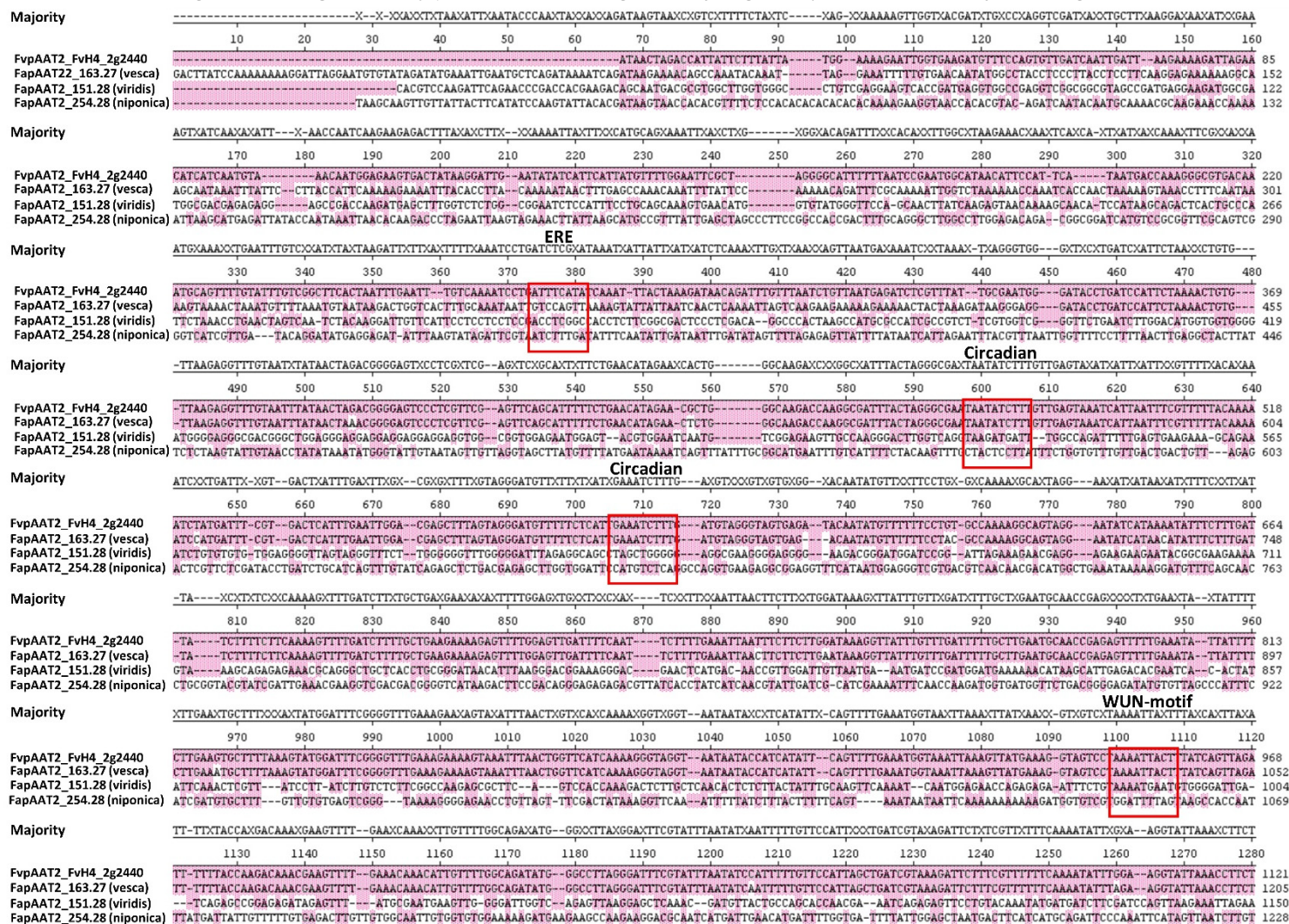

Article

The Intragenesis and Synthetic Biology Approach towards Accelerating Genetic Gains on Strawberry: Development of New Tools to Improve Fruit Quality and Resistance to Pathogens

Supplementary Materials.

Figure S1 Alignment of promoter and regulatory region of the strawberry AAT2 genes



(Cont)

(Cont)



Figure S1: Alignment of promoter and regulatory region of the strawberry AAT2 genes. Alignment of the 2998 bp DNA fragment corresponding to the promoter and regulatory region of FvAAT2 (FvH4_5g24240) with its respective homeologous of *Fragaria x ananassa* FapAAT2_163.27, maker-Fvb5-1-snap-gene-163.27-mRNA-1 (Vesca homeologous); FapAAT2_151.28, maker-Fvb5-2-snap-gene-151.28-mRNA-1 (Viridis homeologous); and FapAAT2_254.28 maker-Fvb3-3-augustus-gene-254.28-mRNA-1 (niponica homeologous). The putative RNA Polymerase II TATA box and transcription start sites (TSS) (Black box) and cis-acting regulatory motifs (Red boxes) were predicted by PlantCare (<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>) and TSSplant v1.2016 (<http://www.softberry.com>). All sequences were retrieved of *Fragaria vesca* v.4.0a1 and *Fragaria x ananassa* Camarosa Genome v1.0.a1 Transcripts database. ERE: Ethylene Response Element; ABRE: Absciscic acid Response element; WUN-motif: wounding-responsive element; TCA element: SA-responsive elements.

Figure S2 Alignment of promoter and regulatory region of the strawberry DOF2 genes



[illegible]

(Cont)

