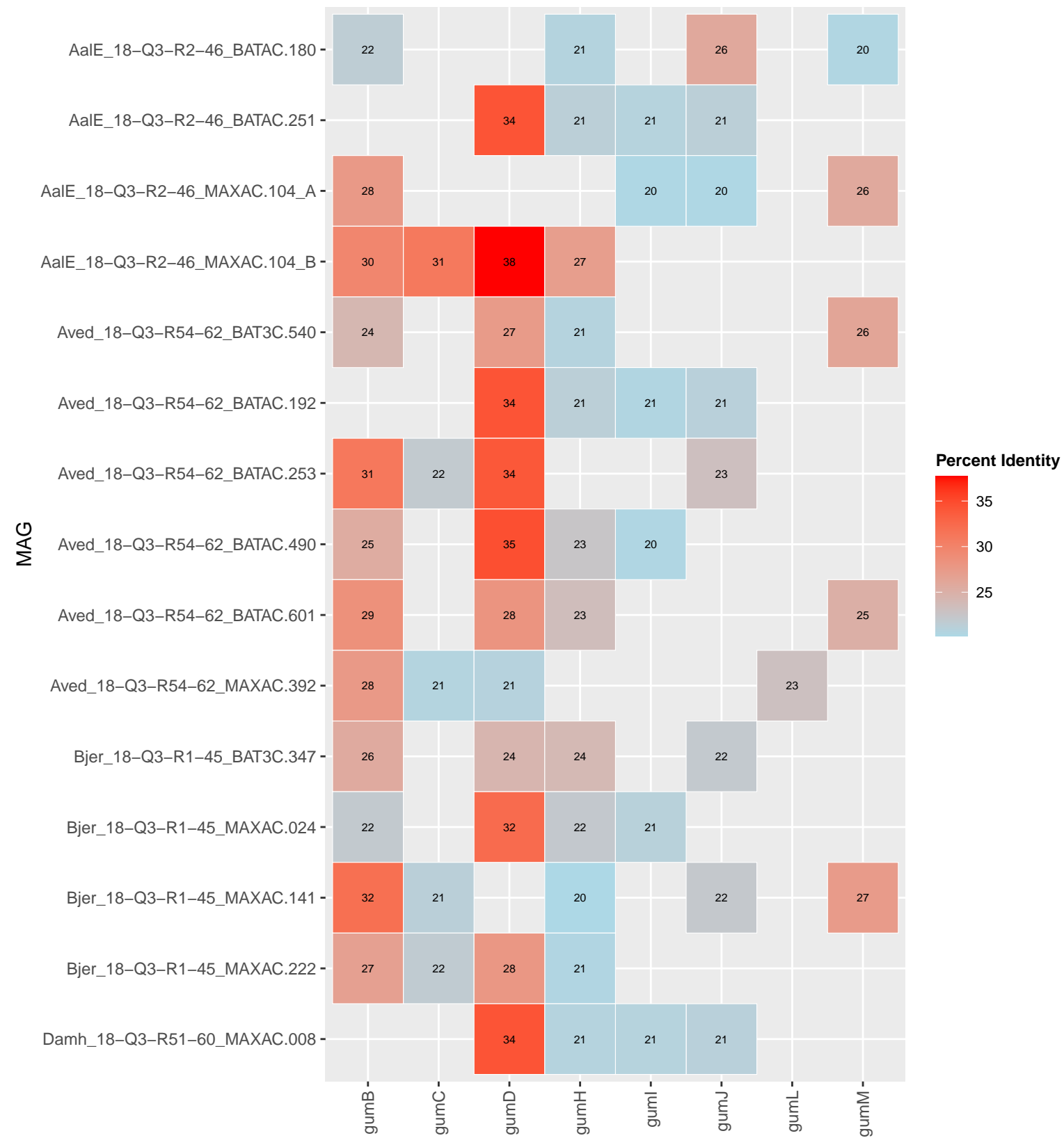
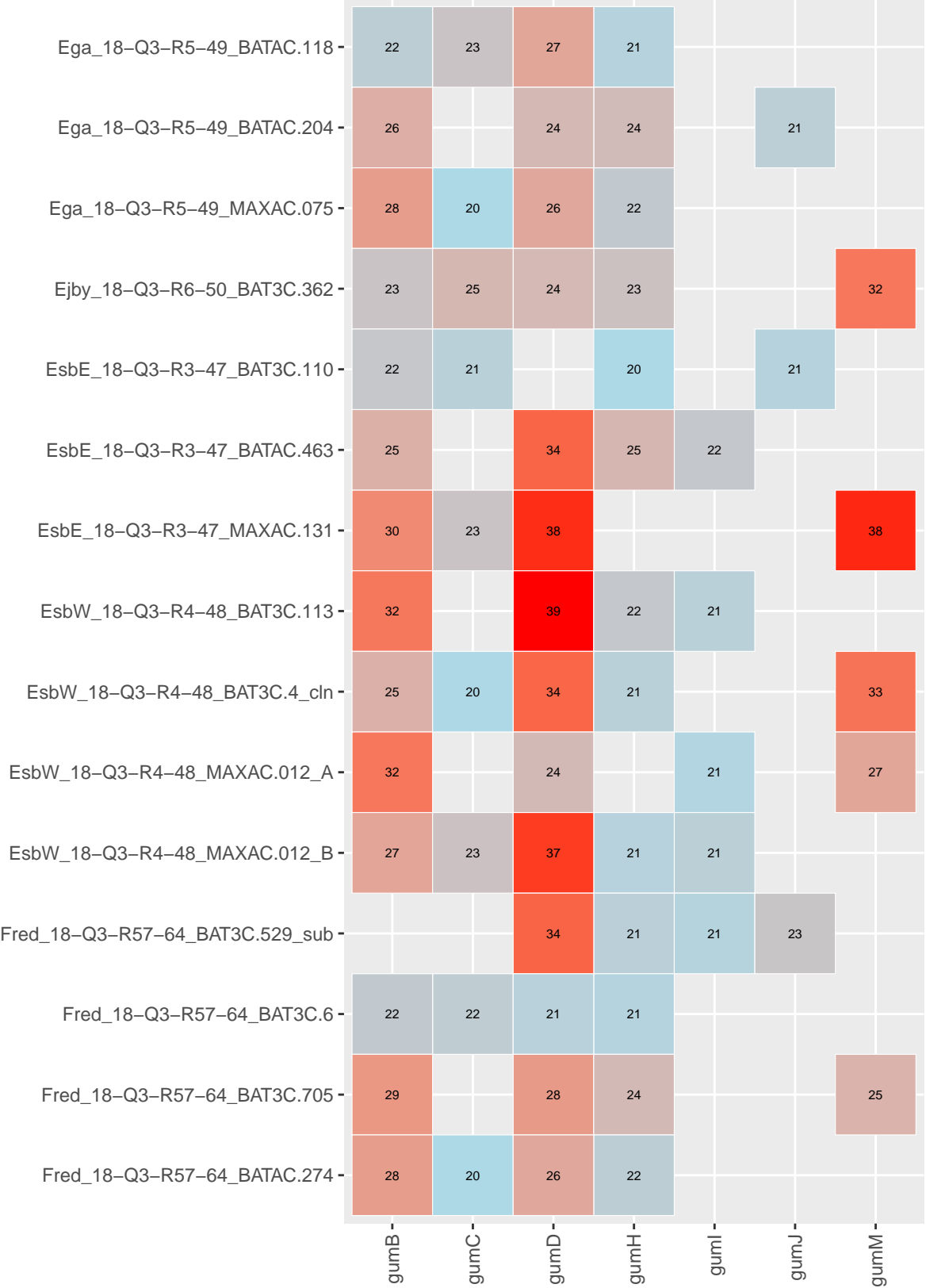


