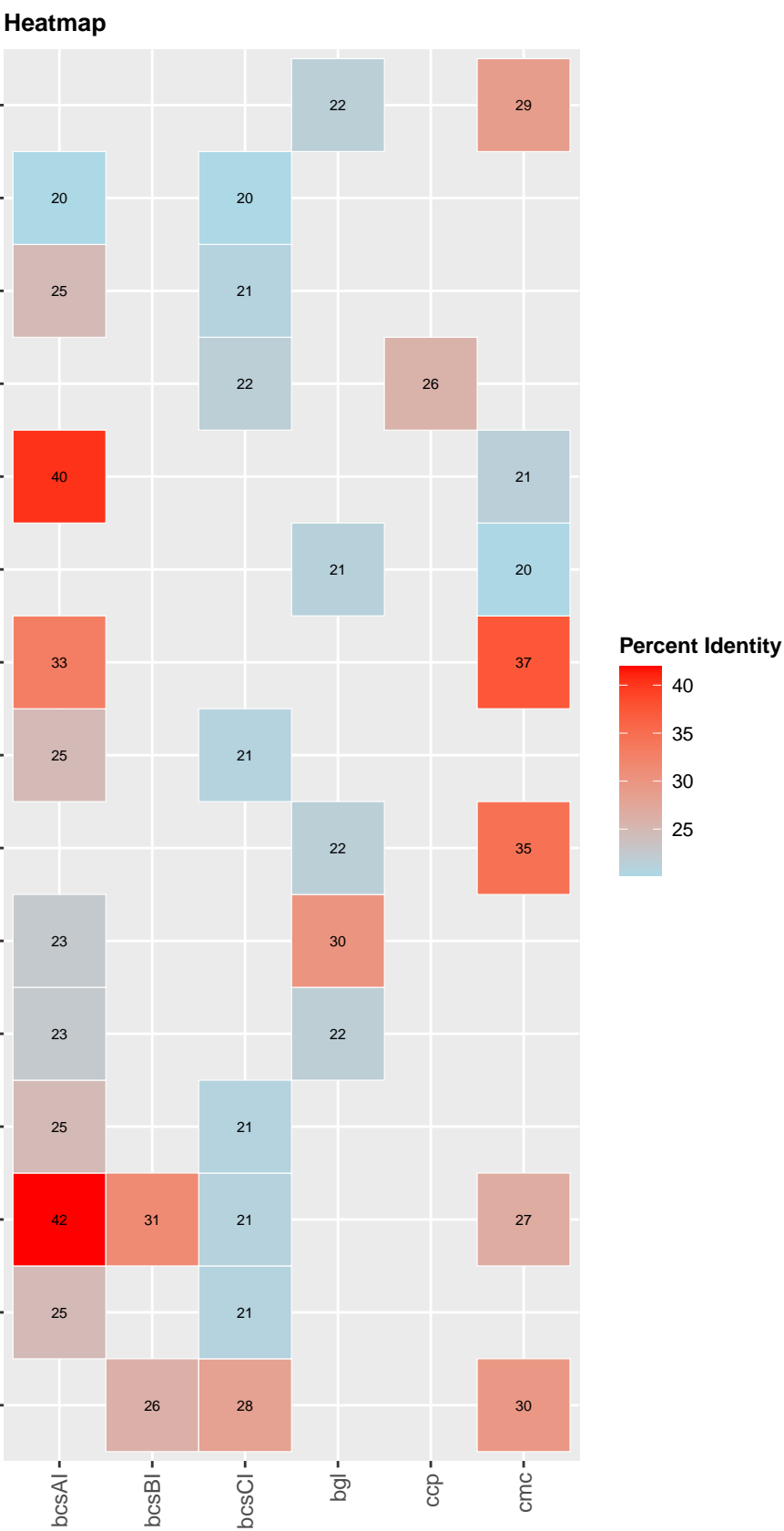
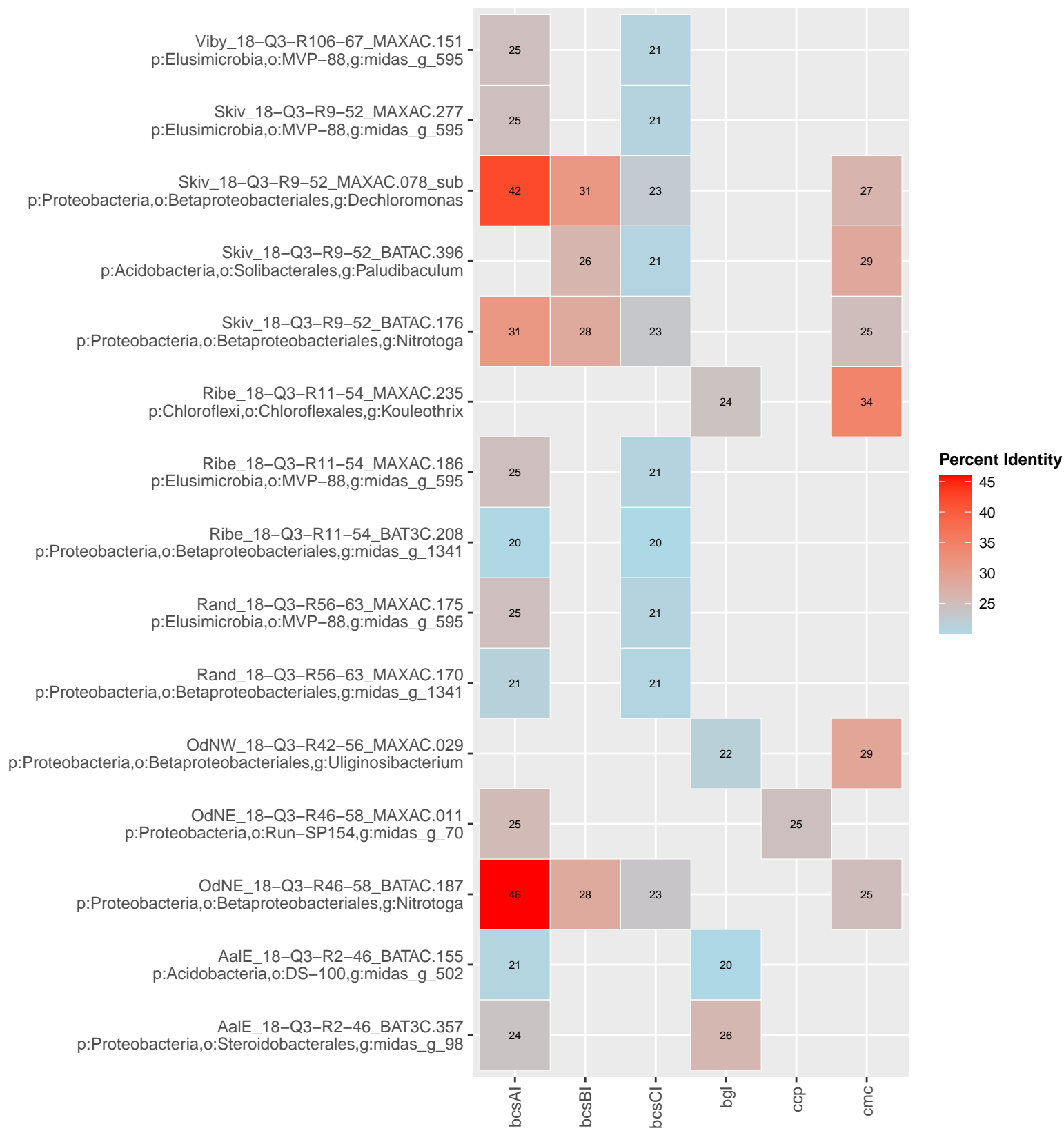


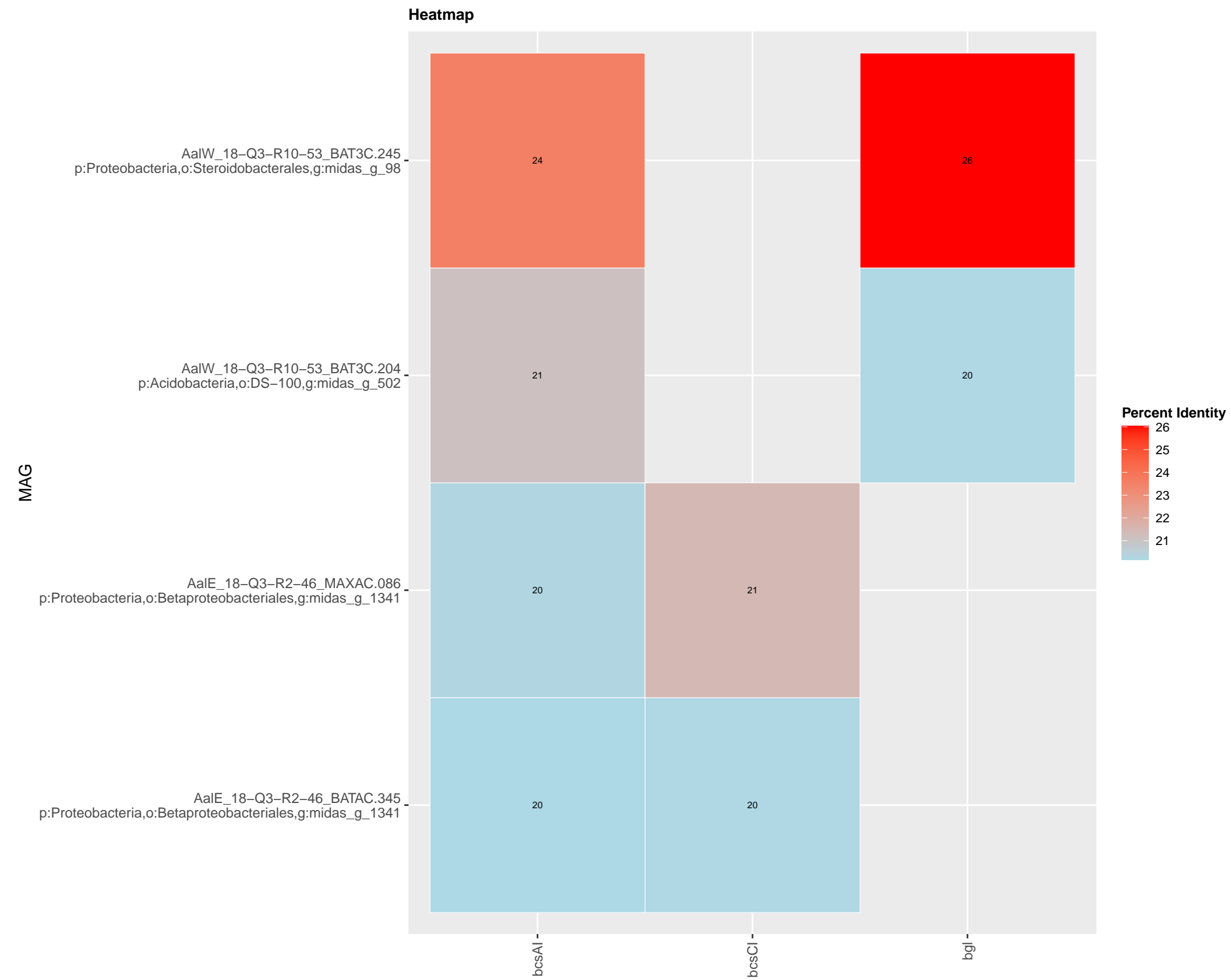
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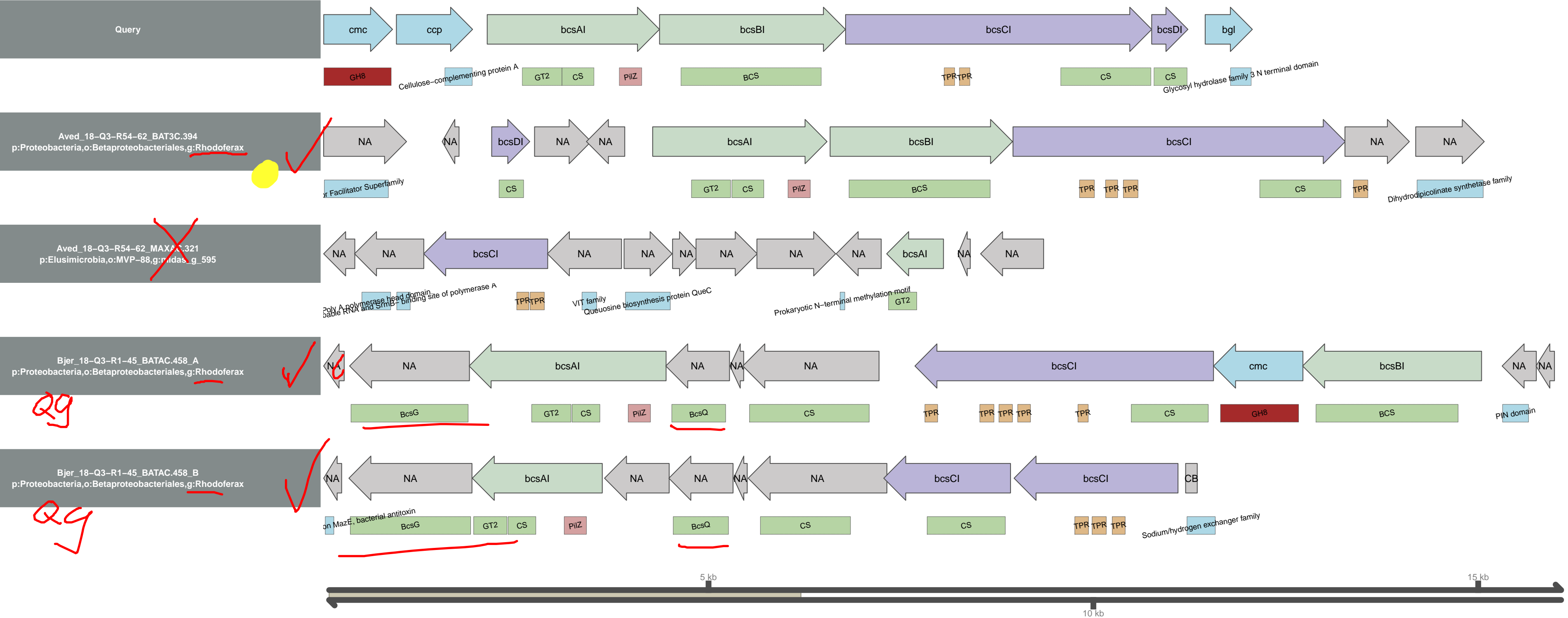
MAG

Heatmap

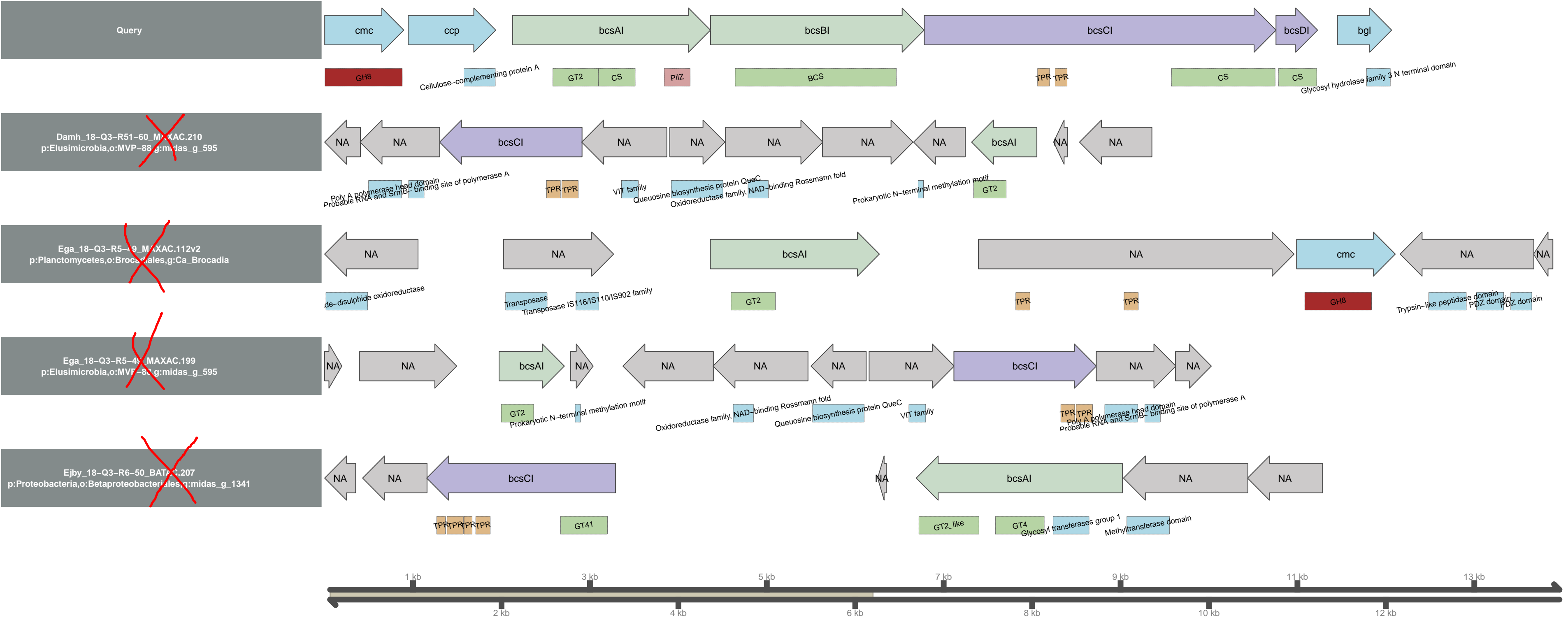




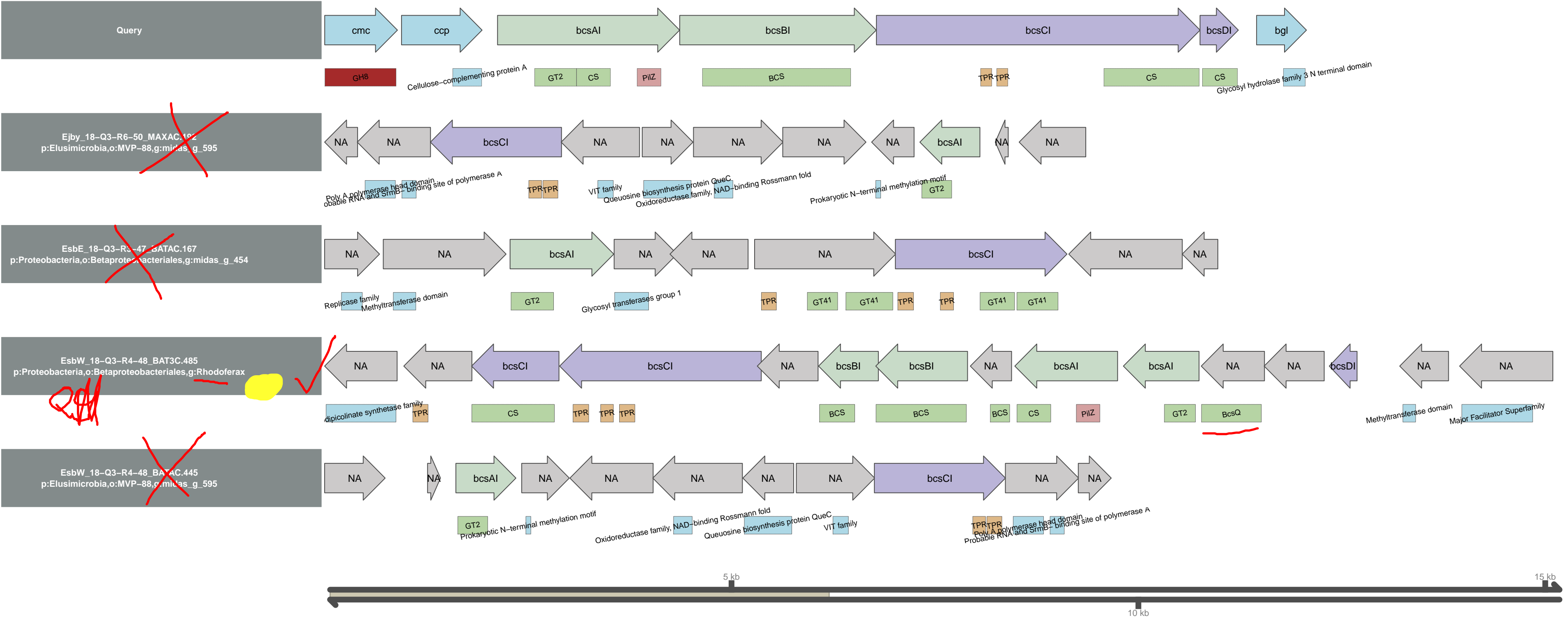
Operon Structure



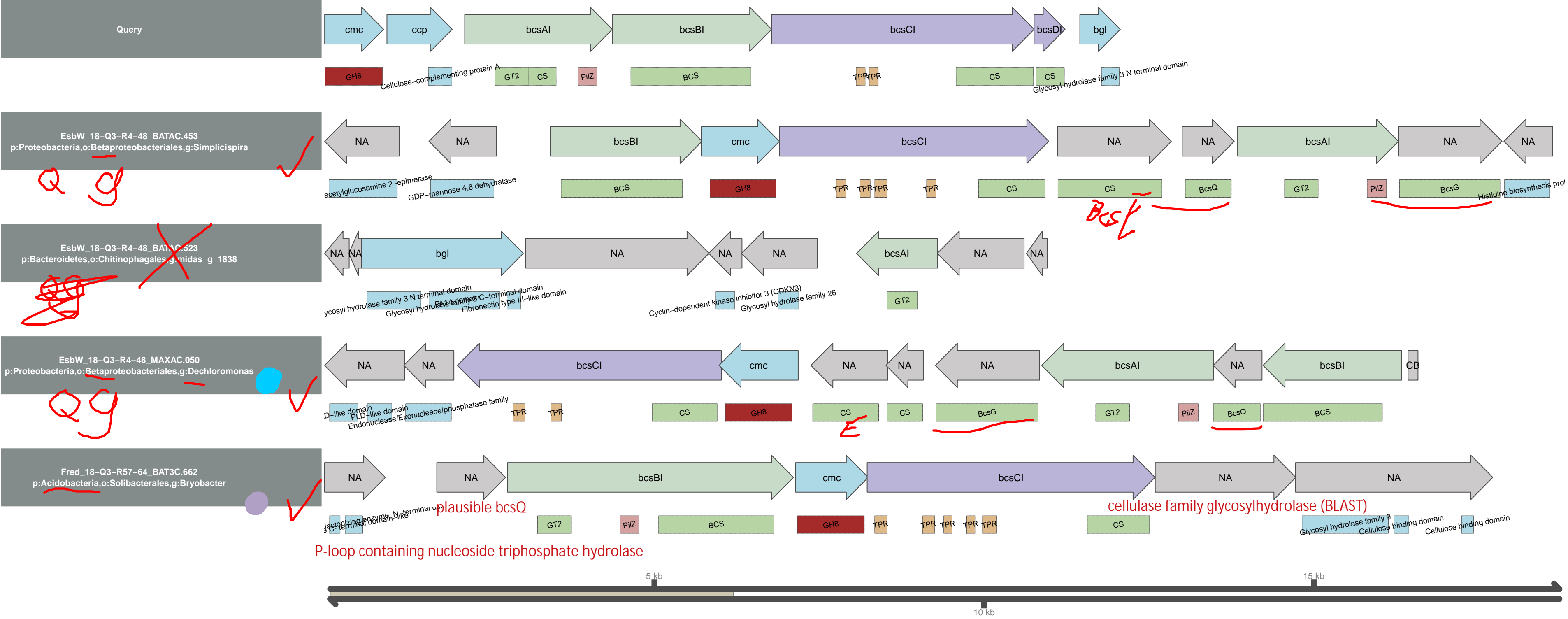
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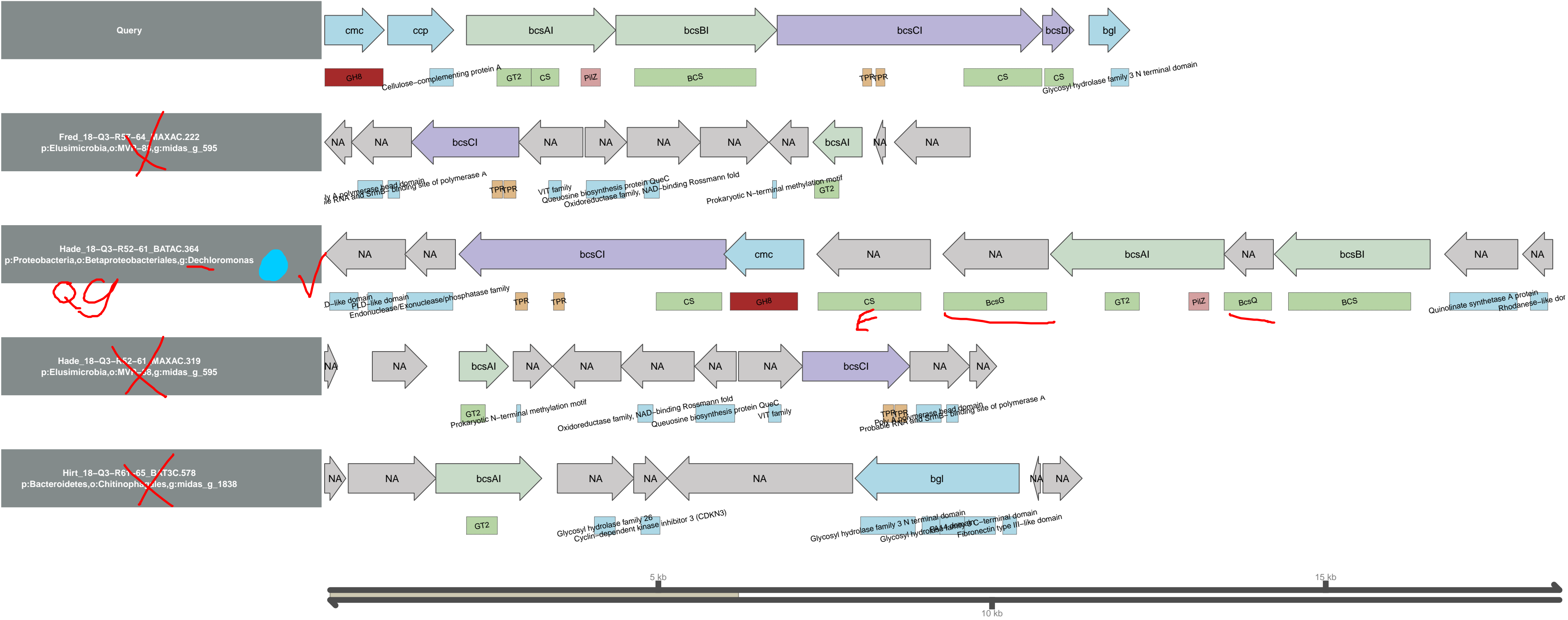
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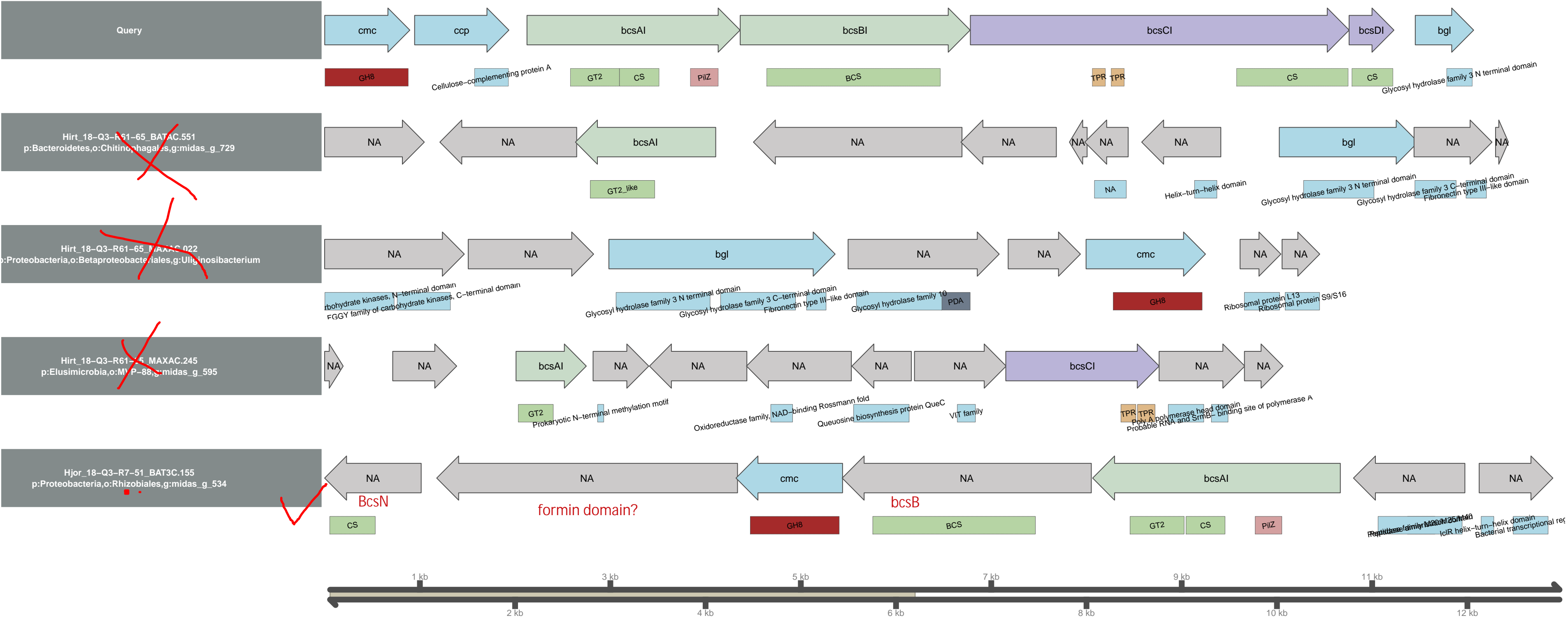
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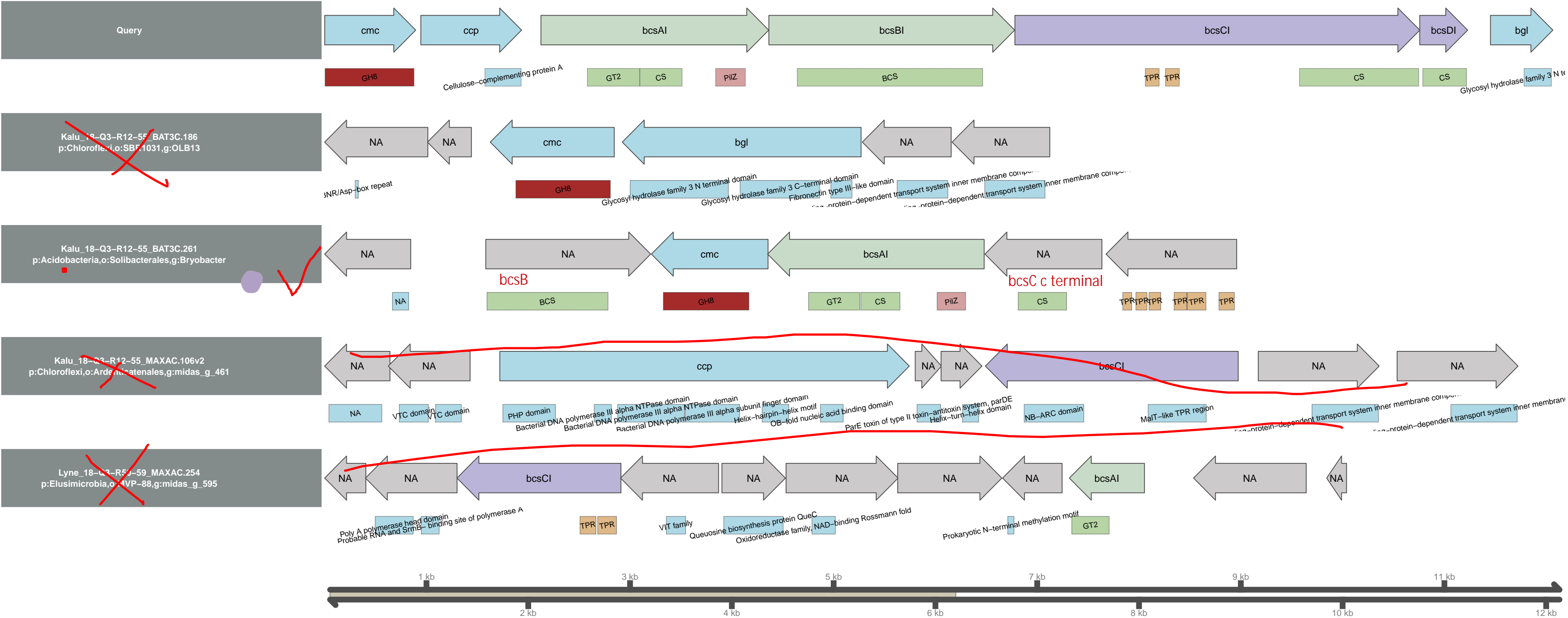
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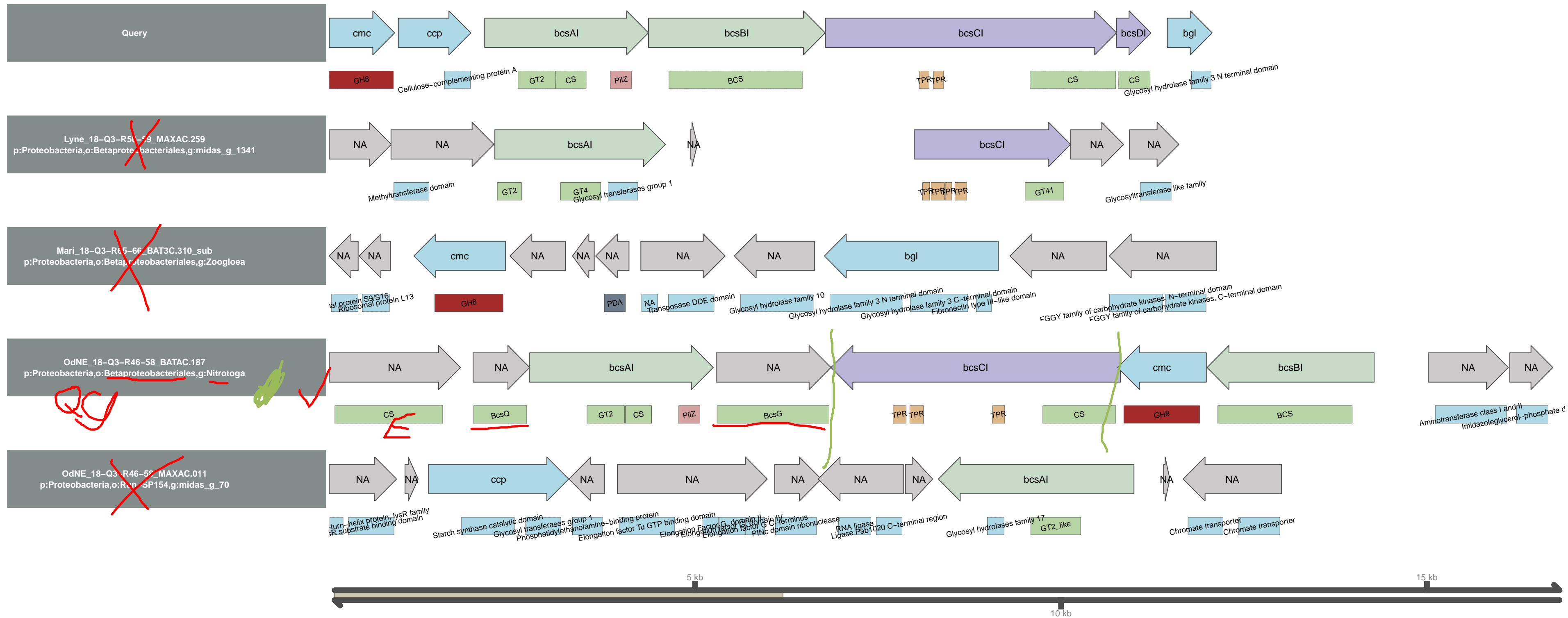
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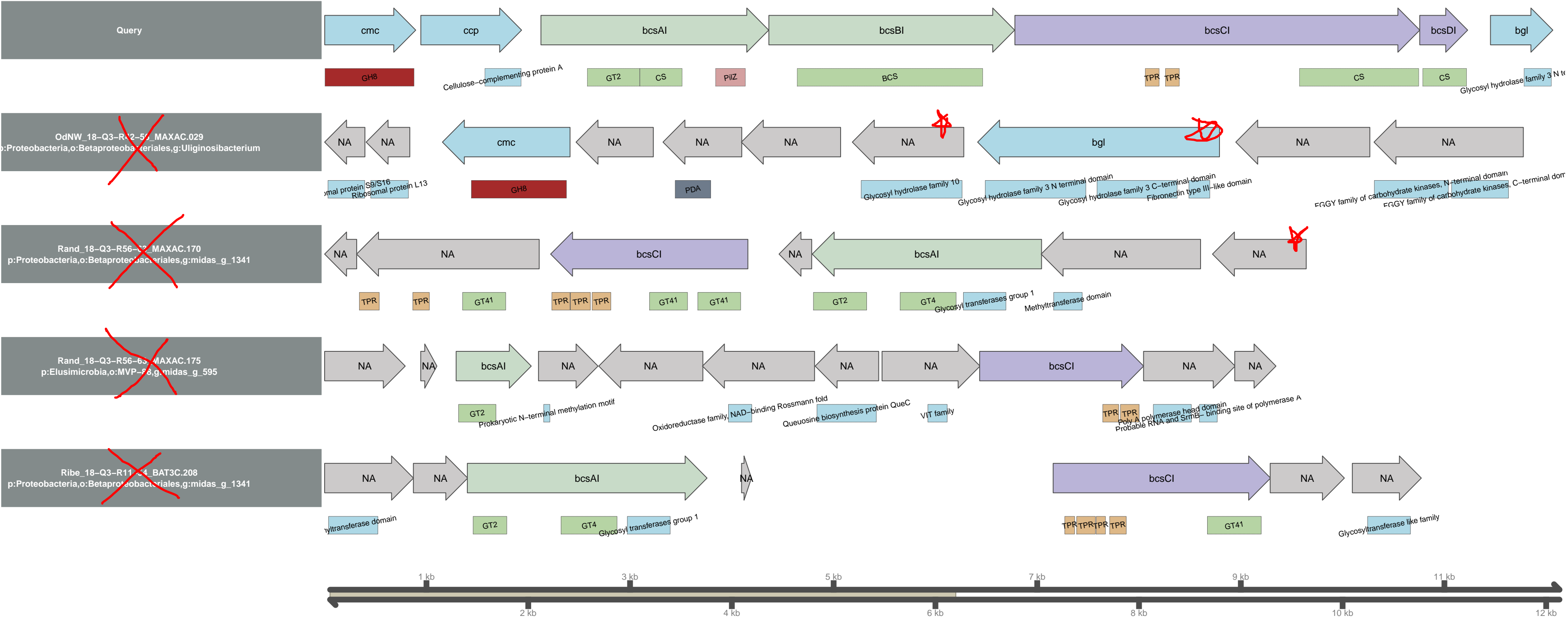
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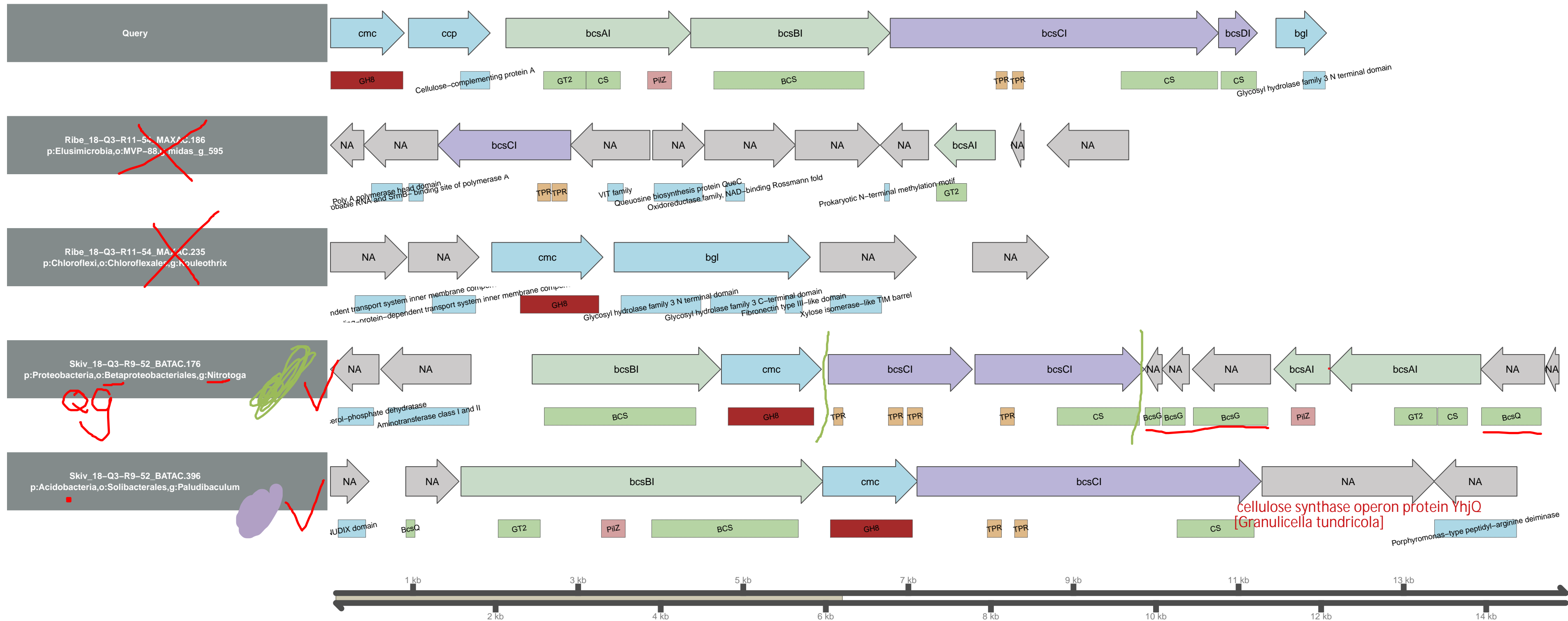
