

IMG ID	GenBank Accession	Taxon ID	infB	lepA	pheS	rplB	rplC	rplD	rplE	rplF	rplK	rplN	rplO	rplP	rpsB	rpsC	rpsE	rpsG	rpsH	rpsI	rpsJ	rpsK	rpsL	rpsM	rpsQ	rpsS	16S rRNA
		<i>Candidatus Synicohabitus palmerolidicus</i>	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
647533243	GCA_000155695	<i>Verrucomicrobiales</i> sp. DG1235	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
2228664034	GCA_000383755	<i>Verrucomicrobia</i> bacterium SCGC AAA300-N18 (unscreened)	+	+	-	+	+	+	-	-	+	-	+	-	+	+	-	+	+	-	+	-	+	-	+	+	+
2228664038	GCA_000385315	<i>Verrucomicrobia</i> bacterium SCGC AAA164-P11 (unscreened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2228664042	GCA_000385235	<i>Verrucomicrobia</i> bacterium SCGC AAA164-A08 (unscreened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2228664043	GCA_000385255	<i>Verrucomicrobia</i> bacterium SCGC AAA164-B23 (unscreened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2228664044	GCA_000385275	<i>Verrucomicrobia</i> bacterium SCGC AAA164-I21 (unscreened)	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
2228664050	GCA_000383735	<i>Verrucomicrobia</i> bacterium SCGC AAA164-M04 (unscreened)	-	-	-	-	-	-	-	-	+	-	+	-	+	+	+	+	+	+	+	+	+	+	+	+	-
2228664051	GCA_000385295	<i>Verrucomicrobia</i> bacterium SCGC AAA164-N20 (unscreened)	-	-	-	+	+	+	+	+	-	+	+	+	-	+	+	+	+	-	+	+	+	+	+	+	+
2236347002	GCA_000383715	<i>Verrucomicrobia</i> bacterium SCGC AAA164-E04 (unscreened)	+	-	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+
2236347003	GCA_000264625	<i>Verrucomicrobia</i> bacterium SCGC AAA168-E21	+	-	+	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2236347021	GCA_000264645	<i>Verrucomicrobia</i> bacterium SCGC AAA168-F10	+	-	+	+	+	+	+	+	+	-	+	+	-	+	-	+	-	-	+	+	+	+	+	+	+
2236661017	GCA_000382665	<i>Verrucomicrobia</i> bacterium SCGC AAA300-K03 (unscreened)	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
2236661018	GCA_000382685	<i>Verrucomicrobia</i> bacterium SCGC AAA300-O17 (unscreened)	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-
2517572138	GCA_000264585	<i>Verrucomicrobia</i> bacterium SCGC AAA164-A21 (unscreened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2517572141	GCA_000264625	<i>Verrucomicrobia</i> bacterium SCGC AAA168-E21 (unscreened)	+	-	+	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2517572140	GCA_000264605	<i>Verrucomicrobia</i> bacterium SCGC AAA164-O14 (unscreened)	-	+	+	+	+	+	+	+	-	+	-	+	+	+	+	+	+	-	+	-	+	-	+	+	+
2517572142		<i>Verrucomicrobia</i> bacterium SCGC AAA168-F10 (unscreened)	+	-	+	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2616645036		<i>D. pulchra</i> bleached metagenome bin377	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
2634166657		<i>Verrucomicrobia</i> bacterium SCGC AC-661-N10 (unscreened)	-	+	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2634166686		<i>Verrucomicrobia</i> bacterium SCGC AD-105-D22 (unscreened)	-	-	+	+	-	-	+	+	-	+	+	+	-	+	+	-	+	-	-	+	-	+	+	+	+
2634166709		<i>Verrucomicrobia</i> bacterium SCGC AD-265-E10 (unscreened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2634166715		<i>Verrucomicrobia</i> bacterium SCGC AAA240-M19 (unscreened)	+	+	+	+	-	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
2634166718		<i>Verrucomicrobia</i> bacterium SCGC AAA242-O13 (unscreened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2634166725		<i>Verrucomicrobia</i> bacterium SCGC AB-606-A23 (unscreened)	-	-	-	+	+	+	+	+	-	+	+	+	-	+	-	+	+	+	+	+	+	+	+	+	+
2634166742		<i>Verrucomicrobia</i> bacterium SCGC AB-661-L11 (unscreened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2634166743		<i>Verrucomicrobia</i> bacterium SCGC AB-661-P22 (unscreened)	-	-	-	-	-	-	-	-	+	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	+
2634166791		<i>Verrucomicrobia</i> bacterium SCGC AC-312-P03 (unscreened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2651870083		unclassified <i>Verrucomicrobiales</i> Bin 11	+	+	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	+	-	+	-	+	-	-	+
2651870084		unclassified <i>Verrucomicrobiales</i> Bin 46	-	-	-	-	-	-	-	-	+	-	-	-	+	-	-	-	-	+	-	+	-	+	-	-	-
2651870085		unclassified <i>Verrucomicrobiales</i> Bin 30	-	-	-	-	-	-	+	+	-	+	-	-	-	+	+	+	+	-	-	+	+	+	-	-	-
2651870086		unclassified <i>Verrucomicrobiales</i> Bin 34	+	-	-	-	-	+	+	-	+	+	+	+	+	+	+	+	+	-	-	+	+	+	+	+	-
2651870087		unclassified <i>Verrucomicrobiales</i> Bin 65	-	-	-	+	-	-	-	-	-	+	-	+	-	+	-	-	-	-	-	-	-	-	-	+	+
