

MAG

EsbW\_18-Q3-R4-48\_MAXAC.012  
p:Nitrospirae,o:Nitrospirales,g:Nitrospira

EsbW\_18-Q3-R4-48\_BATAC.445  
p:Elusimicrobia,o:MVP-88,g:midas\_g\_595

EsbE\_18-Q3-R3-47\_MAXAC.085  
p:Gemmatimonadetes,o:Gemmatimonadales,g:midas\_g\_395

EsbE\_18-Q3-R3-47\_BAT3C.110  
p:Proteobacteria,o:Syntrophobacterales,g:midas\_g\_134

Ejby\_18-Q3-R6-50\_BATAC.338  
p:Ca\_Fermentibacterota,o:midas\_o\_753,g:midas\_g\_753

Ejby\_18-Q3-R6-50\_BAT3C.80  
p:Gemmatimonadetes,o:Gemmatimonadales,g:midas\_g\_395

Ejby\_18-Q3-R6-50\_BAT3C.203  
p:Actinobacteria,o:Micrococcales,g:midas\_g\_724

Ega\_18-Q3-R5-49\_BATAC.239  
p:Proteobacteria,o:midas\_o\_26,g:midas\_g\_523

Damh\_18-Q3-R51-60\_MAXAC.210  
p:Elusimicrobia,o:MVP-88,g:midas\_g\_595

Damh\_18-Q3-R51-60\_MAXAC.107  
p:Bacteroidetes,o:Sphingobacterales,g:midas\_g\_1061

Bjer\_18-Q3-R1-45\_MAXAC.090  
p:Ca\_Fermentibacterota,o:midas\_o\_753,g:midas\_g\_753

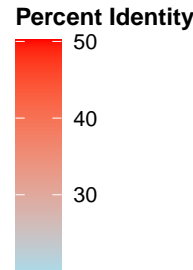
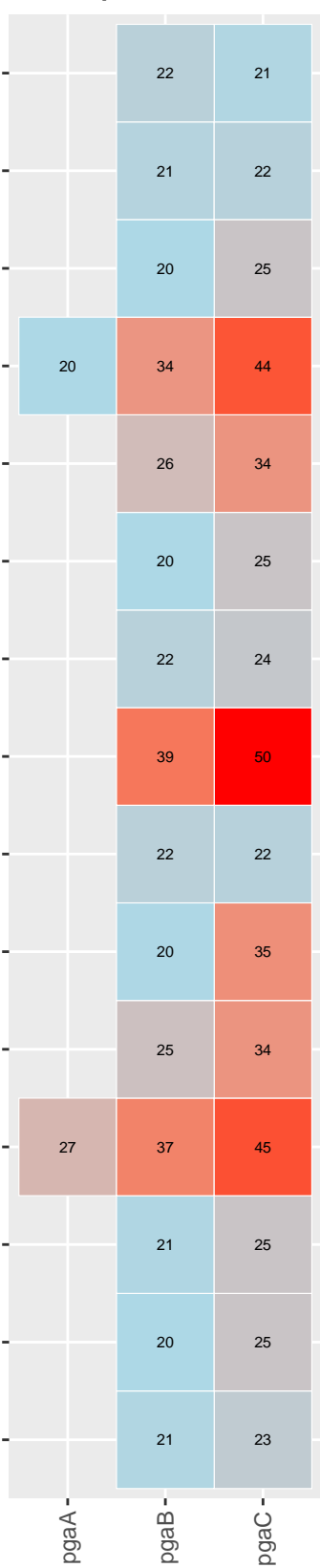
Bjer\_18-Q3-R1-45\_MAXAC.014  
p:Proteobacteria,o:Betaproteobacterales,g:Sulfuritalea

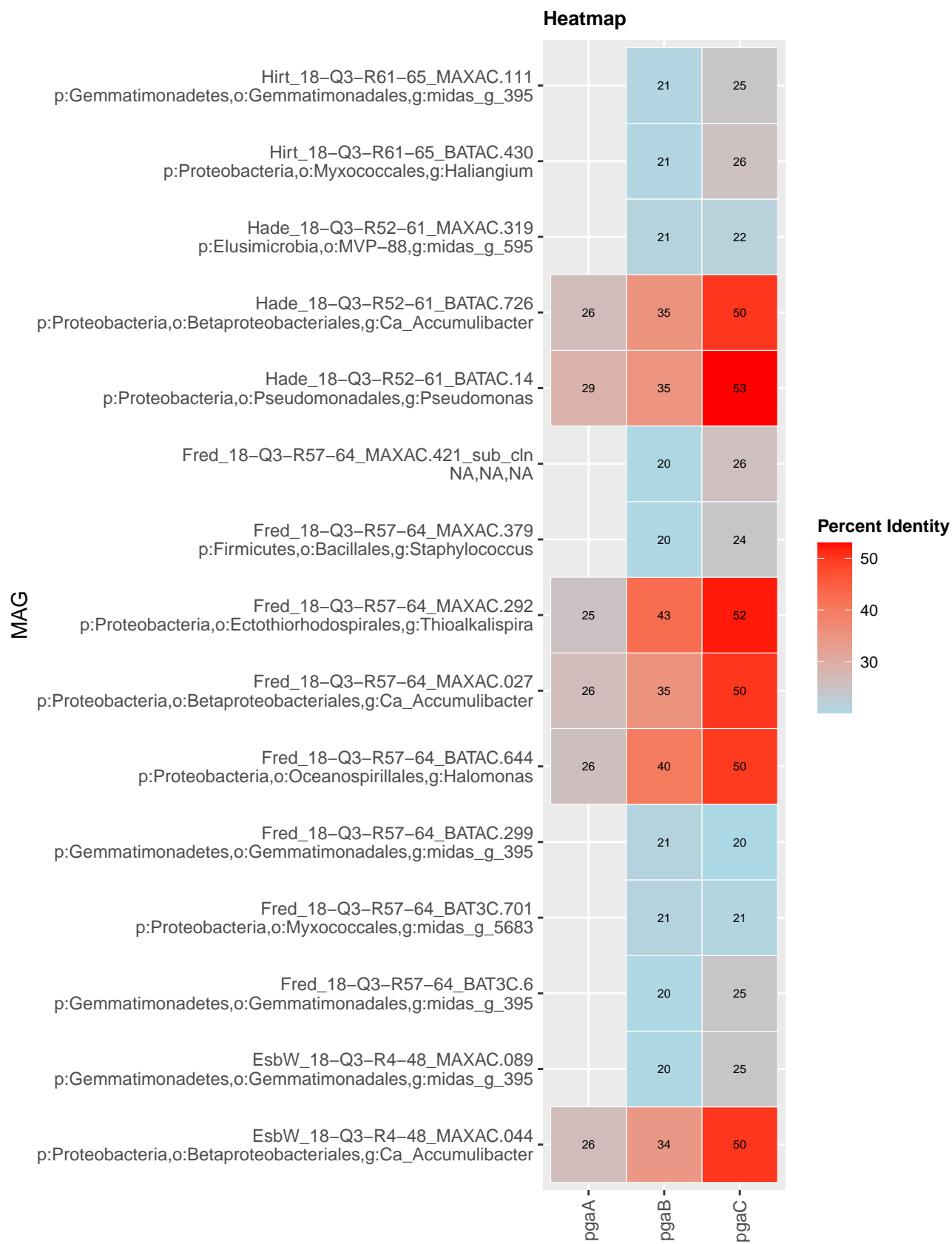
Aved\_18-Q3-R54-62\_BATAC.843  
p:Gemmatimonadetes,o:Gemmatimonadales,g:midas\_g\_395

AalE\_18-Q3-R2-46\_MAXAC.133  
p:Gemmatimonadetes,o:Gemmatimonadales,g:midas\_g\_395

AalE\_18-Q3-R2-46\_BAT3C.204  
p:Epsilonbacteraeota,o:Campylobacterales,g:Arcobacter

