

Title: The effects of promoter variations of the N-Methylcanadine 1-Hydroxylase (CYP82Y1) gene on the noscapine production in opium poppy

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“Including all of the tables, figures, gene sequences”

Supplementary Information 1

Table S1. Analysis of putative cis-acting regulatory elements presented in the insertion segment of CYP82Y1 promoter region from Ps#7 ecotype by plantCARE database. In this table cis regulatory elements name and their sequences, positions in the insertion sequences and their function are presented.

Cis element	Position	sequence	Function
A-box	+495 and -680	CCGTCC	cis-acting regulatory element
Box I	-407 and -417	TTTCAAA	light responsive element
CAAT-box	+29, +136,+129, +651 and 8 positions	CAAAT	common cis-acting element in promoter and enhancer regions
CCGTCC-box	+495 and 680	CCGTCC	cis-acting regulatory element related to meristem specific activation
CGTCA-motif	+661	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
GC-motif	+204	GCCGCGCG	Unknown
GT1-motif	+121	GGTTAA	light responsive element
LAMP-element	+443, +575 and +546	CTTTATCA	part of a light responsive element
MBS	+7	CAACTG	MYB binding site involved in drought-inducibility
Skn-1_motif	+393	GTCAT	cis-acting regulatory element required for endosperm expression
TATA-box	-95, +140, -152, -187 and 15 positions	TATA	core promoter element around -30 of transcription start site
TCA-element	+456	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
TGACG-motif	-661	TGACG	cis-acting regulatory element involved in the MeJA-responsiveness
Unnamed__13	+134	TCCAAGTATA	Unknown

Supplementary Information 2

Fig. S2-A. Agarose gel electrophoresis of cleaned up amplicons of MT1 and SDR1 promoters region from Ps#7 ecotype. Primer used for MT1 were 11 and 12, and for SDR1, 13 and 14. Primer used also are detailed in Table1. M; 100 bp DNA ladder

Fig. S2-B. Agarose gel electrophoresis of MT1 (B1) and SDR1 (B2) promoter region from different geological collected ecotypes of *P. somniferum* L. No variation was detected into amplified fragments; (Ps#1-Ps#16) *P. somniferum* L. ecotypes. M; 100 bp DNA ladder

Fig. S2-C1. Illustration of designed primers based on exon-exon junction method for Real Time PCR assay. The MT1 gene contains three distinct exons. The forward primer (qMT1-F) was designed on 1st exon and the reverse primer (qMT1-R) cover 1st and 2nd exons.

Fig. S2-C2. Illustration of designed primers based on exon-exon junction strategy for qRT-PCR. The SDR1 gene contains four distinct exons. The forward primer (qSDR1-F) was designed to cover 2nd and 3rd exons and the reverse primer (qSDR1-R) on 3rd exon only.

Fig. S2-C3. Illustration of designed primers based on exon-exon junction strategy for qRT-PCR. The CYP82Y1 gene contains three distinct exons. The forward primer (qCYP82Y1-F) was designed to cover 2nd and 3rd exons and the reverse primer (qCYP82Y1-R) on 3rd exon.

Fig. S2-C4. Primers specificity and amplicons length. The PCR amplification products were analyzed on agarose gel electrophoresis; 1; SDR1, 2; MT1, 3; CYP82Y1, M; 100 bp DNA ladder.

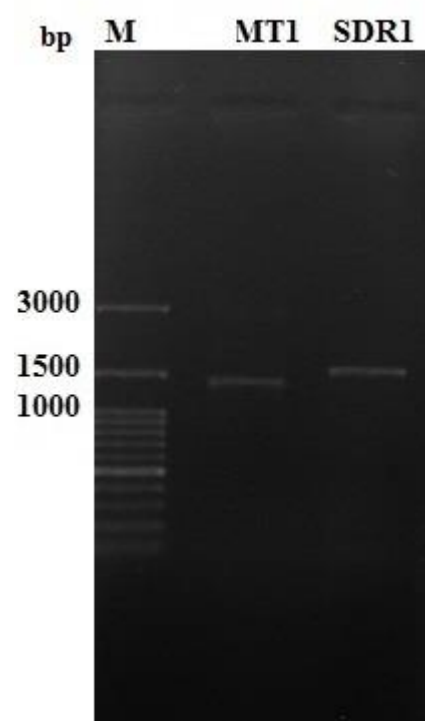


Fig. S2-A.

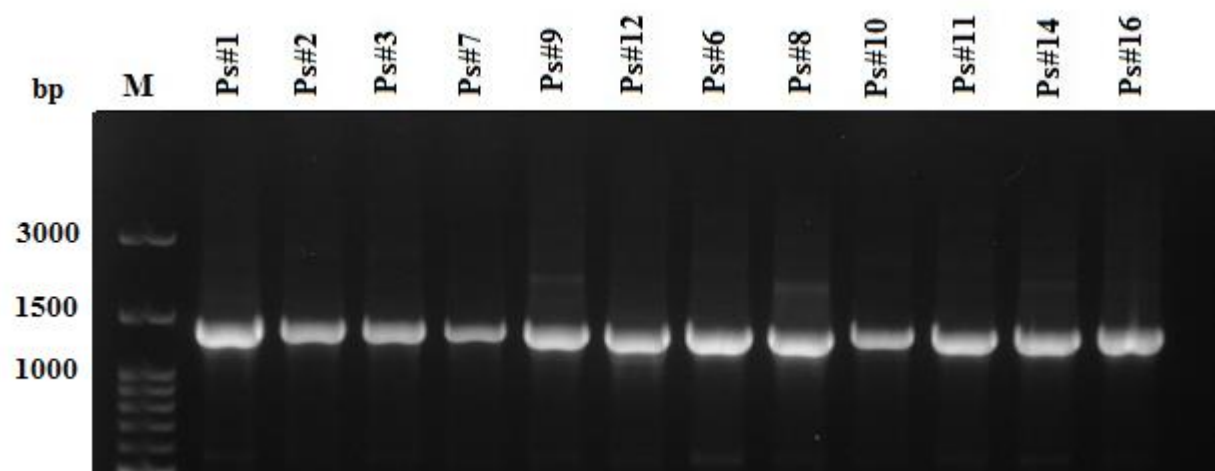


Fig. S2-B1.

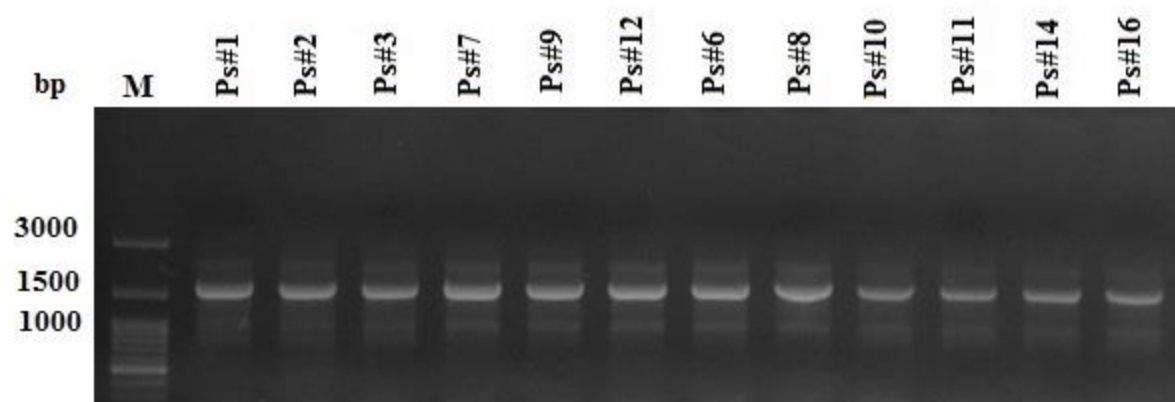


Fig. S2-B2.

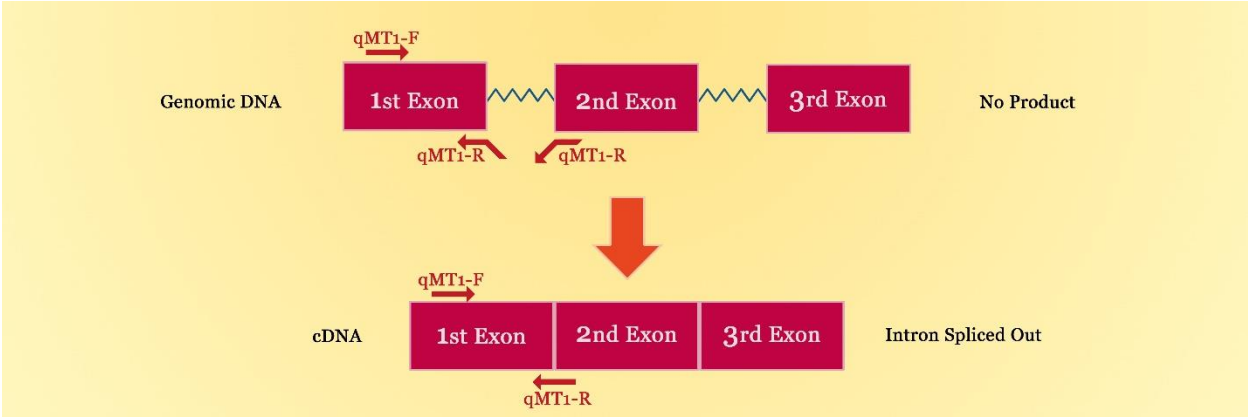


Fig. S2-C1.

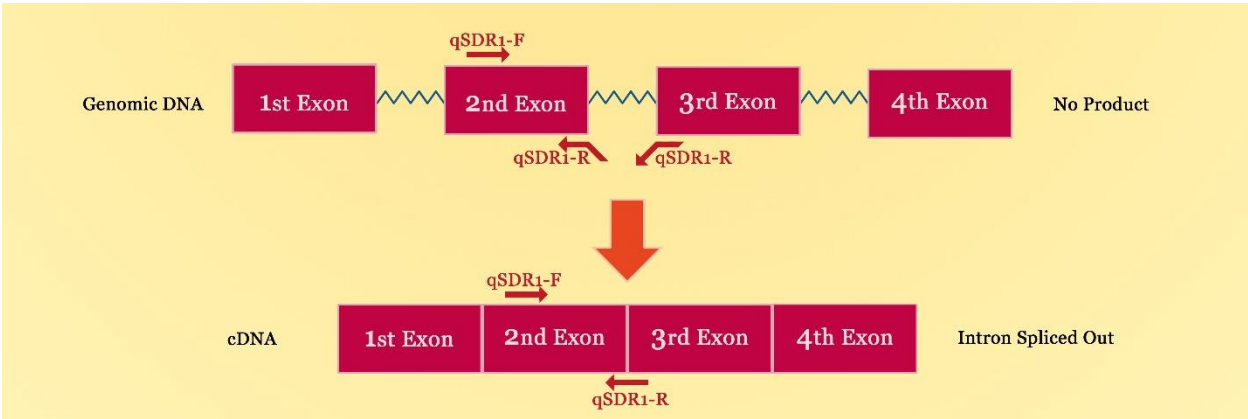


Fig. S2-C2.

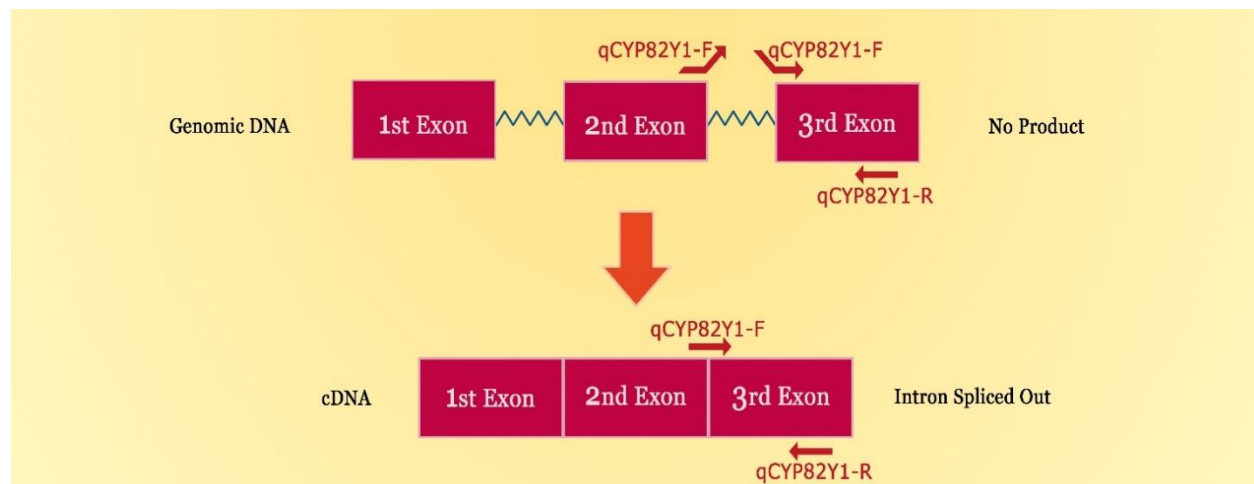


Fig. S2-C3.

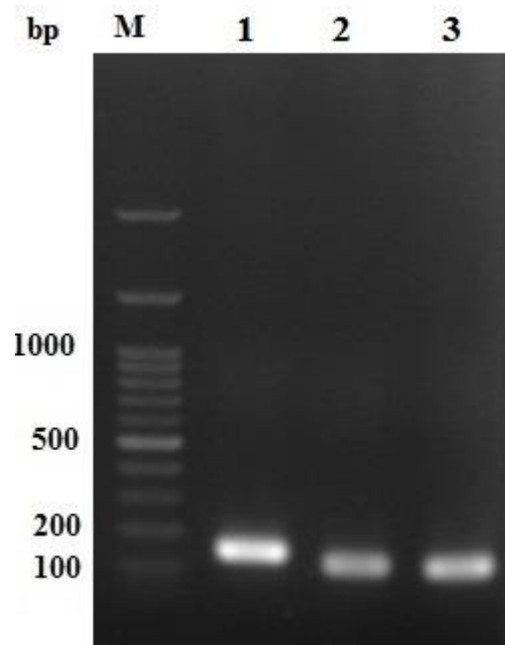


Fig. S2-C4.

Supplementary Information 3

Fig. S3. Pairwise alignment of isolated promoter region of SDR1 (a) and MT1 (b) from Ps#7 and CYP82Y1 (c) from Ps#12, and presumed promoter region of these genes from HN1 variety. High similarity between aligned sequences are visualized utilizing Multiple Alignment Show. The similar nucleotides highlighted in black and the percentage of sequences which must agree for similarity coloring is added 100%.

