The synthesis of L-ascorbic acid in the fruits of different *Fragaria* species

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Table S1. Sequence of the specific primers used for RT-PCR expression studies.

Gene	**Primer**	**Sequence**
FaGME	Forward	TTGCAACTGAGGAGTTGTGC
	Reverse	TCGGGTCTGAAGTCCATCTC
FaG1PP	Forward	TGGTGTAACGGAGCTGACTG
	Reverse	CAGAAATGCACCTCCTCCAC
FaGalUR	Forward	CTGTAATCGGCATGGGAACT
	Reverse	TGATGAGTTGGAGACGGAGA
FaGLDH	Forward	CACATGGTACTGGTGCAAGG
	Reverse	AGGCCACAGCGAGCTAAATA
FaMYOX	Forward	CCCCAAATTGAGCACTTGTT
	Reverse	GGCCTCCAAAGCTAGGAAGT
FaMDHAR	Forward	TTGGCAATAGCCTGGTTTTC
	Reverse	CGTGCTCTTTGGAGACAACA
FaDHAR	Forward	GGTTTAGCCACCCAGTTTGA
	Reverse	GGAATCTTTTGCCAAGACCA
FaRIB413	Forward	ACCGTTGATTCGCACAATTGGTCATCG
	Reverse	TACTGCGGGTCGGCAATCGGACG

Table S2. Table with the different restriction sites and the fragments length of the different cuts in the different alleles.

	*Eco*52I	Fragment Lenght (bp)	*Mbi*I	Fragment Lenght (bp)
Allele 1	+	554 + 406	+	651 + 309
Allele 2	+	554 + 406	+	651 + 309
Allele 3	-	960	-	960

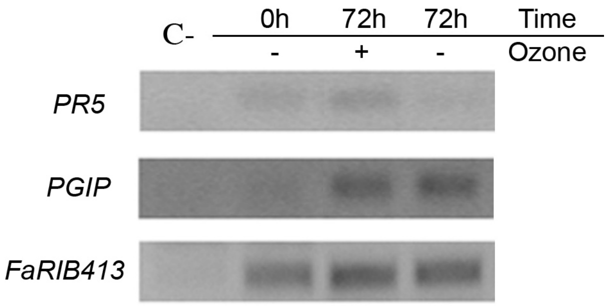


Figure S1. Changes in mRNA levels of *PR5* and *PGIP*, two pathogen-induced genes (Osorio *et al.*, 2008) in fruits before (0 h) and after storage for 72 h in ozone or air atmosphere by semi-quantitative RT-PCR.

