DATA SHEET

Urinary Pathogen ID/ AMR Panel

Highly sensitive, culture-free identification and quantification of common and underrecognized uropathogens

- Identification of > 170 pathogens associated with complicated and uncomplicated infections
- Coverage of > 3700 genes and gene variants associated with antimicrobial resistance
- Compatible with select human and environmental sample types

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Genetic identification of urinary tract infections

Urinary tract infection (UTI) is any infection occurring in the urinary system (ie, kidneys, ureters, bladder, and urethra). They are among the most common bacterial infections, but UTIs can also be caused by fungal, viral, and parasitic agents. Most infections involve the lower urinary tract, including the bladder and the urethra. Bacterial infections are mostly treated with antibiotics but the rise in antibiotic resistance is a major health concern.[1]

The Urinary Pathogen ID/AMR Panel is a research panel that brings the power of precision metagenomics to uropathogen identification. Panel content is developed based on reported correlation with uncomplicated or complicated UTIs and multidrug-resistant infections. The panel is able to detect and quantify 174 organisms, including common and less common uropathogens and some sexually transmitted pathogens (Figure 1, Table 1). In addition, the panel covers > 3700 genes and gene variants associated with antimicrobial resistance (AMR).

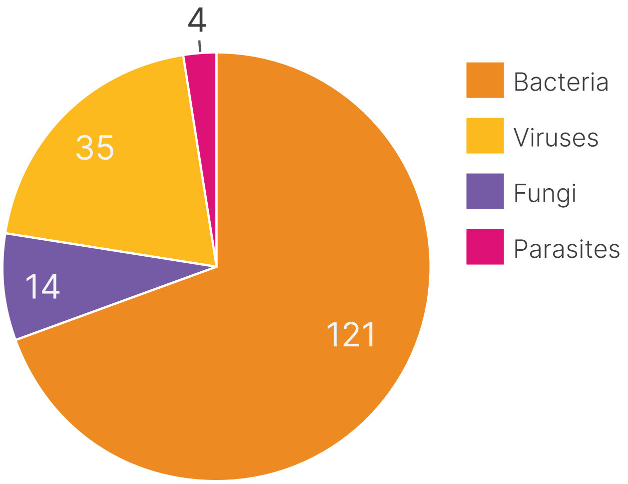

Figure 1: Urinary pathogen categories covered on the Urinary Pathogen ID/AMR Panel.

Workflow

The Urinary Pathogen ID/AMR Panel enriches for pathogen genomes from a range of host and environmental samples. The workflow includes DNA isolation, library preparation, sequencing, and secondary next-generation sequencing (NGS) analysis (Figure 2). The library preparation and sequencing steps can be completed in two days on benchtop sequencing systems.

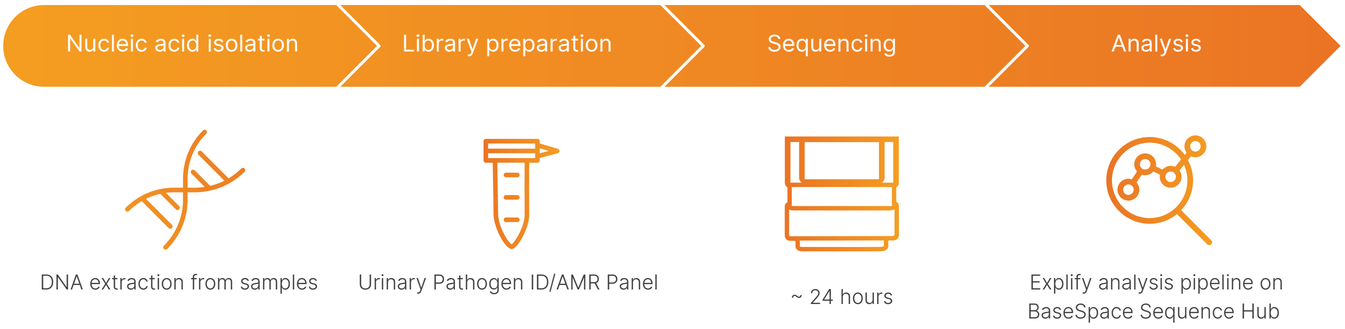

Figure 2: Urinary Pathogen ID/AMR Panel workflow—In a streamlined, comprehensive workflow, libraries are prepared from environmental or host samples, sequenced on any Illumina benchtop sequencing system, and analyzed in the Explify pipeline for pathogen identification, consensus sequence generation, read mapping to pathogen best match, and strain typing. Sequencing time varies with sample read depth and sequencing system used.

