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Supplementary Information for
Complete biosynthesis of the bisbenzylisoquinoline alkaloids guattegaumerine and berbamunine in yeast

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Supplementary Materials and Methods

Chemical compounds and standards

Guattegaumerine and berbamunine were provided by Toni Kutchan. (*R*)-*N*-methylcoclaurine was purchased from BOC Sciences. All other chemicals were purchased from Sigma.

Yeast strain construction

Strains used in this work are listed in Table S1. All strains used are derived from the previously reported strain CSY1171 (10). Strains were grown non-selectively in yeast-peptone media supplemented with 2% w/v dextrose (YPD media), yeast nitrogen base (YNB) defined media (Becton, Dickinson and Company, BD) supplemented with synthetic complete amino acid mixture (YNB-SC; Clontech) and 2% w/v dextrose, or on agar plates made using the aforementioned media. Strains transformed with plasmids bearing auxotrophic selection markers (*URA3* and/or *TRP1*) were grown selectively in YNB media supplemented with 2% w/v dextrose and the appropriate dropout media (YNB-DO; Clontech) or on YNB-DO agar plates.

Yeast genomic modifications were performed using the CRISPRm method (48). Oligonucleotides used in this work (Table S2) were synthesized by the Stanford Protein and Nucleic Acid Facility (Stanford, CA). Biosynthetic genes used in this study (Table S3) were codon-optimized using GeneArt Gene Optimizer software (Thermo Fisher Scientific) either for expression in *S. cerevisiae* or *E. coli* (Table S7) and then synthesized as either gBlock DNA fragments (Integrated DNA Technologies, IDT) or gene fragments (Twist Bioscience). All biosynthetic genes were synthesized with overhangs on both the 5’ end (5’ – CTTAGTTTCGACGGATTCTAGAACTAGTGGATCCTATACA – gene – 3’) and 3’ end (5’ – gene – TAACGCGCCACTTCTAAATAAGCGAATTTCTTATGATTTA – 3’) for ease of cloning. CRISPRm plasmids expressing *Streptococcus pyogenes* Cas9 (SpCas9) and a single guide RNA (sgRNA) targeting a locus of interest in the yeast genome were constructed by assembly PCR and Gibson assembly of DNA fragments encoding SpCas9 (pCS3410), tRNA promoter and HDV ribozyme (pCS3411), a 20-nt guide RNA sequence (synthesized by the Stanford Protein and Nucleic Acid Facility), and tracrRNA and terminator (pCS3414)(49). For gene insertions, integration fragments containing the gene(s) of interest flanked by a promoter and terminator were constructed by PCR amplification such that they possessed 40 bp overhangs on either end with homology to the yeast genome surrounding the site targeted by the guide RNA sequence. Approximately 300 ng of each integration fragment was co-transformed with 300 ng of the CRISPRm plasmid expressing the sgRNA targeting the desired genomic site. Positive integrants were identified by yeast colony PCR, DNA sequencing (Quintara Biosciences; South San Francisco, CA), and/or functional screening by LC-MS.

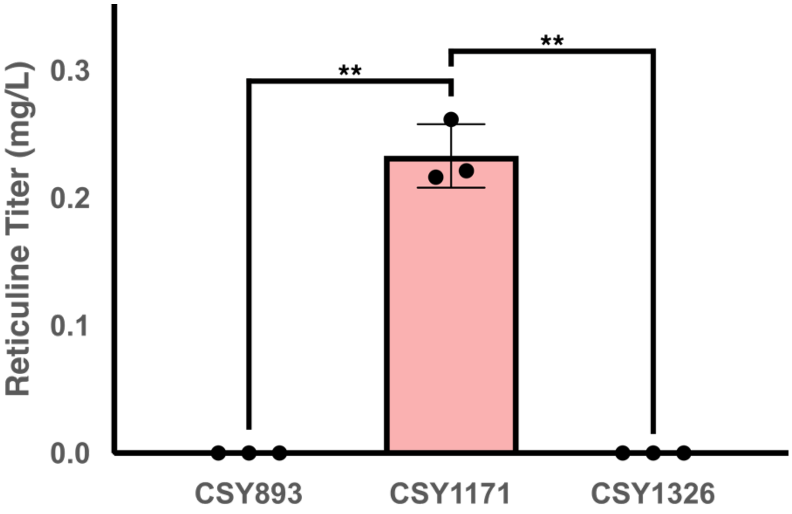
Plasmid construction

Plasmids used in this study (Table S4) were constructed through Gibson assembly. Gibson assembly was performed by amplifying both the gene of interest and the destination plasmid (pCS952(8), pAG414, pAG416, pAG424(50), or pET28) with 40 bp homologous overhangs. PCR amplifications were performed using Q5 DNA polymerase (NEB) and linear DNA fragments were purified using the DNA Clean and Concentrator-5 kit (Zymo Research). Assembled plasmids were propagated in chemically competent *E. coli* (TOP10; Thermo Fisher Scientific) using heat-shock transformation and selection on Luria-Bertani (LB)-agar plates with carbenicillin (100 µg/mL; for pCS952, pAG414, pAG416, and pAG424 derived plasmids) or kanamycin (50 µg/mL; for pET28 derived plasmids). Plasmid DNA was isolated by alkaline lysis from overnight *E. coli* cultures grown at 37 °C and 250 rpm in selective LB media using Econospin columns (Epoch Life Science) according to the manufacturer’s protocol.

Yeast transformations

Yeast strains were chemically transformed using the Frozen-EZ Yeast Transformation II Kit (Zymo Research). Individual colonies were inoculated into YPD media and grown overnight at 30 °C and 250 rpm. Saturated cultures were back-diluted into three new cultures at 1:5, 1:10, and 1:20 dilutions in YPD media and grown for an additional 5–7 hours to reach exponential phase. For each transformation, 1 mL aliquots from each back-diluted culture were pelleted by centrifugation at 500 g for 4 minutes (successively pelleting aliquots from each different dilution into a single pellet in a 1.5 mL microcentrifuge tube) and then washed twice by resuspending the pellet in 1 mL of 50 mM Tris-HCl buffer, pH 8.5. Washed pellets were resuspended in 50 µL of EZ2 solution per transformation and mixed with 100–600 ng of total DNA and 500 µL of the EZ3 solution. The yeast suspensions were incubated at 30 °C with gentle inversion for one hour. For plasmid transformations, the transformed yeast was directly plated onto YNB-DO agar plates. For Cas9-mediated gene integrations, the yeast suspensions in the EZ3 solution were first mixed with 1 mL YPD media, pelleted by centrifugation at 500 g for 4 minutes, and then resuspended in 250 µL of fresh YPD media. The suspensions were incubated at 30 °C with gentle inversion for an additional 90 minutes to allow production of G418 resistance proteins and then spread onto YPD plates containing 400 mg/L G418 sulfate. For all transformations, plates were incubated at 30 °C for 72 hours before being used to inoculate cultures for metabolite assays.

Supplementary Figures



	CSY893	CSY1171	CSY1326
PsNCS	-	+	+
Ps6OMT	-	+	+
PsCNMT	-	+	+
PsCPR	-	+	-
EcCYP80B1	-	+	-
Ps4'OMT	-	+	-

Fig. S1. Titer of reticuline produced by strains CSY893, CSY1171, and CSY1326. All strains were cultured for 96 hr at 30 °C in synthetic complete media and the supernatant was subsequently analyzed by LC-MS/MS using the transitions described in Table S5.

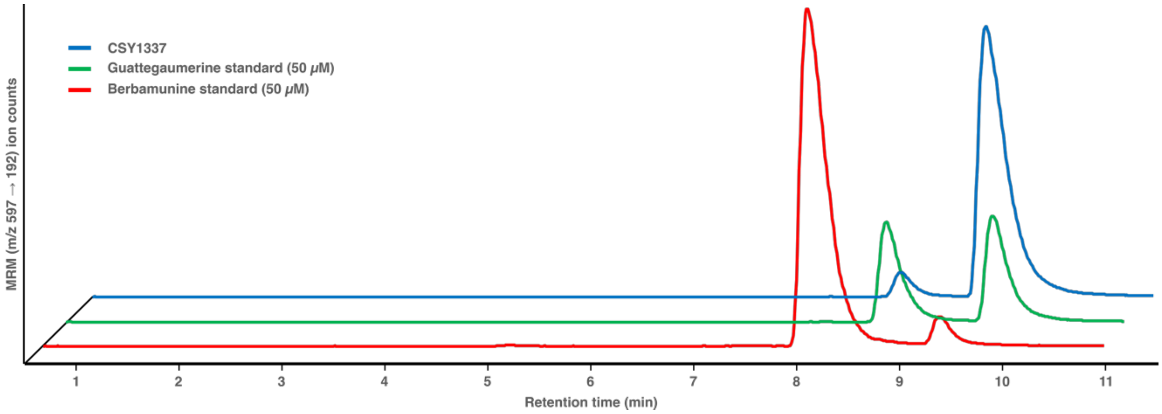
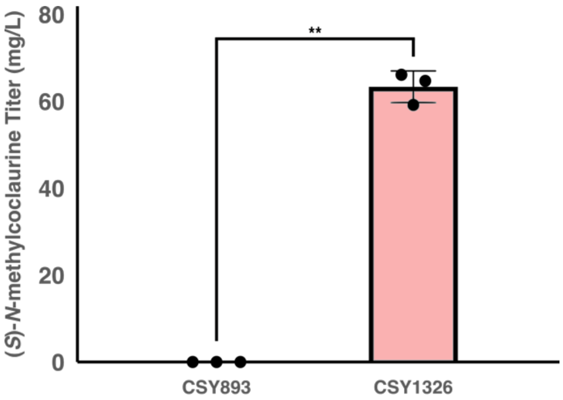


Fig. S2. Comparison of standards of berbamunine (red) and guattegaumerine (green) (both shown here at a concentration of 50 μM; standards were provided by Toni Kutchan) with strain CSY1337 (blue), which produces both berbamunine and guattegaumerine. The guattegaumerine standard contains a nearly equal mixture of both berbamunine and guattegaumerine; concentrations of guattegaumerine were thus determined by first subtracting out the concentration of berbamunine present in the guattegaumerine standard, as determined from the berbamunine standard. Note that the retention times of these peaks would shift slightly over the course of multiple LC-MS/MS runs; whenever such shifts were large enough to result in ambiguous peak assignment, coinjection with berbamunine/guattegaumerine standards was used to verify the identity of the peaks.



PsNCS	-	+
Ps6OMT	-	+
PsCNMT	-	+

Fig. S3. Titer of (*S*)-*N*-methylcoclaurine produced by strains CSY893 and CSY1326 under improved media and growth conditions. Both strains were cultured for 96 hr at 25 °C in synthetic complete media supplemented with 2 mM L-DOPA and 10 mM ascorbic acid and the supernatant was subsequently analyzed by LC-MS/MS using the transitions described in Table S5.

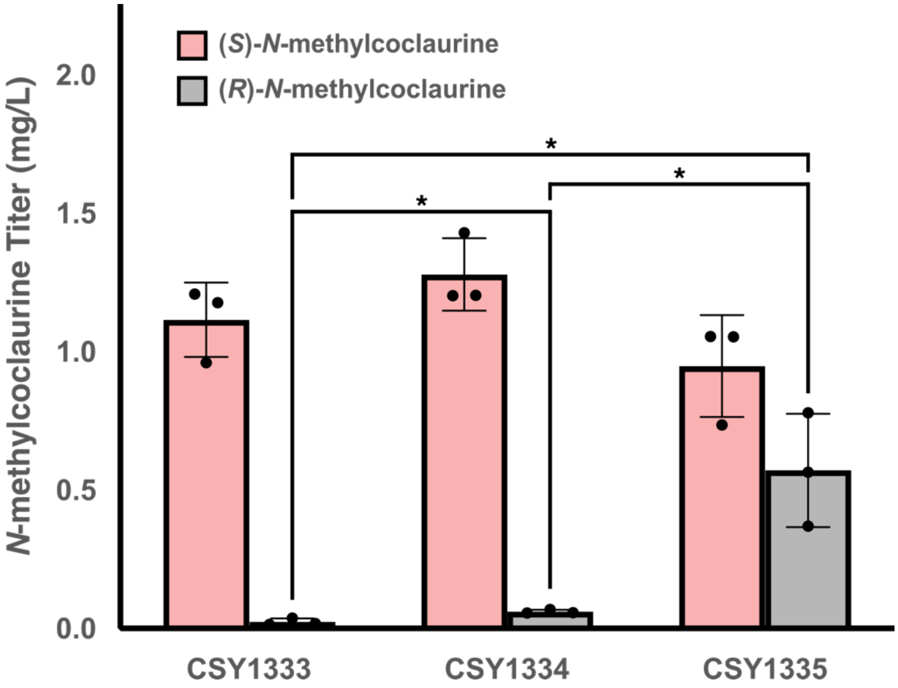


Fig. S4. Titers of residual (*S*)-NMC and (*R*)-NMC in strains containing either one (CSY1333), two (CSY1334), or three (CSY1335) integrated copies of *PbDRS-DRR 1*. All strains were cultured for 96 hr at 25 °C in synthetic complete media supplemented with 2 mM L-DOPA and 10 mM ascorbic acid and the supernatant was subsequently analyzed by LC-MS/MS using the transitions described in Table S5.

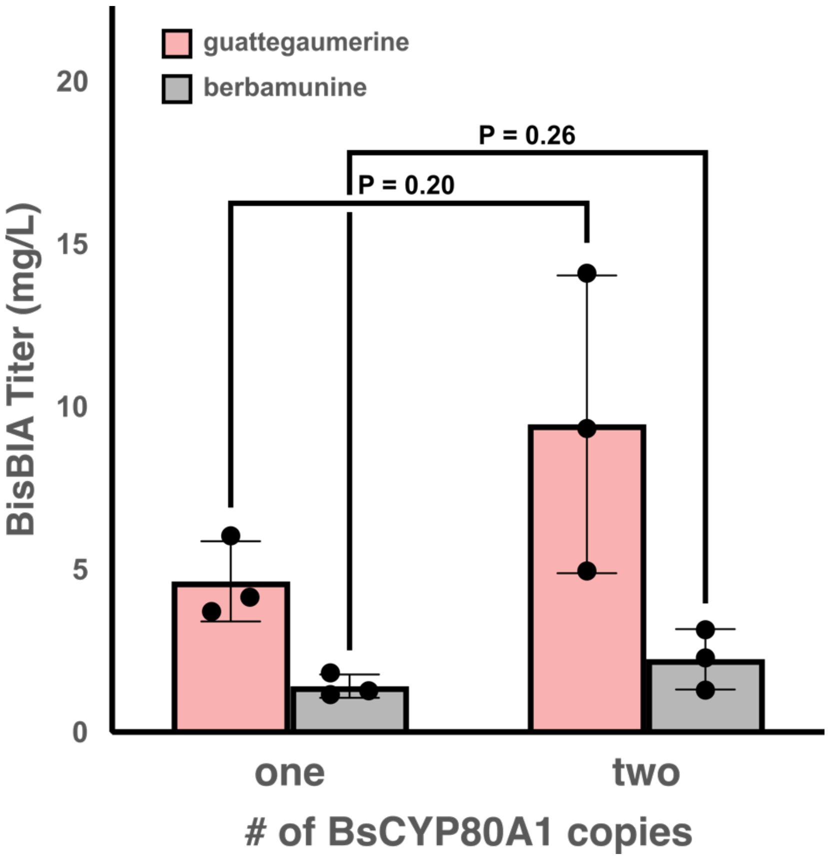


Fig. S5. Effect on bisBIA titer of integration of either a single copy (strain CSY1332) or two copies (strain CSY1336) of *BsCYP80A1*. Data shown were collected after 96 hours growth at 25 °C in synthetic complete media supplemented with 2 mM L-DOPA and 10 mM ascorbic acid.

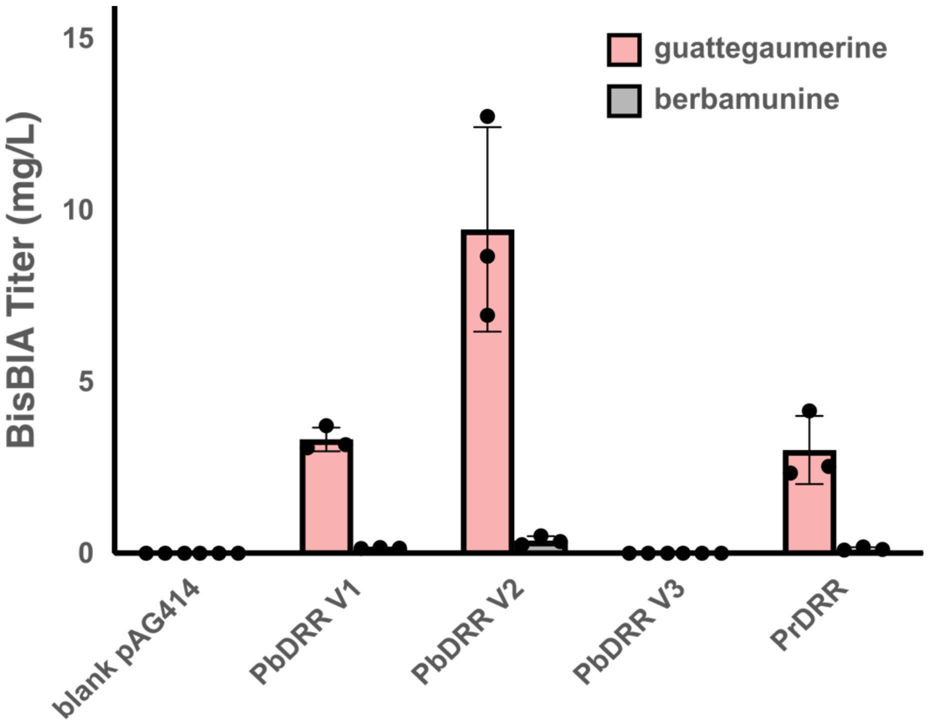


Fig. S6. *De novo* production of bisBIAs in yeast strains expressing PrDRS with different DRR domains as individual polypeptides. Strains were cultured in selective media (YNB-Ura-Trp) with 2% dextrose with 2 mM L-DOPA and 10 mM ascorbic acid at 25 °C for 96 h before LC-MS/MS analysis of the growth media using the MRM transitions reported in Table S5.

