SUPPLEMENTARY MATERIALS

Genome-wide identification and expression profile of *TPS* gene family in *Dendrobium officinale* and the role of *DoTPS10* in linalool biosynthesis

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Supplementary table legends

Table S1 Localization was predicted by Plant-mPLoc (http://www.csbio.sjtu.edu.cn/bioinf/plant-multi/).

Table S2 Localization was predicted by AtSubP tool (http://bioinfo3.noble.org/AtSubP/index.php).

Table S3 Localization was predicted by pLoc-mPlant (http://www.jci-bioinfo.cn/pLoc-mPlant/).

Table S4 Secondary structure of DoTPS proteins.

Table S5 Distribution of conserved motifs in *D. officinale* TPS proteins based on the results of MEME analysis.

Table S6 TPS proteins represented in phylogenetic analysis. TPS proteins from *P. equestris* and *A. shenzhenica* were obtained from their genome databases [25]. The other TPS proteins were downloaded from Phytozome version 12.1 database (http://phytozome.jgi.doe.gov/pz/portal.html).

Table S7 The FPKM values of *DoTPS* genes in different *D. officinale* organs.

Table S8 The expression values of *DoTPS* genes in response to 200 mM mannitol treatment for 48 h.

Table S9 The FPKM values of *DoTPS* genes exposed to cold treatment (0°C) for 20 h.

Table S10 The expression values of *DoTPS* genes in response to 200 mM mannitol treatment for 48 h.

Table S11 The expression values of *DoTPS* genes in at three flowering stages of *D. officinale*.

Table S12 Functional annotation of DoTPS with Terzyme (http://www.nipgr.ac.in/terzyme.html).

Table S13 CGTCA-motif, G-box and MYC motif in the promoter region of *DoTPS* genes.

Table S14 Primers used for RT-qPCR analysis, DoTPS10 cloning and its pET32a and YFP vector construction. Gene-specific primers for real-time reverse transcription quantitative PCR (RT-qPCR) were designed by the PrimerQuest tool (http://www.idtdna.com/Primerquest/Home/Index). The *D. officinale* actin gene (*DoEF-1α*) was obtained from NCBI (GenBank accession no. JF825419). F, forward; R, reverse.

Supplementary figure legends

Figure S1 Distribution of conserved motifs in *D. officinale* TPS proteins based on the results of MEME analysis.

Figure S2 Content of geraniol and linalool in *D. officinale* at three flowering stages: budding (B), semi-flowering (S) and full flowering (F). Each bar represents the mean (± standard error, n = 3) of three independent biological replicates. Different letters above the bars indicate significant differences ($p < 0.05$, Duncan's multiple range test).

Figure S3 Gas chromatograms of products yielded by DoTPS10 using GPP as substrate. Each bar represents the mean (± standard error, n = 3) of three independent biological replicates. Different letters above the bars indicate significant differences ($p < 0.05$, Duncan's multiple range test).

Table S1 Localization was predicted by Plant-mPLoc (http://www.csbio.sjtu.edu.cn/bioinf/plant-multi/).

Protein	Subcellular localization
DoTPS1	Chloroplast
DoTPS2	Chloroplast
DoTPS3	Chloroplast
DoTPS4	Chloroplast
DoTPS5	Chloroplast
DoTPS6	Chloroplast
DoTPS7	Chloroplast
DoTPS8	Chloroplast
DoTPS9	Chloroplast
DoTPS10	Chloroplast
DoTPS11	Chloroplast
DoTPS12	Chloroplast
DoTPS13	Chloroplast
DoTPS14	Chloroplast
DoTPS15	Chloroplast
DoTPS16	Chloroplast
DoTPS17	Chloroplast
DoTPS18	Chloroplast
DoTPS19	Chloroplast
DoTPS20	Chloroplast
DoTPS21	Chloroplast
DoTPS22	Chloroplast
DoTPS23	Chloroplast
DoTPS24	Chloroplast
DoTPS25	Chloroplast
DoTPS26	Chloroplast
DoTPS27	Chloroplast
DoTPS28	Chloroplast
DoTPS29	Chloroplast
DoTPS30	Chloroplast
DoTPS31	Chloroplast
DoTPS32	Chloroplast
DoTPS33	Chloroplast
DoTPS34	Chloroplast

Table S2 Localization was predicted by AtSubP tool (http://bioinfo3.noble.org/AtSubP/index.php).

Protein	Chloro	Cyto	Golgi	Mito	Extracl	Nucl	Celmemb	Prediction
DOTPS1	0.41	-1.25	-1.29	-0.43	-1.04	-1.03	-1.25	Chloroplast
DOTPS2	0.86	-1.14	-1.29	-0.56	-1.06	-1.28	-1.27	Chloroplast
DOTPS3	1.22	-1.29	-1.29	-1.05	-1.06	-1.22	-1.19	Chloroplast
DOTPS4	1.06	-1.25	-1.29	-0.84	-1.08	-1.17	-1.35	Chloroplast
DOTPS5	1.40	-0.99	-1.29	-1.59	-1.04	-1.00	-1.36	Chloroplast
DOTPS6	0.70	-1.11	-1.29	-0.51	-1.04	-0.96	-1.38	Chloroplast
DOTPS7	1.36	-0.75	-1.29	-1.47	-1.06	-1.01	-1.40	Chloroplast
DOTPS8	-1.13	-0.92	-1.29	-0.76	-0.73	-0.48	-0.42	Unknown
DOTPS9	1.82	-1.18	-1.29	-1.62	-1.08	-1.21	-1.37	Chloroplast
DOTPS10	1.20	-1.42	-1.29	-0.93	-1.06	-1.19	-1.35	Chloroplast
DOTPS11	1.35	-0.80	-1.29	-1.21	-1.07	-1.34	-1.08	Chloroplast
DOTPS12	-1.24	1.09	-1.29	-1.74	-0.95	-1.08	-1.22	Cytoplasm
DOTPS13	1.29	-0.68	-1.29	-1.68	-1.06	-1.04	-1.14	Chloroplast
DOTPS14	1.01	-0.98	-1.29	-1.37	-1.05	-1.08	-1.07	Chloroplast
DOTPS15	1.85	-1.01	-1.29	-1.83	-1.10	-1.33	-1.17	Chloroplast
DOTPS16	1.41	-0.96	-1.29	-1.43	-1.06	-1.11	-1.10	Chloroplast
DOTPS17	1.03	-0.70	-1.29	-1.12	-1.06	-0.97	-1.26	Chloroplast
DOTPS18	1.32	-0.99	-1.29	-1.52	-1.05	-1.15	-1.19	Chloroplast
DOTPS19	0.90	-1.04	-1.29	-0.87	-1.02	-0.99	-1.22	Chloroplast
DOTPS20	0.40	-1.32	-1.29	0.00	-1.04	-1.12	-1.40	Chloroplast
DOTPS21	1.19	-1.38	-1.29	-0.97	-1.05	-1.19	-1.28	Chloroplast
DOTPS22	1.54	-0.98	-1.29	-1.52	-1.06	-1.14	-1.44	Chloroplast
DOTPS23	1.50	-1.03	-1.29	-1.59	-1.06	-1.21	-1.21	Chloroplast
DOTPS24	0.54	-0.96	-1.29	-0.73	-1.00	-1.04	-1.07	Chloroplast
DOTPS25	1.13	-1.39	-1.29	-1.23	-1.00	-1.06	-1.27	Chloroplast
DOTPS26	1.21	-0.65	-1.29	-1.47	-1.08	-0.96	-1.21	Chloroplast
DOTPS27	1.44	-1.40	-1.29	-1.33	-1.07	-1.27	-1.15	Chloroplast
DOTPS28	1.28	-1.44	-1.29	-1.19	-1.02	-1.11	-1.28	Chloroplast
DOTPS29	1.33	-1.04	-1.29	-1.06	-1.10	-1.17	-1.33	Chloroplast
DOTPS30	0.87	-1.25	-1.29	-1.08	-1.03	-1.18	-1.28	Chloroplast
DOTPS31	1.49	-1.34	-1.29	-1.32	-1.09	-1.32	-1.28	Chloroplast
DOTPS32	1.15	-1.28	-1.29	-1.05	-1.09	-1.20	-1.24	Chloroplast
DOTPS33	0.77	-1.15	-1.29	-0.72	-1.04	-1.15	-1.15	Chloroplast
DOTPS34	1.50	-1.56	-1.29	-1.30	-1.06	-1.22	-1.35	Chloroplast

Prediction approach followed the best hybrid-based classifier (AA+PSSM+N-Center-C+PSI-BLAST). Chloro, chloroplast; Cyto, cytoplasm; Mito, mitochondrion; Extracl, extracellular; Nucl, nucleus; Celmemb, cell membrane.

Table S3 Localization was predicted by pLoc-mPlant (http://www.jci-bioinfo.cn/pLoc-mPlant/).

