Electronic supplementary information

Rapid biosynthesis of phenolic glycosides and their derivatives from biomass-derived hydroxycinnamates

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1. Supporting Tables

Table S1. Main products synthesized from biomass-derived aromatics and their applications in this study.

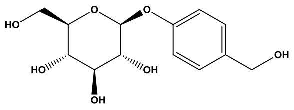
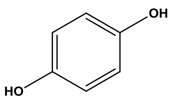
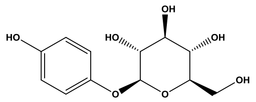
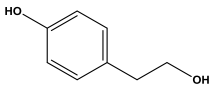
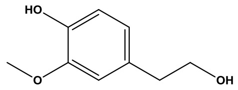
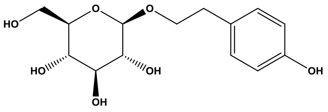
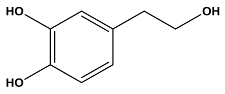
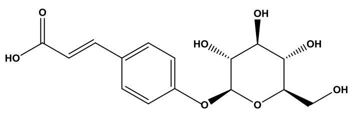
Products	Names/Applications
	**9 Gastrodin**. Treating diseases like headache, dizziness, vertigo and convulsion;[1-3] presenting manifold biological activities, such as anti-inflammation,[4] anxiolytic activity,[5] anti-oxidant, anti-obesity,[6] anti-epilepsy,[7] neuroprotection[8] and memory improvement[9]
	**11 Hydroquinone**. An intermediate used in chemicals, pharmaceutical and polymer industries;[10] a pheromone for termites;[11] a precursor for arbutin biosynthesis[12]
	**12 Arbutin**. A skin-lightener;[13] presenting manifold biological activities, such as anti-oxidant,[14] anti-inflammatory,[15] and anti-bacterial[16]
	**17 Tyrosol**. Presenting manifold biological activities, such as prevention of cardiovascular diseases,[17] osteopenia;[18] anti-inflammatory and antioxidant activity;[19] an intermediate in organic synthesis of critical medicines such as metoprolol,[20] β-xolol,[21] and salidroside[19]
	**18 Homovanilly alcohol**. An antioxidant and a potential medicine for cardiovascular diseases [22]
	**19 Salidroside**. Presenting manifold biological activities, such as anti-inflammation activities,[23] antiaging, anoxia resistance,[24] cardiovascular disease prevention,[25] anticancer,[26] brain cell protection;[27] a potential nutraceutical supplement[28]
	**20 Hydroxytyrosol**. Presenting manifold biological activities, such as anti-oxidant,[29, 30] inhibiting platelet aggregation;[31] antimicrobial,[32] anticarcinogenic[33] and anti-inflammatory activities[34]
	**22 β-glucoside of *p*-coumaric acid.** Potential antibacterial, antiviral, anti-infammatory[35]

Table S2. Main plasmids used in this study

Plasmids	Descriptions	Sources
pET-28a(+)	Single T7 promoter, T7 term, PBR322 ori, Kan^{R}	Novagen
pA7a-RFP	Single T7 promoter, dbl term, P15A ori, Amp^{R}	BglBrick
pACYCDuet-1	Double T7 promoters, T7 term, PBR322 ori, Cm^{R}	Invitrogen
pET28a-Ado	pET28a carrying *ado*	this study
pET28a-TtAdo	pET28a carrying *Ttado*	this study
pET28a-CgAdo	pET28a carrying *Cgado*	this study
pET28a-PaAdo	pET28a carrying *Paado*	this study
pET28a-TtAdo-BLPad	pET28a carrying *Ttado* and *blpad*	this study
pET28a-Fcs-Ech	pET28a carrying *fcs* and *ech*	this study
pET28a-YahK	pET28a carrying *yahK*	this study
pET28a-YqhD	pET28a carrying *yqhD*	this study
pET28a-ScADH6	pET28a carrying *ScADH6*	this study
pET28a-SlPAR1	pET28a carrying *SlPAR1*	this study
pET28a-Fcs-Ech-SlPAR1	pET28a carrying *fcs*, *ech* and *SlPAR1*	this study
pA7a-UGT73B6^{FS}	pA7a carrying *ugt73b6*^{FS}	this study
pET28a-Fcs-Ech-Vdh	pET28a carrying *fsc*, *ech* and *vdh*	this study
pA7a-MNX1	pA7a carrying *MNX1*	this study
pA7a-vibMO1	pA7a carrying *vibMO1*	this study
pA7a-Vdh-MNX1-AS	pA7a carrying *vdh*, *MNX1* and *AS*	this study
pA7a-MNX1-AS	pA7a carrying *MNX1* and *AS*	this study
pA7a-AS-MNX1	pA7a carrying *AS* and *MNX1*	this study
pA7a-AS-7-MNX1	pA7a carrying *AS* and *MN*X1	this study
pACYC-AS-MNX1	pACYCDuet-1 carrying *AS* and *MNX1*	this study
pA7a-BLPad	pA7a carrying *blpad*	this study
pET28a-StyAB	pET28a carrying *styAB*	this study
pET28a-RostyC	pET28a carrying *RostyC*	this study
pET28a-StyAB-RostyC	pET28a carrying *styAB* and *RostyC*	this study
pET28a-StyAB-RostyC-7-BLPad	pET28a carrying *styAB*, *RostyC* and *blpad*	this study
pET28a-StyAB-RostyC-SlPAR1	pET28a carrying *styAB*, *RostyC* and *SIPAR1*	this study
pET28a-StyAB-RostyC-YqhD	pET28a carrying *styAB*, *RostyC* and *yqhD*	this study
pET28a-StyAB-RostyC-YahK	pET28a carrying *styAB*, *RostyC* and *yahK*	this study
pA7a-BLPad-7-SlPAR1	pA7a carrying *blpad* and *SlPAR1*	this study
pA7a-BLPad-7-YqhD	pA7a carrying *blpad* and *yqhD*	this study
pA7a-BLPad-7-YahK	pA7a carrying *blpad* and *yahK*	this study
pA7a-BLPad-7-HpaBC	pA7a carrying *blpad* and *hpaBC*	this study
pA7a-BLPad-7-UGT85A1	pA7a carrying *blpad* and *ugt85a1*	this study
pET28a-UGT85A1	pET28a carrying *ugt85a1*	this study
pET28a-UGT$_{BL}$1	pET28a carrying *ugt*$_{BL}$*1*	this study

Table S3. Main strains used in this study

Strains	Descriptions	Reactions
E. coli BL21 (DE3)	F$^-$ *ompT hsdS$_B$ (r$_B^-$m$_B^-$) gal dcm (DE3)*	
DH5α	Cloning host	
E. coli (pET28a-Fcs-Ech)	*E. coli* BL21 (DE3) with pET28a-Fcs-Ech	**1** to **5** **2** to **6**
E. coli (pET28a-BLPad-TtAdo)	*E. coli* BL21 (DE3) with pET28a-BLPad-TtAdo	**1** to **5** **2** to **6**
E. coli (Fcs-Ech-SlPAR1)	*E. coli* BL21 (DE3) with pET28a-Fcs-Ech-SlPAR1	**1** to **7**
E. coli (UGT73B6^{FS})	*E. coli* BL21 (DE3) with pA7a-UGT73B6^{FS}	**7** to **9**
E. coli (Fcs-Ech-SlPAR1-UGT73B6^{FS})	*E. coli* BL21 (DE3) with pET28a-Fcs-Ech-SlPAR1 and pA7a-UGT73B6^{FS}	**1** to **9**
E. coli (Fcs-Ech-Vdh-MNX1)	*E. coli* BL21 (DE3) with pET28a-Fcs-Ech-Vdh and pA7a-MNX1	**1** to **11**
E. coli (AS)	*E. coli* BL21 (DE3) with pA7a-AS	**11** to **12**
SArbutin 1	*E. coli* BL21 (DE3) with pET28a-Fcs-Ech and pA7a-Vdh-MNX1-AS	**1** to **12**
SArbutin 2	*E. coli* BL21 (DE3) with pET28a-Fcs-Ech-Vdh and pA7a-MNX1-AS	**1** to **12**
SArbutin 3	*E. coli* BL21 (DE3) with pET28a-Fcs-Ech-Vdh and pA7a-AS-MNX1	**1** to **12**
SArbutin 4	*E. coli* BL21 (DE3) with pET28a-Fcs-Ech-Vdh and pA7a-AS-7-MNX1	**1** to **12**
SArbutin 5	*E. coli* BL21 (DE3) with pET28a-Fcs-Ech-Vdh and pACYC-AS-MNX1	**1** to **12**
E. coli (StyAB)	*E. coli* BL21 (DE3) with pET28a-StyAB	**3** to **13**
E. coli (StyAB-RostyC)	*E. coli* BL21 (DE3) with pET28a-StyAB-RostyC	**3** to **15**
Styrosol 1	*E. coli* BL21 (DE3) with pET28a-StyAB-RostyC-7-BLPad	**1** to **17** **2** to **18**
Styrosol 2	*E. coli* BL21 (DE3) with pET28a-StyAB-RostyC and pA7a-BLPad	**1** to **17** **2** to **18**
Styrosol 3	*E. coli* BL21 (DE3) with pET28a-StyAB-RostyC-SlPAR1and pA7a-BLPad	**1** to **17** **2** to **18**
Styrosol 4	*E. coli* BL21 (DE3) with pET28a-StyAB-RostyC-YqhD and pA7a-BLPad	**1** to **17** **2** to **18**
Styrosol 5	*E. coli* BL21 (DE3) with pET28a-StyAB-RostyC-YahK and pA7a-BLPad	**1** to **17** **2** to **18**
Styrosol 6	*E. coli* BL21 (DE3) with pET28a-StyAB-RostyC and pA7a-BLPad-7-SlPAR1	**1** to **17** **2** to **18**

Refer to Table S3 (continued).

Styrosol 7	*E. coli* BL21 (DE3) with pET28a-StyAB-RostyC and pA7a-BLPad-7-YqhD	**1** to **17** **2** to **18**
Styrosol 8	*E. coli* BL21 (DE3) with pET28a-StyAB-RostyC and pA7a-BLPad-**7**-YahK	**1** to **17** **2** to **18**
E. coli (BLPad-StyAB-RostyC-SlPAR1-UGT85A1)	*E. coli* BL21 (DE3) with pET28a-StyAB-RostyC-SlPAR1 and pA7a-BLPad-7-UGT85A1	**1** to **19**
E. coli (HpaBC)	*E. coli* BL21 (DE3) with pA7a-HpaBC	**17** to **20**
E. coli (StyAB-RostyC-SlPAR1-BLPad-HpaBC)	*E. coli* BL21 (DE3) with pET28a-StyAB-RostyC-SlPAR1 and pA7a-BLPad-7-HpaBC	**1** to **20**
E. coli (UGT85A1)	*E. coli* BL21 (DE3) with pET28a-UGT85A1	**17** to **19**
E. coli (UGTBL1)	*E. coli* BL21 (DE3) with pET28a-UGT$_{BL}$1	**1** to **22** **2** to **23**

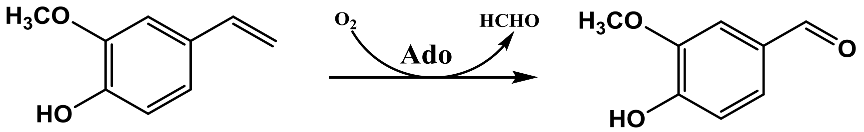
Note: Figures S2, S7, S9, S11, and S13 present detailed information of some *E. coli* strains.

Table S4. Comparison of glucose-based and biomass-derived aromatics-based biosynthesis for gastrodin (**9**), arbutin (**12**), salidroside (**19**), tyrosol (**17**) and hydroxytyrosol (**20**).

Product	Biocatalyst	Production process (Substrate)[a]	Productivity (mg L^{-1} h^{-1})*	Reference
Gastrodin				
	Escherichia coli	Growth system (Glc)	11.35	36
	Escherichia coli	Bioconversion (**1**)	**121±5.6**	This study
Arbutin				
	Escherichia coli	Growth system (Glc)	87.29	37
	Yarrowia lipolytica	Growth system (Glc)	59.7	38
	Escherichia coli	Bioconversion (**1**)	**127±6.1**	This study
Salidroside				
	Escherichia coli	Growth system (Glc)	2.375	39
	Escherichia coli	Growth system (Glc)	12	19
	Escherichia coli	Growth system (Glc)	46.74	40
	Saccharomyces cerevisiae	Growth system (Glc)	4.36	28
	Saccharomyces cerevisiae	Growth system (Glc)	0.03	41
	Saccharomyces cerevisiae	Growth system (Glc)	8.88	42
	Saccharomyces cerevisiae	Growth system (Glc)	9.47	43
	Escherichia coli	Bioconversion (**1**)	**179±9.6**	This study
Tyrosol				
	Escherichia coli	Growth system (Glc)	1.44	44
	Escherichia coli	Growth system (Glc)	15.52	45
	Escherichia coli	Growth system (Glc)	19.26	39
	Escherichia coli	Growth system (Glc)	11.93	46
	Escherichia coli	Growth system (Glc)	18.4	19
	Escherichia coli	Growth system (Glc)	27.42	47
	Escherichia coli	Growth system (Glc)	30.6	48
	Saccharomyces cerevisiae	Growth system (Glc)	8.3	28
	Escherichia coli	Growth system (Glc)	30.4	40
	Saccharomyces cerevisiae	Growth system (Glc)	2.64	49
	Escherichia coli	Growth system (Glc)	16.68	50
	Escherichia coli	Growth system (Glc)	80.5	51
	Saccharomyces cerevisiae	Growth system (Glc)	43.59	43
	Escherichia coli	Bioconversion (**1**)	**170±4.4**	This study
Hydroxytyrosol				
	Escherichia coli	Growth system (Glc)	13.48	48
	Escherichia coli	Growth system (Glc)	7.45	52
	Saccharomyces cerevisiae	Growth system (Glc)	0.064	53
	Escherichia coli	Bioconversion (**1**)	**229±7**	This study

a, Glc, Glucose; **1**, *p*-coumaric acid; *, biomass-derived aromatic-based biosynthesis is reported in this study (Values are presented in bold).

2. Supporting Figures



4 4-vinylguaiacol

6 Vanillin

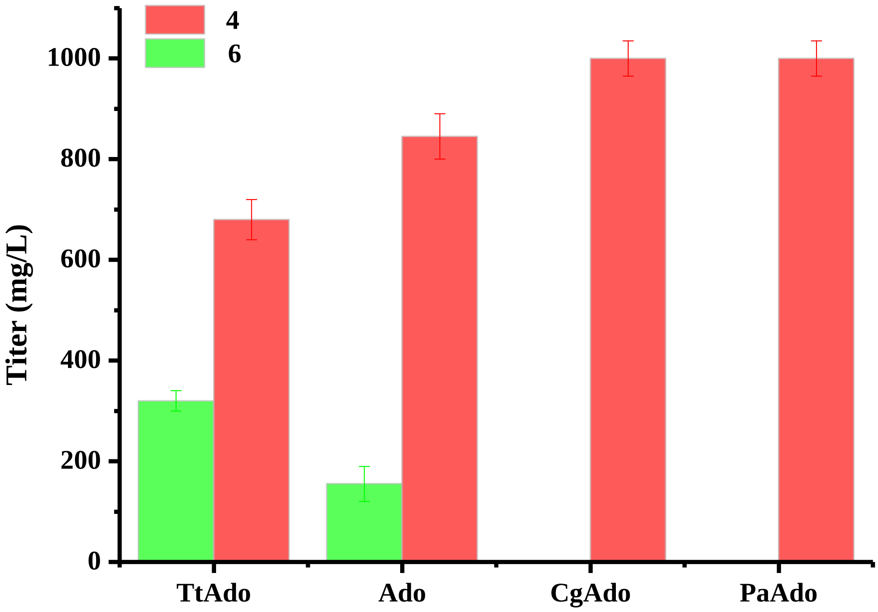


Fig. S1 Bioconversion of 4-vinylguaiacol (**4**) into vanillin (**6**). 1000 mg L^{-1} of **4** was converted into **6** using *E. coli* biocatalysts (OD_{600} of 10) expressing different aromatic dioxygenases (Ado). TtAdo (XP_003653923) from *Thielavia terrestris* NRRL 8126, CgAdo (XP_001219451) from *Chaetomium globosum* CBS 148.51, and PaAdo (XP_001905181) from *Podospora anserina* S mat+ was obtained based on the BLAST search of Ado (XP_00366585) from *Thermothelomyces thermophila*.[54]

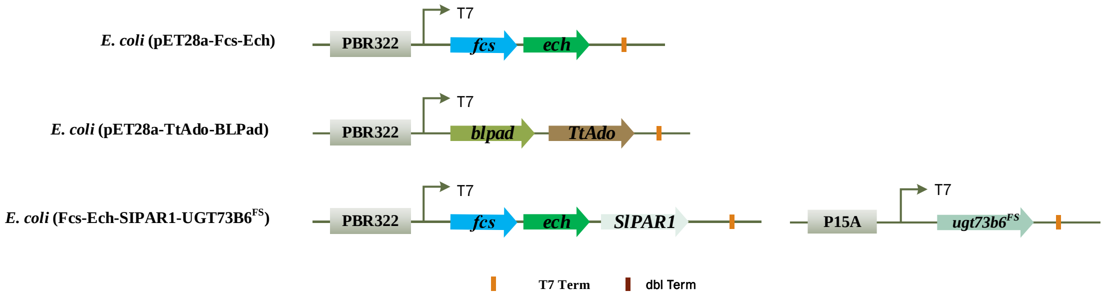


Fig. S2 Biocatalysts for gastrodin (**9**) synthesis. *E. coli* (pET28a-Fcs-Ech) expressing *fcs* and *ech* was engineered as coenzyme-dependent biocatalyst. Genes *fcs* and *ech* are from *Pseudomonas putida* KT2440[55]. *E. coli* (pET28a-BLPad-TtAdo) expressing *blpad* and *TtAdo* was engineered as coenzyme-free biocatalyst. Gene *blpad* is from *Bacillus licheniformis* strain CGMCC 7172.[56] *E. coli* (Fcs-Ech-SlPAR1-UGT73B6^{FS}) expressing *fcs*, *ech*, *SlPAR1* and *ugt73b6*^{FS} was engineered for synthesis of **9** from *p*-coumaric acid (**1**). Gene *slpar1* is from *Solanum lycopersicum*;[57] *ugt73b6*^{FS} is a mutant of *ugt73b6* from *Rhodiola sachalinensis*.[36] The recombinant plasmids and strains were listed in Table S2 and S3, respectively.