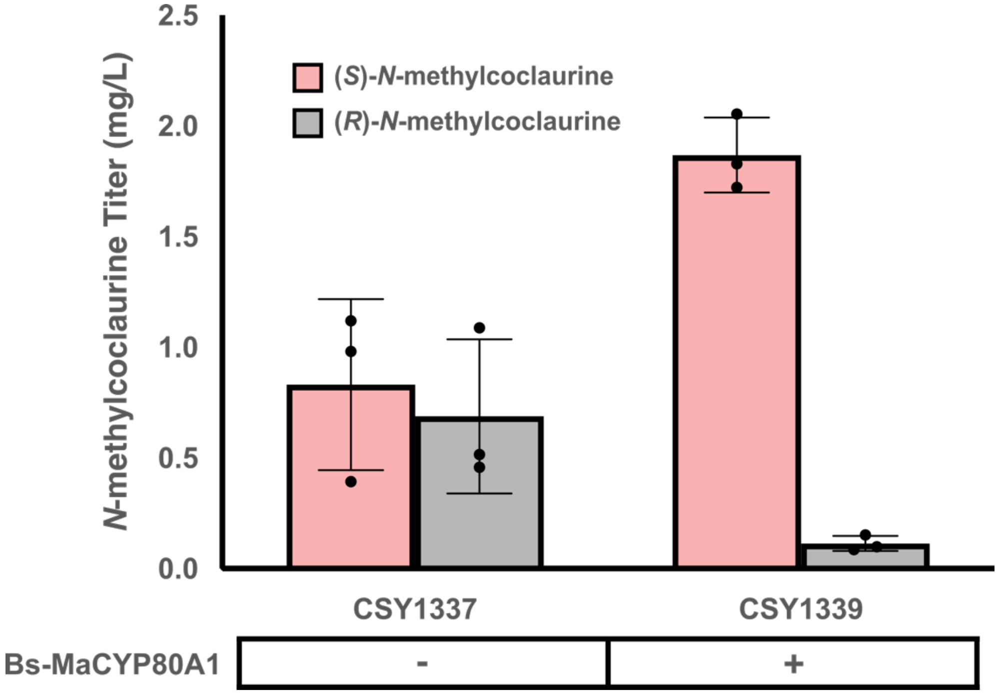


Fig. S7. Titers of residual (*S*)-NMC and (*R*)-NMC in our top guattegaumerine producing strain (CSY1337) and our top berbamunine producing strain (CSY1339 expressing Bs-MaCYP80A1 from a high-copy plasmid). Both strains were cultured for 96 hr at 25 °C in the appropriate dropout media supplemented with 2 mM L-DOPA and 10 mM ascorbic acid and the supernatant was subsequently analyzed by LC-MS/MS using the transitions described in Table S5.

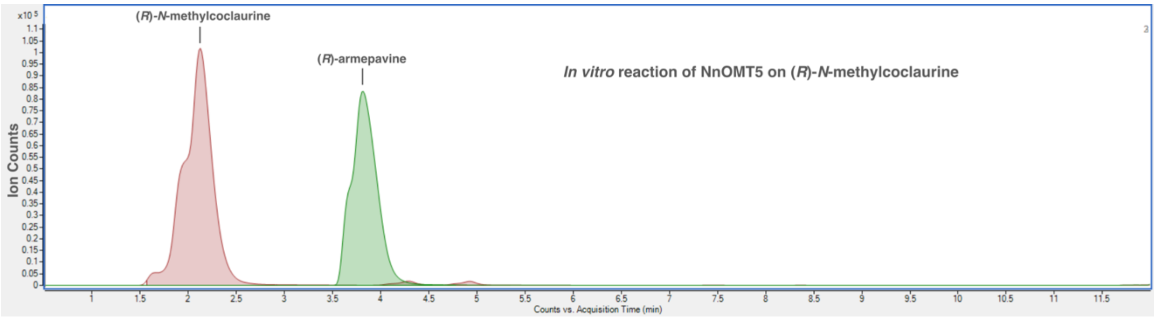
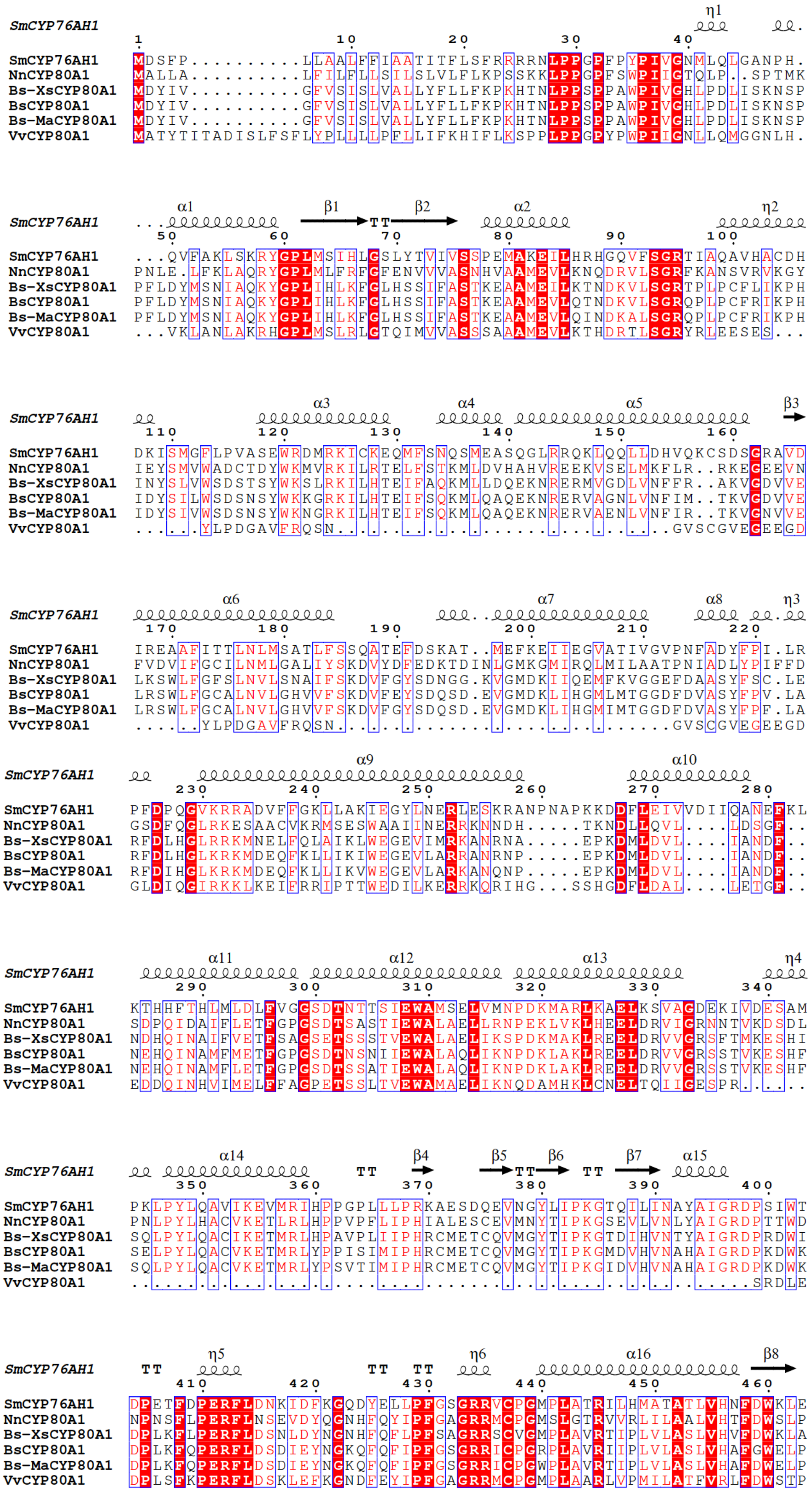


Fig. S8. *In vitro* reaction of NnOMT5 on commercial (*R*)-*N*-methylcoclaurine to produce (*R*)-armepavine. Data shown are representative raw LC-MS/MS traces using the transitions shown in Table S5 for *N*-methylcoclaurine and armepavine.



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SmCYP76AH1    MDSFP..........LLAALFFIAATITFLSFRRRRNLPPGPFPYPIVGNMLQLGANPH.
NnCYP80A1     MALLA..........LFILFLLSILSLVLFLKPSSKKLPPGPFSWPIIGTQLP..SPTMK
Bs-XsCYP80A1  MDYIV..........GFVSISLVALLYFLLFKPKHTNLPPSPPAWPIVGHLPDLISKNSP
BsCYP80A1     MDYIV..........GFVSISLVALLYFLLFKPKHTNLPPSPPAWPIVGHLPDLISKNSP
Bs-MaCYP80A1  MDYIV..........GFVSISLVALLYFLLFKPKHTNLPPSPPAWPIVGHLPDLISKNSP
VvCYP80A1     MATYTITADISLFSFLYPLLLLPFLLIFKHIFLKSPPLPPGPYPWPIIGNLLQMGGNLH.

SmCYP76AH1    ...QVFAKLSKRYGPLMSIHLGSLYTVIVSSPEMAKEILHRHGQVFSGRTIAQAVHACDH
NnCYP80A1     PNLE.LFKLAQRYGPLMLFRFGFENVVVASNHVAAMEVLKNQDRVLSGRFKANSVRVKGY
Bs-XsCYP80A1  PFLDYMSNIAQKYGPLIHLKFGLHSSIFASTKEAAMEILKTNDKVLSGRTPLPCFLIKPH
BsCYP80A1     PFLDYMSNIAQKYGPLIHLKFGLHSSIFASTKEAAMEVLQTNDKVLSGRQPLPCFRIKPH
Bs-MaCYP80A1  PFLDYMSNIAQKYGPLIHLKFGLHSSIFASTKEAAMEVLQINDKALSGRQPLPCFRIKPH
VvCYP80A1     ...VKLANLAKRHGPLMSLRLGTQIMVVASSSAAAMEVLKTHDRTLSGRYRLEESES...

SmCYP76AH1    DKISMGFLPVASEWRDMRKICKEQMFSNQSMEASQGLRRQKLQQLLDHVQKCSDSGRAVD
NnCYP80A1     IEYSMVWADCTDYWKMVRKILRTELFSTKMLDVHAHVREEKVSELMKFLR..RKEGEEVN
Bs-XsCYP80A1  INYSLVWSDSTSYWKSLRKILHTEIFAQKMLLDQEKNRERMVGDLVNFFR..AKVGDVVE
BsCYP80A1     IDYSILWSDSNSYWKKGRKILHTEIFSQKMLQAQEKNRERVAGNLVNFIM..TKVGDVVE
Bs-MaCYP80A1  IDYSIVWSDSNSYWKNGRKILHTEIFSQKMLQAQEKNRERVAENLVNFIR..TKVGNVVE
VvCYP80A1     ......YLPDGAVFRQSN..............................GVSCGVEGEEGD

SmCYP76AH1    IREAAFITTLNLMSATLFSSQATEFDSKAT..MEFKEIIEGVATIVGVPNFADYFPI.LR
NnCYP80A1     FVDVIFGCILNMLGALIYSKDVYDFEDKTDINLGMKGMIRQLMILAATPNIADLYPIFFD
Bs-XsCYP80A1  LKSWLFGFSLNVLSNAIFSKDVFGYSDNGG.KVGMDKIIQEMFKVGGEFDAASYFSC.LE
BsCYP80A1     LRSWLFGCALNVLGHVVFSKDVFEYSDQSD.EVGMDKLIHGMLMTGGDFDVASYFPV.LA
Bs-MaCYP80A1  LRSWLFGCALNVLGHVVFSKDVFGYSDQSD.EVGMDKLIHGMIMTGGDFDVASYFPF.LA
VvCYP80A1     ......YLPDGAVFRQSN..............................GVSCGVEGEEGD

SmCYP76AH1    PFDPQGVKRRADVFFGKLLAKIEGYLNERLESKRANPNAPKKDDFLEIVVDIIQANEFKL
NnCYP80A1     GSDFQGLRKESAACVKRMSESWAAIINERRKNNDH.....TKNDLLQVL....LDSGF..
Bs-XsCYP80A1  RFDLHGLRRKMNELFQLAIKLWEGEVIMRKANRNA.....EPKDMLDVL....IANDF..
BsCYP80A1     RFDLHGLKRKMDEQFKLLIKIWEGEVLARRANRNP.....EPKDMLDVL....IANDF..
Bs-MaCYP80A1  RFDIHGLKRKMDEQFKLLIKVWEGEVLARKANQNP.....EPKDMLDVL....IANDF..
VvCYP80A1     GLDIQGIRKKLKEIFRRIPTTWEDILKERRKQRIHG...SSHGDFLDAL....LETGF..

SmCYP76AH1    KTHHFTHLMLDLFVGGSDTNTTSIEWAMSELVMNPDKMARLKAELKSVAGDEKIVDESAM
NnCYP80A1     SDPQIDAIFLETFGPGSDTSASTIEWALAELLRNPEKLVKLHEELDRVIGRNNTVKDSDL
Bs-XsCYP80A1  NDHQINAIFVETFSAGSETSSSTVEWALAELIKSPDKMAKLREELDRVVGRSFTMKESHI
BsCYP80A1     NEHQINAMFMETFGPGSDTNSNIIEWALAQLIKNPDKLAKLREELDRVVGRSSTVKESHF
Bs-MaCYP80A1  NEHQINAMFLETFGPGSDTSSATIEWALAQLIKNPDKLAKLREELDRVVGRSSTVKESHF
VvCYP80A1     EDDQINHVIMELFFAGPETSSLTVEWAMAELIKNQDAMHKLCNELTQIIGESPR......

SmCYP76AH1    PKLPYLQAVIKEVMRIHPPGPLLLPRKAESDQEVNGYLIPKGTQILINAYAIGRDPSIWT
NnCYP80A1     PNLPYLHACVKETLRLHPPVPFLIPHIALESCEVMNYTIPKGSEVLVNLYAIGRDPTTWD
Bs-XsCYP80A1  SQLPYLQACIKETMRLHPAVPLIIPHRCMETCQVMGYTIPKGTDIHVNTYAIGRDPRDWI
BsCYP80A1     SELPYLQACVKETMRLYPPISIMIPHRCMETCQVMGYTIPKGMDVHVNAHAIGRDPKDWK
Bs-MaCYP80A1  SQLPYLQACVKETMRLYPSVTIMIPHRCMETCQVMGYTIPKGIDVHVNAHAIGRDPKDWK
VvCYP80A1     .......................................................SRDLE

SmCYP76AH1    DPETFDPERFLDNKIDFKGQDYELLPFGSGRRVCPGMPLATRILHMATATLVHNFDWKLE
NnCYP80A1     NPNSFLPERFLNSEVDYQGNHFQYIPFGAGRRMCPGMSLGTRVVRLILAALVHTFDWSLP
Bs-XsCYP80A1  DPLKFLPERFLDSNLDYNGNHFQFLPFSAGRRSCVGMPLAVRTIPLVLASLVHVFDWKLA
BsCYP80A1     DPLKFQPERFLDSDIEYNGKQFQFIPFGSGRRICPGRPLAVRIIPLVLASLVHAFGWELP
Bs-MaCYP80A1  DPLKFQPERFLDSDIEYNGKQFQFIPFGSGRRICPGWPLAVRTIPLVLASLVHAFDWELP
VvCYP80A1     DPLSFKPERFLDSKLEFKGNDFEYIPFGAGRRMCPGMPLAARLVPMILATFVRLFDWSTP
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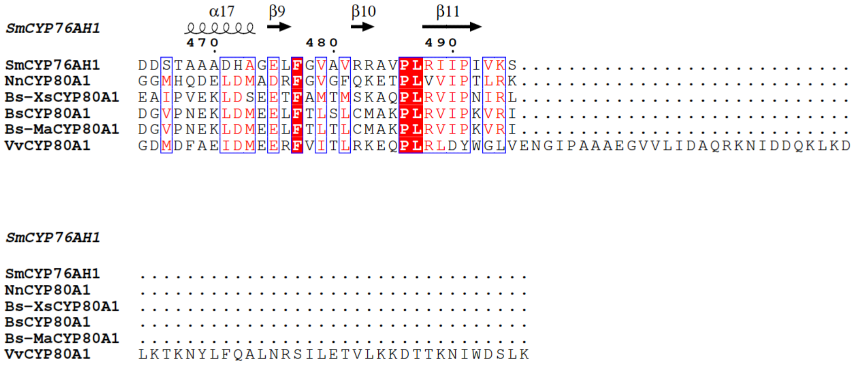

Fig. S9. Alignment of protein sequences of different CYP80A1 variants tested *in vivo* in *S. cerevisiae* for bisBIA biosynthesis. Alignment was generated using ClustalOmega (1, 2) and the visualization shown was generated using ESPript (https://espript.ibcp.fr) (3). As no CYP80A1 crystal structures are currently available, the secondary structural features shown in the alignment are those of the plant P450 with a crystal structure available that is most similar to BsCYP80A1, CYP76AH1 from *Salvia miltiorrhiza* (SmCYP76AH1) (4).

Supplemental Tables

Table S1. Yeast strains used in this work. The prefix “y” here denotes that the gene is codon-optimized for expression in E. coli. CSY1171 contains two different isoforms of the *Ps4’OMT* gene – one that is wild-type, called here *Ps4’OMT*, and one that is codon-optimized for the yeast S. cerevisiae, called here *yPs4’OMT*.

Strain ID	Description	Genotype
CSY893(5)	Control strain	CEN.PK2-1D (MATα ura3-52; trp1-289; leu2-3, 112; trp1-1; his3Δ1; MAL2-8L; SUC2)
CSY1171(6)	*De novo* (*S*)-reticuline strain	CSY1060(7); *ymr206w-CjNCS*Δ:: *yCjNCS-Δ23*; *zwf1-CjNCS*Δ:: *yCjNCS-Δ23*; *ymr206w-RnTyrH*^{WR}:: *yRnTyrH*^{WR}; *ymr206w-RnTyrH*^{WR}:: *yRnTyrH*^{WR} ‡
CSY1326	*De novo* (*S*)-*N*-methylcoclaurine strain	CSY1171; Δ *PsCPR*; Δ *EcCYP80B1*; Δ *Ps4’OMT**
CSY1327	BsCYP80A1 test strain	CSY1326; LEU2:: P_{GPD}-*BsCYP80A1*-T_{ADH1}
CSY1328	First full pathway strain	CSY1327; URA3:: P_{TEF1}-*PsCPR*-T_{CYC1}, P_{HXT7}-*PbDRS-DRR 1*-T_{ADH1}
CSY1329	Integrated *PsCPR*	CSY1327; URA3:: P_{TEF1}-*PsCPR*-T_{CYC1}
CSY1330	Integrated *EcCPR*	CSY1327; URA3:: P_{TEF1}-*EcCPR*-T_{CYC1}
CSY1331	Integrated *AtCPR*	CSY1327; URA3:: P_{TEF1}-*AtCPR*-T_{CYC1}
CSY1332	Integrated *ScCPR*	CSY1327; URA3:: P_{TEF1}-*ScCPR*-T_{CYC1}
CSY1333	First fully integrated *de novo* bisBIA strain	CSY1332; TRP3:: P_{HXT7}-*PbDRS-DRR 1*-T_{ADH1}
CSY1334	Two integrated *PbDRS-DRR 1* copies	CSY1333; HIS3:: P_{GPD}-*PbDRS-DRR 1*-T_{CYC1}
CSY1335	Three integrated *PdDRS-DRR 1* copies	CSY1334; *ydr514c-yPs4’OMT**:: P_{GPD}-*PbDRS-DRR 1*-T_{CYC1}
CSY1336	Two integrated *BsCYP80A1* copies	CSY1332; TRP3:: P_{GPD}-*BsCYP80A1*-T_{ADH1}
CSY1337	*De novo* guattegaumerine strain	CSY1332; TRP3:: P_{GPD}-*PrDRS*-T_{ADH1}, P_{TEF1}-*PbDRR V2*-T_{CYC1}, P_{PGK1}-*BsCYP80A1*-T_{PHO5}
CSY1338	Second integrated bisBIA module	CSY1337; HIS3:: P_{HXT7}-*BsCYP80A1*-T_{PGK1}, P_{TEF1}-*EcTyrA*^{M53I,A354V}-T_{CYC1}(8), P_{GPD}-*PrDRS-PbDRR V2 chimera 1*-T_{ADH1}
CSY1339	*De novo* (R)-NMC strain	CSY1335; Δ Bs*CYP80A1*

Table S2. Oligonucleotides used in this work. CSY1171 contains two different isoforms of the *Ps4'OMT* gene – one that is wild-type, called here *Ps4'OMT*, and one that is codon-optimized for the yeast S. cerevisiae, called here *yPs4'OMT*. The site targeted by guide RNAs is denoted in bold.

