	pDI2E with <i>At</i> target gRNA
H757	pICH47751 with the two <i>At</i> gRNA cassettes from H749 and H753; Addgene: 48002
H761	pAGM4723 with expression cassettes from V181, V182, V183 and H757; for Arabidopsis transformation; Addgene: 48015

Supplementary Table 2. Primers used in this study.

Name	Sequence	Description
P-274	TAGGTCTCCAAACGAAGACAAAAAC	pGTR general reverse
P-294	CGGGTCTCAGGCAGAAGACTAATTG	pGTR general forward
P-307	CCCACATCGCTTAGATAAGAAAACG	Sequencing H386 and H387
P-395	TAAGCCGGTCTCGGTTTCACGTGCTTCTAGAACCCGG GATGGAGCGAGACGAACGTCTCTCGCTATGACTAGT TCGACGTCAGATTTAAATGAGTGTACTTCAAGTC	Multiple Cloning Site
P-860	TAGGTCTCCGAAGGCGGACCAGTTTTAGAGCTAGAA	gRNA1 <i>SlMAR1</i> forward
P-861	ATGGTCTCACTTCCTTACTCTTGCACCAGCCGGGAA	gRNA1 <i>SlMAR1</i> reverse
P-862	TAGGTCTCCTTTACCACGCAAGTTTTAGAGCTAGAA	gRNA2 <i>SlMAR1</i> forward
P-863	ATGGTCTCATAAAGCGAGGAGTGCACCAGCCGGGAA	gRNA2 <i>SlMAR1</i> reverse
P-864	TAGGTCTCCTGGCAGCAGGTGGTTTTAGAGCTAGAA	gRNA3 <i>SlMAR1</i> forward
P-865	ATGGTCTCAGCCATTGCGTTGTGCACCAGCCGGGAA	gRNA3 <i>SlMAR1</i> reverse
P-866	TAGGTCTCCCTGGGTATATGGGTTTTAGAGCTAGAA	gRNA4 <i>SlMAR1</i> forward
P-867	ATGGTCTCACCAGCCAAGCAATGCACCAGCCGGGAA	gRNA4 <i>SlMAR1</i> reverse
P-1248	ATATTCACTGACCACACATC	Genotyping <i>SlMAR1</i>
P-1249	GAATCAACATCACTACTCAC	Genotyping <i>SlMAR1</i>
P-1250	CTGTTAGAGTGAAGACTACTACC	Genotyping <i>SlMAR1</i>
P-1251	GGAACCTCCTGTACAAAAAC	Genotyping <i>SlMAR1</i>
P-1436	ATTGGATAATTGCTGGAGGCCCTG	gRNA <i>AtMAR1</i> forward (H677)
P-1437	AAACCAGGGCCTCCAGCAATTATC	gRNA <i>AtMAR1</i> reverse (H677)
P-1661	ATTGAGCCTATGAGACTAGGCCTG	gRNA <i>At</i> target forward (H677)
P-1662	AAACCAGGCCTAGTCTCATAGGCT	gRNA <i>At</i> target reverse (H677)
P-1663	ATTGGCCTAAGCATGCGTTTGGAG	gRNA <i>At</i> target forward (H677 and H761)
P-1664	AAACCTCCAAACGCATGCTTAGGC	gRNA <i>At</i> target reverse (H677 and H761)
P-1665	ATTGGCCACTCCTGCTCACCCTGA	gRNA <i>AtMAR1</i> forward (H677 and H761)

P-1666	AAACTCAGGGTGAGCAGGAGTGGC	gRNA <i>AtMAR1</i> reverse (H677 and H761)
P-1780	GTAAAACGACGGCCAGTGCTTAGGATTTTCGATGGGA TCG	Capillary sequencing <i>At</i> target
P-1781	CTAACCACTGCAAACACAGCC	Capillary sequencing <i>At</i> target
P-1784	GTAAAACGACGGCCAGTCAGCATTGCCTGTACGTTC	Capillary sequencing <i>AtMAR1</i>
P-1785	GCATTGCAATGGCGGACG	Capillary sequencing <i>AtMAR1</i>
M13- FAM	GTAAAACGACGGCCAGT	Fluorescence-labelled (FAM) for AFLP
M13- JOE	GTAAAACGACGGCCAGT	Fluorescence-labelled (JOE) for AFLP

Supplementary Table 3. Different types of mutations induced by the CRISPR/Cas9-system in *MAR1* and the target gene.

Type of mutation	<i>MAR1</i>		Target gene	
	Number of detected alleles	Percentage of all <i>MAR1</i> mutations	Number of detected alleles	Percentage of all target gene mutations
Insertion > 2 bp	2	2.3	0	0
Insertion 1 bp	57	65.5	41	64.1
Deletion 1 bp	11	12.6	20	31.3
Deletion 2-10 bp	11	12.6	3	4.7
Deletion > 10 bp	6	6.9	0	0
Total	87	100	64	100

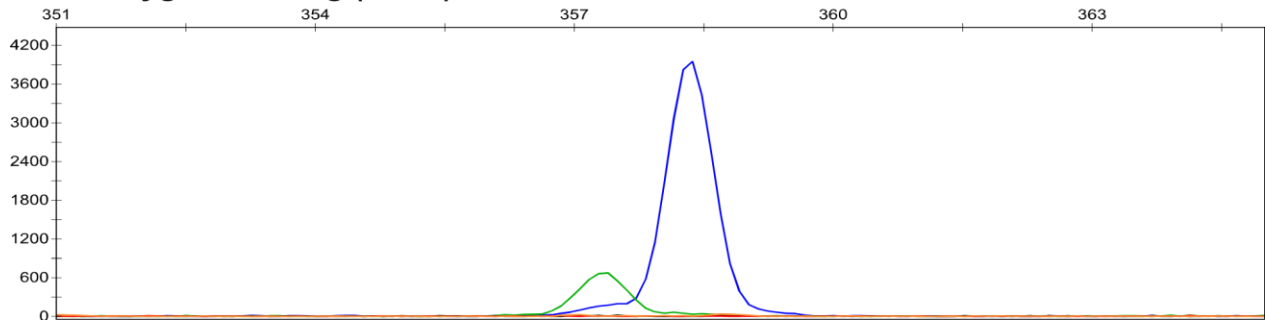
Supplementary Table 4. Putative orthologs of *AtMAR1* with a sequence identity higher than 50% of 56 plant species. Plant species used for phylogenetic analysis are highlighted in grey.

Family	Organism	MAR1- orth.	Locus tag
Brassicaceae	<i>Arabidopsis thaliana</i>	1	AT5G26820.1
	<i>Arabidopsis halleri</i>	1	Araha.25491s000
	<i>Arabidopsis lyrata</i>	1	AL6G38700.t1
	<i>Brassica oleracea</i>	1	Bol012754
	<i>capitata</i>		
	<i>Boechera stricta</i>	1	Bostr.2128s0093.1
	<i>Brassica rapa</i>	1	Brara.B03574.1
	<i>Capsella grandiflora</i>	1	Cagra.0418s0004.1
	<i>Capsella rubella</i>	1	Carubv10000515m
	<i>Eutrema salsugineum</i>	1	Thhalv10003867m
Embryophyte	<i>Marchantia polymorpha</i>	1	Mapoly0001s0146.1
	<i>Physcomitrella patens</i>	2	Pp3c25_630V3; Pp3c5_21200V3
	<i>Sphagnum phallax</i>	1	Sphfalx0092s0074
Tracheophyte	<i>Selaginella</i>	1	62145 (gw1.11.772.1)
	<i>moellendorffii</i>		
Angiosperm	<i>Ananas comosus</i>	1	Aco007359.1
	<i>Amborella trichopoda</i>	1	evm_27.model.AmTr_v1.0_scaffold00003.40
	<i>Musa acuminata</i>	2	GSMUA_Achr8T06360_001; GSMUA_Achr3T08330_001
	<i>Spirodela polyrhiza</i>	1	Spipo3G0069600
	<i>Zostera marina</i>	1	Zosma2g01370.1
Grass	<i>Brachypodium</i>	2	Bradi4g04670.2; Bradi1g67620.2
	<i>distachyon</i>		
	<i>Brachypodium stacei</i>	2	Brast10G052700.1; Brast02G120800.1
	<i>Oryza sativa</i>	2	LOC_Os12g37530.1; LOC_Os05g04120.1
	<i>Oropetium thomaeum</i>	2	Oropetium_20150105_21861A; Oropetium_20150105_15432A
Panicoideae	<i>Panicum hallii</i>	2	Pahal.I04577.1; Pahal.C01213.1
	<i>Panicum virgatum</i>	4	Pavir.Ca02569.1; Pavir.Ca00756.1; Pavir.Cb00583.1; Pavir.J15949.1
	<i>Setaria italica</i>	2	Seita.3G335000.1; Seita.3G051000.1

