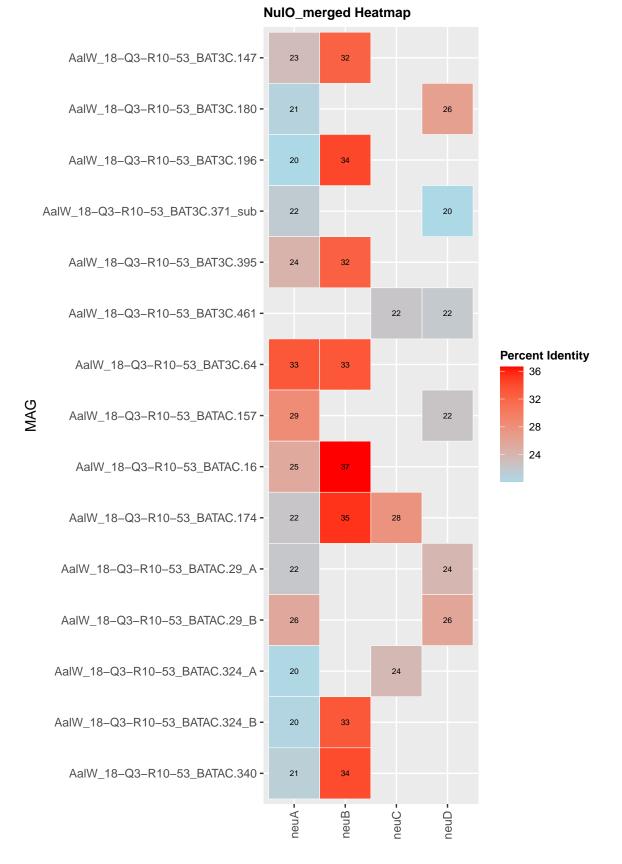
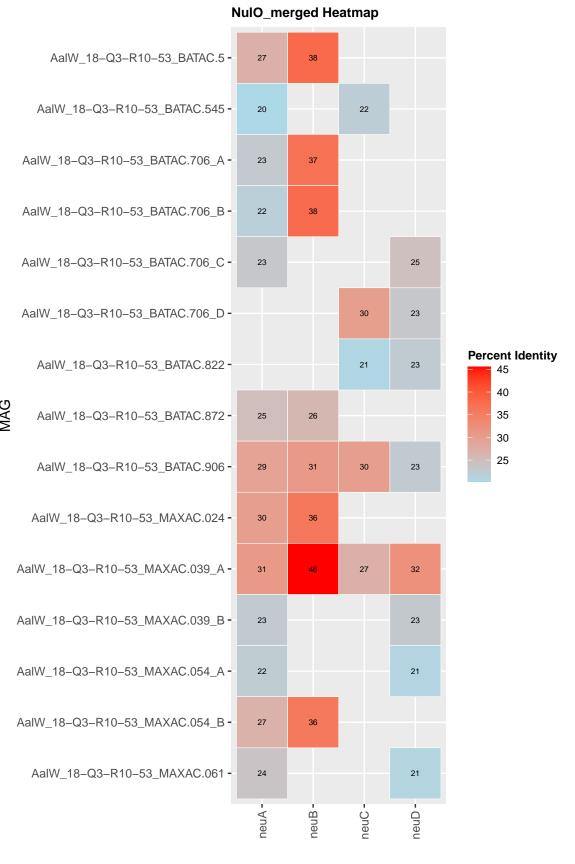
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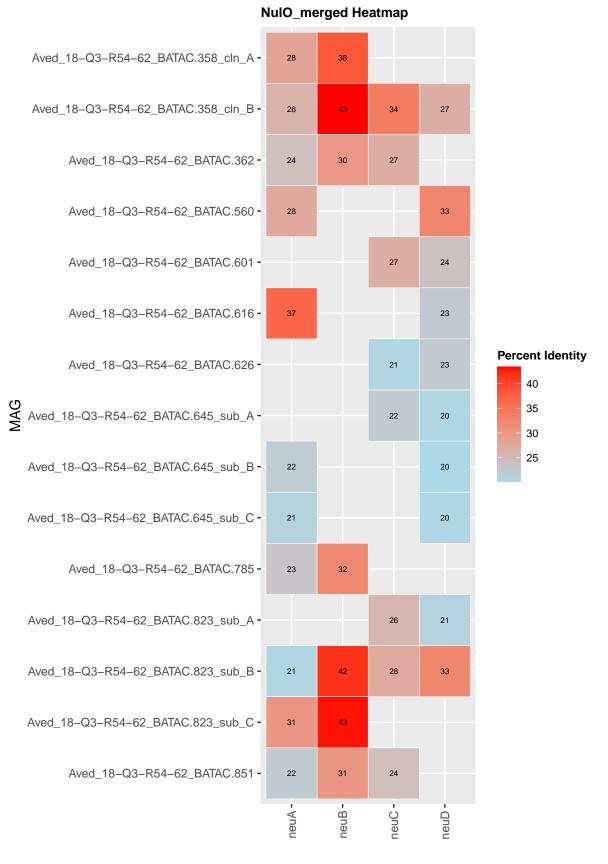
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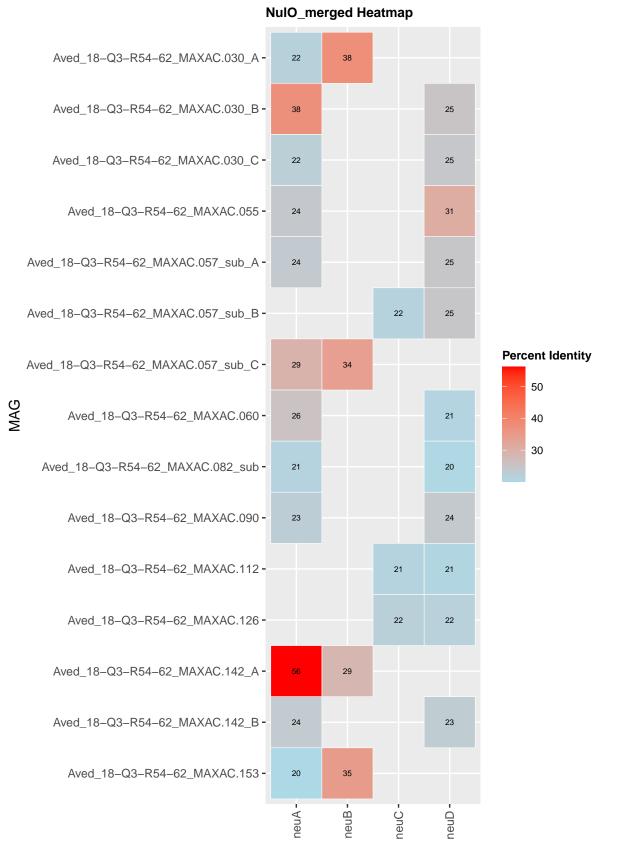


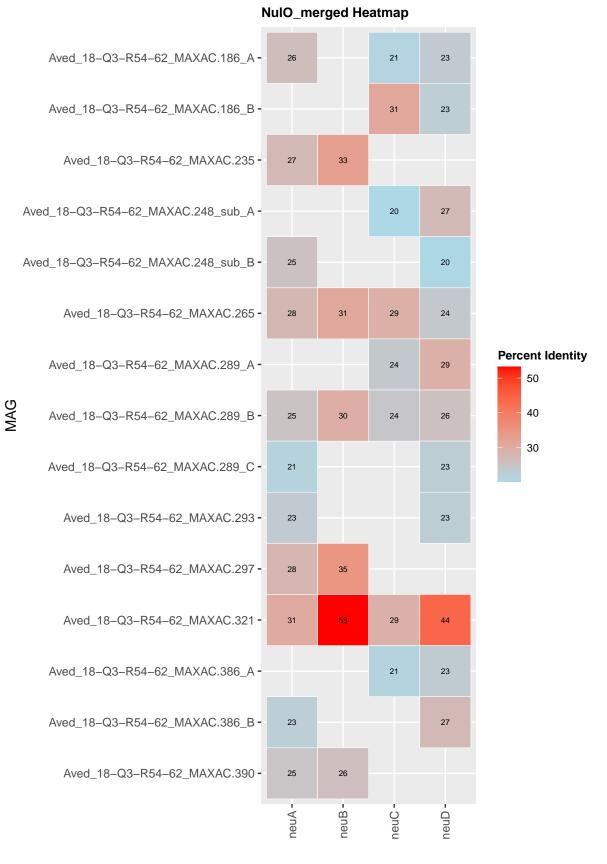


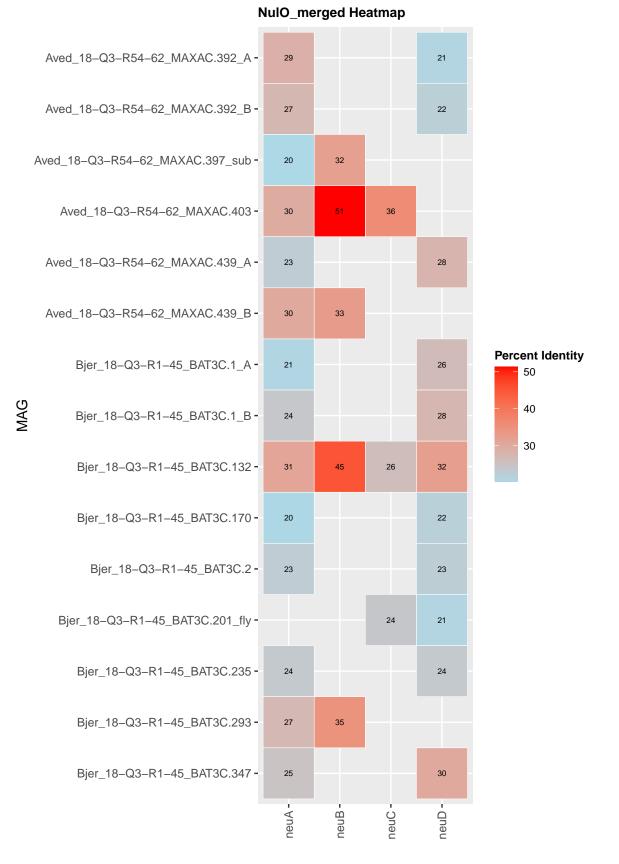
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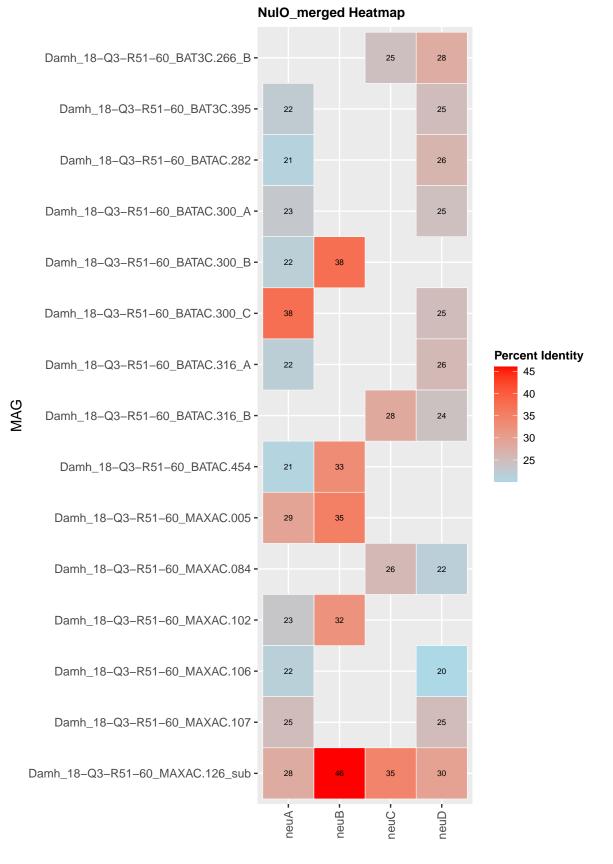






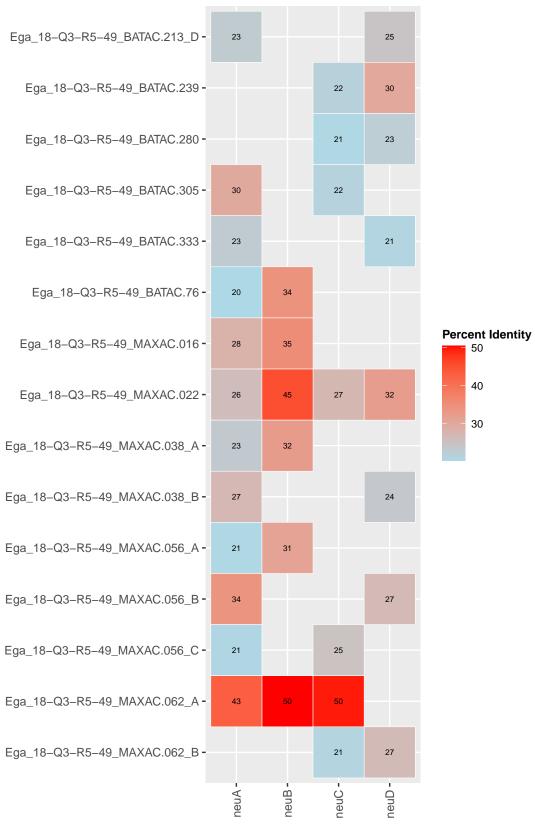
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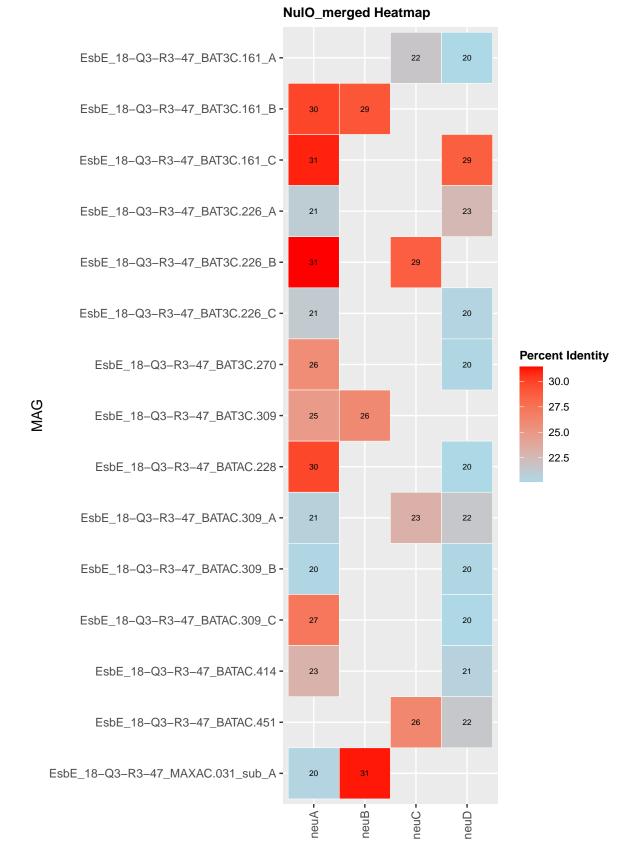
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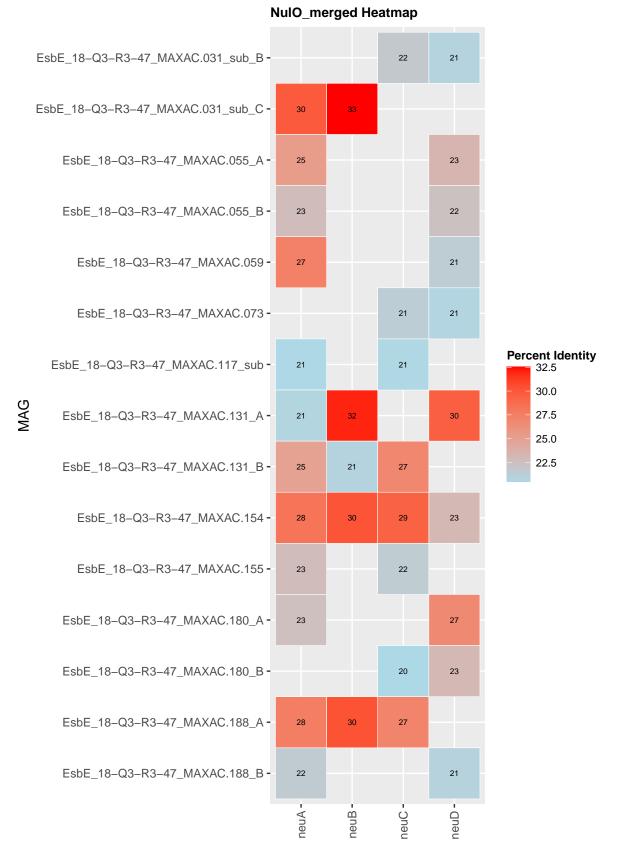
NuIO_merged Heatmap



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NuIO_merged Heatmap Ejby_18-Q3-R6-50_BATAC.215_sub -21 23 Ejby_18-Q3-R6-50_BATAC.240 -Ejby_18-Q3-R6-50_BATAC.262 -20 28 Ejby_18-Q3-R6-50_BATAC.272 -28 23 Ejby_18-Q3-R6-50_BATAC.463 -22 23 Ejby_18-Q3-R6-50_MAXAC.047 -27 Percent Identity Ejby_18-Q3-R6-50_MAXAC.157 - 20 **O** Ejby_18-Q3-R6-50_MAXAC.161_A -40 21 21 30 Ejby_18-Q3-R6-50_MAXAC.161_B -28 Ejby_18-Q3-R6-50_MAXAC.161_C -43 Ejby_18-Q3-R6-50_MAXAC.192 -31 28 44 Ejby_18-Q3-R6-50_MAXAC.193_A -25 24 Ejby_18-Q3-R6-50_MAXAC.193_B -20 Ejby_18-Q3-R6-50_MAXAC.193_C -28 EsbE_18-Q3-R3-47_BAT3C.140 -28 26 21





NulO_merged Heatmap EsbE_18-Q3-R3-47_MAXAC.191 -EsbW_18-Q3-R4-48_BAT3C.13 -EsbW_18-Q3-R4-48_BAT3C.194 -EsbW_18-Q3-R4-48_BAT3C.247 -EsbW_18-Q3-R4-48_BAT3C.275 -EsbW_18-Q3-R4-48_BAT3C.288_A -Percent Identity EsbW_18-Q3-R4-48_BAT3C.288_B -EsbW_18-Q3-R4-48_BAT3C.307 -EsbW_18-Q3-R4-48_BAT3C.4_cln -EsbW_18-Q3-R4-48_BAT3C.485 -EsbW_18-Q3-R4-48_BAT3C.7 -EsbW_18-Q3-R4-48_BATAC.168_A -EsbW_18-Q3-R4-48_BATAC.168_B -EsbW_18-Q3-R4-48_BATAC.233 -EsbW_18-Q3-R4-48_BATAC.313 -

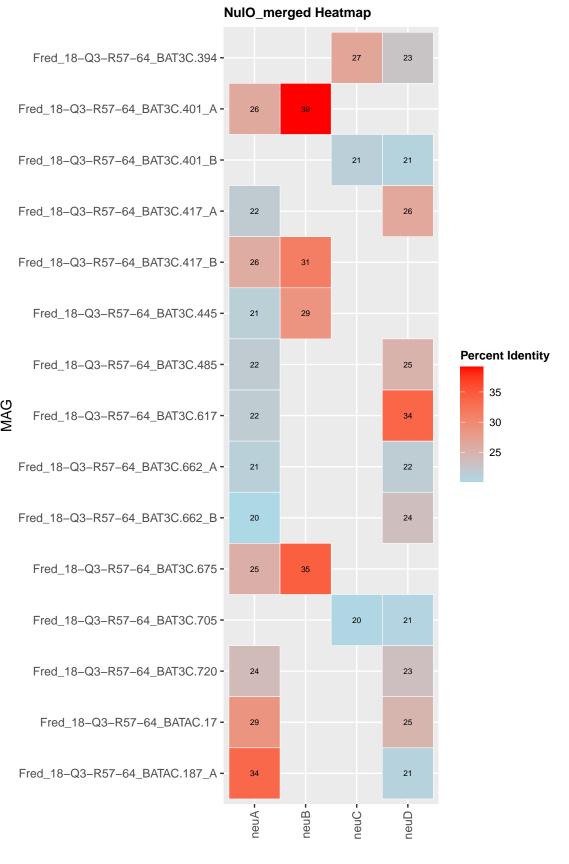
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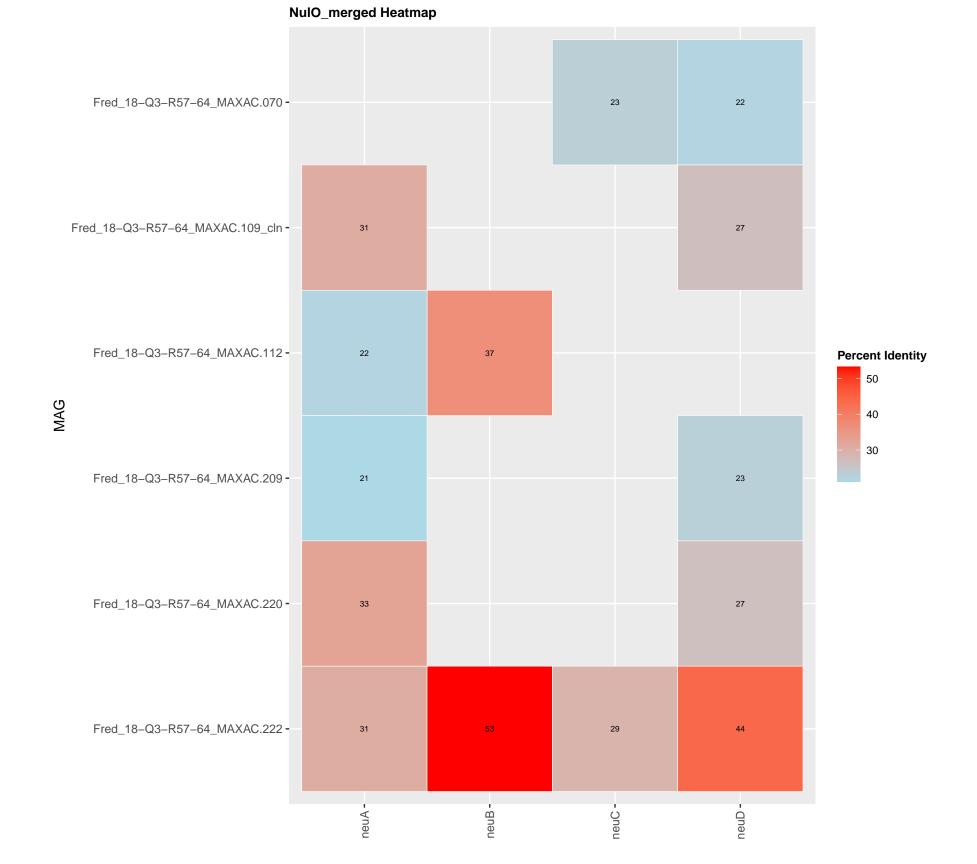
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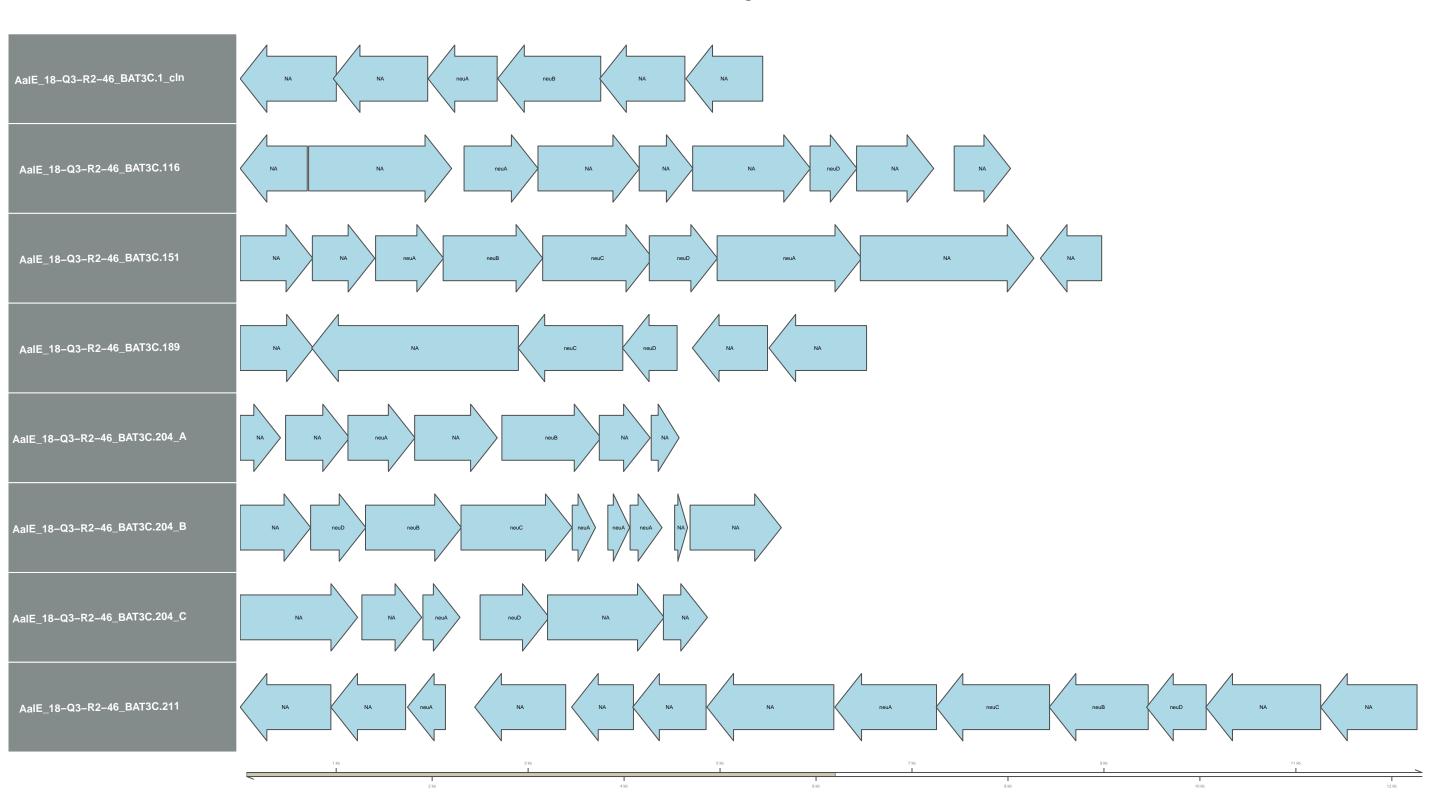


