

Supplemental Data

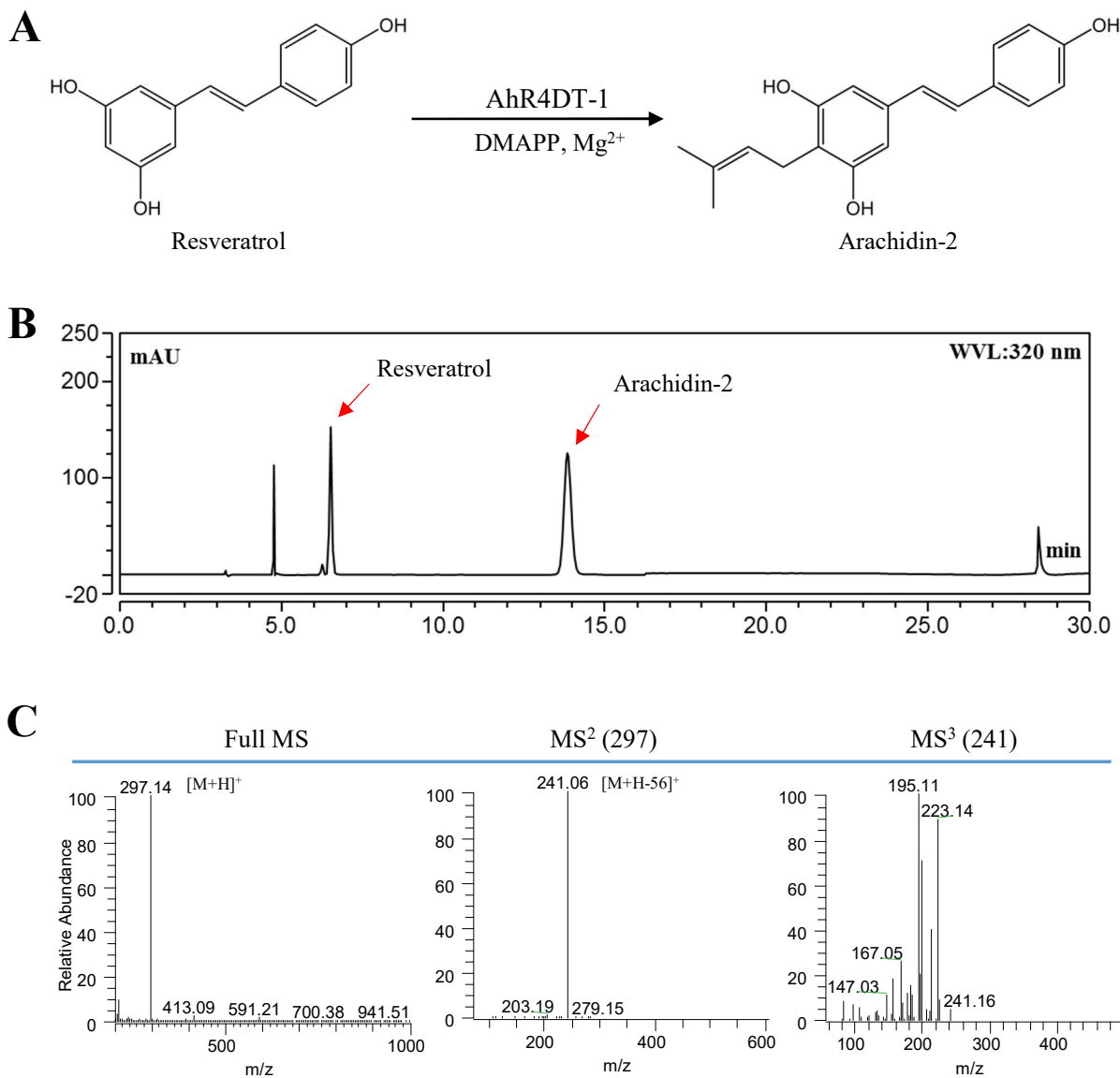


Figure S1. Prenylation of resveratrol by AhR4DT-1.

Prenylation activity of AhR4DT-1 in microsomal fraction of *Nicotiana benthamiana* leaf after vacuum infiltration with *Agrobacterium tumefaciens* LBA4404 harboring pBIB-Kan-AhR4DT-1.

(A) Chemical structures of resveratrol and its prenylated product, arachidin-2.

(B) HPLC chromatograms (UV 320 nm) of ethyl acetate extraction of reaction mixtures contained 100 μM resveratrol, 300 μM DMAPP, 10 mM MgCl_2 , 5 mM DTT and 30 μg microsomal fraction in a pH 9.0 Tris-HCl buffer for 40 min.

(C) HPLC-PAD-ESI- MS^3 analysis of prenylated product, arachidin-2.

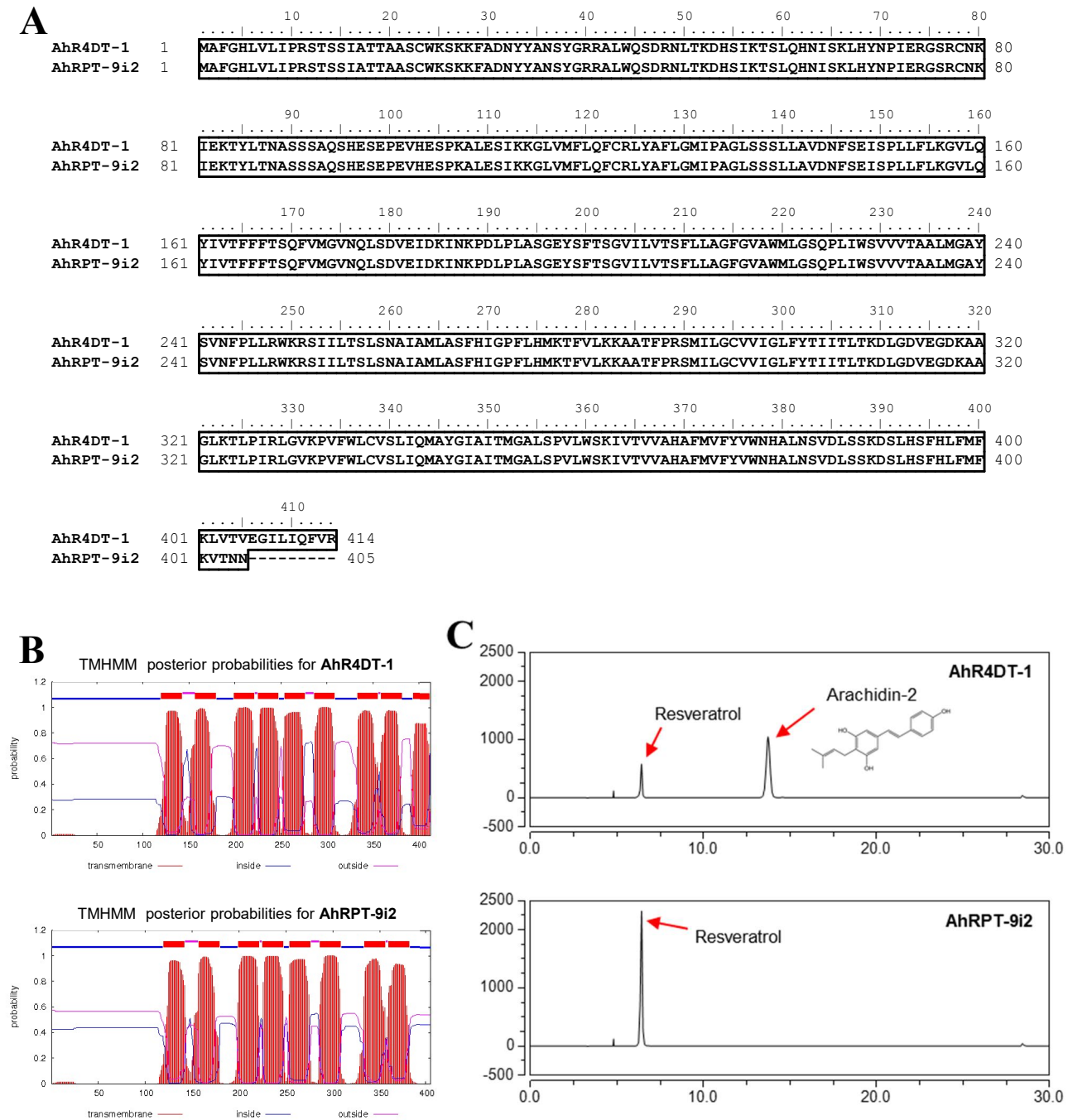


Figure S2. Comparison of AhR4DT-1 and AhRPT-9i2.

(A) Alignment of AhR4DT-1 with AhRPT-9i2 was performed using ClustalX.

(B) Potential transmembrane domains of AhR4DT-1 and AhRPT-9i2 were predicted by TMHMM.

(C) Resveratrol prenylation activity of AhR4DT-1 and AhRPT-9i2 were analyzed by using HPLC.

