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How Do Polymer Coatings Affect the Growth and Bacterial Population of a Biofilm Formed by Total Human Salivary Bacteria? – A Study by 16S-RNA Sequencing

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Table of Contents:

Table S1: Total RNA extracted from biofilm samples grown on **PSB**, **PZI**, and **SMAMP**, uncoated substrates (**NegCtrol**), and uncoated substrates grown in the presence of chlorhexidine digluconate (**CHX**). Data is as concentration (in ng/μl), total mass of extracted RNA (in ng), and relative percentage compared to the mean of the uncoated samples (**NegCtrol**), i.e. the natively biofilm grown.

Table S2: Abundance of bacteria (in counts per million, CPM, and percent), found in a) saliva, b) the native biofilm formed on uncoated substrates, and c) the biofilms formed on uncoated substrates in the presence of **CHX**, listed as Top 20 genera. STD = Standard Deviation. **It should be kept in mind that the amount of 16S rRNA also correlates to a high number of ribosomes, which in turn correlates with the activity of bacteria, since active bacterial cells contain a higher number of ribosomes than inactive ones.**

Table S3: Abundance of bacteria (in counts per million, CPM, and percent), found in a) saliva, b) the native biofilm formed on uncoated substrates, and c) the biofilms formed on uncoated substrates in the presence of **CHX**, listed as Top 20 species. STD = Standard Deviation. **It should be kept in mind that the amount of 16S rRNA also correlates to a high number of ribosomes, which in turn correlates with the activity of bacteria, since active bacterial cells contain a higher number of ribosomes than inactive ones.**



Table S4: Abundance of bacteria (in counts per million, CPM, and percent), found in a) biofilms grown on **PSB**, b) biofilms grown on **PZI**, and c) biofilms grown on **SMAMP**, listed as Top 20 genera. STD = Standard Deviation. It should be kept in mind that the amount of 16S rRNA also correlates to a high number of ribosomes, which in turn correlates with the activity of bacteria, since active bacterial cells contain a higher number of ribosomes than inactive ones.

Table S5: Abundance of bacteria (in counts per million, CPM, and percent), found in a) biofilms grown on **PSB**, b) biofilms grown on **PZI**, and c) biofilms grown on **SMAMP**, listed as Top 20 species. STD = Standard Deviation. It should be kept in mind that the amount of 16S rRNA also correlates to a high number of ribosomes, which in turn correlates with the activity of bacteria, since active bacterial cells contain a higher number of ribosomes than inactive ones.

Table S1: Total RNA extracted from biofilm samples grown on **PSB**, **PZI**, and **SMAMP**, uncoated substrates (**NegCtrl**), and uncoated substrates grown in the presence of chlorhexidine digluconate (**CHX**). Data is as concentration (in ng/ μ l), total mass of extracted RNA (in ng), and relative percentage compared to the mean of the uncoated samples (**NegCtrl**), i.e. the natively biofilm grown.

Sample	ng/ μ l	ng	% of NegCtrl
NegCtrl 1	15.1	211.8	106.6
NegCtrl 2	13.3	186.1	93.6
NegCtrl 3	12.1	169.4	85.3
NegCtrl 4	16.3	227.5	114.5
SMAMP 1	7.4	103.3	52.0
SMAMP 2	6.5	91.3	45.9
SMAMP 3	7.5	104.4	52.6
SMAMP 4	13.4	187.6	94.4
SMAMP 5	7.4	103.9	52.3
PZI 1	1.6	21.8	11.0
PZI 2	1.0	13.7	6.9
PZI 3	1.1	15.8	8.0
PZI 4	0	0	0
PZI 5	1.1	15.3	7.7
PSB 1	1.5	21.6	10.9
PSB 2	2.0	28.3	14.2
PSB 3	0.9	12.4	6.1
PSB 4	1.5	20.6	10.4
CHX	0.6	8.5	4.3