Heatmap





MAG

Skiv\_18-Q3-R9-52\_MAXAC.212  
p:Elusimicrobia,o:MVP-88,g:midas\_g\_595

Skiv\_18-Q3-R9-52\_MAXAC.110  
p:Ca\_Fermentibacterota,o:midas\_o\_753,g:midas\_g\_753

Rand\_18-Q3-R56-63\_MAXAC.104  
p:Gemmatimonadetes,o:Gemmatimonadales,g:midas\_g\_395

OdNW\_18-Q3-R42-56\_BAT3C.388  
p:Ca\_Fermentibacterota,o:midas\_o\_753,g:midas\_g\_753

OdNE\_18-Q3-R46-58\_MAXAC.028  
p:Bacteroidetes,o:Chitinophagales,g:midas\_g\_543

OdNE\_18-Q3-R46-58\_BATAC.493  
p:Elusimicrobia,o:MVP-88,g:midas\_g\_945

OdNE\_18-Q3-R46-58\_BAT3C.415  
p:Proteobacteria,o:Betaproteobacteriales,g:Ca\_Accumulibacter

Lyne\_18-Q3-R50-59\_MAXAC.318  
p:Proteobacteria,o:Oceanospirillales,g:Halomonas

Lyne\_18-Q3-R50-59\_MAXAC.215  
p:Elusimicrobia,o:MVP-88,g:midas\_g\_945

Lyne\_18-Q3-R50-59\_BATAC.420  
p:Actinobacteria,o:Micrococcales,g:midas\_g\_724

Kalu\_18-Q3-R12-55\_MAXAC.185\_cln  
p:Acidobacteria,o:Blastocatellales,g:JGI.fa

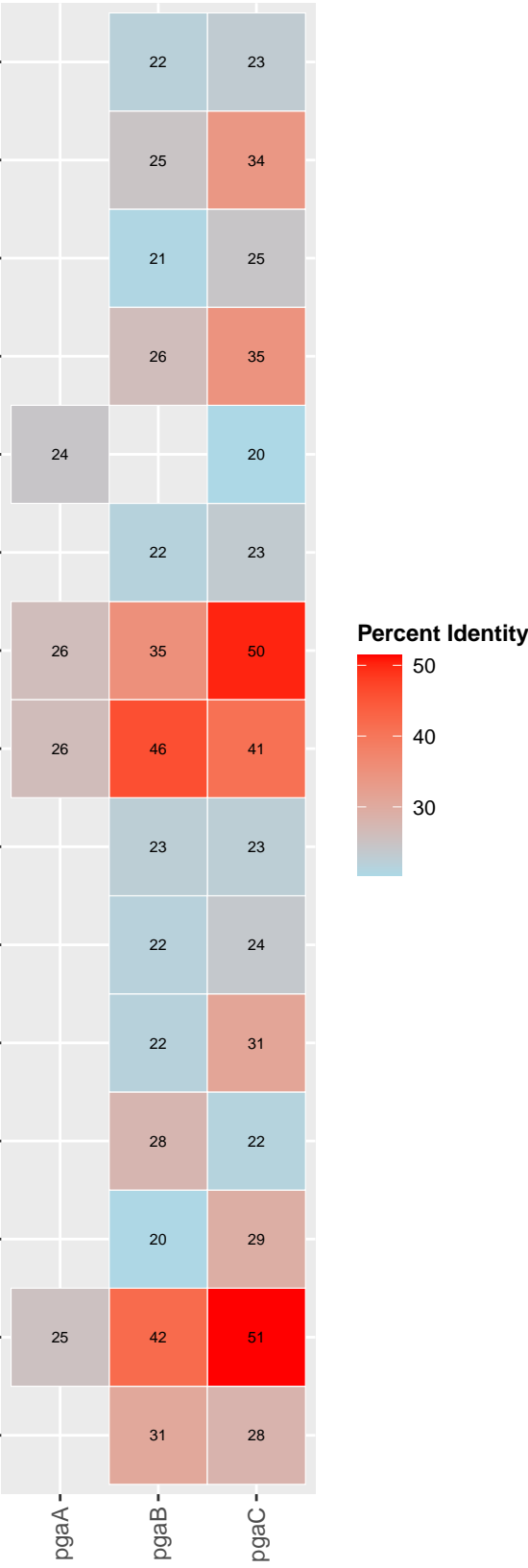
Kalu\_18-Q3-R12-55\_MAXAC.123  
p:Acidobacteria,o:11-24,g:midas\_g\_1424

Kalu\_18-Q3-R12-55\_BAT3C.355  
p:Acidobacteria,o:Blastocatellales,g:JGI.fa

Kalu\_18-Q3-R12-55\_BAT3C.208  
p:Proteobacteria,o:Ectothiorhodospirales,g:Thioalkalispira

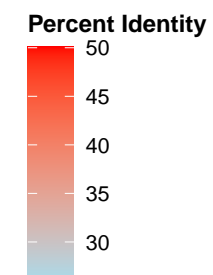
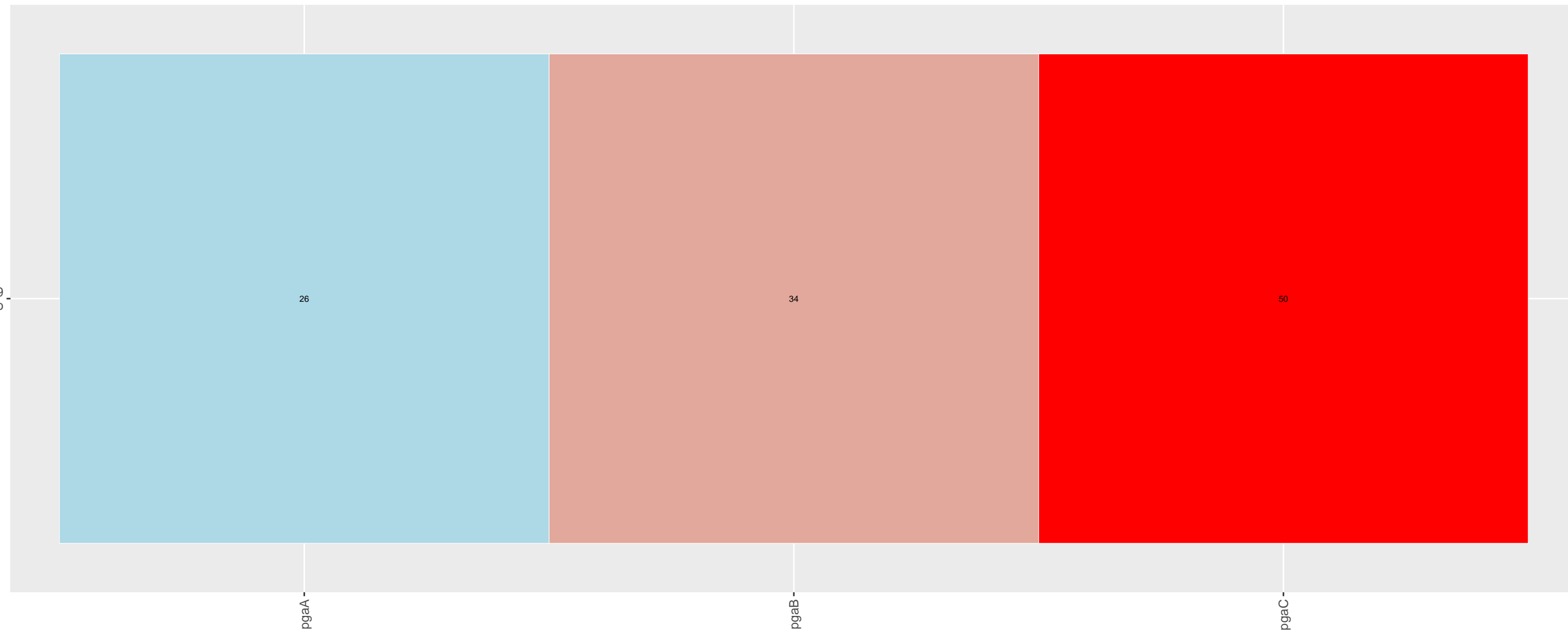
Hirt\_18-Q3-R61-65\_MAXAC.229  
p:Proteobacteria,o:Myxococcales,g:Haliangium

