Table S1. Sequence counts of the rhizosphere and bulk soil metagenomes. The total number of sequences before and after quality filtering, and coverage data of contigs ≥500 bp.

		Original sequence files			**After quality filtering**			**Coverage (Contigs ≥ 500bp long)**
Sample	**Habitat**	**No. of sequences**	**No. of bases**	**Average length**	**No. of sequences**	**No. of bases**	**Average length**	**No. of mapped reads**
1C4	Bulk	20109591	2975984909	147.99	19346238	2849067044	147.265	10693941
2C3	Bulk	16412612	2437520419	148.515	15668391	2292314037	146.305	8488893
4C3	Bulk	17085364	2539362024	148.63	16262162	2381077816	146.415	6679680
8C4	Bulk	19685011	2914204472	148.04	18779173	2764065885	147.185	12713236
	Total	**73292578**	**10867071823**		**70055964**	**10286524781**		**38575750**
21R	Rhizosphere	14059802	2056595556	146.275	13308646	1926423705	144.75	11606054
34R	Rhizosphere	12776790	1887171712	147.7	11983209	1747001863	145.785	5664206
43R	Rhizosphere	12448635	1841092827	147.895	11570365	1687972045	145.89	6966831
51R	Rhizosphere	18734804	2763025902	147.48	17964991	2613876715	145.89	10727283
	Total	**58020031**	**8547885997**		**54827211**	**7975274328**		**34964374**

Table S2. Relative frequencies of open-reading frame (ORF) hit counts for microorganisms (phylum level) in each metagenome.

Number	Pylum	Microorganism	Sample	Habitat	Relative_frequency
1	Unknown_archaea	Archaea	1C4	Bulk_soil	0.000258256
2	Crenarchaeota	Archaea	1C4	Bulk_soil	0
3	Euryarchaeota	Archaea	1C4	Bulk_soil	0.001549537
4	Thaumarchaeota	Archaea	1C4	Bulk_soil	0.000193692
5	Acidobacteria	Bacteria	1C4	Bulk_soil	0.009716887
6	Actinobacteria	Bacteria	1C4	Bulk_soil	0.530942312
7	Aquificae	Bacteria	1C4	Bulk_soil	0
8	Armatimonadetes	Bacteria	1C4	Bulk_soil	0.000258256
9	Bacteroidetes	Bacteria	1C4	Bulk_soil	0.002259741
10	Candidatus Amesbacteria	Bacteria	1C4	Bulk_soil	0
11	Candidatus_Gottesmanbacteria	Bacteria	1C4	Bulk_soil	0
12	Candidatus_Kryptonia	Bacteria	1C4	Bulk_soil	0
13	Candidatus_Saccharibacteria	Bacteria	1C4	Bulk_soil	0
14	Candidatus_Tectomicrobia	Bacteria	1C4	Bulk_soil	0.002808535
15	Candidatus_Woesebacteria	Bacteria	1C4	Bulk_soil	0
16	Candidatus_Yanofskybacteria	Bacteria	1C4	Bulk_soil	0
17	Chlamydiae	Bacteria	1C4	Bulk_soil	0
18	Chlorobi	Bacteria	1C4	Bulk_soil	0
19	Chloroflexi	Bacteria	1C4	Bulk_soil	0.00335733
20	Cyanobacteria	Bacteria	1C4	Bulk_soil	0.00368015
21	Deferribacteres	Bacteria	1C4	Bulk_soil	0
22	Deinococcus-Thermus	Bacteria	1C4	Bulk_soil	0.001323563
23	Fibrobacteres	Bacteria	1C4	Bulk_soil	0
24	Firmicutes	Bacteria	1C4	Bulk_soil	0.009555477
25	Gemmatimonadetes	Bacteria	1C4	Bulk_soil	0.002517997
26	Ignavibacteriae	Bacteria	1C4	Bulk_soil	0
27	Lentisphaerae	Bacteria	1C4	Bulk_soil	0
28	Nitrospinae	Bacteria	1C4	Bulk_soil	0
29	Nitrospirae	Bacteria	1C4	Bulk_soil	0.00016141
30	Planctomycetes	Bacteria	1C4	Bulk_soil	0.002840817
31	Proteobacteria	Bacteria	1C4	Bulk_soil	0.261129225
32	Spirochaetes	Bacteria	1C4	Bulk_soil	0.000225974
33	Synergistetes	Bacteria	1C4	Bulk_soil	0
34	Thermotogae	Bacteria	1C4	Bulk_soil	0
35	Verrucomicrobia	Bacteria	1C4	Bulk_soil	0.00800594
36	candidate_division_Zixibacteria	Bacteria	1C4	Bulk_soil	0.000129128
37	Unknown_bacteria	Bacteria	1C4	Bulk_soil	0.157342544
38	Unknown_Eukaryotes	Eukaryota	1C4	Bulk_soil	0.000451948
39	Pelagophyceae	Eukaryota	1C4	Bulk_soil	0
40	Fungi	Eukaryota	1C4	Bulk_soil	0.000290538
41	Metazoa	Eukaryota	1C4	Bulk_soil	0
42	Viridiplantae	Eukaryota	1C4	Bulk_soil	3.23E-05
43	Unknown_Caudovirales	Viruses	1C4	Bulk_soil	0.000129128
44	Caudovirales|Myoviridae	Viruses	1C4	Bulk_soil	0

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45	Caudovirales|Siphoviridae	Viruses	1C4	Bulk_soil	0
46	Unidentied_microorganisms	Unknown_organisms	1C4	Bulk_soil	0.000839332
47	Unknown_archaea	Archaea	21R	Rhizosphere	0.00016141
48	Crenarchaeota	Archaea	21R	Rhizosphere	0
49	Euryarchaeota	Archaea	21R	Rhizosphere	0.001000742
50	Thaumarchaeota	Archaea	21R	Rhizosphere	0
51	Acidobacteria	Bacteria	21R	Rhizosphere	0.031636375
52	Actinobacteria	Bacteria	21R	Rhizosphere	0.630919715
53	Aquificae	Bacteria	21R	Rhizosphere	0
54	Armatimonadetes	Bacteria	21R	Rhizosphere	0.000419666
55	Bacteroidetes	Bacteria	21R	Rhizosphere	0.002808535
56	Candidatus Amesbacteria	Bacteria	21R	Rhizosphere	0
57	Candidatus_Gottesmanbacteria	Bacteria	21R	Rhizosphere	0
58	Candidatus_Kryptonia	Bacteria	21R	Rhizosphere	0
59	Candidatus_Saccharibacteria	Bacteria	21R	Rhizosphere	0.00080705
60	Candidatus_Tectomicrobia	Bacteria	21R	Rhizosphere	0.000903896
61	Candidatus_Woesebacteria	Bacteria	21R	Rhizosphere	0
62	Candidatus_Yanofskybacteria	Bacteria	21R	Rhizosphere	0
63	Chlamydiae	Bacteria	21R	Rhizosphere	0
64	Chlorobi	Bacteria	21R	Rhizosphere	0
65	Chloroflexi	Bacteria	21R	Rhizosphere	0.001840075
66	Cyanobacteria	Bacteria	21R	Rhizosphere	0.003002227
67	Deferribacteres	Bacteria	21R	Rhizosphere	0
68	Deinococcus-Thermus	Bacteria	21R	Rhizosphere	0.000871614
69	Fibrobacteres	Bacteria	21R	Rhizosphere	0
70	Firmicutes	Bacteria	21R	Rhizosphere	0.008587016
71	Gemmatimonadetes	Bacteria	21R	Rhizosphere	0.007876812
72	Ignavibacteriae	Bacteria	21R	Rhizosphere	0
73	Lentisphaerae	Bacteria	21R	Rhizosphere	0
74	Nitrospinae	Bacteria	21R	Rhizosphere	0
75	Nitrospirae	Bacteria	21R	Rhizosphere	0.000290538
76	Planctomycetes	Bacteria	21R	Rhizosphere	0.003421894
77	Proteobacteria	Bacteria	21R	Rhizosphere	0.190044226
78	Spirochaetes	Bacteria	21R	Rhizosphere	0.000225974
79	Synergistetes	Bacteria	21R	Rhizosphere	0
80	Thermotogae	Bacteria	21R	Rhizosphere	0
81	Verrucomicrobia	Bacteria	21R	Rhizosphere	0.001388127
82	candidate_division_Zixibacteria	Bacteria	21R	Rhizosphere	0
83	Unknown_bacteria	Bacteria	21R	Rhizosphere	0.112341415
84	Unknown_Eukaryotes	Eukaryota	21R	Rhizosphere	0.000613358
85	Pelagophyceae	Eukaryota	21R	Rhizosphere	0
86	Fungi	Eukaryota	21R	Rhizosphere	0.000193692
87	Metazoa	Eukaryota	21R	Rhizosphere	3.23E-05
88	Viridiplantae	Eukaryota	21R	Rhizosphere	6.46E-05
89	Unknown_Caudovirales	Viruses	21R	Rhizosphere	3.23E-05
90	Caudovirales|Myoviridae	Viruses	21R	Rhizosphere	9.68E-05
91	Caudovirales|Siphoviridae	Viruses	21R	Rhizosphere	0.000225974
92	Unidentied_microorganisms	Unknown_organisms	21R	Rhizosphere	0.000193692
93	Unknown_archaea	Archaea	2C3	Bulk_soil	0.000355102
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94	Crenarchaeota	Archaea	2C3	Bulk_soil	0
95	Euryarchaeota	Archaea	2C3	Bulk_soil	0.002324305
96	Thaumarchaeota	Archaea	2C3	Bulk_soil	0.00048423
97	Acidobacteria	Bacteria	2C3	Bulk_soil	0.051909481
98	Actinobacteria	Bacteria	2C3	Bulk_soil	0.567033606
99	Aquificae	Bacteria	2C3	Bulk_soil	0
100	Armatimonadetes	Bacteria	2C3	Bulk_soil	0.000548794
101	Bacteroidetes	Bacteria	2C3	Bulk_soil	0.004035252
102	Candidatus Amesbacteria	Bacteria	2C3	Bulk_soil	0
103	Candidatus_Gottesmanbacteria	Bacteria	2C3	Bulk_soil	0.00016141
104	Candidatus_Kryptonia	Bacteria	2C3	Bulk_soil	0
105	Candidatus_Saccharibacteria	Bacteria	2C3	Bulk_soil	0
106	Candidatus_Tectomicrobia	Bacteria	2C3	Bulk_soil	0.001710947
107	Candidatus_Woesebacteria	Bacteria	2C3	Bulk_soil	0.00016141
108	Candidatus_Yanofskybacteria	Bacteria	2C3	Bulk_soil	0
109	Chlamydiae	Bacteria	2C3	Bulk_soil	0
110	Chlorobi	Bacteria	2C3	Bulk_soil	0.000225974
111	Chloroflexi	Bacteria	2C3	Bulk_soil	0.013203344
112	Cyanobacteria	Bacteria	2C3	Bulk_soil	0.009329503
113	Deferribacteres	Bacteria	2C3	Bulk_soil	0.00016141
114	Deinococcus-Thermus	Bacteria	2C3	Bulk_soil	0.001807793
115	Fibrobacteres	Bacteria	2C3	Bulk_soil	0
116	Firmicutes	Bacteria	2C3	Bulk_soil	0.015398521
117	Gemmatimonadetes	Bacteria	2C3	Bulk_soil	0.00416438
118	Ignavibacteriae	Bacteria	2C3	Bulk_soil	0.00016141
119	Lentisphaerae	Bacteria	2C3	Bulk_soil	0
120	Nitrospinae	Bacteria	2C3	Bulk_soil	0
121	Nitrospirae	Bacteria	2C3	Bulk_soil	0.00032282
122	Planctomycetes	Bacteria	2C3	Bulk_soil	0.004551764
123	Proteobacteria	Bacteria	2C3	Bulk_soil	0.105820447
124	Spirochaetes	Bacteria	2C3	Bulk_soil	0.000355102
125	Synergistetes	Bacteria	2C3	Bulk_soil	0
126	Thermotogae	Bacteria	2C3	Bulk_soil	0
127	Verrucomicrobia	Bacteria	2C3	Bulk_soil	0.001969203
128	candidate_division_Zixibacteria	Bacteria	2C3	Bulk_soil	0.000225974
129	Unknown_bacteria	Bacteria	2C3	Bulk_soil	0.212028279
130	Unknown_Eukaryotes	Eukaryota	2C3	Bulk_soil	0.000710204
131	Pelagophyceae	Eukaryota	2C3	Bulk_soil	0
132	Fungi	Eukaryota	2C3	Bulk_soil	0.00016141
133	Metazoa	Eukaryota	2C3	Bulk_soil	0
134	Viridiplantae	Eukaryota	2C3	Bulk_soil	6.46E-05
135	Unknown_Caudovirales	Viruses	2C3	Bulk_soil	0
136	Caudovirales|Myoviridae	Viruses	2C3	Bulk_soil	0
137	Caudovirales|Siphoviridae	Viruses	2C3	Bulk_soil	0
138	Unidentied_microorganisms	Unknown_organisms	2C3	Bulk_soil	0.000613358
139	Unknown_archaea	Archaea	34R	Rhizosphere	0.000290538
140	Crenarchaeota	Archaea	34R	Rhizosphere	0
141	Euryarchaeota	Archaea	34R	Rhizosphere	0.001388127
142	Thaumarchaeota	Archaea	34R	Rhizosphere	0.000193692

143	Acidobacteria	Bacteria	34R	Rhizosphere	0.018013365
144	Actinobacteria	Bacteria	34R	Rhizosphere	0.438841721
145	Aquificae	Bacteria	34R	Rhizosphere	0
146	Armatimonadetes	Bacteria	34R	Rhizosphere	0.00016141
147	Bacteroidetes	Bacteria	34R	Rhizosphere	0.004228944
148	Candidatus Amesbacteria	Bacteria	34R	Rhizosphere	9.68E-05
149	Candidatus_Gottesmanbacteria	Bacteria	34R	Rhizosphere	0.000129128
150	Candidatus_Kryptonia	Bacteria	34R	Rhizosphere	0
151	Candidatus_Saccharibacteria	Bacteria	34R	Rhizosphere	0
152	Candidatus_Tectomicrobia	Bacteria	34R	Rhizosphere	0.000677922
153	Candidatus_Woesebacteria	Bacteria	34R	Rhizosphere	0
154	Candidatus_Yanofskybacteria	Bacteria	34R	Rhizosphere	9.68E-05
155	Chlamydiae	Bacteria	34R	Rhizosphere	0
156	Chlorobi	Bacteria	34R	Rhizosphere	0
157	Chloroflexi	Bacteria	34R	Rhizosphere	0.006650095
158	Cyanobacteria	Bacteria	34R	Rhizosphere	0.00384156
159	Deferribacteres	Bacteria	34R	Rhizosphere	0
160	Deinococcus-Thermus	Bacteria	34R	Rhizosphere	0.001678665
161	Fibrobacteres	Bacteria	34R	Rhizosphere	0
162	Firmicutes	Bacteria	34R	Rhizosphere	0.010136553
163	Gemmatimonadetes	Bacteria	34R	Rhizosphere	0.021370694
164	Ignavibacteriae	Bacteria	34R	Rhizosphere	9.68E-05
165	Lentisphaerae	Bacteria	34R	Rhizosphere	9.68E-05
166	Nitrospinae	Bacteria	34R	Rhizosphere	0
167	Nitrospirae	Bacteria	34R	Rhizosphere	0.000677922
168	Planctomycetes	Bacteria	34R	Rhizosphere	0.0044872
169	Proteobacteria	Bacteria	34R	Rhizosphere	0.280207896
170	Spirochaetes	Bacteria	34R	Rhizosphere	0.000290538
171	Synergistetes	Bacteria	34R	Rhizosphere	0
172	Thermotogae	Bacteria	34R	Rhizosphere	0
173	Verrucomicrobia	Bacteria	34R	Rhizosphere	0.035413371
174	candidate_division_Zixibacteria	Bacteria	34R	Rhizosphere	0.000225974
175	Unknown_bacteria	Bacteria	34R	Rhizosphere	0.168834942
176	Unknown_Eukaryotes	Eukaryota	34R	Rhizosphere	0.000387384
177	Pelagophyceae	Eukaryota	34R	Rhizosphere	0
178	Fungi	Eukaryota	34R	Rhizosphere	0.000225974
179	Metazoa	Eukaryota	34R	Rhizosphere	0.000129128
180	Viridiplantae	Eukaryota	34R	Rhizosphere	0.000548794
181	Unknown_Caudovirales	Viruses	34R	Rhizosphere	0
182	Caudovirales|Myoviridae	Viruses	34R	Rhizosphere	0
183	Caudovirales|Siphoviridae	Viruses	34R	Rhizosphere	0
184	Unidentied_microorganisms	Unknown_organisms	34R	Rhizosphere	0.000581076
185	Unknown_archaea	Archaea	43R	Rhizosphere	0.00048423
186	Crenarchaeota	Archaea	43R	Rhizosphere	0.000258256
187	Euryarchaeota	Archaea	43R	Rhizosphere	0.002937663
188	Thaumarchaeota	Archaea	43R	Rhizosphere	0.000355102
189	Acidobacteria	Bacteria	43R	Rhizosphere	0.120992995
190	Actinobacteria	Bacteria	43R	Rhizosphere	0.445362688
191	Aquificae	Bacteria	43R	Rhizosphere	0.000225974

192	Armatimonadetes	Bacteria	43R	Rhizosphere	0.000387384
193	Bacteroidetes	Bacteria	43R	Rhizosphere	0.004132098
194	Candidatus Amesbacteria	Bacteria	43R	Rhizosphere	0
195	Candidatus_Gottesmanbacteria	Bacteria	43R	Rhizosphere	0
196	Candidatus_Kryptonia	Bacteria	43R	Rhizosphere	0.000258256
197	Candidatus_Saccharibacteria	Bacteria	43R	Rhizosphere	0
198	Candidatus_Tectomicrobia	Bacteria	43R	Rhizosphere	0.002066049
199	Candidatus_Woesebacteria	Bacteria	43R	Rhizosphere	0
200	Candidatus_Yanofskybacteria	Bacteria	43R	Rhizosphere	0
201	Chlamydiae	Bacteria	43R	Rhizosphere	0
202	Chlorobi	Bacteria	43R	Rhizosphere	0.000129128
203	Chloroflexi	Bacteria	43R	Rhizosphere	0.014623753
204	Cyanobacteria	Bacteria	43R	Rhizosphere	0.007198889
205	Deferribacteres	Bacteria	43R	Rhizosphere	9.68E-05
206	Deinococcus-Thermus	Bacteria	43R	Rhizosphere	0.002840817
207	Fibrobacteres	Bacteria	43R	Rhizosphere	9.68E-05
208	Firmicutes	Bacteria	43R	Rhizosphere	0.028730994
209	Gemmatimonadetes	Bacteria	43R	Rhizosphere	0.0089744
210	Ignavibacteriae	Bacteria	43R	Rhizosphere	0
211	Lentisphaerae	Bacteria	43R	Rhizosphere	0
212	Nitrospinae	Bacteria	43R	Rhizosphere	0.000193692
213	Nitrospirae	Bacteria	43R	Rhizosphere	0.00048423
214	Planctomycetes	Bacteria	43R	Rhizosphere	0.009394067
215	Proteobacteria	Bacteria	43R	Rhizosphere	0.15230655
216	Spirochaetes	Bacteria	43R	Rhizosphere	0.000613358
217	Synergistetes	Bacteria	43R	Rhizosphere	0.00016141
218	Thermotogae	Bacteria	43R	Rhizosphere	0.000225974
219	Verrucomicrobia	Bacteria	43R	Rhizosphere	0.001646383
220	candidate_division_Zixibacteria	Bacteria	43R	Rhizosphere	0.00032282
221	Unknown_bacteria	Bacteria	43R	Rhizosphere	0.191174097
222	Unknown_Eukaryotes	Eukaryota	43R	Rhizosphere	0.000936178
223	Pelagophyceae	Eukaryota	43R	Rhizosphere	0
224	Fungi	Eukaryota	43R	Rhizosphere	0.00096846
225	Metazoa	Eukaryota	43R	Rhizosphere	0.000677922
226	Viridiplantae	Eukaryota	43R	Rhizosphere	0.000355102
227	Unknown_Caudovirales	Viruses	43R	Rhizosphere	9.68E-05
228	Caudovirales|Myoviridae	Viruses	43R	Rhizosphere	0
229	Caudovirales|Siphoviridae	Viruses	43R	Rhizosphere	0
230	Unidentied_microorganisms	Unknown_organisms	43R	Rhizosphere	0.000290538
231	Unknown_archaea	Archaea	4C3	Bulk_soil	0.000258256
232	Crenarchaeota	Archaea	4C3	Bulk_soil	0
233	Euryarchaeota	Archaea	4C3	Bulk_soil	0.001355845
234	Thaumarchaeota	Archaea	4C3	Bulk_soil	0.000290538
235	Acidobacteria	Bacteria	4C3	Bulk_soil	0.057849372
236	Actinobacteria	Bacteria	4C3	Bulk_soil	0.379894761
237	Aquificae	Bacteria	4C3	Bulk_soil	0
238	Armatimonadetes	Bacteria	4C3	Bulk_soil	0.000129128
239	Bacteroidetes	Bacteria	4C3	Bulk_soil	0.00416438
240	Candidatus Amesbacteria	Bacteria	4C3	Bulk_soil	0

241	Candidatus_Gottesmanbacteria	Bacteria	4C3	Bulk_soil	9.68E-05
242	Candidatus_Kryptonia	Bacteria	4C3	Bulk_soil	0
243	Candidatus_Saccharibacteria	Bacteria	4C3	Bulk_soil	0
244	Candidatus_Tectomicrobia	Bacteria	4C3	Bulk_soil	0.001840075
245	Candidatus_Woesebacteria	Bacteria	4C3	Bulk_soil	0.000129128
246	Candidatus_Yanofskybacteria	Bacteria	4C3	Bulk_soil	0
247	Chlamydiae	Bacteria	4C3	Bulk_soil	9.68E-05
248	Chlorobi	Bacteria	4C3	Bulk_soil	9.68E-05
249	Chloroflexi	Bacteria	4C3	Bulk_soil	0.002808535
250	Cyanobacteria	Bacteria	4C3	Bulk_soil	0.00384156
251	Deferribacteres	Bacteria	4C3	Bulk_soil	9.68E-05
252	Deinococcus-Thermus	Bacteria	4C3	Bulk_soil	0.00096846
253	Fibrobacteres	Bacteria	4C3	Bulk_soil	0
254	Firmicutes	Bacteria	4C3	Bulk_soil	0.010007425
255	Gemmatimonadetes	Bacteria	4C3	Bulk_soil	0.013784421
256	Ignavibacteriae	Bacteria	4C3	Bulk_soil	0.000193692
257	Lentisphaerae	Bacteria	4C3	Bulk_soil	0
258	Nitrospinae	Bacteria	4C3	Bulk_soil	0.000258256
259	Nitrospirae	Bacteria	4C3	Bulk_soil	0.000903896
260	Planctomycetes	Bacteria	4C3	Bulk_soil	0.005681635
261	Proteobacteria	Bacteria	4C3	Bulk_soil	0.308583788
262	Spirochaetes	Bacteria	4C3	Bulk_soil	0.000581076
263	Synergistetes	Bacteria	4C3	Bulk_soil	9.68E-05
264	Thermotogae	Bacteria	4C3	Bulk_soil	0
265	Verrucomicrobia	Bacteria	4C3	Bulk_soil	0.001549537
266	candidate_division_Zixibacteria	Bacteria	4C3	Bulk_soil	0.000129128
267	Unknown_bacteria	Bacteria	4C3	Bulk_soil	0.202214546
268	Unknown_Eukaryotes	Eukaryota	4C3	Bulk_soil	0.000613358
269	Pelagophyceae	Eukaryota	4C3	Bulk_soil	9.68E-05
270	Fungi	Eukaryota	4C3	Bulk_soil	0.000548794
271	Metazoa	Eukaryota	4C3	Bulk_soil	0
272	Viridiplantae	Eukaryota	4C3	Bulk_soil	6.46E-05
273	Unknown_Caudovirales	Viruses	4C3	Bulk_soil	0
274	Caudovirales|Myoviridae	Viruses	4C3	Bulk_soil	9.68E-05
275	Caudovirales|Siphoviridae	Viruses	4C3	Bulk_soil	0.000193692
276	Unidentied_microorganisms	Unknown_organisms	4C3	Bulk_soil	0.00048423
277	Unknown_archaea	Archaea	51R	Rhizosphere	0.00032282
278	Crenarchaeota	Archaea	51R	Rhizosphere	0.000129128
279	Euryarchaeota	Archaea	51R	Rhizosphere	0.002776253
280	Thaumarchaeota	Archaea	51R	Rhizosphere	0.00032282
281	Acidobacteria	Bacteria	51R	Rhizosphere	0.028634148
282	Actinobacteria	Bacteria	51R	Rhizosphere	0.402750428
283	Aquificae	Bacteria	51R	Rhizosphere	0
284	Armatimonadetes	Bacteria	51R	Rhizosphere	0.000419666
285	Bacteroidetes	Bacteria	51R	Rhizosphere	0.004874584
286	Candidatus Amesbacteria	Bacteria	51R	Rhizosphere	0
287	Candidatus_Gottesmanbacteria	Bacteria	51R	Rhizosphere	0.00016141
288	Candidatus_Kryptonia	Bacteria	51R	Rhizosphere	0.000129128
289	Candidatus_Saccharibacteria	Bacteria	51R	Rhizosphere	0.000355102

