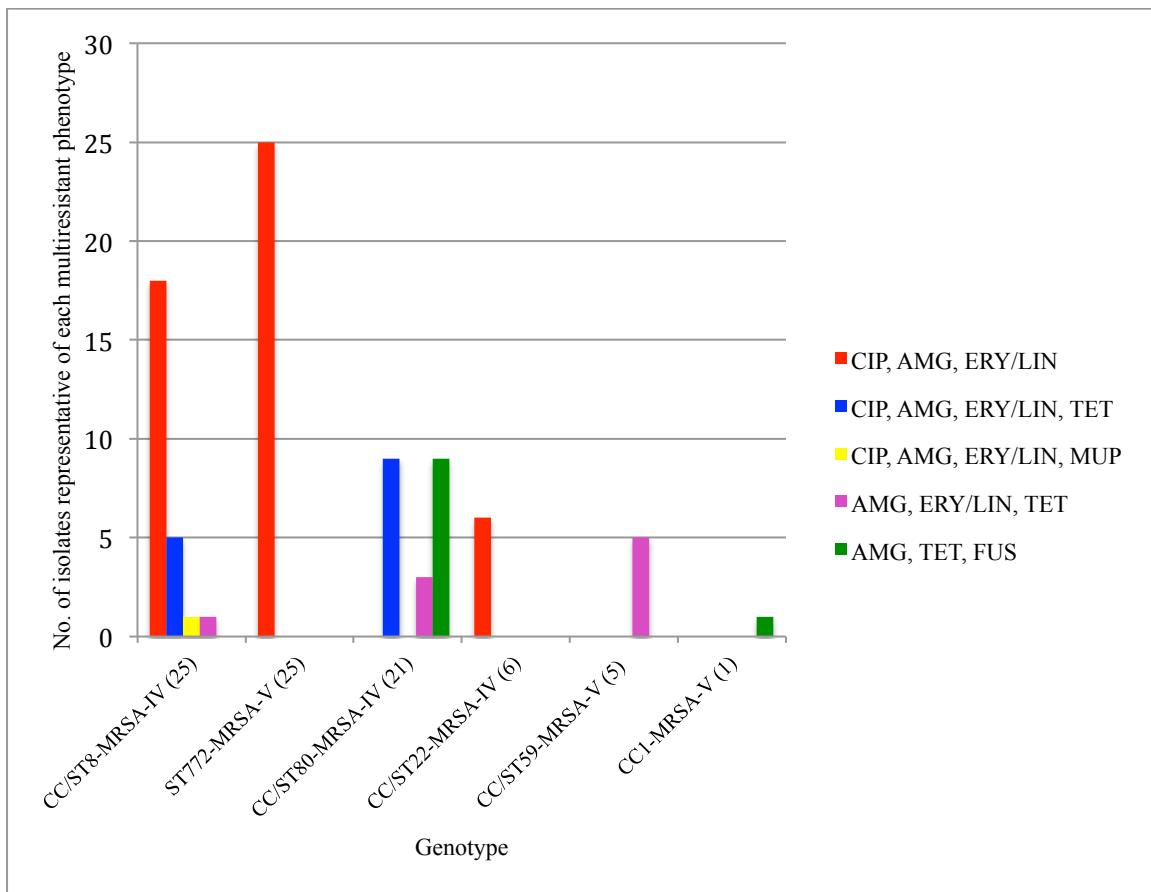
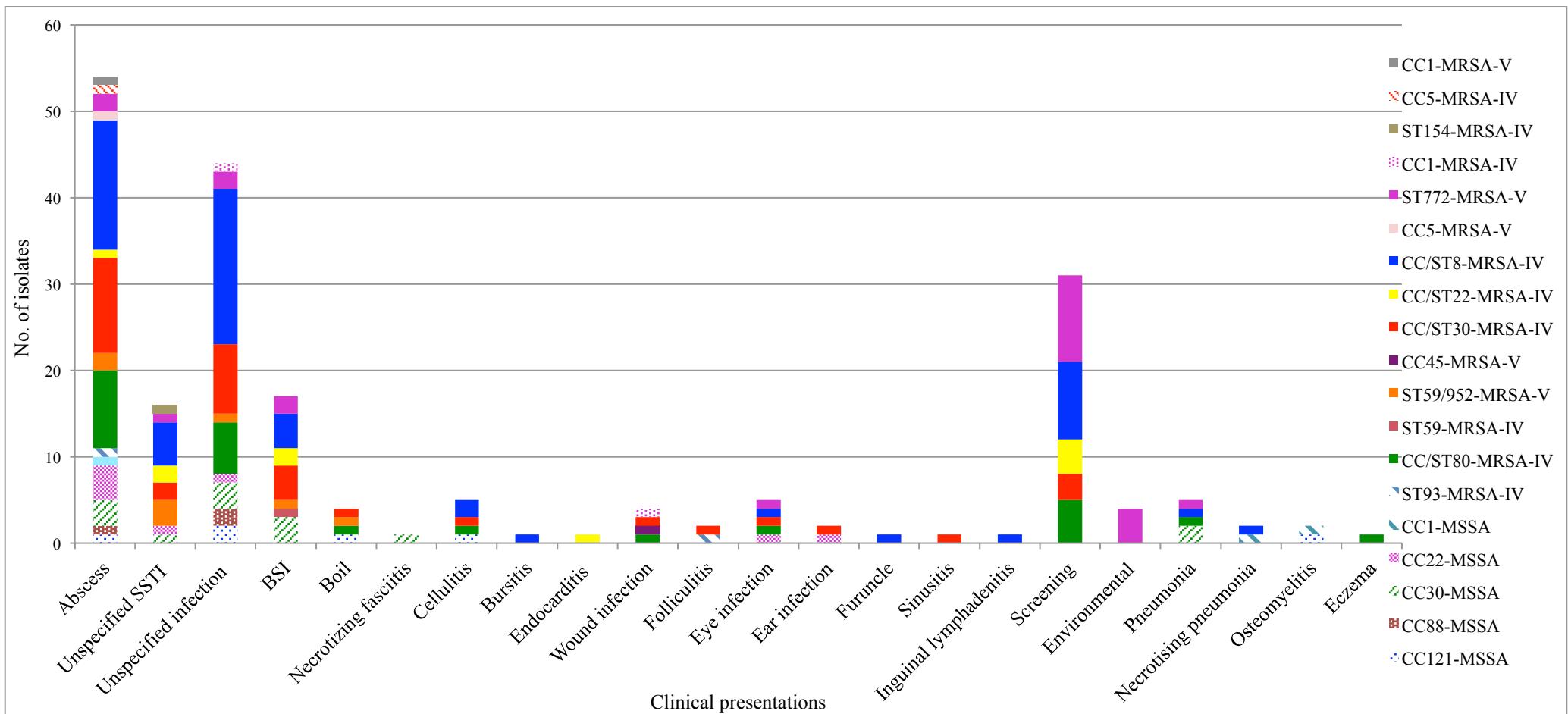


