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Supplementary Datasets

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Dataset S4. Intact AbaRs identified from complete and draft genomes

Dataset S5. *Acinetobacter baumannii* plasmids sequenced alone.

Table S1. Known AbaRs collected by this study.

AbaR	Strain	Accession No.	Location	Size (bp)	GC content	Insertion site	Flanking DR	Ref.
Tn*6019*[a]	*A. baumannii* 3208	FJ172370	27587-39905, 79885-83897	16332	37.77%	*comM*	ACCGC	(1)
Tn*6021*	*A. baumannii* ATCC 17978	CP000521	230361-243463	13103	35.85%	*comM*	ACCGC	(1)
Tn*6022*[b]	*A. baumannii* D36	JN107991	41312-51082, 55897-58123	11998	36.06%	*comM*	ACCGC	(2)
Tn*6022*Δ1[c]	*A. baumannii* A320 (RUH134)	JN247441	30419-39566	9148	35.76%	*comM*	-	(3)
Tn*6022*Δ1[d]	*A. nosocomialis* H06-681	KP888561	53-9200	9148	35.71%	*comM*	ACCGC	(4)
Tn*6022*Δ1[e]	*A. seifertii* C066	KP888562	43-9190	9148	35.71%	*comM*	ACCGC	(4)
Tn*6022*Δ1[f]	*A. baumannii* A9380	JX844629	99-9246	9148	35.71%	*comM*	ACCGC	
Tn*6022*Δ1[g]	*A. baumannii* A50841	JF330267	416-9558	9143	35.81%	*comM*	ACCGC	
AbaR0	*A. baumannii* WM98	KF483599	26869-90504	63636	52.24%	*comM*	ACCGC	(5)
AbaR1	*A. baumannii* AYE	CT025832	6496-92739	86244	52.80%	*comM*	ACCGC	(6)
AbaR2[h]	*A. baumannii* ACICU	CP000863	248016-264298	16283	51.52%	*comM*	ACCGC	(7)
AbaR3	*A. baumannii* AB0057	CP001182	263572-326560	62989	52.20%	*comM*	ACCGC	(8)
AbaR3	*A. baumannii* A85	KC118540	47072-110060	62989	52.20%	*comM*	ACCGC	(9)
AbaR4	*A. baumannii* AB0057	CP001182	582394-599202	16809	36.27%	*pho*	TCAGT	(8)
AbaR4	*A. baumannii* D36	JN107991	41312-58123	16812	36.27%	*comM*	ACCGC	(2)
AbaR4	*A. baumannii* A85 plasmid pA85-3	KJ493819	39244-56049	16806	36.26%	-	CCATT	(9)
AbaR4	*A. nosocomialis* E09-34	KP888559	40-16851	16812	36.27%	*comM*	ACCGC	(4)
AbaR4	*A. nosocomialis* H09-1045	KP888560	99-16910	16812	36.27%	*comM*	ACCGC	(4)
AbaR4a[i]	*A. baumannii* LT-3	JN129845	263-17892	17630	40.83%	*comM*	ACCGC	(10)
AbaR4b[j]	*A. baumannii* LT-11	JN129846	-	-	-	*comM*	-	(10)
AbaR4c[j]	*A. baumannii* LT-V1	JN129847	-	-	-	*comM*	-	(10)
AbaR4d	*A. baumannii* 1656-2	CP001921	257773-291760	33988	40.20%	*comM*	ACCGC	(10)

