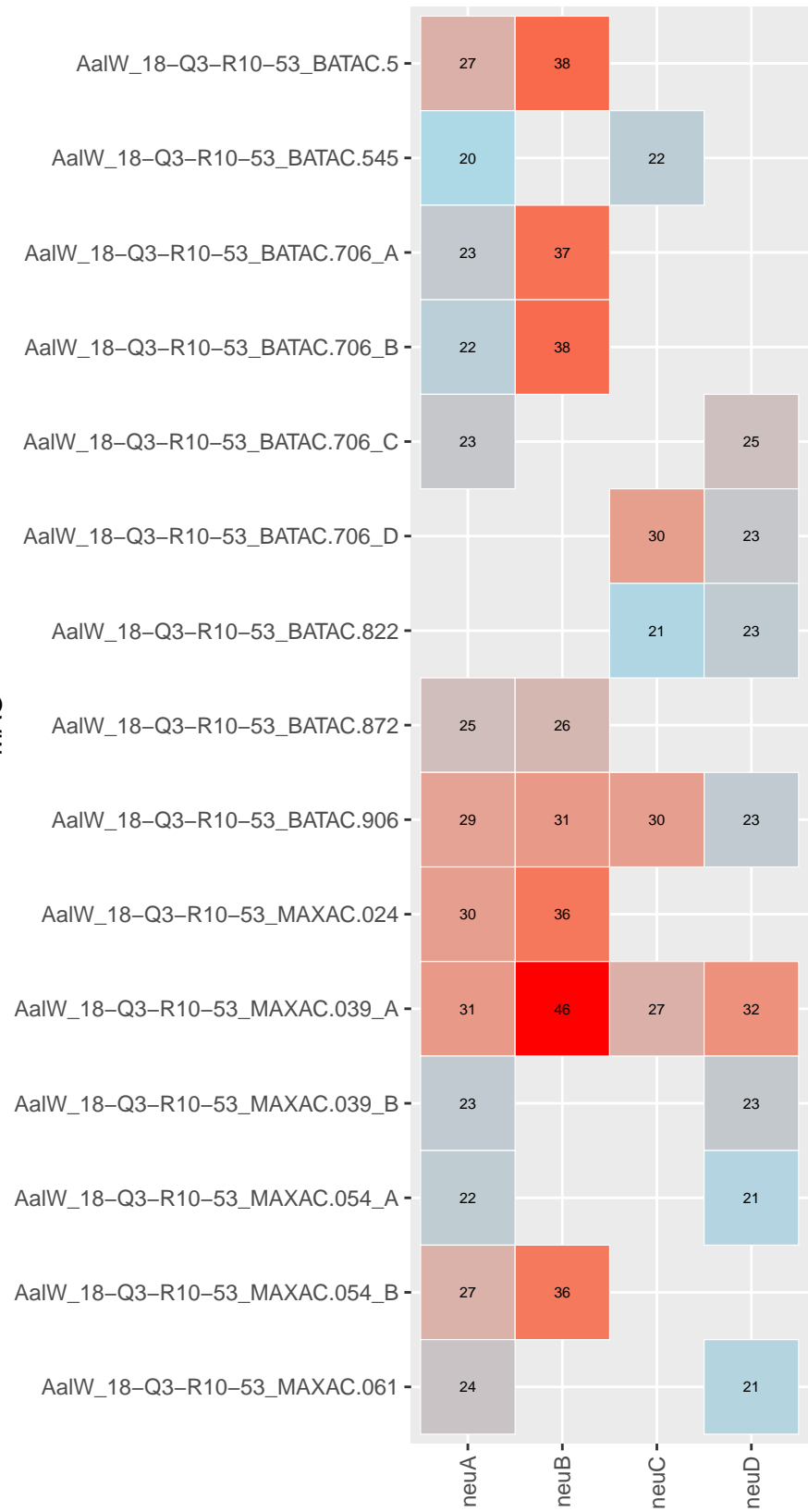
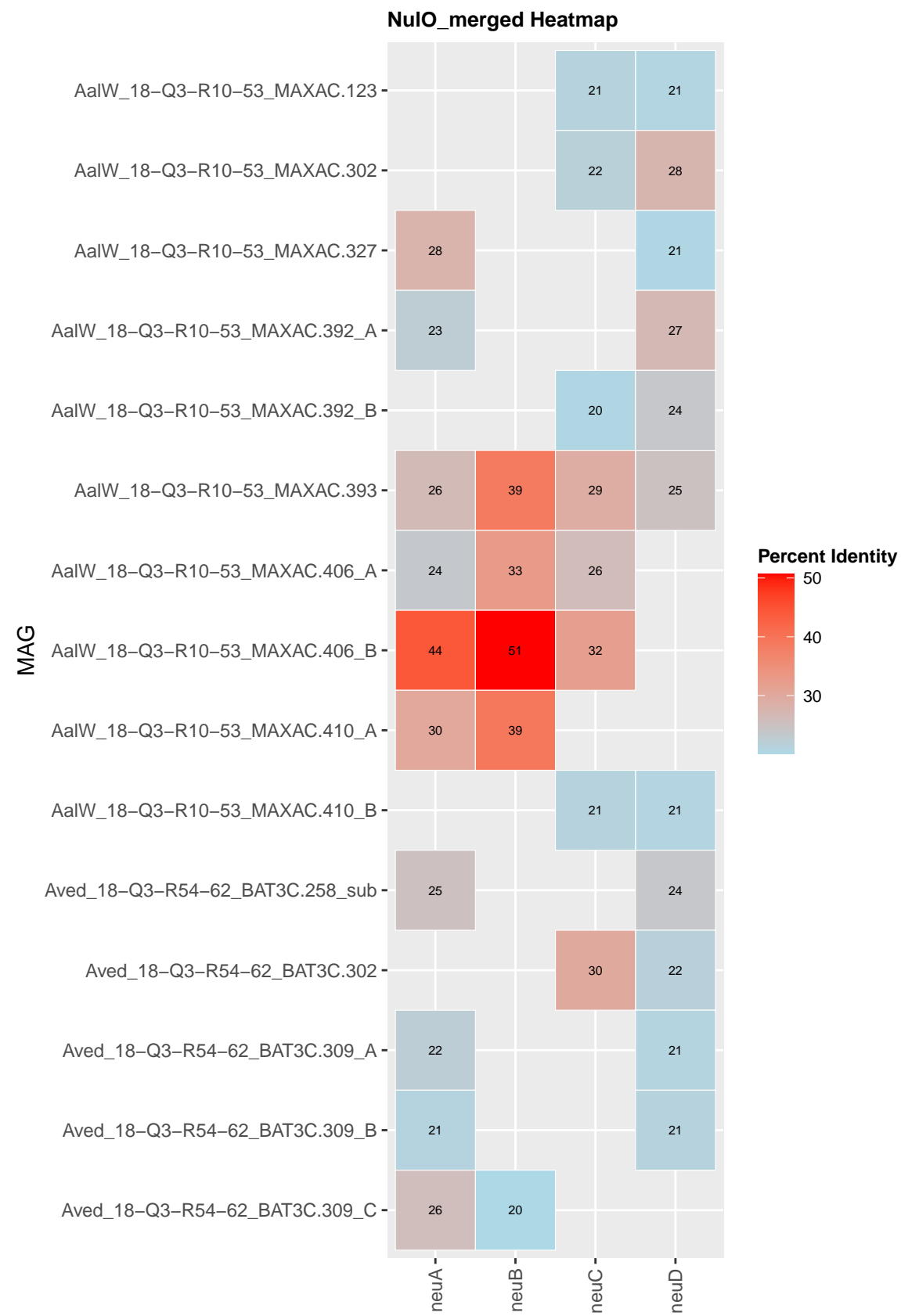


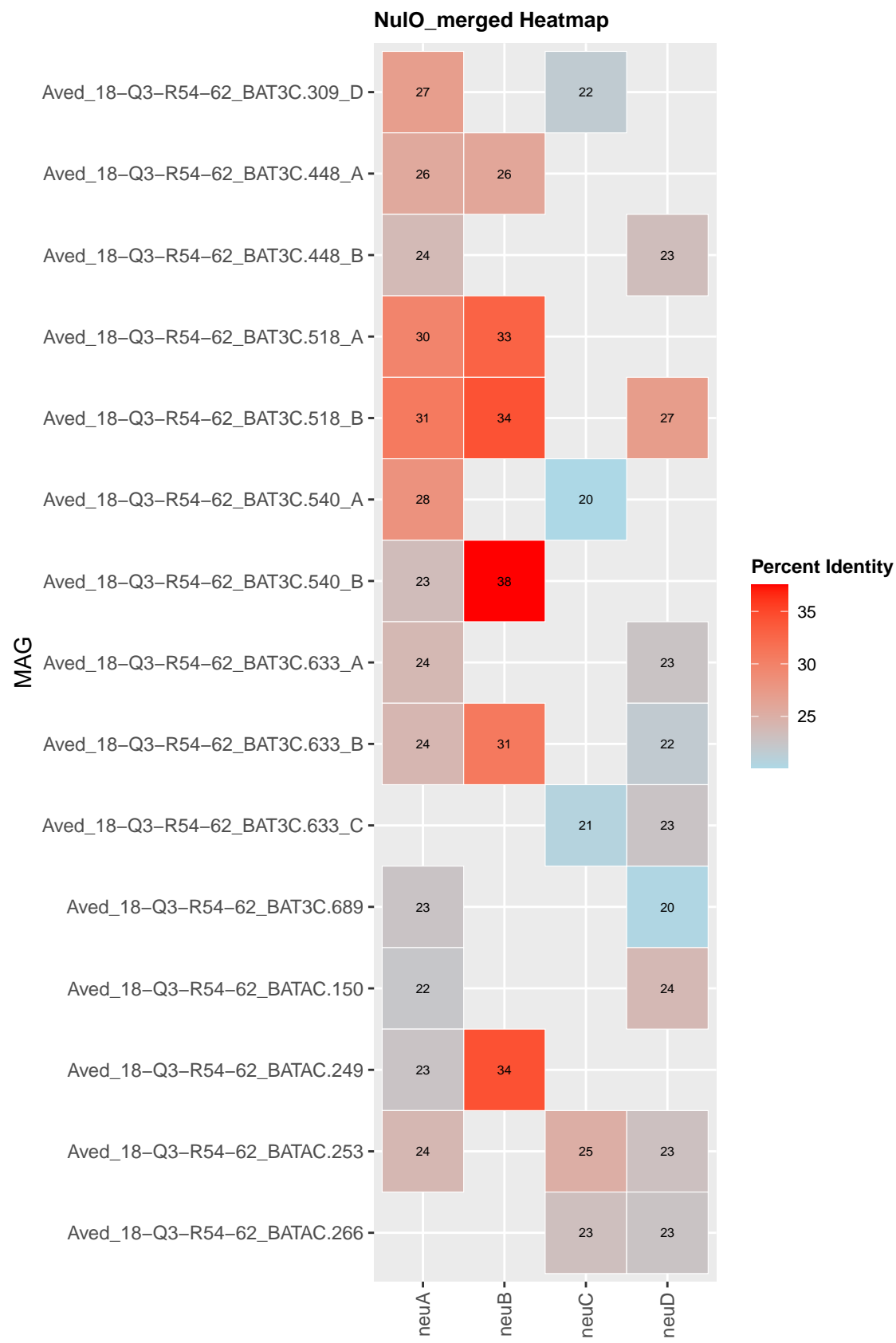


NuIO_merged Heatmap

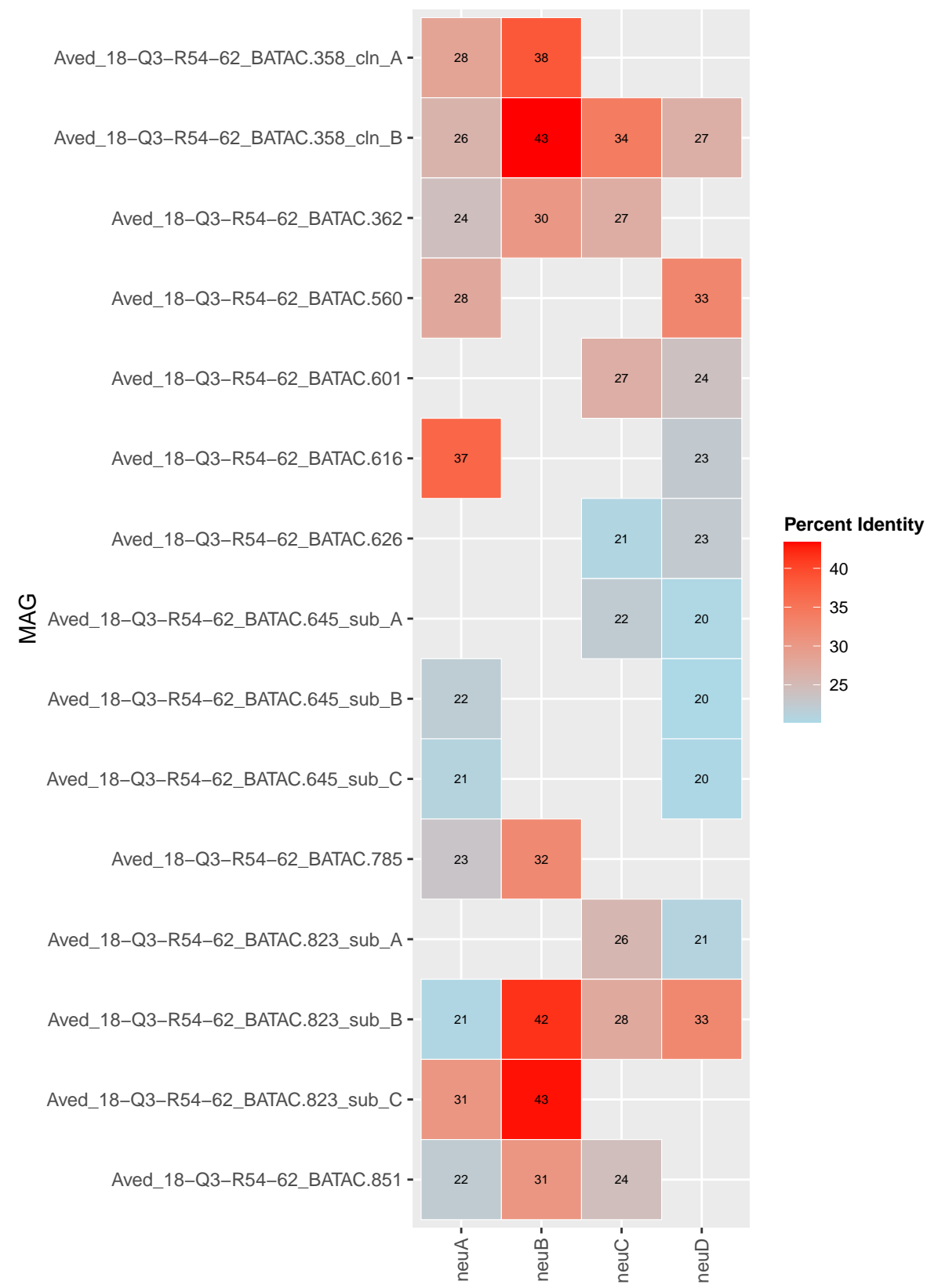
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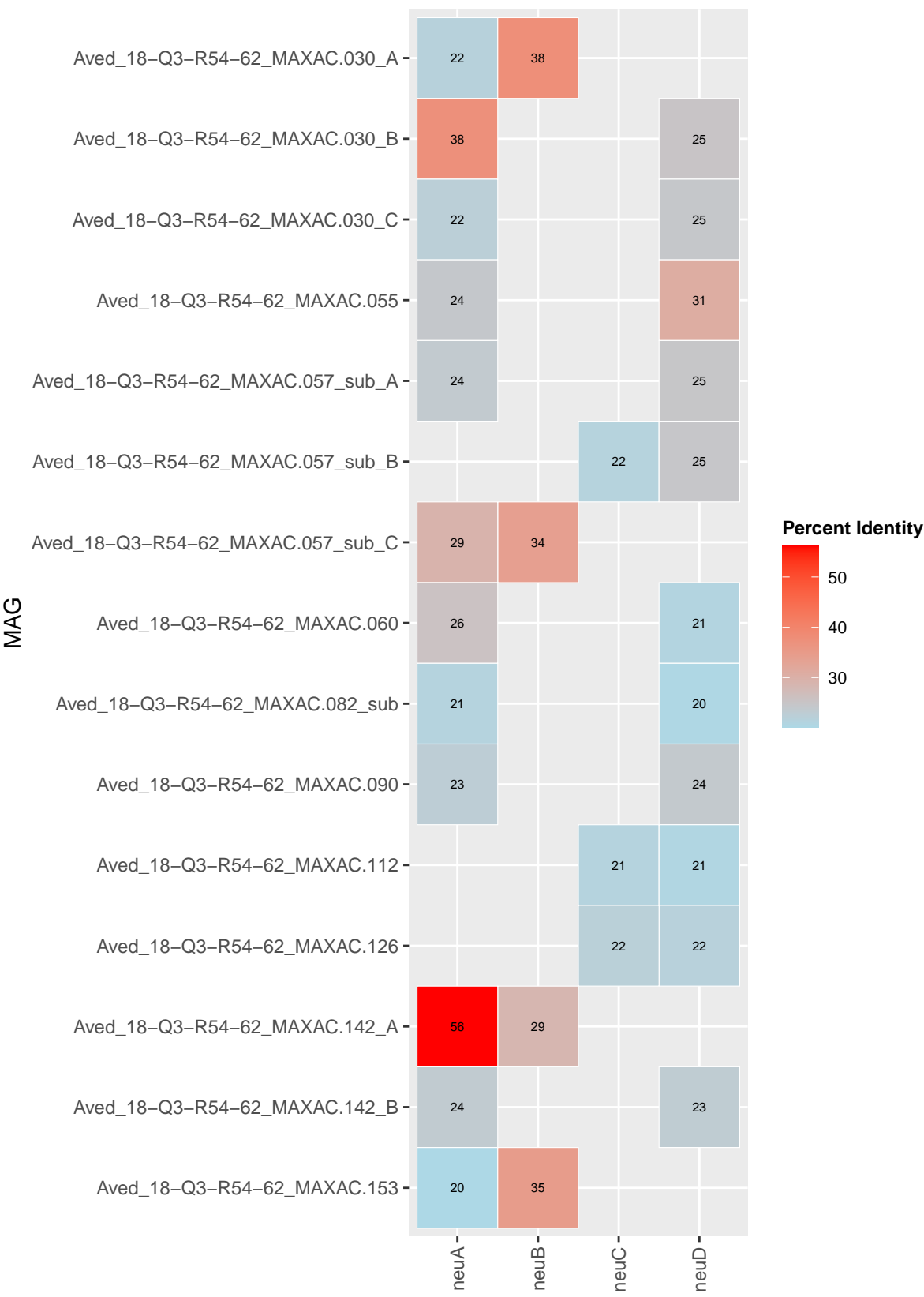




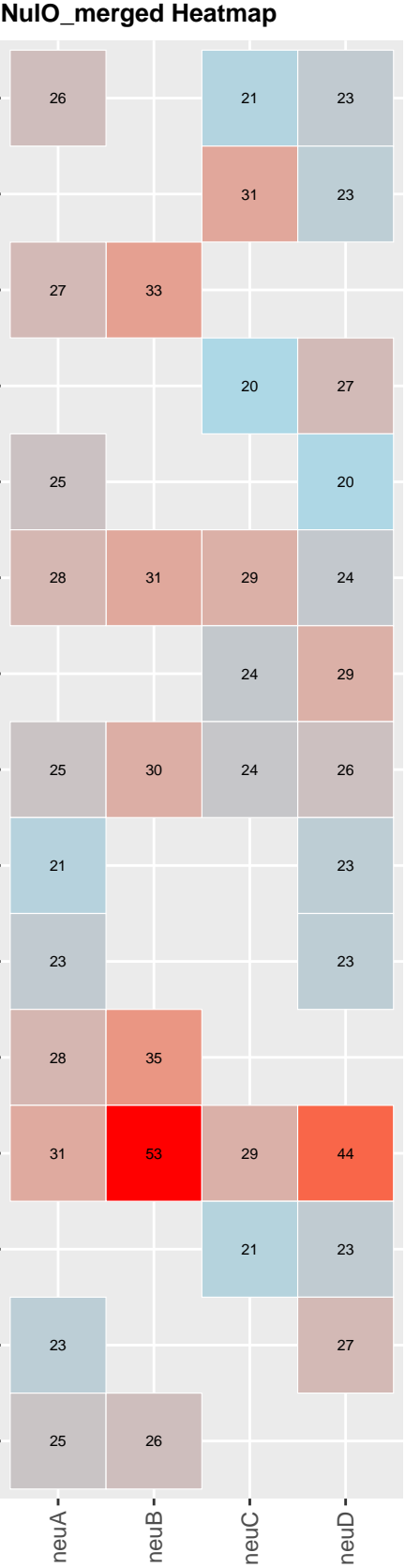
NuIO_merged Heatmap

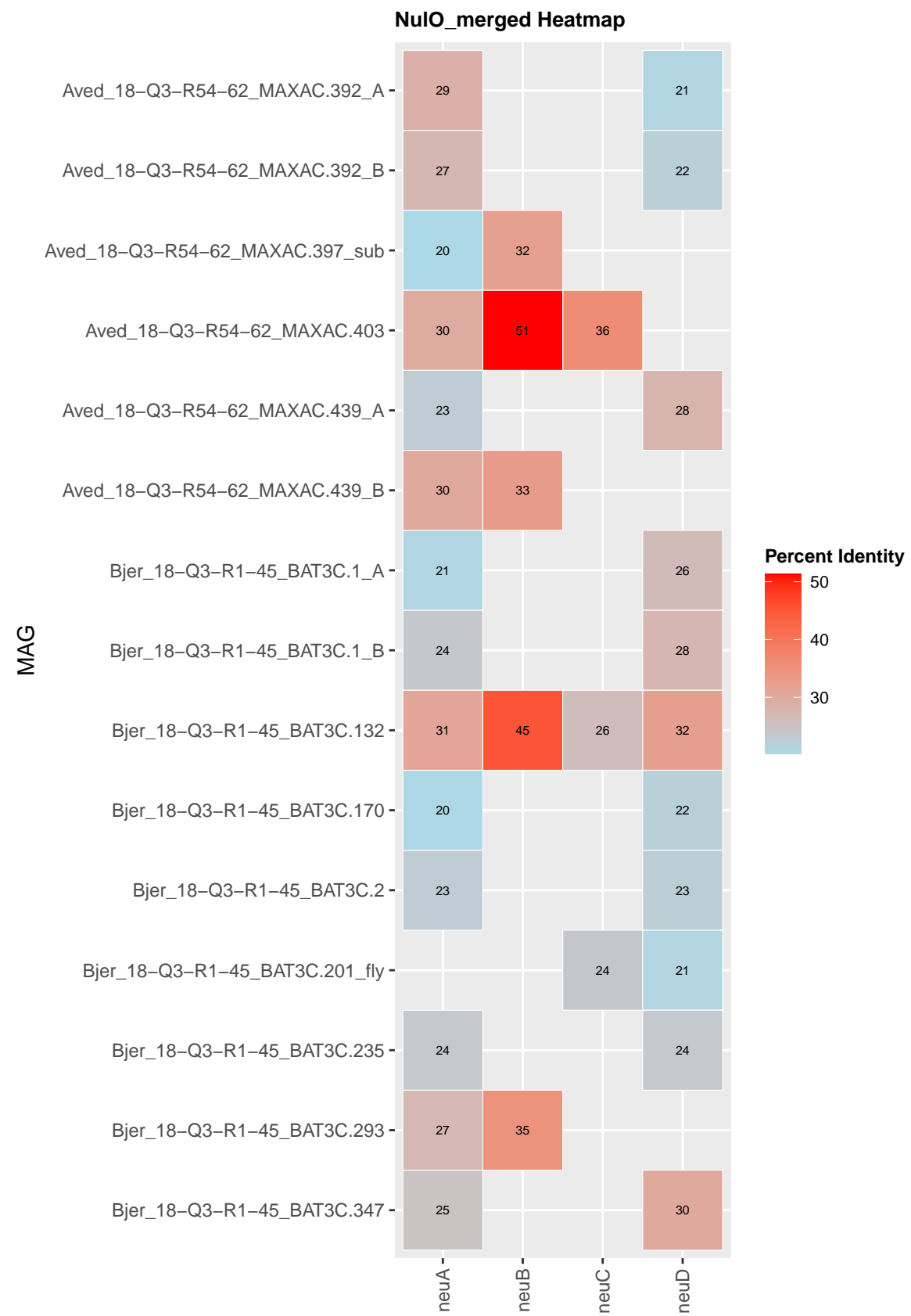


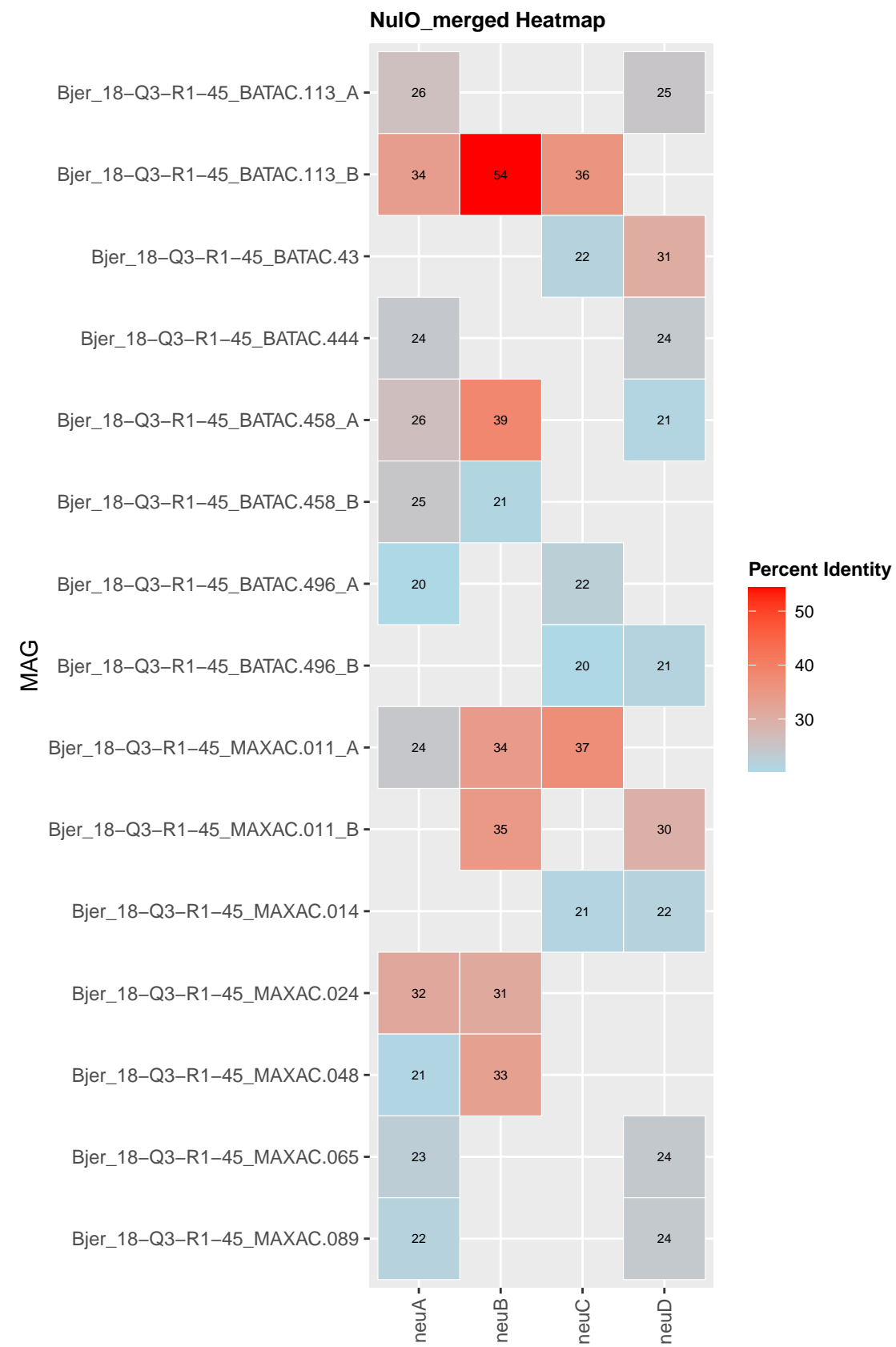
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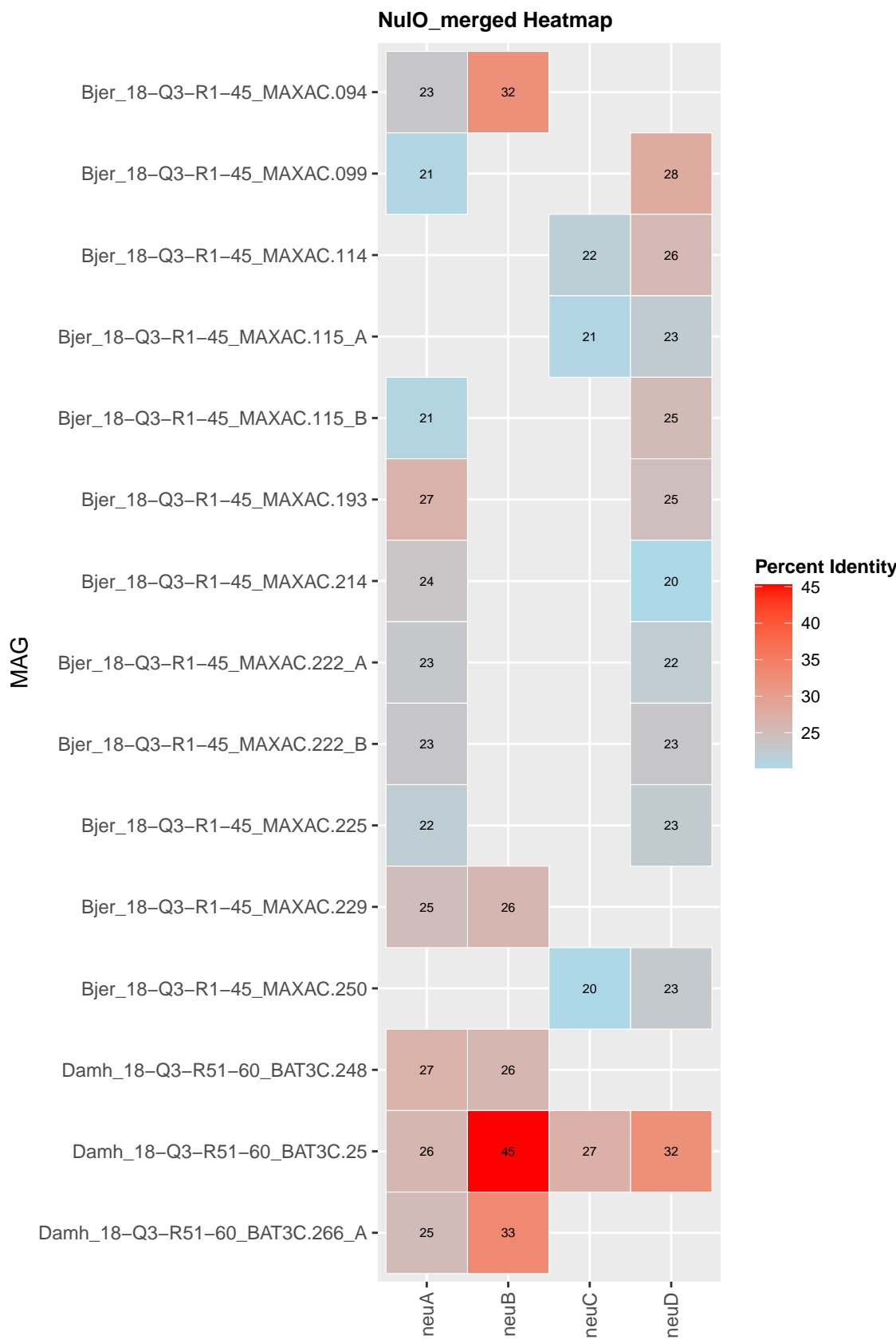


