

Data Visualization Portfolio

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Here are some examples of some of my previous Data Visualizations

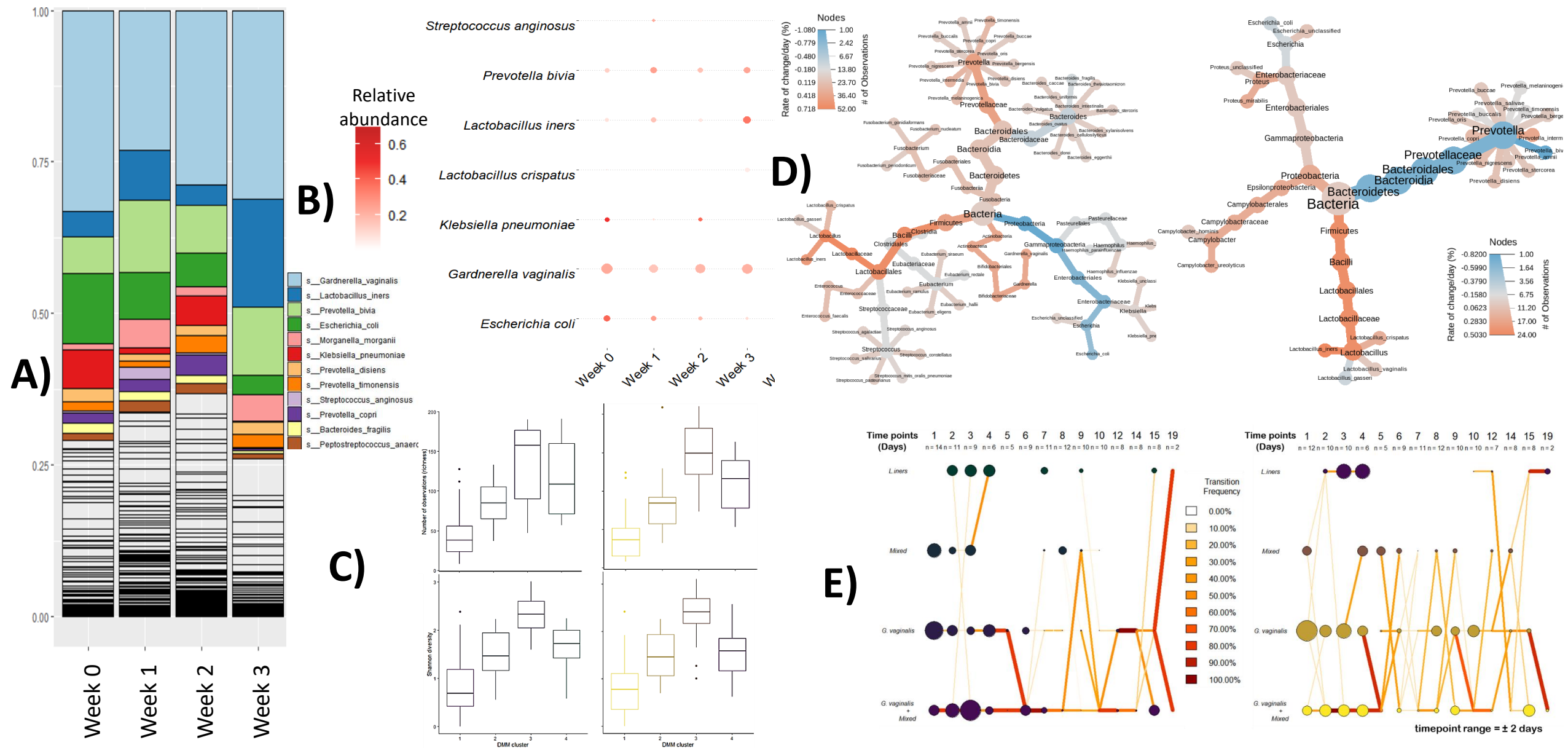


Figure 1. A) Stacked and **B)** bubble bar charts of top vaginal species averaged by week (min. prevalence & detection = 5%). **C)** Alpha diversity boxplot comparisons of richness (top) and Shannon diversity indices (bottom) per DMM cluster in vaginal introitus (left) and posterior fornix (right) samples. **D)** Heat tree taxonomic comparisons of taxa with $> 0.1\% \Delta \text{ day}^{-1}$ post-operative fistula repair in vaginal introitus (left) & posterior fornix (right). **E)** DMM cluster transition model showing vaginal introitus (left) & posterior fornix (right) microbiome progressions from Day 1-21 post-op.

