

Supplementary material

Supplementary Figures

Supplementary Figure 1

An overview of sampling and field soil conditions.

Supplementary Figure 2

The appearance (**A**) and PCS severity (**B**) of potato tubers.

Supplementary Figure 3

The random forest analysis revealed the accuracy of BS and GS bacterial communities in distinguishing between high and low PCS severity.

Supplementary Figure 4

Phylogenetic tree for 16S rRNA gene sequences of the isolated strains using the neighbour-joining method.

Supplementary Figure 5

The effect of pathogen-related strains belonging to the phyla Bacteroidetes and Actinobacteria on pathogen virulence.

Supplementary Figure 6

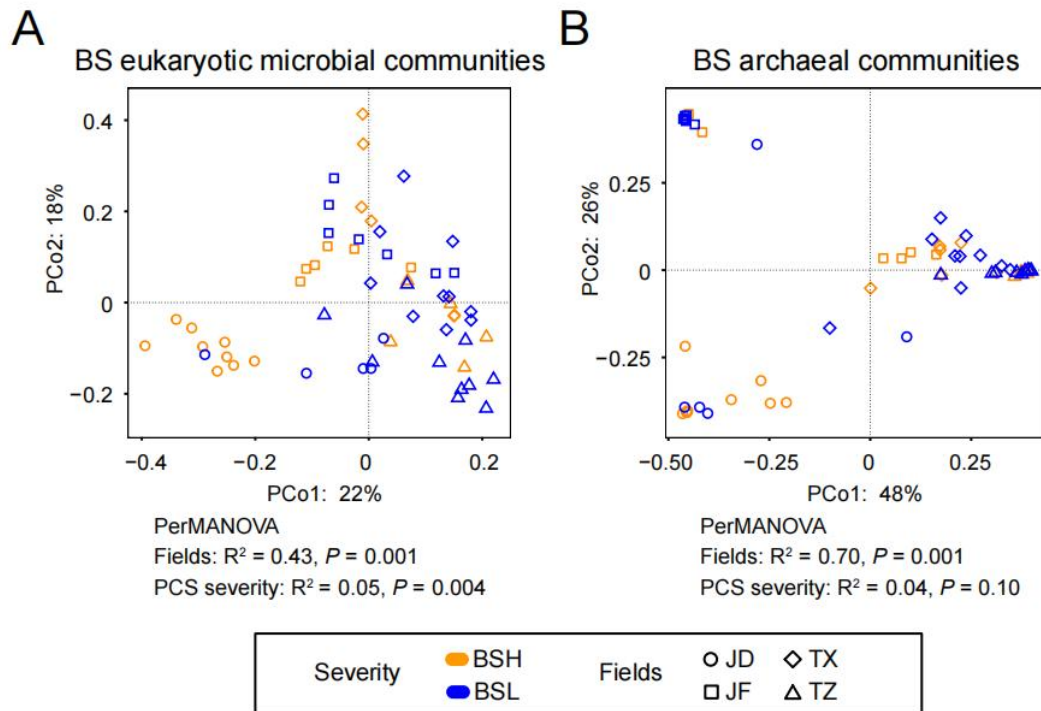
The effect of pathogen-related strains belonging to the phyla Proteobacteria and Firmicutes on pathogen virulence.

Supplementary Figure 7

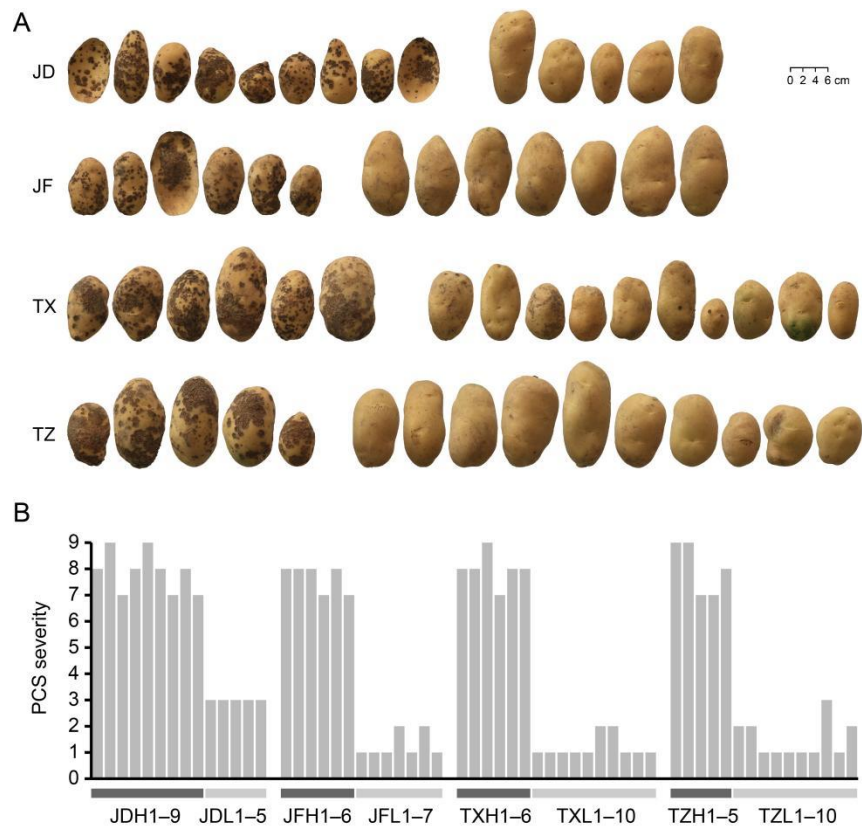
Design and evaluation of eight co-cultivation protocols based on seed suspension cultivation times.

Supplementary Figure 8

The impact of synthetic community FMSS and its constituent strains on the growth indices and enzymatic activities of radish seedlings.

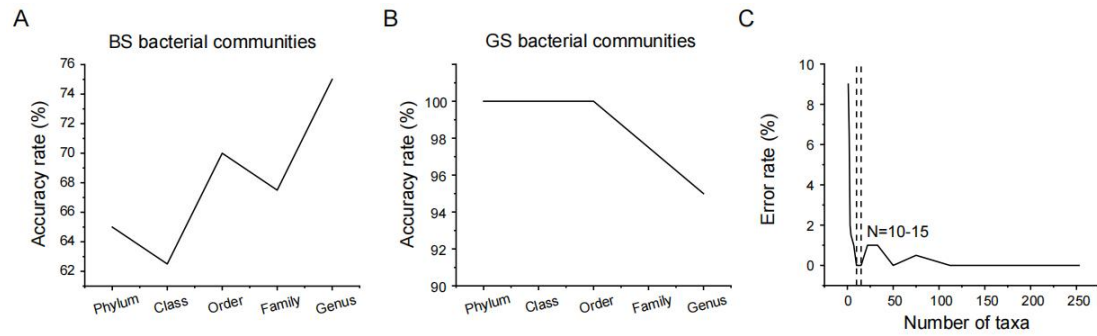


Supplementary Figure 1 Eukaryotic (**A**) microbial communities and Archaeal (**B**) communities of BS significantly differed across these four fields.

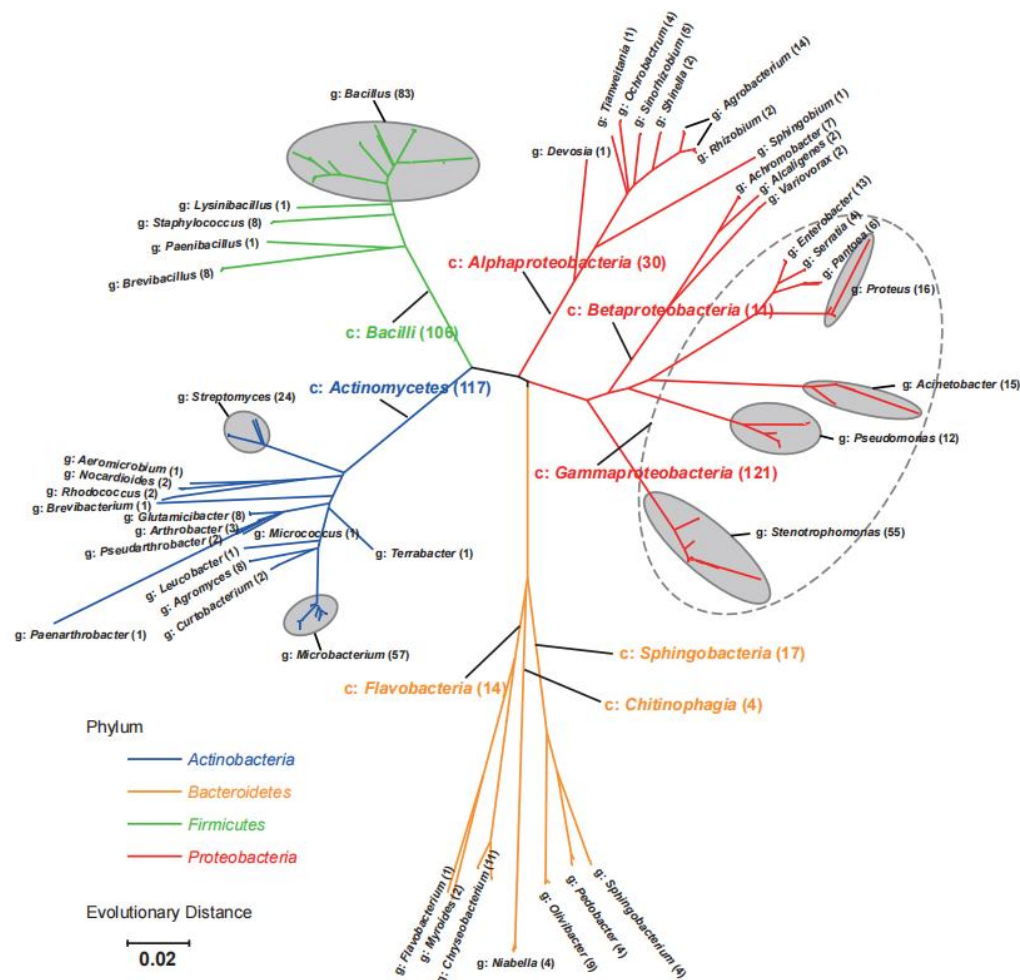


Supplementary Figure 2 The appearance (**A**) and PCS severity (**B**) of potato tubers.