290	Candidatus_Tectomicrobia	Bacteria	51R	Rhizosphere	0.002130613
291	Candidatus_Woesebacteria	Bacteria	51R	Rhizosphere	0.00016141
292	Candidatus_Yanofskybacteria	Bacteria	51R	Rhizosphere	0
293	Chlamydiae	Bacteria	51R	Rhizosphere	0
294	Chlorobi	Bacteria	51R	Rhizosphere	0.00016141
295	Chloroflexi	Bacteria	51R	Rhizosphere	0.010265681
296	Cyanobacteria	Bacteria	51R	Rhizosphere	0.005713917
297	Deferribacteres	Bacteria	51R	Rhizosphere	0.000129128
298	Deinococcus-Thermus	Bacteria	51R	Rhizosphere	0.002324305
299	Fibrobacteres	Bacteria	51R	Rhizosphere	0
300	Firmicutes	Bacteria	51R	Rhizosphere	0.017238596
301	Gemmatimonadetes	Bacteria	51R	Rhizosphere	0.018917261
302	Ignavibacteriae	Bacteria	51R	Rhizosphere	0.00016141
303	Lentisphaerae	Bacteria	51R	Rhizosphere	0
304	Nitrospinae	Bacteria	51R	Rhizosphere	0.00016141
305	Nitrospirae	Bacteria	51R	Rhizosphere	0.000419666
306	Planctomycetes	Bacteria	51R	Rhizosphere	0.004713174
307	Proteobacteria	Bacteria	51R	Rhizosphere	0.220453885
308	Spirochaetes	Bacteria	51R	Rhizosphere	0.000548794
309	Synergistetes	Bacteria	51R	Rhizosphere	0
310	Thermotogae	Bacteria	51R	Rhizosphere	0.000193692
311	Verrucomicrobia	Bacteria	51R	Rhizosphere	0.008748426
312	candidate_division_Zixibacteria	Bacteria	51R	Rhizosphere	0.000355102
313	Unknown_bacteria	Bacteria	51R	Rhizosphere	0.262388224
314	Unknown_Eukaryotes	Eukaryota	51R	Rhizosphere	0.00064564
315	Pelagophyceae	Eukaryota	51R	Rhizosphere	0
316	Fungi	Eukaryota	51R	Rhizosphere	0.002324305
317	Metazoa	Eukaryota	51R	Rhizosphere	0
318	Viridiplantae	Eukaryota	51R	Rhizosphere	6.46E-05
319	Unknown_Caudovirales	Viruses	51R	Rhizosphere	3.23E-05
320	Caudovirales|Myoviridae	Viruses	51R	Rhizosphere	0
321	Caudovirales|Siphoviridae	Viruses	51R	Rhizosphere	0.000129128
322	Unidentied_microorganisms	Unknown_organisms	51R	Rhizosphere	0.000742486
323	Unknown_archaea	Archaea	8C4	Bulk_soil	0.000193692
324	Crenarchaeota	Archaea	8C4	Bulk_soil	0
325	Euryarchaeota	Archaea	8C4	Bulk_soil	0.001194435
326	Thaumarchaeota	Archaea	8C4	Bulk_soil	0.000129128
327	Acidobacteria	Bacteria	8C4	Bulk_soil	0.031313555
328	Actinobacteria	Bacteria	8C4	Bulk_soil	0.50543952
329	Aquificae	Bacteria	8C4	Bulk_soil	0
330	Armatimonadetes	Bacteria	8C4	Bulk_soil	0.000225974
331	Bacteroidetes	Bacteria	8C4	Bulk_soil	0.001904639
332	Candidatus Amesbacteria	Bacteria	8C4	Bulk_soil	0
333	Candidatus_Gottesmanbacteria	Bacteria	8C4	Bulk_soil	0
334	Candidatus_Kryptonia	Bacteria	8C4	Bulk_soil	0
335	Candidatus_Saccharibacteria	Bacteria	8C4	Bulk_soil	0
336	Candidatus_Tectomicrobia	Bacteria	8C4	Bulk_soil	0.003163638
337	Candidatus_Woesebacteria	Bacteria	8C4	Bulk_soil	0
338	Candidatus_Yanofskybacteria	Bacteria	8C4	Bulk_soil	0

339	Chlamydiae	Bacteria	8C4	Bulk_soil	0
340	Chlorobi	Bacteria	8C4	Bulk_soil	0.000129128
341	Chloroflexi	Bacteria	8C4	Bulk_soil	0.003163638
342	Cyanobacteria	Bacteria	8C4	Bulk_soil	0.004422636
343	Deferribacteres	Bacteria	8C4	Bulk_soil	0
344	Deinococcus-Thermus	Bacteria	8C4	Bulk_soil	0.00096846
345	Fibrobacteres	Bacteria	8C4	Bulk_soil	0
346	Firmicutes	Bacteria	8C4	Bulk_soil	0.006553249
347	Gemmatimonadetes	Bacteria	8C4	Bulk_soil	0.001614101
348	Ignavibacteriae	Bacteria	8C4	Bulk_soil	0
349	Lentisphaerae	Bacteria	8C4	Bulk_soil	0
350	Nitrospinae	Bacteria	8C4	Bulk_soil	0
351	Nitrospirae	Bacteria	8C4	Bulk_soil	0.000225974
352	Planctomycetes	Bacteria	8C4	Bulk_soil	0.003873842
353	Proteobacteria	Bacteria	8C4	Bulk_soil	0.277722181
354	Spirochaetes	Bacteria	8C4	Bulk_soil	0.000193692
355	Synergistetes	Bacteria	8C4	Bulk_soil	0
356	Thermotogae	Bacteria	8C4	Bulk_soil	0
357	Verrucomicrobia	Bacteria	8C4	Bulk_soil	0.008393324
358	candidate_division_Zixibacteria	Bacteria	8C4	Bulk_soil	0.000129128
359	Unknown_bacteria	Bacteria	8C4	Bulk_soil	0.147593376
360	Unknown_Eukaryotes	Eukaryota	8C4	Bulk_soil	0.000290538
361	Pelagophyceae	Eukaryota	8C4	Bulk_soil	0
362	Fungi	Eukaryota	8C4	Bulk_soil	0.000548794
363	Metazoa	Eukaryota	8C4	Bulk_soil	0
364	Viridiplantae	Eukaryota	8C4	Bulk_soil	0
365	Unknown_Caudovirales	Viruses	8C4	Bulk_soil	0.000129128
366	Caudovirales|Myoviridae	Viruses	8C4	Bulk_soil	0
367	Caudovirales|Siphoviridae	Viruses	8C4	Bulk_soil	0
368	Unidentied_microorganisms	Unknown_organisms	8C4	Bulk_soil	0.00048423

Table S3 Operational taxonomic units showing microbial taxa which were significantly overrepresented in rhizosphere and bulk soil metagenomes, based on protein-coding ORF data using the STAMP package.

OTU_ID	Taxonomy	Bulk soil: mean rel. freq. (%)	Rhizosphere soil: mean rel. freq. (%)	Habitat_upregulated	p-values (corrected)
otu1018	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Streptomycetales|f__Streptomycetaceae|g__Streptomyces|s__Streptomycesfulvoviolaceus	0,011	0	Bulk soil	
otu1171	d__Bacteria|p__Cyanobacteria|c__Gloeobacteria|o__Gloeobacterales|g__Gloeobacter|s__Gloeobacterkilaueensis|	0,014	0,002	Bulk soil	0,003
otu145	d__Bacteria|p__CandidatusTectomicrobia|g__CandidatusEntotheonella|s__CandidatusEntotheonellasp.TSY2|||	0,075	0,042	Bulk soil	0,019
otu164	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria||||	4,232	1,812	Bulk soil	0,036
otu172	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhizobiales|||	2,33	1,03	Bulk soil	0,045
otu178	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhizobiales|f__Bradyrhizobiaceae||	2,341	0,715	Bulk soil	0,039
otu180	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhizobiales|f__Bradyrhizobiaceae|g__Afipia|s__Afipiabroomeae	0,008	0	Bulk soil	0,034
otu185	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhizobiales|f__Bradyrhizobiaceae|g__Bosea|s__Boseasp.117	0,013	0	Bulk soil	0,04
otu194	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhizobiales|f__Bradyrhizobiaceae|g__Bradyrhizobium|s__Bradyrhizobiumsp.BTAi1	0,011	0	Bulk soil	
otu209	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhizobiales|f__Bradyrhizobiaceae|g__Bradyrhizobium|s__Bradyrhizobiumsp.URHA0002	0,027	0,003	Bulk soil	0,034
otu238	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhizobiales|f__Methylobacteriaceae|g__Methylobacterium|	0,151	0,084	Bulk soil	0,046
otu244	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhizobiales|f__Methylobacteriaceae|g__Microvirga|s__Microvirgalupini	0,013	0	Bulk soil	0,029
otu245	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhizobiales|f__Methylobacteriaceae|g__Microvirga|s__Microvirgasp.JC119	0,043	0,014	Bulk soil	0,01
otu283	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhizobiales|f__Xanthobacteraceae|g__Starkeya|s__Starkeyanovella	0,01	0	Bulk soil	0,015
otu294	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhodobacterales|f__Rhodobacteraceae|g__Rhodovulum|s__Rhodovulumsp.PH10	0,201	0,047	Bulk soil	0,033
otu323	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Rhodospirillales|f__Rhodospirillaceae|g__Skermanella|s__Skermanellaaerolata	0,016	0,003	Bulk soil	0,005
otu351	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|s__alphaproteobacteriumBAL199|||	0,023	0,003	Bulk soil	0,007
otu512	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Chromatiales|f__Chromatiaceae||	0,027	0,022	Bulk soil	0,004
otu764	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Frankiales|f__Frankiaceae|g__Frankia|s__Frankiasp.EUN1f	0,02	0,003	Bulk soil	0,007
otu775	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Geodermatophilales|f__Geodermatophilaceae|g__Blastococcus|s__Blastococcussp.URHD0036	0,026	0,016	Bulk soil	0,043
otu784	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Geodermatophilales|f__Geodermatophilaceae|s__GeodermatophilaceaebacteriumURHB0062|	0,052	0,031	Bulk soil	0,039
otu836	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Micrococcales|f__Intrasporangiaceae|g__Tetrasphaera|s__Tetrasphaerajaponica	0,064	0,031	Bulk soil	0,005
otu876	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Micromonosporales|f__Micromonosporaceae|g__Actinoplanes|	0,231	0,131	Bulk soil	0,049
otu878	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Micromonosporales|f__Micromonosporaceae|g__Actinoplanes|s__Actinoplanesglobisporus	0,08	0,037	Bulk soil	0,02
otu883	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Micromonosporales|f__Micromonosporaceae|g__Actinoplanes|s__Actinoplanessubtropicus	0,074	0,031	Bulk soil	0,021
otu101	d__Bacteria|p__Bacteroidetes|c__Cytophagia|o__Cytophagales|f__Hymenobacteraceae||	0,002	0,016	Rhizosphere	0,045
otu1145	d__Bacteria|p__Chloroflexi|c__Dehalococcoidia|g__Dehalogenimonas|||	0	0,012	Rhizosphere	0,02
otu1198	d__Bacteria|p__Deinococcus-Thermus|c__Deinococci|o__Deinococcales|f__Deinococcaceae|g__Deinococcus|	0,038	0,063	Rhizosphere	0,046
otu1225	d__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Lactobacillaceae|g__Lactobacillus|	0	0,009	Rhizosphere	0,018
otu13	d__Bacteria|p__Acidobacteria|c__Acidobacteriia|o__Acidobacteriales|f__Acidobacteriaceae|g__Granulicella|	0,006	0,014	Rhizosphere	0,015

otu336	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Sphingomonadales|f__Sphingomonadaceae|g__Novosphingobium|	0,014	0,025	Rhizosphere	0,019
otu340	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Sphingomonadales|f__Sphingomonadaceae|g__Sphingomonas|s__Sphingomonasastaxanthinifaciens	0,003	0,019	Rhizosphere	0,043
otu344	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Sphingomonadales|f__Sphingomonadaceae|g__Sphingomonas|s__Sphingomonasjaspsi	0,003	0,034	Rhizosphere	0,034
otu346	d__Bacteria|p__Proteobacteria|c__Alphaproteobacteria|o__Sphingomonadales|f__Sphingomonadaceae|g__Sphingomonas|s__Sphingomonassp.URHD0057	0,034	0,131	Rhizosphere	0,032
otu404	d__Bacteria|p__Proteobacteria|c__Betaproteobacteria|o__Neisseriales|||	0	0,009	Rhizosphere	0,006
otu446	d__Bacteria|p__Proteobacteria|c__Deltaproteobacteria|o__Desulfuromonadales|f__Geobacteraceae||	0,004	0,011	Rhizosphere	0,045
otu541	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Oceanospirillales|f__Halomonadaceae||	0	0,003	Rhizosphere	0,035
otu542	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Oceanospirillales|f__Halomonadaceae|g__Halomonas|	0	0,01	Rhizosphere	0,023
otu559	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Xanthomonadales|||	0,019	0,037	Rhizosphere	0,034
otu566	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Xanthomonadales|f__Xanthomonadaceae||	0,041	0,061	Rhizosphere	0,027
otu567	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Xanthomonadales|f__Xanthomonadaceae|g__Arenimonas|	0,004	0,018	Rhizosphere	0,025
otu573	d__Bacteria|p__Proteobacteria|c__Gammaproteobacteria|o__Xanthomonadales|f__Xanthomonadaceae|g__Xanthomonas|	0,012	0,029	Rhizosphere	0,009
otu611	d__Bacteria|p__Planctomycetes|c__Planctomycetia|o__Planctomycetales|f__Planctomycetaceae|g__Rhodopirellula|	0,022	0,039	Rhizosphere	0,024
otu615	d__Bacteria|p__Planctomycetes|c__Planctomycetia|o__Planctomycetales|f__Planctomycetaceae|g__Schlesneria|s__Schlesneriapaludicola	0	0,015	Rhizosphere	0
otu689	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Actinomycetales|f__Actinomycetaceae||	0,002	0,01	Rhizosphere	0,005
otu709	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Corynebacteriales|f__Corynebacteriaceae|g__Corynebacterium|s__Corynebacteriumvariabile	0	0,009	Rhizosphere	0,013
otu727	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Corynebacteriales|f__Mycobacteriaceae|g__Mycobacterium|s__Mycobacteriumsmegmatis	0,006	0,016	Rhizosphere	0,034
otu770	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Frankiales|f__Sporichthyaceae|g__Sporichthya|s__Sporichthyapolymorpha	0,022	0,054	Rhizosphere	0,019
otu851	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Micrococcales|f__Microbacteriaceae|g__Microbacterium|	0,056	0,074	Rhizosphere	0,032
otu856	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Micrococcales|f__Micrococcaceae||	0,084	0,566	Rhizosphere	0,033
otu857	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Micrococcales|f__Micrococcaceae|g__Arthrobacter|	0,08	0,199	Rhizosphere	0,006
otu863	d__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Micrococcales|f__Micrococcaceae|g__Pseudarthrobacter|	0	0,009	Rhizosphere	0,033

Table S4. Genes overrepresented in either, the rhizosphere or bulk soil metagenomes, based on ORF data analysis using the STAMP package.

MainFunction	Subfunction	KO	EnzymeName	GeneName	Significant_Habitat	Bulk: mean rel. freq. (%)	Rhizosphere: mean rel. freq. (%)	Bulk: std. dev. (%)	Rhizosphere: std. dev. (%)	p-values	p-values (corrected)
AminoAcidMetabolism	Valine,leucineandisoleucinedegradation	K00020	3-hydroxyisobutyratedehydrogenase[EC:1.1.1.31]	mmsB, HIBADH	Bulk	0.064216092	0.032084497	0.015394425	0.012997063	0.03058268	0.03058268
CarbohydrateMetabolism	Pentosephosphatepathway	K00034	glucose1-dehydrogenase[EC:1.1.1.47]	gdh	Bulk	0.024868931	0.011889445	0.00670867	0.004472897	0.029461991	0.029461991
CarbohydrateMetabolism	Fructoseandmannosemetabolism	K00045	mannitol2-dehydrogenase[EC:1.1.1.67]	mtlK	Bulk	0.023349791	0.007862346	0.010268411	0.000865994	0.038065047	0.038065047
CarbohydrateMetabolism	Pyruvatemetabolism	K00102	D-lactatedehydrogenase(cytochrome)[EC:1.1.2.4]	dld, LDHD	Bulk	0.020977915	0.011889445	0.003980011	0.004472897	0.036748824	0.036748824
CarbohydrateMetabolism	Glycolysis/Gluconeogenesis	K00169	pyruvateferredoxinoxidoreductase,alphasubunit[EC:1.2.7.1]	porA	Bulk	0.015214654	0.007862346	0.001170407	0.000865994	0.000278213	0.000278213
EnergyMetabolism	Carbonfixationpathwaysinprokaryotes	K00259	alaninedehydrogenase[EC:1.4.1.1]	ald	Bulk	0.062299779	0.049683338	0.002539973	0.0081976	0.041655956	0.041655956
MetabolismofCofactorsandVitamins	Nicotinateandnicotinamidemetabolism	K00322	NAD(P)transhydrogenase[EC:1.6.1.1]	sthA, udhA	Bulk	0.028788126	0.010442961	0.007595294	0.007383592	0.022379702	0.022379702
UnknownMainFunction	UnknownSubFunction	K00359	UnknownEnzyme	unknown	Bulk	0.013370588	0.005599288	0.003643621	0.003275466	0.031201411	0.031201411
UnknownMainFunction	UnknownSubFunction	K00375	GntR family transcriptional regulator / MocR family aminotransferase	unknown	Bulk	0.097856991	0.052300337	0.019061623	0.024617968	0.042503527	0.042503527
UnknownMainFunction	UnknownSubFunction	K00389	putative membrane protein	yidH	Bulk	0.024744023	0.01345124	0.003885509	0.00566005	0.027413009	0.027413009
UnknownMainFunction	UnknownSubFunction	K00433	non-heme chloroperoxidase [EC:1.11.1.10]	cpo	Bulk	0.040036653	0.012025543	0.009200017	0.007523991	0.00576489	0.00576489
XenobioticsBiodegradationandMetabolism	Naphthalenedegradation	K00480	salicylatehydroxylase[EC:1.14.13.1]	unknown	Bulk	0.038236654	0.019887889	0.00764532	0.007919856	0.026048589	0.026048589
XenobioticsBiodegradationandMetabolism	Toluenedegradation	K00481	p-hydroxybenzoate3-monooxygenase[EC:1.14.13.2]	pobA	Bulk	0.042330553	0.019559938	0.012706682	0.0039801	0.023558777	0.023558777
AminoAcidMetabolism	Tyrosinemetabolism	K00505	tyrosinase[EC:1.14.18.1]	TYR	Bulk	0.017136696	0.007534395	0.003615814	0.005036911	0.034205721	0.034205721
UnknownMainFunction	UnknownSubFunction	K00520	mercuric reductase [EC:1.16.1.1]	merA	Bulk	0.099750853	0.05419906	0.022240147	0.005497233	0.012058777	0.012058777
AminoAcidMetabolism	Cysteineandmethioninemetabolism	K00549	5-methyltetrahydropteroyltriglutamate--homocysteinemethyltransferase[EC:2.1.1.14]	metE	Bulk	0.233606295	0.108408514	0.07159234	0.007004241	0.022016066	0.022016066
UnknownMainFunction	UnknownSubFunction	K00598	trans-aconitate 2-methyltransferase [EC:2.1.1.144]	tam	Bulk	0.037105922	0.01798775	0.011354936	0.005397703	0.036469436	0.036469436
MetabolismofCofactorsandVitamins	Riboflavinmetabolism	K00793	riboflavinsynthase[EC:2.5.1.9]	ribE, RIB5	Bulk	0.041274933	0.029186326	0.005990767	0.002412713	0.016056034	0.016056034
MetabolismofOtherAminoAcids	Glutathionemetabolism	K00799	glutathioneS-transferase[EC:2.5.1.18]	GST, gst	Bulk	0.138889401	0.0806441	0.039496251	0.012715009	0.0491971	0.0491971
LipidMetabolism	Glycerolipidmetabolism	K00901	diacylglycerolkinase(ATP)[EC:2.7.1.107]	dgkA, DGK	Bulk	0.013292612	0.005780747	0.003439632	0.003437612	0.034489812	0.034489812
CarbohydrateMetabolism	Starchandsucrosemetabolism	K01087	trehalose6-phosphatephosphatase[EC:3.1.3.12]	otsB	Bulk	0.039880701	0.030950367	0.003808195	0.003429855	0.021891458	0.021891458
LipidMetabolism	Steroidhormonebiosynthesis	K01130	arylsulfatase[EC:3.1.6.1]	aslA	Bulk	0.121575775	0.043875193	0.040393812	0.034155046	0.041798589	0.041798589
UnknownMainFunction	UnknownSubFunction	K01133	choline-sulfatase [EC:3.1.6.6]	betC	Bulk	0.011573454	0.001764042	0.004371923	0.00305541	0.017450235	0.017450235
MetabolismofOtherAminoAcids	Glutathionemetabolism	K01469	5-oxoprolinase(ATP-hydrolysing)[EC:3.5.2.9]	OPLAH, OXP1, oplAH	Bulk	0.036114593	0.019731003	0.004253296	0.008582142	0.023534875	0.023534875
CarbohydrateMetabolism	Pyruvatemetabolism	K01571	oxaloacetatedecarboxylase,alphasubunit[EC:4.1.1.3]	oadA	Bulk	0.026913015	0.011879051	0.009177664	0.004451415	0.041180643	0.041180643
CarbohydrateMetabolism	Glyoxylateanddicarboxylatemetabolism	K01577	oxalyl-CoAdecarboxylase[EC:4.1.1.8]	oxc	Bulk	0.009326485	0.001753648	0.002587783	0.003037407	0.014994122	0.014994122

