

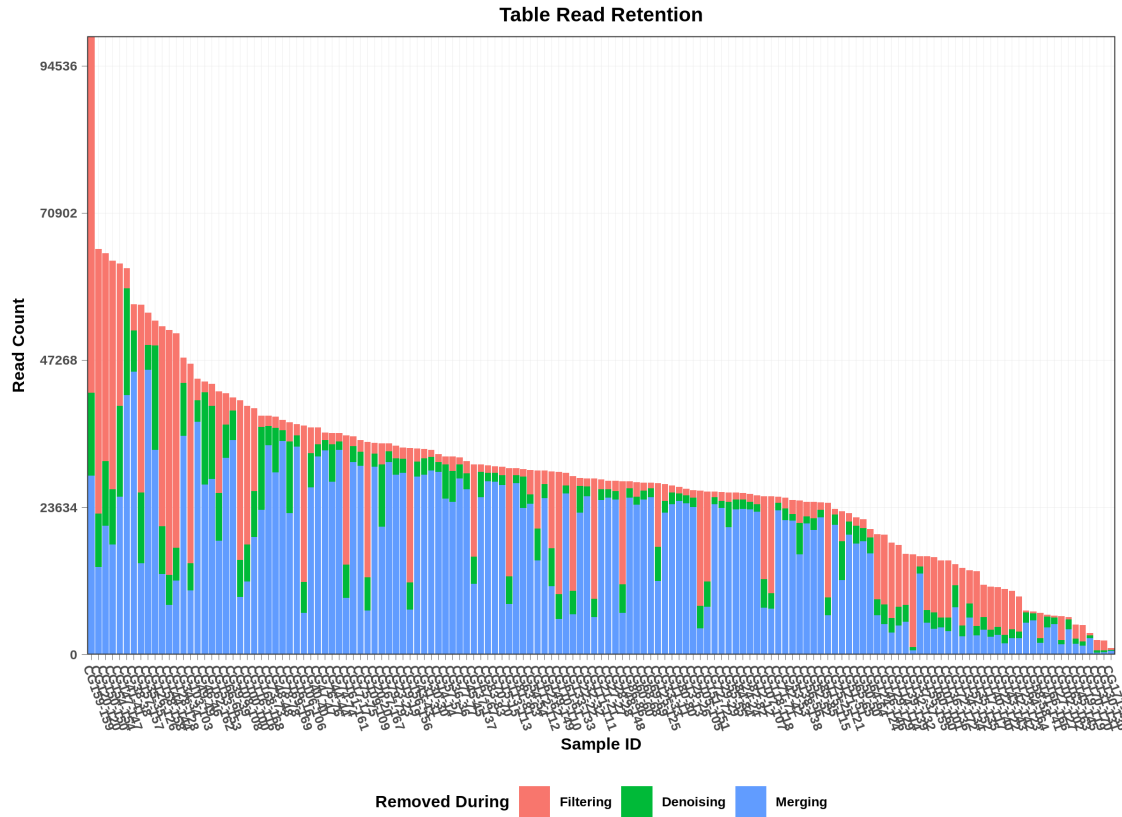
# MMEDS Analysis Summary

Clemente Lab  
*Icahn School of Medicine at Mount Sinai*

(Dated: May 16, 2022)

## I. Table Statistics Summary

### a . Dada2 Statistics



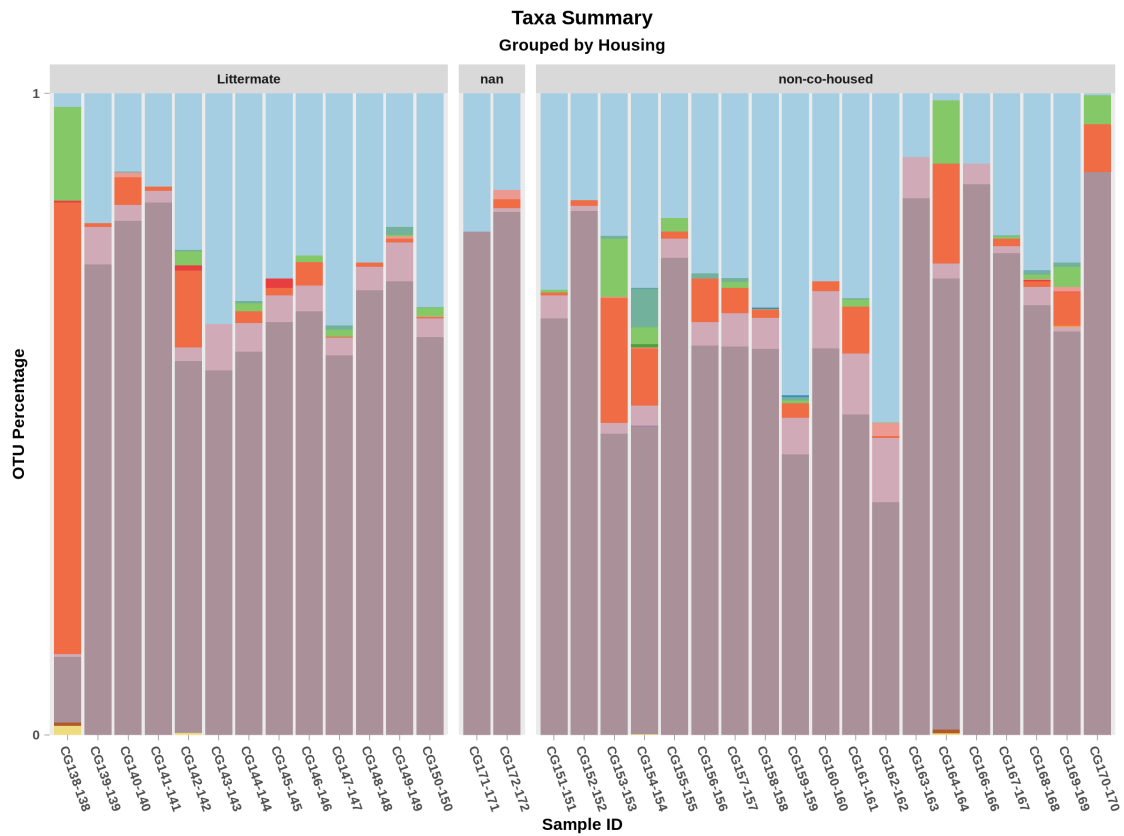
The above plot represents number of input reads (total bar length) and retained (magenta) after quality control filtering, including denoising and chimera checking.

## II. Taxonomy Summary

### a . Interpreting Taxonomy Results

Taxonomy plots represent the abundance of different taxa using stacked plots on a per-sample or per-group (averaged) basis. Data is normalized so that abundances per sample or per group add up to 100%. When using group-based taxonomy plots, it should be noted that only average abundances are shown per group and taxa: this can induce visual biases when a small number of samples in a group have significantly higher abundance of a given taxa compared to the rest of samples in the group, and give the (incorrect) impression that the group as a whole has high abundance of the taxa.

### b . Phylum Level

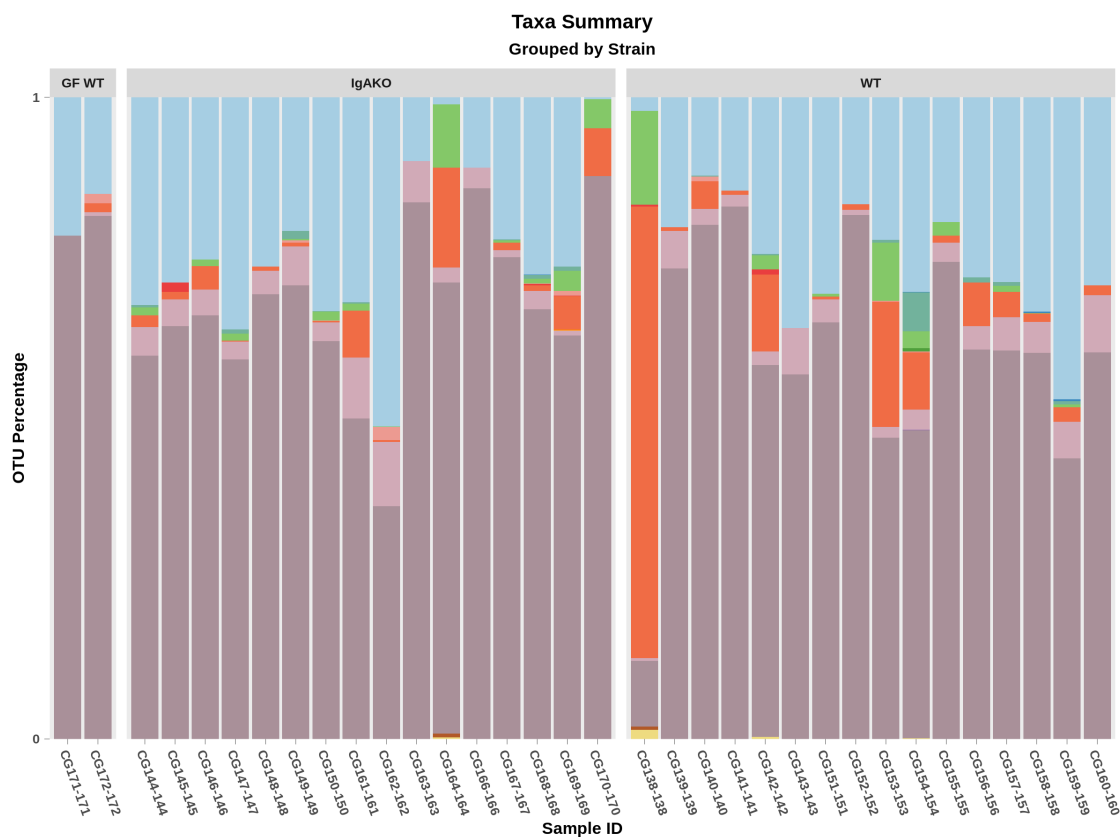


Legend grouped by Housing

Color Abundance OTU

	28.51%	k__Bacteria;__
	17.55%	k__Bacteria;p__Firmicutes
	10.04%	k__Bacteria;p__OD1
	64.21%	k__Bacteria;p__Proteobacteria

The above plot represents the percentage of each sample belonging to particular taxon summarized at the Phylum level.



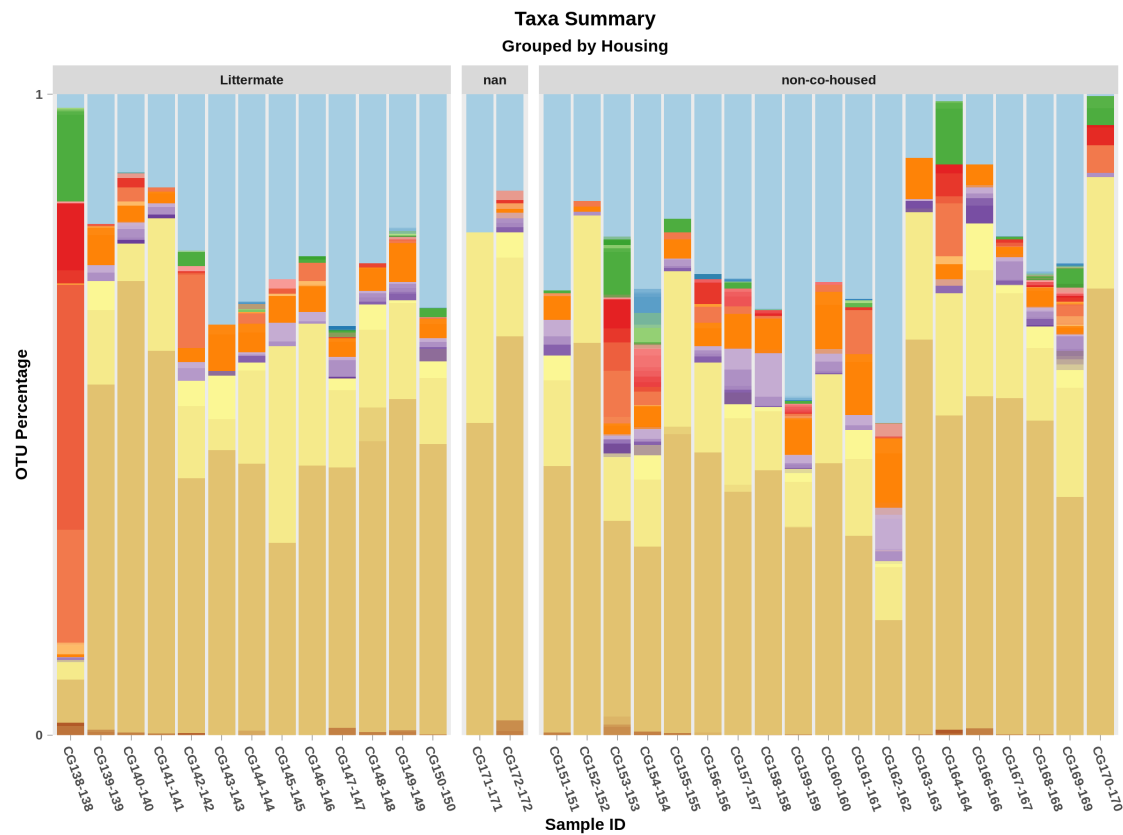
Legend grouped by Strain

Color Abundance OTU

	26.21%	k__Bacteria;__
	14.61%	k__Bacteria;p__Bacteroidetes
	33.94%	k__Bacteria;p__Firmicutes
	60.18%	k__Bacteria;p__Proteobacteria

The above plot represents the percentage of each sample belonging to particular taxon summarized at the Phylum level.