xanthan Heatmap

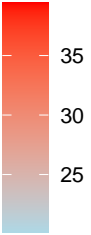


xanthan Heatmap

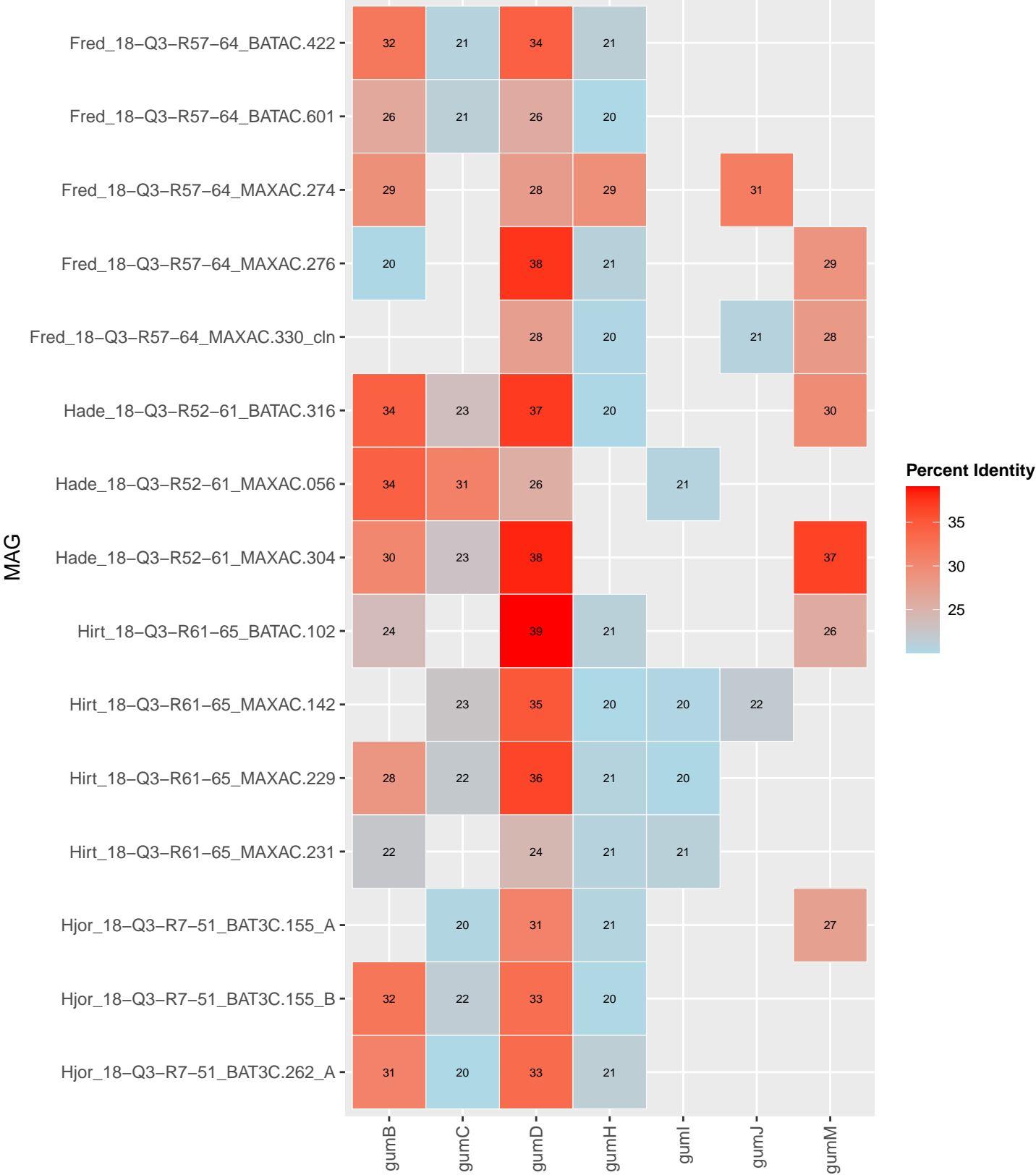
MAG



Percent Identity

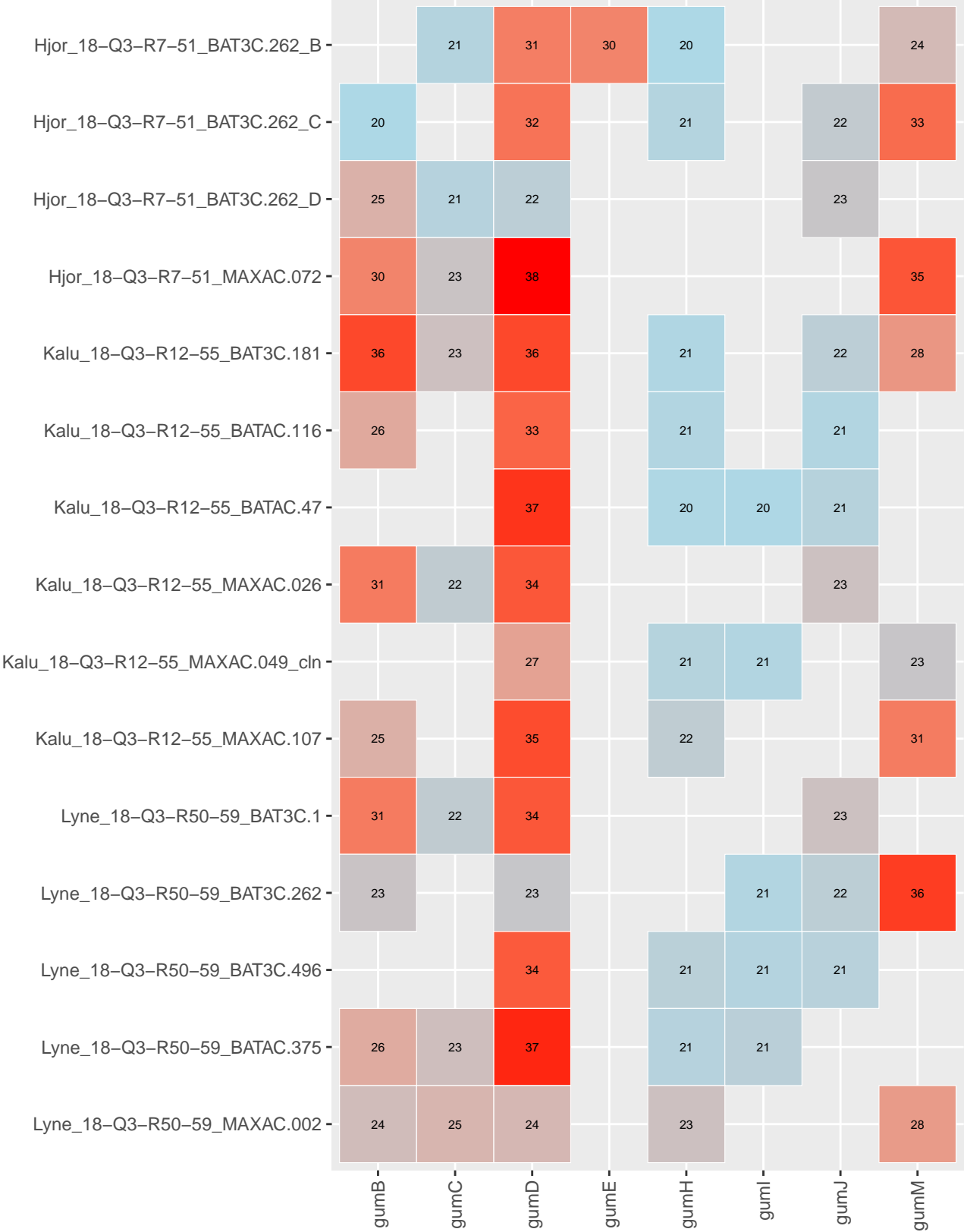


