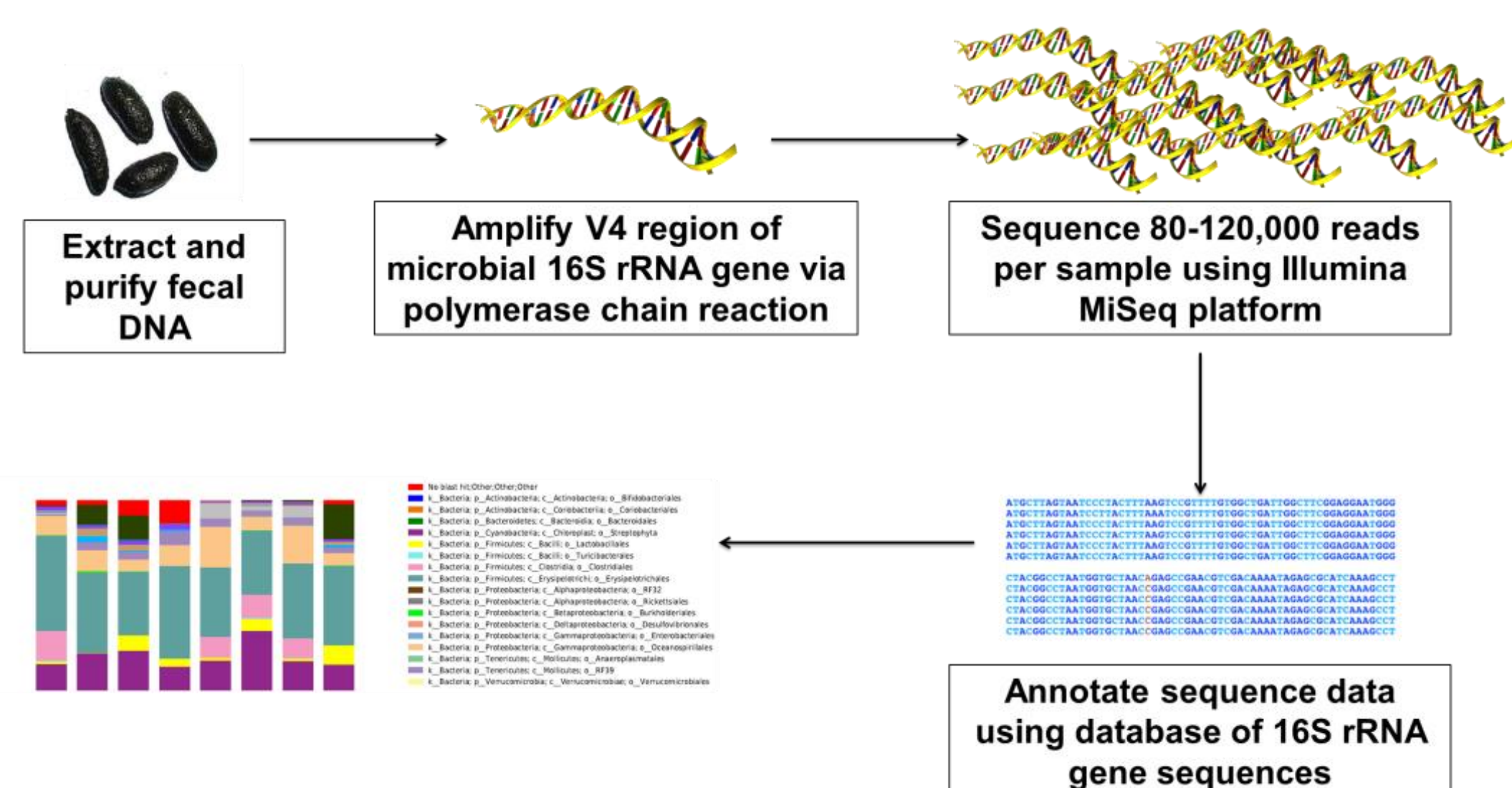


Background

- The gut microbiota (GM) of most species studied to date has been shown to benefit host health by aiding in digestion, immune system development and disease resistance to pathogens.
- Millions of domestic cats are housed in shelters each year and these cats are exposed to many unique factors that may predispose them to disease.
- Study of the feline GM is in its infancy and it is largely unknown how composition and/or complexity change in environmental factors or disease states often encountered in shelter housing.
- Our study aims to characterize the GM of shelter felines exposed to a variety of environmental factors and disease states, as well as compare the GM of shelter felines to client owned felines.

