

Supplementary material

Table S1. SRA accessions and metadata of foreign strains included in the cgSNP-based phylogeny analysis.

Strain	SRA	Country	Year	Specimen	Oxford ST	Pasteur ST
AYP-A2	SRR5891495	Australia	2013	wound	1806, 208	2
11A1213CRGN008	SRR5739056	Canada	2012	NA	1806, 208	2
11A1314CRGN088	SRR5739066	Canada	2013	NA	1806, 208	2
09A16CRGN003B	SRR5739115	Canada	2016	NA	1806, 208	2
AB1251	SRR11589159	Egypt	2013	NA	1816, 195	2
M17	SRR14102306	Egypt	2020	sputum	1050, 2058	2
M18	SRR14102521	Egypt	2020	blood	1078	85
A1829	SRR13327188	Egypt	2018	blood	NA	NA
A1825	SRR13327192	Egypt	2018	bronchoalveolar lavage	2246	113
A1824	SRR13327193	Egypt	2018	bronchoalveolar lavage	1705	2
A1823	SRR13327194	Egypt	2018	bronchoalveolar lavage	2246	113
A1819	SRR13327199	Egypt	2018	blood	2805, 684	570
A1813	SRR13327205	Egypt	2018	blood	1816, 195	2
M11	SRR14100602	Egypt	2020	Pleural fluid	1089	85
A1702	SRR13327208	Egypt	2017	blood	NA	NA
B9	SRR15911746	France	NA	Seine River	1806/208	2
AB1318	SRR11589121	Israel	2014	NA	1806, 208	2
M012.6	SRR15973856	Israel	2019	NA	1816, 195	2
AB1317	SRR11589122	Israel	2014	NA	2054, 502	2
AB1181	SRR11589183	Israel	2010	NA	1806, 208	604
AB1342	SRR11589278	Israel	2014	NA	1808, 348	2
Ab105	SRR16951843	Israel	2019	blood	1806, 208	2
AB1218	SRR11589173	Jordan	2012	NA	1816, 195	2
nasal1	SRR15185780	Jordan	2016	Nasal swab	1806, 208	2
blood3	SRR15185781	Jordan	2016	blood	499	158
ACN-20190830-N22	SRR12905336	Libya	2019	wound	440	25
ACN-20190830-N60	SRR12905337	Libya	2019	wound	NA	NA
ACN-20190830-N54	SRR12905338	Libya	2019	blood	2806, 286	2
ACN-20190830-N45	SRR12905339	Libya	2019	throat swab	NA	NA
ACN-20190830-N27	SRR12905341	Libya	2019	wound	1806, 208	2
AbBAS-1	SRR12349738	Spain	2019	NA	957	85
FDAARGOS_1360	SRR13674446	USA	NA	NA	1114, 1841	2
CFSAN0937	SRR9883198	USA	2005	NA	1806, 208	2
ORAB01	SRR1819797	USA	2012	NA	1806, 208	2
ABUH763	SRR3666894	USA	2015	NA	1839, 281	2

Table S2: Metadata and STs of the isolates included in the current study

Strain	Specimen	Oxford STs	Pasteur STs
20Y0020	Endotracheal Tube	208, 1806	2
20Y0021	Blood	732	602
20Y0022	Endotracheal Tube	732	602
20Y0023	Wound swab	281	2
20Y0024	Endotracheal Tube	281	2
20Y0025	Catheter Tip	281	2
20Y0026	Wound swab	281	2
20Y0028	Blood	208, 1806	2
20Y0030	Catheter Tip	208, 1806	2
20Y0031	Endotracheal Tube	208, 1806	2
20Y0032	Sputum	208, 1806	2
20Y0033	Endotracheal Tube	1114, 1841	2
20Y0035	Sputum	732	602
20Y0036	Catheter Tip	281	2
20Y0037	Sputum	684, 2805	570
20Y0038	Blood	281	2
20Y0039	Endotracheal Tube	281	2
20Y0040	Wound swab	281	2
20Y0041	Sputum	684, 2805	570
20Y0042	Endotracheal Tube	208, 1806	2
20Y0043	Wound swab	684, 2805	570
20Y0045	Sputum	732	602
20Y0046	Endotracheal Tube	732	602
20Y0048	Blood	2026, 2807	570
20Y0054	Blood	208, 1806	604
20Y0055	Blood	195, 1816	2
20Y0056	Blood	195, 1816	2
20Y0057	Blood	2808	85
20Y0058	Sputum	732	602
20Y0059	Blood	195, 1816	2
20Y0060	Blood	195, 1816	2
20Y0062	Blood	502, 2054	600
20Y0063	Blood	1050, 2058	2
20Y0066	Blood	2026, 2807	570
20Y0067	Blood	2026, 2807	570
20Y0068	Blood	195, 1816	2
20Y0070	Blood	286, 2806	570
20Y0075	Endotracheal Tube	208, 1806	2
20Y0076	Sputum	732	602
20Y0077	Wound swab	2246	113
20Y0078	Blood	1115	15
20Y0079	Blood	1115	15
20Y0080	Blood	1580	85
20Y0081	Blood	732	602
20Y0082	Blood	732	602
20Y0083	Pus	1115	15

Table S3: Post-assembly metrics of the draft genomes generated in the current study

