S3 Table. Primers sequences used for RT-qPCR analysis of the genes analyzed in this research. The primers were designed from full-length cDNA sequences of *Fragaria vesca*. The primers for *COI1* and *GAPDH* genes were obtained from Preuss et al. (2014).

Gene (CDS)	Forward (5'-3')	Reverse (5'-3')	Amplicon size (bp)
COI1	TGATCTTTTGGGGATGGCTCGCCC	TGAGCCGGATGCTCAACCACTACC	117
JAZ1	TGGGAGATCTGAACCTCGTC	TTCCTCGGTTTCTCCATCAC	130
JAZ4-1/2/3	AGAAGTGCTGGTGCACATTG	TGGGCATAAATCTGGAGGAC	133
JAZ5	CACCATGAACTTGCTCAACG	GAAAGGTCGCTGAAGACGAG	126
JAZ7	GGATGAGCAGACCAGACAGG	AAACATAAACCCGGCCATCG	59
JAZ8.1	GAGGAGGAACTGCAATTTGG	AAGAGGGAAGCCGGAATTAG	64
JAZ8.2	GTTGCAACCTGGAACTGGAAC	ATGAAGGGACTCAAGGGAGC	71
JAZ9	TCCACAGCTCAATTGCAAAC	ACCATCACCTGTGGAAGGAC	51
JAZ10	TTCCAGAAGTTCCTCGAACG	GATTTCCTGGCTGCAATCAC	116
JAZ11	GGTTGCAGAAAGGGCAAAGC	TTGCCAAAGGTATCCCTGCTC	95
JAZ12	GAAGCGTAGGGACAGATTGG	AACCGGAAGAAGCATCATTG	104
MYC2	AGGGGATCCTGTCGTTTACC	TTCGGGGTCCACAACTCTAC	149
MYC2-like	AGTCCATCCTCAACGACACC	AACCACTCTGCGTCGGATAC	94
NINJA	AAGCGATTTGTTGGATCTGG	ATTTGGGTCCACGCTACTTG	84
TPL1	TGCTTACTCGAGGCACATTG	GCTGCTTATTGGGGTGAGAG	128
TPL2	ATACTCTGTTTGCCCGCATC	TTCCATCAGTTGCTGTCGAG	65
TPL3	ATGATGCTCCTGGACTTTGG	TTCACCGTCTTTACCCGTTC	89
TPL4	CGAATCCTCTGTTCCGAGAG	AATGTCAGGATTTGGCCTTG	128
HDA6.1	GTTTGGCGATTTCTTTCCAG	TCCGAAAATTCTCGTCATCC	116
HDA6.2	ATGGAGCTGAATCGGGTTGG	GCAGTTAGTGTCAGGGGTGG	101
HDA19.1	CTACCTTCAGGACCAGACGC	TGGTTGAGGCCGTAGTTGAC	149
HDA19.2	GGACAAGCAGCATTGTTCTC	ACCTACGTGCAGCATCTATCG	128
JAM1	GCTTTACGAGCTGTTGTGCC	TTGAAGTGCCTCCTGCACTC	139
JAM2	GACAATGGGTGTGCAGCAG	TCCATCGCCCCAAATCAAGG	122
PPD1-1	CCTGAGGGTCAGGCAAGTAG	CTCCAAGGTAGAAGTTGGTCCC	110
GAPDH	TTCATCACTACTGCCACCCAGAAGACTG	AGCAGGCAGAACCTTTCCGACAG	132

COI1, coronatine insensitive 1; GAPDH, glyceraldehyde-3-phospate dehydrogenase; HDA, histone deacetylase; JAM, jasmonate-associated MYC2-like; JAZ, jasmonate-ZIM-domain; NINJA, novel interactor of JAZ; TPL, TOPLESS; PPD, PEAPOD.