Supplementary information figures

Desert Environments Facilitate Unique Evolution of Biosynthetic Potential in *Streptomyces*

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Figure S1

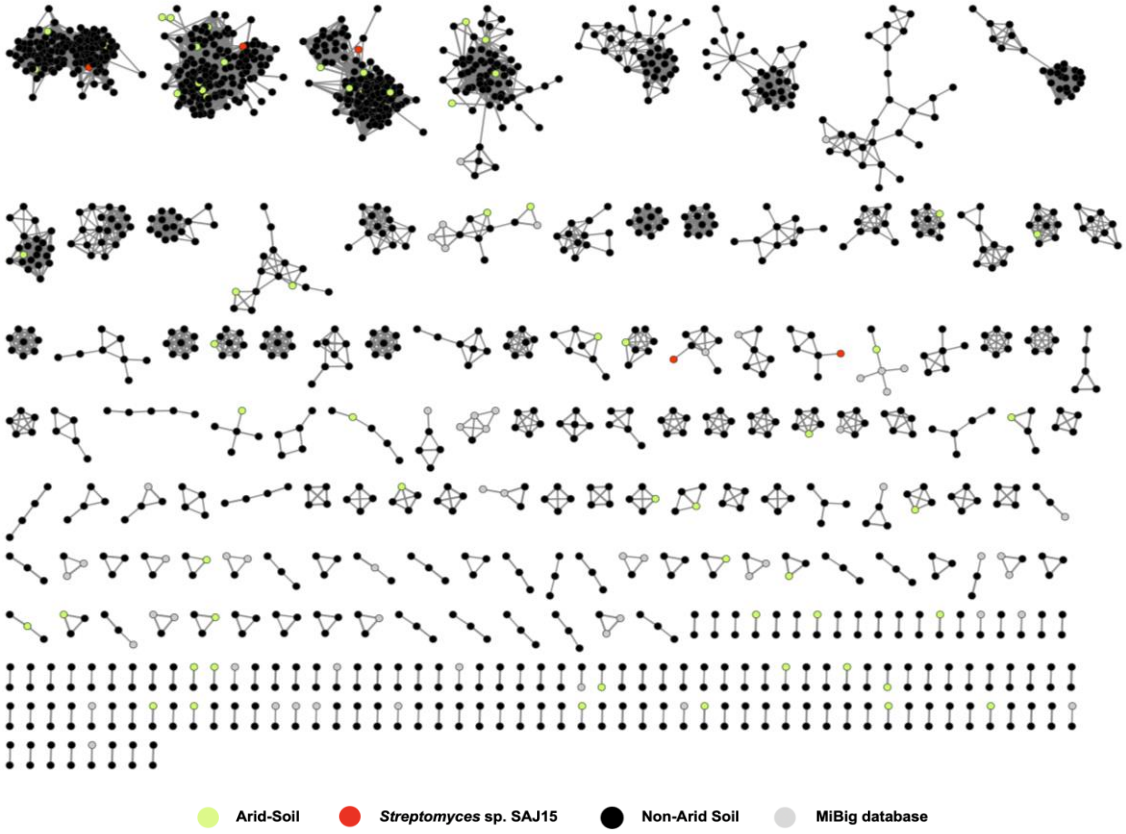


Figure S1. BiG-SCAPE family classified as Others. BGC sequence similarity networks of BGCs from 179 *Streptomyces* genomes. 1,540 *Streptomyces*-BGCs were classified into this GCF.

