Oral Microbiome Test Analysis

Name	Example User	**Age**	24
Country	United Kingdom	**Sample ID**	484682552147
Sampling Date	12 Apr 2024 09:37	**Test Date**	19 Apr 2024 12:48
Test Profile	Oral Microbiome	**Technology**	Shotgun metagenomics

Welcome to your oral microbiome report!

The oral microbiome is the collection of microorganisms – mostly bacteria – that live in your mouth, and it has an important influence on both oral and overall health. The oral environment is very complex, with different micro-environments around the teeth, gums, and tongue. This test uses a saliva sample which is the easiest to collect and provides good information about the overall oral microbiome. This report includes multiple analyses of your oral microbiome – looking at the types and amounts of beneficial (good) and pathogenic (disease-causing) bacteria; important functional capabilities of the microbiome, and patterns associated with specific health risks.

Results at a glance

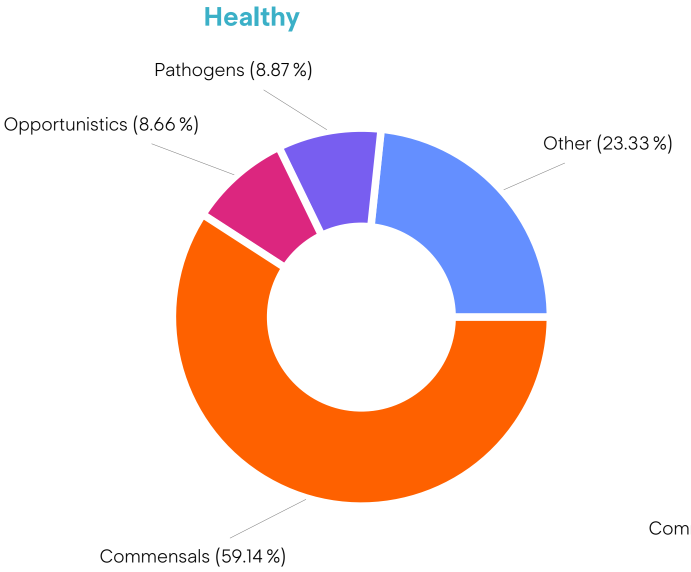
Microbiome balance	Balanced	**Pathogens**	1 above normal levels
Beneficial bacteria	3 below normal levels	**Health risk scores**	1 high-risk scores

Contents

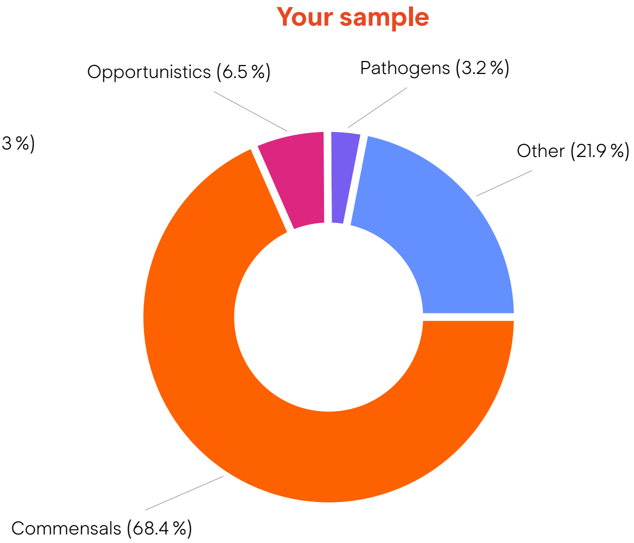
This report will guide you through the key aspects of the oral microbiome that influence your health and wellbeing. Background information and actionable advice is provided in each section. Please note that each section heading is clickable as a link to the relevant section.

Microbiome balance

The oral microbiome contains a huge variety of microbes, many of which are commensal with neutral or beneficial impacts on health, and others which could be pathogens or opportunistic pathogens. The overall balance of your microbiome between commensal and pathogenic is presented here. Unlike the gut or vaginal microbiomes, there are no clear links between oral microbiome diversity and health, so diversity metrics are not included.

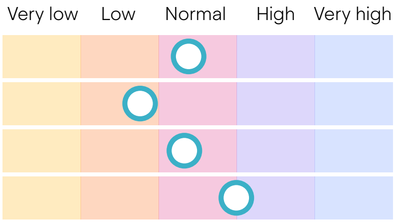


This chart shows the proportions of selected bacterial groups in a representative healthy sample.



This chart shows the proportions of selected bacterial groups in your sample.

Other (21.9 %)	Normal range: 17.36–29.30 %	Normal
Pathogens (3.2 %)	Normal range: 5.02–12.72 %	Low
Opportunistics (6.5 %)	Normal range: 2.34–14.98 %	Normal
Commensals (68.4 %)	Normal range: 49.77–68.51 %	Normal



These doughnut charts compare the balance of commensal and pathogenic or potentially pathogenic microbes in your sample to an average healthy sample. The sliders for each category help to quantify this balance. A healthy oral microbiome will have normal levels of all three groups, whereas an unhealthy microbiome might contain lower levels of commensal bacteria and/or higher levels of pathogens or opportunistic pathogens.

The balance of microbes in your sample is **similar to an average healthy oral microbiome**, though the levels of individual microbes are still important for health – see the following sections of this report. For tips on how to maintain a healthy microbiome see the **Recommendations** section.

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Pathogens

This test checks your sample for 25 microbes with proven pathogenic (disease-causing) potential: *only those detected are reported.* Some of these bacteria may exist harmlessly within the normal oral microbiome, but could be problematic if their population grows too large. Oral pathogens are involved in plaque formation, caries development, and the progression of gum disease and inflammation (see **Key terms**). Your results show what the normal range for each microbe is in a healthy population and how your sample compares.

We detected 14 potential pathogens in your sample, and **1 are above the levels expected in a healthy population**.

You should interpret your results in the context of any symptoms you may have. These results do not equate to a clinical diagnosis, and you should consult a medical professional before making any decisions about treatments. Please see the **Recommendations** section for more information. Please note that descriptions of each of these species are provided in the **Key bacteria** section. You can also click on the name of any of the bacterial species below to jump to the relevant section.

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Schaalia odontolytica: 1.7 %	Normal range: 1.77–9.55 %	Low
Streptococcus pneumoniae: 0.6 %	Normal range: 0.00–1.21 %	Normal
Lancefieldella parvula: 0.5 %	Normal range: 0.07–1.28 %	Normal
Prevotella intermedia: 0.1 %	Normal range: 0.05–0.53 %	Normal
Treponema denticola: 0.09 %	Normal range: 0.00–0.13 %	Normal
Streptococcus mutans: 0.07 %	Normal range: 0.00–0.15 %	Normal
Ligilactobacillus salivarius: 0.05 %	Normal range: 0.00–0.02 %	Very High
Streptococcus pyogenes: 0.03 %	Normal range: 0.00–0.43 %	Normal
Campylobacter rectus: 0.02 %	Normal range: 0.00–0.11 %	Normal
Dialister pneumosintes: 0.02 %	Normal range: 0.00–0.08 %	Normal
Tannerella forsythia: 0.02 %	Normal range: 0.00–0.26 %	Normal
Porphyromonas gingivalis: 0.01 %	Normal range: 0.00–0.26 %	Normal
Selenomonas sputigena: 0.01 %	Normal range: 0.00–0.34 %	Normal
Campylobacter showae: 0.0 %	Normal range: 0.00–0.41 %	Low

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Opportunistic pathogens

This test also checks for 16 microbial taxa that are known to be opportunistic pathogens; as for the pathogens, *only those detected are reported.* Most of the time these microbes do not cause any problems and many will be present in a healthy sample. However, if the level of these microbes are higher than normal this could indicate that they are contributing to disease. Your results show what the normal range for each microbe is in a healthy population and how your sample compares.

We detected 11 potential opportunistic pathogens in your sample, and **3 are above the levels expected in a healthy population**.

You should interpret your results in the context of any symptoms you may have. These results do not equate to a clinical diagnosis, and you should consult a medical professional before making any decisions about treatments. See the **Recommendations** section for more information. Please note that descriptions of each of these species are provided in the **Key bacteria** section. You can also click on the name of any of the bacterial species below to jump to the relevant section.

