

CORRECTION

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# Correction to: Evaluation of the impact of six different DNA extraction methods for the representation of the microbial community associated with human chronic wound infections using a gel-based DNA profiling method

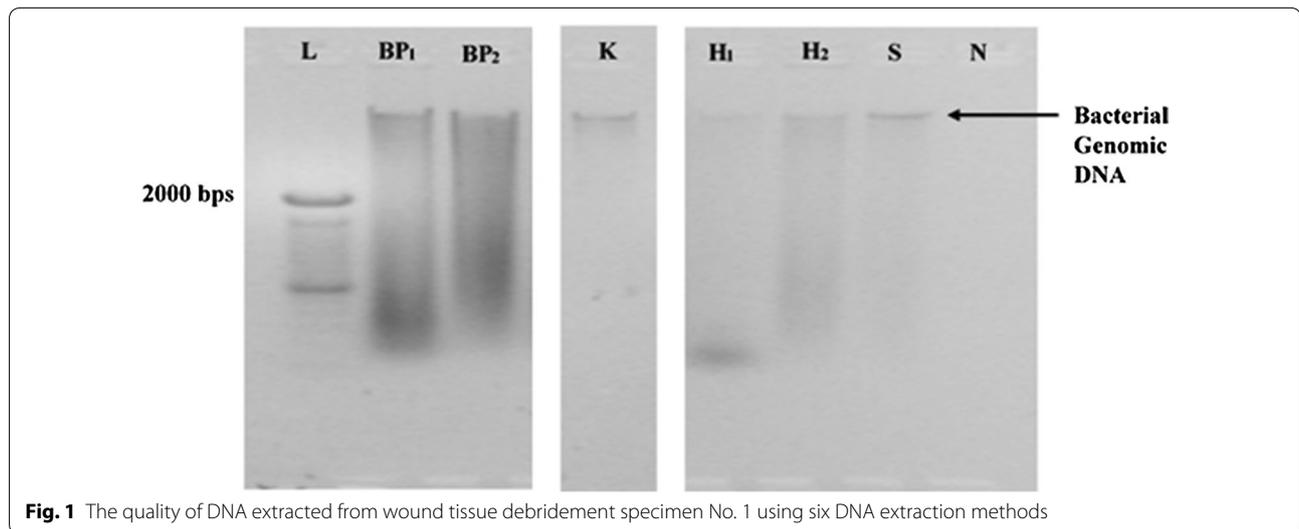
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**Correction to: AMB Expr (2017) 7:179**

<https://doi.org/10.1186/s13568-017-0477-z>

Following publication of the original article (Dilhari et al. 2017), the authors identified an error in Figs. 1 and 3.

The corrected figures are given below.



**Fig. 1** The quality of DNA extracted from wound tissue debridement specimen No. 1 using six DNA extraction methods

The original article can be found online at <https://doi.org/10.1186/s13568-017-0477-z>.

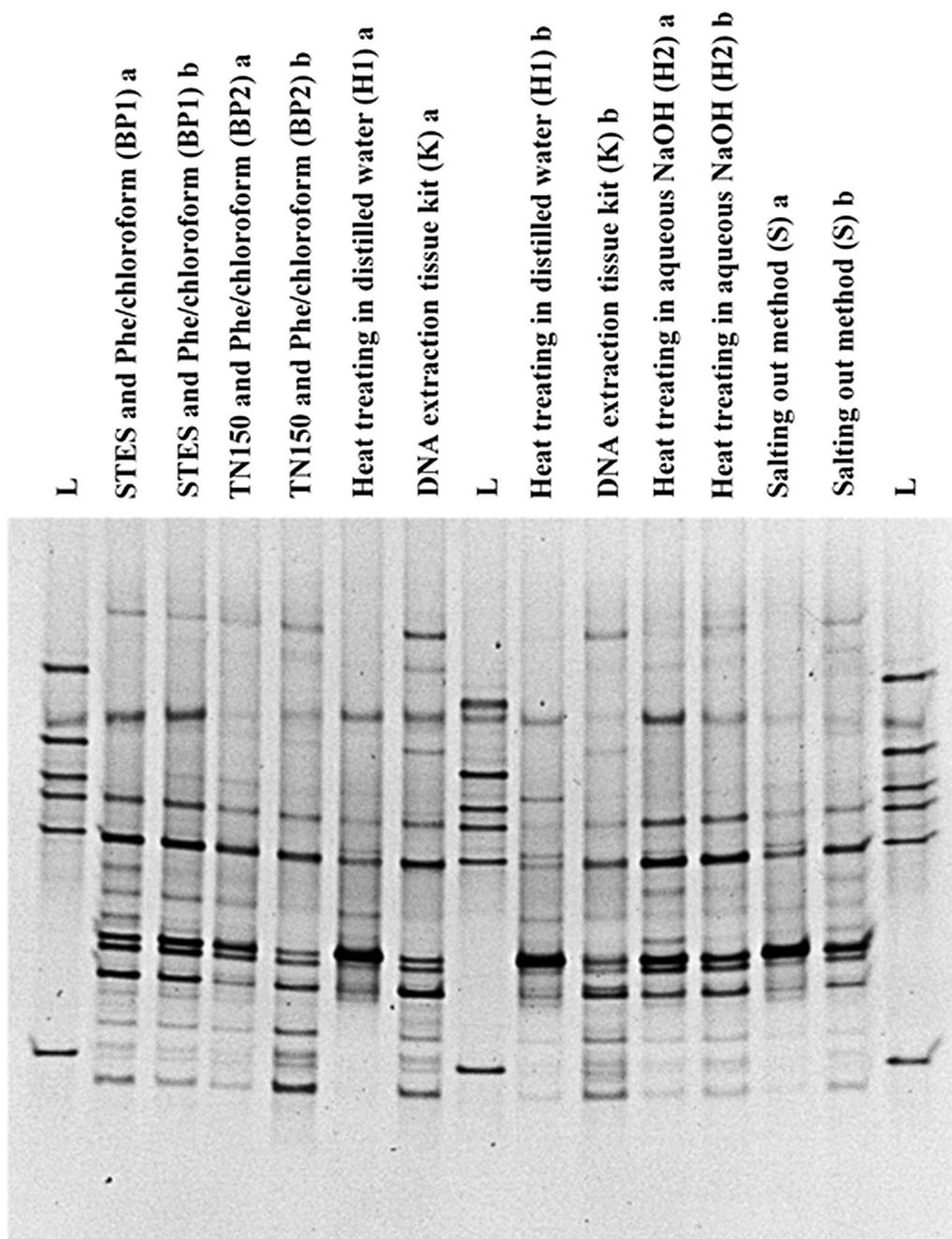
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**Fig. 3** A comparison of DGGE profiles of PCR amplified bacterial 16S rRNA gene for the specimen No: 1. DNA was extracted using six different DNA extraction methods using 25 mg of wound tissue debridement specimen no. 1. Bacterial fingerprinting profile is based on 30–55% denaturing gradient. “L” lanes represent the in house bacterial reference panel which includes *S. aureus*, *Acinetobacter* spp, Group B *Streptococcus* spp., *E. faecalis*, Group A *Streptococcus* spp. and *E. coli* from top to bottom respectively. Other lanes show bacterial fingerprinting profile of each extraction method in duplicate (a, b) for the specimen No. 1, collected from a subject with a chronic wound

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