Supplementary Table S2: Sequences used in phylogenies and their Microbe-BLAST results. Highlighted sequences are those with greater identity scores in the PKS subtypes that they belong (excluding reference-sequences).

	Genbank Accession Number	**Sequence**	**Microbe-BLAST hit**		**Identity of the best score**
			Genome	**Phylum**	
			Sup		
1	ABK01356	A_aerophoba_27p20	Mycobacterium gilvum PYR-GCK CCG.	Actinobacteria	66%
2	ABK01354	A_aerophoba_22b24	Mycobacterium gilvum PYR-GCK CCG	Actinobacteria	67%
3	ABK01355	A_aerophoba_26p15	Mycobacterium gilvum PYR-GCK CCG.	Actinobacteria	62%
4	AAW84190	spTKS62g_D_dissoluta	Mycobacterium_sp._Spyr1	Actinobacteria	65%
5	AAW84230	fosFJ58KS2_D_dissoluta	Mycobacterium_sp._Spyr1	Actinobacteria	63%
6	AAW84206	spTKS15Ci_D_dissoluta	Mycobacterium_gilvum_PYR-GCK	Actinobacteria	67%
7	ABK01329	C_mycofijiensis_cm5KS6	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	67%
8	AAW84181	spUKS40i_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	66%
9	ABK01399	A_aerophoba_Aa23	Mycobacterium gilvum PYR-GCK CCG	Actinobacteria	55%
10	ABK01370	A_aerophoba_23	Mycobacterium gilvum PYR-GCK CCG	Actinobacteria	55%
11	ABK01381	C_mycofijiensis_cmKS20	Mycobacterium_sp._Spyr1	Actinobacteria	67%
12	AAW84184	spUKS52g_D_dissoluta	Mycobacterium gilvum PYR-GCK CCG	Actinobacteria	67%
13	ACX49735	SupA_KS13	Mycobacterium gilvum PYR-GCK CCG.	Actinobacteria	67%
14	AAW84201	spTKS39Bg_D_dissoluta	Mycobacterium_sp._Spyr1	Actinobacteria	68%
15	AAW84227	fosUH105KS68_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG.	Actinobacteria	68%
16	ABK01336	C_mycofijiensis_cmKS41	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	64%
17	AAW84185	spUKS41Ai_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	65%
18	ABK01400	A_aerophoba_Aa40	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	67%
19	ABK01363	A_aerophoba_40	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	67%
20	ABK01369	A_aerophoba_21	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	67%
21	ABK01360	A_aerophoba_Aa21	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	65%

22	ABK01365	A_aerophoba_2	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	67%
23	ABK01358	A_aerophoba_Aa2	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	65%
24	ABK01361	A_aerophoba_Aa32	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	64%
25	ABK01372	A_aerophoba_32	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	67%
26	AAW84219	fosFJ104KS51_D_dissoluta	Mycobacterium smegmatis str. MC2 155 CG	Actinobacteria	67%
27	ABK01337	C_mycofijiensis_cmKSB48	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	66%
28	AAW84179	spUKS13g_D_dissoluta	Gamma proteobacterium HdN1 CG.	Gammaproteobacteria	58%
29	ABK01364	A_aerophoba_1	Gamma proteobacterium HdN1 CG.	Gammaproteobacteria	57%
30	ABK01352	A_aerophoba_16e14	Gamma proteobacterium HdN1 CG.	Gammaproteobacteria	56%
31	ABK01357	A_aerophoba_Aa1	Gamma proteobacterium HdN1 CG	Gammaproteobacteria	50%
32	AAW84204	spTKS12Ci_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	68%
33	AAW84231	cosTM26KS21_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG.	Actinobacteria	70%
34	ABK01351	A_aerophoba_15p20	Stigmatella_aurantiaca_DW4/3-1	Deltaproteobacteria	61%
35	ABK01350	A_aerophoba_1h11	Stigmatella_aurantiaca_DW4/3-1	Deltaproteobacteria	61%
36	ABK01367	A_aerophoba_pgpks16	Stigmatella_aurantiaca_DW4/3-1	Deltaproteobacteria	61%
37	ABK01378	X_muta14	Mycobacterium gilvum PYR-GCK CCG	Actinobacteria	63%
38	AAW84223	fosFK57KS57_D_dissoluta	Stigmatella_aurantiaca_DW4/3-1	Deltaproteobacteria	62%
39	ABK01368	A_aerophoba_20	Myxococcus_fulvus_HW-1 CG.	Deltaproteobacteria	63%
40	ABK01359	A_aerophoba_Aa20	Myxococcus fulvus HW-1 CCG.	Deltaproteobacteria	63%
41	ABK01373	A_aerophoba_aapgpks7	Myxococcus fulvus HW-1 CCG.	Deltaproteobacteria	63%
42	ABK01376	A_cavernicola_22	Granulicella_mallensis_MP5ACTX8 CCG	Acidobacteria	59%
43	ABK01375	P_crassa_7	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	64%
44	AAW84202	spTKS55Bg_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	64%
45	AAW84205	spTKS14Ci_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	65%
46	ABK01377	P_crassa_8	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	65%
47	AAW84189	spTKS54g_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	65%
48	ABK01396	T_swinhoei_swsymb1	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	63%
49	ABK01374	V_gigantea_4	Mycobacterium vanbaalenii PYR-1 CCG.	Actinobacteria	66%

50	AAY00027	SupAKS14	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	69%
51	ABK01347	T_swinhoei_swsymb13	Gamma_proteobacterium_HdN1 CCG	Gammaproteobacteria	57%
52	ABB73281	P_clavata_2368H	Mycobacterium sp. MCS CCG.	Actinobacteria	55%
53	ABK01349	T_swinhoei_swsymb19	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	61%
54	JX012429	meta_2_contig00196_1	Gamma_proteobacterium_HdN1 CG	Gammaproteobacteria	54%
55	ABK01338	C_mycofijiensis_cmKSB56	Gamma_proteobacterium_HdN1 CG	Gammaproteobacteria	58%
56	ABB73280	P_clavata__2368C	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	62%
57	ABK01348	T_swinhoei_swsymb14	Gamma proteobacterium HdN1 CG	Gammaproteobacteria	58%
58	AAQ91805	AAQ91805	Gamma proteobacterium HdN1 CG	Gammaproteobacteria	58%
59	AAQ91804	AAQ91804	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	62%
60	ABB73277	P_clavata_pcks29	Gamma proteobacterium HdN1 CG	Gammaproteobacteria	60%
61	ABK01345	T_swinhoei_swsymb6	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	60%
62	ABK01335	C_mycofijiensis_cmKS13	Gamma proteobacterium HdN1 CG	Gammaproteobacteria	58%
63	ABB73279	P_clavata_2226A	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	60%
64	ABB73276	P_clavata_pcks17	Gamma proteobacterium HdN1 CG	Gammaproteobacteria	55%
65	ABK01332	C_mycofijiensis_cmKS2	Acidobacterium_capsulatum_ATCC_51196	Acidobacteria	47%
66	AAW84183	spUKS44i_D_dissoluta	Gamma proteobacterium HdN1 CG	Gammaproteobacteria	59%
67	ABK01341	T_swinhoei_swsymb3	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	51%
68	ABB73278	P_clavata_2125E	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	54%
69	ABK01344	T_swinhoei_swsymb11	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	54%
70	ABK01328	C_mycofijiensis_cm5KS5	Microcystis aeruginosa NIES-843 CG	Cyanobacteria	48%
71	ABB73275	P_clavata_pcks38	Myxococcus xanthus DK 1622 CCG	Deltaproteobacteria	51%
72	AAQ91802	AAQ91802	Acidobacterium_capsulatum_ATCC	Acidobacteria	51%
73	ABK01327	C_mycofijiensis_cm5KS4	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	52%
74	ABK01342	T_swinhoei_swsymb4	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	63%
75	ABK01334	C_mycofijiensis_cmKS9	Gamma proteobacterium HdN1 CG	Gammaproteobacteria	54%
76	ABK01339	C_mycofijiensis_cmKSH22	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	59%
77	AAW84193	spTKS71i_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	59%

