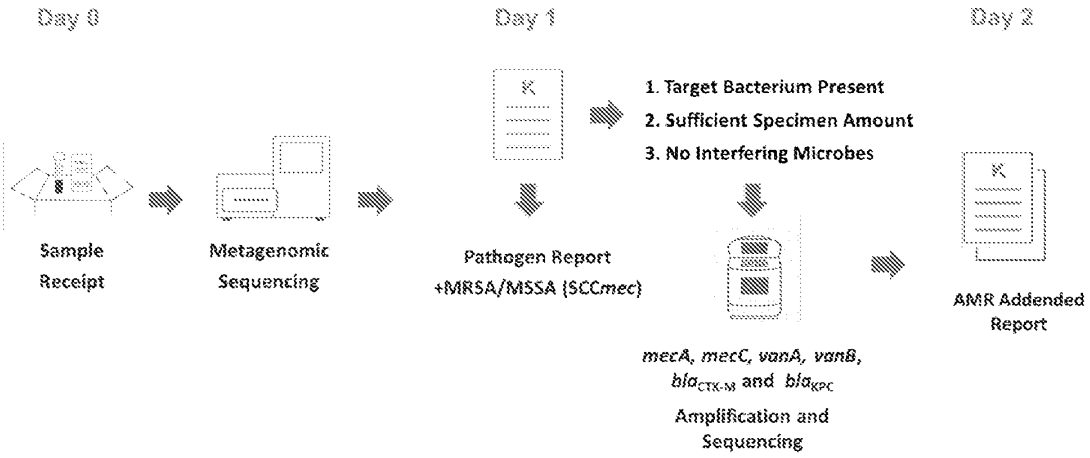

Day 0
Day 1
Day 2
Sample Receipt
Metagenomic Sequencing
Pathogen Report +MRSA/MSSA (SCC*mec*)
1. Target Bacterium Present
2. Sufficient Specimen Amount
3. No Interfering Microbes
mecA, *mecC*, *vanA*, *vanB*, bla_{CTX-M} and bla_{KPC} Amplification and Sequencing
AMR Addended Report