Figure S2

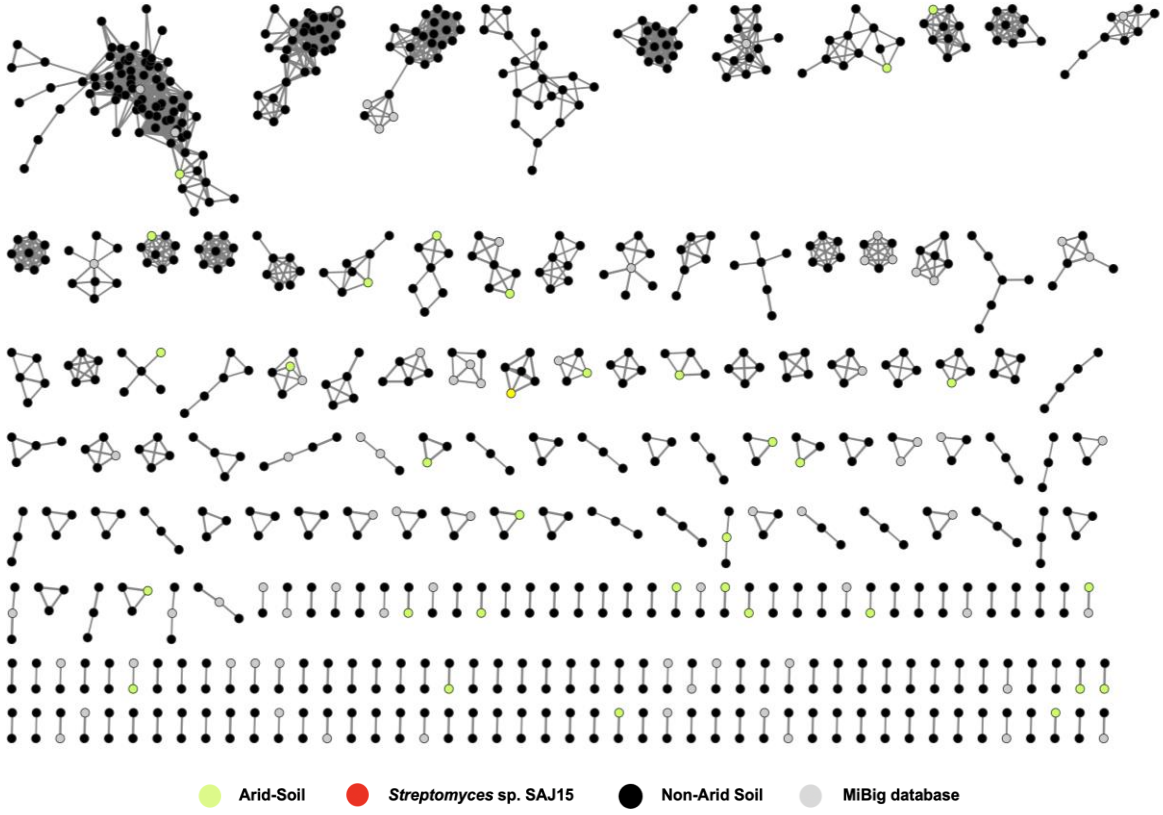


Figure S2 BiG-SCAPE family classified as NRPs. BGC sequence similarity networks of BGCs from 179 *Streptomyces* genomes. 761 *Streptomyces*-BGCs were classified into this GCF.