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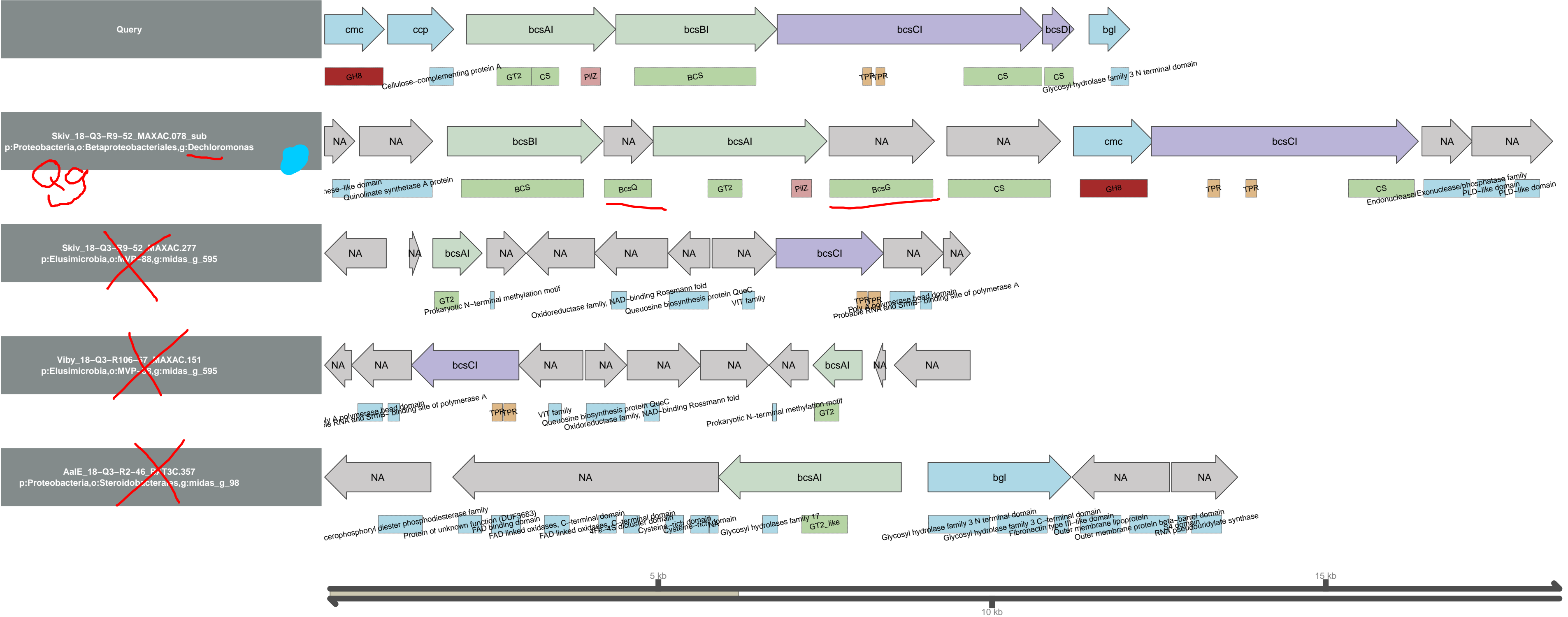
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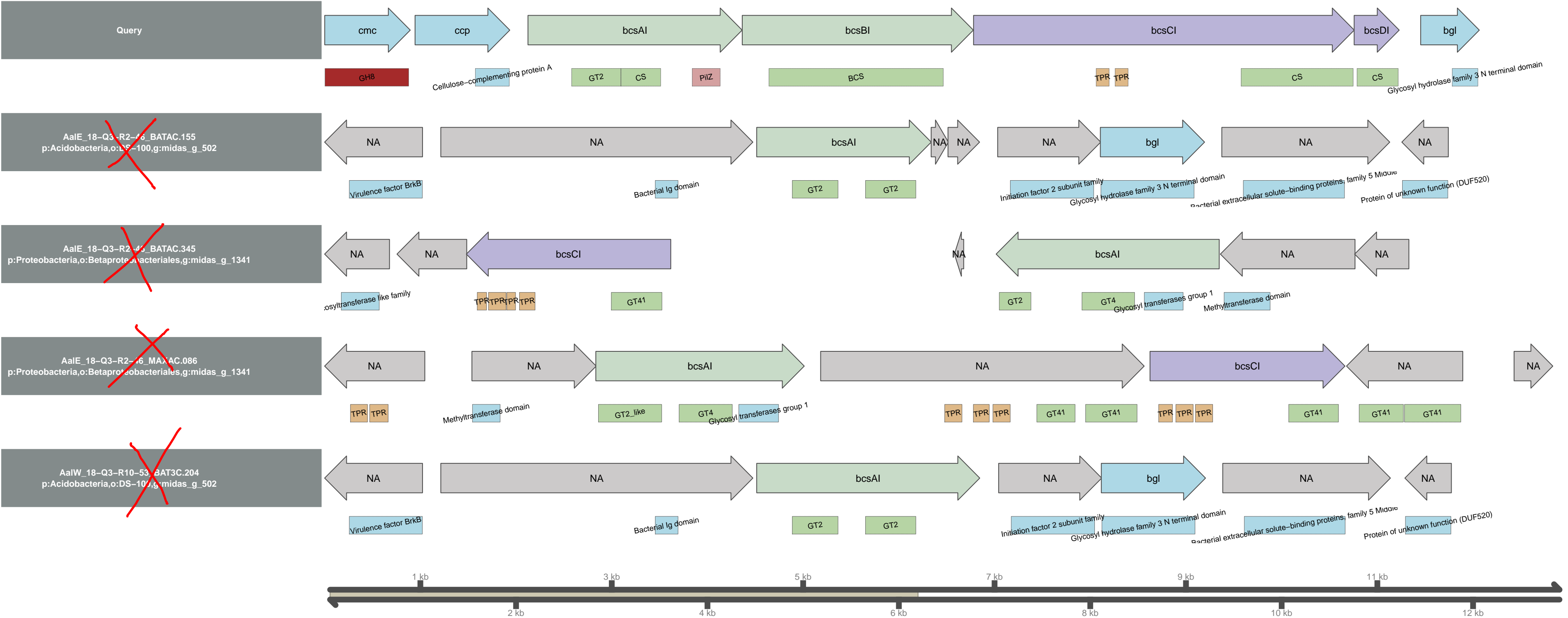
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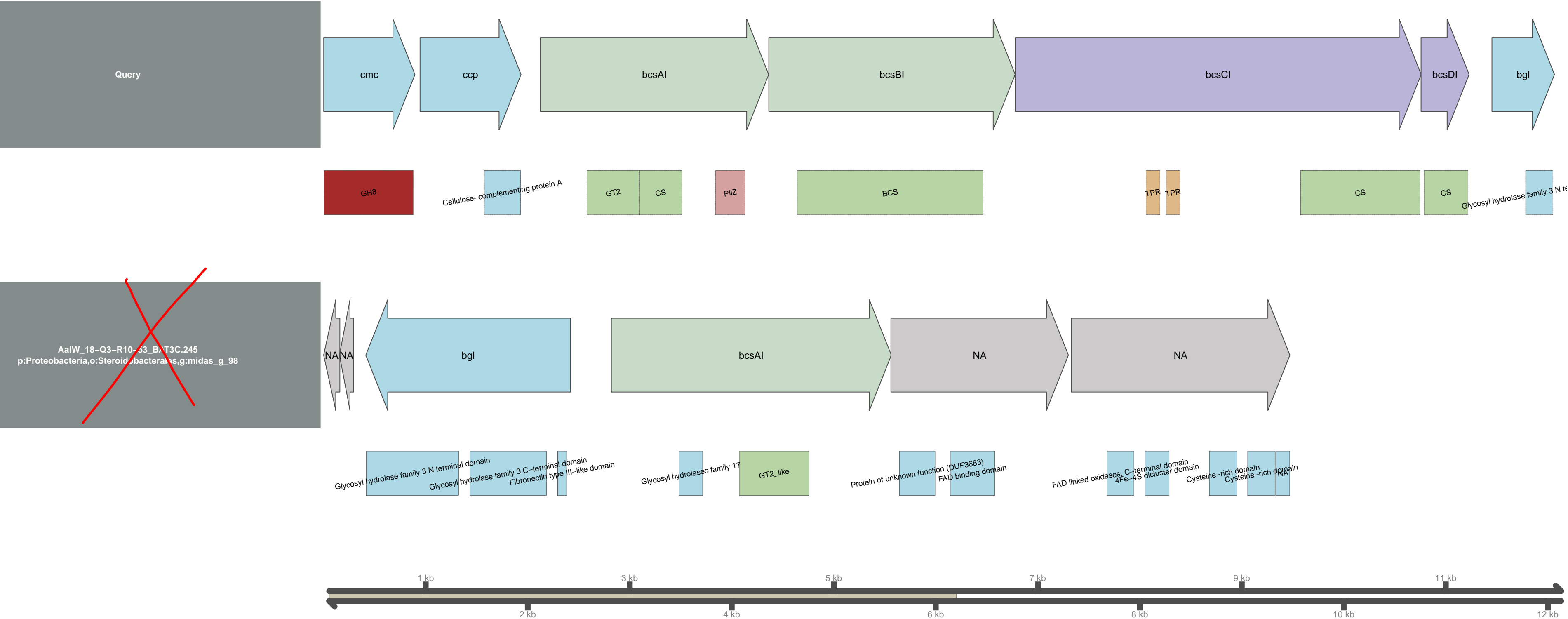
Operon Structure



Operon Structure



Operon Structure



	ID2	plot_tax	seqname	start	Query_label	ProkkaNO
1	AalE_18-Q3-R2-46_BAT3C.357	p:Proteobacteria,o:Steroidobacterales,g:midas_g_98	tig00004397-10-3020980	53916	bcsAI	00957
2	AalE_18-Q3-R2-46_BATAC.155	p:Acidobacteria,o:DS-100,g:midas_g_502	tig00003873-10-3436420	242886	bcsAI	01757
3	AalE_18-Q3-R2-46_BATAC.345	p:Proteobacteria,o:Betaproteobacterales,g:midas_g_1341	tig00002178-10-4724040	236998	bcsAI	00195
4	AalE_18-Q3-R2-46_MAXAC.086	p:Proteobacteria,o:Betaproteobacterales,g:midas_g_1341	tig00015706-10-216600	4737	bcsAI	01656