Table S2: Abundance of bacteria (in counts per million, CPM, and percent), found in a) saliva, b) the native biofilm formed on uncoated substrates, and c) the biofilms formed on uncoated substrates in the presence of **CHX**, listed as Top 20 genera. STD = Standard Deviation. It should be kept in mind that the amount of 16S rRNA also correlates to a high number of ribosomes, which in turn correlates with the activity of bacteria, since active bacterial cells contain a higher number of ribosomes than inactive ones.

a) Saliva				
Genus	CPM Mean	CPM STD	% Mean	% STD
<i>Streptococcus</i>	298653.96	13058.34	29.87	1.31
<i>Campylobacter</i>	202530.06	61853.40	20.25	6.19
<i>Veillonella</i>	164369.75	62496.87	16.44	6.25
<i>Gemella</i>	67682.07	46469.58	6.77	4.65



<i>Prevotella</i>	34458.58	30544.07	3.45	3.05
<i>Haemophilus</i>	32488.68	10128.32	3.25	1.01
<i>Fusobacterium</i>	31683.54	9174.90	3.17	0.92
<i>Neisseria</i>	28694.34	19290.07	2.87	1.93
<i>Schaalia</i>	20082.88	2454.18	2.01	0.25
<i>Actinomyces</i>	14874.74	6317.08	1.49	0.63
<i>Atopobium</i>	14507.75	14025.36	1.45	1.40
<i>Bacillus</i>	9462.43	2549.41	0.95	0.25
<i>Selenomonas</i>	6566.19	3007.45	0.66	0.30
<i>Rothia</i>	6466.50	1436.57	0.65	0.14
<i>Staphylococcus</i>	5781.25	716.37	0.58	0.07
<i>Lactobacillus</i>	5213.19	1120.81	0.52	0.11
<i>Corynebacterium</i>	3970.43	3429.50	0.40	0.34
<i>Enterococcus</i>	3732.74	1439.90	0.37	0.14
<i>Erysipelothrix</i>	2771.61	2110.45	0.28	0.21
<i>Megasphaera</i>	2090.94	1038.76	0.21	0.10

b) Native				
Genus	CPM Mean	CPM STD	% Mean	% STD
<i>Streptococcus</i>	316633.26	28601.86	31.66	2.86
<i>Fusobacterium</i>	187175.01	37219.62	18.72	3.72
<i>Megasphaera</i>	106519.42	23815.29	10.65	2.38
<i>Neisseria</i>	46108.91	44862.71	4.61	4.49
<i>Tannerella</i>	42883.65	34077.78	4.29	3.41
<i>Prevotella</i>	39814.53	36564.89	3.98	3.66
<i>Campylobacter</i>	33569.54	22700.58	3.36	2.27
<i>Veillonella</i>	32888.34	11113.57	3.29	1.11
<i>Staphylococcus</i>	11871.88	5037.34	1.19	0.50
<i>Bacillus</i>	10803.27	1177.49	1.08	0.12
<i>Selenomonas</i>	9247.11	2669.07	0.92	0.27
<i>Actinomyces</i>	9000.47	3912.34	0.90	0.39
<i>Erysipelothrix</i>	7806.01	2268.61	0.78	0.23
<i>Luteimonas</i>	6163.59	7338.72	0.62	0.73
<i>Slackia</i>	5933.55	2958.09	0.59	0.30
<i>Dialister</i>	5791.48	1041.49	0.58	0.10
<i>Atopobium</i>	4728.39	1154.16	0.47	0.12
<i>Olsenella</i>	4550.73	2315.17	0.46	0.23
<i>Schaalia</i>	4362.96	1258.85	0.44	0.13
<i>Gemella</i>	4287.27	1423.55	0.43	0.14