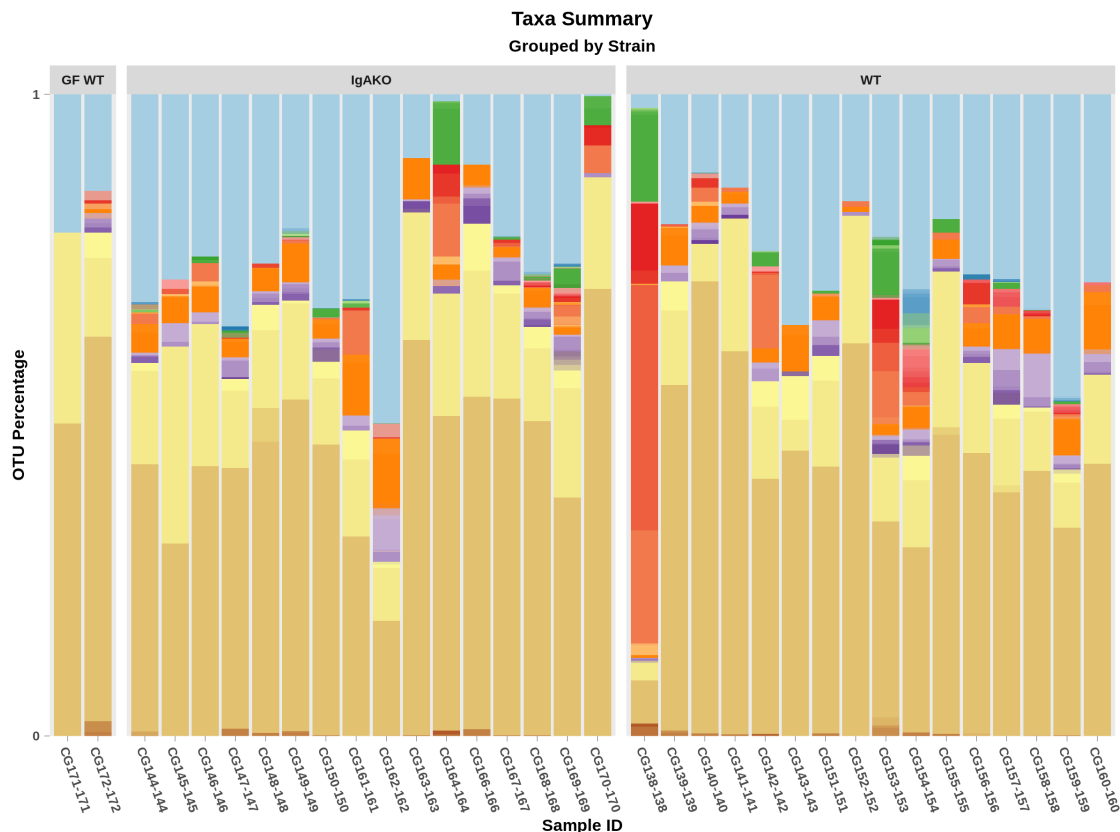
c . Genus Level



Legend grouped by Housing  
Color Abundance OTU

- 28.51% k\_\_Bacteria;\_\_;\_\_;\_\_;\_\_
- 15.92% k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Alteromonadales;f\_\_Shewanellaceae;g\_\_Shewanella
- 43.48% k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Oceanospirillales;f\_\_Halomonadaceae;g\_\_Halomonas

The above plot represents the percentage of each sample belonging to particular taxon summarized at the Genus level.



Legend grouped by Strain

Color Abundance OTU

	26.21%	k__Bacteria;__;__;__;__;__
	13.49%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__S24-7;g__
	10.45%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus
	38.22%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Candidatus Arthromitus
	14.53%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;__
	14.96%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Shewanellaceae;g__Shewanella
	44.98%	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae;g__Halomonas

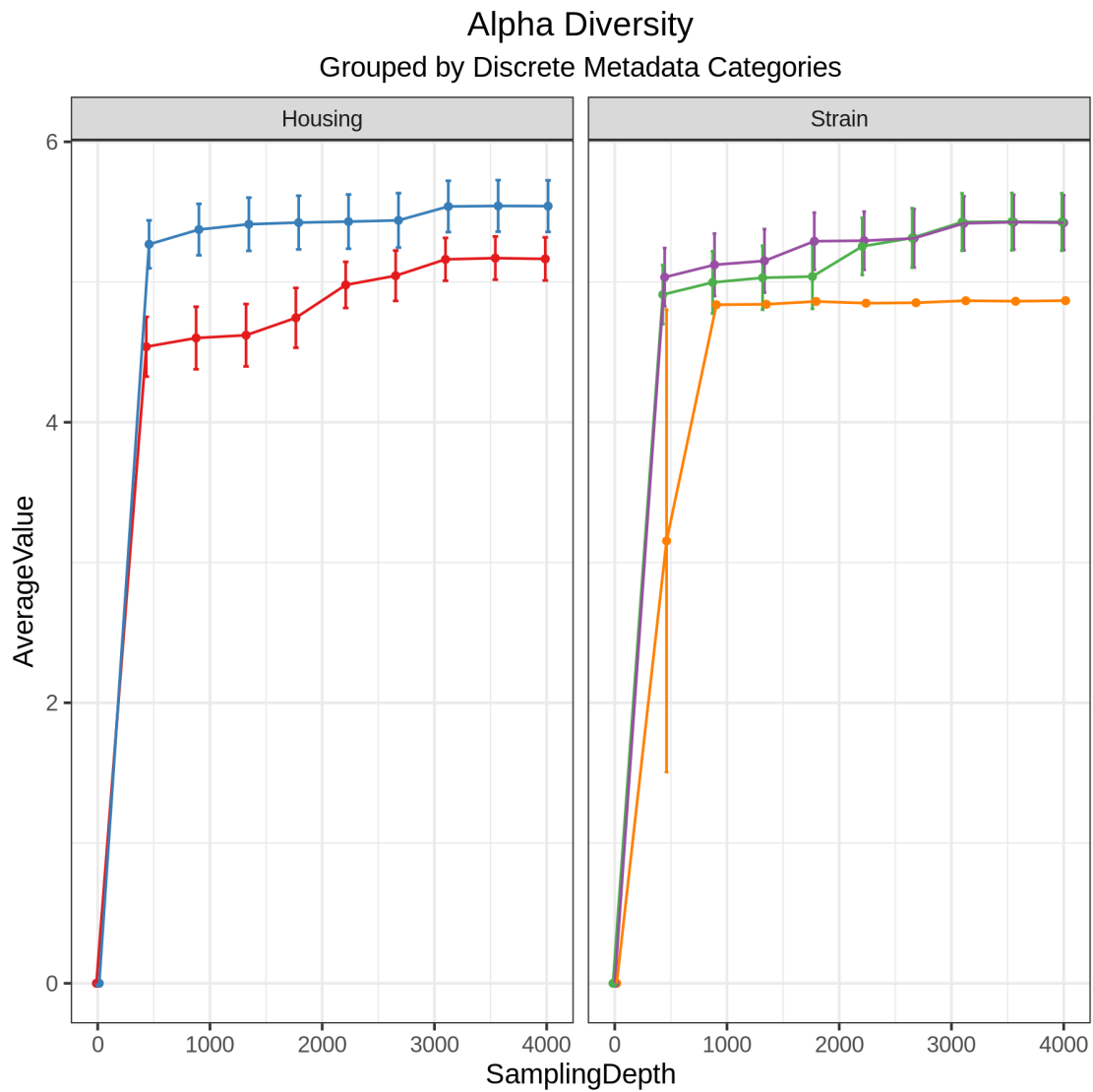
The above plot represents the percentage of each sample belonging to particular taxon summarized at the Genus level.

### III. Alpha Diversity

#### a . Interpreting Alpha Diversity Results

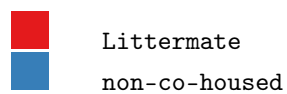
Alpha diversity estimates the amount of microbial diversity present in a sample or group of samples. There are several measures that can be used for alpha diversity, including observed features, Shannon's diversity or Faith's phylogenetic diversity. Because diversity estimates depend on the total number of sequences assigned to each sample, rarefaction curves are constructed to show the relation between alpha diversity (on the vertical axis) and sequencing depth (on the horizontal axis). Curves that gradually plateau as sequencing depth increases suggest that additional sequencing effort would not substantially yield additional results in terms of currently not observed diversity; curves that continue to increase suggest additional sequencing effort might be required to saturate the estimate.

#### b . Shannon Diversity



## Legend for Housing

Color Metadata



## Legend for Strain

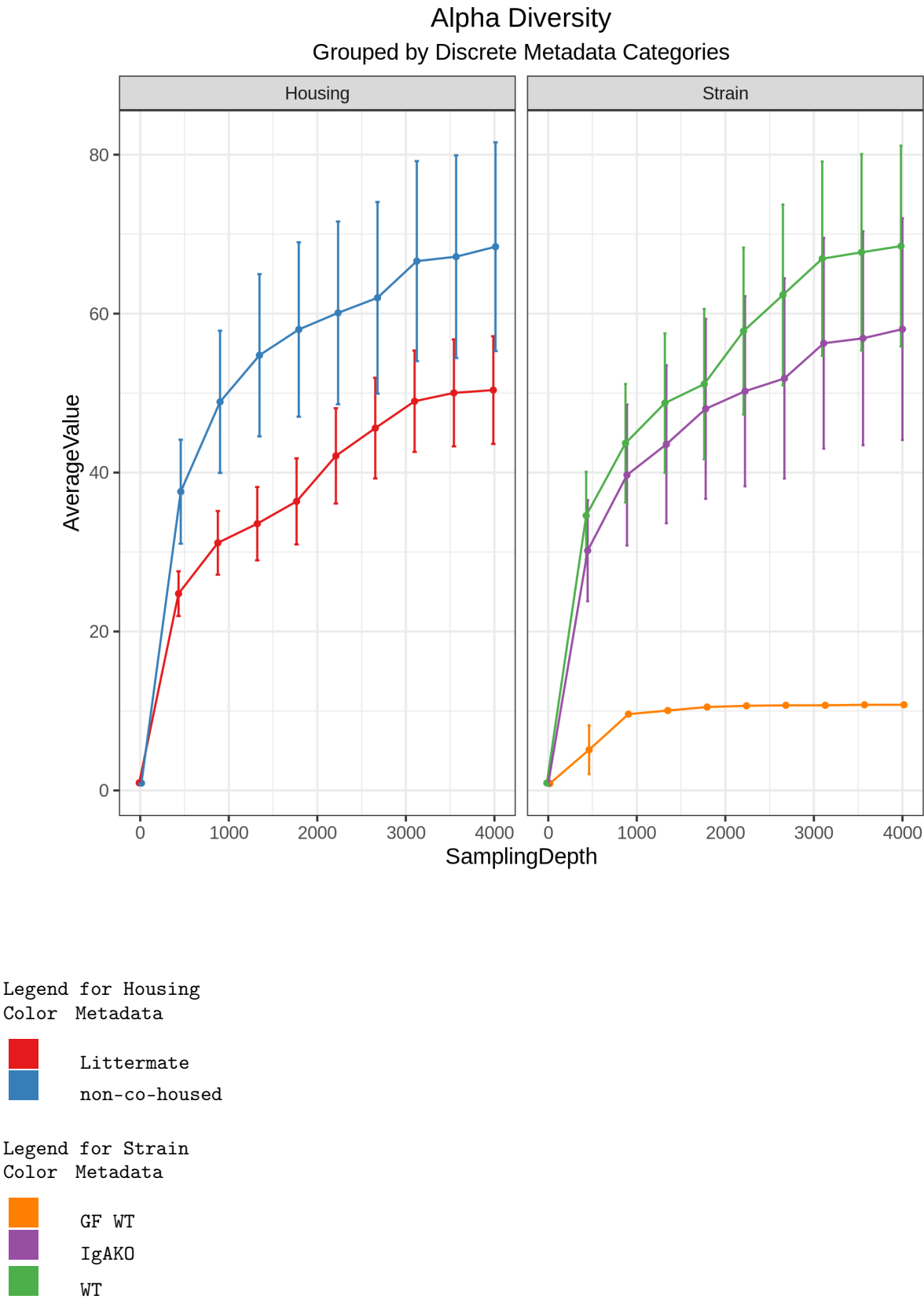
Color Metadata



The above plot represents the average value of alpha diversity at each sampling depth. The error bars show the standard error within each group. Groups are determined by the metadata value in each category specified in the plot.