MAG

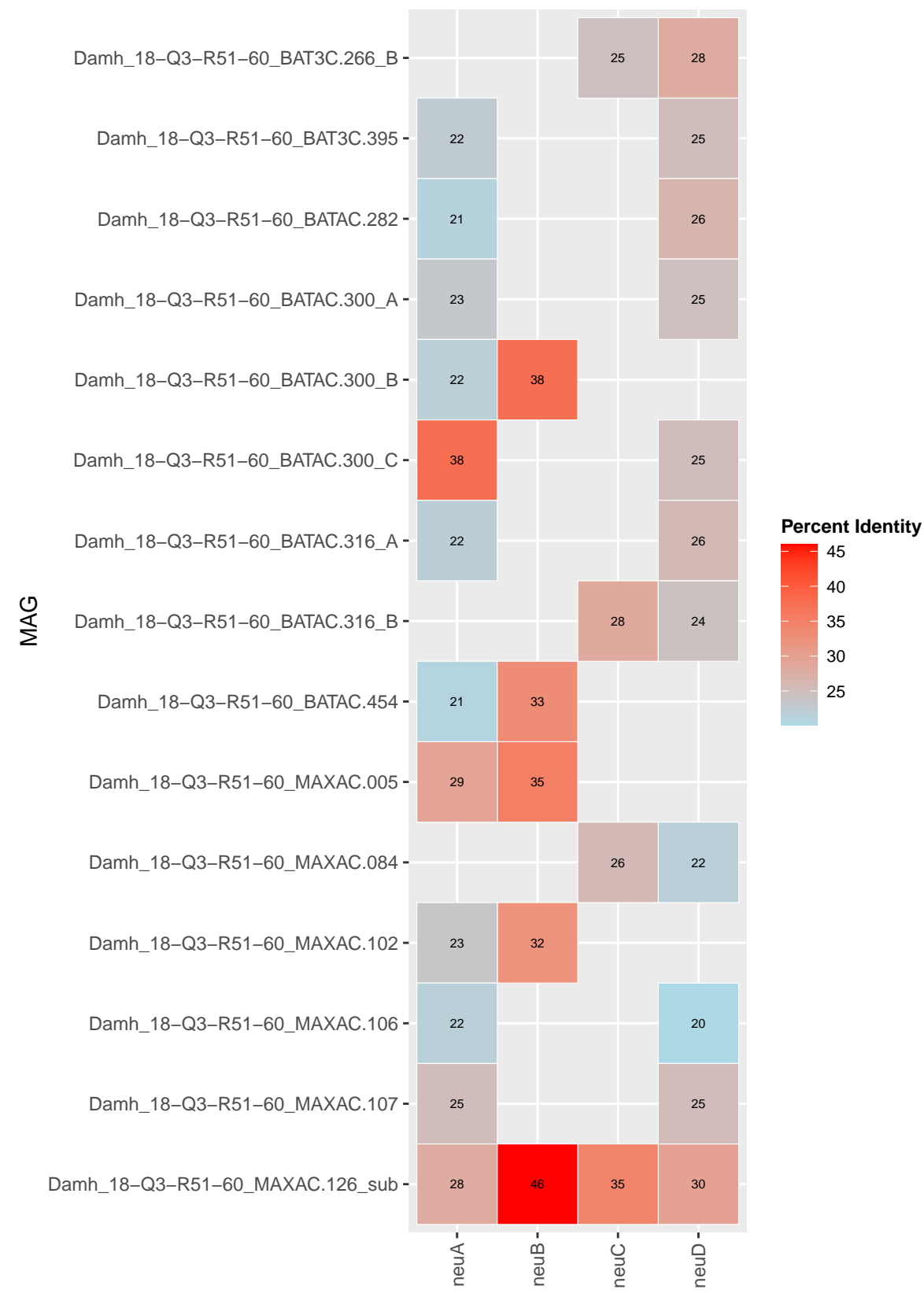


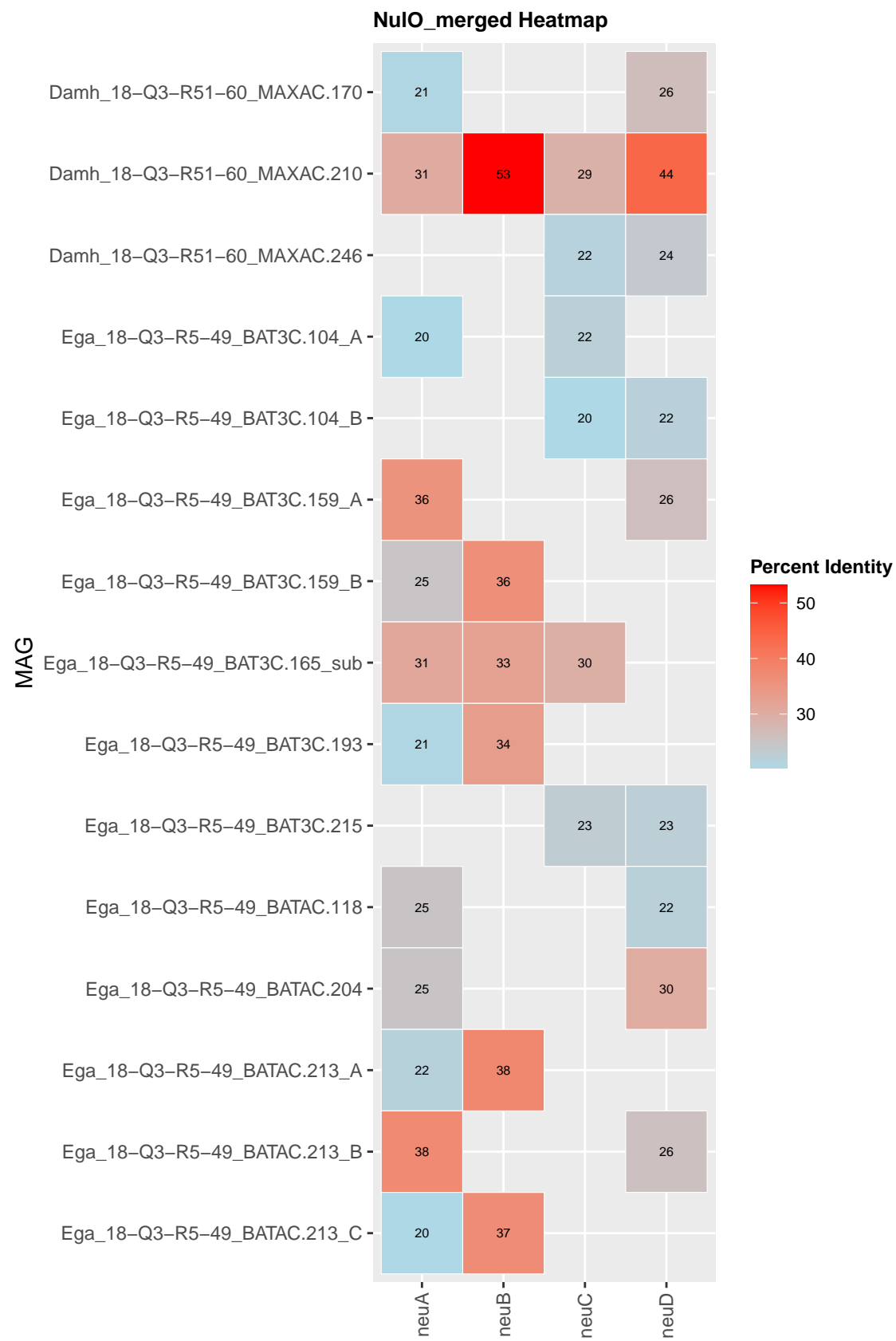


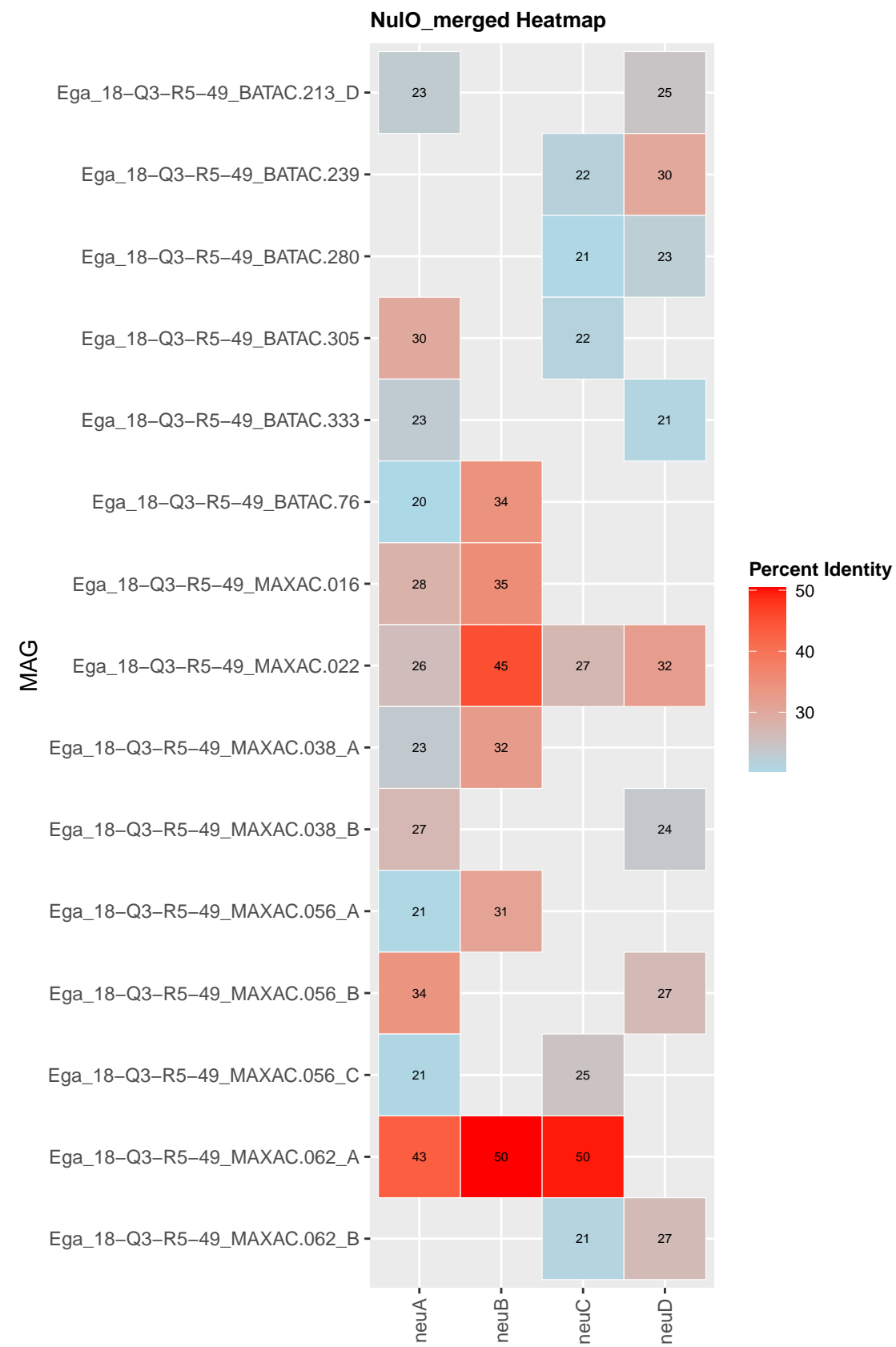


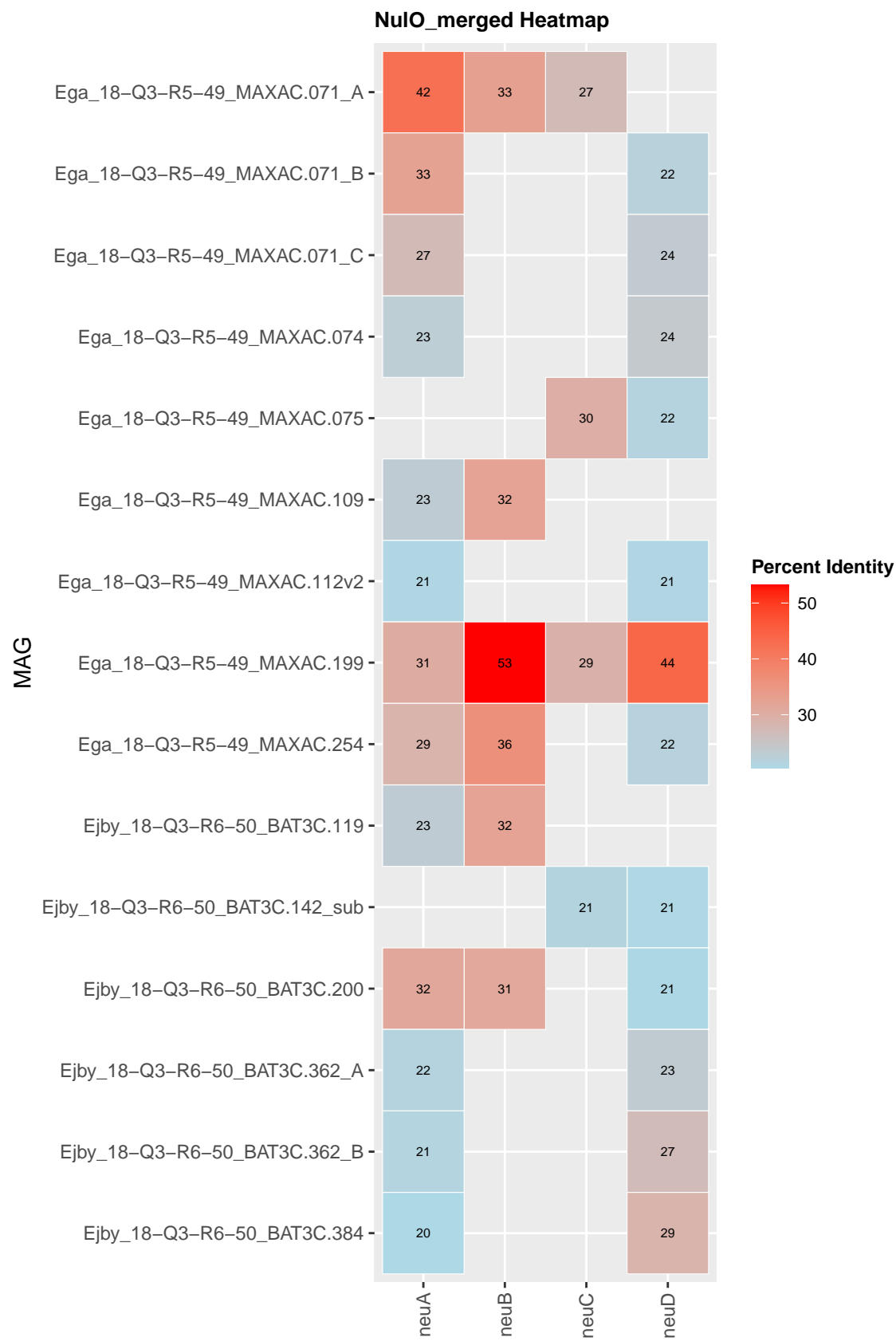


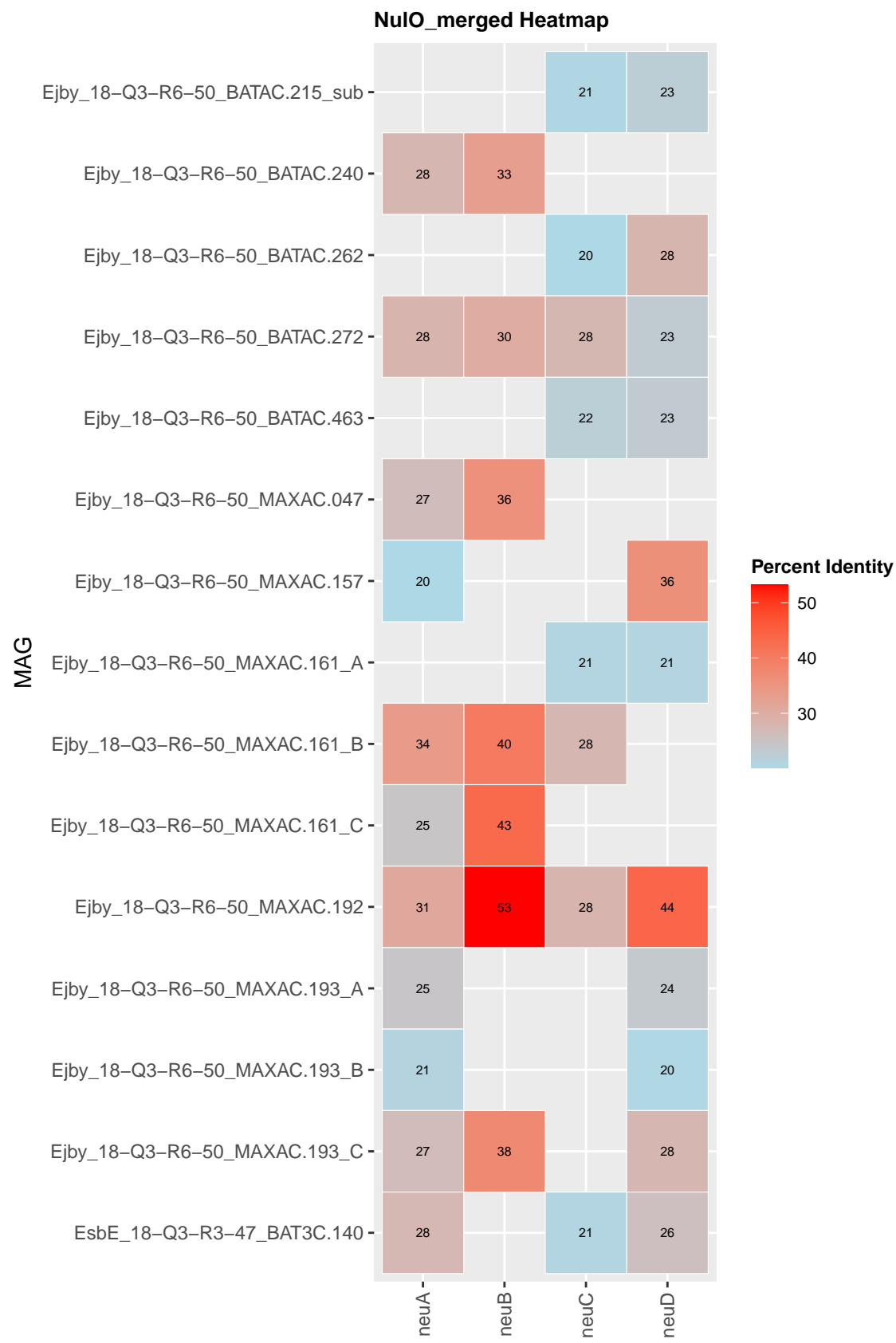
NuIO_merged Heatmap



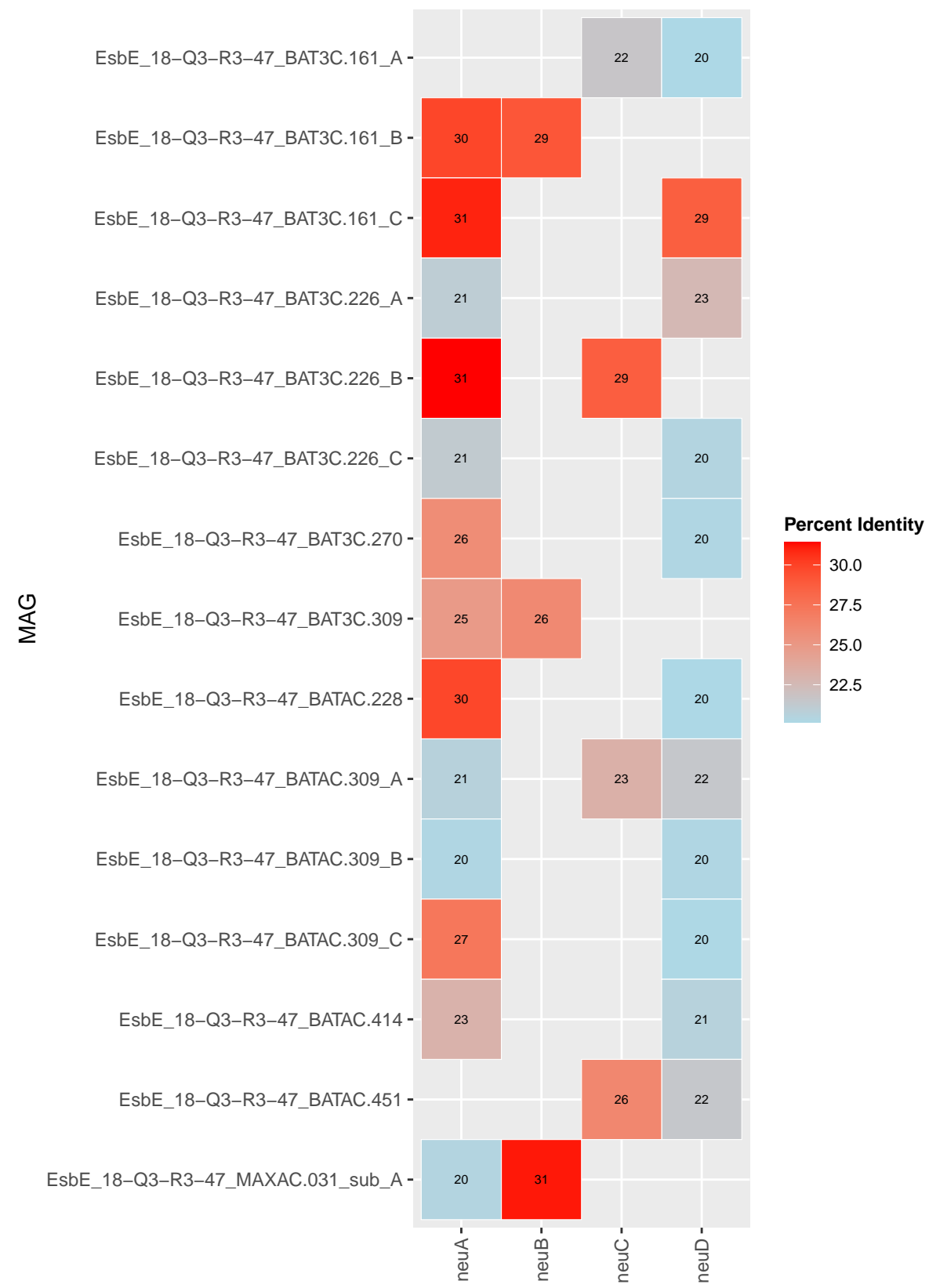




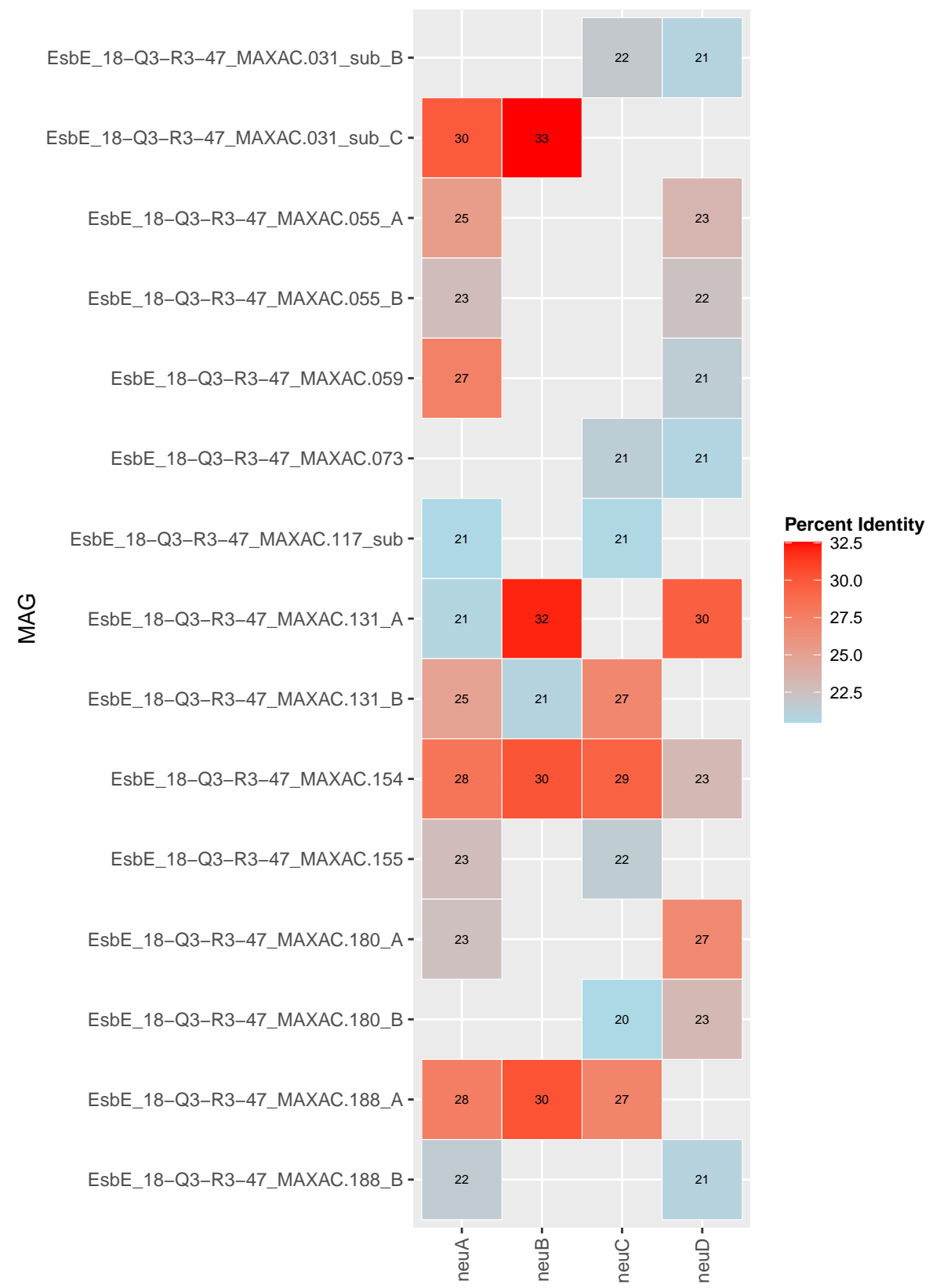


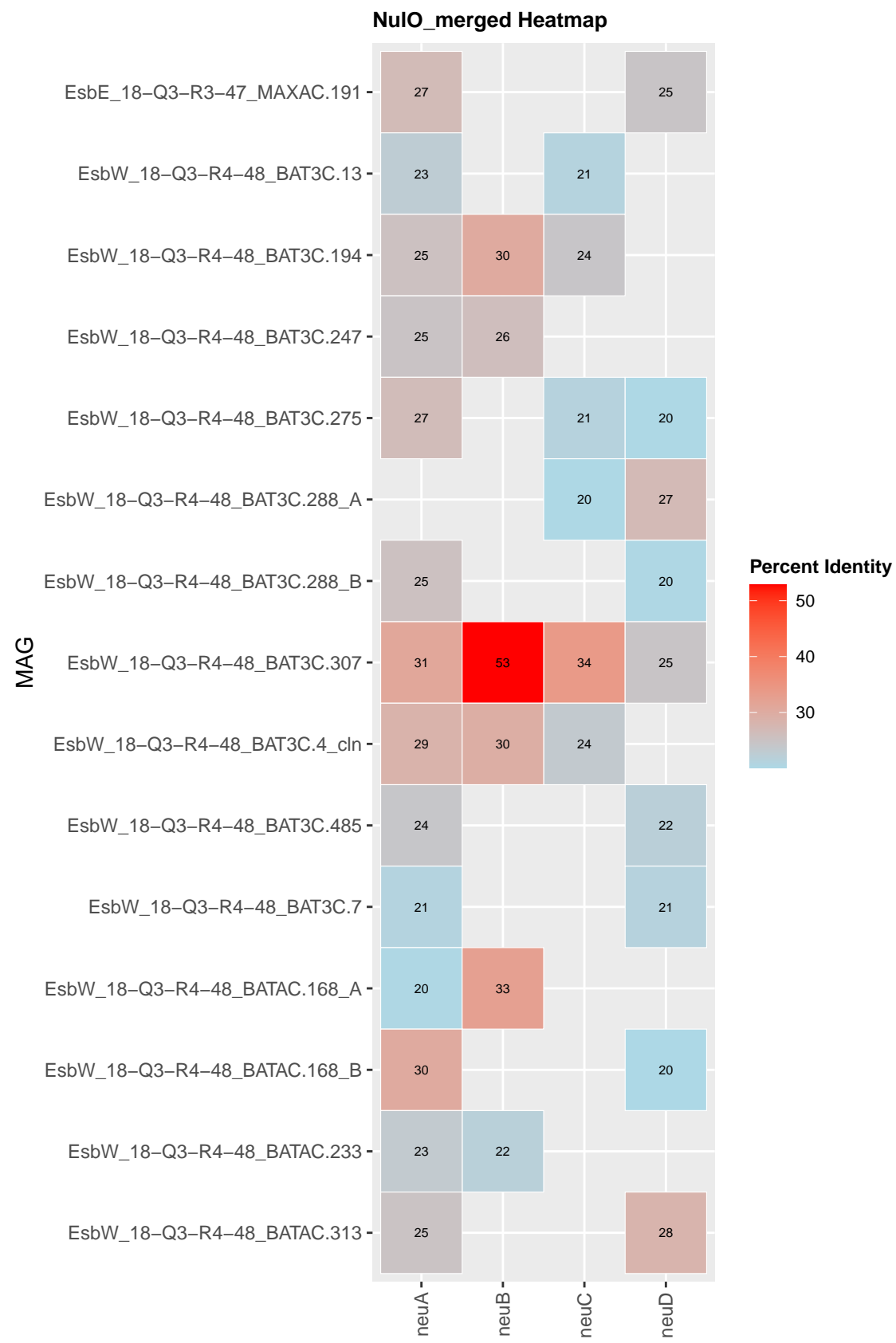


NuIO_merged Heatmap

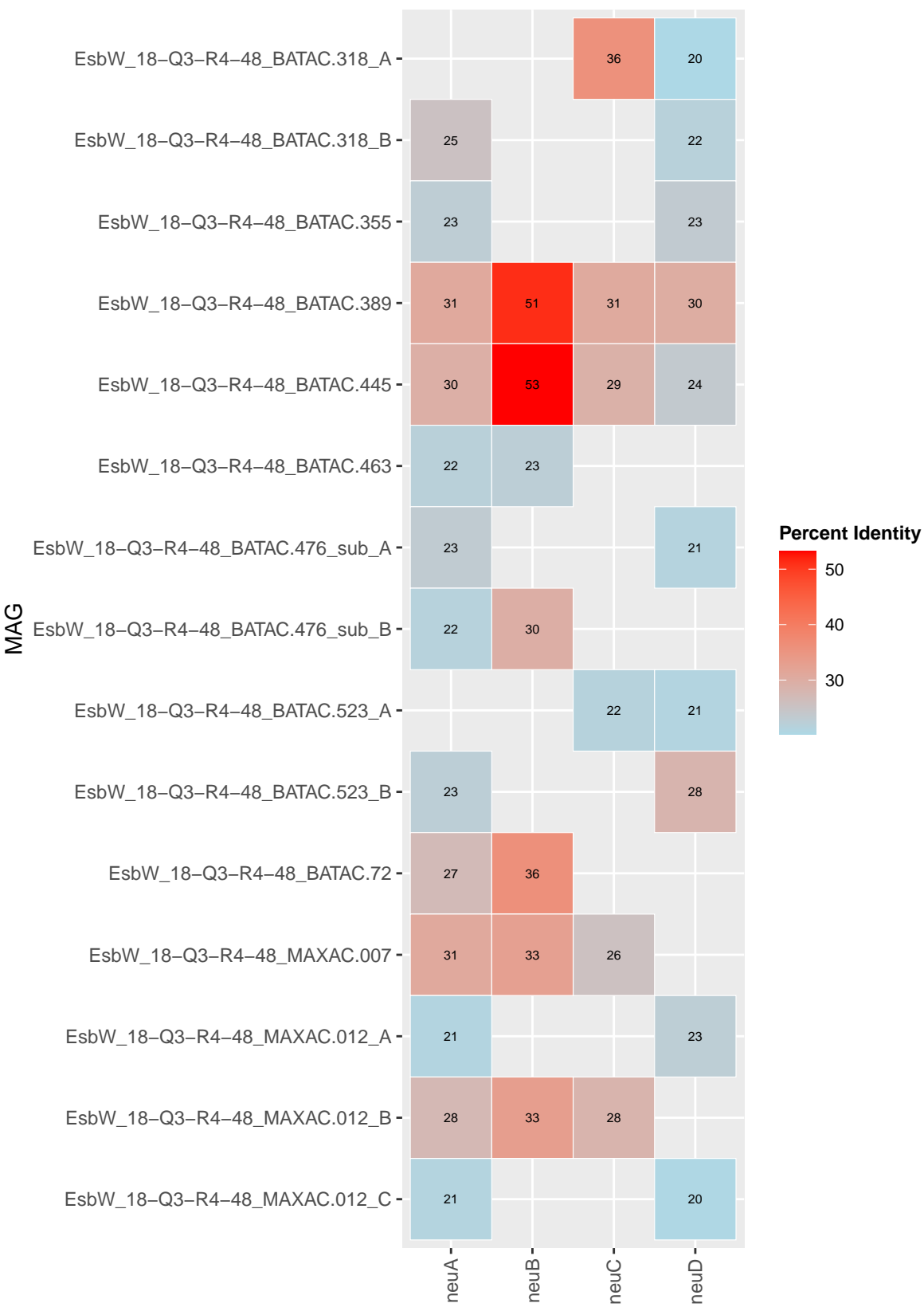


NuLO_merged Heatmap



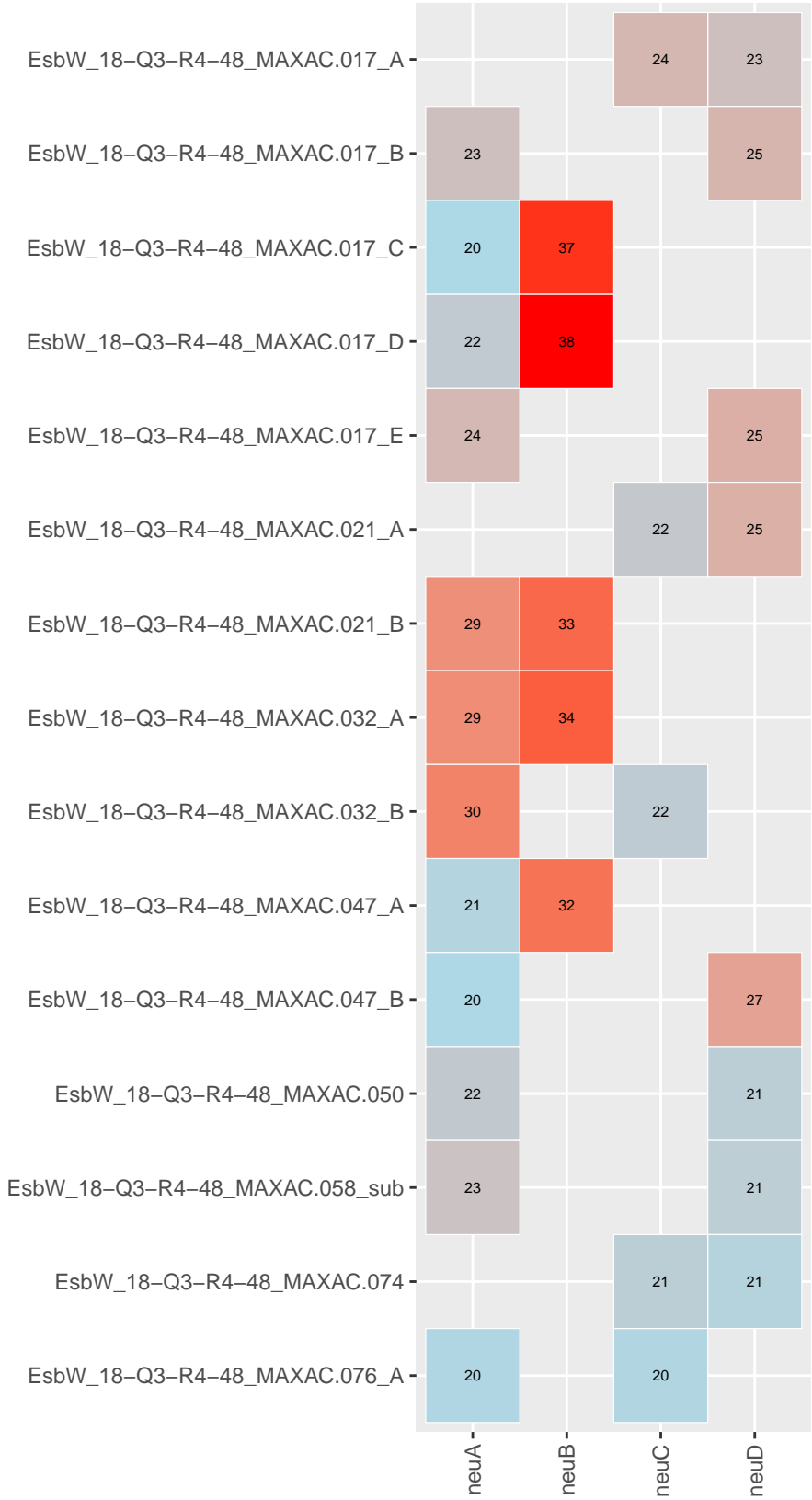


NuIO_merged Heatmap

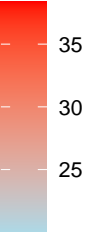


NuIO_merged Heatmap

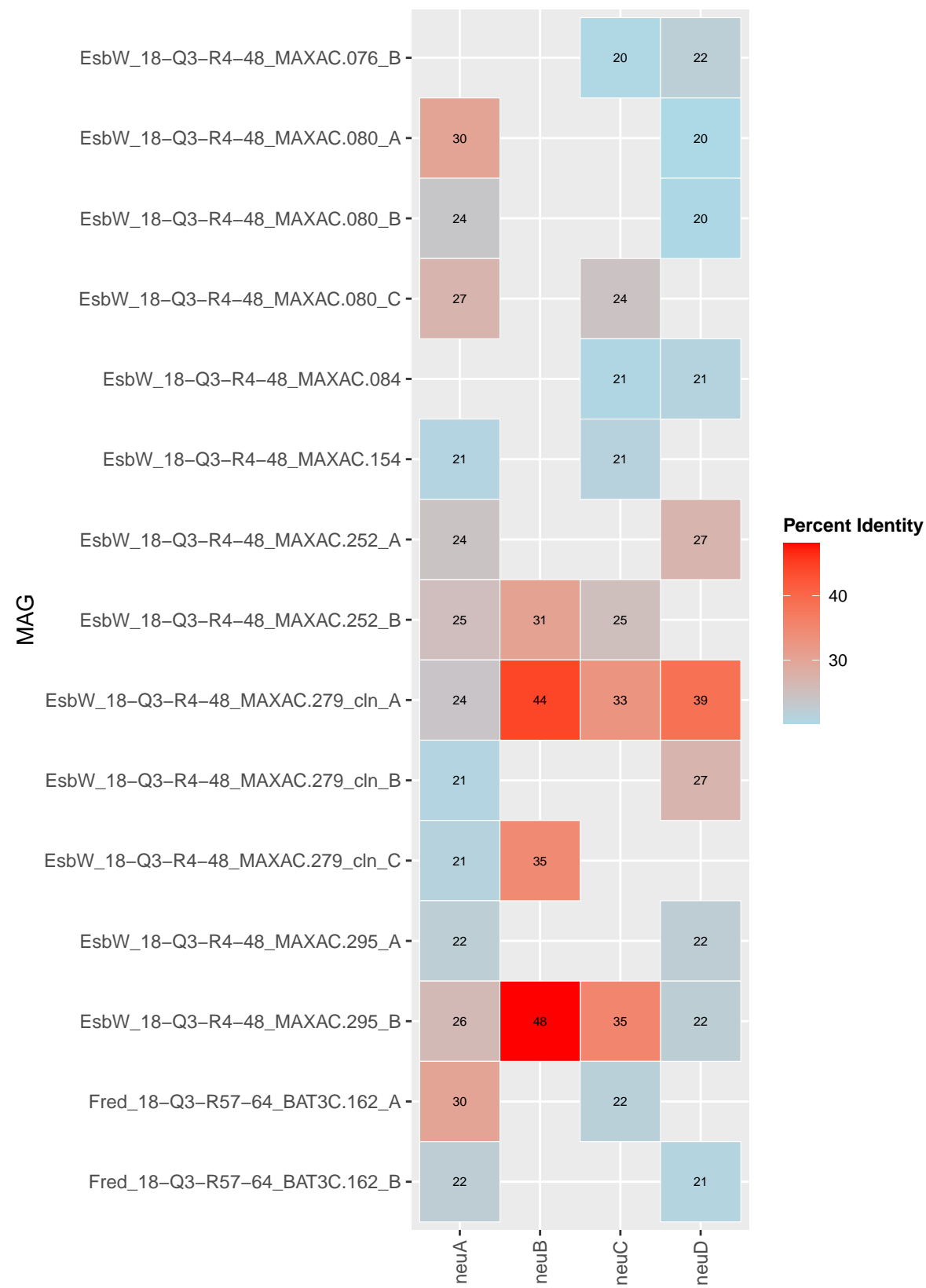
MAG

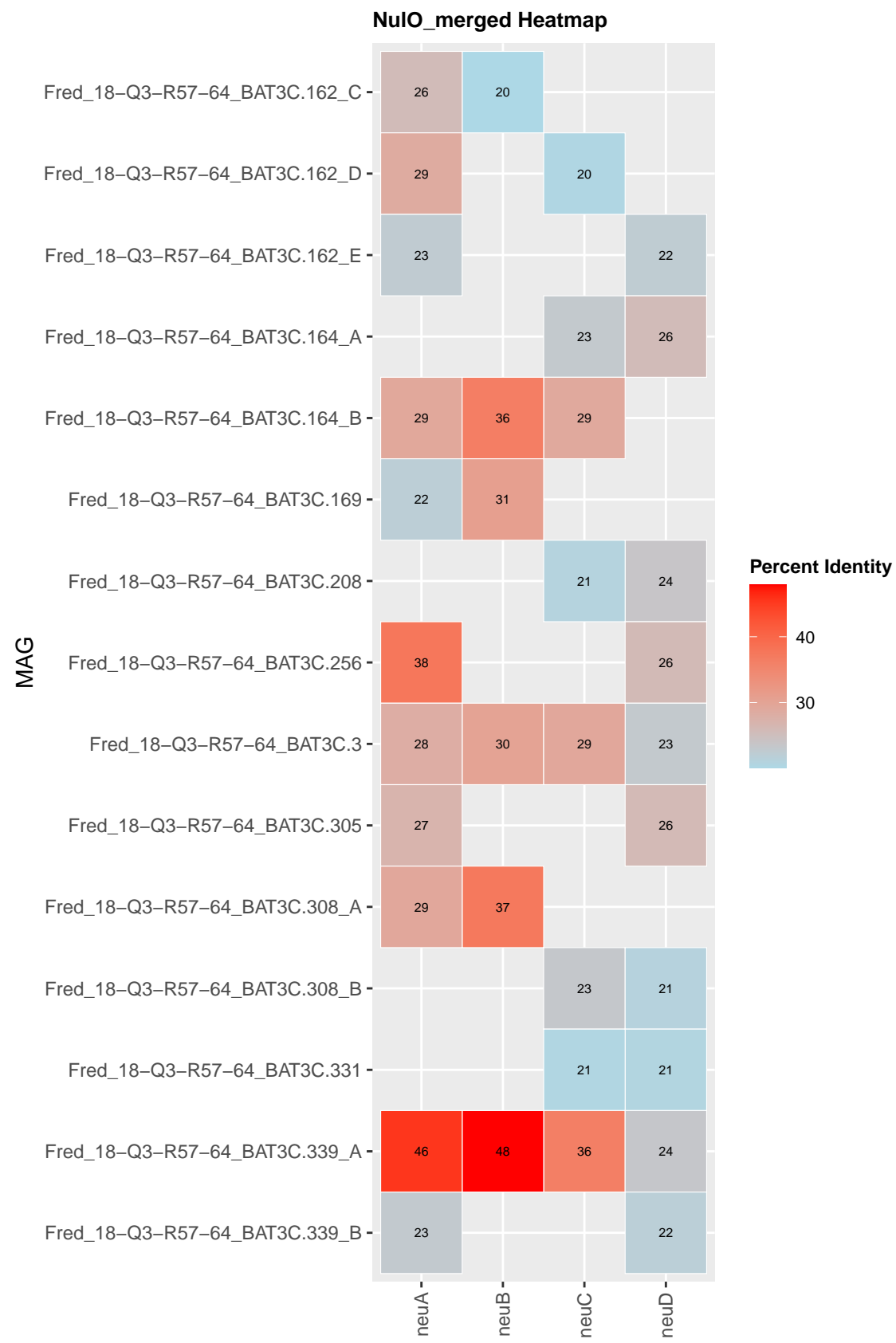


Percent Identity

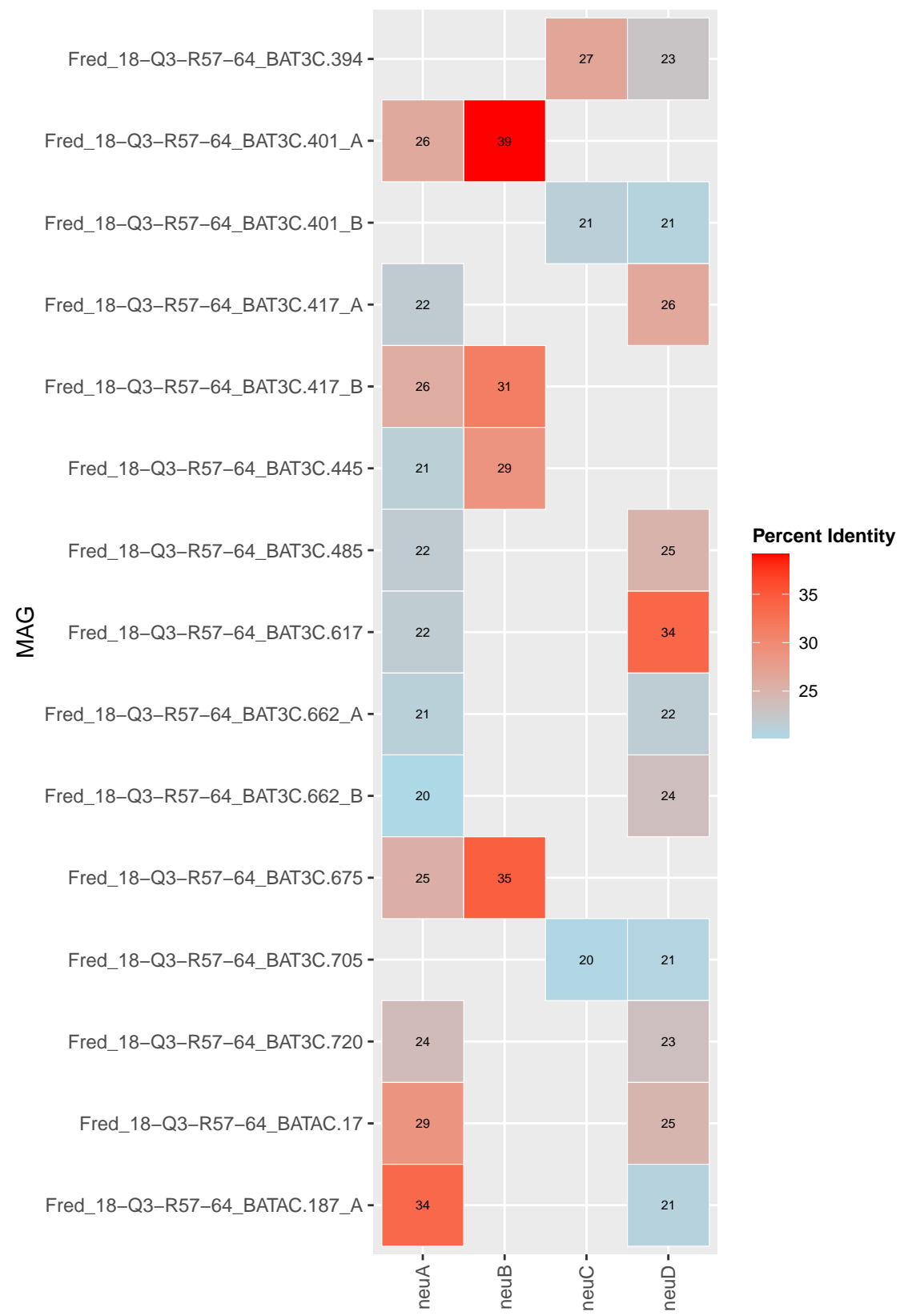


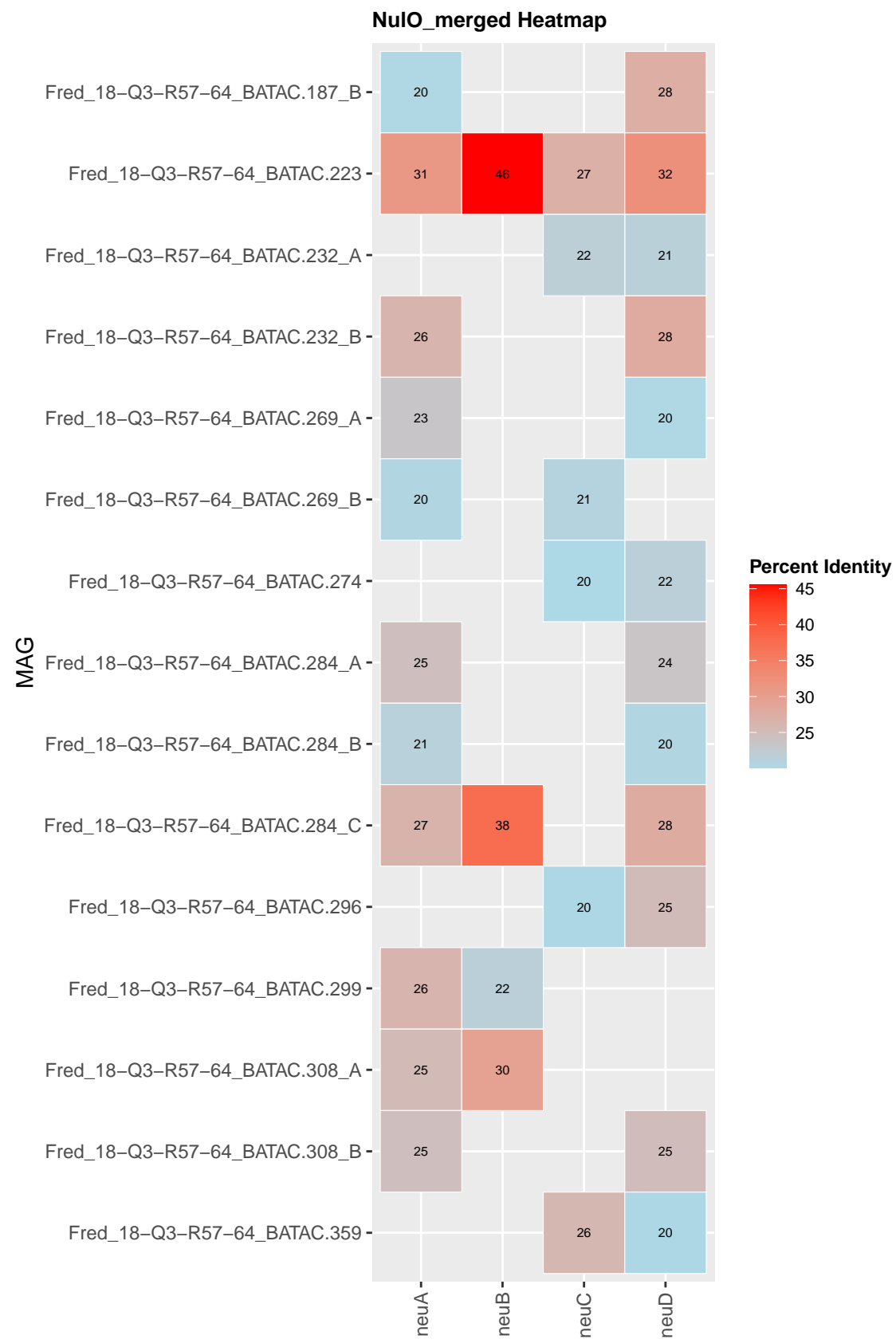
NuIO_merged Heatmap

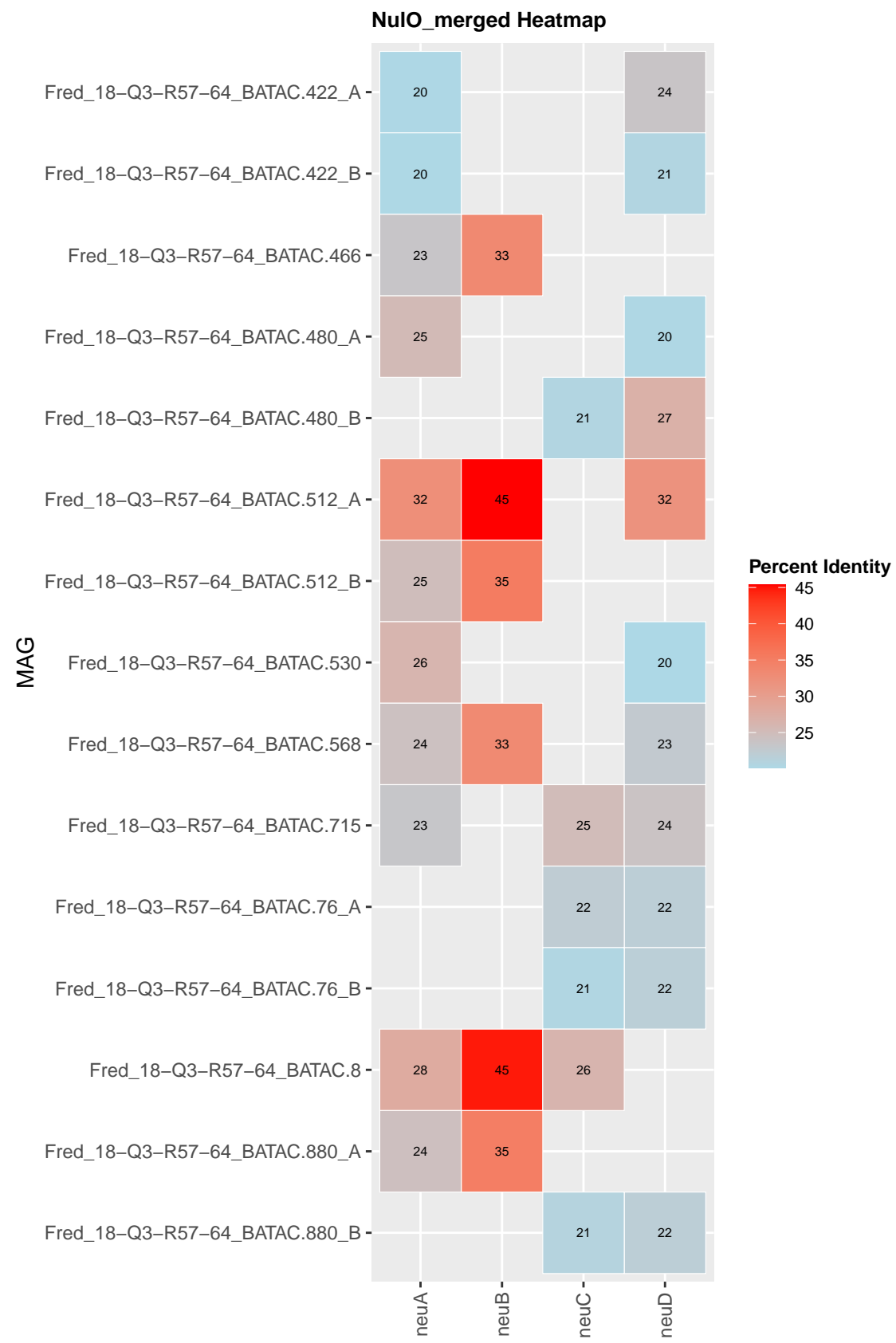




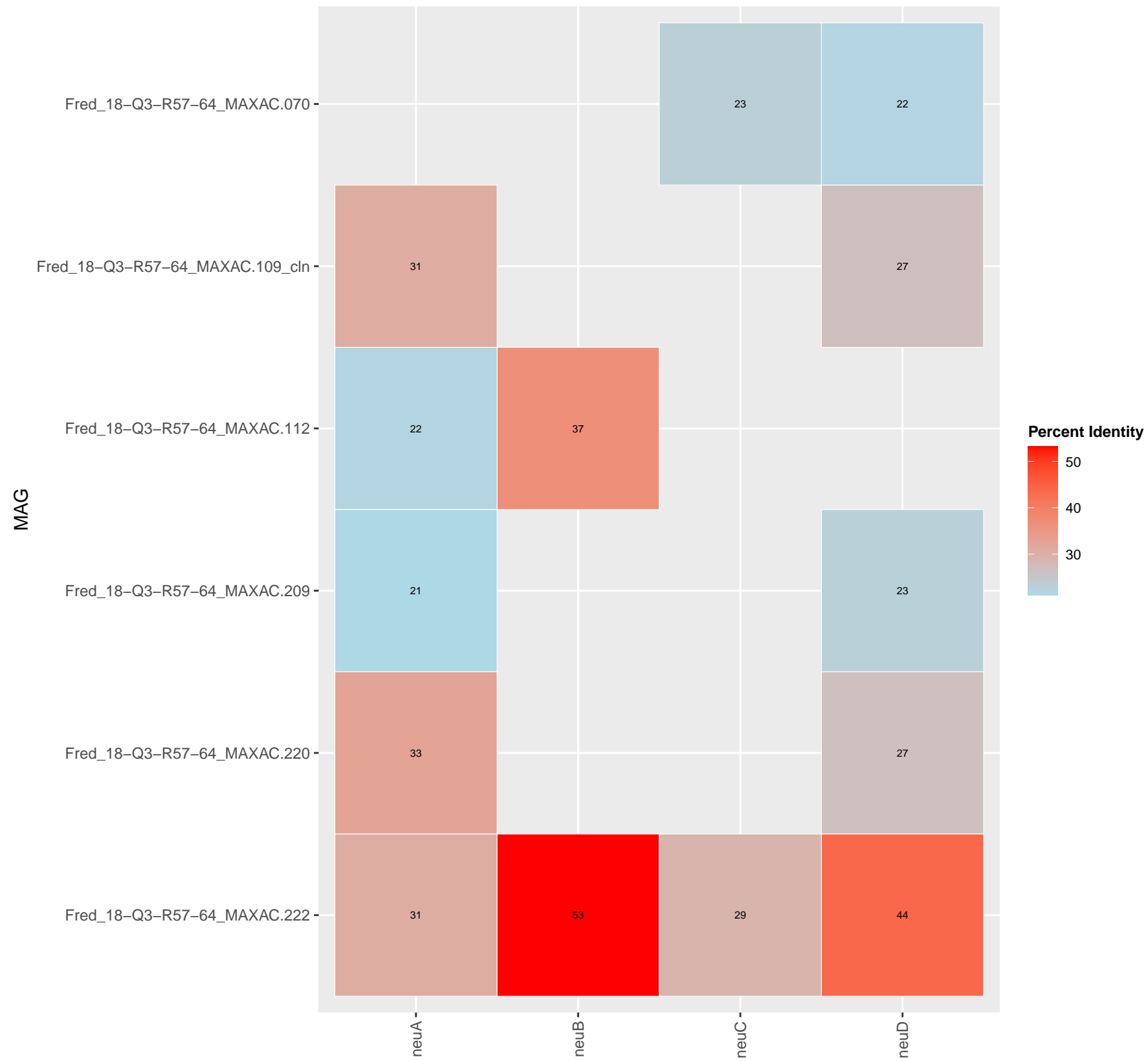
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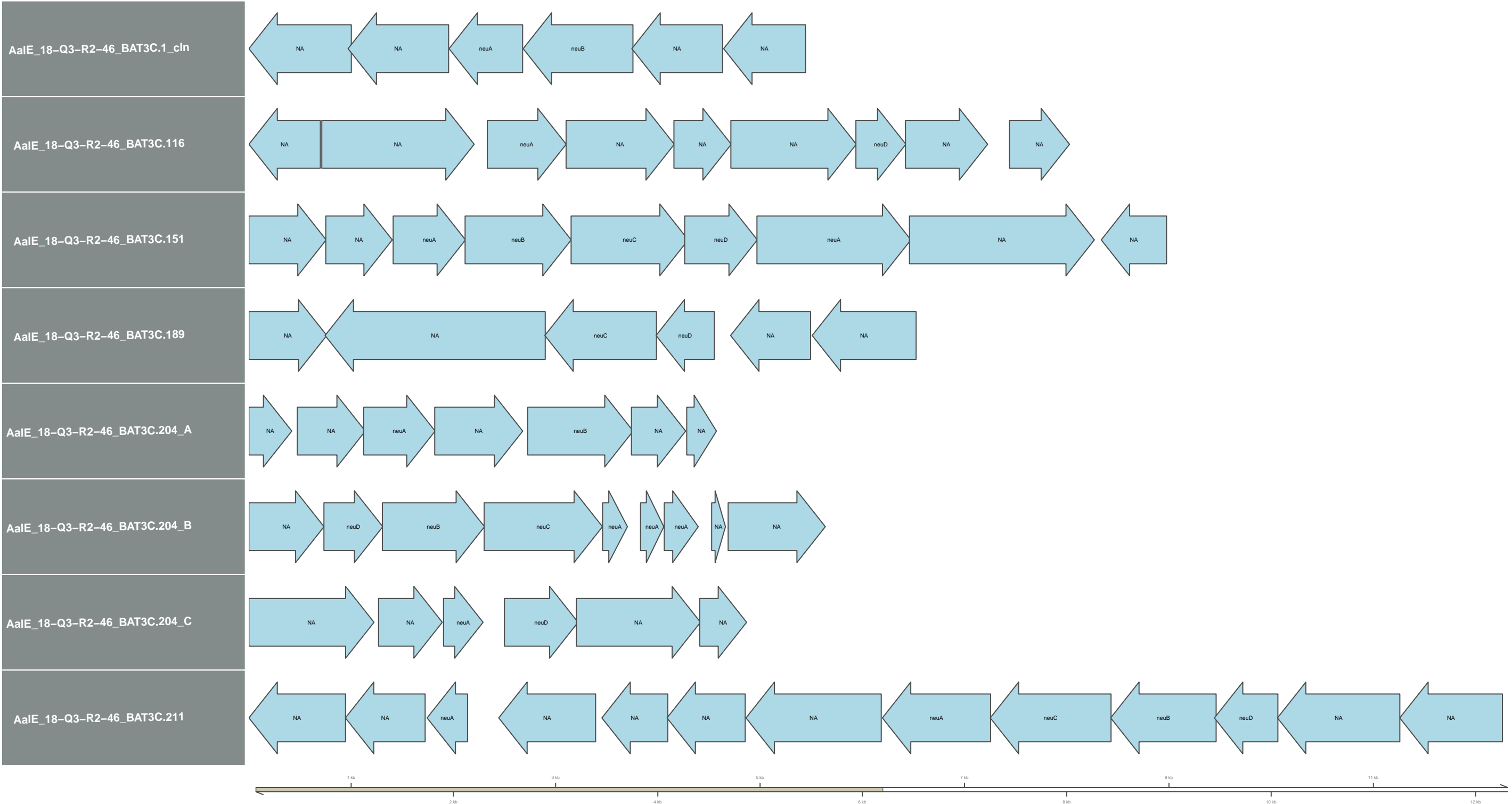




