

In-situ electrochemical regeneration of nanogap hotspots for continuously reusable ultrathin SERS sensors

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ABSTRACT

Surface-enhanced Raman spectroscopy (SERS) harnesses the confinement of light into metallic nanoscale hotspots to achieve highly sensitive label-free molecular detection that can be applied for a broad range of sensing applications. However, challenges related to irreversible analyte binding, substrate reproducibility, fouling, and degradation hinder its widespread adoption. Here we show how *in-situ* electrochemical regeneration can rapidly and precisely reform the nanogap hotspots to enable the continuous reuse of gold nanoparticle monolayers for SERS. Applying an oxidising potential of +1.5 V (vs Ag/AgCl) for 10 s strips a broad range of adsorbates from the nanogaps and forms a metastable oxide layer of few monolayer thickness. Subsequent application of a reducing potential of -0.80 V for 5 s in the presence of a nanogap-stabilising molecular scaffold, cucurbit[5]uril, reproducibly regenerates the optimal plasmonic properties with SERS enhancement factors $\approx 10^6$. The regeneration of the nanogap hotspots allows these SERS substrates to be reused over multiple cycles, demonstrating $\approx 5\%$ relative standard deviation over at least 30 cycles of analyte detection and regeneration. Such continuous and reliable SERS-based flow analysis accesses diverse applications from environmental monitoring to medical diagnostics.

INTRODUCTION

Surface-enhanced Raman Spectroscopy (SERS) has emerged as a powerful analytical technique, unlocking prospects for sensitive label-free molecular fingerprinting across various fields including forensic analysis¹, environmental monitoring², biomedical diagnostics³⁻⁵, and food quality control⁶. SERS is based on the enhancement of Raman scattering that arises from strong electromagnetic fields generated by the optical excitation of localized surface plasmons ('hotspots') on nanostructured metal substrates. The SERS from analytes adsorbed at the hotspots can be enhanced by 10^3 - 10^{10} , enabling the identification and quantification of trace concentrations of analytes.⁷ However, the same sensitivity that endows SERS with its analytical capability renders it particularly susceptible to irreproducibility from variations in substrate nanoscale fabrication⁸ and contamination^{9,10}. Achieving continuous high-throughput SERS measurements is further compromised by irreversible analyte binding at the hotspots (the SERS 'memory effect'), resulting in the need for frequent substrate replacement¹¹. This presents insuperable practical issues, including high operating costs, poor resource utilization, and waste generation. To address these challenges, a promising route is to develop effective SERS substrate recycling strategies to enable multiple sample analyses on the same platform, thus delivering reproducible high-throughput SERS-based analysis.

To reuse SERS sensors, a key requirement is repeatedly removing a broad range of analytes without altering the crucial nanoscale morphology which controls the SERS hotspots and directly affects analyte signal intensities.⁸ Various strategies have been proposed¹², including metal etching and redeposition^{13,14}; analyte decomposition with thermal^{15,16}, plasma^{17,18}, or photochemical^{19,20} treatments; use of protective polymers²¹⁻²³; solvent rinsing²⁴⁻²⁶; analyte displacement with competitive binding²⁷⁻³¹; and electrochemical methods^{28,32-39} (see Supplementary Table 1 for comprehensive comparison). However, previous methods that remove strongly adsorbed molecules can induce significant morphological changes that degrade the SERS hotspots. Electrochemical (EC) strategies are the most promising in terms of speed, *in-situ* implementation, and the range of analytes that can be removed, making EC strategies promising for rapid, high-throughput sequential sample analysis. Still, maintaining analyte signal reproducibility across multiple cleaning cycles remains unfeasible due to degradation of the SERS hotspots⁴⁰. While EC cleaning via oxidation and reduction removes adsorbates from metal surfaces⁴¹⁻⁴³, it leads

53 to significant nanoscale surface restructuring^{44,45}. Achieving reliable scalable SERS-based analysis thus
54 necessitates advances in the precision control of nanoscale morphology to repeatedly regenerate SERS hotspots.
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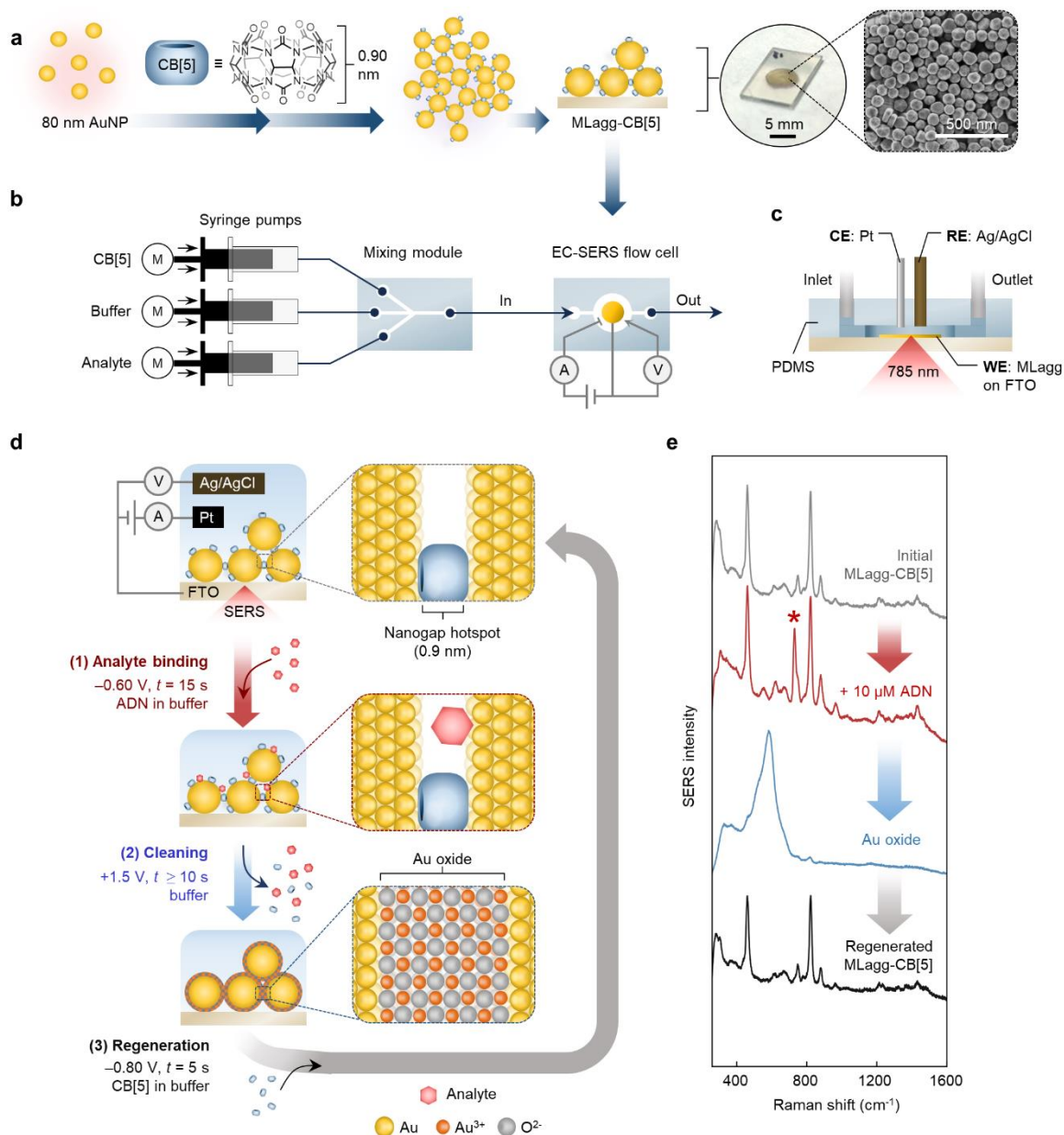
56 Here we present an *in-situ* electrochemical SERS hotspot regeneration scheme ('ReSERS') for the continuous
57 reuse of thin-film gold nanoparticle (AuNP) SERS substrates. Previously, we demonstrated a low-cost scalable
58 method to prepare thin-film SERS substrates through bottom-up self-assembly of AuNPs using a rigid molecular
59 scaffold, cucurbit[*n*]uril (CB[*n*], *n*=5-8), which yields highly reproducible sub-1 nm nanogap hotspots across multi-
60 layer AuNP aggregates ('MLagg')^{9,46,47}. We now show that by integrating MLaggs within electrochemical SERS
61 (EC-SERS) flow cells, the ligand-stabilised ('scaffolded') nanogap hotspots can be anodically stripped of molecular
62 adsorbates with the simultaneous formation of a meta-stable gold oxide plug. A second step precisely
63 regenerates the hotspots by reducing the few-monolayer oxide layer while re-stabilising the metallic nanogaps
64 with the CB[*n*] scaffolding molecule. Using this cleaning and regeneration protocol, the same SERS substrate can
65 be reused with a high level of reproducibility and number of regeneration cycles. We find that the key to
66 reproducibility is the reintroduction of the molecular scaffold, which precisely reforms the nanogap hotspots
67 after oxidative cleaning. Efficient ReSERS enables direct quantitative analysis of complex samples without
68 substrate fouling, and allows us to identify key criteria for its application to different SERS substrates. Fully
69 regenerating nanogaps thus gives continuous high-throughput SERS measurements, with broad applications in
70 health, environment, industrial process, and quality monitoring.
71
72