ID	# Contigs	GC (%)	Genome fraction (%)	L50	N50	Total Length (>= 0 bp)
20Y0020	124	39.12	82.464	17	63,013	3,949,756
20Y0021	120	38.97	84.246	19	67,691	4,052,277
20Y0022	76	38.95	84.320	8	180,645	4,067,317
20Y0023	169	39.08	82.365	25	46,184	3,798,591
20Y0024	88	39.02	82.789	12	86,520	3,815,456
20Y0025	83	39.02	82.606	12	105,392	3,816,242
20Y0026	164	39.07	82.573	23	51,975	3,804,414
20Y0028	112	39.11	82.328	15	83,486	3,954,504
20Y0030	116	39.11	82.477	15	98,676	3,937,117
20Y0031	144	39.13	82.214	21	49,789	3,935,324
20Y0032	76	39.10	82.561	11	133,123	3,946,657
20Y0033	133	39.02	83.217	18	76,709	4,067,300
20Y0035	123	38.99	84.143	11	88,807	4,064,120
20Y0036	116	39.02	82.915	14	89,001	3,855,350
20Y0037	85	38.99	82.079	12	110,515	3,868,356
20Y0038	147	38.95	82.780	19	61,103	3,918,603
20Y0039	120	39.02	82.885	15	75,801	3,855,053
20Y0040	143	39.05	82.584	17	61,060	3,844,840
20Y0041	111	39.01	81.837	17	79,886	3,864,308
20Y0042	150	39.15	82.192	22	61,206	3,932,666
20Y0043	90	38.99	81.748	14	99,619	3,862,699
20Y0045	124	38.99	84.231	15	73,045	4,061,666
20Y0046	96	38.94	84.355	11	122,870	4,061,701
20Y0048	121	38.91	81.782	17	74,174	3,942,770
20Y0054	107	38.90	82.705	16	85,520	4,036,875
20Y0055	88	38.86	82.258	18	78,512	3,960,451
20Y0056	112	38.89	82.195	16	82,756	3,950,723
20Y0057	144	39.02	81.283	15	70,792	3,978,669
20Y0058	77	38.95	84.427	12	105,476	4,066,863
20Y0059	187	38.90	82.697	15	110,212	4,247,432
20Y0060	82	38.86	82.098	13	110,241	3,957,597
20Y0062	126	38.97	81.891	15	81,618	4,108,098
20Y0063	130	38.96	82.611	17	61,439	3,992,810
20Y0066	116	39.01	81.726	16	65,743	3,871,707
20Y0067	150	39.06	81.417	24	54,557	3,865,554
20Y0068	107	39.00	82.190	17	84,571	3,883,930
20Y0070	146	39.05	81.852	21	55,067	3,865,723
20Y0075	95	38.87	82.312	18	79,920	3,969,708
20Y0076	108	38.95	84.284	15	79,196	4,051,733
20Y0077	163	39.08	84.662	20	51,316	4,161,645
20Y0078	152	39.00	86.573	24	51,538	4,136,194
20Y0079	133	38.97	86.861	22	56,881	4,142,505
20Y0080	129	38.86	82.687	15	78,173	3,979,601
20Y0081	82	38.93	84.349	12	97,676	4,053,101
20Y0082	128	38.98	84.191	19	61,878	4,041,800
20Y0083	152	38.96	86.455	24	51,962	4,108,172

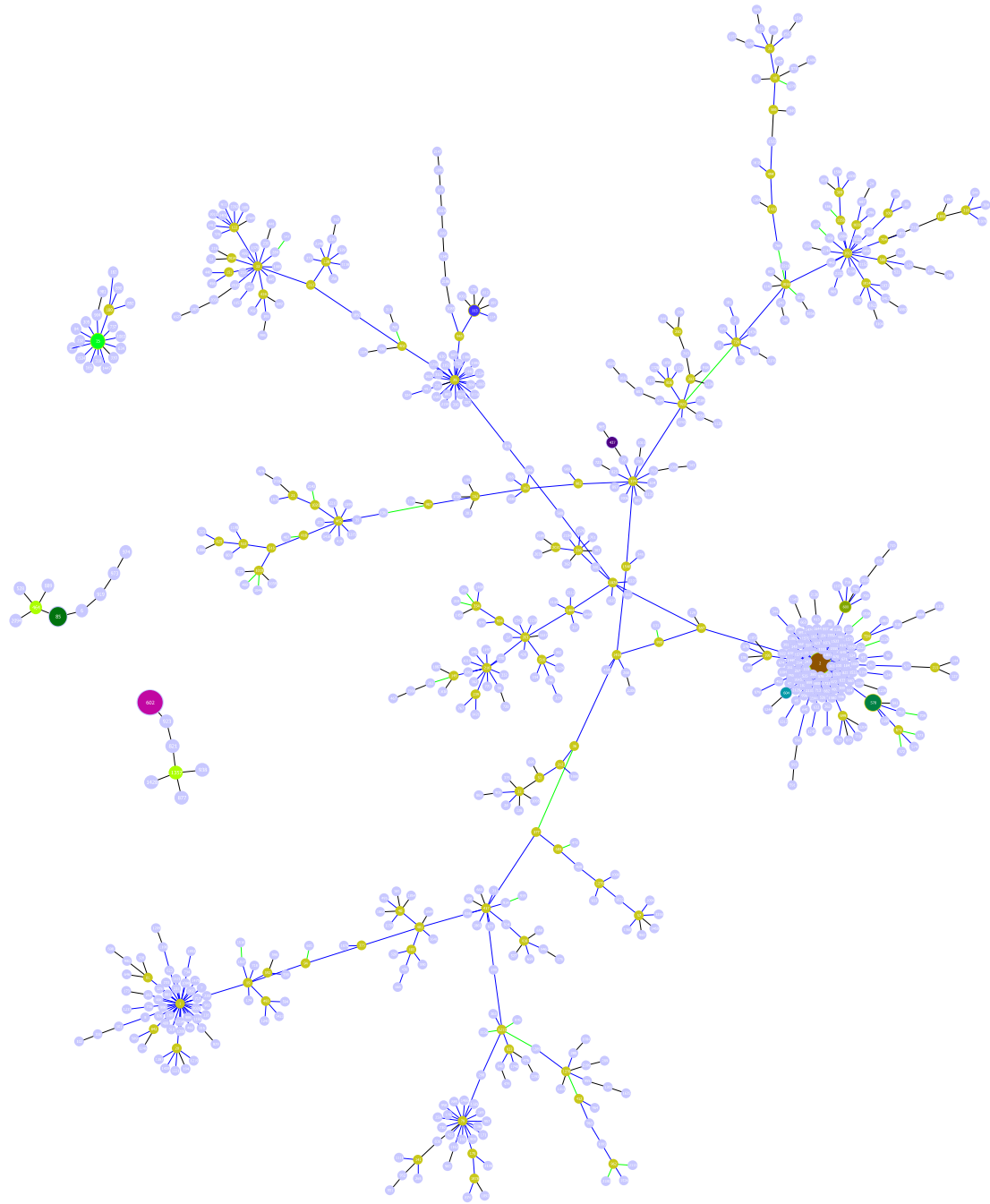


Figure S1: A minimum spanning tree based on Pasteur MLST typing scheme of *A. baumannii*. The numbers inside the circles refer to STs while light blue and light green circles correspond to STs in the database and clonal complexes, respectively. Circles of other colors correspond to the STs of the isolates sequenced in the current study.

