**Bacterial community analysis of stabilized soils in proximity to an exhausted mine**

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(a)



(b)

**Fig. S1.** Correlation between samples and soil bacterial communities at class level (a) Taxonomic compositions of bacterial communities. The bars mean averages, and error bars mean standard deviations of relative portions. (b) Principal component analysis (PCA) based on the relative abundance.



(a)



(b)

**Fig. S2.** Correlation between samples and soil bacterial communities at order level (a) Taxonomic compositions of bacterial communities. The bars mean averages, and error bars mean standard deviations of relative portions. (b) Principal component analysis (PCA) based on the relative abundance.



(a)



(b)

**Fig. S3.** Correlation between samples and soil bacterial communities at family level (a) Taxonomic compositions of bacterial communities. The bars mean averages, and error bars mean standard deviations of relative portions. (b) Principal component analysis (PCA) based on the relative abundance.



(a)



(b)

**Fig. S4.** Correlation between samples and soil bacterial communities at species level (a) Taxonomic compositions of bacterial communities. The bars mean averages, and error bars mean standard deviations of relative portions. The *Methylobacter tundripaludum* is dominant species in stabilized soil (red arrow). (b) PCA based on the relative abundance. The samples from stabilized soil are grouped with *Methylobacter tundripaludum* (red arrows).