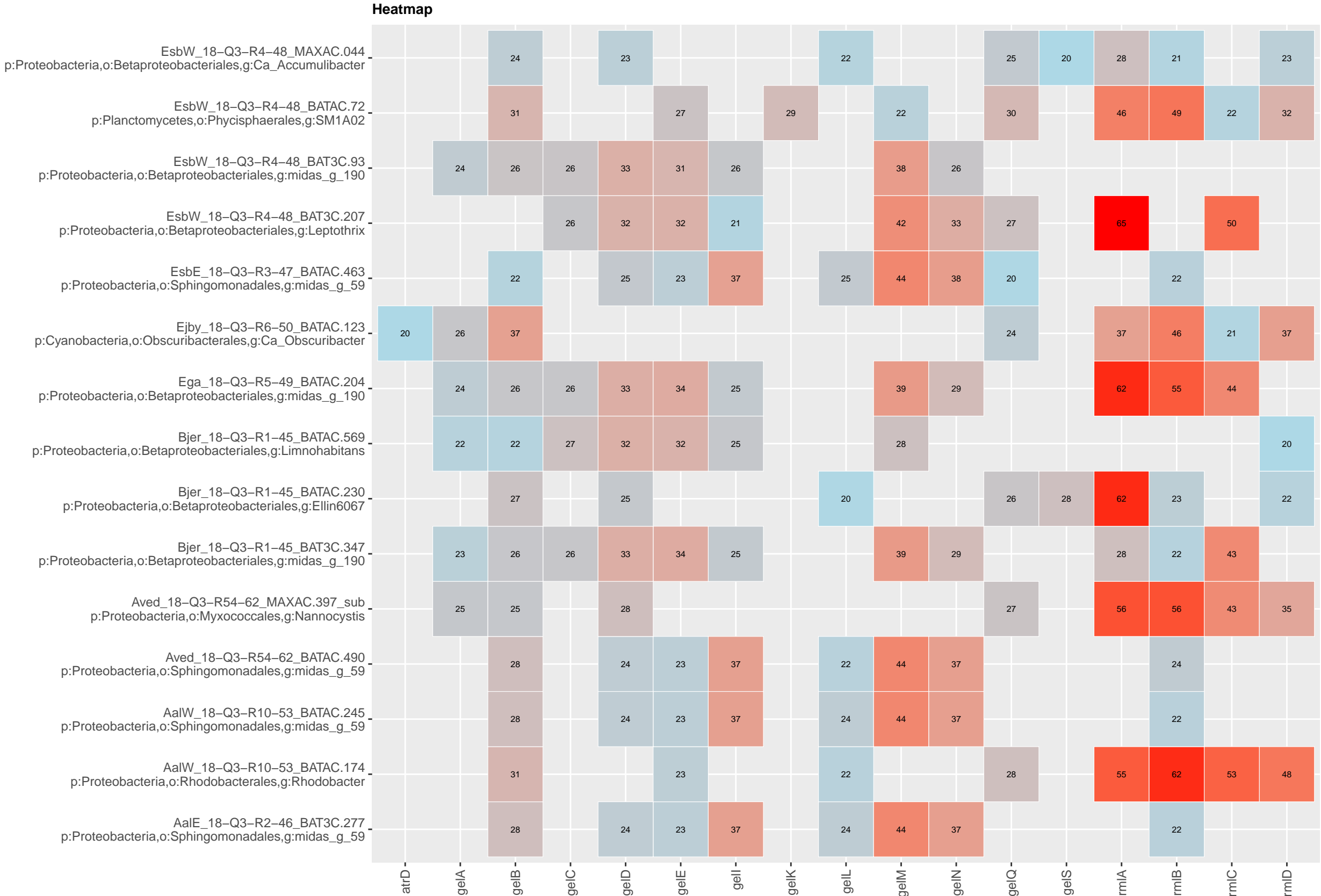
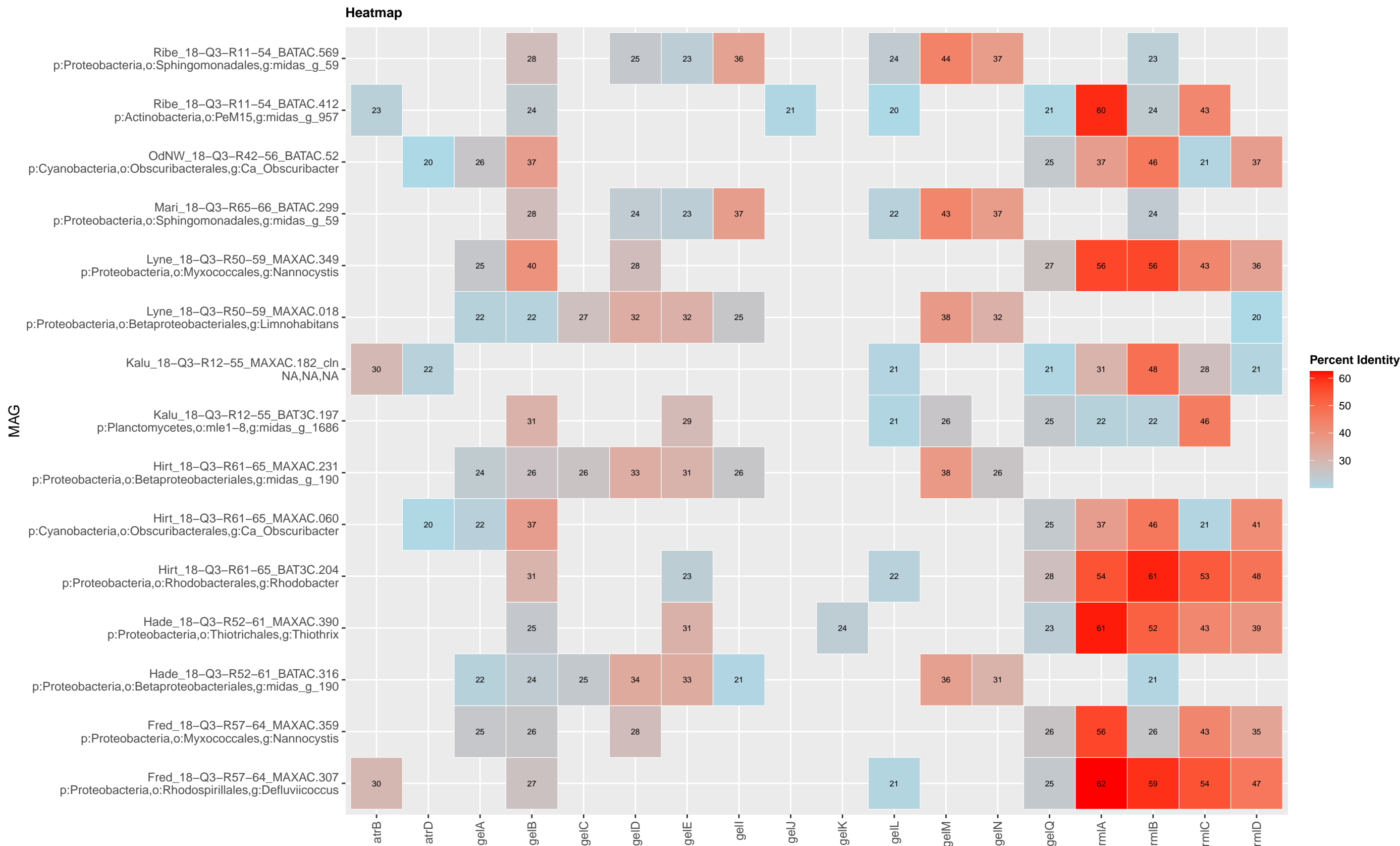


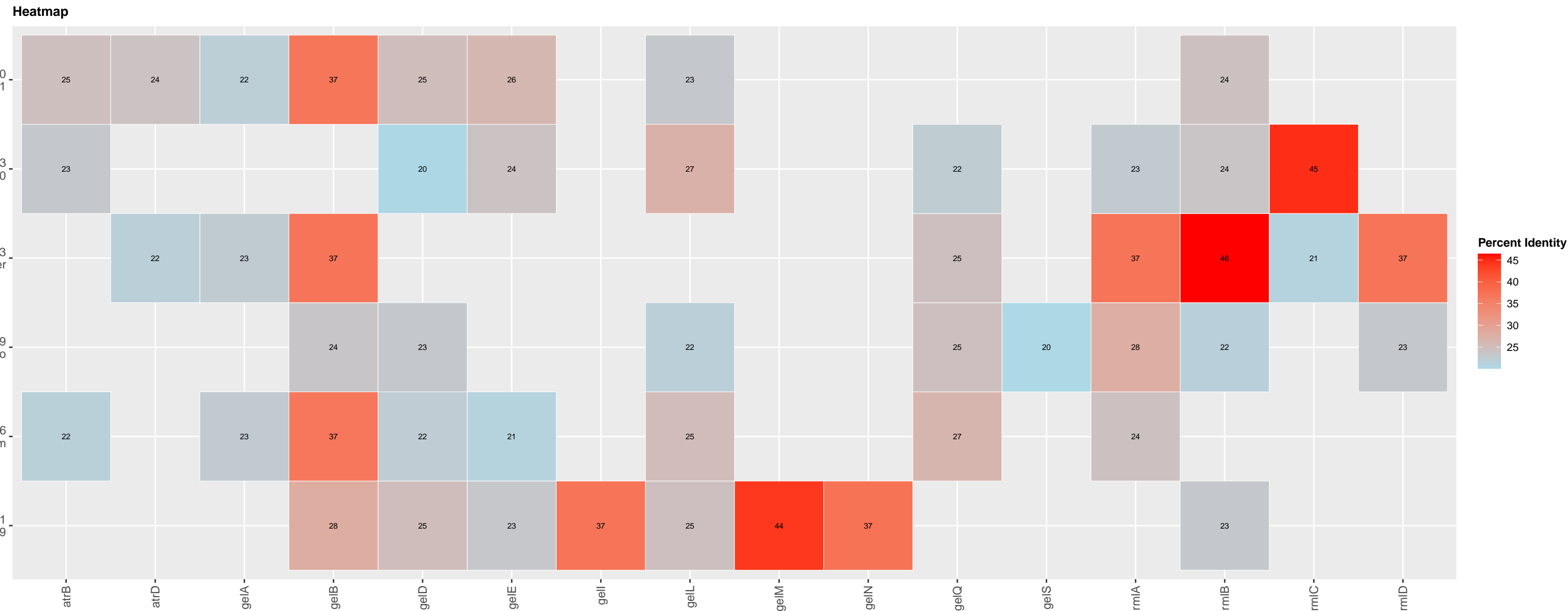
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