Protein	Subcellular localization
DoTPS1	Cytoplasm
DoTPS2	Chloroplast
DoTPS3	Chloroplast
DoTPS4	Chloroplast
DoTPS5	Cytoplasm
DoTPS6	Cytoplasm
DoTPS7	Cytoplasm
DoTPS8	Cytoplasm
DoTPS9	Cytoplasm
DoTPS10	Cytoplasm
DoTPS11	Cytoplasm
DoTPS12	Cytoplasm
DoTPS13	Chloroplast
DoTPS14	Chloroplast
DoTPS15	Chloroplast
DoTPS16	Cytoplasm
DoTPS17	Chloroplast
DoTPS18	Chloroplast
DoTPS19	Chloroplast
DoTPS20	Chloroplast
DoTPS21	Cytoplasm
DoTPS22	Cytoplasm
DoTPS23	Cytoplasm
DoTPS24	Cytoplasm
DoTPS25	Cytoplasm
DoTPS26	Cytoplasm
DoTPS27	Cytoplasm
DoTPS28	Cytoplasm
DoTPS29	Cytoplasm
DoTPS30	Chloroplast
DoTPS31	Chloroplast
DoTPS32	Chloroplast
DoTPS33	Cytoplasm
DoTPS34	Chloroplast

Table S4 Secondary structure of DoTPS proteins.

	Alpha helix (%)	Extended strand (%)	Beta turn (%)	Random coil (%)
DoTPS1	61.44	5.02	4.39	29.15
DoTPS2	64.45	5.21	3.48	26.86
DoTPS3	68.26	3.29	3.29	25.16
DoTPS4	57.71	6.19	3.50	32.59
DoTPS5	69.09	4.80	3.02	23.09
DoTPS6	74.51	2.96	3.75	18.77
DoTPS7	69.98	4.44	3.73	21.85
DoTPS8	76.56	3.65	0.00	19.79
DoTPS9	70.04	3.61	2.89	23.47
DoTPS10	66.72	3.18	3.18	26.92
DoTPS11	80.95	1.30	1.73	16.02
DoTPS12	79.20	12.80	1.60	6.40
DoTPS13	69.20	3.99	2.36	24.46
DoTPS14	57.71	7.42	3.30	31.57
DoTPS15	70.65	3.80	3.08	22.46
DoTPS16	71.77	3.10	3.10	22.04
DoTPS17	69.82	3.27	3.09	23.82
DoTPS18	70.38	2.33	3.23	24.06
DoTPS19	74.84	2.29	3.95	18.92
DoTPS20	69.24	3.61	3.78	23.37
DoTPS21	63.88	4.01	3.01	29.10
DoTPS22	69.27	4.09	3.37	23.27
DoTPS23	71.10	1.97	3.59	23.34
DoTPS24	64.64	5.86	2.17	27.33
DoTPS25	64.99	5.36	3.02	26.63
DoTPS26	71.04	4.01	3.46	21.49
DoTPS27	66.98	4.19	2.95	25.89
DoTPS28	64.35	5.16	3.06	27.42
DoTPS29	69.09	4.73	3.64	22.55
DoTPS30	72.49	2.84	3.49	21.18
DoTPS31	62.15	5.52	3.59	28.73
DoTPS32	64.07	5.80	4.07	26.05
DoTPS33	72.80	2.74	4.31	20.16
DoTPS34	65.72	4.68	3.68	25.92

Table S5 Distribution of conserved motifs in *D. officinale* TPS proteins based on the results of MEME analysis.

Name	Sequences	E-value	Sites	Width
Motif 1	EPHYSRARKEITKVISLITTJDDIYDVYGTLEELZLFTBAI	$2.3\times e^{-657}$	31	41
Motif 2	BVKGLLSLYEASYLAMPGEDILDEAKEFAKKHLK	$2.7\times e^{-503}$	31	34
Motif 3	KREWKDLCKAYLVEAKWYNNGYIPTLDEYLENAWISIAYPL	$2.8\times e^{-468}$	28	41
Motif 4	FYPPIIKYSCIIFRLYBDJGTSEFEQKRGDVAKSIQCYMKE	$1.0\times e^{-474}$	23	41
Motif 5	NPILLEFAKLDFNMVQSIHQEELKEJSRWWR	$6.4\times e^{-463}$	31	31
Motif 6	EISHALELPLHRRMDRLHARWFI	$9.1\times e^{-331}$	33	23
Motif 7	WKIDAVQQLPEYMKICLLALFNTMNDIANELSKEKGLDILP	$2.4\times e^{-369}$	26	41
Motif 8	EQLELIDSJQRLGVAYHFEEEIKBLLSKJ	$6.1\times e^{-354}$	30	29
Motif 9	SSKPARRSANYQPSVWDDSFIQSLPLPSM	$5.9\times e^{-240}$	22	29
Motif 10	ALLFRLLRZHGYHIS	$5.5\times e^{-212}$	32	15
Motif 11	ELPFARDRLVENYFWALGVYF	$1.7\times e^{-262}$	29	21
Motif 12	EARDKJREMIEKYWKILNREY	$9.8\times e^{-179}$	24	21
Motif 13	FYQYGDGYTEPDHETKDQIISVLIEPIPL	$5.1\times e^{-199}$	21	29
Motif 14	TCASYIGMQEVISKEVFDWVT	$1.3\times e^{-101}$	11	21
Motif 15	LFSSFKDEKGSFKPC	$3.6\times e^{-93}$	24	15
Motif 16	EKQKKRREKLKEEVRKLJDDT	$3.1\times e^{-89}$	23	21
Motif 17	NSNYEESFKKVLIBJPRTAQC	$8.0\times e^{-71}$	12	21
Motif 18	SNLYLSTDFVHNYGFFLPLKIQHSAQSFSSTPYLRLRKKCYSVASN	$8.4\times e^{-73}$	4	46
Motif 19	VLTAAYCLSEDLTKEALNSLE	$1.2\times e^{-69}$	13	21
Motif 20	PVSAYETAWVAMVPDPDDPTSPMFPEYLDWILRNQNBLGFWFDQQHG	$8.3\times e^{-39}$	3	47

