

## **Supporting Information**

### **A chromatogram-simplified *Streptomyces albus* host for heterologous production of natural products**

Asif Fazal<sup>1,2,3†</sup>, Divya Thankachan<sup>1,3†</sup>, Ellie Harris<sup>1,3</sup>, Ryan F. Seipke<sup>1,3\*</sup>

<sup>1</sup>School of Molecular and Cellular Biology, <sup>2</sup>School of Chemistry, <sup>3</sup>Astbury Centre for Structural Molecular Biology, University of Leeds, Leeds, LS2 9JT, United Kingdom

†Authors contributed equally to this work

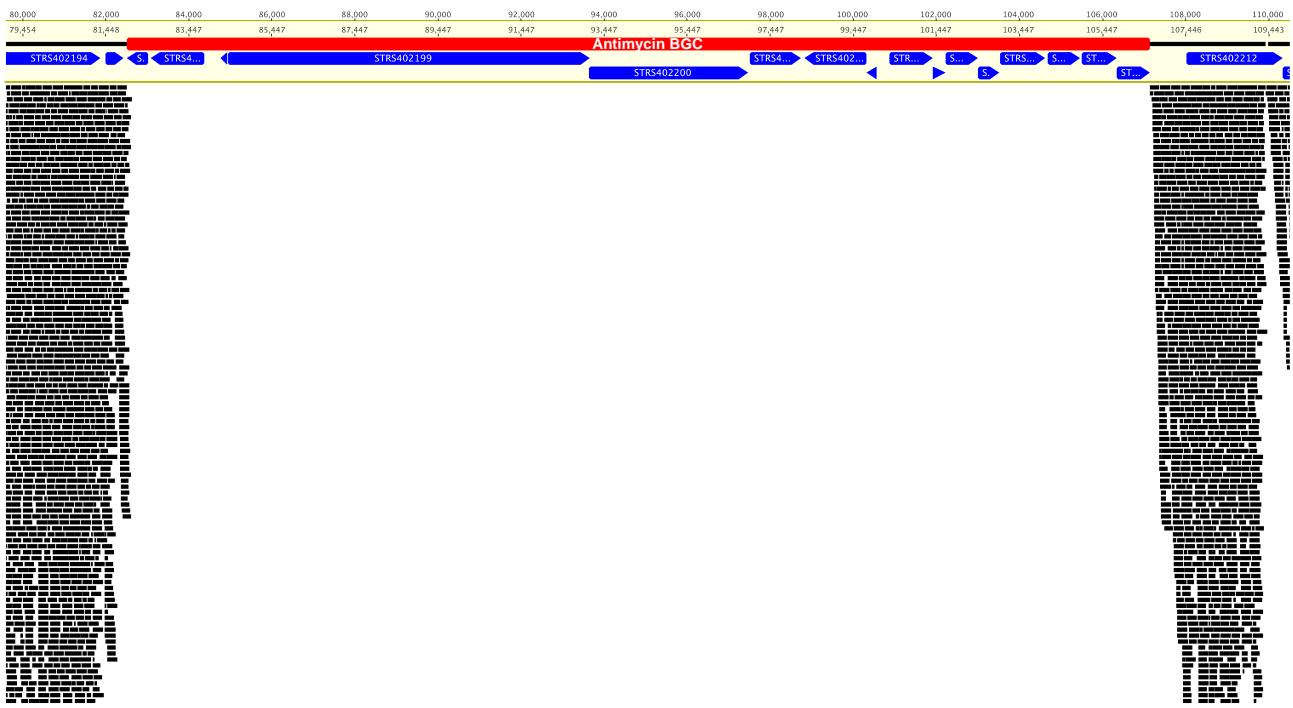
\*Correspondence:

E-mail: [r.seipke@leeds.ac.uk](mailto:r.seipke@leeds.ac.uk)