Figure S3

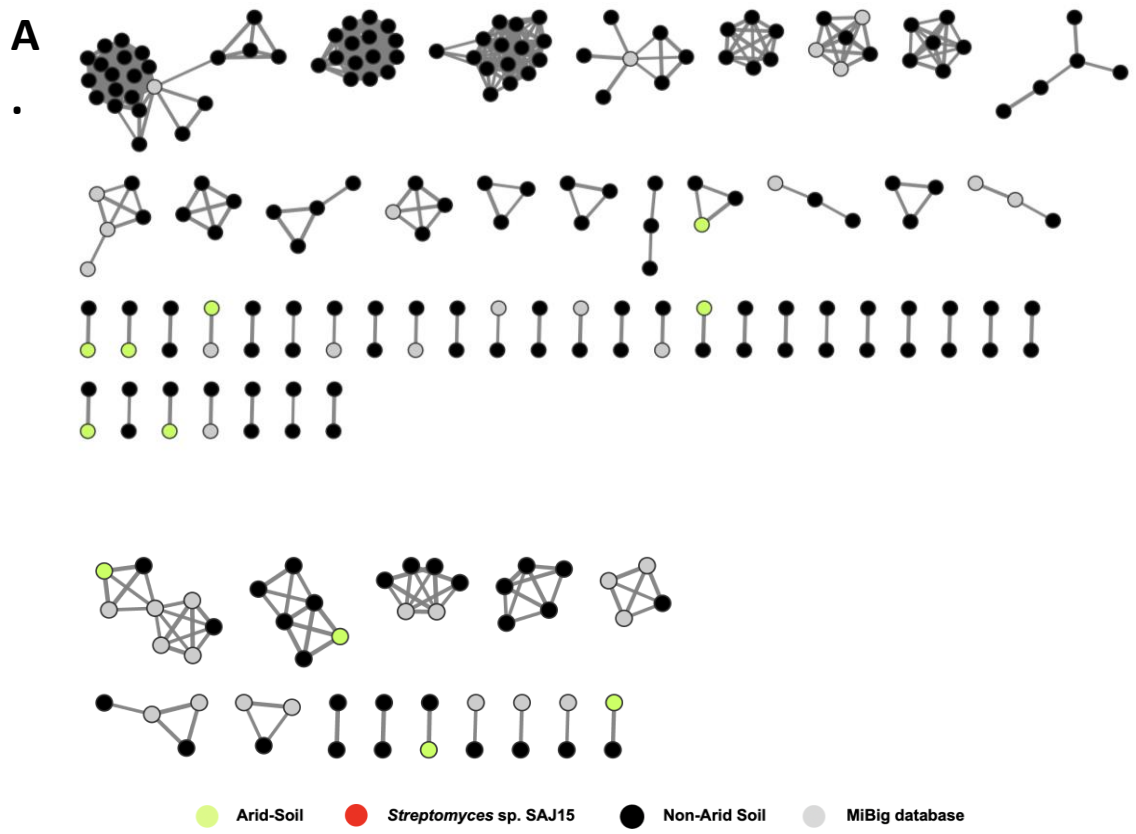


Figure S3. A. BiG-SCAPE family classified as PKS-NRPs hybrid. BGC sequence similarity networks of BGCs from 179 *Streptomyces genomes*. 164 *Streptomyces*-BGCs were classified into this GCF. B. BiG-SCAPE family classified as Saccharides. 33 *Streptomyces*-BGCs were classified into this GCF

Figure S4

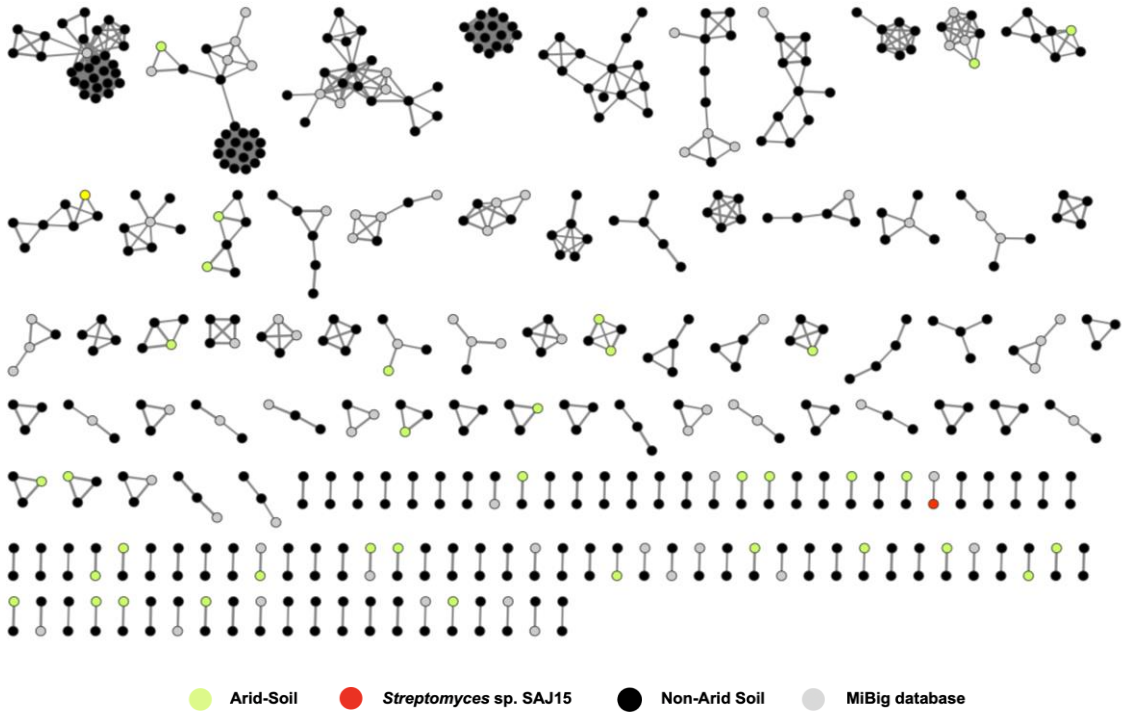


Figure S4. BiG-SCAPE family classified as PKSI. BGC sequence similarity networks of BGCs from 179 *Streptomyces* genomes. 457 *Streptomyces*-BGCs were classified into this GCF.