xanthan Heatmap

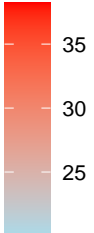


xanthan Heatmap

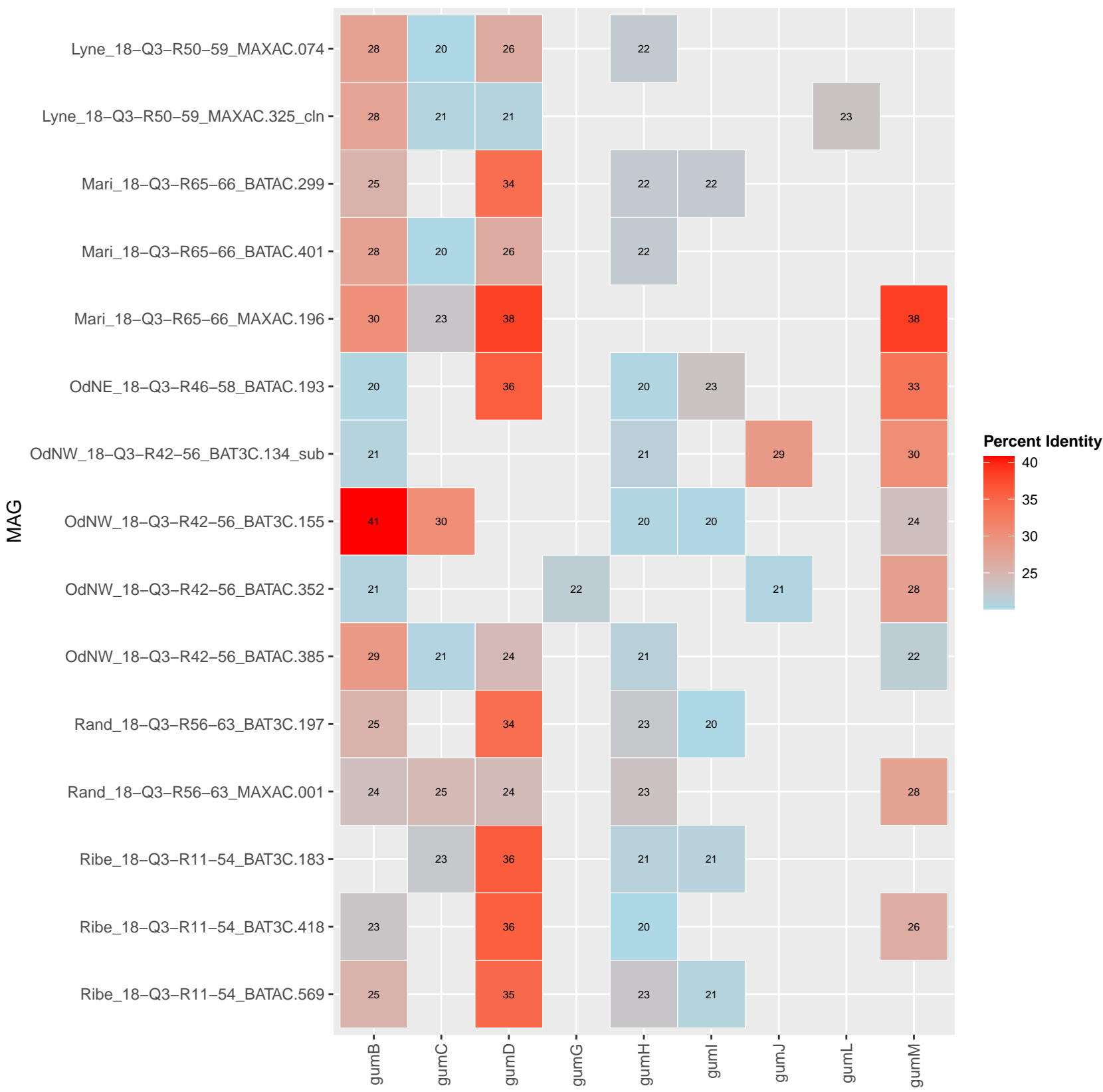
MAG



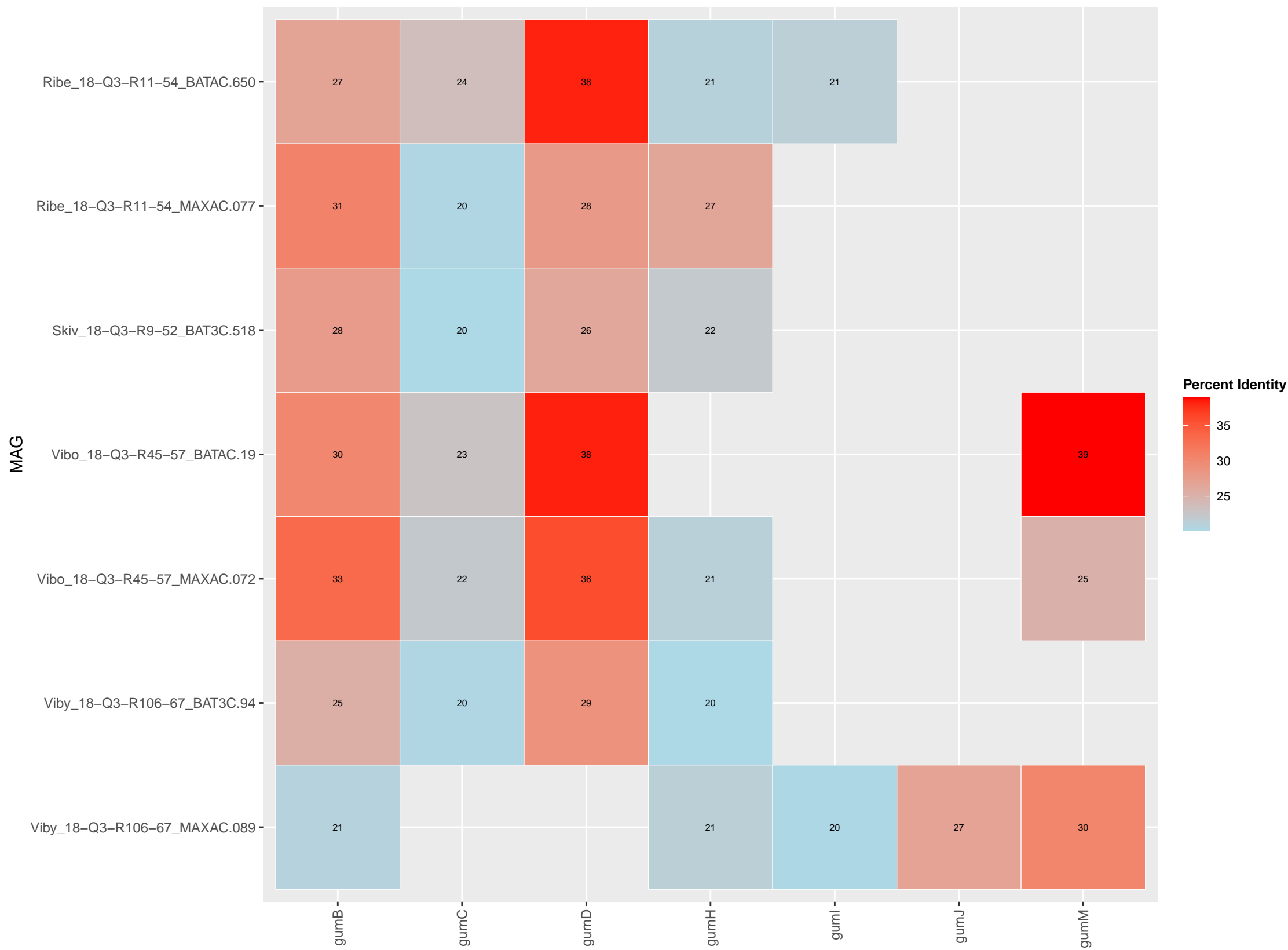
Percent Identity