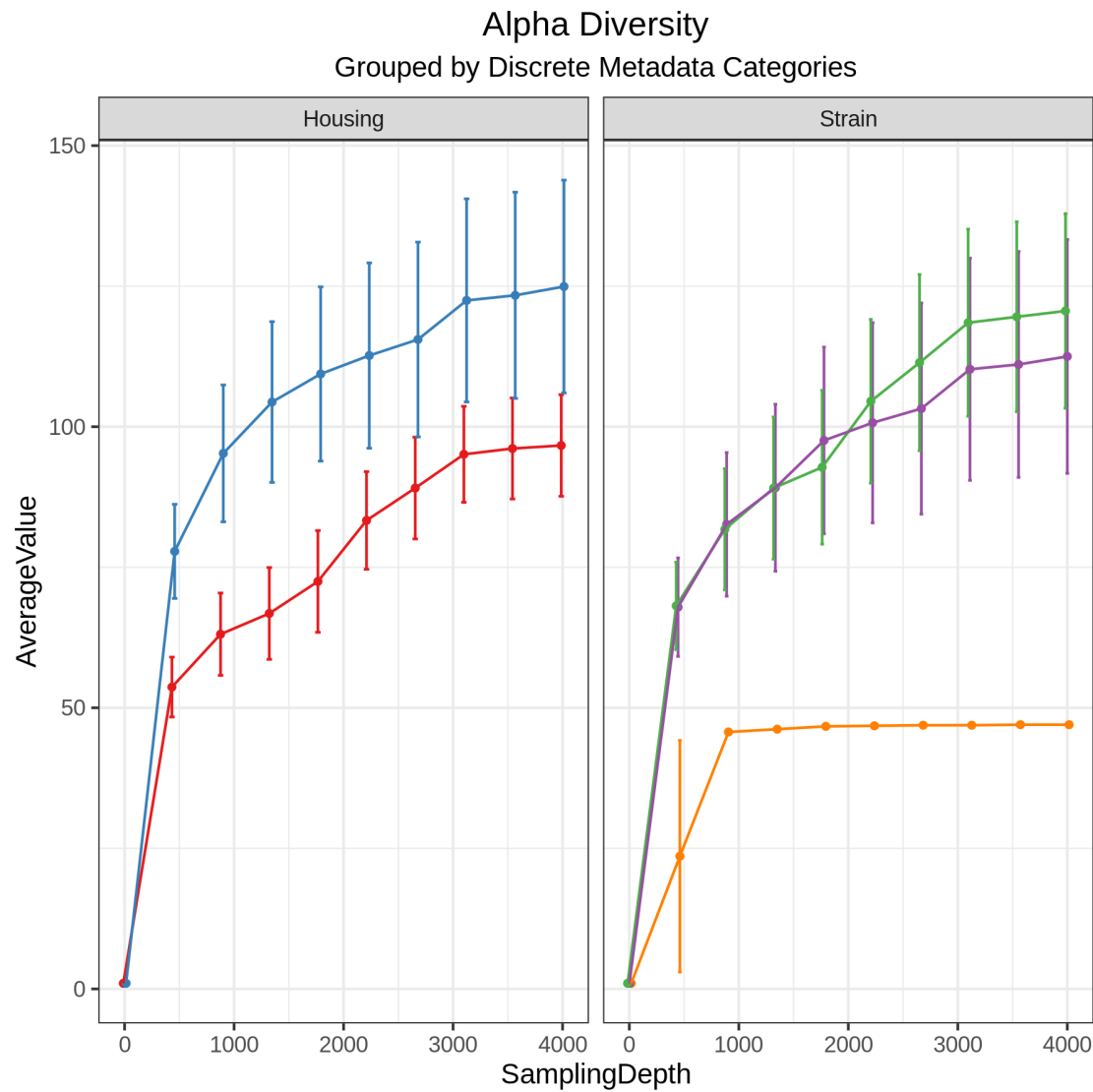


c . Faith's Phylogenetic Diversity



The above plot represents the average value of alpha diversity at each sampling depth. The error bars show the standard error within each group. Groups are determined by the metadata value in each category specified in the plot.

d . Observed ASV



Legend for Housing  
Color Metadata

- Littermate
- non-co-housed

Legend for Strain  
Color Metadata

- GF WT
- IgAKO
- WT

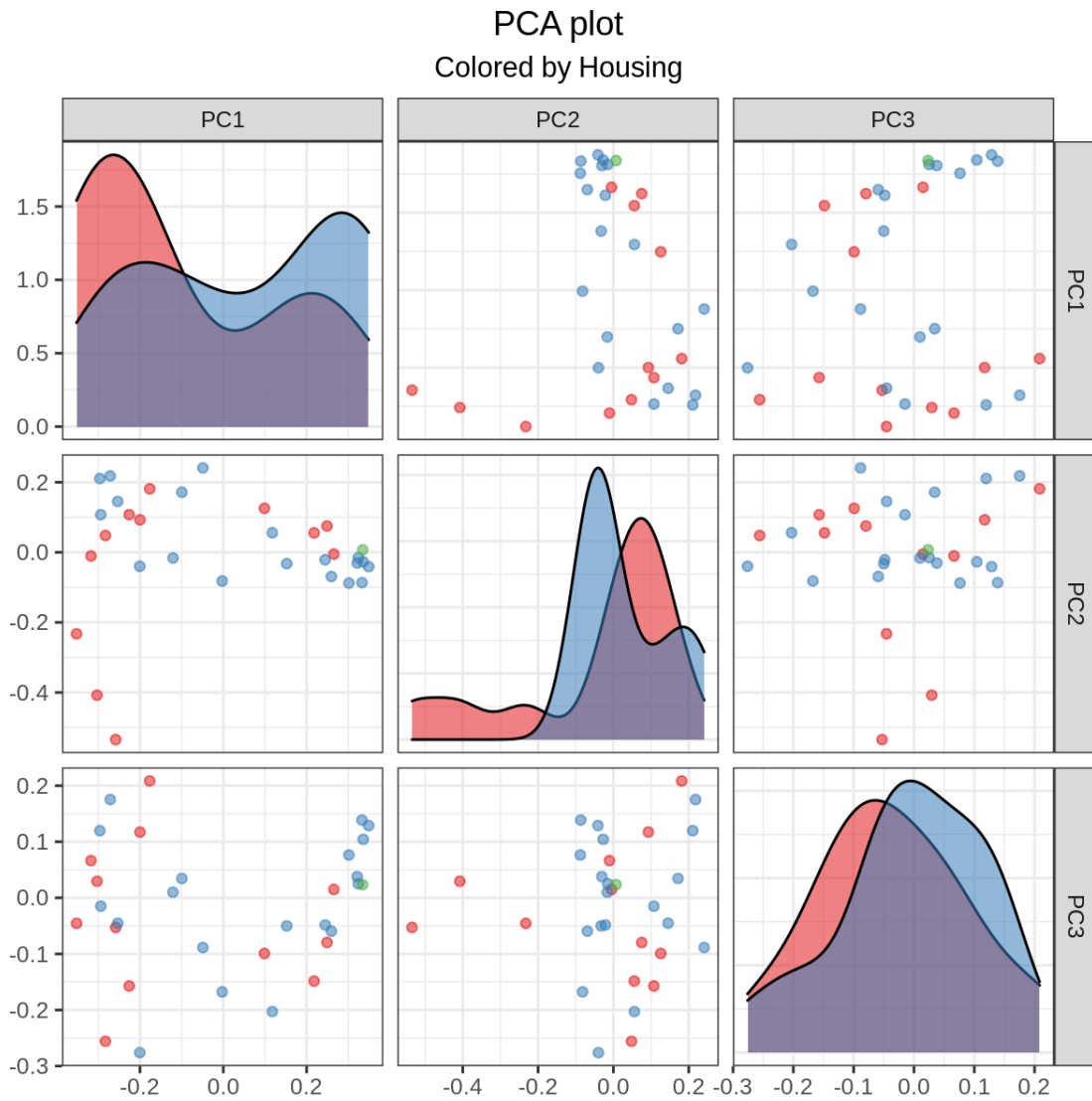
The above plot represents the average value of alpha diversity at each sampling depth. The error bars show the standard error within each group. Groups are determined by the metadata value in each category specified in the plot.

## IV. Beta Diversity

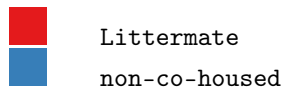
### a . Interpreting Beta Diversity Results

Beta diversity estimates how similar or dissimilar samples are based on their microbiome composition. Different to alpha diversity, which is estimated per sample, beta diversity is a distance that is calculated between pairs of samples. Samples that are similar to each other in their microbiome composition will have a low distance between them based on beta diversity, while those that are very different in their composition will have a large distance. Principal Coordinate Analysis (PCoA) is an ordination technique that visually represents the samples based on their beta diversity distances to facilitate the identification of clusters or gradients of samples. By default, the first three principal coordinates are shown in PCoA plots.

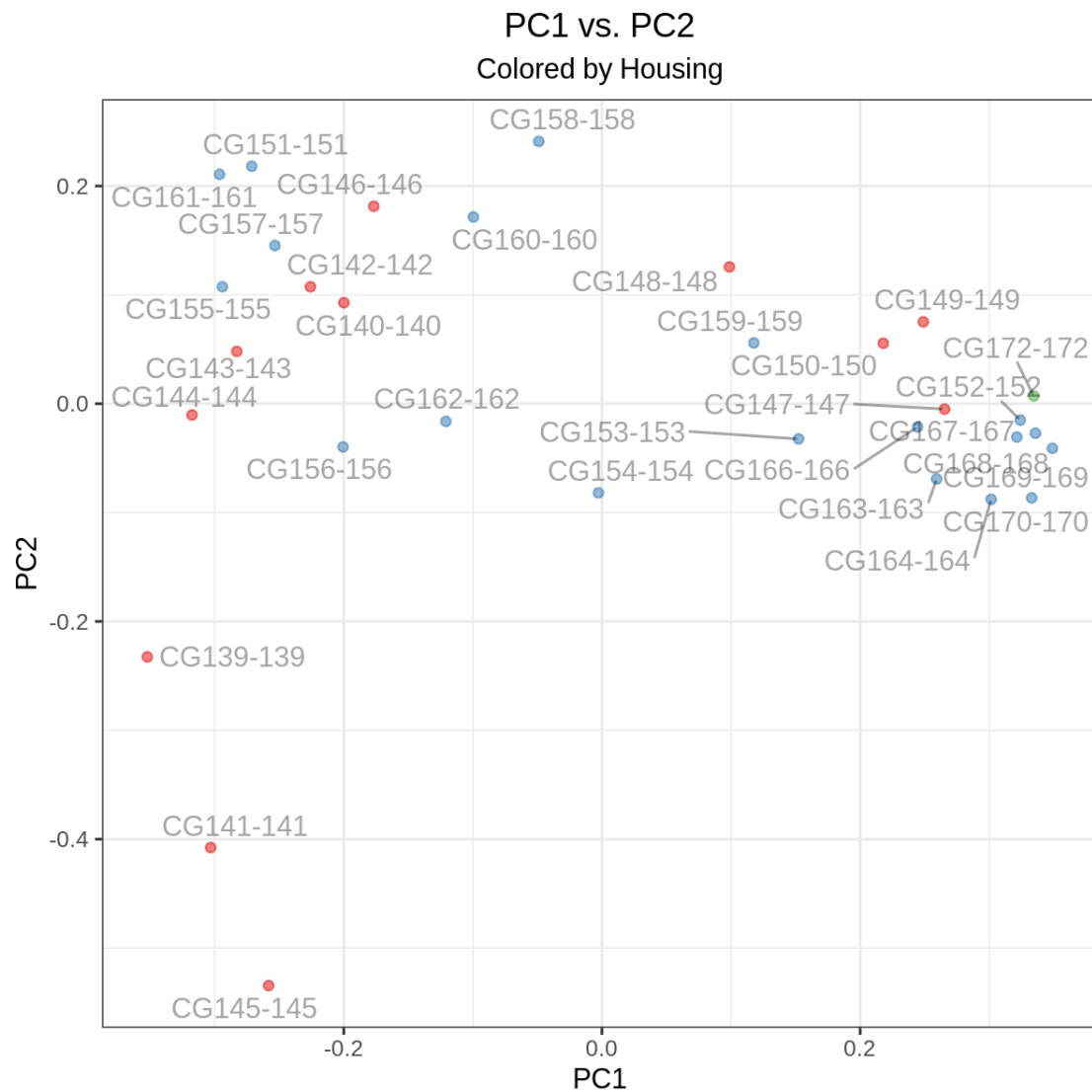
### b . Bray-Curtis, grouped by Housing



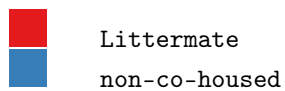
Legend for Housing  
Color Metadata

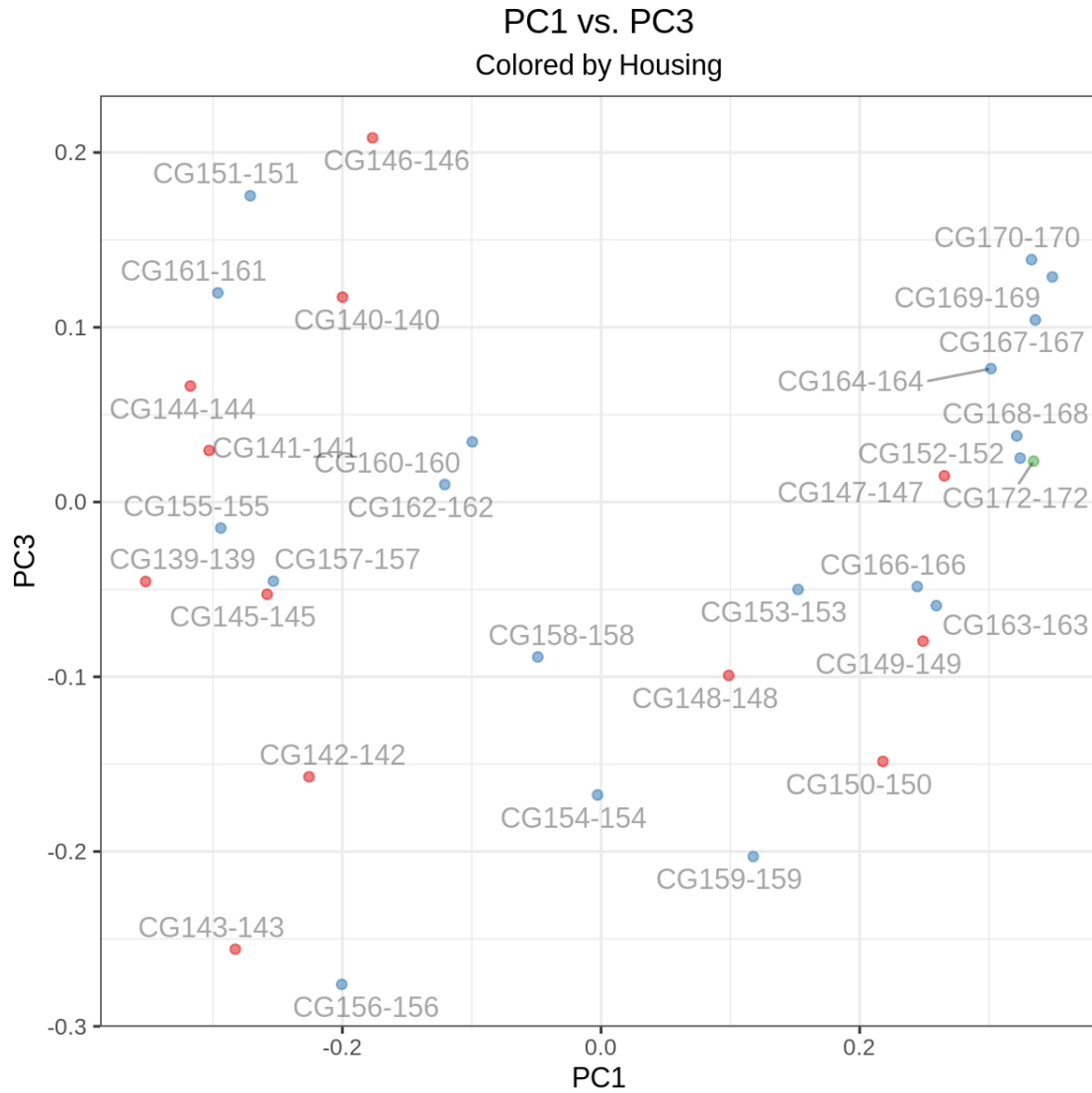


The above plot represents the first three components created when performing Principle Component Analysis on the Beta diversity of the samples.