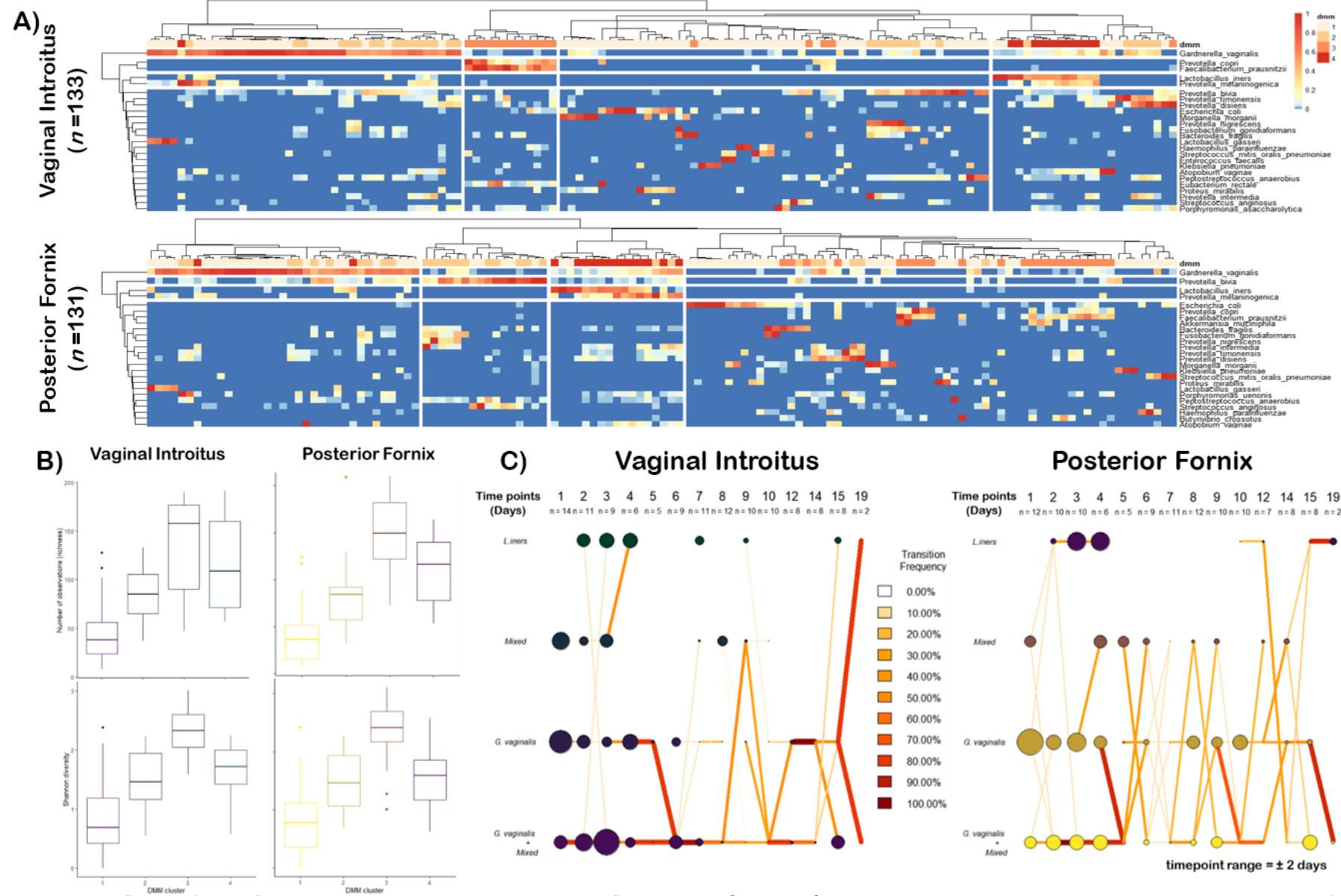
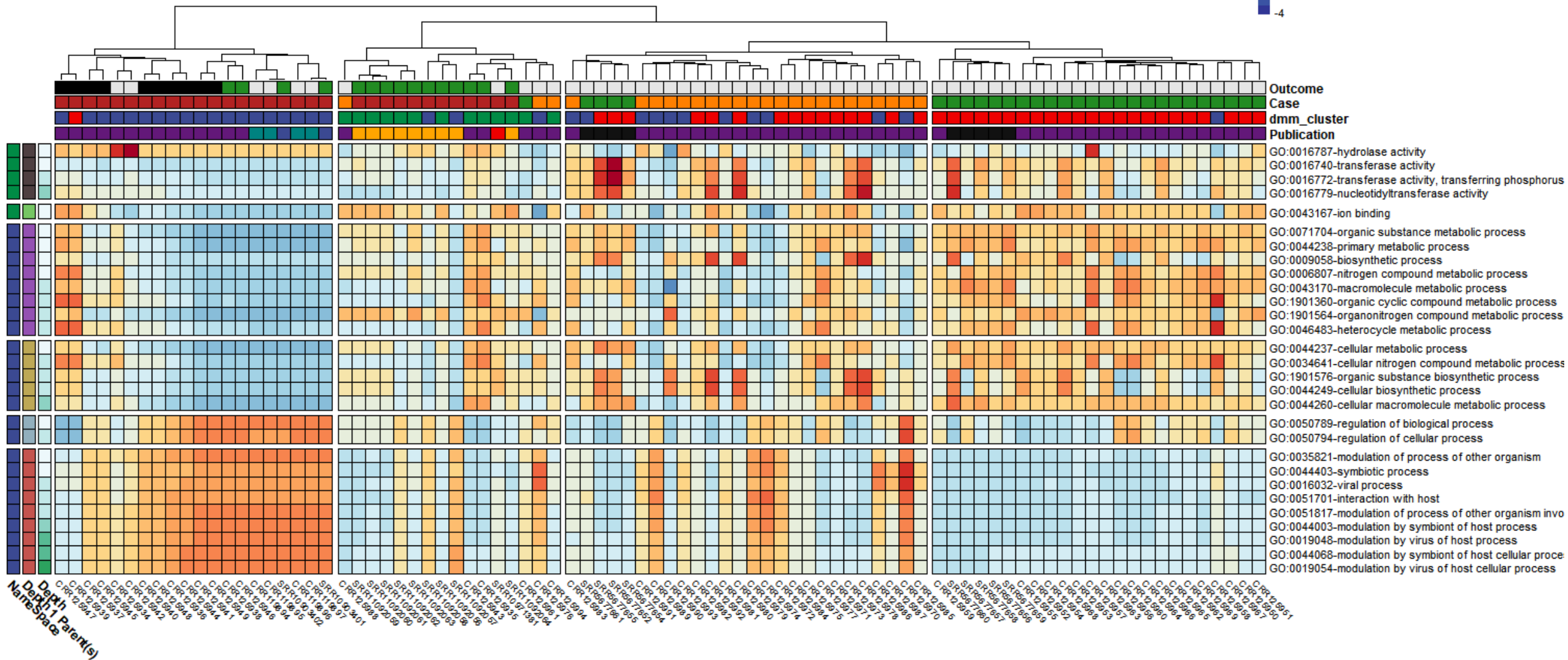
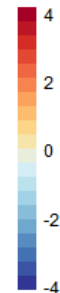
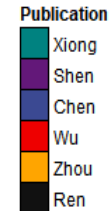
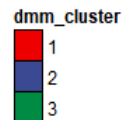
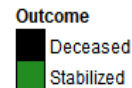
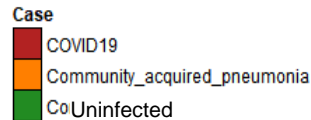
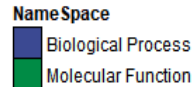
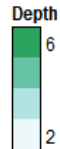
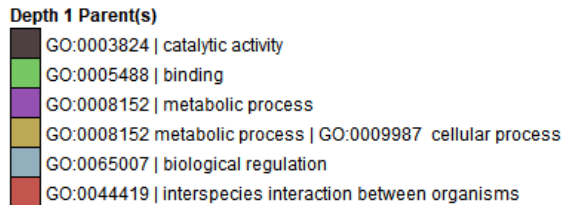


