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Supporting Information

Colonising New Frontiers - Microarrays Reveal Biofilm Modulating Polymers

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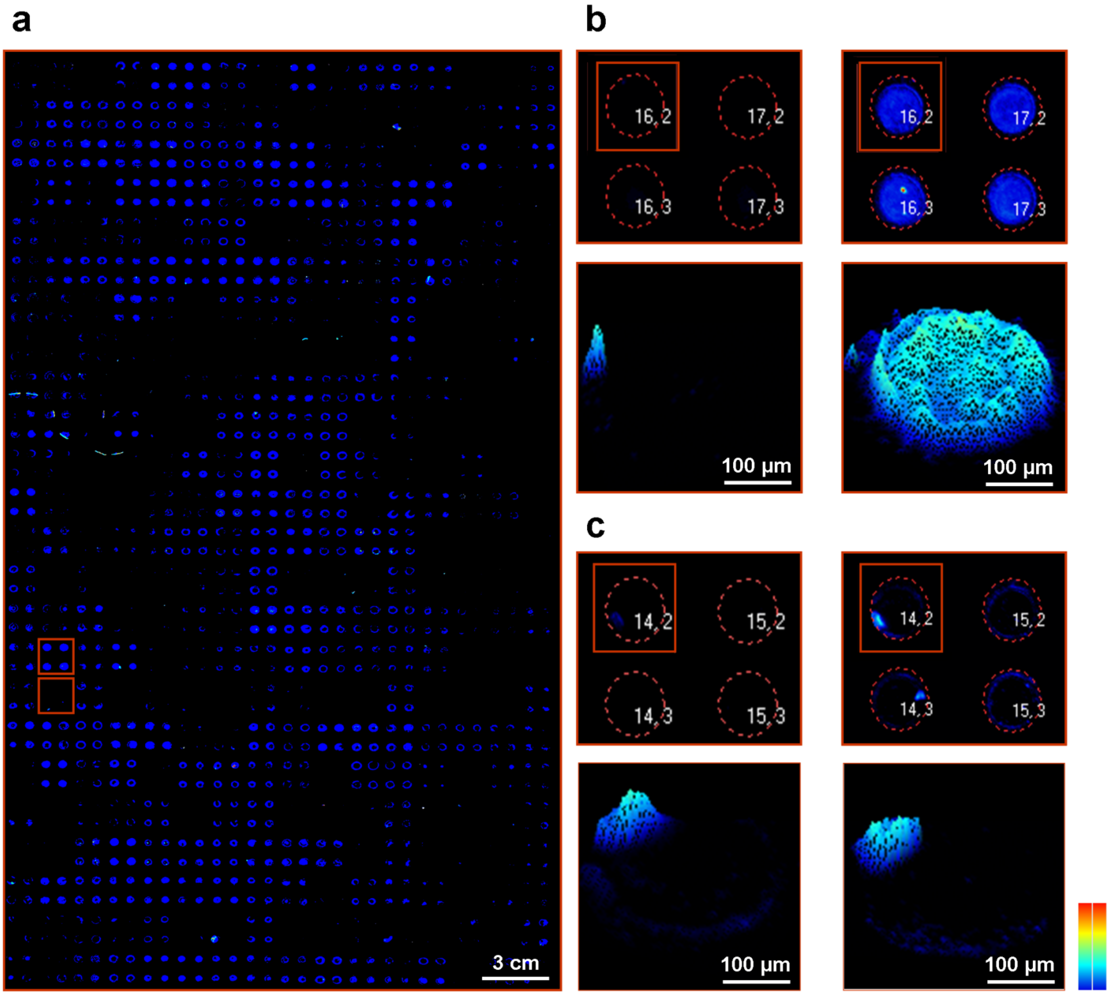


Fig S1 LaVision Bio Analyzer 4F/4S BioTech quantification. (a) Fluorescence associated with the binding of bacteria (expressing GFP) on a library of 370 polyurethanes and polyacrylates (each polymer was printed in quadruplicate). The high-lighted squares show the 4 polymer spots shown in b and c. (b) Strong binding polymer (PA155). Upper-left: background polymer auto-fluorescence prior to bacterial binding; Upper right: fluorescence intensity in the presence of bacteria. 3D image of the spot in the selected area is shown in lower panels, respectively. (c) Poor binding polymer (PA325). Upper-left: background polymer auto-fluorescence prior to bacterial binding; Upper right: fluorescence intensity in the presence of bacteria. 3D image of the spot in the selected area is shown in lower panels, respectively. In b and c: the number in the square is the position of the polymer spot in the array, which was allocated automatically by the software. Intensity scale bar is shown (botton right).