73 RESULTS

74 SERS substrate preparation and oxidative cleaning

75 To prepare a SERS substrate with precisely-controlled nanogap spacing, we self-assemble citrate-stabilised 80 nm
76 AuNPs with CB[5], a barrel-shaped molecule which binds AuNPs together through its carbonyl portals^{8,46} (Fig. 1a,
77 Supplementary Fig. 1a). The AuNP:CB[5] assembly can be concentrated and deposited as a thin film, yielding
78 close-packed multi-layer AuNP aggregates with 0.90 ± 0.05 nm interparticle spacings defined by the CB[5]
79 scaffold^{9,47,48}. These sub-nm hotspots give an enhancement factor of $\approx 10^6$ (see Methods). Such MLaggs also have
80 multiple advantages for delivering in-flow SERS sensing, such as their ease of integration into flow cell systems
81 and their capability to be probed optically from the backside when deposited on transparent solid supports. The
82 MLaggs further allow for tuning the surface chemistry⁹. Interfering native AuNP ligands such as citrate can be
83 completely removed and replaced with desired scaffolding molecules. One way to clean MLagg surfaces is to use
84 oxygen plasma cleaning (O₂-PC), followed by a 're-scaffolding' step in which diverse molecules are used to
85 redefine the nanogaps (Supplementary Fig. 1b)⁹. Here, ligands and contaminants are decomposed in O₂-PC by
86 bombarding the surface with reactive oxygen species, which then react with the bare Au surface to form an oxide
87 layer. This few-monolayer thick Au oxide serves a key role in plugging and stabilising the nanogap when no
88 stabilising ligands are present. The hotspots can then be regenerated by decomposing the Au oxide in the
89 presence of a desired scaffold such as CB[5], which rebinds to and restabilises the nanogap. However, plasma
90 treatment requires an hour to remove analytes from the hotspots (Supplementary Fig. 3) and requires a plasma
91 source incompatible with continuous and/or low-cost measurements.
92

93 Adsorbate removal and Au oxide formation are here achieved electrochemically, offering a strategy to control
94 the surface properties of SERS substrates *in-situ*. By setting the SERS substrate as a working electrode in a three-
95 electrode electrochemical cell, a potential is applied to control the surface charge and induce local reactions
96 directly on its surface^{49,50}. With a Au-based SERS substrate, the application of an anodic potential oxidises and/or
97 desorbs adsorbates as well as oxidises the Au. This process is rapid (seconds) even for nanogaps, as the oxidation
98 process is driven directly at the Au surface⁵¹, in contrast to O₂-PC which relies on reactive oxygen surface
99 collisions. Electrochemical reduction of the Au oxide layer then occurs upon application of a cathodic potential.
100 Aside from analyte removal, EC-SERS can modulate analyte binding, increasing SERS signals by up to 10-fold
101 through the enhanced adsorption of analytes⁴⁹. While EC-SERS is highly promising for offering rapid *in-situ*
102 control of both analyte binding and removal, electrochemical oxidative cleaning has not so far been attempted
103 with nanogap re-scaffolding to regenerate SERS hotspots. We thus examine multiple analyte detection, cleaning,
104 and regeneration cycles to assess both the stripping capability and regeneration repeatability.
105



106

107 **Fig. 1 | Preparation and in-flow EC-SERS analyte detection, cleaning, and regeneration with MLagg-CB[5].** a Preparation of
 108 MLagg-CB[5] SERS aggregate from self-assembly of AuNPs with CB[5], followed by deposition onto solid support. Photo and
 109 scanning electron micrograph (SEM) show MLagg-CB[5] deposited on FTO-coated glass. b Schematic illustrating the
 110 integration of an MLagg-CB[5] into an EC-SERS flow system. c Cross-section of the EC-SERS flow cell (CE = counter electrode,
 111 RE = reference electrode, and WE = working electrode). d Schematic of *in-situ* electrochemical SERS analyte detection and
 112 cleaning/regeneration protocol. Potentials are vs Ag/AgCl. e SERS spectra from: initial MLagg-CB[5] (grey), after detection of
 113 10 μM adenine (ADN) (red), after oxidative cleaning step (blue), and after regeneration step (black). ADN peak at 732 cm^{-1} is
 114 marked by asterisk. SERS spectra are collected with 1s integration time and 1 mW 785 nm laser.

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Electrochemical stability of MLagg-CB[5]

118 To enable electrochemical control of their surface potential, MLaggs are deposited on a fluorine-doped tin oxide
 119 (FTO)-coated glass slide and assembled in an EC-SERS flow cell as the working electrode (Fig. 1b-c, Supplementary
 120 Fig. 4). SERS spectra are recorded by illuminating the MLagg with a 785 nm laser through the transparent FTO-
 121 coated glass, facilitating *in-situ* monitoring of the nanogap while simultaneously controlling the applied potential.
 122

123 The electrochemical stability of MLagg-CB[5] hotspots is initially explored by time-resolved SERS while sweeping
 124 between oxidizing and reducing potentials using cyclic voltammetry (Supplementary Note 1). Desorption of CB[5]

125 is observed during the anodic scan (0.2 to +1.5 V) in 50 mM potassium phosphate buffer (pH 7.0) with formation
126 of Au oxide from +1.0 to +1.5 V (Supplementary Fig. 5). Upon the return cathodic scan, the oxide layer is reduced
127 with re-adsorption of some CB[5] around +0.35 V. However repeated oxidation and reduction results in the
128 continued desorption of CB[5] from the nanogap along with a gradual loss in SERS activity. Addition of excess
129 CB[5] in the buffer solution better stabilises the nanogap hotspots (Supplementary Fig. 6), however chloride ions
130 present (from all CB[n] crystals, $n=5,6,7,8$) dissolve Au complexes leading to the destruction of SERS activity, as
131 previously noted^{52,53}. We thus alternate between Au oxidation in buffer, and reduction in 1 mM CB[5] + buffer
132 (Supplementary Note 2, Supplementary Fig. 7). Stepping the potential to +1.5 V in buffer shows rapid
133 simultaneous desorption of CB[5] and formation of Au oxide in the nanogap, occurring within 5 s. Switching to -
134 0.80 V in CB[5] + buffer reduces the Au oxide and rapidly re-adsorbs CB[5] in the nanogaps within 2-3 s
135 (Supplementary Fig. 8). Importantly, the SERS activity of the MLagg is stable over multiple
136 electrooxidation/reduction repetitions, making this protocol promising for possible SERS substrate recycling
137 (thus termed ReSERS: Re-cycling Scheme via Electrooxidation and Re-Scaffolding).
138

139 **Analyte detection and recycling repeatability**

140 As an initial model analyte for recycling experiments, adenine (ADN) is selected since its potential-dependent
141 binding and SERS spectra are well-studied^{54,55}, and tested in EC-SERS on roughened Ag electrodes³⁴. At pH 7.0,
142 ADN is predominantly neutral and binds to Au⁵⁶ however in electrolyte solutions, ADN competes with ions for
143 binding sites in the nanogaps⁵⁷. Negative potentials enhance ADN binding giving maximum SERS enhancement
144 of the $\nu_{\text{ADN}} = 732 \text{ cm}^{-1}$ peak with a step potential of -0.60 V (Supplementary Note 3, Supplementary Fig. 9). Once
145 adenine binds to the MLagg-CB[5] hotspots, removal of this applied potential does not lead to adenine
146 desorption, nor does application of moderately positive potentials (up to +0.60 V, before the onset of Au
147 oxidation). Adenine is thus strongly bound and rinsing with buffer solutions (pH 2.0, 7.0, or 12.0), 0.1 M HCl, or
148 0.1 M NaOH does not lead to its desorption. Since adsorbed and is not removed with simple rinsing, it is an ideal
149 analyte to test *in-situ* analyte detection, cleaning, and regeneration (Fig. 1d).
150