AbaR4e	*A. baumannii* TCDC-AB0715	CP002522	246596-296176	49581	48.48%	*comM*	ACCGC	(10)
AbaR5	*A. baumannii* 3208	FJ172370	27587-83897	56311	52.49%	*comM*	ACCGC	(11)
AbaR6	*A. baumannii* D2	GQ406245	28298-55689	27392	47.74%	*comM*	ACCGC	(1)
AbaR7	*A. baumannii* A92	GQ406246	755-20422	19668	50.88%	*comM*	ACCGC	(1)
AbaR8	*A. baumannii* D13	HM590877	28552-73689	45138	50.97%	*comM*	ACCGC	(12)
AbaR9[j]	*A. baumannii* AB056	ADGZ00000000	-	-	-	*comM*	-	(13)
AbaR10[j]	*A. baumannii* AB058	ADHA00000000	-	-	-	*comM*	-	(13)
AbaR10[j]	*A. baumannii* NIPH56	JF262165	-	-	-	*comM*	-	(14)
AbaR10[j]	*A. baumannii* NIPH783	JF262166	-	-	-	*comM*	-	(14)
AbaR11[j]	*A. baumannii* NIPH470	JF262167	-	-	-	*comM*	-	(14)
AbaR12[j]	*A. baumannii* LUH6013	JF262168	-	-	-	*comM*	-	(14)
AbaR13[j]	*A. baumannii* LUH6015	JF262169	-	-	-	*comM*	-	(14)
AbaR14[j]	*A. baumannii* LUH5881	JF262170	-	-	-	*comM*	-	(14)
AbaR15[j]	*A. baumannii* LUH6125	JF262171	-	-	-	*comM*	-	(14)
AbaR16[j]	*A. baumannii* LUH7140	JF262172	-	-	-	*comM*	-	(14)
AbaR17[j]	*A. baumannii* LUH8592	JF262173	-	-	-	*comM*	-	(14)
AbaR18[j]	*A. baumannii* NIPH2713	JF262174	-	-	-	*comM*	-	(14)
AbaR19[j]	*A. baumannii* NIPH2554	JF262175	-	-	-	*comM*	-	(14)
AbaR20[j]	*A. baumannii* NIPH2665	JF262178	-	-	-	*comM*	-	
AbaR302[j, k]	*A. baumannii* HK302	HM357806	-	-	-	*comM*	-	(15)
AbaR21	*A. baumannii* A297 (RUH875)	KM921776	754-62030	61277	52.08%	*comM*	ACCGC	(16)
AbaR22	*A. baumannii* MDR-ZJ06	CP001937	255471-294153	38683	37.77%	*comM*	ACCGC	(17)
AbaR23	*A. baumannii* D81	JN409449	34344-85159	50816	52.42%	*comM*	ACCGC	
AbaR24	*A. baumannii* A1	CP010781	252007-304766	52760	52.49%	*comM*	ACCGC	(18)
AbaR25	*A. baumannii* K51-65	JX481978	417-46885	46469	38.29%	*comM*	ACCGC	(19)

ΔAbaR25	*A. baumannii* K51-74	JX481979	417-41063	40647	37.75%	*comM*	ACCGC	(19)
AbaR26 [l]	*A. baumannii* D30	KC665626	1610-20270	18661	51.77%	*comM*	ACCGC	
AbaR25 [m]	*A. baumannii* BJAB07104	CP003846	264350-307196	42847	38.37%	*comM*	ACCGC	(20)
AbaR26 [n]	*A. baumannii* BJAB0868	CP003849	261295-302950	41656	38.45%	*comM*	ACCGC	(20)
AbaR27	*A. baumannii* BJAB0715	CP003847	2986232-3001620	15389	44.04%	*ACICU_02698*	CCAAC	(20)
TnAbaR23 [o]	*A. baumannii* A424	JN676148	2901-51246	48346	52.31%	*comM*	ACCGC	(21)
Tn*6166* [p]	*A. baumannii* A320 (RUH134)	JN247441	30419-48048	17630	40.85%	*comM*	ACCGC	(3)
Tn*6167*	*A. baumannii* A91	JN968483	29721-66788	37068	39.57%	*comM*	ACCGC	(22)
Tn*6168* [q]	*A. baumannii* A9337	JX844630	89-42979	42891	38.39%	*comM*	ACCGC	(23)
RI$_{\text{AB210}}$	*A. baumannii* AB210	HQ700358	135-14096	13962	36.12%	*comM*	ACCGC	(24)
RI$_{\text{MDR-TJ}}$	*A. baumannii* MDR-TJ	CP003500	3672761-3714403	41643	38.45%	*comM*	ACCGC	(25)
RI$_{\text{TYTH-1}}$	*A. baumannii* TYTH-1	CP003856	475548-517205	41658	38.47%	*comM*	ACCGC	(26)

DR, direct repeat. DRs are given in accord with the orientation of the *tni* tranposase genes. Ref., reference.

[a] Represented by the AbaR5 backbone.