c) CHX				
Genus	CPM Mean	CPM STD	% Mean	% STD
<i>Streptococcus</i>	21.01	n.a.	21.01	n.a.
<i>Corynebacterium</i>	10.47	n.a.	10.47	n.a.
<i>Massilia</i>	10.06	n.a.	10.06	n.a.
<i>Actinomyces</i>	7.55	n.a.	7.55	n.a.
<i>Schaalia</i>	6.62	n.a.	6.62	n.a.
<i>Prevotella</i>	4.01	n.a.	4.01	n.a.
<i>Staphylococcus</i>	2.79	n.a.	2.79	n.a.
<i>Neisseria</i>	2.56	n.a.	2.56	n.a.
<i>Rothia</i>	2.14	n.a.	2.14	n.a.
<i>Lautropia</i>	2.12	n.a.	2.12	n.a.
<i>Porphyromonas</i>	2.03	n.a.	2.03	n.a.
<i>Erysipelothrix</i>	1.87	n.a.	1.87	n.a.
<i>Selenomonas</i>	1.87	n.a.	1.87	n.a.



<i>Streptomyces</i>	1.78	n.a.	1.78	n.a.
<i>Brevundimonas</i>	1.68	n.a.	1.68	n.a.
<i>Bacillus</i>	1.43	n.a.	1.43	n.a.
<i>Bradyrhizobium</i>	0.90	n.a.	0.90	n.a.
<i>Fusobacterium</i>	0.79	n.a.	0.79	n.a.
<i>Gemella</i>	0.78	n.a.	0.78	n.a.
<i>Atopobium</i>	0.78	n.a.	0.78	n.a.

Table S3: Abundance of bacteria (in counts per million, CPM, and percent), found in a) saliva, b) the native biofilm formed on uncoated substrates, and c) the biofilms formed on uncoated substrates in the presence of **CHX**, listed as Top 20 species. STD = Standard Deviation. It should be kept in mind that the amount of 16S rRNA also correlates to a high number of ribosomes, which in turn correlates with the activity of bacteria, since active bacterial cells contain a higher number of ribosomes than inactive ones.

a) Saliva				
Species	CPM Mean	CPM STD	% Mean	% STD
<i>Campylobacter concisus</i>	243034.20	57565.27	24.30	5.76
<i>Gemella sanguinis</i>	80512.50	53728.22	8.05	5.37
<i>Veillonella dispar</i>	55877.49	30950.55	5.59	3.10
<i>Streptococcus sp. LPB0220</i>	48460.60	18826.01	4.85	1.88
<i>Haemophilus parainfluenzae</i>	41176.31	15305.59	4.12	1.53
<i>Veillonella parvula</i>	36101.70	9000.34	3.61	0.90
<i>Streptococcus sp. A12</i>	33867.45	25390.49	3.39	2.54
<i>Veillonella rodentium</i>	29574.61	10443.03	2.96	1.04
<i>Atopobium parvulum</i>	18811.03	17446.63	1.88	1.74
<i>Schaalia odontolytica</i>	17907.65	2575.89	1.79	0.26
<i>Prevotella sp. oral taxon 299</i>	17656.55	24036.68	1.77	2.40
<i>Streptococcus koreensis</i>	17615.67	9148.69	1.76	0.91
<i>Streptococcus sp. I-P16</i>	17566.03	13629.89	1.76	1.36
<i>Prevotella melaninogenica</i>	17467.38	13818.00	1.75	1.38
<i>Fusobacterium pseudoperiodonticum</i>	15987.26	3072.26	1.60	0.31
<i>Veillonella atypica</i>	13566.61	4695.02	1.36	0.47
<i>Neisseria subflava</i>	13364.14	9965.92	1.34	1.00
<i>Streptococcus salivarius</i>	12703.52	8865.47	1.27	0.89
<i>Streptococcus pneumoniae</i>	11627.69	5475.84	1.16	0.55
<i>Streptococcus sp. oral taxon 431</i>	10426.36	4820.18	1.04	0.48

