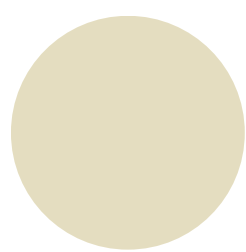


NGS DIAGNOSTICS

PATIENT	
---------	--

SPECIMEN	Semen swab
COMPLETED	

BACTERIAL LOAD (Bacteria/ml)	845,000 =8.45E+5
Yeast Load (Genome copies/ml)	0



Result Summary

(detailed results are provided below)

BACTERIA Detected	Category	RELATIVE %	Absolute levels (Bacteria/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	1.09	9.55E+03
Streptococcus spp (Total)	Commensal	0	0
Corynebacterium spp (Total)	Commensal	5.75	5.04E+04
Lactobacillus spp (Total)	Commensal	0.04	3.50E+02

Key	
Bacterial abundance	This is the absolute measure of the number of bacterial genomes per ml of sample. This is expressed at 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

NGS DIAGNOSTICS

PATIENT	
---------	--

SPECIMEN	Semen swab
COMPLETED	

BACTERIAL LOAD (Bacteria/ml)	876,000 =8.76E+5
Yeast Load (Genome copies/ml)	0

Result Summary
 (detailed results are provided below)

BACTERIA Detected	Category	RELATIVE %	Absolute levels (Bacteria/ml)
Bacteroides Spp (Total)	Opportunistic Anaerobe	0	0
Porphyromonas spp (Total)	Opportunistic Anaerobe	0	0
Prevotella spp (Total)	Opportunistic Anaerobe	0.04	3.50E+02
Anaerococcus spp (Total)	Opportunistic Anaerobe	1.94	1.70E+04
Peptostreptococcus spp (Total)	Opportunistic Anaerobe	0	0
Parvimonas spp (Total)	Opportunistic Anaerobe	0	0
Enterococcus;s__faecalis	Opportunistic Anaerobe	0.06	5.26E+02
Escherichia Coli	Opportunistic Anaerobe	0.02	1.75E+02
Eubacterium spp (Total)	Opportunistic Anaerobe	0	0

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

NGS DIAGNOSTICS

PATIENT	
---------	--

SPECIMEN	Semen swab
COMPLETED	

BACTERIAL LOAD (Bacteria/ml)	876,000 =8.76E+5
Yeast Load (Genome copies/ml)	0

Result Summary
 (detailed results are provided below)

BACTERIA DETCTED	Category	RELATIVE %	Absolute levels (Bacteria/ml)
Gardnerella Vaginalis	BV associated bacteria	0	0
Megasphaera Spp (Total)	BV associated bacteria	0	0
Veillonella Spp (Total)	BV associated bacteria	0	0
Dialister Spp (Total)	BV associated bacteria	0.05	4.38E+02
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	4.71	4.13E+04
Peptoniphilus spp (Total)	BV associated bacteria	0	0

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

PATIENT	
---------	--

SPECIMEN	Semen swab
COMPLETED	

BACTERIAL LOAD (Bacteria/ml)	876,000 =8.76E+5
Yeast Load (Genome copies/ml)	0

Fungal species

Fungus Detected	RELATIVE %	Absolute levels (fungus/ml)
Not Identified*	68.62	0.00E+00
Cutaneotrichosporon;s__curvatus	10.73	0.00E+00
Malassezia;s__restricta	8.22	0.00E+00
Panellus;s__edulis	7.54	0.00E+00
Myriangium;s__NA	4.9	0.00E+00

PATIENT	
---------	--

SPECIMEN	Semen swab
COMPLETED	

BACTERIAL LOAD (Bacteria/ml)	876,000 =8.76E+5
Yeast Load (Genome copies/ml)	0

COMPREHENSIVE IDENTIFICATION NEXT-GEN DNA SEQUENCING RESULTS - (Complete list of bacteria detected.)

BACTERIA DETCTED	RELATIVE %	ABSOLUTE LEVELS (LOAD/ML)
Streptococcus;s__NA	56.26	4.93E+05
Ralstonia;s__pickettii	9.22	8.08E+04
Fingoldia;s__magna	4.71	4.13E+04
Phyllobacterium;s__brassicacearum-myrsinacearum	4.55	3.99E+04
Corynebacterium;s__pyruviciproducens	3.35	2.93E+04
Pseudomonas;s__aeruginosa	2.1	1.84E+04
Anaerococcus;s__hydrogenalis-vaginalis	1.92	1.68E+04
Pseudomonas;s__stutzeri	1.82	1.59E+04
Corynebacterium;s__pseudogenitalium-tuberculostearicum	1.18	1.03E+04
Sphingomonas;s__alpina-echinoides-glacialis	1.17	1.02E+04
NA	1.03	9.02E+03
Peptoniphilus;s__grossensis	1.02	8.94E+03
Sphingobium;s__limneticum	0.98	8.58E+03
Roseomonas;s__gilardii-mucosa	0.96	8.41E+03

Next Generation Sequencing Results

ScreenMe's comprehensive testing (patent pending) is a relative quantitative universal test for bacteria/fungi. DNA sequencing methods are used to identify the microorganisms' genetic signatures and the estimated percentage of organisms present in the specimen. Virtually all bacteria/fungi are screened for and the most predominant populations are reported.

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. For further information on methods and materials please contact us on 0044 20 7842 1000