

Supplemental Table 1. Phenotypic antibiotic resistances of infectious isolates

Patient	Infectious Organism	AMK	ATM	FEP	CAZ	CIP	CST	IPM	MEM	TZP	TIM	TOB	CRO	MXF	PEN	TET	TGC	VAN	AMC	ETP	SXT	CLI	ERY	GEN	LVX	LZD	NIT	OXA	RIF	AMP	SAM	CTX	CPD	CEF	DAP	Q-D	STR	CZA	MIN	C/T	CPT									
B001	<i>Pseudomonas aeruginosa</i>	S	S	I	S	R	S	R	R	S	R	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-								
B002	<i>Streptococcus mitis</i>	-	-	-	-	-	-	-	-	-	-	-	S	R	S	R	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
B003	<i>Escherichia coli</i>	S	-	S	-	R	-	S	S	S	I	S	-	R	-	-	S	-	I	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
B004	<i>Staphylococcus epidermidis</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	S	S	-	-	-	S	R	S	R	S	S	R	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
B005	<i>Streptococcus oralis</i>	-	-	-	-	-	-	-	-	-	-	-	S	R	I	R	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
B006	<i>Staphylococcus epidermidis</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	S	S	-	-	R	R	R	R	R	S	R	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-						
B007	<i>Pseudomonas aeruginosa</i>	S	S	S	-	S	-	S	-	S	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-						
B008	<i>Streptococcus mitis</i>	-	-	-	-	-	-	-	-	-	-	-	S	R	I	R	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-						
B009	<i>Escherichia coli</i>	S	-	S	-	R	-	S	-	S	R	R	-	R	-	-	S	-	R	S	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-					
B010	<i>Escherichia coli</i>	S	S	S	S	R	-	S	S	S	-	S	S	R	-	-	S	-	S	S	-	-	S	R	-	S	R	-	S	-	R	R	S	S	R	-	-	-	-	-	-	-	-	-	-					
B011	<i>Staphylococcus aureus (MRSA)</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	S	S	-	-	S	S	R	S	S	R	S	S	R	S	-	-	-	-	-	-	S	-	-	-	-	-	-	-						
B012	<i>Enterococcus faecium, VRE</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	R	-	-	-	-	-	R	R	I	S	-	R	-	-	-	-	-	-	-	-	S	S	-	-	-	-	-						
B013	<i>Streptococcus oralis</i>	-	-	-	-	-	-	-	-	-	-	-	R	S	R	R	S	S	-	-	-	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	-	S	-	-	-	-	-	-	-					
B014	<i>Pseudomonas aeruginosa</i>	S	S	S	S	S	-	S	S	S	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-					
B015	<i>Staphylococcus epidermidis</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	S	S	-	-	R	R	R	R	R	R	S	R	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-					
B016	<i>Streptococcus sanguinis</i>	-	-	-	-	-	-	-	-	-	-	-	S	R	S	R	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-					
B017	<i>Staphylococcus epidermidis</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	S	S	-	-	-	-	R	R	R	R	-	S	R	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-					
B018	<i>Enterococcus faecalis</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	S	-	-	-	-	-	R	R	S	S	-	S	-	-	-	-	-	-	-	-	S	R	-	-	-	-	-	-					
B019	<i>Escherichia coli</i>	S	R	I	R	R	-	S	S	S	-	S	R	R	-	-	S	-	S	R	-	-	S	R	-	I	-	-	R	R	R	R	R	-	-	-	-	-	-	-	-	-	-	-	-	-				
B021	<i>Streptococcus mitis</i>	-	-	-	-	-	-	-	-	-	-	-	S	S	R	S	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-					
B022	<i>Pseudomonas aeruginosa</i>	S	S	S	S	S	-	S	S	S	I	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-					
B023	<i>Escherichia coli</i>	S	S	S	S	R	-	S	S	S	-	S	S	R	-	-	S	-	-	-	S	R	-	-	R	R	-	S	-	-	R	I	S	-	R	-	-	-	-	-	-	-	-	-	-	-				
B024	<i>Streptococcus mitis</i>	-	-	-	-	-	-	-	-	-	-	-	S	R	S	S	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
B025	<i>Pseudomonas aeruginosa</i>	R	I	R	S	R	-	S	R	R	-	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
B026	<i>Enterococcus faecium</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	R	-	-	-	-	-	R	R	-	-	-	R	-	-	-	-	-	-	-	-	-	S	R	-	-	-	-	-	-				
B027	<i>Staphylococcus aureus (MRSA)</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	S	-	-	S	R	T	S	R	S	-	R	S	-	-	-	-	-	-	-	-	-	S	-	-	-	-	-	-	-				
B028	<i>Streptococcus mitis</i>	-	-	-	-	-	-	-	-	-	-	-	-	S	S	S	R	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
B029	<i>Escherichia coli</i>	S	S	S	S	R	-	S	S	S	-	S	S	R	-	-	S	-	-	S	S	-	-	S	R	-	-	R	R	-	S	-	-	R	I	S	R	R	-	-	-	-	-	-	-	-	-			
B030	<i>Escherichia coli</i>	S	S	S	S	R	-	S	S	S	-	S	S	-	-	-	-	-	S	R	-	-	S	R	-	S	R	-	-	R	I	S	S	I	-	-	-	-	-	-	-	-	-	-	-	-	-			
B032	<i>Staphylococcus epidermidis</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	S	S	-	-	-	R	R	R	-	R	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
B034	<i>Staphylococcus epidermidis</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	S	S	-	-	S	R	S	R	S	-	R	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
B035	<i>Enterococcus faecalis</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	S	-	-	-	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
B036	<i>Pseudomonas aeruginosa</i>	S	I	S	S	S	-	S	S	S	-	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
B037B	<i>Streptococcus salivarius</i>	-	-	-	-	-	-	-	-	-	-	-	-	S	S	I	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
B038	<i>Streptococcus parasanguinis</i>	-	-	-	-	-	-	-	-	-	-	-	-	S	I	R	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
B039	<i>Streptococcus mitis</i>	-	-	-	-	-	-	-	-	-	-	-	-	S	R	I	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
B041	<i>Escherichia coli</i>	S	R	S	R	R	-	S	S	S	-	I	R	R	-	-	-	-	S	S	R	-	-	R	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
B042	<i>Staphylococcus epidermidis</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	R	-	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
B043	<i>Enterococcus faecium, VRE</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
B044	<i>Escherichia coli</i>	S	R	R	R	R	-	S	S	-	R	R	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
B045	<i>Klebsiella pneumoniae</i>	S	R	R	R	R	-	S	R	R	-	R	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
B047	<i>Pseudomonas aeruginosa</i>	I	-	I	S	R	-	S	I	-	S	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
B048	<i>Escherichia coli</i>	S	S	S	S	R	-	S	S	-	S	S	-	-	-	-	-	-	-	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
B049	<i>Staphylococcus aureus</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
B050	<i>Escherichia coli</i>	S	S	R	R	R	-	S	R	-	R	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
B052	<i>Staphylococcus aureus</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
B053	<i>Klebsiella pneumoniae</i>	S	S	S	-	S	-	S	S	-	S	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
B054	<i>Enterococcus faecalis</i>																																																	

