

**Table A. Enterobacteriaceae spp. strain information.**

Species	Strain	Origin	Ciprofloxacin			Gentamicin			Imipenem		
			BMD (MIC; int*)	qPCR assay ( $\Delta$ Cq)	qPCR assay (int*)	BMD (MIC; int*)	qPCR assay ( $\Delta$ Cq)	qPCR assay (int*)	BMD (MIC; int*)	qPCR assay ( $\Delta$ Cq)	qPCR assay (int*)
<i>Escherichia coli</i>	AR0001	CDC	> 32; R	0.2	R	2; S	3.1	S	4; R	-0.5	R
<i>Enterobacter cloacae</i>	AR0002	CDC	16; R	-0.4	R	8; I	3.4	S	32; R	0.2	R
<i>Klebsiella pneumoniae</i>	AR0003	CDC	16; R	0.0	R	4; S	3.3	S	8; R	0.1	R
<i>Klebsiella pneumoniae</i>	AR0004	CDC	16; R	-0.6	R	1; S	3.9	S	32; R	-0.4	R
<i>Klebsiella pneumoniae</i>	AR0005	CDC	32; R	0.2	R	2; S	2.7	S	16; R	-0.8	R
<i>Escherichia coli</i>	AR0006	CDC	> 32; R	-0.3	R	> 64; R	-0.3	R	8; R	0.3	R
<i>Enterobacter aerogenes</i>	AR0007	CDC	32; R	-0.3	R	1; S	6.1	S	0.5; S	7.7	S
<i>Enterobacter cloacae</i>	AR0008	CDC	16; R	0.1	R	≤ 0.5; S	4.5	S	1; S	5.9	S
<i>Enterobacter aerogenes</i>	AR0009	CDC	≤ 0.25; S	3.4	S	1; S	4.6	S	4; R	0.8	R
<i>Klebsiella pneumoniae</i>	AR0010	CDC	≤ 0.25; S	2.3	S	4; S	3.2	S	1; S	5.4	S
<i>Escherichia coli</i>	AR0011	CDC	> 32; R	0.2	R	64; R	-0.2	R	≤ 0.25; S	6.8	S
<i>Klebsiella pneumoniae</i>	AR0012	CDC	16; R	0.1	R	32; R	2.2	R	≤ 0.25; S	6.4	S
<i>Escherichia coli</i>	AR0013	CDC	≤ 0.25; S	3.6	S	> 64; R	-0.3	R	≤ 0.25; S	7.2	S
<i>Escherichia coli</i>	AR0014	CDC	32; R	-0.4	R	64; R	-0.1	R	≤ 0.25; S	6.1	S
<i>Escherichia coli</i>	AR0015	CDC	> 32; R	-0.1	R	> 64; R	0.9	R	≤ 0.25; S	6.9	S
<i>Klebsiella pneumoniae</i>	AR0016	CDC	≤ 0.25; S	2.7	S	≤ 0.5; S	6.1	S	≤ 0.25; S	7.7	S
<i>Escherichia coli</i>	AR0017	CDC	≤ 0.25; S	3.1	S	1; S	1.7	R	1; S	3.7	S
<i>Enterobacter aerogenes</i>	AR0018	CDC	≤ 0.25; S	4.4	S	1; S	5.8	S	1; S	6.3	S
<i>Escherichia coli</i>	AR0019	CDC	> 32; R	-0.2	R	≤ 0.5; S	3.9	S	≤ 0.25; S	6.2	S
<i>Escherichia coli</i>	AR0020	CDC	16; R	-0.3	R	1; S	6.0	S	1; S	7.2	S
<i>Citrobacter freundii</i>	AR0021	CDC	≤ 0.25; S	2.6	S	1; S	5.3	S	1; S	6.5	S
<i>Citrobacter freundii</i>	AR0022	CDC	≤ 0.25; S	3.5	S	≤ 0.5; S	4.6	S	1; S	5.4	S
<i>Citrobacter freundii</i>	AR0023	CDC	≤ 0.25; S	2.6	S	≤ 0.5; S	5.3	S	1; S	6.2	S
<i>Citrobacter koseri</i>	AR0024	CDC	≤ 0.25; S	3.2	S	1; S	5.2	S	≤ 0.25; S	7.0	S
<i>Citrobacter koseri</i>	AR0025	CDC	≤ 0.25; S	4.5	S	64; R	0.7	R	≤ 0.25; S	7.2	S
<i>Providencia stuartii</i>	AR0026	CDC	≤ 0.25; S	3.4	S	1; S	3.9	S	0.5; S	-1.2	R
<i>Serratia marcescens</i>	AR0027	CDC	≤ 0.25; S	0.9	R	≤ 0.5; S	3.4	S	4; R	-0.4	R
<i>Klebsiella oxytoca</i>	AR0028	CDC	≤ 0.25; S	3.5	S	≤ 0.5; S	4.6	S	≤ 0.25; S	7.2	S
<i>Proteus mirabilis</i>	AR0029	CDC	≤ 0.25; S	4.2	S	1; S	3.7	S	8; R	-0.4	R
<i>Shigella sonnei</i>	AR0030	CDC	≤ 0.25; S	4.1	S	1; S	4.6	S	≤ 0.25; S	6.8	S
<i>Salmonella typhimurium</i>	AR0031	CDC	≤ 0.25; S	3.1	S	1; S	3.8	S	≤ 0.25; S	4.8	S
<i>Klebsiella pneumoniae</i>	AR0112	CDC	32; R	-0.3	R	16; R	-0.1	R	4; R	0.0	R
<i>Klebsiella pneumoniae</i>	AR0113	CDC	> 32; R	0.1	R	>64; R	-0.3	R	16; R	-0.3	R
<i>Escherichia coli</i>	AR0114	CDC	16; R	-0.1	R	4; S	3.0	S	> 32; R	0.3	R
<i>Klebsiella pneumoniae</i>	AR0115	CDC	32; R	0.1	R	8; I	1.3	R	> 32; R	-0.1	R
<i>Citrobacter freundii</i>	AR0116	CDC	8; R	0.4	R	16; R	0.5	R	8; R	0.6	R
<i>Klebsiella pneumoniae</i>	AR0117	CDC	4; R	-0.2	R	16; R	0.3	R	16; R	0.5	R

