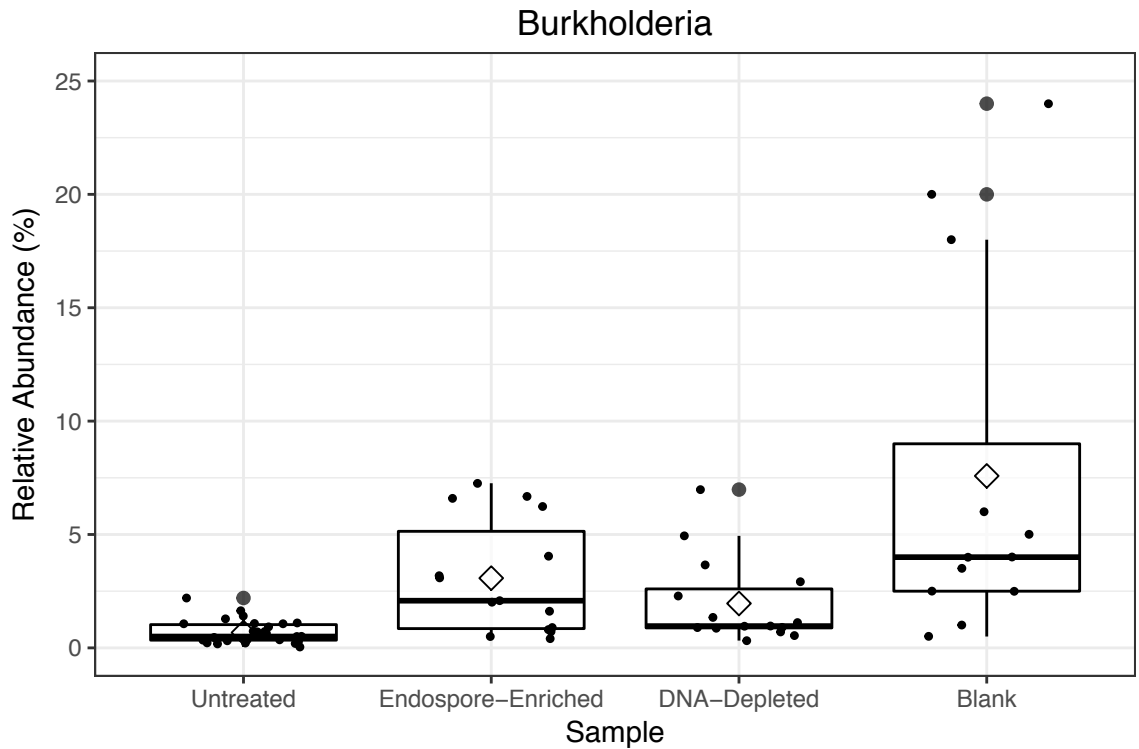
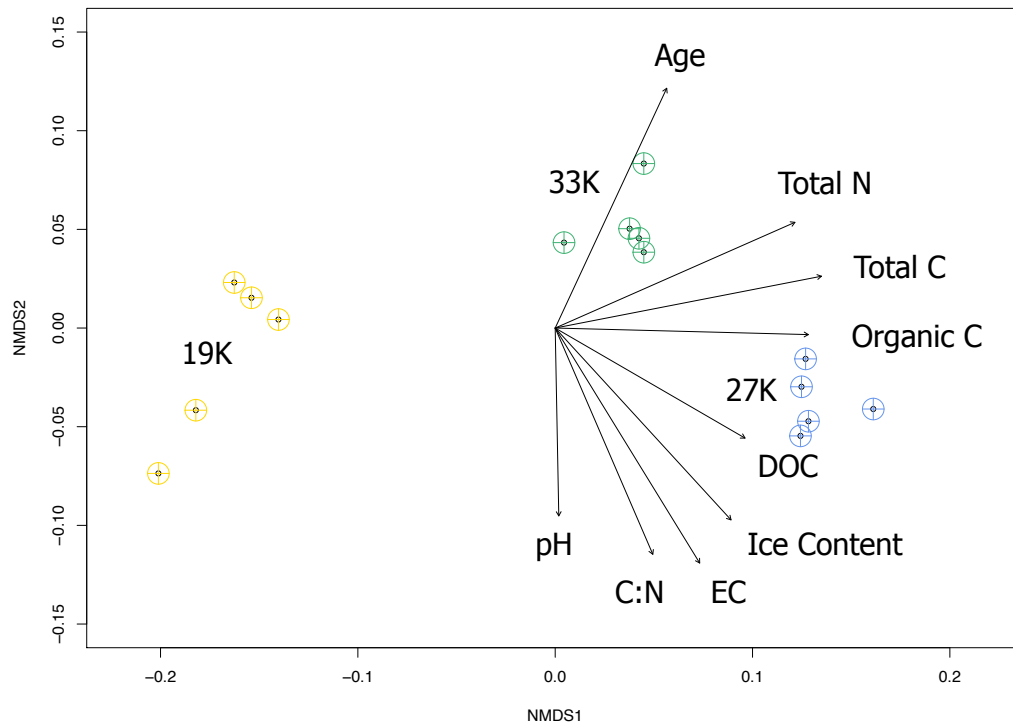


1 **Supplementary Material**



2

3 **Figure S1.** Relative abundance of the genera *Burkholderia* based on 16S rRNA gene
4 sequences. This OTU was only abundant in samples with very low DNA yields (blank
5 controls as well as endospore-enriched and DNA-depleted samples from the oldest time
6 point) indicating it was likely the result of contamination. Therefore, this OTU was
7 removed from subsequent analyses.



8

9 **Figure S2.** Non-metric multidimensional scaling (NMDS) based on weighted Unifrac

10 values of 16S rRNA gene sequences.