78	AAQ91807	AAQ91807	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	61%
79	AAQ91806	AAQ91806	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	62%
80	ABK01346	T_swinhoei_swsymb12	Mycobacterium vanbaalenii PYR-1 CCG.	Actinobacteria	61%
81	ABK01397	T_swinhoei_swsymb5	Acidobacterium capsulatum ATCC 51196 CG.	Acidobacteria	59%
82	ABB73273	ABB73273	Burkholderia_ambifaria_AMMD	Betaproteobacteria	56%
83	ABB73274	ABB73274	Acidobacterium_capsulatum_ATCC	Acidobacteria	60%
84	AAQ91803	AAQ91803	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	63%
85	ABK01331	C_mycofijiensis_cm5KS7	Nostoc_punctiforme_PCC_73102	Cyanobacteria	52%
86	AAW84182	spUKS42i_D_dissoluta	Nostoc_punctiforme_PCC_73102	Cyanobacteria	52%
87	ABK01343	T_swinhoei_swsymb8	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	55%
88	ABK01340	C_mycofijiensis_cmKSH39	Opitutus terrae PB90-1 CCG	Verrucomicrobia	58%
89	ABK01326	C_mycofijiensis_cm5KS3	Opitutus terrae PB90-1 CCG.	Verrucomicrobia	56%
90	AAW84199	spTKS32Bi_D_dissoluta	Mycobacterium gilvum PYR-GCK CCG	Actinobacteria	67%
91	ACX49735	SupA_KS23	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	63%
92	AAW84226	fosUH45KS32_D_dissoluta	Methylobacterium sp. 4-46 CCG.	Alphaproteobacteria	61%
93	AAW84180	spUKS25i_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	61%
94	AAW84200	spTKS35Bg_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	58%
95	AAW84228	fosUH124KS91_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	58%
96	ABK01398	A_aerophoba_Aa5	Mycobacterium_sp._Spyr1 CCG.	Actinobacteria	61%
97	ABK01371	A_aerophoba_24	Mycobacterium_sp._Spyr1 CCG.	Actinobacteria	60%
98	AAW84218	fosFJ16KS31_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	60%
99	JX012430	meta_2_contig00100_1	Mycobacterium_sp._Spyr1 CCG	Actinobacteria	63%
100	AAW84188	spTKS48g_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG.	Actinobacteria	50%
101	AAQ91799	AAQ91799	Mycobacterium gilvum PYR-GCK CCG	Actinobacteria	49%
102	ABK01330	C_mycofijiensis_cm5AKS6	Mycobacterium_sp._Spyr1 CCG	Actinobacteria	56%
103	AAW84229	fosUF104KS49_D_dissoluta	Mycobacterium_intracellulare_MOTT-64	Actinobacteria	61%
104	AAW84214	cosTM40KS52_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG	Actinobacteria	62%
105	AAW84215	cosTM109KS3_D_dissoluta	Mycobacterium_avium_subsp._paratuberculosis	Actinobacteria	55%

106	AAY00027	SupA15	Mycobacterium vanbaalenii PYR-1 CCG.	Actinobacteria	69%
107	**AAW84225**	**fosUF15KS6_D_dissoluta**	**Mycobacterium vanbaalenii PYR-1 CCG**	**Actinobacteria**	**72%**
108	AAW84224	fosUF3KS2_D_dissoluta	Mycobacterium vanbaalenii PYR-1 CCG.	Actinobacteria	69%
109	AAY00025	SupAKS5	Mycobacterium_avium_subsp._paratuberculosis	Actinobacteria	68%
110	AAY00025	SupAKS4	Mycobacterium_gilvum_PYR-GCK	Actinobacteria	70%
111	AAY00025	SupAKS8	Mycobacterium_avium	Actinobacteria	69%
112	AAY00025	SupAKS7	Mycobacterium_avium_subsp._paratuberculosis	Actinobacteria	70%
113	AAY00025	SupAKS3	Mycobacterium_gilvum_PYR-GCK	Actinobacteria	68%
114	AAY00025	SupAKS12	Mycobacterium vanbaalenii PYR-1 CCG.	Actinobacteria	70%
115	AAY00025	SupAKS11	Mycobacterium_sp._Spyr1, CG	Actinobacteria	65%
116	AAY00025	SupA_KS13	Mycobacterium gilvum PYR-GCK CCG.	Actinobacteria	67%
117	AAY00025	SupAKS9	Mycobacterium gilvum PYR-GCK CCG.	Actinobacteria	70%
118	AAY00025	SupAKS6	Mycobacterium avium 104, CG	Actinobacteria	69%
119	AAW84213	cosTM31KS65__D_dissoluta	Mycobacterium gilvum PYR-GCK CCG.	Actinobacteria	61%
120	AAY00025	SupAKS10	Mycobacterium gilvum PYR-GCK CCG.	Actinobacteria	67%
121	AAY00025	SupAKS1	Mycobacterium gilvum PYR-GCK CCG.	Actinobacteria	67%
122	AAY00025	SupAKS0	Mycobacterium gilvum PYR-GCK CCG.	Actinobacteria	70%
123	AAW84212	cosTM11KS1_D_dissoluta	Mycobacterium gilvum PYR-GCK CCG.	Actinobacteria	70%
124	ABK01392	ABK01392	Mycobacterium_avium_subsp._paratuberculosis	Actinobacteria	62%
FAS					
125	NP_218342	PKS2_KS4	Mycobacterium tuberculosis KZN 1435 CG	Actinobacteria	99%
126	NP855206	NP855206	Mycobacterium tuberculosis T17 cont1.179, WGSS	Actinobacteria	100%
127	NP216043	pks5_KS4	Mycobacterium africanum GM041182 CCG.	Actinobacteria	99%
128	NP217456	NP217456	Mycobacterium tuberculosis GM 1503 cont1198 WGSS	Actinobacteria	90%
***Cis*-AT (dark green)**					
129	YP259894	**PltKS1_Pseudomo**	Pseudomonas fluorescens Pf-5 chromosome, CG	Gammaproteobacteria	100%
130	AAW84176	spFKS81i_D_dissoluta	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	62%
131	JX012555	meta_2_contig00151_6	Myxococcus_fulvus_HW-1	Deltaproteobacteria	63%