<i>Escherichia coli</i>	AR0118	CDC	32; R	0.6	R	> 64; R	-0.6	R	1; S	6.5	S
<i>Escherichia coli</i>	AR0119	CDC	> 32; R	-0.4	R	> 64; R	-0.1	R	0.5; S	6.0	S
<i>Klebsiella pneumoniae</i>	AR0120	CDC	32; R	-0.6	R	64; R	0.1	R	16; R	0.8	R
<i>Serratia marcescens</i>	AR0121	CDC	1; S	2.9	S	≤ 0.5; S	3.9	S	> 32; R	0.2	R
<i>Serratia marcescens</i>	AR0122	CDC	≤ 0.25; S	4.0	S	≤ 0.5; S	5.6	S	> 32; R	0.2	R
<i>Serratia marcescens</i>	AR0123	CDC	≤ 0.25; S	2.7	S	≤ 0.5; S	5.5	S	> 32; R	1.2	R
<i>Serratia marcescens</i>	AR0124	CDC	≤ 0.25; S	2.4	S	1; S	3.8	S	> 32; R	0.8	R
<i>Klebsiella pneumoniae</i>	AR0125	CDC	> 32; R	-0.8	R	> 64; R	-0.6	R	16; R	-0.7	R
<i>Klebsiella pneumoniae</i>	AR0126	CDC	≤ 0.25; S	3.3	S	≤ 0.5; S	4.7	S	8; R	0.0	R
<i>Salmonella senftenberg</i>	AR0127	CDC	16; R	0.3	R	> 64; R	0.9	R	2; I	6.7	S
<i>Escherichia coli</i>	AR0128	CDC	32; R	-0.6	R	> 64; R	0.7	R	8; R	6.9	S
<i>Klebsiella pneumoniae</i>	AR0129	CDC	> 32; R	-0.1	R	2; S	5.2	S	8; R	0.5	R
<i>Serratia marcescens</i>	AR0130	CDC	≤ 0.25; S	4.0	S	1; S	3.9	S	> 32; R	0.1	R