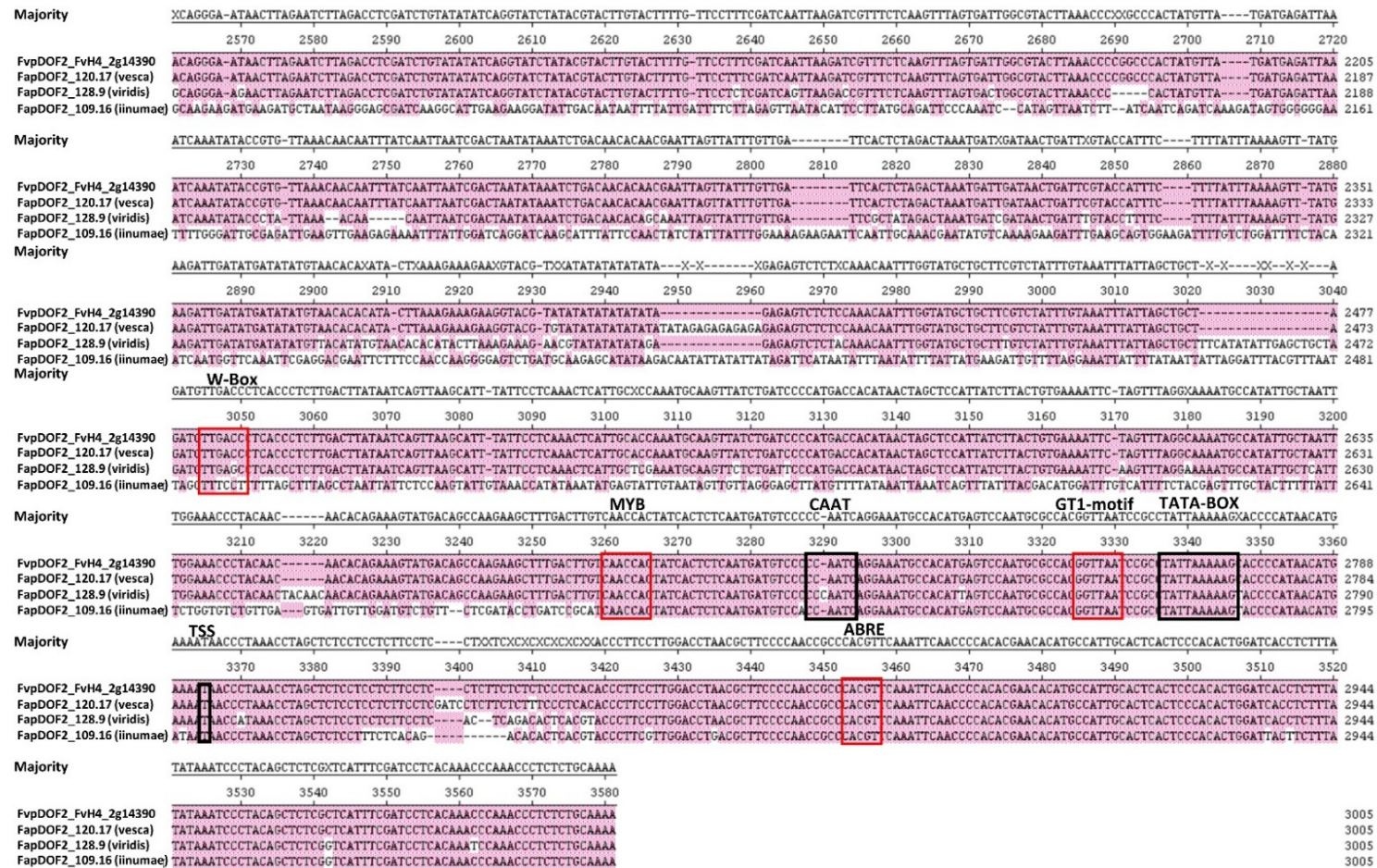


Figure S2: Alignment of promoter and regulatory region of the strawberry DOF2 genes. Alignment of the 3005 bp DNA fragment corresponding to promoter and regulatory region of the FvDOF2 (FvH4_2g14390) with its respective homeologous of *Fragaria x ananassa* FapDOF2_120.17, snap_masked-Fvb2-2-processed-gene-120.17-mRNA-1 (Vesca homeologous); FapDOF2_128.9, augustus_masked-Fvb2-3-processed-gene-128.9-mRNA-1 (Viridis homeologous); and FapDOF2_109.16 snap_masked-Fvb2-4-processed-gene-109.16-mRNA-1 (liunumae homeologous). The putative RNA Polymerase II TATA box and transcription start sites (TSS) (Black box) and cis-acting regulatory motif (Red boxes) were predicted by

PlantCare (<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>) and *TSSplant v1.2016* (<http://www.softberry.com>). All sequences were retrieved of *Fragaria vesca* v.4.0a1 and *Fragaria x ananassa* Camarosa Genome v1.0.a1 Transcripts database. ERE: Ethylene Response Element; ABRE: Absciscic acid Response element; WUN-motif: wounding-responsive element; TCA element: SA-responsive elements.

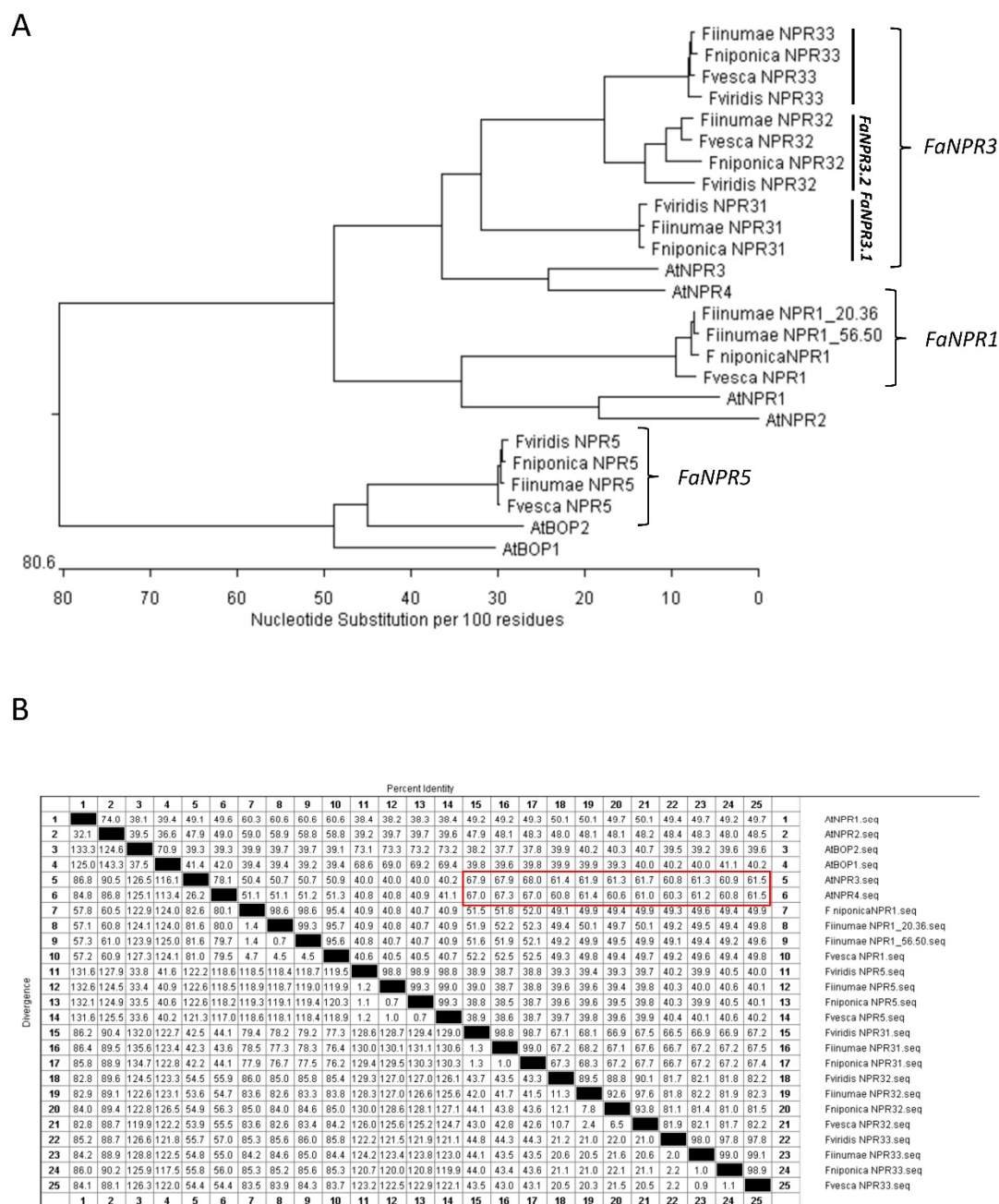
Figure S3 Phylogenetic tree and identity percentage of NPR gene family in strawberry and *A. thaliana*

