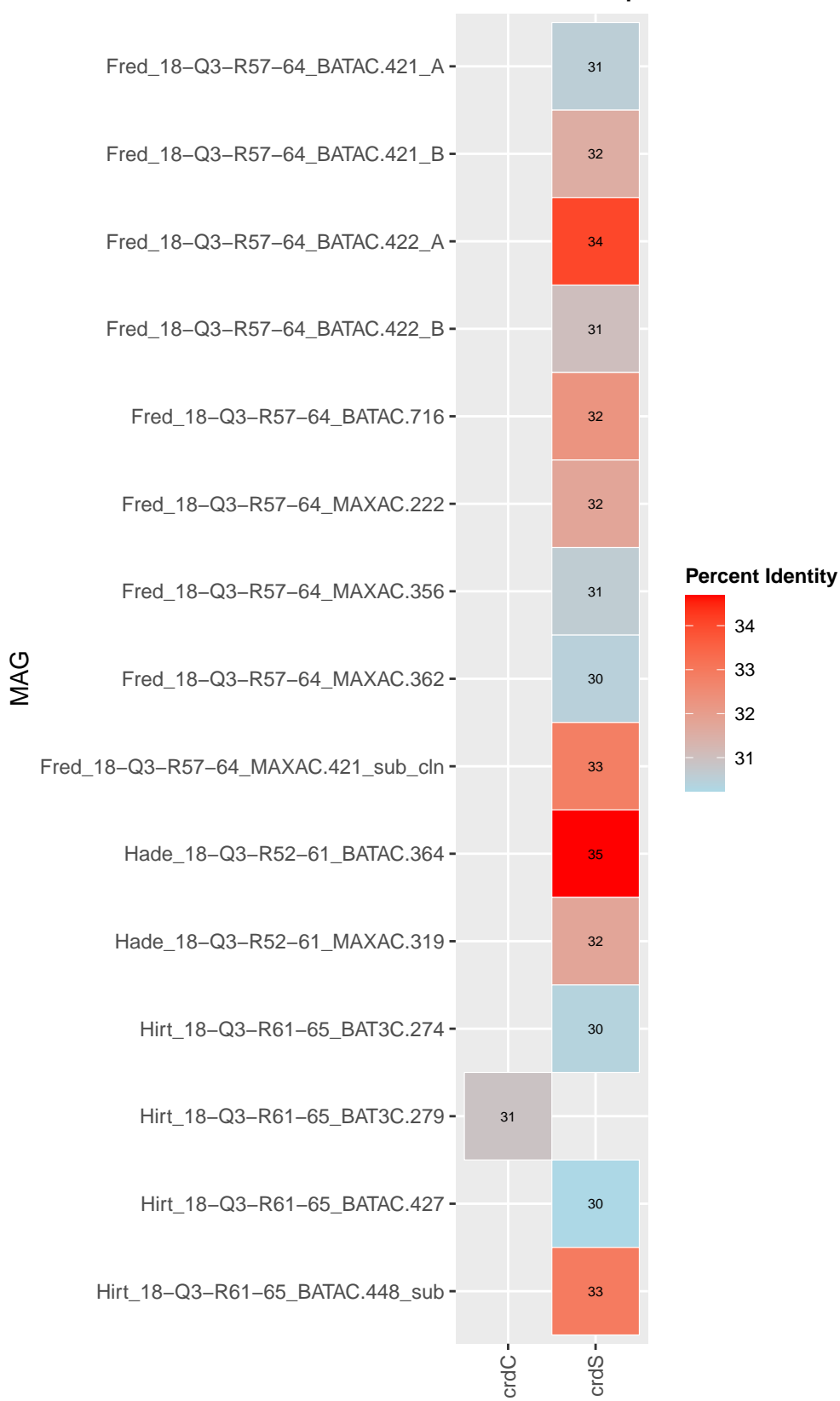
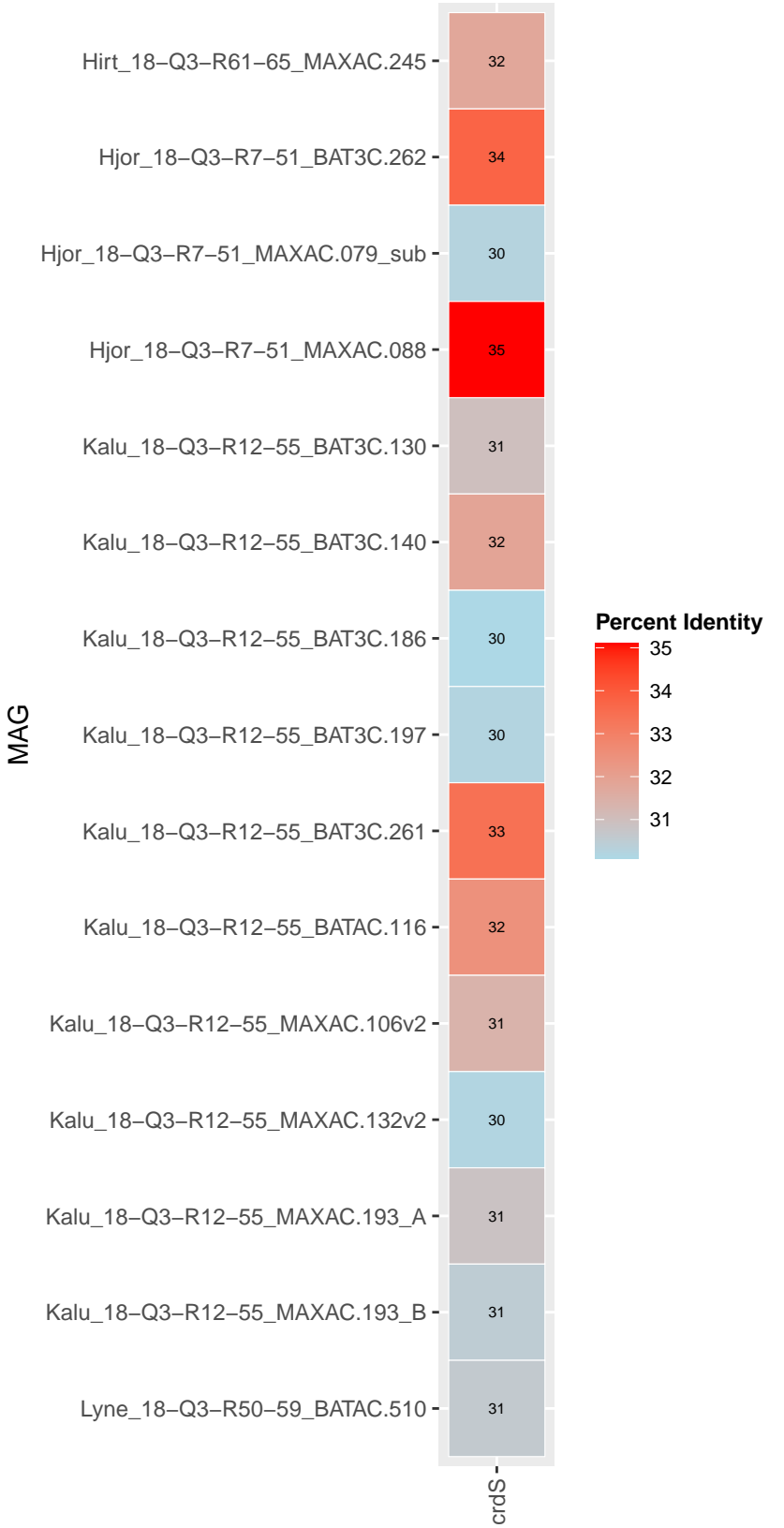
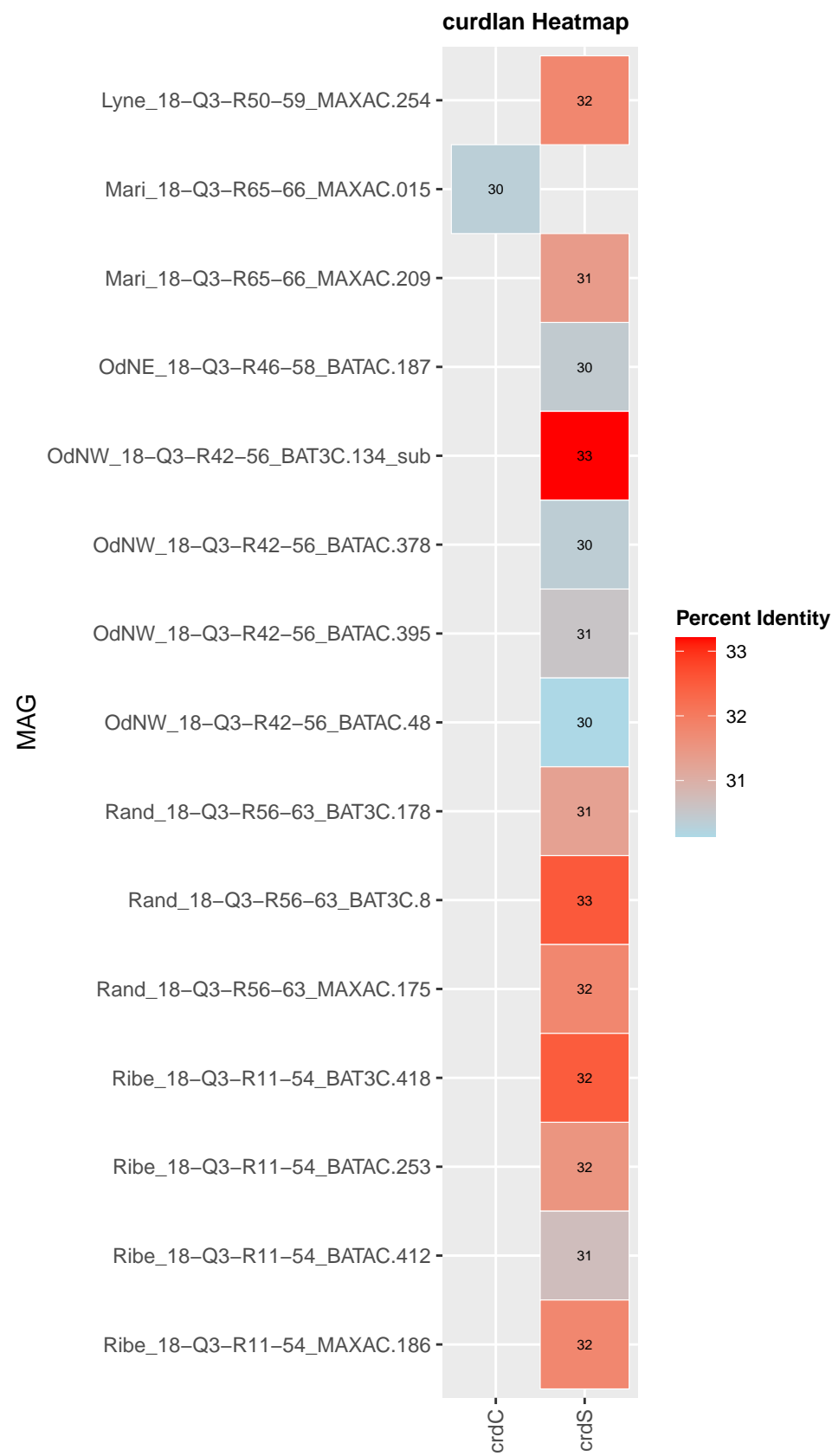


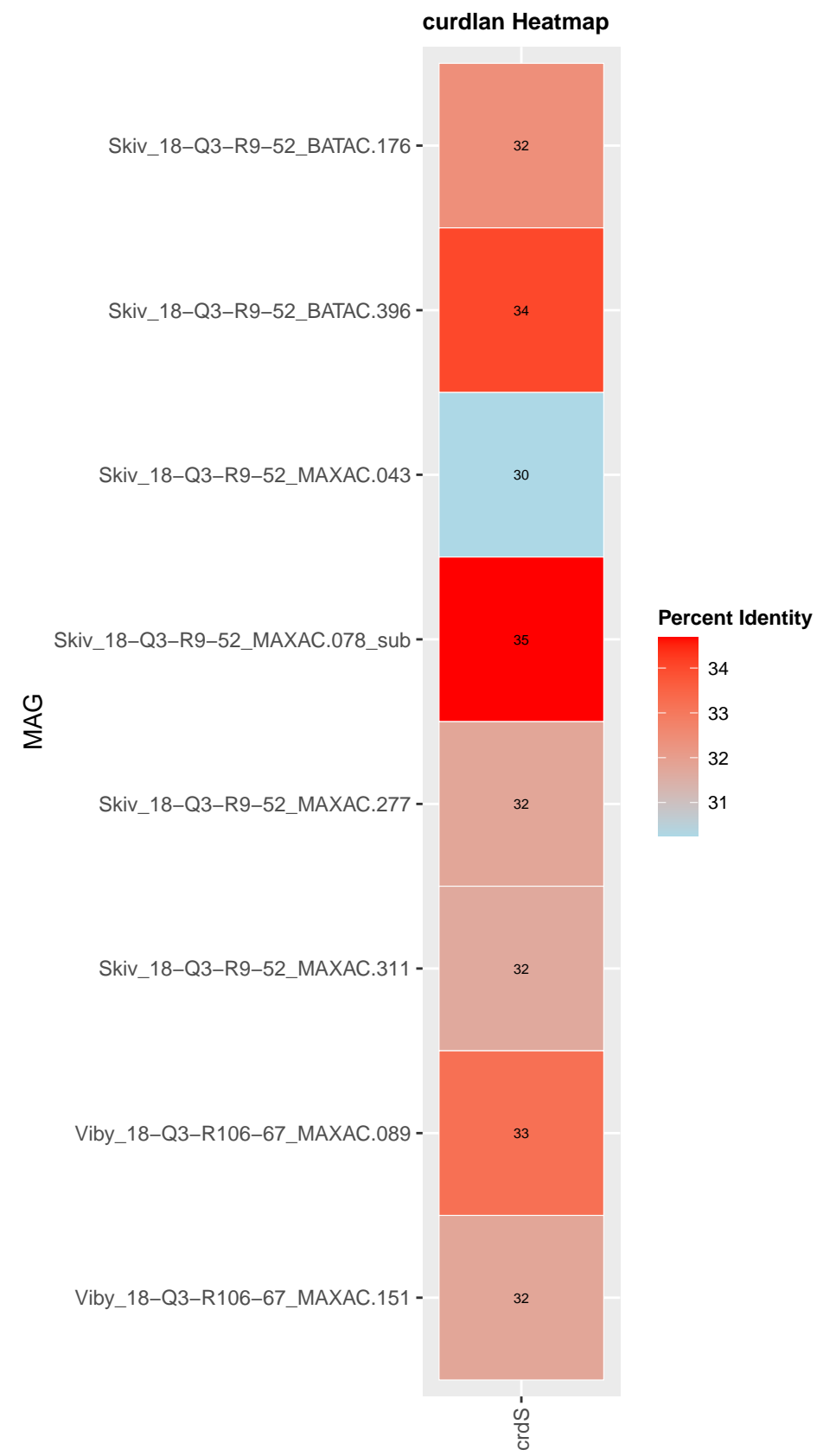
curdIan Heatmap



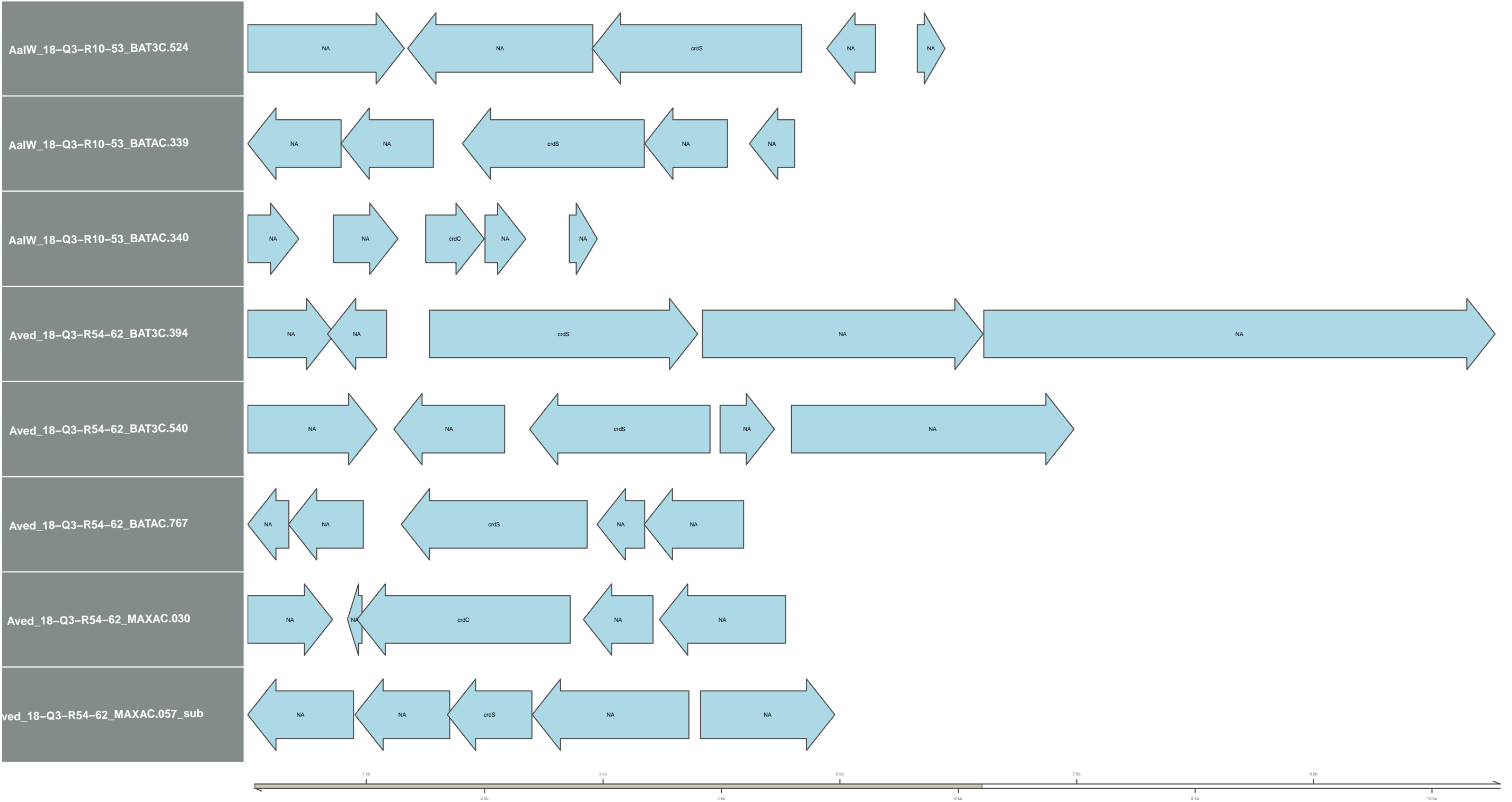
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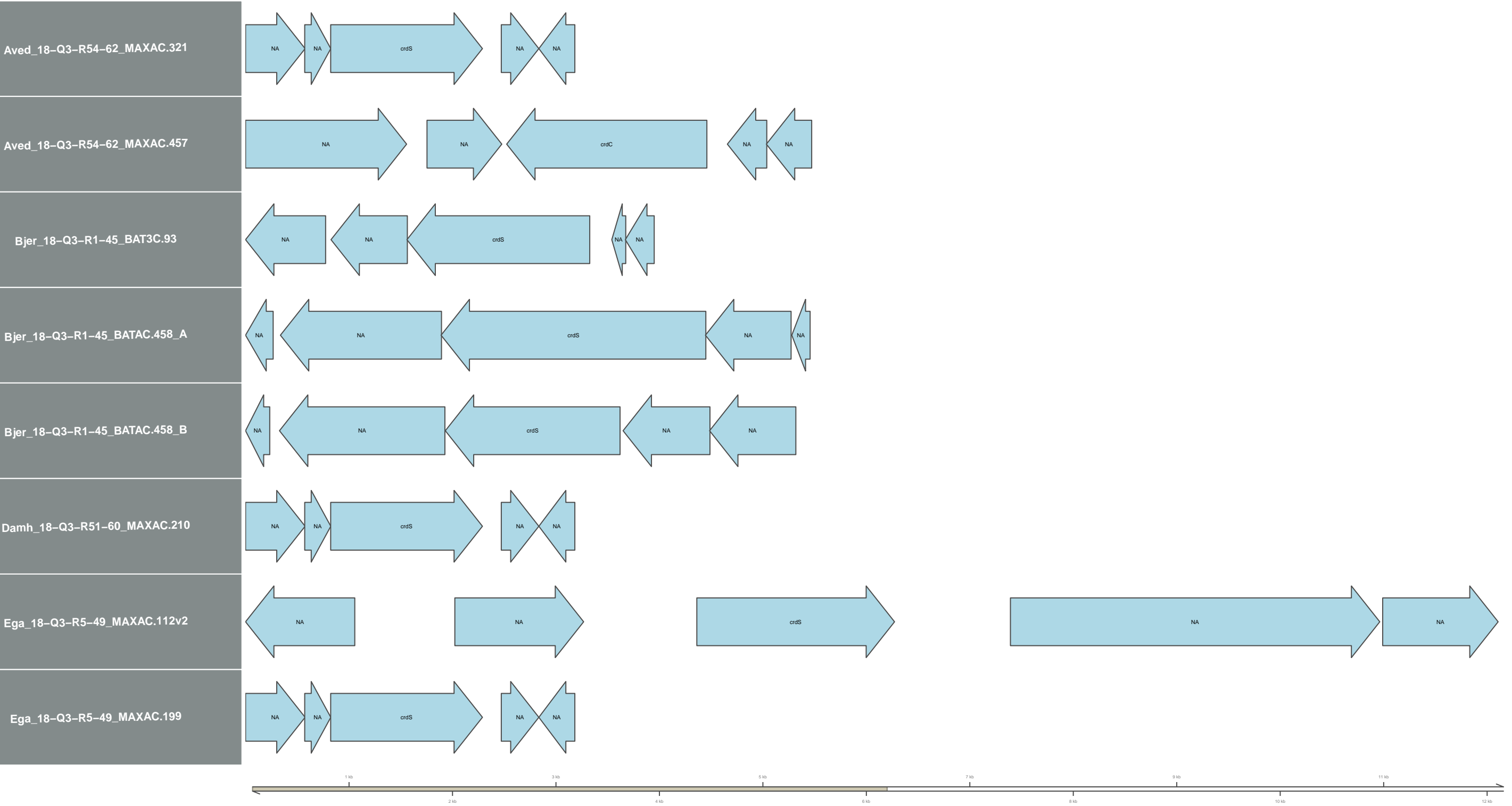




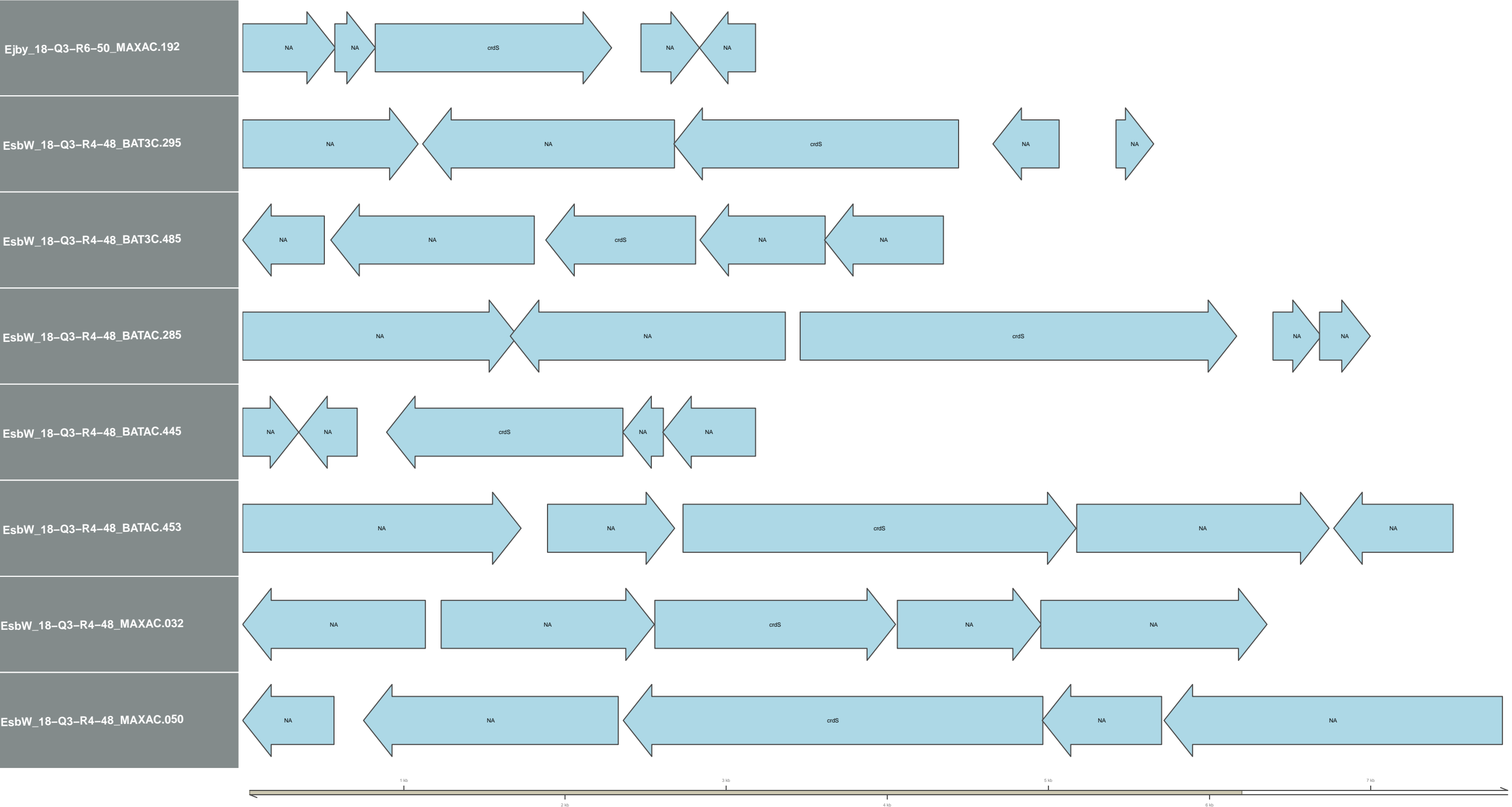
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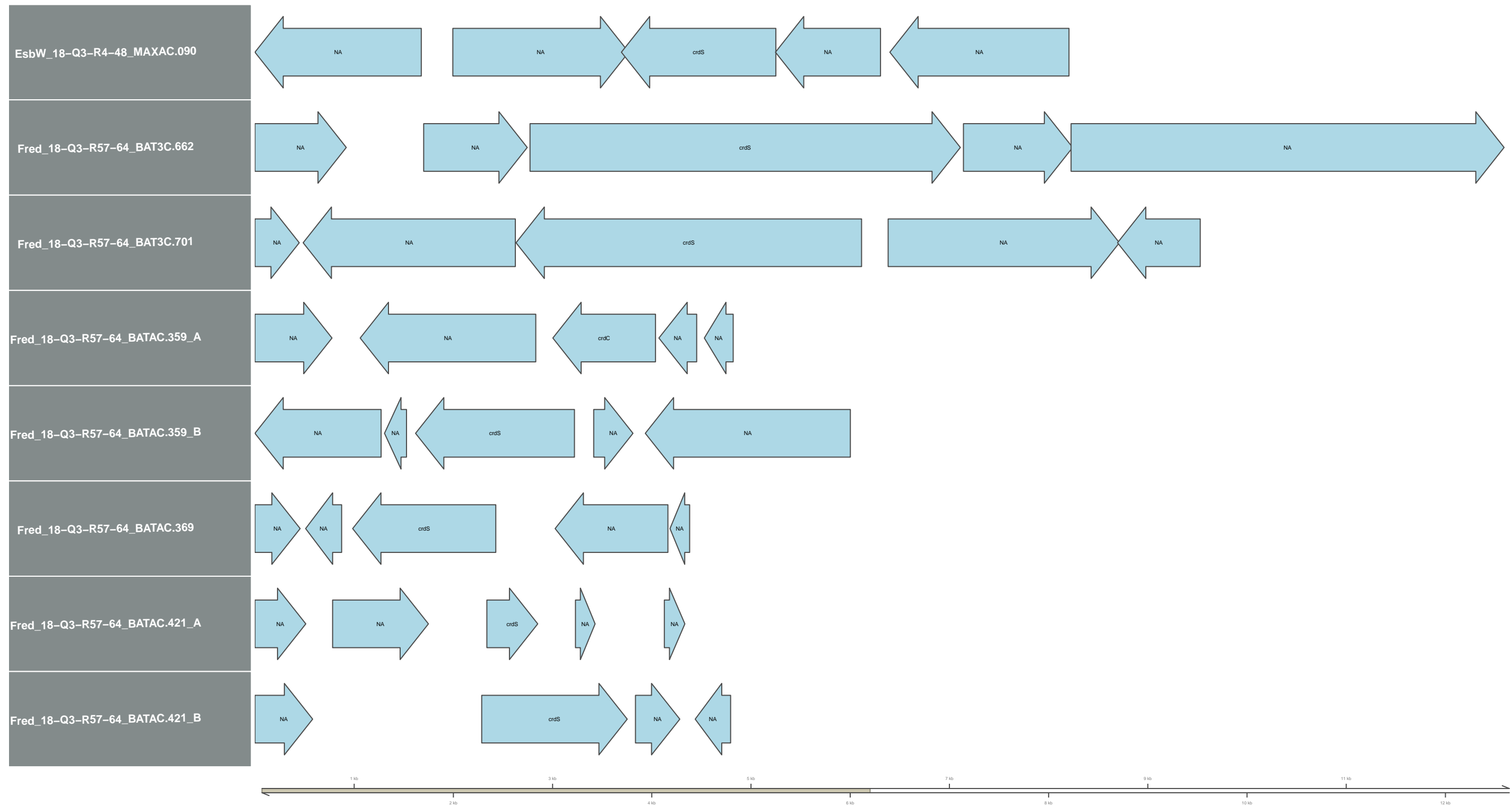
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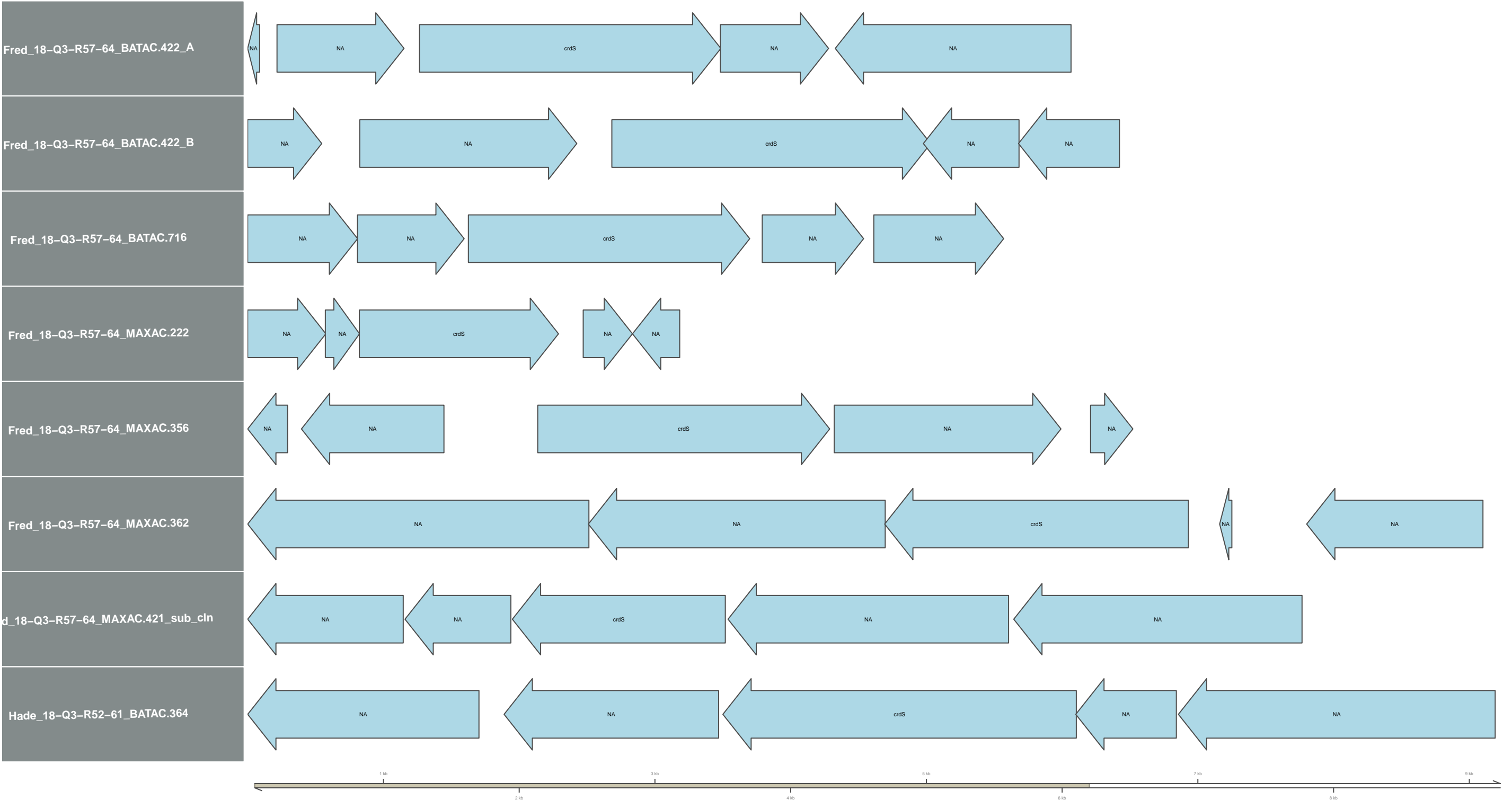
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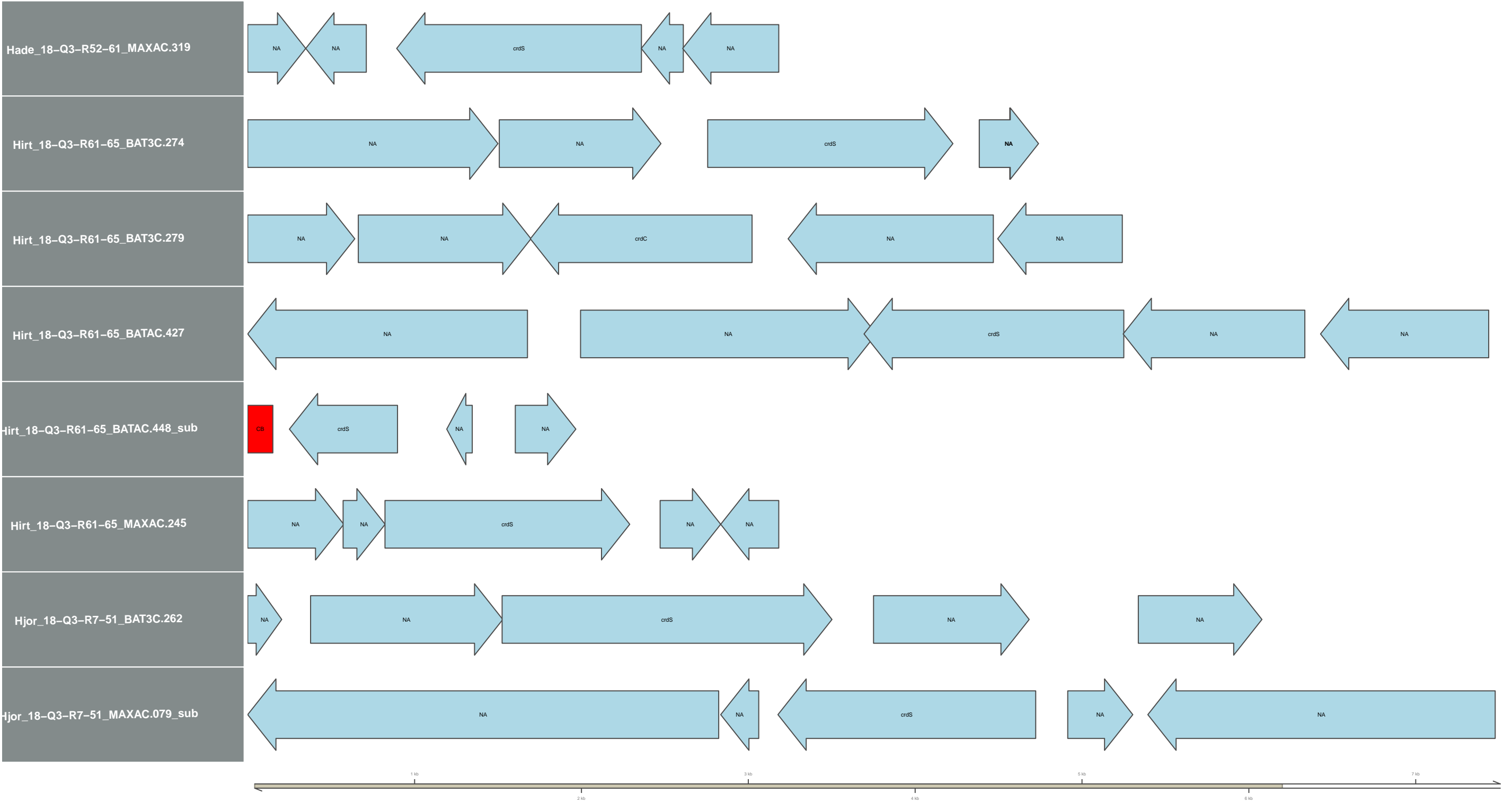
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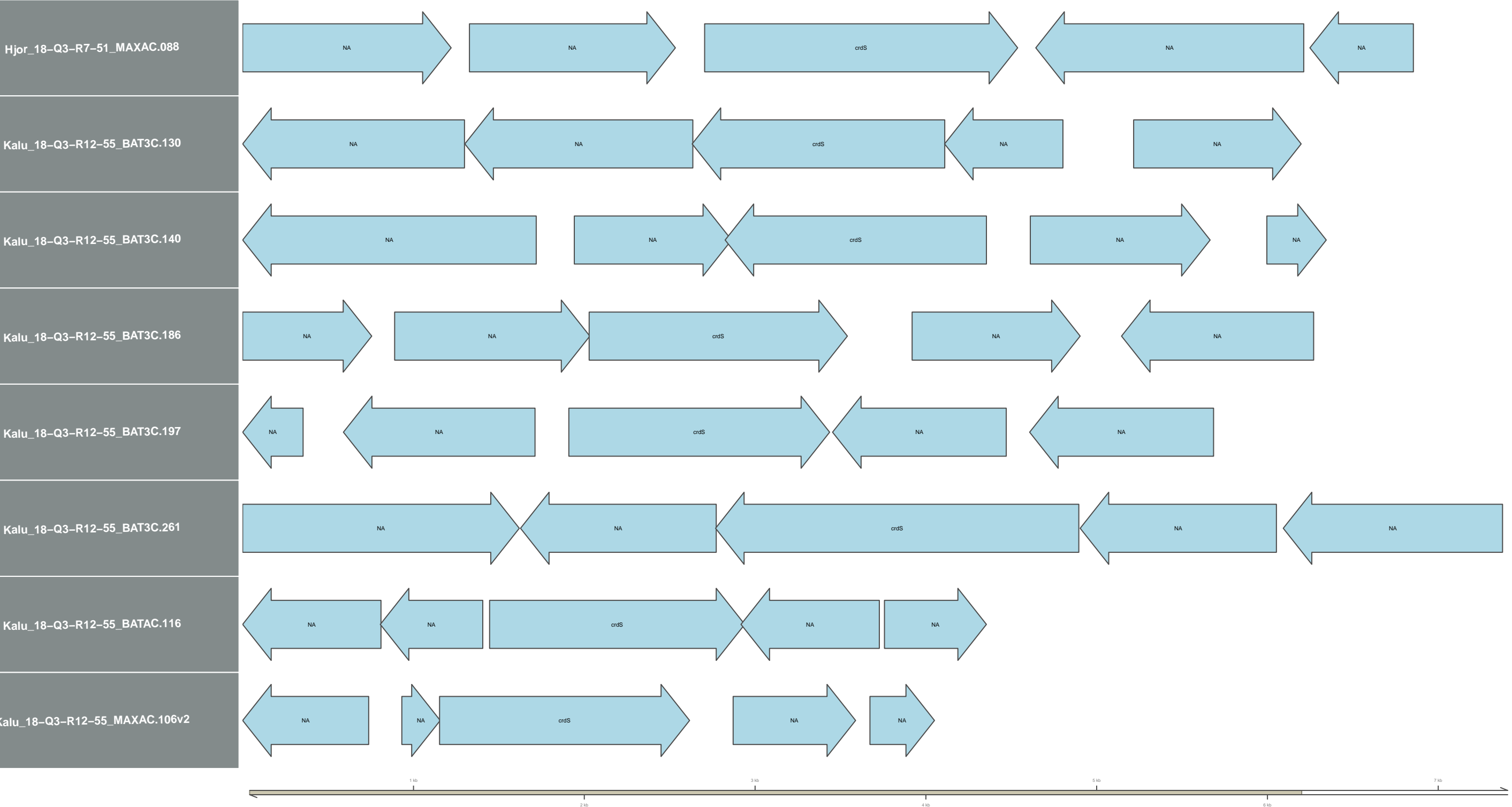
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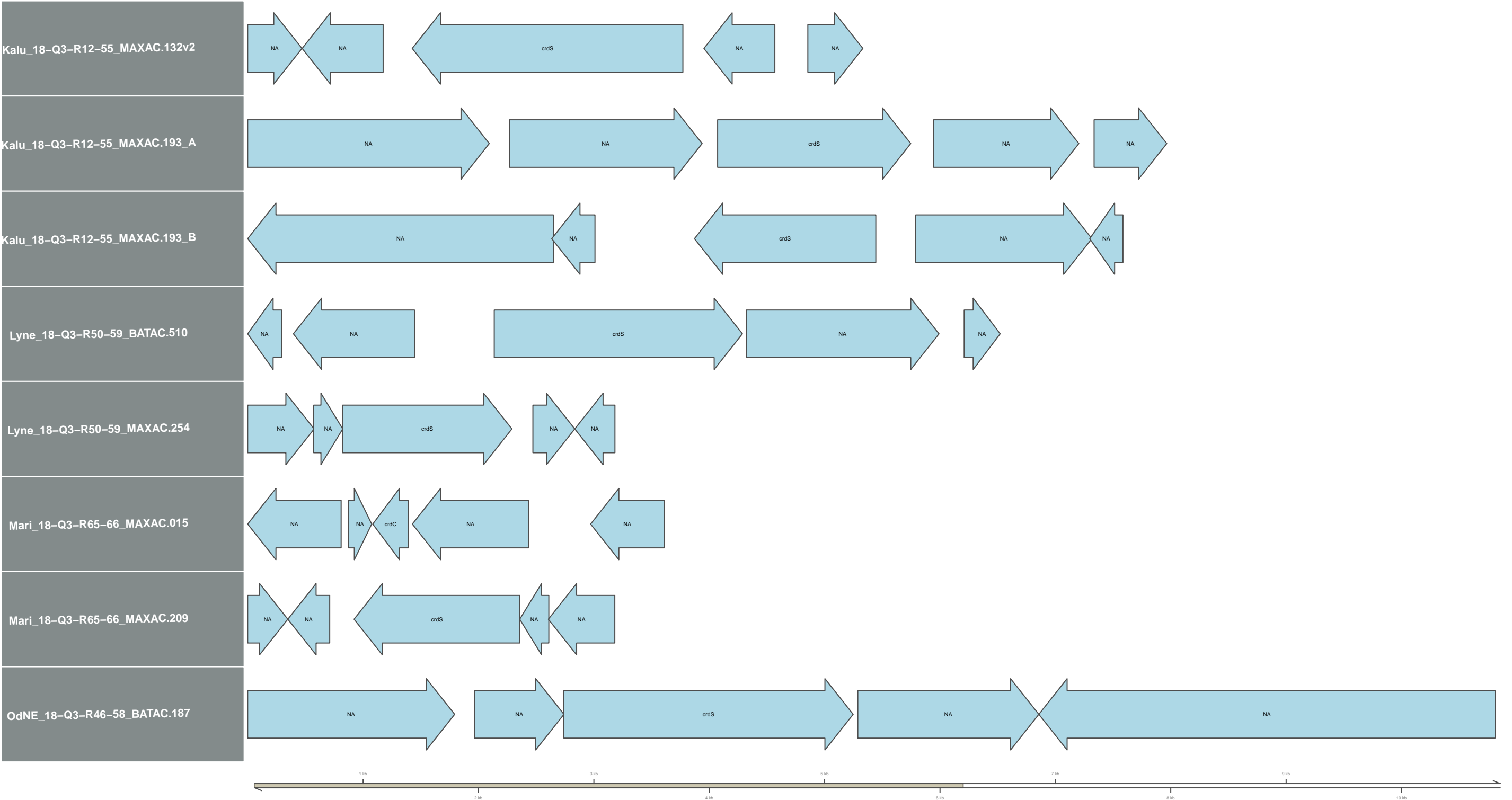
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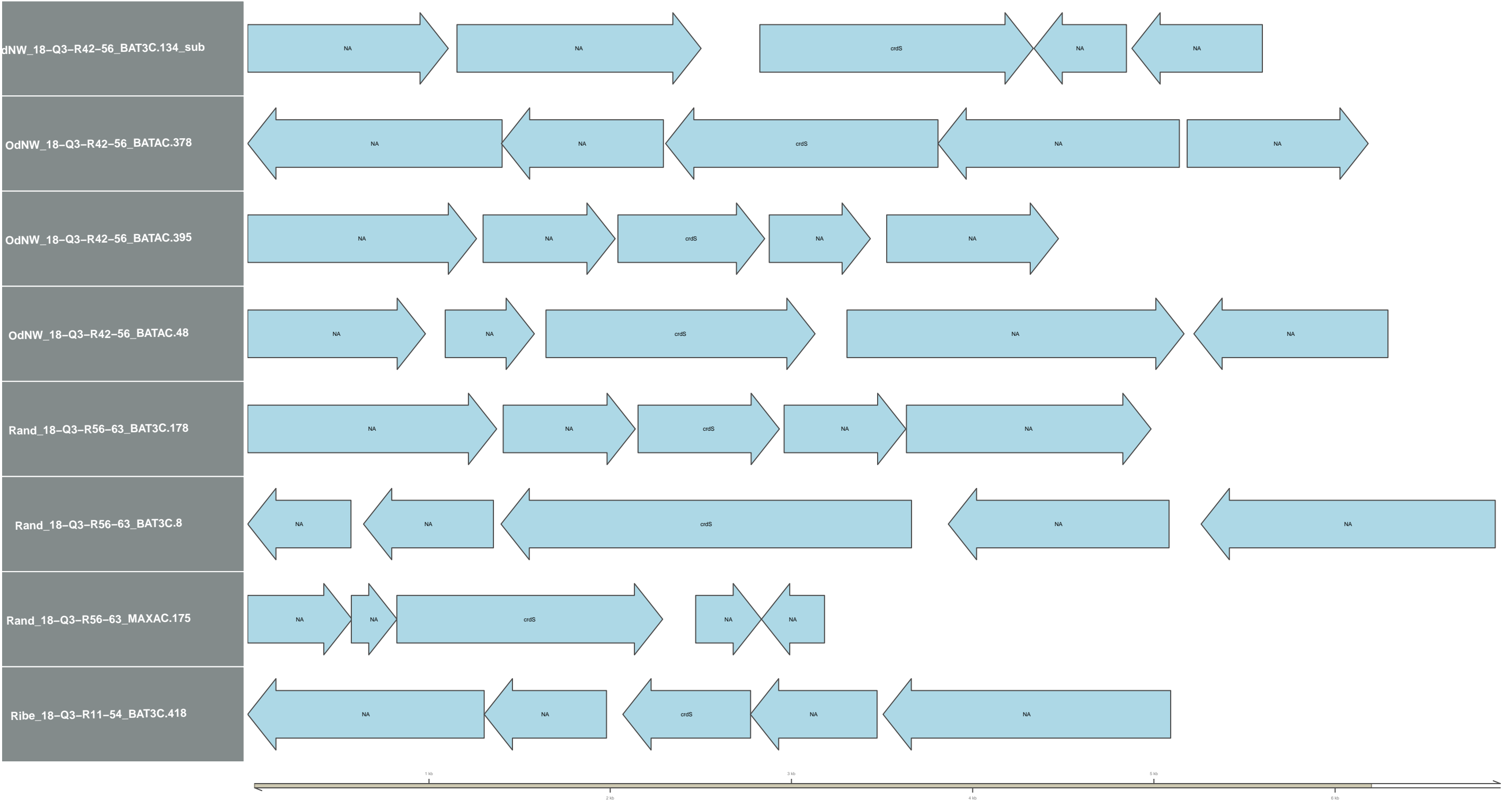
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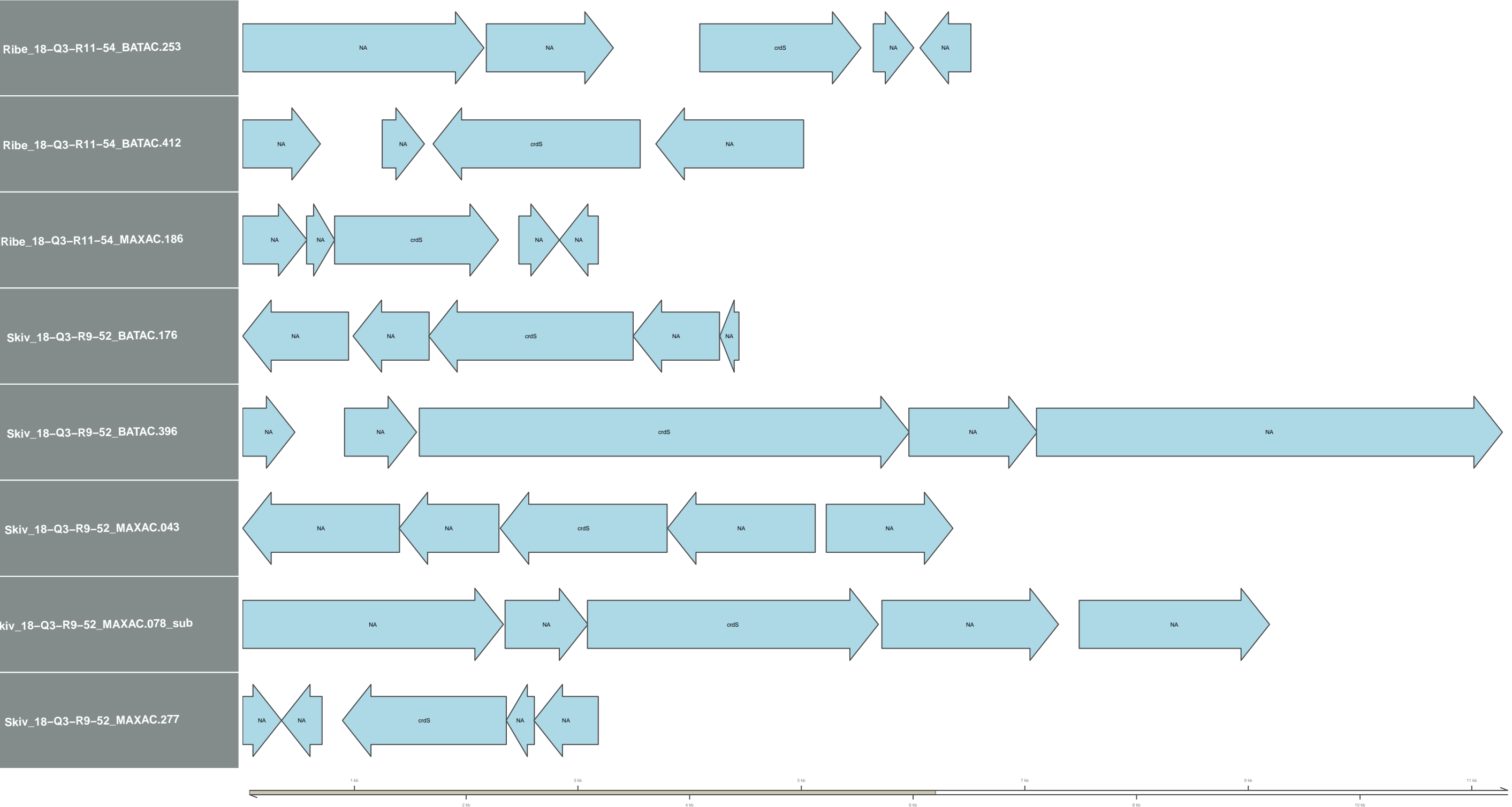
