**Relative abundance findings (anaerobic digester sludge):**

* Highest abundance methanogens:
  1. Acetoclastic
     + Methanosaeta
     + Methanosarcina
  2. Hydrogenotrophic
     + Methanospirillium
     + Methanoculleus
     + Methanoregula
  3. Methylotrophic
     + Methanococcoides
* Highest abundance bacteria:
  1. Clostridium
  2. Treponema
  3. Eubacterium
* Most abundant systems:
  1. Central carbon metabolism
  2. One-carbon metabolism
  3. CO2 fixation
  4. Fermentation
  5. Organic acids

**Relative abundance findings (incoming sewage):**

* Highest abundance methanogens:

1. Methanobrevibacter
2. Methanosarcina

* Highest abundance bacteria:
  1. Acinetobacter
  2. Akkermansia
  3. Trichoccous
  4. Streptococcus

**Overall findings:**

Bacteria are found in a much higher abundance overall than archaea. Incoming sewage has a drastically different community make up than activated sludge. Communities between different digesters can have rather large differences. Acinetobacter is consistently the most prevalent organism even between sewage from different sources.