illumina®

Urinary Pathogen ID/AMR Panel (UPIP)

Urinary tract infection (UTI) — facts and figures

- UTI is the most common outpatient infection affecting ~150 million people worldwide[1]
- It accounts for ~10 million office visits and ~1 million hospitalizations per year in the U.S.
  - Estimated cost of $2.8 billion[2,3]
  - More than 50% of all women will have at least one UTI in their lifetimes[1,2]
- Most common uropathogens[2,3] are: *Escherichia coli* (>80% of all community-acquired infections), *Staphylococcus, Klebsiella, Enterobacter, Proteus,* and *Enterococcus* species
- There is a growing understanding of the bladder microbiome and the complexity of UTIs, especially in patients experiencing recurrent infection
- The prevalence of drug resistance in uropathogens is increasing; antibiotic treatment for acute infection or prophylaxis often do not prevent recurrent infections

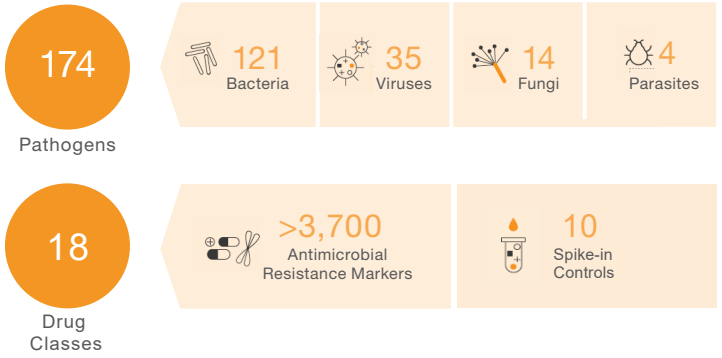
Scope of detection

- UPIP is a research panel that brings the power of Precision Metagenomics to genitourinary pathogen identification
- UPIP detects and quantifies >170 organisms, including common and less common important uropathogens. UPIP also detects >3,700 antimicrobial resistance (AMR) markers
- Panel analytes selected based on reported correlation with uncomplicated or complicated UTIs, hospital-acquired and multidrug-resistant infections
- UPIP has the capability to identify fastidious, slow-growing and anaerobic bacteria linked to UTIs that are typically missed and culture-negative using traditional detection methods

Precision metagenomics — pilot study performance

In a pilot study with remnant urine samples from symptomatic adults, 100% positive agreement was observed between metagenomic and urine culture-based identification for samples in which predicate testing identified a common uropathogen at >100,000 CFU/mL (n=133).

- Precision Metagenomics increased the detection of common uropathogens by >30% compared with standard urine culture
- An anaerobic and/or fastidious potential uropathogen was detected in 1 in 3 urine samples with no growth or no significant growth in culture



Explify process and workflow

Sample Prep

- Sample extraction
- Library prep
- Enrichment with UPIP probes

Sequencing

- Process libraries
- Generate FASTQ file

Metagenomic Analysis

- Automated Analysis
- Sequencing Data Alignment
- Microbial Identification
- Pathogenicity Filterings

Result Review

- Confirm pathogen results
- Confirm run, sample QC
- Result preview
- Result comments

Results Generation

1. Reviewed in McLellan and Hunstad. 2017. Trends Mol Med 22(11): 946-957
2. Flores-Mireles AL et al. Urinary tract infections: epidemiology, mechanisms of infection and treatment options. Nat Rev Microbiol. 2015;13(5):269-84.
3. Simmering JE et al. The Increase in Hospitalizations for UTIs and the Associated Costs in the United States, 1998-2011. Open Forum Infect Dis. 2017;4(1):ofw281.

illumina®

For research use only. Not use for diagnostics procedures.

1.800.809.4566 toll-free (US) | +1.858.202.4566 tel | techsupport@illumina.com | www.illumina.com

© 2022 Illumina, Inc. All rights reserved. All trademarks are the property of Illumina, Inc. or their respective owners. For specific trademark information, see www.illumina.com/company/legal.html.

M-GL-01191