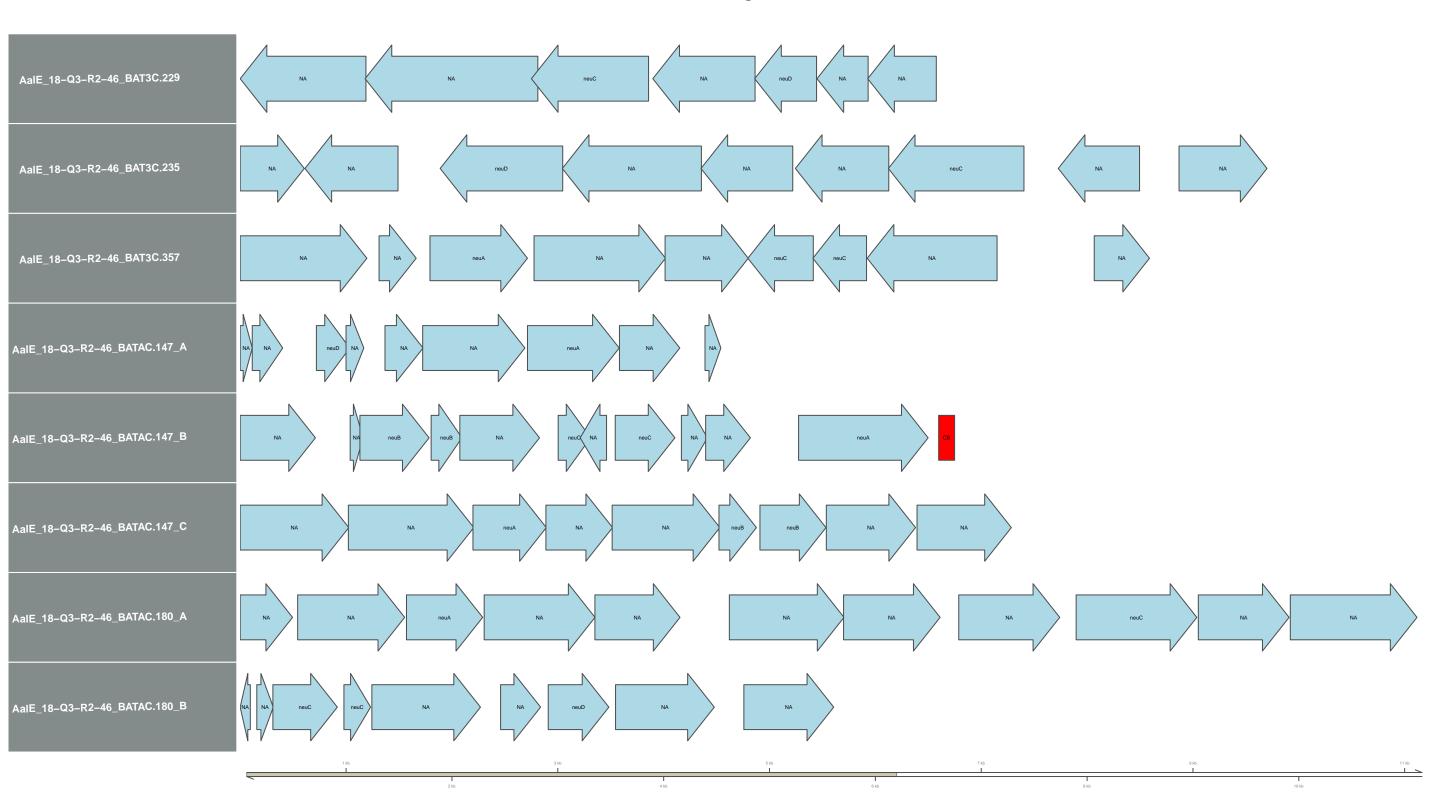
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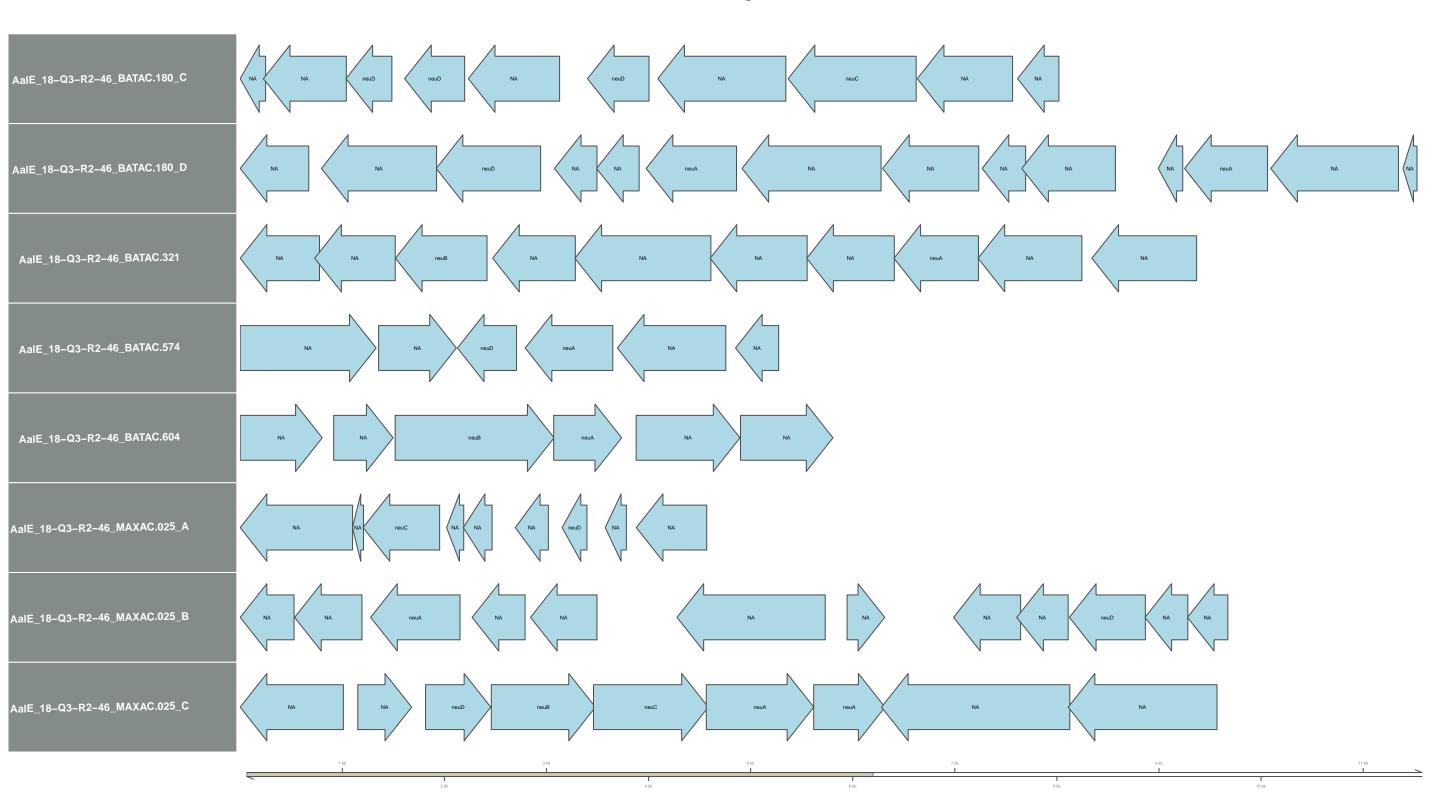
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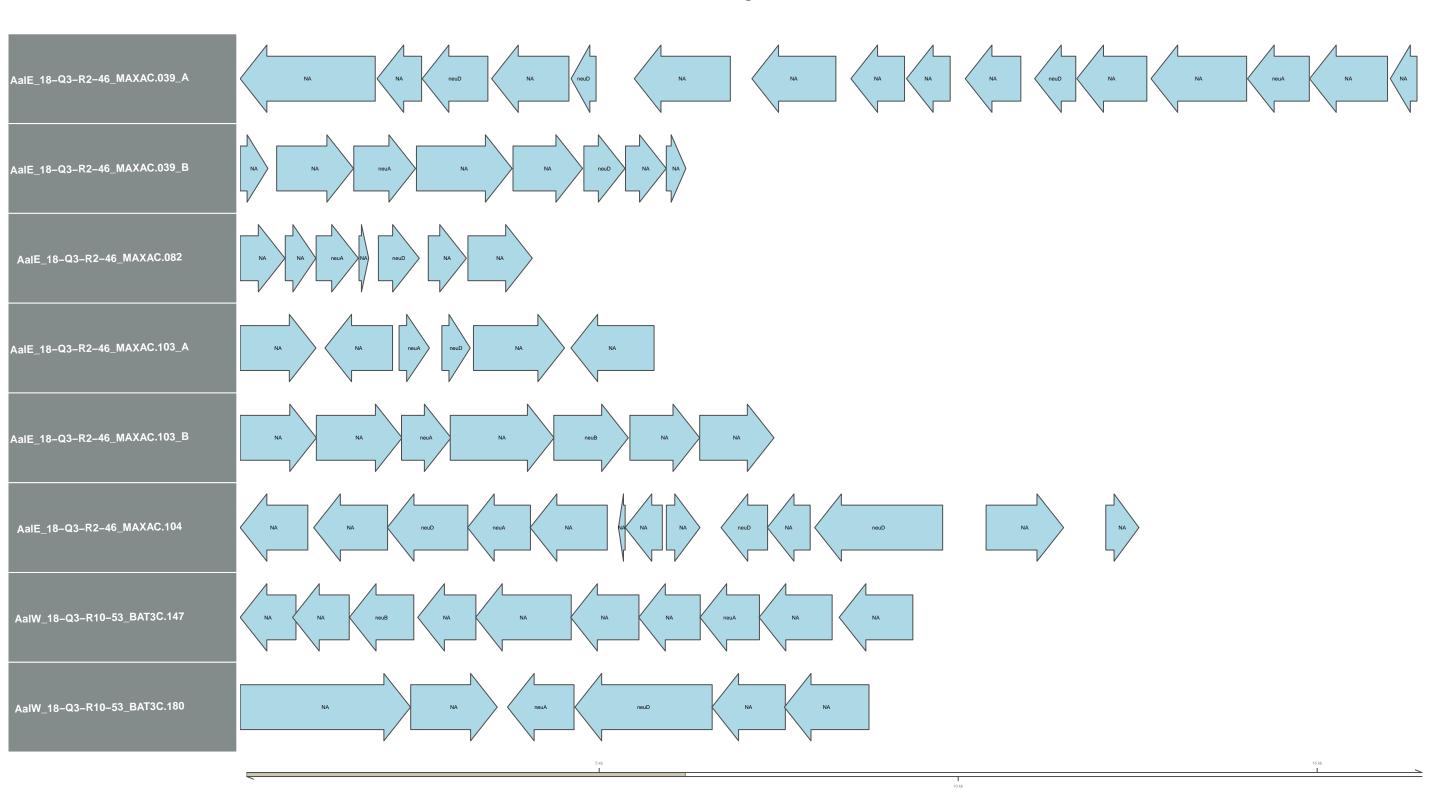
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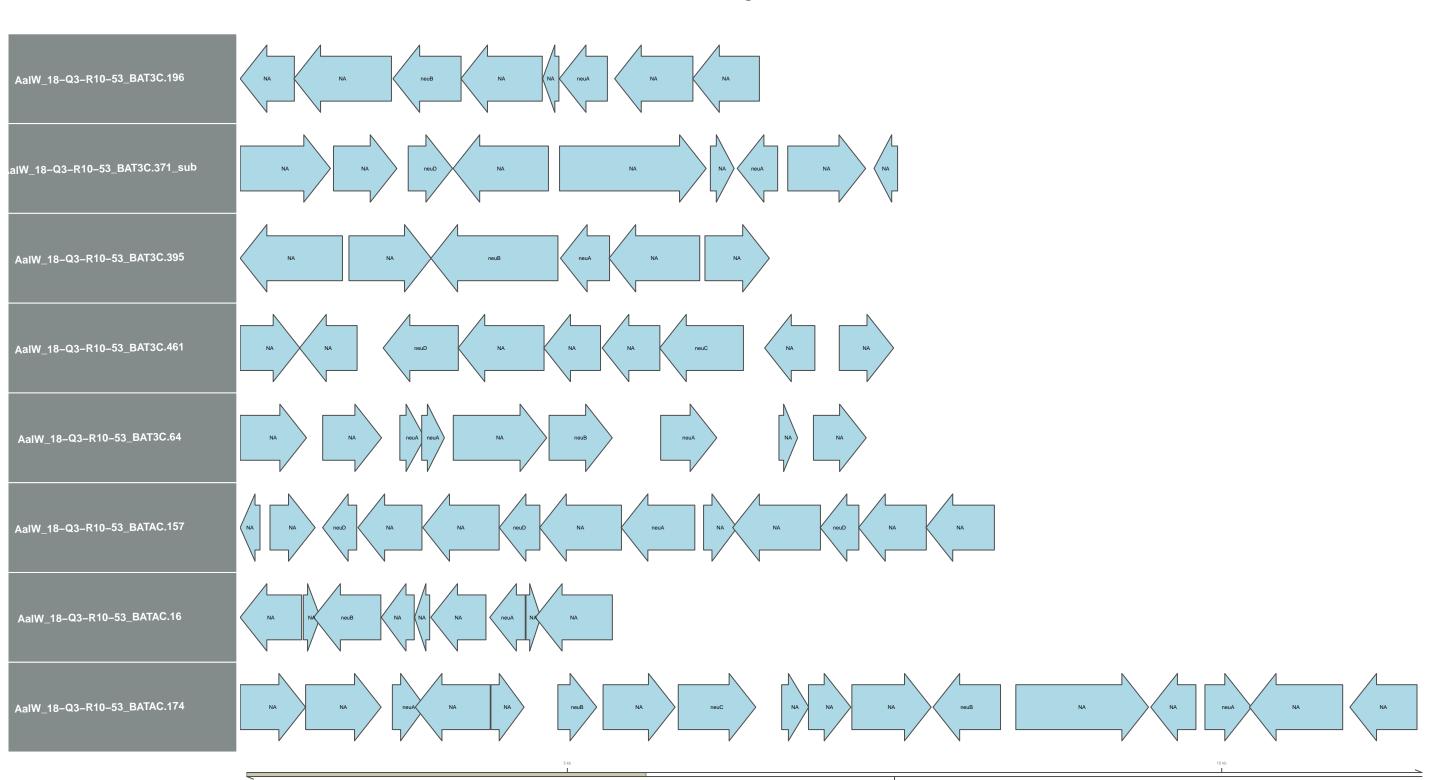