CarbohydrateMetabolism	Butanoatemetabolism	K01652	acetolactatesynthaseI/II/IIIlargesubunit[EC:2.2.1.6]	ilvB, ilvG, ilvI	Bulk	0.289939119	0.237491714	0.023733817	0.015699196	0.017219828	0.017219828
MetabolismofCofactorsandVitamins	Onecarbonpoolbyfolate	K01934	5-formyltetrahydrofolatecyclo-ligase[EC:6.3.3.2]	MTHFS	Bulk	0.030910187	0.013779191	0.009649776	0.006947041	0.044747257	0.044747257
MembraneTransport	ABCtransporters	K02020	molybdatetransportsystemsubstrate-bindingprotein	modA	Bulk	0.075664638	0.039301335	0.018560925	0.006546122	0.017019201	0.017019201
MembraneTransport	ABCtransporters	K02040	phosphatetransportsystemsubstrate-bindingprotein	pstS	Bulk	0.08947343	0.059990201	0.017624471	0.005793424	0.030990596	0.030990596
UnknownMainFunction	UnknownSubFunction	K02426	cysteine desulfuration protein SufE	sufE	Bulk	0.013495496	0.005780747	0.003906544	0.003437612	0.040113636	0.040113636
MembraneTransport	ABCtransporters	K02471	putativeATP-bindingcassettetransporter	yddA	Bulk	0.034114575	0.015215281	0.011439048	0.004336975	0.034467476	0.034467476
UnknownMainFunction	UnknownSubFunction	K03192	ureJ	urease accessory protein	Bulk	0.007529351	0	0.005249069	0	0.045532132	0.045532132
GlycanBiosynthesisandMetabolism	Lipopolysaccharidebiosynthesis	K03273	D-glycero-D-manno-heptose1,7-bisphosphatephosphatase[EC:3.1.3.823.1.3.83]	gmhB	Bulk	0.023224884	0.011380035	0.007176883	0.002703092	0.034524687	0.034524687
EnergyMetabolism	Methanemetabolism	K03520	carbon-monoxidedehydrogenaselargesubunit[EC:1.2.99.2]	coxL, cutL	Bulk	0.396523438	0.233686243	0.104306756	0.013593884	0.034248041	0.034248041
UnknownMainFunction	UnknownSubFunction	K03549	KUP system potassium uptake protein	kup	Bulk	0.097958809	0.047430675	0.020837461	0.013025143	0.010298981	0.010298981
UnknownMainFunction	UnknownSubFunction	K03704	cold shock protein (beta-ribbon, CspA family)	cspA	Bulk	0.153059893	0.131018308	0.003782788	0.014357211	0.039820141	0.039820141
UnknownMainFunction	UnknownSubFunction	K04094	methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase [EC:2.1.1.74]	trmFO, gid	Bulk	0.019180781	0.011380035	0.004798711	0.002703092	0.04768221	0.04768221
UnknownMainFunction	UnknownSubFunction	K06136	pyrroloquinoline quinone biosynthesis protein B	pqqB	Bulk	0.020777896	0.009943945	0.006129311	0.003959928	0.039806818	0.039806818
UnknownMainFunction	UnknownSubFunction	K06139	pyrroloquinoline quinone biosynthesis protein E	pqqE	Bulk	0.019058738	0.007862346	0.006851557	0.000865994	0.028876959	0.028876959
CarbohydrateMetabolism	Pentosephosphatepathway	K06152	gluconate2-dehydrogenasegammachain[EC:1.1.99.3]	unknown	Bulk	0.023149772	0.006426255	0.009596455	0.006965473	0.048378918	0.048378918
MembraneTransport	ABCtransporters	K06160	putativeATP-bindingcassettetransporter	pvdE	Bulk	0.011776337	0	0.006847287	0	0.022958856	0.022958856
UnknownMainFunction	UnknownSubFunction	K06188	aquaporin Z	aqpZ	Bulk	0.041999897	0.021313586	0.012918727	0.005501934	0.041247257	0.041247257
UnknownMainFunction	UnknownSubFunction	K06897	7,8-dihydropterin-6-yl-methyl-4-(beta-D-ribofuranosyl)aminobenzene 5'-phosphate synthase [EC:2.5.1.105]	unknown	Bulk	0.030957118	0.01011501	0.010758659	0.006794569	0.027850705	0.027850705
UnknownMainFunction	UnknownSubFunction	K06978	UnknownEnzyme	unknown	Bulk	0.154630302	0.078991579	0.027705525	0.033875155	0.022529389	0.022529389
UnknownMainFunction	UnknownSubFunction	K07001	NTE family protein	unknown	Bulk	0.14380852	0.111191376	0.008481315	0.010089484	0.004545846	0.004545846
UnknownMainFunction	UnknownSubFunction	K07006	UnknownEnzyme	unknown	Bulk	0.041877854	0.029186326	0.005456466	0.002412713	0.008797022	0.008797022
UnknownMainFunction	UnknownSubFunction	K07058	membrane protein	unknown	Bulk	0.184330308	0.122047822	0.020018521	0.015427924	0.004644592	0.004644592
UnknownMainFunction	UnknownSubFunction	K07102	anomeric MurNAc/GlcNAc kinase [EC:2.7.1.-]	amgK	Bulk	0.016855836	0.007862346	0.005614897	0.000865994	0.031469436	0.031469436
UnknownMainFunction	UnknownSubFunction	K07117	UnknownEnzyme	unknown	Bulk	0.013292612	0.007862346	0.003439632	0.000865994	0.035567398	0.035567398
UnknownMainFunction	UnknownSubFunction	K07390	monothiol glutaredoxin	grxD, GLRX5	Bulk	0.024541139	0.017478339	0.002100385	0.002505786	0.008268417	0.008268417
UnknownMainFunction	UnknownSubFunction	K07481	transposase, IS5 family	unknown	Bulk	0.059948128	0.020329732	0.020065862	0.017921753	0.041420455	0.041420455
UnknownMainFunction	UnknownSubFunction	K07484	transposase	unknown	Bulk	0.060336535	0.02500234	0.01899539	0.011009684	0.029471003	0.029471003
UnknownMainFunction	UnknownSubFunction	K07486	transposase	unknown	Bulk	0.099122616	0.036799645	0.035113256	0.024426986	0.04316105	0.04316105
UnknownMainFunction	UnknownSubFunction	K07577	putative mRNA 3-end processing factor	unknown	Bulk	0.015214654	0.005271337	0.001170407	0.005819352	0.025655956	0.025655956
UnknownMainFunction	UnknownSubFunction	K07734	transcriptional regulator	paiB	Bulk	0.018777878	0.011697592	0.002714502	0.003825279	0.037435345	0.037435345
UnknownMainFunction	UnknownSubFunction	K07812	trimethylamine-N-oxide reductase (cytochrome c) [EC:1.7.2.3]	torZ	Bulk	0.009248509	0	0.005845938	0	0.031519984	0.031519984
UnknownMainFunction	UnknownSubFunction	K08256	phosphatidylinositol alpha-mannosyltransferase [EC:2.4.1.57]	pimA	Bulk	0.067909953	0.048938117	0.008441181	0.00438953	0.011834248	0.011834248
UnknownMainFunction	UnknownSubFunction	K08988	putative membrane protein	unknown	Bulk	0.009854295	0	0.006642995	0	0.039996082	0.039996082
UnknownMainFunction	UnknownSubFunction	K09154	UnknownEnzyme	unknown	Bulk	0.007607327	0	0.000585204	0	5.49E-06	5.49E-06
UnknownMainFunction	UnknownSubFunction	K09936	bacterial/archaeal transporter family-2 protein	TC.BAT2	Bulk	0.018902786	0.005599288	0.006226397	0.003275466	0.015274687	0.015274687
MembraneTransport	ABCtransporters	K10242	cellobiosetransportsystempermeaseprotein	cebG	Bulk	0.007607327	0.002081599	0.000585204	0.003605435	0.03716105	0.03716105

LipidMetabolism	Fattyacidbiosynthesis	K10780	enoyl-[acyl-carrierprotein]reductaseIII[EC:1.3.1.104]	fabL	Bulk	0.011045644	0.001753648	0.005548316	0.003037407	0.041746865	0.041746865
UnknownMainFunction	UnknownSubFunction	K11068	hemolysin III	hlyIII	Bulk	0.043443925	0.023566249	0.004946752	0.010245422	0.021653997	0.021653997
CarbohydrateMetabolism	Glyoxylateanddicarboxylatemetabolism	K11472	glycolateoxidaseFADbindingsubunit	glcE	Bulk	0.043396994	0.033213425	0.004280588	0.003155566	0.014227273	0.014227273
MembraneTransport	ABCtransporters	K11959	ureatransportsystemsubstrate-bindingprotein	urtA	Bulk	0.019180781	0.009626388	0.004798711	0.00269095	0.022153213	0.022153213
UnknownMainFunction	UnknownSubFunction	K12507	acyl-CoA synthetase [EC:6.2.1.-]	fadK	Bulk	0.007607327	0.002081599	0.000585204	0.003605435	0.03716105	0.03716105
UnknownMainFunction	UnknownSubFunction	K12508	feruloyl-CoA synthase [EC:6.2.1.34]	fcs	Bulk	0.032148466	0.013315142	0.002072801	0.008071521	0.006955329	0.006955329
UnknownMainFunction	UnknownSubFunction	K13057	trehalose synthase [EC:2.4.1.245]	treT	Bulk	0.053176178	0.033213425	0.007912925	0.003155566	0.005934561	0.005934561
NucleotideMetabolism	Purinemetabolism	K13481	xanthinedehydrogenasesmallsubunit[EC:1.17.1.4]	xdhA	Bulk	0.017261604	0.007862346	0.006428298	0.000865994	0.043836207	0.043836207
AminoAcidMetabolism	Phenylalanine,tyrosineandtryptophanbiosynthesis	K13503	anthranilatesynthase[EC:4.1.3.27]	trpEG	Bulk	0.021177934	0.007862346	0.007720855	0.000865994	0.023306034	0.023306034
UnknownMainFunction	UnknownSubFunction	K13628	iron-sulfur cluster assembly protein	iscA, ISCA1	Bulk	0.035308788	0.01798775	0.008436305	0.005397703	0.022495298	0.022495298
LipidMetabolism	Glycerolipidmetabolism	K13920	propanedioldehydratasesmallsubunit[EC:4.2.1.28]	pduE	Bulk	0.007404443	0	0.004906851	0	0.03746199	
UnknownMainFunction	UnknownSubFunction	K15371	glutamate dehydrogenase [EC:1.4.1.2]	GDH2	Bulk	0.106349491	0.082579207	0.010502988	0.010330368	0.029329545	0.029329545
UnknownMainFunction	UnknownSubFunction	K16515	4-oxalomesaconate hydratase [EC:4.2.1.83]	galB	Bulk	0.013092593	0.006108698	0.002720633	0.003598488	0.034237069	0.034237069
UnknownMainFunction	UnknownSubFunction	K16927	energy-coupling factor transport system substrate-specific component	cbrT	Bulk	0.022621962	0.011879051	0.005054487	0.004451415	0.030554075	0.030554075
UnknownMainFunction	UnknownSubFunction	K17225	sulfane dehydrogenase subunit SoxC	soxC	Bulk	0.018777878	0.007352936	0.002714502	0.004991833	0.011392241	0.011392241
UnknownMainFunction	UnknownSubFunction	K18457	L-proline amide hydrolase [EC:3.5.1.101]	laaA	Bulk	0.007607327	0	0.000585204	0	5.49E-06	5.49E-06
UnknownMainFunction	UnknownSubFunction	K18928	L-lactate dehydrogenase complex protein LldE	lldE	Bulk	0.024541139	0.013779191	0.002100385	0.006947041	0.040094044	0.040094044
CarbohydrateMetabolism	Pentosephosphatepathway	K00117	quinoproteinglucosedehydrogenase[EC:1.1.5.2]	gcd	Rhizosphere	0.023610427	0.056572225	0.01507453	0.017950338	0.048909875	0.048909875
EnergyMetabolism	Nitrogenmetabolism	K00266	glutamatesynthase(NADPH/NADH)smallchain[EC:1.4.1.131.4.1.14]	gltD	Rhizosphere	0.04319411	0.061890341	0.007118629	0.004578348	0.007572492	0.007572492
MetabolismofCofactorsandVitamins	Nicotinateandnicotinamidemetabolism	K00324	NAD(P)transhydrogenasesubunitalpha[EC:1.6.1.2]	pntA	Rhizosphere	0.05845856	0.073633294	0.005930678	0.009018182	0.048978448	0.048978448
EnergyMetabolism	Nitrogenmetabolism	K00362	nitritereductase(NADH)largesubunit[EC:1.7.1.15]	nirB	Rhizosphere	0.01705872	0.029514277	0.00314121	0.007513477	0.035695141	0.035695141
EnergyMetabolism	Nitrogenmetabolism	K00372	assimilatorynitratereductasecatalyticsubunit[EC:1.7.99.4]	nasA	Rhizosphere	0.017461622	0.032386458	0.00711025	0.006863831	0.037325235	0.037325235
UnknownMainFunction	UnknownSubFunction	K00537	arsenate reductase [EC:1.20.4.1]	ARSC1, arsC	Rhizosphere	0.001922042	0.011879051	0.003329074	0.004451415	0.019634796	0.019634796
AminoAcidMetabolism	Cysteineandmethioninemetabolism	K00548	5-methyltetrahydrofolate--homocysteinemethyltransferase[EC:2.1.1.13]	metH, MTR	Rhizosphere	0.125637819	0.169007838	0.015201968	0.023859449	0.035365987	0.035365987
AminoAcidMetabolism	Arginineandprolinemetabolism	K00611	ornithinecarbamoyltransferase[EC:2.1.3.3]	OTC, argF, argI	Rhizosphere	0.043724785	0.061743849	0.006911107	0.007335285	0.019775078	0.019775078
NucleotideMetabolism	Pyrimidinemetabolism	K00757	uridinephosphorylase[EC:2.4.2.3]	udp, UPP	Rhizosphere	0.003766108	0.011380035	0.003767722	0.002703092	0.027670063	0.027670063
BiosynthesisofPolyketidesandTerpenoids	Terpenoidbackbonebiosynthesis	K00806	undecaprenyldiphosphatesynthase[EC:2.5.1.31]	uppS	Rhizosphere	0.043924804	0.064027695	0.006022403	0.011353591	0.032889498	0.032889498
CarbohydrateMetabolism	Propanoatemetabolism	K00823	4-aminobutyrateaminotransferase[EC:2.6.1.19]	puuE	Rhizosphere	0.034195416	0.060660282	0.004184424	0.01590636	0.029504702	0.029504702
MetabolismofCofactorsandVitamins	Biotinmetabolism	K00833	adenosylmethionine-8-amino-7-oxononanoateaminotransferase[EC:2.6.1.62]	bioA	Rhizosphere	0.022141083	0.043031666	0.008219927	0.012511073	0.04993221	0.04993221
CarbohydrateMetabolism	Galactosemetabolism	K00849	galactokinase[EC:2.7.1.6]	galK	Rhizosphere	0.022821981	0.038994172	0.001755611	0.004954434	0.001681426	0.001681426
NucleotideMetabolism	Purinemetabolism	K00940	nucleoside-diphosphatekinase[EC:2.7.4.6]	ndk, NME	Rhizosphere	0.030429308	0.044265509	0.002340815	0.00653447	0.011882837	0.011882837

CarbohydrateMetabolism	Fructoseandmannosemetabolism	K00971	mannose-1-phosphateguanylyltransferase[EC:2.7.7.13]	manC, cpsB	Rhizosphere	0.014733775	0.031142221	0.006672664	0.008528721	0.036967085	0.036967085
CarbohydrateMetabolism	Starchandsucrosemetabolism	K00975	glucose-1-phosphateadenylyltransferase[EC:2.7.7.27]	glgC	Rhizosphere	0.032751388	0.063539073	0.010750876	0.017230996	0.036847571	0.036847571
CarbohydrateMetabolism	Glyoxylateanddicarboxylatemetabolism	K01091	phosphoglycolatephosphatase[EC:3.1.3.18]	gph	Rhizosphere	0.021180799	0.038484762	0.007184423	0.003867271	0.008920846	0.008920846
LipidMetabolism	Glycerophospholipidmetabolism	K01095	phosphatidylglycerophosphataseA[EC:3.1.3.27]	pgpA	Rhizosphere	0	0.007862346	0	0.000865994	2.19E-05	2.19E-05
LipidMetabolism	Sphingolipidmetabolism	K01186	sialidase-1[EC:3.2.1.18]	NEU1	Rhizosphere	0.001922042	0.007862346	0.003329074	0.000865994	0.022576803	0.022576803
UnknownMainFunction	UnknownSubFunction	K01235	alpha-glucuronidase [EC:3.2.1.139]	aguA	Rhizosphere	0.002122061	0.007862346	0.003675517	0.000865994	0.036508229	0.036508229
NucleotideMetabolism	Pyrimidinemetabolism	K01494	dCTPdeaminase[EC:3.5.4.13]	dcd	Rhizosphere	0.026588089	0.046347108	0.003956462	0.003173343	0.000637931	0.000637931
CarbohydrateMetabolism	Pentosephosphatepathway	K01625	2-dehydro-3-deoxyphosphogluconatealdolase/(4S)-4-hydroxy-2-oxoglutaratealdolase[EC:4.1.2.144.1.3.42]	eda	Rhizosphere	0.013092593	0.033349523	0.002720633	0.009597726	0.010814655	0.010814655
CarbohydrateMetabolism	Butanoatemetabolism	K01640	hydroxymethylglutaryl-CoAlyase[EC:4.1.3.4]	HMGCL, hmgL	Rhizosphere	0.041599859	0.064919408	0.002113434	0.013988837	0.027183386	0.027183386
CarbohydrateMetabolism	Aminosugarandnucleotidesugarmetabolism	K01654	N-acetylneuraminatesynthase[EC:2.5.1.56]	neuB	Rhizosphere	0.003766108	0.013144077	0.003767722	0.005126599	0.041147727	0.041147727
MetabolismofCofactorsandVitamins	Folatebiosynthesis	K01664	para-aminobenzoatesynthetasecomponentII[EC:2.6.1.85]	pabA	Rhizosphere	0.001844066	0.007862346	0.003194016	0.000865994	0.018355799	0.018355799
AminoAcidMetabolism	Glycine,serineandthreoninemetabolism	K01696	tryptophansynthasebetachain[EC:4.2.1.20]	trpB	Rhizosphere	0.056411611	0.072207598	0.004287968	0.007562463	0.018484718	0.018484718
EnergyMetabolism	Nitrogenmetabolism	K01744	aspartateammonia-lyase[EC:4.3.1.1]	aspA	Rhizosphere	0.001719158	0.01780629	0.00297767	0.00445677	0.00185815	0.00185815
CarbohydrateMetabolism	Fructoseandmannosemetabolism	K01809	mannose-6-phosphateisomerase[EC:5.3.1.8]	manA, MPI	Rhizosphere	0.018777878	0.027432678	0.002714502	0.004359258	0.024918887	0.024918887
K2000013Translation	Aminoacyl-tRNAbiosynthesis	K01866	tyrosyl-tRNAsynthetase[EC:6.1.1.1]	YARS, tyrS	Rhizosphere	0.058255676	0.069934146	0.006178349	0.002100576	0.01973942	0.01973942
AminoAcidMetabolism	Arginineandprolinemetabolism	K01941	ureacarboxylase[EC:6.3.4.6]	unknown	Rhizosphere	0	0.007851952	0	0.005036791	0.033290752	0.033290752
CarbohydrateMetabolism	Citratecycle(TCAcycle)	K01958	pyruvatecarboxylase[EC:6.4.1.1]	PC, pyc	Rhizosphere	0.015261585	0.03528463	0.009130736	0.004770507	0.013331505	0.013331505
CarbohydrateMetabolism	Pyruvatemetabolism	K01963	acetyl-CoAcarboxylasecarboxyltransferasesubunitbeta[EC:6.4.1.2]	accD	Rhizosphere	0.033667606	0.051628839	0.006423378	0.008684483	0.026291536	0.026291536
MembraneTransport	ABCtransporters	K02001	glycinebetaine/prolinetransportsystempermeaseprotein	proW	Rhizosphere	0.001719158	0.01488733	0.00297767	0.007924187	0.033696708	0.033696708
MembraneTransport	ABCtransporters	K02013	ironcomplextransportsystemATP-bindingprotein[EC:3.6.3.34]	ABC.FEV.A	Rhizosphere	0.026990991	0.051593872	0.007813087	0.015578754	0.048247649	0.048247649
UnknownMainFunction	UnknownSubFunction	K02014	iron complex outermembrane recepter protein	TC.FEV.OM	Rhizosphere	0.048145837	0.125229547	0.026972547	0.03959517	0.029522727	0.029522727
NucleotideMetabolism	Purinemetabolism	K02083	allantoatedeiminase[EC:3.5.3.9]	allC	Rhizosphere	0.001844066	0.011380035	0.003194016	0.002703092	0.006624216	0.006624216
SignalTransduction	Two-componentsystem	K02106	short-chainfattyacidstransporter	atoE	Rhizosphere	0	0.007352936	0	0.004991833	0.041258229	0.041258229
MetabolismofCofactorsandVitamins	Porphyrinandchlorophyllmetabolism	K02228	precorrin-6Asynthase[EC:2.1.1.152]	cobF	Rhizosphere	0	0.009626388	0	0.00269095	0.000930643	0.000930643
K2000013Translation	Aminoacyl-tRNAbiosynthesis	K02434	aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln)amidotransferasesubunitB[EC:6.3.5.66.3.5.7]	gatB, PET112	Rhizosphere	0.043649673	0.073123884	0.013575703	0.009526577	0.020239812	0.020239812
MembraneTransport	Bacterialsecretionsystem	K02453	generalsecretionpathwayproteinD	gspD	Rhizosphere	0.018930966	0.036741509	0.008099028	0.007866874	0.031876959	0.031876959
UnknownMainFunction	UnknownSubFunction	K02485	two-component system, response regulator	rssB, hnr	Rhizosphere	0	0.00736333	0	0.005020378	0.042043887	0.042043887
UnknownMainFunction	UnknownSubFunction	K02575	MFS transporter, NNP family, nitrate/nitrite transporter	NRT, narK, nrtP, nasA	Rhizosphere	0.011248527	0.026616105	0.00338844	0.009398472	0.034962382	0.034962382
UnknownMainFunction	UnknownSubFunction	K02618	oxepin-CoA hydrolase / 3-oxo-5,6-dehydrosuberyl-CoA semialdehyde dehydrogenase [EC:3.3.2.12 1.2.1.91]	paaZ	Rhizosphere	0.009529369	0.019570332	0.003425779	0.004020664	0.014807994	0.014807994
UnknownMainFunction	UnknownSubFunction	K02654	leader peptidase (prepilin peptidase) / N-methyltransferase [EC:3.4.23.43 2.1.1.-]	pilD, pppA	Rhizosphere	0.028510131	0.043010878	0.006537992	0.007470713	0.042729232	0.042729232

UnknownMainFunction	UnknownSubFunction	K02805	dTDP-4-amino-4,6-dideoxygalactose transaminase [EC:2.6.1.59]	wecE, rffA	Rhizosphere	0.001844066	0.011390429	0.003194016	0.00569241	0.042546238	0.042546238
K2000013Translation	Ribosome	K02874	largesubunitribosomalproteinL14	RP-L14, MRPL14, rplN	Rhizosphere	0.043724785	0.055973496	0.006911107	0.004891047	0.044020768	0.044020768
K2000013Translation	Ribosome	K02914	largesubunitribosomalproteinL34	RP-L34, MRPL34, rpmH	Rhizosphere	0.007404443	0.017488734	0.004906851	0.002578135	0.018336991	0.018336991
Folding,SortingandDegradation	Proteinexport	K03106	signalrecognitionparticlesubunitSRP54	SRP54, ffh	Rhizosphere	0.070387985	0.083067829	0.006451287	0.005856585	0.043302508	0.043302508
MembraneTransport	Bacterialsecretionsystem	K03195	typeIVsecretionsystemproteinVirB10	virB10, lvhB10	Rhizosphere	0	0.011879051	0	0.004451415	0.003100313	0.003100313
SignalTransduction	Two-componentsystem	K03408	purine-bindingchemotaxisproteinCheW	cheW	Rhizosphere	0.014608868	0.034796008	0.007932977	0.007199861	0.015444749	0.015444749
CellMotility	Bacterialchemotaxis	K03411	chemotaxisproteinCheD[EC:3.5.1.44]	cheD	Rhizosphere	0.001844066	0.009626388	0.003194016	0.00269095	0.016344828	0.016344828
UnknownMainFunction	UnknownSubFunction	K03455	monovalent cation:H+ antiporter-2, CPA2 family	TC.KEF	Rhizosphere	0.01165143	0.037284483	0.004563631	0.017292642	0.045795846	0.045795846
UnknownMainFunction	UnknownSubFunction	K03547	exonuclease SbcD	sbcD	Rhizosphere	0.009529369	0.021334374	0.003425779	0.0055803	0.019211207	0.019211207
ReplicationandRepair	Baseexcisionrepair	K03648	uracil-DNAglycosylase[EC:3.2.2.27]	UNG, UDG	Rhizosphere	0.015136678	0.031142221	0.00523614	0.008528721	0.030230799	0.030230799
ReplicationandRepair	Homologousrecombination	K03655	ATP-dependentDNAhelicaseRecG[EC:3.6.4.12]	recG	Rhizosphere	0.077314414	0.099110077	0.006296445	0.004812655	0.002715909	0.002715909
UnknownMainFunction	UnknownSubFunction	K03695	ATP-dependent Clp protease ATP-binding subunit ClpB	clpB	Rhizosphere	0.113335145	0.144858456	0.016089908	0.011293196	0.029856975	0.029856975
MetabolismofCofactorsandVitamins	Lipoicacidmetabolism	K03801	lipoyl(octanoyl)transferase[EC:2.3.1.181]	lipB	Rhizosphere	0.043599877	0.065271932	0.006252014	0.01017738	0.018670455	0.018670455
UnknownMainFunction	UnknownSubFunction	K03811	nicotinamide mononucleotide transporter	pnuC	Rhizosphere	0	0.00736333	0	0.005020378	0.042043887	0.042043887
UnknownMainFunction	UnknownSubFunction	K04485	DNA repair protein RadA/Sms	radA, sms	Rhizosphere	0.049007167	0.065579095	0.004298414	0.007009553	0.011260972	0.011260972
UnknownMainFunction	UnknownSubFunction	K05299	formate dehydrogenase alpha subunit [EC:1.2.1.43]	fdhA	Rhizosphere	0	0.007534395	0	0.005036911	0.038760188	0.038760188
UnknownMainFunction	UnknownSubFunction	K05589	cell division protein FtsB	ftsB	Rhizosphere	0	0.007862346	0	0.000865994	2.19E-05	2.19E-05
UnknownMainFunction	UnknownSubFunction	K05807	outer membrane protein assembly factor BamD	bamD	Rhizosphere	0.011448546	0.021822996	0.004080251	0.004961637	0.029246473	0.029246473
MembraneTransport	ABCtransporters	K05846	osmoprotectanttransportsystempermeaseprotein	opuBD	Rhizosphere	0.041605589	0.070070243	0.0175174	0.008095173	0.040943966	0.040943966
UnknownMainFunction	UnknownSubFunction	K06024	segregation and condensation protein B	scpB	Rhizosphere	0.032273374	0.042330403	0.003503195	0.004687802	0.023105799	0.023105799
UnknownMainFunction	UnknownSubFunction	K06178	23S rRNA pseudouridine2605 synthase [EC:5.4.99.22]	rluB	Rhizosphere	0.039755793	0.050192749	0.002205973	0.004022122	0.006657132	0.006657132
UnknownMainFunction	UnknownSubFunction	K06199	CrcB protein	crcB	Rhizosphere	0.018652971	0.031777335	0.005175567	0.007819586	0.049597571	0.049597571
LipidMetabolism	Fattyaciddegradation	K06445	acyl-CoAdehydrogenase[EC:1.3.99.-]	fadE	Rhizosphere	0.001719158	0.007862346	0.00297767	0.000865994	0.012345219	0.012345219
UnknownMainFunction	UnknownSubFunction	K06929	UnknownEnzyme	unknown	Rhizosphere	0.033867625	0.044401607	0.00456581	0.005575732	0.042627351	0.042627351
UnknownMainFunction	UnknownSubFunction	K06975	UnknownEnzyme	unknown	Rhizosphere	0.005685285	0.013461634	0.003333833	0.002755532	0.019401646	0.019401646
UnknownMainFunction	UnknownSubFunction	K07002	UnknownEnzyme	unknown	Rhizosphere	0	0.007862346	0	0.000865994	2.19E-05	2.19E-05
UnknownMainFunction	UnknownSubFunction	K07042	probable rRNA maturation factor	ybeY, yqfG	Rhizosphere	0.028507266	0.040758214	0.003913964	0.006758382	0.03257837	0.03257837
UnknownMainFunction	UnknownSubFunction	K07044	UnknownEnzyme	unknown	Rhizosphere	0.001719158	0.009615993	0.00297767	0.002646215	0.012298197	0.012298197
UnknownMainFunction	UnknownSubFunction	K07093	UnknownEnzyme	unknown	Rhizosphere	0.001844066	0.020517801	0.003194016	0.012889699	0.048898511	0.048898511
UnknownMainFunction	UnknownSubFunction	K07220	UnknownEnzyme	unknown	Rhizosphere	0.029623503	0.046528567	0.008611612	0.007910121	0.04416105	0.04416105
ReplicationandRepair	Mismatchrepair	K07456	DNAmismatchrepairproteinMutS2	mutS2	Rhizosphere	0.014686844	0.034628728	0.008010728	0.00930191	0.028624216	0.028624216
UnknownMainFunction	UnknownSubFunction	K07507	putative Mg2+ transporter-C (MgtC) family protein	mgtC	Rhizosphere	0.012936641	0.030939973	0.010750861	0.003330303	0.030112853	0.030112853
UnknownMainFunction	UnknownSubFunction	K07560	D-tyrosyl-tRNA(Tyr) deacylase [EC:3.1.-.-]	dtd, DTD1	Rhizosphere	0.022744005	0.043010878	0.005288339	0.007470713	0.007517241	0.007517241
UnknownMainFunction	UnknownSubFunction	K07576	metallo-beta-lactamase family protein	unknown	Rhizosphere	0.01112362	0.032068901	0.007731996	0.011947185	0.04149373	0.04149373