151 The SERS spectrum of the initial MLagg-CB[5] in the buffer-filled EC-SERS flow cell shows a clean MLagg with only
152 the spectral fingerprint of the CB[5] molecular scaffold visible (Fig 1e grey). To detect ADN, the analyte solution
153 is injected into the flow cell using a syringe pump and a potential of -0.6 V applied for 15 s. A spectrum is then
154 recorded at open-circuit potential (Fig 1e red). After analyte binding, the nanogaps are cleaned by flowing buffer
155 at a constant rate of $500 \mu\text{L min}^{-1}$ while applying +1.5 V for >10 s. This oxidises/desorbs the ADN while forming
156 Au oxide at the AuNP surface, seen directly in the SERS spectrum (Fig. 1e blue) as a broad peak $\approx 590 \text{ cm}^{-1}$ from
157 the Au-O stretch^{51,58}. Buffer flow for another 5 s after applying the oxidising potential flushes out any
158 decomposition products and desorbed analytes from the MLagg surface and sample chamber. After cleaning,
159 the nanogap is regenerated by flowing 1 mM CB[5] in buffer and applying -0.8 V for 5 s, which rapidly reduces
160 Au oxide while facilitating the binding of CB[5] onto the Au surface. The resulting SERS spectrum of the
161 regenerated MLagg-CB[5] (Fig. 1e black) is near identical to the initial spectrum and shows no trace of the ADN
162 ν_{ADN} peak, indicating how effectively the MLagg nanogaps are cleaned.
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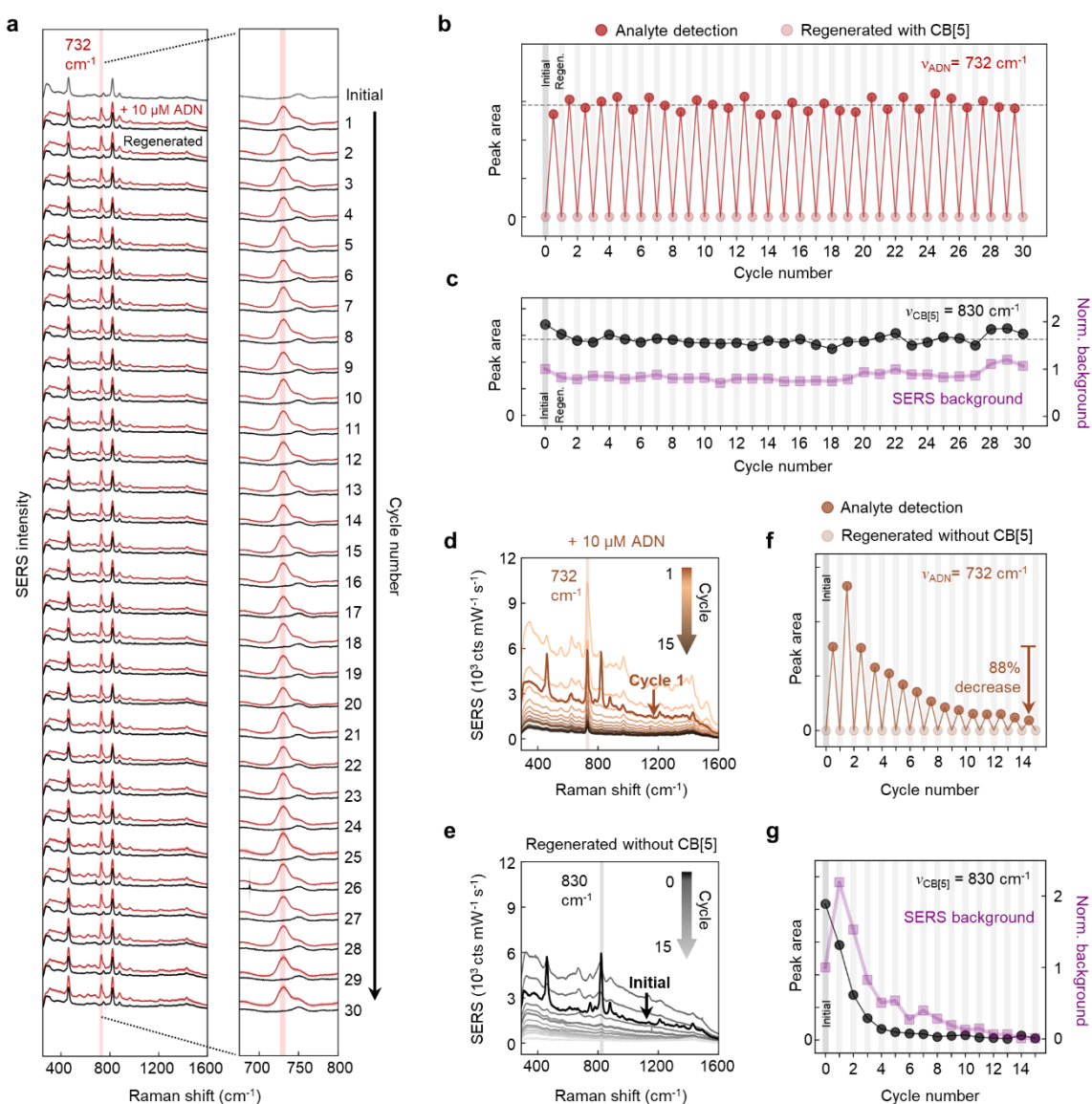
164 This *in-situ* analyte detection and ReSERS cycle is then performed 30 times to evaluate its repeatability (Fig. 2a).
165 To eliminate analyte signal variations due to spot-to-spot variations on the SERS substrate (Supplementary Fig.
166 10), the same substrate spot was probed for all cycles. Tracking the ν_{ADN} peak area every cleaning cycle shows
167 that not only is the analyte successfully removed each time, but the MLagg is also identically regenerated,
168 yielding a 5.5% relative standard deviation (RSD) between all repetitions (Fig. 2b). This variation in analyte
169 detection is comparable to the 5.7% RSD previously observed when detecting and cleaning paracetamol from
170 MLaggs using HCl rinsing over multiple cycles⁹. SERS mapping of the ADN signal at cycles 1, 10, 20, and 30 also
171 shows that the analyte signal and regional uniformity of the substrate remain consistent, implying that all
172 hotspots across the SERS substrate surface area are effectively and reproducibly regenerated (Supplementary
173 Fig. 11**Error! Reference source not found.**). The SERS spectra from the regenerated MLagg are also consistent
174 across the cycles (Fig. 2a,c), while SERS mapping shows the effective removal of the analyte across the probed
175 area of the SERS substrate (Supplementary Fig. 11). In terms of the number of cycles demonstrated and % RSD,
176 this level of recycling repeatability outperforms any reported method (Supplementary Table 1). We note that the
177 MLagg can undergo at least 100 non-continuous analyte detection/ReSERS cycles, even if the MLagg is removed

178 from the cell and dried intermittently. Under flow conditions, effective adhesion of the MLAGg to the FTO-coated
 179 glass is required to ensure its robustness over continuous, prolonged use.

180

181 As a control, the same analyte detection, cleaning, and regeneration cycles are repeated on a new MLAGg-CB[5]
 182 SERS substrate but without using a re-scaffolding molecule during the regeneration step (Fig. 2d,e). Specifically,
 183 after Au oxide formation, only buffer is pumped through the EC-SERS flow cell and -0.80 V is applied for 5 s to
 184 reduce the oxide. With this protocol, the analyte signal per cycle initially fluctuates and then gradually decreases
 185 (Fig. 2f), down to 12% of its strength by cycle 15. SERS maps of the analyte signal at cycles 1, 2, and 10 show
 186 similar variations in analyte signal across the probed area as well as a degradation in the local uniformity from
 187 6% for cycle 1 to 12% and 29% RSD for cycles 2 and 10 respectively (Supplementary Fig. 12). A second cycling
 188 control using 1 mM KCl and buffer in the regeneration step characterises the effect of chloride ions in the CB[5]
 189 solution, giving similar analyte signal fluctuations and a decrease to 21% by cycle 15 (Supplementary Fig. 13). A
 190 further control using MLAGgs prepared from NaCl-aggregated AuNPs (without CB[5]) yields similar results
 191 (Supplementary Fig. 14).

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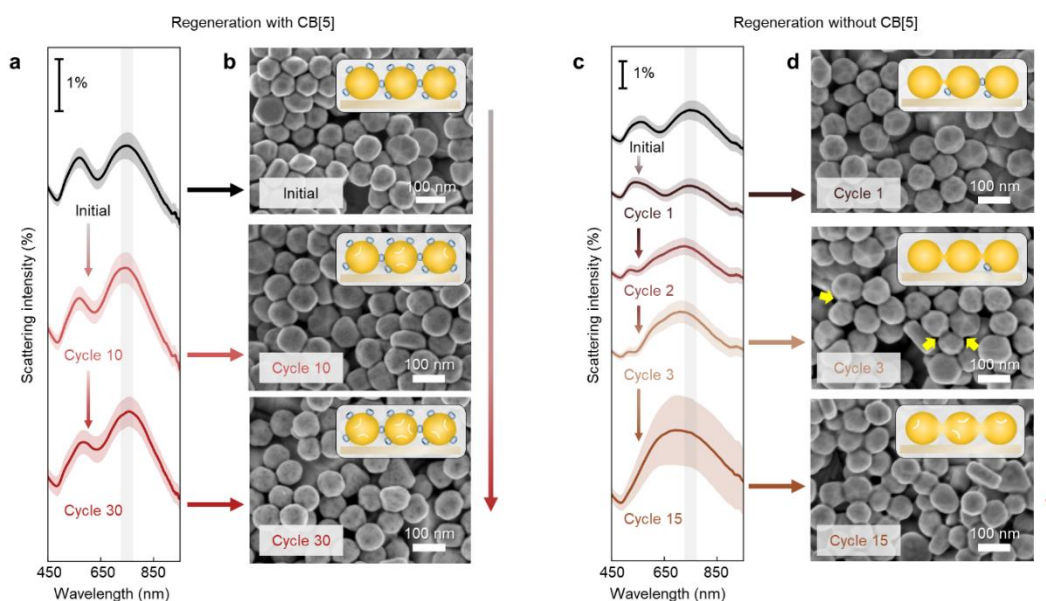
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194 **Fig. 2 | Analyte detection, cleaning, and regeneration cycles with and without CB[5].** a SERS spectra from 30 cycles of 10
 195 μM ADN detection (red) and regeneration with CB[5] (black). Spectra are offset for clarity. b ADN peak areas ($\nu_{\text{ADN}}=732\text{ cm}^{-1}$)
 196 from the SERS spectra of each ADN detection and cleaning/CB[5]-regeneration cycle. Dotted horizontal line represents the
 197 average ADN peak area of all analyte detection cycles. c CB[5] peak areas ($\nu_{\text{CB[5]}}=830\text{ cm}^{-1}$, black circles) and integrated SERS

198 background (purple squares) for the CB[5]-regenerated MLagg. Dotted horizontal line represents the average CB[5] peak area
 199 of all regeneration cycles. **d** Overlaid SERS spectra from 15 cycles of 10 μM ADN detection and **e** after regeneration without
 200 CB[5]. A constant background was subtracted from all spectra to facilitate comparison across 15 cycles. **f** ADN peak areas
 201 ($\nu_{\text{ADN}}=732\text{ cm}^{-1}$) from the SERS spectra of each ADN detection and cleaning/regeneration cycle without CB[5]. **g** CB[5] peak
 202 areas ($\nu_{\text{CB[5]}}=830\text{ cm}^{-1}$, black circles) and integrated SERS background (purple squares) for the MLagg regenerated without
 203 CB[5].
 204
 205