Legend for Housing  
Color Metadata





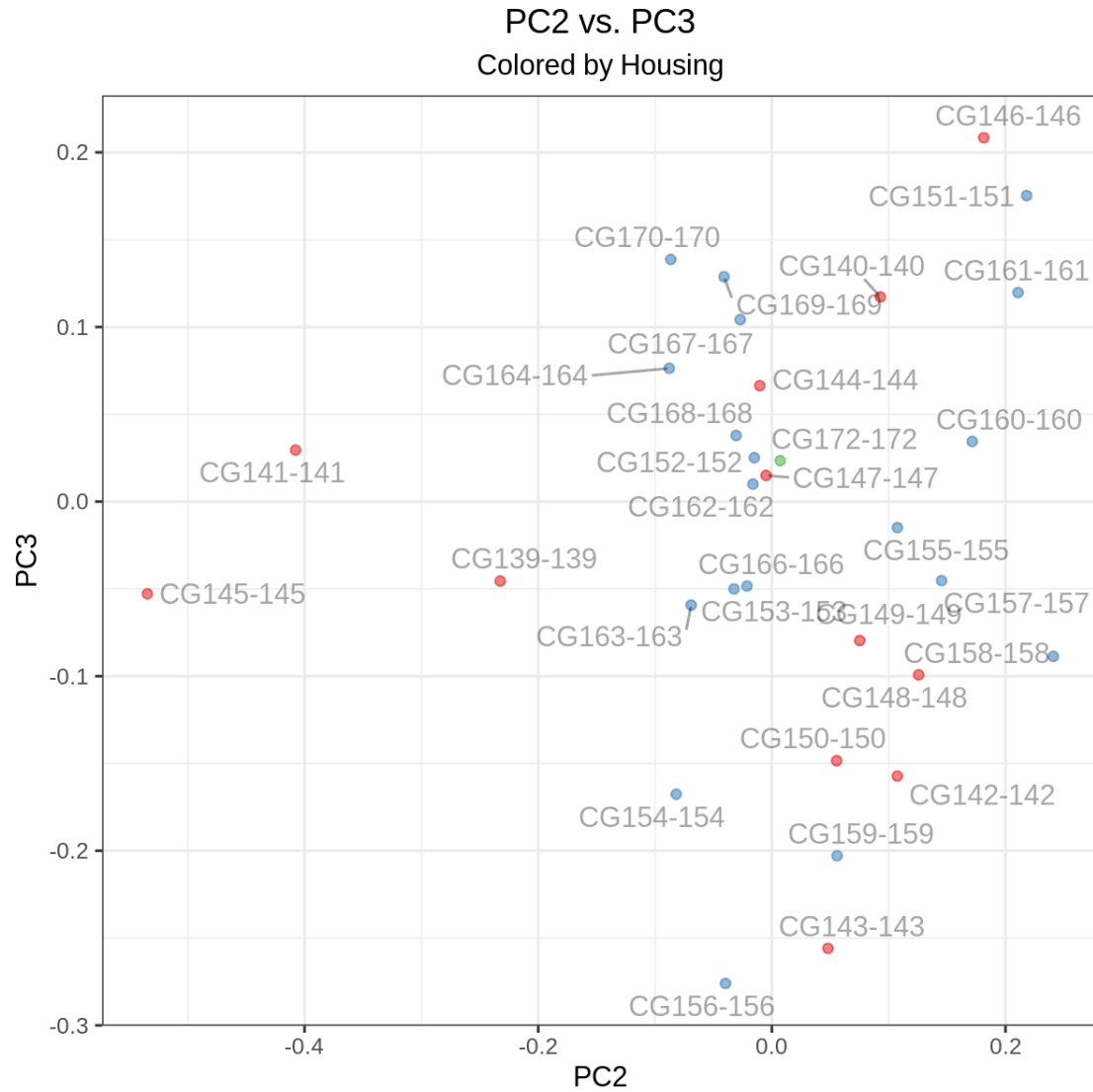
Legend for Housing

Color Metadata



Littermate

non-co-housed





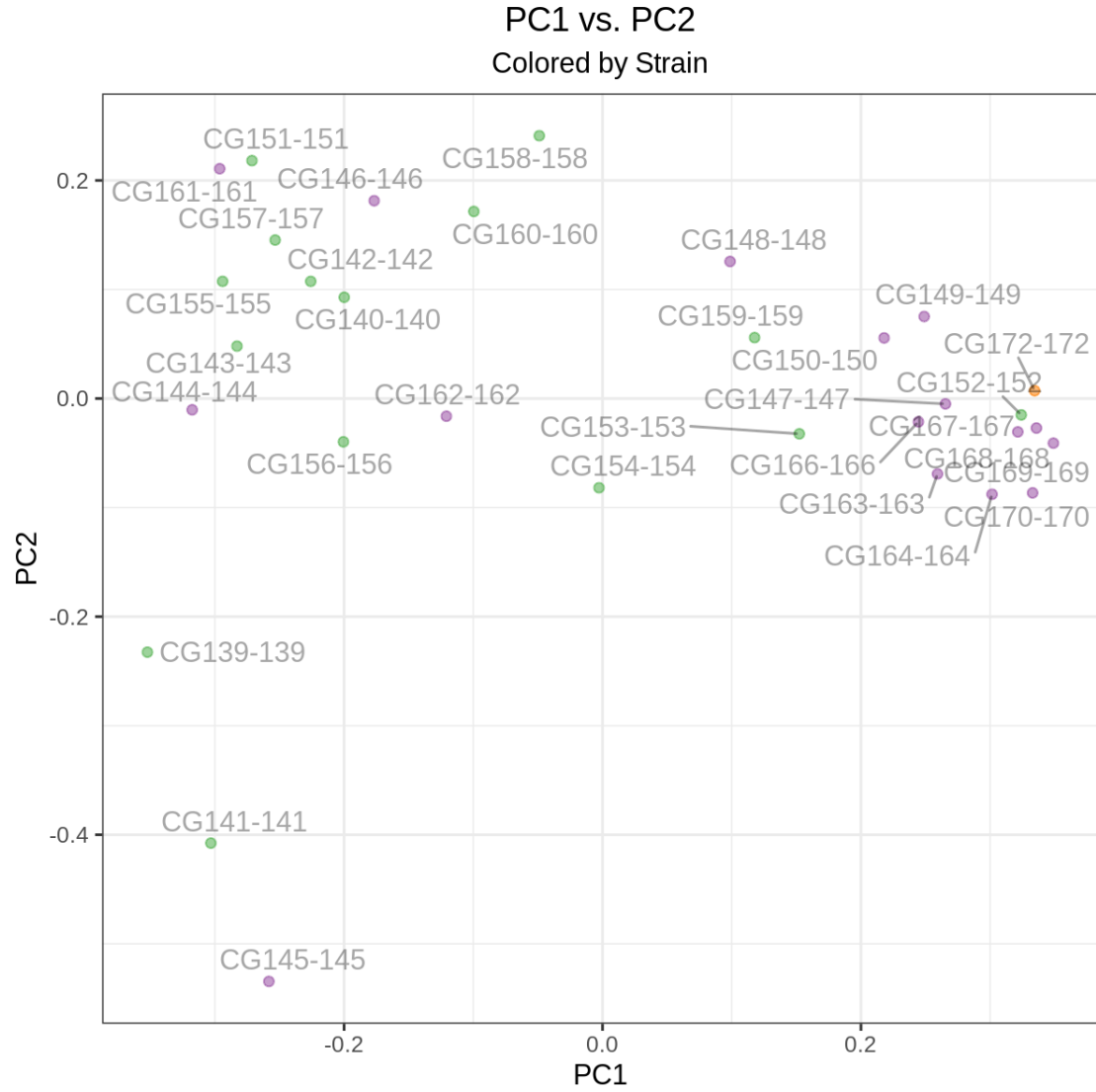
## c . Bray-Curtis, grouped by Strain



Legend for Strain  
Color Metadata

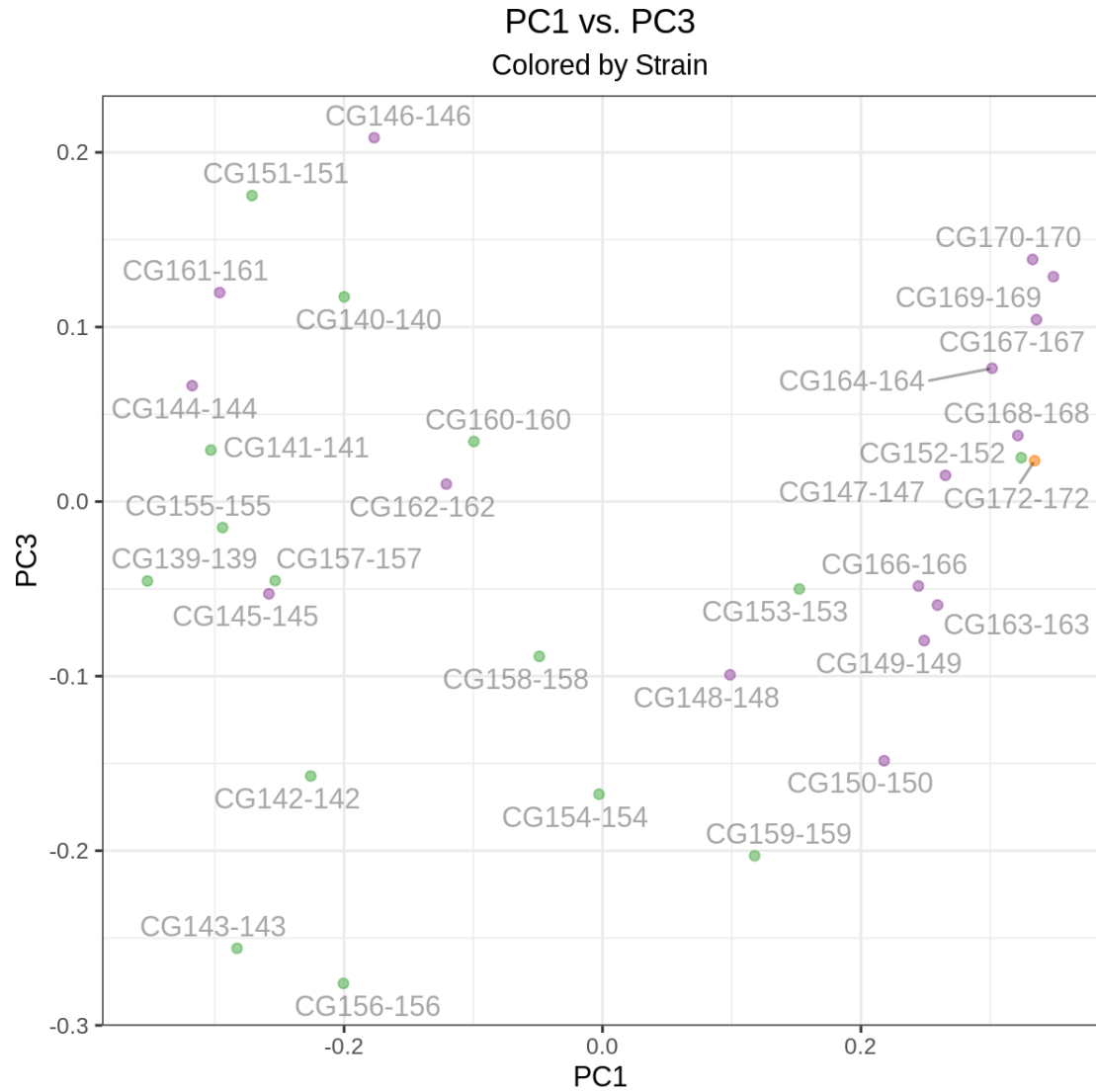


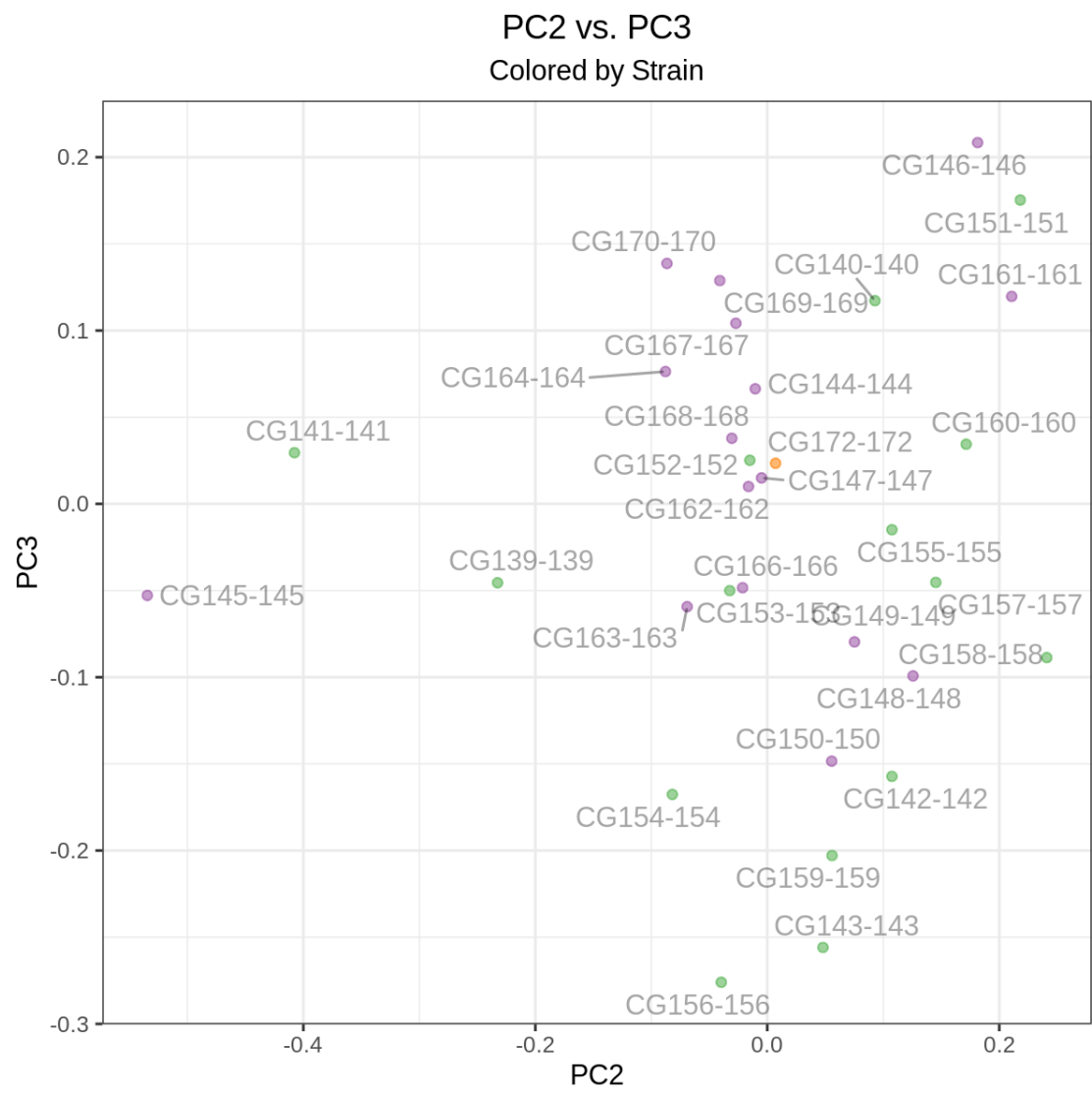