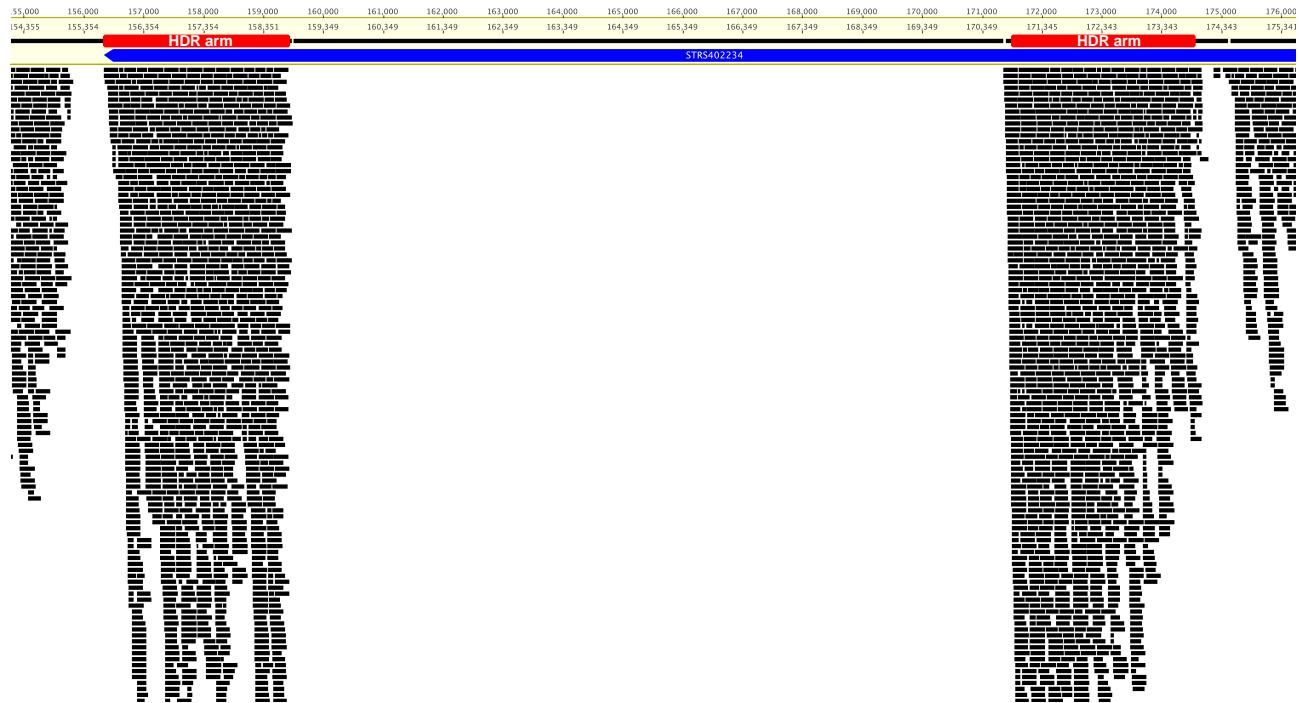
## Table of Contents

### Supporting figures and tables

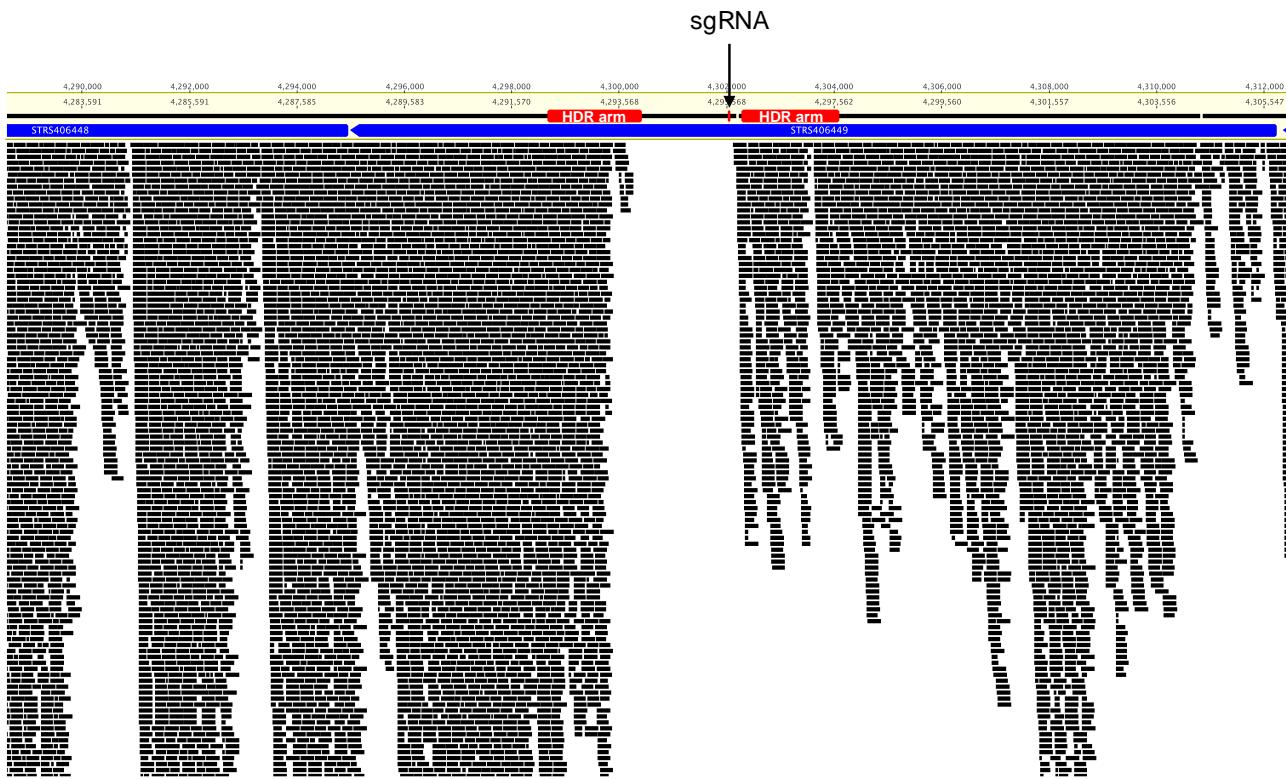
- Figure S1.** Illumina read mapping to the antimycin BGC in *S. albus* S4 Δ5.  
**Figure S2.** Illumina read mapping to the candicidin BGC in *S. albus* S4 Δ5.  
**Figure S3.** Illumina read mapping to the albaflavenone BGC in *S. albus* S4 Δ5.  
**Figure S4.** Illumina read mapping to the surugamide BGC in *S. albus* S4 Δ5.  
**Figure S5.