## 1. Supplemental Methods

### 1.1 *Soil Sampling and Isolation*

All soil sampling was conducted in public settings; as such, no permission, consent, or authorization was necessitated. Soil sampling was performed during years 2019 – 2024 throughout several geographical locations in Georgia, USA (Atlanta, Georgia; Marietta, Georgia; Brunswick, Georgia; Jekyll Island, Georgia, USA) (1, 2). Soil was gathered from the top layer (0 - 100 cm) and stored in clean containers, allowing for aeration until needed. Bacterial isolation was performed as previously stated (2). Initially, Winogradsky columns were created using the following preparations: approximately 500 mL of the collected soil was mixed with 5 g of $MgSO_4$ and 3 bleached paper towels (cut into small pieces) as a source of carbon, and clean glass 500 mL graduated cylinders were filled up to 300 mL with the soil mixture. For most columns, the turmeric (whole root, ground) was added onto the soil surface; the remaining 200 mL was gently filled with di-$H_2O$, leaving 3 inches of air at the top of the column. The Winogradsky columns were loosely sealed with parafilm and left at room temperature. Columns were sampled once visible growth was observed within the column, approximately 4 weeks post setup.

Rapid flask culturing (soil-turmeric RFC) was alternatively used for the rapid culturing of soil bacteria (2). Into 500 mL sterile flasks (three replications), approximately 100 mL of soil was added along with 200 mL ¼ TSB and sterile turmeric powder for a total concentration of approximately 1% relative to the broth volume. Flasks were incubated at 19 - 22°C, shaking with aeration at 200 rpm, for 5 days before sampling. For the Winogradsky columns, samples were taken from the soil surface and water within the column. For the flask cultures, samples were taken at 96 hours of growth for isolating bacteria. All samples were serial diluted and spread-plated onto ¼ TSA plates with 1% turmeric integrated into the agar. All plates were continuously incubated at 19 - 22° C, and colonies were picked and continuously streak-purified on ¼ TSA + 1% turmeric every three days. Colony purification was confirmed using standard Gram-staining and light microscopy. Gram-stain results and colony morphology are listed within the Supplemental Results.

### 1.2 *Soil RNA Extraction*

Total RNA was extracted from soil–turmeric slurry samples using the ZymoBIOMICS™ DNA/RNA Miniprep Kit (Zymo Research) with modifications optimized for soil. Briefly, soil samples (2 mL) collected from three replications of 48 hr soil-turmeric slurry cultures grown in ¼ TSB were immediately transferred into DNA/RNA Shield™ (Zymo) and stored at -80 °C until processing. For extraction, 0.5 g of the preserved soil slurry was added to ZymoBIOMICS lysis tubes and homogenized by bead beating for 5 min to facilitate cell disruption. Total RNA was purified according to the manufacturer's protocol. Residual genomic DNA was removed by DNase I treatment (Thermo Fisher Scientific™), followed by RNA cleanup and concentration using the Zymo Clean & Concentrator™ kit (Zymo). Purified RNA was eluted in RNase-free water. Extracted RNA was stored at −80 °C until downstream analyses.

Absolute transcript abundances were determined by reverse-transcription quantitative PCR (RT-qPCR). Standard curves were generated from five-fold serial dilutions of DNA containing the target gene, allowing conversion of cycle threshold (Ct) values to copies per reaction. Transcript copy numbers were scaled to the total cDNA volume and were normalized to the soil slurry mass. All results are reported as $\log_{10}$-transformed cDNA copies per 0.5 g of soil-turmeric slurry.

1.3 *Growth Analysis*

Overnight cultures were prepared as mentioned above. After 48 hours, the cells were normalized to an optical density ($OD_{600}$) of 0.20 using sterile ¼ TSB broth, and the 1% turmeric samples were prepared alongside the control samples. The control and turmeric samples ($OD_{600}$ = 0.20) were added to six wells of a polystyrene microtiter plate (200 µL/well). The microtiter plate was placed in a Victor3 V Multilabel Plate Reader (Perkin Elmer, USA) which maintained a temperature of 19 - 22°C with aeration at 200 rpm over the course of the experiment. Optical density readings (600 nm) were recorded for each well every hour for 48 hours. Wells with ¼ TSB broth only (no cells) served as the negative control. All growth procedures were replicated in triplicate.

1.6 *Metatranscriptomics Analysis*

RNA library preparation and sequencing: RNA samples from soil-turmeric slurries (RFC-1, RFC-2, and RFC-3) were prepared as described above. Samples were processed and analyzed with the Microbiome Metatranscriptomics Sequencing Service (Zymo Research, Irvine, CA). Sequencing libraries were prepared using the Zymo-Seq RiboFree® Total RNA Library Kit (R3003, Zymo Research, Irvine, CA) with up to 250 ng RNA input following the manufacturer's protocol. This method uses unique dual-Index 8 bp barcodes with TruSeq® adapters (Illumina, San Diego, CA). All libraries were quantified with Qubit™ 1X dsDNA High Sensitivity (HS) (Q33231, Invitrogen™ ThermoFisher Scientific, Waltham, MA) and TapeStation® (Agilent Technologies, Santa Clara, CA), then were pooled in equal abundance. The final pool was quantified using Droplet Digital™ PCR (Bio-Rad Laboratories, Hercules, CA). The final library was sequenced on the NovaSeq® (Illumina, San Diego, CA).

Bioinformatics analysis: Raw sequence reads were trimmed to remove low quality fractions and adapters with Trimmomatic-0.33 (Bolger et al., 2014): quality trimming by sliding window with 6 bp window size and a quality cutoff of 20 and reads with size lower than 70 bp were removed. After that, ribosomal RNA is was filtered away using RiboDetector (3). Subsequently, host-derived reads were removed using Kraken2 (4) against some common eukaryote host genomes. Low-diversity reads were detected and removed using sdust (https://github.com/lh3/sdust). The surviving reads were subjected to further taxonomy and functional analyses as follows. Antimicrobial resistance and virulence factor gene identification was performed with the DIAMOND sequence aligner (5) against reference databases internally curated from NCBI repositories. Microbial composition was profiled using Sourmash (6). The GTDB species representative database (RS207) was used for bacterial and archaeal identification. Preformatted

GenBank databases (v. 2022.03) provided by Sourmash (https://sourmash.readthedocs.io/en/latest/databases.html) were also used for virus, protozoa, and fungi identification. Reads were mapped back to the genomes identified by Sourmash using BWA-MEM (7) and the microbial abundance was determined based on the counts of mapped reads. The resulting taxonomy and abundance information were further analyzed: 1) to perform alpha- and beta-diversity analyses; 2) to create microbial composition barplots with QIIME (8); 3) to create taxa abundance heatmaps with hierarchical clustering (based on Bray-Curtis dissimilarity); and (4) for biomarker discovery with LEfSe (9) with default settings ($p>0.05$ and LDA effect size >2). Functional profiling was performed using Humann3 (10) including identification of UniRef gene family and MetaCyc metabolic pathways.