2657245246		<i>Verrucomicrobia</i> bacterium SCGC AC-312_D05v2 (unscreened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2657245247		<i>Verrucomicrobia</i> bacterium SCGC AC-312_D05v2 (contamination screened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2657245291		<i>Verrucomicrobia</i> bacterium SCGC AC-337_K21 - v2 (unscreened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2657245292		<i>Verrucomicrobia</i> bacterium SCGC AC-337_K21 - v2 (contamination screened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2657245323		<i>Verrucomicrobia</i> bacterium SCGC AC-312_O22 - v2 (unscreened)	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2657245324		<i>Verrucomicrobia</i> bacterium SCGC AC-312_O22 - v2 (contamination screened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2663762693		<i>Verrucomicrobia</i> bacterium SCGC AC-312_N19v2 (unscreened)	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2684622978		<i>Verrucomicrobia</i> bacterium SCGC AG-542-N08	-	-	+	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	+
2684622991		<i>Verrucomicrobia</i> bacterium SCGC AG-542-I16	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2693429924		<i>Verrucomicrobia</i> bacterium SCGC AC-337_A14 - v2 (unscreened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2693429925		<i>Verrucomicrobia</i> bacterium SCGC AC-337_A14 - v2 (contamination screened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2693429980		<i>Verrucomicrobia</i> bacterium SCGC AC-337_J20 - v2 (unscreened)	-	-	-	-	-	-	-	-	+	-	+	-	-	+	-	+	-	-	+	-	+	-	+	-	-
2693429981		<i>Verrucomicrobia</i> bacterium SCGC AC-337_J20 - v2 (contamination screened)	-	-	-	-	-	-	-	-	+	-	+	-	-	+	-	+	-	-	+	-	+	-	+	-	-
2695420979		unclassified <i>Verrucomicrobiales</i> bin 1	-	-	+	+	+	+	+	+	-	-	+	-	+	-	+	+	+	+	+	+	-	-	-	-	-
2695420980		unclassified <i>Verrucomicrobiales</i> bin 2	-	-	-	+	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	+

IMG ID	GenBank Accession	Taxon ID	infB	lepA	pheS	rplB	rplC	rplD	rplE	rplF	rplK	rplN	rplO	rplP	rpsB	rpsC	rpsE	rpsG	rpsH	rpsI	rpsJ	rpsK	rpsL	rpsM	rpsQ	rpsS	16S rRNA
2700988675		Verrucomicrobia bacterium SCGC AC-337_A09v3 (contamination screened)	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2731639125		Verrucomicrobia bacterium SCGC AG-485_L14 (contamination screened)	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2731639127		Verrucomicrobia bacterium SCGC AG-485_G21 (contamination screened)	-	-	-	+	+	+	+	-	+	+	+	+	-	+	+	+	+	-	+	+	+	+	+	+	+
2731639129		Verrucomicrobia bacterium SCGC AG-487_A21 (contamination screened)	-	-	+	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	+
2731639131		Verrucomicrobia bacterium SCGC AG-487_G17 (contamination screened)	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
2739367775		Verrucomicrobiales bacterium JGI_01_E13 (contamination screened)	-	+	-	+	+	+	-	-	+	-	-	-	-	-	-	-	+	-	-	+	-	-	-	+	-
2786546549	GCA_002726435	Opiritae bacterium NP78	-	-	+	+	+	+	+	+	-	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-
2786546550	GCA_002716045	Opiritae bacterium SP85	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-
2786546551	GCA_002722545	Opiritae bacterium SP216	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-
2786546552	GCA_002721705	Opiritae bacterium SP241	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
2786546553	GCA_002713685	Opiritae bacterium SAT156	+	+	-	+	+	+	+	+	-	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+
2786546554	GCA_002730975	Opiritae bacterium NP117	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-
2786546555	GCA_002695645	Opiritae bacterium EAC647	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	-	+	+	+	+	+	+	-
2786546556	GCA_002686835	Opiritae bacterium ARS76	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-
2786546557	GCA_002689665	Opiritae bacterium ARS1007	-	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-
2786546558	GCA_002692605	Opiritae bacterium IN42	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-
2786546559	GCA_002702485	Opiritae bacterium NAT243	-	-	-	+	+	+	+	+	+	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+	-
2786546560	GCA_002694035	Opiritae bacterium IN48	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-
2786546561	GCA_002692535	Opiritae bacterium IN921	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	-
2786546708	GCA_002725655	Opiritales bacterium NP990	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	-	+	+	+	+	+	+	-
2786546709	GCA_002724235	Opiritales bacterium RS400	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2786546710	GCA_002720915	Opiritales bacterium SP2995	+	+	+	+	+	-	-	-	-	-	-	+	+	+	-	-	-	+	-	-	-	-	-	-	-
2786546935	GCA_002713695	Opiritaceae bacterium SAT155	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
