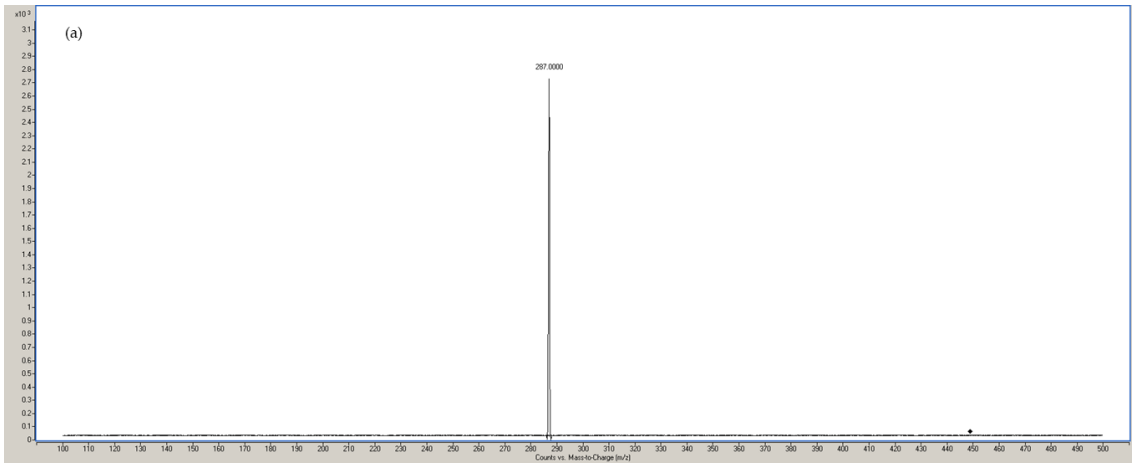

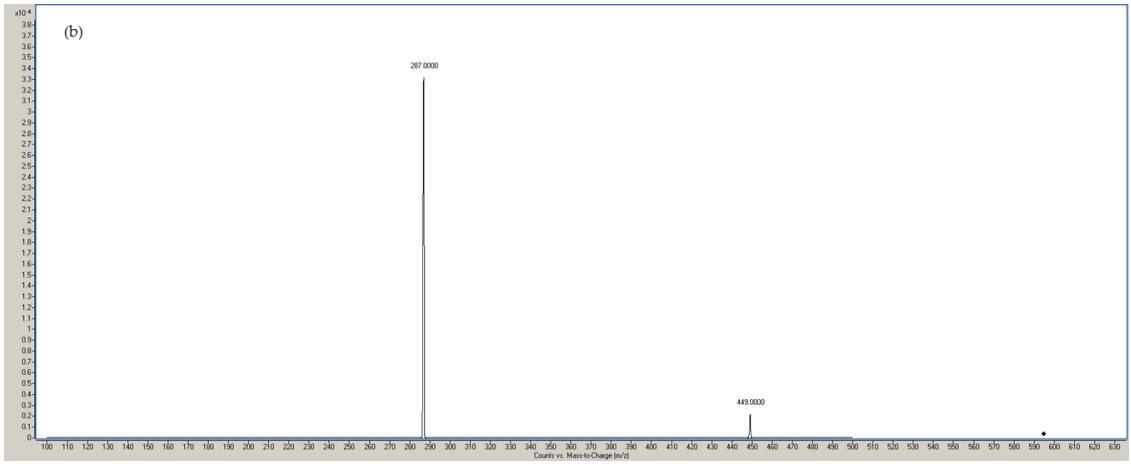

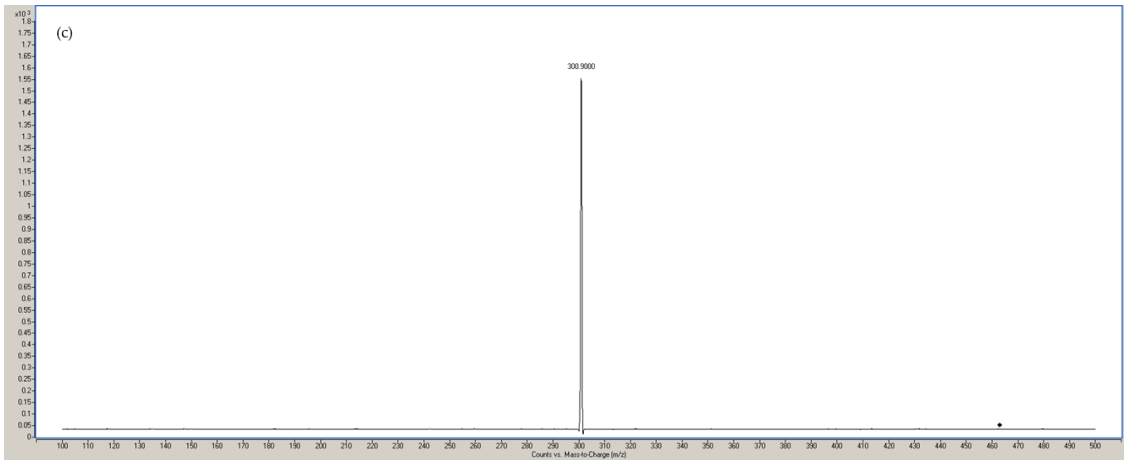

Figure S1. Mass spectra of the four identified peaks in *Cannabis* samples. Second-order mass spectra, obtained with ESI ionization in positive mode, of cyanidin 3-glucoside (peak 1), according to the standard mass spectra as reported by Olivas-Aguirre et al., 2016 (a), second-order mass spectra, obtained with ESI ionization in positive mode, of cyanidin 3-rutinoside (peak 2), according to the standard mass spectra as reported by de Rosso et al., 2008 (b), second-order mass spectra, obtained with ESI ionization in positive mode, of peonidin 3-glucoside (peak 3), according to the standard mass spectra as reported by Castañeda-Ovando et al. (2012) and De Pascual-Teresa et al. (2002)

(c),.second-order mass spectra, obtained with ESI ionization in positive mode, of peonidin 3-rutino-side (peak 4) according to the standard mass spectra as reported by de Rosso et al. (2008) and Pra-dhan and Saha (2016).

Table S1. List of primer pairs used for RT-Qpcr. Forward (Fw) and reverse (Rv) primer sequences, the accession number of cs10 transcript used for primer design, amplicon length expressed in base pairs (bp), PCR efficiency (Eff) are given.

Gene	NCBI transcript	Primer sequences	Effi	Amplicon length
CsF3'H	XM_030637390.1	FW:CGACACATCATCAAGCACAGT RV:CAGCATCACTTACAAGCCTATCTC	0.85	125 bp
