



Fig S2. Core genome maximum likelihood phylogenetic tree of 689 MSSA isolates included those from the US (n=49) and Latin America (n=640). Rings from the inner to outer rim are: *i*) CziE phenotype, *ii*) rapid test result, *iii*) BlaZ type, *iv*) geographic origin of the isolate. Highlighted regions on tree branches highlight the major clonal complex (CC) of *S. aureus*.