FIG. 1

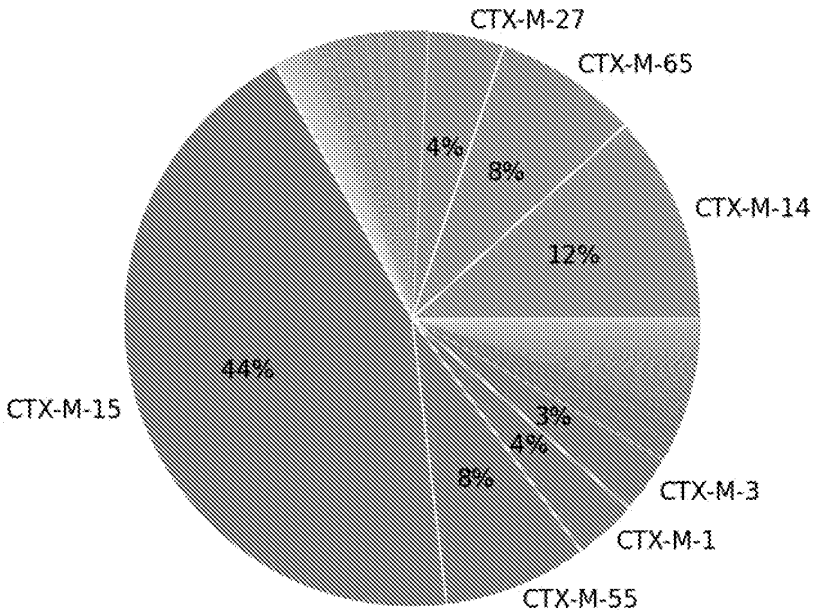

CTX-M-27
CTX-M-65
CTX-M-14
CTX-M-3
CTX-M-1
CTX-M-55
CTX-M-15
4%
8%
12%
3%
4%
8%
44%

FIG. 2

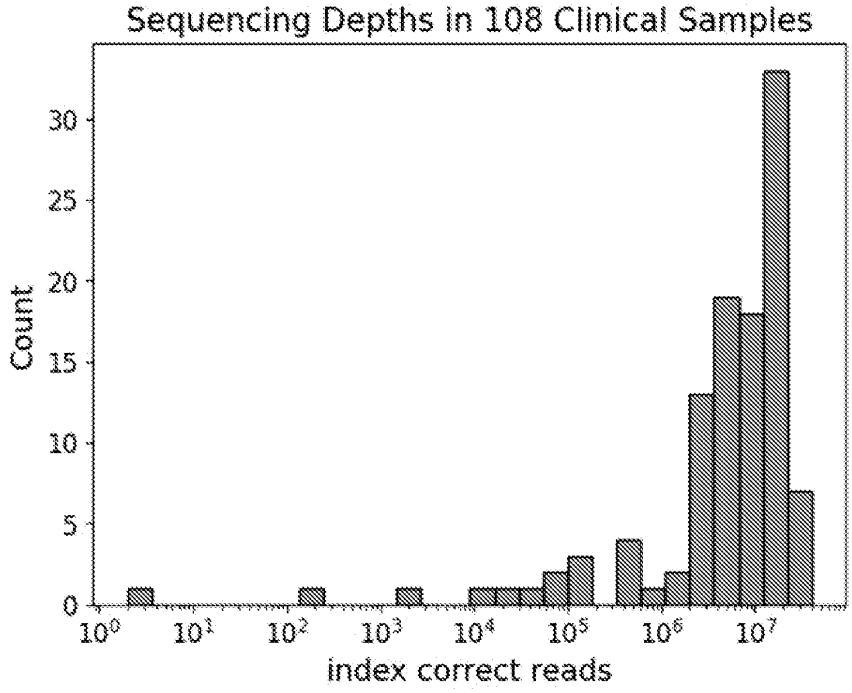

Sequencing Depths in 108 Clinical Samples
Count
index correct reads
0
5
10
15
20
25
30
10^0
10^1
10^2
10^3
10^4
10^5
10^6
10^7

