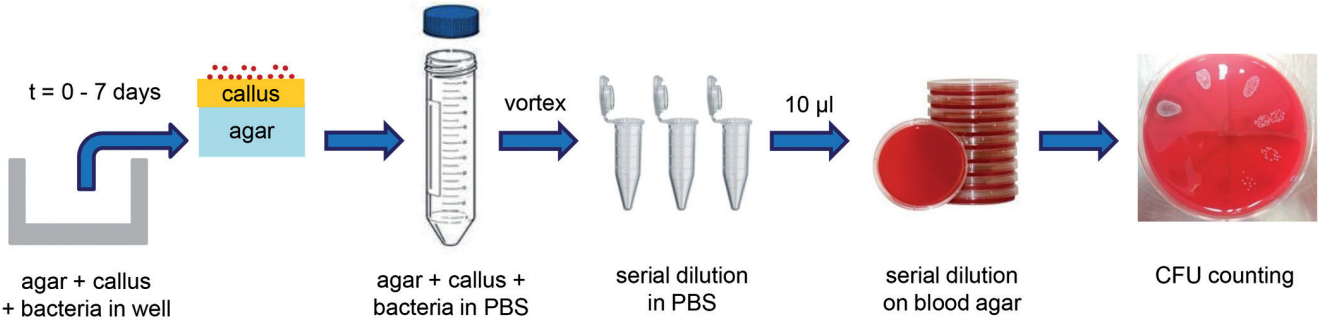

Fig. S1. Bacterial collection and analysis by colony-forming units (CFU) counting. Bacteria are collected by removing the agar + callus + bacteria from the 24-well plate, and transferred to a 50 ml tube containing phosphate-buffered saline (PBS). The bacteria are suspended in the PBS by vortexing the tube, followed by CFU counting. The bacteria are diluted in serial, and grown on blood agar plates overnight at 37°C. On the next day, the number of CFUs for each dilution can be counted.

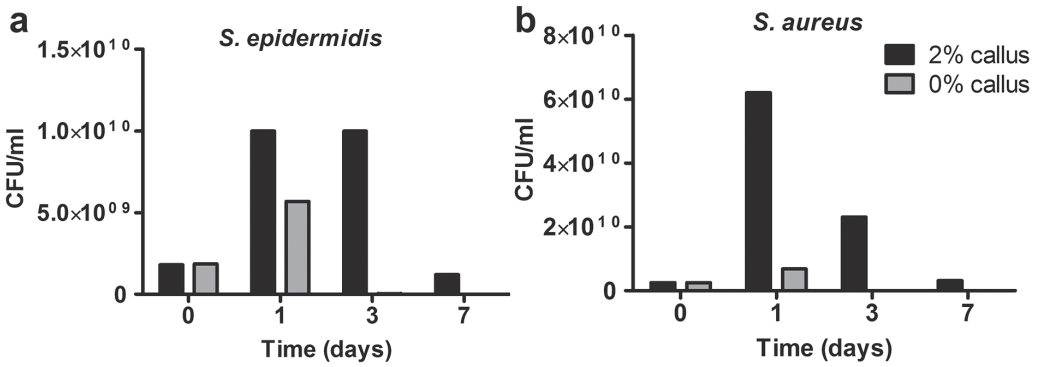

Fig. S2. Effect of the presence of callus on bacterial survival. (a) *S. epidermidis*, and (b) *S. aureus* survival on the model after 1, 3 and 7 days of culture. Model contains 2% callus (*black bars*) or 0% callus (*grey bars*). Both bacterial strains survived for 1 day only on the model without callus, whereas both strains were able to survive for 7 days when 2% callus was applied to the model. The bacterial survival was determined by colony-forming unit (CFU) counting. This figure represents 1 of 2 separate experiments.