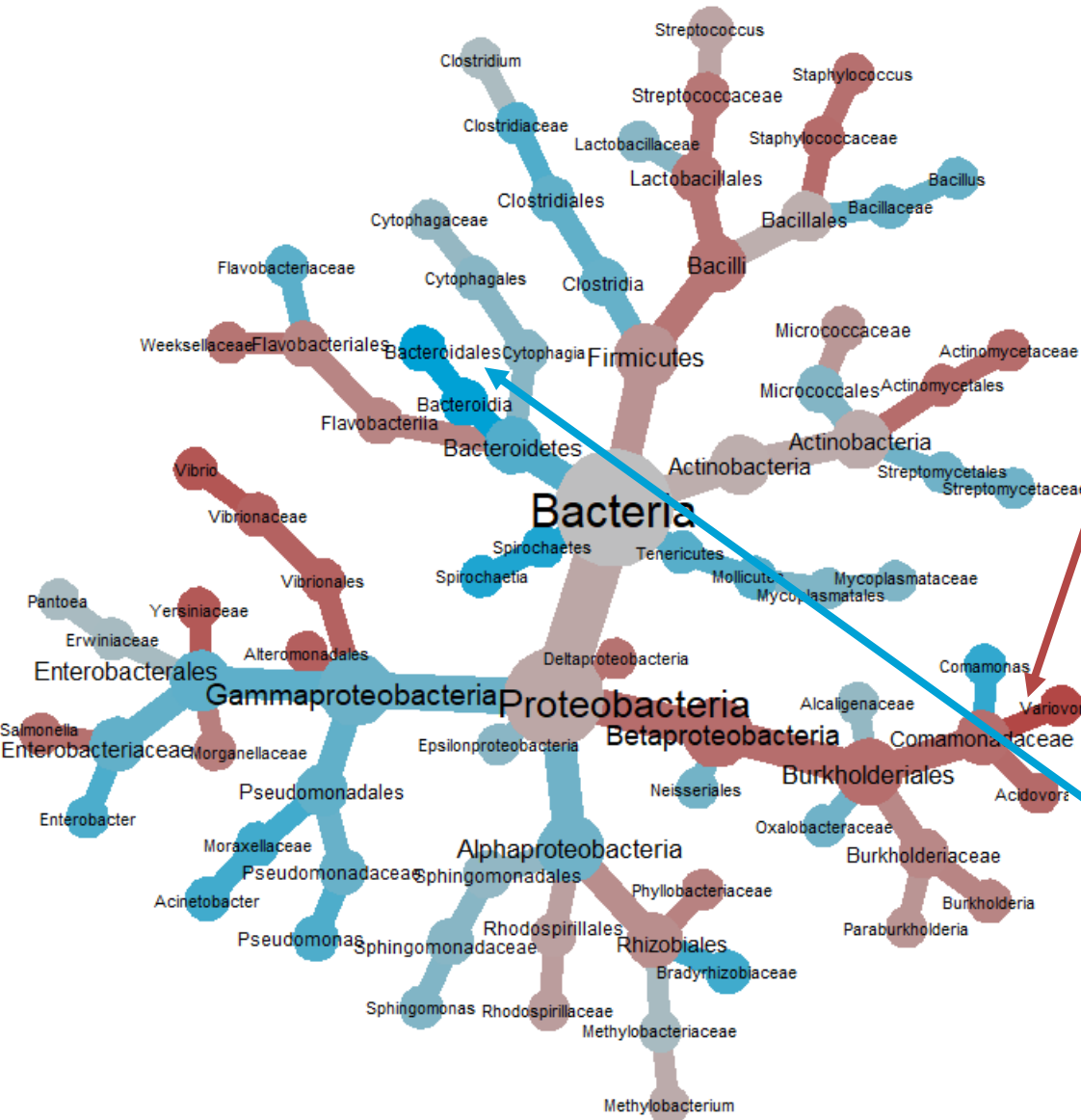
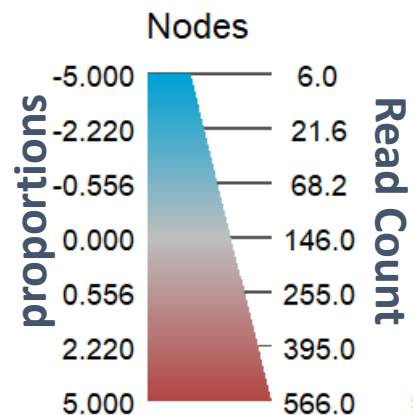
Figure 2. DMM clustering of vaginal shotgun gene sequencing data (n=264). **A.** Heat map showing Ward clustering of the relative abundance of the most dominant bacterial species per DMM cluster **B.** Box plots showing richness and Shannon alpha diversity indices per each DMM cluster (centerline= median, Boxes = 25th and 75th percentiles, whiskers= most distant data point less than 1.5x the box length, with outliers represented by points outside the whiskers) **C.** Transition model showing the progression of vaginal samples through each DMM cluster per each time point from Day 1 to 21 post-operative repair.

COVID19 vs Uninfected & viral pneumonia



COVID-19 Mortality Taxonomic profiles

Log2 ratio of median



Taxonomic comparisons (Deceased vs Survived)

log ₂ median ratio	Median diff	Mean diff	p value	q value	Taxonomy
2.25	0.361	0.371	0.00017	0.00691	<i>Comamonadaceae</i>
5.21	0.405	0.377	0.00017	0.00691	<i>Variovorax</i>
2.97	0.002	0.002	0.00353	0.074	<i>Vibrionales</i>
2.97	0.002	0.002	0.00353	0.074	<i>Vibrionaceae</i>
3.8	0.002	0.00181	0.00492	0.0827	<i>Vibrio</i>
1.84	0.0549	0.13	0.0137	0.124	<i>Bacilli</i>
2.24	0.403	0.297	0.0163	0.124	<i>Burkholderiales</i>
3.16	0.002	0.002	0.0157	0.124	<i>Alteromonadales</i>
3.61	0.004	0.004	0.0156	0.124	<i>Yersiniaceae</i>
2.1	0.005	0.00435	0.0156	0.124	<i>Salmonella</i>
1.77	0.011	0.064	0.0475	0.274	<i>Streptococcaceae</i>
2.29	0.425	0.296	0.0264	0.185	<i>Betaproteobacteria</i>
-5.13	-0.103	-0.104	0.0308	0.199	<i>Bacteroidia</i>
-5.18	-0.099	-0.102	0.00962	0.124	<i>Bacteroidales</i>

