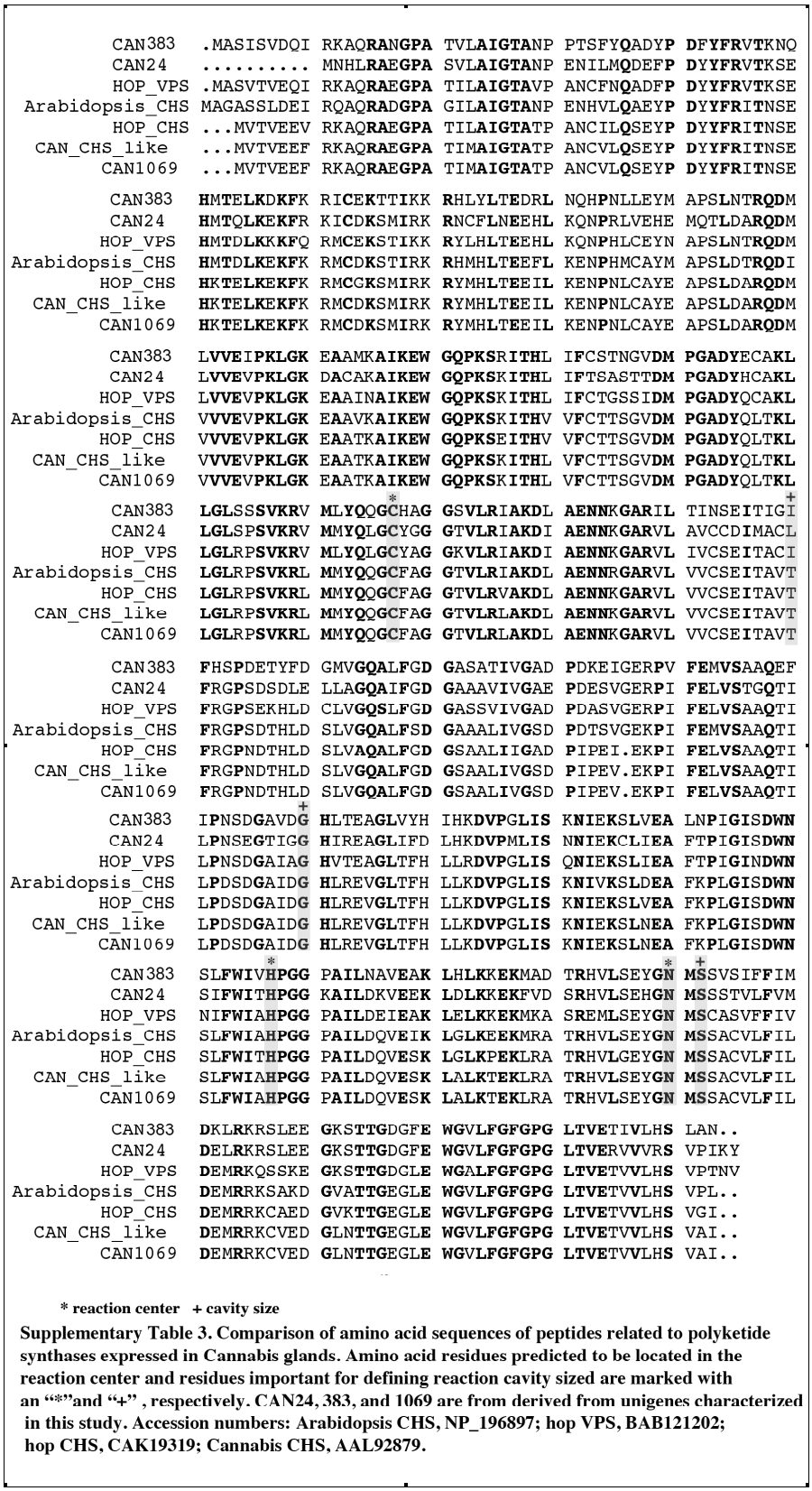


*** reaction center + cavity size**

Supplementary Table 3. Comparison of amino acid sequences of peptides related to polyketide synthases expressed in Cannabis glands. Amino acid residues predicted to be located in the reaction center and residues important for defining reaction cavity sized are marked with an "*"and "+" , respectively. CAN24, 383, and 1069 are from derived from unigenes characterized in this study. Accession numbers: Arabidopsis CHS, NP_196897; hop VPS, BAB121202; hop CHS, CAK19319; Cannabis CHS, AAL92879.

