

Reproductive Seminal Microbiome Test

Name	
Sample ID	
Date of sample taken	
Date of birth	
Sample type	Seminal
Partner	NA
Symptoms	NA

screen*me*



Our labs are subject to rigorous quality systems based on Good Laboratory Practice (GLP), Clinical Laboratory Improvement Amendments (CLIA) regulations and College of American Pathologist (CAP) standards

Next Generation Sequencing Screening

Name

Sample Date

Sample breakdown

Bacterial Load (Genome copies/ml)

2,448,000 = 2.45E+06

Bacterial Diversity (Shannon Index)

3.51

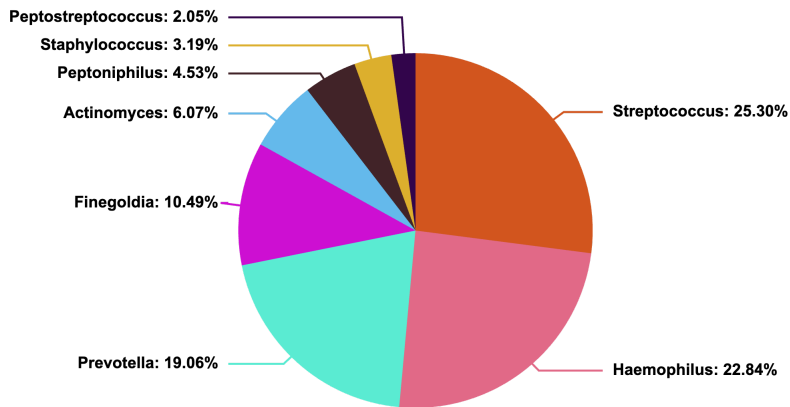
Arbitrary range > 4.5

Yeast Load (Genome copies/ul)

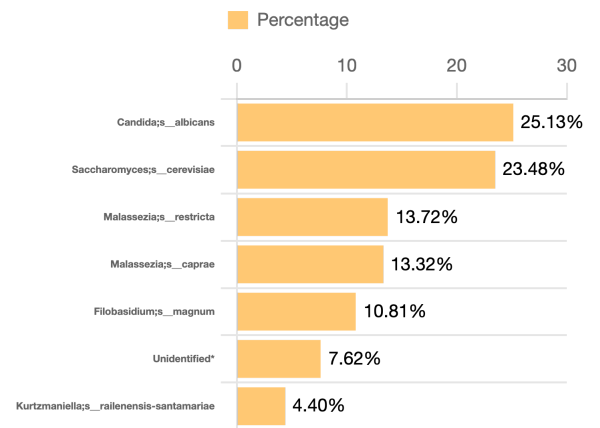
2,000 = 2.00E+03

Arbitrary range < 5,000

Bacterial Genus Chart *



Fungi Species Chart *



*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.

*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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Yeast Load (Genome copies/ul)

2,000 = 2.00E+03

Arbitrary range < 5,000

Result Summary

This table highlights some of the most common bacterial species (or groups) of interest in seminal samples. A complete list of bacteria identified can be found in the 'bacterial species' table.

Bacteria Detected	Category	Relative Quantity (%)	Absolute Quantity* (Genome/per ml)
Chlamydia Trichomonas	Pathogen	0	0
Neisseria gonorrhoeae	Pathogen	0	0
Mycoplasma spp (Total)	Mycoplasma	0	0
Ureaplasma spp (Total)	Mycoplasma	0	0
Staphylococcus spp (Total)	Commensal	3.19	7.81E+04
Streptococcus spp (Total)	Commensal	25.30	6.19E+05
Corynebacterium spp (Total)	Commensal	1.57	3.84E+04
Lactobacillus spp (Total)	Commensal	0	0

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
 $<1E+4$

ScreenMe Scientific



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*percentage relative to the client's entire semen bacterial microbiota



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Arbitrary range < 5,000

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Bacteria Detected	Category	Relative Quantity (%)	Absolute Quantity* (Genome/per ml)
Bacteroides Spp (Total)	Opportunistic Anaerobe	0	0
Porphyromonas spp (Total)	Opportunistic Anaerobe	0	0
Prevotella spp (Total)	Opportunistic Anaerobe	19.06	4.67E+05
Anaerococcus spp (Total)	Opportunistic Anaerobe	0.06	1.47E+03
Peptostreptococcus spp (Total)	Opportunistic Anaerobe	2.05	5.02E+04
Parvimonas spp (Total)	Opportunistic Anaerobe	0	0
Enterococcus;s__faecalis	Opportunistic Anaerobe	0.52	1.27E+04
Escherichia Coli	Opportunistic Anaerobe	0	0
Eubacterium spp (Total)	Opportunistic Anaerobe	0	0
Total sum of opportunistic anaerobes above		21.69	5.31E+05