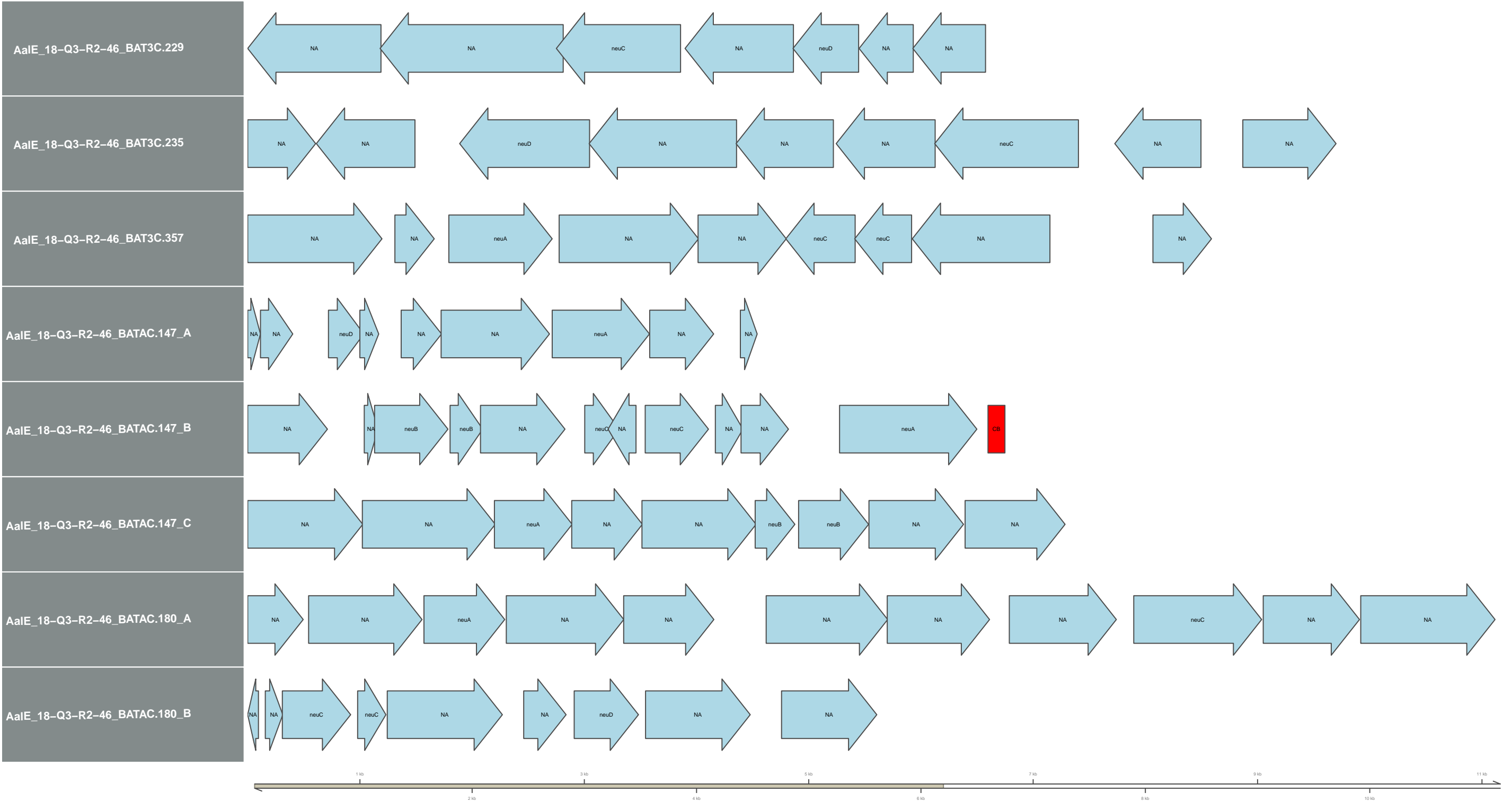
NuIO_merged Heatmap



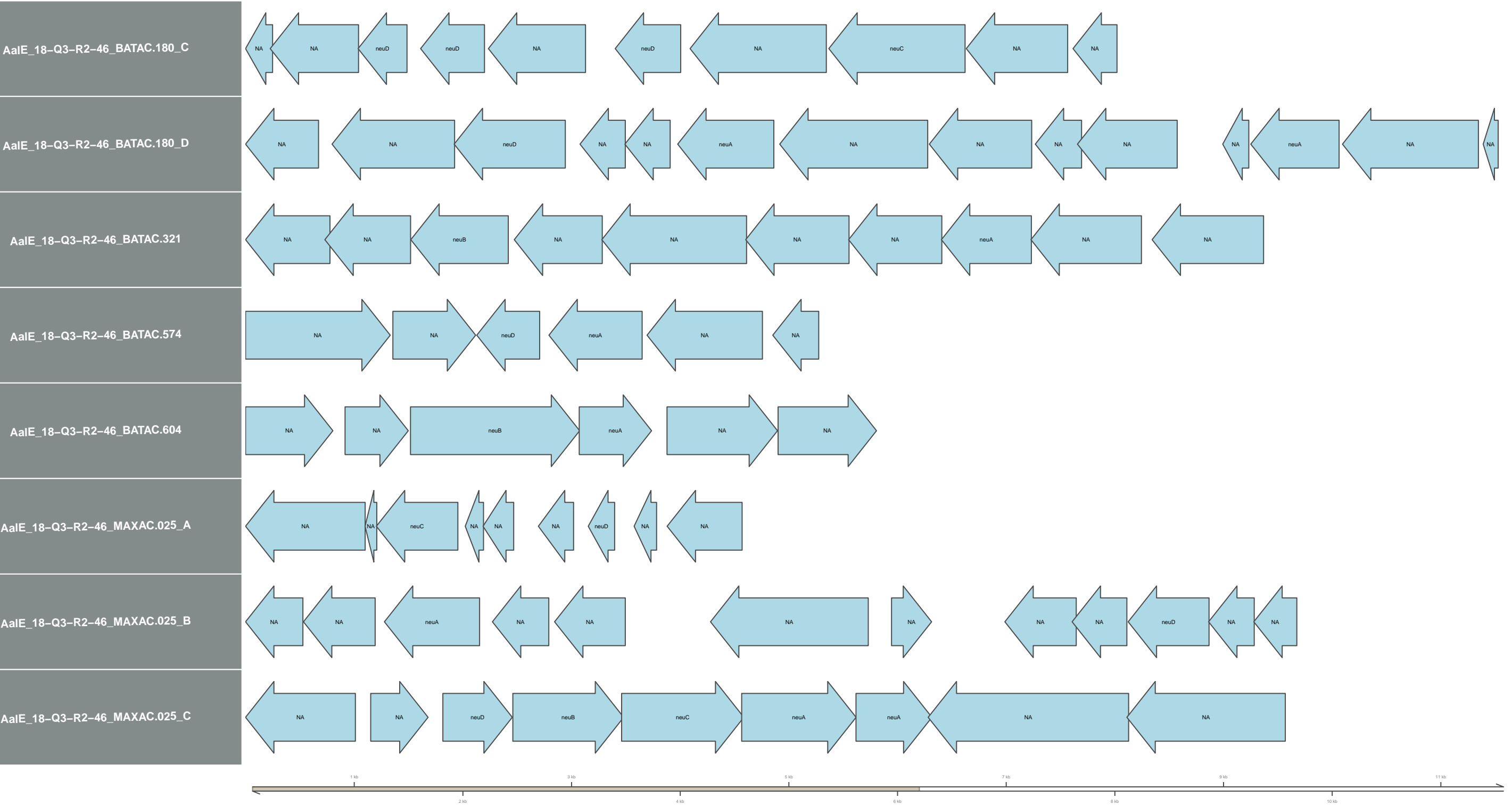
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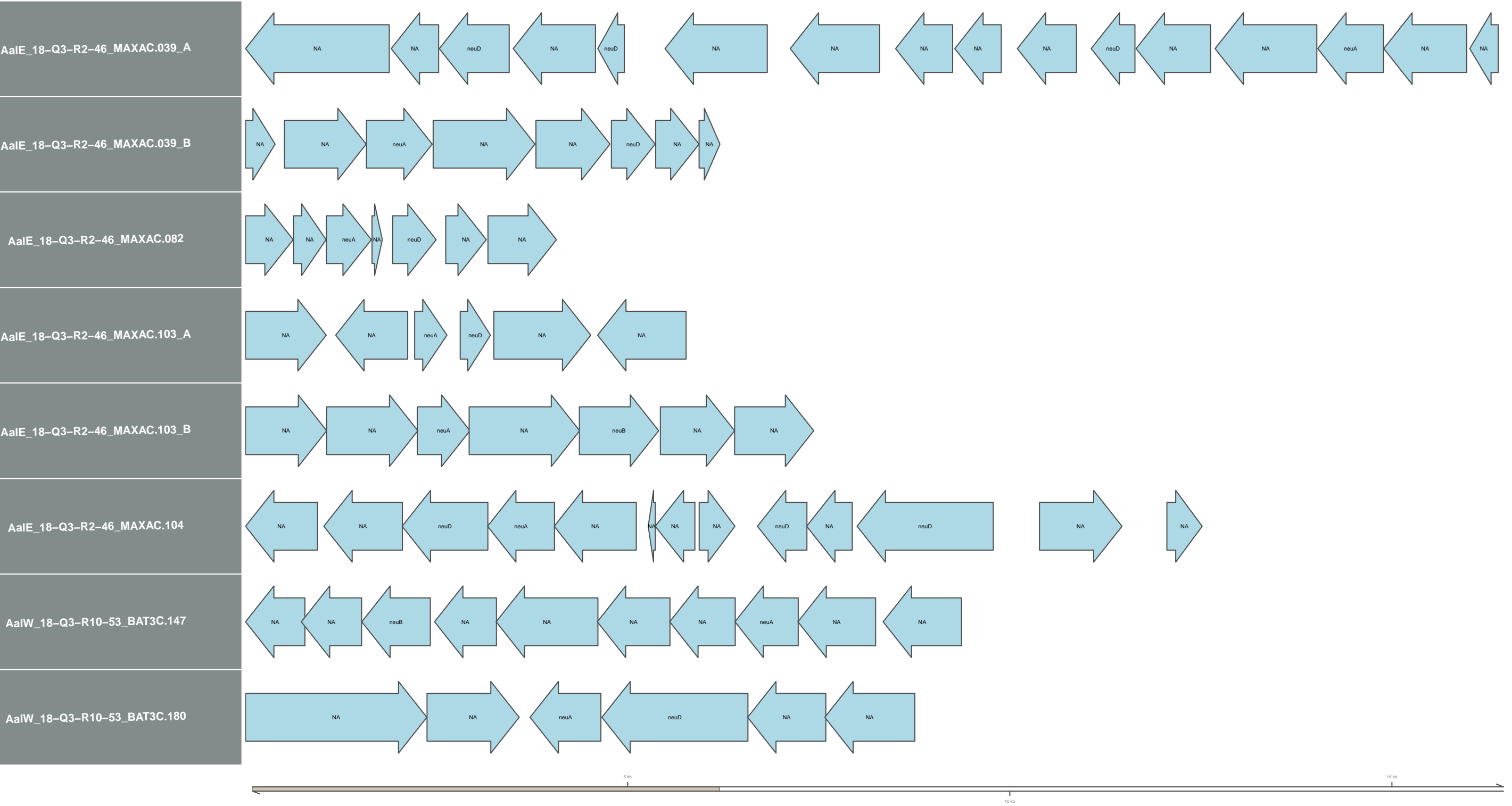
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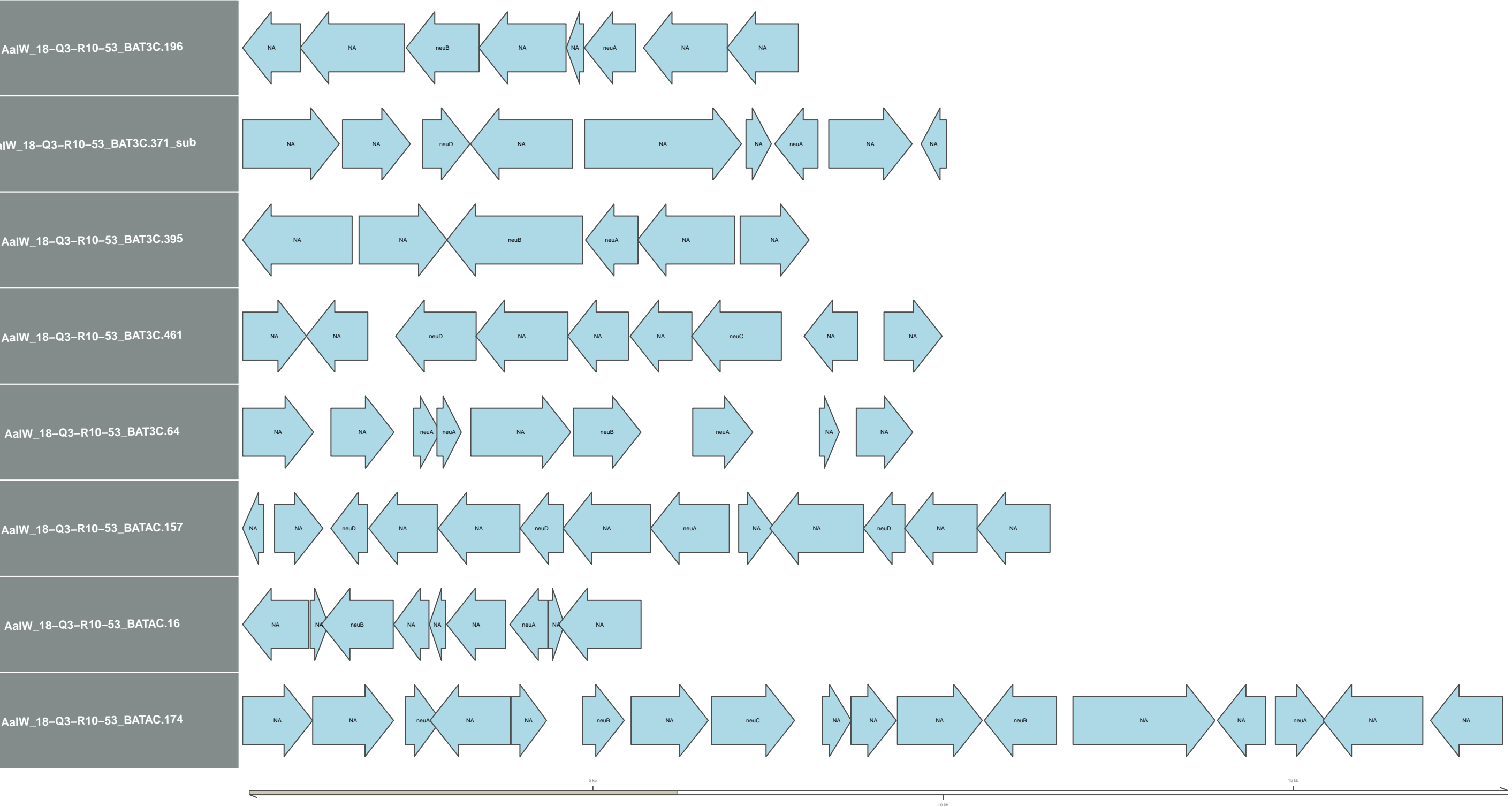
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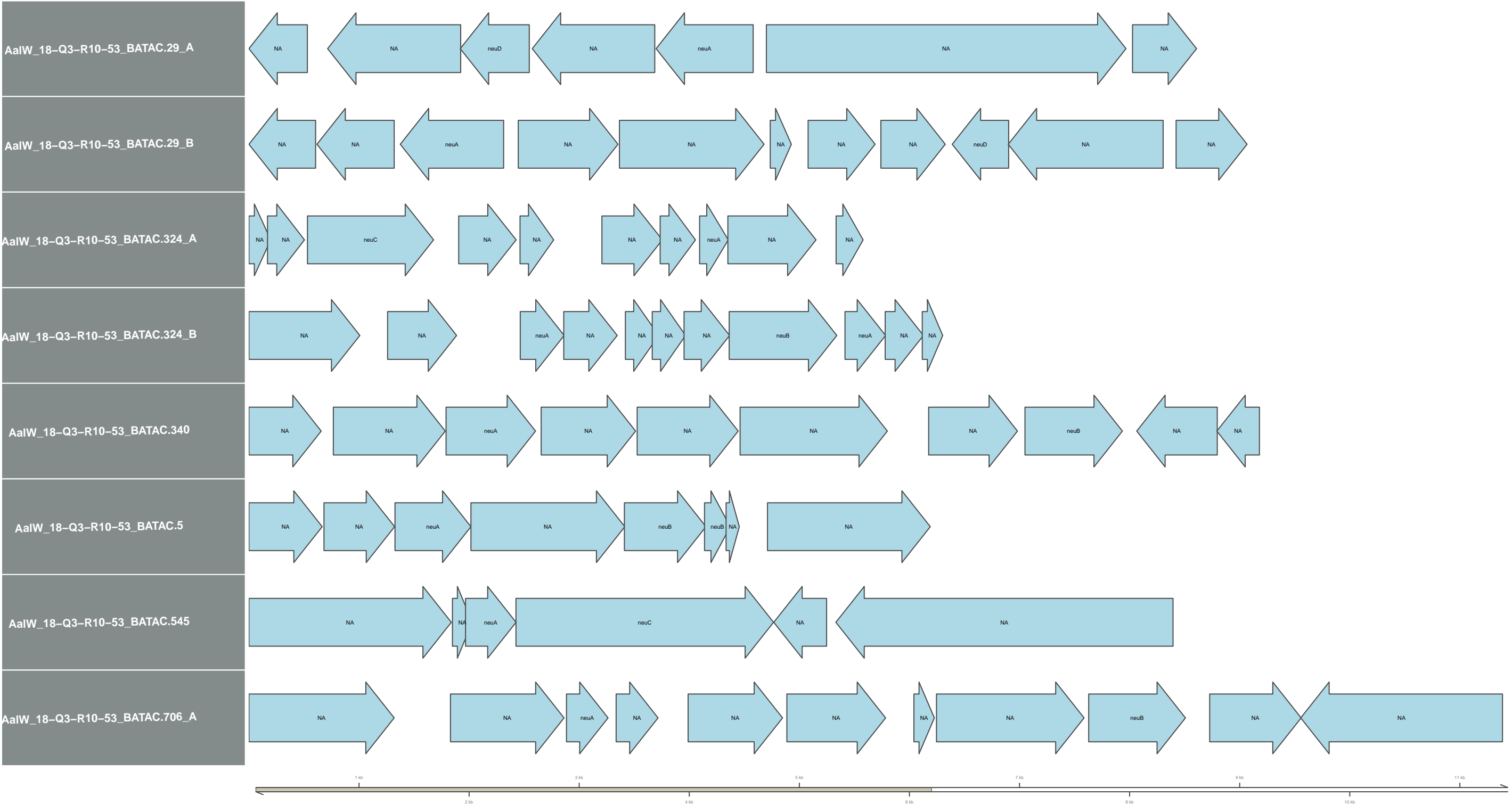
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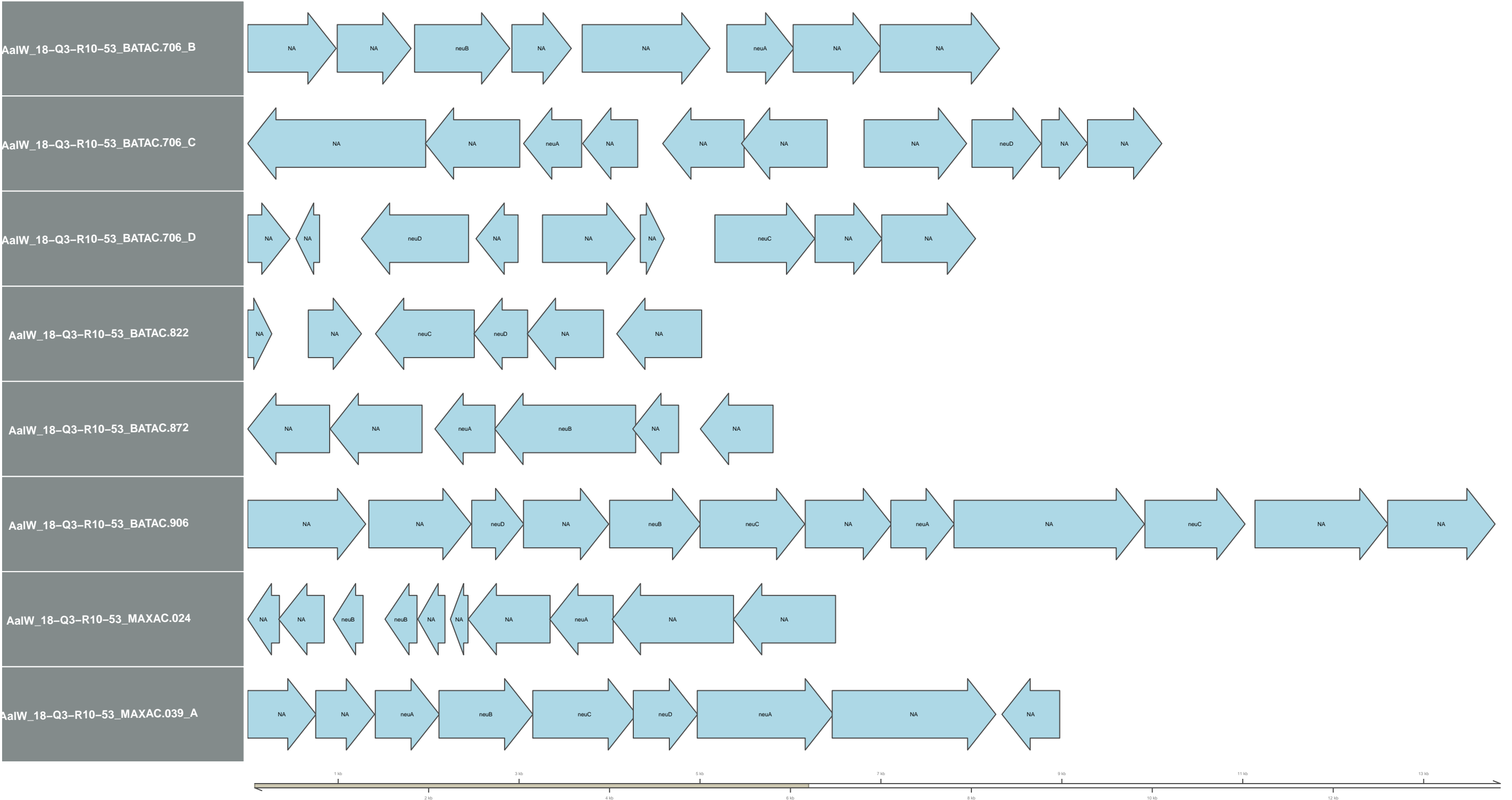
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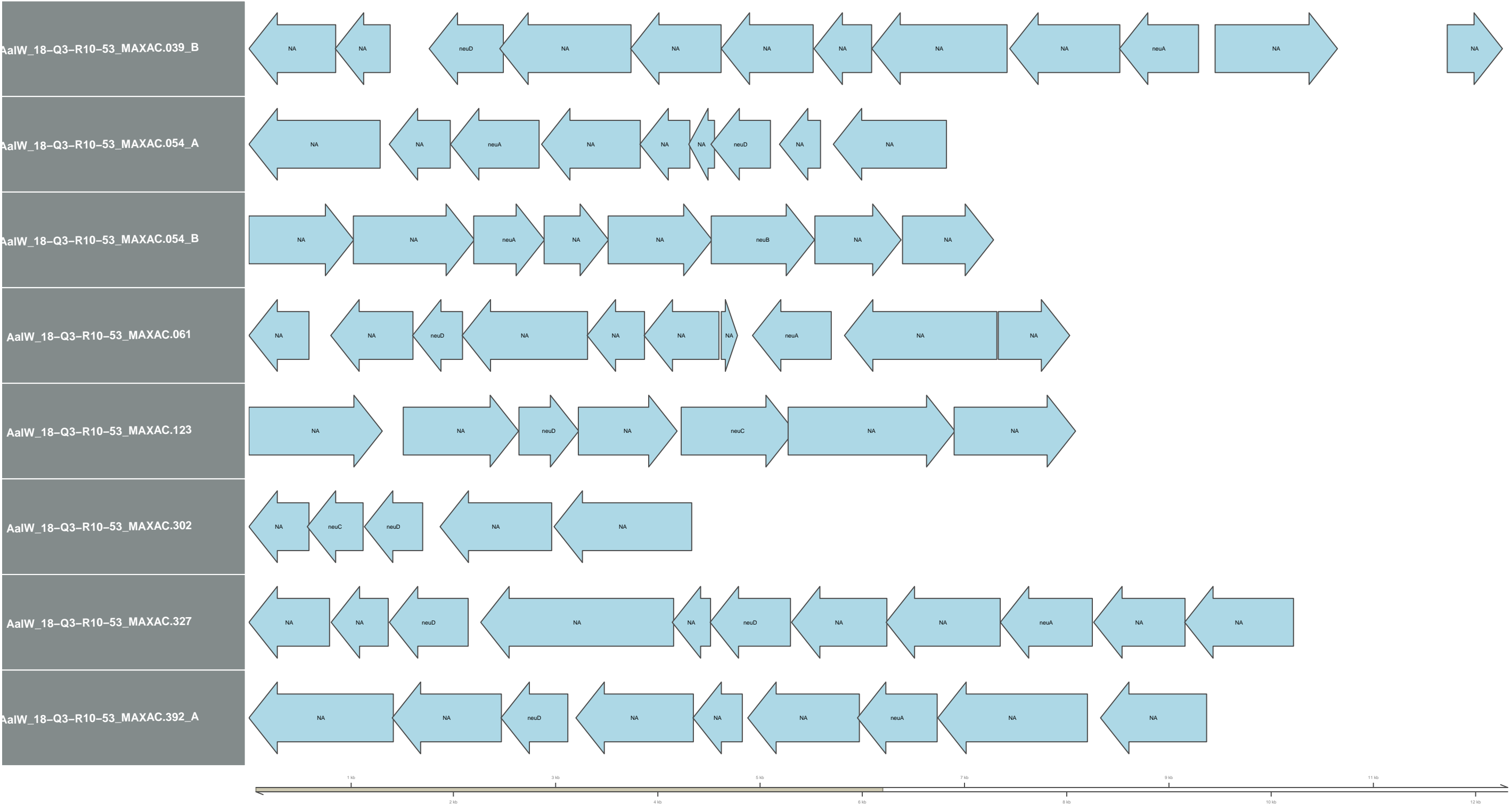
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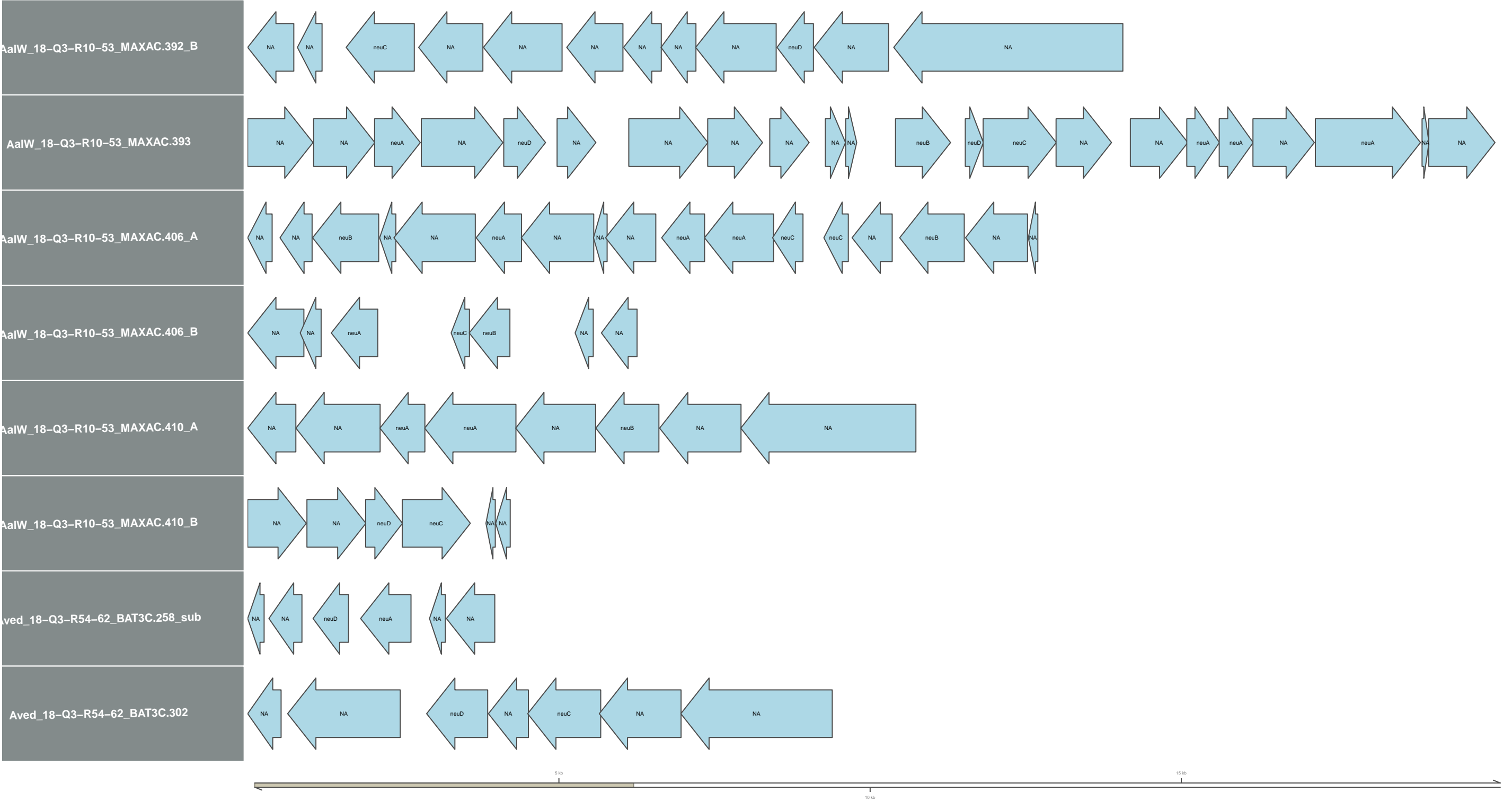
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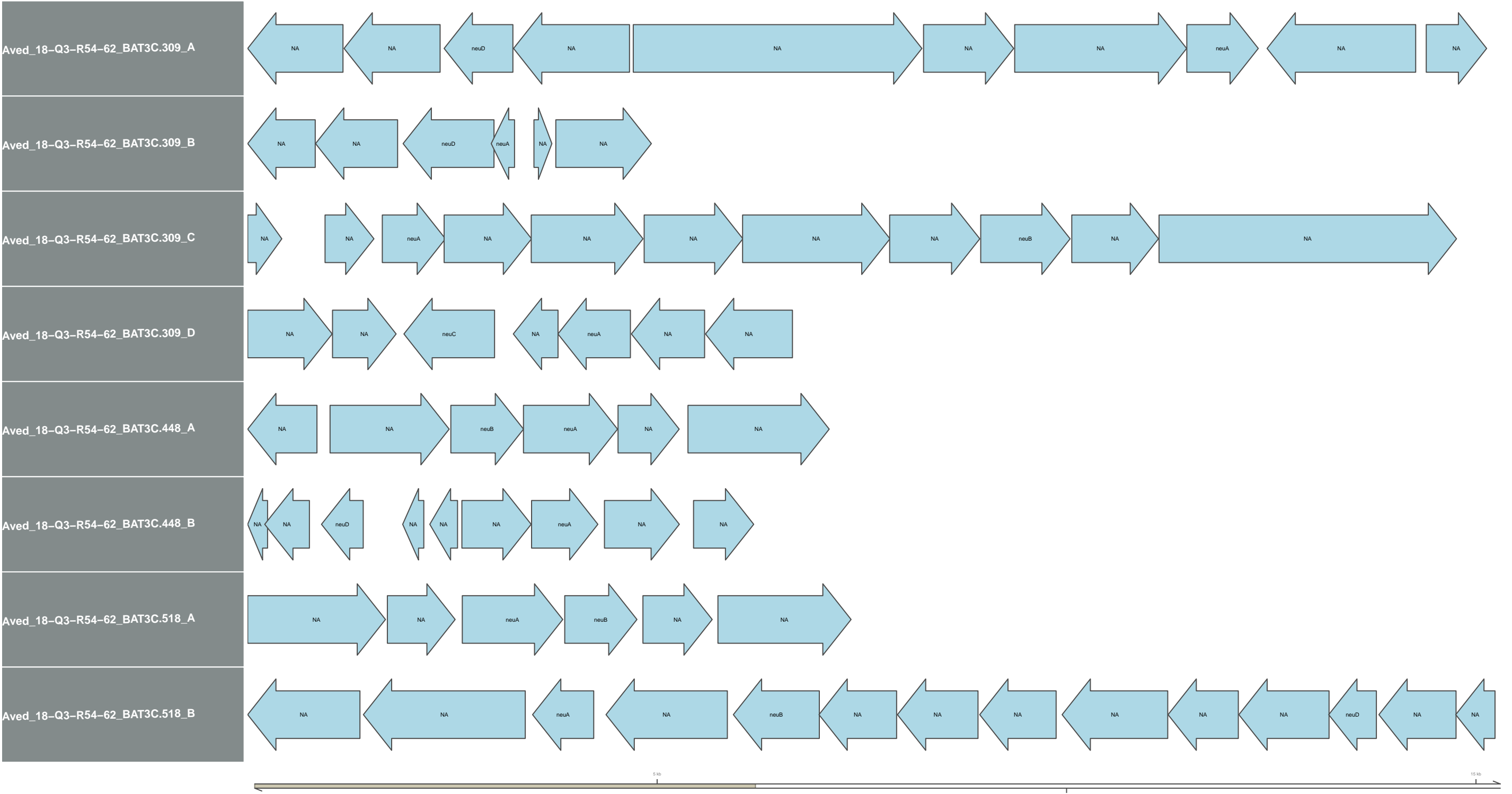
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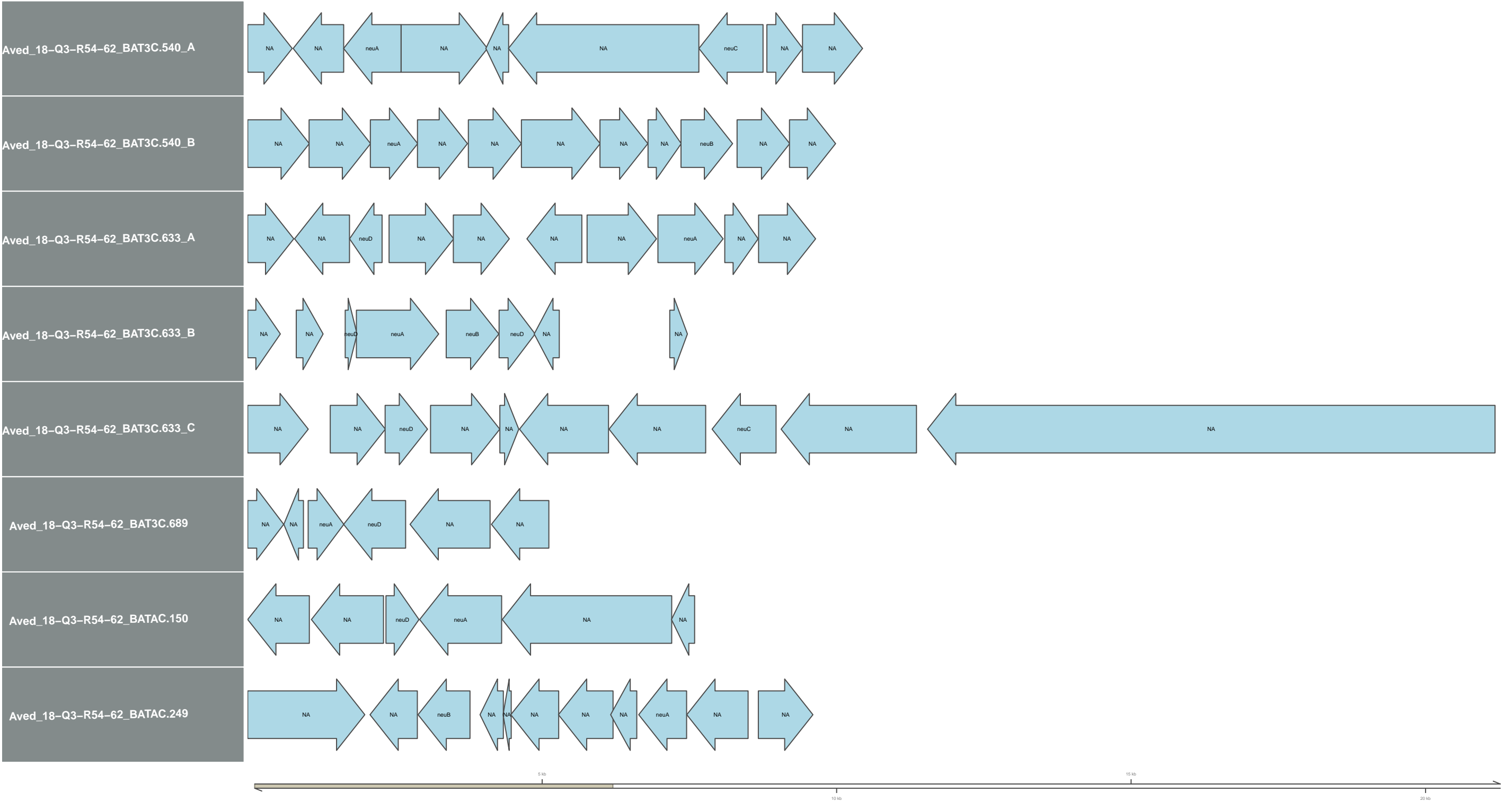
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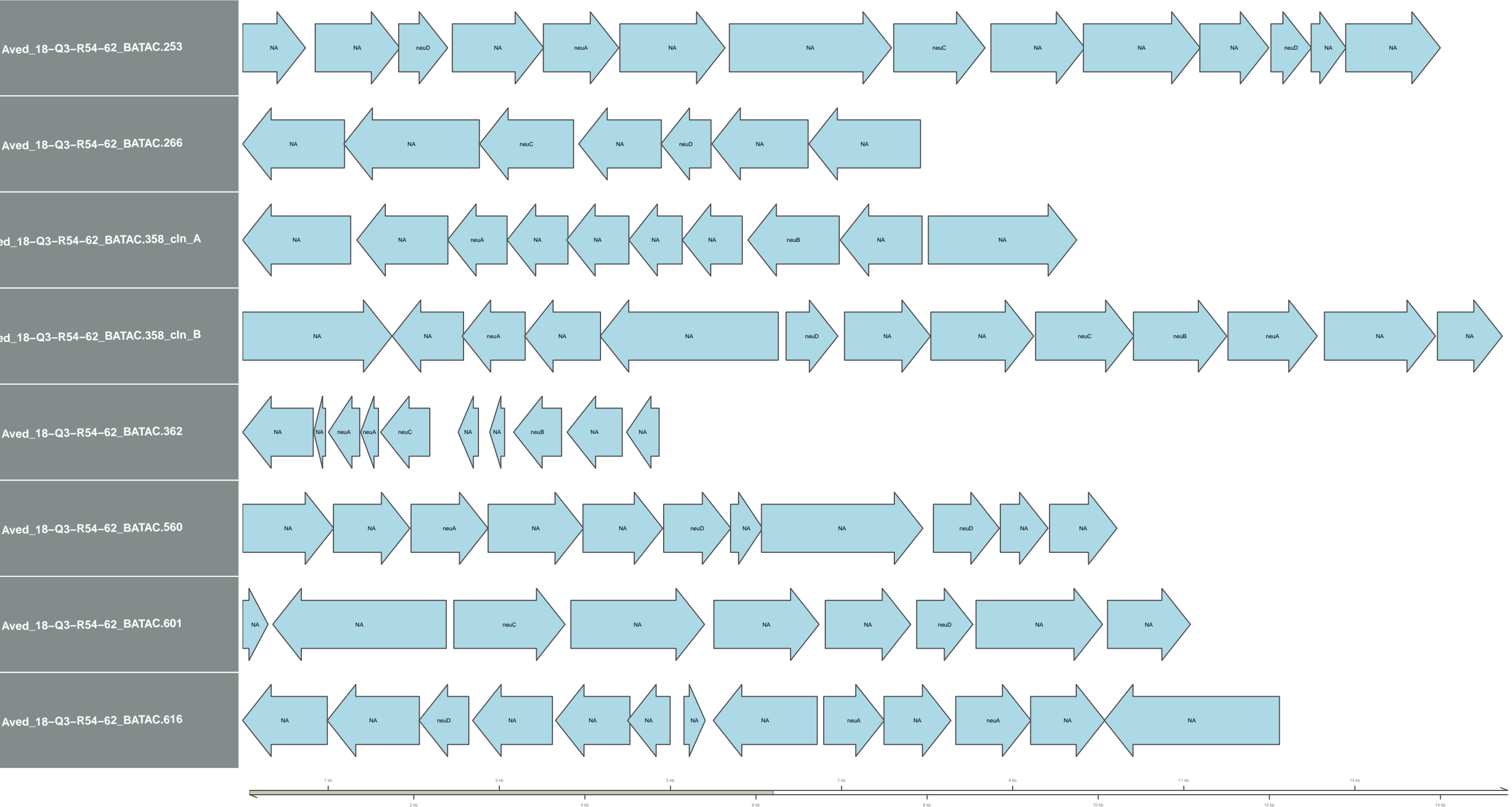
