Nasal microbiome disruption and recovery after mupirocin treatment in *Staphylococcus aureus* carriers and noncarriers

#### **Authors**

Valérie O. Baede¹#, Anaïs Barray <sup>2,3#</sup>, Mehri Tavakol¹, Gérard Lina <sup>2,3</sup>, Margreet C. Vos ¹¶, Jean-Philippe Rasigade<sup>2,3</sup>¶\*

### **Author affiliations**

- 1. Department of Medical Microbiology and Infectious Diseases, Erasmus MC University Medical Center Rotterdam, Rotterdam, the Netherlands
- 2. CIRI, Centre International de Recherche en Infectiologie, Inserm U1111, Université Lyon 1, Ecole Normale Supérieure de Lyon, Lyon, France
- 3. Centre National de Référence des Staphylocoques, Institut des Agents infectieux, Hôpital de la Croix Rousse, Hospices Civils de Lyon, Lyon, France
- \* Corresponding author
- # Contributed equally
- ¶Contributed equally

### Supplementary information file

### Members of the MACOTRA Study Group:

Valérie O. Baede <sup>1</sup>, Anaïs Barray <sup>2,3</sup>, Sake J. de Vlas <sup>4</sup>, Anneke S. de Vos <sup>4</sup>, Arya Gupta <sup>5</sup>, Antoni P. A. Hendrickx <sup>6</sup>, Gwenan M. Knight <sup>7</sup>, Mirjam E. E. Kretzschmar <sup>6,8</sup>, Gérard Lina <sup>2,3</sup>, Jodi A. Lindsay <sup>5</sup>, Jean-Philippe Rasigade <sup>2,3</sup>, Leo Schouls <sup>6</sup>, Mehri Tavakol <sup>1</sup>, Margreet C. Vos <sup>1</sup>, Willem J. B. van Wamel <sup>1</sup>, Adam A. Witney <sup>5</sup>

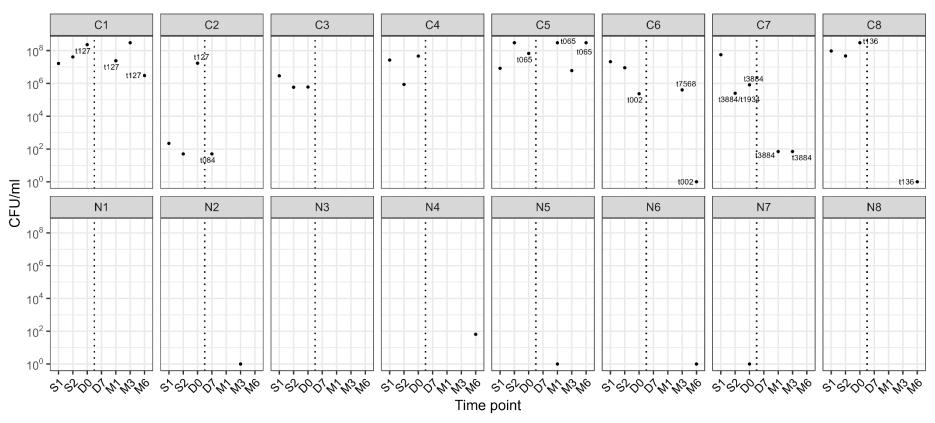
#### **Affiliations**

- 1. Department of Medical Microbiology and Infectious Diseases, Erasmus MC University Medical Center Rotterdam, Rotterdam, the Netherlands
- 2. CIRI, Centre International de Recherche en Infectiologie, Inserm U1111, Université Lyon 1, Ecole Normale Supérieure de Lyon, Lyon, France
- 3. Centre National de Référence des Staphylocoques, Institut des Agent infectieux, Hôpital de la Croix Rousse, Hospices Civils de Lyon, Lyon, France
- 4. Department of Public Health, Erasmus MC University Medical Center Rotterdam, Rotterdam, the Netherlands
- 5. Institute for Infection and Immunity, St George's, University of London, London, United Kingdom
- 6. Center for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands
- 7. Centre for Mathematical Modelling of Infectious Diseases, Infectious Disease Epidemiology, London School of Hygiene and Tropical Medicine, London, United Kingdom
- 8. Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht, Utrecht University, Utrecht, The Netherlands