b) Native				
Species	CPM Mean	CPM STD	% Mean	% STD
<i>Fusobacterium nucleatum</i>	201697.88	44677.38	20.17	4.47
<i>Streptococcus salivarius</i>	167185.28	44236.34	16.72	4.42
<i>Megasphaera stantonii</i>	64882.66	19192.01	6.49	1.92
<i>Megasphaera elsdenii</i>	60280.24	10042.85	6.03	1.00
<i>Prevotella dentalis</i>	29272.85	28919.48	2.93	2.89
<i>Tannerella sp. oral taxon HOT-286</i>	29227.20	24514.84	2.92	2.45
<i>Tannerella forsythia</i>	24046.18	47418.83	2.40	4.74
<i>Neisseria subflava</i>	23884.48	24315.76	2.39	2.43
<i>Streptococcus thermophilus</i>	21101.02	1692.00	2.11	0.17
<i>Streptococcus sp. LPB0220</i>	17507.70	5630.60	1.75	0.56
<i>Campylobacter ureolyticus</i>	14987.13	10940.48	1.50	1.09
<i>Veillonella dispar</i>	12046.56	4916.29	1.20	0.49
<i>Staphylococcus schleiferi</i>	11557.77	5093.23	1.16	0.51
<i>Campylobacter curvus</i>	9809.15	7004.67	0.98	0.70



<i>Fusobacterium pseudoperiodonticum</i>	9788.53	3869.59	0.98	0.39
<i>Luteimonas</i> sp. Gr-4	7552.74	8932.71	0.76	0.89
<i>Slackia heliotrinireducens</i>	7272.81	3535.70	0.73	0.35
<i>Erysipelothrix larvae</i>	6907.04	2090.77	0.69	0.21
<i>Prevotella denticola</i>	6349.18	6035.12	0.63	0.60
<i>Actinomyces radidentis</i>	6251.42	3857.25	0.63	0.39

c) CHX				
Species	CPM Mean	CPM STD	% Mean	% STD
<i>Schaalia odontolytica</i>	56431.94	n.a.	5.64	n.a.
<i>Massilia armeniaca</i>	43702.81	n.a.	4.37	n.a.
<i>Massilia flava</i>	33687.56	n.a.	3.37	n.a.
<i>Lautropia mirabilis</i>	28406.33	n.a.	2.84	n.a.
<i>Prevotella melaninogenica</i>	24918.81	n.a.	2.49	n.a.
<i>Streptococcus sanguinis</i>	24449.29	n.a.	2.44	n.a.
<i>Rothia mucilaginosa</i>	23693.40	n.a.	2.37	n.a.
<i>Actinomyces naeslundii</i>	23493.61	n.a.	2.35	n.a.
<i>Actinomyces radidentis</i>	22014.02	n.a.	2.20	n.a.
<i>Schaalia meyeri</i>	21756.50	n.a.	2.18	n.a.
<i>Streptomyces</i> sp. SCSIO 03032	21525.63	n.a.	2.15	n.a.
<i>Porphyromonas gingivalis</i>	21097.18	n.a.	2.11	n.a.
<i>Streptococcus salivarius</i>	18466.56	n.a.	1.85	n.a.
<i>Erysipelothrix larvae</i>	18052.54	n.a.	1.81	n.a.
<i>Neisseria mucosa</i>	17014.72	n.a.	1.70	n.a.
<i>Staphylococcus schleiferi</i>	16263.27	n.a.	1.63	n.a.
<i>Selenomonas</i> sp. oral taxon 136	16152.27	n.a.	1.62	n.a.
<i>Streptococcus parasanguinis</i>	14562.79	n.a.	1.46	n.a.
<i>Streptococcus thermophilus</i>	14006.70	n.a.	1.40	n.a.
<i>Streptococcus</i> sp. LPB0220	13078.77	n.a.	1.31	n.a.