206 Morphology changes

207 The repeatable analyte detection achieved when CB[5] is added during the Au oxide reduction step suggests that
 208 the nanogaps are precisely regenerated. To investigate changes in morphology, the coupled plasmon modes of the
 209 MLagg are characterised using dark-field (DF) scattering spectroscopy (Fig. 3a), with the peak wavelength
 210 indicative of the gap size and refractive index⁵⁹. In MLaggs the AuNPs are coupled via precisely-spaced nanogaps,
 211 resulting in strong plasmonic interactions between the nanoparticles^{47,48}. Before cycling, the MLagg exhibits a
 212 chain mode at $745\pm 12\text{ nm}$ (shaded), set by the CB[5]-controlled gap size (0.90 nm). This coupled plasmon mode
 213 is highly sensitive to changes in gap size: assuming constant refractive index, a spacing increase by $\approx 0.1\text{ nm}$ results
 214 in a $\approx 20\text{ nm}$ blue shift⁹. After 10 and 30 cycles, we observe peak wavelength shifts to $741\pm 12\text{ nm}$ and $751\pm 8\text{ nm}$
 215 respectively, indicating only minor effects on the plasmonic coupling. Tracking the plasmon mode after every
 216 regeneration step for the first 10 cycles confirms minimal shifts in peak wavelength relative to the initial MLagg
 217 (Supplementary Fig. 15). Representative SEM images of the MLagg-CB[5] before and after 10 and 30 cycles
 218 further evidence that the nanogaps are preserved (Fig. 3b).
 219



220

221 **Fig. 3 | Morphology changes with or without CB[5] during regeneration.** **a** DF scattering spectra and **b** representative SEM
 222 images of the MLagg-CB[5] before and after undergoing 10 and 30 cycles of analyte detection, cleaning, and regeneration
 223 with CB[5]. **c** DF scattering spectra and **d** representative SEM images of the MLagg-CB[5] throughout different cycles of
 224 analyte detection, cleaning, and regeneration without CB[5]. Yellow arrows in **d** point to bridges formed between
 225 neighbouring AuNPs. For the DF spectra, solid lines and shaded area represent mean and $\pm 1\text{ s.d.}$ of $n=150$ spectra obtained
 226 across the area of a MLagg-CB[5]. Grey line highlights initial chain mode peak wavelength. Spectra are offset for clarity.
 227
 228
 229

230 In contrast, when CB[5] is omitted during the regeneration step, changes in nanogap morphology are observed
 231 as the MLagg is repeatedly electrooxidized and reduced. After the first cycle, the regenerated MLagg exhibits a
 232 $\approx 10\text{ nm}$ blue shift in peak wavelength and a decrease in scattering amplitude (Fig. 3c). While SEM imaging shows
 233 no obvious morphology changes (Fig. 3d top), shifts in the coupled plasmon mode suggest partial sintering or
 234 nanoscale roughening at the nanogaps. The CB[5] SERS peaks after this first cycle decrease 30% and broaden
 235 (Fig. 2e, g), either from reduced CB[5] binding or reduced optical fields⁶⁰, while the SERS background more than

236 doubles (Fig. 2g). Further rounds of Au oxide formation and reduction remove more CB[5] sites and induce more
237 pronounced morphology changes. SEM images show formation of bridges between some neighbouring AuNPs
238 after cycle 3 (Fig. 3d centre, yellow arrows) with sintering of every nanogap after cycle 15 (Fig. 3d bottom). The
239 plasmon mode gradually blue shifts to ≈ 700 nm and broadens as the nanogaps collapse and sinter (Fig. 3c),
240 coinciding with the disappearance of SERS (Fig. 2d-g). Similar morphology changes, plasmon mode shifts, and
241 SERS decrease are observed with other controls (Supplementary Figs. 13-14).

242

243 These data show that CB[5] is crucial for regenerating the nanogaps after oxidative cleaning. Time-resolved EC-
244 SERS (Supplementary Figs. 6-8) shows that CB[5] rapidly binds to the Au facets to restabilise the nanogap
245 hotspots as Au oxide is reduced. We propose that the rigid 0.90 nm high CB[5] molecule favourably binds to the
246 two proximate AuNP facets⁴⁶, enabling the reproducible reconstruction of the sub-1 nm nanogap after Au
247 oxidation. The CB[5] molecule acts as an effective molecular scaffold between the facets of neighbouring AuNPs,
248 and its reintroduction prevents the nanogaps from collapsing and sintering. Nanoscale surface roughening visible
249 in SEMs (Fig. 3b,d, Supplementary Figs. 13-14) outside the nanogaps when cycling both with and without CB[5]
250 is thus evidently very different from reconstructing the facet morphology inside the nanogaps with CB[5]. We
251 note that EC-recycling is also possible with CB[6], but that CB[7] is harder to remove electrochemically from the
252 nanogaps, while other scaffolding molecules are also inferior to CB[*n*].

253

254 **Analyte switching**

255 To exemplify how this recycling removes all analytes from MLagg-CB[5] nanogaps, we alternate between
256 detecting different molecules, thus robustly testing for SERS memory effects. If the first analyte is not effectively
257 removed, its signal remains in the SERS spectrum as an interferent when the next analyte is detected. Incomplete
258 analyte removal also results in competition for available binding sites in the SERS hotspots, which in turn affects
259 detection sensitivity.

260

261 Initially we alternate between detection of 100 μ M ADN and 100 μ M cytosine (CYT), selected since their Raman
262 peaks do not overlap. They have similar electrochemical SERS enhancement at -0.60 V³⁴, allowing enhanced
263 binding of both analytes simultaneously. Characteristic ADN and CYT ($\nu_{\text{CYT}} = 792 \text{ cm}^{-1}$) peaks are tracked for
264 every detection/regeneration cycle (Fig. 4 a,b), showing the complete removal of analytes each time and no
265 detectable trace (within the ADN limit of detection $\approx 10^{-7}$ M) of the initial analyte after analyte switching. Analyte
266 quantification is repeatable to 4.6% RSD for ADN and 3.5% RSD for CYT. A 50:50% mixture of 100 μ M ADN and
267 100 μ M CYT is also fully removed.

268

269 In a next set of analyte-switching experiments, ADN is alternated with thiols. Due to their strong interaction with
270 Au, thiols readily displace most other adsorbates from Au surfaces, and are in turn very difficult to remove once
271 bound²⁷. Only a very limited number of SERS substrate recycling methods remove thiols, typically relying on harsh
272 treatments such as the complete etching and redeposition of the metal layer^{13,39}, plasma or ozone
273 treatment^{18,27,61}, or competitive binding with NaBH₄^{29,30}. Electrochemical oxidation-reduction cycling can remove
274 thiol ligands from graphite-supported AuNP catalysts, but requires 25 cycles for complete thiol removal^{42,43}.
275 Thiols are sensitive to oxidising conditions and at positive potentials near the oxidation of Au, surface-bound
276 thiols (Au-SR) are oxidised to form R-SO₂^{-62,63}, which can be more readily removed from the surface with rinsing.

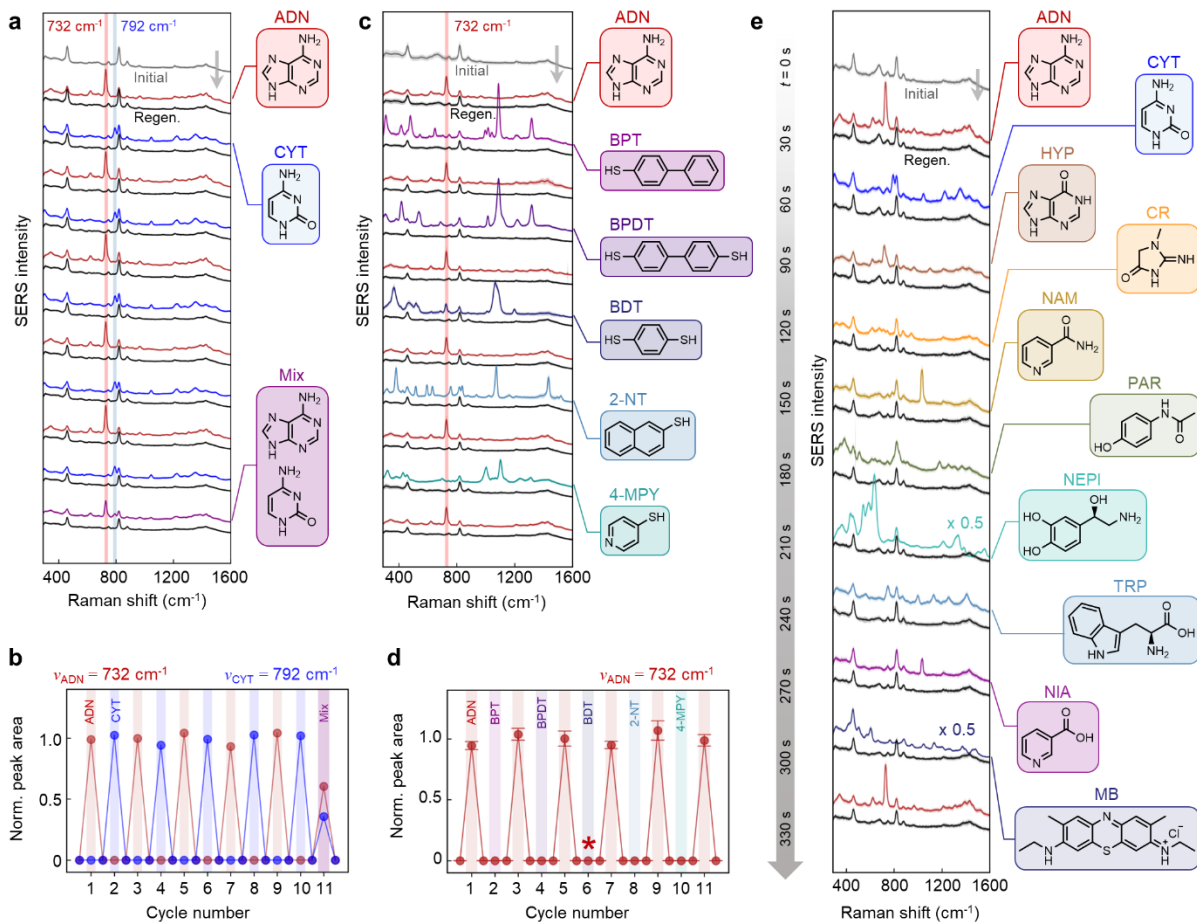
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278 To evaluate the effectiveness of thiol removal using ReSERS, 100 μ M of different aromatic thiols including 4-
279 biphenylthiol (BPT), 4,4-biphenyldithiol (BPDT), 1,4-benzenedithiol (BDT), 2-naphthalenethiol (2-NT), and 4-
280 mercaptopyridine (4-MPY) were each incubated with the MLagg-CB[5] for 1 h and then cleaned. After analyte
281 detection and cleaning by holding the potential at 1.5 V for 30 s under continuous buffer flow, each regenerated
282 MLagg-CB[5] SERS spectrum shows no trace of the previously bound thiol (Fig. 4c), demonstrating its effective
283 removal from the nanogaps. Before and after each thiol detection/cleaning cycle, 100 μ M of ADN was also
284 detected to benchmark the cleaned/regenerated MLagg-CB[5]. This ADN calibration between each thiol
285 detection was reproducible to 5.4% RSD (Fig. 4d), indicating highly effective cleaning and regeneration after thiol
286 detection.

