Beyond HOMINGS

Forsyth Oral Microbiome Core

ADA Forsyth

- New 16S rRNA analyses
- Big data genomic analysis
- Collaborations

Final Data Analysis Report

Project Number **FOMC-17924/300101 FRODO**

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I. Overall Summary

A total of 408 clinical oral samples were collected for two types of next generation sequencing (NGS) – 1) 16S rRNA V1V3 gene amplicon sequencing and 2) Shot-gun meta-transcriptomic RNA sequencing. The 16S rRNA sequencing can help answer the question regarding what bacterial species are in the samples and comparing the species profiles of different sample group can help answer whether a product or a treatment impact the microbial composition. The meta-transcriptomic sequencing determines the RNA levels for the genes expressed in the samples and helps to answer the functional related question and compare different levels of microbial activities in different sample groups.

The 16S rRNA V1V3 NGS sequences were assigned to species level taxonomy using the FOMC reference set (https://microbiome.forsyth.org/ftp/refseq/) and provides the best specie-level taxonomy assignment. Based on the species-level sequence abundance results, overall, the microbiomes were modified more with treatment Product B. In general with the exception of subgingival microbiomes, there appeared to be a microbiological benefit with this treatment.

The metagenomic shotgun sequences were processed with CosmosID-Hub's Host-Agnostic Functional Profiling Pipeline for functional/activity inferencing. Alpha and beta diversities of functional profiles (Gene Ontology, Enzyme Commission and MetaCyc Pathways) were affected by Product A for samples from individual sites - saliva and tongue samples. No significant differences were detected for combined sites, supra- and sub-gingiva sites. For Product B, functional diversities were affected when samples of 4 sites were combined, as well as tongue and supragingival samples. No significant effects were observed for saliva and subgingival samples. When Product A and B were directly compared for effect of treatment, significant differences between these two products were observed for combined and subgingival samples, but not for individual saliva, tongue and subgingival samples. This is also true for bacterial composition analysis. Finally, bacterial compositions and functional profiles for the baseline group differ between the saliva/tongue and supragingival/subgingival grouping. There were only two significant differences in functional diversity between Product A and B at baseline.

II. Data Download Links

1. Raw Sequence Data

16S rRNA V1V3 amplicon sequences

Raw sequence reads can be downloaded from a link in the FOMC 16S report:

https://microbiome.forsyth.org/ftp/fomc/FOMC_project/haleon/ef8268d4-4bde-4eb7-94c8-09aabee1e8bf

Meta-transcriptome shot-gun sequences

Meta-transcriptome shot-gun reads can be downloaded from this link:

https://microbiome.forsyth.org/ftp/fomc/FOMC_project/haleon/b0eb797b-ac3d-43d5-9958-7d86868ad149

2. Analysis Results

16S rRNA V1V3 Bioinformatics Analyses (FOMC Pipeline)

https://microbiome.forsyth.org/ftp/fomc/FOMC_project/haleon/ef8268d4-4bde-4eb7-94c8-09aabee1e8bf

Meta-transcriptomic Analyses (CosmosID Pipeline)

https://microbiome.forsyth.org/ftp/fomc/FOMC_project/haleon/48b41065-dd02-49db-9ebe-da0e7d463cdf

3. Final Report – this document

This report can also be downloaded (and shared) online from this link:

https://microbiome.forsyth.org/ftp/fomc/FOMC_project/haleon/d6e5a990-c912-4a4b-8573-b877c3072f37

III. Project Workflow

Figure 1 shows the overall project workflow that was performed by FOMC starting from the clinical samples.

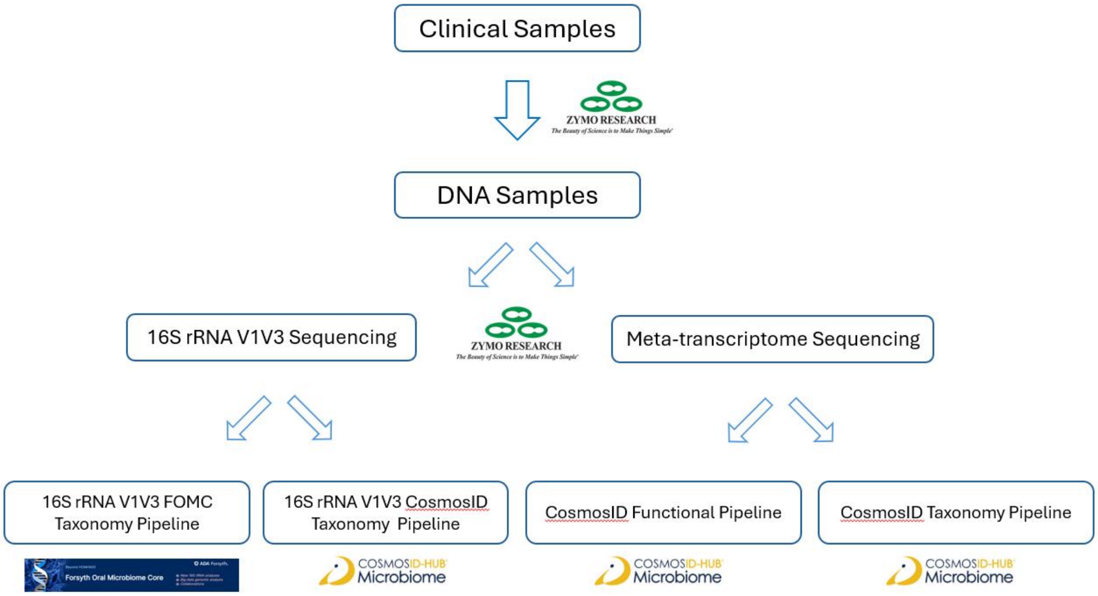
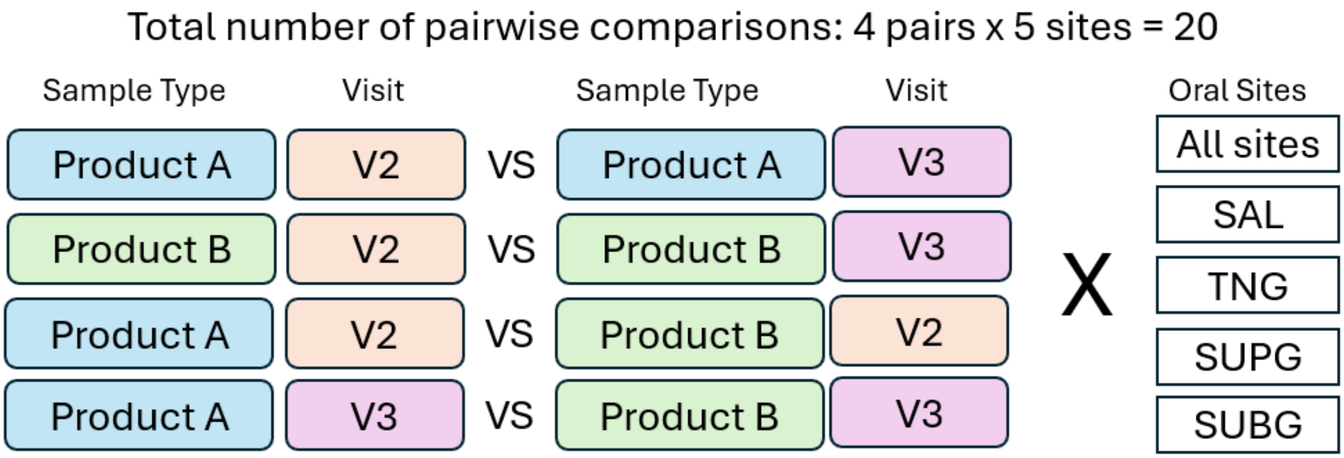


Figure 1. Overall experimental and analytic workflow

IV. Analyses Overview

Figure 2 depicts the number of combinations of sample types, visits and oral sites of all samples. A total of 20 comparisons were performed and the comparison IDs and labeling are listed in Table 1. The VII. Results section focuses on the 4 major questions described in the section V. Objectives and Endpoints. The figures and tables for all the comparison are shown in the Appendix section.



Total number of pairwise comparisons: 4 pairs x 5 sites = 20

Sample Type	Visit		Sample Type	Visit		Oral Sites
Product A	V2	VS	Product A	V3	X	All sites
Product B	V2	VS	Product B	V3		SAL
Product A	V2	VS	Product B	V2		TNG
Product A	V3	VS	Product B	V3		SUPG
						SUBG

Figure 2. Comparative analyses performed in this study

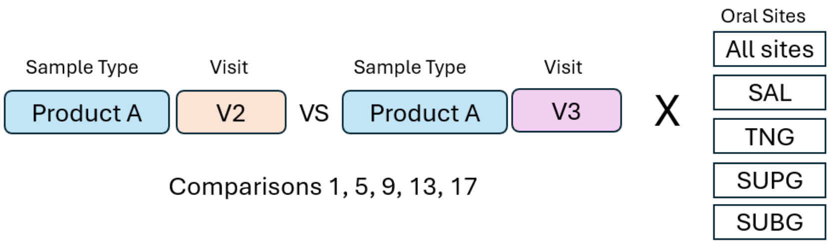
Table 1. List of all comparative analyses

Comparison List		
1. A V2 vs A V3 ALL	9. A V2 TNG vs A V3 TNG	17. A V2 SUBG vs A V3 SUBG
2. B V2 vs B V3 ALL	10. B V2 TNG vs B V3 TNG	18. B V2 SUBG vs B V3 SUBG
3. A V2 vs B V2 ALL	11. A V2 TNG vs B V2 TNG	19. A V2 SUBG vs B V2 SUBG
4. A V3 vs B V3 ALL	12. A V3 TNG vs B V3 TNG	20. A V3 SUBG vs B V3 SUBG
5. A V2 SAL vs A V3 SAL	13. A V2 SUPG vs A V3 SUPG	*A: Product A* *B: Product B* *V2: Baseline* *V3: 6 Weeks* All: All sites SAL: Saliva TNG: Tongue SUPG: Supragingival SUB: Subgingival
6. B V2 SAL vs B V3 SAL	14. B V2 SUPG vs B V3 SUPG	
7. A V2 SAL vs B V2 SAL	15. A V2 SUPG vs B V2 SUPG	
8. A V3 SAL vs B V3 SAL	16. A V3 SUPG vs B V3 SUPG	

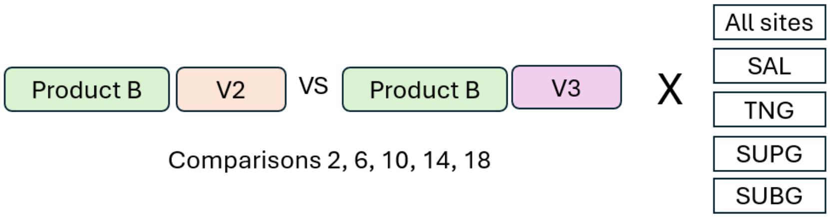
V. Objectives and Endpoints

1. **Describe and compare the bacterial composition by different areas of the mouth at week 6 compared to baseline by treatment.**

   Results related to this objective are depicted in the illustration below and described in section 7. Week 6 vs Baseline Comparisons – Bacterial Composition.



Comparisons 1, 5, 9, 13, 17



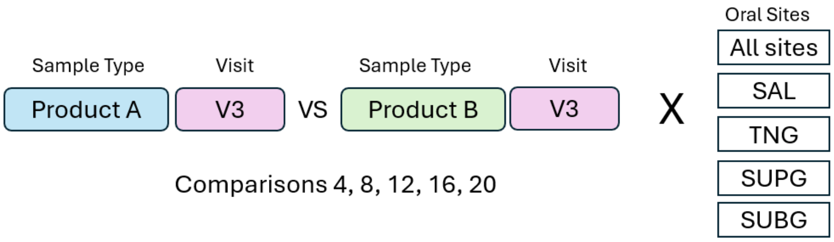
Comparisons 2, 6, 10, 14, 18

2. **Describe and compare the bacterial activity by different areas of the mouth at week 6 compared to baseline by treatment.**

   Results related to this objective are depicted in the illustration <u>above</u> and described in section 8. Week 6 vs Baseline Comparisons – Activities.

3. **Compare the bacterial composition and activity by different areas of the mouth at week 6 between treatment A and treatment B.**

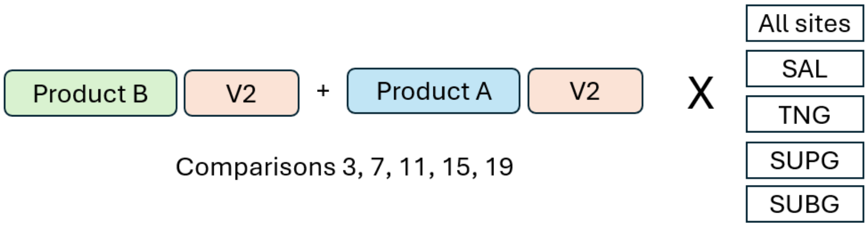
   Results related to this objective are depicted in the illustration below and are described in sections 9. Products A vs B at Week 6 vs– Bacterial Composition and 10. Products A vs B at Week 6 vs– Activities.



Comparisons 4, 8, 12, 16, 20

4. **Describe the bacterial composition of the different areas of the mouth at baseline.**

   Results related to this objective are depicted in the illustration below and are described in section 11. Bacterial Compositions of Oral Sites at Baseline.



Comparisons 3, 7, 11, 15, 19

VI. Methods

4. FOMC 16S rRNA V1V3 Amplicon Analysis Pipeline

Sequence Data Processing

Raw 16S V1V3 amplicon sequences obtained from Zymo Research were quality-filtered, denoised, pair-end merged, and chimera removed with the DADA2 tool [1].

Taxonomy Assignment

Amplicon sequence variants (ASVs) generated by DADA2 were subjected to species level taxonomy assignment based on the approach developed by Al-Hebshi et. al. (2015) [2] against the FOMC Reference Sequence Set (https://microbiome.forsyth.org/ftp/refseq) that consists of 1,015 full-length 16S rRNA sequences from HOMD V15.22, 356 from MOMD V5.1, and 22,126 from NCBI, a total of 23,497 sequences. Altogether these sequences represent a total of 17,035 oral and non-oral microbial species.

Taxonomy bar plots

Graphically displays differences between groups—a good visual aid. Only shown for the first comparison for illustrative purposes. If desired, taxonomy plots can be provided for all comparisons. Dynamic taxonomy bar plot is available in the original analysis report (https://microbiome.forsyth.org/ftp/fomc/FOMC17924_haleon_16S_full/qiime/data_mc100/qiime2/barplot/index.html) using QIIME2 package [3].

Alpha diversity

Alpha diversity (α-diversity) is the mean species diversity in sites or habitats. Data are presented in 3 measurements: 1) number of species (observed), 2) Shannon index, and 3) Simpson index. *p* values were calculated for these metrics. Alpha diversity was calculated with QIIME2 package [3] and R [4] “phyloseq” package [5]. Alpha diversity significance tests were evaluated with QIIME2’ “alpha-group-significance” function [3].

Beta diversity

Compares the similarity (or dissimilarity) of entire microbial profiles between different groups of samples. Presently in dot graphs and p-values are calculated. Best diversity significance tests were evaluated with QIIME2’ “beta-group-significance” function [3].

Differential abundance

ANCOMB-BC2 was used to test significance of differential abundance between two test groups [6]. ANCOM-BC2 (Analysis of Compositions of Microbiomes with Bias Correction) provides the following: (a) statistically valid test with appropriate p-values, (b) provides confidence intervals for differential abundance of each taxon, (c) controls the False Discovery Rate (FDR), (d) maintains adequate power, and (e) is computationally simple to implement. Key here is that p-values are calculated for specific taxa.

LEfSe

Linear discriminant analysis LDA Effect Size (LEfSe), a 2-stage statistical analysis [7]. It uses the non-parametric factorial Kruskal-Wallis (KW) sum-rank test to detect features with significant differential abundance with respect to the class of interest and then biological significance is determined using a set of pairwise tests among subclasses using the (unpaired) Wilcoxon rank-sum test. For the output, LEfSe uses Linear Discriminant Analysis to estimate the effect size of each differentially abundant feature. These data clearly illustrate key microbiological differences among groups. P-values cannot be calculated for Lefse, but I use the p-values as determined from the differential abundance data.

Heat map

Graphically displays differences between groups - a visual aid. Heat maps were done using R's "gplots" function [4].

References

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5. CosmosID-HUB Meta-transcriptomics Analysis Pipeline

Host-Agnostic Functional Profiling

Initial QC, adapter trimming and preprocessing of metagenomic sequencing reads are done using BBduk [1]. The quality controlled reads are then subjected to a translated search against a comprehensive and non-redundant protein sequence database, UniRef 90. The UniRef90 database, provided by UniProt [2], represents a clustering of all non-redundant protein sequences in UniProt, such that each sequence in a cluster aligns with 90% identity and 80% coverage of the longest sequence in the cluster. The mapping of metagenomic reads to gene sequences are weighted by mapping quality, coverage and gene sequence length to estimate community wide weighted gene family abundances as described by Franzosa et al [3]. Gene families are then annotated to MetaCyc [4] reactions (Metabolic Enzymes) to reconstruct and quantify MetaCyc [4] metabolic pathways in the community as described by Franzosa et al [3]. Furthermore, the UniRef_90 gene families are also regrouped to Enzyme Commission Enzymes and GO Terms in order to get an exhaustive overview of gene functions in the community. Lastly, to facilitate comparisons across multiple samples with different sequencing depths, the abundance values are normalized using Total-sum scaling (TSS) normalization to produce "Copies per million" (analogous to TPMs in RNA-Seq) units.

RelativeAbundance Stacked Bars

Stacked Bar figures were generated using phylum, genus, species, and strain-level filtered matrices for bacteria from CosmosID-HUB. Stacked bar figures for each group were generated using the R package ggpubr [5,6].

Heatmaps

Heatmaps were created using the pheatmap R package [7] generated using the phylum, genus, species, and strain matrices for bacteria from CosmosID-HUB. Hierarchical clustering and dendrograms are generated using the hclust and dist functions from the R stats package [8,9], with default parameters using euclidean distance and complete linkage.

Alpha Diversity Boxplots (with Wilcoxon Rank-Sum)

Alpha diversity boxplots were calculated from the phylum, genus, species, and strain level abundance score matrices from CosmosID-HUB analysis. Species or Chao1, Simpson, and Shannon alpha diversity metrics were calculated in R using the R package Vegan [9,10]. Wilcoxon Rank-Sum tests were performed between groups using the R package *ggsignif* [11]. Boxplots with overlaid significance in *p* value format were generated using the R package ggpubr [6].

Beta Diversity PCoA (with PERMANOVA)

Beta Diversity Principal Coordinate Analyses were calculated from phylum, genus, species, and strain-level matrices for bacteria from CosmosID-HUB. Bray-Curtis dissimilarity was calculated in R using the vegan package with the function vegdist, and PCoA tables were generated using ape’s function pcoa [12]. PERMANOVA tests for each distance matrix were generated using vegan’s [10] function adonis2, and beta dispersion was calculated and compared using the anova method for the betadisper function from vegan [10]. Plots were visualized using the R package ggpubr [6].

LEfSe

Linear Discriminant Analysis Effect Size figures were generated using the LEfSe tool [13] from the Huttenhower lab implemented in the R package lefser [14], based on phylum, genus, species, and strain matrices for bacteria from CosmosID-HUB. LEfSe is calculated with a Kruskal-Wallis alpha value of 0.05, a Wilcoxon alpha value of 0.05, and a logarithmic LDA score threshold of 2.0. In the LEfSe figures, red bars to the left convey that the feature in that group is more associated with the "red" group than the other. Blue bars to the right convey that the organism is more associated with the "blue" group.

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VII. Results

6. Summary Statistics

The impact of the treatments/products on microbiome composition and functional profiles can be evaluated in two ways: 1) diversity measures, including both alpha and beta diversities and 2) by the number and significance of the features (i.e., species for composition and GO/EC/pathways for metatranscriptomic functional profiles).

We performed a wide range of statistical tests evaluating the significance of differences between the two groups in each of the 20 comparisons listed in Table 1. *p* values of all the tests were listed in Table 2 to indicate whether there are significant differences between two groups measured by the diversity indices listed in the column “Measurement” of Table 2. When *p* values are ≤ 0.05 they are highlighted in green - the smaller *p* values the darker green shading is used. Gray shading (from white to dark gray) was used for when p values are > 0.05, the larger the darker gray. Thus Table 2 shows where the most significant results are for various types of comparisons.

When many statistical tests were performed (620 in Table 2), naturally some results can be false positive, depending on the confidence level chosen. We did not perform the FDR adjustment because Microbiome studies such as this project, are exploratory in nature. So original p values were presented to allow more flexible interpretation of the significance.

However, we did observe that, unlike simulations of randomly generated data, which result in uniform distributions of *p* values, the *p* values in Table 2 do not follow a uniform distribution. The significant results are twice as numerous as would be expected by chance, which indicates a lower likelihood that these results are false positives (Figure 3).

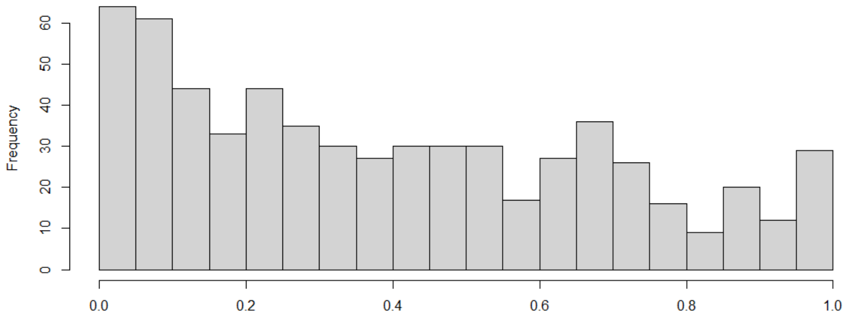


Figure 3. Distribution of all 620 p values for various type of comparisons.

With the exploratory purpose in mind, we can begin to examine the table for the most significant results. Notably comparison 5 (Product A V2 vs V3 saliva) and 6 (Product B V2 vs V3 saliva) show significant differences in alpha and beta diversity between V2 and V3 in MetaCyc Pathway profiles. This indicates that both products impacted metabolic pathways after treatment in the saliva samples.

Sections 7 to 11 are focused result presentation addressing the 4 objectives listed in Section V. Not all comparisons in Table 2 were described in this report.

Table 2. Statistical *p* values of all pairwise comparisons

Sequence_Type	Analysis Type	Pipeline	Analysis Method	Database	Measurement	1. AV2 vs AV3	2. BV2 vs BV3	3. AV2 vs BV2	4. AV3 vs BV3	5. AV2 SAL vs AV3 SAL	6. BV2 SAL vs BV3 SAL	7. AV2 SAL vs BV2 SAL	8. AV3 SAL vs BV3SAL	9. AV2 TNG vs AV3 TNG	10. BV2 TNG vs BV3 TNG	11. AV2 TNG vs BV2 TNG	12. AV3 TNG vs BV3 TNG	13. AV2 SUPG vs AV3 SUPG	14. BV2 SUPG vs BV3 SUPG	15. AV2 SUPG vs BV2 SUPG	16. AV3 SUPG vs BV3 SUPG	17. AV2 SUBG vs AV3 SUBG	18. BV2 SUBG vs BV3 SUBG	19. AV2 SUBG vs BV2 SUBG	20. AV3 SUBG vs BV3 SUBG
					Saliva	🟧	🟧	🟧	🟧	🟧	🟧	🟧	🟧												
					Tongue	🟦	🟦	🟦	🟦					🟦	🟦	🟦	🟦								
					Supragingiva	🟩	🟩	🟩	🟩									🟩	🟩	🟩	🟩				
					Subgingiva	🟪	🟪	🟪	🟪													🟪	🟪	🟪	🟪
					Product A	🟨	🟪	🟨	🟨	🟨	🟪	🟨	🟨	🟨	🟪	🟨	🟨	🟨	🟪	🟨	🟨	🟨	🟪	🟨	🟨
					Product B			🟪	🟪			🟪	🟪			🟪	🟪			🟪	🟪			🟪	🟪
					V2	░	░	░	▓	░	░	░	▓	░	░	░	▓	░	░	░	▓	░	░	░	▓
					V3	▓	▓			▓	▓			▓	▓			▓	▓			▓	▓		
Metatranscriptome	Functions	CosmosID	Alpha	Enzyme Commission	Chao1	0.726182	0.619889	0.340824	0.955539	0.038637	0.398656	0.380941	0.828453	0.131082	0.044623	0.380941	0.962429	0.614766	0.091402	0.200098	0.777458	0.934364	0.449223	0.763052	0.763052
Metatranscriptome	Functions	CosmosID	Alpha	Enzyme Commission	Shannon	0.020333	0.237938	0.3307	0.175523	0.175644	0.225253	0.678487	0.534078	0.007962	0.210758	0.969939	0.637601	0.898063	0.183817	0.073452	0.939921	0.272173	0.281544	0.637601	0.16322
Metatranscriptome	Functions	CosmosID	Alpha	Enzyme Commission	Simpson	0.034423	0.176633	0.276174	0.278272	0.119803	0.148314	0.664745	0.720342	0.042211	0.075838	0.534078	0.835803	0.660496	0.248308	0.076533	0.821118	0.206667	0.171343	0.521759	0.064814
Metatranscriptome	Functions	CosmosID	Alpha	Gene Ontology	Chao1	0.2014	0.086074	0.736201	0.221779	0.64729	0.336833	0.777458	0.355867	0.012812	0.030509	0.678487	0.969939	0.070014	0.036996	0.791941	0.341334	0.43131	0.593633	0.242719	0.250401
Metatranscriptome	Functions	CosmosID	Alpha	Gene Ontology	Shannon	0.287124	0.065073	0.447743	0.636843	0.509997	0.148314	0.31797	1	0.533784	0.690808	0.954922	0.559147	0.521821	0.011339	0.250401	0.266271	0.379696	0.299246	0.497569	0.327187
Metatranscriptome	Functions	CosmosID	Alpha	Gene Ontology	Simpson	0.451203	0.049192	0.269945	0.583667	0.442101	0.225253	0.122331	0.509589	0.783687	0.634523	0.664745	0.29135	0.714347	0.008085	0.235204	0.093551	0.985399	0.976781	0.895067	0.734489
Metatranscriptome	Functions	CosmosID	Alpha	MetaCyc Pathways	Chao1	0.514379	0.546165	0.527994	0.492941	0.003214	0.017926	0.491616	0.720342	0.026176	0.415118	0.917461	0.407072	0.819052	0.14561	0.184054	0.924941	0.783687	0.387903	0.685398	0.692336
Metatranscriptome	Functions	CosmosID	Alpha	MetaCyc Pathways	Shannon	0.6868	0.082775	0.81615	0.032551	0.033759	0.013366	0.485701	0.193562	0.082103	0.961312	0.235204	0.734489	0.64729	0.478819	0.028838	0.168982	0.498315	0.137725	0.386083	0.227855
Metatranscriptome	Functions	CosmosID	Alpha	MetaCyc Pathways	Simpson	0.3838	0.046981	0.939484	0.004316	0.193812	0.042601	0.451036	0.101156	0.128763	0.869004	0.346136	0.428726	0.854789	0.398656	0.093551	0.009316	0.509997	0.153837	0.462433	0.101156
Metatranscriptome	Functions	CosmosID	Beta	Enzyme Commission	Jaccard	0.246	0.108	0.234	0.042	0.006	0.041	0.704	0.726	0.379	0.232	0.639	0.034	0.894	0.031	0.194	0.086	0.393	0.07	0.383	0.157
Metatranscriptome	Functions	CosmosID	Beta	Enzyme Commission	Bray–Curtis	0.28	0.476	0.091	0.072	0.412	0.44	0.514	0.676	0.053	0.45	0.494	0.232	0.609	0.166	0.036	0.444	0.477	0.093	0.594	0.073
Metatranscriptome	Functions	CosmosID	Beta	Gene Ontology	abund_jaccard	0.232	0.09	0.489	0.112	0.221	0.113	0.75	0.389	0.073	0.265	0.882	0.199	0.107	0.027	0.459	0.278	0.597	0.362	0.222	0.336
Metatranscriptome	Functions	CosmosID	Beta	Gene Ontology	Bray–Curtis	0.542	0.271	0.044	0.107	0.473	0.526	0.573	0.505	0.17	0.724	0.651	0.053	0.402	0.031	0.067	0.323	0.221	0.052	0.224	0.08
Metatranscriptome	Functions	CosmosID	Beta	MetaCyc Pathways	Jaccard	0.42	0.068	0.462	0.032	0.001	0.006	0.862	0.59	0.518	0.288	0.847	0.05	0.866	0.096	0.115	0.307	0.79	0.101	0.854	0.11
Metatranscriptome	Functions	CosmosID	Beta	MetaCyc Pathways	Bray–Curtis	0.087	0.007	0.158	0.003	0.401	0.04	0.588	0.534	0.164	0.638	0.666	0.529	0.851	0.044	0.654	0.003	0.351	0.107	0.374	0.058
Metatranscriptome	Taxonomy	CosmosID	Alpha	KEPLER	Chao1	0.018827	0.731376	0.291087	0.313315	0.145685	0.71963	0.584774	0.671602	0.054653	0.455058	0.546541	0.064814	0.248921	0.111602	0.462433	0.300052	0.442101	0.331975	0.29135	0.571892
Metatranscriptome	Taxonomy	CosmosID	Alpha	KEPLER	Shannon	0.034227	0.496972	0.019323	0.302065	0.175644	0.884299	0.407072	0.664745	0.050203	0.99226	0.076533	0.27446	0.256512	0.225253	0.396493	0.417816	0.970802	0.032032	0.093551	0.346136
Metatranscriptome	Taxonomy	CosmosID	Alpha	KEPLER	Simpson	0.032507	0.236	0.00623	0.353601	0.264263	0.961312	0.428726	0.706289	0.064542	0.808365	0.039995	0.706289	0.206667	0.398656	0.193562	0.485701	0.64729	0.010144	0.079718	0.266271
Metatranscriptome	Taxonomy	CosmosID	Beta	KEPLER	Jaccard	0.202	0.076	0.129	0.063	0.093	0.09	0.65	0.396	0.545	0.365	0.769	0.069	0.659	0.072	0.338	0.162	0.903	0.071	0.532	0.104
Metatranscriptome	Taxonomy	CosmosID	Beta	KEPLER	Bray–Curtis	0.554	0.132	0.14	0.086	0.621	0.634	0.281	0.468	0.712	0.585	0.303	0.531	0.848	0.111	0.548	0.054	0.42	0.096	0.319	0.535
16S_V1V3_amplicon	Taxonomy	CosmosID	Alpha	SILVA	Chao1	0.219611	0.697647	0.035972	0.187539	0.64729	0.472816	0.300052	0.33186	0.425973	0.853757	0.308925	0.591265	0.272173	0.097127	0.304467	0.203426	0.213323	0.800858	0.17192	0.977452
16S_V1V3_amplicon	Taxonomy	CosmosID	Alpha	SILVA	Shannon	0.207021	0.663618	0.111404	0.909335	0.714347	0.240446	0.624206	0.664745	0.660496	0.71963	0.485701	0.664745	0.379696	0.71963	0.13661	0.610934	0.103354	0.99226	0.4398	0.610934
16S_V1V3_amplicon	Taxonomy	CosmosID	Alpha	SILVA	Simpson	0.254482	0.377743	0.080378	0.736201	0.660496	0.183817	0.473988	0.521759	0.486776	0.264566	0.250401	0.485701	0.341268	0.99226	0.180962	0.895067	0.128763	0.853757	0.336575	0.417816
16S_V1V3_amplicon	Taxonomy	CosmosID	Beta	SILVA	Jaccard	0.275	0.36	0.005	0.008	0.957	0.633	0.377	0.522	0.993	0.99	0.35	0.738	0.432	0.131	0.126	0.096	0.422	0.891	0.578	0.639
16S_V1V3_amplicon	Taxonomy	CosmosID	Beta	SILVA	Bray–Curtis	0.141	0.062	0.194	0.097	0.999	0.094	0.516	0.54	0.666	0.332	0.478	0.733	0.887	0.081	0.484	0.014	0.007	0.376	0.02	0.109
16S_V1V3_amplicon	Taxonomy	FOMC	Alpha	HOMD/NCBI	Ovserved species	0.21468	0.978556	0.026848	0.442043	0.653817	0.203573	0.262035	0.857899	0.256248	0.756114	0.076373	0.699157	0.172671	0.099025	0.299953	0.327034	0.355274	0.861334	0.406965	0.857899
16S_V1V3_amplicon	Taxonomy	FOMC	Alpha	HOMD/NCBI	shannon	0.133638	0.590891	0.048666	0.479573	0.498315	0.648414	0.086411	0.651115	0.350634	0.76361	0.242719	0.763052	0.43131	0.327163	0.168982	0.13661	0.133434	0.607129	0.678487	0.597789
16S_V1V3_amplicon	Taxonomy	FOMC	Alpha	HOMD/NCBI	simpson	0.09081	0.656539	0.033924	0.538908	0.234213	0.976781	0.062128	0.624206	0.206667	0.67656	0.28282	0.651115	0.64729	0.67656	0.174895	0.11784	0.220131	0.945857	0.909988	0.407072
16S_V1V3_amplicon	Taxonomy	FOMC	Beta	HOMD/NCBI	Bray–Curtis	0.602	0.092	0.249	0.11	0.259	0.027	0.255	0.765	0.942	0.692	0.299	0.691	0.989	0.09	0.74	0.023	0.225	0.679	0.35	0.123
16S_V1V3_amplicon	Taxonomy	FOMC	Beta	HOMD/NCBI	Correlation	0.863	0.084	0.307	0.212	0.847	0.191	0.104	0.738	0.775	0.442	0.128	0.582	0.992	0.093	0.917	0.139	0.215	0.684	0.444	0.145
16S_V1V3_amplicon	Taxonomy	FOMC	Beta	HOMD/NCBI	Aitchison	0.711	0.164	0.046	0.014	1	0.971	0.786	0.51	1	0.968	0.716	0.625	0.976	0.659	0.269	0.016	0.918	0.996	0.331	0.152

The excel file of this table can be downloaded with this link (file name Haleon_Comparisons_pvalues.xlsx)

https://microbiome.forsyth.org/ftp/fomc/FOMC_project/haleon/48b41065-dd02-49db-9ebe-da0e7d463cdf/

7. Week 6 vs Baseline Comparison – Bacterial Compositions

Section summary

Based on the species-level sequence abundance results, overall, the microbiomes were modified more with treatment Product B. In general with the exception of subgingival microbiomes, there appeared to be a microbiological benefit with this treatment.

Product A V2 vs Product A V3:

Comparison 1: All sites

a. No significant differences in Alpha diversity and Beta diversity
b. Little or no change in Differential abundance and Lefse analyses
c. Additional species composition and abundance charts are provided in Appendix A Comparison 1

Comparison 5: Saliva

a. Very little change in all analyses. No trends were observed with Differential abundance and LefSe analyses
b. Treatment did not affect the microbiome.
c. Additional species composition and abundance charts are provided in Appendix A Comparison 5

Comparison 9: Tongue

a. No significant differences in Alpha diversity and Beta diversity
b. Minimal trends were observed with Differential abundance. No change in LefSe analyses
c. Treatment A had little or no effect on tongue microbiomes
d. Additional species composition and abundance charts are provided in Appendix A Comparison 9

Comparison 13: Supragingival

a. No significant differences in Alpha diversity and Beta diversity
b. No or few trends were observed with Differential abundance and LefSe analyses
c. Treatment did not appreciably affect the supragingival microbiome
d. Additional species composition and abundance charts are provided in Appendix A Comparison 13.

Comparison 17: Subgingival

a. No significant differences in Alpha diversity and Beta diversity
b. Subgingival microbiomes were significantly altered with treatment A. higher levels of putative pathogens were observed. Eg., *Fusobacterium, Treponema, Selenomonas* and *Prevotella*. However, *Streptococcus* spp were reduced after treatment

c. Additional species composition and abundance charts are provided in Appendix A Comparison 17

Product B V2 vs Product B V3:

Comparison 2: All sites

a. No significant differences in Alpha diversity and Beta diversity
b. Many differences in Differential abundance and Lefse
c. Some health associated species were prevalent after treatment, e.g., *Streptococcus gordonii, Slackia spp, Abiotrophia defectiva.* However, a few putative pathogens were also more prevalent after treatment, e.g., *Dialister invisus* and species of *Aggregatibacter*
d. Treatment B modified the microbiome as compared to Treatment B baseline
e. Additional species composition and abundance charts are provided in Appendix A Comparison 2

Comparison 6: Saliva

a. No significant differences in Alpha diversity. However, there was a significant difference in Beta diversity with a p value of 0.027
b. Trend observed with a few species using differential abundance, but significance was lost after multiple comparisons
c. Lefse indicated reduced levels of a putative pathogen, *Aggregatibacter* and increased levels of the health-associated *Streptococcus gordonii*
d. Treatment B had more modifications tha~~t~~n with treatment A with an apparent health associated profile
e. Additional species composition and abundance charts are provided in Appendix A Comparison 6.

Comparison 10: Tongue

a. No significant differences in Alpha diversity and Beta diversity
b. Minimal trends were observed with Differential abundance. Not statistically significant.
c. As shown in salivary microbiome analyses, Lefse showed a reduction in *Aggregatibacter*, a putative pathogen
d. Treatment B was more effective than Treatment A. Not as effective as compared to treatment of the salivary microbiomes
e. Additional species composition and abundance charts are provided in Appendix A Comparison 10

Comparison 14: Supragingival

a. No significant differences in Alpha diversity and Beta diversity. However, statistical differences approached significance at 0.09 in each.
b. Differential abundance indicated several differences, although not significantly different

c. Many differences indicated using Lefse. The health-associated *Streptococcus gordonii* again was more prevalent after treatment. Again *Aggregatibacter* sp were reduced after treatment with B.
d. Modulations of other species are difficult to interpret. However, it is clear that treatment B modified the supragingival microbiome
e. Additional species composition and abundance charts are provided in Appendix A Comparison 14

Comparison 18: Subgingival

a. No significant differences in Alpha diversity and Beta diversity
b. Differential abundance indicated several differences, although not significantly different. Not as many with Treatment A.
c. *Aggregatibacter* reduced as before
d. Difficult to assess biological significance. These results conflict with data from other sites. B had fewer modifications as compared to A
e. Additional species composition and abundance charts are provided in Appendix A Comparison 18

8. Week 6 vs Baseline Comparison – Activities

Product A V2 vs Product A V3:

Comparison 1: All sites

Summary: No significant difference after product A treatment based on diversity assessment (all p values > 0.05). Based on differential abundance analysis (LEfSe), there are 6 Gene Ontology terms, 22 enzymes (Enzyme Commission) and 27 metabolic pathways (Metacyc Pathways) that are significantly affected (p value < 0.05).

The top-most (based on LDA scores) increased functions by Product A are:

- hydrolase activity
- Pyridoxal 5'-phosphate synthase
- fatty acid biosynthesis initiation (mitochondria)

The top-most reduced functions by Product A are:

- NADPH:quinone reductase activity
- 1,4-alpha-glucan branching enzyme
- glycogen biosynthesis I (from ADP-D-Glucose)

Detail analysis results are shown in Appendix B. Comparison 1.

Comparison 5: Saliva

Summary: In saliva samples, product A significantly affected the bacterial pathways listed in MetaCyc, when measured by alpha diversity Chao1 (p = 0.003), Shannon (p = 0.034) but not Simpson. This indicates that functions with lower read abundance (low expression level) were impacted. Enzyme activities were also affected when measured with alpha index Chao1 (p = 0.039).

A total of 5 GO terms, 4 enzymes, and 20 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product A are:

- DNA replication
- Alanine--tRNA ligase
- fatty acid β-oxidation I (generic)

The top-most reduced functions by Product A are:

- NADPH:quinone reductase activity
- Glutamine synthetase
- superpathway of anaerobic sucrose degradation

Detail analysis results are shown in Appendix B. Comparison 5.

Comparison 9: Tongue

Summary: On tongue, alpha diversity was significantly affected by Product A based on Chao1 measurement (p = 0.013) of GO terms. Alpha diversity of enzyme profile was also impacted when measured with Shannon and Simpson indexes (p=0.008 and 0.042 respectively). This means medium to higher abundant enzymatic gene expression were affected by Product A. Beta diversity of enzyme activities was affected with marginal significance by Product A (p=0.053). Alpha diversity of pathways was also affected when measured with Chao1 (p=0.026).

A total of 11 GO terms, 52 enzymes, and 28 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product A are:

- metal ion binding
- Formate C-acetyltransferase
- gondoate biosynthesis (anaerobic)

The top-most reduced functions by Product A are:

- hydrolase activity
- Glutamine synthetase

Detail analysis results are shown in Appendix B. Comparison 9.

Comparison 13: Supragingival

Summary: Alpha and Beta diversity of bacterial activities of supragingival samples were not significantly affected by the treatment of Product A.

A total of 17 GO terms, 5 enzymes, and 3 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product A are:

- mitochondrion
- Pyridoxal 5'-phosphate synthase
- UMP biosynthesis

Only one function was significantly reduced by Product A:

- Formimidoyltetrahydrofolate cyclodeaminase

Detail analysis results are shown in Appendix B. Comparison 13.

Comparison 17: Subgingival

Summary:: Alpha and Beta diversity of bacterial activities of subgingival samples were not significantly affected by the treatment of Product A.

A total of 17 GO terms, 28 enzymes, and 18 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product A are:

- periplasmic flagellum
- 3-hydroxybutyryl-CoA dehydrogenase

- fatty acid biosynthesis initiation (mitochondria)

The top-most reduced functions by Product A are:

- phosphoenolpyruvate-dependent sugar phosphotransferase system
- 1,4-alpha-glucan branching enzyme

Detail analysis results are shown in Appendix B. Comparison xxx.

Product B V2 vs Product B V3:

Comparison 2: All sites

Summary: Beat diversity of MetaCyc pathway profile was significantly affected by Product B ($p = 0.007$). Alpha Simpson diversity of Gene Ontology has significant difference ($p=0.049$) after Product B treatment.

A total of 4 GO terms, 21 enzymes, and 38 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product B are:

- extracellular region
- Galactose-6-phosphate isomerase
- glycolysis IV

The top-most reduced functions by Product B are:

- cell outer membrane
- Bacterial non-heme ferritin
- Calvin-Benson-Bassham cycle

Detail analysis results are shown in Appendix B. Comparison 2.

Comparison 6: Saliva

Summary: Alpha and Beta diversity of bacterial activities of saliva samples were not significantly affected by the treatment of Product A.

A total of 3 GO terms, 0 enzymes, and 48 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product B are:

- glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity

The top-most reduced functions by Product B are:

- riboflavin biosynthetic process
- superpathway of glucose and xylose degradation
- glycolysis IV

Detail analysis results are shown in Appendix B. Comparison 6.

Comparison 10: Tongue

Summary: On Tongue, Alpha diversity of both GO and Enzymes profiles were significantly affected by Product B, measured by Chao1 index (p=0.031 and 0.045, respectively). Beta diversity was not significantly affected.

A total of 6 GO terms, 14 enzymes, and 4 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product B are:

- 6-phosphofructokinase
- Rubisco shunt

The top-most reduced functions by Product B are:

- porin activity
- Nitrite reductase (NO-forming)
- phosphatidylglycerol biosynthesis I (plastidic)

Detail analysis results are shown in Appendix B. Comparison 10.

Comparison 14: Supragingival

Summary: Alpha diversity of GO profiles was affected significantly by Product B, measured with Chao1 (p=0.037), Shannon (p=0.011) and Simpson (p=0.008). Beta diversity of GO and MetaCyc profiles were significantly affected by Product B (p=0.031, and 0.044, respectively).

A total of 25 GO terms, 41 enzymes, and 28 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product B are:

- cytoplasm
- Triose-phosphate isomerase
- UMP biosynthesis II

The top-most reduced functions by Product B are:

- integral component of membrane
- Transaldolase
- Calvin-Benson-Bassham cycle

Detail analysis results are shown in Appendix B. Comparison 14.

Comparison 18: Subgingival

Summary: Alpha and Beta diversity of bacterial activities of subgingival samples were not significantly affected by the treatment of Product B.

A total of 17 GO terms, 28 enzymes, and 18 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product B are:

- periplasmic flagellum
- 3-hydroxybutyryl-CoA dehydrogenase

- fatty acid biosynthesis initiation (mitochondria)

The top-most reduced functions by Product B are:

- phosphoenolpyruvate-dependent sugar phosphotransferase system
- 1,4-alpha-glucan branching enzyme
- glucose and glucose-1-phosphate degradation

Detail analysis results are shown in Appendix B. Comparison 18.

9. Product A vs B at Week 6 – Bacterial Composition

Comparison 4: All sites

a. Data indicated that the microbiomes of the subject populations were not similar. Many differences were observed.
b. Longitudinal data should be used to evaluate, as in Comparison 2
c. Additional species composition and abundance charts are provided in Appendix A Comparison 4

Comparison 8: Saliva

a. No significant differences in Alpha diversity and Beta diversity
b. Differential abundance indicated many differences, but statistical significance was lost after multiple comparisons.
c. Lefse also indicated many differences. Many health associated species had increased levels in B, e.g. *S. gordonii, Gemella hemolysans, Abiotrophia defectiva, Granulicatella elegans*. In contrast, species of *Campylobacter*, putative pathogens, were reduced in B
d. Treatment B appeared to be beneficial
e. Additional species composition and abundance charts are provided in Appendix A Comparison 8.

Comparison 12: Tongue

a. No significant differences in Alpha diversity and Beta diversity
b. Differential abundance indicated several differences, although not significantly different between the subject populations
c. Very few differences with Lefse analysis. Campylobacter sp (putative pathogens), were again reduced with Treatment B.
d. Additional species composition and abundance charts are provided in Appendix A Comparison 12

Comparison 16: Supragingival

a. No significant differences in Alpha diversity. However, there was a significant difference in Beta diversity with a p value of 0.023
b. As expected, many differences observed with both differential abundance and Lefse
c. Longitudinal data, and not these cross-sectional data should be used to evaluate
d. Additional species composition and abundance charts are provided in Appendix A Comparison 16

Comparison 20: Subgingival

a. No significant differences in Alpha diversity and Beta diversity
b. Many differences in differential abundance and Lefse, as expected
c. Longitudinal analyses would be a better assessment
d. Additional species composition and abundance charts are provided in Appendix A Comparison 20

10. Product A vs B at Week 6 – Activities

Comparison 4: All sites

Summary: When all sites combined, alpha and beta diversities of MetaCyc pathway profiles are significantly different after 2 weeks of treatment between Product A and Product B. Alpha diversities measured with Shannon and Simpson indexes have p values of 0.033 and 0.004 respectively. Beat diversities of MetaCyc pathway profiles differed at a significant level with p =0.005.

A total of 12 GO terms, 45 enzymes, and 41 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product A are:

- cytolysis
- DNA-directed RNA polymerase
- gondoate biosynthesis (anaerobic)

The top-most increased functions by Product B are:

- glutamine biosynthetic process
- 6-phospho-beta-galactosidase
- glycogen biosynthesis I (from ADP-D-Glucose)

Detail analysis results are shown in Appendix B. Comparison 4.