SignalTransduction	Two-componentsystem	K07652	two-componentsystem,OmpRfamily,sensorhistidinekinaseVicK[EC:2.7.13.3]	vicK	Rhizosphere	0.001844066	0.009626388	0.003194016	0.00269095	0.016344828	0.016344828
UnknownMainFunction	UnknownSubFunction	K07726	putative transcriptional regulator	unknown	Rhizosphere	0.002122061	0.011380035	0.003675517	0.002703092	0.010859718	0.010859718
NucleotideMetabolism	Purinemetabolism	K11175	phosphoribosylglycinamideformyltransferase1[EC:2.1.2.2]	purN	Rhizosphere	0.030351332	0.049875192	0.005403778	0.008300949	0.012547806	0.012547806
CarbohydrateMetabolism	Aminosugarandnucleotidesugarmetabolism	K12410	NAD-dependent deacetylase [EC:3.5.1.-]	npdA	Rhizosphere	0.030429308	0.04023841	0.002340815	0.006067754	0.03756779	0.03756779
UnknownMainFunction	UnknownSubFunction	K12994	alpha-1,3-rhamnosyl/mannosyltransferase [EC:2.4.1.-]	wbpY, wbdB	Rhizosphere	0.003563224	0.013643093	0.0035676	0.003483545	0.011072884	0.011072884
UnknownMainFunction	UnknownSubFunction	K13282	cyanophycinase [EC:3.4.15.6]	cphB	Rhizosphere	0.011373435	0.02276007	0.003741224	0.005406184	0.022353056	0.022353056
CarbohydrateMetabolism	Pyruvatemetabolism	K13788	phosphateacetyltransferase[EC:2.3.1.8]	pta	Rhizosphere	0.001844066	0.007862346	0.003194016	0.000865994	0.018355799	0.018355799
UnknownMainFunction	UnknownSubFunction	K14162	error-prone DNA polymerase [EC:2.7.7.7]	dnaE2	Rhizosphere	0.124071748	0.152876271	0.009649366	0.017011668	0.041395376	0.041395376
UnknownMainFunction	UnknownSubFunction	K14761	ribosome-associated protein	ybcJ	Rhizosphere	0	0.00736333	0	0.005020378	0.042043887	0.042043887
UnknownMainFunction	UnknownSubFunction	K15539	cytoskeleton protein RodZ	rodZ	Rhizosphere	0	0.007862346	0	0.000865994	2.19E-05	2.19E-05
UnknownMainFunction	UnknownSubFunction	K16087	hemoglobin/transferrin/lactoferrin receptor protein	TC.FEV.OM3, tbpA, hemR, lbpA, hpuB, bhuR, hugA, hmbR	Rhizosphere	0	0.007352936	0	0.004991833	0.041258229	0.041258229
UnknownMainFunction	UnknownSubFunction	K16092	vitamin B12 transporter	btuB	Rhizosphere	0.003966127	0.015714298	0.003985564	0.005243095	0.019984326	0.019984326
UnknownMainFunction	UnknownSubFunction	K16692	tyrosine-protein kinase Etk/Wzc [EC:2.7.10.-]	etk-wzc	Rhizosphere	0	0.007862346	0	0.000865994	2.19E-05	2.19E-05
UnknownMainFunction	UnknownSubFunction	K17103	CDP-diacylglycerol---serine O-phosphatidyltransferase [EC:2.7.8.8]	CHO1, pssA	Rhizosphere	0.011448546	0.023597432	0.004080251	0.005646688	0.021770768	0.021770768
UnknownMainFunction	UnknownSubFunction	K17836	beta-lactamase class A [EC:3.5.2.6]	penP	Rhizosphere	0.01653091	0.037059066	0.006885573	0.005711907	0.006513323	0.006513323
UnknownMainFunction	UnknownSubFunction	K18672	diadenylate cyclase [EC:2.7.7.85]	dacA	Rhizosphere	0.005485266	0.017150388	0.003180122	0.007193517	0.040059953	0.040059953

Table S5. Overrepresented genes of the rhizosphere and bulk soil metagenomes, identified using STAMP analysis of ORF hit counts, linked to their associated microbial taxa.

Genus	Rhizosphere_gene_count	Bulk_soil_gene_count	Significant_Habitat	Gene_name	KEGG_orthology	Function
Achromobacter	1	1	Bulk	unknown	K07058	Not known
			Rhizosphere	TC.FEV.OM	K02014	Not known
Acidimicrobium	2	0	Rhizosphere	pntA	K00324	Nicotinate and nicotinamide metabolism
				cphB	K13282	Not known
Acidiphilium	0	2	Bulk	unknown	K07481	Not known
				unknown	K07486	Not known
Acidisphaera	0	7	Bulk	merA	K00520	Not known
				ribE	K00793	Riboflavin metabolism
				coxL,cutL	K03520	Methane metabolism
				kup	K03549	Not known
				cspA	K03704	Not known
				unknown	K07001	Not known
				lldE	K18928	Not known
Acidithrix	1	0	Rhizosphere	cphB	K13282	Not known
Acidobacterium	5	3	Bulk	ribE	K00793	Riboflavin metabolism
				pstS	K02040	ABC transporters
				unknown	K07058	Not known
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				rluB	K06178	Not known
				mgtC	K07507	Not known
				CHO1,pssA	K17103	Not known
Acidothermus	0	1	Bulk	unknown	K07058	Not known
Actinocatenispora	8	3	Bulk	aslA	K01130	Steroid hormone biosynthesis
				pstS	K02040	ABC transporters

				glcE	K11472	Glyoxylate and dicarboxylate metabolism
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				manC,cpsB	K00971	Fructose and mannose metabolism
				glgC	K00975	Starch and sucrose metabolism
				manA,MPI	K01809	Fructose and mannose metabolism
				sbcD	K03547	Not known
				pnuC	K03811	Not known
				radA,sms	K04485	Not known
				opuBD	K05846	ABC transporters
Actinomadura	1	1	Bulk	MTHFS	K01934	One carbon pool byfolate
			Rhizosphere	dnaE2	K14162	Not known
Actinomycetospora	1	0	Rhizosphere	nirB	K00362	Nitrogen metabolism
Actinoplanes	8	6	Bulk	unknown	K00480	Naphthalene degradation
				ribE	K00793	Riboflavin metabolism
				coxL,cutL	K03520	Methane metabolism
				unknown	K07058	Not known
				unknown	K07117	Not known
				hlyIII	K11068	Not known
			Rhizosphere	NEU1	K01186	Sphingolipid metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				clpB	K03695	Not known
				opuBD	K05846	ABC transporters
				scpB	K06024	Not known
				rluB	K06178	Not known
				unknown	K06929	Not known
				cphB	K13282	Not known
Actinopolymorpha	1	1	Bulk	unknown	K07006	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
Actinospica	12	2	Bulk	unknown	K00375	Not known

				pstS	K02040	ABC transporters
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				pntA	K00324	Nicotinate and nicotinamide metabolism
				OTC,argF,argI	K00611	Arginine and prolinemetabolism
				uppS	K00806	Terpenoid backbone biosynthesis
				galK	K00849	Galactose metabolism
				eda	K01625	Pentose phosphate pathway
				manA,MPI	K01809	Fructose and mannose metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				rssB,hnr	K02485	Not known
				recG	K03655	Homologous recombination
				rluB	K06178	Not known
				crcB	K06199	Not known
Aeromicrobium	0	1	Bulk	merA	K00520	Not known
Afipia	1	4	Bulk	ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				modA	K02020	ABC transporters
				unknown	K06897	Not known
				soxC	K17225	Not known
			Rhizosphere	ybeY,yqfG	K07042	Not known
Akkermansia	1	0	Rhizosphere	rluB	K06178	Not known
Alicyclobacillus	1	1	Bulk	unknown	K06978	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
Altererythrobacter	1	0	Rhizosphere	gcd	K00117	Pentose phosphate pathway
Amycolatopsis	53	28	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
				sthA,udhA	K00322	Nicotinate and nicotinamide metabolism
				unknown	K00375	Not known
				yidH	K00389	Not known
				pobA	K00481	Toluene degradation
				merA	K00520	Not known

				metE	K00549	Cysteine and methionine metabolism
				tam	K00598	Not known
				ribE	K00793	Riboflavin metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				MTHFS	K01934	One carbon pool byfolate
				modA	K02020	ABC transporters
				pstS	K02040	ABC transporters
				gmhB	K03273	Lipopolysaccharide biosynthesis
				coxL,cutL	K03520	Methane metabolism
				pqqB	K06136	Not known
				pqqE	K06139	Not known
				unknown	K06978	Not known
				unknown	K07001	Not known
				unknown	K07006	Not known
				unknown	K07058	Not known
				paiB	K07734	Not known
				pimA	K08256	Not known
				cebG	K10242	ABC transporters
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
				fadK	K12507	Not known
				GDH2	K15371	Not known
				cbrT	K16927	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				pntA	K00324	Nicotinate and nicotinamide metabolism
				nirB	K00362	Nitrogen metabolism
				nasA	K00372	Nitrogen metabolism
				ARSC1,arsC	K00537	Not known
				metH,MTR	K00548	Cysteine and methionine metabolism
				uppS	K00806	Terpenoid backbone biosynthesis

				puuE	K00823	Propanoate metabolism
				bioA	K00833	Biotin metabolism
				galK	K00849	Galactose metabolism
				gph	K01091	Glyoxylate and dicarboxylate metabolism
				NEU1	K01186	Sphingolipid metabolism
				dcd	K01494	Pyrimidine metabolism
				eda	K01625	Pentose phosphate pathway
				HMGCL,hmgL	K01640	Butanoate metabolism
				neuB	K01654	Aminosugar and nucleotidesugar metabolism
				pabA	K01664	Folate biosynthesis
				trpB	K01696	Glycine, serine and threonine metabolism
				aspA	K01744	Nitrogen metabolism
				manA,MPI	K01809	Fructose and mannose metabolism
				unknown	K01941	Arginine and prolinemetabolism
				PC,pyc	K01958	Citrate cycle (TCAcycle)
				accD	K01963	Pyruvate metabolism
				ABC.FEV.A	K02013	ABC transporters
				gatB,PET112	K02434	Aminoacyl-tRNA biosynthesis
				NRT,narK,nrtP,nasA	K02575	Not known
				paaZ	K02618	Not known
				pilD,pppA	K02654	Not known
				SRP54,ffh	K03106	Protein export
				TC.KEF	K03455	Not known
				sbcD	K03547	Not known
				UNG,UDG	K03648	Base excision repair
				recG	K03655	Homologous recombination
				clpB	K03695	Not known
				lipB	K03801	Lipoic acid metabolism

				pnuC	K03811	Not known
				radA,sms	K04485	Not known
				opuBD	K05846	ABC transporters
				scpB	K06024	Not known
				crcB	K06199	Not known
				unknown	K06929	Not known
				unknown	K06975	Not known
				unknown	K07044	Not known
				unknown	K07093	Not known
				unknown	K07220	Not known
				mgtC	K07507	Not known
				dtd,DTD1	K07560	Not known
				purN	K11175	Purine metabolism
				npdA	K12410	Aminosugar and nucleotidesugar metabolism
				dnaE2	K14162	Not known
				ybcJ	K14761	Not known
				CHO1,pssA	K17103	Not known
				penP	K17836	Not known
Anaerolinea	1	0	Rhizosphere	radA,sms	K04485	Not known
Anaeromyxobacter	8	7	Bulk	tam	K00598	Not known
				otsB	K01087	Starch and sucrose metabolism
				amgK	K07102	Not known
				unknown	K07484	Not known
				pimA	K08256	Not known
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
				iscA,ISCA1	K13628	Not known
			Rhizosphere	YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				cheD	K03411	Bacterial chemotaxis

				lipB	K03801	Lipoic acid metabolism
				ftsB	K05589	Not known
				mutS2	K07456	Mismatch repair
				unknown	K07576	Not known
				unknown	K07726	Not known
				dnaE2	K14162	Not known
Arenimonas	1	0	Rhizosphere	TC.FEV.OM	K02014	Not known
Arthrobacter	13	8	Bulk	pobA	K00481	Toluene degradation
				metE	K00549	Cysteine and methionine metabolism
				otsB	K01087	Starch and sucrose metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				cspA	K03704	Not known
				unknown	K06152	Pentose phosphate pathway
				unknown	K07001	Not known
				GDH2	K15371	Not known
			Rhizosphere	pntA	K00324	Nicotinate and nicotinamide metabolism
				uppS	K00806	Terpenoid backbone biosynthesis
				manC,cpsB	K00971	Fructose and mannose metabolism
				trpB	K01696	Glycine, serine and threonine metabolism
				PC,pyc	K01958	Citrate cycle (TCAcycle)
				accD	K01963	Pyruvate metabolism
				paaZ	K02618	Not known
				SRP54,ffh	K03106	Protein export
				sbcD	K03547	Not known
				UNG,UDG	K03648	Base excision repair
				recG	K03655	Homologous recombination
				unknown	K06929	Not known
				unknown	K07093	Not known
Asticcacaulis	1	0	Rhizosphere	TC.KEF	K03455	Not known

Azospirillum	4	7	Bulk	oadA	K01571	Pyruvate metabolism
				unknown	K07486	Not known
				GDH2	K15371	Not known
			Rhizosphere	TC.FEV.OM	K02014	Not known
				clpB	K03695	Not known
				opuBD	K05846	ABC transporters
				btuB	K16092	Not known
Bacillus	1	0	Rhizosphere	radA,sms	K04485	Not known
Belnapia	1	5	Bulk	ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				yddA	K02471	ABC transporters
				coxL,cutL	K03520	Methane metabolism
				unknown	K07484	Not known
				unknown	K07486	Not known
			Rhizosphere	dnaE2	K14162	Not known
Beutenbergia	0	1	Bulk	paiB	K07734	Not known
Blastococcus	0	1	Bulk	fcs	K12508	Not known
Bordetella	0	2	Bulk	coxL,cutL	K03520	Methane metabolism
				unknown	K06152	Pentose phosphate pathway
Bradyrhizobium	56	49	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
				dld,LDHD	K00102	Pyruvate metabolism
				ald	K00259	Carbon fixation pathways in prokaryotes
				unknown	K00375	Not known
				yidH	K00389	Not known
				cpo	K00433	Not known
				unknown	K00480	Naphthalene degradation
				pobA	K00481	Toluene degradation
				TYR	K00505	Tyrosine metabolism
				metE	K00549	Cysteine and methionine metabolism
				tam	K00598	Not known

				ribE	K00793	Riboflavin metabolism
				GST,gst	K00799	Glutathione metabolism
				otsB	K01087	Starch and sucrose metabolism
				aslA	K01130	Steroid hormone biosynthesis
				oxc	K01577	Glyoxylate and dicarboxylate metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				MTHFS	K01934	One carbon pool byfolate
				modA	K02020	ABC transporters
				pstS	K02040	ABC transporters
				sufE	K02426	Not known
				yddA	K02471	ABC transporters
				gmhB	K03273	Lipopolysaccharide biosynthesis
				coxL,cutL	K03520	Methane metabolism
				kup	K03549	Not known
				cspA	K03704	Not known
				trmFO,gid	K04094	Not known
				pqqB	K06136	Not known
				pqqE	K06139	Not known
				unknown	K06152	Pentose phosphate pathway
				unknown	K06897	Not known
				unknown	K07001	Not known
				unknown	K07006	Not known
				unknown	K07058	Not known
				unknown	K07117	Not known
				grxD,GLRX5	K07390	Not known
				unknown	K07481	Not known
				unknown	K07484	Not known
				unknown	K07486	Not known
				unknown	K07577	Not known

				paiB	K07734	Not known
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
				urtA	K11959	ABC transporters
				fcs	K12508	Not known
				trpEG	K13503	Phenylalanine, tyrosine and tryptophan biosynthesis
				iscA,ISCA1	K13628	Not known
				GDH2	K15371	Not known
				galB	K16515	Not known
				soxC	K17225	Not known
			Rhizosphere	gcd	K00117	Pentose phosphate pathway
				gltD	K00266	Nitrogen metabolism
				pntA	K00324	Nicotinate and nicotinamide metabolism
				nirB	K00362	Nitrogen metabolism
				nasA	K00372	Nitrogen metabolism
				ARSC1,arsC	K00537	Not known
				metH,MTR	K00548	Cysteine and methionine metabolism
				uppS	K00806	Terpenoid backbone biosynthesis
				bioA	K00833	Biotin metabolism
				ndk,NME	K00940	Purine metabolism
				glgC	K00975	Starch and sucrose metabolism
				gph	K01091	Glyoxylate and dicarboxylate metabolism
				dcd	K01494	Pyrimidine metabolism
				eda	K01625	Pentose phosphate pathway
				HMGCL,hmgL	K01640	Butanoate metabolism
				neuB	K01654	Aminosugar and nucleotidesugar metabolism
				trpB	K01696	Glycine, serine and threonine metabolism
				aspA	K01744	Nitrogen metabolism

				manA,MPI	K01809	Fructose and mannose metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				accD	K01963	Pyruvate metabolism
				ABC.FEV.A	K02013	ABC transporters
				TC.FEV.OM	K02014	Not known
				allC	K02083	Purine metabolism
				atoE	K02106	Two-component system
				gatB,PET112	K02434	Aminoacyl-tRNA biosynthesis
				gspD	K02453	Bacterial secretion system
				NRT,narK,nrtP,nasA	K02575	Not known
				SRP54,ffh	K03106	Protein export
				virB10,lvhB10	K03195	Bacterial secretion system
				cheW	K03408	Two-component system
				TC.KEF	K03455	Not known
				recG	K03655	Homologous recombination
				clpB	K03695	Not known
				lipB	K03801	Lipoic acid metabolism
				radA,sms	K04485	Not known
				bamD	K05807	Not known
				opuBD	K05846	ABC transporters
				scpB	K06024	Not known
				rluB	K06178	Not known
				crcB	K06199	Not known
				fadE	K06445	Fatty acid degradation
				unknown	K06929	Not known
				unknown	K06975	Not known
				unknown	K07002	Not known
				ybeY,yqfG	K07042	Not known
				unknown	K07220	Not known

				mgtC	K07507	Not known
				unknown	K07576	Not known
				unknown	K07726	Not known
				purN	K11175	Purine metabolism
				npdA	K12410	Aminosugar and nucleotidesugar metabolism
				dnaE2	K14162	Not known
				TC.FEV.OM3,tbpA	K16087	Not known
				CHO1,pssA	K17103	Not known
				penP	K17836	Not known
Bryobacter	2	0	Rhizosphere	TC.FEV.OM	K02014	Not known
				rluB	K06178	Not known
Burkholderia	7	9	Bulk	TYR	K00505	Tyrosine metabolism
				merA	K00520	Not known
				GST,gst	K00799	Glutathione metabolism
				betC	K01133	Not known
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				modA	K02020	ABC transporters
				unknown	K06978	Not known
				unknown	K07001	Not known
				unknown	K07006	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				puuE	K00823	Propanoate metabolism
				proW	K02001	ABC transporters
				ABC.FEV.A	K02013	ABC transporters
				TC.KEF	K03455	Not known
				mgtC	K07507	Not known
				etk-wzc	K16692	Not known
Caldilinea	0	1	Bulk	glcE	K11472	Glyoxylate and dicarboxylate metabolism

Candidatus_Accumulibacter	1	2	Bulk	aslA	K01130	Steroid hormone biosynthesis
				unknown	K07484	Not known
			Rhizosphere	SRP54,ffh	K03106	Protein export
Candidatus_Entetheonella	0	5	Bulk	metE	K00549	Cysteine and methionine metabolism
				oxc	K01577	Glyoxylate and dicarboxylate metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				unknown	K06978	Not known
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
Candidatus_Koribacter	28	11	Bulk	unknown	K00375	Not known
				metE	K00549	Cysteine and methionine metabolism
				ribE	K00793	Riboflavin metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				pstS	K02040	ABC transporters
				cspA	K03704	Not known
				trmFO,gid	K04094	Not known
				unknown	K06152	Pentose phosphate pathway
				unknown	K07001	Not known
				unknown	K07058	Not known
				unknown	K07486	Not known
			Rhizosphere	pntA	K00324	Nicotinate and nicotinamide metabolism
				OTC,argF,argI	K00611	Arginine and prolinemetabolism
				uppS	K00806	Terpenoid backbone biosynthesis
				ndk,NME	K00940	Purine metabolism
				glgC	K00975	Starch and sucrose metabolism
				trpB	K01696	Glycine, serine and threonine metabolism
				manA,MPI	K01809	Fructose and mannose metabolism
				accD	K01963	Pyruvate metabolism
				TC.FEV.OM	K02014	Not known
				gatB,PET112	K02434	Aminoacyl-tRNA biosynthesis

				gspD	K02453	Bacterial secretion system
				pilD,pppA	K02654	Not known
				virB10,lvhB10	K03195	Bacterial secretion system
				cheW	K03408	Two-component system
				recG	K03655	Homologous recombination
				lipB	K03801	Lipoic acid metabolism
				bamD	K05807	Not known
				unknown	K06929	Not known
				ybeY,yqfG	K07042	Not known
				unknown	K07220	Not known
				mutS2	K07456	Mismatch repair
				mgtC	K07507	Not known
				unknown	K07576	Not known
				purN	K11175	Purine metabolism
				btuB	K16092	Not known
				CHO1,pssA	K17103	Not known
				penP	K17836	Not known
				dacA	K18672	Not known
Candidatus_Microthrix	0	2	Bulk	OPLAH	K01469	Glutathione metabolism
				unknown	K07058	Not known
Candidatus_Solibacter	18	11	Bulk	metE	K00549	Cysteine and methionine metabolism
				otsB	K01087	Starch and sucrose metabolism
				aslA	K01130	Steroid hormone biosynthesis
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				pstS	K02040	ABC transporters
				cspA	K03704	Not known
				unknown	K06152	Pentose phosphate pathway
				unknown	K06978	Not known
				unknown	K07001	Not known

				unknown	K07058	Not known
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
			Rhizosphere	gcd	K00117	Pentose phosphate pathway
				gltD	K00266	Nitrogen metabolism
				ARSC1,arsC	K00537	Not known
				glgC	K00975	Starch and sucrose metabolism
				gph	K01091	Glyoxylate and dicarboxylate metabolism
				NEU1	K01186	Sphingolipid metabolism
				aguA	K01235	Not known
				TC.FEV.OM	K02014	Not known
				gatB,PET112	K02434	Aminoacyl-tRNA biosynthesis
				rssB,hnr	K02485	Not known
				NRT,narK,nrtP,nasA	K02575	Not known
				lipB	K03801	Lipoic acid metabolism
				rluB	K06178	Not known
				ybeY,yqfG	K07042	Not known
				unknown	K07220	Not known
				wbpY,wbdB	K12994	Not known
				dnaE2	K14162	Not known
				dacA	K18672	Not known
Catelliglobosispora	1	4	Bulk	yidH	K00389	Not known
				tam	K00598	Not known
				unknown	K07058	Not known
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
			Rhizosphere	lipB	K03801	Lipoic acid metabolism
Catenulispora	10	7	Bulk	unknown	K00375	Not known
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				kup	K03549	Not known
				cspA	K03704	Not known

				unknown	K06978	Not known
				unknown	K07006	Not known
				GDH2	K15371	Not known
			Rhizosphere	OTC,argF,argI	K00611	Arginine and prolinemetabolism
				bioA	K00833	Biotin metabolism
				eda	K01625	Pentose phosphate pathway
				ABC.FEV.A	K02013	ABC transporters
				UNG,UDG	K03648	Base excision repair
				radA,sms	K04485	Not known
				unknown	K07220	Not known
				mgtC	K07507	Not known
				dnaE2	K14162	Not known
				penP	K17836	Not known
Catenuloplanes	1	1	Bulk	metE	K00549	Cysteine and methionine metabolism
			Rhizosphere	recG	K03655	Homologous recombination
Caulobacter	3	1	Bulk	unknown	K07001	Not known
			Rhizosphere	manA,MPI	K01809	Fructose and mannose metabolism
				ABC.FEV.A	K02013	ABC transporters
				TC.FEV.OM	K02014	Not known
Cellulomonas	0	1	Bulk	pimA	K08256	Not known
Chloracidobacterium	5	0	Rhizosphere	SRP54,ffh	K03106	Protein export
				recG	K03655	Homologous recombination
				clpB	K03695	Not known
				bamD	K05807	Not known
				TC.FEV.OM3,tbpA	K16087	Not known
Chloroflexus	2	1	Bulk	unknown	K06978	Not known
			Rhizosphere	radA,sms	K04485	Not known
				mutS2	K07456	Mismatch repair
Chondromyces	1	0	Bulk	unknown	K07001	Not known