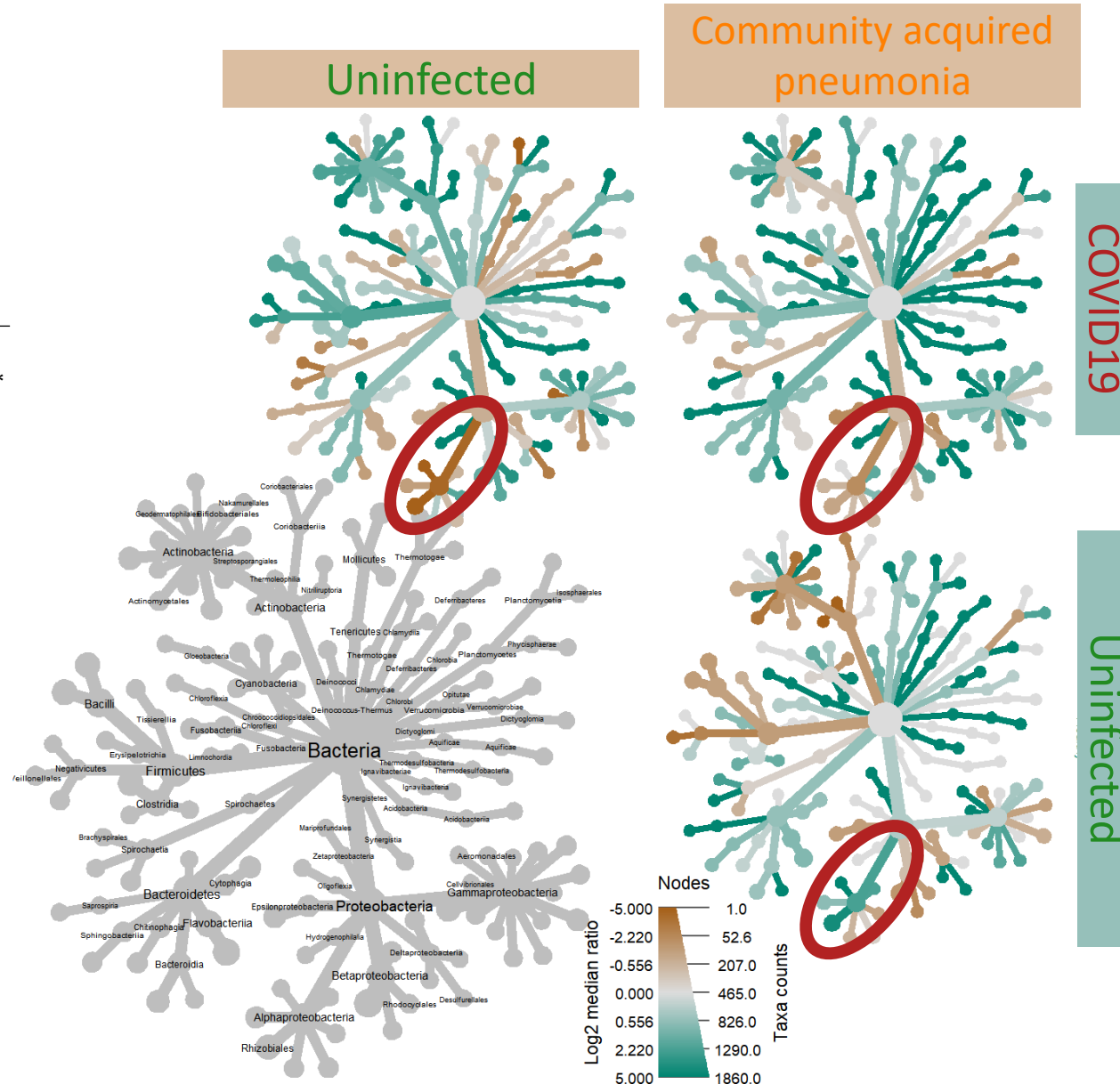
Comparisons were conducted using Wilcoxon rank sum test and adjusted for multiple test comparisons using the benajmini hochberg correction method

COVID19 vs Uninfected & viral pneumonia

Differential Taxonomic abundances

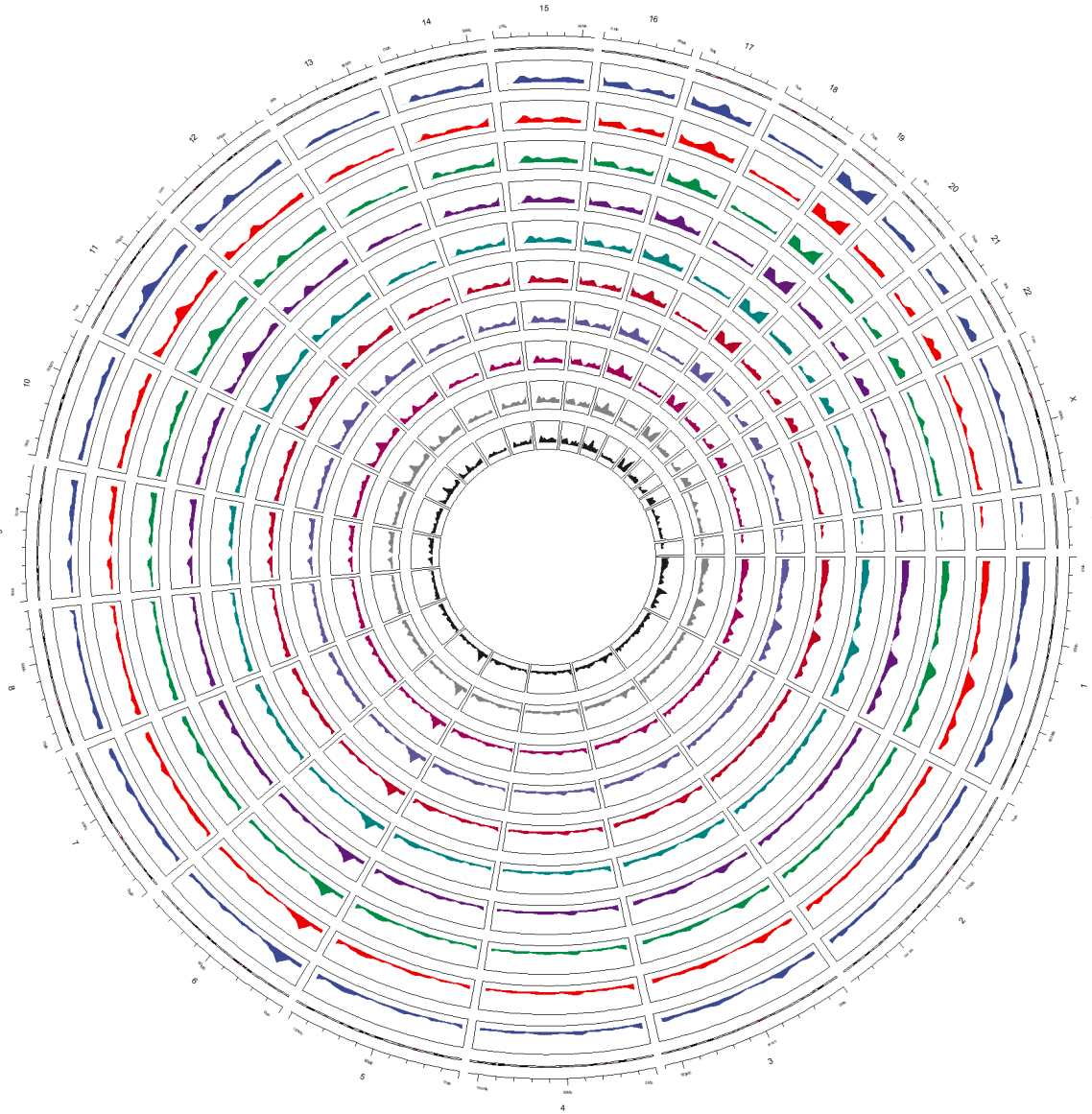
Sphingomonas

treatment	median			
	ratio	p	q	
CAP	-2.05	0.007	<0.05	*
Uninfected	-2.80	<0.0001	<0.0005	***