Ps#7-SDR1 - - T C C T T T A T A G T T C G A G A A T T T T T T T T G C G A A C T A T A A C A A T A T G A C T G T T A G G T A T G C A T G A A T A A T C A G T T A G T G A T T A T
 HN1-SDR1 A T G C C T T T A T A G T T C G A G A A T T T T T T T T G G G A A C T A T A A C A A T A T G A C T G T T A G G T A T G C A T G A A T A A T C A G T T A G T G A T T A T

Ps#7-SDR1 T G T A G C T T A C C T A C A G T C A G A C T A C A C T C A G C C A A A A C A C T C A G T A T T G T G G G G G C A A T G C C G A C A A C A A A G A T G T G G T T A C T
 HN1-SDR1 T G T A G C T T A C C T A C A G T C A G A C T A C A C T C A G C C A A A A C A C T C A G T A T T G T G G G G G C A A T G C C G A C A A C A A A G A T G T G G T T A C T

Ps#7-SDR1 T T A C C A A A A T A A A A A T T G A A T G T T G T A G G T G C A A A C T G T T A T T G T T T G C C T G T T A G T T A A A G A G T C A T A T A A A T G A T T T T T T T
 HN1-SDR1 T T A C C A A A A T A A A A A T T G A A T G T T G T A G G T G C A A A C T G T T A T T G T T T G C C T G T T A G T T A A A G A G T C G T A T A A A T G A T T T T T T T

Ps#7-SDR1 T G T T A T A A G G A C T A C T C T C C A A T A C T C C A A C T G A A C T T C A A T C A C C C A A A T G A T A A T T G A T T G T T T T T T T T T T T C C A A A A A A
 HN1-SDR1 G G T T A T A A G G A C T A C T C T C C A A A A C T C C A A C T G A A C T T C A A T C A C C A A A A T G A T A A T T G A T T G T T C G T T T T T T T T C C G A A G A A

Ps#7-SDR1 G A A A A A G A A A A T T A C A A T T G A C A A A G C T A A T C A C T C T A T C A C G A A A G T T T C C C A T T T G C T C C A A A T G A G G C T A G G A G G A A C A A A
 HN1-SDR1 G A A A A A G A G A A A T A C A A A T G A C A A A G C T A A T C A C T C T C T C A T G A G A G T T T C C C A T T T G T T C C A A A T G A G G C T A G G A G G A A T A A A

Ps#7-SDR1 T C A C A A G A C C T T A A A A C A A C A A G T T T C T T A C A A A G A T C A A T A T T T T T C C G C A A T A C T T T T C T G G A G A C C A C C A A A T A C T C T C C
 HN1-SDR1 T C A C A A G G C C A T A A G A C A A C A A G T T G C T T A C A A A G A T C A A T A T T T T T C C G C A A T A C T T T T C T G G A G A C C A C C A A A T A C T C T C C

Ps#7-SDR1 T A A T A T C C A A C A A A T A G C A T A G T G A A T A A T C T C C C A A C C T C T T T C C T C T T C C T T T A A G C A C A T T G G T A T T C C A A G C T T C A A
 HN1-SDR1 T A A T A T A C A A C A A A T A G C A T A G T G A A T A A T C T T C C A A C C T C T T T C C C T C T T C C T T T A A G C A C A T T G G T A T T C C A A G C T T C A A

Ps#7-SDR1 C T T G G C A T C G G C C A T G A T A T C T T A A A A T C C T T G A T A A A A T A A T C C C A T A T C G C A A A A G A A T A C G G A C G G T G T T G A A A C A T A T G A
 HN1-SDR1 C T T G A C A T C G G C C A T G A T A T C T T A A A A G C C T T G A T A A A A T A A T C C C A T A T C G C A A A A G A A T A C G G A C A G T G T A G A A A C A T A T G A

Ps#7-SDR1 C A T C A T T G C A A A A A A C A C A C A A A T C A G T T T G A A T G C T T A T A C C G C G A T G A A C T A A C A T G T C T C A A T A G G A A G A G A G T C A T G A
 HN1-SDR1 C A T C A T T G C A A A A A A C A C A C A A A T C A G T T T G A A T G C T T A T A C C G C G A T G A A C T A A C A T G T C T C T A G T A G G G A G A G A G T C A T G A

Ps#7-SDR1 G A A G C T T A C C T T G T T T G G A A T A T A T C T C T T C C A T A A A T G A G A A T C G A A A T T A C A T G G A G G A T A A T T A C C T G T C A A A A T C T C G T
 HN1-SDR1 G A A G C T T A C C T T G T T T G G A A T A T A T C T C T T C C A T A A A T G A G A A T C G A A A T T A C A T G G C G G A T A A T T A C C T G T C A A A A T C T C G T

Ps#7-SDR1 A A A T T C T C C A T A A T A T G C A C T T C A T C C T C A A C T T C C C C T A A C T C T G G A A C G G A C A A T C A C G T C T A A G C A A G T C C C A C T C T A A
 HN1-SDR1 A A A T T C T C C A T A A T A T G C A C T T C A T C C T C A A C T T C C C C T A A C T C T G G A A C G A G A C A A T C A C G T C T A A G C A A G T C C C A C T C T A A

Ps#7-SDR1 A A G C C C T C C T G A A A T C A C A A T T C C A T A T A T T G T T C A C A A T C A T A T C A G C T A T T G A C G C A T C T T T C G C C T T G G C C G C C T T G A A A A
 HN1-SDR1 A A G C C C T C C T G A A A T C A C A A T T C C A T C T A T T G T T T A C A A T C A T A T C A T C T A T T G A C G C A T C T T T C G C C T T G G C C G C C T T G A A A A

Ps#7-SDR1 T T G A A G T C T C C C T C T A T T T A G C C A T T T A T C C T T C C A A A C C T T A T C C C T T T T C C G T T C C C A C T G T A A A C T G T G C C A T T T G T T G
 HN1-SDR1 T T G A A G T C T C C C T C T A T C T A G C C A T T T A T C C T T C C A A A C C T T A T C C C T T T T C C G T T C C C A C T G T A A C T G T G C C A T T T G T T G

Ps#7-SDR1 T T C A C T A C A T T C T T C C A C A A A C T T C T G C A T T G A G A C T T T C T A T C A A C A T C T G G C A T T A A C A A A T T C A G A C A T C T C T T G A A T T T A
 HN1-SDR1 T T C A C T A C A T T C T T C C A C A A A C T C T G C A T T G A G A C T T G C T A T C A A C A T C T G G C A T T A A C A A A T T C A G A C A T C T C T T G A A T T T C

Ps#7-SDR1 T C C A C A G G T T G T T T T T G T T C T T T G A G A A T C T C C A A A T C C A T T T T A T T A A C A G A G A T T G A T T A G T A T T T C T T C G A A T C T T C A C T C
 HN1-SDR1 T C C A C A G G T T G T T T T T G T T C T T T G A G A A T C T C C A A A T C C A T T T T A T T A A C A G A G A T T G A T T A G T A T T T C T T A G A A T C T T C A C T C

Fig. S3-a

P₉#7-MT1 TTAGGTTGTTAATAGTAATCATTTCATTAGCAAGAAAGGTGACTAATTACACATCTACCAATCAAACACAGCTAATCAA
 HN1-MT1 TATGGATGGCTATA-GTAATCCATTTCATTAGCAAGAAAGGTGACTAATTACACATCTACCAATCAAACACAGCCAATCAA

P₉#7-MT1 GAATCTATATCAACATTAGCAACCAAGAAGAAGACATTGTATAAAATACTAGTCGAAACTTTAATAACAAAAACAGTTATA
 HN1-MT1 GAATCTATATCAACATTAGCAACCAAGAAGAAGACATTGTATAAAATACTAGTCGAAACTTTAATAACAAAAACAGTTATA

P₉#7-MT1 ACAATAGCGTCATCAAAAAC TCCATTGACGATAGATATGATGTAGAGGTTTCACGTAATAATATTTTTTCACATGTAGTTCC
 HN1-MT1 ACAATAGCGTCATCAAAAAT TCCATTGACGATAGATATGATGTAGAGGTTTCACGTAATAATATTTTTTCACATGTAGTTCC

P₉#7-MT1 CCAACTAAAAATCAATTGGCAATGAGTGGAGAGGTCCTAAGAATTATAAATCACAGGATCTTAGATTGCCCAACAAGATGG
 HN1-MT1 CCAACTAAAAATCAATTGGCAATAAGTGGAGAGGCCCTCAGGATTATAAATCACAGGATCTTAGATTGCCCAACAAGGTGG

P₉#7-MT1 CCCCTCAGTGCTAGCCTCGTTGGGTCTAACACGTGGACAATTAAATCGGGTGACGCGGAGTAAAGGCGCGGTCTAATGAC
 HN1-MT1 CCTCCTCAGTGCTAGCCTCGTTGGGTCTAACACGTGGACAATTAAATCGGGTGACGCGGAGTAAAGGCGCGGTCTAATGAC

P₉#7-MT1 CTGATACCATGTTAGAATACGGGCATCCAAC TCAAAACCAATTGGCAATGAGTGGATAGGCCCTAAGAATTATAAACCGCA
 HN1-MT1 CTGATACCATGTTAGAATACGGGCATCCAAC TCAAAACCAATTAGCAATGAGTGGATAGGCCCTAAGAATTATAAACCGCA

P₉#7-MT1 AAGATGGGACTAATAATCTCAACACCCATGTACCTTGATGCTGTGGTGCACGAGAAGCTCGTGTTCTTTACGCTGTCTCT
 HN1-MT1 AAGATGGGACTAATAATCTCAACACCCATGTACCTTGATGCTGTGGTGCACGAGAAGCTCGTGTTCTTTACGCTGTCTCT

P₉#7-MT1 ATCACCATATCCATTGT TAGCTAGCTAAAAATGATTGAAGAAATTAACAGTAAAGATATGTGATTAAATTTATGCAAAAGTT
 HN1-MT1 ATCACCATATCCATTGC TAGCTAGCTAAAAATGATTGAAGAAATTAACAGTAAAGACATGTGATTAAATTTATGCAAAAGTT

P₉#7-MT1 TCTGGTTCAACCAATACTACACCTAGTGTTTTTTGTTTCATCTAATTGATTAGCCATTAATAGTGTGATATCTTCCTACCCT
 HN1-MT1 TCTGGTTCAACCAATACTACACCTAGTGTTTTTTGTTTCATCTAATTGATTAGCCATTAATAGTGTGATATCTTCCTACCCT

P₉#7-MT1 TGCCAATTAACCTCTACTCTTTAGTGGTGACCCCTCTTGTGTTTAGCAATAAATCATGTGTAATGAATGTGTTGGTGAGCACTAG
 HN1-MT1 TGCCAATTAACCTCTACTCTTTAGTGGTGACCCCTCTTGTGTTAGCATAAAT--CATG-GGTGAAAAGGTTGGGGGGCCAAA

P₉#7-MT1 CTCATGATGCTCTCTTTTTTTGTTGGTGACCCAAAGTAGCCATAAAAAATATCTTGGATTTGTGCCCTTTTCAGTCAAAAAAAAAA
 HN1-MT1 GTCCTGTGTGTCTTTTTTTTTTGGGGGGCCCAAAGTGCCCAAAAAAATTTGGGTTTTTGCCCTTTTCCTCAAAAAAAAAA

P₉#7-MT1 AAAAAAGAGAGAAAAGGGAAAAATAAGTAAATGCGTGAAACACTTTCCACAAGGGGTGTAGAGTCGGTACTGGCATAGCCATAG
 HN1-MT1 AAAAAAGAGAGAAAAGGGAAAAATAAGTAAATGCGTGAAACACTTTCCACAAGGGGTGTAGAGTCGGTACTGGCATAGCCATAG

P₉#7-MT1 ATAAATATGCATGCATATCTTATATAGAAGCATAAACACACCAAACCTTGATCATTGTGCATAAAAAACAGTCCTAATTGTCA
 HN1-MT1 ATAAATATGCATGCATATCTTATATAGAAGCATAAACACACCAAACCTTGATCATTGTGCATAAAAAACAGTCCTAATTGTCA

P₉#7-MT1 AC
 HN1-MT1 AC

Fig. S3-b.

Ps#12-CYP82Y1 - C G C G A A T G C G T T C T G C T G C C G T C A C A C G G T C A C C G C T G A A G A A A A G T A G G A A A T T T A A A T A T A T C T T T G C T T T T T C T C C A A
 HN1-CYP82Y1 T G G G T G G A T T T A C A T T A A G G T C C A A C A A G G T C A C C G C T G A A G A A A A G T A G G A A A T T T A A A T A T A T C T T T G C T T T T T C T C C A A

Ps#12-CYP82Y1 A A C A C T A T C A G T G T A G T G G T T G C T C A T A A C C C C A C C T G C A G A T T T G G C T T A C C T T T A A T T A C A T A T A T C A T T G T T T T T C T T C
 HN1-CYP82Y1 A A C A C T A T C A G T G T A G T G G T T G C T C A T A A C C C C A C C T G C A G A T T T G G C T T A C C T T T A A T T A C A T A T A T C A T T G T T T T T C T T C

Ps#12-CYP82Y1 T G G A T G C T G A T C A A A A A G T T A T G G C A A A A G A G A C G G C G T G A G C G A A C A C G A G C T T C T C G T G C A C C A C A A C A T C A A G G T T
 HN1-CYP82Y1 T G G A T G C T G A T C A A A A A G T T A T G G C A A A A G A G A C G G C G T G A G C G A A C A C G A G C T T C T C G T G C A C C A C A A C A T C A A G G T T

Ps#12-CYP82Y1 G G T G A A A T A C T C C T T A T T C G C G T A G G A C C T C G A A A T C A A T T A T T T T T G G T T C G T T C T T T T C C A A C C A T A A T G T A T C C G A C C
 HN1-CYP82Y1 G G T G A A A T A C T C C T T A T T C G C G T A G G A C C T C G A A A T C A A T T A T T T T T G G T T C G T T C T T T T C C A A C C A T A A T G T A T C C G A C C

Ps#12-CYP82Y1 T C A A A C T T T T G A A C A T A A C G A C T C C C A T A C T C G G A A A T C A C C G A G T C T A T C T T T C T T T T T C T A T T T T T T T A A T A A T T G T
 HN1-CYP82Y1 T C A A A C T T T T G A A C A T A A C G A C T C C C A T A C T C G G A A A T C A C C G A G T C T A T C T T T C T T T T T C T A T T T T T T T A A T A A T T G T

Ps#12-CYP82Y1 A C T T C G A T G G A A T C G A A G G G G A T A A C C C T T T T C T T T T C T T A G A A A A T T G G G G T A T A C C T G G A T T A A T T A G G G T A T A T C T A A
 HN1-CYP82Y1 A C T T C G A T G G A A T C G A A G G G G A T A A C C C T T T T C T T T T C T T G A A A A T T G G G G T A T A C C T G G A T T A A T T A G G G T A T A T C T A A

Ps#12-CYP82Y1 T T A C G A A G T A A C C C C T C A A C T A T T T A T T T C A A A A T G C C T A A T C T A C C C T T T C T T A A T T A A T A C T A A T T A A T C C C G T T T A G G
 HN1-CYP82Y1 T T A C G A A G T A A C C C C T C A A C T A T T T A T T T C A A A A T G C C T A A T C T A C C C T T T C T T A A T T A A C A C T A A T T A A T C C C G T T T A G G

Ps#12-CYP82Y1 G A G C T T T T T C T T T C T T T T T T G A G A A T T T G T T T G T A A C G G A A A T G A A A C A A C A C T A C C C A A A C A C T T A T A A A G A T G G G A C
 HN1-CYP82Y1 G A G C T T T T T C T T T C T T T T T T G A G A A T T T G T T T G T A A C G G A A A T G A A A C A A C A C T A C C C A A A C A C T T A T A A A G A T G G G A C

Ps#12-CYP82Y1 T T C A T G T T C A A A A T T T G A G A A G A A A T G C A C A C T T C T G A A A C A G A A A G T A T G A A A A G T C G G C A G G G T C G A C A T T A T T G G A A G
 HN1-CYP82Y1 T T C A T G T T C A A A A T T T G A G A A G A A A T G C A C A C T T C T G A A A C A G A A A G T A T G A A A A G T C G G C A G G G T C G A C A T T A T T G G A A G

Ps#12-CYP82Y1 G A T A G G A T A G T A A A A A A T C A T T A T G T C A A C T A T A T G A T T T T G A C C T A C A T G A A A G G T G T T A C A A A T G C A C G A T T A T T A G T
 HN1-CYP82Y1 G A T A G G A T A G T A A A A A A T C A T T A T G T C A A C T A T A T G A T T T T G A C C T A C A T G A A A G G T G T T A C A A A T G C A C G A T T A T T A G T

Ps#12-CYP82Y1 T A A C A T G T C G A A T T G T A G T C A T C A A G G T T G A G A A T T G T A A A C A T G A A C G A C T A A A A A T C T T A T T A A T C T C A A A A C C C G A T G
 HN1-CYP82Y1 T A A C A T G T C G A A T T G T A G T C A T C A A G G T T G A G A A T T G T A A A C A T G A A C G A C T A A A A A T C T T A T T A A T C T C A A A A C C C G A T G

Ps#12-CYP82Y1 T C T T G A T T T T A A T T T T T C C G T T T T G A T G C T C G C T T T T G T T T T G G T T T C T T - T T T T G A T T C A T C A T G G A T A G T T A A A T
 HN1-CYP82Y1 T C T T G A T T T T A T T T T T C C G T T T T G A T G C T C G C T T T T G T T T T G T T T T C T T T T T T G A T T T C A T C A T G T A T A G T T A A A T

Ps#12-CYP82Y1 A T T G T T T A A A A A G G T T T A A T C C G G G A A G T G G T G G T T T T T T T T T T T T T G G A A A A A T T G A T T T T T T A A A A C C T T T
 HN1-CYP82Y1 A T T G T T T A G A T A G G T T T T A G T C G G T A T G T - T G T - - - T G T T T T T T T T T T T T T T G G A C A A A T T G A T T T T T T - A A T A C C T T

Ps#12-CYP82Y1 C T A C T T T T G G A T T G A T A T A A C C C A C T T A A T G T G G G T A T A C C C A A T T T A G C A A G G T T T T C C T T T T C A A T T T G T T T T T G C C C T
 HN1-CYP82Y1 C T A A C T T T G A A T T G A T A T A A C C C A C T T A A T G T T G G T A T A C C C A A T T T A G C A A G G T T T C C T T T T C A A T T T G T T T T T G C C C T

Ps#12-CYP82Y1 A A C A C T A T T G A T G T G G A C C A G T C C C A C T C C A C T G G A T T C C T C G A G A A A A T T T G A C A A A T A A T A T A T A T A T A T - - - - -
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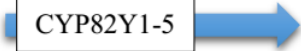
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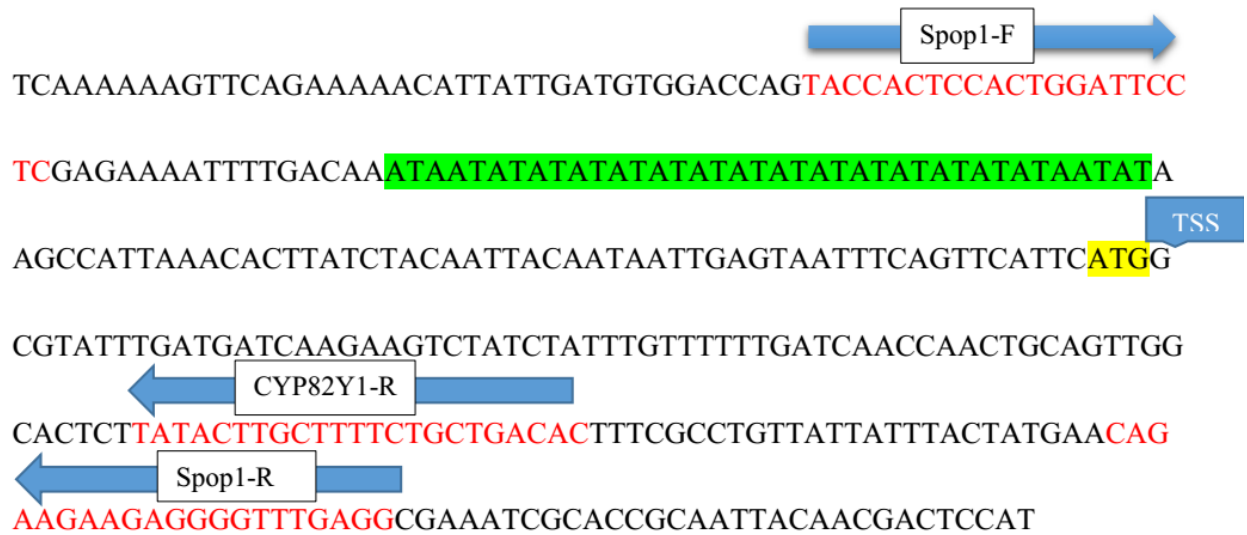
Fig. S3-c.

