

The Lung Cancer Microbiota and Adjacent Healthy Lung Tissue Microbiota

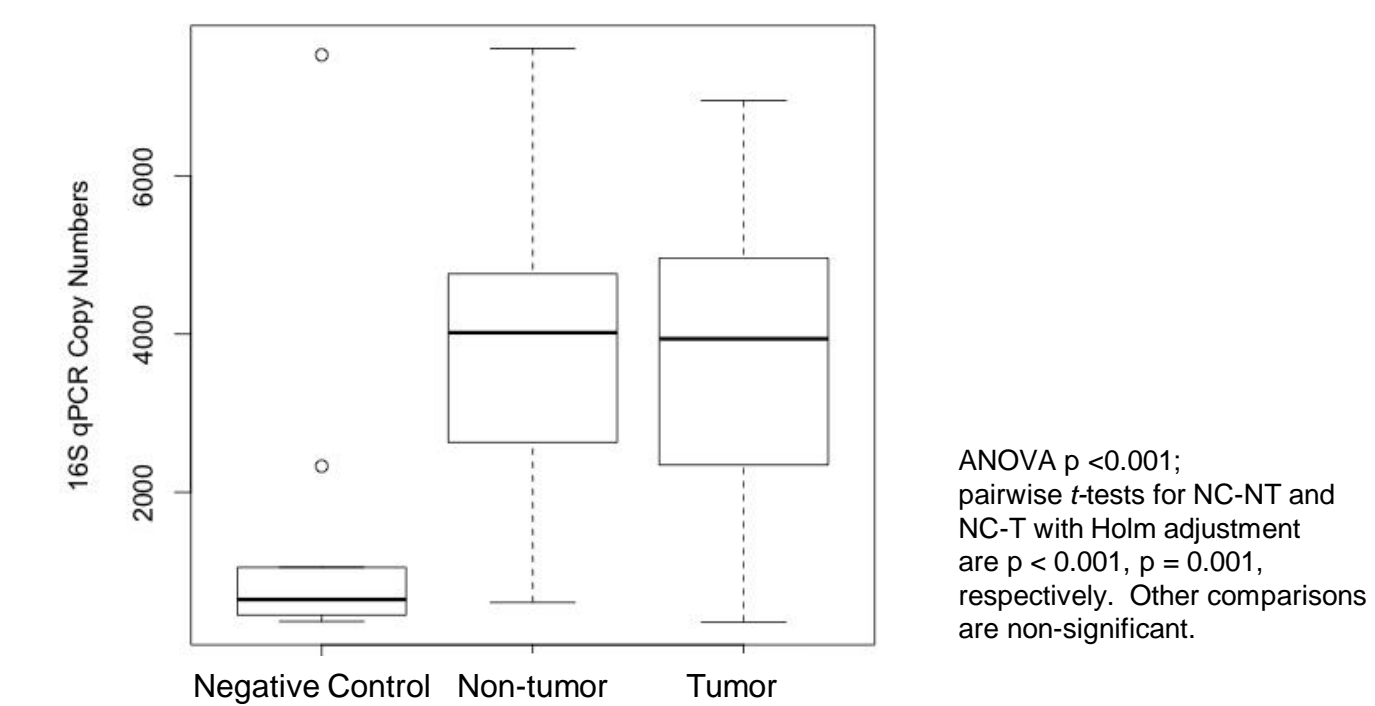
