1	SUPPLEMENTARY INFORMATION
2 3 4 5	Discovery of Cryptic Polyketide Metabolites from Dermatophytes using Heterologous Expression in <i>Aspergillus nidulans</i>
6 7 8 9 10 11 12 13 14 15	 Wen-Bing Yin¹, Yit Heng Chooi¹, Ralph A. Cacho^{1,2}, Youcai Hu¹, Adam R. Smith³, Theodore C. White³, Yi Tang^{1,2} ¹Department of Chemical and Biomolecular Engineering, ²Department of Chemistry and Biochemistry, University of California, Los Angeles, CA 90095, USA, 3School of Biological Sciences, University of Missouri at Kansas City, Kansas City, Missouri, USA. yitang@ucla.edu Running Title: Dermatophyte Polyketide Metabolite Table of Contents
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42 Figure S1. Strategies for assembling of DNA fragment in yeast and transformation

43 of *A. nidulans*

44 (A) SOE PCR and yeast homologous recombination were used for assembling of large DNA 45 fragments as described previously (1). (B) Transformation was performed by replacing of A. 46 nidulans wA PKS gene with targeted core PKS genes plus A. fumigatus pyrG (AfpyrG) maker for the first part of DNA fragment integration. The second integration of DNA fragment with A. 47 48 fumigatus pyroA (AfpyroA) was inserted to the same wA locus with 1 kb flanking regions of 49 AfpyrG and wA. The recipient strain is RJMP1.49 (pyrG89, pyroA4, ΔnkuA::argB, veA). The 50 screening of transformants is performed by picking white spore strains in combination with 51 diagnostic PCR using primers as shown in purple arrows.



73 Figure S2. Phenotypes of control strain and dermatophyte cluster transformants

74 in *A. nidulans*.

Strains were point-inoculated and grown on minimal medium for 3 days at 37 °C. 1: CK
(TWY2.2), 2: TESG_06695 to 6702 (TWY1.1), 3: MCYG_03596 to 3602 (TWY3.3), 4:
TESG_06695 to 6706 (TWY7.1), 5: TESG_06695-6706 (-6696) (TWY8.1), 6: TESG_06695 to
6702 (+6701) (TWY9.1).





Figure S3. LC-MS analysis of *A. nidulans* mutants.

(A) HPLC traces (400 nm) of organic extracts from different strains. Trace 1: isogenic control
(TWY2.2); Trace 2: TESG_06706 to 6695 (-6696) (TWY8.1); Trace 3: TESG_06706 to 6702
(+6701) (TWY9.1); (B) UV absorption of neosartoricin B; (C) Positive and negative masses of
neosartoricin B, m/z 443.0 [M+H]⁺, 465.0 [M+Na]⁺, 441.1 [M-H]⁻.



93 Figure S4. UV absorption and masses of neosartoricins C and D.

94 (A) UV absorption, positive and negative masses of neosartoricin C, m/z 424.9 [M+H]⁺, 423.1
 95 [M-H]⁻; (B) UV absorption, positive and negative masses of neosartoricin D, m/z 424.9 [M+H]⁺,

96 423.1 [M-H].



114 Figure S5. RT-PCR analysis of dermatophyte gene transcription in *A. nidulans*

115 mutants

RT-PCR products were loaded into 1.5 % agarose gel. ANactin from *A. nidulans* was
used for the relative quantification of the cDNA template. Lane M: 100 bp DNA Ladder
(lamda Biotech); lane 1 and 2: TF1 (TESG_06706) and NR-PKS (TESG_06702) from
TWY1.1; lane 3 to 6: TF1, NR-PKS, TESG_06698 and TESG_06701 from TWY7.1;
lane 7 and 8: MCYG_03602 and MCYG_03598 from TWY3.3.

122 Supplementary Tables

Strain/plasmid	Descrption	Reference
RJMP1.49	pyrG89, pyroA4, ΔnkuA::argB, veA	Yin <i>et al.</i> (2)
TWY1.1	pyroA4, pyrG89, Δ wApks::gpdA(p)::TESG_06706 to	This study
	6702::AfpyrG, ∆nkuA::argB, veA	
TWY2.2	pyroA4, pyrG89, \u0355wApks::AfpyrG, \u0355nkuA::argB, veA	This study
TWY3.3	pyroA4, pyrG89, ∆wApks::gpdA(p):: gpdA::MCYG_03602 to	This study
	3596::AfpyrG, ∆nkuA::argB, veA	
TWY7.1	pyroA4, pyrG89, ∆wApks::gpdA(p)::TESG_06706 to	This study
	6702::AfpyrG::TESG_06701 to 6695::AfpyroA, ∆nkuA::argB,	
	veA	
TWY8.1	pyroA4, pyrG89, Δ wApks::gpdA(p)::TESG_06706 to	This study
	6702::AfpyrG::TESG_06701 to 6695(-6696)::AfpyroA,	
	∆nkuA∷argB, veA	
TWY9.1	pyroA4, pyrG89, Δ wApks::gpdA(p)::TESG_06706 to	This study
	6702::AfpyrG::TESG_06701::AfpyroA, ∆nkuA::argB, veA	
pYH-WA-pyrG	URA3, WA flanking, AfpyrG, Amp	This study
pWY13.2	gpdA::TESG_06706 to 6702 in pYH-WA-pyrG	This study
pWY14.1	gpdA::MCYG_03602 to 3596 in pYH-WA-pyrG	This study
pWY15	TESG_06701 to 6695 in pYH-WA-pyrG	This study
pWY16	TESG_06701 to 6695(-6696) in pYH-WA-pyrG	This study
pWY17.1	TESG_06701AfpyroA in pYH-WA-pyrG	This study

