HA_streptococcus Heatmap AaIE_18-Q3-R2-46_BAT3C.188 -24 AaIE_18-Q3-R2-46_BAT3C.202 -24 AaIE_18-Q3-R2-46_BAT3C.320 -22 43 AaIE_18-Q3-R2-46_BATAC.180 -23 AaIE_18-Q3-R2-46_MAXAC.025 -29 AaIE_18-Q3-R2-46_MAXAC.039 -26 23 **Percent Identity** AaIE_18-Q3-R2-46_MAXAC.104 -25 50 24 40 30 AalW_18-Q3-R10-53_BATAC.157 - 21 25 AalW_18-Q3-R10-53_BATAC.377 -26 AalW_18-Q3-R10-53_BATAC.706 -24 AalW_18-Q3-R10-53_MAXAC.084 -44 26 AalW_18-Q3-R10-53_MAXAC.406 -22 22 Aved_18-Q3-R54-62_BAT3C.309 -27 21 Aved_18-Q3-R54-62_BATAC.253 -21 24 pgi

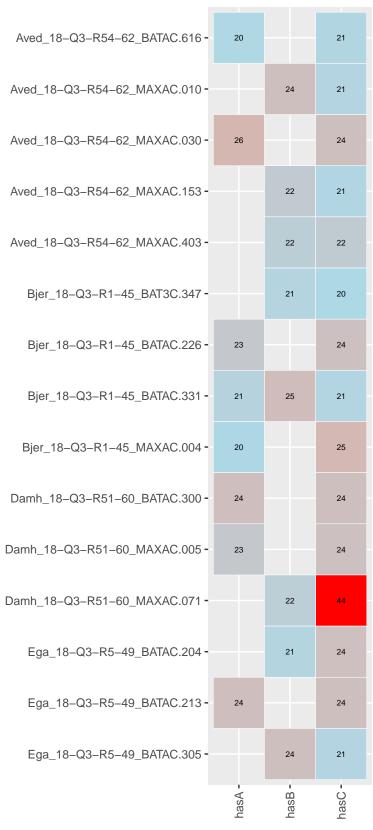
HA_streptococcus Heatmap

Percent Identity

40

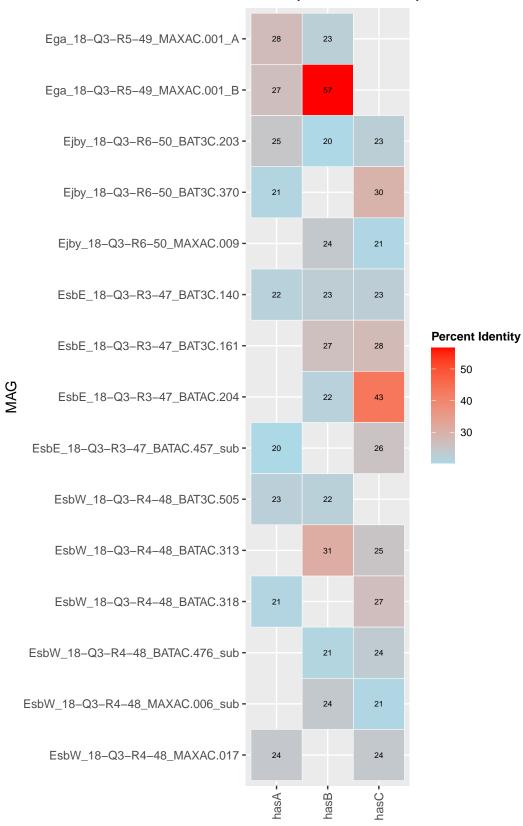
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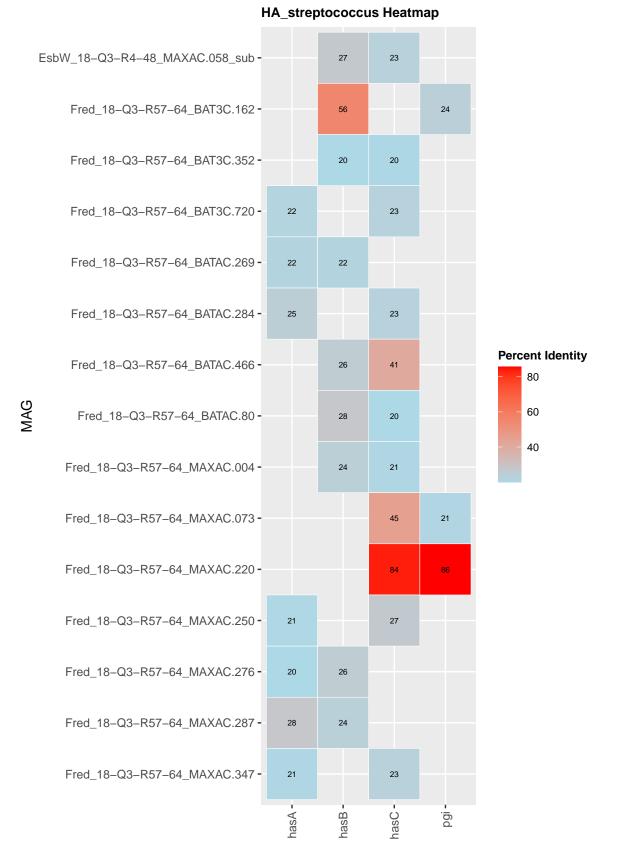
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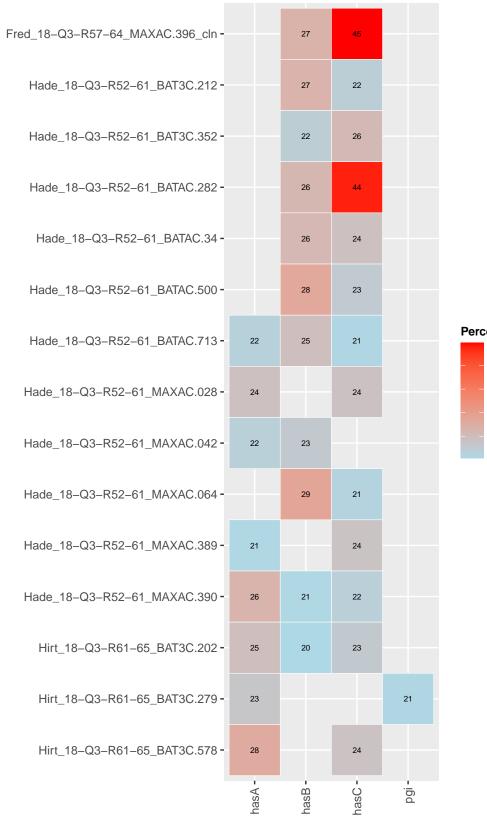
MAG

