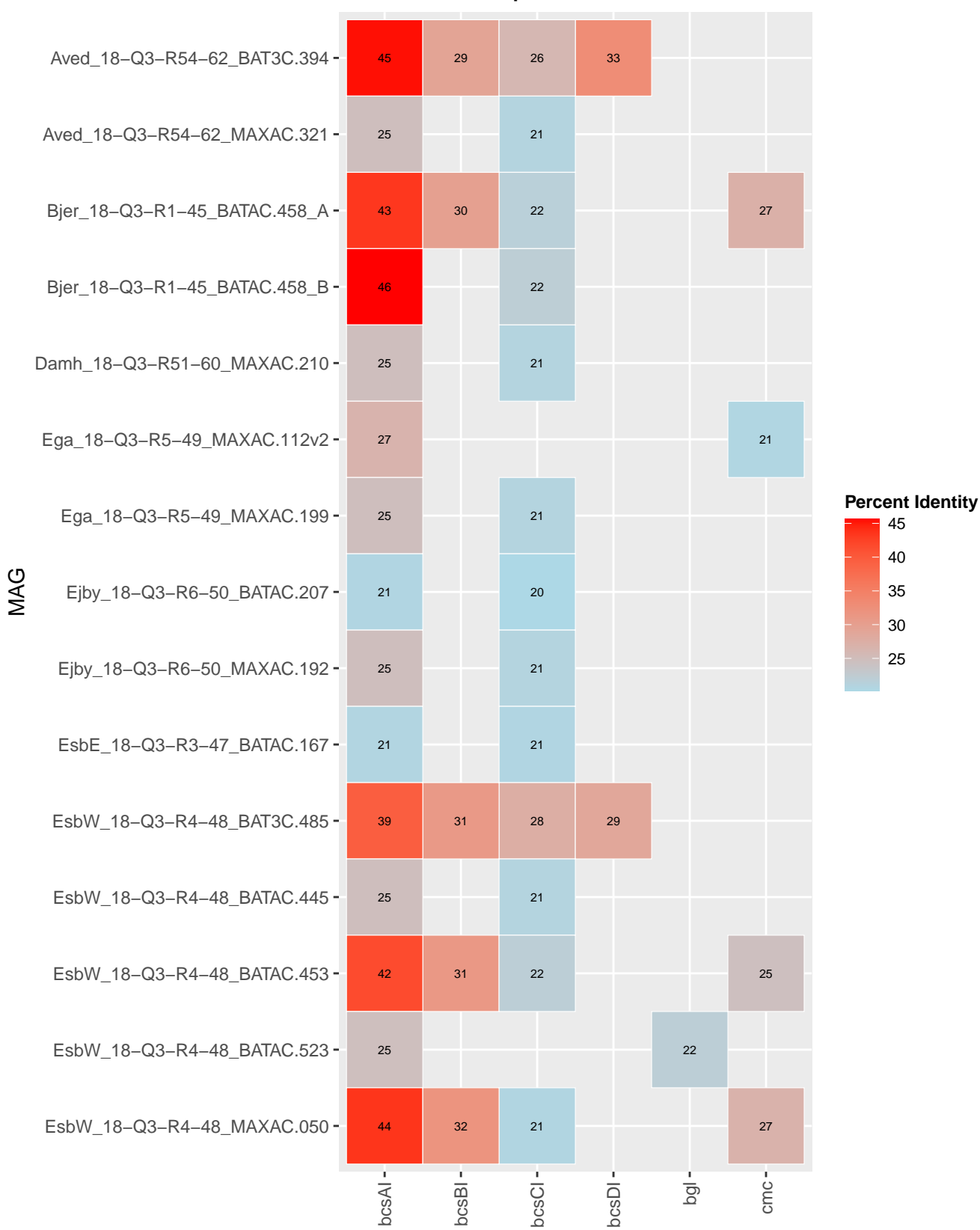
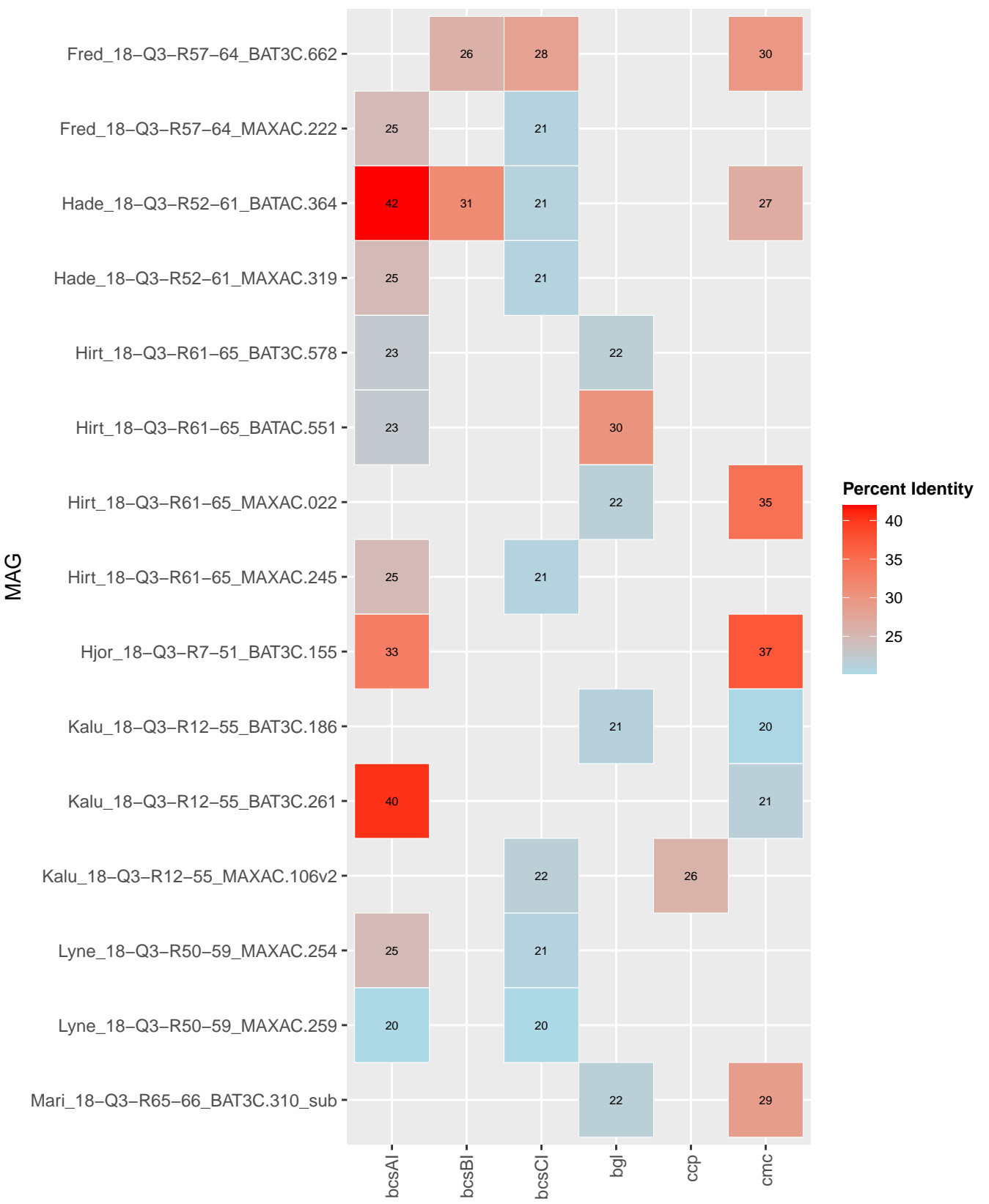


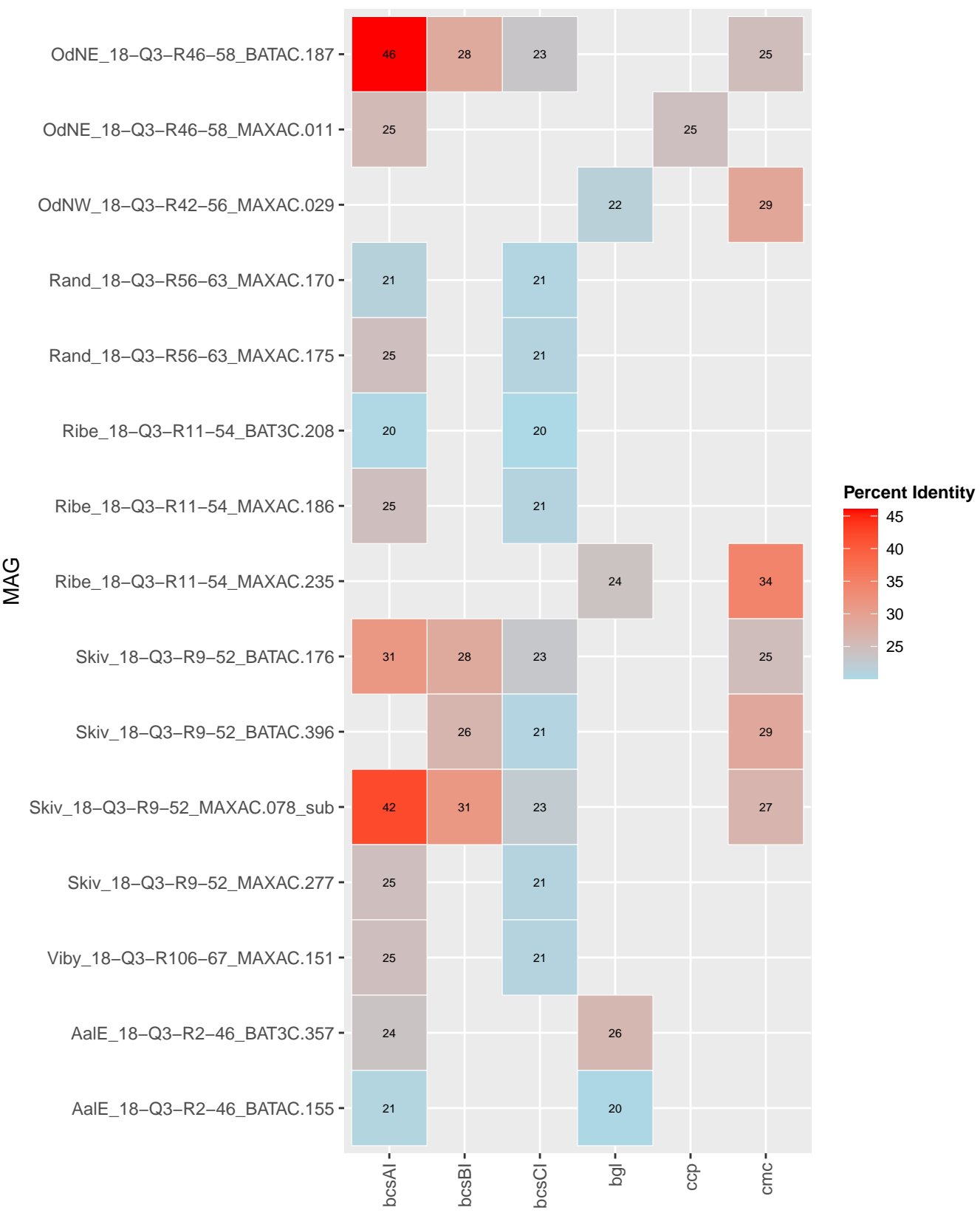
cellulose1 Heatmap



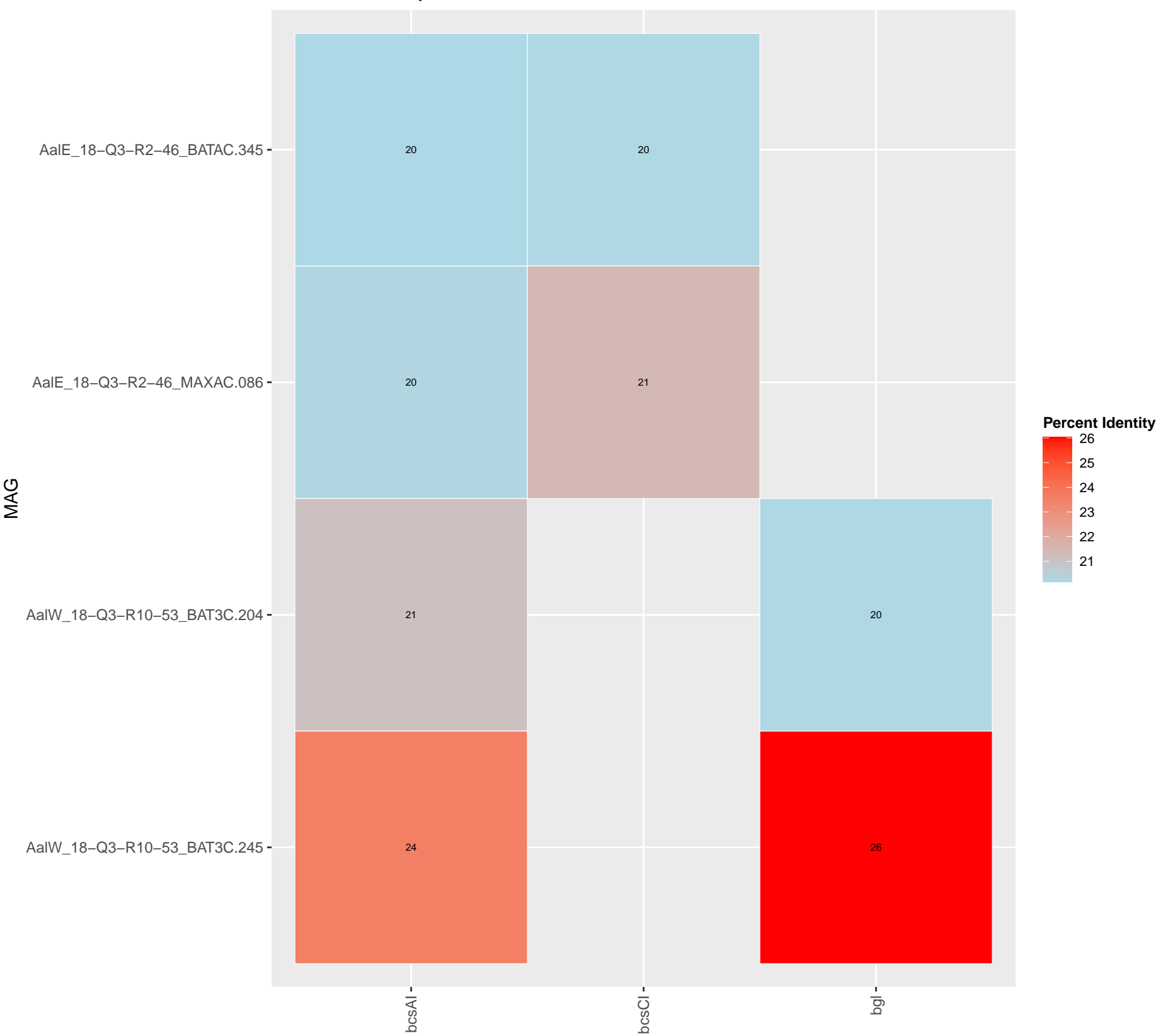
cellulose1 Heatmap



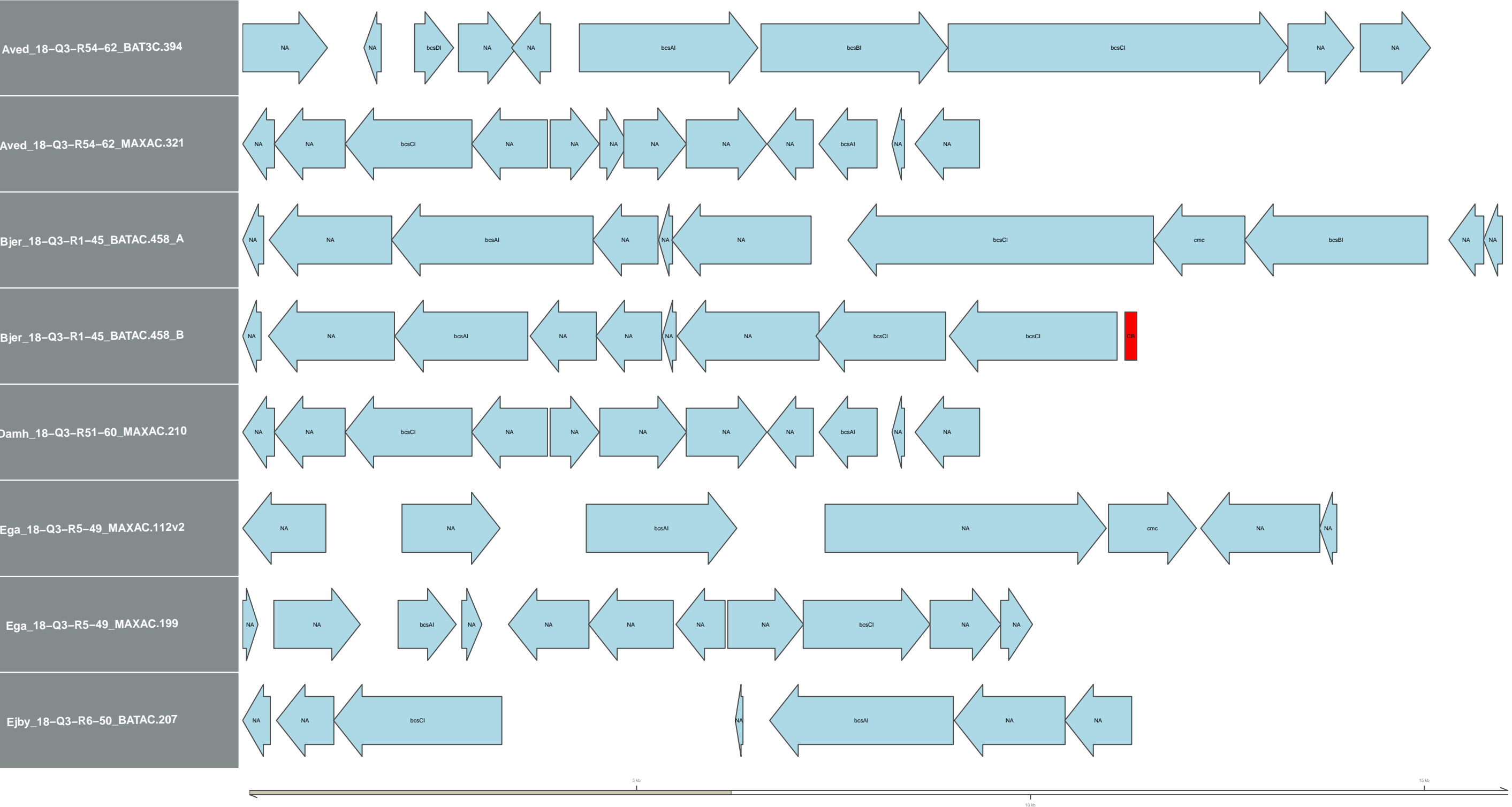
cellulose1 Heatmap



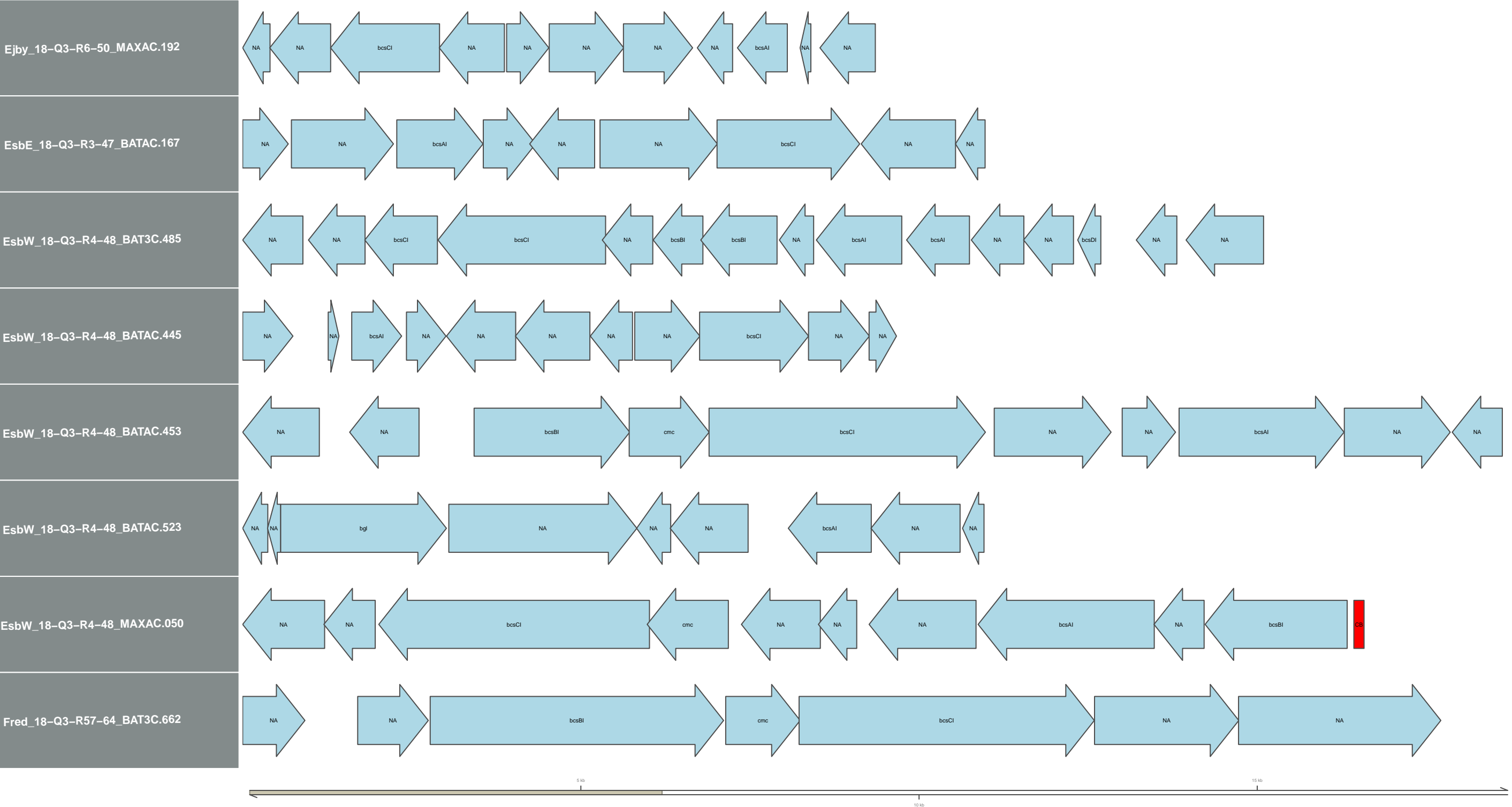
cellulose1 Heatmap



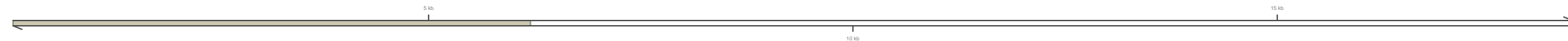
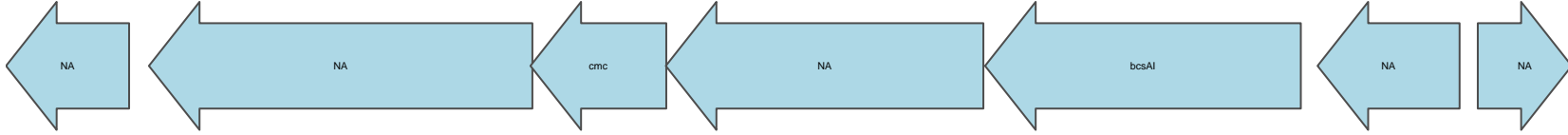
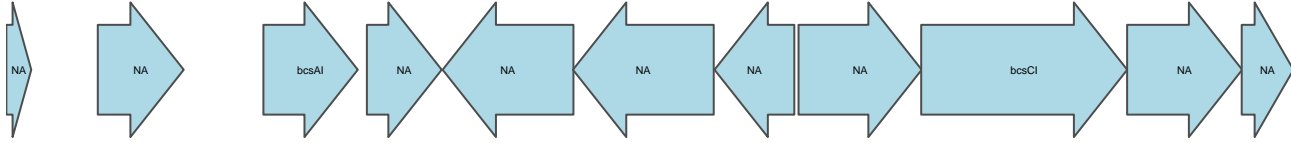
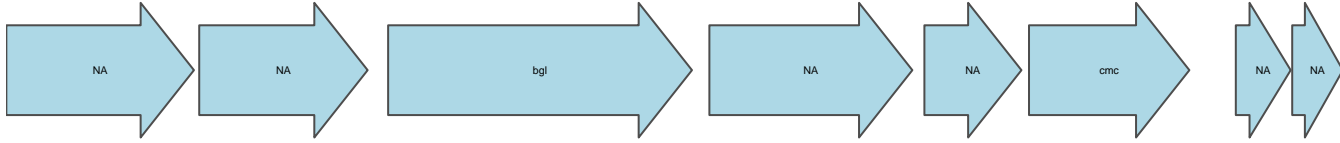
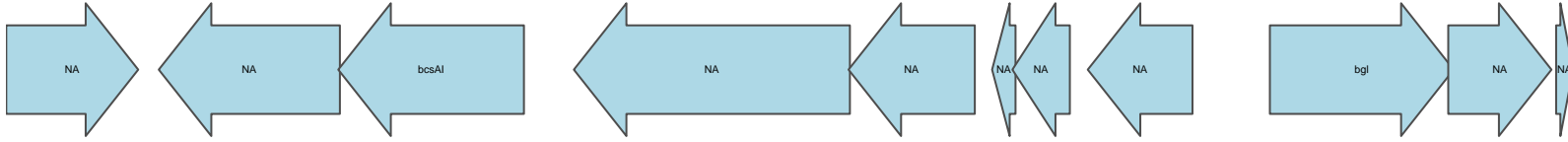
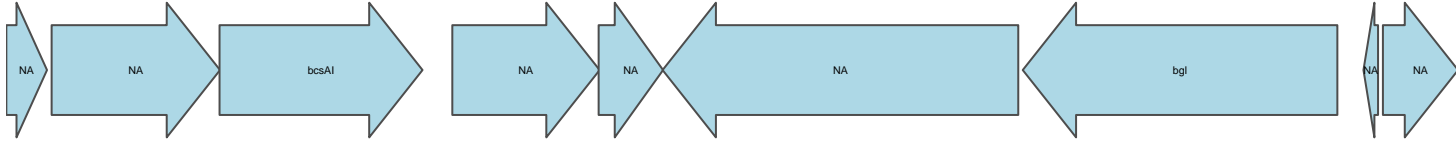
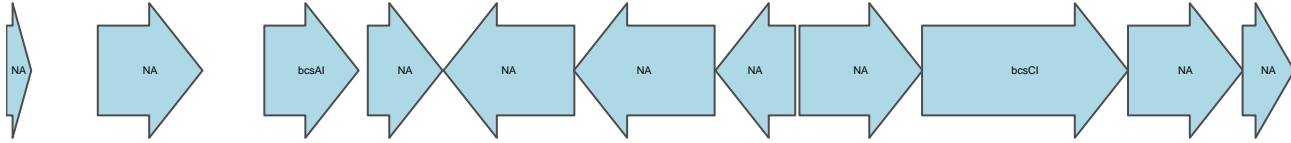
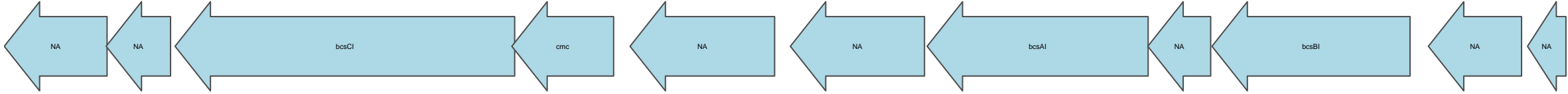
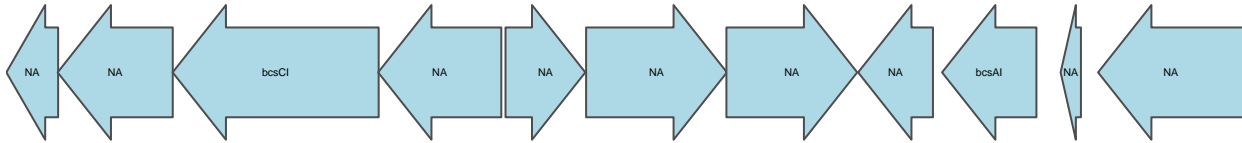
cellulose1



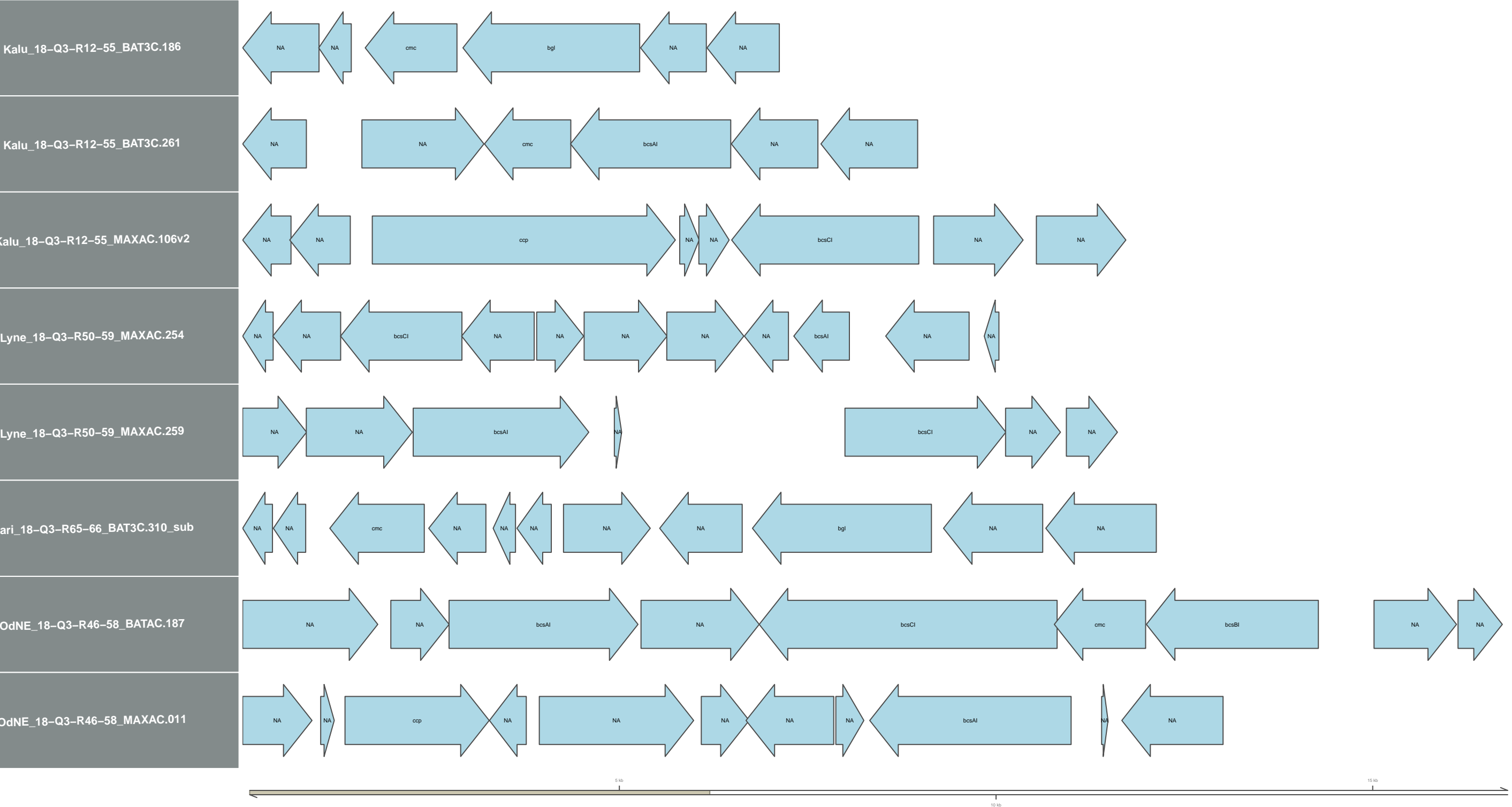
cellulose1



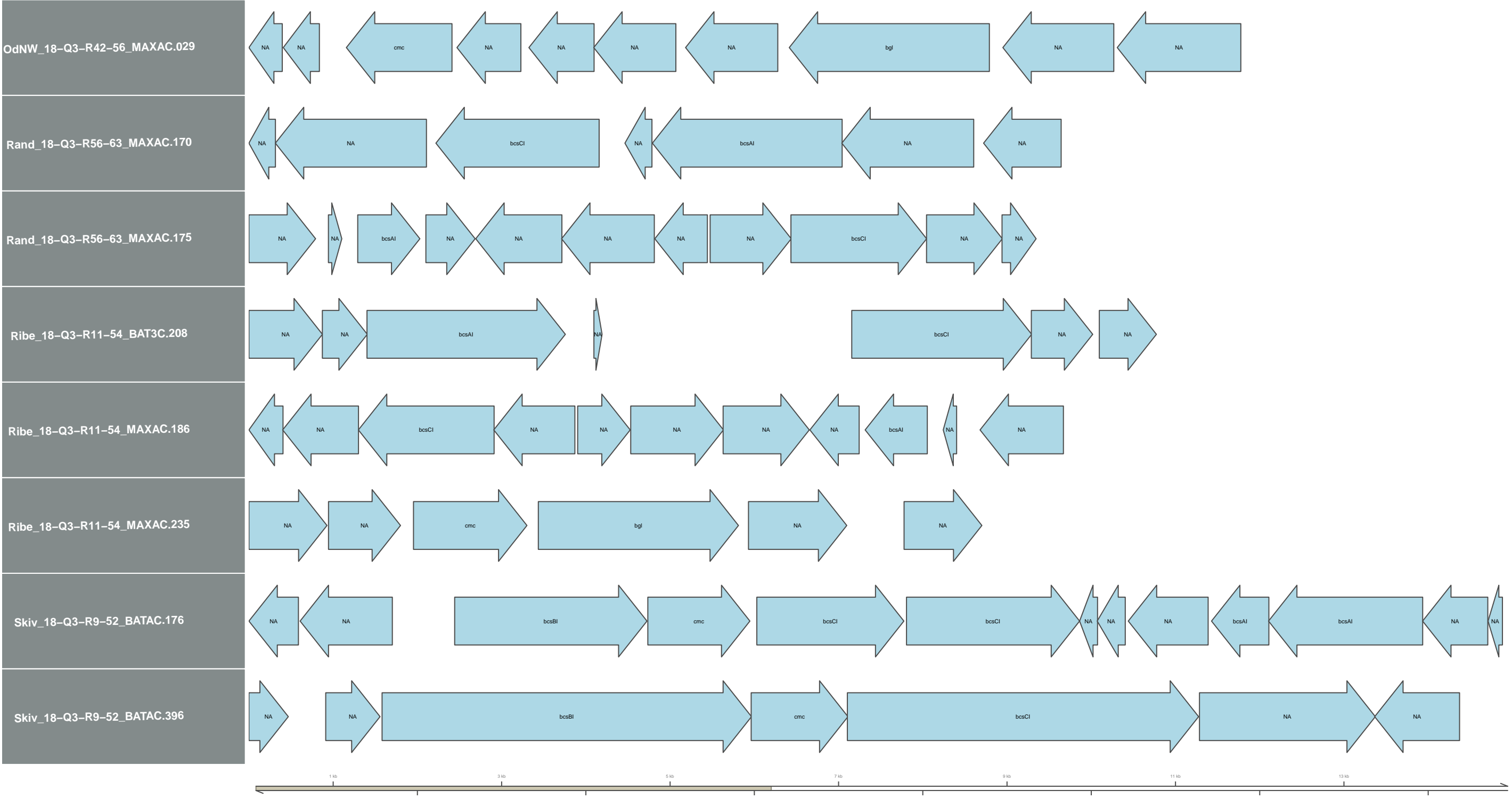
cellulose1



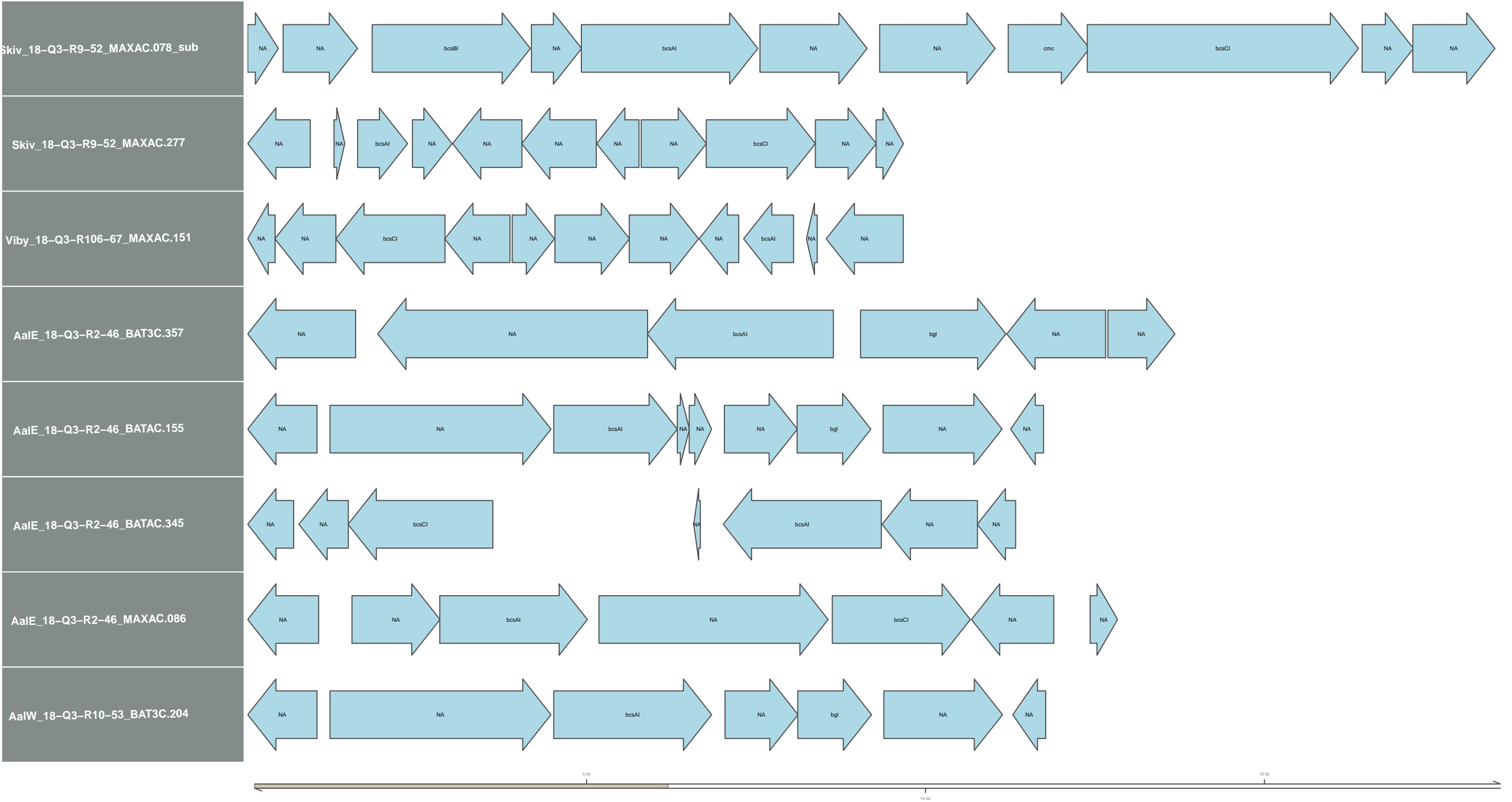
cellulose1



cellulose1

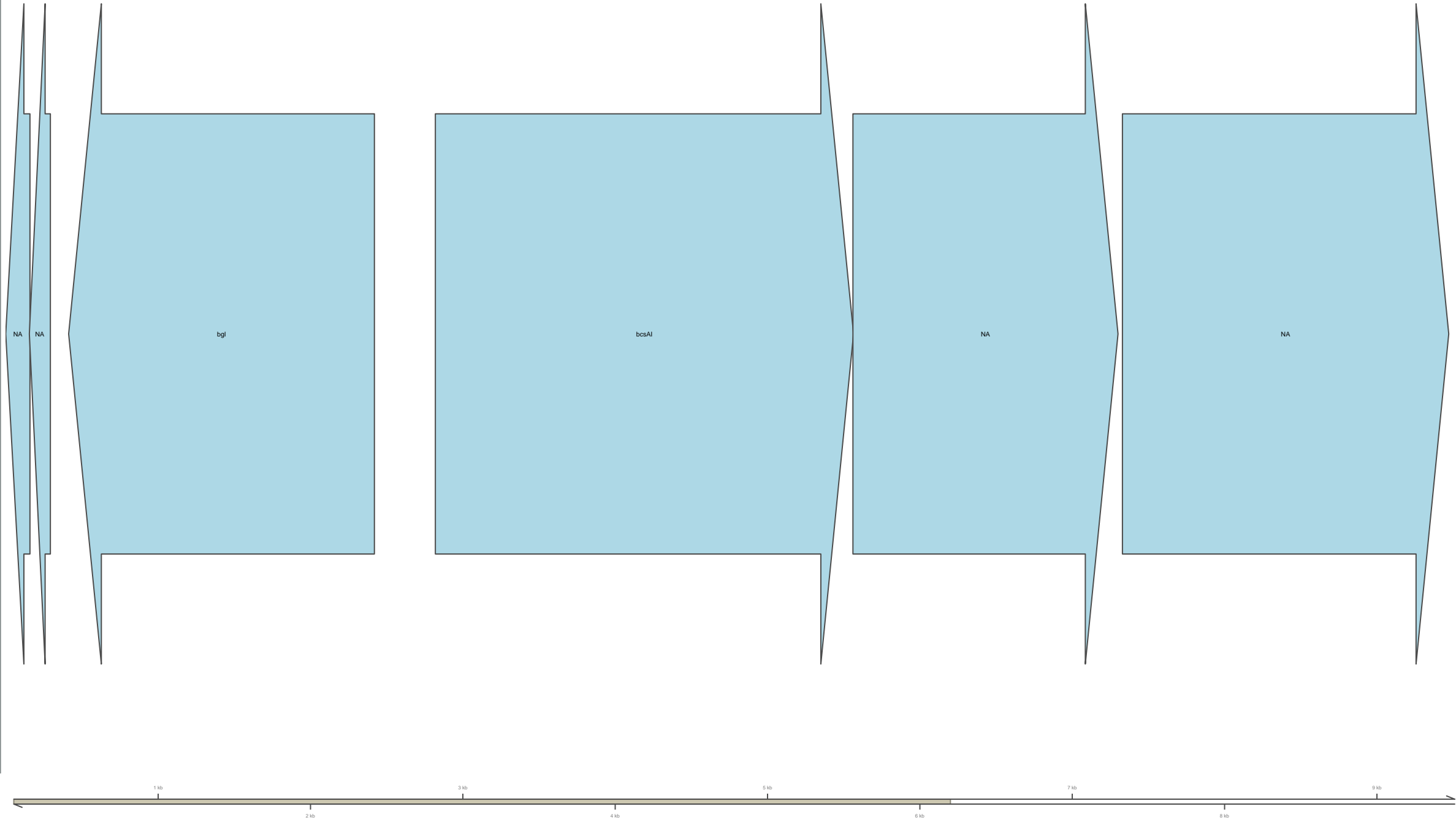