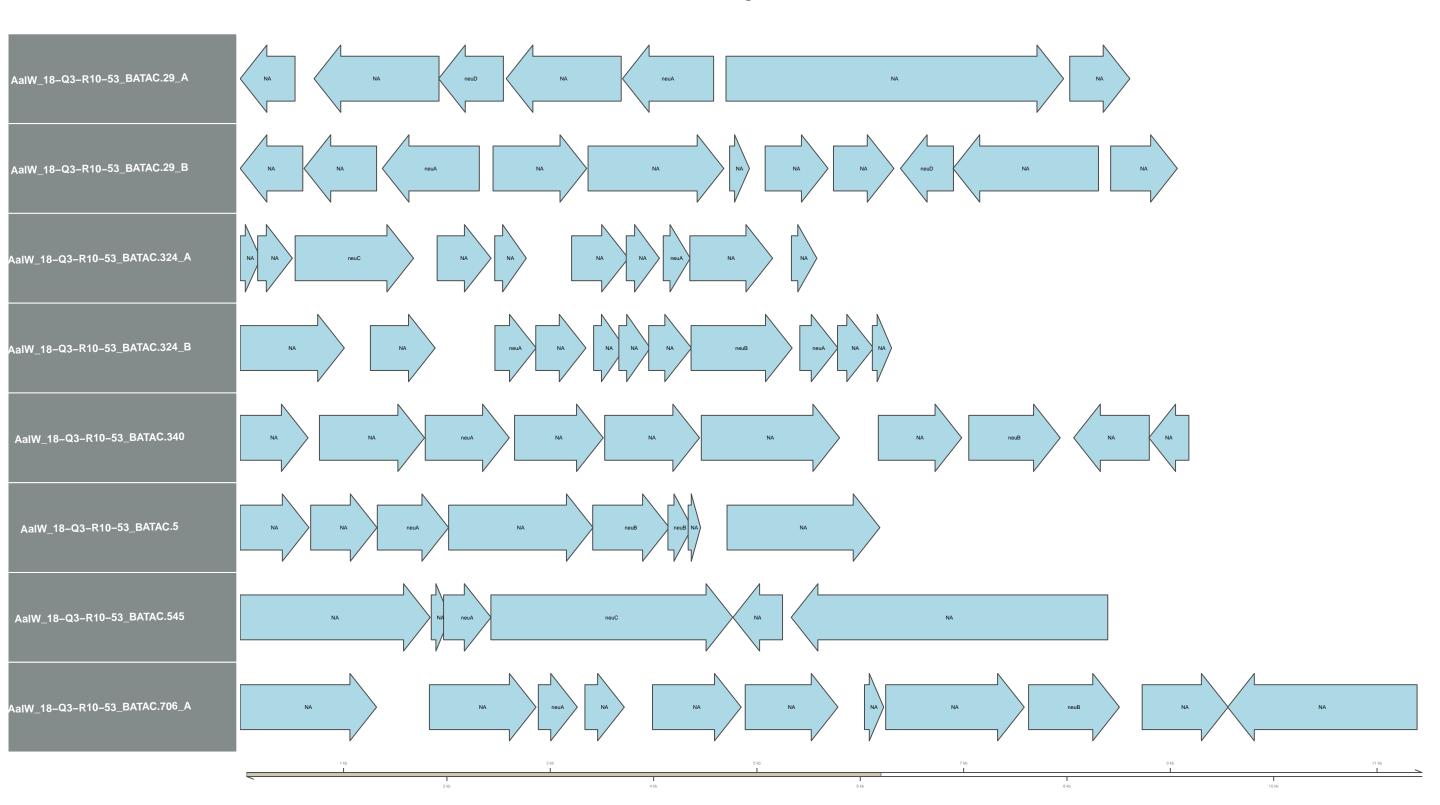


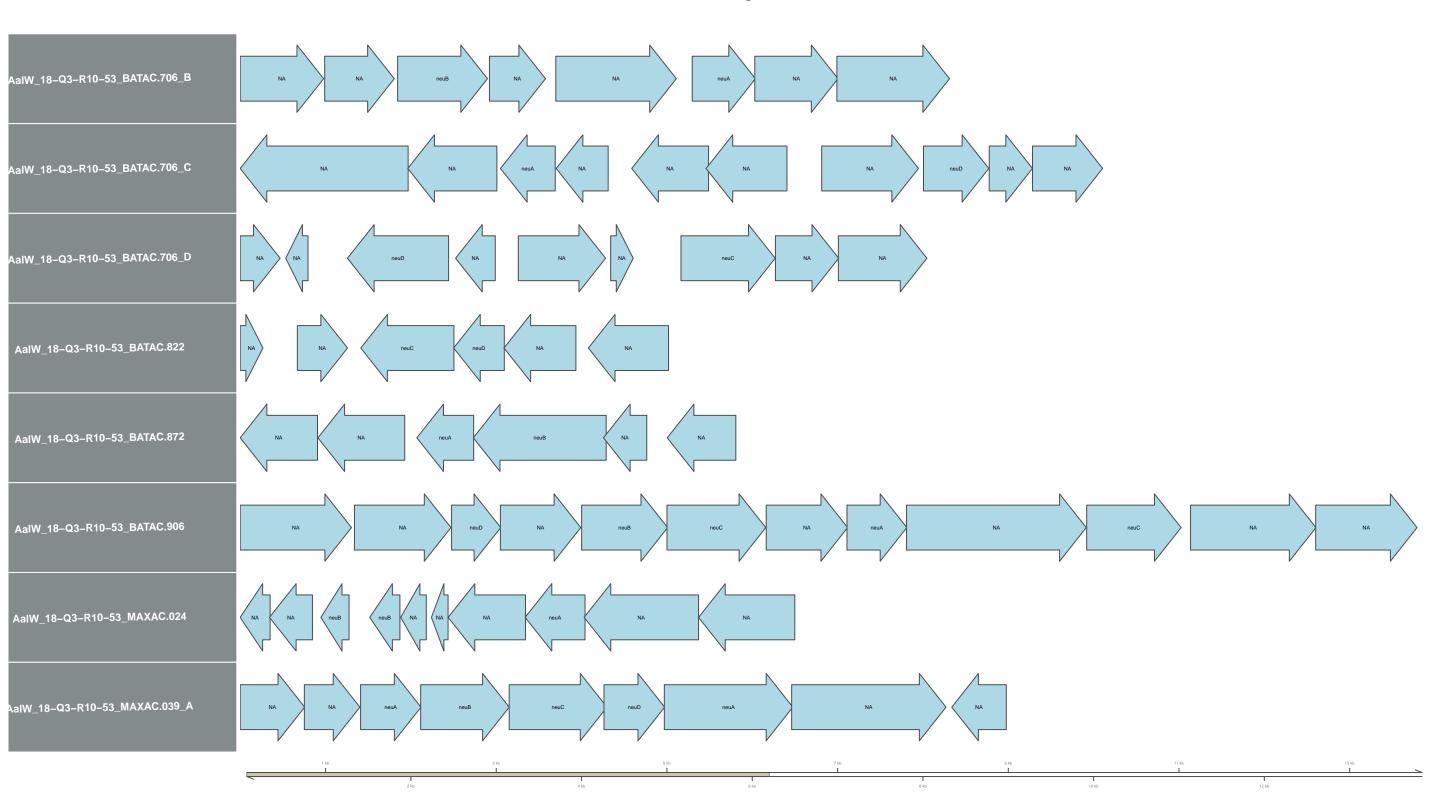


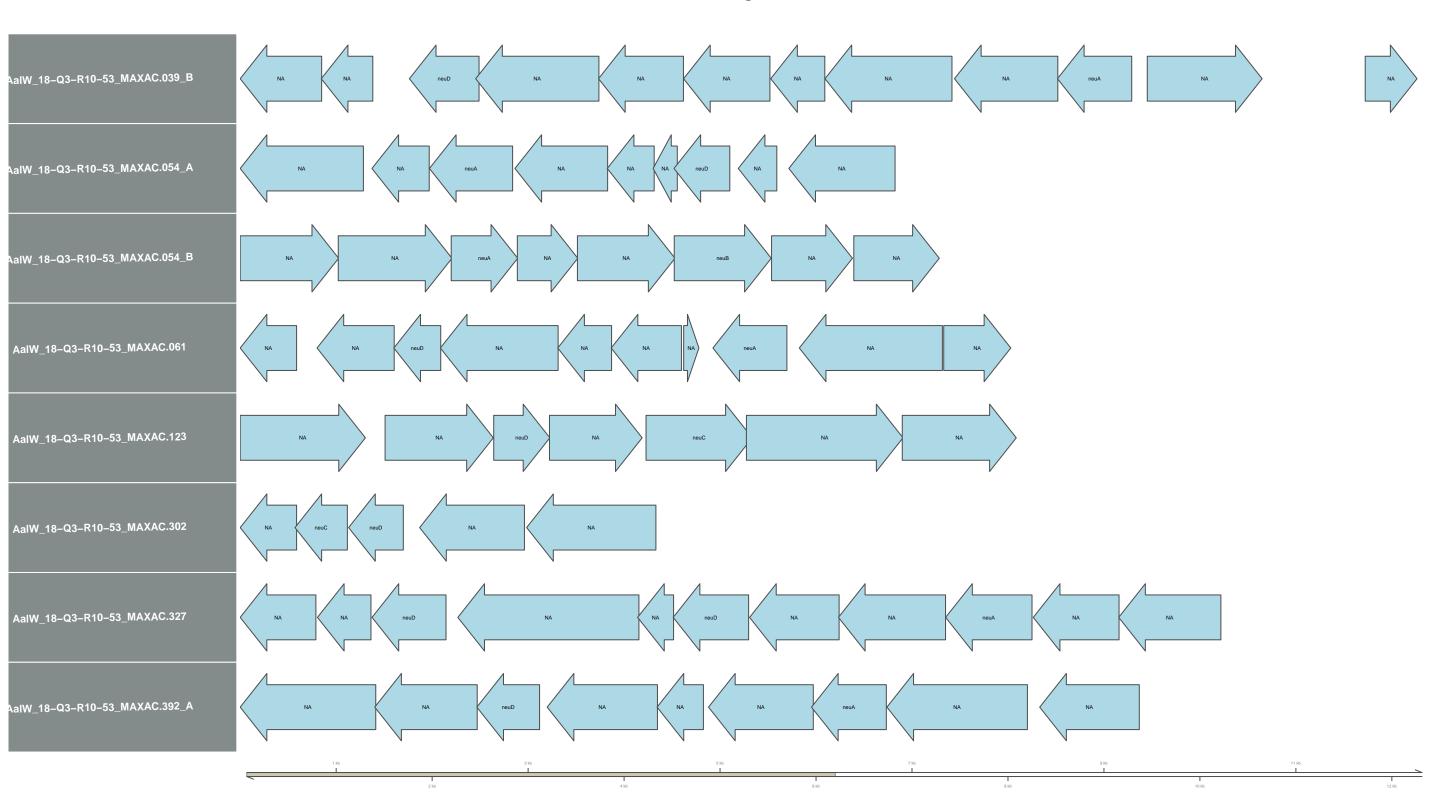


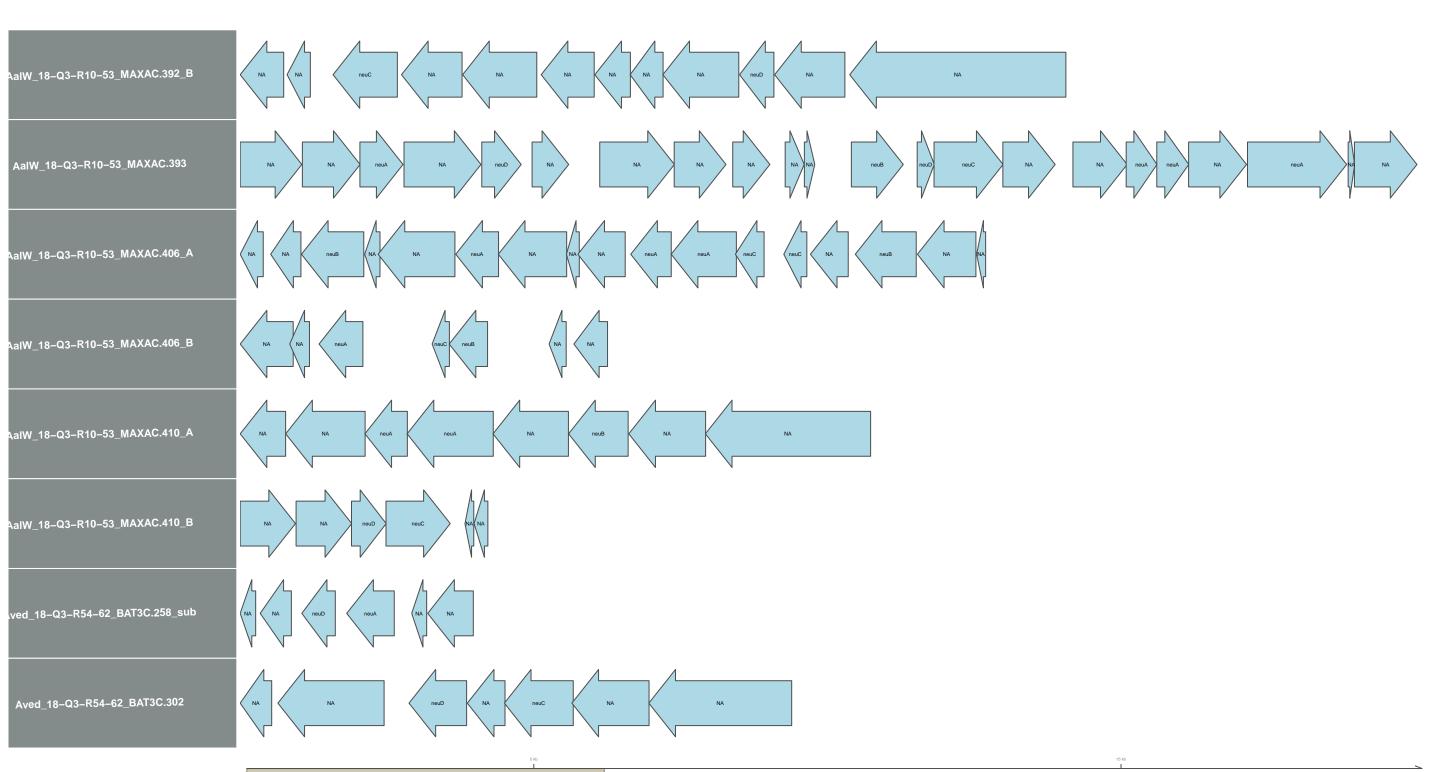




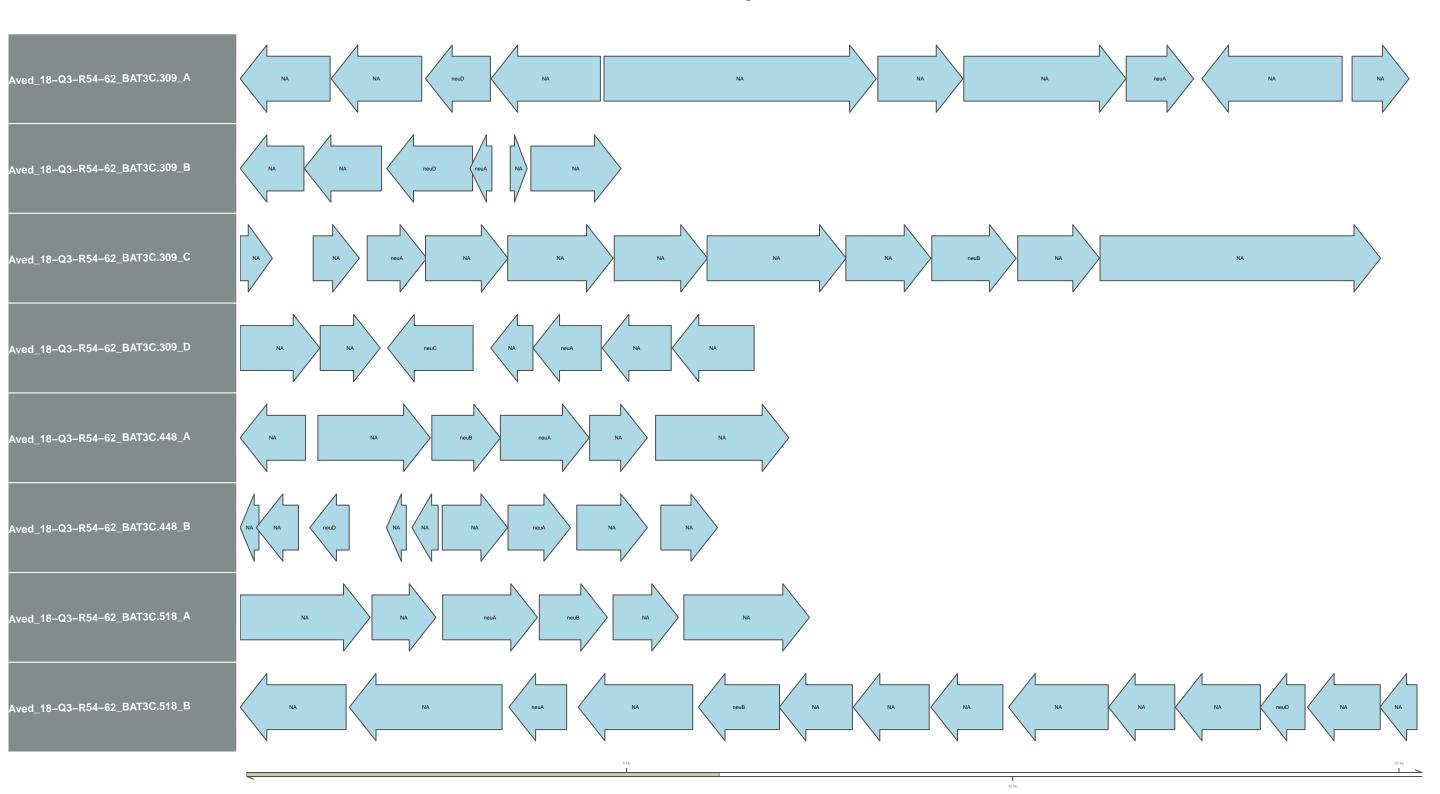


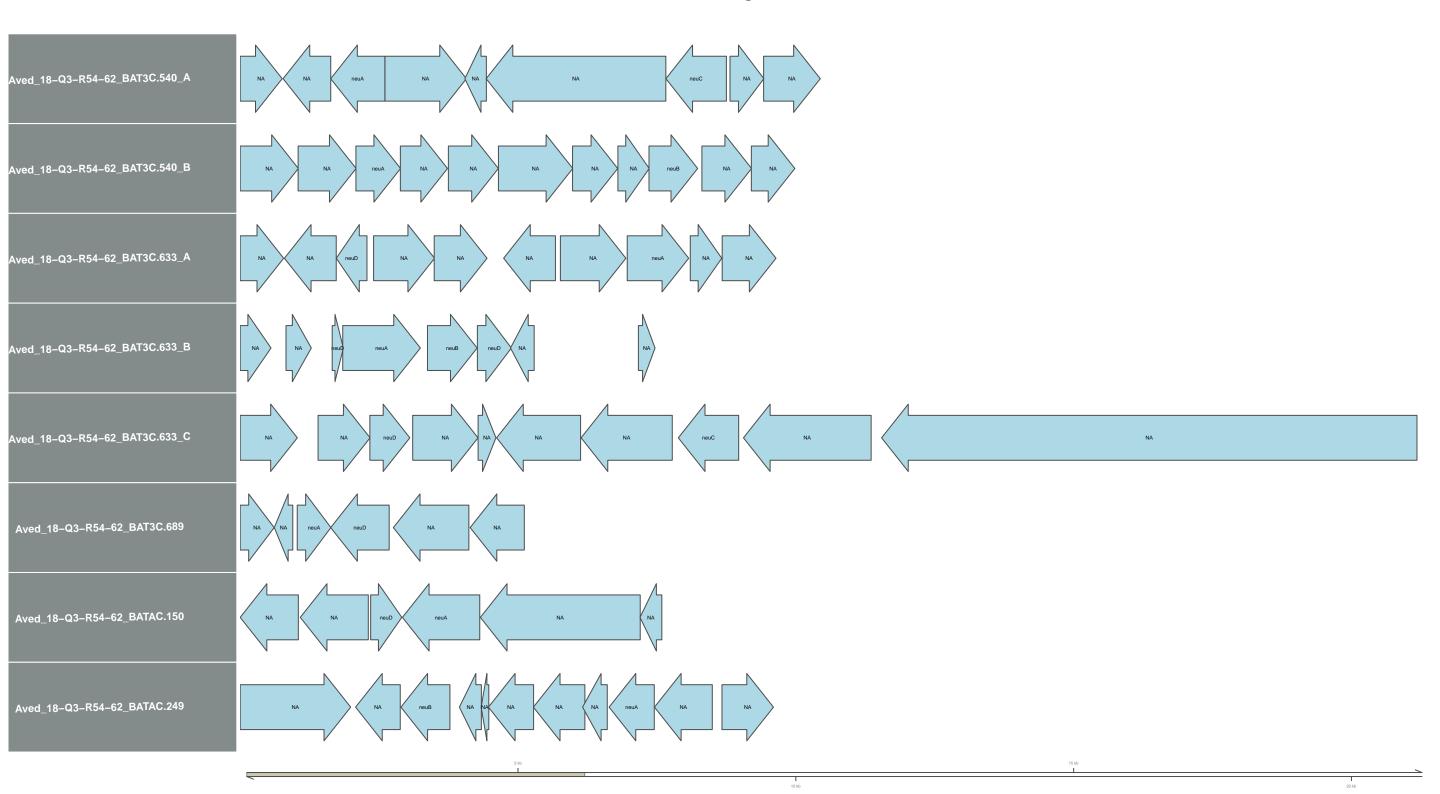


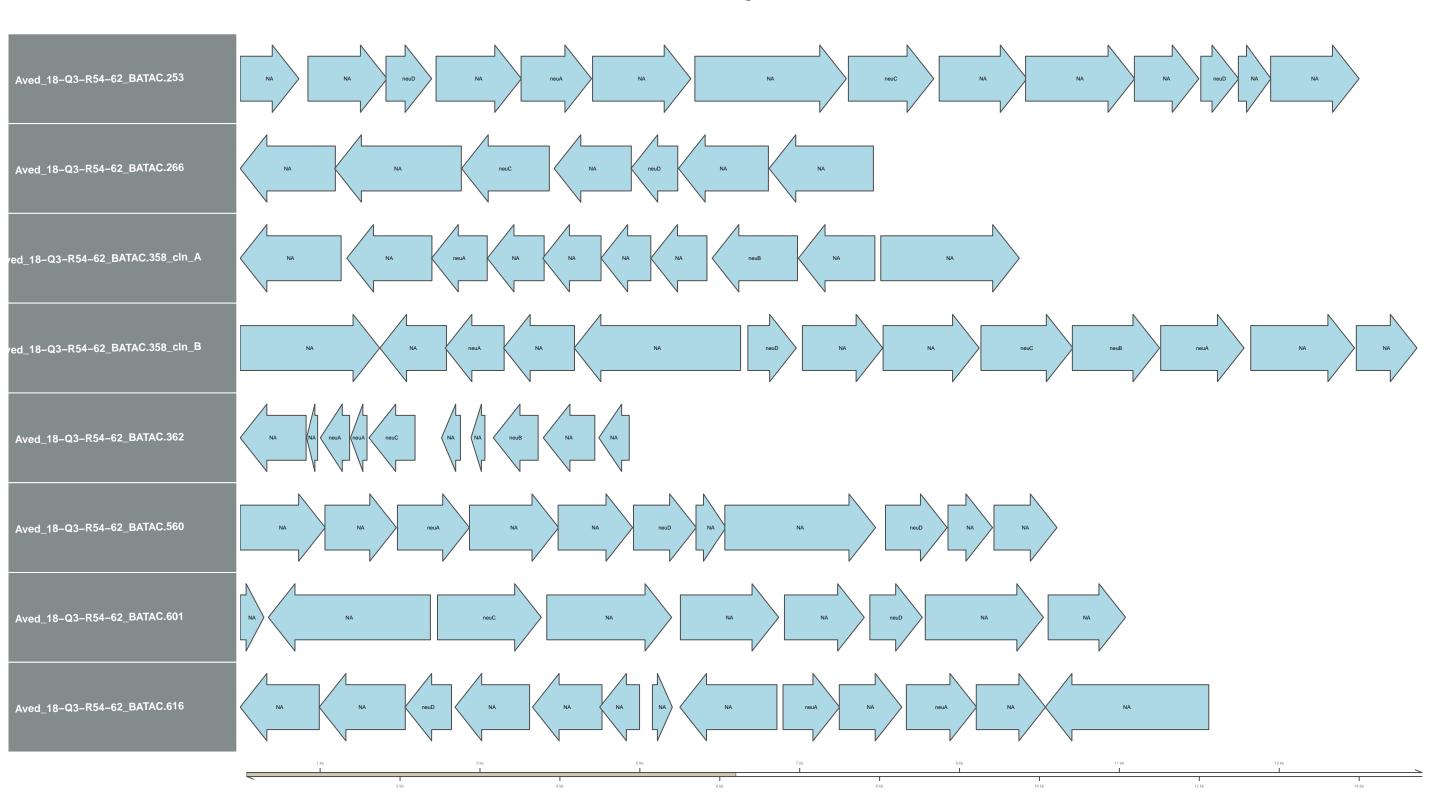


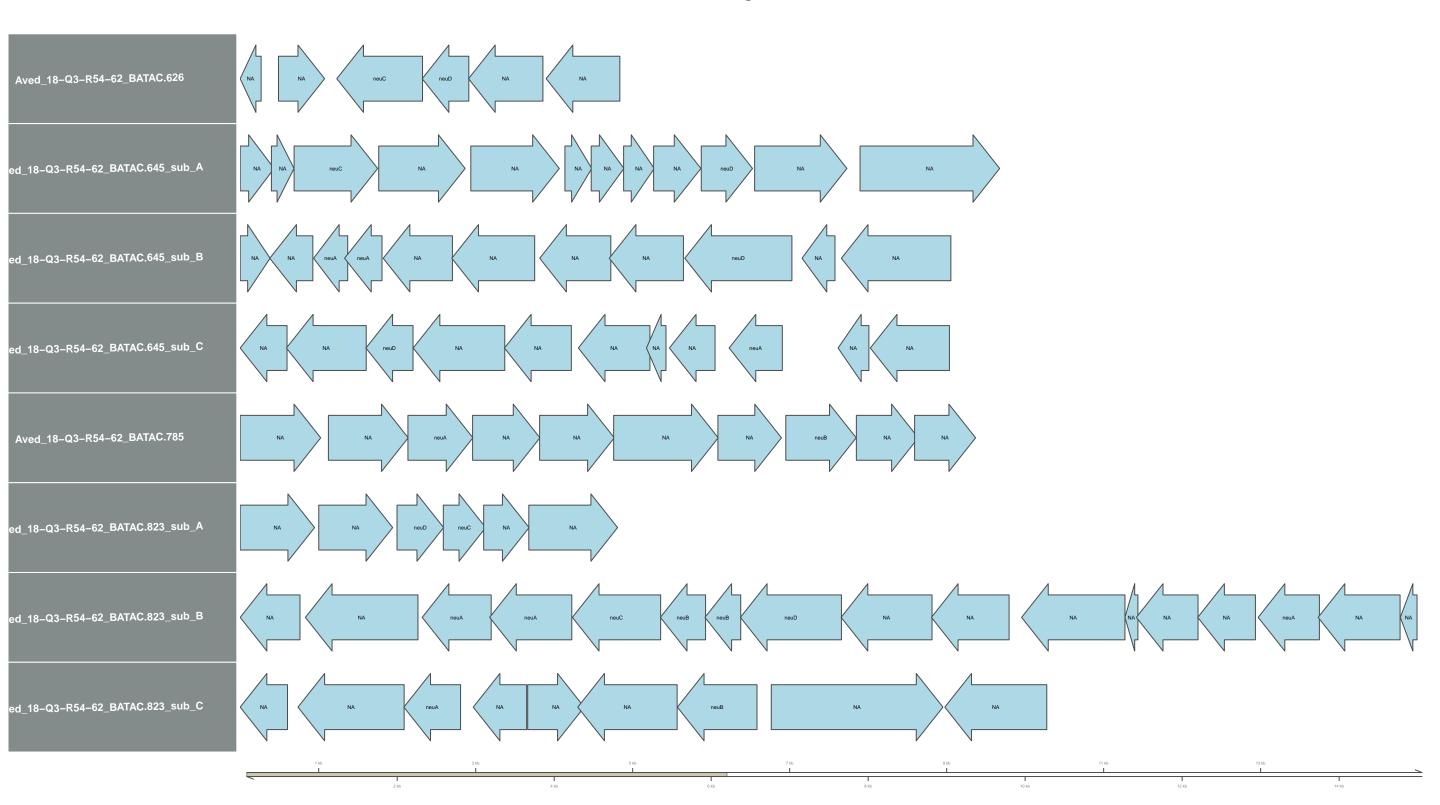


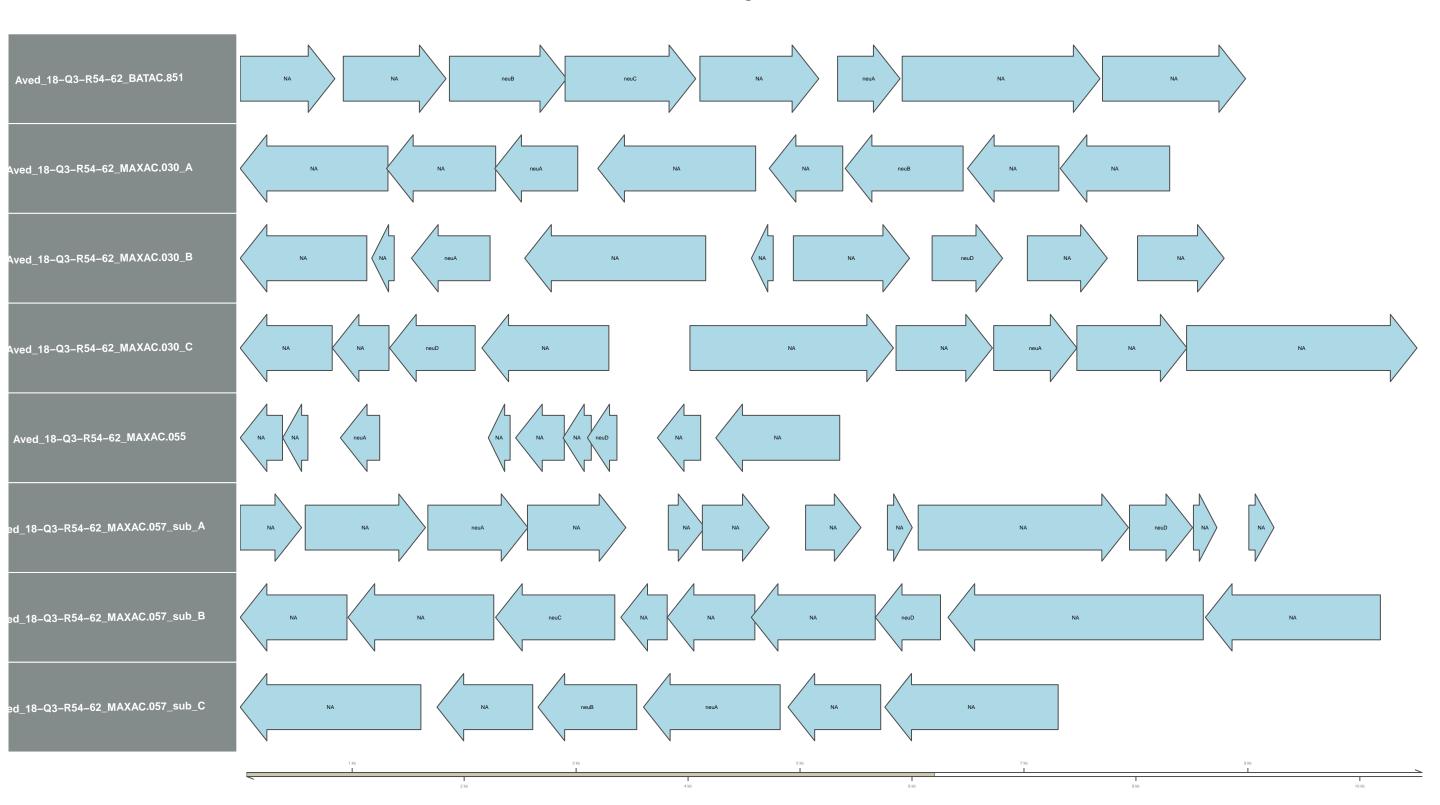
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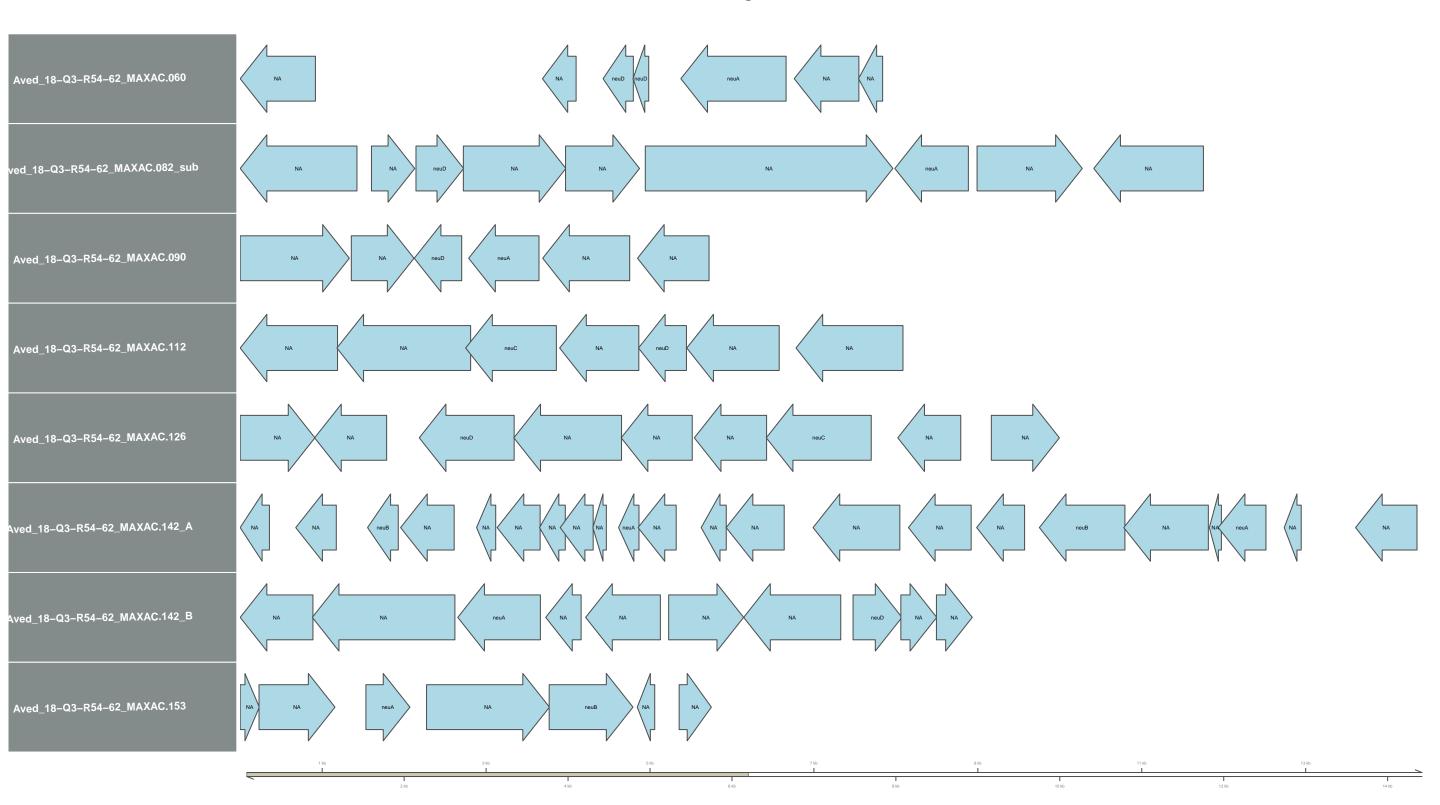