Table S4: Abundance of bacteria (in counts per million, CPM, and percent), found in a) biofilms grown on **PSB**, b) biofilms grown on **PZI**, and c) biofilms grown on **SMAMP**, listed as Top 20 genera. STD = Standard Deviation. It should be kept in mind that the amount of 16S rRNA also correlates to a high number of ribosomes, which in turn correlates with the activity of bacteria, since active bacterial cells contain a higher number of ribosomes than inactive ones.

a) PSB				
Genus	CPM Mean	CPM STD	% Mean	% STD
<i>Streptococcus</i>	265594.50	81644.39	26.56	8.16
<i>Campylobacter</i>	198685.49	79362.69	19.87	7.94
<i>Fusobacterium</i>	118246.36	52794.69	11.82	5.28
<i>Megasphaera</i>	108818.28	53636.62	10.88	5.36
<i>Veillonella</i>	58971.81	21884.42	5.90	2.19
<i>Neisseria</i>	57819.28	75321.98	5.78	7.53
<i>Prevotella</i>	48485.56	14916.20	4.85	1.49
<i>Tannerella</i>	23453.89	10048.99	2.35	1.00
<i>Treponema</i>	8395.22	4023.67	0.84	0.40
<i>Bacillus</i>	7734.32	2490.42	0.77	0.25
<i>Selenomonas</i>	7115.98	4096.00	0.71	0.41
<i>Staphylococcus</i>	7012.64	3555.46	0.70	0.36
<i>Erysipelothrix</i>	5930.60	1931.54	0.59	0.19
<i>Dialister</i>	5367.26	3061.18	0.54	0.31
<i>Slackia</i>	4177.49	4734.10	0.42	0.47
<i>Capnocytophaga</i>	3804.51	4087.29	0.38	0.41



<i>Actinomyces</i>	3683.44	1424.23	0.37	0.14
<i>Porphyromonas</i>	3565.28	1219.20	0.36	0.12
<i>Olsenella</i>	3384.43	3992.79	0.34	0.40
<i>Gemella</i>	2411.59	1257.08	0.24	0.13

b) PZI

Genus	CPM Mean	CPM STD	% Mean	% STD
<i>Streptococcus</i>	312564.78	25573.85	31.26	2.56
<i>Fusobacterium</i>	207524.82	45508.91	20.75	4.55
<i>Megasphaera</i>	99710.25	20991.16	9.97	2.10
<i>Neisseria</i>	67259.26	55640.46	6.73	5.56
<i>Veillonella</i>	59921.59	17969.10	5.99	1.80
<i>Campylobacter</i>	55033.42	31434.41	5.50	3.14
<i>Tannerella</i>	39875.61	18402.07	3.99	1.84
<i>Prevotella</i>	29447.34	11419.90	2.94	1.14
<i>Staphylococcus</i>	9089.19	3394.30	0.91	0.34
<i>Bacillus</i>	8179.89	1356.71	0.82	0.14
<i>Selenomonas</i>	7716.39	2385.99	0.77	0.24
<i>Actinomyces</i>	6706.52	4479.26	0.67	0.45
<i>Porphyromonas</i>	6666.39	8219.77	0.67	0.82
<i>Erysipelothrix</i>	6380.08	2176.81	0.64	0.22
<i>Dialister</i>	5474.05	1586.33	0.55	0.16
<i>Slackia</i>	3122.74	1258.16	0.31	0.13
<i>Rothia</i>	2966.57	2035.97	0.30	0.20
<i>Eikenella</i>	2823.39	540.41	0.28	0.05
<i>Tetragenococcus</i>	2639.59	762.81	0.26	0.08
<i>Bacteroides</i>	2561.54	2662.53	0.26	0.27

c) SMAMP

Genus	CPM Mean	CPM STD	% Mean	% STD
<i>Streptococcus</i>	237743.35	26999.99	23.77	2.70
<i>Fusobacterium</i>	177287.15	32570.35	17.73	3.26
<i>Campylobacter</i>	162427.64	66013.08	16.24	6.60
<i>Megasphaera</i>	102910.17	16333.80	10.29	1.63
<i>Tannerella</i>	75675.60	15826.68	7.57	1.58
<i>Neisseria</i>	56166.63	30690.84	5.62	3.07
<i>Veillonella</i>	46971.14	12631.36	4.70	1.26
<i>Prevotella</i>	19286.51	6632.46	1.93	0.66
<i>Selenomonas</i>	8480.92	1734.02	0.85	0.17
<i>Staphylococcus</i>	8239.61	2098.15	0.82	0.21
<i>Erysipelothrix</i>	7910.86	3407.19	0.79	0.34
<i>Bacillus</i>	7340.60	685.10	0.73	0.07
<i>Lachnoanaerobaculum</i>	5428.10	1737.52	0.54	0.17
<i>Dialister</i>	5308.95	641.20	0.53	0.06
<i>Atopobium</i>	4667.43	2045.56	0.47	0.20
<i>Capnocytophaga</i>	4261.01	5426.32	0.43	0.54
<i>Actinomyces</i>	4028.15	1522.07	0.40	0.15
<i>Slackia</i>	3803.65	1846.80	0.38	0.18
<i>Olsenella</i>	2905.63	1265.99	0.29	0.13
<i>Tetragenococcus</i>	2838.57	1126.21	0.28	0.11



