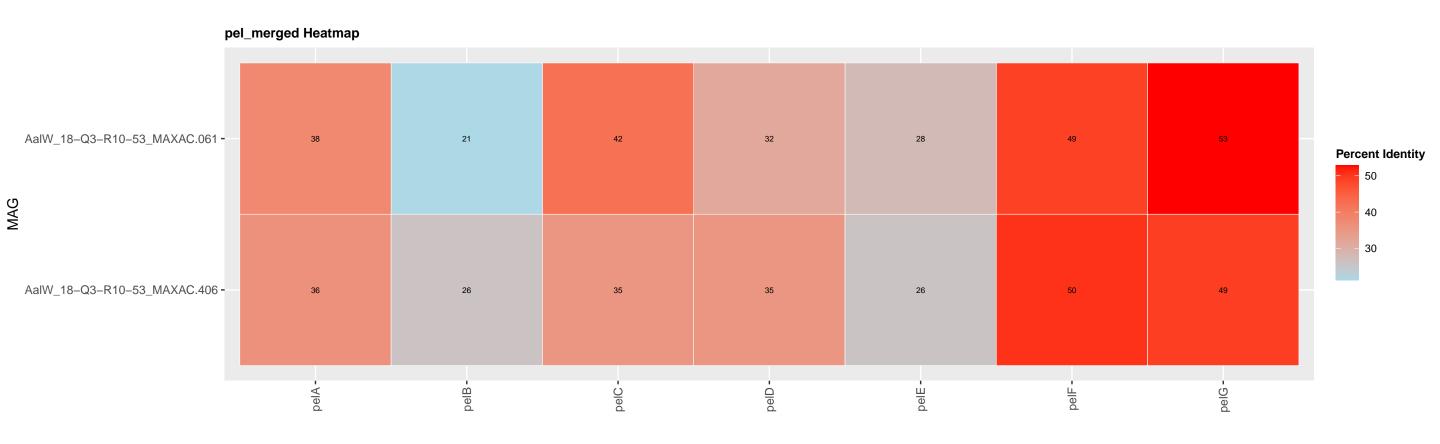


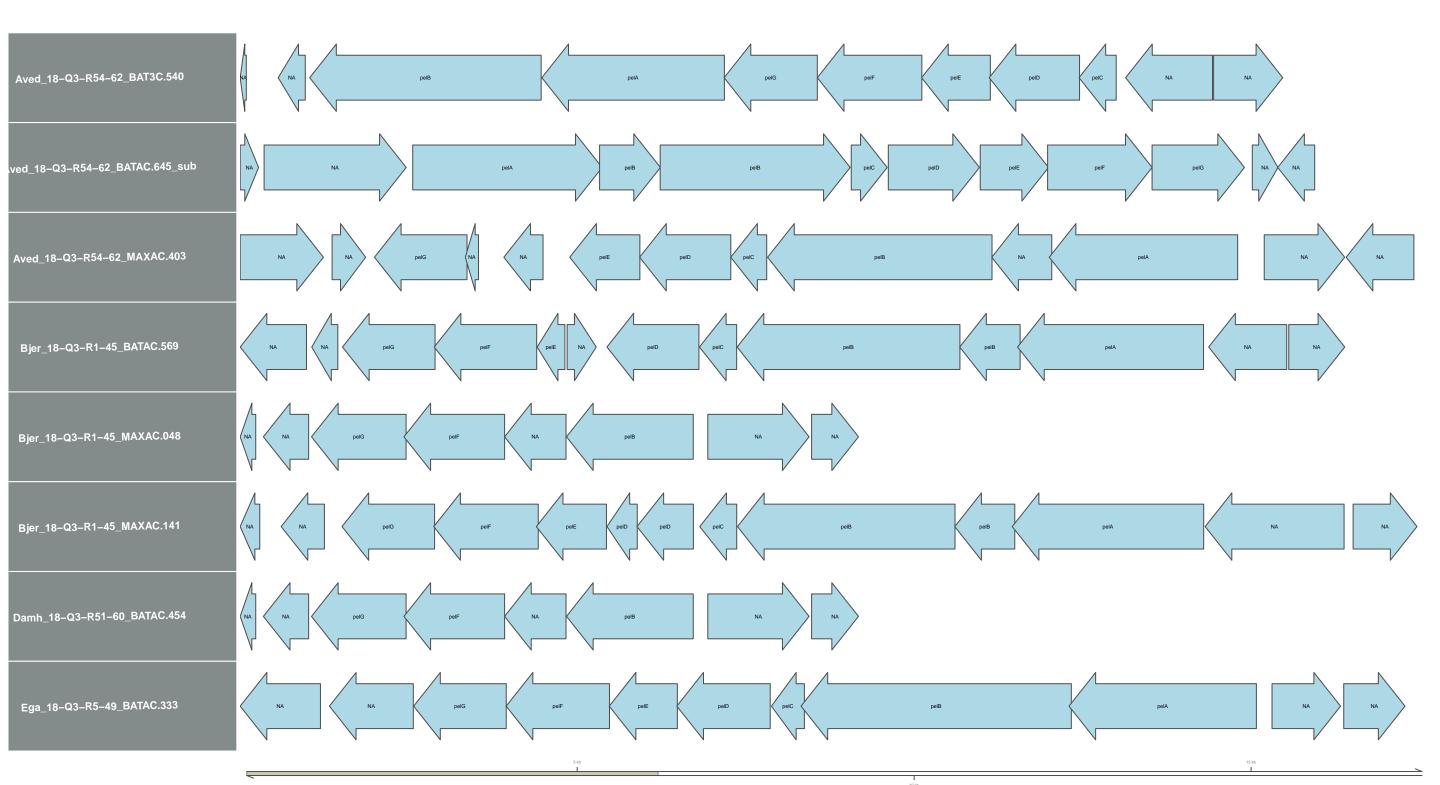
pel_merged Heatmap Hjor_18-Q3-R7-51_BATAC.292 -Hjor_18-Q3-R7-51_MAXAC.072 -Kalu_18-Q3-R12-55_BAT3C.357 -Kalu_18-Q3-R12-55_BATAC.288 -Lyne_18-Q3-R50-59_BAT3C.546 -Lyne_18-Q3-R50-59_BATAC.526 -Lyne_18-Q3-R50-59_MAXAC.018 -MAG Lyne_18-Q3-R50-59_MAXAC.409 -Mari_18-Q3-R65-66_MAXAC.196 -OdNE_18-Q3-R46-58_MAXAC.062_sub -Vibo_18-Q3-R45-57_BAT3C.142 -Vibo_18-Q3-R45-57_BATAC.19 -Viby_18-Q3-R106-67_MAXAC.046 -AalE_18-Q3-R2-46_BAT3C.116 -AalE_18-Q3-R2-46_BAT3C.211 -pelG-

pelD

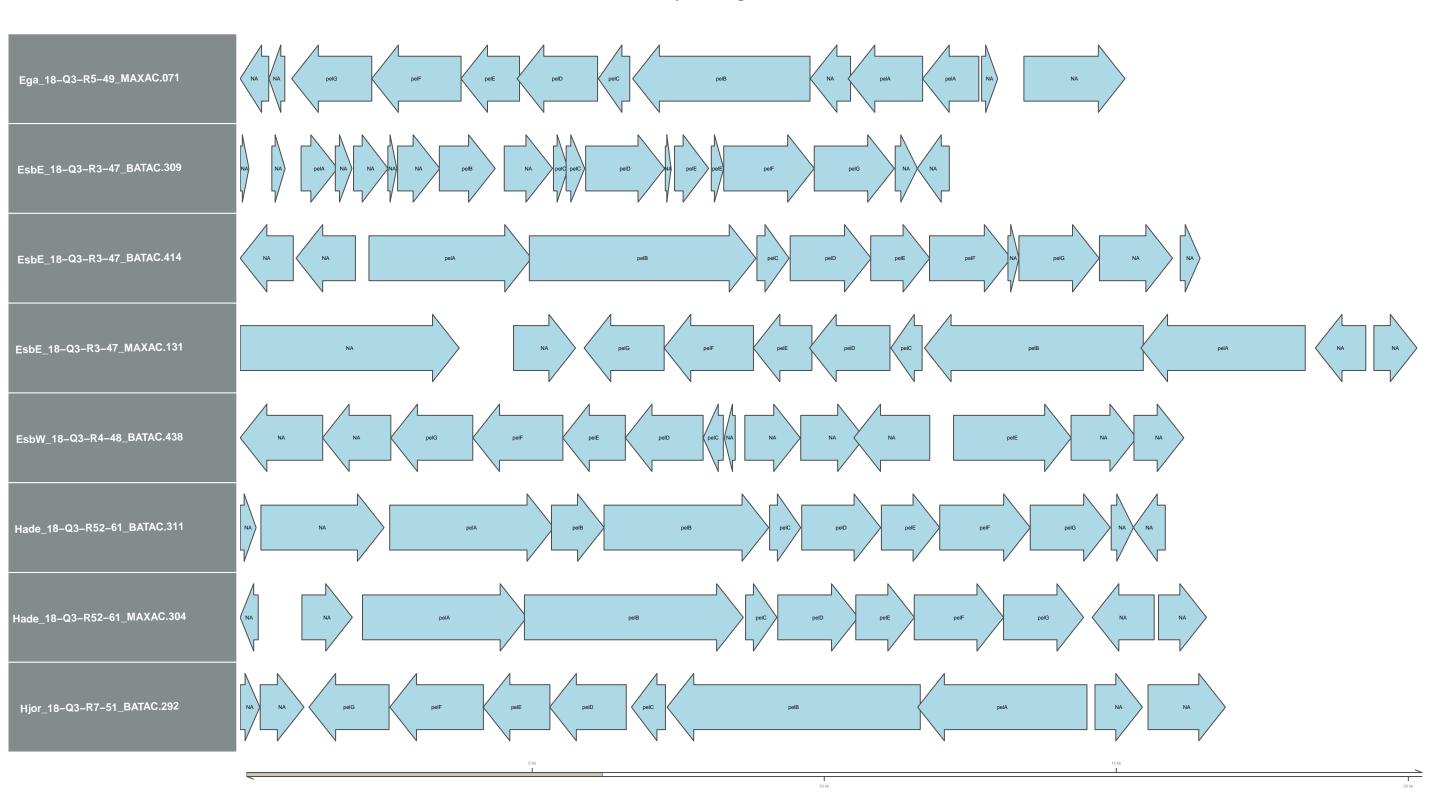
Percent Identity

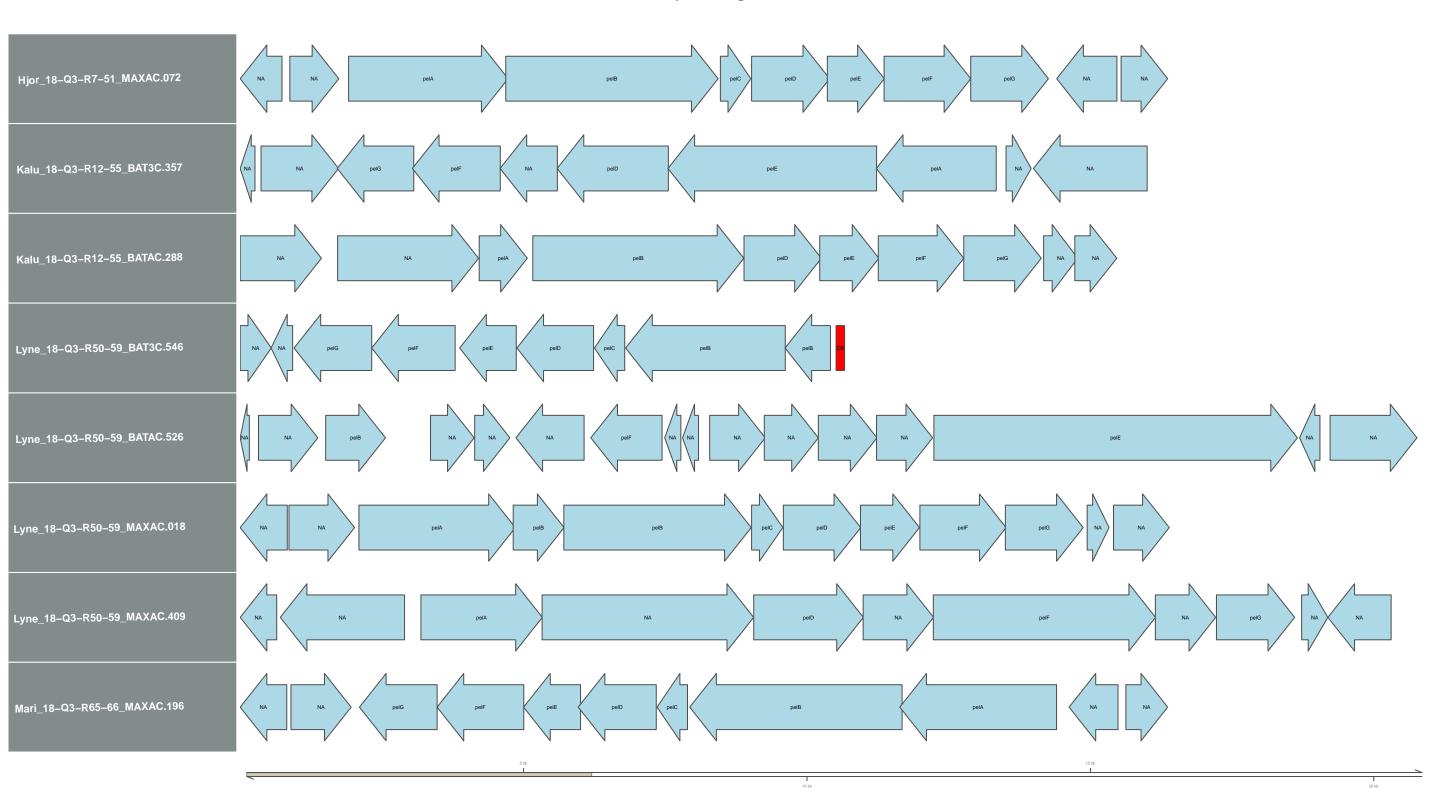


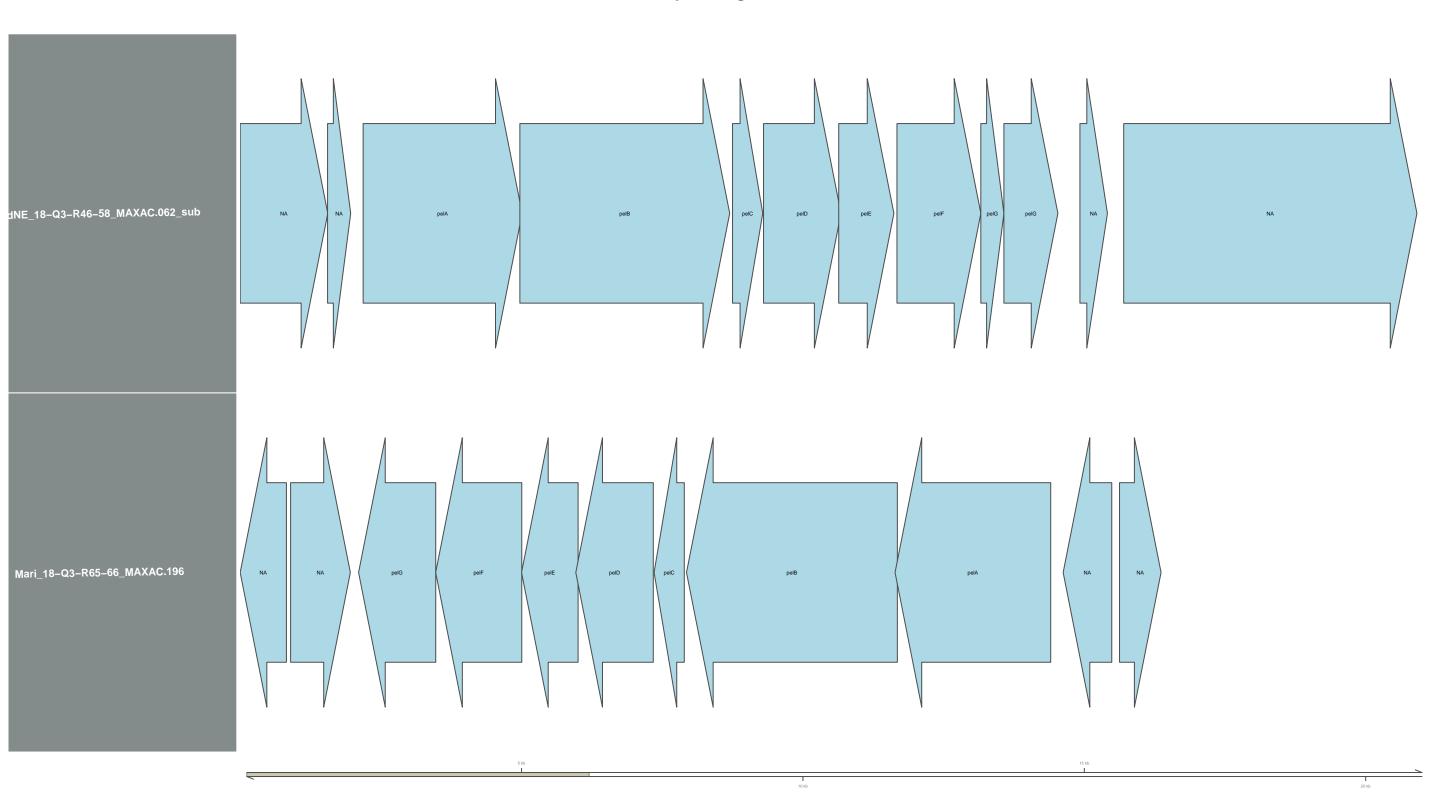
pel_merged



pel_merged







	ID	GTDBTax	seqname	start	Query_label	ProkkaNO
1	Aved_18-Q3-R54-62_BAT3C.540	d_Bacteria;p_Myxococcota;c_UBA727;o_;f_;g_;s_	tig00000023-10-69002250	5051495	pelA	04194
2	2 Aved_18-Q3-R54-62_BATAC.645_sub	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Agitococcus;s_Agitococcus sp002333125	tig00027713-10-400140	7242	pelA	00834
