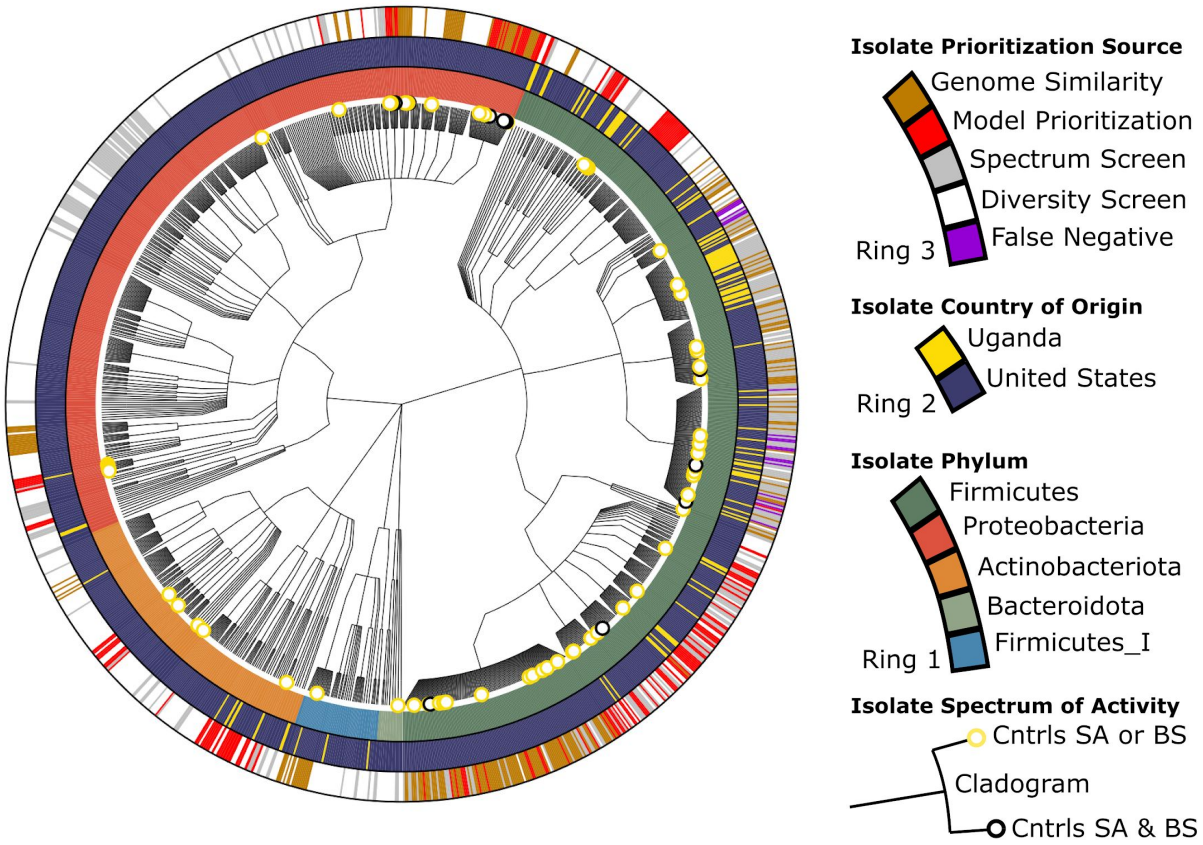
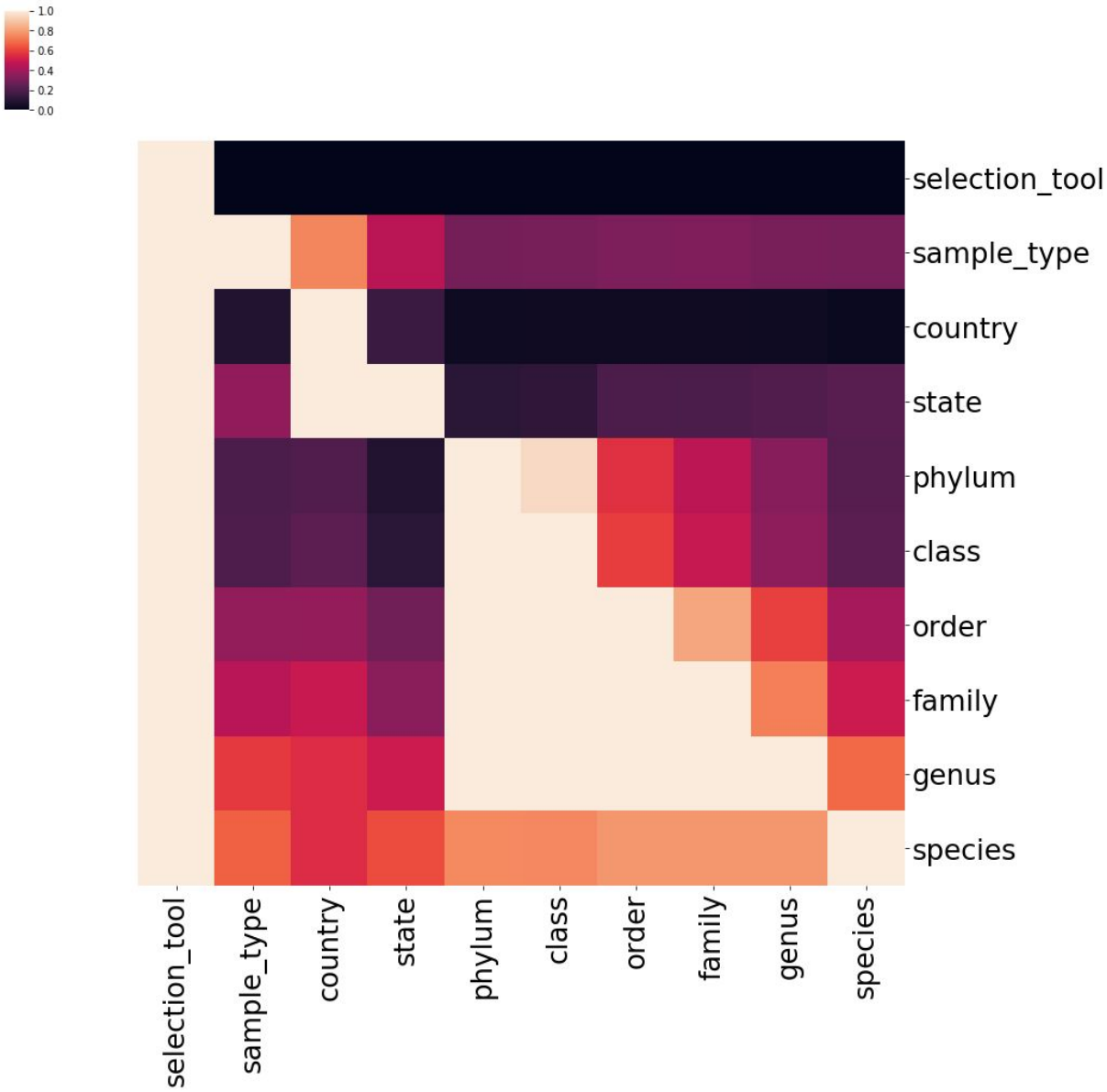
Supplemental Materials for "Genomics-accelerated discovery of diverse fungicidal bacteria"

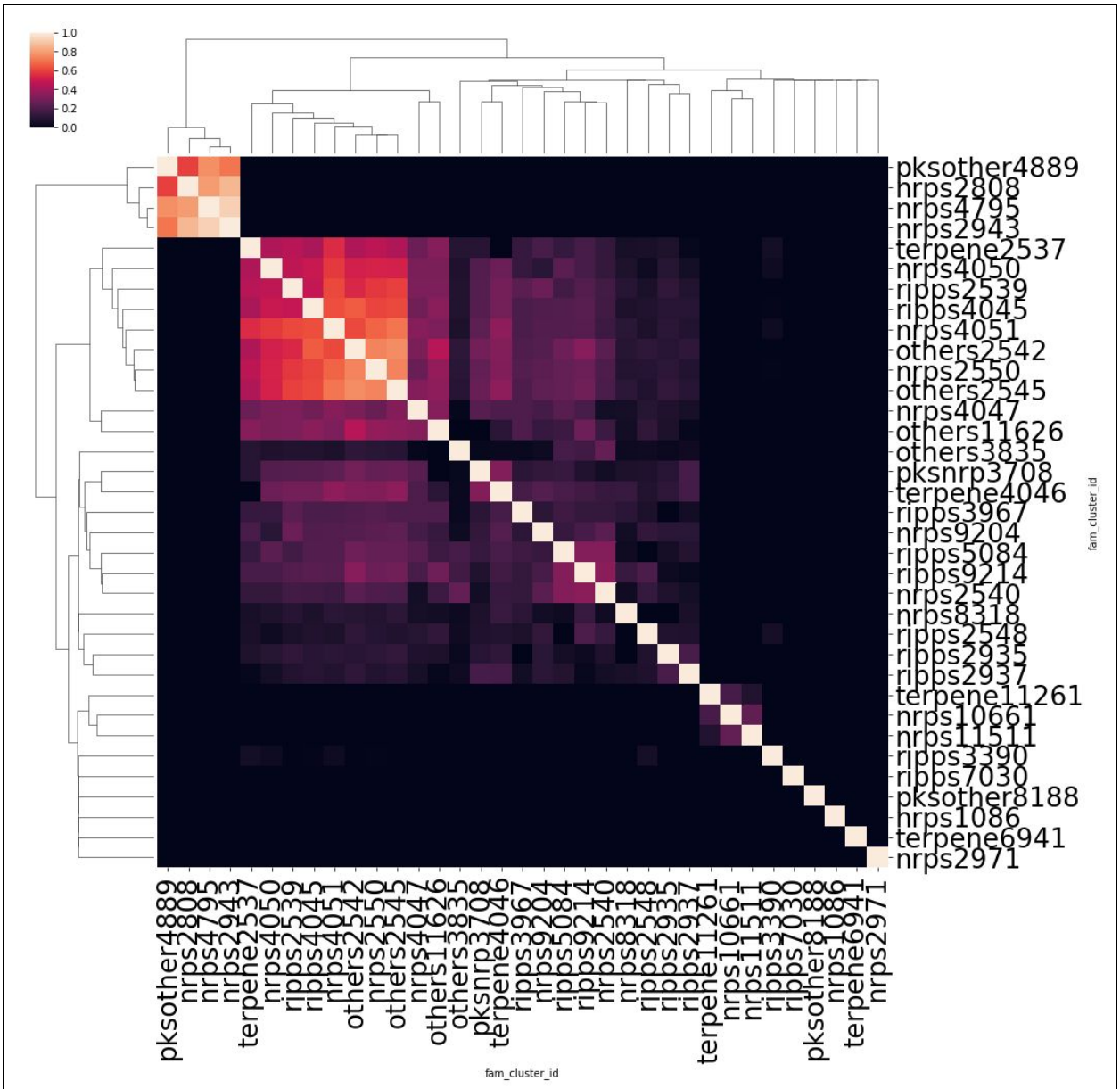


Supplemental Figure 1. Full collection of strains screened against SA and BS. The cladogram in the center highlights the diversity of the biocontrol strains discovered in this work (five phyla represented by the center branches, 14 genera, 22 species). Multiple isolates displayed activity against both diseases (black leaf nodes). The outer ring shows the isolate prioritization strategies that led to each discovery, including predictive models. The "false negative" isolates in purple were predicted to be inactive by all three modeling approaches and yet were reproducibly active against SA.