Table 1: Microorganisms covered on the Urinary Pathogen ID/AMR Panel.

Reporting name					
Acidovorax wautersii	*Candida lusitaniae (Clavispora lusitaniae)*	*Finegoldia magna (Peptostreptococcus magnus)*	Human papillomavirus type 51	*Mycobacterium simiae* complex	*Schistosoma haematobium*
Acinetobacter baumannii	*Candida parapsilosis*	*Francisella tularensis*	Human papillomavirus type 52	*Mycobacterium szulgai*	*Serratia marcescens*
Acinetobacter calcoaceticus	*Candida tropicalis*	*Fusobacterium necrophorum*	Human papillomavirus type 54	*Mycobacterium tuberculosis* complex	Simian virus 40
Acinetobacter pittii	*Chlamydia trachomatis*	*Fusobacterium nucleatum*	Human papillomavirus type 55/44	*Mycobacterium xenopi*	*Sneathia amnii (Leptotrichia amnionii)*
Actinobaculum massiliense	*Chromobacterium violaceum*	*Giardia intestinalis*	Human papillomavirus type 56	*Mycobacteroides chelonae (Mycobacterium chelonae)*	*Staphylococcus aureus*
Actinotignum sanguinis	*Chryseobacterium indologenes*	*Haemophilus ducreyi*	Human papillomavirus type 58	*Mycoplasma genitalium*	*Staphylococcus epidermidis*
Actinotignum schaalii (Actinobaculum schaalii)	*Citrobacter freundii* complex	*Haemophilus influenzae*	Human papillomavirus type 6	*Mycoplasma hominis*	*Staphylococcus haemolyticus*
Aerococcus christensenii	*Citrobacter koseri*	*Haemophilus parainfluenzae*	Human papillomavirus type 66	*Neisseria gonorrhoeae*	*Staphylococcus hominis*
Aerococcus sanguinicola	*Corynebacterium aurimucosum*	*Hafnia alvei*	Human papillomavirus type 68	*Neisseria meningitidis*	*Staphylococcus intermedius*
Aerococcus urinae	*Corynebacterium coyleae*	Herpes simplex virus 1	Human papillomavirus type 70	*Oligella urethralis*	*Staphylococcus lugdunensis*
Aerococcus viridans	*Corynebacterium genitalium*	Herpes simplex virus 2	JC polyomavirus	*Pantoea agglomerans*	*Staphylococcus saprophyticus*
Aeromonas hydrophila	*Corynebacterium glucuronolyticum*	*Histoplasma capsulatum*	*Klebsiella aerogenes (Enterobacter aerogenes)*	*Pasteurella multocida*	*Staphylococcus simulans*
Alloscardovia omnicolens	*Corynebacterium jeikeium*	Human adenovirus B	*Klebsiella oxytoca*	*Peptostreptococcus anaerobius*	*Staphylococcus warneri*
Anaerococcus lactolyticus	*Corynebacterium pseudogenitalium*	Human adenovirus C	*Klebsiella pneumoniae*	*Porphyromonas asaccharolytica*	*Stenotrophomonas maltophilia*
Anaerococcus vaginalis (Peptostreptococcus vaginalis)	*Corynebacterium renale*	Human adenovirus E	*Klebsiella quasipneumoniae*	*Prevotella timonensis*	*Streptococcus agalactiae*
Aspergillus flavus	*Corynebacterium riegelii*	Human herpesvirus 6	*Klebsiella variicola*	*Propionimicrobium lymphophilum*	*Streptococcus anginosus*
Atopobium vaginae	*Corynebacterium urealyticum*	Human herpesvirus 7	*Kluyvera ascorbata*	*Proteus mirabilis*	*Streptococcus constellatus*
Bacillus subtilis	*Cryptococcus neoformans*	Human herpesvirus 8	*Kocuria rosea*	*Proteus penneri*	*Streptococcus intermedius*
Bacteroides fragilis	Cytomegalovirus	Human papillomavirus type 11	*Listeria monocytogenes*	*Proteus vulgaris*	*Streptococcus pneumoniae*
Bifidobacterium breve	*Dialister micraerophilus*	Human papillomavirus type 16	*Mobiluncus curtisii*	*Providencia rettgeri*	*Streptococcus pyogenes*
BK polyomavirus	*Entamoeba histolytica*	Human papillomavirus type 18	*Mobiluncus mulieris*	*Providencia stuartii*	*Treponema pallidum*
Burkholderia cepacia complex	*Enterobacter cloacae* complex	Human papillomavirus type 30	*Molluscum contagiosum virus*	*Pseudomonas aeruginosa*	*Trichomonas vaginalis*
Campylobacter jejuni	*Enterococcus faecalis*	Human papillomavirus type 31	*Moraxella catarrhalis*	*Pseudomonas mendocina*	*Trichosporon asahii*
Candida albicans	*Enterococcus faecium*	Human papillomavirus type 33	*Morganella morganii*	*Pseudomonas putida*	*Trichosporon beigelii (Cutaneotrichosporon cutaneum)*
Candida auris (*Clavispora auris*)	*Enterococcus gallinarum*	Human papillomavirus type 35	*Mycobacterium avium* complex	*Rahnella aquatilis*	*Ureaplasma parvum*
Candida dubliniensis	*Enterococcus raffinosus*	Human papillomavirus type 39	*Mycobacterium gordonae*	*Rhodanobacter denitrificans*	*Ureaplasma urealyticum*
Candida fabianii (Cyberlindnera fabianii)	Epstein-Barr virus	Human papillomavirus type 42	*Mycobacterium kansasii*	*Riemerella anatipestifer*	*Veillonella parvula*
Candida glabrata (Nakaseomyces glabrata)	*Escherichia coli*	Human papillomavirus type 43	*Mycobacterium marinum*	*Rothia kristinae* (*Kocuria kristinae*)	*Vibrio cholerae*
Candida krusei (*Pichia kudriavzevii*)	*Facklamia hominis*	Human papillomavirus type 45	*Mycobacterium scrofulaceum*	*Salmonella enterica*	*Yersinia enterocolitica*