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a) PSB				
Species	CPM Mean	CPM STD	% Mean	% STD
<i>Streptococcus salivarius</i>	173280.61	84957.71	17.33	8.50
<i>Fusobacterium nucleatum</i>	107372.78	61657.44	10.74	6.17
<i>Campylobacter ureolyticus</i>	91127.00	40955.75	9.11	4.10
<i>Megasphaera stantonii</i>	67148.17	31990.75	6.71	3.20
<i>Campylobacter curvus</i>	66476.42	30465.27	6.65	3.05
<i>Megasphaera elsdenii</i>	63067.95	33766.82	6.31	3.38
<i>Prevotella dentalis</i>	35491.59	13921.09	3.55	1.39
<i>Tannerella sp. oral taxon HOT-286</i>	29360.93	13421.85	2.94	1.34
<i>Campylobacter gracilis</i>	25427.38	15465.63	2.54	1.55
<i>Neisseria subflava</i>	24153.68	43798.98	2.42	4.38
<i>Veillonella dispar</i>	19560.27	10960.46	1.96	1.10
<i>Streptococcus thermophilus</i>	16094.37	4529.98	1.61	0.45
<i>Fusobacterium pseudoperiodonticum</i>	15037.92	6136.79	1.50	0.61
<i>Neisseria mucosa</i>	12018.73	15115.77	1.20	1.51
<i>Veillonella parvula</i>	10923.53	2524.97	1.09	0.25
<i>Streptococcus sp. LPB0220</i>	10375.91	9551.32	1.04	0.96
<i>Veillonella rodentium</i>	9242.57	2483.41	0.92	0.25
<i>Staphylococcus schleiferi</i>	6659.69	3259.97	0.67	0.33
<i>Prevotella denticola</i>	6543.12	2144.30	0.65	0.21
<i>Campylobacter concisus</i>	6286.42	1970.64	0.63	0.20

b) PZI				
Species	CPM Mean	CPM STD	% Mean	% STD
<i>Fusobacterium nucleatum</i>	215937.68	51565.22	21.59	5.16
<i>Streptococcus salivarius</i>	205957.66	13785.24	20.60	1.38
<i>Megasphaera stantonii</i>	56966.06	14114.85	5.70	1.41
<i>Megasphaera elsdenii</i>	56478.69	12560.91	5.65	1.26
<i>Tannerella sp. oral taxon HOT-286</i>	38194.94	8229.52	3.82	0.82
<i>Neisseria mucosa</i>	29639.62	52183.58	2.96	5.22
<i>Campylobacter ureolyticus</i>	24100.65	14212.72	2.41	1.42
<i>Prevotella dentalis</i>	21313.02	7829.72	2.13	0.78
<i>Streptococcus thermophilus</i>	17681.01	3802.28	1.77	0.38
<i>Neisseria subflava</i>	16617.37	11621.04	1.66	1.16
<i>Campylobacter curvus</i>	16577.18	9672.69	1.66	0.97
<i>Veillonella dispar</i>	16183.53	3330.48	1.62	0.33
<i>Veillonella parvula</i>	13397.55	5890.40	1.34	0.59
<i>Veillonella rodentium</i>	11080.72	4463.79	1.11	0.45
<i>Fusobacterium pseudoperiodonticum</i>	10494.90	3323.46	1.05	0.33
<i>Staphylococcus schleiferi</i>	9423.84	3660.56	0.94	0.37
<i>Tannerella forsythia</i>	9143.42	17151.17	0.91	1.72
<i>Porphyromonas gingivalis</i>	7551.02	9371.10	0.76	0.94
<i>Streptococcus sp. LPB0220</i>	7251.15	3565.00	0.73	0.36
<i>Streptococcus gordonii</i>	5660.04	2074.54	0.57	0.21