3	B Aved_18-Q3-R54-62_MAXAC.403	${\tt d_Bacteria_p_Proteobacteria_c_Gamma proteobacteria_vo_Burkholderiales_f_Rhodocyclaceae_g__s_$	tig00005102-1973220-6987030	319633	pelA	00550
4	Bjer_18-Q3-R1-45_BATAC.569	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Rhodoferax;s_	tig00858586-10-1255560	55278	pelA	03894
5	5 Bjer_18-Q3-R1-45_MAXAC.048	d_Bacteria;p_Myxococcota;c_Polyangia;o_Haliangiales;f_Haliangiaceae;g_UBA2376;s_	tig00001110-10-1759710	41481	pelB	02226
6	Bjer_18-Q3-R1-45_MAXAC.141	$\label{eq:d_Bacteria} d_Bacteria,p_Proteobacteria,c_Gammaproteobacteria,o_Burkholderiales,f_Burkholderiaceae;g_Rhodoferax;s_leadings. The proteobacteria and the proteobacter$	tig00002058-10-6971940	422657	pelA	01018
7	7 Damh_18-Q3-R51-60_BATAC.454	d_Bacteria;p_Myxococcota;c_Polyangia;o_Haliangiales;f_Haliangiaceae;g_UBA2376;s_	tig00001452-10-3594700	293357	pelB	05351