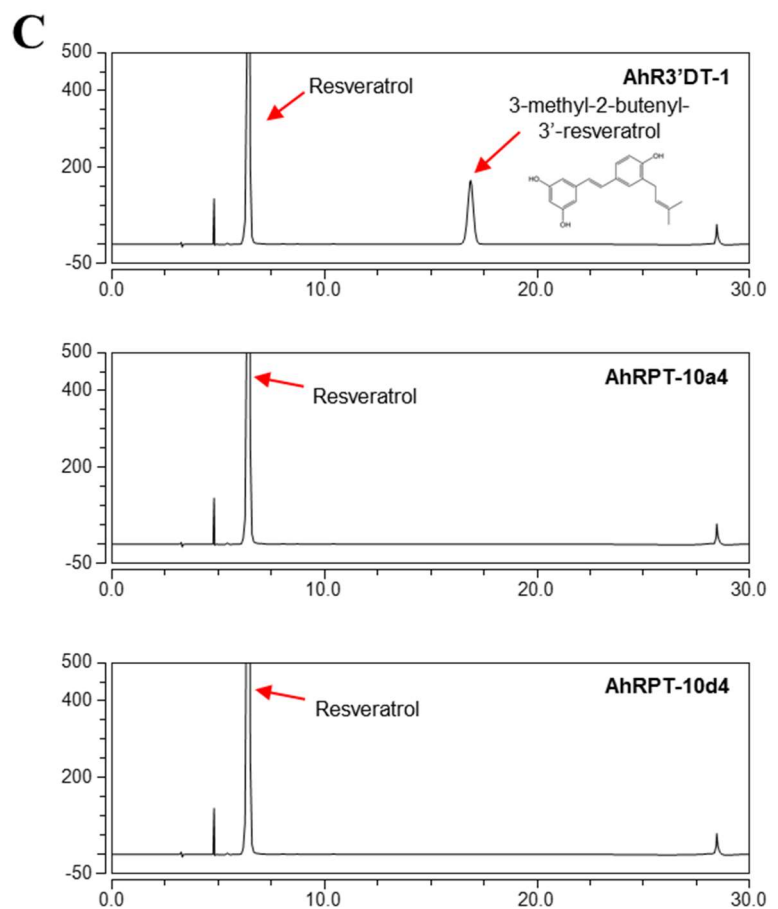
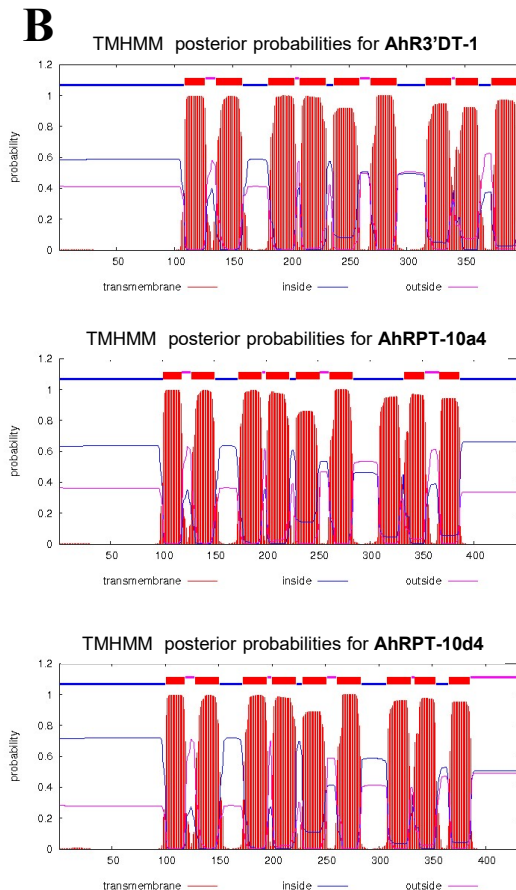
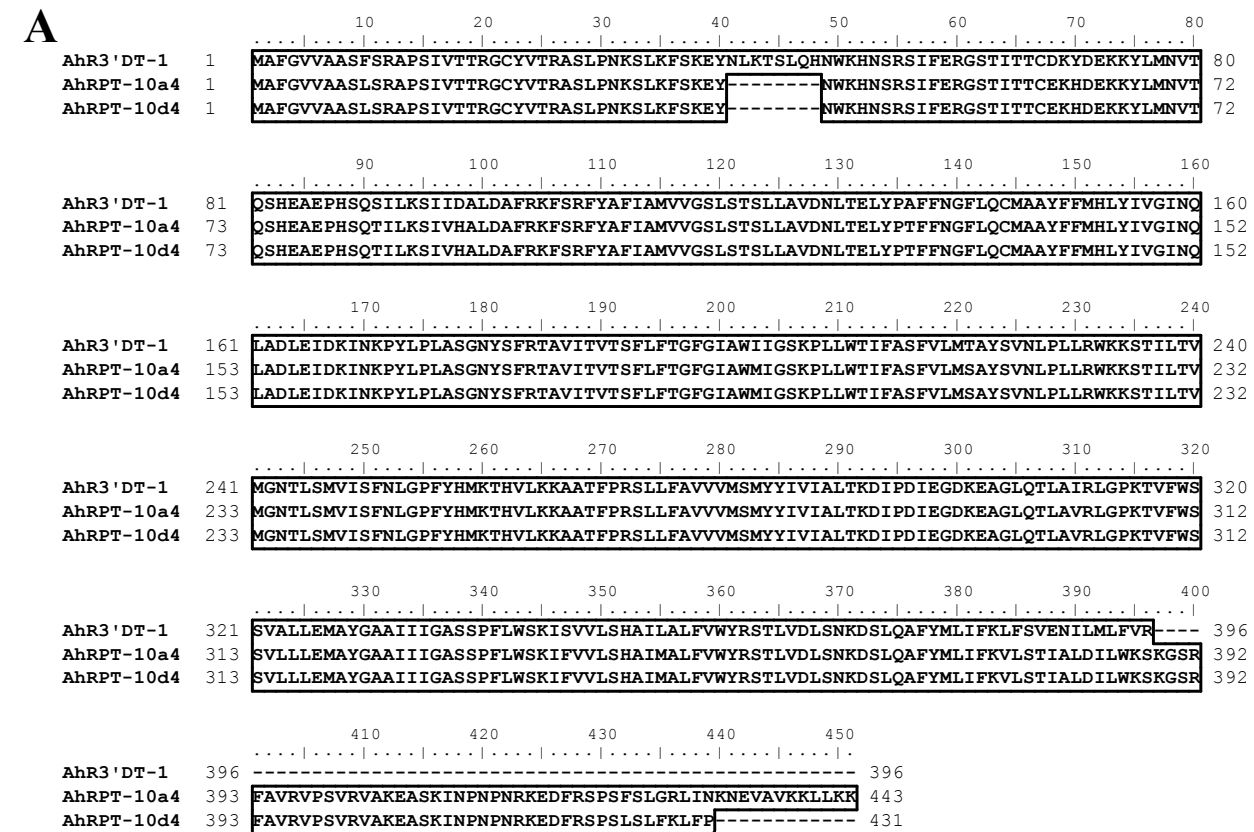


Figure S3. Comparison of AhR3'DT-1, AhRPT-10a4 and AhRPT-10d4.

(A) Alignment of AhR3'DT-1, AhRPT-10a4 and AhRPT-10d4 was performed using ClustalX.

(B) Potential transmembrane domains of AhR3'DT-1, AhRPT-10a4 and AhRPT-10d4 were predicted by TMHMM.

(C) Resveratrol prenylation activity of AhR3'DT-1, AhRPT-10a4 and AhRPT-10d4 were analyzed by using HPLC.

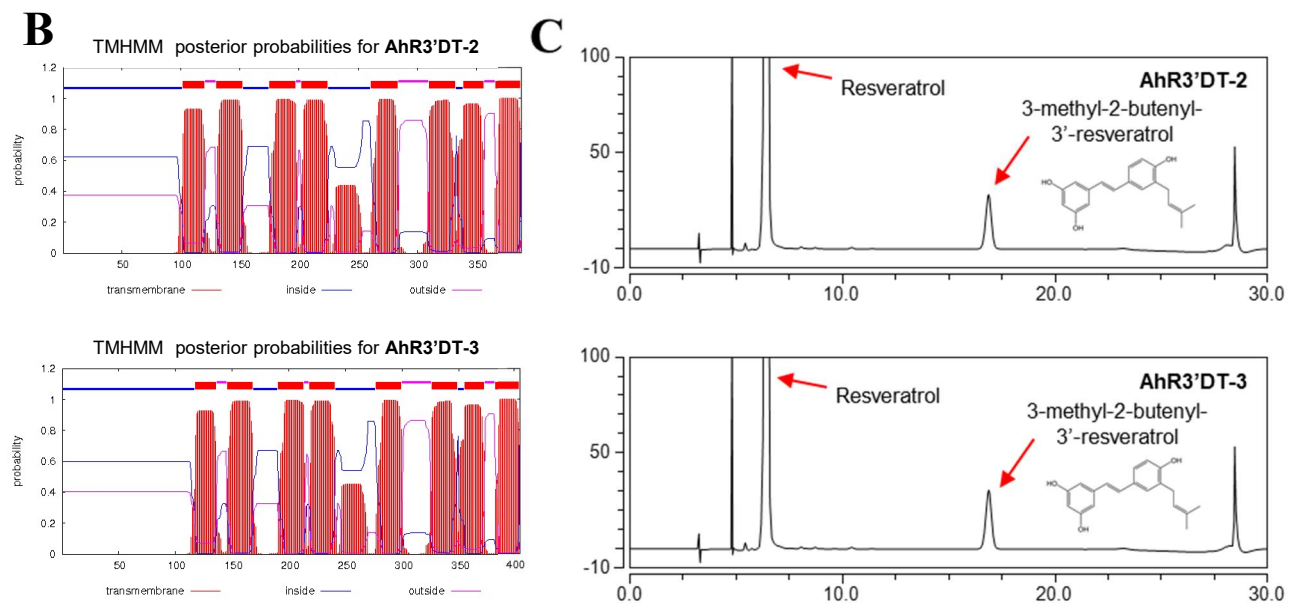
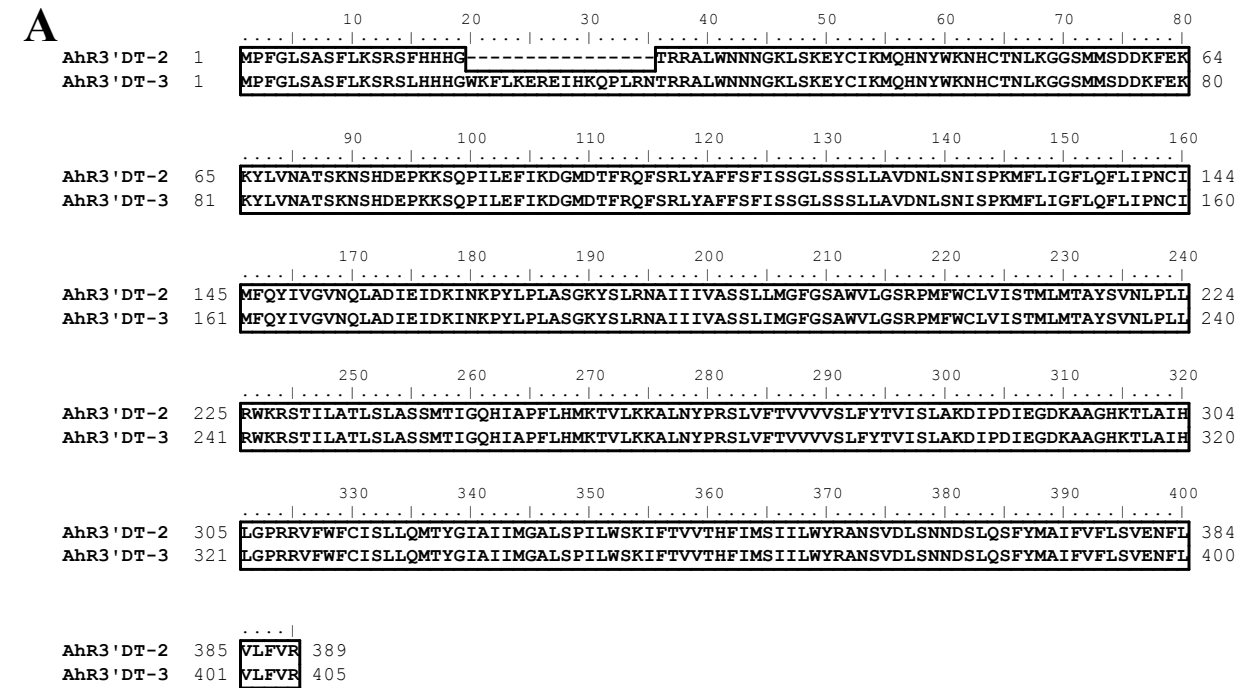