Figure S3. Phylogenetic tree and identity percentage of NPR gene family in strawberry and *A. thaliana*. (A) Phylogenetic analysis of five members of *Fragaria ananassa* NPR gene family and six member of *A. thaliana*. The sequences were aligned and analyzed by clustalW method with 1000 bootstrap replications. Numbers on branches are the bootstrap values. The scale bar at the bottom indicates the evolutionary distance. **(B)** Divergence and percentage identity of nucleotide sequences of NPR gene family between *F. x ananassa* and *Arabidopsis thaliana*. The nucleotide sequence of *AtNPR3/4* present the similar percentage (around 60 to 70%) of homologous with respect to *Fragaria* NPR3 gene family (Red Box). *Fragaria ananassa* sequences correspond to *Fiinumae* NPR1_20.36, *maker-Fvb1-2-augustus-gene-20.36-mRNA-1*; *Fiinumae* NPR1_56.50, *maker-Fvb1-2-augustus-gene-56.50-mRNA-1*; *Fvesca* NPR1, *maker-Fvb1-4-augustus-gene-33.69-mRNA-1*; *Fniponica* NPR1, *maker-Fvb1-3-augustus-gene-37.59-mRNA-1*; *Fniponica* NPR31, *maker-Fvb3-3-augustus-gene-47.46-*

mRNA-1; Fiinumae NPR31, maker-Fvb3-2-augustus-gene-63.42-mRNA-1 and Fviridis NPR31, maker-Fvb3-1-augustus-gene-256.35-mRNA-1. The corresponding homeolog to FaNPR32 and FaNPR33 are named as Fviridis NPR32, maker-Fvb6-4-augustus-gene-288.39-mRNA-1; Fiinumae NPR32, maker-Fvb6-3-augustus-gene-80.33-mRNA-1; Fvesca NPR32, maker-Fvb6-1-augustus-gene-87.19-mRNA-1; Fniponica NPR32, maker-Fvb6-2-snap-gene-357.51-mRNA-1; Fviridis NPR33, maker-Fvb6-4-augustus-gene-288.38-mRNA-1; Fiinumae NPR33, maker-Fvb6-3-augustus-gene-80.34-mRNA-1; Fvesca NPR33, maker-Fvb6-1-augustus-gene-87.20-mRNA-1 and Fniponica NPR33, snap_masked-Fvb6-2-processed-gene-357.26-mRNA-1; Fvesca NPR5, maker-Fvb6-1-augustus-gene-182.42-mRNA-1; Fniponica NPR5, maker-Fvb6-2-augustus-gene-104.36-mRNA-1; Fviridis NPR5, maker-Fvb6-3-augustus-gene-192.35-mRNA-1; Fiinumae NPR5, maker-Fvb6-4-augustus-gene-184.25-mRNA-1. For the Arabidosis NPR sequence, NPR1: At1g64280; NPR2: At4g26120; NPR3At5g45110; NPR4: At4g19660; NPR5(BOP2); At2g41370; NPR6(BOP1); At3g572130.

FigureS4 Candidate DNA fragments of the strawberry *FaWRKY1* gene for dsRNA production (siRNAs).

A

Nº	Sequence (5'-3')	Start
1	GGATACCTACCCAGCATTCTA	3
2	GCATTCTATTCTTCTCATCA	16
3	GGTGAACACTCATCCTCATCA	78
4	GTGAACACTCATCCTCATCAT	79
5	GAGGTTTCGAACAGCATGAGT	175
6	GTTTCGAACAGCATGAGTAGT	178
7	GTGAAAGTAATACAGCAGTAA	213
8	GAAAGTAATACAGCAGTAAGA	215

C

Nº	siRNA	Homeologous	Target Name	E-value	ID
1	1	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	0.000819148	21
2	1	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	0.000819148	21
3	1	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	0.000819148	21
4	2	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	0.000819148	21
5	2	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	0.000819148	21
6	2	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	0.000819148	21
7	3	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	0.000819148	21
8	3	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	0.000819148	21
9	4	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	0.000819148	21
10	4	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	0.000819148	21
11	5	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	0.000819148	21
12	5	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	0.000819148	21
13	5	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	0.000819148	21
14	6	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	0.000819148	21
15	6	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	0.000819148	21
16	6	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	0.000819148	21
17	7	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	0.000819148	21
18	7	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	0.000819148	21
19	7	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	0.000819148	21
20	8	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	0.000819148	21
21	8	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	0.000819148	21
22	8	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	0.000819148	21

B

Nº	Sequence (5'-3')	Start
9	ACCTACCCAGCATTCTATTCTT	7
10	CAGCATTCTATTCTTCTCATCA	14
11	TGCTTCTTCGCTGTCATTGAACA	54
12	TTCGCTGTCATTGAACATGGTGA	60
13	ATGGTGAACACTCATCCTCATCA	76
14	GTGAACACTCATCCTCATCATGC	79
15	AAGCTAGCAATAACAAGGAAAAT	125
16	GTCAGAGATGGAGGTTTCAACA	165
17	TGGAGGTTTCAACAGCATGAGT	173
18	TTCGAACAGCATGAGTAGTATTA	180
19	GGGGAGGGTGAAAGTAATACAGC	226
20	GAGGGTGAAAGTAATACAGCAGT	229
21	CAGCAGTAAGATTAGGGATGAAG	245
22	CAGCAGTAAGATTAGGGATGAAG	246

D

Nº	siRNA	Homeologous	Target Name	E-value	ID
1	9	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	6.71529E-5	23
2	9	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
3	9	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
4	10	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	6.71529E-5	23
5	10	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
6	10	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
7	11	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	6.71529E-5	23
8	11	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
9	11	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
10	12	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	6.71529E-5	23
11	12	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
12	12	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
13	13	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
14	13	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
15	14	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
16	14	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
17	15	<i>F.vescaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
18	16	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	6.71529E-5	23
19	16	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
20	16	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
21	17	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	6.71529E-5	23
22	17	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
23	17	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
24	18	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	6.71529E-5	23
25	18	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
26	18	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
27	19	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	6.71529E-5	23
28	19	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
29	19	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
30	20	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	6.71529E-5	23
31	20	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
32	20	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
33	21	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	6.71529E-5	23
34	21	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
35	21	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23
36	22	<i>F.viridisWRKY1</i>	maker-Fvb4-4-augustus-gene-72.68-mRNA-1	6.71529E-5	23
37	22	<i>F.vescaWRKY1</i>	maker-Fvb4-3-augustus-gene-105.32-mRNA-1	6.71529E-5	23
38	22	<i>F.niponicaWRKY1</i>	maker-Fvb4-2-augustus-gene-73.40-mRNA-1	6.71529E-5	23

