Supporting information for:

Sustained Bauxite Residue Rehabilitation with Gypsum and Organic Matter 16 years after Initial Treatment

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Consists of 18 pages, 8 tables, and 3 figures

Section S1. Aqueous chemical analysis by Inductively Coupled Plasma Optical Emission Spectrometry (ICP-OES).

All samples from aqueous extraction and phosphate extraction were diluted 10 fold in 5% HNO_3 (AnalaR NORMAPUR, VWR) prior to analysis by ICP-OES. Limits of detection were calculated from 3 x the standard deviation of 12 measurements of analytical blank solutions (5% HNO_3).

Table S1. Limits of detection of elements analysed by ICP-OES.

Element	Limit of Detection (mg L^{-1})
Na	0.436
Mg	0.012
K	0.183
Fe	0.016
Si	0.070
Al	0.008
P	0.003
V	0.002
Cr	0.007
Mn	0.001
Ti	0.004
Ca	0.026
As	0.002

Reported aqueous concentration of element i (C_i, mg kg^{-1}) are normalised to mass of bauxite residue following:

$$C_i = \frac{c_i \times \text{DF} \times V_{\text{ex}}}{m_{\text{BR}}}$$

(Eqn. S1)

Where the measured concentration of element i (c_i, mg L^{-1}) is corrected for analytical dilution (DF), multiplied by the volume of extractant used (V_{ex}, L, either ultrapure water or disodium phosphate solution) and divided by the mass of bauxite residue used in each extraction (m_{BR}, kg).

Aqueous concentrations of element i presented in Fig. S2 (M$_i$, mol L^{-1}) are analytical dilution corrected and converted from elemental mass to number of moles following:

$$M_i = \frac{c_i \times \text{DF}}{m_{a,i}}$$

Where $m_{a,i}$ is the atomic mass of element i.

Section S2. Chemical equations describing gypsum addition and CO₂ in-gassing.

Addition of gypsum ($CaSO_4.2H_2O$) to bauxite residue promotes the rapid precipitation of $CaCO_3$ through the net reaction:

$$CaSO_4.2H_2O + 2OH^- + CO_2 \rightleftharpoons CaCO_3 + SO_4^{2-} + 3H_2O$$

(Eqn. S2)
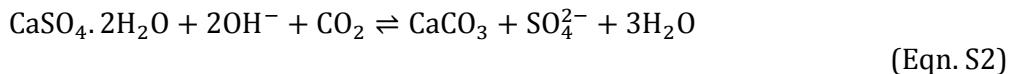
This can be broken down into stepwise reactions (Eqns. S3-S7):

$$CaSO_4.2H_2O \rightleftharpoons Ca^{2+}_{(aq)} + SO^{2-}_{4\,(aq)} + 2H_2O$$

(Eqn. S3)

$$CO_{2(g)} \rightleftharpoons CO_{2(aq)}$$

(Eqn. S4)

$$CO_{2(aq)} + H_2O \rightleftharpoons H_2CO_{3\,(aq)}$$

(Eqn. S5)

$$H_2CO_{3\,(aq)} \rightleftharpoons HCO^-_{3\,(aq)} + H^+ \rightleftharpoons CO^{2-}_{3\,(aq)} + H^+$$

(Eqn. S6)

$$Ca^{2+}_{(aq)} + CO^{2-}_{3\,(aq)} \rightleftharpoons CaCO_{3\,(s)}$$

(Eqn. S7)
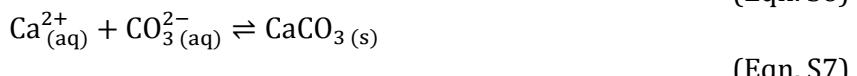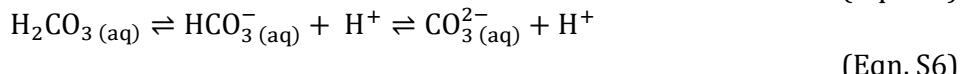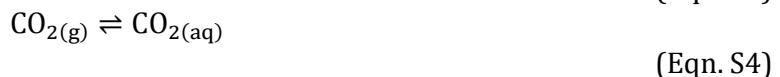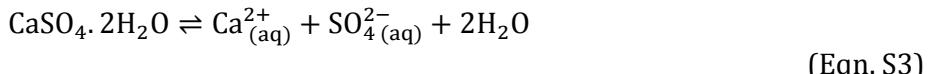
Section S3. DNA extraction, quantification, and post sequence processing.

DNA was extracted from samples using the MPBio FastDNA SPIN Kit for Soil. To account for variability of DNA extraction efficiency, duplicate extractions were conducted on sub samples at selected depths. These samples are represented as individual points in Fig. 3, and Table S6. Extraction was also conducted on 1/10 the mass of the most concentrated sample, to ensure the assay was not over saturated with DNA.

Extracted DNA was quantified using Qubit dsDNA High Sensitivity assay on a Qubit Fluorometer (Life Technologies). This method uses two standards with DNA concentrations of 0 ng µL⁻¹ and 10 ng µL⁻¹. These were diluted 1:5 for measurement in the assay. The analytical uncertainty was determined by performing triplicate assays on sub samples from 3 different extractions, spanning a range in DNA concentration. The maximum analytical uncertainty was 2.6% (2 x RSD), and this was used to calculate uncertainty for all samples (Table S6).

Sequencing generated ~1M clusters of data, and the trimmed overlapping paired-end reads were assembled and relabelled using the *fastq_mergepairs* command (USEARCH version 10).[1,2] The merged reads were then quality filtered with a maximum expected error of 1.0 using the *fastq_filter* command. Unique sequences for each merged read were identified using the *fastx_uniques* command, and clustered into operational taxonomic units (OTUs) for all samples using the *cluster_otus* command, resulting in 6243 OTUs. Chimeras and singletons are removed as part of the *cluster_otus* command. The unfiltered merged reads in each sample were mapped to OTUs with a minimum of 97% sequence matching, using the *usearch_global* command. Unfiltered merged reads were used in case some of the discarded merged reads mapped to an OTU. Taxonomic predications for each OTU

were made using the *sintax* command and the SILVA Living Tree Project 16s database, version 123,[3] with a confidence value of 0.7 (Fig. S2). OTUs which were not classified to the level of bacterial phylum with a confidence of > 0.7 (8-17 % of non-chimeric reads) were excluded from further analysis. Taxonomic assignments below 0.7 confidence were discarded at each taxonomic level. Alpha diversity indices were determined using the *alpha_div* command (Table S7), and rarefaction curves for each sample were created following the *alpha_div_rare* command which subsamples at random without replacement (a read may only be selected once; Fig. S2).