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Prevotella histicola: 3.2 %	Normal range: 0.00–2.95 %	High
Prevotella veroralis: 1.3 %	Normal range: 0.00–2.08 %	Normal
Veillonella parvula: 1.0 %	Normal range: 0.04–1.33 %	Normal
Rothia aeria: 0.3 %	Normal range: 0.00–0.72 %	Normal
Limosilactobacillus fermentum: 0.2 %	Normal range: 0.00–0.02 %	Very High
Prevotella nigrescens: 0.1 %	Normal range: 0.00–2.29 %	Normal
Candidatus Saccharibacteria: 0.1 %	Normal range: Not Detected	High
Fusobacterium nucleatum: 0.09 %	Normal range: 0.00–0.25 %	Normal
Eikenella corrodens: 0.06 %	Normal range: 0.00–0.23 %	Normal
Prevotella denticola: 0.06 %	Normal range: 0.00–1.05 %	Normal
Leptotrichia shahii: 0.01 %	Normal range: 0.00–0.04 %	Normal

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Commensal bacteria

The microbes listed below are usually found in a healthy oral microbiome. Commensal microbes can be beneficial to oral health by preventing pathogenic microbes from attaching to teeth and gums, neutralising acids that could cause tooth decay, and sometimes actively killing harmful bacteria. Your results show what the normal range for each microbe is in a healthy population and how your sample compares.

Not all of the microbes below need to be present for your microbiome to be healthy, though if many are missing or at low levels there may be an imbalance in your overall microbiome – check the **Microbiome balance** section of the report, and see the **Recommendations** section for tips on how to maintain or restore a healthy oral microbiome. Please note that descriptions of each of these species are provided in the **Key bacteria** section. You can also click on the name of any of the bacterial species below to jump to the relevant section.

Streptococcus salivarius: 21.3 %	Normal range: 0.19–9.06 %	Very High
Rothia mucilaginosa: 8.8 %	Normal range: 3.93–20.97 %	Normal
Streptococcus mitis: 2.7 %	Normal range: 0.00–4.73 %	Normal
Veillonella dispar: 1.8 %	Normal range: 0.00–1.06 %	High
Streptococcus sanguinis: 1.7 %	Normal range: 0.05–1.19 %	High
Streptococcus oralis: 1.1 %	Normal range: 0.14–2.26 %	Normal
Streptococcus gordonii: 1.1 %	Normal range: 0.00–0.57 %	High
Veillonella rogosae: 1 %	Normal range: 0.44–4.15 %	Normal
Haemophilus parainfluenzae: 1 %	Normal range: 1.15–8.44 %	Low
Campylobacter concisus: 0.5 %	Normal range: 0.14–2.13 %	Normal
Prevotella melaninogenica: 0.4 %	Normal range: 0.18–10.93 %	Normal
Neisseria sicca: 0.2 %	Normal range: 0.06–1.28 %	Normal
Neisseria mucosa: 0.07 %	Normal range: 0.06–1.57 %	Normal
Actinomyces naeslundii: 0.02 %	Normal range: 0.00–0.47 %	Normal
Corynebacterium durum: 0.02 %	Normal range: 0.00–0.25 %	Normal
Corynebacterium matruchotii: 0.02 %	Normal range: 0.00–0.43 %	Normal
Neisseria flavescens: Not detected	Normal range: 0.02–0.49 %	Low
Neisseria perflava: Not detected	Normal range: 0.00–1.37 %	Low

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Health risks

In this section of your report you can view the levels of microbes that are associated with particular oral diseases, as well as relevant data on symptoms and lifestyle that you entered when registering your sample. This report cannot be used to diagnose any disease, but will provide you with a holistic view of each health risk, helping you to decide whether further investigations may be necessary.

Dental Caries – High risk

Dental caries, commonly known as tooth decay or cavities, are caused when oral microbes ferment sugars from foods and drinks to produce acids. These acids can dissolve the tooth enamel, and is especially problematic when the microbes are trapped close to the tooth in **plaque**. Initially, caries can appear as a white spot, and decay is reversible at this point with good oral hygiene and fluoride toothpaste. If more minerals are lost from the tooth than can be restored the enamel eventually breaks down, forming a cavity. If tooth decay is not treated it can cause pain, infection, and even tooth loss. Dentists commonly treat cavities by removing the decayed tooth tissue and filling the hole. You can reduce the risk of caries by maintaining good oral hygiene, including regular dental check-ups, and reducing your intake of sugary and acidic foods – see the **Recommendations** section for general advice on diet and oral hygiene.

Microbes

Limosilactobacillus fermentum: 0.2 %	Normal range: 0.00–0.02 %	Very High
Prevotella histicola: 3.2 %	Normal range: 0.00–2.95 %	High
Scardovia wiggsiae: Not detected	Normal range: Not Detected	Normal
Streptococcus mutans: 0.07 %	Normal range: 0.00–0.15 %	Normal
Streptococcus sobrinus: Not detected	Normal range: Not Detected	Normal

Symptoms summary

Relevant symptoms from the information registered with this sample are summarised here:

Symptom	Sample information
Tooth pain	No
Bad breath	No
Sensitive teeth	Yes
White spots	No
Yellow film on teeth	Yes
Fuzzy texture	Yes
Holes or pits	No
Grey/brown/black patches	None
Issues with sense of taste	No issues

Assessment

Your overall risk assessment for caries is **high**, as you have both symptoms and above-average levels of microbes that are associated with this disease. It is recommended that you seek a formal assessment from a dentist who can also create a personalised treatment and prevention plan for you.

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Gum disease – Low risk

Gum disease is an infection that can occur when untreated **plaque** builds up on teeth close the gums. **Gingivitis** is the earliest and reversible stage of gum disease, leading to **periodontitis** which is a serious infection that irreversibly damages the gums and tissues that support the teeth, including bone. The different stages of gum disease are associated with different types of bacteria that are involved in colonising and infecting the gums. The severity of gum disease depends on both the microbes that are present and the host immune response, so it is important to take into account both microbes and symptoms when assessing gum disease risk. There are different classification systems for gum disease microbes, but we use three categories here: ***Early colonisers*** come first and allow other microbes to attach to the teeth and gums, and are often present in healthy individuals. ***Bridging species*** attach to early colonisers and create the conditions that allow for aggregation of diverse bacteria including pathogens. ***Advanced infection*** species are associated with more severe disease, and include '**red complex**' bacteria.

Microbes

Early colonisers

Capnocytophaga gingivalis: 0.01 %	Normal range: 0.00–0.52 %	Normal
Capnocytophaga granulosa: Not detected	Normal range: Not Detected	Normal
Eikenella corrodens: 0.06 %	Normal range: 0.00–0.23 %	Normal
Streptococcus gordonii: 1.1 %	Normal range: 0.00–0.57 %	High
Streptococcus oralis: 1.1 %	Normal range: 0.14–2.26 %	Normal

Bridging species

Campylobacter rectus: 0.02 %	Normal range: 0.00–0.11 %	Normal
Campylobacter showae: 0.0 %	Normal range: 0.00–0.41 %	Low
Capnocytophaga periodontitidis: Not detected	Normal range: Not Detected	Normal
Fusobacterium nucleatum: 0.09 %	Normal range: 0.00–0.25 %	Normal
Fusobacterium periodonticum: Not detected	Normal range: 0.00–0.18 %	Low
Prevotella intermedia: 0.1 %	Normal range: 0.05–0.53 %	Normal
Prevotella nigrescens: 0.1 %	Normal range: 0.00–2.29 %	Normal
Veillonella parvula: 1.0 %	Normal range: 0.04–1.33 %	Normal
Veillonella tobetsuensis: Not detected	Normal range: Not Detected	Normal

Advanced infection

Aggregatibacter actinomycetemcomitans: Not detected	Normal range: 0.00–0.09 %	Low
Porphyromonas gingivalis: 0.01 %	Normal range: 0.00–0.26 %	Normal
Tannerella forsythia: 0.02 %	Normal range: 0.00–0.26 %	Normal
Treponema denticola: 0.09 %	Normal range: 0.00–0.13 %	Normal

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Symptoms summary

Gum disease symptoms are grouped here in order of increasing severity, starting with signs of plaque formation, followed by gingivitis and periodontitis.