5	AalW_18-Q3-R10-53_BAT3C.204	p:Acidobacteria,o:DS-100,g:midas_g_502	tig00016875-10-1983350	95163	bcsAI	02939
6	AalW_18-Q3-R10-53_BAT3C.245	p:Proteobacteria,o:Steroidobacterales,g:midas_g_98	tig00010978-10-2850530	34943	bcsAI	01426
7	Aved_18-Q3-R54-62_BAT3C.394	p:Proteobacteria,o:Betaproteobacterales,g:Rhodoferax	tig01608118-10-14295950	484128	bcsAI	03919
8	Aved_18-Q3-R54-62_MAXAC.321	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00000302-10-25166900	1695374	bcsAI	01477
9	Bjer_18-Q3-R1-45_BATAC.458_A	p:Proteobacteria,o:Betaproteobacterales,g:Rhodoferax	tig00001862-10-6955040	304719	bcsAI	00257
10	Bjer_18-Q3-R1-45_BATAC.458_B	p:Proteobacteria,o:Betaproteobacterales,g:Rhodoferax	tig00003241-10-469790	37438	bcsAI	01831
11	Damh_18-Q3-R51-60_MAXAC.210	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00000292-10-7440630	707129	bcsAI	02125
12	Ega_18-Q3-R5-49_MAXAC.112v2	p:Planctomycetes,o:Brocadiales,g:Ca_Brocadia	tig00000002-10-32561090	864182	bcsAI	00815