[b] Represented by the AbaR4 backbone.

[c] Represented as defined in Tn*6166*.

[d] Called ‘Tn*6022*’ in the GenBank entry, but renamed here as being 99% identical to the published Tn*6022*Δ1 (GeneBank accession number: JN247441).

[e] Called ‘Tn*6022*’ in the GenBank entry, but renamed here as being 99% identical to the published Tn*6022*Δ1 (GeneBank accession number: JN247441).

[f] Called ‘Tn*6022*Δ2’ in the GenBank entry, but renamed here as being 99% identical to the published Tn*6022*Δ1 (GeneBank accession number: JN247441).

[g] Called ‘Tn*6021*’ in the GenBank entry, but renamed here as being 99% identical to the published Tn*6022*Δ1 (GeneBank accession number: JN247441).

[h] AbaR2 is not intact with the left-hand end missing.

[i] Also appeared as ‘TnAbaR4a’ in the GenBank entry.

[j] Partially sequenced.

[k] Named by this study since no name had been given before.

[l] AbaR26 (*A. baumannii* D30) is not intact with the left-hand end missing.

[m] Different to the AbaR25 defined in *A. baumannii* K51-65.

[n] Different to the AbaR26 defined in *A. baumannii* D30.

[o] Different to AbaR23.

[p] Also called AbGRI1-1.

[q] The element was named Tn*6168* in the GenBank entry, but is totally different to the published Tn*6168* defined in *A. baumannii* A85 (GenBank accession number: KC118540) (27).

Table S2. Insertion sites of AbaRs.

Locus	Origin	Left DR sequence/ 5-bp flank (5'-3')	Right DR sequence/ 5-bp flank (5'-3')	Left splitting part found	Right splitting part found
comM (c836-840)	chromosome	ACCGC	ACCGC	1790	1890
comM (mutation of ACCGC)	chromosome	GCCGC	GCCGC	5	5
comM (c836-840/c684-688)	chromosome	ACCGC	GTGAG	1	1
comM (c830-834)	chromosome	-	CCCAA	0	6
comM (c836-840/c833-837)	chromosome	ACCGC	GCCCC	1	1
comM (c835-839)	chromosome	-	CCGCC	0	1
comM (c836-840/c838-842)	chromosome	ACCGC	CGCCC	1	4
comM (c1316-1320)	chromosome	ACTAT	-	1	0
pAB3-type locus 2	plasmid	AGAAT	AGAAT	891	79
tetA (B)	transposon	ACTTG	ACTTG	555	1268
tetA (B) (mutation of ACTTG)	transposon	CCTTG	-	1	0
acoA	chromosome	CGATC	CGATC	72	53
pAB3-type locus 1	plasmid	ATTAT	ATAGT	40	720
B7L39_18880	plasmid	CCATT	CCATT	23	19
pho	chromosome	TCAGT	TCAGT	14	19
uup	chromosome	CCTGA	CCTGA	14	14
CBI29_04511- 04512 IGR 2	plasmid	TCCAC	TCCAC	13	14
AB57_05270	prophage	CTCGT	CTCGT	12	8
D721_p10064	plasmid	AATTG	AATTG	10	10
ACICU_02698/ABR2091_2729	chromosome	CCAAC	CCAAC	6	6
ABR2091_0476	chromosome	GTGTT	-	3	0
pilT (511-507)	chromosome	TGCAG	TGCAG	3	3
pip7-thrC IGR	chromosome	GCTGT	GCTGT	3	3
CBI29_04511-04512 IGR 1	plasmid	GTTTA	GTTTA	3	3
ABR2091_0006-0007 IGR	chromosome	CTGTG	CTGTG	3	3
ABR2091_3231-tRNA^{Arg} IGR	chromosome	AGATT	AGATT	3	2
ate	chromosome	GCAGA	GCAGA	2	2
garD	chromosome	TCCGC	TCCGC	2	2
ABR2091_0103	chromosome	CTTGG	CTTGG	2	2
ABR2091_3495 (c1463-1367)	chromosome	ACCAC	ACCAC	2	2
GI sequence	genomic island	TCCAC	TCCAC	2	2
mucK	chromosome	CCTAT	CCTAT	2	2
ompW	chromosome	GTAGA	GTAGA	2	2