\* int = categorical interpretation

**Table B. A. baumannii strain information.**

Species	Strain	Origin	Ciprofloxacin			Gentamicin			Imipenem		
			BMD (MIC; int*)	qPCR assay (ΔCq)	qPCR assay (int*)	BMD (MIC; int*)	qPCR assay (ΔCq)	qPCR assay (int*)	BMD (MIC; int*)	qPCR assay (ΔCq)	qPCR assay (int*)
<i>A. baumannii</i>	AR0033	CDC	32; R	-0.3	R	> 64; R	-0.4	R	2; S	2.8	S
<i>A. baumannii</i>	AR0035	CDC	32; R	-0.3	R	8; I	0.1	R	> 32; R	-0.2	R
<i>A. baumannii</i>	AR0036	CDC	> 32; R	0.3	R	8; I	1.2	R	32; R	0.4	R
<i>A. baumannii</i>	AR0037	CDC	32; R	-0.3	R	> 64; R	-0.3	R	2; S	3.6	S
<i>A. baumannii</i>	AR0045	CDC	16; R	-0.3	R	> 64; R	0.4	R	8; R	-0.1	R
<i>A. baumannii</i>	AR0052	CDC	4; R	0.8	R	> 64; R	0.2	R	8; R	0.1	R
<i>A. baumannii</i>	AR0056	CDC	32; R	-0.7	R	> 64; R	-0.9	R	32; R	-1.1	R
<i>A. baumannii</i>	AR0063	CDC	32; R	-0.8	R	2; S	6.4	S	8; R	0.0	R
<i>A. baumannii</i>	AR0070	CDC	4; R	-0.1	R	64; R	-0.2	R	8; R	0.6	R
<i>A. baumannii</i>	AR0078	CDC	> 32; R	-0.1	R	> 64; R	0.3	R	16; R	0.3	R
<i>A. baumannii</i>	AR0083	CDC	8; R	-0.1	R	> 64; R	0.2	R	32; R	0.0	R
<i>A. baumannii</i>	AR0088	CDC	16; R	-0.4	R	> 64; R	0.2	R	2; S	2.2	S
<i>A. baumannii</i>	AR0101	CDC	32; R	-0.6	R	4; S	4.5	S	> 32; R	-0.3	R
<i>A. baumannii</i>	AR0102	CDC	16; R	-0.4	R	> 64; R	-0.4	R	1; S	4.5	S
<i>A. baumannii</i>	NR-13380	BEI	16; R	-0.3	R	> 64; R	0.2	R	0.5; S	5.4	S
<i>A. baumannii</i>	NR-13383	BEI	> 32; R	-0.5	R	> 64; R	0.1	R	4; I	-0.8	R
<i>A. baumannii</i>	NR-17780	BEI	16; R	0.6	R	> 64; R	0.5	R	0.5; S	6.1	S
<i>A. baumannii</i>	NR-17781	BEI	2; I	0.0	R	> 64; R	0.3	R	1; S	5.3	S
<i>A. baumannii</i>	NR-17782	BEI	32; R	0.1	R	> 64; R	0.0	R	0.5; S	4.9	S
<i>A. baumannii</i>	NR-17784	BEI	> 32; R	-0.5	R	> 64; R	-0.1	R	0.5; S	7.2	S
<i>A. baumannii</i>	NR-13379	BEI	32; R	-0.8	R	> 64; R	0.0	R	16; R	-0.1	R

<i>A. baumannii</i>	NR-13378	BEI	16; R	-0.3	R	8; I	1.8	R	> 32; R	-0.4	R
<i>A. baumannii</i>	NR-17786	BEI	16; R	0.0	R	> 64; R	-0.3	R	1; S	4.8	S
<i>A. baumannii</i>	NR-17778	BEI	≤ 0.25; S	1.2	R	1; S	7.0	S	≤ 0.25; S	5.1	S
<i>A. baumannii</i>	NR-17787	BEI	32; R	-0.4	R	> 64; R	0.1	R	≤ 0.25; S	5.7	S
<i>A. baumannii</i>	NR-13375	BEI	> 32; R	0.2	R	32; R	2.5	S	16; R	-0.5	R
<i>A. baumannii</i>	CNH111	FDA	32; R	0.4	R	2; S	4.6	S	≤ 0.25; S	5.4	S
<i>A. baumannii</i>	CNH151	FDA	≤ 0.25; S	3.0	S	1; S	5.8	S	≤ 0.25; S	5.1	S
<i>A. baumannii</i>	CNH160	FDA	≤ 0.25; S	3.3	S	4; S	6.7	S	≤ 0.25; S	5.8	S
<i>A. baumannii</i>	CNH640	FDA	≤ 0.25; S	3.1	S	2; S	5.5	S	≤ 0.25; S	6.0	S