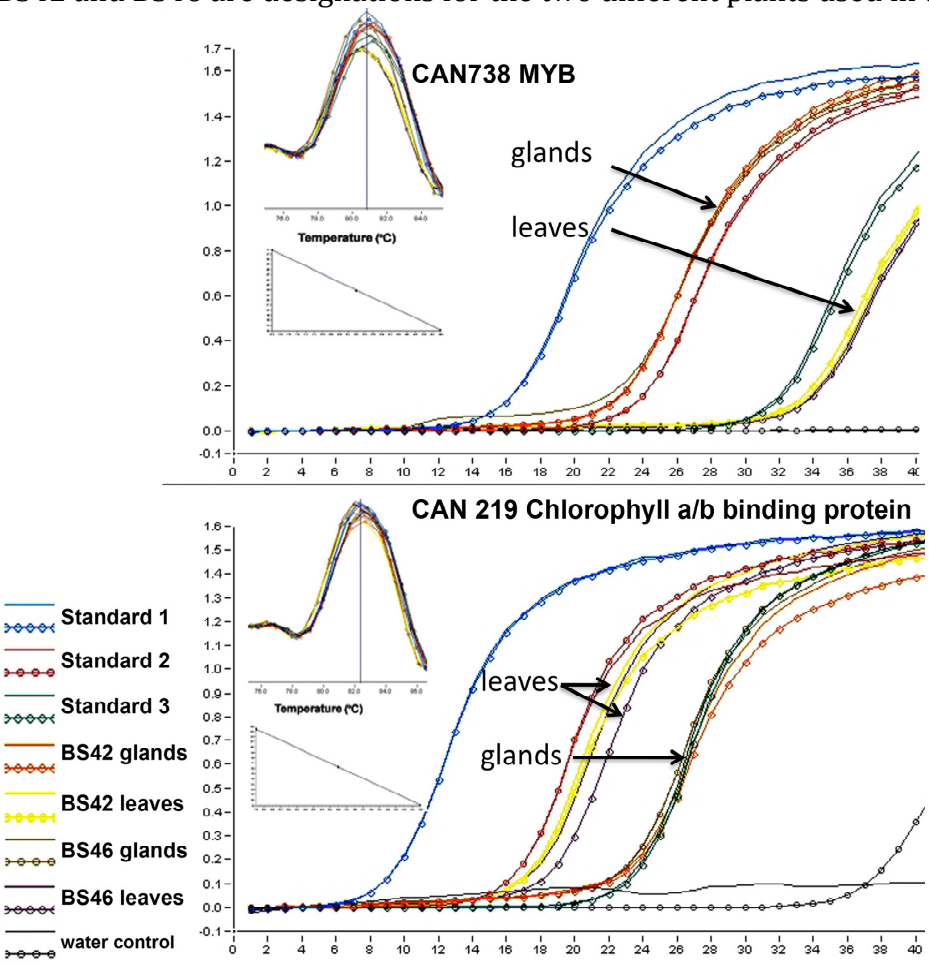
Supplemental Table 4. qPCR analysis of select *Cannabis* unigenes.

A) Relative expression levels of selected genes in glands and leaves.

		Gland mean	Gland std. dev.	Leaf mean	Leaf std. dev.	gland over leaf	P values
DOXP synthase	Can548	1.98E-5	4.58E-6	9.21E-7	3.26E-07	21.5	0.0002
Malic enzyme	Can6	1.55E-5	3.26E-6	2.20E-7	3.99E-08	70.2	0.0001
putative Olivetolic acid synthase	Can24	2.66E-5	7.27E-6	1.59E-8	3.45E-09	1670	0.0003
Chlorophyll A/B Binding protein	Can219	1.08E-7	1.77E-8	4.40E-6	1.62E-06	0.02	0.0019
hydroperoxide lyase	Can413	1.56E-6	3.13E-7	1.71E-7	6.20E-08	9.15	0.0001
COP9 complex subunit	Can747	2.14E-8	4.77E-9	1.80E-9	1.53E-09	11.9	0.0002
AtMYB78&112	Can833	1.47E-6	2.01E-7	1.54E-9	1.04E-09	954	0.0001
beta-keto acylreductase	Can915	1.53E-5	3.11E-6	1.61E-7	4.67E-08	95.3	0.0001
Histone H2A	Can986	6.77E-7	1.24E-7	1.59E-7	2.36E-08	4.24	0.0002
Beta tubulin	Can1084	1.09E-5	5.91E-6	3.16E-6	2.14E-07	3.45	0.0397
THC synthase	Can720	4.15E-6	1.36E-6	9.50E-9	5.51E-09	437	0.0009
CHS-like protein	Can383	5.32E-6	4.03E-6	3.81E-6	2.87E-06	1.40	0.564
acyl carrier	Can498	1.26E-6	1.71E-7	8.49E-9	5.90E-10	148	0.0001
lipoxygenase	Can162	2.34E-8	7.18E-9	3.10E-7	5.38E-08	0.075	0.0001
3-oxoacyl-[acyl-carrier protein] reductase; beta-ketoacyl-ACP reductase	Can82	2.28E-6	6.71E-7	3.10E-9	4.36E-10	735	0.0005
acyl-CoA synthetase [Brassica napus]	Can70	1.18E-6	2.16E-7	5.26E-8	2.74E-08	22.5	0.0001
3-ketoacyl-CoA thiolase; acetyl-CoA acyltransferase	can94	4.17E-7	2.91E-8	6.14E-8	2.35E-08	6.79	0.0001
MYB related	can792	1.15E-7	1.65E-8	1.35E-8	6.56E-09	8.51	0.0001
AtMYB12&111	can738	1.94E-6	7.58E-8	3.31E-9	4.55E-10	586	0.0001
MYB related	can483	7.03E-8	1.65E-8	9.91E-9	2.46E-09	7.09	0.0004
Homeodomain HAT4 Arabidopsis	can227	2.86E-7	7.88E-8	8.22E-8	2.06E-08	3.48	0.0024
CAN CHS	can1069	1.86E-6	6.03E-8	8.43E-9	1.09E-09	220	0.0001
CONSTANS-LIKE3	can618	1.99E-9	1.26E-9	3.74E-7	5.04E-07	.0053	0.1903
lipoxygenase	can295	4.95E-8	1.57E-8	4.81E-8	4.71E-09	1.03	0.87