Figure S5

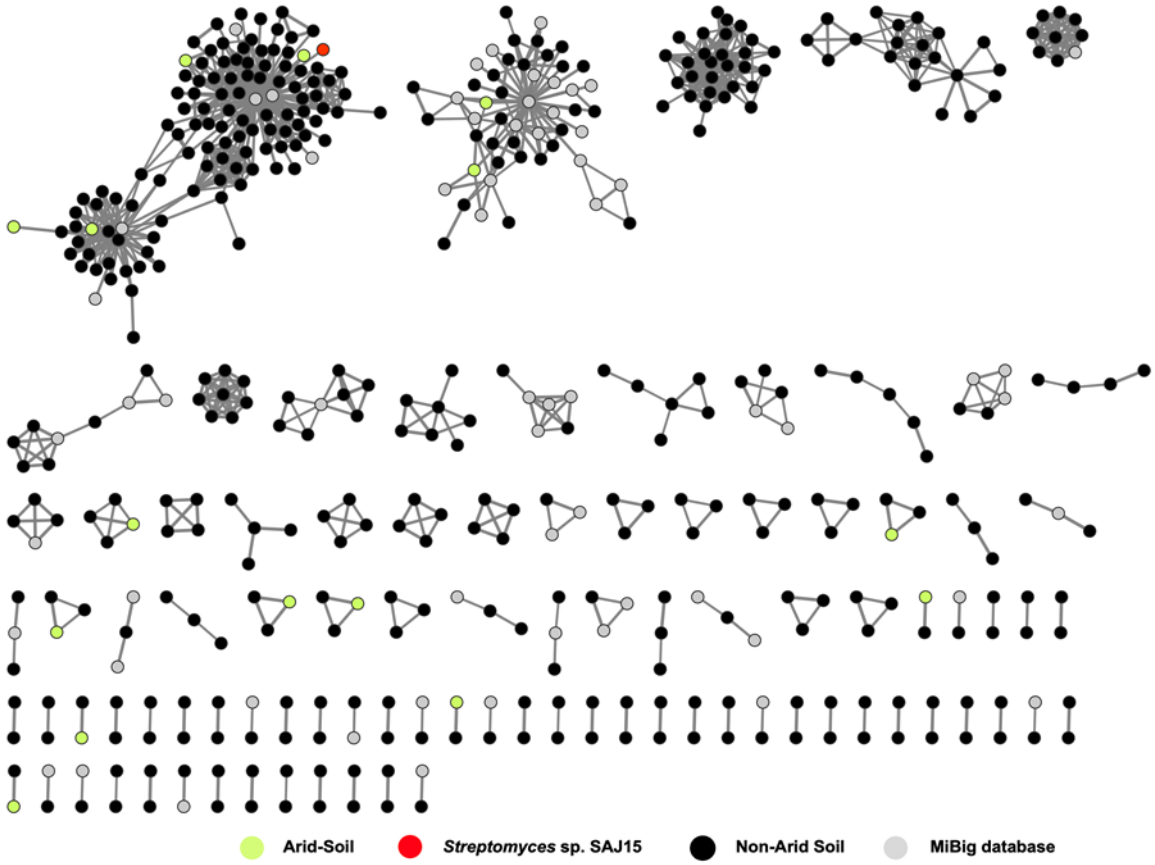


Figure S5. BiG-SCAPE family classified as PKS-Other. BGC sequence similarity networks of BGCs from 179 *Streptomyces* genomes. 423 *Streptomyces*-BGCs were classified into this GCF.