Hill numbers[4,5] are used in this study, providing robust bacterial diversity measures which account for the distortions of rare taxa to traditional biodiversity estimates. Here, biodiversity is defined as the reciprocal mean of proportional abundance, with taxa weighted based on abundance to compensate for the disproportionate impact of rare taxa.[4–7] The unweighted Hill number, $D_0{}^\alpha$, is equivalent to the OTU richness. $D_1{}^\alpha$ is a measure of the number of common species and is equivalent to the exponential of Shannon entropy; and $D_2{}^\alpha$ is a measure of the number of dominant species and is equivalent to the inverse of Simpson concentration.[4–6]
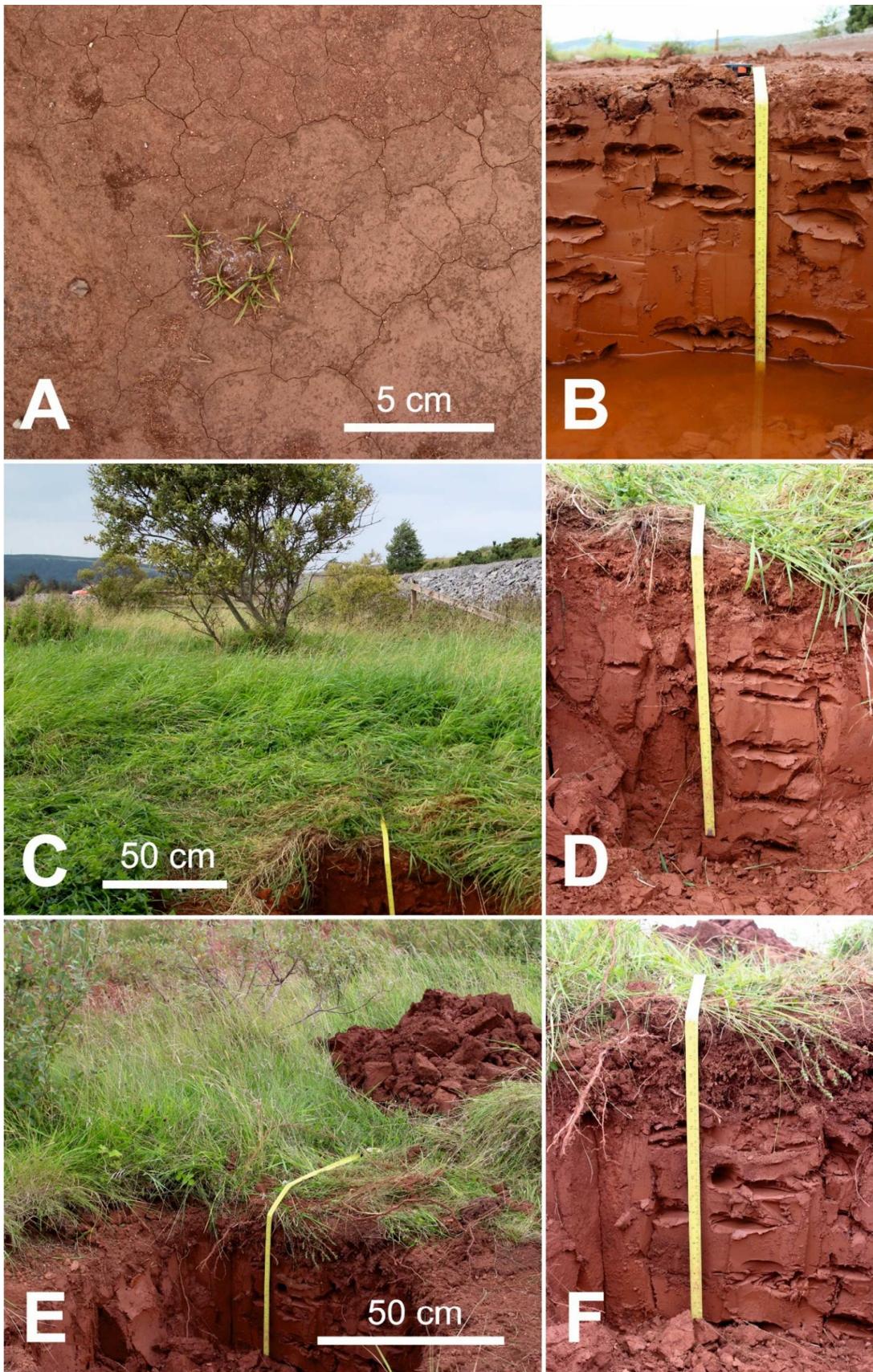
Figure S1. On site photographs of untreated bauxite residue 20 years after deposition (A, B); bauxite residue 16 years after full treatment with