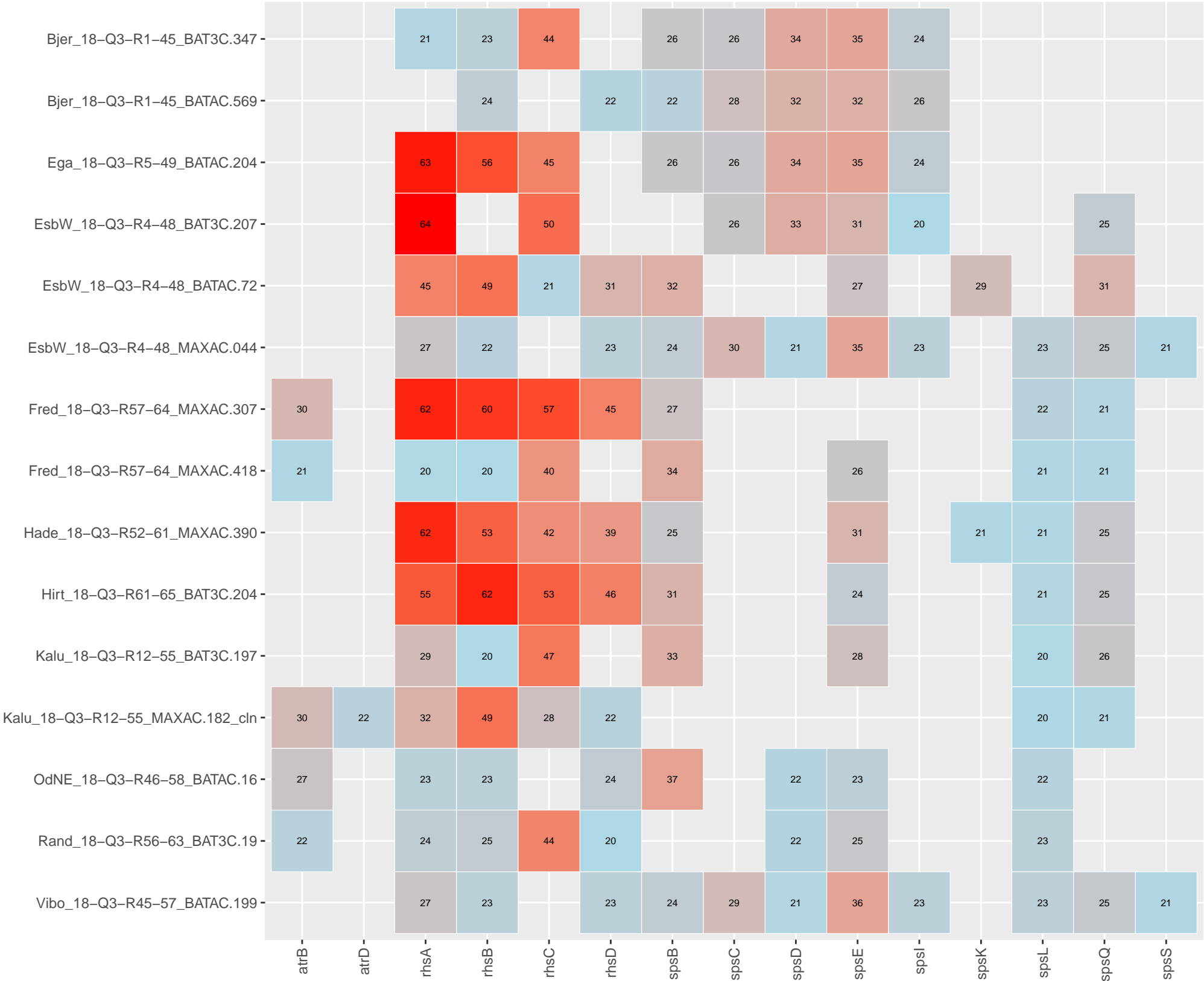
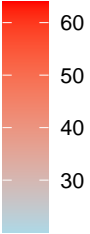


