

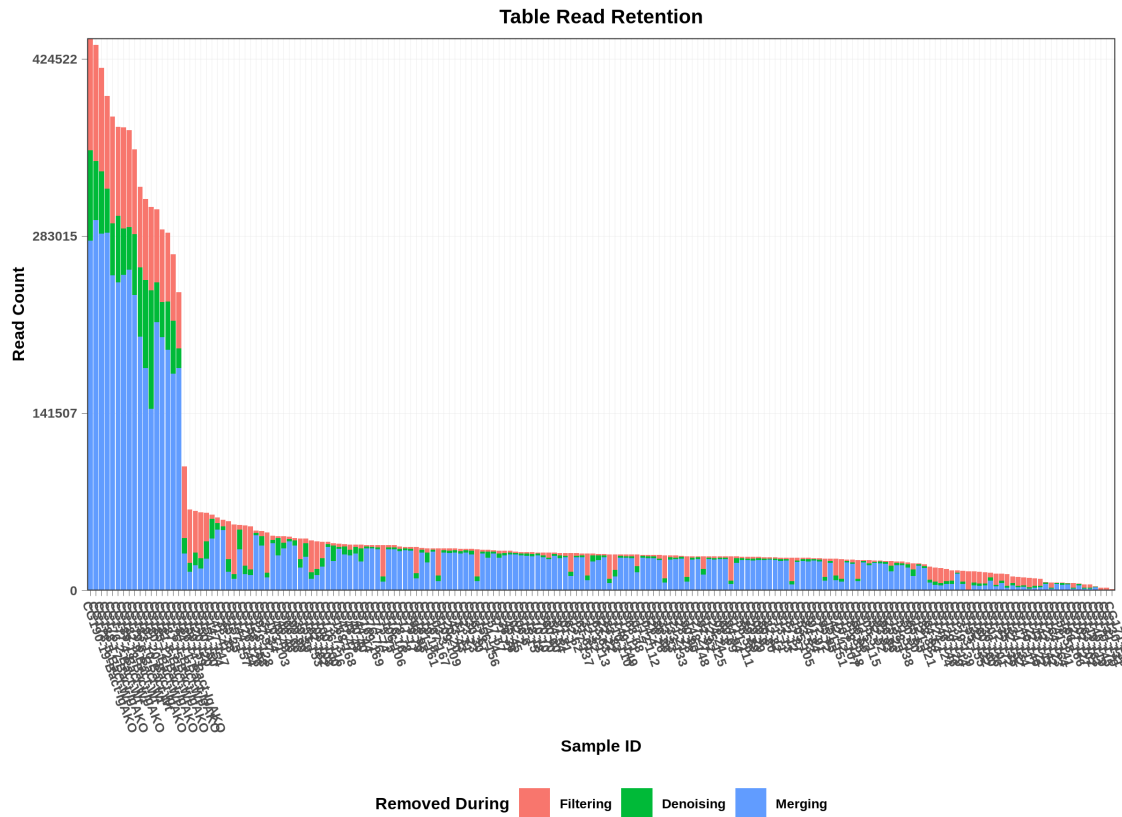
MMEDS Analysis Summary

Clemente Lab
Icahn School of Medicine at Mount Sinai

(Dated: May 17, 2022)

I. Table Statistics Summary

a . Dada2 Statistics



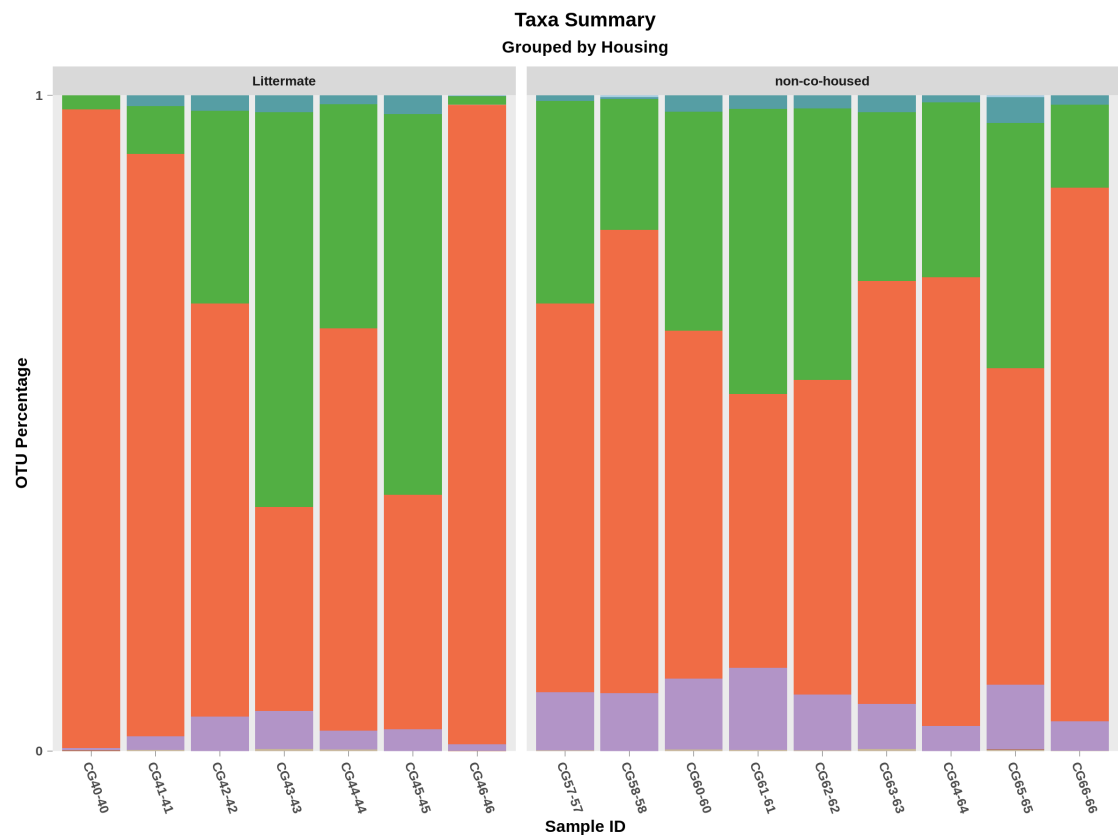
The above plot represents number of input reads (total bar length) and retained (magenta) after quality control filtering, including denoising and chimera checking.

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 high abundance of the taxa.

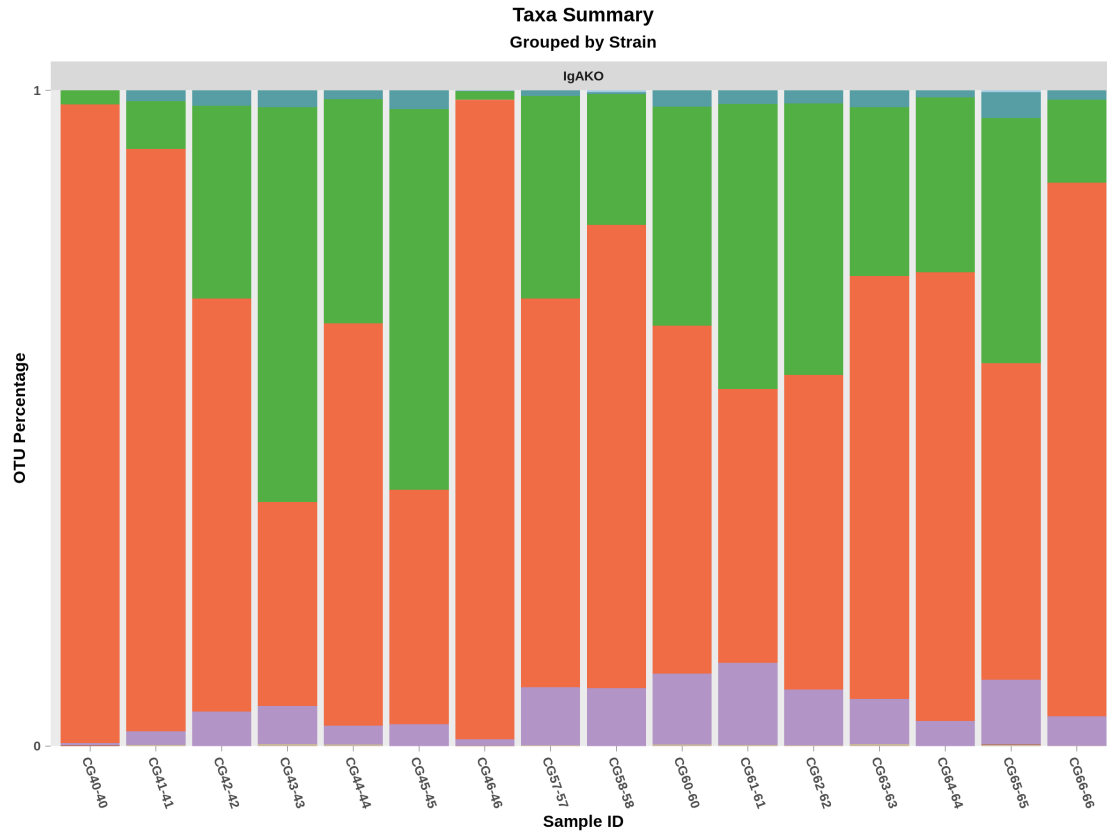
b . Phylum Level



Legend grouped by Housing

Color	Abundance	OTU
<div></div>	30.17%	k__Bacteria;p__Bacteroidetes
<div></div>	59.47%	k__Bacteria;p__Firmicutes
<div></div>	11.67%	k__Bacteria;p__Proteobacteria

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



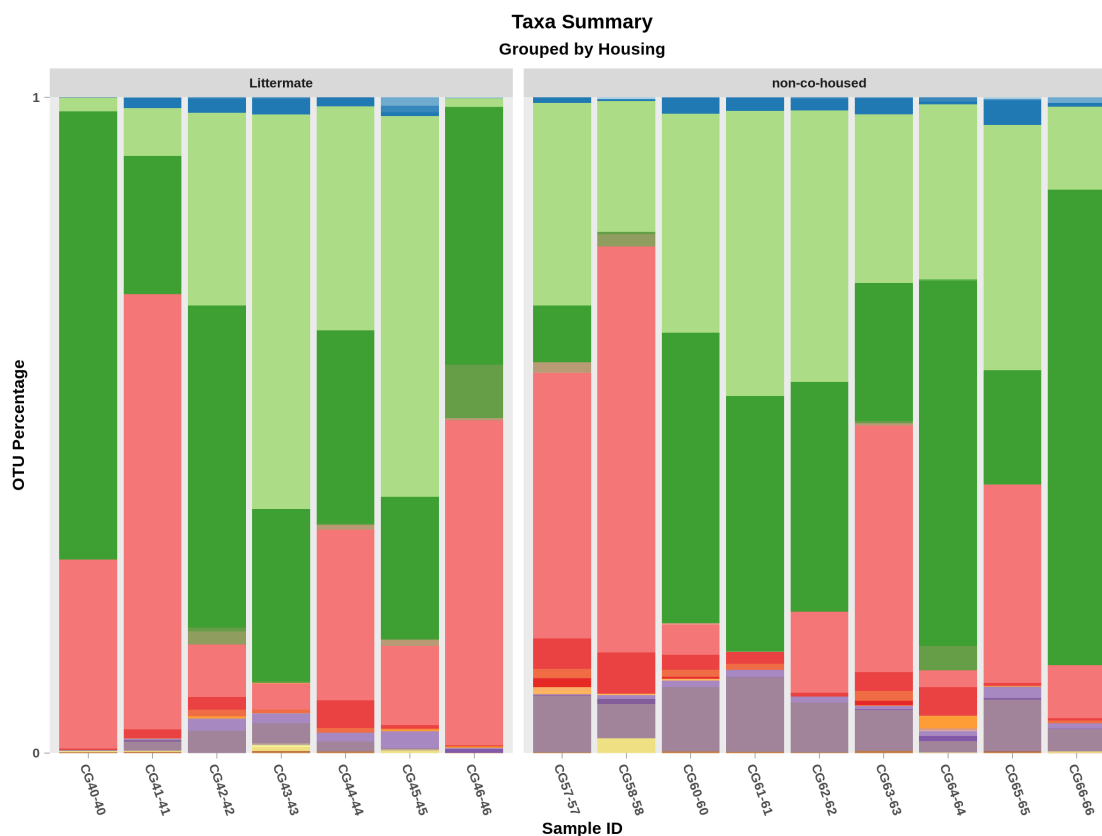
Legend grouped by Strain

Color Abundance OTU

	34.87%	k__Bacteria;p__Bacteroidetes
	63.13%	k__Bacteria;p__Firmicutes
	11.67%	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

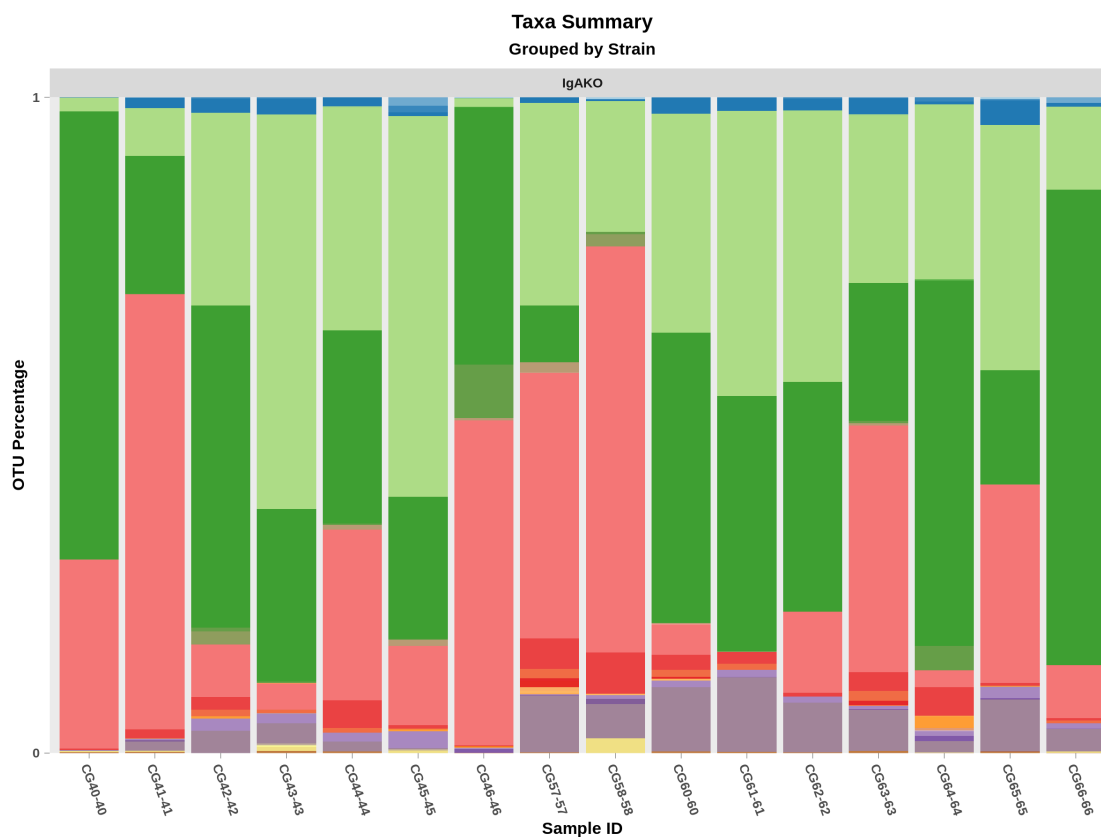


Legend grouped by Housing

Color Abundance OTU

	30.16%	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__S24-7;g__
	40.69%	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus
	36.50%	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Candidatus Arthromitus
	11.34%	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Desulfovibrio

