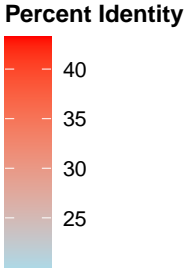
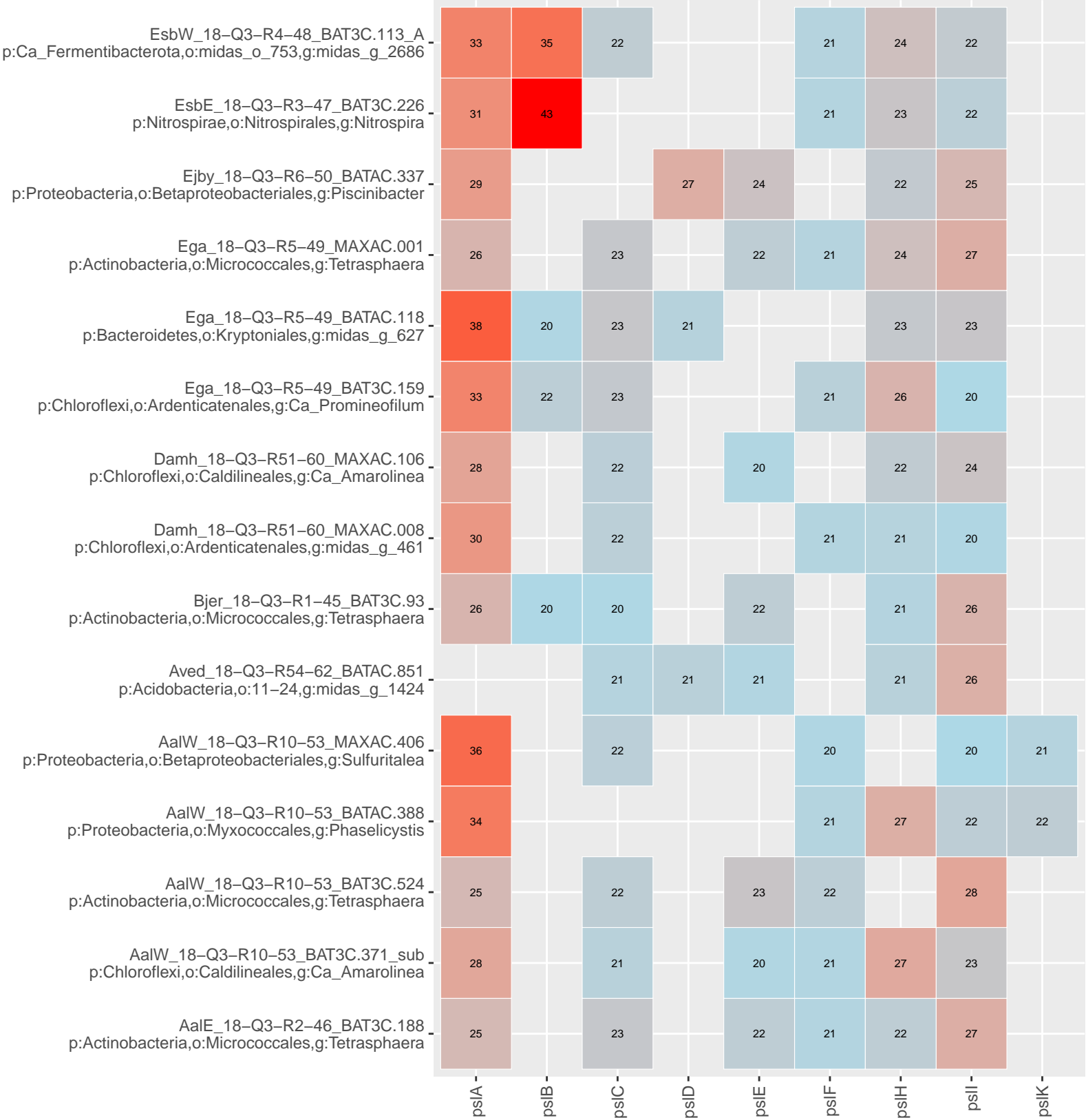


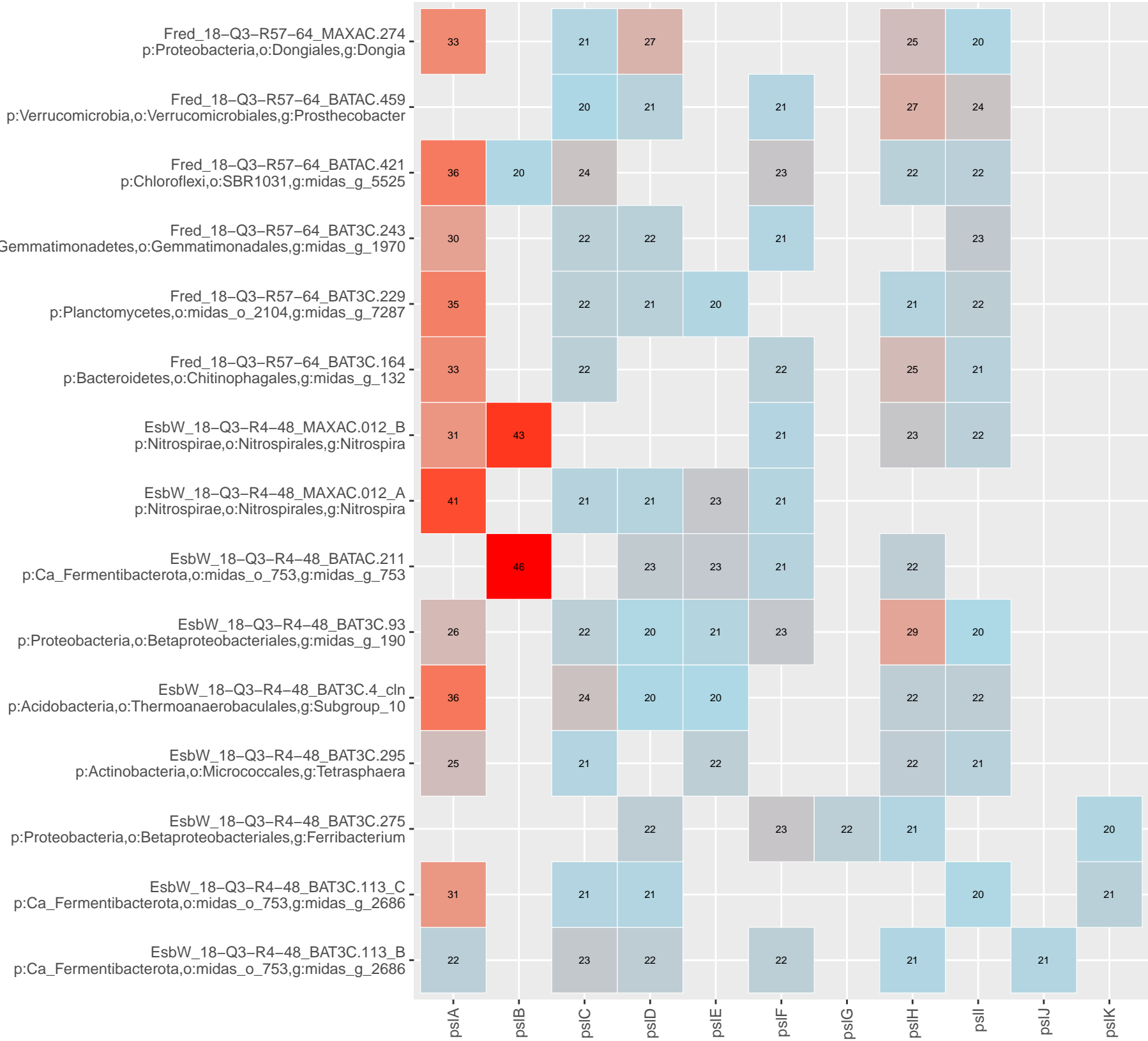
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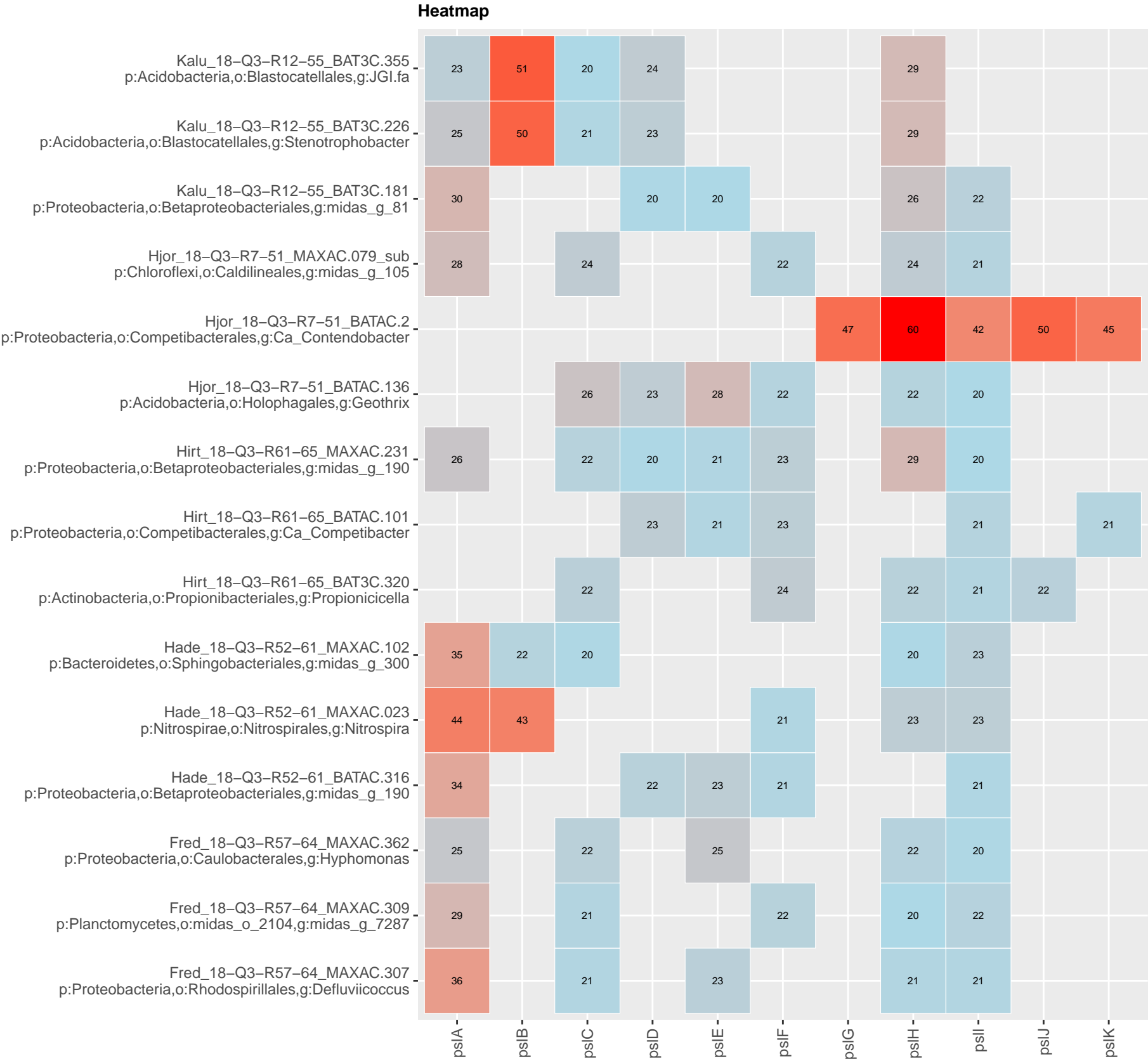