287

288 To simulate the continuous flow-injection analysis of various bioanalytes, different biologically significant
289 compounds, including ADN, CYT, hypoxanthine (HYP), creatinine (CR), nicotinamide (NAM), paracetamol (PAR),
290 norepinephrine (NEPI), tryptophan (TRP), nicotinic acid (NIA), and methylene blue (MB) at 100 μ M each were

291 sequentially detected after 15 s incubation and then cleaned from the same MLagg-CB[5] SERS substrate, with
 292 15 s of ReSERS process between each analyte. SERS spectra from sequential analyte detection and
 293 cleaning/regeneration steps (Fig. 4e) prove the MLagg is effectively cleaned and regenerated. Calibration ADN
 294 detection at the start and end of the series are within 6.0% in peak area, confirming the reliable regeneration of
 295 the SERS substrate throughout analysis of this test set. This demonstrates the capability to perform continuous
 296 measurements of various analytes in aqueous flow systems, such as for flow-injection analysis or the sequential
 297 detection of fractionated chromatographic eluates.
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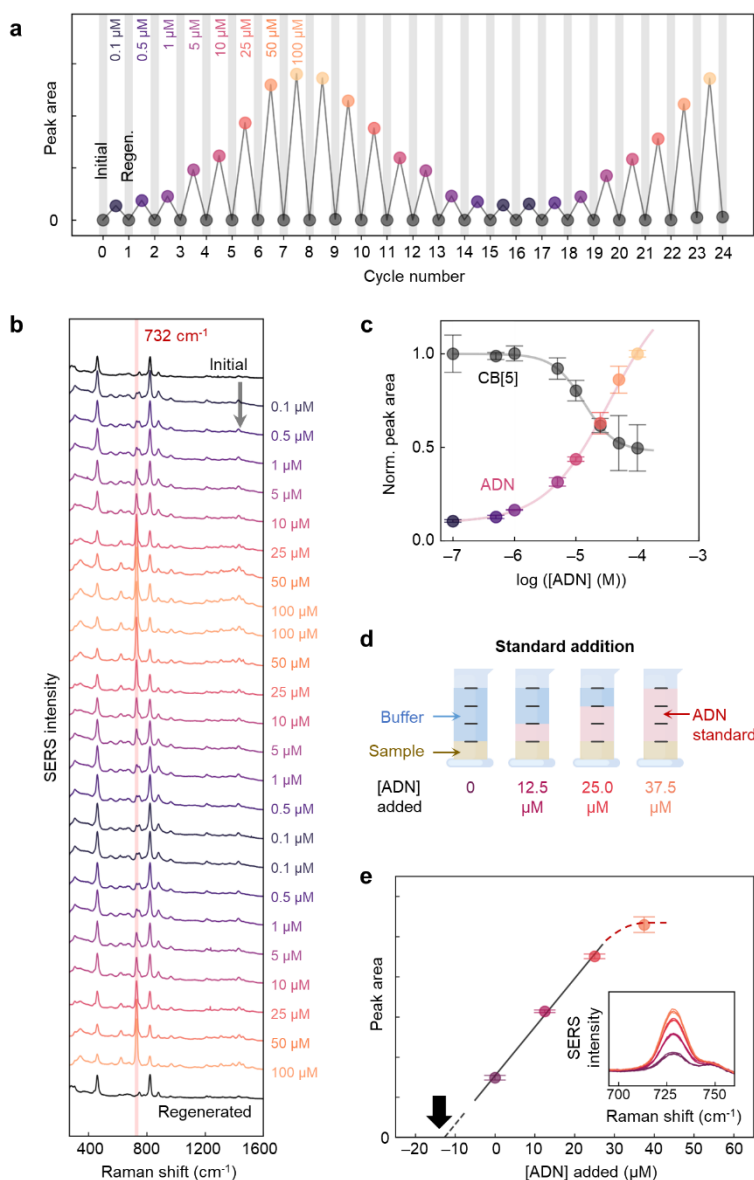
300 **Fig. 4 | In-situ analyte switching.** a Sequential SERS spectra from alternating detection of 100 μM ADN (red) and 100 μM CYT
 301 (blue) with the corresponding regenerated MLagg-CB[5] (black). A 50:50% mixture of 100 μM ADN and 100 μM CYT (purple)
 302 is also tested. b Normalized peak areas of ADN ($\nu_{\text{ADN}}=732\text{ cm}^{-1}$, red) and CYT ($\nu_{\text{CYT}}=792\text{ cm}^{-1}$, blue) per detection-
 303 regeneration cycle. c Sequential spatially-averaged SERS spectra from alternating detection of 100 μM ADN (red) and 100 μM
 304 4-biphenylthiol (BPT), 4,4-biphenyldithiol (BPDT), 1,4-benzenedithiol (BDT), 2-naphthalenethiol (2-NT), and 4-
 305 mercaptopyridine (4-MPY) with the corresponding regenerated MLagg-CB[5] (black). d Normalized peak area of ν_{ADN} per
 306 ADN/thiol detection-regeneration cycle. Peak areas are plotted as the mean with error bars representing ± 1 s.d. of $n=10$
 307 spectra obtained from different points across the MLagg-CB[5] area. For cycle 6 (marked with asterisk), alternative ADN peak
 308 at 970 cm^{-1} is used due to overlap with BDT peak at 732 cm^{-1} . e Sequential SERS spectra from detection of a series of biological
 309 compounds: ADN, CYT, hypoxanthine (HYP), creatinine (CR), nicotinamide (NAM), paracetamol (PAR), norepinephrine (NEPI),
 310 tryptophan (TRP), nicotinic acid (NIA), methylene blue (MB), and ADN (red) again with the corresponding regenerated MLagg-
 311 CB[5] (black). Time (t) axis marks progress of both analyte detection and ReSERS (30 s between each detection cycle). All SERS
 312 spectra collected at 1 s integration time and with 1 mW 785 nm excitation laser.
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316 Quantitative analysis of ADN in biofluids

317 A key application of SERS substrate regeneration is analytical calibration and quantitative analysis. Most works
 318 reporting quantitative SERS analysis rely on using separate SERS substrates for every calibration standard and
 319 test sample³⁻⁵. Reliable quantitative analysis using this approach therefore hinges on the substrate-to-substrate

320 reproducibility of the SERS substrate⁸, and/or the use of the appropriate internal standards to normalise for other
 321 uncontrollable factors^{64,65}. However, if a SERS substrate can be reliably cleaned and regenerated over multiple
 322 uses, then the same SERS substrate can be used for both the calibration and test samples. This greatly enhances
 323 the accuracy, reliability, and efficiency of the analysis by reducing the time and cost needed for SERS substrate
 324 fabrication, maximising materials efficiency, and minimising the uncertainty introduced by substrate-to-substrate
 325 variations.

326
 327 For feasibility of absolute quantitative calibration using the same SERS substrate, ADN in buffer is again used as
 328 a model analyte. ADN calibration standards (0.1 μM to 100 μM) are sequentially detected and cleaned on the
 329 same MLagg-CB[5], extracting the SERS peak areas (Fig. 5a-b). ADN peaks are reproducible with average 5.3%
 330 RSD. Binding site competition is clearly observed as the CB[5] signal drops for higher ADN concentrations $\geq 5 \mu\text{M}$
 331 (Fig. 5c). With such a repeatable system, analyte competition becomes feasible to quantify.
 332



333
 334 **Fig. 5 | Quantitative analysis of ADN.** **a** ADN peak areas at ν_{ADN} from sequentially measured calibration standards (0.1 to
 335 100 μM) in 50 mM potassium phosphate buffer (pH 7.0) and regenerated MLagg-CB[5] (black circles). **b** Sequential SERS
 336 spectra from ADN calibration standards measured from the same MLagg-CB[5] SERS substrate. SERS spectra collected at 1 s
 337 integration time and 1 mW 785 nm laser. **c** Relative peak areas of CB[5] ($\nu_{\text{CB[5]}}=830 \text{ cm}^{-1}$) and ADN ($\nu_{\text{ADN}}=732 \text{ cm}^{-1}$) vs [ADN]
 338 (log scale). Peak areas are plotted as the mean with error bars representing ± 1 s.d. from $n=3$ measurements of an ADN
 339 calibration standard using the same MLagg-CB[5] SERS substrate after multiple ReSERS cycles. Solid lines are fits. **d** Schematic

340 of the standard addition analysis of ADN in urine. **e** ADN peak area vs added [ADN] standard. Points are plotted as mean ± 1
341 s.d. from $n=3$ measurements of an ADN calibration standard using the same MLagg-CB[5] SERS substrate after multiple
342 ReSERS cycles. Grey solid line is linear fit, dashed grey line is linear extrapolation. Black arrow points to the extrapolated x -
343 intercept. Red dashed line highlights the trend towards non-linearity at higher concentration. Inset shows close-up of ADN
344 peak from SERS spectra of calibration standards.