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

- 34.84%
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__S24-7;g__
- 38.57%
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus
- 36.53%
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Candidatus
Arthromitus
- 11.34%
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Desulfovibrio

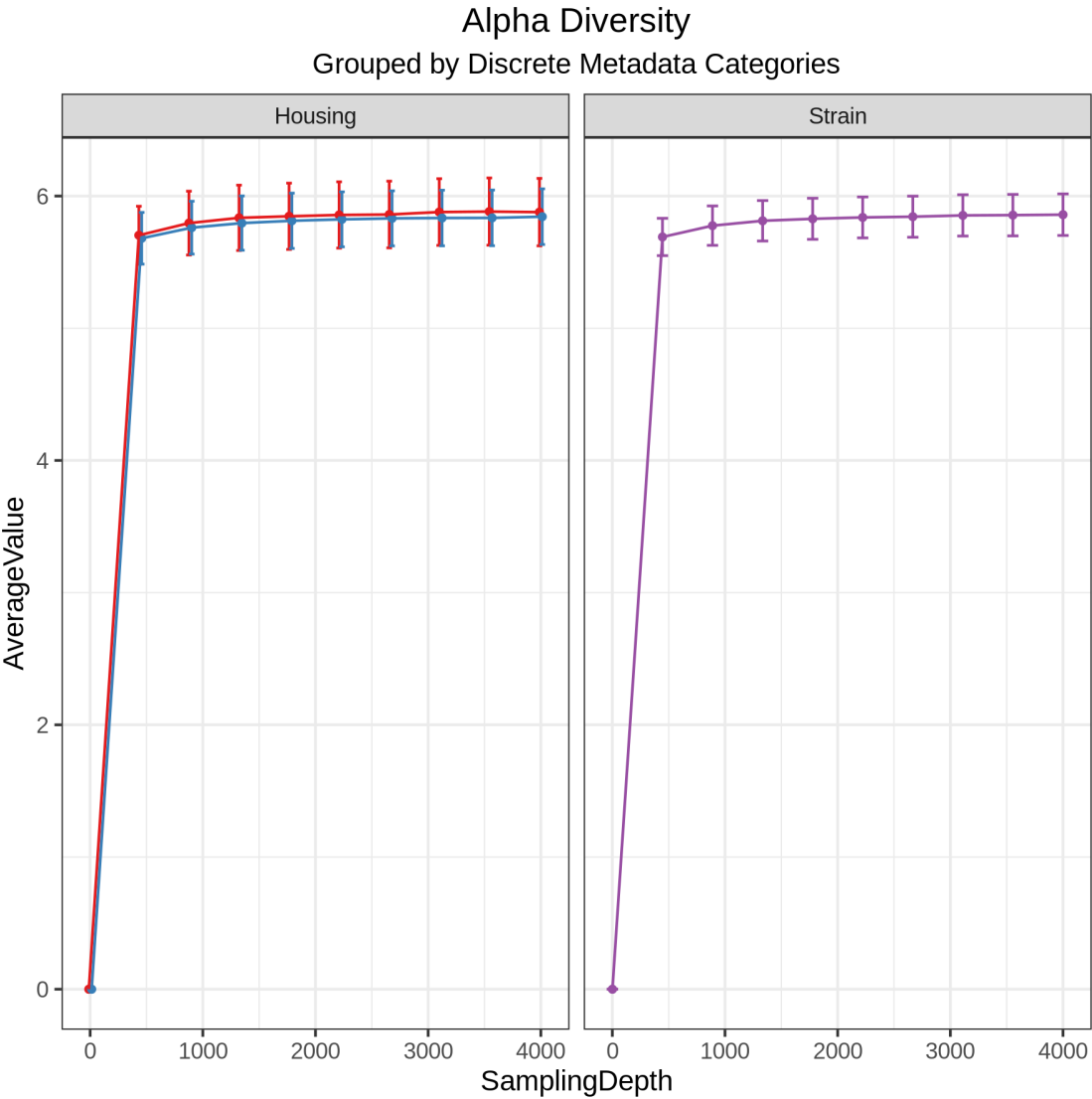
The above plot represents the percentage of each sample belonging to particular taxon summarized at the Genus level.

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

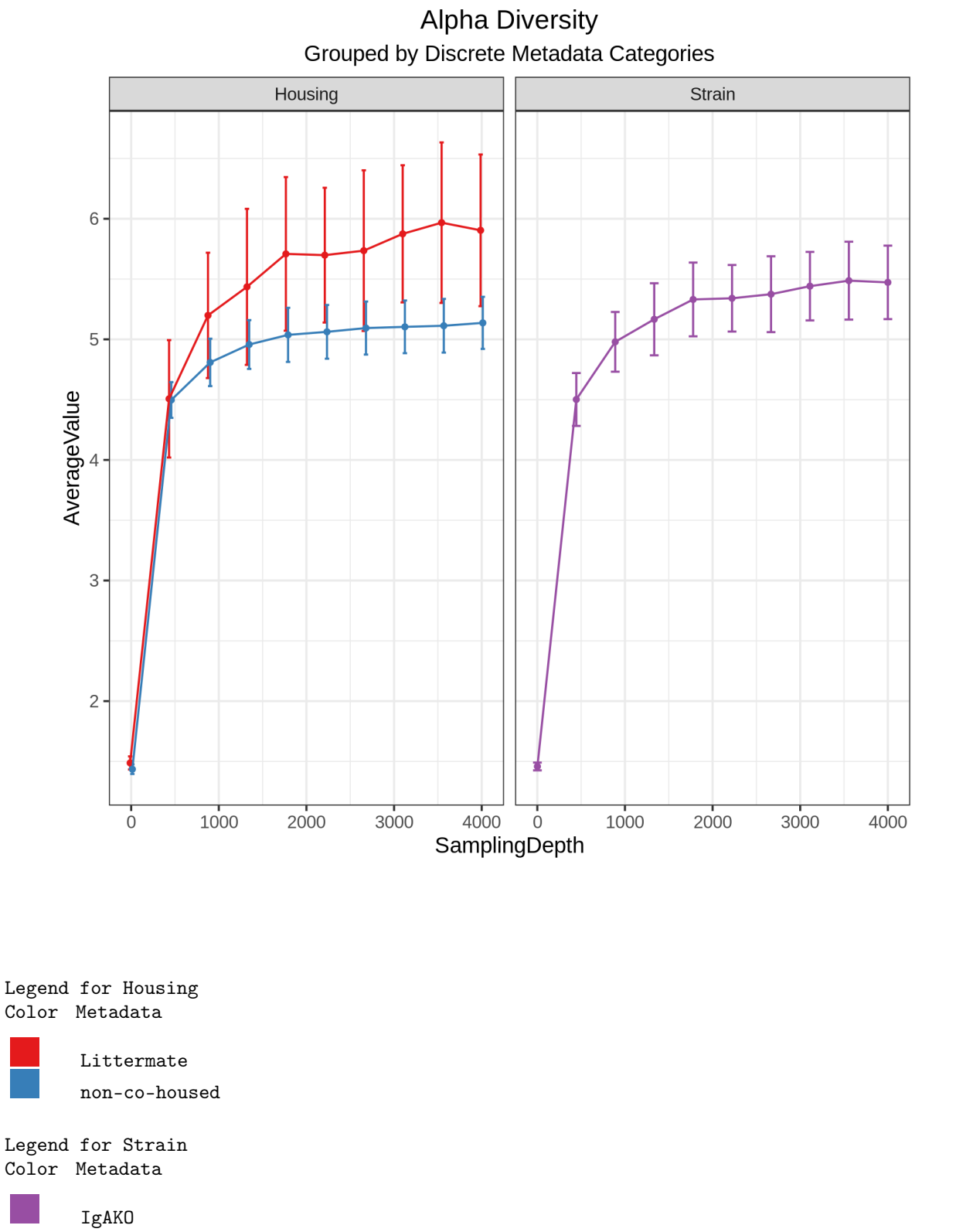
 Littermate
 non-co-housed

Legend for Strain
Color Metadata

 IgAKO

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.

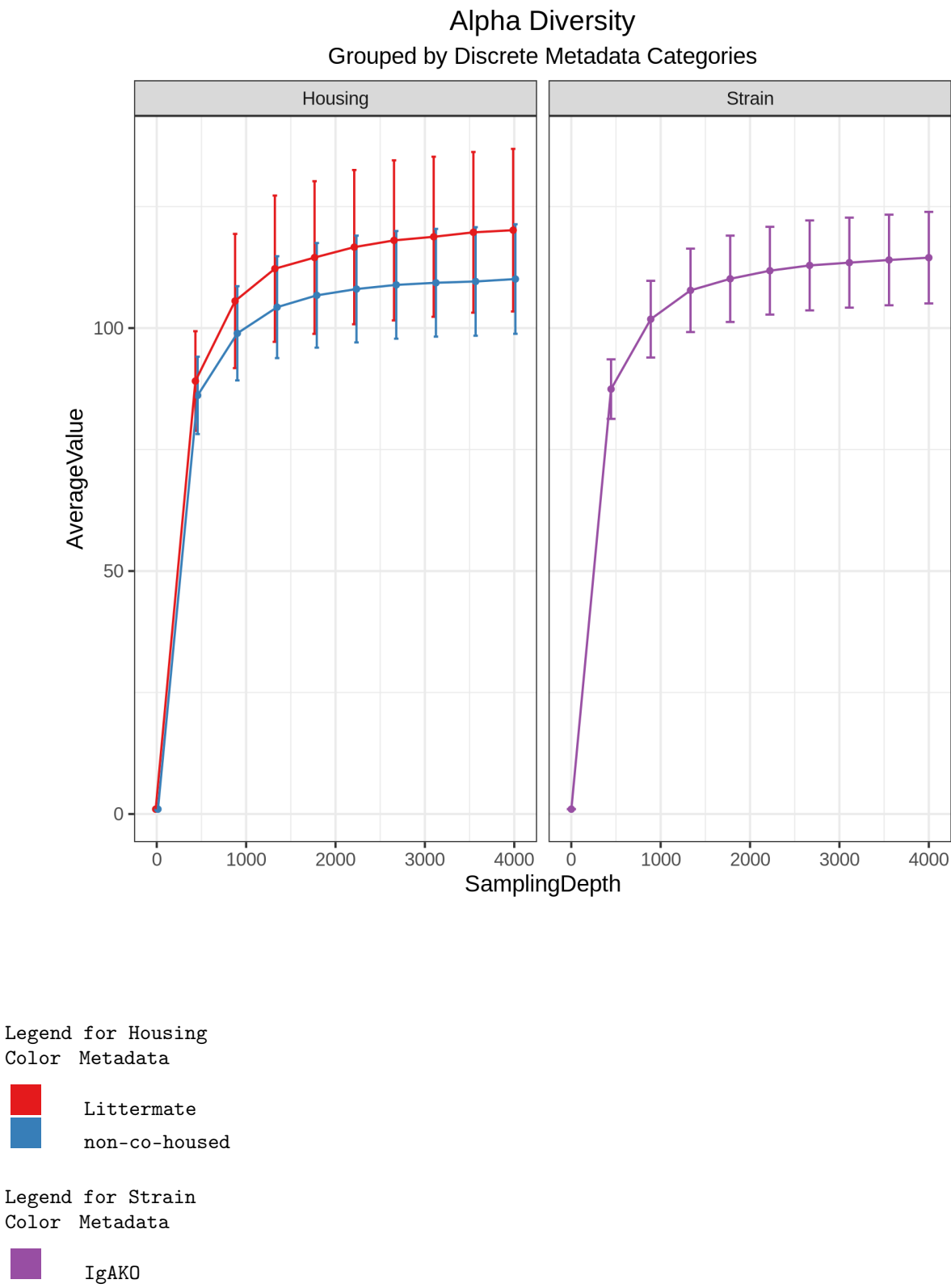
c . Faith's Phylogenetic Diversity



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



The above plot represents the average value of alpha diversity at each sampling depth. The error bars

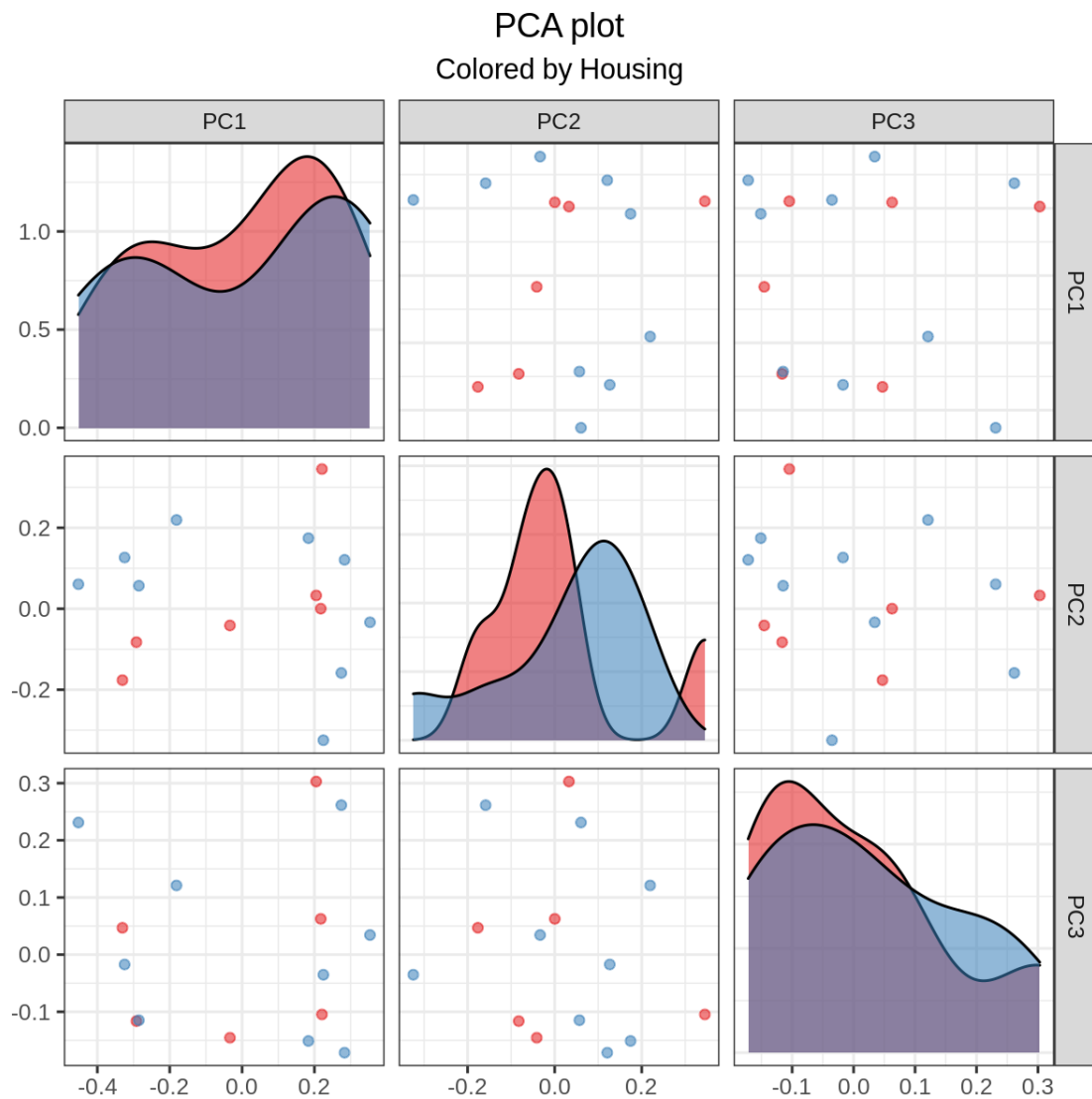
show the standard error within each group. Groups are determined by the metadata value in each category specified in the plot.