Figure S4. Comparison of AhR3'DT-2 and AhR3'DT-3.

(A) Alignment of AhR3'DT-2 with AhR3'DT-3 was performed using ClustalX.

(B) Potential transmembrane domains of AhR3'DT-2 and AhR3'DT-3 were predicted by TMHMM.

(C) Resveratrol prenylation activity of AhR3'DT-2 and AhR3'DT-3 were analyzed by using HPLC.

A

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      10      20      30      40      50      60      70      80
AhR3'DT-4 1  MASTSRLLHSHASLPPPTTSISKTNSSGSHAVIRSIWHNNGKYPKEKTCIETPLLLQHNQKHHTCDQIKRKHVFKATHAQS 80
      90      100     110     120     130     140     150     160
AhR3'DT-4 81  KNEPEPQADSAKPIWNSIKDVMHTIQKFSVFYALIGLLSGILSSLLAVEKLSLSPTEFFISMLQFMAAYSSMQLYTTGV 160
      170     180     190     200     210     220     230     240
AhR3'DT-4 161 NQLADIEIDKINKPYRPLASSKISFGGGLAIVAASLFMSFGLALMIGSKPLLWGLILIFILMTAYSVNLPFLRWKKSTIL 240
      250     260     270     280     290     300     310     320
AhR3'DT-4 241 TLLSGVPTILTAYNLAPYLHMKTFVLKPPFIETRSLAFTTVVMTFFVVISLFDIPDIEGDKKEGLQTLIRLGPKRVF 320
      330     340     350     360     370     380     390
AhR3'DT-4 321 WLCISLLEMTYGIALIMGLTSPFLWSKIFTVMAHAINAWILWFRANSVDLKSKEFQSFYMFIFKLLYLENVLVLFVR 398

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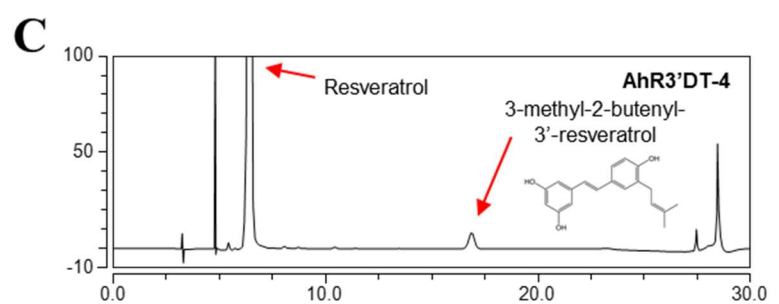
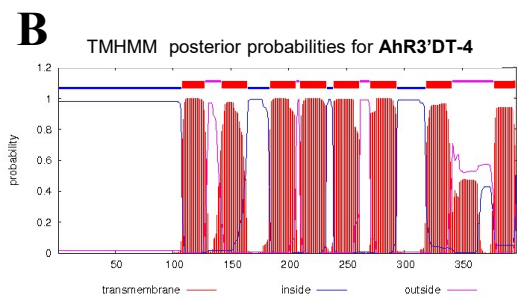


Figure S5. Structural analysis of AhR3'DT-4.

(A) Primary structure of AhR3'DT-4.

(B) Potential transmembrane domains of AhR3'DT-4 was predicted by TMHMM.

(C) Resveratrol prenylation activity of AhR3'DT-4 was analyzed by using HPLC.

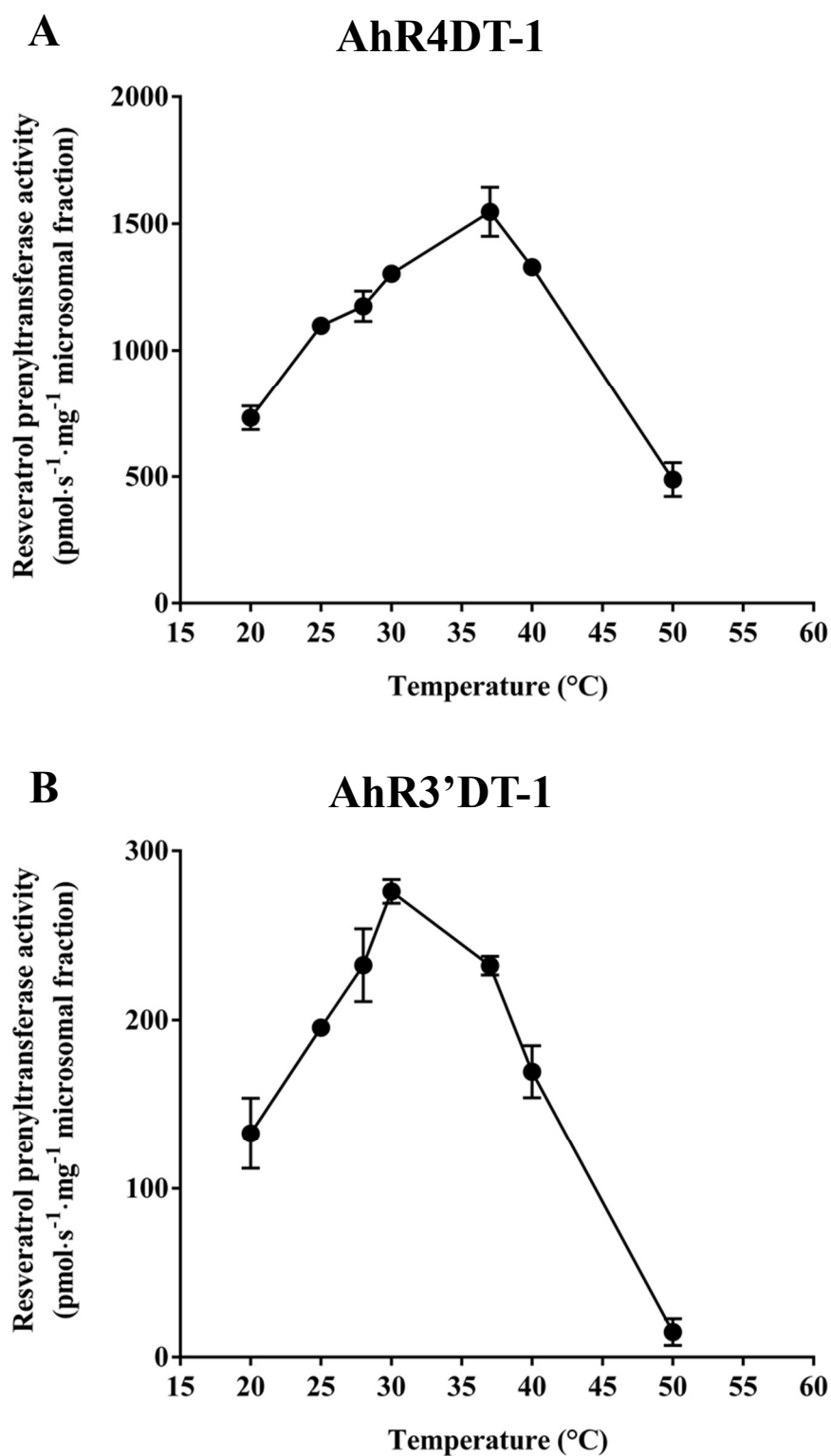


Figure S6. Temperature dependency of AhR4DT-1 and AhR3'DT-1 activity. AhR4DT-1 (A) and AhR3'DT-1 (B) activities were measured at various temperature (20, 25, 28, 30, 37, 40 and 50 °C) in 100 mM Tris-HCl buffer (pH 9.0) for 40 mins.