345
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347

348 To test the viability of quantitative analysis on a real sample matrix using a single MLagg-CB[5] SERS substrate,
349 the direct quantification of ADN in human urine is explored. Urine is a complex biofluid containing >4600
350 different metabolites at concentration levels spanning eleven orders of magnitude, from μM mM^{-1} creatinine to
351 mM mM^{-1} creatinine (normalized to creatinine levels as conventional)⁶⁶. Typical levels of urinary ADN in adults
352 occur at a mid-range concentrations of 1.4 to 5.1 μM mM^{-1} creatinine, or 18-66 μM given average creatinine
353 concentrations of 13 mM ⁶⁶. Other major molecular components of urine such as hippuric acid, citric acid, urea,
354 creatinine, and uric acid occur at mM levels⁶⁶. Direct analysis of a complex sample therefore exposes SERS
355 substrates to a broad range of unknown components of varying concentrations that often result in substrate
356 fouling. Our aim is to mitigate this using the ReSERS cleaning technique since it is proven capable of stripping
357 even thiols.

358

359 The many unknown components in real sample matrices pose not only a challenge to SERS substrate cleaning,
360 but also for the quantitative analysis itself. Due to the complexity of biological matrices, ADN is not usually
361 determined directly, but typically requires chromatographic separation prior to detection⁶⁷. As SERS relies on the
362 interaction of the analyte with the nanogap for detection, direct analysis of a complex sample matrix such as
363 urine inevitably leads to the simultaneous competitive binding of molecular components at the SERS hotspots,
364 thereby limiting the availability of binding sites, and reducing the analysis sensitivity. Calibration standards must
365 thus be prepared in a background that matches that of the sample (e.g. ionic strength, pH, background
366 components) to include interactions of the SERS substrate and analyte with the background matrix. However, for
367 complex matrices such as urine, this can be difficult and/or impractical to prepare.

368

369 To address this challenge, we opt to use the standard addition method to account for matrix interactions in direct
370 analysis⁶⁵. For ADN determination in urine, a test sample of human urine is prepared (see Methods) containing
371 50.0 μM ADN (Supplementary Fig. 16) and with a series of standard addition calibrators of $[\text{ADN}]_{\text{added}} = 0, 12.5,$
372 $25.0,$ and $37.5 \mu\text{M}$ (Fig. 5d). Using the same substrate throughout, the SERS spectrum of each standard is
373 measured after applying the ADN enhancement potential of -0.60 V , followed by cleaning and regeneration
374 (Supplementary Fig. 17). The triplicate measurements at v_{ADN} of each standard are repeatable, with 1.0-3.9%
375 RSD for each (Fig. 5e). To ensure linearity, the standard $[\text{ADN}]_{\text{added}} = 37.5 \mu\text{M}$ is excluded from the calibration fit
376 since analyte saturation is evident ($R^2 = 0.996, p < 0.05$). Extrapolating (Fig. 5e, black arrow) and accounting for
377 dilution returns the ADN concentration in the test sample as 50.8 μM (with error $\pm 6.0 \mu\text{M}$ at 95% confidence),
378 and 101.6% recovery.

379

380 The high accuracy of ADN determination in urine using the same MLagg-CB[5] indicates that our SERS substrate
381 recycling method indeed mitigates substrate fouling, enabling reliable continuous reuse of the SERS substrate for
382 the entire standard addition assay. While standard addition was previously demonstrated for direct
383 quantification of uric acid^{68,69} and moxifloxacin⁷⁰ in urine, new SERS substrates were needed for every
384 measurement, generating high levels of waste, while substrate-to-substrate variations compromise the accuracy
385 and reproducibility (6-9% error, 8-25% RSD reported). By contrast, using single MLagg-CB[5] substrates coupled
386 with effective recycling offers multiple advantages, including cost savings, improved efficiency, enhanced
387 precision, ease of comparison, and the capability for integration. These benefits contribute to more accurate and
388 reliable analytical calibration, supporting high-quality and high-throughput quantitative analysis across various
389 applications, including environmental monitoring, industrial quality control, and medical diagnostics.

390

391 DISCUSSION

392 SERS has been enormously hampered by the difficulty of preserving the metallic nanogaps that deliver the crucial
393 signal enhancements during its practical use for analyte sensing. Here, we demonstrate an *in-situ*
394 electrochemical SERS substrate recycling method that addresses the challenge of substrate degradation and
395 limited reusability. Compared to other previously reported recycling methods, we demonstrate a two-step
396 electrochemical process that rapidly removes a broad range of analytes (all we have tested so far) and

397 reproducibly regenerates the hotspots of the SERS substrate through the unusual and rapid reintroduction of a
398 nanogap-stabilising scaffold molecule. The ability to maintain consistent SERS enhancements after multiple
399 cycles of reuse showcases the robustness of our method and its potential to provide reliable analytical results
400 over extended periods. This can significantly impact the development of highly sensitive and reproducible SERS
401 platforms for diverse applications such as trace-level molecular detection, biosensing, and environmental
402 monitoring.

403

404 Several key conditions are required for this cleaning. Initial gaps between the AuNPs need to be on the few nm
405 scale, so that oxidation reliably and completely plugs them with Au oxide. The MLagg (or equivalent plasmonic
406 nano-geometry) must be fully electrically contacted to act as the working electrode and possess low enough
407 tortuosity that the electrical double layer accesses each nanogap. For instance, we find that stacking six layers of
408 the MLagg (which tunes the resonant modes into the mid-infrared) is also found to be successfully cleaned.
409 Chloride ions must be eliminated from the oxidation step as they evidently interfere with the Au oxide formation.
410 Details of the mechanism for the nanoscale process will need to confirm the crystal structure and stoichiometry
411 with depth of the Au oxide that plugs the nanogaps, as clearly seen in the SERS and scattering spectra. The variety
412 of SERS peaks $\approx 590\text{ cm}^{-1}$ that make up the Au oxide signature have been matched to different positions of oxygen
413 atoms in the upper and lower Au atomic layers⁵⁸. An improved understanding should also show how the CB[n]
414 molecules interact with the Au oxide as it progressively reduces and recreates the separated Au facets that elicit
415 extremely strong SERS signals for analytes. Although we find that other molecules can perform this re-scaffolding
416 (as in Ref⁹), their cleaning repeatability is inferior to CB[5] so far and sintering is progressively observed. An
417 account is also sought for the capability of analytes to diffuse into the SERS hotspots once the CB[n] has re-
418 scaffolded the nanogap. The combination of electrochemical potentials at the nanoscale surfaces, variable
419 oxidation states, labile hydrogen bonding between organic and metal oxide, and confinement at the nanoscale,
420 all highlight the complexity of the Re-SERS process. Because the chemistry of Au is rather unique, it is not clear
421 how well this cleaning can be controlled on other SERS-active metals such as Ag and Cu. However we suggest
422 that analogous approaches may indeed also be successful. We also note this treatment will equally enhance the
423 repeatable performance of sensors for surface-enhanced infrared absorption (SEIRA).

424

425 To ensure the successful integration of this method for real-world SERS applications, further studies will be
426 directed towards optimization, validation, and mechanistic investigations. Specifically, optimising the
427 electrochemical parameters and electrolyte composition to achieve the highest recycling efficiency without
428 compromising long-term substrate integrity is required. Optimisation towards minimising the time needed for
429 the two-step ReSERS process is ongoing, to improve its suitability for rapid on-line detection, while additional
430 rigorous studies involving more complex multi-analyte samples will be explored to validate its performance in
431 real-world scenarios. Further work is underway to understand the nanogap regeneration mechanism, which can
432 provide insights on achieving more rapid implementation and longer-term stability, as well as extending the
433 applicability of the protocol to other SERS substrate metals and scaffolding molecules. Systematically addressing
434 these research avenues can lead to the seamless integration of electrochemical recycling with SERS platforms in
435 microfluidic compact sensor systems, contributing to the enhanced cost-effectiveness, practicality, and reliability
436 of SERS-based analysis.

437

438 **METHODS**

439 **Materials**

440 All chemicals were used as received. Citrate-stabilised 80 nm AuNPs (optical density 1.0 at 555 nm) were
441 purchased from BBI Solutions. Analytical-grade chloroform ($\geq 99.8\%$) was obtained from Merck. HCl (37%) and
442 methylene blue hydrate (MB) ($\geq 96\%$) were from Fisher Scientific. NaCl ($\geq 99\%$), K_2HPO_4 ($\geq 98\%$), and KH_2PO_4
443 ($\geq 98\%$) were from Alfa Aesar. Cucurbit[5]uril hydrate ($\approx 20\%$ water), adenine (ADN, $\geq 99\%$), cytosine (CYT, $\geq 99\%$),
444 1,4-benzenedithiol (BDT, $\geq 99\%$), 2-naphthalenethiol (2-NT, $\geq 99\%$), 4-biphenylthiol (BPT, $\geq 97\%$), 4,4-
445 biphenyldithiol (BPDT, $\geq 95\%$), 4-mercaptopyridine (4-MPY, $\geq 95\%$), hypoxanthine (HYP, $\geq 99.0\%$), creatinine (CR,
446 $\geq 98\%$), nicotinamide (NAM, $\geq 98\%$), paracetamol (PAR, $\geq 99\%$), (\pm)-norepinephrine hydrochloride (NEPI, $\geq 97\%$), L-
447 tryptophan (TRP, $\geq 98\%$), nicotinic acid (NA, $\geq 98\%$), and 96% ethanol (EtOH) were obtained from Sigma-Aldrich.
448 Lyophilised pooled human urine controls (Level II for biogenic amines, Ref 8821, Lot 1066) were from ClinChek
449 Controls. Polydimethylsiloxane (PDMS) was prepared using a SYLGARD 184 kit from DOWSIL (Dow Silicones).
450 Fluorine-doped tin oxide (FTO)-coated glass slides (TEC 10) were purchased from Ossila Ltd and were cleaned
451 and cut to $10 \times 15\text{ mm}^2$ slides prior to use. All aqueous solutions were prepared using deionized (DI) water (>18.2
452 $\text{M}\Omega\text{ cm}^{-1}$) from a Purelab Ultra Scientific water purification system.