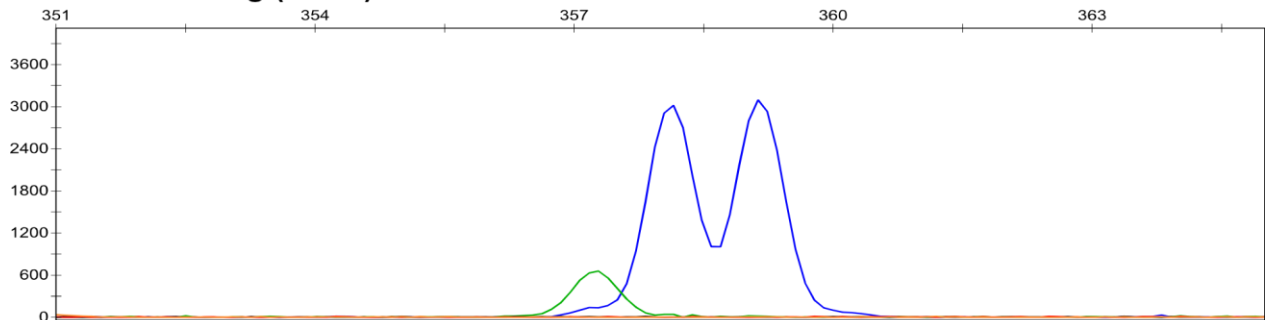
	<i>Setaria viridis</i>	2	Sevir.3G349400.1; Sevir.3G051500.1
	<i>Sorghum bicolor</i>	2	Sobic.008G129900.1; Sobic.009G031000.1
	<i>Zea mays</i>	2	Zm00008a002625_T01; Zm00008a031796_T01
Eudicot	<i>Aquilegia coerulea</i>	1	Aqcoe5G312000.1
Pentapetalae	<i>Amaranthus</i>	1	AHYPO_014711-RA
	<i>hypochoeriacus</i>		
	<i>Kalanchoe fedtschenkoi</i>	2	Kaladp1071s0022.1; Kaladp0034s0193.1
	<i>Kalanchoe laxiflora</i>	4	Kalax.0461s0032.1; Kalax.0334s0009.1; Kalax.0084s0037.1; Kalax.0276s0018.1
Asterid	<i>Daucus carota</i>	1	DCAR_005423
	<i>Mimulus guttatus</i>	1	Migut.B00957.1
	<i>Solanum lycopersicum</i>	1	Solyc01g100610.2.1
	<i>Solanum tuberosum</i>	1	PGSC0003DMT400007140
Rosid	<i>Eucalyptus grandis</i>	1	Eucgr.L00261.1
	<i>Vitis vinifera</i>	1	GSVIVT01031249001
Malpighiales	<i>Linum usitatissimum</i>	4	Lus10029841; Lus10020698; Lus10031421; Lus10010912
	<i>Manihot esculenta</i>	1	Manes.08G110700.1
	<i>Populus trichocarpa</i>	1	Potri.005G012900.3
	<i>Ricinus communis</i>	1	30128.m008918
	<i>Salix purpurea</i>	2	SapurV1A.1038s0110.1; SapurV1A.2359s0010.1
Citrus	<i>Citrus sinensis</i>	3	orange1.1g007569m; orange1.1g010361m; orange1.1g015174m
	<i>Citrus clementina</i>	1	Ciclev10000649m
Brassicales-	<i>Carica papaya</i>	1	evm.model.supercontig_48.168
Malvales			
	<i>Gossypium raimondii</i>	2	Gorai.004G236200.1; Gorai.013G129700.1
	<i>Theobroma cacao</i>	1	Thecc1EG026774t1
Fabidae	<i>Cucumis sativus</i>	1	Cucsa.090580.1
	<i>Fragaria vesca</i>	1	mrna31598.1-v1.0-hybrid
	<i>Glycine max</i>	1	Glyma.10G146600.1
	<i>Malus domestica</i>	2	MDP0000294274; MDP0000150969
	<i>Medicago truncatula</i>	1	Medtr1g084140.1
	<i>Phaseolus vulgaris</i>	1	Phvul.007G201800.1
	<i>Prunus persica</i>	1	Prupe.6G312300.1
	<i>Trifolium pratense</i>	1	Tp57577_TGAC_v2_mRNA2710

Supplementary Figures

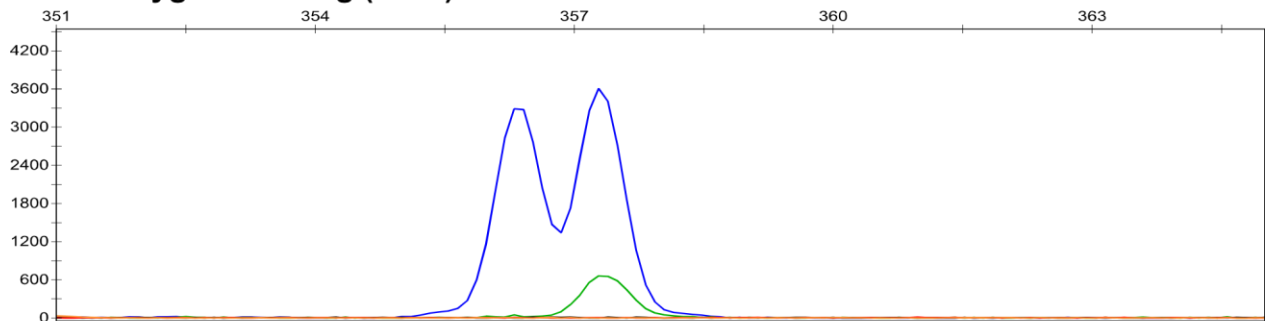
A homozygous editing (+1/+1)



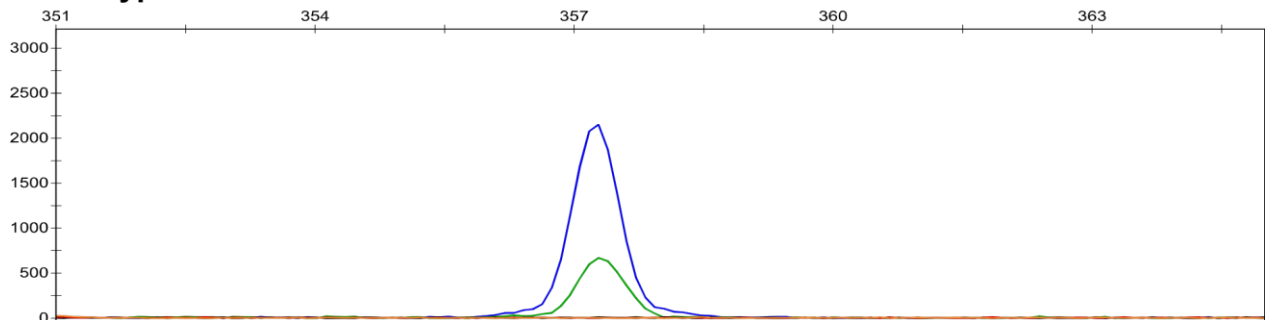
B biallelic editing (+1/+2)



C heterozygous editing (-1/wt)



D wild type



Supplementary Figure 1. Capillary sequencing chromatograms generated with GeneMapperID v3.2. The x-axis indicates the size of the amplicons, the y-axis the strength of detected fluorescence. Green peaks represent JOE-labelled amplicons of wild type plants, blue peaks are 6-FAM-labelled amplicons from H761-plants. Displayed are examples for a (A) homozygous, (B) biallelic, (C) heterozygous and (D) wild type mutation pattern. The numbers in the brackets indicate the number of inserted or deleted nucleotides.