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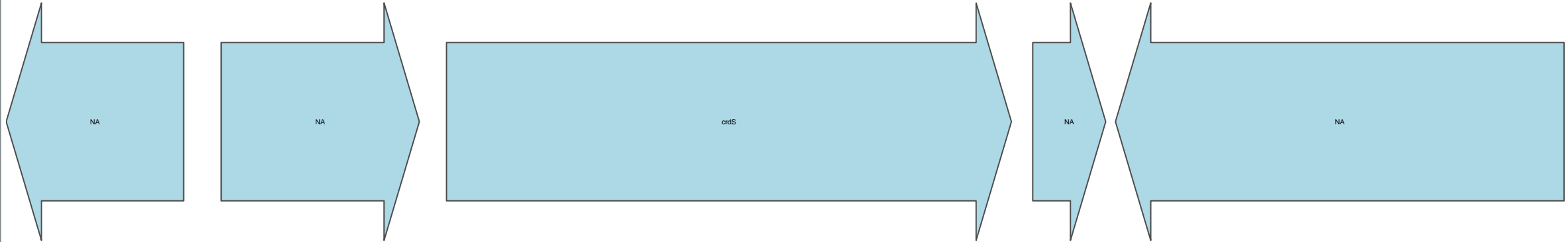


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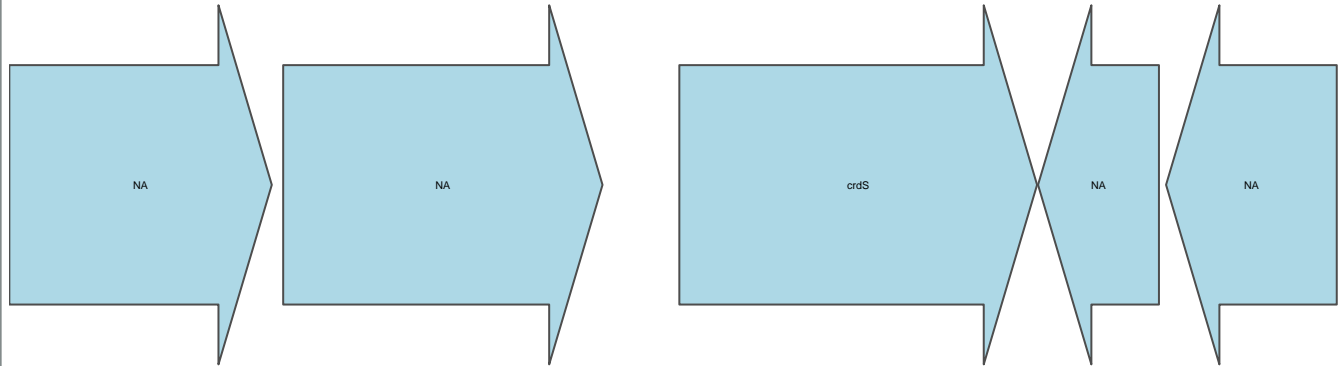


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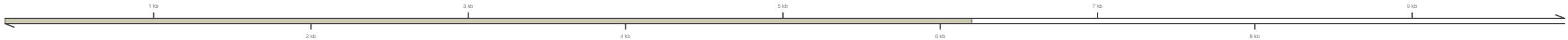
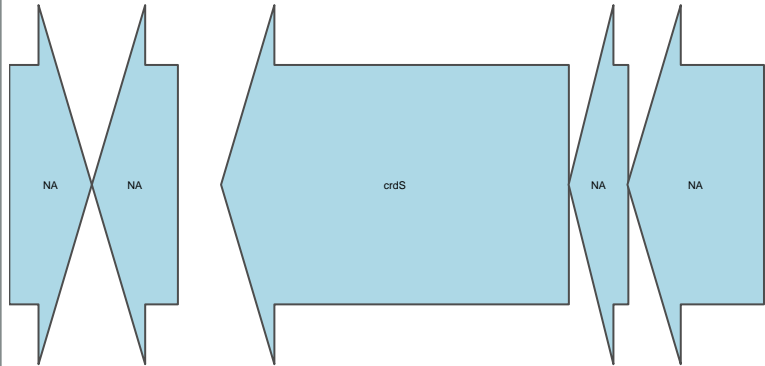
Skiv_18-Q3-R9-52_MAXAC.311



Viby_18-Q3-R106-67_MAXAC.089



Viby_18-Q3-R106-67_MAXAC.151



17	EsbW_18-Q3-R4-48_BAT3C.295	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__GCA-2748155;s__	tig00002188-10-9196560	487823	crdS	00724
18	EsbW_18-Q3-R4-48_BAT3C.485	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__PHCI01;s__	tig00020141-10-609230	22885	crdS	03737
19	EsbW_18-Q3-R4-48_BATAC.285	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Accumulibacter;s__	tig00004813-10-4512910	252292	crdS	01588
20	EsbW_18-Q3-R4-48_BATAC.445	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00002500-10-7312180	144270	crdS	00148
21	EsbW_18-Q3-R4-48_BATAC.453	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Simplicispira_A;s__	tig00014047-10-1285900	106609	crdS	01813
