Colistin

	IpxA	lpxC	lpxD	pmrA	pmrB	Total
in/del	4 (3)	13 (11)	1 (1)	0	0	18 (15)
Substitution	13 (6)	12 (5)	4 (2)	0	0	29 (13)
ISAba11	4 (2)	11 (7)	9 (6)	0	0	24 (15)
Total	21 (11)	36 (22)	14 (9)	0	0	71 (43)

Colistin+Meropenem

	lpxA*	lpxC*	lpxD*	pmrA	pmrB	Total
in/del	0	0	0	0	1	0
Substitution	0	0	0	12 (4)	28 (19)	41 (23)
ISAba11	0	0	0	0	0	0
Total	0	0	0	12 (4)	29 (19)	41 (23)

The numerical value is the number of isolated strains, and (numbers) are the number of independent events. * 21 of 41 strains were analyzed.

Supplemental Table 2 Kamoshida et al.

ATCC 19606 Colistin-resistant strains

Maria	0.1		Genes				And a solution of the second	
Name	Colony	lpxA	IpxC	lpxD	pmrA	pmrB	Amino acid change	wutation gene
KL001	1	591 592delTA	-	-	-	-	1198fs(1198*)	Axal
KI 002	1	591 592delTA	_	_	-	-	1198fs(1198*)	InvA
KL002	1	331_332delTA	-		-	-	113013(1130.)	ipza Imu D
KL003	1	-	-	-220p>ISADaTT(AAG^GTT)	-	-	1 (00) (1 (00)	ipxD
KL004	2	-	394>ISAba11 (Inversion)	-	-	-	L132fs(L132*)	IpxC
KL005	3	82delT	-	-	-	-	I28fs(I28Y)V35*	lpxA
KL006	3	-	-	-	-	-	1	Not detected
KL007	3	-	-	-	-	-	1	Not detected
KL008	3	-	630delT	-	-	-	L211fs(L211*)	lpxC
KI 009	3	461G>A	-	-	-	-	G154D	InvA
KL 010	3	5620> A					G1998	Ipx/1
KLUIU	3	562G>A	-	-	-	-	61665	ipxA
KL011	3	-	-	-	-	-		Not detected
KL012	3	562G>A	-	-	-	-	G188S	lpxA
KL013	3	562G>A	-	-	-	-	G188S	lpxA
KL014	3	562G>A	-	-	-	-	G188S	<i>IpxA</i>
KL015	3	562G>A	-	-	-	-	G188S	Axql
KI 016	3	461G>A	_	_	-	-	G188S	InvA
KL017	3	562G>A					G1998	Ipx/1
KLO10	2	50202A		-	-	-	01000	ipxA
KLU10	3	362G>A	-	-	-	-	01000	ipxA
KL019	4	-	119G>C	-	-	-	R40P	IpxC
KL020	5	-	-	-	-	-		Not detected
KL021	5	-	327_330insATTT	-	-	-	L114fs(L114F)Q122*	lpxC
KL022	5	315G>A	-	-	-	-	M117I	<i>IpxA</i>
KL023	5	-	563C>T	-	-	-	A188V	lpxC
KI 024	5	-	394>ISAba11(Inversion)	-	-	-	132*	InvC.
KL 025	5		562C>T				A199\/	IpxC
KL020	5	-	5030-7	-	-	-	A100V	ipxc IpxC
KLU26	5	-	503051	-	-	-	A188V	ipxC
KL027	5	-	563C>1	-	-	-	A188V	lpxC
KL028	5	-	563C>T	-	-	-	A188V	lpxC
KL029	5	-	563C>T	-	-	-	A188V	lpxC
KL030	6	-	97 98delGT	-	-	-	V33fs(V33G)A52*	Dxql
KI 031	7	-	569C>T	-	-	-	T190I	InvC.
KL 022	7		000021	222-15 16211			179fc(179C)D93*	Ipx0
KL032	- /	-		233213Aba 11	-	-	17013(1700)F03	ipxD
KL033	8	-	391>ISAba11 (Inversion)	-	-	-	1131fs(1131*)	IpxC
KL034	8	-	391>ISAba11 (Inversion)	-	-	-	1131fs(1131*)	lpxC
KL035	8	-	391>ISAba11 (Inversion)	-	-	-	I131fs(I131*)	lpxC
KL036	8	-	391>ISAba11 (Inversion)	-	-	-	I131fs(I131*)	lpxC
KL037	9	-	475 689(215bp)del	-	-	-	D159fs(D159C)D161*	lpxC