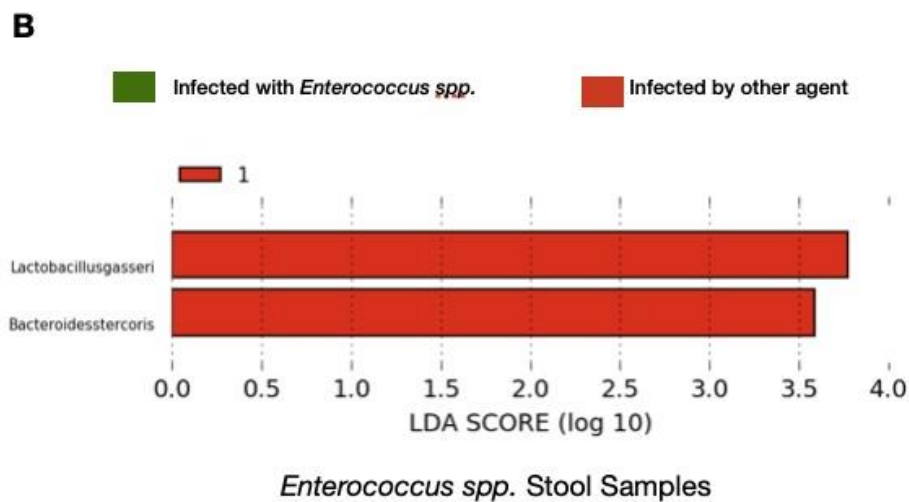
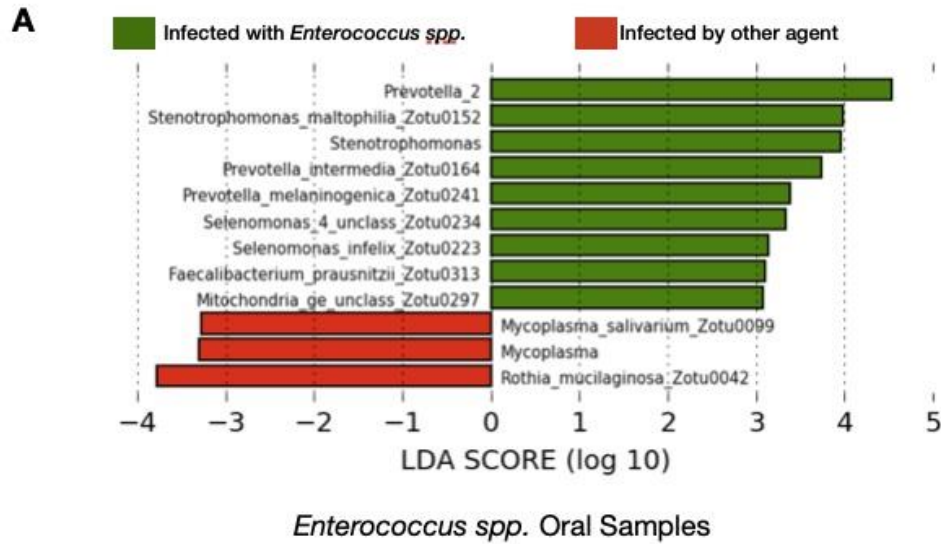
Supplemental Table 2: ddPCR Primers and Probes to Confirm of Infectious Agents in Patient Stool Samples.