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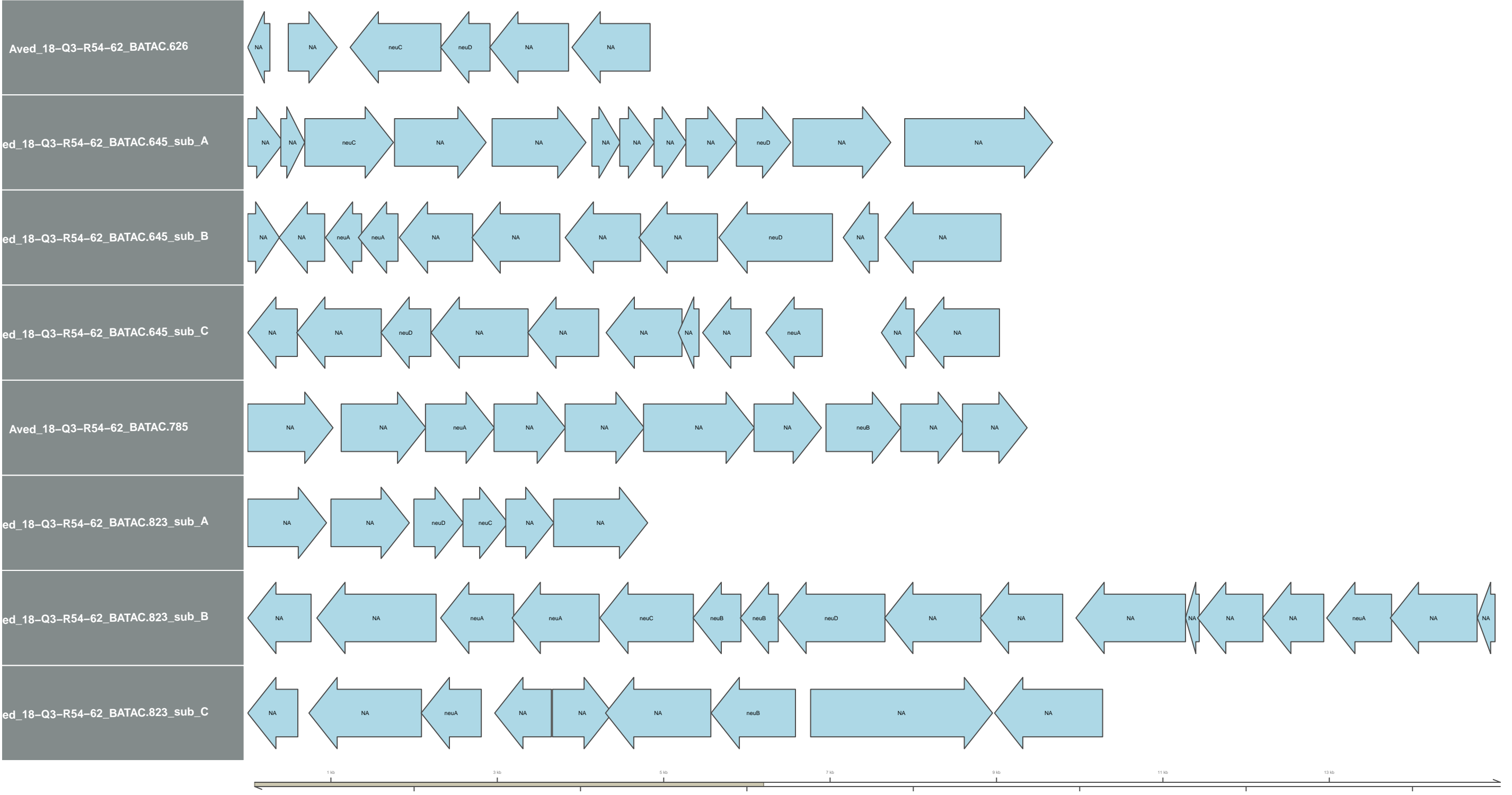
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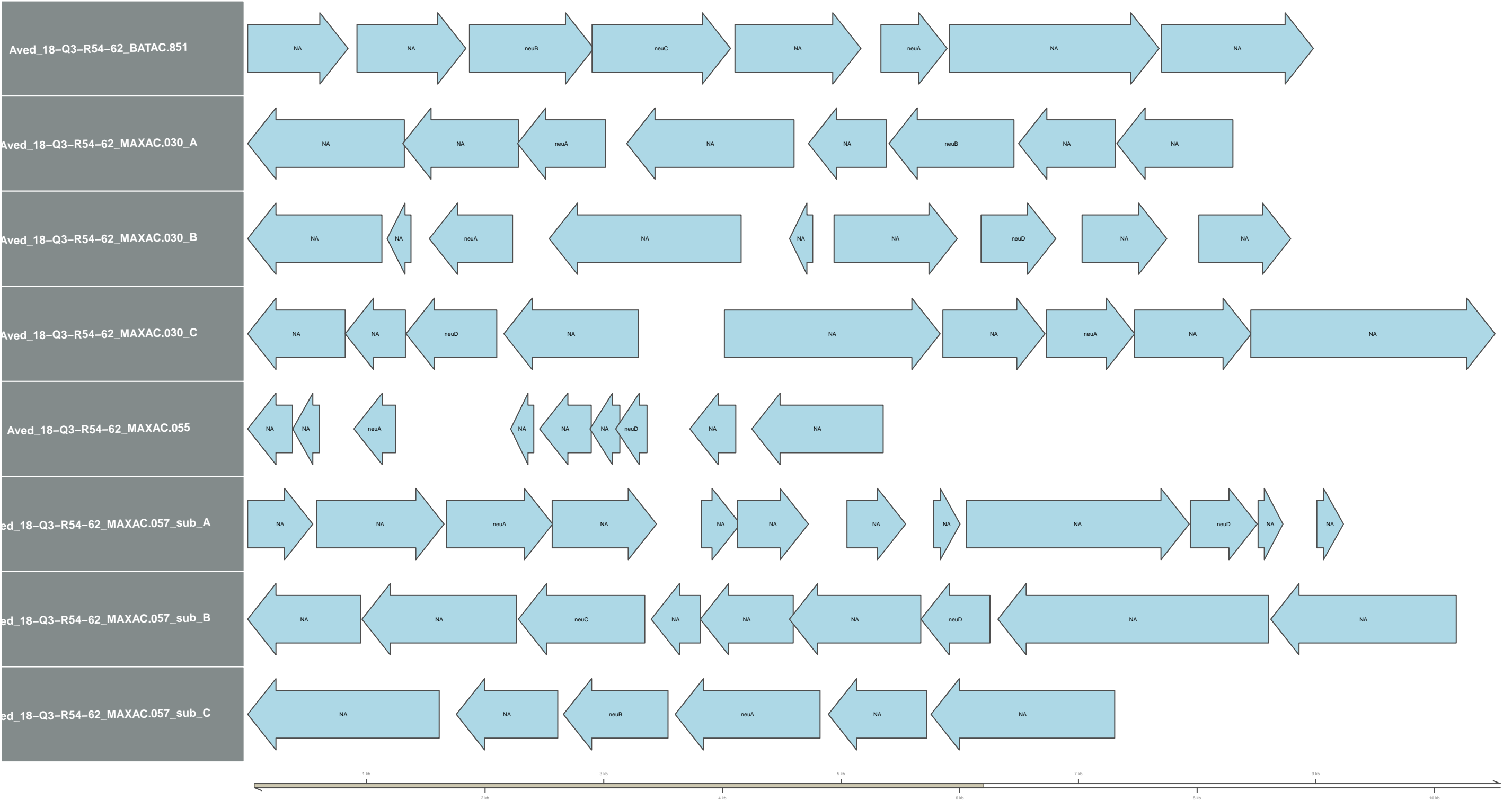
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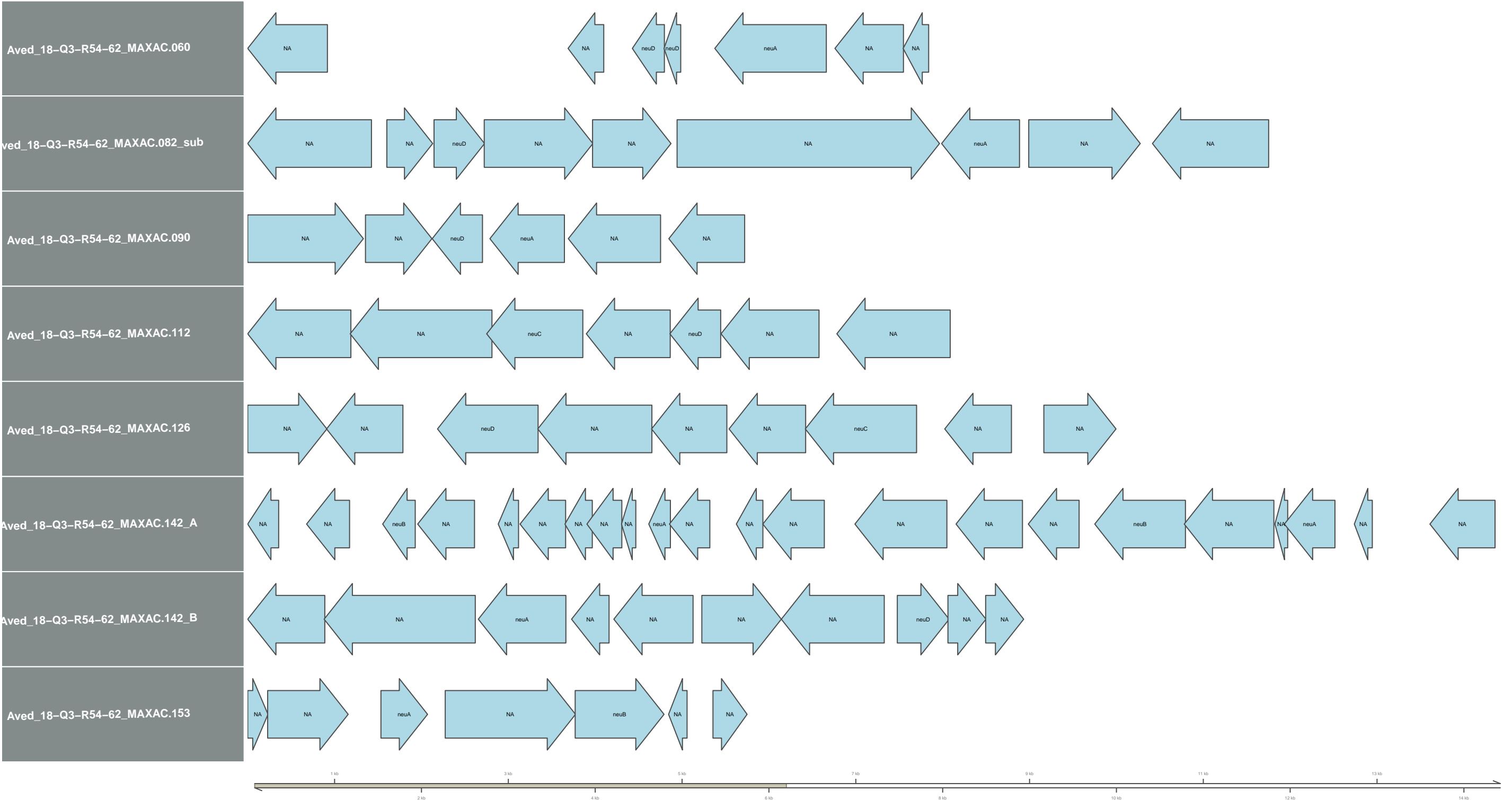
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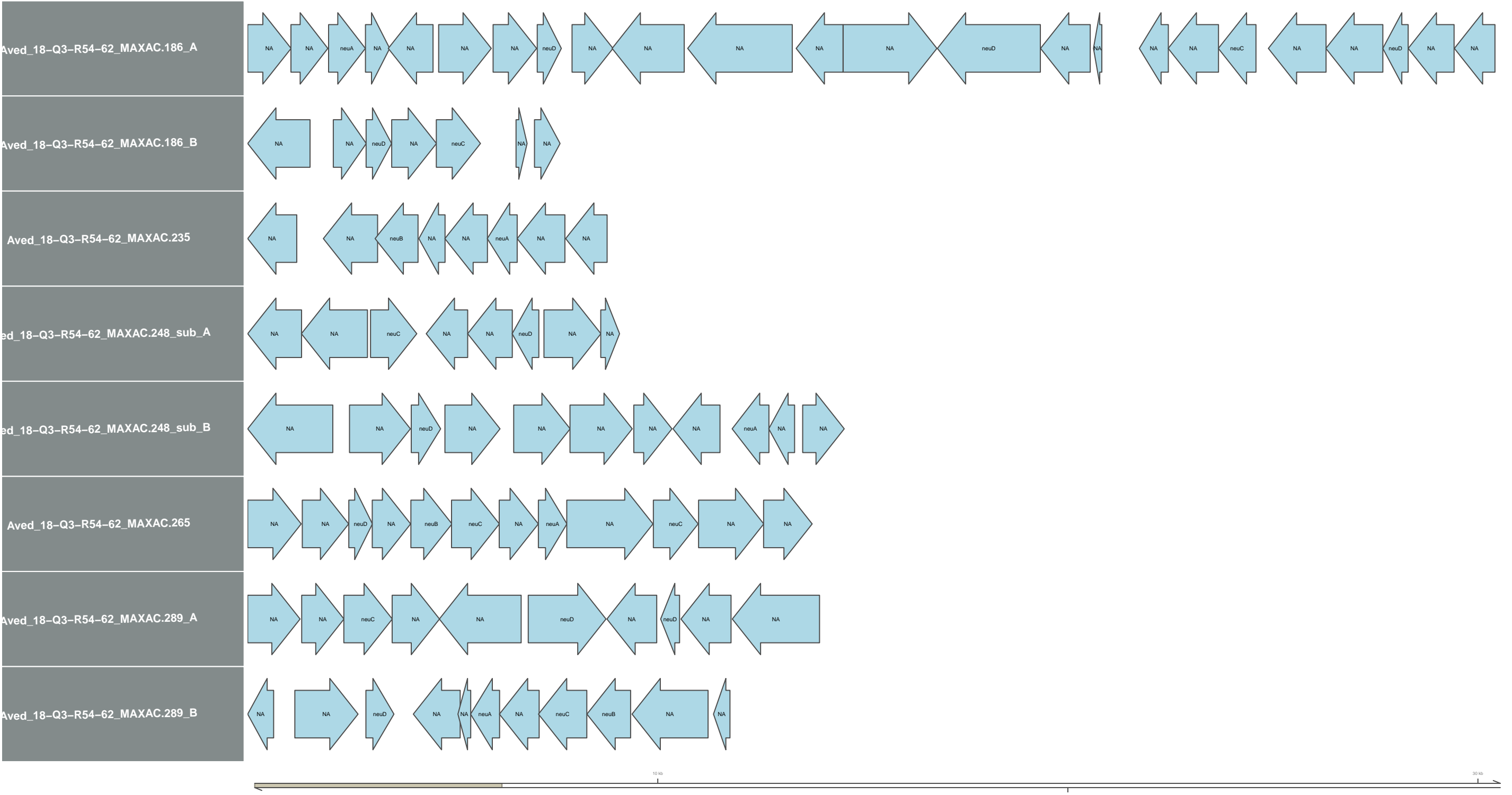
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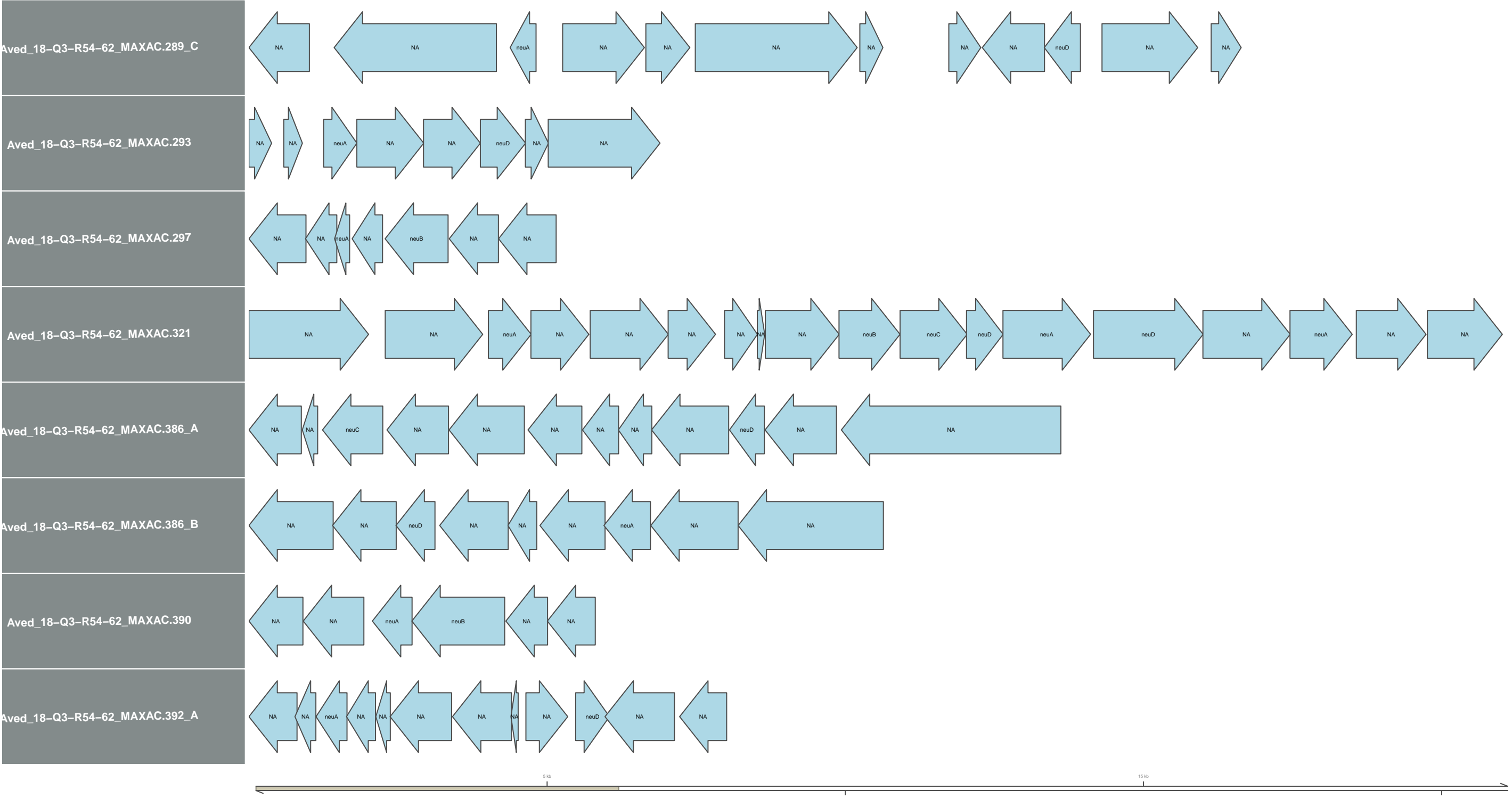
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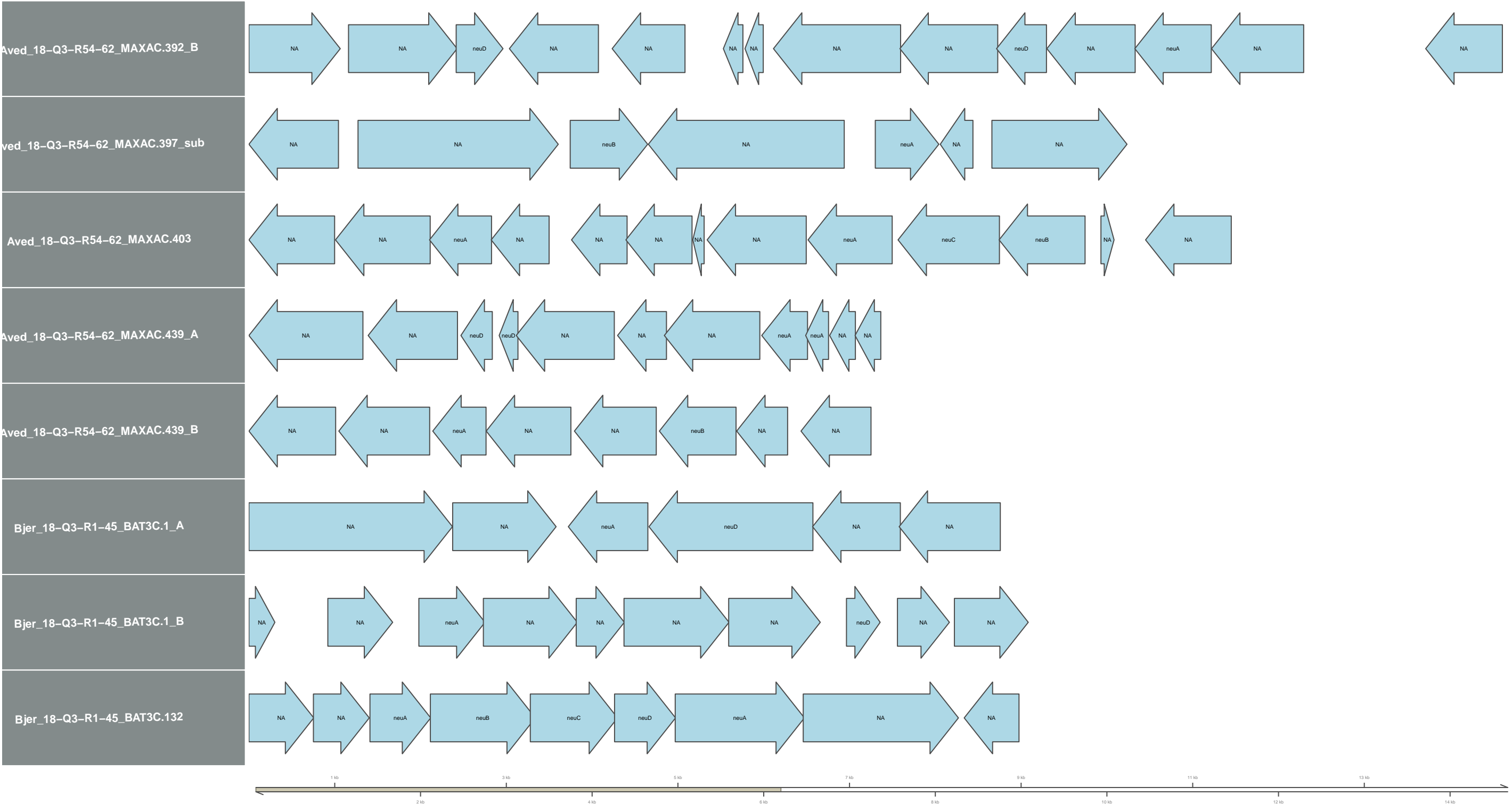
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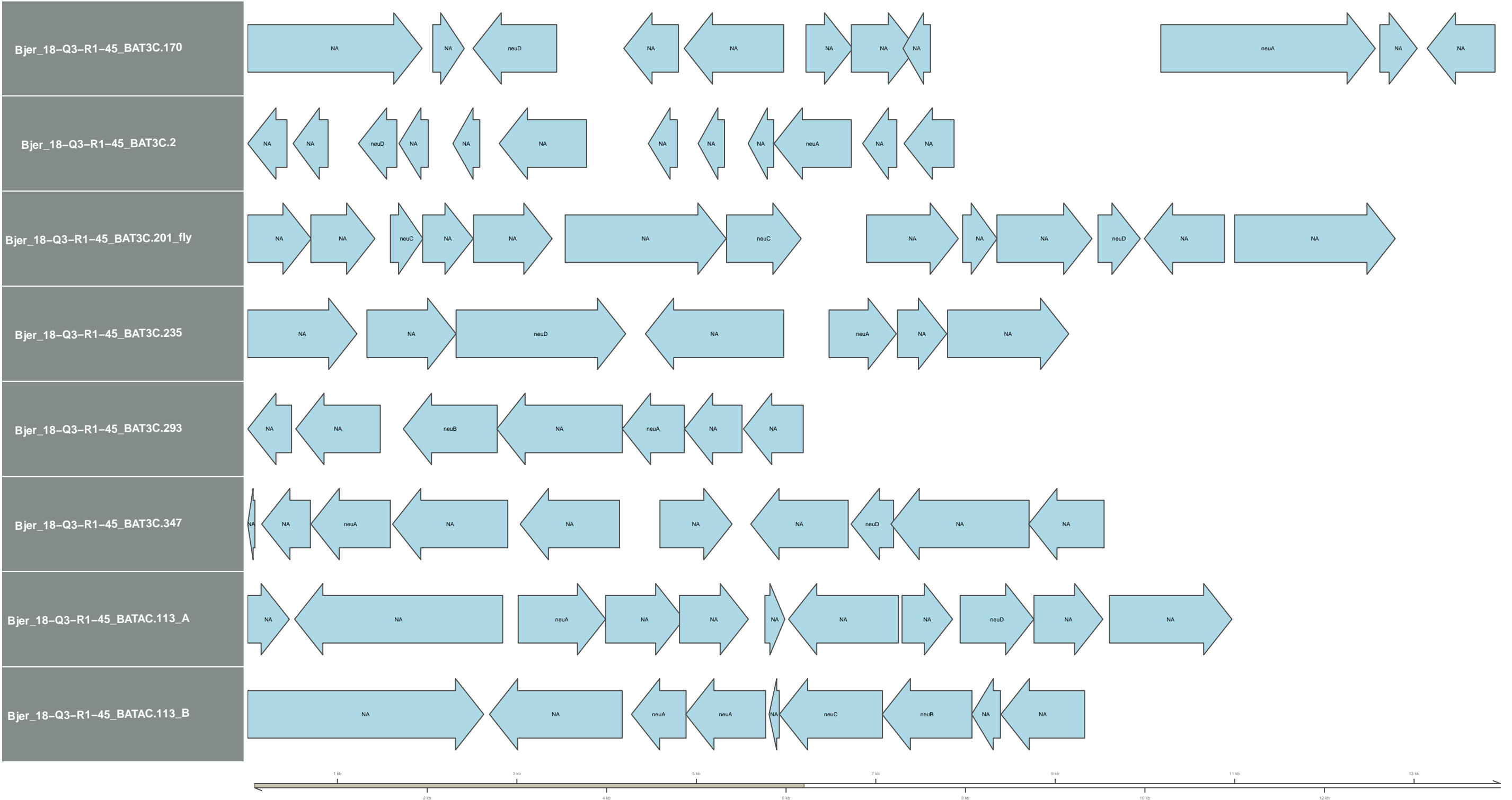
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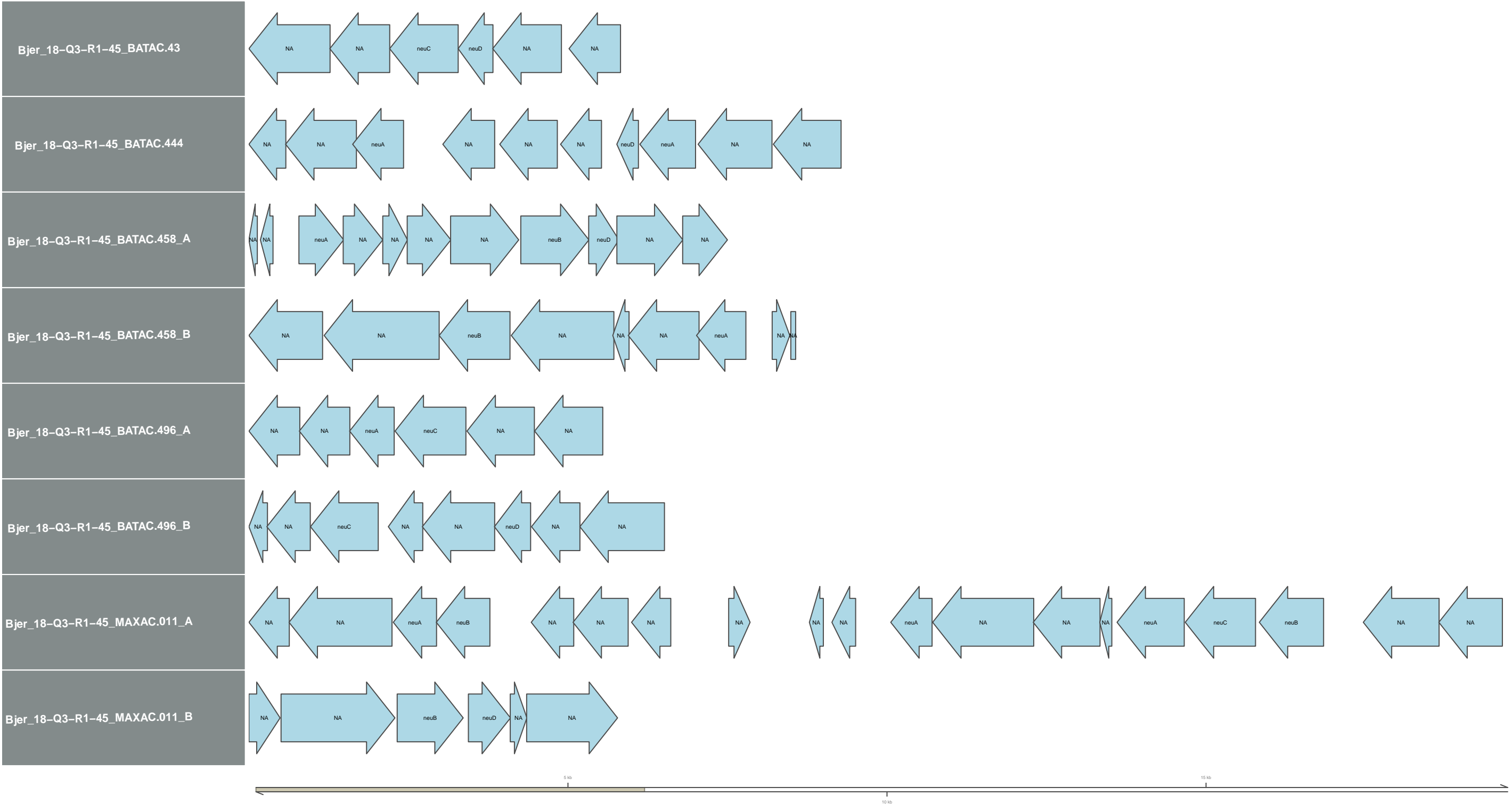
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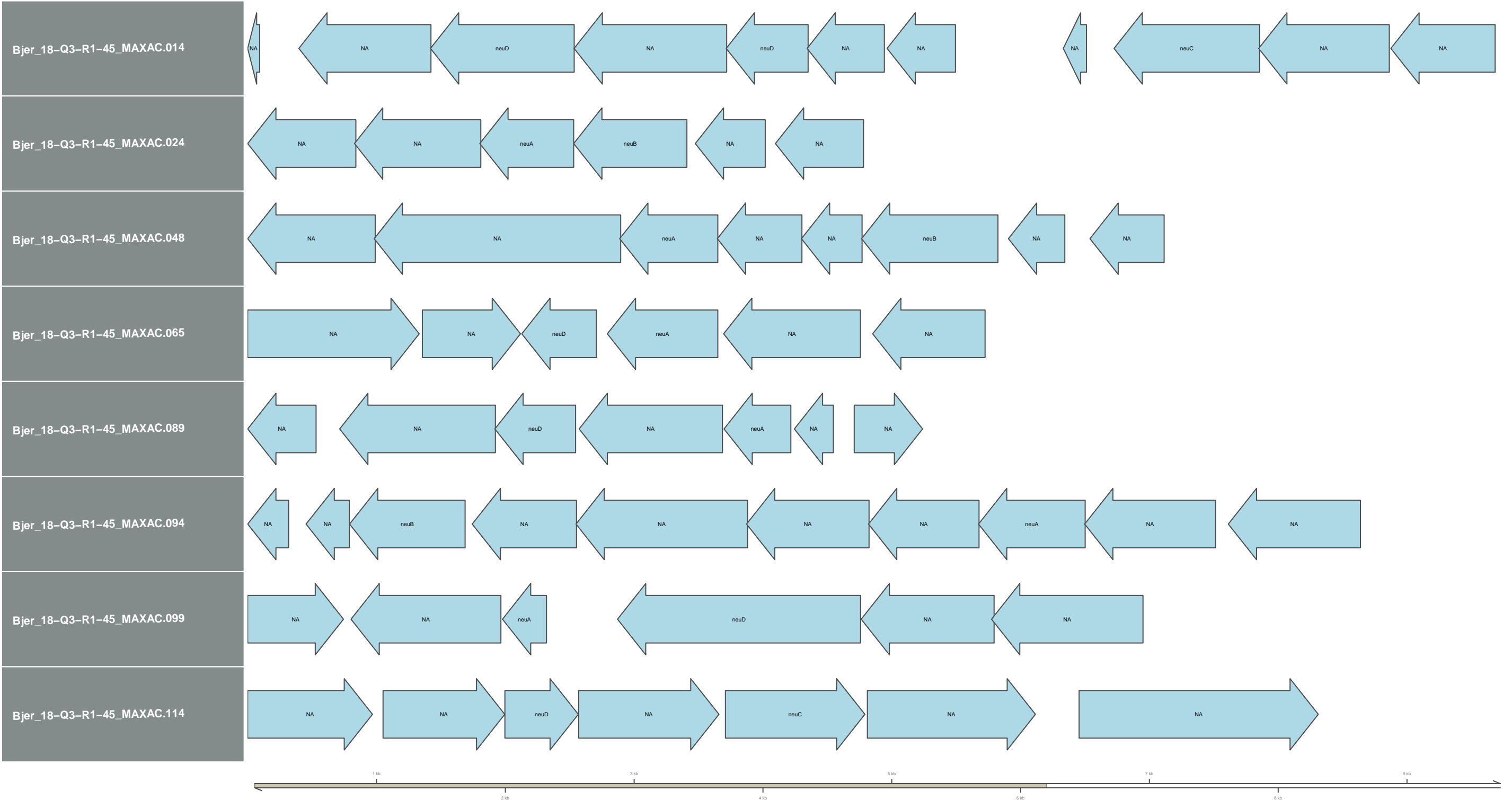
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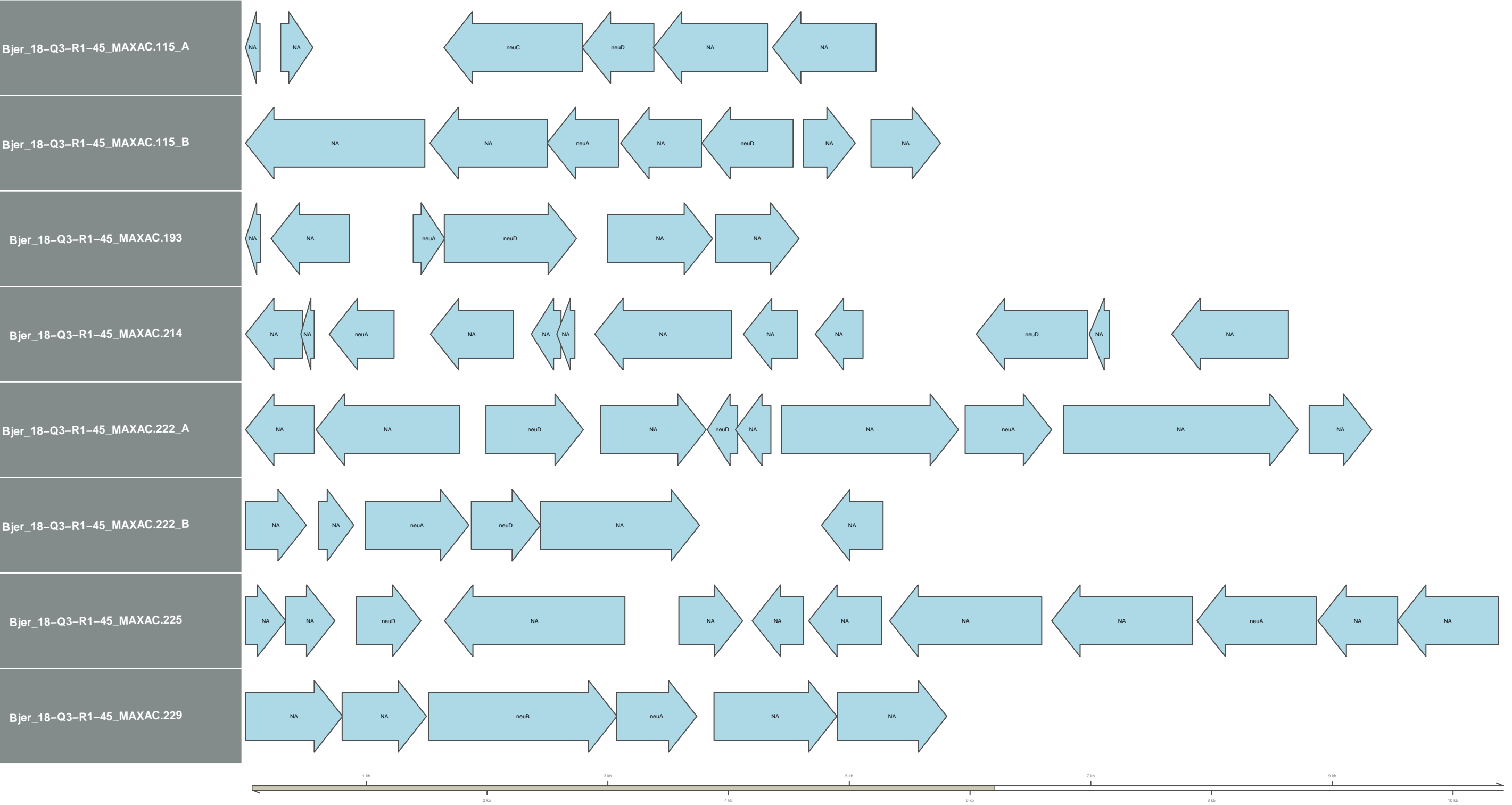