IV. Beta Diversity

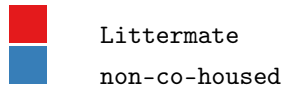
a . Interpreting Beta Diversity Results

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.

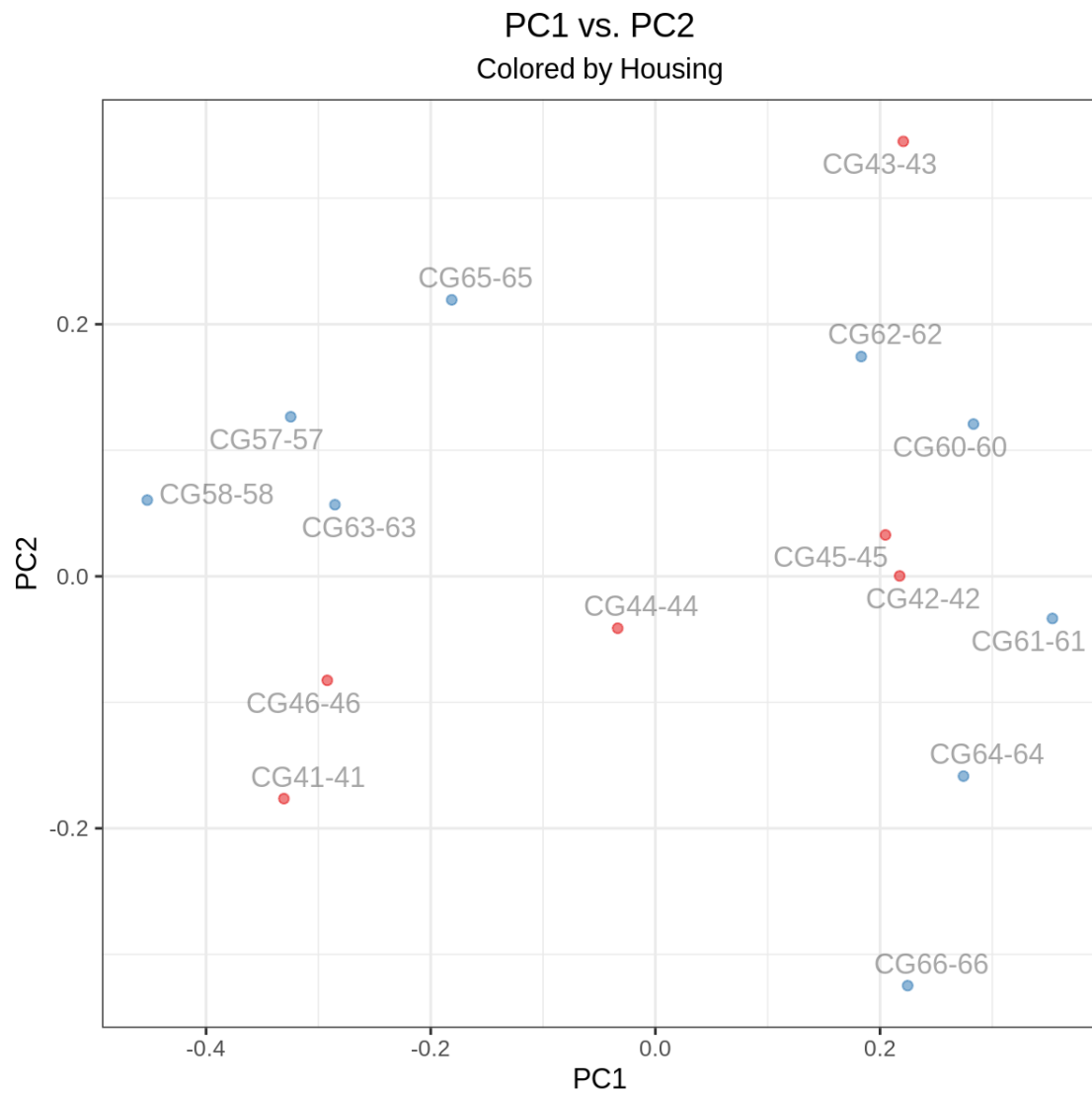
b . Bray-Curtis, grouped by Housing



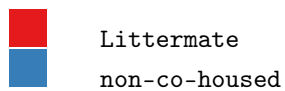
Legend for Housing
Color Metadata

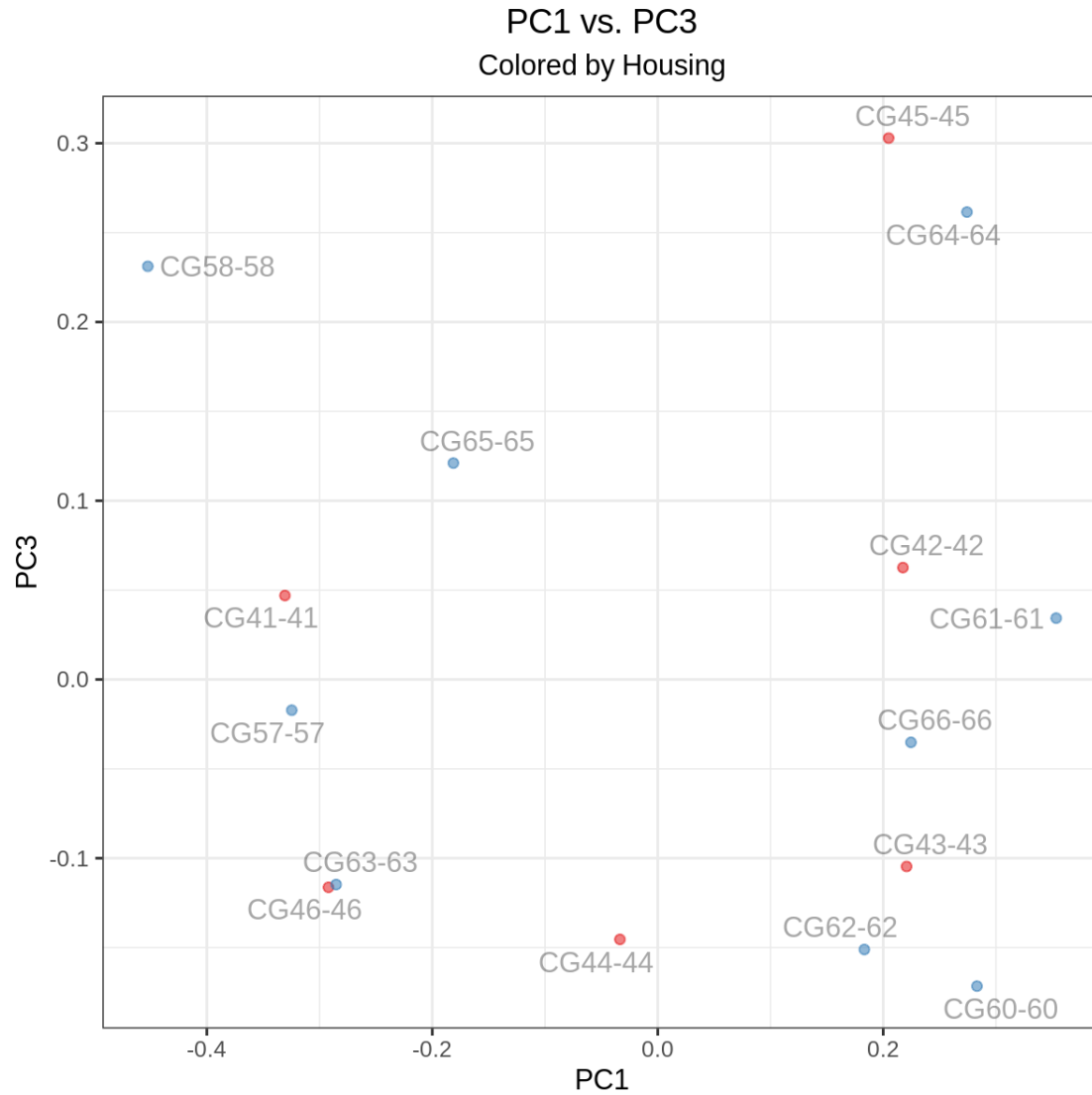


The above plot represents the first three components created when performing Principle Component Analysis on the Beta diversity of the samples.