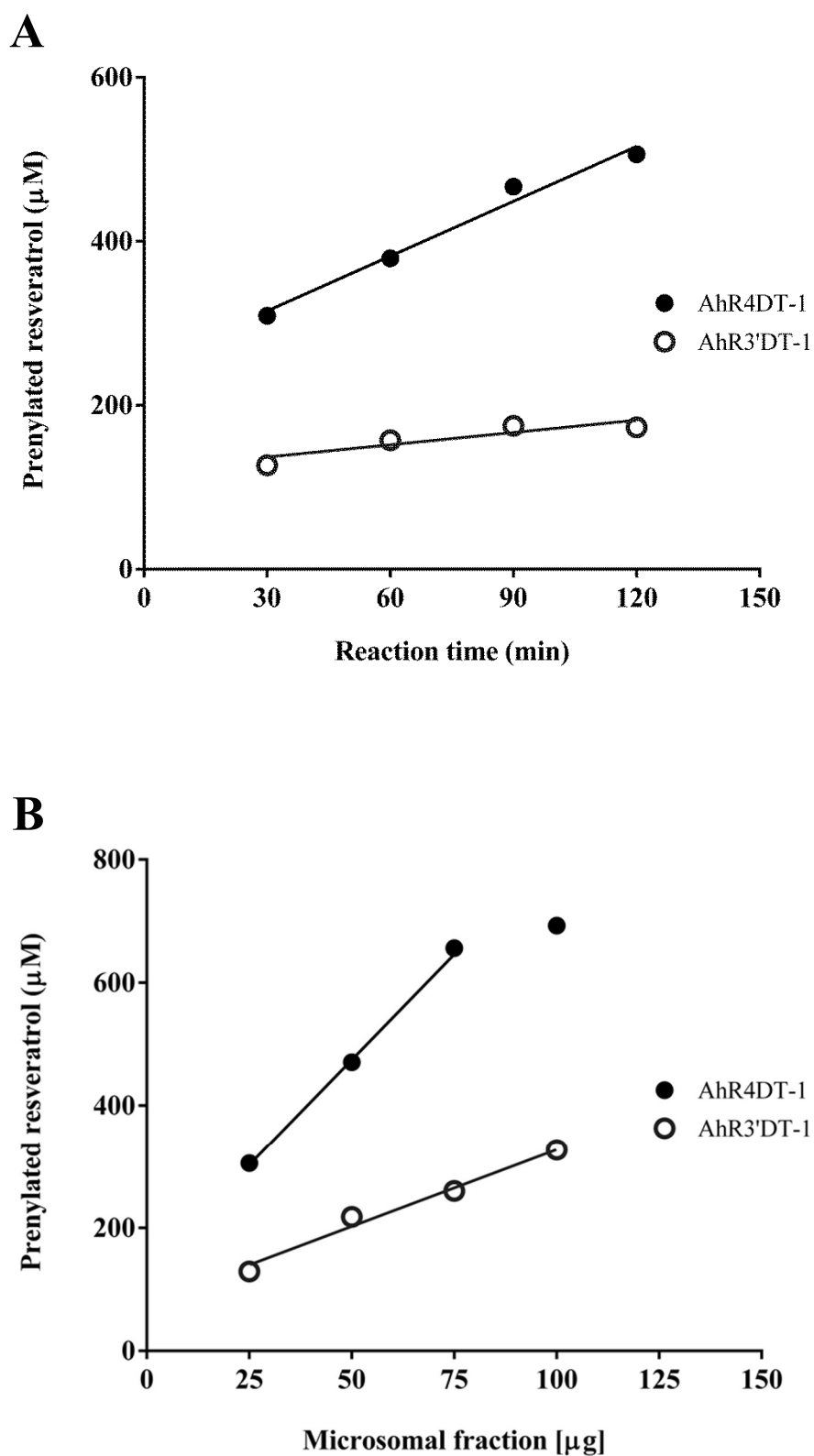


Figure S7. Resveratrol prenylation activity of AhR4DT-1 and AhR3'DT-1.

(A) Concentrations of generated prenylated resveratrol from AhR4DT-1 and AhR3'DT-1 reaction mixtures with varying incubation times (30, 60, 90 and 120 min) were quantified by HPLC.

(B) Concentrations of generated prenylated resveratrol from AhR4DT-1 and AhR3'DT-1 reaction mixtures with varying amounts of microsomal fraction (25, 50, 75 and 100 µg) were quantified by HPLC.

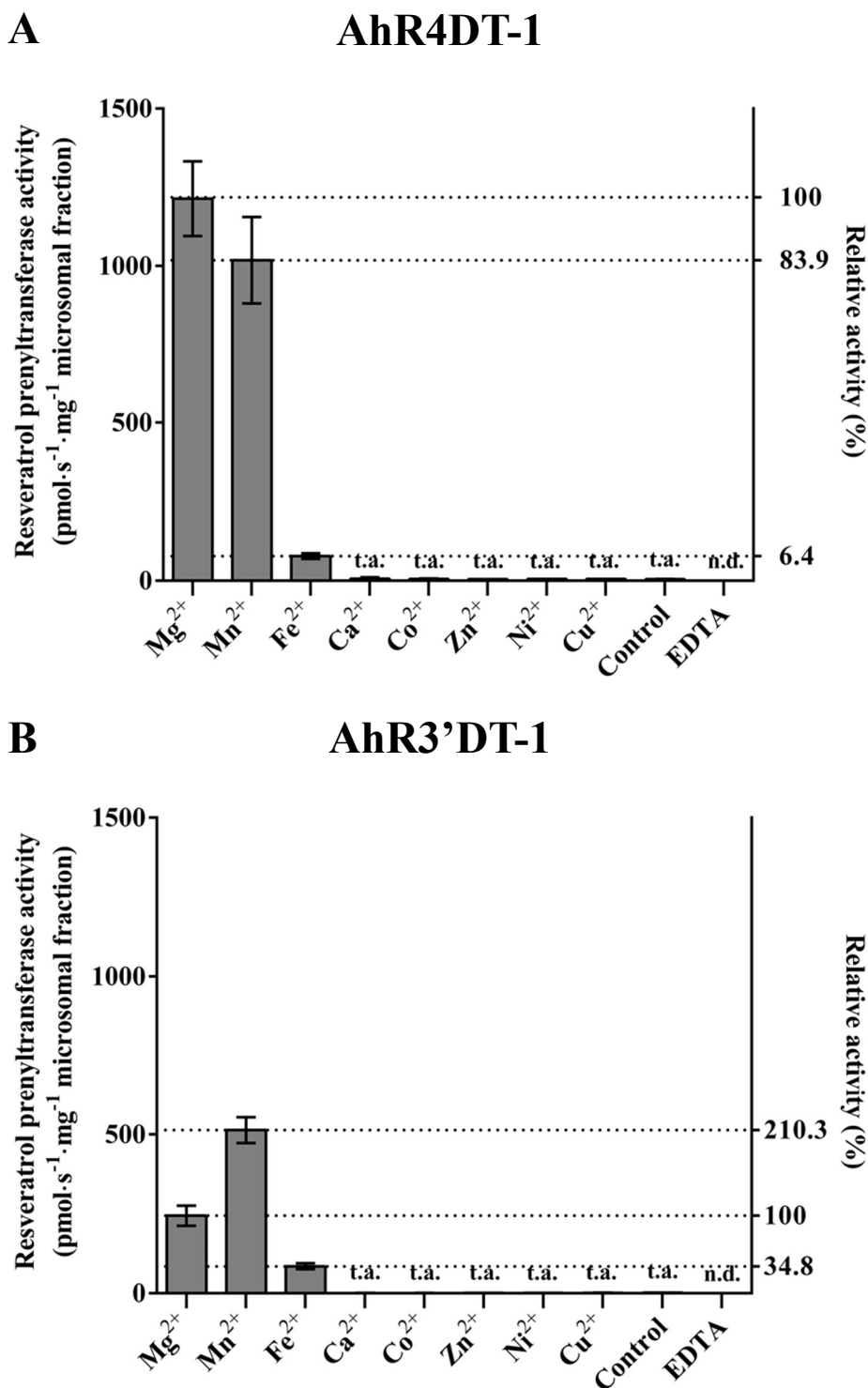
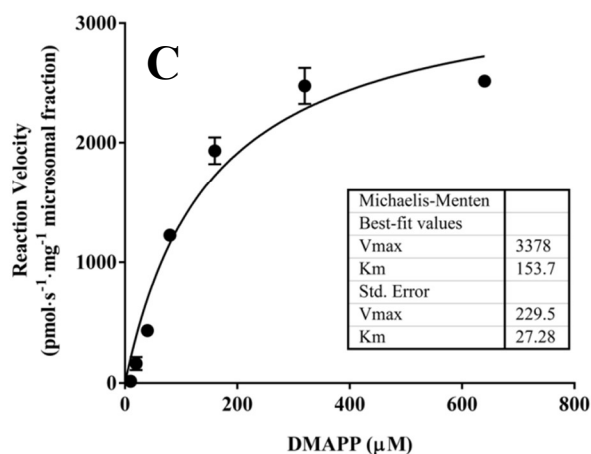
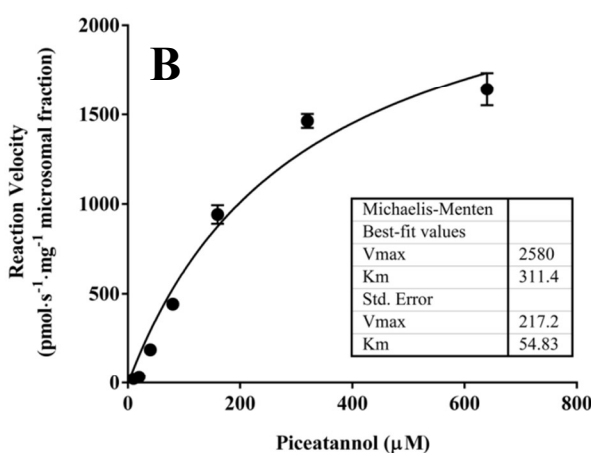
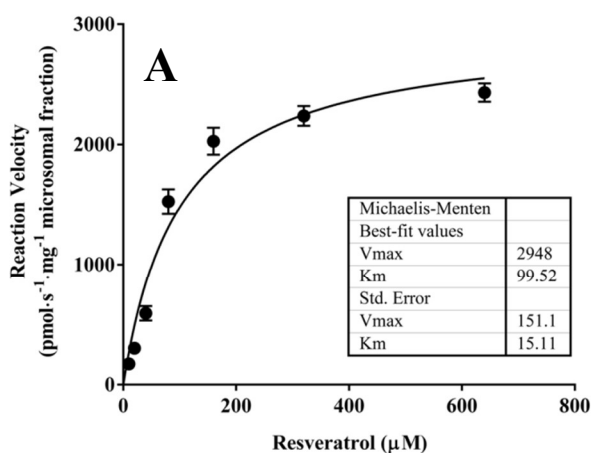


Figure S8. Divalent cation dependency of AhR4DT-1 and AhR3'DT-1 activity.