KI 038	9	469G>A	-	-	-	-	G157R	InxA
KI 030	<u>a</u>	-	_	_	_	_	010111	Not detected
KL040	0	-	420dolA	-	-		A144fo(A1440)M104*	Invit detected
KL040	9	-	4290EIA		-	-	T0501	ipxc
KL041	9	-	-	7490>1	-	-	12501	IpxD
KL042	10	-	327_330delA111	-	-	-	Y112fs(Y112C)F128	IpxC
KL043	10	263>ISAba11 (Inversion)	-	-	-	-	N88fs(N88I)S96*	lpxA
KL044	10	-	327_330delATTT	-	-	-	Y112fs(Y112C)F128*	lpxC
KL045	10	-	-	-3bp>ISAba11 (Inversion) (AAa^tta)	-	-	1	lpxD
KI 046	10	-	327_330delATTT		-	-	Y112fs(Y112C)F128*	InxC.
KL 047	11	_	227_220dolATTT				V112fc(V112C)E128*	lpxC
KL047	11	442:10 46-44	327_33008iATTT	-	-	-	111218(11120)1120	ipxc ImxA
KL048	11	413>ISADa11	-	-	-	-	V140IS(V140L)H143	ίρχΑ
KL049	11	413>ISAba11	-	-	-	-	V140fs(V140L)H143*	IpxA
KL050	11	-	394>ISAba11 (Inversion)	-	-	-	L132fs(L132*)	lpxC
KL051	11	413>ISAba11	-	-	-	-	V140fs(V140L)H143*	lpxA
KL052	11	-	-	271A>C	-	-	T91P	lpxD
KL053	11	-	-	271A>C	-	-	T91P	lpxD
KI 054	11	-	-	271A>C	-	-	T91P	InxD
KL 055	11	-	_	218ins A	-	_	D75fs(D75R)N76*	InvD
KLOEG	12	-		210113A	-	-	DISIS(DISIC)[110	Not detected
KL050	12	-	-	-	-	-	l	Not detected
KL057	12	-	-	-	-	-	04005-(04001) 44005	
KL058	12	306_310delGCAA	-	-	-	-	Q103TS(Q103I)A106*	IpxA
KL059	12	-	-	232>ISAba11 (Inversion)	-	-	178fs(178*)	lpxD
KL060	12	-	-	232>ISAba11 (Inversion)	-	-	I78fs(I78*)	lpxD
KL061	13	-	327_330insATTT	-	-	-	Y112fs(Y112C)F128*	lpxC
KL062	13	-	392>ISAba11	-	-	-	L132fs(L132G)E136*	lpxC
KL063	13	-	703G>T	-	-	-	V235F	lpxC
KI 064	13	-	703G-T	-	-	-	V235E	InvC
KLOCE	10		911-10 Abc11		_	-	274fo/l 274*)	InvC
KL000	13	-	01121SADa11	-	-	-	L2/ 115(L2/11)	ipxc
KL066	13	-	703G>1	-	-	-	V235F	ipxC
KL067	13	-	-	-	-	-		Not detected
KL068	13	-	-35bpA>G	-	-	-		lpxC
KL069	13	-	811>ISAba11	-	-	-	L271fs(L271*)	lpxC
KL070	13	-	-	-2bp>ISAba11(Inversion)(Aat^taA)	-	-		lpxD
KL071	14	-	327 330insATTT	-	-	-	L114fs(L114F)Q122*	lpxC
KI 072	14	-	327 330delATTT	-	-	-	Y112fs(Y112C)F128*	InvC
KL 072	15	-	327 330dolATTT	-			V112fe(V112C)E120*	InvC
KL073	10	-	327_33008ATTT	-	-	-	111213(11120)F128	ipxc
KL074	15	-	-	-	-	-		Not detected
KL075	15	-	-	-	-	-		Not detected
KL076	15	604C>T, 606A>T	-		-	-	R202C	<i>lpxA</i>
KL077	15	-	-	-	-	-		Not detected
KL078	15	-	-	-	-	-		Not detected
KL079	15	-		-	-	-		Not detected
KL 080	15		-		-	-		Not detected
KL 001	15	604C- T					D202*	Invit detected
KL000	10	0046>1	201 10 45 - 11	-	-	-		ipxA
KL082	15	-	394>ISAba11	-	-	-	L132IS(L132^)	ipxC
KL083	16	-	-	-22bp>ISAba11(AAG^GTT)	-	-		lpxD
KL084	16	-	-	-22bp>ISAba11(AAG^GTT)	-	-		lpxD
KL085	16	-	-	-22bp>ISAba11(AAG^GTT)	-	-		lpxD