132	AAW84174	spFKS53g_D_dissoluta	Anabaena variabilis ATCC 29413 CCG.	Cyanobacteria	50%
133	AAW84220	fosFJ13059_D_dissoluta	Cyanothece_sp._ATCC_51142	Cyanobacteria	66%
134	JX012550	meta_2_contig00117_4	Anabaena_variabilis_ATCC_29413 CG	Cyanobacteria	75%
135	AAW84169	spFKS31g_D_dissoluta	Anabaena variabilis ATCC 29413 CCG	Cyanobacteria	64%
136	CAD19087	**StiKS2_Myxo**	Nostoc_sp._PCC_7120 CG	Cyanobacteria	66%
137	JX012436	meta_2_contig00158_1	Microcystis aeruginosa NIES-843 CG	Cyanobacteria	71%
138	AAW84197	spTKS10Bi_D_dissoluta	Microcystis aeruginosa NIES-843 CG.	Cyanobacteria	67%
139	JX012434	meta_2_contig00032_1	Nostoc punctiforme PCC 73102 CG	Cyanobacteria	65%
140	AAW84191	AAW84191	Nostoc punctiforme PCC 73102 CG	Cyanobacteria	60%
141	JX012444	meta_2_contig00162_3	Cyanothece sp. ATCC 51142 chromosome circular CS	Cyanobacteria	64%
142	AF183408_7	**McyKS3_Cyano**	Microcystis aeruginosa NIES-843 chromosome, CG	Cyanobacteria	100%
143	ABI34078	H_perleve	Planctomyces brasiliensis DSM 5305 CCG.	Planctomycetes	99%
144	AAW84196	spTKS42Ai_D_dissoluta	Cyanothece sp. ATCC 51142 chromosome circular CS	Cyanobacteria	73%
145	AAW84186	spTKS36g_D_dissoluta	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	77%
146	AAW84187	spTKS38g_D_dissoluta	Stigmatella_aurantiaca_DW4/3-1 CG.	Deltaproteobacteria	60%
147	JX012545	meta_2_contig00026_6	Nostoc_punctiforme_PCC_73102 CCG	Cyanobacteria	62%
148	ABK01383	C_mycofijiensis_cmKS31	Nostoc punctiforme PCC 73102 CG	Cyanobacteria	59%
149	JX012569	meta_2_contig00028_4	Burkholderia glumae BGR1 plasmid bglu_2p CS	Betaproteobacteria	57%
150	JX012445	meta_2_contig00058_1	Stigmatella_aurantiaca_DW4/3-1	Deltaproteobacteria	53%
151	JX012448	meta_2_contig00048_1	Burkholderia glumae BGR1 plasmid bglu_2p CS	Betaproteobacteria	59%
152	ABI91465	Burkholderia_ambifaria_AMMD	Burkholderia_ambifaria AMMD chromosome 3 CS	Betaproteobacteria	91%
153	ABB73269	P_clavata_F16	Actinoplanes_sp._SE50/110	Actinobacteria	60%
154	AAA79984	**SorKS5_Sorangium**	Haliangium ochraceum DSM 14365 chromosome, CG	Deltaproteobacteria	75%
155	JX012537	meta_2_contig00030_6	Nostoc_punctiforme_PCC_73102	Cyanobacteria	66%
156	AAW84210	spTKS42Ci_D_dissoluta	Stigmatella_aurantiaca_DW4/3-1	Deltaproteobacteria	69%
157	AAW84216	fosFJ4KS21_D_dissoluta	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	67%
158	JX012540	meta_2_contig00163_6	Gamma proteobacterium HdN1 CG.	Gammaproteobacteria	70%
159	AAT68462	Salinospora_M413_Pclavata	Salinispora arenicola CNS-205 CCG	Actinobacteria	89%

160	AAT68460	Salinospora_M403_Pclavata	Salinispora arenicola CNS-205 CCG	Actinobacteria	89%
161	AAT68461	Salinospora_M412_Pclavata	Salinispora arenicola CNS-205 CCG	Actinobacteria	90%
162	AAT68463	Salinospora_SW15_Pclavata	Salinispora arenicola CNS-205 CCG.	Actinobacteria	81%
163	AAT68464	Salinospora_SW17_Pclavata	Salinispora arenicola CNS-205 CCG.	Actinobacteria	87%
164	CAA11036	**RifKS2_Actino**	Amycolatopsis mediterranei U32 chromosome, CG	Actinobacteria	99%
165	ADN37744	MycobactFSD4bSM_10_Fas	Mycobacterium avium 104 CG.	Actinobacteria	80%
166	JX012638	meta_3_contig00018_6	Streptomyces_griseus_subsp._griseus	Actinobacteria	68%
167	YP_001102988	**EryKS2_Actino**	Saccharopolyspora erythraea NRRL 2338 WGSS	Actinobacteria	100%
168	ADN37743	MycobactFSD4bSM_6_Fasc	Mycobacterium marinum M CG	Actinobacteria	69%
169	AAC46024	**NidKS2_Streptomyces**	Saccharopolyspora_erythraea	Actinobacteria	82%
170	JX012513	meta_3_contig00055_3	Streptomyces_violaceusniger_Tu_4113	Actinobacteria	77%
171	ABB73268	P_clavata_Rhodococcus	Rhodococcus jostii RHA1 CCG.	Actinobacteria	91%
172	JX012561	meta_2_contig00168_4	Mycobacterium marinum M CG.	Actinobacteria	82%
173	ADN37742	MycobactFSD4bSM_4_Fasc	Streptomyces_violaceusniger_Tu_4113	Actinobacteria	63%
174	JX012508	meta_3_contig00031_1	Streptomyces_bingchenggensis_BCW-1 CCG.	Actinobacteria	76%
175	JX012634	meta_3_contig00028_4	Streptomyces_bingchenggensis_BCW-1 CCG.	Actinobacteria	73%
176	JX012443	meta_2_contig00043_1	Streptomyces_bingchenggensis_BCW-1 CCG.	Actinobacteria	74%
177	JX012509	meta_3_contig00025_1	Streptomyces_bingchenggensis_BCW-1 CCG.	Actinobacteria	73%
178	JX012558	meta_2_contig00099_4	Streptomyces_griseus_subsp._griseus	Actinobacteria	73%
179	JX012573	meta_2_contig00205_4	Streptomyces_avermitilis_MA-4680	Actinobacteria	74%
180	JX012456	meta_2_contig00245_1	Streptomyces_coelicolor_A3	Actinobacteria	61%
181	JX012635	meta_3_contig00024_4	Streptomyces_avermitilis_MA-4680 CCG.	Actinobacteria	64%
182	JX012464	meta_2_contig00224_3	Stigmatella_aurantiaca_DW4/3-1	Deltaproteobacteria	56%
183	ABK01388	C_mycofijiensis_cmKSA11	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	64%
184	JX012631	meta_3_contig00033_5	Opitutus terrae PB90-1 CCG	Verrucomicrobia	65%
185	JX012438	meta_2_contig00025_1	Opitutus terrae PB90-1 CCG	Verrucomicrobia	65%
186	JX012446	meta_2_contig00031_1	Myxococcus_fulvus_HW-1 CCG	Deltaproteobacteria	59%
187	ABK01390	C_mycofijiensis_cmKSA61	Stigmatella_aurantiaca_DW4/3-1	Deltaproteobacteria	66%