٤	B Ega_18-Q3-R5-49_BATAC.333	$lem:d_Bacteria:p_Proteobacteria:c_Gammaproteobacteria:o_Burkholderiales:f_Burkholderiaceae:g_Rhodolerax:s_defined and the second of t$	tig00192084-10-15636590	420067	pelA	03018
S	Ega_18-Q3-R5-49_MAXAC.071	$\label{lem:decomposition} \mbox{d_Bacteria$,p$_Proteobacteria$,c$_Gammaproteobacteria$,o$_Burkholderiales$,f$_Rhodocyclaceae$,g$_Propionivibrio$,s$_Propionivibrio$,alborgensis$. \label{lem:decomposition}$	tig00003455-10-2480190	13873	pelA	00609
10	EsbE_18-Q3-R3-47_BATAC.309	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Agitococcus;s_Agitococcus sp002333125	tig00682613-10-1292800	13041	pelA	03089
11	EsbE_18-Q3-R3-47_BATAC.414	$lem:d_Bacteria:p_Proteobacteria:c_Gammaproteobacteria:o_Burkholderiales:f_Burkholderiaceae:g_Rhodoferax:s_defined and the second of t$	tig00174989-10-5817180	167615	pelA	03363
12	EsbE_18-Q3-R3-47_MAXAC.131	$\label{lem:d_Bacteria} {\tt d_Bacteria}, {\tt p-Proteobacteria}, {\tt c_Gammaproteobacteria}, {\tt o_Burkholderiales}, {\tt l-Rhodocyclaceae}, {\tt g-Propionivibrio}, {\tt o_Burkholderiales}, {\tt $	tig00001009-10-6140660	210953	pelA	01209