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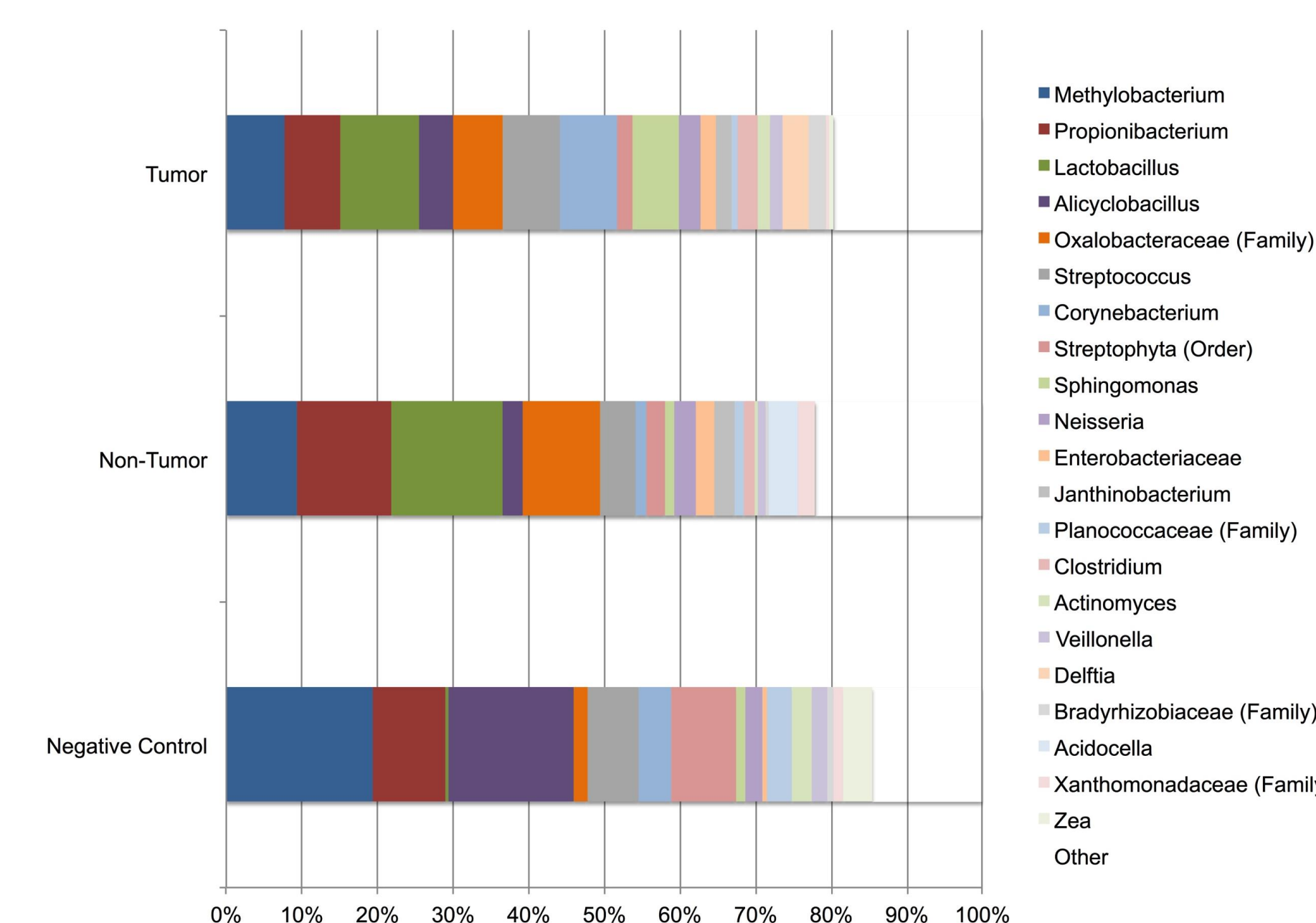
Introduction