123 **Table S1. Fungal strains and plasmids used in this study**

124 pXX = plasmid, TXX = original transformant

Table S2. PCR primer sets utilized in this study

primer primer CatacGaGGCGCGTGTAAGTTACCTCTGGAACAGT Wapks upstream amplification pyrG-wAup-R CATATTTCGTCAGAACACAGAATAACTCTCGCTAGCG ATCAGGAGAAGGAAGGTCAAGTC AfpyrG wAup-pyrG-R GACTTGACCTCTCTCTCTCTCGCTAGCGAGAG TTATTCTGTGTCGAAGGAAGTCACGGCCGCCATA TTCTGTCTCTGCAAGGAAGGCACTG wApks wAdn-pyrG-R TGTCATAGTAAAGTGATTCGCGTCATGCGGCCGCATA TTCTGTCTCTCAGAGAGAGCGCACTG wAPKS geamp-wAdn-F CAGTCCTCTCCTCTCAGACAGAATGGGGCCCGCATAG GGCGAATCACTTTACTATGACA wAPKS pEamp-wAdn-R GTCTTTCCTCGCTATACCCCTGTGCTGTCAGTACG AGACAATACCCTGA wAPKS pVUCA-pEamp-F AGATCTTCGCGTATACTTCGTATAATGTATGGCTCATG AGACAATAACCCTGA gMB1 Ori + AmpR amplification pVUCA-pEamp-F TGGACCCTCATAACTTCGTATAATGTATGGCTCATG AGCACATAACCCTGA CEN/ARS + ura3 amplification wAup-pYUCA-F TCGGGTGTTTGCAGAGAACCGC CCTGTATC gpdA amplification pgdA_F GTCTCCCCAAGGAACCGGC SOE pgdA_R GTCTGCTCATAGAAGATCGC gpdA amplification pgMCY_F GCACCCACAGAAACCGGAC SOE p3MCY_F GAGGATGCGAAGCGCGCACATG SOE p3MCY_F GAGGATGCCGAAACCTGTCTGAGACACACACACCGC MCYG_03602 to 3596 screening <td< th=""><th>Name of the</th><th>Oligonucleotide sequence (5'-3')</th><th>Uses</th></td<>	Name of the	Oligonucleotide sequence (5'-3')	Uses
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pyrG-wAup-RCATATTTCGTCAGACACAGAATAACTCTCGCTAGCG ATCAGGAGAGGAGAGAGAGTCAAGTCwAup-pyrG-RGACTTGACTCTCTTCTCTGTGTCGCAGAGAGA TTATTCTGTGTCTGACGAAGGAGCCCGCA TTCGTCTGAGAGAGGGCACTGAfpyrG amplificationwAdn-pyrG-RTGTCATAGTAAAGTGATTCGCGTCGCGCCGCAT CGCGAATCACATTTACTAGACAwAPKS downstream amplificationpEamp-wAdn-RGTTCTTTCCTGCGTATCGCACAGAGAGAGCACGGGGATAACGC CGAAGATCT CGAAGATCTwAPKS downstream amplificationpYUCA-pEamp-FAGACTCTCGCGTACTGACAGCACAGGGGATAACGC CGAAGATCTpMB1 Ori + AmpR amplificationpYUCA-pEamp-RTGGACCCTGATACTTCGTATAATGTATGGCTCATG AGCAATAACCCTGAcEN/ARS + ura3 amplificationpYUCA-PEAmp-RTGGACCCTGATACTCCATGAGCCATACATTATACGA GCGCGAGCTGTTCCAGAGGTAACTTCACGCGgpdA amplificationpgpdA_FGTCTGCTCATAGAAGATCGC CTCGTATCgpdA amplificationpgpdA_FGTCTGCTCATAGAAGATCGC CTCGTATCgpdA amplificationpgpdA_RTTTGGTTTCGAGACGGAC CTGGTATCSOEPCR for MCYG_03602 to 3596 amplificationpMCY_FCGCTGCAGAAACCTGCGAAGCCGGAC CTAGCCTATGTCTCAGACACAGAACAGAATAACTCTCG CTAGCCTATGTCTAGAACAGAACCGGTCSOEPCR for MCYG_03602 to 3596 screeningpMCY_FCGCTGCAGAAACCTGCGTCATCAGAGAACGGCTGACAATG pMCY_FGCACCAACACATATTTCGCGACAACAGAATAACTCTCG CTAGCCTATGTCTAGCGGTCSOEPCR for TCCAGCGCTGGCGTCTTTCGGAGAGCpMCY_FCGACCTGAGGAAACTGCGGTC CTAGCCTATGTCTGCCGCGTCGTTTC SCESOEPCR for TCCAGCGCGCGCAAACCSOEpMCY_FCGACGCGCGCGCGCGCGGAAGGTGCCGAAAC CTGCCGCGTCGTCGCGCGCGTTTGGAGAGCSOEPCR for TCCGGCGGCGCGGAAGCTGCGGTCpMCY_F<	ртоса-мацр-г	CTCGCCGT	amplification
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Wathpeanip-FAGAAGAACAGGAAGGAACamplificationpYUCA-pEamp-RTGGACCCTGATAACTTCGTATAATGTATGGCTCATG AGACAATAACCCTGAamplificationpEamp-pYUCA-FTCAGGGTTATTGTCTCATGAGCCATACATTATACGA AGTTATCAGGGTCCACEN/ARS + ura3 amplificationwAup-pYUCA-RACGGCGAGACTGTTCCAGAGGTAACTTACACGCGC CTCGTATCgpdA_FpgpdA_FGTCTGCTCATAGAAGATCGCgpdA amplificationpgpdA_RTTTGGTTTCGTTTCTCCATGTCCGGTTCTGTGCTGA ATAGCGATTAAAGGTTCTTGGATGgpdA amplificationp1MCY_FCTATTCAGCACAGAACCGGACSOE PCR forp1MCY_FGCATCCACAGCTACAGAGCAG3596 amplificationp2MCY_FGAGGATGCGGAAGCTGACAATG3596 amplificationp3MCY_FGAGGATGCGGAAGCTGACAATGMCYG_03602 top3MCY_FGAGGATGCGGAAGCTGACAATG3596 screeningpSkr1_FCAACCTGAGGAAACCTGTCGAGMCYG_03602 topScr1_FCAACCTGAGGAAACTGCGGTCMCYG_03602 topScr2_FCTCTCTGGCCGGTCATTCAGAGCACAGAATAACTCTCGSOE PCR forpScr2_RGCTTTCTGAAGCGCTGGTTTTGGGGCCTCGTTTCSOE PCR forpgpdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGGCCTCGTTTCSOE PCR forp3TTR_FGAAGGGTGTTCGACGGGCC6702 amplificationp1TTR_RCAAGAGGCTGTCGACGGGC6702 amplificationp1TR_RCAAGAGGCTGTTCGACGGTC6702 amplificationp1TR_RCAAGAGGCTGTTCGACGGTC6702 amplificationp1TR_RCAAGAGGCTGTTCGACGGCC6702 amplificationp1TR_RCAAGAGGCTGTTCGACGGCC6702 amplificationp1TR_RCAAGAGGTGTATGACTGGGAG6702 amplification	wada a Fama F		nMD1 Ori I AmnD