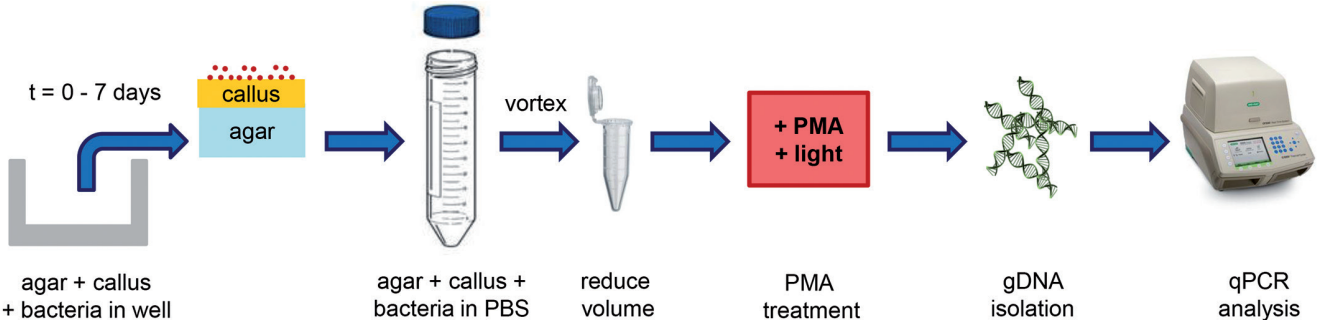

Fig. S3. Bacterial collection and analysis by quantitative PCR (qPCR) analysis. Bacteria were collected by removing the agar + callus + bacteria from the 24-well plate, and transferred to a 50 ml tube containing phosphate-buffered saline (PBS). The bacteria were suspended in the PBS by vortexing the tube. Prior to qPCR analysis, the bacteria were resuspended in a smaller volume, followed by the exposure to propidium monoazide (PMA) and light. Then the gDNA of the viable bacteria was isolated and analysed by qPCR using 16S- or strain-specific primers.

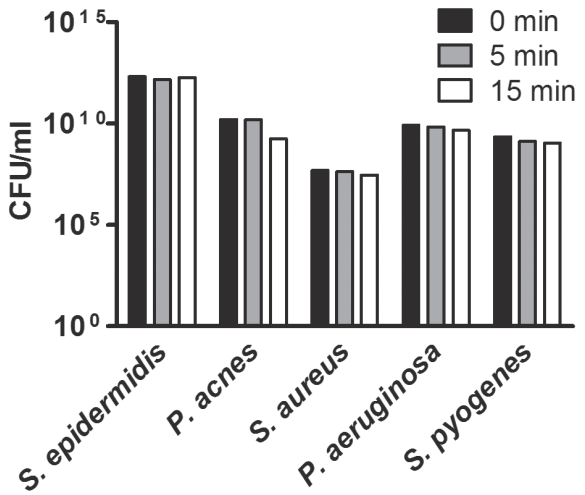

Fig. S4. Effect of light exposure on bacterial survival. *S. epidermidis*, *P. acnes*, *S. aureus*, *P. aeruginosa* and *S. pyogenes* were exposed to intense light for 0 (*black bars*), 5 (*grey bars*) or 15 (*white bars*) min. Bacterial survival was determined by colony-forming unit (CFU) counting. This figure represents 1 of 2 separate experiments.