The above plot represents the first three components created when performing Principle Component Analysis on the Beta diversity of the samples.



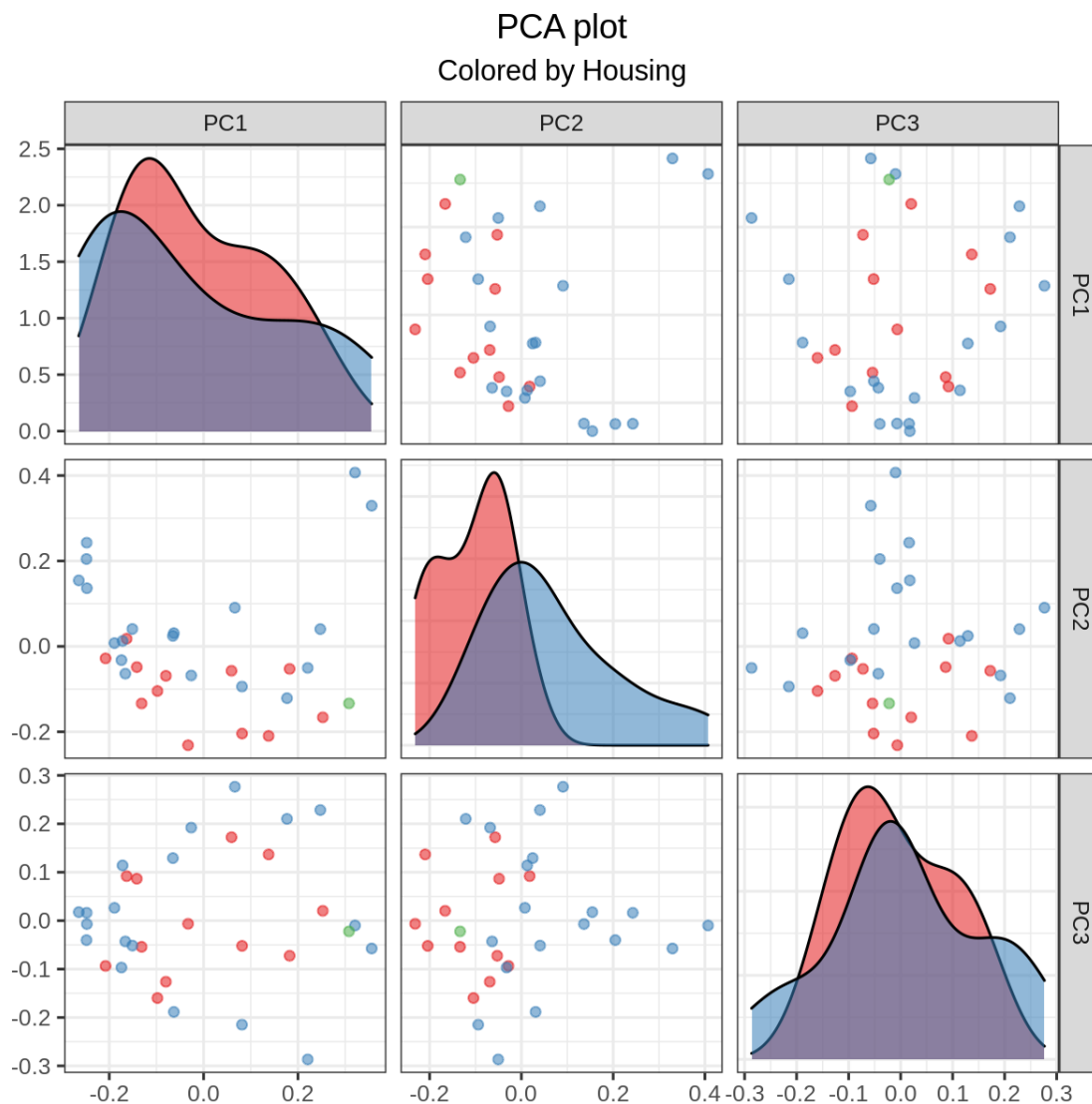
Legend for Strain  
Color Metadata



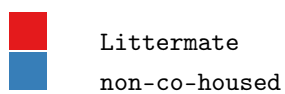




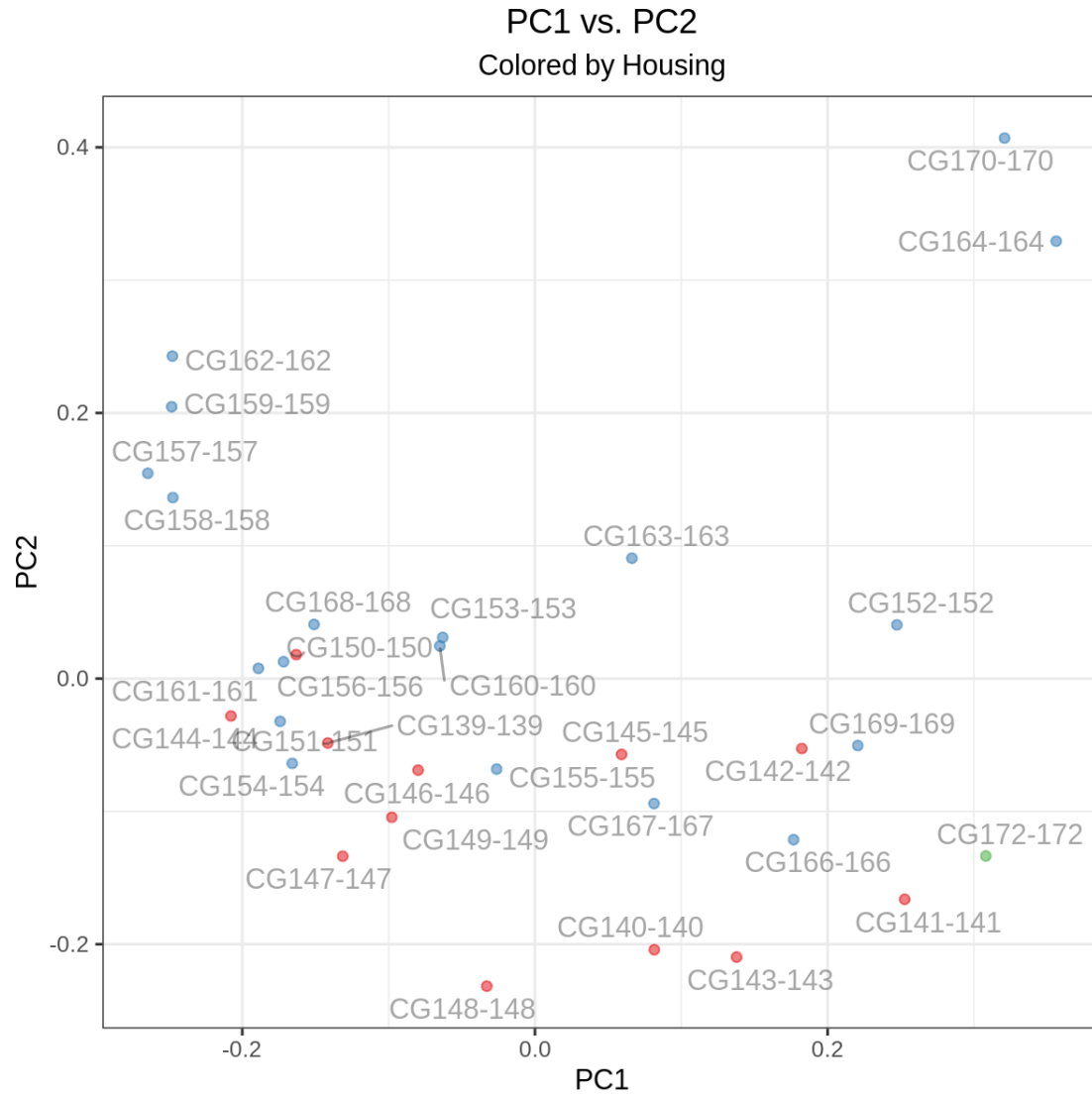
## d . Unweighted UniFrac, grouped by Housing