Oligo ID	Description	Sequence (5' → 3')
p73	Construction of sgRNA-tracrRNA cassette	ATGTGTTATGTCGACTTAATGTGCTTCAGTATTACATTTTT
p74	Construction of sgRNA-tracrRNA cassette	CTAGACCTATATCGTAGTTAATCCACTAGACAGAAGTTTG
pTV5	gRNA for construction of CSY1326 strain (excision of PsCPR, EcCYP80B1, and Ps4'OMT from CSY1171)	GTGGCGAATGGGACTTT**GATTGAACTCGTAAAAGCAA**GTTTTAGAGCTAGAAATAGCAAGT
pTV6	gRNA for construction of CSY1326 strain (excision of PsCPR, EcCYP80B1, and Ps4'OMT from CSY1171)	GTGGCGAATGGGACTTT**AGTGAATGATCTGCCGGTAG**GTTTTAGAGCTAGAAATAGCAAGT
pTV136	gRNA for cutting at *BsCY80A1*	GTGGCGAATGGGACTTT**ATACACGGTATGTTGATGAC**GTTTTAGAGCTAGAAATAGCAAGT
pTV228	gRNA for cutting at *yPs4'OMT*	GTGGCGAATGGGACTTT**GATATCATCAAGAACAACGA**GTTTTAGAGCTAGAAATAGCAAGT
pTV229	gRNA for cutting at *yPs4'OMT*	GTGGCGAATGGGACTTT**GAACAAGAAACTTGTAACGG**GTTTTAGAGCTAGAAATAGCAAGT
pTV356	gRNA for cutting at *ScPDC1*	GTGGCGAATGGGACTTT**CAATTCACCGACACCGAAGG**GTTTTAGAGCTAGAAATAGCAAGT
pTV11	Repair gap in construction of CSY1326 strain after cutting with pCS3695, replacing with Leu marker	CAAAAATGAAAAAAAGGAAGAGTGAATGATCTGCCGGGCTTTAATTTGCGGCCAAG
pTV12	Repair gap in construction of CSY1326 strain after cutting with pCS3695, replacing with Leu marker	TACCTACAAAACTTCTAGCTAGATTGAACTCGTAAAAGTTACGAATTCGAGCTCGGTAC
pTV147	Repair gap in *BsCYP80A1* after cutting with pCS4718, inserting His tag from pET28	GACAGGGAAATAACTAGCTACATCAAAATCACCTCCGGTCTCAGTGGTGGTGGTGGTG
pTV148	Repair gap in *BsCYP80A1* after cutting with pCS4718, inserting His tag from pET28	TGATGAGGTTGGAATGGACAAATTGATACACGGTATGTTGATTAATATGTTTGAAGGAGTACCAAATGCA
pTV230	Repair gap in *yPs4'OMT* after cutting with pCS4719, inserting *ScCPR*	CAATTTAGCAGCCAATTGAGCCAAGGTAATAGCACCATCGCTGAGAGTGCACCATAT
pTV231	Repair gap in *yPs4'OMT* after cutting with pCS4719, inserting *ScCPR*	TGCGCTGTTGAAATTGGTATTGCCGATATCATCAAGAACAACAAATTAAAGCCTTCGAGCG

pTV232	Repair gap in *yPs4'OMT* after cutting with pCS4720, inserting *ScCPR*	TAGATACTTGGTCCACTTGAACATTATCGAACAAGAAACTTGTAACTGAGAGTGCACCATATGCATA
pTV233	Repair gap in *yPs4'OMT* after cutting with pCS4720, inserting *ScCPR*	ACCAACTGGTTTCAAAGAGTAAACCTTTTCGACACCACCGCAAATTAAAGCCTTCGA
pTV246	Repair gap in *yPs4'OMT* after cutting with pCS4720, inserting *yCjNCS-Δ23*	AATCATAAATCATAAGAAATTCGCTTATTTAGAAGTGGCGCTCATTCAGATGACTTATG
pTV247	Repair gap in *yPs4'OMT* after cutting with pCS4720, inserting *yCjNCS-Δ23*	TAGTTTCGACGGATTCTAGAACTAGTGGATCCTATACAATGAACGGTAGACCTTTGTT
pTV361	Repair gap in *ScPDC1* after cutting with pCS4721	GCTGATGGTTACGCTCGTATCAAGGGTATGTCTTGTATCATCACCACCTACAAAAGCTGGAGCTCTT
pTV362	Repair gap in *ScPDC1* after cutting with pCS4721	CCGGCAATACCGTTCAAAGCAGACAATTCACCGACACCGATGATCTGCCGGTAGAG
Module_1-1_fwd	Construction of strain CSY1337; P_{GPD}-*PrDRS*-T_{ADH1} portion	TTAATCGGCAAAAAAAGAAAAGCTCCGGATCAAGATTGTAGAGCTCTTCGAGTTTATCAT
Module_1-1_rev	Construction of strain CSY1337; P_{GPD}-*PrDRS*-T_{ADH1} portion	CGCTCGAAGGCTTTAATTTGTGATCTGCCGGTAGAGGTGT
Module_1-2_fwd	Construction of strain CSY1337; P_{TEF}-*PbDRR V2*-T_{CYC1} portion	CAAATTAAAGCCTTCGAGCGTCCCAAAACCTT
Module_1-2_rev	Construction of strain CSY1337; P_{TEF}-*PbDRR V2*-T_{CYC1} portion	ATATGCATAGCTTCAAAATGTTTCTACTCCTTTTTTACTC
Module_1-3_fwd	Construction of strain CSY1337; P_{PGK1}-*BsCYP80A1*-T_{PHO5} portion	CTGGAAGAGTAAAAAAGGAGTAGAAACATTTTGAAGCTATGCATATAGGCATTTGCAAGAATTACT
Module_1-3_rev	Construction of strain CSY1337; P_{PGK1}-*BsCYP80A1*-T_{PHO5} portion	AGTAGTGGAAGATATTCTTTATTGAAAAATAGCTTGTCACCTTACGTTCACTCTTCCTTTTTTTCATTTTTG
Module_2-1_fwd	Construction of strain CSY1339; P_{HXT7}-*BsCYP80A1*-T_{PGK} portion	ATTTTTTTGTCAAATATCGTATCTATAGAGATAATCTCTATCAACTCAAACTCGTAGGAACAATTTCGGGCCCC
Module_2-1_rev	Construction of strain CSY1339; P_{HXT7}-*BsCYP80A1*-T_{PGK} portion	GGGACGCTCGAAGGCTTTAATTTGAACGAACGCAGAATTTTCGAGTTATTAAACT
Module_2-2_fwd	Construction of strain CSY1339; P_{TEF1}-$EcTyrA^{M53I,A354V}$-T_{CYC1} portion	AGTTTAATAACTCGAAAATTCTGCGTTCGTTCAAATTAAAGCCTTCGAGCGTCCC
Module_2-2_rev	Construction of strain CSY1339; P_{TEF1}-$EcTyrA^{M53I,A354V}$-T_{CYC1} portion	CGAAGAGCTCCAGCTTTTGTCATAGCTTCAAAATGTTTCTACTCCTTTTTTAC
Module_2-3_fwd	Construction of strain CSY1339; P_{GPD}-*PrDRS-PbDRR V2 chimera 1*-T_{ADH} portion	GTAAAAAAGGAGTAGAAACATTTTGAAGCTATGACAAAAGCTGGAGCTCTTCGAGTTTATCATTATCAATACT
Module_2-3_rev	Construction of strain CSY1339; P_{GPD}-*PrDRS-PbDRR V2 chimera 1*-T_{ADH} portion	GATTGTACGGGGAATGGAAAATGTACATATAATATCCAGTATCATGATCTGCCGGTAGAGGTGTGGTC

pJP-243	Amplification of pCS952 backbone	TAAGCGGCCGCTAGGG
pJP-244	Amplification of pCS952 backbone	GTCGACAAAACTTAGATTAGATTGCTAT
pJP-277	Amplification of gBlocks for *ySiCNMT2*, *yNnOMT5*, and *yCt7OMT* for Gibson assembly into pCS952	TAGAAAGAAAGCATAGCAATCTAATCTAAGTTTTGTCGACCTTAGTTTCGACGGATTCTAGAACTAGT
pJP-278	Amplification of gBlocks for *ySiCNMT2*, *yNnOMT5*, and *yCt7OMT* for Gibson assembly into pCS952	TACATGATGCGGCCCTCCTGCAGGGCCCTAGCGGCCGCTTATAAATCATAAGAAATTCGCTTATTTAGAAGTGG
pJP-279	Construction of empty pAG414 control plasmid	GATGGGCCTAGGAAAACTTAGATTAGATTGCTATGC
pJP-280	Construction of empty pAG414 control plasmid	GCTTCAATTAGTTATGTCACGCTTACATTCACG
pJP-281	Amplification of pAG424 backbone	TTCTAGAATCCGTCGAAACTAAGTTCT
pJP-282	Amplification of pAG424 backbone	ATTAGTTATGTCACGCTTACATTCACG
pJP-283	Amplification of *BsCYP80A1* for Gibson assembly into pAG424	GTTTTAAAACACCAGAACTTAGTTTCGACGGATTCTAGAAGGATCCCACAAAATGGACTATATTGTTGGTTTCGTAAGTATTT
pJP-284	Amplification of *BsCYP80A1* for Gibson assembly into pAG424	GGGAGGGCGTGAATGTAAGCGTGACATAACTAATCTCGAGTTACTAAATCCTCACTTTGGGGATAACTCTC
pJP-285	Amplification of *Bs-MaCYP80A1* for Gibson assembly into pAG424	TGTGGGGGGAGGGCGTGAATGTAAGCGTGACATAACTAATCTCGAGTTACTATATACGAACCTTGGGGATTACACG
pJP-286	Amplification of *NnCYP80A1* for Gibson assembly into pAG424	GTTTTAAAACACCAGAACTTAGTTTCGACGGATTCTAGAAGGATCCCACAAAATGGCTTTGTTGGCCCTATTTATC
pJP-287	Amplification of *NnCYP80A1* for Gibson assembly into pAG424	TGTGGGGGGAGGGCGTGAATGTAAGCGTGACATAACTAATCTCGAGTTACTATCACTTCCTAAGAGTCGGGATAAC
pJP-288	Amplification of *VvCYP80A1* for Gibson assembly into pAG424	AGAACTTAGTTTCGACGGATTCTAGAAGGATCCCACAAAATGGCAACATACACGATTACGGCCGATATAAGTTTATTCT
pJP-289	Amplification of *VvCYP80A1* for Gibson assembly into pAG424	TGTGGGGGGAGGGCGTGAATGTAAGCGTGACATAACTAATCTCGAGTTACTACTTCAGAGAGTCCCAAATATTCTTTGTC
pJP-290	Amplification of *Bs-XsCYP80A1* for Gibson assembly into pAG424	TGTGGGGGGAGGGCGTGAATGTAAGCGTGACATAACTAATCTCGAGTTACTAAAGCCTTATGTTCGGTATTACTCTTAAAG
pJP-52	Amplification of pET-28 backbone	CTTGCGGCCGCACTCGAGCA
pJP-53	Amplification of pET-28 backbone	ATGGCTGCCGCGCGGCACCA
pJP-295	Amplification of *yNnOMT5* for Gibson assembly into pET-28	TCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGCCATATGGAGGAAGACATGAAAGCACA
pJP-296	Amplification of *yNnOMT5* for Gibson assembly into pET-28	CTCAGTGGTGGTGGTGGTGGTGCTCGAGTGCGGCCGCAAGTCAGGGAAACACCTCAATGATACTT

pJP-297	Amplification of *yCt7OMT* for Gibson assembly into pET-28	TCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGCCATATGGAGACGATTCTTCAAGGTCAA
pJP-298	Amplification of *yCt7OMT* for Gibson assembly into pET-28	TCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGCCATATGGAGACGATTCTTCAAGGTCAA

Table S3. Genes used in this work.

Gene ID	Description	Source organism	Accession ID
ARO4^{Q166K}	DAHP synthase	*Saccharomyces cerevisiae*	AJQ16674.1
ARO7^{T226I}	Chorismate mutase	*Saccharomyces cerevisiae*	NP_015385
ARO10	Phenylpyruvate decarboxylase	*Saccharomyces cerevisiae*	NP_010668
TKL1	Transketolase	*Saccharomyces cerevisiae*	NP_015399
RnSpr	Sepiapterin reductase	*Rattus norvegicus*	AAA42130
RnPts	6-pyruvoyltetrahydropterin synthase	*Rattus norvegicus*	AAH59140
RnQdpr	Dihydropteridine reductase	*Rattus norvegicus*	P11348
RnPcbd1	Pterin-4-alpha-carbinolamine dehydratase	*Rattus norvegicus*	NP_001007602
RnTyrH^{WT}	Tyrosinase	*Rattus norvegicus*	NP_036872
CjNCS	Norcoclaurine synthase	*Coptis japonica*	BAF45338
Ps6OMT	Norcoclaurine 6-O-methyltransferase	*Papaver somniferum*	AY268894.1
PsCNMT	Coclaurine N-methyltransferase	*Papaver somniferum*	AY217336.1
Ps4'OMT	6-Methyl-*(S)*-laudanosoline 4'-O-methyltransferase	*Papaver somniferum*	MF038041.1
PsCPR	Cytochrome P450 reductase	*Papaver somniferum*	AAC05021
EcCPR	Cytochrome P450 reductase	*Eschscholzia californica*	U67186.1
AtCPR	Cytochrome P450 reductase	*Arabidopsis thaliana*	X66016.1
ScCPR	Cytochrome P450 reductase	*Saccharomyces cerevisiae*	D13788.1
PbDRS-DRR 1	Reticuline epimerase	*Papaver bracteatum*	No ID
PbDRS-DRR 2	Reticuline epimerase	*Papaver bracteatum*	No ID

PsDRS-DRR	Reticuline epimerase	*Papaver somniferum*	KP985715.1
PrDRS	1,2-dehydroreticuline synthase	*Papaver rhoeas*	KP985716.1
PrDRR	1,2-dehydroreticuline reductase	*Papaver rhoeas*	KP985723.1
PbREPI	Reticuline epimerase	*Papaver bracteatum*	KP985719.1
BsCYP80A1	Berbamunine synthase	*Berberis stolonifera*	U09610.1
NnCYP80A1	Berbamunine synthase	*Nelumbo nucifera*	XM_010255688.2
VvCYP80A1	Berbamunine synthase	*Vitis vinifera*	RVW28439.1
MaCYP80A1	Berbamunine synthase	*Mahonia aquifolium*	No ID
XsCYP80A1	Berbamunine synthase	*Xanthorhiza simplicissima*	No ID
SiCNMT2	Coclaurine *N*-methyltransferase	*Stephania intermedia*	MK749413
NnOMT5	(*RS*)-norcoclaurine 6-*O*-methyltransferase	*Nelumbo nucifera*	XM_010277761
Ct7OMT	Norcoclaurine 7-*O*-methyltransferase	*Coptis teeta*	MH165877.1

Table S4. Plasmids used in this work. CSY1171 contains two different isoforms of the *Ps4'OMT* gene – one that is wild-type, called here *Ps4'OMT*, and one that is codon-optimized for the yeast S. cerevisiae, called here *yPs4'OMT*.

Plasmid	Description	Origin	Marker	Source
pCS952	High-copy *S. cerevisiae* expression vector, P$_{\text{TEF1}}$-*TfS9OMT*-T$_{\text{CYC1}}$	2µ	URA3	(9)
pAG414	Empty yeast expression vector; P$_{\text{TDH3}}$-attR1-*CmR*-ccdB-attR2-T$_{\text{CYC1}}$	CEN/ARS	TRP1	(10)
pAG416	Empty yeast expression vector; P$_{\text{TDH3}}$-attR1-*CmR*-ccdB-attR2-T$_{\text{CYC1}}$	CEN/ARS	URA3	(10)
pAG424	Empty yeast expression vector; P$_{\text{TDH3}}$-attR1-*CmR*-ccdB-attR2-T$_{\text{CYC1}}$	2µ	TRP1	(10)
pET-28	*E. coli* expression vector	pBR322	kan	Novagen
pCS3300	Low-copy expression in *S. cerevisiae* of PbDRS-DRR 1; pAG416; P$_{\text{HXT7}}$-*PbDRS-DRR 1*-T$_{\text{CYC1}}$	CEN/ARS	URA3	(11)
pCS3301	Low-copy expression in *S. cerevisiae* of PbDRS-DRR 1; pAG416; P$_{\text{TDH3}}$-*PbDRS-DRR 1*-T$_{\text{CYC1}}$	CEN/ARS	URA3	(11)
pCS3302	Low-copy expression in *S. cerevisiae* of PsDRS-DRR; pAG416; P$_{\text{HXT7}}$-*PsDRS-DRR*-T$_{\text{CYC1}}$	CEN/ARS	URA3	(11)
pCS3304	Low-copy expression in *S. cerevisiae* of PbDRS-DRR 2; pAG416; P$_{\text{HXT7}}$-*PbDRS-DRR 2*-T$_{\text{CYC1}}$	CEN/ARS	URA3	(11)
pCS3410	Cas9 CRISPR vector for sequence-specific yeast genome integration; pUC-P$_{\text{RNR2}}$-*SpCas9-SV40NLS-8xHis*-T$_{\text{CYC1}}$	2µ	KanMX	(12)
pCS3411	sgRNA promoter + HDV ribozyme; pUC; P$_{\text{tRNA}}$-*Phe-HDV*	--	--	(12)
pCS3414	sgRNA tracrRNA + terminator; pUC; *tracrRNA*-T$_{\text{SNR52}}$	--	--	(12)
pCS3695	Cas9 CRISPR vector for double cutting to excise PsCPR, EcCYP80B1, and Ps4'OMT from CSY1171 (*de novo* (*S*)-reticuline strain); pCS3410; P$_{\text{tRNA}}$-*Phe-HDV-sgRNA*$_{pTV5}$-*sgRNA*$_{pTV6}$-*tracrRNA*-T$_{\text{SNR52}}$	2µ	KanMX	This work
pCS3700	Cas9 CRISPR vector for integration at *ura3* locus; pCS3410; P$_{\text{tRNA}}$-*Phe-HDV-sgRNA*$_{ura3}$-*tracrRNA*-T$_{\text{SNR52}}$	2µ	KanMX	(13)
pCS3701	Cas9 CRISPR vector for integration at *leu2* locus; pCS3410; P$_{\text{tRNA}}$-*Phe-HDV-sgRNA*$_{leu2}$-*tracrRNA*-T$_{\text{SNR52}}$	2µ	KanMX	(13)
pCS3702	Cas9 CRISPR vector for integration at *trp3* locus; pCS3410; P$_{\text{tRNA}}$-*Phe-HDV-sgRNA*$_{trp3}$-*tracrRNA*-T$_{\text{SNR52}}$	2µ	KanMX	(13)

