

**Supplemental Table 1**

<b>Sample Method</b>	<b>Sequence Depth (Gbp)</b>	<b>Total Reads (million)</b>	<b>Bacterial Reads (%)</b>
Biopsy	2.04±0.47	14.5±7.2	26.5±11.5
Cytology Brush	4.22±3.03	41.7±31.9	59.1±23.9*

Mean number ± SD of gigabase pairs sequenced (Gbp), sequenced reads (in millions) after removal of poor quality reads, and bacterial percentage of reads following metatranscriptomics sequencing comparing pinch biopsy and cytology brush methods. N=5 samples per group. \*, P<0.05 as determined by Student's t-test comparing biopsy to cytology brush.

**Supplemental Table 2**

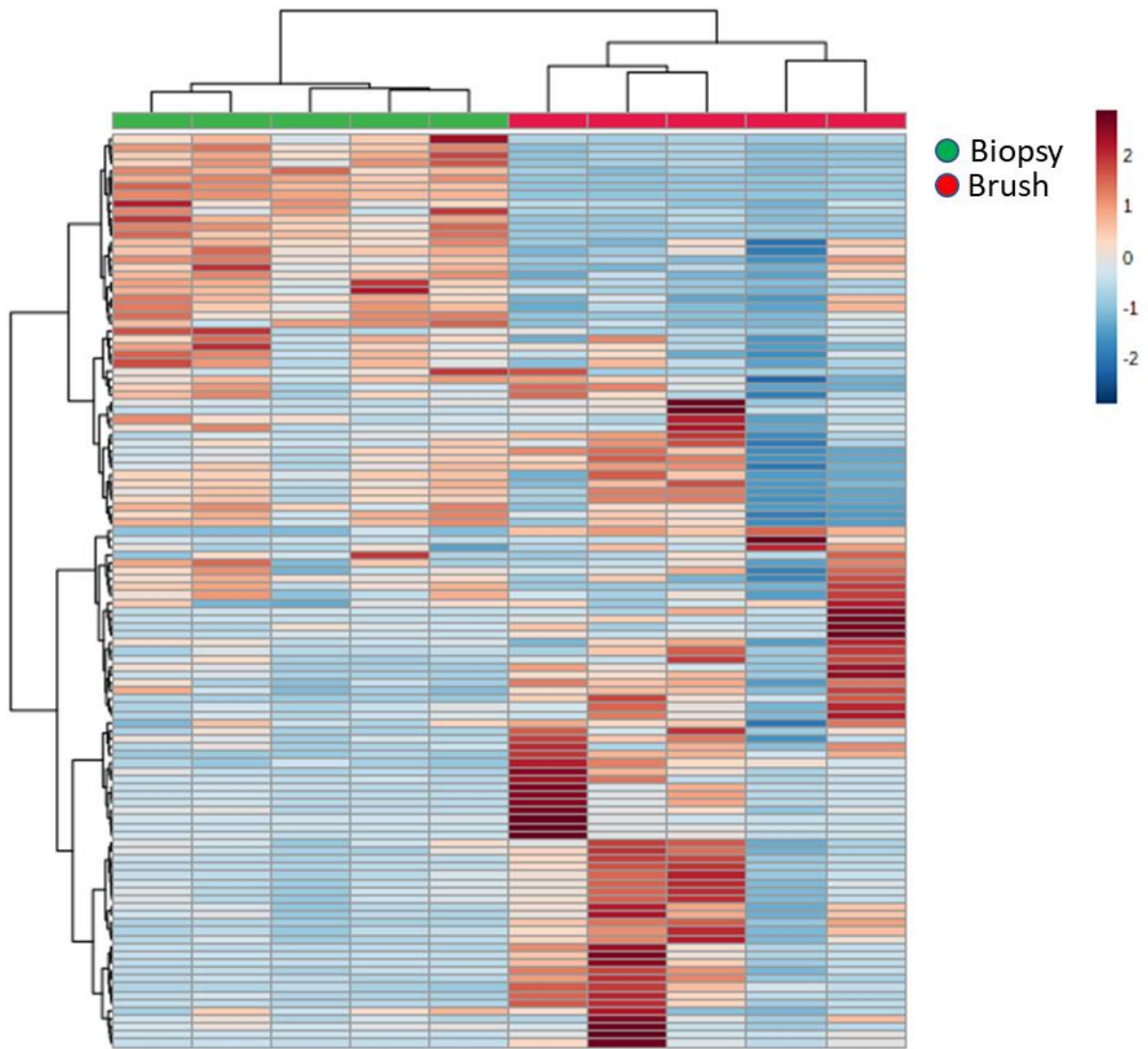
Class	Mean $\pm$ SEM (%)		P value
	Biopsy	Cytology Brush	
Methanobacteria	1.08 $\pm$ 2.42	1.66 $\pm$ 3.71	0.778
Actinobacteria	56.11 $\pm$ 21.16	22.26 $\pm$ 14.88	<b>0.019</b>
Bacteroidia	2.21 $\pm$ 4.95	11.58 $\pm$ 14.89	0.219
Bacilli	29.35 $\pm$ 5.43	10.82 $\pm$ 11.33	<b>0.011</b>
Clostridia	4.11 $\pm$ 7.32	47.71 $\pm$ 10.84	<b>0.00007*</b>
Negativicutes	0.80 $\pm$ 1.78	1.28 $\pm$ 2.85	0.757
Betaproteobacteria	0.03 $\pm$ 0.05	1.28 $\pm$ 2.55	0.306
Deltaproteobacteria	0.00 $\pm$ 0.00	0.65 $\pm$ 1.45	0.346
Epsilonproteobacteria	0.00 $\pm$ 0.00	0.07 $\pm$ 0.16	0.346
Gammaproteobacteria	6.31 $\pm$ 7.00	2.68 $\pm$ 2.32	0.304

Top 10 bacterial classes identified as different between the two collection methods. Data shown as mean  $\pm$  SEM. Three classes noted to be significantly different with p-value <0.05 and one with FDR <0.05 as indicated by the asterisk.