Mutation gene	Name	Mutation	Colistin MIC (µg/ml)
lpxA	KL001	591_592delTA: I198fs	128
lpxA	KL009	461G>A: G154D	128
lpxA	KL010	562G>A: G188S	128
lpxA	KL022	315G>A: M117I	256
lpxA	KL038	469G>A: G157R	128
lpxA	KL076	604C>T, 606A>T: R202C	128
lpxC	KL037	475_689(215)del: D159fs	64
lpxC	KL019	119G>C: R40P	128
lpxC	KL023	563C>T: A188V	256
lpxC	KL031	569C>T: T190I	128
lpxC	KL063	703G>T: V235F	256
lpxD	KL055	218insA: D75fs	64
lpxD	KL041	749C>T: T250I	128
lpxD	KL052	271A>C: T91P	8

Supplemental Table 4 Kamoshida et al.

NCBI BioSan	nple						-
BioSample	Amino acids					Colistin	Mutation
ID	LpxA	LpxC	LpxD	PmrA	PmrB	MIC	wittation
12087735	-	-	-	-	A138T, R263H	>256	PmrB
4901700	-	-	-	K172l	-	8	PmrA
4901699	-	-	-	K172l	-	8	PmrA
4901698	-	-	-	-	P170S	8	PmrB
4901697	-	-	-	-	P170L	>8	PmrB
4901694	-	-	-	-	-	4	Not detected
4901693	-	-	-	-	H266Y, Q270P	>8	PmrB
4901678	-	-	-	-	T235I	>8	PmrB
6837835	-	-	-	D10E	V133G, P154T	>4	PmrAB
6837830	-	-	-	-	L33P	>4	PmrB
6837819	-	-	-	-	20bp>ISAba125(insersion)	>4	PmrB
6837812	-	-	-	-	-	>4	Not detected
6837767	-	-	-	-	L239I	>4	PmrB
6837762	-	-	-	-	-	>4	Not detected
6837757	-	-	-	-	-	>4	Not detected
6837753	-	-	D75G	-	-	4	LpxD
6837751	-	-	-	M6K	-	>4	PmrB
6827875	-	-	-	I173F	-	>4	PmrB
6892294	-	-	S100T	-	-	>4	LpxD
6892290	-	-	-	-	P170L, N337H	>4	PmrB
6892289	-	-	-	I173F	-	>4	PmrA
4254730	-	-	-	E8D	Y116H	>256	PmrAB
4254728	-	-	-	-	S17R	192	PmrB
4254727	-	-	-	-	T232I	128	PmrB

Supplemental Table 5 Kamoshida et al.