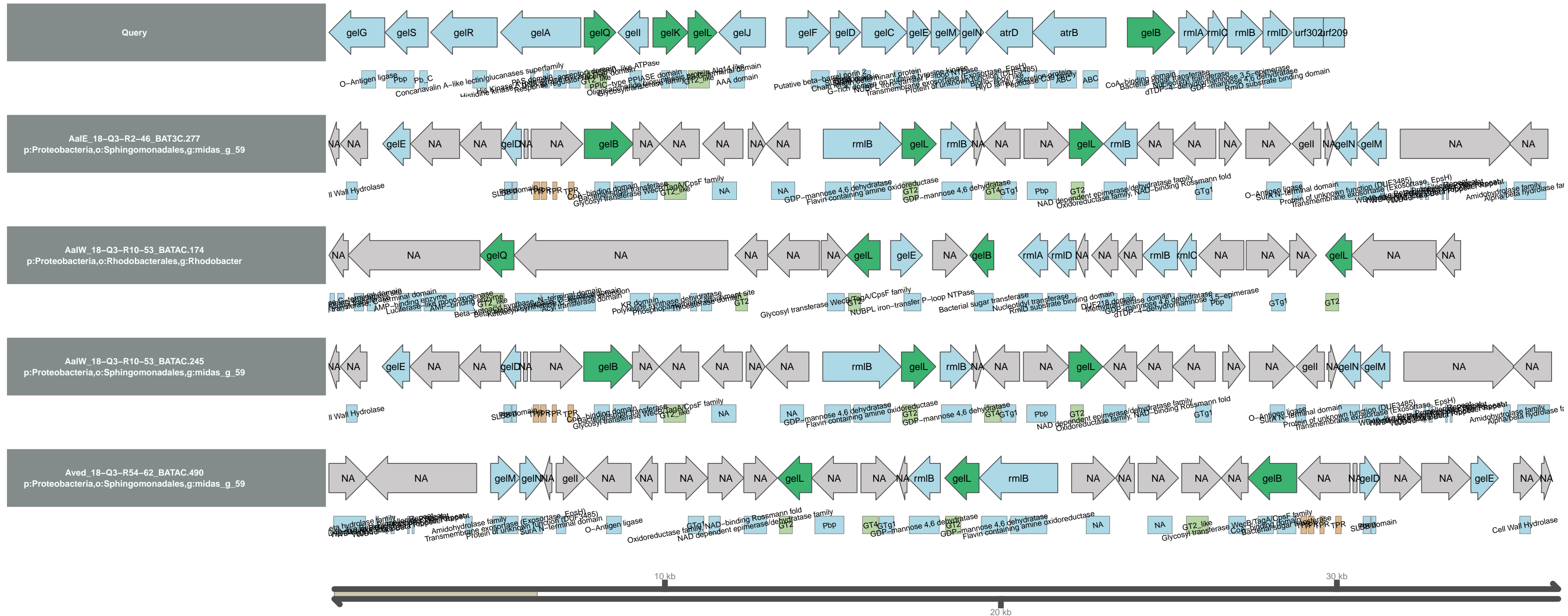
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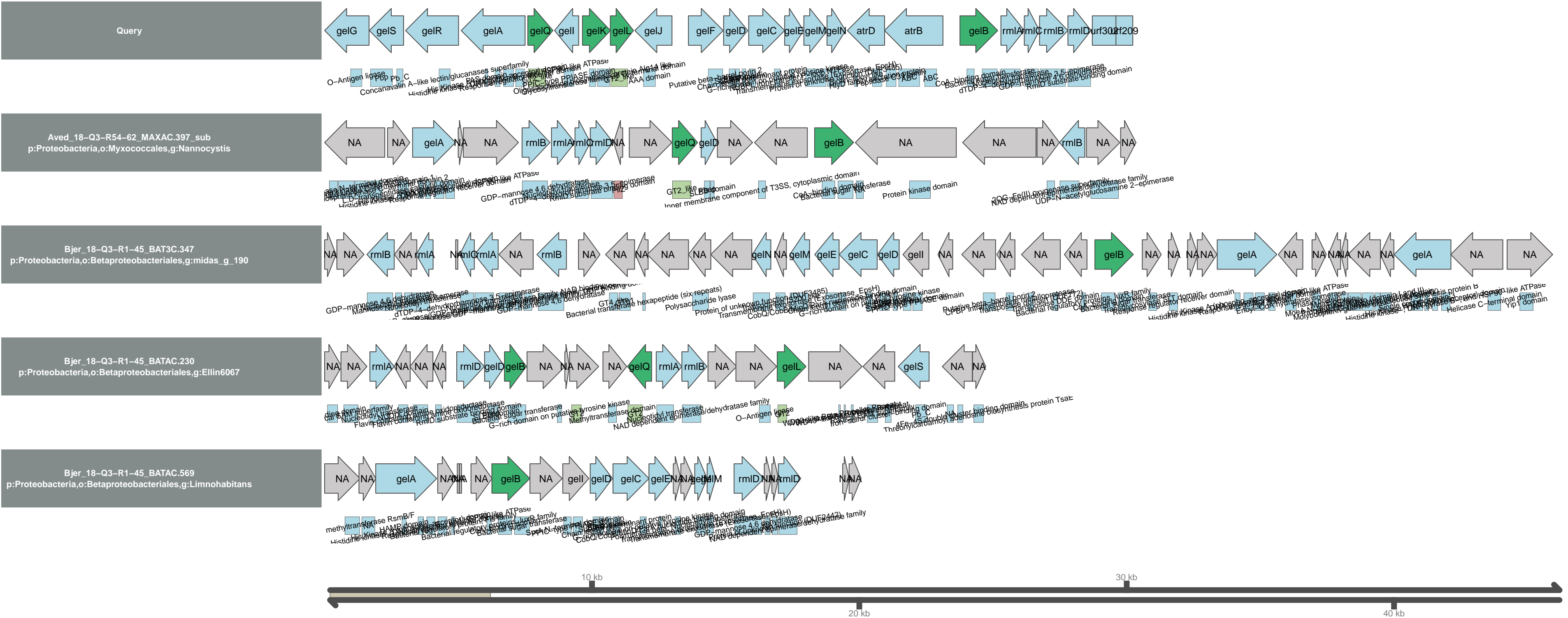
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