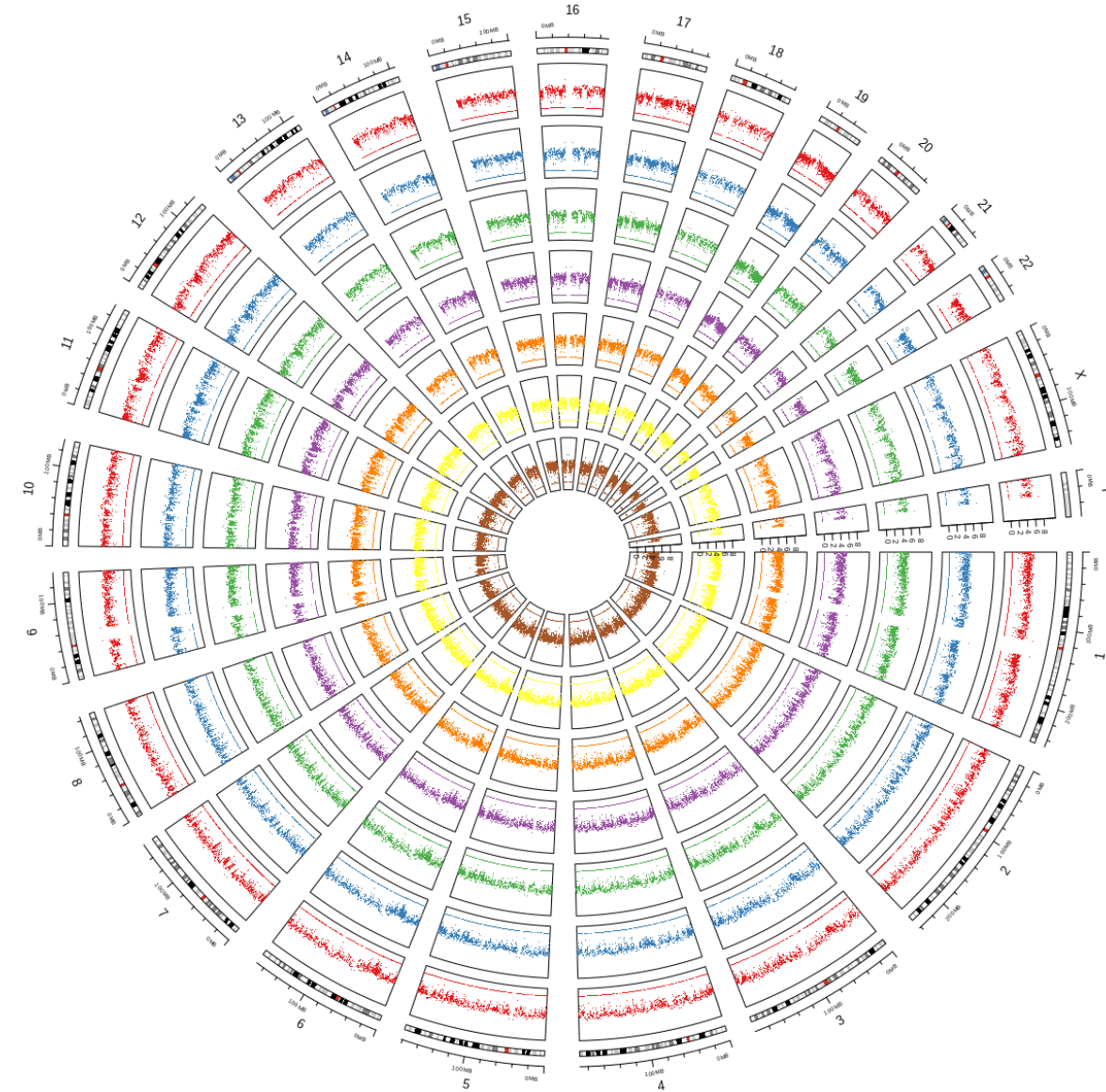
Cohort1 Genomic Density plot

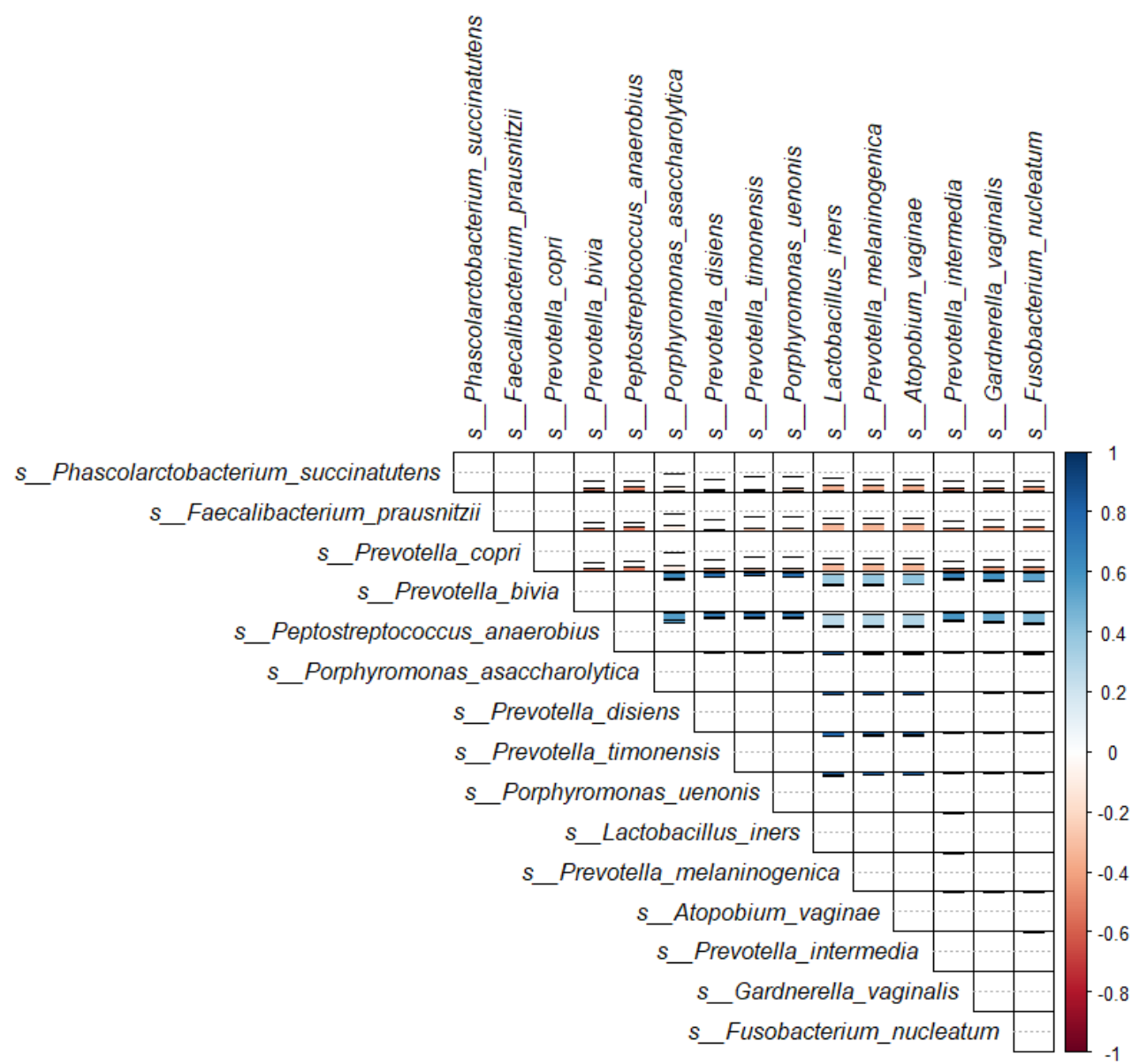
Issue: automatically calculates how much a genomic window is covered by regions in bed. It is also a high-level function and creates a new track.