Table S6 TPS proteins represented in phylogenetic analysis

Species	Sequence
Abies grandis	>AAF61453
	MALVSSAPKSCLHKSLIRSTHHELKPLRRTIPTLGMCRRGKSFTPSVSMSLTTAVSDDGLQRRIGDYHSNLWDDDFIQSLSTPYGEPSYR
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	RTLRLHGYSVSSEVLKVFQDQNGQFAFSPSTKERDIRTVLNLYRASFIAFPGEKVMEEAEIFSSRYLKEAVQKIPVSSLSQEIDYTLEYGW
	HTNMPRLETRNYLDVFGHPTSPWLKKKRTQYLDSEKLLELAKLEFNIFHSLQQKELQYLSRWWIHSGLPELTFGRHRHVEYYTLSSCI
	ATEPKHSAFRLGFAKTCHLITVLDDIYDTFGTMDEIELFNEAVRRWNPSEKERLPEYMKEIYMALYEALTDMAREAEKTQGRDTLNY
	ARKAWEVYLDSYTQEAKWIASGYLPTFEEYLENAKVSSGHRAAALTPLLTLDVPLPDDVLKGIDFPSRFNDLASSFLRLRGDTRCYKA
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	RRTVLEPVPL
	>AAB71084
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	RTLRLHGYTVSPEVLKAFQDQNGQFVCSPGQTEGEIRSVLNLYRASLIAFPGEKVMEEAEIFSTRYLKEALQKIPVSALSQEIKFVMEYG
	WHTNLPRLEARNYIDTLEKDTSAWLNKNAGKKLLELAKLEFNIFNSLQQKELQYLLRWWKESDLPKLTFARHRHVEFYTLASCIAID
	PKHSAFRLGFAKMCHLVTVLDDIYDTFGTIDELELFTSAIKRWNSSEIEHLPEYMKCVYMVVFETVNELTREAEKTQGRNTLNYVRKA
	WEAYFDSYMEEAKWISNGYLPMFEEYHENGKVSSAYRVATLQPILTLNAWLPDYILKGIDFPSRFNDLASSFLRLRGDTRCYKADRDR
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	DLNSTALALRTLRLHGYNVSSDVLEYFKDQKGHFACPAILTEGQITRSVLNLYRASLVAFPGEKVMEEAEIFSASYLKEVLQKIPVSSFS
	REIEYVLEYGWHTNLPRLEARNYIDVYGQDSYESSNEMPYVNTQKLLKLAKLEFNIFHSLQQKELQYISRWWKDSCSSHLTFTRHRHV
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GGLGVLFEPRYSLARIFLAKLTLIMTVVDDTCDAYATLPEVQSLHDAFHRWDLRAMEELPRYMRIIYQSVFETVEDIDREMIARGKHG
RLQLTIDEIKSLMIWYLGIAKWARSDQVPSFEDYMEIGTPSSALDDFASYGFIAMDDCDQKQLKEWFYSKPKIFHALNALFRIRNDIVT
FEQEMSRGEVANGVNCYMKQHGVTKEAAVEELRKMERESYKIMIEEFMAMPRQILVRPVNIARVMDLFY
>AtTPS30
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PTLGLYFEPRFSLGRIIIAKMTIIVVALNDVCDSYATYPEAKSLIDSLQRWDIEAIDELPNYSRIVLRLILETIGEIEREMKPRGRSASVQHTI
DETKSLGRAYLALSKWASEGYMPTFDEYMEVGEVTGGMDDFALYSFIAMEDCDEKPLYEWFDSKPKILQALSVLYRINNDIVTYERE
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>AtTPS31
ARCSHVQDIDDTAMAFRLLRQHGYQVSADVFKNFEKEGEFFCFVGQSNQAVTGMFNLYRASQLAFPREEILKNAKEFSYNYLLEKRE
RELIDKWIIMKDLPGEIGFALEIPWYASLPRVETRFYIDQYGGENDVWIGKTLYRMPYVNNNGYLELAKQDYNNCQAQHQLEWDIF
QKWYEENRLSEWGVRRSELLECYYLAAATIFESERSHERMVWAKSSVLVKAISSSFSSDSSFDQFHEYIANARRSDHNDRNDRPVQAS
RLAGVLIGTLNQMSFDLFMSHGRDVNNLLYLSWGDWMEKWKLYGDEGEGELMVKMIILMKNNDLTNFFTHTHFVRLAEIINRICLP
RQYKARRNDEKEKTIKSMEKEMGKMVELALSESDTFRDVFLDVAKAFYYF
>AtTPS12
DITGDEKDLSTISIMFRVFRTYGHNLPSSVFKRFTGDDGKFQQSLTEDAKGILSLYEAAHLGTTTDYILDEALKFTSSHLKSLLAGGTCRP
HILRLIRNTLYLPQRWNMEAVIAREYISFYEQEEDHDKMLLRLAKLNFKLLQLHYIKELKSFIKWWMELGLTSKWPSQFRERIVEAWL
AGLMMYFEPQFSGGRVIAAKFNYLLTILDDACDHYFSIHELTRLVACVERWSPDGIDTLEDISRSVFKLMLDVFDDIGKGVRSEGSSYH
LKEMLEELNTLVRANLDLVKWARGIQTAGKEAYEWVRSRPRLIKSLAAKGRLMDDITDFDSDMSNGFAANAINYYMKQFVTKEEAI
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>AtTPS13
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HILRLIRNTLYLPQRWNMEAVIAREYISFYEQEEDHDKMLLRLAKLNFKLLQLHYIKELKTFIKWWMELGLTSKWPSQFRERIVEAWL
AGLMMYFEPQFSGGRVIAAKFNYLLTILDDACDHYFSIPELTRLVDCVERWNHDGIHTLEDISRIIFKLALDVFDDIGRGVRSKGCSYY
LKEMLEELKILVRANLDLVKWARGNQLPSFEEHVEVGGIALTTYATLMYSFVGMGEAVGKEAYEWVRSRPRLIKSLAAKGRLMDDIT
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>AtTPS1
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SPHILMRIRNALCMPQHYNAEMIFAREYISFYEQEEDHNKMLLRFAKINFKFLQLNWIQELKTLTKWWKQQDLASKLPPYFRDRLIEC
YLFAIMIYFEPQFSLGRVSLAKINTVFTLVDDTCDRYGNVSEVAALVQCVERWDPDCMDSLPDYMKTVFKFAWNTFEECENAGIMEE
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GFDVNAIMYYMKQYKVTEEETFTRLQKMARDLDTTVNEEILSVPRQILKRAIDFGKMIEFTY
>AtTPS2
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EDETYILEMVKRALETPYHWSIRRLEARWYINVYEKKHEMNPLLLEFAAIDFNMLQANHQEELKLISSWWNSTGLMKQLDFVRDRIT
ESYFWTIGIFYEPEFKYCRKILTKIFMLIVIMDDIYDIYGTLEELELFTNVVEKWDVNHVERLPNYMRMCFLFLYNEINQIGYDVLRDKG
LNVIPYLKQVWTDLFKTFLTESKWYKTGHKPSFEEYMQNGVISSSVPTILLHLFSVLSDHISDQTLTDDSKNHSVVRSCATILRLANDLA
TSTEEMARGDSPKSVQCYMYETRASEEEARRHMQSMISDSWDIINSDLKSLPRGFLAAAANLNRVVQCIY
>AtTPS3
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LRRMVIHALEMPYHRRVGRLEARWYIEVYGERHDMNPILLELAKLDFNFVQAIHQDELKSLSSWWSKTGLTKHLDFVRDRITEGYFS
SVGVMYEPEFAYHRQMLTKVFMLITTIDDIYDIYGTLEELQLFTTIVEKWDVNRLEELPNYMKLCFLCLVNEINQIGYFVLRDKGFNVI
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ARGDTMKSVQCHMHETGASEAESRAYIQGIIGVAWDDLNMESCRLHQGFLEAAANLGRVAQCVY
>AtTPS7
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>AtTPS8
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>AtTPS9
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>AtTPS21
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HLAIRIKNALKHPYHKGISRIETRQYISYYEEEESCDPTLLEFAKIDFNLLQILHREELACVTRWHHEMEFKSKVTYTRHRITEAYLWSL
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>AtTPS11
DLIADENKLHTISTIFRVFRTYGYYMSSDVFKIFKGDDGKFKESLIEDVKGMLSFYEAVHFGTTTDHILDEALSFTLNHLESLATGRRASP
PHISKLIQNALHIPQHRNIQALVAREYISFYEHEEDHDETLLKLAKLNFKFLQLHYFQELKTITMWWTKLDHTSNLPPNFRERTVETW
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Dendrobium officinale	>DoTPS34 NNSNEENNLNGSALLFRLLREHGINNASMLRVNALISCFKKEREKLNQNDEHNVKGMLSLYEASYLAVEGEEELEEAGKLAMEHLKCIDGSLFTQQFIEEIDHALELPLHWRMSRLHTRWFIDAYGRRENFNPTLLELAKLDFNMVQSIYKAELQELSMWWRNLGLVCEELDFVRDRLVENYLISLGITFQPNFARCRKAITKIISLVTTIDDIYDIYGTLDELKLFTNTIEEWKIDTSQQLPDYMKMCWIAIFNTMNDIATSFSMEKALDILPCLKRVWVDLCKSQLLEAKWYHNGYTPTLDEYLENAWVSTSGHCELTAAYCLSDDLTIESLNSLEFYPPIIRYSCILFRLYDDLQTSKEEMKRGDVPKSIQCYMKEKNVSESIARDYIKCLITIYWKKLNQECTTISKLWEPFRNALVGFPRTAQCFY >DoTPS19 SNIIKNNLHYSSLLFRLLREYNIKVPNQSEDFFVRSFKNESGRFNINIMNDVKGMLSLYEASYLAVQGEDDLDDAVEFTTKHLSNYLKEPLLINPLLVEEISHALELPLHWRMSRLHTMWFIDAYERQENMNPYLLEFAKLDFNIVQTIYKKELKEISRWWRSIGLVGDDFSFARDRLMETYLWSVGCAFEPRFWRCRKEITKLGCLITTIDDIYDVYGSLEELVFFTNVVDEWKIAESQHVSTCMKTVLLALFNTVNDIARTISTEKGIDILPHLKRLWGDLCKSYLMEAIWYYIGYIPTINEYMQNAWLSISAPLILTSAYCLSEDLTIEALNSLELYIDATLHSSMITRLYDDLGTSTVRTIMLLYNIYIYI >DoTPS28 NNLIENNNLHDFALLFRLVREHDIHNASILRLDDLISCFKNEEESFNQNNQLDVKGMLNLYEASFLAMEGEDELDEAGKFAMKHLKYHDRSLLSPQLVEQIEHALELPLHWRMSRLHTRWFIDAYGRHKNFNPTLLEFAKLDFNMVQSIYKTELQELSRWWRNINVVRGGLNFVRDRLVENYLWAIGFTFQPELWRIRKAMTQIISFITTIDDIYDIYGTLDELKLFTNAIEAWNIATTQQLPGYMKKCLTTLFNTMDDIASSFSKEKELDILPCLKRMWADLCKAYFIEAMWYHNGYTPTLDEYLDNAWVTISGICVLTATYCLSDDLTFEAIKSLEFYPPIVRYSCMLLRLYDDLGTCTEEIQRGDVPKSIQCYMKEKNVSETTARDYIRCLIRNYWKKLNKEHVISSKYVESFRKVLFDIPRTAQCFY