B7L39_18740	plasmid	GTCG	GTCG	2	3
umuC (935-939)	plasmid	ATAAG	ATAAG	2	2
M3Q_1446	prophage	CTGTC	-	2	0
recR-*rnd* IGR	chromosome	CCGAG	CCGAG	2	2
sequence similar to *A1S_2017*		CCATT	-	2	0
amt	chromosome	TCCAA	-	1	0
btuE	chromosome	CTAAT	CTAAT	1	1
clpA	chromosome	GCCCA	GCCCA	1	1
cobS	chromosome	AAGAC	AAGAC	1	1
ABR2091_0137	chromosome	TTACC	TTACC	1	1
ABR2091_0220	chromosome	CATGC	-	1	0
ABR2091_1099	chromosome	CATTG	CATTG	1	1
ABR2091_1103	chromosome	TTCAG	TTCAG	1	1
ABR2091_1132	chromosome	ATTAT	ATTAT	1	1
ABR2091_1139	chromosome	ACGTG	ACGTG	1	1
ABR2091_1254	chromosome	CTTAC	CTTAC	1	1
ABR2091_1418	chromosome	CCAGA	CCAGA	1	1
ABR2091_1901	chromosome	TACAT	TACAT	1	1
ABR2091_1931	chromosome	CACAT	CACAT	1	1
ABR2091_2130	chromosome	CTTAT	CTTAT	1	1
ABR2091_3010	chromosome	GTTAG	GTTAG	1	1
ABR2091_3384	chromosome	CCACC	CCACC	1	1
ABR2091_3495 (c833-837)	chromosome	TTGGT	TTGGT	1	1
ABR2091_3577	chromosome	TTTGA	TTTGA	1	1
AB57_0815	genomic island	ACGAT	ACGAT	1	1
AB57_1275	genomic island	GAGGC	GAGGC	1	1
gloB (5'-end)	chromosome	AATGC	AATGC	1	1
gutB3	chromosome	TTCAG	TTCAG	1	1
IS*Aba1* (c1162-1166)	IS*Aba1*	AATTT	-	1	0
IS*Aba1* (c419-423)	IS*Aba1*	GTATC	GTATC	1	2
likely plasmid-borne region 2	plasmid	TCTAT	TCTAT	1	2
oprD	chromosome	CCAGC	CCAGC	1	1
pilS	chromosome	CCAAG	CCAAG	1	1
pilT (1039-1043)	chromosome	CGTTT	CGTTT	1	1
Aba10324_18325	plasmid	TTTAT	TTTAT	1	1
Aba9102_19180 (6-10)	plasmid	ATTGC	ATTGC	1	1
Aba9102_19180 (745-749)	plasmid	TCTAC	TCTAC	1	1
B7L39_19070	plasmid	TTAAG	TTAAG	1	1
BSF95_05010	plasmid	CTTGA	CTTGA	1	1

KAB01_03881	plasmid	CTGAT	CTGAT	1	1
repA	plasmid	ATTAC	ATTAC	1	1
ACX61_19590-19595 IGR	plasmid	GCCTT	GCCTT	1	1
umuC (1129-1133)	plasmid	CAAGA	CAAGA	1	2
AB57_0986- 0987 IGR	genomic island	ATGAC	ATGAC	1	1
ABR2091_0111-0112 IGR	chromosome	ATTAT	-	1	0
ABR2091_1794-1795 IGR	chromosome	CTTTT	-	1	0
ABR2091_3550-3551 IGR	chromosome	GCTAT	GCTAT	1	1
styA	chromosome	CTTCT	CTTCT	1	1
tnpA	Tn*1000*-like	CCCAG	CCCAG	1	1
topA	chromosome	TTCAG	TTCAG	1	1
uvrA/drrC	chromosome	ACAAT	ACAAT	1	1
ybaL	chromosome	CCCCT	CCCCT	1	1
ychJ	chromosome	TTTAG	TTTAG	1	1
ABR2091_0123	chromosome	-	GGTGA	0	2
ABR2091_2957	chromosome	-	ATGGC	0	2
IS*Aba1* (712-716)	IS*Aba1*	-	GATTT	0	3
B7L39_18670	plasmid	-	TTCTA	0	1
repeat region	plasmid	-	TTTTG	0	1
strA	Tn*5393*	-	CCAAT	0	1