Heatmap

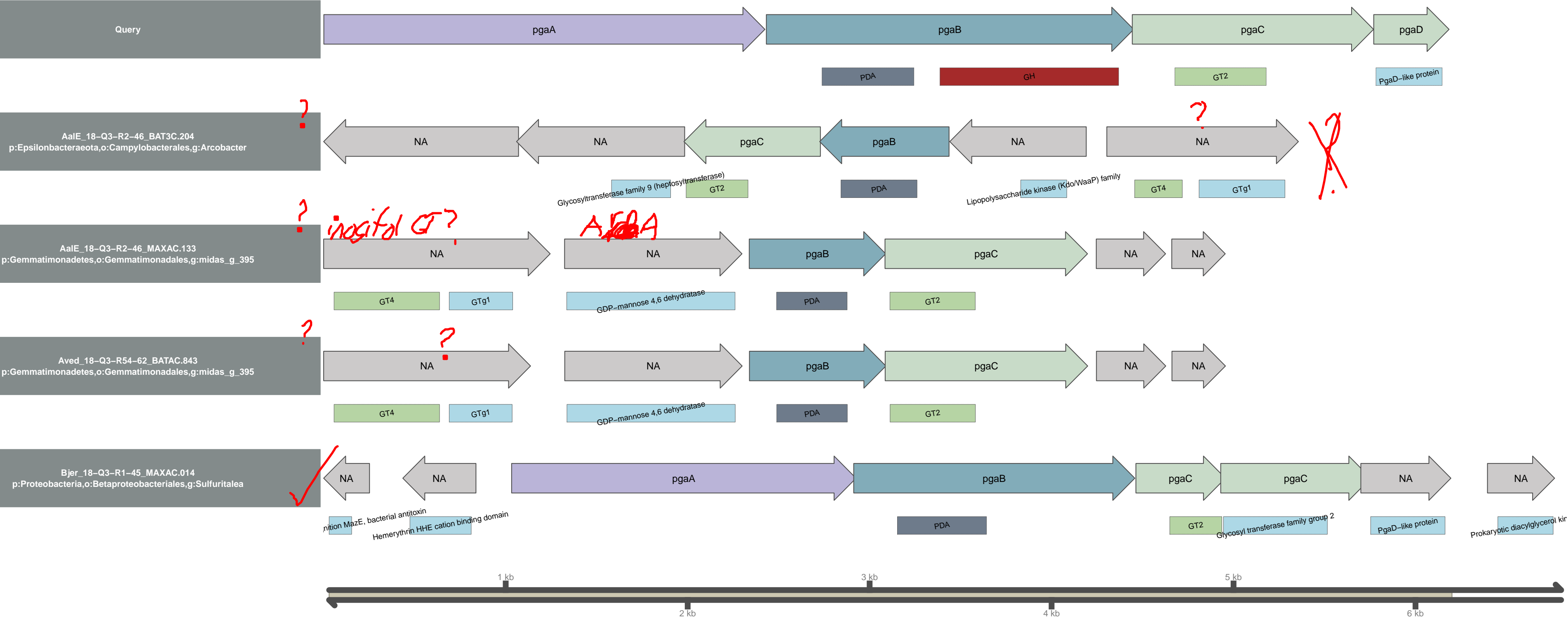


MAG  
Vibo\_18-Q3-R45-57\_BATAC.199  
p:Proteobacteria,o:Betaproteobacteriales,g:Propionivibrio