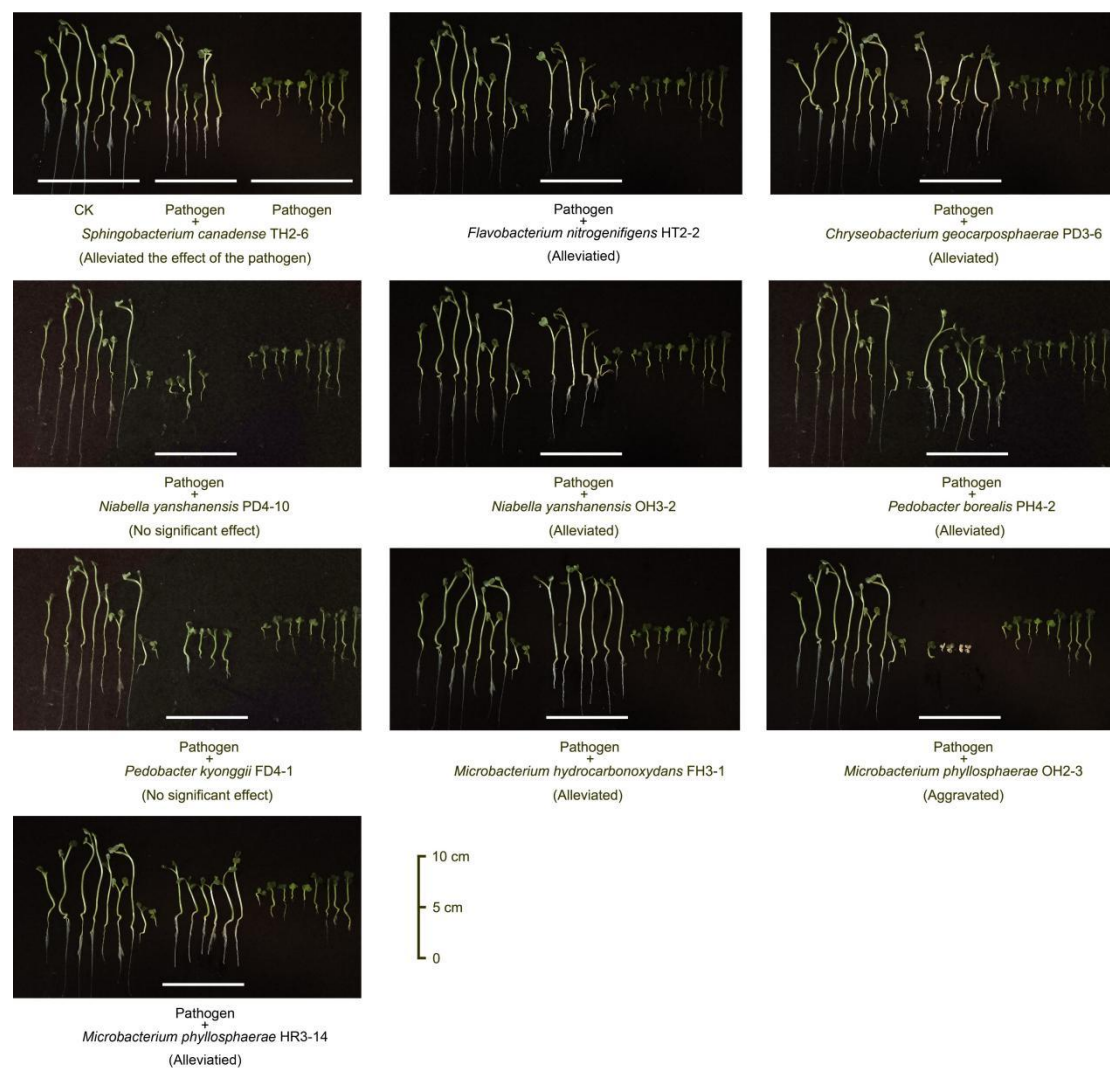
A total of 58 potato plants were selected, including 14 plants in JD, 13 in JF, 16 in TX and 15 in TZ. PCS severity of tubers was assessed on a scale of 1 to 9. According to the severity, the tubers were grouped into H (PCS severity level ≥ 4) or L groups (PCS severity level 1–3).



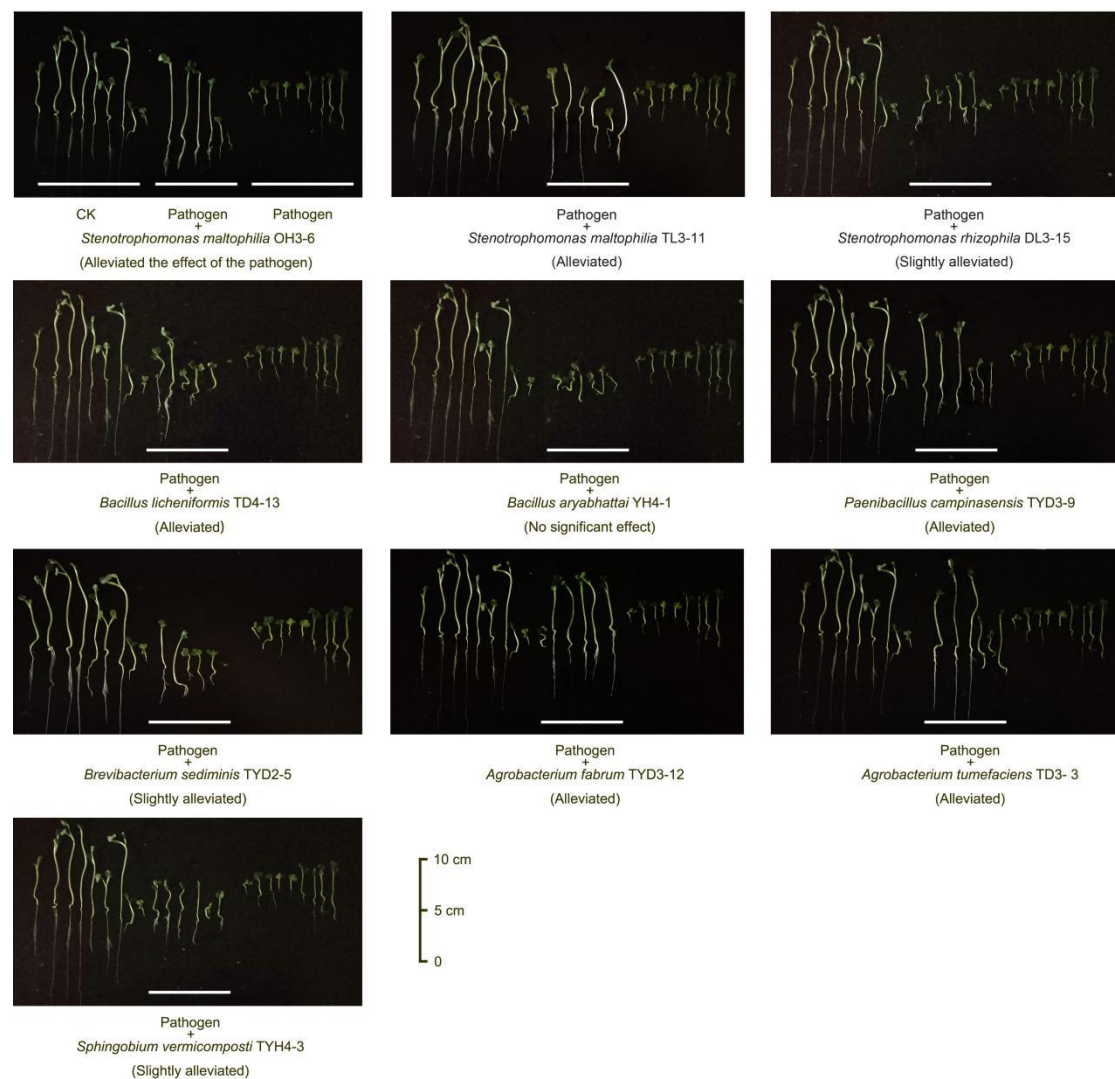
Supplementary Figure 3 The random forest analysis revealed the accuracy of BS and GS bacterial communities in distinguishing between high and low PCS severity. **A-B** The predictive accuracy of BS (**A**) and GS (**B**) bacterial communities in forecasting PCS severity was assessed at the phylum, class, order, family, and genus levels. **C** The importance of GS microbiota members at the order level as biomarkers for PCS severity was evaluated using tenfold cross-validation with five repetitions. The CV error was minimized (at 0) when 10–15 members were selected.



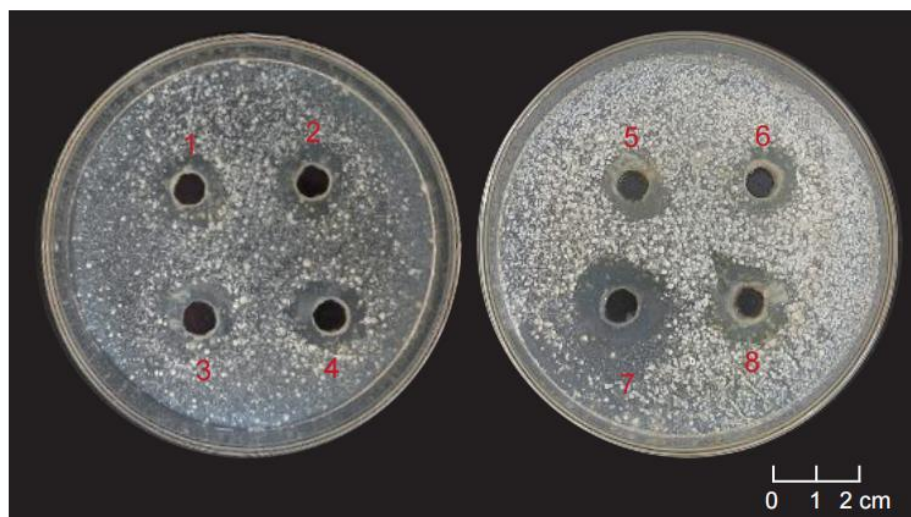
Supplementary Figure 4 Phylogenetic tree for 16S rRNA gene sequences of the isolated strains using the neighbour-joining method. A total of 420 strains were sequenced using the primers Eub 27F (5'-AGAGTTTGATCMTGGCTCAG-3') and Eub 1492 R (5'-ACGGYTACCTTGTTACGACTT-3'). These strains were assigned to a total of 81 species, 45 genera and 4 phyla. The evolutionary distances were computed using the Jukes-Cantor method and are in units of the number of base substitutions per site.



Supplementary Figure 5 The effect of pathogen-related strains belonging to the phyla *Bacteroidetes* and *Actinobacteria* on pathogen virulence. Several strains belonging to the genera *Sphingobacterium*, *Flavobacterium*, *Chryseobacterium*, *Niabella*, *Pedobacter*, and *Microbacterium* were able to alleviate the growth inhibition of radish seedlings by the pathogen *S. scabies*.