*1.7 Methanol Extraction of Curcuminoids from Cells*

Overnight cultures were prepared as mentioned above. After 48 hours, the cells were normalized to an optical density ($OD_{600}$) of 0.20 using sterile ¼ TSB broth, and the 1% turmeric samples were prepared alongside the control samples. The sample cultures were grown at 19 – 22°C with aeration at 200 rpm; 2 mL cells were harvested from the sample cultures at 24, 48, and 72 h of growth. First, the cell suspension was centrifuged at 1,000 rpm for 2 minutes to remove residual turmeric. The supernatants were transferred into new tubes and subsequently centrifuged at 13,000 rpm for 1 minute to pellet the cells, and the cell pellet was washed thrice with dd-$H_2O$. Lastly, the cell pellet was re-suspended in 100% methanol and incubated at 65°C with agitation for 5 minutes, and the tubes were then centrifuged to remove cell debris. The methanol extracts were stored in the dark at 19 – 22°C until analyzed by ATR-FTIR.

*1.8 ATR-FTIR Analysis*

Attenuated Total Reflectance with Fourier Transform Infrared (ATR-FTIR) spectra of methanolic film extracts were collected in rapid-scan mode at 4 cm-1 spectral resolution. Repeated measurements were performed for each sample, and 40 individual interferograms were collected and co-averaged to generate each representative spectrum. Spectra were analyzed in Bruker OPUS 8.2 using processing workflows similar to those applied previously in our ATR-FTIR studies of bacterial cells (11). Baseline correction was performed using a one-iteration concave rubber-band procedure. To facilitate comparison among the cell-derived extract spectra, each film spectrum was scaled to match the absorbance of the ~1510 cm-1 band of the 72 h tur1 tube extract spectrum. For subsequent local comparison of the principal curcuminoid band, spectra were min-max normalized over the 1521-1480 cm-1 region. The spectrum of the methanolic turmeric extract concentrate was baseline-corrected but left unscaled.

Second-derivative spectra were used to aid band identification in regions of band overlap and to suppress broad baseline contributions, consistent with prior FTIR processing approaches for bacterial spectra (11, 12). In a second-derivative spectrum, the negative minimum occurs at the same wavenumber as the maximum in the parent absorbance spectrum; accordingly, the derivative traces shown here were multiplied by -1 for display so that derivative-derived features

visually align with the absorbance bands. This transformation was applied only to improve visualization and does not alter the underlying band positions. As with derivative-based FTIR analysis more generally, this approach improves localization of overlapping spectral features but can also amplify high-frequency noise, and should therefore be interpreted as a peak-resolution tool rather than as an intrinsic improvement in signal-to-noise (11, 12).

**<u>Supplemental Table 1:</u> Primers used for gene amplification.**

| Primer Name | Primer (5' → 3') | Amplicon size (bp) | Source |
|---|---|---|---|
| *16S rRNA*-Fwd | AGA GTT TGA TCC TGG CTC AG | 1542 | IDT, Coralville, IA, USA |
| *16S rRNA*-Rev | ACG GCT ACC TTG TTA CGA CTT | | |
| *ansP*-Fwd | GAA ACG CCG CTG GCT TAA TGC C | 1455 | This study |
| *ansP*-Rev | CTC GCC GTT TCA GGC TTA AAC AC | | |
| *curA*-Fwd | AGC GAT GAG CCA TCT TAT TC | 829 | This study* |
| *curA*-Rev | CGA AGT TTT TAC CCT TCA GC | | |
| *ISAs1*-Fwd | CGC CAG TGC AGC TTA TT | 1012 | This study |
| *ISAs1*-Rev | GAC TAT TTG CGC CGT TAT TTC | | |
| *ISEc*-Fwd | CCT GGA AAG TGG AAC ATA AA | 1063 | This study |
| *ISEc*-Rev | CTG CTA TTA TCG ACC GAA AG | | |
| *mcbR*-Fwd | TGA GAA CGA CCT GAA ACA TC | 581 | This study |
| *mcbR*-Rev | GTT GCA TAA TTT CAG CAA GAC A | | |
| *mnaT*-Fwd | CCG CAA AGC CGA TTG TG | 489 | This study |
| *mnaT*-Rev | TCC GGT TCA GTG CGT TC | | |
| *ortT*-Fwd | ATG TCT CTC TAT CAA CAC ATG CT | 100 | This study |
| *ortT*-Rev | GCC ACC GGG AAA CTC ATC | | |
| *patD*-Fwd | ATC GCA CCG TGG AAT TAT C | 960 | This study |
| *patD*-Rev | GTA ATC CTC CAG CCC ATA AAG | | |
| *rhsC*-Fwd | GGG AGG GAT TAC CTA TGC TAA C | 1148 | This study |
| *rhsC*-Rev | CCT TCT TCA CAA CAC GTT TCA G | | |
| *vgrG*-Fwd | GTG GTG ACC AAA GAC TAC AC | 1193 | This study |
| *vgrG*-Rev | GTG ACG TTA TTC CCT ACA TTG A | | |
| *ydcS*-Fwd | CCG AAC CGC CTA CCA ATT TA | 863 | This study |
| *ydcS*-Rev | AAC TGG CTT TAC ACC CTT CC | | |
| *ydcU*-Fwd | CCT TCA CGT CCA GGT CT | 918 | This study |
| *ydcU*-Rev | CAG AGT GCA TCG AAC GC | | |

| | | | |
|---|---|---|---|
| *ydcV*-Fwd | GAA GAT GAG GAG TTT AG | 612 | This study |
| *ydcV*-Rev | TGC CAC CAC GTT AGT TA | | |
| *ydcY*-Fwd | ATG TCG CAT CTG GAT GAG GTC A | 230 | This study |
| *ydcY*-Rev | CAG AGG ATG GTG CCA CCT | | |
| *ydcZ*-Fwd | TGA ATC AGT CGC TCA CC | 234 | This study |
| *ydcZ*-Rev | AGC AAG CCG GGT ATA AG | | |
| *yncD*-Fwd | CCT GTA TGT GGA CGG TAT TC | 1039 | This study |
| *yncD*-Rev | CGG CAG GTA GCC ATT TAT | | |
| *yncE*-Fwd | CGT GGT TCA TTA CTG TTA GG | 824 | This study |
| *yncE*-Rev | GCT TCC TGC TGT TTA GTG | | |
| *yncL*-Fwd | ATG AAT GTT TCC AGT AGA ACT | 96 | This study |
| *yncL*-Rev | TCA AAT AAA CCA GCC AAA TC | | |

*The forward primer used for *curA* amplification was previously designed (13). The reverse primer for *curA* amplification was designed within the current study.