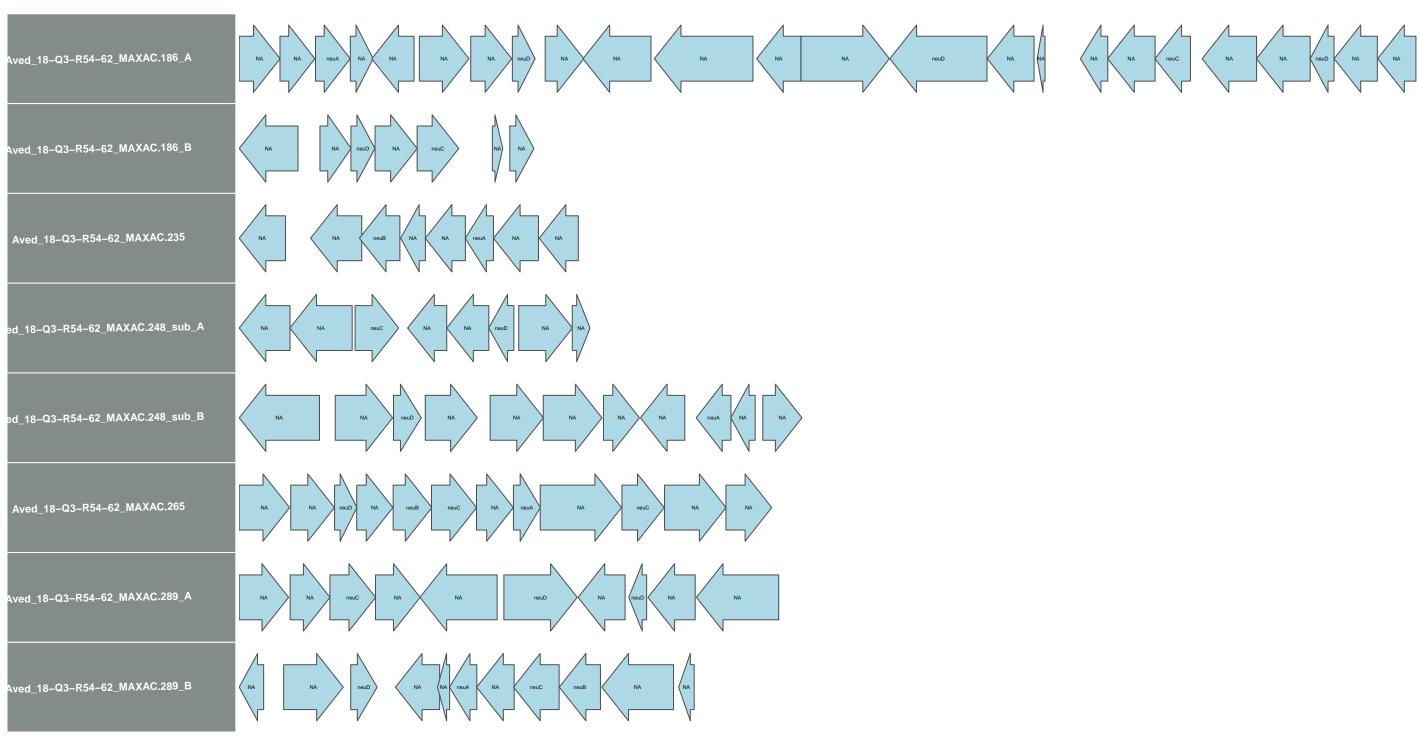




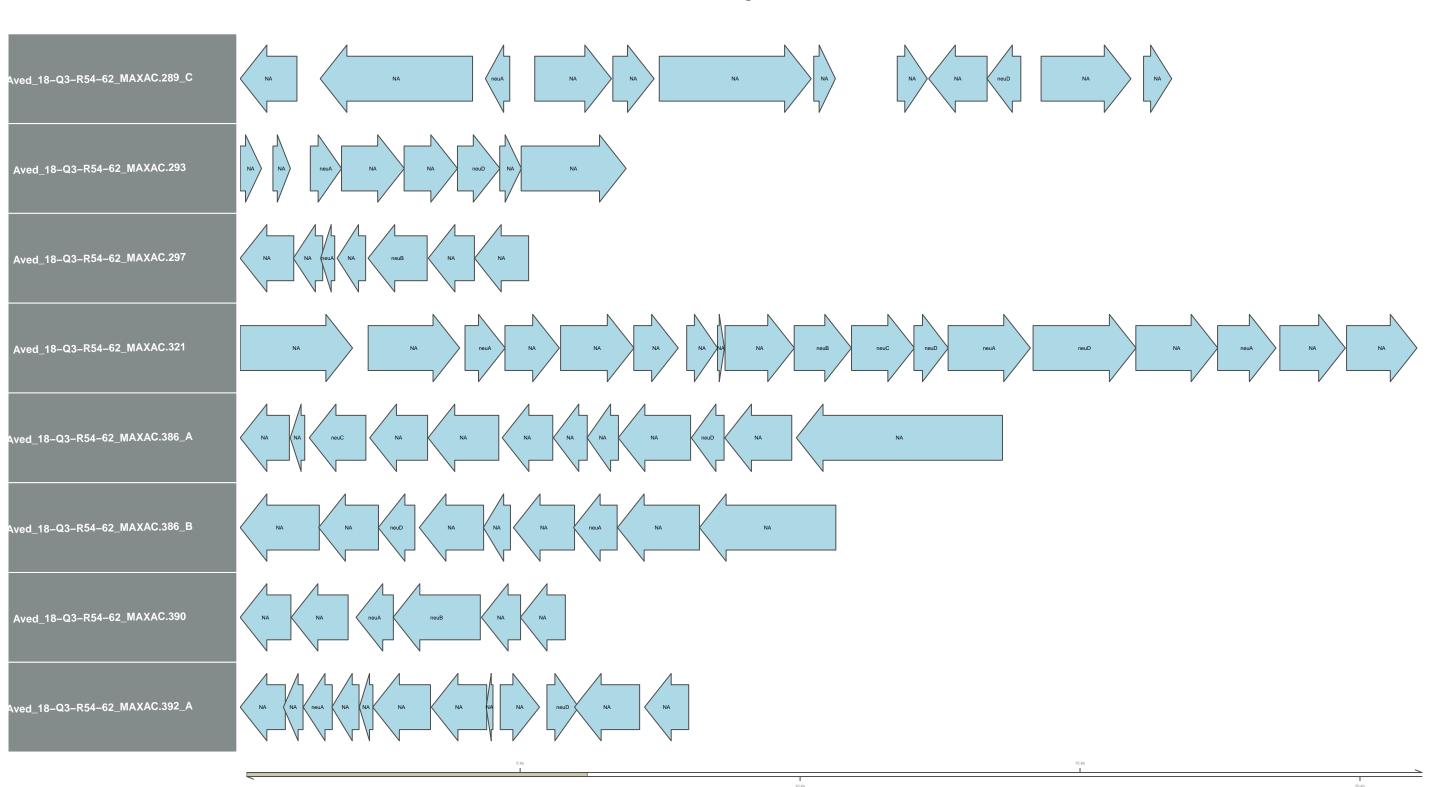


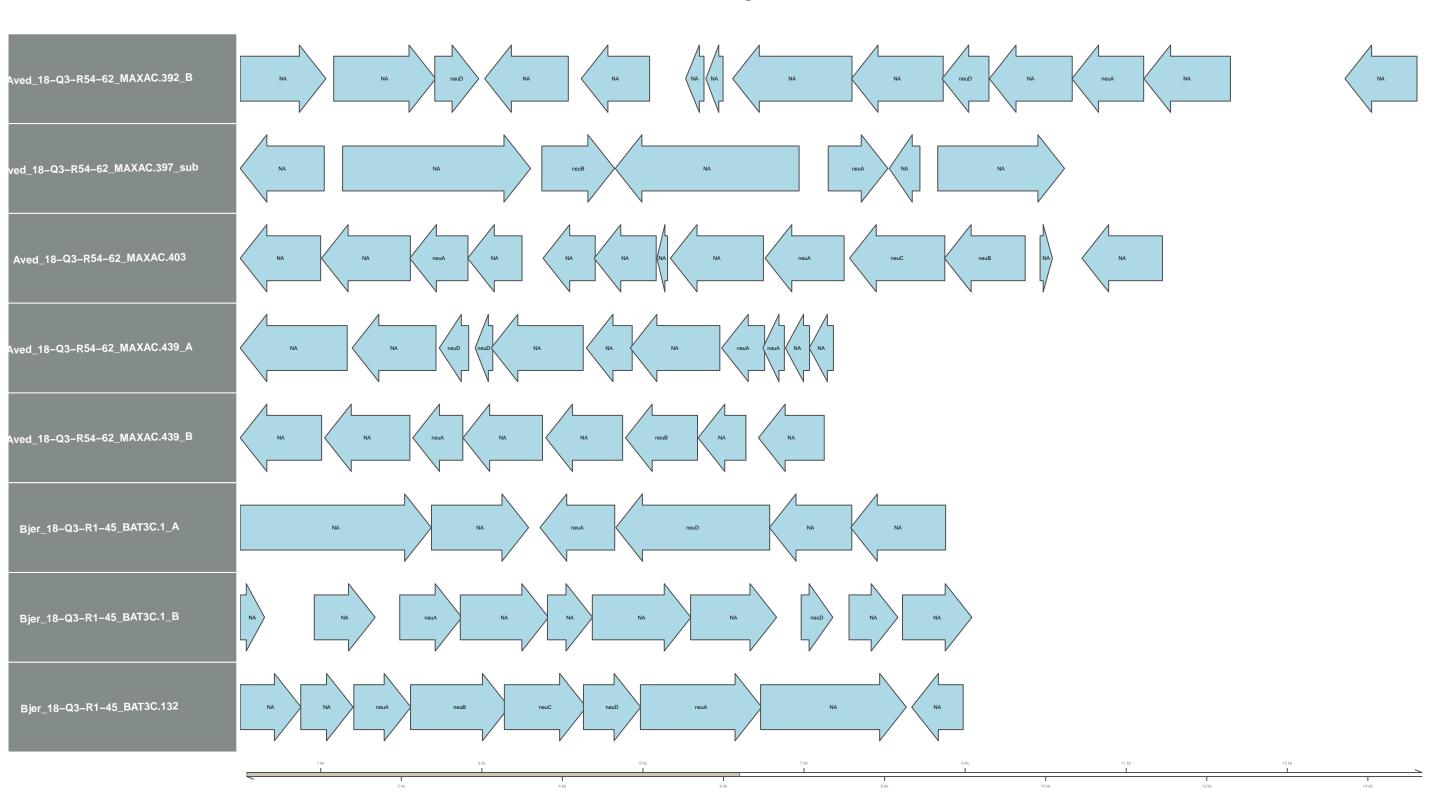


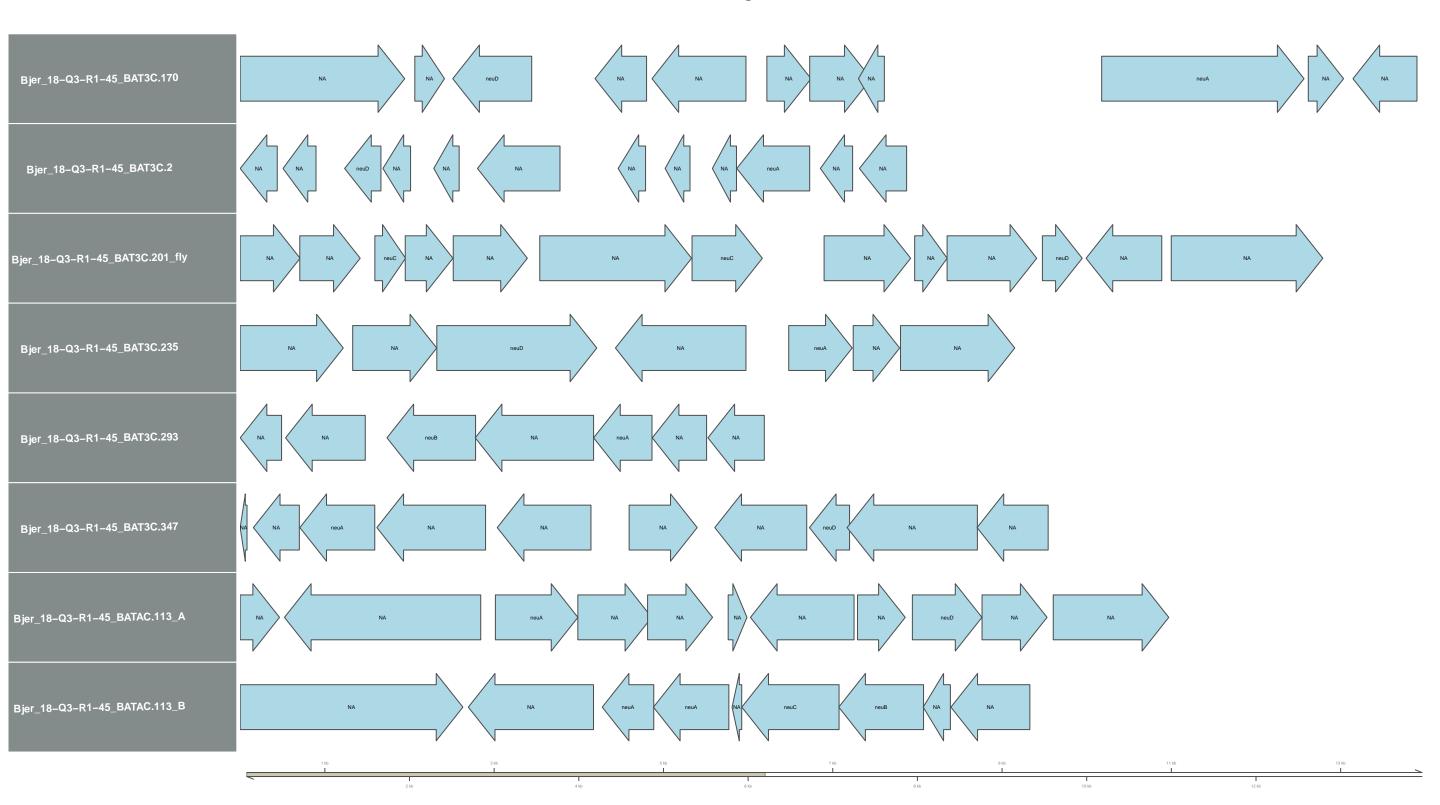


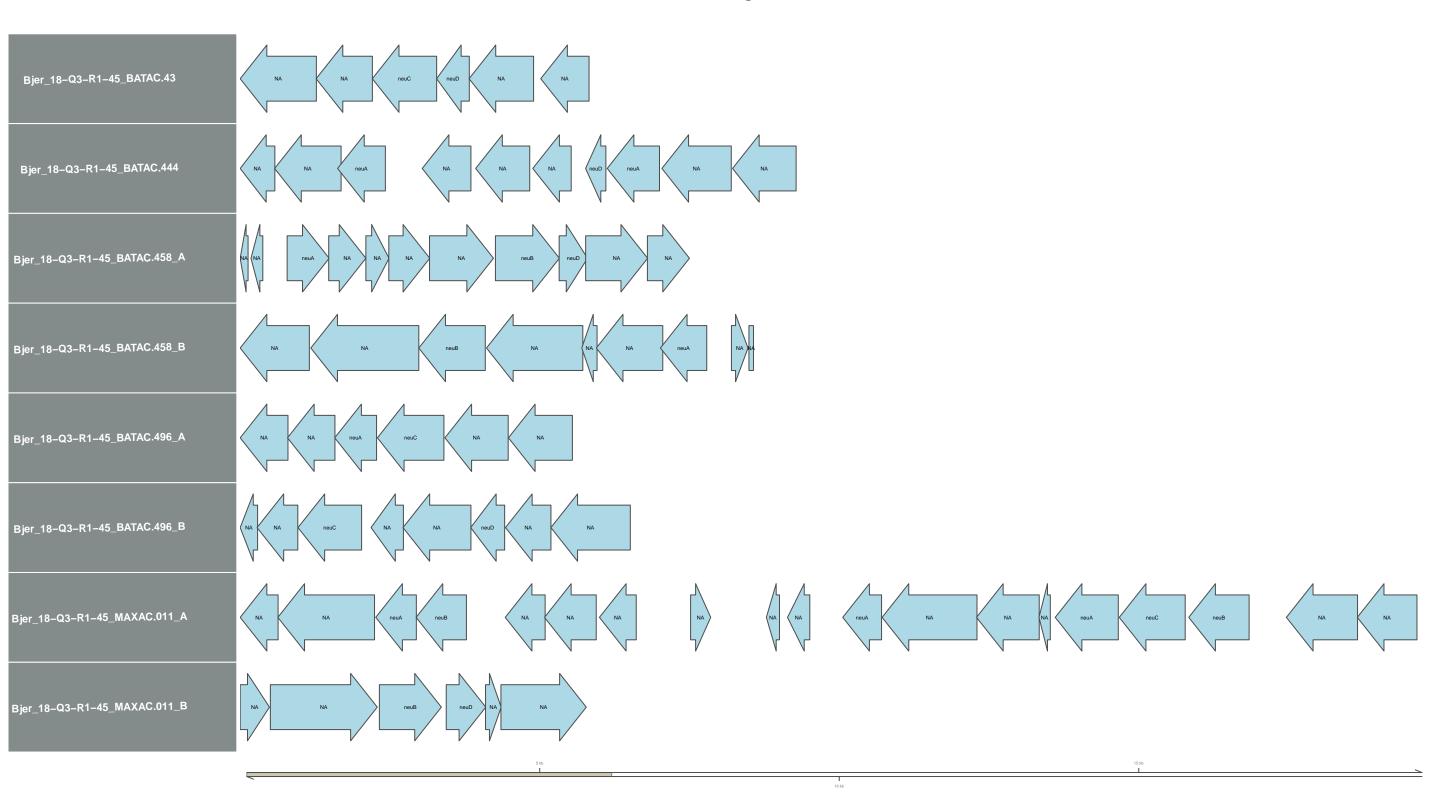


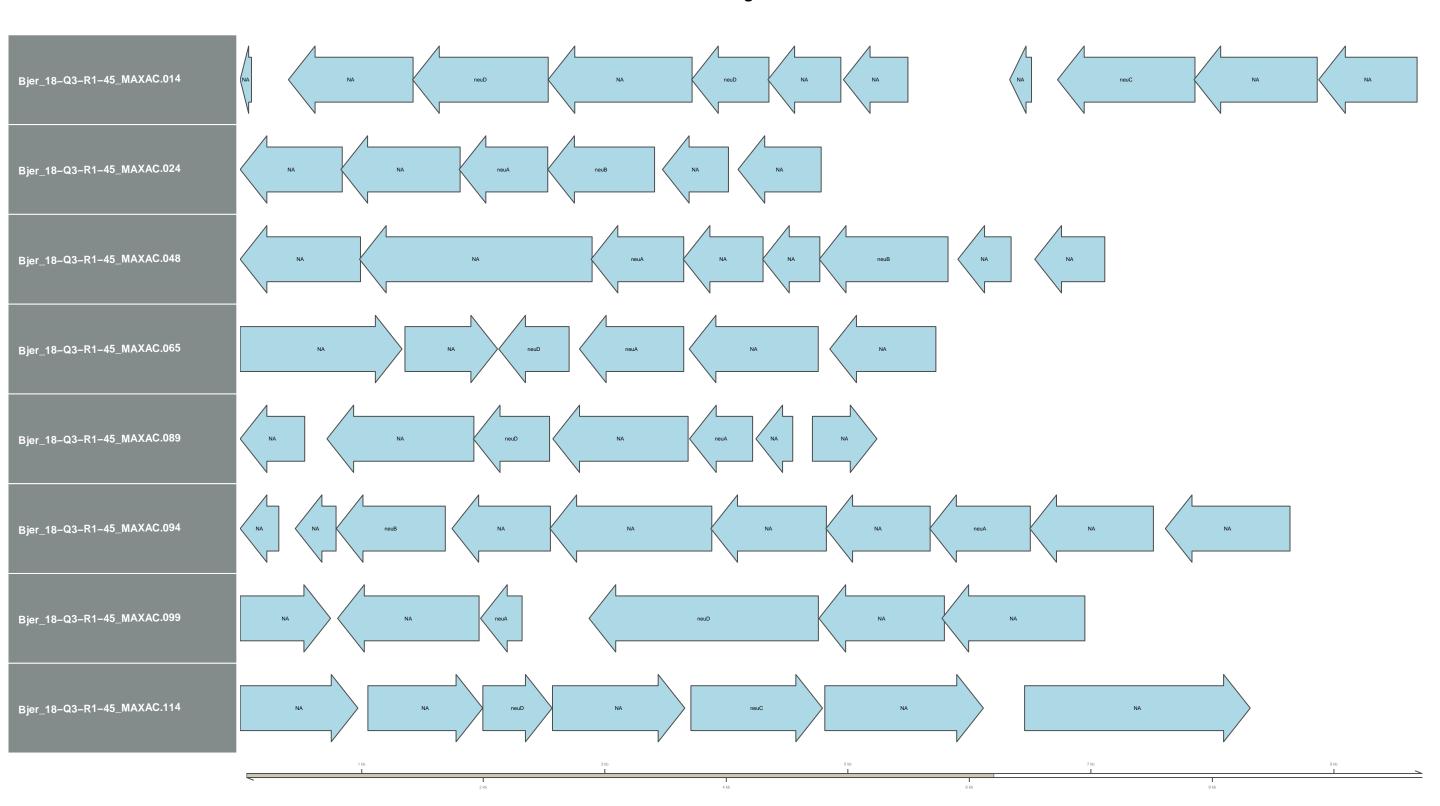
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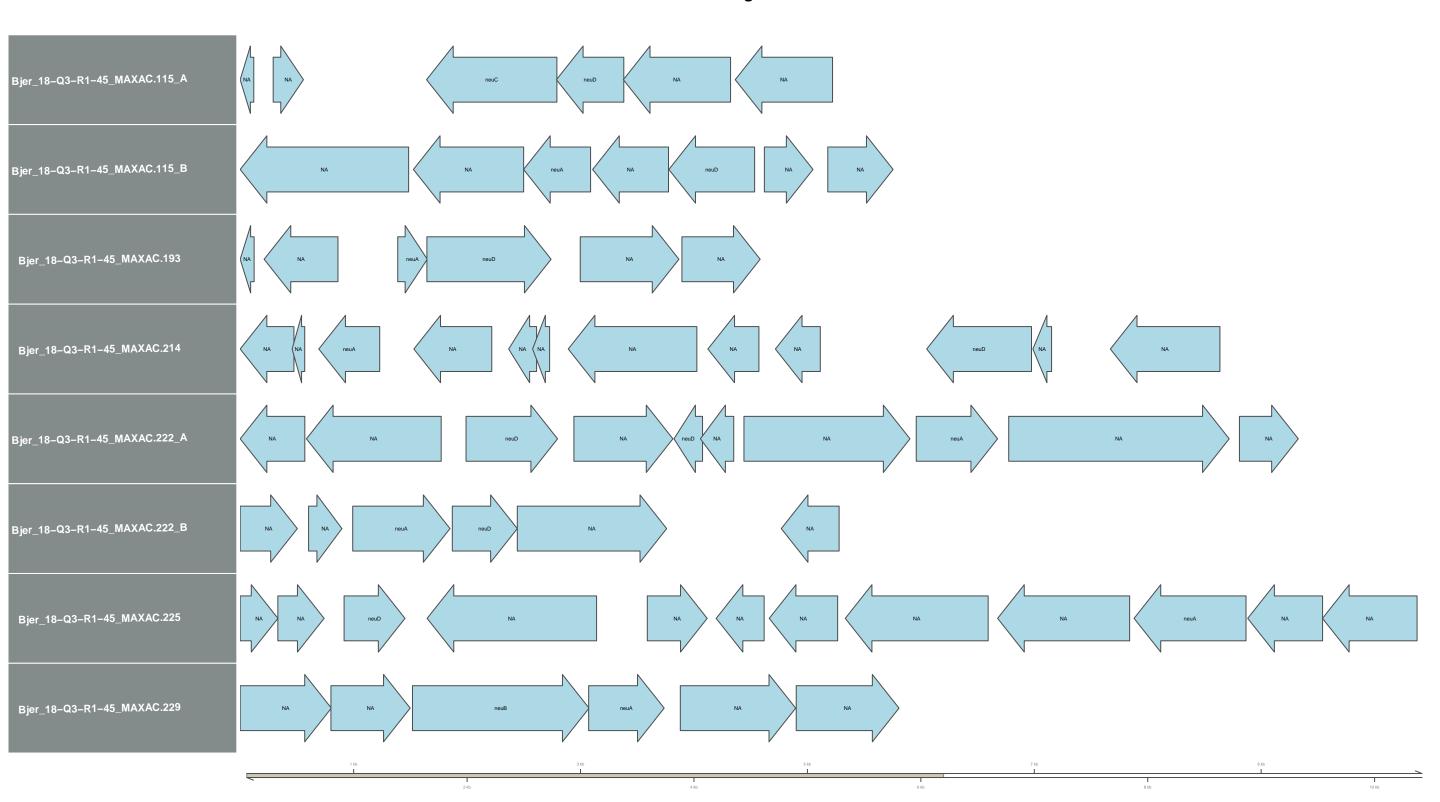