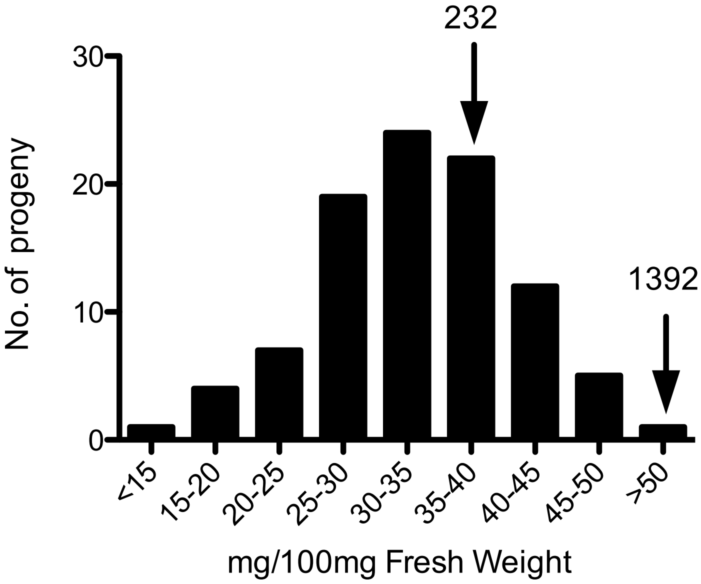
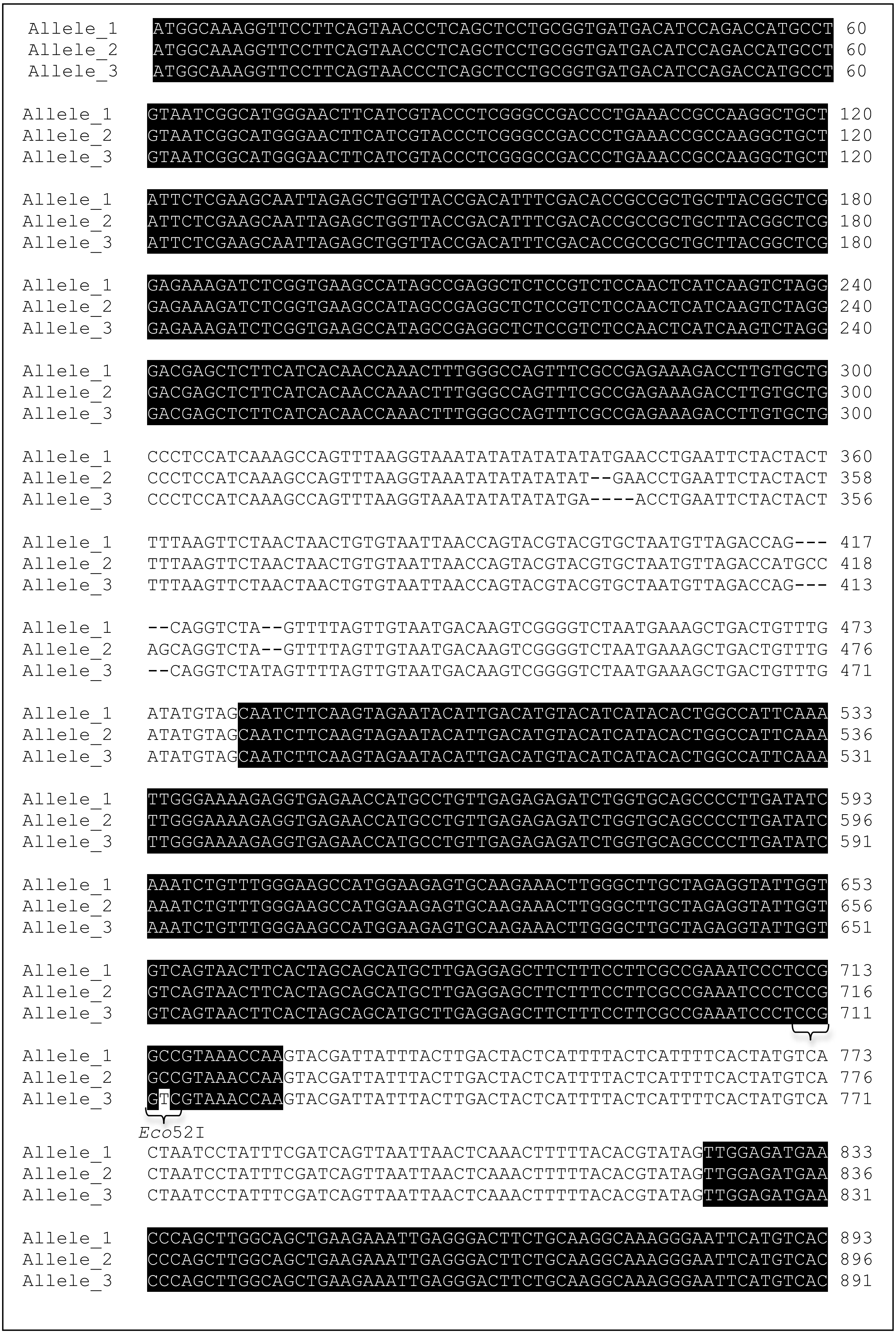


Figure S2. Frequency distributions of AsA for the 95 individuals from the population segregation derived from the cross between '232' and '1392'. Arrows indicate the parental values.



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Allele_1    ATGGCAAAGGTTCCTTCAGTAACCCTCAGCTCCTGCGGTGATGACATCCAGACCATGCCT 60
Allele_2    ATGGCAAAGGTTCCTTCAGTAACCCTCAGCTCCTGCGGTGATGACATCCAGACCATGCCT 60
Allele_3    ATGGCAAAGGTTCCTTCAGTAACCCTCAGCTCCTGCGGTGATGACATCCAGACCATGCCT 60

Allele_1    GTAATCGGCATGGGAACTTCATCGTACCCTCGGGCCGACCCTGAAACCGCCAAGGCTGCT 120
Allele_2    GTAATCGGCATGGGAACTTCATCGTACCCTCGGGCCGACCCTGAAACCGCCAAGGCTGCT 120
Allele_3    GTAATCGGCATGGGAACTTCATCGTACCCTCGGGCCGACCCTGAAACCGCCAAGGCTGCT 120

Allele_1    ATTCTCGAAGCAATTAGAGCTGGTTACCGACATTTCGACACCGCCGCTGCTTACGGCTCG 180
Allele_2    ATTCTCGAAGCAATTAGAGCTGGTTACCGACATTTCGACACCGCCGCTGCTTACGGCTCG 180
Allele_3    ATTCTCGAAGCAATTAGAGCTGGTTACCGACATTTCGACACCGCCGCTGCTTACGGCTCG 180