Pre-gum disease (plaque)

Tooth pain	No
Issues with sense of taste	No issues
Yellow film on teeth	Yes
Fuzzy texture	Yes
Grey/brown/black patches	None

Gingivitis

Redness of the gums	No
Gums that bleed when brushing/flossing	Yes
Tender gums	No
Swollen gums	No
Gums that are receding	No

Periodontitis

Gums with pockets	No
Pus in the mouth	No
Teeth that become loose or have changed position	No

Assessment

Your overall risk assessment for gum disease is **low** as you do not have above-average levels of multiple microbes from the bridging species or advanced infection categories, or multiple symptoms normally associated with either gingivitis or periodontitis. Maintain good oral hygiene and monitor symptoms of plaque build up. Having a low risk assessment is not a formal diagnosis, and if you have any concerns about your oral health you should discuss them with your dentist.

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Halitosis – Low risk

Halitosis, or bad breath, is most often caused by oral microbes breaking down food into foul smelling chemicals, often sulphur-containing chemicals. This risk score is for halitosis caused by oral microbes, but smelly breath may also be a symptom of other non-oral diseases. Dry mouth is a common symptom of halitosis, as is a white coating on the tongue. Because halitosis is often caused by poor oral hygiene it can also occur alongside gum disease. Halitosis can usually be prevented with good oral hygiene, including gentle cleaning of the tongue. It is important to also address any underlying causes of related problems such as dry mouth, for example by staying hydrated. A healthcare professional can help you create a personalised plan to identify and overcome the causes of halitosis.

Microbes

Dialister: 0.02 %	Normal range: Not Detected	High
Fusobacterium nucleatum: 0.09 %	Normal range: 0.00–0.25 %	Normal
Fusobacterium periodonticum: Not detected	Normal range: 0.00–0.18 %	Low
Lancefieldella parvula: 0.5 %	Normal range: 0.07–1.28 %	Normal
Porphyromonas gingivalis: 0.01 %	Normal range: 0.00–0.26 %	Normal
Prevotella intermedia: 0.1 %	Normal range: 0.05–0.53 %	Normal
Solobacterium moorei: Not detected	Normal range: Not Detected	Normal
Streptococcus milleri: Not detected	Normal range: 0.00–0.03 %	Low
[Eubacterium] sulci: Not detected	Normal range: Not Detected	Normal

Symptoms summary

Relevant symptoms from the information registered with this sample are summarised here:

Symptom	Sample information
White coating on a large area of the tongue	No
Bad breath	No
Dry mouth	No
Thick saliva	No

Assessment

Your overall risk assessment for halitosis is **low** as you do not have many symptoms or above-average levels of many of the microbes normally associated with this disease, which indicates a good, healthy result. Having a low risk assessment is not a formal diagnosis however, and if you have any concerns about your health you should discuss them with your dentist or a qualified healthcare practitioner.

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Oral thrush – Low risk

Oral thrush, or candidiasis, is caused by Candida yeast. These yeast are found in low amounts in most healthy microbiomes, but can cause a problem if they grow too much, including symptoms of creamy white patches in the mouth, redness and soreness. Oral thrush is usually treated with antifungal medication, but it is important to understand and solve the underlying cause of oral thrush. Oral thrush may occur due to other health issues, such as diabetes, nutritional deficiencies, or as the result of taking some medications. The results shown are not a diagnosis. Consult with a qualified health practitioner before making decisions about starting or stopping medication or other treatments.

Microbes

Candida: Not detected	Normal range: Not Detected	Normal

Symptoms summary

Relevant symptoms from the information registered with this sample are summarised here:

Symptom	**Sample information**
Redness of the gums	No
Redness of the tongue	No
Redness of the throat	No
Creamy white patches on tongue/gums/inner cheeks	No
Pain in the mouth generally	No
Issues with sense of taste	No issues
Cracks at the corner of the mouth	No
Dry mouth	No

Assessment

Your overall risk assessment for oral thrush is **low** as you do not have above-average levels of Candida yeast or many of the symptoms normally associated with this disease, which indicates a good, healthy result. Having a low risk assessment is not a formal diagnosis however, and if you have any concerns about your health you should discuss them with your dentist or a qualified healthcare practitioner.

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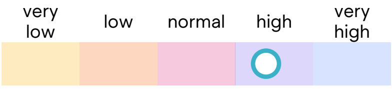
Oral Microbiome Functions

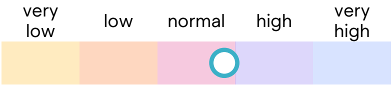
Oral bacteria are involved in a wide range of metabolic processes, which include the ability to break down different components of your diet and to produce chemicals which can damage or protect with your teeth. Our analysis directly detects which functional genes are present in your sample. The higher the score, the more potential your microbiome has to perform that function. Your score is compared to the average score of a healthy population.

Oral - Sugar Degradation High



A high score for this function is linked to a higher risk of tooth decay. Oral microbes break down sugars as the first step towards production of acids that dissolve the tooth enamel, leading to formation of caries.

Oral - Acid Production Normal



Acids produced by oral microbes, especially those found in plaque deposits attached to the tooth surface, cause dental caries by dissolving the outer enamel layer of the teeth. Lactic acid is the major decay-causing acid produced by oral microbes, though short-chain fatty acids such as acetate and propionate also contribute.

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Recommendations

Here is a summary of your test results and actions you can take to improve your oral health. For fully personalised advice, please consult with a dentist or qualified healthcare practitioner.

Pathogens and opportunistic pathogens

We detected **25 potential pathogens or opportunistic pathogens** in your sample, and **4 are above the levels expected** in a healthy population. This means it is more likely that you have or may develop an oral health issue, but you should interpret your results in the context of any symptoms you may have, and consult with a dentist if you have any concerns. Maintaining a healthy oral microbiome through good hygiene and diet is a good general defence against oral pathogens.

Health risks

This test is intended as a tool for assessing disease risk and cannot be used to provide a formal diagnosis. Based on the levels of relevant microbe in your sample and the symptoms you reported, you have:

- A **high risk** of Dental Caries which should be followed up with a healthcare professional if you are concerned.
- A **low risk** of Gum disease, Halitosis, and Oral thrush but trust your instincts about your own health and seek further advice if you are still concerned about these or other diseases.

Diet and lifestyle

A high-sugar diet increases the risk of tooth decay by feeding acid-producing microbes, and acidic food or drink (e.g. orange juice or fizzy drinks) is directly harmful to teeth. A healthy diet should contain a limited amount of sugar and acidic foods, and include fibre from fruit, vegetables and grains which helps stimulate saliva to wash out acids. Sources of calcium, phosphorus and vitamin D, such as dairy, fish, eggs, and nuts. Staying hydrated helps to maintain saliva production; drinking water with meals will also help to rinse out food. You said that you do not eat sugary food or drinks, and that you drink fizzy drinks weekly. You also reported that you smoke or vape. Smoking is a risk factor for many oral diseases, including cancer.

Oral hygiene

Most people will benefit from an oral hygiene routine that includes:

- Brushing at least twice a day with a fluoride toothpaste (your dentist can advise if a hydroxyapatite toothpaste is a suitable alternative for you).
- Flossing daily.
- Visit the dentist at least every two years, but more frequently if you have a history of dental problems.

You reported that you brush your teeth once per day with a toothpaste that contains neither fluoride nor hydroxyapatite. You do not floss daily, and you have visited a dentist within the last two years. Everyone's mouth and oral health needs are unique; your dentist can help create a personalised oral hygiene routine for you.

Probiotics

Following a good oral hygiene routine, with a healthy diet and lifestyle, is the best way to build and maintain a healthy oral microbiome. However, if the oral microbiome is unbalanced, particularly after illness or antibiotic treatment, it may be worthwhile to try probiotic supplements to help rebalance the microbiome. The balance of your microbiome was similar to an average healthy oral microbiome. Oral probiotics usually contain bacteria that have been shown to inhibit the growth of oral pathogens. Discuss possible probiotic supplements with a qualified healthcare practitioner, and be aware of any unwanted side effects such as stomach upset or (rarely) allergic reactions.