Figure S6

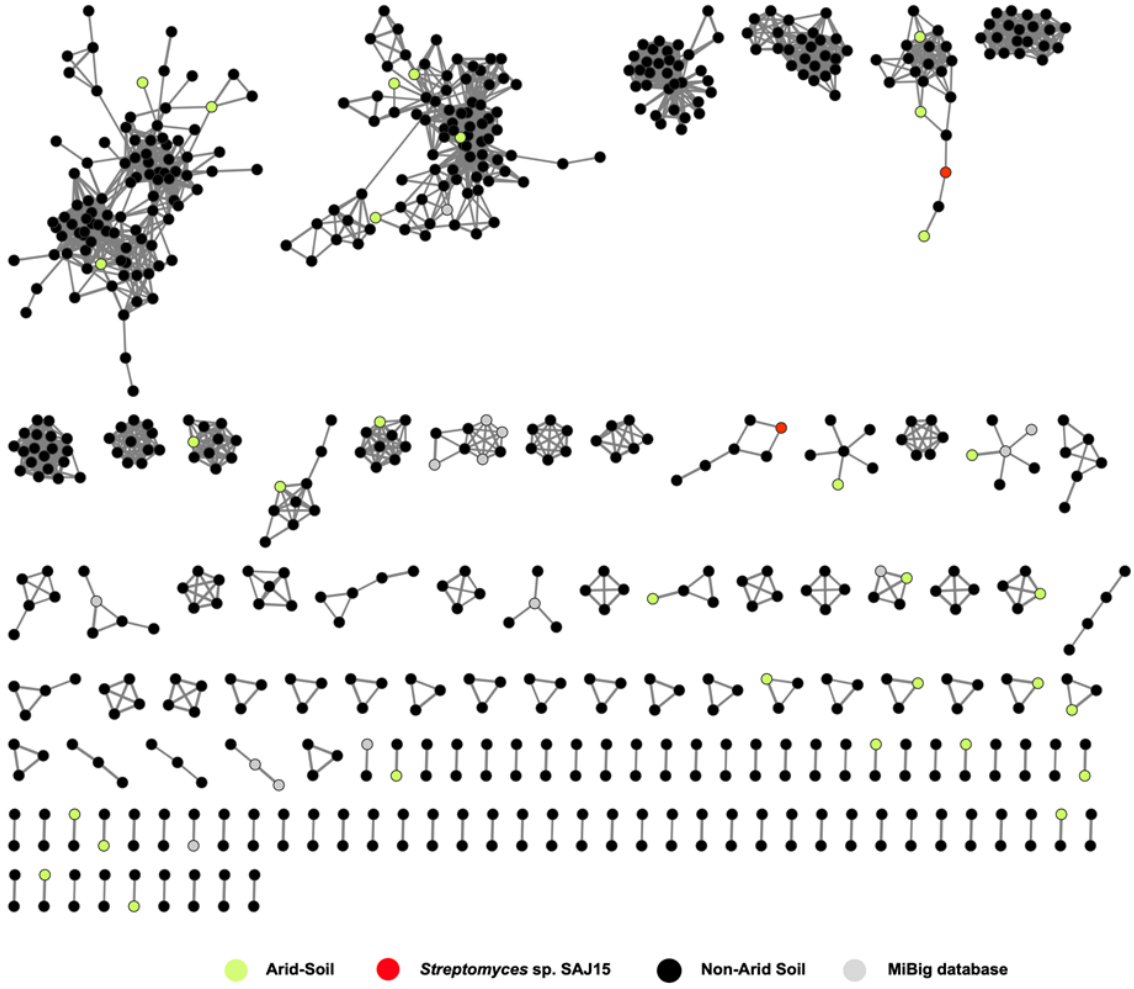


Figure S6. BiG-SCAPE family classified as RiPPs. BGC sequence similarity networks of BGCs from 179 *Streptomyces* genomes. 654 *Streptomyces*-BGCs were classified into this GCF.

