

Supplemental document for “Microbiome composition modulates secondary metabolism in a multispecies bacterial community” by Chevrette et al.

### Table S1 – Detailed BGC annotations

*Pathway-level annotations of all BGCs in this study.*

- Rows = Individual BGCs
- Columns
  - A. organism = Organism in THOR whose genome has this BGC. Either *Bacillus cereus* UW85, *Flavobacterium johnsoniae* UW101, or *Pseudomonas koreensis* CI12.
  - B. bgc = Name of the BGC. For unknown BGCs, the antiSMASH category of biosynthesis is listed (e.g., putative saccharide, NRPS-like, etc.). For known BGCs, colloquial names are used (e.g., petrobactin, bacillibactin, etc.) and exactly match how they are referred to in the manuscript text.
  - C. bgc\_group = Type of biosynthesis (as defined by antiSMASH)
  - D. contig = the accession number of the genomic contig that a BGC is found
  - E. antiSMASH\_bgc = antiSMASH-generated region numbers for each BGC
  - F. Known = Is this BGC previously experimentally described, Y or N (yes or no)
  - G. Manual curation = were the genes and/or start/end sites of this BGC been manually curated from the antiSMASH predictions, Y or N (yes or no)
  - H. start = start location for the BGC on the contig
  - I. end = end location for the BGC on the contig
  - J. size = size of the BGC in basepairs
  - K. ClusterBlast = top % gene identity in antiSMASH ClusterBlast against antiSMASH-db
  - L. KnownClusterBlast = top % gene identity in antiSMASH ClusterBlast against MIBiG
  - M. Lit\_Activity = bioactivity as described in the literature
  - N. Reference = DOI for references of the BGC and/or bioactivity
  - O. Notes = Notes

### Table S2 – Select BGC Annotations

*Manually-curated, gene-level annotations and BGC start/end sites in THOR BGCs. In cases not seen here, cluster boundaries from antiSMASH predictions were used.*

- Rows = Genes
- Columns
  - A. organism = Organism in THOR whose genome has this gene. Either *Bacillus cereus* UW85, *Flavobacterium johnsoniae* UW101, or *Pseudomonas koreensis* CI12.
  - B. bgc = Name of the BGC. For unknown BGCs, the antiSMASH category of biosynthesis is listed (e.g., putative saccharide, NRPS-like, etc.). For known BGCs, colloquial names are used (e.g., petrobactin, bacillibactin, etc.) and exactly match how they are referred to in the manuscript text.
  - C. contig = the accession number of the genomic contig that a BGC is found

- D. gene = unique gene name from prodigal gene calls in antiSMASH
- E. ann = annotated gene name as found in the literature (e.g., zmaR for zwittermicin resistance gene)
- F. replace\_antismash\_bgc = which BGC should this annotation replace. Perfectly matches column E from Table S1.
- G. ann\_verbose = verbose annotation of each gene
- H. ann\_acc = accession number for each annotation
- I. ann\_percent\_prot\_id = % protein identity to the gene used for annotation
- J. notes = Notes

### Table S3 – WT CPM

*Gene-level counts per million reads (CPM) for wildtype mono- and co-culture transcriptomic studies.*

- Rows = unique gene-replicate pair (e.g., Bc\_ctg1\_1 in replicate B1 is its own unique row)
- Columns
  - A. gene = unique gene name from prodigal gene calls in antiSMASH. Note that antiSMASH calls genes with prodigal across the entire genome, not just in BGCs, so every gene in each THOR genome is represented here (not just those that are in BGCs).
  - B. sample = replicate ID. B1 denotes *Bacillus* (B) monoculture, replicate 1. BFK4 denotes *Bacillus* (B), *Flavobacterium* (F), *Pseudomonas* (K), co-culture, replicate 4.
  - C. cpm = Counts per million reads
  - D. condition = mono- or co-culture condition of this replicate. Bcer denotes *Bacillus* monoculture. Bcer.Fjoh denotes *Bacillus-Flavobacterium* coculture.
  - E. cog\_category = COG category as annotated by eggNOG
  - F. organism = Organism in THOR whose genome has this gene. Either Bcer for *Bacillus cereus* UW85, Fjoh for *Flavobacterium johnsoniae* UW101, or Pkor for *Pseudomonas koreensis* CI12.
  - G. is.q = TRUE or FALSE, is this gene annotated as COG category Q (secondary metabolism)?
  - H. bgc = BGC this gene belongs to. NA if outside a BGC.
  - I. gene\_kind = antiSMASH annotation of type of BGC gene
  - J. smcog = antiSMASH SMCOG category