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Bacteria Detected	Category	Relative Quantity (%)	Absolute Quantity* (Genome/per ml)
Gardnerella Vaginalis	BV associated bacteria	0	0
Megasphaera Spp (Total)	BV associated bacteria	0	0
Veillonella Spp (Total)	BV associated bacteria	0.58	1.42E+04
Dialister Spp (Total)	BV associated bacteria	0.58	1.42E+04
Sneathia Spp (Total)	BV associated bacteria	0	0
Leptotrichia Spp (Total)	BV associated bacteria	0	0
Fusobacterium spp (Total)	BV associated bacteria	0	0
Atopobium Spp (Total)	BV associated bacteria	0	0
Fingoldia Magna	BV associated bacteria	10.49	2.57E+05
Peptoniphilus spp (Total)	BV associated bacteria	4.53	1.11E+05
Total sum of BV associated bacteria above		16.18	3.96E+05

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High bacterial load

> 1E+5

Medium bacterial load

1E+4-1E+5

Low bacterial load

<1E+4

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)
Haemophilus;s__pittmaniae	22.84	5.59E+05
Streptococcus;s__urinalis	19.98	4.89E+05
Prevotella;s__bivia	19.06	4.67E+05
Fingoldia;s__magna	10.49	2.57E+05
Actinomyces;s__neuui	6.07	1.49E+05
Streptococcus;s__anginosus	5.26	1.29E+05
Peptoniphilus;s__grossensis	4.53	1.11E+05
Staphylococcus;s__haemolyticus-petrasii	2.06	5.04E+04
Peptostreptococcus;s__anaerobius	2.05	5.02E+04
Corynebacterium;s__pseudogenitalium-tuberculostearicum	1.16	2.84E+04
Unknown	1.02	2.50E+04
Staphylococcus;s__haemolyticus	0.65	1.59E+04
Dialister;s__micraerophilus	0.58	1.42E+04
Enterococcus;s__faecalis	0.52	1.27E+04
f__Corynebacteriaceae;s__sp5023	0.40	9.79E+03
Veillonella;s__parvula	0.35	8.57E+03
Staphylococcus;s__capitis-caprae-epidermidis	0.31	7.59E+03
Propionibacterium;s__acnes	0.29	7.10E+03
Veillonella;s__tobetsuensis	0.21	5.14E+03
Corynebacterium;s__imitans	0.19	4.65E+03
Staphylococcus;s__pasteuri-warneri	0.17	4.16E+03
Pseudomonas;s__NA	0.16	3.92E+03
Sphingomonas;s__alpina-echinoides-glacialis	0.16	3.92E+03

Next Generation Sequencing Screening

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All bacterial species identified

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Bacteria Detected	Relative Quantity (%)	Absolute levels (Genome/ml)
f_Corynebacteriaceae;s__sp5276	0.12	2.94E+03
Enhydrobacter-Moraxella;s__aerosaccus-osloensis	0.11	2.69E+03
Roseomonas;s__vinacea	0.10	2.45E+03
Bradyrhizobium;s__sp43375	0.08	1.96E+03
Acinetobacter;s__haemolyticus-johnsonii-lwoffii	0.08	1.96E+03
Curtobacterium;s__flaccumfaciens-oceanosedimentum	0.08	1.96E+03
Corynebacterium;s__sundsvallense-thomssenii	0.07	1.71E+03
Pseudomonas;s__aeruginosa	0.07	1.71E+03
Anaerococcus;s__hydrogenalis	0.06	1.47E+03
Dermacoccus;s__nishinomiyaensis	0.06	1.47E+03
Micrococcus;s__NA	0.06	1.47E+03
Acidibacter;s__sp65540	0.06	1.47E+03
Corynebacterium;s__kroppenstedtii	0.05	1.22E+03
Streptococcus;s__NA	0.05	1.22E+03
Corynebacterium;s__freneyi-xerosis	0.05	1.22E+03
Corynebacterium;s__falsenii	0.05	1.22E+03
Acinetobacter;s__parvus	0.05	1.22E+03
Acinetobacter;s__beijerinckii-calcoaceticus	0.05	1.22E+03
Acinetobacter;s__johnsonii	0.05	1.22E+03
Dermabacter;s__hominis	0.04	9.79E+02
Gordonia;s__bronchialis	0.04	9.79E+02
Mycobacterium;s__moriokaense	0.03	7.34E+02
Veillonella;s__denticariosi-parvula-tobetsuensis	0.02	4.90E+02

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)
Rubellimicrobium;s__mesophilum	0.02	4.90E+02
Ralstonia;s__insidiosa	0.02	4.90E+02
Burkholderia-Paraburkholderia;s__insulsa	0.01	2.45E+02
Tabrizicola;s__sp45174	0.009	2.20E+02
Burkholderia-Burkholderia-Paraburkholderia;s__cepacia-contaminans-lata	0.009	2.20E+02
Streptococcus;s__lactolyticus	0.005	1.22E+02
Friedmanniella;s__antarctica	0.005	1.22E+02

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)
Candida;s__albicans	25.13	5.03E+02
Saccharomyces;s__cerevisiae	23.48	4.70E+02
Malassezia;s__restricta	13.72	2.74E+02
Malassezia;s__caprae	13.32	2.66E+02
Filobasidium;s__magnum	10.81	2.16E+02
Unidentified*	7.62	1.53E+02
Kurtzmaniella;s__railenensis-santamariae	4.40	8.79E+01
Malassezia;s__globosa	1.52	3.04E+01

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

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