13	Ega_18-Q3-R5-49_MAXAC.199	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00004062-10-2279720	51224	bcsAI	02055
14	Ejby_18-Q3-R6-50_BATAC.207	p:Proteobacteria,o:Betaproteobacterales,g:midas_g_1341	tig00001219-10-4727790	59737	bcsAI	00712
15	Ejby_18-Q3-R6-50_MAXAC.192	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00000024-10-25242610	1615219	bcsAI	01360
16	EsbE_18-Q3-R3-47_BATAC.167	p:Proteobacteria,o:Betaproteobacterales,g:midas_g_454	tig00008171-10-824870	71073	bcsAI	02164
17	EsbW_18-Q3-R4-48_BAT3C.485	p:Proteobacteria,o:Betaproteobacterales,g:Rhodoferax	tig00020141-10-609230	22885	bcsAI	03737
18	EsbW_18-Q3-R4-48_BATAC.445	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00004595-10-3816970	31208	bcsAI	01209
19	EsbW_18-Q3-R4-48_BATAC.453	p:Proteobacteria,o:Betaproteobacterales,g:Simplicispira	tig00014047-10-1285900	106609	bcsAI	01813
20	EsbW_18-Q3-R4-48_BATAC.523	p:Bacteroidetes,o:Chitinophagales,g:midas_g_1838	tig00002958-10-6732880	188715	bcsAI	00832
21	EsbW_18-Q3-R4-48_MAXAC.050	p:Proteobacteria,o:Betaproteobacterales,g:Dechloromonas	tig00018082-10-889440	83447	bcsAI	03083
22	Fred_18-Q3-R57-64_BAT3C.662	p:Acidobacteria,o:Solibacterales,g:Bryobacter	tig00006256-10-5425100	396711	bcsBI	01773
23	Fred_18-Q3-R57-64_MAXAC.222	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00000202-10-25454520	2463238	bcsAI	02108
24	Hade_18-Q3-R52-61_BATAC.364	p:Proteobacteria,o:Betaproteobacterales,g:Dechloromonas	tig00407471-10-3182230	146325	bcsAI	03000
25	Hade_18-Q3-R52-61_MAXAC.319	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00013332-10-1613710	60757	bcsAI	02127

	ID2	plot_tax	seqname	start	Query_label	ProkkaNO
1	Hirt_18-Q3-R61-65_BAT3C.578	p:Bacteroidetes,o:Chitinophagales,g:midas_g_1838	tig00005850-10-2890570	78592	bcsAI	03735