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Key bacteria

[Eubacterium] sulci — Normal range: Not Detected

Eubacterium sulci is known to produce malodorous compounds that contribute to halitosis.

Actinomyces naeslundii — Normal range: Normal range: 0.00–0.65 %

Actinomyces naeslundii is a part of the normal oral microflora, found in dental plaque and gingival pockets. While it contributes to healthy biofilm balance and is associated with good oral health, under certain conditions, it can promote the growth of harmful bacteria like P. gingivalis and contribute to periodontal disease and tooth decay. Its role can shift depending on the oral environment, potentially causing inflammation and tissue damage when biofilms are disrupted by factors like acid exposure.

Aggregatibacter actinomycetemcomitans — Normal range: Normal range: 0.00–0.07 %

Aggregatibacter actinomycetemcomitans is a bacterium commonly associated with aggressive periodontitis, especially localized juvenile periodontitis (LJP), which causes rapid destruction of tooth-supporting tissues, particularly around incisors and molars in young individuals. This pathogen can invade periodontal tissues, evade host defences, and cause significant tissue and bone destruction. It is also linked to various systemic infections, such as endocarditis, osteomyelitis, and abscesses. While it can be found in a small percentage of healthy individuals, it is more prevalent in patients with periodontitis and can remain stable within the host for many years despite treatment.

Campylobacter concisus — Normal range: Normal range: 0.10–1.67 %

Campylobacter concisus is primarily a member of the normal oral flora, colonizing the human oral cavity from an early age. While commonly found in healthy individuals, it has been found in higher prevalence in patients with inflammatory bowel disease (IBD) compared to healthy individuals. Overall, C. concisus may have pathogenic potential, especially in the context of IBD and gastroesophageal reflux disease.

Campylobacter rectus — Normal range: Normal range: 0.00–0.11 %

Campylobacter rectus is a bacterium associated with periodontal disease. While it can be found in healthy individuals, its prevalence significantly increases in those with established periodontitis. This bacterium can act as a pathogen, leading to opportunistic infections, particularly in immunocompromised individuals. Additionally, C. rectus has been implicated in adverse pregnancy outcomes and extraoral infections.

Campylobacter showae — Normal range: Normal range: 0.00–0.36 %

Campylobacter showae has been found in higher frequencies and levels in patients with periodontitis and gingivitis compared to healthy controls, suggesting a potential pathogenic role. Additionally, C. showae has been implicated in other medical conditions, such as inflammatory bowel disease and ulcerative colitis.

Candida albicans — Normal range: Not Detected

Candida albicans is a commensal fungal species that commonly colonizes human mucosal surfaces, particularly in the oral cavity. While it is typically non-pathogenic, it can become an opportunistic pathogen under conditions of immune dysfunction, such as HIV infection, leading to mucosal and systemic infections. It is frequently associated with oral candidiasis, especially in immunocompromised individuals, and has the potential to contribute to dental caries due to its ability to produce and tolerate acids.

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Candidatus Saccharibacteria Normal range: Not Detected

Candidatus Saccharibacteria are ubiquitous members of the human oral microbiota also found in other areas, such as the gastrointestinal tract, urogenital tract, and breast milk. They are considered important, commensal members of the oral microbiota but have also been linked to periodontal disease.

Capnocytophaga granulosa Normal range: Not Detected

Capnocytophaga granulosa is a bacterium that is a normal part of the human oral flora, commonly found in the gingival sulcus. This species, along with others in the Capnocytophaga group, is also present in the mouths of animals like dogs and cats. While it typically coexists without issue, C. granulosa can overgrow and contribute to periodontal disease. In immunocompromised individuals, it may lead to opportunistic infections such as bone infections, bacteremia, and systemic infections.

Capnocytophaga periodontitidis Normal range: Not Detected

Capnocytophaga periodontitidis has been isolated from subgingival plaque of individuals suffering from periodontitis, indicating its potential role in the disease process.

Corynebacterium durum Normal range: Normal range: 0.00–0.27 %

Corynebacterium durum is a commensal bacterium found in the human oral cavity, as well as in the digestive and respiratory tracts. It is associated with periodontal health and is considered a potential producer of beneficial chemical messengers. Studies indicate that it is present alongside Corynebacterium matruchotii in healthy individuals, often being more predominant. Overall, C. durum contributes positively to oral health and is part of the normal oral flora.

Corynebacterium matruchotii Normal range: Normal range: 0.00–0.46 %

Corynebacterium matruchotii is a commensal bacterium abundant in healthy dental plaque, playing a potential role as an indicator of oral health. It is associated with the formation of dental calculi and is thought to help stabilize healthy dental plaque. Its prevalence is significantly higher in periodontally healthy individuals compared to those with periodontitis, particularly in diabetes-negative groups, suggesting a protective role against oral diseases. Additionally, C. matruchotii may act as a marker of a caries-free state, as its abundance correlates with lower caries risk.

Dialister invisus Normal range: Not Detected

Dialister invisus is a bacterium found in the oral cavity and other body sites, typically considered a commensal organism but capable of spreading and causing severe infections, including bacteremia. It is primarily linked to oral diseases such as halitosis, periodontitis and acute necrotizing ulcerative gingivitis.

Dialister micraerophilus Normal range: Not Detected

Dialister micraerophilus is a bacterium found in the oral cavity and other body sites, often linked to halitosis. Although generally considered a commensal organism, it can spread to various organs and potentially cause serious infections.

Dialister pneumosintes Normal range: Normal range: 0.00–0.04 %

Dialister pneumosintes is typically considered a commensal organism, but it can lead to various infections, particularly oral conditions like halitosis, gingivitis and periodontitis. This species is also associated with more severe extra-oral infections, including pneumonia, abscesses, and vaginosis, and has been isolated from various clinical specimens, including bite wounds and brain abscesses. Although primarily linked to dental infections, D. pneumosintes can cause bacteremia, often related to sinusitis or dental issues.

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Eikenella corrodens

Normal range: Normal range: 0.00–0.21 %

Eikenella corrodens is a bacterium that normally resides in the oral cavity, upper respiratory tract, and mucosal surfaces of the digestive and genitourinary tracts. While it is part of the normal flora, it can become an opportunistic pathogen, contributing to conditions such as gingival inflammation and various infections, including periodontitis, brain abscesses, endocarditis, and osteomyelitis. It is often found in the subgingival plaque of patients with advanced periodontitis and has been linked to nonoral infections like arthritis.

Fusobacterium nucleatum

Normal range: Normal range: 0.00–0.22 %

Fusobacterium nucleatum is a prevalent bacterium found in the oral cavity, recognized as both a commensal organism and a significant periodontal pathogen. While it can be associated with periodontal disease, it also plays a role in the formation of dental plaque in a balanced microbiome. It is associated with various oral diseases, including gingivitis, chronic and aggressive periodontitis, and endodontic infections, with its prevalence increasing in relation to disease severity and inflammation. This bacterium is also implicated in several extraoral conditions, such as preterm birth and colorectal cancer, potentially translocating from the oral cavity to other sites in the body. Additionally, F. nucleatum plays a crucial role in dental plaque development by facilitating the co-aggregation of different bacterial species, making it a key player in both oral and systemic health issues. Improving oral hygiene and periodontal treatment has been shown to lower F. nucleatum levels.

Fusobacterium periodonticum

Normal range: Normal range: 0.00–0.20 %

Fusobacterium periodonticum is a bacterium primarily inhabiting the oral cavity and gastrointestinal tract, associated with periodontal disease, particularly periodontitis, and has been linked to conditions like pyogenic liver abscess.

Fusobacterium pseudoperiodonticum

Normal range: Normal range: 0.00–1.83 %

Fusobacterium pseudoperiodonticum is a bacterium found in the tongue and subgingival plaque of individuals with gingivitis.