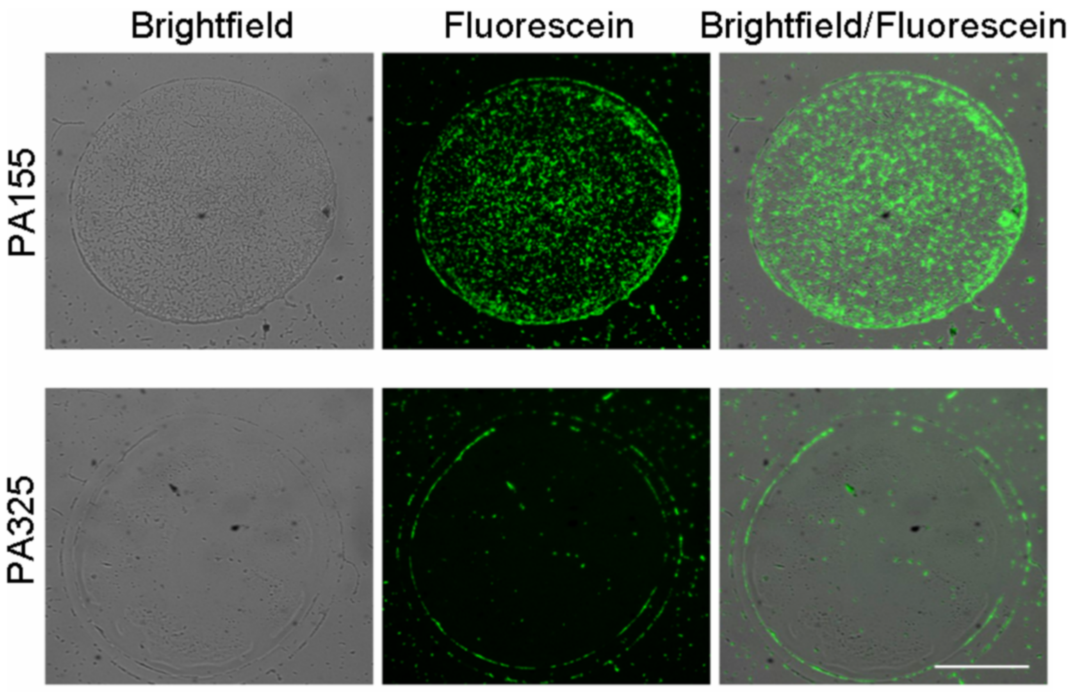
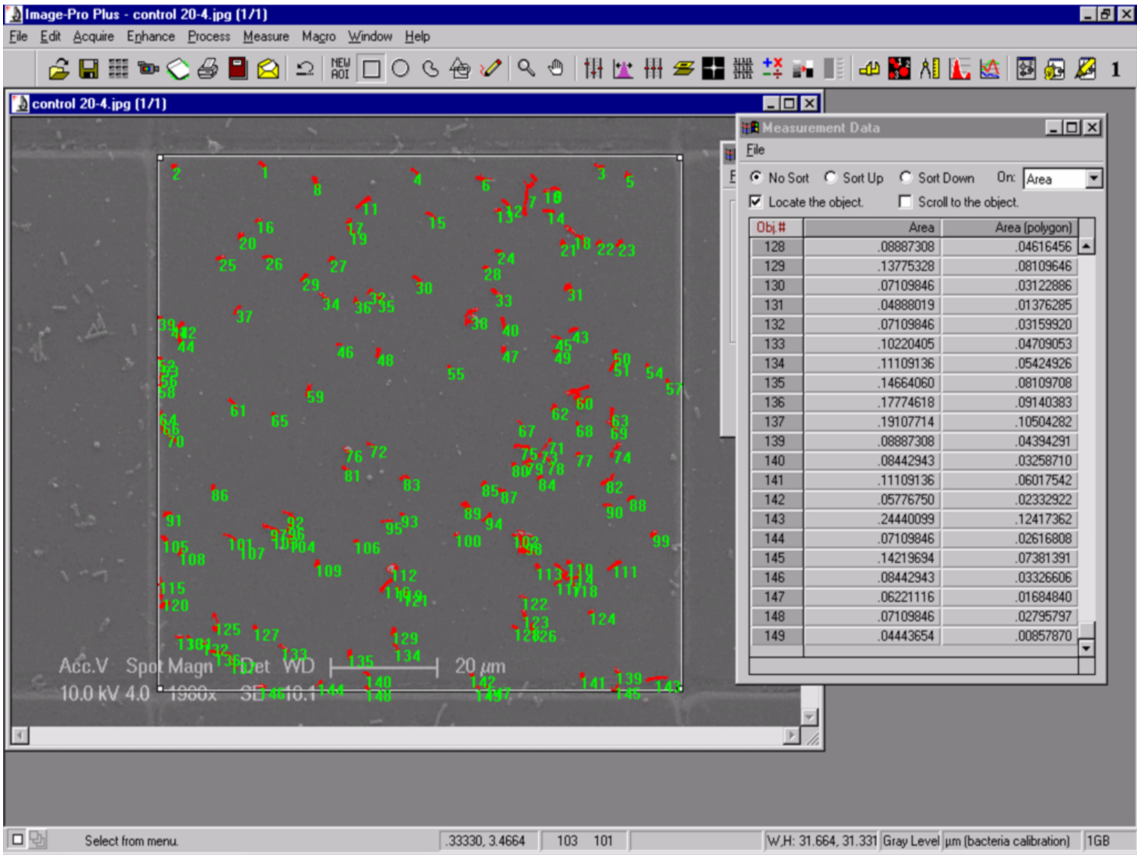