13	B EsbW_18-Q3-R4-48_BATAC.438	d_Bacteria:p_Myxococcota;c_Polyangia;o_Polyangiales;f_;g_;s_	tig00003322-10-6252770	340879	pelC	02090
14	Hade_18-Q3-R52-61_BATAC.311	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Agitococcus;s_Agitococcus sp002333125	tig00409209-10-2044890	2846	pelA	02274
15	5 Hade_18-Q3-R52-61_MAXAC.304	$\label{lem:d_Bacteria} d_Bacteria$,$p$_Proteobacteria$,c_Gammaproteobacteria$,$o$_Burkholderiales$,f_Rhodocyclaceae$,$g$_Propionivibrio$,g_Propionivibrio$,$g$_Propionivibrio$,g_Propionivib$	tig00406327-10-1992640	26284	pelA	01343
16	6 Hjor_18-Q3-R7-51_BATAC.292	$eq:d_Bacteria:p_Proteobacteria:c_Gammaproteobacteria:o_Burkholderiales:f_Burkholderiaceae;g_;s_$	tig00006524-54670-1205970	102133	pelA	01864
17	7 Hjor_18-Q3-R7-51_MAXAC.072	$\label{lem:d_Bacteria} d_Bacteria$,$p$_Proteobacteria$,c_Gammaproteobacteria$,$o$_Burkholderiales$,f_Rhodocyclaceae$,$g$_Propionivibrio$,g_Propionivibrio$,$g$_Propionivibrio$,g_Propionivib$	tig00006634-10-1438320	32747	pelA	01695