Supplementary Information 4

Fig. S4. The location of designed primers to isolation of CYP82Y1 upstream region. Primer sequences are colored in red and the arrows indicate the primer direction, the SSR region are highlighted in green and the start codon (ATG) are highlighted in yellow. Primers are detailed in the Table 1.

```
CGTCCTGCTCTTAGGGAGGAAAATCAAAGCTAGCCCTGTAAGGAATACTAGTATATG
                                PICYP82Y1-2
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TGTAGTTACCCTGAATTAAAAAAGTAGAGCAACAAAAATGTGTAATTCGTTATTTT
PICYP82Y1-4
TCGCGTATTTTGTTCACTGACATTATTCCAATATGTATGCAAGTTTAGAGCTTGA
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                                PICYP82Y1-3
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Supplementary Information 4

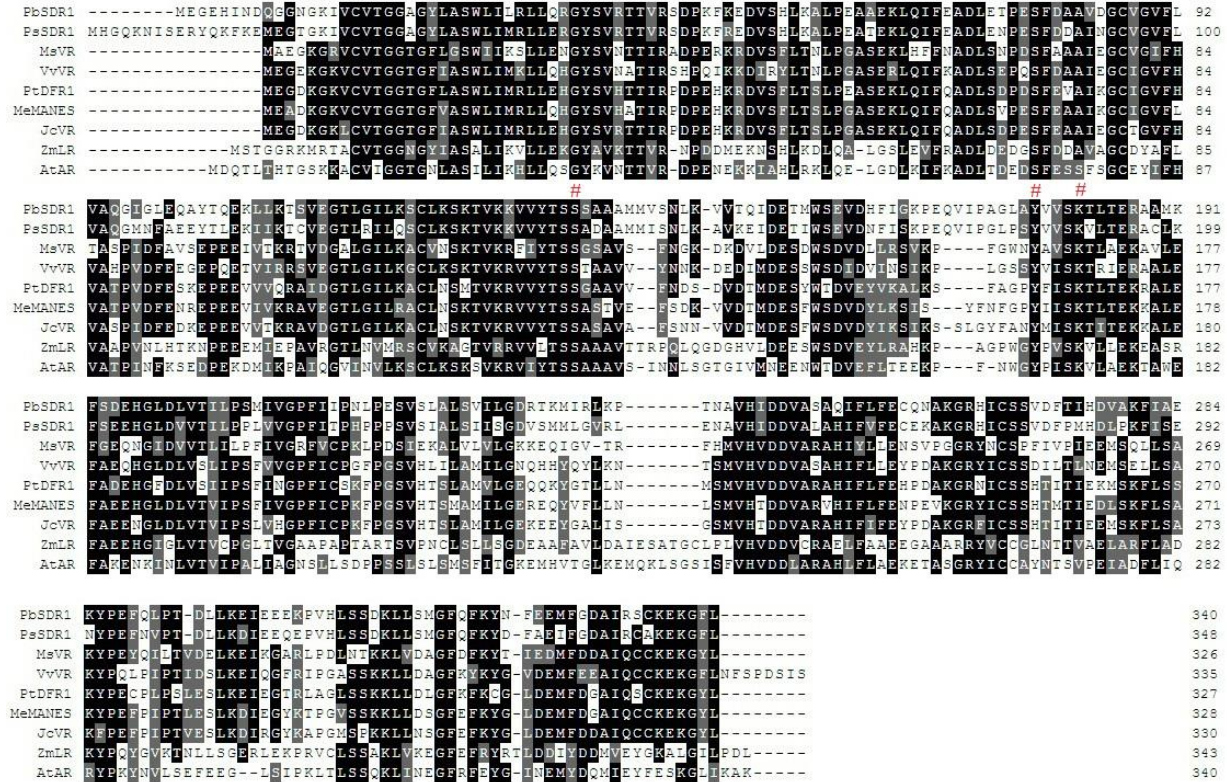


Fig.S5-A1. Sequence alignment of the amino acid sequence of identified SDR1 from *P. bracteatum*. Residues highlighted in black are identical and those in dark gray are similar. Percentage of sequences which must agree for identity or similarity coloring to be added 50%. Hyphens represent gaps inserted for optimal alignment. Catalytic residues (Serine (S), Tyrosine (Y) and lysine (K)) are indicated above the alignment by red # (hash key). These residues are conserved in all the protein sequences and their catalytic functions have recently reported.

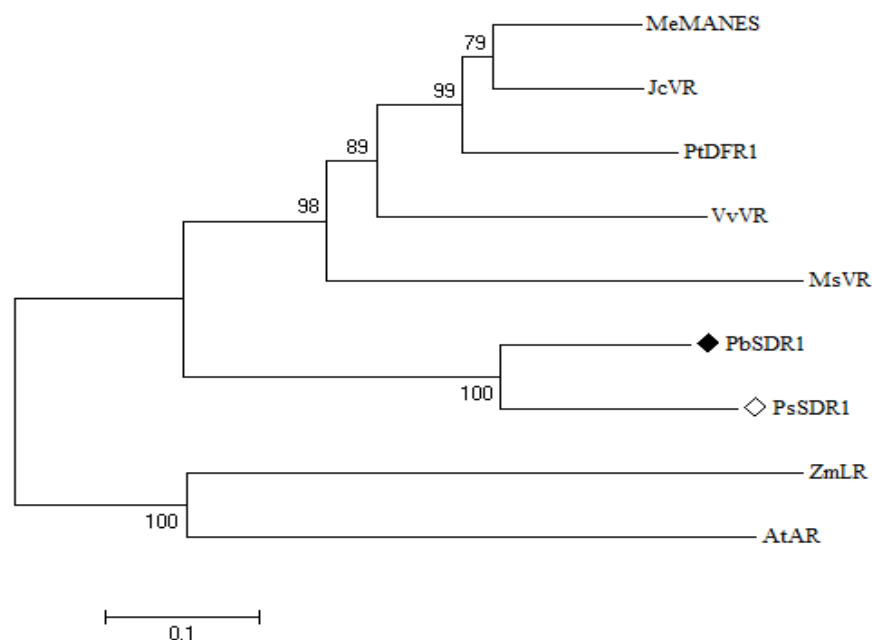


Fig.S5-A2. Unrooted neighbor-joining phylogenetic tree for selected SDR1 consensus sequence exploiting RNA-seq data obtained from *Papaver bracteatum* genus from a BLASTP search of the NCBI non-redundant protein database, constructed using MEGA 7 software. Bootstrap frequencies for each clade were based on 1,000 iterations.

Abbreviated species names are given before gene identifiers for each protein related to SDR1 are as follows:

PbSDR1, *P. bracteatum* short-chain dehydrogenase/reductase; PsSDR1, *P. somniferum* short-chain dehydrogenase/reductase (AFB74619.1); PbSalR, *P. bracteatum* salutaridine reductase (ABO93462.1); MeMANES, *Manihot esculenta* MANES_01G266200 (OAY62412); VvVR, *Vitis vinifera* vestitone reductase isoform X3 (XP_002278819); PtDFR1, *Populus trichocarpa* 2'-hydroxy isoflavone/dihydroflavonol reductase (XP_002301290); JcVR, *Jatropha curcas* vestitone reductase (XP_01208357); AlDFR, *Arabidopsis lyrata* dihydroflavonol 4-reductase (XP_002882011); AtND, *A. thaliana* NAD(P)-binding Rossmann-fold superfamily protein (NP_191681); ZmLR, *Zea mays* leucoanthocyanidin reductase (NP_001148881); MsVR, *Medicago sativa* vestitone reductase (AAB41550); ZmSDR, *Z. mays* short-chain dehydrogenase/reductase (NP_001148440); AtAR, *A. thaliana* anthocyanidin reductase (NP_176365)

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NtCYP82E4v1 -----MVFFIEAIVGLV--F-TLFLFLWTKKs-----KQFSKPLPKIIGGWPVIGHHNFHNDGDDDRFARHLGLIA 67
GmCYP82G4 -----MDSSQHTIAIVS--LVFWHTKRNRG--SKNKSKEAPFAGAWPLIGHHLHLLGG--DDQLLYRTFLGMA 68
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CjCYP82R1 ISLLNNKQKAKACEEIDKVGKDRW-----VEESIDKLVLYLQAIKEVIRLYPFGPLLYPHENVEDCVVSGYHHPGTRLEAVNNVKKGRDPK 434
PbCYP82N4 ISLLNNKQKAKACEEIDKVGKDRW-----VEESIDKLVLYLQAIKEVIRLYPFGPLLYPHENVEDCVVSGYHHPGTRLEAVNNVKKGRDPK 429

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AcCYP82C2 WED-PLTFSPERFINS-----VDRGNDSESLIPFGAGRRICPELPTANQFIALVATFVQNLWCHENGMSVDHHTVVEKGL-PLCKPBLFLVFKS 516
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PbCYP82N4 WED-PLTFSPERFINS-----VDRGNDSESLIPFGAGRRICPELPTANQFIALVATFVQNLWCHENGMSVDHHTVVEKGL-PLCKPBLFLVFKS 523

Fig.S5-B1. Sequence alignment of the amino acid sequence of identified CYP82Y1 from *P. bracteatum* . Residues highlighted in black are identical and those in dark gray are similar. Percentage of sequences which must agree for identity or similarity coloring to be added 50%. Hyphens represent gaps inserted for optimal alignment.

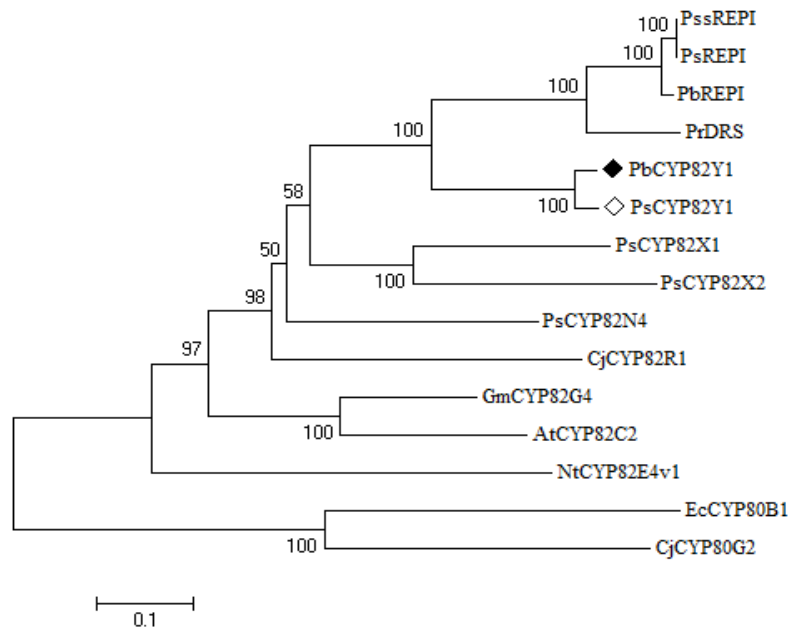


Fig.S5-B2. Unrooted neighbor-joining phylogenetic tree for CYP82Y1 selected consensus sequence exploiting RNA-seq data obtained from *Papaver bracteatum* genus from a BLASTP search of the NCBI non-redundant protein database, constructed using MEGA 7 software. Bootstrap frequencies for each clade were based on 1,000 iterations. Abbreviated species names are given before gene identifiers for each protein related to CYP82Y1 are as follows:

PbCYP82Y1, *P. bracteatum* CYP82Y1; PsCYP82Y1, *P. somniferum* (AFB74617); PssREPI, *P. somniferum* (subsp. *Setigerum*) reticuline epimerase (AKO60180); PsREPI, *P. somniferum* reticuline epimerase (AKO60175); PbREPI, *P. bracteatum* reticuline epimerase (AKO60179); PrDRS, *P. rhoeas* 1,2-dehydroreticuline synthase (AKO60176); PsCYP82X1, *P. somniferum* CYP82X1 (AFB74614); PsCYP82X2, *P. somniferum* CYP82X2 (AFB74616); CjCYP82R1, *C. japonica* var. *dissecta* CYP82R1 (BAF98472); PsCYP82N4, *P. somniferum* (S)-cis-N-methylstylophine 14-hydroxylase (AGC92398.1); EcCYP80B1, *E. californica* (S)-N-methylcoclaurine 3'-hydroxylase (AAC39453.1); CjCYP80G2, *C. japonica* var. *dissecta* corytuberine synthase (BAF80448.1); NtCYP82E4v1, *N. tabacum* CYP82E4v1 (DQ131886); GmCYP82G4, *G. max* CYP82G4 (XP_003523888); AtCYP82C2, *A. thaliana* CYP82C2 (O49394)

Sequence alignment of the amino acid sequence of identified MT1 from *P. bracteatum*. The alignment shows residues highlighted in black as identical and in dark gray as similar. The percentage of identity is indicated on the right side of the alignment.

Residues highlighted in black are identical, and residues highlighted in dark gray are similar. Percentage of identity is indicated on the right side of the alignment.

Fig.S5-C1. Sequence alignment of the amino acid sequence of identified MT1 from *P. bracteatum*. Residues highlighted in black are identical and those in dark gray are similar. Percentage of

sequences which must agree for identity or similarity coloring to be added 50%. Hyphens represent gaps inserted for optimal alignment.

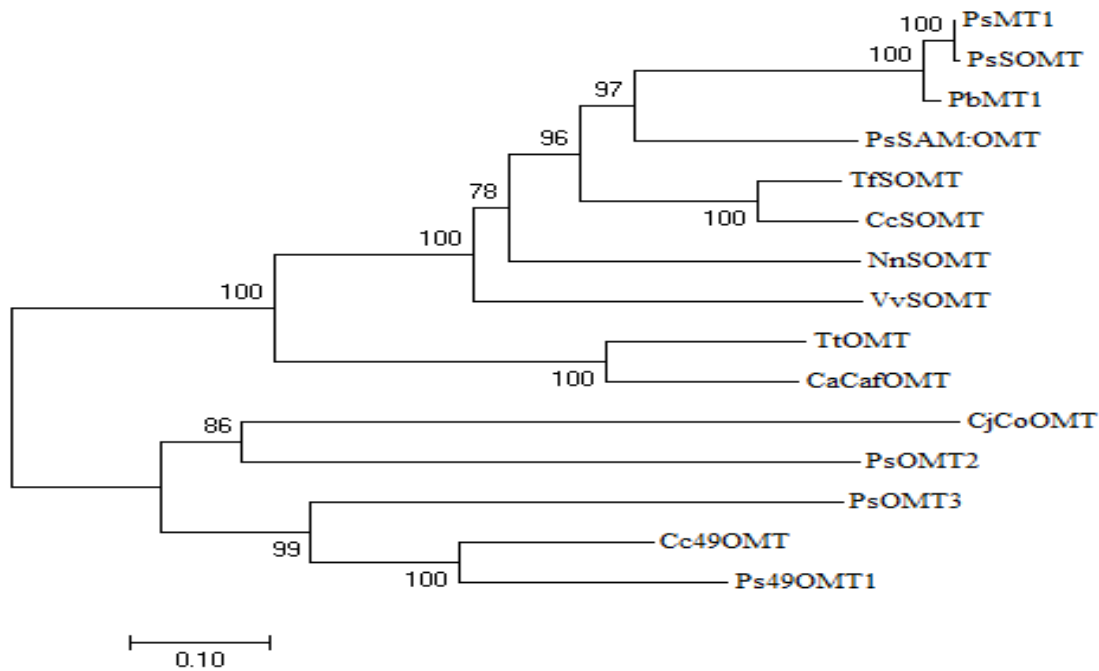


Fig.S5-C2. Unrooted neighbor-joining phylogenetic tree for MT1 selected consensus sequence exploiting RNA-seq data obtained from *Papaver bracteatum* genus from a BLASTP search of the NCBI non-redundant protein database, constructed using MEGA 7 software. Bootstrap frequencies for each clade were based on 1,000 iterations. Abbreviated species names are given before gene identifiers for each protein related to MT1 are as follows:

PbMT1, *P. bracteatum* O-methyltransferase 1; PsMT1, *P. somniferum* O-methyltransferase 1 (AFB74611); PsSOMT, *P. somniferum* scoulerine-9-O-methyltransferase (AFK73709); PsSOMT:OMT, *P. somniferum* S-adenosyl-L-methionine:O-methyltransferase (AKO60157); TfSOMT, *Thalictrum flavum* (S)-scoulerine 9-O-methyltransferase (AAU20770); CcSOMT, *Coptis chinensis* (S)-scoulerine 9-O-methyltransferase (ACL31653); NnSOMT, *Nelumbo nucifera* (S)-scoulerine 9-O-methyltransferase-like (XP_010242195); VvSOMT, *Vitis vinifera* (S)-scoulerine 9-O-methyltransferase (XP_002280092); CjCoOMT, *Coptis japonica* Columbamine O-methyltransferase (Q8H9A8.1); TtOMT, *Thalictrum tuberosum* O-methyltransferase (AAD29845.1); PsOMT2, *P. somniferum* narcotoline-O-methyltransferase (AFK73710.1); PsOMT3, *P. somniferum* O-methyltransferase (AFK73711.1); Cc49OMT, *Coptis chinensis* 3'-hydroxy-N-methylcoclaurine 4'OMT (ABY75613.1); Ps49OMT1, *P. somniferum* 3'-hydroxy-N-methylcoclaurine 4'OMT2 (AAP453141); CaCafOMT, *Capsicum annuum* caffeate O-methyltransferase (AAG43822.1)

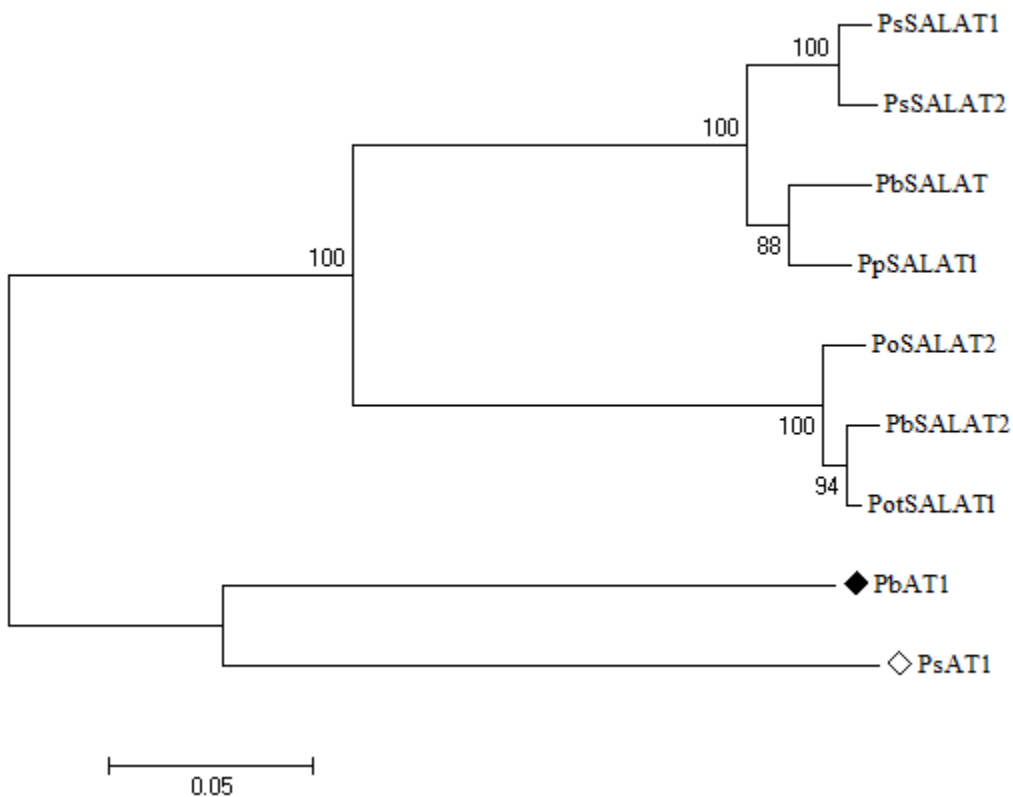


Fig.S5-D2. Unrooted neighbor-joining phylogenetic tree for AT1 selected consensus sequence exploiting RNA-seq data obtained from *Papaver bracteatum* genus from a BLASTP search of the NCBI non-redundant protein database, constructed using MEGA 7 software. Bootstrap frequencies for each clade were based on 1,000 iterations.

Abbreviated species names are given before gene identifiers for each protein related to AT1 are as follows:

PbAT1, *P. bracteatum* acetyltransferase 1; PsAT1, *P. somniferum* acetyltransferase 1 (AFB74620); PbSALAT, *P. bracteatum* salutaridinol 7-O-acetyltransferase (ACI45392.1); PsSALAT1, *P. somniferum* salutaridinol 7-O-acetyltransferase (ACI45390.1); PsSALAT2, *P. somniferum* salutaridinol 7-O-acetyltransferase (BAT70024.1); Posal, *P. orientale* salutaridinol 7-O-acetyltransferase (ACI45395.1); Pbsal2, *P. bracteatum* salutaridinol 7-O-acetyltransferase (ACI45393.1); P-posal, *P. pseudo-orientale* salutaridinol 7-O-acetyltransferase, partial (AKN62840.1); EgVS, *Eucalyptus grandis* vinorine synthase-like (XP_010044504)