For a name-unassigned gene, a representative locus tag identifier of an identical undisrupted gene is given. IGR, intergenic region. If there are two insertion sites in one gene or one IS, the positions of the corresponding DR sequences are given in brackets for distinction and the letter “c” means complement where applicable. The *comM* gene is considered as one insertion with variations at the right splitting part. The locus used to be represented by *ACICU_02698* is tagged with *ABR2091_2729* here to be consistent with other chromosomal loci. The *B7L39_18880* corresponds to the locus having been reported on pA85-3. The pAB3-type locus 1 and pAB3-type locus 2 correspond to the ones seen to be disrupted by Tn*6021* and Tn*6174*, respectively, on plasmid pAB3. The direct repeat sequences are underlined.

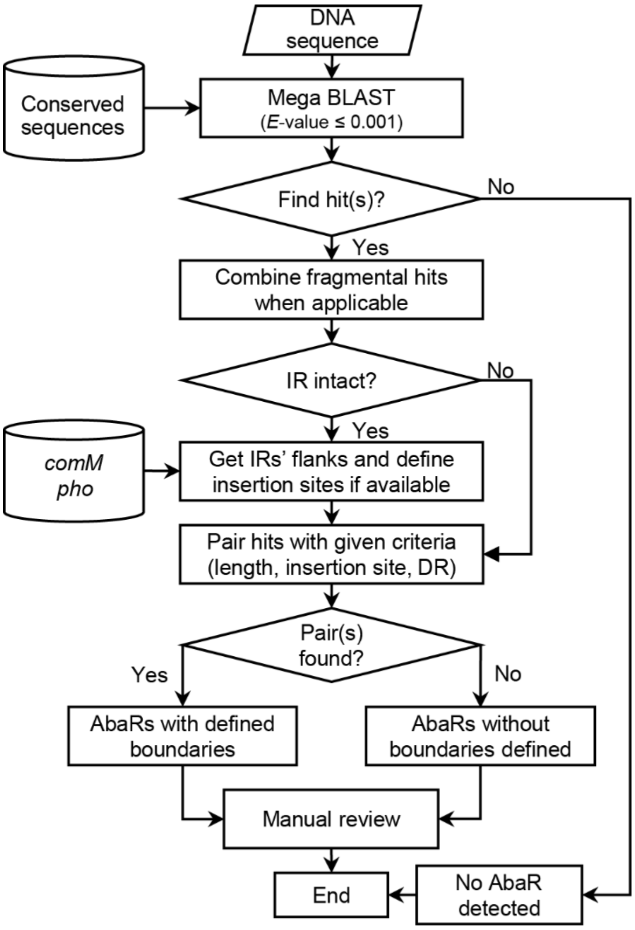

Figure S1. Flow diagram for *in silico* identification of AbaRs. IR, inverted repeat; DR, direct repeat.

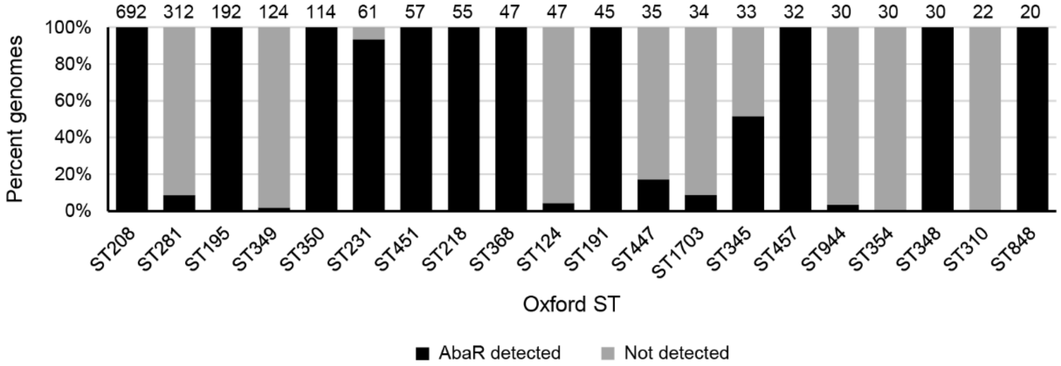

Figure S2. Abundance of AbaRs in different *Acinetobacter baumannii* sequence types (STs) of the Oxford scheme. The numbers above the histograms are the numbers of genomes belonging to the corresponding STs. Only STs with top-20 genome numbers are shown. Note that STs could not be determined in many unfinished genomes.