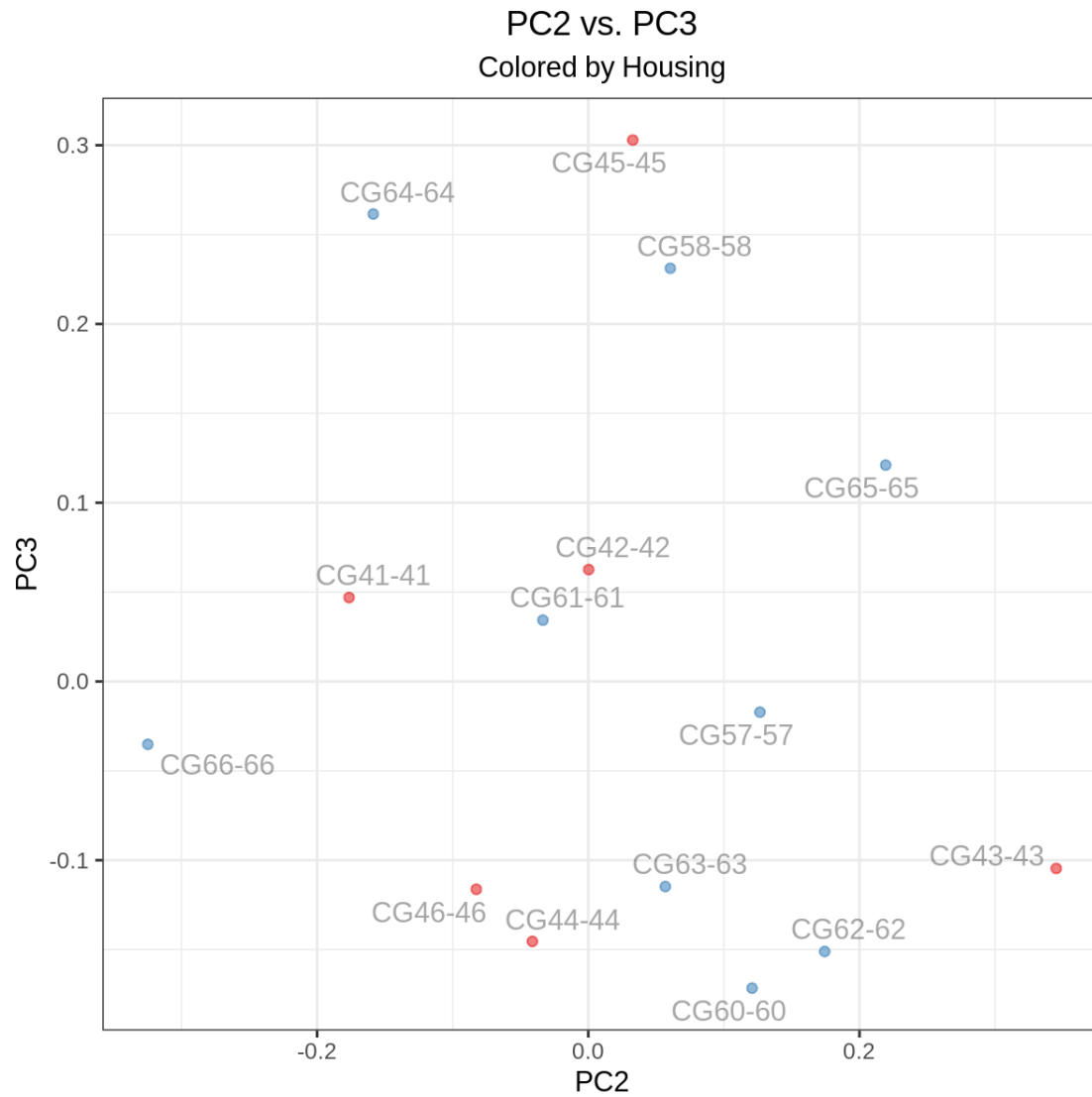
Legend for Housing
Color Metadata





Legend for Housing
Color Metadata

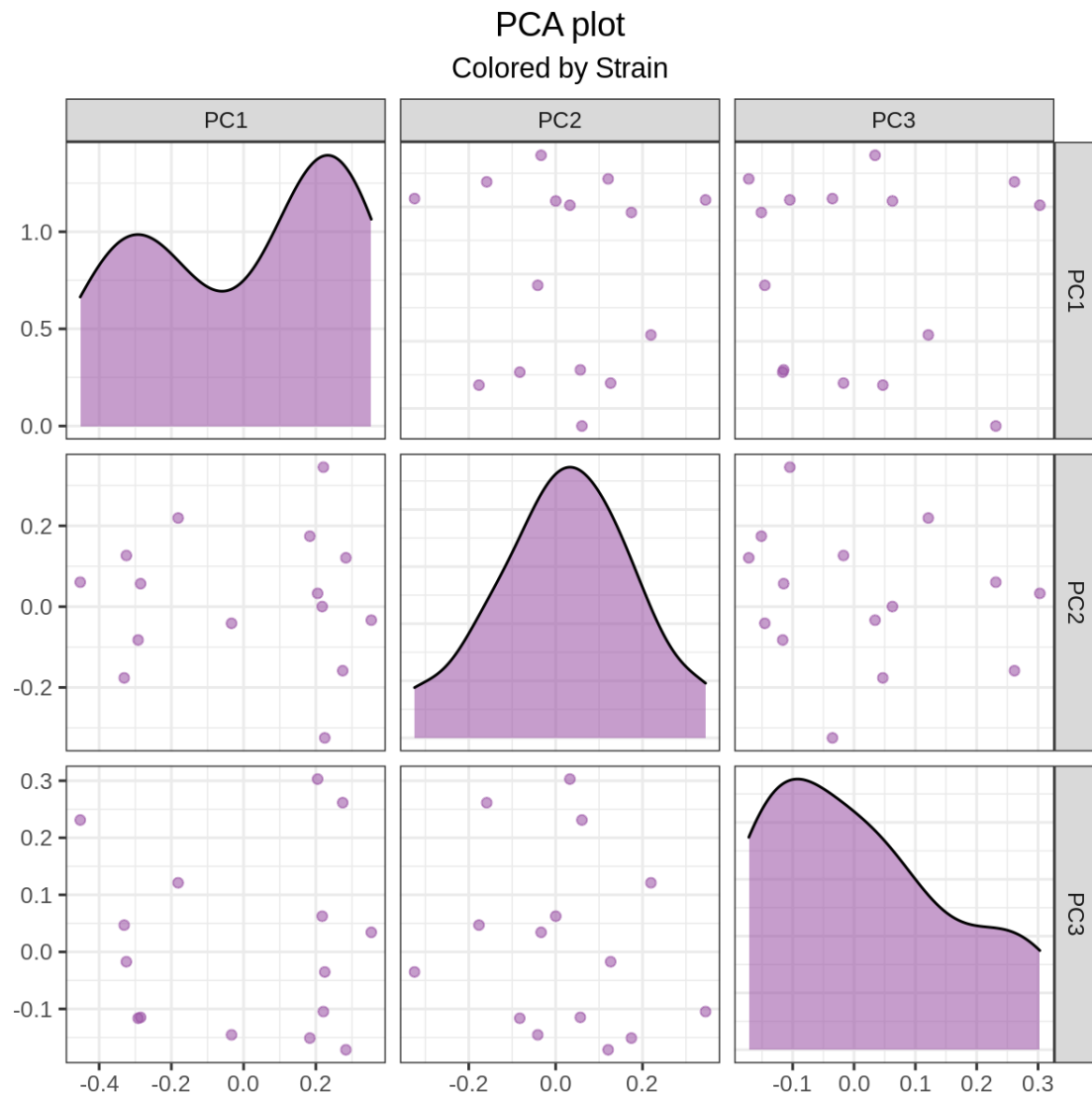
■	Littermate
■	non-co-housed



Legend for Housing
Color Metadata

■	Littermate
■	non-co-housed

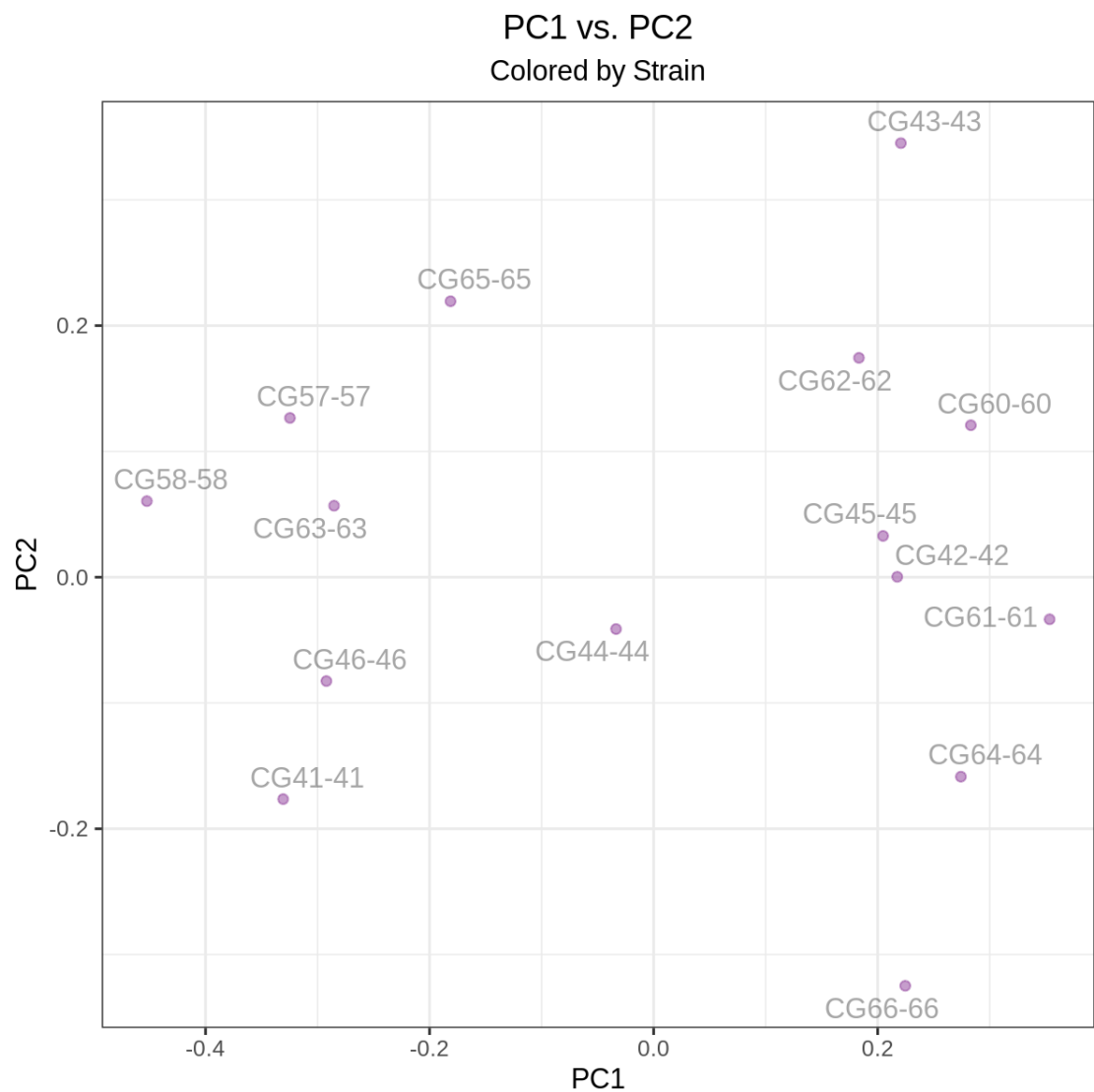
c . Bray-Curtis, grouped by Strain



Legend for Strain
Color Metadata

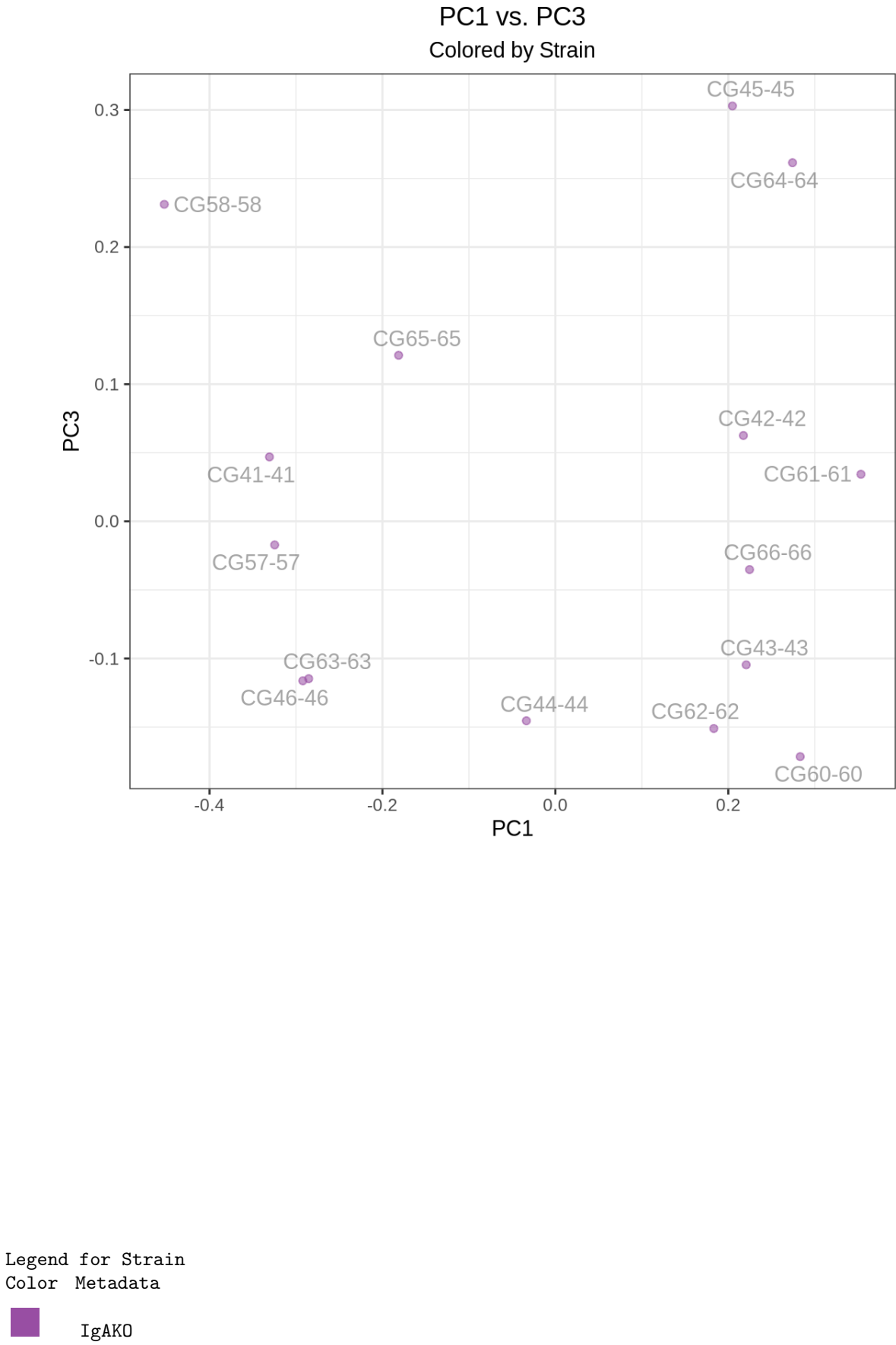
IgAK0

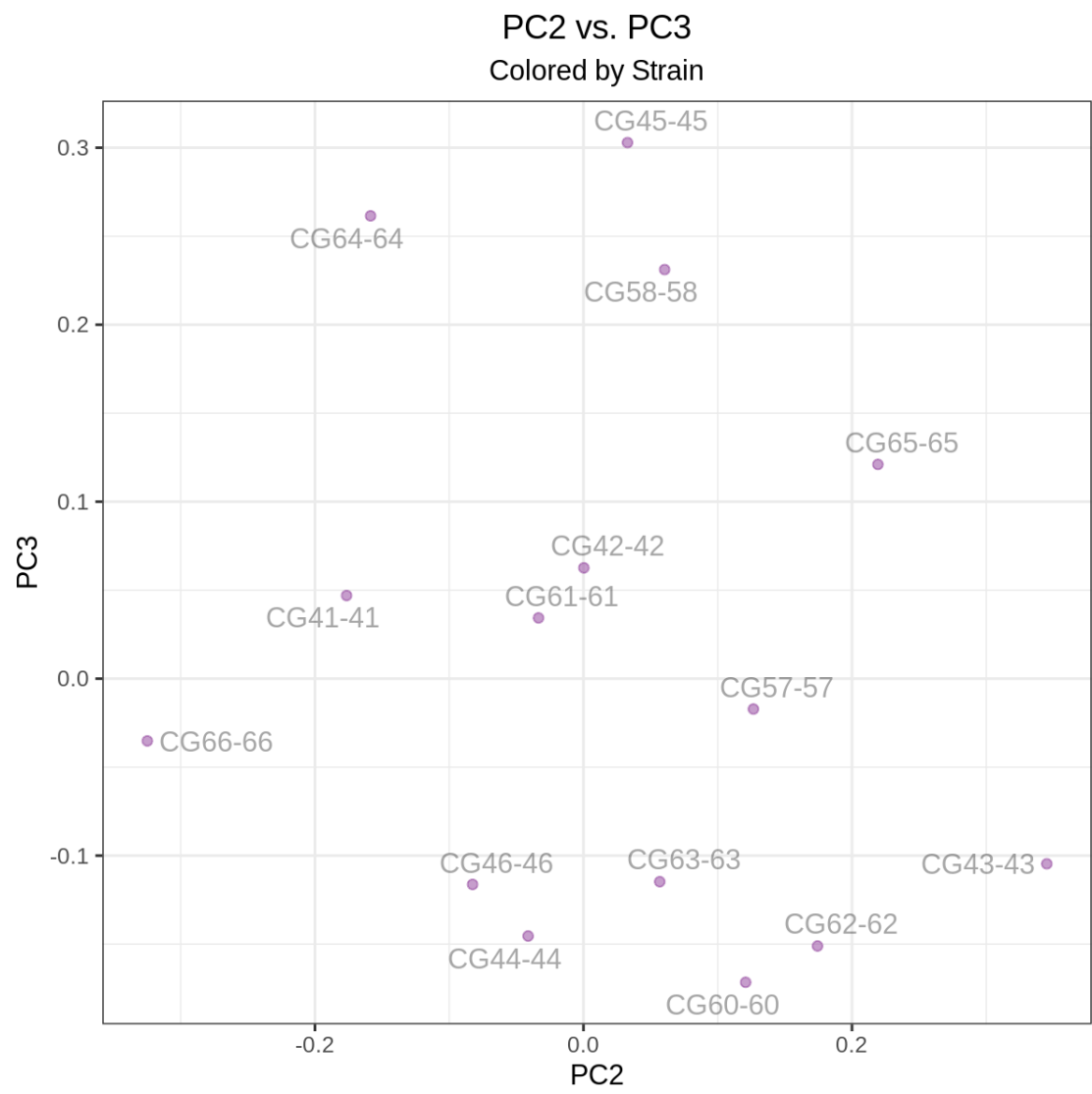
The above plot represents the first three components created when performing Principle Component Analysis on the Beta diversity of the samples.