c) SMAMP

Species	CPM Mean	CPM STD	% Mean	% STD
<i>Streptococcus salivarius</i>	153220.67	14378.33	15.32	1.44
<i>Fusobacterium nucleatum</i>	146497.13	41387.27	14.65	4.14
<i>Tannerella sp. oral taxon HOT-286</i>	87934.60	18984.27	8.79	1.90
<i>Campylobacter ureolyticus</i>	72213.67	27307.05	7.22	2.73
<i>Megasphaera stantonii</i>	59699.90	10939.55	5.97	1.09
<i>Megasphaera elsdenii</i>	57224.07	8603.13	5.72	0.86
<i>Campylobacter curvus</i>	48111.84	18519.94	4.81	1.85
<i>Neisseria mucosa</i>	30299.36	16366.28	3.03	1.64
<i>Fusobacterium pseudoperiodonticum</i>	29892.26	6090.08	2.99	0.61
<i>Campylobacter gracilis</i>	24643.84	15594.11	2.46	1.56
<i>Streptococcus parasanguinis</i>	18325.99	3738.29	1.83	0.37
<i>Veillonella dispar</i>	14443.35	5594.66	1.44	0.56
<i>Prevotella dentalis</i>	12338.09	4972.50	1.23	0.50
<i>Streptococcus thermophilus</i>	12155.04	1759.81	1.22	0.18
<i>Neisseria subflava</i>	10048.90	9011.30	1.00	0.90
<i>Veillonella parvula</i>	8764.01	1937.77	0.88	0.19
<i>Staphylococcus schleiferi</i>	8143.21	2176.82	0.81	0.22
<i>Veillonella rodentium</i>	7185.88	1666.84	0.72	0.17
<i>Erysipelothrix larvae</i>	6683.64	2938.01	0.67	0.29
<i>Lachnoanaerobaculum umeaense</i>	6485.54	2023.36	0.65	0.20

Table S6: About 950 000 to 1 500 000 sequencing reads passing the ONT Q7 quality score were obtained for each sample, and of these >95% in each sample mapped to bacterial sequences as per the centrifuge results

Name	Number of raw reads	Classified reads	Chordate reads	Artificial reads	Unclassified reads	Microbial reads	Bacterial reads	Viral reads	Fungal reads	Protozoan reads
CHX	1,472,476	96.7%	0.11%	0%	3.26%	96.6%	96.6%	0.000407%	0%	0%
NegCtrl_1	1,294,857	97.2%	0.0306%	0%	2.78%	97.2%	97.1%	0.000309%	0%	0%
NegCtrl_2	1,286,644	97.9%	0.0113%	0%	2.11%	97.9%	97.9%	0.00109%	0%	0%
NegCtrl_3	1,241,613	97.7%	0.0166%	0%	2.33%	97.7%	97.6%	0.000161%	0%	0%
NegCtrl_4	1,174,811	98.4%	0.0109%	0%	1.64%	98.3%	98.3%	0%	0%	0%
PSB_1	1,185,297	97.7%	0.0136%	0%	2.28%	97.7%	97.7%	0.000253%	0%	0%
PSB_2	1,271,530	98.4%	0.011%	0%	1.65%	98.3%	98.3%	0.000315%	0%	0%
PSB_3	1,342,889	97.6%	0.0157%	0%	2.37%	97.6%	97.6%	0.00119%	0%	0%
PSB_4	1,001,763	98.2%	0.0197%	0%	1.77%	98.2%	98.2%	0.0002%	0%	0%
PZI_1	1,033,474	97.7%	0.0113%	0%	2.34%	97.6%	97.6%	0.000968%	0%	0%
PZI_2	1,046,485	97.9%	0.0118%	0%	2.07%	97.9%	97.9%	0.000191%	0%	0%
PZI_3	1,122,866	98.6%	0.00989%	0%	1.39%	98.6%	98.6%	0.000267%	0%	0%
PZI_5	1,000,959	98.4%	0.0126%	0%	1.63%	98.4%	98.4%	0.000699%	0%	0%
SMAMP_1	1,007,157	98.6%	0.0109%	0%	1.38%	98.6%	98.6%	0%	0%	0%
SMAMP_2	1,162,149	98.4%	0.00955%	0%	1.64%	98.3%	98.3%	0.000602%	0%	0%
SMAMP_3	1,352,278	98%	0.011%	0%	2.01%	98%	98%	0.000148%	0%	0%
SMAMP_4	950,395	98.3%	0.00705%	0%	1.66%	98.3%	98.3%	0.000316%	0%	0%
SMAMP_5	1,302,290	98.7%	0.00829%	0%	1.34%	98.7%	98.6%	0.000384%	0%	0%

