



## Reproductive Uterine Microbiome Test

Name	
Sample ID	
Date of sample taken	
Date of birth	
Sample type	Menstrual Blood Sample
Partner	
Symptoms	Infertility, miscarriage

screenme



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## Next Generation Sequencing Screening

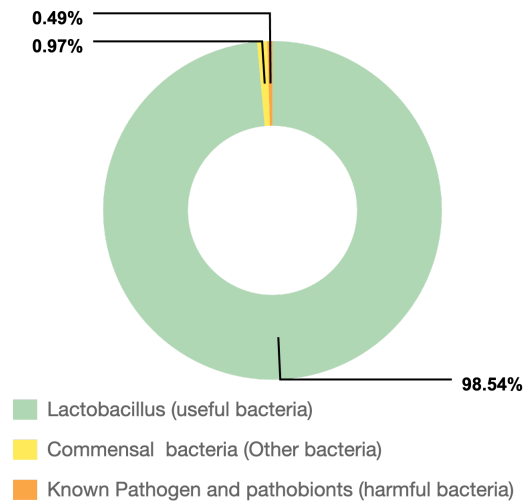
Name

Sample Date

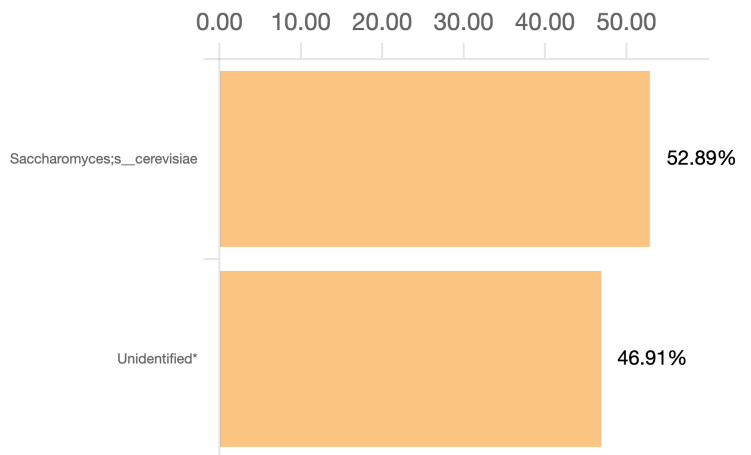
### Result Summary

Parameters		Results	
1	Dysbiosis	-ve	Optimal
2	Uterine community state type	Type III	
3	Uterine microbiome diversity score	0.99	Range: < 4
4	Uterine yeast abundance (yeast/ml)	1,000 = 1.00E+03	Range: < 5,000
5	Candida presence	-ve	

#### Uterine bacterial composition



#### Uterine fungal composition \*



\*Only fungal species with a relative quantity above 2% are represented in the bar chart. For the full list, please refer to the detailed fungal species table.

### Comments:

Dr Golnoush Golshirazi, PhD, MA(Cantab)  
Molecular biologist

# Detailed uterine bacterial compositions

Lactobacillus Species	Relative Quantity	Absolute Quantity*
Genus_Species	Percentage %	Genome/per ml
Lactobacillus;s__iners	98.54	3.98E+08

Key	
Bacterial abundance	This is the absolute measure of the number of bacterial genomes per ml of sample. This is expressed as the specific number and the scientific format of power of 10. I.e. 13,450,354 = 1.3E+7
High bacterial load	> 1E+7
Medium bacterial load	1E+5-1E+7
Low bacterial load	<1E+5

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\*percentage relative to the clients entire Uterine bacterial microbiota



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# Detailed bacterial compositions