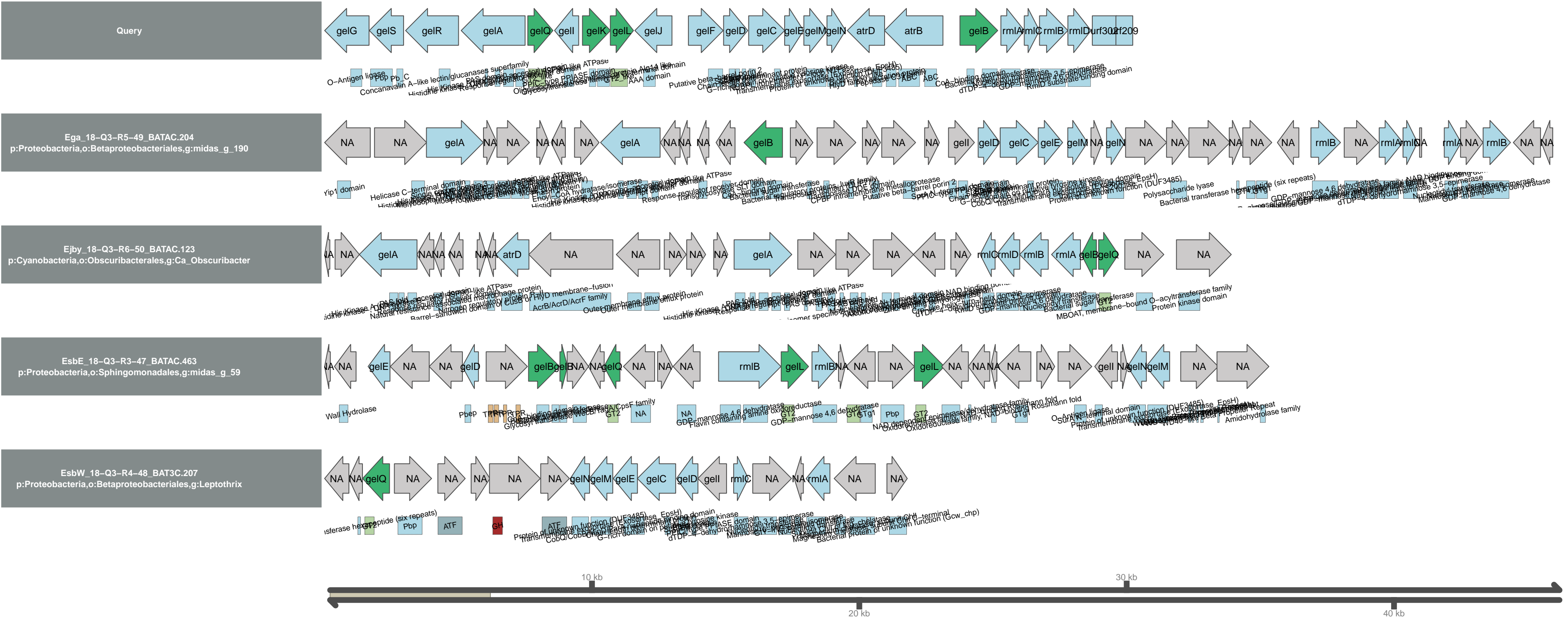
Operon Structure



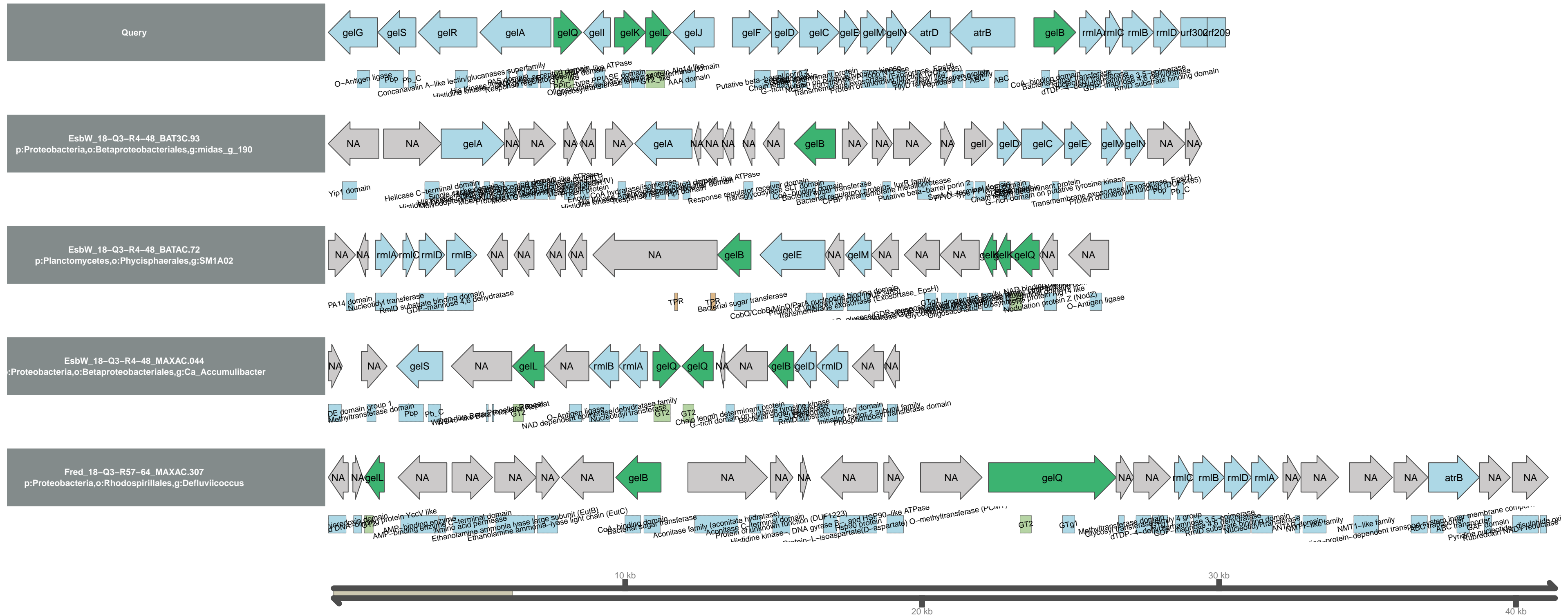
Operon Structure



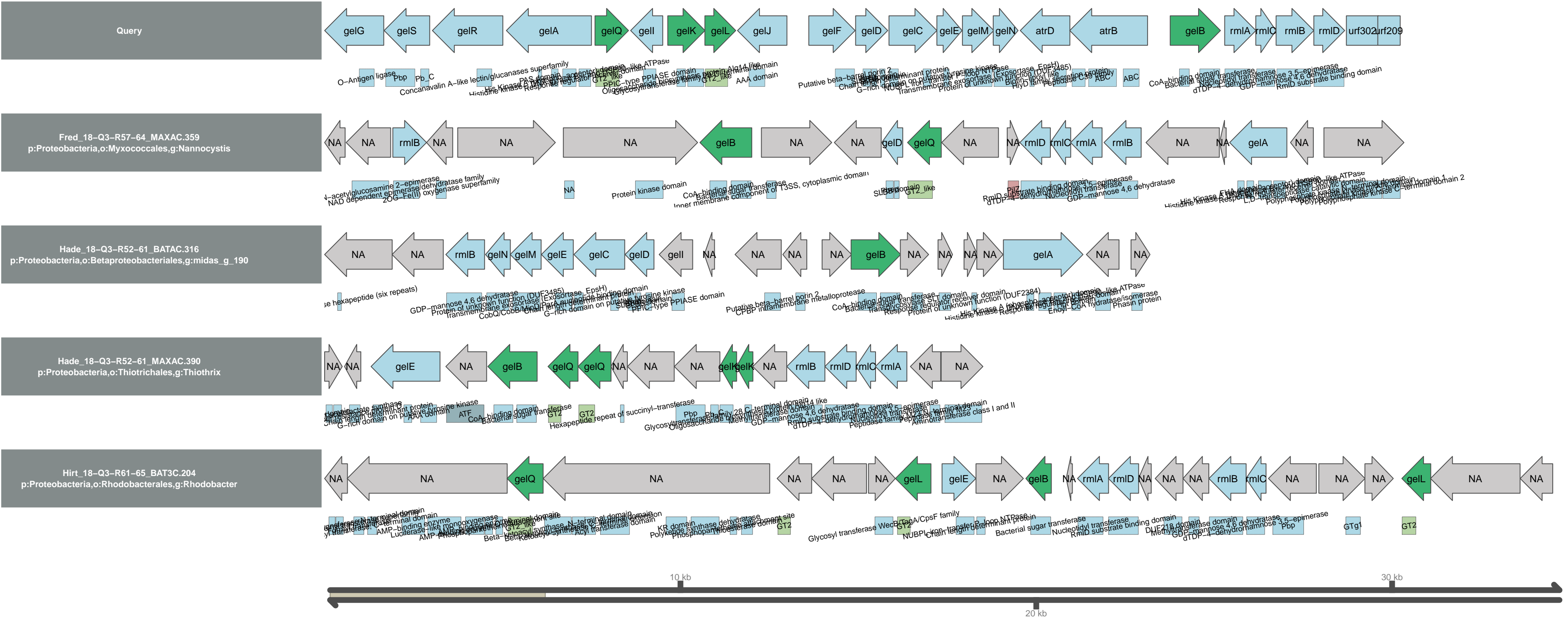
