**Genomic analysis of *Bacillus cereus* NWUAB01 and its heavy metal removal from polluted soil**

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**Table S1. The growth rate of strain NWUAB01 on each of the metal tested and the control**

| | Generation time | Number of generations | Specific growth rate |
|---|---|---|---|
| Cd | 88.87 | 0.27 | 0.01 |
| Cr | 93.67 | 0.26 | 0.01 |
| Pb | 61.34 | 0.39 | 0.01 |
| Control | 88.87 | 0.27 | 0.01 |

**Table S2. Heavy metal removal by strain NWUAB01 and its biosurfactant**

| **Metal** | **Biosurfactant** | **Strain NWUAB01** |
|---|---|---|
| | Percentage removal (%) | Percentage removal (%) |
| Cd | 54.30 | 60.90 |
| Cr | 43.52 | 30.85 |
| Pb | 69.78 | 83.83 |
| Multi-metal | | |
| Cd | 40.13 | 45.80 |
| Cr | 30.45 | 33.72 |
| Pb | 65.23 | 72.39 |

**Table S3. The sampling sites and their corresponding metal concentration**

| Sampling site | Location | Cd (mg/kg) | Cr (mg/kg) | Pb (mg/kg) | Zinc (mg/kg) |
|---|---|---|---|---|---|
| 1 | 26° 10' 5.27" S<br>25° 14' 47.69" E | 0.26±0.00$^{b}$ | 0.35±0.00 $^{c}$ | 1.86±0.00 $^{b}$ | 0.96±0.00 $^{b}$ |
| 2 | 26° 10' 14.28" S<br>25° 14' 14.58" E | 0.02±0.00 $^{d}$ | 0.27±0.01 $^{f}$ | 0.23±0.01 $^{de}$ | 0.3±0.02 $^{c}$ |
| 3 | 26° 10' 3.19" S<br>25° 15' 19.47" E | 0.04±0.00 $^{c}$ | 0.37±0.00 $^{b}$ | 0.3±0.01 $^{c}$ | 0.16±0.00 $^{d}$ |
| 4 | 26° 10' 2.18" S<br>25° 15' 20.66" E | 0.36±0.00 $^{a}$ | 0.41±0.00 $^{a}$ | 2.4±0.04 $^{a}$ | 1.2±0.00 $^{a}$ |
| 5 | 26° 11' 11.03" S<br>25° 15' 20.66" E | 0.03±0.00 $^{d}$ | 0.29±0.00 $^{e}$ | 0.21±0.00 $^{de}$ | 0.07±0.00 $^{g}$ |
| 6 | 26° 11' 11.01" S<br>25° 15' 40.87" E | 0.02±0.00 $^{d}$ | 0.22±0.00 $^{g}$ | 0.2±0.00 $^{e}$ | 0.07±0.00 $^{g}$ |
| 7 | 26° 9' 40.15" S<br>25° 14' 55.40" E | 0.02±0.00 $^{d}$ | 0.27±0.00 $^{f}$ | 0.25±0.00 $^{cd}$ | 0.14±0.00 $^{e}$ |
| 8 (Control) | 26° 6' 42.59" S<br>25° 9' 24.52" E | 0.03±0.00 $^{c}$ | 0.33±0.00 $^{d}$ | 0.28±0.00 $^{c}$ | 0.11±0.00 $^{f}$ |

Values are means of triplicate readings ± standard error
Values with the same letter within a column are not significantly different ($P < 0.05$)

**Table S4. The sequences of the primer sets used for amplification of 16S rRNA and heavy metal-resistant genes**

| Primer | Primer sequence | Expected band size (bp) | Reference |
|---|---|---|---|
| 16S rRNA | F- AGAGTTTGATCCTGGCTCAG<br>R- ACGGCTACCTTGTTACGACTT | 1,500 | Marin, et al. [1] |
| *CzcA* | F- GTTTGAACGTATCATTAGTTTC<br>R - GTAGCCATCCGAAATATTCG | 1,885 | Nies, et al. [2] |
| *CzcD* | F- CAGGTCACTGACACGACCAT<br>R- CATGCTGATGAGATTGATGATC | 398 | Nies, et al. [2] |
| *CzcB* | F- CTATTTCGAACAAACAAAAGG<br>R- CTTCAGAACAAAACTGTTGG | 1,520 | Abou-Shanab, et al. [3] |
| *PbrT* | F- ATGGTGATTGCTTTAGTT<br>R- TTAGGCTTGCTTCTTTTT | | Shin, et al. [4] |
| *PbrA* | F- ATGAGCGAATGTGGCTCGAAG<br>R- TCATCGACGCAACAGCCTCAA | 766 | Shin, et al. [4] |
| *chr*A | F- CTTATACGCTACGCCAACTG<br>R- GTAATGGCATTCAGTCGCTTG | 1,292 | Nies, et al. [5] |
| *chrB* | F- GTCGTTAGCTTGCCAACATC<br>R- CGAAAGCAAGATGTCGATCG | 450 | Nies, et al. [5] |
| *cadA* | F- GACAAGACYGGMACYMTCAC<br>R- GCRTGGTTRATSCGTC | 600 | Dell'Amico, et al. [6] |

