SUPPLEMENTARY MATERIAL

Rapid and sensitive identification of uropathogenic *Escherichia coli* using a Surface-Enhanced-Raman-Scattering-based biochip

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[‡] Univ. Lille, CNRS, Centrale Lille, Univ. Polytechnique Hauts-de-France, UMR 8520-IEMN, F-59000 Lille, France Figure SI1: Fluidic set-up used for the detection of bacteria at low concentration (< 10^4 CFU mL⁻¹): It consists of a fluidic chamber containing the sensing area of the biochip and connected to a peristatic pump with an optimized flow rate of 0.25 mL min⁻¹. The chamber is installed on an optical microscope sample holder connected to a computer in order to follow the trapping of bacteria *in situ*. In the case of bacteria detection in artificial urine, a suspension of 10 mL of artificial urine spiked with bacteria was recirculated inside the cell.



urine spiked with bacteria

Figure SI2: **Type-1 fimbrial and major pilin FimA purification**: (A) 17% SDS-PAGE showing the extraction (lanes 1 & 2) and first purification using 100 mM MgCl₂ of extracellular organelles from *E. coli* strains LF82 (1, 4), K12 MG1655 (2, 5) and AAEC185(pUT2002) (6). The low molecular-weight marker (7) shows that purified FimA migrates at the expected molecular weight of ~17 kDa. The first purification product from LF82 FimA with (9) and without (10) 0.16% TFA in the sample loading buffer; (B) Analysis of the purification in the gel exclusion on an SDS-PAGE: K12 FimA (1), AAEC185(pUT2002) FimA (2), LF82 FimA (3), LMWM (4). As expected, the major fimbrial subunit FimA of the *E. coli* strain LF82 migrates at a higher molecular weight (16268.9 Da for 161 amino acids) than FimA of the uropathogenic UTI89 or the K1 meningitis *E. coli* strains,^[1] FimA encoded on the pUT2002 plasmid carries the K12 FimA sequence.^[2]



Figure SI3: **Polyclonal antibodies towards** *E. coli* **type-1 fimbrial FimA:** generation (A), purification (B), SDS-PAGE analysis (C), and reactivity as determined using surface plasmon resonance (SPR), by subsequently injecting purified IgG fractions (1) and (2) over 87 RU (response units of immobilized FimA pilin protein (D).



Figure SI4: FTIR-ATR spectra of the multi-steps functionalization of a 20 nm-thick thin film a-Si:H deposited on a silicon prism: carboxydecyl-terminated surface, abbreviated as acid surface (a) after the first activation using EDC/NHS (b), the first aminolysis with HOOC-OEG-NH₂ (c) and the second activation using EDC/NHS (d). The reference spectra are the freshly hydrogenated a-Si:H surface with HF vapors. The blue trace corresponds to the spectrum of the surface after its first aminolysis with respect to that of the surface after the first activation allowing for a convenient isolation of the characteristic vibrations of the OEG chains.



Figure SI5. Optical-microscopy images of antibodies spots: before and after incubation of bacteria *E. coli* pMMB66 and *E. coli* Katushka at 10^8 CFU mL⁻¹ in PBS 1X for 1 h (A); optical image of the spot with trapped *E. coli* Katushka after three successive regeneration cycles. One cycle is composed of 5 min interaction in 20 mM NaOH followed by a quick rinse in H₂O and 1-hour incubation with *E. coli* Katushka at 10^9 CFU mL⁻¹ in PBS 1X (B).



Figure SI6. SEM images of *E. coli* **after interaction with AuNRs at different time intervals of exposure:** 15 min, 30 min, 1 h and 3 h. The inset represents the SEM image of the AuNRs.



Figure SI7. SERS spectra of dried drops of gold nanorods AuNR-CTAB deposited on glass (acquisition parameters: acq 10 s, 1 accumulation, 100× objective, excitation: 633 nm, 2.5 mW).



Figure SI8. SERS Mapping of trapped *E. coli* Katushka in PBS 1X on antibodies spots and their extracted spectra obtained: (A) at 10⁸ CFU mL⁻¹ without contact with AuNRs; (B) at 10⁸, 10⁴, 10² and 10 CFU mL⁻¹ after 15 min of interaction with AuNRs



Figure SI9. PCA of the extracted spectra of *E. coli* MG1655 at 10⁸ and 10 CFU mL⁻¹ in PBS 1X and artificial urine.



Reference:

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