Chthoniobacter	12	3	Bulk	ribE	K00793	Riboflavin metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				amgK	K07102	Not known
			Rhizosphere	manC,cpsB	K00971	Fructose and mannose metabolism
				gph	K01091	Glyoxylate and dicarboxylate metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				accD	K01963	Pyruvate metabolism
				gspD	K02453	Bacterial secretion system
				pilD,pppA	K02654	Not known
				SRP54,ffh	K03106	Protein export
				recG	K03655	Homologous recombination
				lipB	K03801	Lipoic acid metabolism
				scpB	K06024	Not known
				purN	K11175	Purine metabolism
				penP	K17836	Not known
Clostridium	1	2	Bulk	dgkA,DGK	K00901	Glycerolipid metabolism
				unknown	K07001	Not known
			Rhizosphere	udp,UPP	K00757	Pyrimidine metabolism
Conexibacter	29	19	Bulk	ald	K00259	Carbon fixation pathways in prokaryotes
				unknown	K00375	Not known
				yidH	K00389	Not known
				metE	K00549	Cysteine and methionine metabolism
				GST,gst	K00799	Glutathione metabolism
				otsB	K01087	Starch and sucrose metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				modA	K02020	ABC transporters
				pstS	K02040	ABC transporters
				coxL,cutL	K03520	Methane metabolism
				cspA	K03704	Not known

				unknown	K06978	Not known
				unknown	K07001	Not known
				unknown	K07058	Not known
				grxD,GLRX5	K07390	Not known
				pimA	K08256	Not known
				treT	K13057	Not known
				cbrT	K16927	Not known
				lldE	K18928	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				metH,MTR	K00548	Cysteine and methionine metabolism
				OTC,argF,argI	K00611	Arginine and prolinemetabolism
				bioA	K00833	Biotin metabolism
				ndk,NME	K00940	Purine metabolism
				gph	K01091	Glyoxylate and dicarboxylate metabolism
				dcd	K01494	Pyrimidine metabolism
				eda	K01625	Pentose phosphate pathway
				trpB	K01696	Glycine, serine and threonine metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				accD	K01963	Pyruvate metabolism
				ABC.FEV.A	K02013	ABC transporters
				gatB,PET112	K02434	Aminoacyl-tRNA biosynthesis
				RP-L14,MRPL14,rplN	K02874	Ribosome
				SRP54,ffh	K03106	Protein export
				cheW	K03408	Two-component system
				cheD	K03411	Bacterial chemotaxis
				sbcD	K03547	Not known
				recG	K03655	Homologous recombination
				clpB	K03695	Not known
				lipB	K03801	Lipoic acid metabolism

				radA,sms	K04485	Not known
				opuBD	K05846	ABC transporters
				scpB	K06024	Not known
				rluB	K06178	Not known
				ybeY,yqfG	K07042	Not known
				unknown	K07220	Not known
				purN	K11175	Purine metabolism
				dnaE2	K14162	Not known
Corallococcus	0	1	Bulk	treT	K13057	Not known
Cryptosporangium	0	5	Bulk	pobA	K00481	Toluene degradation
				unknown	K07001	Not known
				unknown	K07006	Not known
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
				pduE	K13920	Glycerolipid metabolism
Cupriavidus	3	2	Bulk	GST,gst	K00799	Glutathione metabolism
				kup	K03549	Not known
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
				HMGCL,hmgL	K01640	Butanoate metabolism
				penP	K17836	Not known
Cystobacter	1	0	Rhizosphere	cheW	K03408	Two-component system
Dactylosporangium	2	1	Bulk	coxL,cutL	K03520	Methane metabolism
			Rhizosphere	TC.KEF	K03455	Not known
				opuBD	K05846	ABC transporters
Dehalococcoides	0	1	Bulk	pimA	K08256	Not known
Deinococcus	3	3	Bulk	dld,LDHD	K00102	Pyruvate metabolism
				unknown	K00359	Not known
				tam	K00598	Not known
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
				glgC	K00975	Starch and sucrose metabolism

				gspD	K02453	Bacterial secretion system
Deinococcus-Thermus	7	11	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
				dld,LDHD	K00102	Pyruvate metabolism
				porA	K00169	Glycolysis/Gluconeogenesis
				ald	K00259	Carbon fixation pathways in prokaryotes
				unknown	K00359	Not known
				tam	K00598	Not known
				ribE	K00793	Riboflavin metabolism
				pstS	K02040	ABC transporters
				aqpZ	K06188	Not known
				GDH2	K15371	Not known
				lldE	K18928	Not known
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
				galK	K00849	Galactose metabolism
				ndk,NME	K00940	Purine metabolism
				glgC	K00975	Starch and sucrose metabolism
				trpB	K01696	Glycine, serine and threonine metabolism
				gspD	K02453	Bacterial secretion system
				rluB	K06178	Not known
Desulfovibrio	1	0	Rhizosphere	cheW	K03408	Two-component system
Devosia	1	1	Bulk	unknown	K00480	Naphthalene degradation
			Rhizosphere	unknown	K07002	Not known
Dongia	1	1	Bulk	gdh	K00034	Pentose phosphate pathway
			Rhizosphere	crcB	K06199	Not known
Dyella	1	1	Bulk	unknown	K00375	Not known
			Rhizosphere	TC.FEV.OM	K02014	Not known
Edaphobacter	6	5	Bulk	unknown	K00375	Not known
				modA	K02020	ABC transporters
				coxL,cutL	K03520	Methane metabolism

				unknown	K06978	Not known
				unknown	K07058	Not known
			Rhizosphere	uppS	K00806	Terpenoid backbone biosynthesis
				puuE	K00823	Propanoate metabolism
				pgpA	K01095	Glycerophospholipid metabolism
				gspD	K02453	Bacterial secretion system
				sbcD	K03547	Not known
				lipB	K03801	Lipoic acid metabolism
Elioraea	0	2	Bulk	OPLAH	K01469	Glutathione metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
Filomicrobium	0	1	Bulk	hlyIII	K11068	Not known
Frankia	12	14	Bulk	TYR	K00505	Tyrosine metabolism
				otsB	K01087	Starch and sucrose metabolism
				aslA	K01130	Steroid hormone biosynthesis
				modA	K02020	ABC transporters
				pstS	K02040	ABC transporters
				coxL,cutL	K03520	Methane metabolism
				cspA	K03704	Not known
				unknown	K06978	Not known
				unknown	K07001	Not known
				unknown	K07058	Not known
				unknown	K07484	Not known
				paiB	K07734	Not known
				hlyIII	K11068	Not known
				lldE	K18928	Not known
			Rhizosphere	nirB	K00362	Nitrogen metabolism
				metH,MTR	K00548	Cysteine and methionine metabolism
				OTC,argF,argI	K00611	Arginine and prolinemetabolism
				gph	K01091	Glyoxylate and dicarboxylate metabolism

				pabA	K01664	Folate biosynthesis
				NRT,narK,nrtP,nasA	K02575	Not known
				clpB	K03695	Not known
				opuBD	K05846	ABC transporters
				unknown	K07002	Not known
				ybeY,yqfG	K07042	Not known
				purN	K11175	Purine metabolism
				dnaE2	K14162	Not known
Gemmata	4	2	Bulk	ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				unknown	K07484	Not known
			Rhizosphere	glgC	K00975	Starch and sucrose metabolism
				manA,MPI	K01809	Fructose and mannose metabolism
				rluB	K06178	Not known
				purN	K11175	Purine metabolism
Gemmatimonas	4	2	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
				unknown	K07001	Not known
			Rhizosphere	ndk,NME	K00940	Purine metabolism
				TC.FEV.OM	K02014	Not known
				bamD	K05807	Not known
				etk-wzc	K16692	Not known
Gemmatirosa	32	7	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
				ribE	K00793	Riboflavin metabolism
				gmhB	K03273	Lipopolysaccharide biosynthesis
				cspA	K03704	Not known
				unknown	K07001	Not known
				unknown	K07058	Not known
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
			Rhizosphere	gcd	K00117	Pentose phosphate pathway
				OTC,argF,argI	K00611	Arginine and prolinemetabolism

				uppS	K00806	Terpenoid backbone biosynthesis
				bioA	K00833	Biotin metabolism
				galK	K00849	Galactose metabolism
				glgC	K00975	Starch and sucrose metabolism
				eda	K01625	Pentose phosphate pathway
				aspA	K01744	Nitrogen metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				ABC.FEV.A	K02013	ABC transporters
				TC.FEV.OM	K02014	Not known
				gspD	K02453	Bacterial secretion system
				recG	K03655	Homologous recombination
				clpB	K03695	Not known
				lipB	K03801	Lipoic acid metabolism
				radA,sms	K04485	Not known
				ftsB	K05589	Not known
				bamD	K05807	Not known
				scpB	K06024	Not known
				unknown	K06975	Not known
				ybeY,yqfG	K07042	Not known
				unknown	K07220	Not known
				mutS2	K07456	Mismatch repair
				unknown	K07576	Not known
				purN	K11175	Purine metabolism
				cphB	K13282	Not known
				dnaE2	K14162	Not known
				btuB	K16092	Not known
				etk-wzc	K16692	Not known
				CHO1,pssA	K17103	Not known
				penP	K17836	Not known

				dacA	K18672	Not known
Geobacter	3	1	Bulk	pstS	K02040	ABC transporters
			Rhizosphere	pilD,pppA	K02654	Not known
				cheW	K03408	Two-component system
				clpB	K03695	Not known
Geodermatophilus	1	2	Bulk	pqqB	K06136	Not known
				unknown	K07001	Not known
			Rhizosphere	rluB	K06178	Not known
Gimesia	0	1	Bulk	unknown	K07481	Not known
Glycomyces	1	0	Rhizosphere	mgtC	K07507	Not known
Gordonia	1	0	Rhizosphere	uppS	K00806	Terpenoid backbone biosynthesis
Granulicella	7	6	Bulk	aslA	K01130	Steroid hormone biosynthesis
				pstS	K02040	ABC transporters
				aqpZ	K06188	Not known
				unknown	K07058	Not known
				unknown	K07481	Not known
				unknown	K07486	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				TC.FEV.OM	K02014	Not known
				atoE	K02106	Two-component system
				clpB	K03695	Not known
				bamD	K05807	Not known
				dnaE2	K14162	Not known
				penP	K17836	Not known
Haliangium	3	2	Bulk	OPLAH	K01469	Glutathione metabolism
				modA	K02020	ABC transporters
			Rhizosphere	TC.FEV.OM	K02014	Not known
				TC.KEF	K03455	Not known
				mutS2	K07456	Mismatch repair

Haloferula	17	3	Bulk	pstS	K02040	ABC transporters
				unknown	K07058	Not known
				amgK	K07102	Not known
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
				OTC,argF,argI	K00611	Arginine and prolinemetabolism
				bioA	K00833	Biotin metabolism
				gph	K01091	Glyoxylate and dicarboxylate metabolism
				eda	K01625	Pentose phosphate pathway
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				ABC.FEV.A	K02013	ABC transporters
				TC.FEV.OM	K02014	Not known
				gspD	K02453	Bacterial secretion system
				NRT,narK,nrtP,nasA	K02575	Not known
				TC.KEF	K03455	Not known
				sbcD	K03547	Not known
				clpB	K03695	Not known
				lipB	K03801	Lipoic acid metabolism
				bamD	K05807	Not known
				unknown	K07576	Not known
				dnaE2	K14162	Not known
Herbaspirillum	1	0	Rhizosphere	uppS	K00806	Terpenoid backbone biosynthesis
Hyalangium	1	2	Bulk	kup	K03549	Not known
				unknown	K07484	Not known
			Rhizosphere	puuE	K00823	Propanoate metabolism
Hyphomicrobium	1	2	Bulk	unknown	K07001	Not known
				unknown	K07577	Not known
			Rhizosphere	CHO1,pssA	K17103	Not known
Ilumatobacter	0	2	Bulk	aslA	K01130	Steroid hormone biosynthesis
				coxL,cutL	K03520	Methane metabolism

Intrasporangium	2	4	Bulk	ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				coxL,cutL	K03520	Methane metabolism
				unknown	K07058	Not known
				treT	K13057	Not known
			Rhizosphere	cobF	K02228	Porphyrin and chlorophyll metabolism
				pta	K13788	Pyruvate metabolism
Janibacter	1	0	Rhizosphere	eda	K01625	Pentose phosphate pathway
Jiangella	0	2	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
				unknown	K07058	Not known
Kibdelosporangium	0	1	Bulk	pimA	K08256	Not known
Kitasatospora	1	1	Bulk	yidH	K00389	Not known
			Rhizosphere	manA,MPI	K01809	Fructose and mannose metabolism
Knoellia	0	1	Bulk	unknown	K07006	Not known
Kribbella	35	13	Bulk	ald	K00259	Carbon fixation pathways in prokaryotes
				unknown	K00375	Not known
				yidH	K00389	Not known
				merA	K00520	Not known
				tam	K00598	Not known
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				MTHFS	K01934	One carbon pool byfolate
				coxL,cutL	K03520	Methane metabolism
				cspA	K03704	Not known
				unknown	K07006	Not known
				unknown	K07058	Not known
				TC.BAT2	K09936	Not known
				hlyIII	K11068	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				pntA	K00324	Nicotinate and nicotinamide metabolism
				nirB	K00362	Nitrogen metabolism

				nasA	K00372	Nitrogen metabolism
				OTC,argF,argI	K00611	Arginine and prolinemetabolism
				puuE	K00823	Propanoate metabolism
				galK	K00849	Galactose metabolism
				manC,cpsB	K00971	Fructose and mannose metabolism
				glgC	K00975	Starch and sucrose metabolism
				NEU1	K01186	Sphingolipid metabolism
				eda	K01625	Pentose phosphate pathway
				HMGCL,hmgL	K01640	Butanoate metabolism
				pabA	K01664	Folate biosynthesis
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				proW	K02001	ABC transporters
				ABC.FEV.A	K02013	ABC transporters
				atoE	K02106	Two-component system
				gatB,PET112	K02434	Aminoacyl-tRNA biosynthesis
				NRT,narK,nrtP,nasA	K02575	Not known
				pilD,pppA	K02654	Not known
				UNG,UDG	K03648	Base excision repair
				clpB	K03695	Not known
				lipB	K03801	Lipoic acid metabolism
				radA,sms	K04485	Not known
				opuBD	K05846	ABC transporters
				scpB	K06024	Not known
				rluB	K06178	Not known
				unknown	K06975	Not known
				ybeY,yqfG	K07042	Not known
				unknown	K07093	Not known
				dtd,DTD1	K07560	Not known
				purN	K11175	Purine metabolism

				npdA	K12410	Aminosugar and nucleotidesugar metabolism
				cphB	K13282	Not known
				pta	K13788	Pyruvate metabolism
Ktedonobacter	4	6	Bulk	unknown	K00375	Not known
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				coxL,cutL	K03520	Methane metabolism
				unknown	K07058	Not known
				unknown	K07484	Not known
				hlyIII	K11068	Not known
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
				HMGCL,hmgL	K01640	Butanoate metabolism
				SRP54,ffh	K03106	Protein export
				fdhA	K05299	Not known
Kutzneria	1	2	Bulk	unknown	K00375	Not known
				GDH2	K15371	Not known
			Rhizosphere	HMGCL,hmgL	K01640	Butanoate metabolism
Labrenzia	0	1	Bulk	unknown	K07486	Not known
Lactobacillus	0	1	Rhizosphere	mutS2	K07456	Mismatch repair
Lechevalieria	1	0	Bulk	ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				unknown	K07001	Not known
Legionella	0	2	Rhizosphere	crcB	K06199	Not known
Leifsonia	6	5	Bulk	ribE	K00793	Riboflavin metabolism
				MTHFS	K01934	One carbon pool byfolate
				modA	K02020	ABC transporters
				pstS	K02040	ABC transporters
				hlyIII	K11068	Not known
			Rhizosphere	UNG,UDG	K03648	Base excision repair

				clpB	K03695	Not known
				opuBD	K05846	ABC transporters
				scpB	K06024	Not known
				crcB	K06199	Not known
				purN	K11175	Purine metabolism
Leptolyngbya	0	1	Bulk	pimA	K08256	Not known
Leptospira	1	0	Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
Lysobacter	0	1	Bulk	GST,gst	K00799	Glutathione metabolism
Magnetospirillum	0	2	Bulk	unknown	K07484	Not known
				torZ	K07812	Not known
Marinobacter	0	2	Bulk	GST,gst	K00799	Glutathione metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
Marmoricola	11	7	Bulk	ald	K00259	Carbon fixation pathways in prokaryotes
				merA	K00520	Not known
				modA	K02020	ABC transporters
				unknown	K07001	Not known
				hlyIII	K11068	Not known
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
				GDH2	K15371	Not known
			Rhizosphere	ARSC1,arsC	K00537	Not known
				OTC,argF,argI	K00611	Arginine and prolinemetabolism
				galK	K00849	Galactose metabolism
				manC,cpsB	K00971	Fructose and mannose metabolism
				ABC.FEV.A	K02013	ABC transporters
				wecE,rffA	K02805	Not known
				clpB	K03695	Not known
				radA,sms	K04485	Not known
				unknown	K07220	Not known
				purN	K11175	Purine metabolism

				dnaE2	K14162	Not known
Massilia	2	0	Rhizosphere	gltD	K00266	Nitrogen metabolism
				ARSC1,arsC	K00537	Not known
Meiothermus	0	1	Bulk	porA	K00169	Glycolysis/Gluconeogenesis
Mesorhizobium	7	15	Bulk	ald	K00259	Carbon fixation pathways in prokaryotes
				unknown	K00375	Not known
				GST,gst	K00799	Glutathione metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				modA	K02020	ABC transporters
				yddA	K02471	ABC transporters
				coxL,cutL	K03520	Methane metabolism
				unknown	K06978	Not known
				unknown	K07001	Not known
				unknown	K07058	Not known
				amgK	K07102	Not known
				unknown	K07117	Not known
				unknown	K07486	Not known
				paiB	K07734	Not known
				urtA	K11959	ABC transporters
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
				ndk,NME	K00940	Purine metabolism
				eda	K01625	Pentose phosphate pathway
				trpB	K01696	Glycine, serine and threonine metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				gatB,PET112	K02434	Aminoacyl-tRNA biosynthesis
				unknown	K06929	Not known
Methanosarcina	0	1	Bulk	ilvB,ilvG,ilvI	K01652	Butanoate metabolism
Methylibium	0	2	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
				unknown	K07001	Not known

Methylobacterium	5	10	Bulk	MTHFS	K01934	One carbon pool byfolate
				modA	K02020	ABC transporters
				yddA	K02471	ABC transporters
				gmhB	K03273	Lipopolysaccharide biosynthesis
				unknown	K07001	Not known
				unknown	K07484	Not known
				unknown	K07486	Not known
				TC.BAT2	K09936	Not known
				hlyIII	K11068	Not known
				GDH2	K15371	Not known
			Rhizosphere	nasA	K00372	Nitrogen metabolism
				ARSC1,arsC	K00537	Not known
				gph	K01091	Glyoxylate and dicarboxylate metabolism
				gspD	K02453	Bacterial secretion system
				TC.KEF	K03455	Not known
Methyloceanibacter	7	8	Bulk	merA	K00520	Not known
				OPLAH	K01469	Glutathione metabolism
				ureC	K03192	Not known
				cspA	K03704	Not known
				unknown	K07058	Not known
				amgK	K07102	Not known
				unknown	K08988	Not known
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
				bioA	K00833	Biotin metabolism
				dcd	K01494	Pyrimidine metabolism
				SRP54,ffh	K03106	Protein export
				recG	K03655	Homologous recombination
				vicK	K07652	Two-component system

				dnaE2	K14162	Not known
Methylocella	0	1	Bulk	yddA	K02471	ABC transporters
Methylocystis	1	1	Bulk	unknown	K07001	Not known
			Rhizosphere	galK	K00849	Galactose metabolism
Methylosinus	0	2	Bulk	unknown	K07484	Not known
				unknown	K07486	Not known
Microbacterium	3	1	Bulk	ilvB,ilvG,ilvI	K01652	Butanoate metabolism
			Rhizosphere	manA,MPI	K01809	Fructose and mannose metabolism
				NRT,narK,nrtP,nasA	K02575	Not known
				mgtC	K07507	Not known
Microlunatus	0	1	Bulk	unknown	K07058	Not known
Micromonospora	5	5		mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
				unknown	K00359	Not known
				unknown	K00375	Not known
				unknown	K07006	Not known
			Bulk	unknown	K07058	Not known
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
				ABC.FEV.A	K02013	ABC transporters
				lipB	K03801	Lipoic acid metabolism
				unknown	K07002	Not known
				penP	K17836	Not known
Microvirga	1	2	Bulk	unknown	K07001	Not known
				unknown	K07486	Not known
			Rhizosphere	ybeY,yqfG	K07042	Not known
Modestobacter	1	2	Bulk	TYR	K00505	Tyrosine metabolism
				coxL,cutL	K03520	Methane metabolism
			Rhizosphere	pilD,pppA	K02654	Not known
Mumia	0	1	Bulk	cpo	K00433	Not known
Mycobacterium	41	31	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation

				mtlK	K00045	Fructose and mannose metabolism
				ald	K00259	Carbon fixation pathways in prokaryotes
				sthA,udhA	K00322	Nicotinate and nicotinamide metabolism
				unknown	K00375	Not known
				yidH	K00389	Not known
				cpo	K00433	Not known
				merA	K00520	Not known
				metE	K00549	Cysteine and methionine metabolism
				tam	K00598	Not known
				otsB	K01087	Starch and sucrose metabolism
				aslA	K01130	Steroid hormone biosynthesis
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				MTHFS	K01934	One carbon pool byfolate
				modA	K02020	ABC transporters
				pstS	K02040	ABC transporters
				yddA	K02471	ABC transporters
				coxL,cutL	K03520	Methane metabolism
				cspA	K03704	Not known
				unknown	K06897	Not known
				unknown	K06978	Not known
				unknown	K07001	Not known
				unknown	K07006	Not known
				unknown	K07058	Not known
				unknown	K07481	Not known
				pimA	K08256	Not known
				hlyIII	K11068	Not known
				fadK	K12507	Not known
				pduE	K13920	Glycerolipid metabolism
				GDH2	K15371	Not known

				laaA	K18457	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				pntA	K00324	Nicotinate and nicotinamide metabolism
				nirB	K00362	Nitrogen metabolism
				metH,MTR	K00548	Cysteine and methionine metabolism
				OTC,argF,argI	K00611	Arginine and prolinemetabolism
				puuE	K00823	Propanoate metabolism
				bioA	K00833	Biotin metabolism
				galK	K00849	Galactose metabolism
				ndk,NME	K00940	Purine metabolism
				glgC	K00975	Starch and sucrose metabolism
				dcd	K01494	Pyrimidine metabolism
				HMGCL,hmgL	K01640	Butanoate metabolism
				trpB	K01696	Glycine, serine and threonine metabolism
				manA,MPI	K01809	Fructose and mannose metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				unknown	K01941	Arginine and prolinemetabolism
				PC,pyc	K01958	Citrate cycle (TCAcycle)
				accD	K01963	Pyruvate metabolism
				proW	K02001	ABC transporters
				ABC.FEV.A	K02013	ABC transporters
				cobF	K02228	Porphyrin and chlorophyll metabolism
				gatB,PET112	K02434	Aminoacyl-tRNA biosynthesis
				RP-L14,MRPL14,rplN	K02874	Ribosome
				SRP54,ffh	K03106	Protein export
				sbcD	K03547	Not known
				recG	K03655	Homologous recombination
				clpB	K03695	Not known
				lipB	K03801	Lipoic acid metabolism

				radA,sms	K04485	Not known
				opuBD	K05846	ABC transporters
				scpB	K06024	Not known
				rluB	K06178	Not known
				crcB	K06199	Not known
				unknown	K06929	Not known
				ybeY,yqfG	K07042	Not known
				unknown	K07044	Not known
				mgtC	K07507	Not known
				npdA	K12410	Aminosugar and nucleotidesugar metabolism
				pta	K13788	Pyruvate metabolism
				dnaE2	K14162	Not known
				penP	K17836	Not known
Myxococcus	0	2	Bulk	aslA	K01130	Steroid hormone biosynthesis
				unknown	K07484	Not known
Nakamurella	2	3	Bulk	unknown	K07001	Not known
				unknown	K07058	Not known
				xdhA	K13481	Purine metabolism
			Rhizosphere	crcB	K06199	Not known
				unknown	K07220	Not known
Neorhizobium	0	1	Bulk	coxL,cutL	K03520	Methane metabolism
Nitrobacter	1	0	Rhizosphere	NRT,narK,nrtP,nasA	K02575	Not known
Nitrolancea	2	0	Rhizosphere	pntA	K00324	Nicotinate and nicotinamide metabolism
				HMGCL,hmgL	K01640	Butanoate metabolism
Nitrosococcus	0	2	Bulk	unknown	K00375	Not known
				unknown	K07001	Not known
Nitrososphaera	0	2	Bulk	ribE	K00793	Riboflavin metabolism