pCS3703	Cas9 CRISPR vector for integration at *his2* locus; pCS3410; P$_{\text{tRNA}}$-*Phe-HDV-sgRNA*$_{\mathit{his2}}$-*tracrRNA*-T$_{\text{SNR52}}$	2µ	KanMX	(13)
pCS4717	Cas9 CRISPR vector for integration at *PsCNMT* gene to disrupt production; pCS3410; P$_{\text{tRNA}}$-*Phe-HDV-sgRNA*$_{\mathit{PsCNMT}}$-*tracrRNA*-T$_{\text{SNR52}}$	2µ	KanMX	This work
pCS4718	Cas9 CRISPR vector for integration at *PsCYP80A1* gene to disrupt production; pCS3410; P$_{\text{tRNA}}$-*Phe-HDV-sgRNA*$_{\mathit{PsCYP80A1}}$-*tracrRNA*-T$_{\text{SNR52}}$	2µ	KanMX	This work
pCS4719	Cas9 CRISPR vector for integration at *yPs4'OMT* gene to disrupt production; pCS3410; P$_{\text{tRNA}}$-*Phe-HDV-sgRNA*$_{\mathit{Ps4'OMT\ g228}}$-*tracrRNA*-T$_{\text{SNR52}}$	2µ	KanMX	This work
pCS4720	Cas9 CRISPR vector for integration at *yPs4'OMT* gene to disrupt production; pCS3410; P$_{\text{tRNA}}$-*Phe-HDV-sgRNA*$_{\mathit{Ps4'OMT\ g229}}$-*tracrRNA*-T$_{\text{SNR52}}$	2µ	KanMX	This work
pCS4721	Cas9 CRISPR vector for integration at *ScPDC1* gene to disrupt production; pCS3410; P$_{\text{tRNA}}$-*Phe-HDV-sgRNA*$_{\mathit{ScPDC1}}$-*tracrRNA*-T$_{\text{SNR52}}$	2µ	KanMX	This work
pCS4722	Low-copy expression in *S. cerevisiae* of PsCPR; pAG414; P$_{\text{TEF1}}$-*PsCPR*-T$_{\text{CYC1}}$	CEN/ARS	TRP1	This work
pCS4723	Empty pAG416 vector for control	CEN/ARS	URA3	This work
pCS4724	Empty pAG414 vector for control	CEN/ARS	TRP1	This work
pCS4725	Low-copy expression in *S. cerevisiae* of PbREPI; pAG416; P$_{\text{TDH3}}$-*PbREPI*-T$_{\text{ADH1}}$	CEN/ARS	URA3	This work
pCS4726	Low-copy expression in *S. cerevisiae* of PbDRS V1; pAG416; P$_{\text{TDH3}}$-*PbDRS V1*-T$_{\text{ADH1}}$	CEN/ARS	URA3	This work
pCS4727	Low-copy expression in *S. cerevisiae* of PbDRS V2; pAG416; P$_{\text{TDH3}}$-*PbDRS V2*-T$_{\text{ADH1}}$	CEN/ARS	URA3	This work
pCS4728	Low-copy expression in *S. cerevisiae* of PbDRS V3; pAG416; P$_{\text{TDH3}}$-*PbDRS V3*-T$_{\text{ADH1}}$	CEN/ARS	URA3	This work
pCS4729	Low-copy expression in *S. cerevisiae* of PrDRS; pAG416; P$_{\text{TDH3}}$-*PrDRS*-T$_{\text{ADH1}}$	CEN/ARS	URA3	This work
pCS4730	Low-copy expression in *S. cerevisiae* of PbREPI DRS; pAG416; P$_{\text{TDH3}}$-*PbREPI DRS*-T$_{\text{ADH1}}$	CEN/ARS	URA3	This work
pCS4731	Low-copy expression in *S. cerevisiae* of PbDRR V1; pAG414; P$_{\text{TEF1}}$-*PbDRR V1*-T$_{\text{CYC1}}$	CEN/ARS	TRP1	This work
pCS4732	Low-copy expression in *S. cerevisiae* of PbDRR V2; pAG414; P$_{\text{TEF1}}$-*PbDRR V2*-T$_{\text{CYC1}}$	CEN/ARS	TRP1	This work
pCS4733	Low-copy expression in *S. cerevisiae* of PbDRR V3; pAG414; P$_{\text{TEF1}}$-*PbDRR V3*-T$_{\text{CYC1}}$	CEN/ARS	TRP1	This work

pCS4734	Low-copy expression in *S. cerevisiae* of PrDRR; pAG414; $\mathrm{P_{TEF1}}$-*PrDRR*-$\mathrm{T_{CYC1}}$	CEN/ARS	TRP1	This work
pCS4735	Low-copy expression in *S. cerevisiae* of PrDRS-PbDRR V2 chimera 1; pAG416; $\mathrm{P_{TDH3}}$-*PrDRS-PbDRR V2 chimera 1*-$\mathrm{T_{ADH1}}$	CEN/ARS	URA3	This work
pCS4736	Low-copy expression in *S. cerevisiae* of PrDRS-PbDRR V2 chimera 2; pAG416; $\mathrm{P_{TDH3}}$-*PrDRS-PbDRR V2 chimera 2*-$\mathrm{T_{ADH1}}$	CEN/ARS	URA3	This work
pCS4737	Low-copy expression in *S. cerevisiae* of PrDRS-PbDRR V2 chimera 3; pAG416; $\mathrm{P_{TDH3}}$-*PrDRS-PbDRR V2 chimera 3*-$\mathrm{T_{ADH1}}$	CEN/ARS	URA3	This work
pCS4738	High-copy expression in *S. cerevisiae* of BsCYP80A1; pAG424; $\mathrm{P_{TDH3}}$-*BsCYP80A1*-$\mathrm{T_{CYC1}}$	2μ	TRP1	This work
pCS4739	High-copy expression in *S. cerevisiae* of NnCYP80A1; pAG424; $\mathrm{P_{TDH3}}$-*NnCYP80A1*-$\mathrm{T_{CYC1}}$	2μ	TRP1	This work
pCS4740	High-copy expression in *S. cerevisiae* of VvCYP80A1; pAG424; $\mathrm{P_{TDH3}}$-*VvCYP80A1*-$\mathrm{T_{CYC1}}$	2μ	TRP1	This work
pCS4741	High-copy expression in *S. cerevisiae* of Bs-MaCYP80A1; pAG424; $\mathrm{P_{TDH3}}$-*Bs-MaCYP80A1*-$\mathrm{T_{CYC1}}$	2μ	TRP1	This work
pCS4742	High-copy expression in *S. cerevisiae* of Bs-XsCYP80A1; pAG424; $\mathrm{P_{TDH3}}$-*Bs-XsCYP80A1*-$\mathrm{T_{CYC1}}$	2μ	TRP1	This work
pCS4743	High-copy expression in *S. cerevisiae* of ySiCNMT2; pCS952; $\mathrm{P_{TEF1}}$-*ySiCNMT2*-$\mathrm{T_{CYC1}}$	2μ	URA3	This work
pCS4744	High-copy expression in *S. cerevisiae* of yNnOMT5; pCS952; $\mathrm{P_{TEF1}}$-*yNnOMT5*-$\mathrm{T_{CYC1}}$	2μ	URA3	This work
pCS4745	High-copy expression in *S. cerevisiae* of yCt7OMT; pCS952; $\mathrm{P_{TEF1}}$-*yCt7OMT*-$\mathrm{T_{CYC1}}$	2μ	URA3	This work
pCS4746	Low-copy expression in *E. coli* of yNnOMT5; pET-28	pBR322	kan	This work
pCS4747	Low-copy expression in *E. coli* of yCt7OMT; pET-28	pBR322	kan	This work

Table S5. LC-MS/MS multiple reaction monitoring (MRM) transitions and parameters used in this work.

Compound	Quantifier MRM transition (m/z^+)	Fragmentor Voltage	Collision Energy	Reference
Norcoclaurine	272.2 → 107	170	28	(14)
Berbamunine/guattegaumerine	597 → 192	100	37	This work
N-methylcoclaurine	300 → 107	100	37	(15)
Armepavine	314 → 107	100	35	(16)
Magnocurarine	315 → 107	122	30	This work
Dauricine	625 → 206	150	46	This work

Compound	Qualifier MRM transition (m/z^+)	Fragmentor Voltage	Collision Energy	Reference
Norcoclaurine	272.2 → 161	170	15	(14)
Berbamunine/guattegaumerine	597 → 475	110	25	This work
N-methylcoclaurine	300 → 175	100	25	(17)
Armepavine	314 → 283	122	18	This work
Magnocurarine	315 → 58	122	34	This work
Dauricine	625 → 190	150	98	This work

Table S6. Exact *p*-values from Student's two-tailed t-tests in Figures 1-4.

Figure	Test	*p*-value
1b	(*S*)-*N*-methylcoclaurine production with PsNCS/Ps6OMT/PsCNMT vs. without PsNCS/Ps6OMT/PsCNMT	2.02×10^{-3}
1c	Guattegaumerine production with BsCYP80A1 & fed (*R*)-NMC vs. with fed (*R*)-NMC but without BsCYP80A1	0.0322
1c	Guattegaumerine production with BsCYP80A1 & fed (*R*)-NMC vs. with BsCYP80A1 but without fed (*R*)-NMC	0.0321
2a	BisBIA production with PsCPR vs. with no CPR	0.0177
2a	BisBIA production with ScCPR vs. with no CPR	0.0388
4b	Berbamunine production with Bs-MaCYP80A1 vs. without Bs-MaCYP80A1	4.67×10^{-3}
4c	Magnocurarine production with SiCNMT2 vs. without SiCNMT2	0.0261
4d	(*RS*)-armepavine production with NnOMT5 vs. without NnOMT5	6.68×10^{-3}
4d	(*RS*)-armepavine production with Ct7OMT vs. without Ct7OMT	0.0103
S1	*De novo* reticuline production, strain CSY893 vs. CSY1171	3.77×10^{-3}
S1	*De novo* reticuline production, strain CSY1326 vs. CSY1171	3.77×10^{-3}
S3	(*S*)-*N*-methylcoclaurine production with PsNCS/Ps6OMT/PsCNMT vs. without PsNCS/Ps6OMT/PsCNMT, with L-DOPA/ascorbic acid supplementation	2.78×10^{-3}
S4	Residual (*R*)-NMC titer, CSY1333 vs. CSY1334	0.0180
S4	Residual (*R*)-NMC titer, CSY1333 vs. CSY1335	0.0431
S4	Residual (*R*)-NMC titer, CSY1334 vs. CSY1335	0.0496
S5	Effect of a second integrated *BsCYP80A1* copy, guattegaumerine titer	0.203
S5	Effect of a second integrated *BsCYP80A1* copy, berbamunine titer	0.260

Table S7. Sequences of genes used in this work.

Gene ID	Sequence
PbDRS-DRR 1	ATGGAATTGCAATACTTCTCCTACTTCCAACCTACCTCTTCTGTTGTTGCTTTGTTGTTGGCATTGGTCAGTATCTTGTTTTCCGTTGTTGTTTTGAGAAAGACCTTCTCCAACAACTATTCTTCTCCAGCTTCTTCTACTGAAACCGCTGTTTTGTGTCATCAAAGACAACAATCTTGCGCCTTGCCAATTTCTGGTTTGTTGCATGTTTTCATGAACAAGAACGGTTTGATCCATGTTACCTTGGGTAATATGGCTGATAAGTACGGTCCAATTTTCTCTTTTCCAACCGGTTCTCATAGAACCTTGGTTGTTTCTTCTTGGGAAATGGTCAAAGAATGTTTCACCGGTAACAACGATACCGCCTTTTCTAATAGACCAATTCCATTGGCTTTCAAGACCATTTTCTATGCCTGTAGAGGTATCGACTCTTACGGTTTATCTTCTGTTCCATACGGTAAATATTGGAGAGAATTGAGAAAGGTTTGCGTCCACAACTTGTTGTCCAATCAACAATTATTGAAGTTCAGACACTTGATCATCTCCCAAGTTGATACCTCCTTCAACAAGTTATACGAATTGTGCAAGAACTCCGAAGATAATCAAGGTATGGTTAGAATGGATGATTGGTTGGCTCAATTGTCCTTCTCAGTTATTGGTAGAATCGTTTGCGGTTTCCAATCTGATCCAAAAACTGGTGCTCCATCTAGAGTCGAACAATTCAAAGAAGCTATTAACGAAGCCTCCTACTTCATGTCTACTTCTCCAGTTTCTGATAACGTTCCAATGTTGGGTTGGATCGATCAATTGACTGGTTTGACTAGAAACATGACCCATTGTGGTAAGAAGTTGGATTTGGTTGTCGAATCCATCATCAACGATCACAGACAAAAGAGAAGATTCTCCAGAACAAAAGGTGGTGACGAAAAGGATGATGAACAAGATGATTTCATCGACATCTGCTTGTCCATTATGGAACAACCACAATTGCCAGGTAACAACAATCCACCAAAAATCCCAATCAAGTCCATCGTTTTGGATATGATTGGTGCTGGTACTGATACCACTAAGTTGACTATTATTTGGACCTTGTCCTTGTTGTTGAACAACCCAAATGTTTTGGCTAAGGCCAAACAAGAAGTTGACGCTCATTTTGAAACTAAGAAGAGATCTACCAACGAAGCTTCTGTCGTTGTTGATTTCGATGATATTGGTAACTTGGTCTACATCCAAGCCATTATCAAAGAATCCATGAGATTATACCCAGTCTCCCCAGTTGTTGAAAGATTGTCATCTGAAGATTGTGTTGTTGGTGGTTTTCATGTTCCAGCTGGTACTAGATTGTGGGCTAATGTTTGGAAAATGCAAAGAGATCCAAAGGTTTGGGATGACCCTTTGGTTTTTAGACCAGAAAGATTCTTGTCCGACGAACAAAAAATGGTTGATGTTAGAGGTCAAAATTACGAATTATTGCCATTTGGTGCCGGTAGAAGAATTTGTCCAGGTGTTTCTTTCTCCTTGGATTTGATGCAATTGGTCTTGACCAGATTGATCTTGGAATTCGAAATGAAATCTCCATCCGATAAGGTTGATATGACTGCTACTCCAGGTTTGATGTCTTACAAAGTTGTTCCATTGGACATCTTGTTGACCCATAGAAGAATCAAGTCTTGCGTTCAATTGGCCTCTTCTGAAAGAGATATGGAATCTTCTGGTGTTCCAGTTATCACTTTGAGATCTGGTAAAGTTATGCCAGTTTTGGGTATGGGTACTTTTGAAAAAGCTGGTAAGGGTTCCGAAAGAGAAAGATTGGCTATTTTGAAGGCCATCGAAGTTGGTTACAGATACTTTGATACTGCTGCTGCTTACGAAACCGAAGAAGTTTTAGGTGAAGCTATTGCTGAAGCCTTGCAATTGGGTTTAATCAAGTCAAGAGATGAATTATTCATTTCCTCCATGTTGTGGTGTACTGATGCTCATCCAGATAGAGTTTTGTTGGCATTGCAAAACTCATTGAGAAACTTGAAGTTGGAATACGTCGACTTGTACATGTTGCCATTTCCAGCTTCATTGAAGCCAGGTAAGATTACCATGGATATCCCAGAAGAAGATATCTGCCCAATGGATTATAGATCTGTTTGGTCTGCTATGGAAGAATGCCAAAATTTGGGTTTGACCAAGTCCATTGGTGTCTCTAATTTCTCCTGCAAAAAGTTGGAAGAATTGATGGCTACTGCTAACATTCCACCAGCTGTAAATCAAGTTGAAATGTCTCCAGCTTTCCAACAAAAGAAGTTGAGAGAATACTGCAACGCTAACAACATTTTGGTTTCCGCCGTTTCTATTTTGGGTTCTAATGGTACTCCATGGGGTTCAAATGCTGTTTTAGGTTCTGAAGTCTTGAAAAAGATTGCTATGGCCAAGGGTAAATCCGTTGCTCAAGTTTCAATGAGATGGGTTTATGAACAAGGTGCTTCCTTGGTTGTTAAGTCCTTTAGTGAAGAAAGAT

	TAAGAGAAAACTTGAACATCTTCGACTGGCAATTGACCAAAGAAGATAACGAAAAGATCGGTGAAATCCCACAATGCAGAATTTTGTCTGCTTACTTCTTGGTTAGTCCAAAGGGTCCATTCAAGTCTCAAGAAGAATTATGGGATGATAAGGCTTAA
PbDRS-DRR 2	ATGGAATTGCAATACTTCTCCTACTTCCAACCTACCTCTTCTGTTGTTGCTTTGTTGTTGGCATTGGTCAGTATCTTGTTTTCCGTTGTTGTTTTGAGAAAGACCTTCTCCAACAACTATTCTTCTCCAGCTTCTTCTACTGAAACCGCTGTTTTGTGTCATCAAAGACAACAATCTTGCGCCTTGCCAATTTCTGGTTTGTTGCATGTTTTCATGAACAAGAACGGTTTGATCCATGTTACCTTGGGTAATATGGCTGATAAGTACGGTCCAATTTTCTCTTTTCCAACCGGTTCTCATAGAACCTTGGTTGTTTCTTCTTGGGAAATGGTCAAAGAATGTTTCACCGGTAACAACGATACCTTCTTCAGCAACAGACCCATACCATTAGCCTTTAAGATCATTTTCTACGCCGGTGGTGTAGATAGCTATGGACTTGCTTTAGTGCCATATGGCAAGTACTGGAGGGAGTTGAGAAAAATTTGTGTTCATAACTTACTTTCAAACCAGCAACTTTTGAACTTTAGGCACTTAATAATTTCTCAAGTCGATACTTCTTTCAATAAGCTGTATGATTTGTCAAACAAAAAGAAAAATACAACCACTGACTCTGGGACCGTTAGGATGGATGATTGGCTAGCTCAATTGTCCTTTAACGTCATTGGAAGGATTGTATGTGGTTTTCAAACACATACGGAAACCTCCGCCACGTCAAGTGTGGAACGTTTCACAGAAGCAATTGATGAAGCATCAAGATTCATGTCAATTGCTACGGTCTCTGATACTTTTCCATGGTTGGGTTGGATAGATCAATTAACAGGTCTTACCCGTAAGATGAAACATTATGGTAAGAAGTTAGATTTGGTTGTTGAGAGCATTATCGAAGATCACAGGCAAAATAGAAGAATTTCCGGCACCAAACAAGGAGACGATTTTATTGATATATGTCTGTCTATCATGGAGCAACCTCAAATAATTCCAGGAAATAACGATCCTCCGAGGCAAATACCAATAAAATCTATTGTTTTAGATATGATAGGTGGAGGTACCGATACTACTAAATTGACTACAACTTGGACATTAAGCTTATTACTGAACAATCCACATGTTTTAGAAAAAGCCAGAGAAGAAGTAGATGCTCATTTCGGTACAAAGAGGCGTCCAACTAACGATGACGCAGTCATGGTGGAGTTTGATGATATACGTAATCTAGTGTATATTCAAGCTATTATTAAAGAGTCTATGAGACTTTACCCAGCATCACCAGTAGTCGAGCGTTTATCTGGTGAAGACTGTGTAGTTGGCGGTTTCCATGTTCCAGCTGGTACTAGATTATGGGTTAATGTCTGGAAGATGCAGAGAGATCCGAATGTTTGGGCTGACCCGATGGTTTTTAGACCTGAAAGATTCTTGTCTGACGAGCAGAAGATGGTCGACGTTAGAGGACAAAATTATGAATTGTTGCCTTTCGGTGCAGGTAGGAGAATATGTCCTGGTGTTTCTTTCTCCTTGGATTTGATGCAATTGGTCTTGACCAGATTGATCTTGGAATTCGAAATGAAGTCTCCATCCGGTAAGGTTGATATGACTGCTACTCCAGGTTTGATGTCTTACAAAGTTGTTCCATTGGACATCTTGTTGACCCATAGAAGAATCAAGTCTTGCGTTCAATTGGCCTCTTCTGAAAGAGATATGGAATCTTCTGGTGTTCCAGTTATCACTTTGAGATCTGGTAAAGTTATGCCAGTTTTGGGTATGGGTACTTTTGAAAAAGCTGGTAAGGGTTCCGAAAGAGAAAGATTGGCTATTTTGAAGGCCATCGAAGTTGGTTACAGATACTTTGATACTGCTGCTGCTTACGAAACCGAAGAAGTTTTAGGTGAAGCTATTGCTGAAGCCTTGCAATTGGGTTTAATCAAGTCAAGAGATGAATTATTCATTTCCTCCATGTTGTGGTGTACTGATGCTCATCCAGATAGAGTTTTGTTGGCATTGCAAAACTCATTGAGAAACTTGAAGTTGGAATACGTCGACTTGTACATGTTGCCATTTCCAGCTTCATTGAAGCCAGGTAAGATTACCATGGATATCCCAGAAGAAGATATCTGCCCAATGGATTATAGATCTGTTTGGTCTGCTATGGAAGAATGCCAAAATTTGGGTTTGACCAAGTCCATTGGTGTCTCTAATTTCTCCTGCAAAAAGTTGGAAGAATTGATGGCTACTGCTAACATTCCACCAGCTGTAAATCAAGTTGAAATGTCTCCAGCTTTCCAACAAAAGAAGTTGAGAGAATACTGCAACGCTAACAACATTTTGGTTTCCGCCGTTTCTATTTTGGGTTCTAATGGTACTCCATGGGGTTCAAATGCTGTTTTAGGTTCTGAAGTCTTGAAAAAGATTGCTATGGCCAAGGGTAAATCCGTTGCTCAAGTTTCAATGAGATGGGTTTATGAACA

