Table S3 *Information for the metagenomic analysis of* R. odorabile *clones*

Sample	WT-a	WT-b	WT-c	T27-Day4-a	T27-Day4-b	T27-Day4-c	T32-Day3-c	T32-Day4-a	T32-Day4-b	T32-Day4-c
Trace file	BBAY34	BBAY35	BBAY36	BBAY49	BBAY50	BBAY51	BBAY52	BBAY53	BBAY54	BBAY55
Raw read	949133	583576	519285	742998	695928	627630	537954	403759	660167	453805
Average read size (nt)	402.0	377.3	401.6	423.4	428.2	343.5	316.1	311	391	368.1
Unique read	904146	505357	506761	716090	639263	606860	507711	399034	635356	388317
16S rRNA gene containing reads	298 (0.03%)	198 (0.04%)	201 (0.04%)	315 (0.04%)	267 (0.04%)	195 (0.03%)	496 (0.10%)	984 (0.25%)	270 (0.04%)	171 (0.04%)
Constructed 16S Seqs	40	36	34	39	32	31	45	31	41	39
Reads in 16S Seqs	209	149	139	243	210	151	297	776	175	112
Min length of 16S Seqs (nt)	781	781	781	839	934	839	747	747	839	747
Max length of 16S Seqs (nt)	1542	1542	1542	1542	1542	1542	1542	1542	1542	1542
Avg length of 16S Seqs (nt)	1417	1405	1406	1403	1435	1418	1376	1350	1397	1366
Aligned read	460513 (50.9%)	198840 (39.4%)	180893 (35.7%)	397269 (55.5%)	334502 (52.3%)	270894 (44.6%)	67199 (13.2%)	225756 (56.6%)	235761 (37.1%)	81113 (20.9%)
Contig > 500 nt	44408	17286	19306	35262	34102	16733	6420	3796	28674	10205
Average size of contig > 500	902	900	836	1002	894	1092	743	2441	784	687

nt (nt)										
N50 size of contig > 500 nt (nt)	909	909	838	1018	895	1178	724	5055	776	664
Maximum size of contig > 500 nt (nt)	52481	16414	16419	52143	18553	17003	6062	89781	5441	3749
Contig > 100 nt	71479	29504	32819	54685	55119	28502	11648	5262	46143	18175
Singleton /outlier > 100 nt	416488	284341	296611	306056	291996	317341	407146	153752	382667	282041
Non-eukaryotic contig and singleton/outlier	486090 (99.6%)	310735 (99%)	326136 (99%)	359921 (99.8%)	346460 (99.8%)	345197 (99.8%)	417634 (99.7%)	158279 (99.5%)	428032 (99.8%)	299667 (99.8%)
Unique predicted protein	597098	367768	394503	450176	433069	401283	475263	186518	518234	356540
Total protein	828348	457510	480812	645157	609660	515151	505473	254007	636935	396781
Protein annotated by COG ($E<10^{-10}$)	230428 (27.8%)	120728 (26.4%)	123659 (25.7%)	204875 (31.8%)	181301 (29.7%)	134597 (26.1%)	104924 (20.8%)	89516 (35.2%)	175661 (27.6%)	100811 (25.4%)
Protein annotated by Pfam ($E<10^{-10}$)	219205 (26.5%)	115740 (25.3%)	118378 (24.6%)	194148 (30.1%)	173218 (28.4%)	126218 (24.5%)	25965 (5.1%)	85497 (33.7%)	162726 (25.5%)	92386 (23.3%)
Protein annotated by SEED ($E<10^{-10}$)	338201 (40.8%)	180828 (39.5%)	187208 (38.9%)	290960 (45.1%)	266252 (43.7%)	199504 (38.7%)	171954 (34%)	129579 (51%)	255930 (40.2%)	151296 (38.1%)

---

* WT, wild-type.