AcoMar	1	LYASCFAGNVVEQLWNFAWPAAVALLHP-SLLPVAVVGFFTKLAIFIGGPLVGR	LMDHFP
VviMar	1	LYASSFAGGLVEQLWNFAWPAATALLHP-SLQPVAVIGFFTKLAVVGGPLVGLMDYFP	
BraMar	1	LYASCLVGNLVEQLWNFAWPSATAMLHP-SLLPVAVMGFVTKLAIICGPPVVGK	FMDHSP
EsaMar	1	LYASCLVGNLVEQLWNFAWPSATAMLHP-SLLPVAVMGFVTKLAIICGPPVVGK	FMDHSP
CgrMar	1	LYASCLVGNLVEQLWNFAWPSATAMLHP-SLLPVAVMGFVTKLMI IAGGPVVGK	FMDYSP
BstMar	1	LYASCLVGNLVEQLWNFAWPSATAMLHP-SLLPVAVMGFVTKLVIIAGGPVVGK	FMDYSP
AthMar	1	LYASCLVGNLVEQLWNFAWPSATAMLHP-SLLPVAVMGFVTKLAI IAGGPVVGK	FMDYSP
AlyMar	1	LYASCLVGNLVEQLWNFAWPSATAMLHP-SLLPVAVMGFVTKLAI IAGGPVVGK	FMDYSP
CsaMar	1	LYASCIAGNLVEQLWNFAWPSATALLHP-SLLPVAVMGFFTKLALIVGGPLVVGK	FMDNFP
FveMar	1	LYASCLAGNLVEQLWNFAWPSATALIYP-SLLPVALMGFVSKLAI IAGGPVVGK	FMDHLP
PpeMar	1	LYASCLAGNLVEQLWNFAWPSATALIYP-SLLPVAVMGFFSKLAI IAGCPLVGT	LMDHFP
MesMar	1	FYASCLAGNLVEQLWNFAWPSATALLHP-SLLPVAVMGFFTKLAI IAGGPVVGK	LMDHSP
TcaMar	1	FYASCLAGNLVEQLWNFAWPSATALLHP-SLLPVAVMGFFTKLVIIAGGPVVGK	LMDHSP
MguMar	1	LYASCLAGNLVEQLWNFAWPAATSLIHP-SLLPVAVLGFFAKVAVIVGGPLVVGK	LMDYFP
SlyMar	1	LYASCLAGYMVEQLWNFASPAATALIHP-SLLPVALMGFLAKLAVIGGGPLVVGK	LMDHFP
StuMar	1	LYASCLAGYMVEQLWNFASPAATALIHP-SLLPVALMGFLAKLTVIVGGPLVVGK	LMDHFP
Bra3	1	LYVGYFLARWGARTWEFSVALYMIYLWPNSLLLAATYGATIESGSTAIFGP	IVGRWIEGMD
Esa3	1	LYVGYFLARWSARTWEFSVALYMIYLWPNSLLLAATYGATIESGSTAIFGP	IVGQWIEGMD
Ath3	1	LYVGYFLARWSARTWEFSVALYMIHLWPNSLLLAATYGATIESGSTAIFGP	IVGQWVEGMD
Aly3	1	LYVGYFLARWSARTWEFSVALYMIHLWPNSLLLAATYGATIESGSTAIFGP	IVGQWVEGMD
Bst3	1	LYVGYFLARWSARTWEFSVALYMIHLWPNSLLLAATYGATIESGSTAIFGP	VVGQWVEGMD
Cgr3	1	LYVGYFLARWSARTWEFSVALYMIHLWPNSLLLAATYGATIESGSTAIFGP	IVGKWVEGMD
Esa2	1	LYLGYFLARWGARTWEFSVALYMIYLWPNSLFLTAMYGAVESGSTAIFGP	IVGQ MIDGMS
Bra2	1	LYLGYFLARWGARTWEFSVALYMIYLWPNSLFLTAMYGAVESGSTAIFGP	IVGQ MIDGMS
Ath2	1	LYLGYFLARWGARTWEFSVALYMIYLWPNSLFLTAMYGVVESGSATLFGP	IVGQ MIDGMS
Aly2	1	LYLGYFLARWGARTWEFSVALYMIYLWPNSLFLTAMYGVVESGSATLFGP	IVGQ MIDGMS
Bst2	1	LYLGYFLARWGARTWEFSVALYMIYLWPNSLFLTAMYGVVESGSTAIFGP	IVGQ MIDGMS
Cgr2	1	LYLGYFLARWGARTWEFSVALYMIYLWPNSLFLTAMYGAVESGSTAIFGP	IVGQ MIDGMS
Aco2	1	LYVGHFLSRWGARMWEFSVGLYMINIWPDSLLVTATYGAAFAASTMLFGP	ITIGRLVDRIS
Mgu2	1	LYVGHFLLARWGARMWEFSVGLYMINIWPDSLLLAAYGVVESASTALFGP	PLIGHWVDNLS
Sly2	1	LYVGHFLLSRWSARMWEFSVGLYMINIWPDSLLLTAAAYGVVESASTALFGP	PLVGVQWVDRLT
Stu2	1	LYVGHFLLSRWSARMWEFSVGLYMINIWPDSLLLTAAAYGVVESASTALFGP	PLIGQWVDRLT
Csa2	1	-----MWEFSVGLYMISVWPNSLLFAATYGVVESASTAFFGP	ITVGDLDVKLA
Fve2	1	LYIGHFLARWGARMWEFSVGLYMINIWPDSLLFAATYGVVESASTALFGP	PLVGVQWVDKLS
Ppe2	1	LYVGHFLLARWGTRMWEFSVGLYMISIWPDSLLFAATYGAVESASTALFGP	PLIGHWVDRFP
Mes2	1	LYIGQFLARWDARMWEFCVGLYMITLWPNSLLIIPAATYGATESASTALFGP	IVGQCAEKLIT
Mes3	1	LYIAHFFARWDARMWEFSVGLYMITLWPDSLMIAATYGATIESASTAFFGP	IVGQWVERST
Mes4	1	LYIAHFFARWDARMWEFSVGLYMITLWPDSLMIAATYGATIESASTAFFGP	IVGQWVERST
Tca2	1	LYAAHFLARWGARMWEFSVGLYMISVWPDSLLLAATYGAVESASTALFGS	VTIGRWVDRLT
Vvi2	1	LYVGHFLLARWGARMWEFSVGLYMINIWPNSLLLAAYGVVESGSTAFLGPS	IGQWLDRLT
Vvi3	1	LYVGHFLLARWGARMWEFSVGLYMINIWPNSLLLAAYGVVESASTAFLGPS	IGQWLDRLT