Comparison 8: Saliva

Summary: For saliva samples, alpha and beta diversity of bacterial activities were not significantly different between the treatment of Product A and B at week 6.

A total of 14 GO terms, 2 enzymes, and 4 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product A are:

- metal ion transport
- Bacterial non-heme ferritin
- gondoate biosynthesis (anaerobic)

The top-most increased functions by Product B are:

- nucleus
- sucrose biosynthesis II

Detail analysis results are shown in Appendix B. Comparison 8.

Comparison 16: Supragingival

Summary: For supragingival samples, alpha and beta diversity of bacterial activities were not significantly different between the treatment of Product A and B at week 6.

A total of 14 GO terms, 7 enzymes, and 5 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product A are:

- cytolysis
- [Formate-C-acetyltransferase]-activating enzyme
- palmitate biosynthesis (type II fatty acid synthase)

The top-most increased functions by Product B are:

- integral component of membrane
- glucose and glucose-1-phosphate degradation

Detail analysis results are shown in Appendix B. Comparison 16.

Comparison 16: Supragingival

Summary: In supragingival samples, alpha diversity of the MetaCyc Pahtways profiles differ between the treatment of Product A and B at week 6 for the most abundant features. The Simpson index differed with a p value of 0.009 and the beta diversity differed at p = 0.003.

A total of 16 GO terms, 23 enzymes, and 34 pathways were impacted based on LEfSe differential abundance analysis.

The top-most (based on LDA scores) increased functions by Product A are:

- integral component of membrane
- tRNA (guanine(37)-N(1))-methyltransferase
- Calvin-Benson-Bassham cycle

The top-most increased functions by Product B are:

- oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor
- Glucose-1-phosphate adenylyltransferase
- glycogen biosynthesis I (from ADP-D-Glucose)

Detail analysis results are shown in Appendix B. Comparison 16.

Comparison 20: Subgingival

Summary: for subgingival samples, alpha and beta diversity of bacterial activities were not significantly affected between the treatment of Product A and B at week 6.

However, numerous functional features had differential abundance between the treatment of Product A and B at week 6. A total of 40 GO terms, 72 enzymes, and 32 pathways were impacted based on LEfSe differential abundance analysis. Product A triggered higher expression for 72 enzymes and 23 pathway related genes. This suggests that Product B affects the bacterial activities more than Product A does.

The top-most (based on LDA scores) increased functions by Product A are:

- translation
- DNA-directed RNA polymerase

- fatty acid biosynthesis initiation (mitochondria)

The top-most reduced functions by Product B are:

- extracellular exosome
- glycolysis III (from glucose)

Detail analysis results are shown in Appendix B. Comparison 20.

11. Bacterial Compositions of Oral Sites at Baseline (V2)

Summary. Bacterial compositions differ most significantly by sites. Saliva and tongue samples have similar compositions and supra- and sub-gingival samples are similar to each other. At baseline (V2) the difference in compositions was driven by sample source (sites) instead of the two product groups. As Figure 4 shows, the saliva and tongues samples have marked differences than supra- and sub-gingival ones, as measured by both alpha (data not shown) and beta diversity analysis (Figure 4). The microbiome profiles between saliva/tongue and supr-/sub-gingival samples are distinct at any stage of the samples, both at baseline and after the treatment of products. This distinction between saliva/tongue and supra-/sub-gingival samples was also observed in the meta-transcriptomic data for all the samples (Figure 5, all p values are significant for pairwise and group comparisons). This is expected and the distinct microbiome profile separation by sites indicates that the sequence quality was adequate to show this distinction.

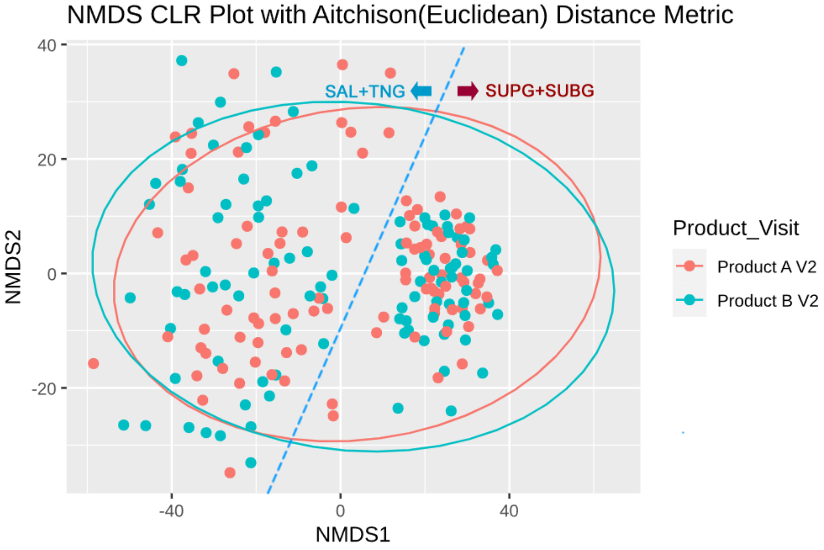


Figure 4. Beta diversity ordinate plots of samples at baseline (V2).

Cohorts	Sample Size	Permutations	Statistic	P-value
All	408	999	36.486	0.001
SUPG ↔ SUBG	204	999	14.106	0.001
SUPG ↔ TNG	204	999	53.781	0.001
SUPG ↔ SAL	204	999	43.394	0.001
SUBG ↔ TNG	204	999	59.21	0.001
SUBG ↔ SAL	204	999	41.06	0.001
TNG ↔ SAL	204	999	8.597	0.001

Figure 5. Beta diversity ordinate plots of all samples.

Comparison 3: Product A V2 vs Product B V2 (All Sites)

a. Data indicated that the microbiomes of the subject populations were not similar. Many differences were observed.
b. Longitudinal data should be used to evaluate, as in comparison 1
c. Additional compositional and abundance charts are available in Appendix A Comparison 3

Comparison 7: Product A V2 SAL vs Product B V2 SAL (Saliva)

a. No significant differences in Alpha diversity and Beta diversity
Only minor differences in Differential abundance and Lefse
b. Data indicates that the salivary microbiomes of subjects in A were similar to those in subjects in B. A good control.
c. Additional compositional and abundance charts are available in Appendix A Comparison 7

Comparison 11: Product A V2 TNG vs Product B V2 TNG (Tongue)

a. No significant differences in Alpha diversity and Beta diversity
b. Differential abundance indicated many differences, although not significantly different between the subject populations. Many differences observed using Lefse
c. Longitudinal analysis would be the preferential comparison (5 and 6 above)
d. Additional compositional and abundance charts are available in Appendix A Comparison 11

Comparison 15: Product A V2 SUPG vs Product B V2 SUPG (Supragingival)

a. No significant differences in Alpha diversity and Beta diversity.
b. Differential abundance indicated several differences, although not significantly different
c. many differences observed with Lefse. Several pathogens were observed, eg., *Treponema* spp., Tm7, and *Prevotella*.
d. These data indicate that there are differences in the 2 populations—longitudinal data should be used to determine the effectiveness of treatment
e. Additional compositional and abundance charts are available in Appendix A Comparison 15

Comparison 19: Product A V2 SUBG vs Product B V2 SUBG (Subgingival)

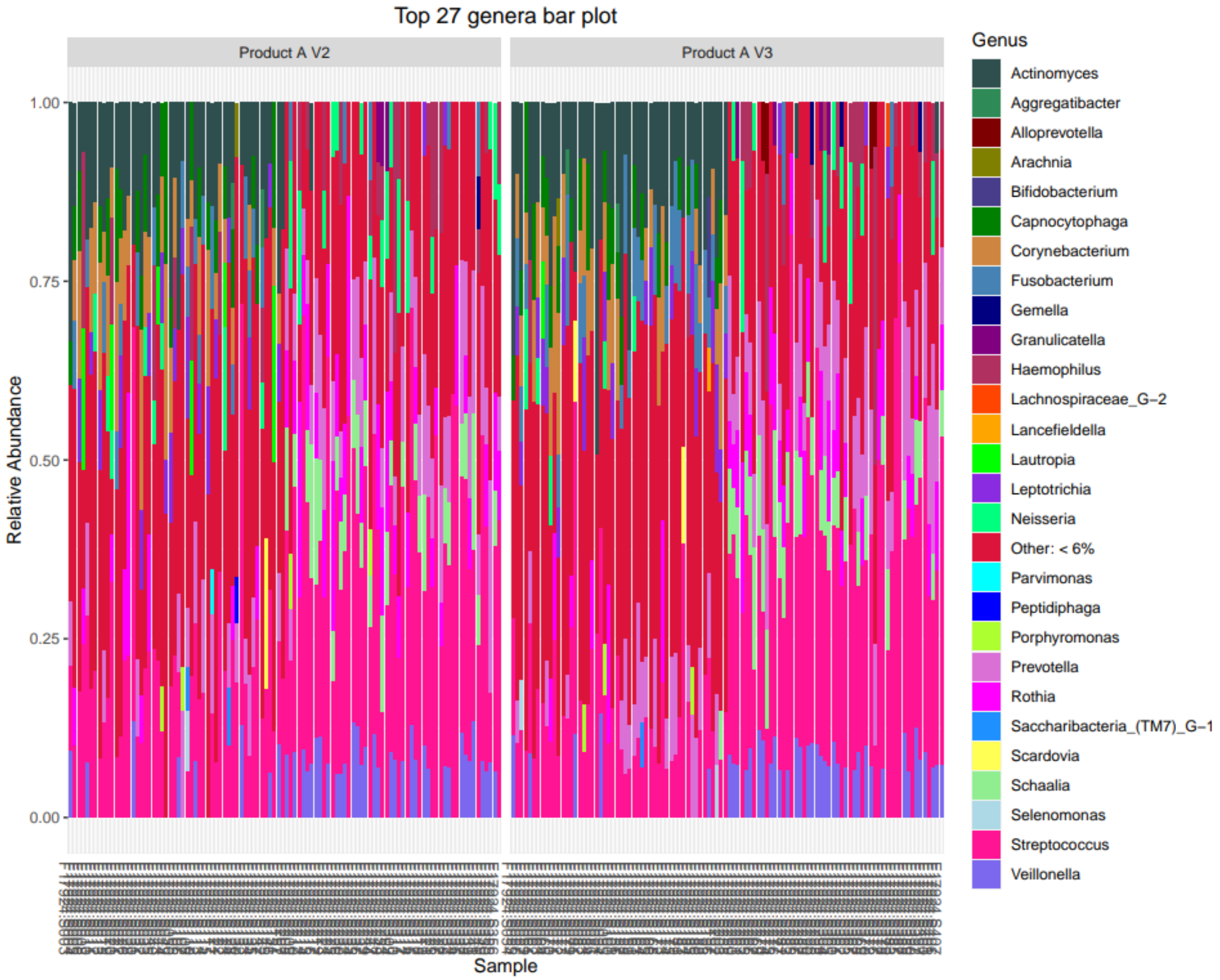
a. No significant differences in Alpha diversity and Beta diversity
b. Differential abundance indicated several differences, although not significantly different
c. Microbiomes are reasonably similar and serve as an adequate control
d. Additional compositional and abundance charts are available in Appendix A Comparison 19

VIII. Appendix

Appendix A – 16S rRNA V1V3 Analysis Figures and Charts

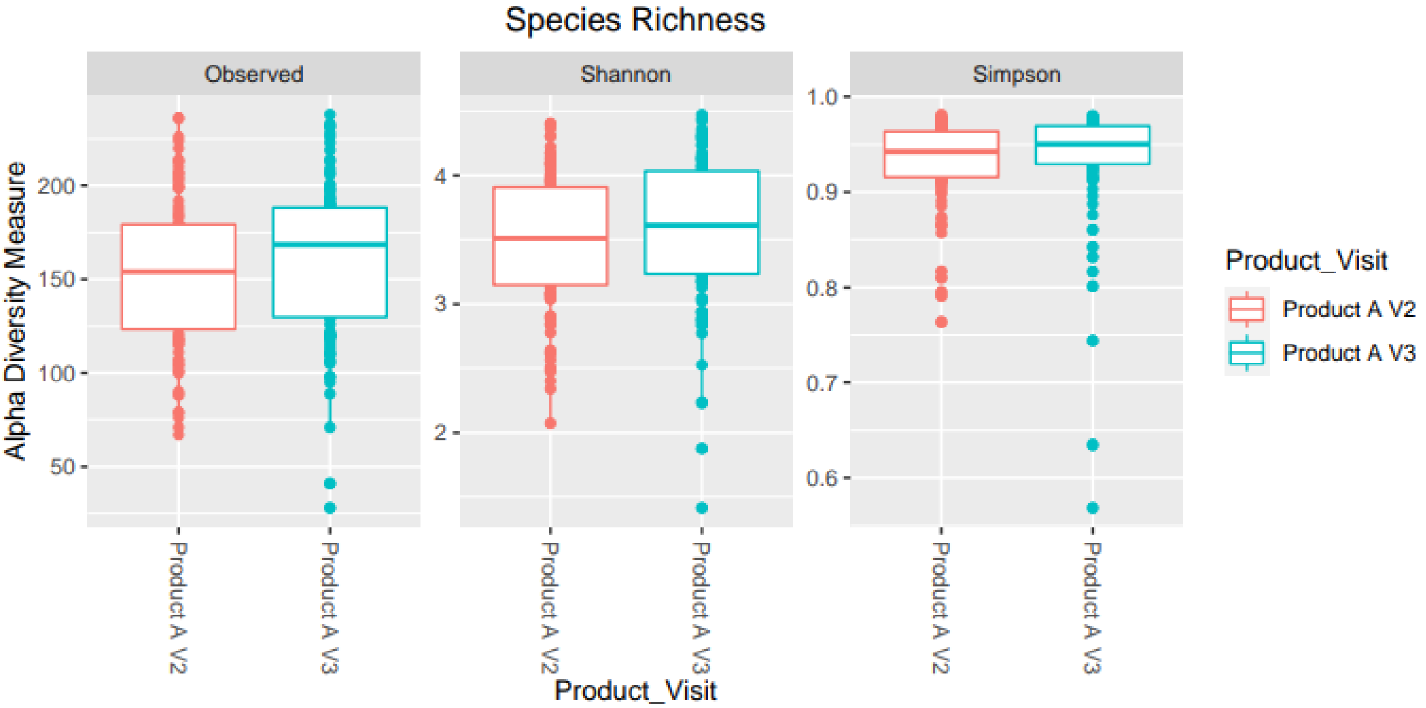
Comparison 1: Product A V2 vs Product A V3

1) Taxonomy bar graph



Too crowded to visualize, but can detect the differences in the different sites

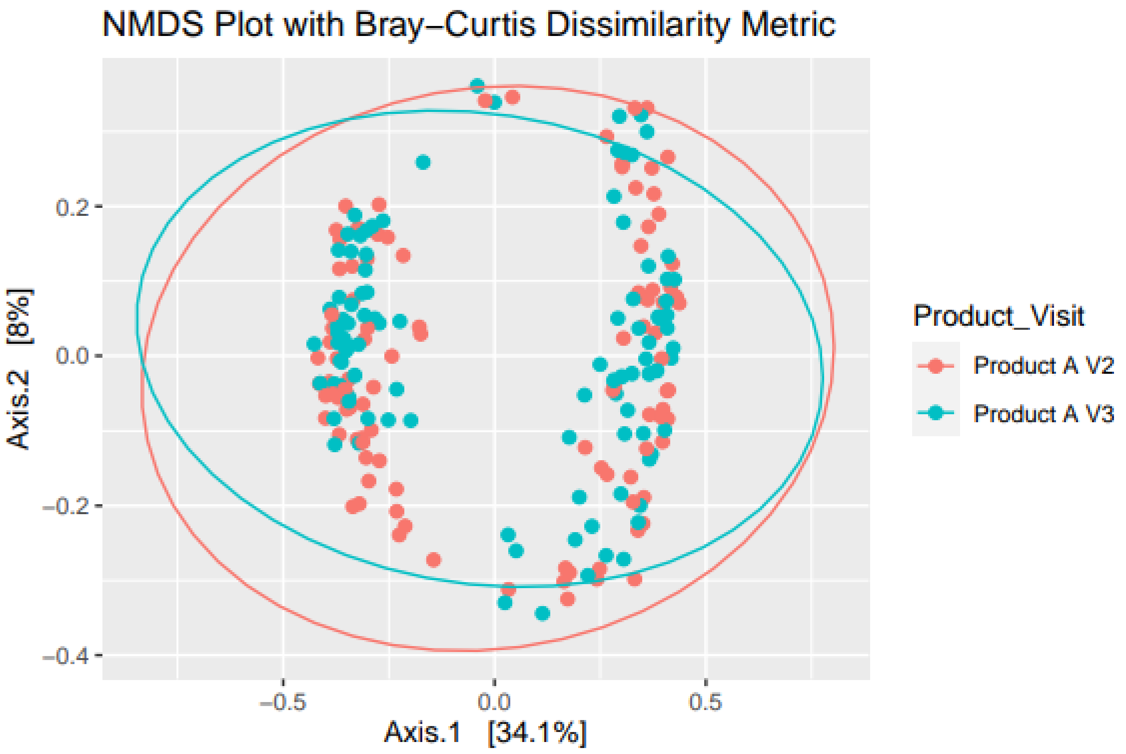
2) Alpha diversity



No statistical differences

Simpson is p=0.09

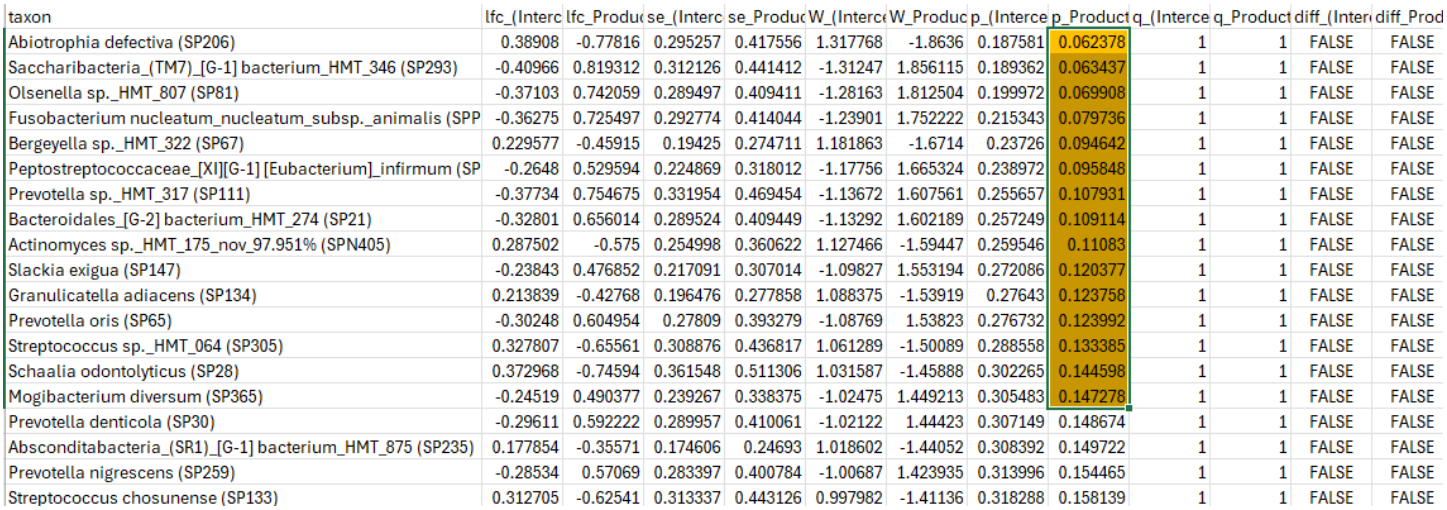
3) Beta diversity



Can see the different sites

Not significantly different.

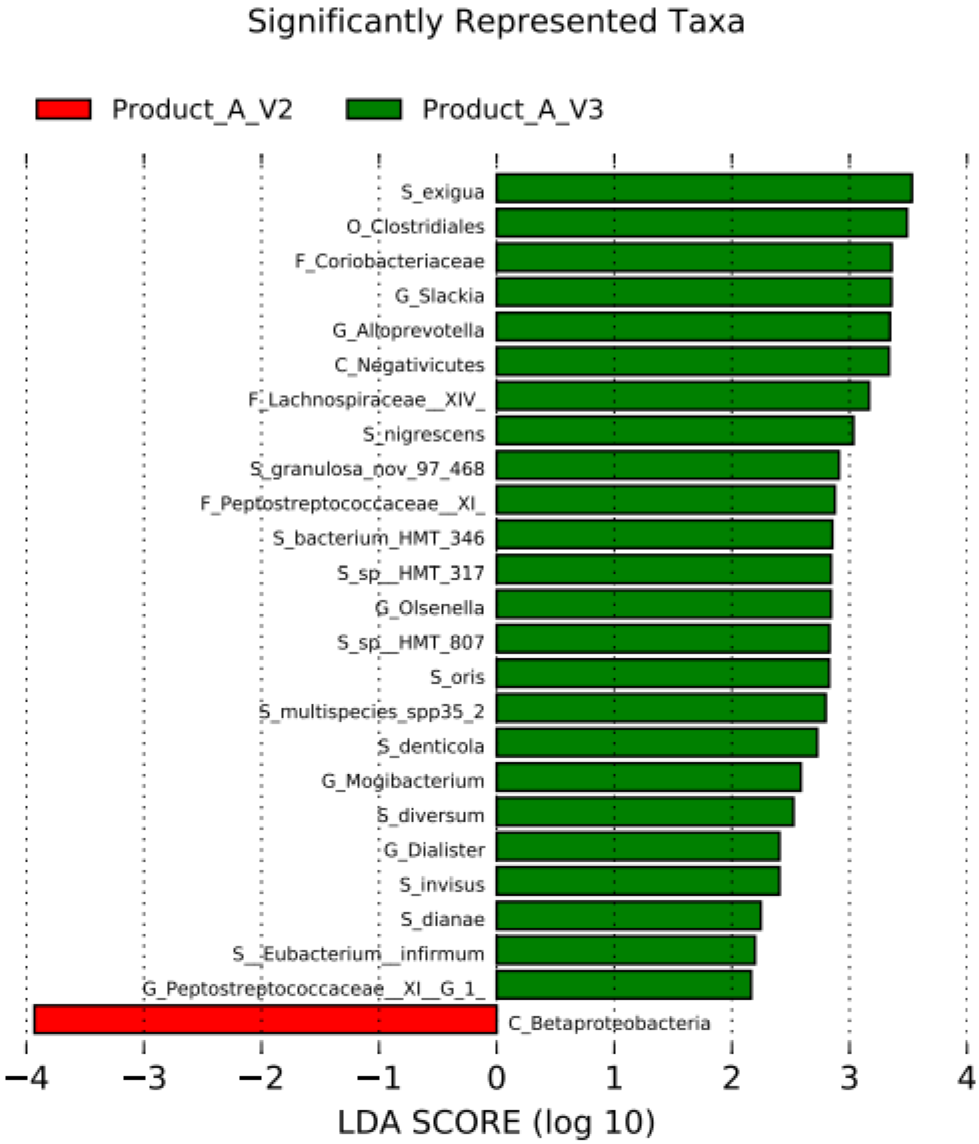
4) Differential abundance

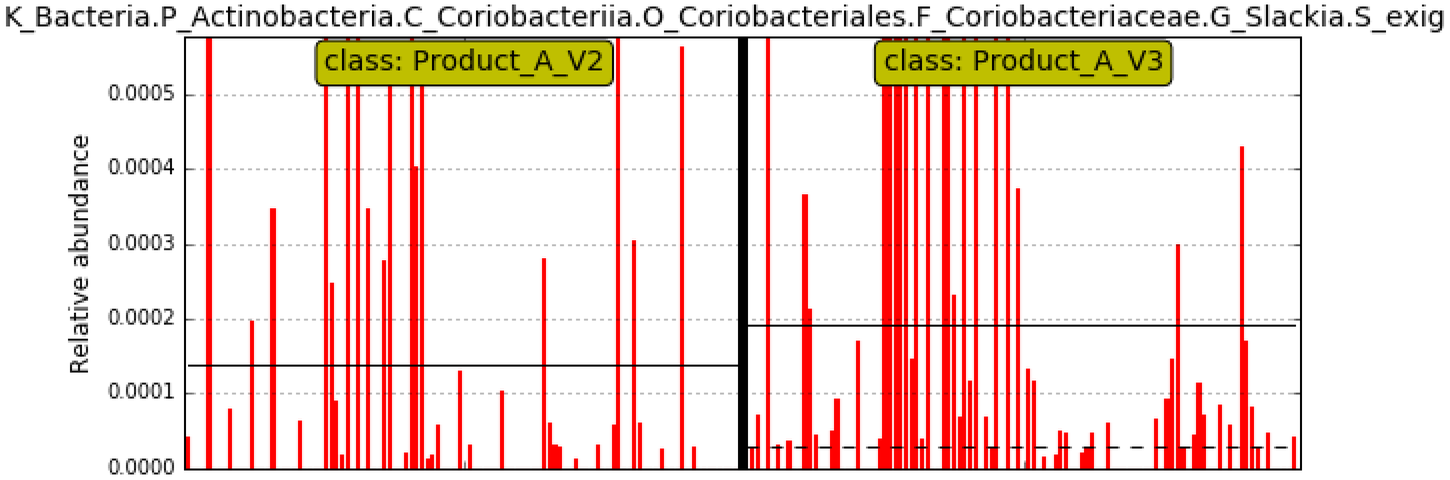


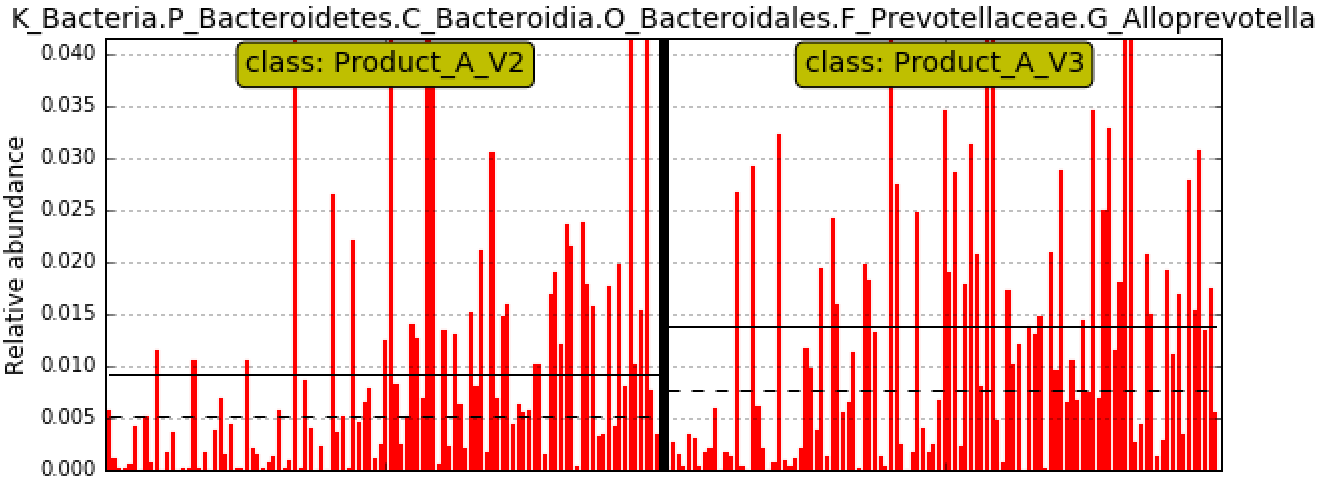
taxon	lfc_(Interc	lfc_Produc	se_(Interc	se_Produc	W_(Interce	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inter	diff_Prod
Abiotrophia defectiva (SP206)	0.38908	-0.77816	0.295257	0.417556	1.317768	-1.8636	0.187581	0.062378	1	1	FALSE	FALSE
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346 (SP293)	-0.40966	0.819312	0.312126	0.441412	-1.31247	1.856115	0.189362	0.063437	1	1	FALSE	FALSE
Olsenella sp._HMT_807 (SP81)	-0.37103	0.742059	0.289497	0.409411	-1.28163	1.812504	0.199972	0.069908	1	1	FALSE	FALSE
Fusobacterium nucleatum_nucleatum_subsp._animalis (SPP	-0.36275	0.725497	0.292774	0.414044	-1.23901	1.752222	0.215343	0.079736	1	1	FALSE	FALSE
Bergeyella sp._HMT_322 (SP67)	0.229577	-0.45915	0.19425	0.274711	1.181863	-1.6714	0.23726	0.094642	1	1	FALSE	FALSE
Peptostreptococcaceae_[XI][G-1] [Eubacterium]_infirmum (SP	-0.2648	0.529594	0.224869	0.318012	-1.17756	1.665324	0.238972	0.095848	1	1	FALSE	FALSE
Prevotella sp._HMT_317 (SP111)	-0.37734	0.754675	0.331954	0.469454	-1.13672	1.607561	0.255657	0.107931	1	1	FALSE	FALSE
Bacteroidales_[G-2] bacterium_HMT_274 (SP21)	-0.32801	0.656014	0.289524	0.409449	-1.13292	1.602189	0.257249	0.109114	1	1	FALSE	FALSE
Actinomyces sp._HMT_175_nov_97.951% (SPN405)	0.287502	-0.575	0.254998	0.360622	1.127466	-1.59447	0.259546	0.11083	1	1	FALSE	FALSE
Slackia exigua (SP147)	-0.23843	0.476852	0.217091	0.307014	-1.09827	1.553194	0.272086	0.120377	1	1	FALSE	FALSE
Granulicatella adiacens (SP134)	0.213839	-0.42768	0.196476	0.277858	1.088375	-1.53919	0.27643	0.123758	1	1	FALSE	FALSE
Prevotella oris (SP65)	-0.30248	0.604954	0.27809	0.393279	-1.08769	1.53823	0.276732	0.123992	1	1	FALSE	FALSE
Streptococcus sp._HMT_064 (SP305)	0.327807	-0.65561	0.308876	0.436817	1.061289	-1.50089	0.288558	0.133385	1	1	FALSE	FALSE
Schaalia odontolyticus (SP28)	0.372968	-0.74594	0.361548	0.511306	1.031587	-1.45888	0.302265	0.144598	1	1	FALSE	FALSE
Mogibacterium diversum (SP365)	-0.24519	0.490377	0.239267	0.338375	-1.02475	1.449213	0.305483	0.147278	1	1	FALSE	FALSE
Prevotella denticola (SP30)	-0.29611	0.592222	0.289957	0.410061	-1.02122	1.44423	0.307149	0.148674	1	1	FALSE	FALSE
Absconditabacteria_(SR1)_[G-1] bacterium_HMT_875 (SP235)	0.177854	-0.35571	0.174606	0.24693	1.018602	-1.44052	0.308392	0.149722	1	1	FALSE	FALSE
Prevotella nigrescens (SP259)	-0.28534	0.57069	0.283397	0.400784	-1.00687	1.423935	0.313996	0.154465	1	1	FALSE	FALSE
Streptococcus chosunense (SP133)	0.312705	-0.62541	0.313337	0.443126	0.997982	-1.41136	0.318288	0.158139	1	1	FALSE	FALSE

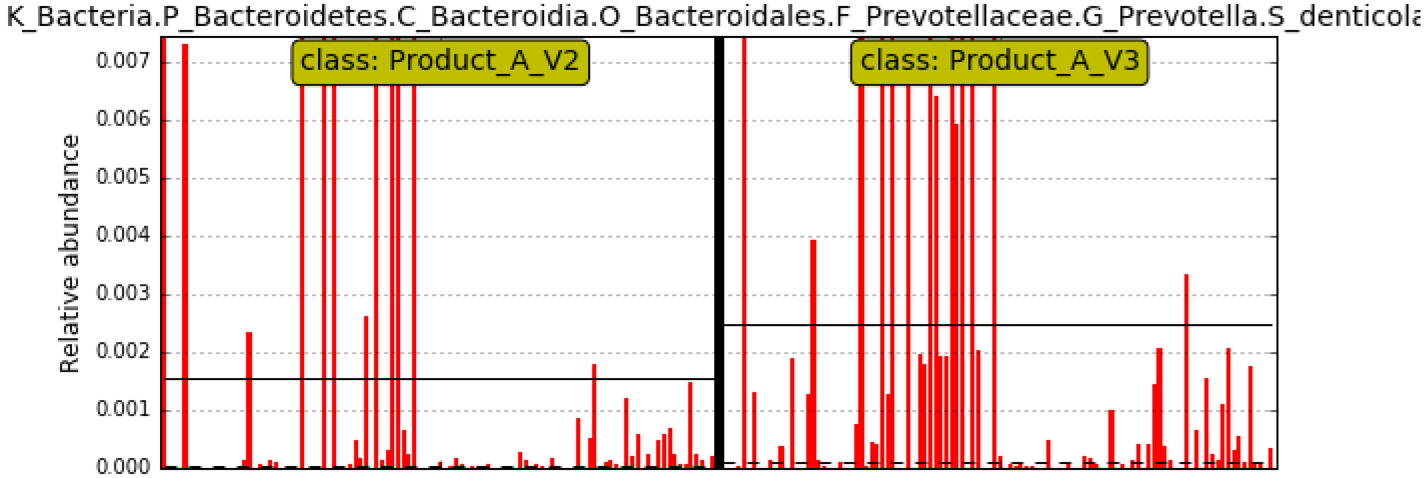
Little or no difference after treatment

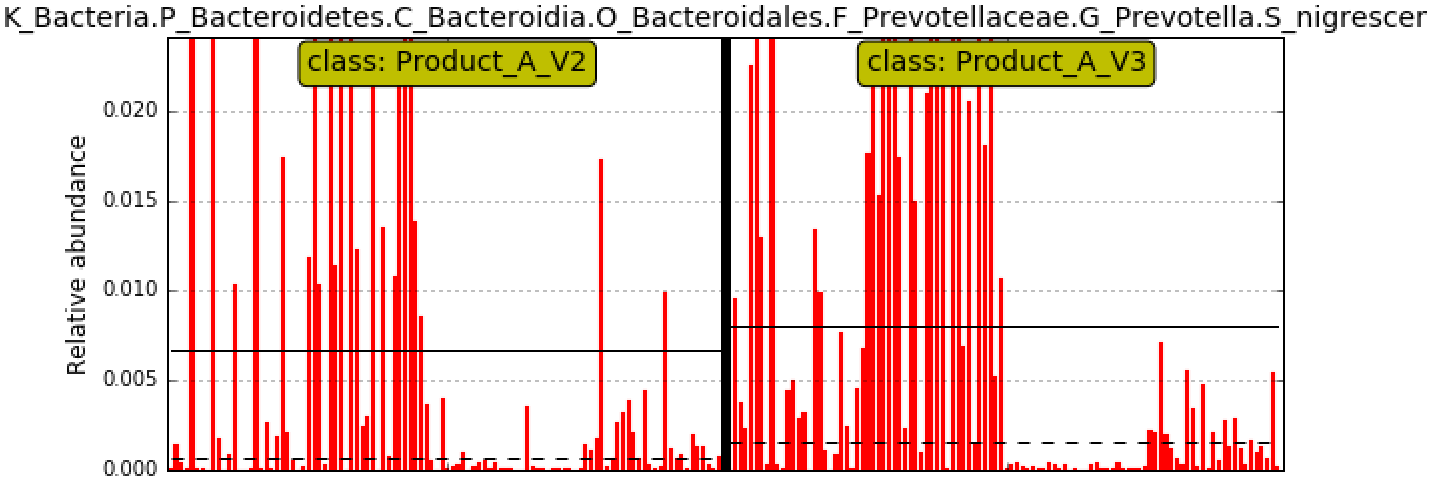
5) Lefse

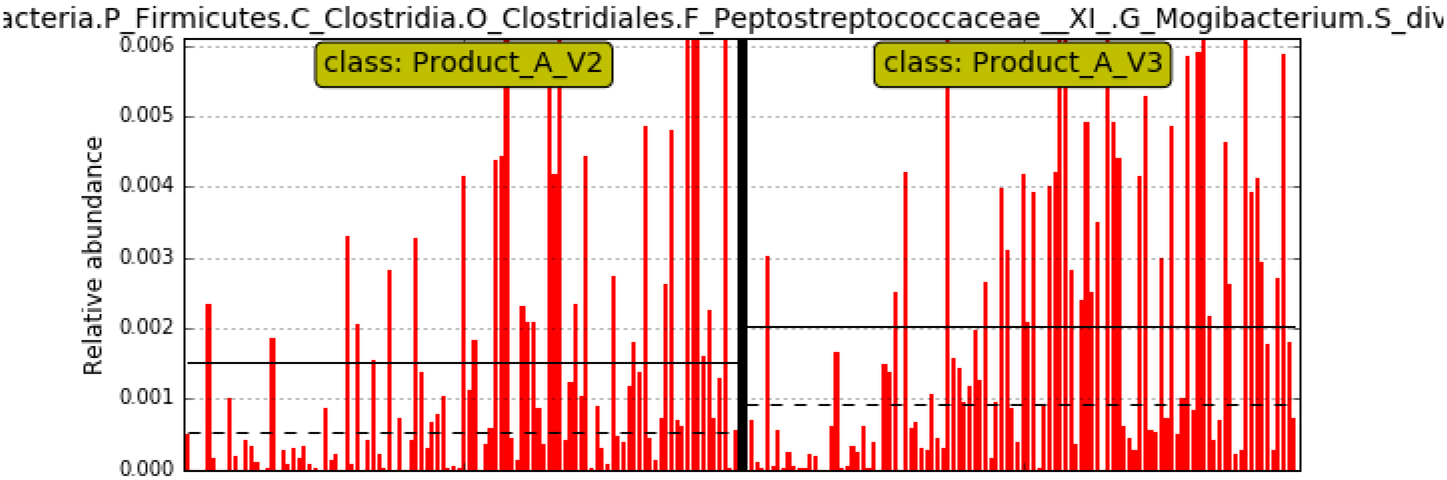

Significantly Represented Taxa
Product_A_V2
Product_A_V3
S_exigua
O_Clostridiales
F_Coriobacteriaceae
G_Slackia
G_Alloprevotella
C_Negativicutes
F_Lachnospiraceae__XIV_
S_nigrescens
S_granulosa_nov_97_468
F_Peptostreptococcaceae__XI_
S_bacterium_HMT_346
S_sp__HMT_317
G_Olsenella
S_sp__HMT_807
S_oris
S_multispecies_spp35_2
S_denticola
G_Mogibacterium
S_diversum
G_Dialister
S_invisus
S_dianae
S__Eubacterium__infirmum
G_Peptostreptococcaceae__XI__G_1_
C_Betaproteobacteria
−4
−3
−2
−1
0
1
2
3
4
LDA SCORE (log 10)

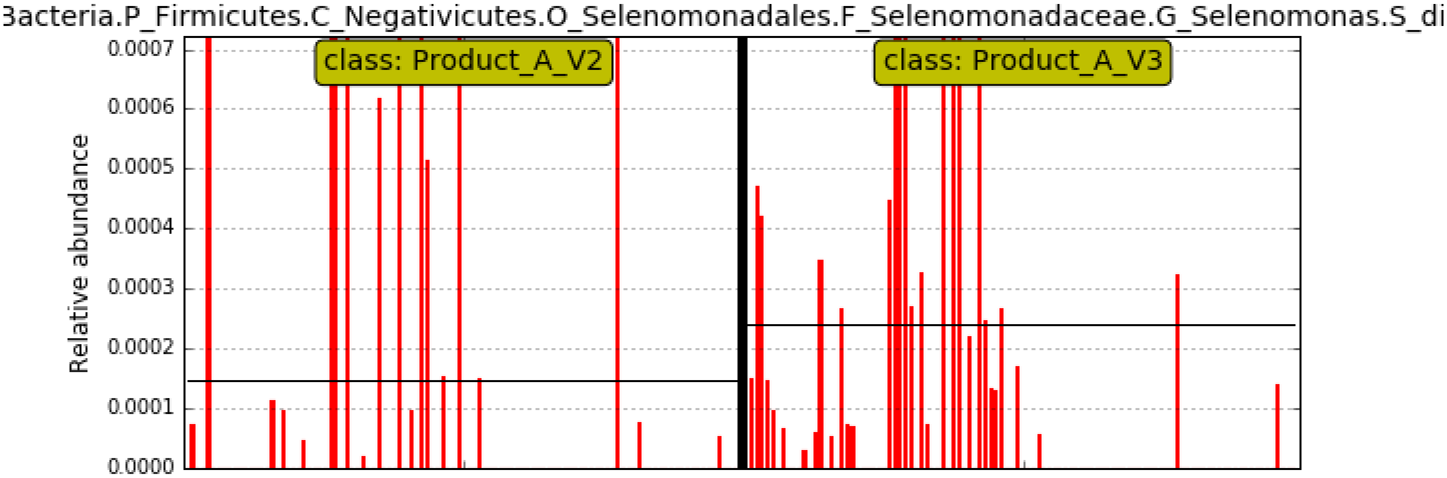

K_Bacteria.P_Actinobacteria.C_Coriobacteriia.O_Coriobacteriales.F_Coriobacteriaceae.G_Slackia.S_exig
class: Product_A_V2
class: Product_A_V3
Relative abundance
0.0000
0.0001
0.0002
0.0003
0.0004
0.0005

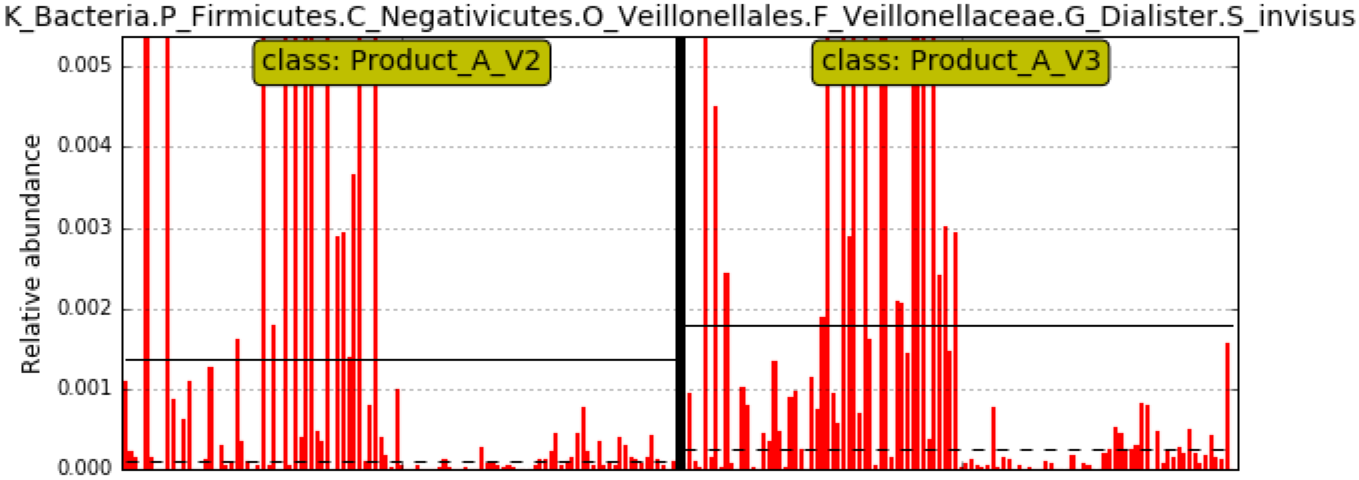

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Alloprevotella
class: Product_A_V2
class: Product_A_V3
Relative abundance
0.040
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000

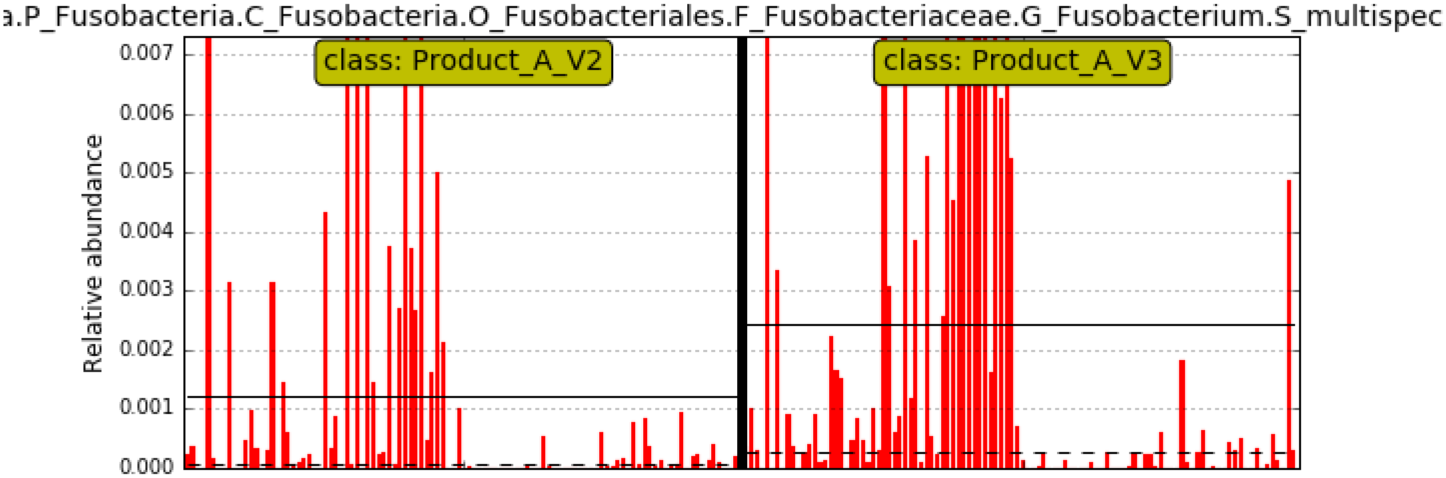

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_denticola
class: Product_A_V2
class: Product_A_V3
Relative abundance
0.007
0.006
0.005
0.004
0.003
0.002
0.001
0.000

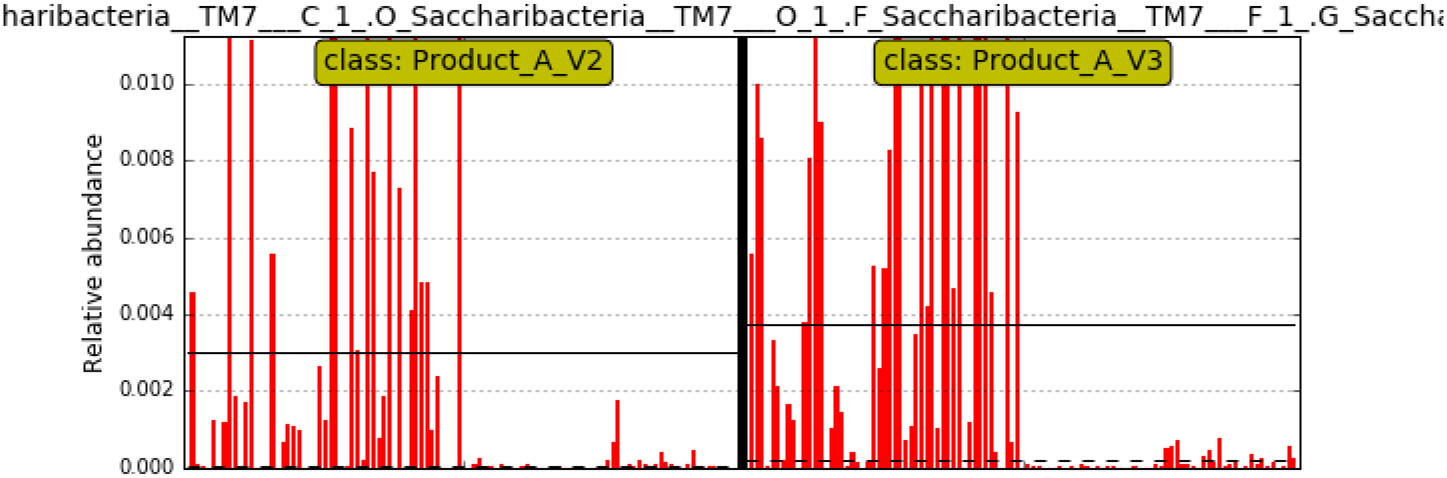

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_nigrescer
class: Product_A_V2
class: Product_A_V3
Relative abundance
0.020
0.015
0.010
0.005
0.000


acteria.P_Firmicutes.C_Clostridia.O_Clostridiales.F_Peptostreptococcaceae__XI_.G_Mogibacterium.S_div


