

Bacterial 16S rRNA Phylogenetic Typing Report

The following report summarises the bacterial taxa detected in the sample. The 16S rRNA assay estimates taxonomic relative abundance based on 16S rRNA gene copy numbers. As the number of 16S rRNA gene copies varies between bacterial taxa, these estimates may not directly reflect the relative abundance of individual bacterial cells. The 16S rRNA gene (V1–V3 regions) was sequenced using Illumina technology and analysed using an in-house developed bioinformatics pipeline, with taxonomic assignment performed against the NCBI Prokaryotic database. As the assay detects bacterial DNA, it cannot establish the viability of the organisms detected. Organisms with a relative abundance of less than 1% are excluded from this report unless considered clinically significant.

Date: 06-10-26

Micropathology Lab Number: 7654321**Your Patient/Lab Number:** 2026-002**Sample Type:** Swab

Result Summary: Staphylococcus aureus**Comments:**

Detailed Findings:

Organism	Relative abundance (%)	Best matches/ Comments
<i>Staphylococcus aureus</i>	100	

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Date: 06-10-26

Micropathology Lab Number: 1234567

Your Patient/Lab Number: 2026-001

Sample Type: Mastoid fluid

Result Summary: Multiple bacterial species detected

Comments:

Detailed Findings:

Final taxonomy	Relative abundance (%)	Best matches/comments
<i>Parvimonas micra</i>	18.9	
<i>Porphyromonas</i> sp.	16.1	<i>Porphyromonas asaccharolytica</i> , <i>Porphyromonas uenonis</i> , <i>Porphyromonas vaginalis</i>
<i>Porphyromonas somerae</i>	7.9	
<i>Peptoniphilus lacrimalis</i>	7.4	
<i>Jonquetella anthropi</i>	5.7	
<i>Campylobacter ureolyticus</i>	5.4	
<i>Peptoniphilus grossensis</i>	4.7	
Clostridia class	3.0	
<i>Porphyromonas uenonis</i>	2.8	
Peptoniphilaceae family	2.7	98.3% ID to <i>Khoudiadiopia massiliensis</i>
Peptoniphilaceae family	2.6	
<i>Gleimia</i> sp.	1.6	97.8% ID to <i>Gleimia europaea</i>
<i>Peptococcus niger</i>	1.6	
<i>Anaerococcus</i> sp.	1.5	
Prevotellaceae family	1.3	