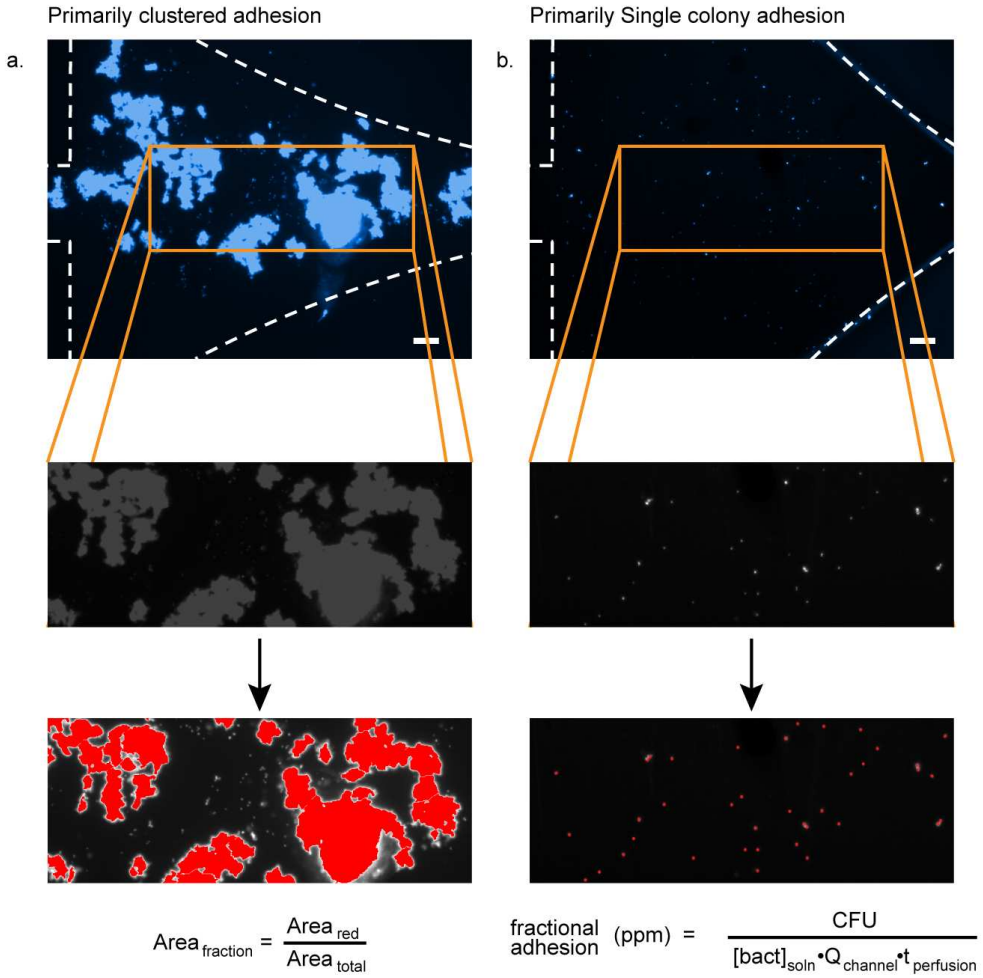
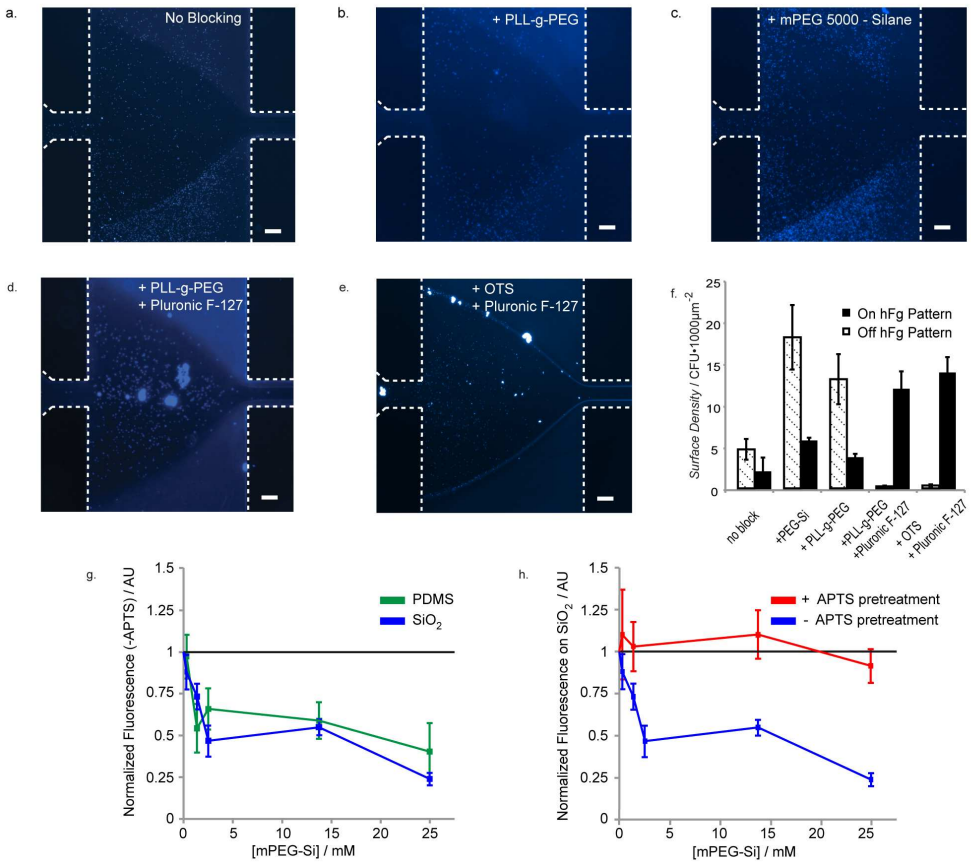
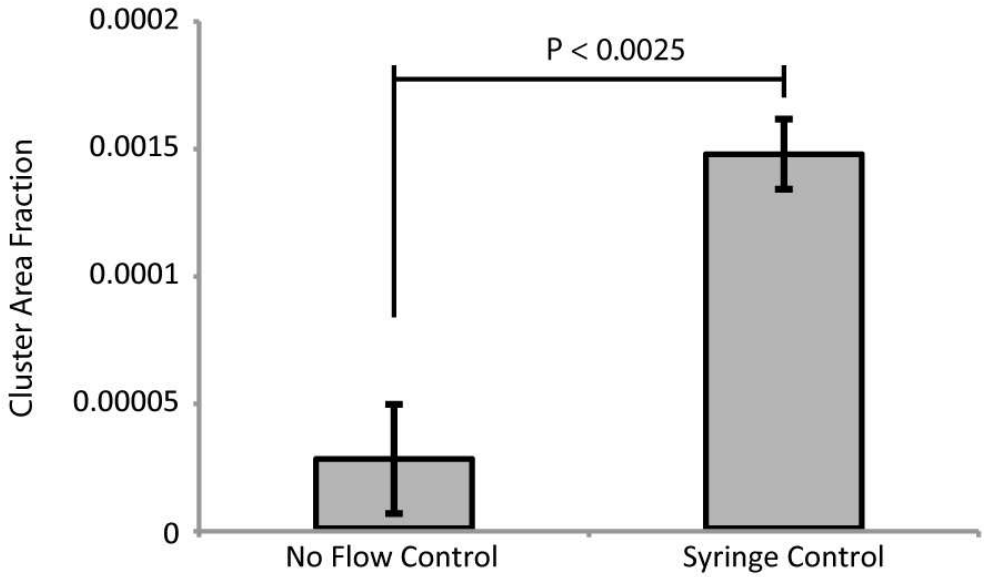