Bacteria.P_Firmicutes.C_Negativicutes.O_Selenomonadales.F_Selenomonadaceae.G_Selenomonas.S_di

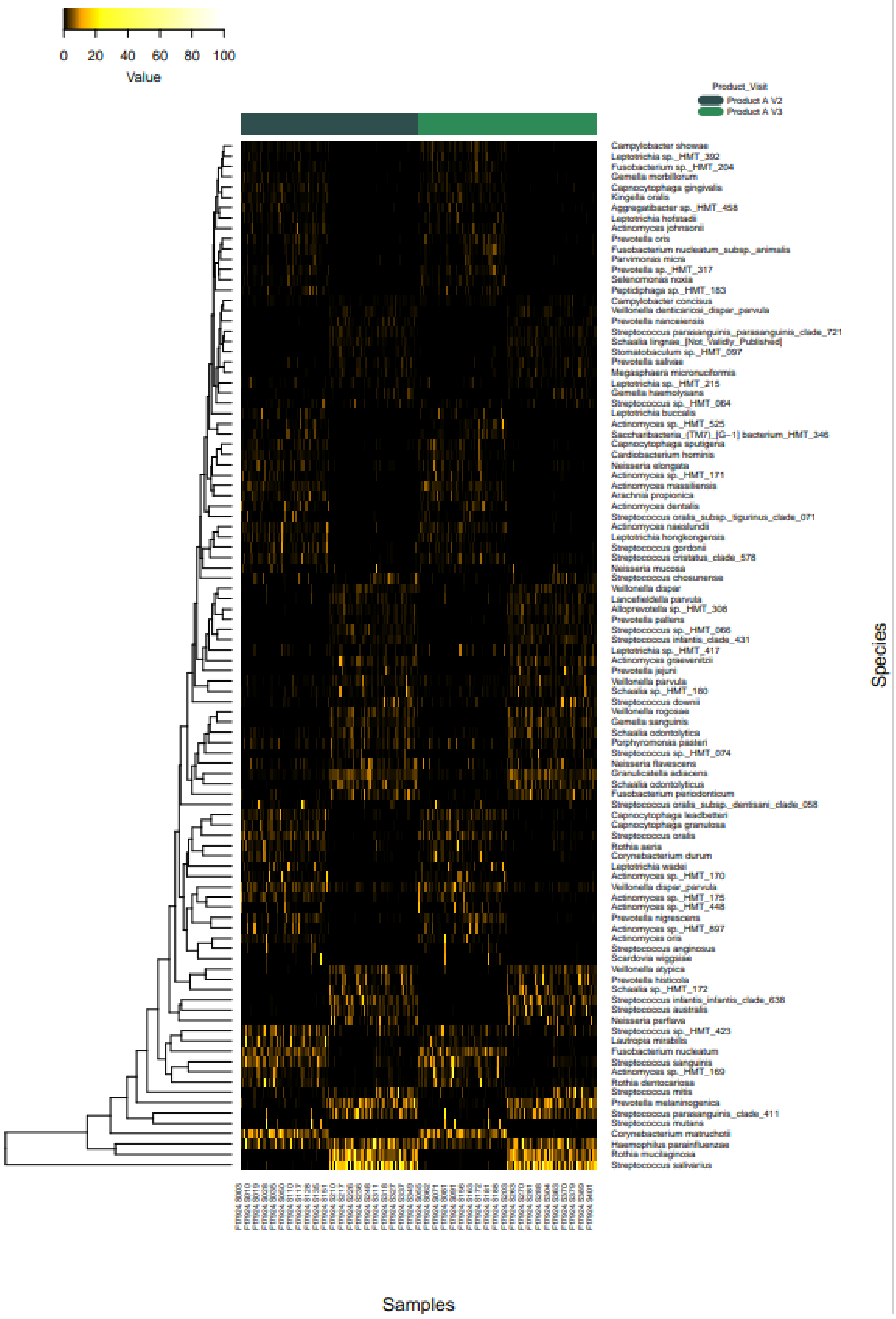

K_Bacteria.P_Firmicutes.C_Negativicutes.O_Veillonellales.F_Veillonellaceae.G_Dialister.S_invisus

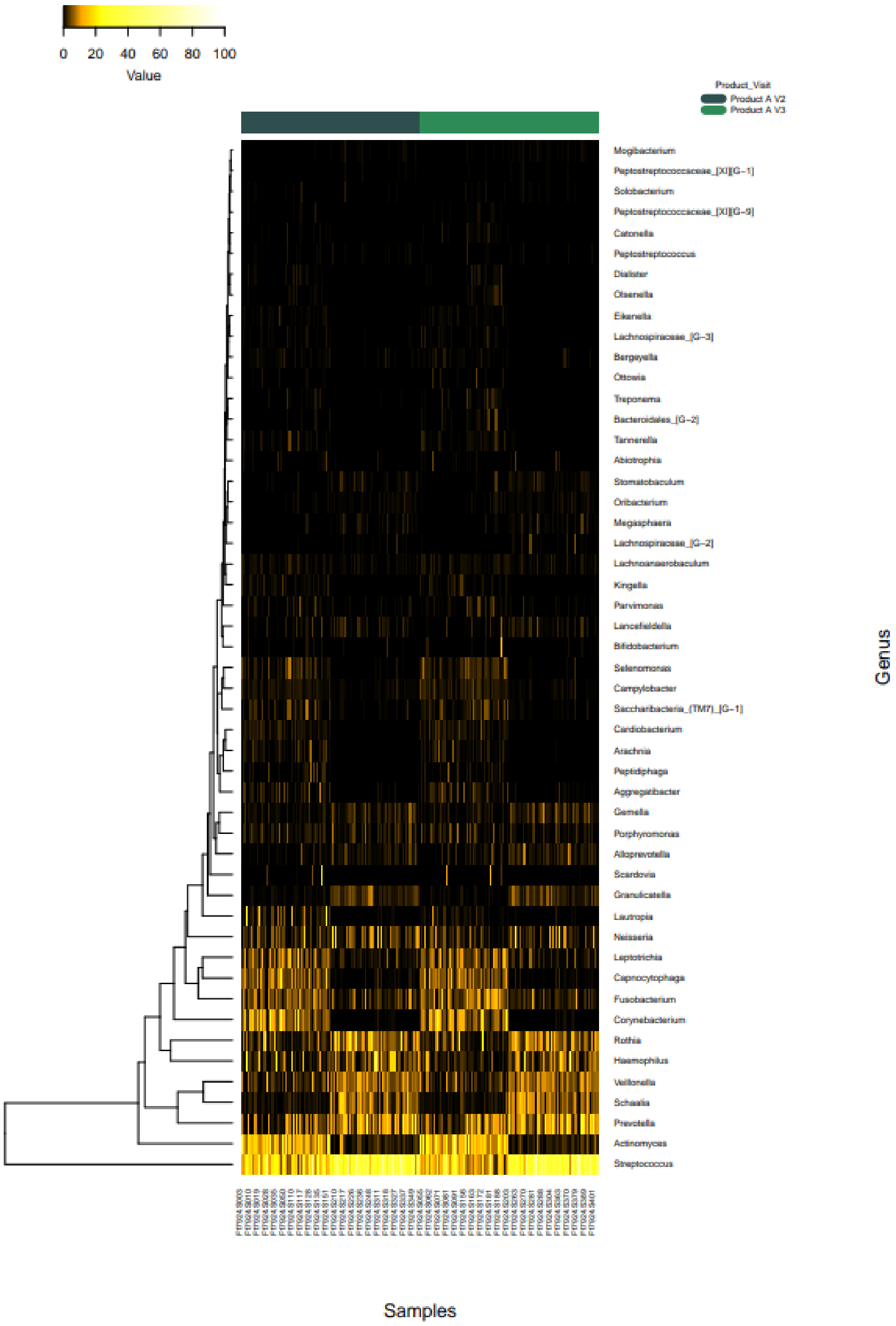

a.P_Fusobacteria.C_Fusobacteria.O_Fusobacteriales.F_Fusobacteriaceae.G_Fusobacterium.S_multispec
Relative abundance
0.000
0.001
0.002
0.003
0.004
0.005
0.006
0.007
class: Product_A_V2
class: Product_A_V3


haribacteria__TM7___C_1_.O_Saccharibacteria__TM7___O_1_.F_Saccharibacteria__TM7___F_1_.G_Sacch
Relative abundance
0.000
0.002
0.004
0.006
0.008
0.010
class: Product_A_V2
class: Product_A_V3

6) Heat maps

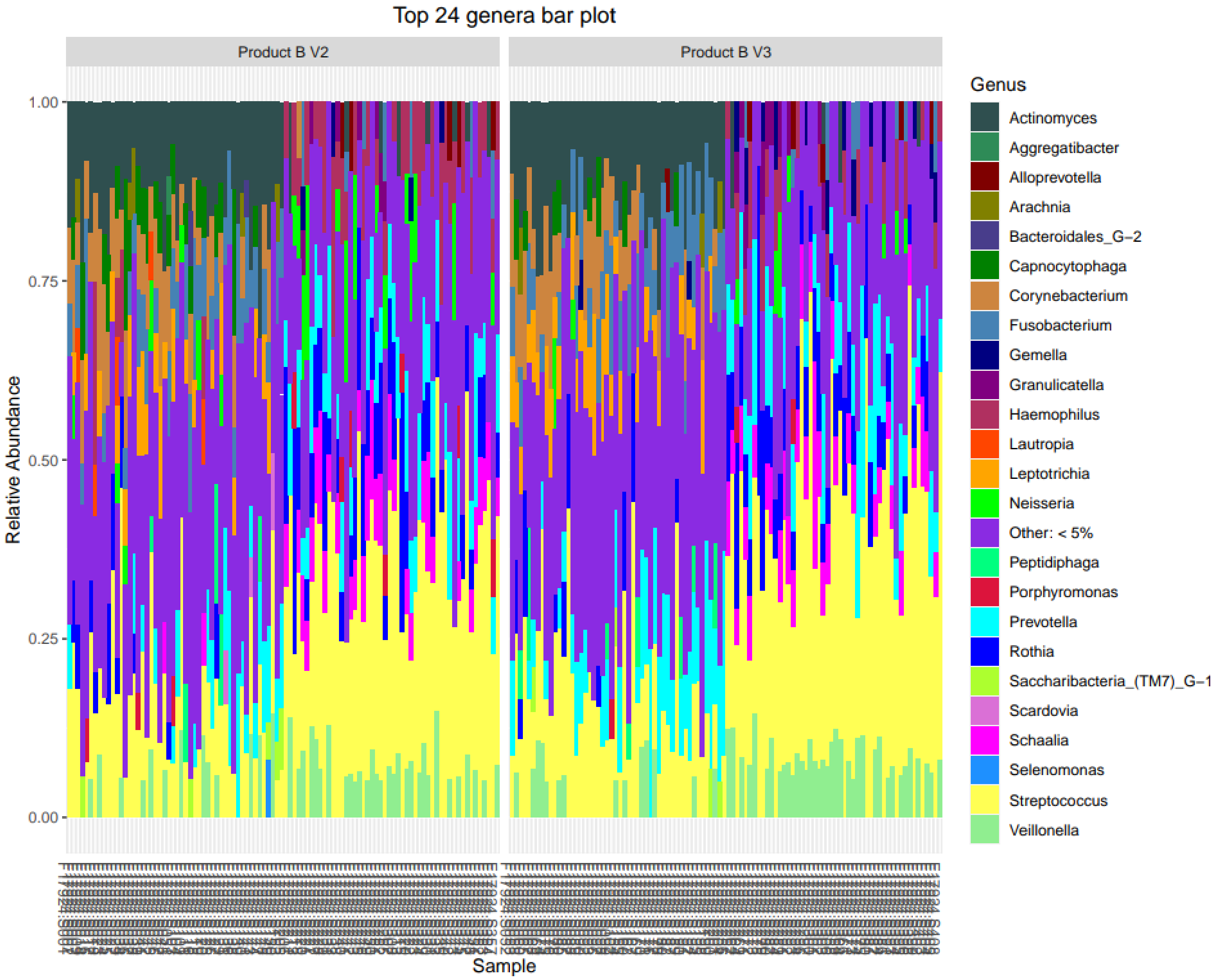
Different sites are clearly seen



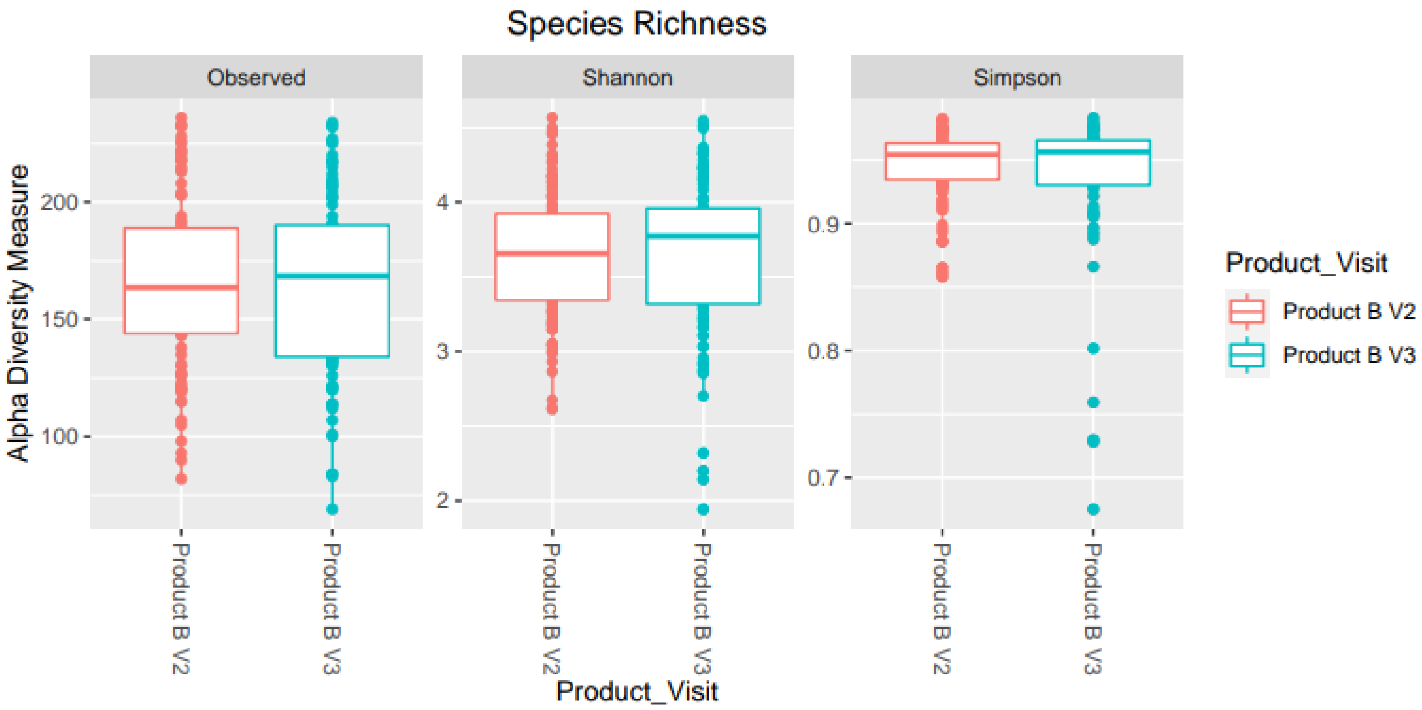

0
20
40
60
80
100
Value
Product_Visit
Product A V2
Product A V3
Mogibacterium
Peptostreptococcaceae_[XI][G-1]
Solobacterium
Peptostreptococcaceae_[XI][G-9]
Catonella
Peptostreptococcus
Dialister
Olsenella
Eikenella
Lachnospiraceae_[G-3]
Bergeyella
Ottowia
Treponema
Bacteroidales_[G-2]
Tannerella
Abiotrophia
Stomatobaculum
Oribacterium
Megasphaera
Lachnospiraceae_[G-2]
Lachnoanaerobaculum
Kingella
Parvimonas
Lancefieldella
Bifidobacterium
Selenomonas
Campylobacter
Saccharibacteria_(TM7)_[G-1]
Cardiobacterium
Arachnia
Peptidiphaga
Aggregatibacter
Gemella
Porphyromonas
Alloprevotella
Scardovia
Granulicatella
Lautropia
Neisseria
Leptotrichia
Capnocytophaga
Fusobacterium
Corynebacterium
Rothia
Haemophilus
Veillonella
Schaalia
Prevotella
Actinomyces
Streptococcus
Genus
Samples

Comparison 2. Product B V2 vs Product B V3

1) Taxonomy bar graphs

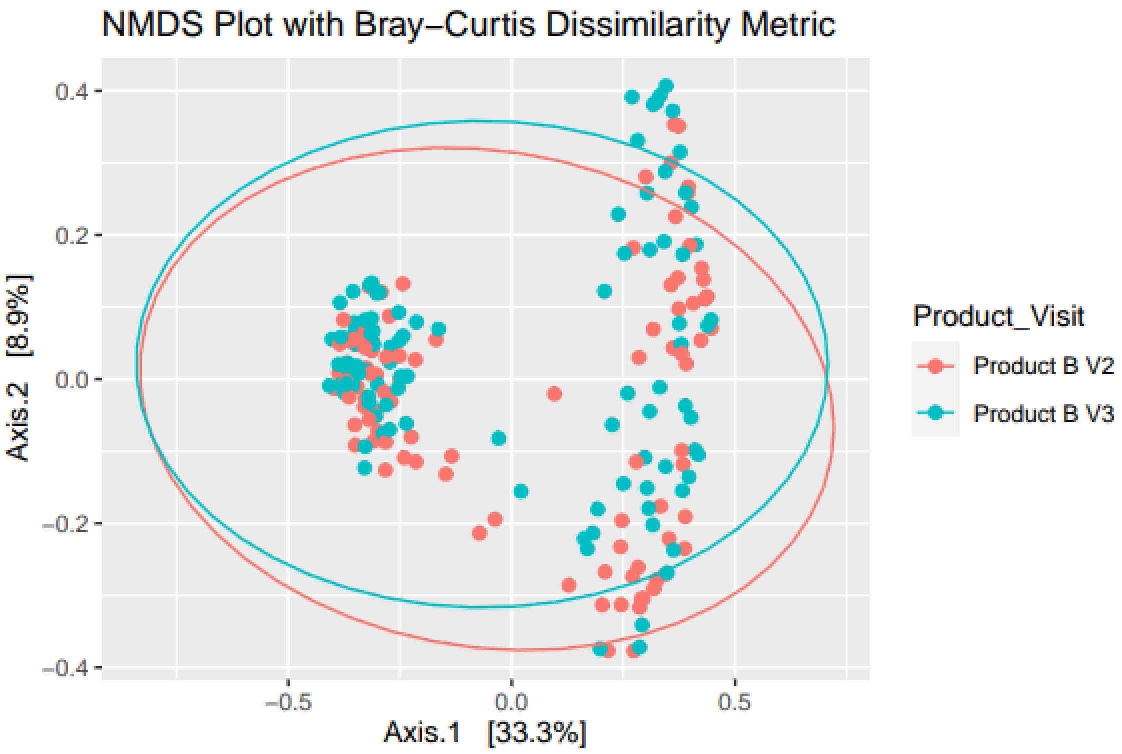


2) Alpha diversity



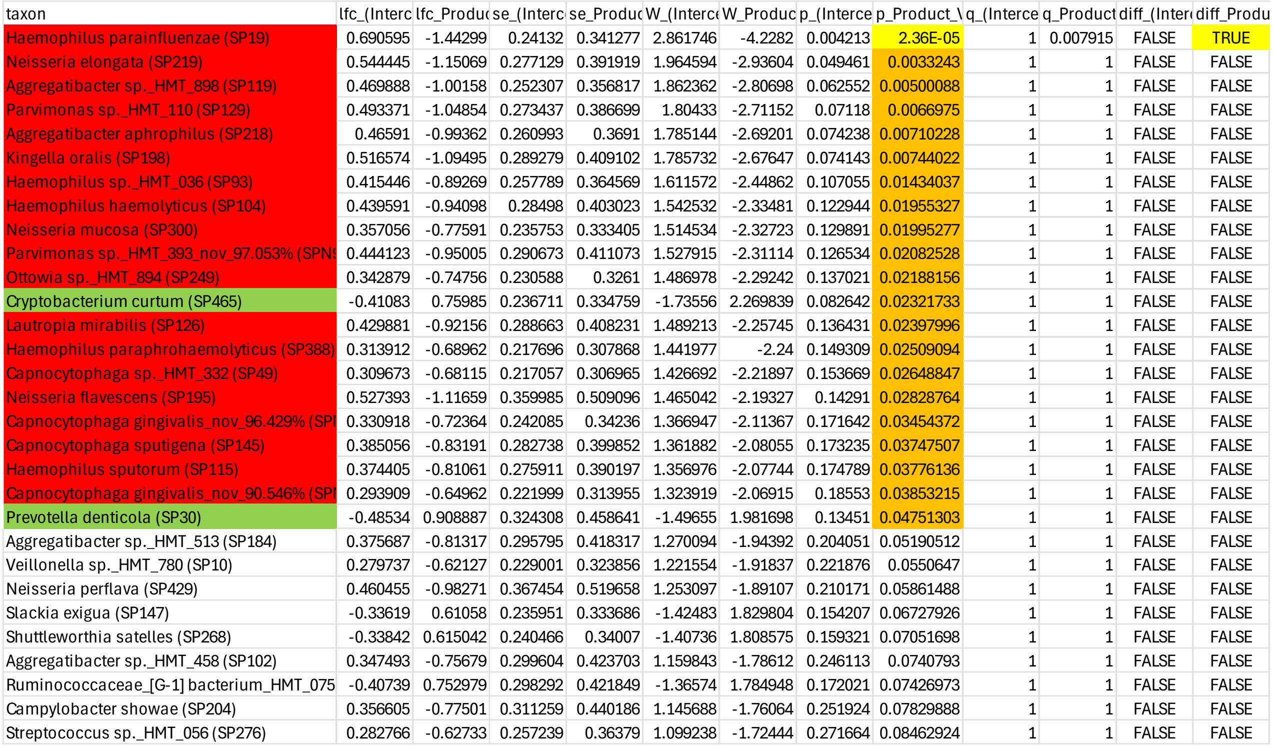
No significant differences

3) Beta diversity



Not significant, but p-value = 0.092

4) Differential abundance

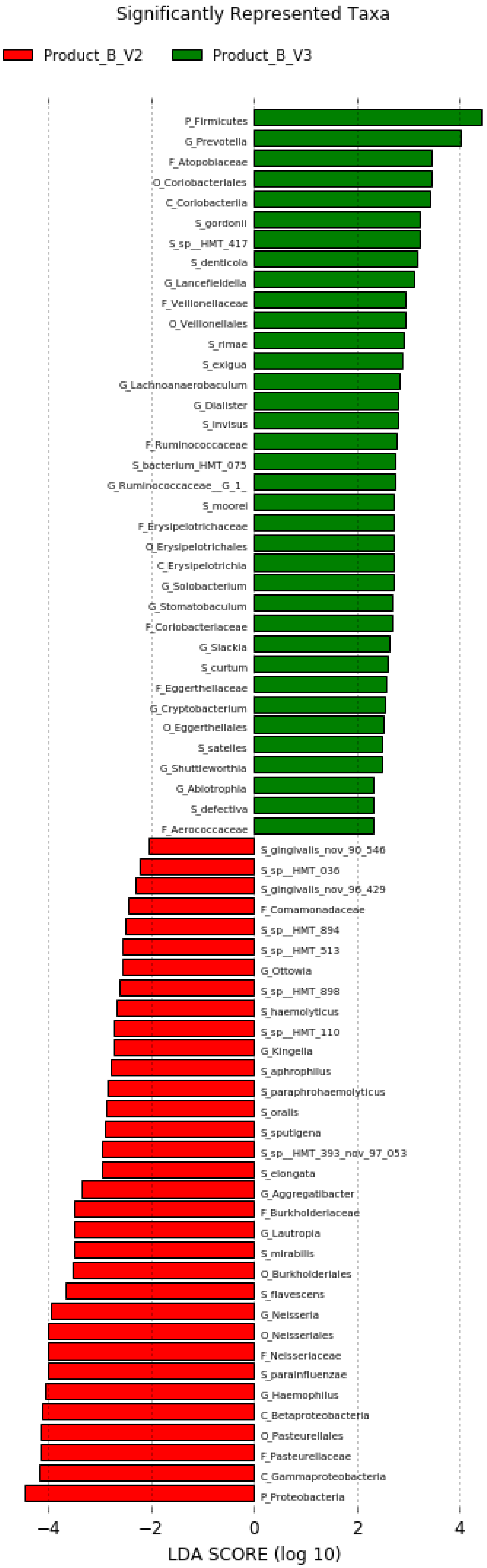


taxon	lfc_(Interc	lfc_Produc	se_(Interc	se_Produc	W_(Interce	W_Produc	p_(Interce	p_Product_\	q_(Interce	q_Product	diff_(Inter	diff_Produ
Haemophilus parainfluenzae (SP19)	0.690595	-1.44299	0.24132	0.341277	2.861746	-4.2282	0.004213	2.36E-05	1	0.007915	FALSE	TRUE
Neisseria elongata (SP219)	0.544445	-1.15069	0.277129	0.391919	1.964594	-2.93604	0.049461	0.0033243	1	1	FALSE	FALSE
Aggregatibacter sp._HMT_898 (SP119)	0.469888	-1.00158	0.252307	0.356817	1.862362	-2.80698	0.062552	0.00500088	1	1	FALSE	FALSE
Parvimonas sp._HMT_110 (SP129)	0.493371	-1.04854	0.273437	0.386699	1.80433	-2.71152	0.07118	0.0066975	1	1	FALSE	FALSE
Aggregatibacter aphrophilus (SP218)	0.46591	-0.99362	0.260993	0.3691	1.785144	-2.69201	0.074238	0.00710228	1	1	FALSE	FALSE
Kingella oralis (SP198)	0.516574	-1.09495	0.289279	0.409102	1.785732	-2.67647	0.074143	0.00744022	1	1	FALSE	FALSE
Haemophilus sp._HMT_036 (SP93)	0.415446	-0.89269	0.257789	0.364569	1.611572	-2.44862	0.107055	0.01434037	1	1	FALSE	FALSE
Haemophilus haemolyticus (SP104)	0.439591	-0.94098	0.28498	0.403023	1.542532	-2.33481	0.122944	0.01955327	1	1	FALSE	FALSE
Neisseria mucosa (SP300)	0.357056	-0.77591	0.235753	0.333405	1.514534	-2.32723	0.129891	0.01995277	1	1	FALSE	FALSE
Parvimonas sp._HMT_393_nov_97.053% (SPN	0.444123	-0.95005	0.290673	0.411073	1.527915	-2.31114	0.126534	0.02082528	1	1	FALSE	FALSE
Ottowia sp._HMT_894 (SP249)	0.342879	-0.74756	0.230588	0.3261	1.486978	-2.29242	0.137021	0.02188156	1	1	FALSE	FALSE
Cryptobacterium curtum (SP465)	-0.41083	0.75985	0.236711	0.334759	-1.73556	2.269839	0.082642	0.02321733	1	1	FALSE	FALSE
Lautropia mirabilis (SP126)	0.429881	-0.92156	0.288663	0.408231	1.489213	-2.25745	0.136431	0.02397996	1	1	FALSE	FALSE
Haemophilus paraphrohaemolyticus (SP388)	0.313912	-0.68962	0.217696	0.307868	1.441977	-2.24	0.149309	0.02509094	1	1	FALSE	FALSE
Capnocytophaga sp._HMT_332 (SP49)	0.309673	-0.68115	0.217057	0.306965	1.426692	-2.21897	0.153669	0.02648847	1	1	FALSE	FALSE
Neisseria flavescens (SP195)	0.527393	-1.11659	0.359985	0.509096	1.465042	-2.19327	0.14291	0.02828764	1	1	FALSE	FALSE
Capnocytophaga gingivalis_nov_96.429% (SP	0.330918	-0.72364	0.242085	0.34236	1.366947	-2.11367	0.171642	0.03454372	1	1	FALSE	FALSE
Capnocytophaga sputigena (SP145)	0.385056	-0.83191	0.282738	0.399852	1.361882	-2.08055	0.173235	0.03747507	1	1	FALSE	FALSE
Haemophilus sputorum (SP115)	0.374405	-0.81061	0.275911	0.390197	1.356976	-2.07744	0.174789	0.03776136	1	1	FALSE	FALSE
Capnocytophaga gingivalis_nov_90.546% (SP	0.293909	-0.64962	0.221999	0.313955	1.323919	-2.06915	0.18553	0.03853215	1	1	FALSE	FALSE
Prevotella denticola (SP30)	-0.48534	0.908887	0.324308	0.458641	-1.49655	1.981698	0.13451	0.04751303	1	1	FALSE	FALSE
Aggregatibacter sp._HMT_513 (SP184)	0.375687	-0.81317	0.295795	0.418317	1.270094	-1.94392	0.204051	0.05190512	1	1	FALSE	FALSE
Veillonella sp._HMT_780 (SP10)	0.279737	-0.62127	0.229001	0.323856	1.221554	-1.91837	0.221876	0.0550647	1	1	FALSE	FALSE
Neisseria perflava (SP429)	0.460455	-0.98271	0.367454	0.519658	1.253097	-1.89107	0.210171	0.05861488	1	1	FALSE	FALSE
Slackia exigua (SP147)	-0.33619	0.61058	0.235951	0.333686	-1.42483	1.829804	0.154207	0.06727926	1	1	FALSE	FALSE
Shuttleworthia satelles (SP268)	-0.33842	0.615042	0.240466	0.34007	-1.40736	1.808575	0.159321	0.07051698	1	1	FALSE	FALSE
Aggregatibacter sp._HMT_458 (SP102)	0.347493	-0.75679	0.299604	0.423703	1.159843	-1.78612	0.246113	0.0740793	1	1	FALSE	FALSE
Ruminococcaceae_[G-1] bacterium_HMT_075	-0.40739	0.752979	0.298292	0.421849	-1.36574	1.784948	0.172021	0.07426973	1	1	FALSE	FALSE
Campylobacter showae (SP204)	0.356605	-0.77501	0.311259	0.440186	1.145688	-1.76064	0.251924	0.07829888	1	1	FALSE	FALSE
Streptococcus sp._HMT_056 (SP276)	0.282766	-0.62733	0.257239	0.36379	1.099238	-1.72444	0.271664	0.08462924	1	1	FALSE	FALSE

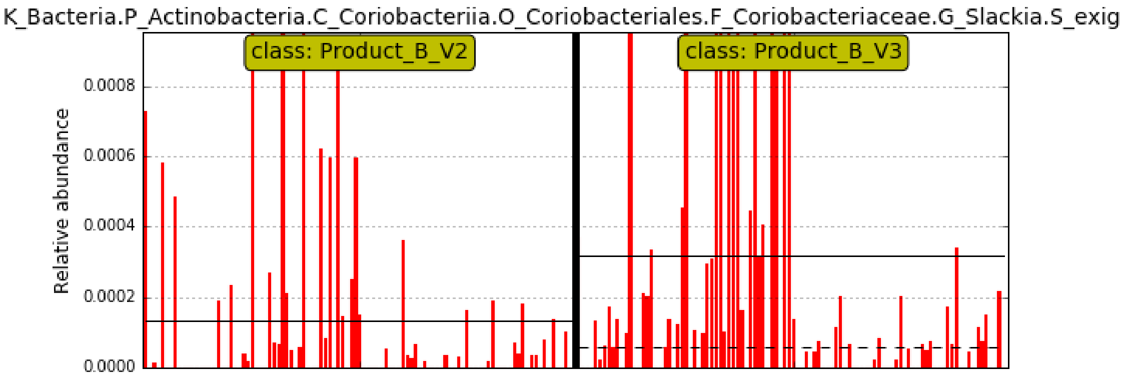
Red, more prevalent in baseline (V2)

Green, more prevalent after treatment (V3)

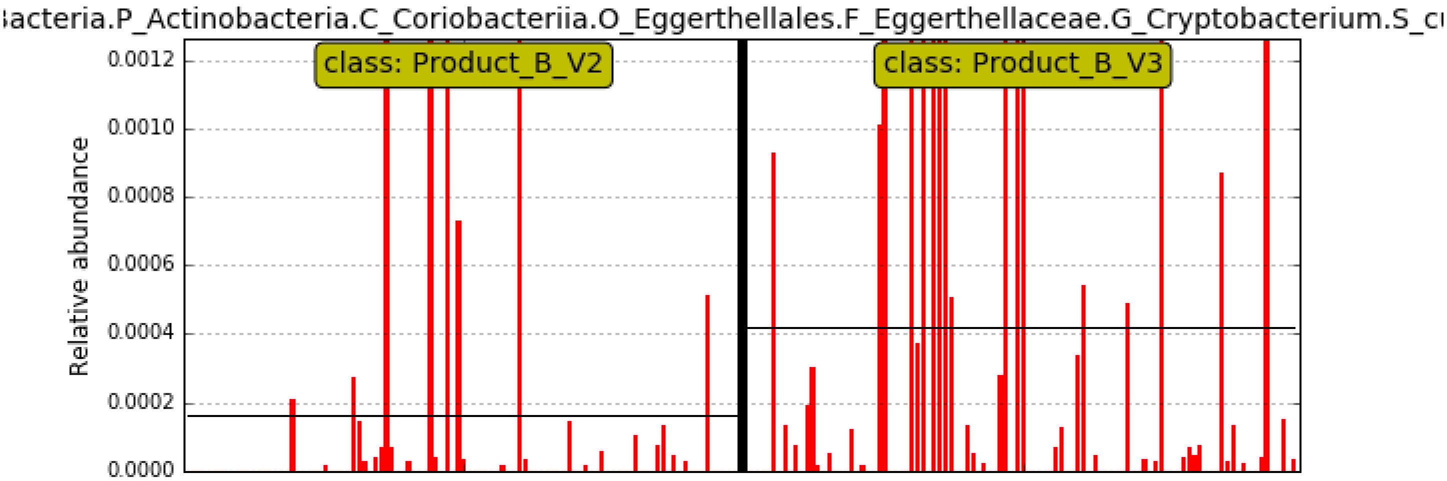
5) Lefse

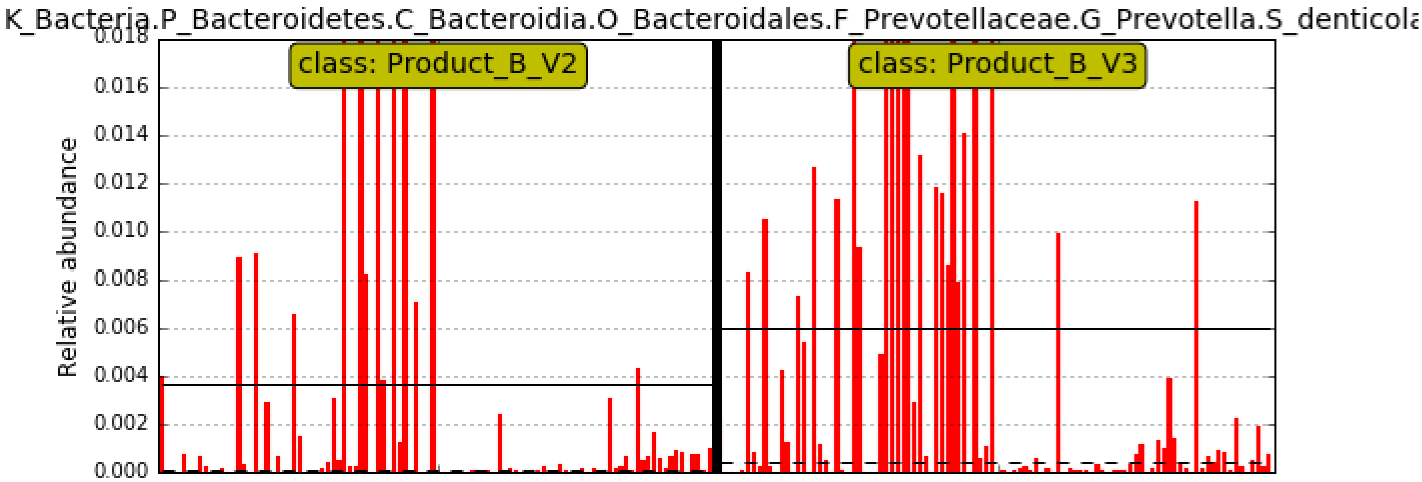

Significantly Represented Taxa
🟥 Product_B_V2
🟩 Product_B_V3
P_Firmicutes
G_Prevotella
F_Atopobiaceae
O_Coriobacteriales
C_Coriobacteriia
S_gordonii
S_sp__HMT_417
S_denticola
G_Lancefieldella
F_Veillonellaceae
O_Veillonellales
S_rimae
S_exigua
G_Lachnoanaerobaculum
G_Dialister
S_invisus
F_Ruminococcaceae
S_bacterium_HMT_075
G_Ruminococcaceae__G_1_
S_moorei
F_Erysipelotrichaceae
O_Erysipelotrichales
C_Erysipelotrichia
G_Solobacterium
G_Stomatobaculum
F_Coriobacteriaceae
G_Slackia
S_curtum
F_Eggerthellaceae
G_Cryptobacterium
O_Eggerthellales
S_satelles
G_Shuttleworthia
G_Abiotrophia
S_defectiva
F_Aerococcaceae
S_gingivalis_nov_90_546
S_sp__HMT_036
S_gingivalis_nov_96_429
F_Comamonadaceae
S_sp__HMT_894
S_sp__HMT_513
G_Ottowia
S_sp__HMT_898
S_haemolyticus
S_sp__HMT_110
G_Kingella
S_aphrophilus
S_paraphrohaemolyticus
S_oralis
S_sputigena
S_sp__HMT_393_nov_97_053
S_elongata
G_Aggregatibacter
F_Burkholderiaceae
G_Lautropia
S_mirabilis
O_Burkholderiales
S_flavescens
G_Neisseria
O_Neisseriales
F_Neisseriaceae
S_parainfluenzae
G_Haemophilus
C_Betaproteobacteria
O_Pasteurellales
F_Pasteurellaceae
C_Gammaproteobacteria
P_Proteobacteria
−4
−2
0
2
4
LDA SCORE (log 10)

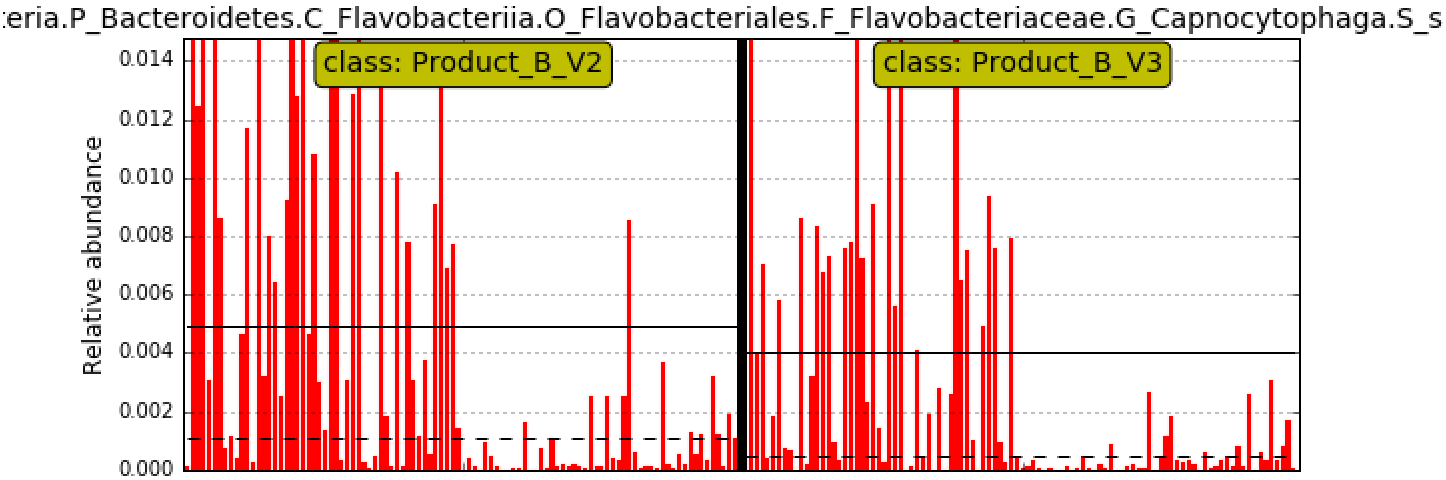
15)