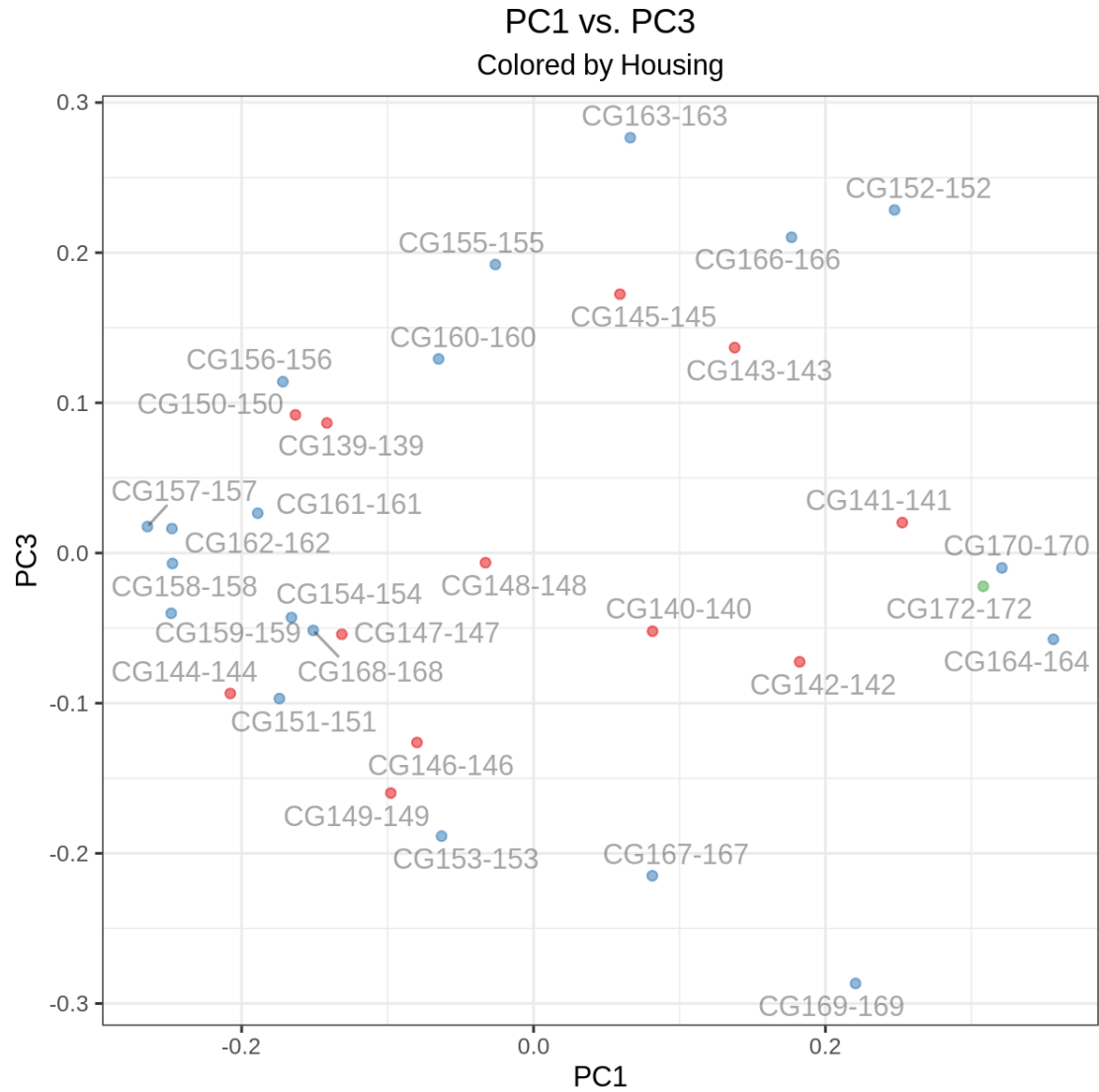


Legend for Housing  
Color Metadata



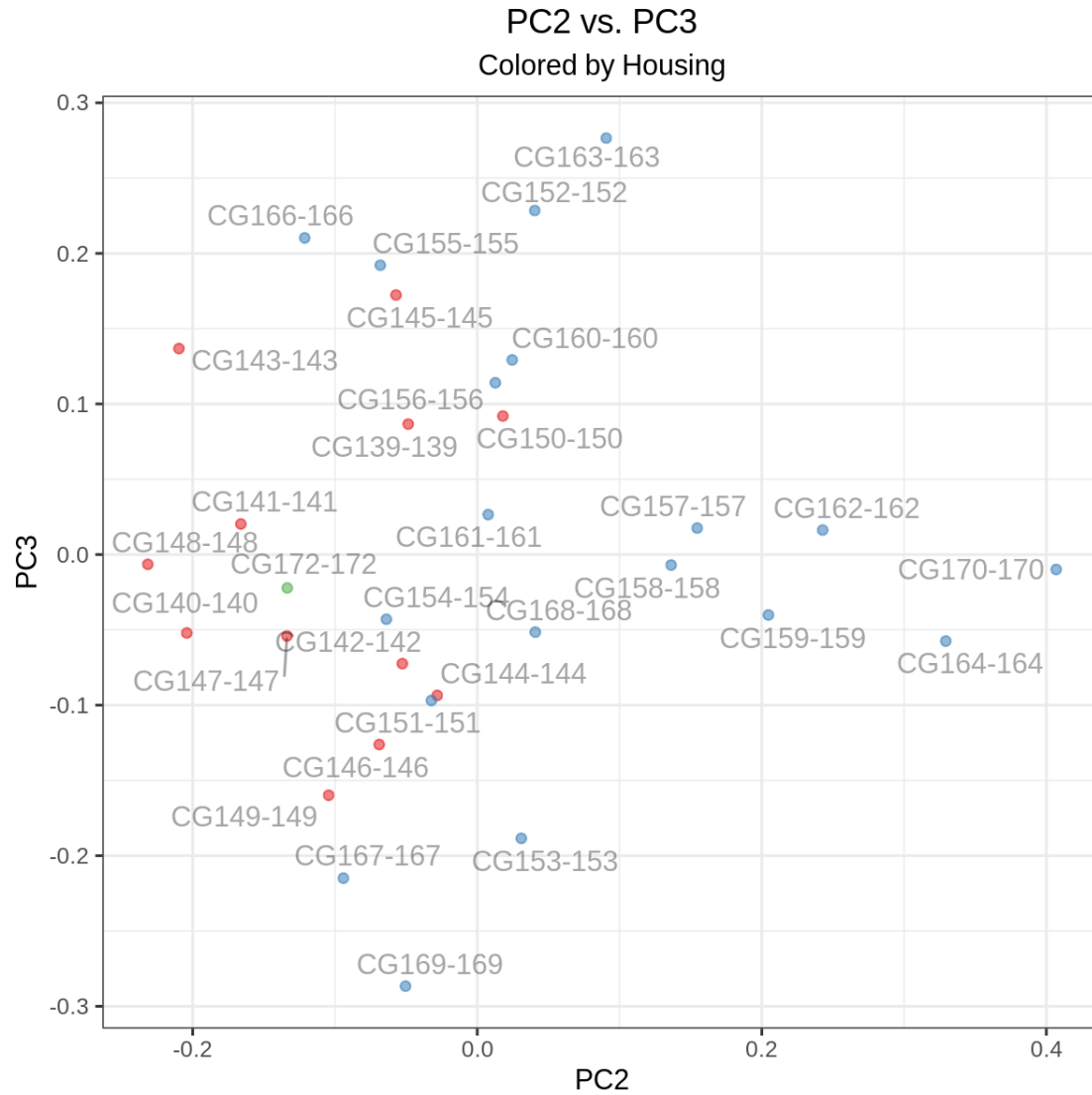
The above plot represents the first three components created when performing Principle Component Analysis on the Beta diversity of the samples.





Legend for Housing  
Color Metadata

<span style="color: red;">■</span>	Littermate
<span style="color: blue;">■</span>	non-co-housed

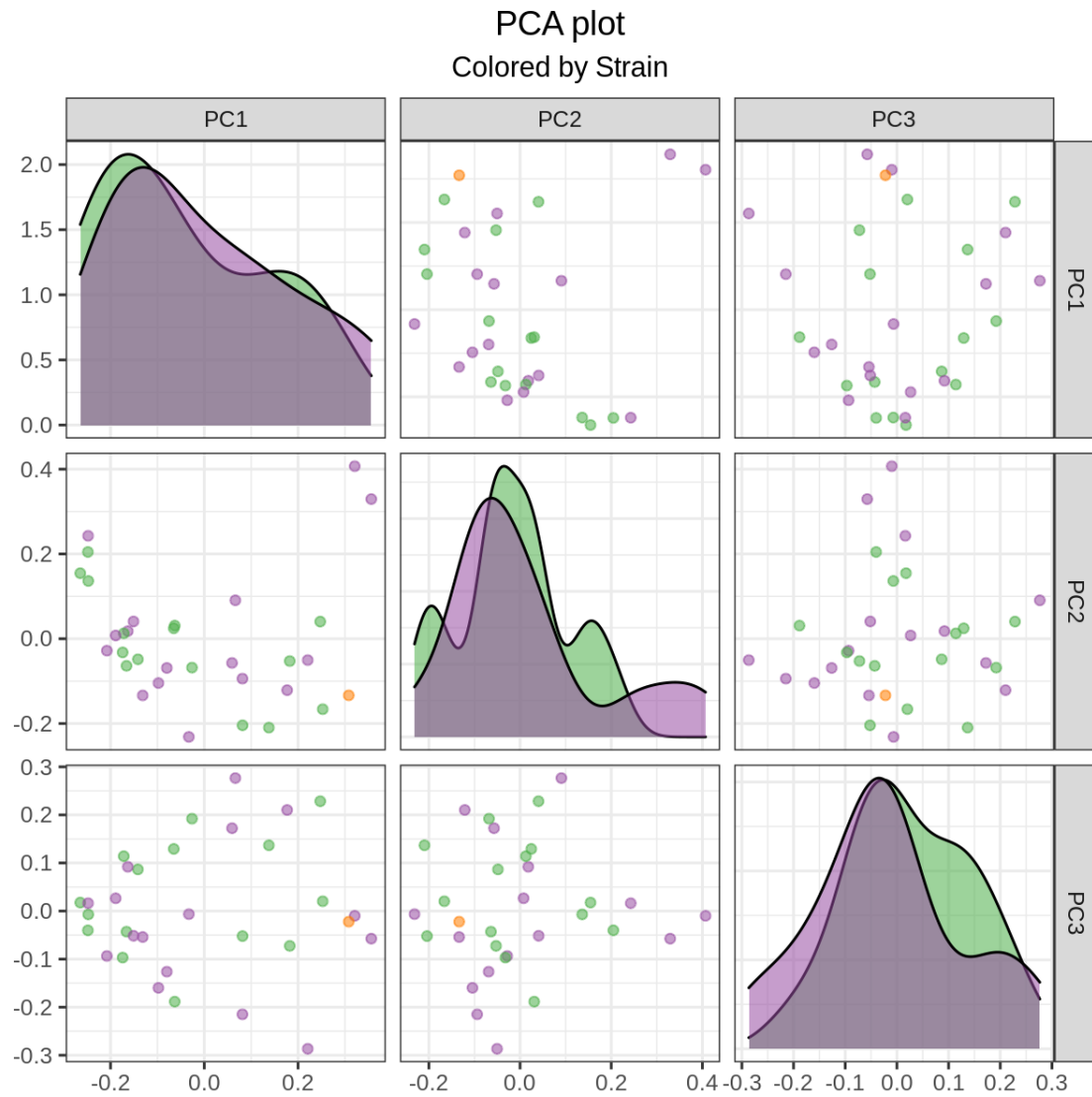


Legend for Housing  
Color Metadata

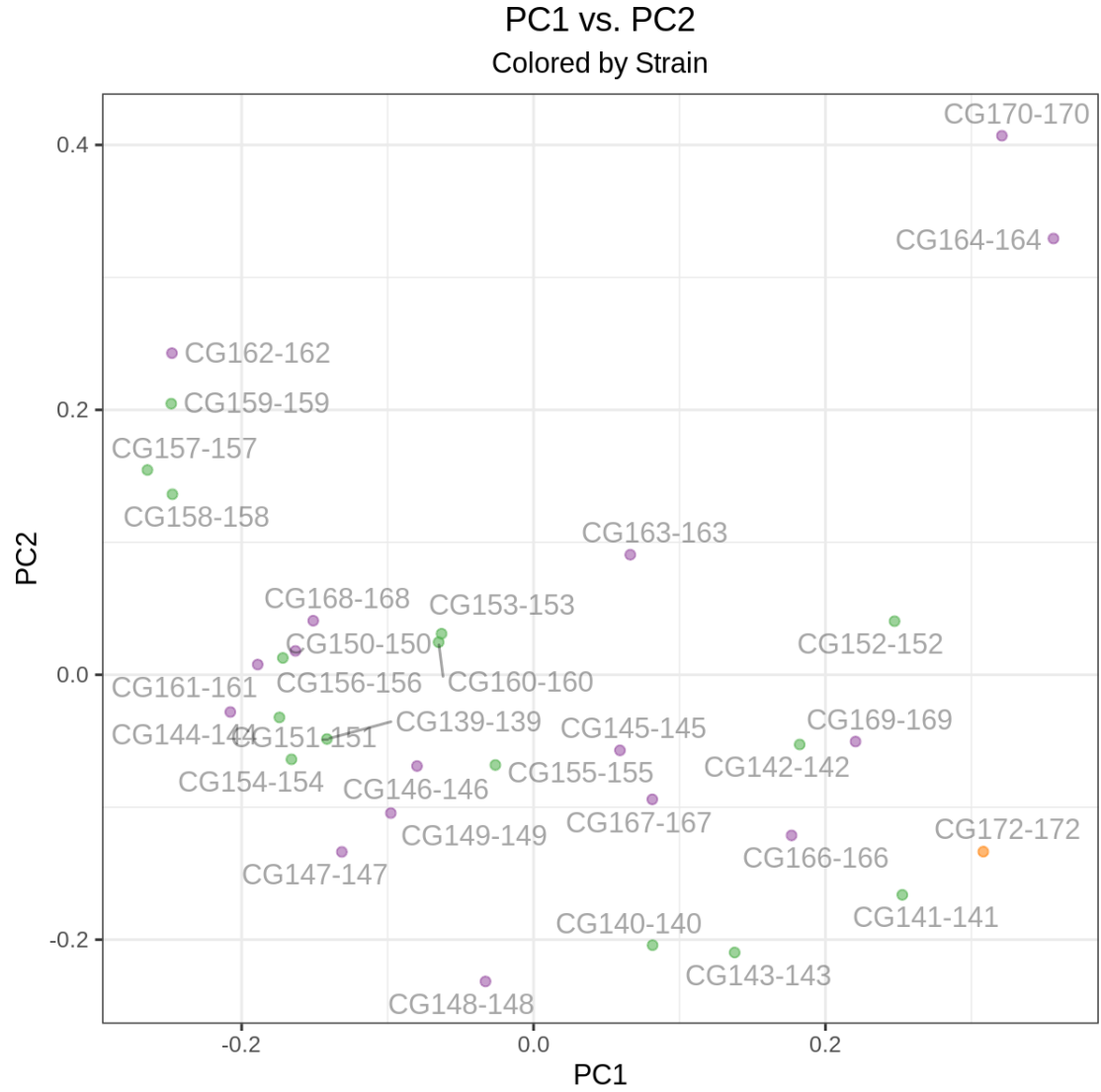
<span style="color: red;">■</span>	Littermate
<span style="color: blue;">■</span>	non-co-housed