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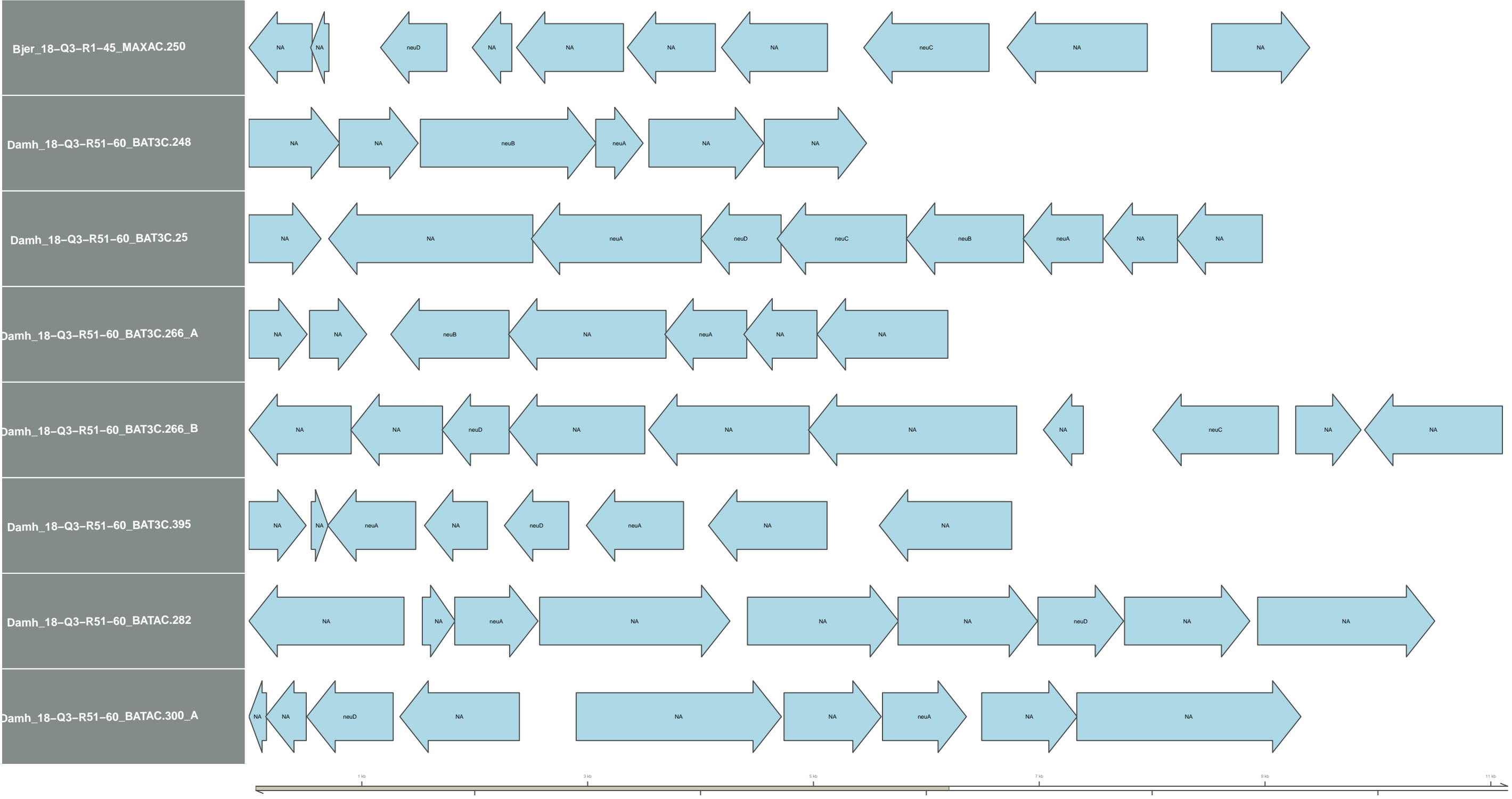
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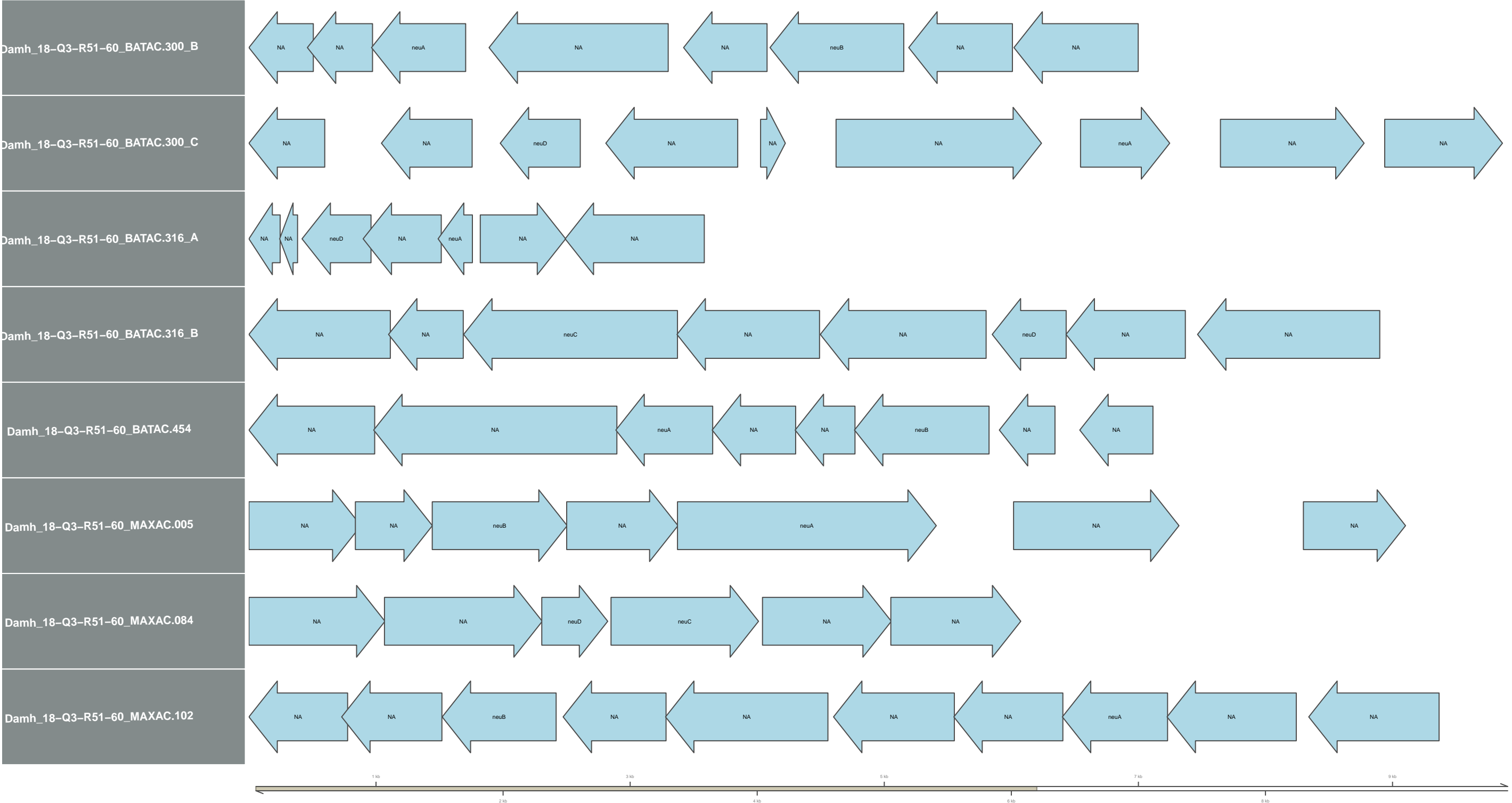
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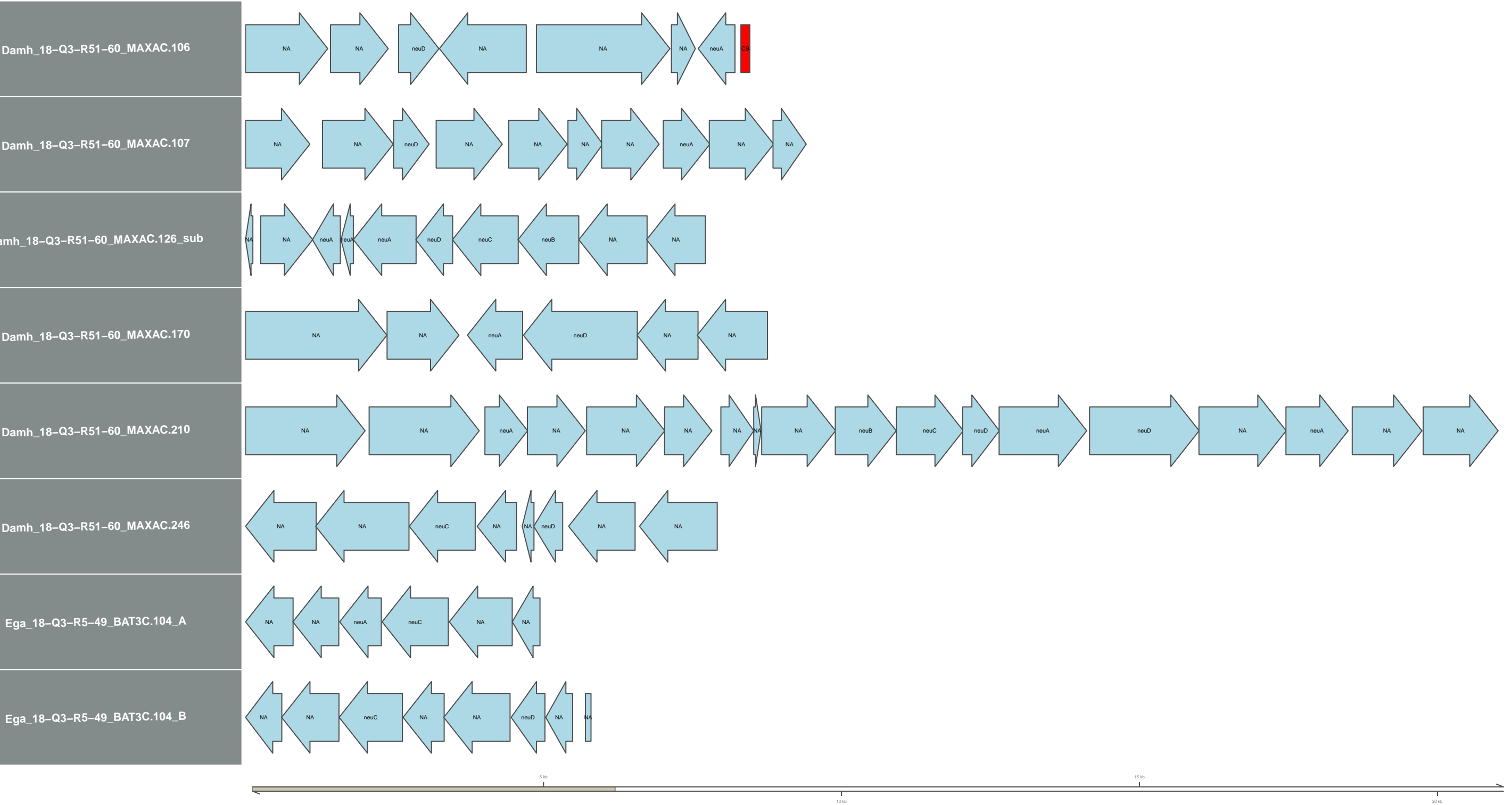
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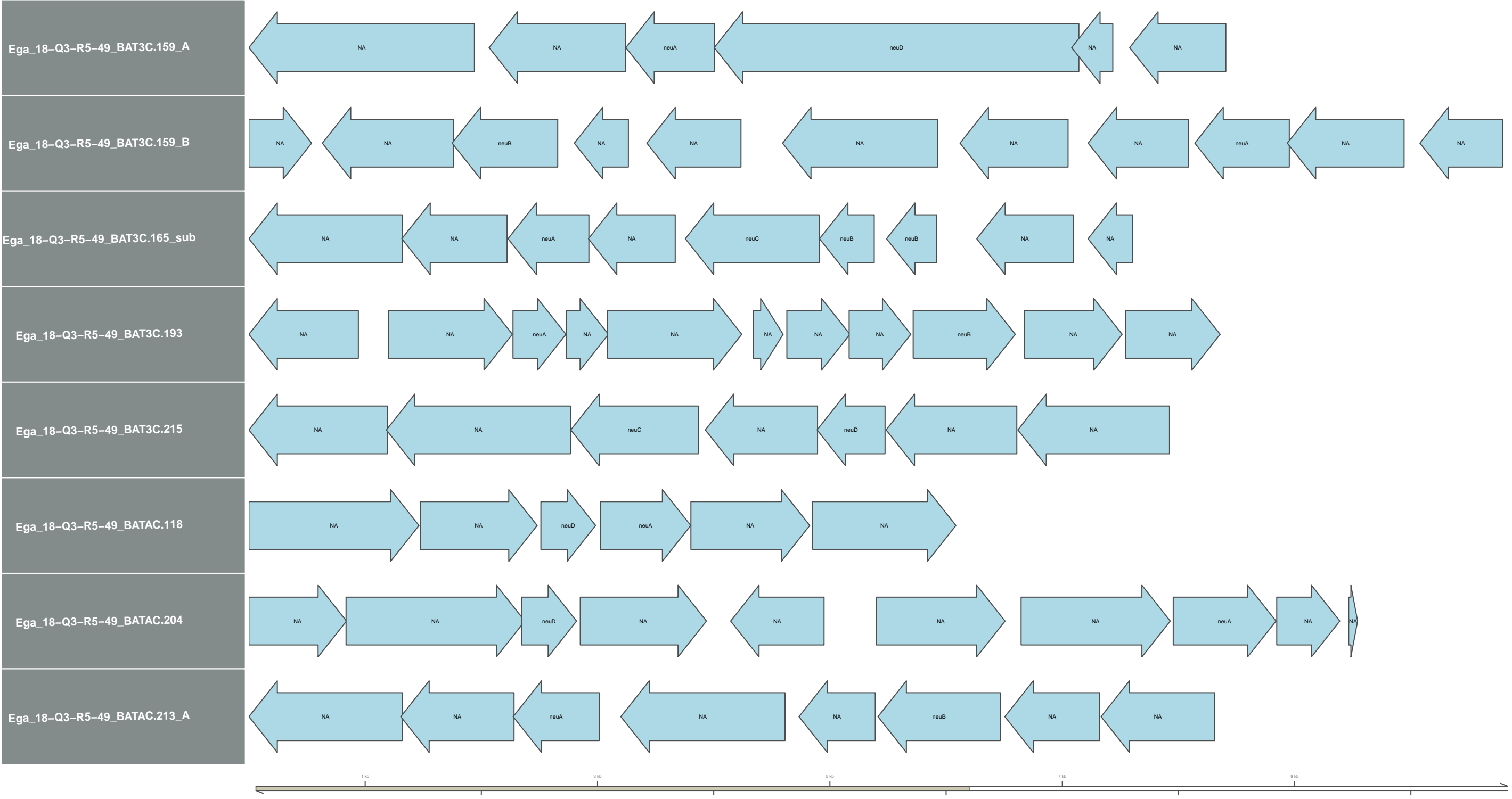
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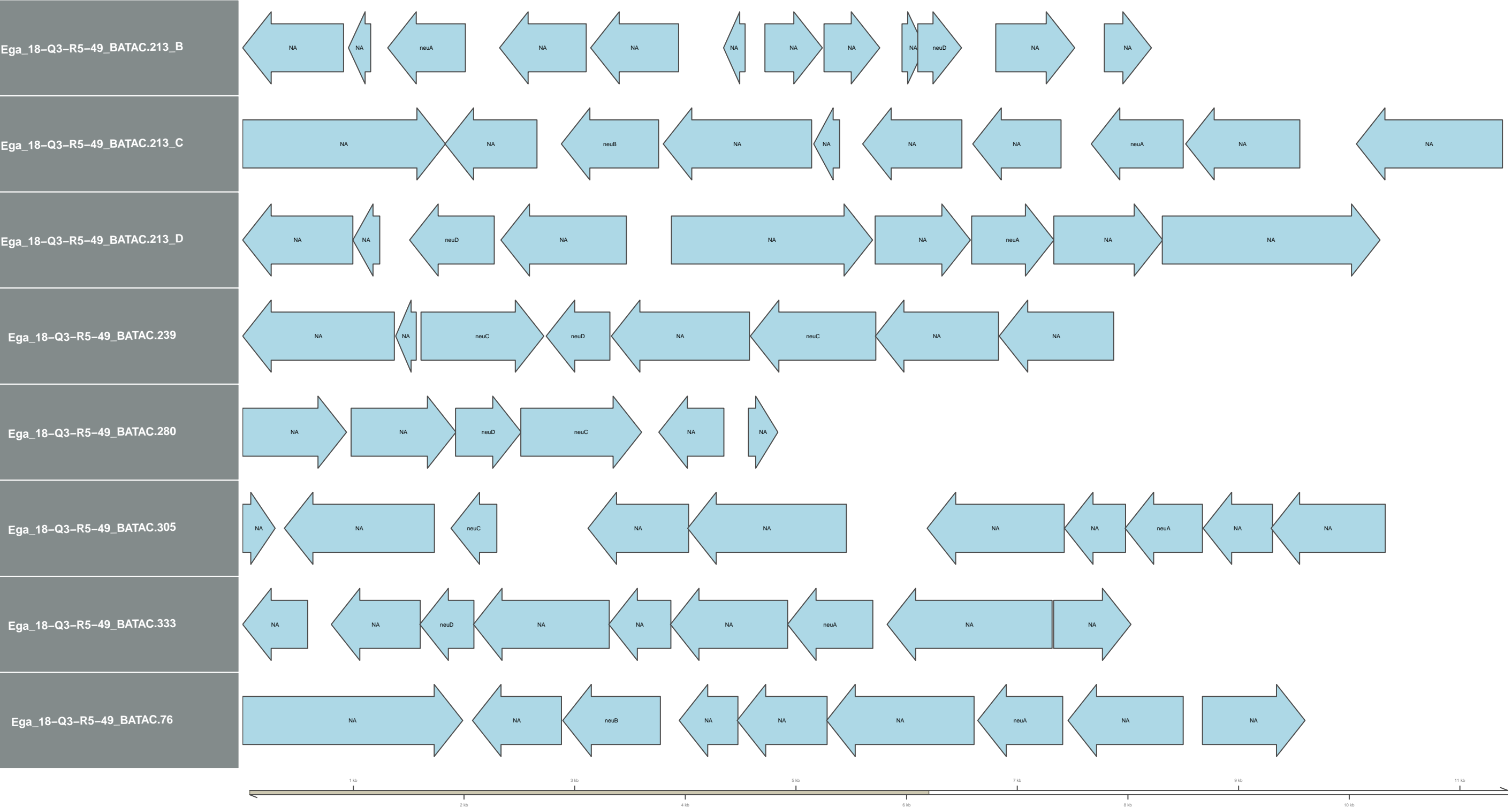
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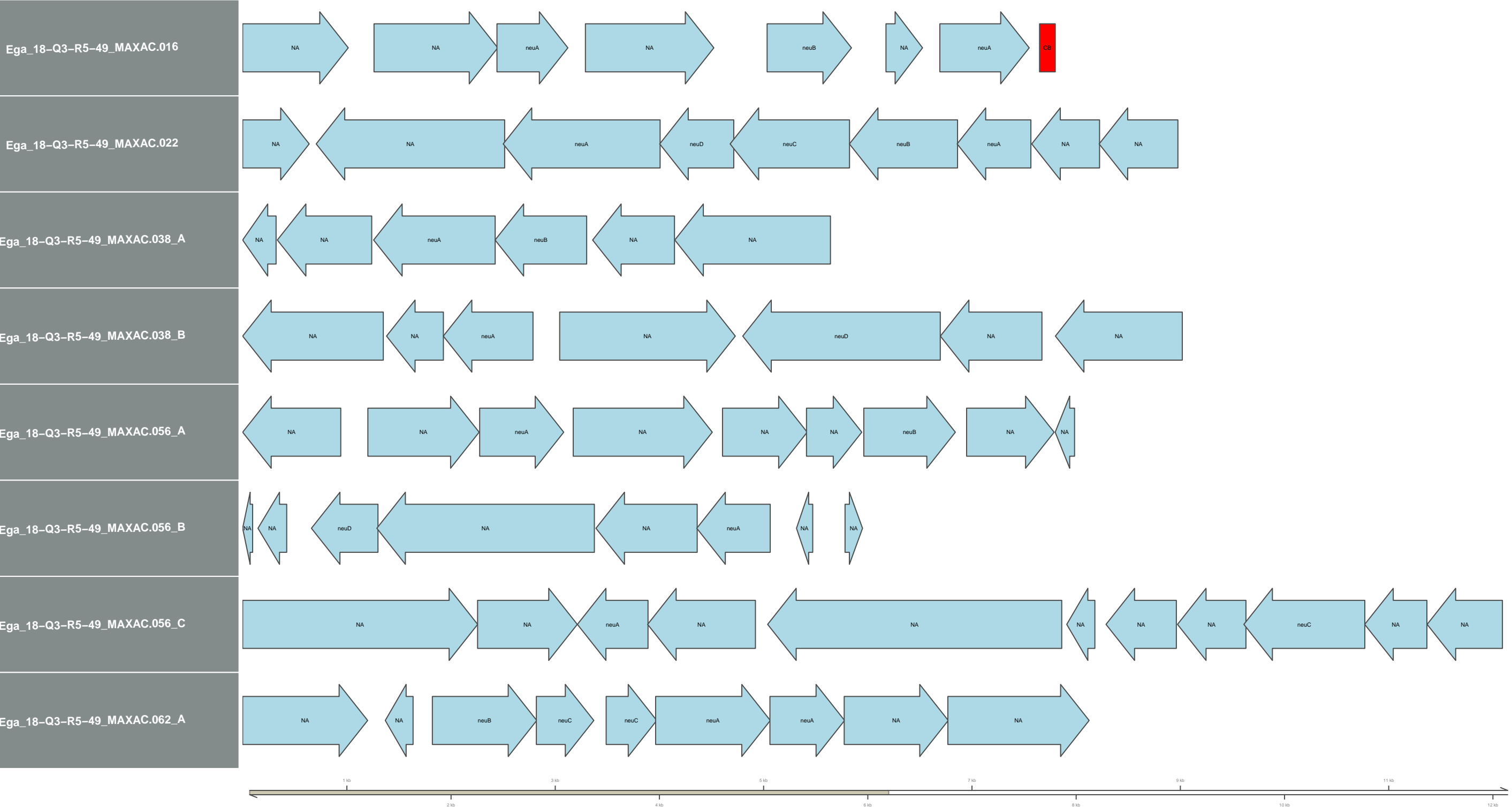
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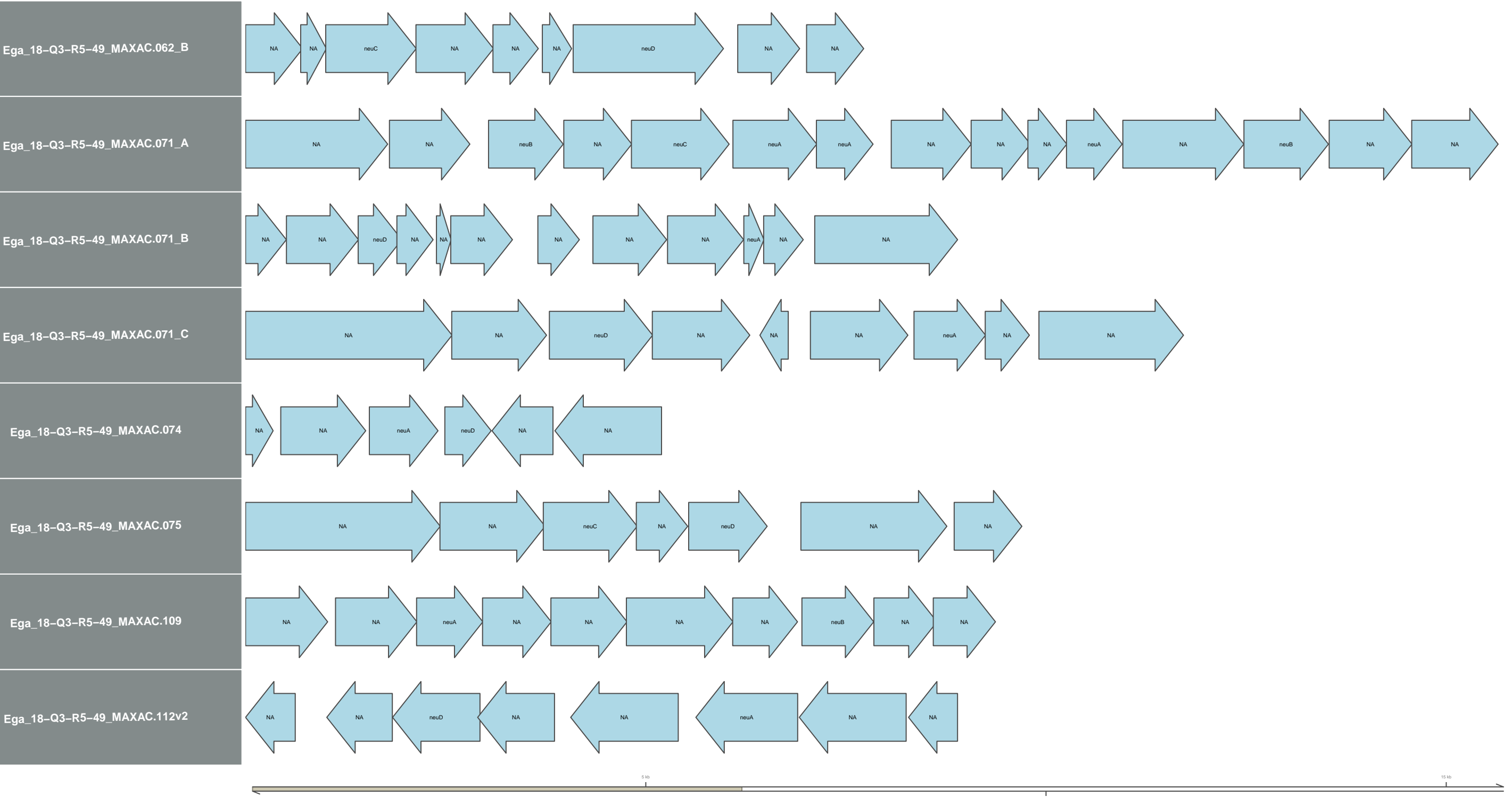
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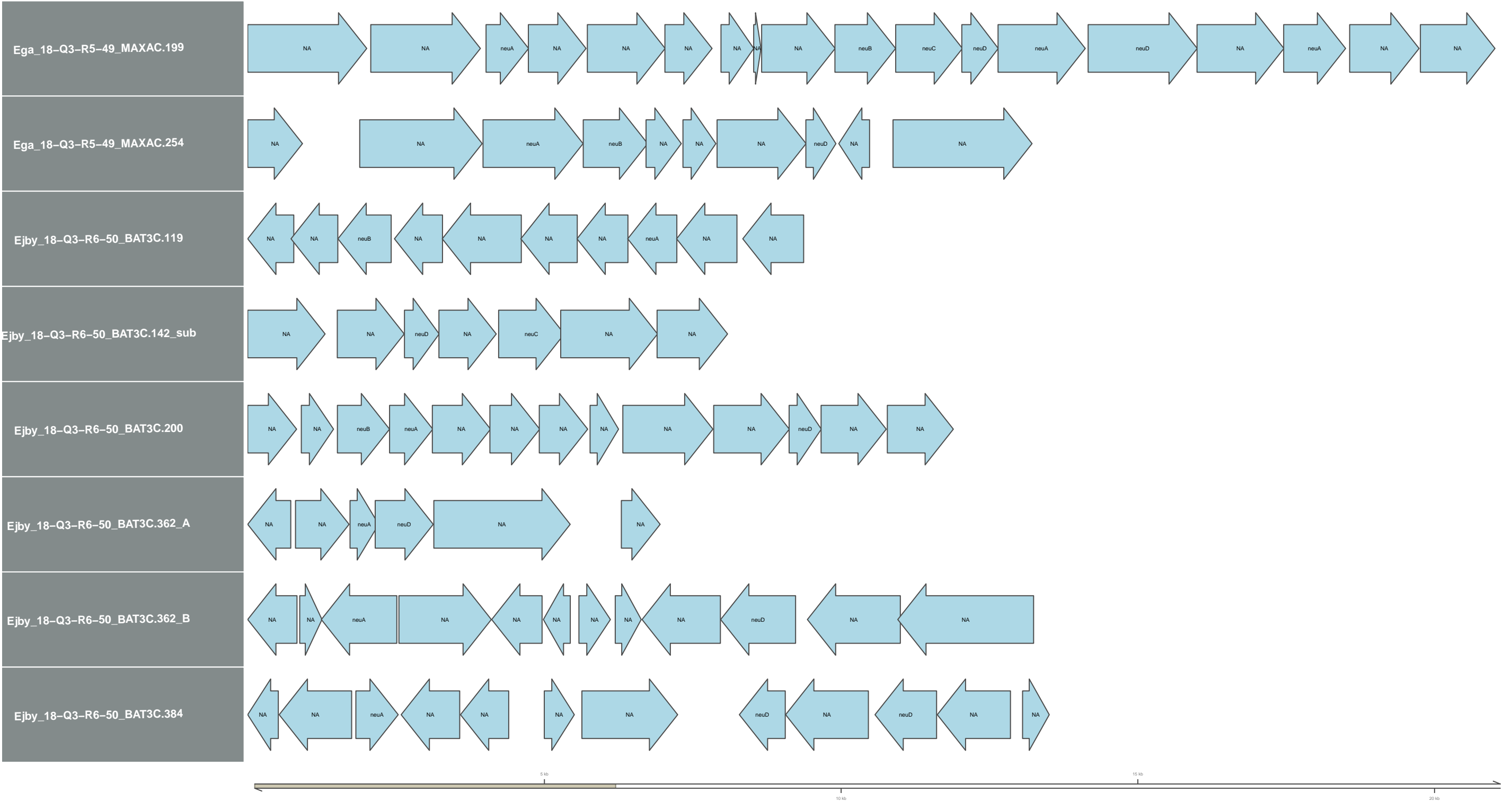
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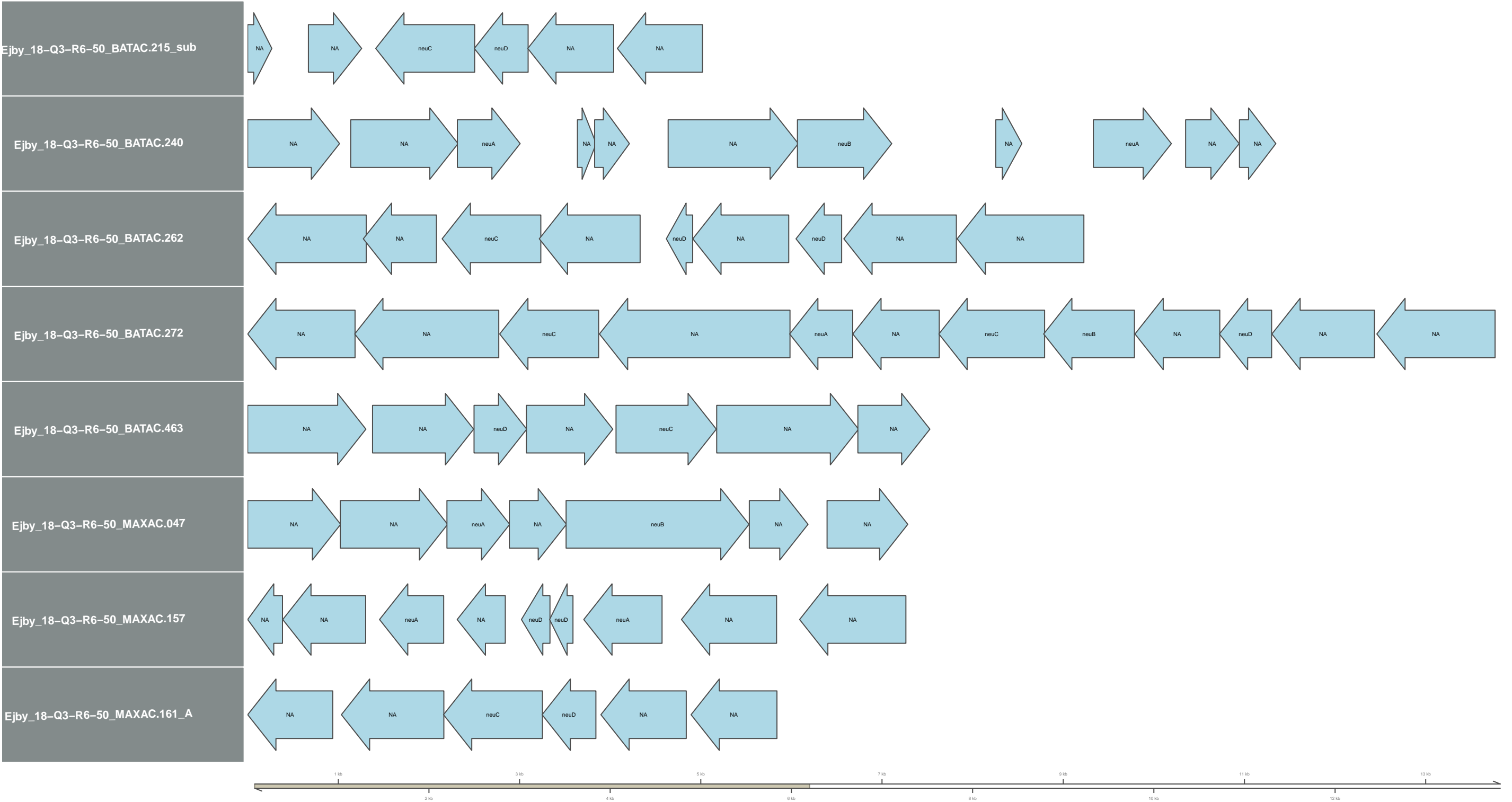
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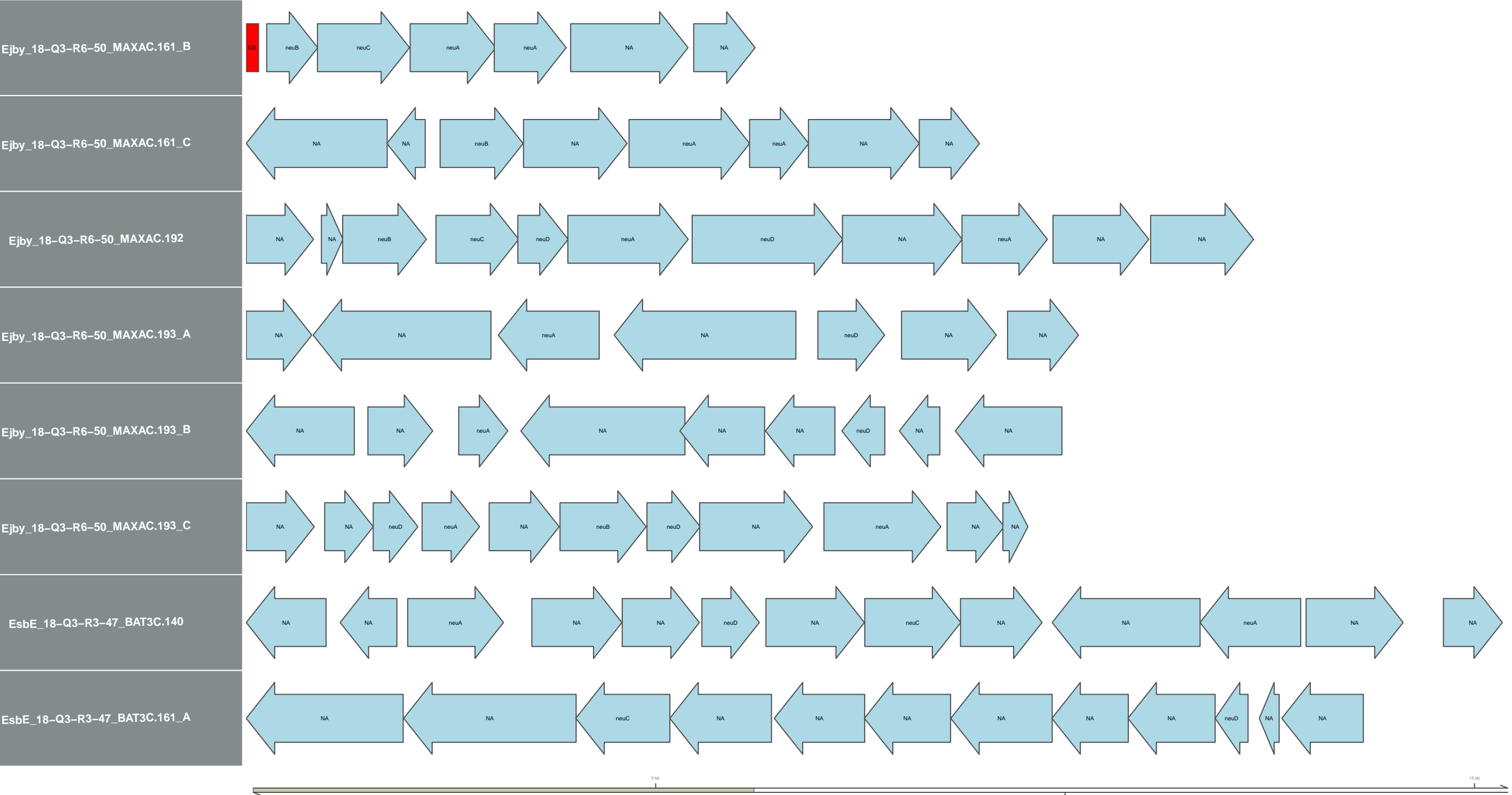