S88 Heatmap

MAG

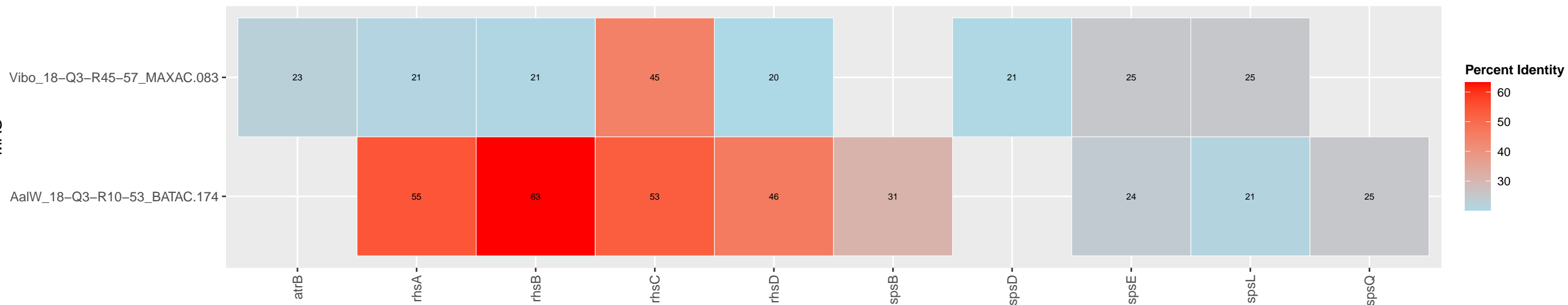


Percent Identity

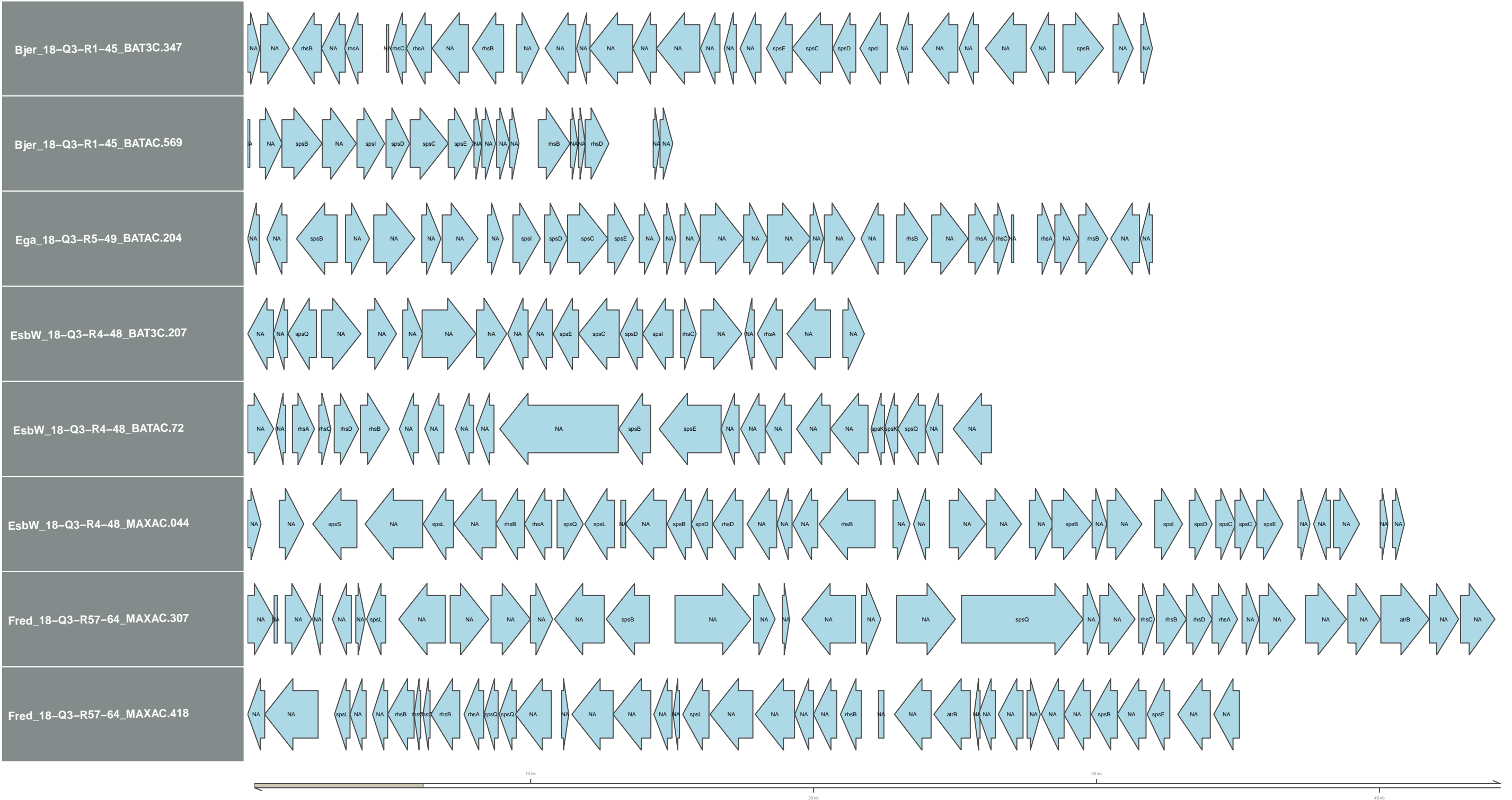