Fig S2 Brightfield and fluorescent microscopy imaging of *S.* Typhimurium binding (Pathfinder^{TM} , IMSTAR). Images of *S.* Typhimurium attachment on spots of polymers: PA155 and PA325. From left to right: brightfield, fluorescein channel and merged images respectively. Scale bar = 100 µm.



● No Sort ○ Sort Up ○ Sort Down On: Area

☑ Locate the object. ☐ Scroll to the object.

Obj.#	Area	Area (polygon)
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142	.05776750	.02332922
143	.24440099	.12417362
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146	.08442943	.03326606
147	.06221116	.01684840
148	.07109846	.02795797
149	.04443654	.00857870

Fig S3 Automated counting of *S.* Typhimurium binding. The image files were transferred to Image-Pro Plus 4.5 for processing. In this example, the number of *S.* Typhimurium on one single square of the uncoated coverslip (control) was counted. Salmonella identified by Image-Pro Plus 4.5 are in red with an associated number in green.

***S. Typhimurium* and *E. coli*-polyacrylate binding analysis**								
	Polymer				*S.* Typhimurium		*E. coli*	
		Monomer (1)	Monomer (2)	Monomer (3)	AVE	SD	AVE	SD
PA for strong	PA55	HBMA	DEAA	-	0.48	0.024	0.16	0.016
	PA155	HEMA	DMAEMA	-	0.46	0.021	0.13	0.005
	PA172	HEMA	BACOEA	-	0.46	0.027	0.25	0.030
	PA181	HEMA	VI	-	0.52	0.035	0.19	0.014
	PA182	HEMA	VI	-	0.48	0.024	0.24	0.014
	Pg17	MEMA	A-H	DEAEA	0.46	0.041	0.13	0.045
PA for poor	PA235	MMA	MA-H	DEAEMA	0.03	0.001	0.02	0.002
	PA236	MMA	MA-H	DEAEMA	0.04	0.008	0.03	0.008
	PA422	MEMA	DEAEMA	BMA	0.04	0.005	0.08	0.027
	PA426	MEMA	DEAEA	BMA	0.04	0.003	0.12	0.008
	PA523	MEMA	DEAEA	St	0.04	0.003	0.13	0.018

Table S1 Polyacrylates for *S.* Typhimurium strong/poor binding. Monomer ratios were Mon1/Mon2/Mon3: PA155 and PA182 (50/50/0); PA172 and PA 181 (70/30/0); PA155 (90/10/0); PA422 and PA426 (40/30/30); Pg17 (50/15/35); PA523 (60/10/30); PA235 (70/25/5); PA236 (70/10/20). Average (AVG) and Standard Deviation (SD) from 8 spots (4 each microarray) were calculated assuming a spot diameter of 300 μm.