>DoTPS10
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LDRSLLSPQLIEEIDHALELPLHWRMPRLHSRWFIDAYGKQENVNPILLELAKLDFNIVQSIYMTELKEISNWWRNLGVLCDELDFIRD
RLVENHLWALGFTFQPKFWRSRKAITKINCLVTTIDDVYDVYGTLDELEIFTNAVEDWKMDAAQQLPNCMKICLMALFNTMNEVA
YSFLKEKELDILPCLKRVWVDLCKAYLIEARWYHNRYTPTLDEYLENAWVTISGNCGLSASYCLSDDLNVEALDSIKFYPPIVQHSCMI
FRLYNDLGTDMAEIQRGDVLKSIQCYMNEKNVSDSAARDYIRCLIRNYWKKLNGEYITFSTSIESFRKALVDVPRTAQSFY
>DoTPS21
NNLIKNNNLYGSALLFRLLREHGINNGAILRVDTLMSCFKKVRESFNPNHQYDVKELLSLYEASYLAMEGEEELDEAGKFAMEHLRR
LDRSLLSPQLIEEIDHALELPLHWRMPRLHSRWFIDAYGKQENVNPILLDLAKLDFNIVQSIYMTELKEISNWWRNLGVLCDELDFIRD
RLVENHLWALGFTFQPKFWRSRKAITKINSLVTTIDDVYDVYGTLDELEIFTNAVEDWKMDAAQQLPNCMKICLMALFNTMNDIAY
SFLKEKGLDILPCLKRVWVDLCKAYLIEARWYHNRYTPTLDEYLENAWVTISGICELSASYCLSDDLNVEALDSINFYPPIVQHSCMIFR
LYNDLGTDMAEIQRGDVLKSIQCYMNEKNVSDSAARDNIRCLIRNYWKKLNGEYMTFSTSIESFRKALVDVPRTAQSFY
>DoTPS27
RMEFNGDVYAMALYFRLSRQHGFEISKDLLVKSYKYESGCFKPSVFDNIKGMLSLYEASFLAMDGEEEIDDAKEFALKHLNDFMRSN
SSTNPLLAQHIAMALELPLHHRIPKFQSQMFIEHSRHIKEINVDSIVLELGQLEFNMTQSIYKRELKEISKWWAEVSNVFDSKLNFARD
WPVESYFLAVGMAVEPQFSTYRKELAKALCFINVIDDIYDIYGLLDELQLFTNAVDRWEFASIKSLPEYMKICLEGLFNMVNSLASKIK
EEKGLDVLPNLKRAWLDLCKAYMVEARWCHTGYCPTFEEYLDNAWISVSTPLLSVISHCLSENLTKLSLESFDFYPTIVRQSSIIFRLYN
DLGTSKGELQRGDVSKSIQCYMKENHVSELVAQECIRNIINKNWKELNREWIKGSIYDETFKTVAINIPRAGHLMY
>DoTPS2
RMEFTEDVNFKALYFRLSRERGFEVSKDLLVKSYKDEKGCFKPCVFHDIKGLLSLYEASFLSMDGEDEIDEAKEFALKHLNDCMRSNS
LTNPALAKHIALALELPLHHRIQKLQAPMFIEHARNMKELDVDPILLEFAQLDFNMTQNIYNKELKEITRWWTKISNLAGGELSFARE
WPVESYFLAVGVAMEPRFSTCRKEFAKAICFINVVDDIYDIYGSLDELQLFTDAIERWDFSTSKSLPEYMKICLSELFNTMNSLACKIME
EKGLNILPYLKRAWLDLCKAYMVEVRWYYNGYCPTFAEYLDNAWISVAAPLGSVMTLCLSENLTNLSLEGFDFYPSIIRQSSIIFRLYN
DLGTSKGELRRGDVSKSLQCYMKEKHVSELEAQKCMKSIINKCWKELNREWIKASRYEETFKMVAINLPRVAHLFY
>DoTPS3
RMEFTEDVHVMALYFRLSREHGFEVSKDLLVKSYKDEKGCFKPCVFHDIKGLLSLYEASFLSMEGEDEIDEAKEFALKHLNDCMRSNS

STNLILAKHIALALELPLHHRIQKLQAPMFIEHARNMKELDVDPILLEFAQLDFNMTQSIYNRELKEITRWWTKISNLAGGELSFARE
WPLESYFLAICLAMEPRFSTCRKEFAKAVCFINVVDDIYDIYGSLDELQHFTDAVEMWDFATSKSLPKYMKICLSELFNTVNNLACKI
MEDKGLDILPYLKRAWLDLCKAYMVEATWYYIGYCPTFDEYLDNAWISVAAPLTSVMALCLSENLTNLSLESFDFYPSIIRQSSIIFRLC
NDLGTSKGELRRGDVSKSIQCYMKEKHVSESEAQKCIRTIIDKCWKDLNNEWMEASKYEETFKMVVINLPRVAHLFY

>DoTPS24

RMEFTEDVHVMALYFRLSREHGFEVSKDLLVKSYKDEKGFFKPYVFHDIKGLLSLYEASFLSMDGEDEIDEAKEFALKHLNDCMRSNS
TTNPLLAKHIALALELPLHHRIQKLQAPMFIEHARNMKELDVDPILFEFAQLDFNMTQSIYNRELKEITRWWAKISNLAGGELSFARE
WPLESYFLAVGLAIEPYFSTCRKEFAKAICFINVIDDIYDIYGSLDELQHFTDAVERWDFATSKSLPQYMKICLSELFNTVNSLACKIMK
DKGLDILPYLKRAVKLLKLLKIFKVLFL

>DoTPS20

SNILKNSLHGSALLFRLLREYGIKALNTREDFLVRSFKNENGSFKVHIVNDVKGMLSLYEASYLSVEGEDDLDEAMEFTTKHLSNYLKE
PSLIHPSLVEQISHALHLPLHWRMPTLHTMWFIDTYEKQENTNYSLFEFAKLDFNMVQSIYKKEVKEMSSWWRSIGLAGDEFSFARDR
LMENYFWAMGCALEPHFWRCRKEITKLVSIITTIDDIYDTYGSIEELVLFTNAVDEWKIIEIQSLPNCMRKALLTLINTMNEIAFAFSKE
KGLDILPQLKRPWGYQCKAYLVEAIWYNTRYIPTLNEYMENAWLSIGTALVLTVAYLLSEDLTKEALNSLELYFDVTRYSCMITRLYD
DLGTSKDELQRGDVPKSIQCYMNETNVLEFVARDHIRQLIKKYWKLLNGEYFSNFNLEESFKRYALNLPRMTQCIY

>DoTPS1

CKEVILCGLRSTAICFQLLRRFGFQISEGIFDDFMDGDHNAFLPTLSDDVIGLLSLYNASYMAFPGENKMESARSFAVKHMNRENMQE
ILPGSIESAIGHALDLPLHRRMPWMEARMYIDMYELEDDMSPPLLHLAKIHFNKVQSIHQKELKHAGSWWRRLDLGKTINFSRDRLM
ECFFYVVGIVHHPDYGFCREKLTQVGRSGHRPGRSVQIKEDRPEHRPGCKTGRLKIGLIVQADLTIILADHFKSEK

>DoTPS33

YKEVILCGLRSTAICFQLLRRFGFQISEGIFDDFMDGDHNTFLPTLSDDLIGLLSLYNASYMAFPGEKKMESARSFALKNMTRKNMQEI
LPGSIESAIGHALDLPLHRRMPWMEARMYIDMYELEDGMSPALLHLAKIHFNKVQSIHQKELKHAGSWWTRLDLGKTISFSRDRLM
ECFFYVVGIVHHPDYGFCREKLTQVGMLIATIDDVYDVYGSLEELELFTQIIDRWDIKGVVELPYYMKICFSALNDTINGVANHLYAD
DRFNILQWADLFKSFLVEAKWHKKGYIPTLKEYLSNASISAAGHVILFLAYILLKCKITKETLQLLQDFPNIIRLPSLIFRLCNDLATSSNI
QVEQERGDVATSVQCYMKETGASEEEARLYISMLISDAWNDMNEEYSTCSKPQFPQRFIDASINLARMASFMY

>DoTPS25

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TPS proteins from *P. equestris* and *A. shenzhenica* were obtained from their genome database [25]. The other TPS proteins were downloaded from Phytozome version 12.1 database (http://phytozome.jgi.doe.gov/pz/portal.html).

Table S7 The FPKM values of *DoTPS* genes in different *D. officinale* organs.