Allele_1    GAGAAAGATCTCGGTGAAGCCATAGCCGAGGCTCTCCGTCTCCAACTCATCAAGTCTAGG 240
Allele_2    GAGAAAGATCTCGGTGAAGCCATAGCCGAGGCTCTCCGTCTCCAACTCATCAAGTCTAGG 240
Allele_3    GAGAAAGATCTCGGTGAAGCCATAGCCGAGGCTCTCCGTCTCCAACTCATCAAGTCTAGG 240

Allele_1    GACGAGCTCTTCATCACAACCAAACTTTGGGCCAGTTTCGCCGAGAAAGACCTTGTGCTG 300
Allele_2    GACGAGCTCTTCATCACAACCAAACTTTGGGCCAGTTTCGCCGAGAAAGACCTTGTGCTG 300
Allele_3    GACGAGCTCTTCATCACAACCAAACTTTGGGCCAGTTTCGCCGAGAAAGACCTTGTGCTG 300

Allele_1    CCCTCCATCAAAGCCAGTTTAAGGTAAATATATATATATATGAACCTGAATTCTACTACT 360
Allele_2    CCCTCCATCAAAGCCAGTTTAAGGTAAATATATATATAT--GAACCTGAATTCTACTACT 358
Allele_3    CCCTCCATCAAAGCCAGTTTAAGGTAAATATATATATGA----ACCTGAATTCTACTACT 356

Allele_1    TTTAAGTTCTAACTAACTGTGTAATTAACCAGTACGTACGTGCTAATGTTAGACCAG--- 417
Allele_2    TTTAAGTTCTAACTAACTGTGTAATTAACCAGTACGTACGTGCTAATGTTAGACCATGCC 418
Allele_3    TTTAAGTTCTAACTAACTGTGTAATTAACCAGTACGTACGTGCTAATGTTAGACCAG--- 413

Allele_1    --CAGGTCTA--GTTTTAGTTGTAATGACAAGTCGGGGTCTAATGAAAGCTGACTGTTTG 473
Allele_2    AGCAGGTCTA--GTTTTAGTTGTAATGACAAGTCGGGGTCTAATGAAAGCTGACTGTTTG 476
Allele_3    --CAGGTCTATAGTTTTAGTTGTAATGACAAGTCGGGGTCTAATGAAAGCTGACTGTTTG 471

Allele_1    ATATGTAGCAATCTTCAAGTAGAATACATTGACATGTACATCATACACTGGCCATTCAAA 533
Allele_2    ATATGTAGCAATCTTCAAGTAGAATACATTGACATGTACATCATACACTGGCCATTCAAA 536
Allele_3    ATATGTAGCAATCTTCAAGTAGAATACATTGACATGTACATCATACACTGGCCATTCAAA 531

Allele_1    TTGGGAAAAGAGGTGAGAACCATGCCTGTTGAGAGAGATCTGGTGCAGCCCCTTGATATC 593
Allele_2    TTGGGAAAAGAGGTGAGAACCATGCCTGTTGAGAGAGATCTGGTGCAGCCCCTTGATATC 596
Allele_3    TTGGGAAAAGAGGTGAGAACCATGCCTGTTGAGAGAGATCTGGTGCAGCCCCTTGATATC 591

Allele_1    AAATCTGTTTGGGAAGCCATGGAAGAGTGCAAGAAACTTGGGCTTGCTAGAGGTATTGGT 653
Allele_2    AAATCTGTTTGGGAAGCCATGGAAGAGTGCAAGAAACTTGGGCTTGCTAGAGGTATTGGT 656
Allele_3    AAATCTGTTTGGGAAGCCATGGAAGAGTGCAAGAAACTTGGGCTTGCTAGAGGTATTGGT 651

Allele_1    GTCAGTAACTTCACTAGCAGCATGCTTGAGGAGCTTCTTTCCTTCGCCGAAATCCCTCCG 713
Allele_2    GTCAGTAACTTCACTAGCAGCATGCTTGAGGAGCTTCTTTCCTTCGCCGAAATCCCTCCG 716
Allele_3    GTCAGTAACTTCACTAGCAGCATGCTTGAGGAGCTTCTTTCCTTCGCCGAAATCCCTCCG 711