	AGGTGCTTCCTTGGTTGTTAAGTCCTTTAGTGAAGAAAGATTAAGAGAAAACTTGAACATCTTCGACTGGCAATTGACCAAAGAAGATAACGAAAAGATCGGTGAAATCCCACAATGCAGAATTTTGTCTGCTTACTTCTTGGTTAGTCCAAAGGGTCCATTCAAGTCTCAAGAAGAATTATGGGATGATAAGGCTTAA
PsDRS-DRR	ATGGAATTGCAATACATCTCCTACTTCCAACCTACCTCTTCTGTTGTTGCTTTGTTGTTGGCATTGGTCAGTATCTTGTCTTCCGTTGTTGTTTTGAGAAAGACCTTCCTAAACAACTATTCTTCTTCACCAGCTTCTTCTACTAAGACCGCTGTTTTGTCTCATCAAAGACAACAATCTTGCGCCTTGCCAATTTCTGGTTTGTTGCATATTTTCATGAACAAGAACGGTTTGATCCATGTTACCTTGGGTAATATGGCTGATAAGTACGGTCCAATTTTCTCTTTTCCAACCGGTTCTCATAGAACCTTGGTTGTTTCTTCTTGGGAAATGGTCAAAGAATGTTTCACCGGTAACAACGATACCGCCTTTTCTAATAGACCAATTCCATTGGCTTTCAAGACCATTTTCTATGCCTGTGGAGGTATCGACTCTTACGGTTTATCTTCTGTTCCATACGGTAAATATTGGAGAGAATTGAGAAAGGTTTGCGTCCACAACTTGTTGTCCAATCAACAATTATTGAAGTTCAGACACTTGATCATCTCCCAAGTTGATACCTCCTTCAACAAGTTATACGAATTGTGCAAGAACTCCGAAGATAATCATGGTAATTACACGACAACAACCACTACAGCTGCAGGTATGGTTAGAATCGATGATTGGTTGGCTGAATTGTCCTTCAACGTTATTGGTAGAATCGTTTGCGGTTTCCAATCTGGTCCAAAAACTGGTGCTCCATCTAGAGTCGAACAATTCAAAGAAGCTATTAACGAAGCCTCCTACTTCATGTCTACTTCTCCAGTTTCTGATAACGTTCCAATGTTGGGTTGGATCGATCAATTGACTGGTTTGACTAGAAACATGAAGCATTGTGGTAAGAAGTTGGATTTGGTTGTCGAATCCATCATCAACGATCACAGACAAAAGAGAAGATTCTCCAGAACAAAAGGTGGTGACGAAAAGGATGATGAACAAGATGATTTCATCGACATCTGCTTGTCCATTATGGAACAACCACAATTGCCAGGTAACAACAATCCATCACAAATCCCAATCAAGTCCATCGTTTTGGATATGATTGGTGGAGGTACTGATACCACTAAGTTGACTACAATTTGGACCTTGTCCTTGTTGTTGAACAACCCACATGTTTTGGATAAGGCCAAACAAGAAGTTGACGCTCATTTTAGGACTAAGAGAAGATCTACCAACGACGCTGCAGCCGCCGTTGTTGATTTCGATGATATTCGTAACTTGGTCTACATCCAAGCCATTATCAAAGAATCCATGAGATTATACCCAGCTTCCCCAGTTGTTGAAAGATTGTCAGGTGAAGATTGTGTTGTTGGTGGTTTTCATGTTCCAGCTGGTACTAGATTGTGGGCTAATGTTTGGAAAATGCAAAGAGATCCAAAGGTTTGGGATGACCCTTTGGTTTTTAGACCAGATAGATTCTTGTCCGACGAACAAAAAATGGTTGATGTTAGAGGTCAAAATTACGAATTATTGCCATTTGGTGCCGGTAGAAGAGTTTGTCCAGGTGTTTCTTTCTCCTTGGATTTGATGCAATTGGTCTTGACCAGATTGATCTTGGAATTCGAAATGAAGTCTCCATCCGGTAAGGTTGATATGACTGCTACTCCAGGTTTGATGTCTTACAAAGTTATTCCATTGGACATCTTGTTGACCCATAGAAGAATCAAGCCTTGCGTTCAATCTGCCGCTTCTGAAAGAGATATGGAATCTTCTGGTGTTCCAGTTATCACTTTGGGTTCTGGTAAAGTTATGCCAGTTTTGGGTATGGGTACTTTTGAAAAAGTCGGTAAGGGTTCCGAAAGAGAAAGATTGGCTATTTTGAAGGCCATCGAAGTTGGTTACAGATACTTTGATACTGCTGCTGCTTACGAAACCGAAGAAGTTTTAGGTGAAGCTATTGCTGAAGCCTTGCAATTGGGTTTAGTAAAGTCAAGAGATGAATTATTCATTTCCTCCATGTTGTGGTGTACTGATGCTCATGCTGATAGAGTTTTGTTGGCATTGCAAAACTCATTGAGAAACTTGAAGTTGGAATACGTCGACTTGTACATGTTGCCATTTCCAGCTTCATTGAAGCCAGGTAAGATTACCATGGATATCCCAGAAGAAGATATCTGCAGAATGGATTATAGATCTGTTTGGGCAGCTATGGAAGAATGCCAAAATTTGGGTTTCACCAAGTCCATTGGTGTCTCTAATTTCTCCTGCAAAAAGTTGCAAGAATTGATGGCTACTGCTAACATTCCACCAGCTGTAAATCAAGTTGAAATGTCTCCAGCTTTCCAACAAAAGAAGTTGAGAGAATACTGCAACGCTAACAACATTTTGGTTTCCGCCATTTCTGTTTTGGGTTCTAATGGTACTCCATGGGGTT

	CAAATGCTGTTTTAGGTTCTGAAGTCTTGAAAAAGATTGCTATGGCCAAGGGTAAATCCGTTGCTCAAGTTTCAATGAGATGGGTTTATGAACAAGGTGCTTCCTTGGTTGTTAAGTCCTTTAGTGAAGAAAGATTAAGAGAAAACTTGAACATCTTCGACTGGGAATTGACCAAAGAAGATCATGAAAAGATCGGTGAAATCCCACAATGCAGAATTTTGTCTGCTTACTTCTTGGTTAGTCCAAACGGTCCATTCAAGTCTCAAGAAGAATTATGGGATGATGAAGCTTAA
PbREPI	ATGGAACTACAATATTTCTCTTACTTCCAGCCCACTAGTAGTGTTGTTGCTCTACTACTGGCTCTTGTTTCCATTTTGTTTAGCGTAGTGGTTCTGCGTAAGACGTTCTCCAACAATTATTCAAGTCCAGCCAGTTCCACCGAGACTGCGGTATTATGCCACCAACGTCAGCAAAGCTGCGCCTTACCGATTAGTGGCTTGTTGCACGTCTTCATGAATAAAAACGGACTAATACACGTAACCTTAGGCAACATGGCGGATAAGTATGGTCCGATATTTTCATTCCCAACGGGTAGCCACAGGACACTGGTGGTTTCCTCTTGGGAAATGGTCAAAGAATGTTTTACAGGAAATAACGACACCGCTTTCAGTAATAGGCCAATCCCTCTAGCATTTCAGACGATTTTTTATGCGTGCGGCGGCATTGACTCATACGGCTTGAGCAGCGTCCCCTACGGAAAGTATTGGCGTGAACTACGTAAAGTTTGTGTGCACAATCTATTAAGCAATCAACAGCTATTGAAATTTAGGCATTTGATAATTTCACAAGTGGACACGTCTTTCAACAAATTATACGAACTGTGTAAAAACAGTGAGGACAATCAGGGGATGGTCAGAATGGATGACTGGCTAGCACAACTGTCCTTTAATGTCATTGGGAGAATCGTGTGCGGGTTTCAATCCGACCCGAAAACGGGCGCACCCAGTAGGGTCGAGCAGTTCAAGGAAGTAATAAATGAGGCCTCCTACTTTATGTCCACGTCCCCTGTGAGCGACAATGTGCCCATGCTTGGCTGGATCGACCAACTGACGGGCCTGACAAGAAATATGAAACATTGCGGAAAGAAACTGGACCTGGTAGTAGAGTCTATCATAAAGGATCACCGTCAGAAGCGTAGATTTAGCAGAACCAAAGGCGGCGACGAGAAAGACGACGAGCAGGATGATTTCATTGACATATGTTTGAGCATTATGGAACAGCCGCAGTTACCCGGGAATAATTCCCCTCCCCAAATCCCAATAAAGAGCATAGTTTTAGACATGATTGGCGGTGGAACGGATACTACTAAGCTGACCACCATATGGACACTAAGTTTGTTGCTAAATAACCCCCATGTCCTAGATAAGGCTAAACAAGAGGTGGATGCCCATTTTAGAAAAAAAAGAAGGTCCACCGACGATGCCGCCGCTGCAGTGGTTGATTTTGATGACATCCGTAACTTAGTTTACATCCAGGCGATCATCAAGGAATCAATGAGGCTGTATCCTGCTTCTCCAGTAGTTGAGAGGTTAAGCGGAGAGGACTGCGTAGTTGGTGGATTTCACGTGCCCGCAGGGACGCGTTTATGGGCCAACGTTTGGAAAATGCAGAGGGACCCGAAAGTGTGGGACGATCCATTAGTTTTTAGGCCGGAAAGATTCTTATCTGATGAGCAGAAAATGGTAGACGTGCGTGGACAGAATTACGAGCTTTTGCCCTTTGGAGCAGGCAGGAGGATTTGCCCCGGGGTGTCATTCAGCTTAGATTTGATGCAACTGGTTCTAACACGTCTAATACTTGAATTTGAAATGAAGAGTCCTTCCGGAAAGGTAGACATGACAGCGACCCCCGGTCTAATGTCCTACAAAGTCGTTCCCTTAGATATCCTGCTTACTCACCGTCGTATTAAAAGTTGTGTCCAATTAGCGTCTAGTGAAAGAGATATGGAGAGTAGTGGGGTTCCAGTGATTACTTTGTCTTCCGGTAAGGTCATGCCTGTATTAGGAATGGGAACGTTCGAAAAAGTCGGCAAGGGCAGCGAACGTGAGAGATTAGCGATTCTGAAGGCTATTGAAGTAGGATACAGATACTTTGACACTGCAGCGGCTTACGAGACGGAAGAGGTGCTGGGTGAAGCAATTGCCGAGGCACTTCAACTAGGACTGATCGAATCCAGAGATGAATTGTTTATCTCTTCTATGCTATGGTGCACGGATGCACACCCTGACCGTGTTCTTCTTGCACTTCAAAACAGCTTGAGGAACCTTAAACTGGAGTACCTAGACCTTTACATGCTGCCTTTCCCGGCTAGCTTAAAACCGGGCAAGATCACGATGGACATTCCGGAGGAGGATATCTGTAGGATGGACTATCGTTCAGTGTGGTCTGCCATGGAGGAATGTCAGAACCTAGGATTTACCAAAAGTATCGGCGTCAGTAACTTTTCCTGCAAGAAACTACAGGAGTTGATGGCGACTGCTAACATCCCCCCAGCCGTCAATCAAGTCGAAATGTCCCCAGCTTTCCAGCA

	GAAAAAATTGAGGGAATATTGTAACGCTAATAATATCCTGGTAAGTGCTGTCTCTATATTGGGGTCTAACGGCACACCGTGGGGCTCAAATGCAGTTCTTGGAAGCGAGGTTCTAAAACAGATAGCTATGGCTAAAGGCAAAAGCGTAGCACAGGTGTCAATGCGTTGGGTTTATGAACAGGGTGCCAGTCTGGTGGTGAAGTCATTCAGCGAAGAGAGACTGAGGGAGAATCTGAACATCTTTGATTGGGAACTAACAAAGGAGGACAACGAGAAGATAGGAGAAATCCCCCAGTGTAGAATCTTGACTGCGTATTTCCTGGTCTCACCTAACGGTCCGTTTAAAAGCCAGGAGGAATTATGGGATGACAAGGCT
PrDRS	ATGGAGTACAGCGATTTACAATTGTTTGGTTTCCAGCCCACAAGCGTCGTAGCATTATTGCTGGCGTTGGTCTCCATTTTGCTAGGCGTCATTGCGGTGTCACACCACAGGGCGAAGCCTTCTTGTGCTCTGCCCATGATCGGTTTATACCACGTTTTTATGAATAAGACAGGTTTAATTCATGTAACACTTGGGAACATGGCAGATAAGTACGGGCCCATCTTCAGCTTCCCAACGGGAGGCCACAGAGCCCTGGTTGTCTCCTCTTGGGAAATGGCCAAGGAATGTTTCACAGGTGACAACGATATCGTCTTCAGTAACCGTCCTATGCCGCTATCCTTCAAGATAATATTCAACGCGGGTGGTATAGATTCCGCCGGACTGACCCAAGTTCCTTATGGGAAGTATTGGCGTGAGTTGAGGAAGATTTGCGTCCACAACCTTTTGAGTAATCAGCAGTTACTTAAATTCCGTCACTTAATAAACTCTCAGGTTGACACATCCTTTACAAAACTATACGAGTCTTGTAACAAGGGGAATAGTGGCATGGTGAGGATGGACGACTGGTTAGGAGAATTGTCATTCAACGTAATAGGACGTATAGTCTGCGGCTTTAGGAGCGATACTGAAACCTCTGCGACAAGTAGTGCGGAAAGGTTCACGGTAGCAATCGATGAAGCAAGTCGTTTTATGTCCATACCAGCGGTCTCTGATACCTTCCCTTGGCTTGGTTGGATTGATCGTCTTACTGGTTTAATCAAGGACATGAAACACCACGCGGAAAAATTAGACCTAGTTGTGGAGTCCATTATAGAGGACCACAGGCAAAAGAGACGTTTCTCTCGTACGAAGAAGGGAGACGAGAATAACACAGAAGACGAGCAGGATGATTTCATAGACATATGTTTGTCCATCATGGAGCAACCAGAGTTACCGGGGAACAACTATGCACGTCAAATGCCTATTAAGAGTATCATTGTTGATATGATTGGCGGTGCCACTGACACGACAAAACTGACAACGATATGGACACTATCCTTATTGCTGAATAACCCCCACGTATTAGGAAAAGCAAAGGAGGAGGTAGATGCGCATTTTGGAAAGAAGCGTAGCAGCACGAACGGTGAAGTAATGGTTGATTTCGACGATATCAGAAGCTTAGTGTACATTCAGGCTATAATAAAGGAAAGCATGAGATTATATCCCGCTTCTCCAGTTGTGGAAAGGTTGAGCAGTGAAGACTGCGTAGTCGGCGGCTTTCACGTCAGTGCCGGAACGAGGCTATGGGTGAATGTGTGGAAGGTGCAACGTGATCCTGAAGTTTGGGATGACCCTAGTGTATTCCGTCCAGAGAGATTCCTGAGTAACGAGCAAAAGATGGTAGATGTCAGGGGGCAGGATTACGAGCTACTTCCTTTTGGAGCTGGACGTCGTATTTGTCCTGGCGTATCCTTTAGCTTGGATTTGATGCATCTAGTCTTAACCAGGTTGATCCTGGAGTTTGAAATCAAATCCCCCGGTGGAGAGGTTGACATGACTGCAACGCAGGGGCTTATGTCTTACAAGGTCGTGCCATTGGACATCCTGCTAACAAGAAGAATGTTG
PrDRR	ATGGATAGTAGCGGGGTCCCTGTAATTCCGCTAAGCAGCGGAAAGGGTATGCCGGCGCTGGCATTAGGGACGTTTGAGACCTTTGGGAAAGGTTCCTCAGAAAGGCAAAGGAGCGCATTTTTGAAGGCGATCGAGGTAGGTTATAGATACTTTGACACTGGCGCATCATATGGGACAGAGGAGGTTCTTGGTGAGGCTATAGACGAGGCACTTCAGTTAGGACTTATAGAAAGCAGAGAGGAGTTATTTATTAGCTCAAATCTATGGTGTACTGACGCCCACCCCGATAGAGTGTTACTTGCTCTACAGAACTCACTTAGGAACCTGAAGTTGGAATACCTTGATCTATACATGATTCCTTTCCCAATAAGTTTAAAACCAGGGAAGATAATGGAAGAGATAACCATGGACATACCGGAAGACGAAATGTTACCGATGGACTACAAAAGCGTCTGGGCCGCTATGGAAGAATGCCAGGATCTAGGGTTCACAAAAAGCATCGGTGTTTCTAACTTTAGTTGTAAGAAACTACAAGAGTTAATGGCAACCGCGAATATCC