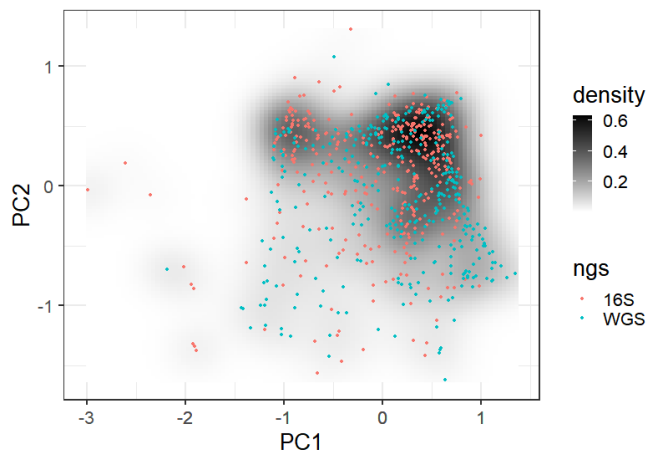
Cohort1 Genomic Rainfall Plot

Issue: The x-axis corresponds to the genomic coordinate, and the y-axis corresponds to the minimal distance (log10 transformed) of the region to its two neighbouring regions. A cluster of regions will appear as a “rainfall” in the plot

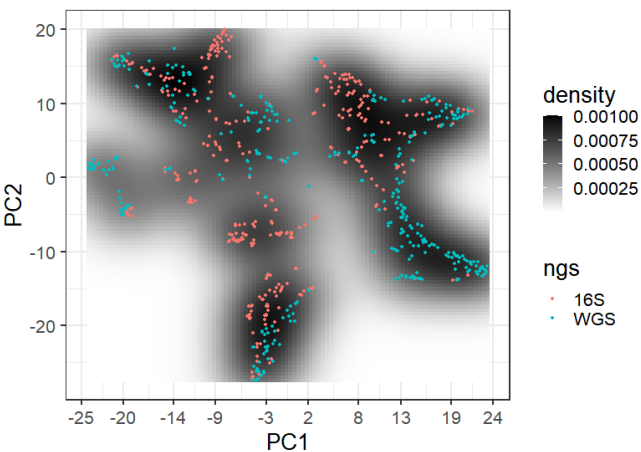


[illegible]