Nama	Colony	Genes			Amino soid change	Mutation gana		
Name	Colony	<i>lpxA</i>	lpxC	lpxD	pmrA	pmrB	Amino aciu change	withation gene
CM001	1	-	-	-	-	695C>T	T232I	pmrB
CM002	1	-	-	-	-	695C>T	T232I	pmrB
CM003	2	-	-	-	-	692G>T	R231L	pmrB
CM004	2	-	-	-	-	692G>T	R231L	pmrB
CM005	2	-	-	-	-	692G>T	R231L	pmrB
CM006	2	-	-	-	-	692G>T	R231L	pmrB
CM008	2	-	-	-	-	692G>T	R231L	pmrB
CM011	3	-	-	-	-	680C>T	A227V	pmrB
CM012	3	-	-	-	-	697C>T	P233S	pmrB
CM015	3	-	-	-	-	680C>T	A227V	pmrB
CM016	3	-	-	-	-	680C>T	A227V	pmrB
CM017	3	-	-	-	-	680C>T	A227V	pmrB
CM018	4	-	-	-	-	787C>G	R263G	pmrB
CM019	5	-	-	-	-	794A>C	Q265P	pmrB
CM020	6	-	-	-	-	697C>T	P233S	pmrB
CM021	7	-	-	-	-	787C>T	R263C	pmrB
CM022	7	-	-	-	36G>T	-	M12I	pmrA
CM023	7	-	-	-	36G>T	-	M12I	pmrA
						42(AATTTTCAGTGTCAT	20.27 position incortion	
CM024	8	-	-	-	-	CTTAGGTTGTATTTT)71		pmrB
						duplication	+VILGUILIF3	
CM025	9	-	-	-	-	937G>T	D313Y	pmrB
CM026	9	-	-	-	-	937G>C	D313H	pmrB
CM027	10	N.T.	N.T.	N.T.	-	794A>C	Q265P	pmrB
CM028	11	N.T.	N.T.	N.T.	36G>T	-	M12I	pmrA
CM029	11	N.T.	N.T.	N.T.	-	680C>T	A227V	pmrB
CM031	12	N.T.	N.T.	N.T.	-	944G>A	G315D	pmrB
CM032	12	N.T.	N.T.	N.T.	-	944G>A	G315D	pmrB
CM033	12	N.T.	N.T.	N.T.	-	680C>T	A227V	pmrB
CM034	12	N.T.	N.T.	N.T.	-	704C>T	T235I	pmrB
CM035	13	N.T.	N.T.	N.T.	-	788G>A	R263H	pmrB
CM036	13	N.T.	N.T.	N.T.	-	788G>A	R263H	pmrB
CM038	14	N.T.	N.T.	N.T.	-	697C>T	P233S	pmrB
CM041	15	N.T.	N.T.	N.T.	34A>G	-	M12V	pmrA
CM042	15	N.T.	N.T.	N.T.	34A>G	-	M12V	pmrA
CM043	15	N.T.	N.T.	N.T.	34A>G	-	M12V	pmrA
CM044	15	N.T.	N.T.	N.T.	34A>G	-	M12V	pmrA
CM045	15	N.T.	N.T.	N.T.	34A>G	-	M12V	pmrA
CM046	15	N.T.	N.T.	N.T.	34A>G	-	M12V	pmrA
CM047	15	N.T.	N.T.	N.T.	-	787C>G	R263G	pmrB
CM048	15	N.T.	N.T.	N.T.	34A>G	-	M12V	pmrA
CM049	15	N.T.	N.T.	N.T.	34A>G	-	M12V	pmrA
CM051	16	N.T.	N.T.	N.T.	38G>T	-	I13S	pmrA