HA_streptococcus Heatmap

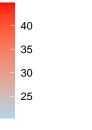




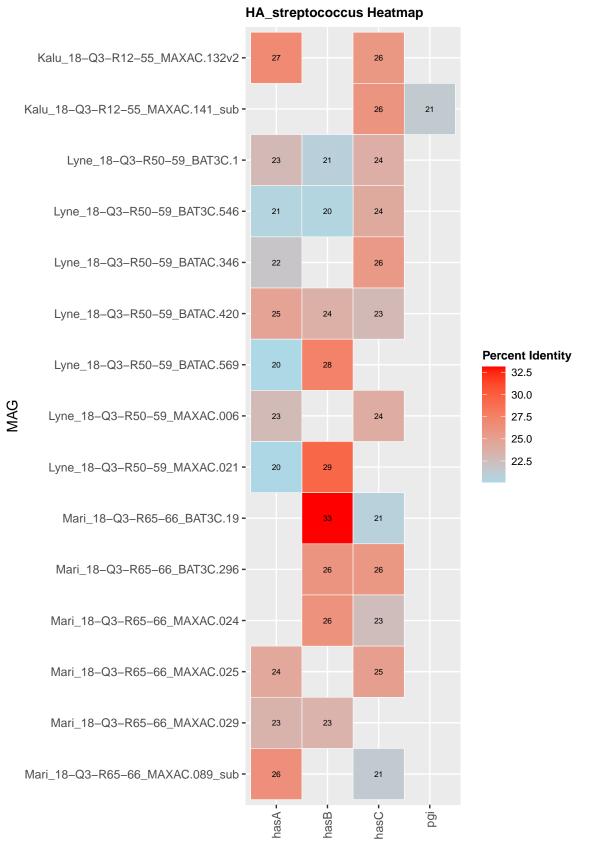
HA_streptococcus Heatmap



Percent Identity



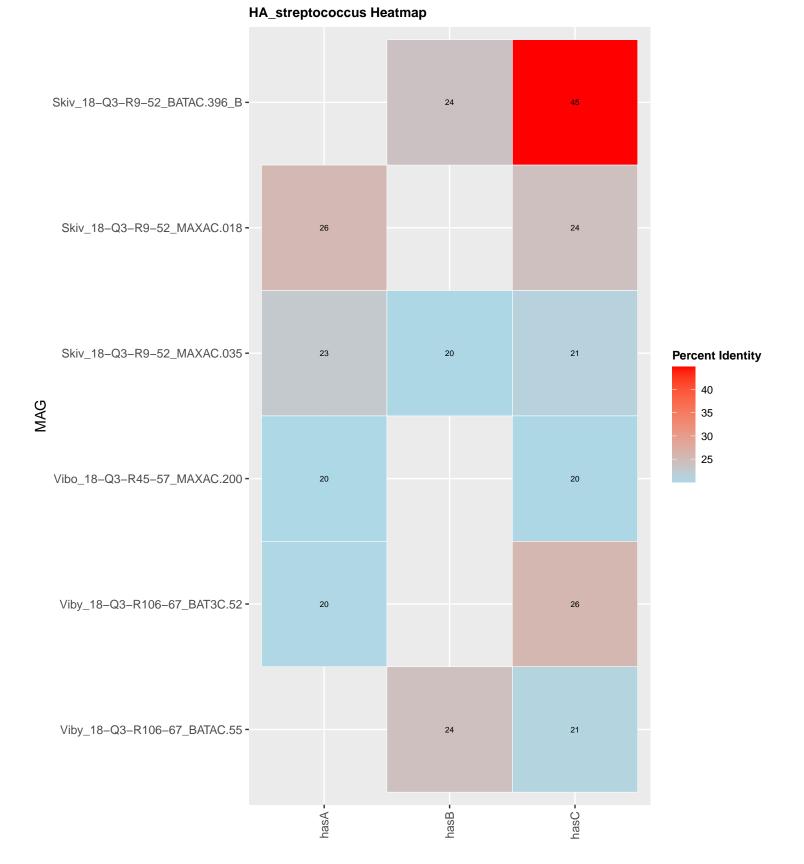
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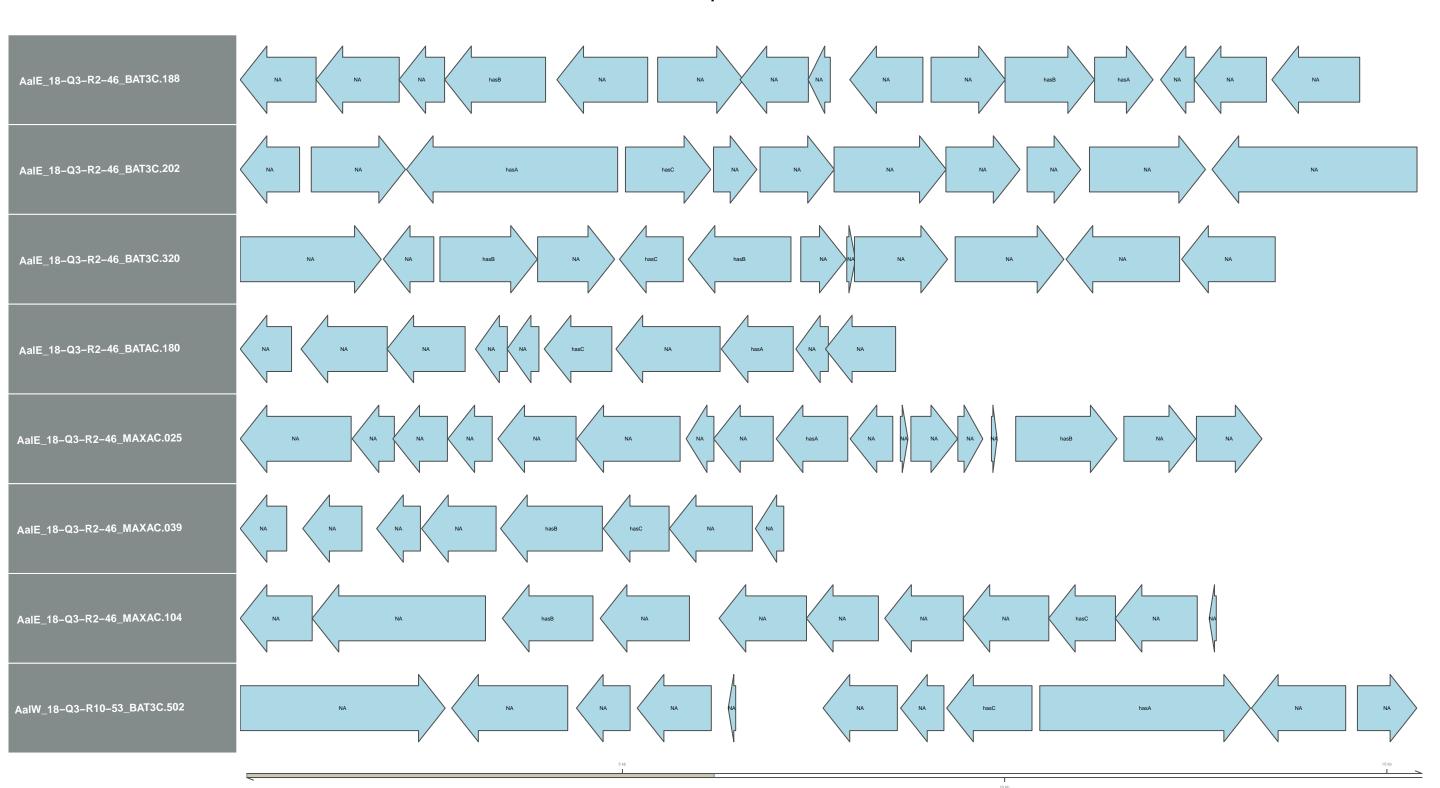


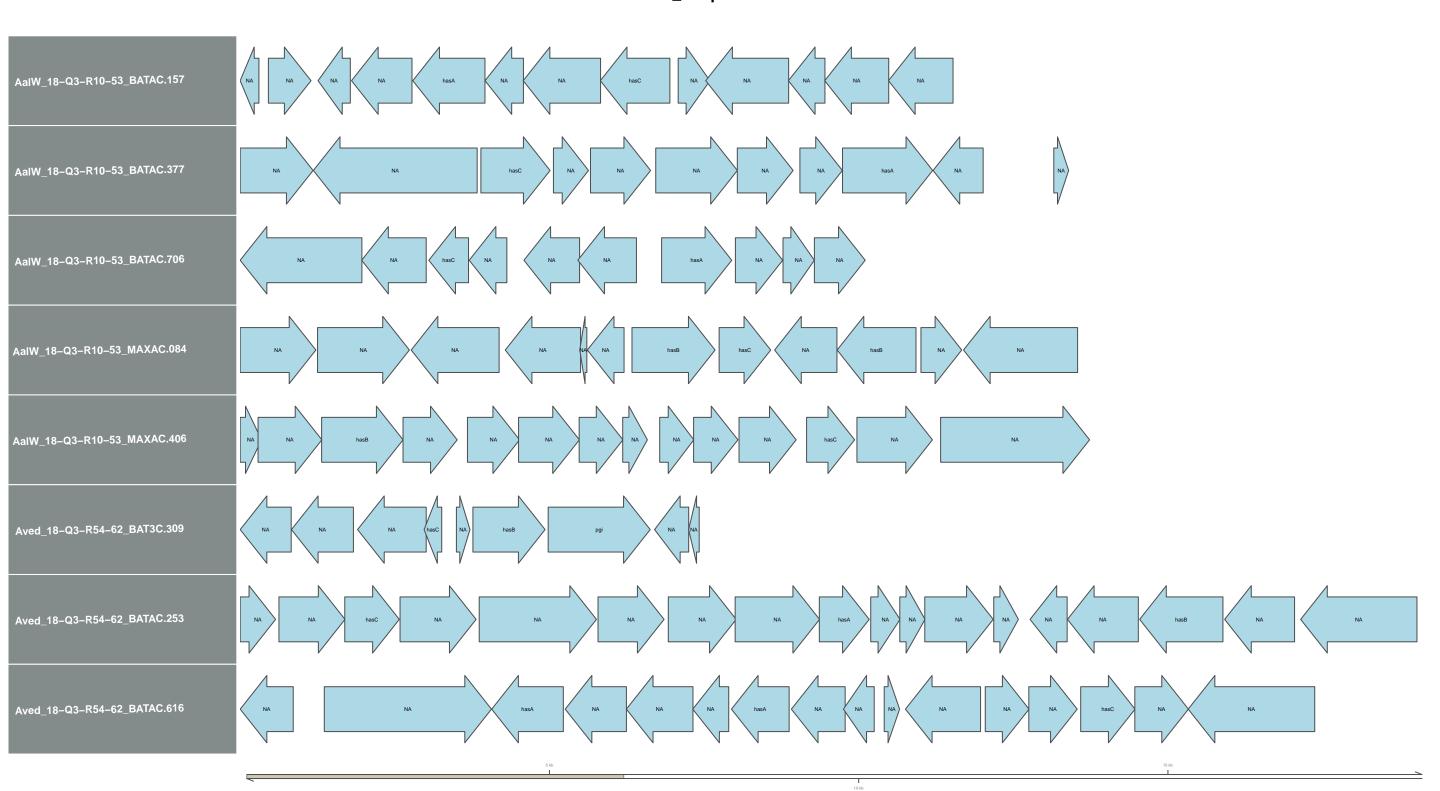
HA_streptococcus Heatmap Mari_18-Q3-R65-66_MAXAC.093 -25 Mari_18-Q3-R65-66_MAXAC.212 - 30 23 OdNE_18-Q3-R46-58_BAT3C.84 -28 21 OdNE_18-Q3-R46-58_BATAC.16 - 21 22 OdNE_18-Q3-R46-58_BATAC.190 -31 24 OdNE_18-Q3-R46-58_BATAC.404 -28 23 Percent Identity OdNE_18-Q3-R46-58_MAXAC.047 - 23 23 40 OdNE_18-Q3-R46-58_MAXAC.056 -28 21 30 OdNE_18-Q3-R46-58_MAXAC.100_sub - 26 21 OdNW_18-Q3-R42-56_BAT3C.339 -22 25 OdNW_18-Q3-R42-56_BATAC.423 -20 24 OdNW_18-Q3-R42-56_BATAC.438 -24 OdNW_18-Q3-R42-56_MAXAC.016 -26 30 OdNW_18-Q3-R42-56_MAXAC.143 -21 Rand_18-Q3-R56-63_BAT3C.13 -24 hasC