Legend for Strain
Color Metadata

IgAKO

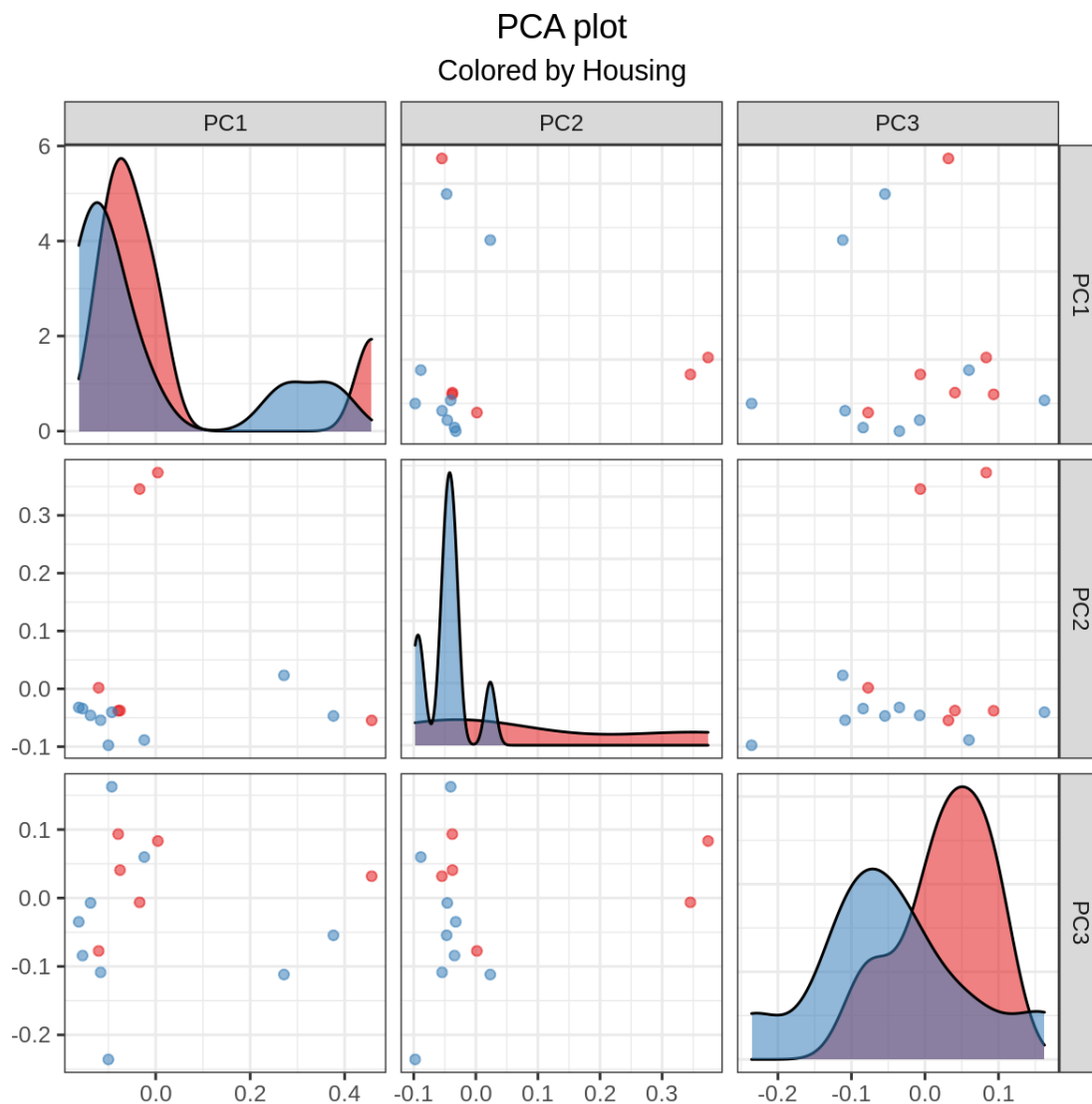




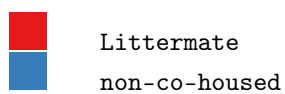
Legend for Strain
Color Metadata

IgAKO

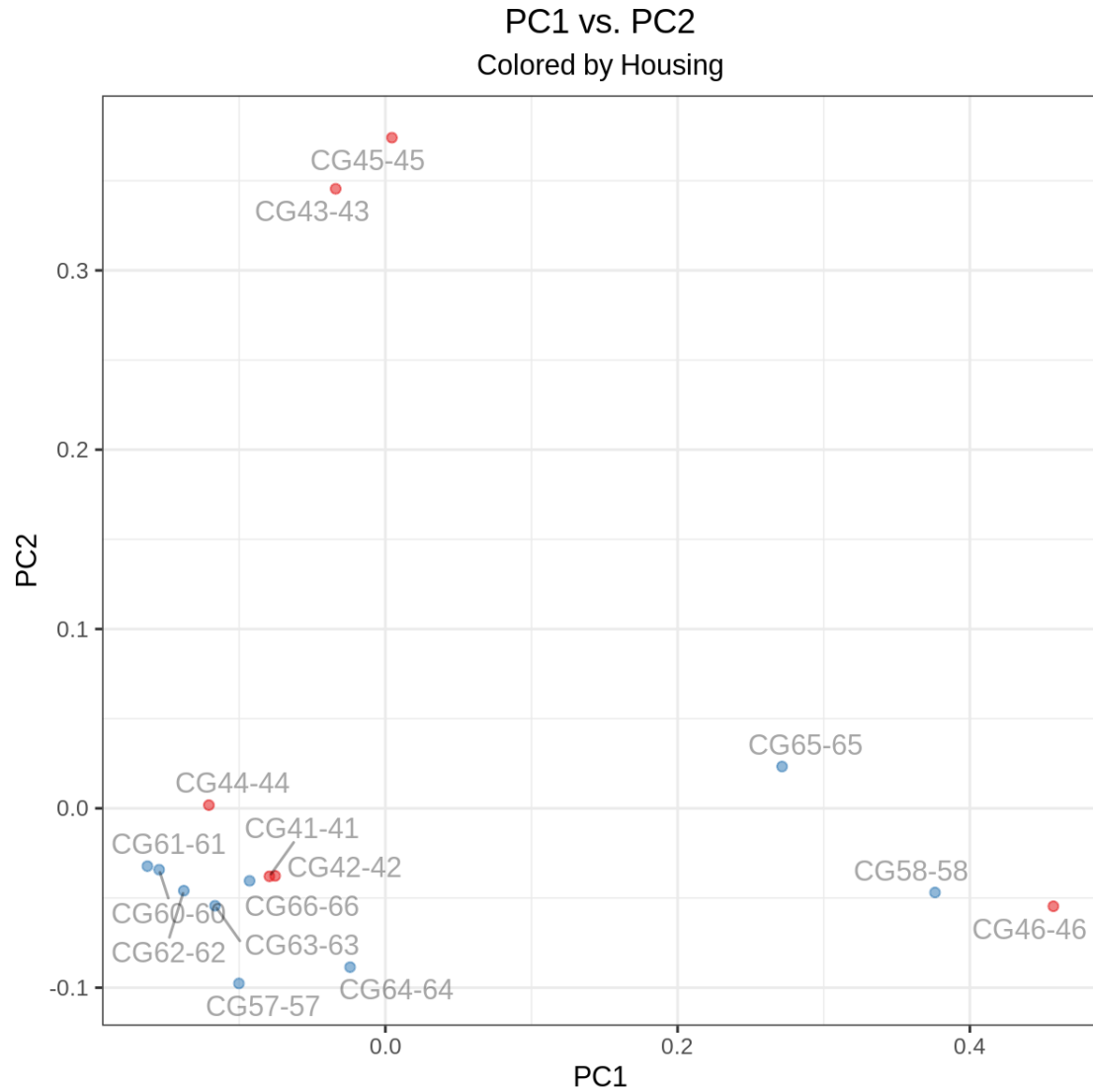
d . Unweighted UniFrac, grouped by Housing



Legend for Housing
Color Metadata

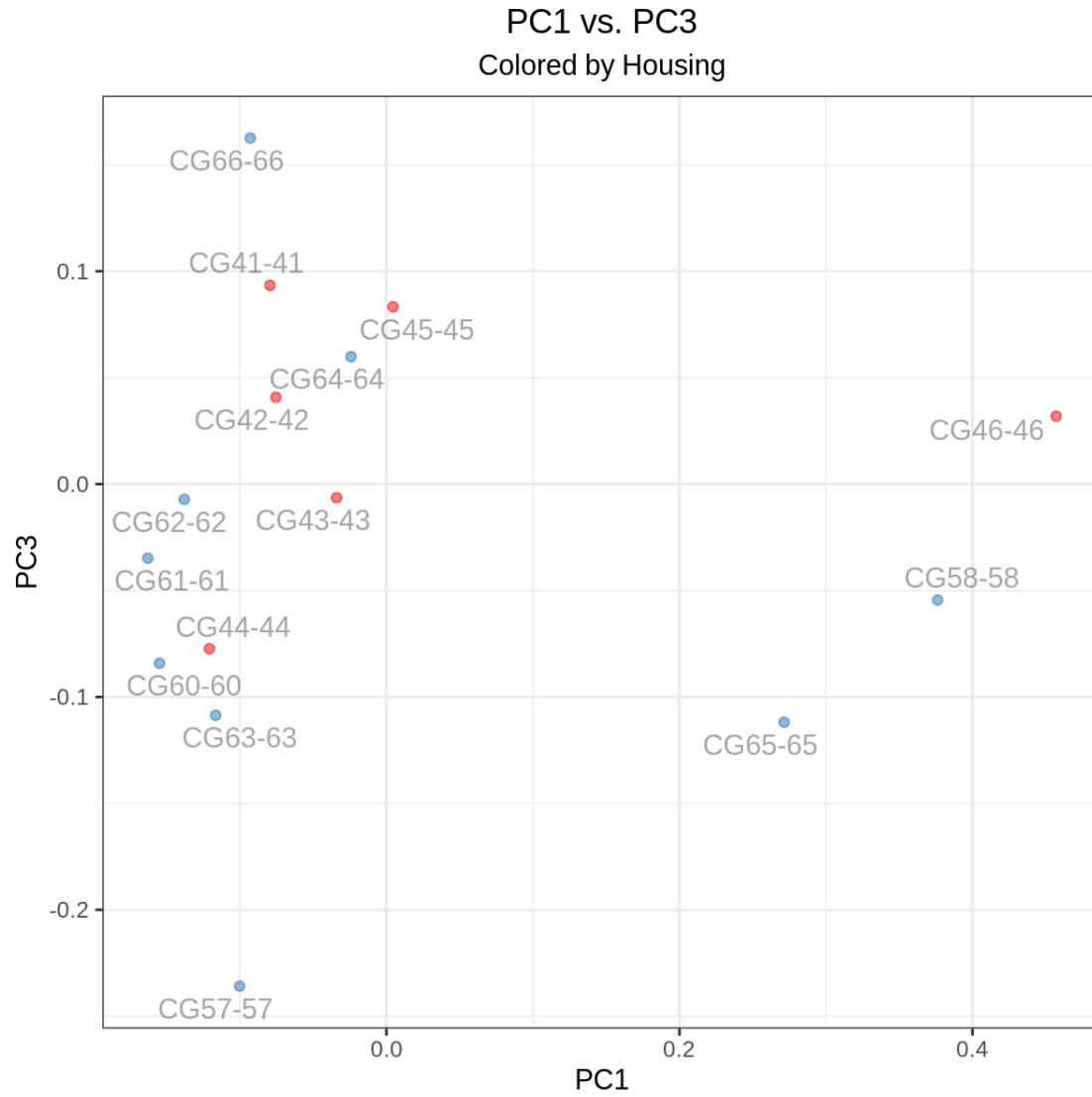


The above plot represents the first three components created when performing Principle Component Analysis on the Beta diversity of the samples.