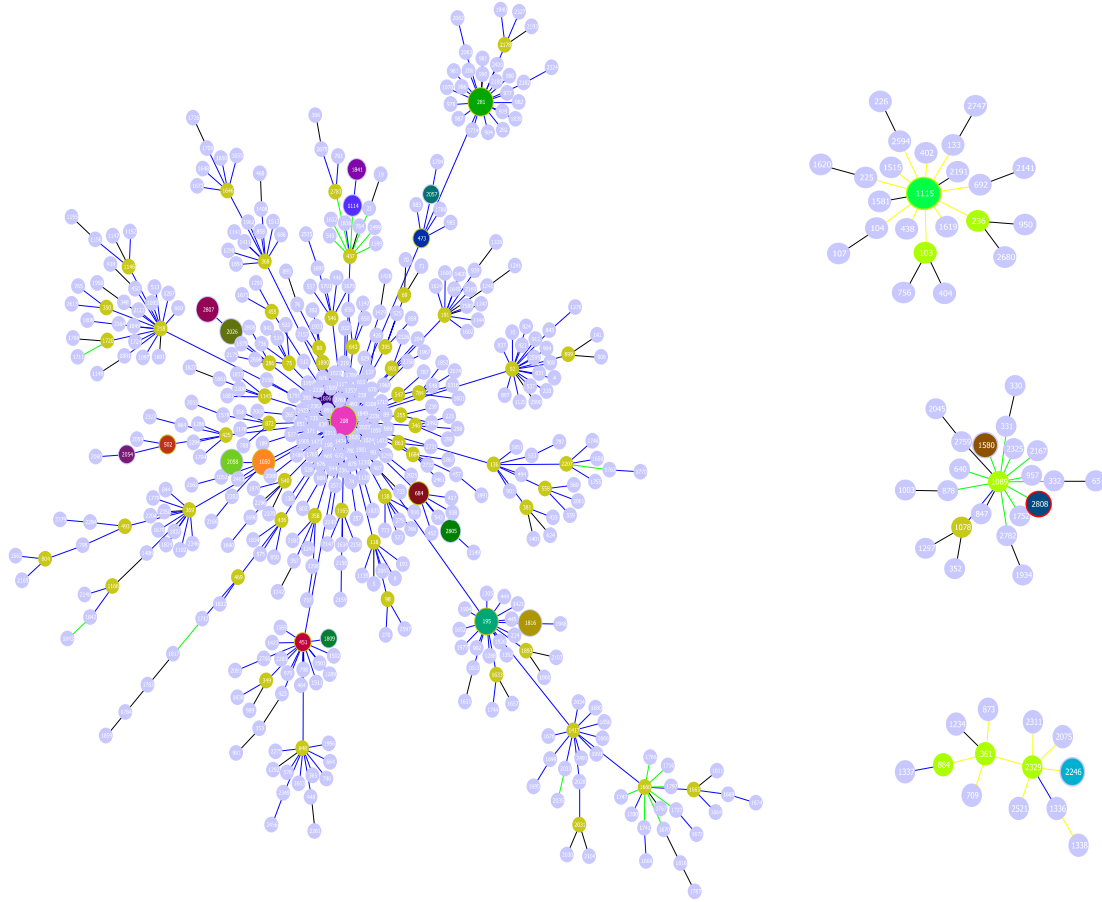
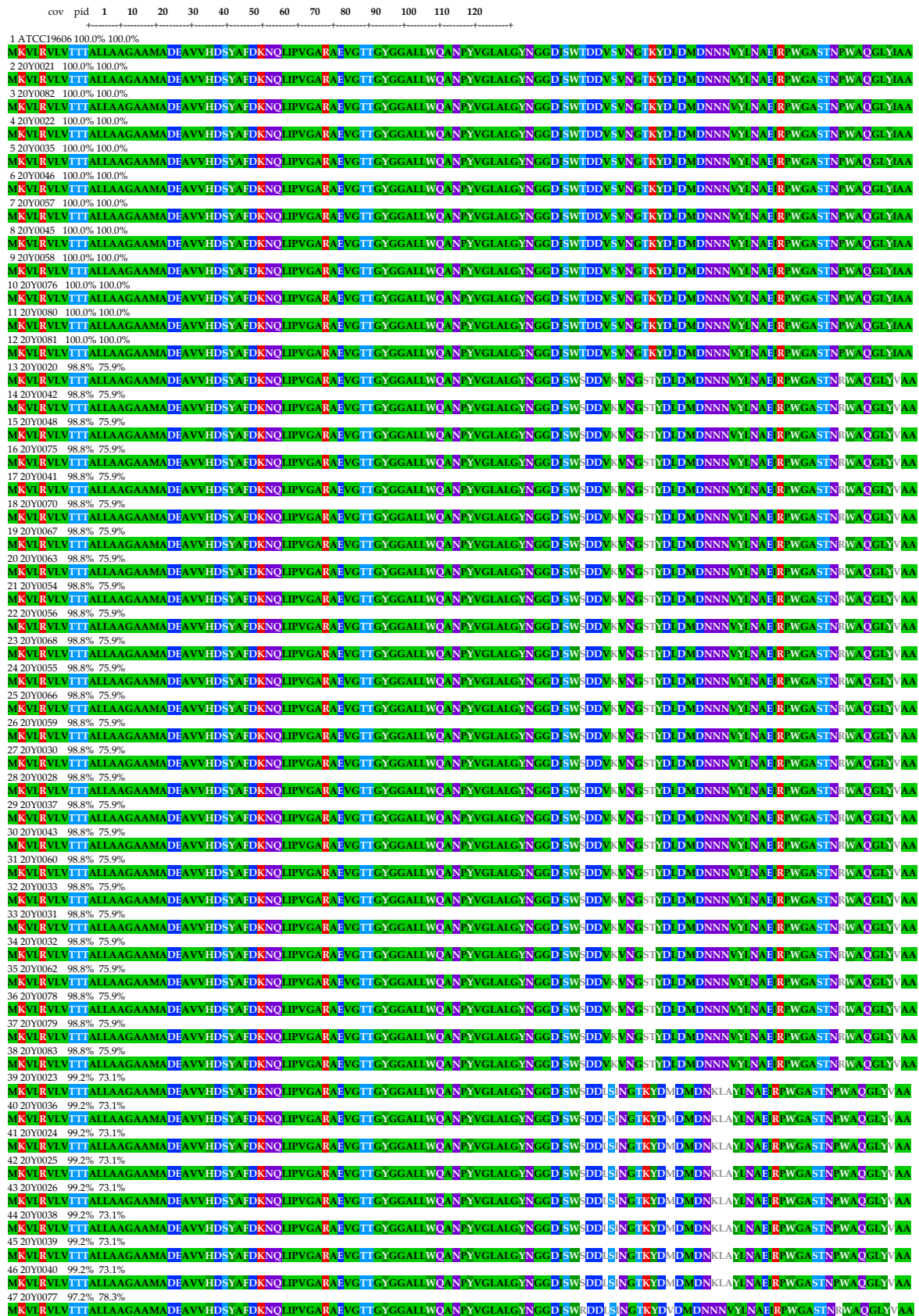


Figure S2: A minimum spanning tree based on Oxford MLST typing scheme of *A. baumannii*. The numbers inside the circles refer to STs while light blue and light green circles correspond to STs in the database and clonal complexes, respectively. Circles of other colors correspond to the STs of the isolates sequenced in the current study.