AhR4DT-1 (A) and AhR3'DT-1 (B) activity with various divalent cation were measured with 10 mM MnCl₂, FeCl₂, CaCl₂, CoCl₂, ZnCl₂, NiCl₂, or CuCl₂ and the enzyme activity was compared with the reaction of 10 mM MgCl₂. Reactions without divalent cation and 10 mM EDTA instead of MgCl₂ were used as controls. All the reactions were performed in 100 mM Tris-HCl buffer (pH 9.0) at 28 °C for 40 min. (t.a., trace amount (<0.5%), n.d., Not detected.). Means and the standard deviation (error bars) were calculated from three replicates.

AhR4DT-1



AhR3'DT-1

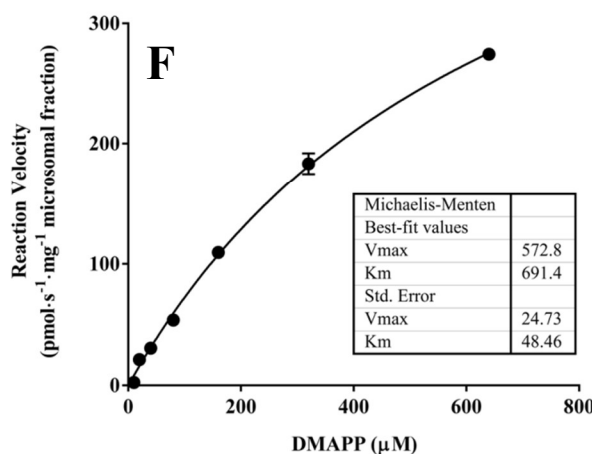
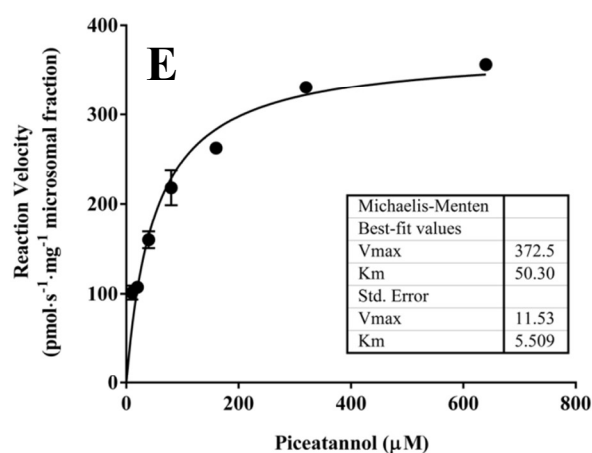
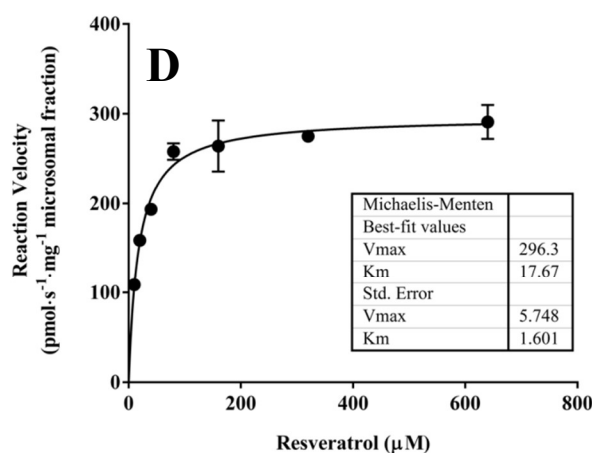


Figure S9. Kinetic values of AhR4DT-1 and AhR3'DT-1.

Dependency of AhR4DT-1 (left) and AhR3'DT-1 (right) on the concentration of resveratrol (A&D), piceatannol (B&E) and DMAPP (C&F) measured with a microsomal fraction from leaves of *Nicotiana benthamiana*. The apparent K_m and V_{max} values for resveratrol and piceatannol were determined with varying concentrations (10~640 μM) using 640 μM DMAPP as prenyl donor, while that for DMAPP were determined with varying concentrations (10~640 μM) using 640 μM resveratrol as prenyl acceptor. All the values were calculated from nonlinear regression analysis with Michaelis-Menten equation by Graphpad Prism 6 software. Means and the standard deviation (error bars) were calculated from three replicates.

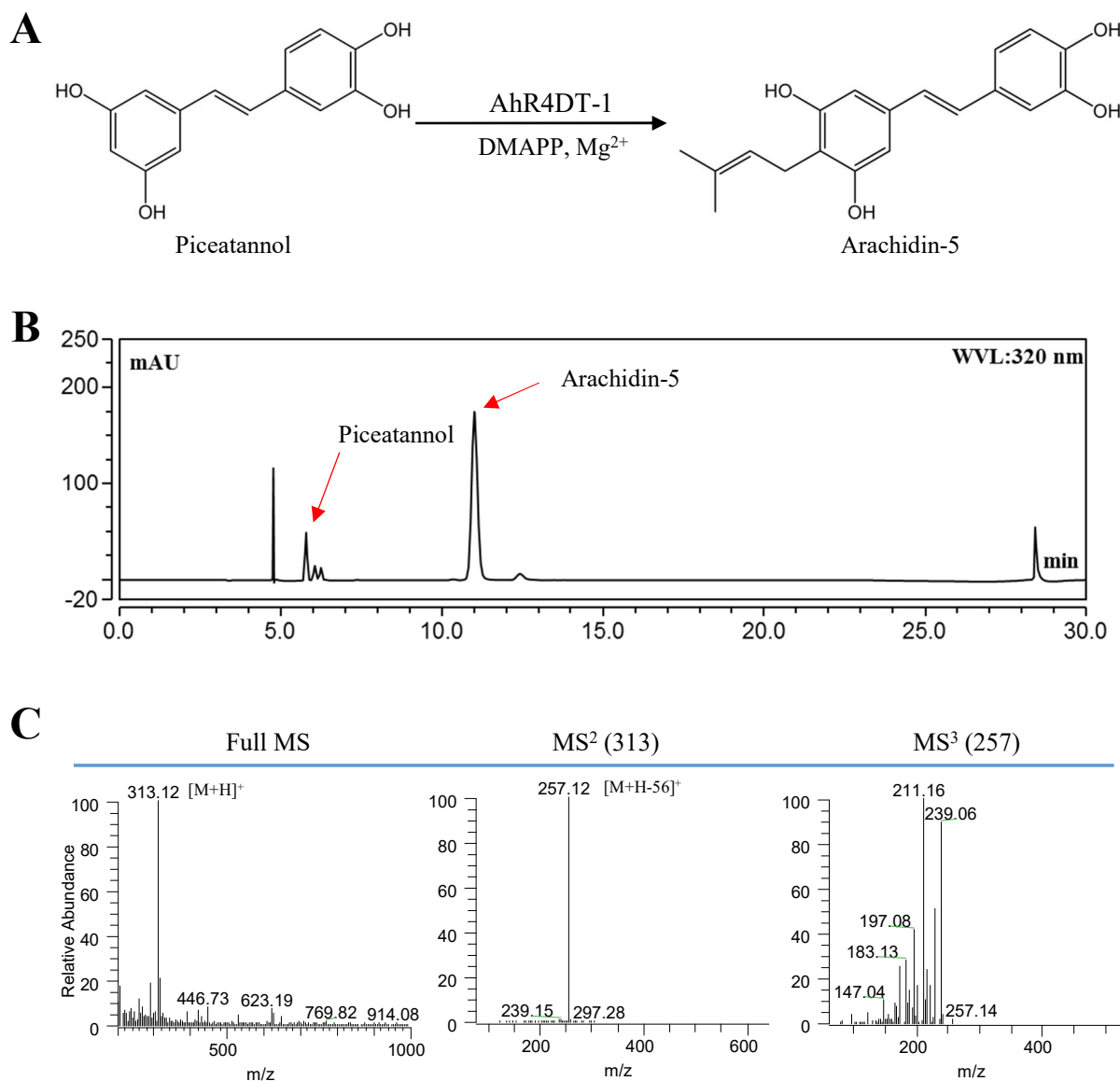


Figure S10. Prenylation of piceatannol by AhR4DT-1.

Substrate specificity of AhR4DT-1 in microsomal fraction of *Nicotiana benthamiana* leaf after vacuum infiltration with *Agrobacterium tumefaciens* LBA4404 harboring pBIB-Kan-AhR4DT-1.

(A) Chemical structures of piceatannol and its prenylated product.

(B) HPLC chromatograms (UV 320 nm) of ethyl acetate extraction of reaction mixtures contained 100 μM piceatannol, 300 μM DMAPP, 10 mM MgCl_2 , 5 mM DTT and 30 μg microsomal fraction in a pH 9.0 Tris-HCl buffer for 40 min.

(C) HPLC-PAD-ESI-MS³ analysis of prenylated product, arachidin-5.