Supplemental Table S1. Novel PCR primers used in the present study

Antimicrobial resistance gene target	Primer name	Nucleotide sequence (5'-3')	Product size (bp)	Genbank accession no.
<i>qacC</i>	qacCF	CCATACCGATTCAATGATTCCCTT	525	Y16944.1
	qacCR	GCATGATGAAGCTGTAAGGC		
<i>msr(A)</i>	msrAF	GCACTTATTGGAGGTAATGGTACTGGC	503	AB013298.1
	msrAR	TGACGTTGTTGTTCTAACTGTTCTT		
<i>dfrS1</i>	dfrS1F	GTCGCTCACGATAAACAAAGAGT	160	AB049452.1
	dfrS1R	TACGTCTATTGGCAATGGCTTCCC		
<i>Inu(A)</i>	InuAF	AAGTTGAGCTCTTGAAATGC	345	AM184101.1
	InuAR	ACTCATTGGTTAGATGGAGGC		
<i>mph(C)</i>	mphCF	ATCAATTACACATCCAACCTCAAAC	348	AB013298.1
	mphCR	CGAGTGTTCAGCTAATGTGTTAAT		
<i>blaZ</i>	blaZF	TTCAAACAGTTCACATGCCAAAGAG	384	AB074882.1
	blaZR	AGAACCGTTGCTGTATTATCAC		



Supplemental Fig. S1. Multiresistant phenotypes detected among *pvl*-positive MRSA. Eighty-three of the 190 *pvl*-positive MRSA isolates exhibited multiresistance (43.7%) i.e. exhibited resistance to three or more classes of clinically used antimicrobial agents tested including fluoroquinolones (ciprofloxacin, CIP), aminoglycosides (AMG), erythromycin/lincomycin (ERY/LIN), tetracycline (TET), mupirocin (MUP) and fusidic acid (FUS). Numbers (*n*) in parenthesis indicate the number of multiresistant isolates within each genotype.



Supplemental Fig. S2. Clinical details for each genotype identified among the *pvl*-positive MRSA and MSSA isolates investigated. Clinical details were available for 170 MRSA and 32 MSSA isolates. Abbreviations: SSTI, skin and soft tissue infection; BSI, bloodstream infection.