	CCCCCGCCGTAAATCAGGTGGAGATGAGCCCCGTCTTTCAACAAAAGAAGTTACGTGAATACTGCAAAGCAAACAACATTTTGGTTTCTGCTGTGAGCGTTTTAGGTTCCAACGGGACAGCATGGGGAAGTAACCAAGTGATGGGATCCGAGGTCTTGAAACAAATTGCTACAGACAGAGGAAAGTCCGTAGCCCAGATAAGCATGCGTTGGGTCTATGAGCAGGGCGCTAGTCTAGTAGTTAAGAGCTTCAACGAGGTGCGTATGAGAGAAAATCTTAACATCTTCAACTGGCAATTGACCAAGGAGGATTTAGAAAAGATTTCCGAGATCCCTCAGTGTAGAATACTGACGGGTGACTTCCTTGTGAGTGCGAATGGCCCCTTCAAAAGCCTACAGGAACTGTGGGATGATCAAGTC
PbDRS V1	ATGGAATTGCAATACTTCTCCTACTTCCAACCTACCTCTTCTGTTGTTGCTTTGTTGTTGGCATTGGTCAGTATCTTGTTTTCCGTTGTTGTTTTGAGAAAGACCTTCTCCAACAACTATTCTTCTCCAGCTTCTTCTACTGAAACCGCTGTTTTGTGTCATCAAAGACAACAATCTTGCGCCTTGCCAATTTCTGGTTTGTTGCATGTTTTCATGAACAAGAACGGTTTGATCCATGTTACCTTGGGTAATATGGCTGATAAGTACGGTCCAATTTTCTCTTTTCCAACCGGTTCTCATAGAACCTTGGTTGTTTCTTCTTGGGAAATGGTCAAAGAATGTTTCACCGGTAACAACGATACCGCCTTTTCTAATAGACCAATTCCATTGGCTTTCAAGACCATTTTCTATGCCTGTAGAGGTATCGACTCTTACGGTTTATCTTCTGTTCCATACGGTAAATATTGGAGAGAATTGAGAAAGGTTTGCGTCCACAACTTGTTGTCCAATCAACAATTATTGAAGTTCAGACACTTGATCATCTCCCAAGTTGATACCTCCTTCAACAAGTTATACGAATTGTGCAAGAACTCCGAAGATAATCAAGGTATGGTTAGAATGGATGATTGGTTGGCTCAATTGTCCTTCTCAGTTATTGGTAGAATCGTTTGCGGTTTCCAATCTGATCCAAAAACTGGTGCTCCATCTAGAGTCGAACAATTCAAAGAAGCTATTAACGAAGCCTCCTACTTCATGTCTACTTCTCCAGTTTCTGATAACGTTCCAATGTTGGGTTGGATCGATCAATTGACTGGTTTGACTAGAAACATGACCCATTGTGGTAAGAAGTTGGATTTGGTTGTCGAATCCATCATCAACGATCACAGACAAAAGAGAAGATTCTCCAGAACAAAAGGTGGTGACGAAAAGGATGATGAACAAGATGATTTCATCGACATCTGCTTGTCCATTATGGAACAACCACAATTGCCAGGTAACAACAATCCACCAAAAATCCCAATCAAGTCCATCGTTTTGGATATGATTGGTGCTGGTACTGATACCACTAAGTTGACTATTATTTGGACCTTGTCCTTGTTGTTGAACAACCCAAATGTTTTGGCTAAGGCCAAACAAGAAGTTGACGCTCATTTTGAAACTAAGAAGAGATCTACCAACGAAGCTTCTGTCGTTGTTGATTTCGATGATATTGGTAACTTGGTCTACATCCAAGCCATTATCAAAGAATCCATGAGATTATACCCAGTCTCCCCAGTTGTTGAAAGATTGTCATCTGAAGATTGTGTTGTTGGTGGTTTTCATGTTCCAGCTGGTACTAGATTGTGGGCTAATGTTTGGAAAATGCAAAGAGATCCAAAGGTTTGGGATGACCCTTTGGTTTTTAGACCAGAAAGATTCTTGTCCGACGAACAAAAAATGGTTGATGTTAGAGGTCAAAATTACGAATTATTGCCATTTGGTGCCGGTAGAAGAATTTGTCCAGGTGTTTCTTTCTCCTTGGATTTGATGCAATTGGTCTTGACCAGATTGATCTTGGAATTCGAAATGAAATCTCCATCCGATAAGGTTGATATGACTGCTACTCCAGGTTTGATGTCTTACAAAGTTGTTCCATTGGACATCTTGTTGACCCATAGAAGAATC
PbDRS V2	ATGGAATTGCAATACTTCTCCTACTTCCAACCTACCTCTTCTGTTGTTGCTTTGTTGTTGGCATTGGTCAGTATCTTGTTTTCCGTTGTTGTTTTGAGAAAGACCTTCTCCAACAACTATTCTTCTCCAGCTTCTTCTACTGAAACCGCTGTTTTGTGTCATCAAAGACAACAATCTTGCGCCTTGCCAATTTCTGGTTTGTTGCATGTTTTCATGAACAAGAACGGTTTGATCCATGTTACCTTGGGTAATATGGCTGATAAGTACGGTCCAATTTTCTCTTTTCCAACCGGTTCTCATAGAACCTTGGTTGTTTCTTCTTGGGAAATGGTCAAAGAATGTTTCACCGGTAACAACGATACCGCCTTTTCTAATAGACCAATTCCATTGGCTTTCAAGACCATTTTCTATGCCTGTAGAGGTATCGACTCTTACGGTTTATCTTCTGTTCCATACGGTAAATATTGGAGAGAATTG

	AGAAAGGTTTGCGTCCACAACTTGTTGTCCAATCAACAATTATTGAAGTTCAGACACTTGATCATCTCCCAAGTTGATACCTCCTTCAACAAGTTATACGAATTGTGCAAGAACTCCGAAGATAATCAAGGTATGGTTAGAATGGATGATTGGTTGGCTCAATTGTCCTTCTCAGTTATTGGTAGAATCGTTTGCGGTTTCCAATCTGATCCAAAAACTGGTGCTCCATCTAGAGTCGAACAATTCAAAGAAGCTATTAACGAAGCCTCCTACTTCATGTCTACTTCTCCAGTTTCTGATAACGTTCCAATGTTGGGTTGGATCGATCAATTGACTGGTTTGACTAGAAACATGACCCATTGTGGTAAGAAGTTGGATTTGGTTGTCGAATCCATCATCAACGATCACAGACAAAAGAGAAGATTCTCCAGAACAAAAGGTGGTGACGAAAAGGATGATGAACAAGATGATTTCATCGACATCTGCTTGTCCATTATGGAACAACCACAATTGCCAGGTAACAACAATCCACCAAAAATCCCAATCAAGTCCATCGTTTTGGATATGATTGGTGCTGGTACTGATACCACTAAGTTGACTATTATTTGGACCTTGTCCTTGTTGTTGAACAACCCAAATGTTTTGGCTAAGGCCAAACAAGAAGTTGACGCTCATTTTGAAACTAAGAAGAGATCTACCAACGAAGCTTCTGTCGTTGTTGATTTCGATGATATTGGTAACTTGGTCTACATCCAAGCCATTATCAAAGAATCCATGAGATTATACCCAGTCTCCCCAGTTGTTGAAAGATTGTCATCTGAAGATTGTGTTGTTGGTGGTTTTCATGTTCCAGCTGGTACTAGATTGTGGGCTAATGTTTGGAAAATGCAAAGAGATCCAAAGGTTTGGGATGACCCTTTGGTTTTTAGACCAGAAAGATTCTTGTCCGACGAACAAAAAATGGTTGATGTTAGAGGTCAAAATTACGAATTATTGCCATTTGGTGCCGGTAGAAGAATTTGTCCAGGTGTTTCTTTCTCCTTGGATTTGATGCAATTGGTCTTGACCAGATTGATCTTGGAATTCGAAATGAAATCTCCATCCGATAAGGTTGATATGACTGCTACTCCAGGTTTGATGTCTTACAAA
PbDRS V3	ATGGAATTGCAATACTTCTCCTACTTCCAACCTACCTCTTCTGTTGTTGCTTTGTTGTTGGCATTGGTCAGTATCTTGTTTTCCGTTGTTGTTTTGAGAAAGACCTTCTCCAACAACTATTCTTCTCCAGCTTCTTCTACTGAAACCGCTGTTTTGTGTCATCAAAGACAACAATCTTGCGCCTTGCCAATTTCTGGTTTGTTGCATGTTTTCATGAACAAGAACGGTTTGATCCATGTTACCTTGGGTAATATGGCTGATAAGTACGGTCCAATTTTCTCTTTTCCAACCGGTTCTCATAGAACCTTGGTTGTTTCTTCTTGGGAAATGGTCAAAGAATGTTTCACCGGTAACAACGATACCGCCTTTTCTAATAGACCAATTCCATTGGCTTTCAAGACCATTTTCTATGCCTGTAGAGGTATCGACTCTTACGGTTTATCTTCTGTTCCATACGGTAAATATTGGAGAGAATTGAGAAAGGTTTGCGTCCACAACTTGTTGTCCAATCAACAATTATTGAAGTTCAGACACTTGATCATCTCCCAAGTTGATACCTCCTTCAACAAGTTATACGAATTGTGCAAGAACTCCGAAGATAATCAAGGTATGGTTAGAATGGATGATTGGTTGGCTCAATTGTCCTTCTCAGTTATTGGTAGAATCGTTTGCGGTTTCCAATCTGATCCAAAAACTGGTGCTCCATCTAGAGTCGAACAATTCAAAGAAGCTATTAACGAAGCCTCCTACTTCATGTCTACTTCTCCAGTTTCTGATAACGTTCCAATGTTGGGTTGGATCGATCAATTGACTGGTTTGACTAGAAACATGACCCATTGTGGTAAGAAGTTGGATTTGGTTGTCGAATCCATCATCAACGATCACAGACAAAAGAGAAGATTCTCCAGAACAAAAGGTGGTGACGAAAAGGATGATGAACAAGATGATTTCATCGACATCTGCTTGTCCATTATGGAACAACCACAATTGCCAGGTAACAACAATCCACCAAAAATCCCAATCAAGTCCATCGTTTTGGATATGATTGGTGCTGGTACTGATACCACTAAGTTGACTATTATTTGGACCTTGTCCTTGTTGTTGAACAACCCAAATGTTTTGGCTAAGGCCAAACAAGAAGTTGACGCTCATTTTGAAACTAAGAAGAGATCTACCAACGAAGCTTCTGTCGTTGTTGATTTCGATGATATTGGTAACTTGGTCTACATCCAAGCCATTATCAAAGAATCCATGAGATTATACCCAGTCTCCCCAGTTGTTGAAAGATTGTCATCTGAAGATTGTGTTGTTGGTGGTTTTCATGTTCCAGCTGGTACTAGATTGTGGGCTAATGTTTGGAAAATGCAAAGAGATCCAAAGGTTTGGGATGACCCTTTGGTTTTTAGACCAGAAAGATTCTTGTCCGACGAACAAAAAATGGTTGATGTTAGAGGTCAAAATTACGAATT

	ATTGCCATTTGGTGCCGGTAGAAGAATTTGTCCAGGTGTTTCTTTCTCCTTGGATTTGATGCAATTGGTCTTGACCAGATTGATCTTGGAATTCGAAATGAAgTCTCCATCCGgTAAGGTTGATATGACTGCTACTCCAGGTTTGATGTCTTACAAAGTTGTTCCATTGGACATCTTGTTGACCCATAGAAGAATCAAGTCTTGCGTTCAATTGGCCTCTTCTGAAAGAGAT
PbREPI DRS	ATGGAACTACAATATTTCTCTTACTTCCAGCCCACTAGTAGTGTTGTTGCTCTACTACTGGCTCTTGTTTCCATTTTGTTTAGCGTAGTGGTTCTGCGTAAGACGTTCTCCAACAATTATTCAAGTCCAGCCAGTTCCACCGAGACTGCGGTATTATGCCACCAACGTCAGCAAAGCTGCGCCTTACCGATTAGTGGCTTGTTGCACGTCTTCATGAATAAAAACGGACTAATACACGTAACCTTAGGCAACATGGCGGATAAGTATGGTCCGATATTTTCATTCCCAACGGGTAGCCACAGGACACTGGTGGTTTCCTCTTGGGAAATGGTCAAAGAATGTTTTACAGGAAATAACGACACCGCTTTCAGTAATAGGCCAATCCCTCTAGCATTTCAGACGATTTTTTATGCGTGCGGCGGCATTGACTCATACGGCTTGAGCAGCGTCCCCTACGGAAAGTATTGGCGTGAACTACGTAAAGTTTGTGTGCACAATCTATTAAGCAATCAACAGCTATTGAAATTTAGGCATTTGATAATTTCACAAGTGGACACGTCTTTCAACAAATTATACGAACTGTGTAAAAACAGTGAGGACAATCAGGGGATGGTCAGAATGGATGACTGGCTAGCACAACTGTCCTTTAATGTCATTGGGAGAATCGTGTGCGGGTTTCAATCCGACCCGAAAACGGGCGCACCCAGTAGGGTCGAGCAGTTCAAGGAAGTAATAAATGAGGCCTCCTACTTTATGTCCACGTCCCCTGTGAGCGACAATGTGCCCATGCTTGGCTGGATCGACCAACTGACGGGCCTGACAAGAAATATGAAACATTGCGGAAAGAAACTGGACCTGGTAGTAGAGTCTATCATAAAGGATCACCGTCAGAAGCGTAGATTTAGCAGAACCAAAGGCGGCGACGAGAAAGACGACGAGCAGGATGATTTCATTGACATATGTTTGAGCATTATGGAACAGCCGCAGTTACCCGGGAATAATTCCCCTCCCCAAATCCCAATAAAGAGCATAGTTTTAGACATGATTGGCGGTGGAACGGATACTACTAAGCTGACCACCATATGGACACTAAGTTTGTTGCTAAATAACCCCCATGTCCTAGATAAGGCTAAACAAGAGGTGGATGCCCATTTTAGAAAAAAAAGAAGGTCCACCGACGATGCCGCCGCTGCAGTGGTTGATTTTGATGACATCCGTAACTTAGTTTACATCCAGGCGATCATCAAGGAATCAATGAGGCTGTATCCTGCTTCTCCAGTAGTTGAGAGGTTAAGCGGAGAGGACTGCGTAGTTGGTGGATTTCACGTGCCCGCAGGGACGCGTTTATGGGCCAACGTTTGGAAAATGCAGAGGGACCCGAAAGTGTGGGACGATCCATTAGTTTTTAGGCCGGAAAGATTCTTATCTGATGAGCAGAAAATGGTAGACGTGCGTGGACAGAATTACGAGCTTTTGCCCTTTGGAGCAGGCAGGAGGATTTGCCCCGGGGTGTCATTCAGCTTAGATTTGATGCAACTGGTTCTAACACGTCTAATACTTGAATTTGAAATGAAGAGTCCTTCCGGAAAGGTAGACATGACAGCGACCCCCGGTCTAATGTCCTACAAAGTCGTTCCCTTAGAT
PbDRR V1	TGTCTTACAAAGTTGTTCCATTGGACATCTTGTTGACCCATAGAAGAATCAAGTCTTGCGTTCAATTGGCCTCTTCTGAAAGAGATATGGAATCTTCTGGTGTTCCAGTTATCACTTTGAGATCTGGTAAAGTTATGCCAGTTTTGGGTATGGGTACTTTTGAAAAAGCTGGTAAGGGTTCCGAAAGAGAAAGATTGGCTATTTTGAAGGCCATCGAAGTTGGTTACAGATACTTTGATACTGCTGCTGCTTACGAAACCGAAGAAGTTTTAGGTGAAGCTATTGCTGAAGCCTTGCAATTGGGTTTAATCAAGTCAAGAGATGAATTATTCATTTCCTCCATGTTGTGGTGTACTGATGCTCATCCAGATAGAGTTTTGTTGGCATTGCAAAACTCATTGAGAAACTTGAAGTTGGAATACGTCGACTTGTACATGTTGCCATTTCCAGCTTCATTGAAGCCAGGTAAGATTACCATGGATATCCCAGAAGAAGATATCTGCCCAATGGATTATAGATCTGTTTGGTCTGCTATGGAAGAATGCCAAAATTTGGGTTTGACCAAGTCCATTGGTGTCTCTAATTTCTCCTGCAAAAAGTTGGAAGAATTGATGGCTACTGCTAACATTCCACCAGCTGTAAATCAAGTTGAAATGTCTCCAGCTTTCCAACAAAAGAAGTTGAGAGAATACTGCAACGCTAACAACATTTT

	GGTTTCCGCCGTTTCTATTTTGGGTTCTAATGGTACTCCATGGGGTTCAAATGCTGTTTTAGGTTCTGAAGTCTTGAAAAAGATTGCTATGGCCAAGGGTAAATCCGTTGCTCAAGTTTCAATGAGATGGGTTTATGAACAAGGTGCTTCCTTGGTTGTTAAGTCCTTTAGTGAAGAAAGATTAAGAGAAAACTTGAACATCTTCGACTGGCAATTGACCAAAGAAGATAACGAAAAGATCGGTGAAATCCCACAATGCAGAATTTTGTCTGCTTACTTCTTGGTTAGTCCAAAGGGTCCATTCAAGTCTCAAGAAGAATTATGGGATGATAAGGCTTAA
PbDRR V2	ATGGAATCTTCTGGTGTTCCAGTTATCACTTTGAGATCTGGTAAAGTTATGCCAGTTTTGGGTATGGGTACTTTTGAAAAAGCTGGTAAGGGTTCCGAAAGAGAAAGATTGGCTATTTTGAAGGCCATCGAAGTTGGTTACAGATACTTTGATACTGCTGCTGCTTACGAAACCGAAGAAGTTTTAGGTGAAGCTATTGCTGAAGCCTTGCAATTGGGTTTAATCAAGTCAAGAGATGAATTATTCATTTCCTCCATGTTGTGGTGTACTGATGCTCATCCAGATAGAGTTTTGTTGGCATTGCAAAACTCATTGAGAAACTTGAAGTTGGAATACGTCGACTTGTACATGTTGCCATTTCCAGCTTCATTGAAGCCAGGTAAGATTACCATGGATATCCCAGAAGAAGATATCTGCCCAATGGATTATAGATCTGTTTGGTCTGCTATGGAAGAATGCCAAAATTTGGGTTTGACCAAGTCCATTGGTGTCTCTAATTTCTCCTGCAAAAAGTTGGAAGAATTGATGGCTACTGCTAACATTCCACCAGCTGTAAATCAAGTTGAAATGTCTCCAGCTTTCCAACAAAAGAAGTTGAGAGAATACTGCAACGCTAACAACATTTTGGTTTCCGCCGTTTCTATTTTGGGTTCTAATGGTACTCCATGGGGTTCAAATGCTGTTTTAGGTTCTGAAGTCTTGAAAAAGATTGCTATGGCCAAGGGTAAATCCGTTGCTCAAGTTTCAATGAGATGGGTTTATGAACAAGGTGCTTCCTTGGTTGTTAAGTCCTTTAGTGAAGAAAGATTAAGAGAAAACTTGAACATCTTCGACTGGCAATTGACCAAAGAAGATAACGAAAAGATCGGTGAAATCCCACAATGCAGAATTTTGTCTGCTTACTTCTTGGTTAGTCCAAAGGGTCCATTCAAGTCTCAAGAAGAATTATGGGATGATAAGGCTTAA
PbDRR V3	ATGGGTACTTTTGAAAAAGCTGGTAAGGGTTCCGAAAGAGAAAGATTGGCTATTTTGAAGGCCATCGAAGTTGGTTACAGATACTTTGATACTGCTGCTGCTTACGAAACCGAAGAAGTTTTAGGTGAAGCTATTGCTGAAGCCTTGCAATTGGGTTTAATCAAGTCAAGAGATGAATTATTCATTTCCTCCATGTTGTGGTGTACTGATGCTCATCCAGATAGAGTTTTGTTGGCATTGCAAAACTCATTGAGAAACTTGAAGTTGGAATACGTCGACTTGTACATGTTGCCATTTCCAGCTTCATTGAAGCCAGGTAAGATTACCATGGATATCCCAGAAGAAGATATCTGCCCAATGGATTATAGATCTGTTTGGTCTGCTATGGAAGAATGCCAAAATTTGGGTTTGACCAAGTCCATTGGTGTCTCTAATTTCTCCTGCAAAAAGTTGGAAGAATTGATGGCTACTGCTAACATTCCACCAGCTGTAAATCAAGTTGAAATGTCTCCAGCTTTCCAACAAAAGAAGTTGAGAGAATACTGCAACGCTAACAACATTTTGGTTTCCGCCGTTTCTATTTTGGGTTCTAATGGTACTCCATGGGGTTCAAATGCTGTTTTAGGTTCTGAAGTCTTGAAAAAGATTGCTATGGCCAAGGGTAAATCCGTTGCTCAAGTTTCAATGAGATGGGTTTATGAACAAGGTGCTTCCTTGGTTGTTAAGTCCTTTAGTGAAGAAAGATTAAGAGAAAACTTGAACATCTTCGACTGGCAATTGACCAAAGAAGATAACGAAAAGATCGGTGAAATCCCACAATGCAGAATTTTGTCTGCTTACTTCTTGGTTAGTCCAAAGGGTCCATTCAAGTCTCAAGAAGAATTATGGGATGATAAGGCTTAA
PrDRS-PbDRR V2 chimera 1	ATGGAGTACAGCGATTTACAATTGTTTGGTTTCCAGCCCACAAGCGTCGTAGCATTATTGCTGGCGTTGGTCTCCATTTTGCTAGGCGTCATTGCGGTGTCACACCACAGGGCGAAGCCTTCTTGTGCTCTGCCCATGATCGGTTTATACCACGTTTTTATGAATAAGACAGGTTTAATTCATGTAACACTTGGGAACATGGCAGATAAGTACGGGCCCATCTTCAGCTTCCCAACGGGAGGCCACAGAGCCCTGGTTGTCTCCTCTTGGGAAATGGCCAAGGAATGTTTCACAGGTGACAACGATATCGTCTTCAGTAACCGTCCT

