

External ID

Name First Name	Date of Birth Sex	Female	Order ID Order Date
Sampling Date Sample Material	Validation by Validation Date	Dr. Herbert Schmidt	Findings Status Findings Date

Final Report

Test	Result	Unit	Standard Range	Previous Result
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Vaginal Diagnostic

Vaginal Microbiomeanalysis

Properties of the vaginal secretion

pH	4,0		4,0 - 4,4		AB NA)
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Biodiversity

Diversity	0,73		< 0,90		AB NA) MGSEQ
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The biodiversity of vaginal microbiota may vary from person to person. A low diversity indicates a healthy physiological vaginal flora. A high diversity may indicate mycosis, pathogenic bacteria or sexually transmitted diseases.

Grad



Vaginal Type / Community State Type (CST)

The composition of the vaginal microbiota can be differentiated into different communities, so-called vaginal types. The five most common vaginal types I, II, III, IV and V are characterized by the respective dominant lactobacillus species.

Vaginaltyp



Bacterial Vaginosis Score

The BV-score assesses the vaginal flora status with regard to a bacterial vaginosis (BV). This involves the inclusion and assessment of the physiological lactobacillus flora, the anaerobic accompanying flora and the BV-associated flora.

< 5		AB NA) MGSEQ
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BV Score

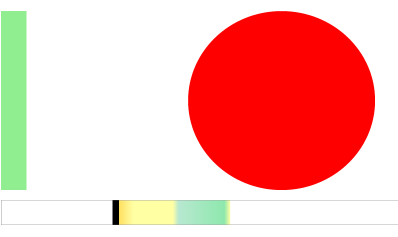
- < 5 normal
- 5 - 8 intermediär
- > 8 positiv

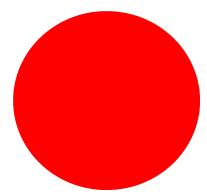


H2O2 production

H2O2 Synthesis index	1,00		> 4		AB NA) MGSEQ
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Lactobacillus (most common)

Lactobacillus crispatus	0,00	%			AB NA) MGSEQ
Lactobacillus gasseri	0,00	%			
Lactobacillus jensenii	0,00	%			
Lactobacillus iners	0,00	%			
Lactobacillus (total)	0,4	%	> 70,0		



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BV-associated Bacteria					
Atopobium vaginae	88,58	%	< 0,01		AB NA) MGSEQ
BVAB*-1	0,00	%	< 0,01		AB NA) MGSEQ
BVAB*-2	<0,01	%	< 0,01		AB NA) MGSEQ
BVAB*-3	0,00	%	< 0,01		AB NA) MGSEQ
Bacteroides fragilis	<0,01	%	< 0,01		AB NA) MGSEQ
Gardnerella vaginalis	9,43	%	< 0,01		AB NA) MGSEQ
Megasphaera spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Eggerthella spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Aerococcus christensenii	<0,01	%	< 0,01		AB NA) MGSEQ
Dialister microaerophilus	<0,01	%	< 0,01		AB NA) MGSEQ
Prevotella spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Dialister spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Mobiluncus spp.	0,00	%	< 0,01		AB NA) MGSEQ
Anaerobic accompanying flora					
Anaerococcus spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Bacteroides spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Corynebacterium spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Escherichia spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Finegoldia spp.	0,00	%	< 0,01		AB NA) MGSEQ
Gemella spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Lachnospiraceae	<0,01	%	< 0,01		AB NA) MGSEQ
Mycoplasma spp.	0,00	%	< 0,01		AB NA) MGSEQ
Parvimonas spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Sneathia spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Streptococcus spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Ureaplasma spp.	0,00	%	< 0,01		AB NA) MGSEQ
Veillonella spp.	<0,01	%	< 0,01		AB NA) MGSEQ
Sonstige	1,56	%			AB NA) MGSEQ
Candidiasis					
Candida albicans	positive		negative		AB NA) QPCR
Candida dubliniensis	negative		negative		AB NA) QPCR
Candida glabrata	negative		negative		AB NA) QPCR
Candida krusei	negative		negative		AB NA) QPCR
Candida lusitaniae	negative		negative		AB NA) QPCR
Candida parapsilosis	negative		negative		AB NA) QPCR
Candida tropicalis	negative		negative		AB NA) QPCR