MAG

Heatmap

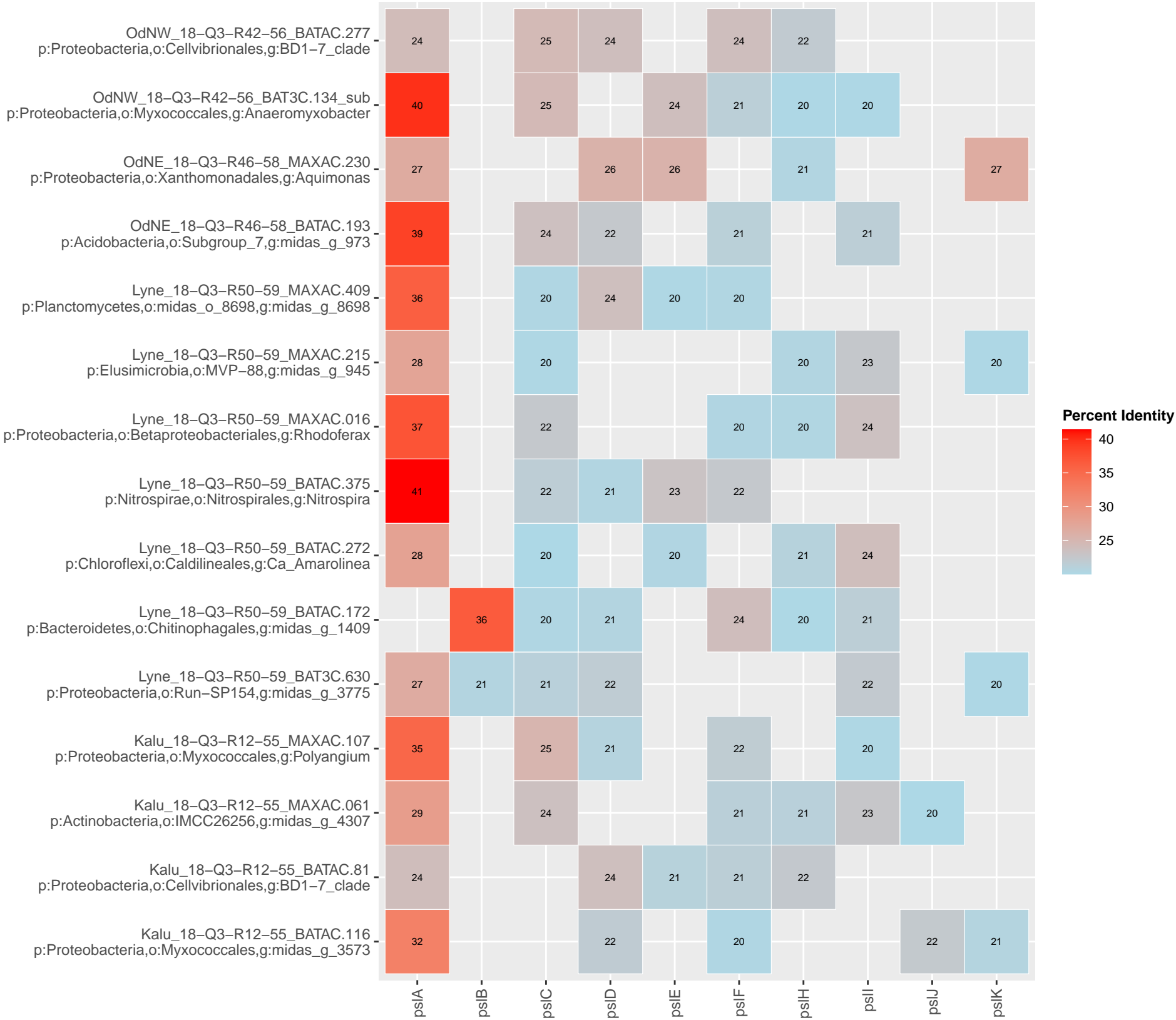


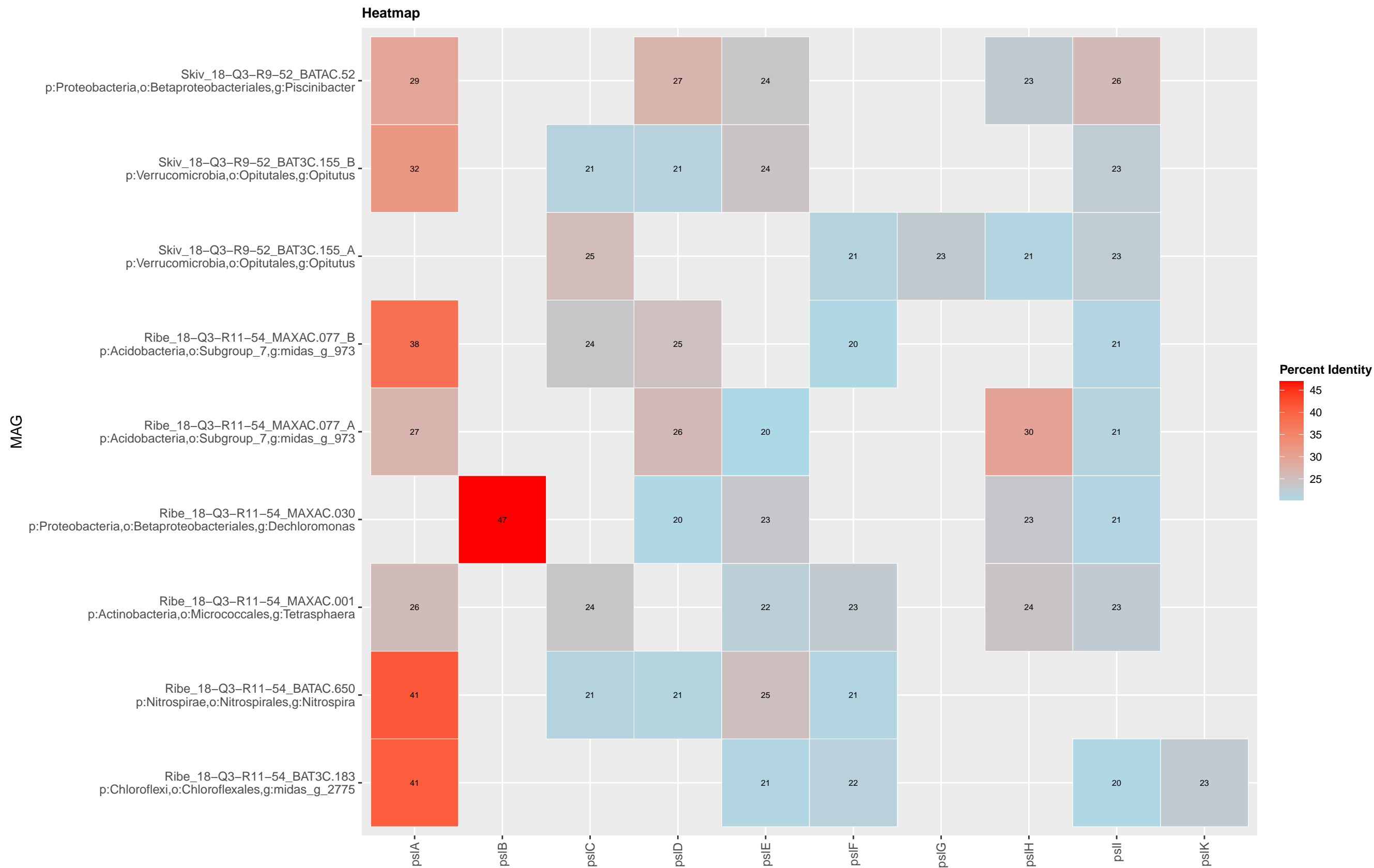
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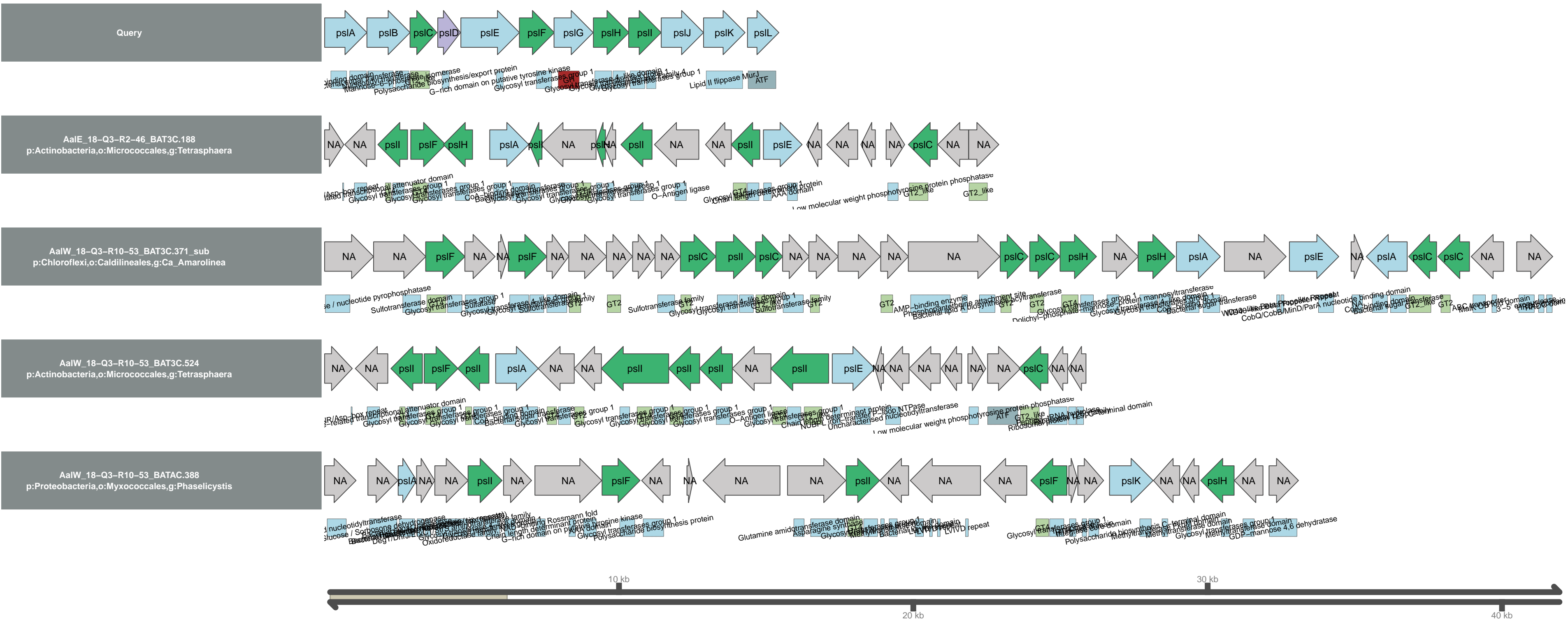
MAG