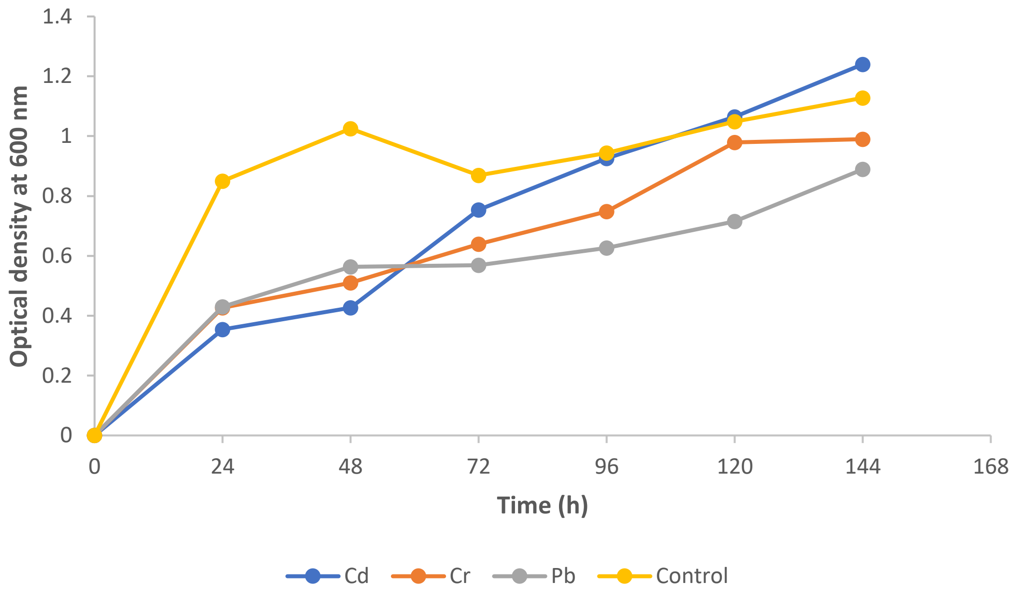



**Fig. S1 Time course growth of *B. cereus* NWUAB01 on different heavy metals**

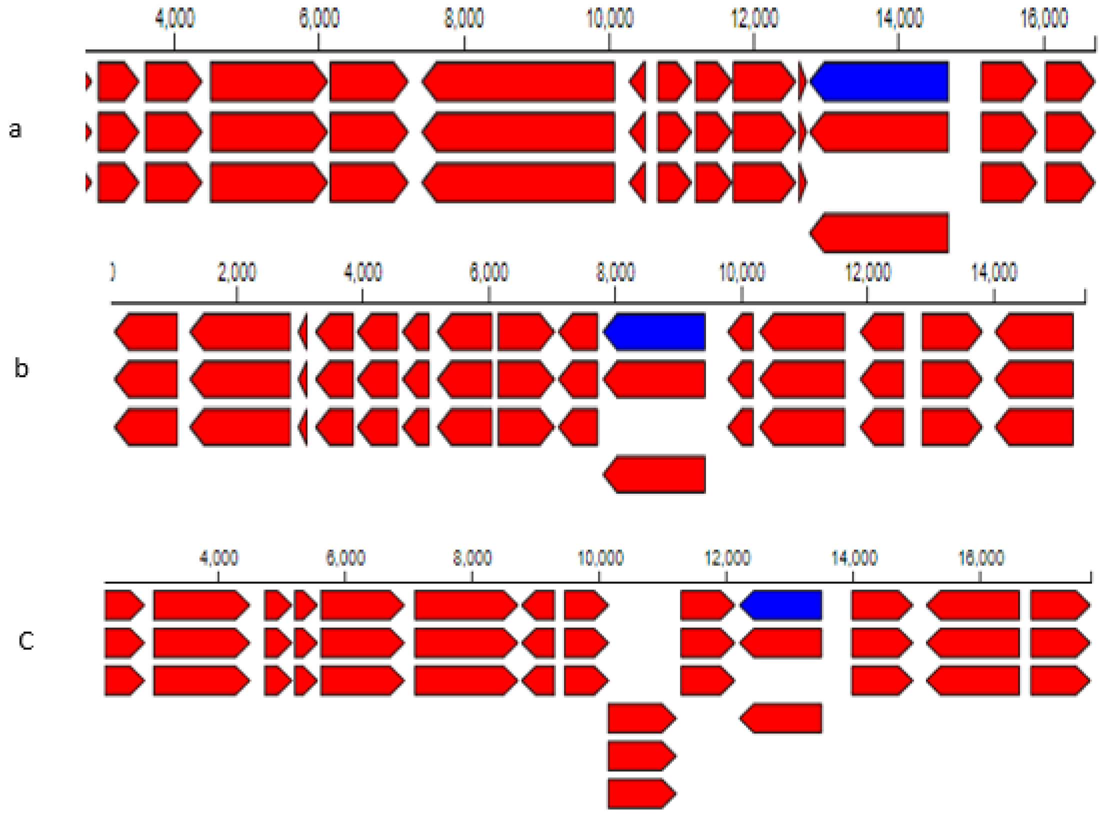



**Fig. S2 The annotation for (a) Lead, cadmium, zinc and mercury transporting ATPase (b) copper resistance protein and (c) manganese transport protein**