22	EsbW_18-Q3-R4-48_MAXAC.032	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__Anaerolineales;f__envOPS12;g__OLB14;s__	tig01102194-10-3390260	19973	crdS	04096
23	EsbW_18-Q3-R4-48_MAXAC.050	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__s__	tig00018082-10-889440	83447	crdS	03083
24	EsbW_18-Q3-R4-48_MAXAC.090	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__f__g__s__	tig00001296-10-13311950	1233231	crdS	02571
25	Fred_18-Q3-R57-64_BAT3C.662	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Bryobacterales;f__Bryobacteraceae;g__s__	tig00006256-10-5425100	396711	crdS	01773
26	Fred_18-Q3-R57-64_BAT3C.701	d__Bacteria;p__Myxococcota;c__UBA9160;o__UBA9160;f__UBA4427;g__s__	tig00006161-10-5807860	249756	crdS	04544
27	Fred_18-Q3-R57-64_BATAC.359	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__Caldilineales;f__Caldilineaceae;g__s__	tig00008971-10-3326960	312313	crdC	00329
28	Fred_18-Q3-R57-64_BATAC.369	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__SBR1031;f__A4b;g__OLB15;s__	tig00353167-10-1684200	19645	crdS	07384
29	Fred_18-Q3-R57-64_BATAC.421	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__SBR1031;f__A4b;g__OLB15;s__	tig00048447-10-384060	36035	crdS	05237
30	Fred_18-Q3-R57-64_BATAC.422	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Ga0077523;g__Ga0077526;s__	tig01546677-10-8895580	749757	crdS	05149
31	Fred_18-Q3-R57-64_BATAC.716	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Verrucomicrobiaceae;g__Prosthecobacter;s__	tig00000726-10-9701610	91681	crdS	01550
32	Fred_18-Q3-R57-64_MAXAC.222	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00000202-10-25454520	583724	crdS	00465
33	Fred_18-Q3-R57-64_MAXAC.356	d__Bacteria;p__Cyanobacteria;c__Vampirovibrionia;o__Obscuribacterales;f__Obscuribacteraceae;g__Obscuribacter;s__	tig00000077-10-70086850	1235022	crdS	01078
34	Fred_18-Q3-R57-64_MAXAC.362	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Hyphomonadaceae;g__Hyphomonas;s__	tig00000777-10-25148860	1123506	crdS	01174