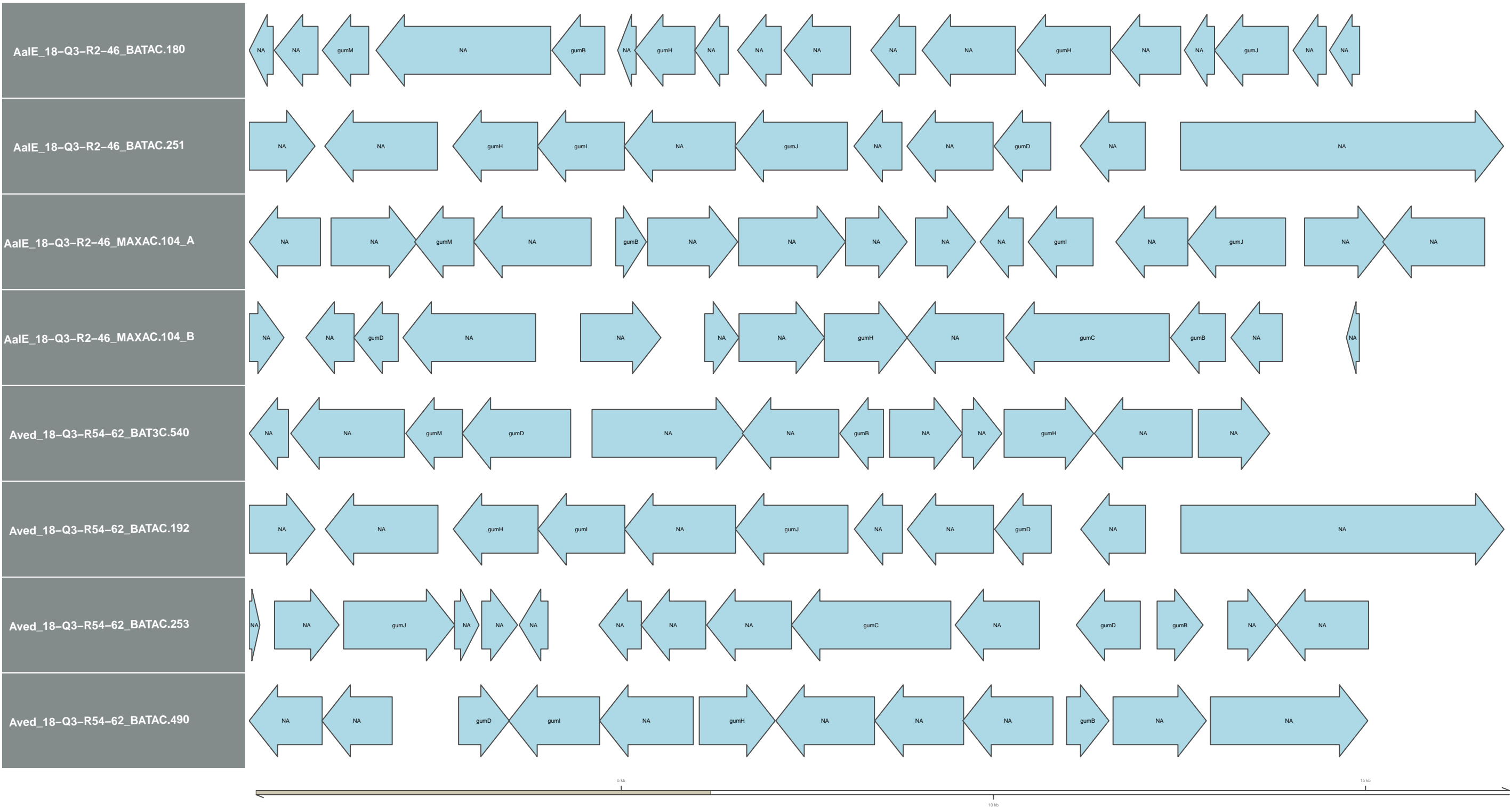
xanthan Heatmap

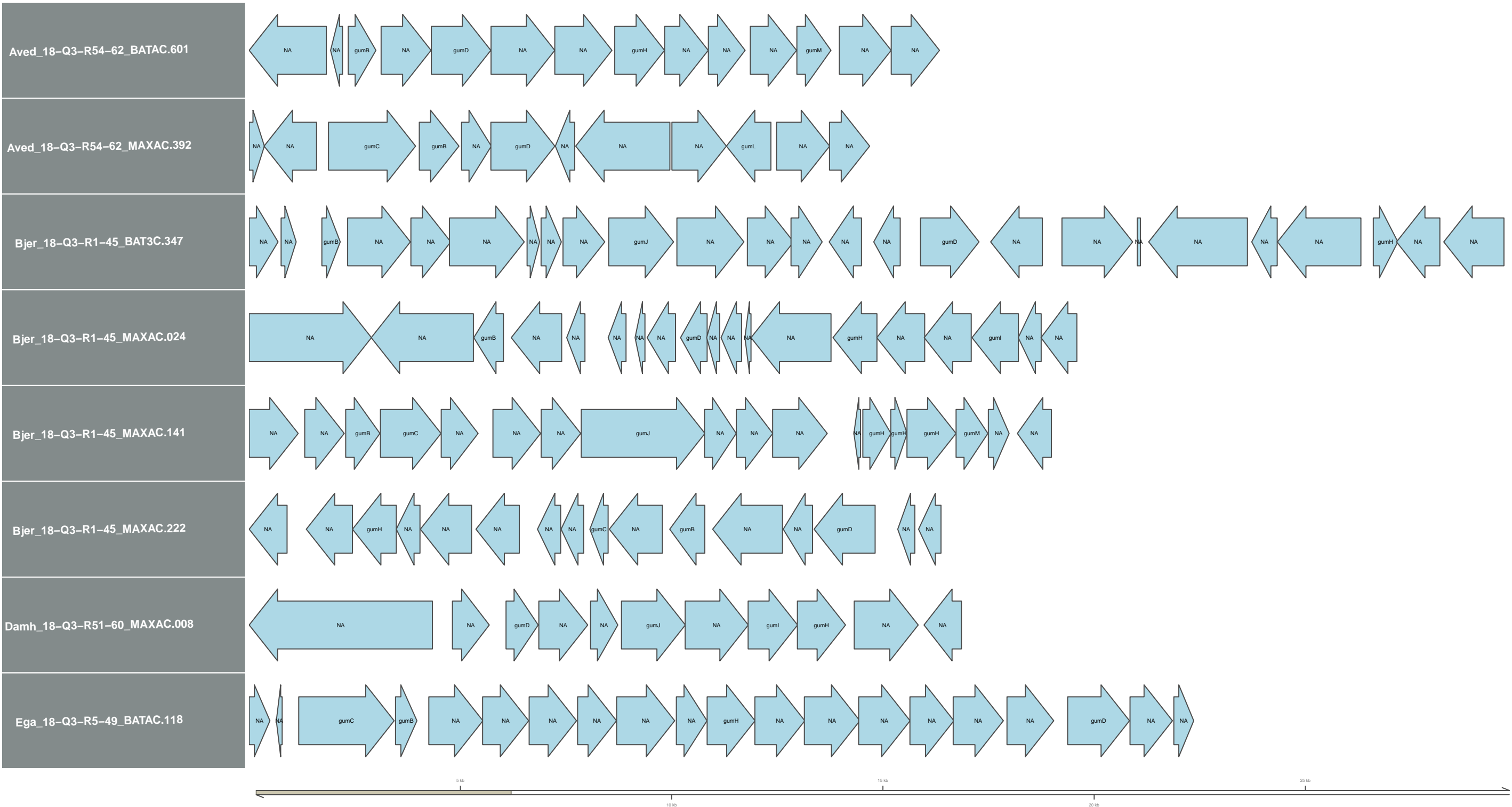


xanthan Heatmap

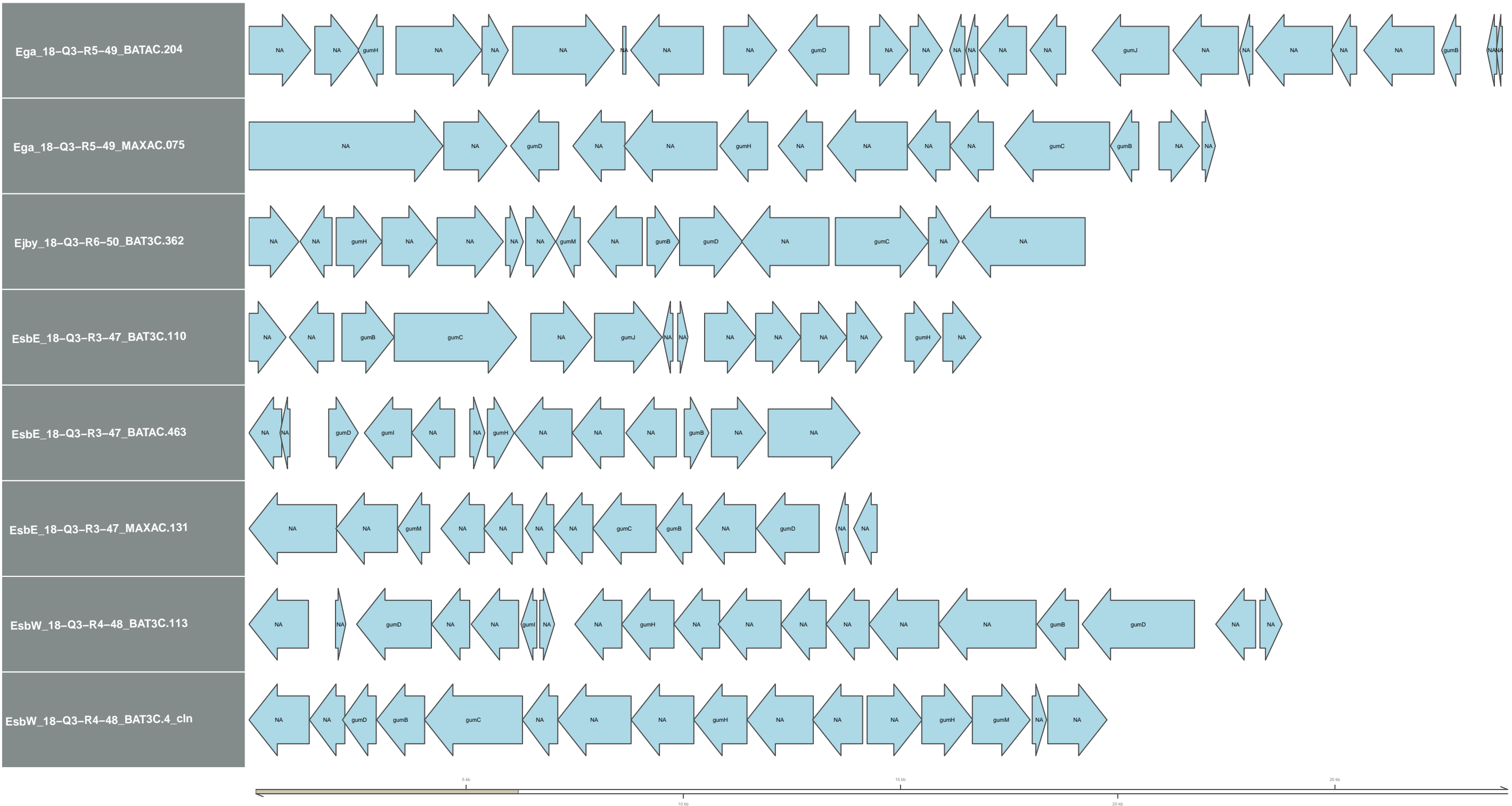


xanthan