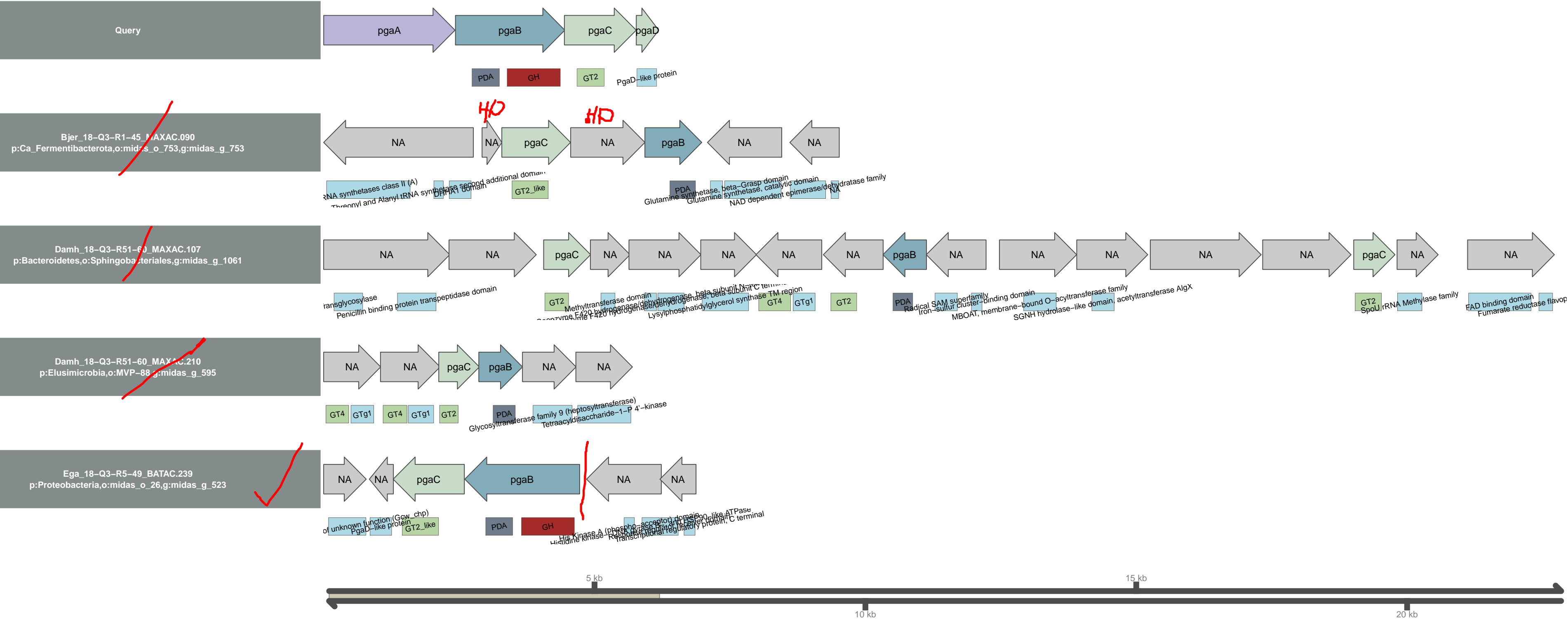
Heatmap



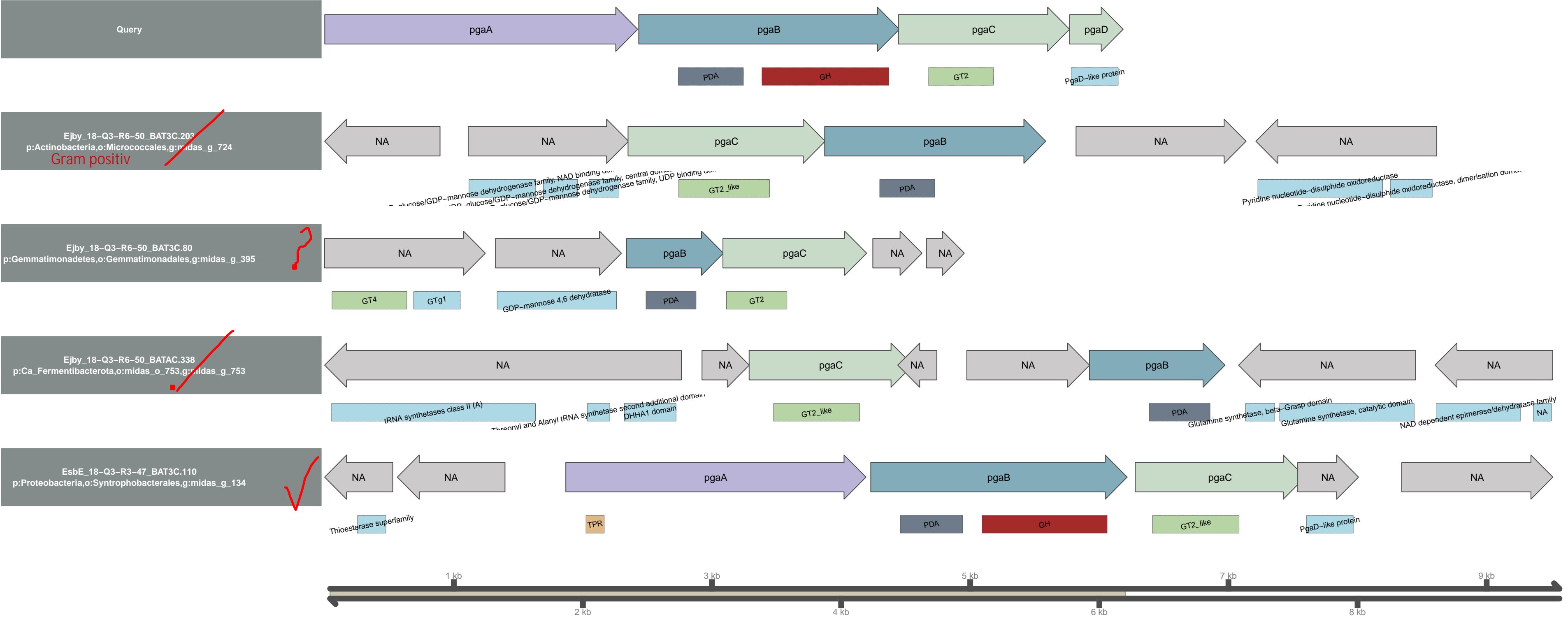
Operon Structure



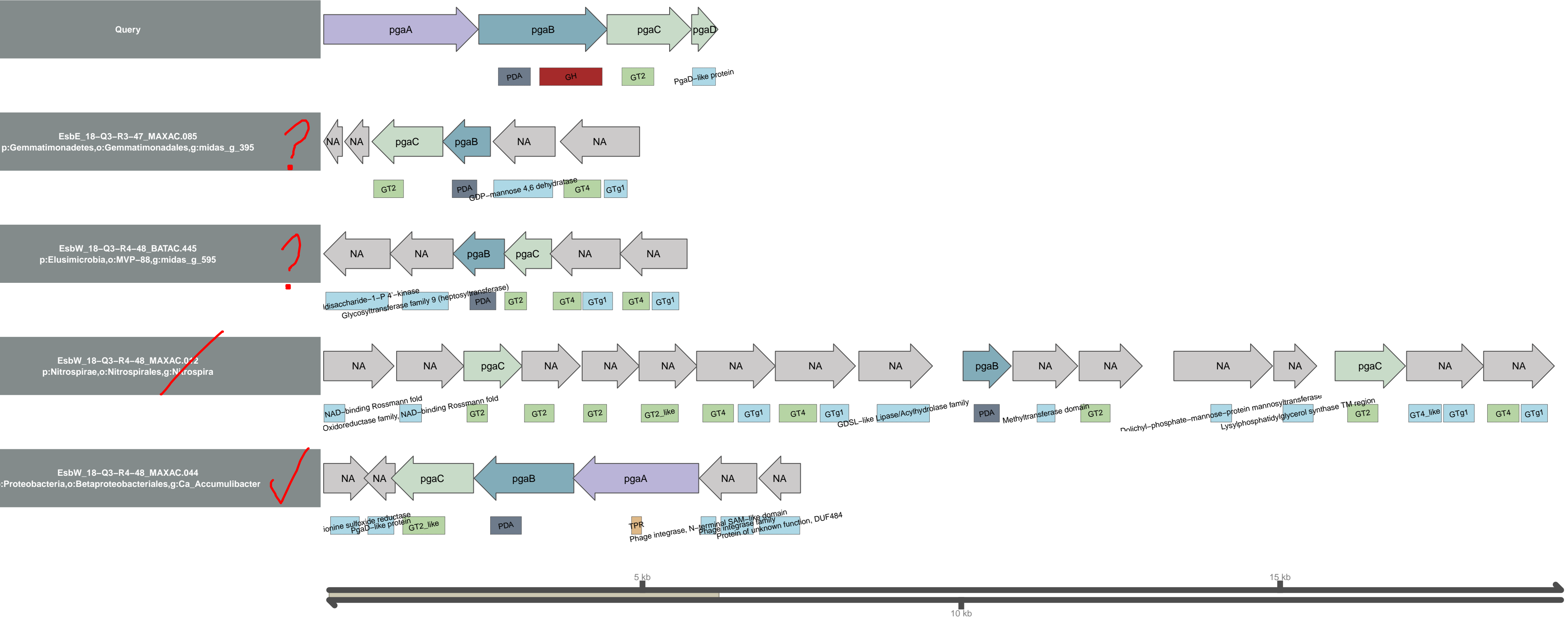
Operon Structure



Operon Structure

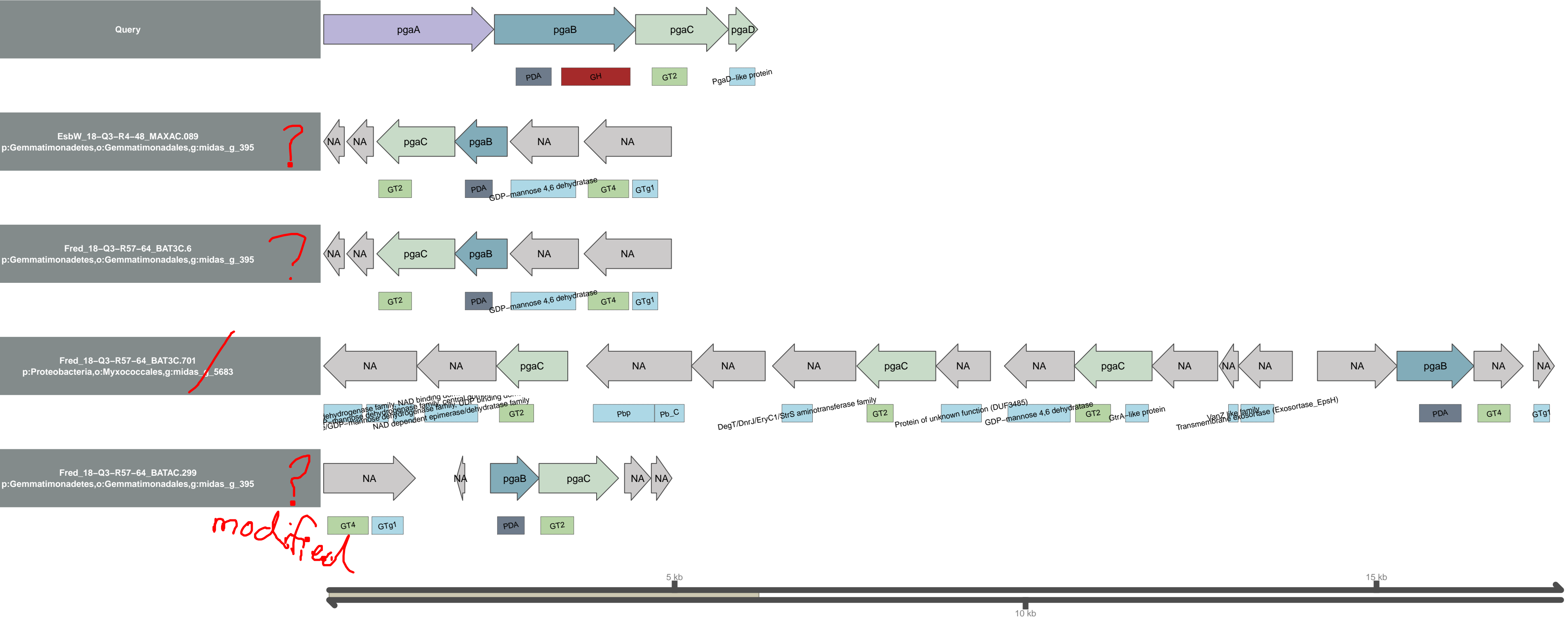


