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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.

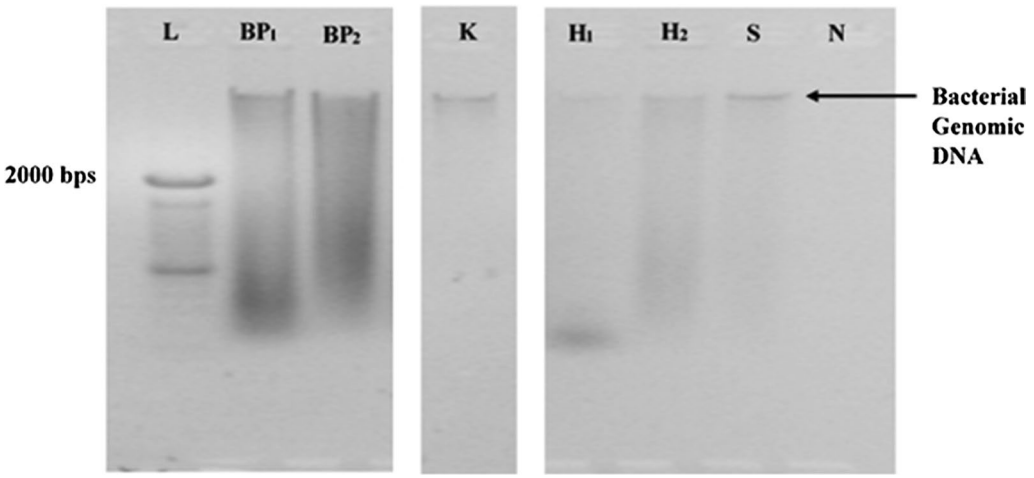

Fig. 1 The quality of DNA extracted from wound tissue debridement specimen No. 1 using six DNA extraction methods

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

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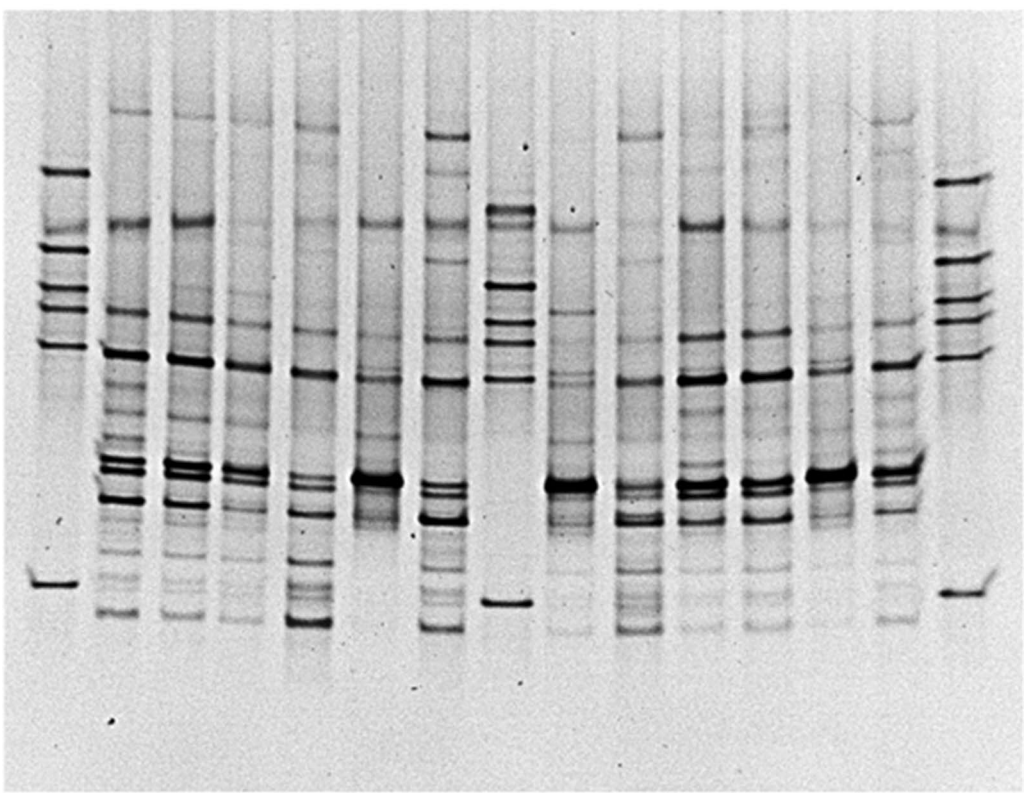

Fig. 3 A comparison of DGGE profiles of PCR amplified bacterial 16S rRNA gene for the specimen No: 1. DNA was extracted using six different DNA extraction methods using 25 mg of wound tissue debridement specimen no. 1. Bacterial fingerprinting profile is based on 30–55% denaturing gradient. "L" lanes 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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