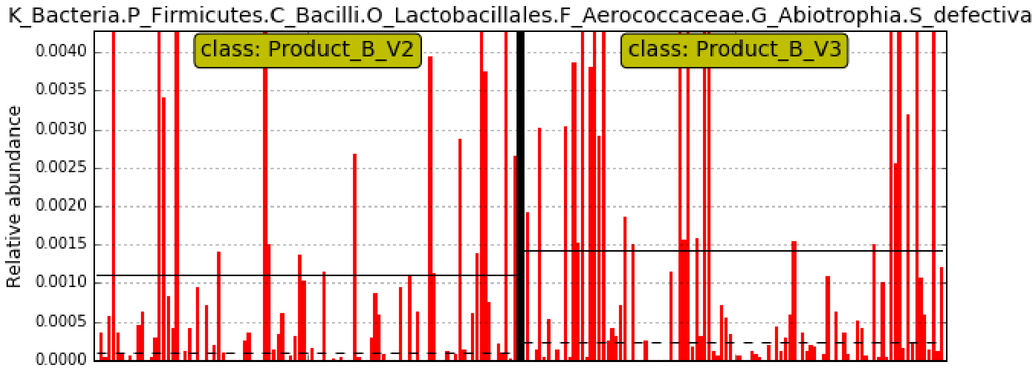


Health associated

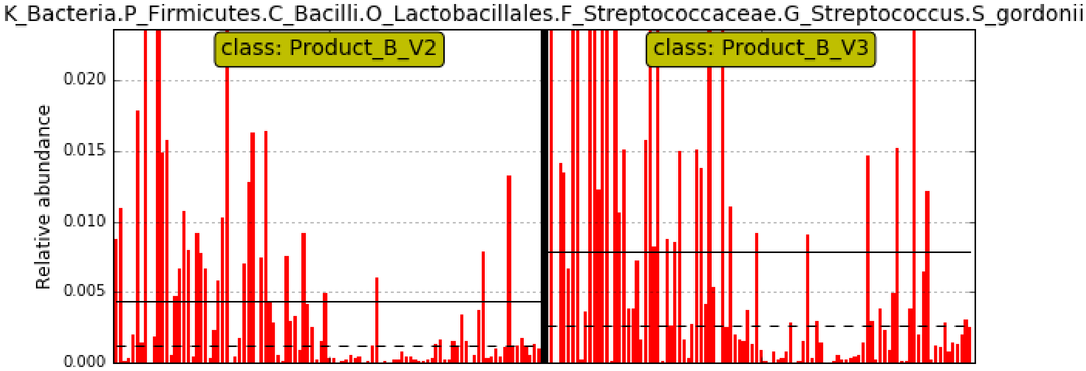




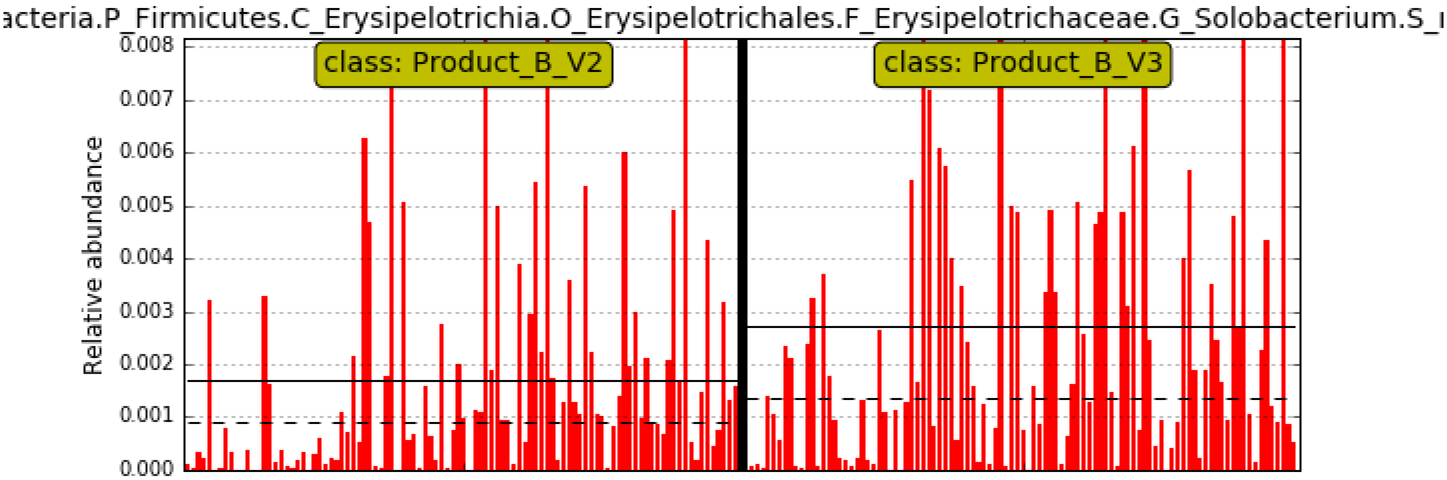


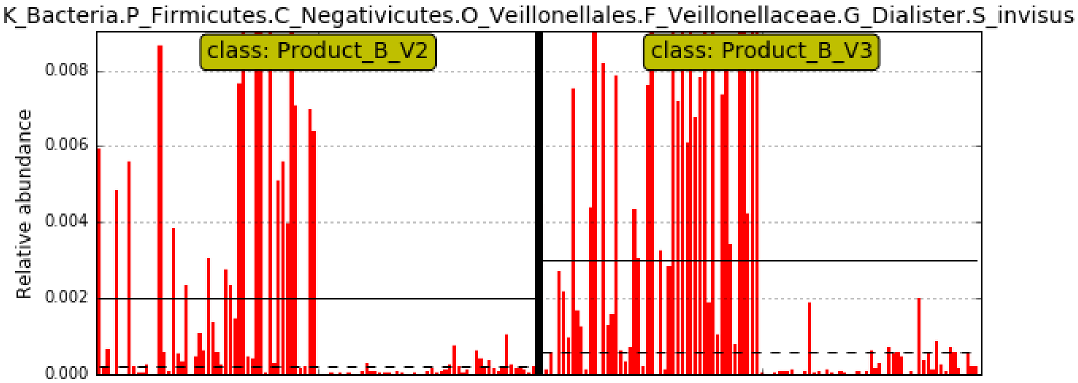


Health associated



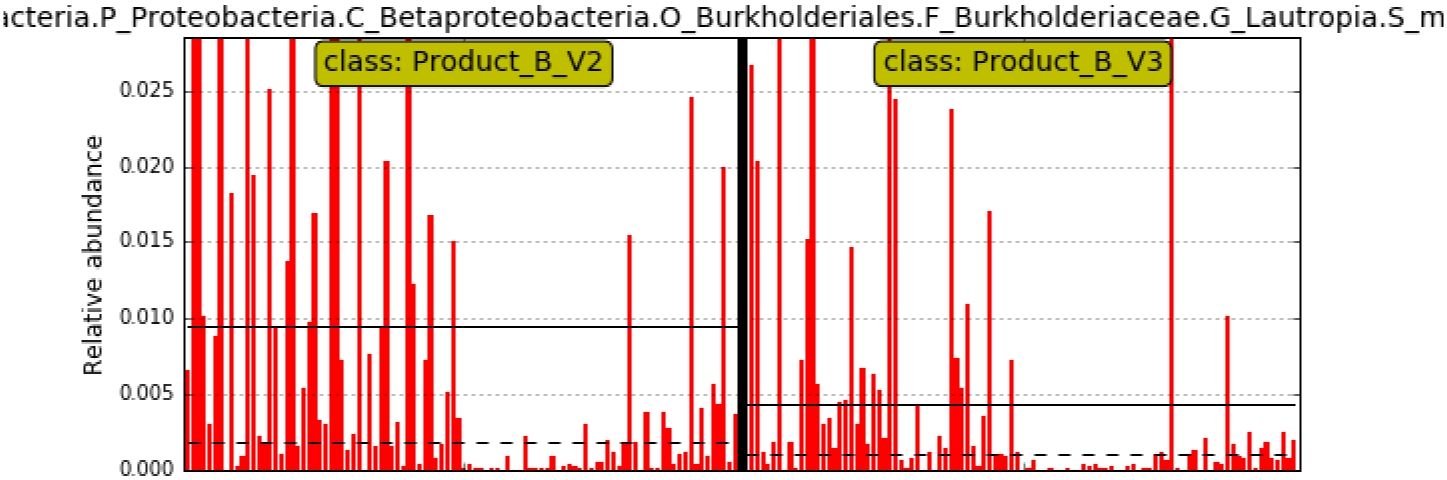
health-associated

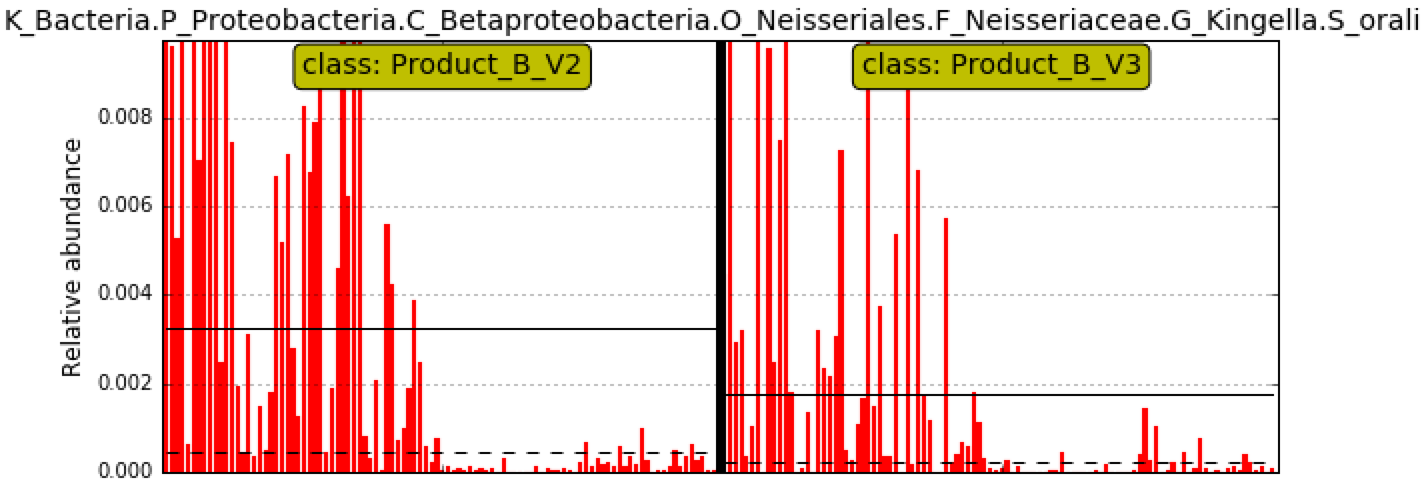


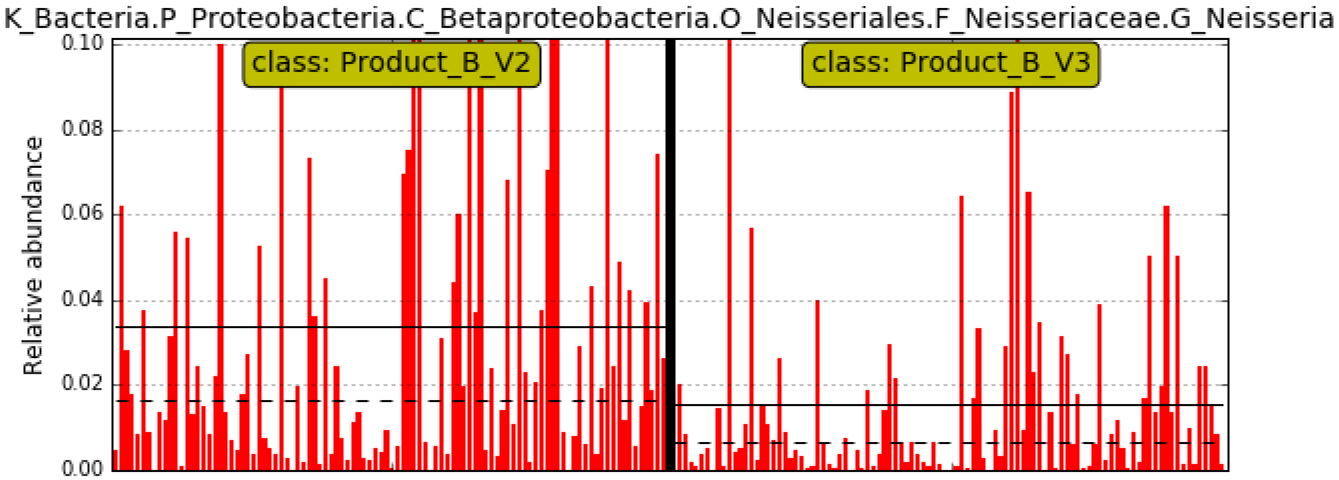


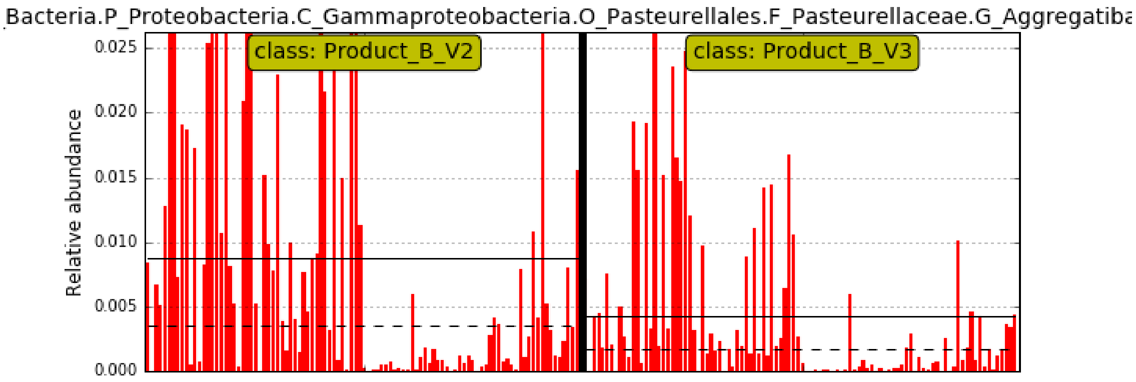
considered

periodontal pathogen

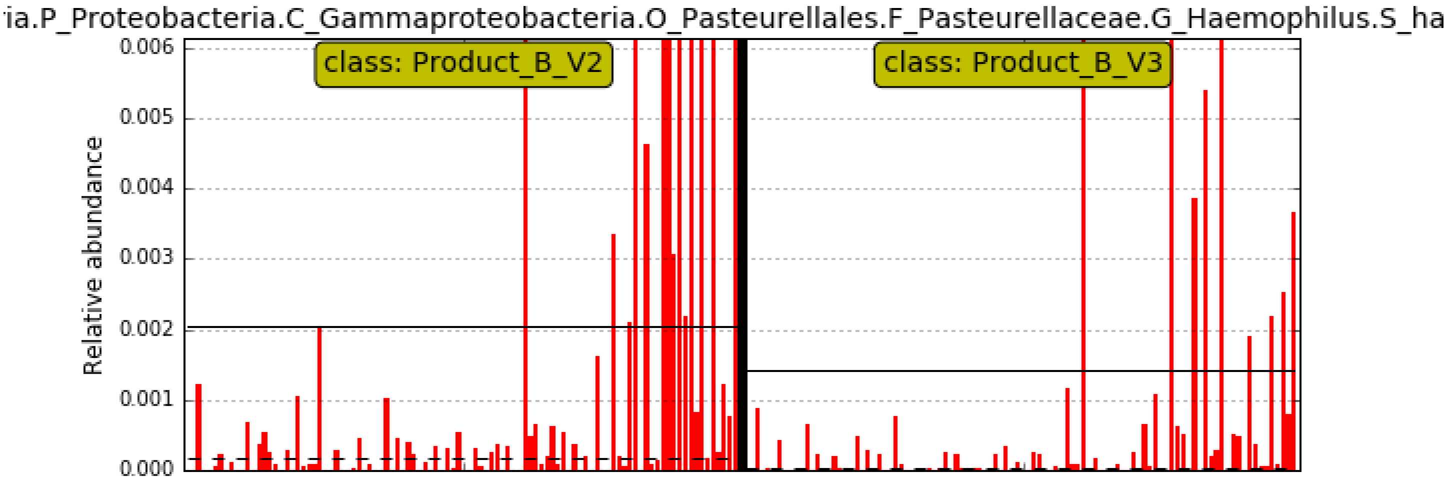


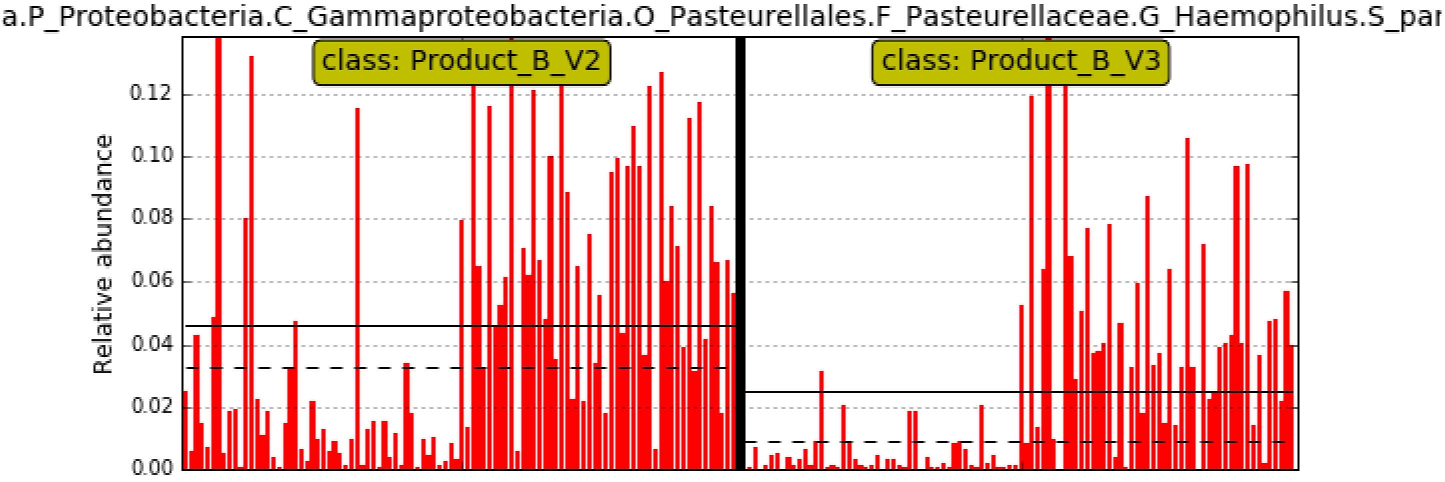

K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Kingella.S_orali


K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Neisseria

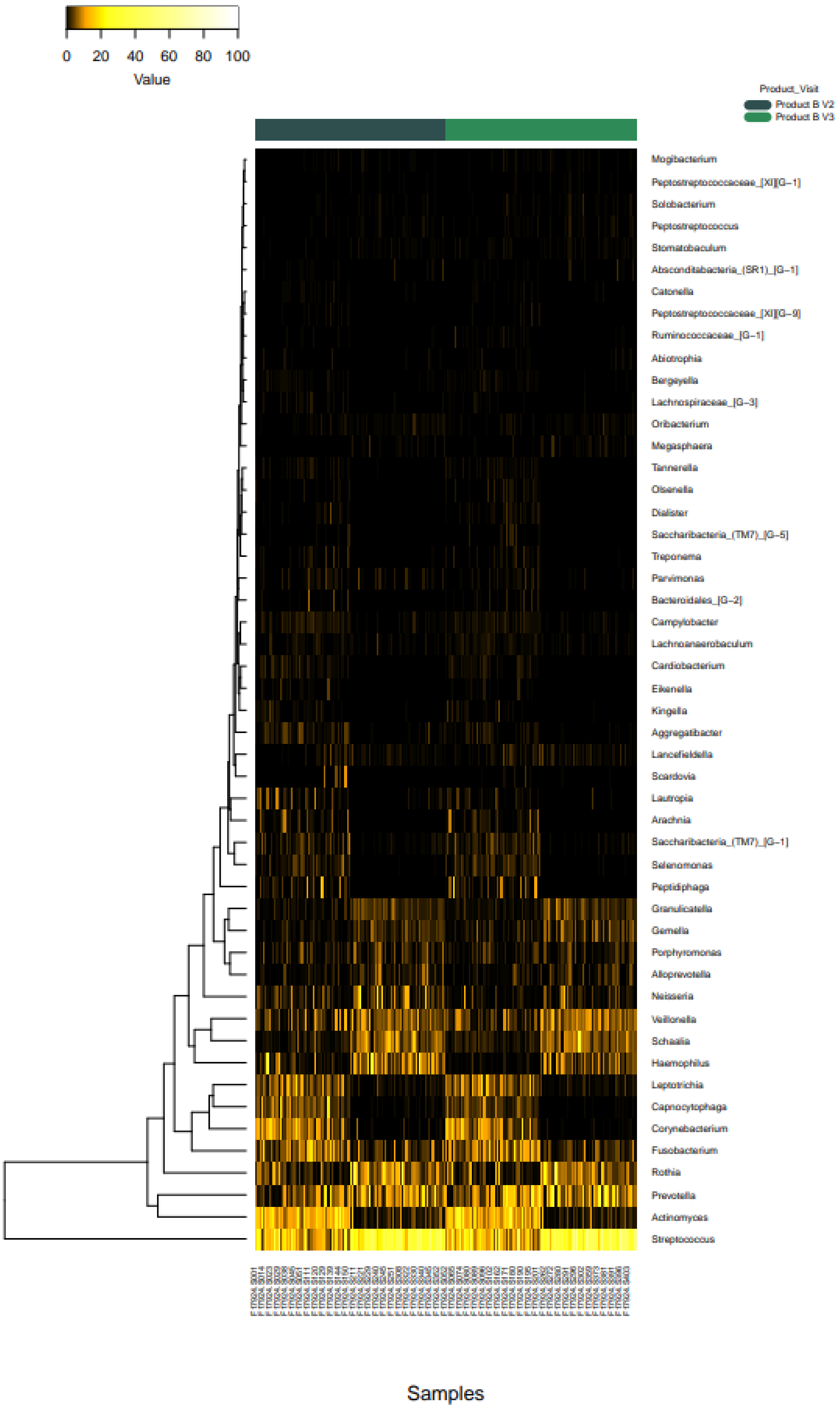

Bacteria.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Aggregatiba

putative pathogen

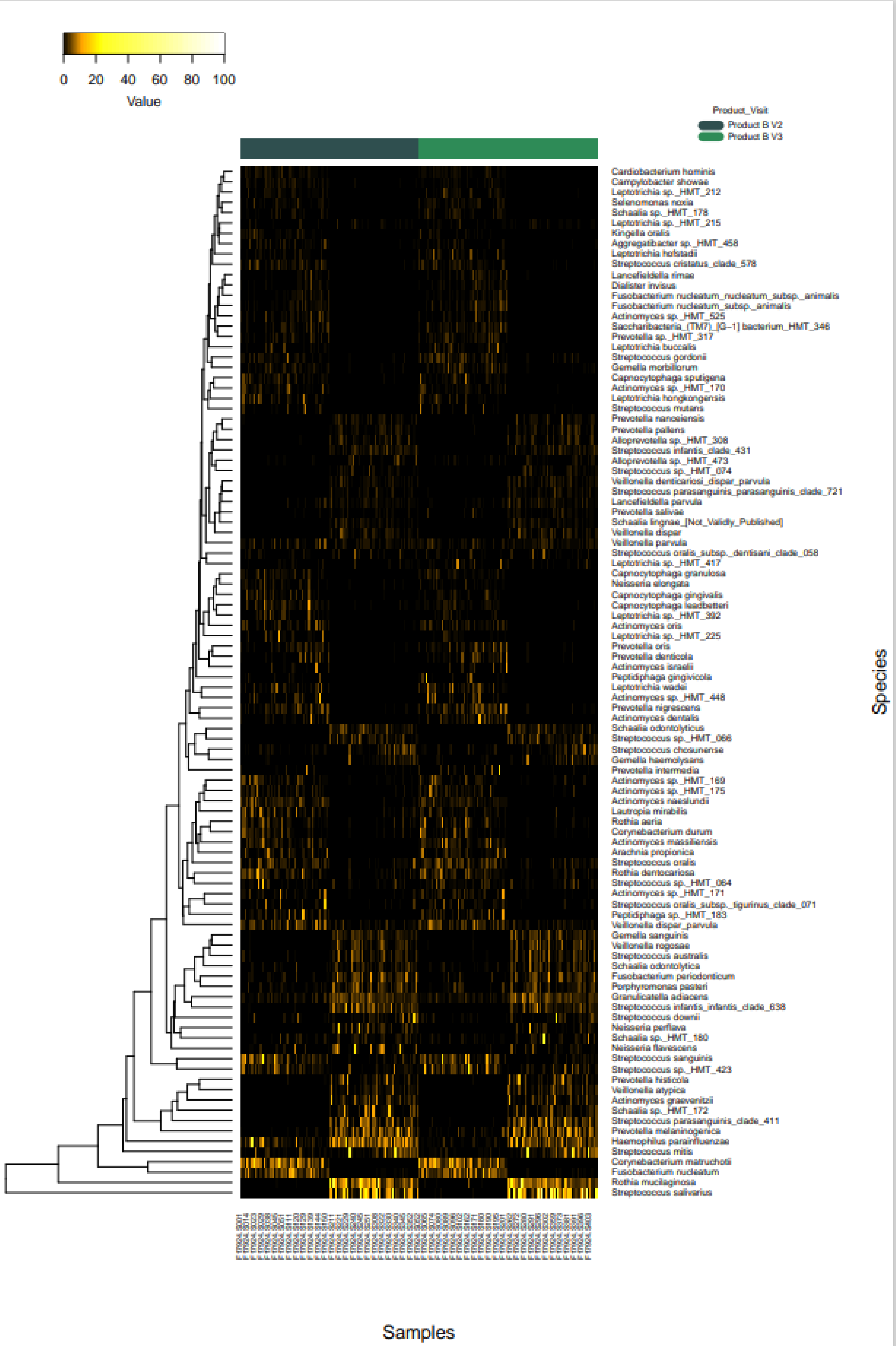

ia.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophilus.S_ha
class: Product_B_V2
class: Product_B_V3
Relative abundance
0.000
0.001
0.002
0.003
0.004
0.005
0.006


a.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophilus.S_par
class: Product_B_V2
class: Product_B_V3
Relative abundance
0.00
0.02
0.04
0.06
0.08
0.10
0.12

6) Heat maps

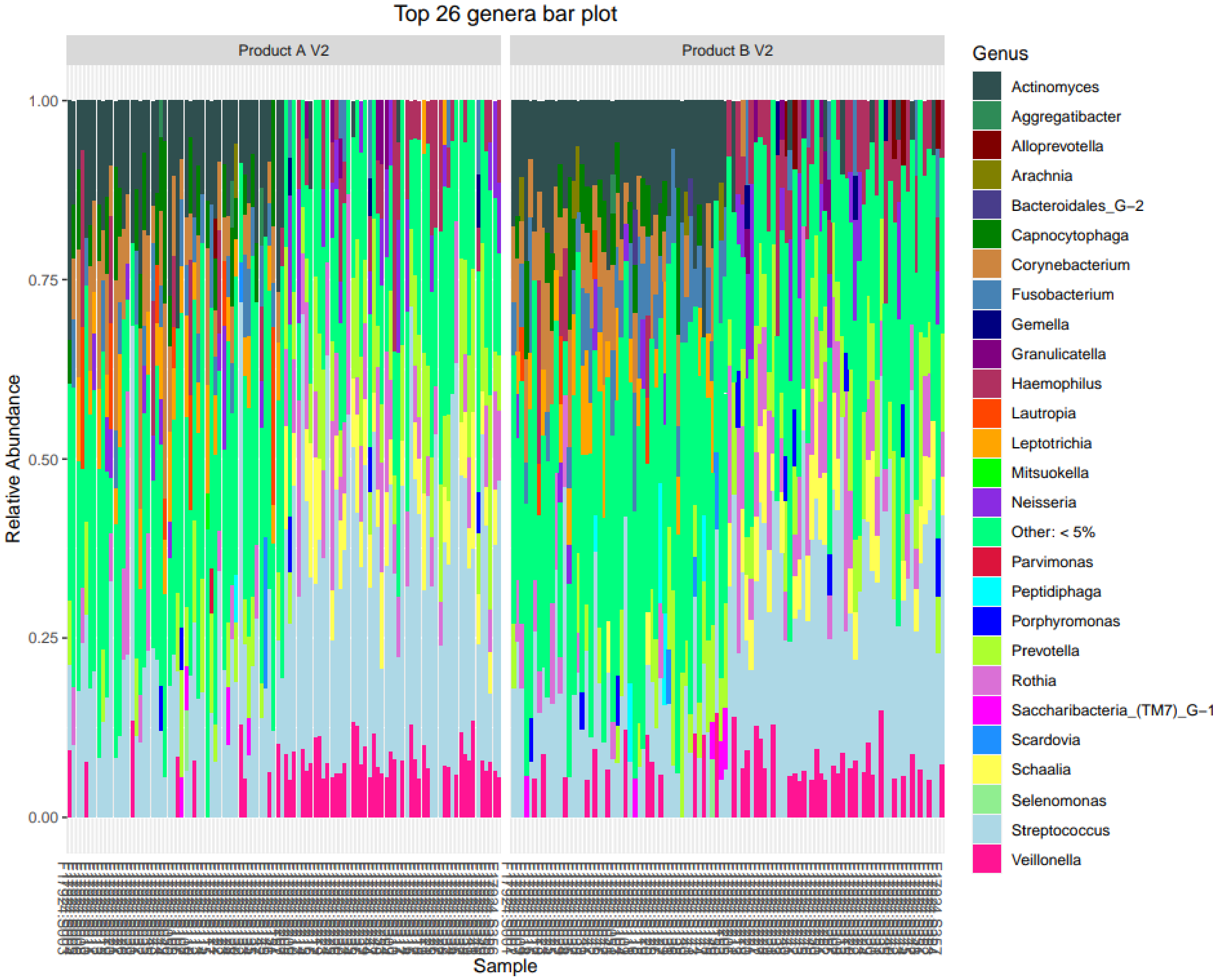


0
20
40
60
80
100
Value
Product_Visit
Product B V2
Product B V3
Mogibacterium
Peptostreptococcaceae_[XI][G-1]
Solobacterium
Peptostreptococcus
Stomatobaculum
Absconditabacteria_(SR1)_[G-1]
Catonella
Peptostreptococcaceae_[XI][G-9]
Ruminococcaceae_[G-1]
Abiotrophia
Bergeyella
Lachnospiraceae_[G-3]
Oribacterium
Megasphaera
Tannerella
Olsenella
Dialister
Saccharibacteria_(TM7)_[G-5]
Treponema
Parvimonas
Bacteroidales_[G-2]
Campylobacter
Lachnoanaerobaculum
Cardiobacterium
Eikenella
Kingella
Aggregatibacter
Lancefieldella
Scardovia
Lautropia
Arachnia
Saccharibacteria_(TM7)_[G-1]
Selenomonas
Peptidiphaga
Granulicatella
Gemella
Porphyromonas
Alloprevotella
Neisseria
Veillonella
Schaalia
Haemophilus
Leptotrichia
Capnocytophaga
Corynebacterium
Fusobacterium
Rothia
Prevotella
Actinomyces
Streptococcus
Samples

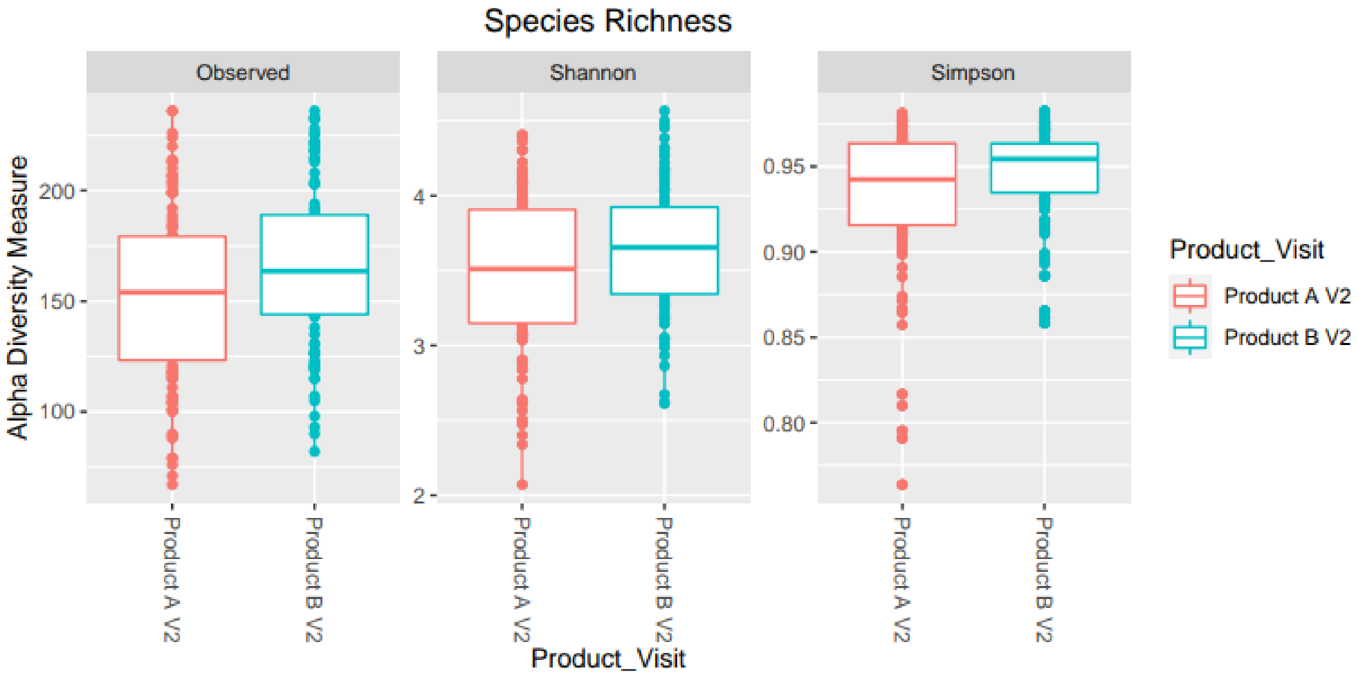

0
20
40
60
80
100
Value
Product_Visit
Product B V2
Product B V3
Cardiobacterium hominis
Campylobacter showae
Leptotrichia sp._HMT_212
Selenomonas noxia
Schaalia sp._HMT_178
Leptotrichia sp._HMT_215
Kingella oralis
Aggregatibacter sp._HMT_458
Leptotrichia hofstadii
Streptococcus cristatus_clade_578
Lancefieldella rimae
Dialister invisus
Fusobacterium nucleatum_nucleatum_subsp._animalis
Fusobacterium nucleatum_subsp._animalis
Actinomyces sp._HMT_525
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346
Prevotella sp._HMT_317
Leptotrichia buccalis
Streptococcus gordonii
Gemella morbillorum
Capnocytophaga sputigena
Actinomyces sp._HMT_170
Leptotrichia hongkongensis
Streptococcus mutans
Prevotella nanceiensis
Prevotella pallens
Alloprevotella sp._HMT_308
Streptococcus infantis_clade_431
Alloprevotella sp._HMT_473
Streptococcus sp._HMT_074
Veillonella denticariosi_dispar_parvula
Streptococcus parasanguinis_parasanguinis_clade_721
Lancefieldella parvula
Prevotella salivae
Schaalia lingnae_[Not_Validly_Published]
Veillonella dispar
Veillonella parvula
Streptococcus oralis_subsp._dentisani_clade_058
Leptotrichia sp._HMT_417
Capnocytophaga granulosa
Neisseria elongata
Capnocytophaga gingivalis
Capnocytophaga leadbetteri
Leptotrichia sp._HMT_392
Actinomyces oris
Leptotrichia sp._HMT_225
Prevotella oris
Prevotella denticola
Actinomyces israelii
Peptidiphaga gingivicola
Leptotrichia wadei
Actinomyces sp._HMT_448
Prevotella nigrescens
Actinomyces dentalis
Schaalia odontolyticus
Streptococcus sp._HMT_066
Streptococcus chosunense
Gemella haemolysans
Prevotella intermedia
Actinomyces sp._HMT_169
Actinomyces sp._HMT_175
Actinomyces naeslundii
Lautropia mirabilis
Rothia aeria
Corynebacterium durum
Actinomyces massiliensis
Arachnia propionica
Streptococcus oralis
Rothia dentocariosa
Streptococcus sp._HMT_064
Actinomyces sp._HMT_171
Streptococcus oralis_subsp._tigurinus_clade_071
Peptidiphaga sp._HMT_183
Veillonella dispar_parvula
Gemella sanguinis
Veillonella rogosae
Streptococcus australis
Schaalia odontolytica
Fusobacterium periodonticum
Porphyromonas pasteri
Granulicatella adiacens
Streptococcus infantis_infantis_clade_638
Streptococcus downii
Neisseria perflava
Schaalia sp._HMT_180
Neisseria flavescens
Streptococcus sanguinis
Streptococcus sp._HMT_423
Prevotella histicola
Veillonella atypica
Actinomyces graevenitzii
Schaalia sp._HMT_172
Streptococcus parasanguinis_clade_411
Prevotella melaninogenica
Haemophilus parainfluenzae
Streptococcus mitis
Corynebacterium matruchotii
Fusobacterium nucleatum
Rothia mucilaginosa
Streptococcus salivarius
Species
Samples

Comparison 3 Product A V2 vs Product B V2

1) Taxonomy barplots



2) Alpha diversity



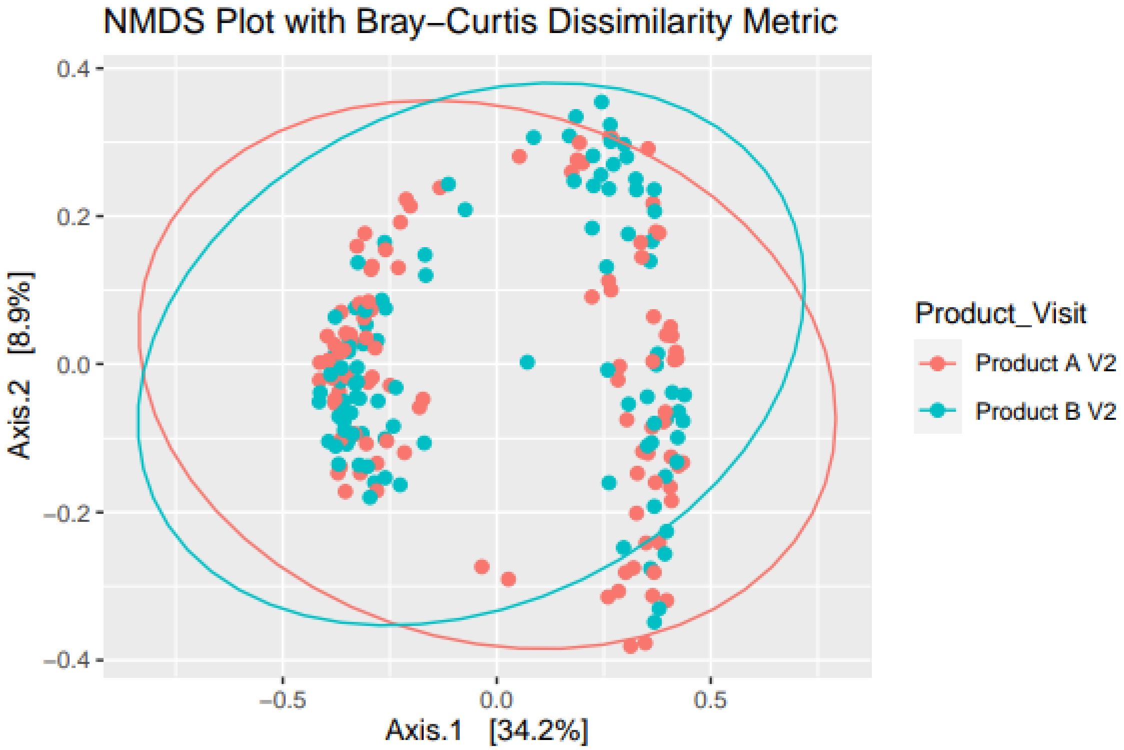
Significant differences—indicates that the populations were different microbiologically at baseline

Observed p= 0.027

Shannon p= 0.049

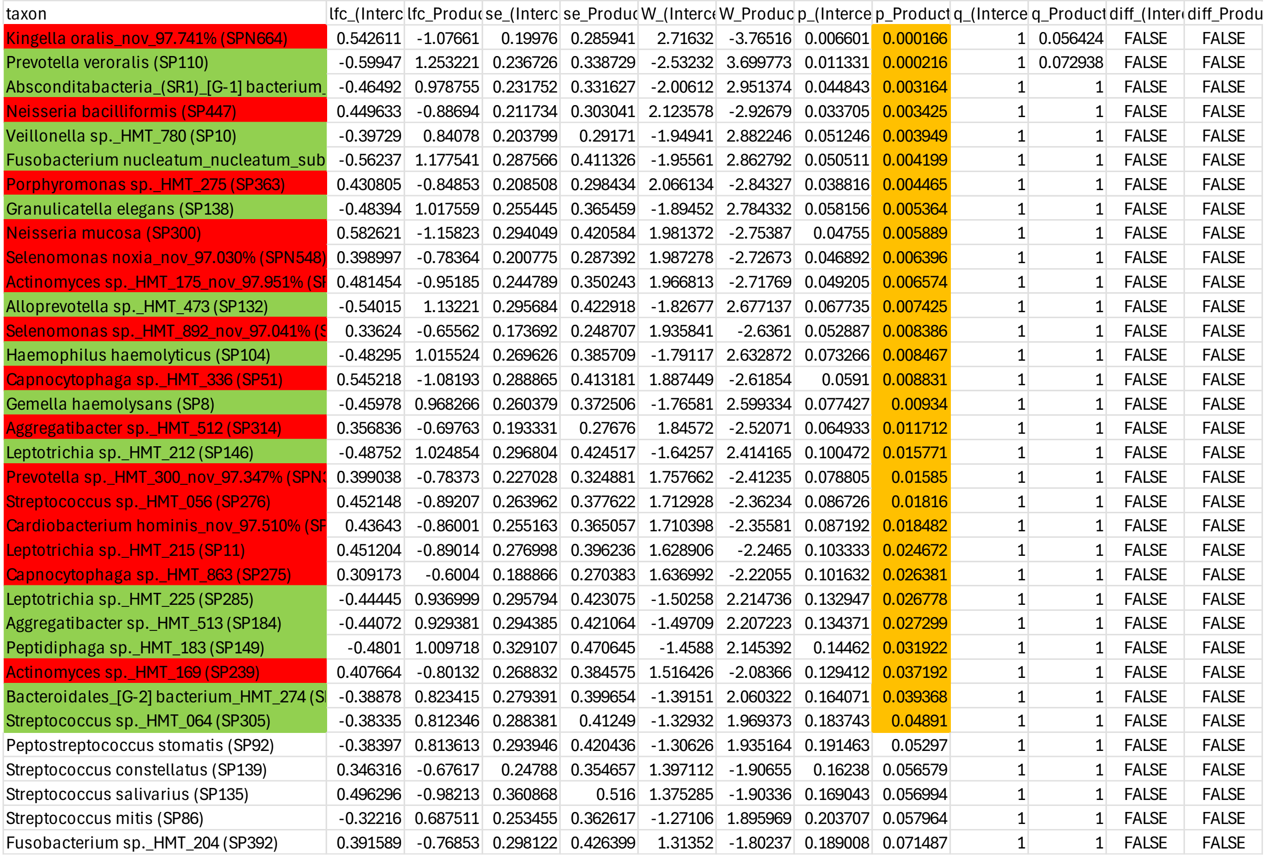
Simpson p= 0.034

3) Beta diversity



No significant differences

4) Differential abundance



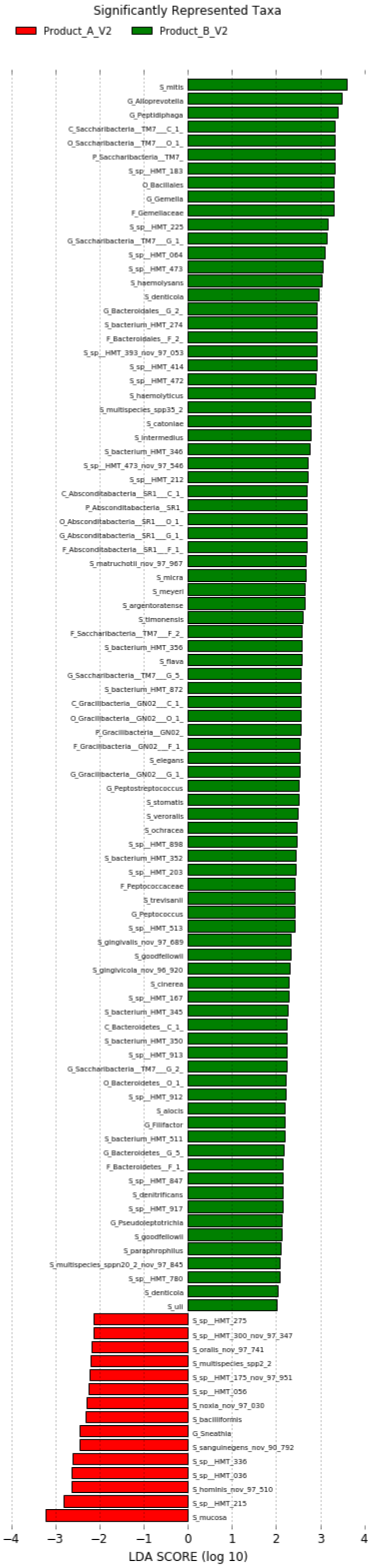
taxon	lfc_(Interc	lfc_Produc	se_(Interc	se_Produc	W_(Interce	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inter	diff_Produ
Kingella oralis_nov_97.741% (SPN664)	0.542611	-1.07661	0.19976	0.285941	2.71632	-3.76516	0.006601	0.000166	1	0.056424	FALSE	FALSE
Prevotella veroralis (SP110)	-0.59947	1.253221	0.236726	0.338729	-2.53232	3.699773	0.011331	0.000216	1	0.072938	FALSE	FALSE
Absconditabacteria_(SR1)_[G-1] bacterium_	-0.46492	0.978755	0.231752	0.331627	-2.00612	2.951374	0.044843	0.003164	1	1	FALSE	FALSE
Neisseria bacilliformis (SP447)	0.449633	-0.88694	0.211734	0.303041	2.123578	-2.92679	0.033705	0.003425	1	1	FALSE	FALSE
Veillonella sp._HMT_780 (SP10)	-0.39729	0.84078	0.203799	0.29171	-1.94941	2.882246	0.051246	0.003949	1	1	FALSE	FALSE
Fusobacterium nucleatum_nucleatum_sub	-0.56237	1.177541	0.287566	0.411326	-1.95561	2.862792	0.050511	0.004199	1	1	FALSE	FALSE
Porphyromonas sp._HMT_275 (SP363)	0.430805	-0.84853	0.208508	0.298434	2.066134	-2.84327	0.038816	0.004465	1	1	FALSE	FALSE
Granulicatella elegans (SP138)	-0.48394	1.017559	0.255445	0.365459	-1.89452	2.784332	0.058156	0.005364	1	1	FALSE	FALSE
Neisseria mucosa (SP300)	0.582621	-1.15823	0.294049	0.420584	1.981372	-2.75387	0.04755	0.005889	1	1	FALSE	FALSE
Selenomonas noxia_nov_97.030% (SPN548)	0.398997	-0.78364	0.200775	0.287392	1.987278	-2.72673	0.046892	0.006396	1	1	FALSE	FALSE
Actinomyces sp._HMT_175_nov_97.951% (SI	0.481454	-0.95185	0.244789	0.350243	1.966813	-2.71769	0.049205	0.006574	1	1	FALSE	FALSE
Alloprevotella sp._HMT_473 (SP132)	-0.54015	1.13221	0.295684	0.422918	-1.82677	2.677137	0.067735	0.007425	1	1	FALSE	FALSE
Selenomonas sp._HMT_892_nov_97.041% (S	0.33624	-0.65562	0.173692	0.248707	1.935841	-2.6361	0.052887	0.008386	1	1	FALSE	FALSE
Haemophilus haemolyticus (SP104)	-0.48295	1.015524	0.269626	0.385709	-1.79117	2.632872	0.073266	0.008467	1	1	FALSE	FALSE
Capnocytophaga sp._HMT_336 (SP51)	0.545218	-1.08193	0.288865	0.413181	1.887449	-2.61854	0.0591	0.008831	1	1	FALSE	FALSE
Gemella haemolysans (SP8)	-0.45978	0.968266	0.260379	0.372506	-1.76581	2.599334	0.077427	0.00934	1	1	FALSE	FALSE
Aggregatibacter sp._HMT_512 (SP314)	0.356836	-0.69763	0.193331	0.27676	1.84572	-2.52071	0.064933	0.011712	1	1	FALSE	FALSE
Leptotrichia sp._HMT_212 (SP146)	-0.48752	1.024854	0.296804	0.424517	-1.64257	2.414165	0.100472	0.015771	1	1	FALSE	FALSE
Prevotella sp._HMT_300_nov_97.347% (SPN	0.399038	-0.78373	0.227028	0.324881	1.757662	-2.41235	0.078805	0.01585	1	1	FALSE	FALSE
Streptococcus sp._HMT_056 (SP276)	0.452148	-0.89207	0.263962	0.377622	1.712928	-2.36234	0.086726	0.01816	1	1	FALSE	FALSE
Cardiobacterium hominis_nov_97.510% (SF	0.43643	-0.86001	0.255163	0.365057	1.710398	-2.35581	0.087192	0.018482	1	1	FALSE	FALSE
Leptotrichia sp._HMT_215 (SP11)	0.451204	-0.89014	0.276998	0.396236	1.628906	-2.2465	0.103333	0.024672	1	1	FALSE	FALSE
Capnocytophaga sp._HMT_863 (SP275)	0.309173	-0.6004	0.188866	0.270383	1.636992	-2.22055	0.101632	0.026381	1	1	FALSE	FALSE
Leptotrichia sp._HMT_225 (SP285)	-0.44445	0.936999	0.295794	0.423075	-1.50258	2.214736	0.132947	0.026778	1	1	FALSE	FALSE
Aggregatibacter sp._HMT_513 (SP184)	-0.44072	0.929381	0.294385	0.421064	-1.49709	2.207223	0.134371	0.027299	1	1	FALSE	FALSE
Peptidiphaga sp._HMT_183 (SP149)	-0.4801	1.009718	0.329107	0.470645	-1.4588	2.145392	0.14462	0.031922	1	1	FALSE	FALSE
Actinomyces sp._HMT_169 (SP239)	0.407664	-0.80132	0.268832	0.384575	1.516426	-2.08366	0.129412	0.037192	1	1	FALSE	FALSE
Bacteroidales_[G-2] bacterium_HMT_274 (SI	-0.38878	0.823415	0.279391	0.399654	-1.39151	2.060322	0.164071	0.039368	1	1	FALSE	FALSE
Streptococcus sp._HMT_064 (SP305)	-0.38335	0.812346	0.288381	0.41249	-1.32932	1.969373	0.183743	0.04891	1	1	FALSE	FALSE
Peptostreptococcus stomatis (SP92)	-0.38397	0.813613	0.293946	0.420436	-1.30626	1.935164	0.191463	0.05297	1	1	FALSE	FALSE
Streptococcus constellatus (SP139)	0.346316	-0.67617	0.24788	0.354657	1.397112	-1.90655	0.16238	0.056579	1	1	FALSE	FALSE
Streptococcus salivarius (SP135)	0.496296	-0.98213	0.360868	0.516	1.375285	-1.90336	0.169043	0.056994	1	1	FALSE	FALSE
Streptococcus mitis (SP86)	-0.32216	0.687511	0.253455	0.362617	-1.27106	1.895969	0.203707	0.057964	1	1	FALSE	FALSE
Fusobacterium sp._HMT_204 (SP392)	0.391589	-0.76853	0.298122	0.426399	1.31352	-1.80237	0.189008	0.071487	1	1	FALSE	FALSE

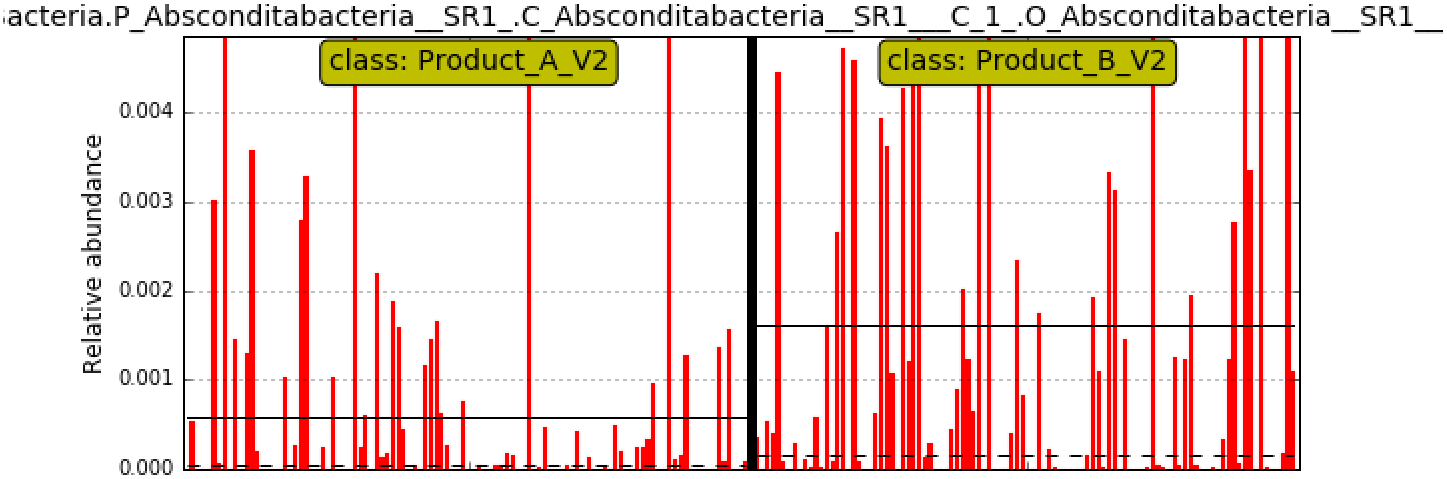
Many differences. Indicates that the 2 subject populations were not similar at baseline.