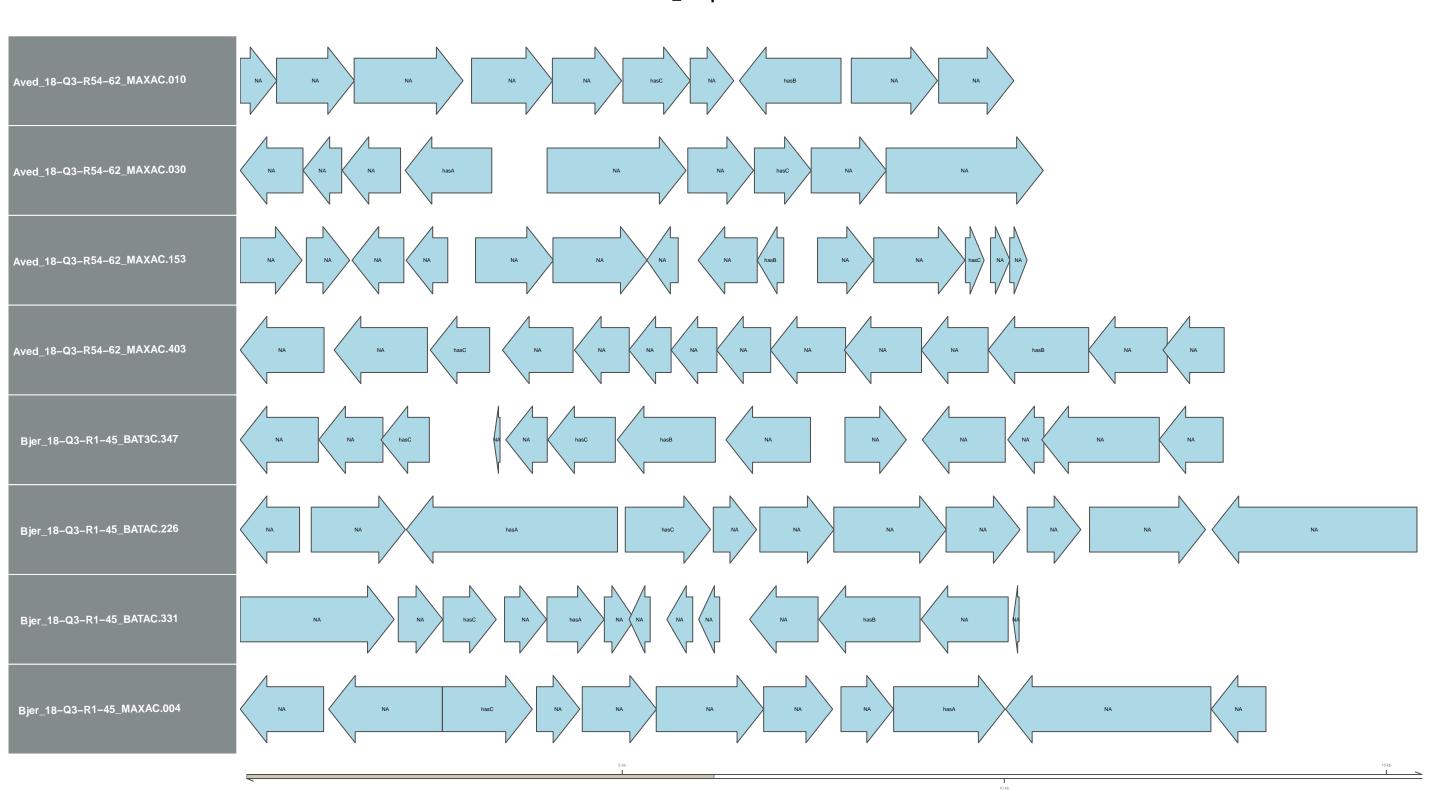
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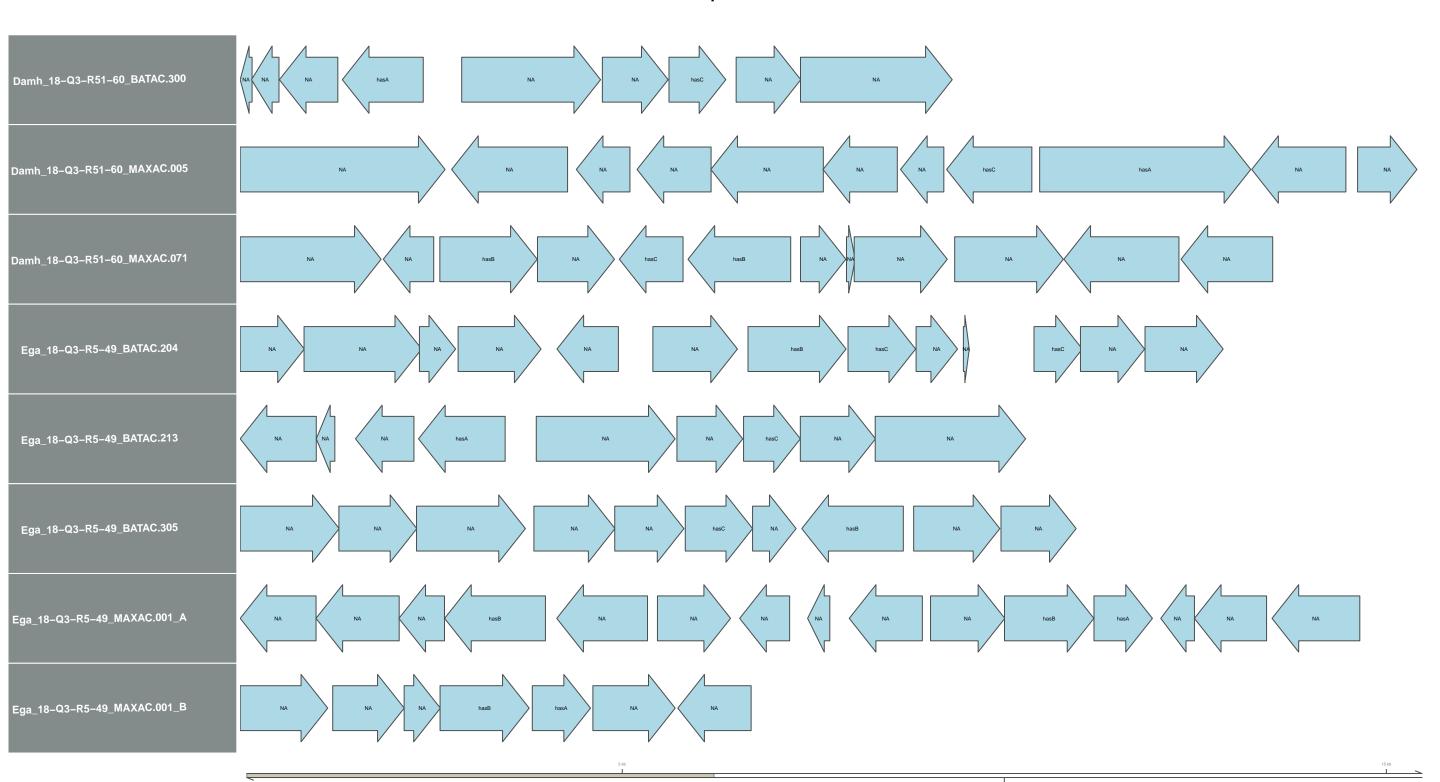
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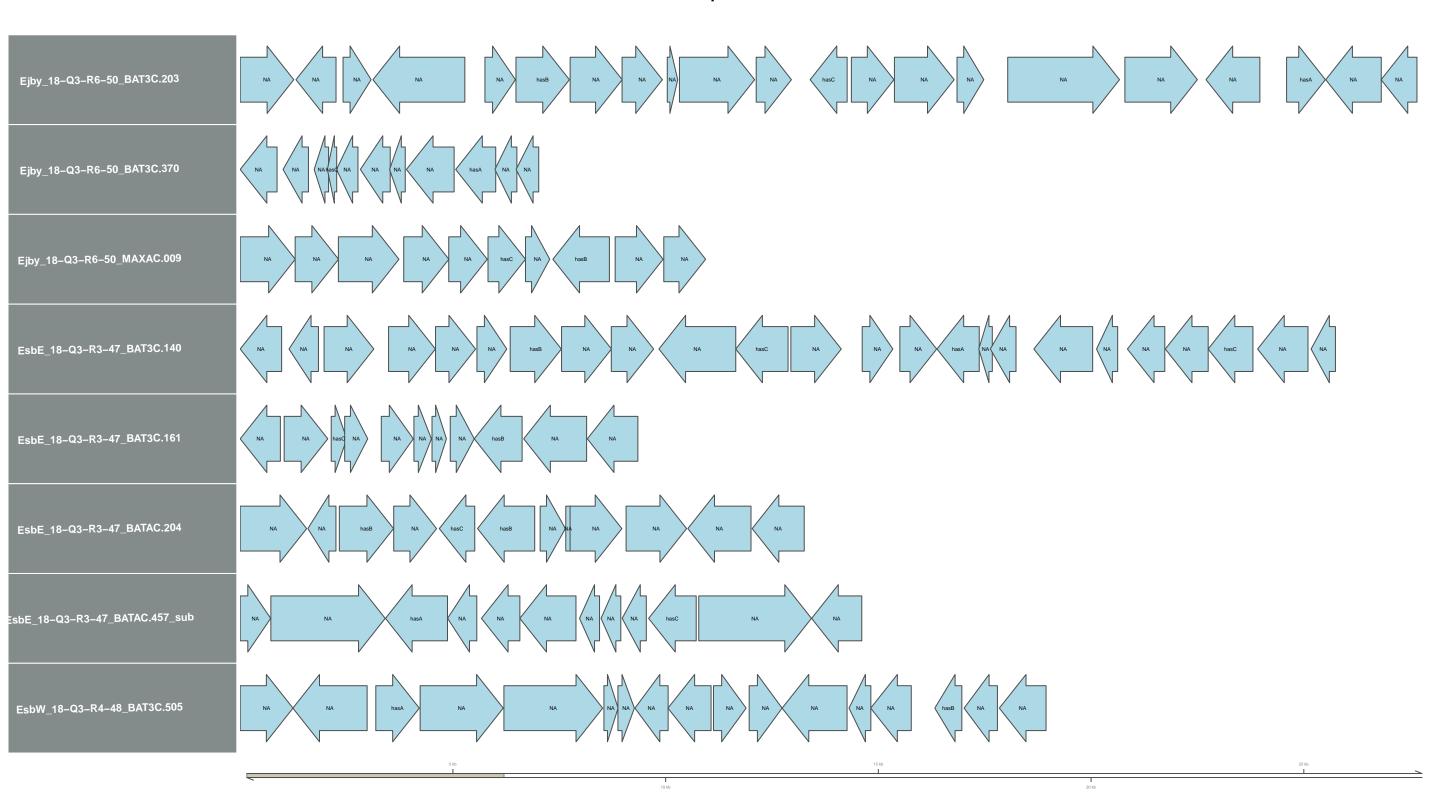