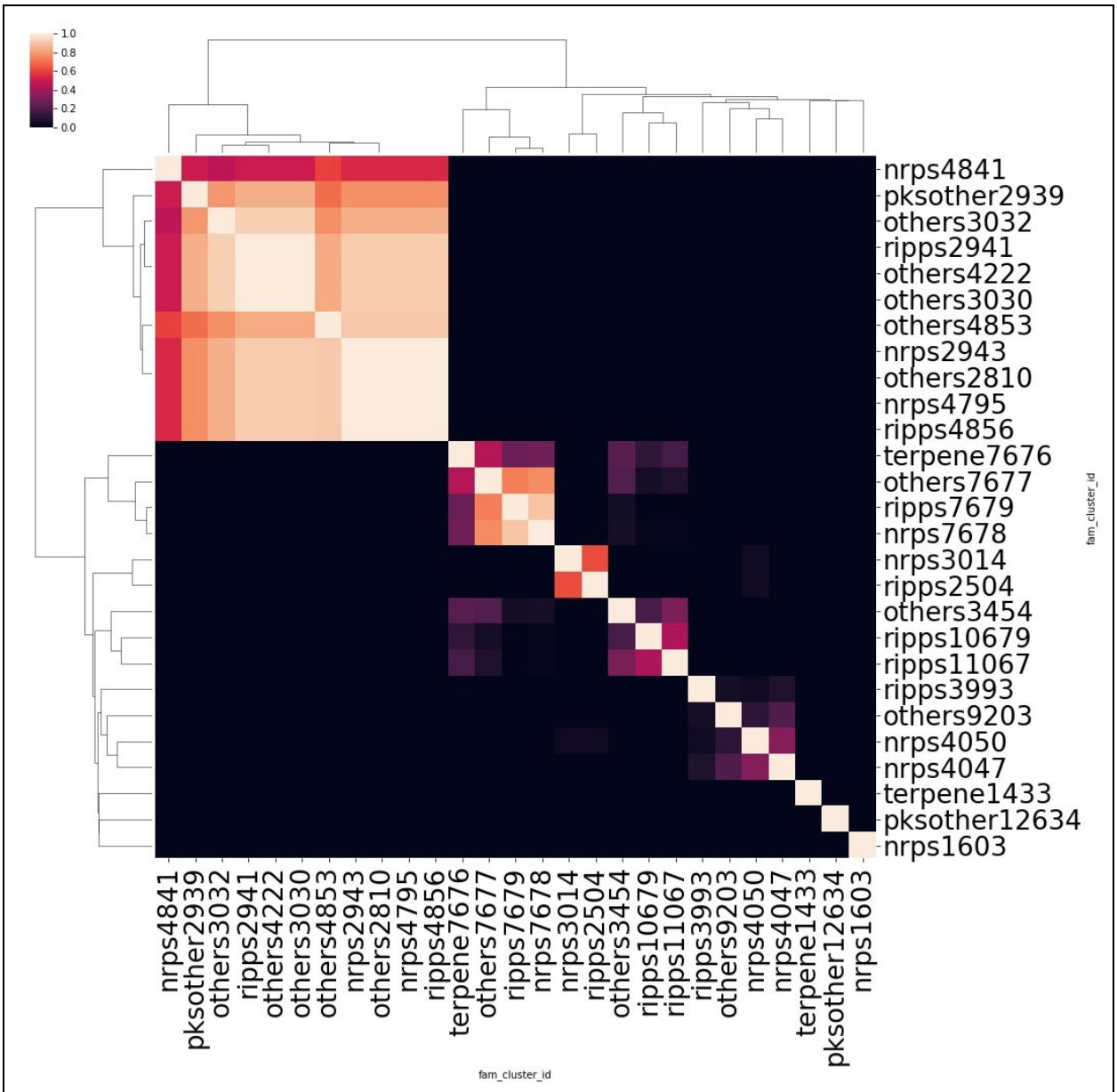


Supplemental Figure 2. **Covariance between metadata categories.** Theil's U is the uncertainty of x given y, where an output close to 0 means y provides no information about x, and a value close to 1 means y provides full information about x. You read the figure as "if you know the value from the row, how much information does that provide about the value in the column?" For example, if you know the **genus**, it gives you full information about the **family**, **order**, **class** and **phylum**, but the opposite is not true.