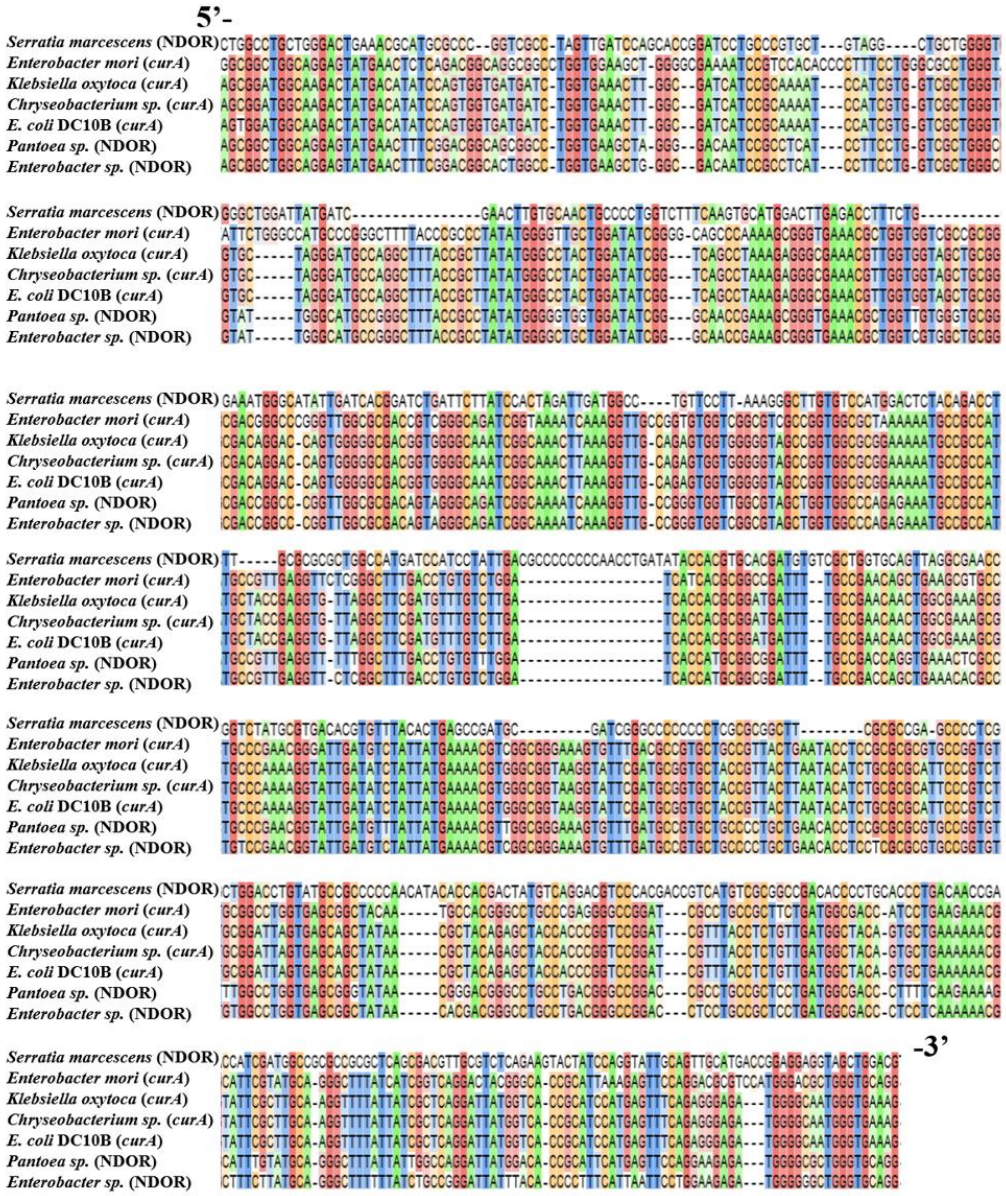
**<u>Supplemental Table 2:</u> Primers used for reverse-transcription quantitative PCR (RT-qPCR) analysis.**

| Primer Name | Primer (5' à 3') | Source |
|---|---|---|
| 1369-Fwd | CGG TGA ATA CGT TCY CGG | (14) |
| 1492-Rev | GGW TAC CTT GTT ACG ACT T | |
| *curA*-RT-Fwd | CAG TGG ATG GCA AGA CTA TG | This study |
| *curA*-RT-Rev | GGC CCA TAT AAG CGG TAA AG | |
| *ansP*-RT-Fwd | GTG CTG ATG GCG TTC GAT TA | This study |
| *ansP*-RT-Rev | CTC GCC GTT TCA GGC TTA AAC AC | |
| *patD*-RT-Fwd | ACA TAA GTT ACT GAT TAA CGG A | This study |
| *patD*-RT-Rev | TCC AGC CCA TAA AGT GAC ATA TC | |
| *yncE*-RT-Fwd | GCT TCC TGC TGT TTA GTG | This study |
| *yncE*-RT-Rev | CGT GGT TCA TTA CTG TTA GG | |
| *yncD*-RT-Fwd | ATG AAG ATT TTT TCC GTC CGA | This study |
| *yncD*-RT-Rev | GGT GTT GCC AGG CGC ATC TC | |
| *mcbR*-RT-Fwd | GGG CGA CAT GGA ACA AAT | This study |
| *mcbR*-RT-Rev | CCC ACA GTT GCT CAA TCA T | |
| *ISEc1*-RT-Fwd | CCC GAT TAC AGA CAA GCC T | This study |
| *ISEc1*-RT-Rev | CCT CTA TAT CTT CCC AGC CTT C | |
| *ISAs*-RT-Fwd | GAA TAA ATA ATC ACC TCC CTG T | This study |
| *ISAs*-RT-Rev | GAG ATT ACA GCT ATC CCA GA | |
| *vgrG*-RT-Fwd | AGG GAA AGA ACA GGT CTA C | This study |
| *vgrG*-RT-Rev | TGA TCG CCT GGT TGT TA | |
| *rhsC*-RT-Fwd | GGA CTA CCG CTT TGA GTA | This study |
| *rhsC*-RT-Rev | CGC ATG TTC CTT CTT CAC | |
| *pptA*-RT-Fwd | TTT CCG CGT GAA CTG GA | This study |
| *pptA*-RT-Rev | GTA GAG CAA TGC TTA TCG AAC TG | |