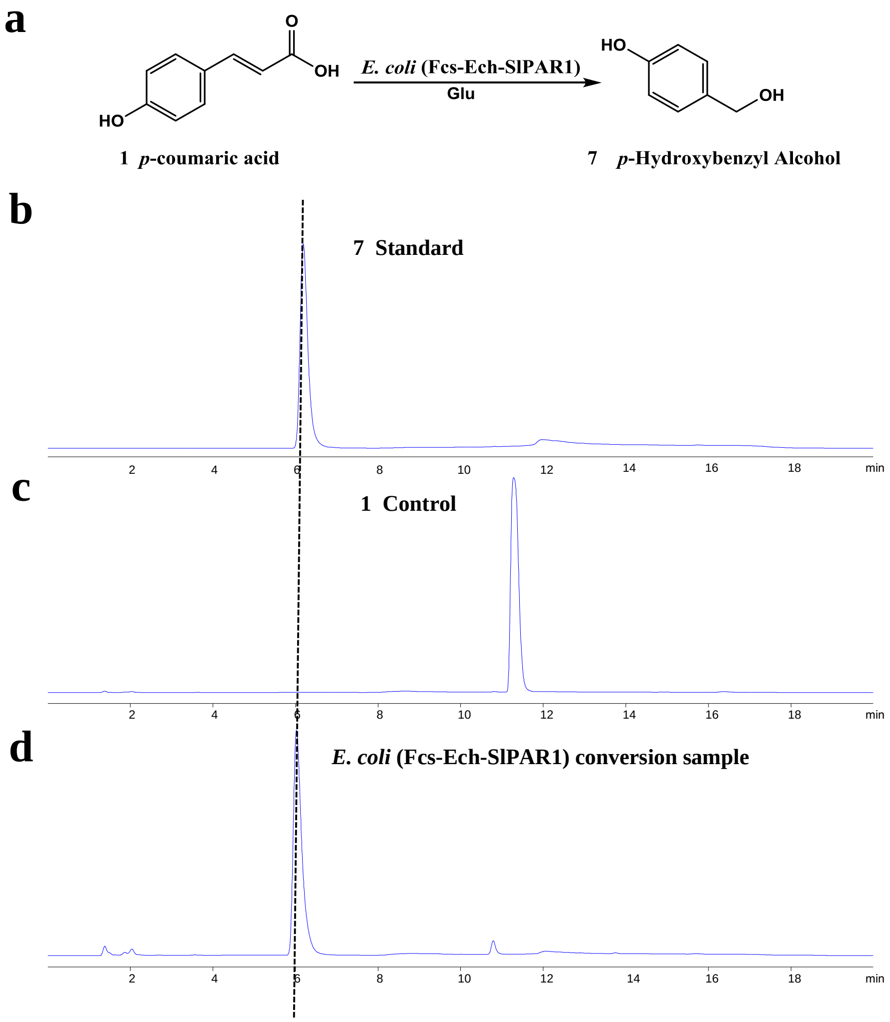


Fig. S3 Biocatalyst strain *E. coli* (Fcs-Ech-SlPAR1) (OD_{600} of 10) for *p*-hydroxybenzyl alcohol (**7**) synthesis from 2000 mg L^{-1} of *p*-coumaric acid (**1**). a) The reaction for **7** synthesis using *E. coli* (Fcs-Ech-SlPAR1). b) HPLC analysis of standard **7**. c) Negative control was performed using strain *E. coli* BL21 (DE3) containing an empty vector with adding 2000 mg L^{-1} of **1**. d) HPLC analysis of conversion product produced by *E. coli* (Fcs-Ech-SlPAR1).

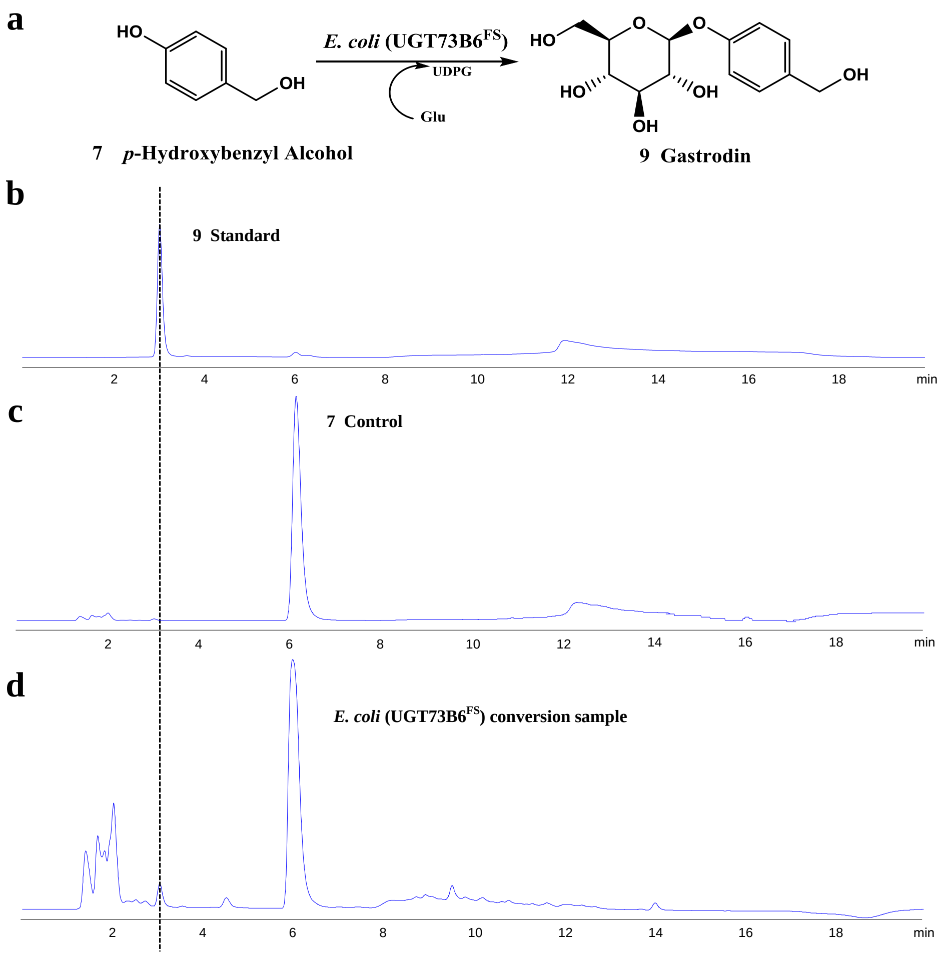
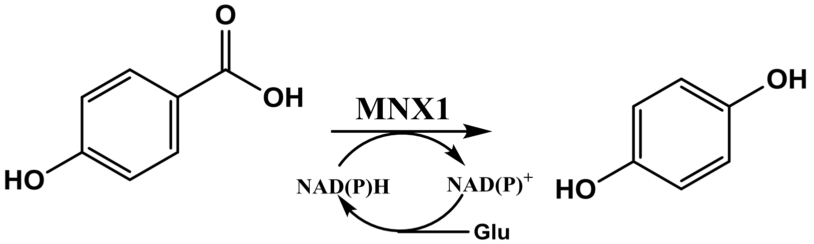


Fig. S4 Biocatalyst strain *E. coli* (UGT73B6^{FS}) (OD$_{600}$ of 10) for gastrodin (**9**) synthesis from 1000 mg L^{-1} of *p*-hydroxybenzyl alcohol (**7**). a) The reaction for **9** synthesis from **7** using *E. coli* (UGT73B6^{FS}). b) HPLC analysis of standard **9**. c) Negative control was performed using strain *E.coli* BL21 (DE3) containing an empty vector with adding 1000 mg L^{-1} of **7**. d) HPLC analysis of conversion product produced by *E. coli* (UGT73B6^{FS}).



10 ***p*-Hydroxybenzoic acid** **11** **Hydroquinone**

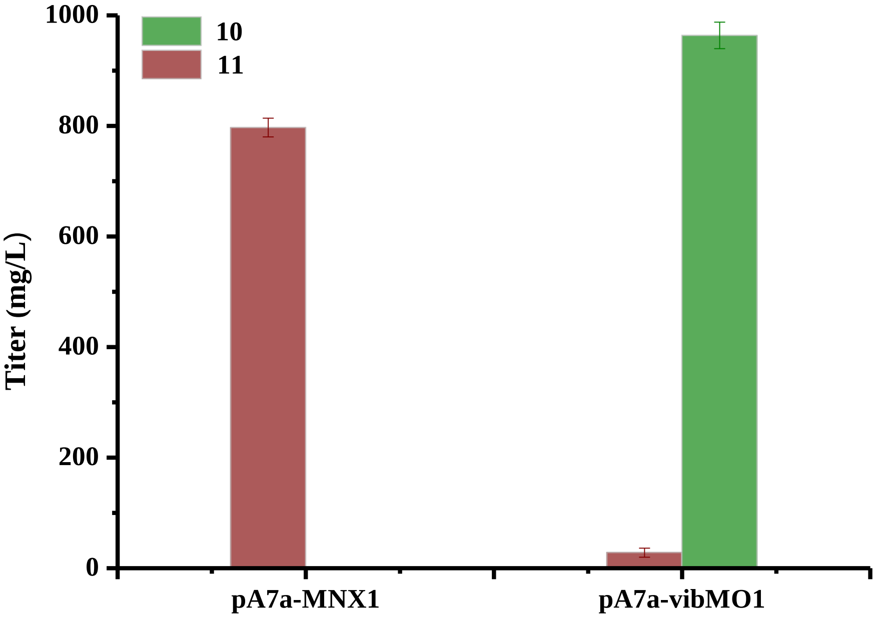


Fig. S5 Conversion of 1000 mg L^{-1} of *p*-hydroxybenzoic acid (**10**) into hydroquinone (**11**) using biocatalyst *E. coli* (OD_{600} of 10) expressing MNX1 or vibMO1. MNX1 from yeast *Candida parapsilosis* CDC317,[58] and vibMO1 from basidiomycete fungus *Boreostereum vibrans*.[59]

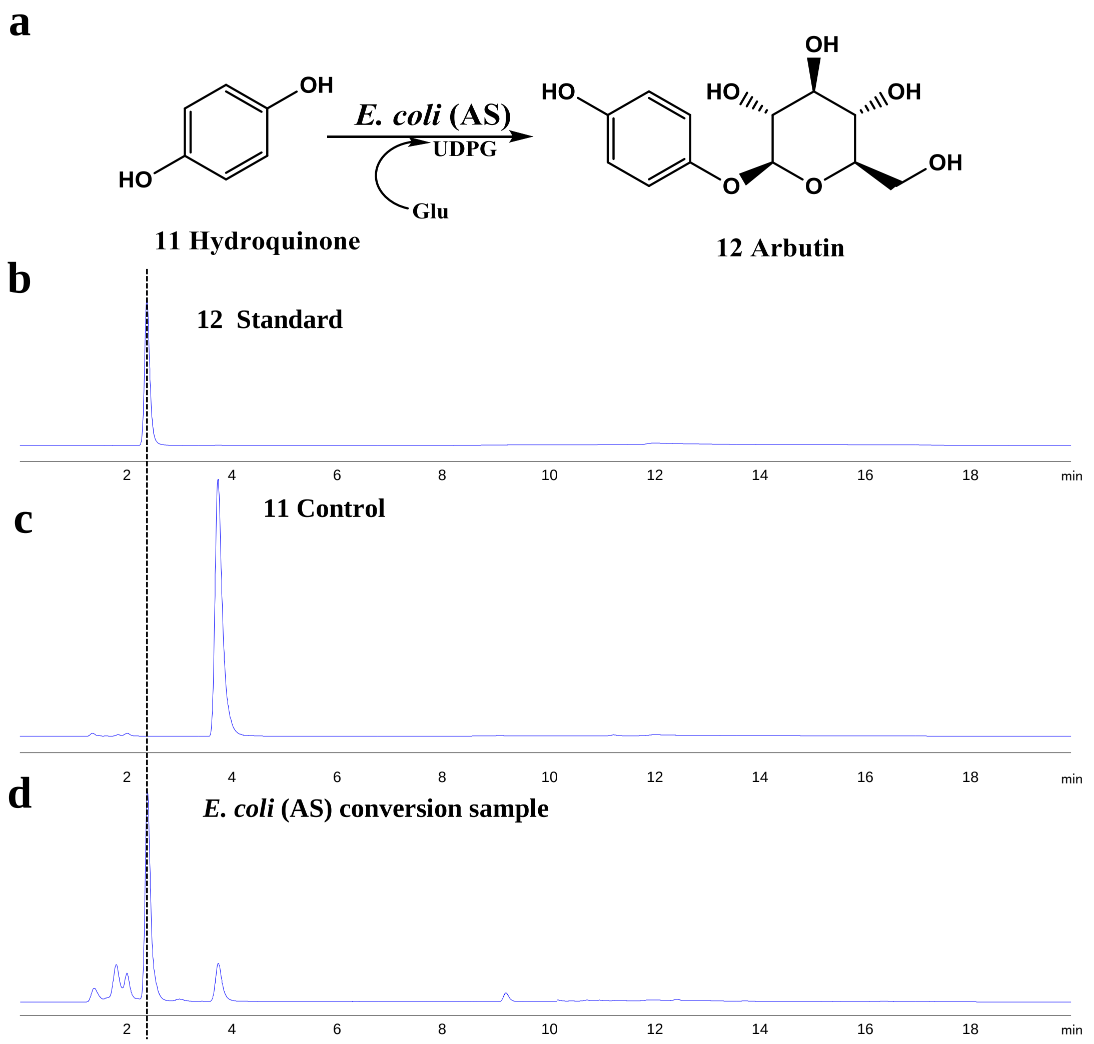


Fig. S6 Arbutin (**12**) synthesis from 2000 mg L^{-1} of hydroquinone (**11**) using biocatalyst *E. coli* (AS) (OD$_{600}$ of 10). a) The reaction for **12** synthesis using *E. coli* (AS). AS is from *Rauvolfia serpentina*.[60] b) HPLC analysis of standard **13**. c) Negative control was performed using strain *E.coli* BL21 (DE3) containing an empty vector with adding 2000 mg L^{-1} of **11**. d) HPLC analysis of conversion product produced by *E. coli* (AS).

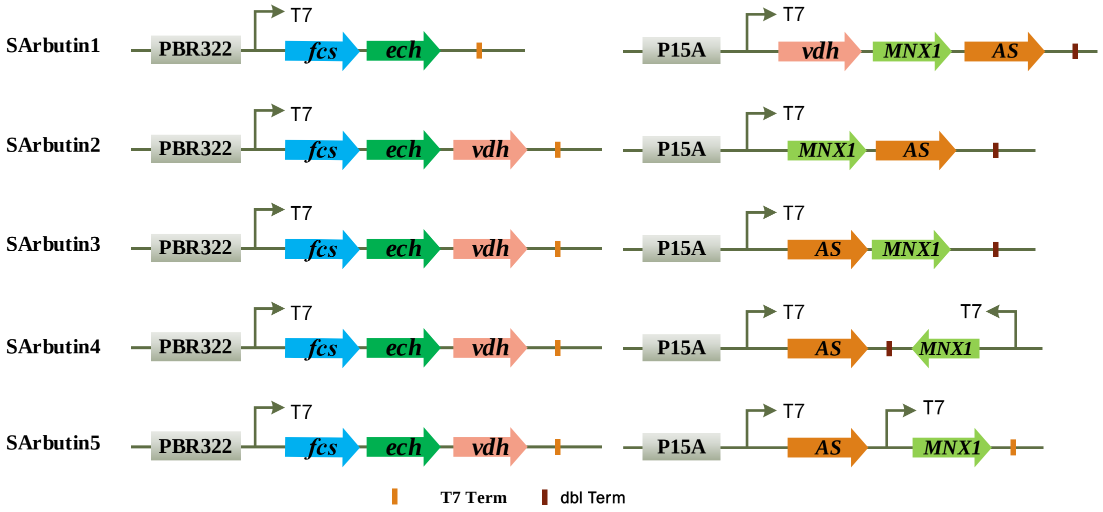


Fig. S7 Conversion of *p*-coumaric acid (**1**) into arbutin (**12**) using different biocatalyst strains expressing *fcs*, *ech*, *vdh*, *MNX1* and *AS* in this study. The genes were cloned into pET-28a (+), pACYCDUet-1 and pA7a-RFP in different organizations, giving SArbutin 1-5.