Library preparation

The Urinary Pathogen ID/AMR Enrichment Kit contains all library prep reagents, indexes, and panel probes for on-bead tagmentation followed by a single hybridization step to provide a rapid workflow for generating enriched libraries. The probe-based enrichment provides:

- Improved sensitivity over shotgun metagenomic sequencing
- Rapid, automation-compatible workflow with minimal hands-on time
- Scalable throughput that supports multiplexing of up to 384 samples in a single run

Learn more about on-bead tagmentation, illumina.com/techniques/sequencing/ngs-library-prep/tagmentation.html

Sequencing

The sensitivity of probe-based target enrichment used with the Urinary Pathogen ID/AMR Panel libraries allows for flexible sequencing options. The panel is ideal for use with the benchtop MiniSeq™, MiSeq™, and NextSeq™ 550, NextSeq 1000, and NextSeq 2000 systems. Nucleic acid sample quality, sample read depth, and the number of reads per sample impact the number of pathogen-specific reads and sequence coverage obtained.

Data analysis

In order to support various experimental workflows, the Urinary Pathogen ID/AMR Panel includes probes targeting 10 commercially available spike-in control options (Table 2). Analysis is performed with the Explify™ secondary analysis pipeline, available on BaseSpace™ Sequence Hub.

The data analysis pipeline provides contig assembly, consensus sequences, and genome coverage metrics for the pathogens featured in the panel. Users can select individual samples or a BaseSpace Sequence Hub project folder containing samples for analysis. The application interface allows for configuration of analysis options, including read quality control metrics, quantitative spike-in control selection, and filtered reporting for AMR markers and microorganisms. Sample results can be output in six different formats: summary PDF report, spreadsheet of results in XLSX format, comprehensive JSON report, interactive HTML web report, annotated TSV variant table with known bacterial AMR marker variants, and consensus genome FASTA sequences for some organisms. Additionally, users can download an aggregate XLSX report for all samples in a BaseSpace Sequence Hub analysis folder to facilitate downstream analysis of results from related samples (eg, results from the same experiment).

Table 2: Spike-in control options.

Allobacillus halotolerans
Armored RNA Quant Internal Process Control
Enterobacteria phage T7
Escherichia virus MS2
Escherichia virus Qbeta
Escherichia virus T4
Imtechella halotolerans
Phocid alphaherpesvirus 1
Phocine morbillivirus
Truepera radiovictrix

Performance

Sensitive pathogen detection

The target enrichment design of the Urinary Pathogen ID/AMR Panel is highly sensitive, outperforming shotgun metagenomics and conventional urine culture methods for identifying common uropathogens. The target enrichment approach also allows for greater analytical sensitivity at a lower number of total reads compared to shotgun metagenomics methods, ~1M vs. ~10M, 1 × 147 bp paired-end reads (Figure 3).