2	Hirt_18-Q3-R61-65_BATAC.551	p:Bacteroidetes,o:Chitinophagales,g:midas_g_729	tig00006048-10-3784910	6222	bcsAI	02345
3	Hirt_18-Q3-R61-65_MAXAC.022	p:Proteobacteria,o:Betaproteobacteriales,g:Uliginosibacterium	tig00008471-10-3272170	86112	bgl	00112
4	Hirt_18-Q3-R61-65_MAXAC.245	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00015913-10-1166340	37940	bcsAI	01910
5	Hjor_18-Q3-R7-51_BAT3C.155	p:Proteobacteria,o:Rhizobiales,g:midas_g_534	tig00002714-1981250-5975520	159282	bcsAI	01030
6	Kalu_18-Q3-R12-55_BAT3C.186	p:Chloroflexi,o:SBR1031,g:OLB13	tig00000584-10-21303060	280325	bgl	00221
7	Kalu_18-Q3-R12-55_BAT3C.261	p:Acidobacteria,o:Solibacterales,g:Bryobacter	tig00004141-10-2319180	89372	bcsAI	03037
8	Kalu_18-Q3-R12-55_MAXAC.106v2	p:Chloroflexi,o:Ardenticatenales,g:midas_g_461	tig00100734-10-59431720	2251808	bcsCI	03824
9	Lyne_18-Q3-R50-59_MAXAC.254	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00002296-10-8929180	853669	bcsAI	00751
