Supplementary Material

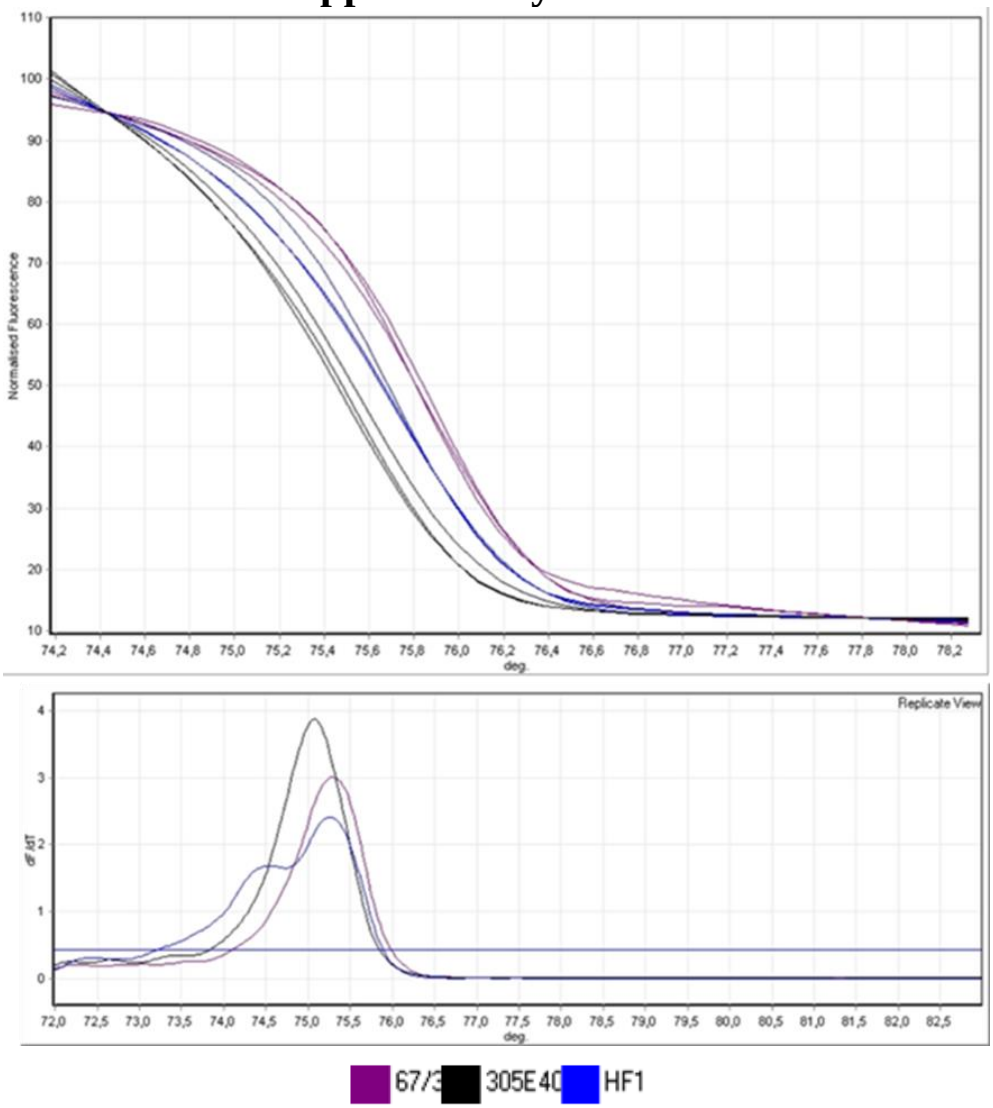


Figure S1. Output of Rotor-Gene 6000 Series Software 1.7 for the Melting curve of the AAT_HRM Marker.

Table S1: List of primers used.