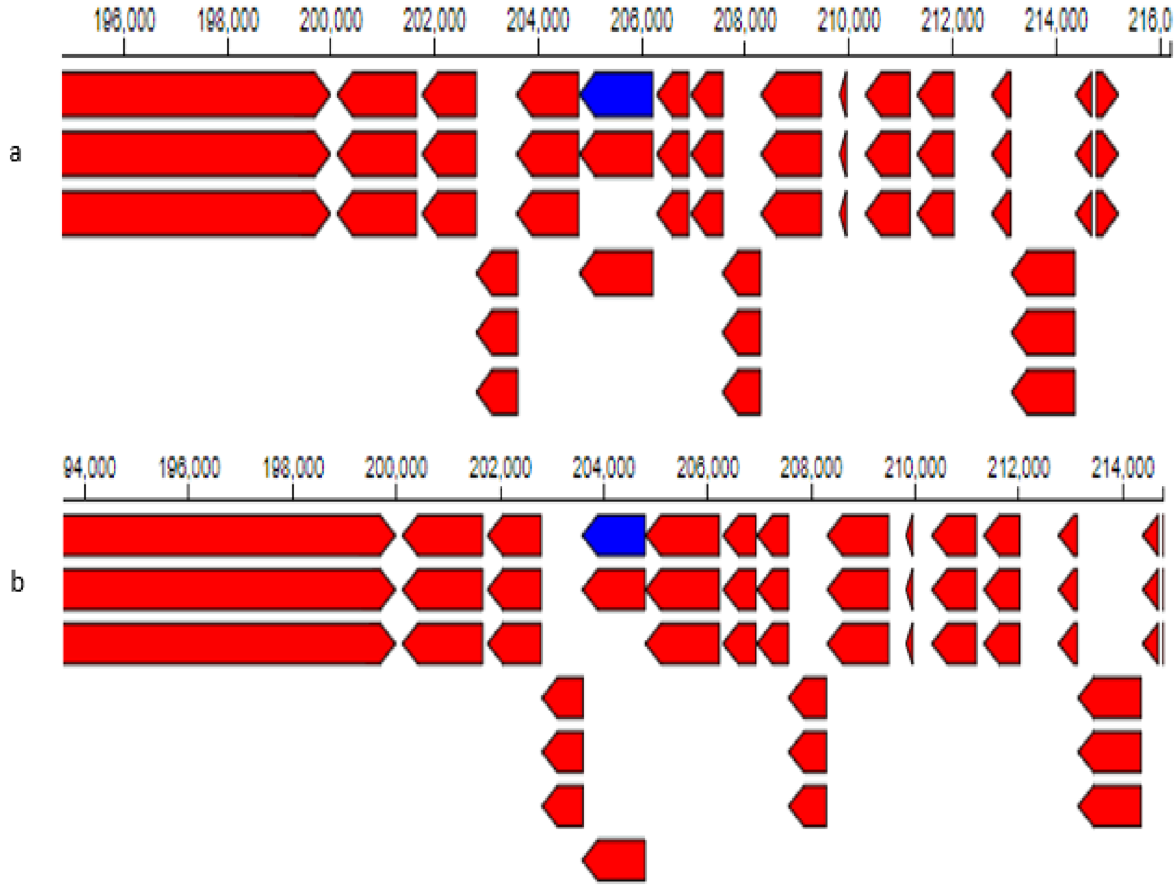



**Fig. S3 Gene annotation of the (a) Wzx and (b) Wzy and their respective locus on the genome of strain NWUAB01**

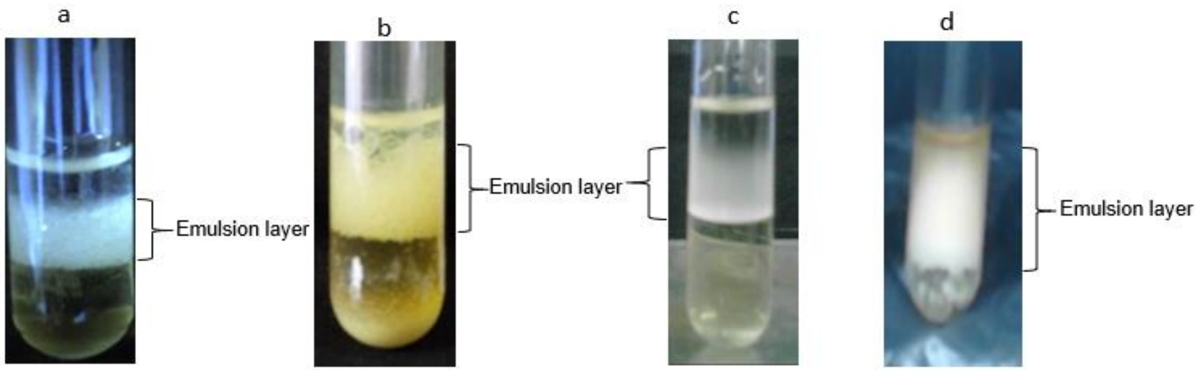
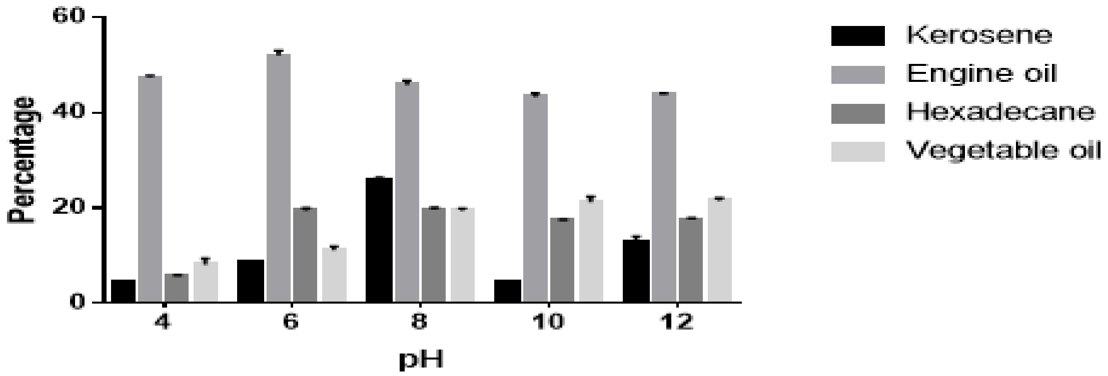



**Fig. S4 Emulsification of (a) kerosene (b) kerosene in the presence of heavy metals (c) vegetable oil (d) engine oil by strain NWUAB01**