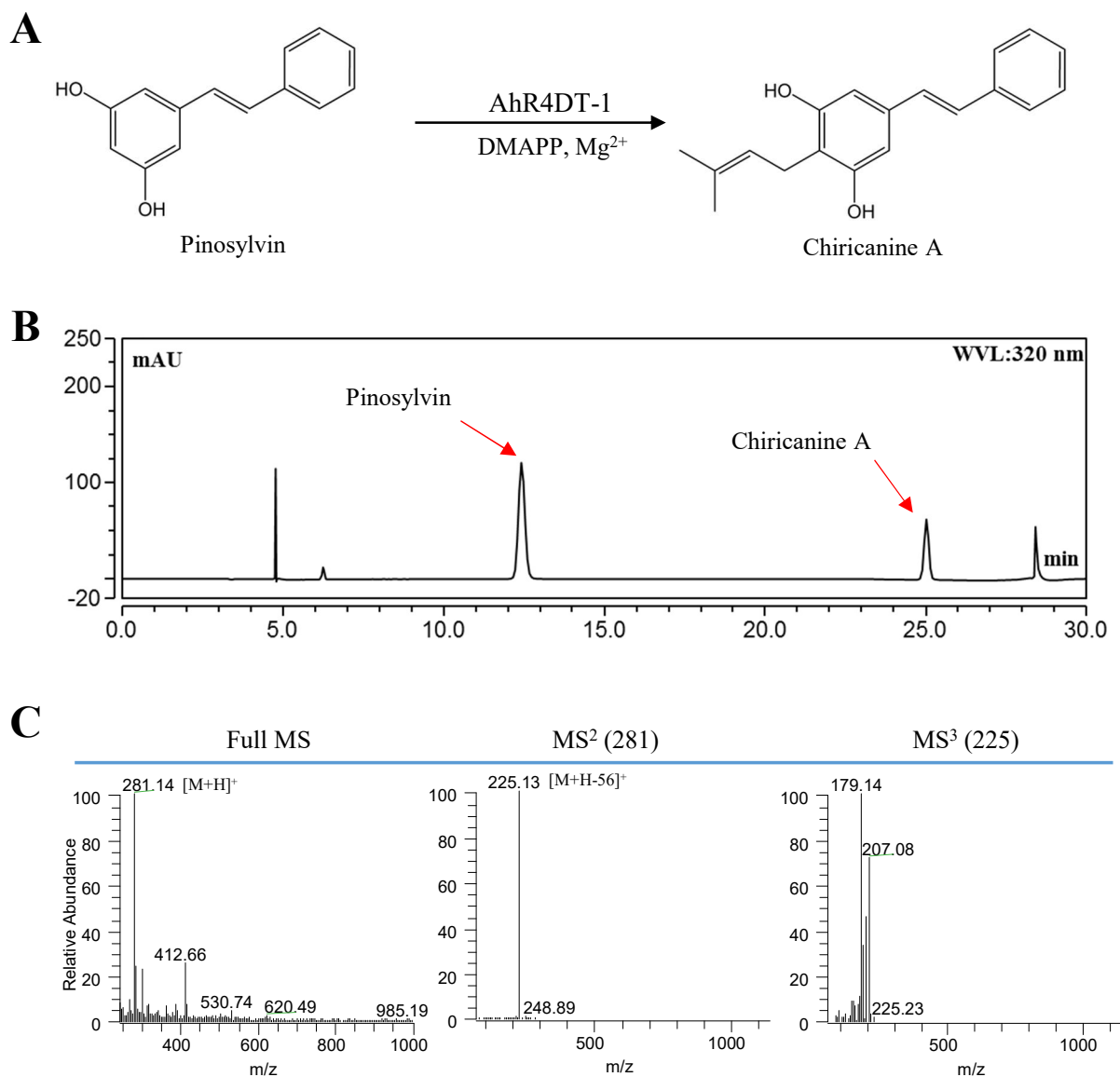


Figure S11. Prenylation of pinosylvin by AhR4DT-1.

Substrate specificity of AhR4DT-1 in microsomal fraction of *Nicotiana benthamiana* leaf after vacuum infiltration with *Agrobacterium tumefaciens* LBA4404 harboring pBIB-Kan-AhR4DT-1.

(A) Chemical structures of pinosylvin and its prenylated product.

(B) HPLC chromatograms (UV 320 nm) of ethyl acetate extraction of reaction mixtures contained 100 μ M pinosylvin, 300 μ M DMAPP, 10 mM $MgCl_2$, 5 mM DTT and 30 μ g microsomal fraction in a pH 9.0 Tris-HCl buffer for 40 min.

(C) HPLC-PAD-ESI-MS³ analysis of prenylated product, chiricanine A.

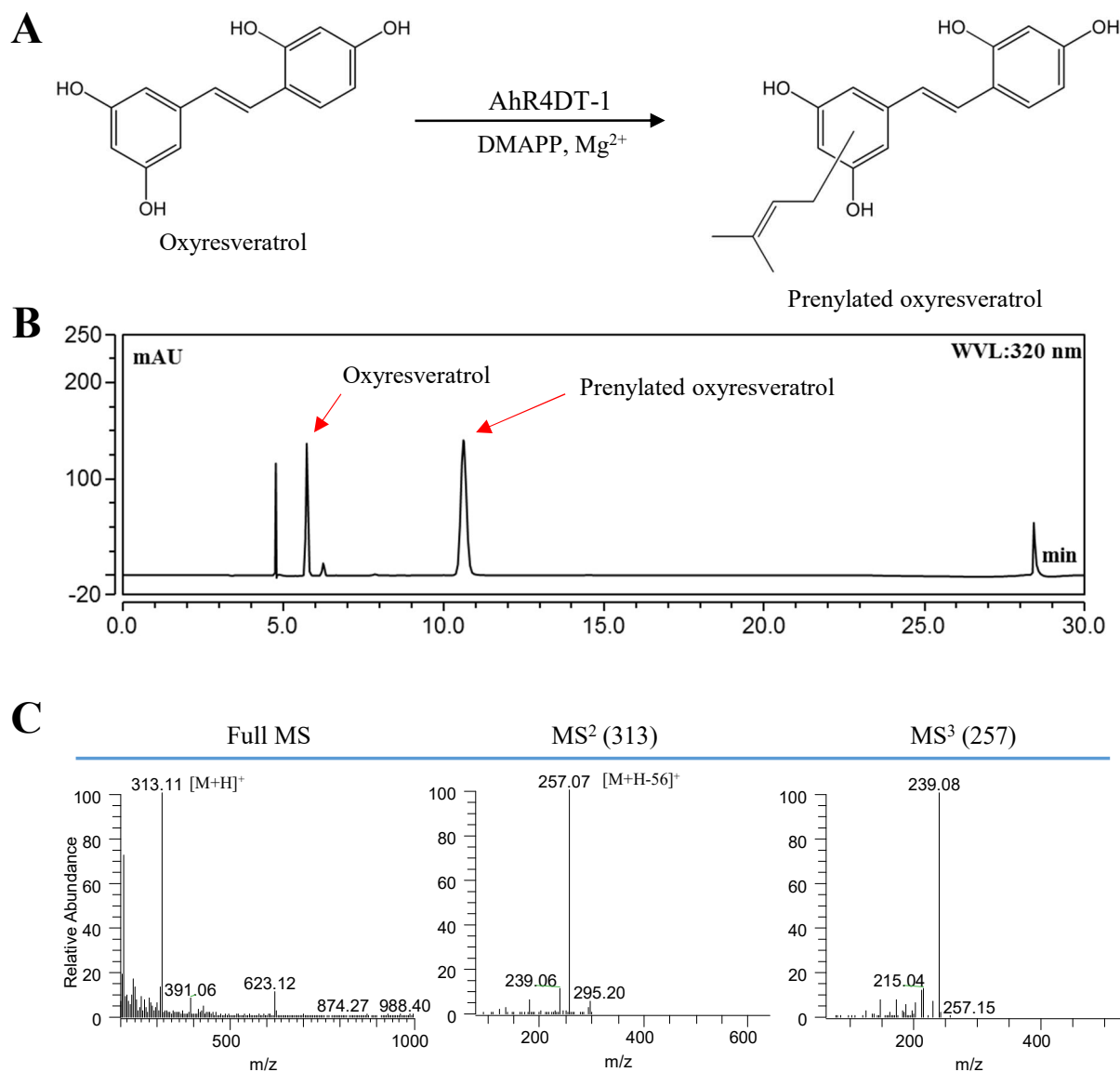


Figure S12. Prenylation of oxyresveratrol by AhR4DT-1.

Substrate specificity of AhR4DT-1 in microsomal fraction of *Nicotiana benthamiana* leaf after vacuum infiltration with *Agrobacterium tumefaciens* LBA4404 harboring pBIB-Kan-AhR4DT-1.

(A) Chemical structures of oxyresveratrol and its prenylated product.

(B) HPLC chromatograms (UV 320 nm) of ethyl acetate extraction of reaction mixtures contained 100 μM oxyresveratrol, 300 μM DMAPP, 10 mM MgCl_2 , 5 mM DTT and 30 μg microsomal fraction in a pH 9.0 Tris-HCl buffer for 40 min.

(C) HPLC-PAD-ESI- MS^3 analysis of prenylated product.