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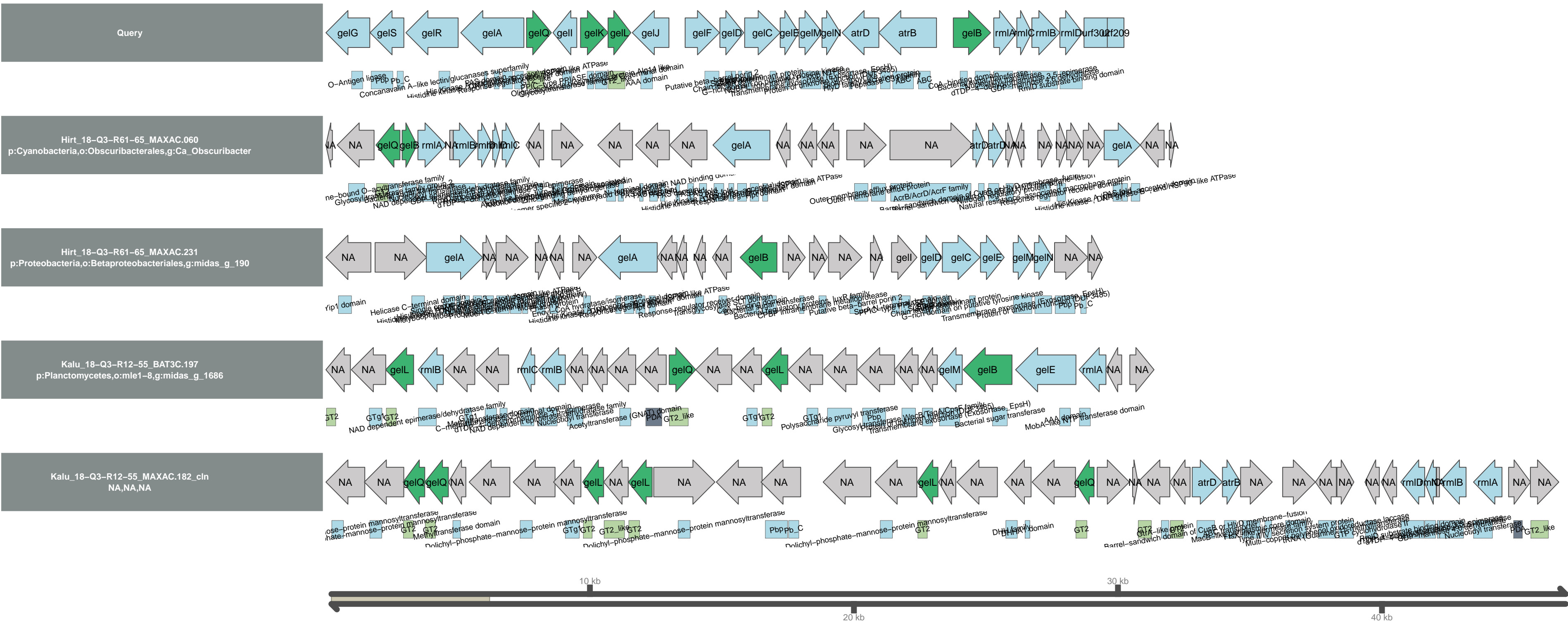
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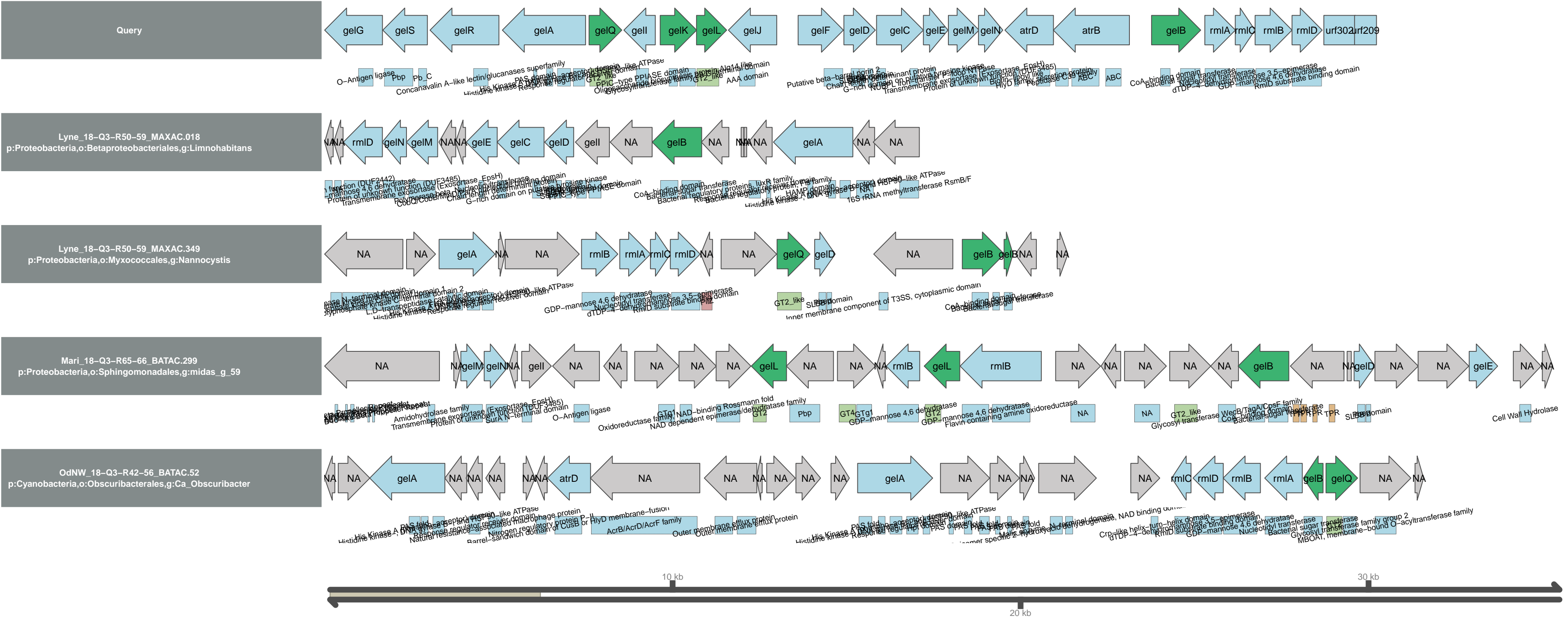