188	AF210843_18	**EpoKS2_Myxo**	Myxococcus xanthus DK 1622 chromosome, CG	Deltaproteobacteria	100%
189	AAW84222	fosFK9KS4_D_dissoluta	Stigmatella_aurantiaca_DW4/3-1	Deltaproteobacteria	64%
Cis-AT 1 (light green)					
190	JX012626	meta_3_contig00009_6	Microcystis aeruginosa NIES-843 CG.	Cyanobacteria	72%
191	JX012536	meta_2_contig00040_5	Microcystis aeruginosa NIES-843 CG.	Cyanobacteria	72%
192	JX012542	meta_2_contig00035_5	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	59%
193	JX012435	meta_2_contig00088_3	Nostoc punctiforme PCC 73102 CG	Cyanobacteria	71%
194	AAW84211	spTKS43Ci_D_dissoluta	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	65%
195	JX012538	meta_2_contig00020_6	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	68%
196	AAW84175	spFKS69i_D_dissoluta	Cyanothece sp. ATCC 51142 chromosome circular CS	Cyanobacteria	78%
197	ACI32874	FAS_Streptomyces_H_simulans	Cyanothece sp. ATCC 51142 chromosome circular CS	Cyanobacteria	65%
198	JX012544	meta_2_contig00074_4	Mycobacterium_intracellulare_MOTT-64	Actinobacteria	68%
199	ABK01382	C_mycofijiensis_cmKS25	Mycobacterium_sp._JLS	Actinobacteria	64%
200	JX012549	meta_2_contig00171_5	Stigmatella_aurantiaca_DW4/3-1	Deltaproteobacteria	72%
201	JX012630	meta_3_contig00038_4	Cyanothece_sp._ATCC_51142	Cyanobacteria	63%
202	JX012439	meta_2_contig00046_2	Nostoc punctiforme PCC 73102 CG	Cyanobacteria	58%
203	**ADN37741**	**A_queenslandica**	**Mycobacterium vanbaalenii PYR-1 CCG.**	**Actinobacteria**	**93%**
204	ADN37739	A_queenslandica	Mycobacterium vanbaalenii PYR-1 CCG.	Actinobacteria	91%
205	AAW84178	spFKS10Ai_D_dissoluta	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	63%
206	JX012556	meta_2_contig00189_4	Rhodopirellula baltica SH 1 CCG.	Planctomycetes	63%
207	JX012619	meta_2_contig00054_4	Streptomyces_violaceusniger_Tu_4113	Actinobacteria	50%
208	JX012440	meta_2_contig00164_1	Nostoc sp. PCC 7120 CG	Cyanobacteria	66%
209	ADN37738	A_queenslandica	Mycobacterium sp. Spyr1 CCG.	Actinobacteria	87%
210	ADN37737	A_queenslandica	Mycobacterium sp. Spyr1 CCG.	Actinobacteria	90%
211	JX012539	meta_2_contig00016_6	Hahella_chejuensis_KCTC_2396	Gammaproteobacteria	65%
212	JX012447	meta_2_contig00214_2	Granulicella_mallensis_MP5ACTX8 CG.	Acidobacteria	66%
213	AAW84209	spTKS39Ci_D_dissoluta	Gamma_proteobacterium_HdN1 CCG.	Gammaproteobacteria	69%
214	JX012629	meta_3_contig00059_6	Cyanothece sp. ATCC 51142 chromosome circular CS	Cyanobacteria	73%

215	JX012431	meta_2_contig00086_1	Cyanothece sp. ATCC 51142 chromosome circular CS	Cyanobacteria	73%
216	JX012548	meta_2_contig00295_6	Anabaena variabilis ATCC 29413 chromosome, CG	Cyanobacteria	76%
217	JX012442	meta_2_contig00057_1	Anabaena_variabilis_ATCC_29413	Cyanobacteria	65%
218	ACI32875	ACI32875	Cyanothece sp. ATCC 51142 chromosome circular CS	Cyanobacteria	63%
219	AAW84172	spFKS44g_D_dissoluta	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	69%
220	AAW84168	spFKS29g_D_dissoluta	Anabaena variabilis ATCC 29413 CCG.	Cyanobacteria	69%
221	JX012455	meta_2_contig00191_3	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	67%
222	JX012554	meta_2_contig00049_6	Corallococcus_coralloides_DSM_2259 CCG	Deltaproteobacteria	59%
223	JX012437	meta_2_contig00038_1	Anabaena_variabilis_ATCC_29413 CCG.	Deltaproteobacteria	70%
224	JX012627	meta_3_contig00021_6	Nostoc punctiforme PCC 73102 CG	Cyanobacteria	68%
225	JX012546	meta_2_contig00126_6	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	68%
226	JX012543	meta_2_contig00064_4	Myxococcus fulvus HW-1 CCG.	Deltaproteobacteria	76%
227	JX012507	meta_3_contig00004_2	Rhodopirellula baltica SH 1 CCG.	Planctomycetes	71%
228	JX012551	meta_2_contig00102_5	Rhodopirellula baltica SH 1 CCG.	Planctomycetes	71%
229	JX012553	meta_2_contig00022_4	Rhodopirellula baltica SH 1 CCG.	Deltaproteobacteria	67%
230	JX012541	meta_2_contig00056_6	Gamma_proteobacterium_HdN1 CG	Gammaproteobacteria	64%
231	JX012451	meta_2_contig00136_1	Anabaena variabilis ATCC 29413 CCG.	Cyanobacteria	61%
New PKS					
232	JX012591	meta_2_contig00115_4	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	53%
233	JX012578	meta_2_contig00085_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	60%
234	JX012495	meta_2_contig00252_1	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	60%
235	JX012468	meta_2_contig00073_1	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	59%
236	JX012427	meta_1_contig00016_1	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	57%
237	JX012599	meta_2_contig00078_4	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	56%
238	JX012534	meta_1_contig00007_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	60%
239	JX012505	meta_2_contig00310_2	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	59%
240	JX012642	meta_3_contig00050_5	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	57%
241	JX012598	meta_2_contig00044_4	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	57%

242	JX012652	meta_3_contig00079_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	58%
243	JX012637	meta_3_contig00036_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	59%
244	JX012589	meta_2_contig00228_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	59%
245	**JX012603**	**meta_2_contig00169_4**	**Corallococcus_coralloides_DSM_2259 CCG.**	**Deltaproteobacteria**	**63%**
246	JX012426	meta_1_contig00014_1	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	58%
247	**JX012657**	**meta_3_contig00104_4**	**Corallococcus_coralloides_DSM_2259 CCG.**	**Deltaproteobacteria**	**63%**
248	JX012512	meta_3_contig00032_1	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	60%
249	JX012593	meta_2_contig00223_5	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	60%
250	JX012502	meta_2_contig00400_1	Cyanothece sp. PCC 7424 CCG	Cyanobacteria	55%
251	JX012612	meta_2_contig00239_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	55%
252	JX012516	meta_3_contig00037_1	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	58%
253	JX012482	meta_2_contig00194_1	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	56%
254	JX012529	meta_3_contig00070_1	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	57%
255	JX012607	meta_2_contig00155_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	57%
256	JX012523	meta_3_contig00076_1	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	60%
257	JX012535	meta_1_contig00009_5	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	60%
258	JX012647	meta_3_contig00012_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	61%
259	JX012594	meta_2_contig00147_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	61%
260	JX012623	meta_2_contig00354_4	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	62%
261	JX012476	meta_2_contig00007_1	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	59%
262	JX012528	meta_3_contig00054_3	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	61%
263	JX012600	meta_2_contig00105_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	61%
264	JX012648	meta_3_contig00041_5	Synechococcus_sp._PCC_7002 CG.	Cyanobacteria	54%
265	JX012641	meta_3_contig00067_6	Nostoc sp. PCC 7120 CG.	Cyanobacteria	53%
266	JX012585	meta_2_contig00144_6	Bacillus_amyloliquefaciens_LL3 CCG	Firmicutes	55%
267	**JX012463**	**meta_2_contig00118_1**	**Corallococcus_coralloides_DSM_2259 CCG.**	**Deltaproteobacteria**	**63%**
268	JX012515	meta_3_contig00042_1	Synechococcus_sp._PCC_7002 CCG.	Cyanobacteria	56%
269	JX012514	meta_3_contig00035_1	Anabaena variabilis ATCC 29413 CCG.	Cyanobacteria	59%