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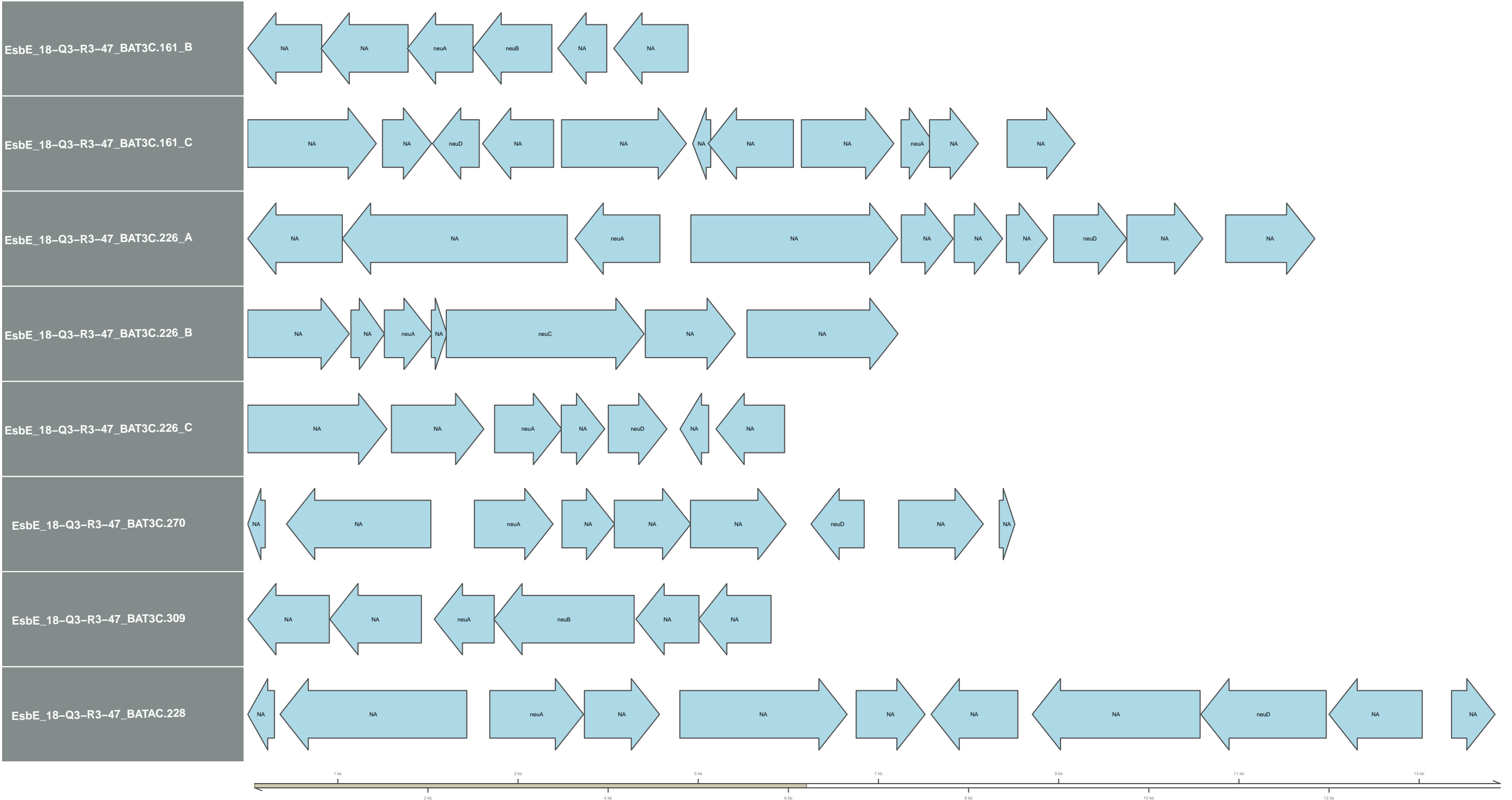
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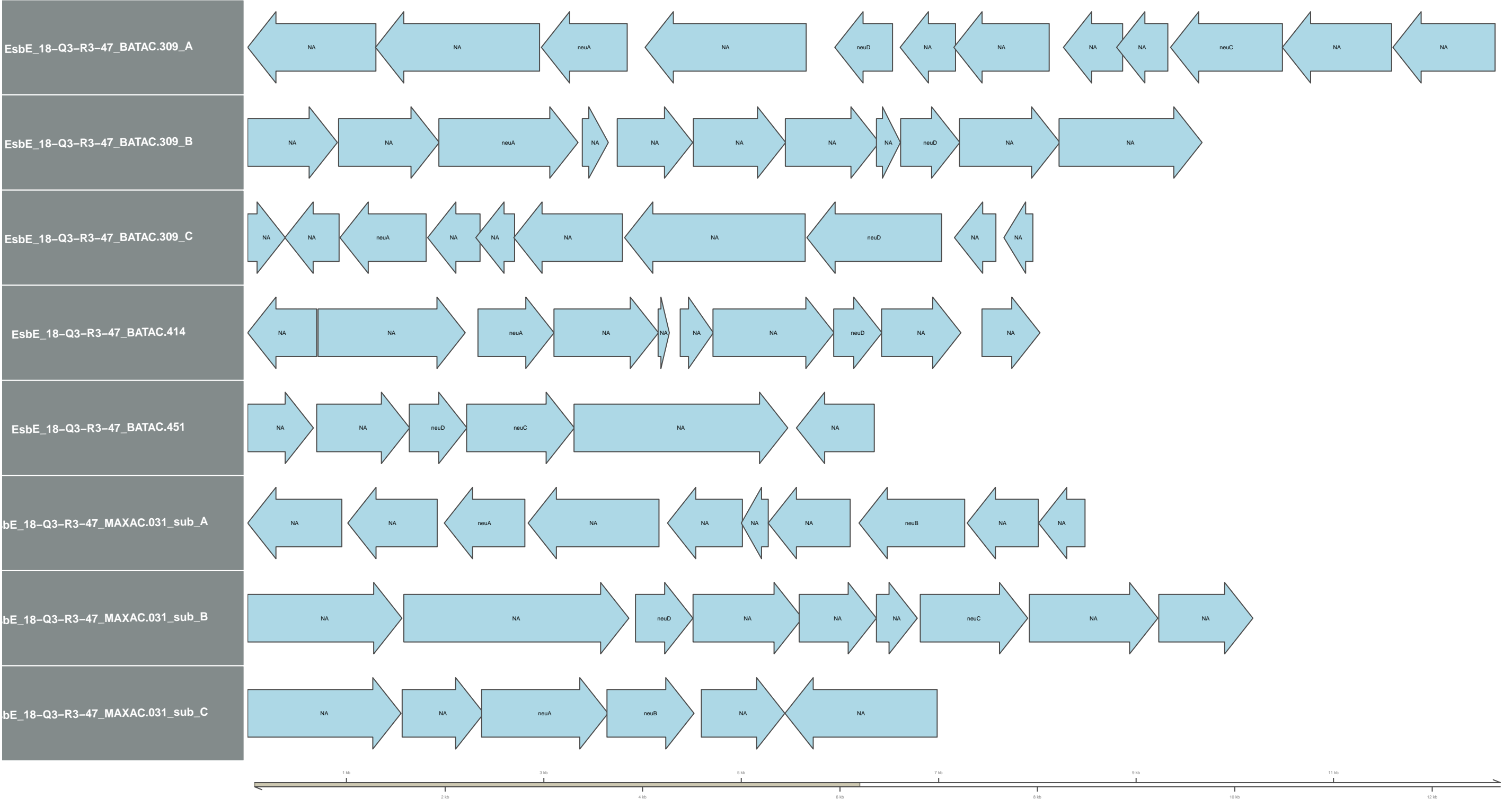
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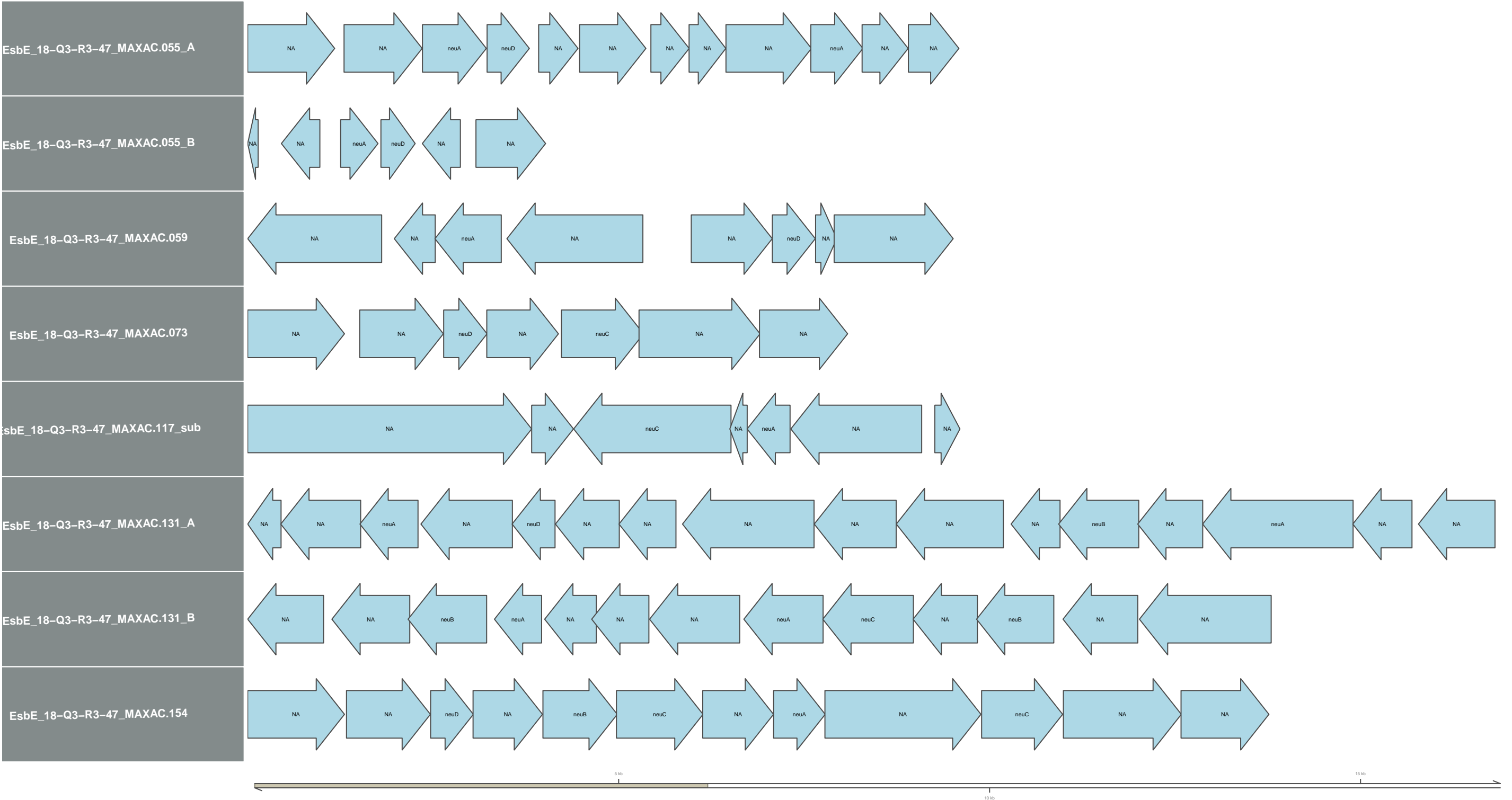
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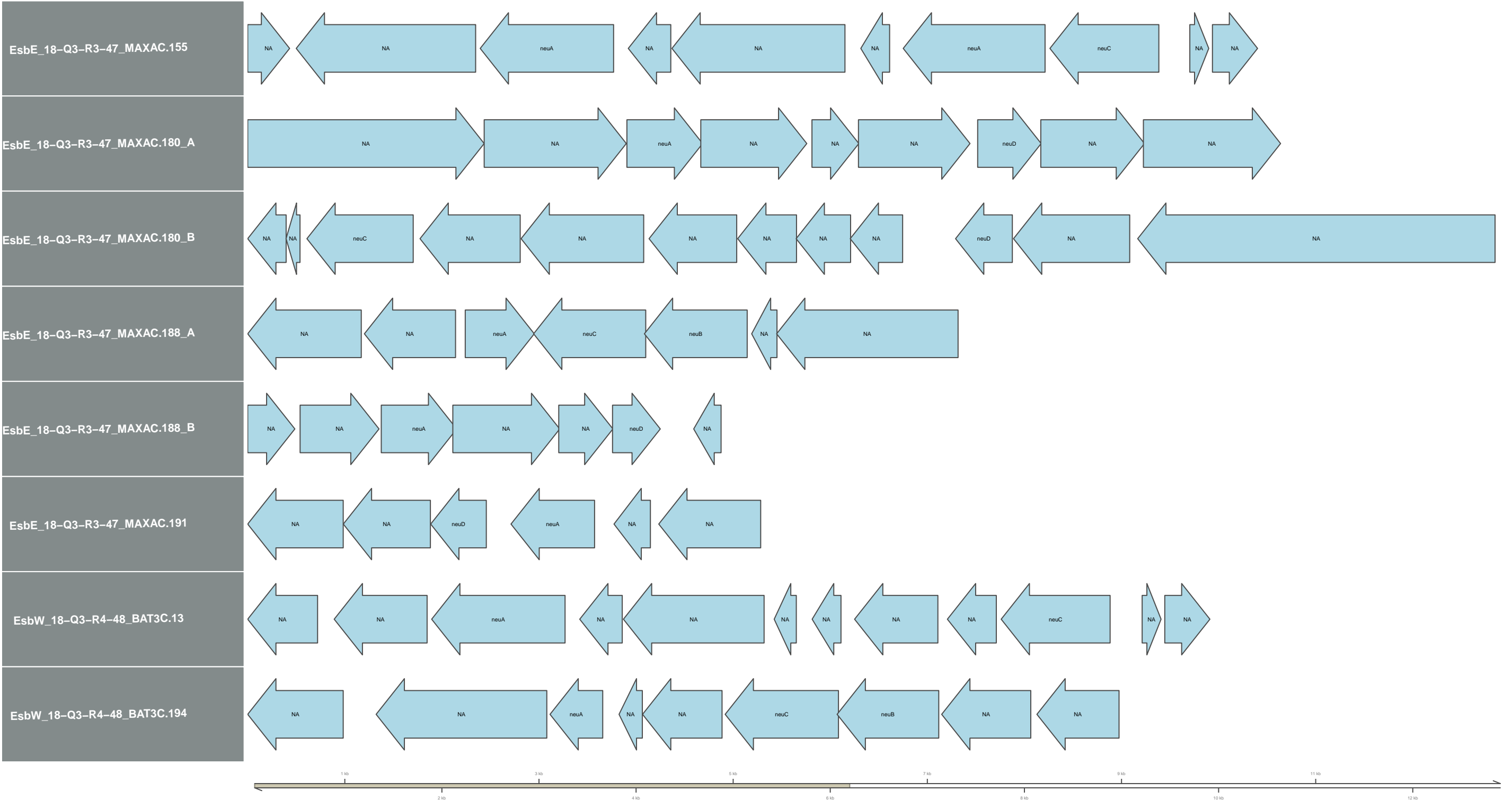
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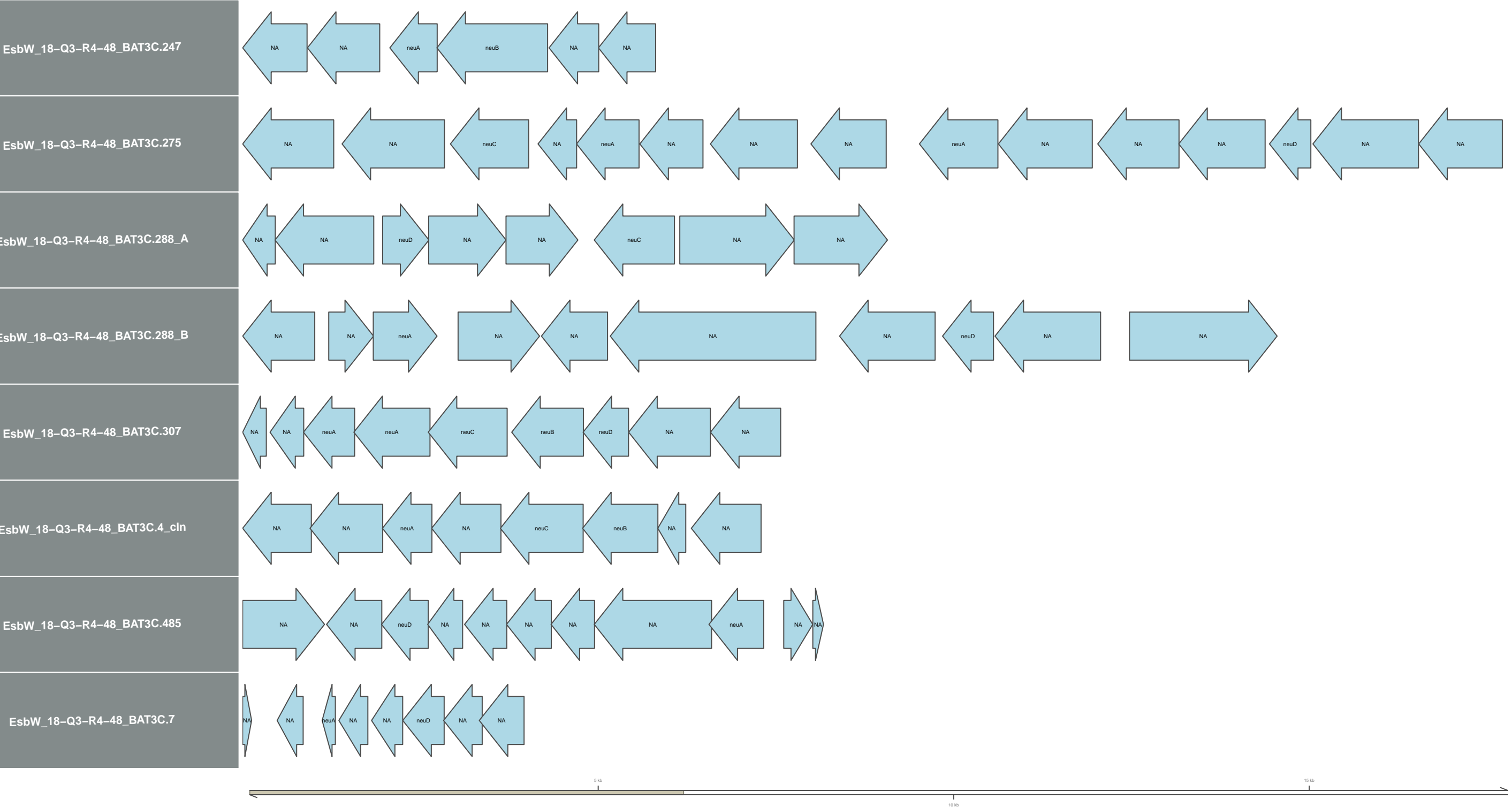
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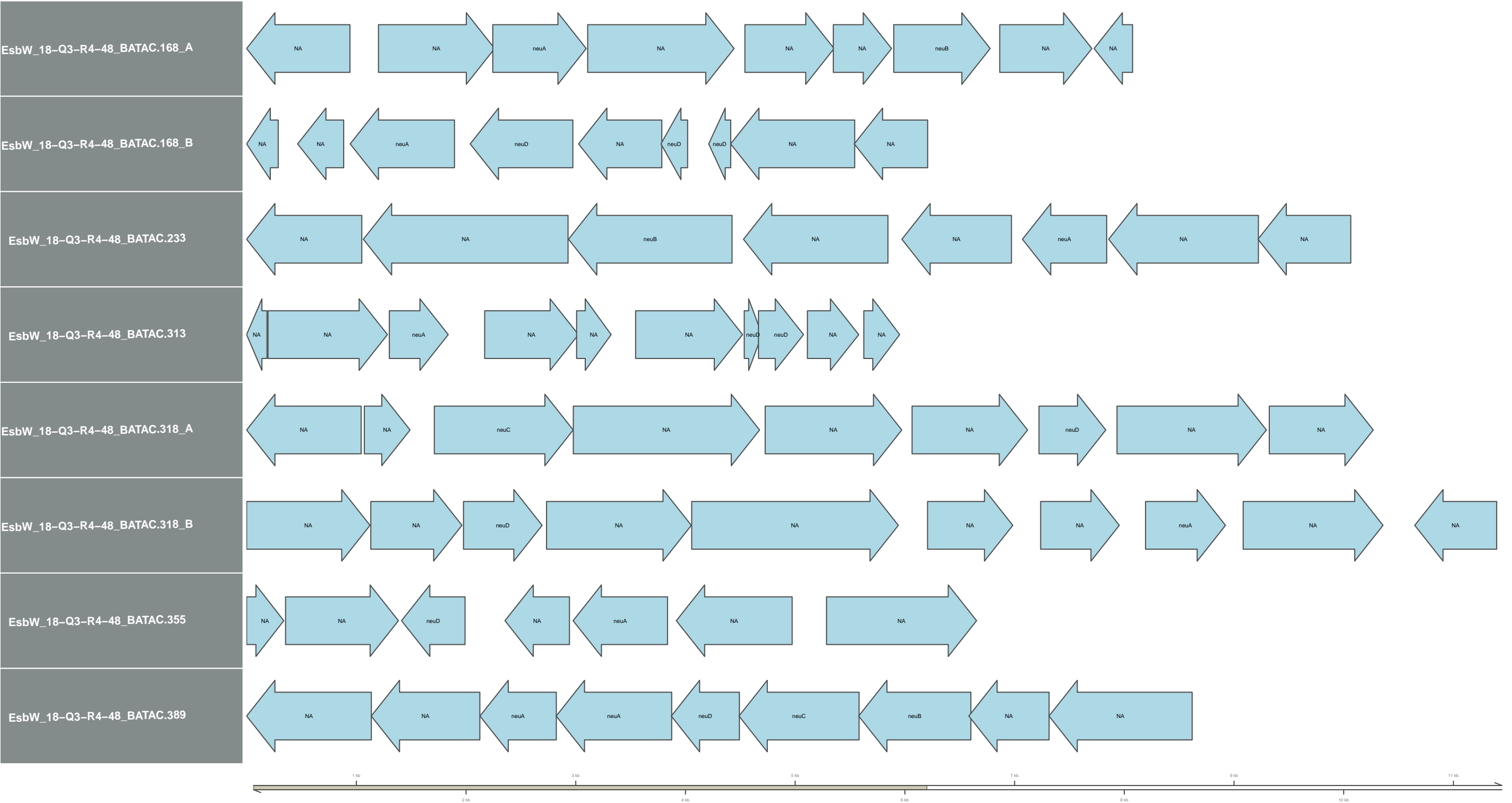
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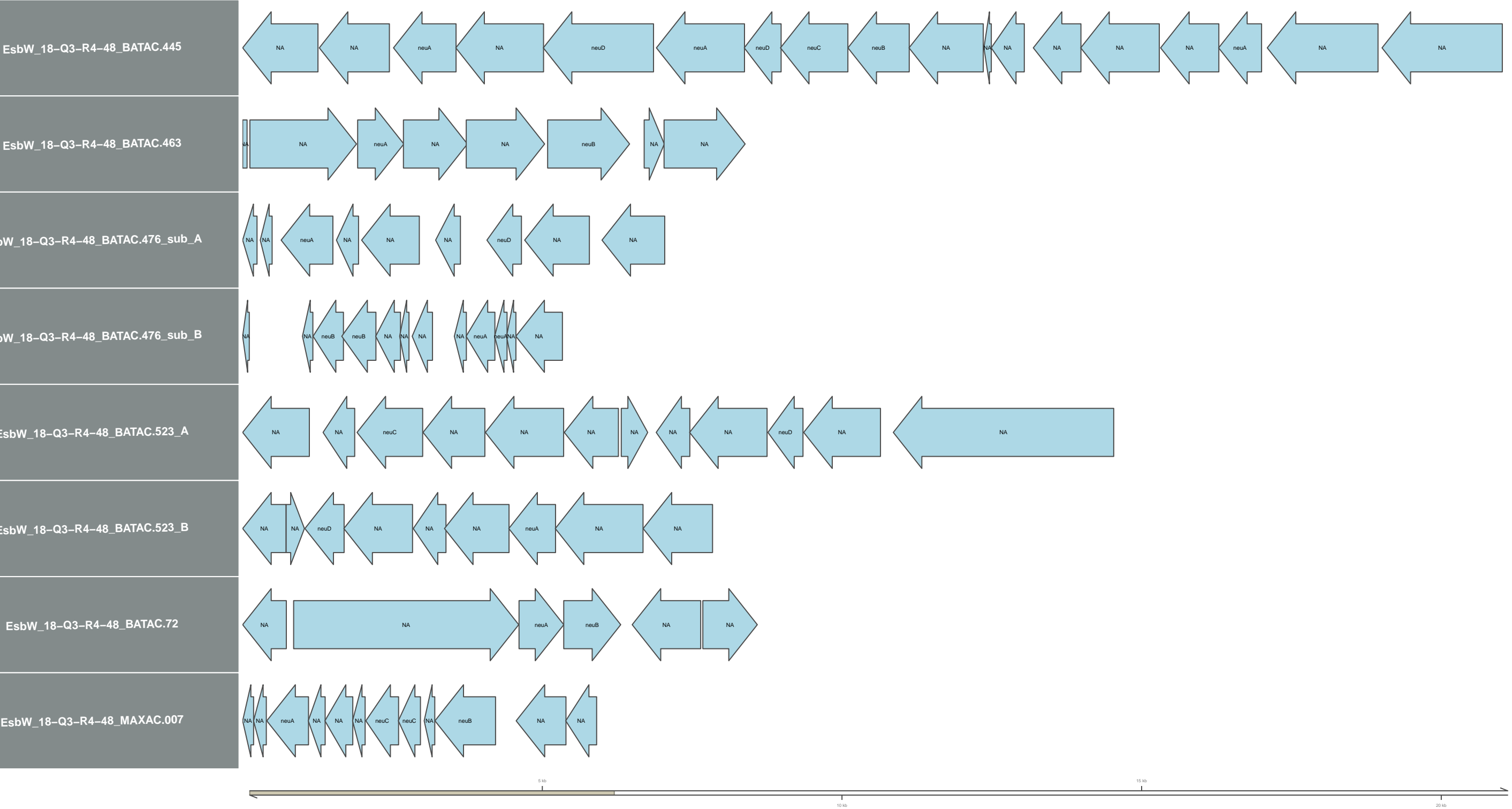
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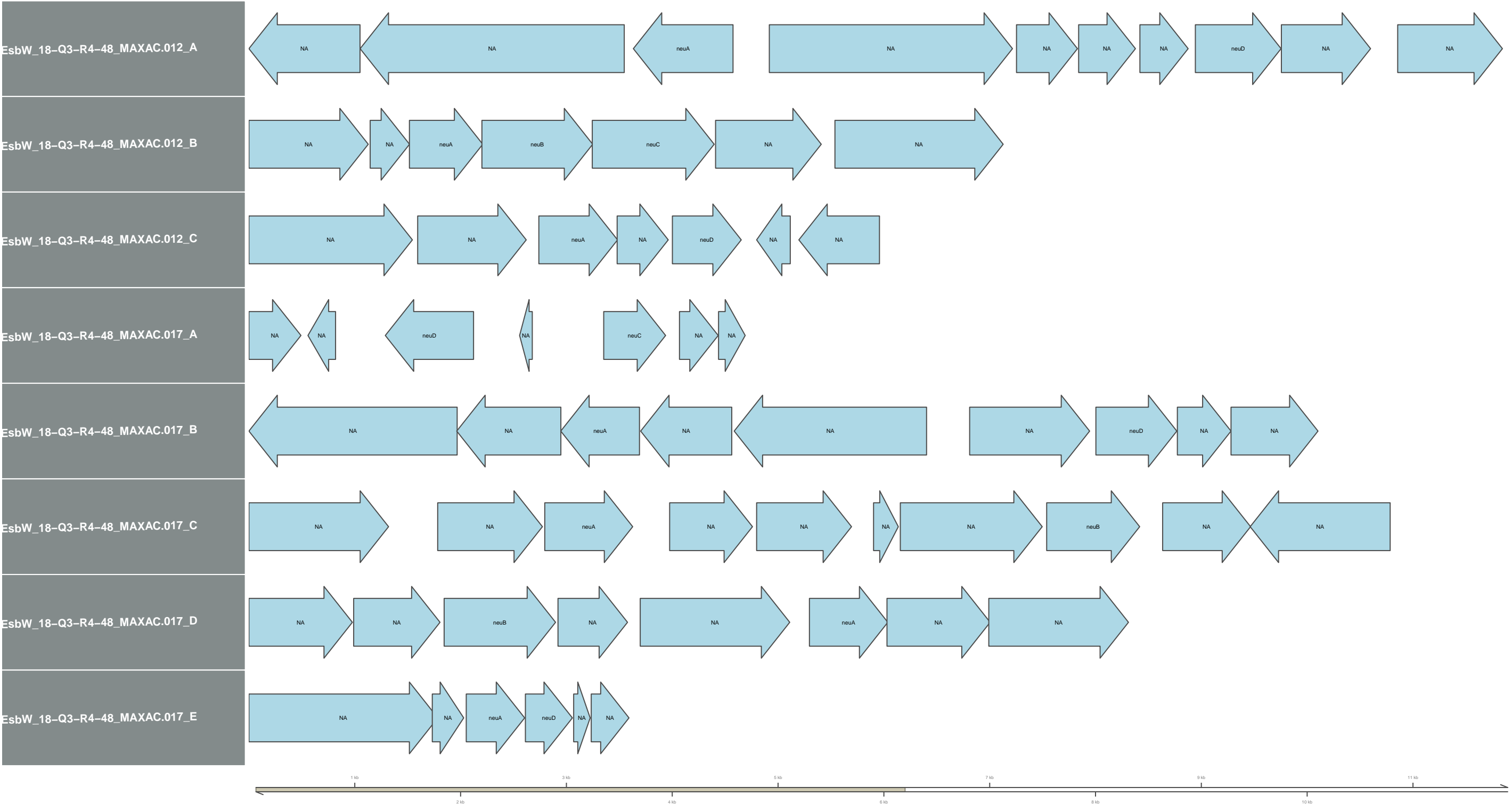
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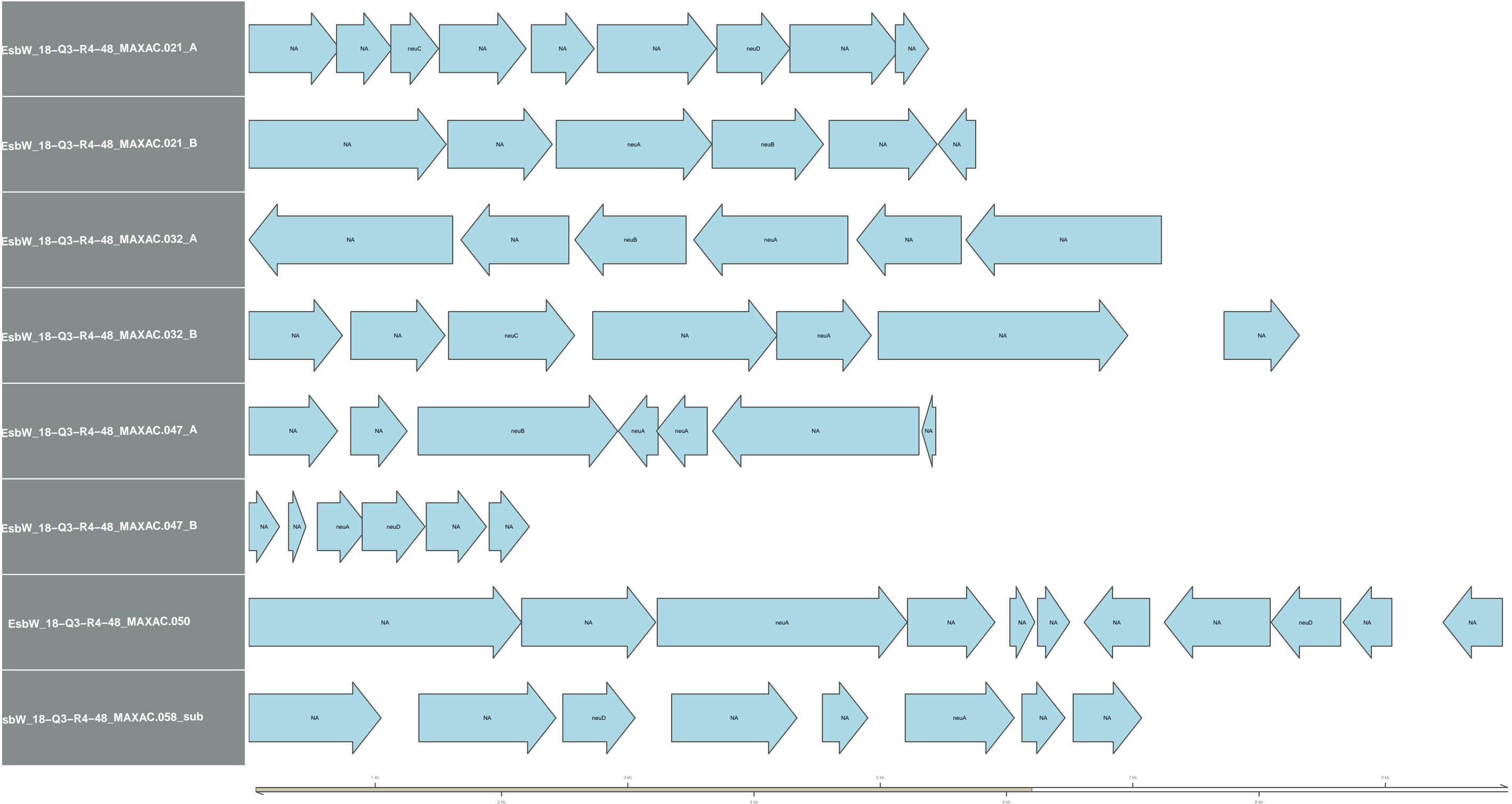
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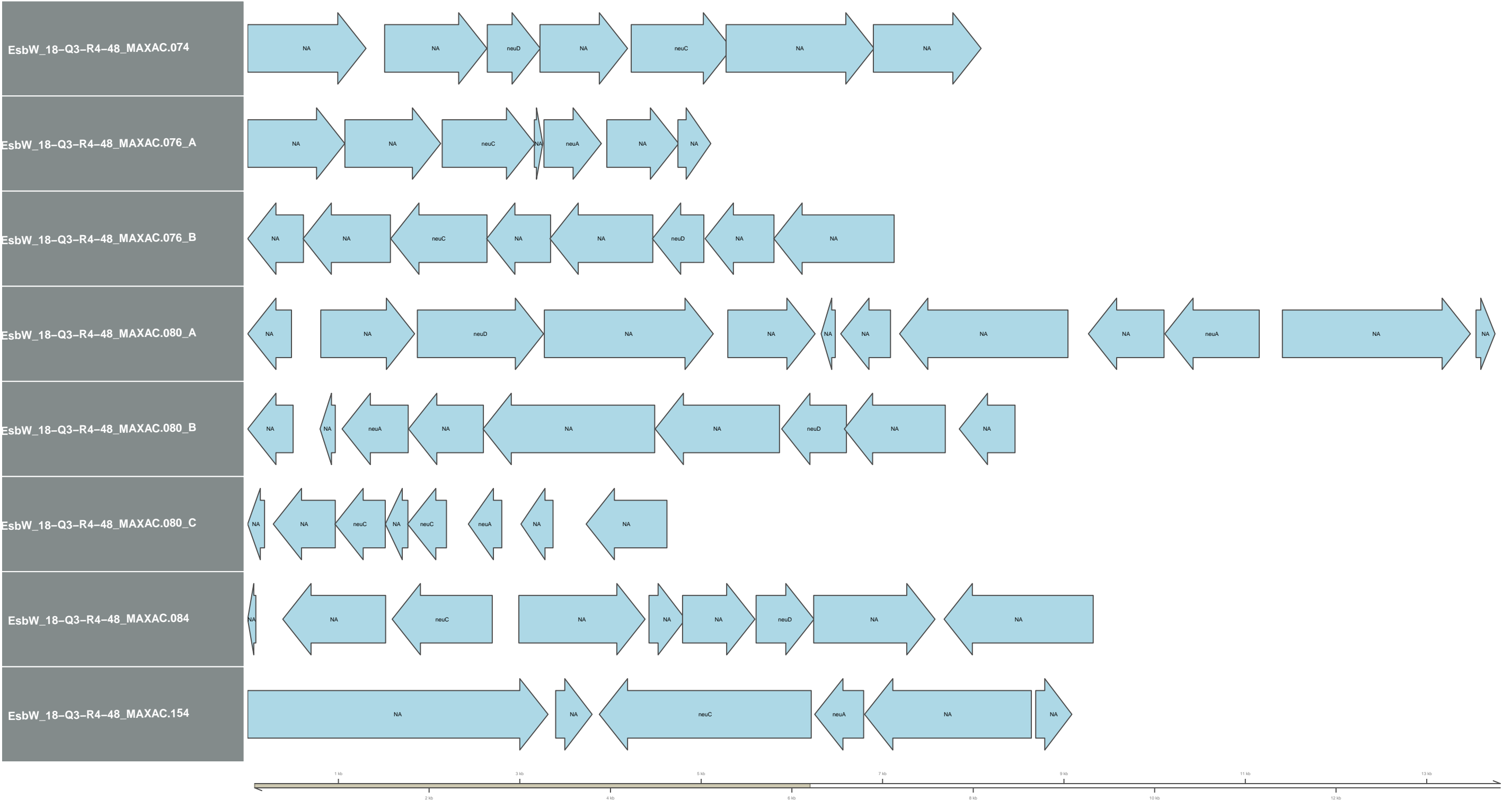