**<u>Supplemental Table 3:</u> Genomes used for gene synteny *in silico* analysis.**

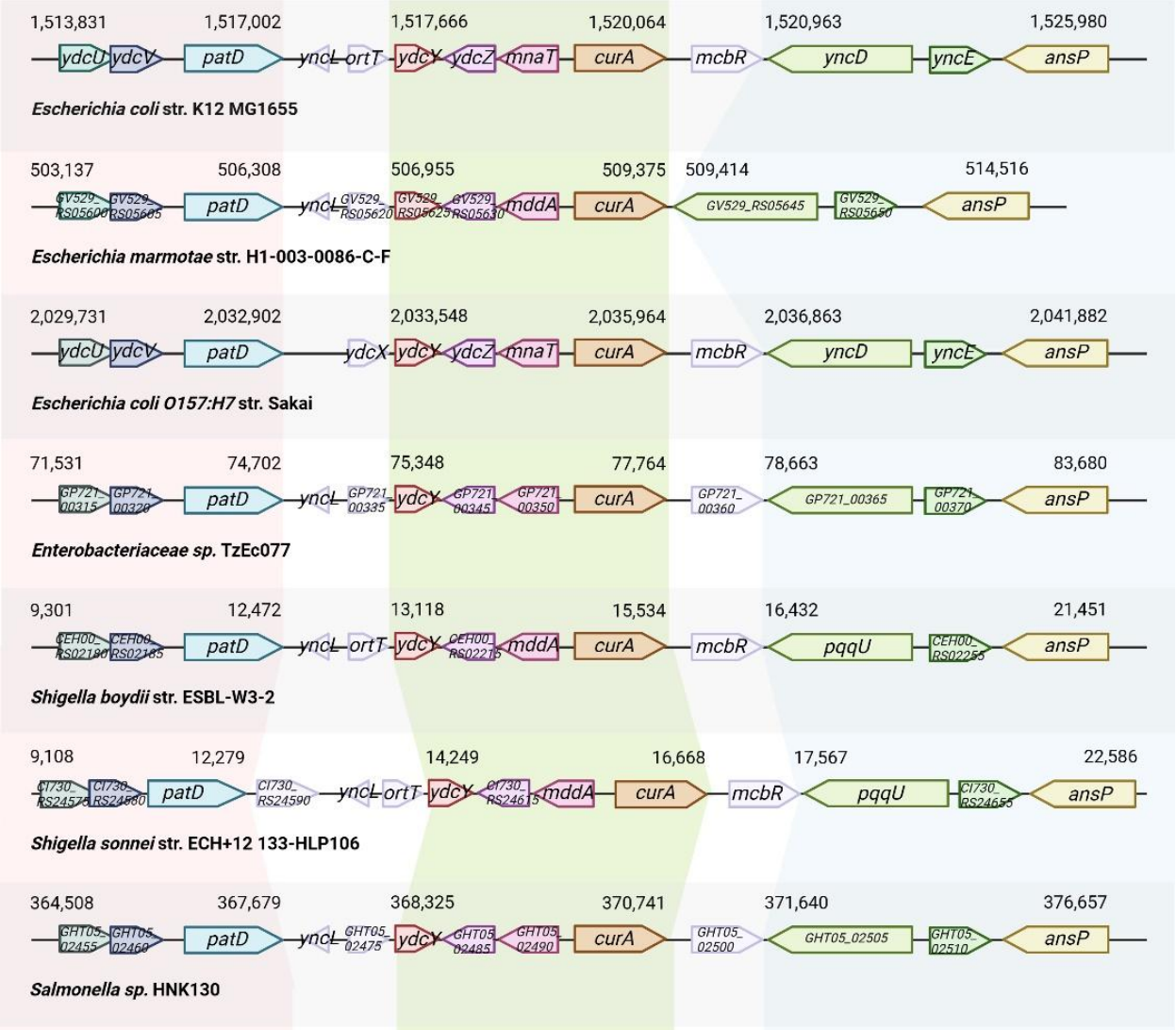
| Species Name | *curA* Gene Location | Sample Collection Information | Year | NCBI Reference |
|---|---|---|---|---|
| *Escherichia coli* str. K-12 substr. MG1655 | 1,519,027 - 1,520,064 | (no information) | - | NC_000913.3 |
| *Escherichia marmotae* str. H1-003-0086-C-F | 508,338 - 509,375 | Creteil, France | 2020 | NZ_CACSXJ020000002.1 |
| *Escherichia coli* O157:H7 str. Sakai | 2,034,927 - 2,035,964 | Fukuyoka, Japan | 2001 | NC_002695.2 |
| *Enterobacteriaceae sp.* TzEc077 | 76,727 - 77,764 | Washington, USA | 2019 | WSGC01000001.1 |
| *Shigella boydii* str. ESBL-W3-2 | 14,497 - 15,534 | Maryland, USA | 2017 | NZ_NIYS01000018.1 |
| *Shigella sonnei* str. ECH+12 133-HLP106 | 15,631 - 16,668 | Maryland, USA | 2017 | NZ_NQBD01000095.1 |
| *Salmonella sp.* HNK130 | 369,704 - 370,741 | Guangzhou, China | 2018 | CP046033.1 |
| *Escherichia fergusonii* str. FDAARGOS | 1,389,434 – 1,390,471 | Maryland, USA | 2021 | NZ_CP083638.1 |
| *Shigella sonnei* str. SE6-1 | 4,408,969 – 4,410,006 | Jellabuk-do, South Korea | 2020 | NZ_CP055292.1 |
| *Shigella dysenteriae* str. SWHEFF | 2,301,012 – 2,302,049 | Hong Kong, China | 2020 | NZ_CP055055.1 |
| *Escherichia ruysiae* str. S1-IND-07-A | 447,576 – 448,646 | Bern, Switzerland | 2022 | NZ_CP112983.1 |
| *Escherichia sp.* E4742 | 4,581,294 – 4,582,331 | Hong Kong, China | 2019 | CP040443.1 |