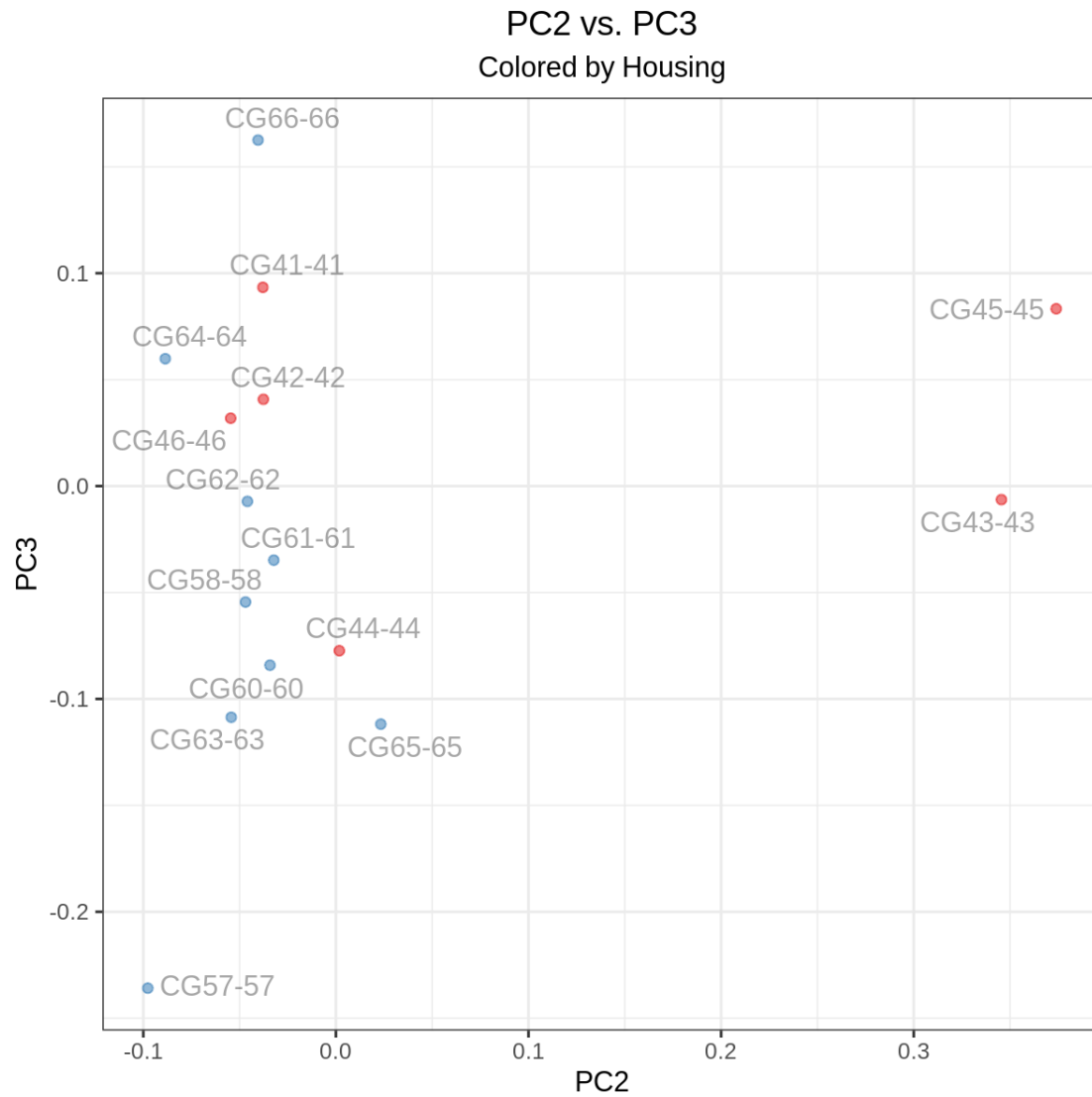
Legend for Housing
Color Metadata

■	Littermate
■	non-co-housed



Legend for Housing
Color Metadata

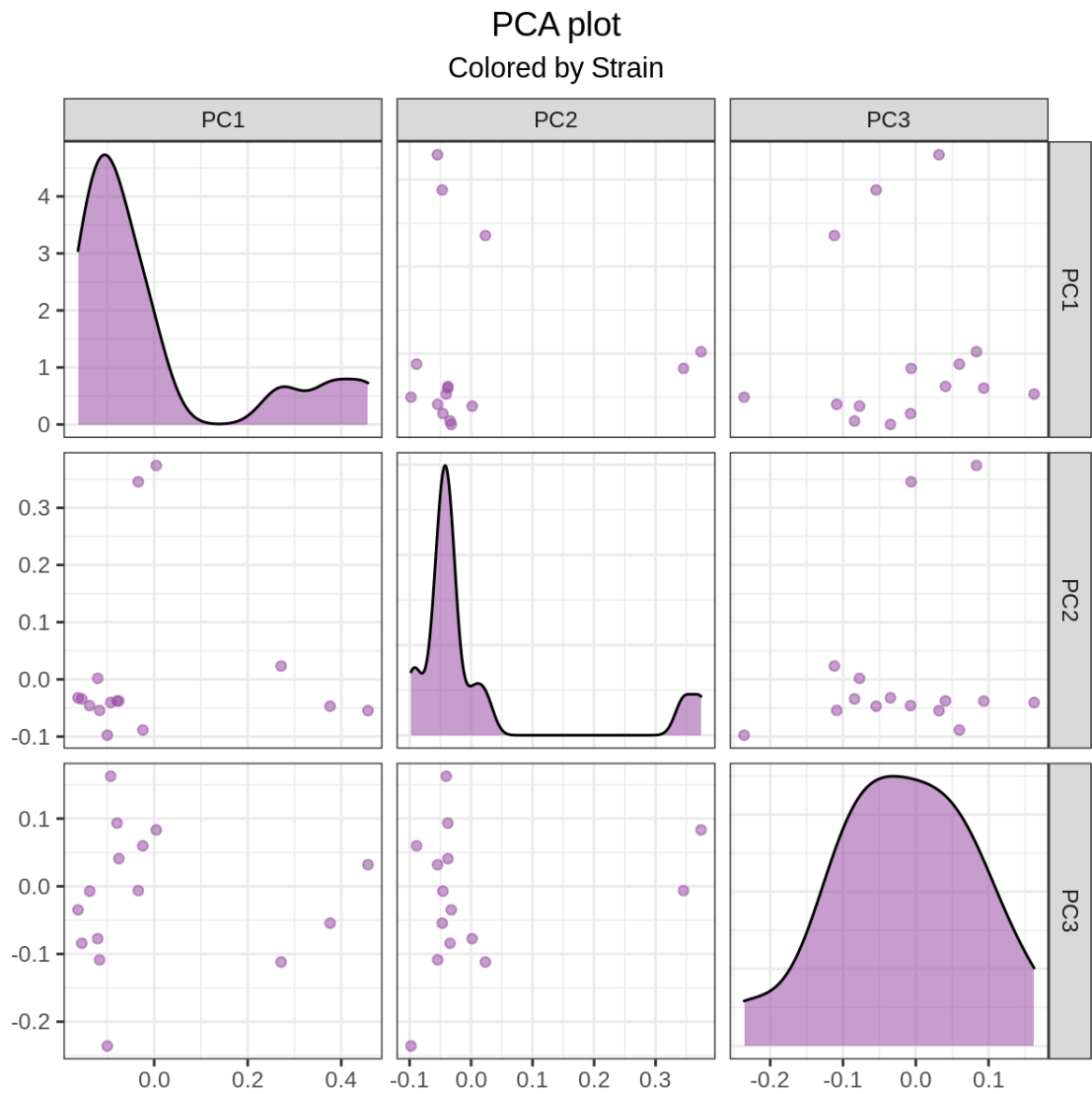
■	Littermate
■	non-co-housed



Legend for Housing
Color Metadata

■	Littermate
■	non-co-housed

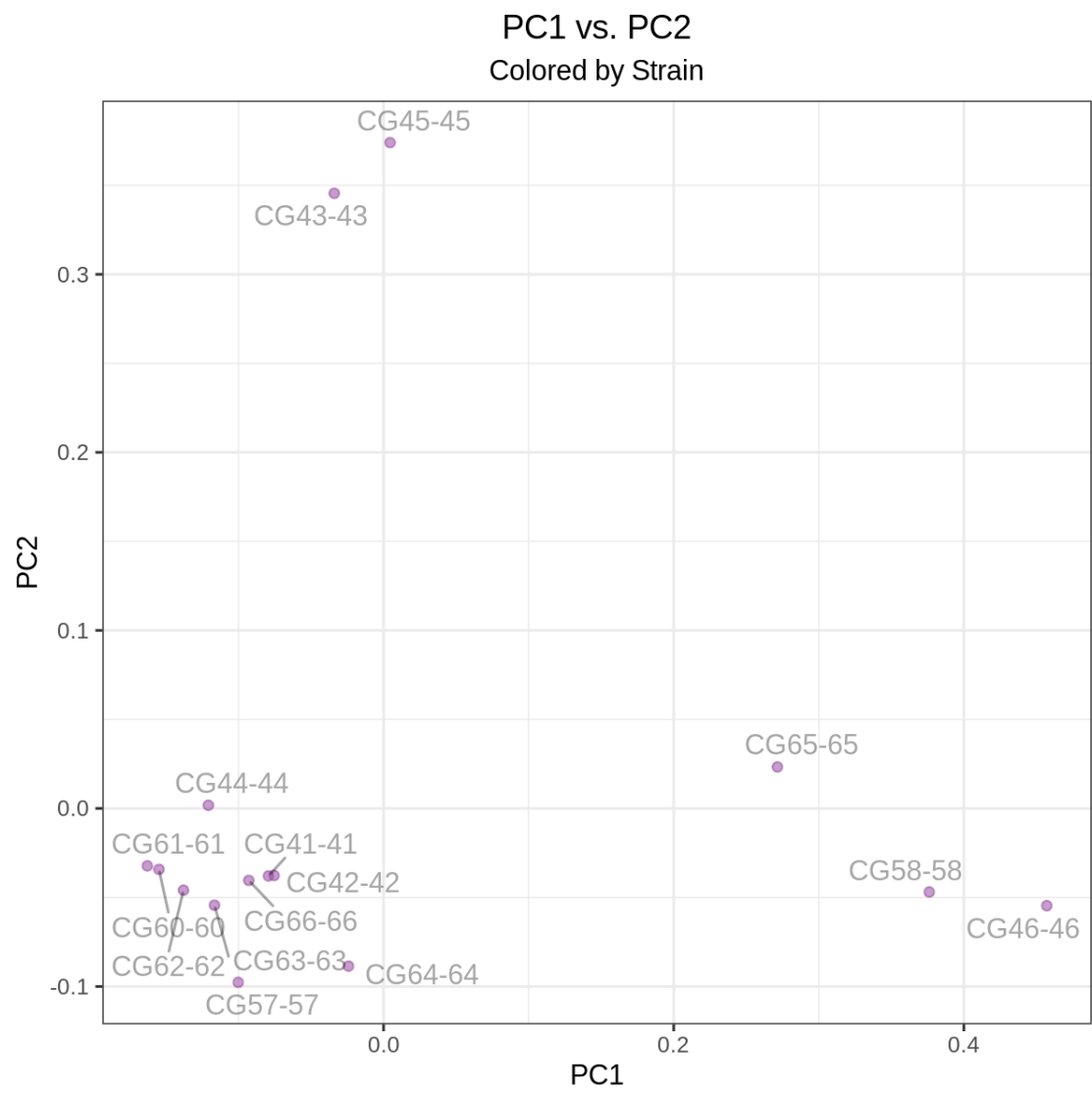
e . Unweighted UniFrac, grouped by Strain