FIG. 3

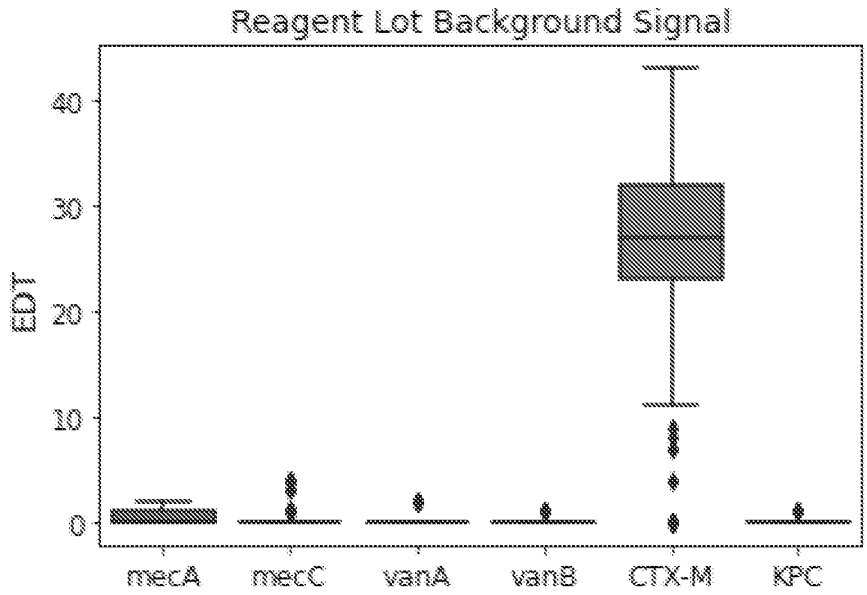

Reagent Lot Background Signal
EDT
0
10
20
30
40
mecA
mecC
vanA
vanB
CTX-M
KPC

FIG. 4

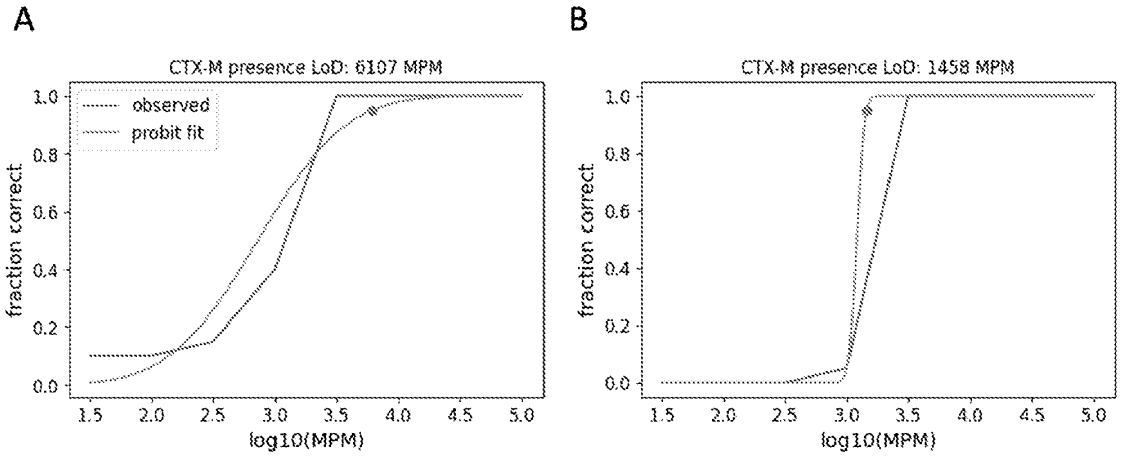


FIG. 5A

FIG. 5B

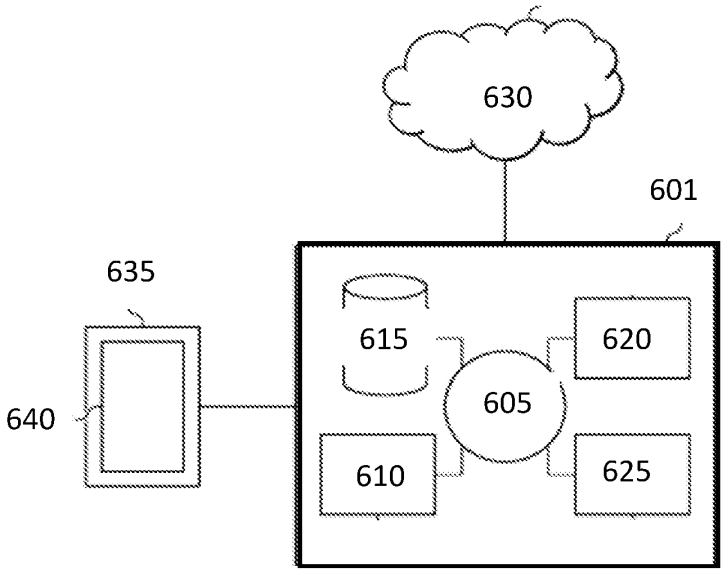


FIG. 6

TABLE 6 *Clinical validation performance summary*

Coverage			Performance metrics[a]			
Bacteria (no.)	Antibiotics	AMR markers	PPA	NPA	CA	DY
S. aureus (58)	Methicillin	SCC*mec*	19/20	21/22	40/42	42/60
S. epidermidis (2)		and *mecA*[b]	(95.0%)	(95.4%)	(95.2%)	(70.0%)
			[75.1–99.9][c]	[77.1–99.9]	[83.8–99.4]	[56.8–81.1]
E. faecium (4)	Vancomycin	*vanA*	3/3	2/2	5/5	5/6
E. faecalis (2)			(100%)	(100%)	(100%) [47.8–100%]	(83.3%) [35.8–99.5]
			[29.2–100]	[15.8–100]		
Gram-negative	Extended spectrum	bla_{CTX-M}	5/6	29/29	34/35	35/49
bacteria (49)	β-lactams[d] (49)		(83.3%)	(100%)	(97.1%)	(71.4%)
			[35.9–99.6]	[88.1–100]	[85.1–99.9]	[56.7–83.4]
	Carbapenems (29)	bla_{KPC}	0/2	23/23	23/25 (92.3%) [73.9–99.0]	25/44 (56.8%) [41.0–71.6]
			(0%)	(100%)		
			[0–84.2]	[85.1–100]		

[a]CA, categorical agreement with orthogonal resistance phenotypes and/or genotypes; DY, diagnostic yield expressed as the sum of presence and absence calls for an AMR marker divided by the sum of all microbes tested (indeterminates excluded).
[b]SCC*mec* and *mecA* results combined as described in the AMR workflow.
[c]95% CI.
[d]Cefepime used as the key indicator drug.

FIG. 7