Table S1. Sequence identities and similarities. Pairwise identity [%]/pairwise positive [%].

	CorA	**HapA1**	**HapA2**	**PpaA1**	**PpaA2**
CorA	100/100	64/76	59/73	48/65	49/66
HapA1		100/100	68/79	49/66	50/66
HapA2			100/100	47/64	47/63
PpaA1				100/100	80/91
PpaA2					100/100

Table S2. Protein sequences used for phylogenetic analysis of quinone synthetases. Substrates are: IP, indole-3-pyruvate; PP, phenylpyruvate; 4-HPP, 4-hydroxyphenylpyruvate.

Organism	Enzyme	Amino acids	Substrate	Direct or pathway product	Accession	Reference
Basidiomycota						
Psilocybe cubensis	PpaA1	1333	PP	polyporic acid	OQ821699	This work
Psilocybe cubensis	PpaA2	1326	PP	none detected	OR105898	This work
Terana caerulea	CorA	994	PP	polyporic acid	UVV38562.1	[1]
Hapalopilus rutilans	HapA1	964	PP	polyporic acid	OQ784619	This work
Hapalopilus rutilans	HapA2	925	PP	polyporic acid	OQ784620	This work
Tapinella panuoides	AtrA	957	4-HPP	atromentin	ACH90386.1	[2]
Serpula lacrymans	Nps3	962	4-HPP	atromentin	EGO23141.1	[3]
Paxillus involutus	InvA1	959	4-HPP	atromentin	A0A0S2E7Z1	[4]
Paxillus involutus	InvA2	953	4-HPP	atromentin	A0A0S1RUN4	[4]
Paxillus involutus	InvA5	953	4-HPP	atromentin	A0A0S2E7W7	[4]
Suillus grevillei	GreA	958	4-HPP	atromentin	AFB76152	[5]
Ascomycota						
Aspergillus nidulans	MicA	938	PP	microperfuranone	Q5B7T4	[6]
Ascocoryne sarcoides	AcyN	930	PP	polyporic acid	P9WES4.1	[7]
Aspergillus terreus	PngA	946	PP	phenguignardic acid	Q0CBN5	[8]
Aspergillus terreus	AtrA	920	4-HPP	atromentin	Q0CT94	[9}
Aspergillus terreus	MelA	925	4-HPP	aspulvinone E	A0A336U965	[10]
Aspergillus terreus	ApvA	925	4-HPP	aspulvinone E	Q0CWD0	[11]
Aspergillus terreus	BtyA	930	4-HPP	butyrolactone II	Q0CU19	[11]
Aspergillus terreus	AtqA	962	IP	didemethylasterriquinone D	Q0D034	[11]
Aspergillus nidulans	TdiA	949	IP	didemethylasterriquinone D	CBF80711.1	[12]
Bacteria						
Streptomyces sp.	EchA	967	PP	echoside	AHN91924	[13]
Ralstonia solanacearum	RalA	937	PP	ralfuranone B	AEC03968.1	[14]

References

1. Lawrinowitz S, Wurlitzer JM, Weiss D, Arndt HD, Kothe E, Gressler M, Hoffmeister D: **Blue Light-Dependent Pre-mRNA Splicing Controls Pigment Biosynthesis in the Mushroom *Terana caerulea***. *Microbiol Spectr* 2022, **10**(5):e0106522.
2. Schneider P, Bouhired S, Hoffmeister D: **Characterization of the atromentin biosynthesis genes and enzymes in the homobasidiomycete *Tapinella panuoides***. *Fungal Genet Biol* 2008, **45**(11):1487-1496.