<i>Enterococcus spp.</i>	Forward	GAGAAATTCCAAACGAACTTG	Tm: 50°C
	Reverse	CAGTGCTCTACCTCCATCATT	Tm: 54.2°C
	Probe, Dye and Quencher	TGGTTCTCTCCGAAATAGCTTTAGGGCTA 6-FAM; BHQ-1	Tm: 60.3°C
<i>Escherichia coli</i>	Forward	TCACGCCGTATGTTATTG	Tm: 49.4°C
	Reverse	GTCGGTAATCACCATTC	Tm: 49.8°C
	Probe, Dye and Quencher	TGCCAGTTCAGTTCGTTGTTCAC 6-FAM; BHQ-1	Tm: 58°C
<i>Klebsiella pneumoniae</i>	Forward	GGGCGAGGTTTACGTCTCAA	Tm: 57.8°C
	Reverse	GCGTGTGGATAAGAGGTGCG	Tm: 58.2°C
	Probe, Dye and Quencher	CCACCACGAGCGGCTGCC 6-FAM; BHQ-1	Tm: 64.7°C
<i>Pseudomonas aeruginosa</i>	Forward	TTCAACGAGAACCTGCTCTG	Tm: 55.5°C
	Reverse	CGGCCTCGATGTAGTTGTT	Tm: 54.9°C
	Probe, Dye and Quencher	CTTCACCAACAACATCCCGCAGC 6-FAM; BHQ-1	Tm: 59°C
<i>Staphylococcus aureus</i>	Forward	GAGTTTGGTGCCTTTACAGATAG	Tm: 53.4°C
	Reverse	AGCAAGCTTTAACTCATAGTGG	Tm: 52.8°C
	Probe, Dye and Quencher	TGCCATACAGTCATTTACGCAAAGTGG 6-FAM; BHQ-1	Tm: 59.8°C
	Forward	ATCAAAAAGTTGGCGAACCTTTTCA	Tm: 56.9°C
	Reverse	CAAAAAGAGCGTGGAGAAAAGTATC	Tm: 54.1°C

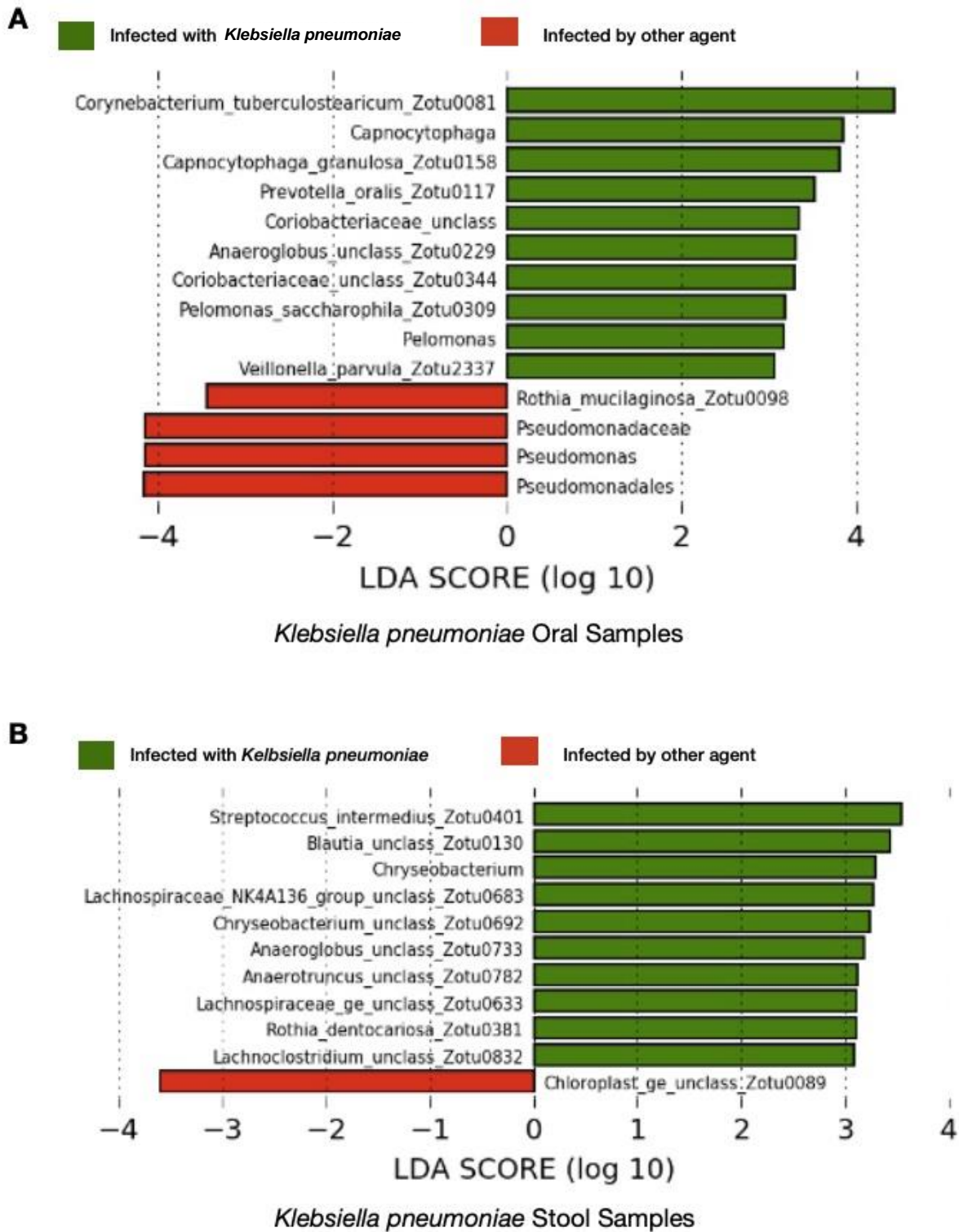
<i>Staphylococcus epidermidis</i>	Probe, Dye and Quencher	CCATTTGCATAGTCTGATTGCTCAAAGTCT 6-FAM; BHQ-1	Tm: 59.0°C
<i>Streptococcus mitis</i>	Forward	TGCCCTTCCACTCAATTAGAC	Tm: 54.9°C
	Reverse	GAACCGTTGTTCCAGTCCTATC	Tm: 55.3°C
	Probe, Dye and Quencher	TACCGTCGTGGTCATGTTGTTGCT 6-FAM; BHQ-1	Tm: 56.2°C
<i>Streptococcus oralis</i>	Forward	GATTACCTTTGCGGAACGTTTG	Tm: 54.8°C
	Reverse	GGCTAGAAGAGAGAGGAGTTGA	Tm: 55.3°C
	Probe, Dye and Quencher	CGATCAATCTGGTGCCCTTCGTGA 6-FAM; BHQ-1	Tm: 61.1°C