Figure S4: Candidate DNA fragments of the strawberry FaWRKY1 for dsRNA production (siRNAs). (A) and (B) indicate the sequence and the position of each predicted siRNA within the 272 bp DNA fragment of the FaWRKY1 used for the construction of the corresponding intragenic dsRNAi inducing cassettes, and (C) and (D) BLAST of each candidate dsRNAi inducing sequence against v1.0.a1 Transcripts database indicating the identity with its corresponding homoeologous in the *Fragaria ananassa* genome. Predicted siRNA sequence were obtained by using the InvivoGen siRNA Wizard software 3.1.(A) and siRNA at Whitehead (B). Search parameters of the BLAST search against *Fragaria x ananassa* Camarosa Genome transcripts database were adjusted to the short sequence (e-value 0,05 and Match/Mismatch Scores 2/-3).

FigureS5 Candidate DNA fragments of the strawberry FaNPR31 gene for dsRNA production (siRNAs).**A**

Nº	Sequence (5'-3')	Start
1	GGCATTAGACTCGGATGATGT	2
2	GCATTAGACTCGGATGATGT	3
3	GAGTATGTTGAACCTTGTA	14
4	GAGTCGAATATAACCTTAGAT	48
5	GTCGAATATAACCTTAGATGA	50
6	GAAGCCCATGCTCTCACTAT	69
7	GCCTACTGTGATCCTAAGGTT	96
8	GGTCTGGGTATGGCTGATGTT	132
9	GTCTGGGTATGGCTGATGTTA	133
10	GGGTATGGCTGATGTTAACT	137
11	GCTGATGTTAACTTCGTAAT	144
12	GGGTTATACCGTGCTTCATAT	170
13	GGTTATACCGTGCTTCATATT	171
14	GCGCAGAGAGCCATCAATAAT	200
15	GATGGTCAAAGTGCAAGTTAGT	267
16	GGTCAAAGTGCAAGTTAGTATT	270
17	GTTGACAAGGGCAAAGGACTA	299
18	GACAAGGGCAAAGGACTATCA	302
19	GGGCAAAGGACTATCATTCAA	307
20	GGCAAAGGACTATCATTCAAA	308

C

Nº siRNA	Homeologous	Target Name	E-value	ID
1	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
2	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.000819148	21
3	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
4	<i>F.niponicaNPR31</i>	maker-Fvb3-2-augustus-gene-47.46-mRNA-1	0.000819148	21
5	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
6	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.000819148	21
7	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
8	<i>F.niponicaNPR31</i>	maker-Fvb3-2-augustus-gene-47.46-mRNA-1	0.000819148	21
9	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	0.000819148	21
10	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
11	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.000819148	21
12	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	0.000819148	21
13	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
14	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.000819148	21
15	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
16	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.000819148	21
17	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.00997927	18
18	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.00997927	18
19	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	0.00997927	18
20	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.00285911	19
21	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.00285911	19
22	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	0.00285911	19
23	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
24	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.000819148	21
25	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	0.000819148	21
26	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.000819148	21
27	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	0.000819148	21
28	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
29	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	0.000819148	21
30	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
31	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	0.000819148	21
32	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
33	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.000819148	21
34	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
35	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.000819148	21
36	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	0.000819148	21
37	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.000819148	21
38	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.000819148	21
39	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	0.000819148	21
40	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	0.00997927	18
41	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	0.00997927	18
42	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	0.00997927	18

B

Nº	Sequence (5'-3')	Start
1	CTCGGATGATGTTGAACCTTGTA	11
2	GAGTCGAATATAACCTTAGATGA	48
3	AGCCTACTGTGATCCTAAGGTTG	95
4	ATGGCTGATGTTAACTTCGTAA	141
5	TGGCTGATGTTAACTTCGTAAT	142
6	GGCTGATGTTAACTTCGTAATC	143
7	GGGTTATACCGTGCTTCATATTG	170
8	TACCGTGCTTCATATTGCTGTGA	176
9	CCGTGCTTCATATTGCTGTGATG	178
10	GCGCAGAGAGCCATCAATAATAGT	201
11	GAGAGCCATCAATAATAGTATTG	205
12	GAGCTGACATCAGATGGTCAAAG	255
13	CTGACATCAGATGGTCAAAGTGC	258
14	CAGATGGTCAAAGTGCAAGTTAGT	265
15	TTGACAAGGGCAAAGGACTATCA	300
16	GACAAGGGCAAAGGACTATCATT	302
17	GGGCAAAGGACTATCATTCAAAA	307
18	AAGGACCGAATTTCATTGATGT	354
19	TAGAGAGAGAAATGCGGAAGAAT	379

D

Nº siRNA	Homeologous	Target Name	E-value	ID
1	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
2	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
3	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
4	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
5	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
6	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
7	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
8	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
9	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
10	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
11	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
12	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
13	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
14	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
15	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
16	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
17	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
18	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
19	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
20	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
21	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
22	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
23	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
24	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
25	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
26	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
27	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
28	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
29	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
30	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
31	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
32	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
33	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
34	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
35	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
36	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
37	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
38	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
39	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
40	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
41	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
42	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
43	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23
44	<i>F.iumaeNPR31</i>	maker-Fvb3-2-augustus-gene-63.42-mRNA-1	6.71529E-5	23
45	<i>F.niponicaNPR31</i>	maker-Fvb3-3-augustus-gene-47.46-mRNA-1	6.71529E-5	23
46	<i>F.viridisNPR31</i>	maker-Fvb3-1-augustus-gene-256.35-mRNA-1	6.71529E-5	23

Figure S5: Candidate DNA fragments of the strawberry FaNPR3.1 for dsRNA production (siRNAs). (A) and (B) indicate the sequence and the position of each predicted siRNA within the 407 bp DNA fragment of the FaNPR3.1 used for the construction of the corresponding intragenic dsRNAi inducing cassettes, and (C) and (D) BLAST of each candidate dsRNA inducing sequence against v1.0.a1 Transcripts database indicating the identity with its corresponding homoeologous in the *F. x ananassa* genome. Predicted siRNA sequence were obtained by using the InvivoGen siRNA Wizard software 3.1.(A) and siRNA at Whitehead (B). Search parameters of the BLAST search against *Fragaria x ananassa* Camarosa Genome transcripts database were adjusted to the short sequence (e-value 0,05 and Match/Mismatch Scores 2/-3).