Gene ID	Fb	Se	La	Po	Gs	St	Le	Ro	Rs	Rw
DoTPS1	1.2173	12.3391	1.7087	0.0947	0.1462	0.0000	0.0506	0.0000	0.0000	0.0000
DoTPS2	0.6080	5.9884	3.2341	0.0000	1.5680	0.9939	0.0319	0.3406	0.1358	0.0000
DoTPS3	8.3954	34.6934	17.0447	0.0000	7.0096	8.1833	0.0000	2.3638	0.3534	0.1604
DoTPS4	1.8939	1.3733	1.1464	0.0000	4.1851	3.5203	0.3542	7.8949	23.4339	16.4147
DoTPS5	0.7914	13.2949	152.6900	0.0448	2.5230	0.0000	0.1076	9.6566	0.8778	15.8660
DoTPS6	0.0400	0.0000	0.0421	0.0000	0.0000	0.0000	0.0000	0.7572	3.9059	0.0000
DoTPS7	0.4317	14.0691	49.8742	0.0895	1.2788	0.2708	9.2217	3.6585	0.9160	0.6236
DoTPS8	9.4823	6.6341	11.0165	0.5050	23.4320	5.9896	0.5539	1.3638	1.1329	0.6170
DoTPS9	4.0618	0.2621	0.0211	0.0374	4.0561	1.2428	0.0000	7.9739	4.5215	7.8422
DoTPS10	0.0000	1028.7356	3268.7298	0.0632	145.0056	0.0956	0.0676	0.0000	0.0000	0.0000
DoTPS11	0.0000	0.0000	0.0000	0.0000	0.0000	0.0823	0.0000	0.0000	0.0000	0.0000
DoTPS12	0.0000	0.0000	0.1695	0.0000	0.0000	0.0000	0.0000	0.1904	2.0500	0.0000
DoTPS13	0.0000	0.1373	0.0000	0.0228	0.0000	5.2483	0.1830	7.2889	3.1529	0.7420
DoTPS14	3.3417	2.8140	2.2112	3.4162	2.7519	1.5051	0.6905	4.7703	3.8745	2.8503
DoTPS15	0.0000	0.0000	0.0772	0.0000	0.0000	0.0000	0.0000	6.8117	24.9504	0.6713
DoTPS16	0.2951	0.0000	4.8930	118.7210	2.5872	0.0694	0.0000	0.0000	0.0783	0.0710
DoTPS17	0.0000	0.1034	0.0000	0.0000	0.4953	759.8893	22.0740	0.0000	0.0781	0.5673
DoTPS18	0.0727	0.0680	1.3780	0.3394	0.5240	0.0000	0.2176	14.4042	1.3501	0.2451
DoTPS19	0.0842	4.0566	14.2685	0.0000	9.7867	78.5955	0.6298	0.3982	0.0447	0.0000
DoTPS20	2.0532	6.7076	29.2717	0.3681	14.9119	6.1246	18.3284	2.9219	0.5169	0.8713
DoTPS21	0.0390	100.6108	2716.5036	0.0243	81.5684	0.0000	0.0000	0.0000	0.0000	0.0376
DoTPS22	0.0719	15.6847	616.6676	0.0000	5.2533	0.0000	0.0000	16.0802	10.3427	68.1060
DoTPS23	0.1091	16.3636	61.3193	1.1765	38.9150	0.1711	0.4715	7.7396	1.5816	0.3501
DoTPS24	0.3074	219.5391	153.9008	0.0273	18.3111	0.2480	0.0438	4.6220	0.6057	0.4229
DoTPS25	19.2802	4.3919	0.0817	0.0000	3.5780	6.8637	0.0387	93.8604	23.4594	19.3139
DoTPS26	0.0369	0.0000	1.2815	1.9052	0.6734	0.0000	0.0000	0.0436	0.0000	0.0000
DoTPS27	0.0000	7.6697	3.0748	0.0000	0.3319	0.0000	0.0313	0.0000	0.0333	0.0000
DoTPS28	260.6178	29.7739	0.9286	0.0203	27.5280	3.6897	0.3585	12.3247	7.6256	8.0543
DoTPS29	0.8101	0.0345	0.0388	0.0458	0.0000	0.2426	0.0000	0.0000	0.9766	0.0355

DoTPS30	0.2087	0.1562	0.3955	0.0000	0.1203	0.3536	0.0000	18.7103	4.4290	9.8092
DoTPS31	28.8962	19.5584	38.1274	68.4811	38.0720	29.1411	16.1677	23.9266	19.2718	24.4360
DoTPS32	13.7093	6.9285	5.0302	9.2781	10.4072	32.5144	24.9788	41.6248	37.2907	25.5609
DoTPS33	1.7942	6.8443	0.8718	0.0286	0.8840	2.6845	0.2753	0.0000	0.0000	0.2215
DoTPS34	0.7452	0.0634	0.1070	0.0211	0.4230	0.1275	0.0000	13.9790	1.1140	33.6942

All FPKM values were downloaded from NCBI under BioProject PRJNA262478 [25].The different tissues were sepals (Se), labellum (la), green root tips (Rt), roots (Ro), white part of roots (Rw), pollinia (Po), flower buds (Fb), gynostemium (Gs), stems (St) and leaves (Le) in two-year-old *D. officinale* adult plants.

Table S8 The expression values of *DoTPS* genes in response to 200 mM mannitol treatment for 48 h.

GeneID	Mannitol-0h	Mannitol-12h	Mannitol-24h	Mannitol-48h
DoTPS1	0.1276	0.1598	0.0000	0.0000
DoTPS2	0.3753	0.3901	0.5617	0.2568
DoTPS3	0.3959	0.1410	0.0564	0.0580
DoTPS4	0.0052	0.0223	0.0877	0.0476
DoTPS5	1.3909	1.8039	1.7631	2.1192
DoTPS6	0.0752	0.0559	0.0333	0.0238
DoTPS7	0.0803	0.4008	0.4808	0.3799
DoTPS8	1.4286	0.0000	0.1358	0.0000
DoTPS9	0.0764	0.0954	0.0763	0.0784
DoTPS10	0.3944	0.6160	0.2956	0.4044
DoTPS11	0.1605	0.1372	0.0016	0.0067
DoTPS12	0.0000	0.0003	0.0003	0.0000
DoTPS13	1.2635	1.1821	2.8364	0.1297
DoTPS14	0.0000	0.4826	0.1544	0.0000
DoTPS15	0.0674	0.0873	0.3506	0.1410
DoTPS16	3.2468	0.0000	0.2592	0.0666
DoTPS17	1.6198	1.3183	1.8725	2.0104
DoTPS18	7.9091	1.2334	0.7234	0.2029
DoTPS19	0.0072	0.0000	0.0000	0.0000
DoTPS20	0.0000	0.0000	0.1637	0.0000
DoTPS21	1.0867	1.0439	1.0018	0.7717
DoTPS22	0.0994	0.0000	0.0000	0.0000
DoTPS23	2.0970	0.1539	0.0615	0.0000
DoTPS24	0.3125	0.2748	0.2256	0.0000
DoTPS25	2.4727	2.2591	1.7555	1.8702
DoTPS26	0.0036	0.0030	0.0000	0.0000
DoTPS27	0.1819	0.0567	0.0000	0.1400
DoTPS28	0.1157	0.1900	0.1350	0.1482
DoTPS29	0.0000	0.9553	4.0462	2.3205
DoTPS30	0.1083	0.1157	0.1886	0.1455
DoTPS31	0.3650	0.2843	0.0910	0.0937
DoTPS32	0.2708	0.0000	0.0000	0.0926
DoTPS33	0.0569	0.0637	0.0965	0.1391
DoTPS34	0.0000	1.9598	0.2137	2.7829

Table S9 The FPKM values of *DoTPS* genes exposed to cold treatment (0°C) for 20 h.

Gene ID	CK1	CK2	CK3	CA1	CA2	CA3
DoTPS1	0.2354	0.0000	0.0000	0.0000	0.0000	1.4929
DoTPS2	0.0000	0.0000	0.0000	0.1970	0.0655	0.0000
DoTPS3	0.0244	0.0000	0.0000	0.8976	0.1642	0.1211
DoTPS4	0.5900	0.3483	0.2700	0.0000	0.0494	0.0000
DoTPS5	0.0577	0.0000	0.0633	12.4024	0.0000	0.0648
DoTPS6	0.0000	0.0000	0.0000	0.0278	0.0000	0.0000
DoTPS7	2.6395	3.4961	2.5775	3.7131	1.8002	4.8149
DoTPS8	0.2326	0.1741	0.2829	0.1317	0.1332	0.0485
DoTPS9	0.0000	0.0000	0.0000	1.1013	0.8665	0.7629
DoTPS10	0.0572	0.0000	0.5597	0.0000	0.0000	5.2860
DoTPS11	1.6998	0.5873	0.9166	5.1072	2.2991	2.4442
DoTPS12	0.0000	0.0000	0.0000	0.0648	0.0633	0.0577
DoTPS13	0.1689	0.0000	0.0371	0.0402	0.0000	0.0000
DoTPS14	0.6177	0.4155	0.4545	1.6973	1.8028	1.0530
DoTPS15	0.0000	0.1376	0.3573	0.0000	0.2571	0.2266
DoTPS16	0.1834	0.0000	0.0965	15.0021	3.5563	4.0863
DoTPS17	0.0000	0.0000	0.0000	0.0268	0.0000	0.0100
DoTPS18	0.9556	0.6541	0.4678	1.2828	1.0808	1.0943
DoTPS19	0.1200	0.0229	0.1218	0.1151	0.1200	0.1753
DoTPS20	1.2828	0.6541	0.4678	0.9556	1.0808	1.0943
DoTPS21	1.2114	0.4076	1.3413	3.3646	2.1892	1.5833
DoTPS22	0.0000	0.0000	0.0000	0.0260	0.0260	0.0000
DoTPS23	0.8701	0.9705	0.7816	0.0611	0.5352	0.0100
DoTPS24	0.0000	0.0000	0.0000	0.1234	0.0274	0.0900
DoTPS25	0.2291	0.1046	0.0000	0.0645	0.2141	5.5846
DoTPS26	0.0258	0.0800	0.0500	0.0000	0.0000	0.0000
DoTPS27	0.0000	0.0000	0.0000	0.0220	0.0000	0.0204
DoTPS28	0.0257	0.0453	0.0239	0.5664	0.3466	0.3113
DoTPS29	0.2685	0.1499	0.2396	12.2277	1.1678	0.1228
DoTPS30	0.0000	0.0000	0.1712	0.5352	0.8701	0.7816
DoTPS31	8.4991	7.3799	7.5907	12.3982	14.3222	10.5718
DoTPS32	14.8624	10.7031	11.3577	11.9571	11.8444	13.2613
DoTPS33	0.0900	0.0374	1.1500	0.0000	0.0000	0.0000
DoTPS34	0.0000	0.0414	0.0000	0.2396	0.1499	0.2685

All FPKM values were retrieved from a reported transcriptome database [29]. Treatments was made up of cold acclimation (0°C for 20 h, CA) and non-acclimation (20°C for 20 h, CK).