18	3 Kalu_18-Q3-R12-55_BAT3C.357	d_Bacteria;p_Planctomycetota;c_UBA1135;o_UBA2386;f_UBA2386;g_;s_	tig00001024-10-13310640	419124	pelA	02447
19	Kalu_18-Q3-R12-55_BATAC.288	$\label{lem:d_bacteria} $$d_Bacteria,p_Proteobacteria,c_Gammaproteobacteria,o_Pseudomonadales,f_Oleiphilaceae,gs_$$$	tig00002468-10-5122030	448739	pelA	02010
20	Lyne_18-Q3-R50-59_BAT3C.546	$\label{local-protocollection} \begin{tabular}{ll} d_Bacteria:p_Proteobacteria:c_Gammaproteobacteria:o_Pseudomonadales:f_Moraxellaceae:g_Agitococcus:s_Agitococcus sp002333125 \end{tabular}$	tig00324356-10-795350	78716	pelB	02877
21	Lyne_18-Q3-R50-59_BATAC.526	d_Bacteria;p_Krumholzibacteriota;c_Krumholzibacteria;o_LZORAL124-64-63;f_LZORAL124-64-63;g_;s_	tig00003255-10-6223550	129643	pelB	00690
22	Lyne_18-Q3-R50-59_MAXAC.018	$\label{lem:def} $$d_Bacteria:p_Proteobacteria:c_Gammaproteobacteria:o_Burkholderiales:f_Burkholderiaceae:g_Rhodoferax:s_f_Burkholderiaceae:g$	tig00321120-10-8711220	279900	pelA	03230
