Supporting Information

Rapid Detection of Urinary Tract Infection in 10 Minutes by Tracking Multiple Phenotypic Features in a 30-Second Large Volume Scattering Video of Urine Microscopy

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S1. The prototype LVSi system

Fig S1. Photo of the prototype LVSi system. The optical system includes one LED light, one zoom lens, and one camera. An electrical heating stage with a temperature control was used to maintain the temperature of the sample in cuvette at 37 ºC.

S2. Evaluation of tracking accuracy

Figure S2. Evaluation of tracking accuracy of an immobilized particle. The intensity and position over time of an immobilized particle is tracked (a). The bright spot in the image is tracked with ~40 nm accuracy (standard deviation) by fitting the intensity distribution with a Gaussian function (b). The detection accuracy (standard deviation) of normalized intensity is ~ 0.002 for the current system (c).

S3. Comparison of intensity fluctuation

Figure S3. Normalized intensity pattern of (a) 1 μm beads and *E. coli* cells with two different swimming patterns (tumbling and running) and the (b) corresponding Fast Fourier Transform (FFT) results.

S4. Differentiation of *E. coli* **and** *K. pneumoniae* **by phenotypic features tracking**

Figure S4. Differentiation of *E. coli* and *K. pneumoniae* by single cell phenotypic features tracking. (a) Single cell motion and intensity mapping for *E. coli* and *K. pneumoniae*. (b) Comparison of the corresponding intensity fluctuation and micro-motion of single *E. coli* and *K. pneumoniae* cells. (c) Training results obtained from individual pure cultures of *E. coli* (n = 215) and *K. pneumoniae* $(n = 230)$ with machine learning classification (Support Vector Machine, SVM) based on mean squared displacement (MSD) of single cell motion and normalized intensity standard deviation (NISD) of single cell intensity. (d) Testing results obtained from individual pure cultures of both *E. coli* cells ($n = 109$) and *K. pneumoniae* cells ($n = 74$) with the trained machine learning classification (Support Vector Machine, SVM) model.

S5. The ROC curve for threshold determination with the first 20 clinical urine samples

To determine an infection threshold, the receiver operating characteristic (ROC) curve was constructed using the relative amounts of cells/all particles (N_{Cell}/N_{Total}) as a predictor, and results were evaluated to determine the infection threshold for UTIs. From the ROC curve for the first 20 samples, of which 10 were positive and 10 were negative via clinical testing, we determined the infection threshold of 0.5 with a sensitivity of 90% and a specificity of 100%.

Figure S5. The ROC curve for threshold determination with the first 20 clinical samples.

S6. Classification of different samples with the trained model of distinguishing *E. coli* **from urine particles**

Figure S6. The testing classification results with the trained model (distinguishing *E. coli* from urine particles) for different samples. (a) Pure culture of *E. coli* cells. (b) Pooled, healthy urine sample with no bacteria present. (c) Pure culture of *K. pneumoniae* cells. (d) Pure culture of *S. saprophyticus* cells. (a-d) The *E. coli* – urine particle trained SVM model classifies bacterial cells as blue dots and non-bacterial particles as black dots.

S7. Clinical urine sample rapid detection results

Table S1. LVSi-RD detection (Ncell/Ntotal) results of UTI for 104 human patient samples compared with clinical results and on-site plating validation results.

*****Reference method; standard microbiological plating results generated by the Mayo Clinic microbiology lab.

On-site validation results generated by standard microbiology plating upon sample receiving.

† Disagreement between LVSi-RD and reference method results.

S8. Initial sample validation results

On-site initial bacterial load validation is performed with sample microbiology plating and colony counting. Upon receipt, urine samples were subjected to serial dilutions and plated on LB agar for colony enumeration. This plating validation provides initial bacterial concentration reference and reveals any viability changes during sample storage and transportation. After LVSi-RD, we obtained an estimation of the bacterial cell number with SVM clustering, which provides the calculated cell concentration per mL for comparison.

Figure S7. Initial plating validation (yellow bar) of 51 clinical positive samples and the calculated cell concentration by LVSi-RD (green bar). The yellow dashed lines indicate the clinical infection threshold $(10^4 \text{-} 10^5 \text{ CFU/mL})$. The stars mark the 8 false negative samples determined by LVSi-RD.

S9. Initial and parallel plating validation result of 8 false negative samples

Parallel plating validation was performed along with LVSi-RD to test the samples postpreparation. Initial plating CFU/mL determinations (described above), calculated CFU/mL based on sample dilution, and parallel plating of sample post-preparation of eight false negative samples are presented here. Of the eight false negative samples, initial on-site plating validation found one sample (#94) to have a bacterial concentration below the clinical threshold of 10⁴ CFU/mL. After all sample handling, including prewarming, filtration and dilution, the parallel microbiological plating validation results show low counts of bacterial cells (below 1,000 cells/mL). Therefore, false negative results are likely due to a combination of low initial bacterial concentration, storage, transport, and the sample handling process, most of which can be avoided with an optimized dilution scheme and quicker handling process at the point of care settings.

Figure S8. The comparison of initial plating, calculated CFU/mL by dilution, and the parallel microbiological plating results of eight false negatives samples. Most of the false negative samples had bacterial concentrations below 1,000 CFU/mL (red dashed line) after sample preparation. The parallel microbiological plating results are the mean value of three technical replicates. The limit of detection for initial microbiological plating (yellow bar) is 100 CFU/mL (yellow dashed line), and the limit for parallel microbiological plating (purple bar) is 200 CFU/mL (purple dashed line).

S10. Flow chart for clinical urine sample preparation

Figure S9. Workflow of sample preparation, LVSi-RD test, and plating-based validations for clinical urine samples.

S11. Flow chart for LVSi video processing and machine learning

Figure S10. Flow chart for LVSi video processing and machine learning.