Haemophilus parainfluenzae

Normal range: Normal range: 1.05–7.60 %

Haemophilus parainfluenzae is a common and abundant part of the oral flora, found in the mouths and upper respiratory tracts of most healthy individuals. It is associated with good oral health but may lead to infections if the immune system is compromised, potentially leading to infections in other parts of the body, such as the lungs, bones, and heart, especially when mucus clearance is impaired. This bacterium has been shown to inhibit the adhesion of harmful bacteria like Porphyromonas gingivalis, highlighting its role in maintaining oral health.

Helicobacter pylori

Normal range: Not Detected

Helicobacter pylori is a bacterium primarily known for its role in gastric diseases such as ustomach ulcers but it can also be found in the oral cavity and may be linked to gum disease. Research indicates that individuals with H. pylori infections show higher levels of periodontal pathogens like Porphyromonas gingivalis and Fusobacterium nucleatum, suggesting that H. pylori may promote the growth of these harmful bacteria and worsen chronic periodontitis.

Lancefieldella parvula

Normal range: Normal range: 0.04–0.83 %

This bacterium is strongly associated with halitosis. It is often isolated from the tongue of individuals suffering from bad breath and can produce sulfur compounds that contribute to the odor.

Leptotrichia buccalis

Normal range: Normal range: 0.00–0.05 %

This bacterium typically exists harmlessly within the oral microbiome, but has occasionally been associated with serious infections, such as septicemia and endocarditis, in immunocompromised individuals or those with existing health issues.

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Leptotrichia shahii Normal range: Normal range: 0.00–0.03 %

Leptotrichia shahii is a bacterium that is part of the normal oral flora but may be associated with periodontal disease or gingivitis. While not typically pathogenic, its presence in gingivitis patients suggests it could play a role in oral health issues.

Ligilactobacillus salivarius Normal range: Normal range: 0.00–0.02 %

L. salivarius is a bacterium primarily associated with caries (tooth decay). It has been found almost exclusively in these decayed areas, suggesting that it may play a significant role in the advanced stages of dental caries. This bacterium thrives in acidic environments, which are common in carious lesions. Its presence indicates a potential link to the progression of tooth decay.

Limosilactobacillus fermentum Normal range: Normal range: 0.00–0.02 %

This bacterium is found in the mouth and gastrointestinal tract, and is known for thriving in acidic environments like those associated with tooth decay. It is commonly present in both caries-free and caries-active individuals, but is one of the most abundant species in dental caries. While it does not significantly differentiate between healthy and decayed teeth, it often co-occurs with other cariogenic bacteria like Streptococcus mutans and Fusobacterium nucleatum. L. fermentum may play a role in the complex interactions of oral microbiota related to tooth decay.

Neisseria flavescens Normal range: Normal range: 0.02–0.47 %

Neisseria flavescens is the most common commensal Neisseria species in the oral microbiome, primarily found on the tongue dorsum alongside N. perflava and N. subflava. While generally non-pathogenic, it can pose risks for immunocompromised and diabetic individuals, being associated with rare cases of meningitis, pneumonia, empyema, endocarditis, and sepsis.

Neisseria mucosa Normal range: Normal range: 0.07–1.78 %

This is one of the most prevalent commensal Neisseria species in the oral microbiome and is generally considered nonpathogenic in healthy individuals. However, it can become opportunistic in those with weakened immune systems, potentially leading to infections like bacterial meningitis, pneumonia, and endocarditis. Interestingly, N. mucosa's abundance is associated with good oral health, and its presence may decrease in smokers, suggesting a protective role in the oral microbiome. Additionally, changes in salivary abundance of N. mucosa have been linked to certain health conditions, such as inflammatory bowel disease and pancreatic cancer.

Neisseria perflava Normal range: Normal range: 0.00–1.39 %

Neisseria perflava is a bacterium that is part of the normal flora of the human oral cavity. While N. perflava is generally considered nonpathogenic, it has been associated with opportunistic infections, particularly in immunocompromised individuals.

Neisseria sicca Normal range: Normal range: 0.06–1.41 %

This bacterium is generally considered non-pathogenic and it may help prevent harmful pathogens from colonizing the oral and nasal areas. In rare cases, particularly in individuals with weakened immune systems, it can cause systemic infections, including meningitis, endocarditis, and septic arthritis.

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Porphyromonas gingivalis Normal range: Normal range: 0.00–0.27 %

Porphyromonas gingivalis is a bacterium that plays a key role in chronic periodontitis, a disease characterized by the destruction of periodontal tissues. P. gingivalis is found primarily in the subgingival sulcus and is part of the "red complex" of bacteria associated with advanced periodontal disease alongside Treponema denticola and Tannerella forsythia. Its presence is linked not only to oral health issues but also to systemic conditions such as cardiovascular disease and diabetes. This bacterium can enter the bloodstream during routine oral activities like brushing or dental procedures.

Prevotella denticola Normal range: Normal range: 0.00–1.16 %

Prevotella denticola is a commensal bacterium found in the mouth and dental plaques from early life. It can be associated with periodontal inflammation and disease, acting as a potential pathogen in oral health issues like periodontitis and cavities.

Prevotella histicola Normal range: Normal range: 0.00–3.72 %

Prevotella histicola is a bacterium normally found in the mouth but can become harmful under certain conditions, contributing to dental issues like cavities (caries) and gum disease (periodontitis). Increased levels in adults have been linked with recurrent tonsillitis.

Prevotella intermedia Normal range: Normal range: 0.08–0.56 %

Prevotella intermedia is a bacterium primarily associated with periodontal infections, including gingivitis and periodontitis. It is often found in conditions like acute necrotizing ulcerative gingivitis and is commonly isolated from dental abscesses. P. intermedia acts as a late colonizer in dental plaque, often facilitating the colonization of other pathogenic bacteria like Porphyromonas gingivalis. Research has demonstrated associations between P. intermedia and systemic diseases, including respiratory and circulatory diseases, neurological disorders, and even adverse pregnancy outcomes like preterm birth and low birth weight. Studies have shown that high levels of P. intermedia correlate with severe asthma and may increase the risk of atherosclerosis by promoting inflammatory responses.

Prevotella melaninogenica Normal range: Normal range: 0.43–14.31 %

Prevotella melaninogenica is a common bacterium found in the mouth from early childhood, particularly on the tongue and in saliva. While it plays a role in normal oral health, shifts in its abundance can signal certain diseases. It's more prevalent in health conditions, like Crohn's disease and asthma, and may be linked to changes in bacterial balance in people with reflux or tonsillitis.

Prevotella nigrescens Normal range: Normal range: 0.00–2.41 %

Prevotella nigrescens is a bacterium commonly found in the mouth as part of the normal oral flora. It is associated with dental plaque and can become pathogenic under certain conditions, contributing to gum diseases like periodontitis.

Prevotella veroralis Normal range: Normal range: 0.00–2.47 %

Prevotella veroralis is a bacterium typically found in the human mouth and is part of the Prevotella genus, which commonly colonizes the oral microbiome and other mucosal surfaces in the respiratory and digestive tracts.

Rothia aeria Normal range: Normal range: 0.00–0.82 %

Rothia aeria is a part of the normal oral and upper gastrointestinal tract microflora. It is usually associated with oral health but it can be contribute to periodontal and dental infections, and in rare cases in immunocompromised individuals can cause systemic infections like bacteremia, endocarditis, and respiratory tract infections.

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Rothia mucilaginosa	Normal range: Normal range: 3.87–20.22 %

Rothia mucilaginosa is a bacterium that is a common resident of the oral cavity and respiratory tract, as a part of the normal flora. While usually benign and associated with oral health, it can act as an opportunistic pathogen, causing infections like septicemia, endocarditis, and lung diseases in immunocompromised individuals. Recent research suggests that R. mucilaginosa may have anti-inflammatory properties, potentially reducing inflammation in chronic respiratory diseases.

Scardovia wiggsiae	Normal range: Not Detected

Scardovia wiggsiae is a bacterium strongly associated with severe early childhood caries, often found alongside Streptococcus mutans. It has been detected in initial and advanced carious lesions, particularly in adolescents with fixed orthodontic appliances. Its acid tolerance and ability to produce acid from various sugars under low pH conditions suggest it may contribute to tooth decay.