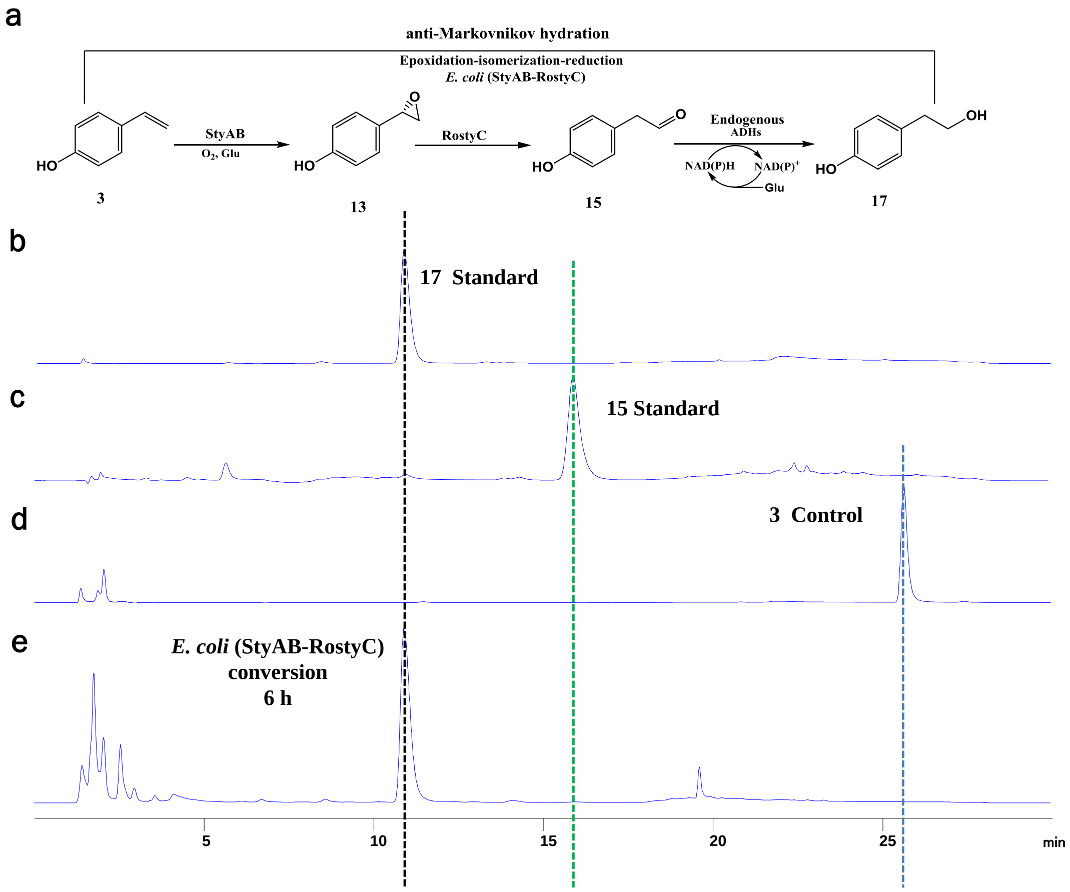


Fig. S8 The anti-Markovnikov hydration of 4-vinylphenol (**3**) using biocatalyst strain *E. coli* (StyAB-RostyC) (OD$_{600}$ of 20). StyAB is from *Pseudomonas* sp. VLB120;[61] RostyC is from *Rhodococcus opacus* 1CP.[62] a) Anti-Markovnikov hydration of 1000 mg L^{-1} of **3** in combination with endogenous dehydrogenases. b) HPLC analysis of standard **17**. c) HPLC analysis of standard **15**. d) Negative control was performed using strain *E.coli* BL21 (DE3) containing an empty vector with adding 1000 mg L^{-1} of **3**. e) HPLC analysis of conversion product produced by *E. coli* (StyAB-RostyC).

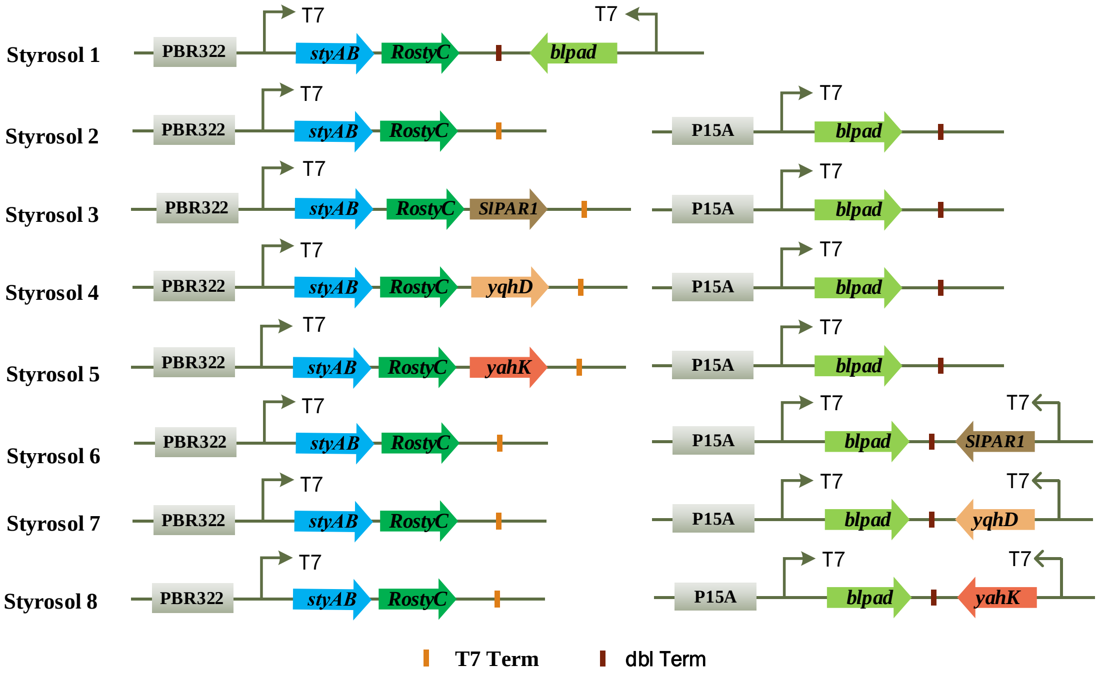
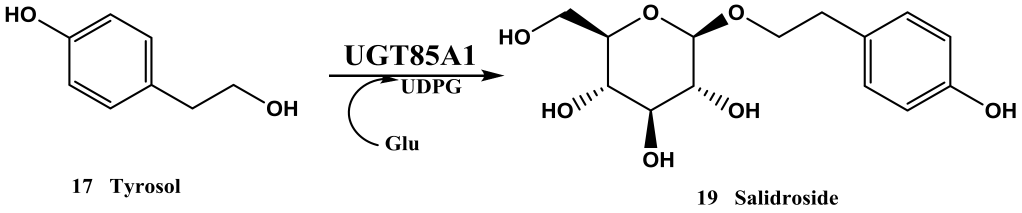
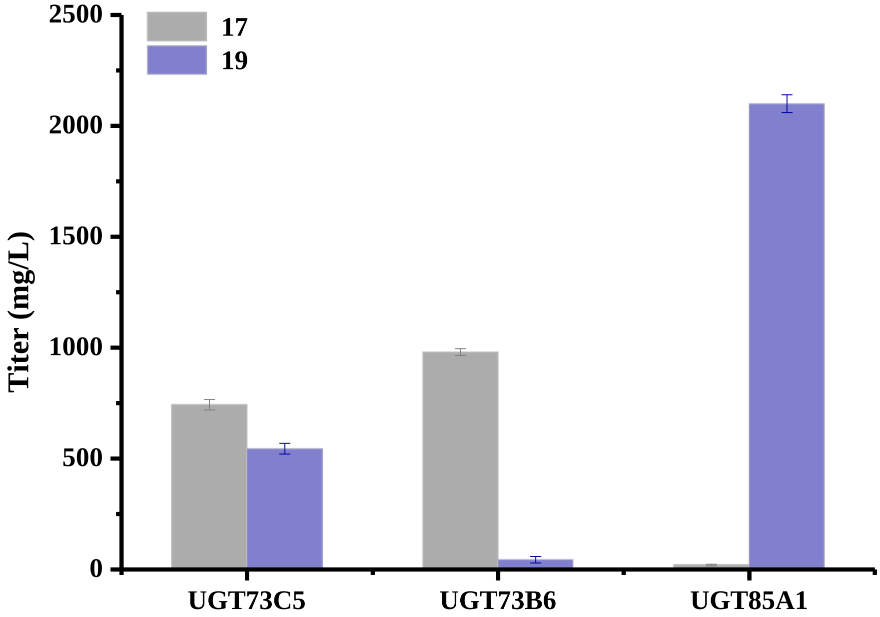


Fig. S9 Different biocatalyst strains expressing *styAB*, *RostyC*, *blpad*, *SlPAR1*, *yqhD* and *yahK* were engineered to convert *p*-coumaric acid (**1**) into tyrosol (**17**) in this study. Genes *yqhD* [63]and *yahK* [64]are from *E. coli* BL21(DE3). The genes were cloned into pET-28a (+) and pA7a-RFP in different organizations, giving Styrosol 1-8 (Table S3).





Fig, S10 Conversion of 1000 mg L^{-1} of tyrosol (**17**) into salidroside (**19**) with *E. coli* BL21 (DE3) (OD$_{600}$ of 10) expressing different glycosyltransferases. UGT73C5 [65]and UGT85A1[66] from *Arabidopsis thaliana*; UGT73B6 from *Rhodiola sachalinensis*.[67]

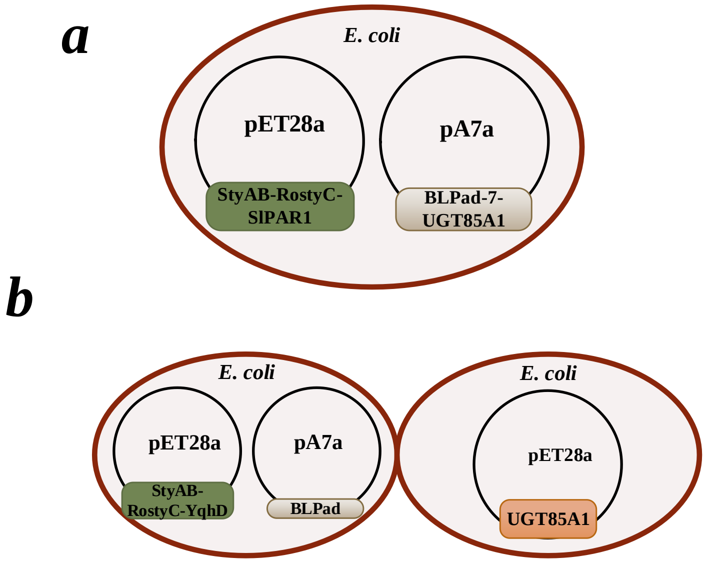


Fig. S11 Engineered biocatalysts for salidroside (**19**) biosynthesis. (a) One-pot, one-step conversion of *p*-coumaric acid (**1**) to **19**. Plasmids pET28a-StyAB-RostyC-SlPAR1 and pA7a-BLPad-UGT85A1 were transformed together into *E. coli* BL21(DE3) to give strain *E. coli* (StyAB-RostyC-SlPAR1-BLPad-UGT85A1) for **19** biosynthesis. (b) One-pot, two-step conversion of **1** to **19**. Step one for tyrosol (**17**) synthesis from **1** using *E. coli* (StyAB-RostyC-YqhD-BLPad) with two plasmids pET28a-StyAB-RostyC-YqhD and pA7a-BLPad. Step two for **19** synthesis from **17** using strain *E. coli* (UGT85A1).

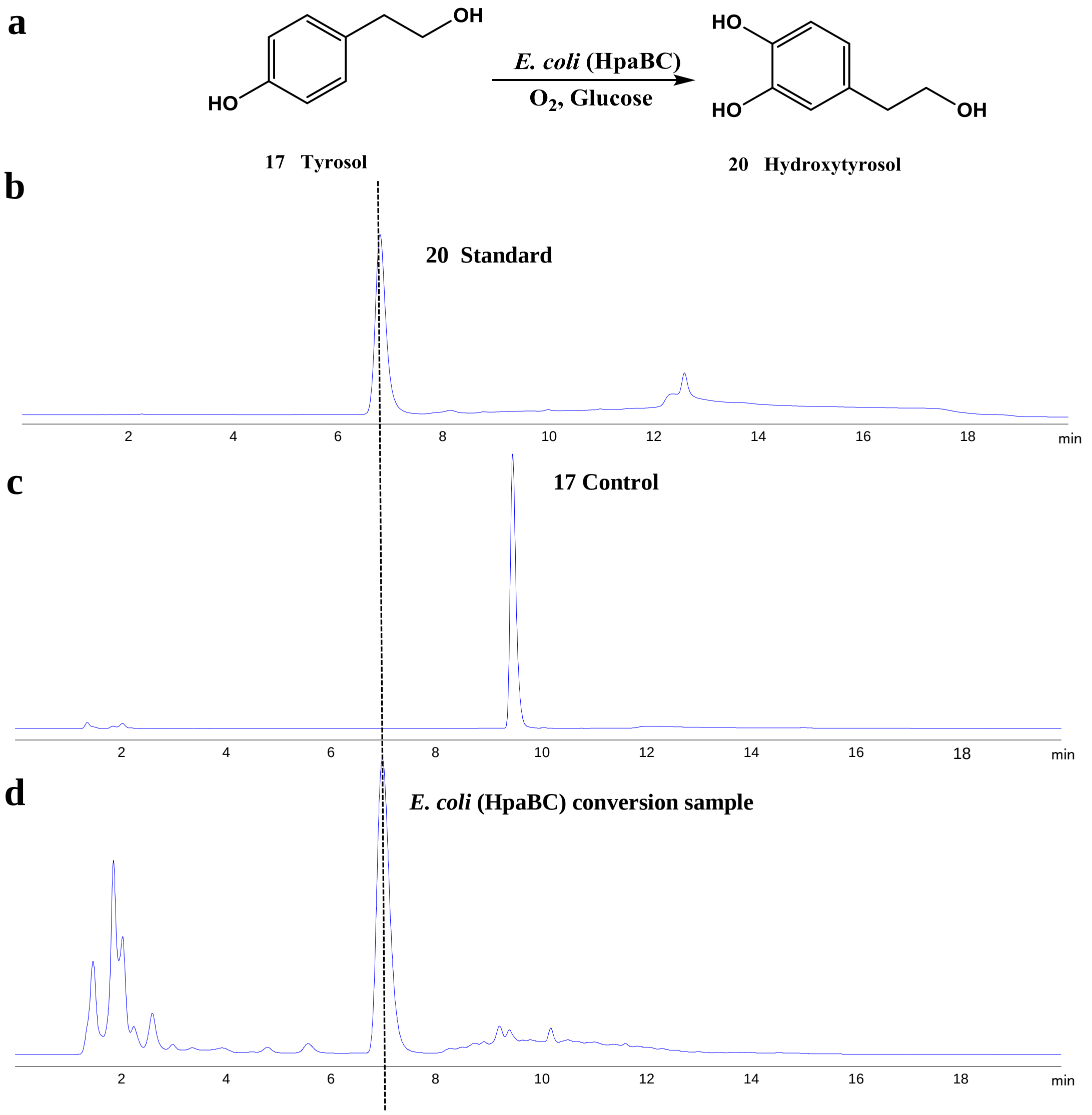


Fig. S12 Hydroxytyrosol (**20**) synthesis from 1000 mg L^{-1} of tyrosol (**17**) using biocatalyst *E. coli* (HpaBC) (OD_{600} of 10). a) The reaction for **20** synthesis using *E. coli* (HpaBC). HpaBC is from *E. coli* BL21(DE3).[68] b) HPLC analysis of standard **20**. c) Negative control was performed using strain *E.coli* BL21 (DE3) containing an empty vector with adding 1000 mg L^{-1} of **17**. d) HPLC analysis of conversion product produced by *E. coli* (HpaBC).

E. coli **(BLPad-StyAB-RostyC-SlPAR1-HpaBC)**

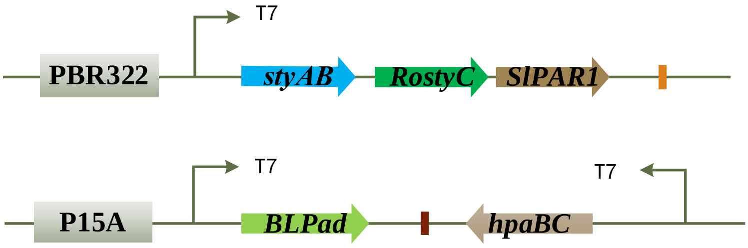


Fig. S13 Constructed biocatalyst *E. coli* (BLPad-StyAB-RostyC-SlPAR1-HpaBC) for hydroxytyrosol (**20**) synthesis from *p*-coumaric acid (**1**). The recombinant plasmids were presented in Table S2.