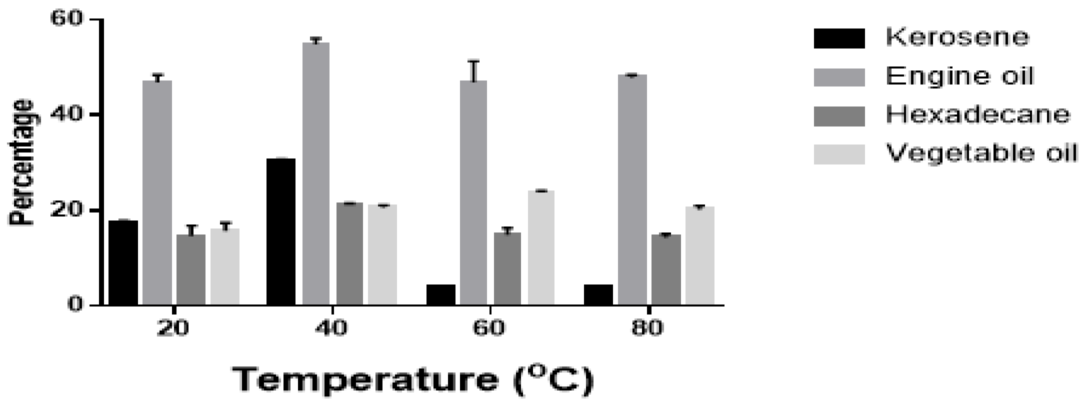




**Fig. S5 Stability of the emulsion produced by strain NWUAB01 at different pH and temperature**

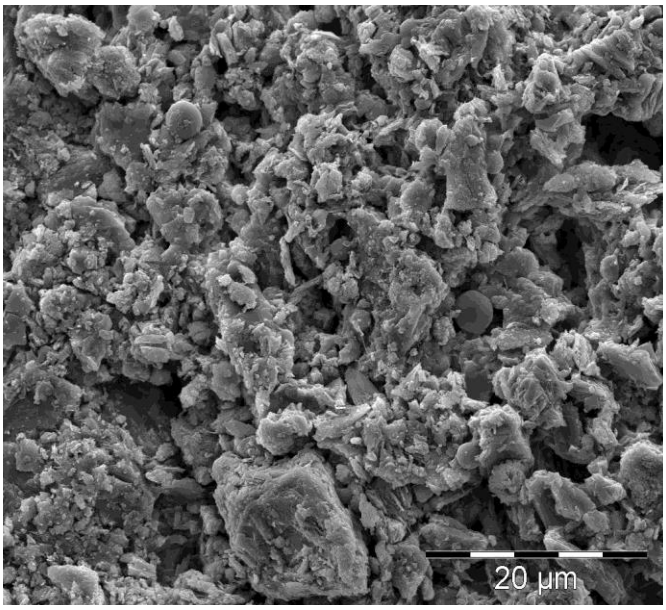



