• Methods
  – DNA Extraction using MoBio Powersoil Kit
  – Illumina Prep
  – HiSeq Sequencing
  – MetaPhlAn for preliminary analysis

• 124 taxa, 33 species found
  – 18 new species not seen on the subway

• Additional collections in winter 2014 and spring 2015
Taxa Breakdown

- Bacteria, 91%
- Unclassified, 7%
- Archaea, 2%
**Potential Pathogens**

<table>
<thead>
<tr>
<th>Species Breakdown (COGEM)</th>
<th># Species</th>
</tr>
</thead>
<tbody>
<tr>
<td>Opportunistic</td>
<td>2</td>
</tr>
<tr>
<td>Non Opportunistic Pathogens</td>
<td>2</td>
</tr>
<tr>
<td>Non Pathogens</td>
<td>11</td>
</tr>
<tr>
<td>Unknown</td>
<td>18</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>33</strong></td>
</tr>
</tbody>
</table>

**Pseudomonas putidas**

**Propionibacterium acnes**

**Escherichia coli**

**Enterococcus faecalis**
DNA Yield and Species Diversity

<table>
<thead>
<tr>
<th>Contamination Level</th>
<th>AVG DNA Yield</th>
<th>AVG Species</th>
</tr>
</thead>
<tbody>
<tr>
<td>Medium</td>
<td>51.23</td>
<td>8.20</td>
</tr>
<tr>
<td>High</td>
<td>29.40</td>
<td>8.11</td>
</tr>
</tbody>
</table>
**Cornell Team**

- Sequencing
  - Chris Mason
- Data Analysis & Visualization
  - Elizabeth Henaff
  - Ebrahim Afshinnekoo

**Genspace Team**

- Sample Collection & Processing
  - Ellen Jorgensen
  - Eric Fernandez
  - Heather Dewey-Hagborg
- Data Analysis
  - Robert Young

**NBW Team**

- Sample Collection & Data Visualization
  - Ian Quate
  - Tom Woltz
  - Matthew Siebert

- and a host of others...