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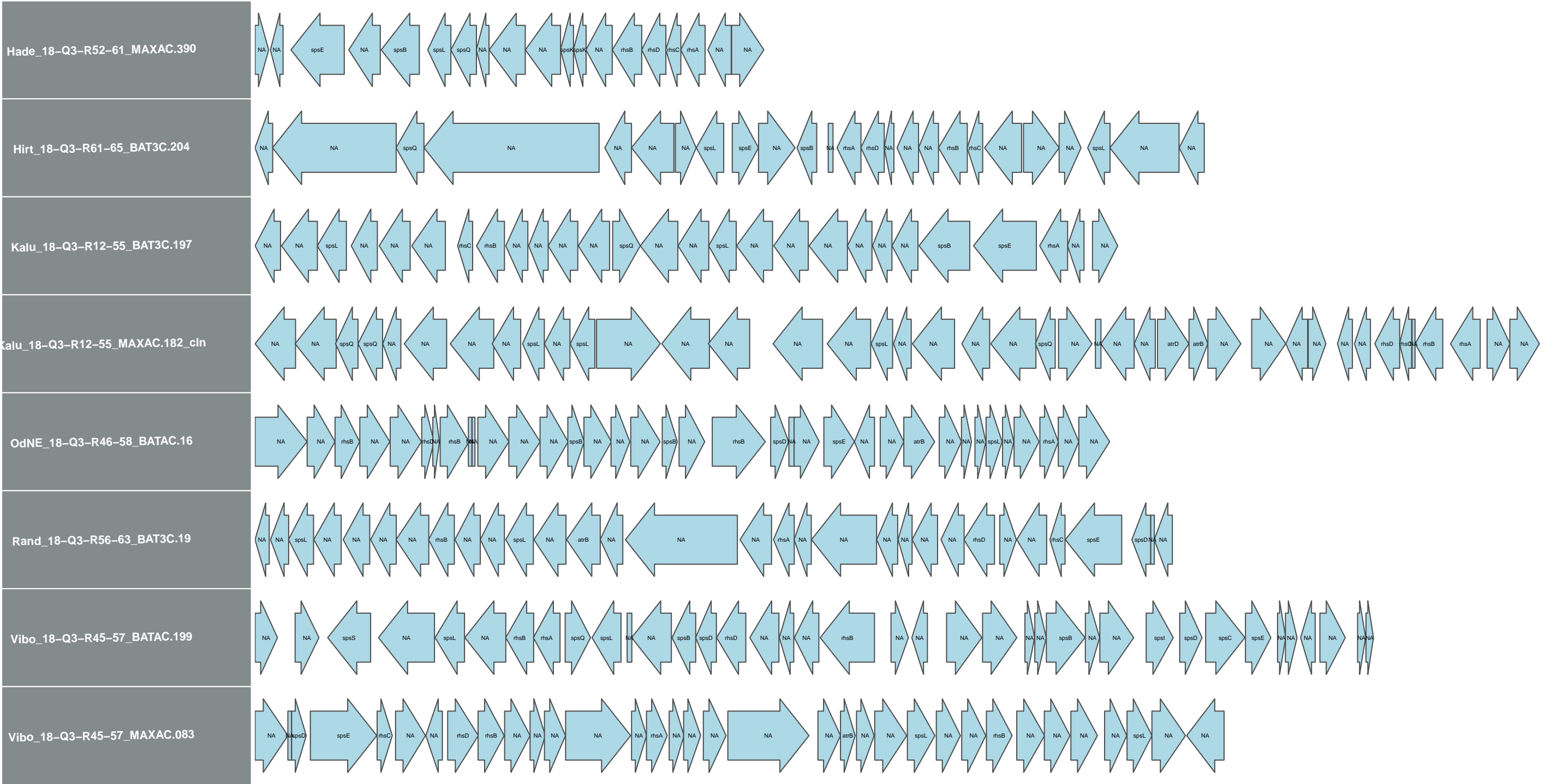
S88 Heatmap