** Illumina read mapping to the fredericamycin BGC in *S. albus* S4 Δ5.  
**Figure S6.** Full scale HPLC trace for *S. albus* S4 WT and *S. albus* S4 Δ5.  
**Table S1.** Bacterial strains, cosmids and plasmids.  
**Table S2.** Oligonucleotide primers used in this study.



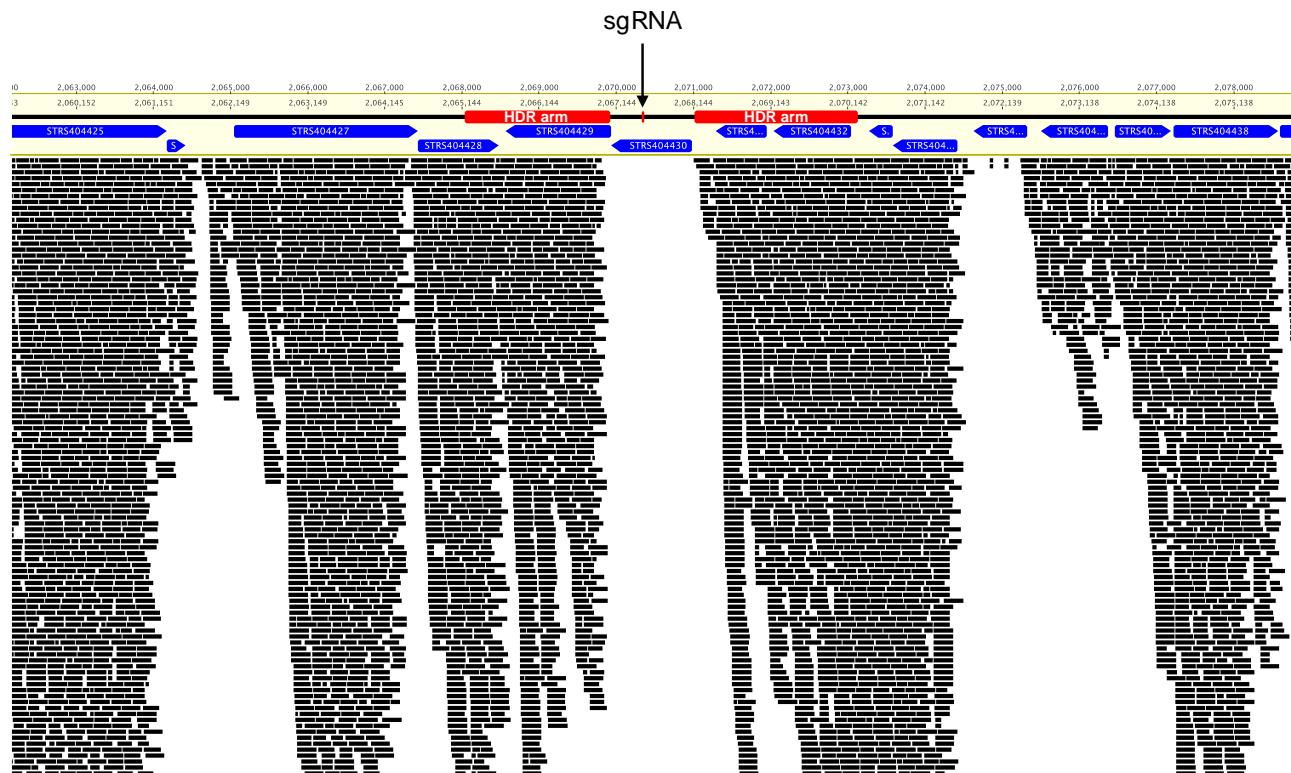
**Figure S1.** Deletion of the entire antimycin BGC in *Streptomyces albus* S4 Δ5. Black rectangles represent Illumina MiSeq reads mapped to the *S. albus* S4 Δ5 genome. The red rectangle indicates the antimycin BGC.