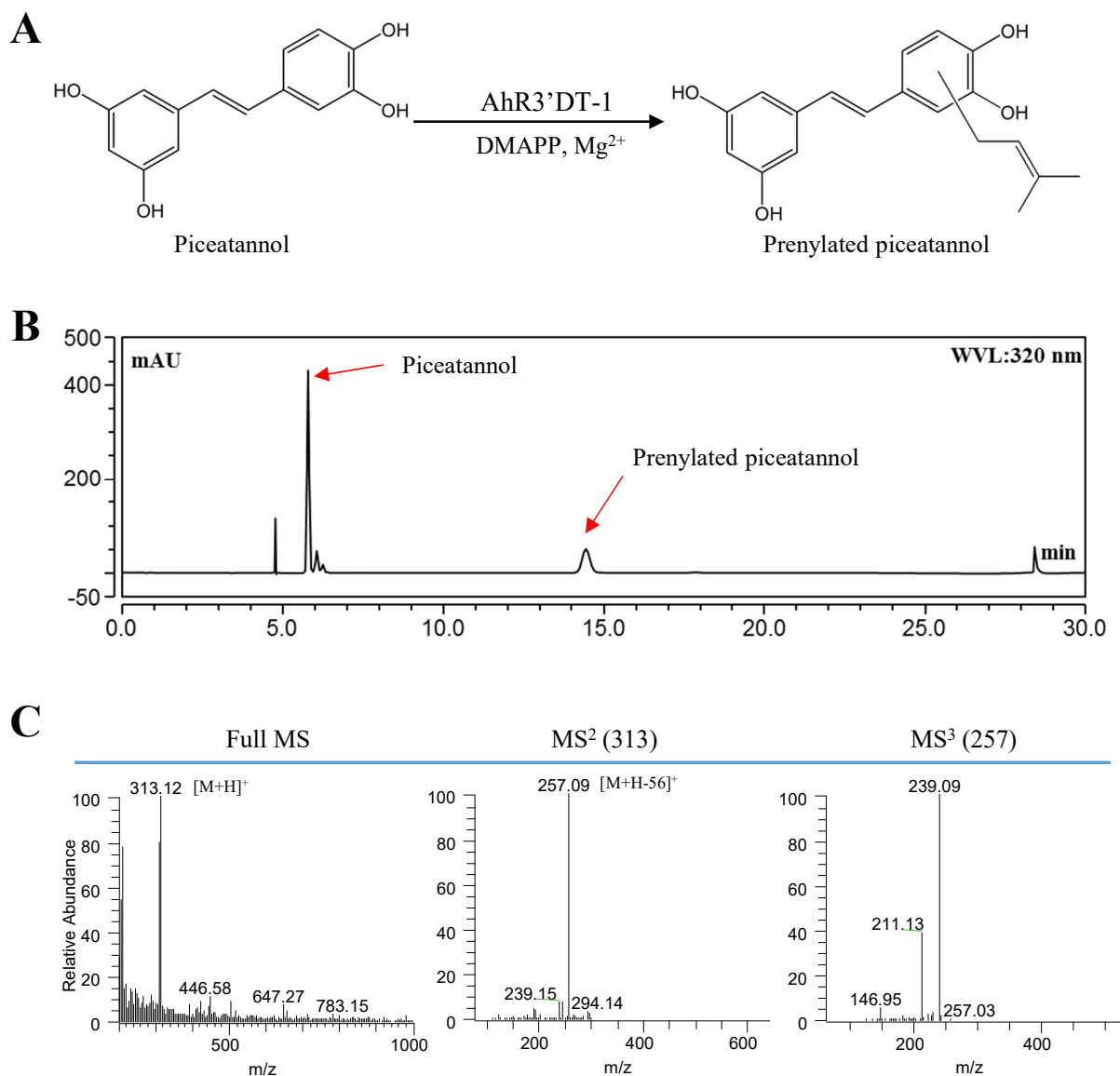


Figure S13. Prenylation of piceatannol by AhR3'DT-1.

Substrate specificity of AhR3'DT-1 in microsomal fraction of *Nicotiana benthamiana* leaf after vacuum infiltration with *Agrobacterium tumefaciens* LBA4404 harboring pBIB-Kan-AhR3'DT-1.

(A) Chemical structures of piceatannol and its prenylated product.

(B) HPLC chromatograms (UV 320 nm) of ethyl acetate extraction of reaction mixtures contained 100 μM piceatannol, 300 μM DMAPP, 10 mM MgCl_2 , 5 mM DTT and 30 μg microsomal fraction in a pH 9.0 Tris-HCl buffer for 40 min.

(C) HPLC-PAD-ESI-MS³ analysis of prenylated product.

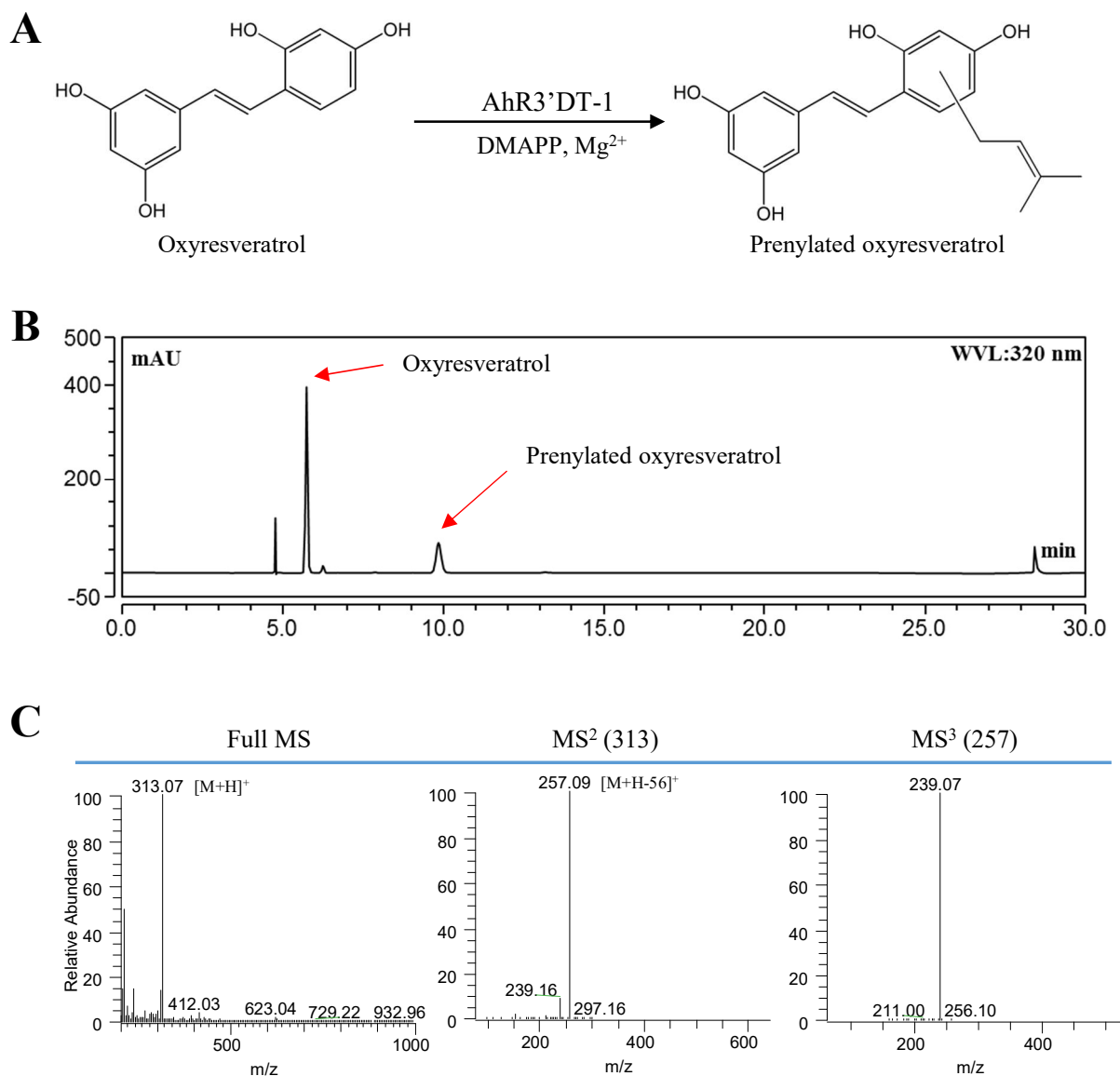


Figure S14. Prenylation of oxyresveratrol by AhR3'DT-1.

Substrate specificity of AhR3'DT-1 in microsomal fraction of *Nicotiana benthamiana* leaf after vacuum infiltration with *Agrobacterium tumefaciens* LBA4404 harboring pBIB-Kan-AhR3'DT-1.

(A) Chemical structures of oxyresveratrol and its prenylated product.

(B) HPLC chromatograms (UV 320 nm) of ethyl acetate extraction of reaction mixtures contained 100 μM oxyresveratrol, 300 μM DMAPP, 10 mM MgCl_2 , 5 mM DTT and 30 μg microsomal fraction in a pH 9.0 Tris-HCl buffer for 40 min.

(C) HPLC-PAD-ESI- MS^3 analysis of prenylated product.

Table S1. List of primers used in this study.

The restriction site on each primer is underlined.

Name	Sequence (5'-3')	Reference
First screening for prenyltransferase gene		
PT-10-FW- <i>NotI</i>	TAG <u>CGGCCGC</u> ATGGCTTTTGGTGTTGTTGCTGC	This study
PT-a-RV- <i>KpnI</i>	ATCGAT <u>GGTACCT</u> ATTTTTTAAGAAGTTTTTTACTGC	This study
PT-d-RV- <i>KpnI</i>	ATCGATG <u>AGGTACCT</u> CATGGAAATAGTTGAACAGAGAG	This study
PT-k-RV- <i>KpnI</i>	CGAT <u>GGTACCT</u> CATCTAACAAAAAGCATAAGAATATTTTC	This study
Second screening for prenyltransferase gene		
PT-4-FW- <i>NotI</i>	TAG <u>CGGCCGC</u> ATGCCTTTCGGACTCTCCGC	This study
PT-5-FW- <i>NotI</i>	TAG <u>CGGCCGC</u> ATGGCTTCCACTTCCAGGCT	This study
PT-6-FW- <i>NotI</i>	TAG <u>CGGCCGC</u> ATGGCTTTTAGGCTTCTAGGATC	This study
PT-9-FW- <i>NotI</i>	TAG <u>CGGCCGC</u> ATGGCTTTTGGGCATTTGGTGT	This study
PT-b-RV- <i>KpnI</i>	CTG <u>AGGTACCT</u> CAACGAACAAATTGTATAAGGATG	This study
PT-c-RV- <i>KpnI</i>	CTG <u>AGGTACCT</u> TATCTCACGAAAAGTATAAGGATG	This study
PT-e-RV- <i>KpnI</i>	CTG <u>AGGTACCT</u> CATCGAACAAAAAGTACAAGGAAG	This study
PT-i-RV- <i>KpnI</i>	CTG <u>AGGTACCT</u> TAGTTATTGGTTACCTTAAACATA	This study
PT-m-RV- <i>KpnI</i>	CTG <u>AGGTACCT</u> TATCTCACAAAAAGCACAAGGACA	This study
Promoter cloning		
Ca35S-FW- <i>SalI</i> -1	ATCGAT <u>GTCGACA</u> AAGCTTGCATGCCTG	This study
TEV-RW- <i>NotI</i>	ATCGAT <u>GCGGCCGC</u> GCTATCGTTCGTAATGGTGA	This study
GFP fusion protein cloning		
mgfp5-FW- <i>BamHI</i>	ATCGAT <u>GGATCC</u> ATGGCTAGTAAAGGAGAAGAAGCTTTTC	This study
mgfp5-FW- <i>NotI</i>	ATCGAT <u>GCGGCCGC</u> ATGGCTAGTAAAGGAGAAGAAGCTTTT	This study
mgfp5-RW- <i>KpnI</i>	ATCGAT <u>GGTACCT</u> CATTTGTATAGTTCATCCAT	This study
PT-10k1-RV- <i>BamHI</i>	ATCGAT <u>GGATCC</u> TCTAACAAAAAGCATAAGAA	This study
PT-9b13-RV- <i>BamHI</i>	AT <u>GGATCC</u> ACGAACAAATTGTATAAGGATG	This study
Ca35S-FW- <i>SalI</i> -2	GATACCGTCGACAAGCTTGCATG	This study
Real time-quantitative PCR		
AHR4DT-1-FW	ACTTCTGGAGTTATACTTGTG	This study
AHR4DT-1-RV	TAGATAGTGATGTGAGGATTATAG	This study
AHR3'DT-1-FW	GCAGCATAATTGGAAGCA	This study
AHR3'DT-1-RV	GGAAAGCATCTAAAGCATCA	This study
JC1-FW	TATGTATTTAACAGAAGAAATAC	(Condori et al., 2009)
JC1-RV	AGTTGCAGCCTCTTTTCCAAC	(Condori et al., 2009)
ACT7-FW	ATGTATGTAGCCATCCAAG	(Condori et al., 2011)
ACT7-RV	ACCAGAGTCCAGAACAATA	(Condori et al., 2011)
EF1 α -FW	GGTGTCAAGCAGATGATT	(Condori et al., 2011)
EF1 α -RV	ACTTCCTCACGATTCA	(Condori et al., 2011)