453

454 **Multilayer aggregate preparation**

455 MLagg SERS substrates were prepared^{9,47} by first placing 500 μL of 80 nm AuNP with an equal volume of
456 chloroform in an Eppendorf tube. Aggregation of the AuNPs was initiated upon addition of 50 μL of 1 mM CB[5]
457 or 1 M NaCl and was facilitated by vigorous shaking for 1 min. The aggregates were then allowed to settle at the
458 aqueous-organic interface. Excess ligands and salts were removed by replacing the aqueous supernatant with
459 fresh DI water. This washing step was repeated three times. The aggregates were then transferred by carefully
460 decreasing the volume of the aqueous phase to $\approx 5 \mu\text{L}$ and depositing the droplet onto a pre-cleaned FTO glass
461 slide. Once deposited, the MLagg was air dried, rinsed with DI, and dried with compressed N_2 . A schematic of
462 the full protocol is summarised in Supplementary Fig. 1a.

463 To remove remaining native AuNP ligands from the MLagg surface, all surface ligands were stripped with
464 oxygen plasma cleaning using 90% RF power and $30 \text{ cm}^3_{\text{STP}} \text{ min}^{-1}$ (Henniker Plasma, HPT-100) for 45 min. The
465 desired scaffolding ligand (e.g. CB[5]) was then introduced by incubating the plasma cleaned MLagg in a 1 mM
466 ligand solution prepared in 0.5 M HCl (Supplementary Fig. 1b-e). After 5 min, the MLagg was rinsed with DI and
467 dried with N_2 . Alternatively, initial MLagg cleaning was also performed with *in-situ* electrochemical cleaning using
468 the regeneration protocol described below (Supplementary Fig. 18).

469

470 **SERS and dark-field measurements**

471 SERS measurements were recorded on a custom-built Raman set-up (Supplementary Fig. 4) using a 785 nm diode
472 laser (Matchbox) set at $\leq 1 \text{ mW}$ power. Excitation and collection were performed through an Olympus
473 LUMPlanFI/IR 40xW NA 0.80 water-immersion objective (in inverted configuration), and spectra were recorded
474 by an Andor Newton 970 EMCCD camera coupled to a Shamrock 168 spectrometer with 1 s integration times.

475 SERS mapping measurements were taken on a commercial Raman instrument (Renishaw inVia) with 1 s
476 integration times, 785 nm excitation (laser line profile) and 2.1 mW laser power using a 20x NA 0.40 objective.
477 Map scans were taken over a $465 \times 330 \mu\text{m}^2$ region over a 31×11 grid with $15 \times 30 \mu\text{m}^2$ spacings.

478 Dark-field (DF) scattering spectra were recorded on a modified Olympus BX51 with an Ocean Optics QE-Pro
479 spectrometer with 0.5 s integration time. Excitation and collection were performed through an Olympus
480 MPlanFL N 20x BD NA 0.45 objective. DF scattering spectra of MLagg samples were collected over a 600×400
481 μm area (in a 10×15 point grid) and then averaged. A white light scattering target (Labsphere) was used as a
482 reference to normalize white light scattering.

483

484 **SEM measurements**

485 SEM measurements of MLaggs deposited on FTO-coated glass slides were taken on a FEI Philips Dualbeam
486 Quanta 3D SEM (dwell 3-10 μs , HV 2 kV, current 50 pA, and $\approx 2.0 \text{ mm}$ WD) or on a FEI Helios NanoLab 650 SEM
487 (dwell 100 ns-1 μs , HV 20 kV, current 100 pA and $\approx 4.0 \text{ mm}$ WD). Magnification ranged from 80,000-200,000x.

488

489 **SERS enhancement factor calculation**

490 The SERS enhancement factor of MLagg-CB[5] was calculated based on the SERS and Raman signal of CB[5]
491 (Supplementary Fig. 2) normalised to an estimated number of probed molecules. The CB[5] SERS spectrum was
492 measured on a MLagg-CB[5] using 1 s integration time and 2.1 mW 785 nm laser excitation. The Raman spectrum
493 of a 2 mM CB[5] solution in water was taken with 200 s integration time and 127 mW 785 nm laser excitation.
494 All measurements were taken using a Renishaw inVia with a 20x NA 0.40 objective.

495 To estimate the number of CB[5] molecules probed per SERS measurement, a diffraction-limited laser
496 spot size of $1 \mu\text{m}^2$ was assumed. The number of nanogaps per μm^2 and the average nanogap diameter was
497 estimated from SEM imaging, while the surface coverage of CB[5] molecules was based on previously reported
498 X-ray photoelectron spectroscopy measurements⁴⁷. From here, the number of CB[5] molecules bound in
499 nanogaps per $1 \mu\text{m}^2$ probed (N_{SERS}) was calculated,

$$N_{\text{SERS}} = \rho_{\text{CB}[5]} \cdot (D_{\text{nanogap}}/2)^2 \cdot n_{\text{gaps}} = 40050 \text{ CB}[5] \text{ molecules} \quad (1)$$

500 where $\rho_{\text{CB}[5]}$ = surface density of CB[5] molecules on MLagg-CB[5] = $9 \times 10^{17} \text{ m}^{-2}$, D_{nanogap} = average lateral width
501 of nanogap = 30 nm, and n_{gaps} = number of gaps within laser focus = 200 on average. The number of CB[5]
502 molecules probed via Raman (N_{Raman}) in a solution of 2 mM CB[5] was then estimated,

$$N_{\text{Raman}} = c \cdot N_{\text{A}} \cdot D^2 z = 6022000 \text{ CB}[5] \text{ molecules} \quad (2)$$

503 where $c = 2 \text{ mM}$ concentration of solution for Raman, N_{A} = Avogadro's number, $D = 1 \mu\text{m}$ diameter of Raman
504 excitation laser spot, $z = 5 \mu\text{m}$ depth of focus. Comparing the normalised Raman peak intensity in counts mW^{-1}
505 s^{-1} with a 785 nm excitation laser for the CB[5] band at 830 cm^{-1} (Eqn. 3) yielded 1.0×10^6 , which is in line with
506 typical SERS enhancements for a variety of substrates and non-resonant SERS molecules.

$$\text{SERS EF} = \frac{I_{\text{SERS}}/N_{\text{SERS}}}{I_{\text{Raman}}/N_{\text{Raman}}} = \left(\frac{1400 \text{ counts mW}^{-1} \text{ s}^{-1}}{40050 \text{ molecules}} \right) / \left(\frac{0.2 \text{ counts mW}^{-1} \text{ s}^{-1}}{6022000 \text{ molecules}} \right) = 1.0 \times 10^6 \quad (3)$$

507

508 **EC-SERS flow set-up**

509 A miniaturized EC-SERS flow cell was designed and fabricated to accommodate a standard three-electrode
 510 electrochemical system: a leakless Ag/AgCl reference electrode (LF-1-45 from Innovative Instruments Ltd), a Pt
 511 wire (Sigma-Aldrich) counter electrode, and a removeable MLagg SERS substrate on FTO-coated glass as the
 512 working electrode (Fig. 1c). The internal volume of the flow cell was 26 μL . The EC-SERS flow cell and a three-
 513 inlet/one-outlet mixer module were fabricated with PDMS using 3D-printed moulds. The EC-SERS flow cell was
 514 sealed and mounted onto the stage of an inverted Raman set-up using custom 3D-printed holders and bases.

515 Custom-built syringe pumps were used to control the flow of solutions (buffer, CB[5] in buffer, and analyte
 516 in buffer) through the EC-SERS flow cell (Supplementary Fig. 4). Electrochemical measurements were conducted
 517 using a portable potentiostat (CompactStat) from Ivium Technologies. All potentials were referenced to the
 518 Ag/AgCl reference electrode. The syringe pumps, electrochemical measurements, and SERS spectra collection
 519 were all controlled and synchronized with Python scripts.

520

521 **Analyte detection**

522 Aqueous analyte solutions were prepared in a background electrolyte of 50 mM potassium phosphate buffer (pH
 523 7.0, 0.5 mS cm^{-1} conductivity) and injected into the EC-SERS flow cell. Under static conditions, an electrochemical
 524 enhancement potential (-0.60 V) was applied where applicable for 15 s. SERS spectra were then collected at open
 525 circuit potential.

526 For the detection of thiols, the MLagg was removed from the EC-SERS flow cell and immersed in a 100
 527 μM thiol solution in EtOH for 1 h. Afterwards, the MLagg was rinsed with EtOH and dried with a stream of N_2 .
 528 The MLagg was then reinstalled into the EC-SERS flow cell for cleaning, regeneration, and reference calibrations
 529 of ADN detection. Since the MLagg was periodically removed from the cell, it was difficult to probe precisely the
 530 same spot on the MLagg surface, so spectra were taken over multiple random spots across the substrate ($n=10$)
 531 and averaged. Variations in the spectra in this case thus also include spatial variation across the MLagg.

532

533 **Cleaning and regeneration**

534 To clean and regenerate the MLagg, 50 mM potassium phosphate buffer (pH 7.0) was pumped into the EC-SERS
 535 flow cell and a potential of +1.5 V vs Ag/AgCl was held for 5-60 s under continuous buffer flow (flow rate = 500
 536 $\mu\text{L min}^{-1}$). For initial MLagg cleaning, 60 s was typically required, while for analyte cleaning, 15-30 s was sufficient.
 537 After cleaning, 1 mM CB[5] in 50 mM potassium phosphate buffer (pH 7.0) was pumped into the flow cell. Under
 538 static conditions, a potential of -0.80 V vs Ag/AgCl was held for 5 s. Buffer was then flushed into the cell to remove
 539 excess scaffold molecules. If traces of previously detected analyte were evident from the SERS spectrum, another
 540 round of cleaning/regeneration was conducted.