AcoMar	60	RVPAYNCLSSVQAAAQLLSVAMIIHAHTVPSTAA--AMLLQPWFVLVLFAGAIERLSGLA
VviMar	60	RVPAYNCLNLVQATAHLLSVAMIIIRAHTVPSTLA-SSVLLRPWFFVLVLAGSVERLSGLA
BraMar	60	RVPTYISLNVVQAAAQVLSAGMIIHAYTVPSTLG-SSILLQPWFFALIFAGAIIDTLCGIA
EsaMar	60	RVPTYISLNVVQAAAQVLSAGMIIHAYTVPSTLG-SSILLQPWFFALIFAGAIIDTLCGIA
CgrMar	60	RVPTYISLNVVQAAAQVLSAGMIIHAYTVPFPSA-SSILLQPWFFALVFAGAIIDSLCGIA
BstMar	60	RVPTYISLNVVQAAAQVLSAGMIIHAYTVPSTSA-SSILLQPWFFALVFAGAIIDSLCGIA
AthMar	60	RVPTYISLNVVQAAAQVLSAGMIIHAYTVPSTSA-SSILLQPWFFALLFAGAIIDSLCGIA
AlyMar	60	RVPTYISLNVVQAAAQVLSAGMIIHAYTVPSTLA-SSILLQPWFFALLFAGAIIDSLCGIA
CsaMar	60	RVPAYTCLNCVQAAAQLLSASMVIYAHTVPHTAASSSILLQPWFVTLIFAGAIERLSGIA
FveMar	60	RVPAYNCLNIIQAAAQLLSAAMIIRAHSVPP--SASSLLIRPWFIVLVLSGAVERLSGVA
PpeMar	60	RVPAYNCLNIIQATAQLLSAAMIIRAHSVPP--SVSSLLLRPWFIVLVLAGAVERLSGVA
MesMar	60	RTPSFIGLNVVQAAAQLLSATMIIRAHTVSPSTA-SSILLRPWFVLVSVGATERLCGVA
TcaMar	60	RVPSYIFLNVVQAAAQLLSASMIIHAAHVSPASA-SSVLRHPWFVAVLVLAGAIERLSGVA
MguMar	60	RVPAYNCLTMVQGAQLLSVGMIIIHAHTIHPTPV-SSVLVQPWFVVLVIALAVERLCGLA
SlyMar	60	RVPAYNCLYIVQTAAQLMSVGMIIHGHTLHPTSA-SSLFRPWFIVLVLVGAVERLSGLA
StuMar	60	RVPAYNCLSIIVQTAAQLMSVGMIIHGHTLHPTSA-SSLFRPWFIVLVLVGAVERLSGLA
Bra3	61	YVKVLRWLWLLQNLSYIIAGGAVIKLLLIDYDLKPRNIPVFATLIALTNVAGAIGVLSTLG
Esa3	61	YVKVLRWLWLLQNLSYTIAGGAVIKLLLSENLSKSNSSVFALVALTNVSGAIGVLSTLG
Ath3	61	YVKVLRWLWLLFQNLSYTIAGGAVIKLLIVSDLKSRNLPVFALIVLTNLAGAIGVLSTLA
Aly3	61	YVKVLRWLWLLFQNLSYTIAGGAVIKLLIVSDLKSRNLAVFALIVLTNVAGAIGVLSTLA
Bst3	61	YVKVLRWLWLLFQNLSYTIAGGAVIKLLIVSDLKSNFNPVFALIVLTNLAGAIGVLSTLA
Cgr3	61	YVKVLRWLWLLFQNLSYTIAGGAVIKLLIVSDLKSNFNLVFALIVLTNVAGAIGVLSTLA
Esa2	61	YVKVLRWLWLVTONLSFIVAGVAVALLAPDLKSNFPLFATLVLTNLSGAVGVLSTLA
Bra2	61	YVKVLRWLWLVTONLSFIVAGGSVIALLLVPDLKSNFNPVFAALVLTNLSGAIGVLSTLA
Ath2	61	YVKVLRWLWLVTONLSFIVAGGAVALLVPDLKSNFNPVFATLVLTNLSGAIGVLSTLA
Aly2	61	YVKVLRWLWLVTONLSFIVAGGAVALLVPDLRSHNFPVFALIVLTNVSGAIGVLSTLA
Bst2	61	YVKVLRWLWLVTONLSFIVAGGAVALLVPDLKSNFNPVFATLVLTNLSGAIGVLSTFA
Cgr2	61	YVKVLRWLWLVTONLSFIVAGGAVALLVPDLKSNFNPVFATLVLTNLSGAIGVLSTLA
Aco2	61	YIQVLRWLWLFIQNISFIVAGGTVTALLIYPGLRISHFPLFISLIITNISGAIGVLATLA
Mgu2	61	YIQVLRWLWLLSQNLSFMVAGGAVAILLAYPNSISANYTSFISLVILINISGAVGVLSTLG
Sly2	61	YVKVLQWLWLLSQNLSFIVAGGAVIALLRADLILVNLTAFISLVSLIYISGAVGVLSSLA
Stu2	61	YVKVLQWLWLLSQNLSFIVAGGAVIALLRADLILVNLTAFISLVSLIYISGAVGVLSSLA
Csa2	48	YVKVLKIWLATQNLSYIVAGVTVALLFYSDLKSSYFTGFILLVILTNIAGAVGALSLSLA
Fve2	61	YVKILRLWLVTQNLSFMIAGGTVMGLLIYPDLKLTNFSAFVSLIILTNISGALGVLSTLA
Ppe2	61	YVKVLWLWLVTQNLSFMIAGGTVMALLVYSDLKLTFSNAFVLLVILTNIISGAVGVLSTLA
Mes2	61	YVKVLRWLWLVTONLSFVIAGLSVIALLVFSTLKSTNFTAFIFLVILTNIISGAIGVLSTLA
Mes3	61	YVKVLRWLWLVTONLSFMVAGCTVIALIVFSTLKTTNFTAFILLVILTNIISGAVGVLSTLA
Mes4	61	YVKVLRWLWLVTONLSFMVAGCTVIALIVFSTLKTTNFTAFILLVILTNIISGAVGVLSTLA
Tca2	61	YVKVLKIWLVTQNLSLIIAGCAVMALLVFSSLKVTNLVAFISLVILTNIISGAVGVLSTLA
Vvi2	61	YVKVLKIWLWVQNLSFVVAGVAVVGLLVYSNLKYTNLAFAFIALVILTNIISGAIGVLSTLA
Vvi3	61	YVKVLQWLWLVTONLSFVVAGAAVVGLLVFSSSLKHTNLAAFITIVALTNIISGAVGVLSTLA

AcoMar	118	LGVA	MERD	WVVL	IAGTNR	-PIA-	LAEANA	ILIS	SRIDLI	CEIV	GASL	FGILL	SKYDP	VVSCLK
VviMar	119	LGVT	VERD	WIVL	IAGPNR	-PIA-	LAEANA	VLNR	IDLV	CEI	AGASL	FGILL	SKYDI	MTYLK
BraMar	119	SGVA	IERD	WVVL	IAGINR	-PIA-	LAQANA	VLNR	IDLL	CEI	AGT	MLFGILL	SKYDP	VVTCLK
EsaMar	119	SGVA	IERD	WVVL	IAGINR	-PIA-	LAQANA	VLNR	IDLL	CEI	AGT	TLLFGILL	SKYDP	VVTCLK
CgrMar	119	SGVA	IERD	WVVL	IAGINR	-PIA-	LAQANA	VLNR	IDLL	CEI	AGT	MLFGILL	SKYDP	VVTCLK
BstMar	119	SGVA	IERD	WVVL	IAGINR	-PIA-	LAQANA	VLNR	IDLL	CEI	AGT	MLFGILL	SKYDP	VVTCLK
AthMar	119	SGVA	IERD	WVVL	IAGINR	-PIA-	LAQANA	VLNR	IDLL	CEI	AGT	MLFGILL	SKYDP	VVTCLK
AlyMar	119	SGVA	IERD	WVVL	IAGINR	-PIA-	LAQANA	VLNR	IDLL	CEI	AGT	MLFGILL	SKYDP	VVTCLK
CsaMar	120	LGVA	MERD	WVVL	IAGINR	-PIA-	LAEANA	VLNR	IDLL	CEI	VGASL	FGILL	SKYDP	VVTCLK
FveMar	118	LGVA	AERD	WVVL	IAGVNR	-PIA-	LAQANA	ILIS	SRIDLL	SEI	AGASL	FGILL	SKYDP	VVTCLK
PpeMar	118	LGVA	MERD	WVVL	IAGVNR	-PIA-	LAQANA	VLNR	IDLL	CEI	AGASL	FGILL	SKYDP	VVTCLK
MesMar	119	LGVA	MERD	WVVL	IAGINR	-PIA-	LAQANA	VLNR	IDLL	CEI	AGASL	FGILL	SKYDP	VVTCLK
TcaMar	119	LGVA	MERD	WVVL	IAGINR	-PIA-	LAQANA	VLNR	INLL	CEI	AGT	LLFGILL	SKYDP	VVTCLK
MguMar	119	LGVA	MERD	WVVL	IAGTSR	-PIA-	LAQANA	ILIS	SRIDLL	CEI	AGASL	FGIFL	SQHEP	VVTCLK
SlyMar	119	LGVA	ERD	WVVL	IAGTNR	-PVA-	LAQANA	VLNR	INLL	CEI	VGAA	FGILL	AKYEL	VLCLK
StuMar	119	LGVA	ERD	WIVL	IAGTNR	-PVA-	LAQANA	VLNR	INLL	CEI	VGAA	FGILL	SKYEL	VVCLK
Bra3	121	GTIL	IERD	WAVV	MSEGHP	-PAV-	LTRM	NSVIR	GIDL	SSKLL	SPVIT	GLIIS	---	FVSLKA
Esa3	121	GTIL	IERD	WAVV	MSEGHP	-PGV-	LTRM	NSVIR	GIDL	SSKLL	SPVIT	GLIIS	---	FVSLKA
Ath3	121	GTIL	IERD	WAVV	MSEGHP	-PAV-	LTKM	NSVIR	GIDL	SSKLL	SPVIT	GLIIS	---	FVSLKA
Aly3	121	GTIL	IERD	WAVV	MSEGHP	-PAV-	LTRM	NSVIR	GIDL	SSKLL	SPVIT	GLIIS	---	FVSLKA
Bst3	121	GTIL	IERD	WAVV	MSEGHP	-LAV-	LTRM	NSVIR	GIDL	SSKLL	SPVIT	GLIIS	---	FVSLKA
Cgr3	121	GTIL	IERD	WAVV	MSEGHP	-PAV-	LTRM	NSVIR	GIDL	SSKLL	SPVIT	GLIIS	---	FVSLKA
Esa2	121	GTIL	IERD	WVVV	MSEGHS	-PAV-	LTRM	NSVIR	SIDL	SSKLL	SPVIT	GLIIS	---	FVSLRA
Bra2	121	GTIL	IERD	WVVV	MSEGHS	-PDV-	LTRM	NSVIR	GIDL	SSKLL	SPVIT	GFIIS	---	FVSLKA
Ath2	121	GTIL	IERD	WVVV	MSEGHS	-PAV-	LTRM	NSVIR	GIDL	SSKLL	SPVIT	GLIIS	---	FVSLRA
Aly2	121	GTIL	IERD	WVVV	MSEGHS	-PTV-	LTRM	NSVIR	GIDL	SSKLL	SPVIT	GLIIS	---	FVSLKA
Bst2	121	GTIL	IERD	WVVV	MSEGHS	-PAV-	LTRM	NSVIR	GIDL	SSKLL	SPVIT	GLIIS	---	FVSLRA
Cgr2	121	GTIL	IERD	WVVV	MSEGHS	-PAV-	LTRM	NSVIR	GIDL	SSKLL	SPVIT	GLIIS	---	FVSLRA
Aco2	121	GTIL	VERD	WVVV	ISEGQP	-PEA-	LTMN	SVIR	RIDL	VCKL	FAPV	VSGFIIS	---	FISLTD
Mgu2	121	GTIL	IERD	WVVV	ISEGQP	-PEV-	QTKM	NSTI	RRIDL	TCKL	FAPV	VSGFIIS	---	FVSLTA
Sly2	121	GTIL	IERD	WVVV	ISEGHP	-PGL-	LTKM	NSTI	RRIDL	TCKL	FAPV	VTGFIIS	---	FVSLTA
Stu2	121	GTIL	IERD	WVVV	ISEGHP	-PGL-	LTKM	NSTI	RRIDL	VCKL	FAPV	ITGFIIS	---	FVSLTA
Csa2	108	GTIL	VERD	WVVV	ISERHP	-PEV-	LTN	INST	RRIDL	VCKL	SPVIT	GFIIS	---	FISLKA
Fve2	121	GTIL	VERD	WVVV	ISEGHS	-PEV-	LTN	MNST	RRIDL	FSKL	CAPV	VTGFIIS	---	FVSLKA
Ppe2	121	GTIL	VERD	WVVV	ISECHSD	PEVLL	LTKM	NSVIR	RRIDL	FCKL	CAPV	LTGFIIS	---	FVSLKA
Mes2	121	GTIL	IERD	WVVV	ISEGHP	-PHV-	LTKM	NSTI	RRIDL	TCKL	LAPV	VAGSIIS	---	FISTKA
Mes3	121	GTIL	IERD	WVVV	ISEGQP	-PGV-	LTN	MNSVIR	RRIDL	TCKL	LAPV	VSGFIIS	---	FISVKA
Mes4	121	GTIL	IERD	WVVV	ISEGQP	-PGV-	LTN	MNSVIR	RRIDL	TCKL	LAPV	VSGFIIS	---	FISVKA
Tca2	121	GTIL	IERD	WVVV	ISEGHP	-PGL-	LTEM	NSVIR	RRIDL	TCKL	VAPV	ITGFIIS	---	FVSLKA
Vvi2	121	GTIL	IERD	WVVV	ISEGHP	-PGV-	LTKM	NSVIR	RRIDL	TCKL	FAPV	VTGLIIS	---	FVSLKA
Vvi3	121	GSIL	IERD	WVVV	MSEGHP	-PDV-	LTRM	NSVIR	RRIDL	TCKL	FAPV	VTGFIIS	---	FVSLKA

