

Table S1. List of genes and q-PCR primers analysed in this paper. Putative orthologs in melon and cucumber are indicated.

Gene ¹	Reference Accession number	Q-PCR primer sequences	Melon Gene ²	Cucumber Gene ³
<i>I8S</i>	[9] AF206895	CCGTTGCTCTGATGATTCATGA GTTGATAGGGCAGAAATTTGAATGAT		
<i>ACTINE</i>	[31] HM594170	CCTCTCAATCCCAAAGCTAACAG CGGCCTGGATAGCAACATACA		
<i>CpACS1</i>	[14] AAA33113	TGTCACTGAGCCAGGTTGGTT GCAACGTCAACGGTGTGTC	MELO3C021182, evaluate 0.0 CM3.5_scaffold00047 (319.775-323.449) LGXI	Csa6M006800, evaluate 0.0 Chr6 (576.828-580.112)
<i>CpACS2</i>	[26] CUTC0483191	ACAAGGAGGTAGCCAAGGTTAAG CCCACGACTCAGTTAAACTTTTG	MELO3C016340, evaluate 7e-66 CM3.5_scaffold00027 (3.936.912 -3.939.367) LGVII	Csa4M049610, evaluate 2e-62 Chr4 (3.925.814-3.928.351)
<i>CpACS4</i>	[26] CUTC036131	CAGCAGCTTCTCCATAATTCTA CGTTAATGAATACCTGGAGACGA	MELO3C006840, evaluate 0.0 CM3.5_scaffold00006 (6.529.439-6.532.788) LGVI	Csa3M177920, evaluate e-176 Chr3 (12.070.103-2.073.483)
<i>CpACS5</i>	[26] CUTC0383771	TGTGCATCTGAAAGCATAGAAGA TTAGAAGATAGCGACCGAGACAG	MELO3C005597, evaluate 0.0 CM3.5_scaffold00005 (6.337.710-6.340.825) LGIX	Csa5M157380, evaluate 0.0 Chr5 (5.575.539-5.578.435)
<i>CpACS6</i>	[26] CUTC0406831	GAAACCAGCTACCAAGAGAAACA TTTTCGTTTCAAGAGTAGATTGC	MELO3C005597, evaluate e-122 CM3.5_scaffold00005 (6.337.710-6.340.825) LGIX	Csa5M157380, evaluate e-115 Chr5 (5.575.539-5.578.435)
<i>CpACS7</i>	This paper KC662095	GGTTTAGAGTCGGAGCGATTTAT CTCTACCAGCATTTTCTGTCTT	MELO3C019008, evaluate 1e-69 CM3.5_scaffold00035 (3.114.060-3.115.032) LGVII	Csa4M099220, evaluate e-122 Chr4 (6.483.187-6.484.884)
<i>CpACO1</i>	unpublished HQ847860	CATTTGGGACAAAAGTGAGTAACTAC GCTCGGAGACCCTTGATCAA	MELO3C014437, evaluate 0.0 CM3.5_scaffold00022 (3.015.704-3.017.224) LGV	Csa6M421630, evaluate 0.0 Chr6 (19.435.577-19.436.822)
<i>CpETRI</i>	unpublished JX014243	AAAGGAGAGCTGCCTGAGAGTC CACGACGCTCTATAAGTTCCGA	MELO3C003906, evaluate 0.0 CM3.5_scaffold00003 (56.561-62.893) LGV	Csa2M070880, evaluate 8e-65 Chr2 (5.520.557-5.526.964)
<i>CpERS1</i>	unpublished JX014245	GAGCGTCGGGTTCTATTCGA AACCTGGGATATGCCTTGTATGTTAC	MELO3C003906, evaluate 3e-93 CM3.5_scaffold00003 (56.561-62.893) LGV	Csa2M070880, evaluate 3e-86 Chr2 (5.520.557-5.526.964)
<i>CpCTR1</i>	[9] FJ917748	ACTAATGATTAGTTGTGGCTGGATACA AACAGTAATGACATTTCTAGCAAACA	MELO3C009433, evaluate 0.0 CM3.5_scaffold00011 (2.117.162-2.125.790) LGIV	Csa3M749850, evaluate e-164 Chr3 (29.127.592-29.136.084)
<i>CpCTR2</i>	[9] FJ917749	ACGTGTTGCTTGGCTGTTAC TCACTCATGAGTACTGGTTGATTGA	MELO3C009433, evaluate 1e-27 CM3.5_scaffold00011 (2.117.162-2.125.790) LGIV	Csa3M749850, evaluate e-164 Chr3 (29.127.592-29.136.084)
<i>CpEIN3.1</i>	This paper KC620381	GCCATCAAATGTTTACAAGACCG AATGAAAAGAGTGCAAGCAGTCTTAC	MELO3C015633, evaluate 3e-31 CM3.5_scaffold00025 (3.608.957-3.612.634)	Csa1M601520, evaluate 2e-22 Chr1 (23.382.449-23.384.803)
<i>CpEIN3.2</i>	This paper KC620382	TAGCAGCCAATTCAACCAGTTTAAGCC CGGTAAAGCATCGAATTGAGATCAGG	MELO3C019008, evaluate 1e-69 CM3.5_scaffold00035 (3.114.060-3.115.032) LGVII	Csa1M601520, evaluate 3e-34 Chr1 (23.382.449-23.384.803)

¹ *Cucurbita pepo* unigenes available at <http://www.cucurbitgene.net>² Best hits of *C. pepo* genes in <https://melonomics.net/>, database that holds the recently released sequence of the melon genome [47]. Position in the melon genome and in the melon genetic map of each melon unigenes is indicated³ Best hits of *C. pepo* genes in <http://www.icugi.org/cgi-bin/ICuGI/index.cgi>, database that holds the last version of the cucumber genome. Position in the cucumber genome of each gen is indicated [48].