270	JX012473	meta_2_contig00133_1	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	58%
271	JX012646	meta_3_contig00022_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	56%
272	JX012580	meta_2_contig00081_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	56%
273	JX012574	meta_2_contig00066_6	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	59%
274	JX012618	meta_2_contig00042_4	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	59%
275	JX012624	meta_2_contig00401_4	Anabaena variabilis ATCC 29413 clone 7-2 pks gene	Cyanobacteria	57%
276	JX012596	meta_2_contig00187_4	Synechococcus_sp._PCC_7002 CCG.	Cyanobacteria	55%
277	JX012469	meta_2_contig00125_1	Synechococcus_sp._PCC_7002 CCG.	Cyanobacteria	56%
278	JX012485	meta_2_contig00284_1	Desulfovibrio_alaskensis_G20 CG	Deltaproteobacteria	52%
279	JX012533	meta_1_contig00013_6	Bacillus_amyloliquefaciens_LL3	Firmicutes	54%
280	JX012501	meta_2_contig00391_2	Desulfovibrio_alaskensis_G20 CG	Deltaproteobacteria	52%
281	JX012491	meta_2_contig00266_3	Anabaena variabilis ATCC 29413 CCG	Cyanobacteria	54%
282	JX012481	meta_2_contig00070_2	Synechococcus_sp._PCC_7002 CCG.	Cyanobacteria	58%
283	JX012649	meta_3_contig00077_5	Cyanothece sp. PCC 7424 CCG	Cyanobacteria	52%
284	JX012605	meta_2_contig00230_6	Cyanothece sp. PCC 7424 CCG	Cyanobacteria	52%
285	JX012477	meta_2_contig00238_1	Mycobacterium avium subsp. paratuberculosis CG.	Actinobacteria	58%
286	**JX012601**	**meta_2_contig00294_4**	**Corallococcus_coralloides_DSM_2259 CCG.**	**Deltaproteobacteria**	**63%**
287	JX012616	meta_2_contig00466_5	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	60%
288	JX012472	meta_2_contig00220_1	Corallococcus_coralloides_DSM_2259 CCG.	Deltaproteobacteria	60%
289	JX012586	meta_2_contig00250_6	Gamma proteobacterium HdN1 CG.	Gammaproteobacteria	60%
290	JX012450	meta_2_contig00186_1	Mycobacterium avium 104 CG.	Actinobacteria	63%
***Cis*-AT 2 (light green)**					
291	AAW84177	spFKS7Ai_D_dissoluta	Anabaena variabilis ATCC 29413 CCG	Cyanobacteria	54%
292	JX012579	meta_2_contig00034_5	Anabaena variabilis ATCC 29413 CCG	Cyanobacteria	54%
293	JX012650	meta_3_contig00073_6	Anabaena variabilis ATCC 29413 CCG.	Cyanobacteria	52%
294	ABK01387	C_mycofijiensis_cmKS88	Methylobacterium sp. 4-46 CCG.	Alphaproteobacteria	57%
295	JX012566	meta_2_contig00181_6	Mycobacterium gilvum PYR-GCK CCG.	Actinobacteria	50%
296	JX012521	meta_3_contig00075_3	Gamma_proteobacterium_HdN1 CCG	Gammaproteobacteria	52%

297	JX012462	meta_2_contig00065_2	Herpetosiphon_aurantiacus_DSM_785 CCG.	Chloroflexi	55%
298	JX012503	meta_2_contig00197_1	Herpetosiphon aurantiacus ATCC 23779 CCG.	Chloroflexi	46%
299	JX012610	meta_2_contig00149_4	Haliangium ochraceum DSM 14365 CG.	Deltaproteobacteria	48%
300	ABK01384	C_mycofijiensis_cmKS37	Stigmatella_aurantiaca_DW4/3-1 CCG	Deltaproteobacteria	56%
301	JX012552	meta_2_contig00077_4	Anabaena_variabilis_ATCC_29413 CG.	Cyanobacteria	63%
302	JX012441	meta_2_contig00061_1	Nostoc sp. PCC 7120 CG	Cyanobacteria	61%
303	JX012633	meta_3_contig00058_6	Burkholderia_ambifaria_AMMD CCG.	Betaproteobacteria	64%
304	JX012433	meta_2_contig00173_1	Anabaena variabilis ATCC 29413 CCG	Cyanobacteria	73%
305	JX012432	meta_2_contig00063_1	Anabaena variabilis ATCC 29413 CCG	Cyanobacteria	63%
306	JX012628	meta_3_contig00011_6	Bacillus_amyloliquefaciens_LL3 CCG	Firmicutes	62%
307	JX012632	meta_3_contig00068_6	Myxococcus_fulvus_HW-1 CCG.	Deltaproteobacteria	69%
308	JX012518	meta_3_contig00047_2	Burkholderia_ambifaria_AMMD chromosome 3 CS	Betaproteobacteria	61%
309	ABK01389	C_mycofijiensis_cmKSA46	Anabaena variabilis ATCC 29413 CCG.	Cyanobacteria	68%
310	ABI34077	S_costatum_H_perleve	Cyanothece_sp._PCC_7424 CG	Cyanobacteria	63%
311	**ADN37740**	**A_queenslandica**	**Mycobacterium vanbaalenii PYR-1 CCG.**	**Actinobacteria**	**93%**
312	JX012454	meta_2_contig00216_3	Stigmatella_aurantiaca_DW4/3-1 CCG	Deltaproteobacteria	67%
313	JX012547	meta_2_contig00159_6	Streptomyces_griseus_subsp._griseus CG	Actinobacteria	67%
314	ABK01385	C_mycofijiensis_cmKS68	Stigmatella_aurantiaca_DW4/3-1 CCG	Deltaproteobacteria	63%
315	JX012581	meta_2_contig00233_6	Stigmatella_aurantiaca_DW4/3-1 CCG	Deltaproteobacteria	67%
316	JX012517	meta_3_contig00078_3	Stigmatella_aurantiaca_DW4/3-1 CCG	Deltaproteobacteria	62%
317	CAO98852	**AufI**	Stigmatella aurantiaca DW4/3-1 chromosome, CG	Deltaproteobacteria	91%
318	JX012449	meta_2_contig00052_1	Haliangium ochraceum DSM 14365 CG.	Deltaproteobacteria	61%
319	JX012532	meta_1_contig00004_6	Stigmatella_aurantiaca_DW4/3-1	Deltaproteobacteria	64%
320	JX012531	meta_1_contig00006_6	Stigmatella_aurantiaca_DW4/3-1 CG.	Deltaproteobacteria	64%
Polysaccharide related FAS-like type I PKS					
321	ADY17925	Pseudovibrio_Ad2_A_dissimilis	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	91%
322	ADY17924	Pseudovibrio_Ad2_A_dissimilis	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	92%