Majority	ATGATGGCTCTTATTATCATGCCCTCTCGGATTCAGGTGAATCGCTGCGAGCCGGCACTTATCACACGACGAAAAACAACACCATACGAAACAAAGCTACTGTGCGGATATCGACAAACCAAGGGCTCAGATTCATGTTCCATTATCATATGTCTTACA	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160
FvAAT2_FvH4_2g2440	ATGATGGCTCTTATTATCATGCCCTCTCGGATTCAGGTGAATCGCTGCGAGCCGGCACTTATCACACGACGAAAAACAACACCATACGAAACAAAGCTACTGTGCGGATATCGACAAACCAAGGGCTCAGATTCATGTTCCATTATCATATGTCTTACA	160															
FaAAT2_163.27 (vesca)	ATGATGGCTCTTATTATCATGCCCTCTCGGATTCAGGTGAATCGCTGCGAGCCGGCACTTATCACACGACGAAAAACAACACCATACGAAACAAAGCTACTGTGCGGATATCGACAAACCAAGGGCTCAGATTCATGTTCCATTATCATATGTCTTACA	160															
FaAAT2_151.28 (viridis)	ATGACGGTCTTATTATCATGCCCTCTCGGATTCAGGTGAATCGCTGCGAGCCGGCACTTATCACACGACGAAAAACAACACCATACGAAACAAAGCTACTGTGCGGATATCGACAAACCAAGGGCTCAGATTCATGTTCCATTATCATATGTCTTACA	160															
FaAAT2_254.28 (niponica)	---ATGGCTCTATTG---CGCTCTCGCATTCAGGTGAATCACTTCGAGCTGCACTTATAACGCCGCAAGGCAACACCGCTCGAAATGAAGCTGTGTGCGAATATCGACGACCGCAATGCTTCAGGTCTCATGTGCCATTATCATATGTCTTACA	154															
Majority	AGAACAATCCTTCAATATCATCGAAACAAAATGACCGCTGCGAGATGATTATTGACGCGCTGAGTAGAGCACTGGAGTTTATACCTCTTGGCTGGTAGGCTAAGGGAAGTGCACAAACAGAAAGCTTGTGTGGATGCACCGGAGAGGCTTCTTGTT	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320
FvAAT2_FvH4_2g2440	AGAACAATCCTTCAATATCATCGAAACAAAATGACCGCTGCGAGATGATTATTGACGCGCTGAGTAGAGCACTGGAGTTTATACCTCTTGGCTGGTAGGCTAAGGGAAGTGCACAAACAGAAAGCTTGTGTGGATGCACCGGAGAGGCTTCTTGTT	320															
FaAAT2_163.27 (vesca)	AGAACAATCCTTCAATATCATCGAAACAAAATGACCGCTGCGAGATGATTATTGACGCGCTGAGTAGAGCACTGGAGTTTATACCTCTTGGCTGGTAGGCTAAGGGAAGTGCACAAACAGAAAGCTTGTGTGGATGCACCGGAGAGGCTTCTTGTT	320															
FaAAT2_151.28 (viridis)	AGAACAATCCTTCAATATCATCGAAACAAAATGACCGCTGCGAGATGATTATTGACGCGCTGAGTAGAGCACTGGAGTTTATACCTCTTGGCTGGTAGGCTAAGGGAAGTGCACAAACAGAAAGCTTGTGTGGATGCACCGGAGAGGCTTCTTGTT	320															
FaAAT2_254.28 (niponica)	AGAACAATCATTTCAATCTGTGGAACCAACGACCGCTGAGTGAATAGGATCGCTGAGCAAGGCACTTCAGTTTATACCTCTTGGCTGGTAGGCTAGGAGGGGCTTACAAAAGCTTATGTTGGATGCACCGGAGAGGCACTTCTTGTT	314															
Majority	CGTCGAGGCAATGCCAATCATCAGCTCGACGAACTCGGTGATGCAATTCTACCACCTTGTCTATTCTTAGACGAGTTCCTGTTTAACTGCCAGGATCTGATGGTATTCTTGTTCTCCTTTGTTGTTAATACAGGTAACCCGCTGTCTATGTGGAGGT	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480
FvAAT2_FvH4_2g2440	CGTCGAGGCAATGCCAATCATCAGCTCGACGAACTCGGTGATGCAATTCTACCACCTTGTCTATTCTTAGACGAGTTCCTGTTTAACTGCCAGGATCTGATGGTATTCTTGTTCTCCTTTGTTGTTAATACAGGTAACCCGCTGTCTATGTGGAGGT	480															
FaAAT2_163.27 (vesca)	CGTCGAGGCAATGCCAATCATCAGCTCGACGAACTCGGTGATGCAATTCTACCACCTTGTCTATTCTTAGACGAGTTCCTGTTTAACTGCCAGGATCTGATGGTATTCTTGTTCTCCTTTGTTGTTAATACAGGTAACCCGCTGTCTATGTGGAGGT	480															
FaAAT2_151.28 (viridis)	CGTCGAGGCAATGCCAAGATCAGCTCGACGAACTCGGTGATGCAATTCTACCACCTTGTCTATTCTTAGACGAGTTCCTGTTTAACTGCCAGGATCTGATGGTATTCTTGTTCTCCTTTGTTGTTAATACAGGTAACCCGCTGTCTATGTGGAGGT	480															
FaAAT2_254.28 (niponica)	CGTTGAGGCAACGCGGAATGCACATCGACGAACTCGGGATGCAATTCTACCGCTTTGTCTATTCTAGATGGTTTCTGTTTAACTGCCAGGCTGATGGTATTCTTGTTCTCCTTTGTTGTTAATACAGGTAACCCGCTGTCTATGTGGAGGT	474															
Majority	TTCATATTTGCAATGCGTTTAAACACACAATGTGTGACACATTGTGGCTTGGTACAATTCTTGAAGGCAGTAGGGAGATTGCCAAGCAAGATGCACCATCTTCTCCACAGTGTGGGAACGACAGCTCTTGAACGCTCGAGAACCCCAATAATT	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640
FvAAT2_FvH4_2g2440	TTCATATTTGCAATGCGTTTAAACACACAATGTGTGACACATTGTGGCTTGGTACAATTCTTGAAGGCAGTAGGGAGATTGCCAAGCAAGATGCACCATCTTCTCCACAGTGTGGGAACGACAGCTCTTGAACGCTCGAGAACCCCAATAATT	640															
FaAAT2_163.27 (vesca)	TTCATATTTGCAATGCGTTTAAACACACAATGTGTGACACATTGTGGCTTGGTACAATTCTTGAAGGCAGTAGGGAGATTGCCAAGCAAGATGCACCATCTTCTCCACAGTGTGGGAACGACAGCTCTTGAACGCTCGAGAACCCCAATAATT	640															
FaAAT2_151.28 (viridis)	TTTCATTTTGCAATGCGTTTAAACACACAATGTGTGACACATTGTGGCTTGGTACAATTCTTGAAGGCAGTAGGGAGATTGCCAAGCAAGATGCACCATCTTCTCCACAGTGTGGGAACGACAGCTCTTGAACGCTCGAGAACCCCAATAATT	640															
FaAAT2_254.28 (niponica)	TTTATATTTGCAATGCGCTTAAACACACAATATGCGATGCACTTGGCTTGGTACAATTCTTGAAGGCAGTAGGGAGATTGCCAAGCAAGATGCACCATCTTATACACAGTGTGGGAACGACAGCTCTTGAAGCCTCGAGATCCCAACGAATT	634															
Majority	CTTGACACATCATGAATTTGATGATACCATTGACCCCTTGTGTCTGAAATCTTCTGCAACAATCAACGATCTTTCTGTTTGTGTTGCCAAGGAGATAAAGGCCCTCAAGGACCATCTTCTCCACACCTTTCTACTTGTTCATCCACATTTGAAGTGAT	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800
FvAAT2_FvH4_2g2440	CTTGACACATCATGAATTTGATGATACCATTGACCCCTTGTGTCTGAAATCTTCTGCAACAATCAACGATCTTTCTGTTTGTGTTGCCAAGGAGATAAAGGCCCTCAAGGAC																