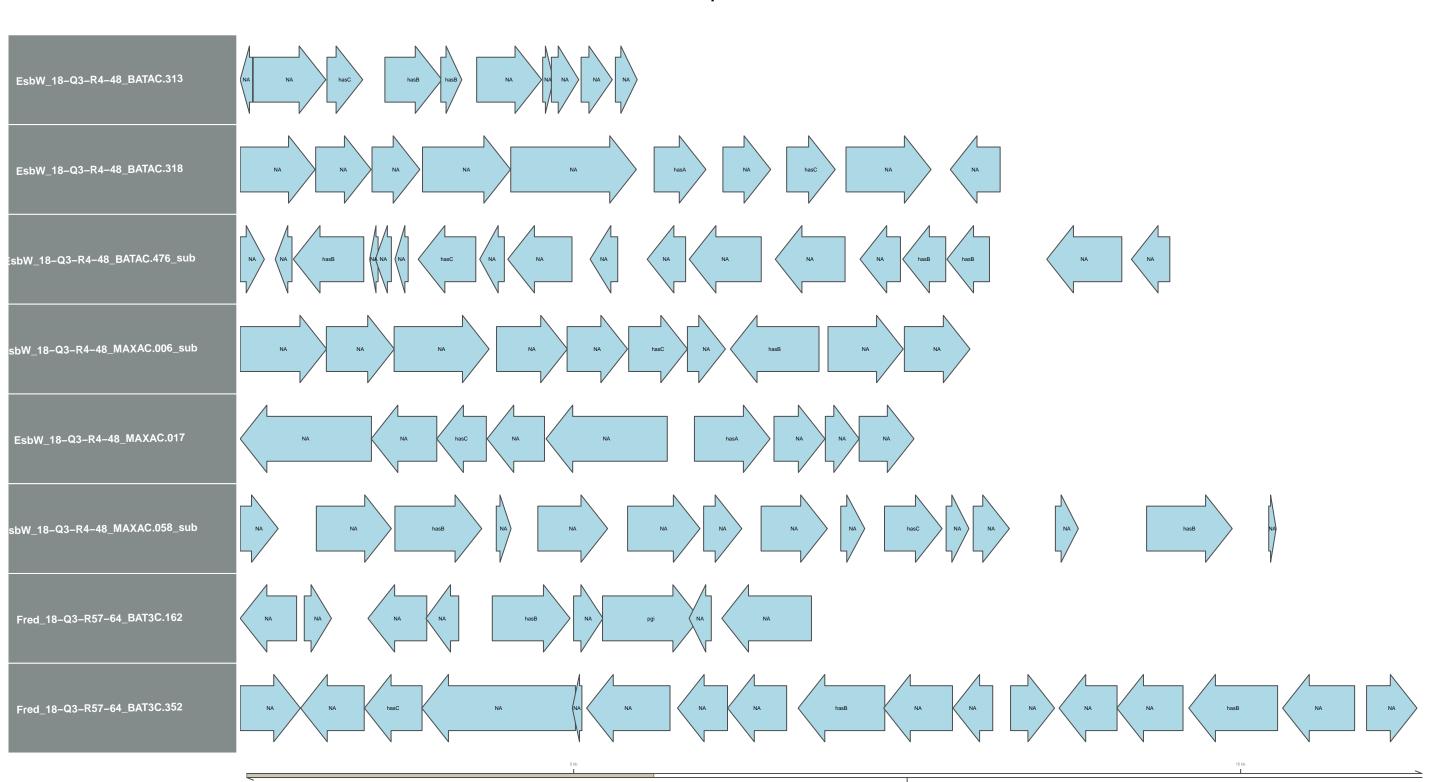


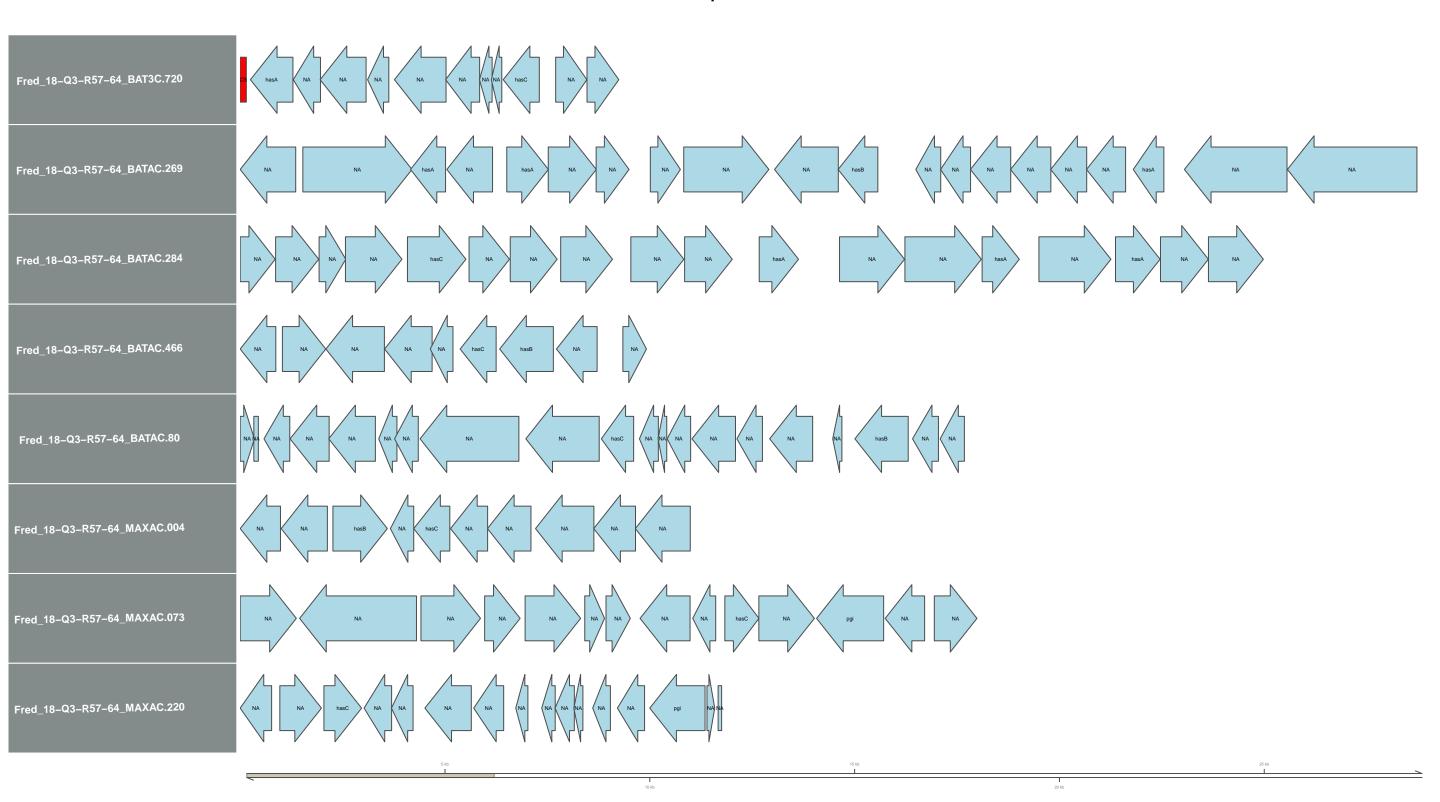


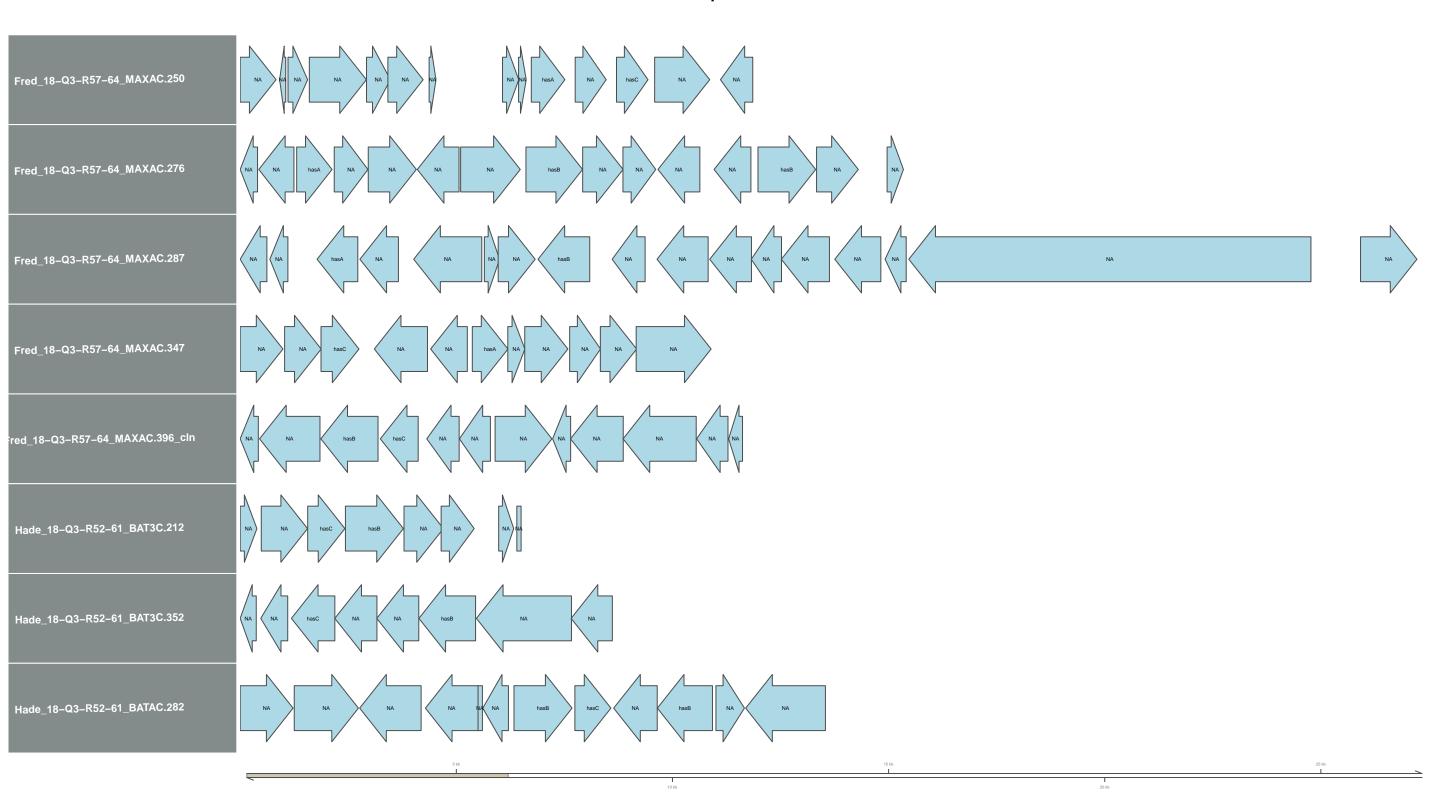


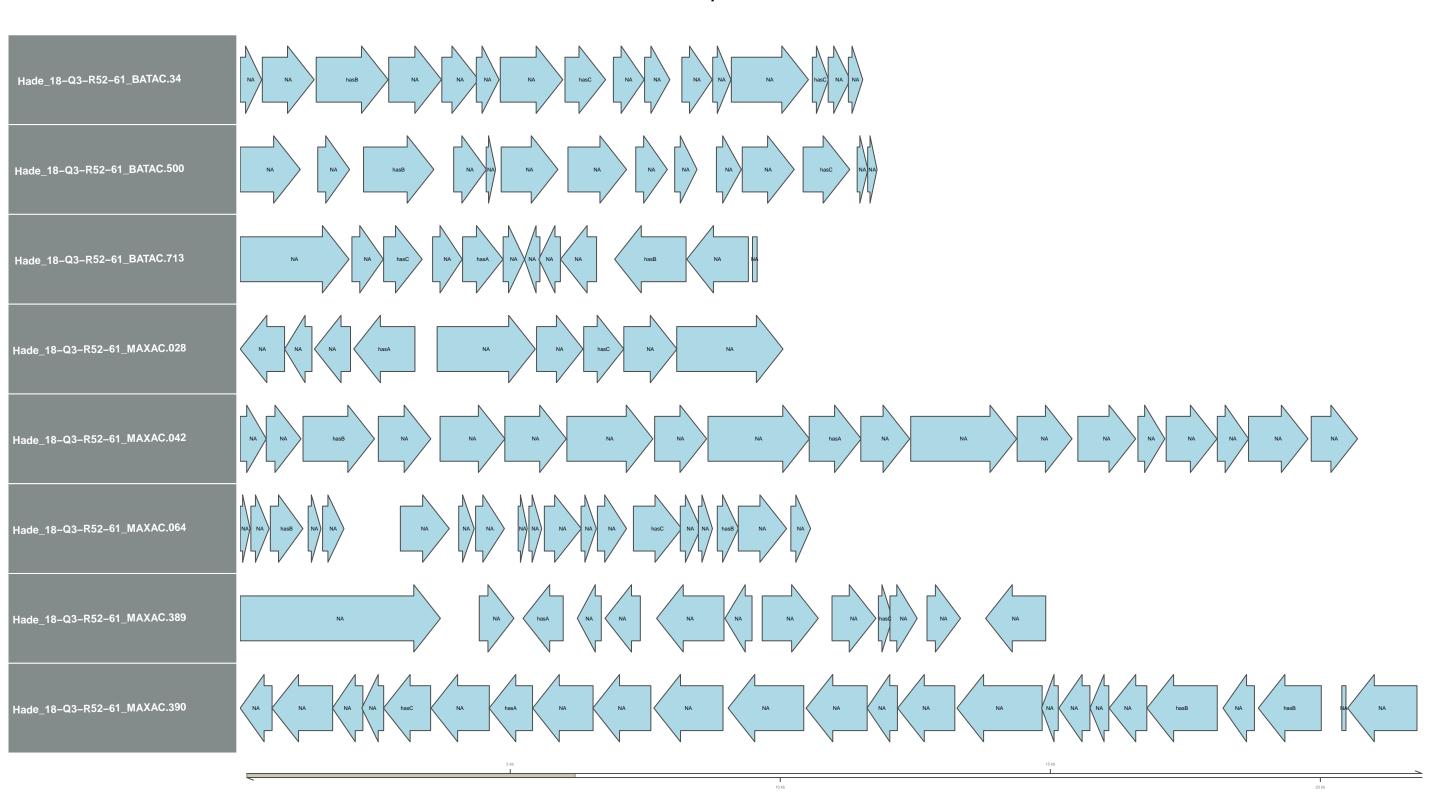


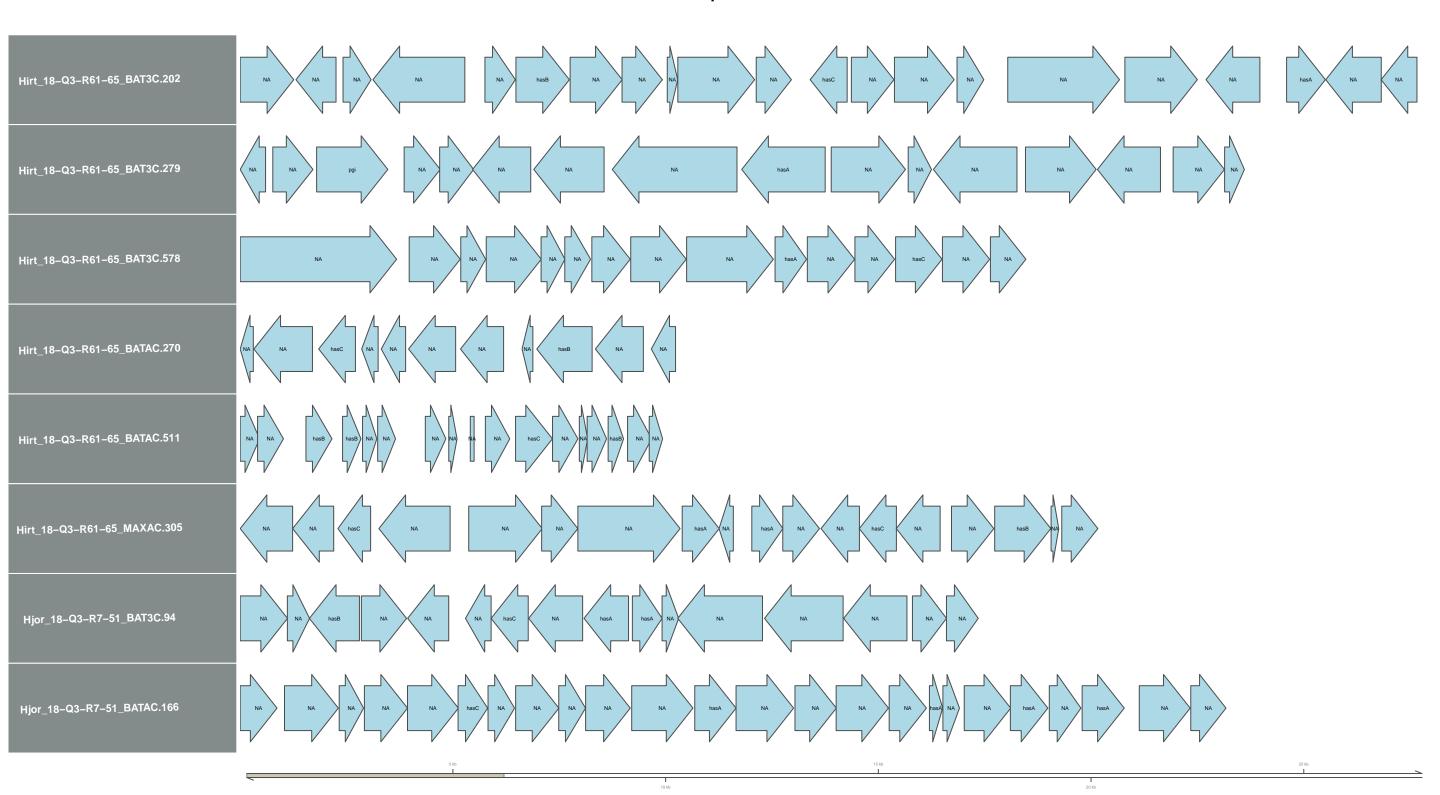


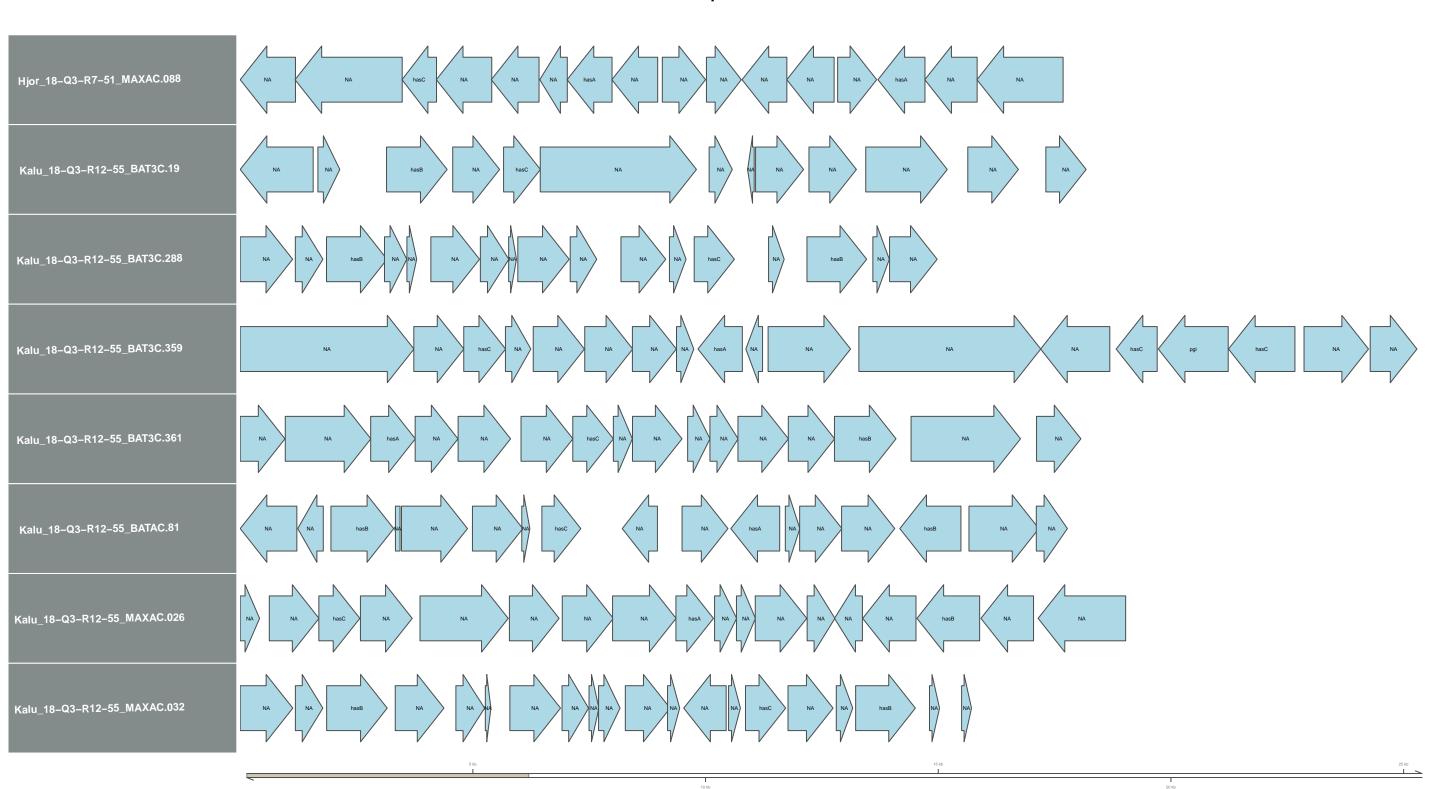


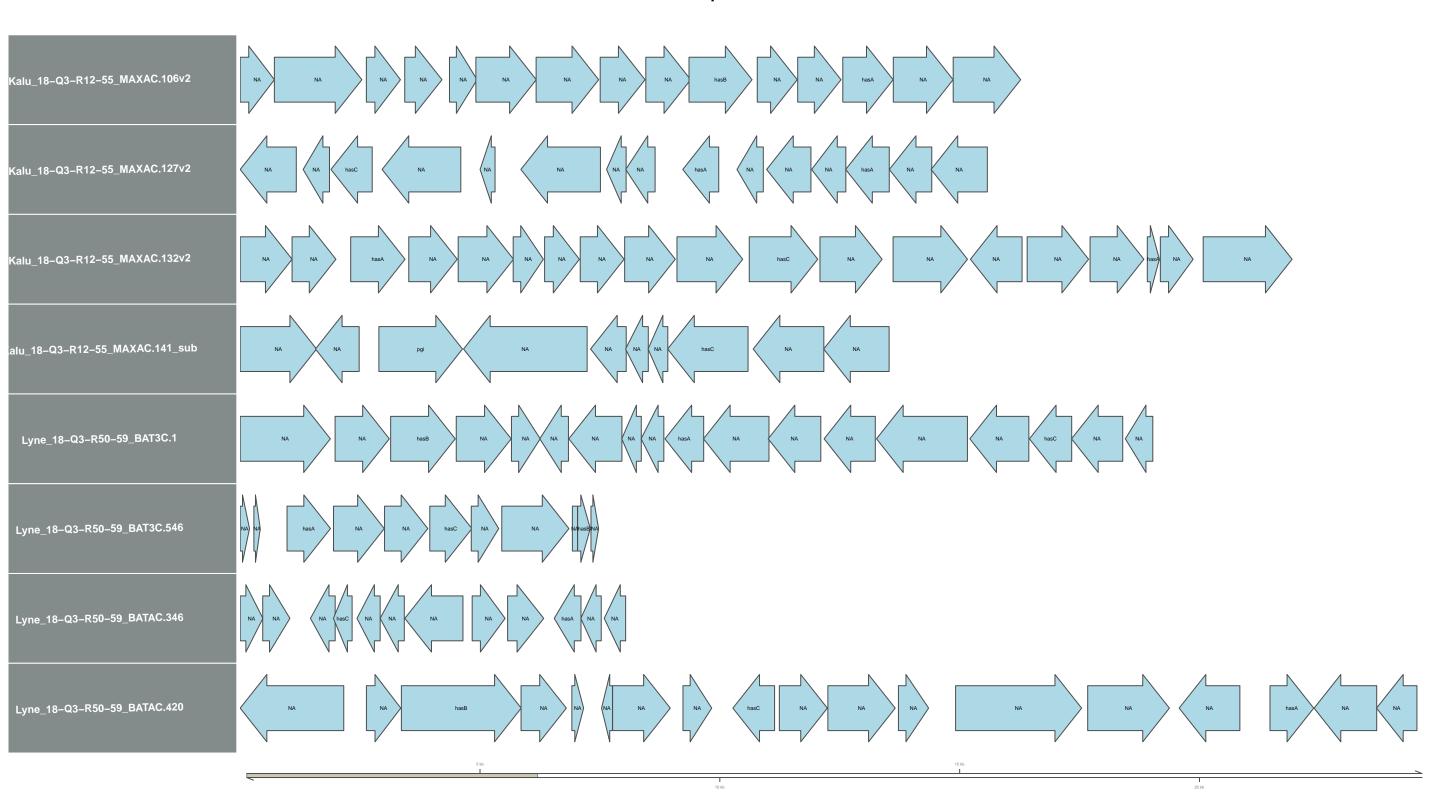


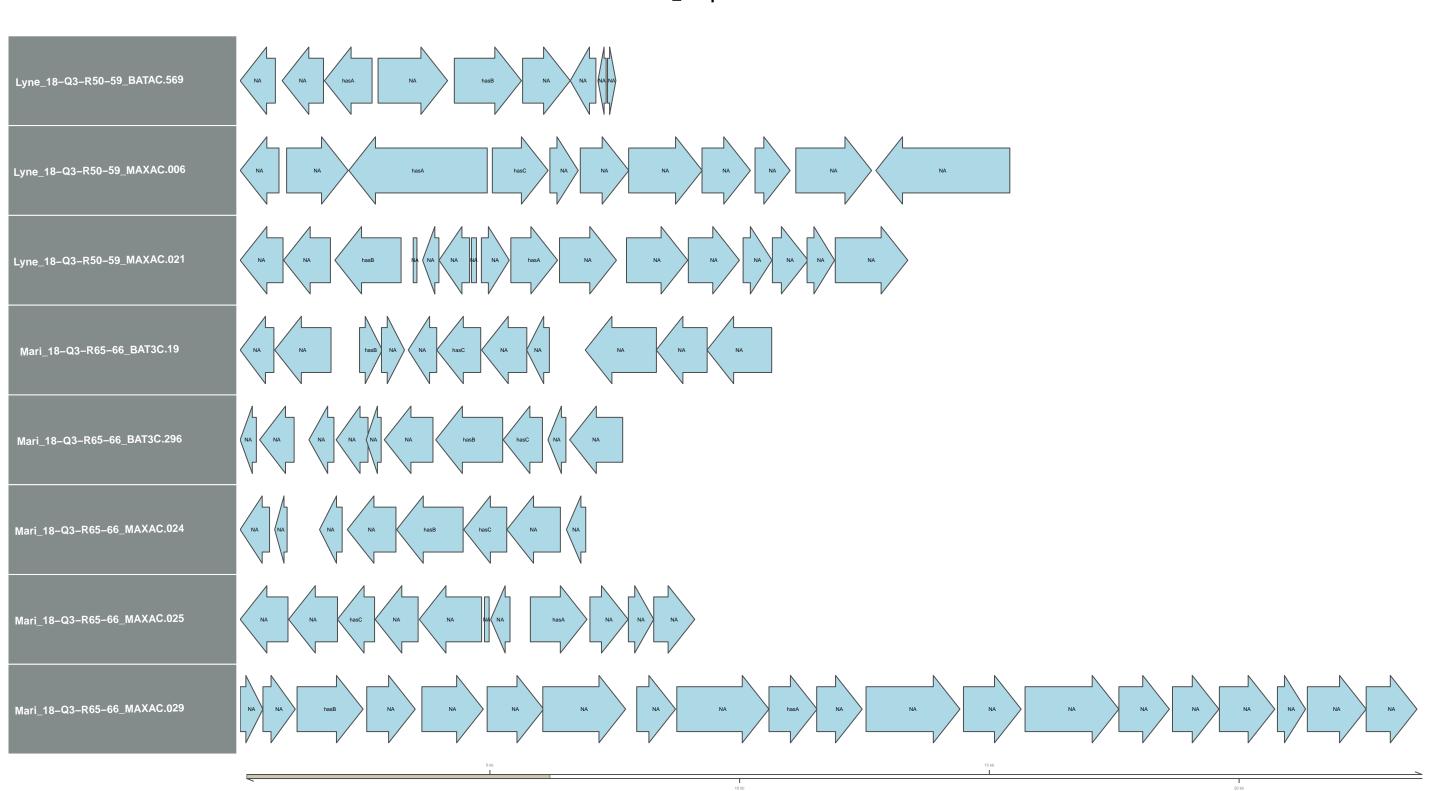


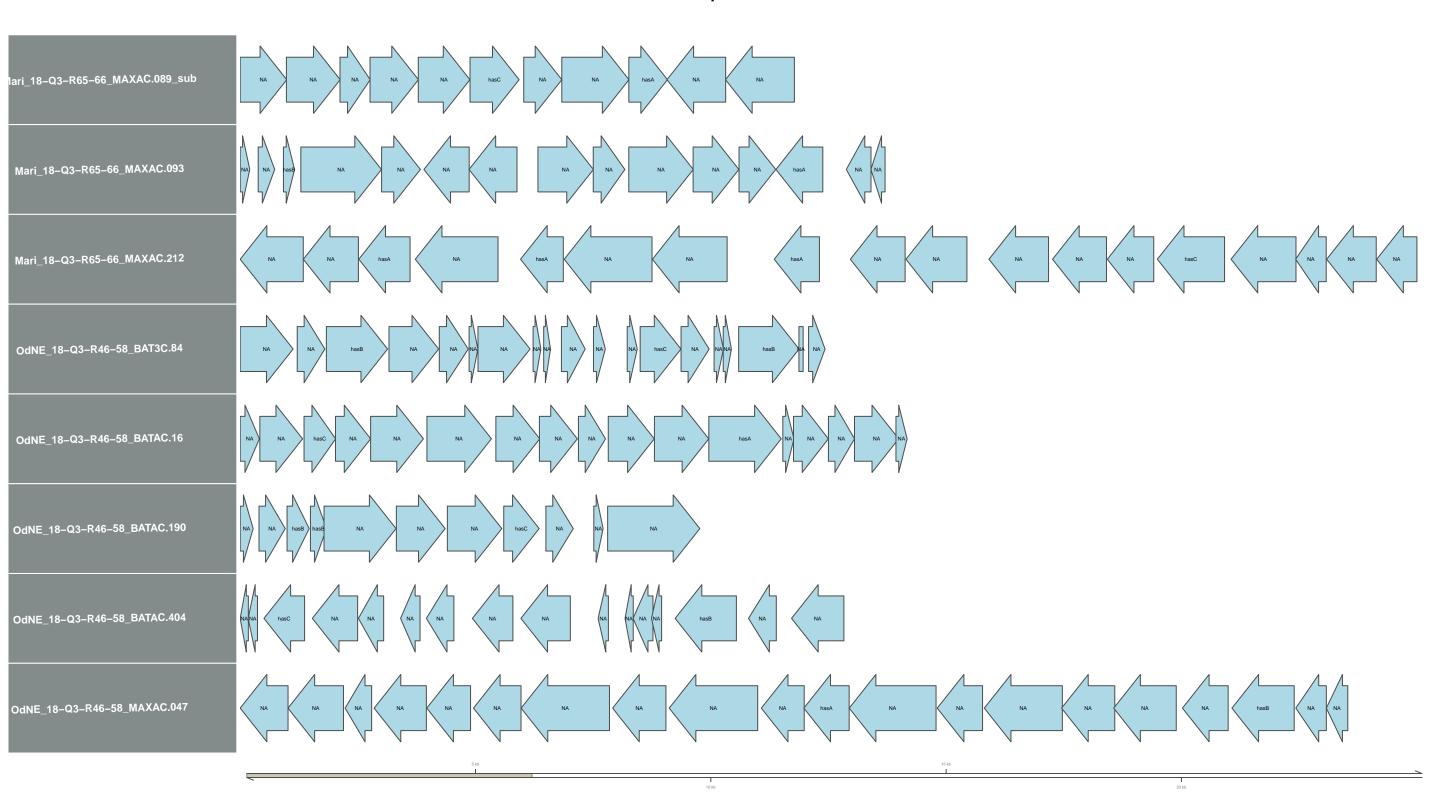


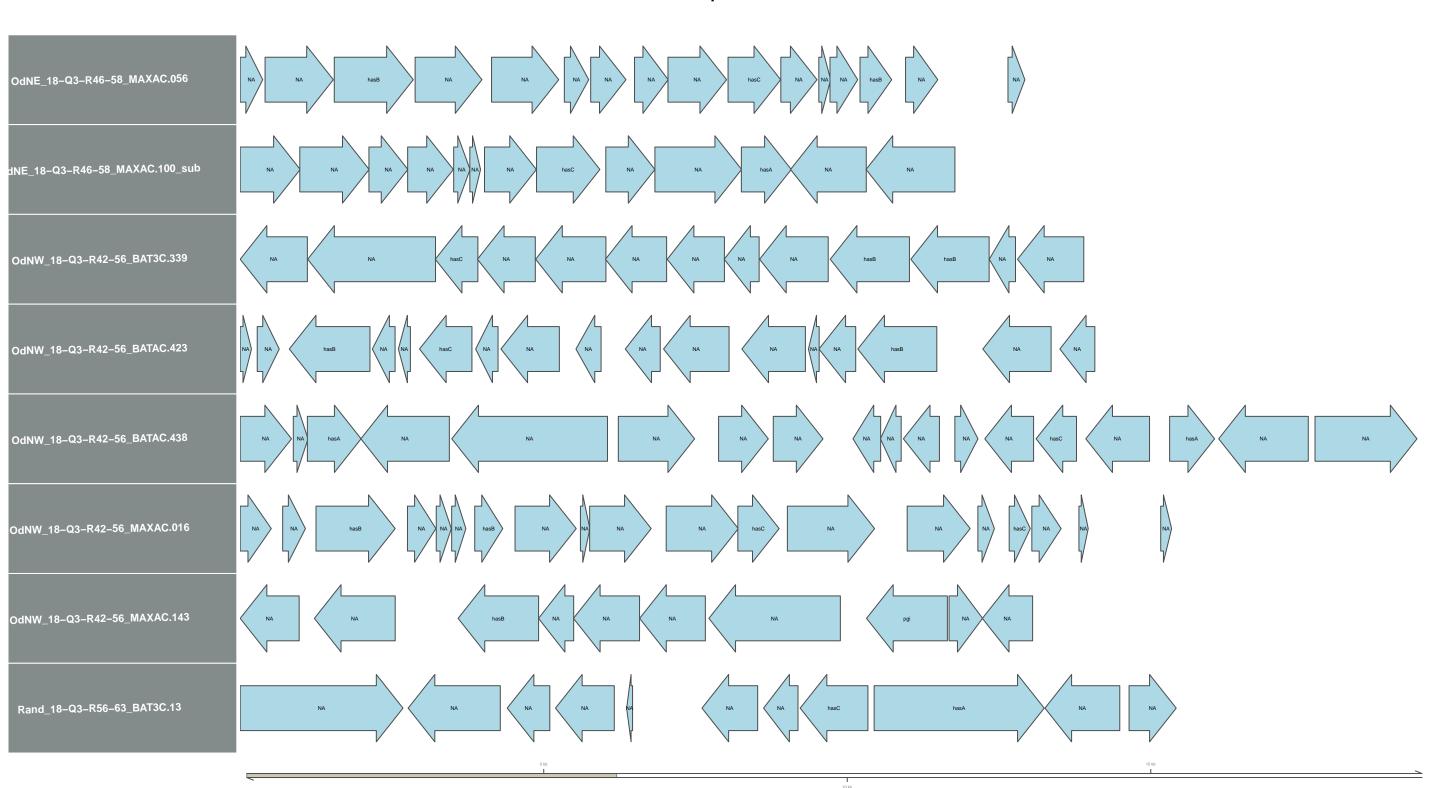


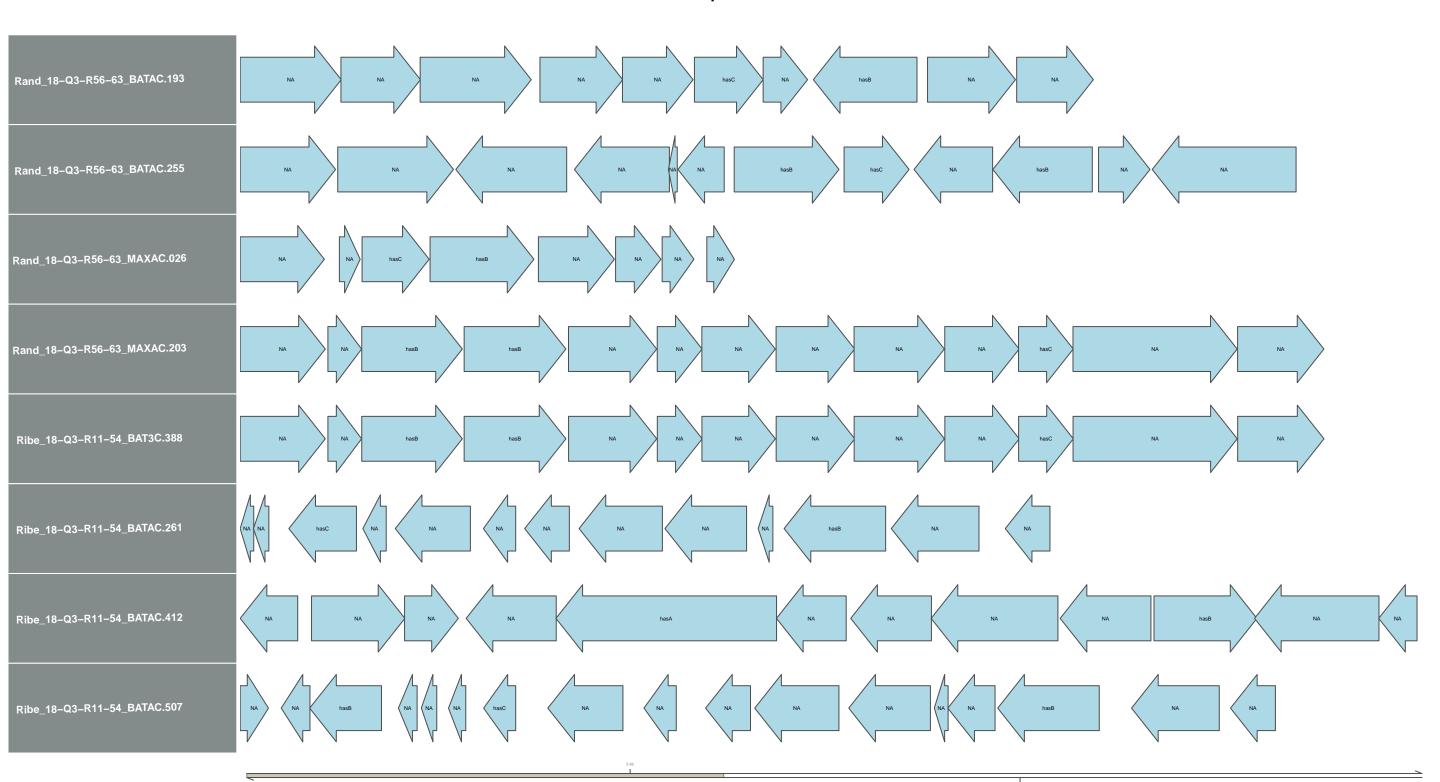


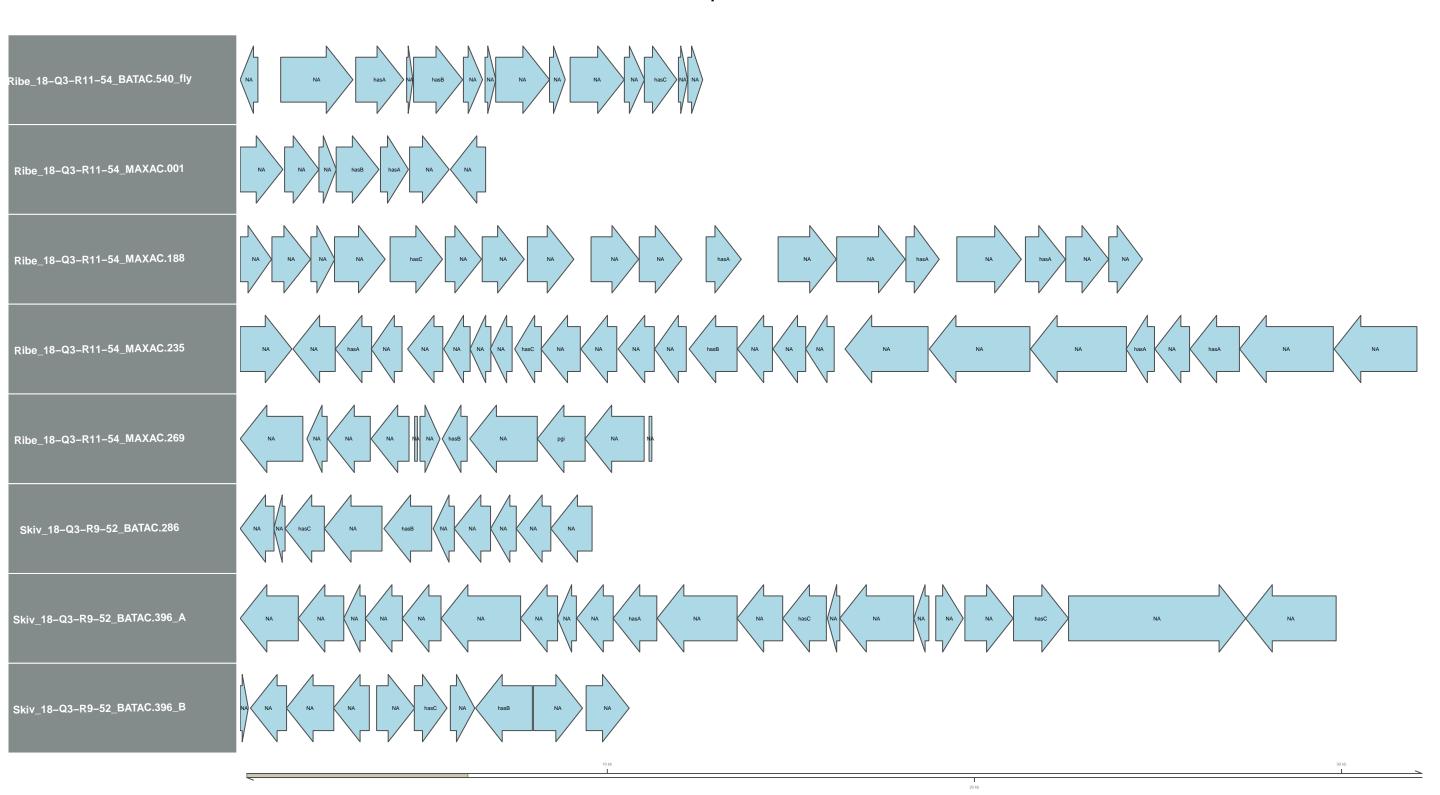


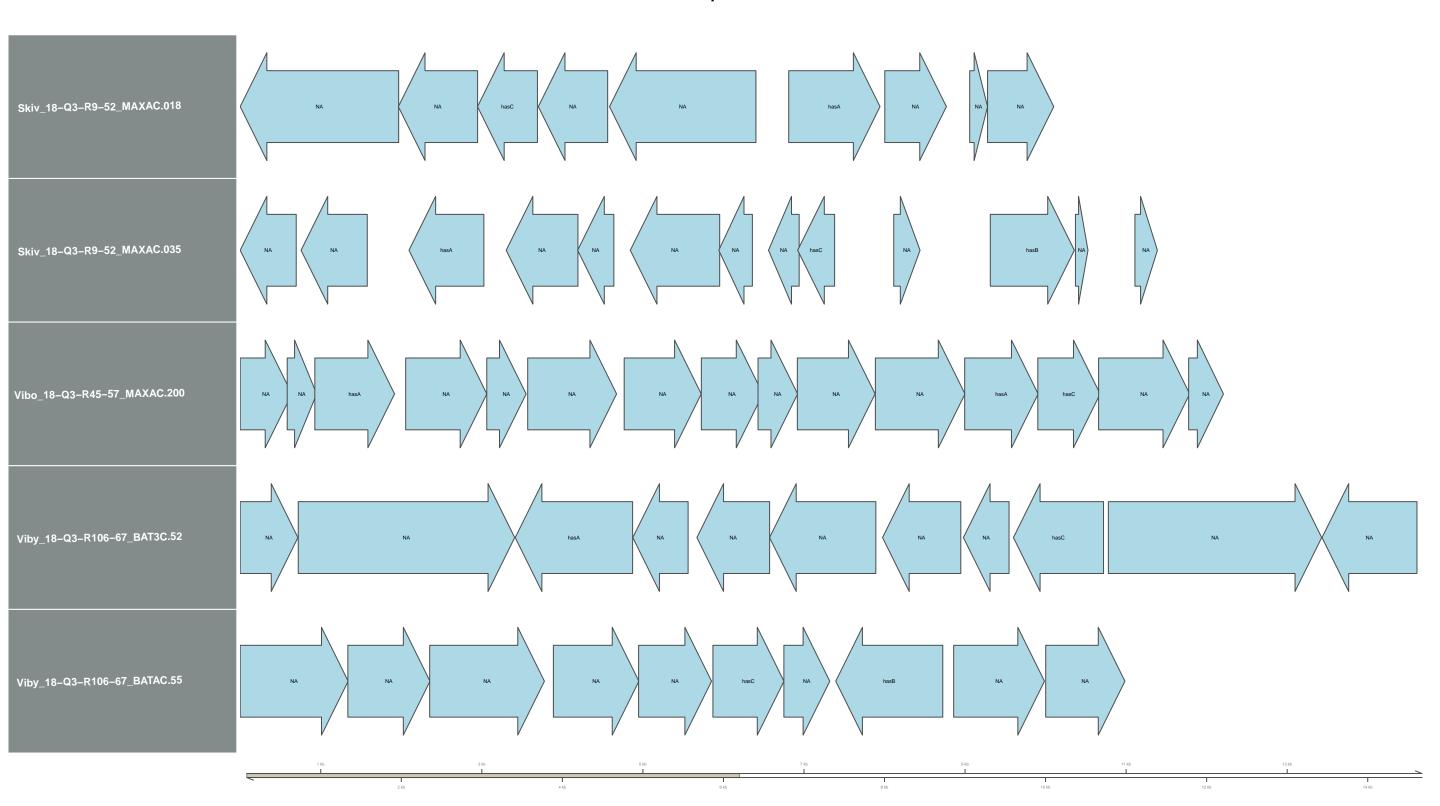












47	Fred_18-Q3-R57-64_BAT3C.352	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Flavobacteriales;f_PHOS-HE28;g_PHOS-HE28;s_	tig00022679-10-905090	52888	hasB	01818
48	Fred_18-Q3-R57-64_BAT3C.720	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Rhodocyclaceae;g_Accumulibacter;s_	tig00351072-10-2609420	661	hasA	01412
49	Fred_18-Q3-R57-64_BATAC.269	d_Bacteria;p_FEN-1099;c_FEN-1099;o_;f_;g_;s_	tig00010798-10-3084350	150044	hasA	02986
50	Fred_18-Q3-R57-64_BATAC.284	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Competibacterales;f_Competibacteraceae;g_Competibacter,s_	tig00002776-10-4696730	89020	hasA	03063
51	Fred_18-Q3-R57-64_BATAC.466	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanithobacteraceae;g_Ga0077548;s_	tig00004636-10-7134330	291854	hasB	01181
52	Fred_18-Q3-R57-64_BATAC.80	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Saprospiraceae;g_OLB9;s_	tig01546531-10-42007240	2870716	hasB	03845
53	Fred_18-Q3-R57-64_MAXAC.004	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Rubrivivax;s_	tig00012388-10-2001380	35851	hasB	01922