	ATGCCGCTATCCTTCAAGATAATATTCAACGCGGGTGGTATAGATTCCGCCGGACTGACCCAAGTTCCTTATGGGAAGTATTGGCGTGAGTTGAGGAAGATTTGCGTCCACAACCTTTTGAGTAATCAGCAGTTACTTAAATTCCGTCACTTAATAAACTCTCAGGTTGACACATCCTTTACAAAACTATACGAGTCTTGTAACAAGGGGAATAGTGGCATGGTGAGGATGGACGACTGGTTAGGAGAATTGTCATTCAACGTAATAGGACGTATAGTCTGCGGCTTTAGGAGCGATACTGAAACCTCTGCGACAAGTAGTGCGGAAAGGTTCACGGTAGCAATCGATGAAGCAAGTCGTTTTATGTCCATACCAGCGGTCTCTGATACCTTCCCTTGGCTTGGTTGGATTGATCGTCTTACTGGTTTAATCAAGGACATGAAACACCACGCGGAAAAATTAGACCTAGTTGTGGAGTCCATTATAGAGGACCACAGGCAAAAGAGACGTTTCTCTCGTACGAAGAAGGGAGACGAGAATAACACAGAAGACGAGCAGGATGATTTCATAGACATATGTTTGTCCATCATGGAGCAACCAGAGTTACCGGGGAACAACTATGCACGTCAAATGCCTATTAAGAGTATCATTGTTGATATGATTGGCGGTGCCACTGACACGACAAAACTGACAACGATATGGACACTATCCTTATTGCTGAATAACCCCCACGTATTAGGAAAAGCAAAGGAGGAGGTAGATGCGCATTTTGGAAAGAAGCGTAGCAGCACGAACGGTGAAGTAATGGTTGATTTCGACGATATCAGAAGCTTAGTGTACATTCAGGCTATAATAAAGGAAAGCATGAGATTATATCCCGCTTCTCCAGTTGTGGAAAGGTTGAGCAGTGAAGACTGCGTAGTCGGCGGCTTTCACGTCAGTGCCGGAACGAGGCTATGGGTGAATGTGTGGAAGGTGCAACGTGATCCTGAAGTTTGGGATGACCCTAGTGTATTCCGTCCAGAGAGATTCCTGAGTAACGAGCAAAAGATGGTAGATGTCAGGGGGCAGGATTACGAGCTACTTCCTTTTGGAGCTGGACGTCGTATTTGTCCTGGCGTATCCTTTAGCTTGGATTTGATGCATCTAGTCTTAACCAGGTTGATCCTGGAGTTTGAAATCAAATCCCCCGGTGGAGAGGTTGACATGACTGCAACGCAGGGGCTTATGTCTTACAAGGTCGTGCCATTGGACATCCTGCTAACAAGAAGAATGTTGAAGTCTTGCGTTCAATTGGCCTCTTCTGAAAGAGATATGGAATCTTCTGGTGTTCCAGTTATCACTTTGAGATCTGGTAAAGTTATGCCAGTTTTGGGTATGGGTACTTTTGAAAAAGCTGGTAAGGGTTCCGAAAGAGAAAGATTGGCTATTTTGAAGGCCATCGAAGTTGGTTACAGATACTTTGATACTGCTGCTGCTTACGAAACCGAAGAAGTTTTAGGTGAAGCTATTGCTGAAGCCTTGCAATTGGGTTTAATCAAGTCAAGAGATGAATTATTCATTTCCTCCATGTTGTGGTGTACTGATGCTCATCCAGATAGAGTTTTGTTGGCATTGCAAAACTCATTGAGAAACTTGAAGTTGGAATACGTCGACTTGTACATGTTGCCATTTCCAGCTTCATTGAAGCCAGGTAAGATTACCATGGATATCCCAGAAGAAGATATCTGCCCAATGGATTATAGATCTGTTTGGTCTGCTATGGAAGAATGCCAAAATTTGGGTTTGACCAAGTCCATTGGTGTCTCTAATTTCTCCTGCAAAAAGTTGGAAGAATTGATGGCTACTGCTAACATTCCACCAGCTGTAAATCAAGTTGAAATGTCTCCAGCTTTCCAACAAAAGAAGTTGAGAGAATACTGCAACGCTAACAACATTTTGGTTTCCGCCGTTTCTATTTTGGGTTCTAATGGTACTCCATGGGGTTCAAATGCTGTTTTAGGTTCTGAAGTCTTGAAAAAGATTGCTATGGCCAAGGGTAAATCCGTTGCTCAAGTTTCAATGAGATGGGTTTATGAACAAGGTGCTTCCTTGGTTGTTAAGTCCTTTAGTGAAGAAAGATTAAGAGAAAACTTGAACATCTTCGACTGGCAATTGACCAAAGAAGATAACGAAAAGATCGGTGAAATCCCACAATGCAGAATTTTGTCTGCTTACTTCTTGGTTAGTCCAAAGGGTCCATTCAAGTCTCAAGAAGAATTATGGGATGATAAGGCTTAA
PrDRS-PbDRR V2 chimera 2	ATGGAGTACAGCGATTTACAATTGTTTGGTTTCCAGCCCACAAGCGTCGTAGCATTATTGCTGGCGTTGGTCTCCATTTTGCTAGGCGTCATTGCGGTGTCACACCACAGGGCGAAGCCTTCTTGTGCTCTGCCCATGATCGGTTTATACCACGTTTTTATGAATAAGACAGGTTTAATTCATGTAACACTTGGGAACATGGCAGATAAGTACGGGCCCATCTTCAGCTTCCCAACGGGAGGCCACAGAGCCCTGGTTGTCTCCTCTTGGGAAATGGCCAAGGAATGTTTCACAGGTGACAACGATATCGTCTTCAGTAACCGTCCT

	ATGCCGCTATCCTTCAAGATAATATTCAACGCGGGTGGTATAGATTCCGCCGGACTGACCCAAGTTCCTTATGGGAAGTATTGGCGTGAGTTGAGGAAGATTTGCGTCCACAACCTTTTGAGTAATCAGCAGTTACTTAAATTCCGTCACTTAATAAACTCTCAGGTTGACACATCCTTTACAAAACTATACGAGTCTTGTAACAAGGGGAATAGTGGCATGGTGAGGATGGACGACTGGTTAGGAGAATTGTCATTCAACGTAATAGGACGTATAGTCTGCGGCTTTAGGAGCGATACTGAAACCTCTGCGACAAGTAGTGCGGAAAGGTTCACGGTAGCAATCGATGAAGCAAGTCGTTTTATGTCCATACCAGCGGTCTCTGATACCTTCCCTTGGCTTGGTTGGATTGATCGTCTTACTGGTTTAATCAAGGACATGAAACACCACGCGGAAAAATTAGACCTAGTTGTGGAGTCCATTATAGAGGACCACAGGCAAAAGAGACGTTTCTCTCGTACGAAGAAGGGAGACGAGAATAACACAGAAGACGAGCAGGATGATTTCATAGACATATGTTTGTCCATCATGGAGCAACCAGAGTTACCGGGGAACAACTATGCACGTCAAATGCCTATTAAGAGTATCATTGTTGATATGATTGGCGGTGCCACTGACACGACAAAACTGACAACGATATGGACACTATCCTTATTGCTGAATAACCCCCACGTATTAGGAAAAGCAAAGGAGGAGGTAGATGCGCATTTTGGAAAGAAGCGTAGCAGCACGAACGGTGAAGTAATGGTTGATTTCGACGATATCAGAAGCTTAGTGTACATTCAGGCTATAATAAAGGAAAGCATGAGATTATATCCCGCTTCTCCAGTTGTGGAAAGGTTGAGCAGTGAAGACTGCGTAGTCGGCGGCTTTCACGTCAGTGCCGGAACGAGGCTATGGGTGAATGTGTGGAAGGTGCAACGTGATCCTGAAGTTTGGGATGACCCTAGTGTATTCCGTCCAGAGAGATTCCTGAGTAACGAGCAAAAGATGGTAGATGTCAGGGGGCAGGATTACGAGCTACTTCCTTTTGGAGCTGGACGTCGTATTTGTCCTGGCGTATCCTTTAGCTTGGATTTGATGCATCTAGTCTTAACCAGGTTGATCCTGGAGTTTGAAATCAAATCCCCCGGTGGAGAGGTTGACATGACTGCAACGCAGGGGCTTATGTCTTACAAGGTCGTGCCATTGGACATCCTGCTAACAAGAAGAATGTTGATGGAATCTTCTGGTGTTCCAGTTATCACTTTGAGATCTGGTAAAGTTATGCCAGTTTTGGGTATGGGTACTTTTGAAAAAGCTGGTAAGGGTTCCGAAAGAGAAAGATTGGCTATTTTGAAGGCCATCGAAGTTGGTTACAGATACTTTGATACTGCTGCTGCTTACGAAACCGAAGAAGTTTTAGGTGAAGCTATTGCTGAAGCCTTGCAATTGGGTTTAATCAAGTCAAGAGATGAATTATTCATTTCCTCCATGTTGTGGTGTACTGATGCTCATCCAGATAGAGTTTTGTTGGCATTGCAAAACTCATTGAGAAACTTGAAGTTGGAATACGTCGACTTGTACATGTTGCCATTTCCAGCTTCATTGAAGCCAGGTAAGATTACCATGGATATCCCAGAAGAAGATATCTGCCCAATGGATTATAGATCTGTTTGGTCTGCTATGGAAGAATGCCAAAATTTGGGTTTGACCAAGTCCATTGGTGTCTCTAATTTCTCCTGCAAAAAGTTGGAAGAATTGATGGCTACTGCTAACATTCCACCAGCTGTAAATCAAGTTGAAATGTCTCCAGCTTTCCAACAAAAGAAGTTGAGAGAATACTGCAACGCTAACAACATTTTGGTTTCCGCCGTTTCTATTTTGGGTTCTAATGGTACTCCATGGGGTTCAAATGCTGTTTTAGGTTCTGAAGTCTTGAAAAAGATTGCTATGGCCAAGGGTAAATCCGTTGCTCAAGTTTCAATGAGATGGGTTTATGAACAAGGTGCTTCCTTGGTTGTTAAGTCCTTTAGTGAAGAAAGATTAAGAGAAAACTTGAACATCTTCGACTGGCAATTGACCAAAGAAGATAACGAAAAGATCGGTGAAATCCCACAATGCAGAATTTTGTCTGCTTACTTCTTGGTTAGTCCAAAGGGTCCATTCAAGTCTCAAGAAGAATTATGGGATGATAAGGCTTAA
PrDRS-PbDRR V2 chimera 3	ATGGAGTACAGCGATTTACAATTGTTTGGTTTCCAGCCCACAAGCGTCGTAGCATTATTGCTGGCGTTGGTCTCCATTTTGCTAGGCGTCATTGCGGTGTCACACCACAGGGCGAAGCCTTCTTGTGCTCTGCCCATGATCGGTTTATACCACGTTTTTATGAATAAGACAGGTTTAATTCATGTAACACTTGGGAACATGGCAGATAAGTACGGGCCCATCTTCAGCTTCCCAACGGGAGGCCACAGAGCCCTGGTTGTCTCCTCTTGGGAAATGGCCAAGGAATGTTTCACAGGTGACAACGATATCGTCTTCAGTAACCGTCCTATGCCGCTATCCTTCAAGATAATATTCAACGCGGGTGGTATAGATTC

	CGCCGGACTGACCCAAGTTCCTTATGGGAAGTATTGGCGTGAGTTGAGGAAGATTTGCGTCCACAACCTTTTGAGTAATCAGCAGTTACTTAAATTCCGTCACTTAATAAACTCTCAGGTTGACACATCCTTTACAAAACTATACGAGTCTTGTAACAAGGGGAATAGTGGCATGGTGAGGATGGACGACTGGTTAGGAGAATTGTCATTCAACGTAATAGGACGTATAGTCTGCGGCTTTAGGAGCGATACTGAAACCTCTGCGACAAGTAGTGCGGAAAGGTTCACGGTAGCAATCGATGAAGCAAGTCGTTTTATGTCCATACCAGCGGTCTCTGATACCTTCCCTTGGCTTGGTTGGATTGATCGTCTTACTGGTTTAATCAAGGACATGAAACACCACGCGGAAAAATTAGACCTAGTTGTGGAGTCCATTATAGAGGACCACAGGCAAAAGAGACGTTTCTCTCGTACGAAGAAGGGAGACGAGAATAACACAGAAGACGAGCAGGATGATTTCATAGACATATGTTTGTCCATCATGGAGCAACCAGAGTTACCGGGGAACAACTATGCACGTCAAATGCCTATTAAGAGTATCATTGTTGATATGATTGGCGGTGCCACTGACACGACAAAACTGACAACGATATGGACACTATCCTTATTGCTGAATAACCCCCACGTATTAGGAAAAGCAAAGGAGGAGGTAGATGCGCATTTTGGAAAGAAGCGTAGCAGCACGAACGGTGAAGTAATGGTTGATTTCGACGATATCAGAAGCTTAGTGTACATTCAGGCTATAATAAAGGAAAGCATGAGATTATATCCCGCTTCTCCAGTTGTGGAAAGGTTGAGCAGTGAAGACTGCGTAGTCGGCGGCTTTCACGTCAGTGCCGGAACGAGGCTATGGGTGAATGTGTGGAAGGTGCAACGTGATCCTGAAGTTTGGGATGACCCTAGTGTATTCCGTCCAGAGAGATTCCTGAGTAACGAGCAAAAGATGGTAGATGTCAGGGGGCAGGATTACGAGCTACTTCCTTTTGGAGCTGGACGTCGTATTTGTCCTGGCGTATCCTTTAGCTTGGATTTGATGCATCTAGTCTTAACCAGGTTGATCCTGGAGTTTGAAATCAAATCCCCCGGTGGAGAGGTTGACATGACTGCAACGCAGGGGCTTATGTCTTACAAGGTCGTGCCATTGGACATCCTGCTAACAAGAAGAATGTTGTCTTACAAAGTTGTTCCATTGGACATCTTGTTGACCCATAGAAGAATCAAGTCTTGCGTTCAATTGGCCTCTTCTGAAAGAGATATGGAATCTTCTGGTGTTCCAGTTATCACTTTGAGATCTGGTAAAGTTATGCCAGTTTTGGGTATGGGTACTTTTGAAAAAGCTGGTAAGGGTTCCGAAAGAGAAAGATTGGCTATTTTGAAGGCCATCGAAGTTGGTTACAGATACTTTGATACTGCTGCTGCTTACGAAACCGAAGAAGTTTTAGGTGAAGCTATTGCTGAAGCCTTGCAATTGGGTTTAATCAAGTCAAGAGATGAATTATTCATTTCCTCCATGTTGTGGTGTACTGATGCTCATCCAGATAGAGTTTTGTTGGCATTGCAAAACTCATTGAGAAACTTGAAGTTGGAATACGTCGACTTGTACATGTTGCCATTTCCAGCTTCATTGAAGCCAGGTAAGATTACCATGGATATCCCAGAAGAAGATATCTGCCCAATGGATTATAGATCTGTTTGGTCTGCTATGGAAGAATGCCAAAATTTGGGTTTGACCAAGTCCATTGGTGTCTCTAATTTCTCCTGCAAAAAGTTGGAAGAATTGATGGCTACTGCTAACATTCCACCAGCTGTAAATCAAGTTGAAATGTCTCCAGCTTTCCAACAAAAGAAGTTGAGAGAATACTGCAACGCTAACAACATTTTGGTTTCCGCCGTTTCTATTTTGGGTTCTAATGGTACTCCATGGGGTTCAAATGCTGTTTTAGGTTCTGAAGTCTTGAAAAAGATTGCTATGGCCAAGGGTAAATCCGTTGCTCAAGTTTCAATGAGATGGGTTTATGAACAAGGTGCTTCCTTGGTTGTTAAGTCCTTTAGTGAAGAAAGATTAAGAGAAAACTTGAACATCTTCGACTGGCAATTGACCAAAGAAGATAACGAAAAGATCGGTGAAATCCCACAATGCAGAATTTTGTCTGCTTACTTCTTGGTTAGTCCAAAGGGTCCATTCAAGTCTCAAGAAGAATTATGGGATGATAAGGCTTAA
BsCYP80A1	ATGGACTATATTGTTGGTTTCGTAAGTATTTCTTTAGTTGCTCTGCTTTACTTCCTTTTGTTCAAACCTAAGCATACTAATCTACCTCCTTCTCCCCCAGCATGGCCGATAGTAGGTCATCTGCCAGACTTGATCTCTAAAAACAGCCCACCATTCCTAGATTATATGTCTAACATCGCTCAGAAATATGGTCCGTTGATTCATTTGAAGTTCGGTCTGCACTCTAGTATTTTTGCCTCTACTAAGGAAGCAGCTATGGAGGTTCTGCAAACTAATGACAAAGTGTTATCTGGTAGACAACCATTGCCTTGTTTTAGAATTAAGCCACATATC