**Fig. S6 The SEM image of the biosurfactant produced be strain NWUAB01**

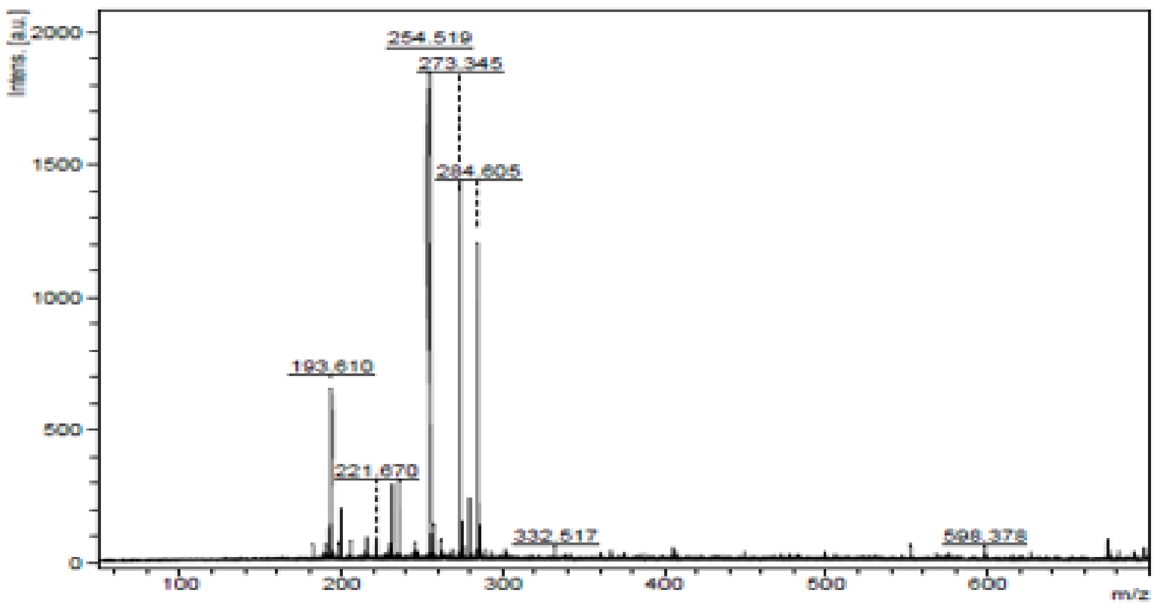



**Fig. S7 The mass spectrum of the purified