Operon Structure

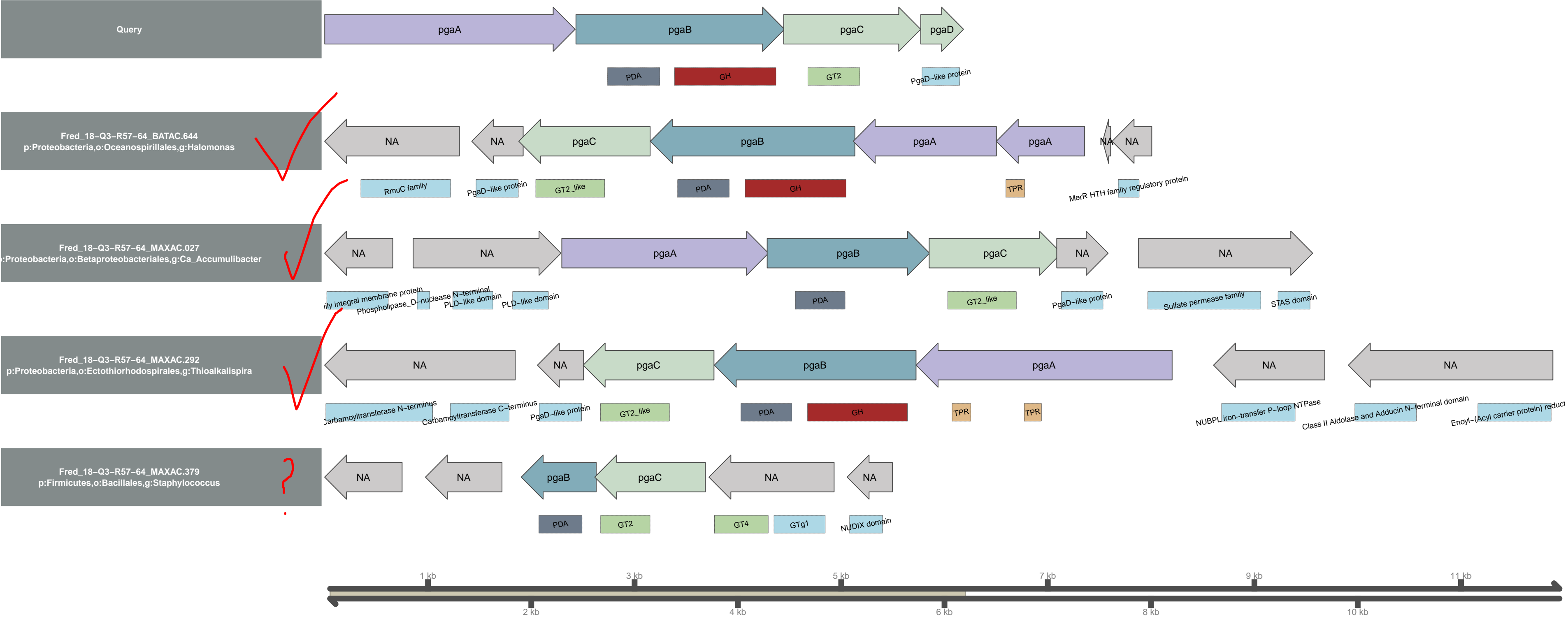




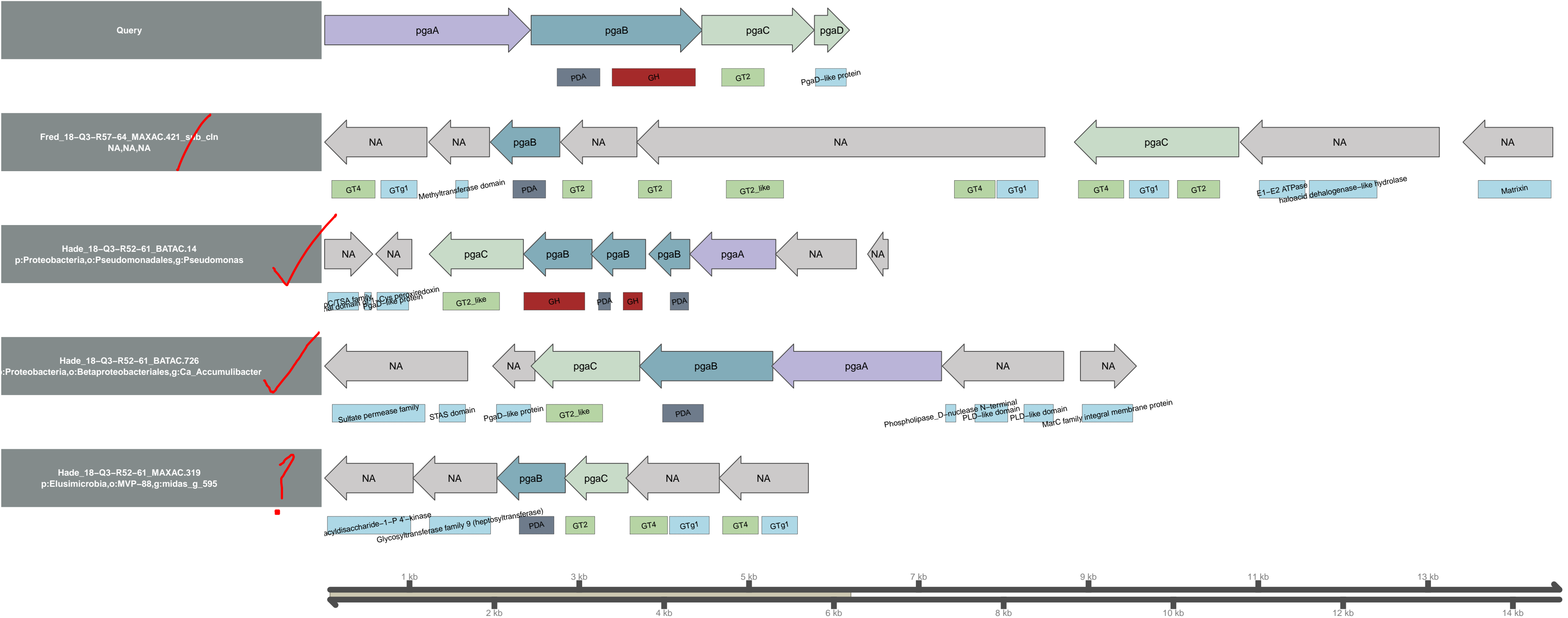
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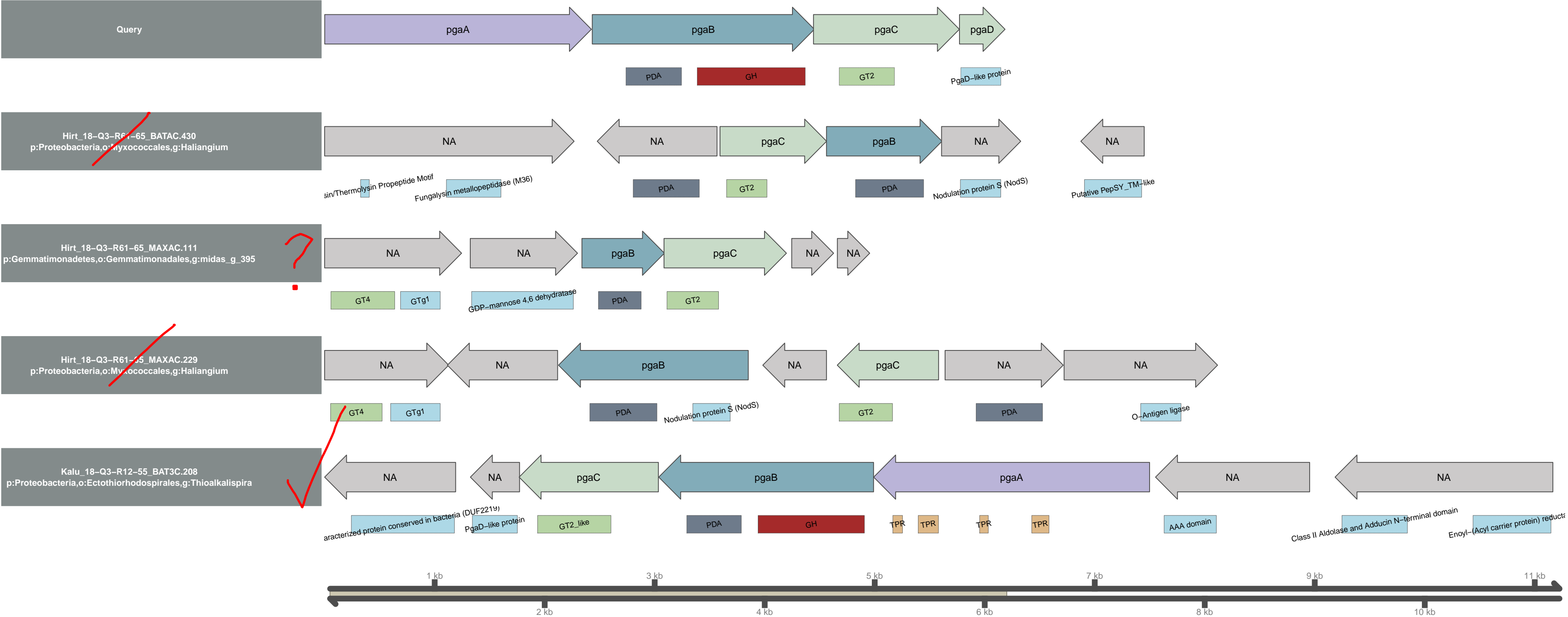