cellulose1



cellulose1

AaIW_18-Q3-R10-53_BAT3C.245



2	Aved_18-Q3-R54-62_MAXAC.321	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00000302-10-25166900	1695374	bcsAI	01477
3	Bjer_18-Q3-R1-45_BATAC.458	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Rhodoferrax;s__	tig00001862-10-6955040	304719	bcsAI	00257
4	Damh_18-Q3-R51-60_MAXAC.210	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00000292-10-7440630	707129	bcsAI	02125
5	Ega_18-Q3-R5-49_MAXAC.112v2	d__Bacteria;p__Planctomycetota;c__Brocadiae;o__Brocadiales;f__Brocadaceae;g__Brocadia;s__Brocadia sapporoensis	tig00000002-10-32561090	864182	bcsAI	00815
6	Ega_18-Q3-R5-49_MAXAC.199	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00004062-10-2279720	51224	bcsAI	02055
7	Ejby_18-Q3-R6-50_BATAC.207	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Palsa-1005;g__PALSA-1003;s__	tig00001219-10-4727790	59737	bcsAI	00712
8	Ejby_18-Q3-R6-50_MAXAC.192	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00000024-10-25242610	1615219	bcsAI	01360
9	EsbE_18-Q3-R3-47_BATAC.167	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Palsa-1005;g__PALSA-1005;s__	tig000008171-10-824870	71073	bcsAI	02164
10	EsbW_18-Q3-R4-48_BAT3C.485	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__PHCI01;s__	tig00020141-10-609230	22885	bcsAI	03737
11	EsbW_18-Q3-R4-48_BATAC.445	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00004595-10-3816970	31208	bcsAI	01209
12	EsbW_18-Q3-R4-48_BATAC.453	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Simplicispira_A;s__	tig00014047-10-1285900	106609	bcsAI	01813
13	EsbW_18-Q3-R4-48_BATAC.523	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__s__	tig00002958-10-6732880	188715	bcsAI	00832
14	EsbW_18-Q3-R4-48_MAXAC.050	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__s__	tig00018082-10-889440	83447	bcsAI	03083
