



Bacterial Typing by Whole Genome
Sequencing

Patient ID SA00338997	Patient Name SAMPLEREPORT, BTWGS	Birth Date 1984-12-25	Gender F	Age 32
Order Number SA00338997	Client Order Number SA00338997	Ordering Physician CLIENT,CLIENT	Report Notes	
Account Information C7028846 DLMP Rochester		Collected 01 May 2017 08:00		

Bacterial Typing, Whole Genome Seq

MCR

SOURCE: APPENDIX

BACTERIAL TYPING, WHOLE GENOME SEQ

FINAL

A link to the interpretive report has been sent to the registered email address provided.

Received: 01 May 2017 09:47

Reported: 01 May 2017 09:49

Performing Site Legend

Code	Laboratory	Address
MCR	Mayo Clinic Laboratories - Rochester Main Campus	200 First Street SW, Rochester, MN 55905



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May 1, 2017

FACILITY NAME
ADDRESS LINE 1
ADDRESS LINE 2
CITY, STATE ZIP

Dear Doctor XYZ:

The following are results of Bacterial Strain Typing by Whole Genome Sequencing performed on isolates of *Staphylococcus aureus* received on January 1, 2017:

Submitted Isolates

Patient Name	Patient ID	Order Number
Patient A	M100000000	B123456789
Patient B	M200000000	B234567890
Patient C	M300000000	B345678901
Patient D	M400000000	B456789012
Patient E	M500000000	B567890123
Patient F	M600000000	B678901234
Patient G	M700000000	B789012345
Patient H	M800000000	B890123456

Result Interpretation (also see attached Minimum Spanning Tree)

- ‘Group 1’: B123456789, B234567890, B345678901 and B456789012 are related to one another
- B567890123, B678901234, B789012345 and B890123456 are unrelated

Methods

Whole genome sequencing was performed using Illumina MiSeq instrumentation and chemistry with Illumina Nextera XT library chemistry. Assembly and core genome multilocus sequence typing analysis were performed with Ridom SeqSphere+ software. Isolate relatedness was based on the total number of allelic differences between each isolate, applying the thresholds shown in the table below. A Minimum Spanning Tree was generated and is attached. Isolates (and type strains for reference) are shown in circles and the allelic differences numerated on linking lines between the circles.

Interpretation Guide For Relatedness Between Test Isolates	
Relationship	Number of Allelic Differences Between Isolates
Unrelated	30 or more differences
Possibly related	9 to 29 differences
Related	0 to 8 differences

This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the U.S. Food and Drug Administration.

Sincerely,

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 Division of Clinical Microbiology
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RP:tjd