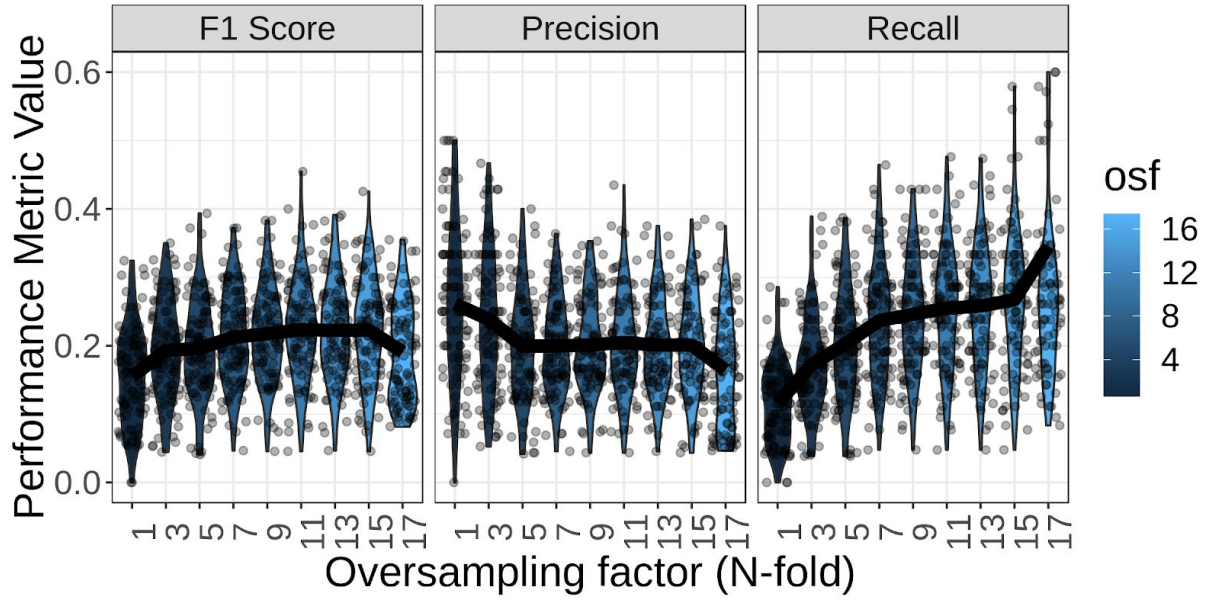
Supplemental Table 1					
BGC Family ID	**99th Percentile Importance**	**Top Enrichment Scores**	**Predicted Product Class**	**Homology to Known BGC**	**Taxonomic Distribution**
nrps4050	TRUE	TRUE	NRPS	Bacillibactin	genus:Bacillus_A
nrps4047	TRUE	TRUE	NRPS;T1PKS	Zwittermycin A	genus:Bacillus_A
others9203	TRUE	TRUE	siderophore	Petrobactin	genus:Bacillus_A
nrps3014	TRUE	FALSE	NRPS	None	species:Bacillus_A toyonensis
others7677	TRUE	FALSE	other	Bacilysin	genus:Bacillus
ripps2504	TRUE	FALSE	LAP;bacteriocin	None	species:Bacillus_A toyonensis
others3454	TRUE	FALSE	betalactone	None	genus:Bacillus
ripps7679	TRUE	FALSE	bacteriocin	None	genus:Bacillus
nrps7678	TRUE	FALSE	NRPS	Surfactin	genus:Bacillus
pksother12634	TRUE	FALSE	NRPS;transAT-PKS;betalactone	Fengycin	species:Bacillus velezensis
ripps11067	TRUE	FALSE	LAP	Plantazolicin	species:Bacillus safensis
terpene7676	TRUE	FALSE	siderophore	Carotenoid	genus:Bacillus
ripps3993	TRUE	FALSE	bacteriocin	None	genus:Bacillus_A
ripps10679	TRUE	FALSE	bacteriocin	None	species:Bacillus safensis
nrps1603	TRUE	FALSE	NRPS	Pyoverdine	species:Pseudomonas_E extremorientalis
terpene1433	TRUE	FALSE	terpene	Carotenoid	species:gtdb_novel_strain