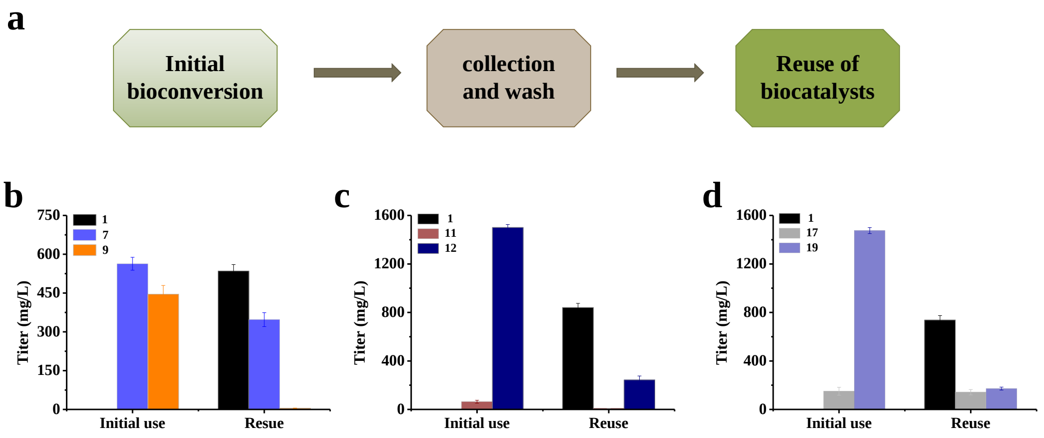


Fig. S14 The reuse tests of biocatalysts for gastrodin (**9**), arbutin (**12**) and salidroside (**19**) biosynthesis. a) The process of reuse of biocatalysts. The conditions for the initial bioconversion: OD_{600} of 10, pH 7.0, 1000 mg L^{-1} of *p*-coumaric acid (**1**), 37 ℃, 250 rpm, 12 h. b) The reuse of *E. coli* (Fcs-Ech-SlPAR1-UGT73B6^{FS}) for **9** biosynthesis. c) The reuse of SArbutin5 for **12** biosyntesis. d) The reuse of *E.coli* (BLPad-StyAB-RostyC-SlPAR1-UGT85A1) for **19** biosynthesis. The reuse tests were performed at conditions as initial bioconversion described.

3. Experimental Section

3.1 Analytical method

HPLC was performed using an Agilent 1200 II HPLC system equipped with a UV detector operating at 280 nm. Separation was achieved using an Agilent Eclipse XDB-C18 column (5 μm, 250 mm×4.6 mm, Santa Clara, USA) working at 30 ℃. Mobile phase A was water with adding 0.1% acetic acid and B was acetonitrile. For regular HPLC analysis, A linear gradient of mobile phase B (0-5min, 5 %; 5-10 min, increased from 5 to 35%; 10-15 min, 35%; 15-20 min, 5%) with a flow rate of 1 mL/min was used. For analysis of **18** and **19**, they were determined using a linear gradient of mobile phase B (0-8min, from 5 % to 8 %; 8-15 min, increased from 8 to 35%; 15-25 min, 35%; 25-30 min, 5%). The concentrations were calculated from the standard curves prepared with corresponding authentic compounds.

LC–MS analysis was performed using Waters Acquity 2D-UPLC & Xevo G2-XS QTOF system and the system was run in negative electrospray (ESI-) mode, scanning masses between 50 Da and 1000 Da. Samples were collected from cell culture and centrifuged at 12000 rpm for 5 min, and the supernatants were precipitated with 50% methanol and followed by a high-speed centrifugiation. The supernatant was analysed by LC-MS. The detailed conditions were as follows: column: ACQUITY CSH Phenyl-Hexyl Column (1.7μm, 2.1*100mm, Milford, USA); Column temperature: 45.0 ℃; solvent system, A: 0.1% formic acid in water, B: 0.1% formic acid in acetonitrile; gradient modes: 99% A (0-1 min), 99-90% A (1-6 min), 90-0% A (6-7 min), 0 % A (7-8.4 min), 0-99% A (8.4-8.5 min) and 99% A (8.5-10 min); injection volume: 2 uL; capillary: 2.0000 kV; sampling cone: 30.0000; Source temperature at 115 ˚C with source offset 60; desolvation temperature: 450 ˚C; cone gas flow: 50 L/Hr; desolvation gas flow: 900 L/Hr. The results were shown as Figure S14-S23.

3.2 DNA sequences used in this study:

Fcs, Vdh and Ech from *Pseudomonas putida* KT2440:[55]

>*fcs*

ATGAATAACGAAGCCCGCTCAGGGTCGACCGACCCTGGCCAACGTCCGCGCTACCGCC
AGGTGGCCATCGGGCATCCCCAGGTGCAGGTCAGTCACGTCGACGACGTGCTGCGCAT
GCAACCTGTCGAGCCACTGGCGCCGCTGCCGGCGCGCCTGCTCGAGCGCCTGGTGCAT
TGGGCCCAGGTGCGCCCGGACACCACTTTCATCGCGGCACGCCAGGCAGACGGTGCC
TGGCGTTCGATCAGCTACGTGCAGATGCTCGCCGATGTGCGCACCATCGCCGCCAACTT

GCTAGGACTGGGCCTCAGTGCCGAGCGCCCGCTGGCGCTGCTTTCCGGCAACGACATC
GAACACCTGCAAATCGCCCTCGGCGCCATGTATGCCGGTATTGCCTATTGCCCGGTGTC
GCCGGCCTACGCGCTGTTGTCGCAAGACTTCGCCAAGTTGCGCCATGTCTGCGAGGTG
CTCACCCCCGGAGTGGTCTTCGTCAGCGACAGCCAGCCGTTCCAGCGCGCCTTCGAGG
CGGTGCTGGACGATTCGGTCGGCGTGATCAGCGTGCGTGGCCAGGTCGCAGGTCGCCC
CCATATAAGCTTCGACAGCCTGTTGCAACCGGGTGACCTGGCGGCGGCCGATGCGGCT
TTCGCCGCCACCGGGCCGGACACCATCGCCAAATTCCTCTTCACCTCGGGCTCGACCA
AGCTGCCCAAGGCGGTGATCACCACCCAGCGCATGCTGTGCGCCAATCAGCAGATGCT
TCTGCAGACTTTTCCGACGTTCGCCGAGGAGCCGCCGGTGCTGGTGGACTGGCTGCCG
TGGAACCACACGTTCGGCGGTAGCCACAACCTCGGCATCGTGCTTTACAACGGGGGCA
GTTTCTACCTGGACGCCGGCAAGCCGACCCCGCAAGGCTTCGCCGAAACCTTGCGCAA
TCTGCGCGAGATTTCCCCCACGGCCTACCTCACCGTACCCAAGGGCTGGGAGGAACTG
GTCAAGGCACTGGAGCAGGACCCCGCGCTACGCGAGGTGTTCTTTGCCCGCATCAAGC
TGTTCTTCTTTGCCGCCGCAGGCCTGTCGCAAAGCGTCTGGGACCGGCTGGACCGCAT
TGCCGAGCAACACTGTGGCGAACGCATCCGCATGATGGCCGGCCTTGGCATGACCGAA
GCCTCGCCATCGTGCACCTTCACCACCGGGCCTTTGTCGATGGCCGGCTATGTCGGGCT
GCCGGCACCTGGCTGCGAAGTGAAGCTGGTGCCGGTGGGCGACAAGCTCGAGGCGCG
CTTCCGTGGCCCGCATATCATGCCGGGCTACTGGCGCTCGCCGCAGCAGACCGCCGAG
GCGTTCGACGAGGAGGGCTTCTACTGTTCGGGCGACGCGTTGAAGCTGGCCGATGCCA
GGCAGCCCGAGCTTGGCCTGATGTTCGATGGCCGTATCGCTGAGGACTTCAAACTTTC
GTCCGGGGTATTCGTCAGTGTCGGGCCGCTGCGCAACCGCGCAGTGCTGGAGGGCTCG
CCTTACGTACAGGACATCGTGGTCACCGCGCCGGACCGTGAATGCCTGGGCCTGCTGG
TGTTCCCGCGTCTGCCCGAGTGTCGGCGCCTGGCCGGGCTGGCAGAGGATGCCAGCGA
TGCGCGGGTGCTGGCCAACGACACCGTGCGCAGTTGGTTCGCTGACTGGCTGGAGCG
CTTGAACCGCGATGCCCAAGGCAACGCCAGCCGTATCGAATGGCTGTCGCTGCTGGCC
GAGCCGCCGTCGATCGACGCCGGTGAAATCACCGACAAGGGCTCGATCAATCAGCGC
GCCGTGCTGCAGCGGCGCGCCGCTCAGGTCGAGGCGCTGTACCGTGGCGAAGACCCC
GACGCATTGCACGCCAAGGTGCGGCCTTGA

>*ech*

ATGAGCAAATACGAAGGCCGCTGGACCACCGTGAAGGTCGAACTGGAAGCGGGCATC
GCCTGGGTGACCCTCAATCGCCCGGAAAAACGCAATGCCATGAGCCCCACCCTGAACC
GGGAAATGGTCGACGTGCTGGAAACCCTTGAGCAGGACGCTGACGCTGGCGTGCTGG
TATTGACCGGTGCCGGCGAGTCCTGGACCGCCGGCATGGACCTGAAGGAGTACTTCCG
CGAGGTGGACGCCGGCCCGGAAATCCTCCAGGAAAAGATTCGTCGCGAAGCCTCGCA
ATGGCAATGGAAGTTGCTGCGTCTGTATGCCAAACCGACCATCGCCATGGTCAACGGC
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ACGAAGCGACCTTCGGCCTGTCGGAAATCAACTGGGGCATCCCGCCTGGTAACCTGGT
CAGCAAGGCCATGGCCGATACCGTTGGCCATCGTCAGTCGCTGTACTACATCATGACCG
GCAAGACCTTCGATGGTCGCAAGGCTGCCGAGATGGGCCTGGTGAACGACAGTGTGC
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ACCCGGTGGTGCTGCGTGCCGCGAAGAATGGCTTCAAGCGTTGCCGCGAGCTGACCT
GGGAACAGAACGAGGACTACCTCTACGCCAAGCTCGACCAGTCGCGCCTGCTGGACA
CTACCGGCGGCCGCGAGCAGGGCATGAAGCAGTTCCTCGACGACAAGAGCATCAAGC
CAGGCCTGCAGGCCTACAAGCGCTGA

>*vdh*

ATGTTGCAGGTGCCTTTGCTGATTGGCGGGCAGTCGCGCCCCGCCAGCGATGGACGAA
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CACTGGCCGATGCCGATGCCGCGGTGGCTGCTGCCAGCGCGGCGTTTCCGGCCTGGGC
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ACGCAGATCACCGGTGAAGTGATCCCCTCGGACGTTCCCGGCAGCTTCGCAATGGCCC
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GGCCACGCGTGCCATTGCCATGCCGCTGGCCTGCGGCAACACCGTGGTGCTCAAGGCC
TCGGAGCTGAGCCCGGCGGTCCATCGGCTGATCGGCCAGGTGCTGCACGATGCAGGCT
CGGCGACGGCGTGGTCAATGTCATCAGCAATGCGCCGCAGGATGCCCCCGCCATCGTC
GAGCGGCTGATCGCCAACCCTGCGGTACGCCGGGTCAACTTCACCGGTTCGACGCACG
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AGCGGCGGCCTTCGGTGCCTACTTCAACCAGGGGCAGATCTGCATGTCCACCGAGCGC
CTTGTGGTGGACAGCTGTATTGCCGACGCTTTCGTCGACAAGCTGGCGGTGAAGATCG
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GGTACTGCGCGCCGAAGGCGACGAAGCCTTGCTGCAGCTGGCCAACGACTCGGAGTT
CGGTCTGTCATCGGCCATTTTCAGCCGCGACACCAGCCGCGCCCTGGCCTTGGCCCAA
CGGGTGGAGTCGGGTATCTGCCATATCAACGGCCCGACCGTTCACGATGAAGCGCAGA
TGCCGTTTGGCGGGGTCAAGTCCAGCGGCTATGGCAGCTTCGGCAGCCGCACGGCCAT
CGATCAGTTCACCCAGTTGCGCTGGGTCACCCTCCAGCACGGCCCGCGTCACTATCCC
ATCTAG

BLPad from *Bacillus licheniformis* strain CGMCC 7172:[56]

> *blpad*

ATGAATCAAGATGTAAAAGAGTTTGTAGGAAGCCATATGATCTATACGTATGAAAACGG
ATGGGAATATGAAATCTACATTAAAAATGACCATACCATCGATTACCGCATTCACAGCGG
AATGGTTGGGGGACGCTGGGTTCGCGATCAAAAAGCCGATATCGTCAAGCTGACTGAA
GGCGTCTATAAAGTATCCTGGACAGAACCGACAGGGACTGACGTTTCCTTGAACTTCA
TGCCGAATGAAAAGCGGATGCACGGCATCATCTTCTTCCCTAAATGGGTTCATGAACGC
CCTGATATTACAGTCTGCTATCAAAATGACCATATCGACTTAATGGAGGAATCGCGCGA
AAAATATGAGACGTATCCAAAATATGTCGTACCGGAATTCGCCGATATCACATTTATTGA
AAATGCCGGAATCGATAATGAAGATCTGATTTCAAAAGCCCCTTATCCCGGAATGACGG
ATGACATCAGGGCAGGAAAGCGGGTATAA

Ado from *Thermothelomyces thermophila*[54] was codon optimized:

>*ado*

ATGGCTCACATCCACGACCTGGCGCCGGAAGTAAGCAACTACTCTTCTGGTCGCCTGA
CCCCGCCGACCCCAGTTAGGTTCCCGCGCACCCCAGTGTTCGCATCTATGAACAAACC

GTGCCGCTTCGAAGGTGACGTTTTCGACCTGGAAGTTTCTGGTGCTATCCCGCCGGAC
ATCGACGGTACCTTCTTCCGCGTTCAGCCGGACCACCGCTTCCCGCCGCTGTTCGAAG
ACGACATCCACTTCAACGGTGACGGTTCTGTTACCGCTATCCGCATCTCTGGTGGTCAC
GCTGACCTGCGCCAGCGCTACGTTCGCACCGAACGCTACCTGCTGGAAACCCGCGCTC
GCCGCTCTCTGTTCGGTCGCTACCGCAACCCGTGGACCGACAACGAATCTGTTCGCGG
TGTTATCCGCACCGCTTCTAACACCAACGTTGTTTTCTGGCGCGGTGCTCTGCTGGCTA
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CTACGACTTCGAAGGTCAGATCCTGTCTCCGACCTTCACCGCTCACCCGAAAATCGAC
CCGGACACCGGTGAAATGGTTTGCTTCGCTTACGAAGCTGGTGGTGACGGTTCTGACT
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CGCTACGTTACCAAACCGTACCGCCACTTCTGGCAGGCTGTTGTTGACCCGACCCGCC
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CCACCTGCCGCTGAAACTGAAACTGGGTCTGCACGGTAACTGGGTTGACTCTCGCGAA
ATCGAAGCTTGGCGCCGCCGCCGCGCTGAAAACGGTGACGTTGGTCCGCTGCGCGTT
GCTAAAGAACCGCTGCCGTGGCAGAAAAAATTCGCTGCTGCTGCTCAGAACGGTTCTA
ACGGTGTTTAA

TtAdo from *Thielavia terrestris* NRRL 8126 was codon optimized:

>*Ttado*

ATGGCGCATATTCATGAGCTGGCGGCGGAGATTAGCAACTACGCGAATAACCGTCTGAC
CGACCCAAGCAAGGTTCGCTTTCCGCGCACCCCGGTTTTCGCGAGTATGAATAAACCG
AGCCGCTTCGAGGGCGACGTGTTTGATCTGGAGATCAGCGGTACGATTCCAGCGGACA
TCGATGGTACCTTCTTCCGCGTTCAGCCAGACCACCGCTTCCCACCGCTGTTTGAGGAT
GACATCCACTTCAACGGCGACGGCAGCGTTACCGCGGTTCGCATCAGTGGTGGTCATG
CCGATCTCAAACAGCGCTACGTGCATACCGATCGCTATGTGCACGAGACGCGTGCCCG
CCGTAGTCTCTTCGGTCGCTATCGTAATCCGTGGACCGACAATGAGAGCGTGAAAGGC
GTTATCCGCACGGCCAGCAACACCAATGTGGTTTTCTGGCGCGGCGTGCTGCTGGCGC
TGAAAGAAGACGGCCCACCGTTCGCCATGGACCCGGTGACGCTGGAAACGCTGGGCC
GTTACGACTTTGAAGGTCAGATTCTGAGCCCGACGTTTACCGCCCATCCAAAGTTCGAT
CCGGATACCGGCGAAATGGTGTGCTTCGCCTACGAAGCGGGCGGTGACGGCAGTGATT

GCAGCGTGGATGTTGCGGTGTGGACGATCGACCGCGATGGTAAGAAAACGGAGGAGT
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TCGATGCCCAACATCTGGCCAAAGGCCCGCTGGCGGTTATCCACCTCCCACTGAAGCT
GAAGCTGGGTCTGCACGGTAATTGGGTGGATCACCGCGATATTGACGCGTGGAAACAA
CGTCGCGCCGAGGGTGGTGACGTTGGTCCGCTGAAAGTGGCCACCGAACCACTGCCG
TGGCAGAAAAAGCTGGCCCAACAGAACGGCACGAATGGCACGCGCGCGTAA

CgAdo from *Chaetomium globosum* CBS 148.51 was codon optimized:

>*Cgado*

ATGGCGCACATCCATGATCTGGCCGCGAGTCTGGCGCCGAACTATACCGCCAATCGTCT
GACGACGCCAACCCCAACCCGCTTTCCGCGTACCCCGACCTTCGCGAGCATGAACAAA
CCGTGCCGTTTTGAAGGCACGGTTGACGATCTGGAAGTTACCGGTACGATTCCGGCGG
ACCTCGATGGTACCTTTTTTCGCGTTCAGCCGGACCATCGCTTTCCGCCGCTGTTCGAG
GATGATATCCACTTCAACGGCGACGGTGCCGTTACCGCCGTTCGCATCGAAAACGGTC
GTGCGGCGCTGCGCCAGCGTTATGTTCGCACCGACCGCTTCGAGAAAGAGGCCCGTGC
GGGCCGTAGTCTCTTTGGTCGCTACCGTAATCCGTGGACCGACAACGAGAGCGTGAAG
GGTGTGATCCGCACGGCGAGCAATACGAACGTTGTGTTCTGGCGCGGTGTGCTGCTGG
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TCGCTACGATTTTGAGGGCCAGATTGTGAGCCCAACGTTCACGGCGCATCCAAAAGTT
GATCCGCGCACGGGCGAAATGGTTTGCTTCGCCTATGAAGCCGGCGGTGATGGTAGCG
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CAACAAGTTCGCGTGGGACCCGAACGAGGATCAGTGGTATGGCGTGGTTCCGCGTCGC
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CGGCAATGTGTTCTTTTTTTTCCCGCCGGACGATAACATCACCCCACCGGATGGCATCG
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GCGCTACAACACGAAGCCGTATCGCCATTTCTGGCAAGCCGTGGTTGACCCAACCAAA
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CTACACGTGGAGTGGTAAGAACTACCACACCGGTGAAAGCACGGAGAACGGTGCGAG
CGGTGAAGGTGAAGGCGATGGCAAATTCGGCCTCGAGGACGTGTATTTCAGCGGCCCG
ACCATGACCTTCCAAGAACCAACGTTCATTCCACGTGAAGGCGGCGCCGAGGGTGAG
GGCTATCTGATTGCGCTGCTGAACCATCTGGACCAGCTGCGCAATGACGTGGTGATCTT
TGACGCCCAGAATCTCGCGAAAGGCCCAGTTGCCGTGATCCATCTCCCGCTGAAGCTG
AAGCTGGGTCTGCACGGCAATTGGGTGGACCATCGCGATATTGATGCGTGGCAGAAAC
GCCGTAGCGAAGATGGTGACATCGGTCCAGTGCAAGTTGCCAAAGAACCGCTCCCGT
GGCAGAAGAAACTCGCGGAACAAAAAGGCGAGACGGGCCTGTAA

PaAdo from *Podospora anserina* S mat+ was codon optimized:

>*Paado*

ATGGCCCATATCTTCCATCTGGCCCCACATATCGACACCAGTCCGAACTATAGCAACAA
CGAGCTCACGAGCCCGGAAAAAGTTGCCTTCCCGAAGACCGATGCCTTTCGCAGCATG
AATGCCCCGAGCCGTTTTGAGGGTAGCGTGTTCAATCTGGAAGTTACCGGTACCATTCC
GCCGGACATTAGCGGCACCTTCTATCGTGTTCAGCCGGACCACCGCTTCCCACCGCTCT
ACGAGGACGACATTCACTTCAACGGTGACGGCAGCGTTACCGCCATCCGTATTGCCAA
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GGCGGCCCGTCGTAGTCTGTTCGGTAAGTACCGCAACCCGTACACCGACAATGAGAGC
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TGCTGGCGATGAAAGAGGATGGCCCGCCGTTTGCCATGGACCCGGACACGCTGGAAA
CGCTGGGCCGCTACGATTTCGAAGGCCAAATTCTGAGCCCGACCTTCTGCGCCCACCC
GAAATTTGATCCGGACACCGGCGAAATGGTGTGCTTTGCGTACGAATGTGGTGGCGAC
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CAAGCGCGGACAGTATCGCGAAGCGTAACAAGCTGAGCAGTCCAACCACCCGCTGGA
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TGTTCAACAGTCTGGGCCACTATACGTGGGGTCCGGAACACTACCACACGGGTAGTAC
CACCAGTAGCGTGACCAATGGCGAAACCAAGAAGGAGAAGGCGGGCCTCGAAGACG
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AACGACGTGCTGATCTTCGATGCGCAGAATCTGAGCCAAGGCCCACTGGCCGTGATCC
ATCTCCCACTCAAACTCAAGCTGGGTCTGCACGGCAACTGGGTGGACAACAAAGACA
TCGAGGAATGGAAAGCCCGTCGTGAAGCGACCGGCGATGTGGGTCCGGTTAAGGTGG
CGAGTGAACCGCTCCCGTGGCAGAAGAAGTTTCAGAGTGGTCAAGCCAATGGCCAAG

AGCGTAGTTTTTAA

YahK[64] and YqhD[63] from bacterium *E. coli* BL21 (DE3):

>*yahK*

ATGAAGATCAAAGCTGTTGGTGCATATTCCGCTAAACAACCACTTGAACCGATGGATAT
CACCCGGCGTGAACCGGGACCGAATGATGTCAAAATCGAAATCGCTTACTGTGGCGTT
TGCCATTCCGATCTCCACCAGGTCCGTTCCGAGTGGGCGGGGACGGTTTACCCCTGCG
TGCCGGGTCATGAAATTGTGGGGCGTGTGGTAGCCGTTGGTGATCAGGTAGAAAAATA
TGCGCCGGGCGATCTGGTCGGTGTCGGCTGCATTGTCGACAGTTGTAAACATTGCGAA
GAGTGTGAAGACGGGTTGGAAAACTACTGTGATCACATGACCGGCACCTATAACTCGC
CGACGCCGGACGAACCGGGCCATACTCTGGGCGGCTACTCACAACAGATCGTCGTTCA
TGAGCGATATGTTCTGCGTATTCGTCACCCGCAAGAGCAGCTGGCGGCGGTGGCTCCT
TTGTTGTGTGCAGGGATCACCACGTATTCGCCGCTACGTCACTGGCAGGCCGGGCCGG
GTAAAAAAGTGGGCGTGGTCGGCATCGGCGGTCTGGGACATATGGGGATTAAGCTGGC
CCACGCGATGGGGGCACATGTGGTGGCATTTACCACTTCTGAGGCAAAACGCGAAGCG
GCAAAAGCCCTGGGGGCCGATGAAGTTGTTAACTCACGCAATGCCGATGAGATGGCGG
CTCATCTGAAGAGTTTCGATTTCATTTTGAATACAGTAGCTGCGCCACATAATCTCGACG
ATTTTACCACCTTGCTGAAGCGTGATGGCACCATGACGCTGGTTGGTGCGCCTGCGAC
ACCGCATAAATCGCCGGAAGTTTTCAACCTGATCATGAAACGCCGTGCGATAGCCGGT
TCTATGATTGGCGGCATTCCAGAAACTCAGGAGATGCTCGATTTTTGCGCCGAACATGG
CATCGTGGCTGATATAGAGATGATTCGGGCCGATCAAATTAATGAAGCCTATGAGCGAA
TGCTGCGCGGTGATGTGAAATATCGTTTTGTTATCGATAATCGCACACTAACAGACTGA

>*yqhD*

ATGAACAACTTTAATCTGCACACCCCAACCCGCATTCTGTTTGGTAAAGGCGCAATCGC
TGGTTTACGCGAACAAATTCCTCACGATGCTCGCGTATTGATTACCTACGGTGGCGGCA
GCGTGAAAAAAACCGGCGTTCTCGATCAAGTTCTGGATGCCCTGAAAGGCATGGACGT
GCTGGAATTTGGCGGTATTGAGCCAAACCCGGCTTATGAAACGCTGATGAACGCCGTG
AAACTGGTTCGCGAACAGAAAGTGACTTTCCTGCTGGCGGTTGGCGGCGGTTCTGTAC
TGGACGGCACCAAATTTATCGCCGCAGCGGCTAACTATCCGGAAAATATCGATCCGTGG
CACATTCTGCAAACGGGCGGTAAAGAGATTAAAAGCGCCATCCCGATGGGCTGTGTGC
TGACGCTGCCAGCAACCGGTTCAGAATCCAACGCAGGCGCGGTGATCTCCCGTAAAAC
CACAGGCGACAAGCAGGCGTTCCATTCTGCCCATGTTCAGCCGGTATTTGCCGTGCTC
GATCCGGTTTATACCTACACCCTGCCGCCGCGTCAGGTGGCTAACGGCGTAGTGGACG
CCTTTGTACACACCGTGGAACAGTATGTTACCAAACCGGTTGATGCCAAAATTCAGGA
CCGTTTCGCAGAAGGCATTTTGCTGACGCTGATCGAAGATGGTCCGAAAGCCCTGAAA
GAGCCAGAAAACTACGATGTGCGCGCCAACGTCATGTGGGGGGCGACGCAGGCGCTG
AACGGTTTGATTGGCGCTGGCGTACCGCAGGACTGGGCAACGCATATGCTGGGCCACG
AACTGACTGCGATGCACGGTCTGGATCACGCGCAAACACTGGCTATCGTCCTGCCTGC
ACTGTGGAATGAAAAACGCGAAACCAAGCGCGCTAAGCTGCTGCAATATGCTGAACG
CGTCTGGAACATCACTGAAGGTTCCGATGATGAGCGTATTGACGCCGCGATTGCCGCA
ACCCGCAATTTCTTTGAGCAATTAGGCGTGCCGACCCACCTCTCCGACTACGGTCTGG
ACGGCAGCTCCATCCCGGCTTTGCTGAAAAAACTGGAAGAGCACGGCATGACCCAAC
TGGGCGAAAATCATGACATTACGTTGGATGTCAGCCGCCGTATATACGAAGCCGCCCGC
TAA

ScADH6 from yeast *Saccharomyces cerevisiae*[69] was codon optimized:

>*Scadh6*

ATGAGTTACCCGGAGAAATTCGAGGGCATTGCCATCCAGAGCCACGAGGACTGGAAG
AACCCGAAGAAGACGAAGTACGACCCGAAGCCGTTCTACGACCACGACATCGATATCA
AGATCGAGGCGTGCGGCGTTTGCGGCAGTGATATCCATTGCGCGGCCGGCCATTGGGG
TAACATGAAAATGCCGCTGGTGGTTGGCCACGAAATCGTTGGCAAGGTGGTGAAACTG
GGCCCGAAAAGTAACAGCGGTCTGAAAGTTGGCCAACGTGTTGGTGTTGGCGCGCAA
GTGTTCAGCTGTCTGGAATGCGATCGCTGCAAGAACGATAACGAGCCGTACTGCACCA
AGTTCGTGACCACCTACAGCCAGCCGTACGAAGATGGCTATGTTAGCCAAGGCGGTTA
CGCCAACTACGTTCGCGTTCACGAACACTTCGTGGTGCCGATCCCGGAAAACATCCCG
AGTCATCTGGCCGCCCCACTGCTGTGTGGTGGTCTGACCGTTTACAGCCCACTGGTTC
GTAATGGTTGCGGCCCGGGCAAAAAAGTGGGCATTGTGGGTCTGGGTGGTATTGGCAG
CATGGGCACGCTGATCAGCAAAGCGATGGGTGCGGAGACGTACGTGATTAGTCGCAGC
AGCCGCAAACGCGAAGACGCCATGAAAATGGGCGCCGATCACTACATCGCGACGCTG
GAAGAAGGCGATTGGGGCGAGAAATACTTCGACACGTTCGACCTCATCGTGGTGTGCG
CGAGCAGCCTCACCGATATCGATTTCAACATCATGCCGAAAGCGATGAAAGTGGGCGG
TCGCATCGTTAGCATCAGCATTCCGGAGCAGCATGAGATGCTGAGTCTCAAGCCATACG
GTCTGAAAGCCGTGAGTATCAGCTATAGCGCGCTGGGCAGCATCAAGGAACTGAACCA
GCTGCTGAAGCTGGTGAGCGAAAAAGACATCAAAATCTGGGTTGAGACGCTGCCGGT
TGGCGAAGCCGGTGTGCATGAGGCCTTCGAACGCATGGAAAAAGGCGATGTTCGCTAC
CGCTTCACCCTCGTGGGCTACGACAAGGAATTTAGCGACTAA

SlPAR1 from tomato *Solanum lycopersicum*[57] was codon optimized:

>*slpar1*

ATGAGTGTGACGGCCAAAACCGTTTGTGTGACCGGTGCCAGCGGCTACATCGCCAGTT
GGCTCGTTAAGTTTCTGCTCCACAGCGGCTACAACGTTAAAGCGAGCGTGCGTGATCC
GAACGATCCGAAAAAGACCCAGCATCTGCTGAGTCTGGGTGGTGCCAAGGAACGTCT
GCATCTGTTCAAGGCCAATCTGCTGGAAGAAGGCAGCTTCGATGCGGTTGTGGATGGC
TGCGAGGGCGTTTTCCACACCGCGAGCCCGTTCTACTACAGCGTTACCGACCCACAAG
CCGAACTGCTGGATCCAGCGGTGAAAGGCACGCTGAATCTGCTGGGTAGCTGCGCCA
AAGCGCCAAGCGTGAAGCGCGTGGTTCTGACCAGCAGCATTGCGGCGGTTGCCTATAG
CGGTCAGCCGCGTACCCCGGAAGTGGTTGTGGATGAAAGCTGGTGGACCAGCCCAGA
CTACTGCAAGGAGAAACAGCTGTGGTACGTGCTGAGTAAGACGCTGGCCGAAGATGC
GGCGTGGAAGTTCGTGAAGGAGAAGGGTATCGACATGGTGGTGGTTAATCCGGCGATG
GTTATCGGCCCACTGCTGCAGCCGACGCTGAATACGAGCAGTGCGGCGGTTCTGAGTC
TGGTTAATGGCGCCGAAACCTACCCGAACAGCAGCTTTGGTTGGGTGAACGTGAAGGA
TGTGGCGAACGCGCATATTCTGGCCTTCGAAAATCCGAGCGCGAATGGCCGTTATCTGA
TGGTTGAGCGCGTGGCGCACTACAGCGATATTCTGAAGATCCTCCGTGATCTGTACCCG
ACCATGCAGCTCCCGGAGAAATGCGCCGATGACAACCCGCTCATGCAGAACTACCAAG
TTAGCAAGGAGAAAGCGAAGAGTCTGGGCATCGAATTCACCACGCTGGAGGAAAGCA
TCAAGGAAACCGTGGAGAGTCTGAAAGAGAAGAAGTTCTTCGGCGGCAGCAGCAGTA
TGTAA

UGT73B6^{FS}, a mutant of *Rhodiola sachalinensis* -derived glycoltransferase[36] was codon optimized:

>*ugt73b6^{FS}*

ATGGGTAGCGAAACGCGCCCGCTCAGCATCTTCTTTTTCCCGTTCATGGCGCATGGCCA
CATGATCCCGATGGTTGATATGGCGCGTCTGTTTGCGAGTCAAGGCGTTCGCTGTACGA
TCGTGACCACCCCGGGCAACCAACCACTCATCGCGCGCAGCATCGGCAAGGTGCAGC
TGCTGGGTTTCGAGATCGGTGTTACCACCATCCCGTTTCGTGGCACCGAGTTCGGCCTC
CCAGATGGCTGCGAAAATCTGGATAGCGTGCCGAGCCCACAGCACGTGTTCCATTTCT
TCGAAGCCGCGGGCAGTCTGCGTGAGCCGTTCGAACAACTGCTGGAGGAACACAAGC
CAGACTGCGTGGTTGGCGATATGTTCTTCCCATGGAGCACCGATAGCGCGGCGAAATTC
GGCATTCCGCGTCTGGTGTTCCATGGCACGAGTTATTTCGCGCTGTGCGCCGGCGAAG
CCGTTCGTATCCATAAGCCGTATCTGAGCGTGAGCAGCGACGATGAACCGTTCGTTATC
CCGGGTCTGCCGGACGAGATCAAGCTCACCAAAAGCCAGCTGCCAATGCATCTGCTCG
AAGGCAAAAAGGACAGCGTGCTGGCCCAGCTGCTGGACGAAGTGAAGGAAACCGAG
GTGAGCAGCTACGGTGTGATCGTGAACAGCATCTACGAGCTGGAGCCGGCGTACGCGG
ACTACTTCCGCAATGTGCTGAAACGTCGCGCGTGGGAAATCGGTCCACTGAGTCTGTG
CAATCGCGACGTGGAGGAGAAAGCGATGCGCGGCATGCAAGCCGCGATTGACCAGCA
CGAGTGTCTGAAATGGCTGGACAGCAAAGAGCCGGATAGCGTTGTTTACGTGTGCTTC
GGCAGCACGTGCAAATTCCCGGATGATCAGCTCGCCGAAATTGCGAGCGGTCTGGAGG
CCAGCGGCCAACAGTTCATCTGGGTTATCCGCCGCATGAGCGACGATAGCAAAGAGGA
CTATCTGCCGAAGGGCTTTGAGGAGCGCGTTAAAGACCGTGCGCTGCTGATTCGTGGT
TGGGCGCCGCAAGTTCTCATCCTCGATCATCAGAGCGTGGGTGGTTTCGTGAGCCATT
GCGGCTGGAACAGTACGCTGGAAGGCATCAGTGCGGGTCTGCCGATGGTTACGTGGCC
AGTGAGCGCCGAACAGTTCTACAACGAGAAGCTGCTGACCGAAGTGCTCAAAATCGG
CGTTGCGGTTGGCGCGCGTAAATGGCGCCAGCTCGTGGGTGACTTTGTGCACAAAGAT
GCGATCCAGCGCGCCGTGCGTGAAATCATGGAGGGCGAAGAAGCGGAAGAGCGTCGC
ATTATCGCCCGCCAGATGGGTAAGATGGCCAAACGCGCGGTTGAGAAAGATGGCAGCA
GTTGGACGAACCTCAACAATCTGCTGCAAGAACTGAAACTGAAGAAAGTGTAA