Supplemental Table 3: ddPCR Primers and Probes to Confirm Antibiotic Resistance Gene Presence in Patient Stool Samples.

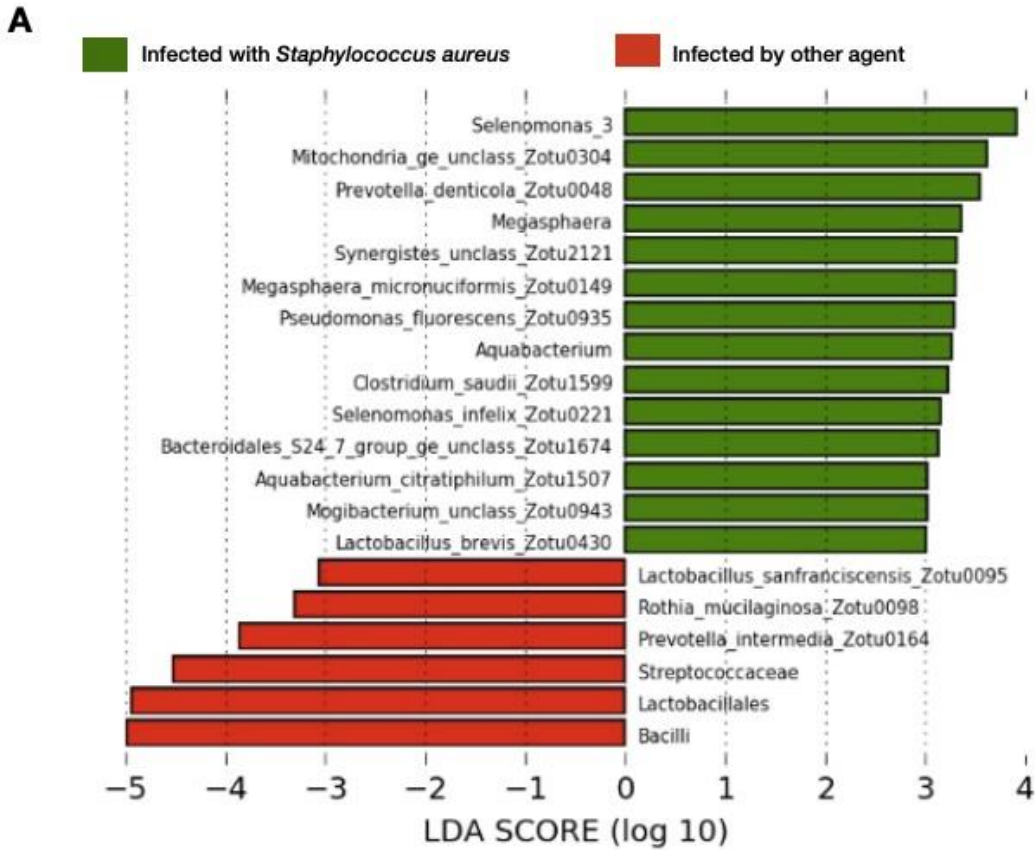
<i>CTX-M-15</i>	Forward	GACTGGGTGTGGCATTGATTAAC	Tm: 64°C
	Reverse	CAGATTCGGTTCGCTTTCACCTT	Tm: 64°C
	Probe, Dye and Quencher	ATGAGCGCTTTGCGATGTGCAGCA 6-FAM; BHQ-1	Tm: 71°C
<i>CTX-M-14</i>	Forward	TGACGTGGCTCAAAGGCAATA	Tm: 64°C
	Reverse	TATCATTGGTGGTGCCGTAGTC	Tm: 64°C
	Probe, Dye and Quencher	TGGA CTGTGGGTGATAAGACCGGCA 6-FAM; BHQ-1	Tm: 71°C
<i>CfrA</i>	Forward	GATTATATCATGTTGCCTGGTGTAATG	Tm: 63°C
	Reverse	CCATACATCTCAGGTGCACTTATTG	Tm: 63°C
	Probe, Dye and Quencher	TCTTGAGCATGCAAACGAGTTGTTAGCCT 6-FAM; BHQ-1	Tm: 70°C
<i>VanA</i>	Forward	TCCTGACCAGTCTACGACCAATAC	Tm: 65°C
	Reverse	CGGTAATCAAGCAGACTATGCGATAC	Tm: 65°C
	Probe, Dye and Quencher	ACAATCCGGGTGTACTTGTTTCCTTTGCA 6-FAM; BHQ-1	Tm: 70°C



