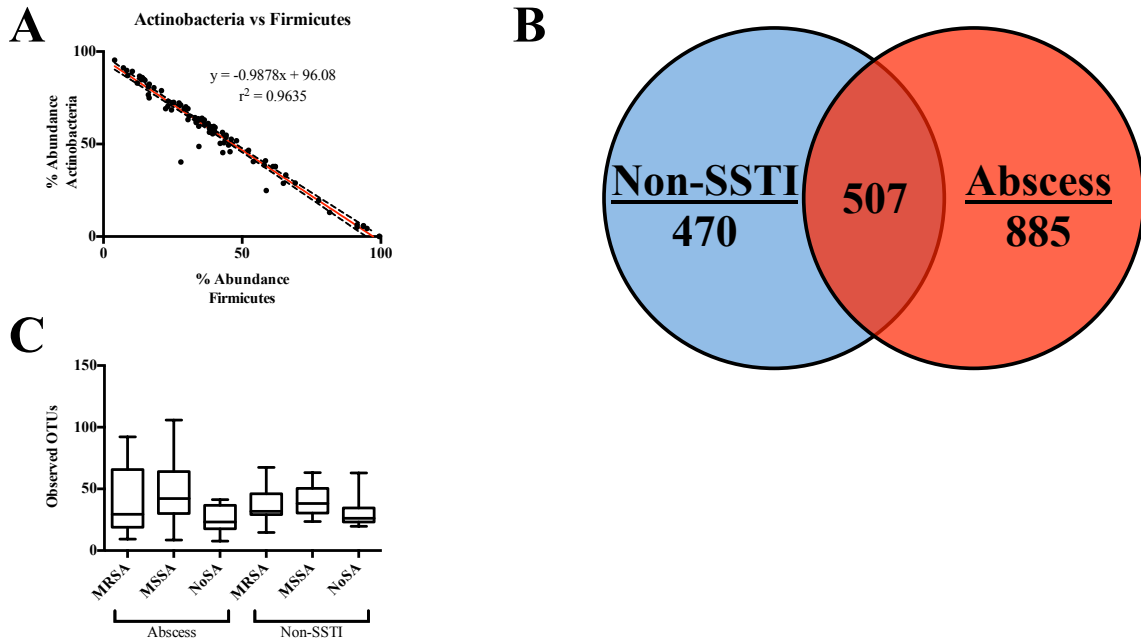
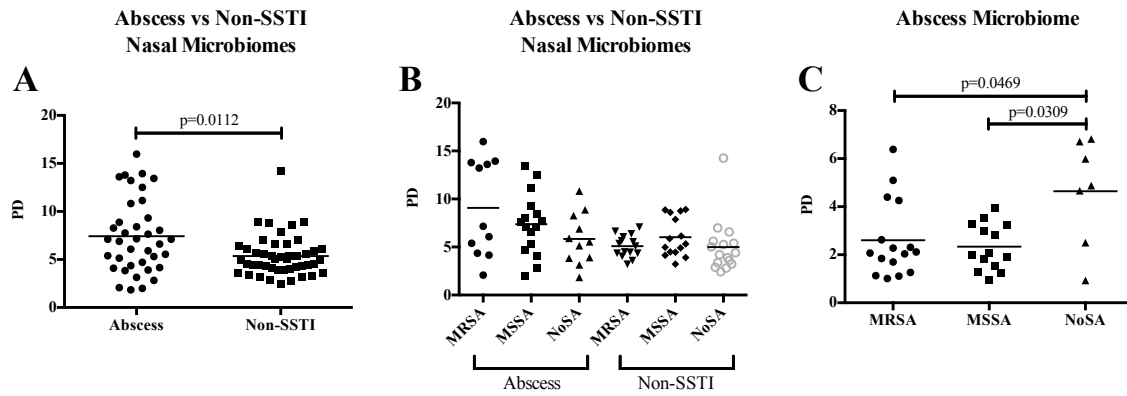


Supplementary Material



Supplementary Figure 1. Characterization of the nasal microbiomes. **A**, Inverse correlation between Actinobacteria and Firmicutes for all nasal samples (slope (m) = -0.9878). Red line and inset equation represent the best fit line ($y = \text{slope}(x) + y\text{-intercept}$). Dashed lines show the 95% confidence interval. $r^2 =$ Coefficient of determination. **B**, Venn-diagram representing the number of Operational Taxonomic Units (OTUs) that were unique as well as shared between the Non-SSTI and abscess nasal groups. **C**, The number of OTUs for individuals colonized (MRSA and MSSA) or not colonized (NoSA) with *S. aureus* that either did (Abscess) or did not develop SSTI (Non-SSTI). Each box represents the interquartile range with the mean shown within. The whiskers spread from the minimum to maximum values.



Supplementary Figure 2. Phylogenetic diversity (PD) as determined using Faith's index between the **A**, abscess and Non-SSTI nasal microbiomes and **B**, various nasal microbiome subgroupings as determined by *S. aureus* colonization status (MRSA, MSSA, NoSA). **C**, PD was also computed for the abscess cavity microbiomes. The various subgrouping are based on infecting *S. aureus* strain (MRSA, MSSA, NoSA).