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EgCXE1 -----MSTENASNLTVNISDSLRALNPDGTLRLARFNIFVTSATL-----NFTSPASPVLSKDVFINPS 61
TcCXE20 -----MSTQTIFSSSIDPFRKRLQTLNPDGTLRLNIFGR-TFAKF-----ESSDNSTAVLGRDIPINYS 60
PbCXE1 -----MADQHSITTSSTIDPYEALMVVHDPDLTLTRNLPLQITNITD-----DPNSKDI-LNAQ 55
PsCXE2 -----MADPYEFLMCHHPDEEDTLTRNFPICAT--FL-----DQNTKDISLNED 42
Ps CXE1 -----MADPYEFLMCHHPDEEDTLTRNFPICAT--FL-----DQNTKDISLNED 42
SOVF -----MDPYKELKISFNPDG-TITRLTPTILVPTTEQQQNINISSETDEDDHTVVSVDVPLNTA 58
ZjCXE8 -----MAFPFSSSSSSSIDPYKELHIVENPDG-SLTRLTPFPVVPFSDS-INT-----NFSPTTISKDLPLNST 64
GhCXE8 -----MEDQSSTISAPSIDPFEKELKIVQNPDG-SLTRQSLFPSSVITDEESTSS-----NTSQAFAFKDIPLPQ 63
TcCXE8 MLSISTTNVNSTIFSAPIQAIISFDLHLKPMTDQSSTAFSSMDPYKELKIVQNPDG-SLTRLAQFESVSVTEG-TTDS-----NTSQAFAFKDIPLPQ 92

EgCXE1 HSTWIRIFPTRLSC---SEKLPVIIVYHGGGFVLSAASSTFHEFCVSLARELSAVVSVSEYRLAPEHRLPMAYDDAVEALHNVKT-----A 148
TcCXE20 NNTWIRIFLPKQALDHSSSTSAKKLPLLVFHHGGGFILFSPDENMSHEFCSNMASELSVIVVSAVYRLAPEHRLPAAYDDAVEALSNVKT-----S 150
PbCXE1 HNTWIRIFKPTI-QDLFT--ANKLPVIIVYHGGGFILCFSTWTFYHDYCKSKANALPAIVSEYRLAPESRLPAAYDDAVDALNVVRQAASG---G-KF 148
PsCXE2 RRTSLRIFRPPF--EEFCVITNKLPLIIYFHGGGFVLFNADSTINHDCCQSIATHLPAVVSVDYRLAPENRLPAAYDDAVDALNVVKDQGLG---KLN 138
Ps CXE1 RRTSLRIFRPPF--KEFPVITNKLPLIIYFHGGGFILFNADSTINHDCCQSIATHPALVVSVDYRLAPENRLPAAYDDAVDALNVVKDQGLG---KLN 138
SOVF KNTFVRIFRPAA-LQH--YSTSKPLIIYFHGGGFVLSAAGTVRFHKSCNMSALIPAVVSVDYRLAPESRLPAAYDDAVEALNVVRQAASGSGGEG 153
ZjCXE8 NNTFIRLRFPLN-LPTNPNNNLPLIIYFHGGGFVLFSAASLPFHSCSRMAHLPALIISLEYRLAPEHRLPAAYDDAVEALNVVRQAQD----NG 159
GhCXE8 NNTFIRLRYRPPF--PF-PTINHKPLPLIIFHGGGFILFSAASRPFHDCSLKAKKLPVAVLSLEYRLAPEHRLPAAYDDAVEALIMVVRQAAMD----NG 156
TcCXE8 NNTFIRVYRPPF--DFF-PTINHKPLPLIIFHGGGFVLFSAASRPFHDCSLKAKKLPVAVLSLEYRLAPEHRLPAAYDDAVEALIMVVRQAAMD----NG 186

EgCXE1 RDEWLAGHADLSMCMGSSGGNLAFCAGLRASASHDELPLKIRGLILHPPFGGIQRTSESLRLVNDQMLPLAKGDTWELSLPLGATRDHVCNPM 248
TcCXE20 HDNWLLENYADFSQIFLMGSSAGGNIAHYGLRAAKQVDSLSPLKIQGLILHPPFGGVERTSESEFRLINDEIFSFCDSDLMWELSLPIGANRDHVCNPT 250
PbCXE1 SEFWLRDYADFNCYIMGSSAGGNIAYNVSLRAS--IDLSPKISGVILNQPFGGTERTSESLRLINDKILSLFVSDLMWELSLPIGSNRHVCNLL 246
PsCXE2 SEFWLKEYGDFSKCFIMGSSGGNIAHASLRAIE--MDLEPVVINGLILHPPFGGSLQRTESDLKVINDQDLPLAVRDVMWELALPLGSSRDHVCNPM 236
Ps CXE1 SEFWLKEYGDFSKCFIMGSSGGNIAHASLRAIE--MDLEPVVINGLILHPPFGGSLERTESDSKVINQDLPLAVRDVMWELALPLGSTRDHVCNPM 236
SOVF ADPWLQEFADFGRCFLMGSSGANIYHAGLRALD--HDLSPMKINGLILNQAFVGGVERTDSESLRLVDDKILPLPANDVMWELALPVGADRNRHVCNPM 253
ZjCXE8 CDPWLRDCADFSRCFLMGSSAGGNIAHAALRALD--IDLSPDLIRGMLNQPVFGGVQRTSEIRLFDRLPLPANDLWELALPEGCDRDHVCNPM 257
GhCXE8 CDPWLKEYVDFSKCFLGSSAGGNMVHAALRALD--IDSPVKIIGLIMNQPVFGGVERTSESEKRVNDRILPLPANDLMWELALPEGADRDRHVCNPM 254
TcCXE8 CDPWLKEYVDFSKCFLMGSSAGGNMVHAALRALN--VDISPVKIIIGLIMNQPVFGGVERTSESEKRSINDRILPLPANDLMWELALPEGADRDRHVCNPM 284

EgCXE1 VDG-GSKIIEGVDKMRSLGWRLVAGCDGDPLEDRQVEFAQMMEKGVSVVRVLTGGGHAIIEVREFDKSKPLLQLKPFMSTTIVS----- 334
TcCXE20 VAH-GST---ALEKIKRLGWRFVFGCDGDLIDRQIELVKMIKKKEIRVVSREVEGGFHGFELADPSKAKALVVALKNFIFSSI----- 331
PbCXE1 INEDDES LRK---KGG-FKKKCLVFGCDGDPLEDRQVEVVKMLEGKGVKVFETFMQEGGYHGMVVFEBEELEIMLPRVKDFILSGASKL----- 330
PsCXE2 IANDGSSSGN---MAG-LIKRCLVFGFGDPLIDRQIQLVKMLEGKGVKVTWIEQGGYHGVLCFDEKIRETLGKIKKFI----- 313
Ps CXE1 IDHDGSSSGN---MVG-LIERCFVVGFGDPLIDRQIQLVKMLEGKGVKVTWIEQGGYHGVLCFDEPMIRETSLERLKHFIINDEFIY----- 320
SOVF AE-NT--HSD---KIG-RIFSCCLVFGFGDPLVDRQKEVVKMLESRGVHVVAVEDEGGFHAVEFEBQRAQALVVMKDFIGSVSPRSTI----- 336
ZjCXE8 AT-NGSSSGG---KIG-RIFRCCLVFGFGDPLVDRQKEVVKMLESRGVEVVAVEDEGGSHGAEIFDVAKARAFYIISQNFINNSSSSSSQAGFVITKSTM 351
GhCXE8 AA-DG-FLKE---KMG-RITRCLVFGFGDPLIDRQRELVLVLEARGVDVVAEAEAGGCGHIEIFDELKAEALLKSIKDFVDTCRCVNSESAAAKSTL 347
TcCXE8 AA-DG-SHKE---KIG-RIFRCCLVFGFGDPLVDRQRELVKMMEARGVEVVAEAEAGGCGHIEIFDELKAKCSLLKSIKDFVNASCQIVNVATANSTL-- 375

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Fig.S5-E1. Sequence alignment of the amino acid sequence of identified CXE1 from *P. bracteatum* and its homologues in *P. somniferum*. Residues highlighted in black are identical and those in dark gray are similar. Percentage of sequences which must agree for identity or similarity coloring to be added 50%. Hyphens represent gaps inserted for optimal alignment. Catalytic residues (Serine (S), Aspartic acid (D) and Histidine (H)) are indicated above the alignment by red # (hash key). These residues are conserved in all the protein sequences and their catalytic functions have recently reported.

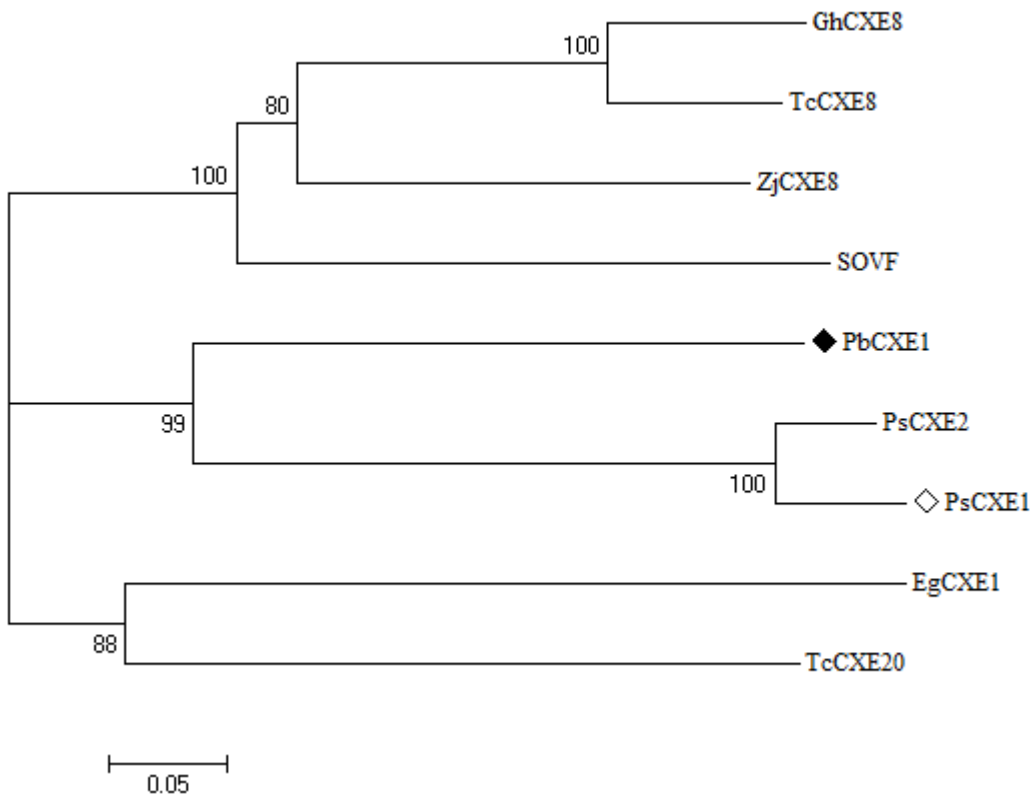


Fig.S5-E2. Unrooted neighbor-joining phylogenetic tree for CXE1 selected consensus sequence exploiting RNA-seq data obtained from *Papaver bracteatum* genus from a BLASTP search of the NCBI non-redundant protein database, constructed using MEGA 7 software. Bootstrap frequencies for each clade were based on 1,000 iterations.

Abbreviated species names are given before gene identifiers for each protein related to CXE1 are as follows:

PsCXE2, *P. somniferum* carboxylesterase 2 (AIY34373.1); PsCXE1, *P. somniferum* carboxylesterase 1 (AFB74618.1); PbCXE1, *P. bracteatum* carboxylesterase 1; SoSOVF, *Spinacia oleracea* SOVF_070390 isoform A (KNA18479.1); GhCXE8, *Gossypium hirsutum* carboxylesterase 8 (XP_016748284.1); TcCXE, *Theobroma cacao* carboxylesterase 8 (XP_017969789.1); ZjCXE8, *Ziziphus jujuba* carboxylesterase 8 (XP_015893007.1); EgCXE1, *Eucalyptus grandis* carboxylesterase 1-like (XP_010061765.1); TcCXE20, *T. cacao* Carboxylesterase 20, putative (EOY13805.1)

Fig.S5-F1. Sequence alignment of the amino acid sequence of identified CYP82X1 from *A. bracteatum* and its homologues in *P. somniferum*. Residues highlighted in black are identical and those in dark gray are similar. Percentage of sequences which must agree for identity or similarity coloring to be added 50%. Hyphens represent gaps inserted for optimal alignment.

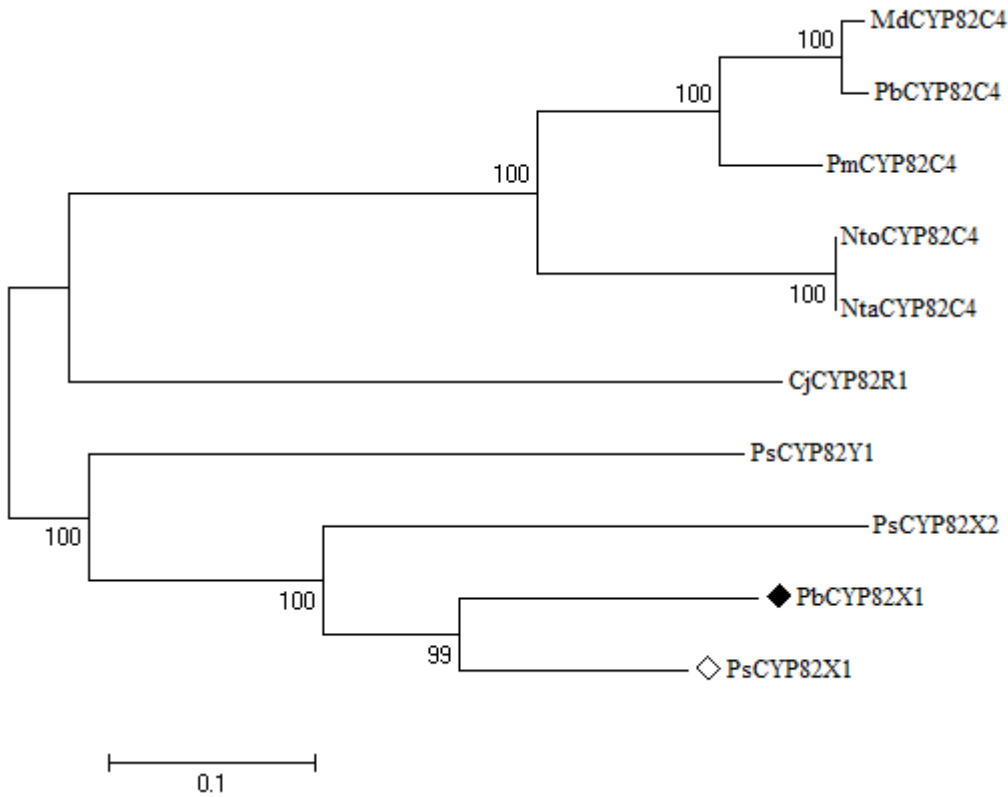


Fig.S5-F2. Unrooted neighbor-joining phylogenetic tree for CYP82X1 selected consensus sequence exploiting RNA-seq data obtained from *Papaver bracteatum* genus from a BLASTP search of the NCBI non-redundant protein database, constructed using MEGA 7 software. Bootstrap frequencies for each clade were based on 1,000 iterations. Abbreviated species names are given before gene identifiers for each protein related to CYP82X1 are as follows:

PbCYP82X1, *P. bracteatum* CYP82X1; PsCYP82X1, CYP82X1 *P. somniferum* (AFB74614); PsCYP82X2, *P. somniferum* CYP82X2 (AFB74616); PsCYP82Y1, *P. somniferum* CYP82Y1 (AFB74617); CjCYP82R1, *Coptis japonica* var. *dissecta* CYP82R1 (BAF98472.1), NtCYP82C4, *N. tomentosiformis* CYP82C4 (XP_009599169); NtCYP82C4, *N. tabacum* CYP82C4 (XP_016458765); PmCYP82C4, *Prunus mume* CYP82C4 (XP_016646999); MdCYP82C4 *Malus domestica* CYP82C4 (XP_008378409); PbCYP82C4, *Pyrus x bretschneideri* CYP82C4 (XP_009364162)

EcCYP719A5 -----MEESLWVVTATVVVFAIA-----KLLK---KSSSISTMEWPKGPKLPIIGNLHQLGGE-AFHVVLNLANLAKHGT 67
AmCYP719A14 -----MDEIWLIIHSTVIVVIGIA-----KFLLGKSSSSSISTMEWPKGPKLPIIGNLHQLGGE-VFHVVLNLANLAKVYGS 70
SoCYP719-Cma-3 -----MEEINVEWISTAAITIGIVV-VF-ATVSMFGRRRKSSMMWPNPGPKTLPIIGNMHLLGGT-ALHVVLHRLAEVYGS 74
PbCYP719A21 -----MMSMSWILTISTILSV-----VFAAVLIIFRRRISASTTEWPKGPKTLPIIGN-HLGGT-ALHVVLHRLAEVYGS 72
SoCYP719-Fbr-3 -----MMSMSWILTISTILSV-----VFAAVLIIFRRRISASTTEWPKGPKTLPIIGN-HLGGT-ALHVVLHRLAEVYGS 72
PbCYP -----MMSNLWILTISTILA-----VFAAVLIIFRRRISASTTEWPKGPKTLPIIGN-HLGGT-ALHVVLHRLAEVYGS 71
PbCYP719A21 -----MMSNLWILTISTILA-----VFAAVLIIFRRRISASTTEWPKGPKTLPIIGN-HLGGT-ALHVVLHRLAEVYGS 71
SoCYP719A21 -----MMSNLWILTISTILA-----VFAAVLIIFRRRISASTTEWPKGPKTLPIIGN-HLGGT-ALHVVLHRLAEVYGS 71
EcCYP719A9 -----MEEMKFLMNNPWLTAATITLLI-----SIFLVIRKSSSTTEWPKGPKTLPIIGNMHLLGGT-ALVVLHNLAKVYGS 74
EcCYP719A21 -----MEEMKILMNNPWLTAATITLLI-----SIFLVIRKSSSTTEWPKGPKTLPIIGNMHLLGGT-ALVVLHNLAKVYGS 73
EcCYP719A21 -----MEEMKFLMNNPWLTAATITLLI-----SIFLVIRKSSSTTEWPKGPKTLPIIGNMHLLGGT-ALVVLHNLAKVYGS 73
AmCYP719A13 -----MEEKIMTNNSPWILTSTSTITITLLSLFTITFILLRRKSSSSSMWVPFGPKTLPIIGNMHLLGGT-ALHVVLHNLAKVYGN 82
SoCYP719-Cma-4 MLLTILINDFRNSRSNINPAKMEELMSDPWILTATTAIVVIL-----L-----TITL-RRKSSSMWVPFGPKTLPIIGNMHLLGGT-ALHVVLHNLAKVYGN 89
SoCYP719-Gf1-3 -----MEWKSSVVFYSFAMEELFMSNPWVITSTFLAVLI-----L-----TITF-RRKSSSMWVPFGPKTLPIIGNMHLLGGT-ALHVVLHNLAKVYGN 83
SoCYP719-Sca-2 -----MEFEKIMSNPWILATTAVVVI-----SITATTF-RRKSSSMWVPFGPKTLPIIGNMHLLGGT-ALHVVLHNLAKVYGN 73
PbSTS -----MEKTFISNPWILTSTILVVIT-----TITMLMVFK-RRKSSSMWVPFGPKTLPIIGNMHLLGGT-ALHVVLHNLAKVYGN 73

EcCYP719A5 VMTIIVGAWRPVIVSDIDKAWELVNKSSDYAGRDPEITKIISANWKNIS SSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 167