gypsum, organic matter, and process sand (C, D); and bauxite residue 16 years after partial treatment with organic matter and process sand (E, F). The tape measure in B, D, and F measures 50 cm depth in each trial pit.
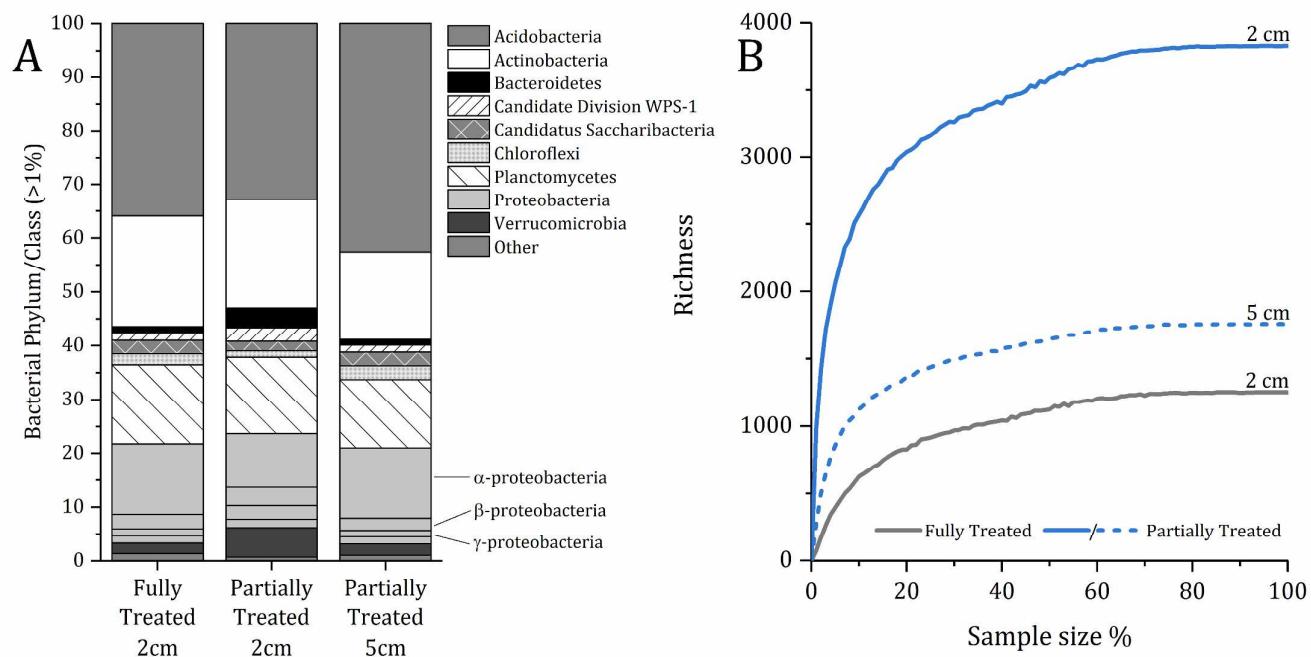
Figure S2. (A)Bacterial phylogenetic diversity with the fully treated and partially treated substrate. The classes of Proteobacteria are labelled from top to bottom Alphaproteobacteria, Betaproteobacteria, Gammaproteobacteria, and other Proteobacteria. Phyla with less than 1% relative abundance are grouped as "Other". Detailed data in Table S7. (B) Rarefaction curves for each sample.
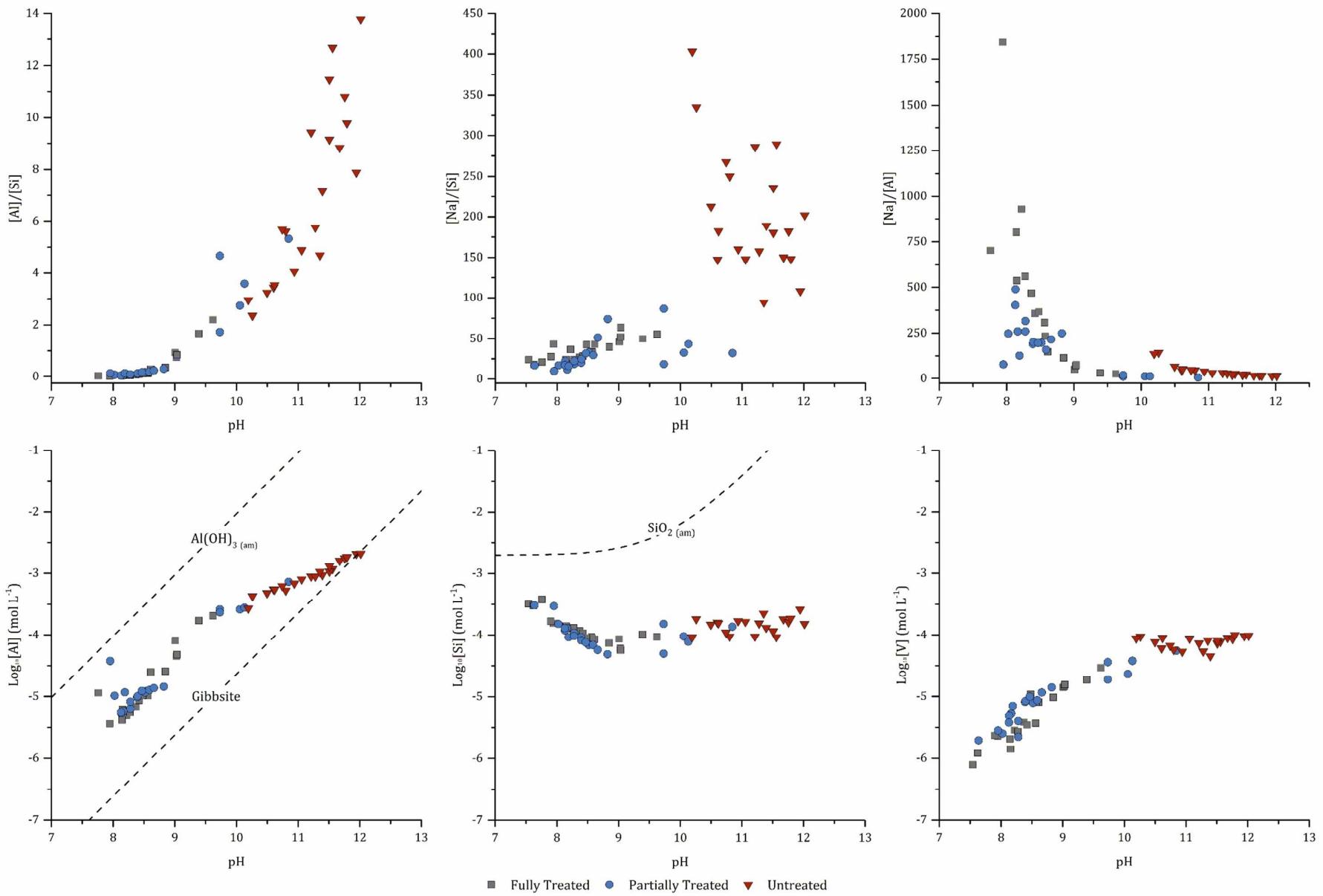
Figure S3. Element ratios and log concentrations of Na, Al, Si, and V aqueously extracted from fully treated, partially treated, and untreated bauxite residue as a function of pH.