Allele_1    GCCGTAAACCAAGTACGATTATTTACTTGACTACTCATTTTACTCATTTTCACTATGTCA 773
Allele_2    GCCGTAAACCAAGTACGATTATTTACTTGACTACTCATTTTACTCATTTTCACTATGTCA 776
Allele_3    GTCGTAAACCAAGTACGATTATTTACTTGACTACTCATTTTACTCATTTTCACTATGTCA 771
           Eco52I
Allele_1    CTAATCCTATTTCGATCAGTTAATTAACTCAAACTTTTTACACGTATAGTTGGAGATGAA 833
Allele_2    CTAATCCTATTTCGATCAGTTAATTAACTCAAACTTTTTACACGTATAGTTGGAGATGAA 836
Allele_3    CTAATCCTATTTCGATCAGTTAATTAACTCAAACTTTTTACACGTATAGTTGGAGATGAA 831

Allele_1    CCCAGCTTGGCAGCTGAAGAAATTGAGGGACTTCTGCAAGGCAAAGGGAATTCATGTCAC 893
Allele_2    CCCAGCTTGGCAGCTGAAGAAATTGAGGGACTTCTGCAAGGCAAAGGGAATTCATGTCAC 896
Allele_3    CCCAGCTTGGCAGCTGAAGAAATTGAGGGACTTCTGCAAGGCAAAGGGAATTCATGTCAC 891
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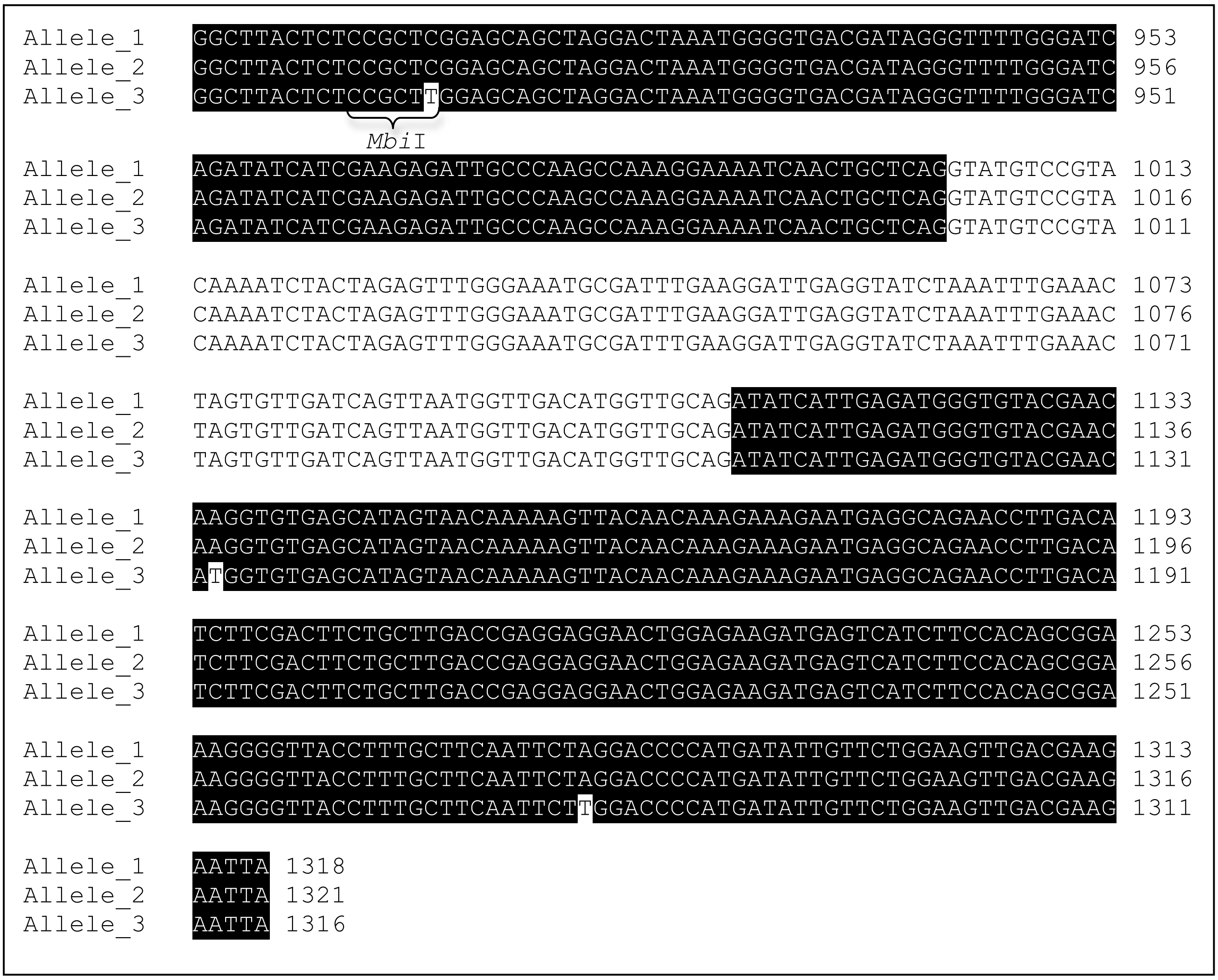