CsF3'5'H	XM_030644276.1	FW:ATTGCGTGTACATCCACCTG RV:GGATTTTCCCAAAGGCTAGG	1.07	147 bp
CsANS	XM_030645652.1	FW: GCAATGTTTTCGAGGAGGAG RV: TCAACTCCTCTCGGCATTTC	1.34	114 bp
CsDFR	XM_030638485.1	Fw:TTCTCCACCTCGGTTACA Rv:TCAGCCTTCCACAGAGTA	1	118 bp
CsOMT	XM_030640905.1	Fw:ACACGAGCAGTTGAAGGAGC Rv:TGTCCTTCATCCACAGGCAC	1.46	87 bp
CsDTX35	XM_030648430.1	Fw:CAATCTTAACGGGTGGGAAG Rv:TTGGACGTTTCCTACCAAGC	1.64	92 bp
Cs3GT	XM_030645093.1	Fw:CCGAGATTGGGAAGGAGGTG Rv:AAGGCCCAGCAGTCCAAAAT	1.54	114 bp
CsTTG1	XM_030645708.1	Fw:ATAGCTTGGGGTGAAGCAAG Rv:AGCAAAGGGGTATCAGGTTG	1.18	128 bp
CsMYB82	XM_030636983.1	Fw:ACCAGGAAGGACAGCCAATG Rv:AGGTCCGAGGACGAGGTTTA	1.21	167 bp
CsMYB87	XM_030622841.1	FW: CGTGGAGAATTTGAGGAGGAC RV: TCTACCGGCAATCAATGACC	1.45	87 bp
CsbHLH112	XM_030646090.1	FW:GCCACTTCATCAGACAAC RV: CTCCTCATCCTCTTCTTCAT	1.47	165 bp
CsbHlH114	XM_030630819.1	FW:GCCACTTCATCAGACAAC RV:CTCCTCATCCTCTTCTTCAT	1.27	162 bp

Table S2. Amino acid sequences used for Neighbour-Joining phylogenetic analysis reported in Figure 2.

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Previously described flavonoid transporter belonging to MATEs were included according to [35]: *Arabidopsis thaliana* FFT, (AT4G25640.2) and AtTT12 (AT3G59030.1); *Vitis vinifera* VvanthoMATE1, (NP_001290007.1) and VvanthoMATE3 (NP_001268037.1); *Medicago truncatula* MtMATE1, (XP_003592215.2) and MtMATE2 (; *Solanum lycopersicum* MTP77 (Solyc03g025220.2.1).

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