Table S2. Substrates used for specificity assay and the prenylated products from reaction mixtures catalyzed by AhR4DT-1 or AhR3'DT-1.

Analysis was done by HPLC-PDA-electrospray ionization-MS³.

No	Analyte	<i>t_R</i> (min)	UV (nm)	[M+H] ⁺ (m/z)	MS ² ions	MS ³ ions
1	Oxyresveratrol	5.74	243, 302, 328	245	227	209 , 199, 157
2	Piceatannol	5.79	240, 324	245	227, 199, 135^a	107
3	Resveratrol	6.50	237, 306, 317	229	211 , 183	107
4	Prenylated oxyresveratrol by AhR3'DT-1	9.85	225, 325	313	257	239
5	Prenylated oxyresveratrol by AhR4DT-1	10.63	225, 304, 329	313	257	239
6	Arachidin-5	11.01	240, 327	313	257	239, 229, 211
7	Pinosylvin	12.42	229, 300, 307	213	135	107
8	Arachidin-2	13.84	239, 311, 323	297	241	223, 213, 195
9	Prenylated piceatannol by AhR3'DT-1	14.44	228, 325	313	257	239 , 211
10	3-methyl-2-butenyl-3'-resveratrol	16.99	230, 320	297	241	223
11	Chiricanine A	25.02	209, 314	281	225	179 , 207

^aMS² ions in boldface were the most abundant ions and were subjected to MS³ fragmentation.

Table S3. List of plasmids used in this study.

For details of the binary vectors, see Materials and Methods.

Name	Description	Reference
pBC KS(-)	Phagemid vector derived from pBluescript II KS(-)	
pBIB-Kan	Binary vector	(Becker, 1990)
pR8-2	<i>CaMV35S::TEV::pat::mGFP5</i> in pBC KS(-)	(Medina-Bolívar and Cramer, 2004)
Prenyltransferase Characterization		
pGEM-CaMV35S-TEV	<i>CaMV35S::TEV</i> in pGEM-T	This study
pBC-CaMV35S-TEV-9b13	<i>CaMV35S::TEV::AhR4DT-1</i> in pBC KS(-)	This study
pBC-CaMV35S-TEV-10k1	<i>CaMV35S::TEV::AhR3'DT-1</i> in pBC KS(-)	This study
pBIB-Kan-AhR4DT-1	<i>CaMV35S::TEV::AhR4DT-1</i> in pBIB-Kan	This study
pBIB-Kan-AhR3'DT-1	<i>CaMV35S::TEV::AhR3'DT-1</i> in pBIB-Kan	This study
pBIB-Kan-AhR3'DT-2	<i>CaMV35S::TEV::AhR3'DT-2</i> in pBIB-Kan	This study
pBIB-Kan-AhR3'DT-3	<i>CaMV35S::TEV::AhR3'DT-3</i> in pBIB-Kan	This study
pBIB-Kan-AhR3'DT-4	<i>CaMV35S::TEV::AhR3'DT-4</i> in pBIB-Kan	This study
Subcellular Localization		
pt-rk	<i>CaMV35S::RS-TP-mCherry</i> in pBIN20	(Nelson et al., 2007)
pGEM-mGFP5-1	<i>mGFP5</i> with <i>Bam</i> HI/ <i>Kpn</i> I sites in pGEM-T	This study
pGEM-mGFP5-2	<i>mGFP5</i> with <i>Not</i> I/ <i>Kpn</i> I sites in pGEM-T	This study
pGEM-CaMV35S-TEV-AhR4DT-1-GFP	<i>CaMV35S::TEV::AhR4DT-1::mGFP5</i> in pGEM-T	This study
pGEM-CaMV35S-TEV-AhR3'DT-1-GFP	<i>CaMV35S::TEV::AhR3'DT-1::mGFP5</i> in pGEM-T	This study
pBC-CaMV35S-TEV-GFP	<i>CaMV35S::TEV::mGFP5</i> in pBC KS(-)	This study
pBIB-Kan-AhR4DT-1-GFP	<i>CaMV35S::TEV::AhR4DT-1::mGFP5</i> in pBIB-Kan	This study
pBIB-Kan-AhR3'DT-1-GFP	<i>CaMV35S::TEV::AhR3'DT-1::mGFP5</i> in pBIB-Kan	This study
pBIB-Kan-GFP	<i>CaMV35S::TEV::mGFP5</i> in pBIB-Kan	This study

Table S4. Accession numbers of proteins used for phylogenetic analysis.

Protein name	Accession number	Description	Organism
AaVTE2-1	ABB70124.1	homogentisate phytyltransferase VTE2-1	<i>Allium ampeloprasum</i>
AhR4DT-1	AQM74172.1	resveratrol-4-dimethylallyltransferase	<i>Arachis hypogaea</i>
AhR3'DT-1	AQM74173.1	resveratrol-3'-dimethylallyltransferase	<i>Arachis hypogaea</i>
AhR3'DT-2	AQM74174.1	resveratrol-3'-dimethylallyltransferase	<i>Arachis hypogaea</i>
AhR3'DT-3	AQM74175.1	resveratrol-3'-dimethylallyltransferase	<i>Arachis hypogaea</i>
AhR3'DT-4	AQM74176.1	resveratrol-3'-dimethylallyltransferase	<i>Arachis hypogaea</i>
AtHPT1	AAM10489.1	homogentisate phytylprenyltransferase	<i>Arabidopsis thaliana</i>
AtPPT1	BAB20818.2	p-hydroxybenzoate polyprenyltransferase	<i>Arabidopsis thaliana</i>
AtVTE2-2	ABB70127.1	homogentisate phytyltransferase VTE2-2	<i>Arabidopsis thaliana</i>
CIPT1a	BAP27988.1	umbelliferone 8-geranyltransferase	<i>Citrus limon</i>
CpVTE2-1	ABB70125.1	homogentisate phytyltransferase VTE2-1	<i>Cuphea pulcherrima</i>
CrVTE2-2	CAL01105.1	homogentisate prenyltransferase	<i>Chlamydomonas reinhardtii</i>
CtIDT	AJD80983.1	isoliquiritigenin 3'-dimethylallyltransferase	<i>Cudrania tricuspidata</i>
GmG4DT	BAH22520.1	pterocarpan 4-dimethylallyltransferase	<i>Glycine max</i>
GmVTE2-1	ABB70126.1	homogentisate phytyltransferase VTE2-1	<i>Glycine max</i>
GmVTE2-2	ABB70128.1	homogentisate phytyltransferase VTE2-2	<i>Glycine max</i>
GuA6DT	AIT11912.1	flavone prenyltransferase	<i>Glycyrrhiza uralensis</i>
HIPT-1	BAJ61049.1	aromatic prenyltransferase	<i>Humulus lupulus</i>
HvHGGT	AAP43911.1	homogentisic acid geranylgeranyl transferase	<i>Hordeum vulgare</i>
LaPT-1	AER35706.1	genistein 3'-dimethylallyltransferase	<i>Lupinus albus</i>
LePGT-1	BAB84122.1	4-hydroxybenzoate geranyltransferase	<i>Lithospermum erythrorhizon</i>
LePGT-2	BAB84123.1	4-hydroxybenzoate geranyltransferase	<i>Lithospermum erythrorhizon</i>
MaIDT	AJD80982.1	isoliquiritigenin 3'-dimethylallyltransferase	<i>Morus alba</i>
OsHGGT	AAP43913.1	homogentisic acid geranylgeranyl transferase	<i>Oryza sativa</i>
OsPPT1	BAE96574.1	p-hydroxybenzoate polyprenyltransferase	<i>Oryza sativa</i>
PcPT	BAO31627.1	umbelliferone 6-dimethylallyltransferase	<i>Petroselinum crispum</i>
SfG6DT	BAK52291.1	genistein 6-dimethylallyltransferase	<i>Sophora flavescens</i>
SfILD	BAK52290.1	isoliquiritigenin dimethylallyltransferase	<i>Sophora flavescens</i>
SfN8DT-1	BAG12671.1	naringenin 8-dimethylallyltransferase	<i>Sophora flavescens</i>
SfN8DT-2	BAG12673.1	naringenin 8-dimethylallyltransferase	<i>Sophora flavescens</i>
SfN8DT-3	BAK52289.1	naringenin 8-dimethylallyltransferase	<i>Sophora flavescens</i>
TaHGGT	AAP43912.1	homogentisic acid geranylgeranyl transferase	<i>Triticum aestivum</i>
TaVTE2-1	ABB70123.1	homogentisate phytyltransferase VTE2-1	<i>Triticum aestivum</i>
ZmVTE2-1	ABB70122.1	homogentisate phytyltransferase VTE2-1	<i>Zea mays</i>