Table S2. pH, water content, carbon content, aqueous extractable and phosphate extractable element concentrations of bauxite residue as a function of treatment and depth.

|	Depth	pH	Soil Water	TIC	TOC	AIC	AOC	Na	Mg	K	Fe	Si	Al	P	V	Cr	Mn	Ti	Ca	As	Al	V	Cr	As
													(H_2O)								(PO_4)			
	cm		%	%	%	%	%						mg kg^{-1}								mg kg^{-1}			
Untreated	1.0	10.3	35.7					1712.26	DL	41.41	3.48	6.24	14.09	0.21	5.81	0.54	DL	1.21	2.99	0.28	29.66	32.19	0.36	1.97
	3.5	10.5	40.0					792.37	DL	26.25	1.87	4.56	14.17	0.09	4.27	0.24	DL	0.83	2.16	0.21	15.14	26.32	0.08	1.75
	5.0	10.6	43.0			0.1	0.1	640.85	DL	32.52	2.70	5.31	17.59	0.16	3.62	0.21	DL	0.86	2.36	0.18	19.01	24.87	DL	1.60
	7.5	10.8	42.9					633.74	DL	25.78	DL	3.10	16.65	0.03	3.40	0.09	DL	DL	0.70	0.14	14.61	28.26	0.07	1.84
	10.0	10.7	49.7			0.1	0.1	757.80	DL	28.83	0.77	3.46	18.88	0.11	3.83	0.20	DL	0.49	1.54	0.17	16.41	26.78	0.06	1.72
	13.5	11.2	46.8					877.57	DL	33.38	0.11	3.75	33.94	0.02	5.22	0.19	DL	DL	0.65	0.17	24.18	29.18	0.12	1.49
	17.0	11.3	42.1					683.36	DL	18.38	0.18	5.30	29.30	0.02	3.34	0.14	DL	0.20	1.31	0.08	11.16	17.82	0.11	1.10
	20.5	11.6	46.4			DL	DL	667.39	DL	21.24	DL	2.82	34.28	0.02	4.25	0.16	DL	DL	0.30	0.11	28.65	29.31	0.10	1.26
	30.0	11.4	40.2			DL	DL	885.91	DL	29.84	DL	5.73	39.45	0.02	3.58	0.12	DL	DL	0.67	0.10	35.55	31.08	0.08	1.46
	40.0	11.9	82.4					857.32	DL	29.68	DL	9.67	73.25	0.02	6.36	0.09	DL	DL	0.51	0.12	48.57	31.88	DL	1.08
	50.0	12.0	44.4					809.82	DL	29.80	DL	4.90	64.91	0.02	5.68	0.19	DL	DL	DL	0.09	47.78	30.91	0.18	1.06
	1.0	10.2	35.9	0.4	0.3			1069.45	DL	45.99	DL	3.24	9.20	0.04	5.63	0.19	DL	DL	0.59	0.20	31.27	73.51	0.10	3.00
	3.5	10.6	80.9	0.3	0.3			916.87	DL	47.59	DL	6.15	20.93	0.02	6.41	0.23	DL	DL	1.09	0.21	37.32	71.64	DL	2.90
	5.0	11.1	43.1	0.3	0.3			789.92	DL	26.34	DL	6.53	30.67	0.02	6.27	0.23	DL	DL	1.05	0.19	31.85	52.75	0.14	2.60
	7.5	10.9	44.7	0.3	0.3			798.53	DL	41.58	DL	6.10	23.76	0.02	3.50	0.19	DL	DL	1.15	0.13	19.77	33.10	0.08	1.70
	10.0	11.4	45.8	0.4	0.0			737.88	DL	37.21	DL	9.55	43.05	0.02	6.18	0.21	DL	DL	1.48	0.17	47.18	54.99	0.21	2.49
	15.0	11.5	46.5	0.3	0.2			818.68	DL	1197.04	DL	5.55	48.81	0.02	6.27	0.21	DL	DL	0.61	0.13	54.09	52.27	0.15	2.21
	20.0	11.5	48.2	0.3	0.2			793.71	DL	35.11	DL	4.11	45.25	0.02	5.31	0.22	DL	DL	0.34	0.12	59.15	49.27	0.18	1.89
	30.0	11.7	42.3	0.3	0.1			763.58	DL	25.27	DL	6.22	52.75	0.02	5.55	0.39	DL	DL	0.23	0.10	47.46	37.35	0.22	1.31
	40.0	11.8	44.7	0.3	0.2			784.83	DL	28.92	DL	5.28	54.78	0.02	5.05	0.22	DL	DL	DL	0.09	43.21	30.18	0.13	0.98
	50.0	11.8	45.5	0.3	0.2			1901.54	DL	74.02	DL	15.69	147.41	0.02	15.08	0.75	DL	DL	DL	0.30	42.91	31.52	0.20	0.99

DL: Sample below detection limit

Table S2. Cont.

	Depth	pH	Soil Water	TIC	TOC	AIC	AOC	Na	Mg	K	Fe	Si	Al	P	V	Cr	Mn	Ti	Ca	As	Al	V	Cr	As
						Carbon		Na	Mg	K	Fe	Si	Al	P	V	Cr	Mn	Ti	Ca	As	Al	V	Cr	As
													(H_2O)									(PO_4)		
	cm		%	%	%	%	%						mg kg^{-1}									mg kg^{-1}		
Fully Treated	1.0	7.8	59.1					242.89	20.80	82.24	0.76	14.12	0.41	0.32	DL	DL	0.16	DL	142.20	DL	50.65	11.92	1.04	0.89
	5.0	7.5	35.6					226.72	11.93	36.44	DL	11.65	DL	DL	0.05	0.01	0.09	DL	120.19	DL	84.48	12.68	1.31	1.05
	7.5	7.9	30.2			DL	0.2	118.57	2.00	18.57	DL	3.36	DL	0.10	0.09	DL	DL	DL	44.45	DL	27.37	28.02	DL	0.94
	10.0	8.2	30.1					86.95	0.70	15.33	DL	2.92	0.11	DL	0.12	DL	DL	DL	22.32	DL	30.56	30.08	DL	1.09
	11.5	7.9	34.7			DL	0.1	124.24	2.23	27.44	DL	5.46	DL	DL	0.14	DL	DL	DL	59.90	DL	34.12	30.99	DL	0.95
	14.0	8.4	29.4					79.99	0.32	17.13	DL	3.61	0.20	DL	0.22	DL	DL	DL	18.21	DL	4.85	23.77	DL	1.10
	17.5	8.4	35.5					93.80	0.14	31.89	DL	4.01	0.31	DL	0.24	DL	DL	DL	15.90	DL	13.51	26.23	DL	0.89
	22.5	8.6	36.5			DL	DL	93.46	DL	21.10	1.89	2.66	0.74	DL	0.45	0.07	DL	DL	7.74	DL	51.27	62.07	DL	2.14
	30.0	9.0	36.2			DL	DL	90.64	DL	18.58	2.74	2.41	2.15	0.06	0.71	0.08	DL	0.17	3.97	DL	53.73	69.07	DL	2.36
	40.0	9.4	35.2					107.09	DL	19.09	5.86	2.63	4.22	0.09	0.87	0.11	DL	0.34	2.42	DL	48.68	72.41	DL	2.35
	50.0	9.6	42.5					103.72	DL	14.48	6.81	2.29	4.83	0.13	1.30	0.14	DL	0.38	1.97	DL	40.43	76.82	DL	2.33
	1.0	7.6	44.0	2.4	1.5			145.87	6.36	25.62	DL	9.85	DL	DL	0.07	0.01	DL	DL	81.56	DL	35.95	14.71	0.58	0.91
	5.0	8.1	29.5	0.8	0.4			87.32	1.24	19.49	DL	4.48	0.13	DL	0.12	0.02	DL	DL	45.84	DL	26.05	28.85	DL	0.81
	7.5	8.2	29.5	0.6	0.4			105.17	2.26	28.55	DL	5.40	0.23	DL	0.10	DL	DL	DL	59.06	DL	34.65	27.91	DL	1.15
	10.5	8.3	32.2	0.4	0.3			74.59	0.59	20.02	DL	3.83	0.16	DL	0.14	DL	DL	DL	22.46	DL	6.78	18.53	DL	0.86
	13.5	8.6	36.5	0.4	0.2			76.47	0.15	28.08	DL	2.78	0.29	0.04	0.20	0.01	DL	DL	10.75	DL	13.95	26.51	DL	1.00
	18.5	8.6	37.2	0.3	0.5			74.89	DL	26.46	DL	2.81	0.38	0.03	0.46	0.03	DL	DL	10.98	DL	23.20	39.99	DL	1.49
	22.5	8.8	38.5	0.4	0.5			82.67	DL	27.88	0.80	2.54	0.85	0.03	0.61	0.04	DL	DL	7.17	DL	32.41	53.32	DL	1.88
	30.0	9.0	37.5	0.4	0.4			87.34	DL	19.66	1.29	2.05	1.46	0.04	0.90	0.10	DL	DL	4.09	DL	20.50	59.84	DL	2.17
	40.0	8.5	38.7	0.4	0.5			106.60	DL	25.96	DL	3.06	0.34	DL	0.67	0.03	DL	DL	13.02	DL	31.87	78.46	DL	2.37
	50.0	9.0	33.8	0.4	0.5			99.39	DL	30.77	0.55	1.91	1.54	0.05	0.95	0.10	DL	DL	4.89	DL	17.51	62.06	0.09	2.14