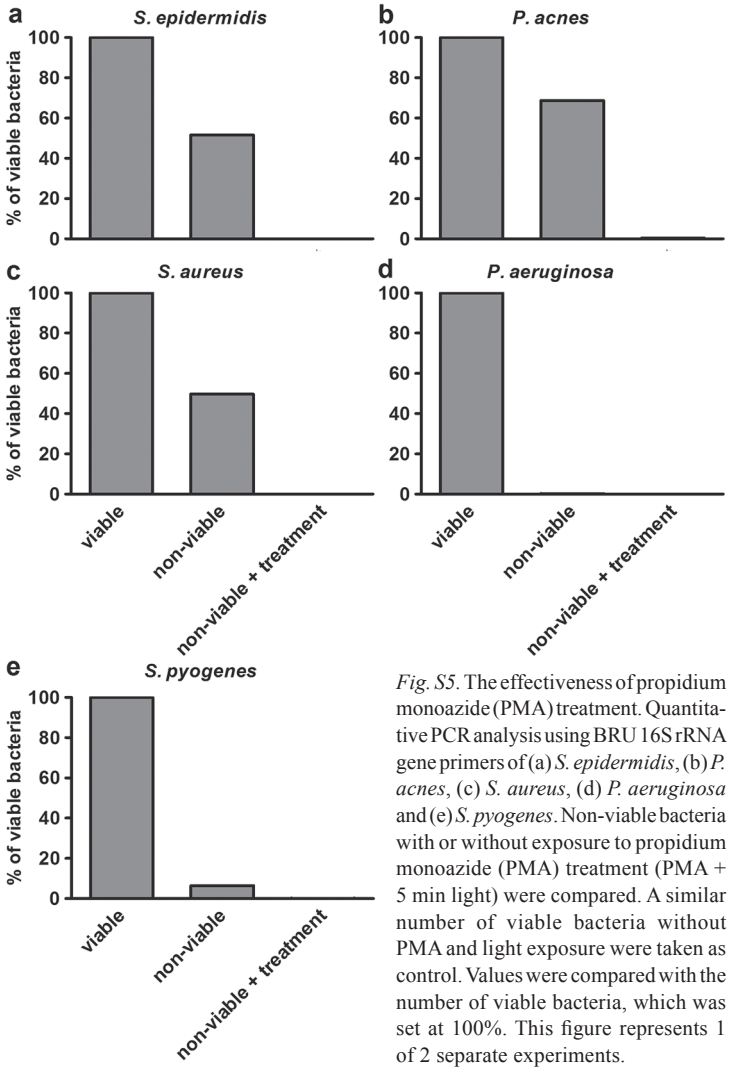

Fig. S5. The effectiveness of propidium monoazide (PMA) treatment. Quantitative PCR analysis using BRU 16S rRNA gene primers of (a) *S. epidermidis*, (b) *P. acnes*, (c) *S. aureus*, (d) *P. aeruginosa* and (e) *S. pyogenes*. Non-viable bacteria with or without exposure to propidium monoazide (PMA) treatment (PMA + 5 min light) were compared. A similar number of viable bacteria without PMA and light exposure were taken as control. Values were compared with the number of viable bacteria, which was set at 100%. This figure represents 1 of 2 separate experiments.

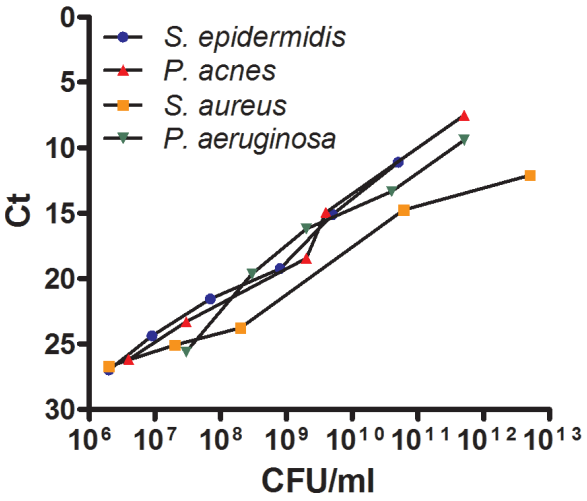

Fig. S6. Correlation between Ct value and colony-forming units (CFU)/ml. Different concentrations of *S. epidermidis*, *P. acnes*, *S. aureus* and *P. aeruginosa* were brought on the model and collected for CFU counting and propidium monoazide (PMA)-quantitative PCR (qPCR) analysis. The Ct values of the qPCR and the CFU/ml are correlated in this figure.

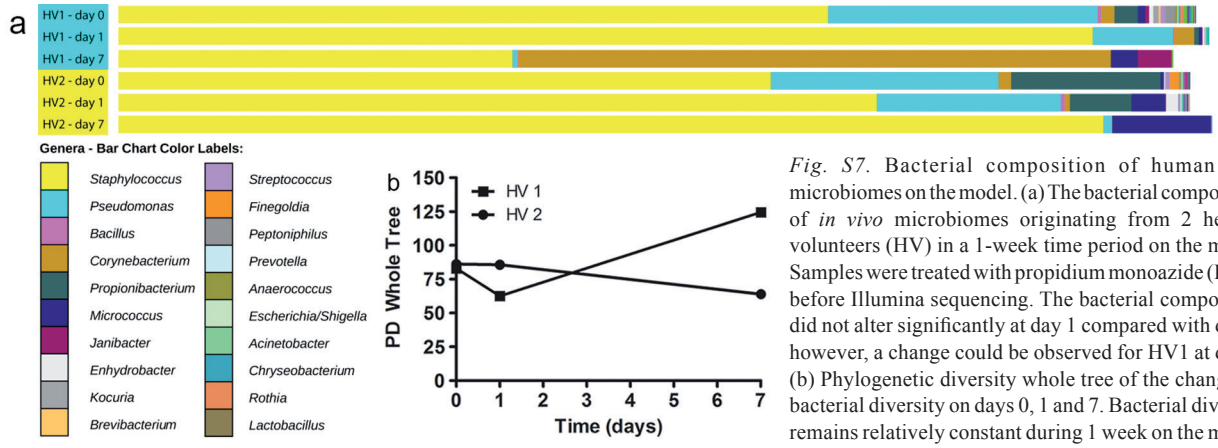

Fig. S7. Bacterial composition of human skin microbiomes on the model. (a) The bacterial composition of *in vivo* microbiomes originating from 2 healthy volunteers (HV) in a 1-week time period on the model. Samples were treated with propidium monoazide (PMA) before Illumina sequencing. The bacterial composition did not alter significantly at day 1 compared with day 0; however, a change could be observed for HV1 at day 7. (b) Phylogenetic diversity whole tree of the changes in bacterial diversity on days 0, 1 and 7. Bacterial diversity remains relatively constant during 1 week on the model.

Appendix S1.