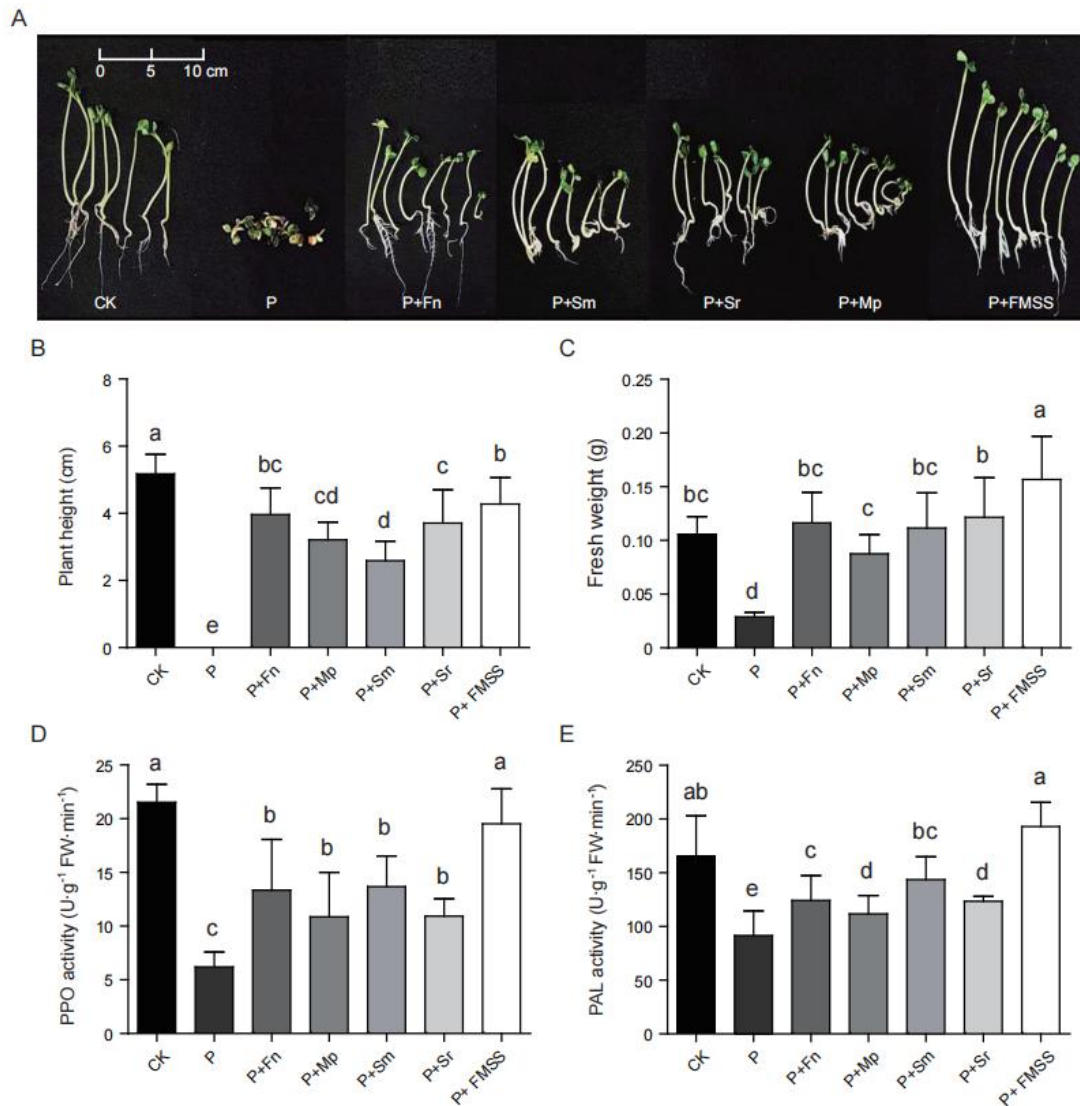


Supplementary Figure 6 The effect of pathogen-related strains belonging to the phyla *Proteobacteria* and *Firmicutes* on pathogen virulence. Several strains belonging to the genera *Stenotrophomonas*, *Bacillus*, *Paenibacillus*, *Brevibacterium*, *Agrobacterium*, and *Sphingobium* were able to alleviate the growth inhibition of radish seedlings by the pathogen *S. scabiei*.



No.	Cultivation protocols	Diameter of inhibition zone (mm)
1	<i>F. nitrogenifigens</i> HT2-2 was cultured individually	8.09±0.54
2	<i>S. maltophilia</i> TL3-11 was cultured individually	9.43±0.22
3	<i>S. rhizophila</i> DL3-15 was cultured individually	3.47±0.49
4	<i>M. phyllosphaerae</i> HR3-14 was cultured individually	11.96±0.19
5	First, <i>F. nitrogenifigens</i> HT2-2 was inoculated and cultured for 24 hours. Next, <i>S. maltophilia</i> TL3-11 and <i>S. rhizophila</i> DL3-15 were inoculated and cultured for 24 hours. Finally, <i>M. phyllosphaerae</i> HR3-14 was inoculated and cultured for 24 hours.	6.14±1.14
6	First, <i>M. phyllosphaerae</i> HR3-14 was inoculated and cultured for 24 hours. Next, <i>S. maltophilia</i> TL3-11 and <i>S. rhizophila</i> DL3-15 were inoculated and cultured for 24 hours. Finally, <i>F. nitrogenifigens</i> HT2-2 was inoculated and cultured for 24 hours.	9.87±0.56
7	First, <i>S. maltophilia</i> TL3-11 and <i>S. rhizophila</i> DL3-15 were inoculated and cultured for 24 hours. Next, <i>F. nitrogenifigens</i> HT2-2 was inoculated and cultured for 24 hours. Finally, <i>M. phyllosphaerae</i> HR3-14 was inoculated and cultured for 24 hours.	21.87±0.36
8	First, <i>F. nitrogenifigens</i> HT2-2 was inoculated and cultured for 24 hours. Next, <i>M. phyllosphaerae</i> HR3-14 was inoculated and cultured for 24 hours. Finally, <i>S. maltophilia</i> TL3-11 and <i>S. rhizophila</i> DL3-15 were inoculated and cultured for 24 hours.	11.38±0.39

Supplementary Figure 7 Design and evaluation of eight co-cultivation protocols based on seed suspension cultivation times. The protocols were based on the strains *F. nitrogenifigens* HT2-2, *M. phyllosphaerae* HR3-14, *S. maltophilia* TL3-11 and *S. rhizophila* DL3-15, with the intention of evaluating the efficacy of each protocol in inhibiting PCS *S. scabies*.



Supplementary Figure 8 The impact of synthetic community FMSS and its constituent strains on the growth indices and enzymatic activities of radish seedlings. **A** Appearance of radish seedlings. **B** Plant height. **C** Fresh weight. **D** Peroxidase (POD) activity. **E** Phenylalanine ammonia lyase (PAL) activity.