Opportunistic & Pathogenic Bacteria	Relative Quantity	Absolute Quantity*
Genus_Species	Percentage %	Genome/per ml
Anaerococcus;s__NA	0.19	7.68E+05
<b>Fingoldia;s__magna</b>	<b>0.16</b>	<b>6.47E+05</b>
<b>Prevotella;s__timonensis</b>	<b>0.12</b>	<b>4.85E+05</b>
Dialister;s__sp36932	0.09	3.64E+05
<b>Prevotella;s__bivia</b>	<b>0.07</b>	<b>2.83E+05</b>
Parvimonas-Tissierella;s__praeacuta-sp31283	0.07	2.83E+05
<b>Prevotella;s__disiens</b>	<b>0.06</b>	<b>2.43E+05</b>
Corynebacterium;s__riegelii	0.05	2.02E+05
Anaerococcus;s__prevotii-tetradius	0.05	2.02E+05
f__Lachnospiraceae;s__sp32831	0.04	1.62E+05
Peptoniphilus;s__lacrimalis	0.03	1.21E+05
Peptoniphilus;s__coxii	0.03	1.21E+05
Peptoniphilus;s__grossensis	0.03	1.21E+05

All bacteria categorised as pathogenic or pathobiont are highlighted in orange. All other bacteria over 1% are also highlighted in orange.

Clinicians and practitioners should refer to the appendix at the back of this report for guidance on the analysis and categorisation methods used in this report.

Key	
<b>Bacterial abundance</b>	This is the absolute measure of the number of bacterial genomes per ml of sample. This is expressed as the specific number and the scientific format of power of 10. I.e. 13,450,354 = 1.3E+7
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# Detailed bacterial compositions

Opportunistic & Pathogenic Bacteria	Relative Quantity	Absolute Quantity*
Genus_Species	Percentage %	Genome/per ml
Parvimonas;s__sp31282	0.03	1.21E+05
Prevotella;s__sp14100	0.02	8.09E+04
Corynebacterium;s__pseudogenitalium-tuberculostearicum	0.02	8.09E+04
Corynebacterium;s__genitalium	0.02	8.09E+04
Peptoniphilus;s__sp31311	0.02	8.09E+04
Dialister;s__micraerophilus	0.02	8.09E+04
Corynebacterium;s__amycolatum	0.02	8.09E+04
Corynebacterium;s__appendicis	0.02	8.09E+04
Corynebacterium;s__aurimucosum	0.02	8.09E+04
Murdochiella;s__sp31271	0.02	8.09E+04
Peptoniphilus;s__duerdenii	0.02	8.09E+04
Campylobacter;s__ureolyticus	0.02	8.09E+04
f__Corynebacteriaceae;s__sp5276	0.02	8.09E+04

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# Detailed bacterial compositions

Opportunistic & Pathogenic Bacteria	Relative Quantity	Absolute Quantity*
Genus_Species	Percentage %	Genome/per ml
Corynebacterium;s__imitans	0.02	8.09E+04
Mobiluncus;s__curtisii	0.01	4.04E+04
Megasphaera;s__sp36951	0.01	4.04E+04
Prevotella;s__buccalis	0.01	4.04E+04
Unknown	0.01	4.04E+04
Corynebacterium;s__freneyi-xerosis	0.01	4.04E+04
Anaerococcus;s__lactolyticus	0.01	4.04E+04
Porphyromonas;s__bennonis	0.01	4.04E+04
Corynebacterium;s__coyleae	0.01	4.04E+04
Arthrobacter;s__cumminsii	0.01	4.04E+04
Helcococcus;s__sp31256	0.009	3.64E+04
Anaerococcus;s__hydrogenalis	0.008	3.23E+04
Ezakiella;s__sp31234	0.008	3.23E+04

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# Detailed bacterial compositions

Opportunistic & Pathogenic Bacteria	Relative Quantity	Absolute Quantity*
Genus_Species	Percentage %	Genome/per ml
Corynebacterium;s__sundsvallense-thomssenii	0.007	2.83E+04
Brevibacterium;s__massiliense	0.007	2.83E+04
Staphylococcus;s__capitis-caprae-epidermidis	0.007	2.83E+04
Dialister;s__propionicifaciens	0.007	2.83E+04

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# Detailed uterine fungal composition