## 2. Supplemental Data

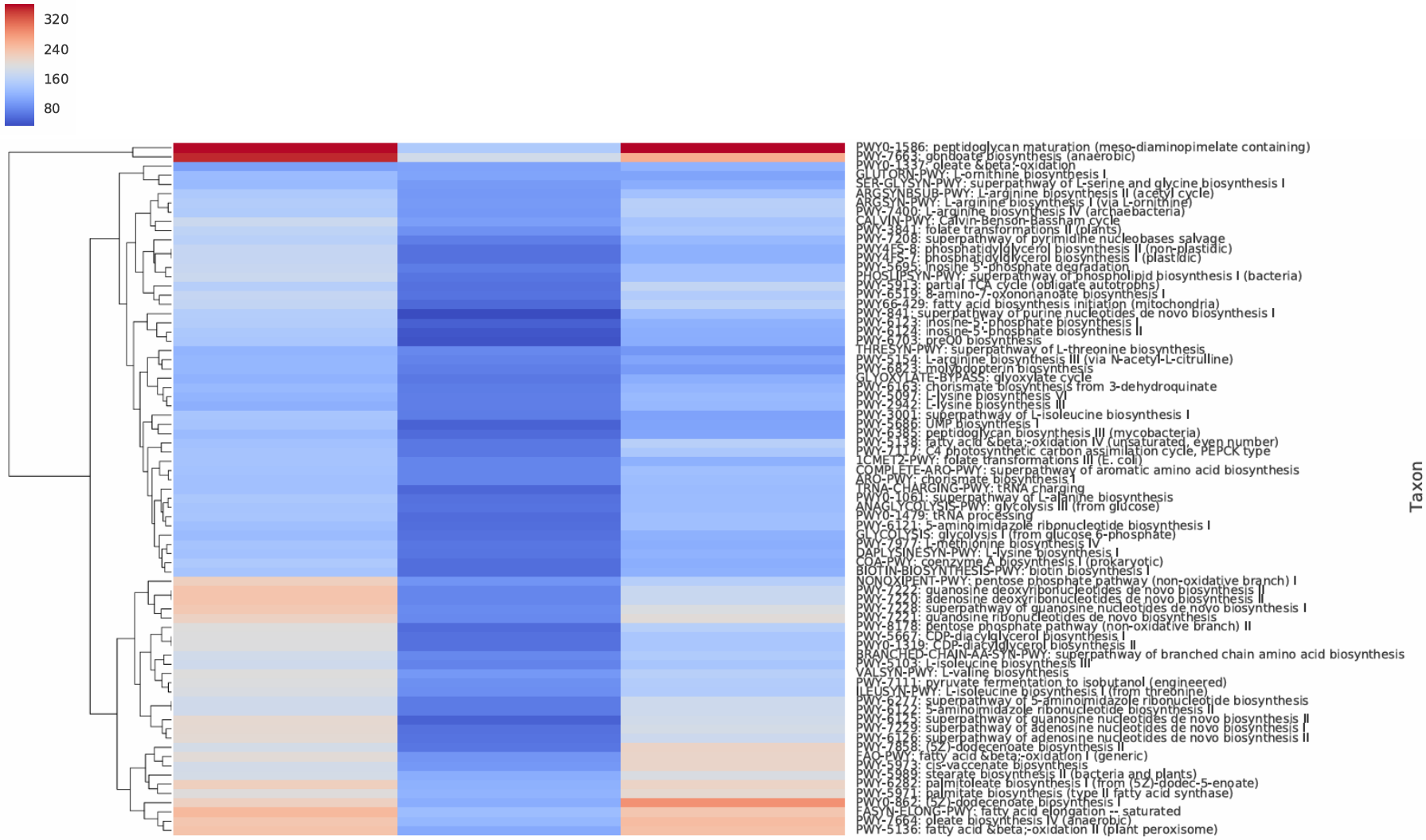



**<u>Supplemental Figure 1:</u> Nucleic acid sequence alignment of *curA* and NDOR genes.** Multiple sequence alignment of *curA* and NDOR amino acid sequences (15). The *curA* gene from *E. coli* DC10B was used for sequence comparison (16). For *E. coli* DC10B, the *curA* sequence is showing nucleotides (5') 298 – 616 (3').


**<u>Supplemental Figure 2:</u> Synteny analysis of genes surrounding *curA*.** *In silico* synteny identification software using multiple sequence alignment (17) found three total regions of synteny surrounding *curA* within 10 genomes that included *Escherichia sp*., *Enterobacteriaceae sp*., *Salmonella sp*., and *Shigella sp*. (Supplemental Table 3).

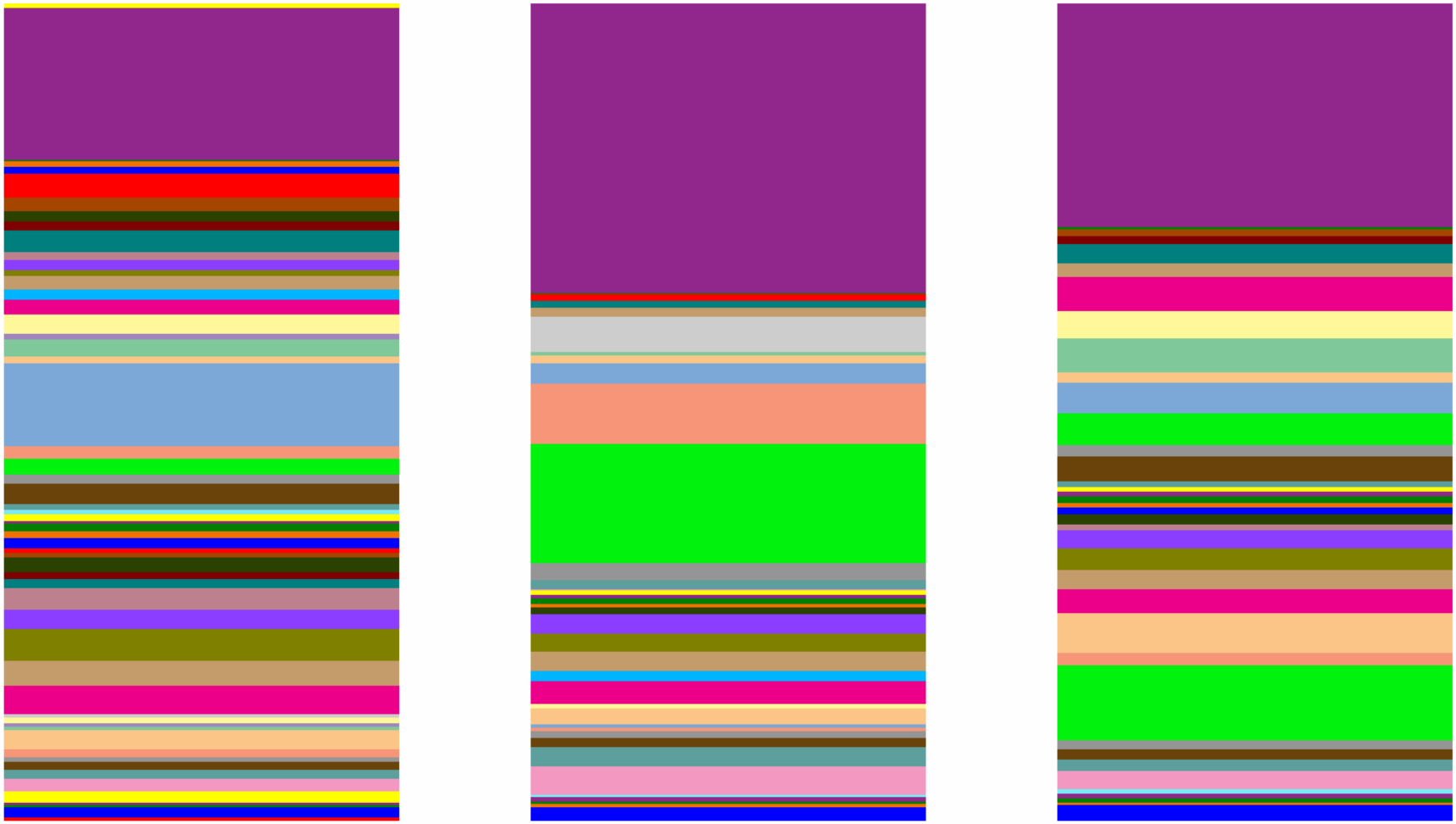



**<u>Supplemental Figure 3:</u> Depiction of the synteny cluster identified during *in silico* analysis.** This illustration shows the first two synteny regions that contain curA (Figure 4); the third synteny region is not depicted here but contains the putative secretion system genes (Figure 6). The gene accession numbers are listed accordingly with the representative genomes (Supplemental Table 3).