Supplementary Table 1: Study Participant Characteristics*

	Abscess (n=38)	Non-SSTI (n=46)
Age		
Median years (range)	20 (17-33)	20.5 (18-39)
Race / Ethnicity^a		
White, non-Hispanic	28 (74)	- ^b
Hispanic	5 (13.2)	-
Black, non-Hispanic	3 (7.9)	-
Other, non-Hispanic	1 (2.6)	-
Nasal Colonization		
MRSA	11 (28.9)	15 (32.6)
MSSA	16 (42.1)	15 (32.6)
NoSA	11 (28.9)	16 (34.8)
Abscess Colonization		
MRSA	16 (42.1)	NA
MSSA	15 (39.5)	NA
NoSA	7 (18.4)	NA
Site of Infection^c		
Lower extremity	19 (50)	NA
Ankle	1 (2.6)	
Buttock	5 (13.2)	
Foot	1 (2.6)	
Knee	7 (18.4)	
Thigh	5 (13.2)	
Upper extremity	11 (28.9)	NA
Arm	2 (5.3)	
Elbow	5 (13.2)	
Finger	1 (2.6)	
Forearm	3 (7.9)	
Thorax	4 (10.5)	NA
Axilla	3 (7.9)	
Back	1 (2.6)	
Head and neck	3 (7.9)	NA
Neck	2 (5.3)	
Scalp	1 (2.6)	
Hygiene Study Group^d		
Standard	8 (21)	20 (43.5)
Enhanced Standard	11 (28.9)	20 (43.5)
Chlorhexidine	19 (50)	6 (13)
Known/Suspected SSTI/MRSA Infection in the Past Year^e	2 (5.3)	

*Unless specified, numbers in parenthesis correspond to percentage of total individuals in either Abscess or Non-SSTI groups.

Abbreviations: Abscess, individuals that developed SSTI; Non-SSTI, individuals that did not develop SSTI; MRSA, Methicillin-Resistant *Staphylococcus aureus*; MSSA, Methicillin-Sensitive *Staphylococcus aureus*; NoSA, No *Staphylococcus aureus*; NA, Not Applicable

^aRace / Ethnicity data for Non-SSTI individuals as well as one abscess individual was not obtained.

^bDashes correspond to data not available

^cSite of Infection data for one individual was not obtained

^dMilitary trainees were enrolled in an ongoing hygiene trial aimed at preventing SSTI prior to this study.

^eData for 2 individuals was not obtained.

Supplementary Table 2: Microbiome Composition Differences

Community-1	Community-2	Jaccard p-value^a	Φ_{yc} p-value^a
Nasal microbiomes- <20 years old	Nasal microbiomes- Ages 20-29	0.180	0.490
Nasal microbiomes- Ages 20-29	Nasal microbiomes- >29 years old	0.612	0.731
Nasal microbiomes- <20 years old	Nasal microbiomes- >29 years old	0.276	0.675
Abscess microbiomes- Upper extremities	Abscess microbiomes- Lower extremities	0.378	0.257
Abscess microbiomes- Upper extremities	Abscess microbiomes- Thorax	0.486	0.515
Abscess microbiomes- Upper extremities	Abscess microbiomes- Head/Neck	0.536	0.725
Abscess microbiomes- Lower extremities	Abscess microbiomes- Thorax	0.305	0.379
Abscess microbiomes- Lower extremities	Abscess microbiomes- Head/Neck	0.519	0.512
Abscess microbiomes- Head/Neck	Abscess microbiomes- Thorax	0.435	0.063

^aP-values are the result of performing analysis of molecular variance (AMOVA) on the Jaccard and Φ_{yc} distance matrices.

Supplementary Table 3. Percent abundance of each taxon per sample according to the GreenGenes database. Each column represents one sample and is labeled with sample ID, sample location (abscess cavity or nasal), and SSTI/*S. aureus* colonization status (Abscess or Non-SSTI; MRSA, MSSA, or NoSA). The total number of reads associated with each sample is included at the bottom of each column (See excel file in Supplemental Materials).

Supplementary Table 4: Differential abundance of OTUs using Metastats

OTU^a	Taxonomy^b	Community-1 (Mean Percent Abundance)	Community-2 (Mean Percent Abundance)	p-value	q-value
0001	<i>Staphylococcus</i> (g)	<i>S. aureus</i> positive nares (34.78)	<i>S. aureus</i> negative nares (20.63)	0.004	0.018
0003	<i>Corynebacterium</i> (g)	<i>S. aureus</i> positive nares (2.19)	<i>S. aureus</i> negative nares (9.15)	0.002	0.009
0014	Proteobacteria (p)	Abscess nares (0.29)	Non-SSTI nares (0.99)	0.002	0.005
0022	Proteobacteria (p)	Abscess nares (0.005)	Non-SSTI nares (0.45)	0.021	0.041
0029	Proteobacteria (p)	Abscess nares (0.02)	Non-SSTI nares (0.17)	0.005	0.011

^aOperational Taxonomic Unit (OTU) designation as assigned by mothur

^b(g), Genus; (p), Phylum