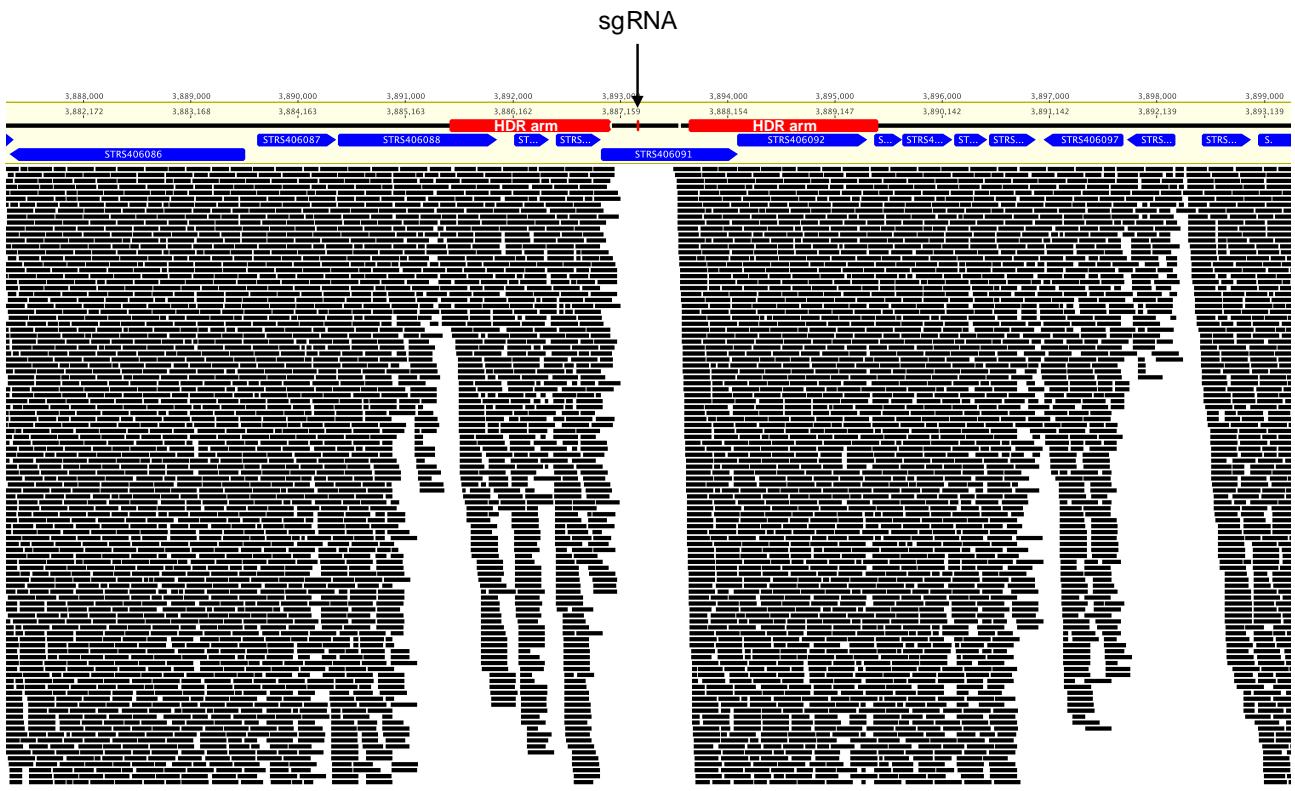
**Figure S2.** Mutagenesis of the candididin BGC in *Streptomyces albus* S4 Δ5. Black rectangles represent Illumina MiSeq reads mapped to the *S. albus* S4 Δ5 genome. Red rectangles indicate the homology-directed repair arms used to delete the STRS402234 gene (also known as *fscC*). HDR, homology-directed repair arm.