\* int = categorical interpretation

**Table C. *P. aeruginosa* strain information.**

Species	Strain	Origin	Ciprofloxacin			Gentamicin			Imipenem		
			BMD (MIC; int*)	qPCR assay (ΔCq)	qPCR assay (int*)	BMD (MIC; int*)	qPCR assay (ΔCq)	qPCR assay (int*)	BMD (MIC; int*)	qPCR assay (ΔCq)	qPCR assay (int*)
<i>P. aeruginosa</i>	AR0054	CDC	8; R	-0.1	R	> 64; R	-0.4	R	> 32; R	0.4	R
<i>P. aeruginosa</i>	AR0064	CDC	8; R	0.3	R	1; S	4.2	S	> 32; R	0.1	R
<i>P. aeruginosa</i>	AR0090	CDC	16; R	-0.5	R	> 64; R	0.3	R	> 32; R	0.3	R
<i>P. aeruginosa</i>	AR0092	CDC	32; R	-1.5	R	> 64; R	-0.5	R	> 32; R	-0.1	R
<i>P. aeruginosa</i>	AR0094	CDC	16; R	-0.7	R	16; R	0.1	R	32; R	0.2	R
<i>P. aeruginosa</i>	AR0095	CDC	16; R	0.0	R	0.5; S	4.0	S	16; R	0.8	R
<i>P. aeruginosa</i>	AR0100	CDC	16; R	0.0	R	> 64; R	-0.2	R	32; R	-0.8	R
<i>P. aeruginosa</i>	AR0103	CDC	16; R	-0.3	R	> 64; R	-1.3	R	> 32; R	-0.2	R
<i>P. aeruginosa</i>	AR0105	CDC	> 32; R	-0.4	R	> 64; R	0.1	R	1; S	3.7	S
<i>P. aeruginosa</i>	AR0108	CDC	16; R	-0.4	R	> 64; R	-0.3	R	> 32; R	0.4	R
<i>P. aeruginosa</i>	AR0110	CDC	16; R	0.6	R	> 64; R	0.5	R	> 32; R	0.7	R
<i>P. aeruginosa</i>	AR0111	CDC	8; R	-0.6	R	> 64; R	-0.1	R	> 32; R	0.0	R
<i>P. aeruginosa</i>	105898	USAMRIID	8; R	0.1	R	> 64; R	0.3	R	0.5; S	2.6	S
<i>P. aeruginosa</i>	105819	USAMRIID	4; R	0.4	R	> 64; R	0.5	R	8; R	-0.1	R
<i>P. aeruginosa</i>	CNH770	FDA	≤ 0.25; S	2.4	S	≤ 0.5; S	4.2	S	1; S	4.1	S
<i>P. aeruginosa</i>	105756	USAMRIID	4; R	0.0	R	> 64; R	0.3	R	4; I	1.6	R
<i>P. aeruginosa</i>	105857	USAMRIID	16; R	-0.2	R	32; R	2.0	S	> 32; R	-0.2	R
<i>P. aeruginosa</i>	000006	USAMRIID	32; R	-0.6	R	16; R	1.1	R	1; S	2.1	S
<i>P. aeruginosa</i>	CNH363	FDA	≤ 0.25; S	3.1	S	≤ 0.5; S	6.0	S	1; S	5.7	S
<i>P. aeruginosa</i>	NR-31041	BEI	≤ 0.25; S	2.8	S	64; R	-0.6	R	2; S	2.3	S
<i>P. aeruginosa</i>	NR-50573	BEI	≤ 0.25; S	2.0	S	≤ 0.5; S	4.6	S	0.5; S	5.4	S
<i>P. aeruginosa</i>	NR-48928	BEI	≤ 0.25; S	1.8	S	> 64; R	0.2	R	1; S	3.1	S