AcoMar 176 LAAGLMIATVPVVIILMWLSNKLSSGVLDRSKSPQAGK----MFNDMPKAGNLVEMGLDS
VviMar 177 FTAGLMTWTVPVVLVLTWLTNKLSSGVLNRTKSH-----DAEVTVKIGVGA
BraMar 177 FAATLMVGSLLPTMTALIWLTKNFSSGVLDRPKCSQSSCA---SEGPRSETESIFDLGMEA
EsaMar 177 FAATLMVGSLLPTMTALIWLTKNFSSGVLDRPKCSQSNCA---TEAPRSNKSIVDIGMEA
CgrMar 177 FAATLMVGSLLPTMTALIWLTKNFSSGVLDRPKCSQGSYA---FEGPRSATNSISDI-VET
BstMar 177 FAATLMVGSLLPTMTALIWLTKNFSSGVLDRPKCSQSSCA---AEGPRSATDSIFDIGMET
AthMar 177 FAATLMVGSLLPTMTALIWLTKNFSSGVLDRPKCSLNSCS---AEGSRTNTDSIFDIGMET
AlyMar 177 FAATLMVGSLLPTMTALIWLTKNFSSGVLDRPKCSLSSCS---AEGSRTNTDSIFDIGMET
CsaMar 178 CAAGLMLWSLPVVVLLTWLTNQLSTGVLDRAKCLQTCC-----GDPTEVTSFVNVEV
FveMar 176 FATCLMVWSLPFAVFLTCLTNKLSSGVLDRPKCSQTCCRTS-TEGPLLDTNINIVDKGVEV
PpeMar 176 FAGGLMVWSLPFAIVLTCLTNKLSSGVLDRPKCSQTCCAS-TEGPLIDTNDILDKGVA
MesMar 177 FATGLMIWSLPIMIGLALLTNKLSTGVLDHTRFSQTCCRE--SNGTAVDDNSLVDRGLET
TcaMar 177 FAAGLMMGSLPVMISLTWLTNKLSTGVLDRAKCSQSCCRTS-DEGQLPDADNFVNTGLEA
MguMar 177 LAAGLMIWSLPVVVLLTWLTNMLSAGVLDRAKCSQCCCGSS-SADSIPTDSNIFATSVEV
SlyMar 177 IAAGLMMGTLPVIVSLTWLTNKLSSGVLDRAVETCLSC----SFPSSLKSENIVGVGLEA
StuMar 177 IAAGLMMGALPVIIVSLTWLTNKLSSGVLDRAVETCLSC----SFPSSLKSENIVGVGLEA
Bra3 176 SAITFAFWAITAWVEYWLFI SVYSGVPAIAQSNERRILRS-ITRPVEETDAPVSVSIVP
Esa3 176 SAITFAAWATITAWVEYWLFI SVYIGVPAIIRSNERRILRS-RTKPVEGKDAAPVVCIEE
Ath3 176 SAITFAAWATITAWVEYWLFI SVYSGVPAITRSNERRILRS-RTKQVEGRDAPVSVSIVP
Aly3 176 SAITFAAWATITAWVEYWLFI SVYSGVPAIARSNERRILRS-RTKQVEGT DAPVSVSNAP
Bst3 176 SAITFAAWATLTAWLEYWLFI SVFSGVPAIARSNEGRILRS-RTKPEEGTDAPVAISTVP
Cgr3 176 SAITFAAWATITAWLEYWLFI SVYSGVPAIARSNERRILRS-RTDPVEETDAPVAISTVL
Esa2 176 SAITFAAWATITVWIEYWLFI SVYSGVPAIVQSDARRSSRLMSRTQAEETDIASRYLHVP
Bra2 176 SAVTFAAWATITVWIEYWLFI SVYNGVPAVLQSDERRSLRL-----SSQTDIASQYYVPL
Ath2 176 SAITFAAWATITVWIEYWLFI SVYNGVPAIVQSDERRSLRS-SQSQAETDSASSFYVPL
Aly2 176 SAITFAAWATITVWIEYWLFI SVYNGVPAIVQSDERRRLRL-SQSQGEETESASSFYVPL
Bst2 176 SAIAFAAWATITVWIEYWLFI SVYNGVPAIVQSDRRSLRL-SQSQAETDIASSYYVPL
Cgr2 176 SAITFAGWATITVWIEYWLFI SVYNGVPAIVQSNERRSLRL-SQSLAEETDFASSYDVPL
Aco2 176 SAVTFTLWNIVSVSVIYWLSSVYNGIPALIENSQKRNF-PPNDIESPPSLQETESL
Mgu2 176 SAVTLALWNVLSVFLQYWLMSVYKGIPILRQFSQRRVSKS-SVMEVDESTSTHQEQDES
Sly2 176 SAMTLALWNVISVCLYWL LTSVYNGIPALSESSLRRVSRSLPEH-SDLSPSISHEQKS
Stu2 176 SAMTLALWNVISVFLEYWL LTSVYNGIPALSESSLRRASRS-SPEH-SDLSPSISHEQKS
Csa2 163 SAMTLAVWNIISVWLEYWLFTSVYDGIPALEESSQRRVSRALGDVGESSSVSQIERL
Fve2 176 SALTALWNTISVWLEYWLFI SVFNGIPALGESSQRKITRP-SQSDLEGIGASTSQERS
Ppe2 178 SALTALWNTISIWLEYWLFI SVYNGIPALGESSQRKISRPSRTDVEESTSTSDQERIS
Mes2 176 SAMALAFWNMSAVWMEYWFFTSVYKGIPALGESSRRRNSRL-SPSNMEEGVPTSTKPENL
Mes3 176 SAMTLALWNTIAVWMEYWLFTSVYKGIPALGESSQRKVLRF-SHSDHEETASLSSQQASL
Mes4 176 SAMTLALWNTIAVWMEYWLFTSVYKGIPALGESSQRKVLRF-SHSDHEETASLSSQQASL
Tca2 176 SAMTLALWTTITVWVEYWLFM SVYNGIPALGESSLRRISEV-SPSDVAEESTSASQETPD
Vvi2 176 SAMTLAIWNTLSIWLEYWL LTSVYNGIPALSERSQKKISKI-SQGDPGESTSADQEI KSS
Vvi3 176 SAMTLAIWNTVSVWLQYWLMSVYNGIPALRESNQKRTSKIAERSAGEST SACQGVN SSP