Figure S7

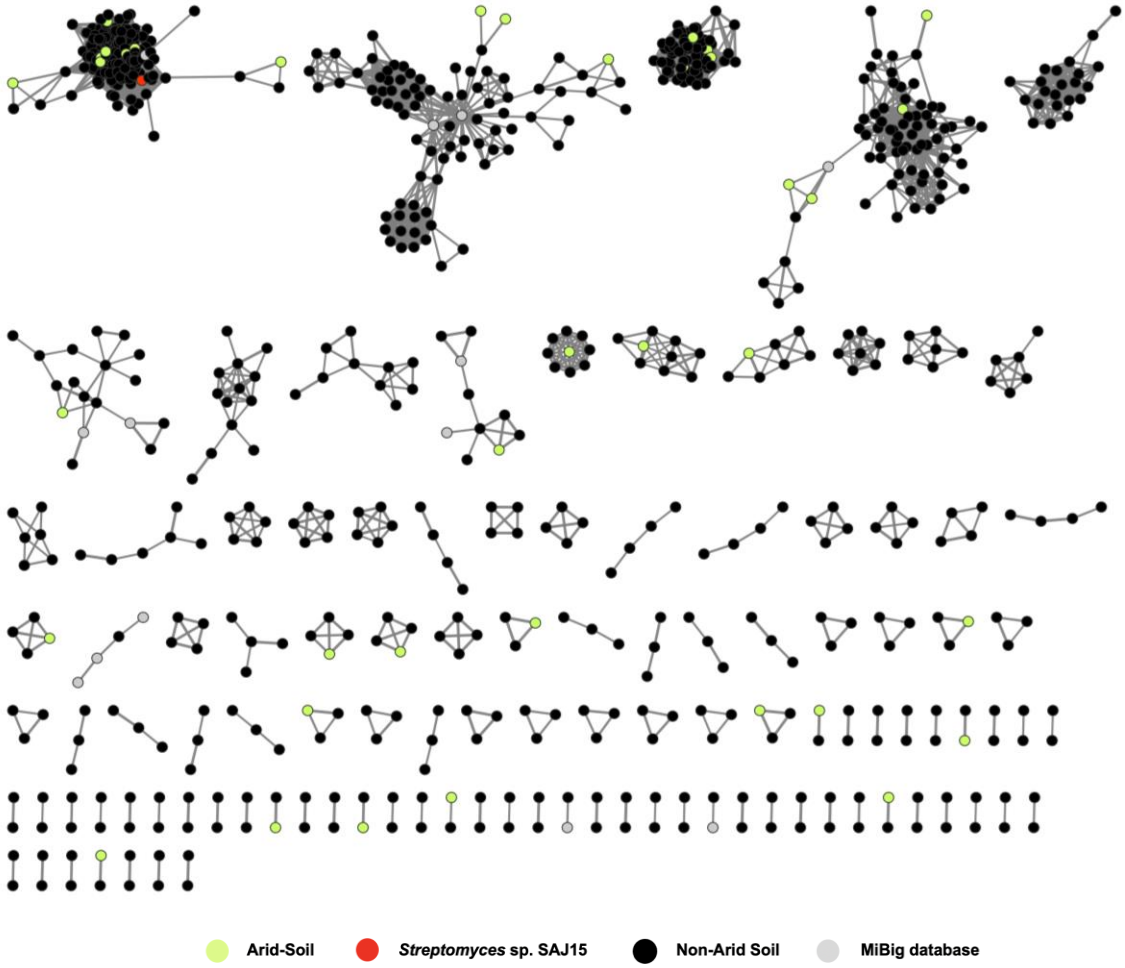


Figure S7. BiG-SCAPE family classified as Terpenes. BGC sequence similarity networks of BGCs from 179 *Streptomyces* genomes. 