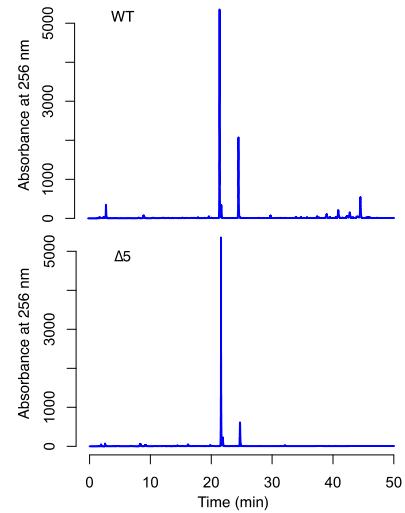
**Figure S3.** Mutagenesis of the surugamide BGC in *Streptomyces albus* S4 Δ5. Black rectangles represent Illumina MiSeq reads mapped to the *S. albus* S4 Δ5 genome. Red rectangles indicate the homology-directed repair arms used to repair the double strand break generated by the Cas9 targeting the *STRS406449* gene. HDR, homology-directed repair arm; sgRNA, single guide RNA.



**Figure S4.** Mutagenesis of the albaflavenone BGC in *Streptomyces albus* S4 Δ5. Black rectangles represent Illumina MiSeq reads mapped to the *S. albus* S4 Δ5 genome. Red rectangles indicate the homology-directed repair arms used to repair the double strand break generated by the Cas9 targeting the *STRS404430* gene. HDR, homology-directed repair arm; sgRNA, single guide RNA.



**Figure S5.** Mutagenesis of the fredericamycin BGC in *Streptomyces albus* S4  $\Delta 5$ . Black rectangles represent Illumina MiSeq reads mapped to the *S. albus* S4  $\Delta 5$  genome. Red rectangles indicate the homology-directed repair arms used to repair the double strand break generated by the Cas9 targeting the *STRS406091* gene. HDR, homology-directed repair arm; sgRNA, single guide RNA.