Heatmap

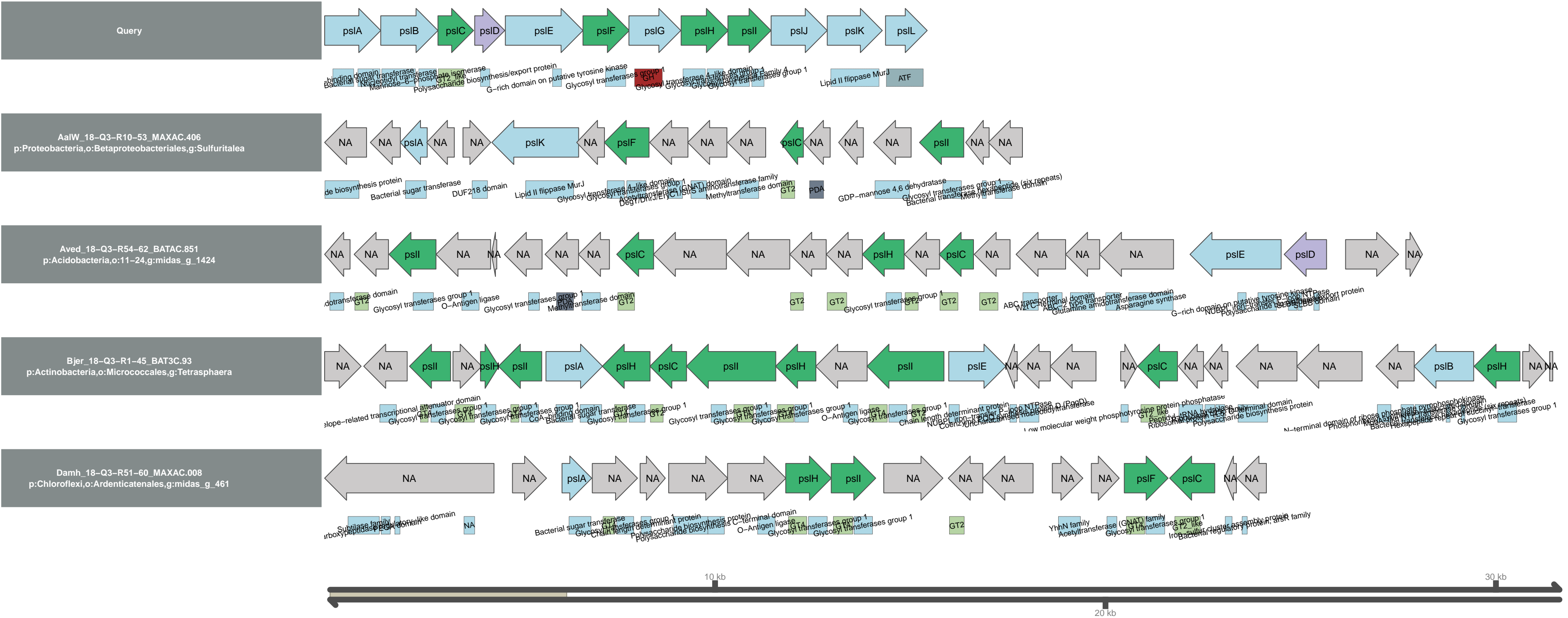




Operon Structure

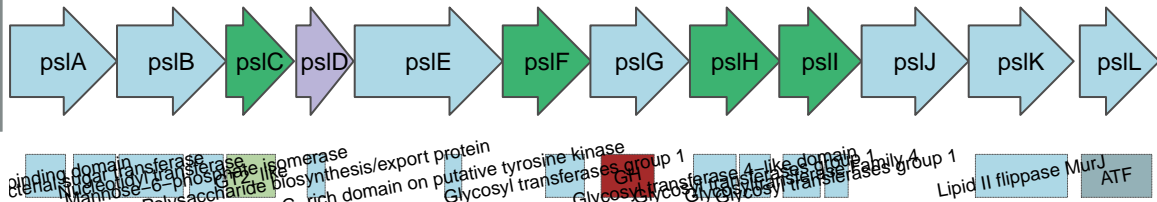


Operon Structure

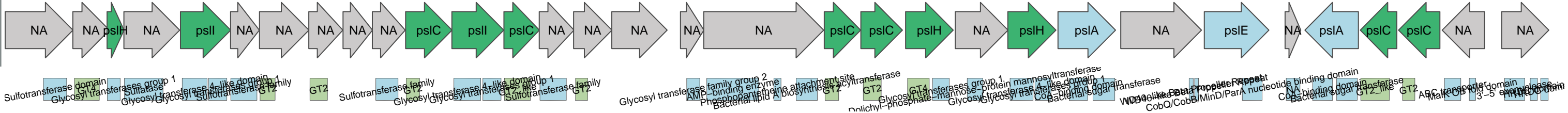


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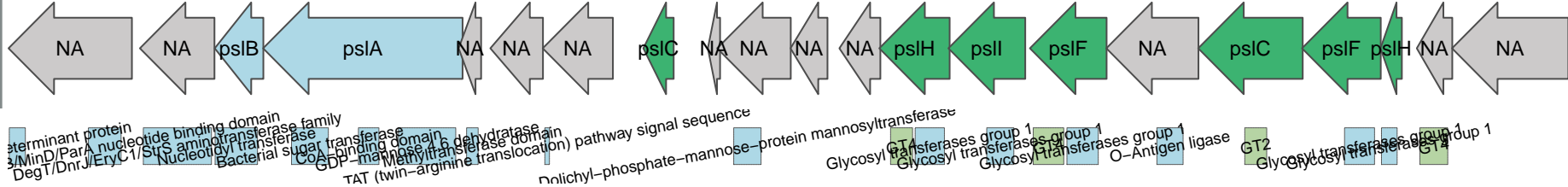
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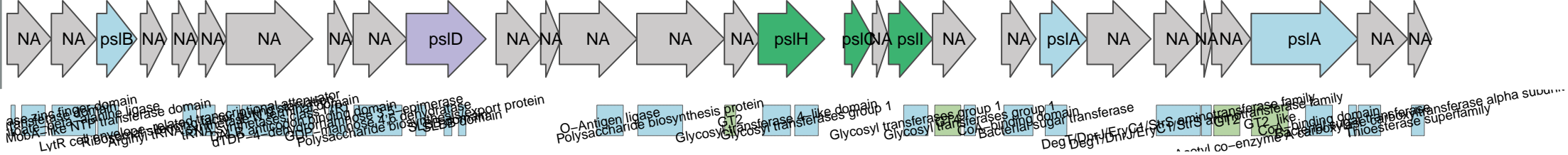
Damh_18-Q3-R51-60_MAXAC.106
p:Chloroflexi,o:Caldilineales,g:Ca_Amarolinea



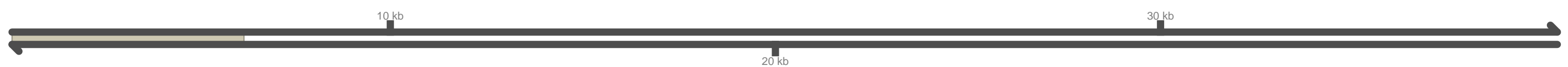
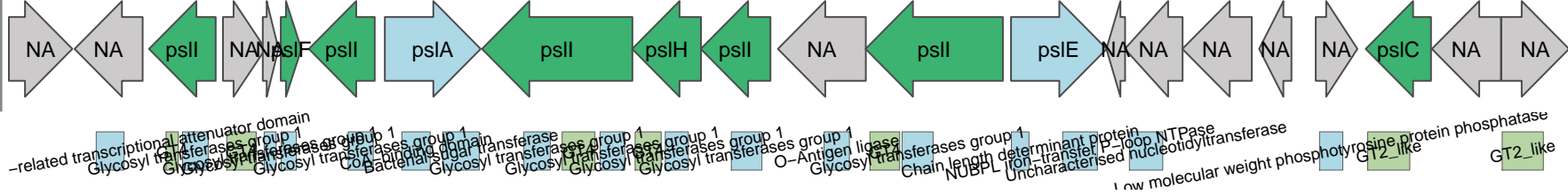
Ega_18-Q3-R5-49_BAT3C.159
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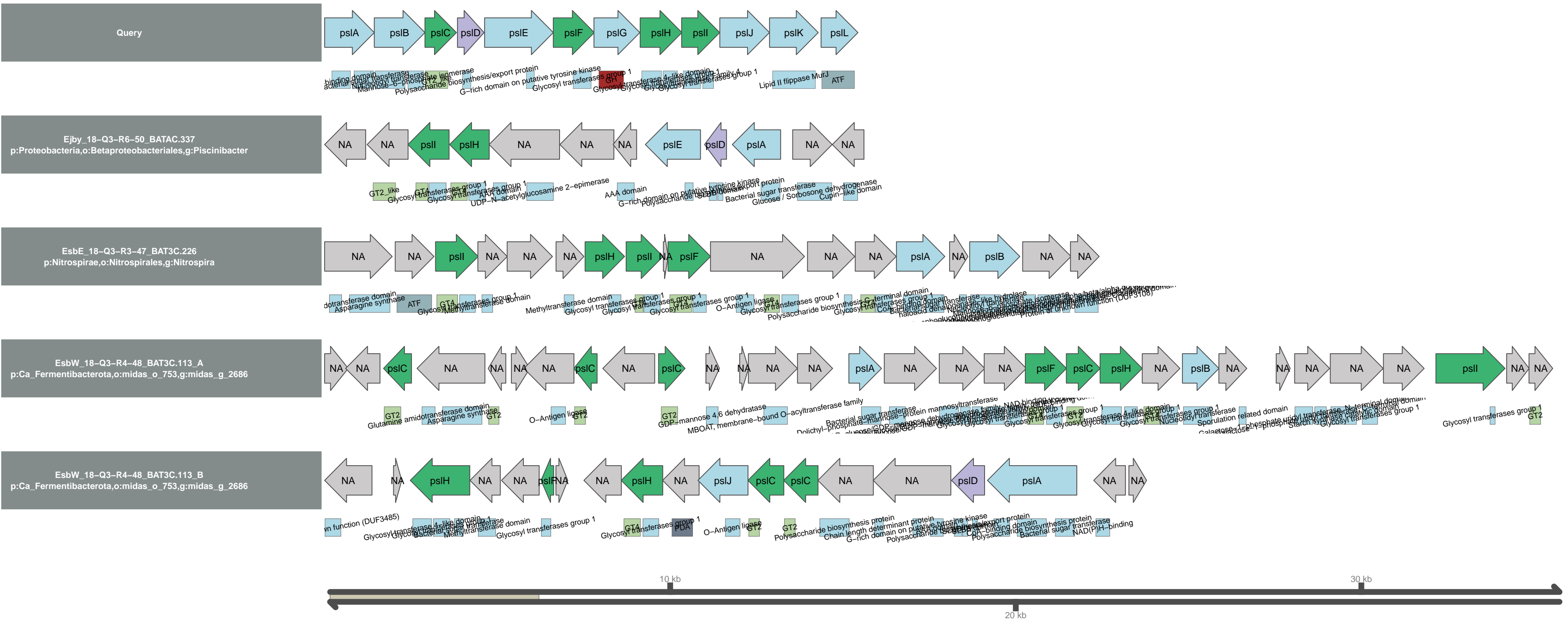
Ega_18-Q3-R5-49_BATAC.118
p:Bacteroidetes,o:Kryptoniales,g:midas_g_627



Ega_18-Q3-R5-49_MAXAC.001
p:Actinobacteria,o:Micrococcales,g:Tetrasphaera

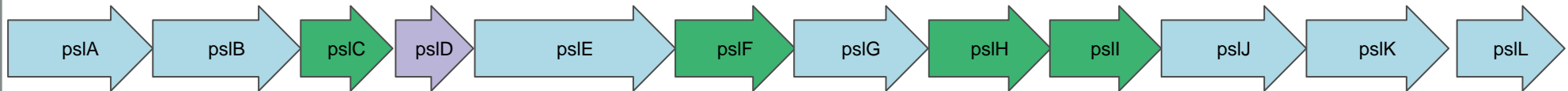


Operon Structure



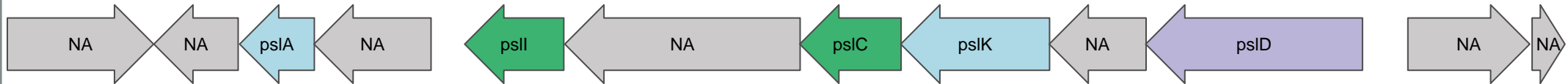
Operon Structure

Query



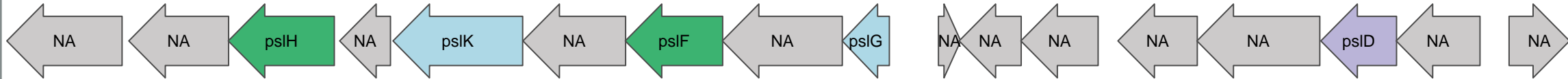
A-binding domain
Bacterial sugar transferase
Nucleotidyl transferase
Mannose-6-phosphate isomerase
GT2-like
Polysaccharide biosynthesis/export protein
G-rich domain on putative tyrosine kinase
Glycosyl transferases group 1
GH
Glycosyl transferase 4-like domain
Glycosyl transferases group 1
Glycosyl transferases group 1
Glycosyl transferases group 1
Lipid II flippase MurJ
ATF