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AGACAATAACCCTGApEamp-pYUCA-FTCAGGGTTATTGTCTCATGAGCCATACATTATACGA AGTTATCAGGGTCCACEN/ARS + ura3 amplificationwAup-pYUCA-RACGCCGAGACTGTTCCAGAGGTAACTTACACGCGC CTCGTATCgpdA_FpgpdA_FGTCTGCTCATAGAAGATCGCgpdA amplificationpgpdA_RTTTGGTTTCGTTCTCCATGTCCGGTCTGTGCGGAgpdA amplificationp1MCY_FCTATTCAGCACAGAACCGGACSOEp2MCY_RGGCTGTGTTTGAGAAGATAAGGCMCYG_03602 to 3596 amplificationp3MCY_FGAGGATGCGGAAGCTGACAAGG3596 amplificationp3MCY_FGAGGATGCGGAAGCTGACAATG3596 amplificationp3MCY_FGAGGATGCGGAAGCTGACAATG3596 amplificationp3MCY_FGAGGATGCGGAAGCTGACAATG3596 amplificationp3MCY_FGAGGATGCGGAAGCTGCACAATGMCYG_03602 to 3596 amplificationp3MCY_FGAGGATGCGGAAGCTGCTGCAGACACGGAACACGGAACACGGAACACGCACAGAAACTGCTCGMCYG_03602 to 3596 amplificationpScr1_FCGCTCATGTCTACGCGAAGCTGCGTCMCYG_03602 to 3596 screeningpScr2_FCTCTGGCCCGTCATTTCCGCGMCYG_03602 to 3596 screeningpScr2_RGCTTTCTGAAGCGCTGGAATGSOEpScr2_RGCTTTCTGAAGCGCTGGCATTGGATGSOEpGAdttr_RGAGCAGCTTGCTGCCGCCGTCGTTTTGGGATGSOEp1TTR_FATGGAAAACGAGGCCCAAAAC6702 amplificationp1TTR_RCAAGAGGTGTATGACTTGGGAG502p2TTR_FGGAAGTGTATGACTGGGAG502p2TTR_FCATGCTGTTCCAAATGGCGAAC6702 amplificationp1TTR_RCAAGGTGTATGACTGGGAG502p2TTR_FCATGCTGTTCCAAATGGCGAAC6702 amplif	pYUCA-pEamp-R	TGGACCCTGATAACTTCGTATAATGTATGGCTCATG	
pEamp-pYUCA-FTCAGGGTTATTGTCTCATGAGCCATACATTATACGA AGTTATCAGGGTCCACEN/ARS + ura3 amplificationwAup-pYUCA-RACGGCGAGACTGTTCCAGAGGTAACTTACACGCGC CTCGTATCgpdA_CTTACAGGGTCCAgpdA amplificationpgpdA_FGTCTGCTCATAGAAGATCGC ATAGCGATTAAAGGTTCTTGGATGgpdA amplificationp1MCY_FCTATTCAGCACAGAACCGGACSOE PCR forp1MCY_RCGGCTGTGTTTGAGAACAGAGCAG CGCTCATCCACAGCTACAGAGCCGGACSOE PCR forp2MCY_FGCATCCACAGCTACAGAGCAGG3596 amplificationp3MCY_FGAGGATGCGGAAGCTGACAATG p3MCY_RGCCTCATGTCAGAGCAGGACp4MCY_FCGCTGCAGAAACTGTCTGCG CTAGCTATGTCTACGAGCACGGACMCYG_03602 top3MCY_RGCCTCATGTTCAGAGCATGAC CTAGCTATGTCTTACGAGCATGACMCYG_03602 top3MCY_FGAGGATGCGGAAACTGCTGCCG CTAGCTATGTCTTACCGATCTGCMCYG_03602 topScr1_FCAACCAACATATTTCGTCAGACACAGAATAACTCTCG CTAGCCTATGTCTTACCGGTCMCYG_03602 topScr2_RGCTTTCTGAAGCGCTGGAATG PgpdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGGCCTCGTTTC TCCATCGATTAAAGGTTCTTGGATGSOE PCR forpStTR_FGAAGAGGTGTTCGACGGTCSOE PCR forp2TTR_RCAAGAGGCTGTTCGACGGTC50E PCR forp2TTR_FGGAAGTGTGTATGACTTGGGAG6702 amplificationp3TTR_FCATGCTGTTCCAAATGGCGAAC6702 amplification		AGACAATAACCCTGA	
wAup-pYUCA-RACGGCGAGACTGTTCCAGAGGTAACTTACACGCGC CTCGTATCannpinicationpgpdA_FGTCTGCTCATAGAAGATCGCgpdA amplificationpgpdA_RTTTGGTTTCGTTTCTCCATGTCCGGTTCTGTGCTGA ATAGCGATTAAAGGTCTTGGATGgpdA amplificationp1MCY_FCTATTCAGCACAGAACCGGACSOEp2MCY_FGCATCCACAGCTACAGAGCCGGACSOEp3MCY_FGAGGATGCGGAAGCTGACAATGp3MCY_FGAGGATGCGGAAGCTGACAATGp4MCY_FCGCTCACAGCTGCGAAGCTGACAATGp3MCY_RGCCTCATGTTCAGAGCACAGAATAACTCTCGp4MCY_FCGCTGCAGAAACCTGTCTGAGp4MCYPRCCACCACACATATTTCGTCAGACACAGAATAACTCTCGp5cr1_FCAACCAGGAACTGCGTCpScr2_FCTCTGGCCCGTCATTCAATCpScr2_RGCTTTCTGAAGCGCTGGAATGpgpdAttr_RGAGCAGCTTGCCGCGTCGTTTGGGCCTCGTTCp1TTR_FATGGAGAAACGGGCCAAAACp1TTR_RCAAGAGGCTGTCGACGGTCp2TTR_FGGAAGTGTATGACTGGGAGp2TTR_FCATGCTGTTCGAAGCACAAGAACCp2TTR_FCATGCTGTTCCAAATGGCGAACp2TTR_FCATGCTGTTCCAAATGGCGAACp2TTR_FCATGCTGTTCCAAATGGCGAAC	pEamp-pYUCA-F	TCAGGGTTATTGTCTCATGAGCCATACATTATACGA	CEN/ARS + ura3
CTCGTATCgpdA_FGTCTGCTCATAGAAGATCGCgpdA amplificationpgpdA_RTTTGGTTTCGTTTCGTTCCCATGTCCGGTTCTGTGCTGA ATAGCGATTAAAGGTTCTTGGATGTTGGTGTGCGTGGTTGGTGGAGAGAGGGAGSOE PCR forp1MCY_FCTATTCAGCACAGAACCGGACSOE PCR forMCYG_03602 top2MCY_FGCATCCACAGCTACAGAGCAG3596 amplificationp2MCY_FGAGGATGCGGAAGCTGACAGAGCAG3596 amplificationp3MCY_FGAGGATGCGGAAGCTGACAGGACAATGJampa and a complete and a com	wAup-pYUCA-R	ACGGCGAGACTGTTCCAGAGGTAACTTACACGCGC	amplification
pgpdA_FGTCTGCTCATAGAAGATCGCgpdA amplificationpgpdA_RTTTGGTTTCGTTTCGTTGTCCGGTTCTGTGCTGA ATAGCGATTAAAGGTTCTTGGATGSOEPCRforp1MCY_FCTATTCAGCACAGAACCGGACSOEPCRforp1MCY_RCGGCTGTGTTTGAGAATAAGGCMCYG_03602top2MCY_FGCATCCACAGCTACAGAGCAG3596 amplificationp2MCY_FGAGGATGCGGAAGCTGACAGAGCAG3596 amplificationp3MCY_FGAGGATGCGGAAGCTGACAATGp3MCY_RGCCTCATGTTCAGAGCATGACp4MCY_FCGCTGCAGAAACCTGCTCTGAGp4MCY_FCGCTGCAGGAAACCTGCGTCp5cr1_FCAACCTGAGGAAACTGCGTCpScr2_FCTCTGGCCCGTCATTCAATCp5cr2_RGCTTTCTGAAGCGCGGGAATGpgpdAttr_RCAAGCAGCTTGCTGCGCGTCGTTTTGGATGGp4TTR_FATGGAGAAACGAGGCCCAAAACp1TTR_RCAAGAGGCTGTTCGACGGTCp3TTR_FCATGCTGTATGAAGAACCTGGGAG		CTCGTATC	