### Table S4 – WT BGC Expression Changes

*BGC-level changes in expression compared to monoculture.*

- Rows = unique BGC-condition pair (e.g., antiSMASH BGC region Bc\_Ga0417192\_01\_rn01 in condition “Pairwise with Fjoh” is its own unique row)
- Columns
  - A. bgc = antiSMASH BGC region
  - B. BGC of = organism whose genome has this BGC. Either Bcer, Fjoh, or Pkor.
  - C. coculture = coculture condition to compare to monoculture

- D. LFC = Psi log fold change (see methods) of coculture vs. monoculture. Positive values indicate higher expression in coculture, negative values indicate higher expression in monoculture.

#### Table S5 – LC-MS Abundance Matrix

*LC-MS abundance of molecular features in each replicate (n=5 each condition).*

- Rows = unique compound ID for each molecular feature
- Columns = replicate ID. B1 denotes *Bacillus* (B) monoculture, replicate 1. BFK4 denotes *Bacillus* (B), *Flavobacterium* (F), *Pseudomonas* (K), co-culture, replicate 4.
- Data in matrix = LC-MS abundance value (see methods)

#### Table S6 – LC-MS Annotations

*Annotation information for LC-MS molecular features from Table S5.*

- Rows = unique compound ID for each molecular feature. Perfectly matches row names in Table S5.
- Columns
  - A. Compounds.ID = unique compound ID for each molecular feature. Perfectly matches row names in Table S5.
  - B. Name = Compound Discoverer™ Annotation
  - C. Tags = Notes and/or manual annotation
  - D. Formula = Compound Discoverer™ predicted molecular formula
  - E. RT\_min = Compound Discoverer™ retention time
  - F. Calc\_MW = Compound Discoverer™ calculated molecular weight

#### Table S7 – Koreenceine Mutant CPM

*Gene-level counts per million reads (CPM) for koreenceine deletion-mutant mono- and co-culture transcriptomic studies.*

- Rows = unique gene-replicate pair (e.g., Bc\_ctg1\_1 in replicate B1 is its own unique row)
- Columns
  - A. gene = unique gene name from prodigal gene calls in antiSMASH. Note that antiSMASH calls genes with prodigal across the entire genome, not just in BGCs, so every gene in each THOR genome is represented here (not just those that are in BGCs).
  - B. sample = replicate ID. B1 denotes *Bacillus* (B) monoculture, replicate 1. BFK4 denotes *Bacillus* (B), *Flavobacterium* (F), *Pseudomonas* (K), co-culture, replicate 4. “delkeck” denotes the koreenceine deletion mutant of *Pseudomonas*.
  - C. cpm = Counts per million reads

- D. condition = mono- or co-culture condition of this replicate. Bcer denotes *Bacillus* monoculture. Bcer.Fjoh denotes *Bacillus-Flavobacterium* coculture. Pkor denotes wildtype *Pseudomonas* and Pkor\* denotes the *Pseudomonas* koreenceine deletion mutant.
- E. cog\_category = COG category as annotated by eggNOG
- F. organism = Organism in THOR whose genome has this gene. Either Bcer for *Bacillus cereus* UW85, Fjoh for *Flavobacterium johnsoniae* UW101, or Pkor for *Pseudomonas koreensis* CI12.
- G. is.q = TRUE or FALSE, is this gene annotated as COG category Q (secondary metabolism)?
- H. bgc = BGC this gene belongs to. NA if outside a BGC.
- I. gene\_kind = antiSMASH annotation of type of BGC gene
- J. smcog = antiSMASH SMCOG category