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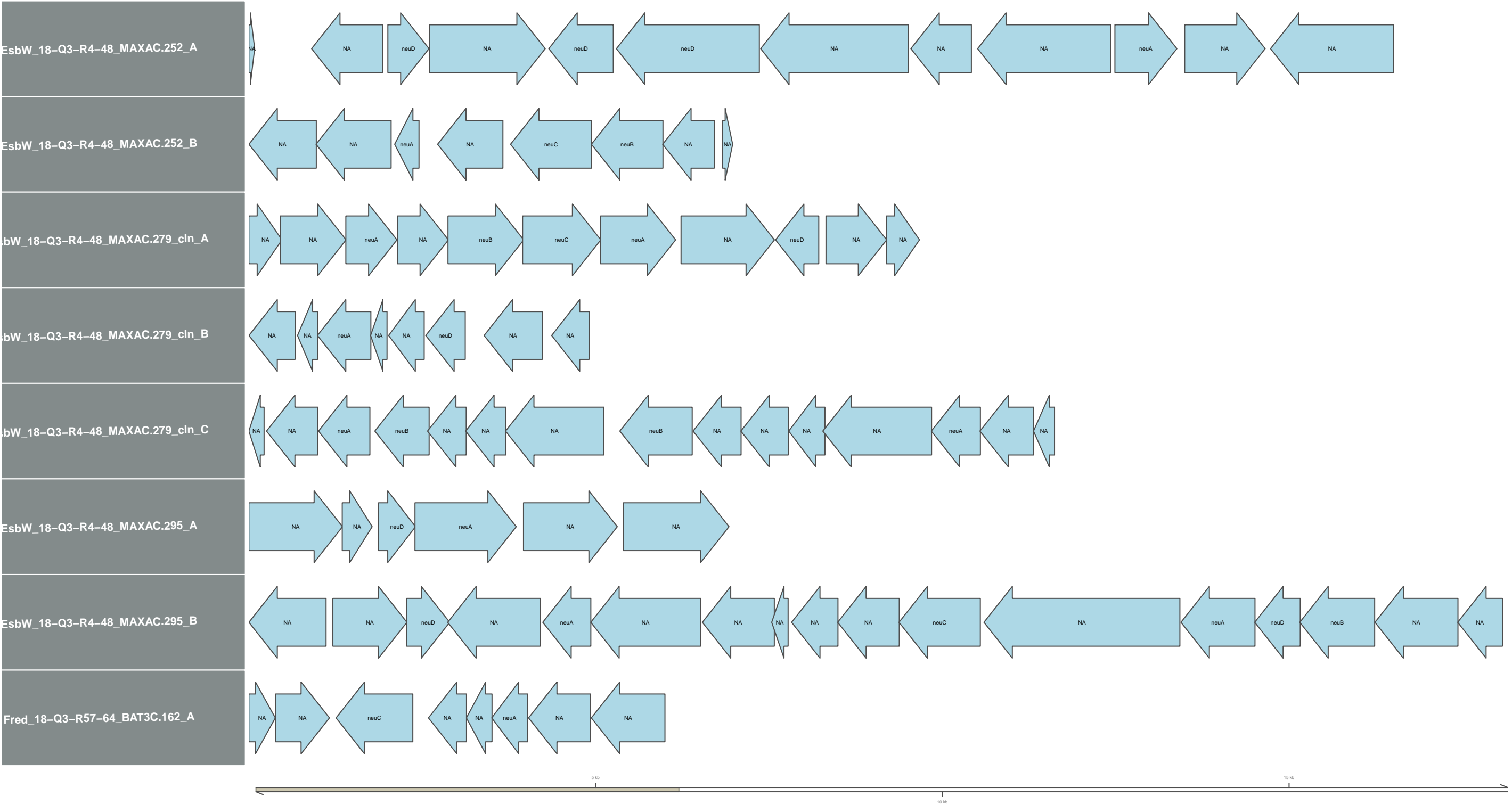
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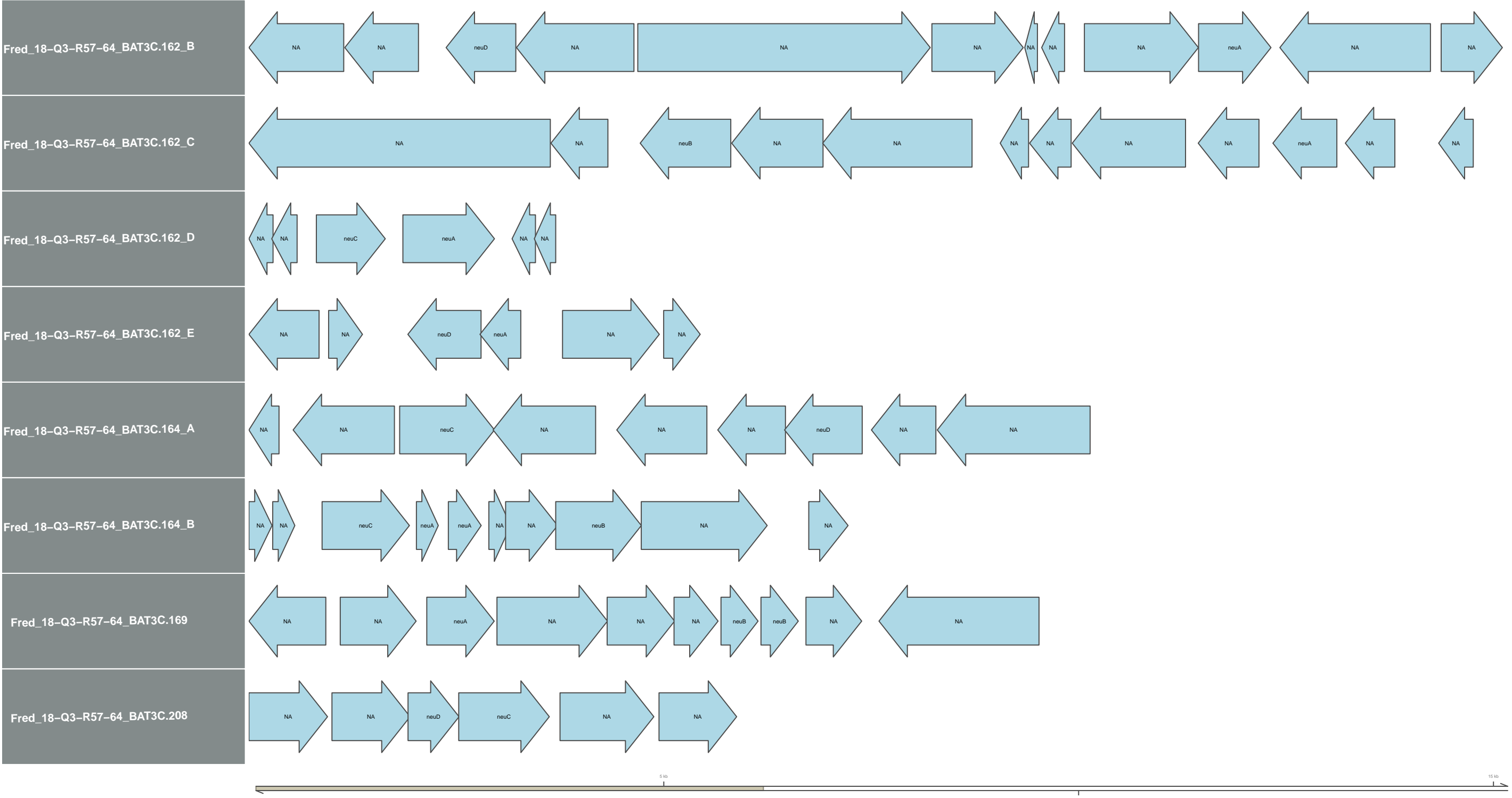
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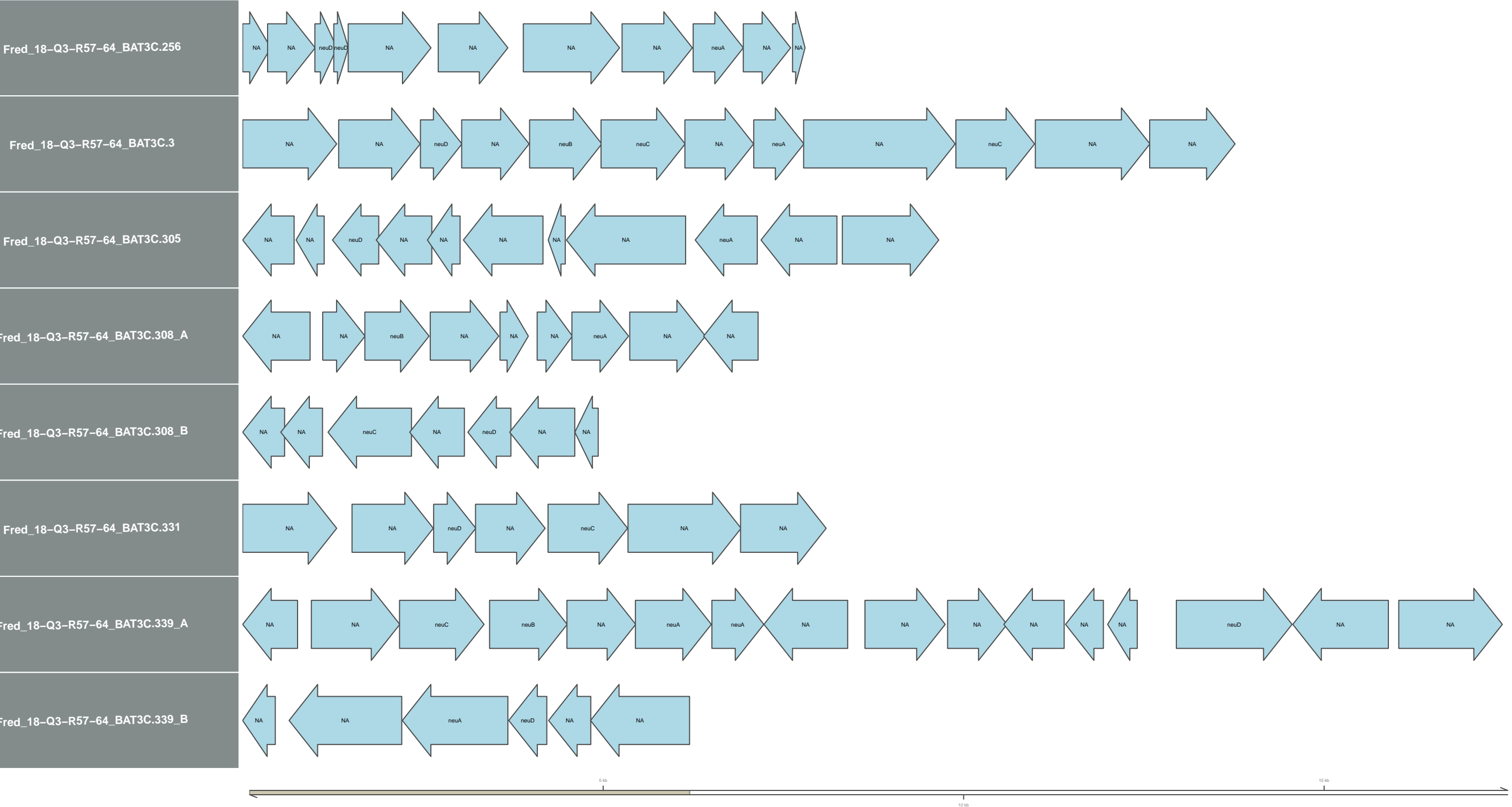
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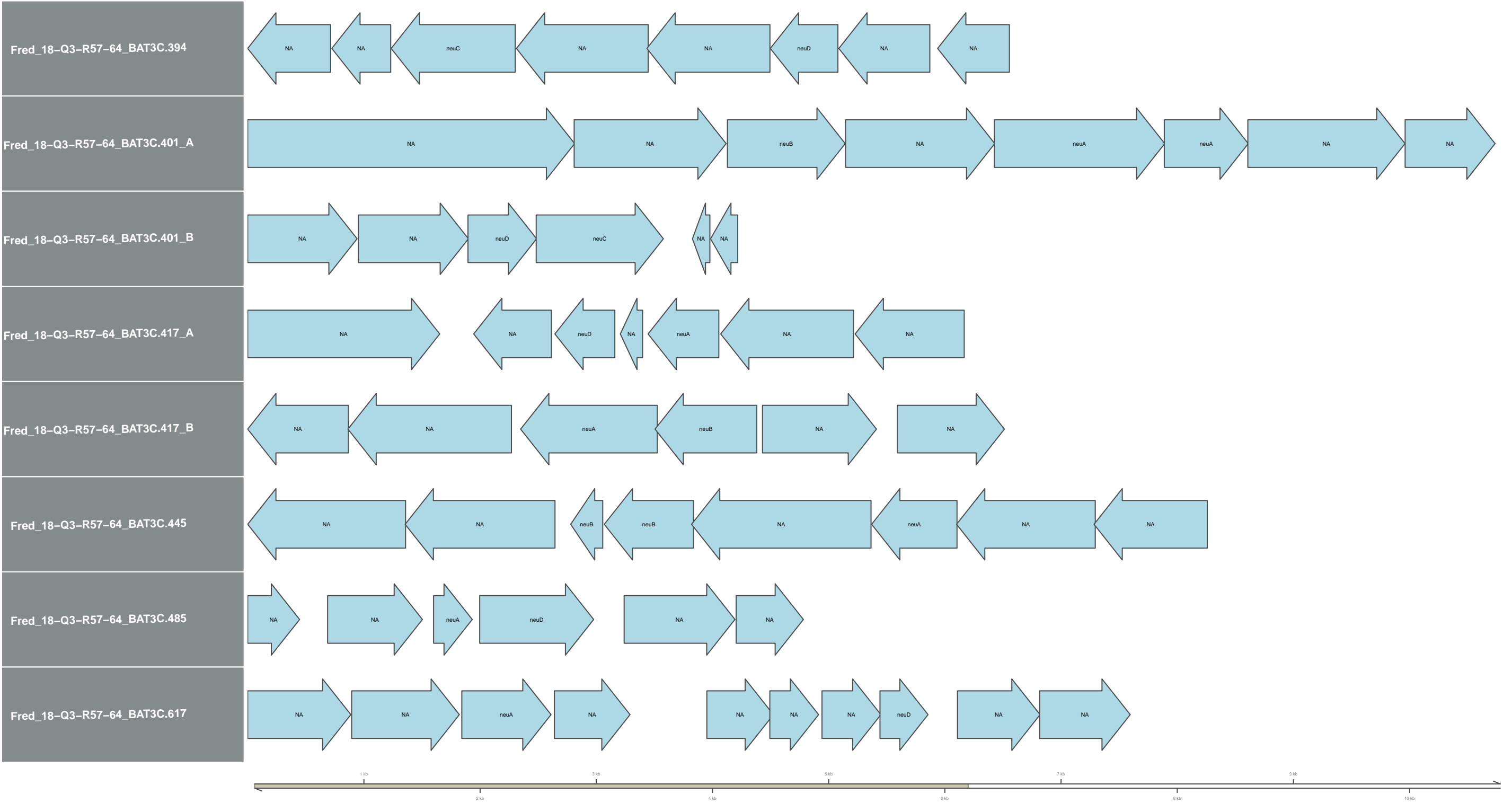
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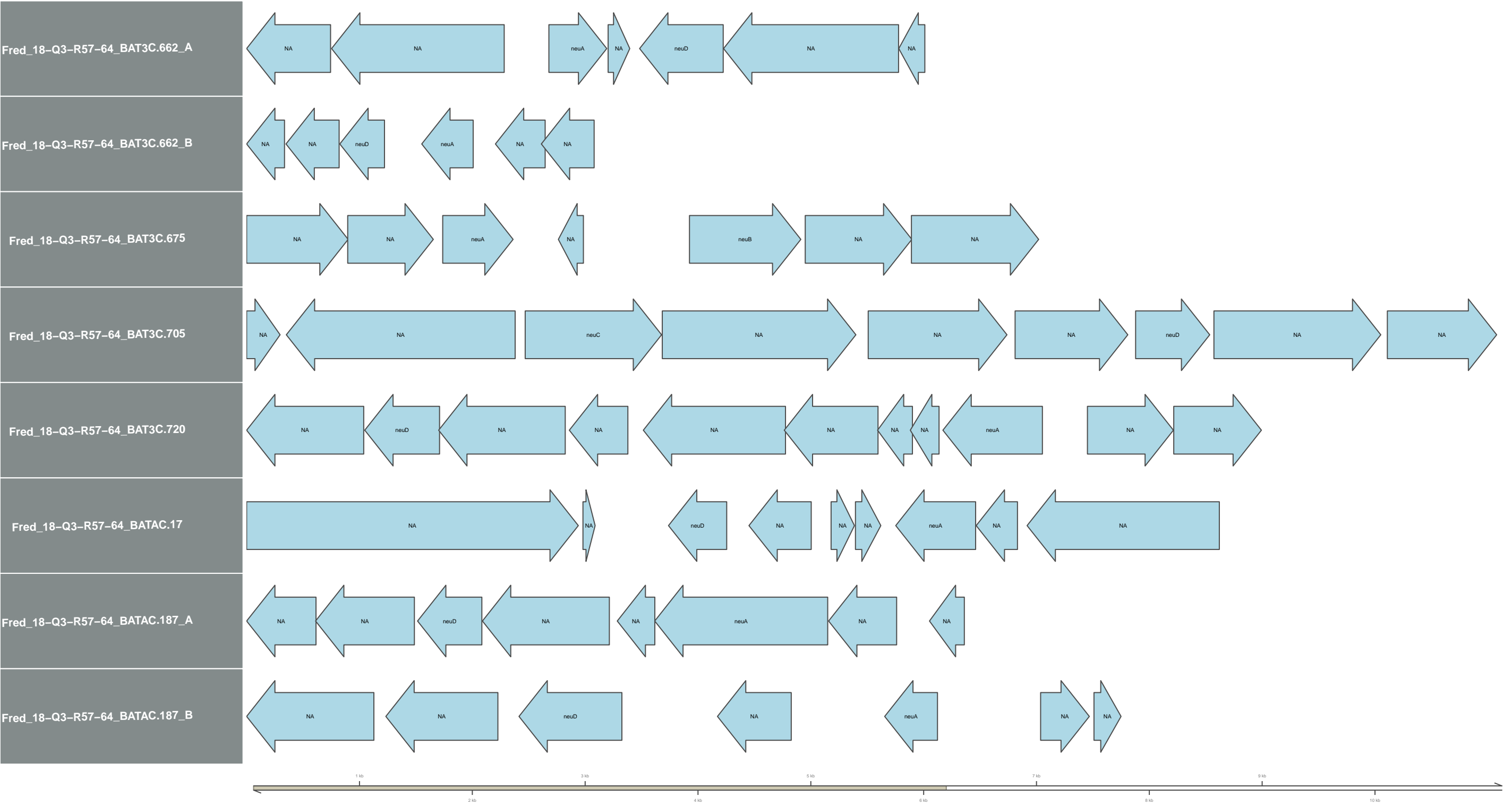
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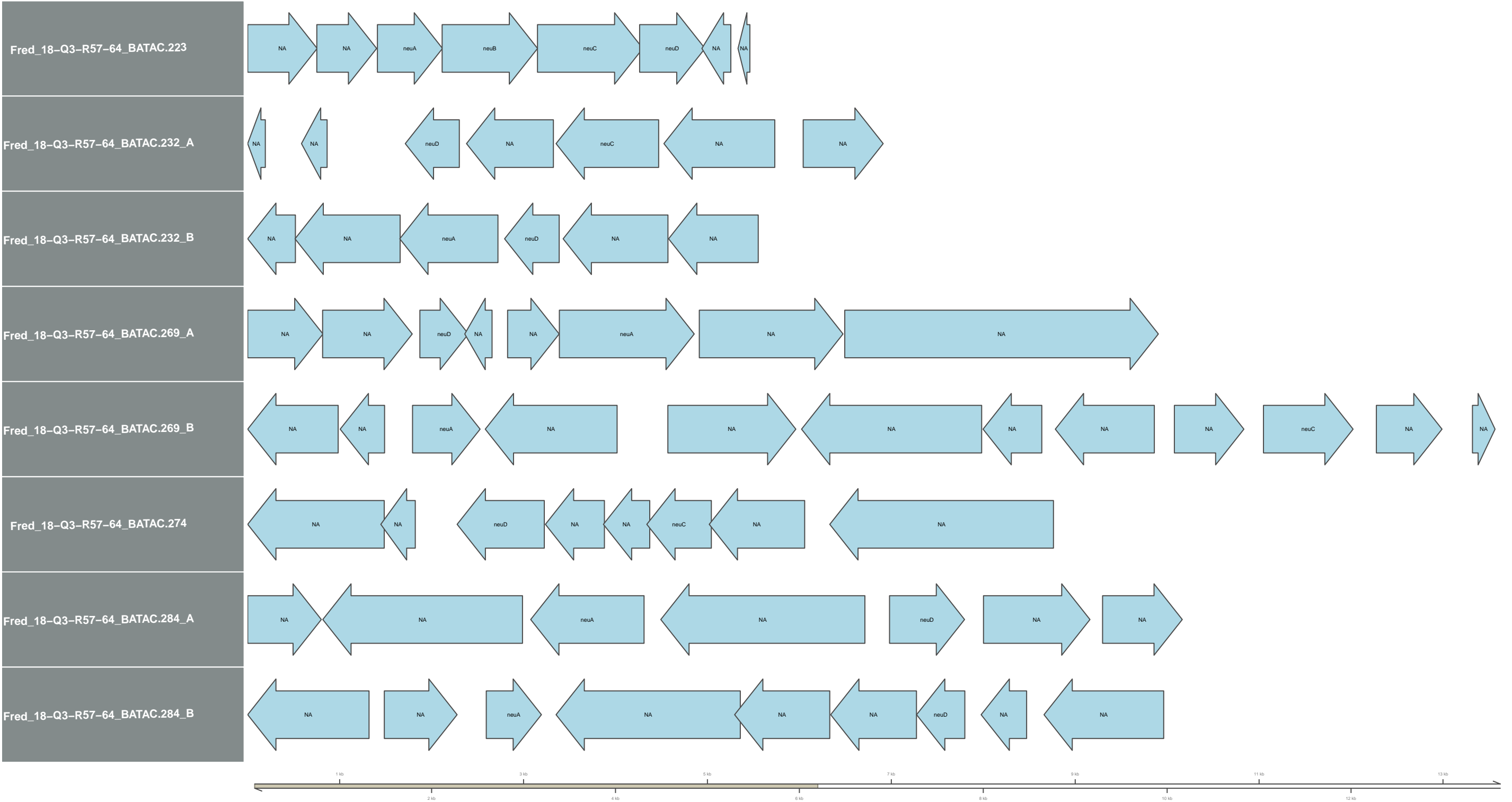
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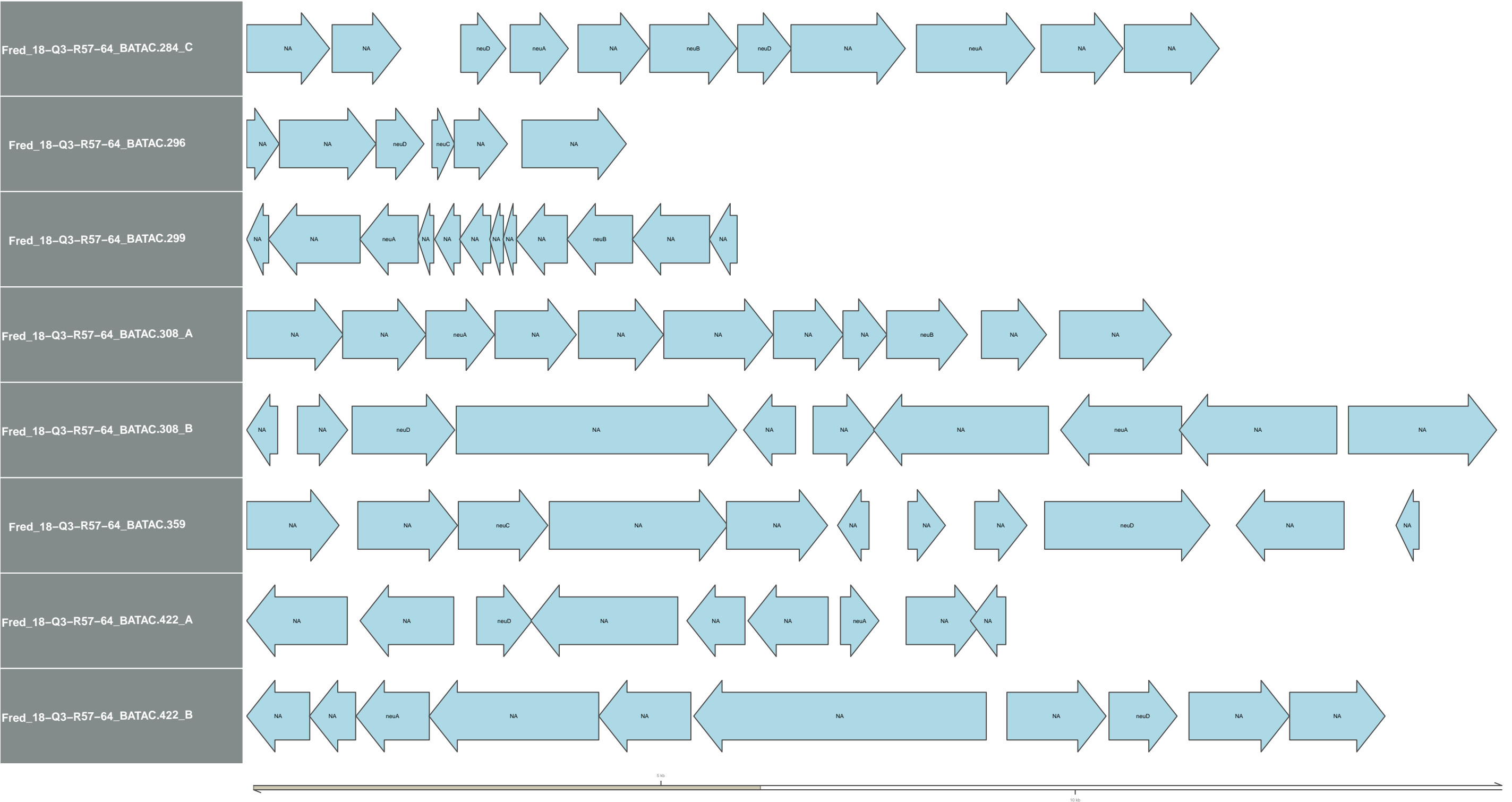
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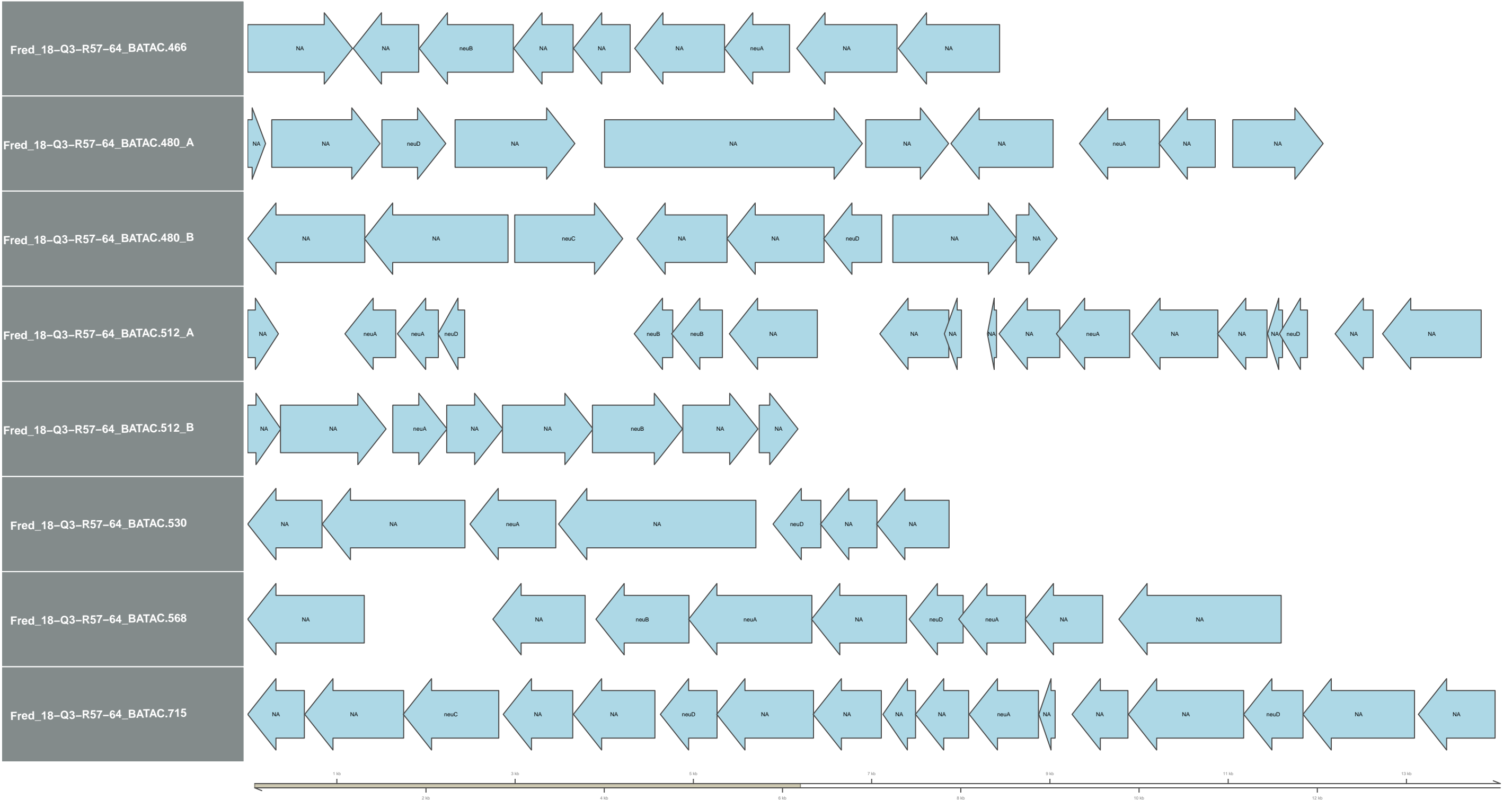
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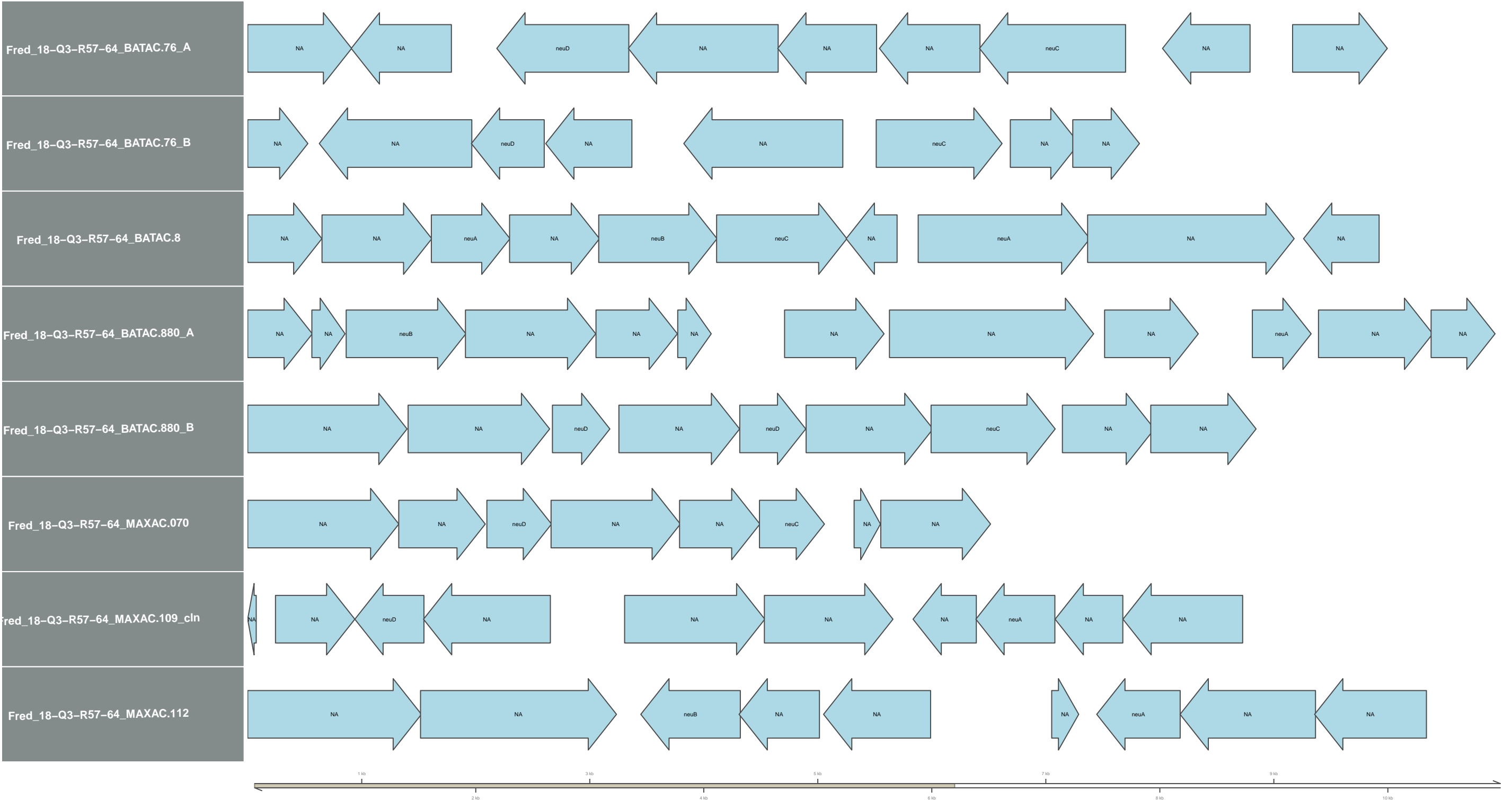
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NuIO_merged