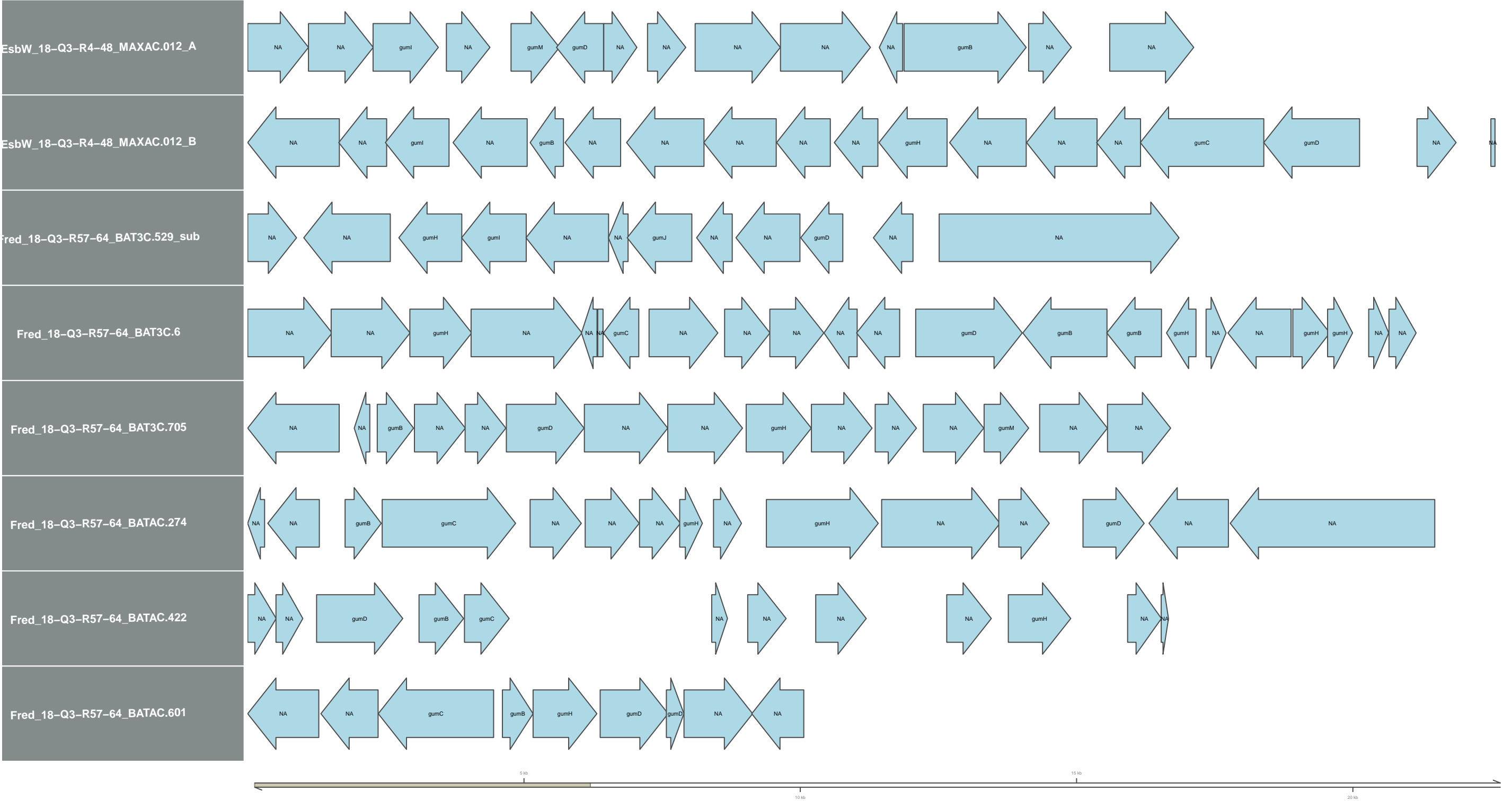


xanthan

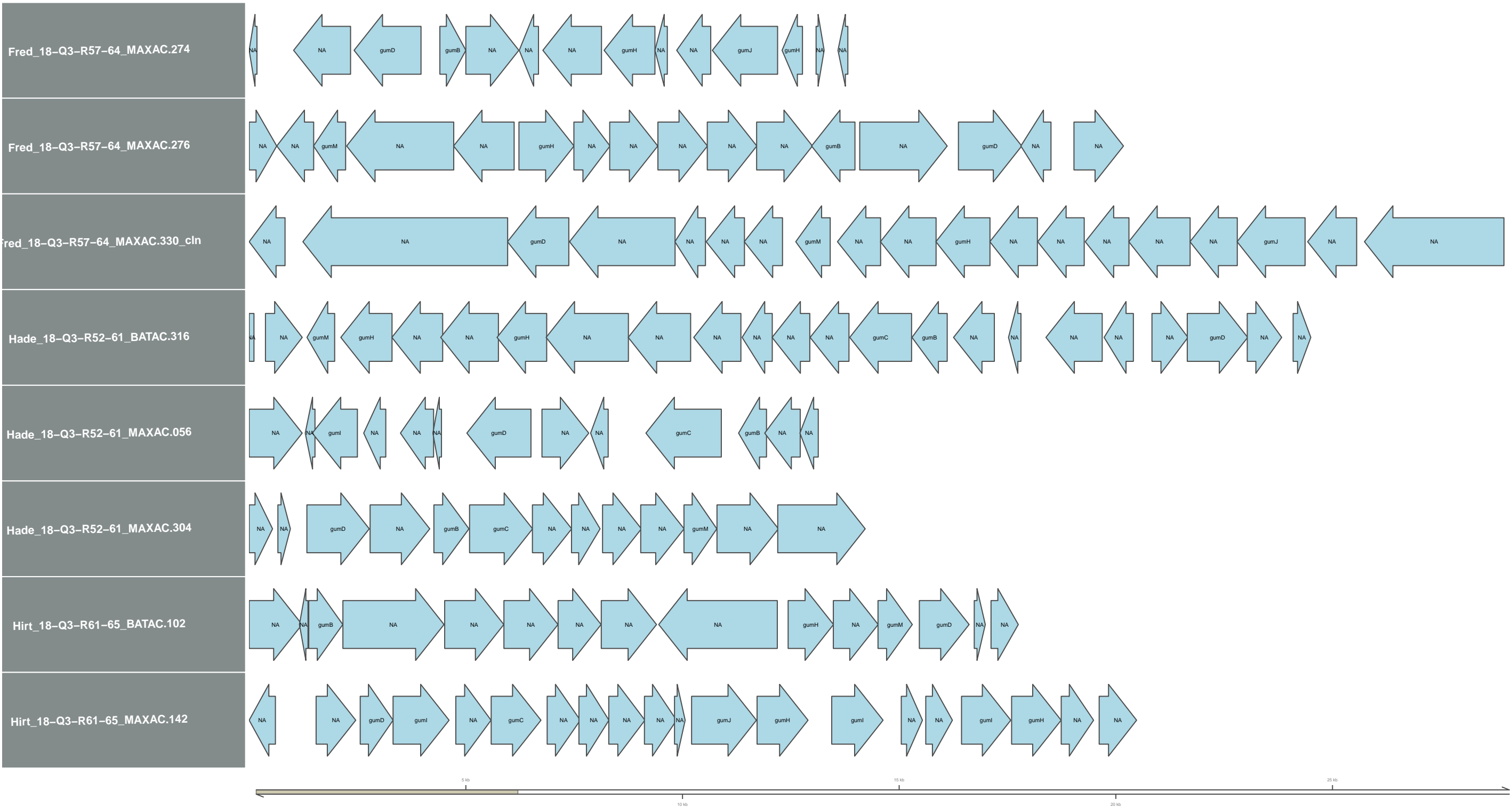
xanthan

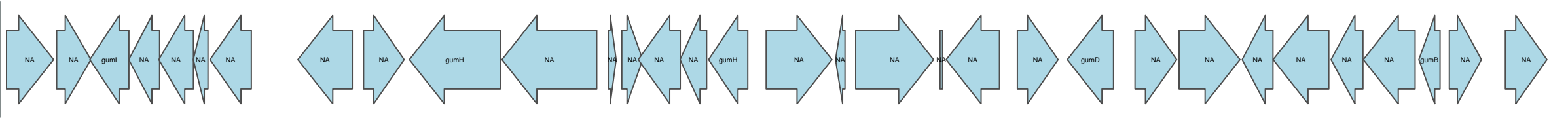
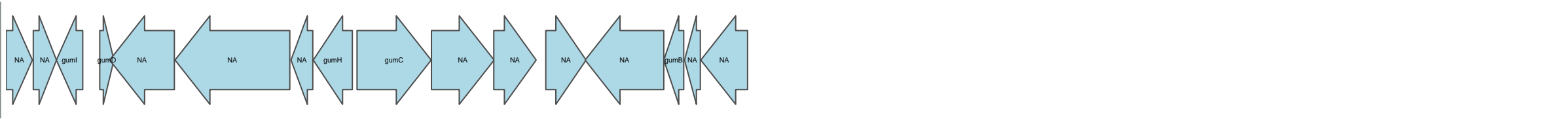