others4222	TRUE	FALSE	CDPS	None	genus:Pseudomonas_E
ripps2941	TRUE	FALSE	bacteriocin	None	genus:Pseudomonas_E
nrps4841	TRUE	FALSE	NRPS	Syringomycin	species:Pseudomonas_E protegens
nrps4795	FALSE	TRUE	NRPS	Pyoverdine	species:Pseudomonas_E protegens
nrps2943	FALSE	TRUE	NRPS	Lipopeptide 8D1-1/2	species:Pseudomonas_E protegens
others2810	FALSE	TRUE	other	Pyrrolnitrin	class:Gammaproteobacteria
pksother4889	FALSE	TRUE	PKS-like	Anikasin	species:Pseudomonas_E protegens
others3032	FALSE	TRUE	arylpolyene	APE Vf	genus:Pseudomonas_E
ripps4856	FALSE	TRUE	bacteriocin	None	genus:Pseudomonas_E
pksother2939	FALSE	TRUE	T3PKS	2,4-Diacetylphloroglucinol	family:Pseudomonadaceae
nrps2808	FALSE	TRUE	NRPS	Thiazostatin	genus:Pseudomonas_E
others3030	FALSE	TRUE	NAGGN	None	family:Pseudomonadaceae



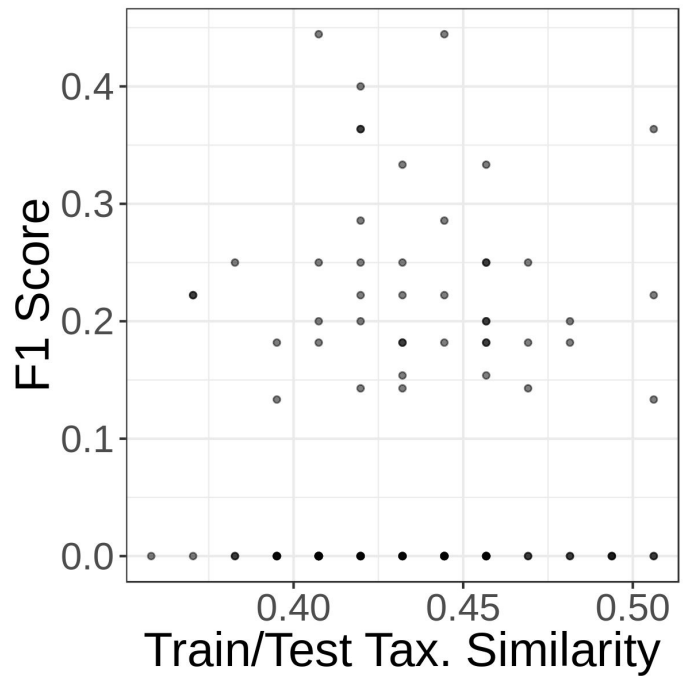
Supplemental Figure 3. **SA features co-occurrence, calculated as the Jaccard similarity between the sets of isolate genomes that contain members of the BGC families.** For example, “pksother4889” was not found in any of the same genomes as “nrps7030”, and so the Jaccard similarity is 0. On the other hand, “terpene2537” was found in many of the same genomes as “nrps4051”.