Figure S1: Z-section galleries of representative confocal laser scanning microscopic (CLSM) images depicting the ex vivo biofilm formation (3 days) after live/dead staining. The panels illustrate the live (green) and dead (red) microbial populations of biofilms grown on the PSB coating. The multiple Z-sections in the panels were generated by vertical sectioning at 2.0- μm intervals through the sample above the PSB surface. Bars, 20 μm ."

PSB

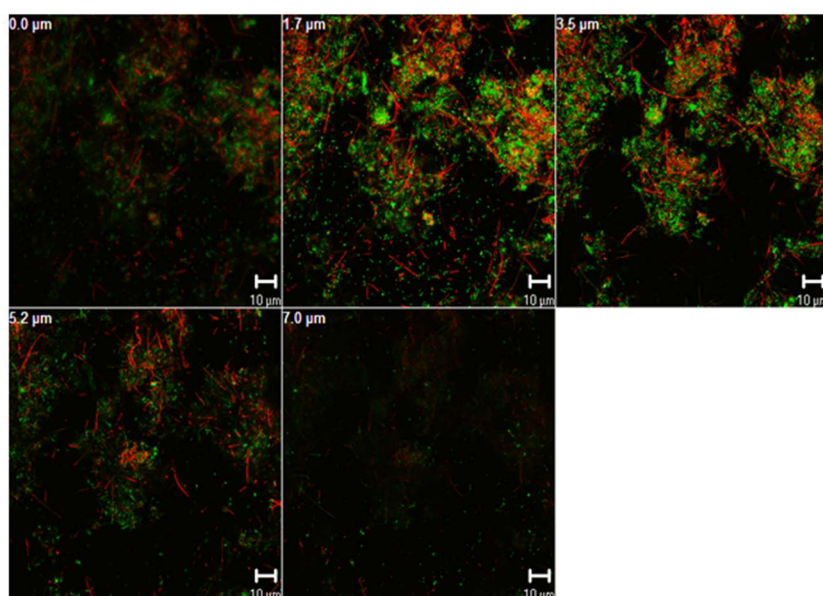




Figure S2: Alpha (A) and beta (B) diversity measures were calculated using the R package *vegan* (Community Ecology Package, R package version 2.5-7., <https://CRAN.R-project.org/package=vegan>, published by J. Oksanen, F. Guillaume Blanchet, Michael Friendly, Roeland Kindt, Pierre Legendre, Dan McGlinn, Peter R. Minchin, R. B. O'Hara, Gavin L. Simpson, Peter Solymos, M. Henry H. Stevens, Eduard Szoecs and Helene Wagner 2020) and visualized using the *ggplot* and *pheatmap* packages (Raivo Kolde 2019: R package version 1.0.12. <https://CRAN.R-project.org/package=pheatmap>)

