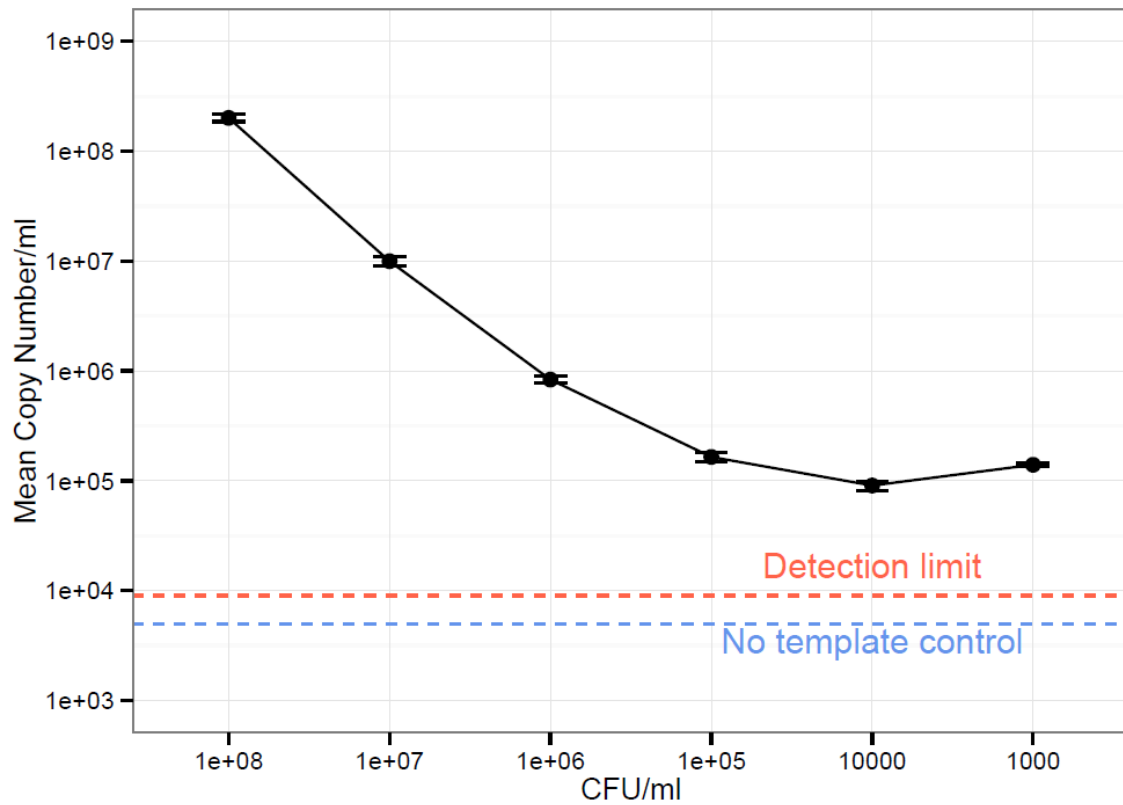


Supplementary Figure S1:

16S rRNA gene profile of *S. bongori* pure culture serial dilutions amplified with 20 PCR cycles.

S. bongori is shown in black; other taxa are grouped by Class. Stars mark samples that had fewer than 50 sequence reads: the most diluted samples gave no visible bands on electrophoresis gels after 20 PCR cycles, and these samples therefore tended to be under-represented in the sequence libraries. The centres that performed the DNA extraction and PCR steps are shown at the bottom of the figure (ICL = Imperial College London, UB = University of Birmingham, WTSI = Wellcome Trust Sanger Institute).



Supplementary Figure S2:

Copy number of total 16S rRNA genes present in a dilution series of *S. bongori* culture.

Total bacterial DNA present in serial ten-fold dilutions of a pure *S. bongori* culture was quantified using qPCR. While the copy number initially reduces in tandem with increased dilution, plateauing after four dilutions indicates consistent background levels of contaminating DNA. Error bars indicate standard deviation of triplicate reactions. The broken red line indicates the detection limit of 45 copies of 16S rRNA genes. The no template internal control for the qPCR reactions (shown in blue) was below the cycle threshold selected for interpreting the fluorescence values (i.e. less than 0), indicating the contamination did not come from the qPCR reagents themselves.

Supplementary Table S1:

OTUs with significant correlation in PCoA plot Figures 3b and 3c.

All taxa with a p-value of <0.05 are shown, with $P < 0.01$ highlighted in bold. Although the data is from human nasopharyngeal swabs, many of the taxa are environmental bacteria associated with the DNA extraction kit.