pgpdA_RTTTGGTTTCGTTTCGCATGTCCGGTTCTGTGCTGA ATAGCGATTAAAGGTTCTTGGATGp1MCY_FCTATTCAGCACAGAACCGGACSOE PCR forp1MCY_RCGGCTGTGTTTGAGAATAAGGCMCYG_03602 top2MCY_FGCATCCACAGCTACAGAGCAG3596 amplificationp2MCY_FGCATCCACAGCTACAGAGCAG3596 amplificationp3MCY_FGAGGATGCGGAAGCTGACAATGp3MCY_FCGCTCATGTTCAGAGCATGACp4MCY_FCGCTGCAGAAACCTGTCTGAGp4MCYpyrG_RACACAACATATTTCGTCAGACACAGAATAACTCTCG CTAGCCTATGTCTTACCGATCTGCpScr1_FCAACCTGAGGAAACTGCGTCpScr2_FCTCTGGCCCGTCATTCAATCpScr2_RGCTTTCTGAAGCGCTGGAATGpgpdAttr_RGAGCAGCTTGCACGGTCCp1TTR_FATGGAGAAACGAGGCCCAAAAACp1TTR_RCAAGAGGCTGTTCGACGGTCp2TTR_FGGAAGTGTGTATGACTTGGGAGp2TTR_RCAAGGGTAGCAAGAAACCGATCp3TTR_FCATGCTGTTCCAAATGGCGAAC	pgpdA_F	GTCTGCTCATAGAAGATCGC	gpdA amplification
p1MCY_FCTATTCAGCACAGAACCGGACSOEPCRforp1MCY_RCGGCTGTGTTTGAGAATAAGGCMCYG_03602top2MCY_FGCATCCACAGCTACAGAGCAG3596 amplificationp2MCY_RGTGTAGCACTTGTCGGTAGTTGp3MCY_FGAGGATGCGGAAGCTGACAATGp3MCY_FCGCTGCAGAAACCTGTCTGAGp4MCY_FCGCTGCAGAAACCTGTCTGAGp4MCY_FCGCTGCAGAAACCTGTCTGAGp4MCY_FCGCTGCAGAAACCTGTCTGCp5cr1_FCAACCAACATATTTCGTCAGACACAGAATAACTCTCGpScr2_FCTATCTCGATCTTTTCCGCGpScr2_RGCTTTCTGAAGCGCTGGAATGpgdAttr_RGAGCAGCTTGCTGCGCGTCGTTTTGGGCCTCGTTTC TCCATCGATTAAAGGTTCTTGGATGp1TTR_FATGGAGAAACGAGGCCCAAAACp1TTR_RCAAGAGGCTGTTCGACGGTCp2TTR_RCGATGGTAGCAAGAATCCGATCp2TTR_RCGATGGTAGCAAGAATCCGATCp3TTR_FCATGCTGTTCCAAATGGCGAAC	pgpdA_R	TTTGGTTTCGTTTCTCCATGTCCGGTTCTGTGCTGA ATAGCGATTAAAGGTTCTTGGATG	
p1MCY_RCGGCTGTGTTTGAGAATAAGGCMCYG_03602 to 3596 amplificationp2MCY_FGCATCCACAGCTACAGAGCAG3596 amplificationp2MCY_RGTGTAGCACTTGTCGGTAGTTG93MCY_Fp3MCY_FGAGGATGCGGAAGCTGACAATG94MCY_FcGCTCATGTTCAGAGCATGACCTAGCCTATGTTCAGAGCATGACp4MCY_FCGCTGCAGAAACCTGTCTGAGp4MCYpyrG_RACACAACATATTTCGTCAGACACAGAATAACTCTCGp5cr1_FCAACCTGAGGAAACTGCGTCpScr1_RCTATCTCGATCTTTCCGCGpScr2_FCTCTGGCCCGTCATTCAATCpScr2_RGCTTTCTGAAGCGCTGGAATGpgpdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGACGp1TTR_FATGGAGAAACGAGGCCCAAAACp1TTR_FGGAAGGGTGTTCGACGGTCp2TTR_FGGAAGTGTGTATGACTTGGGAGp2TTR_RCATGCTGTTCCAAATGGCGAACp3TR_FCATGCTGTTCCAAATGGCGAAC	p1MCY F	CTATTCAGCACAGAACCGGAC	SOE PCR for
p2MCY_FGCATCCACAGCTACAGAGCAG3596 amplificationp2MCY_RGTGTAGCACTTGTCGGTAGTTGp3MCY_FGAGGATGCGGAAGCTGACAATGp3MCY_RGCCTCATGTTCAGAGCATGACp4MCY_FCGCTGCAGAAACCTGTCTGAGp4MCYpyrG_RACACAACATATTTCGTCAGACACAGAATAACTCTCGp5cr1_FCAACCTGAGGAAACTGCGTCMCYG_03602 top5cr2_FCTCTGGCCCGTCATTCAATCp5cr2_RGCTTTCTGAAGCGCTGGAATGpgpdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGCCTCGTTTCp1TTR_FATGGAGAAACGAGGCCCAAAAC6702 amplificationp1TTR_FGGAGGTGTGTATGACTTGGGAGp2TTR_FGGAAGTGTGTATGACTTGGGAGp2TTR_FCATGCTGTTCCAAATGGCGAACp3TTR_FCATGCTGTTCCAAATGGCGAAC	p1MCY_R	CGGCTGTGTTTGAGAATAAGGC	MCYG_03602 to
p2MCY_RGTGTAGCACTTGTCGGTAGTTGp3MCY_FGAGGATGCGGAAGCTGACAATGp3MCY_RGCCTCATGTTCAGAGCATGACp4MCY_FCGCTGCAGAAACCTGTCTGAGp4MCYpyrG_RACACAACATATTTCGTCAGACACAGAATAACTCTCGcTAGCCTATGTCTTACCGATCTGCMCYG_03602 topScr1_FCAACCTGAGGAAACTGCGTCpScr2_FCTCTGGCCCGTCATTCAATCpScr2_RGCTTTCTGAAGCGCTGGAATGpgpdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGCCTCGTTTCp1TTR_FATGGAGAAACGAGGCCCAAAACp1TTR_FGAGAGGCTGTATGACTGGGAGp2TTR_FGGAAGTGTGTATGACTTGGGAGp2TTR_FCATGCTGTCCAAATGGCGAACp3TTR_FCATGCTGTTCCAAATGGCGAAC	p2MCY_F	GCATCCACAGCTACAGAGCAG	3596 amplification
p3MCY_FGAGGATGCGGAAGCTGACAATGp3MCY_RGCCTCATGTTCAGAGCATGACp4MCY_FCGCTGCAGAAACCTGTCTGAGp4MCYpyrG_RACACAACATATTTCGTCAGACACAGAATAACTCTCGpScr1_FCAACCTGAGGAAACTGCGTCpScr1_RCTATCTCGATCTTTCCGCGpScr2_FCTCTGGCCCGTCATTCAATCpScr2_RGCTTTCTGAAGCGCTGGAATGpgdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGCCCGTCGTTTCp1TTR_FATGGAGAAACGAGGCCCAAAACp1TTR_RCAAGAGGCTGTTCGACGGTCp2TTR_FGGATGGTAGCAAGAATCCGATCp3TTR_FCATGCTGTTCCAAATGGCGAAC	p2MCY_R	GTGTAGCACTTGTCGGTAGTTG	
p3MCY_RGCCTCATGTTCAGAGCATGACp4MCY_FCGCTGCAGAAACCTGTCTGAGp4MCYpyrG_RACACAACATATTTCGTCAGACACAGAATAACTCTCGpScr1_FCAACCTGAGGAAACTGCGTCpScr1_RCTATCTCGATCTTTCCGCGpScr2_FCTCTGGCCCGTCATTCAATCpScr2_RGCTTTCTGAAGCGCTGGAATGpgpdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGCCTCGTTTCp1TTR_FATGGAGAAACGAGGCCCAAAACp1TTR_FGGAAGTGTGTATGACTTGGGAGp2TTR_FGGAAGTGTGTATGACTTGGGAGp2TTR_FCAAGGGTAGCAAGAATCCGATCp3TTR_FCATGCTGTTCCAAATGGCGAAC	p3MCY_F	GAGGATGCGGAAGCTGACAATG	