(Cont)

Majority	TTTCGGATAACACAAGAACAGGTTTGGGAGGAATTGATTTTCGGGTGGGGAAGCCAGTATATGCTGGAGTTGCTAAGTCCATCGATCTTATTAGCTTCTATGTCAGGAAAAACAACAAAGAGGAGAAATATGAGATTTTGGTACCATTATGCTTGCCATT	
	1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280	
FvAAT2_FvH4_2g2440	TTTCGGATAACACAAGAACAGGTTTGGGAGGAATTGATTTTCGGGTGGGGAAGCCAGTATATGCTGGAGTTGCTAAGTCCATCGATCTTATTAGCTTCTATGTCAGGAAAAACAACAAAGAGGAGAAATATGAGATTTTGGTACCATTATGCTTGCCATT	1280
FaAAT2_163.27 (vesca)	TTTCGGATAACACAAGAACAGGTTTGGGAGGAATTGATTTTCGGGTGGGGAAGCCAGTATATGCTGGAGTTGCTAAGTCCATCGATCTTATTAGCTTCTATGTCAGGAAAAACAACAAAGAGGAGAAATATGAGATTTTGGTACCATTATGCTTGCCATT	1280
FaAAT2_151.28 (viridis)	TTTCGGATAACACAAGAACAGGTTTGGGAGGAATTGATTTTCGGGTGGGGAAGCCAGTATATGCTGGAGTTGCTAAGTCCATCGATCTTATTAGCTTCTATGTCAGGAAAAACAACAAAGAGGAGAAATATGAGATTTTGGTACCATTATGCTTGCCATT	1280
FaAAT2_254.28 (niponica)	TTTCGGATAACACAAGAACAGGTTTGGGAGGATCGATTTTGGGTTCGGAAAGCCAGTGTATGCTGGAGTTGCCAAGTCCACCGATCTGATCAGCTTCTATGTCAGGAGCACAACAAAGAGAGAGA---GAAATCTTGGTGCCAGTATGCTTGCCATT	1271
Majority	ATCGTCCATGGAGAGGTTTCAGCAAGAGTTCAAGAAGATGATTAGTTTGGACAAAGTGGAAATGTCATCATATATATGTAATTCATATTAA	
	1290 1300 1310 1320 1330 1340 1350 1360 1370	
FvAAT2_FvH4_2g2440	ATCGTCCATGGAGAGGTTTCAGCAAGAGTTCAAGAAGATGATTAGTTTGGACAAAGTGGAAATGTCATCATATATATGTAATTCATATTAA	
FaAAT2_163.27 (vesca)	ATCGTCCATGGAGAGGTTTCAGCAAGAGTTCAAGAAGATGATTAGTTTGGACAAAGTGGAAATGTCATCATATATATGTAATTCATATTAA	1371
FaAAT2_151.28 (viridis)	ATCGTCCATGGAGAGGTTTCAGCAAGAGTTCAAGAAGATGATTAGTTTGGACAAAGTGGAAATGTCATCATATATATGTAATTCATATTAA	1371
FaAAT2_254.28 (niponica)	ATCGTCCATGGAGAGGTTTCAGCAAGAGTTCAAGAAGATGATTAGTTTGGACAAAGTGGAAATGTCATCATATATATGTAATTCATATTAA	1371

Figure S6: Alignment of the coding DNA sequence of the strawberry AAT2 genes. Alignment of the 1371 bp DNA fragment corresponding to coding sequence of the FvAAT2 (FvH4_5g24240) with its respective homeologous of *F. x ananassa* FaAAT2_163.27, maker-Fvb5-1-snap-gene-163.27-mRNA-1 (Vesca homeologous); FaAAT2_151.28, maker-Fvb5-2-snap-gene-151.28-mRNA-1 (Viridis homeologous); and FaAAT2_254.28 maker-Fvb3-3-augustus-gene-254.28-mRNA-1 (niponica homeologous).

Figure S7: Alignment of the coding DNA sequence of the strawberry DOF2 genes.