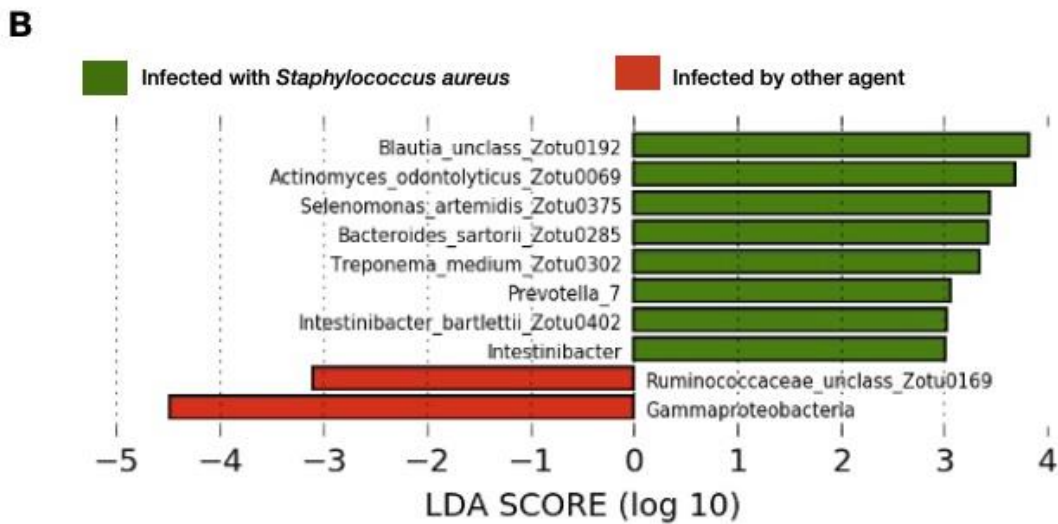
Supplemental Figure 1. LEfSe analysis of *Enterococcus spp.* infections. Linear discriminant analysis of effect size was done on oral (A) and stool (B) samples to compare the microbiomes of patients with an *Enterococcus spp.* infection to those without. Organisms with a red bar show enrichment in patients without an *Enterococcus spp.* infection while those with a green bar show enrichment in patients with an *Enterococcus spp.* infection.



Supplemental Figure 2. LEfSe analysis of *Klebsiella pneumoniae* infections. Linear discriminant analysis of effect size was done on oral (A) and stool (B) samples to compare the microbiomes of patients with a *Klebsiella pneumoniae* infection to those without. Organisms with a red bar show enrichment in patients without a *K. pneumoniae* infection while those with a green bar show enrichment in patients with a *K. pneumoniae* infection.

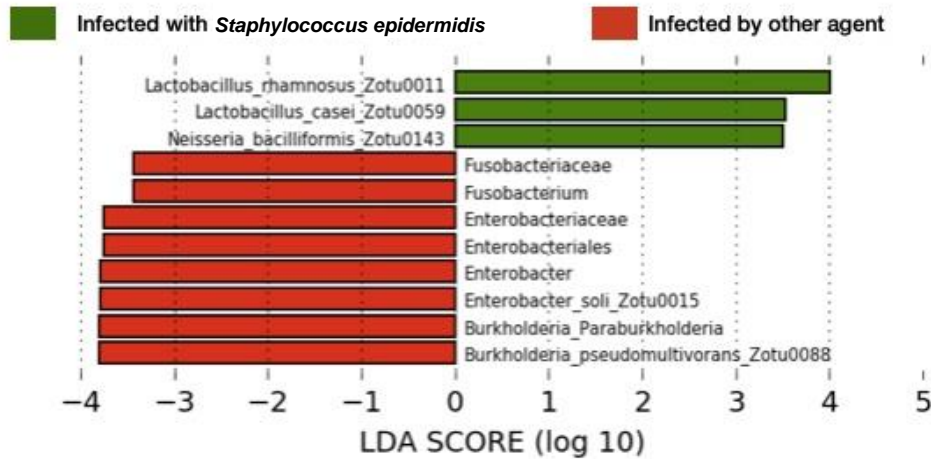
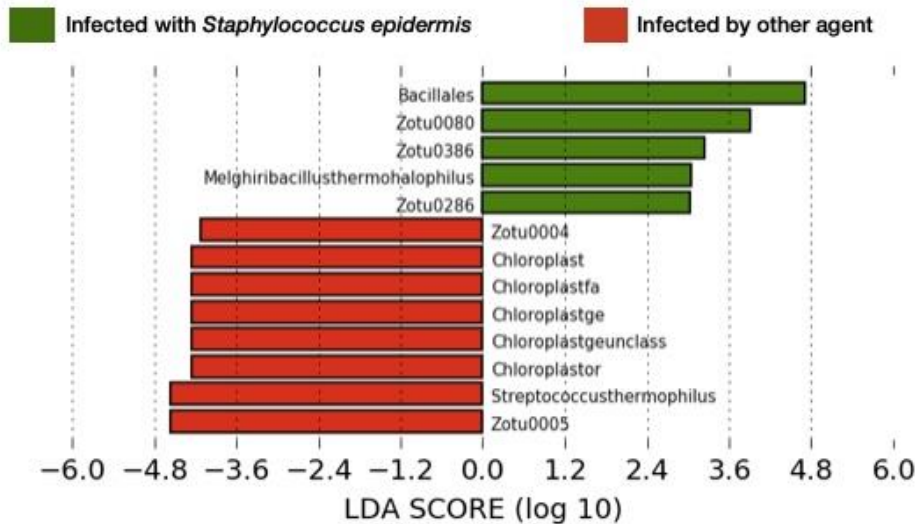