\* int = categorical interpretation

**Table D. *E. faecium* strain information.**

Species	Strain	Origin	Ciprofloxacin			Vancomycin			Ampicillin		
			BMD (MIC; int*)	qPCR assay ( $\Delta$ Cq)	qPCR assay (int*)	BMD (MIC; int*)	qPCR assay ( $\Delta$ Cq)	qPCR assay (int*)	BMD (MIC; int*)	qPCR assay ( $\Delta$ Cq)	qPCR assay (int*)
<i>E. faecium</i>	NR-32065	BEI	4; R	0.9	R	> 32; R	0.1	R	4; S	2.1	S
<i>E. faecium</i>	NR-32094	BEI	> 32; R	0.2	R	32; R	0.3	R	32; R	0.0	R
<i>E. faecium</i>	HM-463	BEI	32; R	-0.5	R	0.5; S	2.4	S	16; R	0.7	R
<i>E. faecium</i>	NR-32053	BEI	$\leq$ 0.25; S	2.7	S	> 32; R	1.5	R	2; S	3.3	S
<i>E. faecium</i>	NR-31967	BEI	8; R	-0.1	R	1; S	5.2	S	> 64; R	0.6	R
<i>E. faecium</i>	NR-31916	BEI	1; S	1.6	S	> 32; R	2.6	S	8; S	2.8	S
<i>E. faecium</i>	NR-31937	BEI	2; I	1.5	R	0.5; S	0.9	R	$\leq$ 0.5; S	1.7	S
<i>E. faecium</i>	NR-28979	BEI	2; I	0.2	R	1; S	3.1	S	64; R	-0.5	R
<i>E. faecium</i>	NR-28982	BEI	> 32; R	-0.7	R	1; S	3.8	S	64; R	0.2	R
<i>E. faecium</i>	HM-204	BEI	1; S	1.2	R	1; S	4.8	S	2; S	3.9	S
<i>E. faecium</i>	NR-31963	BEI	4; R	0.9	R	1; S	4.8	S	16; R	-0.5	R
<i>E. faecium</i>	NR-31954	BEI	16; R	2.2	S	1; S	3.4	S	2; S	4.2	S
<i>E. faecium</i>	NR-28976	BEI	$\leq$ 0.25; S	2.4	S	1; S	4.1	S	2; S	4.8	S
<i>E. faecium</i>	NR-31955	BEI	> 32; R	-1.1	R	0.5; S	4.5	S	32; R	0.1	R
<i>E. faecium</i>	NR-31912	BEI	32; R	-0.2	R	> 32; R	1.2	R	32; R	-0.4	R
<i>E. faecium</i>	NR-31913	BEI	1; S	2.1	S	0.5; S	11.4	S	8; S	4.6	S
<i>E. faecium</i>	NR-32052	BEI	0.5; S	1.6	S	> 32; R	0.8	R	4; S	1.6	S
<i>E. faecium</i>	NR-32054	BEI	1; S	2.4	S	> 32; R	1.0	R	4; S	3.6	S
<i>E. faecium</i>	GRIM718	USAMRIID	> 32; R	-0.5	R	> 32; R	2.8	S	64; R	0.6	R
<i>E. faecium</i>	GRIM725	USAMRIID	2; I	0.8	R	1; S	3.9	S	> 64; R	-0.8	R
<i>E. faecium</i>	GRIM726	USAMRIID	> 32; R	-0.2	R	1; S	4.3	S	64; R	0.5	R
<i>E. faecium</i>	10857	USAMRIID	> 32; R	-0.4	R	1; S	3.8	S	64; R	0.1	R