Supplementary Note 1

Qiime2 offline data processing

```
conda /home/qiime2-2023.5
find /home/miniconda3/bin/activate -name "*R1.fq.gz"
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find /home -name "*.extendedFragments.fastq.gz" > result.txt
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  --input-path rawdata.txt \
  --output-path scab_five_sample_seqs.qza \
  --input-format PairedEndFastqManifestPhred33V2
qiime demux summarize \
  --i-data scab_five_sample_seqs.qza \
  --o-visualization five_sample_seqs.qzv
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qiime dada2 denoise-paired \
  --i-demultiplexed-seqs scab_five_sample_seqs.qza \
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  --p-trim-left-r 20 \
  --p-trunc-len-f 0 \
  --p-trunc-len-r 0 \
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  --o-representative-sequences rep-seqs.qza \
  --o-denoising-stats denoising-stats.qza \
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  --o-visualization denois/table.qzv \
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  --i-data denois/rep-seqs.qza \
  --o-visualization denois/rep-seqs.qzv
qiime metadata tabulate \
  --m-input-file denois/denoising-stats.qza \
  --o-visualization denois/denoising-stats.qzv
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  --i-table denois/table.qza \
  --p-min-samples 2 \
  --p-min-frequency 5 \
  --o-filtered-table denois/filtered-table.qza
qiime feature-table summarize \
  --i-table denois/filtered-table.qza \
```

```

--o-visualization denois/filtered-table.qzv \
--m-sample-metadata-file denois/metadata.txt
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--i-data rep-seqs.qza \
--i-table filtered-table.qza \
--o-filtered-data filtered-rep-seqs.qza
qiime feature-table tabulate-seqs \
--i-data filtered-rep-seqs.qza \
--o-visualization filtered-rep-seqs.qzv
qiime feature-table filter-seqs \
--i-data rep-seqs.qza \
--i-table filtered-tableping2.qza \
--o-filtered-data filtered-rep-seqs3.qza
qiime feature-table tabulate-seqs \
--i-data filtered-rep-seqs3.qza \
--o-visualization filtered-rep-seqs3.qzv
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biom convert -i feature-table.txt -o feature-table.biom --to-hdf5 --table-type="ASV table"
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--type 'FeatureTable[Frequency]' \
--input-format BIOMV210Format \
--output-path feature-table.qza
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--type 'FeatureData[Sequence]' \
--input-path dna-sequences.fasta \
--output-path bacASVseq.qza
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--o-visualization feature-table.qzv \
--m-sample-metadata-file metadata.txt
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--i-data bacASVseq.qza \
--o-visualization bacASVseq.qzv
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--o-masked-alignment masked-aligned-rep-seqs.qza \
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```

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--verbose  
qiime metadata tabulate \  
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--o-visualization aligned-rep-seqs.qzv
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Supplementary Tables

Supplementary Table 1

Physicochemical properties of BS

Supplementary Table 2

Composition and preparation of bacterial growth media used for isolation

Supplementary Table 3

Statistical analysis of different KEGG pathways of the bacterial communities of GS and BS between H and L

Supplementary Table 4

Taxonomic information for the 63 ASVs belonging to *Streptomyces* genus

Supplementary Table 5

Characteristic values of soil physicochemical properties and microbial communities of BS and GS

Supplementary Table 6

Spearman's correlation analysis between microbial community characteristics, pathogen population and PCS severity

Supplementary Table 7

Evaluating of the effect of GS and BS factors on PCS severity through hierarchical partitioning analysis

Supplementary Table 8

Taxonomy information for 157 ASVs in the Green cluster

Supplementary Table 9

Evaluating of the effect of BS factors on GS bacterial communities and pathogen populations through hierarchical partitioning analysis

Supplementary Table 10

Sequence alignment information between the synthetic community and the green cluster microorganisms

Supplementary Table 1 Physicochemical properties of BS

Groups	pH	EC ($\mu\text{S}/\text{cm}$)	MC (%)	OM (g/kg)	TN (g/kg)	TP (g/kg)	TK (g/kg)	TS (mg/kg)	NH_4^+ (mg/kg)	NO_3^- (mg/kg)	SO_4^{2-} (mg/kg)	Fe^{3+} (g/kg)
JDH	7.08 ± 0.42	92.29 ± 39.17	12.10 ± 9.89	5.15 ± 0.30	1.2 ± 0.39	0.38 ± 0.34	1.99 ± 0.25	61.7 ± 27.60	1.48 ± 1.43	2.19 ± 2.49	189.41 ± 47.05	2.41 ± 0.22
JDL	6.47 ± 1.16	77.15 ± 18.37	8.09 ± 0.81	5.39 ± 1.51	1.06 ± 0.24	0.26 ± 0.14	2.12 ± 0.29	42.48 ± 37.81	0.96 ± 0.30	1.23 ± 1.21	219.35 ± 42.86	2.58 ± 0.28
JFH	4.37 ± 0.42	345.99 ± 227.18	12.69 ± 0.55	15.87 ± 12.67	1.62 ± 0.18	0.31 ± 0.38	2.18 ± 0.15	304.08 ± 146.71	15.71 ± 18.16	15.62 ± 8.68	145.22 ± 30.27	2.65 ± 0.18
JFL	3.96 ± 0.15	368.71 ± 143.36	12.73 ± 2.13	10.03 ± 1.34	1.53 ± 0.47	0.39 ± 0.35	2.22 ± 0.18	204.91 ± 101.33	53.19 ± 50.31	21.12 ± 7.65	129.90 ± 41.36	2.56 ± 0.13
TXH	4.63 ± 0.45	454.31 ± 233.30	13.14 ± 1.11	11.68 ± 1.17	2.00 ± 0.44	1.11 ± 0.49	1.85 ± 0.40	137.22 ± 76.68	6.98 ± 7.28	30.59 ± 10.62	111.29 ± 108.86	2.35 ± 0.32
TXL	4.59 ± 0.44	371.61 ± 208.63	14.03 ± 1.07	11.59 ± 2.12	1.86 ± 0.29	1.44 ± 0.71	2.01 ± 0.17	175.53 ± 58.99	5.92 ± 9.42	22.42 ± 13.64	181.47 ± 243.04	2.65 ± 0.36
TZH	4.36 ± 0.63	404.86 ± 204.84	13.71 ± 0.60	12.74 ± 0.91	1.96 ± 0.23	1.65 ± 0.46	2.04 ± 0.29	213.88 ± 149.36	8.24 ± 14.26	21.12 ± 11.73	138.64 ± 75.33	2.42 ± 0.29
TZL	4.09 ± 0.30	528.14 ± 148.05	13.94 ± 0.67	11.49 ± 1.49	1.84 ± 0.34	1.57 ± 0.88	2.18 ± 0.33	162.82 ± 102.06	2.68 ± 1.20	23.33 ± 12.52	114.03 ± 126.75	2.60 ± 0.44

Supplementary Table 2 Composition and preparation of bacterial growth media used for isolation

Media	Compounds and amounts/L	Instructions
Flour Medium [1]	Plain flour 4 g, CaCO ₃ 0.4 g, (Agar 16 g)	Sterilization at 115°C for 20 minutes, pH: 7.0
Oatmeal Agar Medium (OMA Medium) [2]	Oatmeal 60 g, Agar 12.5 g	Sterilization at 121°C for 15 minutes, pH: 7.2 ± 0.2
Potato Dextrose Agar Medium (PDA Medium) [2]	Infusion from potatoes 5 g, Dextrose 20 g, Agar 20 g	Sterilization at 121°C for 15 minutes, pH: 6.0 ± 0.2
Tryptic Soy Broth Medium (TSB Medium) [1]	Casein (pancreatic digest) 17 g, Soya peptone (papaic digest) 3 g, NaCl 5 g, K ₂ HPO ₄ 2.5 g, Dextrose 2.5 g, (Agar 20 g)	Sterilization at 121°C for 15 minutes, pH: 7.2 ± 0.2
Tryptone Yeast extract Glucose Medium (TYG Medium) [1]	Tryptone 1 g, Yeast extract 1 g, D-glucose 0.5 g, KCl 6.34 g, NaCl 1.2 g, MgSO ₄ · 7H ₂ O 0.25 g, K ₂ HPO ₄ 0.13 g, CaCl ₂ · 2H ₂ O 0.22 g, K ₂ SO ₄ 0.17 g, Na ₂ SO ₄ 2.4 g, NaHCO ₃ 0.5 g, Na ₂ CO ₃ 0.09 g, Fe EDTA 0.07 g, (Agar 20 g)	Sterilization at 121°C for 15 minutes, pH: 7.0
Yeast Extract Mannitol Medium (YEM Medium) [1]	Yeast extract 0.5 g, Mannitol 5 g, K ₂ HPO ₄ 0.5 g, MgSO ₄ · 7H ₂ O 0.2 g, NaCl 0.1 g, (Agar 20 g)	Sterilization at 121°C for 15 minutes, pH: 7.0

1. Bai Y, Müller DB, Srinivas G, Garrido-Oter R, Potthoff E, Rott M, et al. Functional overlap of the *Arabidopsis* leaf and root microbiota. *Nature*. 2015;528(7582):364–9.
2. Pradeep FS, Begam MS, Palaniswamy M, Pradeep BV. Influence of culture media on growth and pigment production by *Fusarium moniliforme* KUMBF1201 isolated from paddy field soil. *World Appl Sci J*. 2013;22(1):70–7.

Supplementary Table 3 Statistical analysis of different KEGG pathways of the bacterial communities of GS and BS between H and L

KEGG Pathway level 3	Level 2	Level 1	GS# Mean	GS# Std.	GSL# Mean	GSL# Std.	P- values	Difference between	BS# Mean	BS# Std.	BSL# Mean	BSL# Std.	P- values	Difference
Ubiquinone and other terpenoid-quinone biosynthesis	1.8 Metabolism of cofactors and vitamins	1. Metabolism	0.7388	0.0547	0.7537	0.0358	0.2446	-0.0150	0.7631	0.0192	0.7687	0.0133	0.2238	-0.0056
Phosphotransferase system (PTS)	3.1 Environmental Information Processing	3. Environmental Information Processing	0.2322	0.0325	0.2206	0.0210	0.2102	0.0291	0.2106	0.0291	0.2106	0.0291	0.2106	0.0004
Thiamine metabolism	1.8 Metabolism of cofactors and vitamins	1. Metabolism	7.3386	0.6102	7.7791	0.3811	0.0031	-0.4405	7.6947	0.2591	7.7075	0.2050	0.8408	-0.0128
Riboflavin metabolism	1.8 Metabolism of cofactors and vitamins	1. Metabolism	0.9562	0.1219	1.2181	0.1703	0.0000	-0.2619	1.2764	0.1138	1.2637	0.1659	0.3750	-0.0128
Lysine degradation	1.5 Amino acid metabolism	1. Metabolism	1.4609	0.1155	1.6269	0.1049	0.0000	-0.1660	1.6205	0.0441	1.6569	0.0536	0.0074	-0.0363
Calcium signaling pathway	3.2 Signal transduction	3. Environmental Information Processing	1.1977	0.0512	1.2025	0.0297	0.6840	-0.0047	1.1797	0.0210	1.1778	0.0328	0.7947	0.0019
Clavulanic acid biosynthesis	1.10 Biosynthesis of other secondary metabolites	1. Metabolism	4.7212	0.2072	4.8746	0.2623	0.0176	-0.1535	4.8078	0.1615	4.7705	0.2469	0.4991	0.0373
Biotin metabolism	1.8 Metabolism of cofactors and vitamins	1. Metabolism	1.1126	0.0819	1.2407	0.0489	0.0000	-0.1281	1.2600	0.0358	1.2498	0.0735	0.4997	0.0102
Purine metabolism	1.4 Nucleotide metabolism	1. Metabolism	2.3232	0.0955	2.4184	0.0721	0.0002	-0.0952	2.4361	0.0375	2.4441	0.0585	0.5393	-0.0080
Photosynthesis - antenna proteins	1.2 Energy metabolism	1. Metabolism	0.9517	0.0670	1.0454	0.0564	0.0000	-0.0937	1.0534	0.0253	1.0592	0.0449	0.5452	-0.0058