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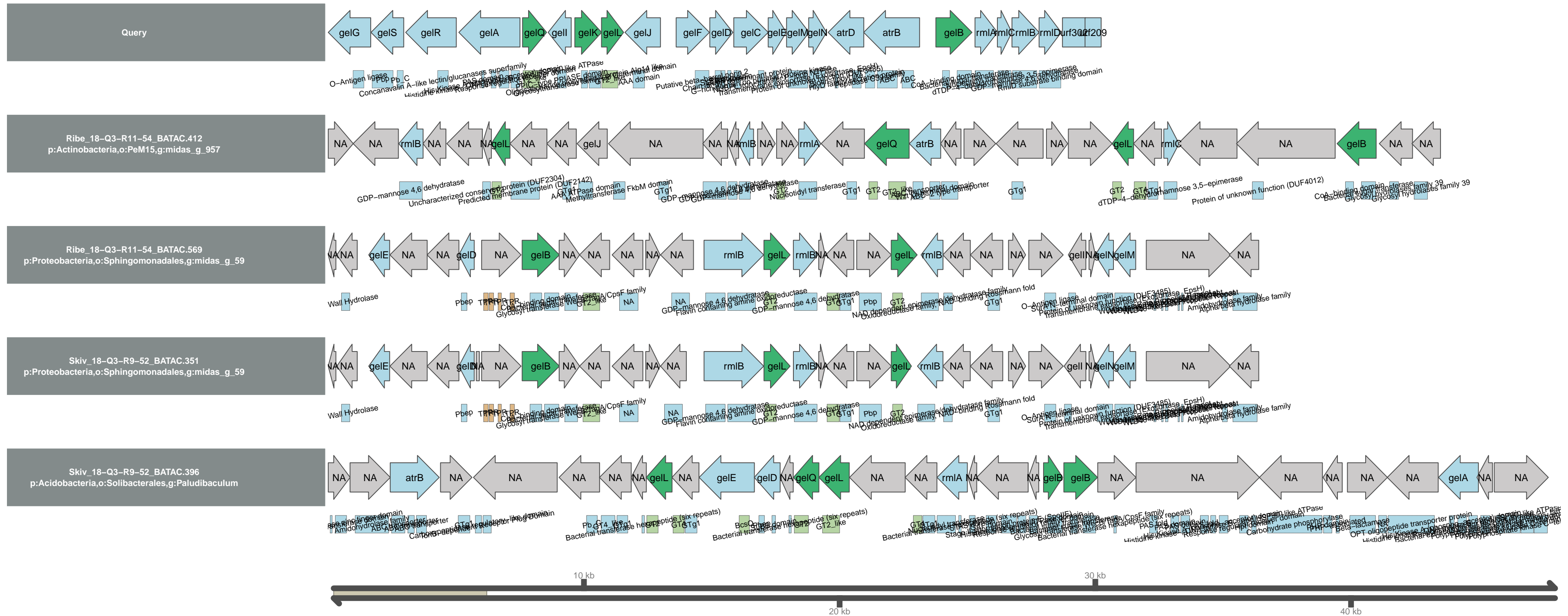
Operon Structure



Operon Structure



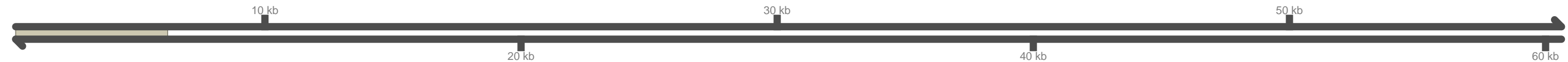
Operon Structure



Operon Structure

[illegible][illegible]

Genomic map of the *gel* locus in *E. coli* O157:H7. The map shows genes *gelA*, *atrD*, *atrB*, *gelD*, *gelE*, *gelL*, and *gelM*. Gene *gelL* is highlighted in green. Below the map, various protein families and domains are listed, including norylase superfamily, ATPase, ABC transporter, and various transferases and kinases.