SUPPLEMENTARY METHODS

Quantitative PCR

Microbial gDNA was used as template for qPCR amplification with SYBR Green using the Bio-Rad CFX Connect apparatus (Bio-Rad, Hercules, CA, USA). One reaction contained 5 µl gDNA, 12.5 µl SYBR Green, 1.5 µl of each forward and reverse primer (10 µM) and 4.5 µl sterile water. Strain-specific quantitative PCR primers were designed manually on unique (i.e. strain-specific) protein-coding DNA sequences that were identified using a customized workflow of in-house built programming scripts (Table SI[1]). Briefly, this workflow determines unique genes by OrthoMCL (S1) on publicly-available reference genomes of the 5 bacterial strains used in this study. The genome sequences are segmented into DNA fragments of 40 nt with a sliding window of 10 nt. Subsequently, these 40 nt sequences were aligned to the 5 reference genomes by BLAST. Only sequences that aligned perfectly with the genome sequence they originated from, and did not align with the other 4 genomes, were retained. Primers were developed manually on the strain-specific 40-bp fragments. Cross-reactivity of candidate primers was: (*i*) validated by BLAST, and (*ii*) by an *in silico* PCR using Primer Prospector (S2) on the BLAST database of the 5 genomes. BRU 16S qPCR primers were adopted and applied as described in Nadkarni et al. (S3). qPCR primers (from Biolegio, Nijmegen, The Netherlands) were used to obtain Ct values. Colony-forming units (CFU)/ml were calculated from Ct values using calibration curves (Fig. S6[1]).

16S amplification prior to sequencing

Microbiota samples derived from skin of the lower back contained small amounts of microbial gDNA. The following universal primers were applied for amplification: forward primer (338F), 5'-ACTCCTACGGGAGGCAGCAG-3'; reverse primer (1061R), 5'-CRRCACGAGCTGACGAC -3'. The PCR mixture contained 5 µl microbial gDNA, 1 µl KOD DNA polymerase (1 U/µl; Novagen, Madison, WI, USA), 5 µl KOD-buffer (10×), 3 µl KOD $MgSO_4$ (25 mM), 5 µl KOD dNTP mixture (2 mM each), 1 µl of each forward and reverse primer (10 µM) and 29 µl sterile water. PCR conditions were: 2 min at 95°C, followed by 30 cycles of 20 s at 95°C, 10 s at 55°C, 15 s 70°C and ending at 70°C for 10 min. The amplicons were purified using the MSB Spin PCRapace kit (Invitek, Westburg, The Netherlands). The concentration of the purified DNA samples was determined with NanoDrop 2000 spectrophotometer (Thermo Scientific, Wilmington, DE, USA).

16S metagenomic library preparation and Illumina sequencing

Illumina 16S metagenomic amplicon libraries were generated and sequenced at BaseClear BV (Leiden, The Netherlands). A pre-amplified full-length 16S PCR amplicon, as described above, was used as input for a 2-step PCR-based library preparation protocol targeting the V3-V4 regions of the 16S rRNA gene. The resultant libraries were checked on a Bioanalyzer (Agilent Technologies, Waldbronn, Germany) and quantified. The libraries were multiplexed, clustered and sequenced on an Illumina MiSeq with paired-end 250 cycles protocol and indexing. The sequencing run was analysed with the Illumina CASAVA pipeline (v1.8.3) with demultiplexing based on sample-specific barcodes. The raw sequencing data produced was processed removing the sequence reads of too low quality (only "passing filter" reads were selected) and discarding reads containing adaptor sequences or failing PhiX Control with an in-house filtering protocol. A quality assessment on the remaining reads was performed using the FASTQC quality control tool version 0.10.0.

REFERENCES

S1. Li L, Stoeckert CJ Jr, Roos DS. OrthoMCL: identification of ortholog groups for eukaryotic genomes. Genome Res 2003; 13: 2178–2189.
S2. Walters WA, Caporaso JG, Lauber CL, Berg-Lyons D, Fierer N, Knight R. PrimerProspector: de novo design and taxonomic analysis of barcoded polymerase chain reaction primers. Bioinformatics 2011; 27: 1159–1161.
S3. Nadkarni MA, Martin FE, Jacques NA, Hunter N. Determination of bacterial load by real-time PCR using a broad-range (universal) probe and primers set. Microbiology 2002; 148: 257–266.

Table SI. *Primers for quantitative PCR (qPCR)*

Detection of	Forward primer (5' → 3')	Reverse primer (5' → 3')
S. epidermidis	TCTTCAAGAAGCTCACTCAGAG	ATTCCCACGCTAACGATTTACG
P. acnes	CGAGGAGCAATTTCTGGGAT	ATGGATGACTTCGACGATGA
S. aureus	AGGACAATCATGGCAAGCGTAC	AACGGACAACATCTAAACTGGC
P. aeruginosa	ACCGAATACCTGATGGCTCA	CTGGCAGCAATACCTGTTTG
S. pyogenes	ACAGTAAGGTTAGACACCCT	CTACAACAGACGGAAACTGA
BRU 16S	TCCTACGGGAGGCAGCAGT	GGACTACCAGGGTATCTAATCCTGTT