3. Tauber JP, Schroeckh V, Shelest E, Brakhage AA, Hoffmeister D: **Bacteria induce pigment formation in the basidiomycete *Serpula lacrymans***. *Environ Microbiol* 2016, **18**(12):5218-5227.
4. Braesel J, Götze S, Shah F, Heine D, Tauber J, Hertweck C, Tunlid A, Stallforth P, Hoffmeister D: **Three Redundant Synthetases Secure Redox-Active Pigment Production in the Basidiomycete *Paxillus involutus***. *Chem Biol* 2015, **22**(10):1325-1334.
5. Wackler B, Lackner G, Chooi YH, Hoffmeister D: **Characterization of the *Suillus grevillei* quinone synthetase GreA supports a nonribosomal code for aromatic α-keto acids**. *ChemBioChem* 2012, **13**(12):1798-1804.
6. Yeh HH, Chiang YM, Entwistle R, Ahuja M, Lee KH, Bruno KS, Wu TK, Oakley BR, Wang CC: **Molecular genetic analysis reveals that a nonribosomal peptide synthetase-like (NRPS-like) gene in *Aspergillus nidulans* is responsible for microperfuranone biosynthesis**. *Appl Microbiol Biotechnol* 2012, **96**(3):739-748.
7. Wieder C, Peres da Silva R, Witts J, Jager CM, Geib E, Brock M: **Characterisation of ascocorynin biosynthesis in the purple jellydisc fungus *Ascocoryne sarcoides***. *Fungal Biol Biotechnol* 2022, **9**(1):8.
8. Sun WW, Guo CJ, Wang CCC: **Characterization of the product of a nonribosomal peptide synthetase-like (NRPS-like) gene using the doxycycline dependent Tet-on system in *Aspergillus terreus***. *Fungal Genet Biol* 2016, **89**:84-88.
9. Hühner E, Backhaus K, Kraut R, Li SM: **Production of alpha-keto carboxylic acid dimers in yeast by overexpression of NRPS-like genes from *Aspergillus terreus***. *Appl Microbiol Biotechnol* 2018, **102**(4):1663-1672.
10. Geib E, Gressler M, Viediernikova I, Hillmann F, Jacobsen ID, Nietzsche S, Hertweck C, Brock M: **A Non-canonical Melanin Biosynthesis Pathway Protects *Aspergillus terreus* Conidia from Environmental Stress**. *Cell Chem Biol* 2016, **23**(5):587-597.
11. Guo CJ, Knox BP, Sanchez JF, Chiang YM, Bruno KS, Wang CC: **Application of an efficient gene targeting system linking secondary metabolites to their biosynthetic genes in *Aspergillus terreus***. *Org Lett* 2013, **15**(14):3562-3565.
12. Schneider P, Weber M, Rosenberger K, Hoffmeister D: **A one-pot chemoenzymatic synthesis for the universal precursor of antidiabetes and antiviral bis-indolylquinones**. *Chem Biol* 2007, **14**(6):635-644.
13. Zhu J, Chen W, Li YY, Deng JJ, Zhu DY, Duan J, Liu Y, Shi GY, Xie C, Wang HX *et al*: **Identification and catalytic characterization of a nonribosomal peptide synthetase-like (NRPS-like) enzyme involved in the biosynthesis of echosides from *Streptomyces* sp. LZ35**. *Gene* 2014, **546**(2):352-358.
14. Wackler B, Schneider P, Jacobs JM, Pauly J, Allen C, Nett M, Hoffmeister D: **Ralfuranone biosynthesis in *Ralstonia solanacearum* suggests functional divergence in the quinone synthetase family of enzymes**. *Chem Biol* 2011, **18**(3):354-360.

Table S3. HR-MS and MS/MS data of polyporic acid and phlebiopsins A and B.

Compound	Formula	Neutral mass [M]	Parental ion *m/z* $[M-H]^-$	MS/MS specific ions	
				Ion mass *m/z* $[M-H]^-$	Formula*
Polyporic acid	$C_{18}H_{12}O_4$	292.0736	291.066		
				263.017	$C_{17}H_{11}O_3$
				191.086	$C_{15}H_{11}$
				117.033	C_8H_5O
Phlebiopsin A	$C_{18}H_{14}O_5$	310.0841	309.077		
				291.066	$C_{18}H_{11}O_4$
				281.081	$C_{17}H_{13}O_4$
				265.087	$C_{17}H_{13}O_3$
				251.071	$C_{16}H_{11}O_3$
				235.076	$C_{16}H_{11}O_2$
				191.086	$C_{15}H_{11}$
				187.039	$C_{11}H_7O_3$
				147.044	$C_9H_7O_2$
				119.049	C_8H_7O
				117.033	C_8H_5O
Phlebiopsin B	$C_{17}H_{12}O_4$	280.0736	279.066		
				251.071	$C_{16}H_{11}O_3$
				235.076	$C_{16}H_{11}O_2$
				191.086	$C_{15}H_{11}$
				179.086	$C_{14}H_{11}$
				121.028	$C_7H_5O_2$
				117.033	C_8H_5O
				105.033	C_7H_5O
				77.038	C_6H_5
Atromentin	$C_{18}H_{12}O_6$	324.0634	323.056		
				295.061	$C_{17}H_{11}O_5$
				251.071	$C_{16}H_{11}O_3$
				223.076	$C_{15}H_{11}O_2$
				133.028	$C_8H_5O_2$
				117.033	C_8H_5O
				105.033	C_7H_5O

*Predicted with ChemCalc [1] and CFM-ID (version 4.0) [2-6]