Methods

- Fecal samples obtained from litter boxes of cats handled for brief examination.
- Approximately 100 shelter felines and 20 client owned felines assessed for various parameters including: age, sex, disease states (oral, dermatological, ocular, aural, upper respiratory, and retroviral), daily enrichment, adequate housing size, housing density, diet, vaccinations received, behavior/stress, body condition, and fecal consistency.
- DNA extracted from fecal samples and subjected to next generation sequencing and Qime analysis to categorize microbiota as shown below:



- For microbiota analysis, OTUs with reads of less than 10,000 were excluded from the data set. Stacked bar charts were generated with Microsoft Excel and principal component analysis (PCA) plots generated with Paleontological Statistics Software Package for Education and Data Analysis (PAST). Bar charts were visually inspected for consistency between samples and PCAs were inspected for clustering of samples within groups. Differences in beta-diversity were analyzed by PERMANOVA in PAST. Richness was calculated in Excel and alpha diversity was computed based on Chao1 indices. Two-tailed student's t-tests were performed on the latter using SigmaPlot.

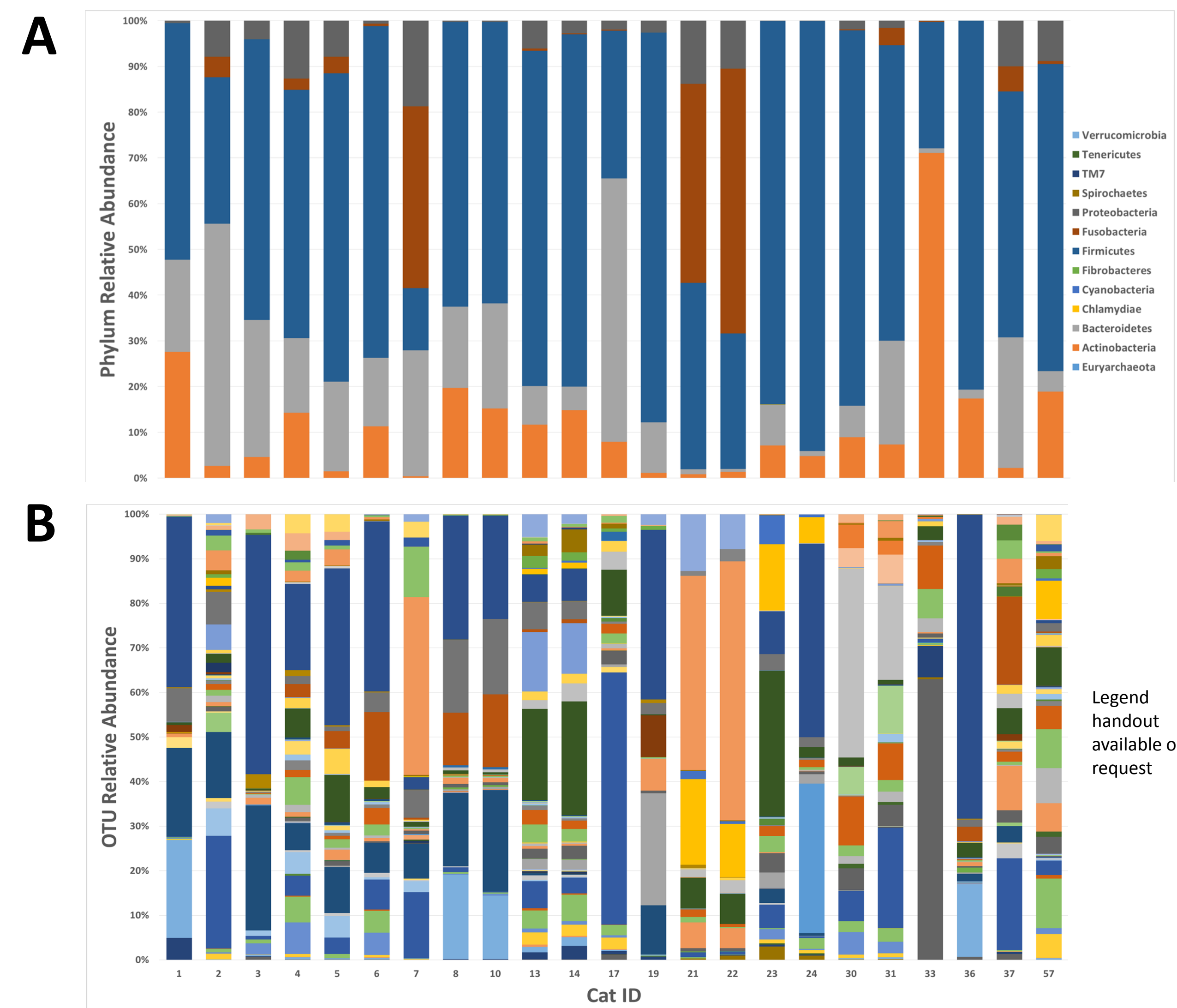


Figure 1: Stacked bar charts of initial 18 samples showing marked variation in GM at all phylogenetic levels from phylum (A) to operational taxonomic unit / species (B).