List of abbreviations (polyacrylate library):

Monomer (1)
HBMA:Hydroxybutylmethacrylate
HEMA: 2-hydroxyethylmethacrylate
MEMA: 2-methoxyethylmethacrylate
MMA: methyl methacrylate

Monomer (2)/(3)
DEAA: diethylacrylamide
DMAEMA: 2-(dimethylamino)ethyl methacrylate
BACOEA: 2-[[(Butylamino)carbonyl]oxy]ethyl acrylate
VI: 1-Vinylimidazol
MA-H: methacrylic acid
BMA: butyl methacrylate
St: styrene
DEAEMA: 2-(diethylamino)ethyl methacrylate
DEAEA: 2-(diethylamino)ethyl acrylate

***S.* Typhimurium and *E. coli*-polyurethane binding analysis**

	Polymer				*S.* Typhimurium		*E. coli*	
	Diol	Mn	Dis.	Ext.	AVE	SD	AVE	SD
PU39	PTMG	2000	HDI	BD	0.56	0.042	0.23	0.017
PU92	PTMG	1000	HDI	-	0.65	0.015	0.17	0.014
PU104	PHNGAD	1800	MDI	DEAPD	0.51	0.018	0.28	0.032
PU116	PPG	425	BICH	-	0.47	0.018	0.18	0.009
PU119	PPG	1000	MDI	DMAPD	0.45	0.009	0.23	0.026
PU120	PPG	425	BICH	DEAPD	0.63	0.020	0.27	0.009
PU126	PPG	425	TDI	DMAPD	0.90	0.030	0.28	0.013
PU138	PTMG	250	BICH	EG	0.48	0.018	0.29	0.022
PU159	PTMG	250	MDI	BD	0.45	0.026	0.19	0.007
PU178	PTMG	1000	HDI	NMPD	0.47	0.022	0.13	0.007
PU208	PPG	1000	MDI	OFHD	0.47	0.032	0.18	0.017
PU219	PHNAD	900	BICH	DMAPD	0.51	0.027	0.21	0.018
PU222	PHNAD	900	BICH	OFHD	0.64	0.035	0.41	0.041

Table S2 Polyurethanes showing *S.* Typhimurium binding. Monomer ratios were: Diol/Dis/Ext (25/5/25) except 92 and 116 (Diol/Dis: 50/50). Average (AVG) and Standard Deviation (SD) from 8 spots (4 each microarray) were calculated assuming a spot diameter of 300 μm.

List of abbreviations (polyurethane library)

Diol
PPG: poly(propylene glycol)
PTMG: poly(butylene glycol)
PHNGAD: poly[1,6-hexanediol/neopentyl glycol/diethylene glycol-alt-(adipic acid)]diol
PHNAD: poly[1,6-hexanediol/neopentyl glycol-alt-(adipic acid)]diol

Chain extender (Ext.)
BD: 1,4-butanediol
EG: ethylene glycol
DMAPD: 3-dimethylamino-1,2-propanediol
NMPD: 2-nitro-2-methyl-1,3-propanediol
OFHD: 2,2,3,3,4,4,5,5-octafluoro-1,6-hexanediol
DEAPD: 3-(Diethylamino)-1,2-propanediol

Diisocryanate (Dis.)
HDI: 1,6-diisocyanohexane
MDI: 4,4’-methylenebis(phenylisocyanate)
TDI: 4-methyl-1,3-phenylene diisocyanate
BICH: 1,3-bis(isocynanatomethyl)cyclohexane

***S.* Typhimurium and *E. coli* -polyacrylate binding analysis**					
	Functionalisation Amines	*S.* Typhimurium		*E. coli*	
		AVE	SD	AVE	SD
PA306	Di-n-Butylamine	0.04	0.005	0.12	0.013
PA321	cycloheanemethylamine	0.04	0.002	0.17	0.020
PA322	cycloheanemethylamine	0.04	0.017	0.17	0.019
PA323	cycloheanemethylamine	0.04	0.005	0.16	0.021
PA325	Benzylmethylamine	0.03	0.006	0.15	0.018
PA326	Benzylmethylamine	0.04	0.006	0.05	0.016
PA327	2-(2-Methylaminoethyl) pyridine	0.04	0.004	0.12	0.025
PA331	Pyrrole	0.04	0.003	0.56	0.080
PA336	N-methylaniline	0.03	0.002	0.22	0.021
PA337	N-methylaniline	0.04	0.002	0.49	0.044
PA338	N-methylaniline	0.04	0.002	0.51	0.021

Table S3 Polyacrylate series with poor *S.* Typhimurium binding. These polyacrylates had similar polymer backbones (MMA and GMA) but different functionalisation of amines. Monomer ratios between MMA and GMA were: PA306, PA321, PA327 and PA336 (90/10), PA322, PA325, PA331, and PA337 (70/30); PA323, PA326, and PA338 (50/50). Average (AVG) and Standard Deviation (SD) from 8 spots (4 each microarray) were calculated assuming a spot diameter of 300 μm.