Fungal species	Relative Quantity	Absolute Quantity*
Genus_Species	Percentage %	Genome/per ml
Saccharomyces;s__cerevisiae	52.89	5.29E+02
Unidentified*	46.91	4.69E+02
Microstroma;s__NA	0.19	1.90E+00

\*Indicate that the species has not been classified and therefore cannot be named  
**All Candida and Aspergillus are highlighted in orange.**



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## Next Generation Sequencing Screening

ScreenMe's comprehensive testing (patent pending) is a relative and absolute quantitative universal test for bacteria and fungi. DNA sequencing methods are used to identify the microorganisms' genetic signatures and the estimated percentage and absolute levels of organisms present in the specimen. All bacteria/fungi are screened for alongside positive and negative controls and all findings are reported. This test is not intended for diagnosing, preventing, curing, treating or mitigating diseases or medical conditions.

## DISCLAIMER

DISCLAIMER: (i) This test was developed and performance characteristics have been determined by Zymmo Scientific Laboratory. It has not been cleared or approved by the U.S. Food and Drug Administration (FDA), however, the FDA has determined that such clearance or approval is not necessary. (ii) A negative result does not rule out the presence of PCR inhibitors, or DNA extraction inhibitors such as lidocaine, in patients' specimens or microbial DNA concentrations below the level of detection of the assay. The information and data provided in this document is not to replace the healthcare systems, precision health practices, or any physician's duty of care or advice. Any result should be interpreted in context of clinical finding by a clinical trained professional alongside diagnostic testing. For further information on methods and materials please contact us on support@screenme.co.uk



# Appendix 1



## Definitions:

<b>Lactobacilli</b>	Lactobacilli are beneficial bacteria, particularly in the gastrointestinal tract and the Uterine microbiome. They contribute to maintaining a healthy microbial balance, known as microbiota, by competing with harmful bacteria for nutrients and colonisation sites.
<b>Commensal bacteria</b>	Commensal bacteria, also known as commensals, are microorganisms that live in or on the body of a host organism without causing harm. However some commensal bacteria above a certain levels can be considered pathogenic.
<b>Pathobiont bacteria</b>	Pathobionts are microorganisms that are part of the normal microbial flora (microbiota) of the human body but can become pathogenic under certain conditions. These conditions may include alterations in the host's immune system, changes in the microbiota composition.
<b>Pathogenic bacteria</b>	Pathogenic bacteria are harmful bacteria that can causes disease or illness in the Uterine microbiome. Pathogens can be transmitted through various means such as bodily fluids, and direct contact with infected individuals. They often lead to the manifestation of symptoms associated with the particular disease or infection they cause.

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\*percentage relative to the clients entire Uterine bacterial microbiota

# Appendix 2

## List of Pathogenic and Pathobiont Bacteria\*

The list below is used to calculate the relative percentages of pathogenic and pathobiont bacteria.

- Atopobium vaginae
- Gardnerella;s\_\_Uterineis
- Prevotella species
- Megasphaera species
- Sneathia species
- Mobiluncus species
- Ureaplasma parvum
- Ureaplasma urealyticum
- Chlamydia trachomatis
- Neisseria gonorrhoea
- Mycoplasma genitalium
- Mycoplasma hominis
- Trichomonas Uterineis
- Finegoldia Magna
- Varibaculum;s\_\_cambriense
- Fusobacterium species
- Veillonella;s\_\_tobetsuensis
- Veillonella atypical
- Aerococcus;s\_\_urinae
- Enterococcus faecalis
- Escherichia Coli
- Staphylococcus aureus
- Klebsiella pneumoniae
- Klebsiella oxytoca
- Klebsiella variicola
- Streptococcus agalactiae
- Streptococcus anginosus
- Peptostreptococcus species
- Corynebacterium pseudogenitalium-tuberculostearium



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### DISCLAIMER

DISCLAIMER: \*It is important to note that upon overgrowth, commensal bacteria can also be pathogenic, and this list is for guidance only. It is, therefore, key to always look at the bigger picture, relative levels, and clinical context rather than just the presence or absence of individual bacterial species.