AmCYP719A14 VTIWIGSWRPVIVSDIDKAWELVNKSSDYASARDMPITKIISANWKNIS SSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 170
SoCYP719-Cma-3 VMTIIVGAWRPVIVSDIDKAWELVNKSSDYASARDMPITKIISANWKNIS SSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 174
PbCYP719A21 VMTIIVGAWRPVIVSDIDKAWELVNKSSDYASAREMPEITKIISTANWRTIS SSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 172
SoCYP719-Fbr-3 VMTIIVGAWRPVIVSDIDKAWELVNKSSDYASAREMPEITKIISTANWRTIS SSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 172
PbCYP VMTIIVGAWRPVIVSDIDKAWELVNKSSDYASAREMPEITKIISTANWRTIS SSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 171
PbCYP719A21 VMTIIVGAWRPVIVSDIDKAWELVNKSSDYASAREMPEITKIISTANWRTIS SSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 171
EcCYP719A21 VMTIIVGAWRPVIVSDIDKAWELVNKSSDYASAREMPEITKIISTANWRTIS SSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 171
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EcCYP719A21 VMTIIVGAWRPVIVSDIDKAWELVNKSSDYASARDMPITKIISADWKTISTSSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 173
AmCYP719A13 VMTIIVGAWRPVIVSDIDKAWELVNKSSDYASARDMPITKIISADWKTISTSSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 182
SoCYP719-Cma-4 VMTIIVGAWRPVIVSDIDKAWELVNKSSDYASARDMPITKIISADWKTISTSSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 189
SoCYP719-Gf1-3 VMTIIVGAWRPVIVSDIDKAWELVNKSSDYASARDMPITKIISADWKTISTSSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 183
SoCYP719-Sca-2 VMTIIVGAWRPVIVSDIDKAWELVNKSSDYASARDMPITKIISADWKTISTSSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 173
PbSTS VMTIIVGAWRPVIVSDIDKAWELVNKSSDYASARDMPITKIISADWKTISTSSGSPFWNLKRGQLGQALAFINWISQYQERDMKNLITSMQKAS 173

EcCYP719A5 HNNGILKPLDYLKKEITRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 267
AmCYP719A14 HNNGILKPLDYLKKEITRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 270
SoCYP719-Cma-3 LNSGIVKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 274
PbCYP719A21 LNSGIVKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 272
SoCYP719-Fbr-3 LNSGIVKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 272
PbCYP LNSGIVKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 271
PbCYP719A21 --SGMWKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 269
SoCYP719A21 --SGMWKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 269
EcCYP719A9 NNNGIVKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 274
EcCYP719A21 NNNGIVKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 273
EcCYP719A21 NNNGIVKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 273
AmCYP719A13 NNNGIVKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 282
SoCYP719-Cma-4 NNNGIVKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 289
SoCYP719-Gf1-3 NNNGIVKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 283
SoCYP719-Sca-2 NNNGIVKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 273
PbSTS NNNGIVKPLDHLKKATVRLISRLIFGQDFDDEYVEEMHHAELIRISGYALAEAFYYAKYLPSSHKKAVRVEEACRRVQNLVLPFLSNPPTNTYHL 273

EcCYP719A5 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 363
AmCYP719A14 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 366
SoCYP719-Cma-3 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 374
PbCYP719A21 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 370
SoCYP719-Fbr-3 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 370
PbCYP FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 369
PbCYP719A21 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 367
EcCYP719A21 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 367
EcCYP719A9 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 372
EcCYP719A21 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 371
EcCYP719A21 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 371
AmCYP719A13 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 380
SoCYP719-Cma-4 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 387
SoCYP719-Gf1-3 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 381
SoCYP719-Sca-2 FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 371
PbSTS FLNSQKQVDEEVIIFAIPEAYLLGVDSSTTAWALAFILREBPVQEKLYQELKNFTANN--RMLKVEDVNLKPYLQAVVKETMRMKPIAPLAIPHAK 371

EcCYP719A5 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 461
AmCYP719A14 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 466
SoCYP719-Cma-3 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 467
PbCYP719A21 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 462
SoCYP719-Fbr-3 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 462
PbCYP KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 461
PbCYP719A21 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 459
SoCYP719A21 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 459
EcCYP719A9 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 468
EcCYP719A2 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 468
EcCYP719A3 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 468
AmCYP719A13 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 477
SoCYP719-Cma-4 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 482
SoCYP719-Gf1-3 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 477
SoCYP719-Sca-2 KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 469
PbSTS KDTSLMGKKVNDGKTVMVNIYALHNNKVVNPEYKPFPERFLOKQ--SKYGDIKMEQSLPFSAGMRICAGMELGKIQFSSFLANLVNAFAFKWNSCVSDG 467

EcCYP719A5 HLPDLSBDDHCFLLMKNPLEARIPRCQL 490
AmCYP719A14 HLPDLSBDDHCFLLMKNPLEARIPRCQL 494
SoCYP719-Cma-3 KFPDMSDLGLGVFLMKTPLEARIVPRV-- 495
PbCYP719A21 VLPDMSDLGLGVFLMKTPLEARIVPRV-- 489
SoCYP719-Fbr-3 VLPDMSDLGLGVFLMKTPLEARIVPRV-- 489
PbCYP VLPDMSDLGLGVFLMKTPLEARIVPRV-- 488
PbCYP719A21 VLPDMSDLGLGVFLMKTPLEARIVPRV-- 486
SoCYP719A21 VLPDMSDLGLGVFLMKTPLEARIVPRV-- 485
EcCYP719A9 VLPDMSDLGLGVFLMKTPLEARIVPRV-- 495
EcCYP719A2 VLPDMSDLGLGVFLMKTPLEARIVPRV-- 495
EcCYP719A3 VLPDMSDLGLGVFLMKTPLEARIVPRV-- 495
AmCYP719A13 VLPDMSDLGLGVFLMKTPLEARIVPRV-- 504
SoCYP719-Cma-4 VLPDMSDLGLGVFLMKTPLEARIVPRV-- 509
SoCYP719-Gf1-3 VLPDMSDLGLGVFLMKTPLEARIVPRV-- 504
SoCYP719-Sca-2 VLPDMSDLGLGVFLMKTPLEARIVPRV-- 496
PbSTS VLPDMSDLGLGVFLMKTPLEARIVPRV-- 494

Fig.S5-G1. Sequence alignment of the amino acid sequence of identified AT1 from *P. bracteatum*. Residues highlighted in black are identical and those in dark gray are similar. Percentage of sequences which must agree for identity or similarity coloring to be added 50%. Hyphens represent gaps inserted for optimal alignment. The red line above the alignment indicates the position of the conserved KPIAPXXXPH motif among CYP719s.

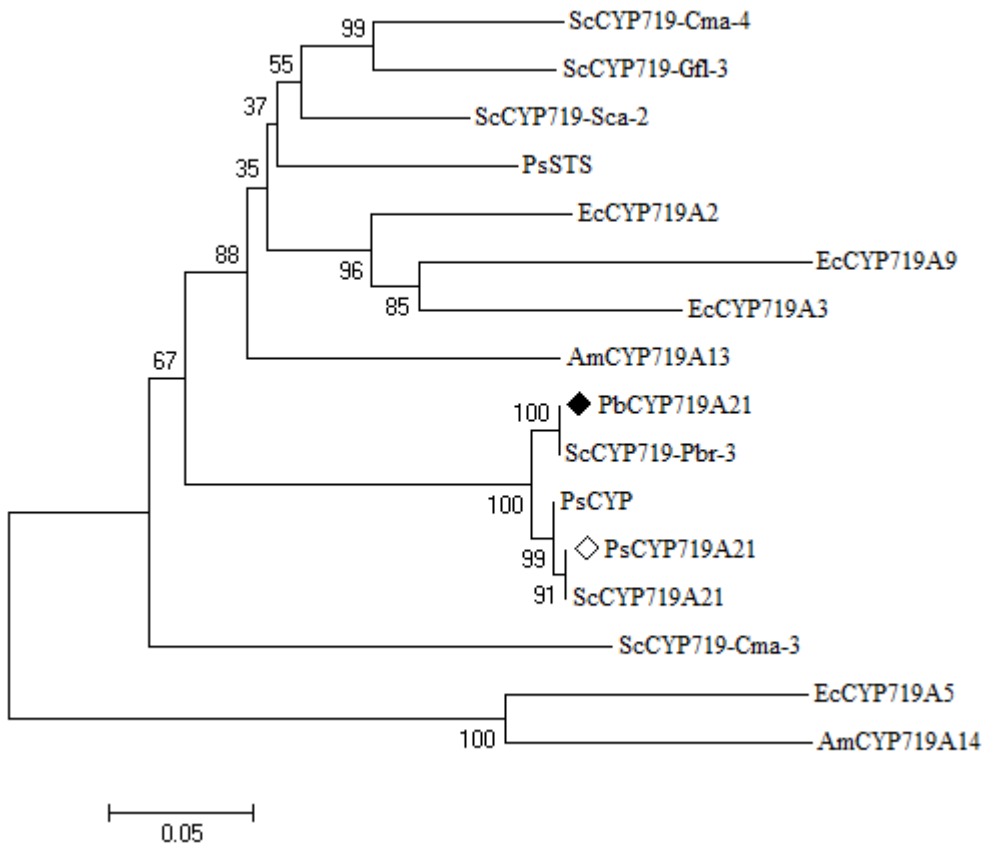


Fig.S5-G2. Unrooted neighbor-joining phylogenetic tree for CYP719A21 selected consensus sequence exploiting RNA-seq data obtained from *Papaver bracteatum* genus from a BLASTP search of the NCBI non-redundant protein database, constructed using MEGA 7 software. Bootstrap frequencies for each clade were based on 1,000 iterations. Abbreviated species names are given before gene identifiers for each protein related to CYP719A21 are as follows:

PsCYP719A21, *P. somniferum* CYP719A21 (AFB74615); PbCYP719A21, *P. bracteatum* CYP719; ScCYP719, synthetic construct CYP719 (ANY58171); EcCYP719A2, *Eschscholzia*

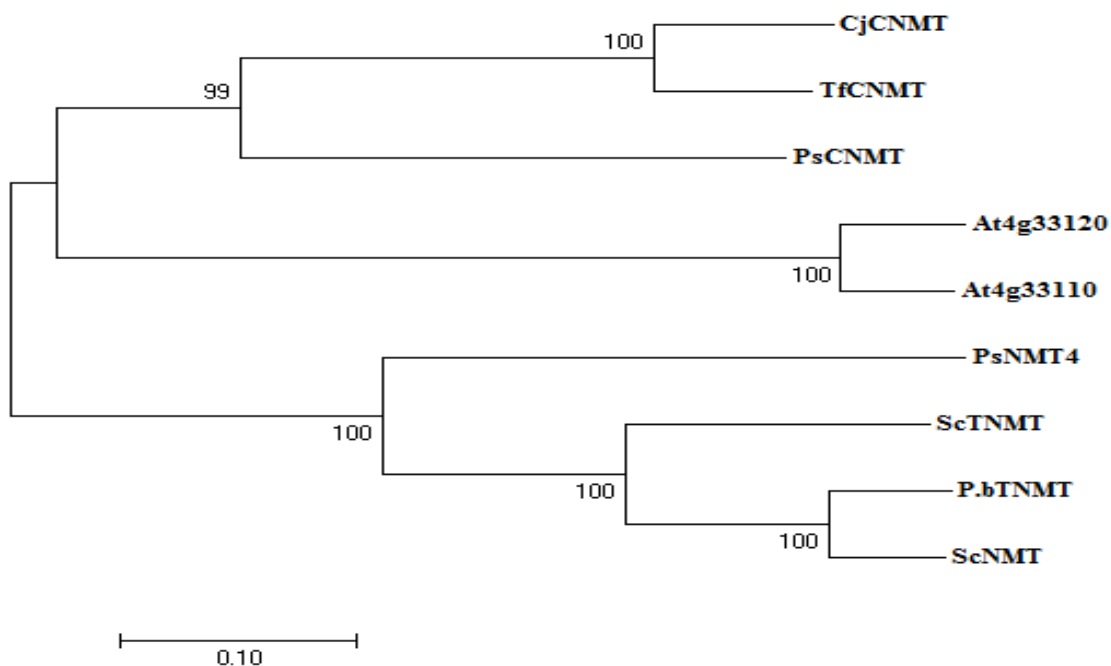


Fig.S5-H2. Unrooted neighbor-joining phylogenetic tree for TNMT selected consensus sequence exploiting RNA-seq data obtained from *Papaver bracteatum* genus from a BLASTP search of the NCBI non-redundant protein database, constructed using MEGA 7 software. Bootstrap frequencies for each clade were based on 1,000 iterations. Abbreviated species names are given before gene identifiers for each protein related to TNMT are as follows:

PbTNMT, *P. bracteatum* tetrahydroprotoberberine N-methyltransferase (ACO90237.1); NMT, N-methyltransferase synthetic construct (ANY58200); TNMT, tetrahydroprotoberberine N-methyltransferase synthetic construct (ANY58195); PsNMT4, *P. somniferum* N-methyltransferase (AOR51553); CjCNMT, *Coptis japonica* coclaurine N-methyltransferase (BAB71802); PsCNMT, *P. somniferum* S-adenosyl-L-methionine:coclaurine N-methyltransferase (AAP45316); TfCNMT, *Thalictrum flavum* (S)-coclaurine N-methyltransferase (AAU20766); At4g33120, *A. thaliana* At4g33120 ORF (NP_195038); At4g33110, *A. thaliana* At4g33110 ORF (AAM65762)

Supplementary Information 7

S7. The illustration of alignment of CYP82Y1 promoter region in Ps#7 and HN1 variety. The insertion has been accrued in, approximately, 400 base pair upstream of Translation Start Site (TSS). The ATG codon is highlighted in yellow, and blue sequences indicate the part of first exon.