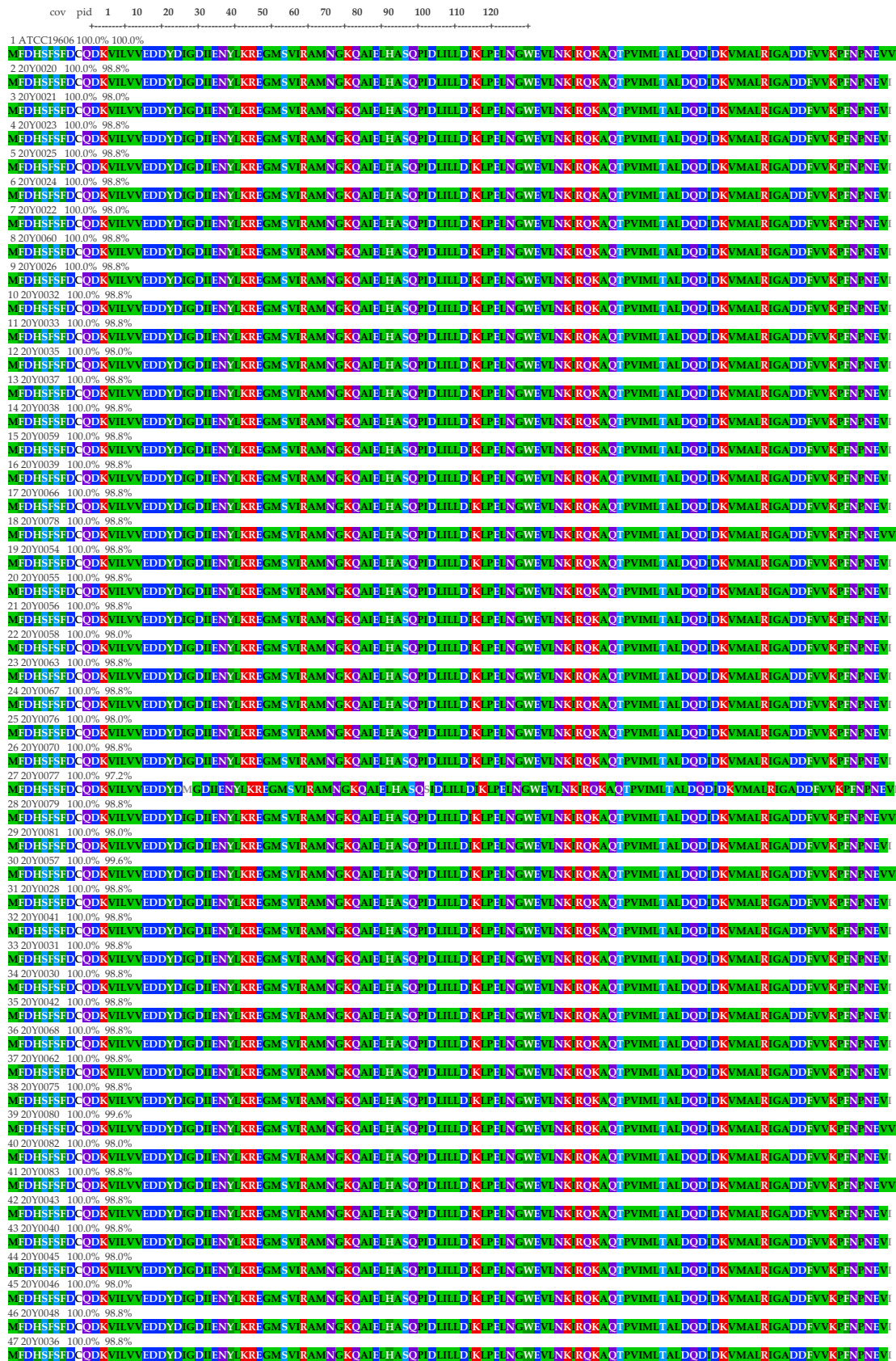


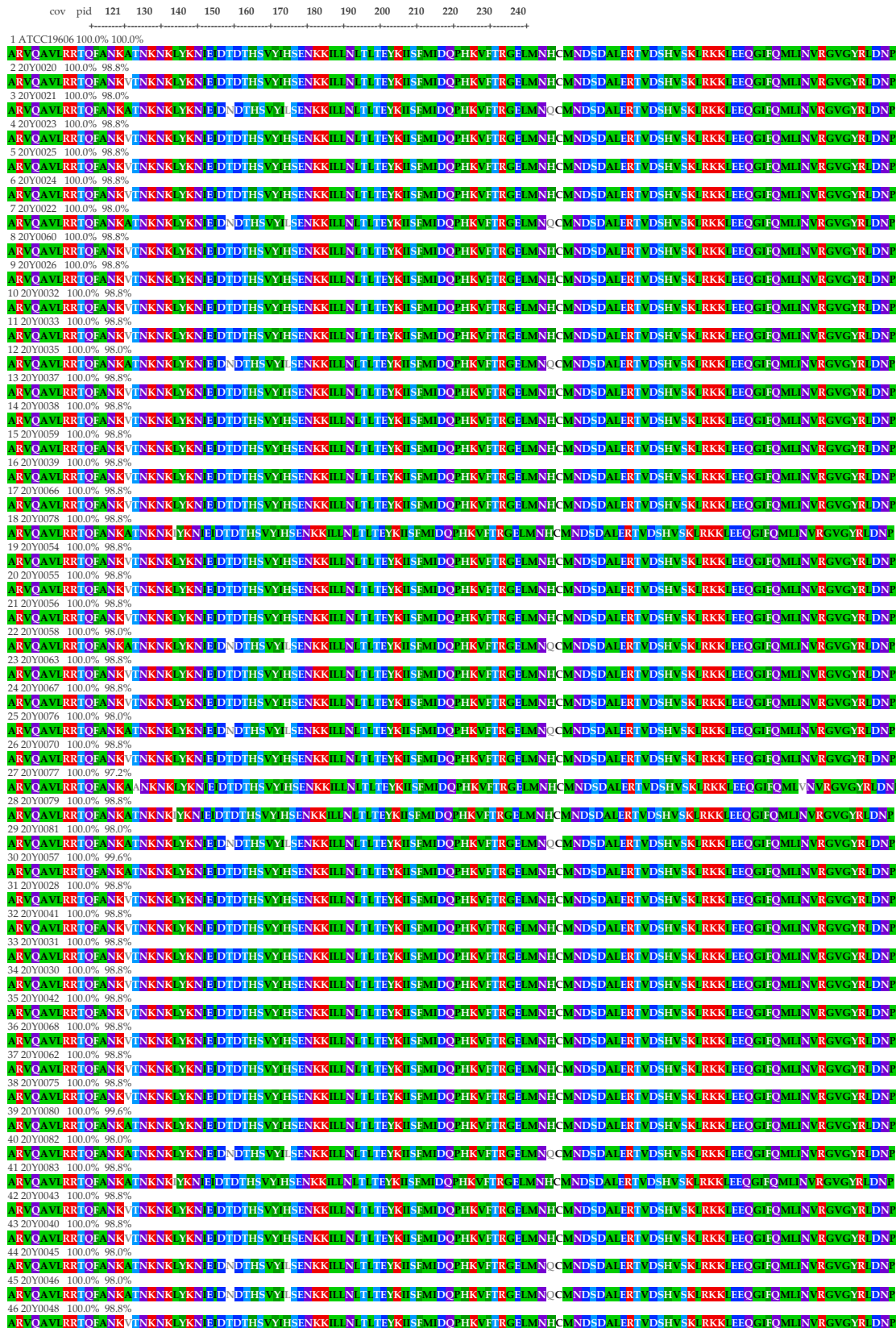
47 20Y0077 97.2% 78.3% **Q**A**A****Y****D****N****D****Y****D****H****R****S****S****D****E****H****K****N****E****T****N****Y**---SYN**E****S****N****E****Q****L****S****Y****K****N****D****A****D****Y****L****G****E****G****F****A****K****N****K****N****W****G****V****L****G****E****V****G****A****Y****T****C****N****T****E****D**KQGT-