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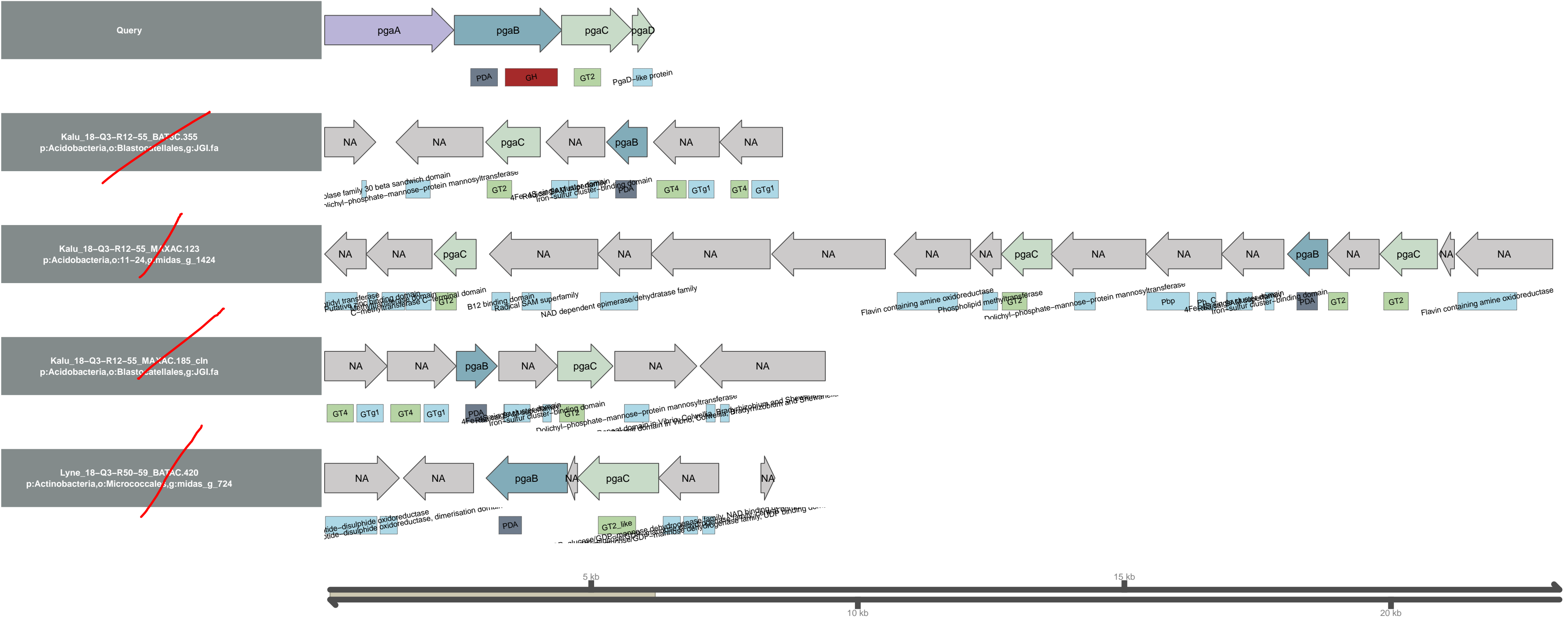
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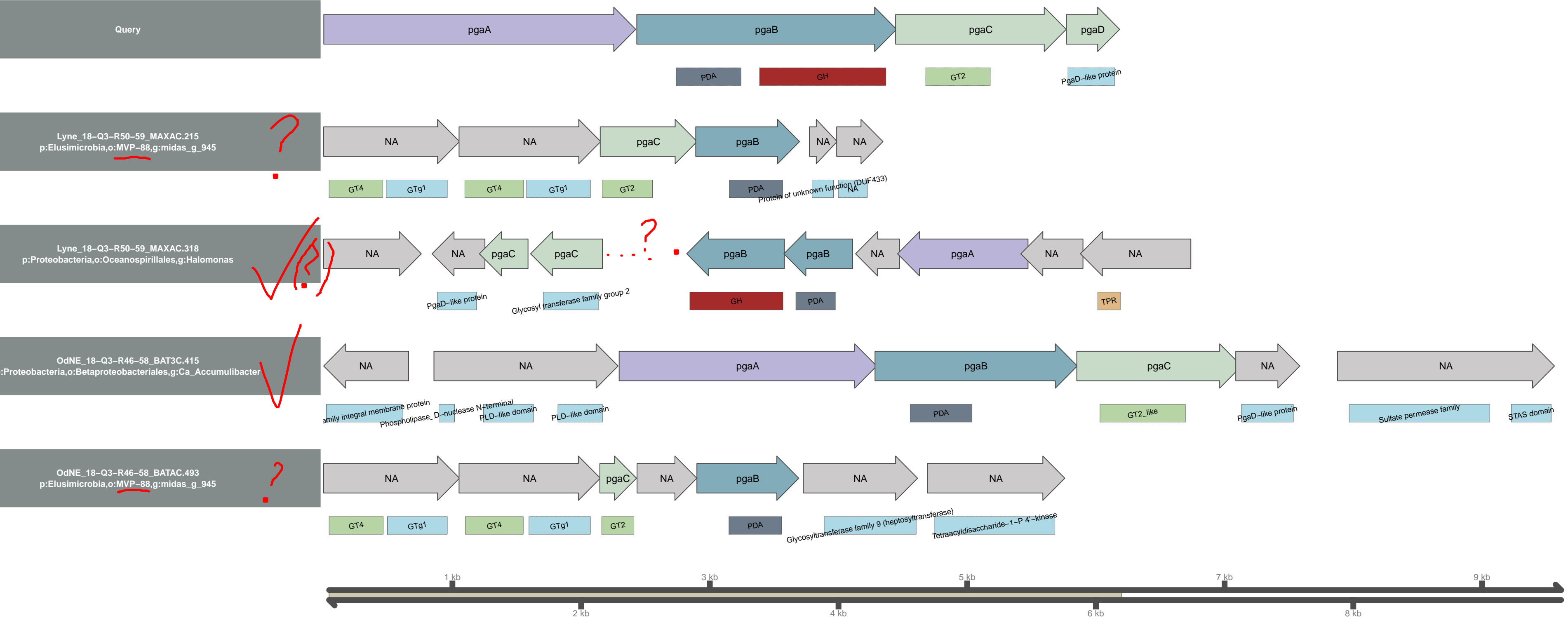
Operon Structure