EsbW_18-Q3-R4-48_BAT3C.113_C
p:Ca_Fermentibacterota,o:midas_o_753,g:midas_g_2686



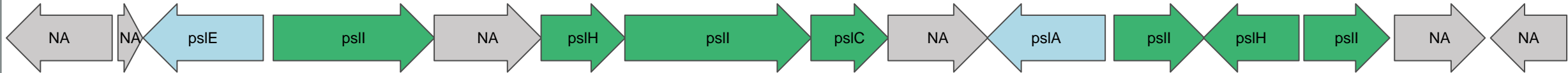
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Methyltransferase domain
Bacterial sugar transferase
DegT/DnrJ/EryC1/StrS aminotransferase family
GT4
Glycosyl transferases group 1
Glycosyl transferases group 1
Glycosyl transferases group 1
Polysaccharide biosynthesis/export protein
G-rich domain on putative tyrosine kinase
GlcC
His Kinase A (phospho-acceptor domain)
His Kinase B
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EsbW_18-Q3-R4-48_BAT3C.275
p:Proteobacteria,o:Betaproteobacteriales,g:Ferribacterium



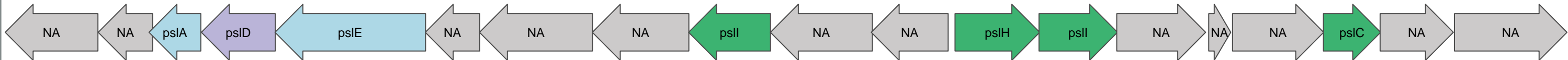
hydrogenase family, NAD binding, iron-binding domain
Mannose-6-phosphate isomerase
Glycosyl transferases group 1
Glycosyl transferases group 1
Hexapeptide repeat of succinyl-transferase
Lipid II flippase MurJ
GT4
Glycosyl transferases group 1
Glycosyl transferases group 1
O-Antigen ligase
Protein of unknown function (DUF3485)
Transmembrane exosortase (Exosortase EpsH)
NUBPL iron-transfer E-loop NTPase protein
G-rich domain on putative tyrosine kinase
PPIase domain
PEP-CTERM motif

EsbW_18-Q3-R4-48_BAT3C.295
p:Actinobacteria,o:Micrococcales,g:Tetrasphaera



Coenzyme PQQ synthase protein O (PqqO)
Chain length determinant protein
NUBPL iron-transfer P-loop NTPase
Glycosyl transferases group 1
GT2
O-Antigen ligase
GT4
Glycosyl transferases group 1
Glycosyl transferases group 1
GT4
Glycosyl transferases group 1
Glycosyl transferases group 1
GT4
Glycosyl transferases group 1
CoA-binding domain
Bacterial sugar transferase
Glycosyl transferases group 1
GT4
Glycosyl transferases group 1
Glycosyl transferases group 1
Glycosyl transferases group 1
Cell envelope-related transcriptional attenuator domain

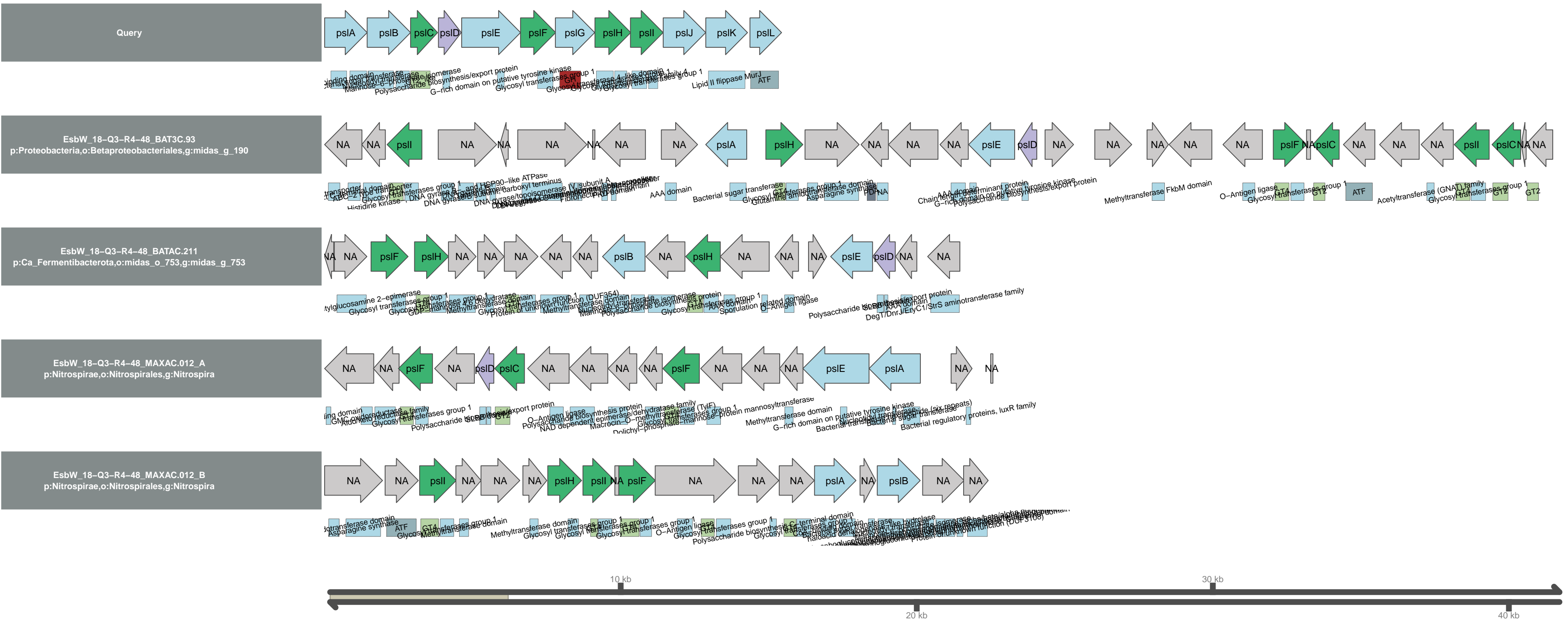
EsbW_18-Q3-R4-48_BAT3C.4_cln
p:Acidobacteria,o:Thermoanaerobaculales,g:Subgroup_10



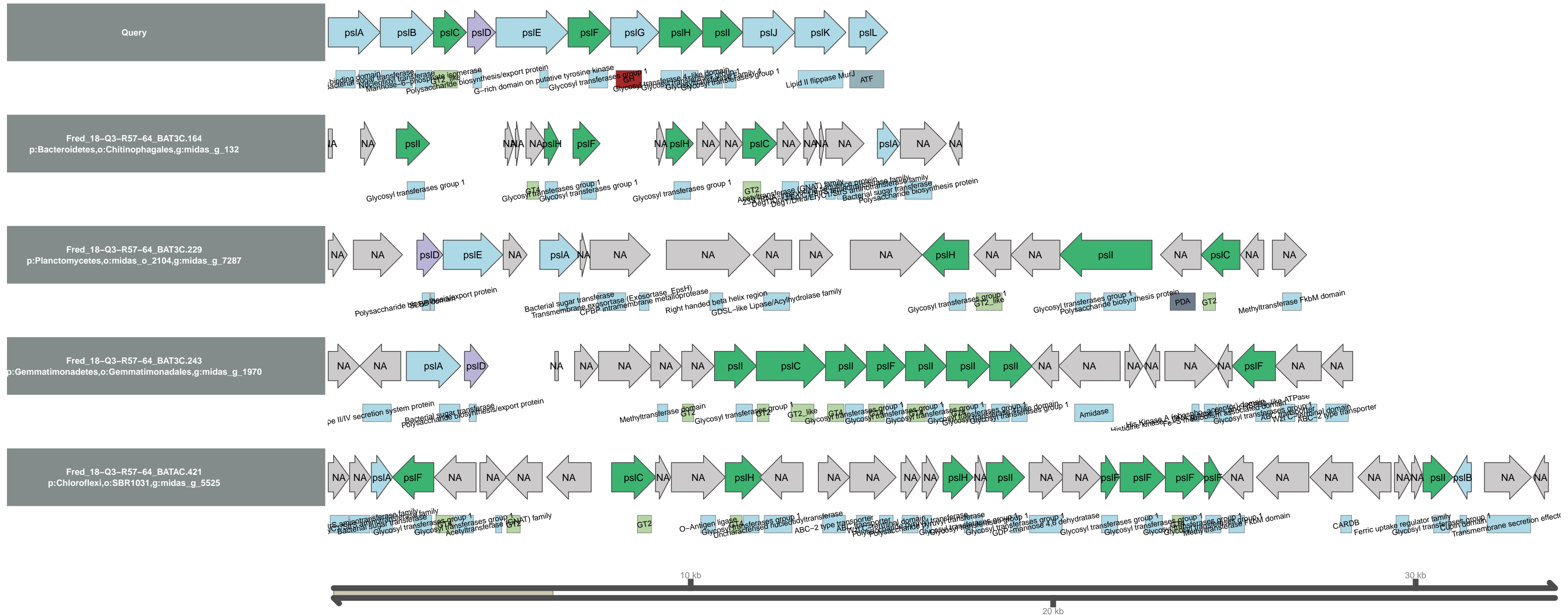
GT2
Bacterial sugar transferase
Polysaccharide biosynthesis/export protein
G-rich domain on putative tyrosine kinase
AAA domain
methyl-phosphate-mannose-protein mannosyltransferase
Glycosyl transferase 4-like domain
Glycosyl transferases group 1
Polysaccharide biosynthesis protein
Polysaccharide biosynthesis C-terminal domain
Type I phosphodiesterase
nucleotide pyrophosphatase
GT4
Glycosyl transferases group 1
Glycosyl transferases group 1
Glycosyl transferases group 1
Glycosyl transferases group 1
Bacterial sugar transferase
WecB/StaA/CpsF family
STAS domain
O-Antigen ligase
GT2
Response regulator receiver domain
Stage II sporulation protein E (SpoE)
Histidine kinase-like ATPase