NAAG**N****A**D**A**D**L**R**A****E****N****K****R****N****D****K****Y****K****W****L****V**

	cov	pid	241	249
			←-----→	
1 ATCC19606	100.0%	100.0%	G	K V G V N F Y W
2 20Y0021	100.0%	100.0%	G	K V G V N F Y W
3 20Y0082	100.0%	100.0%	G	K V G V N F Y W
4 20Y0022	100.0%	100.0%	G	K V G V N F Y W
5 20Y0035	100.0%	100.0%	G	K V G V N F Y W
6 20Y0046	100.0%	100.0%	G	K V G V N F Y W
7 20Y0057	100.0%	100.0%	G	K V G V N F Y W
8 20Y0045	100.0%	100.0%	G	K V G V N F Y W
9 20Y0058	100.0%	100.0%	G	K V G V N F Y W
10 20Y0076	100.0%	100.0%	G	K V G V N F Y W
11 20Y0080	100.0%	100.0%	G	K V G V N F Y W
12 20Y0081	100.0%	100.0%	G	K V G V N F Y W
13 20Y0020	98.8%	75.9%	G	K V G V N F Y W
14 20Y0042	98.8%	75.9%	G	K V G V N F Y W
15 20Y0048	98.8%	75.9%	G	K V G V N F Y W
16 20Y0075	98.8%	75.9%	G	K V G V N F Y W
17 20Y0041	98.8%	75.9%	G	K V G V N F Y W
18 20Y0070	98.8%	75.9%	G	K V G V N F Y W
19 20Y0067	98.8%	75.9%	G	K V G V N F Y W
20 20Y0063	98.8%	75.9%	G	K V G V N F Y W
21 20Y0054	98.8%	75.9%	G	K V G V N F Y W
22 20Y0056	98.8%	75.9%	G	K V G V N F Y W
23 20Y0068	98.8%	75.9%	G	K V G V N F Y W
24 20Y0055	98.8%	75.9%	G	K V G V N F Y W
25 20Y0066	98.8%	75.9%	G	K V G V N F Y W
26 20Y0059	98.8%	75.9%	G	K V G V N F Y W
27 20Y0030	98.8%	75.9%	G	K V G V N F Y W
28 20Y0028	98.8%	75.9%	G	K V G V N F Y W
29 20Y0037	98.8%	75.9%	G	K V G V N F Y W
30 20Y0043	98.8%	75.9%	G	K V G V N F Y W
31 20Y0060	98.8%	75.9%	G	K V G V N F Y W
32 20Y0033	98.8%	75.9%	G	K V G V N F Y W
33 20Y0031	98.8%	75.9%	G	K V G V N F Y W
34 20Y0032	98.8%	75.9%	G	K V G V N F Y W
35 20Y0062	98.8%	75.9%	G	K V G V N F Y W
36 20Y0078	98.8%	75.9%	G	K V G V N F Y W
37 20Y0079	98.8%	75.9%	G	K V G V N F Y W
38 20Y0083	98.8%	75.9%	G	K V G V N F Y W
39 20Y0023	99.2%	73.1%	G	K V G V N F Y W
40 20Y0036	99.2%	73.1%	G	K V G V N F Y W
41 20Y0024	99.2%	73.1%	G	K V G V N F Y W
42 20Y0025	99.2%	73.1%	G	K V G V N F Y W
43 20Y0026	99.2%	73.1%	G	K V G V N F Y W
44 20Y0038	99.2%	73.1%	G	K V G V N F Y W
45 20Y0039	99.2%	73.1%	G	K V G V N F Y W
46 20Y0040	99.2%	73.1%	G	K V G V N F Y W
47 20Y0077	97.2%	78.3%	G	K V G V N F Y W

Figure S3: Multiple sequence alignment of the predicted amino acid sequences of CarO in all isolates compared to that of *A. baumannii* ATCC 19606. The alignment was visualized using MView version 1.63. cov, coverage; pid, percent identity.