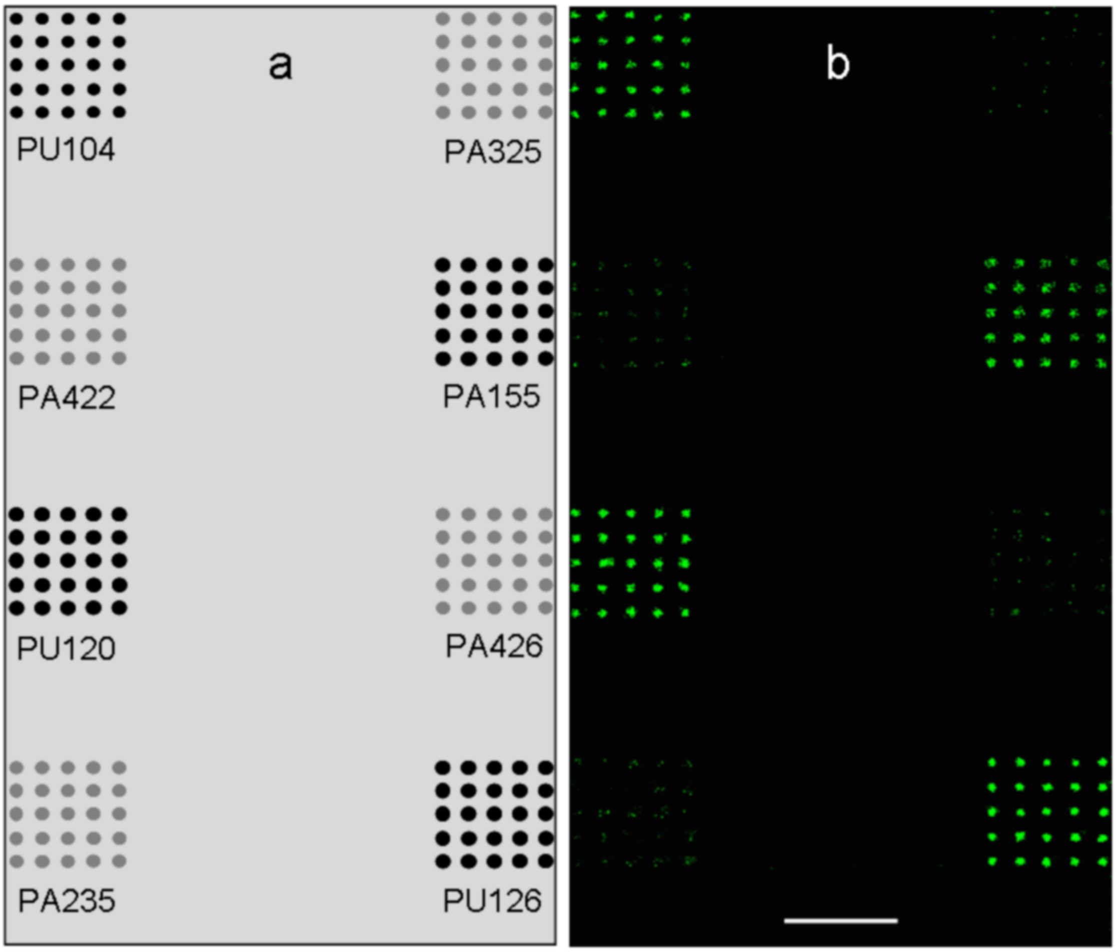

Fig S4 (a) Slide template with 8 fields of 25 polymer spots (PU104, PA325, PA422, PA155, PU120, PA426, PA235 and PU126, respectively), and array design with the binding polymers (in black) and the poor binding polymers (in grey). (b) Fluorescent microscopy image of *S.* Typhimurium-GFP (fluorescein channel) binding. Scale bar = 3 cm.