				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
Nitrospira	2	1	Bulk	modA	K02020	ABC transporters
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
				dtd,DTD1	K07560	Not known
Nocardia	4	3	Bulk	yddA	K02471	ABC transporters
				aqpZ	K06188	Not known
				unknown	K06978	Not known
			Rhizosphere	nasA	K00372	Nitrogen metabolism
				OTC,argF,argI	K00611	Arginine and prolinemetabolism
				eda	K01625	Pentose phosphate pathway
				manA,MPI	K01809	Fructose and mannose metabolism
Nocardioides	31	15	Bulk	gdh	K00034	Pentose phosphate pathway
				merA	K00520	Not known
				ribE	K00793	Riboflavin metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				pstS	K02040	ABC transporters
				coxL,cutL	K03520	Methane metabolism
				kup	K03549	Not known
				aqpZ	K06188	Not known
				unknown	K06978	Not known
				unknown	K07001	Not known
				unknown	K07058	Not known
				unknown	K07577	Not known
				hlyIII	K11068	Not known
				GDH2	K15371	Not known
				cbrT	K16927	Not known
			Rhizosphere	pntA	K00324	Nicotinate and nicotinamide metabolism
				nirB	K00362	Nitrogen metabolism
				nasA	K00372	Nitrogen metabolism

				ARSC1,arsC	K00537	Not known
				OTC,argF,argI	K00611	Arginine and prolinemetabolism
				uppS	K00806	Terpenoid backbone biosynthesis
				bioA	K00833	Biotin metabolism
				manC,cpsB	K00971	Fructose and mannose metabolism
				trpB	K01696	Glycine, serine and threonine metabolism
				manA,MPI	K01809	Fructose and mannose metabolism
				PC,pyc	K01958	Citrate cycle (TCAcycle)
				accD	K01963	Pyruvate metabolism
				ABC.FEV.A	K02013	ABC transporters
				NRT,narK,nrtP,nasA	K02575	Not known
				pilD,pppA	K02654	Not known
				SRP54,ffh	K03106	Protein export
				sbcD	K03547	Not known
				recG	K03655	Homologous recombination
				clpB	K03695	Not known
				lipB	K03801	Lipoic acid metabolism
				pnuC	K03811	Not known
				radA,sms	K04485	Not known
				opuBD	K05846	ABC transporters
				scpB	K06024	Not known
				rluB	K06178	Not known
				crcB	K06199	Not known
				unknown	K07220	Not known
				mutS2	K07456	Mismatch repair
				npdA	K12410	Aminosugar and nucleotidesugar metabolism
				cphB	K13282	Not known
				dnaE2	K14162	Not known

Nocardiopsis	4	3	Bulk	otsB	K01087	Starch and sucrose metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				GDH2	K15371	Not known
			Rhizosphere	uppS	K00806	Terpenoid backbone biosynthesis
				puuE	K00823	Propanoate metabolism
				proW	K02001	ABC transporters
				radA,sms	K04485	Not known
Nostoc	0	1	Bulk	fabL	K10780	Fattyacidbiosynthesis
Novosphingobium	3	2	Bulk	unknown	K07001	Not known
				unknown	K07481	Not known
			Rhizosphere	HMGCL,hmgL	K01640	Butanoate metabolism
				TC.FEV.OM	K02014	Not known
				ybeY,yqfG	K07042	Not known
Opitutus	1	0	Rhizosphere	manC,cpsB	K00971	Fructose and mannose metabolism
Paenibacillus	1	0	Rhizosphere	galK	K00849	Galactose metabolism
Pandoraea	0	2	Bulk	pobA	K00481	Toluene degradation
				unknown	K07117	Not known
Paraburkholderia	2	3	Bulk	unknown	K00480	Naphthalene degradation
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				modA	K02020	ABC transporters
			Rhizosphere	unknown	K07002	Not known
				mgtC	K07507	Not known
Patulibacter	6	7	Bulk	unknown	K00375	Not known
				unknown	K00480	Naphthalene degradation
				GST,gst	K00799	Glutathione metabolism
				unknown	K06978	Not known
				unknown	K07058	Not known
				grxD,GLRX5	K07390	Not known
				pimA	K08256	Not known

			Rhizosphere	gltD	K00266	Nitrogen metabolism
				cobF	K02228	Porphyrin and chlorophyll metabolism
				recG	K03655	Homologous recombination
				lipB	K03801	Lipoic acid metabolism
				ybeY,yqfG	K07042	Not known
				purN	K11175	Purine metabolism
Pedobacter	0	2	Bulk	otsB	K01087	Starch and sucrose metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
Pedosphaera	3	2	Bulk	unknown	K07486	Not known
				lldE	K18928	Not known
			Rhizosphere	eda	K01625	Pentose phosphate pathway
				opuBD	K05846	ABC transporters
				penP	K17836	Not known
Pelobacter	1	0	Rhizosphere	fdhA	K05299	Not known
Phycicoccus	1	0	Rhizosphere	proW	K02001	ABC transporters
Phycisphaera	2	0	Rhizosphere	dcd	K01494	Pyrimidine metabolism
				bamD	K05807	Not known
Pimelobacter	1	0	Rhizosphere	UNG,UDG	K03648	Base excision repair
Pirellula	0	2	Bulk	glcE	K11472	Glyoxylate and dicarboxylate metabolism
				iscA,ISCA1	K13628	Not known
Prauserella	0	1	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
Pseudomonas	1	5	Bulk	ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				unknown	K07001	Not known
				unknown	K07006	Not known
				unknown	K07058	Not known
				GDH2	K15371	Not known
			Rhizosphere	CHO1,pssA	K17103	Not known
Pseudonocardia	31	28	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
				mtlK	K00045	Fructose and mannose metabolism

				ald	K00259	Carbon fixation pathways in prokaryotes
				unknown	K00359	Not known
				unknown	K00375	Not known
				unknown	K00480	Naphthalene degradation
				merA	K00520	Not known
				metE	K00549	Cysteine and methionine metabolism
				tam	K00598	Not known
				ribE	K00793	Riboflavin metabolism
				otsB	K01087	Starch and sucrose metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				MTHFS	K01934	One carbon pool byfolate
				modA	K02020	ABC transporters
				pstS	K02040	ABC transporters
				coxL,cutL	K03520	Methane metabolism
				cspA	K03704	Not known
				aqpZ	K06188	Not known
				unknown	K06978	Not known
				unknown	K07001	Not known
				unknown	K07006	Not known
				unknown	K07058	Not known
				pimA	K08256	Not known
				hlyIII	K11068	Not known
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
				fadK	K12507	Not known
				fcs	K12508	Not known
				GDH2	K15371	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				pntA	K00324	Nicotinate and nicotinamide metabolism
				nirB	K00362	Nitrogen metabolism

				ARSC1,arsC	K00537	Not known
				metH,MTR	K00548	Cysteine and methionine metabolism
				OTC,argF,argI	K00611	Arginine and prolinemetabolism
				uppS	K00806	Terpenoid backbone biosynthesis
				puuE	K00823	Propanoate metabolism
				bioA	K00833	Biotin metabolism
				glgC	K00975	Starch and sucrose metabolism
				eda	K01625	Pentose phosphate pathway
				manA,MPI	K01809	Fructose and mannose metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				allC	K02083	Purine metabolism
				gatB,PET112	K02426	Aminoacyl-tRNA biosynthesis
				paaZ	K02618	Not known
				pilD,pppA	K02654	Not known
				SRP54,ffh	K03106	Protein export
				TC.KEF	K03455	Not known
				sbcD	K03547	Not known
				UNG,UDG	K03648	Base excision repair
				recG	K03655	Homologous recombination
				clpB	K03695	Not known
				radA,sms	K04485	Not known
				opuBD	K05846	ABC transporters
				unknown	K06929	Not known
				ybeY,yqfG	K07042	Not known
				unknown	K07044	Not known
				unknown	K07093	Not known
				dnaE2	K14162	Not known
				CHO1,pssA	K17103	Not known
Pyrinomonas	22	10	Bulk	ald	K00259	Carbon fixation pathways in prokaryotes

				ribE	K00793	Riboflavin metabolism
				pstS	K02040	ABC transporters
				gmhB	K03273	Lipopolysaccharide biosynthesis
				coxL,cutL	K03520	Methane metabolism
				cspA	K03704	Not known
				trmFO,gid	K04094	Not known
				unknown	K06978	Not known
				amgK	K07102	Not known
				iscA,ISCA1	K13628	Not known
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
				uppS	K00806	Terpenoid backbone biosynthesis
				puuE	K00823	Propanoate metabolism
				galK	K00849	Galactose metabolism
				glgC	K00975	Starch and sucrose metabolism
				aguA	K01235	Not known
				dcd	K01494	Pyrimidine metabolism
				trpB	K01696	Glycine, serine and threonine metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				accD	K01963	Pyruvate metabolism
				TC.FEV.OM	K02014	Not known
				gatB,PET112	K02434	Aminoacyl-tRNA biosynthesis
				gspD	K02453	Bacterial secretion system
				RP-L14,MRPL14,rplN	K02874	Ribosome
				virB10,lvhB10	K03195	Bacterial secretion system
				clpB	K03695	Not known
				ybeY,yqfG	K07042	Not known
				mutS2	K07456	Mismatch repair
				dtd,DTD1	K07560	Not known
				rodZ	K15539	Not known

				penP	K17836	Not known
				dacA	K18672	Not known
Ralstonia	3	2		pobA	K00481	Toluene degradation
			Bulk	GST,gst	K00799	Glutathione metabolism
			Rhizosphere	HMGCL,hmgL	K01640	Butanoate metabolism
				purN	K11175	Purine metabolism
				dnaE2	K14162	Not known
Reyranella	4	8	Bulk	metE	K00549	Cysteine and methionine metabolism
				GST,gst	K00799	Glutathione metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				modA	K02020	ABC transporters
				pstS	K02040	ABC transporters
				coxL,cutL	K03520	Methane metabolism
				cspA	K03704	Not known
				hlyIII	K11068	Not known
			Rhizosphere	manC,cpsB	K00971	Fructose and mannose metabolism
				TC.KEF	K03455	Not known
				clpB	K03695	Not known
				npdA	K12410	Aminosugar and nucleotidesugar metabolism
Rhizobium	11	9	Bulk	dld,LDHD	K00102	Pyruvate metabolism
				GST,gst	K00799	Glutathione metabolism
				betC	K01133	Not known
				yddA	K02471	ABC transporters
				unknown	K06152	Pentose phosphate pathway
				unknown	K07001	Not known
				unknown	K07006	Not known
				unknown	K07486	Not known
				paiB	K07734	Not known

			Rhizosphere	nirB	K00362	Nitrogen metabolism
				ndk,NME	K00940	Purine metabolism
				glgC	K00975	Starch and sucrose metabolism
				unknown	K01941	Arginine and prolinemetabolism
				proW	K02001	ABC transporters
				ABC.FEV.A	K02013	ABC transporters
				TC.FEV.OM	K02014	Not known
				cobF	K02228	Porphyrin and chlorophyll metabolism
				TC.KEF	K03455	Not known
				TC.FEV.OM3,tbpA	K16087	Not known
				penP	K17836	Not known
Rhodococcus	2	8	Bulk	mtlK	K00045	Fructose and mannose metabolism
				otsB	K01087	Starch and sucrose metabolism
				aslA	K01130	Steroid hormone biosynthesis
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				coxL,cutL	K03520	Methane metabolism
				unknown	K07001	Not known
				unknown	K07058	Not known
				fadK	K12507	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				recG	K03655	Homologous recombination
Rhodopirellula	0	3	Bulk	unknown	K07001	Not known
				unknown	K07484	Not known
				iscA,ISCA1	K13628	Not known
Rhodopseudomonas	5	8	Bulk	tam	K00598	Not known
				dgkA,DGK	K00901	Glycerolipid metabolism
				coxL,cutL	K03520	Methane metabolism
				unknown	K07486	Not known
				unknown	K07577	Not known

				fcs	K12508	Not known
			Rhizosphere	nirB	K00362	Nitrogen metabolism
				nasA	K00372	Nitrogen metabolism
				glgC	K00975	Starch and sucrose metabolism
				TC.FEV.OM	K02014	Not known
				radA,sms	K04485	Not known
Rhodothermus	1	0	Rhizosphere	gltD	K00266	Nitrogen metabolism
Rhodovulum	2	4	Bulk	unknown	K00480	Naphthalene degradation
				GST,gst	K00799	Glutathione metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				cheW	K03408	Two-component system
Roseiflexus	1	2	Bulk	metE	K00549	Cysteine and methionine metabolism
				unknown	K06897	Not known
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
Roseomonas	0	3	Bulk	coxL,cutL	K03520	Methane metabolism
				kup	K03549	Not known
				unknown	K07486	Not known
Rubritepida	0	1	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
Rubrobacter	31	30	Bulk	gdh	K00034	Pentose phosphate pathway
				porA	K00169	Glycolysis/Gluconeogenesis
				ald	K00259	Carbon fixation pathways in prokaryotes
				unknown	K00375	Not known
				yidH	K00389	Not known
				pobA	K00481	Toluene degradation
				TYR	K00505	Tyrosine metabolism
				metE	K00549	Cysteine and methionine metabolism
				tam	K00598	Not known

				ribE	K00793	Riboflavin metabolism
				GST,gst	K00799	Glutathione metabolism
				dgkA,DGK	K00901	Glycerolipid metabolism
				otsB	K01087	Starch and sucrose metabolism
				oadA	K01571	Pyruvate metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				pstS	K02040	ABC transporters
				coxL,cutL	K03520	Methane metabolism
				cspA	K03704	Not known
				trmFO,gid	K04094	Not known
				unknown	K06978	Not known
				unknown	K07001	Not known
				unknown	K07006	Not known
				unknown	K07058	Not known
				unknown	K07577	Not known
				pimA	K08256	Not known
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
				treT	K13057	Not known
				iscA,ISCA1	K13628	Not known
				GDH2	K15371	Not known
				lldE	K18928	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				pntA	K00324	Nicotinate and nicotinamide metabolism
				metH,MTR	K00548	Cysteine and methionine metabolism
				OTC,argF,argI	K00611	Arginine and prolinemetabolism
				uppS	K00806	Terpenoid backbone biosynthesis
				puuE	K00823	Propanoate metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				PC,pyc	K01958	Citrate cycle (TCAcycle)

				accD	K01963	Pyruvate metabolism
				proW	K02001	ABC transporters
				allC	K02083	Purine metabolism
				atoE	K02106	Two-component system
				gatB,PET112	K02434	Aminoacyl-tRNA biosynthesis
				rssB,hnr	K02485	Not known
				pilD,pppA	K02654	Not known
				RP-L14,MRPL14,rplN	K02874	Ribosome
				SRP54,ffh	K03106	Protein export
				TC.KEF	K03455	Not known
				recG	K03655	Homologous recombination
				lipB	K03801	Lipoic acid metabolism
				opuBD	K05846	ABC transporters
				unknown	K07002	Not known
				ybeY,yqfG	K07042	Not known
				unknown	K07093	Not known
				mgtC	K07507	Not known
				unknown	K07576	Not known
				vicK	K07652	Two-component system
				purN	K11175	Purine metabolism
				dnaE2	K14162	Not known
				ybcJ	K14761	Not known
				penP	K17836	Not known
Saccharomonospora	0	3	Bulk	unknown	K06978	Not known
				unknown	K07058	Not known
				TC.BAT2	K09936	Not known
Saccharopolyspora	0	1	Bulk	coxL,cutL	K03520	Methane metabolism
Salinispora	1	1	Bulk	ald	K00259	Carbon fixation pathways in prokaryotes
			Rhizosphere	OTC,argF,argI	K00611	Arginine and prolinemetabolism

Sandaracinus	4	2	Bulk	sthA,udhA	K00322	Nicotinate and nicotinamide metabolism
				gmhB	K03273	Lipopolysaccharide biosynthesis
			Rhizosphere	manC,cpsB	K00971	Fructose and mannose metabolism
				TC.FEV.OM	K02014	Not known
				gspD	K02453	Bacterial secretion system
				SRP54,ffh	K03106	Protein export
Sciscionella	1	2	Bulk	gdh	K00034	Pentose phosphate pathway
				coxL,cutL	K03520	Methane metabolism
			Rhizosphere	neuB	K01654	Aminosugar and nucleotidesugar metabolism
Singulisphaera	7	8	Bulk	merA	K00520	Not known
				metE	K00549	Cysteine and methionine metabolism
				aslA	K01130	Steroid hormone biosynthesis
				kup	K03549	Not known
				pvdE	K06160	ABC transporters
				unknown	K06978	Not known
				unknown	K07058	Not known
				unknown	K07117	Not known
			Rhizosphere	galK	K00849	Galactose metabolism
				glgC	K00975	Starch and sucrose metabolism
				PC,pyc	K01958	Citrate cycle (TCAcycle)
				NRT,narK,nrtP,nasA	K02575	Not known
				unknown	K07726	Not known
				cphB	K13282	Not known
				penP	K17836	Not known
Skermanella	0	1	Bulk	kup	K03549	Not known
Solirubrobacter	19	27	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
				mtlK	K00045	Fructose and mannose metabolism
				dld,LDHD	K00102	Pyruvate metabolism

				ald	K00259	Carbon fixation pathways in prokaryotes
				sthA,udhA	K00322	Nicotinate and nicotinamide metabolism
				unknown	K00359	Not known
				unknown	K00375	Not known
				yidH	K00389	Not known
				metE	K00549	Cysteine and methionine metabolism
				ribE	K00793	Riboflavin metabolism
				GST,gst	K00799	Glutathione metabolism
				otsB	K01087	Starch and sucrose metabolism
				aslA	K01130	Steroid hormone biosynthesis
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				modA	K02020	ABC transporters
				coxL,cutL	K03520	Methane metabolism
				cspA	K03704	Not known
				unknown	K07001	Not known
				unknown	K07058	Not known
				grxD,GLRX5	K07390	Not known
				unknown	K07481	Not known
				pimA	K08256	Not known
				fcs	K12508	Not known
				treT	K13057	Not known
				iscA,ISCA1	K13628	Not known
				GDH2	K15371	Not known
				lldE	K18928	Not known
			Rhizosphere	pntA	K00324	Nicotinate and nicotinamide metabolism
				metH,MTR	K00548	Cysteine and methionine metabolism
				OTC,argF,arg	K00611	Arginine and prolinemetabolism
				uppS	K00806	Terpenoid backbone biosynthesis
				galK	K00849	Galactose metabolism

				dcd	K01494	Pyrimidine metabolism
				HMGCL,hmgL	K01640	Butanoate metabolism
				trpB	K01696	Glycine, serine and threonine metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				gatB,PET112	K02434	Aminoacyl-tRNA biosynthesis
				pilD,pppA	K02654	Not known
				SRP54,ffh	K03106	Protein export
				cheD	K03411	Bacterial chemotaxis
				clpB	K03695	Not known
				opuBD	K05846	ABC transporters
				rluB	K06178	Not known
				crcB	K06199	Not known
				purN	K11175	Purine metabolism
				dnaE2	K14162	Not known
Sorangium	7	4	Bulk	metE	K00549	Cysteine and methionine metabolism
				GST,gst	K00799	Glutathione metabolism
				pstS	K02040	ABC transporters
				amgK	K07102	Not known
			Rhizosphere	nasA	K00372	Nitrogen metabolism
				bioA	K00833	Biotin metabolism
				aguA	K01235	Not known
				ABC.FEV.A	K02013	ABC transporters
				TC.FEV.OM	K02014	Not known
				clpB	K03695	Not known
				dnaE2	K14162	Not known
Sphaerobacter	4	7	Bulk	otsB	K01087	Starch and sucrose metabolism
				OPLAH	K01469	Glutathione metabolism
				gmhB	K03273	Lipopolysaccharide biosynthesis
				unknown	K06978	Not known

				pimA	K08256	Not known
				glcE	K11472	Glyoxylate and dicarboxylate metabolism
				treT	K13057	Not known
			Rhizosphere	puuE	K00823	Propanoate metabolism
				allC	K02083	Purine metabolism
				TC.KEF	K03455	Not known
				UNG,UDG	K03648	Base excision repair
Sphingobium	2	1	Bulk	metE	K00549	Cysteine and methionine metabolism
			Rhizosphere	TC.FEV.OM	K02014	Not known
				bamD	K05807	Not known
Sphingomonas	26	16	Bulk	metE	K00549	Cysteine and methionine metabolism
				ribE	K00793	Riboflavin metabolism
				GST,gst	K00799	Glutathione metabolism
				otsB	K01087	Starch and sucrose metabolism
				OPLAH	K01469	Glutathione metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				pstS	K02040	ABC transporters
				kup	K03549	Not known
				unknown	K06978	Not known
				unknown	K07001	Not known
				amgK	K07102	Not known
				grxD,GLRX5	K07390	Not known
				unknown	K07481	Not known
				unknown	K07486	Not known
				unknown	K08988	Not known
				GDH2	K15371	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				nasA	K00372	Nitrogen metabolism
				metH,MTR	K00548	Cysteine and methionine metabolism

				uppS	K00806	Terpenoid backbone biosynthesis
				galK	K00849	Galactose metabolism
				TC.FEV.OM	K02014	Not known
				gatB,PET112	K02434	Aminoacyl-tRNA biosynthesis
				gspD	K02453	Bacterial secretion system
				paaZ	K02618	Not known
				virB10,lvhB10	K03195	Bacterial secretion system
				cheW	K03408	Two-component system
				TC.KEF	K03455	Not known
				UNG,UDG	K03648	Base excision repair
				recG	K03655	Homologous recombination
				lipB	K03801	Lipoic acid metabolism
				radA,sms	K04485	Not known
				bamD	K05807	Not known
				scpB	K06024	Not known
				unknown	K06929	Not known
				unknown	K07044	Not known
				unknown	K07576	Not known
				purN	K11175	Purine metabolism
				npdA	K12410	Aminosugar and nucleotidesugar metabolism
				dnaE2	K14162	Not known
				btuB	K16092	Not known
				penP	K17836	Not known
Starkeya	0	1	Bulk	unknown	K06897	Not known
Streptacidiphilus	2	2	Bulk	tam	K00598	Not known
				unknown	K07058	Not known
			Rhizosphere	eda	K01625	Pentose phosphate pathway
				aspA	K01744	Nitrogen metabolism

Streptomyces	24	19	Bulk	mmsB,HIBADH	K00020	Valine, leucine and isoleucine degradation
				ald	K00259	Carbon fixation pathways in prokaryotes
				sthA,udhA	K00322	Nicotinate and nicotinamide metabolism
				unknown	K00375	Not known
				unknown	K00480	Naphthalene degradation
				TYR	K00505	Tyrosine metabolism
				metE	K00549	Cysteine and methionine metabolism
				otsB	K01087	Starch and sucrose metabolism
				OPLAH	K01469	Glutathione metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				modA	K02020	ABC transporters
				pstS	K02040	ABC transporters
				coxL,cutL	K03520	Methane metabolism
				unknown	K06152	Pentose phosphate pathway
				unknown	K07001	Not known
				unknown	K07058	Not known
				paiB	K07734	Not known
				cebG	K10242	ABC transporters
				fcs	K12508	Not known
			Rhizosphere	gltD	K00266	Nitrogen metabolism
				nirB	K00362	Nitrogen metabolism
				metH,MTR	K00548	Cysteine and methionine metabolism
				gph	K01091	Glyoxylate and dicarboxylate metabolism
				aguA	K01235	Not known
				dcd	K01494	Pyrimidine metabolism
				eda	K01625	Pentose phosphate pathway
				HMGCL,hmgL	K01640	Butanoate metabolism
				trpB	K01696	Glycine, serine and threonine metabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis

				proW	K02001	ABC transporters
				pilD,pppA	K02654	Not known
				RP-L14,MRPL14,rplN	K02874	Ribosome
				SRP54,ffh	K03106	Protein export
				TC.KEF	K03455	Not known
				sbcD	K03547	Not known
				UNG,UDG	K03648	Base excision repair
				lipB	K03801	Lipoic acid metabolism
				opuBD	K05846	ABC transporters
				unknown	K07044	Not known
				unknown	K07220	Not known
				dtd,DTD1	K07560	Not known
				npdA	K12410	Aminosugar and nucleotidesugar metabolism
				pta	K13788	Pyruvate metabolism
Streptosporangium	0	1	Bulk	unknown	K07001	Not known
Sulfobacillus	1	0	Rhizosphere	pntA	K00324	Nicotinate and nicotinamide metabolism
Terrabacter	2	3	Bulk	unknown	K00480	Naphthalene degradation
				cebG	K10242	ABC transporters
				GDH2	K15371	Not known
			Rhizosphere	opuBD	K05846	ABC transporters
				dnaE2	K14162	Not known
Terriglobus	4	2	Bulk	unknown	K00375	Not known
				unknown	K07058	Not known
			Rhizosphere	gcd	K00117	Pentose phosphate pathway
				TC.FEV.OM	K02014	Not known
				clpB	K03695	Not known
				dnaE2	K14162	Not known
Tetrasphaera	1	3	Bulk	betC	K01133	Not known

				modA	K02020	ABC transporters
				cebG	K10242	ABC transporters
			Rhizosphere	proW	K02001	ABC transporters
Thermaerobacter	3	2	Bulk	coxL,cutL	K03520	Methane metabolism
				unknown	K06978	Not known
			Rhizosphere	OTC,argF,argI	K00611	Arginine and prolinemetabolism
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				lipB	K03801	Lipoic acid metabolism
Thermoanaerobacter	0	1	Bulk	pstS	K02040	ABC transporters
Thermoanaerobaculum	5	1	Bulk	coxL,cutL	K03520	Methane metabolism
			Rhizosphere	uppS	K00806	Terpenoid backbone biosynthesis
				YARS,tyrS	K01866	Aminoacyl-tRNA biosynthesis
				TC.FEV.OM	K02014	Not known
				recG	K03655	Homologous recombination
				TC.FEV.OM3,tbpA	K16087	Not known
Thermobaculum	2	5	Bulk	gdh	K00034	Pentose phosphate pathway
				unknown	K07058	Not known
				pimA	K08256	Not known
				cebG	K10242	ABC transporters
				treT	K13057	Not known
			Rhizosphere	nasA	K00372	Nitrogen metabolism
				unknown	K07093	Not known
Thermobispora	1	0	Rhizosphere	puuE	K00823	Propanoate metabolism
Thermocrispum	0	1	Bulk	coxL,cutL	K03520	Methane metabolism
Thermomicrobium	2	0	Rhizosphere	uppS	K00806	Terpenoid backbone biosynthesis
				glgC	K00975	Starch and sucrose metabolism
Thermomonospora	0	2	Bulk	OPLAH	K01469	Glutathione metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
Thermus	5	3	Bulk	ribE	K00793	Riboflavin metabolism

				lldE	K18928	Not known
			Rhizosphere	ndk,NME	K00940	Purine metabolism
				trpB	K01696	Glycine, serine and threonine metabolism
				rluB	K06178	Not known
Thiobacillus	2	0	Rhizosphere	TC.FEV.OM	K02014	Not known
				gspD	K02453	Bacterial secretion system
Variovorax	3	2	Bulk	merA	K00520	Not known
				yddA	K02471	ABC transporters
			Rhizosphere	nirB	K00362	Nitrogen metabolism
				TC.FEV.OM	K02014	Not known
				cheW	K03408	Two-component system
Verrucomicrobium	1	1	Bulk	unknown	K07001	Not known
			Rhizosphere	uppS	K00806	Terpenoid backbone biosynthesis
Xanthomonas	2	1	Bulk	laaA	K18457	Not known
			Rhizosphere	metH,MTR	K00548	Cysteine and methionine metabolism
				eda	K01625	Pentose phosphate pathway
Zavarzinella	2	3	Bulk	metE	K00549	Cysteine and methionine metabolism
				ilvB,ilvG,ilvI	K01652	Butanoate metabolism
				paiB	K07734	Not known
			Rhizosphere	gspD	K02453	Bacterial secretion system
				unknown	K07576	Not known

Table S6. Statistical information of the CONCOCT genome bins as revelled by CheckM analysis.