References

1. Patiny L, Borel A: **ChemCalc: a building block for tomorrow's chemical infrastructure**. *J Chem Inf Model* 2013, **53**(5):1223-1228.
2. Wang F, Liigand J, Tian S, Arndt D, Greiner R, Wishart DS: **CFM-ID 4.0: More Accurate ESI-MS/MS Spectral Prediction and Compound Identification**. *Anal Chem* 2021, **93**(34):11692-11700.
3. Djoumbou-Feunang Y, Pon A, Karu N, Zheng J, Li C, Arndt D, Gautam M, Allen F, Wishart DS: **CFM-ID 3.0: Significantly Improved ESI-MS/MS Prediction and Compound Identification**. *Metabolites* 2019, **9**(4).
4. Allen F, Pon A, Greiner R, Wishart D: **Computational Prediction of Electron Ionization Mass Spectra to Assist in GC/MS Compound Identification**. *Anal Chem* 2016, **88**(15):7689-7697.
5. Allen F, Greiner R, Wishart D: **Competitive fragmentation modeling of ESI-MS/MS spectra for putative metabolite identification**. *Metabolomics* 2015, **11**:98-110.
6. Allen F, Pon A, Wilson M, Greiner R, Wishart D: **CFM-ID: a web server for annotation, spectrum prediction and metabolite identification from tandem mass spectra**. *Nucleic Acids Res* 2014, **42**(Web Server issue):W94-99.

Table S4. Plasmids.

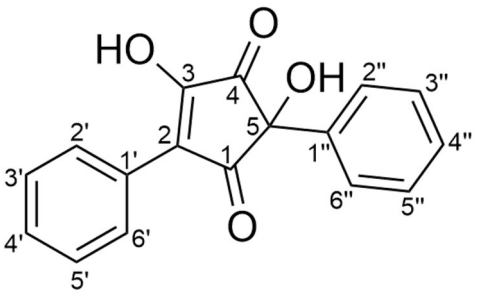
Plasmid name	Vector backbone	Gene product	Position of His_6-tag	Reference
pSMX2-URA	pUC19	- (vector)	-	[1]
pMG49	pMD03	LpaA	-	[2]
pPS13	pSMX2-URA	PpaA2	N-terminus	this study
pPS14	pSMX2-URA	PpaA1	N-terminus	this study
pPS29	pMG49	- (vector)	-	this study
pPS35	pPS29	PpaA2	C-terminus	this study
pPS36	pPS29	PpaA1	C-terminus	this study
pPS37	pSMX2-URA	$PpaA1^{S628A}$	N-terminus	this study
pPS39	pSMX2-URA	$PpaA1^{D1188A}$	N-terminus	this study
pPS40	pSMX2-URA	$PpaA1^{H1243A}$	N-terminus	this study
pPS41	pSMX2-URA	$PpaA1^{H1186A/D1188A/H1243A}$	N-terminus	this study
pPS42	pSMX2-URA	PpaA1ΔD-domain	N-terminus	this study
pPS50	pPS29	PpaA1ΔD-domain	C-terminus	this study
pPS51	pPS29	PpaA1(A-T)::CorA(TE)	C-terminus	this study
pPS52	pPS29	CorA(A-T)::PpaA1(TE)	C-terminus	this study
pPS53	pPS29	CorA(A-T-TE)::PpaA1(D)	C-terminus	this study
pPS54	pPS29	CorA(A-T)::PpaA1(TE-D)	C-terminus	this study
pPS57	pPS29	$CorA^{I298N}$	C-terminus	this study
pPS58	pPS29	$PpaA1^{V302N}$	C-terminus	this study
pPS59	pPS29	$Nps3^{N323I}$	C-terminus	this study
pPS60	pPS29	$Nps3^{N323V}$	C-terminus	this study
pPS61	pPS29	Nps3	C-terminus	this study
pSS06	pMG49	CorA	-	[3]
pSS10	pMG49	HapA1	-	this study
pSS11	pMG49	HapA2	-	this study

References

1. Geib E, Brock M: **ATNT: an enhanced system for expression of polycistronic secondary metabolite gene clusters in *Aspergillus niger***. *Fungal Biol Biotechnol* 2017, **4**:13.
2. Seibold PS, Lenz C, Gressler M, Hoffmeister D: **The *Laetiporus* polyketide synthase LpaA produces a series of antifungal polyenes**. *J Antibiot (Tokyo)* 2020, **73**(10):711-720.
3. Lawrinowitz S, Wurlitzer JM, Weiss D, Arndt HD, Kothe E, Gressler M, Hoffmeister D: **Blue Light-Dependent Pre-mRNA Splicing Controls Pigment Biosynthesis in the Mushroom *Terana caerulea***. *Microbiol Spectr* 2022, **10**(5):e0106522.