799 *Streptomyces*-BGCs were classified into this GCF.

Figure S8

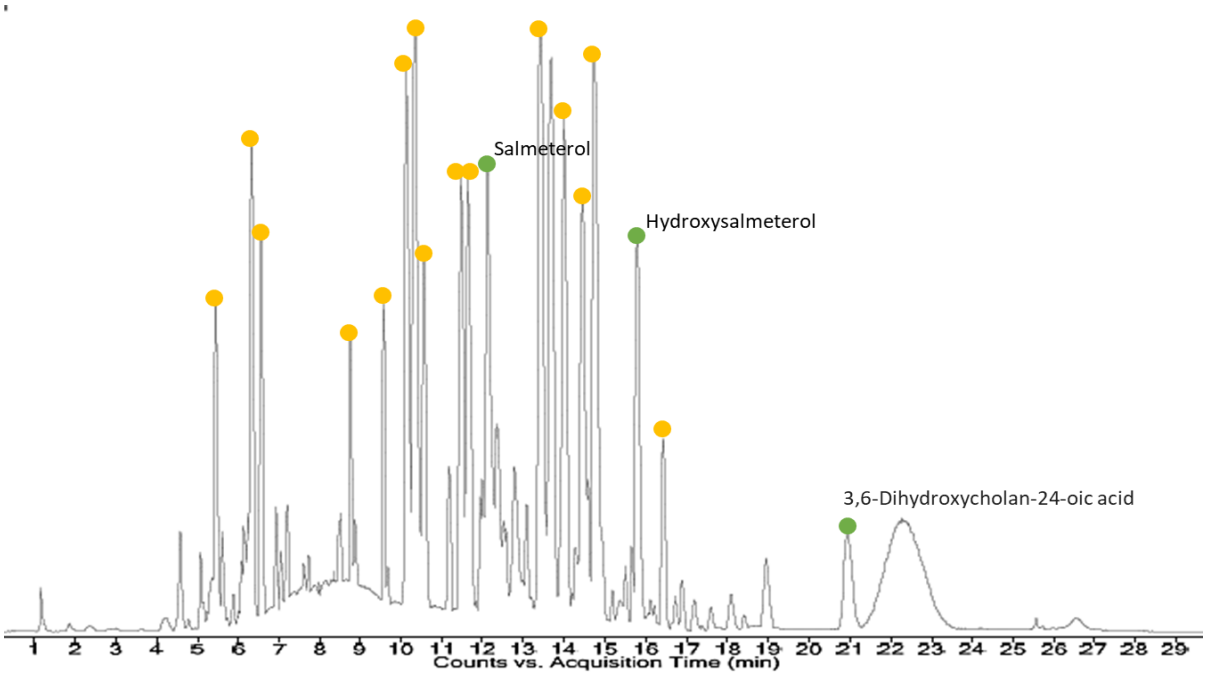
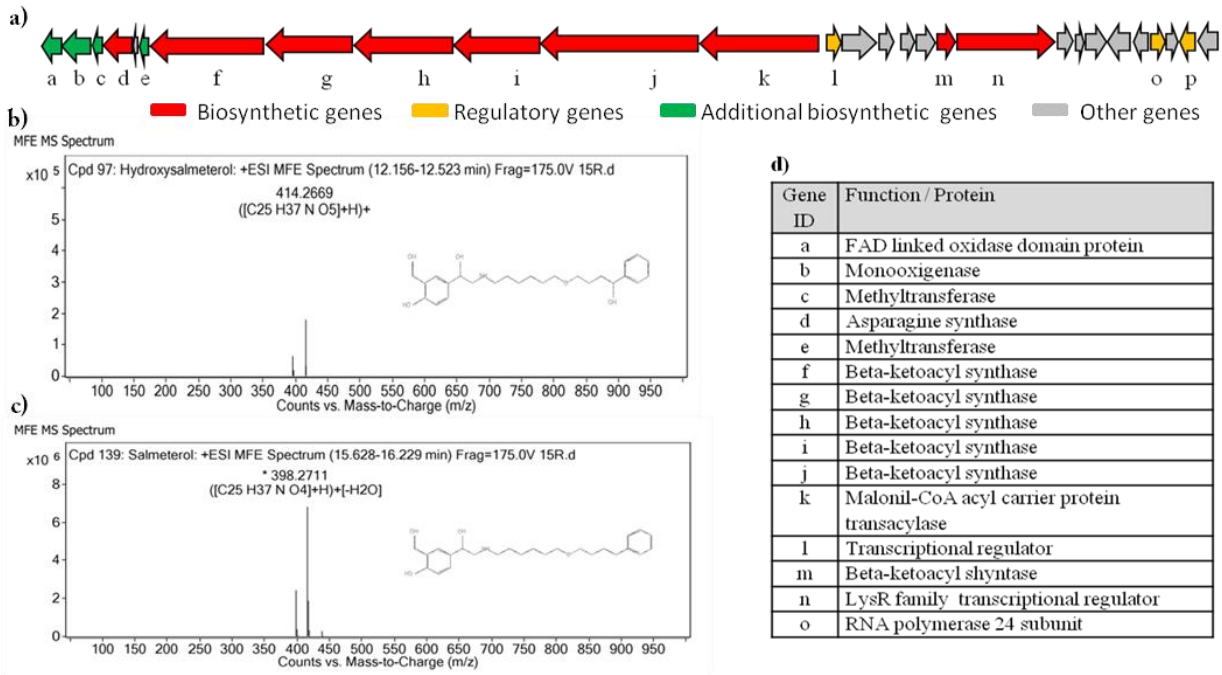