DL: Sample below detection limit

Table S2. Cont.

Depth	pH	Soil Water	TIC	TOC	AIC	AOC	Na	Mg	K	Fe	Si	Al	P	V	Cr	Mn	Ti	Ca	As	Al	V	Cr	As
					Carbon								(H_2O)									(PO_4)		
cm		%	%	%	%	%							mg kg^{-1}									mg kg^{-1}		
1.0	7.6	37.5					169.30	9.37	202.60	DL	12.34	DL	0.06	0.14	DL	0.02	DL	143.81	DL	23.12	12.14	0.45	0.70
5.0	8.0	33.8					57.12	2.48	30.48	0.47	4.14	0.27	0.52	0.13	0.02	DL	DL	52.30	DL	33.20	24.74	DL	1.05
7.5	8.3	28.1			DL	DL	66.50	2.13	21.38	DL	4.38	0.25	0.04	0.16	DL	DL	DL	67.55	DL	7.57	25.93	DL	1.24
10.0	8.2	27.0					53.52	1.74	49.28	DL	5.65	0.24	DL	0.42	0.02	DL	DL	42.54	DL	25.24	41.51	DL	1.39
12.5	8.1	39.7			DL	0.1	56.61	1.87	29.76	DL	3.12	0.14	DL	0.23	0.01	DL	DL	37.75	DL	68.13	51.46	0.17	1.73
15.0	8.4	47.2					52.82	0.86	36.28	DL	3.21	0.33	DL	0.51	0.01	DL	DL	21.25	DL	38.16	43.72	DL	1.67
17.5	8.5	44.1					60.31	0.57	33.23	DL	2.22	0.36	DL	0.46	0.01	DL	DL	13.31	DL	49.62	62.03	DL	2.39
25.0	9.7	45.8			DL	DL	85.60	0.20	54.28	1.33	5.68	9.43	0.77	1.28	0.08	0.05	1.07	7.81	DL	61.75	59.09	DL	2.68
30.0	10.1	42.2			DL	DL	93.12	0.16	24.61	1.02	3.49	9.18	1.98	1.54	0.07	0.04	0.78	8.80	DL	96.81	62.29	DL	2.94
40.0	10.1	48.0					84.38	DL	18.26	0.63	2.38	8.20	0.90	2.10	0.06	0.02	0.59	5.01	DL	55.77	62.97	DL	2.63
50.0	10.8	56.1					139.21	DL	26.19	2.84	5.30	27.12	0.57	3.92	0.07	DL	0.26	3.48	DL	129.07	66.53	DL	2.62
1.0	8.0	50.9					95.78	8.91	50.40	3.43	12.01	1.46	0.83	0.21	0.05	DL	0.24	118.51	DL	44.17	11.46	0.78	1.23
6.0	8.1	40.5					63.69	2.69	17.24	0.11	4.51	0.19	0.09	0.24	0.02	DL	DL	47.49	DL	33.67	33.95	0.30	1.31
9.0	8.2	32.6					42.06	1.37	39.05	0.58	3.22	0.39	1.98	0.44	0.02	DL	DL	31.02	DL	43.66	55.54	0.10	2.02
12.5	8.3	34.4					55.04	2.16	25.18	DL	3.03	0.25	0.19	0.23	0.01	DL	DL	39.55	DL	18.62	42.76	DL	1.49
16.0	8.4	42.7					51.24	1.00	23.06	DL	2.51	0.30	0.07	0.47	0.02	DL	DL	21.04	DL	22.83	52.20	DL	1.88
19.0	8.6	49.1					79.84	0.66	39.39	DL	3.31	0.59	DL	0.76	0.02	DL	DL	15.93	DL	34.99	60.08	DL	2.10
25.0	8.5	46.3					99.07	0.60	31.31	DL	3.79	0.59	DL	0.90	0.04	DL	DL	23.23	DL	45.25	70.27	DL	2.71
30.0	8.7	45.7					93.31	DL	26.54	DL	2.22	0.51	DL	0.81	0.02	DL	DL	9.95	DL	35.85	59.87	0.11	2.41
40.0	8.8	43.1					75.72	DL	12.18	DL	1.25	0.36	DL	0.65	0.02	DL	DL	4.43	DL	36.70	69.84	DL	2.75
50.0	9.7	44.5					93.48	DL	25.54	2.95	1.32	5.93	0.64	1.73	0.06	DL	0.27	3.33	0.05	42.42	72.90	DL	3.10