OTU identity	Classification	Environmental/human associated	X axis		Y axis	
			Correlation coefficient	p-value	Correlation coefficient	p-value
Otu003	<i>Herbaspirillum</i>	Environmental	-0.753	0.000		
Otu009	<i>Pseudomonas</i>	Both	-0.591	0.000	0.250	0.001
Otu012	<i>Ochrobactrum</i>	Environmental	-0.568	0.000		
Otu014	<i>Rhodococcus</i>	Environmental	-0.486	0.000	0.198	0.007
Otu030	<i>Pedobacter</i>	Environmental	-0.438	0.000	0.264	0.000
Otu040	<i>Aminobacter</i>	Environmental	-0.435	0.000		
Otu025	<i>Sphingomonas</i>	Environmental	-0.403	0.000	-0.159	0.030
Otu031	<i>Brevundimonas</i>	Environmental	-0.374	0.000	0.249	0.001
Otu015	<i>Stenotrophomonas</i>	Both	-0.366	0.000	-0.163	0.027
Otu013	<i>Achromobacter</i>	Environmental	-0.357	0.000		
Otu026	<i>Phyllobacterium</i>	Environmental	-0.277	0.000		
Otu116	<i>Afipia</i>	Environmental	-0.208	0.005		
Otu092	<i>Moraxella</i>	Human	-0.152	0.040		
Otu004	<i>Haemophilus</i>	Human	0.151	0.041		
Otu081	<i>Pseudonocardia</i>	Environmental	0.151	0.041	0.202	0.006
Otu067	<i>Bradyrhizobium</i>	Environmental	0.154	0.037		
Otu007	<i>Corynebacterium</i>	Human	0.157	0.033		
Otu036	<i>Burkholderia</i>	Both	0.159	0.031		
Otu060	<i>Curvibacter</i>	Environmental	0.164	0.026		
Otu016	<i>Ralstonia</i>	Environmental	0.195	0.008	0.148	0.044
Otu017	<i>Acidaminococcus</i>	Environmental	0.210	0.004		
Otu006	<i>Moraxella</i>	Human	0.232	0.001		
Otu008	Unclassified <i>Flavobacteriaceae</i>	Human	0.242	0.001		
Otu010	<i>Helcococcus</i>	Human	0.380	0.000		
Otu001	<i>Moraxella</i>	Human	0.404	0.000		
Otu197	<i>Bordetella</i>	Both			0.147	0.046
Otu090	<i>Aeromonas</i>	Environmental			0.148	0.045
Otu161	<i>Kineosphaera</i>	Environmental			0.150	0.042
Otu250	<i>Perlucidibaca</i>	Environmental			0.153	0.038
Otu117	<i>Rheinheimera</i>	Environmental			0.153	0.038
Otu058	<i>Dyella</i>	Environmental			0.153	0.038
Otu020	<i>Actinobacillus</i>	Human			0.154	0.036
Otu251	Unclassified <i>Chitinophagaceae</i>	Environmental			0.155	0.036
Otu120	<i>Veillonella</i>	Human			0.156	0.034
Otu113	<i>Herbaspirillum</i>	Environmental			0.157	0.033
Otu138	<i>Perlucidibaca</i>	Environmental			0.157	0.033
Otu146	<i>Granulicatella</i>	Human			0.161	0.029
Otu131	<i>Actinomyces</i>	Both			0.162	0.028
Otu159	<i>Pseudoxanthomonas</i>	Environmental			0.163	0.027
Otu094	<i>Pseudomonas</i>	Both			0.164	0.026
Otu075	<i>Wautersiella</i>	Environmental			0.175	0.017
Otu115	<i>Micrococcus</i>	Both			0.176	0.017
Otu072	<i>Massilia</i>	Both			0.177	0.016

Otu022	<i>Acinetobacter</i>	Both	0.178	0.016
Otu119	<i>Stigmatella</i>	Environmental	0.178	0.015
Otu078	<i>Paracoccus</i>	Environmental	0.180	0.015
Otu091	<i>Aeromicrobium</i>	Environmental	0.181	0.014
Otu166	<i>Arthrobacter</i>	Environmental	0.184	0.012
Otu124	<i>Moraxella</i>	Human	0.186	0.012
Otu055	<i>Pseudomonas</i>	Both	0.189	0.010
Otu034	<i>Janibacter</i>	Environmental	0.189	0.010
Otu043	<i>Kocuria</i>	Both	0.196	0.008
Otu029	<i>Brachybacterium</i>	Human	0.202	0.006
Otu155	<i>Tistrella</i>	Environmental	0.210	0.004
Otu054	<i>Corynebacterium</i>	Human	0.213	0.004
Otu059	<i>Luteimonas</i>	Environmental	0.217	0.003
Otu095	<i>Nocardioides</i>	Environmental	0.227	0.002
Otu048	<i>Veillonella</i>	Human	0.232	0.001
Otu127	<i>Nocardioides</i>	Environmental	0.242	0.001
Otu046	<i>Paracoccus</i>	Environmental	0.244	0.001
Otu024	<i>Acinetobacter</i>	Both	0.249	0.001