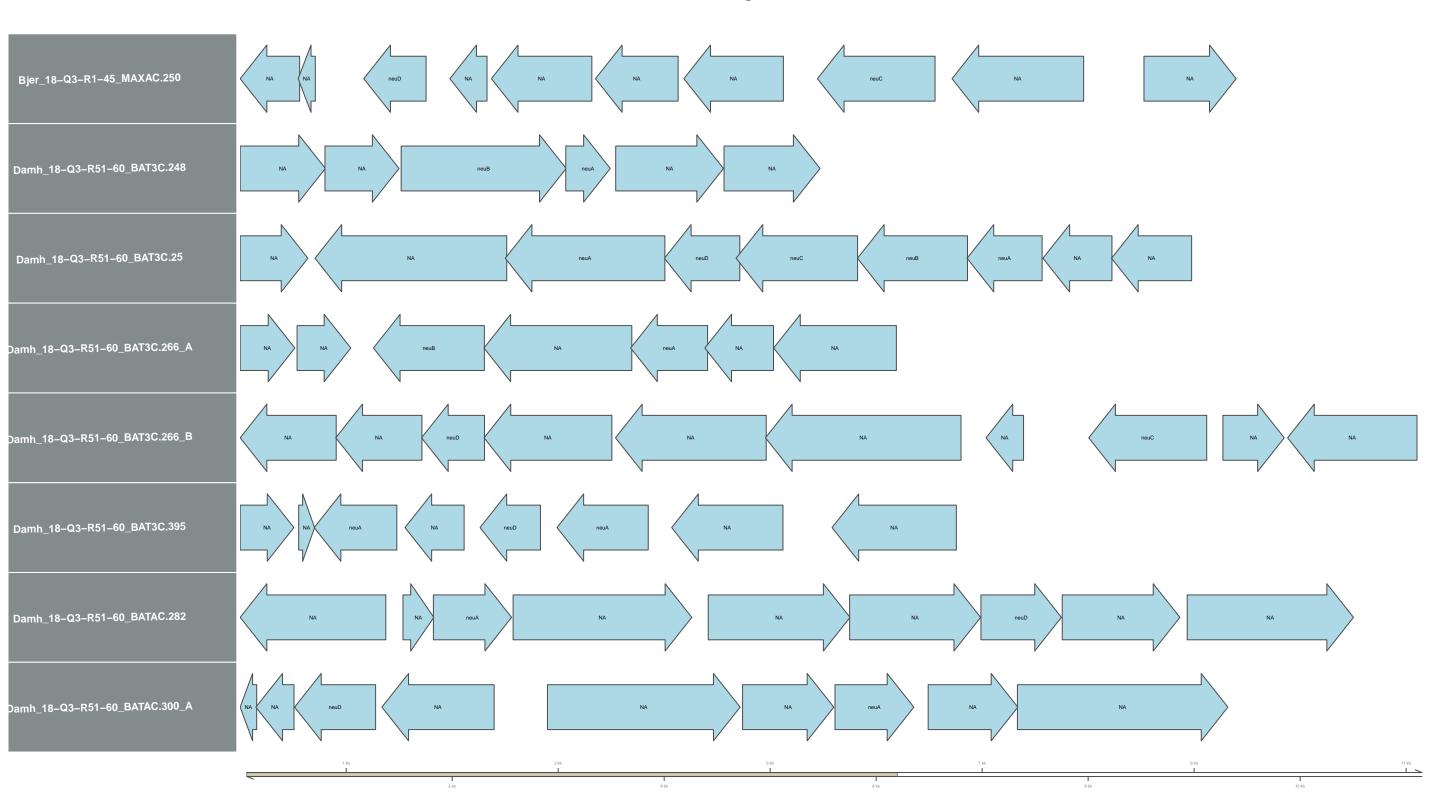


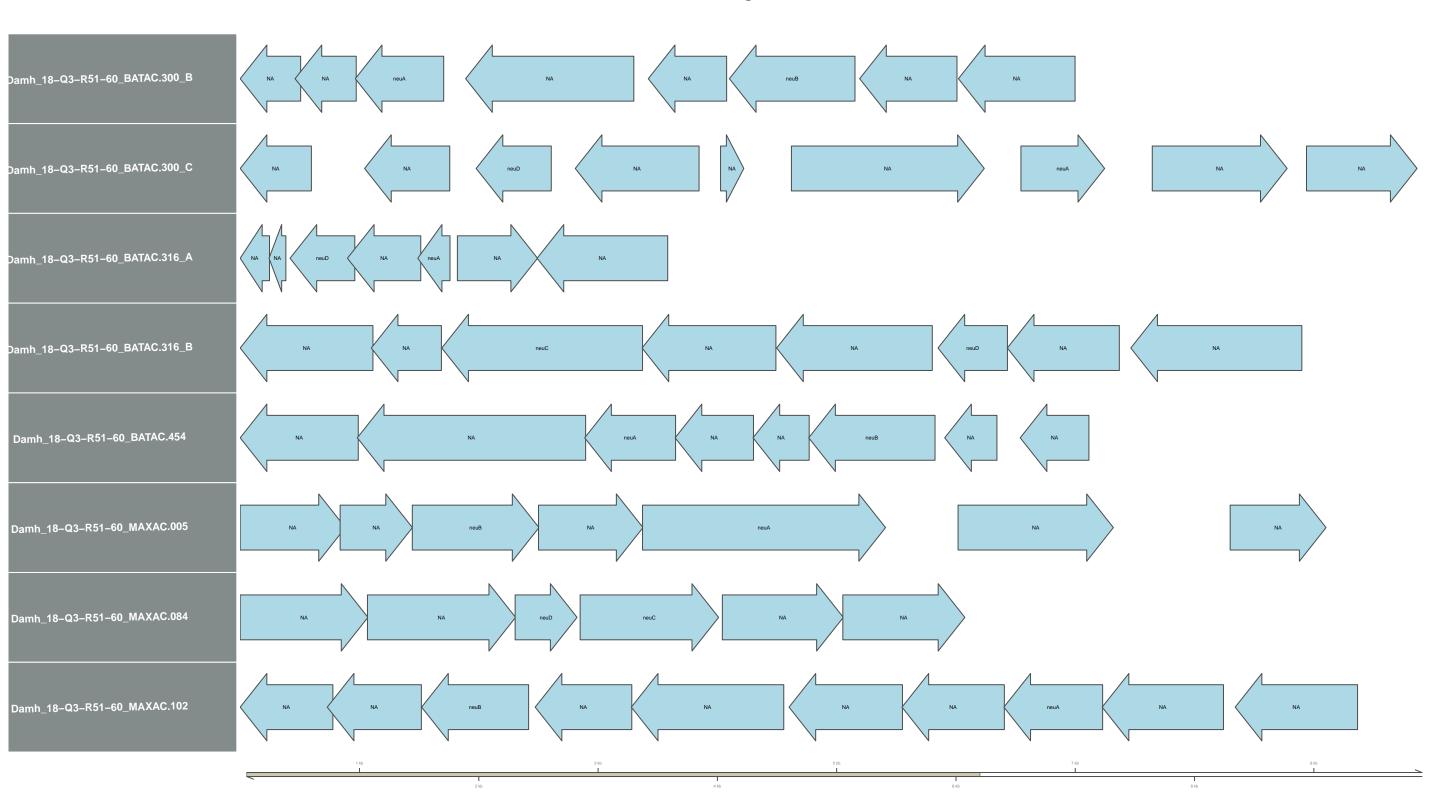


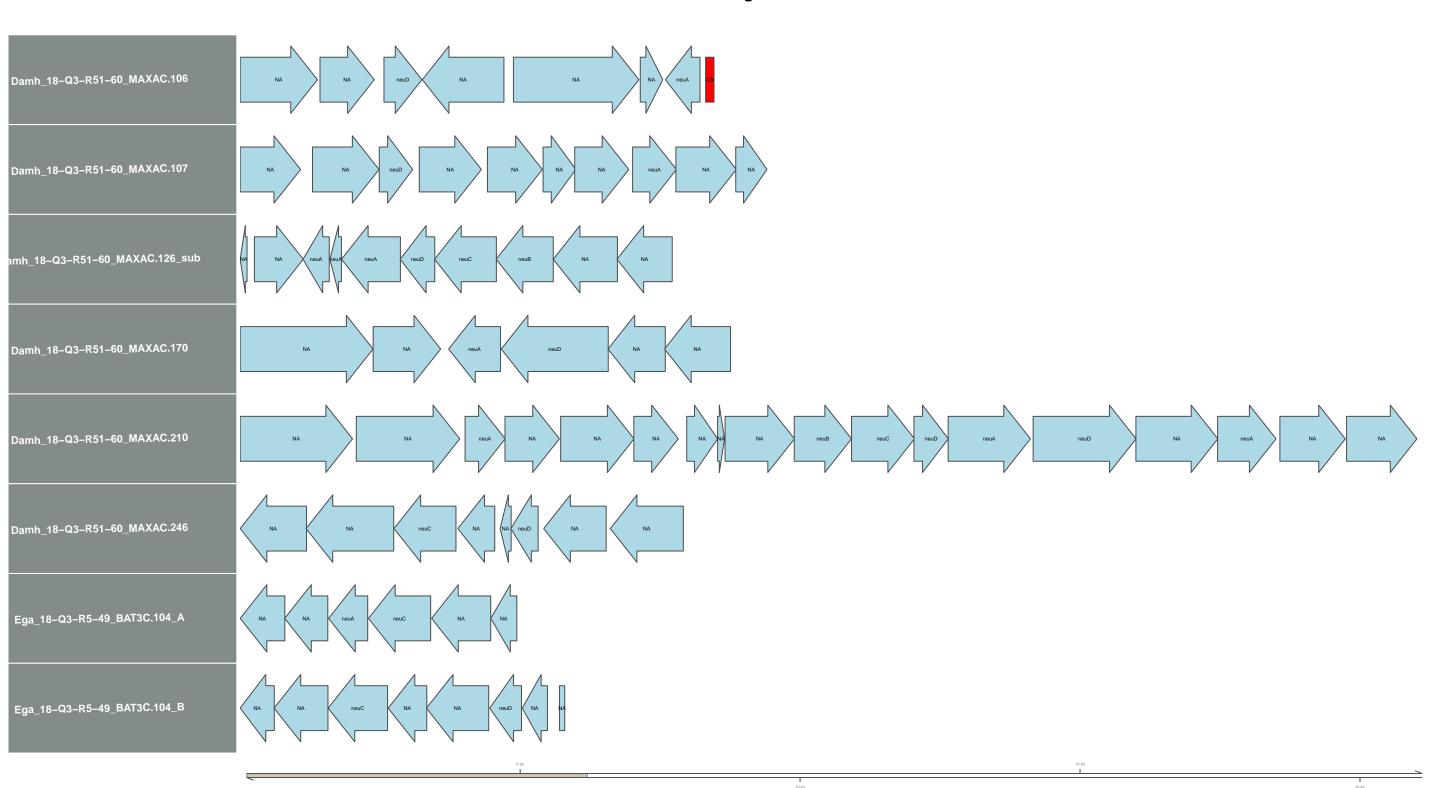


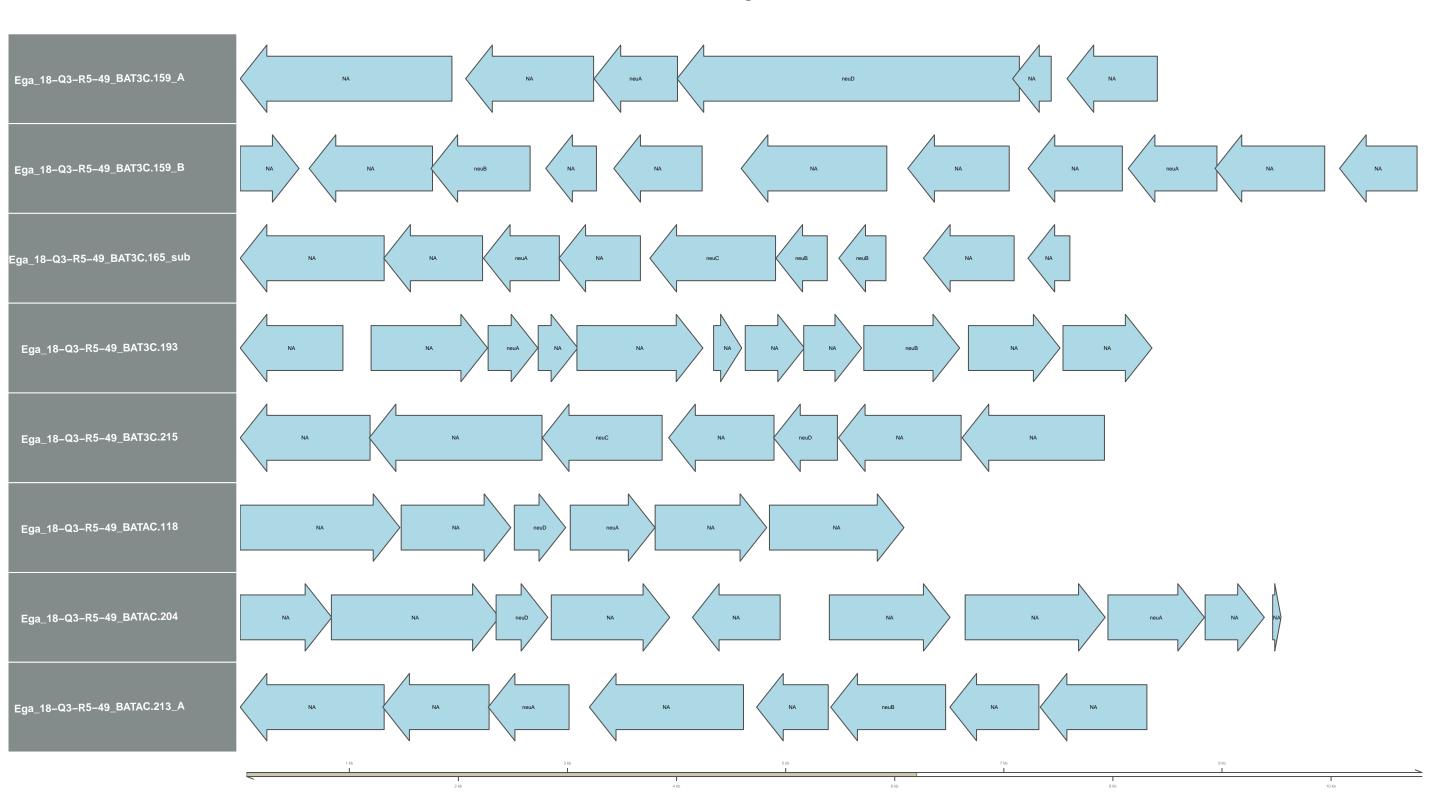


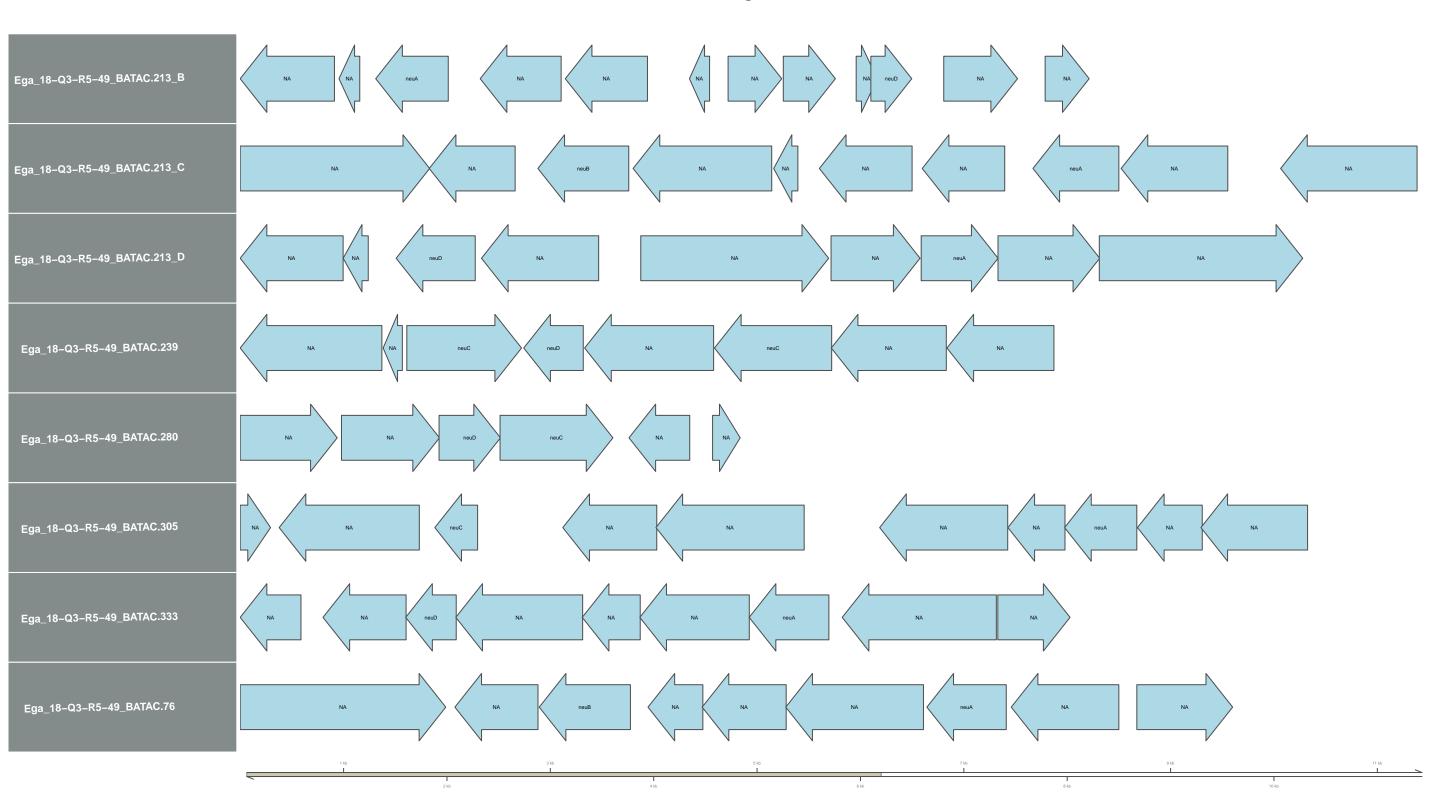


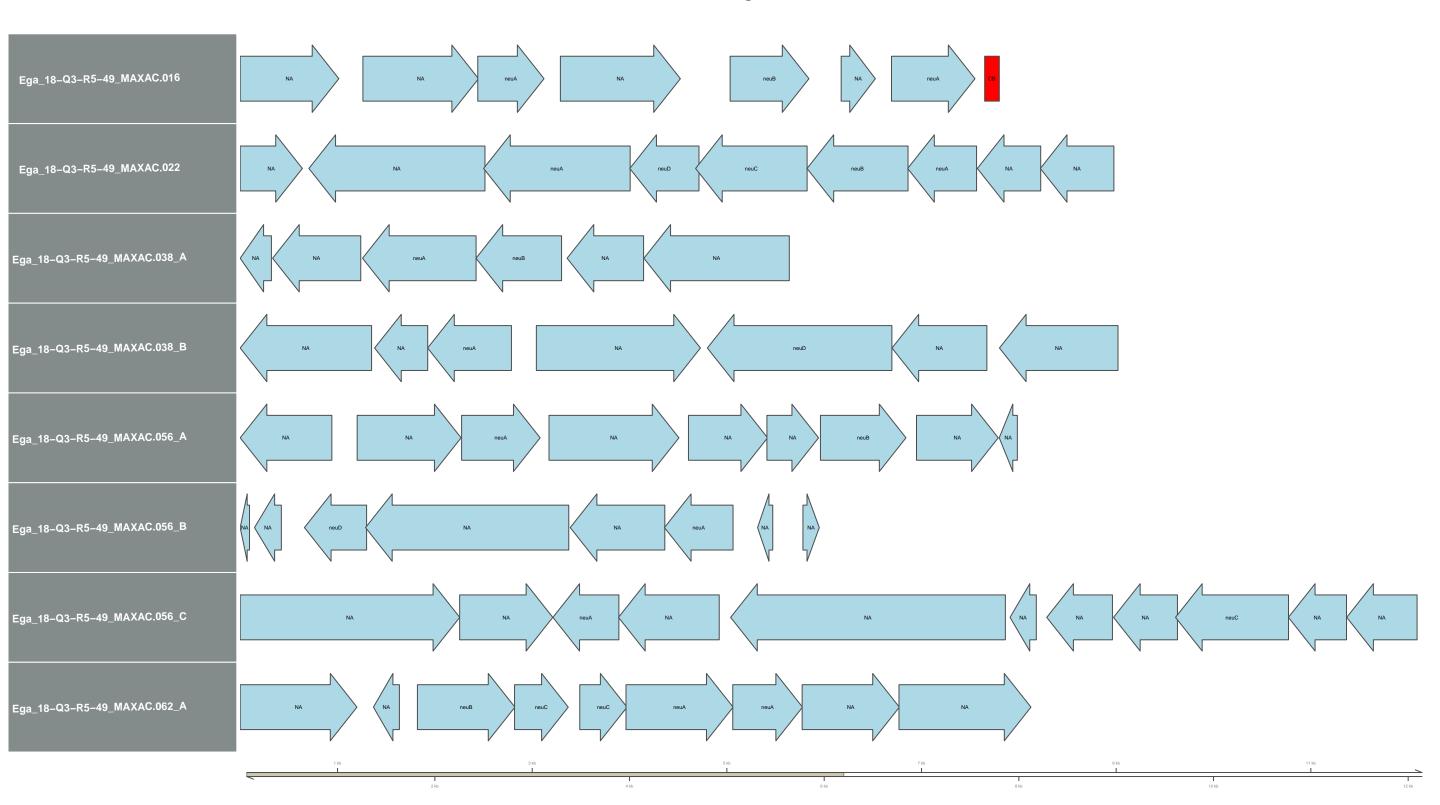


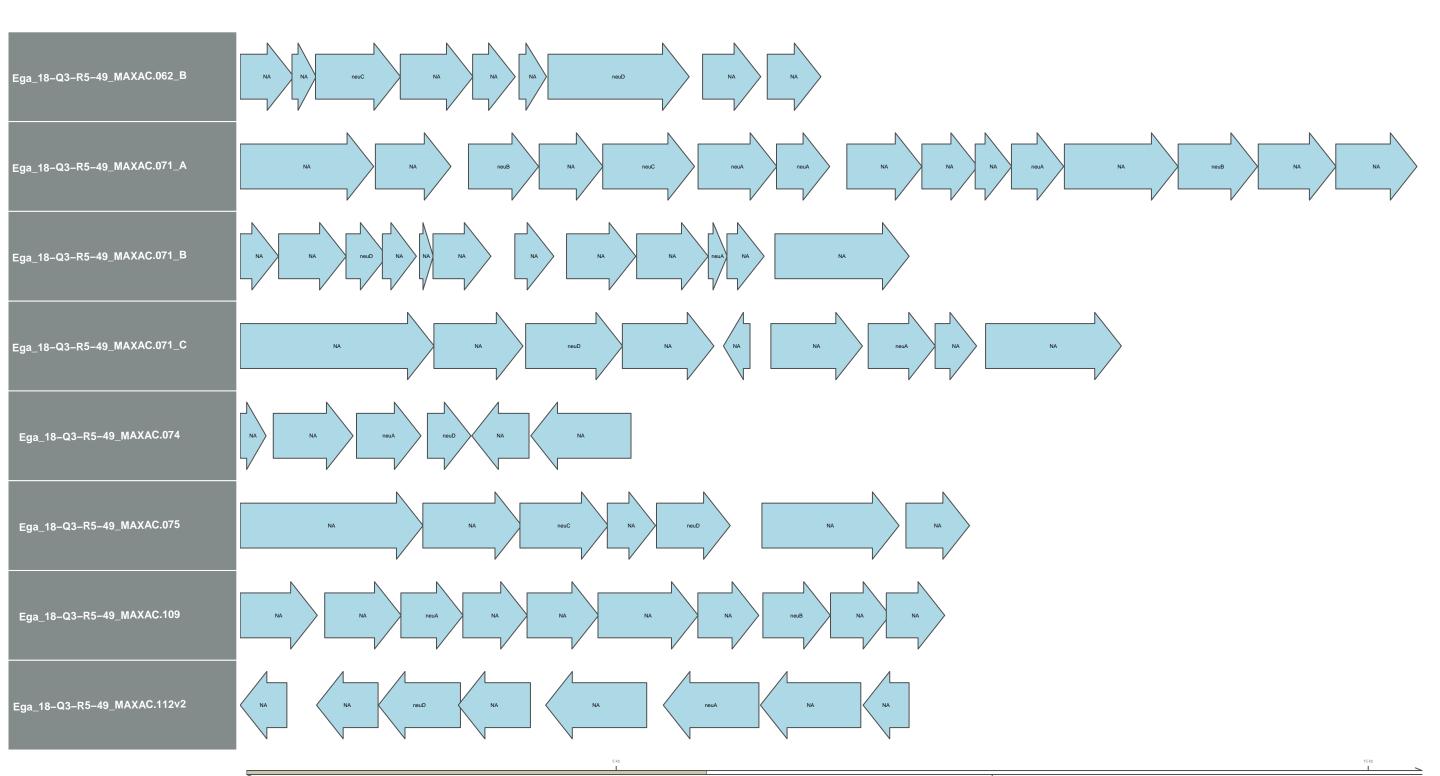