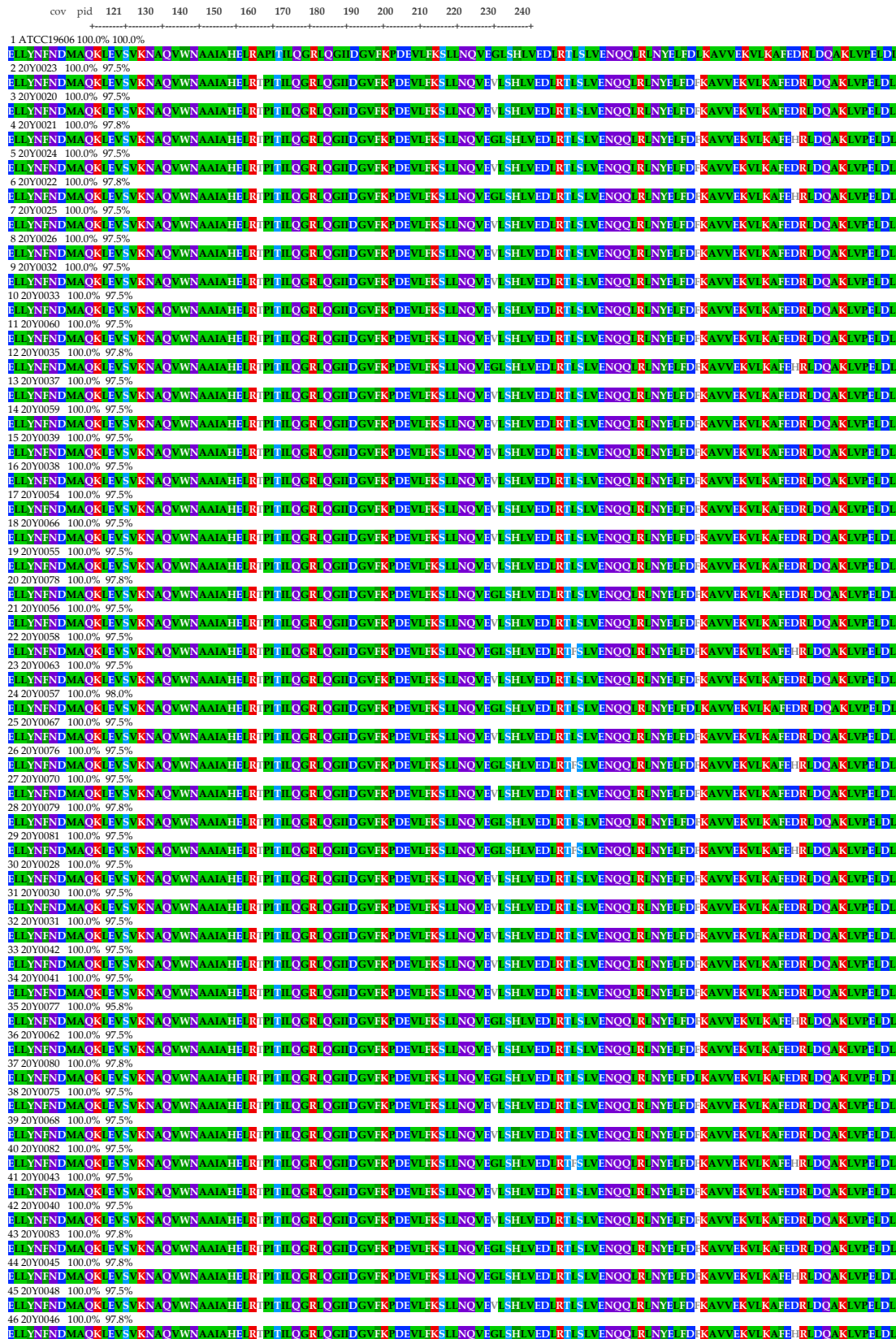


47 20Y0036 100.0% 98.8%

R Q A V L R R T Q F N K V I N K N K Y K N E D I D T H S Y H S E N K K I L N T I T E Y K I S E M D Q H K V F T R E L M N H C M N D S D M E R T V D S H Y S K I R K K E E Q G I F Q M L N V R G V G Y R D N

	cov	pid	241	247	
			←-----→		
1 ATCC19606	100.0%	100.0%	P	A	V
2 20Y0020	100.0%	98.8%	L	A	V
3 20Y0021	100.0%	98.0%	L	A	V
4 20Y0023	100.0%	98.8%	L	A	V
5 20Y0025	100.0%	98.8%	L	A	V
6 20Y0024	100.0%	98.8%	L	A	V
7 20Y0022	100.0%	98.0%	L	A	V
8 20Y0060	100.0%	98.8%	L	A	V
9 20Y0026	100.0%	98.8%	L	A	V
10 20Y0032	100.0%	98.8%	L	A	V
11 20Y0033	100.0%	98.8%	L	A	V
12 20Y0035	100.0%	98.0%	L	A	V
13 20Y0037	100.0%	98.8%	L	A	V
14 20Y0038	100.0%	98.8%	L	A	V
15 20Y0059	100.0%	98.8%	L	A	V
16 20Y0039	100.0%	98.8%	L	A	V
17 20Y0066	100.0%	98.8%	L	A	V
18 20Y0078	100.0%	98.8%	L	K	D
19 20Y0054	100.0%	98.8%	L	A	V
20 20Y0055	100.0%	98.8%	L	A	V
21 20Y0056	100.0%	98.8%	L	A	V
22 20Y0058	100.0%	98.0%	L	A	V
23 20Y0063	100.0%	98.8%	L	A	V
24 20Y0067	100.0%	98.8%	L	A	V
25 20Y0076	100.0%	98.0%	L	A	V
26 20Y0070	100.0%	98.8%	L	A	V
27 20Y0077	100.0%	97.2%	L	K	D
28 20Y0079	100.0%	98.8%	L	A	V
29 20Y0081	100.0%	98.0%	L	A	V
30 20Y0057	100.0%	99.6%	L	A	V
31 20Y0028	100.0%	98.8%	L	A	V
32 20Y0041	100.0%	98.8%	L	A	V
33 20Y0031	100.0%	98.8%	L	A	V
34 20Y0030	100.0%	98.8%	L	A	V
35 20Y0042	100.0%	98.8%	L	A	V
36 20Y0068	100.0%	98.8%	L	A	V
37 20Y0062	100.0%	98.8%	L	A	V
38 20Y0075	100.0%	98.8%	L	A	V
39 20Y0080	100.0%	99.6%	L	A	V
40 20Y0082	100.0%	98.0%	L	A	V
41 20Y0083	100.0%	98.8%	L	K	D
42 20Y0043	100.0%	98.8%	L	A	V
43 20Y0040	100.0%	98.8%	L	A	V
44 20Y0045	100.0%	98.0%	L	A	V
45 20Y0046	100.0%	98.0%	L	A	V
46 20Y0048	100.0%	98.8%	L	A	V
47 20Y0036	100.0%	98.8%	L	A	V

Figure S4: Multiple sequence alignment of the predicted amino acid sequences of AdeR in all isolates compared to that of *A. baumannii* ATCC 19606. The alignment was visualized using MView version 1.63. cov, coverage; pid, percent identity.



47 20Y0036 100.0% 97.5%

E L I Y N F N D M A Q K L E V S V K N A Q V W N A A I A H E R T L I I L Q G R Q G I D G V F K D E V I F K S I I N Q V E V S H I A E D R I L S A E N Q Q R N Y E F D R K A V V E K V I K A F E D R D Q K A V I E D I



Figure S5: Multiple sequence alignment of the predicted amino acid sequences of AdeS in all isolates compared to that of *A. baumannii* ATCC 19606. The alignment was visualized using MView version 1.63. cov, coverage; pid, percent identity.

	cov	pid	1	10	20	30	40	50	60	70	80	90	100	110	120	
1	ATCC19606	100.0%	100.0%													
2	20Y0024	100.0%	100.0%													
3	20Y0056	100.0%	100.0%													
4	20Y0055	100.0%	100.0%													
5	20Y0063	100.0%	100.0%													
6	20Y0077	100.0%	99.6%													
7	20Y0037	100.0%	100.0%													
8	20Y0032	100.0%	100.0%													
9	20Y0059	100.0%	100.0%													
10	20Y0081	100.0%	100.0%													
11	20Y0076	100.0%	100.0%													
12	20Y0036	100.0%	100.0%													
13	20Y0030	100.0%	100.0%													
14	20Y0033	100.0%	100.0%													
15	20Y0068	100.0%	100.0%													
16	20Y0042	100.0%	100.0%													
17	20Y0062	100.0%	100.0%													
18	20Y0066	100.0%	100.0%													
19	20Y0045	100.0%	100.0%													
20	20Y0020	100.0%	100.0%													
21	20Y0070	100.0%	100.0%													
22	20Y0041	100.0%	100.0%													
23	20Y0038	100.0%	100.0%													
24	20Y0025	100.0%	100.0%													
25	20Y0022	100.0%	100.0%													
26	20Y0079	100.0%	100.0%													
27	20Y0043	100.0%	100.0%													
28	20Y0040	100.0%	100.0%													
29	20Y0054	100.0%	100.0%													
30	20Y0057	100.0%	100.0%													
31	20Y0028	100.0%	100.0%													
32	20Y0080	100.0%	100.0%													
33	20Y0078	100.0%	100.0%													
34	20Y0023	100.0%	100.0%													
35	20Y0058	100.0%	100.0%													
36	20Y0075	100.0%	100.0%													
37	20Y0083	100.0%	100.0%													
38	20Y0048	100.0%	100.0%													
39	20Y0035	100.0%	100.0%													
40	20Y0046	100.0%	100.0%													
41	20Y0031	100.0%	100.0%													
42	20Y0067	100.0%	100.0%													
43	20Y0026	100.0%	100.0%													
44	20Y0082	100.0%	100.0%													
45	20Y0060	100.0%	100.0%													
46	20Y0021	100.0%	100.0%													
47	20Y0039	100.0%	100.0%													