35	Fred_18-Q3-R57-64_MAXAC.421_sub_cln	d__Bacteria;p__Patescibacteria;c__Paceibacteria_A;o__Moranbacteriales;f__UBA1568;g__s__	tig00000963-10-10881080	77102	crdS	00084
36	Hade_18-Q3-R52-61_BATAC.364	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Dechloromonas;s__	tig00407471-10-3182230	146325	crdS	03000
37	Hade_18-Q3-R52-61_MAXAC.319	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00000703-10-10596450	1005217	crdS	00935
38	Hirt_18-Q3-R61-65_BAT3C.274	d__Bacteria;p__Myxococcota;c__Polyangia;o__GCA-2747355;f__GCA-2747355;g__s__	tig00001291-10-13242390	153378	crdS	00116
39	Hirt_18-Q3-R61-65_BAT3C.279	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Micropruina;s__	tig00001155-10-14562110	122894	crdC	01804
40	Hirt_18-Q3-R61-65_BATAC.427	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__f__g__s__	tig00317876-10-1787950	69253	crdS	03602
41	Hirt_18-Q3-R61-65_BATAC.448_sub	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Hyphomonadaceae;g__SWB02;s__	tig00016717-10-1660250	679	crdS	01699
42	Hirt_18-Q3-R61-65_MAXAC.245	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00004079-10-4916730	332594	crdS	00784
43	Hjor_18-Q3-R7-51_BAT3C.262	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Hyphomicrobium;s__	tig00003782-10-3351080	88894	crdS	00521
44	Hjor_18-Q3-R7-51_MAXAC.079_sub	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__Caldilineales;f__Caldilineaceae;g__Caldilinea;s__	tig00004638-10-2386320	199176	crdS	01433
45	Hjor_18-Q3-R7-51_MAXAC.088	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Actinomycetales;f__Dermatophilaceae;g__GCA-2748155;s__	tig00120094-10-3563900	252625	crdS	02950
46	Kalu_18-Q3-R12-55_BAT3C.130	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__PHOS-HE28;g__PHOS-HE28;s__	tig00000285-10-36554120	534273	crdS	00440
47	Kalu_18-Q3-R12-55_BAT3C.140	d__Bacteria;p__Planctomycetota;c__Phycisphaerae;o__UBA1845;f__Fen-1342;g__Fen-1342;s__	tig00000016-10-42368670	3464226	crdS	02765
48	Kalu_18-Q3-R12-55_BAT3C.186	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__SBR1031;f__A4b;g__OLB13;s__	tig00442631-10-4027980	341967	crdS	04728