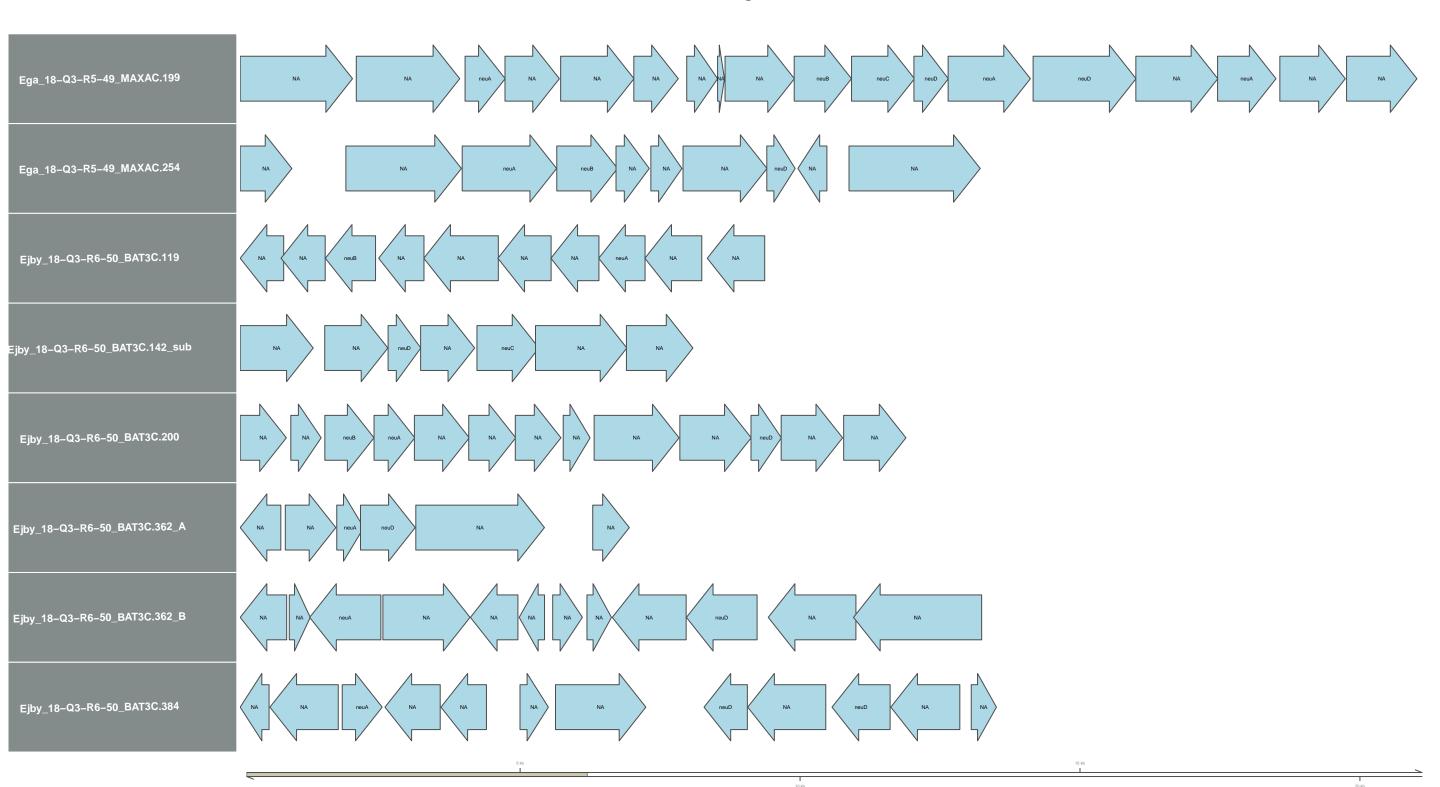


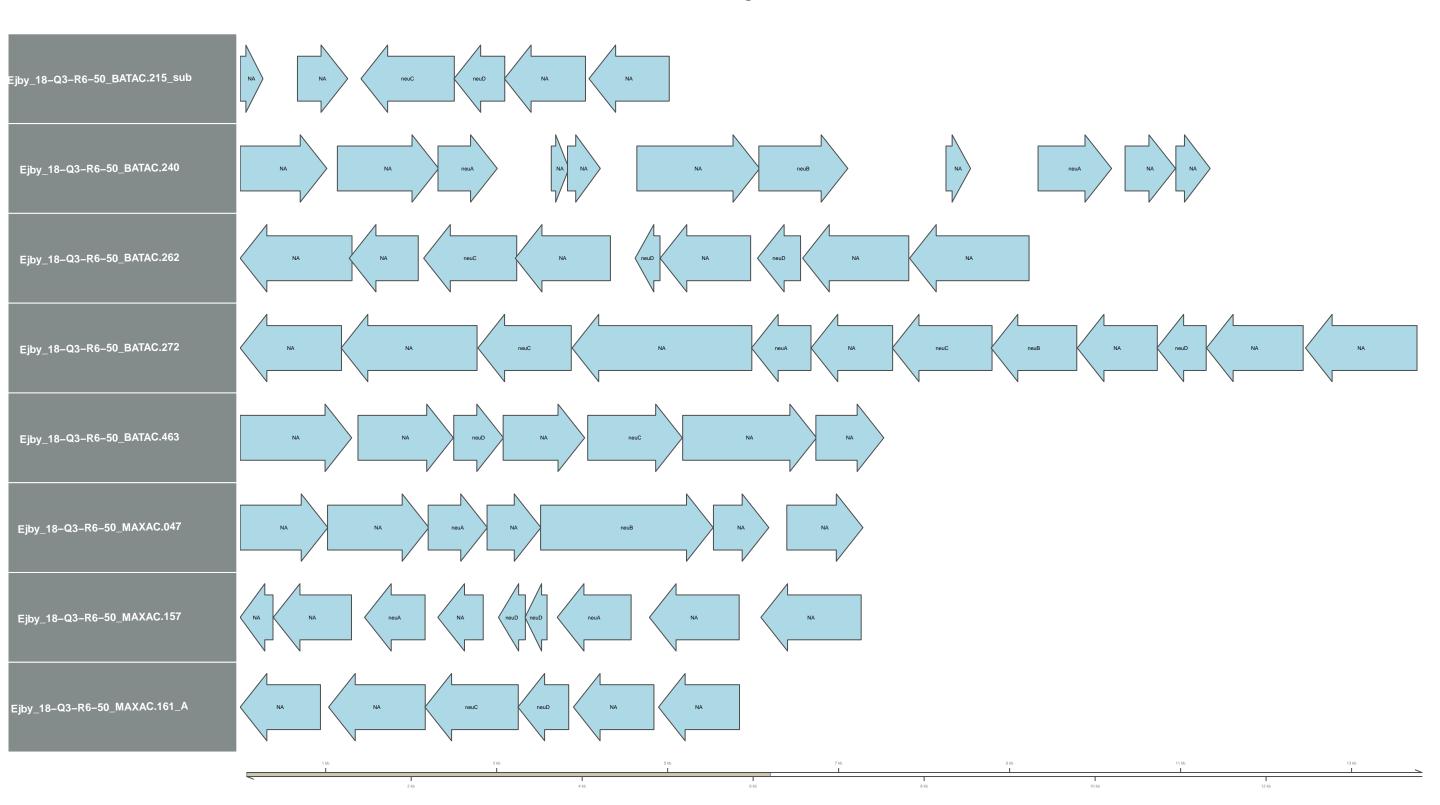


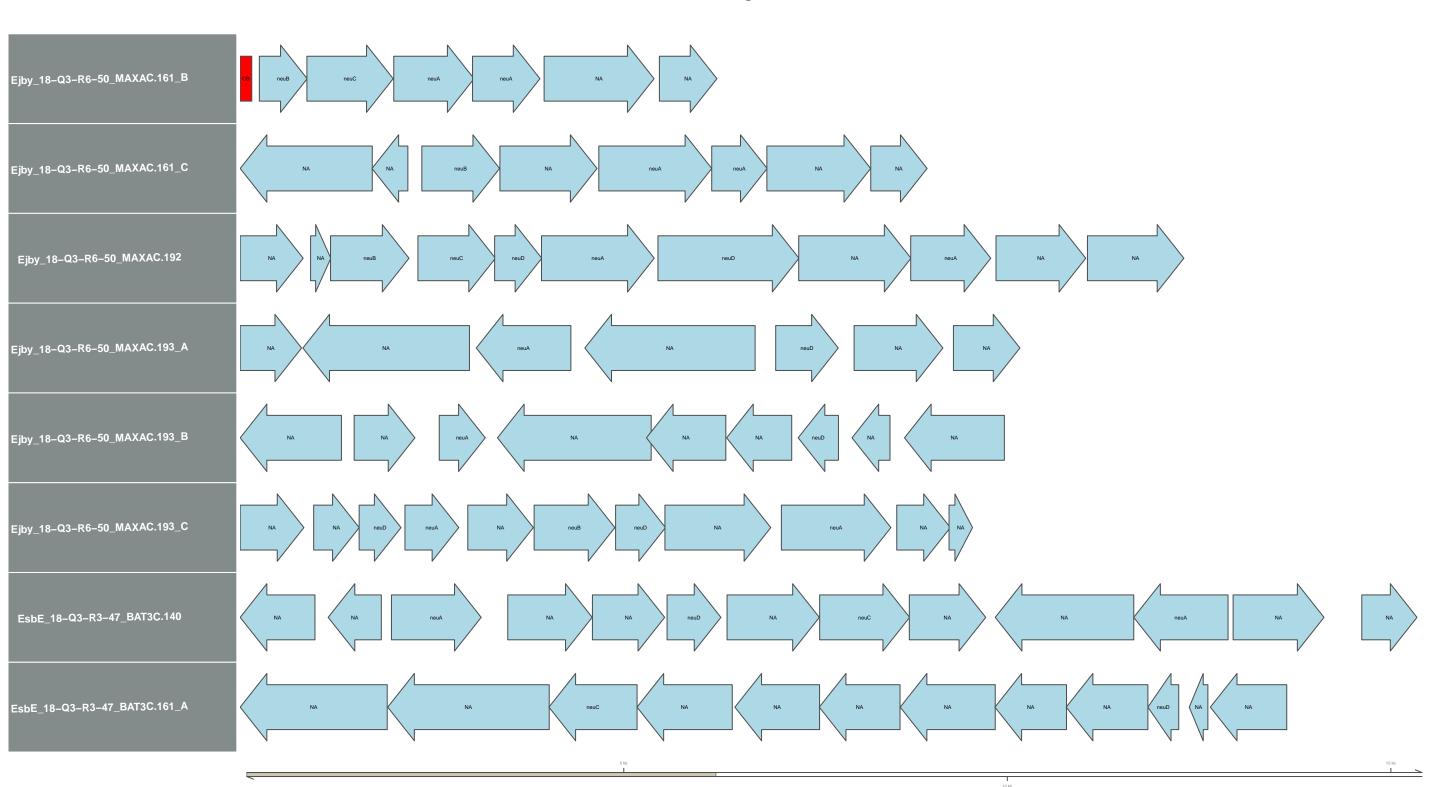


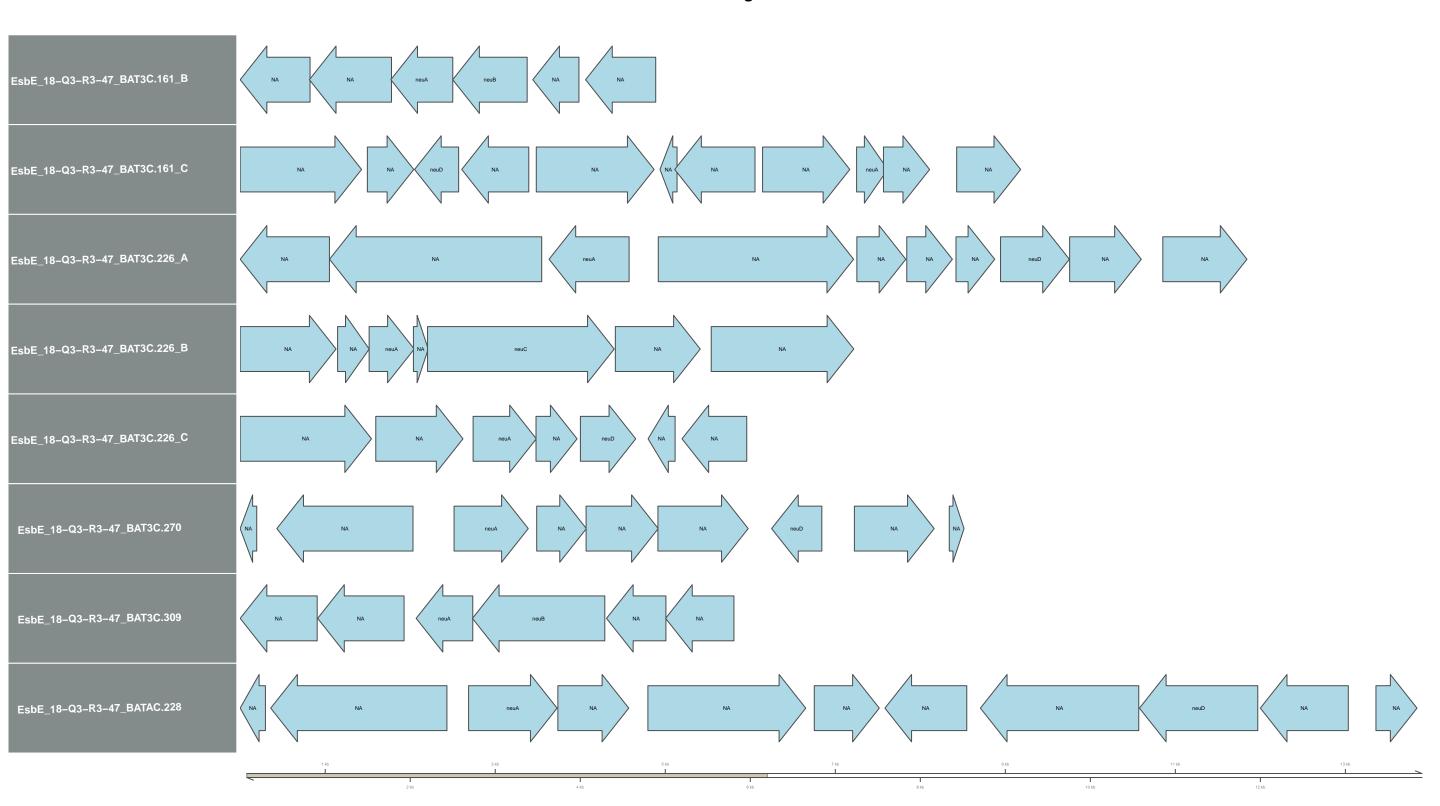


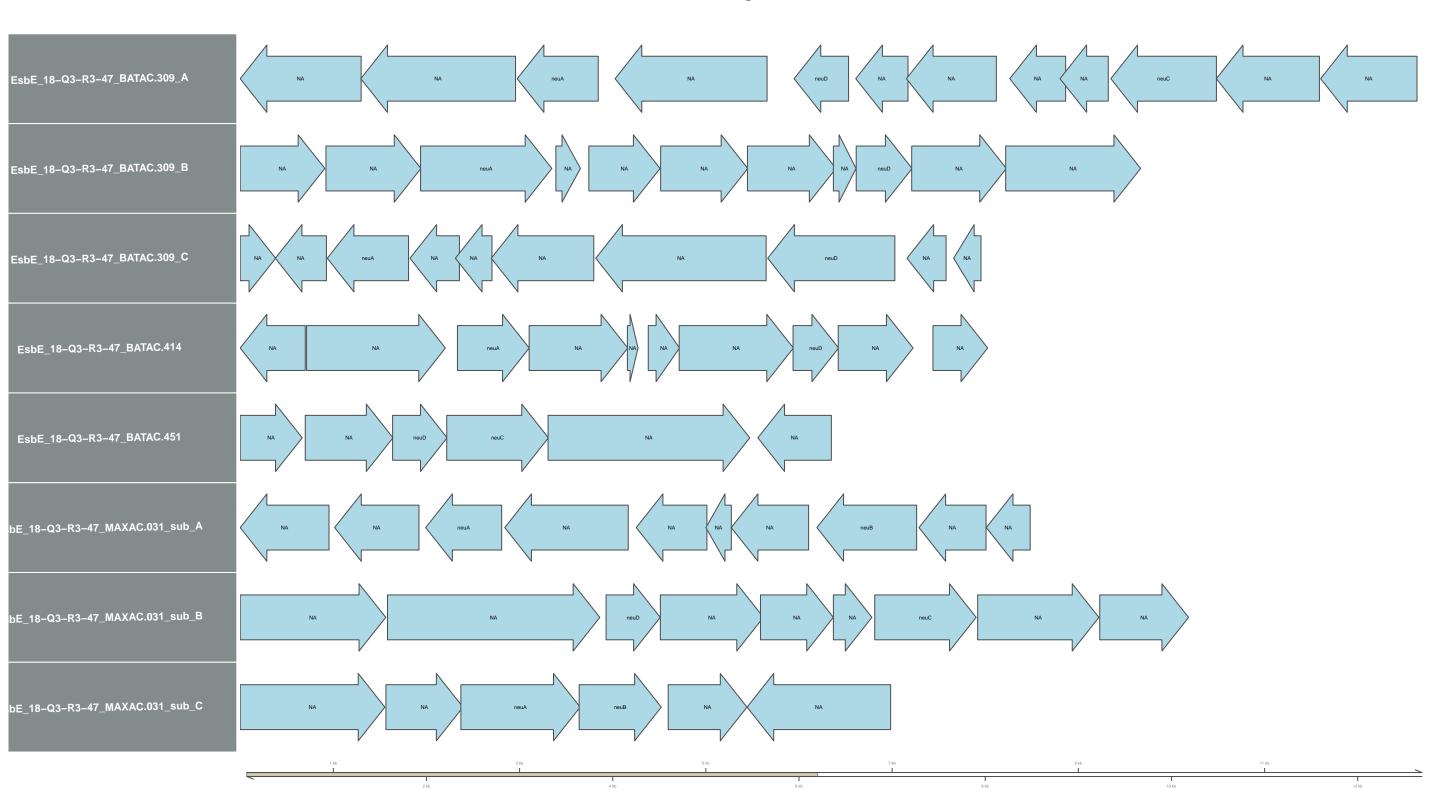
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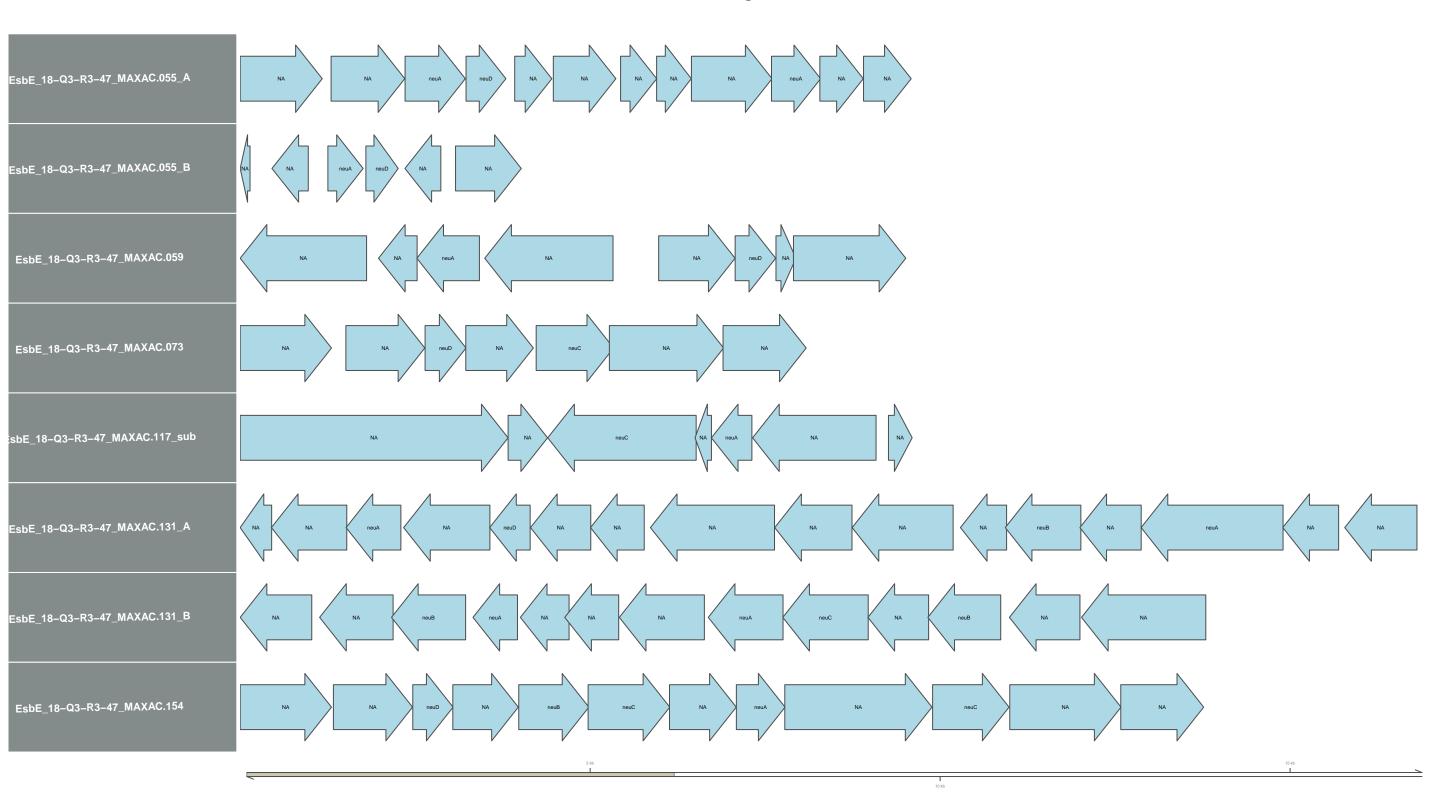