AcoMar	232	IKH-----	GWIEYKQQPVLPASLAYVLLYFNVVLT
VviMar	223	IKH-----	GWMEYLQQPVLPASLAYVLLYFN-VLM
BraMar	234	IKL-----	GWKEYIQQPVLPAASLAYVLLCFNIVLT
EsaMar	234	IKL-----	GWKEYIQQPVLPAASLAYVLLYFNIVLT
CgrMar	233	IKL-----	GWKEYIQQPVLPAASLAYVLLYFNIILT
BstMar	234	IKL-----	GWKEYIQQPVLPAASLAYVLLYFNIVLT
AthMar	234	IKL-----	GWKEYIQQPVLPAASLAYVLLYFNIVLT
AlyMar	234	IKL-----	GWKEYIQQPVLPAASLAYVLLYFNIVLT
CsaMar	232	IKN-----	GWKEYLQQPALPASLAYVLLYFNAVLA
FveMar	235	IKL-----	GWKEYLQQPVLPASLAYVLLYFNVVLT
PpeMar	235	IKL-----	GWKEYMQQPVLPAASLAYVLLYFNVVLT
MesMar	235	IKL-----	GWKEYMHQPVLPAASLAYVLLCFNVVLA
TcaMar	236	IKL-----	GWREYIQQPVLPAASLAYVLLYLNVVLT
MguMar	236	IKN-----	GWFEYIQQPVLPAASLAYVLLYFNVVLA
SlyMar	233	IKH-----	GWFEYIRQPVLPAASLAYVLLYFNVVLA
StuMar	233	IKH-----	GWFEYIRQPVLPAASLAYVLLYFNVVLA
Bra3	235	GTE-----EGNPPRRTAMLKVFDRI	SKSSFVGAWRVIYIKQEVVLPGVSLALLFFT-VLS
Esa3	235	GSQ-----GNPPCRTGMLKILDRI	SESSFVGAWRVIYINQEVVLPGVSLALLFFT-VLS
Ath3	235	GTE---EGYTGNPPTSRTGILVILDR	MSKSSFVGAWRVIYFNQEVVLPGVSLALLFFT-VLS
Aly3	235	GTE---ESSTGNPPCRTGIRKILNR	VSKSSFVSAWRVIYFNQEVVLPGVSLPLLFFT-VLS
Bst3	235	GTE---EGSQGTPPRRIGILKIVDR	ISDSSFVGAWRVIYFNQEVVLPGVSLALLFFT-VLS
Cgr3	235	RTE---EGSQGPPPCRTGILKIVDR	ISNSSFVGAWRVIYFNQEVVLPGVSLALLFFT-VLS
Esa2	236	LLQ---GTTSEDNIPSRSGIMRIL	ERISGSSFVAAWRNYLNQETVLPGV
Bra2	231	LTD-----QNTRSRSGNMRIL	ERISDSSFVNAWRNYLNQDIVLPGV
Ath2	235	LHE---EESYRNTQSRSRILRIL	ERISSESSFVSAWRNYLNQETVLPGV
Aly2	235	LHE---EESYRKSQSRSGIFRIL	ERISSESSFVSAWRNYLNQETVLPGV
Bst2	235	LKGTTEDESYRNTQRGSGILRIL	ERIFESSFVSAWRNYLNQETVLPGV
Cgr2	235	LQGTTEDESYGNTQRRSGILRIL	DRISSESSFVGAWRNYLNQETVLPGV
Aco2	235	LPH-----KGSDSAVRHHLIER	VSKIPYVQAWTVYLQDDVVLPGIALALLFFT-VLS
Mgu2	235	SSS-----KGTTHIERFLNLPYI	SAWILYFKQDDVVLPGLSLALLYFT-VLS
Sly2	234	SLH---SDGIGLEQSENLRKIVGS	ISRLPCLSAWKVYLQDDVVLPGIALALLFFT-VLS
Stu2	234	TFH---LDRIGLEQSENLRKIVGS	ISRLPCLSAWKVYLQDDVVLPGIALALLFFT-VLS
Csa2	222	IPN----DVDARSAERSWKVKMF	NWFSKVPFVTAWKVYLEQDVLPGVALALLFFT-VLS
Fve2	235	LLS---KDENDSDFAKESWITRV	IKMVSRLPYVNAWSVYLQDDVVLPGVSLALLFFT-VLS
Ppe2	237	LLS---HDENDSQPAEESWIKRI	TEAVSRIPYVGAWKVYLQDDVVLPGVALALLFFT-VLS
Mes2	235	HSQ---NGENSALMERKWRRKL	TVWVSKAPFVGAWKVYLQDDVLLPGVALALLYFT-VLS
Mes3	235	LSQ---NEETSALEDKSWRKKL	SEWISQAPFLGAWSTYLQDDVAVPGVALALLYFT-VLS
Mes4	235	LSQ---NEETSALEDKSWRKKL	SEWISQAPFLGAWSTYLQDDVAVPGVALALLYFT-VLS
Tca2	235	SLS---NNGENSAAAGKNSGSK	FIIEWAKVPYIDAWRVYLQDDVVLPGVALALLYFT-VLS
Vvi2	235	PSF---DGGDSALAENSWKRKM	IEWWKALSTISAWTVYLQDDVVLPGIALALLYFT-VLS
Vvi3	236	LAD-----NSWKRKMIKCV	WKVLCISAWNVYLRQDDVVLSGVALALLYFT-VLS