323	ADY17927	Pseudovibrio_Ad9_A_dissimilis	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	96%
324	ADY17932	Pseudovibrio_Ad26_A_dissimilis	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	95%
325	ADY17930	Pseudovibrio_Ad23_A_dissimilis	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	96%
326	ACI32870	FAS_Pseudovibrio_H_simulans	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	96%
327	ADY17940	PseudovibAd48_A_dissimilis	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	95%
328	ACI32869	FAS_Pseudovibrio_H_simulans	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	95%
329	ADY17936	Pseudovibrio_Ad35_A_dissimilis	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	96%
330	ADY17934	Pseudovibrio_Ad28_A_dissimilis	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	96%
331	ADY17938	PseudovibAd37_A_dissimilis	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	95%
332	ADY17928	Pseudovibrio_Ad11_A_dissimilis	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	94%
333	ADY17929	Pseudovibrio_Ad17_A_dissimilis	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	95%
334	ADY17935	Pseudovibrio_Ad30_A_dissimilis	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	96%
335	**ABK01380**	**C_mycofijiensis_cmKS17**	**Pseudovibrio_sp._FO-BEG1**	**Alphaproteobacteria**	**84%**
336	AAW78650	**RkpA_KS2**	Sinorhizobium fredii HH103 CCG.	Alphaproteobacteria	90%
337	JX012504	meta_2_contig00243_2	Sinorhizobium medicae WSM419 CCG.	Alphaproteobacteria	56%
338	JX012620	meta_2_contig00179_6	Sinorhizobium medicae WSM419 CCG.	Alphaproteobacteria	57%
339	JX012655	meta_3_contig00014_6	Sinorhizobium fredii NGR234 CCG.	Alphaproteobacteria	55%
340	JX012654	meta_3_contig00027_6	Azorhizobium caulinodans ORS 571 CG.	Alphaproteobacteria	53%
341	JX012530	meta_3_contig00013_1	Sinorhizobium_meliloti_SM11 CG	Alphaproteobacteria	48%
342	JX012602	meta_2_contig00166_6	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	57%
343	JX012625	meta_2_contig00313_5	Pseudovibrio_sp._FO-BEG1	Alphaproteobacteria	62%
344	JX012592	meta_2_contig00051_6	Nocardia farcinica IFM 10152 CCG.	Actinobacteria	48%
345	JX012428	meta_1_contig00008_3	Legionella longbeachae NSW150 CCG	Gammaproteobacteria	45%
346	ACB47226	Phakellia_fusca	Segniliparus rotundus DSM 44985 CCG.	Actinobacteria	48%
347	JX012484	meta_2_contig00148_3	Mycobacterium_avium_subsp._paratuberculosis	Actinobacteria	54%
348	ABI34079	Karlodinium_NBA5_H_perleve	Xanthobacter_autotrophicus_Py2	Alphaproteobacteria	59%
349	AAW84195	spTKS37Ai_D_dissoluta	Streptomyces_bingchenggensis_BCW-1	Actinobacteria	53%
350	ABK01333	C_mycofijiensis_cmKS7	Legionella longbeachae NSW150 CCG.	Gammaproteobacteria	63%

351	AAW84194	spTKS35i_D_dissoluta	Frateuria_aurantia_DSM_6220	Gammaproteobacteria	66%
352	B1HAZ6	**BURPS_WcbR_KS**	Burkholderia_mallei_ATCC_23344	Betaproteobacteria	100%
353	Q82UT4	**NITEU_WcbR_KS**	Nitrosomonas europaea ATCC 19718 CG.	Betaproteobacteria	99%
354	JX012571	meta_2_contig00029_6	Clostridium_acetobutylicum_EA_2018	Firmicutes	58%
355	ABG57047	Pseudoalteromonas_H_perleve	Saccharophagus degradans 2-40 CCG.	Gammaproteobacteria	68%
356	JX012559	meta_2_contig00023_6	Paenibacillus_mucilaginosus_K02	Firmicutes	65%
357	JX012453	meta_2_contig00174_1	Paenibacillus_mucilaginosus_K02	Firmicutes	60%
358	**JX012576**	**meta_2_contig00237_4**	**Rhodopirellula baltica SH 1 CCG**	**Planctomycetes**	**80%**
359	AAW84208	spTKS25Ci_D_dissoluta	Rhodopirellula baltica SH 1 CCG	Planctomycetes	75%
360	JX012557	meta_2_contig00106_5	Rhodopirellula baltica SH 1 CCG.	Planctomycetes	65%
361	ABK01401	A_aerophoba_2m14	Burkholderia_ambifaria_AMMD	Betaproteobacteria	62%
362	AAW84192	spTKS63g_D_dissoluta	Burkholderia_ambifaria_AMMD	Betaproteobacteria	60%
363	AAQ91800	AAQ91800	Paenibacillus curdlanolyticus YK9 ctg108, WGSS	Firmicutes	64%
Trans-AT					
364	JX012639	meta_3_contig00045_6	Paenibacillus polymyxa SC2 CCG	Firmicutes	71%
365	ABK51301	**BryKS8**	Paenibacillus polymyxa ATCC 842 contig26, WGSS	Firmicutes	76%
366	JX012604	meta_2_contig00178_4	Paenibacillus polymyxa SC2 CCG	Firmicutes	81%
367	JX012575	meta_2_contig00087_6	Paenibacillus polymyxa E681 CCG.	Firmicutes	77%
368	JX012640	meta_3_contig00064_6	Dickeya dadantii Ech703 CCG	Gammaproteobacteria	77%
369	JX012487	meta_2_contig00130_3	Paenibacillus_polymyxa_M1	Firmicutes	64%
370	JX012588	meta_2_contig00160_6	Dickeya dadantii Ech703 CCG	Gammaproteobacteria	64%
371	AAW84173	spFKS44i_D_dissoluta	Paenibacillus_polymyxa_M1	Firmicutes	71%
372	JX012480	meta_2_contig00236_2	Paenibacillus polymyxa E681 CCG	Firmicutes	65%
373	JX012425	meta_1_contig00011_1	Paenibacillus polymyxa SC2 CCG.	Firmicutes	68%
374	JX012467	meta_2_contig00199_1	Paenibacillus polymyxa SC2 CCG	Firmicutes	69%
375	JX012452	meta_2_contig00101_1	Paenibacillus_polymyxa_E681	Firmicutes	61%
376	JX012587	meta_2_contig00091_4	Dickeya dadantii Ech703 CCG	Gammaproteobacteria	64%
377	JX012562	meta_2_contig00165_6	Paenibacillus polymyxa SC2 CCG	Firmicutes	67%

378	JX012570	meta_2_contig00142_6	Paenibacillus polymyxa E681 CCG	Firmicutes	66%
379	JX012577	meta_2_contig00036_6	Paenibacillus polymyxa E681 CCG	Firmicutes	60%
380	JX012460	meta_2_contig00190_1	Myxococcus xanthus DK 1622 CCG	Deltaproteobacteria	53%
381	AAQ91801	AAQ91801	Paenibacillus_polymyxa_M1 CG	Firmicutes	63%
382	JX012461	meta_2_contig00083_1	Myxococcus_xanthus_DK_1622	Deltaproteobacteria	63%
383	JX012645	meta_3_contig00072_6	Paenibacillus_polymyxa_M1	Firmicutes	65%
384	JX012489	meta_2_contig00248_3	Burkholderia_gladioli_BSR3	Betaproteobacteria	55%
385	JX012479	meta_2_contig00232_1	Chitinophaga pinensis DSM 2588 CG	Bacteroidetes	56%
386	JX012583	meta_2_contig00217_6	Bacillus_amyloliquefaciens_subsp._plantarum	Firmicutes	77%
387	JX012563	meta_2_contig00131_6	Chitinophaga pinensis DSM 2588 CG	Bacteroidetes	78%
388	JX012459	meta_2_contig00116_1	Sorangium_cellulosum_'So_ce_56' CG	Deltaproteobacteria	74%
389	JX012478	meta_2_contig00129_1	Paenibacillus_mucilaginosus_K02 CCG	Firmicutes	70%
390	JX012568	meta_2_contig00111_6	Bacillus_amyloliquefaciens_subsp._plantarum CG	Firmicutes	67%
391	JX012471	meta_2_contig00092_1	Paenibacillus_mucilaginosus_K02 CCG.	Firmicutes	74%
392	JX012525	meta_3_contig00016_2	Paenibacillus_mucilaginosus_K02	Firmicutes	68%
393	JX012564	meta_2_contig00079_6	Burkholderia gladioli BSR3 chromosome 1 CS	Betaproteobacteria	72%
394	AEA60792	PKS_NRPS_Burkholderia_gladioli	Burkholderia_gladioli	Betaproteobacteria	100%
395	AAW84171	spFKS39i_D_dissoluta	Brevibacillus brevis NBRC 100599 CG.	Firmicutes	70%
396	JX012522	meta_3_contig00061_2	Burkholderia gladioli BSR3 chromosome 1 CS	Betaproteobacteria	62%
397	JX012567	meta_2_contig00138_6	Burkholderia gladioli BSR3 chromosome 1 CS	Betaproteobacteria	63%
398	JX012458	meta_2_contig00112_1	Burkholderia gladioli BSR3 chromosome 1 CS	Betaproteobacteria	61%
399	JX012526	meta_3_contig00051_1	Paenibacillus polymyxa E681 CCG.	Firmicutes	62%
400	JX012497	meta_2_contig00103_1	Paenibacillus polymyxa E681 CCG.	Firmicutes	56%
401	AAW84198	spTKS31Bi_D_dissoluta	Paenibacillus polymyxa E681 CCG	Firmicutes	56%
402	JX012565	meta_2_contig00134_6	Paenibacillus_polymyxa_E681 CCG.	Firmicutes	79%
403	JX012608	meta_2_contig00262_6	Ralstonia_solanacearum_CFBP2957 CG.	Betaproteobacteria	71%
404	JX012611	meta_2_contig00246_6	Pseudomonas fluorescens Pf-5 CCG.	Gammaproteobacteria	70%
405	JX012597	meta_2_contig00242_4	Burkholderia_rhizoxinica_HKI_454	Betaproteobacteria	70%