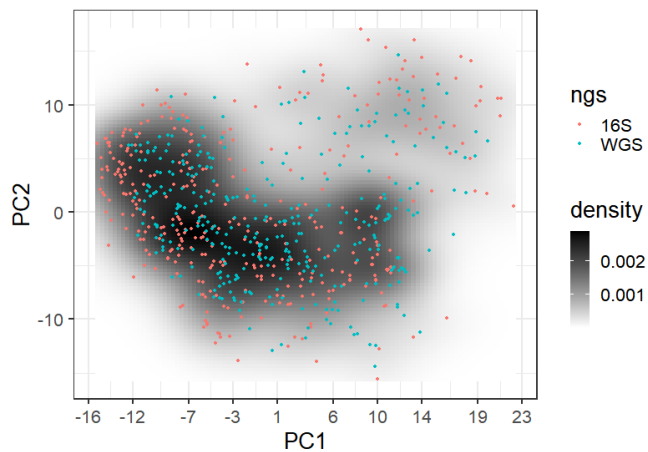
NMDS / Bray-Curtis



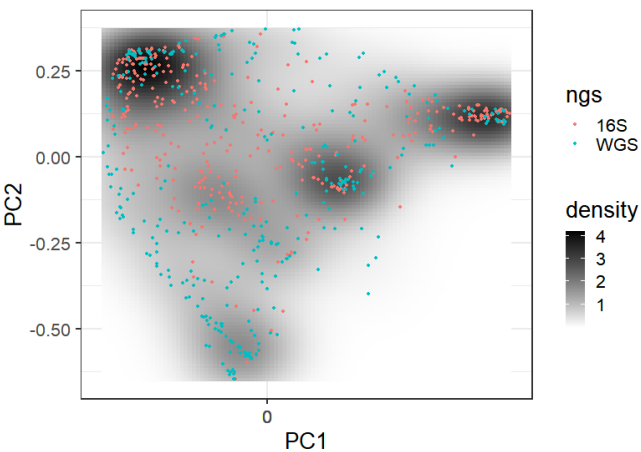
t-SNE / compositional / Euclidean



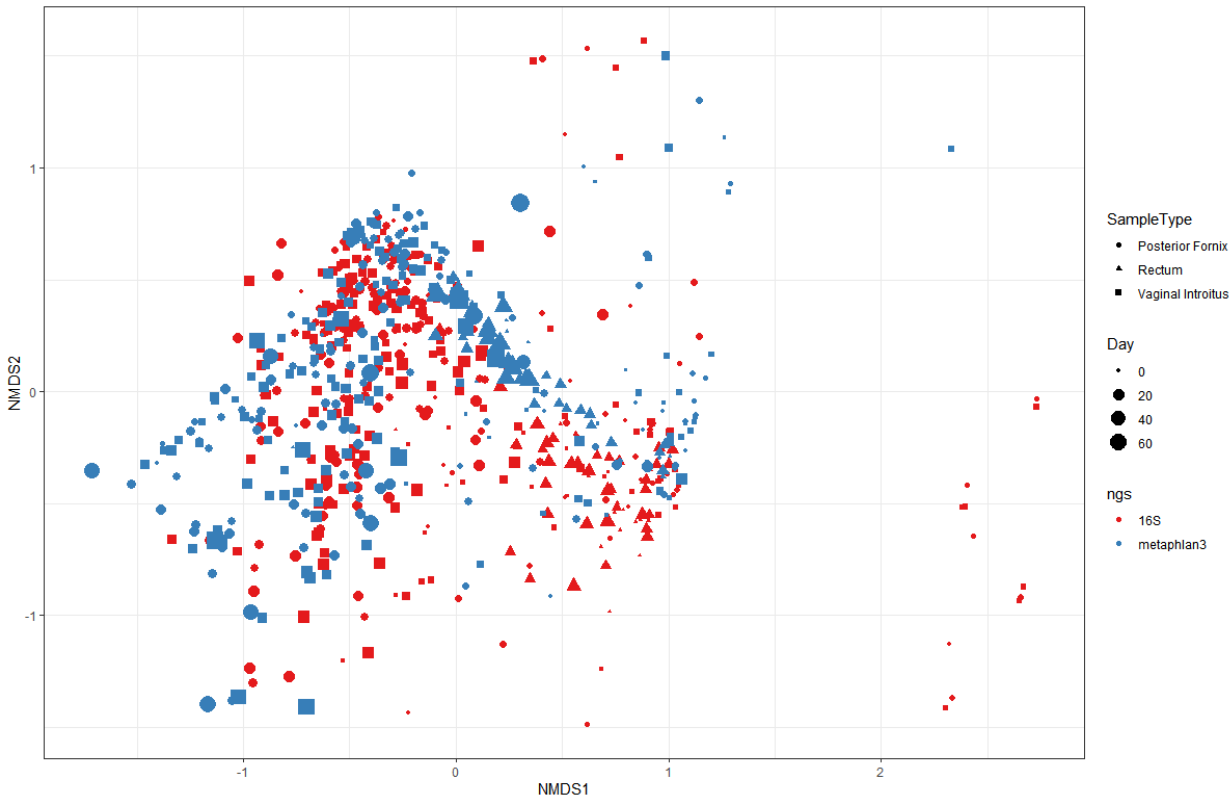
PCA



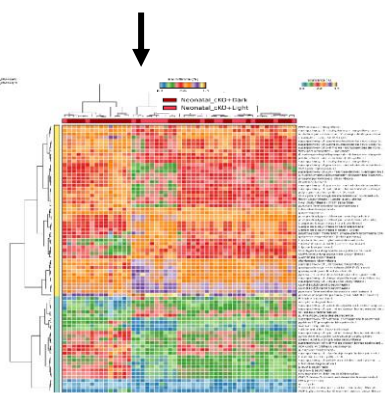
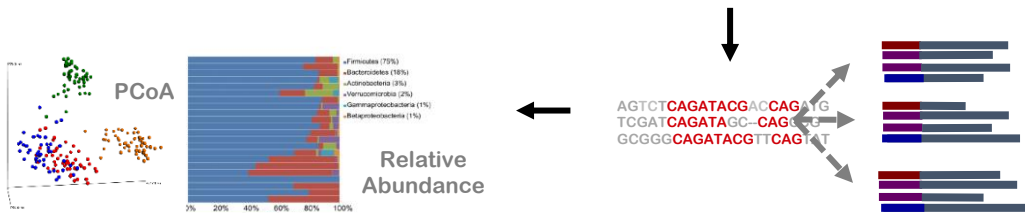
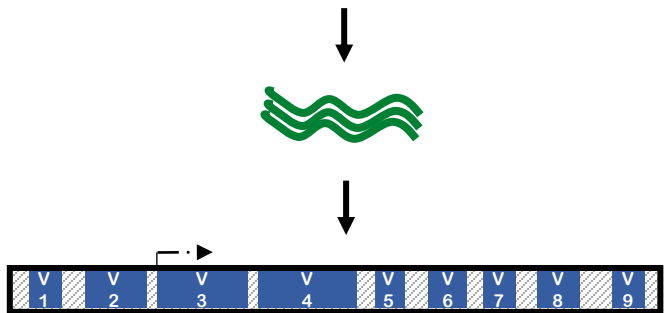
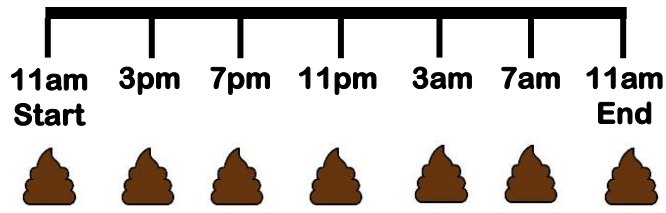
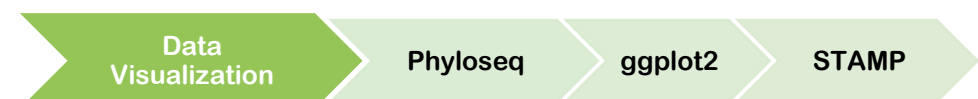
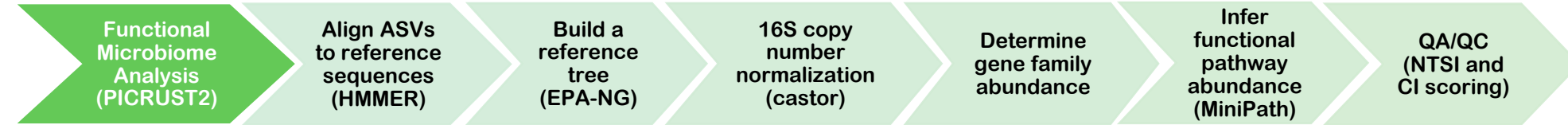
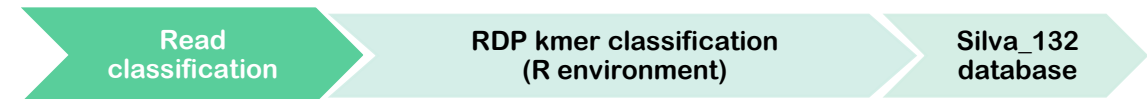
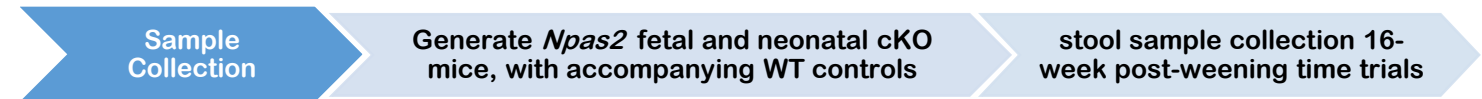
PCoA / Compositional / Bray-Curtis