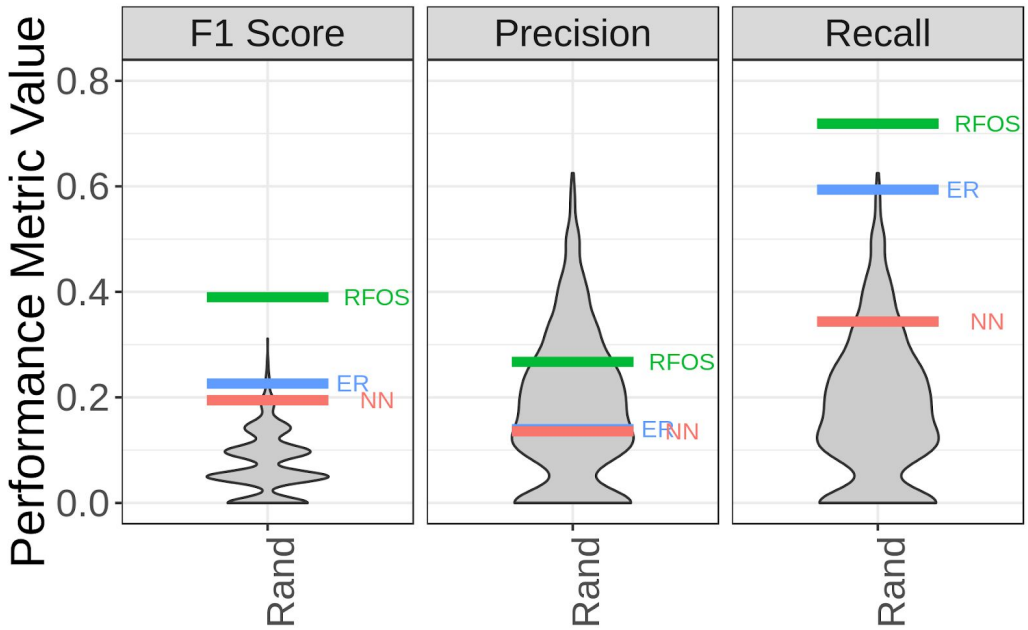
Supplemental Figure 4. BS features co-occurrence, calculated as the Jaccard similarity between the sets of isolate genomes that contain members of the BGC families. For example, “nrps4841” was not found in any of the same genomes as “pksother12634”, and so the Jaccard similarity is 0. On the other hand, “nrps4841” was found in many of the same genomes as “pksother2939”.



Supplemental Figure 5. The effect on random forest model performance of oversampling positive observations in the SA primary screen data set.



Supplemental Figure 6. Correlation between the taxonomic overlap of the training/test set and the model performance.



Supplemental Figure 7. Performance of predictive models during *in vivo* validation experiment with 176 isolates. The gray distribution represents the results of 1,000 draws from a random, null model. The horizontal lines indicate how each predictive model performed on this single validation set of 176 isolates. The closer to the upper tail of the null distribution, the more valuable the performance. The closer to the mean, the less different from random chance. In this case, the models tended to achieve better recall (driving up the F1 score) than random chance would suggest.

Supplemental Table 2	
BGC Family ID	**Feature Selected By**
ripps7574	random_forest
nrps4051	enrichment
nrps9204	random_forest
others3835	random_forest
nrps2567	random_forest
terpene7676	random_forest
nrps4050	enrichment
nrps8190	random_forest
ripps3390	both

nrps2597	random_forest
ripps2539	both
others7673	random_forest
nrps4071	random_forest
nrps2936	random_forest
others2545	both
nrps2969	random_forest
nrps10526	random_forest
nrps8318	random_forest
others9203	random_forest
ripps2548	random_forest
pksother4889	enrichment
nrps9044	random_forest
ripps3967	random_forest
others4222	random_forest
nrps6166	random_forest
nrps4047	random_forest
ripps10679	random_forest
ripps3960	random_forest
ripps4045	enrichment
nrps2550	enrichment
nrps2943	both
nrps4795	enrichment