320
240
160
80
PWY0-1586: peptidoglycan maturation (meso-diaminopimelate containing)
PWY-7663: gondoate biosynthesis (anaerobic)
PWY0-1337: oleate β-oxidation
GLUTORN-PWY: L-ornithine biosynthesis I
SER-GLYSYN-PWY: superpathway of L-serine and glycine biosynthesis I
ARGSYNBSUB-PWY: L-arginine biosynthesis II (acetyl cycle)
ARGSYN-PWY: L-arginine biosynthesis I (via L-ornithine)
PWY-7400: L-arginine biosynthesis IV (archaebacteria)
CALVIN-PWY: Calvin-Benson-Bassham cycle
PWY-3841: folate transformations II (plants)
PWY-7208: superpathway of pyrimidine nucleobases salvage
PWY4FS-8: phosphatidylglycerol biosynthesis II (non-plastidic)
PWY4FS-7: phosphatidylglycerol biosynthesis I (plastidic)
PWY-5695: inosine 5'-phosphate degradation
PHOSLIPSYN-PWY: superpathway of phospholipid biosynthesis I (bacteria)
PWY-5913: partial TCA cycle (obligate autotrophs)
PWY-6519: 8-amino-7-oxononanoate biosynthesis I
PWY66-429: fatty acid biosynthesis initiation (mitochondria)
PWY-841: superpathway of purine nucleotides de novo biosynthesis I
PWY-6123: inosine-5'-phosphate biosynthesis I
PWY-6124: inosine-5'-phosphate biosynthesis II
PWY-6703: preQ0 biosynthesis
THRESYN-PWY: superpathway of L-threonine biosynthesis
PWY-7254: L-arginine biosynthesis III (via N-acetyl-L-citrulline)
PWY-6823: molybdopterin biosynthesis
GLYOXYLATE-BYPASS: glyoxylate cycle
PWY-6163: chorismate biosynthesis from 3-dehydroquinate
PWY-5097: L-lysine biosynthesis VI
PWY-2942: L-lysine biosynthesis III
PWY-3001: superpathway of L-isoleucine biosynthesis I
PWY-5686: UMP biosynthesis I
PWY-6385: peptidoglycan biosynthesis III (mycobacteria)
PWY-5138: fatty acid β-oxidation IV (unsaturated, even number)
PWY-7117: C4 photosynthetic carbon assimilation cycle, PEPCK type
1CMET2-PWY: folate transformations III (E. coli)
COMPLETE-ARO-PWY: superpathway of aromatic amino acid biosynthesis
ARO-PWY: chorismate biosynthesis I
TRNA-CHARGING-PWY: tRNA charging
PWY0-1061: superpathway of L-alanine biosynthesis
ANAGLYCOLYSIS-PWY: glycolysis III (from glucose)
PWY0-1479: tRNA processing
PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I
GLYCOLYSIS: glycolysis I (from glucose 6-phosphate)
PWY-7977: L-methionine biosynthesis IV
DAPLYSINESYN-PWY: L-lysine biosynthesis I
COA-PWY: coenzyme A biosynthesis I (prokaryotic)
BIOTIN-BIOSYNTHESIS-PWY: biotin biosynthesis I
NONOXIPENT-PWY: pentose phosphate pathway (non-oxidative branch) I
PWY-7222: guanosine deoxyribonucleotides de novo biosynthesis II
PWY-7220: adenosine deoxyribonucleotides de novo biosynthesis II
PWY-7228: superpathway of guanosine nucleotides de novo biosynthesis I
PWY-7221: guanosine ribonucleotides de novo biosynthesis
PWY-8178: pentose phosphate pathway (non-oxidative branch) II
PWY-5667: CDP-diacylglycerol biosynthesis I
PWY0-1319: CDP-diacylglycerol biosynthesis II
BRANCHED-CHAIN-AA-SYN-PWY: superpathway of branched chain amino acid biosynthesis
PWY-5103: L-isoleucine biosynthesis III
VALSYN-PWY: L-valine biosynthesis
PWY-7111: pyruvate fermentation to isobutanol (engineered)
ILEUSYN-PWY: L-isoleucine biosynthesis I (from threonine)
PWY-6277: superpathway of 5-aminoimidazole ribonucleotide biosynthesis
PWY-6122: 5-aminoimidazole ribonucleotide biosynthesis II
PWY-6125: superpathway of guanosine nucleotides de novo biosynthesis II
PWY-7229: superpathway of adenosine nucleotides de novo biosynthesis I
PWY-6126: superpathway of adenosine nucleotides de novo biosynthesis II
PWY-7858: (5Z)-dodecenoate biosynthesis II
FAO-PWY: fatty acid β-oxidation I (generic)
PWY-5973: cis-vaccenate biosynthesis
PWY-5989: stearate biosynthesis II (bacteria and plants)
PWY-6282: palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate)
PWY-5971: palmitate biosynthesis (type II fatty acid synthase)
PWY0-862: (5Z)-dodecenoate biosynthesis I
FASYN-ELONG-PWY: fatty acid elongation -- saturated
PWY-7664: oleate biosynthesis IV (anaerobic)
PWY-5136: fatty acid β-oxidation II (plant peroxisome)
Taxon
RFC-1
RFC-2
RFC-3

**<u>Supplemental Figure 4:</u> Metatranscriptomics analysis of soil-turmeric RFCs after 48 h of growth.** Heatmap of metabolic pathway transcript abundance without hierarchical clustering. Color intensity corresponds to normalized transcript read abundance, with dark red indicating the highest abundance and dark blue indicating the lowest abundance. The data represents three biological replicates of soil-turmeric RFCs (RFC-1, RFC-2, and RFC-3).