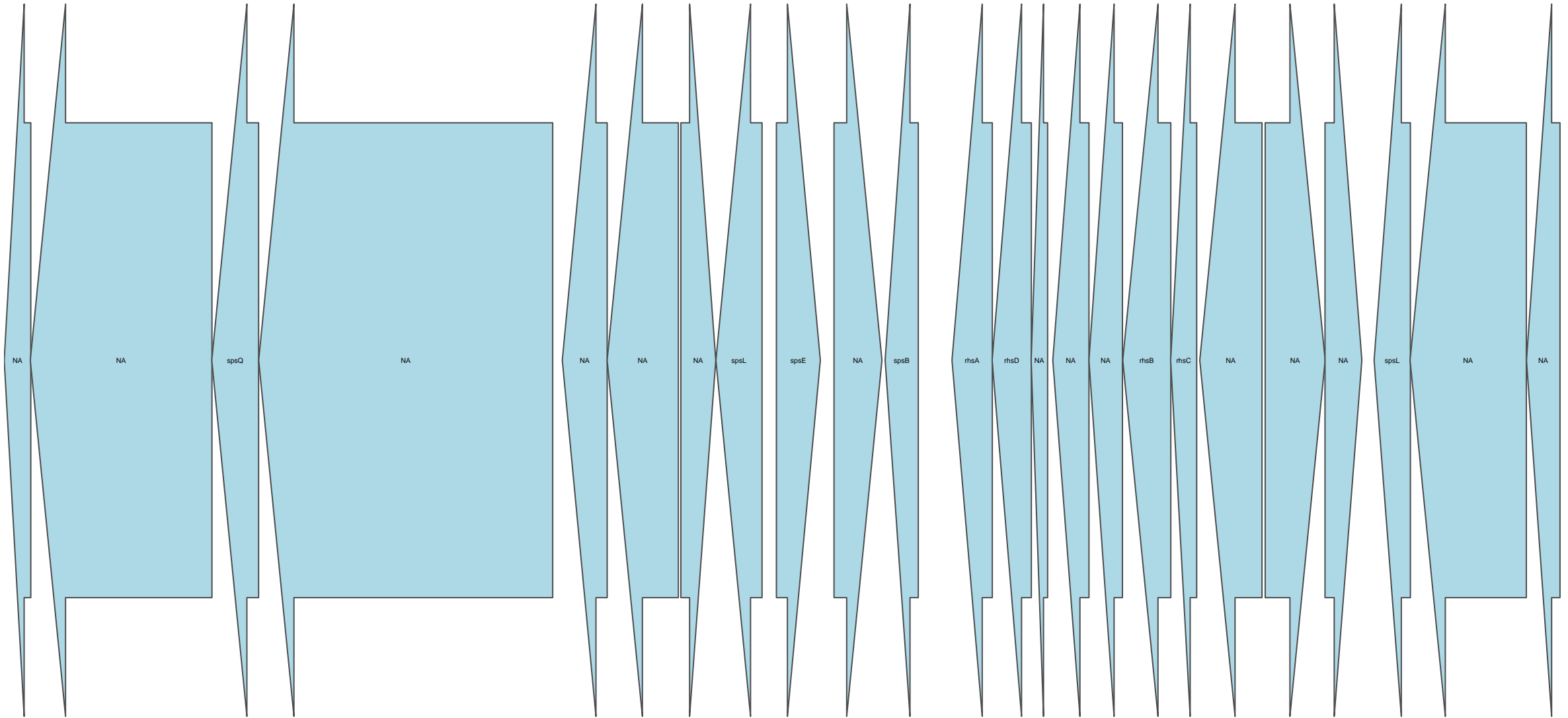
S88



S88



AalW\_18-Q3-R10-53\_BATAC.174



	ID	GTDBTax	seqname	start	Query_label	ProkkaNO
1	Bjer_18-Q3-R1-45_BAT3C.347	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__s__	tig00199796-10-9414780	52822	rhsA	03815
2	Bjer_18-Q3-R1-45_BATAC.569	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Rhodoferax;s__	tig00012007-10-1205650	112483	rhsB	02388
3	Ega_18-Q3-R5-49_BATAC.204	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__s__	tig00004277-10-2003480	190040	rhsA	03686
4	EsbW_18-Q3-R4-48_BAT3C.207	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Vitreoscilla_A;s__	tig00001176-10-9861400	280141	rhsA	02020
5	EsbW_18-Q3-R4-48_BATAC.72	d__Bacteria;p__Planctomycetota;c__Phycisphaerae;o__Phycisphaerales;f__SM1A02;g__s__	tig00011125-10-1386600	93278	rhsA	03051
6	EsbW_18-Q3-R4-48_MAXAC.044	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Propionivibrio;s__	tig00033796-10-615360	23940	rhsA	03339
7	Fred_18-Q3-R57-64_MAXAC.307	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales_A;f__2-12-FULL-67-15;g__s__	tig00002301-10-12040470	1011128	atrB	03305
8	Fred_18-Q3-R57-64_MAXAC.418	d__Bacteria;p__Planctomycetota;c__Phycisphaerae;o__UBA1845;f__UTPLA1;g__UTPLA1;s__	tig00010737-10-2712970	157344	atrB	00729