NMDS



Study Design and Microbiome Pipeline



Stool Sampling

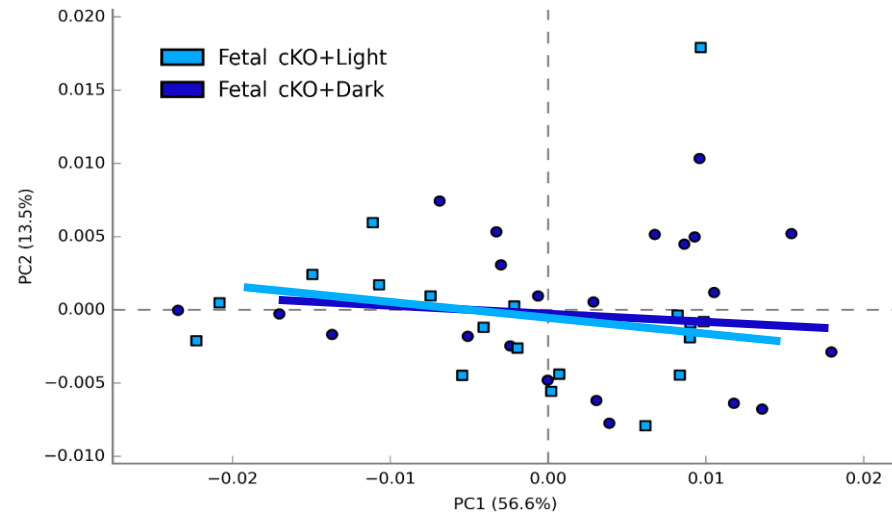
DNA Extract/PCR

Microbiome Analysis

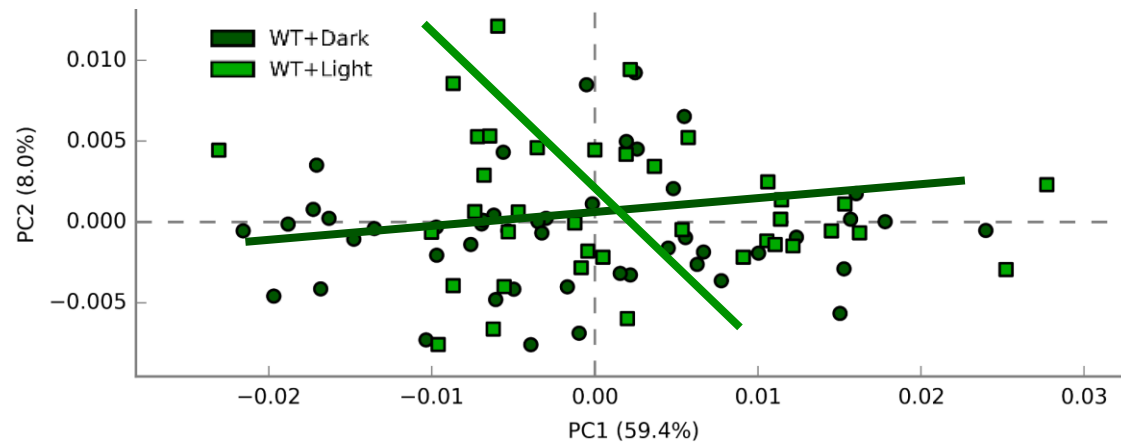
Functional Analysis

Npas2 Fetal cKO Impairs Functional Microbiome to Light:Dark Cues

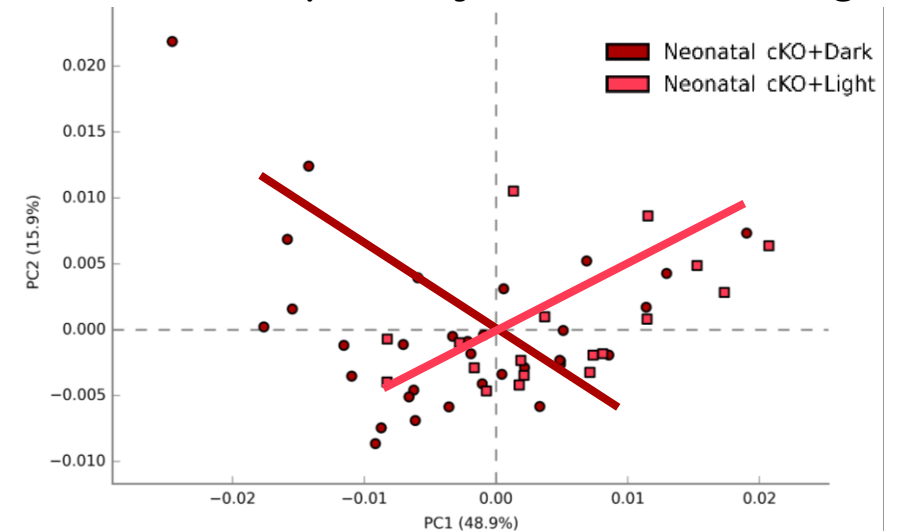
Fetal cKO: little to no significant light to dark pathway changes



Wild Type: pathway abundance changes

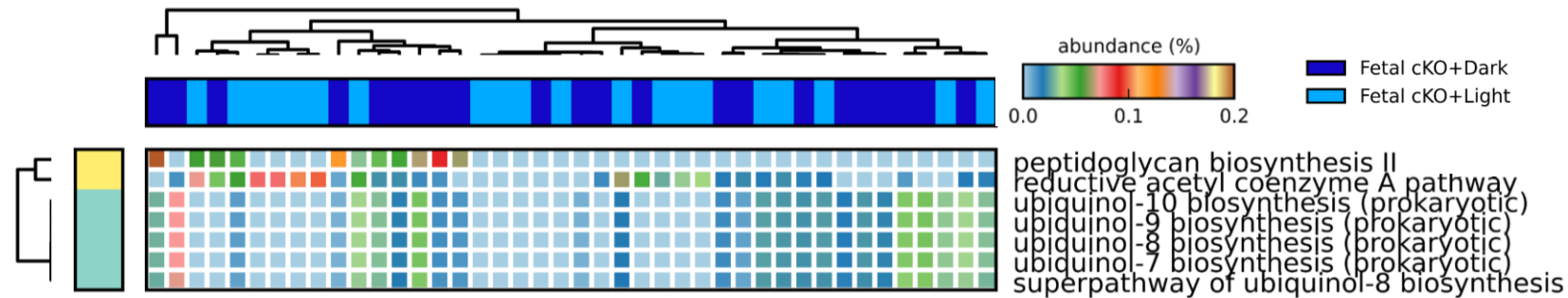


Neonatal cKO: pathway abundance changes



In utero Npas2 Deletion Impairs Functional Microbiome Light:Dark Transitions

Fetal cKO: little to no significant light to dark pathway changes



Neonatal cKO: pathway abundance changes



Wild Type: pathway abundance changes