ATCC 19606 Colistin-meropenem-resistant strains

N.T. Not Tested

Namo	Colony			Amina agid abanga	Mutation cono
Name	Colony	pmrA	pmrB	Amino aciu change	Mutation gene
CpCL001	1	-	689C>T	A226V	pmrB
CpCL002	1	-	787C>T	R263C	pmrB
CpCL003	1	-	787C>T	R263C	pmrB
CpCL004	1	-	787C>T	R263C	pmrB
CpCL005	2	239C>T	-	A80V	pmrA
CpCL006	2	-	821T>G	L274W	pmrB
CpCL007	3	-	794A>C	Q265P	pmrB
CpCL008	3	-	944G>C	G315D	pmrB
CpCL009	4	-	697C>T	P233S	pmrB
CpCL010	4	-	49A>C	S17R	pmrB
CpCL011	5	-	676G>A	A226T	pmrB
CpCL012	5	-	676G>A	A226T	pmrB
CpCL013	6	-	680C>T	A227V	pmrB
CpCL014	6	-	692G>A	R231Q	pmrB
CpCL015	6	-	716T>C	L239S	pmrB
CpCL016	6	-	716T>C	L239S	pmrB
CpCL017	6	-	716T>C	L239S	pmrB

ATCC 19606 Colistin-ciprofloxacin-resistant strains

Supplemental Table 7 Kamoshida et al.

Namo	Colony	Gei	nes	Amino acid chango	Mutation gono
Name	Colony	pmrA	pmrB	Amino aciu change	mutation gene
BAAC001	1	60G>C	-	L20F	pmrA
BAAC002	1	60G>T	-	L20F	pmrA
BAAC003	1	60G>T	-	L20F	pmrA
BAAC009	2	-	704C>T	T235I	pmrB
BAAC010	2	-	704C>T	T235I	pmrB
BAAC033	6	-	707C>A	T235I	pmrB
BAAC044	7	-	697C>T	P233S	pmrB
BAAC045	7	-	686A>C	E229A	pmrB
BAAC046	7	-	944G>T	G315V	pmrB
BAAC066	10	-	944G>A	G315D	pmrB
BAAC067	10	-	944G>A	G315D	pmrB

ATCC BAA-1605 Colistin-resistant strains

ATCC BAA-1605 Colistin-meropenem-resistant strains

Namo	Colony	Gei	nes	Amino acid chango	Mutation cono
Name	Colony	pmrA	pmrB	Amino aciu change	Mutation gene
BAACM001	1	60G>C	-	L20F	pmrA
BAACM002	1	60G>T	-	L20F	pmrA
BAACM003	1	60G>T	-	L20F	pmrA
BAACM004	1	60G>C	-	L20F	pmrA
BAACM005	1	60G>T	-	L20F	pmrA
BAACM006	1	60G>T	-	L20F	pmrA
BAACM007	1	-	704C>T	T235I	pmrB
BAACM008	1	60G>C	-	L20F	pmrA
BAACM009	1	60G>C	-	L20F	pmrA
BAACM010	1	60G>T	-	L20F	pmrA
BAACM011	1	60G>T	-	L20F	pmrA
BAACM012	4	-	697C>T	P233S	pmrB
BAACM013	5	-	938A>T	D313V	pmrB
BAACM014	5	60G>C	-	L20F	pmrA
BAACM015	6	60G>C	-	L20F	pmrA
BAACM016	6	60G>C	-	L20F	pmrA
BAACM017	7	-	944G>T	G315V	pmrB
BAACM018	7	-	787C>G	R263G	pmrB
BAACM019	7	60G>C	-	L20F	pmrA
BAACM020	7	60G>C	-	L20F	pmrA
BAACM021	7	-	699A>C	E229D	pmrB
BAACM022	7	-	699A>C	E229D	pmrB
BAACM023	8	-	698A>C	P233H	pmrB
BAACM024	8	-	788G>A	R263H	pmrB
BAACM025	8	-	698A>C	P233H	pmrB
BAACM026	9	-	787C>G	R263G	pmrB
BAACM027	10	-	788G>A	R263H	pmrB

Supplemental Table 8 Kamoshida et al.