Propanoate metabolism	1.1 Carbohydrate metabolism	1. Metabolism	0.0012	0.0024	0.0019	0.0022	0.2847	-0.0007	0.0017	0.0015	0.0017	0.0006	0.8863	-0.0000
Ascorbate and aldarate metabolism	1.1 Carbohydrate metabolism	1. Metabolism	1.4494	0.0698	1.5316	0.0447	0.0000	-0.0821	1.5328	0.0391	1.5405	0.0641	0.5848	-0.0077
Nicotinate and nicotinamide metabolism	1.8 Metabolism of cofactors and vitamins	1. Metabolism	1.5571	0.0633	1.6286	0.0403	0.0000	-0.0715	1.6298	0.0202	1.6330	0.0237	0.5881	-0.0032
Valine, leucine and isoleucine biosynthesis	1.5 Amino acid metabolism	1. Metabolism	0.8332	0.0532	0.8961	0.0470	0.0000	-0.0629	0.9291	0.0104	0.9108	0.0641	0.2005	0.0183
Tetracycline biosynthesis	1.9 Metabolism of terpenoids and polyketides	1. Metabolism	0.0162	0.0040	0.0187	0.0055	0.0560	-0.0025	0.0222	0.0036	0.0199	0.0055	0.7466	0.0004
Various types of N-glycan biosynthesis	1.1 Carbohydrate metabolism	1. Metabolism	0.0692	0.0158	0.0681	0.0069	0.7486	0.011	0.0749	0.0096	0.0762	0.0082	0.5905	-0.0013
Steroid biosynthesis	1.3 Lipid metabolism	1. Metabolism	1.8889	0.0525	1.8957	0.0460	0.1444	-0.0068	1.9345	0.0380	1.9404	0.0667	0.6778	-0.0059
Retinol metabolism	1.8 Metabolism of cofactors and vitamins	1. Metabolism	2.3534	0.0568	2.4123	0.0615	0.0005	-0.0588	2.4231	0.0447	2.4315	0.0486	0.5954	-0.0084
Other glycan degradation	1.7 Glycan biosynthesis and metabolism	1. Metabolism	0.1269	0.0209	0.1675	0.0219	0.0000	-0.0406	0.1752	0.0162	0.1732	0.0199	0.5200	0.0031
Glycosaminoglycan degradation	1.7 Glycan biosynthesis and metabolism	1. Metabolism	0.0492	0.0091	0.0519	0.0105	0.3046	-0.0027	0.0534	0.0071	0.0500	0.0072	0.7778	0.0035
Toluene degradation	1.11 Xenobiotics biodegradation and metabolism	1. Metabolism	0.2214	0.0278	0.2602	0.0319	0.0000	-0.0388	0.2593	0.0172	0.2664	0.0228	0.1869	-0.0071
Zeaxanthin biosynthesis	1.9 Metabolism of terpenoids and polyketides	1. Metabolism	0.4339	0.0317	0.4706	0.0267	0.0000	-0.0366	0.4918	0.0188	0.4667	0.0442	0.5184	-0.0049
Amino sugar and nucleotide sugar metabolism	1.1 Carbohydrate metabolism	1. Metabolism	0.7449	0.0543	0.7746	0.0237	0.0160	-0.0297	0.7973	0.0177	0.7935	0.0173	0.4177	0.0038
Biosynthesis of siderophore group nonribosomal peptides	1.9 Metabolism of terpenoids and polyketides	1. Metabolism	0.4338	0.0263	0.4365	0.0207	0.6698	-0.0028	0.4444	0.0081	0.4462	0.0118	0.4983	-0.0018
Pentose phosphate pathway	1.1 Carbohydrate metabolism	1. Metabolism	0.0626	0.0144	0.0596	0.0090	0.3606	0.0031	0.0690	0.0085	0.0641	0.0101	0.0542	0.0049
Cysteine and methionine metabolism	1.5 Amino acid metabolism	1. Metabolism	0.6204	0.0323	0.6125	0.0263	0.2388	0.0079	0.6251	0.0153	0.6267	0.0296	0.7917	-0.0016
Aminobenzoate degradation	1.11 Xenobiotics biodegradation and metabolism	1. Metabolism	0.3957	0.0257	0.4251	0.0254	0.0001	-0.0274	0.4419	0.0171	0.4280	0.0218	0.0998	0.0139
Biosynthesis of ansamycins	1.9 Metabolism of terpenoids and polyketides	1. Metabolism	0.0000	0.0000	0.0000	0.0000	0.9317	-0.0000	0.0000	0.0000	0.0000	0.0000	0.6147	-0.0000
Phenylalanine metabolism	1.5 Amino acid metabolism	1. Metabolism	0.6900	0.0481	0.7144	0.0264	0.0289	-0.0244	0.7064	0.0167	0.7115	0.0162	0.2504	-0.0052
Peptidoglycan biosynthesis	1.7 Glycan biosynthesis and metabolism	1. Metabolism	0.1253	0.0243	0.1478	0.0194	0.0005	-0.0225	0.1634	0.0223	0.1610	0.0193	0.6681	0.0024
Ether lipid metabolism	1.3 Lipid metabolism	1. Metabolism	2.5841	0.0695	2.5511	0.0518	0.0551	0.0329	2.5460	0.0326	2.5373	0.0315	0.3219	0.0086
Betalain biosynthesis	1.10 Biosynthesis of other secondary metabolites	1. Metabolism	0.5106	0.0223	0.5317	0.0259	0.0018	-0.0211	0.5280	0.0157	0.5355	0.0130	0.0600	-0.0075
Fatty acid metabolism	1.0 Global and overview maps	1. Metabolism	0.0452	0.0107	0.0486	0.0103	0.2415	-0.0033	0.0523	0.0067	0.0555	0.0185	0.3756	-0.0032
Secondary bile acid biosynthesis	1.3 Lipid metabolism	1. Metabolism	0.1115	0.0199	0.1319	0.0150	0.0001	-0.0203	0.1393	0.0076	0.1503	0.0181	0.0038	-0.0110
Caffeine metabolism	1.10 Biosynthesis of other secondary metabolites	1. Metabolism	0.0059	0.0036	0.0058	0.0027	0.9148	0.0001	0.0065	0.0021	0.0065	0.0020	0.9495	0.0000
Pyruvate metabolism	1.1 Carbohydrate metabolism	1. Metabolism	0.4084	0.0274	0.4277	0.0171	0.0038	-0.0193	0.4379	0.0084	0.4404	0.0097	0.3000	-0.0025
Pentose and glucuronate interconversions	1.1 Carbohydrate metabolism	1. Metabolism	0.1481	0.0258	0.1634	0.0184	0.0162	-0.0153	0.1756	0.0158	0.1756	0.0205	0.9969	0.0000
Starch and sucrose metabolism	1.1 Carbohydrate metabolism	1. Metabolism	0.1072	0.0130	0.1202	0.0093	0.0001	-0.0130	0.1258	0.0083	0.1223	0.0064	0.9942	0.0034
Isoquinoline alkaloid biosynthesis	1.10 Biosynthesis of other secondary metabolites	1. Metabolism	0.0756	0.0143	0.0872	0.0116	0.0019	-0.0117	0.0976	0.0110	0.0982	0.0193	0.8786	-0.0006
Carotenoid biosynthesis	1.9 Metabolism of terpenoids and polyketides	1. Metabolism	0.1007	0.0139	0.1116	0.0137	0.0050	-0.0109	0.1189	0.0125	0.1186	0.0136	0.9305	0.0003
Phosphatidylinositol signaling system	3.2 Signal transduction	3. Environmental Information Processing	0.0097	0.0050	0.0203	0.0125	0.0001	-0.0106	0.0128	0.0047	0.0120	0.0061	0.5917	0.0008
One carbon pool by folate	1.8 Metabolism of cofactors and vitamins	1. Metabolism	0.0356	0.0071	0.0438	0.0090	0.0000	-0.0103	0.0426	0.0042	0.0408	0.0127	0.0873	-0.0043
Lipoic acid metabolism	1.8 Metabolism of cofactors and vitamins	1. Metabolism	0.0901	0.0099	0.0901	0.0001	0.6653	-0.0000	0.0901	0.0001	0.0901	0.0001	0.8805	-0.0000
Indole alkaloid biosynthesis	1.10 Biosynthesis of other secondary metabolites	1. Metabolism	0.0896	0.0126	0.0995	0.0078	0.0015	-0.0099	0.1039	0.0065	0.1058	0.0062	0.2636	-0.0019
Arginine and proline metabolism	1.5 Amino acid metabolism	1. Metabolism	0.0816	0.0131	0.0903	0.0140	0.0187	-0.0088	0.0952	0.0069	0.0938	0.0118	0.5787	0.0014
ABC transporters	3.1 Membrane transport	3. Environmental Information Processing	1.9659	0.0884	1.9991	0.0584	0.1140	-0.0332	1.9473	0.0366	1.9568	0.0404	0.3618	-0.0095
Steroid hormone biosynthesis	1.3 Lipid metabolism	1. Metabolism	0.1825	0.0136	0.1912	0.0097	0.0099	-0.0087	0.1931	0.0084	0.1919	0.0065	0.5437	0.0012
Fluorobenzoate degradation	1.11 Xenobiotics biodegradation and metabolism	1. Metabolism	0.0398	0.0082	0.0469	0.0065	0.0010	-0.0070	0.0525	0.0101	0.0507	0.0081	0.4585	-0.0019
Phenanthrene and CoA biosynthesis	1.8 Metabolism of cofactors and vitamins	1. Metabolism	0.4815	0.0197	0.4736	0.0097	0.0776	0.0079	0.4721	0.0062	0.4771	0.0054	0.0026	-0.0050
alpha-Linolenic acid metabolism	1.3 Lipid metabolism	1. Metabolism	0.0987	0.0183	0.0986	0.0109	0.5793	0.0001	0.1057	0.0092	0.1036	0.0109	0.4568	0.0021
Biosynthesis of type II polyketide products	1.9 Metabolism of terpenoids and polyketides	1. Metabolism	0.0104	0.0059	0.0171	0.0122	0.0075	-0.0068	0.0209	0.0071	0.0368	0.0552	0.1049	-0.0159
Lipopolysaccharide biosynthesis	1.7 Glycan biosynthesis and metabolism	1. Metabolism	0.0201	0.0082	0.0261	0.0092	0.0125	-0.0060	0.0270	0.0050	0.0301	0.0094	0.1117	-0.0032
Pyrimidine metabolism	1.4 Nucleotide metabolism	1. Metabolism	2.5158	0.0839	2.5067	0.0394	0.6198	0.0091	2.4970	0.0193	2.4684	0.0355	0.0004	0.0286
Terpenoid backbone biosynthesis	1.9 Metabolism of terpenoids and polyketides	1. Metabolism	0.0130	0.0034	0.0187	0.0047	0.0000	-0.0057	0.0175	0.0055	0.0175	0.0035	0.0026	-0.0003
Flavonoid biosynthesis	1.10 Biosynthesis of other secondary metabolites	1. Metabolism	2.1386	0.1637	2.1562	0.2269	0.7368	-0.0177	2.1441	0.0920	2.1494	0.1127	0.8454	-0.0054
Fructose and mannose metabolism	1.1 Carbohydrate metabolism	1. Metabolism	0.0047	0.0024	0.0052	0.0012	0.2939	-0.0006	0.0056	0.0011	0.0054	0.0012	0.5421	0.0002
Glycolysis / Gluconeogenesis	1.1 Carbohydrate metabolism	1. Metabolism	0.0082	0.0026	0.0104	0.0051	0.0464	-0.0022	0.0109	0.0017	0.0110	0.0017	0.8005	-0.0001
Arachidonic acid metabolism	1.3 Lipid metabolism	1. Metabolism	0.6815	0.0601	0.6658	0.0360	0.2576	0.0157	0.6795	0.0217	0.6892	0.0486	0.3278	-0.0096
C5-Branched dibasic acid metabolism	1.1 Carbohydrate metabolism	1. Metabolism	0.0094	0.0051	0.0094	0.0031	0.2002	-0.0020	0.0131	0.0022	0.0157	0.0097	0.1561	-0.0026
Naphthalene degradation	1.11 Xenobiotics biodegradation and metabolism	1. Metabolism	0.4764	0.0204	0.4684	0.0153	0.1103	-0.0080	0.4669	0.0101	0.4713	0.0092	0.0991	-0.0044
Benzoate degradation	1.1332	0.0085	0.1351	0.0082	0.3918	-0.0019	0.1329	0.0039	0.1344	0.0039	0.1367	0.0039	0.1567	-0.0015
Biosynthesis of type II polyketide backbone	1.9 Metabolism of terpenoids and polyketides	1. Metabolism	0.0954	0.0179	0.0943	0.0116	0.8035	0.0010	0.1037	0.0101	0.0941	0.0090	0.0006	0.0995
N-Glycan biosynthesis	1.7 Glycan biosynthesis and metabolism	1. Metabolism	0.0031	0.0010	0.0039	0.0011	0.0057	-0.0008	0.0033	0.0011	0.0028	0.0005	0.0523	0.0005
Fatty acid biosynthesis	1.3 Lipid metabolism	1. Metabolism	0.0005	0.0003	0.0009	0.0006	0.0013	-0.0004	0.0005	0.0002	0.0006	0.0003	0.7539	-0.0000
Taurine and hypotaurine metabolism	1.6 Metabolism of other amino acids	1. Metabolism	0.1902	0.0135	0.1844	0.0069	0.0617	0.0057	0.1852	0.0033	0.1828	0.0071	0.1063	0.0024
Sulfur metabolism	1.2 Energy metabolism	1. Metabolism	0.0002	0.0001	0.0004	0.0003	0.0007	-0.0002	0.0003	0.0003	0.0005	0.0004	0.0075	-0.0002
Phenylalanine, tyrosine and tryptophan biosynthesis	1.5 Amino acid metabolism	1. Metabolism	0.0001	0.0001	0.0001	0.0001	0.0227	-0.0000	0.0001	0.0001	0.0001	0.0001	0.8325	0.0000
Galactose metabolism	1.1 Carbohydrate metabolism	1. Metabolism	0.0011	0.0007	0.0007	0.0003	0.2676	0.0004	0.0012	0.0005	0.0008	0.0021	0.0004	-0.0004