- The lung harbors a complex microbiota.
- The lung microbiota has been described in healthy subjects as well as those with chronic inflammatory lung diseases such as COPD.
- Inflammation related to lung malignancy may correlate with changes in the lung tissue microbiota.
- We undertook the present study to describe the lung tumor tissue microbiota in relationship to the adjacent lung microbiota
- Our **hypothesis** is that the lung tumor tissue microbiota is altered in comparison to the adjacent lung tissue microbiota.

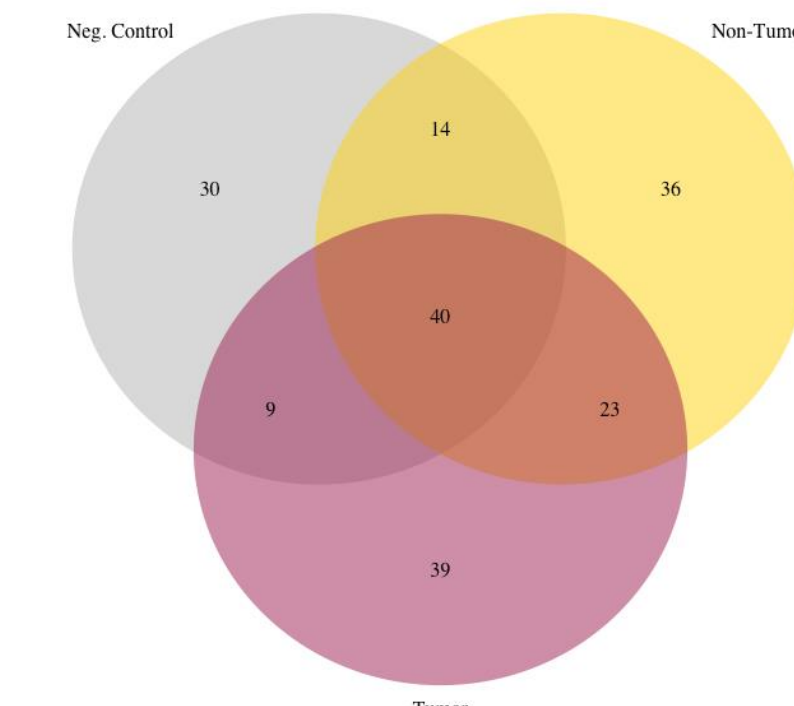
Bacterial DNA Yield



Taxonomy



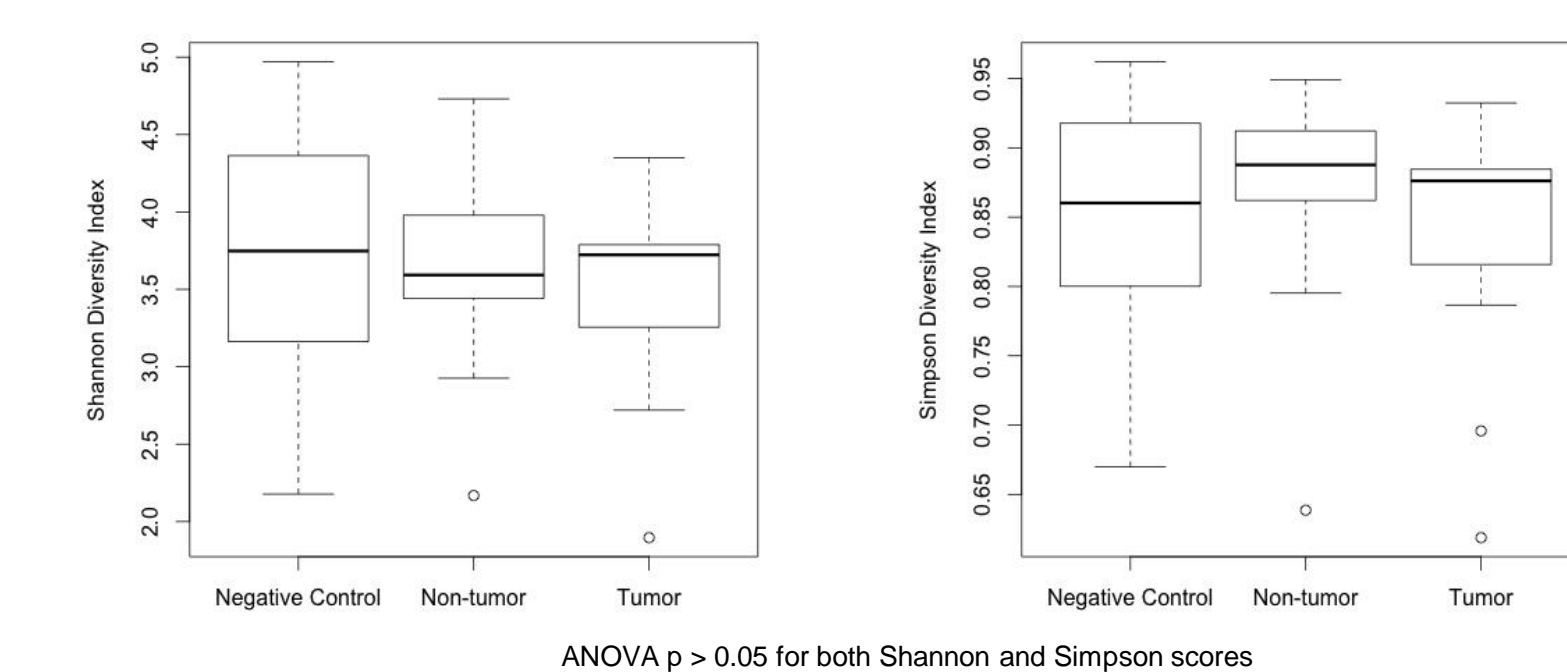
Core Lung Tissue Taxa



Subject Characteristics

- Average age 70
- 70% male
- Average FEV₁ 1.8 L
- COPD severity: 55% GOLD 3/4; 45% GOLD 0/1

No Change in Alpha Diversity



Methods

Samples

- 21 matched pairs of lung tissue samples were obtained per Lung Tissue Research Consortium procedures.
- Each pair of tissue samples consisted of a "tumor" sample obtained from within the tumor or tumor edge and a "non-tumor" sample obtained from unaffected lung at least 5 cm from the tumor.

Sample Processing

- Samples were flash-frozen in liquid nitrogen and maintained at -80° C until DNA extraction using tissue pulverization and mechanical and chemical bacterial lysis.
- Negative control samples were included to evaluate for contamination.

