



## Reproductive Urine Microbiome Test

Name	
Sample ID	
Date of sample taken	
Date of birth	
Sample type	Urine
Partner	NA
Symptoms	Abnormal smell, UTI, BV

screenme



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## Next Generation Sequencing Screening

Name

Sample Date

### Sample breakdown

**Bacterial Load (Genome copies/ml)**

6,330,000 = 6.33E+06

**Bacterial Diversity (Shannon Index)**

3.39

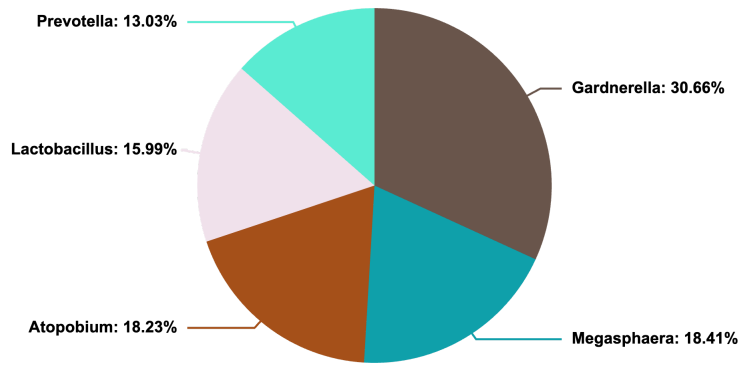
Arbitrary range > 4.5

**Yeast Load (Genome copies/ul)**

0

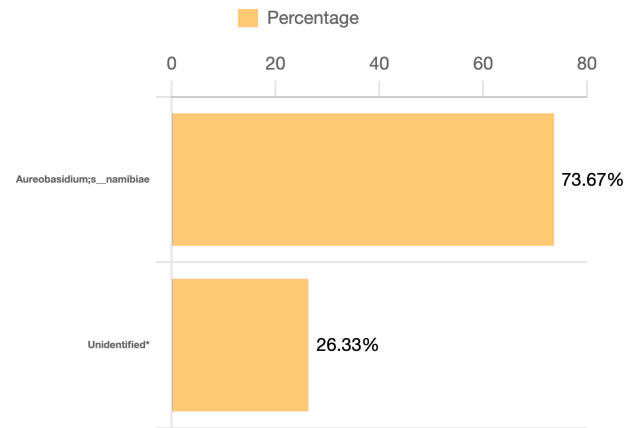
Arbitrary range < 5,000

### Urine bacterial composition \*



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

### Urine 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:

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### Sample breakdown

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6,330,000 = 6.33E+06

**Bacterial Diversity (Shannon Index)**

3.39

Arbitrary range &gt; 4.5

**Yeast Load (Genome copies/ul)**

0

Arbitrary range &lt; 5,000

## Bacterial groups over 1%

(This table consists of a genus of bacteria found to be over 1%. Detailed results are in the 'comprehensive identification' table)

Bacteria Detected Above 1%	Relative Quantity (%)	Absolute Quantity* (Genome/per ml)
Gardnerella	30.66	1.94E+06
Megasphaera	18.41	1.17E+06
Atopobium	18.23	1.15E+06
Lactobacillus	15.99	1.01E+06
Prevotella	13.03	8.25E+05
Senegalimassilia	1.31	8.29E+04

### 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. ie. 13,450,354 = 1.3E+7

**High bacterial load**
 $> 1E+5$ 
**Medium bacterial load**
 $1E+4-1E+5$ 
**Low bacterial load**
 $<1E+4$

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**Bacterial Diversity (Shannon Index)**

3.39

Arbitrary range &gt; 4.5

**Yeast Load (Genome copies/ul)**

0

Arbitrary range &lt; 5,000

## Pathogenic and Pathobiont Bacteria

(This table shows the bacteria present that are categorised as pathogenic or pathobiont)

Pathogenic & Pathobiont Bacteria Detected	Relative Quantity (%)	Absolute Quantity* (Genome/per ml)
Megasphaera;s__sp36945	18.41	1.17E+06
Atopobium;s__vaginae	18.23	1.15E+06
Prevotella;s__disiens	8.99	5.69E+05
Prevotella;s__timonensis	3.17	2.01E+05
Prevotella;s__buccalis	0.79	5.00E+04
Finegoldia;s__magna	0.09	5.70E+03
Pseudomonas;s__aeruginosa	0.06	3.80E+03
Prevotella;s__sp14100	0.05	3.17E+03
Prevotella;s__bivia	0.03	1.90E+03
Streptococcus;s__anginosus	0.03	1.90E+03
Enterococcus;s__faecalis	0.02	1.27E+03

### 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

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 $> 1E+5$ 
**Medium bacterial load**
 $1E+4-1E+5$ 
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 $<1E+4$ 

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\*percentage relative to the client's entire urine bacterial microbiota

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## Next Generation Sequencing Screening