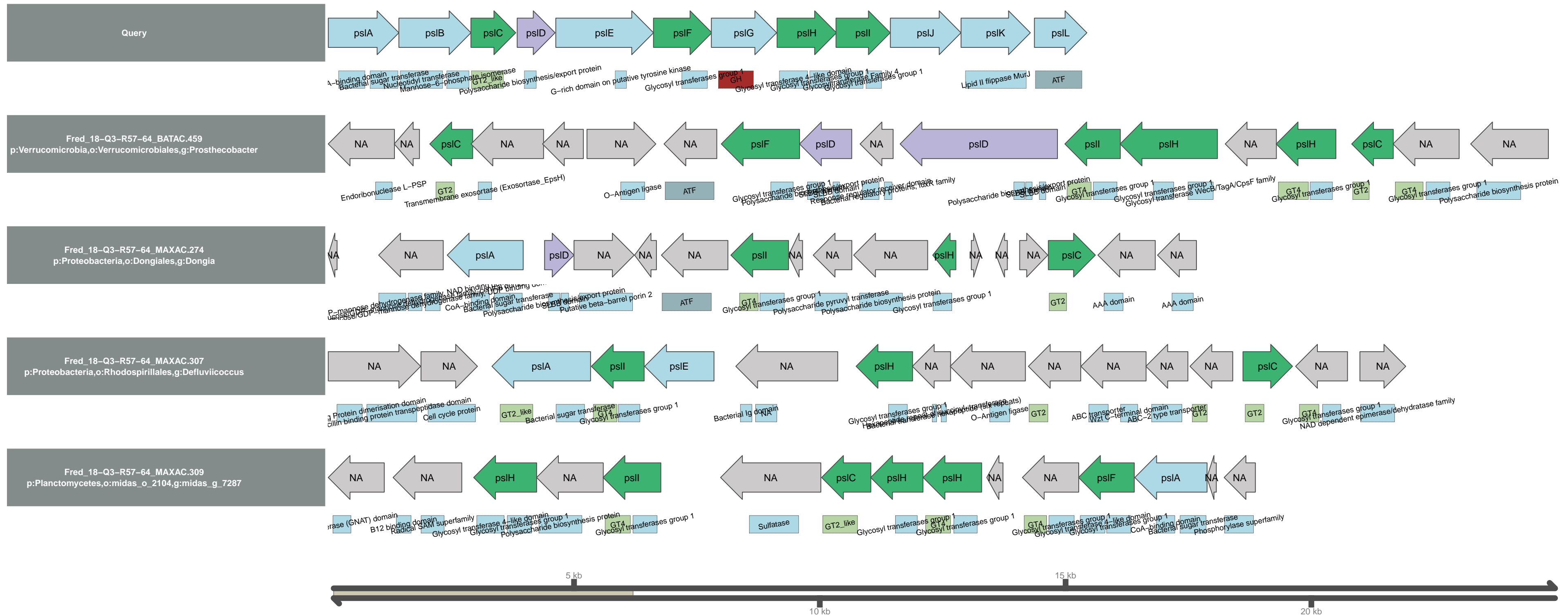
Operon Structure



Operon Structure

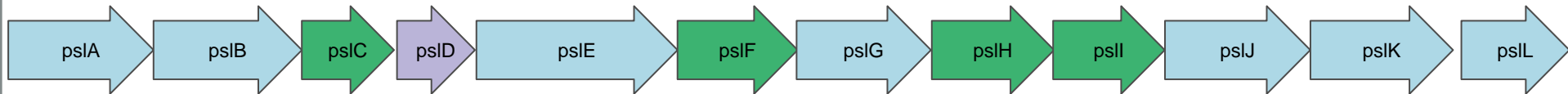


Operon Structure



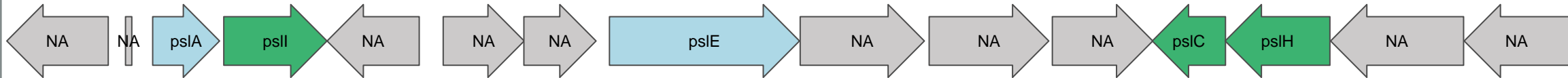
Operon Structure

Query



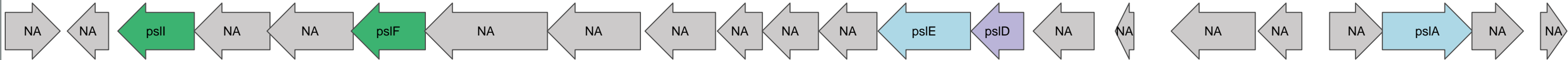
A-binding domain transferase Bacterial sugar nucleotidyl transferase Mannose-6-phosphate isomerase Polysaccharide biosynthesis/export protein G-rich domain on putative tyrosine kinase Glycosyl transferases group 1 GH Glycosyl transferase 4-like domain Glycosyl transferases group 1 Family 4 Glycosyl transferases group 1 Lipid II flippase MurJ ATF

Fred_18-Q3-R57-64_MAXAC.362
p:Proteobacteria,o:Caulobacteriales,g:Hyphomonas



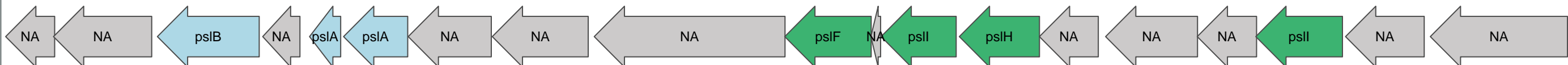
Cytochrome P-450 Cytochrome P-450 Bacterial sugar transferase GT4 transferases group 1 Glycosyl transferases group 1 Glycosyl transferase family 8 Glycosyl hydrolases family 16 Chain length determinant protein G-rich domain on putative tyrosine kinase Polysaccharide biosynthesis protein Polysaccharide pyruvyl transferase GT2-like GT4 Glycosyl transferases group 1

Hade_18-Q3-R52-61_BATAC.316
p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_190



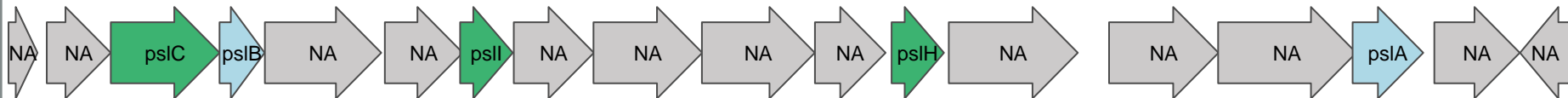
yltransferase domain Web/TagA/CpsF family A-binding domain transferase 4-like domain GT4 transferases group 1 Glycosyl transferases group 1 Glycosyl hydrolases family 39 GT4 transferases group 1 Bacterial transferase hexapeptide (six repeats) GDP-mannose 4,6 dehydratase Protein of unknown function (DUF3485) Exosortase (Exosortase-EpsH) Transmembrane protein of unknown function (DUF3485) CobQ/CobB/MinD/ParA nucleotide binding domain G-rich domain on putative tyrosine kinase Polysaccharide biosynthesis protein PPI-type PPIASE domain Putative beta-barrel porin 2 CPBP intramembrane metalloprotease CoA-binding domain Bacterial sugar transferase SLT domain Response regulator

Hade_18-Q3-R52-61_MAXAC.023
p:Nitrospirae,o:Nitrospirales,g:Nitrospira



own function (DUF3108) beta/alpha domain C-terminal domain... Nucleotidyl transferase Mannose-6-phosphate isomerase halocacid dehalogenase Bacterial sugar CoA-binding domain Glycosyl transferases group 1 Polysaccharide biosynthesis C-terminal domain O-Antigen ligase GT4 transferases group 1 Glycosyl transferases group 1 Glycosyl transferases group 1 Glycosyl transferases group 1 Glycosyl transferases group 1 Methyltransferase domain Methyltransferase domain GT4 transferases group 1 ATF Glutamine amidotransferase domain Asparagine synthase

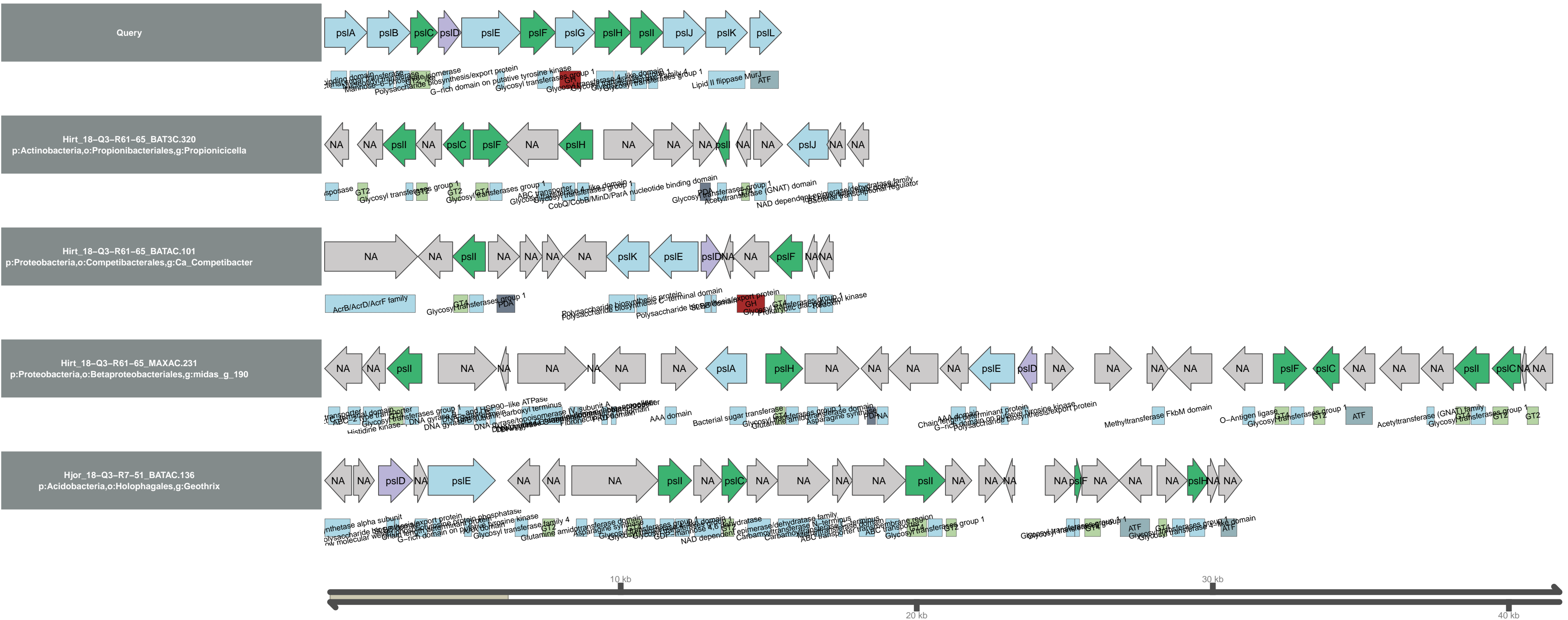
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p:Bacteroidetes,o:Sphingobacteriales,g:midas_g_300



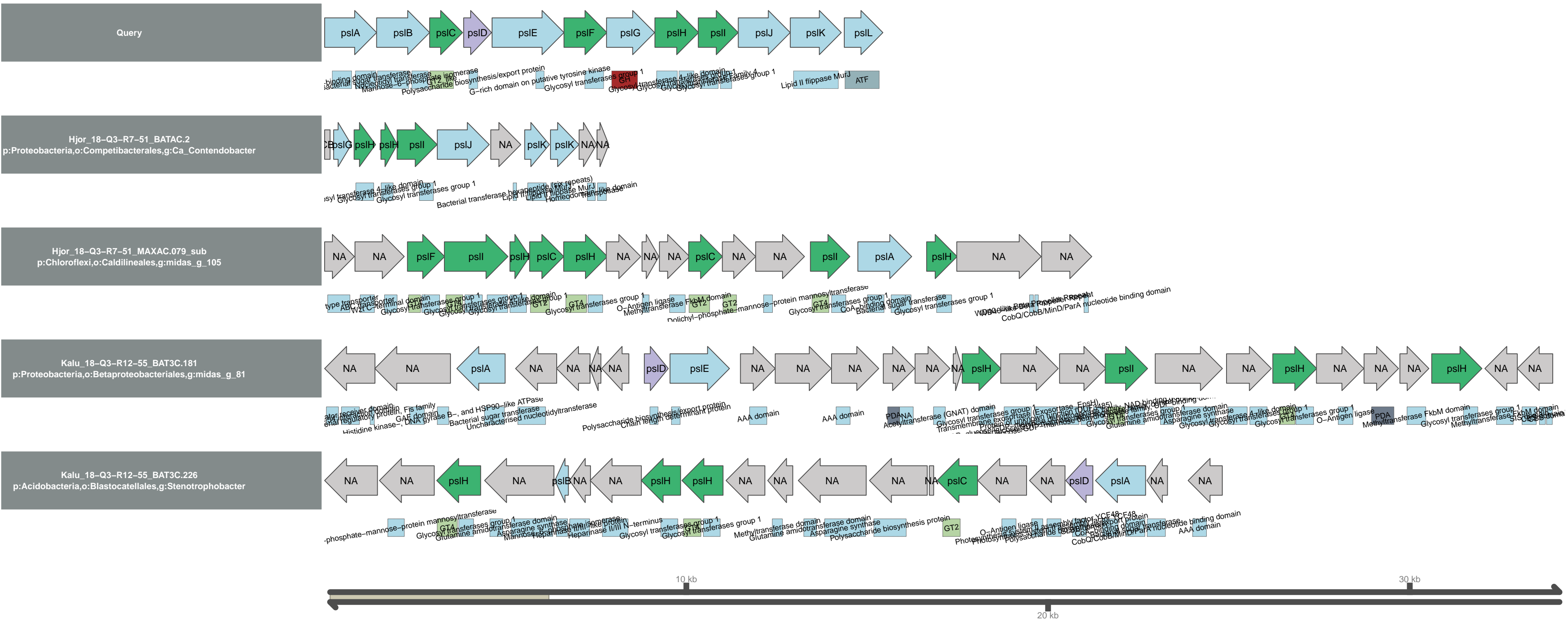
GT2 DegT/DnrJ/EryC1/StrS aminotransferase family Glycosyl transferases group 1 Glycosyl transferase 4-like GT4 transferases group 1 UDP-N-acetylglucosamine 2-epimerase Glycosyl transferases group 1 O-Antigen ligase DegT/DnrJ/EryC1/StrS aminotransferase family Protein of unknown function (DUF3887) S33 Serine aminotransferase Bacterial sugar transferase Kozal-type serine protease inhibitor domain