23	B Lyne_18-Q3-R50-59_MAXAC.409	d_Bacteria;p_Planctomycetota;c_UBA1135;o_;f_;g_;s_	tig00000050-10-70511450	3564857	pelA	02706
24	Mari_18-Q3-R65-66_MAXAC.196	${\tt d_Bacteria; p_Proteobacteria; c_Gamma proteobacteria; o_Burkholderiales; f_Rhodocyclaceae; g_Propionivibrio; s_results for the propionity of the propio$	tig00010843-10-947990	13613	pelA	01211
25	OdNE_18-Q3-R46-58_MAXAC.062_sub	$\label{thm:continuous} $$d_Bacteria,p_Proteobacteria;c_Gammaproteobacteria,o_Burkholderiales,f_Rhodocyclaceae;g_Propionivibrio;s_Propionivibrio aalborgensis$	tig00228155-10-4339090	339429	pelA	02068
26	Vibo_18-Q3-R45-57_BAT3C.142	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Agitococcus;s_Agitococcus sp002333125	tig00004470-10-1735850	100416	pelA	00907
27	7 Vibo_18-Q3-R45-57_BATAC.19	${\tt d_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Burkholderiales; f_Rhodocyclaceae; g_Propionivibrio; s_results for the propionity of the propion$	tig00004818-10-1680160	39736	pelA	01458