# Appendix 3



## Characterisation of Bacteria key

<b>Lactobacillus &lt; 90%</b>	Dysbiosis
<b>Lactobacillus &lt; 50%</b>	Uterine Community type 4
<b>Commensal Bacteria</b>	Any commensal bacteria above 1% is highlighted in red to be discussed with practitioner/physician.
<b>Pathogenic</b>	Any bacteria categorised as pathogenic or pathobiont is highlighted in red to be discussed with practitioner/physician.
<b>Bacterial load</b>	<ul style="list-style-type: none"><li>• High &gt;1E+7</li><li>• Medium 1E+5-1E+7</li><li>• Low &lt;1E+5</li></ul>

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# Appendix 4

## Community state type:

Community State Type	Dominant Lactobacillus (Above 50%)	Definition
Type I	Crispatus - Optimal	This is a classification of the uterine microbial community. Different Types are strong indicators of uterine health and comfort, reproductive health, fertility and other immune factors such as susceptibility to infections and STDs. <b>Community State Type:</b> Community State Type I is dominated by beneficial Lactobacilli bacteria. The dominant strain is Lactobacillus crispatus and Gallinarum . This community type is ideal and shows the most resilience and stability. People with a CST I have a lower risk of infections like vaginosis, stronger immune response to sexually transmitted infections (STIs), including chlamydia and an increased chance of full-term delivery.
Type II	Gasseri - Healthy	This is a classification of the uterine microbial community. Different Types are strong indicators of uterine health and comfort, reproductive health, fertility and other immune factors such as susceptibility to infections and STDs. <b>Community State Type:</b> Community State Type II is considered healthy and is dominated by beneficial Lactobacillus bacteria. The dominant strain is Lactobacillus gasseri. This community type is less resilient than Type I. They still show clinical significance in promoting a healthy vagina. People with a CST II classification have a decreased risk of developing bacterial vaginosis, UTIs, and STI
Type III	Iners - Healthy but not optimal	This is a classification of the uterine microbial community. Different Types are strong indicators of uterine health and comfort, reproductive health, fertility and other immune factors such as susceptibility to infections and STDs. <b>Community State Type:</b> Community State Type III consists of at least 50% acid-producing Lactobacillus bacteria. However, this type is dominated by Lactobacillus iners, which can be relatively unstable and allow the overgrowth of pathobiont and pathogenic bacteria, increasing the risk of infection and disease.

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# Appendix 4

## Community state type:

Community State Type	Dominant Lactobacillus (Above 50%)	Definition
Type IV	No Lacto dominance - Not Healthy	<p>This is a classification of the uterine microbial community. Different Types are strong indicators of uterine health and comfort, reproductive health, fertility and other immune factors such as susceptibility to infections and STDs.</p> <p><b>Community State Type:</b> Community State Type IV may indicate a bacterial imbalance in the uterine microbiome with high bacterial diversity and low levels of the beneficial Lactobacilli bacteria. This community type increases your risk of harmful bacteria growth, recurrent infections, STDs and complications on your fertility journey, including preterm birth. It is recommended to share these results with your health professional and take extra care of your uterine and reproductive health.</p>
Type V	Jensenii - Normal	<p>This is a classification of the uterine microbial community. Different Types are strong indicators of uterine health and comfort, reproductive health, fertility and other immune factors such as susceptibility to infections and STDs.</p> <p><b>Community State Type:</b> Community State Type V is considered normal and is dominated by beneficial Lactobacillus bacteria. The dominant strain is Lactobacillus jensenii. This community type is relatively resistant and stable. People with a community state type V have a decreased risk of developing bacterial vaginosis, UTIs, and STIs.</p>