	GATTATAGTATCTTGTGGTCTGACTCAAACTCTTATTGGAAAAAAGGTAGGAAAATCTTGCATACGGAAATTTTCTCCCAGAAGATGTTGCAAGCTCAAGAAAAGAATAGAGAAAGAGTAGCTGGTAATTTGGTTAACTTCATTATGACTAAAGTTGGTGATGTTGTCGAGTTGCGTAGTTGGTTGTTTGGCTGTGCTTTGAATGTCTTGGGTCATGTTGTTTTTTCTAAGGATGTATTTGAATACTCCGATCAATCTGATGAGGTTGGAATGGACAAATTGATACACGGTATGTTGATGACCGGAGGTGATTTTGATGTAGCTAGTTATTTCCCTGTCCTAGCCAGATTCGATCTGCATGGGCTGAAGAGAAAAATGGATGAACAGTTTAAGTTGTTGATAAAGATTTGGGAAGGCGAAGTATTGGCACGTAGAGCGAATCGTAACCCTGAGCCAAAAGATATGTTGGATGTCCTAATTGCGAACGACTTTAACGAACACCAGATTAACGCTATGTTTATGGAAACTTTTGGTCCAGGGTCTGATACGAATAGCAACATTATAGAATGGGCTCTTGCTCAGTTGATTAAGAACCCAGACAAACTTGCTAAGTTGAGGGAAGAATTAGATAGAGTTGTCGGACGTTCTAGCACCGTCAAGGAATCCCATTTTAGCGAACTGCCGTATTTGCAGGCTTGTGTTAAAGAGACTATGAGATTGTATCCACCCATTTCTATTATGATTCCACATAGATGTATGGAGACTTGCCAAGTTATGGGTTATACAATACCGAAAGGGATGGATGTGCACGTTAATGCGCACGCTATAGGCAGAGATCCCAAGGATTGGAAGGACCCACTGAAGTTTCAACCAGAACGTTTTTTGGATTCTGACATTGAGTATAATGGTAAGCAATTTCAGTTTATTCCCTTTGGAAGCGGTAGGAGAATTTGCCCAGGTAGACCACTTGCTGTTAGAATAATTCCATTGGTATTAGCCTCTTTGGTTCACGCCTTCGGTTGGGAATTGCCCGATGGAGTTCCAAATGAGAAACTAGACATGGAGGAATTGTTCACCCTTTCTTTGTGTATGGCTAAACCGTTGAGAGTTATCCCCAAAGTGAGGATT
NnCYP80A1	ATGGCTTTGTTGGCCCTATTTATCCTATTCCTTTTAAGCATCCTGTCACTTGTCCTATTCTTGAAACCGAGTAGTAAAAAGTTGCCCCCAGGACCTTTCTCTTGGCCAATTATCGGCACACAACTGCCCAGCCCGACTATGAAACCTAATCTTGAACTATTCAAACTGGCACAAAGATACGGCCCTCTAATGTTGTTTCGTTTCGGTTTCGAAAACGTGGTTGTAGCTTCCAATCACGTAGCCGCAATGGAAGTCCTGAAGAACCAGGACCGTGTGCTTAGCGGCAGATTCAAAGCCAATTCAGTCAGAGTAAAAGGGTACATAGAATATTCAATGGTATGGGCGGATTGCACAGATTATTGGAAGATGGTCCGTAAAATTCTGAGGACCGAGCTATTTTCAACAAAAATGTTGGACGTCCATGCACACGTAAGGGAGGAAAAAGTTTCCGAATTGATGAAATTCTTAAGGAGAAAGGAAGGGGAGGAGGTAAATTTCGTAGATGTTATATTTGGCTGCATCCTGAATATGCTAGGCGCTTTGATCTACTCTAAAGATGTCTATGATTTTGAGGATAAAACCGACATAAACTTGGGTATGAAGGGGATGATAAGGCAGCTTATGATACTTGCTGCGACACCCAATATCGCTGACCTATACCCTATCTTCTTTGACGGTTCAGACTTTCAAGGCTTGAGAAAGGAATCTGCTGCTTGCGTTAAGAGAATGAGTGAGAGCTGGGCGGCCATAATAAACGAGAGAAGGAAAAATAACGACCATACGAAGAATGATTTATTGCAGGTCTTACTGGACAGCGGTTTCTCTGATCCACAAATTGACGCTATATTTCTAGAAACCTTCGGTCCCGGGTCTGATACTTCAGCATCTACGATTGAATGGGCTCTAGCAGAGCTTTTACGTAACCCAGAAAAACTTGTGAAATTGCATGAGGAGTTGGATAGGGTAATCGGACGTAACAACACCGTCAAGGATAGCGACTTACCCAACTTGCCTTACCTTCATGCCTGCGTCAAGGAAACATTGAGACTGCACCCTCCAGTTCCTTTCCTTATTCCGCACATAGCGCTTGAAAGCTGTGAAGTAATGAATTATACTATACCCAAAGGGAGTGAGGTACTAGTCAACCTATATGCAATCGGGCGTGACCCAACTACGTGGGATAACCCAAACAGCTTTCTTCCTGAGAGGTTCCTTAATAGCGAGGTAGATTACCAAGGCAACCATTTCCAATATATACCATTTGGAGCCGGCAGAAGGATGTGCCCCGGAATGAGCTTAGGGACTCGTGTTGTAAGGTTGATTTTAGCTGCCTTAGTTCATACGTTCGACTGGTCCTTACCAGGAGGGATGCACCAGGATGAGTTGGACATGGCTGACCGTTTCGGAGTAGGGTTCCAGAAAGAAACGCCTCTGGTCGTTATCCCGACTCTTAGGAAGtga

VvCYP80A1	ATGGCAACATACACGATTACGGCCGATATAAGTTTATTCTCTTTTTTGTACCCGCTTCTTTTATTGCCCTTTCTATTAATATTTAAGCACATATTCCTAAAGAGTCCACCTTTGCCCCCGGGTCCGTACCCATGGCCTATTATAGGCAACCTGCTGCAAATGGGTGGCAACTTACATGTCAAGCTTGCGAATTTGGCTAAGAGACATGGGCCCCTAATGAGCCTTAGACTAGGAACTCAAATAATGGTAGTTGCGAGTAGTTCCGCCGCTGCTATGGAGGTTTTGAAAACTCATGACCGTACCCTGTCAGGCAGATATAGGTTGGAAGAGTCTGAGTCTTATTTGCCAGATGGCGCAGTATTTAGACAGTCAAACGGCGTGTCATGCGGAGTTGAAGGAGAAGAAGGAGATGGTATTGGAGGTGTCTTTGGGAAGAAGGGTAGAGATGTTAGAGGAGTGTTATTAAAAGATCTGCTTAACGAGAATGCAGAACTAGGTGCTACCGACATCCTAGATTTCTACCCTATTTTGGGGGGCTTAGACATACAAGGGATTCGTAAAAAATTGAAAGAAATATTTAGGCGTATCCCAACGACTTGGGAAGATATATTAAAAGAACGTAGAAAGCAAAGGATACATGGAAGCTCACATGGCGATTTCCTGGATGCCCTGCTTGAGACGGGTTTTGAAGACGATCAGATCAACCATGTTATCATGGAGCTGTTTTTTGCCGGCCCTGAAACGTCCTCCCTGACCGTGGAATGGGCAATGGCCGAGCTAATTAAGAACCAGGATGCTATGCACAAGCTGTGTAATGAATTGACTCAGATCATCGGTGAAAGCCCGAGGTCCAGGGATTTAGAAGATCCTTTATCATTTAAGCCCGAAAGATTCTTAGATTCAAAGTTAGAGTTTAAGGGAAACGATTTCGAGTACATACCTTTCGGAGCTGGAAGACGTATGTGCCCCGGTATGCCGCTGGCAGCAAGACTGGTCCCTATGATCTTAGCCACGTTTGTGCGTCTTTTTGATTGGTCAACGCCGGGTGATATGGACTTCGCAGAGATAGACATGGAAGAACGTTTTGTTATTACTTTGAGGAAGGAACAACCCTTAAGATTAGACTATTGGGGATTAGTTGAAAATGGAATCCCTGCTGCGGCTGAAGGAGTCGTACTTATCGATGCGCAACGTAAAAACATCGACGATCAGAAGCTAAAAGATCTAAAAACGAAAAACTACTTATTCCAGGCACTGAACAGGTCCATCTTGGAGACTGTACTAAAAAAAGACACGACAAAGAATATTTGGGACTCTCTGAAG
Bs-MaCYP80A1	ATGGACTATATTGTTGGTTTCGTAAGTATTTCTTTAGTTGCTCTGCTTTACTTCCTTTTGTTCAAACCTAAGCATACTAATCTACCTCCTTCTCCCCCAGCATGGCCGATAGTAGGTCATCTGCCAGACTTGATCTCTAAAAACAGCCCACCATTCCTAGATTATATGTCTAACATCGCTCAGAAATATGGTCCGTTGATTCATTTGAAGTTCGGTCTGCACTCTAGTATTTTTGCCTCTACTAAGGAAGCAGCTATGGAGGTCTTACAGATTAACGACAAGGCTTTGAGCGGGAGACAGCCTCTTCCCTGCTTTAGGATAAAGCCCCATATAGACTATTCTATCGTCTGGTCCGACTCTAATAGTTACTGGAAGAACGGACGTAAGATACTTCACACCGAAATATTTTCCCAGAAAATGCTTCAAGCGCAGGAAAAAAATAGGGAGAGGGTGGCAGAAAACCTGGTGAACTTTATCCGTACAAAAGTGGGTAACGTTGTCGAACTAAGGAGCTGGCTATTTGGCTGTGCGCTGAATGTATTAGGCCATGTTGTATTTTCAAAGGATGTGTTCGGCTACTCAGATCAATCAGACGAAGTTGGTATGGATAAGCTGATTCATGGTATGATCATGACGGGCGGAGACTTCGATGTAGCATCCTACTTCCCGTTCTTGGCAAGATTTGATATACACGGTCTTAAAAGGAAAATGGATGAACAGTTTAAATTACTAATCAAGGTTTGGGAGGGAGAAGTATTAGCGAGGAAAGCTAACCAGAACCCCGAGCCGAAGGATATGTTAGATGTGCTAATTGCGAATGACTTTAATGAACATCAGATAAATGCTATGTTCTTAGAAACGTTCGGTCCAGGGAGCGATACGAGCTCAGCAACAATAGAATGGGCGTTGGCACAATTGATAAAAAACCCAGACAAGTTGGCAAAACTAAGGGAAGAGCTGGACAGGGTTGTAGGAAGATCATCCACGGTGAAGGAGAGCCACTTCTCACAGTTGCCATATCTTCAGGCTTGCGTCAAAGAGACGATGAGACTGTATCCGTCCGTTACGATCATGATCCCACACCGTTGTATGGAAACGTGCCAAGTCATGGGCTATACTATTCCTAAAGGTATTGATGTTCATGTCAATGCCCATGCGATTGGCAGGGACCCTAAGGATTGGAAAGACCCACTTAAGTTTCAGCCTGAGAGGTTCTTAGACTCCGATATAGAGTACAATGGGAAGCAATTCCAGTTTATTCCGTTTGGTT

	CCGGCAGAAGAATTTGCCCTGGATGGCCCCTGGCCGTTCGTACCATCCCGCTGGTCTTAGCGTCACTGGTCCATGCATTCGATTGGGAATTACCTGATGGAGTTCCCAACGAAAAGCTTGACATGGAAGAATTGTTTACCCTAACTCTTTGCATGGCCAAGCCATTACGTGTAATCCCCAAGGTTCGTATA
Bs-XsCYP80A1	ATGGACTATATTGTTGGTTTCGTAAGTATTTCTTTAGTTGCTCTGCTTTACTTCCTTTTGTTCAAACCTAAGCATACTAATCTACCTCCTTCTCCCCCAGCATGGCCGATAGTAGGTCATCTGCCAGACTTGATCTCTAAAAACAGCCCACCATTCCTAGATTATATGTCTAACATCGCTCAGAAATATGGTCCGTTGATTCATTTGAAGTTCGGTCTGCACTCTAGTATTTTTGCCTCTACTAAGGAAGCAGCTATGGAGATCCTAAAAACTAACGATAAAGTATTATCAGGAAGGACCCCGTTGCCGTGCTTTTTAATCAAGCCTCATATTAACTATTCCCTTGTTTGGAGCGATTCAACAAGTTATTGGAAATCACTGAGAAAAATACTACACACGGAGATATTTGCTCAAAAAATGTTACTAGATCAAGAAAAAAACCGTGAGAGGATGGTCGGGGATTTAGTTAACTTCTTCCGTGCAAAAGTAGGGGACGTTGTTGAATTGAAAAGCTGGCTGTTTGGGTTCTCATTAAACGTGCTTTCTAACGCGATATTTAGCAAGGACGTTTTCGGCTATTCAGACAACGGGGGCAAAGTTGGTATGGACAAAATAATTCAGGAGATGTTTAAGGTCGGGGGGGAATTTGACGCCGCAAGTTATTTCTCCTGCCTAGAAAGGTTCGATCTGCACGGCTTGCGTCGTAAAATGAATGAATTGTTCCAATTAGCAATTAAACTTTGGGAAGGAGAAGTTATTATGCGTAAGGCCAACCGTAATGCGGAGCCAAAAGATATGTTAGATGTGCTTATTGCGAATGATTTTAACGATCATCAGATTAACGCGATATTTGTGGAGACATTCAGTGCAGGGTCAGAAACTTCCAGTAGCACGGTTGAATGGGCCCTAGCCGAATTAATCAAATCACCGGATAAGATGGCCAAACTGAGGGAAGAACTAGACAGGGTCGTAGGGAGGTCCTTTACCATGAAGGAATCTCATATTTCTCAATTGCCCTACCTGCAAGCATGCATTAAAGAAACCATGAGGTTACACCCTGCCGTTCCCTTAATCATACCGCACCGTTGTATGGAGACCTGTCAGGTAATGGGCTATACCATCCCCAAGGGTACCGATATACACGTGAATACTTATGCTATTGGAAGGGATCCGAGAGATTGGATCGATCCCCTAAAGTTTCTTCCAGAGAGGTTCCTGGATAGTAATTTAGATTACAACGGGAATCACTTTCAATTCCTTCCCTTTTCCGCAGGAAGACGTTCCTGCGTCGGTATGCCCCTGGCGGTACGTACCATTCCACTGGTCTTAGCTTCTTTGGTACATGTGTTTGACTGGAAGTTGGCGGAGGCCATACCTGTAGAGAAGCTGGACTCTGAGGAAACCTTTGCCATGACCATGTCCAAGGCTCAGCCTTTAAGAGTAATACCGAACATAAGGCTT
ySiCNMT2	ATGGAAGCACCCCAACGTAATCGTGCGGAAGTAACGGAGGTGATGCGTAAGTTAGGTTTGGGGCTGATACCTGACGAGGAGCTTCGTTCACTAATCAGCGTGCAAGTGGAAAGGAGATTGAGATGGGGATACAAGCCTACCTTTGAACAGCAGCTTGCCCAGCTGGTCCAATTCGTGCATTCACTAAAACAAATGAGTATCTCCCTAGAGGCAGAAGTTTTGGAGTCTCAAGTGTACGAAATTCCTAATTCTTTTATGAAATTGTTGCACGGCTCCAGTATGAAGGCCAGCTGGTGTTTTTTCATCAACGACTCAACCACCCTAGACGAGGCTGAGATTGCAATGTTGGAATTGTACTGCGATCGTTCCCAGATTCGTGACGGTGATAGGGTTTTAGACCTAGGGTGTGGCTTCGGCGCCTTGGCGACATATATCGCGAGAAAATACCCCAACTGCCAAGTTACGGGCGTCACTAATTCAGAATTTCAAAAAGAGTTCATCGAGGAGCAATGCAAAAAAGATAACTTAGTCAATGTAGAAGTGATTCTTGCCGACGTCACAACCCTTGAAATGGATAAAGAATTTGACCGTGTTATGGCTATTGGAGTAATAGAACATATGAAGTCCTATGAACTGCTACTGAAGAAGATCTCCAAGTGGATGAAACAAGATGGATTGCTTTTTGTGGACCATATTTGTCATAAAGCCTTCGCTTATCATTTTGAGCCAATTGGCGAGGAGGACTGGATAGAGGAATACATTTTCCCAGGAGGAGTTATGACAATTCCGTCCGCTGATCTGTTGCTGTATTTTCAGGACGATATTAGTGTTGTAAACCACTGGGCTGTCAATGGTAAACATTATTCCCGTACTAATGAGGAATGGTTGAAG

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yNnOMT5	ATGGAGGAAGACATGAAAGCACAAGCGCAGGTCTGGAAACATATATATGGATTTGTCGAATCCTTTACCTTAAAGTGCGCTATCGAGTTGGGTATCGCTGATATTTTATATGAACATGGTCAGCCGATGACGCTGAGTGAGCTGGCTAGCAGCATACCCCTACCATCTGTCTCTCAGGACGGTCTATATCGTGTACTAAGATACCTGGTTCATATGAAATTGTTTGACCTACAGGTCGATTCAGATGGCCTGAAAAAGTATAGGTTGACGCCGGCTTCAAAATTGCTAGTAAAAAATCAAGAAAAGAACTTGGCCTCCTTTGTCTTGCTACAGCTTTACGAGATAGACACGTGGAACCATTTAAGCGCGGCTGTCGAAGGTACTGTTACGCCATGGGAAAAATGCCATGGTGGCGTCGACTATATCGAATACTTTAAAAAAGACAGTGTTGCCAACCAGTTATTGTCCGATGCGATGACCTCCCATACATCAATGGTCACAGACGCCTTAGTGAAAGGGTGCAAGAAAGCCCATATCTTGGACGGAGTCGGGTCACTAATCGATGTGGGAGGTTGTACGGGCGTTGCTGCAAGAGCTATCGCCAAGTGGTTTCCTTCAATAAAGTGTGCCGTTTTCGATCTTCCGCATGTGGTAGCGAACGCCCCTGAGTGTCCAGAGGTCACTCGTATAGGTGGAGATATGTTTGTTTCTATCCCTAAGACGGATGTAGTCTTTATGAAGTCTGTGTTGCATGACTGGGGTGATGAAGACTGCGTCAAGATCCTAAAGAAGTGCAAGGAGGCCATTAGCGAAAAAGGTGGGAAGGCAGTGATAGTTGACATCGTCATGGACGTTGAATCATCTCCTAATGAATTTACAGGCGCTAGGTTAGGCATGGAGATGGATATGCTGGTTGCAGTGGGAGGTAAAGAAAGGAGTGAAAAAGAATGGCATAAGCTATTTAAGGAAGCTGGGTACTCCGGATACAAAATTACTCCCATAGTCGCAATAGAAAGTATCATTGAGGTGTTTCCCTGA
yCt7OMT	ATGGAGACGATTCTTCAAGGTCAACAGAACATTACTAAATTACTATTTGCATTTGCGGATACGATGGCTTTAAAATGCGTAGTCGAGCTGCGTATCGCCGACATTATCAACAGTCATGGGCTGCCTATAAGTTTGTCAGAAATCGCTGCGGGCATACAATCCACCAGTTCCAGTTCTTCTCCCCCGAATATAAACTACCTTTTTAGGATAATGCGTCTGCTGGTTCGTAAAGGAGTTTTCTCAAGTCATGCGCCTAATCAAAACGAAGAAACACTGTACGGTTTAACTAACAGCTCTAAGTGGTTGCTAAGGGACGCTAACTTTTCAATGACACCAATAATTCAGGCGCTGACCCATCATTGTAGTATGGATTCATTCCATAAGCTAAATAAGTGCGTTGAAGAAGGAGGTTATGCGTTTGCCAAAGCCAATGGTTGTGAAATATGGGAATTTGCTTCCATGAACCCGGAATTCAATAGACTGTTCAACTCAGCGATGGCTTCTACCTCCAAGATAGCGGTTGACGCTATTCTAAGCGGATATAAGAATGGATTCGACGGGTTACGTTCCTTAGTCGATGTAGGAGGCGGTACAGGAACATTGATTGGGGAGATAGTGAAAGCCTATCCTCACCTAACCGGGACCAATTTTGACCTACCTCACGTAGTTGCTACAGCACCAGAACACACTGGGGTAGTTCACGTCGGTGGGGACATGTTCGTCGAAATTCCCCACGCGGACGCAATCATTTTGAAGTGGATTCTACATGATTGGAATGACGAGGATTGCGTGAAGATTTTAAAGAACTGCCATAAGGCCATAGCGAATAGGGGCGTAAAAGTAATCATTGTCGAAATTGTGCTGCAACCGGATGGAGTTGCGCCATTAGACGAAACTAGGCTAATTTTCGATCTGTCAATGATAGCACATAGCTCCGGTGGTAAAGAGCGTACAGAGACAGAATGGGAGAAGCTATTGAGGGACGGAGGCTTCAGCAGGCACCGTATAATCCAGATCCCGGATGTCACCAGCATTATAGAAGCTTATCCT

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