Staphylococcus aureus Oral Samples

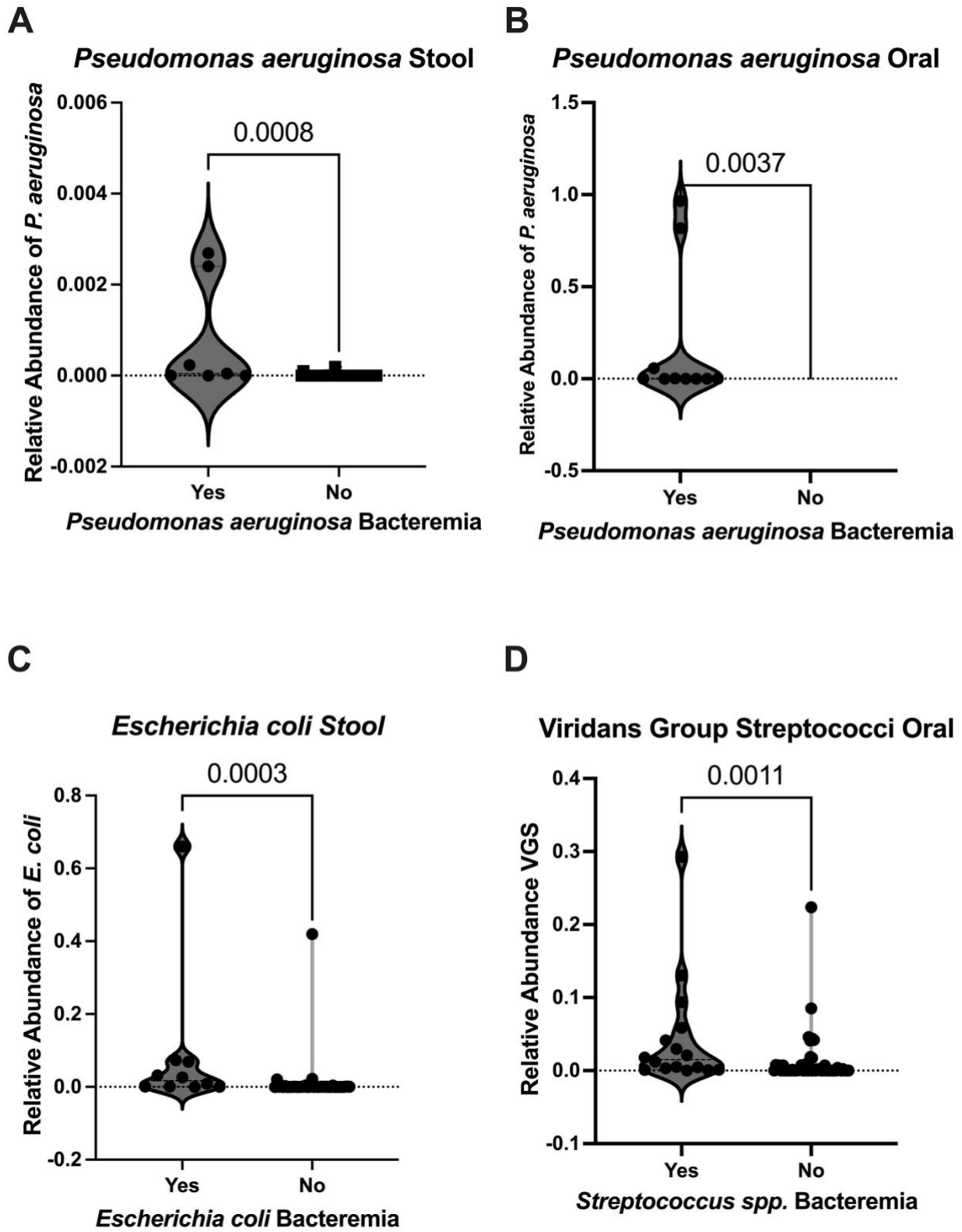


Staphylococcus aureus Stool Samples

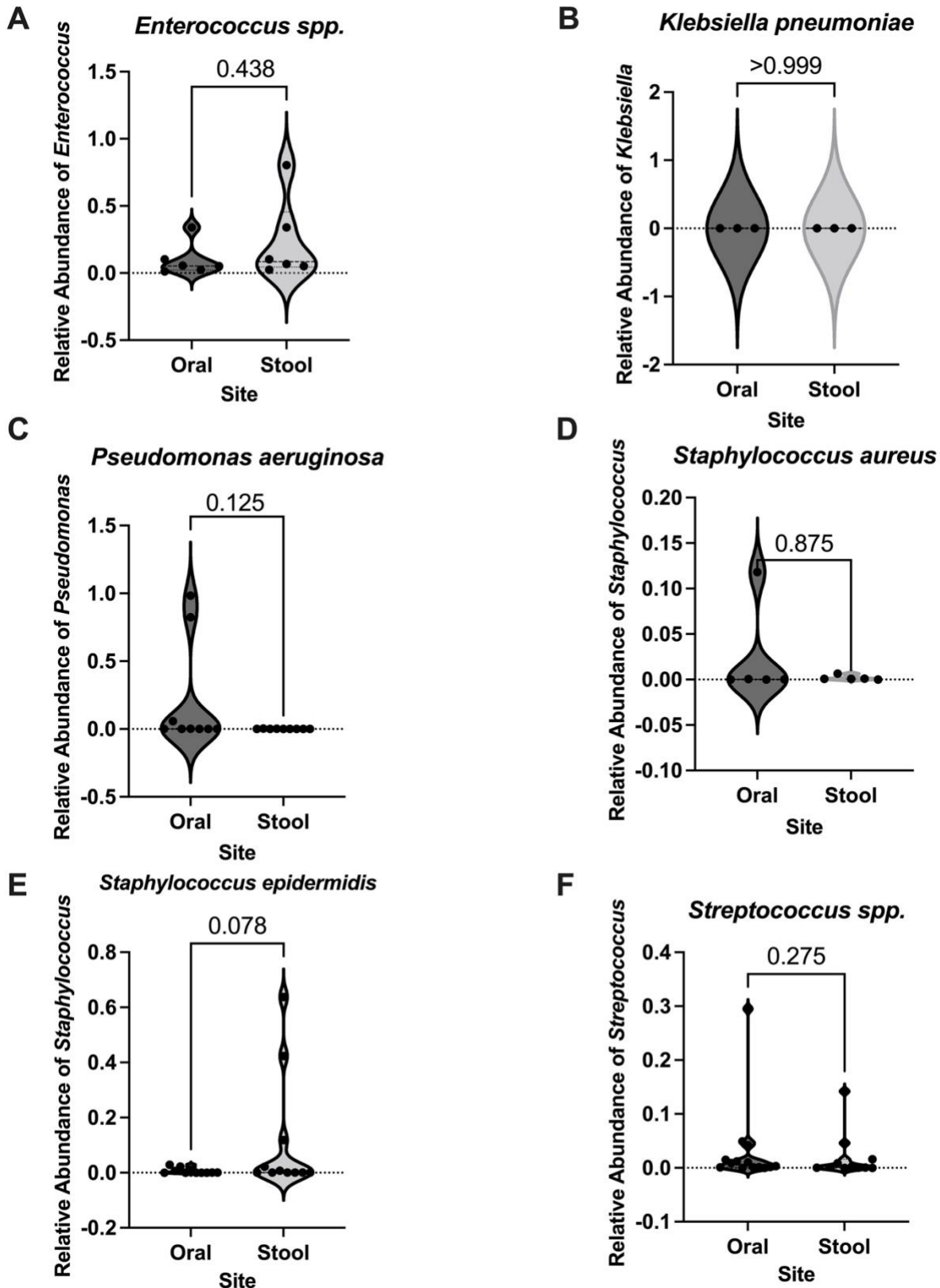
Supplemental Figure 3. LEfSe analysis of *Staphylococcus aureus* infections. Linear discriminant analysis of effect size was done on oral (A) and stool (B) samples to compare the microbiomes of patients with a *Staphylococcus aureus* infection to those without. Organisms with a red bar show enrichment in patients without a *S. aureus* infection while those with a green bar show enrichment in patients with a *S. aureus* infection.

A*Staphylococcus epidermidis* Oral Samples**B***Staphylococcus epidermidis* Stool Samples