Polyketide sugar unit biosynthesis	1.9 Metabolism of terpenoids and polyketides	1. Metabolism	0.0026	0.0010	0.0026	0.0009	0.8161	0.0001	0.0031	0.0007	0.0029	0.0008	0.2756	0.0002
Glutathione metabolism	1.6 Metabolism of other amino acids	1. Metabolism	0.0373	0.0087	0.0406	0.0069	0.1190	-0.0034	0.0484	0.0072	0.0459	0.0085	0.2337	0.0025
Nitrotoluene degradation	1.11 Xenobiotics biodegradation and metabolism													

Supplementary Table 4 Taxonomic information for the 63 ASVs belonging to *Streptomyces* genus

ASV	Species information	Reference sequence ID	Consistency (%)
BASV9	<i>Streptomyces acidiscabies</i>	NR_025866.2	100
BASV75	<i>Streptomyces turgidiscabies</i>	NR_040828.2	100
BASV124	<i>Streptomyces bikiniensis</i>	NR_112436.1	100
BASV175	<i>Streptomyces monticola</i>	NR_164930.1	100
BASV187	<i>Streptomyces avermitilis</i>	NR_074747.2	100
BASV252	<i>Streptomyces caldifontis</i>	NR_149197.1	100
BASV346	<i>Streptomyces graminilatus</i>	NR_125579.1	100
BASV354	<i>Streptomyces neyagawaensis</i>	NR_025868.2	100
BASV399	<i>Streptomyces eurythermus</i>	NR_025869.2	100
BASV510	<i>Streptomyces deserti</i>	NR_116355.1	100
BASV566	<i>Streptomyces prasinosporus</i>	NR_115671.1	100
BASV617	<i>Streptomyces asenjonii</i>	NR_152642.1	100
BASV863	<i>Streptomyces steffisburgensis</i>	NR_178228.1	100
BASV890	<i>Streptomyces verrucosispurus</i>	NR_151951.1	99.51
BASV908	<i>Streptomyces clavifer</i>	NR_112453.1	100
BASV918	<i>Streptomyces aridus</i>	NR_149222.1	100
BASV939	<i>Streptomyces qinzhouensis</i>	NR_180506.1	100
BASV1121	<i>Streptomyces verrucosispurus</i>	NR_151951.1	100
BASV1164	<i>Streptomyces polymachus</i>	NR_136769.1	100
BASV1226	<i>Streptomyces blattellae</i>	NR_180531.1	100
BASV1244	<i>Streptomyces hawaiiensis</i>	NR_114824.2	100
BASV1354	<i>Streptomyces flavidoviren</i>	NR_115445.1	100
BASV1408	<i>Streptomyces jeddahensis</i>	NR_156945.1	100
BASV1414	<i>Streptantibioticus parmotrematis</i>	NR_181850.1	100
BASV1510	<i>Streptomyces mimosae</i>	NR_170412.1	95.32
BASV1972	<i>Streptomyces verrucosispurus</i>	NR_151951.1	99.27
BASV2010	<i>Streptomyces panacagri</i>	NR_112566.1	99.51
BASV2157	<i>Streptomyces broussonetiae</i>	NR_180862.1	100
BASV2218	<i>Streptomyces verrucosispurus</i>	NR_151951.1	98.54
BASV2903	<i>Streptomyces hawaiiensis</i>	NR_114824.2	99.76
BASV3107	<i>Streptomyces gossypisoli</i>	NR_180846.1	100
BASV3438	<i>Streptomyces lavendulae</i>	NR_117992.2	100
BASV3534	<i>Streptomyces griseorubiginosus</i>	NR_114835.1	100
BASV3574	<i>Streptomyces toxytricini</i>	NR_112291.1	100
BASV3648	<i>Streptomyces monomycini</i>	NR_112592.1	99.27
BASV4118	<i>Streptomyces paromomycinus</i>	NR_112468.1	99.27
BASV4488	<i>Streptomyces zhaozhouensis</i>	NR_133874.1	100
BASV5249	<i>Streptomyces physcomitrii</i>	NR_180163.1	99.76
BASV5323	<i>Streptomyces triticiradicis</i>	NR_169450.1	100
BASV5385	<i>Streptomyces acidiscabies</i>	NR_025866.2	98.3
BASV5908	<i>Streptomyces xiangtanensis</i>	NR_164877.1	99.03
BASV6406	<i>Streptomyces hokutonensis</i>	NR_134197.1	99.76
BASV6489	<i>Streptomyces qinzhouensis</i>	NR_180506.1	99.76
BASV6609	<i>Streptomyces triticiradicis</i>	NR_169450.1	99.03
BASV7474	<i>Streptomyces xiaopingdaonensis</i>	NR_148293.1	99.76
BASV7504	<i>Streptomyces tremellae</i>	NR_178504.1	100
BASV7766	<i>Streptomyces neyagawaensis</i>	NR_025868.2	98.55
BASV8204	<i>Streptomyces pinistramenti</i>	NR_181887.1	99.02
BASV8233	<i>Streptomyces avermitilis</i>	NR_074747.2	98.54
BASV8236	<i>Streptomyces acidiscabies</i>	NR_025866.2	98.79
BASV8270	<i>Streptomyces coffeae</i>	NR_180665.1	99.02
BASV8386	<i>Streptomyces clavifer</i>	NR_112453.1	99.27
BASV8958	<i>Streptomyces acidiscabies</i>	NR_025866.2	97.32
BASV9014	<i>Streptomyces graminilatus</i>	NR_125579.1	98.55
BASV9415	<i>Streptomyces triticisoli</i>	NR_179791.1	100
BASV9466	<i>Streptomyces reniochaliniae</i>	NR_171447.1	100
BASV9982	<i>Streptomyces acidiscabies</i>	NR_025866.2	98.06
BASV10044	<i>Streptomyces poriferorum</i>	NR_181639.1	100
BASV10108	<i>Streptomyces acidiscabies</i>	NR_025866.2	98.54
BASV10126	<i>Streptomyces decoyicus</i>	NR_116226.1	99.52
BASV10387	<i>Streptomyces bikiniensis</i>	NR_112436.1	100
BASV10764	<i>Streptomyces cinnabarinus</i>	NR_041097.1	100
BASV10777	<i>Streptomyces gelaticus</i>	NR_112308.1	100

Supplementary Table 5 Characteristic values of soil physicochemical properties and microbial communities of BS and GS

	BS Soil PCo1	BS Bac PCo1	BS Euk PCo1	BS Arc PCo1	GS Bac PCo1	GS Euk PCo1	GS Arc PCo1
JDH_1	-621.2381128	-0.335113102	-0.135108144	-0.389827371	-0.402389948	-0.363892813	-0.4000595
JDH_2	-536.4953189	-0.328861551	-0.327124956	-0.400918531	-0.318065562	-0.421356805	-0.40251919
JDH_3	-753.5227976	-0.297815714	-0.140816152	-0.391338218	-0.272611236	-0.391900101	-0.34733279
JDH_4	-802.6260804	-0.310994317	-0.261973127	-0.191613927	-0.396989343	-0.401252569	-0.3914632
JDH_5	-897.4303494	-0.232483182	-0.117432078	-0.288632743	-0.438689313	-0.393162049	-0.38349988
JDH_6	-499.0563912	-0.282459454	-0.188999948	-0.393890465	-0.434709565	-0.353367634	-0.39044678
JDH_7	270.1151864	-0.22783658	-0.062327332	-0.229427076	-0.395507888	-0.489870156	-0.37059658
JDH_8	-729.9245701	-0.318770726	-0.087135697	-0.154926409	-0.425706288	-0.235415938	-0.37950568
JDH_9	-661.18493	-0.285615935	-0.12557697	-0.403221562	-0.344527617	-0.12514783	-0.33314436
JFH_1	-867.875247	0.014129111	0.064063097	0.142661516	-0.201718584	-0.138195345	-0.08267358
JFH_2	-793.2277589	0.008127221	-0.009771719	0.114103877	-0.142639311	0.028164078	-0.14934839
JFH_3	-699.6968774	0.013094812	-0.022633329	0.065889943	-0.254172616	-0.096858325	0.057397607
JFH_4	-673.099238	0.139435988	-0.036307479	0.207557809	-0.190204135	-0.139650546	0.190900152
JFH_5	-854.9090803	0.206805624	0.153196512	-0.404836219	-0.043043106	0.041698061	-0.4069628
JFH_6	173.3258984	0.014267546	0.037820143	-0.359910021	-0.04569558	-0.072968651	-0.37379929
TXH_1	742.3920061	0.054446354	0.042916383	0.207547489	-0.239757728	0.035550967	0.227726596
TXH_2	396.5466345	0.130015595	0.079076705	0.360898995	-0.290543045	0.100021458	0.22615989
TXH_3	362.6977899	0.085962134	0.207134229	0.223201615	-0.264213208	-0.103402728	0.119519401
TXH_4	-354.4202821	0.088113858	0.103972536	0.043214975	-0.25469434	0.107833027	0.055012625
TXH_5	-449.4817598	0.173456114	0.18772545	0.274915198	-0.196230774	0.119447592	0.096946154
TXH_6	402.8473958	0.165240579	0.017496035	0.213220311	-0.11929513	0.093210972	0.264732575
TZH_1	686.978449	0.199104424	0.035577242	0.422537301	-0.119509931	-0.258732644	0.408083724
TZH_2	114.6298541	0.14919728	0.057927208	0.436759647	-0.08943244	-0.023675831	0.391619131
TZH_3	844.7752946	0.209044537	0.229528931	0.402352876	-0.165234064	-0.338049413	0.324050171
TZH_4	560.3423756	0.177405192	0.154521157	0.438506554	-0.12343408	0.032325693	0.407610941
TZH_5	1382.936599	0.259667193	0.141726336	0.444289304	-0.027085312	-0.022199329	0.430662123
JDL_1	-630.4040688	-0.337093587	-0.140292617	-0.400635642	-0.364938742	-0.095529967	-0.39012814
JDL_2	-918.4277484	-0.068741875	0.097273591	-0.245170514	0.024642463	0.115432366	-0.3158077
JDL_3	-557.7470906	-0.308879412	0.091627486	-0.369324751	-0.034053133	-0.124141755	-0.08983513
JDL_4	-742.8827201	-0.282158614	-0.023631637	-0.353243691	-0.338986899	-0.314204445	-0.33539997
JDL_5	-650.3991566	-0.139264743	0.094444614	0.138130427	-0.268662402	-0.188743421	-0.38355255
JFL_1	-563.897586	0.246197896	0.09996095	-0.401677806	0.190189616	0.06034873	-0.41310133
JFL_2	-760.5553583	0.07957486	0.037508594	-0.40859466	0.112319898	0.038557945	-0.41112584
JFL_3	-742.8277795	0.239793979	0.011682169	-0.416724908	0.110954174	-0.077224366	-0.42508356
JFL_4	265.0942565	0.237074695	0.187207383	-0.414101343	0.066583177	0.11312427	-0.40157638
JFL_5	-600.6177543	0.242033	0.06108953	-0.408268653	0.176331202	0.139404677	-0.42401154
JFL_6	-642.031847	0.223186102	-0.001046707	-0.410057063	0.143981031	-0.061476667	-0.41567923
JFL_7	-715.0257324	0.203467957	0.235626927	-0.413463554	0.193270404	-0.026526848	-0.41590534
TXL_1	-798.4326261	0.159624212	0.252515317	0.274369265	0.153924759	0.172410465	0.185336551
TXL_2	761.5657425	0.165483259	0.095905653	0.257941719	0.02917146	0.164717638	-0.23382069
TXL_3	478.6631557	0.174094446	0.1334445	0.26627368	0.123407453	0.157262786	0.106520186
TXL_4	554.4966223	0.261634289	0.204319787	0.285863349	0.022065249	0.168730828	0.089592526
TXL_5	775.5855207	0.247443911	0.238245454	0.377582695	0.177724875	0.189239771	0.134390392
TXL_6	454.2931269	0.281305672	0.200507185	0.216929322	0.226453106	0.130315004	-0.37885843
TXL_7	1069.111771	0.225387518	0.187404994	0.320646655	0.095562473	0.184091985	-0.17345979
TXL_8	1042.976677	0.223430424	0.054981413	0.184300845	0.201246259	0.055728503	-0.04328754
TXL_9	1349.155433	0.283573049	0.205313372	0.398528546	0.163933048	0.178269325	-0.14529844
TXL_10	-660.1126117	0.059112659	0.061362853	-0.04879267	-0.077705486	-0.011020128	-0.20769631
TZL_1	-870.1603247	0.258791073	0.183723849	0.432742552	0.063210963	-0.064132901	0.365272396
TZL_2	1486.903576	0.245569574	0.073765716	0.440579803	0.127574941	-0.222731143	0.371863615
TZL_3	617.6270902	0.243183926	0.23133418	0.448662523	0.183147818	-0.024218434	0.362534663
TZL_4	557.906475	0.266778238	0.16979343	0.34372082	0.093493472	-0.006337985	0.419912096
TZL_5	340.1947609	0.260590013	0.167145755	0.20608685	0.169457998	0.145586385	0.302783267
TZL_6	1176.49793	0.234902784	0.127650528	0.353032226	0.156614045	-0.032140287	0.316408845
TZL_7	1427.848146	0.168558025	-0.054404981	0.423022185	-0.025120316	-0.058686391	0.320143416
TZL_8	-610.8906177	0.059299914	-0.148271729	0.431930765	0.08739356	-0.034612985	0.346344016
