APERIOMICS®

CLIN–PATHO℠ REPORT

Patient	Ordering Provider	Sample Information
▉▉▉▉▉▉	▉▉▉▉▉▉▉▉	**Urine DNA**
Gender: Fe		Specimen#: 11790504
Patient ID: ▉▉▉▉		Collected: 02/20/2021
Request ID: 111		Received: 02/24/2021
		Reported: 03/08/2021

CLIN-PATHO℠ SUMMARY

DNA Viruses Identified	**Detected**	Total DNA Fragments	41,871,632
Parasite & Other Identified	**Detected**	Human DNA Fragments	17,405,928
Fungi Identified	**Detected**	Total Classified DNA Fragments	5,195,848
Bacteria Identified	**Detected**	Microbial Burden	20.697%

FINDINGS

The findings of this test are POSITIVE. Microbial burden is higher than expected in healthy female urine, suggesting significant microbial overgrowth. Uropathogens are present at elevated levels. Evidence of infection is present.

Clin-PATHO™ Urine Test identifies every known, sequenced microorganism physically collected in the urine sample tested. Sample collection procedure, patient history, diet/dietary supplements, occupation, and exposures should be taken into consideration when reviewing findings. If infection is present, sexual partners should be evaluated as a possible reservoir of re-infection. This summary is based on the current understanding of female urinary microbiomes and scientific knowledge of microorganisms, which regularly evolves, and views may change over time.

PATHOGENS
Propionimicrobium lymphophilum was identified at high levels and has been documented in urinary tract infections (https://jcm.asm.org/content/53/9/3077).

POTENTIAL PATHOGENS
Actinotignum timonense was identified at high levels and is not found at high levels in healthy female urine. Related species have been documented to cause UTIs (https://pubmed.ncbi.nlm.nih.gov/26577137/).

Prevotella species were identified at higher levels than expected in healthy urine and have been documented in UTI cases (https://onlinelibrary.wiley.com/doi/full/10.1111/j.1442-2042.2003.00756.x).

Peptoniphilus was higher than expected and a documented uropathogen (https://www.mathewsopenaccess.com/full-text/cutaneous-vasculitis-as-a-first-sign-of-isolated-peptoniphilus-spp-in-urinary-tract-infection-a-case-report).

Porphyromonas, Varibaculum, and Aerococcus were all higher than expected and known uropathogens.

OTHER MICROORGANISMS
Many enteric bacteria, archaea, and fungi were identified at low levels, some of which are not expected in healthy urine. These may have been introduced into the sample if clean-catch instructions were not followed. They may also be colonizing the bladder/urethra if a clean catch was taken. A number of healthy urinary flora were identified at low levels.

Reviewed by: Crystal R Icenhour, PhD – CEO, Infectious Disease Expert
Approved by: C Alexander Valencia, PhD - CCO and Laboratory Director
Approved by: Yaping Qian, PhD - Laboratory Director

Note: This summary of findings is intended to give clinicians information to gain a deeper understanding of the microbial populations identified in each sample tested . This summary of findings highlights microorganism(s) presence and abundance, compared to healthy samples and relevant peer-reviewed literature. We can provide additional support to clinicians on a case-by-case basis, however, it is beyond our scope of practice to provide diagnosis, drug susceptibility, or treatment guidance. It is recommended that a pharmacist with expertise in infectious diseases be consulted with regard to treatment guidance. If you would like to schedule an appointment to speak to one of our infectious disease experts, please email support@aperiomics.com.

CLIN-PATHO℠ IDENTIFIED DNA VIRUS

Species	RPM
Staphylococcus phage Twillingate	342
Streptococcus phage Javan32	295
Staphylococcus phage Quidividi	121
Staphylococcus virus CNPH82	15

CLIN-PATHO^{SM} IDENTIFIED PARASITE & OTHER

Kingdom	Species	Abundance %	RPM
Archaea	*Methanobrevibacter smithii*	0.294	1946.17
Archaea	*Methanobrevibacter sp. A54*	0.002	15.782