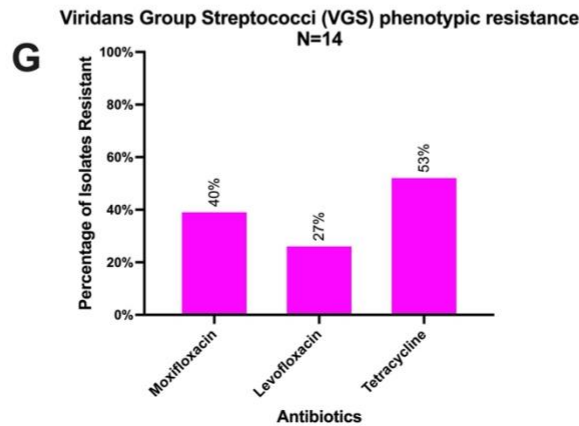
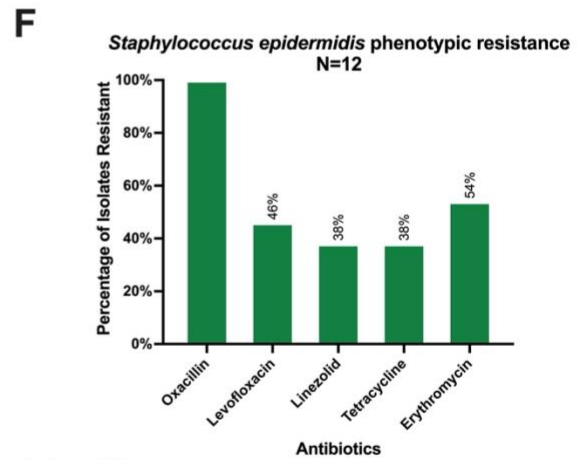
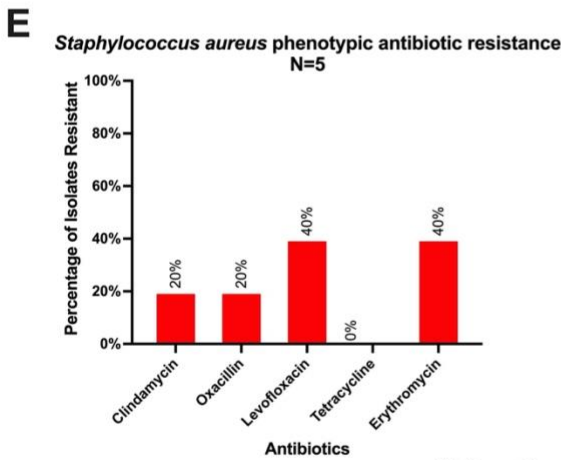
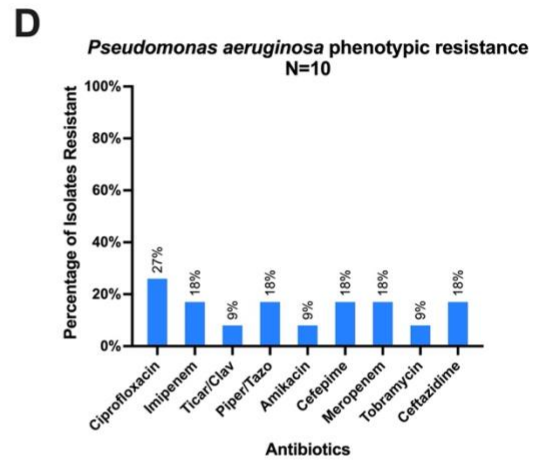
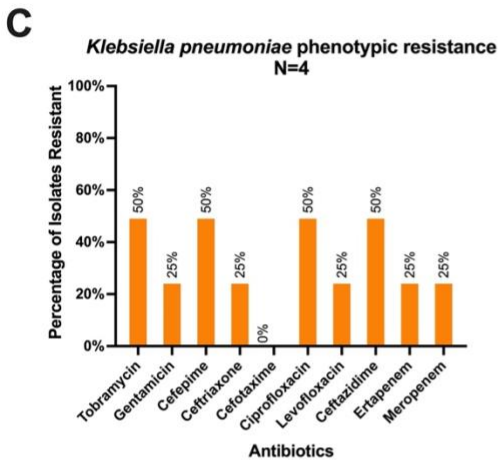
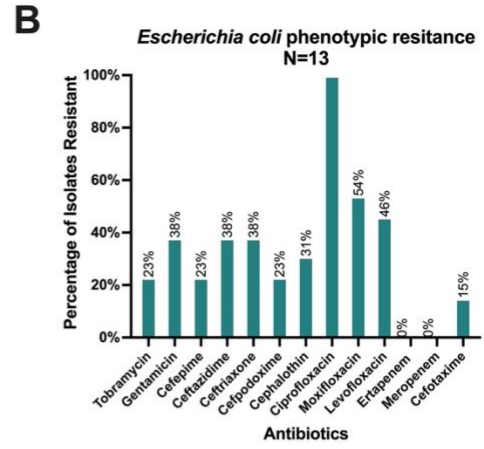
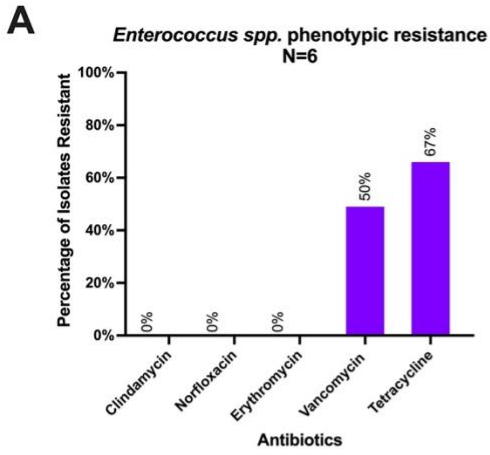
Supplemental Figure 4. LEfSe analysis of *Staphylococcus epidermidis* infections. Linear discriminant analysis of effect size was done on oral (A) and stool (B) samples to compare the microbiomes of patients with a *Staphylococcus epidermidis* infection to those without. Organisms with a red bar show enrichment in patients without a *S. epidermidis* infection while those with a green bar show enrichment in patients with a *S. epidermidis* infection.



Supplemental Figure 5. Distribution of infectious taxa between patients with and without respective bacteremias. Mann-Whitney testing demonstrates that patients with *E. coli* and *P. aeruginosa* bacteremia had higher abundance of the infectious taxa in their stool. Additionally, patients with *P. aeruginosa* and VGS bacteremia had increased abundance of the infectious taxa in the oral samples.



Supplemental Figure 6. Demonstration of differences in abundance based on site and species specificity. Demonstration of differences in abundance based on site specificity per species. Mann-Whitney testing was performed using the relative abundance of each genera compared between stool and oral samples of patients infected with A) *Enterococcus spp.*, B) *Klebsiella pneumoniae*, C) *Pseudomonas aeruginosa*, D) *Staphylococcus aureus*, E) *Staphylococcus epidermidis* and F) *Streptococcus spp.*



Supplemental Figure 7. Graphical representation of phenotypic antibiotic resistance. The percentage of isolates resistant to various antibiotics for A) *Enterococcus spp.*, B) *Escherichia coli*, C) *Klebsiella pneumoniae*, D) *Pseudomonas aeruginosa*, E) *Staphylococcus aureus*, F) *Staphylococcus epidermidis* and G) Viridians Group Streptococci (VGS). Each graph was made by looking at what antibiotics were tested for sensitivity for each species of interest, and determining what percentage of isolates were resistant to each antibiotic.