15	Fred_18-Q3-R57-64_BAT3C.662	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Bryobacteriales;f__Bryobacteraceae;g__s__	tig00006256-10-5425100	396711	bcsBI	01773
16	Fred_18-Q3-R57-64_MAXAC.222	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00000202-10-25454520	2463238	bcsAI	02108
17	Hade_18-Q3-R52-61_BATAC.364	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Dechloromonas;s__	tig00407471-10-3182230	146325	bcsAI	03000
18	Hade_18-Q3-R52-61_MAXAC.319	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00013332-10-1613710	60757	bcsAI	02127
19	Hirt_18-Q3-R61-65_BAT3C.578	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__s__	tig00005850-10-2890570	78592	bcsAI	03735
20	Hirt_18-Q3-R61-65_BATAC.551	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__s__	tig00006048-10-3784910	6222	bcsAI	02345
21	Hirt_18-Q3-R61-65_MAXAC.022	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Uliginosibacterium;s__	tig000008471-10-3272170	86112	bgl	00112
22	Hirt_18-Q3-R61-65_MAXAC.245	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00015913-10-1166340	37940	bcsAI	01910
23	Hjor_18-Q3-R7-51_BAT3C.155	d__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__s__	tig00002714-1981250-5975520	159282	bcsAI	01030
24	Kalu_18-Q3-R12-55_BAT3C.186	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__SBR1031;f__A4b;g__OLB13;s__	tig00000584-10-21303060	280325	bgl	00221
25	Kalu_18-Q3-R12-55_BAT3C.261	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Bryobacteriales;f__Bryobacteraceae;g__s__	tig00004141-10-2319180	89372	bcsAI	03037
26	Kalu_18-Q3-R12-55_MAXAC.106v2	d__Bacteria;p__Chloroflexota;c__Anaerolineae;o__Promineofillales;f__Promineofillaceae;g__GCA-2699125;s__	tig00100734-10-59431720	2251808	bcsCI	03824
27	Lyne_18-Q3-R50-59_MAXAC.254	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00002296-10-8929180	853669	bcsAI	00751