xanthan

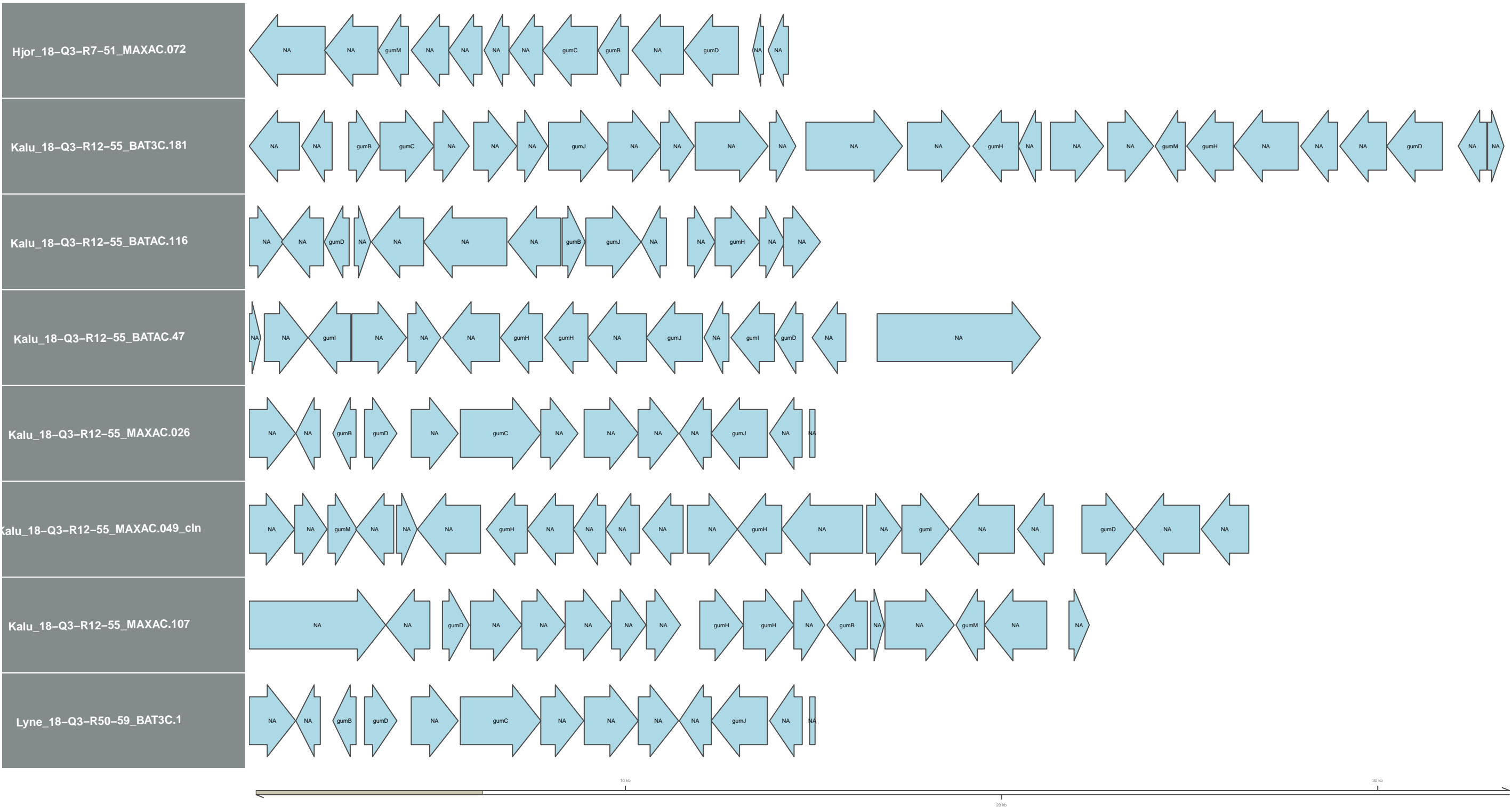


xanthan



[illegible]

xanthan



xanthan

The figure displays a genomic map of the *xanthan* locus, comparing gene organization across seven different strains. The strains are listed on the left: Lyne_18-Q3-R50-59_BAT3C.262, Lyne_18-Q3-R50-59_BAT3C.496, Lyne_18-Q3-R50-59_BATAC.375, Lyne_18-Q3-R50-59_MAXAC.002, Lyne_18-Q3-R50-59_MAXAC.074, lyne_18-Q3-R50-59_MAXAC.325_cln, Mari_18-Q3-R65-66_BATAC.299, and Mari_18-Q3-R65-66_BATAC.401. Genes are represented by blue arrows indicating their orientation and relative position. Some genes are labeled with names like gumD, gumJ, gumH, gumL, gumB, gumM, gumI, gumC, and NA. A scale bar at the bottom indicates distances in kilobases (kb), with markers at 5 kb, 10 kb, 15 kb, and 20 kb.