Bin Identity	Marker lineage	No. of genomes	No. of markers	No. of marker sets	Completeness	Contamination	Strain heterogeneity
Bin_1	k__Bacteria (UID203)	5449	104	58	88.65	175.91	0.00
Bin_2	k__Bacteria (UID203)	5449	104	58	86.76	51.93	67.53
Bin_3	k__Bacteria (UID203)	5449	104	58	78.57	38.90	47.06
Bin_4	k__Bacteria (UID203)	5449	104	58	89.66	81.84	11.82
Bin_5	k__Bacteria (UID203)	5449	104	58	32.34	6.90	0.00
Bin_6	k__Bacteria (UID203)	5449	104	58	63.56	49.11	1.14
Bin_7	o__Actinomycetales (UID1696)	455	311	187	48.95	16.09	28.26
Bin_8	k__Bacteria (UID203)	5449	104	58	82.62	35.87	75.00
Bin_9	k__Bacteria (UID3187)	2258	188	117	55.42	11.50	20.00
Bin_10	o__Rhizobiales (UID3642)	107	485	316	70.19	11.00	6.67
Bin_11	p__Actinobacteria (UID1454)	732	200	117	48.30	13.38	7.50
Bin_12	k__Bacteria (UID3187)	2258	188	117	88.29	6.43	0.00
Bin_13	p__Actinobacteria (UID1454)	732	199	116	37.63	10.63	5.00
Bin_14	k__Bacteria (UID203)	5449	104	58	40.92	3.45	50.00
Bin_15	g__Bradyrhizobium (UID3699)	37	824	336	90.40	0.74	16.67
Bin_16	k__Bacteria (UID3187)	2258	188	117	17.60	0.85	0.00
Bin_17	o__Actinomycetales (UID1802)	274	388	214	88.96	26.38	1.01
Bin_18	k__Bacteria (UID203)	5449	104	58	2.66	0.00	0.00
Bin_19	k__Bacteria (UID203)	5449	104	58	1.19	0.00	0.00
Bin_20	o__Actinomycetales (UID1697)	387	330	193	91.11	3.10	0.00
Bin_21	k__Bacteria (UID1452)	924	161	108	73.49	0.00	0.00
Bin_22	k__Bacteria (UID1453)	901	171	117	34.82	1.71	50.00
Bin_23	k__Bacteria (UID203)	5449	103	57	17.54	0.00	0.00
Bin_24	k__Bacteria (UID203)	5449	104	58	11.19	0.00	0.00
Bin_25	k__Bacteria (UID203)	5449	104	58	29.08	0.00	0.00
Bin_26	k__Bacteria (UID1453)	901	171	117	9.83	3.85	0.00
Bin_27	o__Rhizobiales (UID3642)	107	485	316	14.15	1.36	8.70
Bin_28	p__Actinobacteria (UID1454)	732	199	116	39.16	1.64	25.00
Bin_29	k__Bacteria (UID203)	5449	104	58	36.29	25.85	13.04
Bin_30	k__Bacteria (UID203)	5449	104	58	13.81	2.59	0.00
Bin_31	k__Bacteria (UID203)	5449	103	57	8.77	0.00	0.00
Bin_32	k__Bacteria (UID203)	5449	104	58	15.52	0.00	0.00
Bin_33	root (UID1)	5656	56	24	0.00	0.00	0.00
Bin_34	k__Bacteria (UID203)	5449	103	58	2.41	0.00	0.00
Bin_35	k__Bacteria (UID203)	5449	103	58	22.54	35.55	14.99
Bin_36	k__Bacteria (UID203)	5449	104	58	5.96	0.00	0.00
Bin_37	k__Bacteria (UID203)	5449	104	58	6.03	1.72	0.00
Bin_38	root (UID1)	5656	56	24	0.00	0.00	0.00
Bin_39	root (UID1)	5656	56	24	0.00	0.00	0.00
Bin_40	root (UID1)	5656	56	24	0.00	0.00	0.00
Bin_41	root (UID1)	5656	56	24	0.00	0.00	0.00
Bin_42	root (UID1)	5656	56	24	0.00	0.00	0.00
Bin_43	root (UID1)	5656	56	24	0.00	0.00	0.00
Bin_44	root (UID1)	5656	56	24	0.00	0.00	0.00
Bin_45	root (UID1)	5656	56	24	0.00	0.00	0.00
Bin_46	root (UID1)	5656	56	24	0.00	0.00	0.00

Table S7. Statistical information of the Anvio's refined genome bins as revelled by CheckM analysis.

Bin ID	Marker lineage	No. of genomes	No. of markers	No. of marker sets	0	1	2	3	4	5+	Completeness	Contamination	Strain heterogeneity
Bin15.1	g__Bradyrhizobium (UID3699)	37	824	336	94	724	6	0	0	0	89.56	0.74	16.67
Bin20.1	o__Actinomycetales (UID1697)	387	330	193	54	265	11	0	0	0	85.11	3.02	0
Bin17.1	o__Actinomycetales (UID1802)	274	388	214	80	302	6	0	0	0	83.64	1.64	0
Bin12.2	k__Bacteria (UID3187)	2258	188	117	33	146	9	0	0	0	80.17	4.55	0
Bin21	k__Bacteria (UID1452)	924	161	108	46	115	0	0	0	0	73.49	0	0
Bin7	o__Actinomycetales (UID1696)	455	311	187	170	105	31	5	0	0	48.95	16.09	28.26
Bin11	p__Actinobacteria (UID1454)	732	200	117	102	73	19	5	1	0	48.3	13.38	7.5
Bin9.1	k__Bacteria (UID3187)	2258	188	117	103	73	11	1	0	0	46.52	10.31	7.14
Bin1.1.1	p__Actinobacteria (UID1454)	732	200	117	111	73	15	1	0	0	46.37	8.94	0
Bin1.3	k__Bacteria (UID203)	5449	104	58	67	28	7	1	1	0	45.67	19.83	0
Bin2.2	o__Actinomycetales (UID1663)	488	309	185	153	136	18	2	0	0	44.37	4.46	66.67
Bin2.3	k__Bacteria (UID203)	5449	104	58	67	32	4	1	0	0	43.59	6.03	42.86
Bin8.2	o__Actinomycetales (UID1696)	455	311	187	170	134	7	0	0	0	43.19	1.37	85.71
Bin6.1.2	p__Actinobacteria (UID1454)	732	199	116	124	49	21	5	0	0	41.69	14.77	0
Bin14	k__Bacteria (UID203)	5449	104	58	73	29	2	0	0	0	40.92	3.45	50
Bin2.1	o__Actinomycetales (UID1663)	488	310	185	185	118	7	0	0	0	40.49	1.89	14.29
Bin28	p__Actinobacteria (UID1454)	732	199	116	119	76	4	0	0	0	39.16	1.64	25
Bin10.1.2	o__Rhizobiales (UID3642)	107	485	316	298	179	8	0	0	0	37.79	1.9	37.5
Bin13	p__Actinobacteria (UID1454)	732	199	116	118	67	11	3	0	0	37.63	10.63	5
Bin4.3	k__Bacteria (UID203)	5449	104	58	51	33	15	3	2	0	37.58	12.88	13.89
Bin29	k__Bacteria (UID203)	5449	104	58	45	22	22	9	1	5	36.29	25.85	13.04
Bin22	k__Bacteria (UID1453)	901	171	117	117	52	2	0	0	0	34.82	1.71	50
Bin1.4	k__Bacteria (UID3187)	2258	188	117	130	51	7	0	0	0	34.29	3.8	0
Bin3.1	o__Rhizobiales (UID3642)	107	485	316	320	153	12	0	0	0	34.12	2.14	16.67
Bin4.1	o__Actinomycetales (UID2014)	33	350	203	216	116	14	4	0	0	32.6	1.88	7.69
Bin6.2	k__Bacteria (UID1452)	924	161	108	102	48	11	0	0	0	32.42	4.64	0
Bin5	k__Bacteria (UID203)	5449	104	58	81	19	4	0	0	0	32.34	6.9	0
Bin3.2.1.1	o__Rhizobiales (UID3642)	107	485	316	332	148	5	0	0	0	32.01	1	20
Bin4.2	k__Bacteria (UID203)	5449	102	58	78	18	6	0	0	0	31.69	9.48	16.67
Bin1.2.2	k__Bacteria (UID203)	5449	104	58	83	16	4	1	0	0	30.8	10.34	0
Bin25	k__Bacteria (UID203)	5449	104	58	80	24	0	0	0	0	29.08	0	0
Bin3.2.1.2	o__Rhizobiales (UID3642)	107	485	316	342	139	4	0	0	0	26.93	0.58	25
Bin1.2.3	k__Bacteria (UID203)	5449	103	57	85	17	1	0	0	0	26.48	1.75	0
Bin8.3	k__Bacteria (UID203)	5449	104	58	82	22	0	0	0	0	25.08	0	0
Bin1.1.2	k__Bacteria (UID203)	5449	104	58	85	18	1	0	0	0	23.04	1.72	0
Bin35	k__Bacteria (UID203)	5449	103	58	52	6	12	13	4	16	22.54	35.55	14.99
Bin4.4	k__Bacteria (UID203)	5449	104	58	82	22	0	0	0	0	21.94	0	0
Bin6.1.1	k__Bacteria (UID203)	5449	104	58	82	22	0	0	0	0	20.75	0	0
Bin10.2	c__Alphaproteobacteria (UID3305)	564	349	230	273	72	4	0	0	0	20.73	1.45	0
Bin3.3	k__Bacteria (UID203)	5449	104	58	87	14	3	0	0	0	19.75	0.47	66.67
Bin17.2	k__Bacteria (UID203)	5449	104	58	88	16	0	0	0	0	18.1	0	0
Bin16	k__Bacteria (UID3187)	2258	188	117	151	36	1	0	0	0	17.6	0.85	0

Bin23	k__Bacteria (UID203)	5449	103	57	90	13	0	0	0	0	17.54	0	0
Bin32	k__Bacteria (UID203)	5449	104	58	93	11	0	0	0	0	15.52	0	0
Bin8.4	k__Bacteria (UID203)	5449	104	58	90	11	3	0	0	0	15.28	2.04	100
Bin27	o__Rhizobiales (UID3642) 8.7		107	485	316	391	79	11	4	0	0	14.15	1.36
Bin30	k__Bacteria (UID203)	5449	104	58	84	18	2	0	0	0	13.81	2.59	0
Bin8.1	k__Bacteria (UID203)	5449	104	58	85	19	0	0	0	0	13.48	0	0
Bin9.2	k__Bacteria (UID203)	5449	104	58	90	14	0	0	0	0	13.01	0	0
Bin10.1.1	k__Bacteria (UID203)	5449	104	58	93	11	0	0	0	0	11.83	0	0
Bin24	k__Bacteria (UID203)	5449	104	58	93	11	0	0	0	0	11.19	0	0
Bin26	k__Bacteria (UID1453)	901	171	117	146	21	2	2	0	0	9.83	3.85	0
Bin1.1.3	k__Bacteria (UID203)	5449	104	58	98	6	0	0	0	0	9.48	0	0
Bin31	k__Bacteria (UID203)	5449	103	57	95	8	0	0	0	0	8.77	0	0
Bin12.1	root (UID1)	5656	56	24	54	2	0	0	0	0	8.33	0	0
Bin1.2.1	k__Bacteria (UID203)	5449	103	57	98	5	0	0	0	0	7.02	0	0
Bin37	k__Bacteria (UID203)	5449	104	58	100	3	1	0	0	0	6.03	1.72	0
Bin36	k__Bacteria (UID203)	5449	104	58	96	8	0	0	0	0	5.96	0	0
Bin4.5	o__Actinomycetales (UID1802) 11.11		274	388	214	347	32	9	0	0	0	4.98	0.75
Bin10.1.3	root (UID1)	5656	56	24	55	1	0	0	0	0	4.17	0	0
Bin18	k__Bacteria (UID203)	5449	104	58	97	7	0	0	0	0	2.66	0	0
Bin6.3	k__Bacteria (UID203)	5449	104	58	97	7	0	0	0	0	2.51	0	0
Bin34	k__Bacteria (UID203)	5449	103	58	100	3	0	0	0	0	2.41	0	0
Bin19	k__Bacteria (UID203)	5449	104	58	100	4	0	0	0	0	1.19	0	0
Bin20.2	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
Bin3.2.2	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
Bin33	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
Bin38	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
Bin39	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
Bin40	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
Bin41	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
Bin42	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
Bin43	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
Bin44	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
Bin45	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0
Bin46	root (UID1)	5656	56	24	56	0	0	0	0	0	0	0	0

Table S8. Functional potential of the *Bradyrhizobium* genome based on RAST and KAAS annotations.

##****The Bradyrhizobium composite genome functional potential (ie., functions that influence plant fitness)

Functional category	Number of genes	Sub-functional category	Examples of genes identified
1. Carbohydrate metabolism			
Citrate cycle	24		K00024 (mdh), K01682 (acnB), K01902 (sucD), K00031 (IDH1)
Fructose and mannose metabolism	16		K01809 (manA), K01805 (xylA), K01624 (FBA), K01628 (fucA)
Galactose metabolism	9		K01684 (dgoD), K01784 (galE), K01785 (galM), K00845 (glK)
Starch and sucrose metabolism	18		K00963 (UGP2), K00975 (glgC), K01176 (AMY), K00694 (bcsA)
Propanoate metabolism	29		K01908 (prpE), K01895 (ACSS), K03417 (prpB), K01035 (atoA)
2. Nitrogen metabolism	19		
		Dissimilatory N reduction	K02568 (napB), K00363 (nirD)
		Assimilatory N reduction	K00366 (nirA)
		Denitrification	K02567 (napA), K02568 (napB), K00368 (nirK), K04561 (norB), K02305 (norC)
		Nitrogen fixation	K02586 (nifD), K02591 (nifK), K02588 (nifH)
		Anamox system	K00368 (nirK)
		Glutamate metabolism	K00265 (gltB), K00266 (gltD)
3. Sulphur metabolism	30		
		Assimilatory sulfate reduction	K00955 (cysNC), K00956 (cysN), K00390 (cysH), K00860 (cysC), K00390 (cysH)
		Sox system	K17224 (soxB), K17226 (soxY), K17227 (soxZ), K17222 (soxA), K08738 (cyc)
4. Essential amino acids			
Cysteine and methionine metabolism	25		K14454 (GOT1), K00812 (aspB), K01758 (CTH), K17217 (mccB)
Arginine and proline metabolism	22		K00819 (rocD), K00147 (proA)
Glutathione metabolism	13		K21456 (GSS), K01920 (gsh)
5. Vitamin metabolism			
Thiamine metabolism	9		K00946 (thiL), K00788 (thiE), K21220 (thiN), K03149 (thiG)
Riboflavin metabolism	9		K01497 (ribA), K00793 (ribE), K14652 (ribBA)
Pyridoxine (Vitamin B6) metabolism	5		K03474 (pdxJ), K00097 (pdxA)
Biotin metabolism	12		K01012 (bioB), K00833 (bioA)
Lipoic acid metabolism	2		K03644 (lipA), K03801 (lipB)
Folate (Vitamin B9) metabolism	19		K00287 (folA), K11754 (folC)
6. Antibiotics biosynthesis			
Vancomycin group antibiotics	1		K01710
Penicillin and cephalosporin	1		K17836 (penP)
Carbapenem	2		K00931 (proB), K00147 (proA)
Monobactam	7		K00215 (dapB)
Streptomycin	6		K01790 (rfbC)
7. Dedradation of elements with potential hazards on plant growth (ie., polyphenols)			
Benzoate degradation	10		K00446 (dmpB), K07104 (catE), K01782 (fadJ), K01825 (fadB)
Aminobenzoate degradation	10		K14333 (DHBD), K01034 (atoD), K01035 (atoA), K19709 (ydiF)
Chlorocyclohexane and chlorobenzene degradation	4		K00446 (dmpB), K07104 (catE)
Nitrotoluene degradation	6		K06281 (hyaB), K06282 (hyaA), K03518 (coxS), K07104 (catE)

Styrene degradation	7	K00446 (dmpB), K07104 (catE), K00451 (HGD)
Atrazine degradation	4	K01457 (atzF), K14541 (DUR1)
8. ABC transporters	104	
(A) Mineral and organic ion transporters		
Sulphate		K02048 (cysP), K02046 (cysU), K02047 (cysW), K02045 (cysA)
Nitrate/Nitrite/Cyanate		K15576 (nrtA), K15577 (nrtB)
Taurine		K15552 (tauC), K10831 (tauB)
Alkanesulfonate		K15553 (ssuA), K15554 (ssuC), K15555 (ssuB)
Molybdate		K02018 (modB), K02017 (modC)
Iron (III)		K02010 (afuC)
Spermidine/Putrescine		K11070 (potC), K11071 (potB), K11072 (potA)
Osmoprotectant		K05846 (opuBD), K05847 (opuA)
(B) Oligosaccharide, polyol and lipid transporters		
Maltose/Maltodextrin		K10111 (malK), K10112 (msmX)
Galactose oligomer/Maltooligosaccharide		K15771 (ganP), K15772 (ganQ), K10111 (malK), K10112 (msmX)
Raffinose/Starchyose/Melibiose		K10117 (msmE), K10118 (msmF), K10119 (msmG), K10112 (msmX)
Sorbitol/Mannitol		K10111 (malK), K10112 (msmX)
?-Glucoside		K10235 (aglK), K10112 (msmX)
Trehalose/Maltose		K10236 (thuE), K10111 (malK)
Cellulose		K10112 (msmX)
Chitobiose		K10112 (msmX), K17245 (chiF)
Arabinooligosaccharide		K10112 (msmX)
Phospholipid		K02067 (mlaD), K02066 (mlaE), K02065 (mlaF)
(C) Monosaccharide transporters		
Glucose/Mannose		K10112 (msmX)
D-Xylose		K10543 (xylF), K10544 (xylH)
Ribose/Autoinducer 2/D-Xylose		K10439 (rbsB), K10440 (rbsC), K10441 (rbsA)
sn-Glycerol 3-phosphate		K05813 (ugpB), K05814 (ugpA), K05815 (ugpE)
(D) Phosphate and amino acid transporters		
Phosphate		K02040 (pstS)
Phosphonate		K02044 (phnD), K02042 (phnE), K02041 (phnC)
Glutamine		K10039 (ABC.GLN1.S)
Arginine		K09997 (artI)
Glutamate/Aspertate		K10001 (gltI), K10002 (gltK), K10003 (gltJ), K10004 (gltL)
General L-Amino acid		K09970 (aapQ), K09971 (aapM), K09972 (aapP)
Cysteine		K02424 (fliY), K10009 (ABC.CYST.P), K10010 (ABC.CYST.A)
Branched-chain amino acid		K01999 (livK), K01997 (livH), K01998 (livM), K01995 (livG), K01996 (livF)
Neutral amino acid/Histidine		K11955 (natC), K11956 (natD), K11958 (natE)
Urea		K11959 (urtA), K11960 (urtB), K11961 (urtC), K11962 (urtD), K11963 (urtE)
D-Methionine		K02073 (metQ)
(E) Peptide and nickel transporters		
Oligopeptide		K15581 (oppB), K15582 (oppC), K15583 (oppD), K10823 (oppF)
Dipeptide/Heme/?-Aminolenolevulinic acid		K12368 (dppA), K12369 (dppB), K12372 (dppF)
Dipeptide		K16201 (dppC)

Glutathione K13889 (gsiB), K13890 (gsiC)
Microcin C K13894 (yejB), K13895 (yejE), K13896 (yejK), K13893 (yejA)
(F) Metallic cation, iron-siderophore and vitamin B12 transporters
Iron complex K02016 (ABC.FEV.S)
Biotin K03523 (bioY), K16786 (ecfA1)
9. Bacterial secretion system 14
(A) Type I system
Outer membrane protein (OMP) K12340 (tolC)
Membrane fusion protein K11003 (hlyD)
ABC transporter K11004 (hlyB)
(B) Type IV system
Outer membrane protein (OMP) K03204 (virB9)
ATPase K03199 (virB4), K03196 (virB11), K03205 (virD4)
(C) Sec-SRP
Inner membrane protein (IMP) K03072 (secD), K03074 (secF), K12257 (secDF), K03210 (yajC), K03217 (yidC)
SRP recepter K03110 (ftsY)
Targeting protein K03071 (secB), K03106 (SRP54)
Twin arginine targeting (Tat) K03118 (tatC)
10. Two-component system 81
(A) OmpR family
Phosphate limitation K07636 (phoR), K07657 (phoB), K07658 (phoB1), K02040 (pstS)
Phosphate assimilation K01077 (phoA), K01113 (phoD)
Magnesium starvation K07637 (phoQ), K07660 (phoP)
Osmotic uptake (K+) and Outer membraneK07638 (envZ), K07659 (ompR)
Cell envelope protein folding and degradation K04771 (degP)
Secretion stress/Misfolded proteins K07641 (creC), K04771 (degP)
Multidrug efflux K07799 (mdtA), K07788 (mdt)
Copper ions/Cu-Si efflux K07644 (cusS), K07665 (cusR), K07798 (cusB), K07787 (cusA)
Potassium limitation/Potassium transport K07646 (kdpD), K01546 (kdpA), K01547 (kdpB), K01548 (kdpC)
Qurum sensing and flagella regulon K07645 (qseC), K02556 (motA)
Trimethylamine N-oxide K07647 (torS)
Temperature K07652 (vicK)
Vancomycin resistance K08641 (vanX)
(B) Sporulation family
Sporulation and biofilm formation K02491 (kinA), K07698 (kinC), K02490 (spoOF)
(C) CitB family
Citrate fermentation K01644 (citE), K09477 (citT)
C4-Dicarboxyrate transport K11103 (dctA)
(D) NarL family
Nitrite/Nitrate (N-metabolism) K07684 (narL), K07685 (narP), K00244 (frdA)
Carbon storage regulator K07689 (uvrY), K07782 (sdiA)
beta-lactam resistance K01467 (ampC)
Salt stress/Degradative enzymes K07777 (degS), K07692 (degU)
Cell wall-active antibiotics/Cationic antimicrobial peptide K11617 (liaS)
(E) NtrC family
Nitrogen availability low K07708 (glnL), K07712 (glnG), K01915 (glnA), K13599 (ntrX), K02584 (nifA)
Acetoacetate (Short fatty acid metabolism) K07710 (atoS), K07714 (atoC), K01034 (atoD), K00626 (atoB)
C4-dicarboxyrate transport K11103 (dctA)

- Hormone-like molecules K07645 (qseC)
- Attaching and effacing (AE) lessions K03092 (SIG54)
- [NiFe] hydrogenase K03620 (hyaC)

(F) Chemotaxis family

- Attractant/Repellent K03776 (aer), K05874 (tsr), K05875 (tar), K05877 (tap), K03406 (mcp)
- Bacterial chemotaxis K03408 (cheW), K03407 (cheA), K00575 (cheR), K13924 (cheBR)
- Flageller motor switch adaptation K03413 (cheY)
- Twitching motility K02660 (pilJ)
- Phytochrome growth and development K11355 (rcp1)

(G) Cell cycle family

- Pole morphogenesis K07716 (pleC), K02488 (pleD)
- Feeding-specific signal/Glycerol uptake and utilization K18444 (rrp1)

(H) LuxR family

- Nitrogen fixation K02584 (nifA)

11. Plant hormone signal transduction 1

- Zeatin biosynthesis (A cytokinin) K14491 (ARR-B)

12. Bacterial chemotaxis 14

(A) Bacterial chemotaxis genes

- Bacterial chemotaxis K03408 (cheW), K03407 (cheA), K00575 (cheR), K13924 (cheBR)
- Flageller motor switch adaptation K03413 (cheY)

(B) Flagella assembly

- Hook-filament junction K02396 (flgK)
- Hook K02390 (flgE
- Distal rod K02392 (flgG)
- L ring (Outer membrane) K02393 (flgH)
- P ring (Peptidoglycan layer) K02394 (flgI)
- Proximal rod (Basal boby) K02388 (flgC), K02557 (motB)
- MS ring K02409 (fliF), K02556 (motA)
- C ring (Motor/Switch) K02410 (fliG), K02416 (fliM), K02417 (fliNY), K02400 (flhA), K02401 (flhB)
- Type III secretion system K02412 (fliI), K02419 (fliP), K02421 (fliR), K13820 (fliR-flhB)

Table S9. Functional potential of the *Geodermatophilus* genome based on RAST and KAAS annotations.