Table S5. NMR spectroscopy data. ^{1}H and ^{13}C NMR spectroscopy data for phlebiopsin B (600 MHz for ^{1}H, 150 MHz for ^{13}C, CD_3OD, 300 K).

Position	δ_C	δ_H, mult. (J [Hz])	^{1}H-^{1}H COSY	HMBC ($^{1}H \rightarrow ^{13}C$)
1	199.6	–	–	6'
2	130.1	–	–	–
3	167.9	–	–	2'
4	199.1	–	–	2''
5	77.7	–	–	2'', 3'', 5'', 6''
1’	130.8	–	–	3', 5'
2’	130.3	8.14, d (7.6)	3'	4', 6'
3’	129.3	7.41, d (7.9)	2', 4'	–
4’	130.3	7.36, t (7.4)	3', 5'	2', 6'
5’	129.3	7.41, d (7.9)	4', 6'	–
6’	130.3	8.14, d (7.6)	5'	2', 4'
1’’	139.0	–	–	3'', 5''
2’’	127.0	7.42, m	3''	4'', 6''
3’’	129.6	7.32, t (7.5)	2'', 4''	5''
4’’	129.4	7.27, t (7.2)	3'', 5''	–
5’’	129.6	7.32, t (7.5)	4'', 6''	3''
6’’	127.0	7.42, m	5''	2'', 4''
5-OH	–	n.d.*	–	–



*Not detected

Table S6. Fungal strains and genotypes. JMRC = Jena Microbial Resource Collection; FGSC = Fungal Genetics Stock Center.

Strain	Genotype	Reference/ Source
Hapalopilus rutilans CBS 490.95	wild type	Westerdijk Institute
Psilocybe cubensis FSU12407	dikaryon	JMRC
Terana caerulea CBS 452.86	wild type	Westerdijk Institute
Serpula lacrymans S7	wild type	[1]
Aspergillus nidulans FGSC A4	wild type	FGSC
Aspergillus niger ATNT16Δ*pyrG*x24	TetOn:*terR_ble*; Δ*pyrG*::*ptrA*	[2]
Aspergillus niger tNAL000	TetOn:*terR_ble*; Δ*pyrG*::*ptrA*; P*terA*:*His$_6$_pyrG*	[3]
Aspergillus niger tPS10	TetOn:*terR_ble*; Δ*pyrG*::*ptrA*; P*terA*:*ppaA2_pyrG*	This study
Aspergillus niger tPS11	TetOn:*terR_ble*; Δ*pyrG*::*ptrA*; P*terA*:*ppaA1_pyrG*	This study
Aspergillus nidulans tPS15	P*alcA*:*His$_6$_ptrA*	This study
Aspergillus nidulans tPS18	P*alcA*:*ppaA2*:*His$_6$_ptrA*	This study
Aspergillus nidulans tPS19	P*alcA*:*ppaA1*:*His$_6$_ptrA*	This study
Aspergillus niger tPS20	TetOn:*terR_ble*; Δ*pyrG*::*ptrA*; P*terA*:*His$_6$*:*ppaA1*(S628A)*_pyrG*	This study
Aspergillus niger tPS21	TetOn:*terR_ble*; Δ*pyrG*::*ptrA*; P*terA*: *His$_6$*:*ppaA1*(D1188A)*_pyrG*	This study
Aspergillus niger tPS22	TetOn:*terR_ble*; Δ*pyrG*::*ptrA*; P*terA*: *His$_6$*:*ppaA1*(H1243A)*_pyrG*	This study
Aspergillus niger tPS23	TetOn:*terR_ble*; Δ*pyrG*::*ptrA*; P*terA*: *His$_6$*:*ppaA1*(H1186A_D1188A_H1243A)*_pyrG*	This study
Aspergillus niger tPS24	TetOn:*terR_ble*; Δ*pyrG*::*ptrA*; P*terA*: *His$_6$*:*ppaA1*ΔD*_pyrG*	This study
Aspergillus nidulans tPS28	P*alcA*:*ppaA1ΔD*:*His$_6$_ptrA*	This study
Aspergillus nidulans tPS29	P*alcA*:*ppaA1(A-T)*:*corA(TE)*:*His$_6$_ptrA*	This study
Aspergillus nidulans tPS30	P*alcA*:*corA(A-T)*:*ppaA1(TE)*:*His$_6$_ptrA*	This study
Aspergillus nidulans tPS31	P*alcA*:*corA(A-T-TE)*:*ppaA1(D)*:*His$_6$_ptrA*	This study
Aspergillus nidulans tPS32	P*alcA*:*corA(A-T)*:*ppaA1(TE-D)*:*His$_6$_ptrA*	This study
Aspergillus nidulans tPS35	P*alcA*:*corA*(I298N):*His$_6$_ptrA*	This study
Aspergillus nidulans tPS36	P*alcA*:*ppaA1*(V302N):*His$_6$_ptrA*	This study
Aspergillus nidulans tPS37	P*alcA*:*nps3*(N323I):*His$_6$_ptrA*	This study
Aspergillus nidulans tPS38	P*alcA*:*nps3*(N323V):*His$_6$_ptrA*	This study
Aspergillus nidulans tPS39	P*alcA*:*nps3*:*His$_6$_ptrA*	This study
Aspergillus nidulans tStL04	P*alcA*:*corA_ptrA*	[4]
Aspergillus nidulans tStL07	P*alcA*:*hapA1_ptrA*	This study
Aspergillus nidulans tStL08	P*alcA*:*hapA2_ptrA*	This study