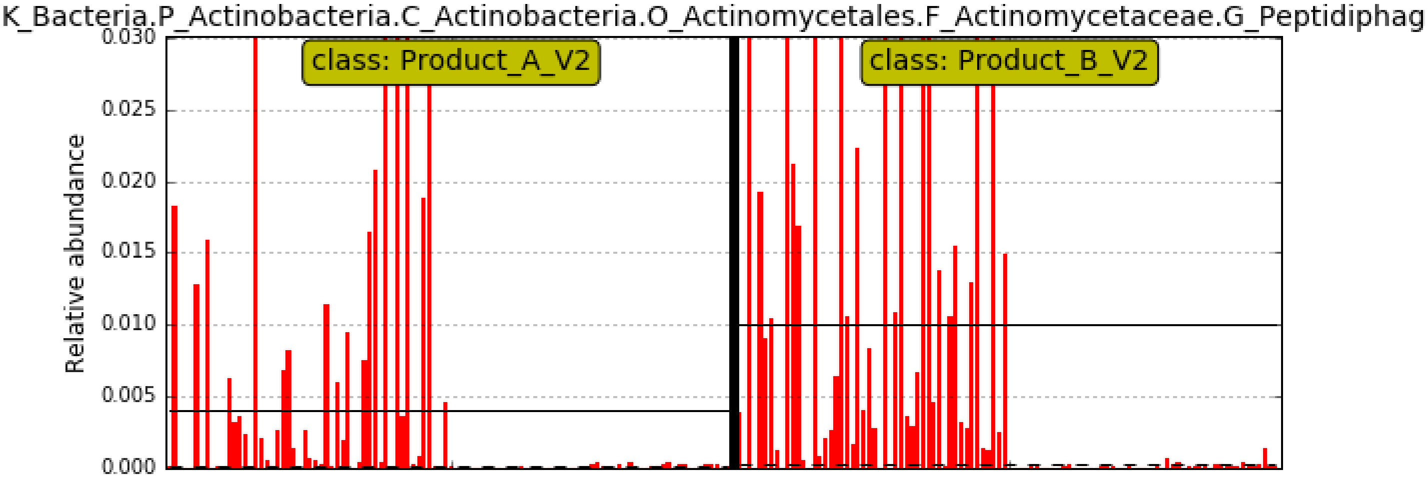
Red, more prevalent in B at baseline

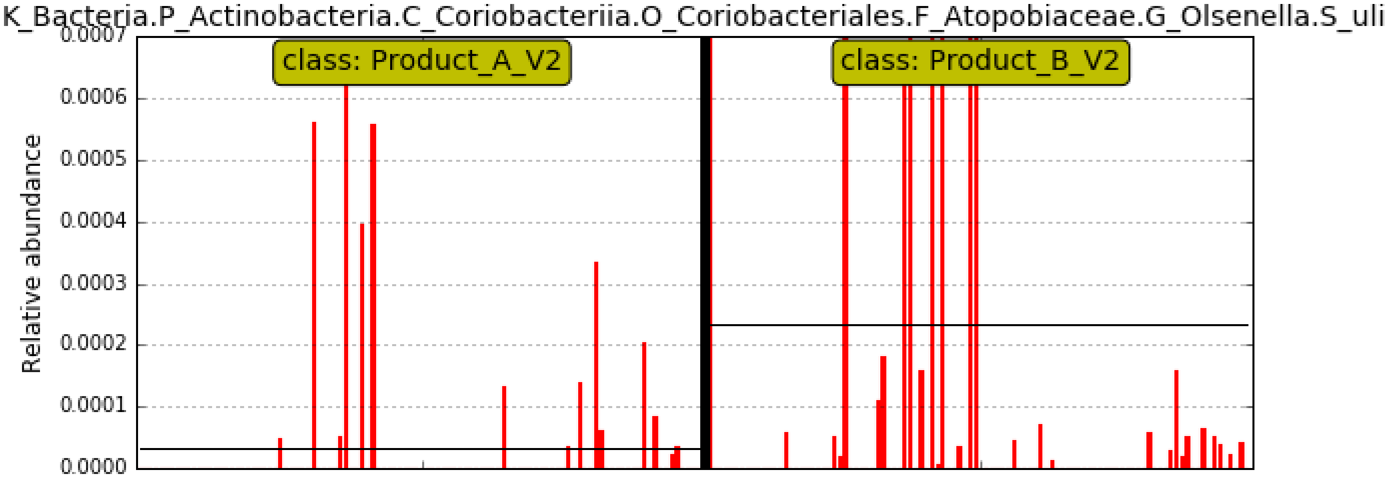
Green, more prevalent in A at baseline

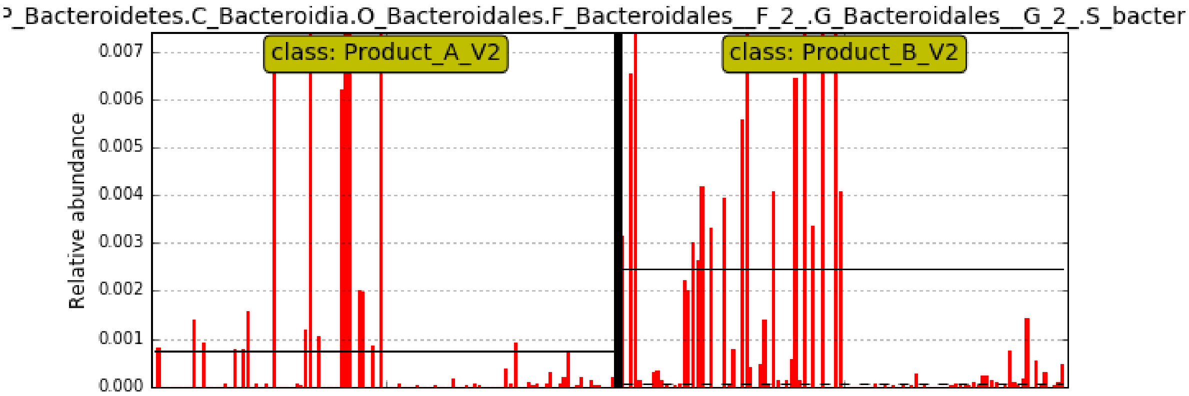
5) Lefse—Many differences



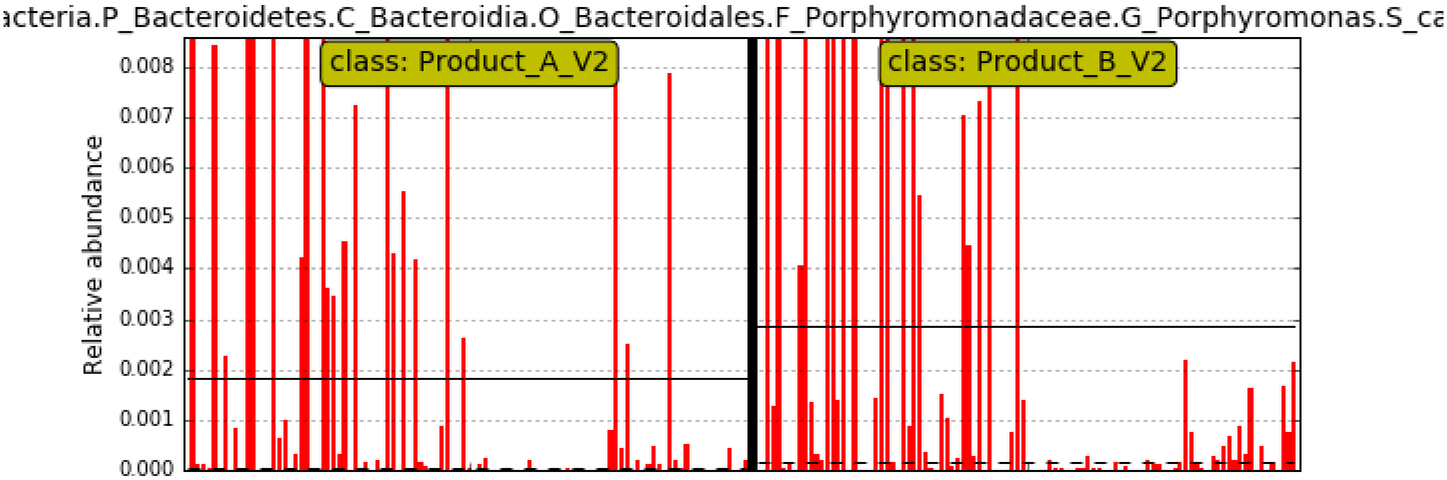

acteria.P_Absconditabacteria__SR1_.C_Absconditabacteria__SR1___C_1_.O_Absconditabacteria__SR1__

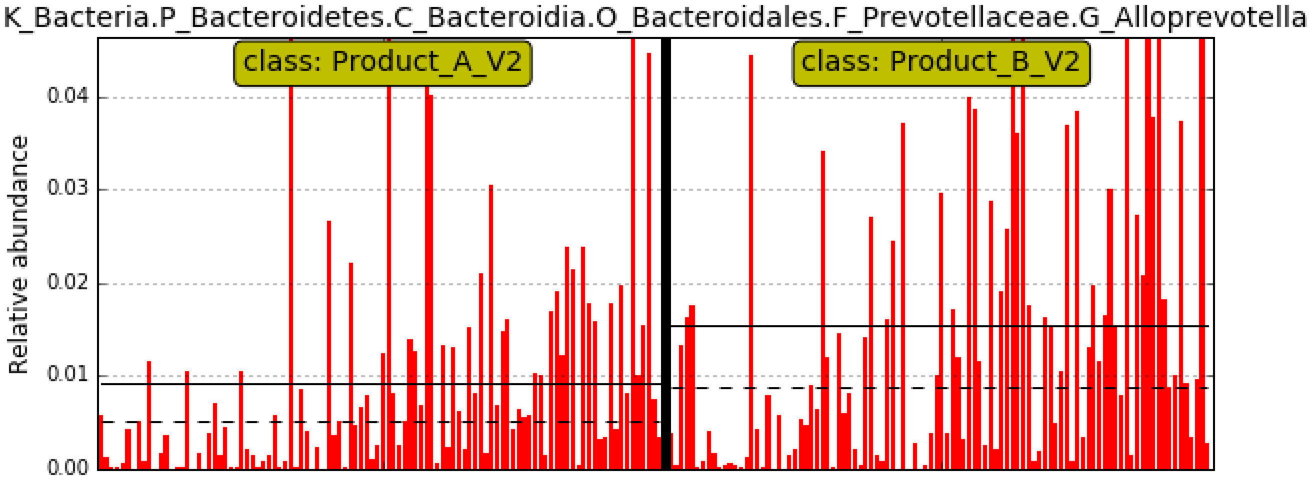

K_Bacteria.P_Actinobacteria.C_Actinobacteria.O_Actinomycetales.F_Actinomycetaceae.G_Peptidiphag

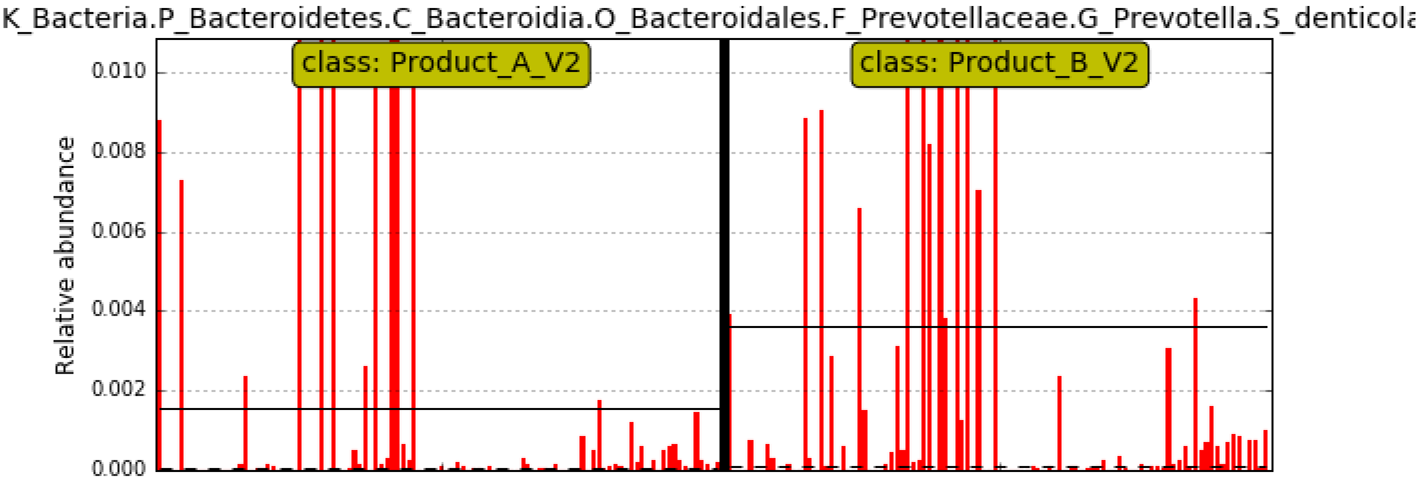

K_Bacteria.P_Actinobacteria.C_Coriobacteriia.O_Coriobacteriales.F_Atopobiaceae.G_Olsenella.S_uli

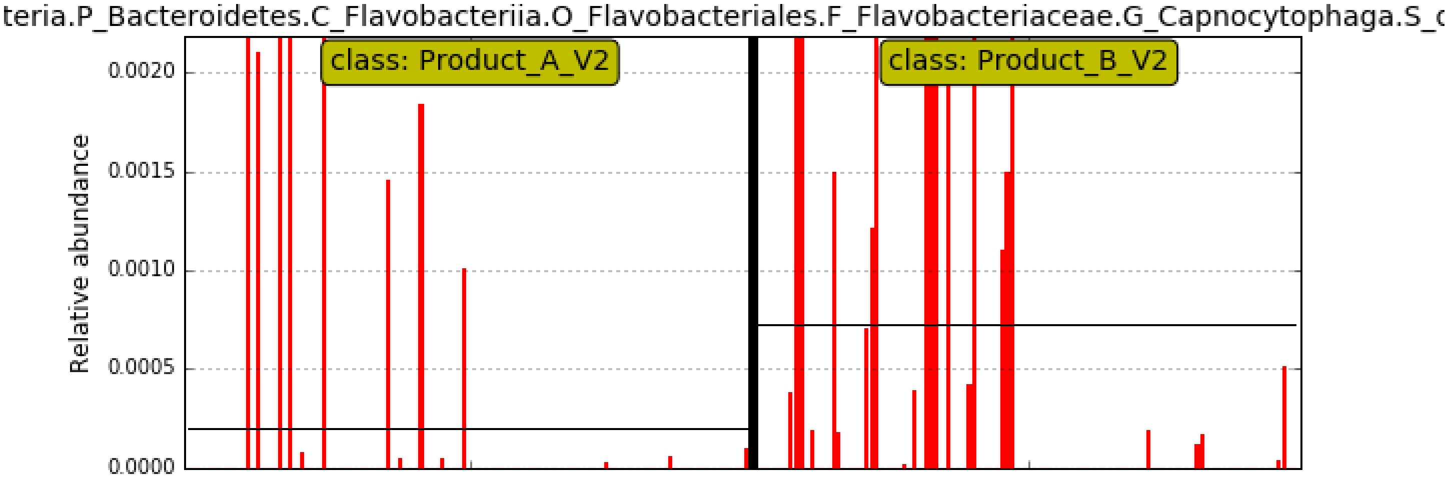

P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Bacteroidales__F_2_.G_Bacteroidales__G_2_.S_bacter
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.007
0.006
0.005
0.004
0.003
0.002
0.001
0.000

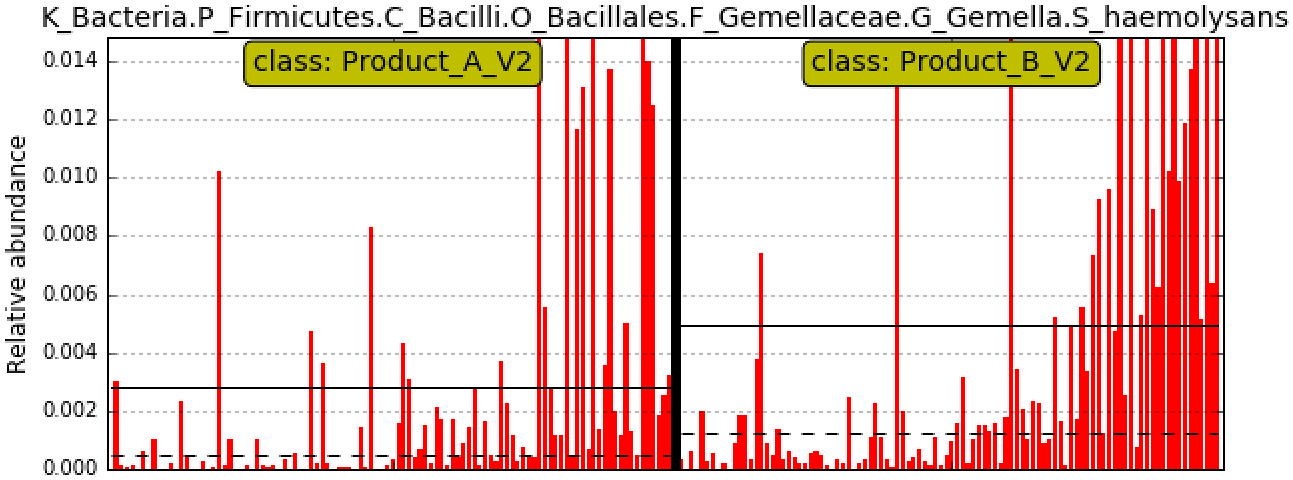
HMT274

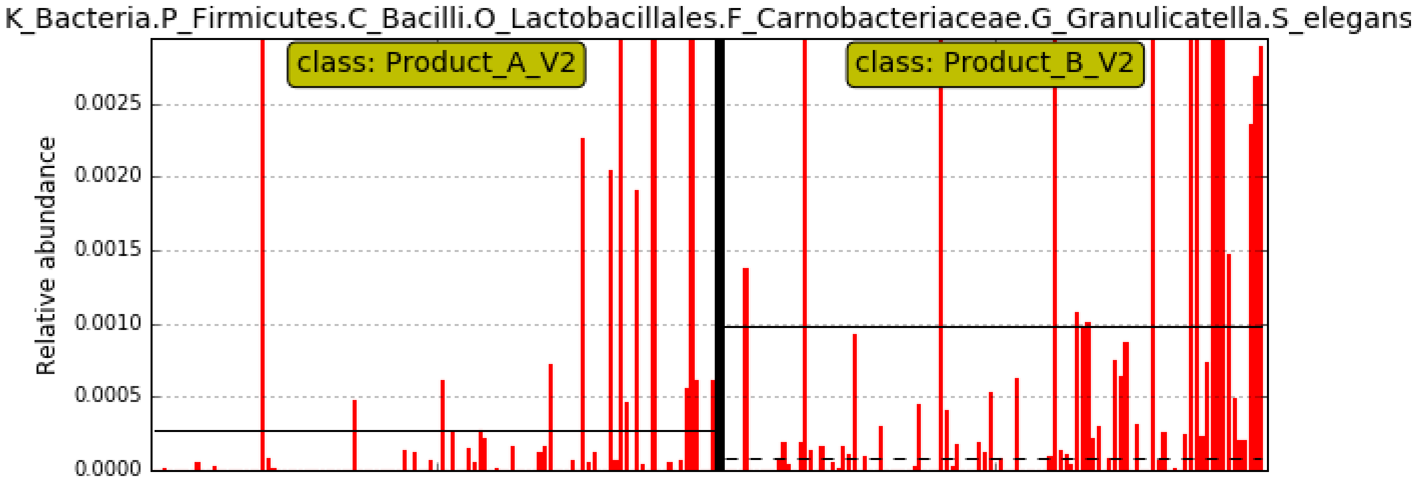

acteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Porphyromonadaceae.G_Porphyromonas.S_ca
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.008
0.007
0.006
0.005
0.004
0.003
0.002
0.001
0.000

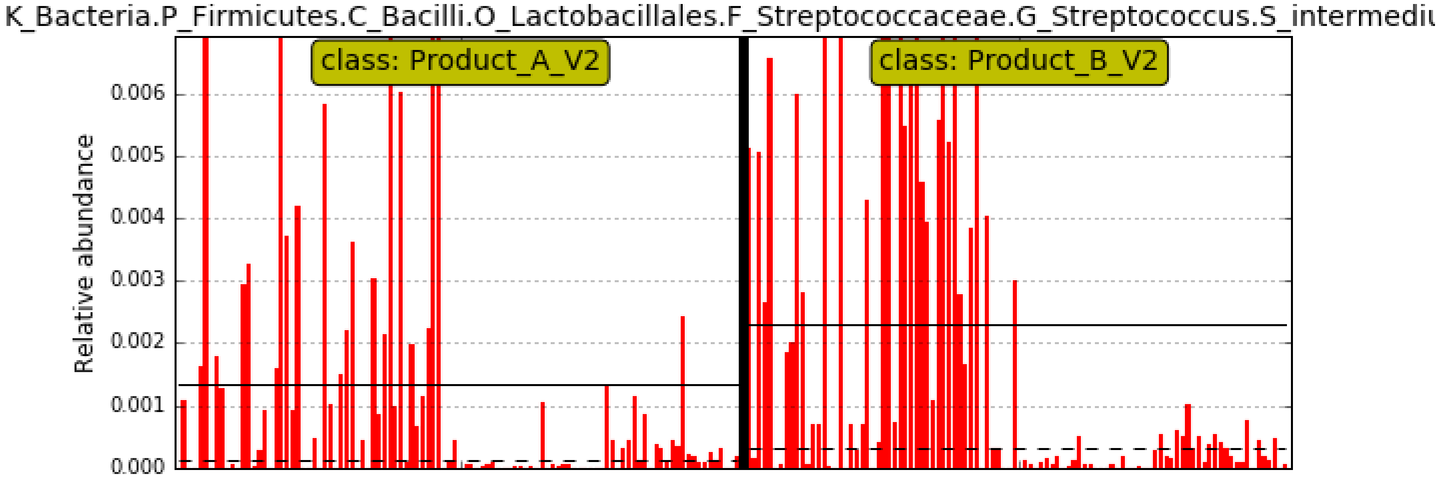

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Alloprevotella
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.04
0.03
0.02
0.01
0.00

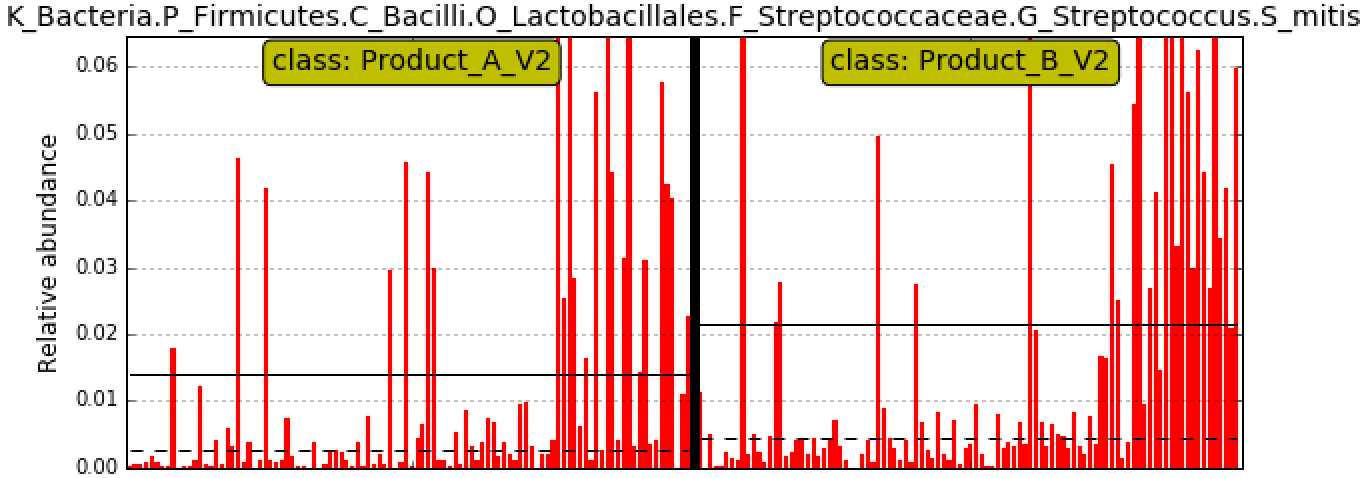

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_denticola
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.010
0.008
0.006
0.004
0.002
0.000

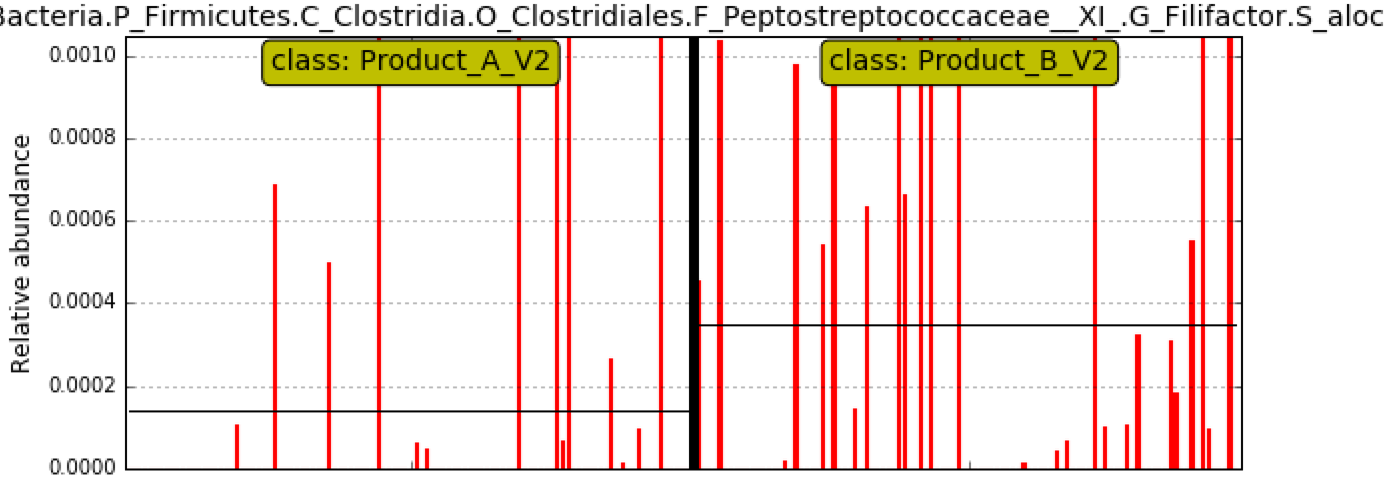

teria.P_Bacteroidetes.C_Flavobacteriia.O_Flavobacteriales.F_Flavobacteriaceae.G_Capnocytophaga.S_
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.0020
0.0015
0.0010
0.0005
0.0000

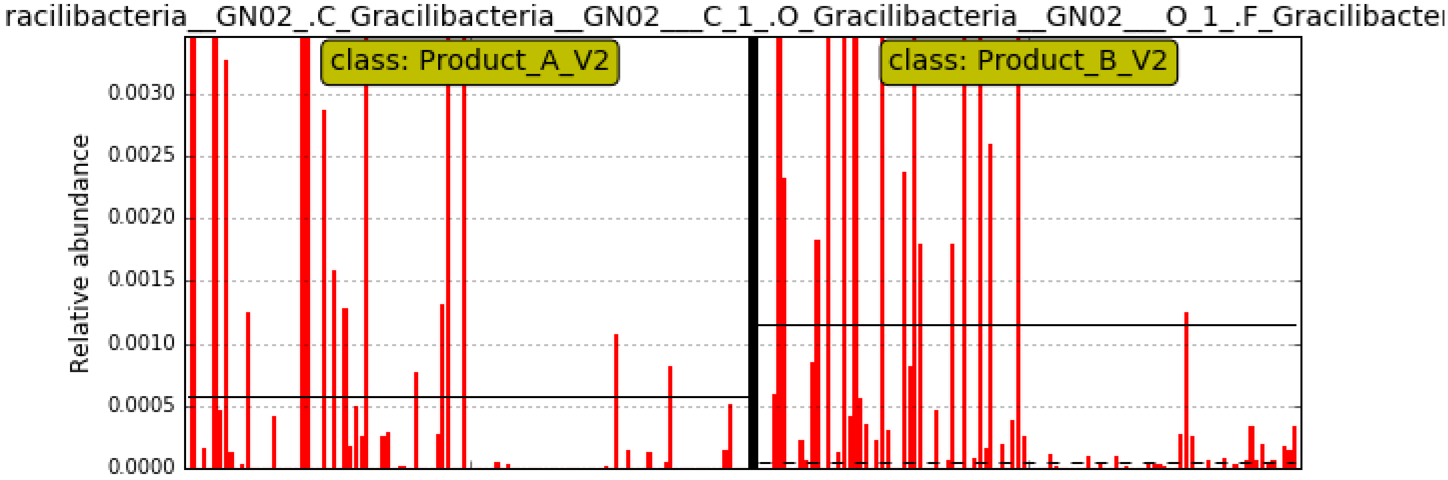

K_Bacteria.P_Firmicutes.C_Bacilli.O_Bacillales.F_Gemellaceae.G_Gemella.S_haemolysans
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000

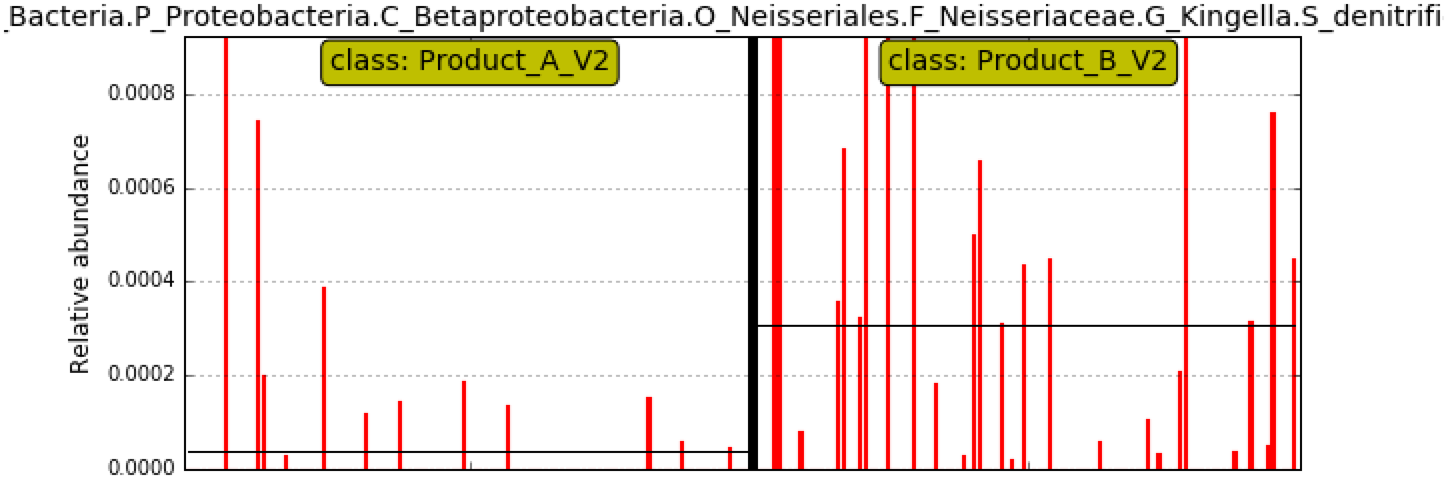

K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Carnobacteriaceae.G_Granulicatella.S_elegans
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000

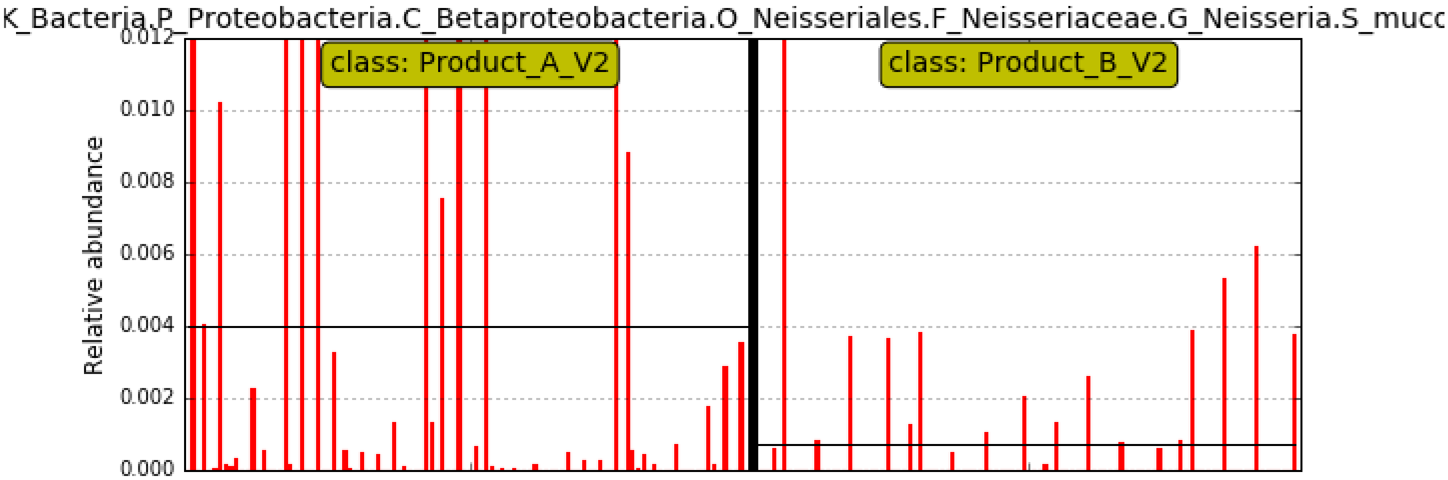

K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_intermediu
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.006
0.005
0.004
0.003
0.002
0.001
0.000

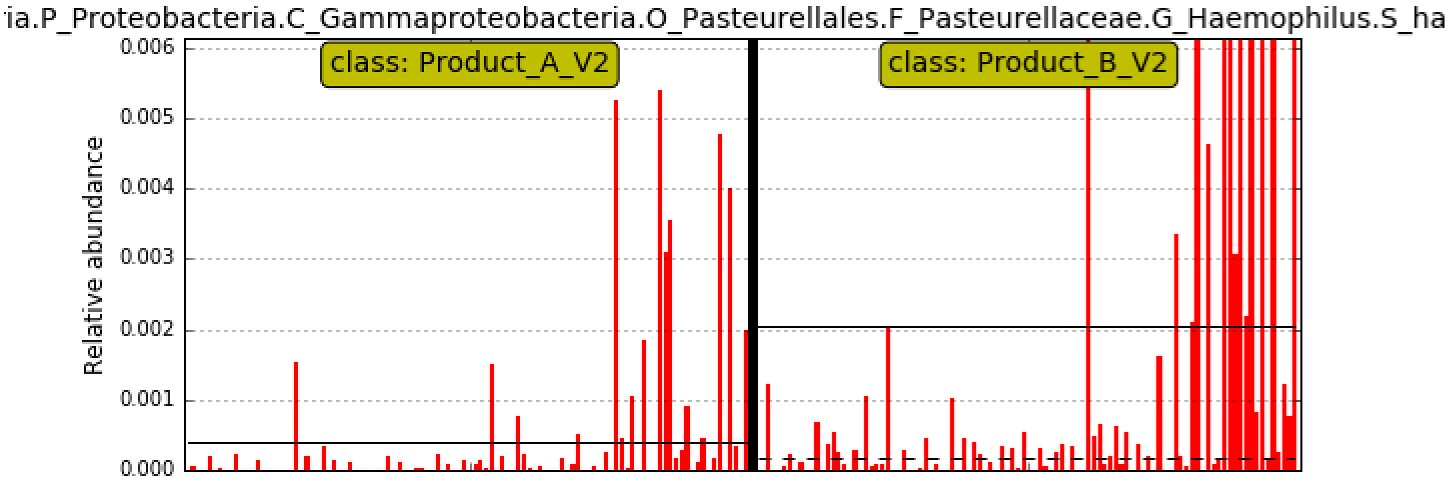

K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_mitis
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.06
0.05
0.04
0.03
0.02
0.01
0.00

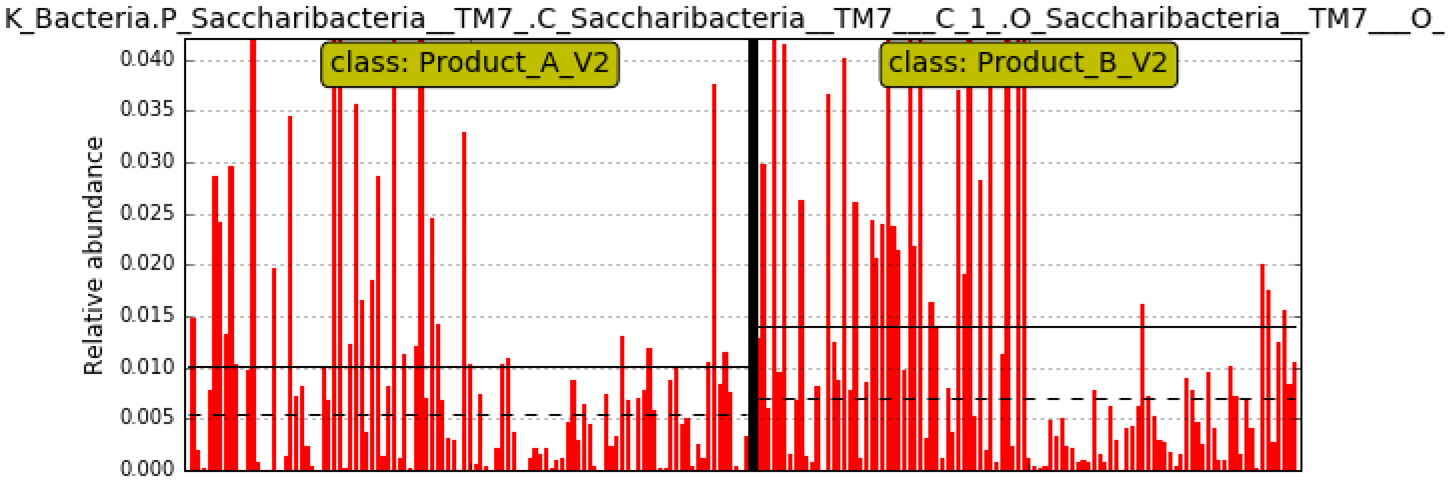

K_Bacteria.P_Firmicutes.C_Clostridia.O_Clostridiales.F_Peptostreptococcaceae__XI_.G_Filifactor.S_aloc

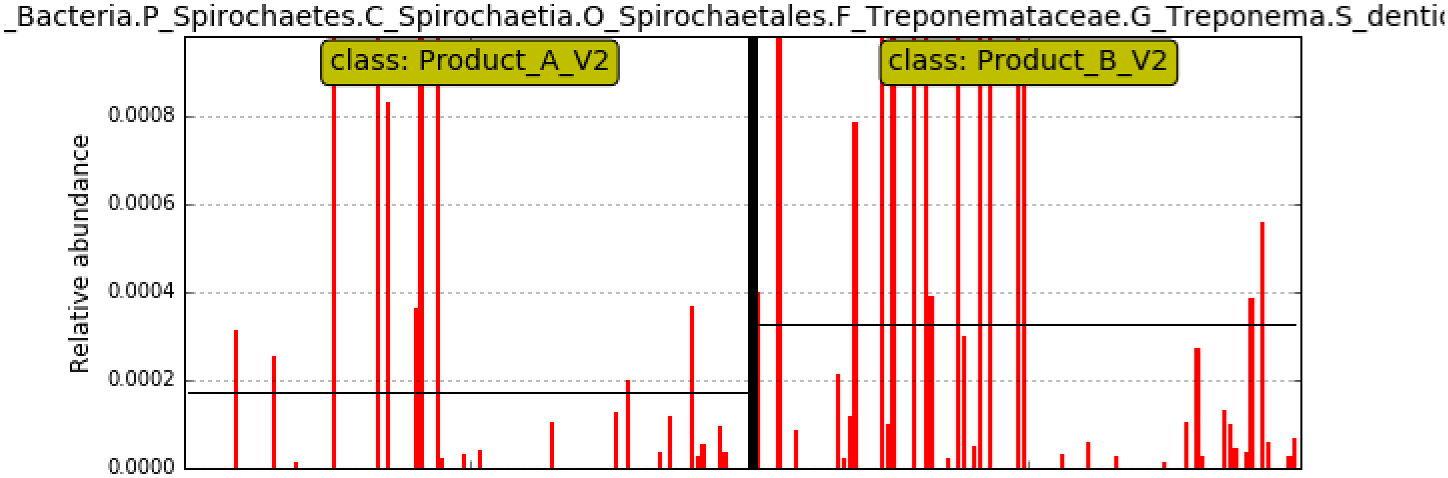

racilibacteria__GN02_.C_Gracilibacteria__GN02___C_1_.O_Gracilibacteria__GN02___O_1_.F_Gracilibacter


_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Kingella.S_denitrifi

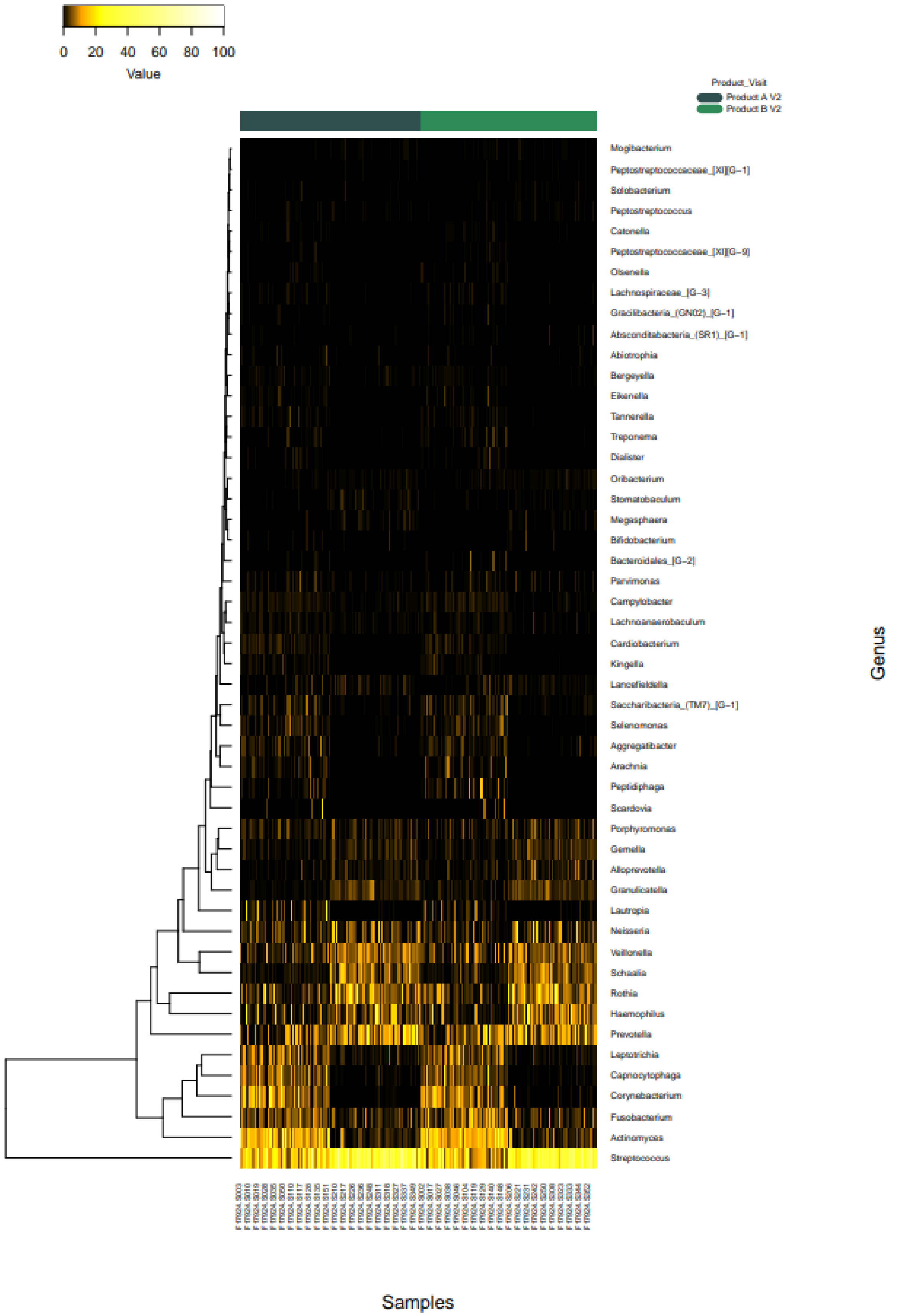

K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Neisseria.S_mucc
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.012
0.010
0.008
0.006
0.004
0.002
0.000