```

Ps#7   GTAACGGAAATGAAACAACACTACCCAAATACTTATAAAGATGGGACTGTAAAGCTATTG  60
HN1   GTAACGGAAATGAAACAACACTACCCAAACACTTATAAAGATGGGACTGTAAAGCTATTG  60
*****

Ps#7   AGAGATTTTCATGTTCAAAATTTGAGAAGAAATGCACACTTCTGAAACAGAAAGTATGAGA  120
HN1   AGAGATTTTCATGTTCAAAATTTGAGAAGAAATGCACACTTCTGAAACAGAAAGTATGAAA  120
*****

Ps#7   AGTCGGCAGGATCGACATTGTTGGAAGGTAACGACCACAAATAGCCGATAGGATAGTAAA  180
HN1   AGTCGGCAGGTCGACATTATTGGAAGATAATGACCACAAATAGCCGATAGGATAGTAAA  180
*****

Ps#7   AAATCATTATGTCAACTATATGATTTTTGACCTACATGAAAGGTGTTACAAATGCACTAT  240
HN1   AAATCATTATGTCAACTATATGATTTTTGACCTACATGAAAGGTGTTACAAATGCACGAT  240
*****

Ps#7   TATTAGTCGGCAATATATTAATTTTCATAACATGTCTGAATTATAGTCGTCAAGGTTGAGAA  300
HN1   TATTAGTCGGCAATATATTAATTTTCATAACATGTCTGAATTGTAGTCATCAAGGTTGAGAA  300
*****

Ps#7   TTGTAAACATGAACGACTAAAAATCTTATTAATCTCAAAACCCGATGATCCAAATTTTCA  360
HN1   TTGTAAACATGAACGACTAAAAATCTTATTAATCTCAAAACCCGATGATCCAAATTTTCA  360
*****

Ps#7   ATTTTTCTTGATTTTTATTGTTCCGTTTGTATGCTTCGCTTTTGTTTTGTTTTCTTT  420
HN1   ATTTTTCTTGATTTTTATTTTCCGTTTGTATGCTTCGCTTTTGTTTTGTTTTCTTT  420
*****

Ps#7   TTTGATTCATCATGTATAGTTATAGTCTTGAAGAAAGATTGAAAATTGTTTAGATAGG  480
HN1   TTTGATTCATCATGTATAGTTATAATCTTGAAGAAAGATTGAAAATTGTTTAGATAGG  480

Ps#7   TTTTAGTCGGTATG - -GTTG- - - - - -TTTTTTTGGAACCAATTGATCTTTAAATATCT  530
HN1   TTTTAGTCGGTATGTTGTTGTTTTTTTTTTTTTTTGGACAATTGATTTTTTAATACCT  540
*****

Ps#7   CAAAAACACCCTTAAGAGCAACTGCATGGACGACTAAATTCAAATTTGAATGTCGA  586
HN1   TTAAACACCC - - - - - - - - - - - - - - - - - - - - - - - - - - - -

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Ps#7 AAGACCAATTCCAAATATAGTCGGGCGTTTATAATAATGTCCGCCTACCCGACGGG 642

HN1 -----

Ps#7 CGTTGGTAAAATGTCCGTCTGTAGCCGCGCGTTTCGTAAAGTTAACGCCTGATGCAGG 699

HN1 -----

Ps#7 GCGTTGGTATAATGTCCGCCTGGATGGGGCGTTGGTATAATGTCCGCCTGAATGGG 755

HN1 -----

Ps#7 GCATTGGTATAATCAAACGCCTGGCATGGGGCGTTGGTATAATGTCCGCATGGATGG 812

HN1 -----

Ps#7 GGCGTACGTAAAGTTAACGCCGGACACCCAGGCGTTGATATAGTCATGATCCCAAATTT 871

HN1 -----

Ps#7 GAAAAGTTTTGAAAACTTTACTTGGGGCGTTGTCTTTATCAACGCCCCATTTTTTTTTTC 931

HN1 -----

Ps#7 TTGAACCCGGGCGAACGTATAATCTCCGTCCCACACACCAGGCGTTGCTATAGTTCAC 989

HN1 -----

Ps#7 GCCCCATACAGGCGTTATCTTTATCAACGCCCCATACCAGGCGTTATCTTTATCAACGC 1048

HN1 -----

Ps#7 CCCATGCCAGGCGTAATCTTTATCTACGCTGGACGATGAAACGGACTTTATATCAAC 1105

HN1 ----- AAA-----

Ps#7 GCGCGACCAAATTTACTCGTCACCCGCTACGCCACAGGACGGACTAAGCCCAAATTT 1162
HN1 ----- CACCC -----

Ps#7 AATTTTTTTTTTAGTCTTTGGTATTTAGTTATGCTGGCACCCTGTGAACGAT 1215
HN1 -----

Ps#7 CTTAGCCCCTAGTTTGAATTGATATAACCCACTTAATGTTGGTATACCCAATTTAGCAA 1355
HN1 CTTAGCCCCTAACTTGAATTGATATAACCCACTTAATGTTGGTATACCCAATTTAGCAA 611

Ps#7 GGTTTTCCTTTTCAATTTTTTTTTTGCCCTTTTCAAAAAAGTTCAGAAAAACATTATTGA 1415
HN1 GGTTTTCCTTTTCAATTTGTTTTTTTGCCCTTTTCAAAAAAGTTCAGAAAAACATTATTGA 671

Ps#7 TGTGGACCAGTACCACTCCACTGGATTCTCGAGAAAATTTTGACAAATA ----- 1465
HN1 TGTGGACCAGTACCACTCCACTGGATTCTCGAGAAAATTTTGACAAATAATATATATAT 731

Ps#7 ----- ATATATATATATATATAATATAAGCCATTAAACACTTATCTACAATTACAATAATT 1521
HN1 ATATATATATATATATATATAATATAAGCCATTAAACACTTATCTACAATTACAATAATT 791

Ps#7 GAGTAATTTTCAGTTCATTCATGCGGTATTTGATGATCAAGAAATCTATCTATTTGTTTTT 1581
HN1 GAGTAATTTTCAGTTCATTCATGCGGTATTTGATGATCAAGAAATCTATCTATTTGTTTTT 851

Ps#7 TGATCAACCAACTGCAGTTGGCACTCTTATACTTGCTTTTCTGCTGACAC 1631
HN1 TGATCAACCAACTGCAGTTGGCACTCTTATACTTGCTTTTCTGCTGACAC 901

Supplementary Information 8

S8. Putative identified genes (full CDS), involved in noscapine biosynthesis pathway, and protein sequences obtained from CDS prediction from *papaver bracteatum*

transcriptome data which are accessible on Sequence Read Archive (SRA) database. These Reads are assembled with the “align-then assemble” strategy utilizing

Codon Code Aligner v. 5. 0.1. Program.

>Putative *papaver bracteatum* acetyltransferase1 (PbAT1) (FULL CDS)

```
ATGGAAGCTTTGTCTAGTGTTGATGTCGAAGTGATCTCCAAGGAAACAATTAAACCCACAACCTCCAACCCCATATC
AACT
TAGAAACTTCAATCTGTCCCTTCTTGATCAATATTGTCCTATAGTTTATGTTCCAATCATTCTTTCTACCTGCTGCA
G
TCTACTAATAGTTCTGGTAGTAAGCACACGATGATCTTAACTTGCTTAAGAGTTCTCTTTCTGAAACGCTGGGTCAA
TTT
TATCCACTGGCCGGTAGGATGAAAGACAACATTGTAGTCGACTGTAACGATGAAGGTATCGACTTTATCGAAGTA
AAAAT
CAAGAGTAAATTGTGCGACTTCATGATGAATCCAGATGTACGCTTAAGTCTGCTTCTCCCATCTGGAGTCGTTTCCA
TGA
ACTTCGTTAAGGAAGCACAGGTGATTGTTCAAGTGAACATATTTGATTGCGGTGGAGCAGCCATTTGTTTGTGTAT
ATCA
CACAAGATTGCAGATGCATGCACCATGAGTACATTCACTCGTTATTGGGCAGCCACCACCAACACAGCTCGTCTTG
GGGG
AGCTATCGGTCCTCCAAACACAAATCCGTTGTTTCTTCCTTCTTCGACTCGGCATCTCTTTTCCACCTAACGAACA
AT
TGGCATCTCAATCAGCGATGCCATCCGTTACTTATCCTACTGAGGATAGCCGAAGACATATAGTTGTCAGCAAAAG
ATTT
GTGTTTCGATGCGGTAAAGTTAAAATCTGTACGTGAAAAGCTACAAGTATTGATGCATGATAAATACAGATCCCGTA
AGCC
AACAAGGGTTGAGGTGGTTTCCGCTCTAATATGGAAGGCAGCCATGAAATCCGCTCCGCTCTGGTGCTTCATCGAC
GGTAA
ACCATGCCGTGAACTTTAGAAAGAAAATGGACCCACCTTTACAAGATGTGTCATTCGGAAATCTTTGTCAGGTCGT
TGCA
```

GCATTATTACCAGCAACAACGCCGGCAACAACAGAAAATTCAGATAACAAGACAGTTAATAGTACAAGTAATGAA
GTGCA

AGTGGCACTTGATGAGTTAAATGATTTCGTAGCTCAATTGAGAGGCGAAATAGATAAGGTAAAGGGCGACAAAG
GTTGCA

TGGAGAGAATGTTTCTAAATTTTCATGAATGGTTATGATGCCTCCGTAACGAAAGACAGTGATGTTGAAGATGAAG
TGATA

GCTTTTTGGATGACTAGCTGGTGCAACTTTGGTTTATATGATGCTGATTTTCGGTTGGGGAAAGCCAATTTGGGTAA
CTAC

TGATCCATTTATCGAGCCGAACAAGAACATAATTTACATGATTGATACAAAATGTGGTGAAGGAATAGAAGTGTG
GGTAA

ACTTTCTTGAGGATGATATGGCTAAGTTCGAGCATCACCTAAGCGAGATCCTCGAATTGTTTTGA

>PbAT1 (Protein sequence)

MEALSSVDVEISKETIKPTTPTYQLRNFNLSDQYCPVYVPIILFYPAAVTNSSGSKHHDDLNLKSSLSETLGQF
YPLAGRMKDNIVVDCNDEGIDFIEVKIKSKLCDFMNPDPVRLSLLPSGVVSMNFVKEAQVIVQVNIFDCGGAAICLCIS
HKIADACTMSTFTRYWAATTNTARLGAIGPPNTNPLFLPSFDSASLFPNEQLASQSAMPSVTYPTEDSRRHIVVSKRF
VFDAVKLKSAREKLQVLMHDKYRSRKPTRVEVVSALIWKAAMKSAPSGASSTVNHAVNFRKKMDPPLQDVSFGNLCQ
VVA