IS insertion in ATCC BAA-1605 Colistin-resistant strains

Nama	Calany	Genes		Pomark	
Name	Colony	IpxA	IpxC	lpxD	Remark
BAAC001	1	-	-	-	pmrA mutation
BAAC002	1	-	-	-	pmrA mutation
BAAC003	1	-	-	-	pmrA mutation
BAAC004	1	-	-	0	-
BAAC005	1	-	0	-	-
BAAC006	1	_	0	_	-
BAAC007	1	_	0	_	
BAAC000	1		0		pmrP mutation
BAAC008	2	-	-	-	piniB indiation
BAAC009	2	-	-	-	pmrB mutation
BAACUIU	2	-	-	-	-
BAACUTT	2	-	-	-	-
BAAC012	2	-	0	-	-
BAAC013	2	-	0	-	-
BAAC014	2	-	-	-	-
BAAC015	2	0	-	-	-
BAAC016	2	-	0	-	-
BAAC017	3	-	-	-	-
BAAC018	3	-	-	-	-
BAAC019	3	-	0	-	-
BAAC020	3	-	0	-	-
BAAC021	4	-	ñ	-	-
BAAC022	4	-	ñ	-	-
BAAC022	4	-	0	-	-
BAAC023	-	-	-		-
BAAC024	-+		0	-	-
BAAC020	5	-		-	-
BAAC020	5 F		-	-	-
DAACU27	5 -	-	-	-	-
BAAC028	5	-	0	-	-
BAAC029	5	-	-	-	-
BAAC030	5	-	•	-	-
BAAC031	5	-	0	-	-
BAAC032	5	-	-	-	-
BAAC033	6	-	-	-	pmrB mutation
BAAC034	6	-	0	-	-
BAAC035	6	-	-	-	-
BAAC036	6	-	0	-	-
BAAC037	6	-	0	-	-
BAAC038	6	-	-	-	-
BAAC039	6	-	0	-	-
BAAC040	6	-	-	-	-
BAAC041	6	-	-	-	-
BAAC042	6	-	-	-	-
BAAC043	6	-	0	-	-
BAAC044	7	-	-	-	pmrB mutation
BAAC045	7	-	-	-	pmrB mutation
BAAC046	7	-	-	-	pmrB mutation
BAAC047	7	-	-	-	-
BAAC049	7				
BAAC040	7		-	_	
BAACOSO	7	_	_	_	
BAAC051	7	_	_	_	
BAACOES	7	-	-	-	-
BAACU52	7	-	-	-	-
DAACU53	1	-	-	-	-
BAACU54	/	-		-	-
BAAC055	/	-	0	-	-
BAAC056	/	-	-	0	-
BAAC057	(0	-	-	-
BAAC058	8	-	•	-	-
BAAC059	8	-	0	-	-
BAAC060	9	-	0	-	-
BAAC061	9	-	-	0	-
BAAC062	9	-	0	-	-
BAAC063	9	-	-	-	-
BAAC064	9	-	-	-	-
BAAC065	9	-	-	-	-
BAAC066	10	-	-	-	pmrB mutation
BAAC067	10	-	-	-	pmrB mutation
BAAC068	10	-	0	-	-
BAAC069	10	-	0	-	-
BAAC070	10	-	0	-	-
BAAC071	10	-	0	-	-

Supplemental Fig. 1 Kamoshida et al.











Supplemental Fig. 4 Kamoshida et al.



Supplemental TABLE 1 Types of mutations in colistin-resistant strains of *A. baumannii* ATCC 19606.