28	3 Viby_18-Q3-R106-67_MAXAC.046	$lem:d_Bacteria:p_Proteobacteria:c_Gammaproteobacteria:o_Burkholderiales:f_Burkholderiaceae:g_Rhodolerax:s_defined and the second of t$	tig00000252-10-9187680	165856	pelA	00179
29	AalE_18-Q3-R2-46_BAT3C.116	$lem:d_Bacteria:p_Proteobacteria:c_Gammaproteobacteria:o_Burkholderiales:f_Burkholderiaceae:g_Rhodoferax:s_defined and the second of t$	tig00000745-10-10299200	67953	pelA	01326
30	AalE_18-Q3-R2-46_BAT3C.211	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Rhodocyclaceae;g_Dechloromonas;s_	tig00000166-10-3784970	217739	pelA	00228
31	AalW_18-Q3-R10-53_MAXAC.061	$lem:d_Bacteria:p_Proteobacteria:c_Gammaproteobacteria:o_Burkholderiales:f_Burkholderiaceae:g_Rhodoferax:s_defined and the second of t$	tig00404314-10-12352360	415816	pelA	03233
32	2 AaIW_18-Q3-R10-53_MAXAC.406	$\label{eq:d_Bacteria} $$d_Bacteria, p_Proteobacteria, c_Gamma proteobacteria, o_Burkholderiales, f_Rhodocyclaceae, g_, s_, and the substitution of the substitution $	tig00038307-10-634890	17882	pelA	03241