Partially Treated

DL: Sample below detection limit

Table S3. Statistical significance of each treatment for chemical parameters calculated by ANCOVA (Analysis of Co-Variance) using a General Linear Model to assess difference in average concentrations across the treatments and with depth of sample as a co-variate. Pairwise comparisons were tested by post-hoc Tukey test (p = 0.05). Treatments sharing letters (A or B) have overlapping means.

	pH	Soil Water	TIC	TOC	Na[a]	Mg[b]	K	Fe	Si	Al[a]	P (H_2O)	V[a]	Cr	Mn[b]	Ti	Ca	As	Al	V (PO_4)	Cr	As
Untreated	A	A	A	A	A	-	A	A	A	A	B	A	A	-	A	B	A	A	A	A	AB
Fully Treated	B	B	A	B	B	-	A	A	A	B	B	B	B	-	A	A	B	A	A	A	B
Partially Treated	B	AB	-	-	B	-	A	A	A	B	A	B	B	-	A	A	B	A	A	A	A
Treatment significance	**	**	no s.f.	*	**		no s.f.	no s.f.	no s.f.	**	**	**	**		no s.f.	**	**	no s.f.	no s.f.	no s.f.	*
Depth significance	**	no s.f.	no s.f.	no s.f.	no s.f.		no s.f.	no s.f.	no s.f.	**	no s.f.	**	no s.f.		no s.f.	**	no s.f.	*	**	*	*

*: ANCOVA significant at p < 0.05
**: ANCOVA significant at p < 0.001
no s.f.: ANCOVA not significant, p > 0.05
[a]: Data log-transformed prior to analysis
[b]: Inadequate sample size for analysis

Table S4. Semi-quantitative percentage of crystalline phases present in bauxite residue as a function of treatment and depth, fitted using Rietveld refinement. Uncertainty on the Rietveld refinement is approximately 5 %.

	Depth	Fe Oxyhydroxides			Gibbsite	Al oxyhydroxides		Katoite	Desilication Products	
		Goethite	Hematite	Magnetite		Boehmite	Diaspore		Cancrinite	Sodalite
		α-FeO(OH)	Fe_2O_3	$Fe^{(II)}Fe^{(III)}_2O_4$	$Al(OH)_3$	γ-AlO(OH)	α-AlO(OH)	$Ca_3Al_2(OH)_{12}$	$Na_6Ca_2Al_6Si_6O_{24}(CO_3)_2$	$Na_8Al_6Si_6O_{24}(OH)_2$
	cm	%	%	%	%	%	%	%	%	%
Untreated	7.5	21	16	< 0.5	6	11	3	2	16	< 0.5
	13.5	20	15	< 0.5	7	12	2	1	14	< 0.5
	20.5	20	15	< 0.5	7	11	1	3	14	1
	30	22	17	< 0.5	11	8	1	2	14	< 0.5
	40	21	17	< 0.5	9	8	1	2	13	< 0.5
Fully Treated	7.5	25	20	< 0.5	10	10	1	1	8	< 0.5
	11.5	23	18	< 0.5	9	9	1	2	12	ND
	22.5	23	20	< 0.5	6	6	1	4	10	< 0.5
	30	24	20	1	7	6	< 0.5	3	11	< 0.5
	40	23	19	< 0.5	6	6	1	7	9	< 0.5
Partially Treated	7.5	20	18	< 0.5	13	12	1	10	7	ND
	15	22	16	< 0.5	14	10	< 0.5	2	10	< 0.5
	17.5	17	16	< 0.5	12	9	2	11	10	< 0.5
	30	19	16	< 0.5	11	9	1	12	10	< 0.5
	40	20	16	< 0.5	7	12	< 0.5	12	11	ND

ND: not detected

Table S4. Cont.

	Depth	Ti oxides					Other minerals			
		Perovskite	Rutile	Ilmenite	Anatase	Calcite	Kaolinite	Quartz	Zircon	Wuelfingite
		$CaTiO_3$	TiO_2	$FeTiO_3$	TiO_2	$CaCO_3$	$Al_2Si_2O_5(OH)_4$	SiO_2	$ZrSiO_4$	$Zn(OH)_2$
	cm	%	%	%	%	%	%	%	%	%
Untreated	7.5	20	3	< 0.5	< 0.5	< 0.5	1	< 0.5	1	1
	13.5	20	3	1	< 0.5	1	1	1	1	< 0.5
	20.5	20	3	2	< 0.5	< 0.5	1	< 0.5	< 0.5	1
	30	20	2	< 0.5	< 0.5	< 0.5	1	< 0.5	1	1
	40	21	3	1	ND	< 0.5	1	< 0.5	1	1
Fully Treated	7.5	17	4	1	< 0.5	2	1	1	< 0.5	< 0.5
	11.5	18	0	1	< 0.5	1	1	< 0.5	1	1
	22.5	21	3	1	< 0.5	1	1	1	< 0.5	< 0.5
	30	21	3	1	< 0.5	< 0.5	2	< 0.5	< 0.5	< 0.5
	40	21	3	1	< 0.5	1	1	< 0.5	< 0.5	1
Partially Treated	7.5	14	3	1	< 0.5	1	1	< 0.5	1	0
	15	17	3	3	ND	< 0.5	1	1	< 0.5	1
	17.5	16	3	2	< 0.5	< 0.5	1	1	ND	< 0.5
	30	16	1	2	< 0.5	< 0.5	1	1	< 0.5	1
	40	12	3	2	< 0.5	< 0.5	2	< 0.5	< 0.5	1

ND: not detected

Table S5. Oxide wt.% measured by pXRF as a function of treatment and depth.