A



RFC-1 RFC-2 RFC-3

B

| Legend | Taxonomy | Total % | Flask1 % | Flask2 % | Flask3 % |
|---|---|---|---|---|---|
| | d__Bacteria;p__Actinobacteriota;o__Actinomycetales;f__Dermatophilaceae;g__Piscicoccus;s__Piscicoccus intestinalis;z__GCF_001515525.1 Piscicoccus intestinalis NBRC 104926 strain=NBRC 104926, ASM151552v1 | 0.1% | 0.4% | 0.0% | 0.0% |
| | d__Bacteria;p__Actinobacteriota;o__Actinomycetales;f__Micrococcaceae;g__Galactobacter;s__Galactobacter valinilphilus;z__GCF_003575975.1 Galactobacter valinilphilus strain=JZ R-35, ASM357597v1 | 1.6% | 1.2% | 1.7% | 1.9% |
| | d__Bacteria;p__Actinobacteriota;o__Mycobacteriales;f__Mycobacteriaceae;g__Mycobacterium;s__Mycobacterium phocaicum;z__GCF_010731115.1 Mycolicibacterium phocaicum strain=JCM 15301, ASM1073111v1 | 0.3% | 0.0% | 0.4% | 0.4% |
| | d__Bacteria;p__Actinobacteriota;o__Propionibacteriales;f__Propionibacteriaceae;g__Cutibacterium;s__Cutibacterium acnes;z__GCF_003030305.1 Cutibacterium acnes strain=ATCC 6919, ASM303030v1 | 0.4% | 0.2% | 0.2% | 0.6% |
| | d__Bacteria;p__Firmicutes;o__Bacillales;f__Bacillaceae_G;g__Bacillus_A;s__Bacillus_A paranthracis;z__GCF_001883995.1 Bacillus paranthracis strain=Mn5, ASM188399v1 | 0.5% | 0.4% | 0.5% | 0.5% |
| | d__Bacteria;p__Firmicutes;o__Bacillales;f__Bacillaceae_H;g__Priestia;s__Priestia megaterium_A;z__GCF_009497655.1 Bacillus megaterium strain=A, ASM949765v1 | 0.4% | 1.3% | 0.0% | 0.0% |
| | d__Bacteria;p__Firmicutes;o__Staphylococcales;f__Staphylococcaceae;g__Staphylococcus;s__Staphylococcus aureus;z__GCF_001027105.1 Staphylococcus aureus subsp. aureus DSM 20231 strain=DSM 20231, ASM102710v1 | 0.3% | 0.0% | 0.4% | 0.6% |
| | d__Bacteria;p__Proteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Comamonas;s__Comamonas acidovorans;z__GCF_001598795.1 Delftia acidovorans NBRC 14950 strain=NBRC 14950, ASM159879v1 | 2.4% | 1.6% | 3.4% | 2.1% |
| | d__Bacteria;p__Proteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Comamonas;s__Comamonas tsuruhatensis;z__GCF_001571325.1 Delftia tsuruhatensis NBRC 16741 strain=NBRC 16741, ASM157132v1 | 1.6% | 1.1% | 2.3% | 1.5% |
| | d__Bacteria;p__Proteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Herbaspirillum;s__Herbaspirillum huttiense;z__GCF_004367745.1 Herbaspirillum huttiense strain=NFYY 53159, ASM436774v1 | 1.1% | 0.9% | 1.2% | 1.3% |
| | d__Bacteria;p__Proteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Undibacterium;s__Undibacterium sp014284195;z__GCF_014284195.1 Undibacterium sp. FT31W strain=FT31W, ASM1428419v1 | 0.8% | 0.6% | 0.8% | 1.0% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter ludwigii;z__GCF_001750725.1 Enterobacter ludwigii strain=EN-119, ASM175072v1 | 3.1% | 0.0% | 0.0% | 9.2% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Enterobacter;s__Enterobacter mori;z__GCF_000211415.1 Enterobacter mori LMG 25706 strain=LMG 25706, ASM21141v1 | 0.9% | 1.0% | 0.4% | 1.5% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Erwinia;s__Erwinia billingiae;z__GCF_000196615.1 Erwinia billingiae Eb661 strain=Eb661, ASM19661v1 | 0.2% | 0.0% | 0.5% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Erwinia_B;s__Erwinia_B gerundensis;z__GCF_001517405.1 Erwinia gerundensis, EM595 | 3.0% | 2.3% | 1.9% | 5.0% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella aerogenes;z__GCF_000215745.1 Klebsiella aerogenes KCTC 2190 strain=KCTC 2190, ASM21574v1 | 0.2% | 0.5% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella planticola;z__GCF_000735435.1 Raoultella planticola ATCC 33531 strain=ATCC 33531, GRPL_DRAFTv1 | 0.2% | 0.5% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Klebsiella;s__Klebsiella sp004342285;z__GCF_004342285.1 Raoultella sp. BIGb0138 strain=BIGb0138, ASM434228v1 | 0.4% | 0.6% | 0.5% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Kosakonia;s__Kosakonia cowanii;z__GCF_001975225.1 Kosakonia cowanii JCM 10956 = DSM 18146 strain=888-76, ASM197522v1 | 0.1% | 0.4% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Leclercia;s__Leclercia adecarboxylata;z__GCA_901472455.1 Leclercia adecarboxylata strain=NCTC13032, 28863_C01 | 3.1% | 3.5% | 2.9% | 2.8% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Leclercia;s__Leclercia adecarboxylata_A;z__GCF_006171285.1 Leclercia adecarboxylata strain=Z96-1, ASM617128v1 | 0.4% | 0.0% | 1.2% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Leclercia;s__Leclercia adecarboxylata_B;z__GCA_002360945.1 Leclercia adecarboxylata, ASM236094v1 | 2.6% | 3.1% | 2.3% | 2.4% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Leclercia;s__Leclercia adecarboxylata_C;z__GCF_006874705.1 Leclercia adecarboxylata strain=R25, ASM687470v1 | 2.9% | 3.8% | 2.2% | 2.7% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Leclercia;s__Leclercia sp003024485;z__GCF_011290365.1 Leclercia sp. 29361 strain=29361, ASM1129036v1 | 2.3% | 2.5% | 2.4% | 2.1% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Lelliottia;s__Lelliottia nimipressuralis;z__GCF_004115925.1 Lelliottia nimipressuralis strain=CCUG 25894, ASM411592v1 | 1.1% | 2.5% | 0.0% | 0.8% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Pantoea;s__Pantoea agglomerans;z__GCF_001598475.1 Pantoea agglomerans NBRC 102470 strain=NBRC 102470, ASM159847v1 | 0.4% | 1.1% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Pantoea;s__Pantoea endophytica;z__GCF_002858935.1 Pantoea endophytica strain=596, ASM285893v1 | 0.3% | 0.9% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Pantoea;s__Pantoea eucalypti;z__GCF_009646115.1 Pantoea eucalypti strain=LMG 24197, ASM964611v1 | 1.2% | 1.7% | 0.8% | 1.2% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Pantoea;s__Pantoea eucrina;z__GCF_002095385.1 Pantoea eucrina strain=LMG 5346, ASM209538v1 | 0.2% | 0.6% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Pantoea;s__Pantoea ludwigii_A;z__GCF_900068845.1 Enterobacter ludwigii strain=EnVs2, EnVs2.FASTA | 0.2% | 0.6% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Pantoea;s__Pantoea ludwigii_B;z__GCF_900068835.1 Enterobacter ludwigii strain=EnVs6, EnVs6.FASTA | 0.7% | 1.1% | 0.0% | 0.8% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Pantoea;s__Pantoea vagans;z__GCF_004792415.1 Pantoea vagans strain=LMG 24199, ASM479241v1 | 0.6% | 0.8% | 0.5% | 0.6% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Pseudescherichia;s__Pseudescherichia sp002298805;z__GCF_007680145.1 Enterobacter sp. DE0047 strain=DE0047, ASM768014v1 | 0.8% | 0.9% | 0.6% | 0.7% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Pseudescherichia;s__Pseudescherichia sp002480085;z__GCA_002480085.1 Enterobacteriaceae bacterium UBA7338, ASM248008v1 | 0.4% | 0.4% | 0.4% | 0.5% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Pseudescherichia;s__Pseudescherichia vulneris;z__GCF_000759795.1 Pseudescherichia vulneris NBRC 102420 strain=NBRC 102420, ASM75979v1 | 0.7% | 0.8% | 0.5% | 0.7% |