e . Unweighted UniFrac, grouped by Strain

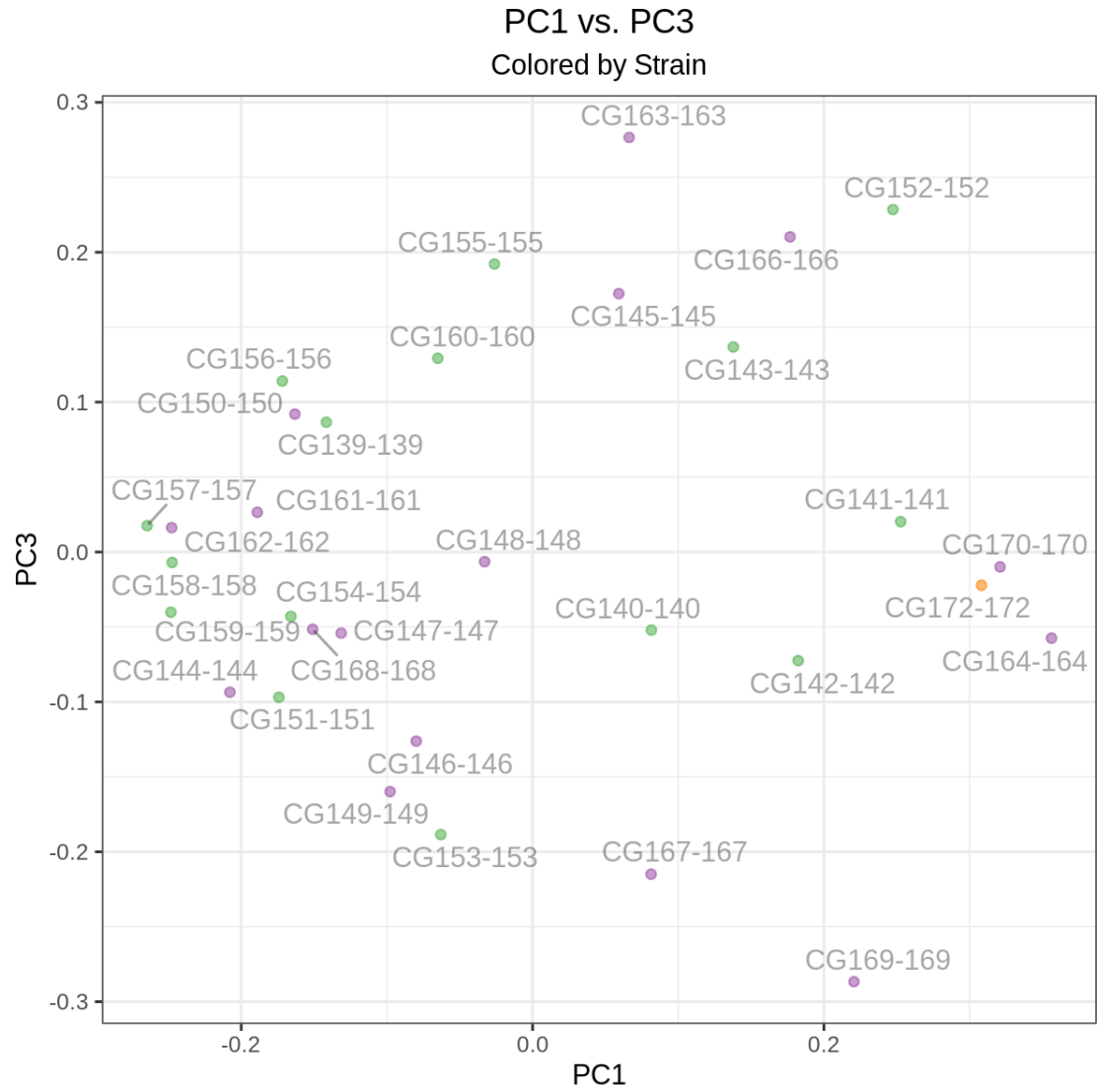


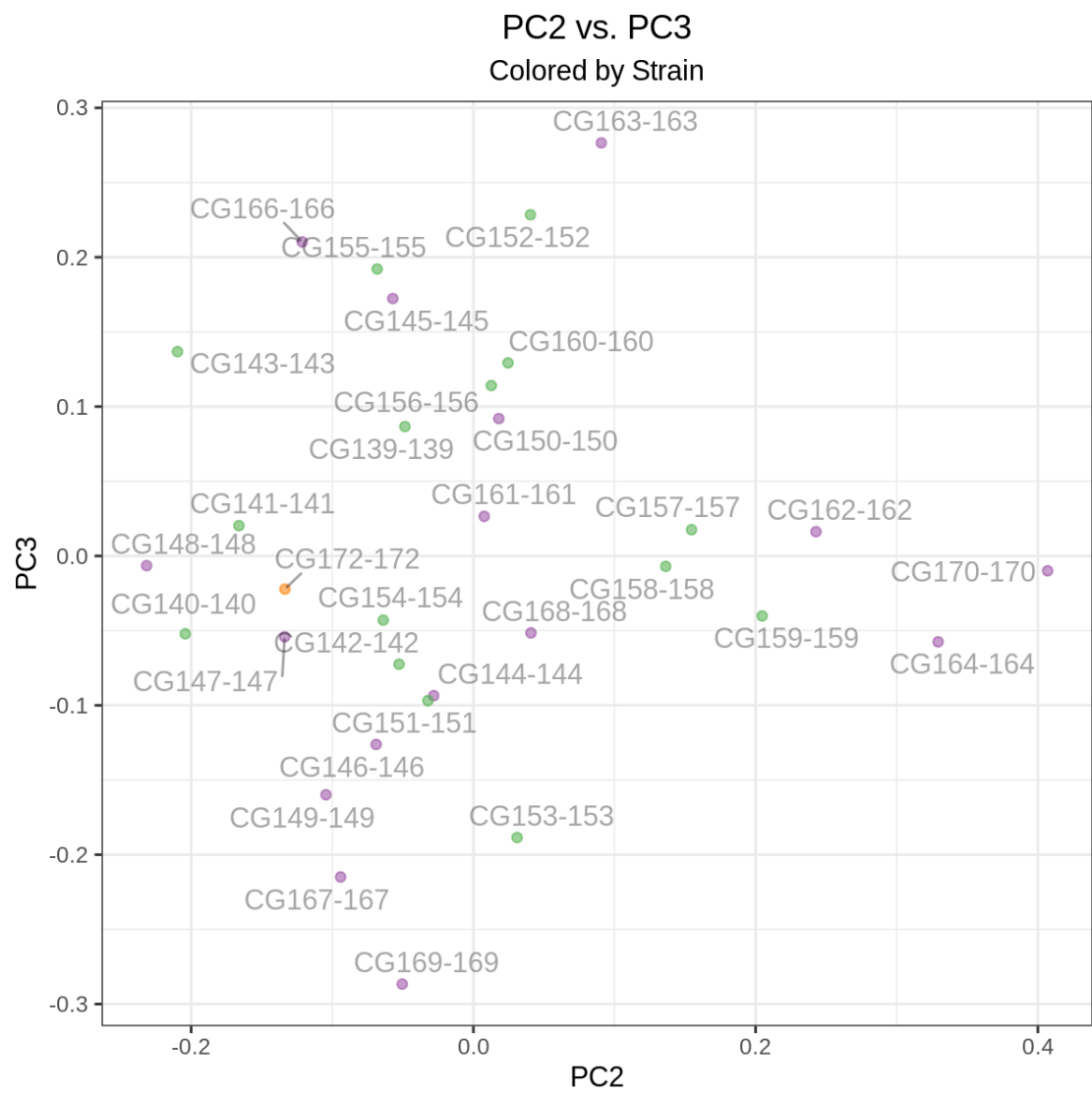
The above plot represents the first three components created when performing Principle Component Analysis on the Beta diversity of the samples.



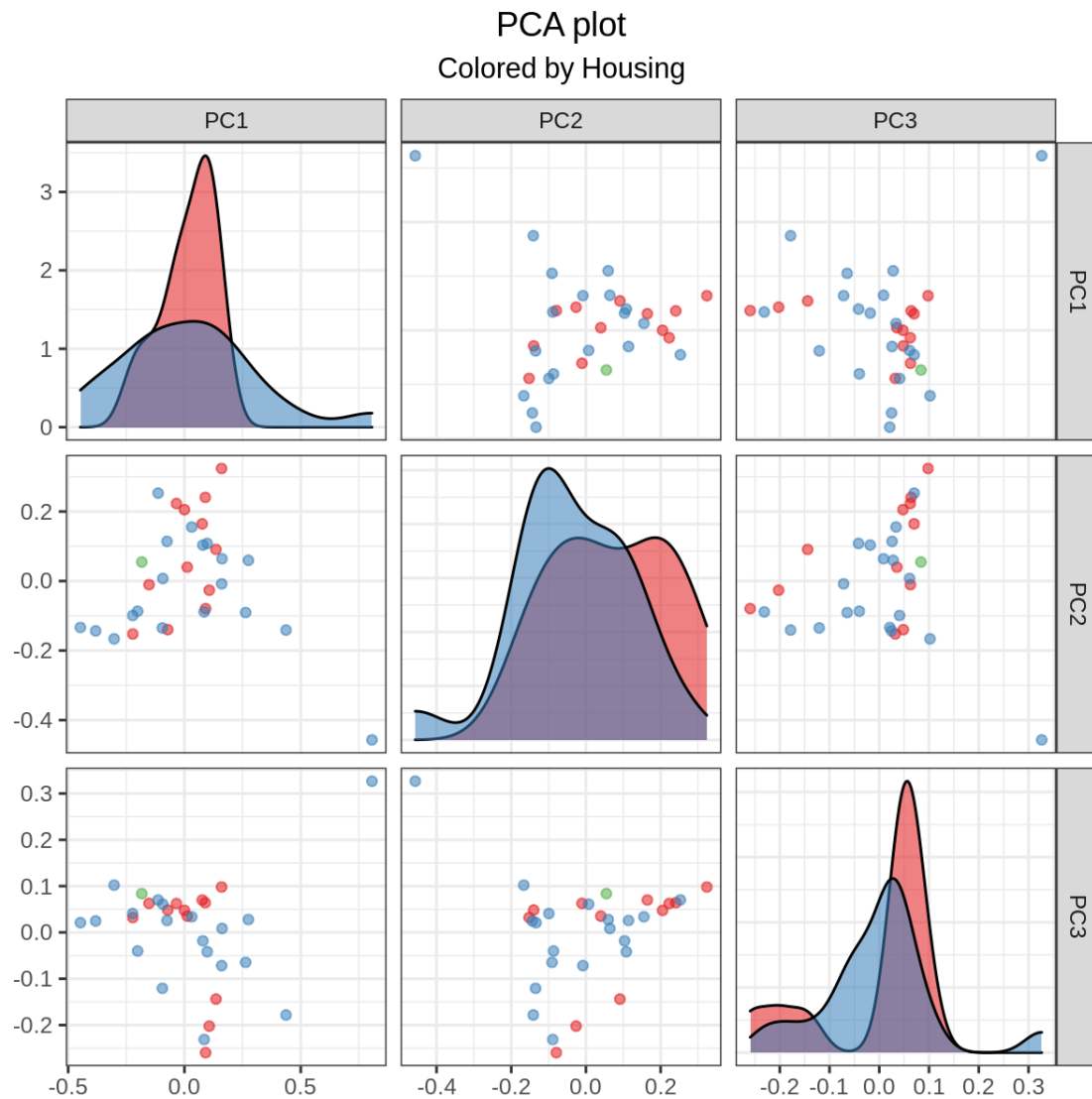
Legend for Strain  
Color Metadata







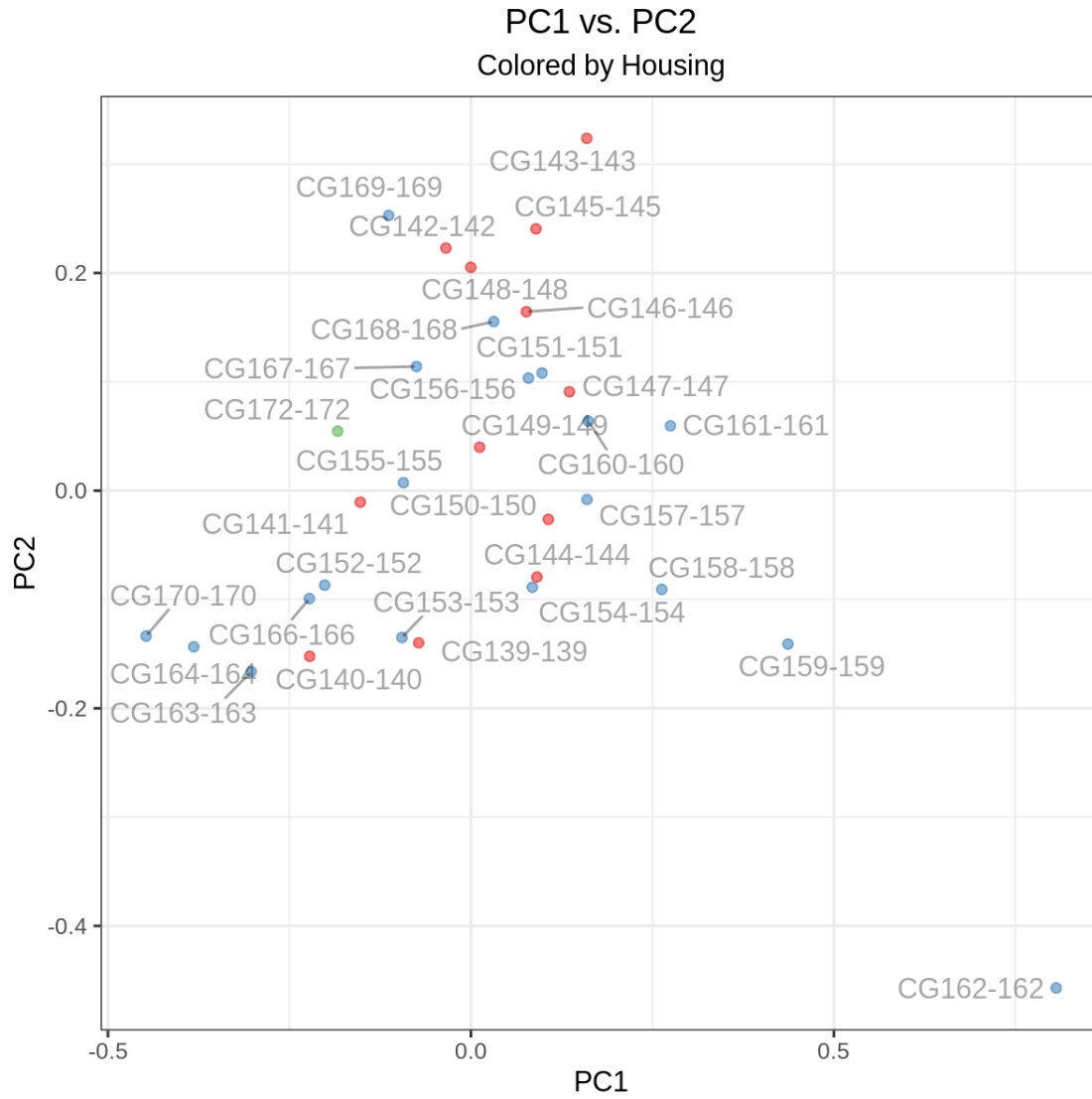
f . Weighted UniFrac, grouped by Housing



Legend for Housing  
Color Metadata

■ Littermate  
■ non-co-housed

The above plot represents the first three components created when performing Principle Component Analysis on the Beta diversity of the samples.