**Figure S6.** Full scale version of the HPLC chromatogram depicted in Figure 3 in the main text.

**Table S1.** Bacterial strains, cosmids and plasmids used in this study

Strain/cosmid/plasmid	Description <sup>a</sup>	Reference
<i>Candida albicans</i>	<i>Candida albicans</i> strain CA-6	[1]
<i>Micrococcus luteus</i>	<i>Micrococcus luteus</i> NCTC 9379	NCTC
<i>Streptomyces</i>		
S4	Wild type <i>Streptomyces albus</i> S4	[2]
Δ1	S4 harbouring a complete deletion of the antimycin BGC	This study
Δ2	Δ1 harbouring a deletion in the <i>STRS402234 (fscC)</i> of the candidicin BGC	This study
Δ3	Δ2 harbouring a deletion in the <i>STRS406449</i> gene of the surugamide BGC	This study
Δ4	Δ3 harbouring a deletion in the <i>STRS404430</i> gene of the albaflavenone BGC	This study
Δ5	Δ4 harbouring a deletion in the <i>STRS406091</i> gene of the fredericamycin BGC	This study
Δ5/Act	<i>S. albus</i> S4 Δ5 harbouring the actinorhodin BGC ( <i>attB</i> ΦC31::pAH77); Apr <sup>R</sup>	This study
Δ5/Cin	<i>S. albus</i> S4 Δ5 harbouring the cinnamycin BGC ( <i>attB</i> ΦC31:: pIJ10109); Apr <sup>R</sup>	This study
Δ5/Prun	<i>S. albus</i> S4 Δ5 harbouring the neoantimycin/prunustatin BGC split over two cosmids ( <i>attB</i> ΦC31::cosmid813 <i>attB</i> ΦBT1::cosmid69); Apr <sup>R</sup> , Hyg <sup>R</sup> , Kan <sup>R</sup>	[3]
<i>Escherichia coli</i>		
BW25113	Host for REDIRECT PCR targeting system	[4]
NEBa	General cloning host	New England Biolabs
ET12567	Non-methylating host for transfer of DNA into <i>Streptomyces</i> spp. ( <i>dam</i> , <i>dcm</i> , <i>hsdM</i> ); Cam <sup>R</sup>	[5]
GB05-red	Host for RecET recombination	[6]
<b>Cosmids and BACs</b>		
Supercos1	Cosmid backbone for <i>S. albus</i> S4 Cosmid 213; Carb <sup>R</sup> , Kan <sup>R</sup>	Stratagene
Cosmid 213	Supercos1 derivative containing the entire antimycin biosynthetic gene cluster; Carb <sup>R</sup> , Kan <sup>R</sup>	[7]
Cosmid 213Δ <i>antF</i>	Cosmid 213 derivative harbouring an apramycin-marked deletion of <i>antF</i> ; Carb <sup>R</sup> , Kan <sup>R</sup> , Apr <sup>R</sup>	This study
Cosmid 213Δ <i>antA-antO</i>	Cosmid 213 derivative harbouring an apramycin-marked deletion in the entire antimycin biosynthetic gene cluster ( <i>antABCDEFHIJKLMNO</i> ); <i>antF</i> ; Carb <sup>R</sup> , Kan <sup>R</sup> , Apr <sup>R</sup>	This study
Cosmid 213Δ <i>antA-antO</i> -FLP	Cosmid 213Δ <i>antA-antO</i> derivative in which the apramycin resistance cassette was removed by the FLP recombinase; Carb <sup>R</sup> , Kan <sup>R</sup>	This study

Cosmid 213 $\Delta$ <i>antA-antO</i> -FLPHygoriT	Cosmid 213 $\Delta$ <i>antA-antO</i> -FLP derivative in which the <i>bla</i> resistance gene on the cosmid backbone was disrupted with a <i>hyg</i> <sup>R</sup> - <i>oriT</i> cassette	This study
pIJ10109	Derivative of pOJ436 harbouring the cinnamycin biosynthetic gene cluster from <i>Streptomyces cinnamoneus</i> ; Carb <sup>R</sup> , Apr <sup>R</sup>	[8]
Cosmid 813	Supercos1 derivative harbouring <i>natABCDEF</i> from the neoantimycin biosynthetic gene cluster; Carb <sup>R</sup> , Kan <sup>R</sup>	[3]
Cosmid 69	Supercos1 derivative harbouring a partial <i>natB</i> gene and <i>natCDEFGQF'G'HJKLMNOP</i> genes from the neoantimycin biosynthetic gene cluster; Carb <sup>R</sup> , Kan <sup>R</sup>	[3]
Cosmid 69-ΦBT1	Cosmid 69 derivative engineered to integrate into the ΦBT1 <i>attB</i> site; Carb <sup>R</sup> , Hyg <sup>R</sup>	[3]
<b>Plasmids</b>		
pCRISPomyces-2	pGM1190 derivative harbouring the CRISPR/Cas9 machinery; Apr <sup>R</sup>	[9]
pCRISPomyces-2-sur	Derivative of pCRISPomyces-2 derivative containing the <i>STRS406449</i> -targeting protospacer cloned into the BbsI site and homology-directed repair arms cloned into the XbaI site; Apr <sup>R</sup>	This study
pCRISPomyces-2-alb	Derivative of pCRISPomyces-2 derivative containing the <i>STRS404430</i> -targeting protospacer cloned into the BbsI site and homology-directed repair arms cloned into the XbaI site; Apr <sup>R</sup>	This study
pCRISPomyces-2-fdm	Derivative of pCRISPomyces-2 derivative containing the <i>STRS406091</i> -targeting protospacer cloned into the BbsI site and homology-directed repair arms cloned into the XbaI site; Apr <sup>R</sup>	This study
pIJ773	ReDirect PCR template plasmid harbouring an apramycin resistance cassette and <i>oriT</i> ; Carb <sup>R</sup> , Apr <sup>R</sup>	[4]
pIJ10701	ReDirect PCR template plasmid harbouring a hygromycin resistance cassette and <i>oriT</i> ; Hyg <sup>R</sup>	[4]
pKC1132-UpDn	Derivative of suicide plasmid pKC1132 [10] containing ~3kb of homologous DNA upstream and downstream of the region of <i>fscC</i> targeted for deletion; Apr <sup>R</sup>	[11]
pUZ8002	Encodes conjugation machinery for mobilisation of plasmids from <i>E. coli</i> to <i>Streptomyces</i> ; Kan <sup>R</sup>	[5]