# Supplementary table 1. Risk factors for S. aureus acquisition

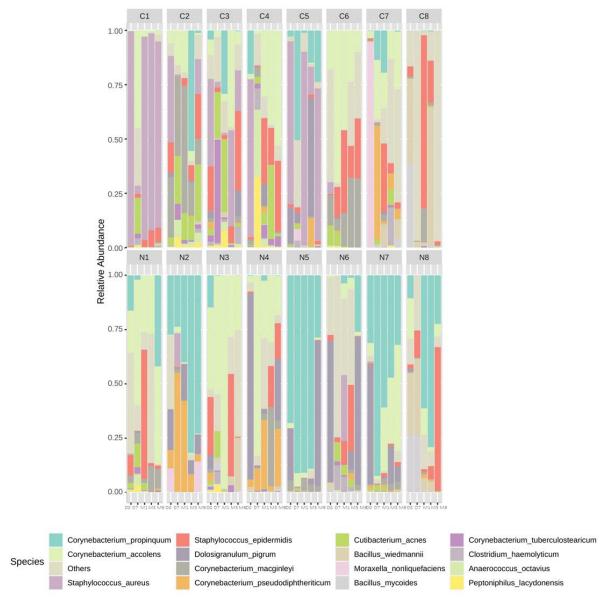
		Cohort	Cohorts	
		Noncarrier	Carrier	
Total		8	8	
Hormonal contraception		1	4	
Dairy consumption				
	Daily	6	6	
	Weekly	1	1	
	Monthly	0	1	
Disinfectants				
	Daily	3	1	
	Weekly	2	1	
Smoking				
	Daily	1	0	
Alcohol consumption				
	Daily	1	2	
	Weekly	2	2	
	Monthly	2	3	
	< 1x per month	2	1	
Nose picking				
	Daily	5	2	
	Weekly	2	5	
	Monthly		1	
	< 1x per month	1		
Household size				
	1		1	
	2	5	5	
	3	3	1	
	4		1	
Team sport or communal	gym			
	Weekly	2	2	
	Monthly		1	
Sauna visits				
	< 1x per month	1	3	
Healthcare or beauty pract	tice			
	< 1x per month	1	2	
Public transport				
	Daily	1	4	
	Weekly	0	3	
	Monthly	1	0	
	< 1x per month	3	1	

### Supplementary Figure 1. S. aureus culture dynamics in carriers and noncarriers.



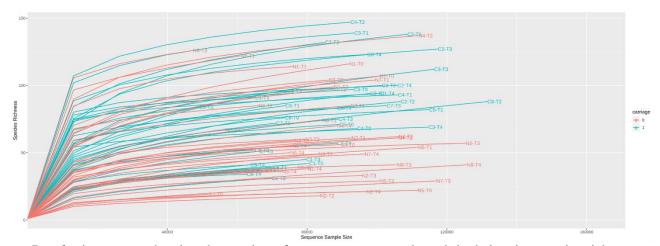
Sampling took place at screening time points S1 and S2. During the study phase, nasal samples were taken 1 day pre-treatment (D0) and 2 days (D7), 1 month (M1), 3 months (M3) and 6 months (M6) post-treatment. *S. aureus*-positive cultures are depicted as black dots, with bacterial load given on the y-axis. The vertical dotted line shows time of treatment. Spa-typing results are given as dot labels. Recolonization was defined as a *S. aureus* positive culture (>8 CFU/ml) post-decolonization

### Supplementary Figure 2. Nasal microbiota of study participants in time.



Shown are the detailed species proportions in nasal samples from 8 *S. aureus* carriers (top panel) and noncarriers (bottom panel), inferred through 16S rRNA metabarcoding. Samples were taken immediately before decolonization (D0) and after 7 days (D7) and 1 (M1), 3 (M3), and 6 (M6) months.

## **Supplementary Figure 3. Rarefaction plot**



Rarefaction curves showing the number of sequences per sample and the belonging species richness uncovered; carriers in red, noncarriers in blue. Curves reaching a plateau mean that a deeper sequencing would not result in significant species richness increase.