ALLPATTPATTENSNDKTVNSTSNEVQVALDELNDFVAQLRGEIDKVKGDKGCMERMFLNFMNGYDASVTKDSDVED
EVI

AFWMTSWCNFGLYDADFGWGKPIWVTTDPFIEPNKNIYMIDTKCGEGIEVWVNFLEDDMAKFEHHLSEILELF

>Putative papaver bracteatum carboxylesterase1 PbCXE1 (full CDS)

TAATTTTGAAGCTCCTGATAAAATGAAGTCTTTGACTCTTGGAACATGATTTCAAGTTCTTCAGGCTCAAAGTAA
CCA

TTCCATGATACCCGCCTTCTGCATAAAAGTTTCAACCTTGACACCTTTTCCTTCCAACATCTTCACAAATTCAACTG
TC

TATCAATCAATGGATCTCCATCACACCAATAACCAAACATTTCTTTATAAACCCACATTTCTTCGTAACGATTCGT
CG

TCTTCGTTGATCAAAAGATTACAATAAGGATGATTTCTATTAGACCCAATCGGCAAAGACAATTCCCACATCAAGTC
AC

TTACCGGGAGAGACAAAATCTTGTCATTGATTAGTCTCAGTTCAGAACTAGTCCTTTCAATTCCGCCCAGAAATGGT
TGATT

CAATATAACCCCGGAAATTTTCAAAGGGCTAAGATCCAATTCCGATGCTCTTAAAGAAACGTTGTAAGCAATATTTCCACCT

GCACTTTCTCCATAATATAACAATTTGTAAAATCAGCGTAATCCCTTAGCCACGGCTCACTTGGTTTACCTCCGGAAGCTT

GATGTTTGACCCAGTTTAGAGCATCAACAGCATCATCATAAGCAGCCGGTAATCGACTTTCCGGTGCAAGACGATCTC

TACTGAAAGTACTATTGCCGGCAAAGCGTTTGCCTTGGATTGTCAGTAATCATGATATATAGTCCAAAATGTGCTGCAAAG

AATGAACCCACCACCATGGTAATAAATTATGACCGGAAGCTTATTTGCTGTGGGTAAATCTTGAATTGTGGGTTGAAGATA

CGAATCCAAGTATTGTGTTGAGCATTGAGAAGTATGTCTTTGGAATTTGGATCATCTGTCGTGTTTGAATTTGAAGTGGG

AGATTTCTTGTGAGGGTATCAAGATCAGGATCGTGAACAACCATTAAAGCTTCGTAAGGATCGATGGTACTACTAGTAGTAG

TTGAATGTTGATCTGCCAT

>PbCXE1 (Protein sequence)

MADQHSTTSSSTIDPYEALMVVHDPDLTLRNLPLQITNTTDDPNSKDILLNAQHNTWIRIFKPTIQDLPTANKLPVIIY YHG

GGFILCSTFWTIYHDYCKSKANALPAIVLSVEYRLAPESRLPAAYDDAVDALNWVKHQASGGKPSEPWL RDYADFTNCYIMGES

AGGNIAYNVSLRASELDLSPKISGVILNQPFLLGGIERTSSELRLINDKILSLPVSDLMWELSLPIGNSNRNHPYC NLLINEDDE

SLRKKCGFIKKCLVIGCDGDPLDRQVEFVKMLEGKGVK VETFMQEGGYHGMVYFEPEELEIMLPVKDFILSGASKL

>Putative papaver bracteatum cytochrome p450 CYP82X1 (PbCYP82X1) (full CDS)

ATGGAGTTCTTGATGAAGTTATTATTGTTACTTGAACCAATCACTTTTAGTATTTTCTTGGTATAGGTTCTATTGTTCTTCTAT

ACAATGTCTTCTTCTTGGTTATTAACAAGAAAAAGAAGAAGAAAGCACCAAATGCATCAGGGGCATGGCCGTTGATAGGCCATCT

CAATCTTTTCATGAATGATAAGGAAGCGTTGTATAAAACACTAGGAACCATGGCCGACAAGTACGGACCTGCATTCAACGTTCTGA

TTAGGCAACCAAGAAATCCTTGTGGTGAGTAATTGGAAGATGGTAAAAGAATGTTTTAACACTCAAAATGATAAGCTATTTCTGA

ATCGTCGAACTACATTGGGTGTGAAATACATGCTTAACAAGAAGACCTCTGTTGCCTTTTCACCATATGGAACATAT
TGGAGGGA

GCTACGAAAGCTAACGGTGCAACAATTGCTCTCTAAGCAACGTTTAGATTCTGTGGAAACATTTGAAAATCAAAGAA
ATAGATGCT

TCATTTGGTAGACTTAACGATTTATGCAGCAACAACAAGGGTACTGGAGCAGCTACCCCAATTAGGATGGACAGTT
GGTTTGCCG

AGTTGACGTTCAACGTGTTTCGCAAGAATTGTCTTTGGCTACCAAAGTGGAGAAAGGTTGATGCTATCAGGTGATAC
GGCATCCAA

CGGGGAGAGGTACAAGAAAACATTAGAAGAAGCATTTCTCCTTATGTCAAGCTTTCGCGTTTCTGACGTATTCCCA
TGCTTAGAG

TGGGTAGACAGATCAAGAGGCCTTGTAAGGAGCATGAAACGCTTTGGAGATCAGCTAAATTCAATTGCAGGGTGT
CTTATTGAGG

AGCATCGCCAAAAGAGATCACAATCCGTATCAGCATCAAATTCTACAAATGATAAAGGAGTTGGTGATGAACAAG
ACTTCATTGA

TGTTCTCTTATCGGTTGCTGAACAATCACAATTCTGGAGATGACCCTGATTTGGTCATCAAGTCTATGATTTTG
AAGCCTTA

GCAGGTGGGAGTGACACAACAACATCAACCCTAACTTGGGTCTTTCACTGCTATTGAACCACCCCAAAGTGTTAA
AGACGGCAA

AAGAGGAAATAGATATGCACGTCGGACGTAATCGATGCGTAGAAGAGTCAGATATTCCAAGCTCGTTTATGTCA
ATGCAATTAT

CAAAGAATCAATGAGATTGTATCCAAATGGGTCATTGGTTGATCGATTGACGTTGGAAGAGTGTGAAGTTGGTGG
ATTCCATGTC

CCAGCTGAGGGGACACTTATTCGTAAACGTTTGGAAGATCCATAGAGATCCGAGTGTGTGGGAGAATCCTCTGGAG
TTCAAGCCAG

AGAGATTTTTGAGTAATGATTGCAAGGTGGATATGGATTTTATAAGTCAAAAATATGAATTCATACCATTCGGGAT
AGGTCGGAG

GATATGTCCTGGTATGCTTTCAGCATTACAGGTGATGCATTTTGTGGTAGCCCGTCTTATTCATGGGTTTGATATGG
AAGCAGCA

AGTGCCGATGGGAAAGTGGATATGGCAGAAAAGCCAGGCATGACTTGCTATAAGATGACACCTCTTGAAGTTATG
CTCACGGCTC

GACAGTAG

>PbCYP82X1 (Protein sequence)

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ILVVSNWKMVKECFNTQNDKLFSNRRTTLGVKYMLNKKTSVAFSPYGTYWRELKRLTVQQLSKQRLDSWKHLKIKEIDASFGRNLNDCS

NNKGTGAATPIRMDSWFAELTFNVFARIVFGYQSGERLMLSGDTASNGERYKKTLEEAFLLMSSFAVSDVFPCLWVDRSRGLVRSMKRF

GDQLNSIAGCLIEHRQKRSQSVSASNSTNDKGVGDEQDFIDVLLSVAEQSQIPGDDPDLVIKSMILEALAGGSDTTTSTLTWVLSLLN

HPKVLKTAKEEIDMHVGRNRCVEESDIPKLVYVNAIKESMRLYPNGSLVDRLTLEECEVGGFHVPAEGHLFVNVWVKIHRDPSVWENPLEF

KPERFLSNDCKVDMDFISQKYEIPFGIGRRICPGMLSALQVMHFVVARLIHGFDMEAASADGKVDMAEKPGMTCYKMTPLEVMLTARQ

>Putative papaver bracteatum cytochrome p450 CYP82Y1 (PbCYP82Y1) (FULL CDS)

ATCTAGTGTCGTGGGGTGAGTAGAACATCTAGTGGCACTACCTTGTTGTTGAAAAACCTGGTCTTGCCCTCATGTCAATTTCCCCCTCTGGTG

CCTTCATCTCGAACTCAAGAATAAGACGAGTGAGGACCAAATGCAAGACTTCTAAGGCAAAAGATGCACCGGGACATATCCGCCTGCCTGTTCCGA

ATGGTATCAGTTCATAATTCTGACCCTTCACATCTACCATCCCTTTGTCATTGCTCAAGAATCTCTCAGGTCGAAATACCAATGGATCATTCCAAA

CCCTTGGGTCTCGTTGCATCTTCATACGTTAACCATAATCTCGTCCCAGCTGGAACGTGGAAGCCACCAACCTCGCAATCATCACTGGTCATCCG

CTCCATTATTGTGCTGGCGGGGTATAATCGCATTGATTCTTTGATGATAGCTTGGATGTAGACGAGGTTAGGAACATCAGAAGCATCAACGACAGCC

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ACTTTGTAGTGCTACTCCACCCGATAACATGTCCAAGGCAATAGATTGACAGAGATTTGGGGTTGTTTCCCGGAATCTGTGATTGCTCCATAAT

CGACAAGCAAACATCGATGAAGTCTTCTTCTCATGCTCCGTAAGTTCTCCTGCGGTATTTCTAGAAATTTTGAGTTCTTTTGGCGATGAACCTCC

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CATCTGAAACGGCAAATGTTGCCATAAGATTTGACACTTCATCGATTGCAAGCTTGATTTTTCTGGCTGCTTGTGACACCTGACACTGCATTTGA

TTGGAATCCGCTGACAATCCGTCCTATTACGTTGAATGTCAAGTAAGCGAACCAATCATCCATTCTCACAAGATTAG
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CCCTGTTTGTTGTTGCTGCATAACTCATGAAGCCTTTTAAAGGAGTTGTCCACTTCAGAAATCCGCAAGTGTTTGAA
CTTCTCTAATTGCTGATTAG

AGAGGAGTTTATGTGTAGATATCTTCCGCAACTCTCTCCAGTACTTCCCATAAGGTGCAAAACCATAAGACTCAGT
GTCATAAAACATAAGTTTAAC

CGCCAAGGAGGAAGGACGATTGAAAAAACTTGTCATTGGCACCTGTAAACACTCCTTTACCATCTCCCAACTA
CTAACAACTAGAGTTCTATGA

CTACCGAATCTTAAGCTGAAAAATAGGTCCATATTTATCAGCCATGTTACCGAGAGTTGCATGATTTAAATCGTTTTC
GTTTCATGAAAAGAAGAAGAT

GACCTATCACTGGCCACGCACCTGATGCCTCTGGTAACGGAGTCGTTGTAATTGCGGTACATGACGATGAGGTCC
GATTCGCCTCAAACCCCTCTT

CTTCTGTTCATAGTAAATAATAACAGGTGAAAGTGTCAGTAGAAAAGCAAGTACTATAAGAGTGGAAGTGAAGT
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AAAGATTTCTTGA

>PbCYP82Y1 (Protein sequence)

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DLNHATLGNMADKYG

PIFSLRFGSHRTLVSWSWEMVKECFTGANDKFFSNRPSSLAVKLMFYDTESYGFAPYGKYWRELKISTHKLLSNQQLEK
FKHLRISEVDNSFKRLHE

LCSNNKQGGETTSVANLVRMDDWFAYLTFNVIGRIVSGFQSNVSGATSSQEKYKLAIDEVSNLMATFAVSDVVPCLG
WIDRLTGLTGKMKKCGKKLD

AVVGDAVEVHRQKKLKISRNTAGELTEHEEEDFIDVCLSIMEQSQIPGNNPEISVKIALDMLSGGSDTTKLIMTWTLSSL
LNHPDILDKAKEEVDTY

FRKKKMAVVDASDVPNLVYIQAIKESMRLYPASTIMERMTSDDCEVGGFHVPAIGTRLWVNVWKMQRDPRVWNDP
LVFRPERFLSNDKGMVDVKGQNY

ELIPFGTGRRICPGASFALEVLHLVLTRLILEFEMKAPEGEIDMRARPGFFNNKVPLDVLLTPRTL

>Putative papaver bracteatum cytochrome p450 PbCYP719A21 (PbCYP719A21) (FULL CDS)

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GTCGTCTTACATAAACTAGCTGAAGTTT

ACGGCAGTGTAATGACGATATGGATTGGTAGTTGGAAACCTGTTATTATTGTTTCTGACTTTGATCGAGCTTGGGA
AGTTCTTGTTAACAATCTTCAGATTAT

TCAGCTCGTGAAATGCCTGAGATCACTAAAATCGGCACTGCAAATTGGAGAACAATTTCAAGTTCTGATTCTGGTC
CATTTTGGGCCACTCTTCGTAAAGGTCT

TCAGAGTGTAGCATTATCCCCTCAGCATTTAGCATCGCAAACCTGCACACCAAGAGAGAGATATAATAAAGTTGATC
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>PbCYP719A21 (Protein sequence)

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VIIVSDFDRAWEVLVNK

SSDYSAREMPEITKIGTANWRTISSSDSGPFWATLRKGLQSVALSPQHLASQTAHQERDIIKLIKLNKDEALNSGTVKPL
DHLKKATVRLISRLIFGQDF

DDDKYVEDMHDVIEFLIRISGYAQLAEVFYAKYLP SHKRAVTGAE EAKRRVIALVRPFLQSNPATNTYLHFLKSQHYPEE
VIIFAIFEAYLLGVDSTSS

TTAWALAFIREPSVQEKLQELKNFTANNNR TMLKVEDVNKLPYLQAVVKETMRMKPIAPLAIPHKACKDTS LMGKK
VDKGTKVMVNIHALHHTK VWK

EPYKFMPPERFLQKQDKAMEQSLLPFSAGMRICAGMELGKLQFSFLANLVYAFKWSCVSDGVL PDMSDLLGFVLFMK
TPLEARVVPRL

>Putative papaver bracteatum O-methyltransferases (PbMT1) (FULL CDS)

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TCTTTCAGAAACGGCTAACTTAGGGAAGTTAATATGCATTCCAATGGCATTAAAGAGCTGCGATGGAGCTAAATGTG
TTCCAATTATCTCAAAGTTTGGAAGT

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AGATAGAGTTCTTCGACTGCTCGGTGCC

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AGTTTTTCAAAGTAAATCTGTGGTGG

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GTCTTCATGTCATTGAGTTTCACAAA

PbMT1 (Protein sequence)

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KMPNTTSNPTAAIYLDRVLRL

LGASSILSVSTRKKLINGGGEDRVVHEKVYGLTNSSCCLVPREEDGVSLVEELLFTSDKVVVDSFFKLKSVVEEKDSVPFEV
AHGAKIFEYAATEPRMNKV

FNDGMAVFSIVVFEAVFRVYDGFLDMKELLDVGGGIGTSVSKIVAKYPFIRGVNFDLPHVISVAPQYPGVEHVAGDMFE
EVPKGQNMMLLKWVLHDWGDERC

VKLLKNCWKSLPAGGKVLIIIEFVLPNELGNNAESFNALIPDLLLMALNPGGKERTISEYDDLAKAAGFIKTIPIISNGLHVI
EFHK

Putative papaver bracteatum short-chain dehydrogenase/reductase (PbSDR1) (FULL CDS)

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GGCATCTTGGCTCATCTTGAGATTGCTTCAA

CGTGGTTACTCTGTTCCGACCACCGTTCGGTCCGACCCCAAATTTAAGGAAGATGTAAGCCACCTGAAAGCCCTTC
CTGAGGCTGCCGAGAAGCTCCAAATTTT

GAAGCAGATCTCGAAACCCGAAAGTTTTGATGCTGCAGTTGACGGATGTGTGGTGTCTTTCTCGTTGCTCAAG
GAATTGGTCTTGAACAAGCCTACACTCAA

GAAAAATTACTCAAGACATCCGTGGAAGGAACTCTTGAATTCTCAAGTCATGCTTGAAGTCCAAAACAGTGAAA
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GCAATGATGGTAAGTAATCTCAAAGTTGTAACACAAATTGACGAGACAATGTGGTCAGAAGTTGACCATTTCATTG
GCAAACCCGAACAAGTCATTCCTGCTGGT

CTCGCATATGTGGTTTCAAAGACACTGACAGAAAGAGCTGCCATGAAATTTTCTGACGAACATGGATTGGATCTTG
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CCATTTATCATCCCCAACCTTCCTGAGAGTGTTTCTCTGGCTCTTTCTGTAATTTTGGGTGATAGGACGAAGATGAT
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TGATTTTACAATACATGATGTGGCTAAA

TTTATAGCTGAAAAATATCCAGAATTTAGTTACCAACTGATTTACTAAAGGAAATTGAGGAGGAAAAACCAAGTTC
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GGATTTAGTTCAAATATAATTTTGAGGAGATGTTTGGTGATGCAATTCGAAGCTGCAAGAGAAAGGTTTCCTT