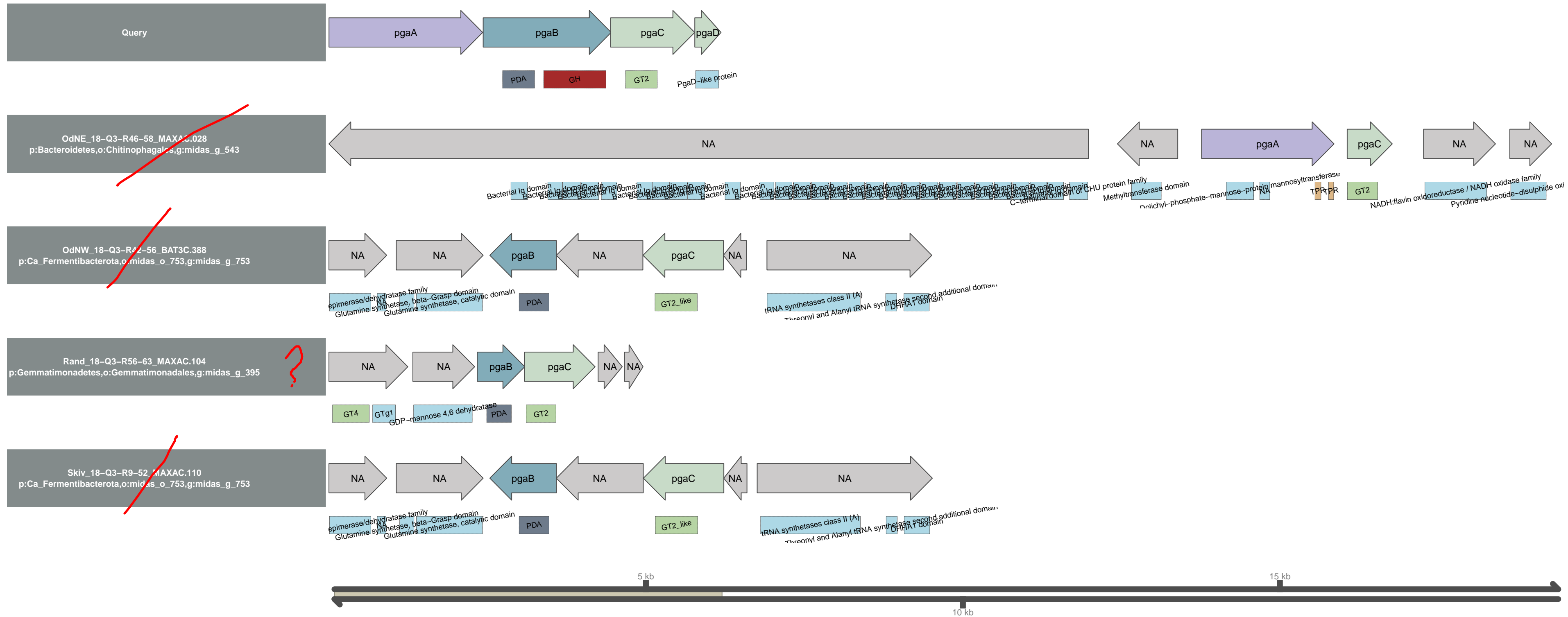
Operon Structure



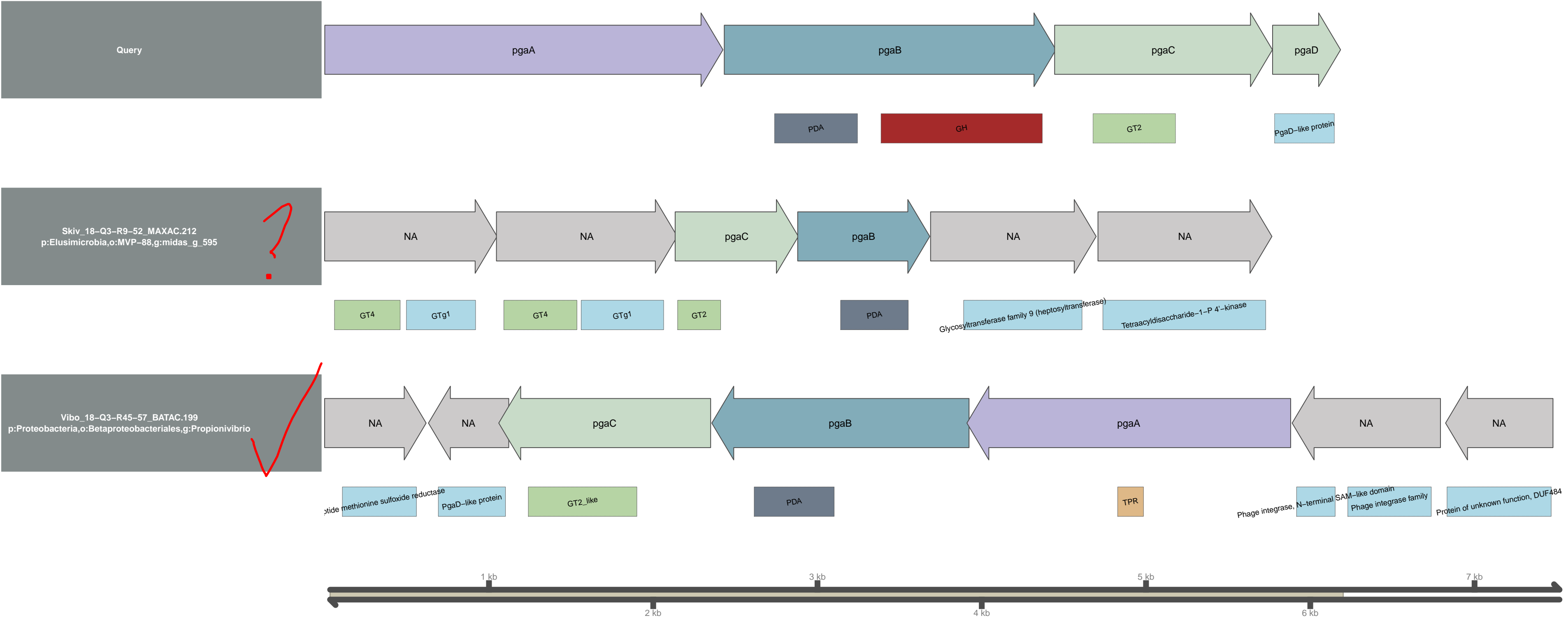
Operon Structure



## Operon Structure



Operon Structure





	ID2	plot_tax	seqname	start	Query_label	ProkkaNO
1	AalE_18-Q3-R2-46_BAT3C.204	p:Epsilonbacteraeota,o:Campylobacterales,g:Arcobacter	tig00009949-10-1090220	106178	pgaB	00805
2	AalE_18-Q3-R2-46_MAXAC.133	p:Gemmatimonadetes,o:Gemmatimonadales,g:midas_g_395	tig00000473-10-14677400	264569	pgaB	00218
3	Aved_18-Q3-R54-62_BATAC.843	p:Gemmatimonadetes,o:Gemmatimonadales,g:midas_g_395	tig00000726-10-21197290	46816	pgaB	00037
4	Bjer_18-Q3-R1-45_MAXAC.014	p:Proteobacteria,o:Betaproteobacterales,g:Sulfuritalea	tig00013944-10-761410	16473	pgaA	03044
5	Bjer_18-Q3-R1-45_MAXAC.090	p:Ca_Fermentibacterota,o:midas_o_753,g:midas_g_753	tig00000439-10-26518310	2009055	pgaB	01692
6	Damh_18-Q3-R51-60_MAXAC.107	p:Bacteroidetes,o:Sphingobacterales,g:midas_g_1061	tig00008676-10-965710	64179	pgaB	02953
7	Damh_18-Q3-R51-60_MAXAC.210	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00000227-10-17572600	1418462	pgaB	01210
8	Ega_18-Q3-R5-49_BATAC.239	p:Proteobacteria,o:midas_o_26,g:midas_g_523	tig00001202-10-4363950	347494	pgaB	00343
9	Ejby_18-Q3-R6-50_BAT3C.203	p:Actinobacteria,o:Micrococcales,g:midas_g_724	tig00214211-10-16152460	504691	pgaB	02216
10	Ejby_18-Q3-R6-50_BAT3C.80	p:Gemmatimonadetes,o:Gemmatimonadales,g:midas_g_395	tig00003915-10-2303560	35528	pgaB	02090
11	Ejby_18-Q3-R6-50_BATAC.338	p:Ca_Fermentibacterota,o:midas_o_753,g:midas_g_753	tig00005712-10-1957820	15220	pgaB	01453
12	EsbE_18-Q3-R3-47_BAT3C.110	p:Proteobacteria,o:Syntrophobacterales,g:midas_g_134	tig00004325-10-2346120	134330	pgaA	02223
13	EsbE_18-Q3-R3-47_MAXAC.085	p:Gemmatimonadetes,o:Gemmatimonadales,g:midas_g_395	tig00000236-10-21381660	1575826	pgaB	01524
14	EsbW_18-Q3-R4-48_BATAC.445	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00004868-10-4039950	177021	pgaB	01706
15	EsbW_18-Q3-R4-48_MAXAC.012	p:Nitrospirae,o:Nitrospirales,g:Nitrospira	tig00000127-10-30891270	1438364	pgaB	01476
16	EsbW_18-Q3-R4-48_MAXAC.044	p:Proteobacteria,o:Betaproteobacterales,g:Ca_Accumulibacter	tig01107798-10-2245570	120621	pgaA	04464
17	EsbW_18-Q3-R4-48_MAXAC.089	p:Gemmatimonadetes,o:Gemmatimonadales,g:midas_g_395	tig00000105-10-26971300	1569593	pgaB	01516
18	Fred_18-Q3-R57-64_BAT3C.6	p:Gemmatimonadetes,o:Gemmatimonadales,g:midas_g_395	tig01546545-10-26760560	1942079	pgaB	03448
19	Fred_18-Q3-R57-64_BAT3C.701	p:Proteobacteria,o:Myxococcales,g:midas_g_5683	tig00002470-10-11917410	472851	pgaB	00434
20	Fred_18-Q3-R57-64_BATAC.299	p:Gemmatimonadetes,o:Gemmatimonadales,g:midas_g_395	tig00007168-10-4655090	210650	pgaB	03098
21	Fred_18-Q3-R57-64_BATAC.644	p:Proteobacteria,o:Oceanospirillales,g:Halomonas	tig00000788-10-24304590	16305	pgaA	00015
22	Fred_18-Q3-R57-64_MAXAC.027	p:Proteobacteria,o:Betaproteobacterales,g:Ca_Accumulibacter	tig00351383-10-3762090	221106	pgaA	03687