MNX1 from yeast *Candida parapsilosis* CDC317[58] was codon optimized:

>*MNX1*

ATGGCAGTGCAAGCTCCGAGCAAAACCTATGGCTTTCAGAAAGCCCCGATTCAGCTGA
CCTTCGTGGTGGTTGGTGCTGGTCTGGGTGGCGTGGCCGCAAGCATTTGTCTGCGTCT
GGCTGGTCATCGTGTGATTTTACTGGAGGCCGCCACCGAACTGGGTGAAGTTGGCGCT
GGTATCCAAATTCCGCCGCCGAGTACCAAGATTTTAAAGGCCATTGGTGTGCTGGACGC
AGTTGACAAGGTGAGCATCCACCCGCACGATATTTTAGTGAAAAAGTATAAGGGCGAG
CTGCTGAGCACCCAGAATCTGGTGCCGTATGTGCTGGAAAAGTACGACGGCATGTATTT
ACACATCCACCGCGCAGACTATCACAAGGTTTTAGTGGACCGTGCCGAGGAGCTGGGC
GTTGAGATCCATACCAACAGCCGCGTTGTGGACATCGACTTCGAGAAAGCAACCGTGA
CCACCGCAACCGGTAAGCAGTATAGCGGCGATGTGATTGTGGGTTACGATGGCGTTCGT
AGTCAGACCCGTGCTTTACTGACTGGTGATAGCAGCGGCGCCTATGATACCGGCGATCT
GGCCTACCGTGCTTTAATTAAGGTGGAGGATATGAAAAAGGTGCCGGGTCTGGAGAAG
TTCTACGCCAACCCGAATATCAACTTCTGGTGGGGTCCGACCATGCATATTGTGATGTAT

TTCTTACACGAGGGCGAAATTTGCAACGTGGTGGCTTTATGCCCCGATACCTTACCGAA
GGGCGTTCTGAAACAAGATGCAAGCCAAGAGGAACTGCTGGATTTAGTGAAAGGTTG
GGACCAAGATTTAACCACCGTTTTTAAACTGATCACCAGTGTTAGCAAATGGCGTTTAC
AAGACAGCCGCGAACTGAAGACTTGGGTGAATAGCAAAACCGGCAACTTTATCATTCT
GGGCGATGCCAGCCATAGCACACTGCCTTATCTGGCCAGCGGCGCCAGTCAAGCTGTT
GAAGATGGCGCAGTGCTGGCCGGTTTATTCAGCAAGATCGAGTTACGTGACCAGATTC
CGCAGCTGCTGCAGATGACCGAAAATCTGCGCAAGTGGCGCAGTAGCCAAGTTGTTCG
TGGTAGCCATCAGTGCCAAGATATCTACCATCTGCCGGACGGTGAGCTGCAAGAAATC
CGTGACAGCTATTTATATGACAAGCAACCGGAATTAGGCTGCCCGAATCGCTTTGCCGA
TCCCGTTTTCCAAGATTTTCTGTGGGGTTACAACGCCTTCGACGAAGTGGAACGCGCA
TGGAAGGAATTCAAAGCCGGCGGCAACCCGACATATACCTACCCGAATTTATATAAACC
GAAGAGCAGCGGCGAAAAGGATGTTAGCGGTGGTGGTGCAGCAGCCACCTTAGCAGC
CGGCAATACACCCGCTGCACCTCTGAGCGCCAGTGGCTAA

vibMO1 from basidiomycete fungus *Boreostereum vibrans*[59] was codon optimized:

>*vibMO1*

ATGAGCACGAGCACCAGCACGAGCTATCAATGCCGCGTTGCGGTTGTTGGTGCGGGTC
TGGGCGGTCTGAGTGCGGCCATTGGTATTACGCTGGCGGGCCACAAAGTGACCATTCT
GGAACAAGCCCCACAACTGGGCGAAGTTGGTGCGGGCATCCAGATCCCGCCAAATAG
CAGTCGCATTCTCCGTCAGTGGGGTCTGCTGCCAGCGCTGGAAGAAGTGAGCGTTCGC
CCACTGGACAGCGTGCTGCGCAGCTATCGCGATGGTAAAGTTCTGAGCCGCATCAATC
TGGTTCCGGGCTACGAAGAGCGCTTTGGCGCCCCGTACTATCATATCCACCGCGCGGAC
TTTCACCGCATTCTGGTTGACAAAGCCCGCGCGCTGGGTGTTGAAATTCTGCTCGGCA
AAAGCGTGCGCACCATCGATTTCAACGCCCCGAGTCTGACGATGGCCGATGGCAGCGT
GTACAACGATGCCGACGTTATCATTGGCGCGGATGGTCTGAAAAGCGTTTGTCGCGAA
CAGATGCTGGGCCACCCAGATCCACCGCACTTTACCGGCGATCTGGCCTACCGTATCAT
CGTGAAAGCCGAGGACATGAAGAAGCACGACAGTCTGCGTGAACTCGTGGAACACCC
GAGCATCAACCATTGGATGGGTCCAAACAGCCACGTTGTGTGCTATCTGCTGAAAGGT
GGCGGTCTGTACAACATCGTTCTGGCGTGCCCAGACGATCTGCCGGAGCTGGTTAATA
CCGCCAAGGCCGATCTGAAAGAGATGCGTGAGCGCTTTGAAGGCTGGGATCCGCGTCT
GACGCTGCTGCTGAGTCTGGTGCAAGAAACCAGCAAATGGCGCCTCCAGAATAGCGA
AGAGATGGACAAGTGGAGCCACGAGAGCGGCAAATTCGTTCTGATGGGTGACGCGTG
CCATGCGACGCTGCCATATCTGGCGCAAGGCGCGGCCATCGCGGTTGAAGATGGTGCG
GCGCTGGGTACCCTCTTTGCCCACGCCACCCATCCGAGTCTGGTGCCAGACGTGCTGA
CCATCTACGAACAGATCCGCAAGAGCCGCACGACCCGTGTGGTTCGCGGTAGTACCAA
ACAGCGTGACATCTTCCACATGCCAGATGGTCCACGCCAGCGTGAACGCGATCGCCAG
CTGCTCACCTACGCGGACAATCTGTTTGAAGGCTACCCGAACCAGTGGGCGGATCCGG
TTTTCCAGCCATGGCTGTACGGCTACAATGCGTTCGAAGAGGCCGAAAAAGCGTGGCA
GAAGTATCTGCGCGGCCATATCTTCGGCACCACCGGTGCGTTTCGCGAACTCGGCATG
GGCCTCGAAGATGCGAAACTGTAA

AS from *Rauvolfia serpentina*[60] was codon optimized:

>*AS*

ATGGAACACACCCCACACATCGCGATGGTTCCGACCCCGGGCATGGGCCATCTGATCC

CGCTCGTTGAATTCGCGAAACGTCTGGTGCTCCGCCACAACTTCGGTGTGACGTTTATC
ATCCCGACGGATGGCCCGCTCCCAAAAGCGCAGAAAAGCTTTCTGGACGCCCTCCCA
GCCGGTGTGAATTATGTTCTGCTGCCGCCGGTTAGCTTCGATGATCTGCCGGCGGATGT
TCGTATTGAGACGCGCATCTGTCTGACCATTACCCGCAGTCTGCCGTTTGTTCGTGATG
CGGTGAAGACGCTGCTGGCCACCACCAAACTGGCCGCGCTGGTGGTGGATCTGTTCG
GCACCGATGCCTTCGACGTGGCCATTGAGTTCAAGGTGAGCCCGTACATCTTCTACCCG
ACCACGGCCATGTGTCTGAGTCTGTTCTTTCACCTCCCAAAGCTCGATCAGATGGTGA
GCTGTGAATACCGCGACGTGCCAGAGCCACTGCAGATTCCGGGTTGCATCCCGATTCAT
GGCAAGGACTTTCTGGATCCGGCGCAAGATCGCAAAAACGACGCCTACAAGTGTCTG
CTGCACCAAGCGAAACGTTATCGCCTCGCCGAGGGCATCATGGTTAACACGTTTAACG
ATCTGGAGCCGGGCCCACTGAAAGCGCTCCAAGAAGAAGATCAAGGCAAGCCGCCAG
TTTATCCGATCGGTCCGCTCATCCGCGCCGATAGCAGTAGCAAAGTGGACGACTGCGAA
TGTCTGAAATGGCTGGACGATCAGCCACGCGGTAGCGTGCTGTTTATCAGCTTCGGTAG
CGGCGGTGCCGTTAGCCACAACCAGTTCATCGAACTGGCGCTGGGTCTGGAGATGAGC
GAACAGCGCTTTCTGTGGGTGGTGCGTAGCCCGAACGATAAAATCGCCAACGCGACCT
ACTTCAGCATTCAAAACCAGAATGACGCGCTGGCCTATCTGCCGGAAGGCTTTCTGGA
ACGCACCAAAGGCCGTTGTCTGCTGGTTCCGAGTTGGGCGCCGCAAACCGAGATCCTC
AGTCATGGCAGTACGGGTGGTTTTCTGACCCACTGCGGCTGGAACAGCATCCTCGAAA
GCGTTGTTAACGGCGTTCCACTGATTGCGTGGCCACTGTACGCCGAGCAGAAAATGAA
CGCCGTGATGCTGACGGAGGGCCTCAAAGTGGCGCTGCGTCCGAAAGCCGGCGAAAA
TGGTCTGATTGGTCGCGTTGAGATCGCGAACGCCGTTAAAGGTCTGATGGAAGGCGAA
GAGGGCAAGAAGTTCCGCAGCACCATGAAGGATCTGAAAGATGCGGCGAGTCGTGCG
CTGAGTGATGATGGCAGCAGTACCAAAGCGCTGGCCGAACTGGCGTGTAAATGGGAG
AATAAAATTAGCAGCACGTAA

StyAB from *Pseudomonas sp*. strain VLB120[61] was codon optimized:

>*styA*

ATGAAAAAGCGTATCGGTATTGTTGGTGCAGGCACTGCCGGCCTCCATCTTGGCCTCTT
CCTTCGTCAGCATGACGTCGACGTCACTGTGTACACTGATCGTAAGCCCGATGAGTACA
GCGGACTGCGTCTCCTGAATACCGTTGCTCACAACGCGGTGACGGTGCAGCGGGAGG
TTGCCCTCGACGTCAATGAGTGGCCGTCTGAGGAGTTTGGTTATTTCGGCCACTACTAC
TACGTAGGTGGGCCGCAGCCCATGCGTTTCTACGGTGATCTCAAGGCTCCCAGCCGTG
CAGTGGACTACCGTCTCTACCAGCCGATGCTGATGCGTGCACTGGAAGCCAGGGGCGG
CAAGTTCTGCTACGACGCGGTGTCTGCCGAAGATCTGGAAGGGCTGTCGGAGCAGTAC
GATCTGCTGGTTGTGTGCACTGGTAAATACGCCCTCGGCAAGGTGTTCGAGAAGCAGT
CCGAAAACTCGCCCTTCGAGAAGCCGCAACGGGCACTGTGCGTTGGCCTCTTCAAGG
GCATCAAGGAAGCACCGATTCGCGCGGTGACTATGTCCTTCTCGCCAGGGCATGGCGA
GCTGATTGAGATTCCAACCCTGTCGTTCAATGGCATGAGCACAGCGCTGGTGCTCGAA
AACCATATTGGTAGCGATCTGGAAGTTCTCGCCCACACCAAGTATGACGATGACCCGCG
TGCGTTCCTCGATCTGATGCTGGAGAAGCTGGGTAAGCATCATCCTTCCGTTGCCGAGC
GCATCGATCCGGCTGAGTTCGACCTTGCCAACAGTTCTCTGGACATCCTCCAGGGTGG
TGTTGTGCCGGCATTCCGCGACGGTCATGCGACCCTCAATAACGGCAAAACCATCATTG
GGCTGGGCGACATCCAGGCAACTGTCGATCCGGTCTTGGGCCAGGGCGCGAACATGG
CGTCCTATGCGGCATGGATTCTGGGCGAGGAAATCCTTGCGCACTCTGTCTACGACCTG

CGCTTCAGCGAACACCTGGAGCGTCGCCGCCAGGATCGCGTGCTGTGTGCCACGCGAT
GGACCAACTTCACTCTGAGCGCTCTCTCGGCACTTCCGCCGGAGTTCCTCGCCTTCCTT
CAGATCCTGAGCCAGAGCCGTGAAATGGCTGATGAGTTCACGGACAACTTCAACTACC
CGGAACGTCAGTGGGATCGCTTCTCCAGCCCGGAACGTATCGGACAGTGGTGCAGTCA
GTTCGCACCCACTATCGCGGCCTGA

>*styB*

ATGACGTTAAAAAAAGATATGGCGGTGGATATCGACTCCACCAACTTCCGCCAGGCGG
TTGCATTGTTCGCGACGGGAATTGCGGTTCTCAGCGCGGAGACTGAAGAGGGCGATGT
GCACGGCATGACCGTGAACAGTTTCACCTCCATCAGTCTGGATCCGCCGACTGTGATG
GTTTCCCTGAAATCGGGCCGTATGCATGAGTTGCTGACTCAAGGCGGACGCTTCGGAG
TTAGCCTCTTGGGTGAAAGCCAGAAGGTGTTCTCGGCATTCTTCAGCAAGCGCGCGAT
GGATGACACGCCTCCCCCCGCCTTCACCATTCAGGCCGGCCTTCCCACTCTGCAGGGC
GCCATGGCCTGGTTCGAATGCGAGGTGGAGAGCACGGTTCAAGTACACGACCACACG
CTCTTCATTGCGCGCGTTAGCGCCTGTGGAACGCCTGAGGCGAATACCCCCCAGCCGC
TGCTGTTCTTTGCCAGCCGTTATCACGGCAACCCGTTGCCACTGAATTGA

RostyC from *Rhodococcus opacus* 1CP[62] was codon optimized:

>*RostyC*

ATGAAAACGCTGGAACGCAAAATCTACGGCCACGGCGTGCTGATGATTCTGAGCACGC
TGATCTTCGGTCTGTTTCTGTGGATGAATCTGGTTGGCGGCTTCGAGATCGTGCCGGGC
TACATCATCAACTTCAACATCCCGGGTACGGCGGAAGGTTGGGCGAAAGCCCATGTTG
GCCCGGCGCTGAATGGCATGATGGTTATCGCGATCGGTCTGGTTCTGCCAAAACTGGC
GTTCCCGCTGAAGACGGCCAAGAAACTGGGCTATATCATCGTGCTGGACGGCTGGGGC
AATGTGTGCTTCTACTTCTTCAGCAACTTCGCGCCGAGCCGTGGTCTGAGTTTCGGCAG
CAATCGTCTGGGCGAAACCAACATCTTCGGCGTTCTGGCGCTGGCCCCGGCCTATGTTT
TTGGCGTGCTGGCGATTGGCGCGCTGGCGATCATCGGCTTTAAAGCGCTGCGCCAGAC
GGATGCCGAAGATCGCGCCATCGAAAGCGCGAACGCCTAA

UGT73C5[65] and UGT85A1[66] from *Arabidopsis thaliana* were codon optimized:

>*ugt73c5*

ATGGTTAGCGAAACCACCAAAAGCAGCCCACTGCACTTCGTTCTGTTCCCGTTCATGG
CCCAAGGCCACATGATCCCGATGGTTGATATTGCCCGTCTGCTGGCGCAGCGTGGTGTG
ATCATCACCATCGTGACCACCCCACATAATGCCGCGCGCTTCAAAAACGTGCTGAATCG
CGCGATCGAAAGCGGTCTGCCGATCAATCTGGTTCAAGTTAAGTTCCCATATCTGGAAG
CGGGTCTGCAAGAGGGTCAAGAAAACATCGATAGCCTCGACACCATGGAGCGCATGAT
CCCGTTCTTTAAGGCCGTGAACTTCCTCGAGGAGCCAGTTCAGAAGCTGATCGAGGAG
ATGAATCCGCGCCCAAGCTGCCTCATCAGTGATTTCTGCCTCCCGTACACGAGCAAGAT
CGCGAAGAAGTTCAACATCCCGAAGATTCTGTTCCATGGCATGGGTTGTTTCTGTCTGC
TGTGCATGCACGTGCTGCGCAAGAACCGCGAGATTCTGGACAATCTGAAGAGCGACA
AAGAGCTCTTCACCGTGCCGGACTTTCCGGATCGCGTTGAATTCACCCGCACCCAAGT
TCCGGTGGAAACCTATGTGCCGGCGGGTGATTGGAAGGACATCTTCGACGGCATGGTG
GAAGCCAATGAGACGAGCTACGGCGTGATCGTGAACAGTTTTCAAGAACTGGAGCCA
GCGTACGCGAAAGACTACAAAGAAGTGCGCAGTGGCAAGGCGTGGACCATCGGTCCG
GTGAGTCTGTGCAATAAGGTTGGCGCGGATAAAGCCGAGCGCGGCAACAAAAGCGAC