54	Fred_18-Q3-R57-64_MAXAC.073	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Porticoccaceae;g_;s_	tig00351274-10-13806640	1211426	hasC	02948
55	Fred_18-Q3-R57-64_MAXAC.220	d_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_Streptococcus infantarius	tig00001084-10-19102340	675892	hasC	00765
56	Fred_18-Q3-R57-64_MAXAC.250	d_Bacteria;p_Acidobacteriota;c_Blastocatellia;o_Pyrinomonadales;t_Pyrinomonadaceae;g_;s_	tig00013653-10-380590	8895	hasA	03179
57	Fred_18-Q3-R57-64_MAXAC.276	d_Bacteria;p_Myxococcota;c_Polyangia;o_Polyangiales;f_Sandaracinaceae;g_;s_	tig00000756-10-19749050	624654	hasA	00551
58	Fred_18-Q3-R57-64_MAXAC.287	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Competibacterales;f_Competibacteraceae;g_Competibacter;s_	tig01547371-10-1541370	25899	hasA	04536
59	Fred_18-Q3-R57-64_MAXAC.347	d_Bacteria;p_Myxococcota;c_Polyangia;o_Polyangiales;f_Polyangiaceae;g_;s_	tig00000646-10-27274520	525962	hasA	00462
60	Fred_18-Q3-R57-64_MAXAC.396_cln	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Reyranellales;f_Reyranellaceae;g_;s_	tig00000039-10-53363560	239600	hasB	00233
61	Hade_18-Q3-R52-61_BAT3C.212	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_JJ008;s_	tig00407653-10-1926590	184766	hasB	02514
62	Hade_18-Q3-R52-61_BAT3C.352	d_Bacteria;p_Actinobacteriota;c_Thermoleophilia;o_Solirubrobacterales;f_70-9;g_67-14;s_	tig00000830-10-14143930	47639	hasB	00048
63	Hade_18-Q3-R52-61_BATAC.282	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_UBA5518;g_UBA5518;s_UBA5518 sp002396625	tig00005254-10-4088780	374350	hasB	02060
