

Table S1. Oligonucleotide sequences used in this work.

Primer	Sequence	Gene Model	Utilization	Reference
1B	<u>AGCACTTATGGGCCTGTTCA</u> CAGCGCATCTTGAGTGTGTT	Solyc01g088100	CAPS marker	This work
2A	<u>ACAACGACTAGAACGGCTGG</u> CCCATCACAAACCTAACATGTCTAAGG	Solyc02g092570	CAPS marker	This work
2B	<u>GCACAACATCCACCCTTCTT</u> CAAGCACATACTGATTGCAGA	Solyc02g093030	CAPS marker	This work
2C	<u>GAAGGGTCGGGTACAAGGTAA</u> CCACTCTCTTAGCCTGAATGG	Solyc02g094500	CAPS marker	This work
3A	<u>GCTCTGAAGATCCTACACATGAAA</u> TCCCATGCTCTTCTGGAAC	Solyc03g019800	CAPS marker	This work
3B	<u>CGCGTAAGACAAACACGTT</u> GCATTATCAACTCATCTACCAGTCC	Solyc03g083830	CAPS marker	This work
3C	<u>TTGGGAGATTAGCGTAAGGAG</u> ATAGGAGCAACAAGGTACATGC	Solyc03g093610	CAPS marker	This work
6A	<u>GCAGTGTGATGCTGGTGT</u> AGGCGACTTGGTTGTCACTC	Solyc06g005060	CAPS marker	This work
6B	<u>TGTTGTTCCCTTGTGCAG</u> GCCAGTTGAACCAGACCAG	Solyc06g009730	CAPS marker	This work
6C	<u>AGCTAAGATGGAGGGAGATGC</u> CCCGAGGGTGTAAACTGTAAACG	Solyc06g048460	CAPS marker	This work
6D	<u>AAAACACGGCGATGAGAAAT</u> TTTCCTCTCCAATTCCCAAT	Solyc06g060210	CAPS marker	This work
FW2.2	<u>GGTGGTGTGATGTGGAGTGAGTG</u> GGCAGATACATAGTGAGGAGGAAC	Solyc02g090730	CAPS marker	This work
DWARF	<u>TGATCCATATTGTTCAATCCA</u> CGTGATTATGTTAGCGGGAAT	Solyc02g089730	CAPS marker	This work

<i>FW3.2</i>	<u>GAGATAACGGGTTAAATAGAGT</u> TAGTTAGGATAGTTATAGTTGC	Solyc03g114940	CAPS marker	This work
<i>EJ-2</i>	<u>CACAATTCATGCTGGATCAGC</u> CGGAGTAATCTATTAGATTCTGC	Solyc03g114840	CAPS marker	This work
<i>SP5G</i>	<u>TAATTACGCCAGTGACGAAGCA</u> TTGACACAGAGTTCGAGAACG	Solyc05g053850	CAPS marker	This work
<i>SP</i>	<u>GGGTTGAAGTTCATGGTGGT</u> AGTGCCTGGAATGTCTGTGA	Solyc06g074350	CAPS marker	This work
<i>PTS</i>	<u>AGGAAGTGATTGACCCATGC</u> CCCCAACACCAACTATCTAAGC	Solyc06g072480	CAPS marker	This work
<i>ASAT1</i>	<u>GGGAGGCCAAGACAAGTTGATA</u> TGGAGAACCAAAGTGAAGAAAATC	Solyc12g006330	qPCR	
<i>ASAT2</i>	<u>GACTCCATTGTCCATCTTACTTC</u> TTTGACTTCTCCTCTCCTTCTTA	Solyc04g012020	qPCR	[12]
<i>ASAT3</i>	<u>TTTCTCCCTTACCGTCTGAA</u> TGAACAAAGTGTGAGGCAAC	Solyc11g067270	qPCR	This work
<i>ASAT4</i>	<u>GGTGGTCGTGATGTCCCTAA</u> GCCCTCCTTGTAGCAGTTG	Solyc01g105580	qPCR	This work
<i>ASH1</i>	<u>TCTTCATCCAACGTGATTAACATT</u> ATCTACACCACAGAACACTACCAATA	Solyc05g051660	qPCR	This work
<i>ASH2</i>	<u>GCGACCCACTGAATAGCATC</u> GGCGGAGGATTGTATTAGGA	Solyc05g051670	qPCR	This work
<i>ASH3</i>	<u>CTACACTCAAATCAACTCCATACCATA</u> ATAGAACCGTTGACTCGACCATT	Solyc09g075710	qPCR	[51]
ABC transporter	<u>TCCGAAGGGATGATGGAG</u> GCAGAACGACCAAAATACAGGGTAA	Solyc03g005860	qPCR	This work
<i>ACTIN</i>	<u>GGTCCCCTCTATTGTCCACAG</u> TGCATCTCTGGTCCAGTAGGA	Solyc04g011500	qPCR	[71]

<i>EF1α</i>	AAGCCCATGGTTGTTGAGAC TTCTTGACAACACCCACAGC	Solyc06g005060	qPCR	[72]
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References

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Table S2. Genomic coordinates (ITAG2.5) of the genetic variation from *S. galapagense* present at high frequencies (≥ 0.8) in the *Get*-like phenotypical group of the MT-*Get* segregating population.

Chromosome	Corresponding Region (bp)
1	82,558,349 – 83,597,817
2	53,604,856 - 55,297,272
3	61,495,951 - 65,007,167
5	19,540,000 - 19,637,400
6	3,688 - 38,647,717

Table S3. GC-MS content of acyl groups in *S. galapagense*, MT-*Get* and Micro-Tom (MT).

RT	Acyl Groups Content	Genotypes		
		<i>S. galapagense</i>	MT- <i>Get</i>	MT
1	2-Methyl Butanoate	0.77 ± 0.30	0.00	0.00
2	3-Methyl Butanoate	2.86 ± 1.20	0.00	0.00
3	Methyl Decanoate	0.18 ± 0.07	0.00	0.00
4	Methyl Dodecanoate	2.92 ± 0.90	0.06 ± 0.00	0.00

Data are means (n =8) ± SD.