p4MCY_FCGCTGCAGAAACCTGTCTGAGp4MCYpyrG_RACACAACATATTTCGTCAGACACAGAATAACTCTCG CTAGCCTATGTCTTACCGATCTGCpScr1_FCAACCTGAGGAAACTGCGTCpScr1_RCTATCTCGATCTTTTCCGCGpScr2_FCTCTGGCCCGTCATTCAATCpScr2_RGCTTTCTGAAGCGCTGGAATG PgpdAttr_RpgdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGCCTCGTTTC TCCATCGATTAAAGGTTCTTGGATGp1TTR_FATGGAGAAACGAGGCCCAAAACp1TTR_RCAAGAGGCTGTTCGACGGTCp2TTR_FGGAAGTGTGTATGACTTGGGAGGp2TTR_FCGATGGTAGCAAGAATCCGATCp3TTR_FCATGCTGTTCCAAATGGCGAAC	p3MCY_R	GCCTCATGTTCAGAGCATGAC	
p4MCYpyrG_RACACAACATATTTCGTCAGACACAGAATAACTCTCG CTAGCCTATGTCTTACCGATCTGCpScr1_FCAACCTGAGGAAACTGCGTCMCYG_03602 to 3596 screeningpScr1_RCTATCTCGATCTTTTCCGCG3596 screeningpScr2_FCTCTGGCCCGTCATTCAATCpScr2_RpgdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGGCCTCGTTTC TCCATCGATTAAAGGTTCTTGGATGSOEp1TTR_FATGGAGAAACGAGGCCCAAAAC6702 amplificationp1TTR_FGGAAGTGTGTATGACTTGGGAG6702 amplificationp2TTR_FGGAAGTGTGTATGACTTGGGAGp3TTR_FCATGCTGTTCCAAATGGCGAACCATGCTGTTCCAAATGGCGAAC	p4MCY_F	CGCTGCAGAAACCTGTCTGAG	
pScr1_FCAACCTGAGGAAACTGCGTCMCYG_03602 topScr1_RCTATCTCGATCTTTTCCGCG3596 screeningpScr2_FCTCTGGCCCGTCATTCAATCpScr2_RpgpdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGCCTCGTTTCSOE PCR forrCCATCGATTAAAGGTTCTTGGATGTESG_06706 top1TTR_FATGGAGAAACGAGGCCCAAAAC6702 amplificationp1TTR_FGGAAGTGTGTATGACTTGGGAG6702 amplificationp2TTR_FGGAAGTGTGTATGACTTGGGAGp2TTR_RcAAGAGGCTGTTCCAAAGAATCCGATCp3TTR_FCATGCTGTTCCAAATGGCGAAC	p4MCYpyrG_R	ACACAACATATTTCGTCAGACACAGAATAACTCTCG	
pScr1_RCTATCTCGATCTTTTCCGCG3596 screeningpScr2_FCTCTGGCCCGTCATTCAATCpScr2_RpgpdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGCCTCGTTTCSOEp2TTR_FATGGAGAAACGAGGCCCAAAAC6702 amplificationp1TTR_FGGAAGTGTGTATGACTTGGGAG6702 amplificationp2TTR_FGGAAGTGTGTATGACTTGGGAG22TTR_Fp3TTR_FCATGCTGTTCCAAATGGCGAAC5702 amplification	pScr1 F	CAACCTGAGGAAACTGCGTC	MCYG 03602 to
pScr2_FCTCTGGCCCGTCATTCAATCpScr2_RGCTTTCTGAAGCGCTGGAATGpgpdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGCCTCGTTTCp1TTR_FATGGAGAAACGAGGCCCAAAACp1TTR_RCAAGAGGCTGTTCGACGGTCp2TTR_FGGAAGTGTGTATGACTTGGGAGp2TTR_RCGATGGTAGCAAGAATCCGATCp3TTR_FCATGCTGTTCCAAATGGCGAAC	pScr1_R	CTATCTCGATCTTTTCCGCG	3596 screening
pScr2_RGCTTTCTGAAGCGCTGGAATGpgpdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGCCTCGTTTCDTTR_FGAGCAGCTTGCTGCCGTCGTTTGGATGp1TTR_RATGGAGAAACGAGGCCCAAAACp1TTR_RCAAGAGGCTGTTCGACGGTCp2TTR_FGGAAGTGTGTATGACTTGGGAGp2TTR_RCGATGGTAGCAAGAATCCGATCp3TTR_FCATGCTGTTCCAAATGGCGAAC	pScr2_F	CTCTGGCCCGTCATTCAATC	
pgpdAttr_RGAGCAGCTTGCTGCCGTCGTTTTGGGCCTCGTTTC TCCATCGATTAAAGGTTCTTGGATGSOE TESG_06706PCR for TESG_06706for TESG_06706p1TTR_FATGGAGAAACGAGGCCCAAAAC6702 amplificationp1TTR_RCAAGAGGCTGTTCGACGGTC6702 amplificationp2TTR_FGGAAGTGTGTATGACTTGGGAG2p2TTR_RCGATGGTAGCAAGAATCCGATC2p3TTR_FCATGCTGTTCCAAATGGCGAAC2	pScr2 R	GCTTTCTGAAGCGCTGGAATG	
TCCATCGATTAAAGGTTCTTGGATGTESG_06706top1TTR_FATGGAGAAACGAGGCCCAAAAC6702 amplificationp1TTR_RCAAGAGGCTGTTCGACGGTCp2TTR_FGGAAGTGTGTATGACTTGGGAGp2TTR_RCGATGGTAGCAAGAATCCGATCp3TTR_FCATGCTGTTCCAAATGGCGAAC	pgpdAttr_R	GAGCAGCTTGCTGCCGTCGTTTTGGGCCTCGTTTC	SOE PCR for
p1TTR_FATGGAGAAACGAGGCCCAAAAC6702 amplificationp1TTR_RCAAGAGGCTGTTCGACGGTCp2TTR_FGGAAGTGTGTATGACTTGGGAGp2TTR_RCGATGGTAGCAAGAATCCGATCp3TTR_FCATGCTGTTCCAAATGGCGAAC		TCCATCGATTAAAGGTTCTTGGATG	TESG_06706 to
p1TTR_RCAAGAGGCTGTTCGACGGTCp2TTR_FGGAAGTGTGTATGACTTGGGAGp2TTR_RCGATGGTAGCAAGAATCCGATCp3TTR_FCATGCTGTTCCAAATGGCGAAC	p1IIR_F	AIGGAGAAACGAGGCCCAAAAC	6702 amplification
p2TTR_F GGAAGTGTGTATGACTTGGGAG p2TTR_R CGATGGTAGCAAGAATCCGATC p3TTR_F CATGCTGTTCCAAATGGCGAAC	p1TTR_R	CAAGAGGCTGTTCGACGGTC	
p2TTR_R CGATGGTAGCAAGAATCCGATC p3TTR_F CATGCTGTTCCAAATGGCGAAC	p2TTR_F	GGAAGTGTGTATGACTTGGGAG	
p3TTR_F CATGCTGTTCCAAATGGCGAAC	p2TTR_R	CGATGGTAGCAAGAATCCGATC	
. –	p3TTR_F	CATGCTGTTCCAAATGGCGAAC	
p3TTR_R GCATTCGACGAGAAGACGTAG	p3TTR_R	GCATTCGACGAGAAGACGTAG	
p4TTR_F GCACGGAAGATCGTATCACTC	p4TTR_F	GCACGGAAGATCGTATCACTC	
p411RpyrG_R CACAACATATTTCGTCAGACACAGAATAACTCTCGC	p4TTRpyrG_R		
p5TTR_F TTGGCATCACGCATCAGTGCCTCCTCAGACAGA SOE PCR for	p5TTR F	TTGGCATCACGCATCAGTGCCTCCTCTCAGACAGA	SOE PCR for