Lyne_18-Q3-R50-59_BAT3C.262

Lyne_18-Q3-R50-59_BAT3C.496

Lyne_18-Q3-R50-59_BATAC.375

Lyne_18-Q3-R50-59_MAXAC.002

Lyne_18-Q3-R50-59_MAXAC.074

lyne_18-Q3-R50-59_MAXAC.325_cln

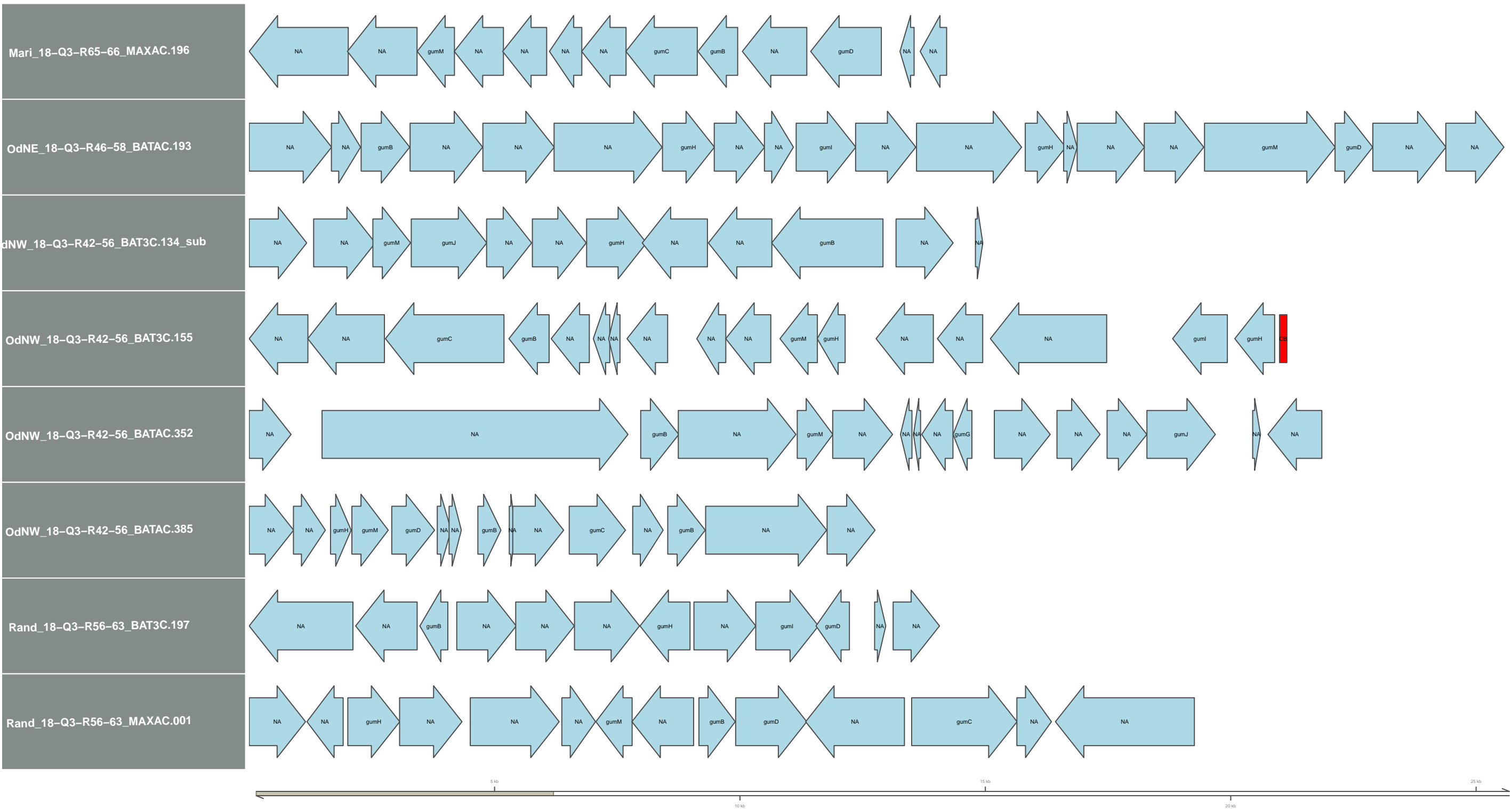
Mari_18-Q3-R65-66_BATAC.299

Mari_18-Q3-R65-66_BATAC.401

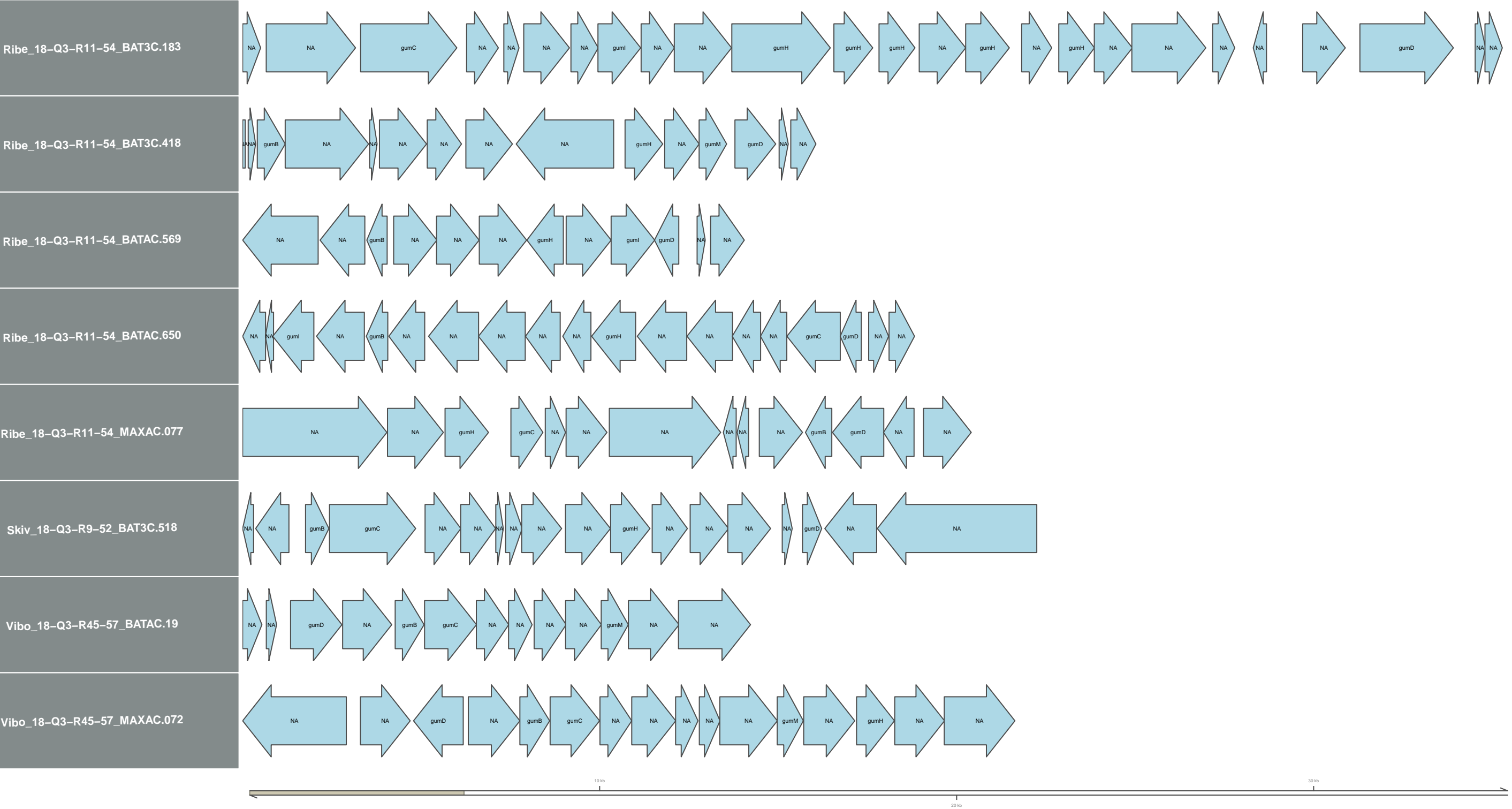
5 kb 10 kb 15 kb 20 kb

Mari_18-Q3-R65-66_BATAC.401

xanthan

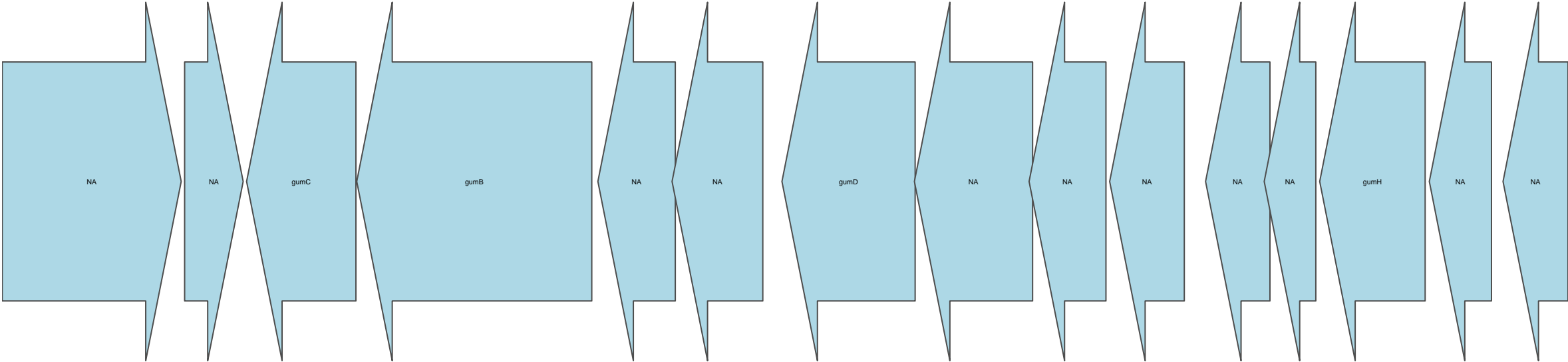


xanthan

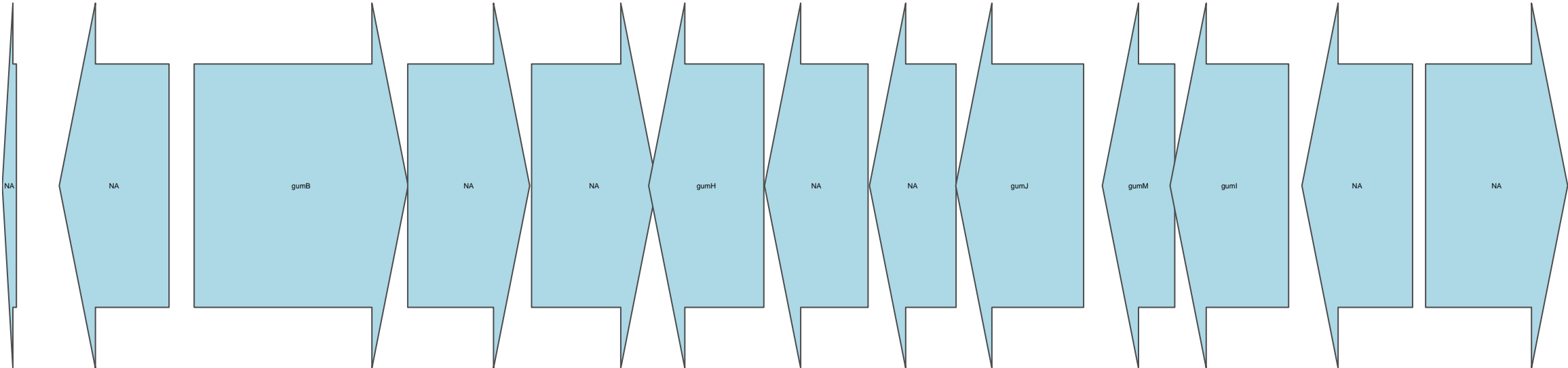


xanthan

Viby_18-Q3-R106-67_BAT3C.94



Viby_18-Q3-R106-67_MAXAC.089



16	Ega_18-Q3-R5-49_BATAC.204	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__s__	tig00192215-10-2989550	294342	gumB	04063
17	Ega_18-Q3-R5-49_MAXAC.075	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__AKYH767-A;f__OLB10;g__s__	tig00001589-10-4219360	268659	gumB	00629
18	Ejby_18-Q3-R6-50_BAT3C.362	d__Bacteria;p__Myxococcota;c__UBA796;o__UBA796;f__g__s__	tig00007529-10-1033940	79033	gumB	02517
19	EsbE_18-Q3-R3-47_BAT3C.110	d__Bacteria;p__Desulfohalobacterota;c__Syntrophia;o__Syntrophales;f__UBA2192;g__s__	tig00019446-10-685040	53907	gumB	03007
20	EsbE_18-Q3-R3-47_BATAC.463	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__UBA1936;s__	tig00686159-10-2149040	92977	gumB	03291
21	EsbE_18-Q3-R3-47_MAXAC.131	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Propionivibrio;s__	tig00001009-10-6140660	444305	gumB	01431
22	EsbW_18-Q3-R4-48_BAT3C.113	d__Bacteria;p__Eisenbacteria;c__RBG-16-71-46;o__RBG-16-71-46;f__RBG-16-71-46;g__s__	tig00010058-10-1919270	80600	gumB	01006
23	EsbW_18-Q3-R4-48_BAT3C.4_cln	d__Bacteria;p__Acidobacteriota;c__Thermoanaerobaculia;o__UBA5704;f__g__s__	tig00000001-10-52256180	2106508	gumB	01765
24	EsbW_18-Q3-R4-48_MAXAC.012	d__Bacteria;p__Nitrospirota;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira_A;s__Nitrospira_A sp900170025	tig00000531-10-3969200	313277	gumB	03432
25	Fred_18-Q3-R57-64_BAT3C.529_sub	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__Promineofillales;f__Promineofillaceae;g__GCA-2746795;s__	tig00003031-10-9702930	50025	gumD	00066
26	Fred_18-Q3-R57-64_BAT3C.6	d__Bacteria;p__Gemmatimonadota;c__Gemmatimonadetes;o__Gemmatimonadales;f__GWC2-71-9;g__s__	tig01546545-10-26760560	369917	gumB	01925
27	Fred_18-Q3-R57-64_BAT3C.705	d__Bacteria;p__Acidobacteriota;c__Blastocatellia;o__Pyrinomonadales;f__Pyrinomonadaceae;g__OLB17;s__	tig00000736-10-28401940	58645	gumB	00053
28	Fred_18-Q3-R57-64_BATAC.274	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__AKYH767-A;f__OLB10;g__s__	tig00006488-10-4803740	153988	gumB	01801
29	Fred_18-Q3-R57-64_BATAC.422	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Ga0077523;g__Ga0077526;s__	tig00025436-10-865720	59530	gumB	04324
30	Fred_18-Q3-R57-64_BATAC.601	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Devosiaceae;g__Devosia;s__	tig00007732-10-4356870	282840	gumB	00830
31	Fred_18-Q3-R57-64_MAXAC.274	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Dongiiales;f__Dongiaceae;g__s__	tig00002610-10-11133940	940124	gumB	04577
32	Fred_18-Q3-R57-64_MAXAC.276	d__Bacteria;p__Myxococcota;c__Polyangia;o__Polyangiales;f__Sandaracinaceae;g__s__	tig00001056-10-18270440	829007	gumB	02484
33	Fred_18-Q3-R57-64_MAXAC.330_cln	d__Bacteria;p__Planctomycetota;c__Phycisphaerae;o__Phycisphaerales;f__SM1A02;g__UBA2402;s__	tig00000055-10-33509940	2621859	gumD	02153
34	Hade_18-Q3-R52-61_BATAC.316	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__s__	tig00000808-10-11321960	733220	gumB	00665
35	Hade_18-Q3-R52-61_MAXAC.056	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Ga0077559;s__	tig00002424-10-6316380	630401	gumB	02446
36	Hade_18-Q3-R52-61_MAXAC.304	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Propionivibrio;s__	tig00406325-10-5610210	358947	gumB	01123