10	Lyne_18-Q3-R50-59_MAXAC.259	p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_1341	tig00005124-10-3344470	80195	bcsAI	01658
11	Mari_18-Q3-R65-66_BAT3C.310_sub	p:Proteobacteria,o:Betaproteobacteriales,g:Zoogloea	tig00004204-10-2745170	212189	bgl	00260
12	OdNE_18-Q3-R46-58_BATAC.187	p:Proteobacteria,o:Betaproteobacteriales,g:Nitrotoga	tig00013603-10-1108760	12689	bcsAI	01449
13	OdNE_18-Q3-R46-58_MAXAC.011	p:Proteobacteria,o:Run-SP154,g:midas_g_70	tig00001185-10-6730500	406363	bcsAI	03704
14	OdNW_18-Q3-R42-56_MAXAC.029	p:Proteobacteria,o:Betaproteobacteriales,g:Uliginosibacterium	tig00008739-10-1323550	51832	bgl	02965
15	Rand_18-Q3-R56-63_MAXAC.170	p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_1341	tig00224048-10-1871190	154794	bcsAI	03451
16	Rand_18-Q3-R56-63_MAXAC.175	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00052853-10-132870	3044	bcsAI	01612
17	Ribe_18-Q3-R11-54_BAT3C.208	p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_1341	tig01078798-10-7283700	84619	bcsAI	02150
18	Ribe_18-Q3-R11-54_MAXAC.186	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00001126-10-9167150	12722	bcsAI	00014
19	Ribe_18-Q3-R11-54_MAXAC.235	p:Chloroflexi,o:Chloroflexales,g:Kouleothrix	tig00000009-10-56372800	5353663	bgl	04180
20	Skiv_18-Q3-R9-52_BATAC.176	p:Proteobacteria,o:Betaproteobacteriales,g:Nitrotoga	tig00025195-10-609250	40291	bcsAI	01730
21	Skiv_18-Q3-R9-52_BATAC.396	p:Acidobacteria,o:Solibacterales,g:Paludibaculum	tig00002691-10-6419970	11117	bcsBI	00856
22	Skiv_18-Q3-R9-52_MAXAC.078_sub	p:Proteobacteria,o:Betaproteobacteriales,g:Dechloromonas	tig00014165-10-544790	30935	bcsAI	00765
23	Skiv_18-Q3-R9-52_MAXAC.277	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig01148445-10-14237630	760958	bcsAI	01708
24	Viby_18-Q3-R106-67_MAXAC.151	p:Elusimicrobia,o:MVP-88,g:midas_g_595	tig00591490-10-8803150	834623	bcsAI	02104