RNA was isolated from the glands and leaves of two different plants. Each sample was tested in two 2-step qPCR reactions. Thus, each mean and standard deviation is derived from four qPCR reactions as described in Materials and methods.

B) qPCR Primers used in this analysis.

Unigene	qFor	qRev
CAN548	GGT GGA TCA GTA CAT GAA TTG	GCA ATG GAT CAA GAC TGG AC
CAN6	CAA GCT CTC TCT GTC ATT TTA AGC	CGC TTT CCA TCA CAA CGG
CAN24	CAC ACA TAC ACA ACT CAT TAT TAT C	GAG TTG AGT CAT GTG TTC AC
CAN219	GGC CAC AAA CCA AAG AAG AAG	CTG TTT GGA AGC AAA CCA C
CAN413	GGC GAG CTC CTA TGC G	GCC GTA AGC GTG ACG ATA TC
CAN747	GCA AAT CGG CGA AAA TAA G	GAT GTG GTG GTT GCA TCT G
CAN833	CTC TCT CTC TCT CTC CAT C	CAA CAG TCC ATG GAC CTC
CAN915	CAT CAA CAT ATA GCT ATA TGG AGT TCC	CCA GAA TCA GAC TCA GAC CTT TC
CAN986	CCC TCC AAA ACT CGA ATC G	GAC TTC TTC CTG TCT CCG C
CAN1084	GGC GCT GAG TTG ATC GAT TC	GTA TGG TTC CAC AAC TGT GTC
CAN720	GGA CTG AAG AAA AAT GAA TTG C	GGT CGT GTT GAG TGT ATA CG
CAN383	CCG TGC TAG CCA TCG GAA C	CCC TAG CTT GGG AAT CTC
CAN498	CCCAGATCTCTCTCACTCTTG	GCG CCT AGG CTG CAT CTT TAG
CAN162	GCC GGA GGA AGC ACT TAT G	CTC CAC ACC GAT TCT TCA AAT C
CAN82	GCC CAC AAC AAT CTT CGG	CCC TGA GCT TTA ACA ACA CC
CAN70	GGA GGT TTA TGA TTG TGT GAT AAA AC	GCA CCT AAG GTG TCA TAC AAC
CAN94	CCC CAC CGA CCT AGA TAT G	CCG GTA AGC TGC GAC AAT AAC
CAN792	CCC TAA CAT TTG CCG ATC TG	CGG ATC GAC CCG TCA GTC
CAN738	GAA GAG GAT GAG ATC TTG ACC AAG	GCC TAA TGT AGA ATG CAG GTT G
CAN483	GAG CCA AAC CCA GAT AAG AAA AAT TG	GGT TCA CTA GCT CCA AAC ACA AAG
CAN227	CCC ACT TTC TCA CCA TCC AAA C	CGG AAC AAA CGA GGA GAG C
CAN1069	CCT CAA GTT TAC CAA ATA TGG T	GAG CTC AGT TTT GTG TTC ACT ATT G
CAN618	CTC CTT CTC GAA TCT CCT AC	GCC ACA ACA TCA AAA CGA C
CAN295	GAA CAC TCT ATG GAT CAA GAA C	GGA CAT GAG CTT TTG CAA G

C) Representative real time qPCR tracings. Relative fluorescence and cycle number are shown
on the Y- and X-axes, respectively. Standards 1, 2, and 3 were generated by sequential 100-fold
dilutions of the target fragments. Inserted into the figures are standard curves (cycle number
vs. log of the dilution factor of the target fragment) and the melting temperatures of the qPCR products.
BS42 and BS46 are designations for the two different plants used in the analyses.