9	Hade_18-Q3-R52-61_MAXAC.390	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiotrichales;f__Thiotrichaceae;g__Thiofilum;s__	tig00000011-10-40151770	1776295	rhsA	01713
10	Hirt_18-Q3-R61-65_BAT3C.204	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rhodobacter_E;s__	tig00317261-10-8095540	423353	rhsA	02779
11	Kalu_18-Q3-R12-55_BAT3C.197	d__Bacteria;p__Planctomycetota;c__Phycisphaerae;o__UBA1845;f__Fen-1342;g__Fen-1342;s__	tig00000698-10-18309200	1185863	rhsA	00991
12	Kalu_18-Q3-R12-55_MAXAC.182_cln	d__Bacteria;p__Patescibacteria;c__Microgenomatia;o__GWA2-44-7;f__UBA8517;g__s__	tig00000428-10-12728800	970939	atrB	00954
13	OdNE_18-Q3-R46-58_BATAC.16	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium;s__	tig00004974-10-2765880	36694	atrB	00735
14	Rand_18-Q3-R56-63_BAT3C.19	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__AKYH767-A;f__2013-40CM-41-45;g__s__	tig00000438-10-7606690	171442	atrB	01709
15	Vibo_18-Q3-R45-57_BATAC.199	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Propionivibrio;s__	tig00008044-10-802880	42325	rhsA	01866
16	Vibo_18-Q3-R45-57_MAXAC.083	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__AKYH767-A;f__2013-40CM-41-45;g__s__	tig00004163-10-3243870	299574	atrB	00314
17	AalIW_18-Q3-R10-53_BATAC.174	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rhodobacter_E;s__	tig00006255-10-4666680	183632	rhsA	00804