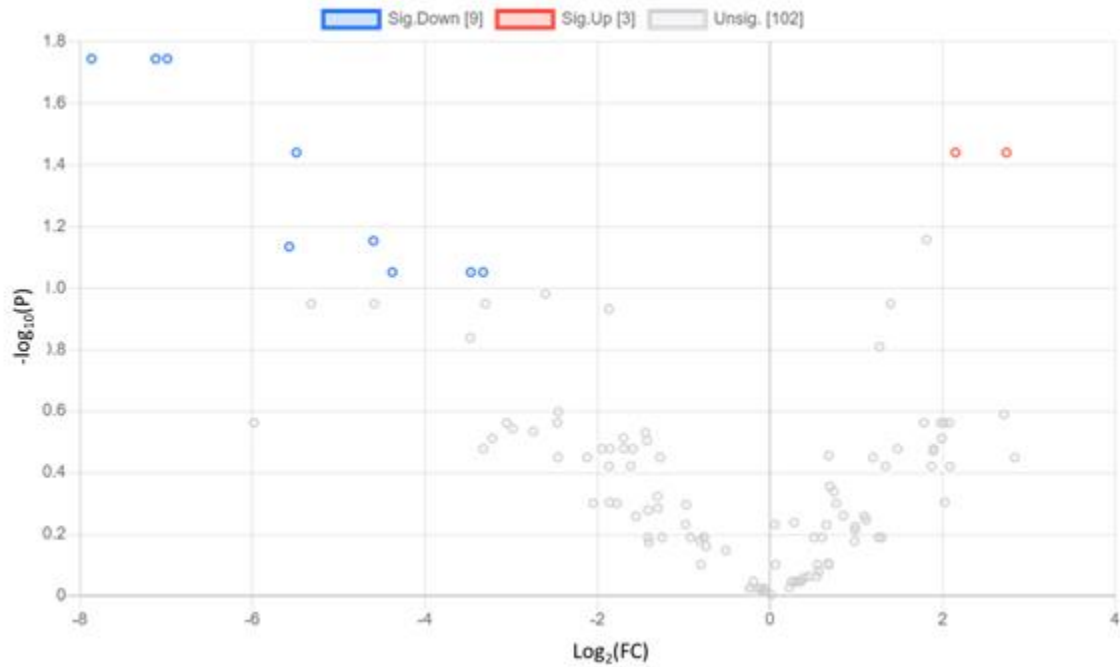
**Supplemental Table 3**

Species	Mean $\pm$ SEM (%)		P-value
	Biopsy	Cytology Brush	
Faecalibacterium prausnitzii	2.27 $\pm$ 3.36	17.37 $\pm$ 11.62	<b>0.023</b>
Fingoldia magna	0.00 $\pm$ 0.00	12.49 $\pm$ 19.77	0.195
Methanobrevibacter unclassified	1.08 $\pm$ 2.42	2.11 $\pm$ 4.72	0.676
Parabacteroides unclassified	1.55 $\pm$ 3.46	8.52 $\pm$ 11.94	0.246
Propionibacterium acnes	53.2 $\pm$ 18.44	13.76 $\pm$ 12.17	<b>0.004*</b>
Pseudomonas unclassified	5.13 $\pm$ 6.44	0.93 $\pm$ 2.07	0.202
Ruminococcus lactaris	0.01 $\pm$ 0.02	3.27 $\pm$ 3.02	<b>0.042</b>
Ruminococcus torques	1.72 $\pm$ 3.84	12.22 $\pm$ 14.01	0.145
Streptococcus thermophilus	32.14 $\pm$ 4.69	13.54 $\pm$ 15.18	<b>0.031</b>
Subdoligranulum unclassified	0.13 $\pm$ 0.29	4.35 $\pm$ 5.54	0.127
Others	2.68 $\pm$ 2.09	11.44 $\pm$ 7.71	<b>0.039</b>

Top 10 bacterial species identified as different between the two collection methods. Data shown as mean  $\pm$  SEM. Four species noted to be significantly different with p-value <0.05 and one with FDR <0.05 as indicated by the asterisk.



**Supplemental Figure 1.** Heat map demonstrating all 114 metabolites comparing the pinch biopsy versus cytology brush collection methods.



**Supplemental Figure 2.** Volcano plot demonstrating 114 metabolites identified as significantly up (red), down (blue), or unchanged (gray) comparing the pinch biopsy versus cytology brush collection method. Significance determined by fold change  $>2.0$  and Wilcoxon signed-rank test with FDR adjusted p-value  $<0.1$ .

**Supplemental Table 4**

<b>Metabolite</b>	<b>Log<sub>2</sub>(FC)</b>	<b>P-value (FDR adjusted)</b>
D-Glucono-1-5-lactone 6-phosphate*	-7.86	0.018
Cys-Gly	-7.12	0.018
alpha-D-Glucosamine 1-phosphate*	-6.98	0.018
5-hydroxytryptophan†	-5.45	0.036
2-Hydroxyglutarate/Citramalate	2.74	0.036
Itaconate	2.15	0.036
L-cysteine	-4.59	0.070
D-Erythrose 4-phosphate	-5.57	0.073
N5-Methyl-L-glutamine	-4.38	0.089
N-Acetyl-L-citrulline	-3.47	0.089
CMP	-3.32	0.089

Metabolites identified as significant (fold change, FC >2.0 and paired-t-test with FDR adjusted p-value <0.1) for comparison between pinch biopsy and cytology brush collection method.