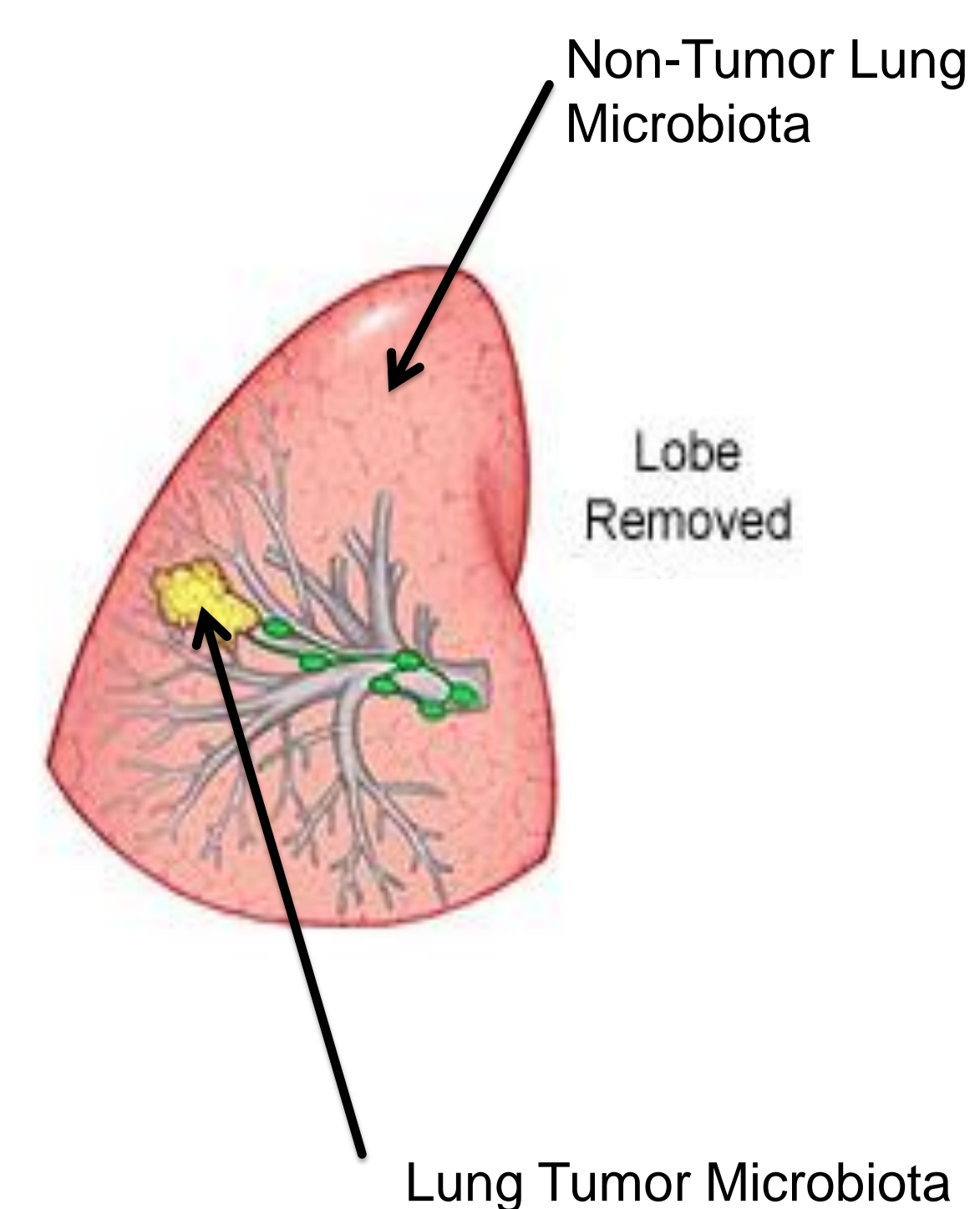
Quantification and Sequencing

- 16S rRNA qPCR was performed to quantify total 16S abundance.
- The 16S rRNA V4 region was sequenced on the Illumina MiSeq at the University of Minnesota.