TZL_9	1768.873088	0.149788815	0.118879374	0.411029207	0.075140682	-0.098230014	0.346936194
TZL_10	594.2209607	0.250286809	0.061812382	0.446666806	0.116181127	-0.076770427	0.389420812

Supplementary Table 6 Spearman's correlation analysis between microbial community characteristics, pathogen population and PCS severity

Factor1	Factor2	ρ	P	FDR
GS bacterial communities	PCS severity	-0.77271619	1.20E-12	2.64E-11
GS eukaryotic microbial communities	PCS severity	-0.51026758	4.28E-05	0.00011525
GS pathogen populations	PCS severity	0.729027601	8.65E-11	1.43E-09
GS txtAB gene copy numbers	PCS severity	0.616498287	2.57E-07	1.31E-06
BS pathogen populations	PCS severity	0.336816889	0.00972938	0.01528902
BS bacterial communities	PCS severity	-0.56610032	3.63E-06	1.26E-05
BS eukaryotic microbial communities	PCS severity	-0.38618431	0.00275198	0.0050453

Supplementary Table 7 Evaluating of the effect of GS and BS factors on PCS severity through hierarchical partitioning analysis
Evaluating of the effect of GS on PCS severity through hierarchical partitioning analysis

Factor	Label	Individual	I.perc(%)
GS bacterial communities	GS_Bac_PCo1	0.3928	57.76
GS eukaryotic microbial communities	GS_Euk_PCo1	0.0679	9.99
GS archaeal communities	GS_Arc_PCo1	0.0053	0.78
GS txtAB gene copy numbers	GS_txtAB	0.0701	10.31
GS pathogen populations	GS_BASV9	0.1439	21.16

Evaluating of the effect of BS on PCS severity through hierarchical partitioning analysis

Factor	Label	Individual	I.perc(%)
BS bacterial communities	BS_Bac_PCo1	0.1596	47.81
BS eukaryotic microbial communities	BS_Euk_PCo1	0.0667	19.98
BS archaeal communities	BS_Arc_PCo1	0.0327	9.80
BS txtAB gene copy numbers	BS_txtAB	0.0015	0.45
BS pathogen populations	BS_BASV9	0.0733	21.96
BS physicochemical properties	BS_Soil_PCo1	0	0

Note: Negative values that appear after correction are treated as 0.

Supplementary Table 8 Taxonomy information for 157 ASVs in the Green cluster

ASV ID	Average relative abundance	Average relative abundance	Taxonomy
BASV023	0.0645%	0.0011%	d_Bacteria; p_Actinobacteriota; c_Actinobacteriota; o_Micrococcales; f_Microbacteriaceae; g_Microbacterium
BASV4852	0.0980%	0.0117%	d_Bacteria; p_Actinobacteriota; c_Actinobacteriota; o_Micrococcales; f_Microbacteriaceae
BASV1414	0.0355%	0.0242%	d_Bacteria; p_Actinobacteriota; c_Actinobacteriota; o_Streptomyces; f_Streptomycetaceae; g_Streptomyces
BASV5185	0.0697%	0.0011%	d_Bacteria; p_Actinobacteriota; c_Actinobacteriota; o_Streptomyces; f_Streptomycetaceae; g_Streptomyces
BASV8958	0.0168%	0.0030%	d_Bacteria; p_Actinobacteriota; c_Actinobacteriota; o_Streptomyces; f_Streptomycetaceae; g_Streptomyces
BASV9	1.5641%	0.0229%	d_Bacteria; p_Actinobacteriota; c_Actinobacteriota; o_Streptomyces; f_Streptomycetaceae; g_Streptomyces
BASV1142	0.0099%	0.0001%	d_Bacteria; p_Bacteroidia; c_Bacteroidia
BASV1470	0.0179%	0.0009%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Chitinophages; f_Chitinophagaceae
BASV1592	0.0277%	0.0022%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Chitinophages; f_Chitinophagaceae; g_Chitinophaga
BASV1728	0.0123%	0.0051%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Chitinophages; f_Chitinophagaceae; g_Chitinophaga
BASV524	0.3368%	0.0023%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Chitinophages; f_Chitinophagaceae; g_Chitinophaga
BASV2613	0.0068%	0.0028%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Chitinophages; f_Chitinophagaceae; g_Chitinophaga
BASV80	0.2067%	0.0185%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Chitinophages; f_Chitinophagaceae; g_Chitinophaga; s_Chitinophaga_arvensicola
BASV3072	0.0094%	0.0026%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Chitinophages; f_Chitinophagaceae; g_Chitinophaga; s_Chitinophaga_arvensicola
BASV2535	0.0084%	0.0030%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Chitinophages; f_Chitinophagaceae; g_Chitinophaga; s_Chitinophaga_arvensicola
BASV2660	0.0113%	0.0011%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Chitinophages; f_Chitinophagaceae; g_Chitinophaga; s_Chitinophaga_arvensicola
BASV459	0.0346%	0.0004%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Chitinophages; f_Chitinophagaceae; g_Chitinophaga; s_Chitinophaga_arvensicola
BASV651	0.0258%	0.0023%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Chitinophages; f_Chitinophagaceae; g_Chitinophaga; s_Chitinophaga_arvensicola
BASV159	0.0855%	0.0013%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Cytophages; f_Spirochaetales; g_Dyadobacter; s_Dyadobacter_fermentans
BASV8	1.2245%	0.0069%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Cytophages; f_Spirochaetales; g_Dyadobacter; s_Dyadobacter_fermentans
BASV2033	0.0434%	0.0013%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium
BASV223	0.0769%	0.0504%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium
BASV6	0.1758%	0.0171%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium
BASV852	0.0305%	0.0077%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium; s_cf_Chrysobacterium
BASV2619	0.0625%	0.0021%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium; s_Flavobacterium_abundans
BASV3	2.3244%	0.0005%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium; s_Flavobacterium_abundans
BASV51	0.3061%	0.0206%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium; s_Flavobacterium_abundans
BASV056	0.0337%	0.0015%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium; s_Flavobacterium_abundans
BASV279	0.0225%	0.0007%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium; s_Flavobacterium_abundans
BASV67	0.1224%	0.0005%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium; s_Flavobacterium_johannae
BASV57	0.1241%	0.0026%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium; s_Flavobacterium_sp.
BASV300	0.0414%	0.0007%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium; s_Flavobacterium_sp.
BASV86	0.0314%	0.0002%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Flavobacteriales; f_Flavobacteriaceae; g_Flavobacterium; s_Flavobacterium_sp.
BASV2	0.2204%	0.0041%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_cf_Chrysobacterium
BASV96	0.1379%	0.0009%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_cf_Chrysobacterium
BASV1028	0.0462%	0.0005%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_cf_Chrysobacterium
BASV1024	0.0272%	0.0005%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_cf_Chrysobacterium
BASV601	0.0153%	0.0002%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_cf_Chrysobacterium
BASV234	0.0098%	0.0005%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_cf_Chrysobacterium
BASV31	0.2301%	0.0017%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_Mucilaginibacter
BASV7650	0.0092%	0.0001%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_Mucilaginibacter
BASV740	0.0192%	0.0001%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_Mucilaginibacter
BASV989	0.0255%	0.0001%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_Mucilaginibacter
BASV2149	0.0094%	0.0005%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_Mucilaginibacter; s_Mucilaginibacter_gossypii
BASV10019	0.0110%	0.0001%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter
BASV11	0.5820%	0.0013%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter
BASV158	0.1851%	0.0014%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter
BASV210	0.0859%	0.0001%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter
BASV268	0.0576%	0.0004%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter
BASV271	0.0712%	0.0004%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter
BASV400	0.0644%	0.0004%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter
BASV429	0.0205%	0.0006%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter
BASV986	0.0115%	0.0001%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter
BASV981	0.0118%	0.0007%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter
BASV298	0.0555%	0.0002%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter; s_Pedobacter_africanus
BASV238	0.0787%	0.0048%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter; s_Pedobacter_sp.
BASV555	0.0269%	0.0005%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter; s_Pedobacter_sp.
BASV588	0.0086%	0.0007%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Pedobacter; s_Pedobacter_sp.
BASV9204	0.0105%	0.0001%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium
BASV4	0.6707%	0.0013%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium
BASV6	0.1317%	0.0005%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium
BASV543	0.0123%	0.0001%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium
BASV9878	0.0666%	0.0002%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium
BASV1076	0.0316%	0.0004%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_Sphingobacterium_multivorum
BASV172	0.0764%	0.0004%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_Sphingobacterium_multivorum
BASV201	0.0832%	0.0004%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_Sphingobacterium_multivorum
BASV243	0.0679%	0.0004%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_Sphingobacterium_multivorum
BASV514	0.0291%	0.0005%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_Sphingobacterium_multivorum
BASV186	0.0648%	0.0002%	d_Bacteria; p_Bacteroidia; c_Bacteroidia; o_Sphingobacteriales; f_Sphingobacteriaceae; g_Sphingobacterium; s_Sphingobacterium_zygense
BASV10262	0.0063%	0.0029%	d_Bacteria; p_Firmicutes; c_Bacilli; o_Peumocillales; f_Peumocillaceae; g_Peumocillus