Name

Sample Date

### Sample breakdown

**Bacterial Load (Genome copies/ml)**

6,330,000 = 6.33E+06

**Bacterial Diversity (Shannon Index)**

3.39

Arbitrary range > 4.5

**Yeast Load (Genome copies/ul)**

0

Arbitrary range < 5,000

## Pathogenic and Pathobiont Bacteria

(This table shows the bacteria present that are categorised as pathogenic or pathobiont)

Pathogenic & Pathobiont Bacteria Detected	Relative Quantity (%)	Absolute Quantity* (Genome/per ml)
Ureaplasma;s__parvum-urealyticum	0.02	1.27E+03
Corynebacterium;s__pseudogenitalium-tuberculostearicum	0.01	6.33E+02

### Key

**Bacterial abundance**

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**Next Generation Sequencing Screening**

Name

Sample Date

**Fungal species**

This table presents all bacterial species identified in the sample

Fungus detected	Relative quantity (%)	Absolute levels (Genome/ml)
Aureobasidium;s__namibiae	73.67	Below Threshold
Unidentified*	26.33	Below Threshold

## Next Generation Sequencing Screening

Name

Sample Date

### All bacterial species identified

This table is a comprehensive list of all bacterial species found in the sample

Bacteria Detected	Relative Quantity (%)	Absolute levels (Genome/ml)
Gardnerella;s__vaginalis	30.66	1.94E+06
Megasphaera;s__sp36945	18.41	1.17E+06
Atopobium;s__vaginae	18.23	1.15E+06
Lactobacillus;s__iners	15.99	1.01E+06
Prevotella;s__disiens	8.99	5.69E+05
Prevotella;s__timonensis	3.17	2.01E+05
Senegalimassilia;s__sp10471	1.31	8.29E+04
Dialister;s__propionicifaciens	0.83	5.25E+04
Prevotella;s__buccalis	0.79	5.00E+04
Unknown	0.77	4.87E+04
Dialister;s__microaerophilus	0.17	1.08E+04
Fingoldia;s__magna	0.09	5.70E+03
Pseudomonas;s__stutzeri	0.07	4.43E+03
Staphylococcus;s__capitis-caprae-epidermidis	0.07	4.43E+03
Pseudomonas;s__aeruginosa	0.06	3.80E+03
Prevotella;s__sp14100	0.05	3.17E+03
Sphingomonas;s__alpina-echinoides-glacialis	0.05	3.17E+03
Staphylococcus;s__epidermidis-hominis	0.04	2.53E+03
Prevotella;s__bivia	0.03	1.90E+03
Streptococcus;s__anginosus	0.03	1.90E+03
Enterococcus;s__faecalis	0.02	1.27E+03
Ureaplasma;s__parvum-urealyticum	0.02	1.27E+03
Corynebacterium;s__pilbarensis	0.02	1.27E+03

Next Generation Sequencing Screening

Name

Sample Date

All bacterial species identified

This table is a comprehensive list of all bacterial species found in the sample

Bacteria Detected	Relative Quantity (%)	Absolute levels (Genome/ml)
Staphylococcus;s__pasteuri-warneri	0.02	1.27E+03
Corynebacterium;s__pseudogenitalium-tuberculostearicum	0.01	6.33E+02
Actinomyces;s__neuui	0.01	6.33E+02
Burkholderia-Paraburkholderia;s__caledonica	0.01	6.33E+02
Ralstonia;s__pickettii	0.01	6.33E+02
Propionibacterium;s__acnes	0.01	6.33E+02
Campylobacter;s__hominis	0.01	6.33E+02
Peptoniphilus;s__grossensis	0.01	6.33E+02
Corynebacterium;s__simulans	0.009	5.70E+02
Enterobacter;s__aerogenes-asburiae	0.009	5.70E+02
Sutterella;s__sp48272	0.007	4.43E+02



# Appendix 1

## List of bacteria categorised as pathogenic and pathobiont

- Atopobium vaginae
- Prevotella species
- Megasphaera species
- Sneathia species
- Mobiluncus species
- Ureaplasma parvum
- Ureaplasma urealyticum
- Chlamydia trachomatis
- Neisseria gonorrhoea
- Mycoplasma genitalium
- Mycoplasma hominis
- Trichomonas vaginalis
- Finegoldia Magna
- Varibaculum;s\_\_cambriense
- Fusobacterium species
- Veillonella;s\_\_tobetsuensis
- Veillonella atypical
- Aerococcus;s\_\_urinae
- Enterococcus faecalis
- Escherichia Coli
- Staphylococcus aureus
- Streptococcus agalactiae
- Streptococcus anginosus
- Peptostreptococcus species
- Corynebacterium pseudogenitalium-tuberculostearium
- Actinotignum schaalii
- Aerococcus urinae
- Staphylococcus saprophyticus
- Streptococcus agalactiae
- Citrobacter freundii
- Enterococcus faecalis
- Klebsiella pneumoniae
- Proteus mirabilis
- Pseudomonas aeruginosa
- Serratia marcescens
- Staphylococcus;s\_\_epidermidis
- Staphylococcus;s\_\_lugdunensis

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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.

# Next Generation Sequencing Results

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.

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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 the 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

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\*percentage relative to the client's entire urine bacterial microbiota



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