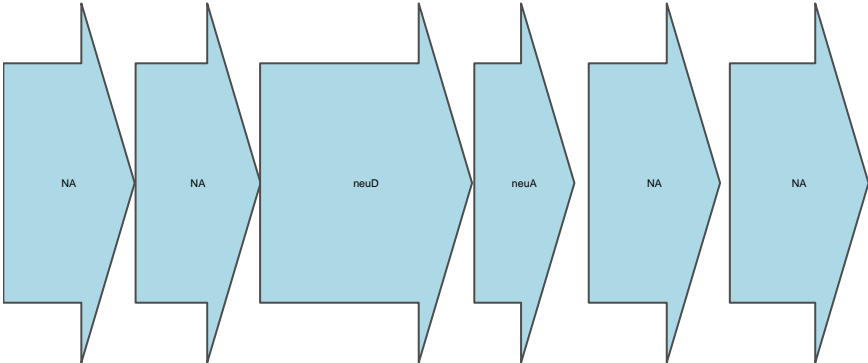


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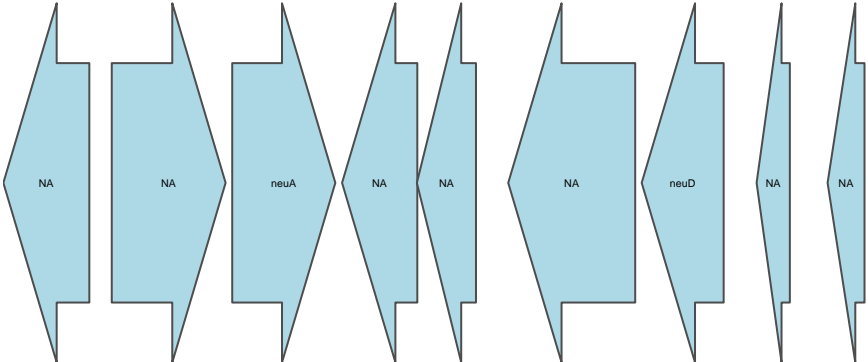


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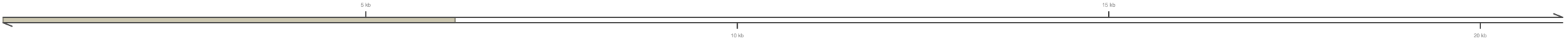
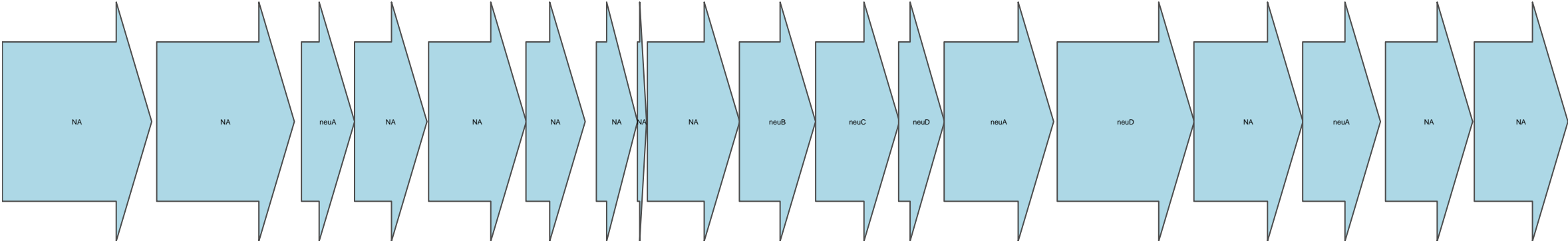
Fred_18-Q3-R57-64_MAXAC.209



Fred_18-Q3-R57-64_MAXAC.220



Fred_18-Q3-R57-64_MAXAC.222



298	Fred_18-Q3-R57-64_MAXAC.362	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Hyphomonadaceae;g__Hyphomonas;s__	tig00000777-10-25148860	43526	neuC	00043
299	Fred_18-Q3-R57-64_MAXAC.370	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__s__	tig00004330-10-6116250	349696	neuA	00291
300	Fred_18-Q3-R57-64_MAXAC.373	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Cellvibrionaceae;g__Cellvibrio;s__	tig00351555-10-10341640	198952	neuA	02800
301	Fred_18-Q3-R57-64_MAXAC.378	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__2-12-FULL-67-15;g__s__	tig00014337-10-1933470	189905	neuA	02195
302	Fred_18-Q3-R57-64_MAXAC.379	d__Bacteria;p__Cyanobacteria;c__Vampirovibrionia;o__Vampirovibrionales;f__Vampirovibrionaceae;g__s__	tig00350858-10-25518060	773694	neuA	01019
303	Fred_18-Q3-R57-64_MAXAC.396_cln	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Reyraneliales;f__Reyraneliaceae;g__s__	tig00000039-10-53363560	3447195	neuA	03312
304	Fred_18-Q3-R57-64_MAXAC.423	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;g__SCN-70-22;s__	tig00351211-10-13155530	1248463	neuA	04247
305	Hade_18-Q3-R52-61_BAT3C.141	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__UBA3362;s__	tig00406178-10-51613330	694285	neuC	00620
306	Hade_18-Q3-R52-61_BAT3C.212	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__JJ008;s__	tig00407653-10-1926590	183893	neuA	02513
307	Hade_18-Q3-R52-61_BAT3C.248	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__UBA3362;s__	tig00000101-10-30037980	2066444	neuA	01803
308	Hade_18-Q3-R52-61_BAT3C.250	d__Bacteria;p__Nitrospirota;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira;s__Nitrospira sp002254365	tig00001106-10-11150850	996349	neuA	02092
309	Hade_18-Q3-R52-61_BATAC.14	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__UBA7239;g__UBA7239;s__UBA7239 sp002333095	tig00003613-10-4728920	172570	neuA	00193
310	Hade_18-Q3-R52-61_BATAC.180	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Cytophagales;f__Cyclobacteriaceae;g__ELB16-189;s__	tig00012467-10-1924820	111466	neuA	03057
311	Hade_18-Q3-R52-61_BATAC.255	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__PHOS-HE28;g__PHOS-HE28;s__	tig00017526-10-1471930	82432	neuA	01730
312	Hade_18-Q3-R52-61_BATAC.287	d__Bacteria;p__Acidobacteriota;c__Blastocatellia;o__Pyrinomonadales;f__g__s__	tig00002277-10-6540280	288880	neuA	00817
313	Hade_18-Q3-R52-61_BATAC.311	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Agitococcus;s__Agitococcus sp002333125	tig00409785-10-1220310	106567	neuA	02645
314	Hade_18-Q3-R52-61_BATAC.34	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__JJ008;s__	tig00001009-10-10233600	548344	neuA	00571
315	Hade_18-Q3-R52-61_BATAC.364	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Dechloromonas;s__	tig00406547-10-1384150	24959	neuA	02712
316	Hade_18-Q3-R52-61_BATAC.500	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__OLB9;s__	tig00408953-10-2470440	242381	neuA	03358
317	Hade_18-Q3-R52-61_BATAC.692	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__OLB11;s__	tig00406607-10-5482930	482605	neuA	00746
318	Hade_18-Q3-R52-61_BATAC.713	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__AKYH767;f__b-17BO;g__UBA4416;s__	tig00018913-10-1413430	140541	neuA	02849
319	Hade_18-Q3-R52-61_BATAC.786	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__BACL12;g__UBA7236;s__	tig00004038-10-4381940	205513	neuA	00649
320	Hade_18-Q3-R52-61_MAXAC.021	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__OLB8;s__	tig00027690-10-776110	9086	neuA	02857
321	Hade_18-Q3-R52-61_MAXAC.023	d__Bacteria;p__Nitrospirota;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira_A;s__Nitrospira_A sp900170025	tig00007806-10-2904650	118130	neuA	01896
322	Hade_18-Q3-R52-61_MAXAC.026	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__s__	tig00002623-10-6181280	332442	neuA	00327
323	Hade_18-Q3-R52-61_MAXAC.028	d__Bacteria;p__Bacteroidota;c__Ignavibacteria;o__SJA-28;f__B-1AR;g__UBA2330;s__	tig00012776-10-1965300	83949	neuA	02184
324	Hade_18-Q3-R52-61_MAXAC.042	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__Anaerolineales;f__envOPS12;g__OLB14;s__	tig00014449-10-1135470	107562	neuA	01575
325	Hade_18-Q3-R52-61_MAXAC.064	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__s__	tig00406432-10-6385110	444546	neuA	02632
326	Hade_18-Q3-R52-61_MAXAC.088	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__AKYH767-A;f__OLB10;g__s__	tig00001683-10-7580860	747730	neuC	00701
327	Hade_18-Q3-R52-61_MAXAC.102	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__AKYH767-A;f__2013-40CM-41-45;g__s__	tig00001256-10-8309610	11644	neuA	00013
328	Hade_18-Q3-R52-61_MAXAC.112	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__UBA3362;s__	tig00000876-10-10999120	706276	neuC	00588
329	Hade_18-Q3-R52-61_MAXAC.228	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__s__	tig00043586-10-480900	34573	neuA	04119
330	Hade_18-Q3-R52-61_MAXAC.236_sub	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__Promineofilales;f__g__s__	tig00014149-10-1752310	124430	neuA	01194
331	Hade_18-Q3-R52-61_MAXAC.304	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Propionivibrio;s__	tig01683464-10-7939650	304893	neuA	02810
332	Hade_18-Q3-R52-61_MAXAC.319	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00001472-10-7732770	360930	neuA	01295
333	Hade_18-Q3-R52-61_MAXAC.344	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__UBA3362;s__	tig00406197-10-29585390	2250656	neuA	02997
334	Hade_18-Q3-R52-61_MAXAC.360	d__Bacteria;p__Acidobacteriota;c__Blastocatellia;o__Pyrinomonadales;f__Pyrinomonadaceae;g__OLB17;s__	tig00000009-10-41445700	3000312	neuA	02492
335	Hade_18-Q3-R52-61_MAXAC.389	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__UBA2359;g__s__	tig00009717-10-1997970	143319	neuA	02708
336	Hade_18-Q3-R52-61_MAXAC.390	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiotrichales;f__Thiotrichaceae;g__Thiofilum;s__	tig00000011-10-40151770	2371088	neuA	02277
337	Hirt_18-Q3-R61-65_BAT3C.167	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Nigerium;s__	tig00004005-10-6400670	67499	neuA	00075
338	Hirt_18-Q3-R61-65_BAT3C.204	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rhodobacter_E;s__	tig01347854-10-6912630	102275	neuA	03523
339	Hirt_18-Q3-R61-65_BAT3C.235	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Opitutales;f__Opitutaceae;g__s__	tig00010562-10-1944820	19355	neuA	01869
340	Hirt_18-Q3-R61-65_BAT3C.274	d__Bacteria;p__Myxococcota;c__Polyangia;o__GCA-2747355;f__GCA-2747355;g__s__	tig00001721-10-10109740	437277	neuA	01397
341	Hirt_18-Q3-R61-65_BAT3C.279	d__Bacteria;p__Actinobacteriota;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Micropruina;s__	tig00001155-10-14562110	1196983	neuA	02776
342	Hirt_18-Q3-R61-65_BAT3C.307	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__UBA3362;s__	tig00002262-10-8186640	229614	neuA	02249