Table S5
PCR and RT-PCR programs for the amplification of 16S rRNA and 16S rRNA gene fragments of *Bacteria* and bacterial subgroups used for DGGE fingerprint analysis. All RT-PCR programs started with a reverse transcriptase step of 30 min at 50°C followed by a step for reverse transcriptase inactivation and *Taq*-DNA polymerase activation at 95°C for 15 min. All RT-PCR programs finished with a final elongation step at 72°C. This step was elongated to 30 min to prevent the formation of DNA double bands during DGGE analysis [1].

Target group	***Bacteria***	***Betaproteobacteria***	***Actinobacteria***	***Sphingomonadaceae***
Primer-system	GC-339F 907R	GC-Beta359F Beta680R	GC-HGC236F HGC664R	Sphingo108F ADF681R Nested-PCR: GC-339F/907R
Fragment length (nt)	588 (+40)	336 (+40)	428 (+40)	871 Nested-PCR: 588 (+40)
PCR cycles	94°C 30 sec 55°C 30 sec 72°C 40 sec 28 cycles	94°C 30 sec 52°C 30 sec 72°C 35 sec 28-30 cycles	94°C 30 sec 52°C 30 sec 72°C 35 sec 28 cycles	94°C 30 sec 55°C 40 sec 72°C 54 sec 28 cycles

Reference

1. Janse I, Bok J, Zwart G (2004) A simple remedy against artifactual double bands in denaturing gradient gel electrophoresis. J Microbiol Met 57: 279-281.