<sup>a</sup> Carb, carbenicillin; Apr, apramycin; Hyg, hygromycin, Kan, kanamycin; Cam, chloramphenicol; *oriT*, origin of conjugal transfer

**Table S2.** Oligonucleotide primers used in this study

Primer alias	Sequence (5'-3') <sup>a</sup>	Description
RFS196	<b>ctcggtcgtttcaggtggagagggtgcgtgcgcgtcatgttagcc</b> tggagctgcttc	PCR: <i>antF</i> REDIRECT knockout cassette
RFS236	cgcctacaacaccggtgagt	PCR: confirmation of Δ <i>ant</i> mutation
RFS237	aggggacgatgttgcgacc	PCR: confirmation of Δ <i>ant</i> mutation
RFS197	<b>gaegggccccggggggggggacggccgggggtgcgtatgtattcc</b> ggggatccgtcgacc	PCR: <i>antF</i> REDIRECT knockout cassette
RFS219	<b>cacggccccgggtgttcacccgcatggtgccgtcaattccggggatccgtcgacc</b>	PCR: <i>antABCDEHIJKLMNO</i> REDIRECT knockout cassette
RFS203	<b>ccgcctggccgggtcgggagacatctggccggccgtcatgttagctggagctgcgttc</b>	PCR: <i>antABCDEHIJKLMNO</i> REDIRECT knockout cassette
RFS242	atcacgcggctgtcgacca	PCR: confirmation of Δ <i>antF</i> mutant strain
RFS243	tggaggaactgcggaccatc	PCR: confirmation of Δ <i>antF</i> mutant strain
EH_S3	acgctccggggccgcgcgagaaaa	CRISPR protospacer targeting <i>STRS4_04430</i> (albaflavenone BGC)
EH_S4	aaaccttctcgccggccggca	CRISPR protospacer targeting <i>STRS4_04430</i> (albaflavenone BGC)
EH_S7	acgcgtacgcctgtccatggaga	CRISPR protospacer targeting <i>STRS4_06091</i> (fredericamycin BGC)
EH_S8	aaactctccatggagcaggcgtac	CRISPR protospacer targeting <i>STRS4_06091</i> (fredericamycin BGC)
EH_S9	acgccacccacgcggcaccggaa	CRISPR protospacer targeting <i>STRS4_06449</i> (surugamide BGC)
EH_S10	aaactccgggtccgcgtgaggta	CRISPR protospacer targeting <i>STRS4_06449</i> (surugamide BGC)
EH_P7	<b>tgcgcggggcggttttatgtgtactggttccgtc</b>	PCR: <i>STRS4_04430</i> homology-directed repair arm
EH_P8	<b>tttgtcgctgtttccgaatccaccaccgaac</b>	PCR: <i>STRS4_04430</i> homology-directed repair arm
EH_P9	<b>gggttcgggtggattcggaaaggcaggcacgaac</b>	PCR: <i>STRS4_04430</i> homology-directed repair arm
EH_P10	<b>cgcccttttacggttctggcctgggtggatcgcaagagg</b>	PCR: <i>STRS4_04430</i> homology-directed repair arm
EH_P15	<b>tgcgcggggcggttttatcgcttccgtgttgtgg</b>	PCR: <i>STRS4_06091</i> homology-directed repair arm
EH_P16	<b>ggtcatgtggtagccgttgggtggccctcacatctcc</b>	PCR: <i>STRS4_06091</i> homology-directed repair arm
EH_P17	<b>agatgategtgaaggccaaaccaacggctaccacatgacc</b>	PCR: <i>STRS4_06091</i> homology-directed repair arm
EH_P18	<b>cgcccttttacggttctggcctatggcttgaggcggtgaagc</b>	PCR: <i>STRS4_06091</i> homology-directed repair arm
EH_P19	<b>tgcgcggggcggttttatgtacgtcatgtccacatcc</b>	PCR: <i>STRS4_06449</i> homology-directed repair arm
EH_P31	<b>cgttaaggctgggtgttgcgtacagctcgctcgttc</b>	PCR: <i>STRS4_06449</i> homology-directed repair arm
EH_P27	<b>cgcgaactgagggagctgtaggacaacaccaggcttacg</b>	PCR: <i>STRS4_06449</i> homology-directed repair arm
EH_P28	<b>cgcccttttacggttctggcctctccgtaccgacttcagc</b>	PCR: <i>STRS4_06449</i> homology-directed repair arm