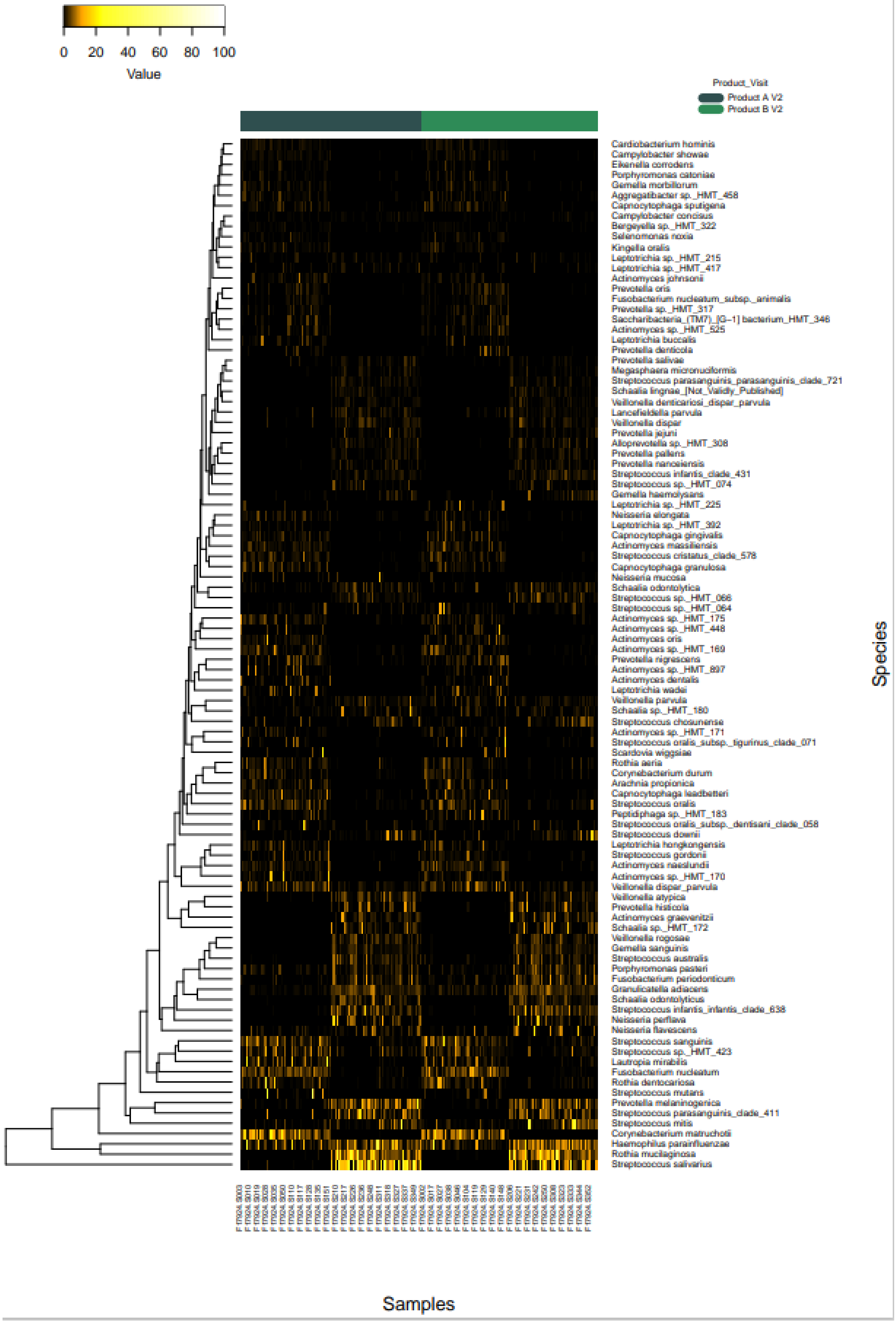

ia.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophilus.S_ha
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.006
0.005
0.004
0.003
0.002
0.001
0.000


K_Bacteria.P_Saccharibacteria__TM7_.C_Saccharibacteria__TM7___C_1_.O_Saccharibacteria__TM7___O_
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.040
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000


_Bacteria.P_Spirochaetes.C_Spirochaetia.O_Spirochaetales.F_Treponemataceae.G_Treponema.S_dentic
class: Product_A_V2
class: Product_B_V2
Relative abundance
0.0008
0.0006
0.0004
0.0002
0.0000

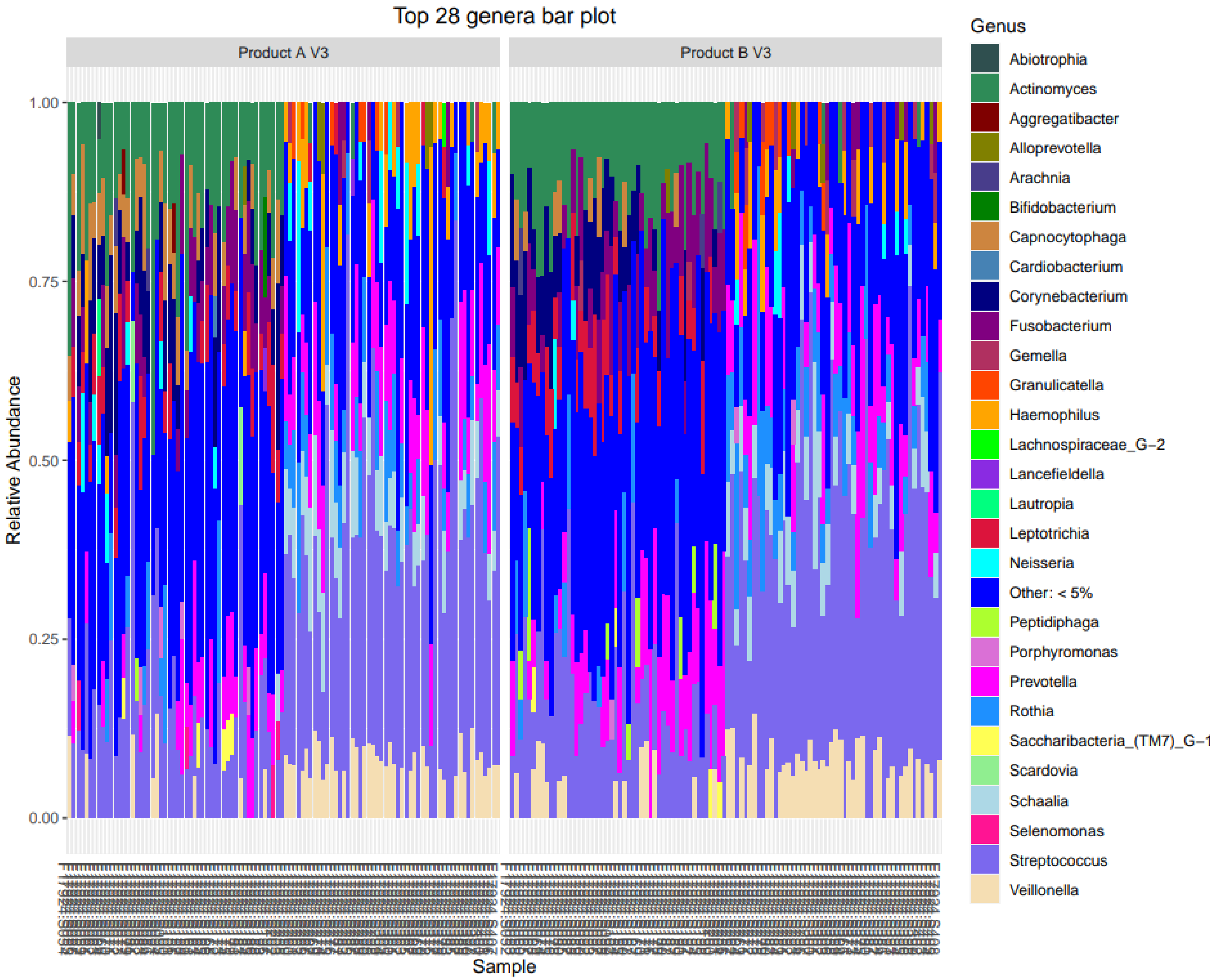
6) Heat maps


0
20
40
60
80
100
Value
Product_Visit
Product A V2
Product B V2
Mogibacterium
Peptostreptococcaceae_[XI][G-1]
Solobacterium
Peptostreptococcus
Catonella
Peptostreptococcaceae_[XI][G-9]
Olsenella
Lachnospiraceae_[G-3]
Gracilibacteria_(GN02)_[G-1]
Absconditabacteria_(SR1)_[G-1]
Abiotrophia
Bergeyella
Eikenella
Tannerella
Treponema
Dialister
Oribacterium
Stomatobaculum
Megasphaera
Bifidobacterium
Bacteroidales_[G-2]
Parvimonas
Campylobacter
Lachnoanaerobaculum
Cardiobacterium
Kingella
Lancefieldella
Saccharibacteria_(TM7)_[G-1]
Selenomonas
Aggregatibacter
Arachnia
Peptidiphaga
Scardovia
Porphyromonas
Gemella
Alloprevotella
Granulicatella
Lautropia
Neisseria
Veillonella
Schaalia
Rothia
Haemophilus
Prevotella
Leptotrichia
Capnocytophaga
Corynebacterium
Fusobacterium
Actinomyces
Streptococcus
Genus
Samples

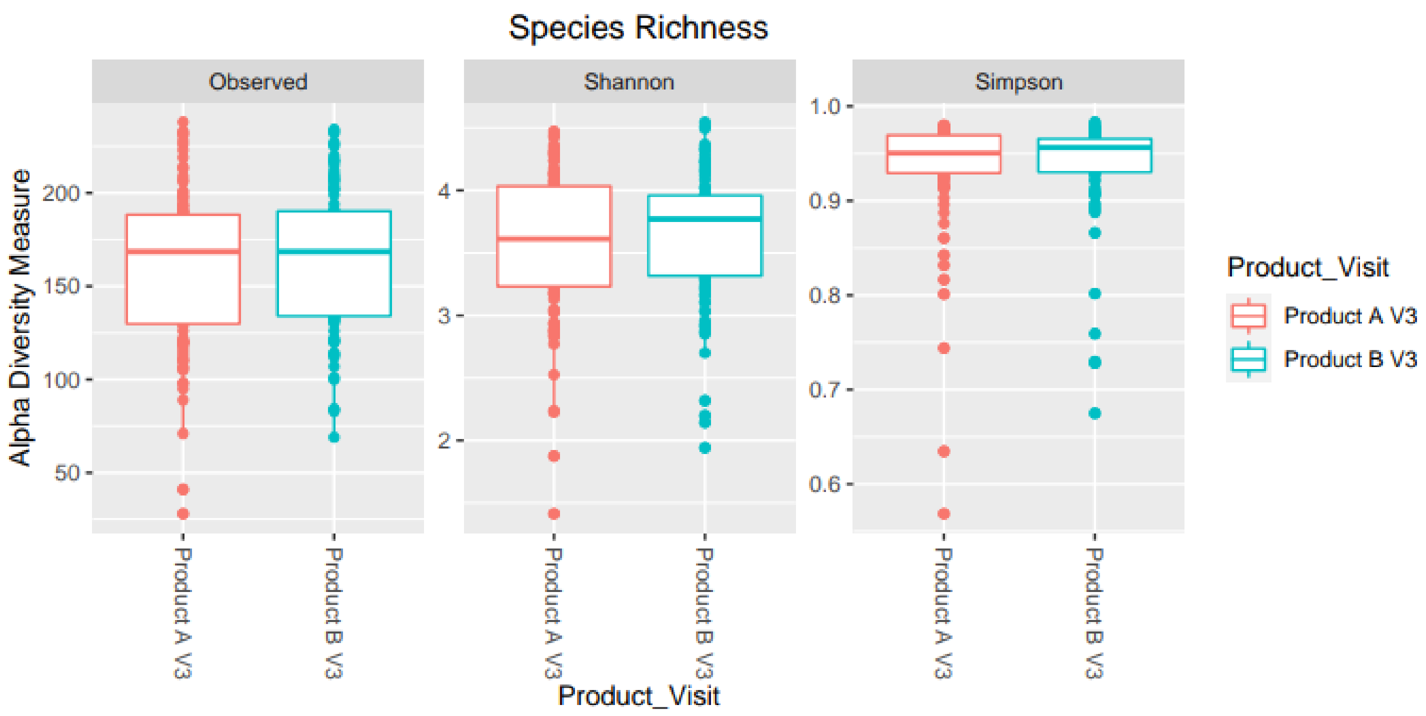

0
20
40
60
80
100
Value
Product_Visit
Product A V2
Product B V2
Cardiobacterium hominis
Campylobacter showae
Eikenella corrodens
Porphyromonas catoniae
Gemella morbillorum
Aggregatibacter sp._HMT_458
Capnocytophaga sputigena
Campylobacter concisus
Bergeyella sp._HMT_322
Selenomonas noxia
Kingella oralis
Leptotrichia sp._HMT_215
Leptotrichia sp._HMT_417
Actinomyces johnsonii
Prevotella oris
Fusobacterium nucleatum_subsp._animalis
Prevotella sp._HMT_317
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_348
Actinomyces sp._HMT_525
Leptotrichia buccalis
Prevotella denticola
Prevotella salivae
Megasphaera micronuciformis
Streptococcus parasanguinis_parasanguinis_clade_721
Schaalia lingnae_[Not_Validly_Published]
Veillonella denticariosi_dispar_parvula
Lancefieldella parvula
Veillonella dispar
Prevotella jejuni
Alloprevotella sp._HMT_308
Prevotella pallens
Prevotella nanceiensis
Streptococcus infantis_clade_431
Streptococcus sp._HMT_074
Gemella haemolysans
Leptotrichia sp._HMT_225
Neisseria elongata
Leptotrichia sp._HMT_392
Capnocytophaga gingivalis
Actinomyces massiliensis
Streptococcus cristatus_clade_578
Capnocytophaga granulosa
Neisseria mucosa
Schaalia odontolytica
Streptococcus sp._HMT_066
Streptococcus sp._HMT_064
Actinomyces sp._HMT_175
Actinomyces sp._HMT_448
Actinomyces oris
Actinomyces sp._HMT_169
Prevotella nigrescens
Actinomyces sp._HMT_897
Actinomyces dentalis
Leptotrichia wadei
Veillonella parvula
Schaalia sp._HMT_180
Streptococcus chosunense
Actinomyces sp._HMT_171
Streptococcus oralis_subsp._tigurinus_clade_071
Scardovia wiggsiae
Rothia aeria
Corynebacterium durum
Arachnia propionica
Capnocytophaga leadbetteri
Streptococcus oralis
Peptidiphaga sp._HMT_183
Streptococcus oralis_subsp._dentisani_clade_058
Streptococcus downii
Leptotrichia hongkongensis
Streptococcus gordonii
Actinomyces naeslundii
Actinomyces sp._HMT_170
Veillonella dispar_parvula
Veillonella atypica
Prevotella histicola
Actinomyces graevenitzii
Schaalia sp._HMT_172
Veillonella rogosae
Gemella sanguinis
Streptococcus australis
Porphyromonas pasteri
Fusobacterium periodonticum
Granulicatella adiacens
Schaalia odontolyticus
Streptococcus infantis_infantis_clade_638
Neisseria perflava
Neisseria flavescens
Streptococcus sanguinis
Streptococcus sp._HMT_423
Lautropia mirabilis
Fusobacterium nucleatum
Rothia dentocariosa
Streptococcus mutans
Prevotella melaninogenica
Streptococcus parasanguinis_clade_411
Streptococcus mitis
Corynebacterium matruchotii
Haemophilus parainfluenzae
Rothia mucilaginosa
Streptococcus salivarius
Species
Samples

Comparison 4. Product A V3 vs Product B V3

1) Taxonomy barplots

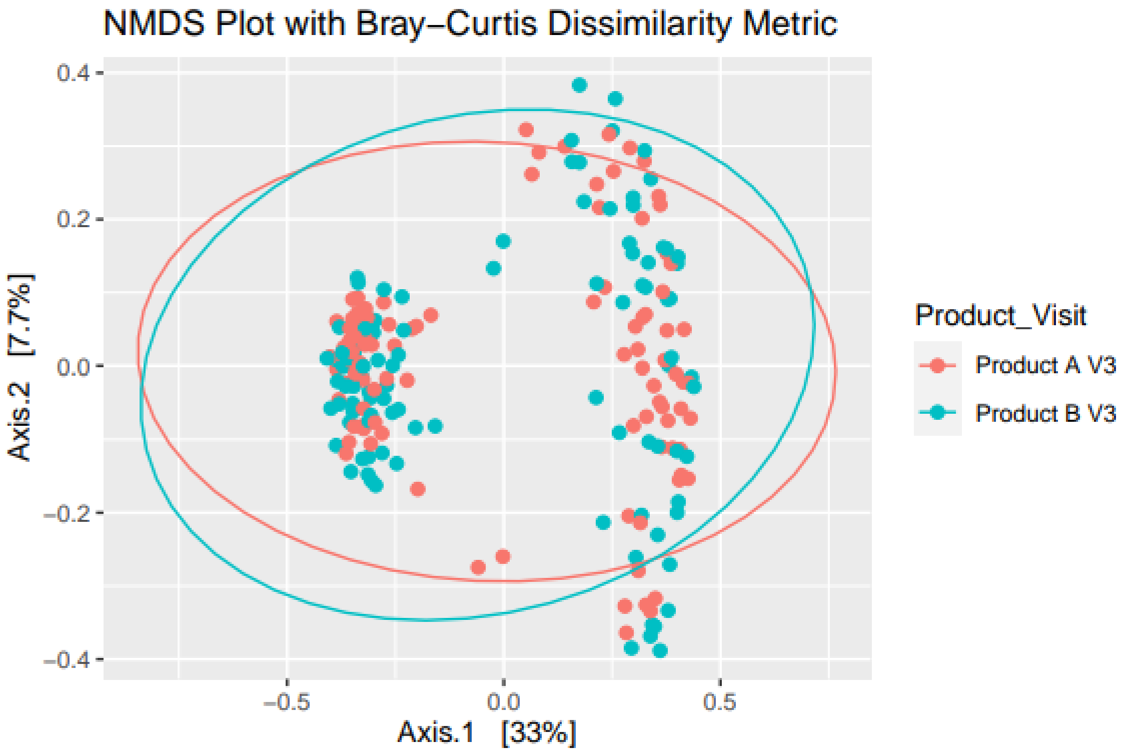


2) Alpha diversity



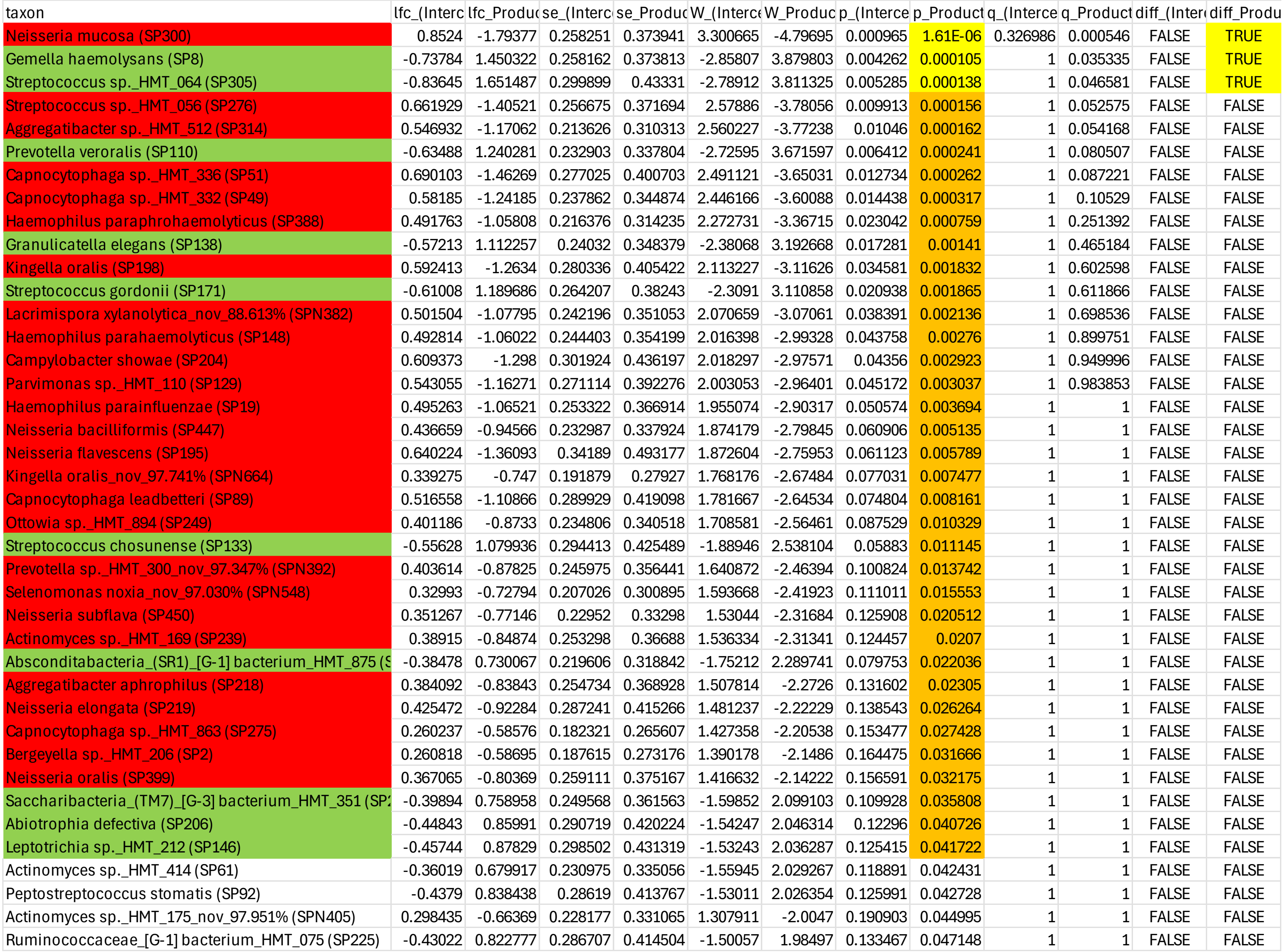
No significant difference

3) Beta diversity



P= 0.11

4) Differential abundance

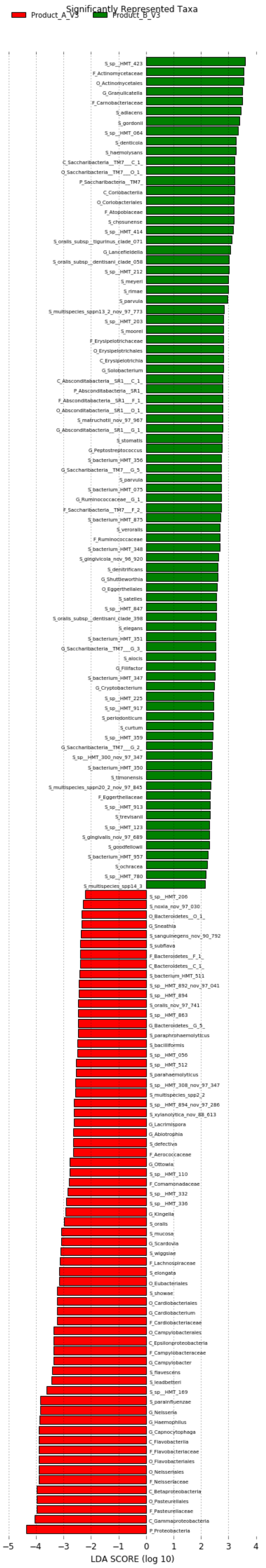


taxon	lfc_(Interc	lfc_Produc	se_(Interc	se_Produc	W_(Interce	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inter	diff_Produ
Neisseria mucosa (SP300)	0.8524	-1.79377	0.258251	0.373941	3.300665	-4.79695	0.000965	1.61E-06	0.326986	0.000546	FALSE	TRUE
Gemella haemolysans (SP8)	-0.73784	1.450322	0.258162	0.373813	-2.85807	3.879803	0.004262	0.000105	1	0.035335	FALSE	TRUE
Streptococcus sp._HMT_064 (SP305)	-0.83645	1.651487	0.299899	0.43331	-2.78912	3.811325	0.005285	0.000138	1	0.046581	FALSE	TRUE
Streptococcus sp._HMT_056 (SP276)	0.661929	-1.40521	0.256675	0.371694	2.57886	-3.78056	0.009913	0.000156	1	0.052575	FALSE	FALSE
Aggregatibacter sp._HMT_512 (SP314)	0.546932	-1.17062	0.213626	0.310313	2.560227	-3.77238	0.01046	0.000162	1	0.054168	FALSE	FALSE
Prevotella veroralis (SP110)	-0.63488	1.240281	0.232903	0.337804	-2.72595	3.671597	0.006412	0.000241	1	0.080507	FALSE	FALSE
Capnocytophaga sp._HMT_336 (SP51)	0.690103	-1.46269	0.277025	0.400703	2.491121	-3.65031	0.012734	0.000262	1	0.087221	FALSE	FALSE
Capnocytophaga sp._HMT_332 (SP49)	0.58185	-1.24185	0.237862	0.344874	2.446166	-3.60088	0.014438	0.000317	1	0.10529	FALSE	FALSE
Haemophilus paraphrohaemolyticus (SP388)	0.491763	-1.05808	0.216376	0.314235	2.272731	-3.36715	0.023042	0.000759	1	0.251392	FALSE	FALSE
Granulicatella elegans (SP138)	-0.57213	1.112257	0.24032	0.348379	-2.38068	3.192668	0.017281	0.00141	1	0.465184	FALSE	FALSE
Kingella oralis (SP198)	0.592413	-1.2634	0.280336	0.405422	2.113227	-3.11626	0.034581	0.001832	1	0.602598	FALSE	FALSE
Streptococcus gordonii (SP171)	-0.61008	1.189686	0.264207	0.38243	-2.3091	3.110858	0.020938	0.001865	1	0.611866	FALSE	FALSE
Lacrimispora xylanolytica_nov_88.613% (SPN382)	0.501504	-1.07795	0.242196	0.351053	2.070659	-3.07061	0.038391	0.002136	1	0.698536	FALSE	FALSE
Haemophilus parahaemolyticus (SP148)	0.492814	-1.06022	0.244403	0.354199	2.016398	-2.99328	0.043758	0.00276	1	0.899751	FALSE	FALSE
Campylobacter showae (SP204)	0.609373	-1.298	0.301924	0.436197	2.018297	-2.97571	0.04356	0.002923	1	0.949996	FALSE	FALSE
Parvimonas sp._HMT_110 (SP129)	0.543055	-1.16271	0.271114	0.392276	2.003053	-2.96401	0.045172	0.003037	1	0.983853	FALSE	FALSE
Haemophilus parainfluenzae (SP19)	0.495263	-1.06521	0.253322	0.366914	1.955074	-2.90317	0.050574	0.003694	1	1	FALSE	FALSE
Neisseria bacilliformis (SP447)	0.436659	-0.94566	0.232987	0.337924	1.874179	-2.79845	0.060906	0.005135	1	1	FALSE	FALSE
Neisseria flavescens (SP195)	0.640224	-1.36093	0.34189	0.493177	1.872604	-2.75953	0.061123	0.005789	1	1	FALSE	FALSE
Kingella oralis_nov_97.741% (SPN664)	0.339275	-0.747	0.191879	0.27927	1.768176	-2.67484	0.077031	0.007477	1	1	FALSE	FALSE
Capnocytophaga leadbetteri (SP89)	0.516558	-1.10866	0.289929	0.419098	1.781667	-2.64534	0.074804	0.008161	1	1	FALSE	FALSE
Ottowia sp._HMT_894 (SP249)	0.401186	-0.8733	0.234806	0.340518	1.708581	-2.56461	0.087529	0.010329	1	1	FALSE	FALSE
Streptococcus chosunense (SP133)	-0.55628	1.079936	0.294413	0.425489	-1.88946	2.538104	0.05883	0.011145	1	1	FALSE	FALSE
Prevotella sp._HMT_300_nov_97.347% (SPN392)	0.403614	-0.87825	0.245975	0.356441	1.640872	-2.46394	0.100824	0.013742	1	1	FALSE	FALSE
Selenomonas noxia_nov_97.030% (SPN548)	0.32993	-0.72794	0.207026	0.300895	1.593668	-2.41923	0.111011	0.015553	1	1	FALSE	FALSE
Neisseria subflava (SP450)	0.351267	-0.77146	0.22952	0.33298	1.53044	-2.31684	0.125908	0.020512	1	1	FALSE	FALSE
Actinomyces sp._HMT_169 (SP239)	0.38915	-0.84874	0.253298	0.36688	1.536334	-2.31341	0.124457	0.0207	1	1	FALSE	FALSE
Absconditabacteria_(SR1)_[G-1] bacterium_HMT_875 (S	-0.38478	0.730067	0.219606	0.318842	-1.75212	2.289741	0.079753	0.022036	1	1	FALSE	FALSE
Aggregatibacter aphrophilus (SP218)	0.384092	-0.83843	0.254734	0.368928	1.507814	-2.2726	0.131602	0.02305	1	1	FALSE	FALSE
Neisseria elongata (SP219)	0.425472	-0.92284	0.287241	0.415266	1.481237	-2.22229	0.138543	0.026264	1	1	FALSE	FALSE
Capnocytophaga sp._HMT_863 (SP275)	0.260237	-0.58576	0.182321	0.265607	1.427358	-2.20538	0.153477	0.027428	1	1	FALSE	FALSE
Bergeyella sp._HMT_206 (SP2)	0.260818	-0.58695	0.187615	0.273176	1.390178	-2.1486	0.164475	0.031666	1	1	FALSE	FALSE
Neisseria oralis (SP399)	0.367065	-0.80369	0.259111	0.375167	1.416632	-2.14222	0.156591	0.032175	1	1	FALSE	FALSE
Saccharibacteria_(TM7)_[G-3] bacterium_HMT_351 (SP	-0.39894	0.758958	0.249568	0.361563	-1.59852	2.099103	0.109928	0.035808	1	1	FALSE	FALSE
Abiotrophia defectiva (SP206)	-0.44843	0.85991	0.290719	0.420224	-1.54247	2.046314	0.12296	0.040726	1	1	FALSE	FALSE
Leptotrichia sp._HMT_212 (SP146)	-0.45744	0.87829	0.298502	0.431319	-1.53243	2.036287	0.125415	0.041722	1	1	FALSE	FALSE
Actinomyces sp._HMT_414 (SP61)	-0.36019	0.679917	0.230975	0.335056	-1.55945	2.029267	0.118891	0.042431	1	1	FALSE	FALSE
Peptostreptococcus stomatis (SP92)	-0.4379	0.838438	0.28619	0.413767	-1.53011	2.026354	0.125991	0.042728	1	1	FALSE	FALSE
Actinomyces sp._HMT_175_nov_97.951% (SPN405)	0.298435	-0.66369	0.228177	0.331065	1.307911	-2.0047	0.190903	0.044995	1	1	FALSE	FALSE
Ruminococcaceae_[G-1] bacterium_HMT_075 (SP225)	-0.43022	0.822777	0.286707	0.414504	-1.50057	1.98497	0.133467	0.047148	1	1	FALSE	FALSE

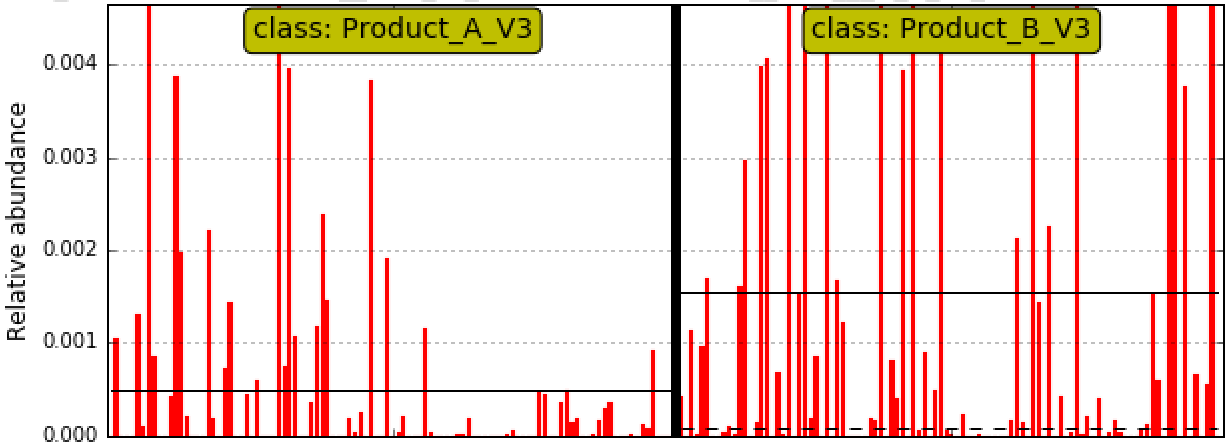
Green, more abundant in B after treatment

Red, more abundant in A after treatment

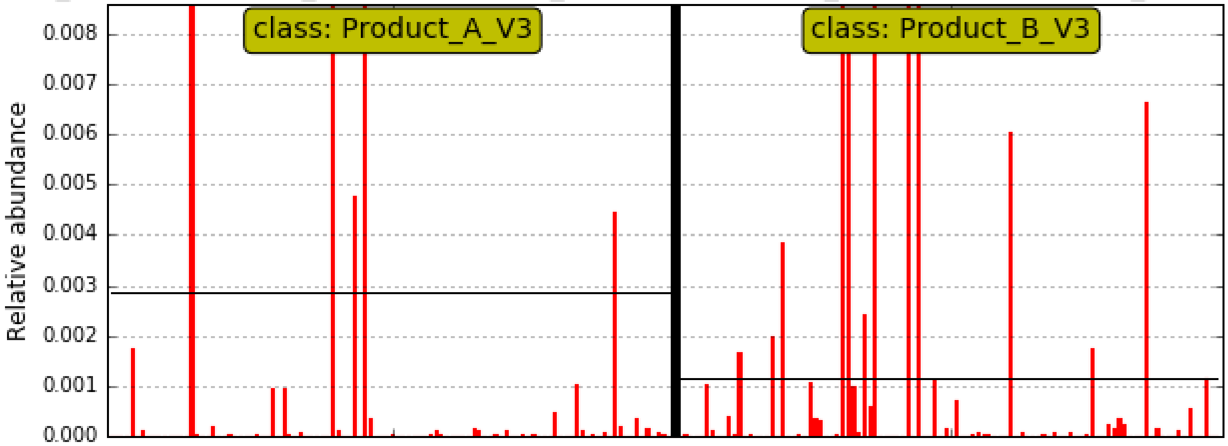
5) Lefse—as expected, many differences



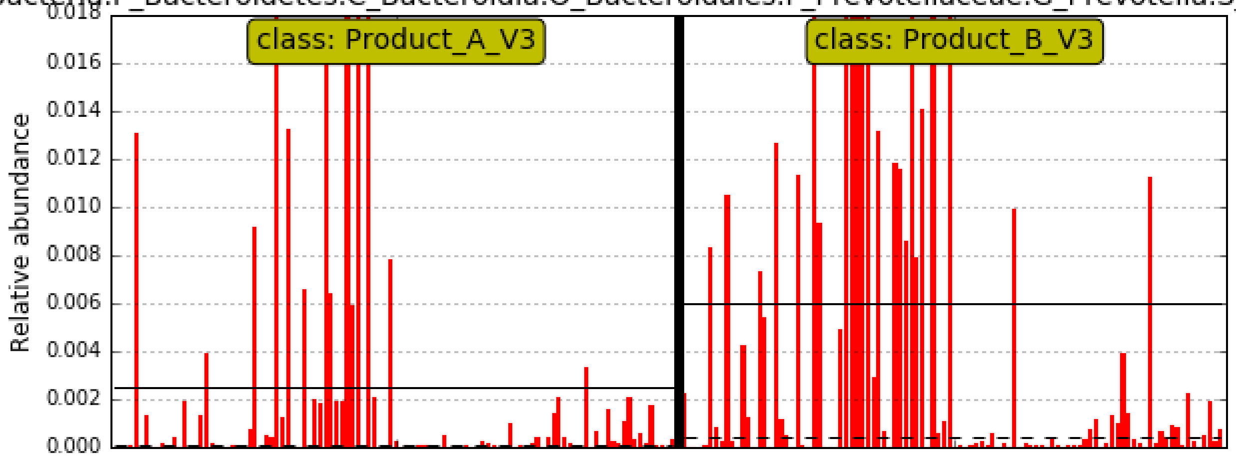
acteria.P_Absconditabacteria__SR1_.C_Absconditabacteria__SR1___C_1_.O_Absconditabacteria__SR1__

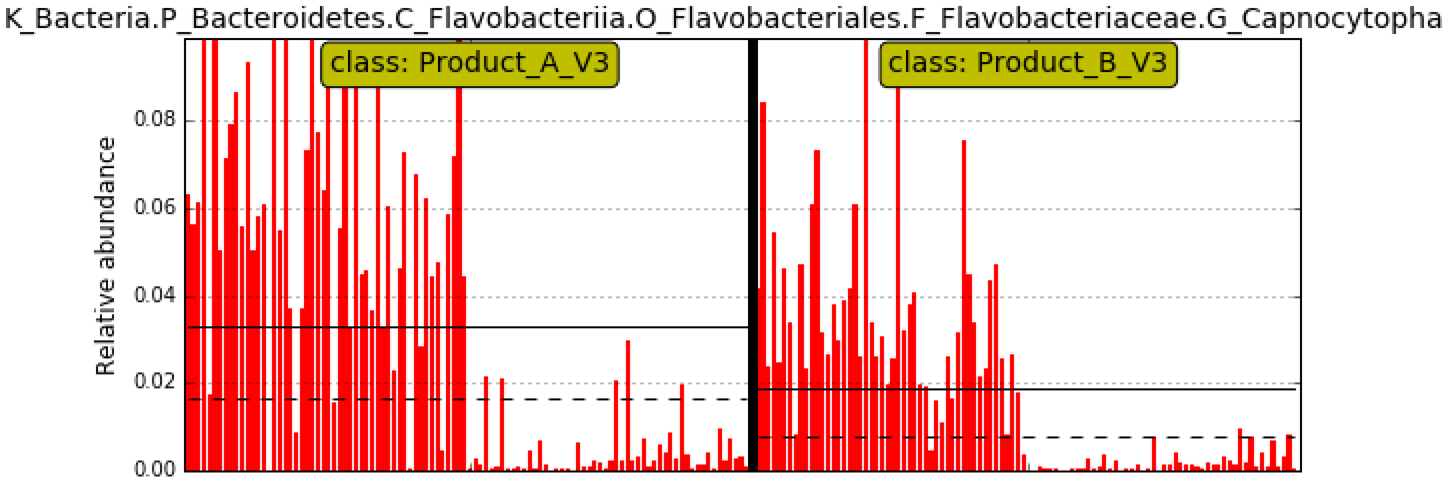


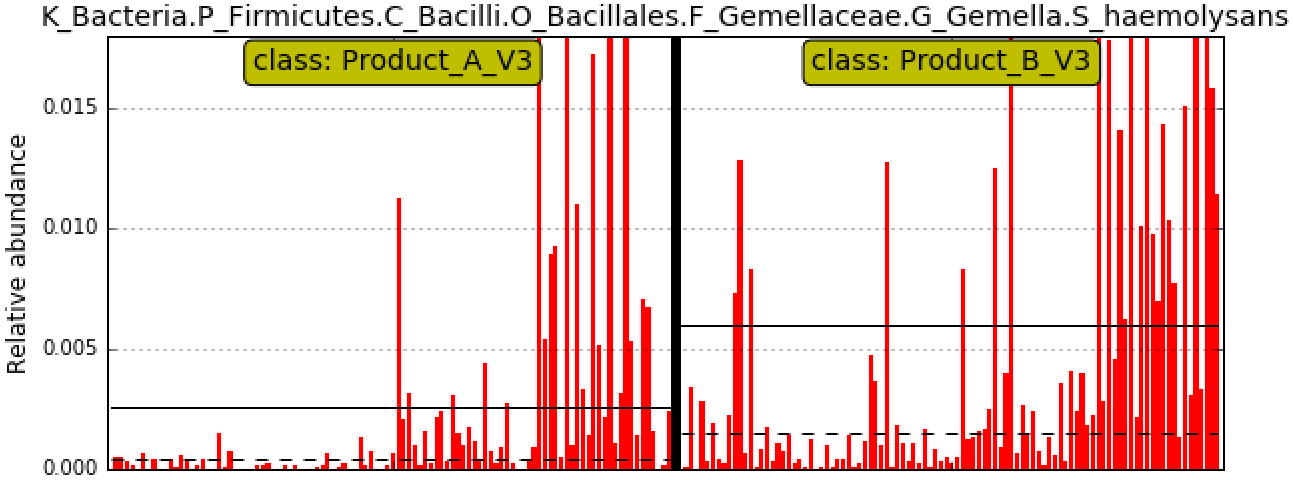
acteria.P_Actinobacteria.C_Actinobacteria.O_Bifidobacteriales.F_Bifidobacteriaceae.G_Scardovia.S_wig

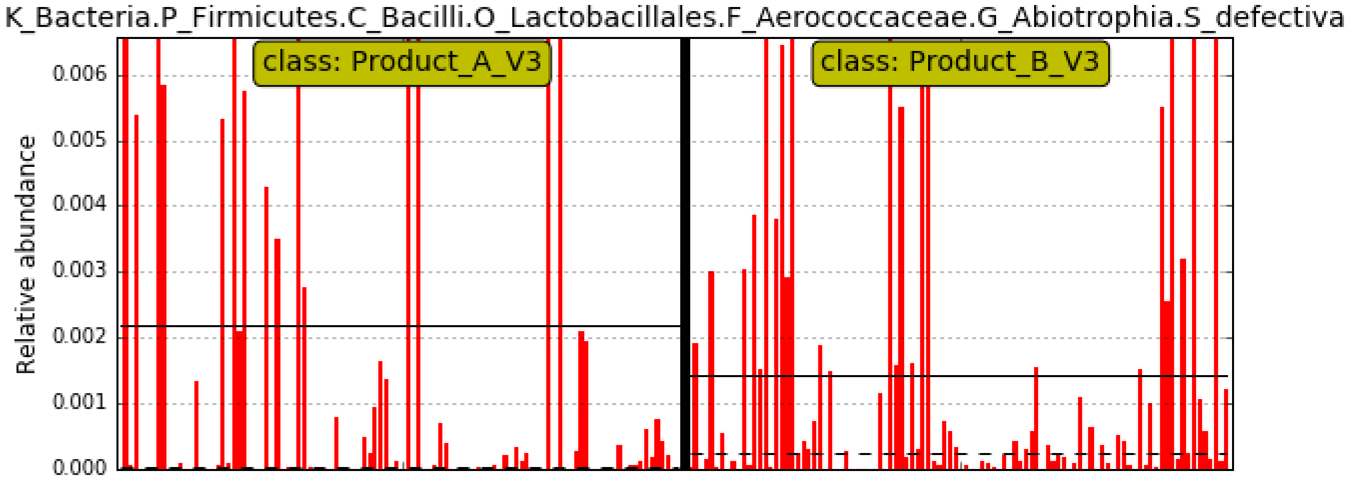


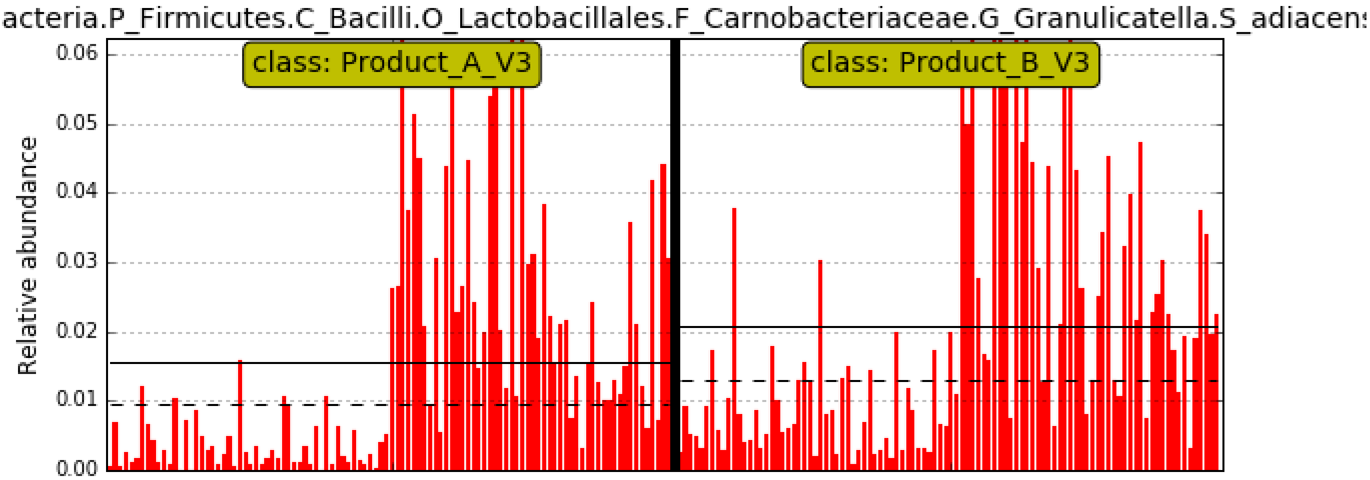
K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_denticola