64	Hade_18-Q3-R52-61_BATAC.34	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_JJ006;s_	tig00001009-10-10233600	538865	hasB	00559
65	Hade_18-Q3-R52-61_BATAC.500	dBacteria.pBacteroidota.cBacteroidia.oChitinophagales:fSaprospiraceae.gOLB9;s	tig00408953-10-2470440	234242	hasB	03349
66	Hade_18-Q3-R52-61_BATAC.713	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_AKYH767;f_b-17BO;g_UBA4416;s_	tig00011384-10-1936590	74757	hasA	01644
67	Hade_18-Q3-R52-61_MAXAC.028	d_Bacteria;p_Bacteroidota;c_lgnavlbacteria;o_SJA-28;f_B-1AR;g_UBA2330;s_	tiq00011331-10-1976460	67338	hasA	01975
68	Hade_18-Q3-R52-61_MAXAC.042	d_Bacteria;p_Chloroflexota;c_Anaerolineae;o_Anaerolineales;f_envOPS12;g_OLB14;s_	tig00014449-10-1135470	35254	hasA	01507
69	Hade_18-Q3-R52-61_MAXAC.064	d_Bacteria.p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Saprospiraceae;g_;s_	tig00406432-10-6385110	446099	hasB	02635
70	Hade_18-Q3-R52-61_MAXAC.389	d_Bacteria.p_Bacteroidota.c_Bacteroidia.o_Chitinophagales.f_UBA2359.g_;s_	tig00002297-10-7587310	98472	hasA	00664
71	Hade_18-Q3-R52-61_MAXAC.390	d_Bacteria.p_Proteobacteria;c_Gammaproteobacteria;o_Thiotrichales;f_Thiotrichaceae.g_Thiofilim;s_	tiq0000011-10-40151770	2373044	hasA	02279
72	Hirt_18-Q3-R61-65_BAT3C.202	d_Bacteria.p_Actinobacteriota;c_Actinobacteria.p_Actinomycetales;f_Dermatophilaceae;g_Austwickia;s_	tig00316410-10-10243700	713713	hasA	02919
73	Hirt_18-Q3-R61-65_BAT3C.279	d_Bacteria.p_ Actinobacteriota;c_Actinobacteria.o_Propionibacteriales;f_Propionibacteriaceae;g_Micropruina.s_	tig00001155-10-14562110	894799	hasA	02505