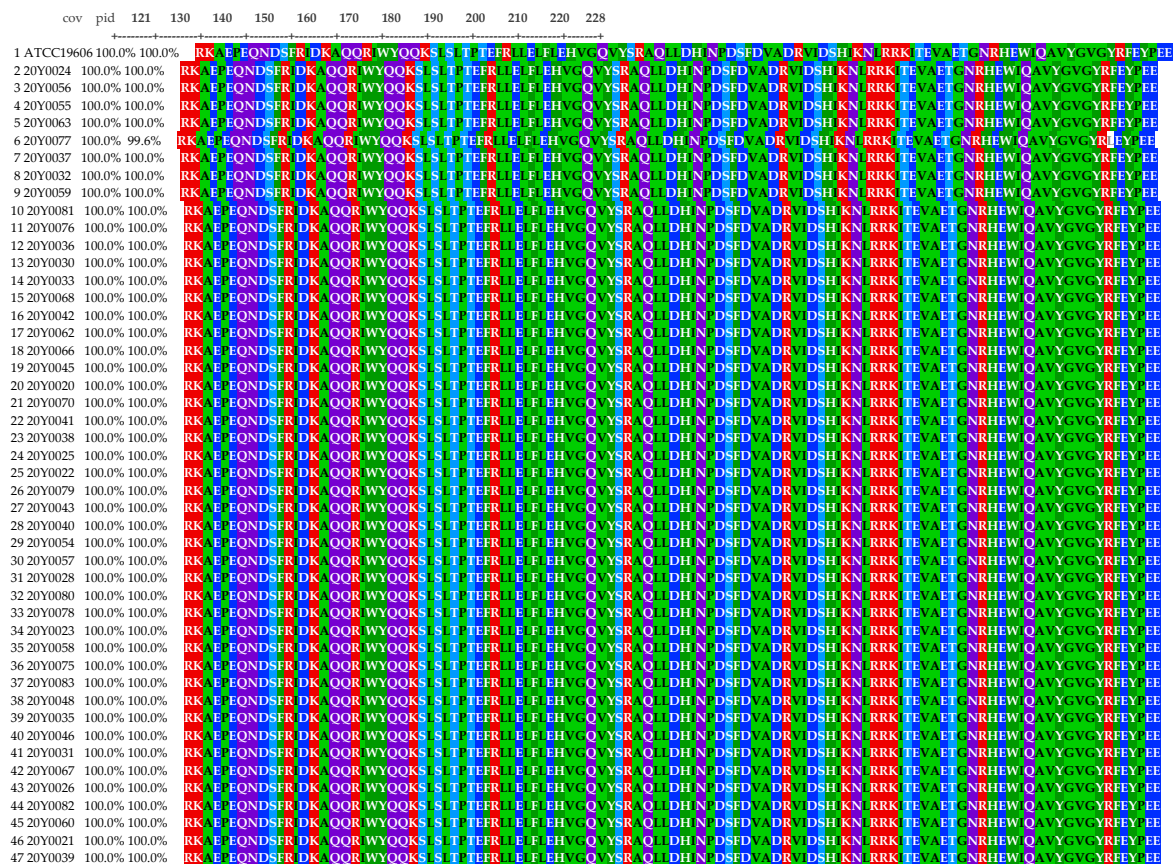
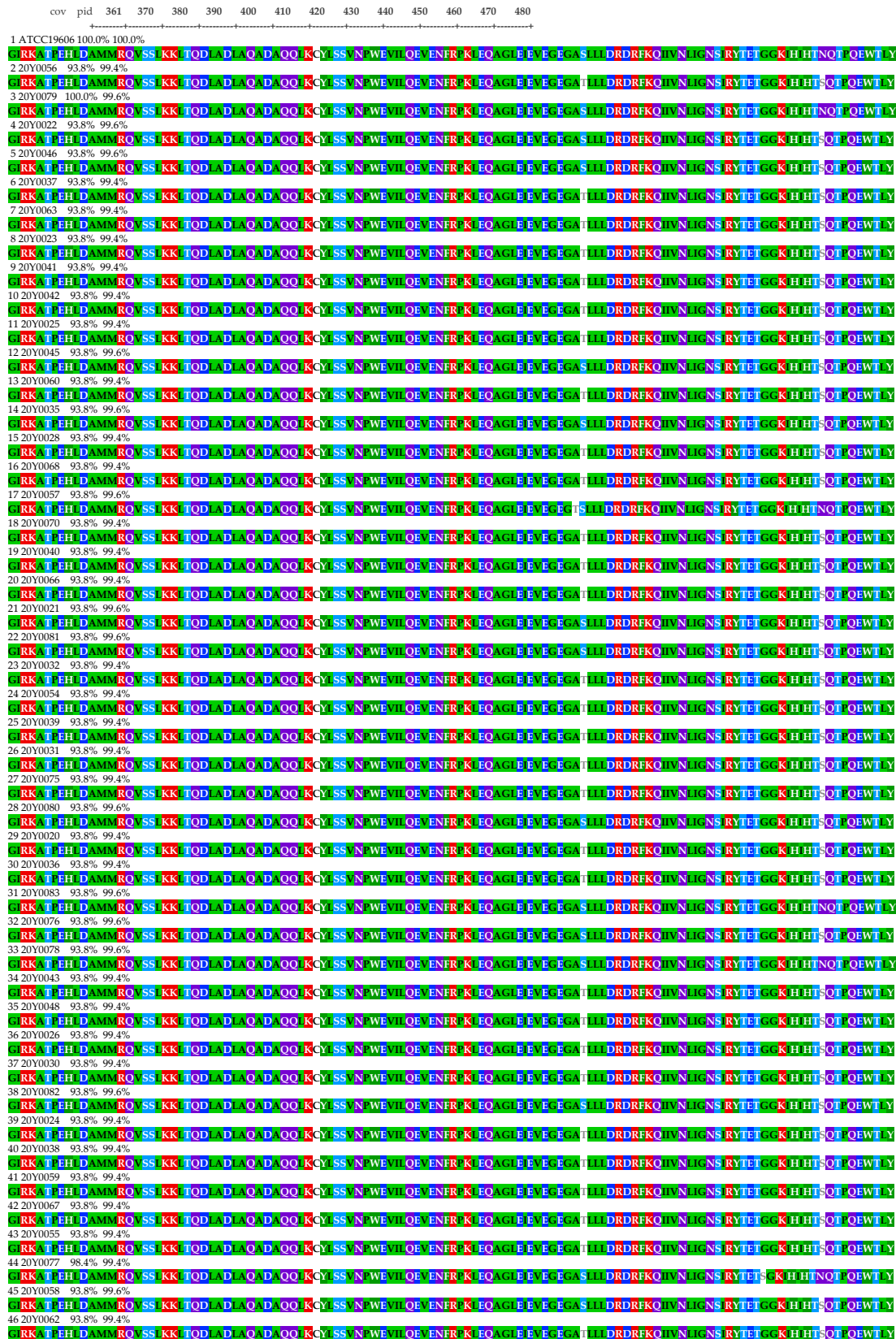