Primers Name	Sequences 5'-3'	Use
Seq_SmelAAT_FW	tttatacttccctgggagttg	Sequencing
Seq_SmelAAT_RV	aataaggtacgctcccagaag	Sequencing
HRM_AAT_FW	atgagccaaattacaaaacaaaacttaaatg	HRM
HRM_AAT_RV	aggcacagcaaaattaggagc	HRM
GW_SmelAAT_FW	caccatgagccaaattacaaaacaaaa	Gateway cloning
GW_SmelAAT_RV	tagaaattccaaaatctttcaag	Gateway cloning
NPTII_FW	tgctcctgccgagaaagtat	PCR
NPTII_RV	agaactcgtcaagaaggcgatag	PCR
qPCR_SmelAAT FW	cgtgcaaatggtccacacat	RT-qPCR
qPCR_SmelAAT RV	ttccccttccccatacgact	RT-qPCR
qPCR_Smel5GT1_FW	tccattcaacttcctggcct	RT-qPCR
qPCR_Smel5GT1_RV	aggcttccttttgcacttga	RT-qPCR
qPCR_SmelAAT_3'UTR FW	attgaagctagagtttgctt	RT-qPCR
qPCR_SmelAAT_3'UTR_RV	aataaggtacgctcccagaa	RT-qPCR
qPCR_SmelAAT_35S:3'UTR_RV	gctgaacttgtggccgttta	RT-qPCR
qPCR_SmGAPDH_FW	ggtgccaagaaggttgtgat	RT-qPCR
qPCR_SmGAPDH_RV	ccaatgctagttgcacaacg	RT-qPCR
qPCR_Sm18S_FW	atgataactcgacggatcgc	RT-qPCR
qPCR_Sm18S_RV	aaacggctaccacatccaag	RT-qPCR

Table S2: F2 population from the cross 305E40 × 67/3. For each F2 individuals: Individual number, HRM haplotype (SmelAAT=AA, 305E40_aat=aa, Heterozygous=Aa), peel colour (lilac=L, purple=P), HPLC phenotype (nasunin=NAS, delphinidin-3-rutinoside =D3R). The individuals where marker and phenotype (colour and/or HPLC) do not match are marked (*). The statistical analysis was performed by using the Spearman's rank correlation.

Individual	HRM Haplotype	Peel Colour Phenotype	HPLC Phenotype
Parental			
67/3	AA	L	NAS
305E40	aa	P	D3R
HF1	Aa	L	NAS
F2 Population			
1	aa	P	D3R
2	Aa	L	NAS
3	Aa	L	NAS
4	aa	P	D3R
5	Aa	L	NAS
6	Aa	L	NAS
7	Aa	L	NAS
8	aa	P	D3R
11	Aa	L	NAS
12	Aa	L	NAS
13	AA	L	NAS
14	Aa	L	NAS
15	aa	P	D3R
16	Aa	L	NAS
17	aa	P	D3R
19	aa	P	D3R
20	Aa	L	NAS
21	Aa	L	NAS
22	AA	L	NAS
23	aa	P	D3R
24	AA	L	NAS
25	AA	L	NAS
26	AA	L	NAS
27	AA	L	NAS
28	AA	P*	NAS
29	Aa	L	NAS
30	AA	L	NAS
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32	Aa	L	NAS
33	Aa	L	NAS
34	Aa	L	NAS
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36	AA	L	NAS
37	AA	L	NAS
38	Aa	L	NAS
39	Aa	L	NAS
40	AA	L	NAS
41	AA	L	NAS
42	Aa	L	NAS
43	Aa	L	NAS
44	AA	L	NAS
45	Aa	L	NAS
46	Aa	L	NAS
47	Aa	L	NAS
48	Aa	L	NAS
49	Aa	L	NAS
50	aa	P	D3R
51	Aa	P*	NAS

52	AA	L	NAS
53	Aa	L	NAS
54	AA	L	NAS
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57	Aa	L	NAS
58	AA	L	NAS
59	Aa	L	NAS
60	AA	L	NAS
61	AA	L	NAS
62	Aa	L	NAS
63	AA	L	NAS
64	aa	P	D3R
65	AA	P*	NAS
66	aa	P	D3R
67	Aa	L	NAS
68	aa	P	D3R
69	AA	L	NAS
70	aa	P	D3R
71	Aa	L	NAS
72	aa	L*	D3R
73	Aa	L	NAS
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81	Aa	L	NAS
83	AA	L	NAS
84	aa	P	D3R
85	AA	L	NAS
86	Aa	L	NAS
88	aa	L*	D3R
90	aa	L*	D3R
91	aa	P	D3R

File S1: Sequences from NCBI and Sol Genomics databases used to identify putative acyltransferase amino acid sequences from S. melongena, S. lycopersicum, S. tuberosum, Capsicum annuum and Petunia axillaris used to obtain a molecular phylogenetic tree.

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File S2: SmelAAT and 305E40_aat cDNA and putative peptides sequences.

- cDNA

*>SmAAT*_cDNA

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- Peptides

>*SmelAAT*_peptide

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