49	Kalu_18-Q3-R12-55_BAT3C.197	d__Bacteria;p__Planctomycetota;c__Phycisphaerae;o__UBA1845;f__Fen-1342;g__Fen-1342;s__	tig00000838-10-15342620	1191470	crdS	02560
50	Kalu_18-Q3-R12-55_BAT3C.261	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Bryobacterales;f__Bryobacteraceae;g__s__	tig00004141-10-2319180	89372	crdS	03037
51	Kalu_18-Q3-R12-55_BATAC.116	d__Bacteria;p__Myxococcota;c__Polyangia;o__Polyangiales;f__Polyangiaceae;g__s__	tig00003199-10-3514140	311636	crdS	03703
52	Kalu_18-Q3-R12-55_MAXAC.106v2	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__Promineofilales;f__Promineofilaceae;g__GCA-2699125;s__	tig00100734-10-59431720	1790220	crdS	03426
53	Kalu_18-Q3-R12-55_MAXAC.132v2	d__Bacteria;p__Nitrospirota;c__Nitrospiria;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira;s__	tig00002484-10-4863410	3590	crdS	02057
54	Kalu_18-Q3-R12-55_MAXAC.193	d__Bacteria;p__Planctomycetota;c__Phycisphaerae;o__UBA1845;f__Fen-1342;g__s__	tig00000220-10-42251120	1900593	crdS	01523