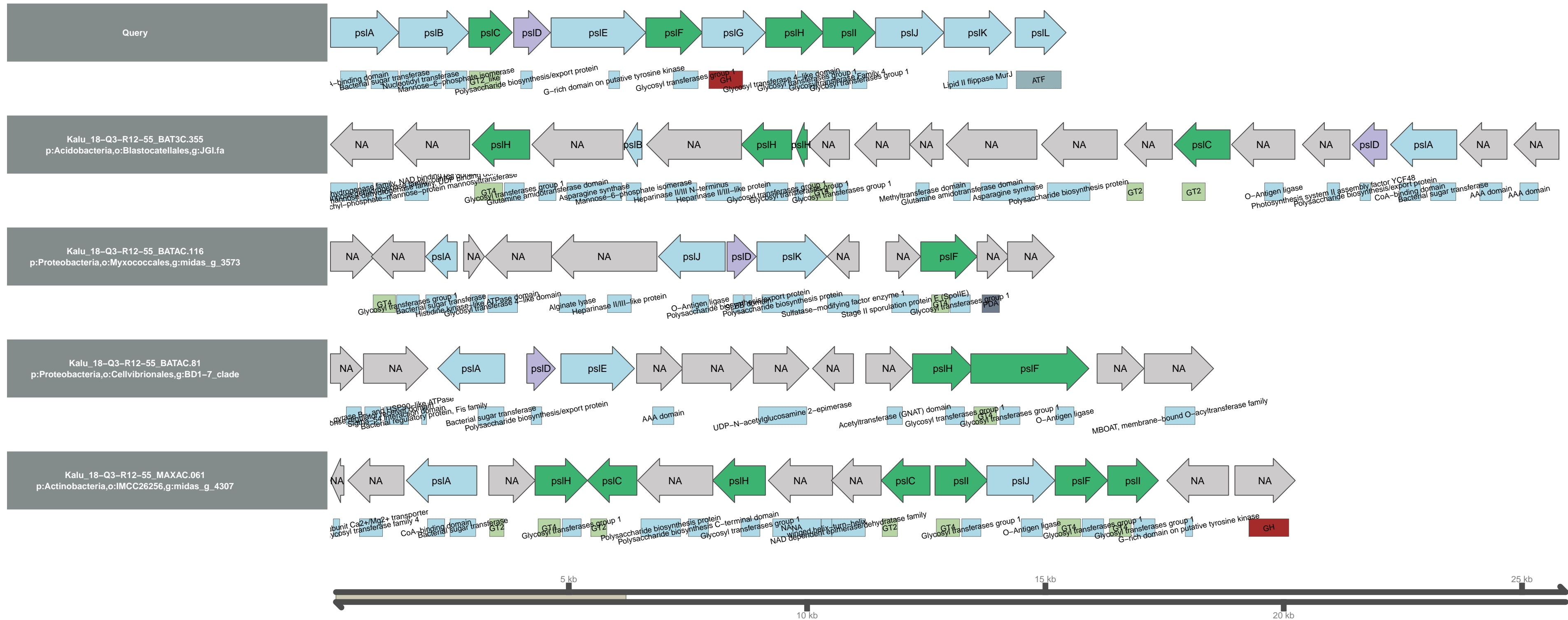
Operon Structure



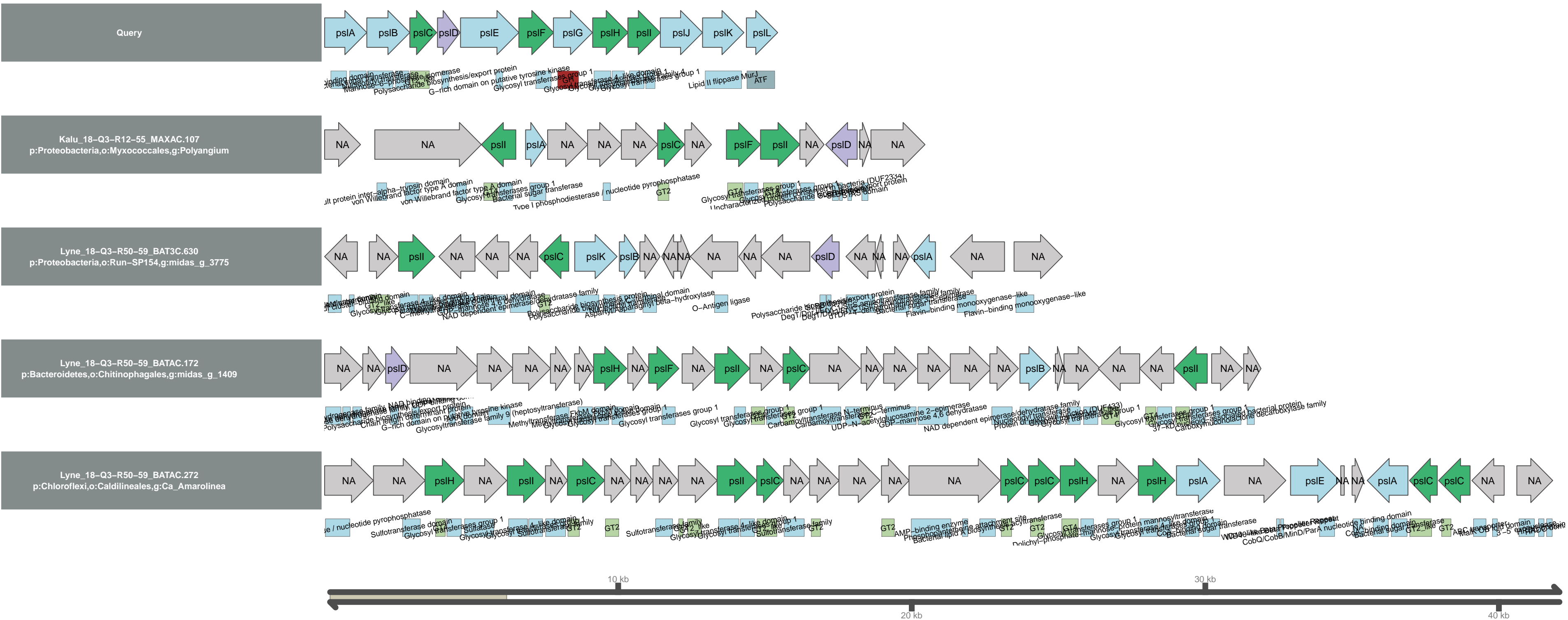
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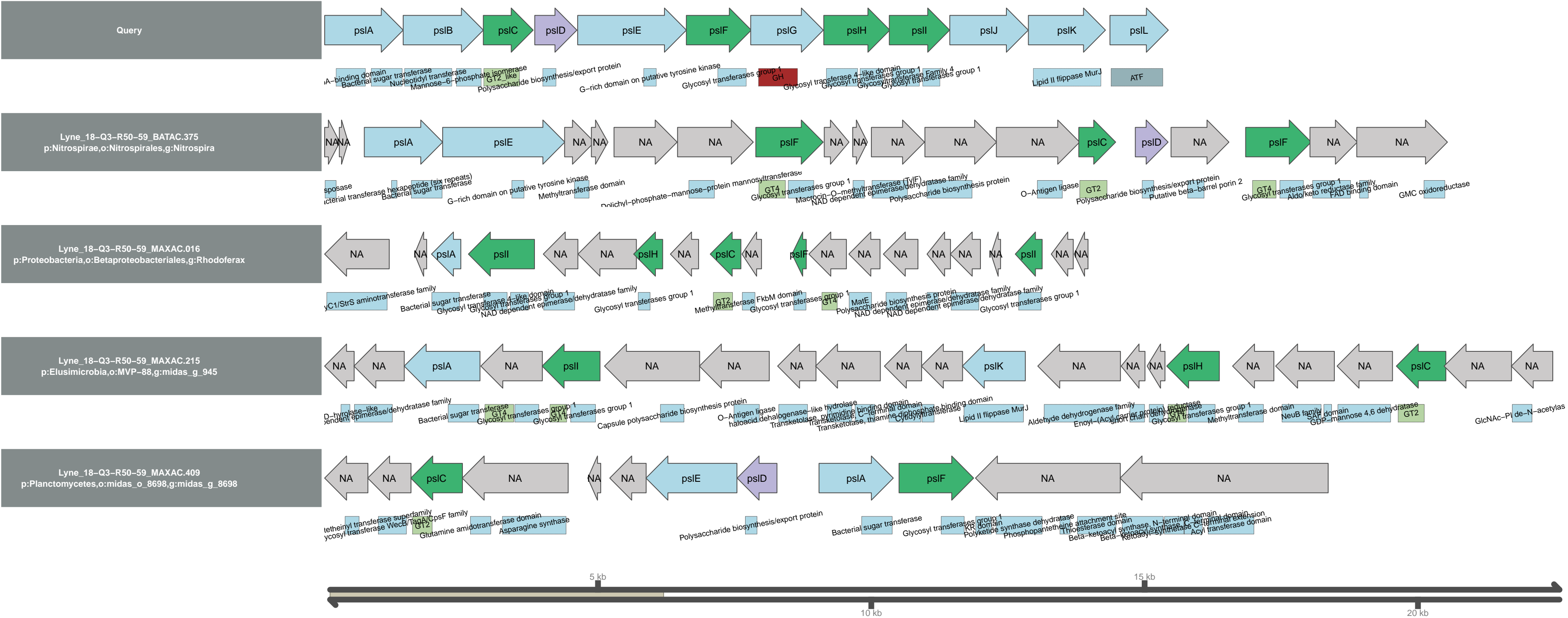
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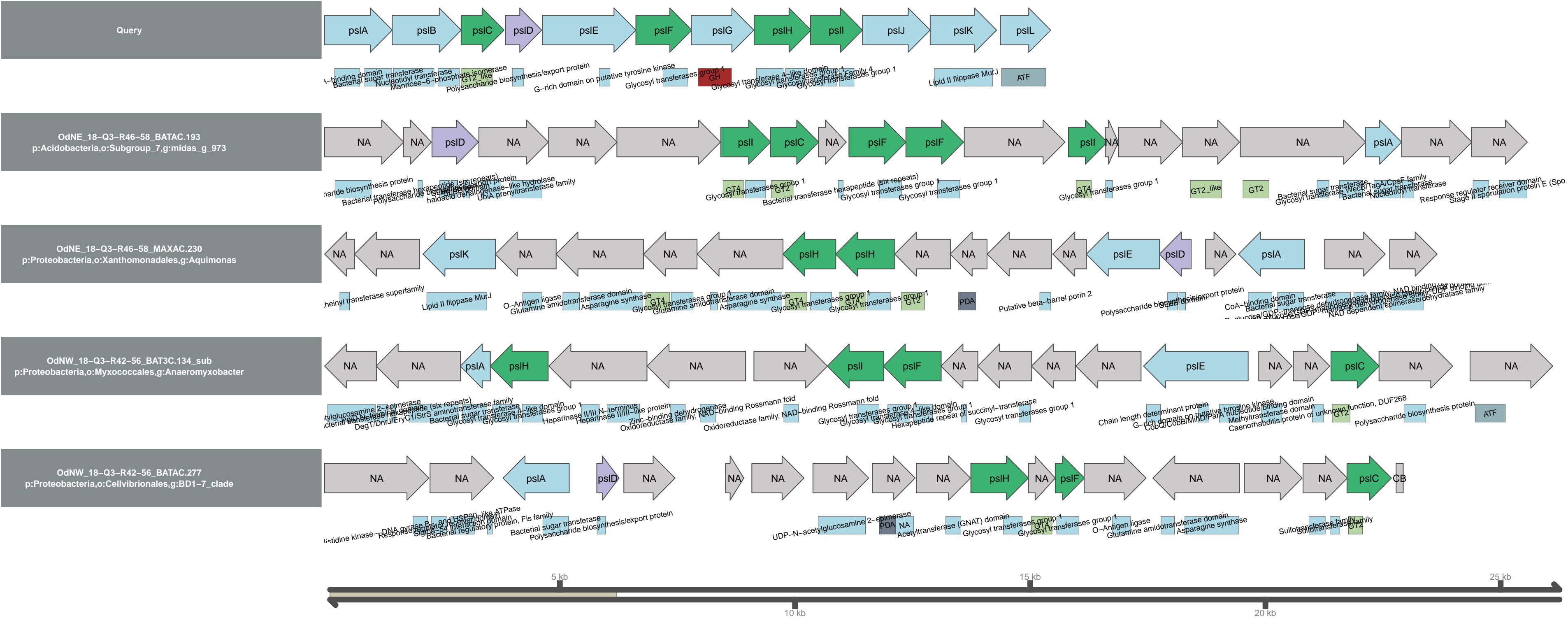
