Electronic Supplementary Material (ESI) for Analyst.

Facile syringe filter-enabled bacteria separation, enrichment, and buffer exchange for clinical isolation-free digital detection and characterization of bacterial pathogens in urine

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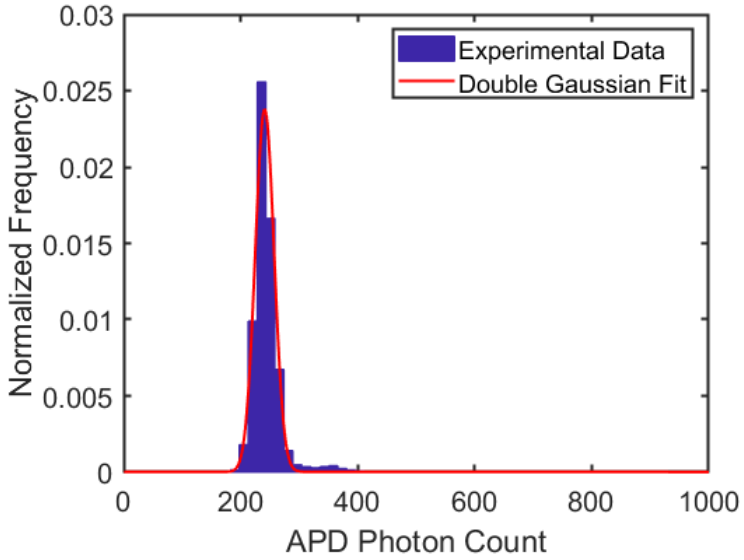
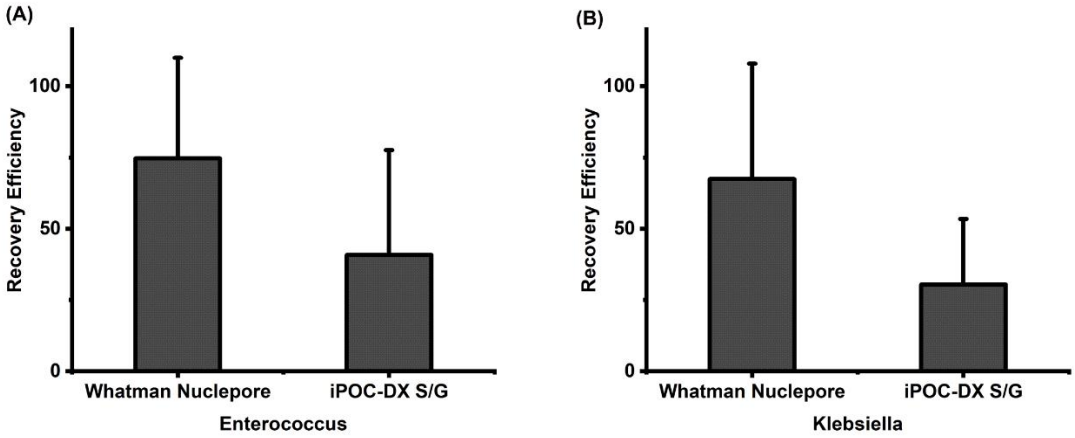
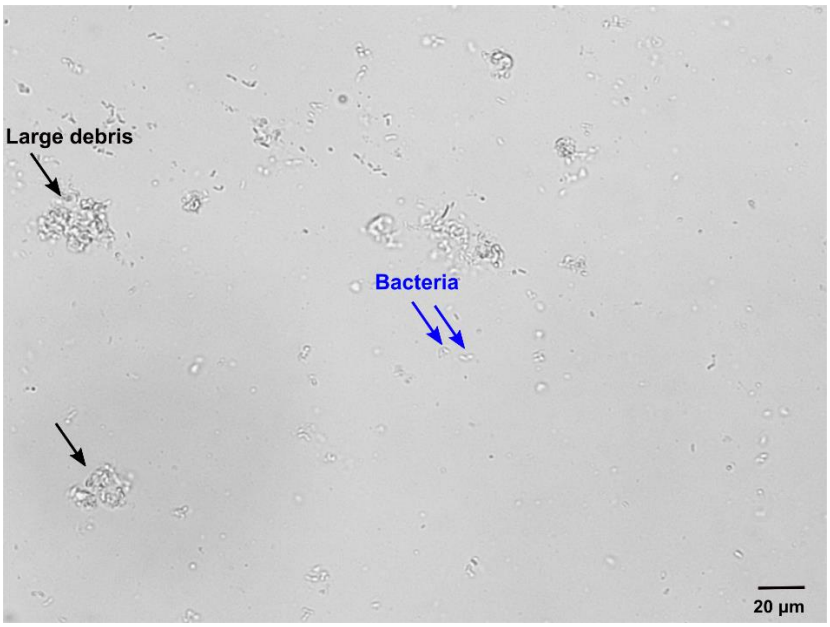
Supplementary Information



Supplementary Figure 1. **Droplet data analysis using the histogram-based modelling**. We fit a Gaussian mixture model using the 'fitgmdist' function in MATLAB to the droplet data. The histogram model typically fits the empty droplet population well from which we calculated the mean intensity and standard deviation of the empty droplet population. We then set a threshold for positive droplets as the empty droplet mean intensity plus 4.5 standard deviations (for probe-based hybridization assay) or 6 standard deviations (for resazurin-based growth assay). The frequency of positive droplets, λ, is then calculated to determine bacteria concentration.



Supplementary Figure 2. ***Enterococcus* and *Klebsiella* filtration recovery efficiency**. Whatman Nuclepore and iPOC-DX S/G can recover both (A) *Enterococcus* and (B) *Klebsiella* even though the recovery efficiency is slightly inferior to that of *E. coli*. The error bars are standard deviations of replicated experiment (n=3 for A, n=5 for B).



Supplementary Figure 3. **Large debris present after Whatman Nuclepore filtration**. Large debris can leak through Whatman Nuclepore filter (indicated by black arrows) even though Whatman Nuclepore filter showed slightly higher recovery efficiency of bacteria (indicated by blue arrows) from urine compared with iPOC-DX S/G filter.