ATCGACCAAGACGAGTGTCTGAAATGGCTCGACAGCAAGAAACACGGCAGCGTGCTC
TATGTGTGTCTGGGCAGCATTTGCAATCTGCCACTGAGCCAGCTGAAAGAACTCGGCC
TCGGCCTCGAAGAAAGCCAGCGCCCGTTTATCTGGGTGATTCGCGGCTGGGAAAAGTA
CAAGGAGCTCGTGGAGTGGTTCAGCGAAAGCGGCTTTGAGGACCGCATCCAAGATCG
CGGTCTGCTGATTAAGGGCTGGAGTCCACAGATGCTCATTCTGAGCCATCCGAGTGTTG
GTGGCTTTCTGACCCATTGCGGTTGGAACAGTACGCTGGAAGGCATCACGGCCGGTCT
GCCGCTGCTGACGTGGCCACTGTTCGCGGATCAGTTCTGCAACGAAAAGCTCGTGGTG
GAGGTTCTGAAGGCGGGCGTTCGTAGTGGCGTTGAACAGCCGATGAAATGGGGCGAA
GAAGAAAAGATCGGCGTGCTGGTTGACAAGGAAGGCGTGAAAAAGGCCGTGGAAGA
ACTCATGGGCGAAAGCGATGATGCCAAGGAACGTCGCCGCCGTGCCAAAGAGCTCGG
TGATAGCGCCCATAAGGCGGTGGAAGAAGGCGGCAGTAGCCACAGCAACATCAGCTTT
CTGCTGCAAGATATCATGGAGCTGGCCGAACCAAATAACTAA

>*ugt85a1*

ATGGGCAGCCAGATCATCCATAACAGCCAAAAGCCGCACGTGGTGTGTGTGCCGTATC
CGGCCCAAGGTCACATCAACCCAATGATGCGCGTGGCCAAACTGCTGCACGCGCGTG
GCTTCTACGTGACCTTCGTGAATACCGTGTACAACCACAACCGCTTTCTGCGTAGTCGC
GGTAGTAATGCGCTGGATGGTCTGCCGAGCTTCCGCTTCGAAAGCATCGCGGATGGTC
TGCCAGAAACCGATATGGACGCGACCCAAGATATTACCGCCCTCTGCGAGAGCACCAT
GAAGAATTGTCTGGCGCCATTCCGCGAGCTGCTGCAGCGCATTAACGCGGGCGATAAT
GTGCCACCGGTGAGTTGCATCGTTAGCGATGGCTGCATGAGCTTCACGCTGGATGTTGC
CGAGGAGCTGGGTGTTCCGGAAGTTCTGTTTTGGACCACGAGCGGTTGTGCCTTTCTG
GCGTATCTGCACTTCTATCTGTTCATCGAGAAGGGTCTGTGTCCGCTCAAGGATGAGAG
CTATCTGACGAAGGAGTATCTGGAGGACACCGTGATCGACTTCATCCCGACCATGAAG
AACGTGAAGCTGAAAGATATCCCGAGCTTCATCCGTACCACGAACCCGGATGACGTGA
TGATCAGCTTTGCGCTGCGTGAAACGGAACGTGCGAAACGTGCGAGCGCCATTATTCT
GAACACGTTCGACGACCTCGAACATGATGTGGTGCACGCGATGCAAAGCATTCTGCCG
CCGGTTTATAGCGTGGGCCCACTGCATCTGCTGGCCAATCGCGAAATCGAAGAGGGTA
GCGAGATCGGCATGATGAGCAGCAATCTGTGGAAGGAAGAGATGGAGTGTCTGGACT
GGCTGGACACGAAAACGCAGAACAGTGTTATCTACATCAACTTCGGCAGTATCACCGT
GCTGAGCGTTAAACAGCTGGTGGAATTTGCGTGGGGTCTGGCCGGTAGCGGCAAAGA
GTTTCTGTGGGTTATTCGCCCGGATCTGGTTGCGGGTGAAGAAGCGATGGTGCCGCCG
GATTTTCTGATGGAAACCAAAGATCGCAGCATGCTGGCCAGCTGGTGCCCACAAGAAA
AAGTGCTGAGCCATCCAGCCATCGGCGGTTTTCTGACCCATTGCGGCTGGAATAGCATT
CTGGAAAGTCTGAGCTGTGGCGTGCCGATGGTGTGTTGGCCGTTCTTTGCCGACCAGC
AGATGAACTGCAAGTTCTGCTGCGACGAATGGGATGTTGGTATCGAGATCGGCGGTGA
CGTTAAGCGCGAAGAAGTGGAAGCGGTTGTGCGCGAGCTGATGGATGGCGAAAAGGG
CAAGAAGATGCGCGAGAAAGCGGTTGAATGGCAACGCCTCGCCGAAAAAGCGACGG
AACATAAGCTGGGCAGCAGCGTGATGAACTTCGAGACGGTGGTGAGCAAGTTTCTGCT
GGGTCAGAAGAGCCAAGATTAA

UGT73B6 from *Rhodiola sachalinensis*[67] was codon optimized:

>*ugt73b6*

ATGGGTAGCGAAACGCGCCCGCTCAGCATCTTCTTTTTCCCGTTCATGGCGCATGGCCA
CATGATCCCGATGGTTGATATGGCGCGTCTGTTTGCGAGTCAAGGCGTTCGCTGTACGA

TCGTGACCACCCCGGGCAACCAACCACTCATCGCGCGCAGCATCGGCAAGGTGCAGC
TGCTGGGTTTCGAGATCGGTGTTACCACCATCCCGTTTCGTGGCACCGAGTTCGGCCTC
CCAGATGGCTGCGAAAATCTGGATAGCGTGCCGAGCCCACAGCACGTGTTCCATTTCT
TCGAAGCCGCGGGCAGTCTGCGTGAGCCGTTCGAACAACTGCTGGAGGAACACAAGC
CAGACTGCGTGGTTGGCGATATGTTCTTCCCATGGAGCACCGATAGCGCGGCGAAATTC
GGCATTCCGCGTCTGGTGTTCCATGGCACGAGTTATTTCGCGCTGTGCGCCGGCGAAG
CCGTTCGTATCCATAAGCCGTATCTGAGCGTGAGCAGCGACGATGAACCGTTCGTTATC
CCGGGTCTGCCGGACGAGATCAAGCTCACCAAAAGCCAGCTGCCAATGCATCTGCTCG
AAGGCAAAAAGGACAGCGTGCTGGCCCAGCTGCTGGACGAAGTGAAGGAAACCGAG
GTGAGCAGCTACGGTGTGATCGTGAACAGCATCTACGAGCTGGAGCCGGCGTACGCGG
ACTACTTCCGCAATGTGCTGAAACGTCGCGCGTGGGAAATCGGTCCACTGAGTCTGTG
CAATCGCGACGTGGAGGAGAAAGCGATGCGCGGCATGCAAGCCGCGATTGACCAGCA
CGAGTGTCTGAAATGGCTGGACAGCAAAGAGCCGGATAGCGTTGTTTACGTGTGCTTC
GGCAGCACGTGCAAATTCCCGGATGATCAGCTCGCCGAAATTGCGAGCGGTCTGGAGG
CCAGCGGCCAACAGTTCATCTGGGTTATCCGCCGCATGAGCGACGATAGCAAAGAGGA
CTATCTGCCGAAGGGCTTTGAGGAGCGCGTTAAAGACCGTGCGCTGCTGATTCGTGGT
TGGGCGCCGCAAGTTCTCATCCTCGATCATCAGAGCGTGGGTGGTTTCGTGAGCCATT
GCGGCTGGAACAGTACGCTGGAAGGCATCAGTGCGGGTCTGCCGATGGTTACGTGGCC
AGTGTTCGCCGAACAGTTCTACAACGAGAAGCTGCTGACCGAAGTGCTCAAAATCGG
CGTTGCGGTTGGCGCGCGTAAATGGCGCCAGCTCGTGGGTGACTTTGTGCACAAAGAT
GCGATCCAGCGCGCCGTGCGTGAAATCATGGAGGGCGAAGAAGCGGAAGAGCGTCGC
ATTATCGCCCGCCAGATGGGTAAGATGGCCAAACGCGCGGTTGAGAAAGATGGCAGCA
GTTGGACGAACCTCAACAATCTGCTGCAAGAACTGAAACTGAAGAAAGTGTAA

UGTBL1 from *Bacillus licheniformis* ZSP01:[35]

>*ugtbl1*

ATGGGACATAAACATATCGCGATTTTTAATATTCCCGCTCACGGGCATATTAATCCGACG
CTTGCTTTAACGGCAAGCCTTGTCAAACGCGGTTATCGGGTAACATATCCGGTAACGGA
TGAGTTTGTGAAAGCTGTTGAGGAAACTGGGGCAGAGCCGCTCAACTACCGCTCAAC
TTTAAATATCGATCCGCAGCAAATTCGGGAGCTGATGAAAAATAAAAAGGATATGACAC
AGGCTCCGATGATGTTTATGAAAGAAATGGAGGAGGTTCTTCCTCAGCTTGAAGCGCT
TTATGAGAATGACAAGCCTGACCTCATCCTTTTTGACTTTATGGCCATGGCGGGAAAAA
TGCTGGCTGAGAAGTTTGGAATAGAGGCGGTTCGCCTTTGTTCTACATATGCACAGAAC
GAACATTTTTCATTCAAATCAATGTCTGAAGAGTTTAAGATCGAGCTCACGCCTGAGCA
AGAAGCCGCTTTGAAAAATGCGAATCTTCCGTCATTTAATTTTGAAGAGATGTTCGAAC
CGGCAAAATTGAACATTGTATTTATGCCTCGTGCTTTTCAGCCTTACGGCGAAACGTTT
GATGAACGGTTCTCTTTTGTCGGTCCTTCTCTAGCCAAACGCAAGTTTCAGGAAAAAG
ACACGCCGGTTATTTCGGACAGCGGCCGTCCTGTCATGCTGATTTCTTTAGGGACGGCG
TTCAATGCCTGGCCGGAATTTTATCATATGTGCATCGAAGCATTCAGGGACACGAAGTG
GCAGGTGATCATGGCTGTCGGCACGACAATCGATCCTGAAAGCTTTGACGACATACCT
GATAACTTTTCGATTCATCAGCGCGTTCCCCAGCTGGAAATCCTGAAGAAAGCAGAGC
TTTTCATCACCCATGGGGGTATGAACAGTACGATGGAAGGATTGAATGCCGGTGTACCG
CTTGTTGCCGTCCCGCAAATGCCTGAACAGGAAATCACTGCCCGCCGCGTCGAAGAAC
TCGGGCTTGGCAAGCATTTGCAGCCGGAGGACACAACAGTTGCTTCATTGCGGGAAG

CCGTCTCCCAGACGGACGGTAACCTGGATGTCCTGAAACGCGTAAAGGACATGCAAG
AGCACATTAAACAAGCAGGAGGAGCCGAGAAAGCCGCAGATGAAATTGAGTCATTTTT
AGCACCCGCAGGAGTAAAATAA

HpaBC from bacterium *E. coli* BL21 (DE3):[68]

>*hpaB*

ATGAAACCAGAAGATTTCCGCGCCAGTACCCAACGTCCTTTCACCGGGGAAGAGTATC
TGAAAAGCCTGCAGGATGGTCGCGAGATCTATATCTATGGCGAGCGAGTGAAAGACGT
CACCACTCATCCGGCATTTCGTAATGCGGCAGCGTCTGTTGCCCAGCTGTACGACGCAC
TGCACAAACCGGAGATGCAGGACTCTCTGTGTTGGAACACCGACACCGGCAGCGGCG
GCTATACCCATAAATTCTTCCGCGTGGCGAAAAGTGCCGACGACCTGCGCCAGCAACG
CGACGCCATCGCTGAGTGGTCACGCCTGAGCTATGGCTGGATGGGCCGTACCCCAGAC
TACAAAGCCGCTTTCGGTTGCGCACTGGGCGCGAATCCGGGCTTTTACGGTCAGTTCG
AGCAGAACGCCCGTAACTGGTACACCCGTATTCAGGAAACTGGCCTCTACTTTAACCA
CGCGATTGTTAACCCACCGATCGATCGTCATTTGCCGACCGATAAAGTGAAAGACGTTT
ACATCAAGCTGGAAAAAGAGACTGACGCCGGGATTATCGTCAGCGGTGCGAAAGTGG
TTGCCACCAACTCGGCGCTGACTCACTACAACATGATTGGCTTCGGCTCGGCACAAGT
GATGGGCGAAAACCCGGACTTCGCACTGATGTTCGTTGCGCCAATGGATGCCGATGGC
GTGAAATTAATCTCCCGCGCCTCTTATGAGATGGTCGCGGGTGCTACCGGCTCGCCATA
CGACTACCCGCTCTCCAGCCGCTTCGATGAGAACGATGCGATTCTGGTGATGGATAACG
TGCTGATTCCATGGGAAAACGTGCTGATCTACCGCGATTTTGATCGCTGCCGTCGCTGG
ACGATGGAAGGCGGTTTTGCCCGTATGTATCCGCTGCAAGCCTGTGTGCGCCTGGCAG
TGAAATTAGACTTCATTACGGCACTGCTGAAAAAATCACTCGAATGTACCGGCACCCTG
GAGTTCCGTGGTGTGCAGGCCGATCTCGGTGAAGTGGTAGCGTGGCGCAACACCTTCT
GGGCATTGAGTGACTCGATGTGTTCAGAAGCAACGCCGTGGGTCAACGGGGCTTATTT
ACCGGATCATGCCGCACTGCAAACCTATCGCGTACTGGCACCAATGGCCTACGCGAAG
ATCAAAAACATTATCGAACGCAACGTTACCAGTGGCCTGATCTATCTCCCTTCCAGTGC
CCGTGACCTGAATAATCCGCAGATCGACCAGTATCTGGCGAAGTATGTGCGCGGTTCGA
ACGGTATGGATCACGTCCAGCGCATCAAGATCCTCAAACTGATGTGGGATGCTATTGGC
AGCGAATTTGGTGGTCGTCACGAACTGTATGAAATCAACTACTCCGGTAGCCAGGATG
AGATTCGCCTGCAGTGTCTGCGCCAGGCACAAAACTCCGGCAATATGGACAAGATGAT
GGCGATGGTTGATCGCTGCCTGTCGGAATACGACCAGGACGGCTGGACTGTGCCGCAC
CTGCACAACAACGACGATATCAACATGCTGGATAAGCTGCTGAAATAA

>*hpaC*

ATGCAATTAGATGAACAACGCCTGCGCTTTCGTGACGCGATGGCCAGCCTGTCGGCAG
CGGTAAATATTATCACCACCGAGGGCGACGCCGGACAATGCGGGATTACGGCAACGGC
CGTCTGCTCGGTCACGGATACACCACCGTCGCTGATGGTGTGCATTAACGCCAACAGT
GCGATGAACCCGGTTTTTCAGGGCAACGGCAAGTTGTGCGTCAACGTCCTCAACCATG
AGCAGGAACTGATGGCACGCCACTTCGCGGGCATGACAGGCATGGCGATGGAAGAGC
GTTTTAGCCTCTCATGCTGGCAAAAAGGTCCGCTGGCGCAGCCGGTGCTAAAAGGTTC
GCTGGCCAGTCTTGAAGGTGAGATCCGCGATGTGCAGGCAATTGGCACACATCTGGTG
TATCTGGTGGAGATTAAAAACATCATCCTCAGTGCAGAAGGTCATGGACTTATCTACTTT
AAACGCCGTTTCCATCCGGTGATGCTGGAAATGGAAGCTGCGATTTAA

4. LC-MS or LC-MS/MS Spectra:

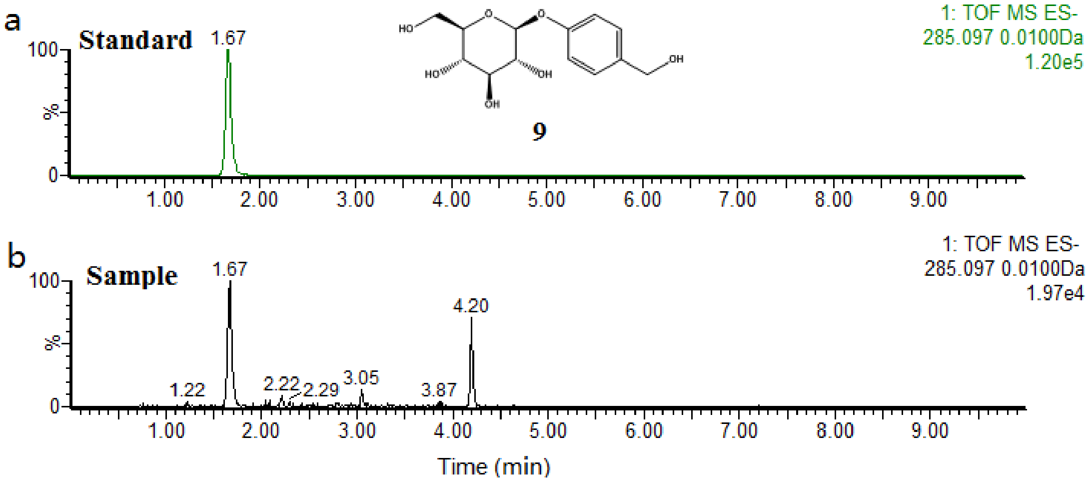


Fig. S15 LC-MS analysis of gastrodin (**9**) produced by *E. coli* (Fcs-Ech-SlPAR1-UGT73B6^{FS}) from *p*-coumaric acid (**1**). a) LC-MS analysis of standard **9**. b) LC-MS analysis of conversion product.