References

1. Eastwood DC, Floudas D, Binder M, Majcherczyk A, Schneider P, Aerts A, Asiegbu FO, Baker SE, Barry K, Bendiksby M *et al*: **The plant cell wall-decomposing machinery underlies the functional diversity of forest fungi**. *Science* 2011, **333**(6043):762-765.

2. Geib E, Brock M: **ATNT: an enhanced system for expression of polycistronic secondary metabolite gene clusters in *Aspergillus niger***. *Fungal Biol Biotechnol* 2017, **4**:13.
3. Löhr NA, Eisen F, Thiele W, Platz L, Motter J, Hüttel W, Gressler M, Müller M, Hoffmeister D: **Unprecedented Mushroom Polyketide Synthases Produce the Universal Anthraquinone Precursor**. *Angew Chem Int Ed* 2022, **61**(24):e202116142.
4. Lawrinowitz S, Wurlitzer JM, Weiss D, Arndt HD, Kothe E, Gressler M, Hoffmeister D: **Blue Light-Dependent Pre-mRNA Splicing Controls Pigment Biosynthesis in the Mushroom *Terana caerulea***. *Microbiol Spectr* 2022, **10**(5):e0106522.

Table S7. Oligonucleotides used for expression analysis by qRT-PCR.

Oligonucleotide	5´-3´sequence	Target gene	Fragment size (gDNA) [bp]	Fragment size (cDNA) [bp]	Primer efficiency
oMG390	TCGGAATCGCTGAAAATGGC	*enoA*	186	120	1.00
oMG391	GGAGACGTTGGGAGCAAAGC				
oPS447	TGAAAGACCTGCTCACATCG	*ppaA2*	202	153	0.99
oPS448	TTCAGCTCCAAGTTCAGGATAC				
oPS453	TAATTCTCCTTCTCTGCGCG	*ppaA1*	178	125	1.03
oPS545	AGAAAGGCACATCTGGACTG				

Table S8. PCR methods.

Method	Reaction Mix		Thermal cycling		
	Component	**Volume [µL]**	**Temperature [°C]**	**Time**	**Cycles**
A	5 × PrimeSTAR GXL Buffer	10	98	10 s	
	2.5 mM dNTP Mix	4	60	15 s	35-40
	Primer forward 10 pmol μL^{-1}	1.5	68	1 min kb^{-1}	
	Primer reverse 10 pmol μL^{-1}	1.5	10	∞	1
	DNA template*	1			
	PrimeSTAR GXL DNA Polymerase (1.25 U μL^{-1})	1			
	dH_2O	to 50			
B	5 × Phusion GC Buffer	4	98	2 min	1
	10 mM dNTP Mix	0.4	98	30 s	
	Primer forward 10 pmol μL^{-1}	1	60	30 s	35-40
	Primer reverse 10 pmol μL^{-1}	1	72	30 s kb^{-1}	
	DNA template*	1	72	5-10 min	1
	Phusion DNA Polymerase (2 U μL^{-1})	0.1	10	∞	
	DMSO (optional)	1.5			
	dH_2O	to 20			
C	2 × Xtreme Buffer	25	94	2 min	1
	2 mM dNTP Mix	10	98	10 s	
	Primer forward 10 pmol μL^{-1}	1.5	60	30 s	35-40
	Primer reverse 10 pmol μL^{-1}	1.5	68	1 min kb^{-1}	
	DNA template*	1	68	5-10 min	1
	KOD Xtreme Hot Start DNA Polymerase (1 U μL^{-1})	1	10	∞	
	dH_2O	to 50	94		
D	10 × DreamTaq Buffer	2	95	2 min	1
	10 mM dNTP Mix	0.4	95	30 s	
	Primer forward 10 pmol μL^{-1}	0.4	60	30 s	31
	Primer reverse 10 pmol μL^{-1}	0.4	72	1 min kb^{-1}	
	DNA template*	X**	72	5-10 min	1
	DreamTaq Polymerase (5 U μL^{-1})	0.1	10	∞	
	dH_2O	to 20	95		
E	5 × Phusion HF Buffer	4	98	2 min	1
	10 mM dNTP Mix	0.4	98	30 s	
	Primer forward 10 pmol μL^{-1}	1	60	30 s	35-40
	Primer reverse 10 pmol μL^{-1}	1	72	30 s kb^{-1}	
	DNA template*	1	72	5-10 min	1
	Phusion DNA Polymerase (2 U μL^{-1})	0.2	10	∞	
	dH_2O	to 20			

