1   **Supplemental materials**

2   **Table S1.** Total numbers of raw and effective sequences, OTU (operational taxonomic unit)

3   counts and Good's coverage in each tested layer of the Kam Kotia Mine NIT profile at four

4   different locations (Site 1, 3, 4 and 5), as determined by high-throughput amplicon sequencing.

Site	Soil sample	Total raw sequences	Effective sequences for analysis	OTU counts	Good's coverage
1	soil	148,178	101,006	2,725	0.938
	sand	130,678	100,556	2,306	0.957
	clay	181,464	146,547	1,391	0.972
	cushion sand	206,340	159,922	1,229	0.975
	rock	212,867	177,480	481	0.989
	tailings	309,508	260,002	434	0.992
		439,041	383,915	326	0.993
		284,231	239,249	381	0.992
		249,384	203,543	545	0.989
		385,551	324,406	683	0.988
		267,878	231,617	509	0.992
3	soil	185,267	136,692	2,458	0.943
	sand	188,633	154,522	1,581	0.980
	clay	181,466	147,377	2,466	0.965
	cushion sand	303,908	247,134	1,928	0.970
	rock	255,407	195,348	975	0.977
	tailings	88,667	75,552	481	0.996
		37,176	32,817	225	0.997
		205,889	175,984	1,367	0.978
		178,999	158,967	729	0.994
4	soil	180,296	129,448	2,642	0.942
	sand	210,021	165,248	2,449	0.955
	clay	170,360	145,565	1,113	0.976
	cushion sand	273,237	214,533	1,556	0.968
	rock	203,340	159,079	515	0.990
	tailings	32,576	24,652	113	0.998
		71,596	64,786	134	0.998
		156,773	136,372	454	0.996
5	soil	115,576	82,329	2,884	0.940
	sand	187,709	156,580	1,200	0.988
	clay	62,592	55,181	374	0.996

	cushion sand	296,958	230,846	1,929	0.959
	rock	261,873	200,930	898	0.981
		79,563	68,132	159	0.998
	tailings	170,801	145,536	355	0.997
		53,564	42,068	284	0.997

5

6   **Table S2.** Mean proportions of total reads of major prokaryotic genera (accounting for > 0.5% of

7   total amplicons), and sum of minor genera (< 0.5%), determined in Kam Kotia Mine NIT samples.

8   Higher taxa that could not be identified on the genus level are marked with asterisks.

Genus	Mean % of total reads	
	Cover system	Tailings
Sum of minor genera	67.3	74.1
Bacteria*	5.1	4.2
Burkholderiaceae*	4.1	2.4
Betaproteobacteriales*	2.8	0.3
Subgroup_6_ge	3.2	1.2
Gammaproteobacteria*	1.1	0.4
Alphaproteobacteria*	0.9	0.4
Sphingomonadaceae*	0.9	0.3
Rhizobiales*	0.8	0.3
Parcubacteria*	0.7	1.5
uncultured	1.0	0.3
Chitinophagaceae*	0.7	0.1
uncultured	1.5	0.8
Proteobacteria*	0.4	0.9
Acidobacteriaceae_(Subgroup_1)*	0.1	1.9
KD4-96_ge	1.2	0.8
AD3_ge	0.5	1.4
Xanthobacteraceae*	0.9	0.8
Acidimicrobiia*	0.4	0.9
Flavobacterium	0.9	1.0
uncultured	0.1	1.6
Deltaproteobacteria*	0.6	0.5
Chloroflexi*	0.6	0.2
Subgroup_7_ge	1.3	0.2
Micrococcaceae*	0.6	1.1
Actinobacteria*	0.3	0.5
Pedosphaeraceae_ge	0.6	0.3
Myxococcales*	0.5	0.1
Sphingobacteriaceae*	0.4	0.1
Babeliales*	0.3	0.5
BSV13	0.2	1.0

9

10   **Table S3:** Permutation test for homogeneity of multivariate dispersions of a 3D-NMDS plot of

11   Bray-Curtis similarity matrices of microbial communities at the four Kam Kotia Mine NIT sampling

12   sites (shown in Fig. S1). Pairwise comparisons: observed p-values below diagonal, permuted p-

13   value above diagonal.

14

Site	1	3	4	5
1	-	0.13387	0.43856	0.3147
3	0.14870	-	0.65035	0.7153
4	0.42071	0.62835	-	0.8921
5	0.29546	0.73918	0.87550	-

15   **Table S4:** Results of the pairwise PERMANOVA for 3D-NMDS plot of Bray-Curtis similarity

16   matrices of microbial communities at the four Kam Kotia Mine NIT sampling sites (shown in Fig.

17   S1). P-value adjustment method: fdr.

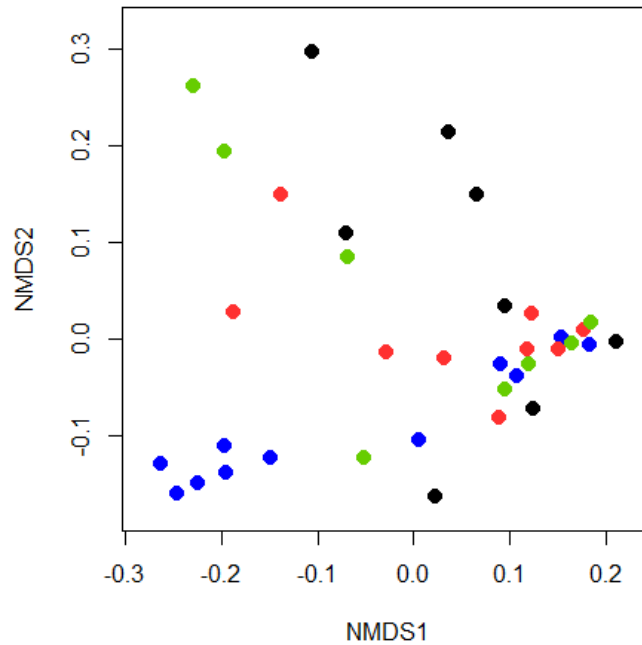| Site	1	3	4
3	0.13	-	-
4	0.13	0.92	-
5	0.13	0.82	0.92

18

19 **Table S5:** Permutation test for homogeneity of multivariate dispersions of NMDS plots of Bray-

20 Curtis similarity matrices of microbial communities in different layers of the Kam Kotia Mine NIT

21 profile (shown in Fig. 2). Pairwise comparisons: observed p-values below diagonal, permuted p-

22 value above diagonal.

Layer	Clay	Cushion sand	Rock	Sand	Soil	Tailings
Clay	-	0.0450	0.8402	0.5295	0.2727	0.001
Cushion sand	0.0317	-	0.0639	0.1798	0.2378	0.001
Rock	0.8511	0.0504	-	0.4486	0.2697	0.001
Sand	0.5451	0.1504	0.4817	-	0.6284	0.001
Soil	0.2820	0.2429	0.2697	0.6740	-	0.001
Tailings	3.03E-06	1.80E-10	2.64E-05	5.74E-07	4.71E-08	-

23

24

25

Fig. S1. Two-dimensional non-metric multidimensional scaling (2D-NMDS, stress = 0.116) plot of

Bray-Curtis similarity matrices of microbial communities at NIT Site (●) 1, (●) 3, (●) 4, and (●) 5

at the Kam Kotia Mine. Points represent the composition of a community, and the distance

between any two points represents the difference between those two communities.