CLIN-PATHO^{SM} IDENTIFIED FUNGI

Species	Abundance %	RPM
Saccharomyces cerevisiae	0.001	26.175

CLIN-PATHO^{SM} IDENTIFIED BACTERIA

Species	Abundance %	RPM
Propionimicrobium lymphophilum	9.1	81979.3
Actinotignum timonense	5.3	45760
Prevotella timonensis	5.1	63035.7
Peptoniphilus harei	5	34435.2
Prevotella corporis	5	53213.6
Porphyromonas uenonis	4.5	43268.4
Porphyromonas somerae	4.4	40782.9
Porphyromonas asaccharolytica	3.9	37565.8
Prevotella buccalis	3.7	43951.6
Varibaculum cambriense	3.5	34223.9
Aerococcus urinae	3.3	26623.6
Anaerococcus lactolyticus	2.9	23629.6
Peptoniphilus lacrimalis	2.7	18640.7
Finegoldia magna	2.6	18858.5
Streptococcus dysgalactiae	2.6	20003.7
Campylobacter ureolyticus	2.6	16383.9
Porphyromonas bennonis	2.5	20412.5
Prevotella colorans	2.2	24175.1
Varibaculum massiliense	1.4	16454.3
Mobiluncus curtisii	1.4	14921.5

Species	Abundance %	RPM
Fenollaria timonensis	1.2	7924
Peptoniphilus grossensis	1.2	9476.4
Facklamia hominis	1.2	7872.1
Corynebacterium imitans	1	11225.5
Levyella massiliensis	1	6181.5
Atopobium deltae	0.8	4352.7
Lagierella massiliensis	0.8	6122.2
Peptoniphilus pacaensis	0.8	5306.9
Alterileibacterium massiliense	0.7	4009.7
Anaerococcus obesiensis	0.7	5473.6
Corynebacterium aurimucosum	0.7	8290.9
Corynebacterium frankenforstense	0.6	6372
Porphyromonadaceae bacterium FC4	0.6	4655.6
Bacteroides vulgatus	0.6	10467.2
Ezakiella massiliensis	0.5	3410.4
Corynebacterium jeikeium	0.5	5161.8
Peptococcus niger	0.5	3653.3
Clostridiales bacterium S5-A14a	0.5	3057.8
Peptoniphilus urinimassiliensis	0.5	3319.2
Corynebacterium glucuronolyticum	0.5	5047.5
Anaerococcus prevotii	0.4	2948.9
Corynebacterium tuberculostearicum	0.4	3445.8
Lachnospiraceae bacterium 3_1_46FAA	0.4	4183
Tissierellia bacterium S7-1-4	0.4	2939.3
Fusobacterium naviforme	0.4	3053.2
Corynebacterium pseudogenitalium	0.3	3405.8
Anaerococcus vaginalis	0.3	2205.2
Corynebacterium pyruviciproducens	0.3	3285.7
Gleimia europaea	0.3	2434.3
Tissierellia bacterium S5-A11	0.3	3182.2
Campylobacter hominis	0.2	1502
Prevotella bergensis	0.2	2996.2
Staphylococcus epidermidis	0.2	2041.6
[Bacteroides] coagulans	0.2	1594.3
Corynebacterium ihumii	0.2	2269.5

Species	Abundance %	RPM
Peptoniphilus obesi	0.2	1224.8
Varibaculum vaginae	0.2	2148.3
Anaerococcus mediterraneensis	0.2	1460
Peptoniphilus vaginalis	0.2	1167.1
Anaerococcus marasmi	0.2	1323.4
Urinicoccus massiliensis	0.1	1174.4
Corynebacterium coyleae	0.1	2006.6
Bacteroides dorei	0.1	2509.3
Corynebacterium minutissimum	0.1	1523.9
Corynebacteriaceae bacterium 'ARUP UnID 227'	0.1	1259.9
Winkia neuii	0.1	1030.1
Faecalibacterium prausnitzii	0.1	1497.3
Bacteroides uniformis	0.1	2197.5
Escherichia coli	0.1	2272.6
Blautia obeum	0.1	1621.7
Anaerococcus provencensis	0.1	1069.7
Arcanobacterium urinimassiliense	0.1	793.3
Anaerococcus urinomassiliensis	0.1	1050.8
Anaeroglobus geminatus	0.1	762.1
Megasphaera massiliensis	0.1	1135.9
Evtepia gabavorous	0.1	1012.3
Acidaminococcus intestini	0.1	966.9
Ruminococcaceae bacterium cv2	0.1	1659.4
Ezakiella peruensis	0.1	691.3
Peptoniphilus senegalensis	0.1	772.5
Corynebacterium hadale	0.1	1386.9
Anaerococcus octavius	0.1	592.4
Bacteroides ovatus	0.1	1913.1
Bacteroides thetaiotaomicron	0.1	1746
Negativicoccus succinicivorans	0.1	404.9
Parabacteroides distasonis	0.1	1351.8
Enterococcus faecalis	0.1	832.2
Clostridiales bacterium SIT11	0.1	466.5
Blautia massiliensis	0.1	930.4
Corynebacterium jeddahense	0.1	1083.9