Schaalia odontolytica	Normal range: Normal range: 1.82–10.07 %

Schaalia odontolytica (formerly Actinomyces odontolyticus) is a bacterium commonly found in the human oral cavity, often associated with dental and periodontal diseases. It can cause actinomycosis, including serious infections like mediastinal masses, particularly in immunocompromised individuals.

Selenomonas sputigena	Normal range: Normal range: 0.00–0.34 %

Selenomonas sputigena is found in the oral cavity, especially in the supragingival biofilm, where it significantly promotes childhood dental caries in combination with Streptococcus mutans. While incapable of causing cavities on its own, S. sputigena enhances biofilm virulence, forming a protective honeycomb structure around S. mutans, which increases acid production and tooth enamel damage.

Solobacterium moorei	Normal range: Not Detected

Solobacterium moorei is a bacterium commonly found in patients with halitosis, or bad breath. It can thrive in subgingival plaque and is linked to various oral infections, including peri-implantitis and endodontic infections. S. moorei is known to produce volatile organic compounds and biofilms, which may contribute to the development of halitosis.

Staphylococcus aureus	Normal range: Normal range: 0.00–0.01 %

Staphylococcus aureus is a common bacterium found in the oral cavity, although its role as a permanent member of the oral microbiota is still debated. It can act as both a commensal and pathogen, causing infections such as angular cheilitis, parotitis, and mucositis, particularly in vulnerable populations. S. aureus is often found in the oral cavities of denture wearers, individuals with carious lesions, or those with periodontal disease, and it may contribute to dental implant failure. Additionally, the oral cavity may serve as a reservoir for S. aureus, potentially leading to auto-infection and transmission throughout the body.

Streptobacillus	Normal range: Not Detected

Streptobacillus bacteria are not typically linked to oral diseases but have been found in higher amounts in the dental plaque of patients with active caries. This suggests they may play a role in the development of cavities.

Streptococcus gordonii	Normal range: Normal range: 0.00–0.54 %

Streptococcus gordonii is a common bacterium found in the mouth that helps form dental plaque and can protect against tooth decay by inhibiting harmful bacteria like Streptococcus mutans. While it usually lives harmlessly in the oral cavity, it can become an opportunistic pathogen and lead to serious infections, such as infective endocarditis, if it enters the bloodstream. S. gordonii is one of the first bacteria to colonize teeth, playing a crucial role in establishing a healthy oral environment.

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Streptococcus mitis Normal range: Normal range: 0.00–3.70 %

Streptococcus mitis is a bacterium that is a normal part of the healthy human oral microbiome, found abundantly in dental plaque and other oral sites. As a pioneer colonizer, it comprises a significant portion of the early biofilm population on newly emerged or professionally cleaned teeth. While S. mitis is generally considered benign and has been associated with oral health, it can cause infections under certain conditions. Its presence helps prevent the adhesion of pathogenic bacteria like Porphyromonas gingivalis.

Streptococcus mutans Normal range: Normal range: 0.00–0.12 %

Streptococcus mutans is the primary pathogen responsible for dental caries, often found in high abundance in carious lesions. It plays a key role in the initiation and progression of cavities and it thrives in dental plaque, creating an acidic environment that favours its survival over non-cariogenic species. Additionally, it has been linked to other health issues, including endocarditis and cardiovascular conditions.

Streptococcus oralis Normal range: Normal range: 0.18–1.78 %

Streptococcus oralis is a common bacterium found in the mouth that plays a key role in the early stages of dental plaque formation. While it normally lives harmlessly in the oral cavity, it can become an opportunistic pathogen, entering the bloodstream and potentially causing serious infections like bacteremia and infective endocarditis. Poor oral hygiene and dental procedures can increase the risk of S. oralis entering the bloodstream. Though it's involved in dental caries, its exact role in tooth decay is still not fully understood.

Streptococcus pneumoniae Normal range: Normal range: 0.00–1.07 %

Streptococcus pneumoniae is a bacterium that can enter the body through the mouth and nose, commonly colonizing the oropharynx and nasopharynx. It is a significant cause of community-acquired pneumonia, particularly in children, although most people's immune systems can usually eliminate the bacteria before they cause infection. Historically, S. pneumoniae was the leading cause of pneumonia before the widespread use of antibiotics, but it still accounts for a notable percentage of pneumonia cases today.

Streptococcus pyogenes Normal range: Normal range: 0.00–0.31 %

Streptococcus pyogenes, often referred to as group A streptococcus, is a bacteria that can cause various oral infections, including strep throat and cellulitis. It is the leading cause of pharyngitis in children and teens, with symptoms like a sore throat, fever, and swollen lymph nodes. While it is not a primary player in dental plaque formation like some other Streptococci, it can be linked to periodontal disease and may lead to more serious infections if it enters the bloodstream through activities like brushing teeth or dental procedures.

Streptococcus salivarius Normal range: Normal range: 0.18–8.58 %

Streptococcus salivarius is a friendly bacterium that naturally inhabits the mouth and is usually one of the first to colonize after birth. It plays a crucial role in maintaining oral health by regulating the balance of other bacteria and contributing to immune system stability. This bacterium is generally harmless and can even help reduce inflammation and fight off harmful pathogens, making it beneficial for overall health. Certain strains, like S. salivarius K12, are used as probiotics to treat oral issues such as bad breath and throat infections, promoting a healthier oral environment.

Streptococcus sanguinis Normal range: Normal range: 0.04–1.16 %

Streptococcus sanguinis is a common bacterium found in the mouth that plays a protective role in oral health. It helps prevent tooth decay by inhibiting harmful bacteria like Streptococcus mutans through the production of hydrogen peroxide. S. sanguinis is often seen as a sign of good periodontal health, as it can prevent the colonization of harmful bacteria associated with gum disease.

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Streptococcus sobrinus Normal range: Not Detected

Streptococcus sobrinus is a type of bacteria commonly found in the mouth, and it plays a significant role in the development of dental caries (tooth decay). Studies have shown that higher levels of S. sobrinus are linked to an increased occurrence of cavities, particularly in children. This bacterium, along with Streptococcus mutans, is known for its ability to produce acid leading to the demineralization of tooth enamel, contributing to the cariogenic process.

Tannerella forsythia Normal range: Normal range: 0.00–0.34 %

Tannerella forsythia is a key bacterium associated with severe periodontal disease, frequently found alongside Porphyromonas gingivalis in cases of chronic periodontitis. T. forsythia relies on other bacteria in the biofilm for survival, particularly for a crucial sugar necessary for its cell wall. Parent-child transmission of T. forsythia has been noted, indicating its potential for familial spread. Overall, T. forsythia plays a significant role in the inflammatory processes underlying periodontal disease, affecting millions globally.

Treponema denticola Normal range: Normal range: 0.00–0.14 %

Treponema denticola is a bacterium commonly found in the mouth, particularly in areas with gum disease. It plays a significant role in the progression of periodontal disease, especially when present in large numbers in periodontal pockets. This bacterium is part of the "red complex" of pathogens implicated in the progression of periodontitis. Research has linked the presence of T. denticola is linked to worsening periodontal health, with higher levels associated with increased plaque, gum bleeding, and pocket depth. This bacterium is also being studied for its potential connections to neurodegenerative diseases.

Treponema putidum Normal range: Normal range: 0.00–0.00 %

Treponema putidum is a bacterium found in the human mouth, particularly in areas affected by periodontal disease. It is closely related to Treponema denticola, which is well-known for its role in gum disease. T. putidum has been isolated from subgingival plaque in deep periodontal lesions, suggesting its involvement in oral infections. Despite being linked to periodontal disease, much about T. putidum — including its clinical significance and how it contributes to gum health — is still not well understood.

Veillonella dispar Normal range: Normal range: 0.00–0.98 %

Veillonella dispar is a bacterium commonly found in the human oral cavity, particularly on the tongue and in saliva. This species constitutes a portion of dental plaque biomass and is predominantly located on soft tissues in the mouth. While it is typically considered a commensal organism, and usually lives harmlessly as part of the healthy oral flora, it may contribute to tooth decay and caries progression, and gum disease, especially in combination with Streptococcus mutans. Its role in shifting from oral health to disease states, such as gingivitis and periodontitis, cannot be overlooked. People with inflammatory bowel disease often have higher levels of Veillonella and related bacteria in their saliva compared to those without the condition.