biosurfactant produced by strain NWUAB01**

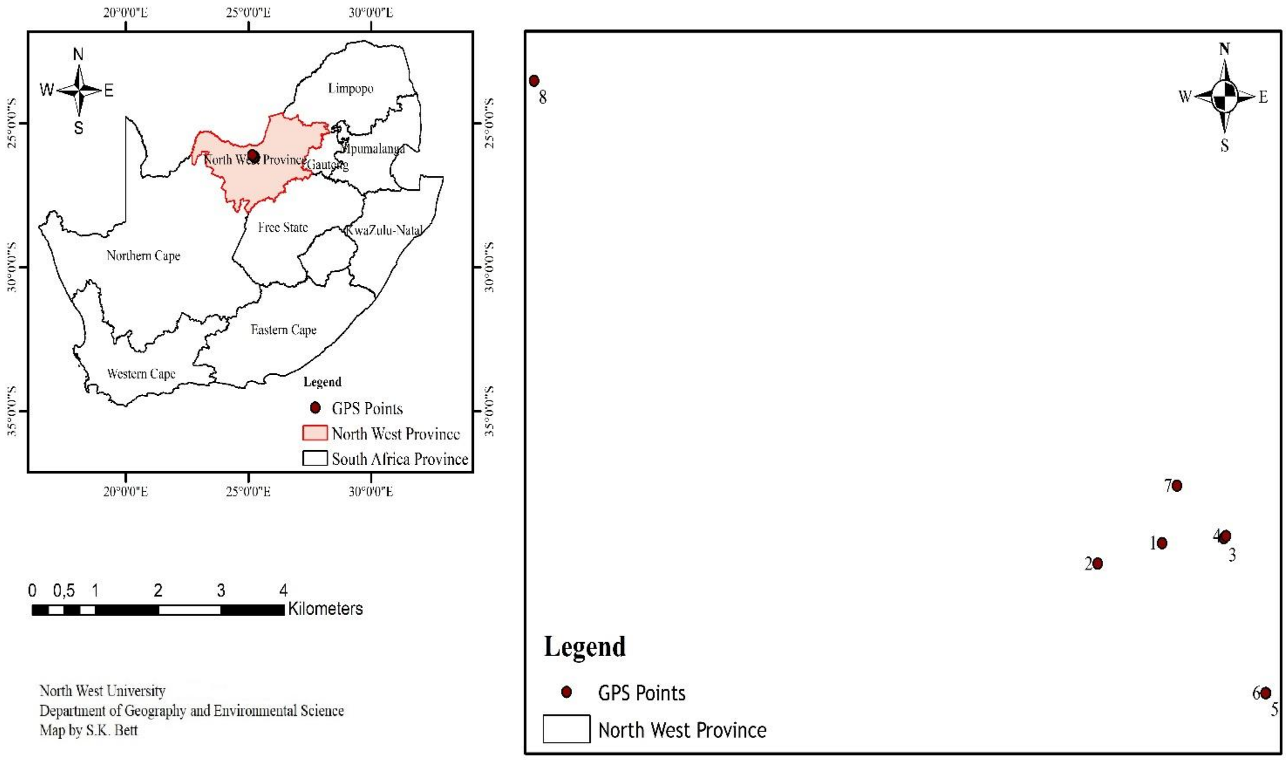
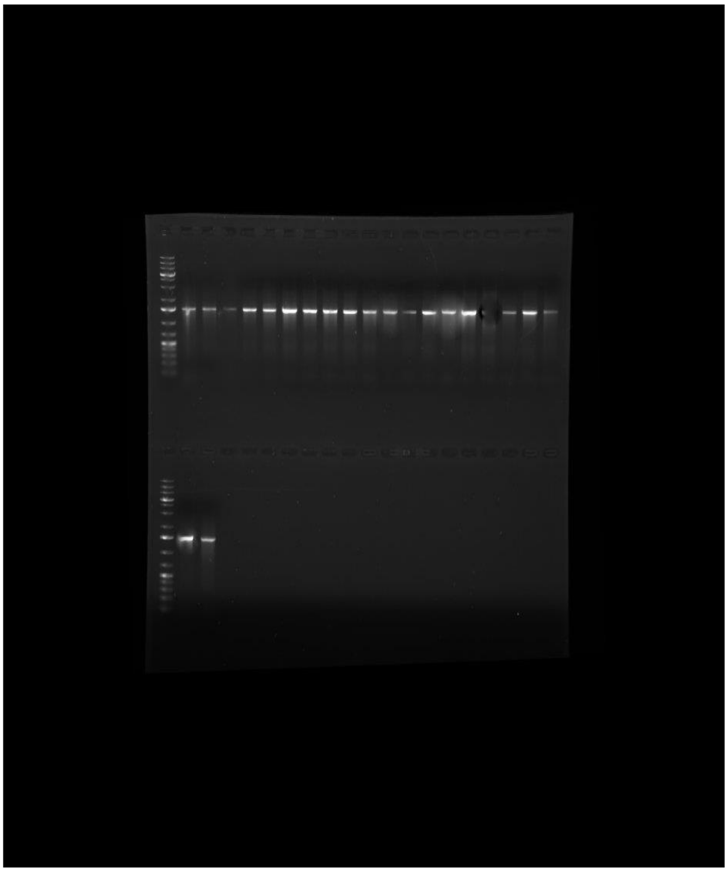
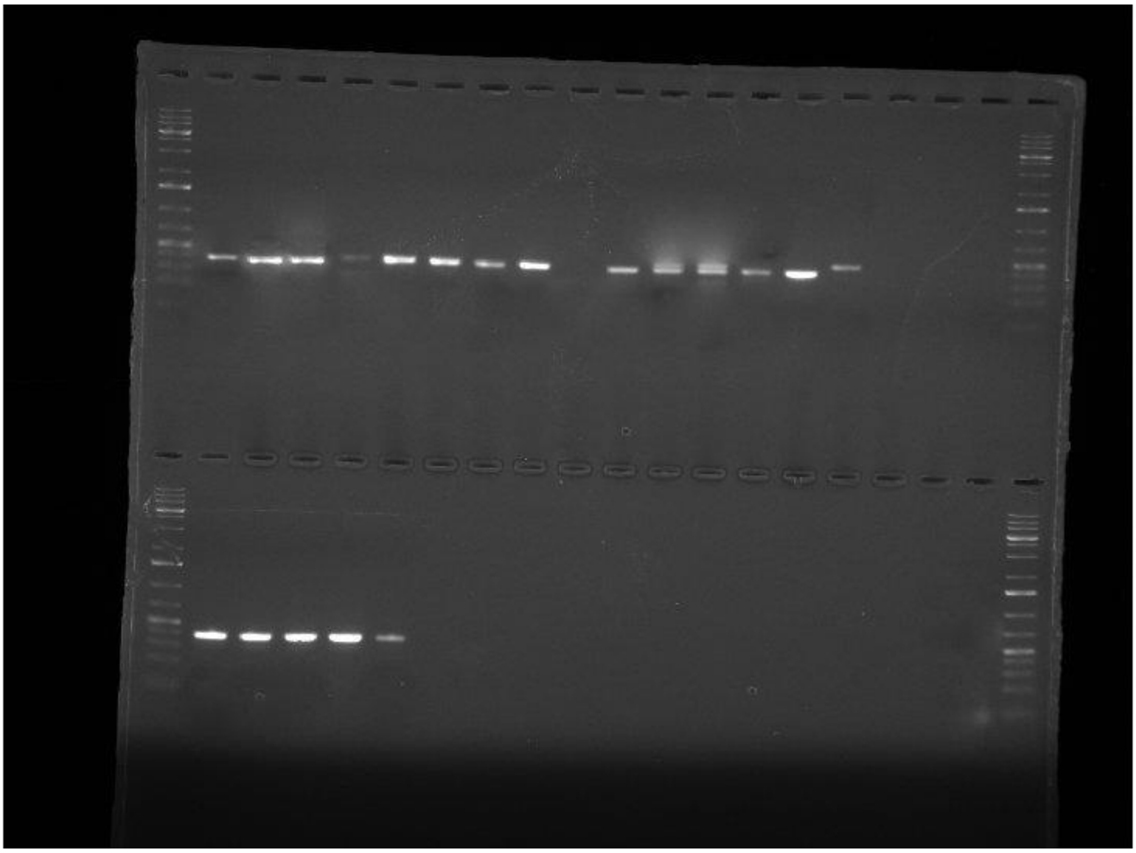