541 During detection/cleaning cycling experiments, solution syringes were refilled every 12-15 cycles. The
 542 flow system was allowed to stabilise before measurements were resumed. Care was also taken to record the
 543 SERS spectra from the same substrate spot throughout the cycling experiments. However, the continuous
 544 operation of the flow system was occasionally halted to replenish the water droplet on the water immersion
 545 objective, which tended to dry over prolonged use. Since this required moving the EC-SERS flow cell, some
 546 variation in the probed substrate spot can occur.

547

548 **Standard addition**

549 For direct ADN detection in urine, a test sample was prepared from a pooled human urine control matrix, which
 550 initially contained no detectable trace of ADN (Supplementary Fig. 16). The test sample was prepared by
 551 dissolving the lyophilised matrix in 50 mM potassium phosphate buffer and adding ADN standards for a final
 552 concentration of 50 μM ADN. Calibration standards were prepared by taking equal volume aliquots of the test
 553 sample and adding different volumes of 100 μM ADN standard and 50 mM potassium phosphate buffer. The final
 554 concentrations of added ADN for each standard were 0, 12.5, 25.0, and 37.5 μM . The final dilution factor of the
 555 test sample in all the standards was 4.

556

557 **Data analysis**

558 SERS spectra are presented here with minimal data processing, except for background correction to eliminate
 559 the broad glass background signal centred at 1400 cm^{-1} that arises from back-side optical measurements. Analyte
 560 peak areas were determined by iteratively fitting a polynomial to correct for the SERS background, followed by
 561 fitting Gaussian curves to the narrow analyte peaks of interest. To determine the peak wavelength of the MLagg

562 coupled plasmon mode from DF scattering spectra, Gaussian curves were fitted for each DF spectrum. The peak
563 wavelength was determined from the centre of the fitted Gaussian.

564

565 DATA AVAILABILITY

566 The data that support the findings of this study are available from the corresponding author upon request. In
567 addition, data is deposited in the Cambridge Open Data archive⁷¹.

568

569

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742 AUTHOR CONTRIBUTIONS STATEMENT

743 S.M.S.-T. and J.J.B. conceived and designed the experiments. EC-SERS flow set-up was developed by S.M.S.-T., D.-
744 B.G. and G.K., with input from M.N., E.W., and B.d.N. S.M.S.-T. performed fabrication and spectroscopic
745 experiments with input from D.-B.G., G.K., M.N., E.W., and B.d.N. S.M.S.-T. and E.W. analysed the data with input
746 from M.N. Sample fabrication was aided by M.N. and E.W. SEM image collection was carried out by N.S. and A.R.
747 S.M.S.-T. and J.J.B. wrote the manuscript with input from all authors.

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750 COMPETING INTERESTS STATEMENT

751 J.J.B., S.M.S.-T., D.-B.G., M.N., and E.W. acknowledge a patent has been filed, patent: Surface-enhanced
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754 FIGURE LEGENDS/CAPTIONS

755 **Fig 1 | Preparation and in-flow EC-SERS analyte detection, cleaning, and regeneration with MLagg-CB[5].** **a** Preparation of
756 MLagg-CB[5] SERS aggregate from self-assembly of AuNPs with CB[5], followed by deposition onto solid support. Photo and
757 scanning electron micrograph (SEM) show MLagg-CB[5] deposited on FTO-coated glass. **b** Schematic illustrating the
758 integration of an MLagg-CB[5] into an EC-SERS flow system. **c** Cross-section of the EC-SERS flow cell (CE = counter electrode,
759 RE = reference electrode, and WE = working electrode). **d** Schematic of *in-situ* electrochemical SERS analyte detection and
760 cleaning/regeneration protocol. Potentials are vs Ag/AgCl. **e** SERS spectra from: initial MLagg-CB[5] (grey), after detection of
761 10 μM adenine (ADN) (red), after oxidative cleaning step (blue), and after regeneration step (black). ADN peak at 732 cm^{-1} is
762 marked by asterisk. SERS spectra are collected with 1s integration time and 1 mW 785 nm laser.

763 **Fig 2 | Analyte detection, cleaning, and regeneration cycles with and without CB[5].** **a** SERS spectra from 30 cycles of 10
764 μM ADN detection (red) and regeneration with CB[5] (black). Spectra are offset for clarity. **b** ADN peak areas ($\nu_{\text{ADN}}=732\text{ cm}^{-1}$)
765 from the SERS spectra of each ADN detection and cleaning/CB[5]-regeneration cycle. Dotted horizontal line represents the
766 average ADN peak area of all analyte detection cycles. **c** CB[5] peak areas ($\nu_{\text{CB[5]}}=830\text{ cm}^{-1}$, black circles) and integrated SERS
767 background (purple squares) for the CB[5]-regenerated MLagg. Dotted horizontal line represents the average CB[5] peak area
768 of all regeneration cycles. **d** Overlaid SERS spectra from 15 cycles of 10 μM ADN detection and **e** after regeneration without
769 CB[5]. A constant background was subtracted from all spectra to facilitate comparison across 15 cycles. **f** ADN peak areas
770 ($\nu_{\text{ADN}}=732\text{ cm}^{-1}$) from the SERS spectra of each ADN detection and cleaning/regeneration cycle without CB[5]. **g** CB[5] peak
771 areas ($\nu_{\text{CB[5]}}=830\text{ cm}^{-1}$, black circles) and integrated SERS background (purple squares) for the MLagg regenerated without
772 CB[5].

773 **Fig 3 | Morphology changes with or without CB[5] during regeneration.** **a** DF scattering spectra and **b** representative SEM
774 images of the MLagg-CB[5] before and after undergoing 10 and 30 cycles of analyte detection, cleaning, and regeneration
775 with CB[5]. **c** DF scattering spectra and **d** representative SEM images of the MLagg-CB[5] throughout different cycles of
776 analyte detection, cleaning, and regeneration without CB[5]. Yellow arrows in **d** point to bridges formed between
777 neighbouring AuNPs. For the DF spectra, solid lines and shaded area represent mean and ± 1 s.d. of $n=150$ spectra obtained
778 across the area of a MLagg-CB[5]. Grey line highlights initial chain mode peak wavelength. Spectra are offset for clarity.

779 **Fig 4 | In-situ analyte switching.** **a** Sequential SERS spectra from alternating detection of 100 μM ADN (red) and 100 μM CYT
780 (blue) with the corresponding regenerated MLagg-CB[5] (black). A 50:50% mixture of 100 μM ADN and 100 μM CYT (purple)
781 is also tested. **b** Normalized peak areas of ADN ($\nu_{\text{ADN}}=732\text{ cm}^{-1}$, red) and CYT ($\nu_{\text{CYT}}=792\text{ cm}^{-1}$, blue) per detection-
782 regeneration cycle. **c** Sequential spatially-averaged SERS spectra from alternating detection of 100 μM ADN (red) and 100 μM
783 4-biphenylthiol (BPT), 4,4-biphenyldithiol (BPDT), 1,4-benzenedithiol (BDT), 2-naphthalenethiol (2-NT), and 4-

784 mercaptopyridine (4-MPY) with the corresponding regenerated MLagg-CB[5] (black). **d** Normalized peak area of ν_{ADN} per
785 ADN/thiol detection-regeneration cycle. Peak areas are plotted as the mean with error bars representing ± 1 s.d. of $n=10$
786 spectra obtained from different points across the MLagg-CB[5] area. For cycle 6 (marked by asterisk), alternative ADN peak
787 at 970 cm^{-1} is used due to overlap with BDT peak at 732 cm^{-1} . **e** Sequential SERS spectra from detection of a series of biological
788 compounds: ADN, CYT, hypoxanthine (HYP), creatinine (CR), nicotinamide (NAM), paracetamol (PAR), norepinephrine (NEPI),
789 tryptophan (TRP), nicotinic acid (NIA), methylene blue (MB), and ADN (red) again with the corresponding regenerated MLagg-
790 CB[5] (black). Time (t) axis marks progress of both analyte detection and ReSERS (30 s between each detection cycle). All SERS
791 spectra collected at 1 s integration time and with 1 mW 785 nm excitation laser.

792 **Fig 5 | Quantitative analysis of ADN.** **a** ADN peak areas at ν_{ADN} from sequentially measured calibration standards (0.1 to 100
793 μM) in 50 mM potassium phosphate buffer (pH 7.0) and regenerated MLagg-CB[5] (black circles). **b** Sequential SERS spectra
794 from ADN calibration standards measured from the same MLagg-CB[5] SERS substrate. SERS spectra collected at 1 s
795 integration time and 1 mW 785 nm laser. **c** Relative peak areas of CB[5] ($\nu_{\text{CB}[5]}=830\text{ cm}^{-1}$) and ADN ($\nu_{\text{ADN}}=732\text{ cm}^{-1}$) vs [ADN]
796 (log scale). Peak areas are plotted as the mean with error bars representing ± 1 s.d. from $n=3$ measurements of an ADN
797 calibration standard using the same MLagg-CB[5] SERS substrate after multiple ReSERS cycles. Solid lines are fits. **d** Schematic
798 of the standard addition analysis of ADN in urine. **e** ADN peak area vs added [ADN] standard. Points are plotted as mean ± 1
799 s.d. from $n=3$ measurements of an ADN calibration standard using the same MLagg-CB[5] SERS substrate after multiple
800 ReSERS cycles. Grey solid line is linear fit, dashed grey line is linear extrapolation. Black arrow points to the extrapolated x -
801 intercept. Red dashed line highlights the trend towards non-linearity at higher concentration. Inset shows close-up of ADN
802 peak from SERS spectra of calibration standards.