Species	Abundance %	RPM
Parabacteroides merdae	0.1	1081.2
Corynebacterium genitalium	0.1	739.1
Olegusella massiliensis	0.1	440
Corynebacterium amycolatum	0.1	605.1
Desulfovibrionaceae bacterium	0.1	856.1
Kallipyga massiliensis	0.1	428.8
Alistipes finegoldii	0.1	797.9
Anaerococcus hydrogenalis	0.1	555.1
Peptoniphilus duerdenii	0.1	492.7
Coprococcus catus	0.1	677.8
Fastidiosipila sanguinis	0.1	406.5
Facklamia ignava	0.1	331.8
Facklamia languida	0.1	314.9
Fenollaria massiliensis	0.1	333

METHODS

Total DNA was isolated using commercial DNA extraction kits from each sample type. Libraries were prepared using the KAPA HyperPlus Prep Kit (Roche, Wilmington, MA) followed by flourometry DNA quality quantification assessment and shotgun metagenomic sequencing on NextSeq500 or HiSeq2500 (Illumina, San Diego, CA) using 75 bp paired-end or 100 bp paired-end modes. For shotgun metagenomic sequencing analysis, Xplore-ID software and Xplore-DB database (Aperiomics, Inc., Sterling, VA) were utilized for quality assessment, background removal, alignment, genome binning, microbial identification, and abundance / RPM calculations.

DEFINITIONS

- **SHOTGUN METAGENOMICS SEQUENCING -** A DNA sequencing method where millions of sequencing reactions are carried out in parallel, increasing the sequencing throughput and generating a raw DNA data file for DNA present in the sample. This method allows unbiased sequencing of all or nearly all DNA in a sample, including microbial genetic information.

- **XPLORE ID -** Analysis software that rapidly and accurately defines the proportions of reads from individual microbial species present in shotgun metagenomic sequencing data obtained from samples.

- **XPLORE DB -** A comprehensive database containing the complete genomes of every high quality, validated genome from every sequenced microorganism.

- **TOTAL DNA FRAGMENTS -** The shotgun sequencing output total number of DNA fragments sequenced.

- **HUMAN DNA FRAGMENTS -** The number of DNA fragments that specifically match to the host. The host in most clinical samples is human.

- **CLASSIFIED DNA FRAGMENTS -** The reads that align to any known microorganism.

- **RPM (Read Per Million) -** The number of reads mapped to a genome per million microbial DNA reads in the sample.

- **MICROBIAL BURDEN -** Microbial Burden is the number of microbial reads found compared to the total host and microbial reads. Microbial burden can mean different things based on what type of sample is being examined. This can sometimes be above 0% in a sample with no microbes due to sequencing noise.

- **ABUNDANCE -** The Abundance % category is the estimated amount of [microbial DNA that matches each listed species] in the sample compared to other microbes present. The relative abundance is defined as:

$$S_i = \frac{C_i/g_i}{\sum C_i/g_i}$$

where i represents the index of the given species; S is the relative abundance; C is number of reads assigned to the given species; g is the size of the reference genome (bp). Because virus genome size is very small, viruses are not included in this calculation to prevent bias.

LIMITATIONS OF THE TESTS AND ADDITIONAL INFORMATION

While the results of **CLIN-PATHO**^{SM} testing is accurate, the presence and/or absence of microorganisms may vary due to a number of circumstances. Such circumstances may includesample collection procedure, use of probiotics and anti-infective medications, and other factors. Samples testing positive for potential pathogens should be referred to a healthcareprovider for interpretation of the results in relation to all other clinical symptoms and testing. The results of this testing, including the benefits and limitations, should be discussed with a qualified health care provider and are required for diagnosis and treatment. The healthcare provider is responsible for the use of this information in the management of their patient. Pursuant to the requirements of CLIA '88, this test was developed and its performance validated by Aperiomics. It has not been cleared or approved by the U.S. Food and Drug Administration (FDA). The FDA has determined that such clearance or approval is not necessary. This test is used for clinical purposes. Aperiomics CLIA number is 49D2181329. Aperiomics, Inc. is required by law to maintain the privacy and security of your protected health information. **APERIOMICS ® is trademark of Aperiomics, Inc. © 2020 Aperiomics, Inc All rights reserved.**