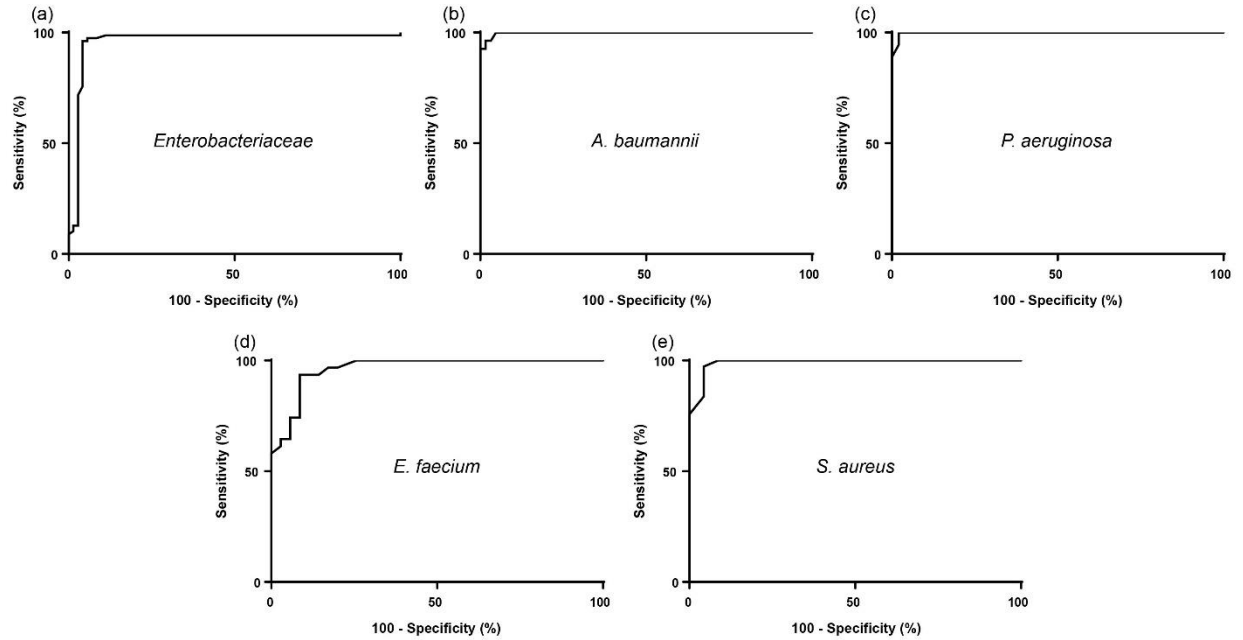
\* int = categorical interpretation

**Table E. *S. aureus* strain information.**

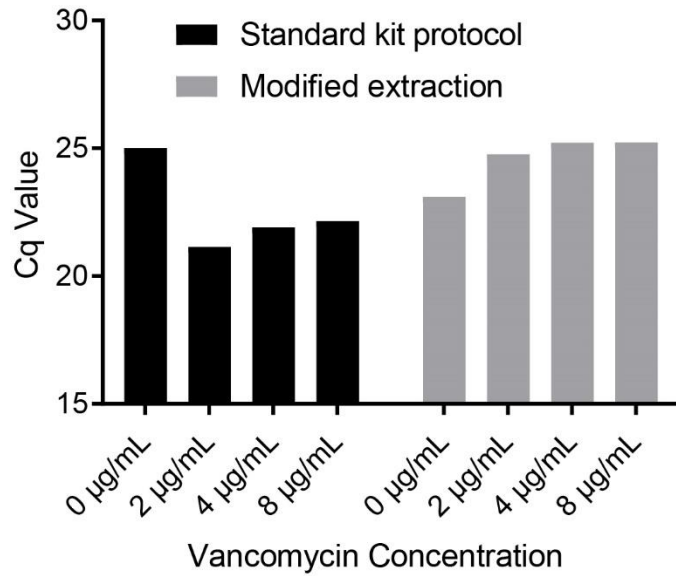
Species	Strain	Origin	Ciprofloxacin			Vancomycin			Oxacillin		
			BMD (MIC; int*)	qPCR assay ( $\Delta$ Cq)	qPCR assay (int*)	BMD (MIC; int*)	qPCR assay ( $\Delta$ Cq)	qPCR assay (int*)	BMD (MIC; int*)	qPCR assay ( $\Delta$ Cq)	qPCR assay (int*)
<i>S. aureus</i>	ATCC BAA-38	ATCC	$\leq$ 0.25; S	3.3	S	1; S	3.7	S	32; R	0.1	R
<i>S. aureus</i>	ATCC BAA-39	ATCC	4; R	0.7	R	2; S	4.9	S	32; R	0	R
<i>S. aureus</i>	ATCC BAA-40	ATCC	$\leq$ 0.25; S	2.9	S	2; S	5	S	> 32; R	-0.3	R
<i>S. aureus</i>	ATCC BAA-41	ATCC	8; R	0.4	R	2; S	5.7	S	> 32; R	1.7	R
<i>S. aureus</i>	ATCC BAA-43	ATCC	32; R	0.4	R	1; S	4.4	S	> 32; R	0.2	R
<i>S. aureus</i>	ATCC BAA-44	ATCC	4; R	0.7	R	2; S	3.1	S	> 32; R	0.7	R
<i>S. aureus</i>	GRIM48	USAMRIID	$\leq$ 0.25; S	3.3	S	1; S	3.5	S	$\leq$ 0.25; S	3.3	S