| | d__Bacteria;p__Proteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__UBA7405;s__UBA7405 sp000755535;z__GCF_017348915.1 Leclercia sp. 4-9-1-25 strain=4-9-1-25, ASM1734891v1 | 0.2% | 0.5% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Halomonadaceae;g__Halomonas;s__Halomonas hamiltonii;z__GCF_014651775.1 Halomonas hamiltonii strain=KCTC 22154, ASM1465177v1 | 0.1% | 0.0% | 0.2% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter calcoaceticus_B;z__GCF_000399665.1 Acinetobacter calcoaceticus ANC 3811 strain=ANC 3811, Acin_calc_ANC_3811_V1 | 0.9% | 0.8% | 1.1% | 0.7% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter courvalinii;z__GCF_014635545.1 Acinetobacter courvalinii strain=CCM 8635, ASM1463554v1 | 1.8% | 2.4% | 0.0% | 3.0% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter oleivorans;z__GCF_000196795.1 Acinetobacter oleivorans DR1 strain=DR1, ASM19679v1 | 1.5% | 1.1% | 2.0% | 1.5% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter sp002365595;z__GCA_002365595.1 Acinetobacter sp. UBA3106, ASM236559v1 | 6.9% | 2.1% | 14.7% | 3.8% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter sp002455755;z__GCA_002455755.1 Acinetobacter sp. UBA6641, ASM245575v1 | 2.9% | 1.4% | 7.2% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter sp004331285;z__GCF_004331285.1 Acinetobacter sp. ANC 3781 strain=ANC 3781, ASM433128v1 | 5.6% | 10.2% | 2.6% | 3.9% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_A;s__Pseudomonas_A stutzeri;z__GCF_000219605.1 Pseudomonas stutzeri strain=CGMCC 1.1803, ASM21960v1 | 1.0% | 0.9% | 1.0% | 1.1% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E atacamensis;z__GCF_004801935.1 Pseudomonas sp. M7D1 strain=M7D1, ASM480193v1 | 2.2% | 2.0% | 0.4% | 4.1% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E chlororaphis_E;z__GCF_001023535.1 Pseudomonas chlororaphis strain=UFB2, ASM102353v1 | 0.3% | 0.8% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E fluorescens_AO;z__GCF_000817895.1 Pseudomonas fluorescens strain=SF39a, ASM81789v1 | 1.8% | 2.2% | 0.0% | 3.3% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E fulva;z__GCF_000730565.1 Pseudomonas fulva NBRC 16637 = DSM 17717 strain=NBRC 16637, ASM73056v1 | 1.4% | 0.0% | 4.2% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E koreensis_C;z__GCF_001605965.1 Pseudomonas koreensis strain=D26, ASM160596v1 | 2.0% | 1.9% | 0.0% | 4.3% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E moraviensis_A;z__GCF_900105805.1 Pseudomonas moraviensis strain=LMG 24280, IMG-taxon 2639762633 annotated assembly | 0.4% | 1.2% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E putida;z__GCF_000412675.1 Pseudomonas putida NBRC 14164 strain=NBRC 14164, ASM41267v1 | 1.5% | 1.8% | 1.2% | 1.7% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E putida_B;z__GCF_001636055.1 Pseudomonas putida strain=PC2, ASM163605v1 | 0.2% | 0.7% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E putida_H;z__GCF_002356095.1 Pseudomonas putida strain=KF715, ASM235609v1 | 0.4% | 1.1% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E putida_J;z__GCF_002025705.1 Pseudomonas putida strain=AA7, ASM202570v1 | 0.4% | 1.1% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E putida_M;z__GCF_002736125.1 Pseudomonas putida strain=E41, ASM273612v1 | 1.9% | 2.5% | 0.8% | 2.4% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E putida_Q;z__GCF_000498395.2 Pseudomonas putida S13.1.2 strain=S13.1.2, ASM49839v3 | 0.7% | 1.2% | 0.0% | 0.8% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E putida_R;z__GCF_000708715.2 Pseudomonas putida W15Oct28 strain=W15Oct28, W15Oct28 99 scaffold | 0.4% | 1.3% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E sp000282535;z__GCF_000282535.1 Pseudomonas sp. GM84 strain=GM84, GM84.fsa | 0.8% | 1.6% | 0.0% | 0.9% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E sp002843585;z__GCF_002843585.1 Pseudomonas sp. 02C 26 strain=02C 26, ASM284358v1 | 1.3% | 3.0% | 0.8% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas_E;s__Pseudomonas_E sp900108875;z__GCF_900108875.1 Pseudomonas sp. NFR16 strain=NFR16, IMG-taxon 2600255283 annotated assembly | 0.3% | 0.8% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Bradyrhizobium;s__Bradyrhizobium sp003020075;z__GCF_016839165.1 Bradyrhizobium sp. PSBB068, ASM1683916v1 | 0.2% | 0.7% | 0.0% | 0.0% |
| | d__Bacteria;p__Proteobacteria;o__Rhizobiales_A;f__Rhizobiaceae_A;g__Phyllobacterium;s__Phyllobacterium sp900539805;z__GCA_900539805.1 uncultured Phyllobacterium sp., UMGS170 | 0.2% | 0.2% | 0.2% | 0.3% |
| | d__Bacteria;p__Proteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Stenotrophomonas;s__Stenotrophomonas maltophilia_AJ;z__GCF_001274595.1 Stenotrophomonas maltophilia strain=ISMMS3, ASM127459v1 | 27.1% | 18.6% | 35.4% | 27.3% |
| | d__Bacteria;p__Proteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Stenotrophomonas;s__Stenotrophomonas rhizophila_A;z__GCF_001704155.1 Stenotrophomonas rhizophila strain=QL-P4, ASM170415v1 | 0.2% | 0.5% | 0.0% | 0.0% |

**<u>Supplemental Figure 5:</u> Taxonomic analysis of soil-turmeric RFCs.** A) Taxonomic composition of soil-turmeric (1%) RFCs at the species level, presented as the relative transcript abundance using QIIME (18). B) The color legend for taxonomy and percentage matches.

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