Table S10 The expression values of *DoTPS* genes in response to 200 mM mannitol treatment for 48 h.

Gene ID	MeJA-0 h	MeJA-12 h	MeJA-24 h	MeJA-48 h
DoTPS1	0.1933	1.6602	1.1917	0.0750
DoTPS2	0.8195	13.8851	8.6327	2.4095
DoTPS3	6.1303	39.9956	16.9366	4.3490
DoTPS4	1.2011	21.9405	20.1309	0.4633
DoTPS5	0.4101	1.2579	1.2293	0.8729
DoTPS6	0.0361	0.3785	0.6501	0.0916
DoTPS7	0.1185	2.7562	1.8431	0.3405
DoTPS8	23.5785	67.9417	85.4984	33.8374
DoTPS9	0.8135	36.7045	21.6445	2.4708
DoTPS10	0.5484	13.8014	20.4691	0.5889
DoTPS11	0.1555	0.1789	0.1521	0.0499
DoTPS12	0.1481	0.1598	0.1419	0.0958
DoTPS13	26.8832	156.4808	140.3864	47.9339
DoTPS14	0.1290	0.8303	0.4973	0.1922
DoTPS15	0.1598	0.5396	0.6297	0.2608
DoTPS16	0.4317	3.5311	4.6591	0.3621
DoTPS17	2.5886	5.6565	4.4752	3.8197
DoTPS18	9.7912	35.5316	30.2294	5.3614
DoTPS19	0.5337	0.9874	0.4997	0.5743
DoTPS20	0.2734	0.3123	0.7531	0.1291
DoTPS21	0.7547	25.4705	34.7946	0.6974
DoTPS22	1.5664	10.0653	6.8606	0.2356
DoTPS23	5.7882	11.4549	9.8674	2.5557
DoTPS24	0.9002	0.9873	0.8631	0.7432
DoTPS25	0.0566	0.8189	0.7273	0.1050
DoTPS26	5.5219	10.1560	12.4607	23.2561
DoTPS27	4.5398	22.5801	9.6888	4.7090
DoTPS28	6.8520	4.5228	4.9056	5.8451
DoTPS29	9.5300	17.8871	15.5421	11.6043
DoTPS30	0.3827	1.0406	1.0023	0.6329
DoTPS31	1.1175	0.4629	0.6216	1.5712
DoTPS32	0.9362	0.4098	0.5825	0.8163
DoTPS33	1.2334	2.3022	3.4734	1.7218
DoTPS34	0.0345	0.7113	0.2138	0.0780

Table S11 The expression values of *DoTPS* genes in at three flowering stages of *D. officinale*.

	B1	B2	B3	S1	S2	S3	F1	F2	F3
DoTPS1	0.8354	0.8348	0.5920	5.5536	6.1455	5.1733	43.3164	37.8553	44.3107
DoTPS2	0.0771	0.0000	0.0000	0.2770	0.1674	0.6346	0.4768	0.7810	0.6779
DoTPS3	3.9852	4.8716	3.3371	17.1842	22.9828	20.7984	24.9471	29.9034	28.2281
DoTPS4	0.0000	0.0395	0.0000	0.1083	0.1239	0.1783	0.0389	0.0000	0.0000
DoTPS5	0.0000	0.0000	0.6293	0.3093	1.0851	0.0000	0.6199	0.0000	0.2888
DoTPS6	0.0057	0.0040	0.0044	0.0040	0.0044	0.0040	0.0044	0.0000	0.0000
DoTPS7	2.9934	2.2824	2.7800	0.9494	1.1183	1.5537	0.2612	0.5734	0.6133
DoTPS8	0.0000	0.0006	0.0000	0.4696	0.3430	0.2595	0.0000	0.3431	0.0299
DoTPS9	0.0120	0.0134	0.0112	0.0000	0.0040	0.0044	0.0000	0.0004	0.0000
DoTPS10	223.2744	229.3890	216.2026	3234.7494	3217.9300	3179.3628	891.4052	652.9398	630.1163
DoTPS11	0.0090	0.0047	0.0035	0.0040	0.0037	0.0040	0.0044	0.0000	0.0000
DoTPS12	0.0000	0.0003	0.0001	0.0000	0.0000	0.0000	0.1042	0.0000	0.0000
DoTPS13	0.0000	0.0000	0.0000	0.1851	0.2798	0.2012	0.8726	0.1745	0.2143
DoTPS14	0.8456	0.7260	1.1031	0.3094	0.3188	0.3702	4.7988	4.8901	4.5217
DoTPS15	0.0003	0.0000	0.0003	0.0287	0.0295	0.0000	0.0002	0.0004	0.0000
DoTPS16	2.3237	2.7277	2.4948	0.0000	0.2986	0.0324	0.5068	0.0328	0.3382
DoTPS17	0.0023	0.0013	0.0022	0.0040	0.0044	0.0000	0.0040	0.0070	0.0000
DoTPS18	0.0807	0.0640	0.1211	0.0000	0.0011	0.0000	0.0053	0.0000	0.0023
DoTPS19	5.4240	5.0955	6.1791	17.2144	19.5407	18.3601	11.1548	12.3520	10.0018
DoTPS20	14.2348	15.0919	15.4891	13.7248	13.6509	14.0405	4.4426	6.9192	5.0905
DoTPS21	84.8295	77.6592	88.9460	627.2865	656.8730	774.5678	139.1584	134.5610	130.4231
DoTPS22	0.1041	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
DoTPS23	15.3781	18.0934	14.8088	13.3106	20.8759	12.2737	3.9390	3.5389	3.4028
DoTPS24	7.3896	7.8489	9.5586	114.7701	102.1070	112.7620	160.4668	196.0226	135.9785
DoTPS25	0.0761	0.0177	0.0583	1.0937	0.8031	0.0239	0.0332	0.1064	0.0893
DoTPS26	0.3991	0.3511	0.9803	0.0000	0.0117	0.0641	0.0000	0.0001	0.0000
DoTPS27	0.0012	0.0000	0.0012	0.0067	0.0038	0.0000	33.3199	37.7800	35.2909
DoTPS28	249.8680	227.5599	232.3214	2.4423	2.9088	3.2606	0.6343	0.5608	0.4010
DoTPS29	0.0003	0.0007	0.0005	0.0000	0.0017	0.0270	0.0691	0.0514	0.1174
DoTPS30	0.0466	0.0000	0.0266	0.0367	0.0000	0.0000	0.0003	0.0001	0.0000
DoTPS31	16.6555	12.2840	15.7901	12.6694	6.0019	25.8597	2.7267	8.9457	7.8824
DoTPS32	10.8991	10.4409	10.5708	3.0542	5.2010	4.7502	5.1282	4.6255	5.3851
DoTPS33	1.1276	0.4167	0.9774	2.3825	4.2775	5.0569	24.3645	21.7366	24.4755
DoTPS34	0.0167	0.0709	0.1117	0.0000	0.0004	0.0003	0.0001	0.0002	0.0000

Three flowering stages of *D. officinale* include budding (B), semi-flowering (S) and full flowering (F).

Table S12 Functional annotation of DoTPS with Terzyme (http://www.nipgr.ac.in/terzyme.html).

Gene sequence ID	Score	E-value	No. of domains
Putative monoterpene synthase			
DoTPS28	657.1	$3.8\times e^{-200}$	1
DoTPS10	649.4	$8.4\times e^{-198}$	1
DoTPS21	643.2	$6.2\times e^{-196}$	1
DoTPS34	642.9	$7.5\times e^{-196}$	1
DoTPS25	637.0	$4.7\times e^{-194}$	1
DoTPS23	631.6	$2.0\times e^{-192}$	1
DoTPS18	622.9	$8.7\times e^{-190}$	1
DoTPS20	619.6	$9.0\times e^{-189}$	1
DoTPS27	604.7	$2.9\times e^{-184}$	1
DoTPS3	604.0	$4.6\times e^{-184}$	1
DoTPS2	598.2	$2.6\times e^{-182}$	1
DoTPS33	554.1	$5.9\times e^{-169}$	1
DoTPS30	534.5	$5.2\times e^{-163}$	1
DoTPS19	477.7	$8.0\times e^{-146}$	2
DoTPS24	394.2	$1.6\times e^{-120}$	1
DoTPS1	233.4	$7.4\times e^{-72}$	1
Putative sesquiterpene synthase			
DoTPS9	701.4	$1.6\times e^{-213}$	1
DoTPS5	673.8	$3.2\times e^{-205}$	1
DoTPS29	672.6	$8.1\times e^{-205}$	1
DoTPS7	670.8	$2.6\times e^{-204}$	1
DoTPS22	669.9	$4.8\times e^{-204}$	1
DoTPS17	668.3	$1.7\times e^{-203}$	1
DoTPS6	663.6	$4.3\times e^{-202}$	1
DoTPS26	661.8	$1.4\times e^{-201}$	1
DoTPS16	658.7	$1.3\times e^{-200}$	1
DoTPS15	637.5	$3.5\times e^{-194}$	1
DoTPS13	615.2	$2.1\times e^{-187}$	1
DoTPS11	309.7	$6.2\times e^{-95}$	1
DoTPS8	211.9	$2.7\times e^{-65}$	1
DoTPS12	156.5	$1.6\times e^{-48}$	2
Putative diterpene synthase			
DoTPS32	1029.5	0.0	1
DoTPS4	622.0	$2.4\times e^{-189}$	1
DoTPS14	592.3	$2.3\times e^{-180}$	1
DoTPS31	249.0	$1.5\times e^{-76}$	2

Table S13 CGTCA-motif, G-box and MYC motif in the promoter region of *DoTPS* genes.