Majority	ATGTTTCACAGCTCCAGTTCTCGAACAGATGCTTCAATGTCAATCCGGACAACCAATTGATCATGAATTCXAXAAGCCCTTCGTGGAAGCCXACGTCGAGATCGCTCCXAACTGCCCCCGGTGCGCGTCTTCCAACACCAAGTTCTGCTACTACAACAACT	
	10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160	
FvDOF2_FvH4_2g14390	ATGTTTCACAGCGCCAGTTCTCGAACAGATGCTTCAATGTCAATCCGGACAACCAATTGATCATGAATTCXAXAAGCCCTTCGTGGAAGCCXACGTCGAGATCGCTCCXAACTGCCCCCGGTGCGCGTCTTCCAACACCAAGTTCTGCTACTACAACAACT	160
FaDOF2_120.17 (vesca)	ATGTTTCACAGCTCCAGTTCTCGAACAGATGCTTCAATGTCAATCCGGACAACCAATTGATCATGAATTCXAXAAGCCCTTCGTGGAAGCCXACGTCGAGATCGCTCCXAACTGCCCCCGGTGCGCGTCTTCCAACACCAAGTTCTGCTACTACAACAACT	160
FaDOF2_128.9 (viridis)	ATGTTTCACAGCTCCAGTTCTCGAACAGATGCTTCAATGTCAATCCGGACAACCAATTGATCATGAATTCXAXAAGCCCTTCGTGGAAGCCXACGTCGAGATCGCTCCXAACTGCCCCCGGTGCGCGTCTTCCAACACCAAGTTCTGCTACTACAACAACT	160
FaDOF2_109.16 (liunumae)	ATGTTTCACAGCTCCAGTTCTCGAACAGATGCTTCAATGTCAATCCGGACAACCAATTGATCATGAATTCXAXAAGCCCTTCGTGGAAGCCXACGTCGAGATCGCTCCXAACTGCCCCCGGTGCGCGTCTTCCAACACCAAGTTCTGCTACTACAACAACT	160
Majority	ACAGCCTCTCACAGCCTCGCTACTTCTGCAAAGGCTGCCGGAGATACTGGACCAAAGGCGGGTCTTAXAGGAACGTCCCGCTGCGCGGCGGTGTAGAAAAGAACCGCCGACGAGGTCXGCCAGXCTCTCGCAGGCTGACCGGATXTCGATGAGTTACTA	
	170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320	
FvDOF2_FvH4_2g14390	ACAGCCTCTCACAGCCTCGCTACTTCTGCAAAGGCTGCCGGAGATACTGGACCAAAGGCGGGTCTTAXAGGAACGTCCCGCTGCGCGGCGGTGTAGAAAAGAACCGCCGACGAGGTCXGCCAGGCTCTCGCAGGCTGACCGGATXTCGATGAGTTACTA	320
FaDOF2_120.17 (vesca)	ACAGCCTCTCACAGCCTCGCTACTTCTGCAAAGGCTGCCGGAGATACTGGACCAAAGGCGGGTCTTAXAGGAACGTCCCGCTGCGCGGCGGTGTAGAAAAGAACCGCCGACGAGGTCXGCCAGGCTCTCGCAGGCTGACCGGATXTCGATGAGTTACTA	320
FaDOF2_128.9 (viridis)	ACAGCCTCTCACAGCCTCGCTACTTCTGCAAAGGCTGCCGGAGATACTGGACCAAAGGCGGGTCTTAXAGGAACGTCCCGCTGCGCGGCGGTGTAGAAAAGAACCGCCGACGAGGTCXGCCAGGCTCTCGCAGGCTGACCGGATXTCGATGAGTTACTA	320
FaDOF2_109.16 (liunumae)	ACAGCCTCTCACAGCCTCGCTACTTCTGCAAAGGCTGCCGGAGATACTGGACCAAAGGCGGGTCTTAXAGGAACGTCCCGCTGCGCGGCGGTGTAGAAAAGAACCGCCGACGAGGTCXGCCAGGCTCTCGCAGGCTGACCGGATXTCGATGAGTTACTA	320
Majority	TCGTCGCAACAGCTCGAGTAGTAGCGGTGATGATCTGTCCGAGCAGCACTCCAAGGAAGGAGCCAAACGGGTGGATATCGACATGGCTGCTGTGTTTGCTAATTTCTTGAACCAAACTCTXGCAACGGACATGATCCCAATXTGGTTGGATCAGAATCG	
	330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480	
FvDOF2_FvH4_2g14390	TCGTCGCAACAGCTCGAGTAGTAGCGGTGATGATCTGTCCGAGCAGCACTCCAAGGAAGGAGCCAAACGGGTGGATATCGACATGGCTGCTGTGTTTGCTAATTTCTTGAACCAAACTCTXGCAACGGACATGATCCCAATXTGGTTGGATCAGAATCG	480
FaDOF2_120.17 (vesca)	TCGTCGCAACAGCTCGAGTAGTAGCGGTGATGATCTGTCCGAGCAGCACTCCAAGGAAGGAGCCAAACGGGTGGATATCGACATGGCTGCTGTGTTTGCTAATTTCTTGAACCAAACTCTXGCAACGGACATGATCCCAATXTGGTTGGATCAGAATCG	480
FaDOF2_128.9 (viridis)	TCGTCGCAACAGCTCGAGTAGTAGCGGTGATGATCTGTCCGAGCAGCACTCCAAGGAAGGAGCCAAACGGGTGGATATCGACATGGCTGCTGTGTTTGCTAATTTCTTGAACCAAACTCTXGCAACGGACATGATCCCAATXTGGTTGGATCAGAATCG	480
FaDOF2_109.16 (liunumae)	TCGTCGCAACAGCTCGAGTAGTAGCGGTGATGATCTGTCCGAGCAGCACTCCAAGGAAGGAGCCAAACGGGTGGATATCGACATGGCTGCTGTGTTTGCTAATTTCTTGAACCAAACTCTXGCAACGGACATGATCCCAATXTGGTTGGATCAGAATCG	480
Majority	ATCCCTGATGATGTTTCATGAGCAAAATGCATTATCCGATCACTCCCAAAATTTCTTGAACCCCGCGGAAGATCTTCTTGAATCAGTGGAGCTACTTCAAGGACTCGTACTTCTGATCATGATCATCAACAATCACACGAAGAGGATAATTCACAATX	
	490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640	
FvDOF2_FvH4_2g14390	ATCCCTGATGATGTTTCATGAGCAAAATGCATTATCCGATCACTCCCAAAATTTCTTGAACCCCGCGGAAGATCTTCTTGAATCAGTGGAGCTACTTCAAGGACTCGTACTTCTGATCATGATCATCAACAATCACACGAAGAGGATAATTCACAATG	640
FaDOF2_120.17 (vesca)	ATCCCTGATGATGTTTCATGAGCAAAATGCATTATCCGATCACTCCCAAAATTTCTTGAACCCCGCGGAAGATCTTCTTGAATCAGTGGAGCTACTTCAAGGACTCGTACTTCTGATCATGATCATCAACAATCACACGAAGAGGATAATTCACAATG	640
FaDOF2_128.9 (viridis)	ATCCCTGATGATGTTTCATGAGCAAAATGCATTATCCGATCACTCCCAAAATTTCTTGAACCCCGCGGAAGATCTTCTTGAATCAGTGGAGCTACTTCAAGGACTCGTACTTCTGATCATGATCATCAACAATCACACGAAGAGGATAATTCACAATA	640
FaDOF2_109.16 (liunumae)	ATCCCTGATGATGTTTCATGAGCAAAATGCATTATCCGATCACTCCCAAAATTTCTTGAACCCCGCGGAAGATCTTCTTGAATCAGTGGAGCTACTTCAAGGACTCGTACTTCTGATCATGATCATCAACAATCACACGAAGAGGATAATTCACAATA	640
Majority	TTATGGGAAATCATCAATACCATCAGGATTTGAGTATTCATGAATTTGGTTTGCAGGCTCTGTAGACGATGAGGATGTGTTTGGTCTGATACAAACAGCAAGTTTGACCACTACTACTAGTTTCAATTGGCAAGAGTTGGATAATTCATCCCATC	
	650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800	
FvDOF2_FvH4_2g14390	TTATGGGAAATCATCAATACCATCAGGATTTGAGTATTCATGAATTTGGTTTGCAGGCTCTGTAGACGATGAGGATGTGTTTGGTCTGATACAAACAGCAAGTTTGACCACTAGTACTACTAGTTTCAATTGGCAAGAGTTGGATAATTCATCCCATC	800
FaDOF2_120.17 (vesca)	TTATGGGAAATCATCAATACCATCAGGATTTGAGTATTCATGAATTTGGTTTGCAGGCTCTGTAGACGATGAGGATGTGTTTGGTCTGATACAAACAGCAAGTTTGACCACTAGTACTACTAGTTTCAATTGGCAAGAGTTGGATAATTCATCCCATC	800
FaDOF2_128.9 (viridis)	TTATGGGAAATCATCAATACCATCAGGATTTGAGTATTCATGAATTTGGTTTGCAGGCTCTGTAGACGATGAGGATGTGTTTGGTCTGATACAAACAGCAAGTTTGACCACTAATACTACTAGTTTCAATTGGCAAGAGTTGGATAATTCATCCCATC	800
FaDOF2_109.16 (liunumae)	TTATGGGAAATCATCAATACCATCAGGATTTGAGTATTCATGAATTTGGTTTGCAGGCTCTGTAGACGATGAGGATGTGTTTGGTCTGATACAAACAGCAAGTTTGACCACTAATACTACTAGTTTCAATTGGCAAGAGTTGGATAATTCATCCCATC	800
Majority	TGATGATGATGATCATATGAAGATAXCGACCACCACAACGAATCTATGTAGCGAAXAAGTGGAGCTCCTTTGATTTTTCAGGCTTGGGAGTTTCTCAGGATCTTAA	
	810 820 830 840 850 860 870 880 890 900	
FvDOF2_FvH4_2g14390	TGATGATGATGATCATATGAAGATAXCGACCACCACAACGAATCTATGTAGCGAAXAAGTGGAGCTCCTTTGATTTTTCAGGCTTGGGAGTTTCTCAGGATCTTAA	906
FaDOF2_120.17 (vesca)	TGATGATGATGATCATATGAAGATAXCGACCACCACAACGAATCTATGTAGCGAAXAAGTGGAGCTCCTTTGATTTTTCAGGCTTGGGAGTTTCTCAGGATCTTAA	906
FaDOF2_128.9 (viridis)	TGATGATGATGATCATATGAAGATAXCGACCACCACAACGAATCTATGTAGCGAAXAAGTGGAGCTCCTTTGATTTTTCAGGCTTGGGAGTTTCTCAGGATCTTAA	906
FaDOF2_109.16 (liunumae)	TGATGATGATGATCATATGAAGATAXCGACCACCACAACGAATCTATGTAGCGAAXAAGTGGAGCTCCTTTGATTTTTCAGGCTTGGGAGTTTCTCAGGATCTTAA	906