3 Supplemental TABLE 2 List of mutations in colistin-resistant strains of A. baumannii

4 ATCC 19606.

5 Supplemental TABLE 3 Minimum inhibitory concentrations (MICs) of colistin in 6 representative *A. baumannii* strains with amino acid substitutions and frameshift

7 mutations in LpxACD.

8 Supplemental TABLE 4 List of mutations and minimum inhibitory concentrations

9 (MICs) of colistin in *A. baumannii* strains (NCBI BioSample).

10 Supplemental TABLE 5 List of mutations in colistin-meropenem-resistant strains of A.

11 baumannii ATCC 19606.

12 Supplemental TABLE 6 List of mutations in colistin-ciprofloxacin-resistant strains of A.

13 baumannii ATCC 19606.

14 Supplemental TABLE 7 List of mutations in colistin-resistant and colistin-meropenem-

15 resistant strains of *A. baumannii* ATCC BAA-1605.

16 Supplemental TABLE 8 Insertion sequences (ISs) in colistin-resistant strains of A.

17 baumannii ATCC BAA-1605.

18

19 Supplemental FIGURE LEGENDS

Supplemental FIG 1 Expression of *lpxCD* mRNA in colistin-resistant strains with upstream mutations (*lpxC*: KL068; *lpxD*: KL003, KL045, KL070, KL083; and wild-type: ATCC 19606) was analyzed using quantitative reverse transcription-PCR (qRT-PCR). *A. baumannii* was grown in LB broth at 37 °C with shaking until OD₆₀₀ reached 0.75. Total RNA was extracted and reverse-transcribed; RT-qPCR was performed using the intercalator method (TB Green). Data are presented as the mean \pm SD (n = 3 per group). Comparison using one-way ANOVA. ***p < 0.001, **p < 0.01, *p < 0.05.

27

28 Supplemental FIG 2 Growth and biofilm formation of colistin-resistant A. baumannii 29 strains. (A) ATCC 19606 (wild-type strain) and representative strains with initial OD₆₀₀ 30 0.001 were grown in LB broth at 37 °C for 24 h. Absorbance at 595 nm was measured at 31 the indicated time points. Data are presented as the mean \pm SD; n = 3 per group compared by two-way ANOVA. n.s., not significant, ***p < 0.001. (B) The biofilm formation ability 32 33 of the representative strains was analyzed by the crystal violet staining method. Data are 34 presented as the mean \pm SD; n = 3 per group. Compared by one-way ANOVA. n.s., not significant, ****p* < 0.001. 35

36

37	Supplemental FIG 3 Bactericidal activity of antibiotics against LPS-modified and LPS-
38	deficient strains of A. baumannii ATCC 19606. (A) Representative images of KL001S and
39	CM012S, LPS-deficient and LPS-modified strains, respectively, and ATCC 19606 as the
40	wild-type strain spotted on each plate. The culture (OD ₆₀₀ 1.0) was serially diluted (10^{-1}
41	to 10^{-6}) and $10 \ \mu$ L of each dilution was spotted onto the plates. The upper part of the plate
42	does not contain any antibiotics, the middle part contains $5 \times MIC (10 \ \mu g/mL)$ of colistin,
43	and the lower part contains 10 $\mu g/mL$ of colistin and 1/5× MIC (0.1 $\mu g/mL)$ of
44	meropenem. (B) The CFU obtained on the non-antibiotic plates was used to calculate the
45	percentage of surviving bacteria. Data are presented as the mean \pm SD ($n = 3$ per group).
46	

Supplemental FIG 4 Frequency of resistance to rifampicin alone or in combination with 1/5× MIC (0.1 μ g/mL) of meropenem. The culture (0.1 mL of *A. baumannii* ATCC 19606 overnight culture) was plated on LB agar containing 5× MIC (10 μ g/mL) of rifampicin with or without 0.1 μ g/mL of meropenem. Data are shown as box plots; *n* = 20 independent assays compared by the Mann–Whitney *U*-test. n.s., not significant.