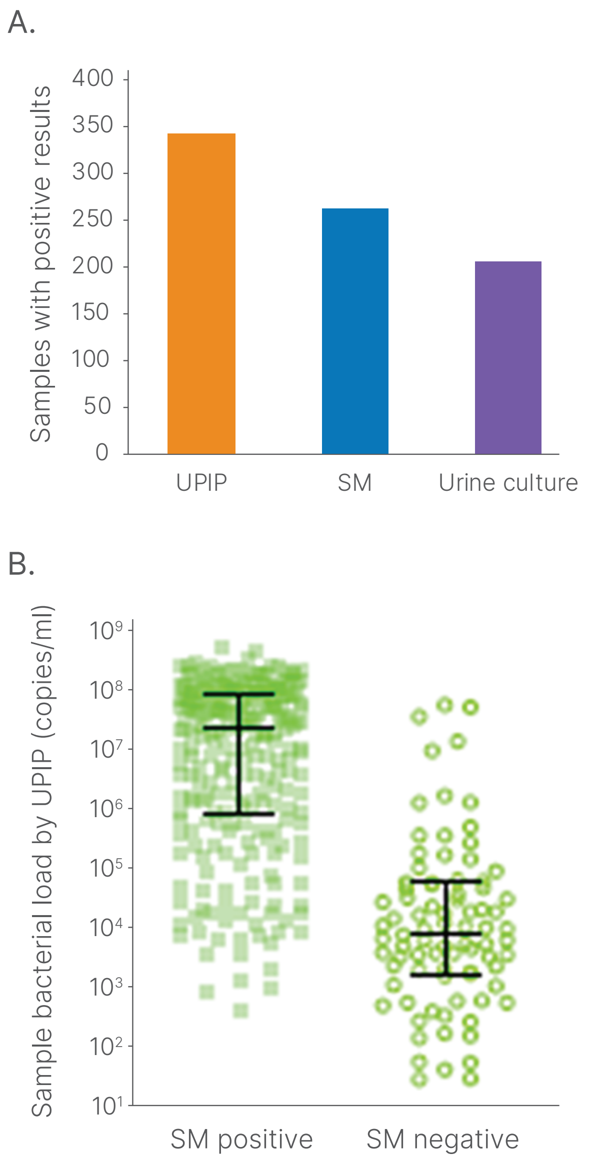

Figure 3: Sensitivity of Urinary Pathogen ID/AMR Panel—The Urinary Pathogen ID/AMR Panel (UPIP) offers more sensitive pathogen identification than shotgun metagenomics (SM) and culture methods. Sequencing was performed on a NextSeq 550 system. (A) One or more uropathogens were detected in 342/399 (86%) urine samples by UPIP, in 262/399 samples (66%) by SM, and in 205/399 samples (51%) by urine culture. (B) Bacterial load by UPIP was higher in SM-positive than in SM-negative samples ($p < 0.0001$), consistent with the prediction of improved analytical sensitivity of targeted enrichment sequencing compared with SM.

Summary

The Urinary Pathogen ID/AMR Panel offers sensitive detection of > 170 common and underrecognized uropathogens. The panel is also able to identify > 3700 antimicrobial resistance markers for the included pathogens, enabling investigations into resistance profiles. The target–capture approach of the Urinary Pathogen ID/AMR Panel means greater detection sensitivity than shotgun metagenomics sequencing methods and makes it ideal for benchtop sequencing systems. The panel is compatible with a range of environmental and biological research sample types.

Learn more

Urinary Pathogen ID/AMR Panel, illumina.com/products/by-type/sequencing-kits/library-prep-kits/urinary-pathogen-id-amr-enrichment-kit.html

BaseSpace applications, illumina.com/products/by-type/informatics-products/basespace-sequence-hub.html

Illumina sequencing platforms, illumina.com/systems/sequencing-platforms.html

Ordering information

Product	Catalog no.
Urinary Pathogen ID/AMR Enrichment Kit Set A (RUO) (96 indexes,96 samples)	20090308
Urinary Pathogen ID/AMR Enrichment Kit Set B (RUO) (96 indexes,96 samples)	20090309
Urinary Pathogen ID/AMR Enrichment Kit Set C (RUO) (96 indexes, 96 samples)	20090310
Urinary Pathogen ID/AMR Enrichment Kit Set D (RUO) (96 indexes, 96 samples)	20090311

References

1. Bono MJ, Leslie SW, Reygaert WC. Urinary Tract Infection. In: *StatPearls*. Treasure Island (FL): StatPearls Publishing; June 15, 2022.

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