Treatment site	Depth	MgO	Al_2O_3	SiO_2	SO_3	CaO	TiO_2	V_2O_5	Cr_2O_3	MnO_2	Fe_2O_3	ZnO	As_2O_5	SrO	Y_2O_3	ZrO_2	SnO_2	ThO_2	Oxides Sum	LE*
	cm	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%
Untreated	1.0	3.73	16.61	6.76	1.57	9.69	4.89	0.21	0.41	0.09	33.73	0.01	0.02	0.01	0.01	0.61	ND	0.02	78.38	21.62
	5.0	4.68	15.34	6.63	1.77	9.96	5.01	0.21	0.41	0.09	32.27	0.01	0.02	0.01	0.03	0.66	ND	0.02	77.12	22.88
	7.5	5.42	14.83	6.36	1.72	9.66	5.12	0.21	0.41	0.09	33.03	0.01	0.02	0.01	0.03	0.62	ND	0.02	77.56	22.44
	10.0	4.74	15.36	6.35	1.70	9.63	5.13	0.21	0.41	0.11	32.43	0.01	0.02	0.01	0.01	0.65	ND	0.02	76.81	23.19
	11.5	4.20	14.85	6.20	1.60	9.58	5.01	0.21	0.42	0.09	31.96	0.01	0.02	0.02	0.03	0.63	ND	0.02	74.86	25.14
	14.0	2.70	14.36	6.23	1.35	9.85	5.05	0.21	0.41	0.11	32.84	0.01	0.02	0.01	0.03	0.65	0.01	0.02	73.86	26.14
	17.5	4.18	14.93	6.35	1.57	9.63	4.95	0.21	0.41	0.11	32.93	0.01	0.02	0.01	0.03	0.66	ND	0.02	76.02	23.98
	22.5	4.71	13.76	5.92	1.40	9.89	5.01	0.23	0.41	0.09	32.61	0.01	0.02	0.02	0.03	0.65	ND	0.02	74.78	25.22
	30.0	4.01	14.53	5.85	2.12	9.41	5.27	0.23	0.42	0.11	34.50	0.01	0.02	0.01	0.03	0.63	ND	0.02	77.18	22.82
	40.0	4.39	14.13	5.55	1.92	9.41	5.25	0.23	0.42	0.09	33.98	0.01	0.02	0.01	0.01	0.66	ND	0.02	76.14	23.86
	50.0	4.46	14.02	5.70	2.02	9.35	5.27	0.23	0.42	0.11	34.21	0.01	0.02	0.01	0.03	0.65	ND	0.02	76.54	23.46
Fully treated	1.0	4.56	13.42	5.24	1.67	8.12	3.65	0.18	0.39	0.09	34.36	0.01	0.02	0.02	0.01	0.58	ND	0.02	72.35	27.65
	5.0	5.64	14.66	5.30	1.60	8.42	4.25	0.20	0.44	0.09	37.69	0.01	0.02	0.02	0.01	0.53	ND	0.02	78.90	21.10
	7.5	5.31	15.83	5.51	1.82	8.97	4.39	0.20	0.45	0.09	38.87	0.01	0.02	0.02	0.01	0.55	ND	0.02	82.09	17.91
	10.0	4.20	14.59	5.33	1.22	8.94	4.40	0.21	0.45	0.11	38.37	0.01	0.02	0.02	0.01	0.55	0.01	0.02	78.48	21.52
	12.5	5.97	14.98	5.27	1.67	9.16	4.44	0.21	0.44	0.09	37.83	0.01	0.02	0.02	0.01	0.51	ND	0.02	80.67	19.33
	15.0	2.77	14.15	4.97	1.75	8.62	4.49	0.21	0.47	0.09	37.92	0.01	0.02	0.02	0.01	0.59	0.01	0.02	76.15	23.85
	17.5	3.15	14.28	5.04	1.45	8.94	4.58	0.21	0.48	0.09	37.87	0.01	0.02	0.02	0.01	0.61	ND	0.02	76.81	23.19
	25.0	3.13	12.21	4.87	1.80	11.09	4.76	0.23	0.47	0.09	37.89	0.01	0.03	0.02	0.03	0.62	0.01	0.02	77.30	22.70
	30.0	5.14	12.21	4.89	1.50	11.22	4.73	0.25	0.45	0.09	38.40	0.01	0.03	0.02	0.01	0.58	0.01	0.03	79.60	20.40
	40.0	5.02	11.73	4.85	1.15	11.60	4.87	0.25	0.45	0.11	38.54	0.01	0.03	0.02	0.01	0.61	ND	0.02	79.30	20.70
	50.0	3.93	11.37	4.69	1.05	11.40	4.69	0.23	0.44	0.09	36.93	0.01	0.03	0.02	0.01	0.59	0.01	0.02	75.53	24.47
Partially Treated	1.0	4.31	15.02	5.42	1.15	11.21	4.09	0.21	0.37	0.11	35.74	0.01	0.02	0.01	0.01	0.43	ND	0.01	78.13	21.87
	3.5	3.35	15.21	5.73	1.57	11.77	4.27	0.23	0.39	0.09	36.26	0.01	0.02	0.01	0.01	0.47	ND	0.02	79.43	20.57
	5.0	5.42	16.10	5.38	1.27	11.03	3.92	0.23	0.41	0.11	39.67	0.01	0.02	0.01	0.01	0.42	ND	0.02	84.04	15.96
	7.5	5.79	15.78	5.26	1.40	10.38	3.69	0.23	0.41	0.11	43.91	0.01	0.02	0.01	0.01	0.39	ND	0.01	87.41	12.59
	10.0	4.84	15.32	5.79	1.22	12.01	4.40	0.25	0.39	0.11	35.11	0.01	0.02	0.01	0.01	0.51	ND	0.02	80.05	19.95
	13.5	3.17	13.77	5.29	1.25	11.66	4.47	0.23	0.39	0.09	32.20	0.01	0.02	0.01	0.01	0.54	ND	0.02	73.15	26.85
	17.0	4.20	14.02	5.37	1.35	11.59	4.57	0.25	0.39	0.09	32.51	0.01	0.02	0.01	0.01	0.55	ND	0.02	74.98	25.02
	20.5	3.75	14.91	5.88	1.50	12.68	4.63	0.23	0.41	0.11	34.64	0.01	0.02	0.02	0.03	0.55	ND	0.02	79.39	20.61
	30.0	4.48	14.66	5.43	1.72	12.60	4.47	0.25	0.39	0.11	33.37	0.01	0.02	0.01	0.01	0.54	ND	0.02	78.11	21.89
	40.0	3.30	14.93	5.25	1.42	11.21	4.46	0.23	0.39	0.09	33.76	0.01	0.02	0.01	0.01	0.50	0.01	0.02	75.63	24.37
	50.0	4.68	15.91	5.93	1.25	11.03	4.31	0.27	0.39	0.09	36.17	0.01	0.02	0.01	0.01	0.50	ND	0.02	80.61	19.39

*LE, light elements, calculated by subtraction of oxides from 100%. Includes 5-10% Na_2O and 7-13% LOI, typical for bauxite residue. [8]

Table S6. Concentrations of extracted DNA as a function of depth and bauxite residue treatment, normalised to dry weight of bauxite residue.

