SUPPLEMENTARY MATERIAL

Identification of organisms

The microorganisms on the agar plates were identified using 16S rRNA gene sequencing. Briefly, distinct colony types were aseptically collected and resuspended in 100µL of sterile Milli-Q water (Millipore Corporation, Billerica, USA) followed by heating for 10 minutes at 100°C. Only Milli-Q water was used as negative control. The cell lysate and negative control were then cooled on ice and spun at 10,000 rpm for 1 minute with the supernatant being used as a template for 16S rRNA gene amplification using the bacterial universal primers F27 (5'-AGA GTT TGA TCM TGG CTC AG-3') and R1492 (5'-TAC GGY TAC CTT GTT ACG ACT T-3').[16] Thermal cycling was performed using Multigene Gradient thermal cycler (Labnet International Incorporated, Edison, USA). Thermal cycling started with 5 minutes at 94ºC for the initial denaturation step, 30 cycles of 94ºC for 30 seconds, 56ºC for 30 seconds and 72ºC for 90 seconds, ending with a final extension step of 10 minutes at 72ºC.

Amplicons were visually inspected for size and success of amplification with a Gel documentation system (GelDoc, BioRad,) after electrophoresis in a 1% agarose gel stained with 30 ppm of GelRed™ 10000x solution in DMSO (Biotium, Hayward, USA). PCR products were cleaned using exonuclease I (ThermoFisher, Austin, USA) and Shrimp Alkaline Phosphatase (Sigma, St. Louis, USA)., 5µL of PCR product were added to 2µL of Exo-Sap-it (Affymetrix, Santa Clara, USA) and incubated at 37°C for 20 minutes followed by incubation at 80°C for 15 minutes. Subsequently, 1µL of cleaned PCR product was used for sequencing reaction with either 1µL of forward (27F) or reverse (1492R) primer in addition to 1µL BigDye Terminator v3.1

(Applied Biosystems, Austin, USA), 4µL of sequencing buffer 5x and 13µL of molecular biology grade water (5prime, Hilden, Germany). Following this products were subjected to sequencing in an Applied Biosystems 3730 DNA Analyzer, at the Ramaciotti Centre for Genomics (University of New South Wales, Sydney, Australia). Negative controls worked as expected. Sequences were manually trimmed using the Sequence Scanner v1.0 software (Applied Biosystems, sequence scanner software v.2) and related sequences were identified using the Basic Local Alignment Search Tool (BLAST) of the National Centre for Biotechnology Information (NCBI) database.