The indigenous microbiota of the nasal cavity plays important roles in human health and disease. Patterns of spatial variation in microbiota composition may help explain Staphylococcus aureus colonization and reveal interspecies and species-host interactions. To assess the biogeography of the nasal microbiota, we sampled healthy subjects, representing both S. aureus carriers and noncarriers at three nasal sites (anterior naris, middle meatus, and sphenoid recess). Phylogenetic compositional and sparse linear discriminant analyses revealed communities that differed according to site epithelium type and S. aureus culture-based carriage status. Corynebacterium accolens and C. pseudodiphtheriticum were identified as the most important microbial community determinants of S. aureus carriage, and competitive interactions were only evident at sites with ciliated pseudostratified columnar epithelium. In vitro cocultivation experiments provided supporting evidence of interactions among these species. These results highlight spatial variation in nasal microbial communities and differences in community composition between S. aureus carriers and noncarriers.