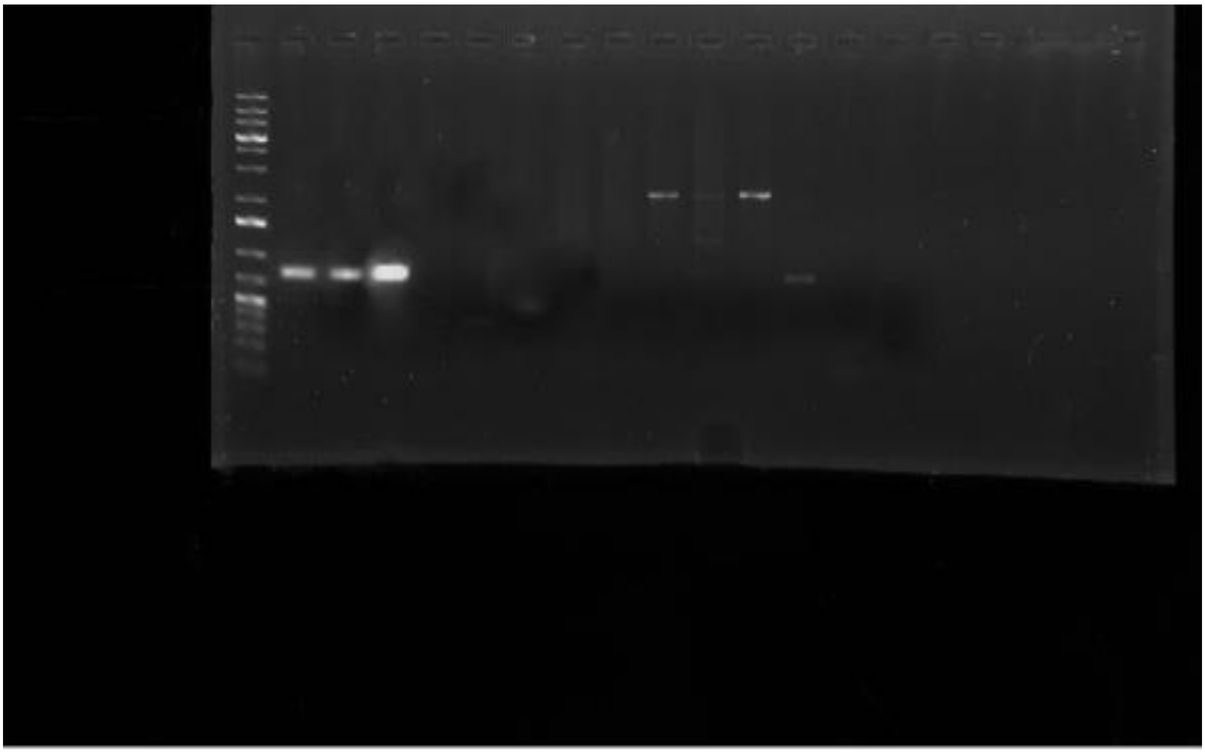

**Fig. S8 The map showing the sampling sites. The map was generated using ArcMap (version 10.5.1) (https://desktop.arcgis.com/en/arcmap/)**