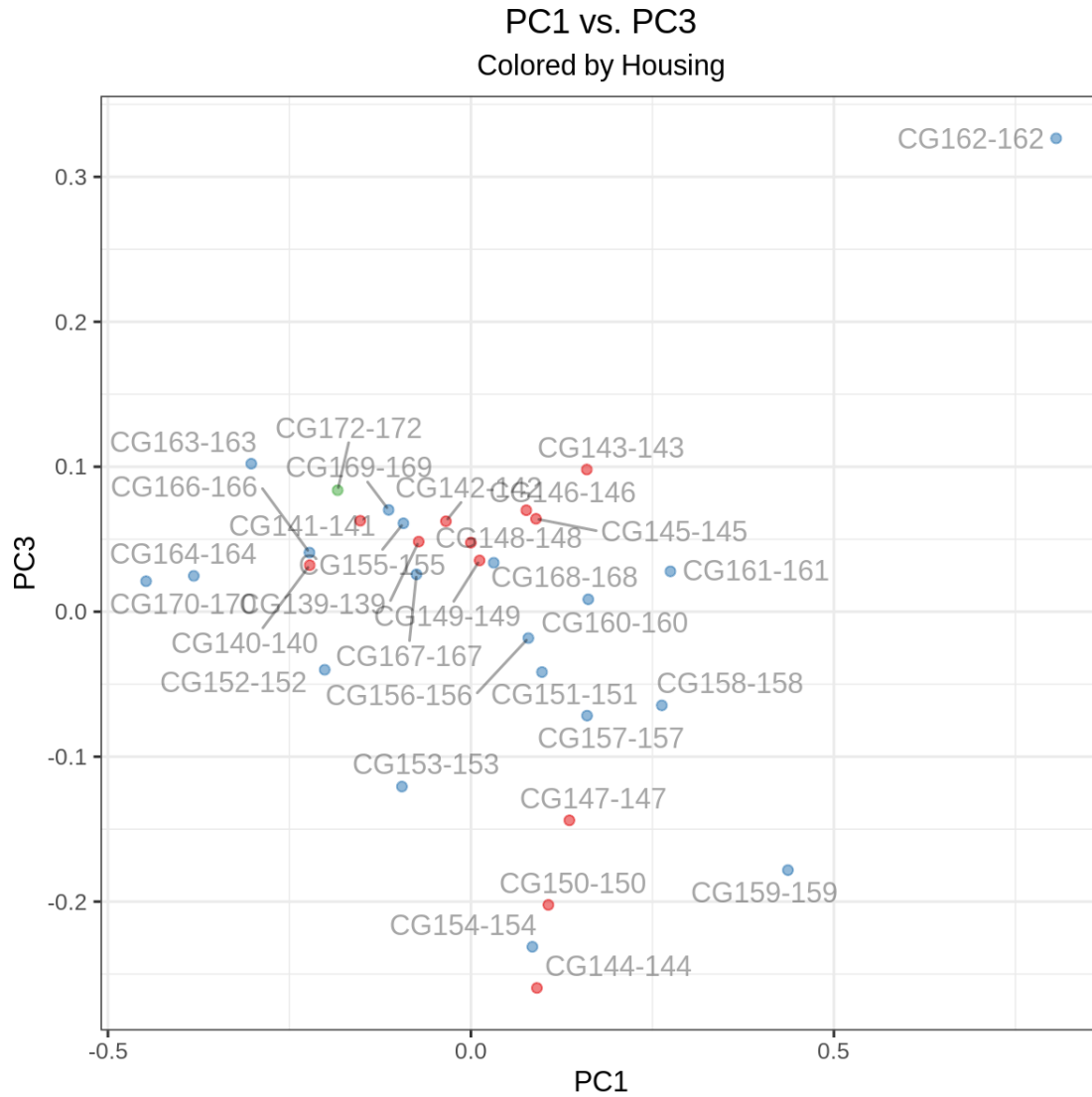
Legend for Housing

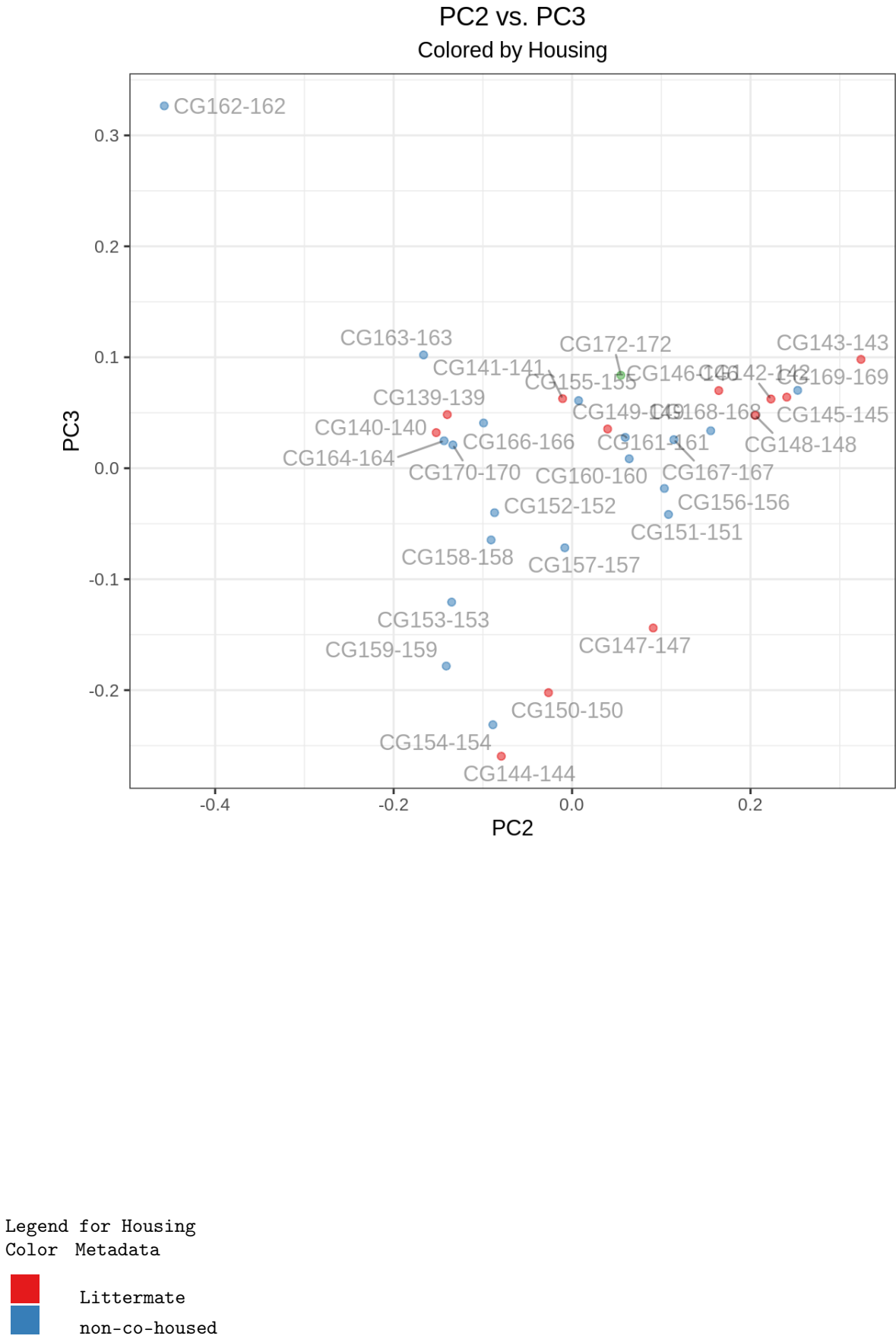
Color Metadata



Littermate

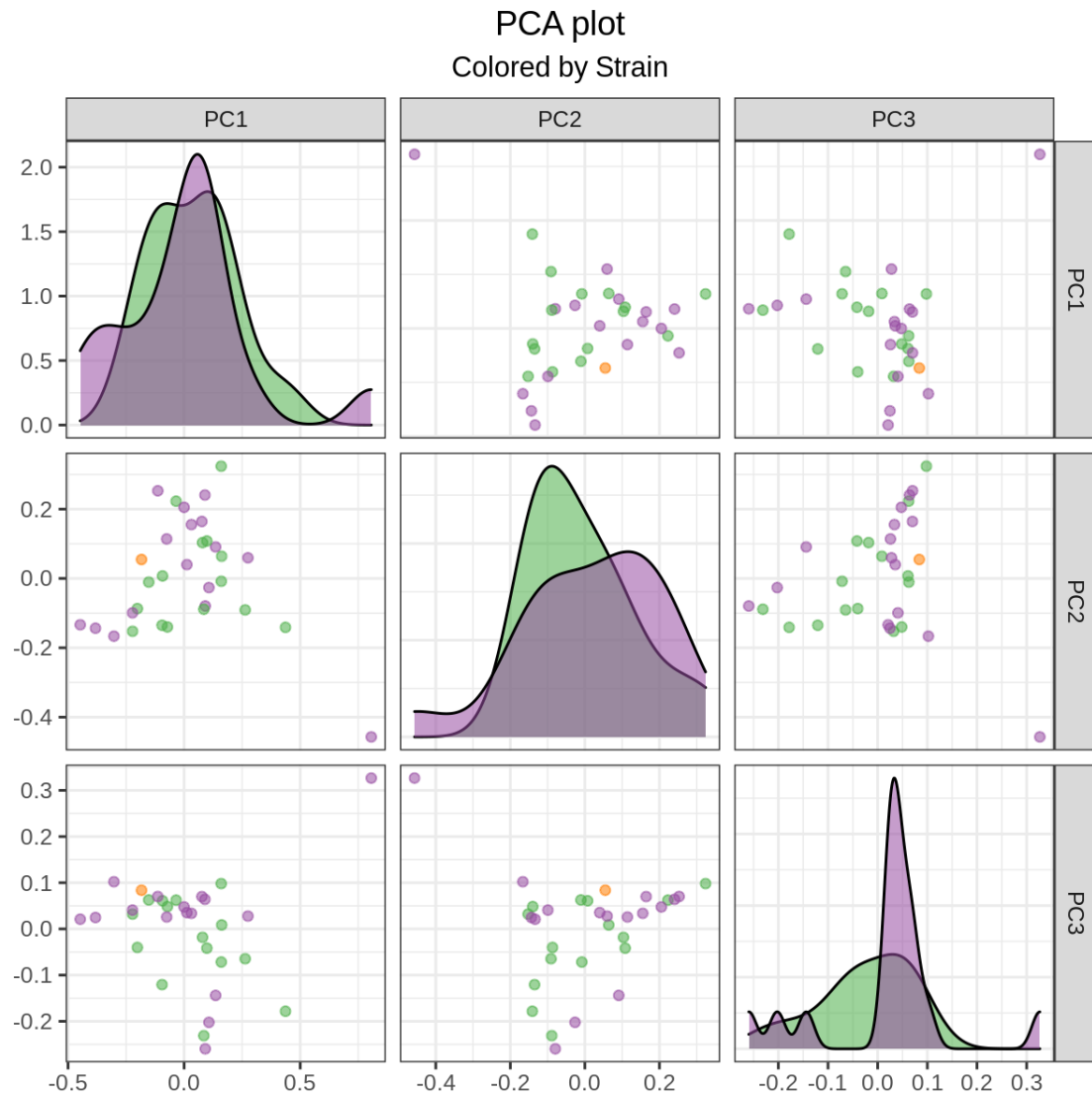
non-co-housed







g . Weighted UniFrac, grouped by Strain



The above plot represents the first three components created when performing Principle Component Analysis on the Beta diversity of the samples.