Figure S7: Alignment of the coding DNA sequence of the strawberry DOF2 genes. Alignment of the 906bp DNA fragment corresponding to the coding sequence of FvDOF2 (FvH4_2g14390) with its respective homeologous of *F. x ananassa* FaDOF2_120.17, snap_masked-Fvb2-2-processed-gene-120.17-mRNA-1 (Vesca homeologous); FaDOF2_128.9, augustus_masked-Fvb2-3-processed-gene-128.9-mRNA-1 (Viridis homeologous); and FaDOF2_109.16 snap_masked-Fvb2-4-processed-gene-109.16-mRNA-1 (iinumae homeologous). All sequences were retrieved of *Fragaria vesca* v.4.0a1 and *Fragaria x ananassa* Camarosa Genome v1.0.a1 Transcripts database

FigureS8. Expression analysis of the strawberry FaDOF2 in green and red fruit receptacles of *F. vesca* and *F. × ananassa* cv. *Camarosa*

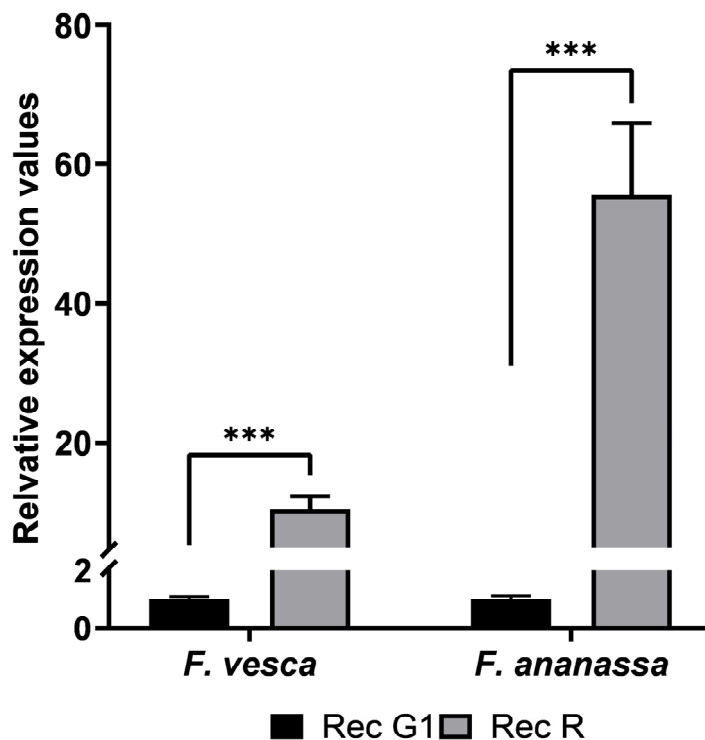


Figure S8. Expression analysis of the strawberry FaDOF2 in green and red fruit receptacles of *F. vesca* and *F. × ananassa* cv. *Camarosa*. qRT-PCR results were obtained using specific primers for FaDOF2 (Molina-Hidalgo et al., 2017). The increase in the mRNA value was relative to the receptacle G1 in all experiments, which was assigned an arbitrary value equal to 1. Means values \pm SD of five independent experiments are shown. Rec G1: small-sized green fruit receptacle; Rec R: red stage fruit receptacle. Statistical significance with respect to reference sample was determined by the Student's t-test in all experiments. (***) p -value < 0.001 .

Table S1. Primers

Name	Description	Chain	RT-qPCR (5'-3')	Observation
NptII_Fw	NPTII	sense	GACCACCAAGCGAAACATCG	Amplicon of 356 bp of kanamycin cassettes in the pKGWFS7.0 used as housekeeping
NptII_Rv		anti-sense	TGCGAATCGGGAGCGGCGATACCG	
GUS_Fw	GUS	sense	AATTATGCGGGCAACGTCTGGTAT	Amplicon of 203 bp of Glucuronidase gene in pKGWFS7.0
GUS_RV		anti-sense	CGTACACTTTTCCCGGCAATAACA	

Table S1. Primers used in the RT-qPCR in this study