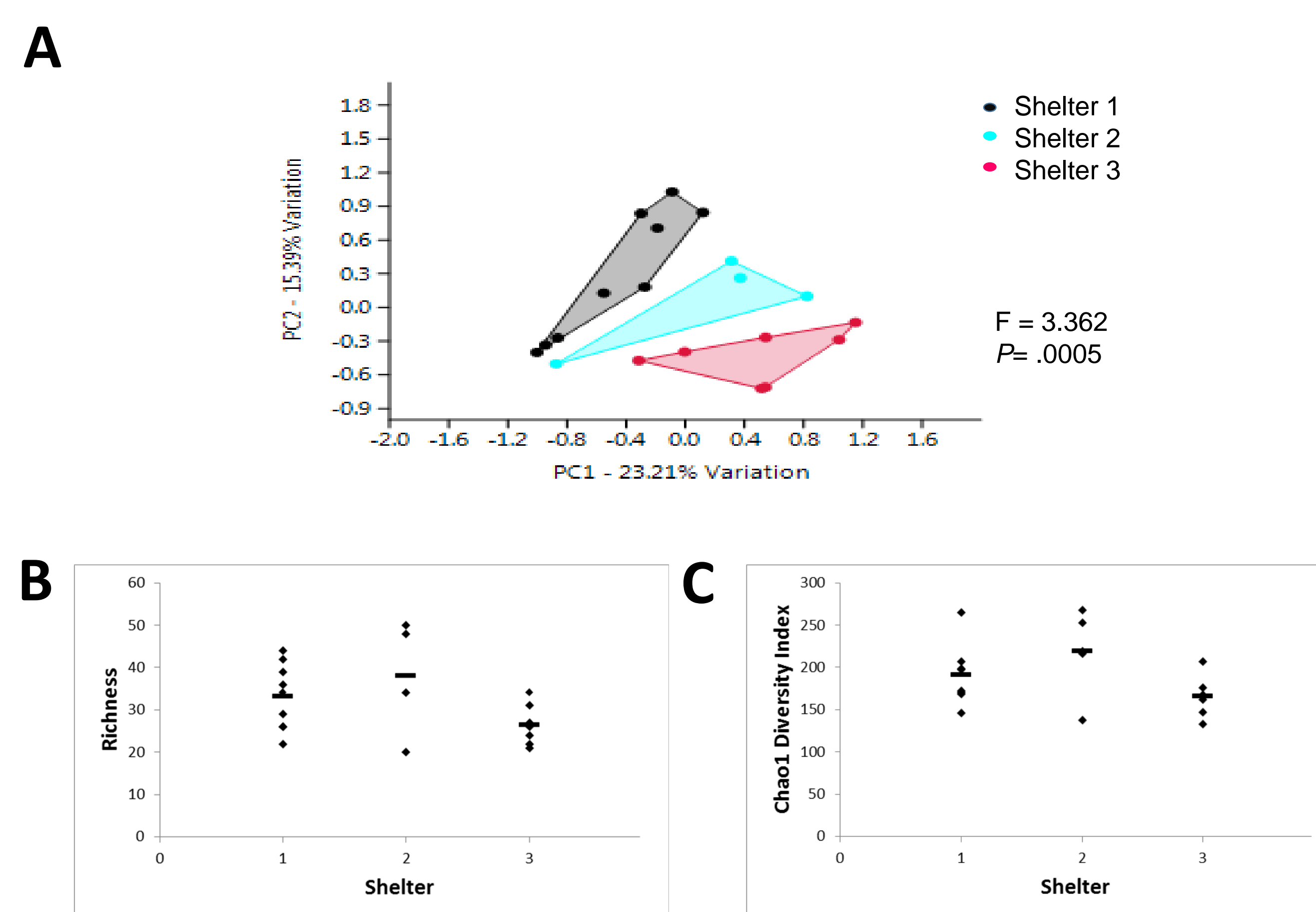


Figure 2: Analysis of samples collected at three separate shelters. A) Principal component analysis shows distinct clustering of samples taken at each location. PERMANOVA analysis revealed statistically significant differences between shelter 1 and 3 (Shelter 1 vs 2 $p=.0394$, Shelter 1 vs 3 $p=.0002$, Shelter 2 vs 3 $p=.0573$). No significant differences were seen in richness (B) or diversity (C).