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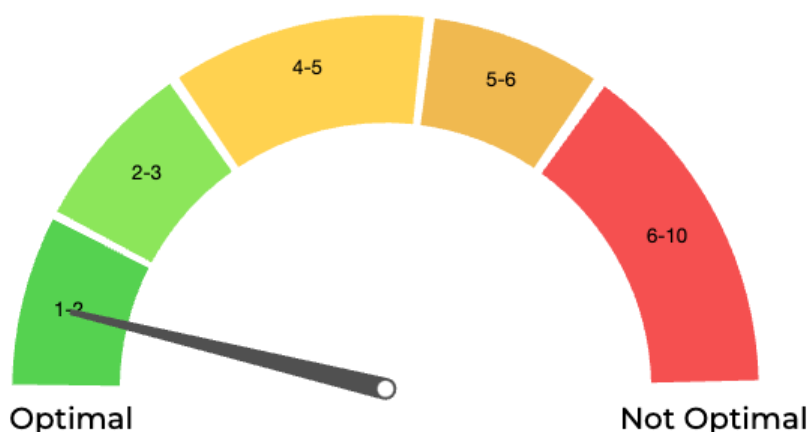
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# Appendix 5

## Uterine microbiome diversity

Range: < 4

Optimal



- Uterine health is typically associated with low microbial diversity. Especially when associated with Lactobacillus species' dominance, it indicates a balanced Uterine microbiome.
- When the diversity increases, the Uterine microbiome is out of balance (dysbiosis).
- An imbalanced microbiome can predispose you to bacterial vaginosis (BV) and put you at higher risk of contracting urinary tract infection (UTI) or sexually transmitted infection (STI)
- Often, Uterine microbiome balance is controlled by your levels of estrogen. Low levels of estrogen may lead to higher diversity.
- \*An overgrowth of lactobacillus which reduces the diversity of the Uterine microbiome, may also lead to cytolytic vaginosis in some women. This will be discussed in your consultation.
- \*Community state type IV Uterine microbiome will also result in a low diversity score. This is due to the dominance of non-lacto strains of bacteria and so not reflective of healthy diversity.

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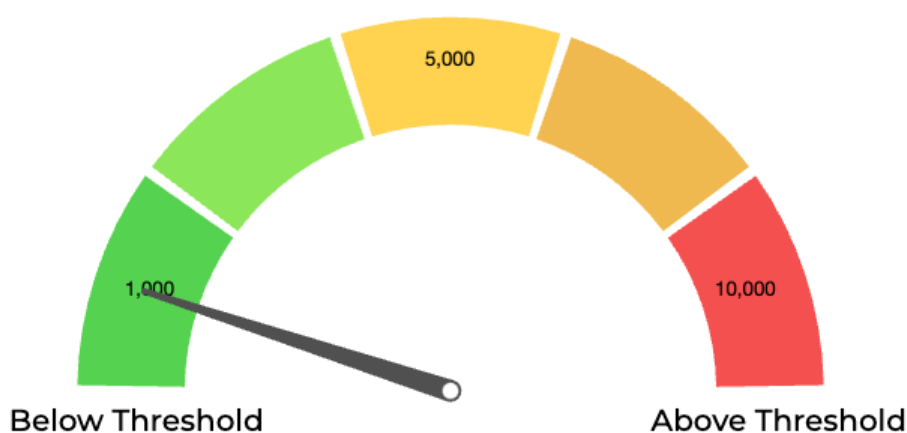
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# Appendix 6

## Uterine yeast abundance

Threshold: < 5000



- Absolute abundance of yeast is measured by looking at the number of yeast genetic material per ul of sample.
- When the yeast absolute abundance is increased, it may indicate an overgrowth of yeast in the Uterine microbiome.
- Increased yeast growth can predispose you to vulvoUterine candidiasis and symptoms of thrush.
- Often, Uterine yeast levels are affected by your levels of estrogen. High levels of estrogen may lead to yeast overgrowth.
- If your absolute yeast levels are higher than average, please refer to the yeast species in section 5b for relative levels of specific yeast strains, allowing more accurate treatment where necessary.

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