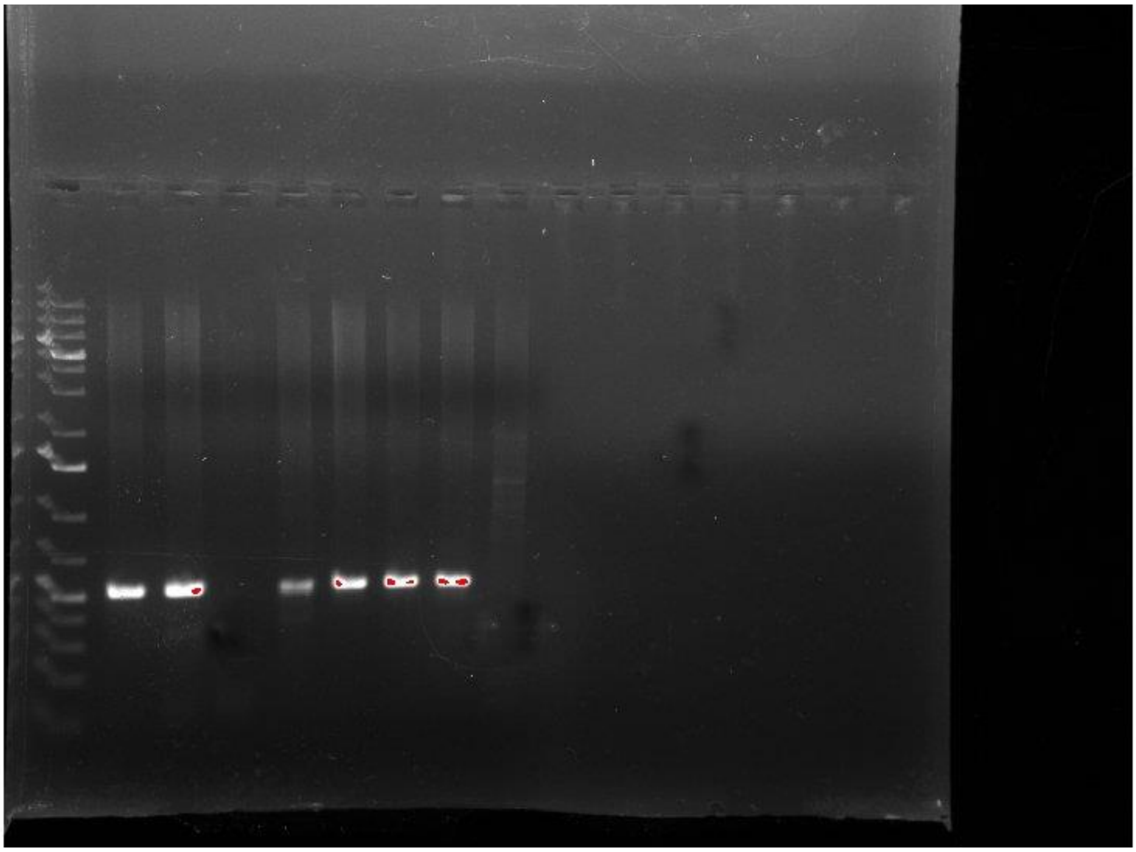
**Gel electrophoresis of the 16S rRNA gene of bacterial isolates from mining soil. It shows the predicted 1,500 bp amplicons of the isolates and negative for the control**



**Gel electrophoresis of the *CzcD* gene of bacterial isolates from mining soil. It shows the predicted 398 bp amplicons for positive isolates and negative for the control**



**Gel electrophoresis of the *PbrA* gene of bacterial isolates from mining soil. It shows the predicted 756 bp amplicons for positive isolates and negative for the control**



**Gel electrophoresis of the *cadA* gene of bacterial isolates from mining soil. It shows the predicted 600 bp amplicons for positive isolates and negative for the control**

**References**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6 Dell'Amico, E., Mazzocchi, M., Cavalca, L., Allievi, L. & Andreoni, V. Assessment of bacterial community structure in a long-term copper-polluted ex-vineyard soil. *Microbiol. Res.* **163**, 671-683, doi:https://doi.org/10.1016/j.micres.2006.09.003 (2008).