	CGTCA-motif		MYC motif		G-box	
Gene	Number	Position	Number	Position	Number	Position
DoTPS1	1	+638	4	-327, +207, +474, +1329	4	-884, -1065, +636, +1140
DoTPS2	2	-1464, -1756	4	-469, -505, -710, +576	1	-209
DoTPS3	3	-331, -1745, +293	8	-18, -122, -1149, -1182, -1304, -1591, +1040, +1197	4	-998, -1835, +455, +1834
DoTPS4	0		1	-294	1	+684
DoTPS5	3	+832, +858, +1870	7	-77, -1187, -1412, +31, +69, +83, -730	2	+1868, +1916
DoTPS6	1	+95	4	-992, -1154, -1800, -1911	5	-341, -365, -724, +724, +1548
DoTPS7	1	+312	3	-212, -629, +70	3	+652, +698, +762
DoTPS8	3	-468, -789, +419	3	-1152, -1282, +924	0	
DoTPS9	0		7	-26, -1582, -1614, -1654, +128, +1628, +1978	2	-241, -1513
DoTPS10	2	-737, -782	7	-548, -687, -1049, -1129, -1470, +216, +519	3	-93, -1114, -1848
DoTPS11	0		1	-506	0	
DoTPS12	1	-1933	2	-1159, +845	3	-1548, +1229, +1545
DoTPS13	0		2	-781, +1090	1	-638
DoTPS14	1	-1150	7	-290, -359, -1805, -1913, +246, +673, +1320	2	-621, -1151
DoTPS15	0		5	-234, -1269, -1466, -1860, +159	2	+899, +900
DoTPS16	7	-53, -967, -981, -1024, +1045, -1218, +886	5	-49, -889, -1258, +902, +995	0	
DoTPS17	1	+1511	4	-427, -821, -1650, +414	2	-483, +612
DoTPS18	0		3	-1288, +633, +1501	1	-1910
DoTPS19	1	-1048	5	-276, -1252, +1399, +1835, +1927	0	
DoTPS20	2	-663, +1720	7	-222, -785, -833, +191, +690, +1079, -1112	0	
DoTPS21	1	-1093	6	-1154, -1465, -1646, -1692, +165, +518	1	-1223
DoTPS22	2	+741, +750	1	+175	1	+1916
DoTPS23	1	-1877	4	-584, +124, +771, +1346	2	-1052, -1878

DoTPS24	0		2	+797, +1950	0	
DoTPS25	7	-175, -1072, -1209, -1337, +583, +677, +1000	4	-384, +72, +1733, +1783	4	-1666, +613, +1066, +1225
DoTPS26	0		2	-669, +115	1	+662
DoTPS27	2	-1544, +1112	4	+436, +726, +1230, +1951	2	-1545, +976
DoTPS28	0		4	-630, -664, -1403, +1901	5	-156, -180, +183, +203, +489
DoTPS29	0		1	-431	0	
DoTPS30	1	+1443	6	-1000, -1448, +282, +495, +968, +1663	1	+231
DoTPS31	1	-774	1	+183	1	-1713
DoTPS32	2	+875, +906	1	-1212	3	-585, -1106, +587
DoTPS33	0		3	-1336, -1503, +1781	1	+1626
DoTPS34	1	-651	4	-468, -1502, -1715, +973	2	-955, +1451

Table S14 Primers used for RT-qPCR analysis, DoTPS10 cloning and vector construction.

Gene		Primer
DoTPS1	F	CCTCACTCTTCCATGAGGAAAT
	R	CGAAGAAGCTGGAAGCAAATAG
DoTPS2	F	AGCACAGCGCTCAGTATTT
	R	TCTTCGAAAGGAAGTGGAAGAG
DoTPS3	F	GTAATCTAGCTGGTGGTGAGTT
	R	GTTGAGAAACGAGGTTCCATTG
DoTPS4	F	ACATTGAAGGAGGAGGGATCTA
	R	GCAAGTTGGAGGAGGTCATTAT
DoTPS5	F	TGTTTATGGGACAGTCGAAGAG
	R	GGAACTCGTGTTGCATGTATTG
DoTPS6	F	ACACTTATTACTGCTGGCTACTC
	R	TGATCTCTGGGAAGCTTGTAAC
DoTPS7	F	GGGTAACTGGTATGCCTCTAATC
	R	TAGCATTGGACAGCTGAAGG
DoTPS8	F	GAAGTCATTGATCTGCAAGATGG
	R	CTTGAACCGATCAGGTGTTCTA
DoTPS9	F	ACACTTATTACTGCTGGCTACTC
	R	GGAAGCTTGTAACCCAATCAAAG
DoTPS10	F	GCTGCCTCTCAACAGCTAATA
	R	CTGGAAGCGATTGGATGTAGT
DoTPS11	F	CAGAGTGGTGGAAAGGATTAGG
	R	GTGAATAGCAGGGTTCAGAGTAA
DoTPS12	F	CTACTGAGGCAGCAACGATTTA
	R	TCAAAGTATGTGCCTGTCATCC
DoTPS13	F	CGATGAGCATGAAGAGAGAGAC
	R	CCATGCATCCTCCACCATTA
DoTPS14	F	AGTCATTGTGGTTCGAGGAAG
	R	CAGATACTGGTACGAAGGCATAC
DoTPS15	F	AGCATCTAGGAGTGGCCTAT
	R	AATCGTTGCTGCCTCAGTAG
DoTPS16	F	GATCTGCTAGCTGTTGCTCTAA
	R	TGCTCTTAAACCTCCCTTCATC
DoTPS17	F	TAGGCTTCTCCAAACACTTACC
	R	GGGCATCACCTTTGACATAATC
DoTPS18	F	TGATGCTTATGAGAGGCAAGAG
	R	TCATCGCTAGCAAGACCAATAC
DoTPS19	F	GCAAGAGATAGGTTGATGGAGAC
	R	TGAGGCAACCTAGTTTGGTAATC
DoTPS20	F	GCCTTTACGAGGCTTCTTATCT
	R	TTGTTCCACTAACGAGGGATG
DoTPS21	F	GCCAACCATTTGGGATGATAAC
	R	AAACACCTGACTTCCTCCTTC

DoTPS22	F	ACCTCAAAGAGGAGGAGAAGA
	R	AAGGCTGACGGCCAAATAA
DoTPS23	F	GCTTATGAGAGGCAAGAGAACA
	R	CCACCAACTAGACATCTCCTTAAC
DoTPS24	F	TTACAAGGTGGTGGGCAAA
	R	TGCTAAACCTACGGCTAAGAAG
DoTPS25	F	CTTGTATGAGGCTTCCTTCCTT
	R	GTAGCTCCAAGGCATGTTCTAT
DoTPS26	F	TGAGAGAGAGGGTGGAAGAA
	R	GCCTAGGCGTTGAAGAGAAT
DoTPS27	F	AAGTGGTGGGCAGAAGTAAG
	R	CAGCCATACCAACAGCTAGAA
DoTPS28	F	CCTCACCATCGCTTCCTATTC
	R	AGCAGAAGAAGATGTTGCAGTA
DoTPS29	F	TCATGCGTACCTTCAGGAATC
	R	GAGTACCCAGCTGTAATCAGTG
DoTPS30	F	ATAGATCACGCCTTGGAGTTAC
	R	AAAGTTCTCTCGTCTCCCATAAG
DoTPS31	F	CTGAAGCTGCCGATCCATATT
	R	GCTCAATCGACCGAACTAACA
DoTPS32	F	CAAACACTCAGCGCAAACAT
	R	ACATACTCCTCACCAACATTCC
DoTPS33	F	GCAACGACTTAGCAACATCATC
	R	GATATGTACAGGCGAGCTTCTT
DoTPS34	F	TGCTTATGGGAGACGAGAGA
	R	GTTCTTGTAGCTCCGCCTTAT
DoEF-1α	F	GCTTGAGAAGGAGCCCAAGT
	R	CCAACAGCCACAGTTTGTCG
DoTPS10-ORF	F	ATGGCTTTGTATTTTCGCCCT
	R	AAGTGGAATTGGTTCAATCATCA
DoTPS10-pET32a	F	TTCGAGCTCCGTCGACATGGCTTTGTATTTTCGCCCT
	R	GGTGGTGGTGCTCGAGAAGTGGAATTGGTTCAATCATCA
DoTPS10-YFP	F	CGAACGATAGCCATGGATGGCTTTGTATTTTCGCCCT
	R	TGAGTCCGGACCATGGAAGTGGAATTGGTTCAATCATCA

Gene-specific primers for real-time reverse transcription quantitative PCR (RT-qPCR) were designed by the PrimerQuest online tool (http://www.idtdna.com/Primerquest/Home/Index). The *D. officinale* actin gene (DoEF-1*α*) was obtained from NCBI (GenBank accession no. JF825419). F, forward; R, reverse.