PbSDR1 (Protein sequence)

MEGEHINDQGGNGKIVCVTGGAGYLASWLILRLLRGYSVRTTVRSDPKFKEDVSHLKALPEAAEKLQIFEADLETPESE
DAAVDGCVGVLVAQIGLEQAYTQE

KLLKTSVEGTLGILKSCLKSKTVKKVVYTSSSAAAMMVSNLKVVTQIDETMWSEVDHFIGKPEQVIPAGLAYVVSRTLTER
AAMKFSDEHGLDLVTILPSMIVGPF

IIPNLPESVSLALSILGDRTKMIRLKPTNAVHIDDVASAQIFLFECQNAKGRHICSSVDFTIHDVAKFIAEKYPEFQLPTDLL
KEIEEEKPVHLSSDKLLSMGFQ

FKYNFEEMFGDAIRSCKEKGFL

Putative papaver bracteatum tetrahydroxyprotoberberine N-methyltransferase (PbTNMT) (Full CDS)

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AGATGAGGAACTGAAGAAGCTGATCAAGTTTCA

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CCTTAAAAAAGATGGAAATGTCAGGAGAGA

TTGAGACAATGAACAAGGAACTTATGAATTACCCTCAGAATTCTTAGAGGCAGTTTTTGGAAAAACAGTCAAGCA
AAGTATGTGTTACTTCAAACATGAATCAGCA

ACAATAGACGAAGCAGAAGAAGCTGCACATGAATTATACTGTGAACGAGCACAGATCAAAGATGGACAACTGTT
CTCGACATTGGTTGTGGTCAAGGTGGTCTAGT

TCTATACATTGCTCGGAAATATAAGAAATGTCATGTTACAGGGCTCACTAATTCAAAGGCACAAGTCAATTACTTAC
TCAAGCAAGCAGAGAAGCTTGGGCTGACAA

ATGTCGACGCCATACTAGCAGATGTCACCTCAATATGAATCTGACAAGACATACGATCGACTACTTATGATTGAAGC
CATAGAGCACATGAAAACTTACAACTGTTC

ATGAAGAACTATCAACTTGGATGACAGAAGAAAGTCTTCTCTTTGTGGACCATGTCTGCCATAAAACCTTTGCTC
ACTTTTTTGAGGCAGTCGACGAGGATGACTG

GTAATCAGGTTTCATCTTCCCCCAGGTTGTGCAACCATACTAGCTGCTAATAGTCTCCTCTATTTCCAGGATGATGT
TTCAGTTGTGGATCATTGGGTTGTCAACG

GAATGCACATGGCTCGTTCAGTAGACATTTGGAGAAAGGCACTAGACAAAAATATGGAAGCTGCAAAAGAAATTC
TATTACCTGGACTTGGAGGAAGCCACGAAGCA

GTAATGGAGTCGTTACTCACATTAGAACATTCTGTATGGGAGGCTATGAACAATTCTCAATGAACGATGGAGAT
GAGTGGATGGTTGCGCAGCTGCTTTCAAGAA

GAAGTAG

PbTNMT (Protein sequence)

MGSIDEVKKESAGETLGRLLKGEIKDEELKKLIKQFEKRLQWGYKSSHQEQLSFNLDFIKSLKKMEMSGEIETMKNKETYE
LPSEFLEAVFGKTVKQSMCYFKHESAT

IDEAEEAAHELYCERAQIKDGQTVLDIGCGQGGLVLYIARKYKKCHVTGLTNSKAQVNYLLQAEKLGLTNVDAILADVT
QYESDKTYDRLLMIEAIEHMKNLQLFMK

KLSTWMTEESLLFVDHVCHKTFAHFFEAVDEDDWYSGFIFPPGCATILAANSLLYFQDDVSVVDHWVVGMMHMARS
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VVTHIRTFMGGYEQFSMNDGDEWMVAQLLFKKK

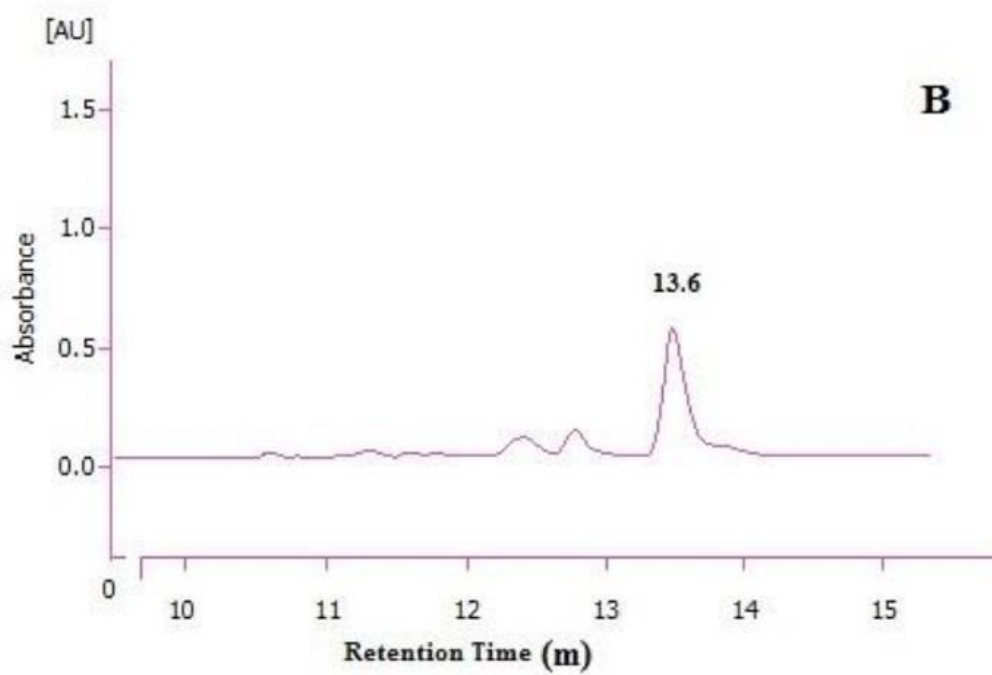
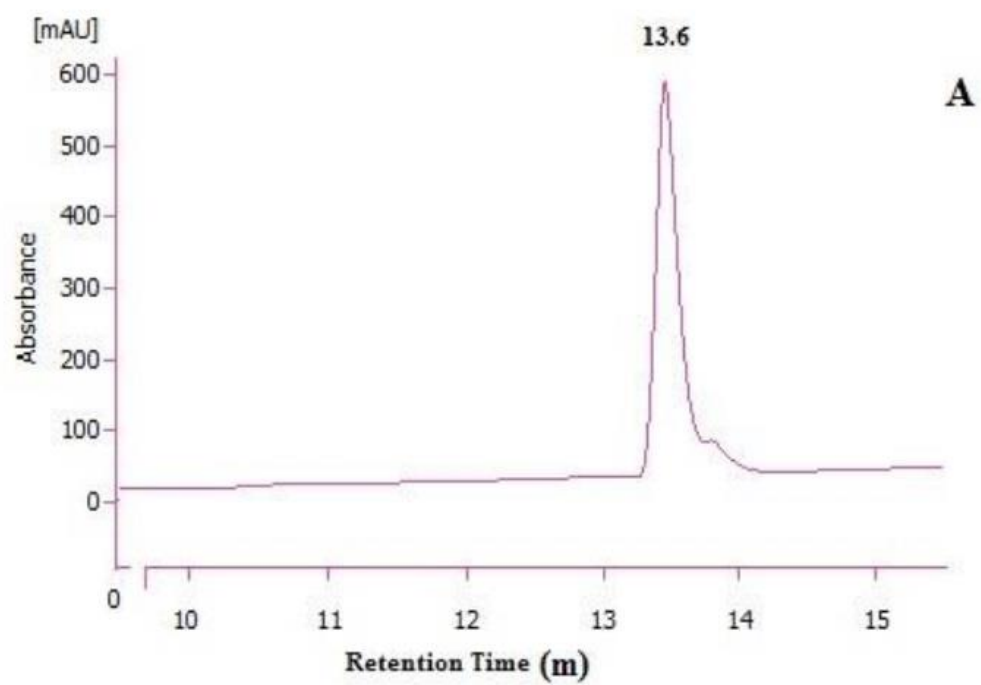
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Table S9. The labels, origins and geographic coordinates of studied ecotypes of *P. somniferum* L in this research.

No.	Label	Origin	above mean sea level (meter)	Longitude (degrees minutes seconds)	Latitude (degrees minutes seconds)
1	Ps#1	Iran, Mazandaran, Yoush	2598.3	51° 42' 6.286"	36° 10' 19.720"
2	Ps#2	Iran, Hamedan, Nahavand	1529.0	48° 16' 16.554"	34° 16' 26.883"
3	Ps#3	Iran, Fars, Komareh sorkhi	1855.6	53° 17' 11.486"	29° 26' 9.231"
4	Ps#6	Iran, Zanjan, Abhar	1520.9	49° 14' 14.023"	36° 8' 43.922"
5	Ps#7	Iran, Hamedan, Nahavand	1643.0	48° 21' 42.848"	34° 11' 16.326"
6	Ps#8	Iran, Kermanshah	1357.7	47° 4' 55.182"	34° 19' 2.087"
7	Ps#9	Iran, Lorestan, Kohdasht	1186.9	47° 38' 42.160"	33° 29' 47.888"
8	Ps#10	Iran, Kurdistan, Sanandaj	1482.3	46° 59' 58.551"	35° 18' 17.763"
9	Ps#11	Iran, Lorestan, Aleshtar	1607.1	48° 13' 48.239"	33° 53' 31.094"
10	Ps#12	Iran, West Azarbaijan, Salmas	1367.4	44° 46' 59.181"	38° 11' 14.514"
11	Ps#14	Iran, Kerman	1745.4	56° 58' 50.436"	30° 21' 17.965"
12	Ps#16	Iran, Hamedan, Nahavand	1593.5	48° 20' 23.746"	34° 12' 13.484"

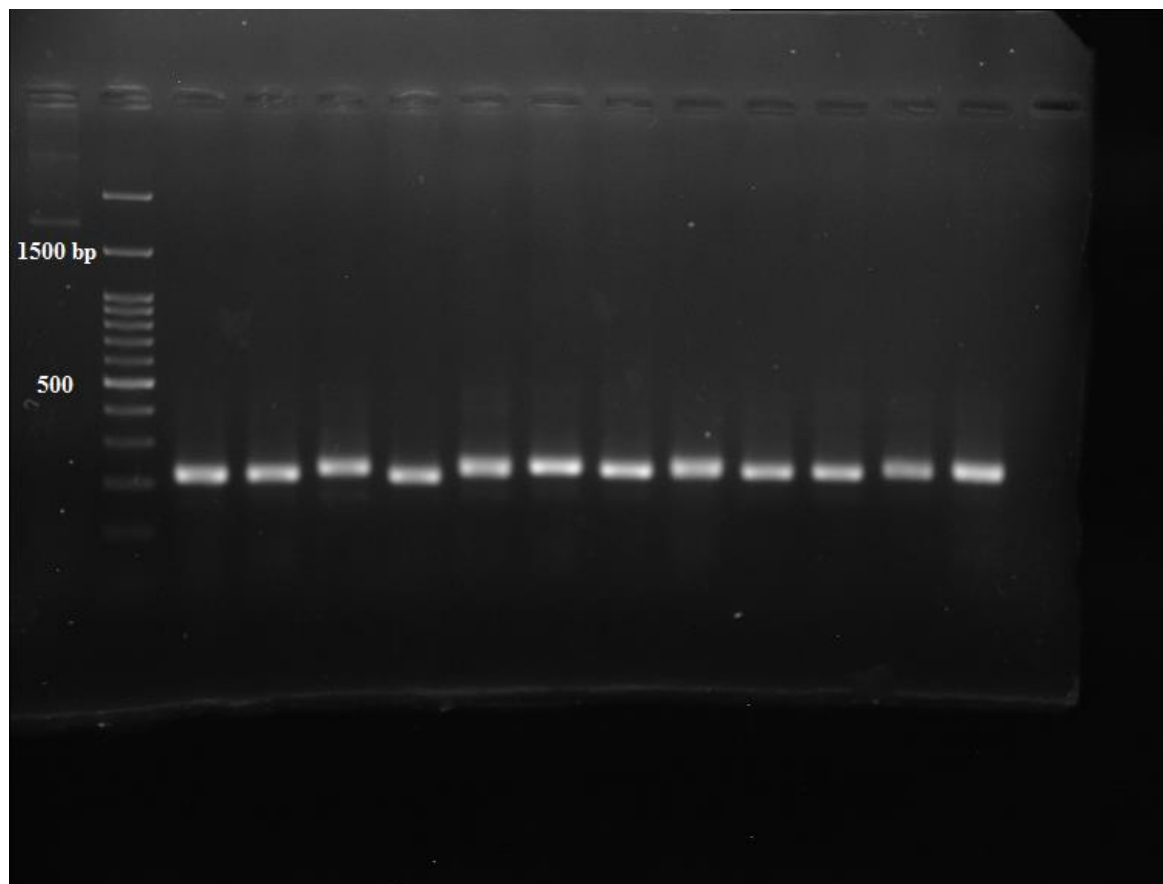
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S10. HPLC chromatograms of noscapine extracted from *Papaver somniferum*. L. The standard sample (noscapine) at 50 ug/ml (**A**) and Ps#12 (**B**), which showed high amount of noscapine into collected ecotypes, are illustrated. The absorption is given in: absorption units (**AU**) and milli absorption units (**mAU**).

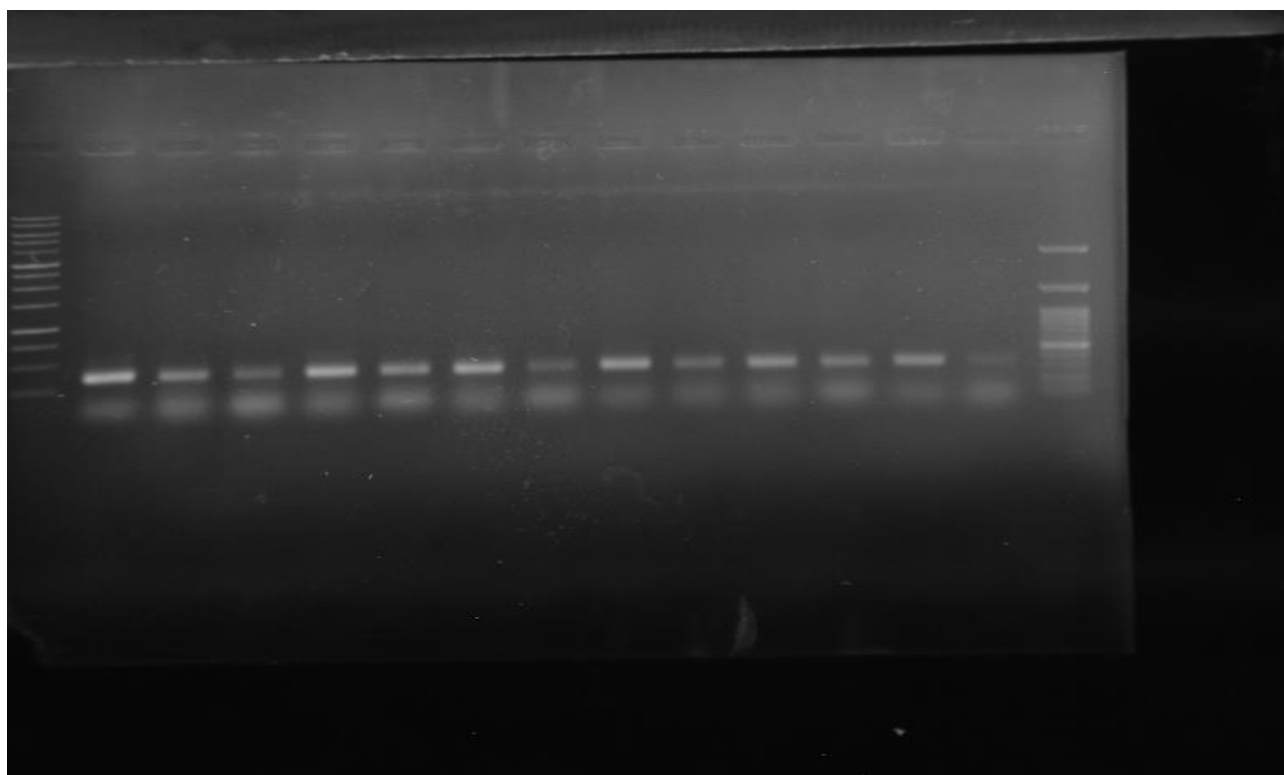


Supplementary Information 10

S11. The full-length of gel pictures sued in the article



Full-length gel of Fig. 1. a



Full-length gel of Fig. 2