Veillonella parvula Normal range: Normal range: 0.04–1.19 %

Veillonella parvula is a common bacterium found in the oral cavity, especially in dental plaque. It is generally a harmless commensal organism but can occasionally be linked to serious infections, although such instances are rare. This bacterium tends to be more prevalent in individuals with poor oral hygiene; its presence is often noted in the saliva of children who do not maintain good oral care.

Veillonella rogosae Normal range: Normal range: 0.44–3.84 %

Veillonella rogosae is a bacterium typically found in the oral cavity, particularly in dental plaque, the tongue, and buccal mucosa. It is considered a health-associated species and plays a role as an early colonizer in the formation of oral biofilms. Studies show that V. rogosae is more prevalent in individuals with good oral hygiene, while its detection decreases in those with poorer hygiene.

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Veillonella tobetsuensis	Normal range: Not Detected

Veillonella tobetsuensis is a bacterium that commonly coexists with other Veillonella species in saliva and tongue biofilms. It was not found in the saliva of individuals with good oral hygiene but was detected in 14.3% of those with moderate oral hygiene and 17.8% of those with poor oral hygiene.

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Key terms

Microbe / Microorganism – A general term for microscopic organisms, very small living things that can only be seen using a microscope, and include bacteria, fungi, viruses and other single-celled organisms. Microbes can exist in a huge range of environments, including soil, water, air, and they also exist on and within larger organisms (such as humans). Whilst some microbes can cause infections, many are beneficial or even essential for human health. All organisms are classified by how closely related (or genetically similar) they are to each other, which also usually determines how similarly they behave. This is their taxonomic classification, or taxon (plural: taxa). We normally talk about organisms at the level of species, which in sexual organisms describes those that are similar enough to produce fertile offspring. Species are grouped together into a genus. An example here is the genus *Streptococcus* which contains many different species, but some are usually found in specific environments, e.g. *Streptococcus salivarius* in the mouth and *Streptococcus agalactiae* in the gut. Sometimes it is useful to talk about strains, which are organisms from the same species that have a handful of genetic differences: these might not be important, or may result in key differences such as antibiotic resistance. At a much higher level organisms can be grouped into phyla.

Microbiome – This is the term for a group of microbes that live in a particular habitat, either in the environment or in association with a host organism. There are microbiomes associated with almost all parts of the body, including the mouth, skin, and gut. When we talk about a microbiome we are often interested in the overall behaviours of the microbial community, for example a microbiome's ability to break down certain foods. We can predict the behaviour of a microbiome by measuring which microbes are present and how many there are of each type.

Dysbiosis – This refers to an imbalance in a microbiome, away from a 'healthy' community of microbes, and is often associated with disease. In general this can be a useful description, but it is important to remember that the collection of microbes in a microbiome is always changing, that those changes may not always be harmful, that they are often temporary, and there is rarely only one definition of a 'healthy' microbiome.

Diversity (of the microbiome) – A measure of the number of microbes in a microbiome and their relative amounts.

Commensal – If a microorganism is commensal it is able to exist in the microbiome without harming the host or other microorganisms.

Opportunistic pathogen – A microorganism that is able to cause infections if the host's resistance to disease is reduced, for example after injury or another infection, or in immunocompromised people. Opportunistic infections often involve the microorganism invading parts of the body where they are not normally found, for example a typically commensal bacterium might become an opportunistic pathogen if it enters the bloodstream.

Plaque – Plaque is a biofilm growing on the teeth. A biofilm is a community of bacteria that live within a biological structure they have created to stick to surfaces and protect the bacteria within. Initially white, it hardens to form brown/yellow tartar. Plaque leads to caries and gum disease.

Caries – Also known as cavities or tooth decay, caries occur when acid produced by oral bacteria break down the outer layers of the tooth.

Gingivitis – An early form of gum disease, usually caused by plaque on tooth surfaces. Symptoms are red, swollen, and bleeding gums. If untreated, gingivitis may lead to periodontitis.

Periodontitis – Also known as gum disease, periodontitis is a long-term infection of the gums and tooth support structures, leading to tooth loss and possible bone damage. The "Red complex" consists of the bacteria *Porphyromonas gingivalis*, *Treponema denticola*, and *Tannerella forsythia*, and is associated with severe periodontitis.

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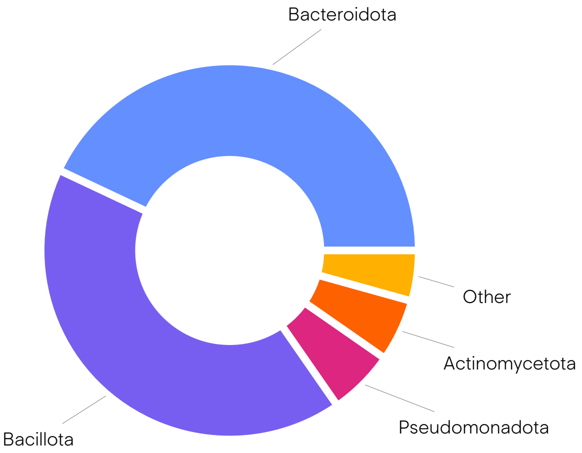
Full taxonomy report

Phyla overview

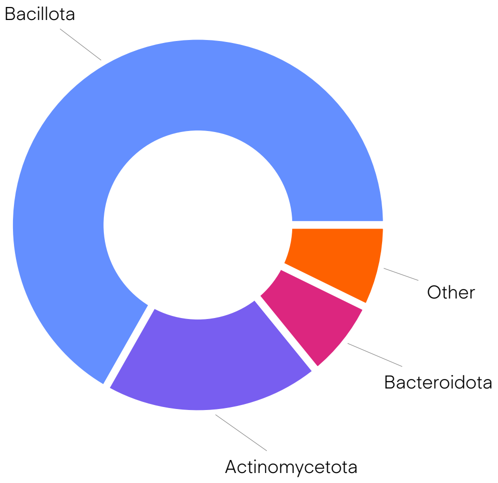
The doughnut charts show the proportion of different microbial phyla in your sample, alongside an average healthy sample for comparison. Everybody's oral microbiome is unique – if your sample is not an exact match it is not necessarily an indicator of poor oral health.

Healthy



This chart shows the proportions of the different bacterial phyla in a representative healthy sample.

Your sample



This chart shows the proportions of the different bacterial phyla in your sample.

Top species

Here are all the species present in your sample, ordered by relative abundance.

Taxonomic name	Relative abundance
Streptococcus salivarius	21.3 %
Veillonella atypica	9.6 %
Rothia mucilaginosa	8.8 %
Rothia dentocariosa	6.8 %
Streptococcus parasanguinis	3.4 %
Streptococcus vestibularis	3.4 %
Prevotella histicola	3.2 %
Streptococcus mitis	2.7 %
Streptococcus sp. LPB0220	2.7 %
Veillonella nakazawae	2.6 %
Streptococcus sp. HSISM1	2.2 %
Veillonella dispar	1.8 %
Streptococcus sanguinis	1.7 %
Schaalia odontolytica	1.7 %