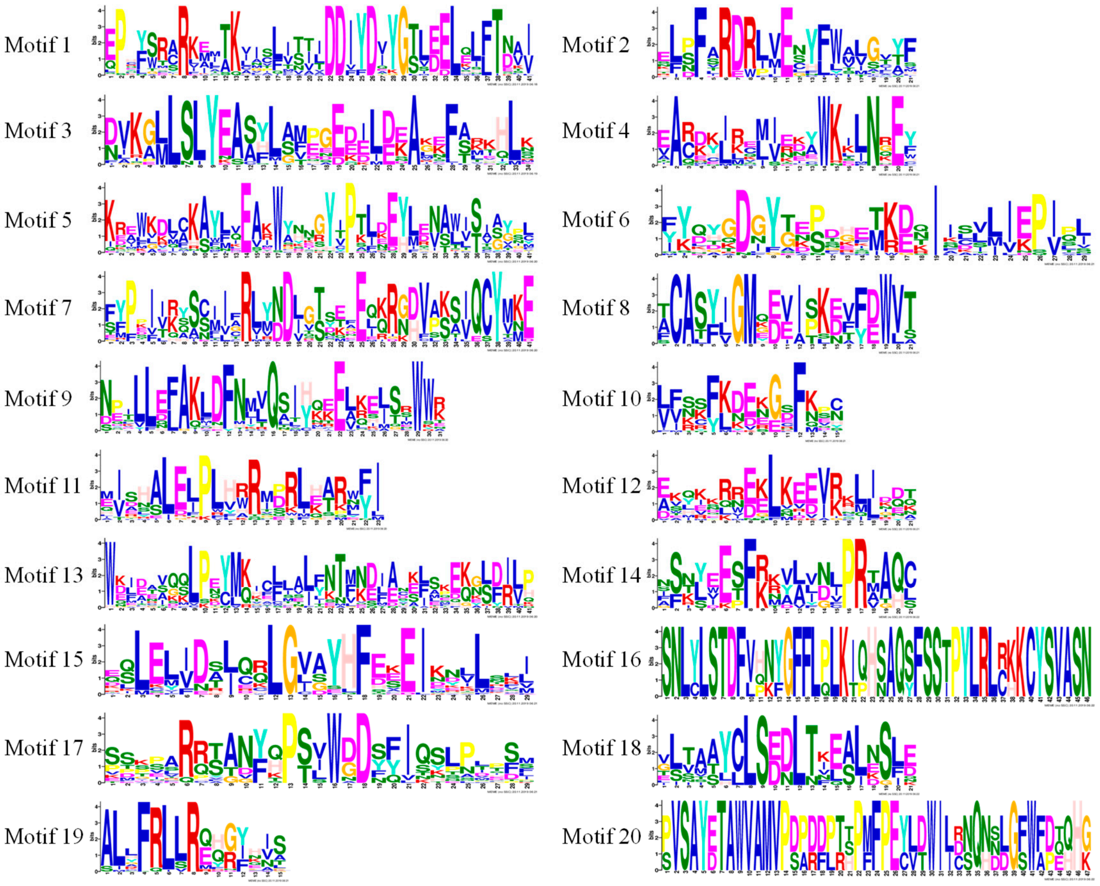

Figure S1 Distribution of conserved motifs in *D. officinale* TPS proteins based on the results of MEME analysis.

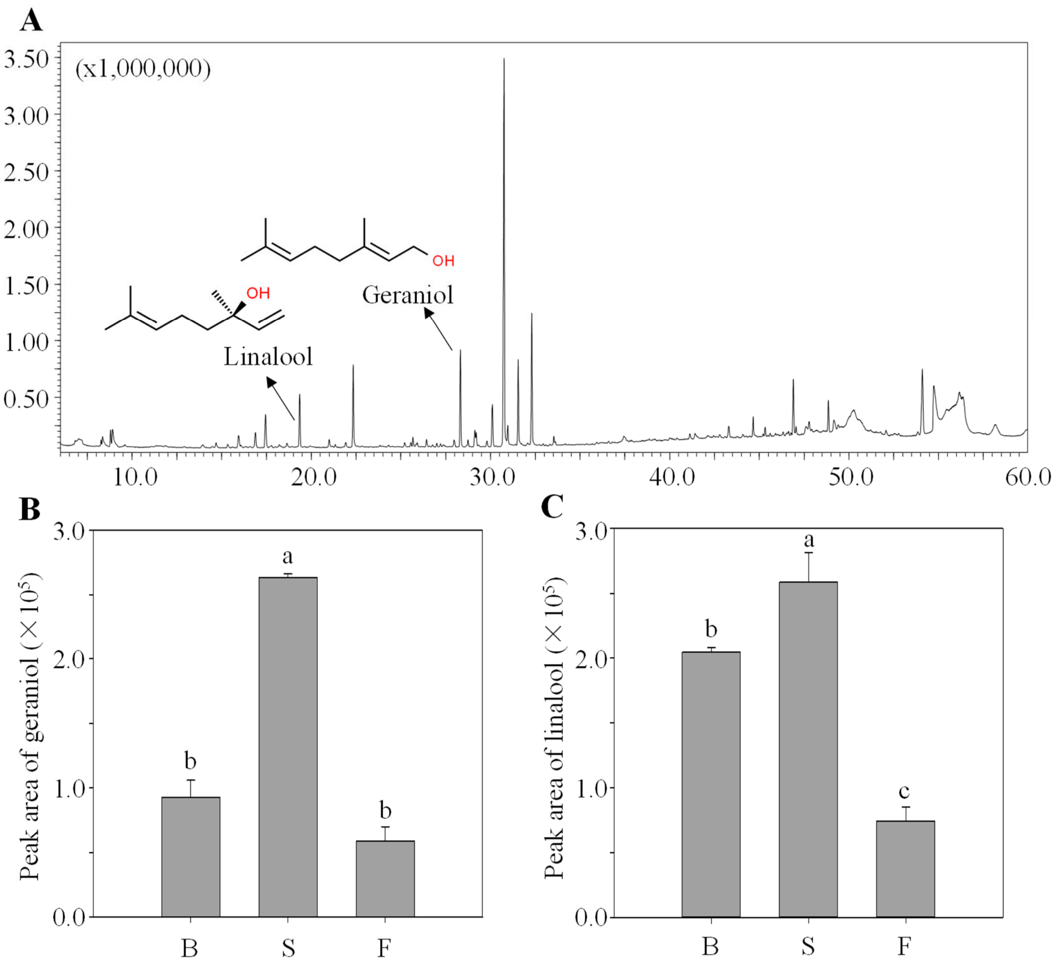

Figure S2 Content of geraniol and linalool in *D. officinale* at three flowering stages: budding (B), semi-flowering (S) and full flowering (F). Each bar represents the mean (± standard error, n = 3) of three independent biological replicates. Different letters above the bars indicate significant differences ($p < 0.05$, Duncan's multiple range test).

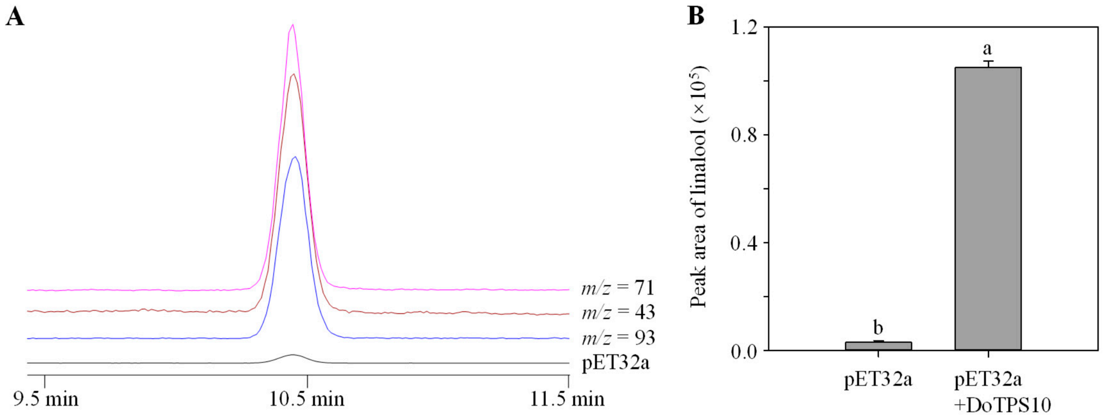

Figure S3 Gas chromatograms of products yielded by DoTPS10 using GPP as substrate. Each bar represents the mean (± standard error, n = 3) of three independent biological replicates. Different letters above the bars indicate significant differences ($p < 0.05$, Duncan's multiple range test).