BASV46	0.0592%	0.0007%	d_Bacteria; p_Firmicutes; c_Bacilli; o_Peumocillales; f_Peumocillaceae; g_Peumocillus
BASV721	0.0327%	0.0005%	d_Bacteria; p_Firmicutes; c_Bacilli; o_Peumocillales; f_Peumocillaceae; g_Peumocillus
BASV604	0.0059%	0.0007%	d_Bacteria; p_Firmicutes; c_Bacilli; o_Peumocillales; f_Peumocillaceae; g_Peumocillus; s_uncultured_actinobacterium
BASV230	0.0114%	0.0028%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Caulobacteriales; f_Caulobacteriaceae; g_Brevundimonas
BASV234	0.0214%	0.0001%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Caulobacteriales; f_Caulobacteriaceae; g_Caulobacter
BASV792	0.0272%	0.0039%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Caulobacteriales; f_Caulobacteriaceae; g_Caulobacter; s_Caulobacter_sp.
BASV83	0.2109%	0.0234%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Caulobacteriales; f_Caulobacteriaceae; g_Caulobacter; s_Caulobacter_sp.
BASV1267	0.0221%	0.0020%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Bejerinckia; g_Besou; s_Besou_sp.
BASV177	0.0070%	0.0005%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Bejerinckia; g_Besou; s_Besou_sp.
BASV1003	0.0081%	0.0001%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Devosia; g_Devosia
BASV1232	0.0564%	0.0007%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Devosia; g_Devosia
BASV5079	0.0063%	0.0007%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Devosia; g_Devosia
BASV594	0.0138%	0.0004%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Devosia; g_Devosia
BASV56	0.2216%	0.0037%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Devosia; g_Devosia
BASV166	0.0109%	0.0017%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Devosia; g_Devosia
BASV74	0.1869%	0.0008%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Devosia; g_Devosia
BASV8351	0.0057%	0.0016%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Devosia; g_Devosia
BASV968	0.0104%	0.0001%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Devosia; g_Devosia
BASV91	0.2832%	0.0147%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Devosia; g_Devosia; s_Devosia_rhizovivans
BASV96	0.2109%	0.0028%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Devosia; g_Devosia; s_Devosia_rhizovivans
BASV2451	0.0076%	0.0004%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae
BASV411	0.0122%	0.0004%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae
BASV454	0.0195%	0.0005%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae
BASV759	0.0105%	0.0003%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae
BASV971	0.0075%	0.0013%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae
BASV1013	0.0313%	0.0010%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Allorhizobium_Norluzibium-Pararhizobium-Rhizobium
BASV159	0.1560%	0.0245%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Allorhizobium_Norluzibium-Pararhizobium-Rhizobium
BASV230	0.0850%	0.0145%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Allorhizobium_Norluzibium-Pararhizobium-Rhizobium
BASV062	0.0257%	0.0002%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Allorhizobium_Norluzibium-Pararhizobium-Rhizobium
BASV60	0.0108%	0.0001%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Allorhizobium_Norluzibium-Pararhizobium-Rhizobium
BASV824	0.0196%	0.0017%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Allorhizobium_Norluzibium-Pararhizobium-Rhizobium
BASV893	0.1152%	0.0029%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Allorhizobium_Norluzibium-Pararhizobium-Rhizobium
BASV10	0.8728%	0.1565%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Allorhizobium_Norluzibium-Pararhizobium-Rhizobium; s_Agrobacterium_puniceum
BASV338	0.0390%	0.0005%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Allorhizobium_Norluzibium-Pararhizobium-Rhizobium; s_Agrobacterium_puniceum
BASV6	1.1291%	0.0312%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Allorhizobium_Norluzibium-Pararhizobium-Rhizobium; s_Agrobacterium_puniceum
BASV3650	0.0110%	0.0027%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Mesorhizobium
BASV404	0.0057%	0.0014%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Mesorhizobium
BASV191	0.0270%	0.0057%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Ochrobium
BASV1001	0.0262%	0.0010%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Shinella
BASV462	0.0071%	0.0038%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Rhizobiaceae; g_Shinella; s_uncultured_bacterium
BASV219	0.0079%	0.0005%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Xanthobacteriaceae
BASV475	0.0535%	0.0196%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Rhizobiales; f_Xanthobacteriaceae; g_Rhodopseudomonas
BASV295	0.0089%	0.0017%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae
BASV771	0.0115%	0.0005%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Ellia655
BASV238	0.0260%	0.0023%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Sphingobium
BASV142	0.0476%	0.0024%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Sphingobium
BASV1	0.2495%	0.0003%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Sphingobium
BASV960	0.0121%	0.0008%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Sphingobium
BASV1390	0.0263%	0.0008%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Sphingobium; s_Sphingobium_herbicidovorans
BASV929	0.0649%	0.0023%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Sphingobium; s_Sphingobium_herbicidovorans
BASV193	0.0322%	0.0118%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Sphingomonas
BASV234	0.0259%	0.0047%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Sphingomonas
BASV7046	0.0150%	0.0004%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Sphingomonas
BASV737	0.0657%	0.0003%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Sphingomonas
BASV983	0.0076%	0.0004%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; g_Sphingomonas
BASV839	0.0469%	0.0021%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; s_Sphingomonas_koreensis
BASV145	0.1560%	0.0102%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; s_Sphingomonas_koreensis
BASV169	0.0409%	0.0029%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; s_Sphingomonas_koreensis
BASV1054	0.0229%	0.0022%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; s_Sphingomonas_koreensis
BASV94	0.0444%	0.0030%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; s_Sphingopyxis
BASV211	0.1046%	0.0085%	d_Bacteria; p_Proteobacteria; c_Alphaproteobacteria; o_Sphingomonadales; f_Sphingomonadaceae; s_Sphingopyxis; s_Sphingopyxis_alaskensis
BASV1004	0.0084%	0.0001%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Gammaproteobacteria
BASV10028	0.0094%	0.0001%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Gammaproteobacteria
BASV81	0.0597%	0.0160%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Gammaproteobacteria
BASV264	0.0041%	0.0011%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Gammaproteobacteria
BASV245	0.0109%	0.0015%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Gammaproteobacteria; s_Gammaproteobacteria_koreensis
BASV719	0.0991%	0.0016%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Gammaproteobacteria; s_Gammaproteobacteria_koreensis
BASV1180	0.0214%	0.0004%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Gammaproteobacteria; s_Pseudomonas; s_uncultured_bacterium
BASV175	0.0091%	0.0017%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Gammaproteobacteria; s_Pseudomonas; s_uncultured_bacterium
BASV838	0.0060%	0.0009%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Gammaproteobacteria; s_Pseudomonas
BASV83	0.0362%	0.0037%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Methylobacteriaceae
BASV1077	0.0277%	0.0028%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Methylobacteriaceae; g_Methylobacterium; s_uncultured_bacterium
BASV22	0.0559%	0.0017%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Methylobacteriaceae; g_Methylobacterium; s_uncultured_bacterium
BASV35	0.0593%	0.0034%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Methylobacteriaceae; g_Methylobacterium; s_uncultured_bacterium
BASV26	0.0602%	0.0034%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Methylobacteriaceae; g_MM2; s_uncultured_bacterium
BASV25	0.0423%	0.0016%	d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Methylobacteriaceae; g_MM2; s_uncultured_bacterium

Supplementary Table 9 Evaluating of the effect of BS factors on GS bacterial communities and pathogen populations through hierarchical partitioning analys

Evaluating of the effect of BS on GS bacterial communities through hierarchical partitioning analysis

Factor	Label	Individual	I.perc(%)
BS physicochemical properties	BS_Soil_PCo1	0.0318	4.8
BS pathogen populations	BS_BASV9	0.0104	1.57
BS bacterial communities	BS_Bac_PCo1	0.4202	63.38
BS eukaryotic microbial communities	BS_Euk_PCo1	0.1678	25.31
BS archaeal communities	BS_Arc_PCo1	0.0324	4.89

Evaluating of the effect of BS on GS pathogen populations through hierarchical partitioning analysis

Factor	Label	Individual	I.perc(%)
BS physicochemical properties	BS_Soil_PCo1	0.0048	4.17
BS pathogen populations	BS_BASV9	0.0076	6.61
BS bacterial communities	BS_Bac_PCo1	0.0561	48.78
BS eukaryotic microbial communities	BS_Euk_PCo1	0.0514	44.7
BS archaeal communities	BS_Arc_PCo1	-0.0044	-3.83

Note: Negative values that appear after correction are treated as 0.

Supplementary Table 10 Sequence alignment information between the synthetic community and the green cluster microorganism

ID	ASV ID	Similarity
HT2-2	BASV51	98.36
HR3-14	BASV623	99.27
TL3-11	BASV1660	99.77
DL3-15	BASV362	97.45