Legend for Strain
Color Metadata

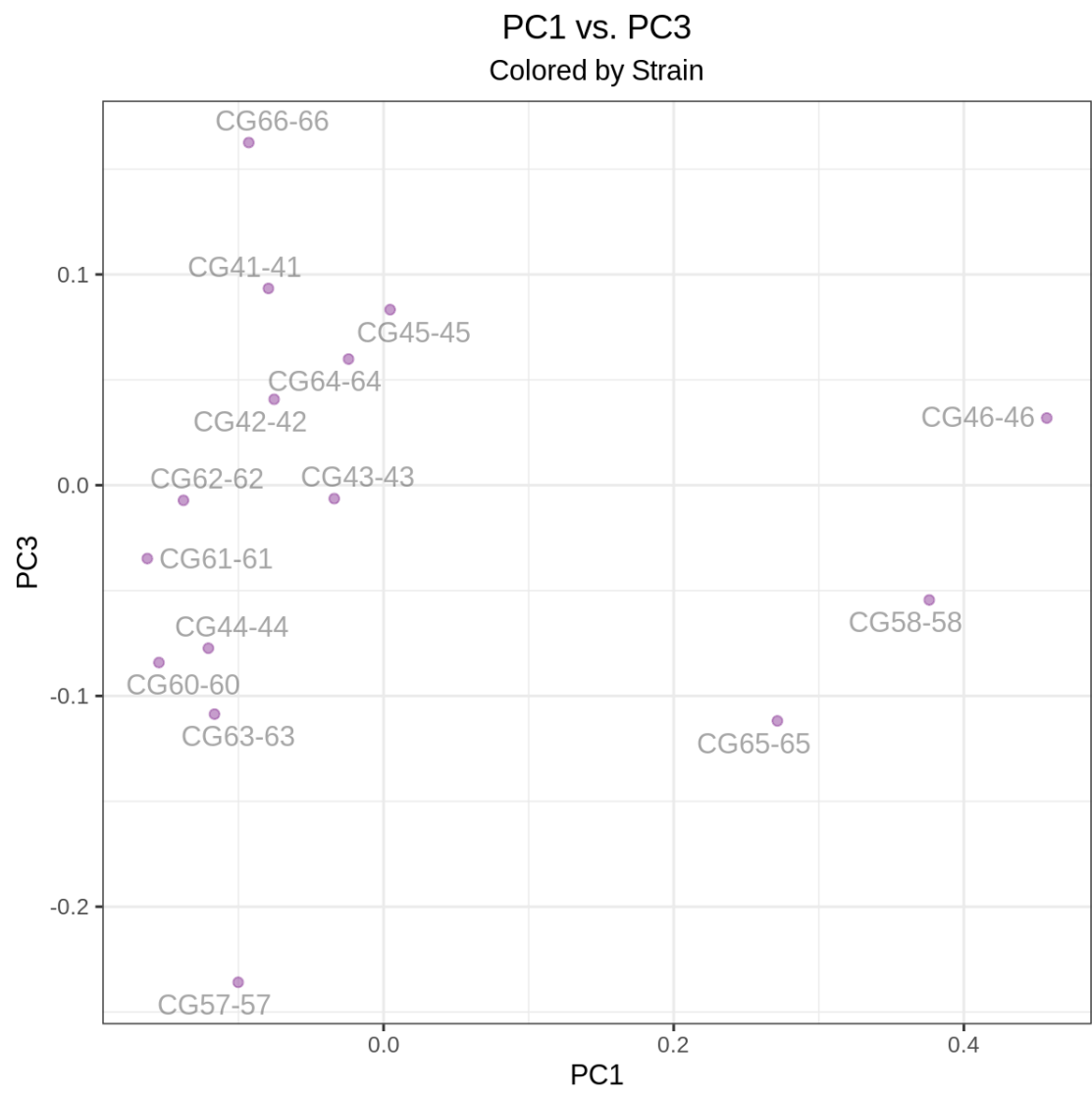
IgAK0

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



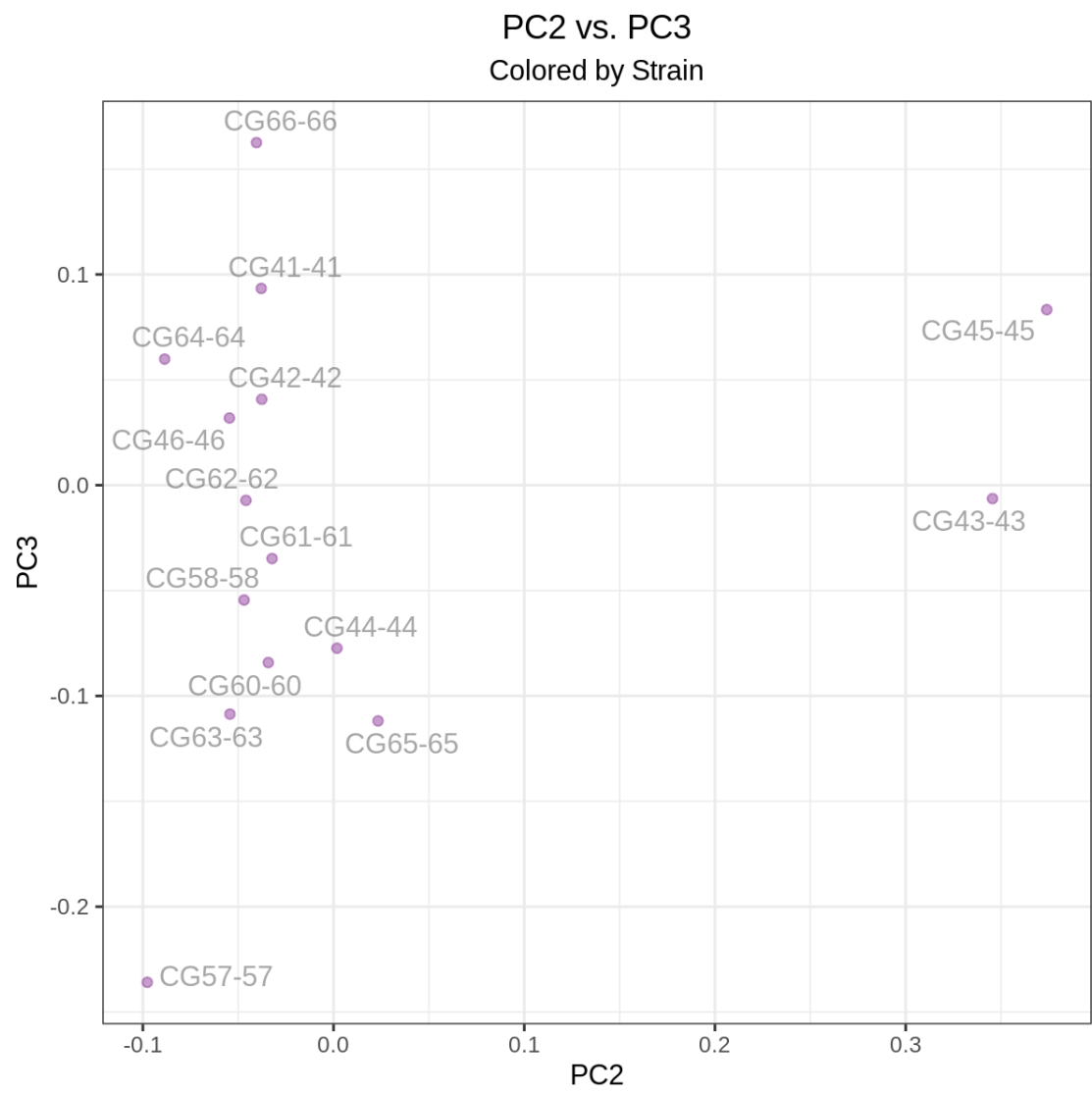
Legend for Strain
Color Metadata

IgAKO



Legend for Strain
Color Metadata

IgAKO



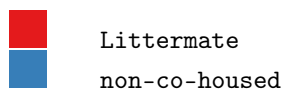
Legend for Strain
Color Metadata

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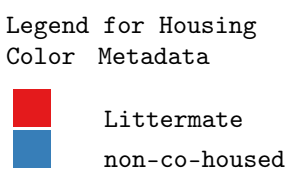
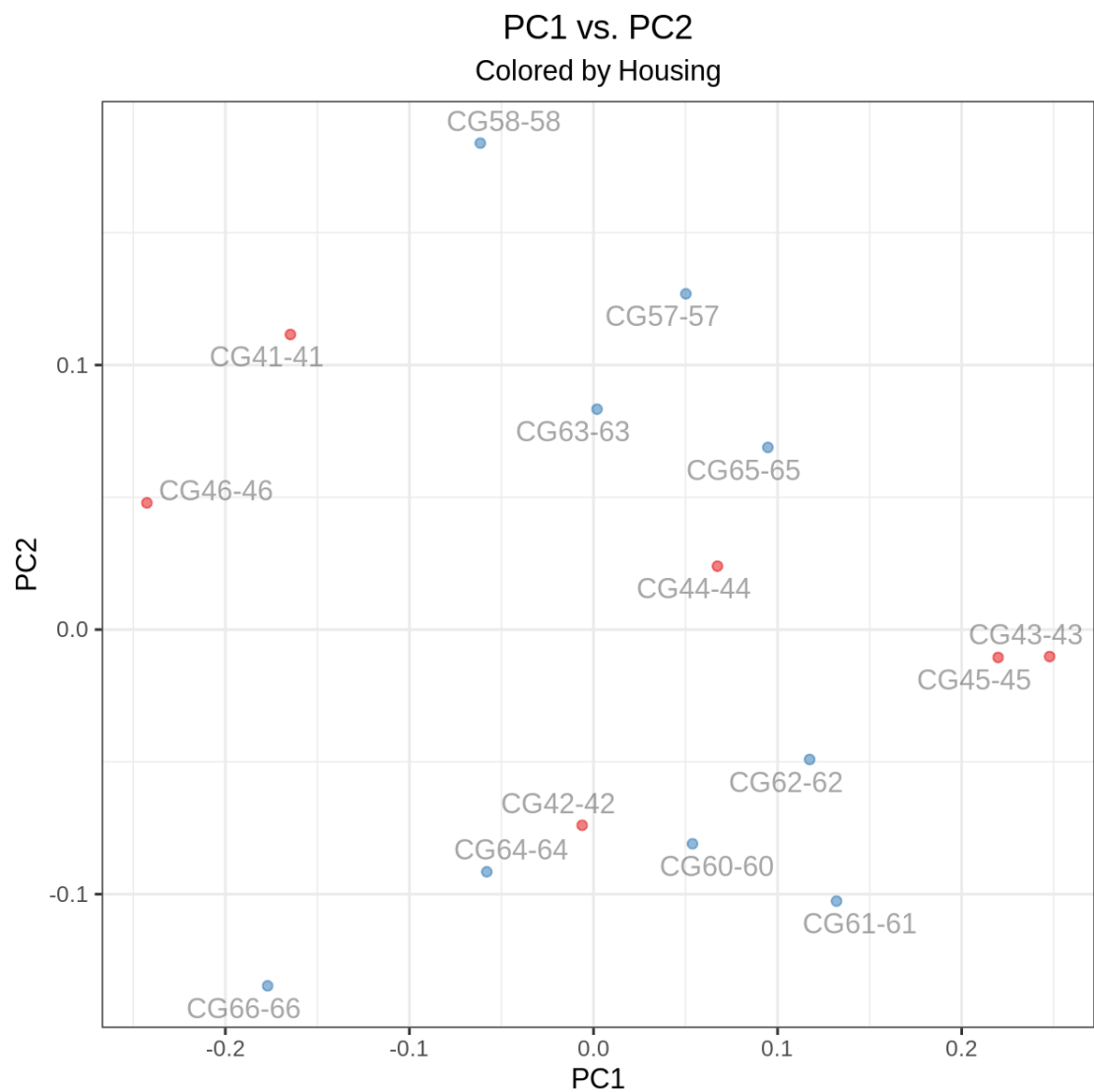
f . Weighted UniFrac, grouped by Housing

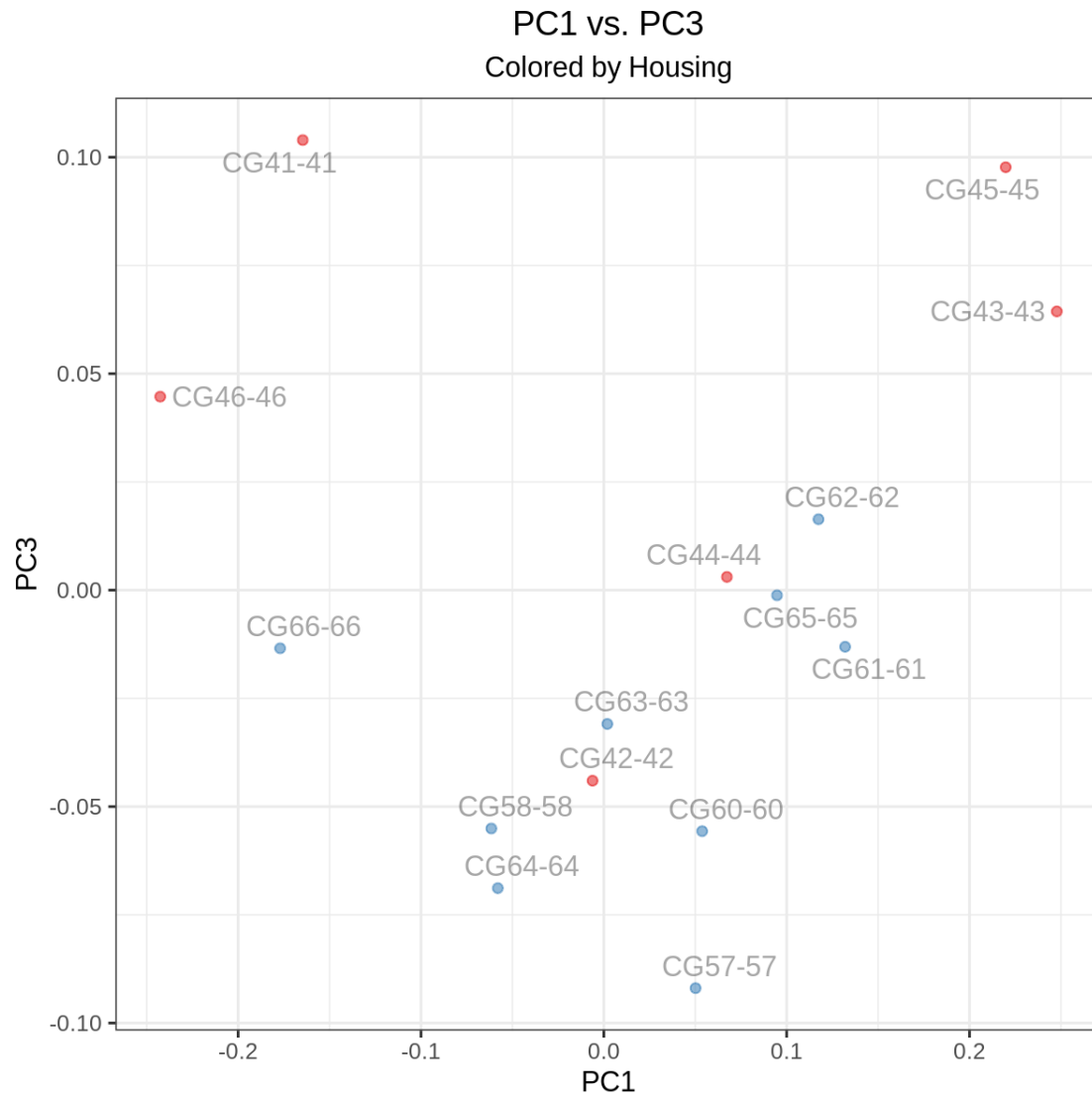


Legend for Housing
Color Metadata



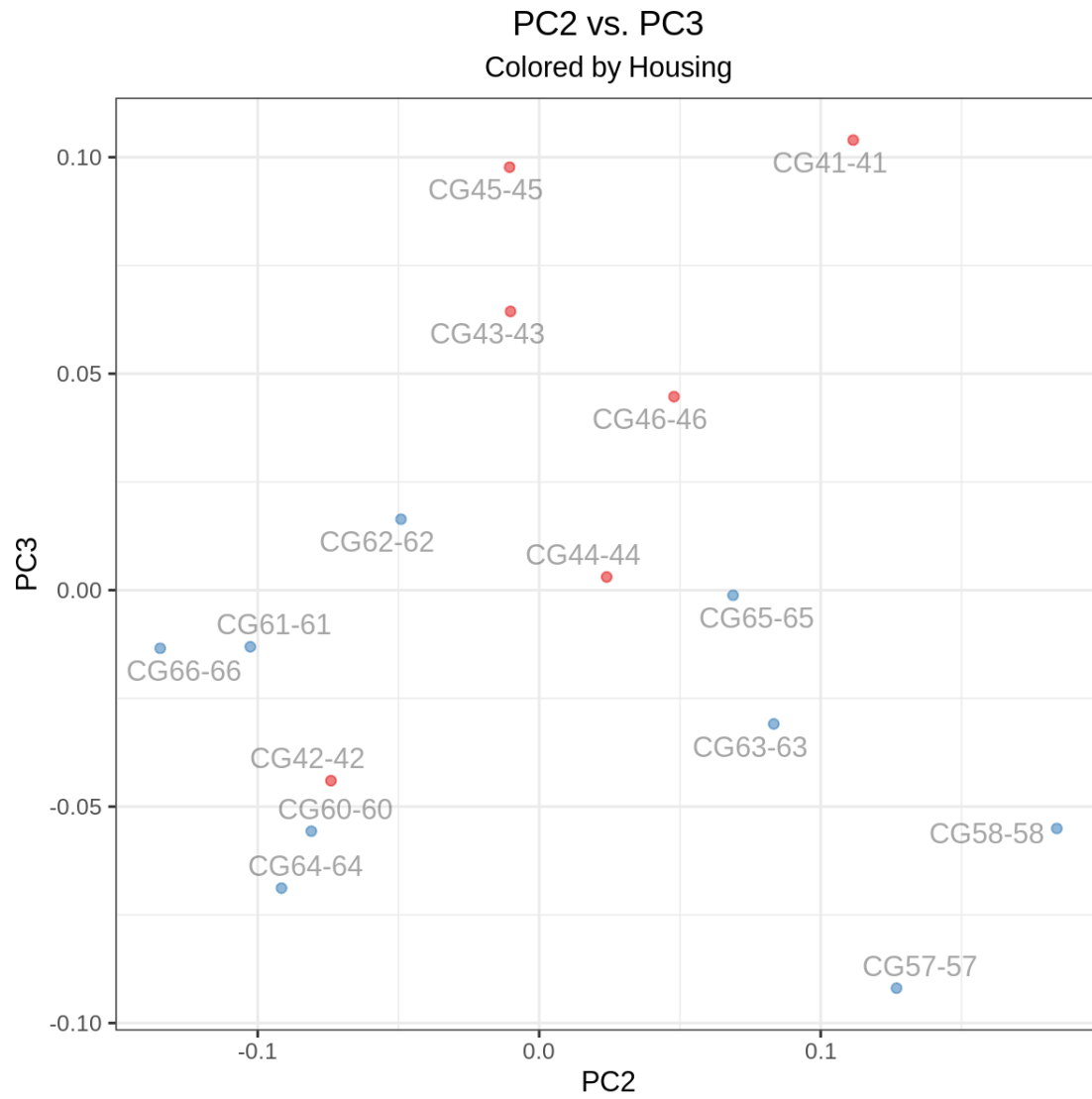
The above plot represents the first three components created when performing Principle Component Analysis on the Beta diversity of the samples.