Figure S8: UHPLC-MS-Q-TOF chromatogram of culture extract (CE15-PM01) of *Streptomyces* sp. SAJ15. Peaks marked with green corresponds predicted to be known compounds, while yellow corresponds putatively new compounds (didn't match with mass features of known compounds).

Figure S9



d)

Gene ID	Function / Protein
a	FAD linked oxidase domain protein
b	Monooxigenase
c	Methyltransferase
d	Asparagine synthase
e	Methyltransferase
f	Beta-ketoacyl synthase
g	Beta-ketoacyl synthase
h	Beta-ketoacyl synthase
i	Beta-ketoacyl synthase
j	Beta-ketoacyl synthase
k	Malonil-CoA acyl carrier protein transacylase
l	Transcriptional regulator
m	Beta-ketoacyl shyntase
n	LysR family transcriptional regulator
o	RNA polymerase 24 subunit

Figure S9: Putative relationship between the BGC14 and salmeterol derivatives detected by UHPLC-MS-Q-TOF; arrangements of genes in the identified I pks - arylpolyene BGC (a), structure of hydroxysalmeterol (b) and salmeterol (c), and identified functions/proteins of genes found in type I pks - arylpolyene BGC (d).

Figure S10

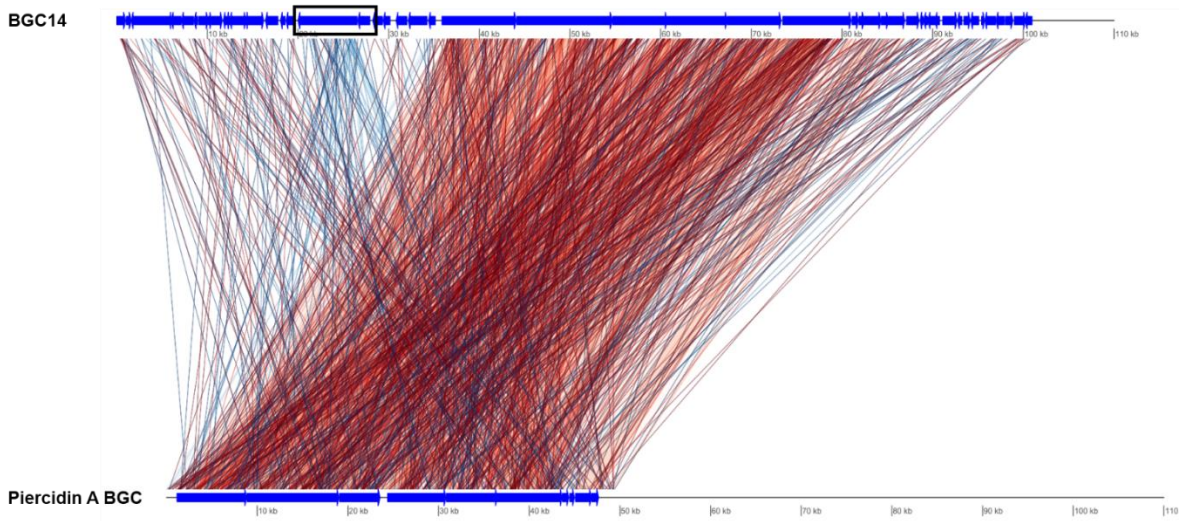
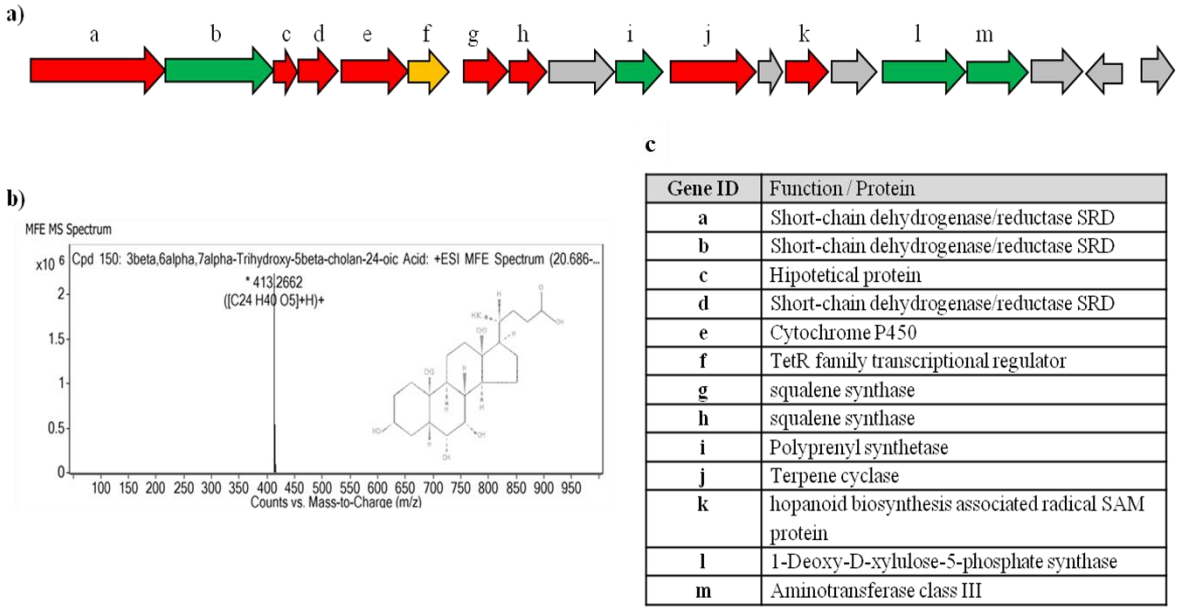


Figure S10: Hybrid PKs - arylpolyene BGC of SAJ15 had two additional beta-ketoacyl synthase compared to piericidin A BGC.

Figure S11



Gene ID	Function / Protein
a	Short-chain dehydrogenase/reductase SRD
b	Short-chain dehydrogenase/reductase SRD
c	Hipotetical protein
d	Short-chain dehydrogenase/reductase SRD
e	Cytochrome P450
f	TetR family transcriptional regulator
g	squalene synthase
h	squalene synthase
i	Polyprenyl synthetase
j	Terpene cyclase
k	hopanoid biosynthesis associated radical SAM protein
l	1-Deoxy-D-xylulose-5-phosphate synthase
m	Aminotransferase class III

Figure S11: Putative relationship between the BGC_06 and cholyglycine related compound (hydroxycholan-24-oic acid) detected by UHPLC-MS-Q-TOF. Arrangements of genes in the identified BGC_06 (a), structure of 3,6-Dihydroxycholan-24-oic acid (b), and identified functions/proteins of genes found in BGC_06 (c).