*DNA template: 1 µL of 100 ng μL^{-1} gDNA, 10 ng μL^{-1} plasmid DNA, reverse transcription reaction (1:5 diluted with dH_2O), **or 10 µL water with resuspended *E. coli* cells (for colony PCR).

Table S9. Oligonucleotides used for cloning, colony PCRs, and DNA sequencing.

Oligonucleotide	5´-3´sequence	Target	Purpose
oMG116	GAGATGTGGTAGACGATTGATCC	pSMX2-URA (T*trpC* from *A. niger*)	sequencing/colony PCR
oMG169	GCGCTTACACAGTACACGAGG	pMG49 (T*trpC* from *A. oryzae*)	sequencing/colony PCR
oMG172	ATGGTCATGCGCCGTCCCGC	pPS29 (*ptrA*)	sequencing
oMG234	TTACGCCGGCGCGCCGTAGATATTTTCGAAGGGATTC	pMG49 (P*alcA*)	sequencing/colony PCR
oMG360	CCTCCAAGAGAGATCCAGAC	pSMX2-URA (P*terA*)	sequencing/colony PCR
oMG361	GAATTTTACCAGTGGCCTAGG	pSMX2-URA (T*trpC* from *A. niger*)	sequencing/colony PCR
oMG370	GATCCTCTCTCTGATATTGTCG	pSMX2-URA (P*terA*)	sequencing/colony PCR
oMG468	ACTTAACGTTACTGAAATCATCAAACAG	pMG49 (T*trpC* from *A. oryzae*)	vector amplicfication
oMG469	TTTGAGGCGAGGTGATAGGATTG	pMG49 (P*alcA*)	vector amplicfication
oMG474	CATCCCCGCATAGCTGAACATC	pPS29 (P*alcA*)	sequencing/ colony PCR
oPS355	TTGAAATCACTGCTGTTATCCATGTTAGACGATACCTAGCTGCCTTGC	*ppaA2*	cloning of pPS13
oPS356	CACCATGCATCATCATCACCATCACCATACCACTGAACCGACGACAA	*ppaA2*	cloning of pPS13
oPS357	CACCATGCATCATCATCACCATCACGAATCAACAGGGCCCACAAC	*ppaA1*	cloning of pPS14
oPS358	GAAATCACTGCTGTTATCCATGTTAAACAATTCCCAACTTCTTTGCC	*ppaA1*	cloning of pPS14
oPS362	ATCAAAACTCTAAGCGCCGA	*ppaA2*	colony PCR *ppaA2*
oPS363	ATAACCCTGAGCGCTGATAG	*ppaA1*	colony PCR *ppaA1*
oPS429	GGTGATGGTGATGATGTCGCGATCGGACGATACCTAGCTGCCTTG	*ppaA2*	cloning of pPS35
oPS430	TCCAATCCTATCACCTCGCCTCAAAATGCATACCACTGAACCGAC	*ppaA2*	cloning of pPS35
oPS431	TCCAATCCTATCACCTCGCCTCAAAATGGAATCAACAGGGCCCAC	*ppaA1*	cloning of pPS36 and pPS50
oPS432	GGTGATGGTGATGATGTCGCGATCGAACAATTCCCAACTTCTTTGCCTC	*ppaA1*	cloning of pPS36
oPS438	CTTAACTATGCGGCATCAGAGC	pMG49	cloning of pPS29
oPS439	GCTCTGATGCCGCATAGTTAAG	pMG49	cloning of pPS29
oPS441	TCGCGACATCATCACCATCACCATTAGACTTAACGTTACTGAAATCATCAAACAG	pMG49	cloning of pPS29
oPS442	AATGGTGATGGTGATGATGTCGCGATCGCATTTTGAGGCGAGGTGATAGGA	pMG49	cloning of pPS29
oPS459	ACCAGGATAGAGAGCATTGTCTG	pSMX2-URA (P*pyrG*)	sequencing
oPS460	CAGACAATGCTCTCTATCCTGGT	pSMX2-URA (P*pyrG*)	sequencing

Table S9 (continued). Oligonucleotides used for cloning, colony PCRs, and DNA sequencing.