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Taxonomic name	Relative abundance
Rothia phage Spartoi	1.6 %
Veillonella sp. S12025-13	1.6 %
Prevotella veroralis	1.3 %
Streptococcus phage PH15	1.2 %
Streptococcus oralis	1.1 %
Streptococcus gordonii	1.1 %
Streptococcus thermophilus	1.1 %
Veillonella parvula	1.0 %
Veillonella rogosae	1 %
Haemophilus parainfluenzae	1 %
Prevotella fusca	0.7 %
Streptococcus sp. oral taxon 431	0.6 %
Streptococcus sp. FDAARGOS_192	0.6 %
Gemella haemolysans	0.6 %
Streptococcus phage PH10	0.6 %
Streptococcus pneumoniae	0.6 %
Campylobacter concisus	0.5 %
Lancefieldella parvula	0.5 %
Gemella sanguinis	0.5 %
Streptococcus infantis	0.4 %
Streptococcus sp. Marseille-Q6470	0.4 %
Prevotella melaninogenica	0.4 %
Streptococcus sp. oral taxon 061	0.4 %
Granulicatella adiacens	0.4 %
Rothia aeria	0.3 %
Streptococcus lactarius	0.3 %
Prevotella jejuni	0.3 %
Actinomyces oris	0.3 %
Streptococcus agalactiae	0.3 %
Streptococcus gwangjuense	0.3 %
Streptococcus australis	0.3 %
Streptococcus sp. Marseille-Q3533	0.3 %
Neisseria sicca	0.2 %
Streptococcus ilei	0.2 %
Leptotrichia wadei	0.2 %
Limosilactobacillus fermentum	0.2 %
Streptococcus toyakuensis	0.2 %
Haemophilus parahaemolyticus	0.2 %
Prevotella oris	0.1 %
Prevotella nigrescens	0.1 %
Streptococcus sp. oral taxon 064	0.1 %
Leptotrichia sp. oral taxon 221	0.1 %
Haemophilus haemolyticus	0.1 %
Streptococcus sp. A12	0.1 %
Neisseria macacae	0.1 %
Capnocytophaga sputigena	0.1 %

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Taxonomic name	**Relative abundance**
Selenomonas sp. oral taxon 478	0.1 %
Selenomonas sp. oral taxon 136	0.1 %
Kingella oralis	0.1 %
Streptococcus koreensis	0.1 %
Mogibacterium diversum	0.1 %
Parvimonas micra	0.1 %
Candidatus Nanosynbacter sp. HMT-352	0.1 %
Actinomyces sp. HMT 175	0.1 %
Prevotella intermedia	0.1 %
Streptococcus pseudopneumoniae	0.1 %
Haemophilus sp. oral taxon 036	0.1 %
Haemophilus influenzae	0.1 %
Actinomyces sp. oral taxon 169	0.09 %
Treponema denticola	0.09 %
Bifidobacterium breve	0.09 %
Fusobacterium nucleatum	0.09 %
Actinomyces pacaensis	0.09 %
Streptococcus sp. 116-D4	0.09 %
Granulicatella elegans	0.08 %
Neisseria mucosa	0.07 %
Streptococcus mutans	0.07 %
Neisseria subflava	0.07 %
Fusobacterium vincentii	0.07 %
Prevotella denticola	0.06 %
Neisseria bacilliformis	0.06 %
Neisseria sp. oral taxon 014	0.06 %
Eikenella corrodens	0.06 %
Streptococcus intermedius	0.06 %
Abiotrophia defectiva	0.06 %
Streptococcus anginosus	0.06 %
Prevotella amnii	0.05 %
Porphyromonas endodontalis	0.05 %
Ligilactobacillus salivarius	0.05 %
Lautropia mirabilis	0.04 %
Hoylesella pleuritidis	0.04 %
Prevotella buccae	0.04 %
Veillonella rodentium	0.04 %
Streptococcus rubneri	0.04 %
Schaalia meyeri	0.04 %
Fusobacterium animalis	0.04 %
Lactobacillus ultunensis	0.04 %
Streptococcus sp. D7B5	0.04 %
Lachnoanaerobaculum gingivalis	0.03 %
Arachnia rubra	0.03 %
Treponema sp. OMZ 803	0.03 %
Segatella copri	0.03 %

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Taxonomic name	Relative abundance
Filifactor alocis	0.03 %
Treponema vincentii	0.03 %
Streptococcus cristatus	0.03 %
Streptococcus sp. NPS 308	0.03 %
Streptococcus sp. 1643	0.03 %
Streptococcus pyogenes	0.03 %
Lachnoanaerobaculum umeaense	0.02 %
Tannerella forsythia	0.02 %
Treponema sp. OMZ 906	0.02 %
Prevotella disiens	0.02 %
Leptotrichia hongkongensis	0.02 %
Campylobacter rectus	0.02 %
Fusobacterium polymorphum	0.02 %
Streptococcus constellatus	0.02 %
Leptotrichia trevisanii	0.02 %
Streptococcus dysgalactiae	0.02 %
Streptococcus suis	0.02 %
Streptococcus lutetiensis	0.02 %
Lactiplantibacillus plantarum	0.02 %
Neisseria elongata	0.02 %
Mogibacterium pumilum	0.02 %
Faecalibacterium prausnitzii	0.02 %
Neisseria sp. RH3002v2g	0.02 %
Actinomyces sp. oral taxon 171	0.02 %
Actinomyces naeslundii	0.02 %
Cutibacterium acnes	0.02 %
Corynebacterium durum	0.02 %
Corynebacterium matruchotii	0.02 %
Collinsella aerofaciens	0.02 %
Prevotella bivia	0.02 %
Prevotella scopos	0.02 %
Hoylesella timonensis	0.02 %
Limosilactobacillus vaginalis	0.02 %
Dialister pneumosintes	0.02 %
Gemella morbillorum	0.02 %
Morococcus cerebrosus	0.01 %
Dorea longicatena	0.01 %
Pseudomonas aeruginosa	0.01 %
Capnocytophaga sp. FDAARGOS_737	0.01 %
Capnocytophaga gingivalis	0.01 %
Prevotella corporis	0.01 %
Hoylesella shahii	0.01 %
Latilactobacillus sakei	0.01 %
Lactobacillus crispatus	0.01 %
Limosilactobacillus oris	0.01 %
Neisseria sp. Marseille-Q5346	0.01 %

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Taxonomic name	Relative abundance
Prevotella micans	0.01 %
Leptotrichia sp. oral taxon 218	0.01 %
Cardiobacterium hominis	0.01 %
Prevotella baroniae	0.01 %
Leptotrichia sp. oral taxon 212	0.01 %
Porphyromonas gingivalis	0.01 %
Selenomonas sputigena	0.01 %
Fusobacterium hwasookii	0.01 %
Leyella stercorea	0.01 %
Anaerobutyricum hallii	0.01 %
Prevotella multiformis	0.01 %
Catenibacterium sp. co_0103	0.01 %
Pauljensenia hongkongensis	0.01 %
Lactococcus lactis	0.01 %
Bifidobacterium longum	0.01 %
Hoylesella oralis	0.01 %
Hoylesella marshii	0.01 %
Cryptobacterium curtum	0.01 %
Streptococcus equi	0.01 %
Capnocytophaga ochracea	0.01 %
Capnocytophaga leadbetteri	0.01 %
Capnocytophaga endodontalis	0.01 %
Leptotrichia hofstadii	0.01 %
Leptotrichia shahii	0.01 %
Fusobacterium canifelinum	0.01 %
Fusobacterium sp. oral taxon 203	0.01 %
Hoylesella enoeca	0.01 %
Prevotella sp. oral taxon 299	0.01 %
Prevotella sp. oral taxon 475	0.01 %
Neisseria meningitidis	0.01 %
Streptococcus uberis	0.01 %
Lancefieldella sp. Marseille-Q7238	0.01 %
Toxoplasma gondii	0.0 %
Saccharomyces cerevisiae	0.0 %
Prevotella dentalis	0.0 %
Selenomonas sp. oral taxon 126	0.0 %
Lacticaseibacillus paracasei	0.0 %
Eubacterium limosum	0.0 %
Actinomyces viscosus	0.0 %
Fretibacterium fastidiosum	0.0 %
Hoylesella loescheii	0.0 %
Hoylesella buccalis	0.0 %
Campylobacter showae	0.0 %
Kingella denitrificans	0.0 %
Lacticaseibacillus rhamnosus	0.0 %
Mobiluncus sp. Marseille-Q7826	0.0 %

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Taxonomic name	Relative abundance
Treponema medium	0.0 %
Eikenella exigua	0.0 %
Streptococcus pseudoporcinus	0.0 %
Treponema socranskii	0.0 %
Selenomonas sp. oral taxon 920	0.0 %

This test was performed by Salient Bio. These results reflect only the state of the sample as received and identified by the sample ID referenced in this document. This test was conducted in Unit 507 Cocoa Studios, The Biscuit Factory, 100 Drummond Road, London, SE16 4DG. Salient Bio is a trading name of Salient Labs Limited, a registered company in England and Wales, company number 12662440.

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