

**invivo<sup>®</sup>**

The Human Microbiome Company

TEST REPORTED: 28/10/2022  
 TEST RECEIVED: 28/10/2022  
 PATIENT NAME: FIRST LAST  
 PATIENT DOB: 20/10/2022

CLINICIAN NAME: CLINICIAN  
 SAMPLE TYPE: SALIVA  
 SEX: FEMALE

Lab Director:  
 Emma Beamish, PhD



## Opportunistic Bacteria (Orange Complex)

RESULTS:

RANGE:

			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
<i>Campylobacter rectus</i>	9.0							3.5-10.5
<i>Capnocytophaga gingivalis</i>	11.7							8.9-14.0
<i>Enterococcus faecalis</i>	<DL							<DL
<i>Fusobacterium nucleatum</i>	14.1							3-16.5
<i>Lactobacillus spp.</i>	6.9	HIGH						< 5.6
<i>Parvimonas micra</i>	11.8	HIGH						2.2-11.3
<i>Peptostreptococcus anaerobius</i>	11.7							6.5-15.0
<i>Prevotella intermedia</i>	13.3	HIGH						<4.9
<i>Streptococcus mutans</i>	2.7							<3.8



Scan for more information and resources on Oral EcologiX

**Disclaimer:** This test was developed, and its performance characteristics determined by Invivo Diagnostics. This test is not intended for use by consumers or physicians as a means to cure, treat, prevent, diagnose or mitigate any disease or other medical condition. The information contained in this document is in no way to be taken as prescriptive nor to replace the physicians duty of care and personalised care practices.

**Pathogens (Red Complex) RESULTS:**

**RANGE:**

			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
	<i>A. actinomycetemcomitans</i>	<DL						<DL
	<i>Porphyromonas gingivalis</i>	12.6						<DL
	<i>Tannerella forsythia</i>	13.9						<DL
	<i>Treponema denticola</i>	2.7						<DL

**Fungi**

**RESULTS:**

**RANGE:**

			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
	<i>Candida albicans</i>	<DL						<2.6

The Oral EcologiX™ profile utilises the highly sensitive quantitative PCR (qPCR) TaqMan technology for analysis of the oral microbiota. Microbial genes of interest are quantified within a sample and their abundances are normalised to an endogenous and highly conserved gene. The qPCR results are therefore reported as the relative abundance of a microorganism as proportional to the whole microbial community.



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