Image analysis of adhered clumps and single colonies: each method of analysis was performed on each shear stress chamber. a) To quantify clumped adhesion, a 10X magnification image was cropped within the fibrinogen-patterned area. This cropped image was then post processed further by calculating the area in (px^2) corresponding to pixels that were over 10,000 intensity (AU). This px area was converted to μm^2 using the pixel to μm conversion for the given objective. This area was divided by the total area of the cropped image to arrive at a unitless area fraction, reported in figure 5 and used for statistical analysis. b) Single colonies were quantified by cropping the images with the same crop from (a). These images were used to count the single colonies and the part per million (ppm) of adhered bacteria to that that passed over the surface during the shear attachment assay was reported in figure 5 and used for statistical analysis.
113x114mm (300 x 300 DPI)



Hydrophobic based surface passivation is sufficient to create a high fidelity protein pattern. a – e) DAPI images of live *S. epidermidis* adhered to the channel walls, modified or otherwise. Successful patterning was achieved only when a hydrophobic and hydrophilic combination (d) or hydrophobic only (e) mechanism of PEG adsorption to the channel walls was used. f) quantification of surface densities of bacteria adhering on and off the protein pattern for each experimental case. g) passivation of freshly O_2 plasma treated PDMS and SiO_2 (glass) using a covalently linked mPEG(triethoxy)silane (MW 5000). It is possible to significantly reduce protein adsorption with larger concentrations of mPEG-silane. h) Glass surfaces treated with mPEG-silane were protected against covalent protein linkage, where as pretreatment of the glass surface with APTS retained the ability to undergo further covalent linkage. This implies the possibility of creating a surface pattern using only silane chemistry, as long as the deposition area can be controlled. (1 corresponds to positive control protein linkage (no blocking) and 0 corresponds to a negative control blank glass slide to PDMS piece). Protein was FITC conjugated and the fluorescent intensities of surfaces were measured. All scale bars are 100 μm.

171x150mm (300 x 300 DPI)



Controls for clump induction from experimental procedure prior to introduction into the device platform. a) Fractional clumped area after bacteria have been stained and vortexed, prior to loading into the syringe and experiencing and flow. b) Clumped area fraction after staining, vortexing and flowing through only the syringe and PEEK tubing. Although there is significant difference between the two, all data points in figure 5 are measured against the syringe control here, indicating that the majority of clumping is resulting form shear stresses within the device.
76x45mm (300 x 300 DPI)