	ATGCATCGGGATTGATTATCAAATG	TESG_06701 to
p5TTR_R	GCATACTTGCCAGAATTTGCAG	6695 amplification
p6TTR_F	CTTACTACAAAAGTCCCTTGC	
p6TTR_R	GTTTCAGTTAATTCTCCCTTTC	
p6AbTv_R	AGGATGCTGATAACTAGTTAACGTAACGGCATGCT	SOE PCR for
	GGAGTTTCAGTTAATTCTCCCTTTC	TESG_06701 to
p7TTR_F	GATATTTATCGTCCGCTGTAAG	6695(-6696)
p7AbTv_F	GCTCTTCTCGCAGCGGGAAAGGGAGAATTAACTGA	amplification
	AACTCCAGCATGCCGTTACGTTAAC	
p7TTR_R	CGTTTATTTACAAACGCCGAACTTGAATACACACCC	
	TGGTCTCGCTAACTAACTAACCAG	
pAfpyroA_F	CGGAGCATCTAGCTAGCTGGTTAGTTAGTTAGCGA	A fumigatus pyroA
	GACCAGGGTGTGTATTCAAGTTCGG	amplification
pAfpyroA_R	CCTTTTCGCCCTTTGTCATAGTAAAGTGATTCGCGT	
	CATGAGTGTTCGCGTTGGCATGCG	
ppyrscr_F	CCAGTCATCTAGCAAGTGAG	screening and
p5Ttscr_R	GGCAAGTGGACAATCTGTTC	sequencing
ppyroscr_F	GTAACATCCTCTTCTGAGATCG	
ppyroscr_R	GATGTCCCTATGAATAAACCCG	
ppyroseq_R	CTGAGACCACTACCCAGTTG	sequencing
pTtDo_F	TGGCATCACGCATCAGTGCCTCCTCTCAGACAGAA	TESG_06701
	TGCCATTGCCCAGGGATTCTATTTC	amplification
pTtDo_R	ACGTTTATTTACAAACGCCGAACTTGAATACACACC	
	CTGGTTTCCTAGAGGTAACTATTG	
pAfpyroAdo_F	TACTTTACTTAACAGATCAATAGTTACCTCTAGGAA	
	ACCAGGGTGTGTATTCAAGTTCGG	
pWAscr_F	GAGTTACGACCGGCCGAATG	transformant
pgpdAscr_R	CACACCAGCCTTTCCACTTC	screening
pWY15Scr_F	GATGCGACATTAGCTCGTG	transformant
pWY15Scr_R	CAGGATCTCGCAGAGAGC	screening
pWY16Scr_R	CGCATCATAATCGTGGAC	
AfpyrG_F	GAGAGTTATTCTGTGTCTGAC	A fumigatus pyroA
AfpyrG_R	CTGTCTGAGAGGAGGCACTG	screening
Tt6698_F	CCCTTTGTCTCCTTGATC	RT-PCR
Tt6698_R	ATGCGCGTCTCGATCATC	RT-PCR
Tt6701_F	CCTTGGGTCGATATTCCAG	RT-PCR
Tt6701_R	CAGATGATGTGAAGGAGC	RT-PCR
Tt6702_F	CCAGGACAGAGTGTTCTC	RT-PCR
Tt6702_R	GTCTGTGTTGCGTTTTCCG	RT-PCR
Tt6706_F	GAGGTCAGAGGATCCAAG	RT-PCR
Tt6706_R	GCTGTCGTCCAAGACCAG	RT-PCR
Mc3598_F	GTTCCATCGCGAACTGTC	RT-PCR
Mc3598_R	CCTGCATCAAAATAGCCTG	RT-PCR
Mc3602_F	CGTATGGACGTTAATGGC	RT-PCR
Mc3602_R	GTGAAAGCTCTGTTGCTG	RT-PCR
ANactin_F	GATCGGTATGGGTCAGAAGGAC	RT-PCR
ANactinM R	CTTCATCAGGTAGTCCGTCAGG	RT-PCR
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Protein				Identity (%)	to genes of				putative function
Trichophyton tonsurans CBS 112818	Trichophyton equinum CBS 127.97	Arthroderma benhamiae CBS 112371	Trichophyton verrucosum HKI 0517	Arthroderma gypseum CBS 118893	Trichophyton rubrum CBS 118892	Arthroderma otae CBS 113480	Neosartorya fischeri NRRL 181	Aspergillus fumigatus Af293	
TESG_06706	TEQG_05350 (100 %)	ARB_00534 (88%)	TRV_00390 (83%)	MGYG_0659 2 (75%)	TERG_08361 (90%)	MCYG_0360 2 (77 %)	NFIA_1122 00 (57%)	AFUA_7G0 0200 (52%)	C6 transcription factor
TESG_06705	TEQG_05349 (100 %)	ARB_00535 (91%)	TRV_00389 (75%)	MGYG_0659 1 (79%)	TERG_08360 (91%)	MCYG_0360 1 (79 %)	NFIA_1122 10 (66%)	AFUA_7G0 0190 (65%)	metallo- β-lactamase- like thioesterase
TESG_06704	TEQG_05348 (41 %)*	ARB_00536 (90%)	TRV_00388 (91%)	MGYG_0659 0 (80%)	TERG_08359 (89%)	MCYG_0360 0 (83 %)	NFIA_1122 20 (67%)	AFUA_7G0 0180 (67%)	flavin-dependent monooxygenase
TESG_06703	TEQG_05347 (99 %)	ARB_00537 (96%)	TRV_00387 (95%)	MGYG_0658 9 (92%)	TERG_08358 (94%)	MCYG_0359 9 (90 %)	NFIA_1122 30 (64%)	AFUA_7G0 0170 (65%)	prenyltransferase
TESG_06702	TEQG_05346 (98 %)	ARB_00538 (94%)	TRV_00386 (93%)	MGYG_0658 8 (88%)	TERG_08357 (94%)	MCYG_0359 8 (89 %)	NFIA_1122 40 (77%)	AFUA_7G0 0160 (76%)	non-reducing polyketide synthase
TESG_06701	TEQG_05345 (71 %)	ARB_00539 (93%)	TRV_00385 (93%)	MGYG_0658 7 (90%)	TERG_08356 (74%)	-	-	-	dioxygenase
TESG_06700	TEQG_05344 (95 %)	ARB_00540 (88%)	TRV_00384 (88%)	MGYG_0886 7 (90%)	-	-	-	-	hypothetical protein
TESG_06699	TEQG_05343 (91 %)	ARB_00541 (88%)	TRV_00383 (88%)	MGYG_0886 6 (76%)	-	-	-	-	major facilitator superfamily transporter
TESG_06698	Poor sequence*	ARB_00542 (97%)	TRV_00382 (96%)	MGYG_0886 5 (95%)	-	-	-	-	asp/glu racemase
TESG_06697	TEQG_05342 (100 %)	ARB_00543 (95%)	TRV_00381 (96%)	MGYG_0886 4 (92%)	-	-	-	-	dioxygenase
TESG_06696	TEQG_05341 (99 %)	-	-	MGYG_0886 1 (42%)	-	-	-	-	glycoside hydrolase
TESG_06695	TEQG_05340 (99 %)	ARB_00544 (90%)	TRV_00380 (90%)	MGYG_0886 0 (91%)	TERG_08355 (94%)	-			alcohol dehydrogenase