28	Lyne_18-Q3-R50-59_MAXAC.259	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Palsa-1005;g__PALSA-1003;s__	tig00005124-10-3344470	80195	bcsAI	01658
29	Mari_18-Q3-R65-66_BAT3C.310_sub	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Uliginosibacterium;s__	tig00004204-10-2745170	212189	bgl	00260
30	OdNE_18-Q3-R46-58_BATAC.187	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Gallionellaceae;g__UBA7399;s__	tig00013603-10-1108760	12689	bcsAI	01449
31	OdNE_18-Q3-R46-58_MAXAC.011	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Chromatiales;f__Chromatiaceae;g__s__	tig00001185-10-6730500	406363	bcsAI	03704
32	OdNW_18-Q3-R42-56_MAXAC.029	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Uliginosibacterium;s__	tig000008739-10-1323550	51832	bgl	02965
33	Rand_18-Q3-R56-63_MAXAC.170	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Palsa-1005;g__PALSA-1003;s__	tig00224048-10-1871190	154794	bcsAI	03451
34	Rand_18-Q3-R56-63_MAXAC.175	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00052853-10-132870	3044	bcsAI	01612
35	Ribe_18-Q3-R11-54_BAT3C.208	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Palsa-1005;g__PALSA-1003;s__	tig01078798-10-7283700	84619	bcsAI	02150
36	Ribe_18-Q3-R11-54_MAXAC.186	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00001126-10-9167150	12722	bcsAI	00014
37	Ribe_18-Q3-R11-54_MAXAC.235	d__Bacteria;p__Chloroflexota;c__Chloroflexia;o__Chloroflexales;f__Roseiflexaceae;g__Kouleothrix;s__	tig00000009-10-56372800	5353663	bgl	04180
38	Skiv_18-Q3-R9-52_BATAC.176	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Gallionellaceae;g__UBA7399;s__	tig00025195-10-609250	40291	bcsAI	01730
39	Skiv_18-Q3-R9-52_BATAC.396	d__Bacteria;p__Acidobacteriota;c__Acidobacteriae;o__Bryobacteriales;f__Bryobacteraceae;g__UBA690;s__	tig00002691-10-6419970	11117	bcsBI	00856
40	Skiv_18-Q3-R9-52_MAXAC.078_sub	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Rhodocyclaceae;g__Dechloromonas;s__	tig00014165-10-544790	30935	bcsAI	00765
41	Skiv_18-Q3-R9-52_MAXAC.277	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig01148445-10-14237630	760958	bcsAI	01708
42	Viby_18-Q3-R106-67_MAXAC.151	d__Bacteria;p__Elusimicrobiota;c__Elusimicrobia;o__F11;f__FEN-1173;g__s__	tig00591490-10-8803150	834623	bcsAI	02104
43	AalE_18-Q3-R2-46_BAT3C.357	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Steroidobacteriales;f__Steroidobacteraceae;g__s__	tig00004397-10-3020980	53916	bcsAI	00957
44	AalE_18-Q3-R2-46_BATAC.155	d__Bacteria;p__Acidobacteriota;c__Blastocatellia;o__UBA7656;f__g__s__	tig00003873-10-3436420	242886	bcsAI	01757
45	AalE_18-Q3-R2-46_BATAC.345	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Palsa-1005;g__PALSA-1003;s__	tig00002178-10-4724040	236998	bcsAI	00195
46	AalE_18-Q3-R2-46_MAXAC.086	d__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Palsa-1005;g__s__	tig00015706-10-216600	4737	bcsAI	01656