Treatment site	Depth cm	DNA µg g^{-1}	Uncertainty µg g^{-1}
Untreated	1.0	0.02	< 0.01
	2.0	2.33	0.06
	3.5	0.94	0.02
	5.0	0.22	0.01
	5.0	0.72	0.02
	7.5	0.19	0.01
	10.0	0.34	0.01
	11.0	0.02	< 0.01
	13.5	0.17	< 0.01
	17.0	0.36	0.01
	19.0	0.02	< 0.01
	20.5	0.45	0.01
	30.0	0.01	< 0.01
	40.0	0.03	< 0.01
	50.0	0.04	< 0.01
Fully Treated	1.0	12.75	0.33
	2.0	13.53	0.35
	5.0	11.60	0.30
	5.0	14.35	0.38
	7.5	3.17	0.08
	10.0	0.65	0.02
	11.0	9.81	0.26
	11.5	7.39	0.19
	14.0	0.33	0.01
	17.5	0.13	< 0.01
	19.0	0.06	< 0.01
	22.5	0.10	< 0.01
	30.0	0.07	< 0.01
	40.0	0.45	0.01
	50.0	0.28	0.01
Partially Treated	2.0	13.97	0.37
	5.0	10.24	0.27
	11.0	9.30	0.24
	19.0	0.31	0.01

Table S7. Bacterial community composition within samples. Values are relative abundance of taxa at the Phylum level (bold type) and Class/Order/Genus, as labelled. Data shown in Figure S2.

Classification	Fully treated	Partially treated	
	2 cm	2 cm	5 cm
Acidobacteria	**35.9**	**32.8**	**42.5**
Acidobacteria Gp1	-	< 0.01	0.01
Acidobacteria Gp2	-	< 0.01	0.09
Acidobacteria Gp3	0.07	0.36	0.32
Acidobacteria Gp4	1.58	7.75	11.17
Acidobacteria Gp5	0.10	0.01	0.04
Acidobacteria Gp6	18.58	17.07	16.67
Acidobacteria Gp7	0.07	0.14	0.07
Acidobacteria Gp10	0.01	< 0.01	< 0.01
Acidobacteria Gp11	-	< 0.01	-
Acidobacteria Gp15	-	< 0.01	-
Acidobacteria Gp16	11.61	5.74	7.33
Acidobacteria Gp17	3.09	1.57	6.47
Acidobacteria Gp18	0.23	0.09	0.10
Acidobacteria Gp20	0.01	< 0.01	0.01
Acidobacteria Gp22	0.02	-	-
Other Acidiobacteria	0.52	0.05	0.20
Actinobacteria	**20.5**	**20.1**	**16.2**
Acidimicrobiales	1.94	1.82	1.22
Actinomycetales	11.66	12.39	10.87
Gaiellales	1.91	1.15	0.79
Solirubrobacterales	1.02	2.17	0.80
Other Actinobacteria	3.97	2.55	2.58
Bacteroidetes	**1.2**	**3.7**	**1.0**
Cytophagia	0.62	1.10	0.37
Flavobacteriia	0.06	0.63	0.03
Sphingobacteriia	0.46	1.74	0.46
Other Bacteroidetes	0.02	0.22	0.19
Candidate Division WPS-1	**1.4**	**2.6**	**1.3**
Candidatus Saccharibacteria	**2.5**	**1.7**	**2.6**
Chloroflexi	**2.0**	**1.2**	**2.6**
Anaerolineae	0.01	< 0.01	0.01
Caldilineae	0.01	< 0.01	< 0.01
Chloroflexia	< 0.01	< 0.01	< 0.01
Ktedonobacteria	-	< 0.01	-
Thermomicrobia	-	< 0.01	< 0.01
Other Chloroflexi	< 0.01	< 0.01	0.01

The left margin labels (vertical): Class (for Acidobacteria subgroups), Order (for Actinobacteria), Class (for Bacteroidetes), Class (for Chloroflexi).

Table S7 Cont.

	Classification	Fully treated	Partially treated	
		2 cm	2 cm	5 cm
Planctomycetes		**14.7**	**14.2**	**12.6**
Genus	*Aquisphaera*	-	0.05	0.02
	Blastopirellula	0.17	0.29	0.23
	Gemmata	0.86	0.63	0.36
	Gimesia	-	< 0.01	-
	Pirellula	1.47	1.09	2.40
	Planctomicrobium	0.31	0.05	0.12
	Planctopirus	0.05	0.33	0.17
	Rhodopirellula	0.01	0.09	0.02
	Rubinisphaera	0.02	0.02	< 0.01
	Singulisphaera	0.12	0.20	0.08
	Telmatocola	-	0.03	-
	Tepidisphaera	-	< 0.01	-
	Thermogutta	0.01	0.14	0.12
	Zavarzinella	0.68	0.45	0.29
	Other Planctomycetaceae	10.96	10.81	8.80
Proteobacteria		**18.5**	**17.4**	**17.8**
Class	*Alphaproteobacteria*	13.05	9.91	13.04
	Betaproteobacteria	2.71	3.39	2.22
	Deltaproteobacteria	0.84	1.26	0.81
	Gammaproteobacteria	1.34	2.56	1.23
	Oligoflexia	-	0.04	-
	Other Proteobacteria	0.53	0.25	0.54
Verrucomicrobia		**1.9**	**5.5**	**2.1**
Class	*Opitutae*	0.07	0.16	< 0.01
	Spartobacteria	1.16	3.56	1.63
	Subdivision3	0.21	0.23	0.04
	Verrucomicrobiae	0.21	0.31	0.27
	Other Verrucomicrobia	0.28	1.22	0.15
Other Bacteria		**1.35**	**0.71**	**1.05**

Table S8. Alpha diversity indices for each microbiological sample. $D_0{}^\alpha$, OTU richness; $D_1{}^\alpha$, a measure of the number of common species and equivalent to the exponential of Shannon entropy; $D_2{}^\alpha$, a measure of the number of dominant species and is equivalent to the inverse of Simpson concentration.

Depth	Untreated			Fully treated			Partially treated		
cm	$D_0{}^\alpha$	$D_1{}^\alpha$	$D_2{}^\alpha$	$D_0{}^\alpha$	$D_1{}^\alpha$	$D_2{}^\alpha$	$D_0{}^\alpha$	$D_1{}^\alpha$	$D_2{}^\alpha$
2	IR	IR	IR	1253	424	150	3832	750	240
5	IR	IR	IR	IR	IR	IR	2125	337	64
11	IR	IR	IR	IR	IR	IR	IR	IR	IR

IR: Insufficient DNA recovery

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