<i>S. aureus</i>	FDAARGOS_159	FDA	≤ 0.25; S	3.7	S	2; S	4.9	S	≤ 0.25; S	4.1	S
<i>S. aureus</i>	FDAARGOS_169	FDA	1; S	3.8	S	1; S	4.4	S	16; R	-0.1	R
<i>S. aureus</i>	ATCC 700698	ATCC	32; R	-0.1	R	2; S	2.4	S	> 32; R	-0.6	R
<i>S. aureus</i>	FDAARGOS_135	FDA	4; R	0.8	R	1; S	5.2	S	8; R	3.3	S
<i>S. aureus</i>	FDAARGOS_140	FDA	4; R	0.4	R	1; S	5.9	S	8; R	0.6	R
<i>S. aureus</i>	71080	BEI	32; R	1.3	R	> 32; R	0.3	R	> 32; R	0.7	R
<i>S. aureus</i>	ATCC 25923	ATCC	≤ 0.25; S	5.8	S	2; S	4.8	S	≤ 0.25; S	4	S
<i>S. aureus</i>	ATCC 29213	ATCC	≤ 0.25; S	4.3	S	1; S	6	S	≤ 0.25; S	3.7	S
<i>S. aureus</i>	ATCC 12600	ATCC	≤ 0.25; S	5.1	S	1; S	5.9	S	≤ 0.25; S	2.7	S
<i>S. aureus</i>	ATCC 13565	ATCC	≤ 0.25; S	4.9	S	1; S	4.8	S	≤ 0.25; S	4.1	S
<i>S. aureus</i>	ATCC 14458	ATCC	≤ 0.25; S	3.2	S	1; S	5.2	S	0.5; S	1.7	R
<i>S. aureus</i>	ATCC 8095	ATCC	≤ 0.25; S	4.2	S	1; S	6.6	S	≤ 0.25; S	5.6	S
<i>S. aureus</i>	880 (BR-VRSA)	BEI	16; R	0.1	R	16; R	-0.8	R	> 32; R	-0.1	R

\* int = categorical interpretation



**Figure A.** ROC curves derived from the experimental  $\Delta Cq$  values. ROC curves were generated such that resistance was considered the “control”. Sensitivity is then defined as the ability of the assay to call true susceptibility and is a measure of the major error rate. Specificity is defined as the ability of the assay to call true resistance and is a measure of the very major error rate. Cutoff values were selected to maximize the likelihood ratio for a correct susceptibility call. (a) *Enterobacteriaceae*, (b) *A. baumannii*, (c) *P. aeruginosa*, (d) *E. faecium*, (e) *S. aureus*.



**Figure B.** Example of insufficient bacterial lysis. The RAMAST assay was performed on cultures of *S. aureus* ATCC 25923, utilizing two different DNA extraction methods. For the standard kit protocol, DNA was extracted using an automated EZ1 instrument (Qiagen, Hilden, Germany) following the manufacturer's protocol with a DNA tissue kit and a DNA bacteria card. The modified extraction protocol is described in the materials and methods. Using the standard kit protocol resulted in inconsistent lysis / extraction for high loads of Gram positive bacteria, a situation that is often the case for no-antibiotic samples and for resistant strains.

**Table F. Retesting of strain-antibiotic combinations originally resulting in errors.**

Species	Strain	Antibiotic	BMD (MIC; int*)	qPCR assay ( $\Delta$ Cq)	qPCR assay (int*)
<i>E. coli</i>	AR0017	Gentamicin	1; S	1.5	R
<i>P. stuartii</i>	AR0026	Imipenem	0.5; S	-0.8	R
<i>S. marcescens</i>	AR0027	Ciprofloxacin	$\leq$ 0.25; S	1.5	R
<i>E. coli</i>	AR0128	Imipenem	8; R	5.6	S
<i>A. baumannii</i>	NR-17778	Ciprofloxacin	$\leq$ 0.25; S	-1.7	R
<i>A. baumannii</i>	NR-13375	Gentamicin	32; R	-0.1	R
<i>P. aeruginosa</i>	105857	Gentamicin	32; R	0.3	R
<i>E. faecium</i>	NR-31916	Vancomycin	> 32; R	5.4	S
<i>E. faecium</i>	NR-31937	Vancomycin	0.5; S	2.7	S
<i>E. faecium</i>	HM-204	Ciprofloxacin	1; S	3.5	S
<i>E. faecium</i>	NR-31954	Ciprofloxacin	16; R	2	S
<i>E. faecium</i>	GRIM718	Vancomycin	> 32; R	2.6	S
<i>S. aureus</i>	ATCC 14458	Oxacillin	0.5; S	0.6	R
<i>S. aureus</i>	FDAARGOS_135	Oxacillin	8; R	-1.2	R

