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## Genomic analysis report

### Archive\_test

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*Contact:*

Deborah MERDA

*Phone:*

01 49 77 28 33

*E-mail:*

deborah.merda@anses.fr

*Anses*

Laboratory for Food Safety  
Maisons-Alfort Location

*Test report addressed to*  
XXXXXXXXXXXXXXXXXX

Request	
Archive name	Archive_test
Number of analyzed strains	2
Unanalyzed strains	NA
Date of analysis	May 28, 2020

## 1 Results

### 1.1 Background

Strains ID	Context of Isolation
05CEB51	Food
05CEB52	Milk

### 1.2 Quality report

Strains ID	Number of contigs	N50	Closest reference genome
05CEB51	5	2786542	Staphylococcus_aureus_AJ_938182
05CEB52	2	2586542	Staphylococcus_aureus_CP_000703

### 1.3 Identification and typing strains

Strains ID	Species	Sequence Type
05CEB51	<i>aureus</i>	5
05CEB52	<i>aureus</i>	2

### 1.4 Enterotoxin detected

Strain ID	Enterotoxins detected
05CEB51	seu(2), sex(2), seg(1), sec(1), seo(19), sen(1), sem(1), sel(1), sei(1), seh(1)
05CEB52	seo(99), sen(1)

*\*in red, are indicated enterotoxin coding gene for which a new variant was identified.*

1.5 Strain clustering

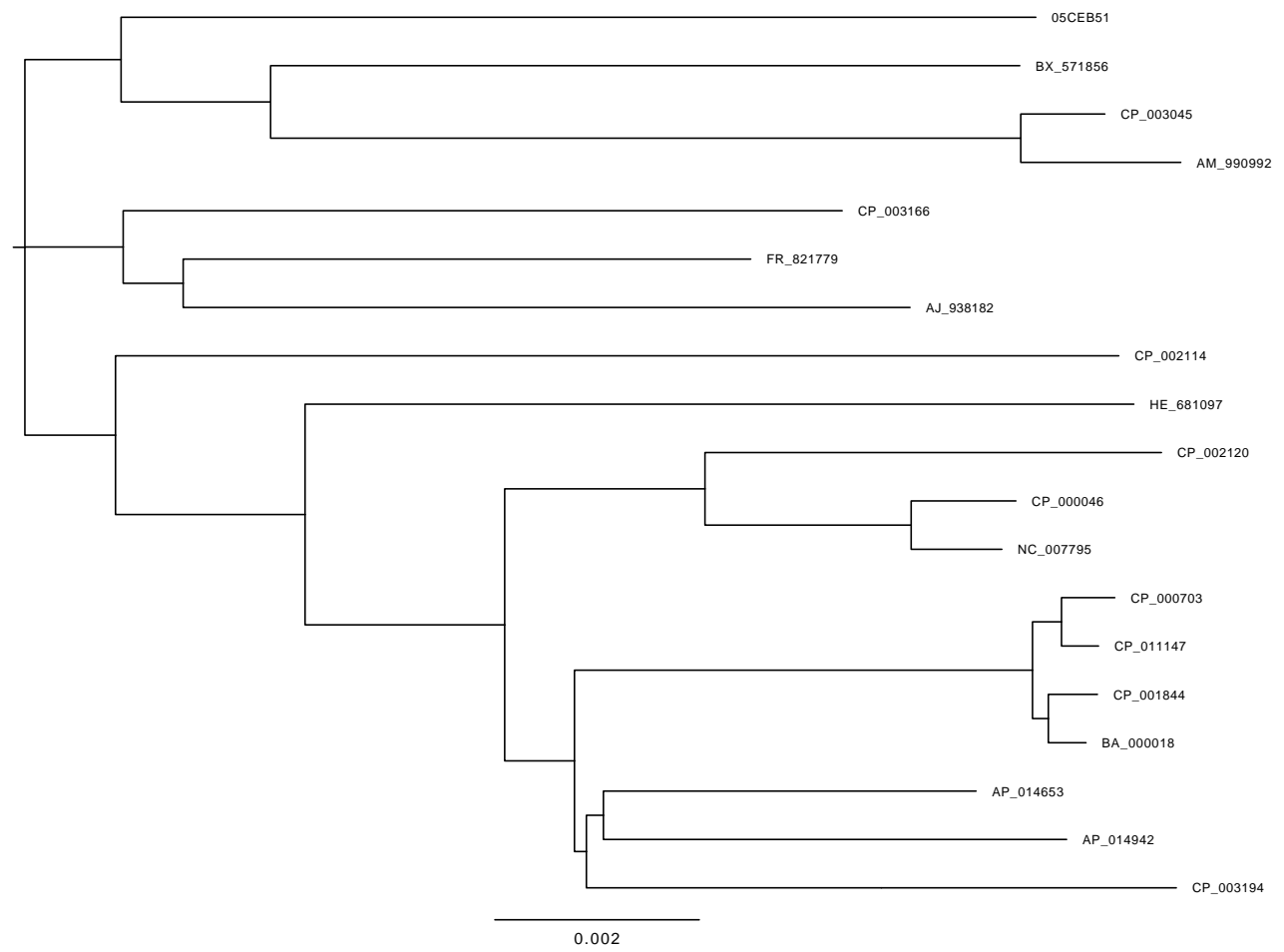


Figure 1: Phylogeny relatedness between reference genome of Staphylococcus sp. and genomes from this study. This phylogeny was obtained using Neighbor joining algorithm and based on distance matrix from k-mer analysis implemented in Fastosh.

2 Complementary informations

The parameters to evaluate quality of reads and assembly are presented in the quast report available in result archive. The thresholds used for assembly are presented in Anses procedure LSA-INS-1477 and the recommendations of quality parameters are described in guidance document XXX.

Report automatically edited, the May 28, 2020.

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It includes X annex(s)