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Allele_1    GGCTTACTCTCCGCTCGGAGCAGCTAGGACTAAATGGGGTGACGATAGGGTTTTGGGATC 953
Allele_2    GGCTTACTCTCCGCTCGGAGCAGCTAGGACTAAATGGGGTGACGATAGGGTTTTGGGATC 956
Allele_3    GGCTTACTCTCCGCTTGGAGCAGCTAGGACTAAATGGGGTGACGATAGGGTTTTGGGATC 951
                      MbiI

Allele_1    AGATATCATCGAAGAGATTGCCCAAGCCAAAGGAAAATCAACTGCTCAGGTATGTCCGTA 1013
Allele_2    AGATATCATCGAAGAGATTGCCCAAGCCAAAGGAAAATCAACTGCTCAGGTATGTCCGTA 1016
Allele_3    AGATATCATCGAAGAGATTGCCCAAGCCAAAGGAAAATCAACTGCTCAGGTATGTCCGTA 1011

Allele_1    CAAAATCTACTAGAGTTTGGGAAATGCGATTTGAAGGATTGAGGTATCTAAATTTGAAAC 1073
Allele_2    CAAAATCTACTAGAGTTTGGGAAATGCGATTTGAAGGATTGAGGTATCTAAATTTGAAAC 1076
Allele_3    CAAAATCTACTAGAGTTTGGGAAATGCGATTTGAAGGATTGAGGTATCTAAATTTGAAAC 1071

Allele_1    TAGTGTTGATCAGTTAATGGTTGACATGGTTGCAGATATCATTGAGATGGGTGTACGAAC 1133
Allele_2    TAGTGTTGATCAGTTAATGGTTGACATGGTTGCAGATATCATTGAGATGGGTGTACGAAC 1136
Allele_3    TAGTGTTGATCAGTTAATGGTTGACATGGTTGCAGATATCATTGAGATGGGTGTACGAAC 1131

Allele_1    AAGGTGTGAGCATAGTAACAAAAAGTTACAACAAAGAAAGAATGAGGCAGAACCTTGACA 1193
Allele_2    AAGGTGTGAGCATAGTAACAAAAAGTTACAACAAAGAAAGAATGAGGCAGAACCTTGACA 1196
Allele_3    ATGGTGTGAGCATAGTAACAAAAAGTTACAACAAAGAAAGAATGAGGCAGAACCTTGACA 1191

Allele_1    TCTTCGACTTCTGCTTGACCGAGGAGGAACTGGAGAAGATGAGTCATCTTCCACAGCGGA 1253
Allele_2    TCTTCGACTTCTGCTTGACCGAGGAGGAACTGGAGAAGATGAGTCATCTTCCACAGCGGA 1256
Allele_3    TCTTCGACTTCTGCTTGACCGAGGAGGAACTGGAGAAGATGAGTCATCTTCCACAGCGGA 1251

Allele_1    AAGGGGTTACCTTTGCTTCAATTCTAGGACCCCATGATATTGTTCTGGAAGTTGACGAAG 1313
Allele_2    AAGGGGTTACCTTTGCTTCAATTCTAGGACCCCATGATATTGTTCTGGAAGTTGACGAAG 1316
Allele_3    AAGGGGTTACCTTTGCTTCAATTCTTGGACCCCATGATATTGTTCTGGAAGTTGACGAAG 1311

Allele_1    AATTA 1318
Allele_2    AATTA 1321
Allele_3    AATTA 1316
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Figure S3. Alignment of the three differents alleles of *FaGalUR*. Exons are indicated with Black backgrounds and introns with grey backgrounds. Gaps are indicated by dashes and letters with background are identical nucleotides. The different between Allele 1 and 2 is only the length of the SSR, although the different between alleles 1 and 2 with allele 3 is the SSR length and the changes in four nucleotides that produce changes in two aminoacids and different restriction sites. The restriction sites used are indicated with brackets.

Osorio S, Castillejo C, Quesada MA, Medina-Escobar N, Brownsey GJ, Suau R, Heredia A, Botella MA, Valpuesta V. 2008. Partial demethylation of oligogalacturonides by pectin methyl esterase 1 is required for eliciting defence responses in wild strawberry (Fragaria vesca). *Plant J* **54**, 43-55.