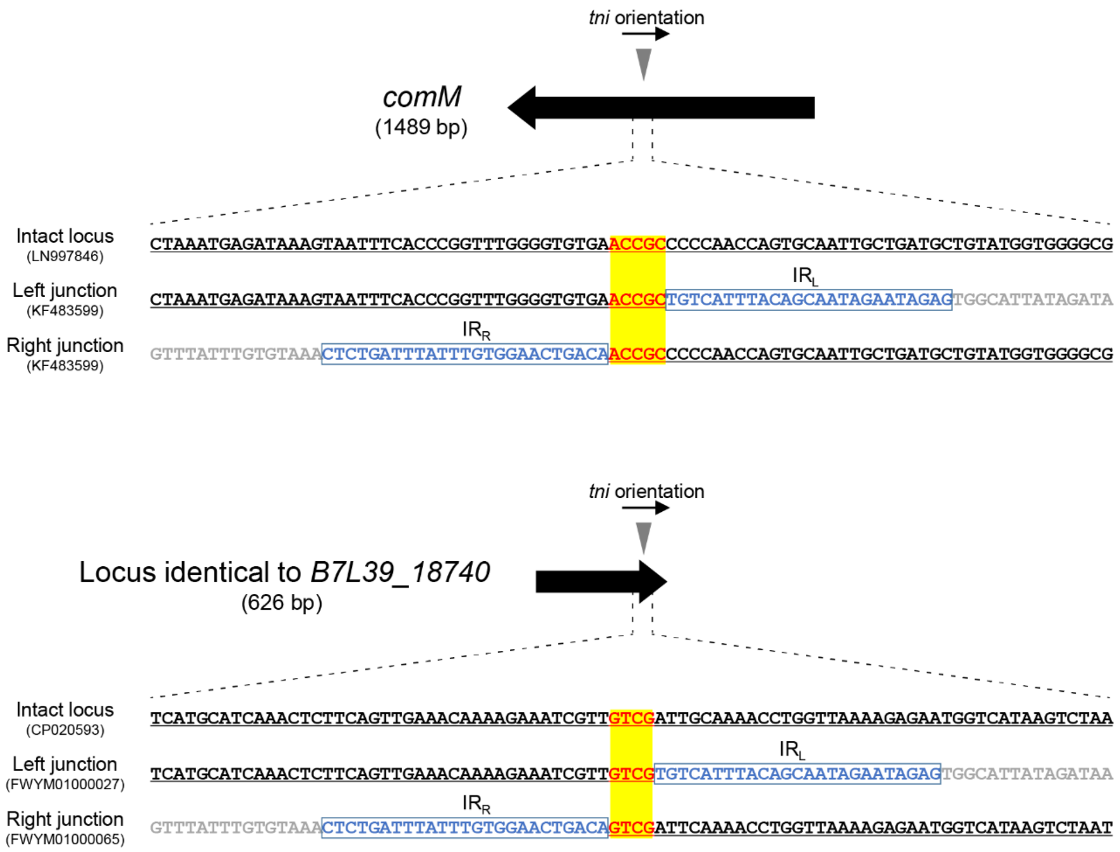

Figure S3. Examples of target site duplication generated by AbaR insertion. The *comM* locus is used as a representative sample for the loci with 5-bp target site duplication. The locus identical to *B7L39_18740* is the one with 4-bp target site duplication. Black bold arrows indicate genes. Grey triangles indicate AbaR insertion positions. Sequences at the insertion positions and the junctions generated by insertion are shown below the genes. Direct repeats (DRs) are indicated in red. Same DRs are connected by yellow. Insertion site sequences (intact or disrupted) are underlined. Inverted repeats (IRs) of AbaRs are indicated in blue and denoted by blue blocks. The sequences in grey are internal AbaR sequences. In the brackets are the GenBank accession numbers for the example sequences.

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