2786546936	GCA_002694885	Opiritaceae bacterium EAC85	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
2786546938	GCA_002722675	Opiritaceae bacterium SP211	+	+	-	+	+	+	+	+	-	+	+	+	-	+	+	+	+	+	+	-	+	+	-	+	+
2786546939	GCA_002717045	Opiritaceae bacterium SP4023	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+
	GCA_002591725	Candidatus Didemnitatus mandela	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+
	GCA_003525105	Opiritae bacterium UBA10075	+	-	+	+	+	-	-	-	-	-	-	+	+	-	+	-	-	+	+	+	+	+	+	+	-
	GCA_003482665	Opiritaceae bacterium UBA8745	+	-	-	+	+	+	+	+	-	+	-	+	-	+	-	+	-	+	+	+	+	+	+	+	-
	GCA_002420265	Opiritales bacterium UBA5691	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	+	+	+	+	-	+	+	+	+	-
	GCA_002420185	Opiritales bacterium UBA5694	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-
	GCA_002450395	Opiritales bacterium UBA6958	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_002474325	Opiritales bacterium UBA7389	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-
	GCA_002367815	Opiritaceae bacterium UBA3033	+	-	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-
	GCA_002471335	Opiritaceae bacterium UBA7327	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-
	GCA_000019965	Opiritus terrae PB90-1	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_000025905	Caraliomargarita akajimensis DSM 45221	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_000171235	Geminisphaera coliterminum TAV2	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_000172555	Pedosphaera parvula Ellin514	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_000173075	Chthoniobacter flavus Ellin428	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_000378105	Rubritalea marina DSM 17716	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_000972765	Verrucomicrobia bacterium IMCC26134	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_001017655	Kiritimiella glycovarans L21-Fru-AB	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_001438005	Verrucomicrobia BAEL9 MAG-120507-bin52	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_001580015	Cephalotococcus primus CAG34	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_001650175	Opiritaceae bacterium TSB47	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_001746835	Lacunisphaera limnophila IG16b	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_000020225	Akkermansia muciniphila ATCC BAA-835	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_000172155	Verrucomicrobium spinosum DSM 4136	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_000526255	Verrucomicrobium sp. LP2A	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_000953475	Methylacidiphilum fumarolicum SolV	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
2786546940	GCA_003054665	Albicoccus flocculans EW11	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	-	+
	GCA_002455175	Opiritaceae bacterium UBA6669	-	+	+	-	-	-	-	+	+	+	+	+	-	+	-	-	+	+	-	+	-	+	-	-	-
	GCA_002344205	Opiritaceae bacterium UBA2377	-	+	+	+	+	+	+	+	+	+	+	+	-	+	-	+	+	+	+	+	+	+	+	-	+

IMG ID	GenBank Accession	Taxon ID	infB	lepA	pheS	rplB	rplC	rplD	rplE	rplF	rplK	rplN	rplO	rplP	rpsB	rpsC	rpsE	rpsG	rpsH	rpsI	rpsJ	rpsK	rpsL	rpsM	rpsQ	rpsS	16S rRNA
	GCA_003142615	Fen-1467 sp003142615	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+
	GCA_002310495	<i>Nibricoccus aquaticus</i>	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+
	GCA_003096195	<i>Ereboglobus luteus</i> Ho45	-	+	+	+	+	-	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	-	+	+
	GCA_003641745	B12-G4 sp003641745	-	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+
	GCA_002382525	IMCC26134 sp002382525	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+
	GCA_003694825	J108 sp003694825	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-
	GCA_003402695	Opi-474 sp003402695	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	-	+	-
	GCA_003151515	Palsa-1447 sp003151515	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+
	GCA_002304445	Tous-C4FEB sp002304445	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+	+	+	+	-	+	-	+	-
	JAABVE000000000	<i>Petrosia ficiformis</i> - associated bin0 (227c)	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+
	JAABVD000000000	<i>Petrosia ficiformis</i> - associated bin01 (287ce)	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+
	GCA_014529625.1	Strain F3	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+
	GCA_014529675.1	Strain E3	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
	GCA_014529665.1	Strain A3	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+