EH_P35	gtcgtgaatctccgtatcg	PCR: confirmation of STRS4_04430 mutation
EH_P36	tacggctacacctacatcgacc	PCR: confirmation of STRS4_04430 mutation
EH_P37	tggccgaacccttactcc	PCR: confirmation of STRS4_06091 mutation
EH_P38	ccatgtccaggcgttcagc	PCR: confirmation of STRS4_06091 mutation
EH_P39	caccaggacttccacg	PCR: confirmation of STRS4_06449 mutation
EH_P40	gagggagaagaagtgtcgtgg	PCR: confirmation of STRS4_06449 mutation

<sup>a</sup> non-homologous sequences are underlined and engineered restriction endonuclease sites are bolded

## References

1. **Maconi P, Bistoni F, Boncio A, Boncio L, Bersiani A, et al.** Utilizzazione di una soluzione salina ipertonica di cloruro di potassio (3M KCl) per l'estrazione di antigeni solubili da *Candida albicans*. *Ann Sclavo* 1976;18: 61–66.
2. **Barke J, Seipke RF, Grüschorow S, Heavens D, Drou N, Bibb MJ, et al.** A mixed community of actinomycetes produce multiple antibiotics for the fungus farming ant *Acromyrmex octospinosus*. *BMC Biol* 2010;8: 109.
3. **Skyrud W, Liu J, Thankachan D, Cabrera M, Seipke RF, Zhang W.** Biosynthesis of the 15-Membered Ring Depsipeptide Neoantimycin. *ACS Chem Biol* 2018;13: 1398–1406.
4. **Gust B, Challis GL, Fowler K, Kieser T, Chater KF.** PCR-targeted *Streptomyces* gene replacement identifies a protein domain needed for biosynthesis of the sesquiterpene soil odor geosmin. *Proc Natl Acad Sci USA* 2003;100: 1541–1546.
5. **MacNeil DJ, Gewain KM, Ruby CL, Dezeny G, Gibbons PH, MacNeil T.** Analysis of *Streptomyces avermitilis* genes required for avermectin biosynthesis utilizing a novel integration vector. *Gene* 1992;111: 61–68.
6. **Fu J, Bian X, Hu S, Wang H, Huang F, Seibert PM, et al.** Full-length RecE enhances linear-linear homologous recombination and facilitates direct cloning for bioprospecting. *Nat Biotechnol* 2012;30: 440–446.
7. **Seipke RF, Patrick E, Hutchings MI.** Regulation of antimycin biosynthesis by the orphan ECF RNA polymerase sigma factor  $\sigma^{\text{AntA}}$ . *PeerJ* 2014;2: e253.
8. **Widdick DA, Dodd HM, Barraille P, White J, Stein TH, Chater KF, et al.** Cloning and engineering of the cinnamycin biosynthetic gene cluster from *Streptomyces cinnamoneus cinnamoneus* DSM 40005. *Proc Natl Acad Sci USA*; 2003;100: 4316–4321.
9. **Cobb RE, Wang Y, Zhao H.** High-efficiency multiplex genome editing of *Streptomyces* species using an engineered CRISPR/Cas system. *ACS Synth Biol* 2015;4: 723–728.
10. **Bierman M, Logan R, O'Brien K, Seno ET, Rao RN, Schoner BE.** Plasmid cloning vectors for the conjugal transfer of DNA from *Escherichia coli* to *Streptomyces* spp. *Gene* 1992;116: 43–49.
11. **Seipke RF, Barke J, Brearley C, Hill L, Yu DW, Goss RJM, et al.** A Single *Streptomyces* symbiont makes multiple antifungals to support the fungus farming ant *Acromyrmex octospinosus*. *PLoS ONE* 2011;6: e22028–8.