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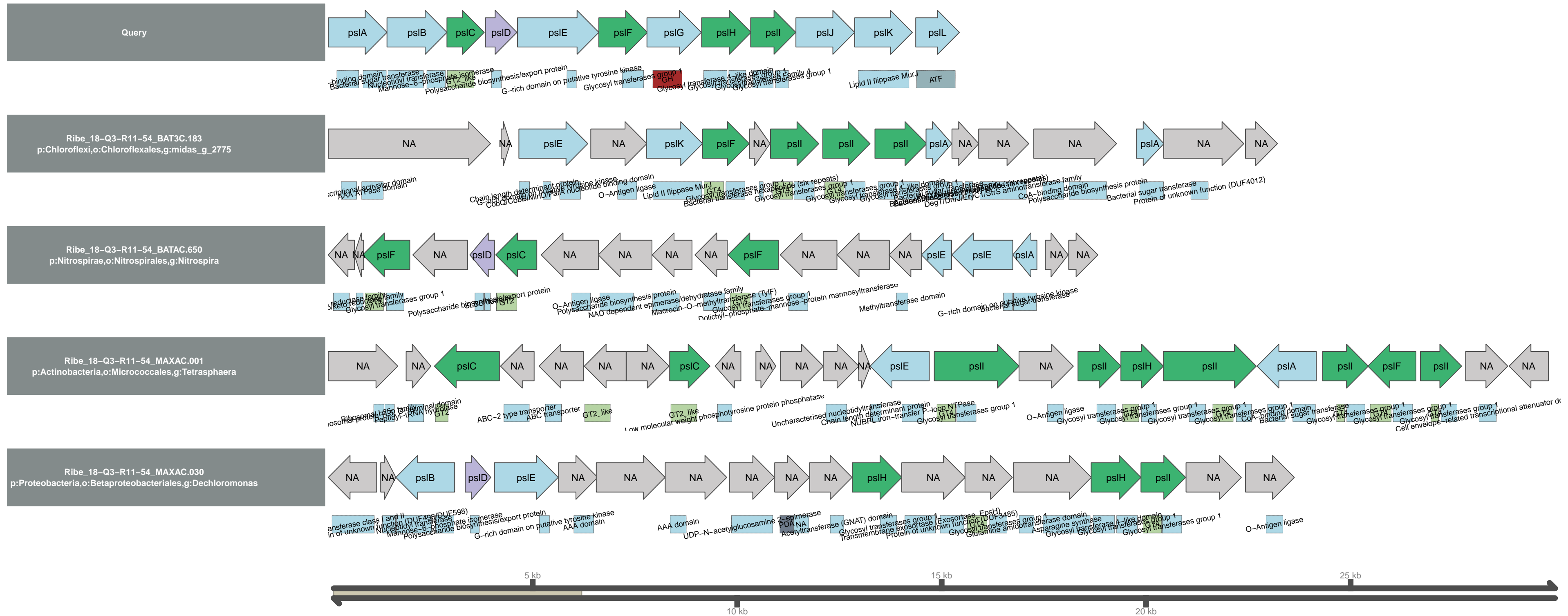
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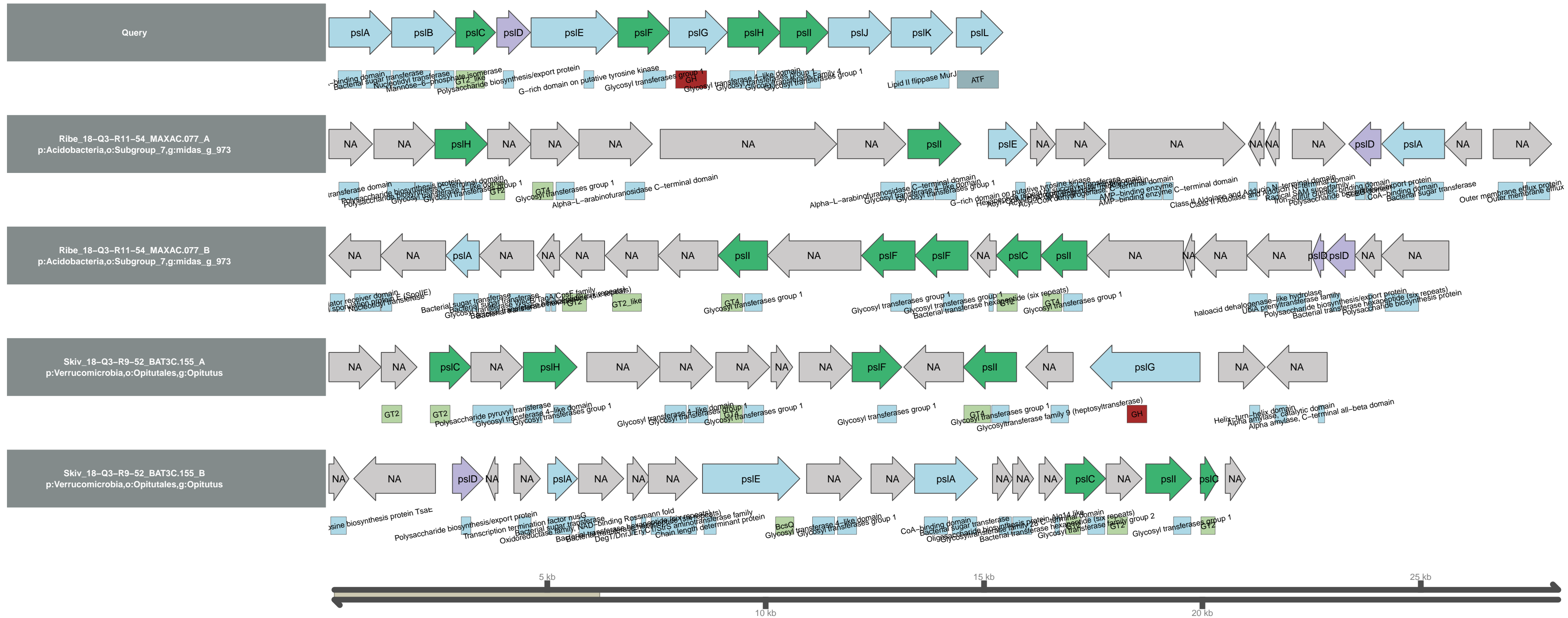
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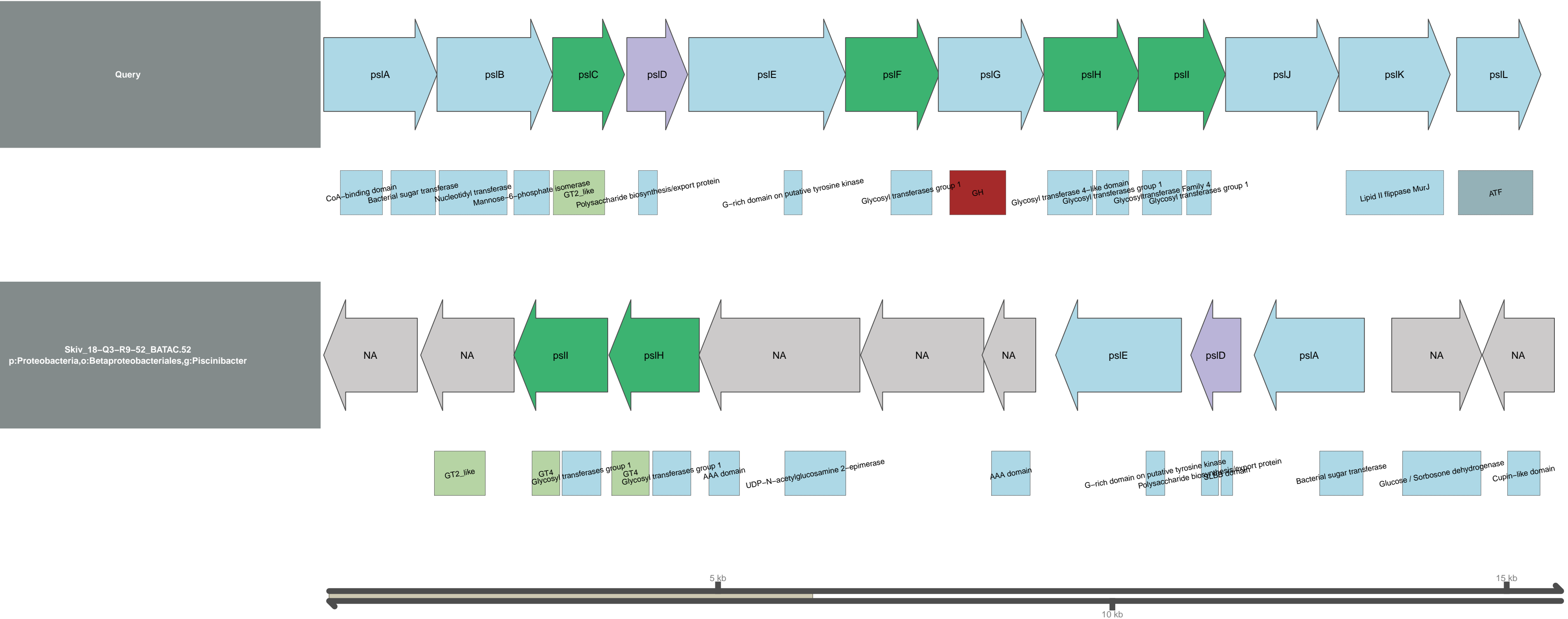
Operon Structure