AcoMar	262	PGGLMTAFLTQRGIDPSIIIGGFSGLCAFMGVAATFISATLVKRLGILKAGAAGLVFQASL
VviMar	252	PGGLMTAFLTQRGINPSIIVGGFSGLCFAFMGVAATFISANLVRRIGMLKAGAAGLIFQAF
BraMar	264	PGSLMTAFLTQRCVNPSVIGGFTGLCAVMGVAATFISANLVKRFGLKAGAVGLFFQASL
EsaMar	264	PGSLMTAFLTQRCVNPSVIGGFSALCAVMGVAATFISANLVKRFGLKAGAVGLFFQASL
CgrMar	263	PGSLMTAFLTQRSVNPSVIGGFSGLCAVMGVAATFISANLVKRFGLKAGAVGLFFQASL
BstMar	264	PGSLMTAFLTQRCVNPSVIGGFSGLCAVMGVAATFISANLVKRFGLKAGAVGLFFQASL
AthMar	264	PGSLMTAFLTQRCVNPSVIGGFSGLCAVMGVAATFISANLVKRVGILKAGAVGLFFQASL
AlyMar	264	PGSLMTAFLTQRCVNPSVIGGFSGLCAVMGVAATFISANLVKRVGILKAGAVGLFFQASL
CsaMar	262	PGSLMTAFLTQQGLSPSIIIGGFSGLCAFMGVATFVSANLVRRQFGILKAGAVGLIFQAA
FveMar	265	PGSLMTAYLTQSGINPSIIIGGFSGLCAFMGVAATFVSASLVRRIGILKAGAAGLIIFQASL
PpeMar	265	PGSLMTAYLTQSGINPSIIIGGFSGLCAFMGVAATFVSASLVRRIGILKAGAAGLIIFQASL
MesMar	265	PGSLMTAFLTQRCVNPSIIIGGFSGLCASMGVATFISATLVKRLGILKAGAAGLVFQASL
TcaMar	266	PGSLMTAFLTQRCVNPSVIGSFSGLCAFMGVATFISATLVRRFGILKAGAVGLIFQASL
MguMar	266	PGSLMTAFLTQHGHNPTLIGGFSGLCAFMGVAATFVSAMVKRLGILKAGAAGLIFQASL
SlyMar	263	PGGLMTAFLTQQGLNPSIIIGGFSGLCAFMGVAATFVSAMVKHLGILKAGAAGLVFHASL
StuMar	263	PGGLMTAFLTQQGLNPSIIIGGFSGLCAFMGVAATFVSAMVKHLGILKAGAAGLVFHASL
Bra3	288	FGTLMTATLQWEGIPTYYIIGIGRGISATVGLAATVVYPLMQSRLSTLRTGLWSFWSQWSC
Esa3	287	FGTLMTATLQWEGIPTYYIIGIGRGISATVGLAATVVYPLMQSRLSTLRTGLWSFWSQWSC
Ath3	291	FGTLMTATLQWEGIPTYYIIGIGRGISATVGLAATLVYPLMQSRLSTLRTGLWSFWSQWSC
Aly3	291	FGTLMTATLQWEGIPTYYIIGIGRGISATVGLAATLVYPLMQSRLSTLRTGLWSFWSQWSC
Bst3	291	FGTLMTATLQWEGIPTYYIIGIGRGISATVGLAATFVYPLMQSRLSTLRTGLWSFWSQWSC
Cgr3	291	FGTLMTATLQWEGIPTYYIIGIGRGISAMVGLAATFVYPLMQSRLSTLRTGLWSFWSQWSC
Esa2	293	FGTLMTATLEWKGIPYIIGIGRGISAGVGLAATVVYPLMQSRLSPLRTGLWSFWSQWTC
Bra2	283	FGTLMTATLEWKGIPYIIGIGRGISAGVGLAATVVYPLLSRLSPLRTGLWSFWSQWTC
Ath2	291	FGTLMTATLEWKGIPYIIGIGRGISAGVGLAATVLYPLMQSRLSPLRTGLWSFWSQWTC
Aly2	291	FGTLMTATLEWKGIPYIIGIGRGISAGVGLAATVLYPLMQSRLSPLRTGLWSFWSQWTC
Bst2	294	FGTLMTATLEWKGIPYIIGIGRGISAGVGLAATVVYPLMQSRLSSLRTGLWSFWSQWTC
Cgr2	294	FGTLMTATLEWKGIPYIIGIGRGISAGVGLAATVVYPLMQSRLSPLRTGLWSFWSQWTC
Aco2	286	FGTLMTATLQWEGIPAYVIGIMRGISATIGIAATLLYPILHSRLSTLRTGLWSIWSQWTF
Mgu2	280	FGTLMTAALEWQGIPIAYVIGIARGISATVGLAATFLYPVLQSRMSTLRTGLWSIWSQWTC
Sly2	290	FGTLMTATLEWEGIPAYVIGIARGVSATIGIAATFLYPILSHISTLRTGLWSIWSQWTF
Stu2	290	FGTLMTATLEWEGIPAYVIGIARGVSATIGIAATFLYPILSHISTLRTGLWSIWSQWTS
Csa2	277	FGTLMTATLEWEGIPAYIIGIARGVSATIGIAATLVYPIVQSRLTLRTGLWSIWSQWTC
Fve2	292	FGTLMTATLEWEGIPVYTIGIARGISAAIGITATIVYPILQSHILTTLRTGLWSIWSQWTF
Ppe2	294	FGTLMTATLEWQGTPIAYAIIGIARGISAAIGIAATIVYPVLQSHILTTLRTGLWSIWSQWTF
Mes2	291	FGTLMTAALKWEGVPFAVIGIGRGISAIIGIGATVVYPILQSRILTTLRTGLWSIWSQWSC
Mes3	291	FGTLMTATLEWEGIPALVIGIARGASALIGIGATLVYPILQSHIHTVTLRTGLWSIWSQWSC
Mes4	291	FGTLMTATLEWEGIPALVIGIARGASALIGIGATLVYPILQSHIHTVTLRTGLWSIWSQWSC
Tca2	292	FGTLMTAALEWEGIPAFVIGIARGISASIGIAATVVYPMLQSRILTTLRTGLWSVWSQWNC
Vvi2	291	FGTLMTAALEWEGIPAYIIGIGRGISATIGIAATFVYPILQSRISILTTLRTGLWSIWSQWAF
Vvi3	283	FGTLMTVALQWEGIPAYVIGIARGISAAIGIAATFVYPILQSHISTLRTGLWSIWSQWAF

AcoMar	322	LVIAVAVVYWSGSLSRRTPLLFFFLCLIVLSKLGHMSYDVVGSQIILQTGIPASKANLIGTTE
VviMar	312	LTIIVAVAVYWSGSLSQQTPLLFFFLCLIVLSRLGHMSYDVVGTQIILQTGIPSSKANLIGTTE
BraMar	324	LGVAIVAVYWSSSLSQKSPLFFFLSMIVLSRLGHMSYGVVGAQIILQTGIPSSKANLIGATE
EsaMar	324	LGVAIVAVYWSSSLSQKSPLFFFLSMIVLSRLGHMSYGVVGAQIILQTGIPSSKANLIGATE
CgrMar	323	LAVAVTVYCSSLSSHKSPLFFFLSMIVLSRLGHMSYGLVGAQIILQTGIPSSKANLIGATE
BstMar	324	LAVAVTVYCSSLSQKSPLFFFLSMIVLSRLGHMSYGVVGAQIILQTGIPSSKANLIGATE
AthMar	324	LAVAVAVYCSSLSSHKSPLFFFLSMIVLSRLGHMSYGVVGAQIILQTGIPSSKANLIGATE
AlyMar	324	LAVAVAVYCSSLSQKSPLFFFLSMIVLSRLGHMSYGVVGAQIILQTGIPSSKANLIGATE
CsaMar	322	LTVAIVAVYLSGSLSRQSPLLFFFLVMIIVLSRLGHMSYNVVGQIILQTGIPSSKTNLIATTE
FveMar	325	LTVAIVAVYCSRSSSQSPLLFFFLCLIVLSRLGHMSYDVVAAQIILQTGIPPSKVNIIIGTTE
PpeMar	325	LTAIVAVYCSRSSSQSPLLFFFLCLIVLSRLGHMSYDVVAVQIILQTGIPSSKANIIIGTTE
MesMar	325	LTIIVAVAVYWSGSLSRQSPLLFFFLGLIVLSRLGHMSYDVVGAQIILQSGIPSSKANLIGATE
TcaMar	326	LTIIVAVAVYQSGSLSQKGPLLFFFLCLIVLSRFGHMSYDIVGAQIILQTGIPSSKANLIGTTE
MguMar	326	LTIIVAVAVYWSGSLSQKVPVLFLLCLIVLSRLGHMSYDVVGAQIILQTGIPASKVNIIIGTTE
SlyMar	323	LTTAVAVVYWSGCLSQQTPIVFFFLALIVLSRLGHMSYDVIGQQIILQTGIPASKANLIGTTE
StuMar	323	LTTAVAVVYWSGCLSQQTPIVFFFLALIVLSRLGHMSYDVIGQQIILQTGIPASKANLIGTTE
Bra3	348	LLVCVGSIIWVK--RDNVASYMLMGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Esa3	347	LLVCVGSIIWVK--KDNIGSYMLMAGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Ath3	351	LLVCVGSIIWVK--KDKIASYMLMAGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Aly3	351	LLVCVGSIIWVK--KDKIASYMLMAGVAASRLGLWMFDLSVIQQMQDQVSESDRCVVGGVQ
Bst3	351	LLVCVGSIIWVK--RDKIASYMLMAGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Cgr3	351	LLVCVGSIIWVE--KDKIASYMLMAGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Esa2	353	LLVCVGSIIWVE--TEKIASYMLMAGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Bra2	343	LLVCVGSIIWVQ--KEKIASYMLMAGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Ath2	351	LLVCVGSIIWVE--KEKIASYMLMAGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Aly2	351	LLVCVGSIIWVE--KEKIASYMLMAGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Bst2	354	LLVCVGSIIWVE--KEKIASYMLMAGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Cgr2	354	LLVCVGSIIWVE--KEKIASYMLMAGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Aco2	346	LLVCVASIIVVR--NSYLSAYMLMGVAASRLGLWMFDLSVIQQMQDQVSESDRCVVGGVQ
Mgu2	340	LLICVASIIVK--GKMVSAYMLMGVAASRLGLWMFDLSVIQQMQDQVSESDRCVVGGAQ
Sly2	350	LLICVASIIVH--KKFLSAFMLMAGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Stu2	350	LLICVASIIVH--KKFLSAFMLMAGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Csa2	337	LLVCVSIWIQ--NSLLSAYMLMGVAASRLGLWMFDLAVIQMQDQVSESDRCVVGGAQ
Fve2	352	LLICVASIIVH--KSLWSAYMLMAGVATSRGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Ppe2	354	LLICVASIIVH--NSLLSAYMLMAGVATSRGLWMFDLAVIQMQDQVSESDRCVVGGVQ
Mes2	351	LLICVGSIIWVQ--NRQLSACMLMAGVATSRGLWMFDLSVIQQMQDQVSESDRCVVGAVQ
Mes3	351	LLICVASIIVQ--NNLLSAYMLMAGVATSRGLWMFDLSVIQQMQDQVSESDRCVVGGAQ
Mes4	351	LLICVASIIVQ--NNLLSAYMLMAGVATSRGLWMFDLSVIQQMQDQVSESDRCVVGGAQ
Tca2	352	LLICVASIIVK--NSHLSAYMLMGVATSRGLWMFDLSVIQQMQDQVSESDRCVVGAVQ
Vvi2	351	LLICIASIWIQ--NHITSAYMLMGVATSRGLWMFDLSVIQQMQDQVSESDRCVVGGVQ
Vvi3	343	LLICVASIIVH--NHITSAYMLMGVATSRGLWMFDLSVTQQMQDQVSESDRCVVGGVQ