##****The Geodermatophilus (Actinomyceteles) composite genome functional potential (ie., functions that influence plant fitness)

Functional category	Number of genes	Sub-functional category	Examples of genes identified
1. Carbohydrate metabolism			
Citrate cycle	14		K01902 (sucD), K00382 (DLD), K00174 (korA), K00025 (MDH1)
Fructose and mannose metabolism	11		K01809 (manA), K01808 (rpiB), K02446 (glpX), K01840 (manB)
Galactose metabolism	11		K01785 (galM), K00845 (glK), K00965 (galT), K07406 (melA)
Starch and sucrose metabolism	22		K00963 (UGP2), K00975 (glgC), K01176 (AMY), K01187 (malZ)
Propanoate metabolism	21		K00048 (fucC), K01965 (PCCA), K11381 (bkdA), K01895 (ACSS)
2. Nitrogen metabolism	6		
		Glutamate metabolism	K00265 (gltB), K00266 (gltD)
3. Sulphur metabolism	16		
		Assimilatory sulfate reduction	K00955 (cysNC), K00956 (cysN), K00390 (cysH), K00860 (cysC), K00390 (cysH), K00392 (Sir)
		Dissimilatory sulphate reduction and oxidation	K00958 (sat)
4. Essential amino acids			
Cysteine and methionine metabolism	19		K14454 (GOT1), K00812 (aspB), K00640 (cysE), K00813 (aspC)
Arginine and proline metabolism	18		K01438 (argE), K00611 (OTC)
Glutathione metabolism	9		K00681 (ggt), K01919 (gshA)
5. Vitamin metabolism			
Thiamine metabolism	9		K00788 (thiE), K21220 (thiN), K00939 (adk), K06949 (rsgA)
Riboflavin metabolism	6		K00793 (ribE), K00794 (ribH), K00861 (RFK), K11753 (ribF)
Pyridoxine (Vitamin B6) metabolism	5		K00275 (pdxH), K01733 (thrC)
Biotin metabolism	5		K00833 (bioA), K16593 bioI)
Lipoic acid metabolism	2		K03644 (lipA), K03801 (lipB)
Folate (Vitamin B9) metabolism	10		K00796 (folP), K01633 (folB)
6. Antibiotics biosynthesis			
Penicillin and cephalosporin	1		K01434 (E3.5.1.11)
Carbapenem	1		K00931 (proB)
Monobactam	7		K00215 (dapB)
Streptomycin	5		K00010 (iolG)
7. Dedradation of elements with potential hazards on plant growth (ie., polyphenols)			
Benzoate degradation	9		K18364 (bphH), K18365 (bphI), K04073 (K04073 (mhpF)
Aminobenzoate degradation	4		K01512 (acyP), K01692 (paaF)
Chlorocyclohexane and chlorobenzene degradation	2		K01061 (E3.1.1.45), K01563 (dhaA)
Nitrotoluene degradation	5		K06281 (hyaB), K06282 (hyaA), K03518 (coxS), K03519 (coxM)
Styrene degradation	2		K01426 (E3.5.1.4), K16171 (faaH)
Atrazine degradation	3		K01428 (ureC), K01430 (ureA)
8. ABC transporters	64		
(A) Mineral and organic ion transporters			
		Sulphate	K02048 (cysP), K02045 (cysA), K02047 (cysN)
		Alkanesulfonate	K15554 (ssuC)
		Molybdate	K02018 (modB), K02017 (modC), K02020 (modA)
		Spermidine/Putrescine	K11070 (potC), K11071 (potB), K11072 (potA), K11069 (potD)
		Osmoprotectant	K05846 (opuBD), K05847 (opuA), K05845 (opuC)
		Bicarbonate	K11951 (cmpB), K11952 (cmpC)
(B) Oligosaccharide, polyol and lipid transporters			

Maltose/Maltodextrin K10111 (malK), K10112 (msmX)
Galactose oligomer/Maltooligosaccharide K15771 (ganP), K10111 (malK)
Raffinose/Starchyose/Melibiose K10117 (msmE), K10118 (msmF), K10119 (msmG), K10112 (msmX)
Sorbitol/Mannitol K10111 (malK), K10112 (msmX)
?-Glucoside K10235 (aglK), K10234 (aglG), K01235 (aglK)
Trehalose/Maltose K10238 (thuG)
Cellulose K10112 (msmX)
Chitobiose K10112 (msmX), K17245 (chiF), K17244 (chiE)
Arabinooligosaccharide K10112 (msmX)
Phospholipid K02067 (mlaD), K02066 (mlaE), K02065 (mlaF)
(C) Monosaccharide transporters
Glucose/Mannose K10112 (msmX)
D-Xylose K10543 (xylF), K10544 (xylH)
Ribose/Autoinducer 2/D-Xylose K10440 (rbsC), K10441 (rbsA)
sn-Glycerol 3-phosphate K05814 (ugpA), K05815 (ugpE)
Autoinducer 2 K10555 (lsrB), K10556 (lsrC)
myo-inositol K17208 (lbpA)
(D) Phosphate and amino acid transporters
Phosphate K02040 (pstS), K02037 (pstC), K02038 (pstA), K02036 (pstB)
Cysteine K02424 (fliY), K10009 (ABC.CYST.P)
Branched-chain amino acid K01999 (livK), K01997 (livH), K01998 (livM), K01995 (livG), K01996 (livF)
Urea K11959 (urtA)
(E) Peptide and nickel transporters
Oligopeptide K15583 (oppD)
(F) Metallic cation, iron-siderophore and vitamin B12 transporters
Iron complex K02016 (ABC.FEV.S), K02015 (ABC.FEV.P), K02013 (ABC.FEV.A)
Biotin K16786 (ecfA1)
Zinc K09817 (znuC)
9. Bacterial secretion system 8
(A) Type I system
(B) Type IV system
(C) Sec-SRP
Inner membrane protein (IMP) K03072 (secD), K03074 (secF), K12257 (secDF), K03210 (yajC), K03217 (yidC)
SRP recepter K03110 (ftsY)
Targeting protein K03106 (SRP54)
(D) Twin arginine targeting (Tat)
Inner membrane protein (IMP) K03118 (tatC)
10. Two-component system 81
(A) OmpR family
Phosphate limitation K07636 (phoR), K07768 (senX3), K07776 (regX3)
Phosphate assimilation K02040 (pstS), K07768 (senX3)
Cell envelope protein folding and degradation K04771 (degP)
Secretion stress/Misfolded proteins K04771 (degP)
Potassium limitation/Potassium transport K07646 (kdpD), K01548 (kdpC), K07667 (kdpE)
Oxygen limitation K07775 (resD), K02259 (coxl5)
Cell replication/Cell envelope stress, osmoregulation, cell division K07654 (mtrB), K07670 (mtrA), K02313 (dnaA)
Ni2+ ions/Changes in the PQ redox poise K11330 (nrsR)
(B) Sporulation family
(C) CitB family

	Citrate fermentation	K01644 (citE)
	C4-Dicarboxyrate transport	K11103 (dctA)
	Malate utilization	K11614 (yufL), K00027 (ME2)
(D) NarL family		
	Nitrite/Nitrate (N-metabolism)	K07684 (narL), K07685 (narP), K07673 (narX), K08349 (fdnH)
	Salt stress/Degradative enzymes	K07692 (degU)
	Cell wall-active antibiotics/Cationic antimicrobial peptide	K11617 (liaS)
	Hypoxia	K07682 (devS), K07695 (devR)
(E) NtrC family		
	Nitrogen availability low	K07708 (glnL),K01915 (glnA), K00990 (glnD), K04751 (glnB)
	Acetoacetate (Short fatty acid metabolism)	K00626 (E2.3.1.9)
(F) Chemotaxis family		
	Bacterial chemotaxis	K00575 (cheR), K13924 (cheBR)
	Phytochrome growth and development	K11355 (rcp1), K11354 (cph1)

Table S10. Functional potential of the *Kribbela* genome based on RAST and KAAS annotations.

"##****The Kribbela (Actinomyceteles) composite genome functional potential (ie., functions that influence plant fitness)"

Functional category	Number of genes	Sub-functional category	Examples of genes identified
1. Carbohydrate metabolism			
Citrate cycle	19		"K01647 (CS), K01682 (acnB), K01902 (sucD), K00658 (DLST)"
Fructose and mannose metabolism	17		"K01809 (manA), K03332 (frucA), K01840 (manB), K00971 (manC)"
Galactose metabolism	16		"K01785 (galM), K00845 (glK), K00965 (galT), K00963 (UGP2)"
Starch and sucrose metabolism	26		"K00975 (glgC), K01176 (AMY), K00700 (GBE1), K01214 (ISA)"
Propanoate metabolism	21		"K00382 (DLD), K11381 (bkdA), K00925 (ackA), K01895 (ACSS)"
2. Nitrogen metabolism	10		
		Dissimilatory N reduction	"K02568 (napB), K00363 (nirD)"
		Assimilatory N reduction	"K00366 (nirA), K00360 (nasB)"
		Glutamate metabolism	"K00265 (gltB), K00266 (gltD), K01915 (glnA)"
3. Sulphur metabolism	12		
		Assimilatory sulfate reduction	"K00955 (cysNC), K00956 (cysN), K00390 (cysH), K00860 (cysC), K00390 (cysH)"
4. Essential amino acids			
Cysteine and methionine metabolism	22		"K14454 (GOT1), K00812 (aspB), K01738 (cysK), K11358 (yhdR)"
Arginine and proline metabolism	15		"K01755 (argH), K01478 (arcA), K01940 (argG)"
Glutathione metabolism	9		"K21456 (GSS), K01920 (gshB)"
5. Vitamin metabolism			
Thiamine metabolism	11		"K00946 (thiL), K00788 (thiE), K21220 (thiN), K00939 (adk)"
Riboflavin metabolism	10		"K00794 (ribH), K00793 (ribE), K11752 (ribD)"
Pyridoxine (Vitamin B6) metabolism	5		"K00275 (pdxH), K00868 (pdxK)"
Biotin metabolism	8		"K01012 (bioB), K00833 (bioA)"
Lipoic acid metabolism	3		"K03644 (lipA), K03801 (lipB)"
Folate (Vitamin B9) metabolism	13		"K11754 (folC), K00796 (folP)"
6. Antibiotics biosynthesis			
Penicillin and cephalosporin	3		"K00273 (DAO), K01060 (cah), K01434 (E3.5.1.11)"
Carbapenem	2		"K00931 (proB), K00147 (proA)"
Monobactam	6		K00215 (dapB)
Streptomycin	6		K01790 (rfbC)
"7. Dedradation of elements with potential hazards on plant growth (ie., polyphenols)"			
Benzoate degradation	5		"K01782 (fadJ), K01825 (fadB), K00252 9GCDH), K01692 (paaF)"
Aminobenzoate degradation	6		"K10215 (ethA), K01692 (paaF)"
Chlorocyclohexane and chlorobenzene degradation	1		K01061 (E3.1.1.45)
Nitrotoluene degradation	4		"K03518 (coxS), K00196 (cooF), K00622 (nat)"
Styrene degradation	3		"K01426 (E3.5.1.4), K01555 (FAH), K16171 (faaH)"
Atrazine degradation	3		"K01428 (ureC0, K01430 (ureA)"
8. ABC transporters	105		

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(A) Mineral and organic ion transporters
                Taurine  K15552 (tauC)
                Molybdate        "K02018 (modB), K02017 (modC), K02020 (modA), K05776 (modF)"
                Iron (III)       K02010 (afuC)
                Spermidine/Putrescine    "K11070 (potC), K11072 (potA)"
                Osmoprotectant   "K05846 (opuBD), K05847 (opuA), K05845 (opuC)"
                Glycine betaine/proline  "K02001 (proW), K02000 (proV)"
"(B) Oligosaccharide, polyol and lipid transporters"
                Maltose/Maltodextrin     "K10111 (malK), K10112 (msmX)"
                Galactose oligomer/Maltooligosaccharide   "K15771 (ganP), K15772 (ganQ), K10112 (msmX), K15770 (cycB)"
                Raffinose/Starchyose/Melibiose    "K10117 (msmE), K10118 (msmF), K10119 (msmG), K10112 (msmX)"
                Sorbitol/Mannitol        "K10111 (malK), K10112 (msmX)"
                ?-Glucoside      "K10235 (aglK), K10112 (msmX), K10232 (aglE)"
                Trehalose/Maltose        "K10236 (thuE), K10237 (thuF), K10238 (thuG)"
                Cellulose        K10112 (msmX)
                Chitobiose       "K10112 (msmX), K17245 (chiF), K17244 (chiE), K17246 (chiG)"
                Arabinooligosaccharide   "K10112 (msmX), K17234 (araN), K17235 (araP)"
                Phospholipid     "K02067 (mlaD), K02066 (mlaE), K02065 (mlaF)"
                Aldoronane       "K17319 (lplB), K17320 (lplC)"
(C) Monosaccharide transporters
                Glucose/Mannose  K10112 (msmX)
                D-Xylose "K10543 (xylF), K10544 (xylH)"
                Ribose/Autoinducer 2/D-Xylose     "K10440 (rbsC), K10441 (rbsA)"
                sn-Glycerol 3-phosphate  "K05813 (ugpB), K05814 (ugpA), K05815 (ugpE)"
                D-Allose K10549 (alsB)
                myo-inositol 1-phosphate "K17238 (inoF), K17239 (inoG)"
                Autoinducer 2    "K10555 (lsrB), K10557 (lsrD)"
(D) Phosphate and amino acid transporters
                Phosphate        "K02040 (pstS), K02037 (pstC), K02038 (pstA), K02036 (pstB)"
                Glutamine        K10036 (glnH)
                Cysteine "K02424 (fliY), K10009 (ABC.CYST.P), K10010 (ABC.CYST.A)"
                Branched-chain amino acid "K01999 (livK), K01997 (livH), K01998 (livM), K01995 (livG), K01996 (livF)"
                Amino acid       "K16961 (yxeM), K16962 (yxeN)"
(E) Peptide and nickel transporters
                Oligopeptide     "K15581 (oppB), K15582 (oppC), K15583 (oppD), K10823 (oppF), K15580 (oppA)"
                Dipeptide/Heme/?-Aminolenolevulinic acid  "K12368 (dppA), K12369 (dppB), K12372 (dppF), K12370 (dppC)"
                Dipeptide        K16199 (dppF)
                Glutathione      "K13889 (gsiB), K13891 (gsiD)"
                Microcin C       K13893 (yejA)
"(F) Metallic cation, iron-siderophore and vitamin B12 transporters"
                Iron complex     "K02016 (ABC.FEV.S), K02015 (ABC.FEV.P), K02013 (ABC.FEV.A)"
                Biotin  K16786 (ecfA1)
                manganese        K11602 (mntB)
                zinc    "K09815 (znuA), K09816 (znuB), K09817 (znuC)"
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                manganese/zinc   K19971 (psaA)
                zinc/manganese/iron (III) K11710 (troB)
                cobalt  "K02007 (cbiM), K02008 (cbiQ), K02006 (cbiO)"
                nickel  "K02007 (cbiM), K02008 (cbiQ), K02006 (cbiO)"
9. Bacterial secretion system     9
(A) Type I system
(B) Type IV system
                ATPase  K03205 (virD4)
(C) Sec-SRP
                Inner membrane protein (IMP)      "K03072 (secD), K03074 (secF), K12257 (secDF), K03210 (yajC), K03217 (yidC)"
                SRP recepter     K03110 (ftsY)
                Targeting protein        K03106 (SRP54)
(D) Twin arginine targeting (Tat)
                Inner membrane protein (IMP)      K03118 (tatC)
10. Two-component system 54
(A) OmpR family
                Phosphate limitation     "K07636 (phoR), K07658 (phoB1), K07768 (senX3), K07777 (regX3)"
                Phosphate assimilation   " K01113 (phoD), K02040 (pstS), K07768 (senX3)"
                Magnesium starvation     K07660 (phoP)
                Cell envelope protein folding and degradation      K04771 (degP)
                Secretion stress/Misfolded proteins       K04771 (degP)
                Copper ions/Cu-Si efflux K07665 (cusR)
                Potassium limitation/Potassium transport  "K07646 (kdpD), K01546 (kdpA), K01547 (kdpB), K01548 (kdpC), K07667
(kdpE)"
                Temperature      K07652 (vicK)
                Vancomycin resistance    K08641 (vanX)
                Aerobic and anaerobic respiration K02259 (cox15)
                Bacitracin efflux        "K11631 (bceA), K11632 (DceB)"
                Manganese transport      K11602 (mntB)
                "DNA replication/Cell envelope stress, osmoprotection, cell division"       "K07654 (mtrB), K07670 (mtrA),
K02313 (dnaA)"
                Serine protease  "K07653 (mprB), K07669 (mprA), K08372 (pepD)"
(B) Sporulation family
                Sporulation and biofilm formation K07698 (kinC)
(C) CitB family
                Citrate fermentation     "K01644 (citE), K07702 (dpiA)"
                C4-Dicarboxyrate transport        K11103 (dctA)
                Anaerobic fumarate respiration system     K07701 (dcuS)
                Malate utilization       K00027 (ME2)
(D) NarL family
                Nitrite/Nitrate (N-metabolism)    K07673 (narX)
                Carbon storage regulator K07689 (uvrY)
                Salt stress/Degradative enzymes   "K07777 (degS), K07692 (degU)"
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Cell wall-active antibiotics/Cationic antimicrobial peptide "K11617 (liaS), K11618 (liaR), K11617 (liaS), K11618 (liaR)"

Hypoxia "K07682 (devS), K07695 (devR)"

Low temperature "K07778 (desK), K07693 (desR)"

(E) NtrC family

Nitrogen availability low "K01915 (glnA), K00990 (gln), K04751 (glnB)"

Acetoacetate (Short fatty acid metabolism) "K02106 (atoE), K00626 (E2.3.1.9)"

C4-dicarboxyrate transport K11103 (dctA)

11. Plant hormone signal transduction 1

Zeatin biosynthesis (A cytokinin) K14491 (ARR-B)

Table S11. Functional potential of the *Sphaerobacter* genome based on RAST and KAAS annotations.

##****The Sphaerobacter composite genome functional potential (ie., functions that influence plant fitness)

Functional category	Number of genes	Sub-functional category	Examples of genes identified
1. Carbohydrate metabolism			
Citrate cycle	15		K01647 (CS), K01681 (ACO), K00163 (aceE), K00658 (DLST)
Fructose and mannose metabolism	7		K01840 (manB), K02446 (glpX), K01623 (ALDO), K00971 (manC)
Galactose metabolism	6		K01784 (galE), K00845 (glK), K00965 (galT), K01189 (GLA)
Starch and sucrose metabolism	12		K00700 (GBE1), K00703 (glgA), K00688 (PYG), K16147 (glgE)
Propanoate metabolism	16		K00925 (ackA), K01895 (ACSS), K11381 (bdkA), K00382 (DLD)
2. Nitrogen metabolism	6		
		Dissimilatory N reduction	K00370 (narG), K00371 (narH), K00374 (narI), K00362 (nirB), K00363 (nirD)
		Denitrification	K00370 (narG), K00371 (narH), K00374 (narI)
		Glutamate metabolism	K01915 (glnA), K00261 (GLUD1_2)
		Nitrification	K00370 (narG), K00371 (narH)
3. Sulphur metabolism	3		
		Assimilatory sulfate reduction	""""
		Sox system	""""
4. Essential amino acids			
Cysteine and methionine metabolism	14		K14454 (GOT1), K01738 (cysK), K01760 (metC), K00813 (aspC)
Arginine and proline metabolism	9		K01480 (speB), K00318 (PRODH)
Glutathione metabolism	5		K00681 (ggt), K18592 (GGT1_5)
5. Vitamin metabolism			
Thiamine metabolism	8		K00788 (thiE), K21220 (thiN), K06949 (rsgA), K00939 (adk)
Riboflavin metabolism	2		K00082 (ribD2), K11753 (ribF)
Pyridoxine (Vitamin B6) metabolism	2		K00275 (pdxH), K01733 (thrC)
Biotin metabolism	4		K03524 (birA), K00208 (fabI)
Lipoic acid metabolism	1		K03800 (lpiA)
Folate (Vitamin B9) metabolism	6		K11754 (folC), K13939 (FOL1)
6. Antibiotics biosynthesis			
Penicillin and cephalosporin	1		K01434 (E3.5.1.11)
Monobactam	3		K00215 (dapB)
Streptomycin	7		K01790 (rfbC)
7. Dedradation of elements with potential hazards on plant growth (ie., polyphenols)			
Benzoate degradation	4		K00446 (dmpB), K07104 (catE), K01607 (pcaC)
Aminobenzoate degradation	2		K01512 (acyP), K01426 (E3.5.1.4)
Chlorocyclohexane and chlorobenzene degradation	3		K00446 (dmpB), K07104 (catE)
Nitrotoluene degradation	1		K01061 (E3.1.1.45)
Styrene degradation	2		K07104 (catE)
8. ABC transporters	34		
(A) Mineral and organic ion transporters			
		Molybdate	K02017 (modC), K02020 (modA)

  - Osmoprotectant K05846 (opuBD), K05847 (opuA), K05845 (opuC)
- (B) Oligosaccharide, polyol and lipid transporters
  - Maltose/Maltodextrin K10111 (malK), K10112 (msmX)
  - Galactose oligomer/Maltooligosaccharide K10111 (malK), K10112 (msmX)
  - Raffinose/Starchyose/Melibiose K10112 (msmX)
  - Sorbitol/Mannitol K10111 (malK), K10112 (msmX)
  - ?-Glucoside K10235 (aglK), K10234 (aglG), K10232 (aglE)
  - Chitobiose K10112 (msmX)
  - Phospholipid K10112 (msmX)
- (C) Monosaccharide transporters
  - Glucose/Mannose K10112 (msmX)
  - D-Xylose K10543 (xylF), K10544 (xylH)
  - Ribose/Autoinducer 2/D-Xylose K10439 (rbsB)
  - sn-Glycerol 3-phosphate K05813 (ugpB), K05815 (ugpE)
- (D) Phosphate and amino acid transporters
  - Branched-chain amino acid K01999 (livK), K01997 (livH), K01998 (livM), K01995 (livG), K01996 (livF)
  - Neutral amino acid/Histidine K11958 (natE)
- (E) Peptide and nickel transporters
  - Oligopeptide K15581 (oppB), K15582 (oppC), K15583 (oppD), K10823 (oppF), K15580 (oppA)
  - Glutathione K13889 (gsiB)
- (F) Metallic cation, iron-siderophore and vitamin B12 transporters
  - Iron complex K02016 (ABC.FEV.S)
  - Biotin K16786 (ecfA1)

9. Bacterial secretion system 6

- (A) Type I system
- (B) Type IV system
  - ATPase K03196 (virB11)
- (C) Sec-SRP
  - Inner membrane protein (IMP) K03072 (secD), K03074 (secF), K12257 (secDF)
  - Targeting protein K03106 (SRP54)
- Twin arginine targeting (Tat)
  - Inner membrane protein (IMP) K03118 (tatC)

10. Two-component system 25

- (A) OmpR family
  - Phosphate limitation K07636 (phoR), K07658 (phoB1)
  - Cell envelope protein folding and degradation K04771 (degP)
  - Secretion stress/Misfolded proteins K04771 (degP)
  - Multidrug efflux K07642 (baeS)
  - Potassium limitation/Potassium transport K07646 (kdpD), K07667 (kdpE)
  - Cationic antimicrobial peptide (AMP) K14205 (mprF)
  - DNA replication K02313 (dnaA)
  - Serine protease K07669 (mprA)
- (B) Sporulation family
- (C) CitB family

(D) NarL family

- Nitrite/Nitrate (N-metabolism) K07684 (narL), K00371 (narH), K00374 (narI), Koo373 (narJ)
- Carbon storage regulator K07678 (barA)
- Cell wall-active antibiotics/Cationic antimicrobial peptide K11617 (liaS)
- Hypoxia K07682 (devS), K07695 (devR)

(E) NtrC family

- Nitrogen availability low K01915 (glnA)
- Acetoacetate (Short fatty acid metabolism) K07710 (atoS), K00626 (E2.3.1.9)

(F) Chemotaxis family

- Bacterial chemotaxis K00575 (cheR), K13924 (cheBR), K03412 (cheB)

11. Bacterial chemotaxis 14

(A) Bacterial chemotaxis genes

- Bacterial chemotaxis K00575 (cheR), K13924 (cheBR), K03412 (cheB)