Oligonucleotide	5´-3´sequence	Target	Purpose
oPS461	GCTTCTGCCATGCATCTCATAC	*ppaA1*	cloning of pPS37 (*ppaA1*_S628A)
oPS462	GTATGAGATGCATGGCAGAAGC	*ppaA1*	cloning of pPS37 (*ppaA1*_S628A)
oPS465	CATCGCGCTCCTTCCACATT	*ppaA1*	cloning of pPS39 (*ppaA1*_D1188A)
oPS466	AATGTGGAAGGAGCGCGATG	*ppaA1*	cloning of pPS39 (*ppaA1*_D1188A)
oPS467	CCACCACTGCTCGAGTAAATAC	*ppaA1*	cloning of pPS40 (*ppaA1*_H1243A)
oPS468	GTATTTACTCGAGCAGTGGTGG	*ppaA1*	cloning of pPS40 (*ppaA1*_H1243A)
oPS469	AATGCACGAGGCTCGCGCTC	*ppaA1*	cloning of pPS41 (*ppaA1*_H1186A_D1188A_H1243A)
oPS470	GAGCGCGAGCCTCGTGCATT	*ppaA1*	cloning of pPS41 (*ppaA1*_H1186A_D1188A_H1243A)
oPS471	ATTGAAATCACTGCTGTTATCCATGTTAAGAGTCAAAATTCTGTCGGGAA	*ppaA1*	cloning of pPS42 (*ppaA1* D domain deletion)
oPS472	ATCACACTAGCCAAGGCGTA	*ppaA1*	sequencing
oPS473	AAGATGAGAACTTCGCCGAC	*ppaA1*	sequencing
oPS474	CAAATCAATGGCCCAAGGAC	*ppaA1*	sequencing
oPS490	GGTGATGGTGATGATGTCGCGATCGAGAGTCAAAATTCTGTCGGGAA	*ppaA1*	cloning of pPS50 (*ppaA1* D-domain deletion)
oPS491	CGAGGAAGACAGGCGGCTTCGATCCCTGAGGGTTCAGGCAAAGAAG	*ppaA1*	cloning of pPS51 (*ppaA1*/*corA* domain swap)
oPS492	GGATCGAAGCCGCCTGTCTT	*corA*	cloning of pPS51 (*ppaA1*/*corA* domain swap)
oPS493	GGTGATGGTGATGATGTCGCGATCGCAGCGCAGCACTCGCGC	*corA*	cloning of pPS51 (*ppaA1*/*corA* domain swap)
oPS494	TCCAATCCTATCACCTCGCCTCAAAATGCTATATAATCTCTCCTCGCCCG	*corA*	cloning of pPS52, pPS53 and pPS54 (*ppaA1*/*corA* domain swap)
oPS495	CAAGGTAAATGGGTGGCTTTGAGCCGTGCGGGTTCATGCAGACCA	*corA*	cloning of pPS52 and pPS54 (*ppaA1*/*corA* domain swap)
oPS496	CCCGCTGGTCTGCATGAACCCGCACGGCTCAAAGCCACCCATTTA	*ppaA1*	cloning of pPS52 and pPS54 (*ppaA1*/*corA* domain swap)
oPS497	GGTGATGGTGATGATGTCGCGATCGAGAGTCAAAATTCTGTCGGGAA	*ppaA1*	cloning of pPS52 (*ppaA1*/*corA* domain swap)
oPS498	CGTCCCTCATCTTAGCGGCGAAGGACACGACGTGCTCCTCGGAGA	*corA*	cloning of pPS53 (*ppaA1*/*corA* domain swap)
oPS499	GATGCTCTCCGAGGAGCACGTCGTGTCCTTCGCCGCTAAGATGAG	*ppaA1*	cloning of pPS53 (*ppaA1*/*corA* domain swap)
oPS500	GGTGATGGTGATGATGTCGCGATCGAACAATTCCCAACTTCTTTGCCT	*ppaA1*	cloning of pPS53 and pPS54 (*ppaA1*/*corA* domain swap)
oPS501	CTTCCATGCATCTCATACGTCTC	*ppaA1*	sequencing
oPS502	CGTCTGCAGGTGCTTGAAGA	*corA*	colony PCR
oPS503	ATCACGAAGCTCACGCGGAT	*corA*	sequencing
oPS504	TGGCTCGAGGTGCTCATCAA	*corA*	sequencing

Table S9 (continued). Oligonucleotides used for cloning, colony PCRs, and DNA sequencing.