A H387

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WT  AATAACAATGGTGGTTGTCGTTTCTCACGCTCAGCCTTGGTCCGCCTTCCTTACTCTC
Line1 A1  AATAA-----TTACTCTC
      A2  AATAACAATGGTGGTTGTCGTTTCTCACGCTCAGCCTTGGTCCGCCTTCCTTACTCTC
Line2 A1  AATAACAATGGTGGTTGTCGTTTCTCACGCTCAG-----TCCGCCTTCCTTACTCTC
      A2  AATAACAATGGTGGTTGTCGTTTCTCACGCTCAGCCTTGGT-----
Line3 A1  AATAACAATGGTGGTTGTCGTTTCTCACGCTCAGCCTTGGTTCCGCCTTCCTTACTCTC
      A2  AATAACAATGGTGGTTGTCGTTTCTCACGCTCAGCCTTGGTCCGCCTTCCTTACTCTC

WT  CGTCAAGTTCCTCTTACCTCCTCCTCTTCTTTTAGAATACGAACCTTAACTCCTCGCTT
Line1 A1  CGTCAAGTTCCTCTTACCTCCTCCTCTTCTTTTAGAATACGAACCTTAACTCCTCGCTT
      A2  CGTCAAGTTCCTCTTACCTCCTCCTCTTCTTTTAGAATACGAACCTTAACTCCTCGCTT
Line2 A1  CGTCAAGTTCCTCTTACCTCCTCCTCTTCTTTTAGAATACGAACCTTAACTCCTCGCTT
      A2  -----
Line3 A1  CGTCAAGTTCCTCTTACCTCCTCCTCTTCTTTTAGAATACGAACCTTAACTCCTCGCTT
      A2  CGTCAAGTTCCTCTTACCTCCTCCTCTTCTTTTAGAATACGAACCTTAACTCCTCGCTT

WT  TCGATCGTTAACTCCTCGCTTTACCACGCAAAGGTGCGATGCTTTTCCTTGTAATTTGA
Line1 A1  TCGATCGTTAACTCCTCGCTTTACCACGCAAAGGTGCGATGCTTTTCCTTGTAATTTGA
      A2  TC-----
Line2 A1  TCGATCGTTAACTCCTCGCTTTACCACGACAAAGGTGCGATGCTTTTCCTTGTAATTTGA
      A2  -----AAAGGTGCGATGCTTTTCCTTGTAATTTGA
Line3 A1  TCGATCGTTAACTCCTCGCTTTACCAC-CAAAGGTGCGATGCTTTTCCTTGTAATTTGA
      A2  TCGATCGTTAACTCCTCGCTTTACCAC-CAAAGGTGCGATGCTTTTCCTTGTAATTTGA

WT  CAATGTAAATGAATGAGTTGCTACTGTGTGATCATGATCTTAC
Line1 A1  CAATGTAAATGAATGAGTTGCTACTGTGTGATCATGATCTTAC -46 bp
      A2  -----GATCATGATCTTAC -86 bp
Line2 A1  CAATGTAAATGAATGAGTTGCTACTGTGTGATCATGATCTTAC -6 bp, +1 bp
      A2  CAATGTAAATGAATGAGTTGCTACTGTGTGATCATGATCTTAC -112 bp
Line3 A1  CAATGTAAATGAATGAGTTGCTACTGTGTGATCATGATCTTAC +1 bp, -1 bp
      A2  CAATGTAAATGAATGAGTTGCTACTGTGTGATCATGATCTTAC -1 bp
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B H386

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WT   AGATTTCTGATGTCAAGTGCATTCAAACAGCTTTATATGCTAGTTGCTTGGCTGGGTAT
Line4 A1  AG-----
      A2  AGATTTCTGATGTCAAGTGCATTCAAACAGCTTTAT-----
      A3  AGATTTCTGATGTCAAGTGCATTCAAACAGCTTTATATGCTAGTTGCTTGGCTGGGTAT
Line5 A1  AGATTTCTGATGTCAAGTGCATTCAAACAGCTTTATATGCT-----
      A2  AGATTTCTGATGTCAAGTGCATTCAAACAGCTTTATATGCTAGTTGCTTGGCTGGGTAT
Line6 A1  AGATTTCTGATGTCAAGTGCATTCAAACAGCTTTATATGCTAGTTGCTTGGCTGGGTAT
      A2  AGATTTCTGATGTCAAGTGCATTCAAACAGCTTTATATGCTAGTTGCTTGGCTGGGTAT
Line7 A1  AGATTTCTGATGTCAAGTGCATTCAAACAGCTTTAT-----
      A2  AGATTTCTGATGTCAAGTGCATTCAAACAGCTTTATATGCTAGTTGCTTG-----
      A3  AGATTTCTGATGTCAAGTGCATTCAAACAGCTTTATATGCTAGTTGCTTGGCTGG--AT

WT   ATGGTGGGAACAACCTTTGGAATTTGCCCTCACCTGCTGCCATTGCGTTGATT
Line4 A1  -----TTGATT -102 bp
      A2  -----TTCGCCTCA----CTGCCATTGCGTTGATT -44 bp, -5 bp
      A3  --GGTGGGAACAACCTTTGGAATTTGCCCTCAC-TGCTGCCATTGCGTTGATT -2 bp, -1 bp
Line5 A1  -----GCCATTGCGTTGATT -54 bp
      A2  --GGTGGGAACAACCTTTGGAATTTGCCCTCACCTGCTGCCATTGCGTTGATT -2 bp
Line6 A1  -----AACTTTGGAATTTGCCCTCACCTGCTGCCATTGCGTTGATT -10 bp
      A2  --GGTGGGAACAACCTTTGGAATTTGCCCTCACCTGCTGCCATTGCGTTGATT -2 bp
Line7 A1  -----TTCGCCTCACCTGCTGCCATTGCGTTGATT -44 bp
      A2  -----CTGCCATTGCGTTGATT -43 bp
      A3  ATGGTGGGAACAACCTTTGGAATTTGCCCTCACCTGCTGCCATTGCGTTGATT -2 bp
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Supplementary Figure 3. Mutated *SIMAR1* alleles detected in regenerated shoots selected on kanamycin-containing medium. (A) Sequences from shoots transformed with H387. (B) Sequences from shoots transformed with H386. The PAM sequence is indicated with bold letters and the gRNA target sites are highlighted in grey.