37	Hirt_18-Q3-R61-65_BATAC.102	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Flavobacteriales;f__PHOS-HE28;g__PHOS-HE28;s__	tig01348459-10-1367200	103999	gumB	03593
38	Hirt_18-Q3-R61-65_MAXAC.142	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__Promineofillales;f__Promineofillaceae;g__s__	tig01348138-10-3112950	119382	gumC	06335
39	Hirt_18-Q3-R61-65_MAXAC.229	d__Bacteria;p__Myxococcota;c__Polyangia;o__Hallangiales;f__Hallangiaceae;g__s__	tig00000107-10-33104080	3075418	gumB	02698
40	Hirt_18-Q3-R61-65_MAXAC.231	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__s__	tig00000003-10-42710140	1889679	gumB	01711
41	Hjor_18-Q3-R7-51_BAT3C.155	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiales;g__s__	tig00003356-10-3515290	161190	gumB	02414
42	Hjor_18-Q3-R7-51_BAT3C.262	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Hyphomicrobium;s__	tig00004932-10-2452570	156228	gumB	01908
43	Hjor_18-Q3-R7-51_MAXAC.072	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Propionivibrio;s__	tig00004613-10-2298940	140291	gumB	01331
44	Kalu_18-Q3-R12-55_BAT3C.181	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Rubrivivax;s__	tig00442601-10-5717870	161867	gumB	03105
45	Kalu_18-Q3-R12-55_BATAC.116	d__Bacteria;p__Myxococcota;c__Polyangia;o__Polyangiales;f__Polyangiaceae;g__s__	tig00001774-10-6877420	526899	gumB	02528
46	Kalu_18-Q3-R12-55_BATAC.47	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__Promineofillales;f__Promineofillaceae;g__GCA-2746795;s__	tig00001562-10-10503890	253097	gumD	00227
47	Kalu_18-Q3-R12-55_MAXAC.026	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Ga0077559;s__	tig00001104-10-10424950	546243	gumB	00584
48	Kalu_18-Q3-R12-55_MAXAC.049_cln	d__Bacteria;p__Actinobacteriota;c__Acidimicrobia;o__Microtrichiales;f__Ilumatobacteraceae;g__s__	tig00000091-10-32885210	1153833	gumD	01100
49	Kalu_18-Q3-R12-55_MAXAC.107	d__Bacteria;p__Myxococcota;c__Polyangia;o__Polyangiales;f__Polyangiaceae;g__s__	tig00100908-10-3475500	214058	gumB	04304
50	Lyne_18-Q3-R50-59_BAT3C.1	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Ga0077559;s__	tig00320340-10-18168060	1056683	gumB	01012
51	Lyne_18-Q3-R50-59_BAT3C.262	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__UBA10428;g__UBA10428;s__	tig00000116-10-39646440	3024331	gumB	02592
52	Lyne_18-Q3-R50-59_BAT3C.496	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__Promineofillales;f__Promineofillaceae;g__GCA-2746795;s__	tig00019390-10-1493580	79377	gumD	03989
53	Lyne_18-Q3-R50-59_BATAC.375	d__Bacteria;p__Nitrospirota;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira_A;s__Nitrospira_A sp900170025	tig01430579-10-3014800	128687	gumB	04047
54	Lyne_18-Q3-R50-59_MAXAC.002	d__Bacteria;p__Myxococcota;c__UBA796;o__UBA796;f__g__s__	tig00028176-10-743750	48652	gumB	04719
55	Lyne_18-Q3-R50-59_MAXAC.074	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__AKYH767-A;f__OLB10;g__s__	tig01430395-10-4954860	328099	gumB	05039
56	Lyne_18-Q3-R50-59_MAXAC.325_cln	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Micavibrionales;f__Micavibrionaceae;g__s__	tig00000079-10-27418810	2216763	gumB	02186
57	Mari_18-Q3-R65-66_BATAC.299	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__UBA1936;s__	tig00869297-10-2867490	117217	gumB	02869
58	Mari_18-Q3-R65-66_BATAC.401	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__AKYH767-A;f__OLB10;g__s__	tig00869093-10-16704040	667055	gumB	02622
59	Mari_18-Q3-R65-66_MAXAC.196	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Propionivibrio;s__	tig00869273-10-3115520	153353	gumB	02964
60	OdNE_18-Q3-R46-58_BATAC.193	d__Bacteria;p__Acidobacteriota;c__Thermoanaerobaculia;o__UBA5066;f__UBA5066;g__UBA5066;s__	tig00026008-10-446880	3888	gumB	04801