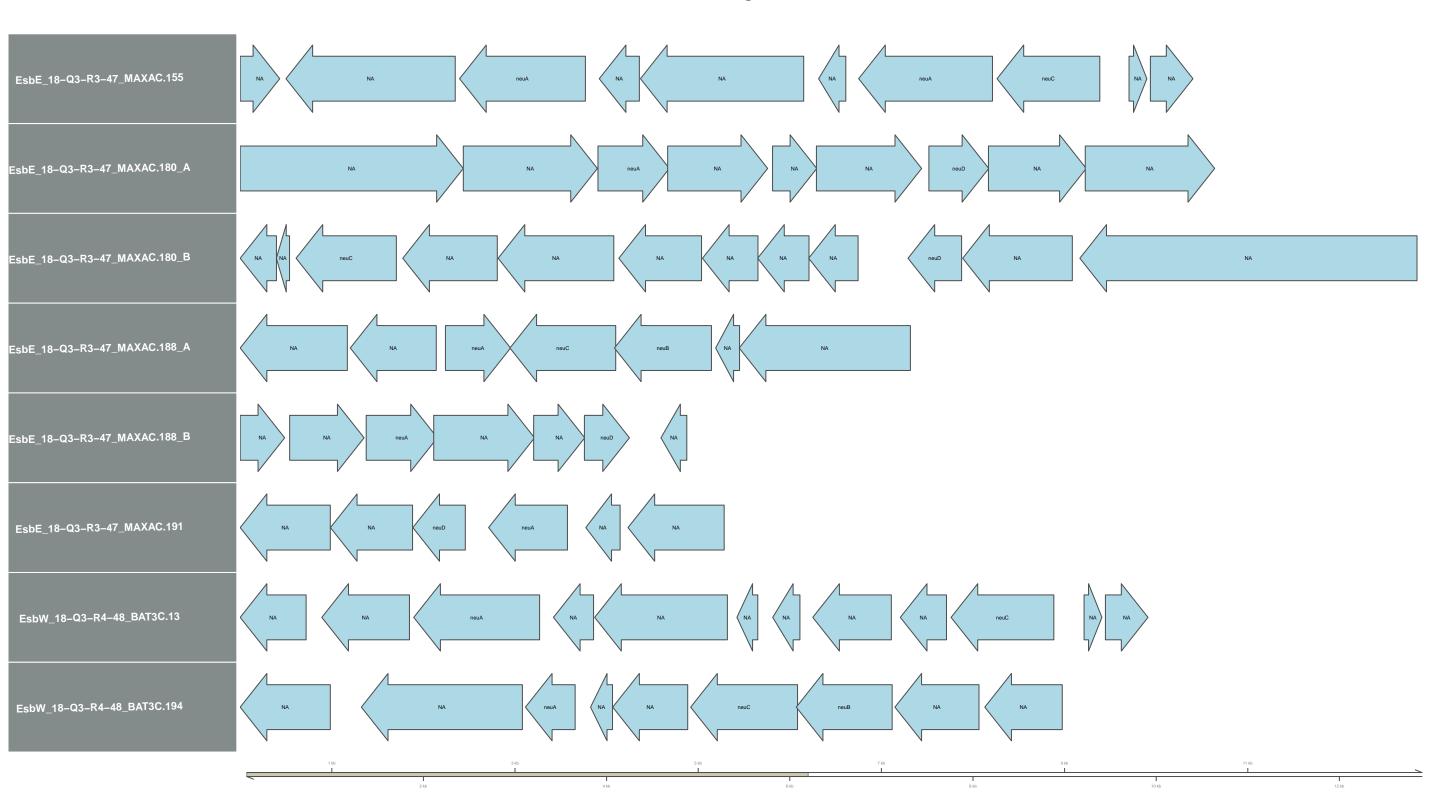


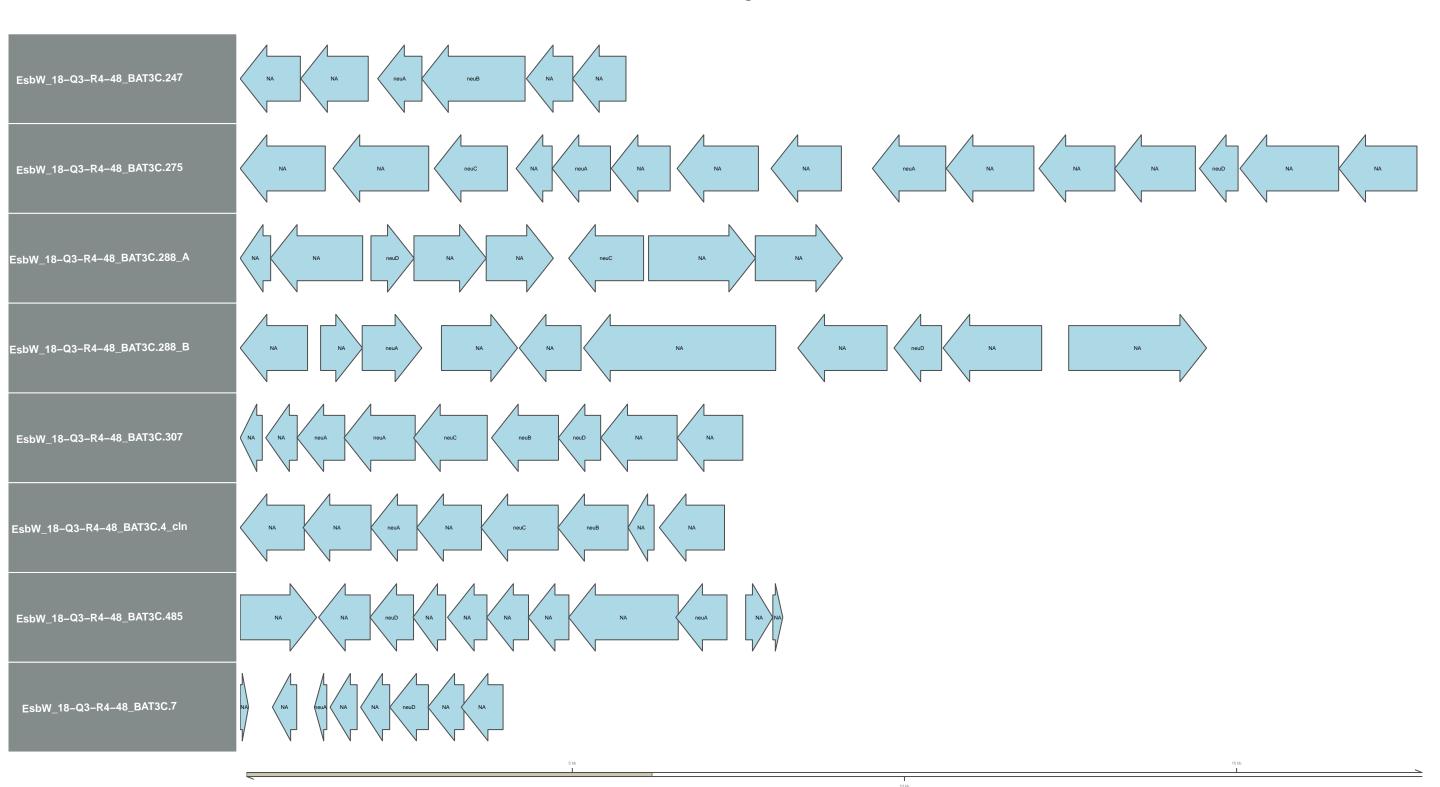


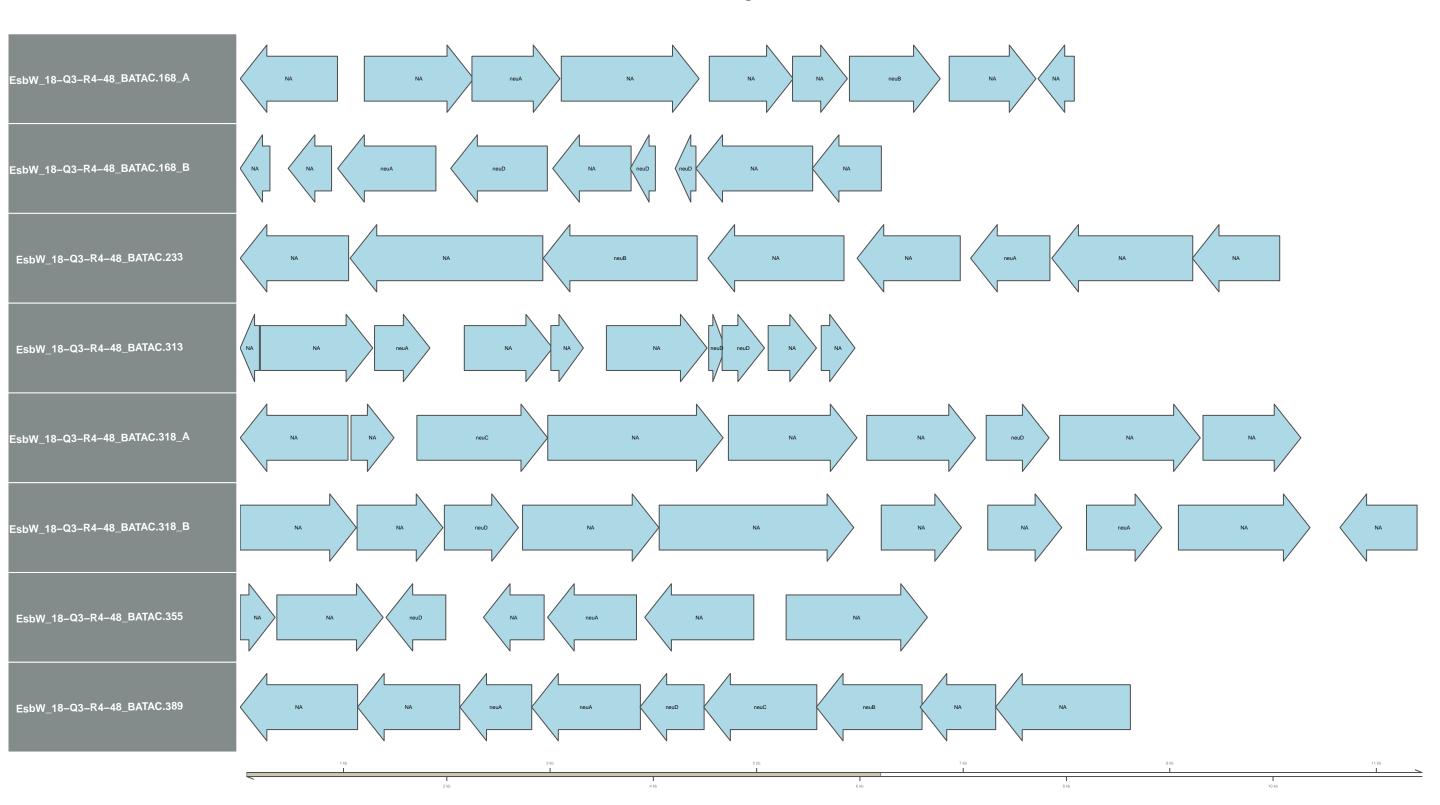


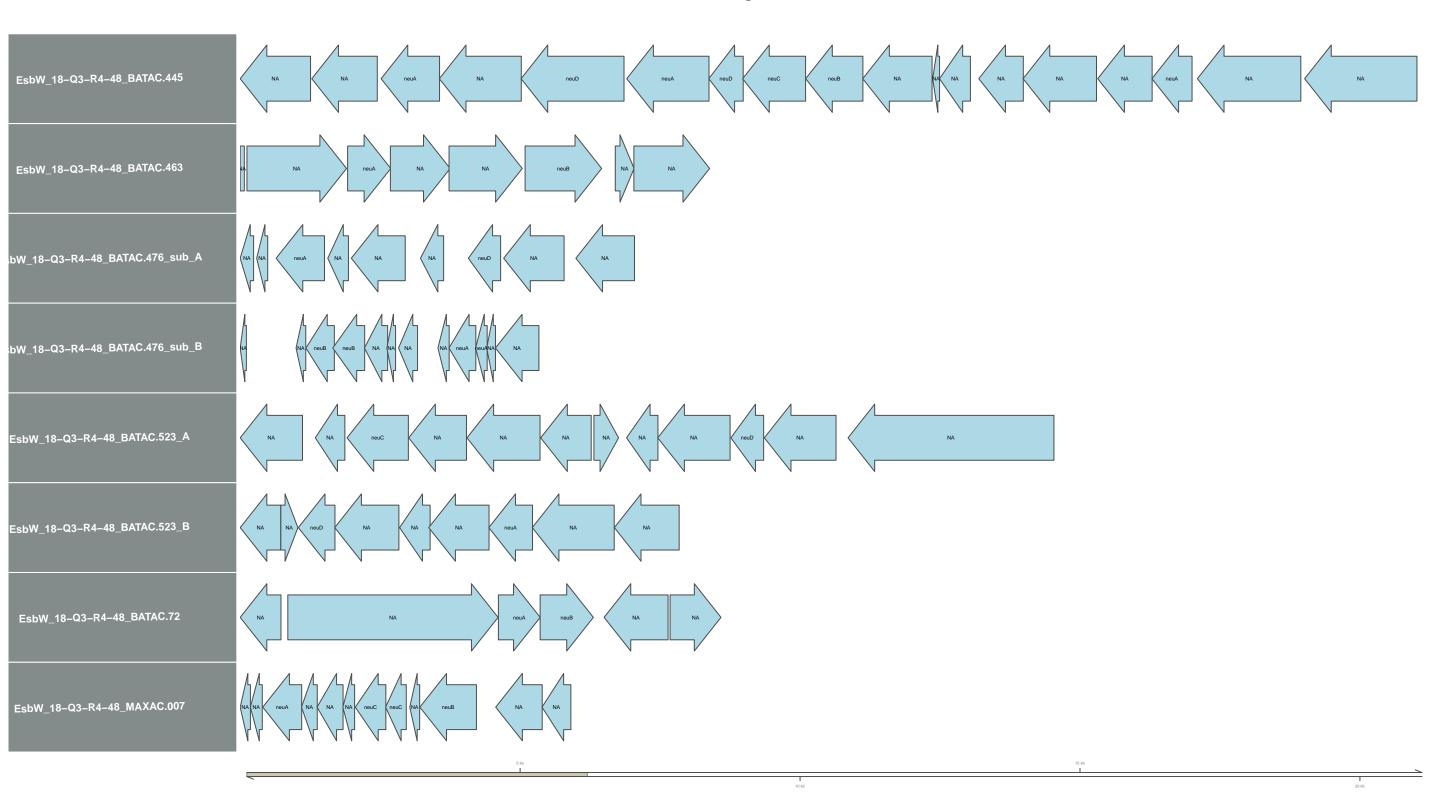


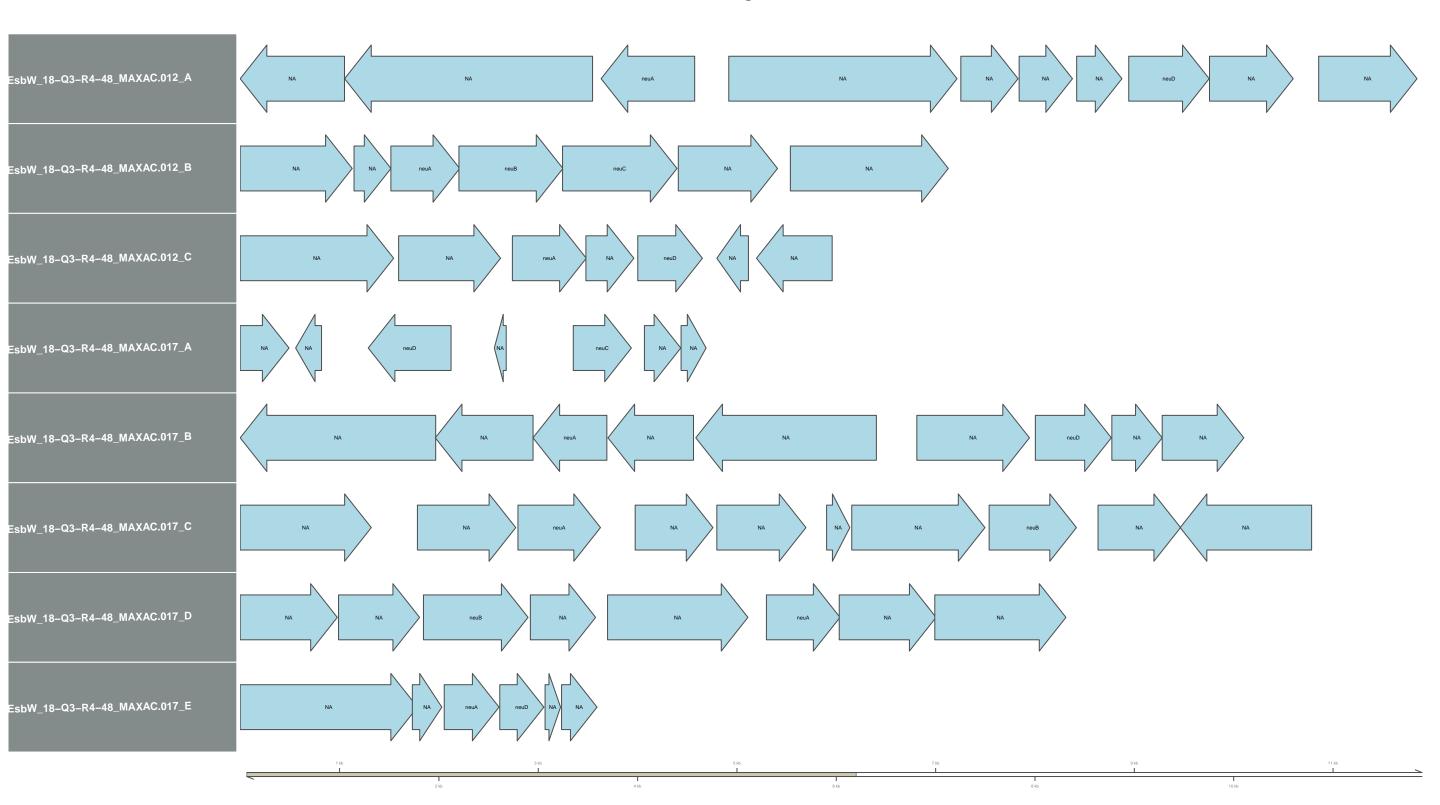


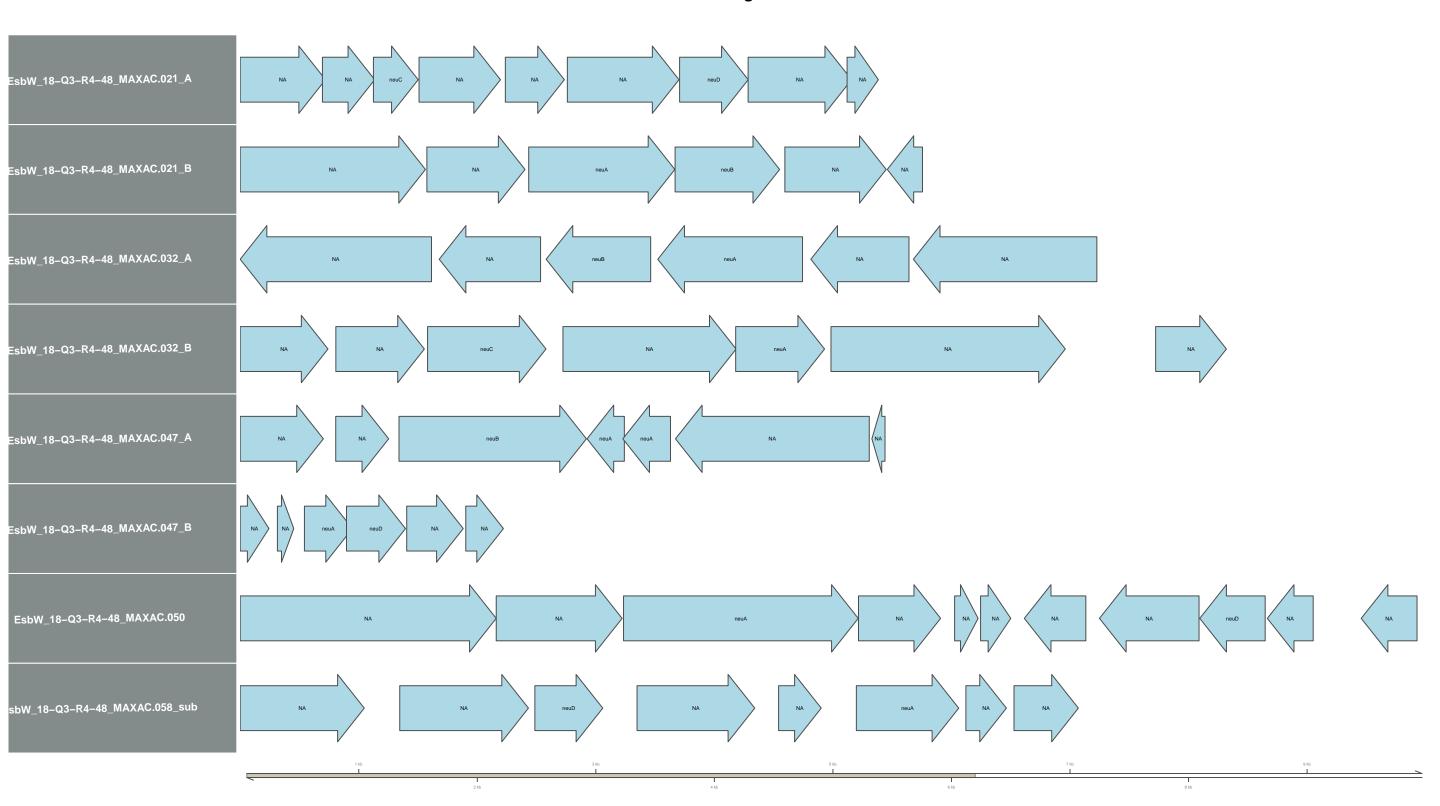


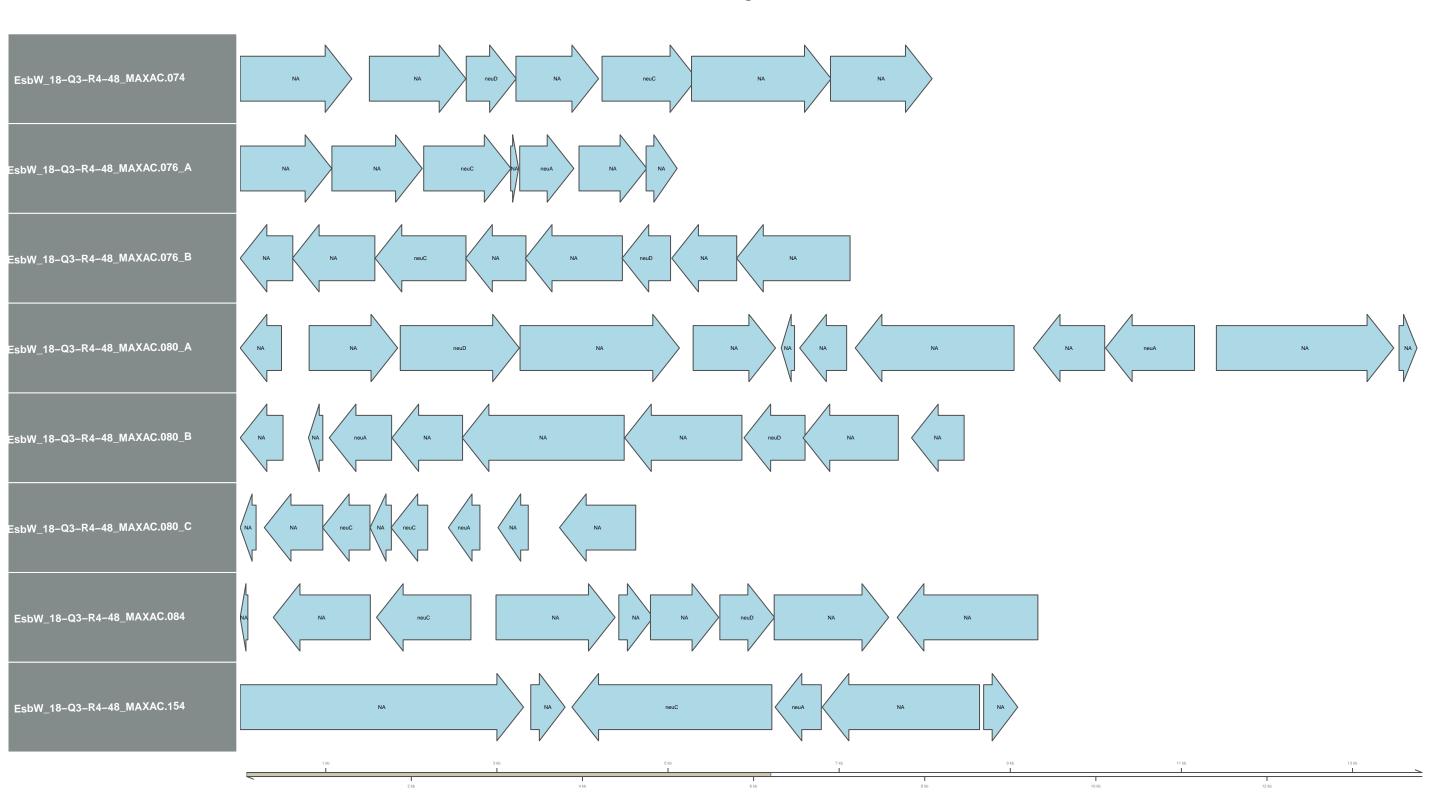


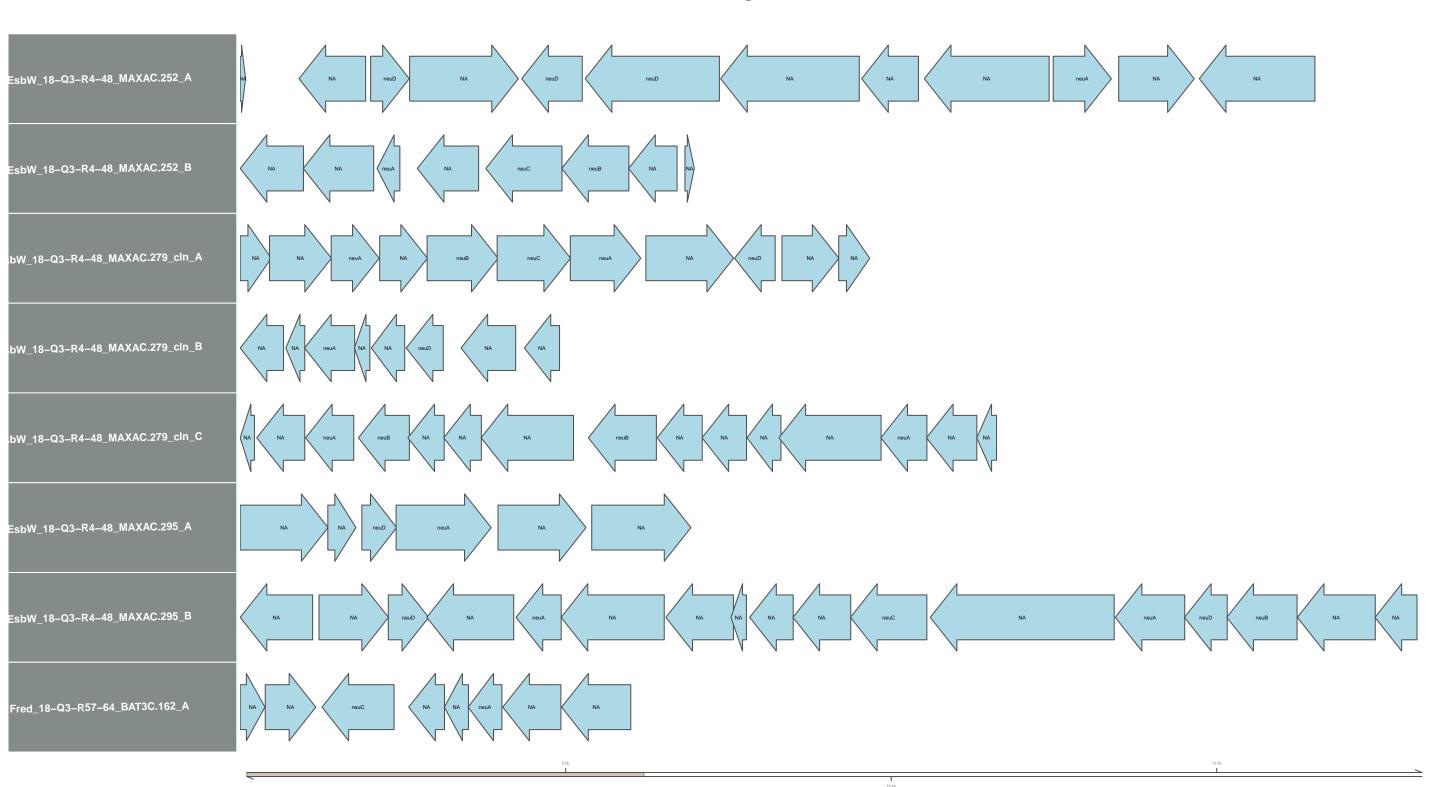


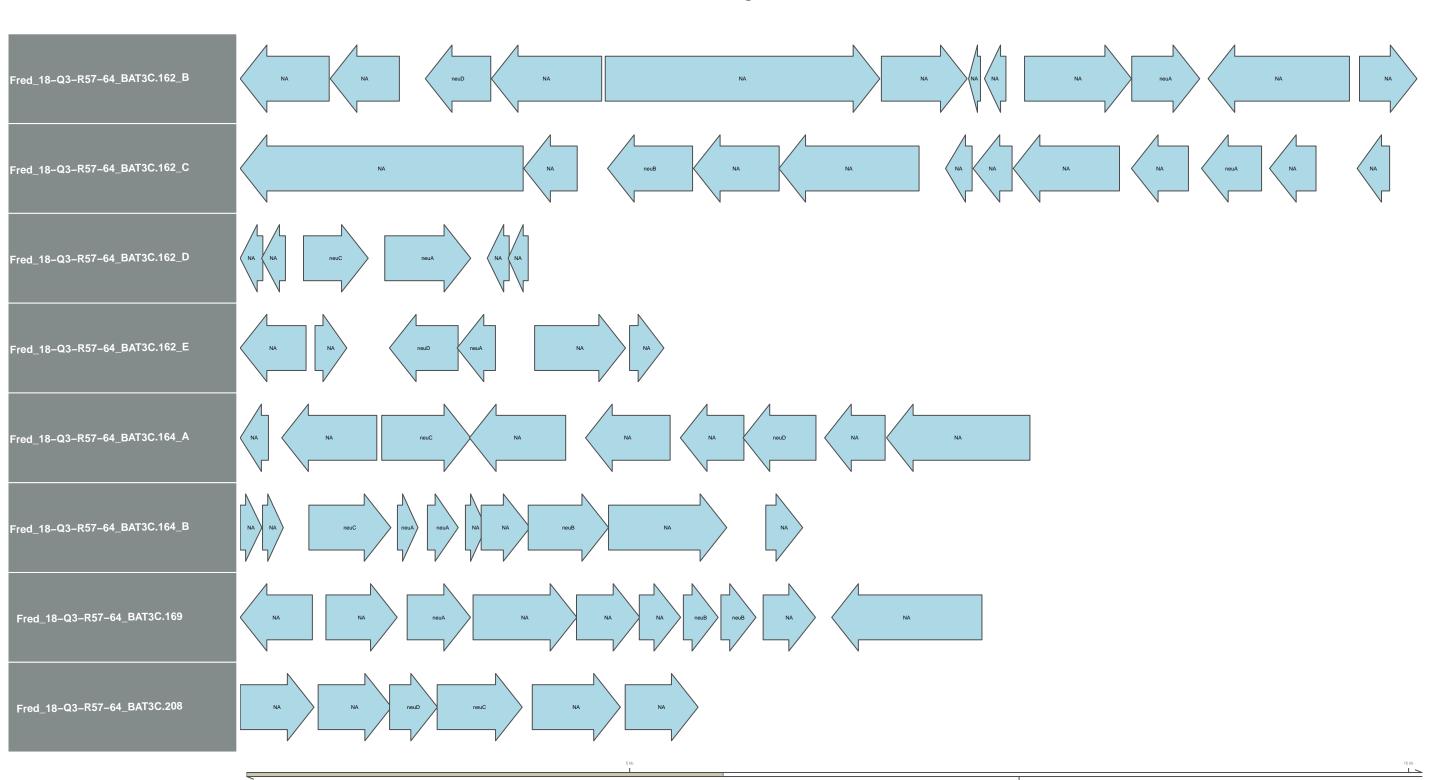


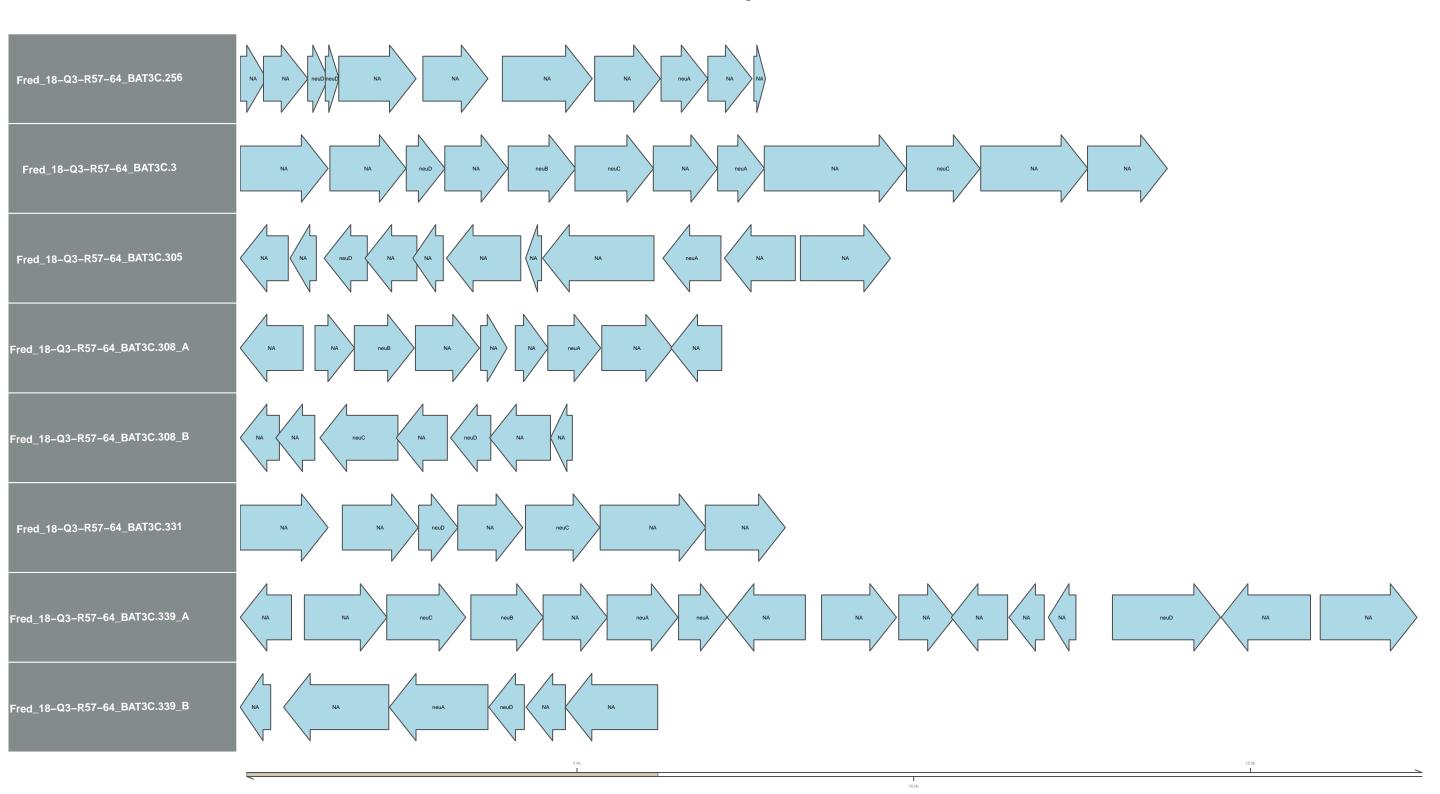


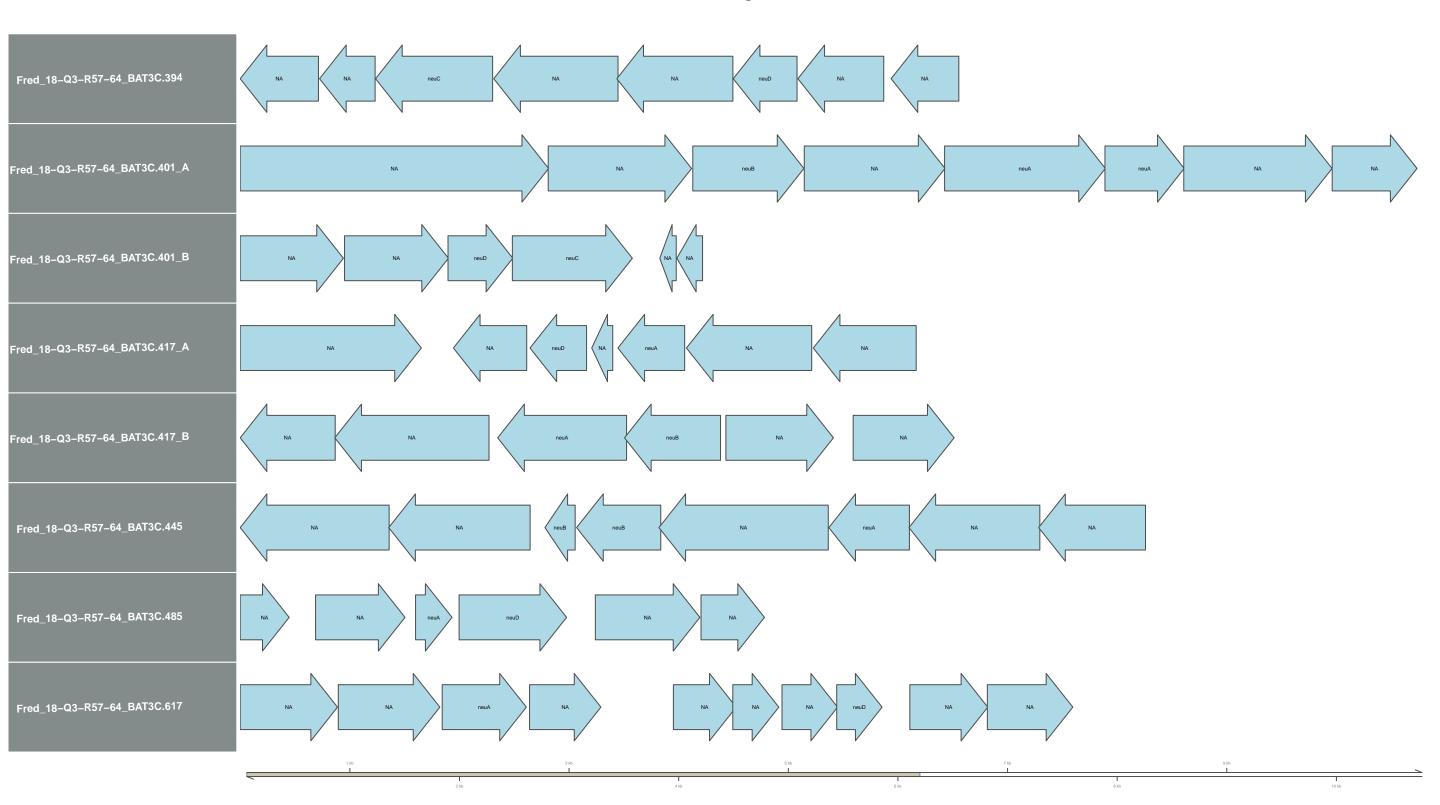


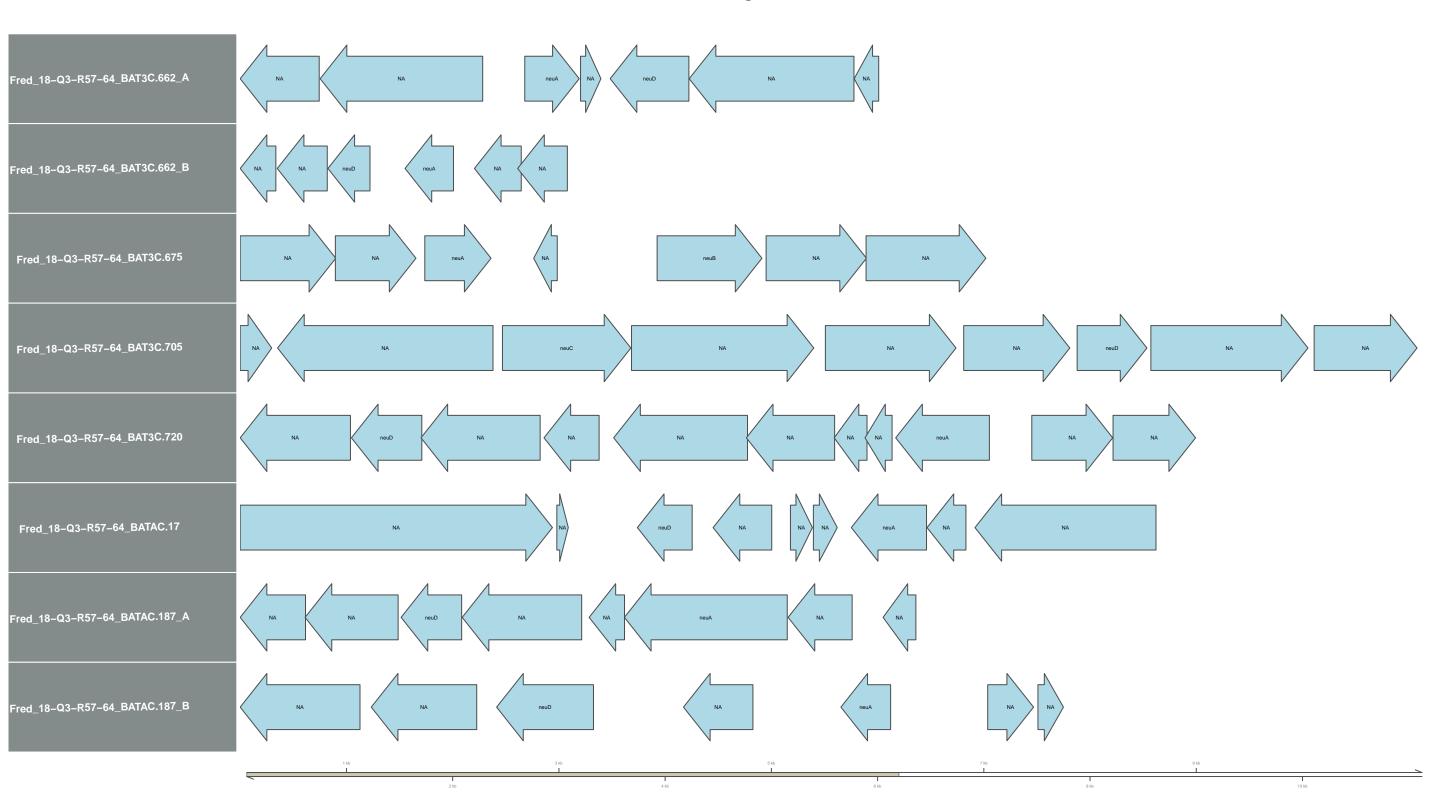


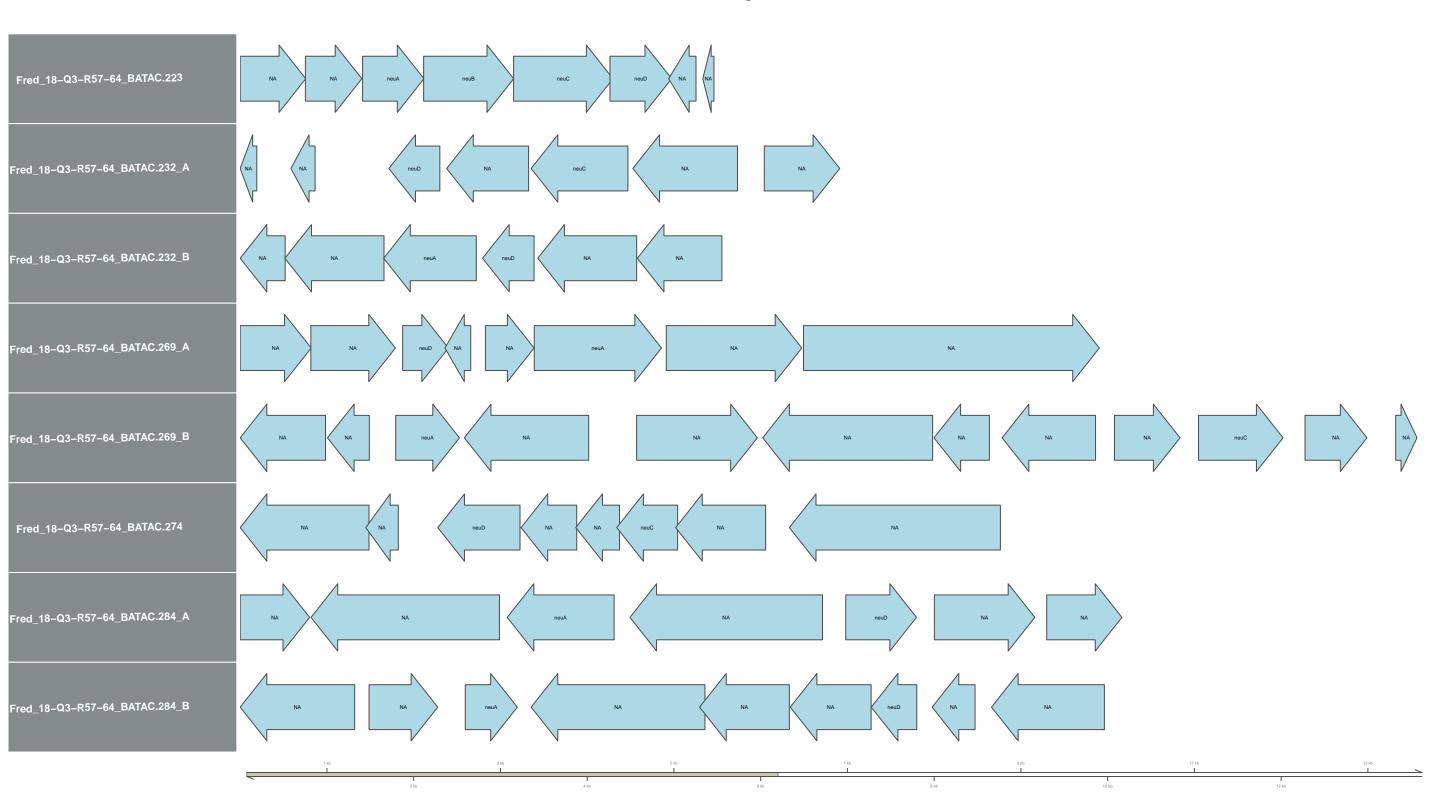


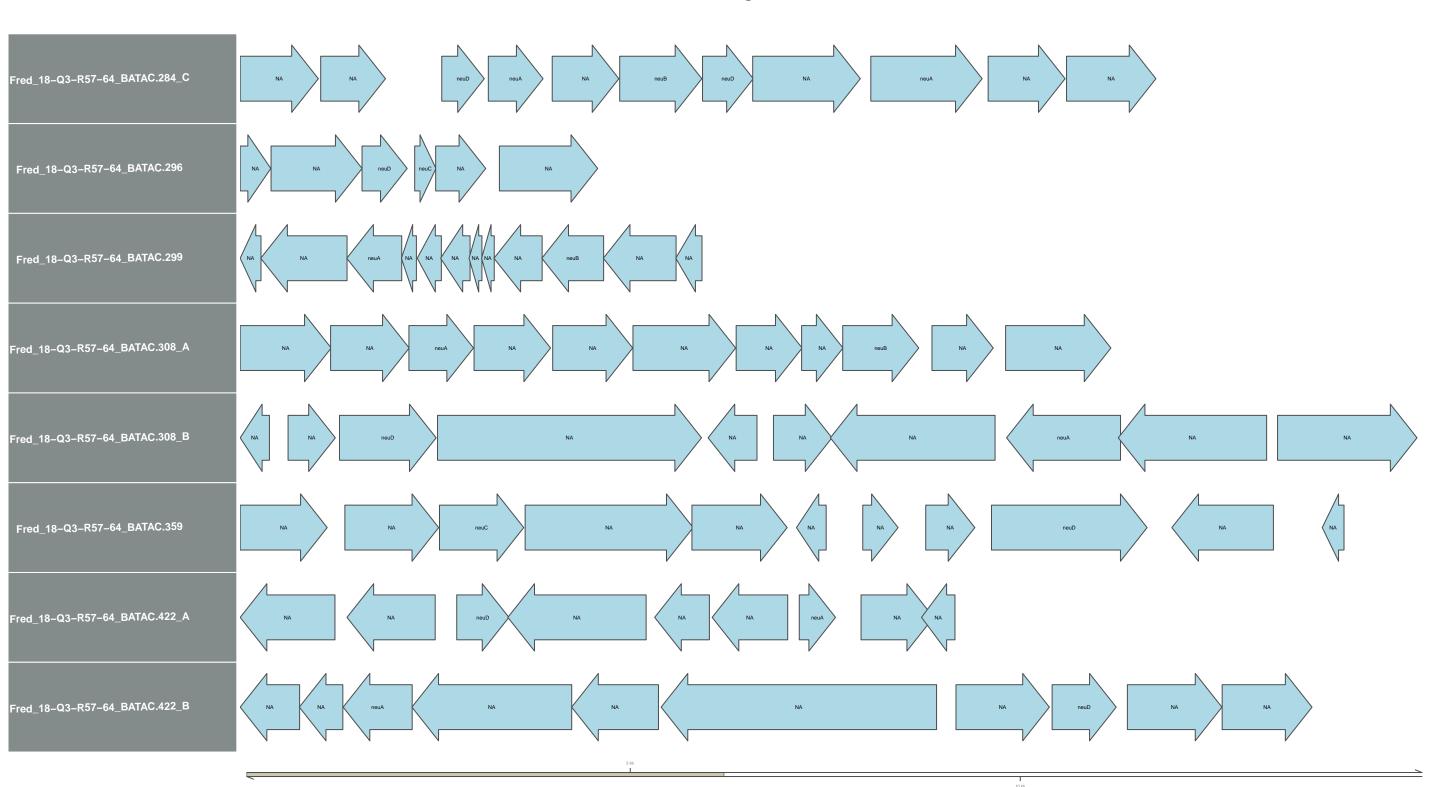


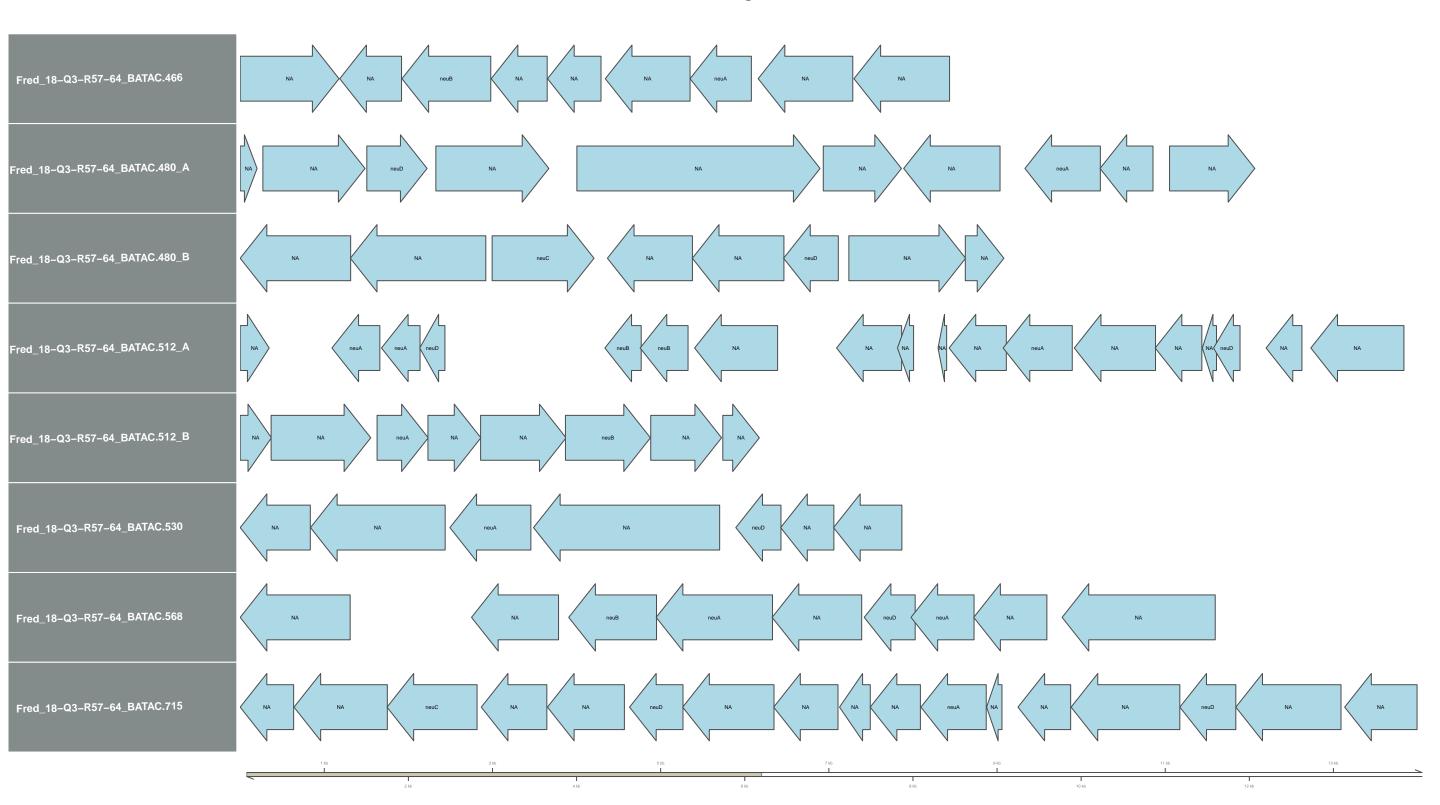


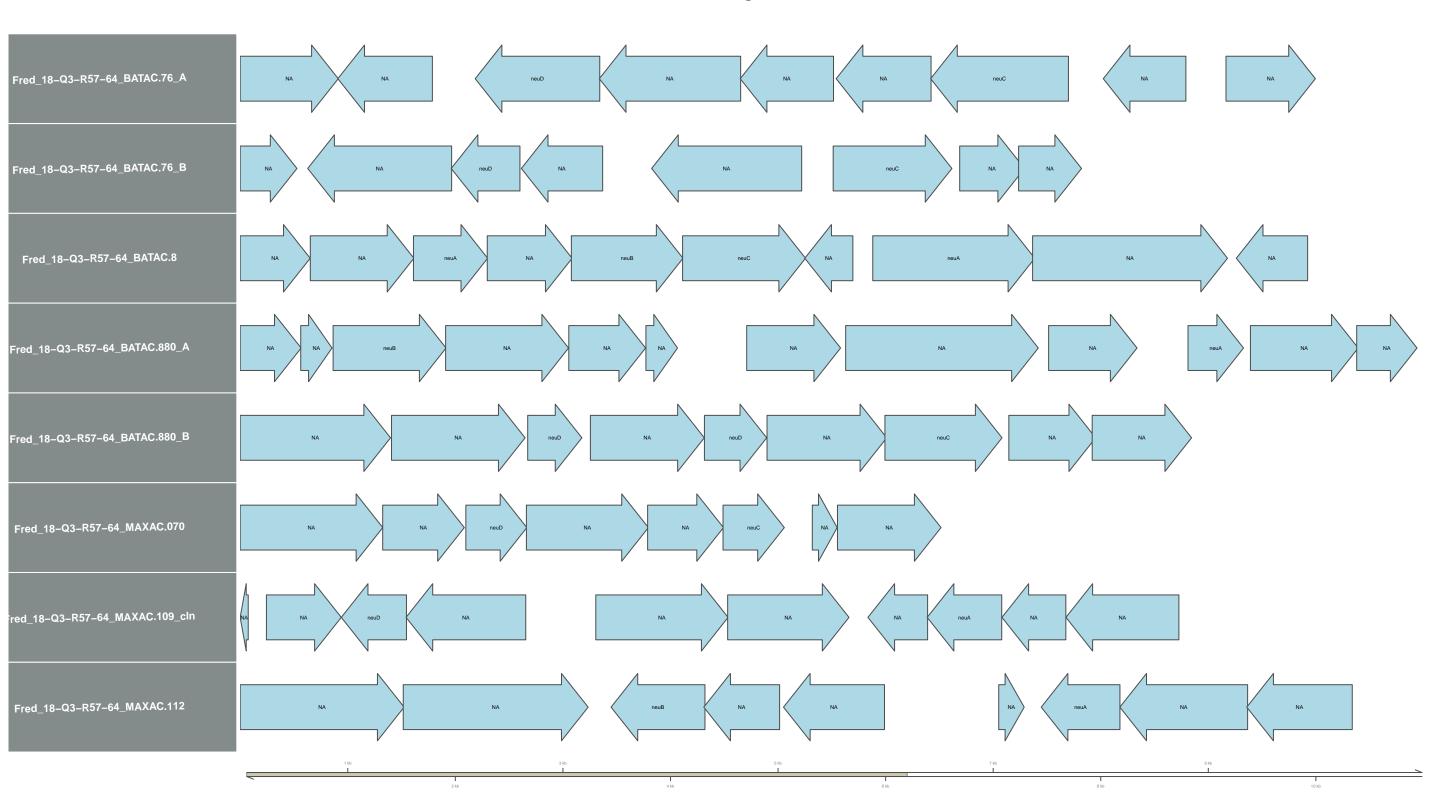


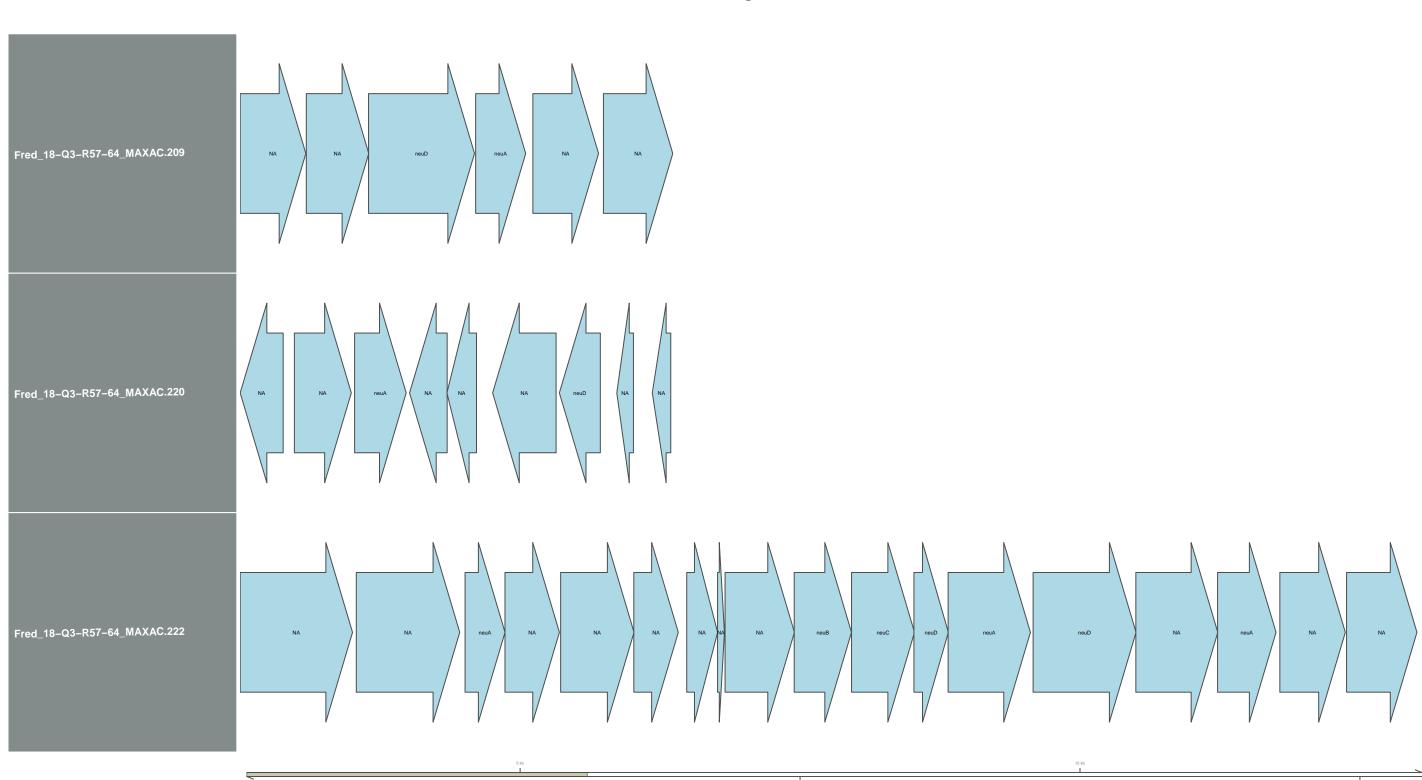












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298	Fred_18-Q3-R57-64_MAXAC.362	d_Bacteria.p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Hyphomonadaceae;g_Hyphomonas;s_	tig00000777-10-25148860	43526	neuC	00043
299	Fred_18-Q3-R57-64_MAXAC.370	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Saprospiraceae;g_;s_	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_A;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_Reyranellales;f_Reyranellaceae;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_Nitrospiria;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;t_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;t_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	${\tt d_Bacteria,p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales,f_Rhodocyclaceae;g_Dechloromonas;s_matching and the control of the c$	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;1_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_Nitrospiraico_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;t_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	dBacteria;pBacteroidota;cBacteroidia;oChitinophagales;fSaprospiraceae;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_Bacteriap_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	dBacteria;pBacteroidota;cBacteroidia;oChitinophagales;fUBA2359;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_Thiofillum;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_Opitutaeeae;g_;s_	tiq00010562-10-1944820	19355	neuA	01869
340	Hirt_18-Q3-R61-65_BAT3C.274	d_Bacteria;p_Myxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx	tig00001721-10-10109740	437277	neuA	01397
341	Hirt_18-Q3-R61-65_BAT3C.279	d_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Propionibacteriales;t_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