55	Lyne_18-Q3-R50-59_BATAC.510	d__Bacteria;p__Cyanobacteria;c__Vampirovibrionia;o__Obscuribacterales;f__Obscuribacteraceae;g__Obscuribacter;s__	tig00001484-10-13208630	25519	crdS	02574
56	Lyne_18-Q3-R50-59_MAXAC.254	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00321322-10-6191890	470728	crdS	01957
57	Mari_18-Q3-R65-66_MAXAC.015	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprosiraceae;g__OLB8;s__	tig00004287-10-3280880	182314	crdC	01566
58	Mari_18-Q3-R65-66_MAXAC.209	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00018235-10-733950	35196	crdS	01438
59	OdNE_18-Q3-R46-58_BATAC.187	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Gallionellaceae;g__UBA7399;s__	tig00013603-10-1108760	12689	crdS	01449
60	OdNW_18-Q3-R42-56_BAT3C.134_sub	d__Bacteria;p__Myxococcota;c__Myxococcia;o__Myxococcales;f__Anaeromyxobacteraceae;g__Anaeromyxobacter;s__	tig00000032-10-15659720	974051	crdS	00842
61	OdNW_18-Q3-R42-56_BATAC.378	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__Anaerolineales;f__envOPS12;g__OLB14;s__	tig00896855-10-3266290	63195	crdS	04539