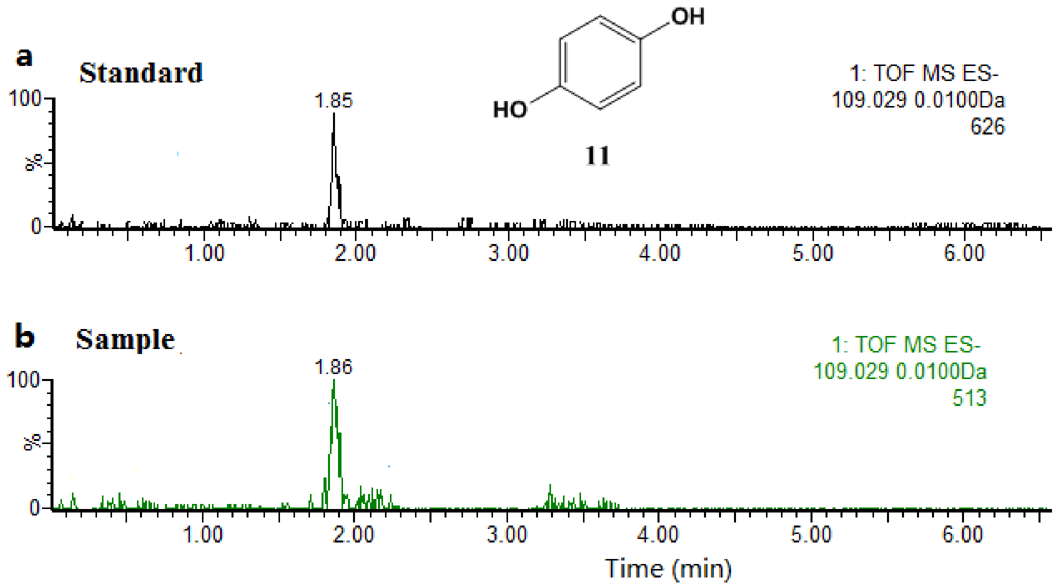


Fig. S16 LC-MS analysis of hydroquinone (**11**) produced by *E. coli* (Fcs-Ech-Vdh-MNX1) from *p*-coumaric acid (**1**). a) LC-MS analysis of standard **11**. b) LC-MS analysis of conversion product.

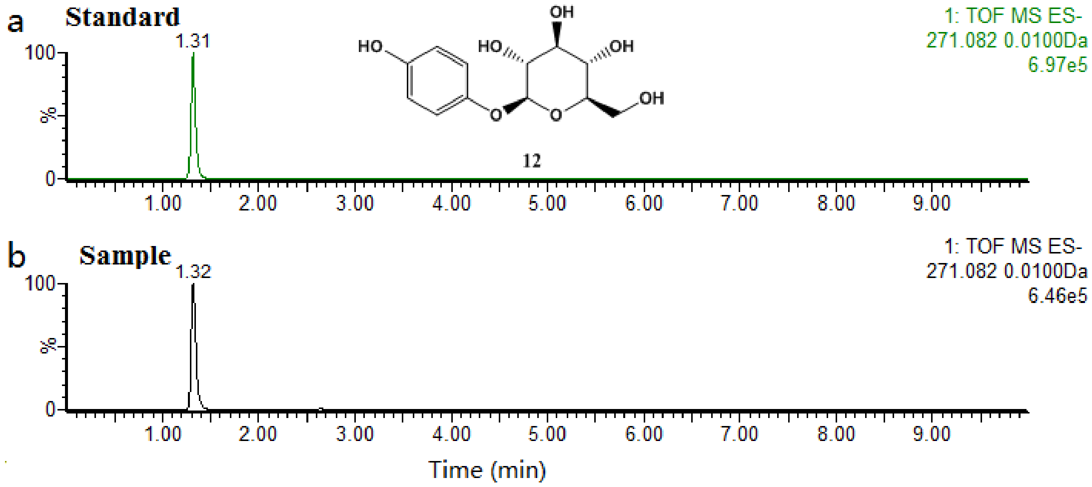


Fig. S17 LC-MS analysis of arbutin (**12**) produced by SArbutin 5 from *p*-coumaric acid (**1**). a) LC-MS analysis of standard **12**. b) LC-MS analysis of conversion product.

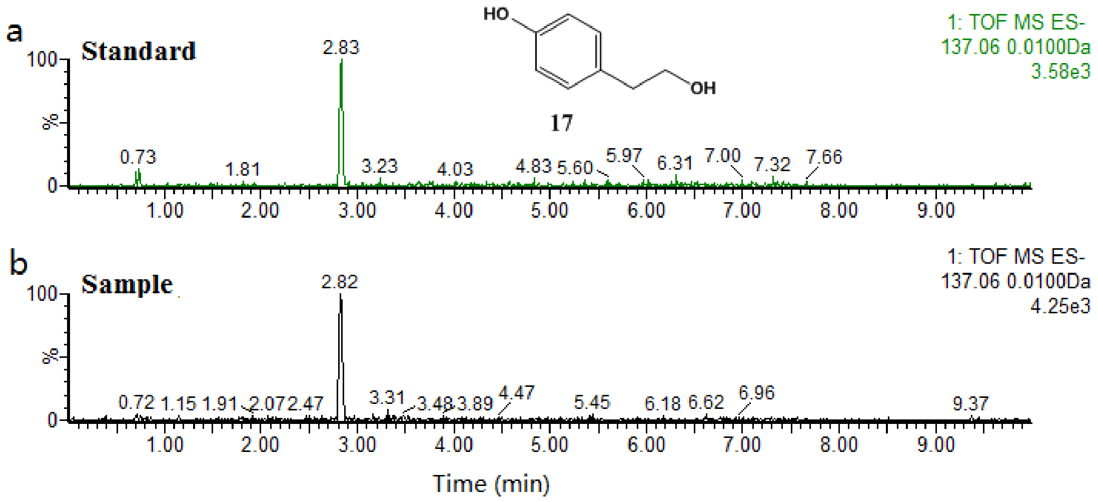


Fig. S18 LC-MS analysis of tyrosol (**17**) produced by Styrosol 7 from *p*-coumaric acid (**1**). a) LC-MS analysis of standard **17**. b) LC-MS analysis of conversion product.

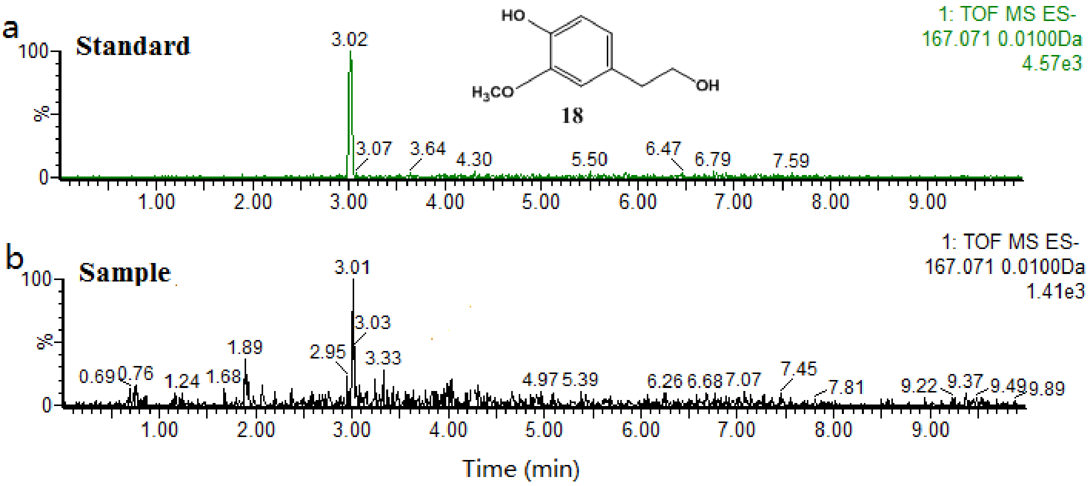


Fig. S19 LC-MS analysis of homovanilly alcohol (**18**) produced by Styrosol 7 from ferulic acid (**2**). a) LC-MS analysis of standard **18**. b) LC-MS analysis of conversion product.

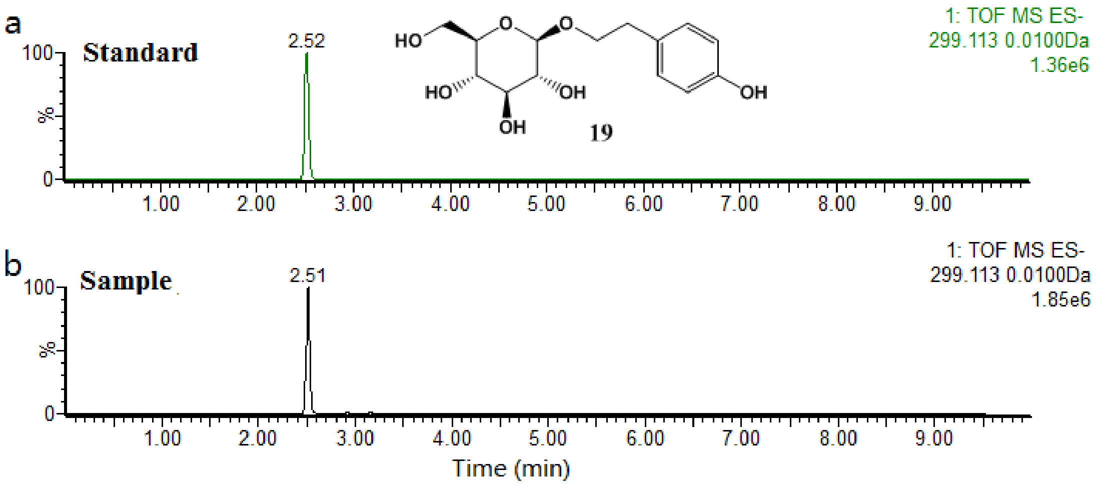


Fig. S20 LC-MS analysis of salidroside (**19**) produced by *E. coli* (BLPad-StyAB-RostyC-SlPAR1-UGT85A1) from *p*-coumaric acid (**1**). a) LC-MS analysis of standard **19**. b) LC-MS analysis of conversion product.

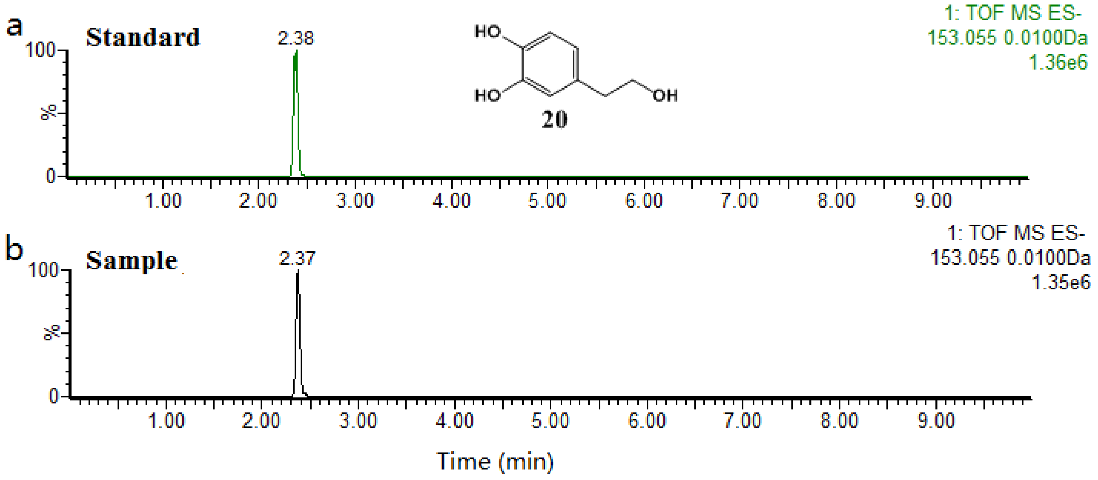


Fig. S21 LC-MS analysis of hydroxytyrosol (**20**) produced by *E. coli* (StyAB-RostyC-SlPAR1-BLPad-HpaBC) from *p*-coumaric acid (**1**). a) LC-MS analysis of standard **20**. b) LC-MS analysis of conversion product.

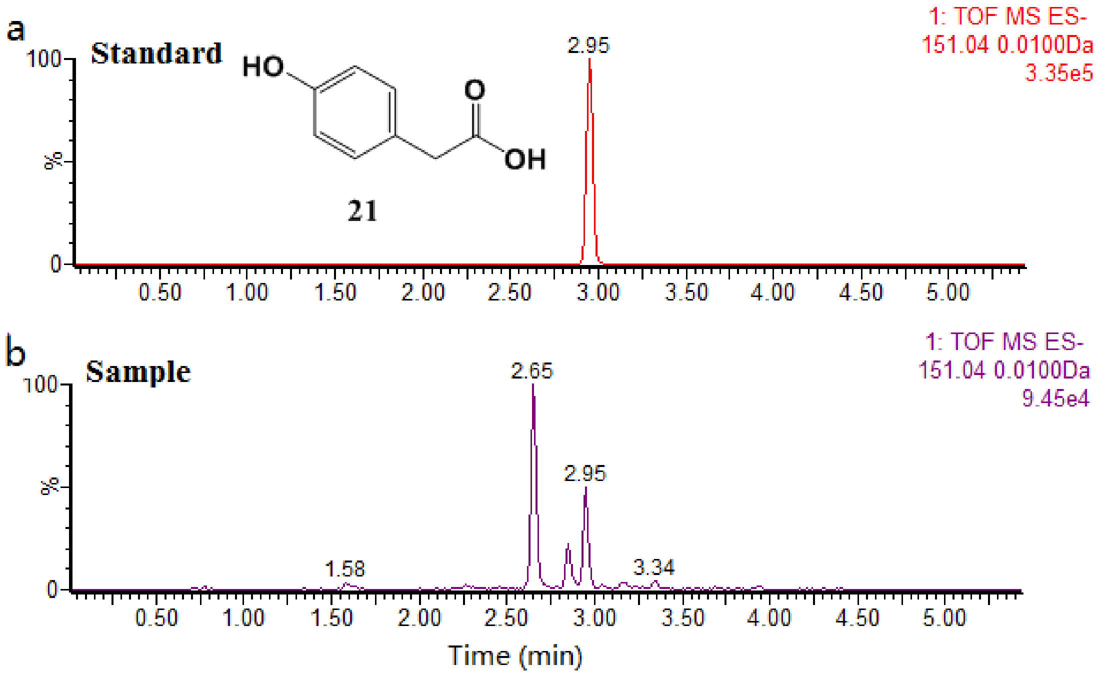
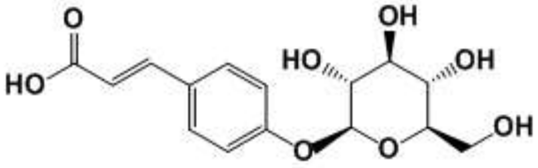


Fig. S22 LC-MS analysis of 4-hydroxyphenylacetic acid (**21**) produced by Styrosol 7. a) LC-MS analysis of standard **21**. b) LC-MS analysis of conversion byproduct.



22

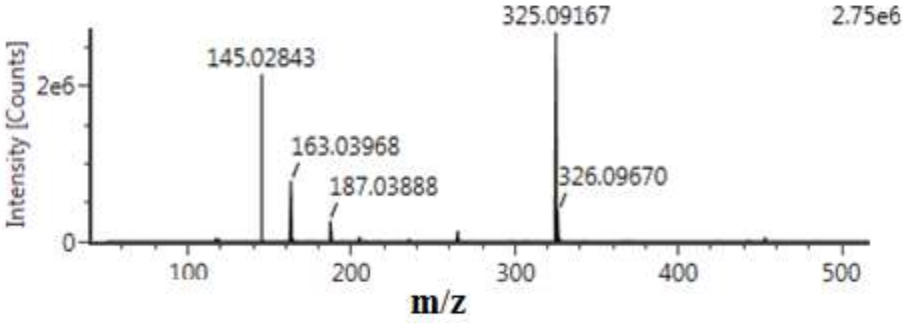


Fig. S23 LC-MS/MS analysis of conversion product produced by E. coli (UGTBL1) from *p*-coumaric acid (**1**). The compound **22** corresponding to $[M-H]^-$ has a molecular ion at 325.0916 (m/z).

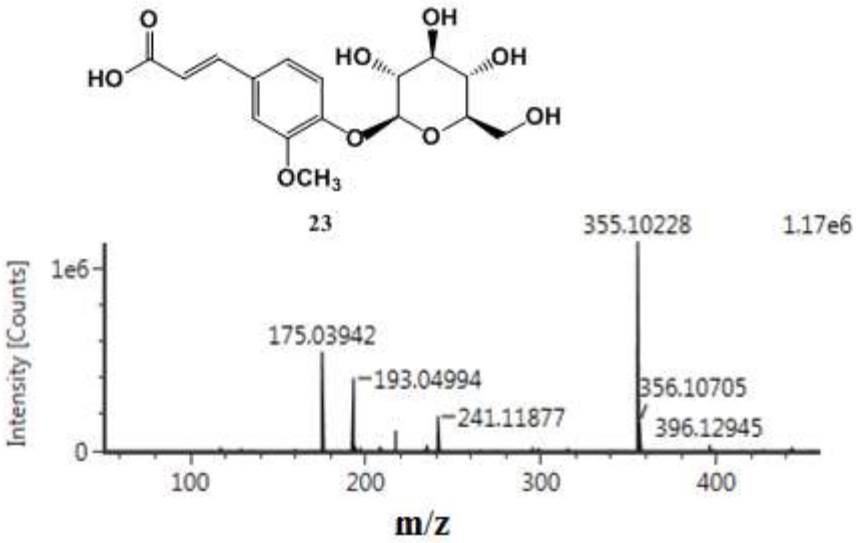


Fig. S24 LC-MS/MS analysis of conversion product produced by *E. coli* (UGT$_{BL}$1) from ferulic acid (**2**). The compound **23** corresponding to [M-H]$^{-}$ has a molecular ion at 355.1022 (m/z).

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