74	Hirt_18-Q3-R61-65_BAT3C.578	d_Bacteria.p_Bacteroidota;c_Bacteroidfa;o_Chifinophagales:f_Saprospiraceae;g_;s_	tig00001406-10-10549010	895651	hasA	00761
75	Hirt_18-Q3-R61-65_BATAC.270	d_Bacteria.p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Saprospiraceae;g_OLB9;s_	tig00002097-10-8877200	666017	hasB	00598
76	Hirt_18-Q3-R61-65_BATAC.511		tig00002097=10-8877200	699132	hasB	01870
		d_Bacteria;p_Bacterioidota;c_Bacterioida;o_Chitinophagales;f_Saprospiraceae;g_;s_	tig00001443-10-11952200			
77	Hirt_18-Q3-R61-65_MAXAC.305	d_Bacteria;p_Bdellovibrionota;c_Bdellovibrionia;o_Bdellovibrionales;f_UBA1609;g_;s_	.,,	474635	hasA	02148
78	Hjor_18-Q3-R7-51_BAT3C.94	d_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Actinomycetales;f_Dermatophilaceae;g_Phycicoccus;s_	tig00001034-10-18376270	668318	hasA	00662
79	Hjor_18-Q3-R7-51_BATAC.166	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Chitinophagaceae;g_Ferruginibacter;s_	tig00120023-10-2656750	77633	hasA	02846
80	Hjor_18-Q3-R7-51_MAXAC.088	d_Bacteria;p_Actinobacteriota;c_Actinobacteria;o_Actinomycetales;f_Dermatophilaceae;g_GCA-2748155;s_	tig00120094-10-3563900	340725	hasA	03029
81	Kalu_18-Q3-R12-55_BAT3C.19	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Pedosphaerales;f_UBA9464;g_;s_	tig00001403-10-8768320	83245	hasB	00062
82	Kalu_18-Q3-R12-55_BAT3C.288	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chilinophagales;f_Saprospiraceae;g_;s_	tig00003588-10-2760750	46719	hasB	01149