Legend for Housing
Color Metadata

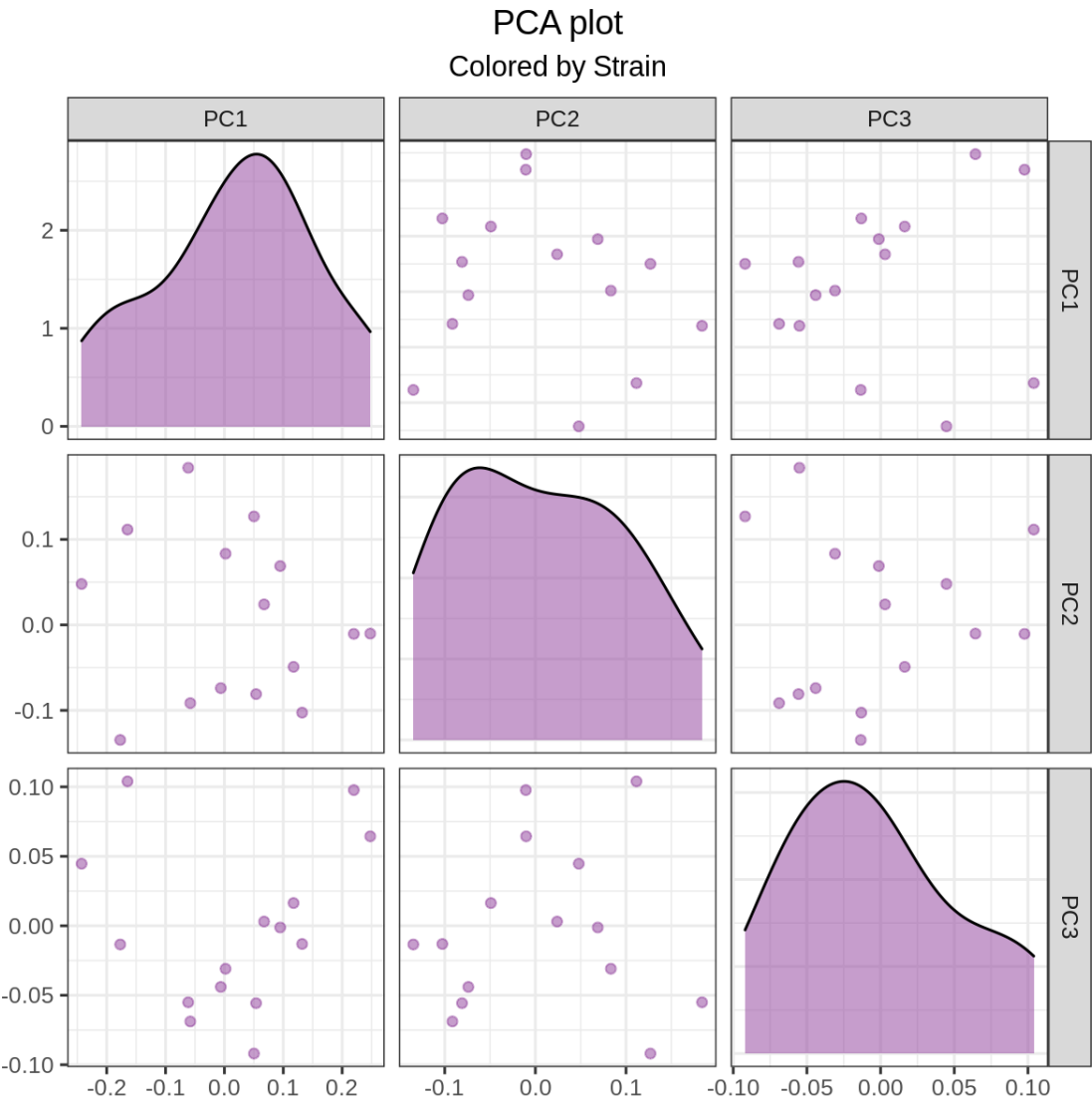
■	Littermate
■	non-co-housed



Legend for Housing
Color Metadata

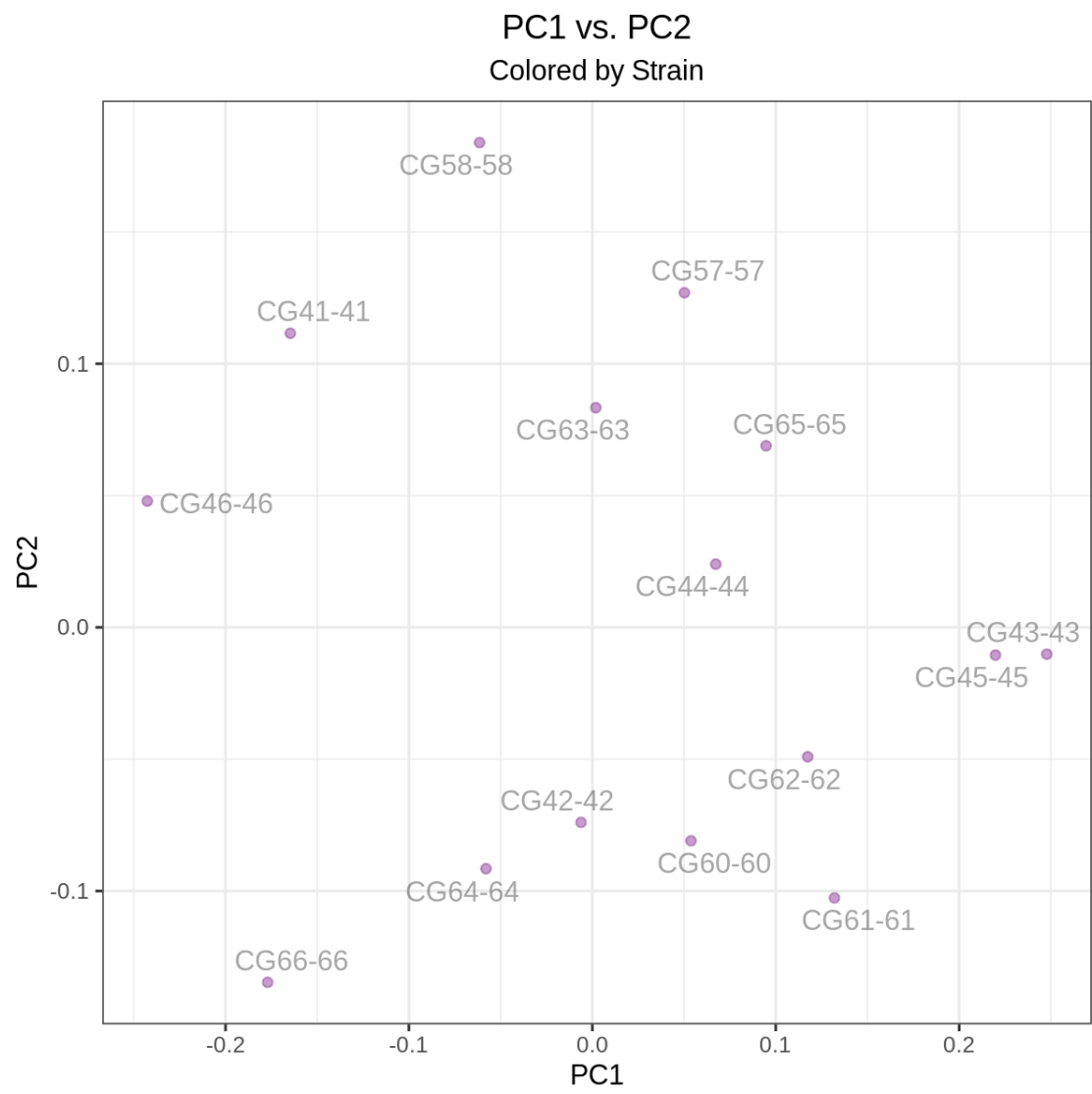
■	Littermate
■	non-co-housed

g . Weighted UniFrac, grouped by Strain



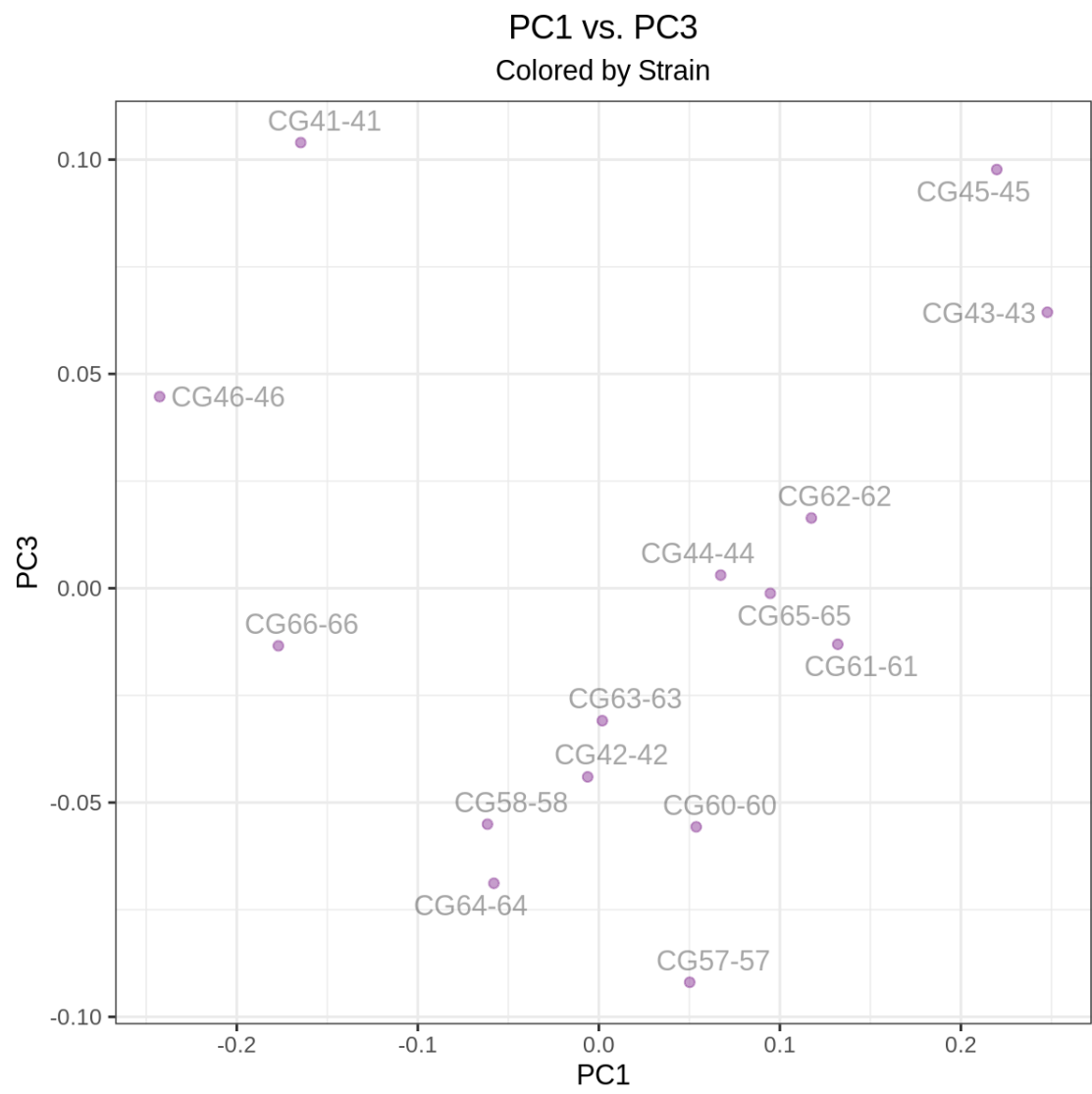
Legend for Strain
Color Metadata
IgAK0

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



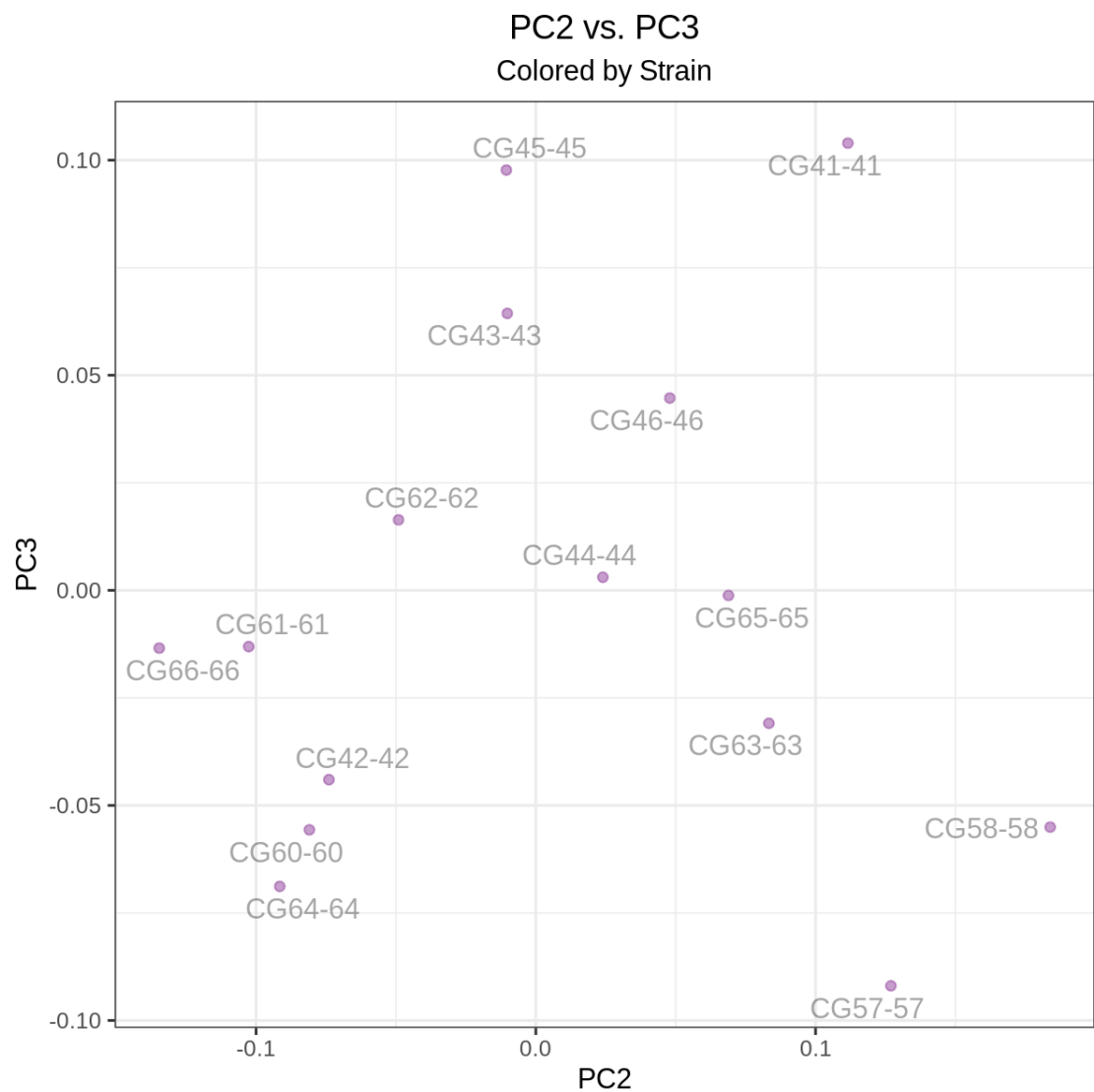
Legend for Strain
Color Metadata

IgAKO



Legend for Strain
Color Metadata

IgAKO



Legend for Strain
Color Metadata

IgAKO