Table S3. Genes and enzymes predicted through	n deep bioinformatic annotation	of the putative <i>nrc</i> -like cluster in	n fungi
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* Poor sequencing in the genome database to lead to TEQG_05348 shorter coding region than other FMO homologs.

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		$5 \qquad \bigcirc H_{11}$	12 13 14 15
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no.	$\delta_{\rm H,}$ mult. (J in Hz)	$\delta_{ m C}$	HMBC
1		200.4	
2	4.45, s	76.6	C-1
3		75.5	
4	3.04, d (17.2)	36.4	C-3, C-4a, C-5
-	3.37, d (17.5)	00.1	
4a		140.8	
5		130.2	
5a		125.8	
6	6.61, d, 1.6	100.5	C-5a, C-8
7		160.7	
8	6.32, brs	101.6	C-6, C-7, C-9a
9		160.2	
9a		106.6	
10		163.1	
10a		107.6	
11	2.78, d (15)	46.7	C-3, C-4, C-12
	2.93, d (15)		C-3, C-4, C-12
12		193.2	
13	5.68, s	102.2	C-14, C-15, C-11
14	.	190.4	
15	2.11, s	24.5	C-13, C-14
16	3.42, d (6.3)	27.3	C-4a, C-5, C-5a, C-17
17	4.98.5	121.6	C-20, C-19, C-5
18	1.00, 0	132.8	
19	1.81. s	18.2	C-17, C18, C-20
20	1.69. s	25.8	C-17, C-19, C18
2-0H	2.31 (1H, s)	2010	C-1, C-2
3-OH	6.04 (1H, brs)		
7-OH	n.a		
9-OH	9.79 (1H. s)		C-9, C-8. C-9a
10-OH	14.9 (1H. s)		C-10, C-9a. C-9
14-OH(a)	15.37 (1H, brs)		,,