406	JX012466	meta_2_contig00213_1	Ralstonia solanacearum PSI07 megaplasmid CS	Betaproteobacteria	70%
407	AAW84217	fosFJ8KS38_D_dissoluta	Ralstonia_solanacearum_CFBP2957	Gammaproteobacteria	71%
408	JX012465	meta_2_contig00218_1	Ralstonia_solanacearum_CFBP2957	Betaproteobacteria	71%
409	JX012582	meta_2_contig00211_6	Ralstonia_solanacearum_CFBP2957	Betaproteobacteria	70%
410	ZP_02371244	**TaiKS2**	Burkholderia thailandensis, WGSS	Betaproteobacteria	100%
411	YP_439868	YP_439868	Burkholderia thailandensis E264	Betaproteobacteria	100%
412	JX012644	meta_3_contig00056_5	Mycobacterium_vanbaalenii_PYR-1	Actinobacteria	51%
413	JX012511	meta_3_contig00019_1	Myxococcus xanthus DK 1622 CCG.	Deltaproteobacteria	77%
414	JX012595	meta_2_contig00226_4	Myxococcus xanthus DK 1622 CCG.	Deltaproteobacteria	76%
415	ACB47225	Berenicea_ampulliformis	Paenibacillus polymyxa E681 CCG.	Firmicutes	70%
416	JX012524	meta_3_contig00049_2	Dickeya_dadantii_Ech703	Gammaproteobacteria	69%
417	JX012584	meta_2_contig00072_6	Dickeya_dadantii_Ech703	Gammaproteobacteria	69%
418	ABB73272	P_clavata_Bacillus_M118	Streptomyces_scabiei_87.22 CG	Actinobacteria	85%
419	**ABB73271**	**P_clavata_Bacillus_M115**	**Streptomyces_scabiei_87.22 CG**	**Actinobacteria**	**86%**
420	ABB73270	P_clavata_Bacillus_SW21	Streptomyces_scabiei_87.22 CG	Actinobacteria	85%
421	JX012636	meta_3_contig00017_5	Paenibacillus_polymyxa_M1 CG	Firmicutes	71%
422	JX012490	meta_2_contig00209_2	Paenibacillus_polymyxa_M1 CG	Firmicutes	67%
423	JX012457	meta_2_contig00060_1	Paenibacillus_polymyxa_M1 CG	Firmicutes	70%
424	JX012510	meta_3_contig00020_1	Bacillus amyloliquefaciens FZB42 CG.	Firmicutes	63%
425	JX012560	meta_2_contig00075_6	Teredinibacter_turnerae_T7901	Gammaproteobacteria	60%
426	AAS47564	**PedKS4**	Myxococcus_xanthus_DK_1622 CCG	Deltaproteobacteria	65%
427	AAV97870	**OnnKS1**	Burkholderia_gladioli_BSR3 CCG	Betaproteobacteria	57%
428	AAQ91798	AAQ91798	Burkholderia_gladioli_BSR3 CCG	Betaproteobacteria	57%
429	JX012572	meta_2_contig00045_4	Sorangium_cellulosum_'So_ce_56'	Deltaproteobacteria	54%
430	JX012527	meta_3_contig00052_1	Chitinophaga pinensis DSM 2588 CG.	Bacteroidetes	53%
431	JX012643	meta_3_contig00029_6	Chitinophaga pinensis DSM 2588 CG.	Bacteroidetes	53%
432	JX012651	meta_3_contig00048_6	Bacillus_subtilis_subsp._spizizenii	Firmicutes	57%
433	JX012617	meta_2_contig00203_6	Sorangium_cellulosum_'So_ce_56' CCG	Deltaproteobacteria	58%

434	YP_004029397	**RhiKS4**	Burkholderia_rhizoxinica_HKI_454	Betaproteobacteria	96%
435	YP_004029397	Burkholderia rhizoxinica	Burkholderia_rhizoxinica_HKI_455	Betaproteobacteria	96%
436	JX012613	meta_2_contig00251_4	Pseudomonas fluorescens Pf-5 CCG.	Gammaproteobacteria	56%
437	JX012609	meta_2_contig00222_6	Bacillus_amyloliquefaciens_subsp._plantarum	Firmicutes	61%
438	JX012488	meta_2_contig00139_1	Clostridium cellulolyticum H10 CG.	Firmicutes	62%
439	JX012520	meta_3_contig00030_1	Clostridium cellulolyticum H10 CG.	Firmicutes	62%
440	ZP_04523236	_Burkholderia	Burkholderia_mallei_ATCC_23344	Betaproteobacteria	84%
441	ABK51301	**BryKS11**	Clostridium_cellulolyticum_H10	Firmicutes	52%
442	YP_439860	**TaiKS9**	Burkholderia thailandensis, WGSS	Betaproteobacteria	100%
443	YP_004360747	YP_004360747	Burkholderia gladioli BSR3	Betaproteobacteria	91%
444	AAM12911	AAM12911	Paenibacillus_polymyxa_E681	Firmicutes	69%
445	ADI59533	**CorKS8_Deltaproteo**	Streptomyces_cattleya_NRRL_8057	Actinobacteria	54%
446	ABK01379	C_mycofijiensis_cmKS12	Clostridium_clariflavum_DSM_19732 CCG	Firmicutes	56%
PKS/NRPS					
447	JX012653	meta_3_contig00001_6	Paenibacillus mucilaginosus K02 CCG	Firmicutes	62%
448	AAW84207	spTKS19Ci_D_dissoluta	Paenibacillus_mucilaginosus_K02	Firmicutes	66%
449	JX012496	meta_2_contig00093_1	Paenibacillus_mucilaginosus_K03	Firmicutes	65%
450	JX012622	meta_2_contig00153_5	Photorhabdus asymbiotica subsp. asymbiotica CCG	Gammaproteobacteria	67%
451	AAW84221	fosFJ132KS34_D_dissoluta	Cyanothece sp. ATCC 51142 chromosome circular CS	Cyanobacteria	71%
452	JX012606	meta_2_contig00008_6	Acaryochloris marina MBIC11017 plasmid pREB1 CS	Cyanobacteria	72%
453	ABK01394	C_mycofijiensis_cmKSH71	Paenibacillus_mucilaginosus_3016	Firmicutes	63%
454	ABK01386	C_mycofijiensis_cmKS79	Anabaena variabilis ATCC 29413 CCG	Cyanobacteria	66%
455	JX012499	meta_2_contig00253_1	Myxococcus fulvus_HW-1 CCG	Deltaproteobacteria	79%
456	JX012486	meta_2_contig00122_1	Trichodesmium_erythraeum_IMS101	Cyanobacteria	71%
457	ABK01391	C_mycofijiensis_cmKSA81	Trichodesmium_erythraeum_IMS101	Cyanobacteria	62%
458	JX012483	meta_2_contig00009_1	Paenibacillus_mucilaginosus_K02 CG	Firmicutes	68%
459	AAS98784	**JamM_Cyanob_NRPS_PKS**	Anabaena_variabilis_ATCC_29413 CCG	Cyanobacteria	74%
460	JX012614	meta_2_contig00037_4	Paenibacillus_mucilaginosus_K02 CCG	Firmicutes	68%