Oligonucleotide	5´-3´sequence	Target	Purpose
oPS574	GCTTGGACGCGTTCAACTC	*corA*	cloning of pPS57 (*corA*_I298N)
oPS575	GAGTTGAACGCGTCCAAGC	*corA*	cloning of pPS57 (*corA*_I298N)
oPS576	AATCCTATCACCTCGCCTCAAAATGGCCCCAGCCCCGACATC	*nps3*	cloning of pPS59, pPS60 and pPS61
oPS577	GGTGATGGTGATGATGTCGCGATCGAACTCCACGGGCTTCAAGAC	*nps3*	cloning of pPS59, pPS60 and pPS61
oPS578	TGAAACGCATCATCAGTGGTG	*nps3*	cloning of pPS59 (*nps3*_N323I)
oPS579	CACCACTGATGATGCGTTTCA	*nps3*	cloning of pPS59 (*nps3*_N323I)
oPS580	TGAAACGCATCGTCAGTGGTG	*nps3*	cloning of pPS60 (*nps3*_N323V)
oPS581	CACCACTGACGATGCGTTTCA	*nps3*	cloning of pPS60 (*nps3*_N323V)
oPS582	GTTATGAACACTGGAGGAGAGG	*ppaA1*	cloning of pPS58 (*ppaA1*_V302N)
oPS583	CCTCTCCTCCAGTGTTCATAAC	*ppaA1*	cloning of pPS58 (*ppaA1*_V302N)
oPS584	TAACGGAAGCCAATACCACG	*corA*	sequencing
oPS585	TCAAATCCGCAAAGTCCACG	*corA*	sequencing, colony PCR
oPS586	CTCGAGATGCACATAACACCTT	*nps3*	sequencing
oPS587	GACCACAAAAGAGACCTTCGAG	*nps3*	sequencing, colony PCR
oPS588	CACGTCACTCACACTTTCAGTC	*ppaA1*	sequencing
oPS589	CAGTTTCAGTCATCCCAAACG	*ppaA1*	sequencing, colony PCR
oSS189	CAATCCTATCACCTCGCCTCAAAATGGCCGCAACATCCTCTACACTTCC	*hapA1*	cloning of pSS10
oSS190	GCTGTTTGATGATTTCAGTAACGTTAAGTTTACGAGCTGGTAGTAGGG	*hapA1*	cloning of pSS10
oSS191	CAATCCTATCACCTCGCCTCAAAATGAGCACCTCATTCAACCCCTCC	*hapA2*	cloning of pSS11
oSS192	GCTGTTTGATGATTTCAGTAACGTTAAGTCTACAGCTGCTTGGCTGCGCG	*hapA2*	cloning of pSS11

Table S10. HPLC and flash chromatography methods.

Method	Column	Parameters	Eluents	Gradient	
				Time [min]	B [%]
A	Macherey-Nagel EC UHPLC column, Nucleodur C18 Gravity, 50 × 2 mm, 1.8 µm	T: 30°C flow: 1 mL min^{-1}	A: water + 0,1% formic acid B: acetonitrile	0.0 4.0 4.5 5.0	5 72 95 95
B	Büchi FlashPure Silica 40 g 40 µm irregular	flow: 45 mL min^{-1}	A: dichloromethane B: methanol	0.0 8.0 16.0 20.0 32.0	0 0 20 100 100
C	Büchi FlashPure ID C18 12 g 40 µm irregular	flow: 30 mL min^{-1}	A: water + 0,1% formic acid B: acetonitrile	0.0 2.0 5.0 8.0 10.0 12.0 16.0	0 0-20 20-40 40-60 60-80 80-100 100
D	Agilent ZORBAX Eclipse XDB C18 250 × 9.4 mm, 5 µm	T: 12°C flow: 2 mL min^{-1}	A: water + 0,1% formic acid B: acetonitrile	0.0 9.0 9.5 20.0 20.5 25.0 26.5 28.5	30 30 35 35 40 40 100 100
E	Thermo Scientific Accucore C18 100 × 2.1 mm, 2.6 µm	flow: 0.2 mL min^{-1}	A: water + 0,1% formic acid B: acetonitrile	0.0 7.0	5 98
F	Thermo Scientific Accucore C18 100 × 2.1 mm, 2.6 µm	flow: 0.2 mL min^{-1}	A: water + 0,1% formic acid B: acetonitrile	0.0 10.0	5 98