Table S4. NMR assignment for neosartoricin B in CDCI₃ (500 MHz)

n.a: not assigned

	2 HO 9	$\begin{array}{c} 19 \\ 17 \\ 6 \\ 54 \\ 98 \\ 10 \\ 10 \\ 10 \\ 10 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0$	D 12 14 0 15 H
		c	
no.	$\partial_{\rm H_{\rm i}}$ mult. (J in Hz)		HMBC
1	4.45	199.2	
2	4.45, S	76.2	C-1
3		84.6	
4	2.69, d (17.0)		C-5, C-4a
	3.86, d (17.0)	32.4	C-3, C-2, C-10a, C-5, C- 4a
4a		129.3	
5		125.0	
5a		140.8	
6	6 75 d (2 1)	100.5	C-8 C-9a C-7 C-5
7		160.6	
8	652 d(21)	102.0	C-6 C-9a C-9
9	0.02, 4 (2.1)	161.0	
92		107.8	
10		163.0	
10		105.0	
10a	2 42 4 (16 4)	100.5	C 12 C 4
	2.43, 0(10.4)	41.0	
40	3.44, 0 (16.4)	404.0	0-12, 0-4, 0-3, 0-2
12	5.04 -	191.3	0.44.0.45
13	5.34, S	103.9	<u> </u>
14		172.1	
15	1.73, s	21.1	C-14, C-13
16	3.38, m	27.2	C-18, C-4a, C-17, C5, C5a
17	4.82, m	121.1	C-5, C-19, C-20
18		133.4	
19	1.78, s	18.3	
20	1.66. s	25.7	
10-OH	14.86. s	-	C-10, C-10a, C-9a
9-OH	9.85, s		C-9, C9a, C-8

Table S5. NMR assignment for neosartoricin C in CDCI₃ (500 MHz)

n.a: not assigned

Table S6. NMR assignment for neosartoricin D in CDCI₃ (500 MHz)

	20 19 18 17 16 HO 7 6 54 4 4 3 9 9 10 10 10 1 2 9 0H OH OH OH	11 12 11 12 13 14 15
no.	$\delta_{\rm H,}$ mult. (J in Hz)	$\delta_{ m C}$
1		203.6
2	4.46, s	80.5
3		78.3
4	2.99, d (17.6) 3.63, d (17.6)	32.2
4a		128.9
5		125.2
5a		141.5
6	6.69. d (2.1)	100.9
7		160.9
8	6.46. d (2.1)	101.7
9		162.0
9a		108.2
10		168.9
10a		106.2
11	2.59. d (16.8)	51.1
	2.76. d (16.8)	-
12		196.3
13	2.70, s	50.1
14	,	108.6
15	1.72. s	24.6
16	3.48. m	27.4
17	4.99. t (6.7)	121.2
18		133.4
19		
20	1.85, s	18.4
40.011	1.85, s 1.51, s	18.4 25.8
10-OH	1.85, s 1.51, s n.a	18.4 25.8
9-OH	1.85, s 1.51, s n.a 10.4, s	18.4 25.8

n.a: not assigned

Supplementary NMR spectra for neosartoricin B





assignments)





¹H-¹³C HMBC spectrum of neosartoricin B in CDCl₃ measured on 500 MHz Bruker NMR spectrometer (see Table S4 for peak assignments)





assignments)



assignments)



peak assignments)



peak assignments)

Supplementary NMR spectra for neosartoricin D



assignments)



¹³C-NMR spectrum of neosartoricin D in CDCI₃ measured on 500 MHz Bruker NMR spectrometer (see Table S6 for peak assignments)



Supplementary References

- 1. Colot, H. V., Park, G., Turner, G. E., Ringelberg, C., Crew, C. M., Litvinkova, L., Weiss, R. L., Borkovich, K. A., and Dunlap, J. C. (2006) A high-throughput gene knockout procedure for *Neurospora* reveals functions for multiple transcription factors, *Proc Natl Acad Sci U S A 103*, 10352-10357.
- 2. Yin, W. B., Amaike, S., Wohlbach, D. J., Gasch, A. P., Chiang, Y. M., Wang, C. C., Bok, J. W., Rohlfs, M., and Keller, N. P. (2012) An *Aspergillus nidulans* bZIP response pathway hardwired for defensive secondary metabolism operates through *aflR*, *Mol. Microbiol.* 83, 1024-1034.