Figure S6: Multiple sequence alignment of the predicted amino acid sequences of BaeR in all isolates compared to that of *A. baumannii* ATCC 19606. The alignment was visualized using MView version 1.63. cov, coverage; pid, percent identity.



47 20Y0033 93.8% 99.4%

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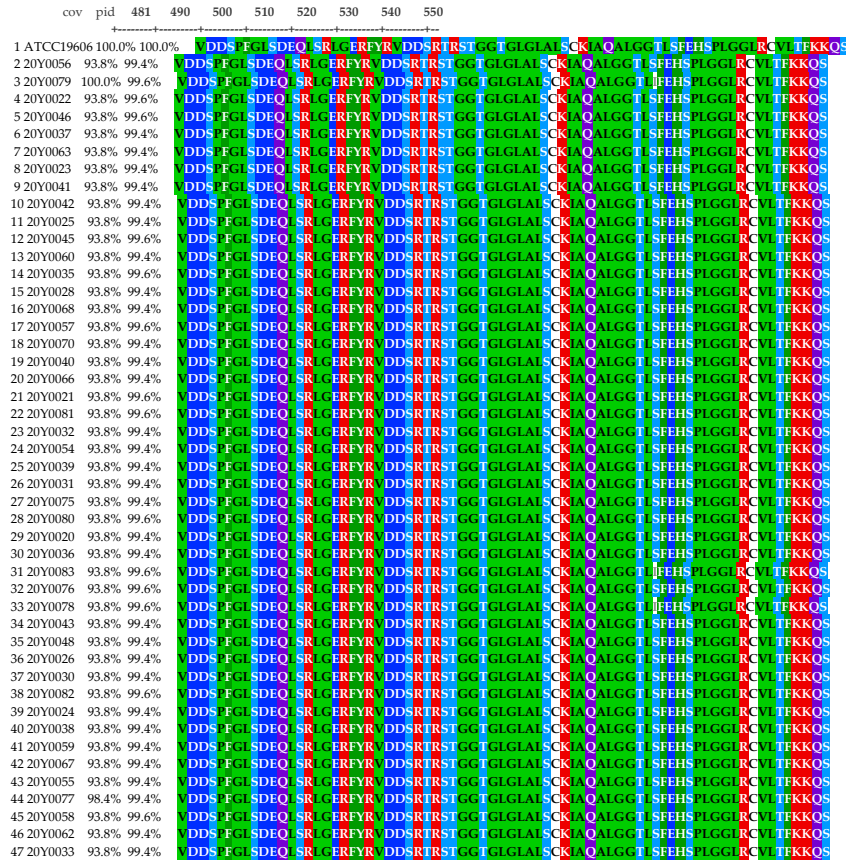


Figure S7: Multiple sequence alignment of the predicted amino acid sequences of BaeS in all isolates compared to that of *A. baumannii* ATCC 19606. The alignment was visualized using MView version 1.63. cov, coverage; pid, percent identity.

Table S4: Summary of mutations affecting *adeRS* and *baeRS* and correlation to tigecycline resistance

Gene	Codon	Wildtype	Mutation	No. of Affected Strains	GC	TG ^R
<i>adeR</i>	24	Ile	Met	1	7	100.0%
	56	Pro	Ser	1	7	100.0%
	120	Val	Ile	41	All except 4 and 9	75.6%
	136	Ala	Val	31	2	70.9%
	137	Thr	Ala	1	7	100.0%
	142	Leu	Ile	3	4	66.7%
	150	Thr	Asn	9	5	88.9%
	158	His	Leu	9	5	88.9%
	195	His	Gln	9	5	88.9%
	228	Ile	Val	1	7	100.0%
	241	Pro	Leu	46	All	74.0%
<i>AdeS</i>	243	Val	Ile	4	4 and 7	75.0%
	153	Ala	Thr	46	All	74.0%
	186	Gly	Val	15	All except 2	80.0%
	197	Leu	Phe	4	Subset of GC5	75.0%
	214	Leu	Phe	44	All except 9	75.0%
	227	Asp	His	10	5 and 7	90.0%
	263	Ser	Ala	46	All	74.0%
	268	Asn	His	26	Subset of GC2, GC9 and GC7	61.5%
			Tyr	8	Subset of GC2	100.0%*
	280	Ala	Ser	46	All	74.0%
	281	Asp	Gln	46	All	74.0%
	312	Ser	Ala	3	4	66.7%
	318	Gly	Ser	1	One isolate of GC9 (20Y0080)	0.0%
	331	Val	Ile	44	All except GC9	72.7%
	332	Val	Met	2	9	50.0%
	337	Thr	Ser	1	7	100.0%
	346	Lys	Arg	1	7	100.0%
	348	Val	Ile	32	2 and 7	71.8%
	353	Ile	Thr	1	7	100.0%
	354	Ser	Pro	15	All except GC2	80.0%
	356	Asn	Asp	1	7	100.0%
	357	Asn	Asp	1	7	100.0%
<i>baeR</i>	223	Phe	Leu	1	7	100.0%
<i>baeS</i>	10	Leu	Met	1	7	100.0%
	230	Arg	Gln	46	All	74.0%
	436	Ala	Thr	1	One GC9 isolate (20Y0057)	100.0%*
	437	Ser	Thr	31	2	70.9%
	463	Gly	Ser	1	7	100.0%
	471	Asn	Ser	41	5, 2 and one GC9 isolate (20Y0080)	75.6%
	533	Ser	Ile	3	4	66.7%

*Mutations were only found in TG-resistant but not in TG-sensitive strains of the same GC/ST.