23	Fred_18-Q3-R57-64_MAXAC.292	p:Proteobacteria,o:Ectothiorhodospirales,g:Thioalkalispira	tig00005391-10-5845880	141858	pgaA	01551
24	Fred_18-Q3-R57-64_MAXAC.379	p:Firmicutes,o:Bacillales,g:Staphylococcus	tig00350858-10-25518060	1871207	pgaB	02036
25	Fred_18-Q3-R57-64_MAXAC.421_sub_cln	NA,NA,NA	tig00000963-10-10881080	453729	pgaB	00483

	ID2	plot_tax	seqname	start	Query_label	ProkkaNO
1	Hade_18-Q3-R52-61_BATAC.14	p:Proteobacteria,o:Pseudomonadales,g:Pseudomonas	tig00035928-10-409280	33209	pgaA	02499
2	Hade_18-Q3-R52-61_BATAC.726	p:Proteobacteria,o:Betaproteobacteriales,g:Ca_Accumulibacter	tig00035480-10-796120	20578	pgaA	02529
3	Hade_18-Q3-R52-61_MAXAC.319	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00000703-10-10596450	173054	pgaB	00165
4	Hirt_18-Q3-R61-65_BATAC.430	p:Proteobacteria,o:Myxococcales,g:Haliangium	tig00018336-10-1151760	55580	pgaB	04370
5	Hirt_18-Q3-R61-65_MAXAC.111	p:Gemmatimonadetes,o:Gemmatimonadales,g:midas_g_395	tig01347732-10-21894770	273989	pgaB	02519
6	Hirt_18-Q3-R61-65_MAXAC.229	p:Proteobacteria,o:Myxococcales,g:Haliangium	tig00008943-10-2562490	90421	pgaB	03776
7	Kalu_18-Q3-R12-55_BAT3C.208	p:Proteobacteria,o:Ectothiorhodospirales,g:Thioalkalispira	tig00000943-10-15208620	287561	pgaA	00283
8	Kalu_18-Q3-R12-55_BAT3C.355	p:Acidobacteria,o:Blastocatellales,g:JGI.fa	tig00100729-10-33526130	75106	pgaB	00448
9	Kalu_18-Q3-R12-55_MAXAC.123	p:Acidobacteria,o:11-24,g:midas_g_1424	tig00002634-10-3925280	235889	pgaB	01888
10	Kalu_18-Q3-R12-55_MAXAC.185_cln	p:Acidobacteria,o:Blastocatellales,g:JGI.fa	tig00000010-10-44899860	418360	pgaB	00347
11	Lyne_18-Q3-R50-59_BATAC.420	p:Actinobacteria,o:Micrococcales,g:midas_g_724	tig00000369-10-34189540	2020477	pgaB	01841
12	Lyne_18-Q3-R50-59_MAXAC.215	p:Elusimicrobia,o:MVP-88,g:midas_g_945	tig00322439-10-3427020	325955	pgaB	02923
13	Lyne_18-Q3-R50-59_MAXAC.318	p:Proteobacteria,o:Oceanospirillales,g:Halomonas	tig00001263-10-14707330	1255095	pgaA	01259
14	OdNE_18-Q3-R46-58_BAT3C.415	p:Proteobacteria,o:Betaproteobacteriales,g:Ca_Accumulibacter	tig00005627-10-3059890	245887	pgaA	00719
15	OdNE_18-Q3-R46-58_BATAC.493	p:Elusimicrobia,o:MVP-88,g:midas_g_945	tig00013005-10-906310	50279	pgaB	01614
16	OdNE_18-Q3-R46-58_MAXAC.028	p:Bacteroidetes,o:Chitinophagales,g:midas_g_543	tig00006143-10-1534100	97019	pgaA	00950
17	OdNW_18-Q3-R42-56_BAT3C.388	p:Ca_Fermentibacterota,o:midas_o_753,g:midas_g_753	tig00896689-10-23573170	385032	pgaB	02180
18	Rand_18-Q3-R56-63_MAXAC.104	p:Gemmatimonadetes,o:Gemmatimonadales,g:midas_g_395	tig00004841-10-1679030	39676	pgaB	02258
19	Skiv_18-Q3-R9-52_MAXAC.110	p:Ca_Fermentibacterota,o:midas_o_753,g:midas_g_753	tig00003286-10-5785960	399384	pgaB	02350
20	Skiv_18-Q3-R9-52_MAXAC.212	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00000460-10-8469010	736871	pgaB	00667
21	Vibo_18-Q3-R45-57_BATAC.199	p:Proteobacteria,o:Betaproteobacteriales,g:Propionivibrio	tig00006229-10-1467280	33613	pgaA	01088