\* int = categorical interpretation



**Table G. Categorical agreement and errors for each strain and antibiotic.**

	Isolates resistant by BMD		Isolates susceptible by BMD		Isolates intermediate by BMD		Total replicates	Very major error rate	Major error rate	Number of minor errors	Categorical agreement
	Susceptible by BQ	Resistant by BQ	Susceptible by BQ	Resistant by BQ	Susceptible by BQ	Resistant by BQ					
<i>Enterobacteriaceae</i>											
Ciprofloxacin	0	27	22	1	0	0	50	0.0%	4.3%	0	98.0%
Gentamicin	0	17	30	1	1	1	50	0.0%	3.2%	1	96.0%
Imipenem	1	24	23	1	1	0	50	4.0%	4.2%	1	94.0%
Overall	1	68	75	3	2	1	150	1.4%	3.8%	2	96.0%
<i>A. baumannii</i>											
Ciprofloxacin	0	25	3	1	0	1	30	0.0%	25.0%	0	96.7%
Gentamicin	1	19	7	0	0	3	30	5.0%	0.0%	0	96.7%
Imipenem	0	13	16	0	0	1	30	0.0%	0.0%	0	100.0%
Overall	1	57	26	1	0	5	90	1.7%	3.7%	0	97.8%
<i>P. aeruginosa</i>											
Ciprofloxacin	0	17	5	0	0	0	22	0.0%	0.0%	0	100.0%
Gentamicin	1	16	5	0	0	0	22	5.9%	0.0%	0	95.5%
Imipenem	0	13	8	0	0	1	22	0.0%	0.0%	0	100.0%
Overall	1	46	18	0	0	1	66	2.1%	0.0%	0	98.5%
<i>E. faecium</i>											
Ciprofloxacin	1	11	6	1	0	3	22	8.3%	14.3%	0	90.9%
Vancomycin	2	6	13	1	0	0	22	25.0%	7.1%	0	86.4%
Ampicillin	0	12	10	0	0	0	22	0.0%	0.0%	0	100.0%
Overall	3	29	29	2	0	3	66	9.4%	6.5%	0	92.4%
<i>S. aureus</i>											
Ciprofloxacin	0	9	11	0	0	0	20	0.0%	0.0%	0	100.0%
Vancomycin	0	2	18	0	0	0	20	0.0%	0.0%	0	100.0%
Oxacillin	1	11	7	1	0	0	20	8.3%	12.5%	0	90.0%
Overall	1	22	36	1	0	0	60	4.3%	2.7%	0	96.7%

**Table H. Vancomycin concentration optimization for *E. faecium***

Species	Strain	Vancomycin						
		BMD	qPCR 0.25 µg/mL	qPCR 0.5 µg/mL	qPCR 1 µg/mL	qPCR 2 µg/mL	qPCR 4 µg/mL	qPCR 8 µg/mL
<i>E. faecium</i>	NR-32065	> 32; R	R	R	R	R	S	S
<i>E. faecium</i>	NR-32094	32; R	R	R	R	R	R	R
<i>E. faecium</i>	HM-463	0.5; S	R	S	S	S	S	S
<i>E. faecium</i>	NR-32053	> 32; R	R	R	R	R	S	S
<i>E. faecium</i>	NR-31967	1; S	R	R	S	S	S	S
<i>E. faecium</i>	NR-31916	> 32; R	R	R	S	S	S	S
<i>E. faecium</i>	NR-31937	0.5; S	R	R	R	R	S	S
<i>E. faecium</i>	NR-28979	1; S	R	R	S	S	S	S
<i>E. faecium</i>	NR-28982	1; S	R	R	S	S	S	S
<i>E. faecium</i>	HM-204	1; S	R	R	S	S	S	S
<i>E. faecium</i>	NR-31963	1; S	R	R	S	S	S	S
<i>E. faecium</i>	NR-31954	1; S	R	R	S	S	S	S
<i>E. faecium</i>	NR-28976	1; S	R	S	S	S	S	S
<i>E. faecium</i>	NR-31955	0.5; S	R	S	S	S	S	S
<i>E. faecium</i>	NR-31912	> 32; R	R	R	R	R	S	S
<i>E. faecium</i>	NR-31913	0.5; S	R	S	S	S	S	S
<i>E. faecium</i>	NR-32052	> 32; R	R	R	R	R	R	S
<i>E. faecium</i>	NR-32054	> 32; R	R	S	R	S	S	S
<i>E. faecium</i>	GRIM718	> 32; R	R	R	S	S	S	S
<i>E. faecium</i>	GRIM725	1; S	R	S	S	S	S	S
<i>E. faecium</i>	GRIM726	1; S	R	S	S	S	S	S
<i>E. faecium</i>	10857	1; S	R	S	S	S	S	S