83	Kalu_18-Q3-R12-55_BAT3C.359	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Burkholderiales;t_Burkholderiaceae;g_;s_	tig00001165-10-8548430	648471	hasA	00618
84	Kalu_18-Q3-R12-55_BAT3C.361	d_Bacteria;p_Chloroflexota;c_Anaerolineae;o_Anaerolineales;f_envOPS12;g_UBA12294;s_	tig00000461-10-23099880	1405172	hasA	01305
85	Kalu_18-Q3-R12-55_BATAC.81	d_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_UBA5518;g_UBA5518;s_	tig00007458-10-904370	59826	hasA	03756
86	Kalu_18-Q3-R12-55_MAXAC.026	d_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Ga0077559;s_	tig00440498-10-14308980	1386948	hasA	02822
87	Kalu_18-Q3-R12-55_MAXAC.032	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Chitinophagales;f_Saprospiraceae;g_;s_	tig00000001-10-55188560	2721544	hasB	02091
88	Kalu_18-Q3-R12-55_MAXAC.106v2	d_Bacteria;p_Chloroflexota;c_Anaerolineae;o_Promineofilales;t_Promineofilaceae;g_GCA-2699125;s_	tig00000173-10-21988890	341844	hasA	00291
89	Kalu_18-Q3-R12-55_MAXAC.127v2	d_Bacteria;p_Bacteroidota;c_Ignavibacteria;o_Ignavibacteriales;f_Ignavibacteriaceae;g_;s_	tig00000009-10-45985110	3815982	hasA	03184
90	Kalu_18-Q3-R12-55_MAXAC.132v2	d_Bacteria;p_Nitrospirota;c_Nitrospiria;o_Nitrospirales;f_Nitrospiraceae;g_Nitrospira;s_	tig00001930-10-7323120	329488	hasA	01636
91	Kalu_18-Q3-R12-55_MAXAC.141_sub	d_Bacteria;p_Acidobacteriota;c_Blastocatellia;o_Pyrinomonadales;f_Pyrinomonadaceae;g_OLB17;s_	tig00000024-10507670-32924090	2164334	hasC	03014
92	Lyne_18-Q3-R50-59_BAT3C.1	$\label{lem:d_bacteria} d_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Sphingomonadales.f_Sphingomonadaceae:g_Ga0077559;s_$	tig00320340-10-18168060	361818	hasA	00344