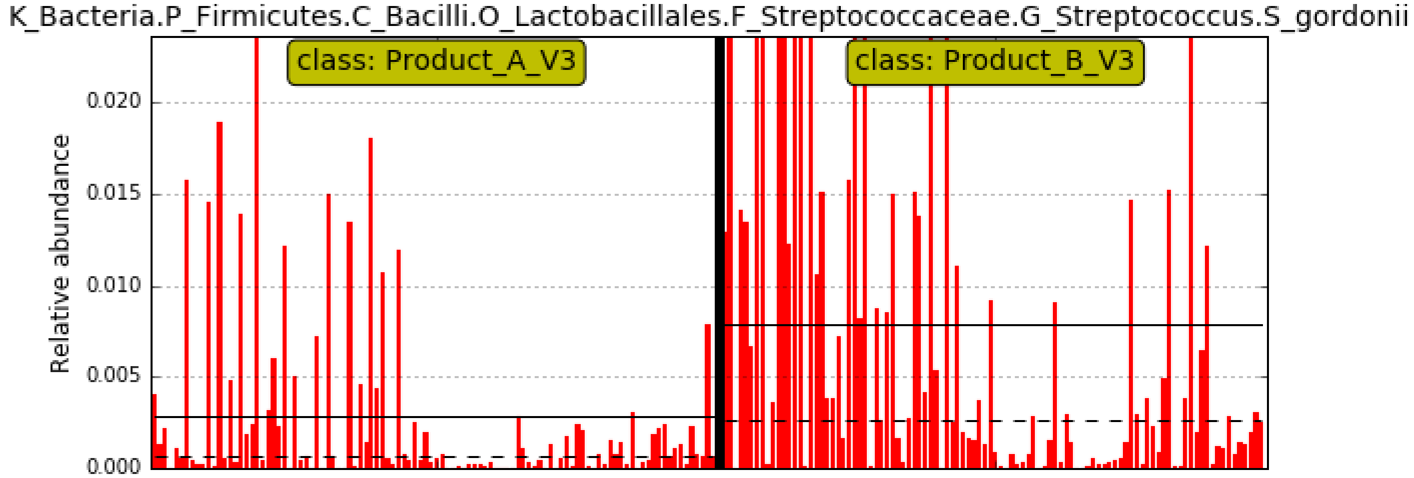


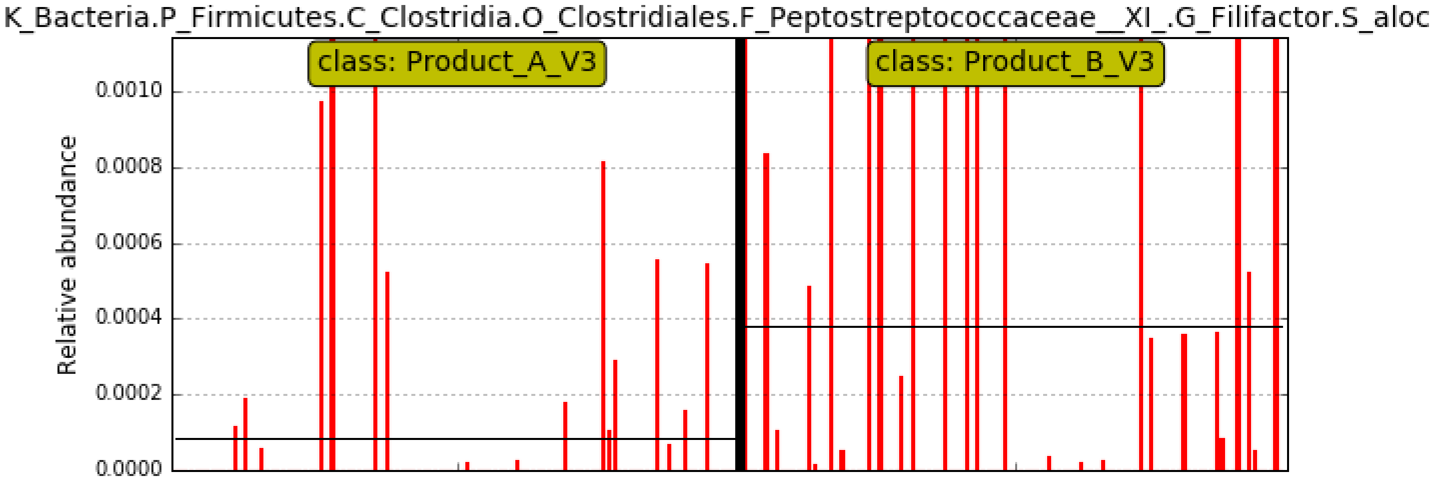

K_Bacteria.P_Bacteroidetes.C_Flavobacteriia.O_Flavobacteriales.F_Flavobacteriaceae.G_Capnocytopha

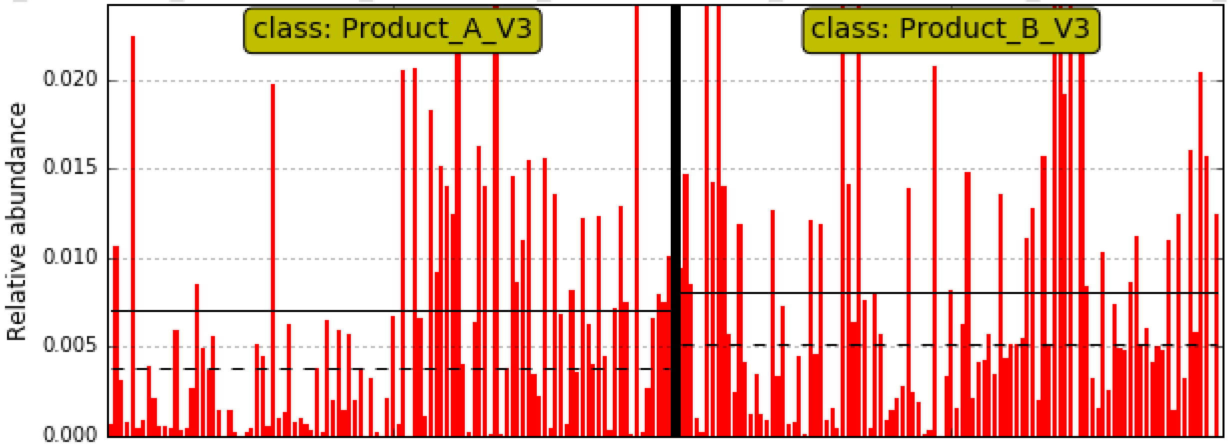

K_Bacteria.P_Firmicutes.C_Bacilli.O_Bacillales.F_Gemellaceae.G_Gemella.S_haemolysans

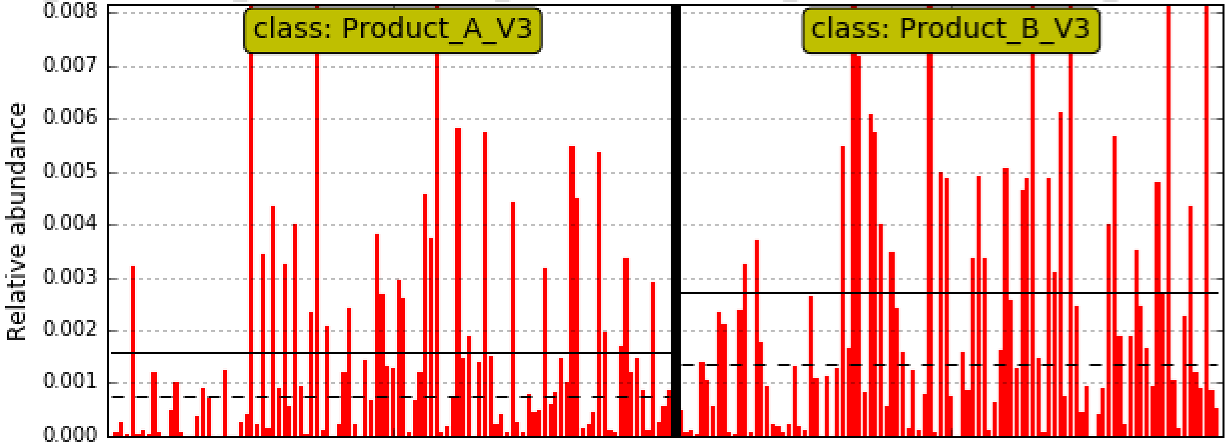

K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Aerococcaceae.G_Abiotrophia.S_defectiva

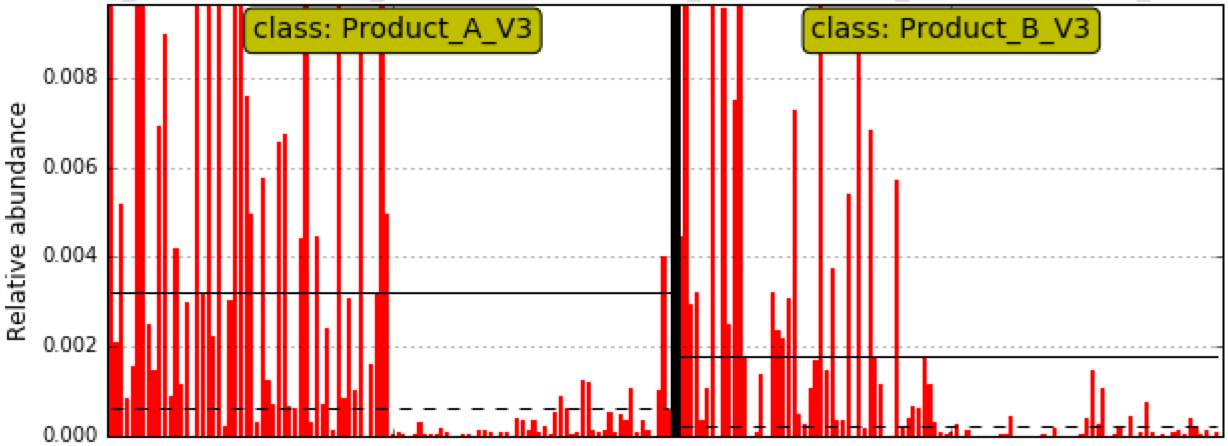

K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Carnobacteriaceae.G_Granulicatella.S_adiacen

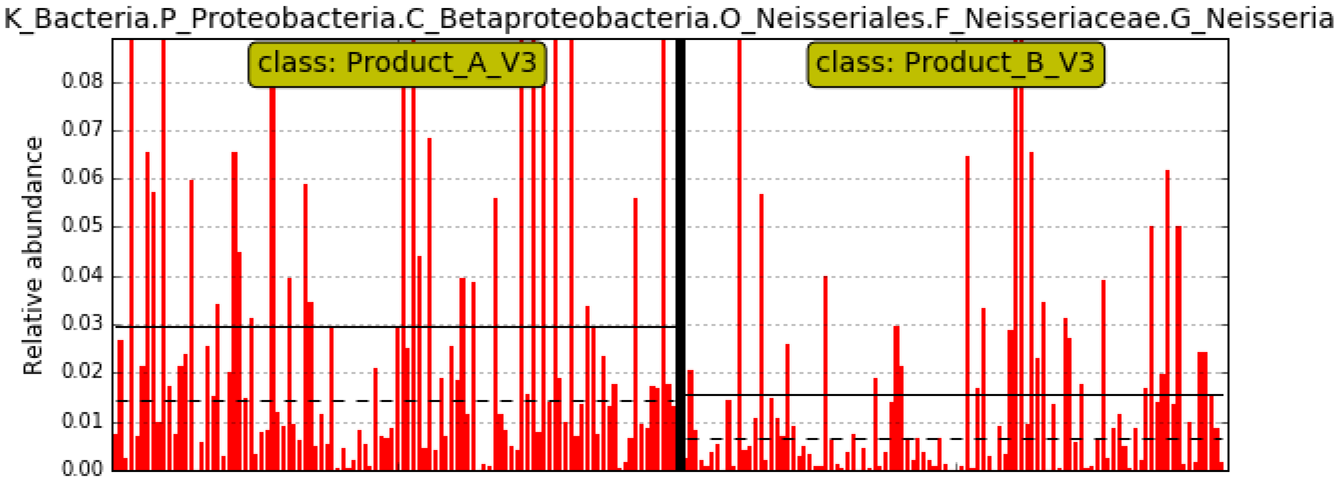

K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_gordonii

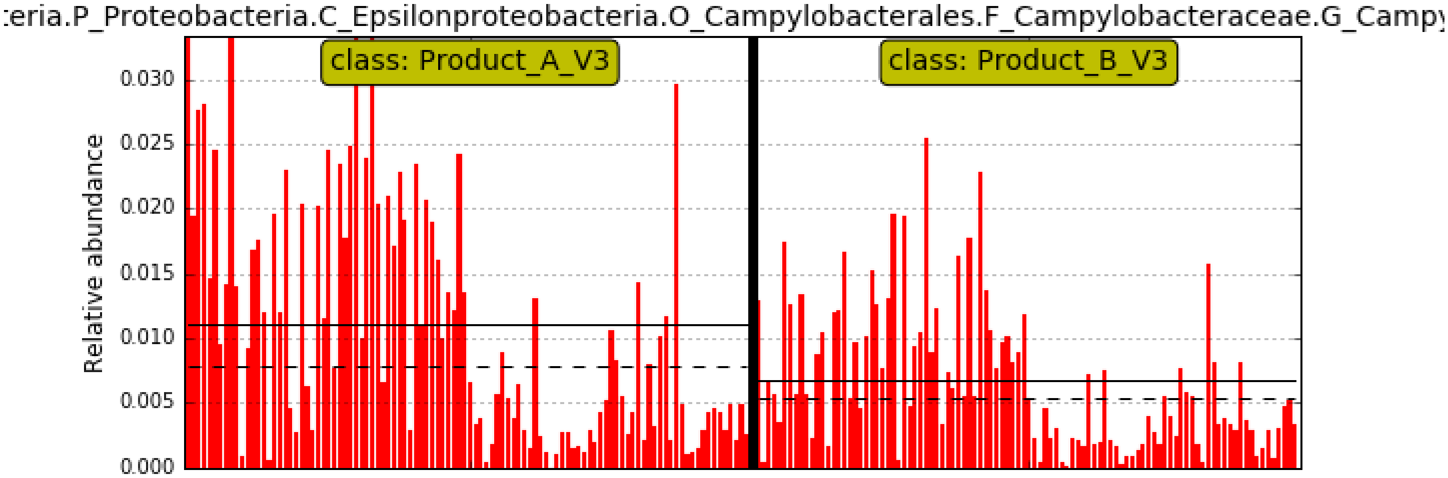

K_Bacteria.P_Firmicutes.C_Clostridia.O_Clostridiales.F_Peptostreptococcaceae__XI_.G_Filifactor.S_aloc

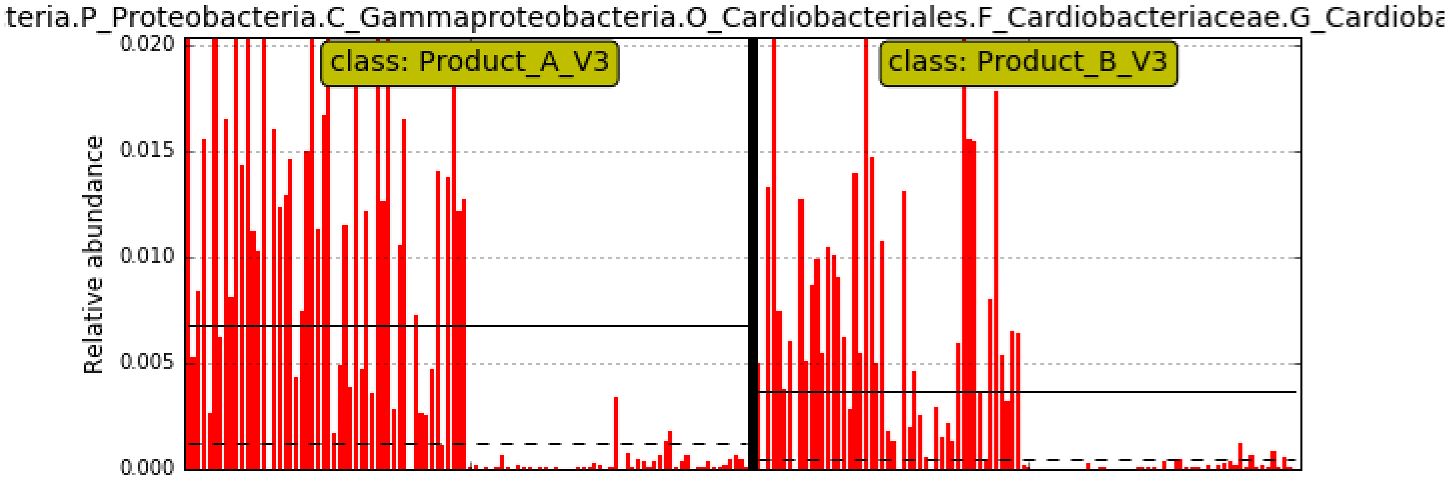

K_Bacteria.P_Firmicutes.C_Clostridia.O_Negativicutes.F_Veillonellaceae.G_Veillonella.S_parvula

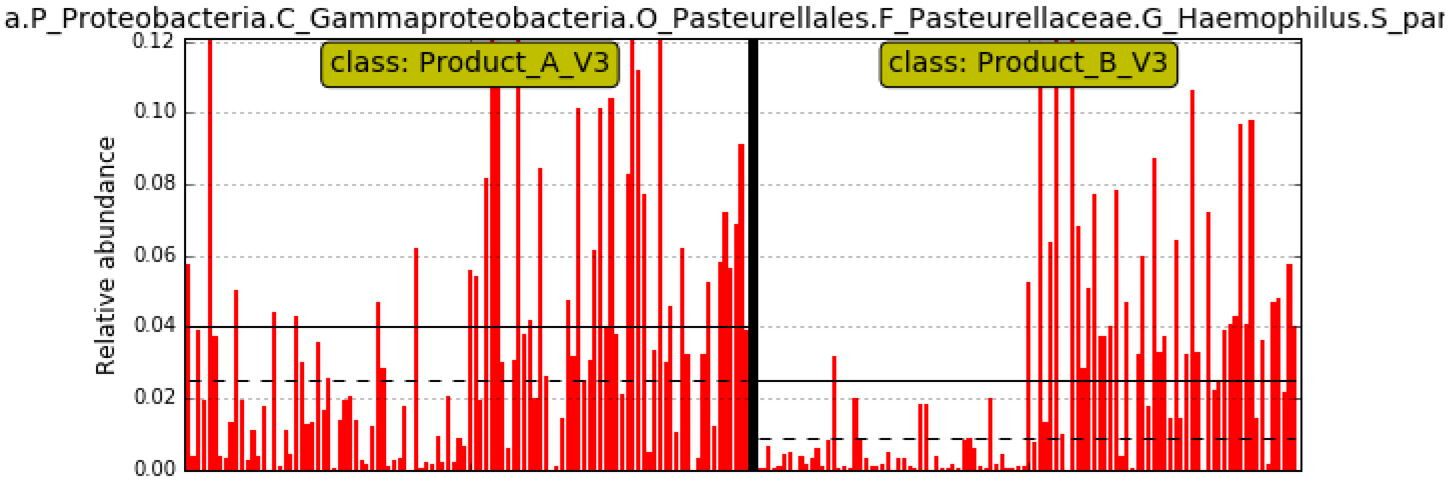

acteria.P_Firmicutes.C_Erysipelotrichia.O_Erysipelotrichales.F_Erysipelotrichaceae.G_Solobacterium.S_

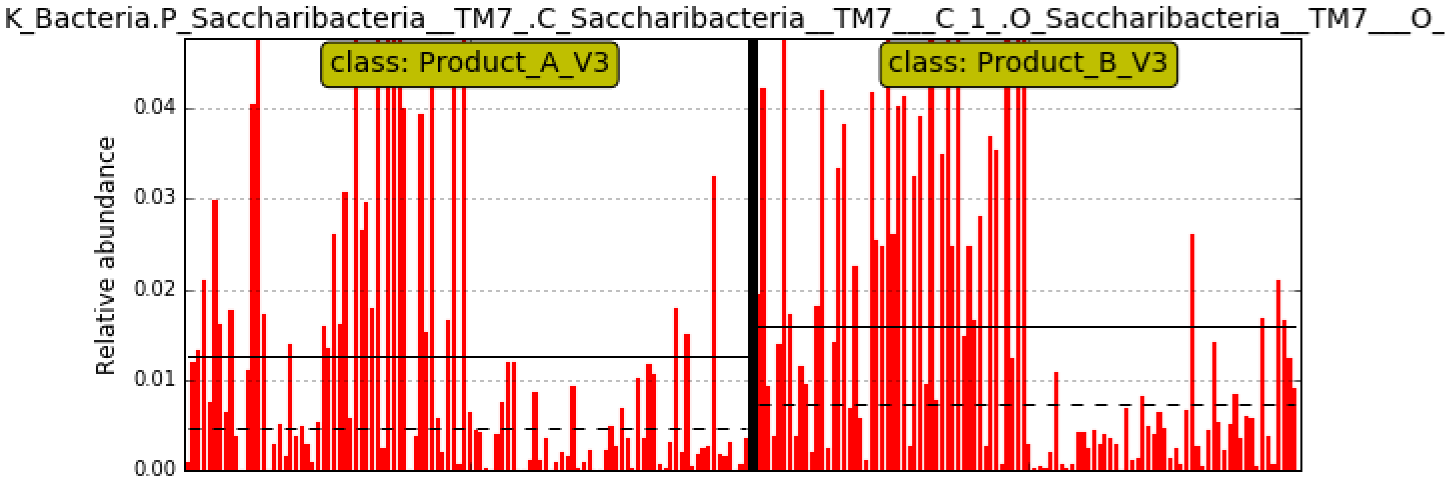

K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Kingella.S_orali


K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Neisseria
class: Product_A_V3
class: Product_B_V3
Relative abundance
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0.00


:eria.P_Proteobacteria.C_Epsilonproteobacteria.O_Campylobacterales.F_Campylobacteraceae.G_Campy
class: Product_A_V3
class: Product_B_V3
Relative abundance
0.030
0.025
0.020
0.015
0.010
0.005
0.000

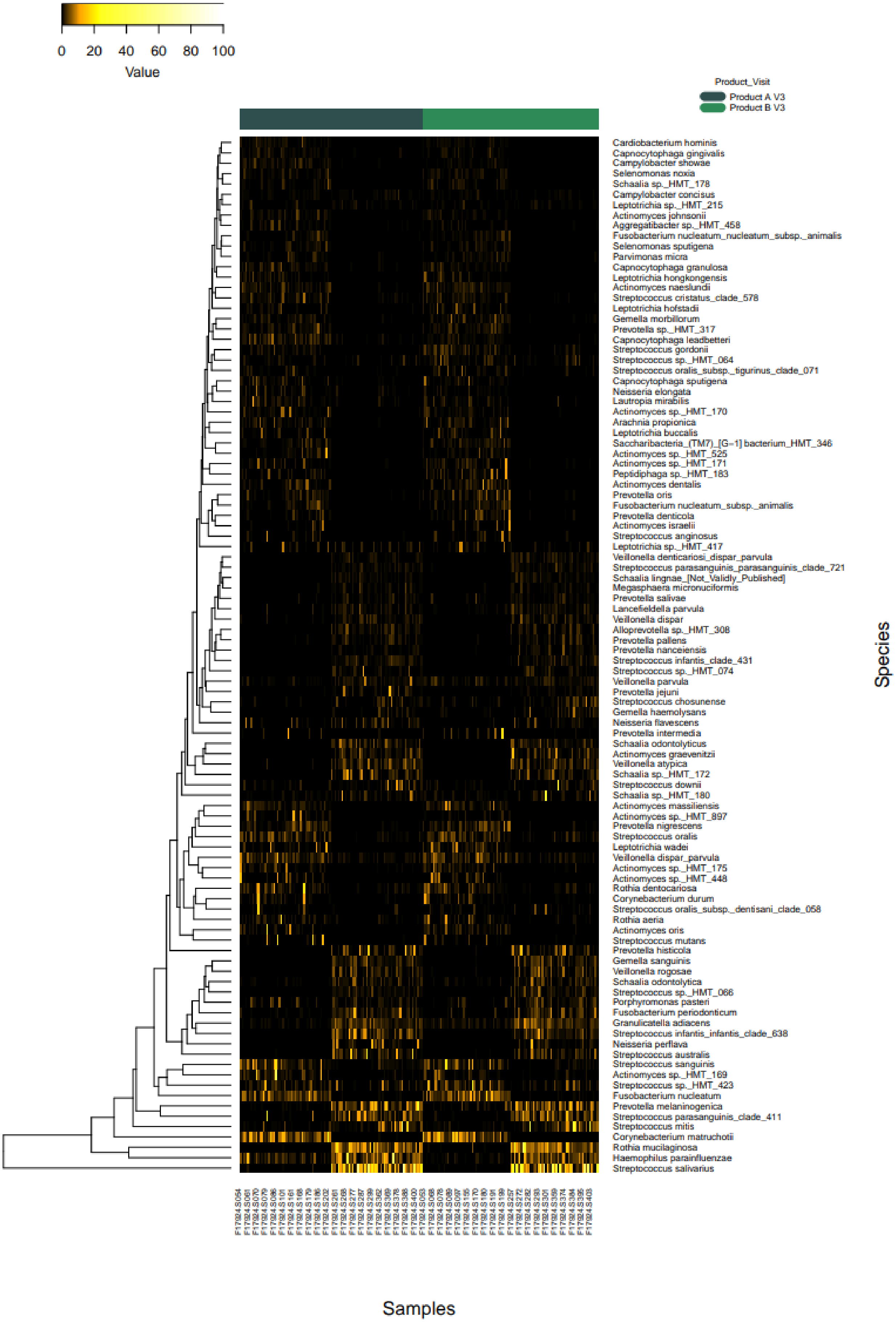

teria.P_Proteobacteria.C_Gammaproteobacteria.O_Cardiobacteriales.F_Cardiobacteriaceae.G_Cardioba
class: Product_A_V3
class: Product_B_V3
Relative abundance
0.020
0.015
0.010
0.005
0.000


a.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophilus.S_par


K_Bacteria.P_Saccharibacteria__TM7_.C_Saccharibacteria__TM7___C_1_.O_Saccharibacteria__TM7___O_

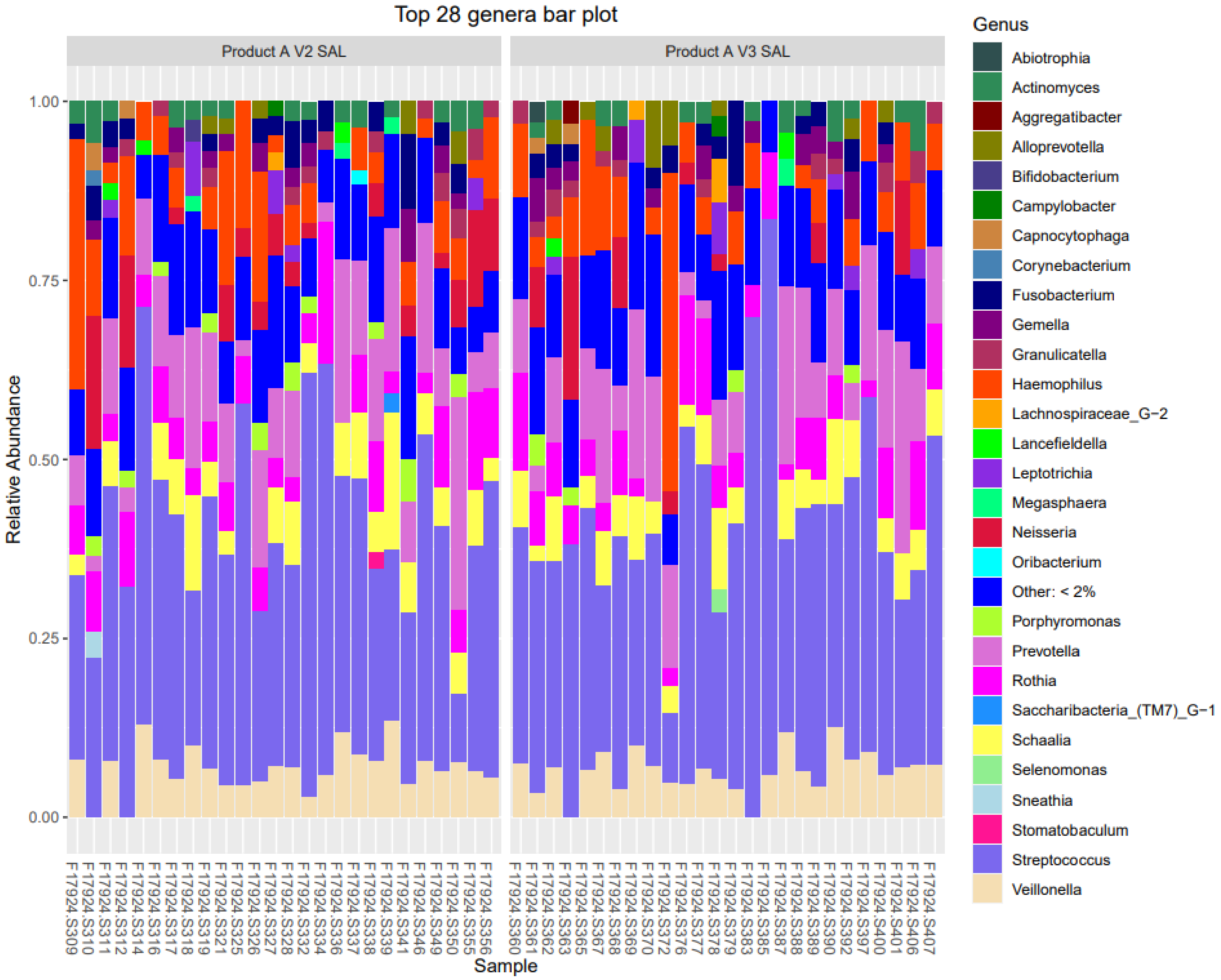
6) Heat maps


0
20
40
60
80
100
Value
Product_Visit
Product A V3
Product B V3
Campylobacter
Lachnoanaerobaculum
Cardiobacterium
Aggregatibacter
Lautropia
Arachnia
Saccharibacteria_(TM7)_[G-1]
Selenomonas
Porphyromonas
Catonella
Peptostreptococcaceae_[XI][G-9]
Ruminococcaceae_[G-1]
Lachnospiraceae_[G-3]
Bergeyella
Eikenella
Mogibacterium
Solobacterium
Peptostreptococcus
Dialister
Olsenella
Saccharibacteria_(TM7)_[G-5]
Tannerella
Treponema
Bacteroidales_[G-2]
Oribacterium
Stomatobaculum
Megasphaera
Lachnospiraceae_[G-2]
Kingella
Abiotrophia
Parvimonas
Lancefieldella
Bifidobacterium
Scardovia
Peptidiphaga
Granulicatella
Gemella
Alloprevotella
Neisseria
Veillonella
Schaalia
Haemophilus
Rothia
Leptotrichia
Capnocytophaga
Corynebacterium
Fusobacterium
Prevotella
Actinomyces
Streptococcus
Genus
Samples


0
20
40
60
80
100
Value
Product_Visit
Product A V3
Product B V3
Cardiobacterium hominis
Capnocytophaga gingivalis
Campylobacter showae
Selenomonas noxia
Schaalia sp._HMT_178
Campylobacter concisus
Leptotrichia sp._HMT_215
Actinomyces johnsonii
Aggregatibacter sp._HMT_458
Fusobacterium nucleatum_nucleatum_subsp._animalis
Selenomonas sputigena
Parvimonas micra
Capnocytophaga granulosa
Leptotrichia hongkongensis
Actinomyces naeslundii
Streptococcus cristatus_clade_578
Leptotrichia hofstadii
Gemella morbillorum
Prevotella sp._HMT_317
Capnocytophaga leadbetteri
Streptococcus gordonii
Streptococcus sp._HMT_064
Streptococcus oralis_subsp._tigurinus_clade_071
Capnocytophaga sputigena
Neisseria elongata
Lautropia mirabilis
Actinomyces sp._HMT_170
Arachnia propionica
Leptotrichia buccalis
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346
Actinomyces sp._HMT_525
Actinomyces sp._HMT_171
Peptidiphaga sp._HMT_183
Actinomyces dentalis
Prevotella oris
Fusobacterium nucleatum_subsp._animalis
Prevotella denticola
Actinomyces israelii
Streptococcus anginosus
Leptotrichia sp._HMT_417
Veillonella denticariosi_dispar_parvula
Streptococcus parasanguinis_parasanguinis_clade_721
Schaalia lingnae_[Not_Validly_Published]
Megasphaera micronuciformis
Prevotella salivae
Lancefieldella parvula
Veillonella dispar
Alloprevotella sp._HMT_308
Prevotella pallens
Prevotella nanceiensis
Streptococcus infantis_clade_431
Streptococcus sp._HMT_074
Veillonella parvula
Prevotella jejuni
Streptococcus chosunense
Gemella haemolysans
Neisseria flavescens
Prevotella intermedia
Schaalia odontolyticus
Actinomyces graevenitzii
Veillonella atypica
Schaalia sp._HMT_172
Streptococcus downii
Schaalia sp._HMT_180
Actinomyces massiliensis
Actinomyces sp._HMT_897
Prevotella nigrescens
Streptococcus oralis
Leptotrichia wadei
Veillonella dispar_parvula
Actinomyces sp._HMT_175
Actinomyces sp._HMT_448
Rothia dentocariosa
Corynebacterium durum
Streptococcus oralis_subsp._dentisani_clade_058
Rothia aeria
Actinomyces oris
Streptococcus mutans
Prevotella histicola
Gemella sanguinis
Veillonella rogosae
Schaalia odontolytica
Streptococcus sp._HMT_066
Porphyromonas pasteri
Fusobacterium periodonticum
Granulicatella adiacens
Streptococcus infantis_infantis_clade_638
Neisseria perflava
Streptococcus australis
Streptococcus sanguinis
Actinomyces sp._HMT_169
Streptococcus sp._HMT_423
Fusobacterium nucleatum
Prevotella melaninogenica
Streptococcus parasanguinis_clade_411
Streptococcus mitis
Corynebacterium matruchotii
Rothia mucilaginosa
Haemophilus parainfluenzae
Streptococcus salivarius
Species
F17924-S054
F17924-S061
F17924-S070
F17924-S079
F17924-S086
F17924-S101
F17924-S161
F17924-S168
F17924-S170
F17924-S186
F17924-S202
F17924-S261
F17924-S268
F17924-S277
F17924-S287
F17924-S289
F17924-S362
F17924-S369
F17924-S376
F17924-S388
F17924-S400
F17924-S053
F17924-S068
F17924-S078
F17924-S089
F17924-S097
F17924-S155
F17924-S170
F17924-S180
F17924-S191
F17924-S199
F17924-S257
F17924-S272
F17924-S282
F17924-S283
F17924-S301
F17924-S359
F17924-S374
F17924-S384
F17924-S395
F17924-S403
Samples

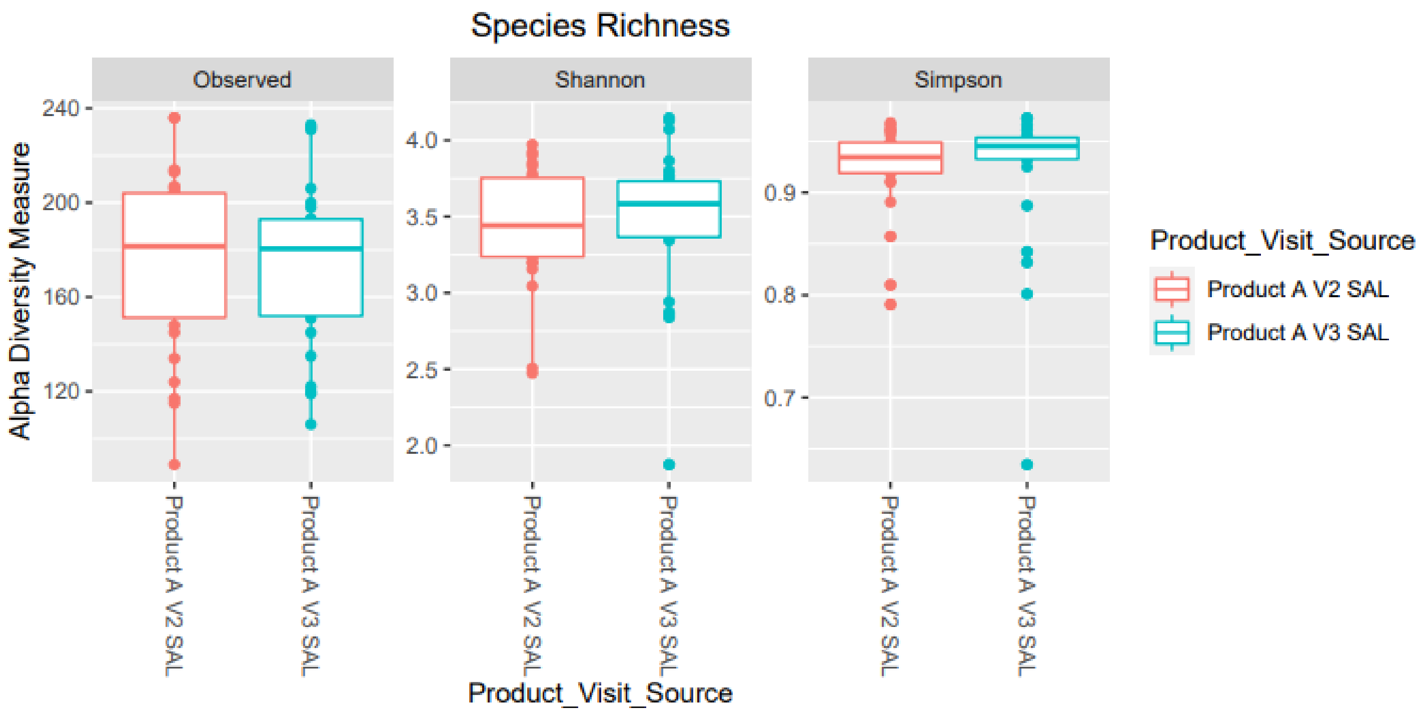
Comparison 5. Product A V2 SAL vs Product A V3 SAL

1) Taxonomy bar plots



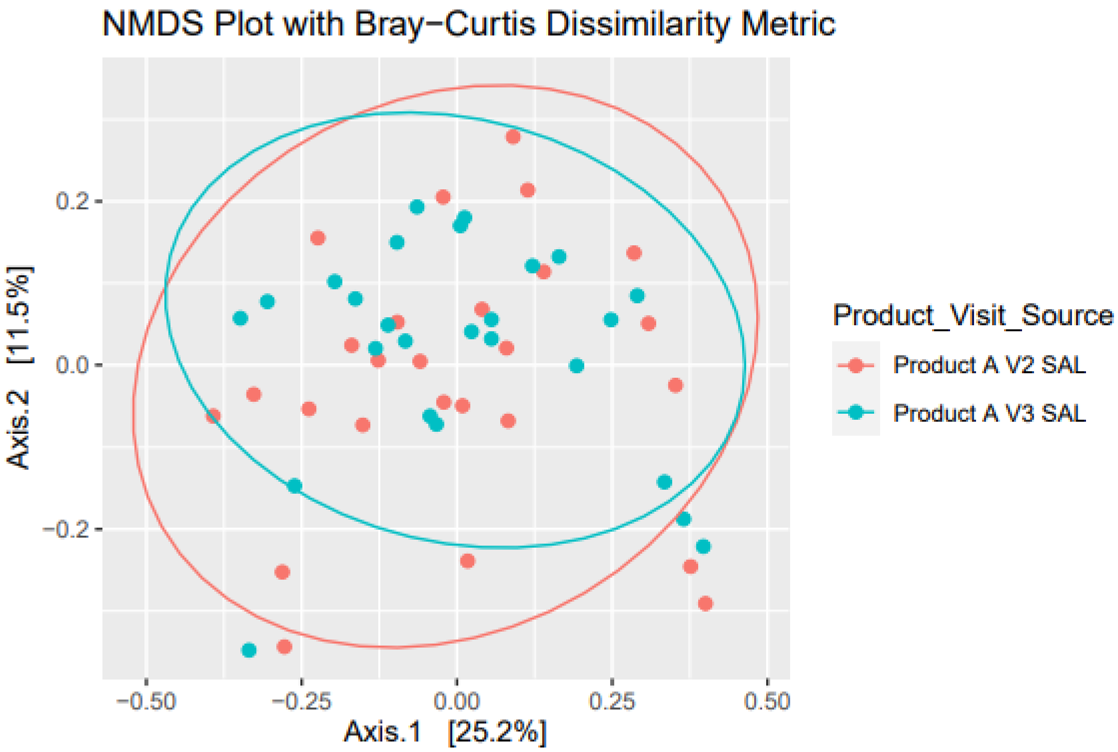
Difficult to see any major differences. However, expected taxa are present. Will see specific taxa in subsequent analyses.

2) Alpha diversity



Not Statistically significant

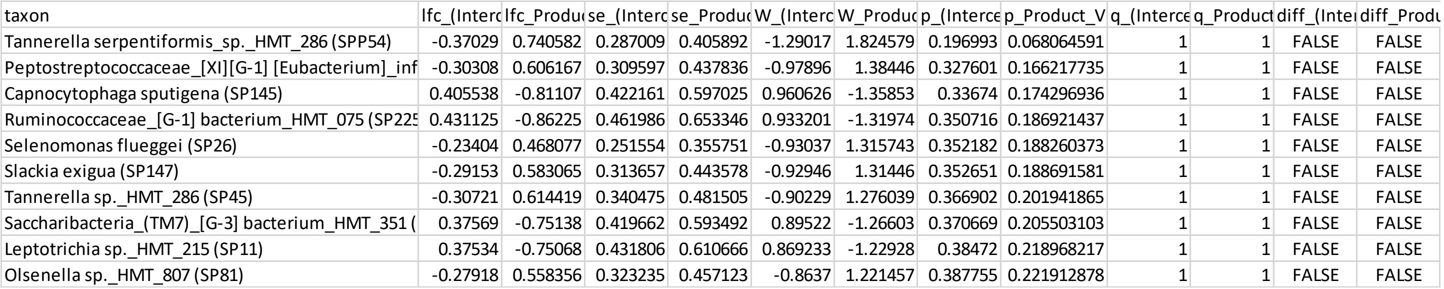
3) Beta diversity



Not Statistically significant

p=0.259

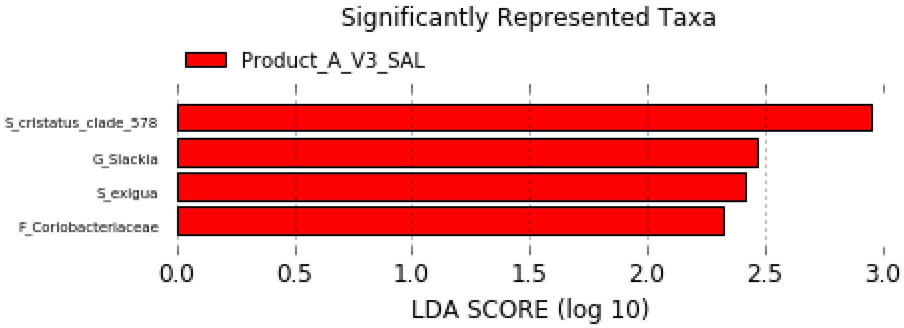
4) Differential abundance



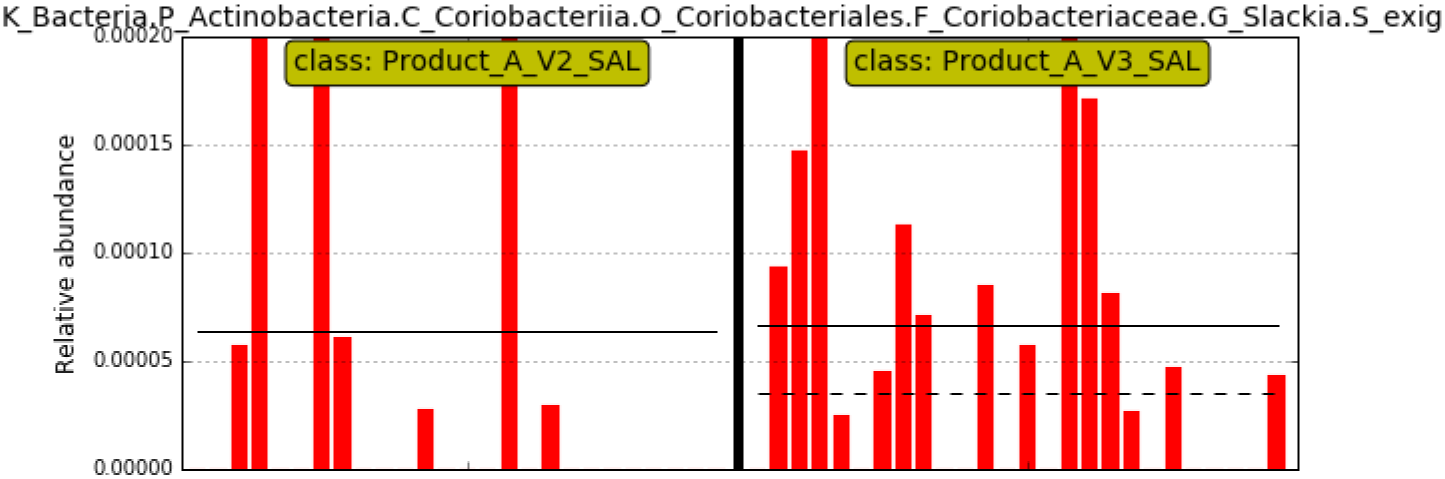
taxon	lfc_(Interc	lfc_Produ	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product_V	q_(Interce	q_Product	diff_(Inte	diff_Produ
Tannerella serpentiformis_sp._HMT_286 (SPP54)	-0.37029	0.740582	0.287009	0.405892	-1.29017	1.824579	0.196993	0.068064591	1	1	FALSE	FALSE
Peptostreptococcaceae_[XI][G-1] [Eubacterium]_inf	-0.30308	0.606167	0.309597	0.437836	-0.97896	1.38446	0.327601	0.166217735	1	1	FALSE	FALSE
Capnocytophaga sputigena (SP145)	0.405538	-0.81107	0.422161	0.597025	0.960626	-1.35853	0.33674	0.174296936	1	1	FALSE	FALSE
Ruminococcaceae_[G-1] bacterium_HMT_075 (SP225	0.431125	-0.86225	0.461986	0.653346	0.933201	-1.31974	0.350716	0.186921437	1	1	FALSE	FALSE
Selenomonas flueggei (SP26)	-0.23404	0.468077	0.251554	0.355751	-0.93037	1.315743	0.352182	0.188260373	1	1	FALSE	FALSE
Slackia exigua (SP147)	-0.29153	0.583065	0.313657	0.443578	-0.92946	1.31446	0.352651	0.188691581	1	1	FALSE	FALSE
Tannerella sp._HMT_286 (SP45)	-0.30721	0.614419	0.340475	0.481505	-0.90229	1.276039	0.366902	0.201941865	1	1	FALSE	FALSE
Saccharibacteria_(TM7)_[G-3] bacterium_HMT_351 (	0.37569	-0.75138	0.419662	0.593492	0.89522	-1.26603	0.370669	0.205503103	1	1	FALSE	FALSE
Leptotrichia sp._HMT_215 (SP11)	0.37534	-0.75068	0.431806	0.610666	0.869233	-1.22928	0.38472	0.218968217	1	1	FALSE	FALSE
Olsenella sp._HMT_807 (SP81)	-0.27918	0.558356	0.323235	0.457123	-0.8637	1.221457	0.387755	0.221912878	1	1	FALSE	FALSE

No statistically significant differences

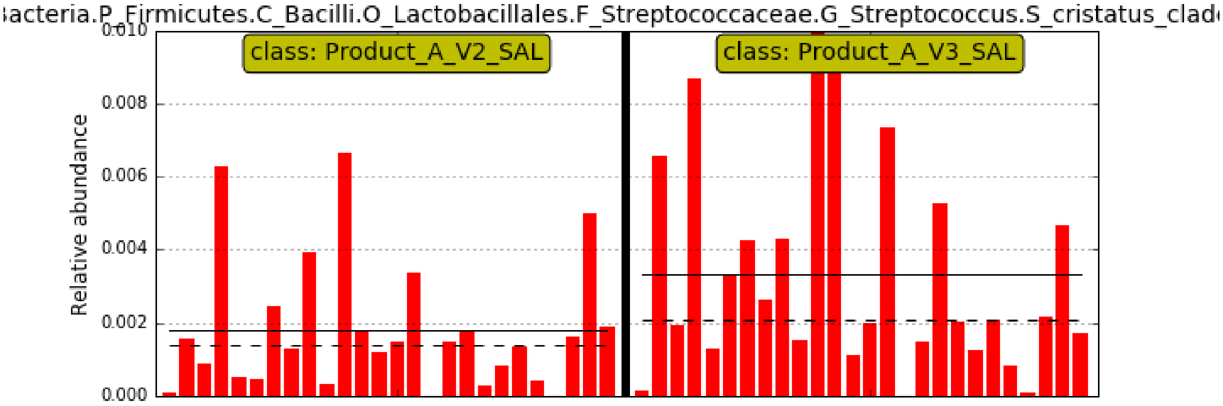
5) Lefse—only 2 species that differentiated—no clear differences—product A had little or no effect