11 **Table S1.** Table of barcodes used on the 806R primer for each sample during
 12 multiplexed sequencing.

SampleID	BarcodeSequence	LinkerPrimerSequence	Treatment	Age
D.19K6	TGTGTAGCCATG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	19K
D.19K7	GAGCATTACATG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	19K
D.19K8	CGGAGAGACATG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	19K
D.19K9	AGTCATCGAATG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	19K
D.19K10	CAGCAGTCTTCG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	19K
D.27K6	AGTGTGCGATTCG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	27K
D.27K7	TGTCAGCTGTGCG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	27K
D.27K8	AATAGCATGTGCG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	27K
D.27K9	AACACTCGATCG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	27K
D.27K10	TCTGGTGCATCG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	27K
D.33K6	TTGACGACATCG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	33K
D.33K7	ATAACATGTGCG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	33K
D.33K8	ATAGACTCCG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	33K
D.33K9	TGTACATCGCCG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	33K
D.33K10	AGTAGACTTACG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	33K
D.Blank	GATAACTGTACG	GGACTACHVGGGTWTCTAAT	Endospore-Enriched	Blank
DC.19K6	GACATTGTCACG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	19K
DC.19K7	GGAGAGATCACG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	19K
DC.19K8	TGATAATGCACG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	19K
DC.19K9	CTGATGTACACG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	19K
DC.19K10	CACCTGTAGTAG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	19K
DC.27K6	CGATATCAGTAG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	27K
DC.27K7	AGTGC GTTCTAG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	27K
DC.27K8	AAGAGTCTCTAG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	27K
DC.27K9	CTGCATACTGAG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	27K
DC.27K10	ACTGTACATGAG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	27K
DC.33K6	TCTCATGTGGAG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	33K
DC.33K7	AGACAGTAGGAG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	33K
DC.33K8	CTGTCGTGTCAG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	33K
DC.33K9	CGCGTATCTCAG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	33K
DC.33K10	GACTCTGCTCAG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	33K
DC.Blank	TAAGTACTGCAG	GGACTACHVGGGTWTCTAAT	NonEnriched-Control	Blank
V.19K6	TCACAGACAATG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	19K
V.19K7	ACGATCATCTGG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	19K
V.19K8	TGCATACACTGG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	19K
V.19K9	AGCTATGTATGG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	19K

V.19K10	ACACATAAGTCG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	19K
V.27K6	GCGTAACTCTCG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	27K
V.27K7	ATGTGCTGCTCG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	27K
V.27K8	TACTGAGCCTCG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	27K
V.27K9	TTCTAGAGTGCG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	27K
V.27K10	AGTCTGTCTGCG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	27K
V.33K6	TATACCGCTGCG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	33K
V.33K7	GATCCTCATGCG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	33K
V.33K8	CAGTCTAGTACG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	33K
V.33K9	GCACGTTCTACG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	33K
V.33K10	TTCGCAGATACG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	33K
V.Blank	ATACAGCATACG	GGACTACHVGGGTWTCTAAT	DNA-Depleted	Blank
VC.19K6	CCTGATCACACG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	19K
VC.19K7	GCTCTAGTAACG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	19K
VC.19K8	GTGTACATAACG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	19K
VC.19K9	TCTATGCGAACG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	19K
VC.19K10	GATGTTGCTAG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	19K
VC.27K6	CTAGTGACCTAG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	27K
VC.27K7	TCAGCTGACTAG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	27K
VC.27K8	ACACGACTATAG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	27K
VC.27K9	CGTACTCTCGAG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	27K
VC.27K10	GATCTAATCGAG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	27K
VC.33K6	TATATGTGCGAG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	33K
VC.33K7	CTACTCCACGAG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	33K
VC.33K8	TCTTCGCAGCAG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	33K
VC.33K9	CTATGAGTCCAG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	33K
VC.33K10	GTCATGCTCCAG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	33K
VC.Blank	TCATACAGCCAG	GGACTACHVGGGTWTCTAAT	NonDepleted-Control	Blank

14 **Table S2.** Average percent difference in relative abundance between the endospore-enriched samples and non-enriched controls
 15 across the three age categories. A negative value shows underrepresentation in the endospore-enriched sample compared to the non-
 16 enriched control while a positive value shows overrepresentation. Values are averages of five replicate cores. U-value is a test statistic
 17 generated during a Mann-Whitney-Wilcoxon test which represents the level of difference between two groups. Lower U-values
 18 indicate that two groups are more different.

Taxa	19K (%)	U-value	27K (%)	U-value	33K (%)	U-value
Proteobacteria	-4.3 ± 2.2	6	-4.0 ± 0.3 **	0	-6.2 ± 2.1	5
Alphaproteobacteria	3.6 ± 0.7	6	-3.8 ± 0.3 **	0	-0.6 ± 0.3	9
Deltaproteobacteria	-8.8 ± 0.3 **	0	-0.2 ± 0.1 *	1.5	-6.0 ± 0.7 **	0
Bacteroidetes	-3.9 ± 0.7 **	0	0.0 ± 0.0	4.5	-2.9 ± 0.9 **	0
Acidobacteria	-3.2 ± 0.3 *	0	-0.1 ± 0.0 *	1.5	-0.1 ± 0.1	4.5
Chloroflexi	-1.4 ± 0.3 **	0	-0.6 ± 0.1 **	0	-0.1 ± 0.1	7
Planctomycetes	-1.3 ± 0.1 **	0	-0.8 ± 0.1 *	0	-0.3 ± 0.1	4

(Mann-Whitney-Wilcoxon test, ** = p < 0.01, * = p < 0.05)