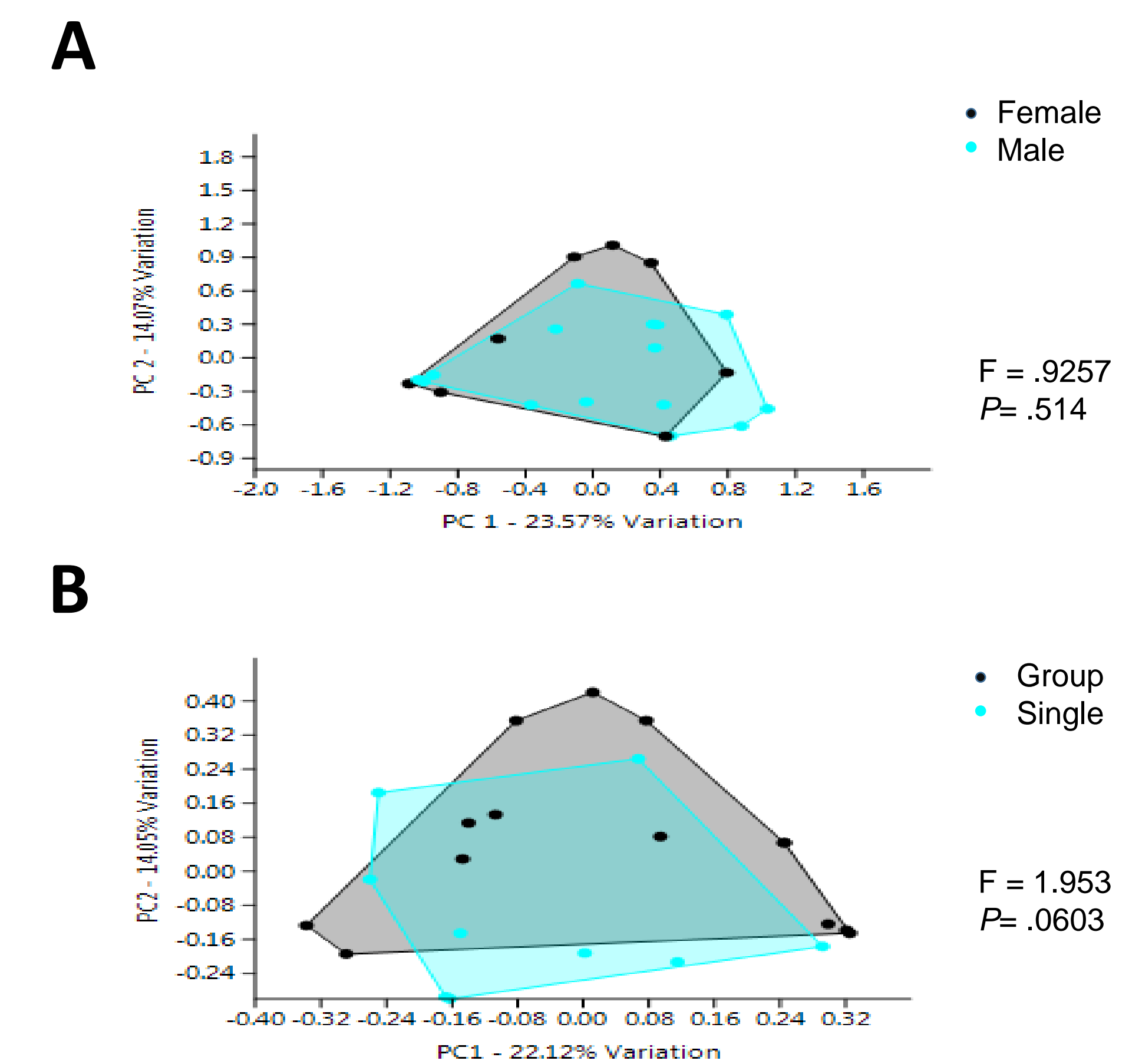


Figure 3: Principal component analysis of several other factors including sex (A) and housing density (B) have shown no distinct clustering of samples suggesting that these factors do not significantly contribute to alteration or unique composition of GM in shelter felines.

Conclusions and Future Directions

- There are significant differences in GM of cats housed at different shelters.
- Sex and housing density did not have a significant association with changes in the GM of felines sampled.
- At this time it is unclear if other parameters measured such as behavior, body condition, diet, etc., correlate to changes in GM due to underpowered sample size.
- Awaiting data on client owned felines as well as more shelter locations to evaluate differences between client vs. shelter feline GM and to increase power for other parameters outlined.
- Future directions include increasing sample sizes and assessing the GM of felines for parameters listed such as behavior, diet, or body condition in a controlled setting.

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