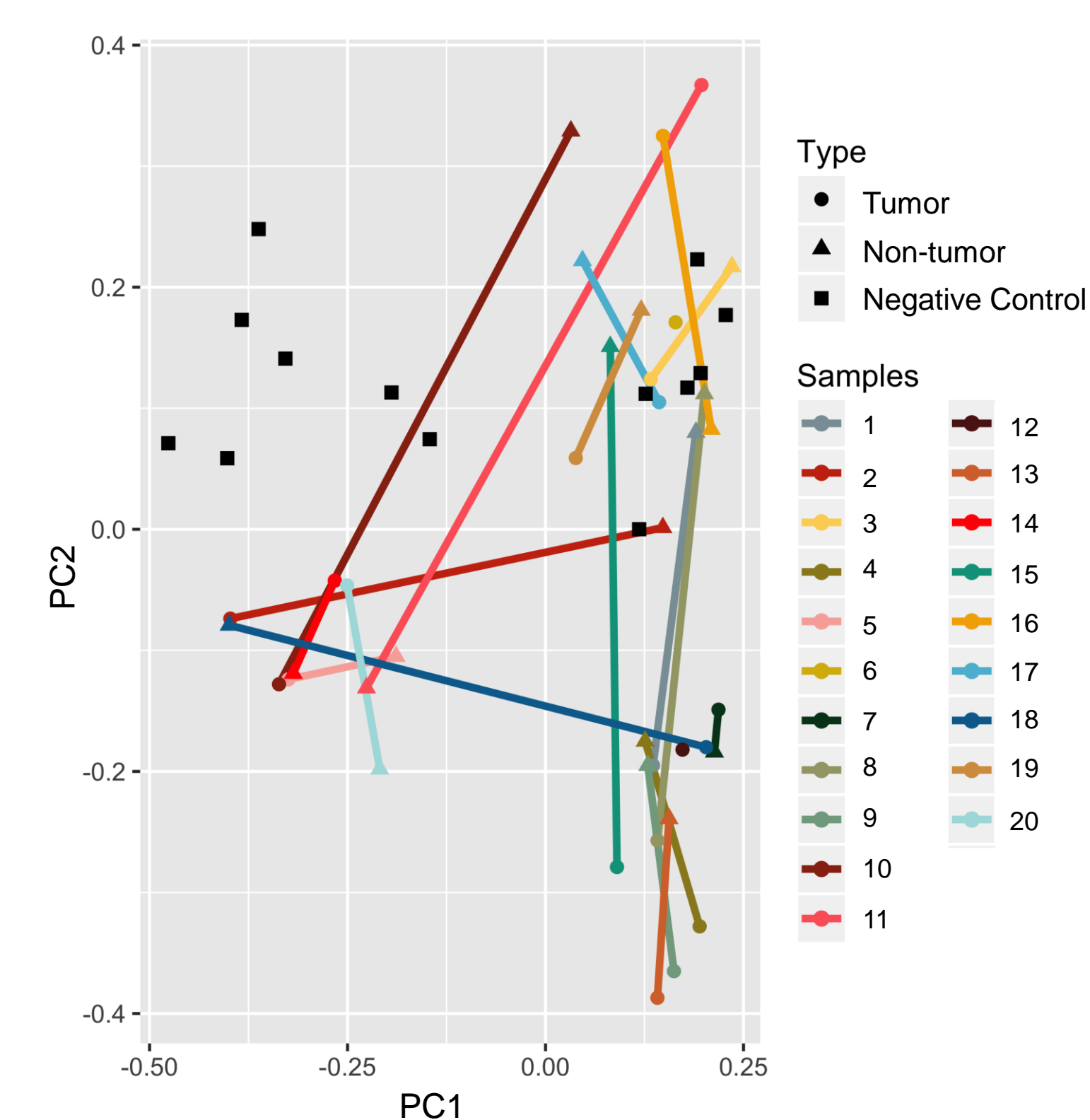
Data Analysis

- Human sequences and contaminating OTUs were removed from the dataset.
- Sequence filtering, denoising, chimera removal, α and β diversity calculations, principal coordinate analysis (PCoA), and taxonomic identification using the Greengenes database were accomplished with QIIME.
- Statistical analyses were carried out in R.

Lung Tissue Samples



Tumor Sample Clustering is Not Observed



Lung Taxa

Lung Only Taxa	Unique to Non-Tumor Lung	Unique to Lung Tumor
Clostridium	<i>Parabacteroides</i>	<i>Fingoldia</i>
<i>S24_7</i> (Family)	<i>Deinococcus</i>	<i>Chryseobacterium</i>
Peptostreptococcaceae (Family)	<i>Actinobacillus</i>	
Clostridiaceae (Family)		
Clostridiales (Order)		
<i>Oscillospira</i>		
<i>Ruminococcus</i>		
SMB53		
Ruminococcaceae (Family)		
Janthinobacterium		
<i>Knoellia</i>		
Burkholderiales (Order)		
Pirellulaceae (Family)		
<i>Dorea</i>		
<i>Escherichia</i>		
<i>Micrococcus</i>		
<i>Campylobacter</i>		
Phyllobacteriaceae (Family)		
<i>Stenotrophomonas</i>		
<i>Selenomonas</i>		
Rhodocyclaceae (Family)		
Streptococcaceae (Family)		
Lachnospiraceae (Family)		

Bolded taxa are found at > 1% relative abundance across all taxa

Conclusions

In our small data set, we did not detect a characteristic lung tumor microbiota

Acknowledgments

This project was supported by Grant Number 11K2CX001095-01A2 from the Veterans Affairs Office of Research and Development (VAORD). Its contents are solely the responsibility of the authors and do not necessarily represent the official views of the VA. Additional funding provided by the University of Minnesota Department of Medicine and Medical School.