Operon Structure



Operon Structure



	ID2	plot_tax	seqname	start	Query_label	ProkkaNO
1	AalE_18-Q3-R2-46_BAT3C.188	p:Actinobacteria,o:Micrococcales,g:Tetrasphaera	tig00263858-10-13527630	845862	pslA	01794
2	AalW_18-Q3-R10-53_BAT3C.371_sub	p:Chloroflexi,o:Caldilineales,g:Ca_Amarolinea	tig01688844-10-2276140	169599	pslA	05189
3	AalW_18-Q3-R10-53_BAT3C.524	p:Actinobacteria,o:Micrococcales,g:Tetrasphaera	tig00000279-10-13903780	202213	pslA	00185
4	AalW_18-Q3-R10-53_BATAC.388	p:Proteobacteria,o:Myxococcales,g:Phaselicystis	tig00404814-10-8851510	689071	pslA	05653
5	AalW_18-Q3-R10-53_MAXAC.406	p:Proteobacteria,o:Betaproteobacteriales,g:Sulfuritalea	tig00010828-17461810596-2816800	60513	pslA	01091
6	Aved_18-Q3-R54-62_BATAC.851	p:Acidobacteria,o:11-24,g:midas_g_1424	tig00005012-10-6570710	506791	pslC	03566
7	Bjer_18-Q3-R1-45_BAT3C.93	p:Actinobacteria,o:Micrococcales,g:Tetrasphaera	tig00200464-10-3864580	156502	pslA	02152
8	Damh_18-Q3-R51-60_MAXAC.008	p:Chloroflexi,o:Ardenticatenales,g:midas_g_461	tig00001610-10-4755440	422017	pslA	00347
9	Damh_18-Q3-R51-60_MAXAC.106	p:Chloroflexi,o:Caldilineales,g:Ca_Amarolinea	tig00005679-10-2001250	163115	pslA	00855
10	Ega_18-Q3-R5-49_BAT3C.159	p:Chloroflexi,o:Ardenticatenales,g:Ca_Promineofilum	tig00001204-10-4325980	222231	pslA	01917
11	Ega_18-Q3-R5-49_BATAC.118	p:Bacteroidetes,o:Kryptoniales,g:midas_g_627	tig00000655-10-8431380	452811	pslA	00383
12	Ega_18-Q3-R5-49_MAXAC.001	p:Actinobacteria,o:Micrococcales,g:Tetrasphaera	tig00000580-10-8759820	291170	pslA	00274
13	Ejby_18-Q3-R6-50_BATAC.337	p:Proteobacteria,o:Betaproteobacteriales,g:Piscinibacter	tig00000693-10-7110010	197896	pslA	00169
14	EsbE_18-Q3-R3-47_BAT3C.226	p:Nitrospirae,o:Nitrospirales,g:Nitrospira	tig00003164-10-2864500	236936	pslA	01734
15	EsbW_18-Q3-R4-48_BAT3C.113_A	p:Ca_Fermentibacterota,o:midas_o_753,g:midas_g_2686	tig00007934-10-2213370	166713	pslA	00419
16	EsbW_18-Q3-R4-48_BAT3C.113_B	p:Ca_Fermentibacterota,o:midas_o_753,g:midas_g_2686	tig00010058-10-1919270	81640	pslA	01007
17	EsbW_18-Q3-R4-48_BAT3C.113_C	p:Ca_Fermentibacterota,o:midas_o_753,g:midas_g_2686	tig01102786-10-645960	10996	pslA	03606
18	EsbW_18-Q3-R4-48_BAT3C.275	p:Proteobacteria,o:Betaproteobacteriales,g:Ferribacterium	tig00250523-10-12255480	1097099	pslD	03931
19	EsbW_18-Q3-R4-48_BAT3C.295	p:Actinobacteria,o:Micrococcales,g:Tetrasphaera	tig00250755-10-1848950	23113	pslA	02101
20	EsbW_18-Q3-R4-48_BAT3C.4_cln	p:Acidobacteria,o:Thermoanaerobaculales,g:Subgroup_10	tig00000001-10-52256180	2105723	pslA	01764
21	EsbW_18-Q3-R4-48_BAT3C.93	p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_190	tig00000038-10-43439960	3516253	pslA	03241
22	EsbW_18-Q3-R4-48_BATAC.211	p:Ca_Fermentibacterota,o:midas_o_753,g:midas_g_753	tig00001333-10-11043260	224813	pslB	00167
23	EsbW_18-Q3-R4-48_MAXAC.012_A	p:Nitrospirae,o:Nitrospirales,g:Nitrospira	tig00000531-10-3969200	326553	pslA	03443
24	EsbW_18-Q3-R4-48_MAXAC.012_B	p:Nitrospirae,o:Nitrospirales,g:Nitrospira	tig00000864-10-8618410	617349	pslA	04061
25	Fred_18-Q3-R57-64_BAT3C.164	p:Bacteroidetes,o:Chitinophagales,g:midas_g_132	tig00004085-10-7592960	126352	pslA	01986

	ID2	plot_tax	seqname	start	Query_label	ProkkaNO
1	Fred_18-Q3-R57-64_BAT3C.229	p:Planctomycetes,o:midas_o_2104,g:midas_g_7287	tig00003168-10-9053500	423480	psIA	01121
2	Fred_18-Q3-R57-64_BAT3C.243	p:Gemmatimonadetes,o:Gemmatimonadales,g:midas_g_1970	tig00006435-10-4437130	67703	psIA	02150
3	Fred_18-Q3-R57-64_BATAC.421	p:Chloroflexi,o:SBR1031,g:midas_g_5525	tig00020854-10-1213840	81246	psIA	03962
4	Fred_18-Q3-R57-64_BATAC.459	p:Verrucomicrobia,o:Verrucomicrobiales,g:Prostheco bacter	tig01554389-10-7478300	261406	psIC	05474
5	Fred_18-Q3-R57-64_MAXAC.274	p:Proteobacteria,o:Dongiales,g:Dongia	tig00002610-10-11133940	938144	psIA	04576
6	Fred_18-Q3-R57-64_MAXAC.307	p:Proteobacteria,o:Rhodospirillales,g:Defluviicoccus	tig00002301-10-12040470	10278	psIA	02412
7	Fred_18-Q3-R57-64_MAXAC.309	p:Planctomycetes,o:midas_o_2104,g:midas_g_7287	tig00005467-10-5804700	194061	psIA	01804
8	Fred_18-Q3-R57-64_MAXAC.362	p:Proteobacteria,o:Caulobacterales,g:Hyphomonas	tig00008145-10-2998620	87420	psIA	03359
9	Hade_18-Q3-R52-61_BATAC.316	p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_190	tig00000808-10-11321960	739573	psIA	00671
10	Hade_18-Q3-R52-61_MAXAC.023	p:Nitrospirae,o:Nitrospirales,g:Nitrospira	tig00007806-10-2904650	46163	psIA	01834
11	Hade_18-Q3-R52-61_MAXAC.102	p:Bacteroidetes,o:Sphingobacteriales,g:midas_g_300	tig00001256-10-8309610	27607	psIA	00031
12	Hirt_18-Q3-R61-65_BAT3C.320	p:Actinobacteria,o:Propionibacteriales,g:Propionice lla	tig00006819-10-4318190	297720	psIC	00766
13	Hirt_18-Q3-R61-65_BATAC.101	p:Proteobacteria,o:Competibacterales,g:Ca_Competibacter	tig00316338-10-11255780	748620	psID	03369
14	Hirt_18-Q3-R61-65_MAXAC.231	p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_190	tig00000003-10-42710140	1879132	psIA	01704
15	Hjor_18-Q3-R7-51_BATAC.136	p:Acidobacteria,o:Holophagales,g:Geothrix	tig00003541-10-3610990	53758	psIC	00577
16	Hjor_18-Q3-R7-51_BATAC.2	NA,NA,NA	tig00014981-10-232450	-247	CB	03135
17	Hjor_18-Q3-R7-51_MAXAC.079_sub	p:Chloroflexi,o:Caldilineales,g:midas_g_105	tig00006381-10-1988830	189909	psIA	03120
18	Kalu_18-Q3-R12-55_BAT3C.181	p:Proteobacteria,o:Betaproteobacteriales,g:midas_g_81	tig00100781-10-9553470	566646	psIA	02641
19	Kalu_18-Q3-R12-55_BAT3C.226	p:Acidobacteria,o:Blastocatellales,g:Stenotrophobacter	tig00100838-10-13854540	965043	psIA	03274
20	Kalu_18-Q3-R12-55_BAT3C.355	p:Acidobacteria,o:Blastocatellales,g:JGI.fa	tig00100729-10-33526130	119544	psIA	00484
21	Kalu_18-Q3-R12-55_BATAC.116	p:Proteobacteria,o:Myxococcales,g:midas_g_3573	tig00001774-10-6877420	520573	psIA	02523
22	Kalu_18-Q3-R12-55_BATAC.81	p:Proteobacteria,o:Cellvibrionales,g:BD1-7_clade	tig00007458-10-904370	68640	psIA	03764
23	Kalu_18-Q3-R12-55_MAXAC.061	p:Actinobacteria,o:IMCC26256,g:midas_g_4307	tig00000109-10-36236620	1387510	psIA	01360
24	Kalu_18-Q3-R12-55_MAXAC.107	p:Proteobacteria,o:Myxococcales,g:Polyangium	tig00100908-10-3475500	203837	psIA	04295
25	Lyne_18-Q3-R50-59_BAT3C.630	p:Proteobacteria,o:Run-SP154,g:midas_g_3775	tig00011870-10-2387850	37093	psIA	02664

	ID2	plot_tax	seqname	start	Query_label	ProkkaNO
1	Lyne_18-Q3-R50-59_BATAC.172	p:Bacteroidetes,o:Chitinophagales,g:midas_g_1409	tig00011674-10-2255570	62886	pslB	02431
2	Lyne_18-Q3-R50-59_BATAC.272	p:Chloroflexi,o:Caldilineales,g:Ca_Amarolinea	tig00010316-10-1820800	73049	pslA	02902
3	Lyne_18-Q3-R50-59_BATAC.375	p:Nitrospirae,o:Nitrospirales,g:Nitrospira	tig01430579-10-3014800	114583	pslA	04034
4	Lyne_18-Q3-R50-59_MAXAC.016	p:Proteobacteria,o:Betaproteobacteriales,g:Rhodoferax	tig00015905-10-344520	22131	pslA	01500
5	Lyne_18-Q3-R50-59_MAXAC.215	p:Elusimicrobia,o:MVP-88,g:midas_g_945	tig00007776-10-3541520	238479	pslA	00579
6	Lyne_18-Q3-R50-59_MAXAC.409	p:Planctomycetes,o:midas_o_8698,g:midas_g_8698	tig00000050-10-70511450	4762296	pslA	03664
7	OdNE_18-Q3-R46-58_BATAC.193	p:Acidobacteria,o:Subgroup_7,g:midas_g_973	tig00026008-10-446880	23732	pslA	04816
8	OdNE_18-Q3-R46-58_MAXAC.230	p:Proteobacteria,o:Xanthomonadales,g:Aquimonas	tig00000122-2938940-21812760	1827605	pslA	01837
9	OdNW_18-Q3-R42-56_BAT3C.134_sub	p:Proteobacteria,o:Myxococcales,g:Anaeromyxobacter	tig00009616-10-535830	19683	pslA	03787
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11	Ribe_18-Q3-R11-54_BAT3C.183	p:Chloroflexi,o:Chloroflexales,g:midas_g_2775	tig00000361-10-32415980	2896169	pslA	02288
12	Ribe_18-Q3-R11-54_BATAC.650	p:Nitrospirae,o:Nitrospirales,g:Nitrospira	tig00003583-10-3606900	277616	pslA	00894
13	Ribe_18-Q3-R11-54_MAXAC.001	p:Actinobacteria,o:Micrococcales,g:Tetrasphaera	tig01078875-10-4739290	129595	pslA	02872
14	Ribe_18-Q3-R11-54_MAXAC.030	p:Proteobacteria,o:Betaproteobacteriales,g:Dechloromonas	tig00000123-10-10923850	928357	pslB	00938
15	Ribe_18-Q3-R11-54_MAXAC.077_A	p:Acidobacteria,o:Subgroup_7,g:midas_g_973	tig00006461-10-2087570	40803	pslA	03113
16	Ribe_18-Q3-R11-54_MAXAC.077_B	p:Acidobacteria,o:Subgroup_7,g:midas_g_973	tig00008766-10-1744070	106566	pslA	04112
17	Skiv_18-Q3-R9-52_BAT3C.155_A	p:Verrucomicrobia,o:Opitutales,g:Opitutus	tig00019076-10-986110	46048	pslC	02600
18	Skiv_18-Q3-R9-52_BAT3C.155_B	p:Verrucomicrobia,o:Opitutales,g:Opitutus	tig00019131-10-661300	58108	pslA	02705
19	Skiv_18-Q3-R9-52_BATAC.52	p:Proteobacteria,o:Betaproteobacteriales,g:Piscinibacter	tig00007198-10-2887380	77885	pslA	01567