	ID2	plot_tax	seqname	start	Query_label	ProkkaNO
1	AalE_18-Q3-R2-46_BAT3C.277	p:Proteobacteria,o:Sphingomonadales,g:midas_g_59	tig00006887-10-1241280	47318	gelB	02089
2	AalW_18-Q3-R10-53_BATAC.174	p:Proteobacteria,o:Rhodobacterales,g:Rhodobacter	tig00006255-10-4666680	182185	gelB	00803
3	AalW_18-Q3-R10-53_BATAC.245	p:Proteobacteria,o:Sphingomonadales,g:midas_g_59	tig01697704-10-12945580	678564	gelB	02968
4	Aved_18-Q3-R54-62_BATAC.490	p:Proteobacteria,o:Sphingomonadales,g:midas_g_59	tig00373198-10-16596610	605926	gelB	02143
5	Aved_18-Q3-R54-62_MAXAC.397_sub	p:Proteobacteria,o:Myxococcales,g:Nannocystis	tig00000424-10-34564120	673176	gelA	00566
6	Bjer_18-Q3-R1-45_BAT3C.347	p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_190	tig00199796-10-9414780	87217	gelA	03848
7	Bjer_18-Q3-R1-45_BATAC.230	p:Proteobacteria,o:Betaproteobacteriales,g:Ellin6067	tig00009630-10-1594380	67661	gelB	02865
8	Bjer_18-Q3-R1-45_BATAC.569	p:Proteobacteria,o:Betaproteobacteriales,g:Limnohabitans	tig00012007-10-1205650	99079	gelA	02373
9	Ega_18-Q3-R5-49_BATAC.204	p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_190	tig00004277-10-2003480	158480	gelA	03657
10	Ejby_18-Q3-R6-50_BATAC.123	p:Cyanobacteria,o:Obscuribacterales,g:Ca_Obscuribacter	tig00018983-10-500140	16135	atrD	05458
11	EsbE_18-Q3-R3-47_BATAC.463	p:Proteobacteria,o:Sphingomonadales,g:midas_g_59	tig00004449-10-2095470	173883	gelB	00746
12	EsbW_18-Q3-R4-48_BAT3C.207	p:Proteobacteria,o:Betaproteobacteriales,g:Leptothrix	tig00001176-10-9861400	273828	gelC	02014
13	EsbW_18-Q3-R4-48_BAT3C.93	p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_190	tig00000038-10-43439960	2137457	gelA	02037
14	EsbW_18-Q3-R4-48_BATAC.72	p:Planctomycetes,o:Phycisphaerales,g:SM1A02	tig00011125-10-1386600	104804	gelB	03060
15	EsbW_18-Q3-R4-48_MAXAC.044	p:Proteobacteria,o:Betaproteobacteriales,g:Ca_Accumulibacter	tig00033796-10-615360	28982	gelB	03344
16	Fred_18-Q3-R57-64_MAXAC.307	p:Proteobacteria,o:Rhodospirillales,g:Defluviicoccus	tig00002301-10-12040470	1011128	atrB	03305
17	Fred_18-Q3-R57-64_MAXAC.359	p:Proteobacteria,o:Myxococcales,g:Nannocystis	tig00001995-10-14076520	736276	gelA	04240
18	Hade_18-Q3-R52-61_BATAC.316	p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_190	tig00000808-10-11321960	743853	gelA	00676
19	Hade_18-Q3-R52-61_MAXAC.390	p:Proteobacteria,o:Thiotrichales,g:Thiothrix	tig00000011-10-40151770	1765403	gelB	01701
20	Hirt_18-Q3-R61-65_BAT3C.204	p:Proteobacteria,o:Rhodobacterales,g:Rhodobacter	tig00317261-10-8095540	421901	gelB	02777
21	Hirt_18-Q3-R61-65_MAXAC.060	p:Cyanobacteria,o:Obscuribacterales,g:Ca_Obscuribacter	tig00010514-10-2077950	78969	atrD	02874
22	Hirt_18-Q3-R61-65_MAXAC.231	p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_190	tig00000003-10-42710140	580316	gelA	00552
23	Kalu_18-Q3-R12-55_BAT3C.197	p:Planctomycetes,o:mle1-8,g:midas_g_1686	tig00000698-10-18309200	1181474	gelB	00989
24	Kalu_18-Q3-R12-55_MAXAC.182_cln	NA,NA,NA	tig00000428-10-12728800	970939	atrB	00954
25	Lyne_18-Q3-R50-59_MAXAC.018	p:Proteobacteria,o:Betaproteobacteriales,g:Limnohabitans	tig00321118-10-792010	14257	gelA	02866

ID2		plot_tax	seqname	start	Query_label	ProkkaNO
1	Lyne_18-Q3-R50-59_MAXAC.349	p:Proteobacteria,o:Myxococcales,g:Nannocystis	tig00007064-10-3813790	226741	gelA	05638
2	Mari_18-Q3-R65-66_BATAC.299	p:Proteobacteria,o:Sphingomonadales,g:midas_g_59	tig00869144-10-6422420	425053	gelB	02515
3	OdNW_18-Q3-R42-56_BATAC.52	p:Cyanobacteria,o:Obscuribacterales,g:Ca_Obscuribacter	tig00000564-10-8675060	796195	atrD	04582
4	Ribe_18-Q3-R11-54_BATAC.412	p:Actinobacteria,o:PeM15,g:midas_g_957	tig00001979-10-5826140	263605	atrB	01129
5	Ribe_18-Q3-R11-54_BATAC.569	p:Proteobacteria,o:Sphingomonadales,g:midas_g_59	tig01084768-10-3860630	331823	gelB	03107
6	Skiv_18-Q3-R9-52_BATAC.351	p:Proteobacteria,o:Sphingomonadales,g:midas_g_59	tig00287756-10-1221250	85581	gelB	03425
7	Skiv_18-Q3-R9-52_BATAC.396	p:Acidobacteria,o:Solibacterales,g:Paludibaculum	tig00003208-10-5214800	237399	atrB	01745
8	Vibo_18-Q3-R45-57_BATAC.199	p:Proteobacteria,o:Betaproteobacteriales,g:Propionivibrio	tig00008044-10-802880	47367	gelB	01871
9	Vibo_18-Q3-R45-57_BATAC.463	p:Cyanobacteria,o:Obscuribacterales,g:Ca_Obscuribacter	tig00002248-10-4417980	430639	atrD	05130
10	Vibo_18-Q3-R45-57_MAXAC.083	p:Bacteroidetes,o:Sphingobacteriales,g:midas_g_300	tig00004163-10-3243870	299574	atrB	00314
11	Viby_18-Q3-R106-67_BAT3C.260	p:Acidobacteria,o:Holophagales,g:midas_g_201	tig00000170-10-6009320	315735	atrB	01137