461	JX012474	meta_2_contig00012_1	Acaryochloris_marina_MBIC11017	Cyanobacteria	65%
462	JX012656	meta_3_contig00003_5	Burkholderia phymatum STM815 chromosome 1 CS	Betaproteobacteria	59%
463	**JX012498**	**meta_2_contig00109_1**	**Agrobacterium vitis S4 plasmid pAtS4e CS**	**Alphaproteobacteria**	**82%**
464	JX012493	meta_2_contig00011_2	Nostoc punctiforme PCC 73102 CG	Cyanobacteria	65%
465	JX012492	meta_2_contig00067_1	Nostoc_punctiforme_PCC_73102 CG	Cyanobacteria	61%
466	JX012494	meta_2_contig00010_2	Nostoc punctiforme PCC 73102 CG	Cyanobacteria	64%
467	ACB47224	H_perlevis	Nostoc punctiforme PCC 73102 CG	Cyanobacteria	65%
468	JX012500	meta_2_contig00137_1	Acaryochloris_marina_MBIC11017	Cyanobacteria	62%
469	JX012615	meta_2_contig00006_4	Paenibacillus mucilaginosus K02 CCG	Firmicutes	70%
470	JX012590	meta_2_contig00013_6	Myxococcus_fulvus_HW-1	Deltaproteobacteria	67%
471	JX012621	meta_2_contig00039_4	Xanthobacter_autotrophicus_Py2 CCG	Alphaproteobacteria	64%
472	AAW84203	spTKS10Ci_D_dissoluta	Paenibacillus_mucilaginosus_K02	Firmicutes	55%
473	JX012519	meta_3_contig00002_1	Paenibacillus_mucilaginosus_K03	Firmicutes	56%
474	JX012470	meta_2_contig00017_1	Nostoc punctiforme PCC 73102 CG.	Cyanobacteria	61%
475	JX012475	meta_2_contig00014_1	Myxococcus_fulvus_HW-1 CCG	Deltaproteobacteria	63%
476	AAW84170	spFKS32i_D_dissoluta	Cyanothece sp. ATCC 51142 chromosome circular CS	Cyanobacteria	71%
477	ADY17941	PseudovibHs3_H_simulans	Pseudomonas syringae pv. syringae B728a CG	Gammaproteobacteria	69%
478	ADY17931	Pseudovibrio_Ad23_A_dissimilis	Pseudomonas syringae pv. syringae B728a CG.	Gammaproteobacteria	69%
479	ADY17939	PseudovibAd48_A_dissimilis	Pseudomonas fluorescens Pf0-1 CCG.	Gammaproteobacteria	68%
480	ACI32873	FAS_Pseudovibrio_H_simulans	Pseudomonas syringae pv. syringae B728a CG.	Gammaproteobacteria	68%
481	ADY17933	Pseudovibrio_Ad28_A_dissimilis	Pseudomonas syringae pv. syringae B728a CG.	Gammaproteobacteria	68%
482	ACI32872	FAS_Pseudovibrio_H_simulans	Pseudomonas fluorescens Pf0-1 CCG	Gammaproteobacteria	67%
483	ADY17926	Pseudovibrio_Ad8_A_dissimilis	Pseudomonas fluorescens Pf0-1 CCG.	Gammaproteobacteria	68%
484	ACI32871	FAS_Pseudovibrio_H_simulans	Pseudomonas fluorescens Pf0-1 CCG.	Gammaproteobacteria	68%
485	ADY17937	Pseudovibrio_Ad35_A_dissimilis	Pseudomonas fluorescens Pf0-1 CCG.	Gammaproteobacteria	67%
486	ABG57048	Pseudoalteromonas_H_perleve	Delftia_sp._Cs1-4 CCG	Betaproteobacteria	63%
487	ABK01395	C_mycofijiensis_cmKSH79	Paenibacillus mucilaginosus K02 CCG	Firmicutes	60%
488	ABK01393	C_mycofijiensis_cmKSH23	Myxococcus_fulvus_HW-1 CCG	Deltaproteobacteria	60%

489	ZP_02371233	**TaiKS5**	Burkholderia_thailandensis_E264	Betaproteobacteria	100%
490	AAV97877	**OnnKS5**	Paenibacillus_polymyxa_E681	Firmicutes	68%
			Outgroup		
491	BAI44079	Streptomyces_H_simulans	Streptomyces_scabiei_87.22 CCG	Actinobacteria	85%
492	BAI44075	Streptomyces_H_simulans	Streptomyces_scabiei_87.22 CCG	Actinobacteria	85%
493	BAI44077	Streptomyces_H_simulans	Streptomyces_scabiei_87.22 CCG	Actinobacteria	86%
494	ABP57802	Streptomyces_dendra	Streptomyces_hygroscopicus_subsp._jinggangensis	Actinobacteria	84%
495	BAI44069	Streptomyces_H_simulans	treptomyces_hygroscopicus_subsp._jinggangensis	Actinobacteria	91%
496	BAI44072	Streptomyces_H_simulans	Streptomyces_flavogriseus_ATCC_33331	Actinobacteria	72%
497	BAI44071	Streptomyces_H_simulans	Streptomyces_flavogriseus_ATCC_33331	Actinobacteria	85%
498	ACG50689	Streptomyces_sp_PKSII	Streptomyces_sp._SirexAA-E CCG	Actinobacteria	65%
499	ABQ42685	typeII_Streptomyces13_42_Iotrochota	Streptomyces_sp._SirexAA-E CCG	Actinobacteria	77%
500	BAI44073	Streptomyces_H_simulans	Streptomyces sp. SirexAA-E CCG	Actinobacteria	75%
501	ACV31767	Streptomyces_sp._MAD01	Streptomyces sp. SirexAA-E CCG	Actinobacteria	72%
502	NP_629237	ActI_ORF1_Streptomyces	Streptomyces_coelicolor_A3 CCG	Actinobacteria	99%
503	ABO33015	typeII_ks_Micromonospora_H_simulans	Streptosporangium_roseum_DSM_43021	Actinobacteria	75%
504	BAI44070	Streptomyces_H_simulans	Streptomyces sp. SirexAA-E CCG	Actinobacteria	78%
505	BAI44076	Streptomyces_H_simulans	Salinispora tropica CNB-440 CCG.	Actinobacteria	71%
506	BAI44078	Streptomyces_H_simulans	Saccharomonospora viridis DSM 43017 CCG.	Actinobacteria	72%
507	BAI44074	Streptomyces_H_simulans	Saccharomonospora viridis DSM 43017 CCG.	Actinobacteria	71%
508	**JX945643**	**contig00144_6_KSRegion_(KSA)_468aa**	**Aromatoleum_aromaticum_EbN1 CCG**	**Betaproteobacteria**	**63%**