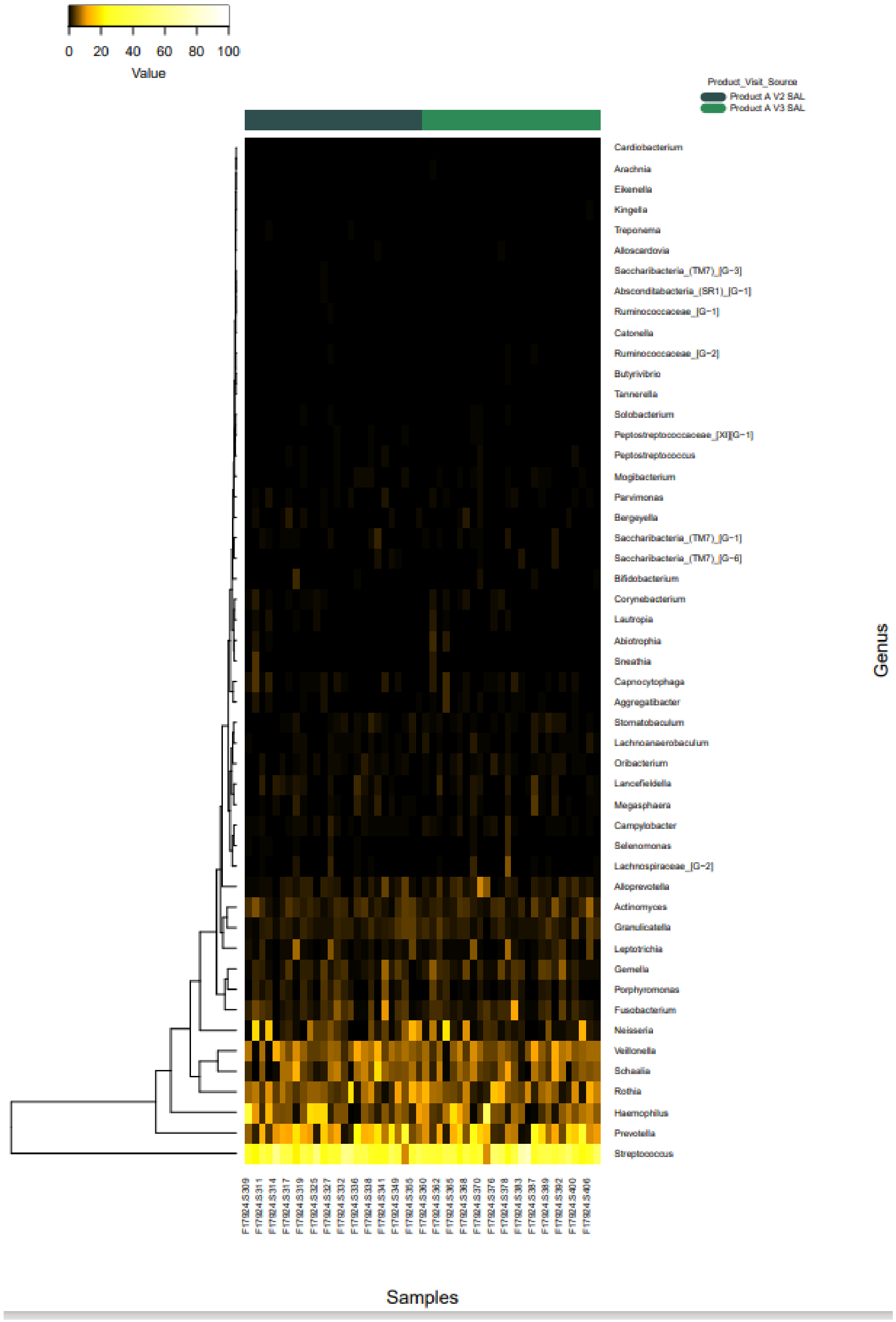
Differences can be better seen in the following graphs for individual taxa

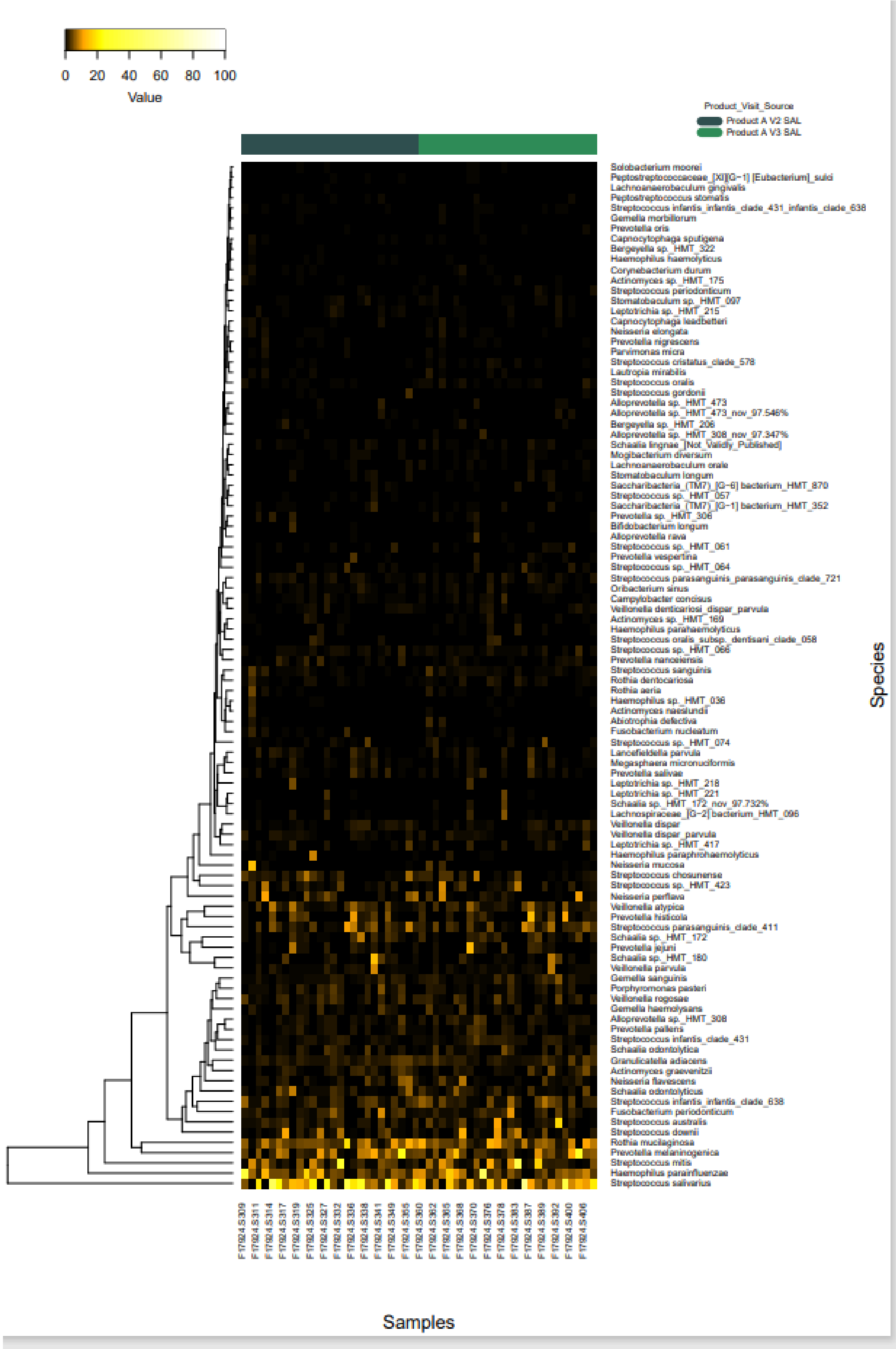


very low levels. Likely not biologically significant



6. Heat maps—difficult to see, visualization of the differences at the species and genus levels is shown below.

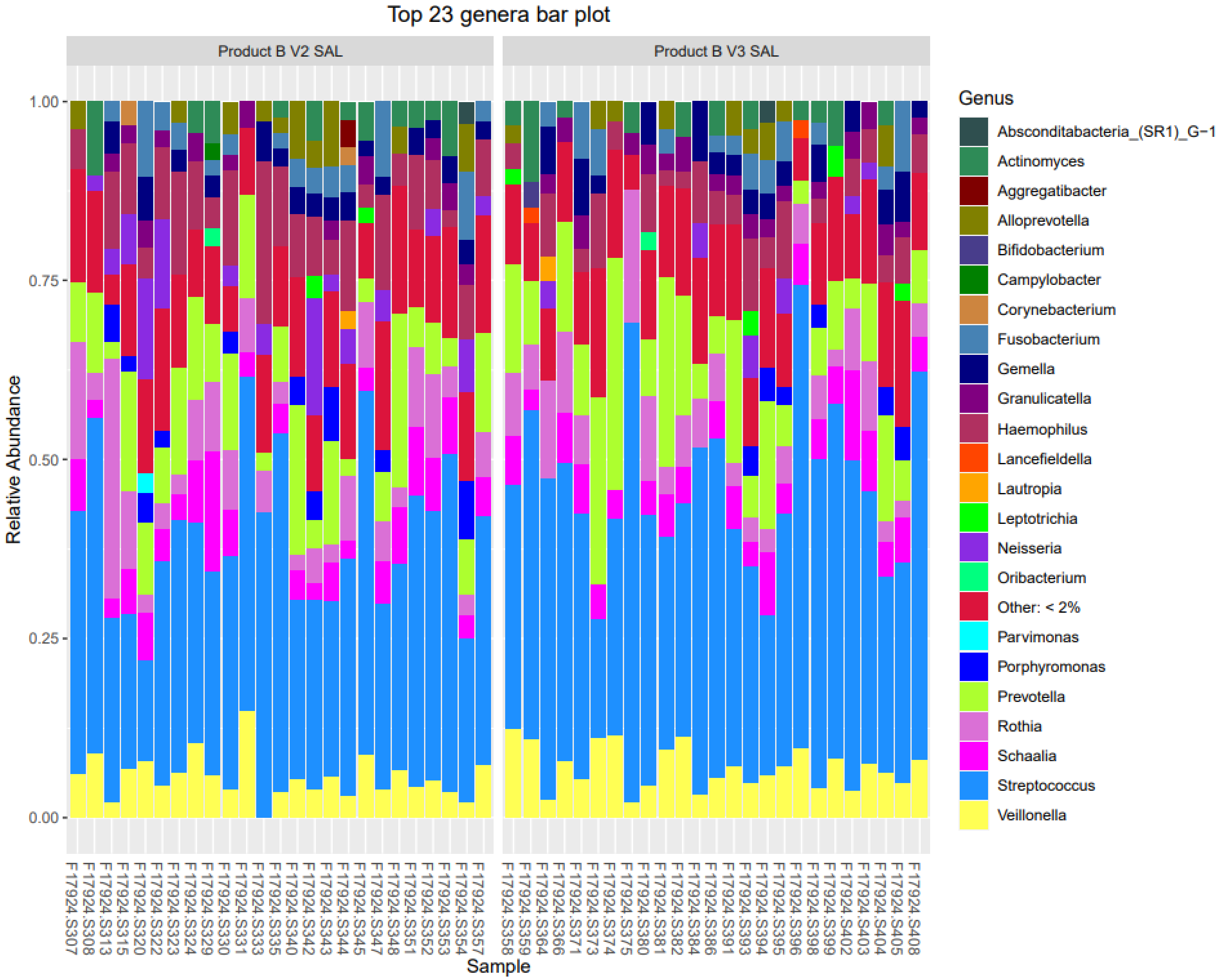



0
20
40
60
80
100
Value
Product_Visit_Source
Product A V2 SAL
Product A V3 SAL
Solobacterium moorei
Peptostreptococcaceae_[XI][G−1] [Eubacterium]_sulci
Lachnoanaerobaculum gingivalis
Peptostreptococcus stomatis
Streptococcus infantis_infantis_clade_431_infantis_clade_638
Gemella morbillorum
Prevotella oris
Capnocytophaga sputigena
Bergeyella sp._HMT_322
Haemophilus haemolyticus
Corynebacterium durum
Actinomyces sp._HMT_175
Streptococcus periodonticum
Stomatobaculum sp._HMT_097
Leptotrichia sp._HMT_215
Capnocytophaga leadbetteri
Neisseria elongata
Prevotella nigrescens
Parvimonas micra
Streptococcus cristatus_clade_578
Lautropia mirabilis
Streptococcus oralis
Streptococcus gordonii
Alloprevotella sp._HMT_473
Alloprevotella sp._HMT_473_nov_97.546%
Bergeyella sp._HMT_206
Alloprevotella sp._HMT_308_nov_97.347%
Schaalia lingnae_[Not_Validly_Published]
Mogibacterium diversum
Lachnoanaerobaculum orale
Stomatobaculum longum
Saccharibacteria_(TM7)_[G−6] bacterium_HMT_870
Streptococcus sp._HMT_057
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_352
Prevotella sp._HMT_306
Bifidobacterium longum
Alloprevotella rava
Streptococcus sp._HMT_061
Prevotella vespertina
Streptococcus sp._HMT_064
Streptococcus parasanguinis_parasanguinis_clade_721
Oribacterium sinus
Campylobacter concisus
Veillonella denticariosi_dispar_parvula
Actinomyces sp._HMT_169
Haemophilus parahaemolyticus
Streptococcus oralis_subsp._dentisani_clade_058
Streptococcus sp._HMT_066
Prevotella nanceiensis
Streptococcus sanguinis
Rothia dentocariosa
Rothia aeria
Haemophilus sp._HMT_036
Actinomyces naeslundii
Abiotrophia defectiva
Fusobacterium nucleatum
Streptococcus sp._HMT_074
Lancefieldella parvula
Megasphaera micronuciformis
Prevotella salivae
Leptotrichia sp._HMT_218
Leptotrichia sp._HMT_221
Schaalia sp._HMT_172_nov_97.732%
Lachnospiraceae_[G−2] bacterium_HMT_096
Veillonella dispar
Veillonella dispar_parvula
Leptotrichia sp._HMT_417
Haemophilus paraphrohaemolyticus
Neisseria mucosa
Streptococcus cheounense
Streptococcus sp._HMT_423
Neisseria perflava
Veillonella atypica
Prevotella histicola
Streptococcus parasanguinis_clade_411
Schaalia sp._HMT_172
Prevotella jejuni
Schaalia sp._HMT_180
Veillonella parvula
Gemella sanguinis
Porphyromonas pasteri
Veillonella rogosae
Gemella haemolysans
Alloprevotella sp._HMT_308
Prevotella pallens
Streptococcus infantis_clade_431
Schaalia odontolytica
Granulicatella adiacens
Actinomyces graevenitzii
Neisseria flavescens
Schaalia odontolyticus
Streptococcus infantis_infantis_clade_638
Fusobacterium periodonticum
Streptococcus australis
Streptococcus downii
Rothia mucilaginosa
Prevotella melaninogenica
Streptococcus mitis
Haemophilus parainfluenzae
Streptococcus salivarius
Species
F17924.S309
F17924.S311
F17924.S314
F17924.S317
F17924.S319
F17924.S325
F17924.S327
F17924.S332
F17924.S336
F17924.S338
F17924.S341
F17924.S349
F17924.S355
F17924.S360
F17924.S362
F17924.S365
F17924.S368
F17924.S370
F17924.S376
F17924.S378
F17924.S383
F17924.S387
F17924.S389
F17924.S392
F17924.S400
F17924.S406
Samples

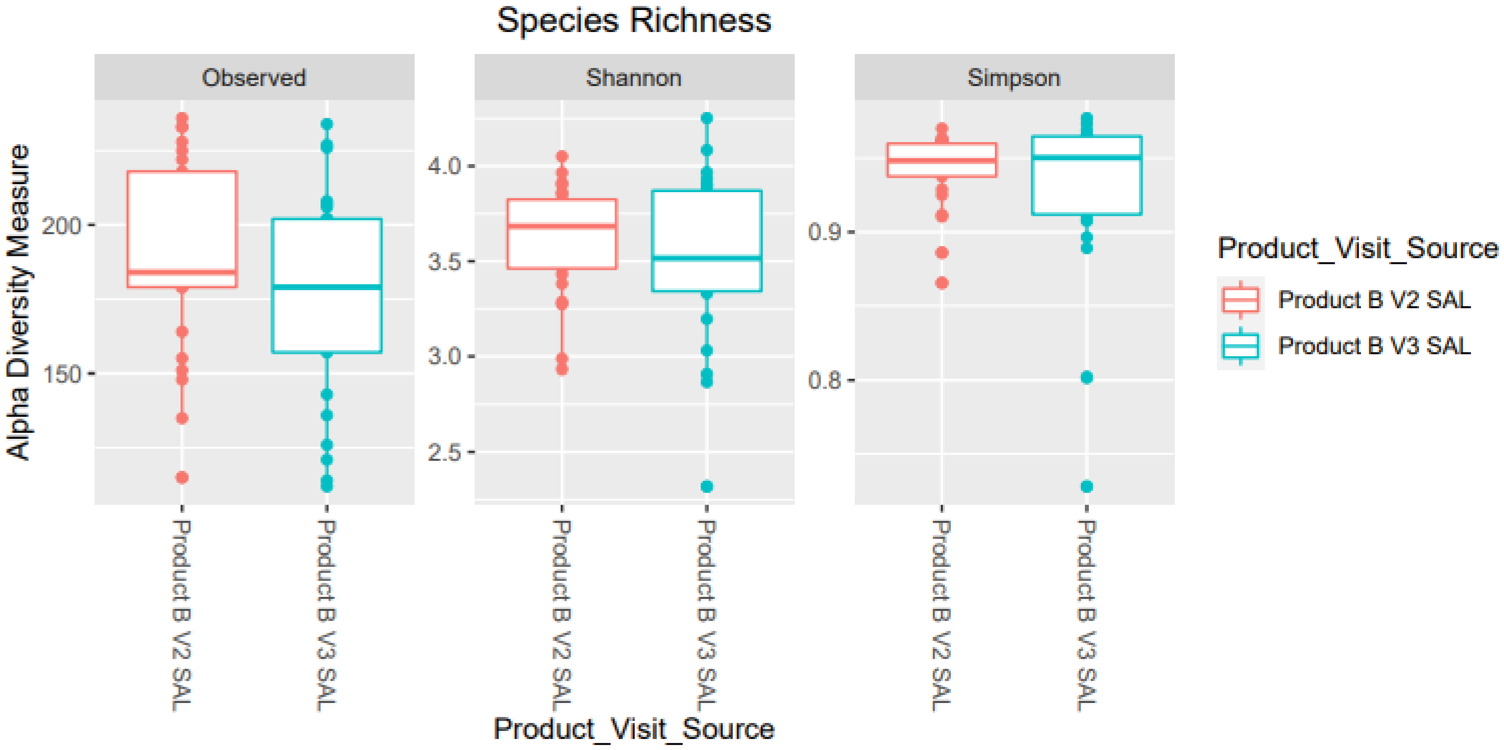
.

Comparison 6. Product B V2 vs Product B V3

1) Taxonomy barplots

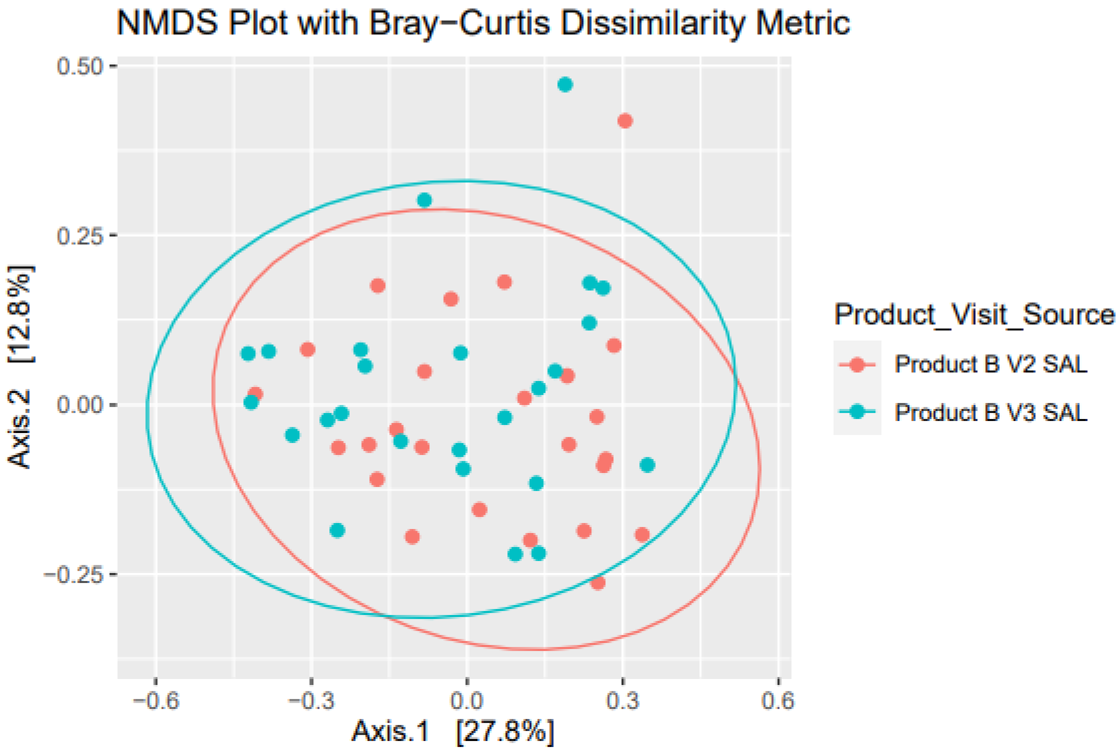


2) Alpha diversity



No significant differences

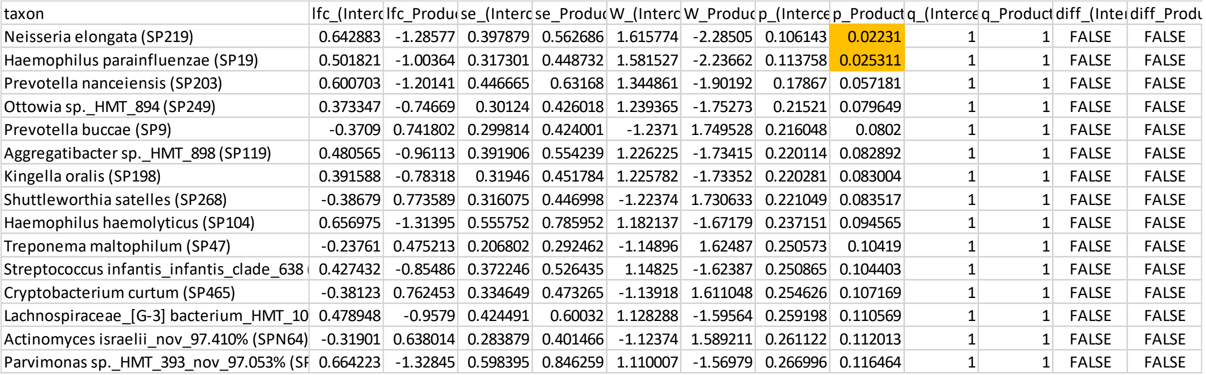
3) Beta diversity



Significant difference

Group 1	Group 2	Sample size	Permutations	pseudo-F	p-value
Product B V2 SAL	Product B V3 SAL	50	999	2.081426	0.027

4) Differential abundance

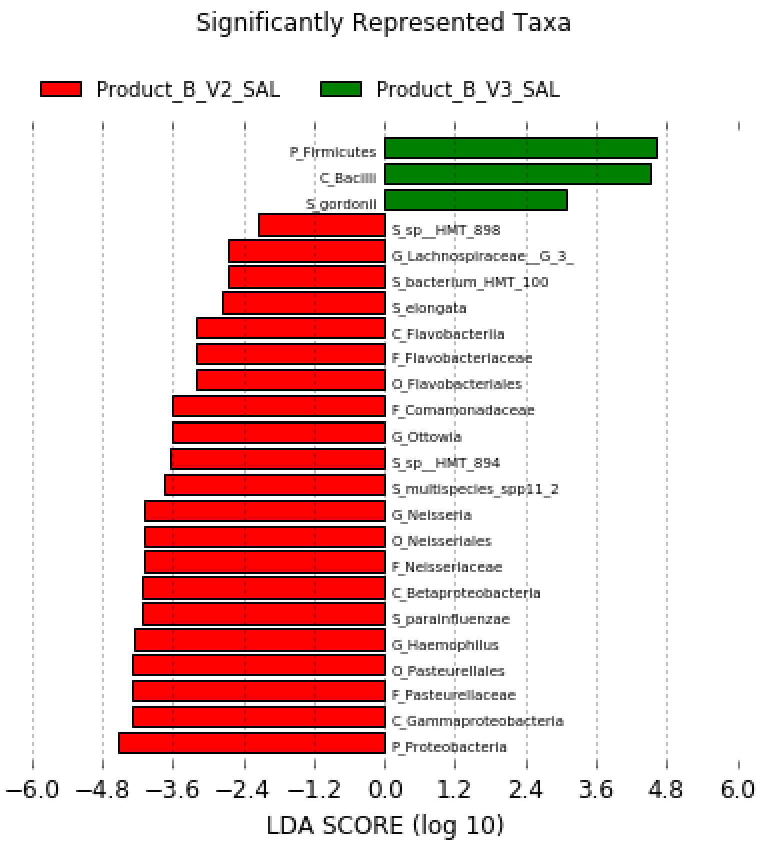


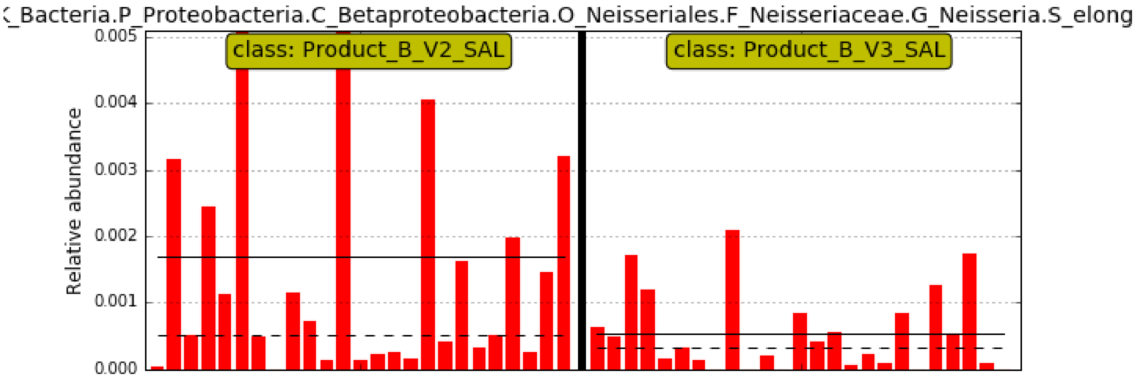
taxon	lfc_(Interc	lfc_Produ	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inte	diff_Produ
Neisseria elongata (SP219)	0.642883	-1.28577	0.397879	0.562686	1.615774	-2.28505	0.106143	0.02231	1	1	FALSE	FALSE
Haemophilus parainfluenzae (SP19)	0.501821	-1.00364	0.317301	0.448732	1.581527	-2.23662	0.113758	0.025311	1	1	FALSE	FALSE
Prevotella nanceiensis (SP203)	0.600703	-1.20141	0.446665	0.63168	1.344861	-1.90192	0.17867	0.057181	1	1	FALSE	FALSE
Ottowia sp._HMT_894 (SP249)	0.373347	-0.74669	0.30124	0.426018	1.239365	-1.75273	0.21521	0.079649	1	1	FALSE	FALSE
Prevotella buccae (SP9)	-0.3709	0.741802	0.299814	0.424001	-1.2371	1.749528	0.216048	0.0802	1	1	FALSE	FALSE
Aggregatibacter sp._HMT_898 (SP119)	0.480565	-0.96113	0.391906	0.554239	1.226225	-1.73415	0.220114	0.082892	1	1	FALSE	FALSE
Kingella oralis (SP198)	0.391588	-0.78318	0.31946	0.451784	1.225782	-1.73352	0.220281	0.083004	1	1	FALSE	FALSE
Shuttleworthia satelles (SP268)	-0.38679	0.773589	0.316075	0.446998	-1.22374	1.730633	0.221049	0.083517	1	1	FALSE	FALSE
Haemophilus haemolyticus (SP104)	0.656975	-1.31395	0.555752	0.785952	1.182137	-1.67179	0.237151	0.094565	1	1	FALSE	FALSE
Treponema maltophilum (SP47)	-0.23761	0.475213	0.206802	0.292462	-1.14896	1.62487	0.250573	0.10419	1	1	FALSE	FALSE
Streptococcus infantis_infantis_clade_638	0.427432	-0.85486	0.372246	0.526435	1.14825	-1.62387	0.250865	0.104403	1	1	FALSE	FALSE
Cryptobacterium curtum (SP465)	-0.38123	0.762453	0.334649	0.473265	-1.13918	1.611048	0.254626	0.107169	1	1	FALSE	FALSE
Lachnospiraceae_[G-3] bacterium_HMT_10	0.478948	-0.9579	0.424491	0.60032	1.128288	-1.59564	0.259198	0.110569	1	1	FALSE	FALSE
Actinomyces israelii_nov_97.410% (SPN64)	-0.31901	0.638014	0.283879	0.401466	-1.12374	1.589211	0.261122	0.112013	1	1	FALSE	FALSE
Parvimonas sp._HMT_393_nov_97.053% (S	0.664223	-1.32845	0.598395	0.846259	1.110007	-1.56979	0.266996	0.116464	1	1	FALSE	FALSE

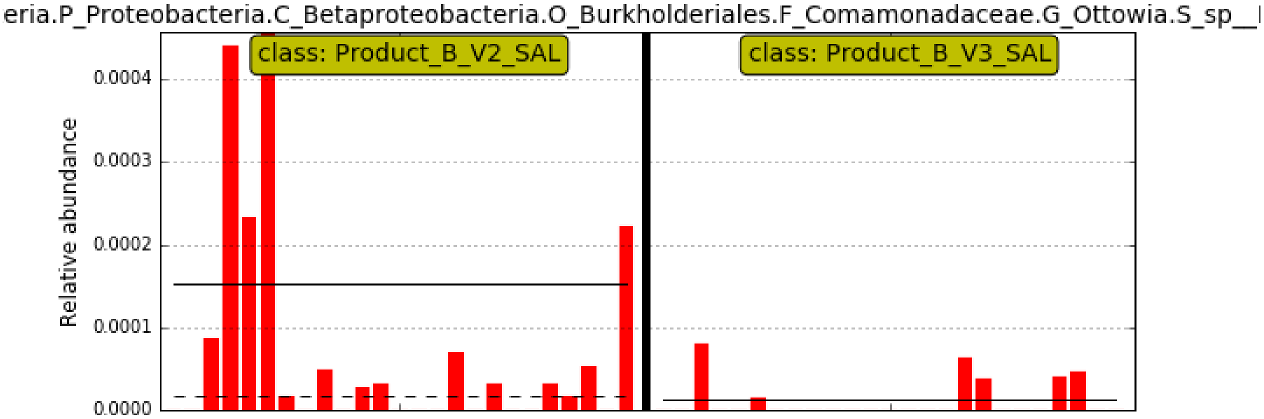
16)

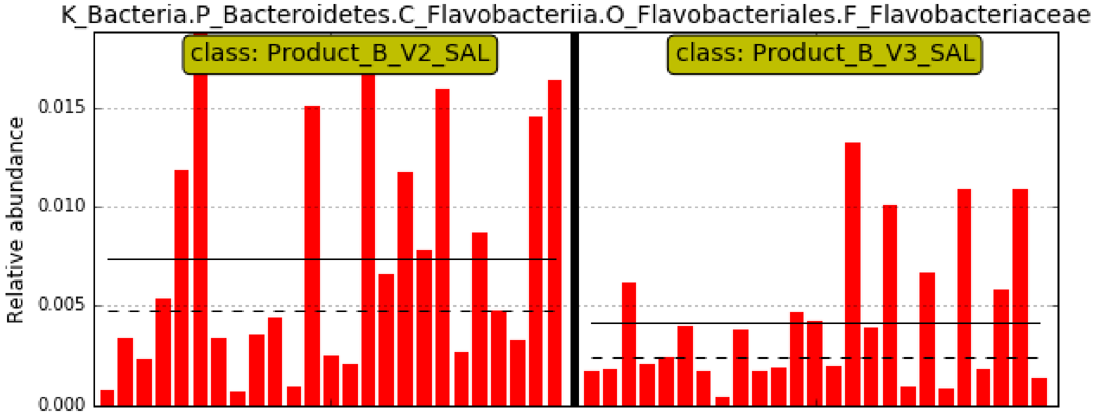
Not significantly different, but a trend. P value is no longer significant after multiple comparisons.

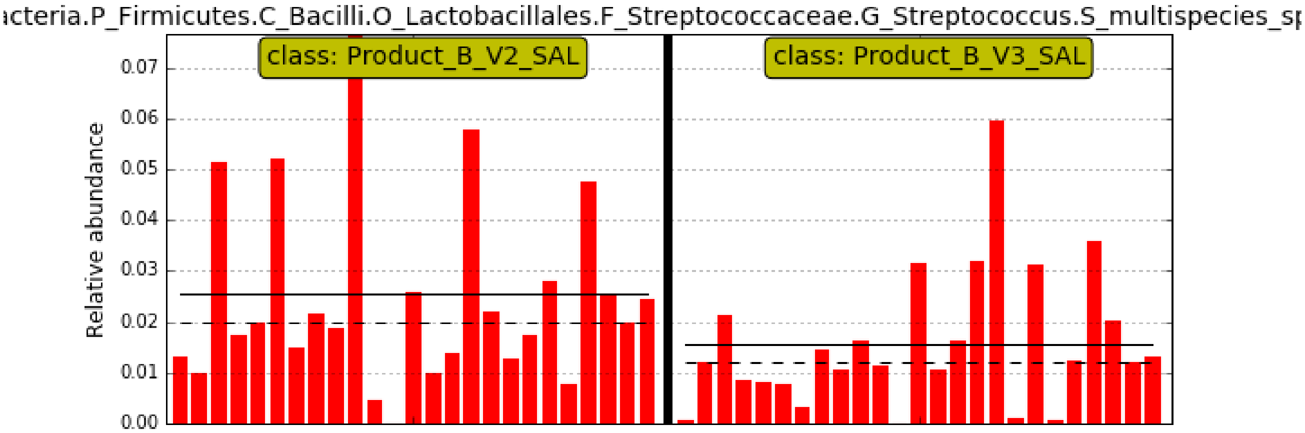
5) LefSe

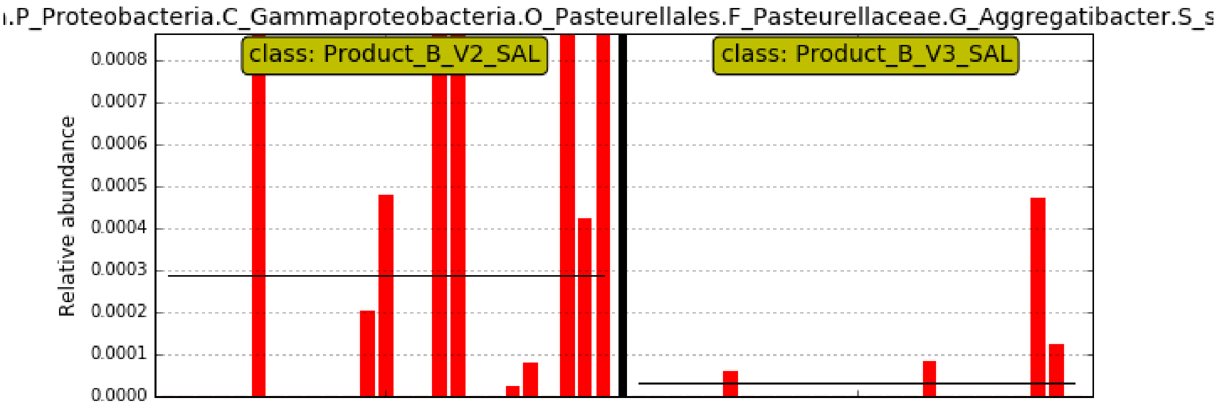

Significantly Represented Taxa
Product_B_V2_SAL
Product_B_V3_SAL
P_Firmicutes
C_Bacilli
S_gordonii
S_sp__HMT_898
G_Lachnospiraceae__G_3_
S_bacterium_HMT_100
S_elongata
C_Flavobacteriia
F_Flavobacteriaceae
O_Flavobacteriales
F_Comamonadaceae
G_Ottowia
S_sp__HMT_894
S_multispecies_spp11_2
G_Neisseria
O_Neisseriales
F_Neisseriaceae
C_Betaproteobacteria
S_parainfluenzae
G_Haemophilus
O_Pasteurellales
F_Pasteurellaceae
C_Gammaproteobacteria
P_Proteobacteria
−6.0
−4.8
−3.6
−2.4
−1.2
0.0
1.2
2.4
3.6
4.8
6.0
LDA SCORE (log 10)

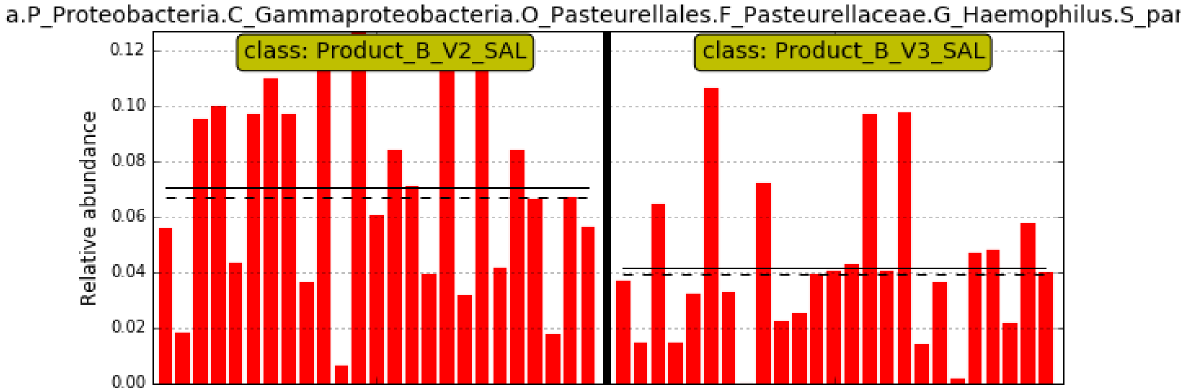

‹_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Neisseria.S_elong
class: Product_B_V2_SAL
class: Product_B_V3_SAL
Relative abundance
0.005
0.004
0.003
0.002
0.001
0.000

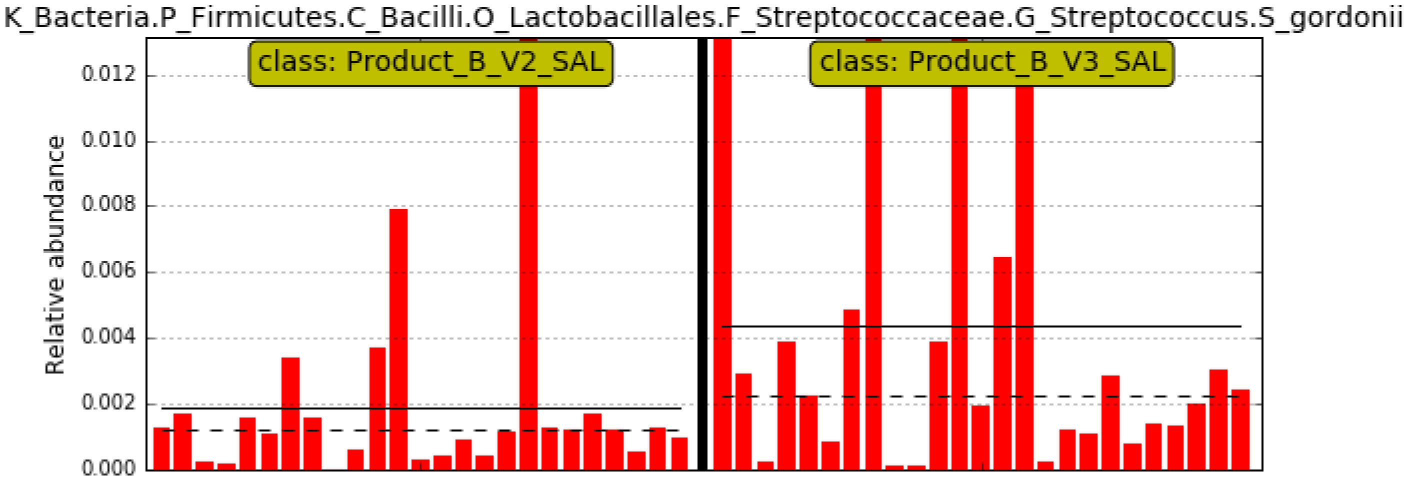

eria.P_Proteobacteria.C_Betaproteobacteria.O_Burkholderiales.F_Comamonadaceae.G_Ottowia.S_sp__
class: Product_B_V2_SAL
class: Product_B_V3_SAL
Relative abundance
0.0004
0.0003
0.0002
0.0001
0.0000


K_Bacteria.P_Bacteroidetes.C_Flavobacteriia.O_Flavobacteriales.F_Flavobacteriaceae
class: Product_B_V2_SAL
class: Product_B_V3_SAL
Relative abundance
0.015
0.010
0.005
0.000

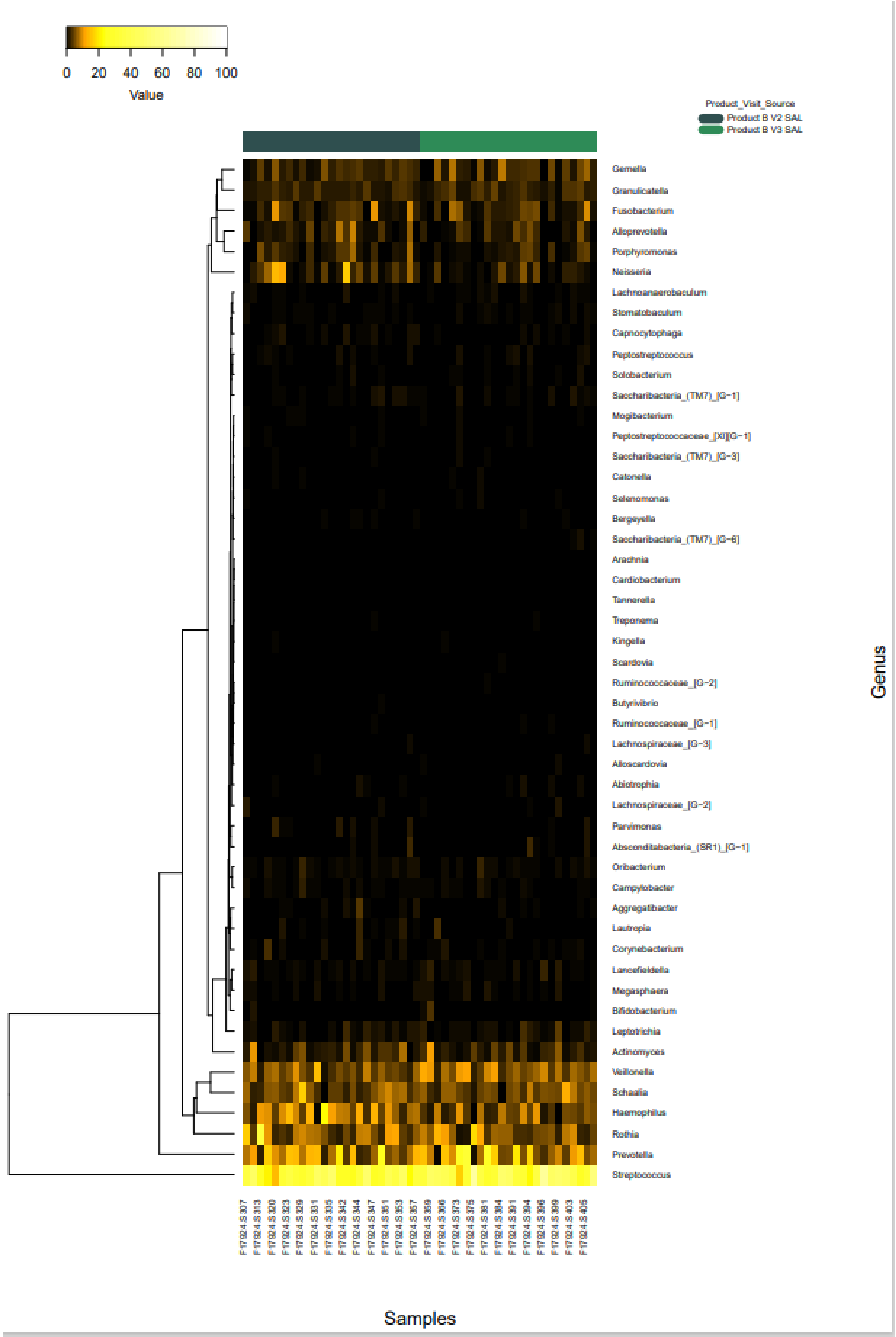

ıcteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_multispecies_s
class: Product_B_V2_SAL
class: Product_B_V3_SAL
Relative abundance
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0.00


ı.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Aggregatibacter.S_s


a.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophilus.S_par


K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_gordonii

6) Heat maps


0
20
40
60
80
100
Value
Product_Visit_Source
Product B V2 SAL
Product B V3 SAL
Gemella
Granulicatella
Fusobacterium
Alloprevotella
Porphyromonas
Neisseria
Lachnoanaerobaculum
Stomatobaculum
Capnocytophaga
Peptostreptococcus
Solobacterium
Saccharibacteria_(TM7)_[G-1]
Mogibacterium
Peptostreptococcaceae_[XI][G-1]
Saccharibacteria_(TM7)_[G-3]
Catonella
Selenomonas
Bergeyella
Saccharibacteria_(TM7)_[G-6]
Arachnia
Cardiobacterium
Tannerella
Treponema
Kingella
Scardovia
Ruminococcaceae_[G-2]
Butyrivibrio
Ruminococcaceae_[G-1]
Lachnospiraceae_[G-3]
Alloscardovia
Abiotrophia
Lachnospiraceae_[G-2]
Parvimonas
Absconditabacteria_(SR1)_[G-1]
Oribacterium
Campylobacter
Aggregatibacter
Lautropia
Corynebacterium
Lancefieldella
Megasphaera
Bifidobacterium
Leptotrichia
Actinomyces
Veillonella
Schaalia
Haemophilus
Rothia
Prevotella
Streptococcus
Genus
F17924.S307
F17924.S313
F17924.S320
F17924.S323
F17924.S329
F17924.S331
F17924.S335
F17924.S342
F17924.S344
F17924.S347
F17924.S351
F17924.S353
F17924.S357
F17924.S359
F17924.S366
F17924.S373
F17924.S375
F17924.S381
F17924.S384
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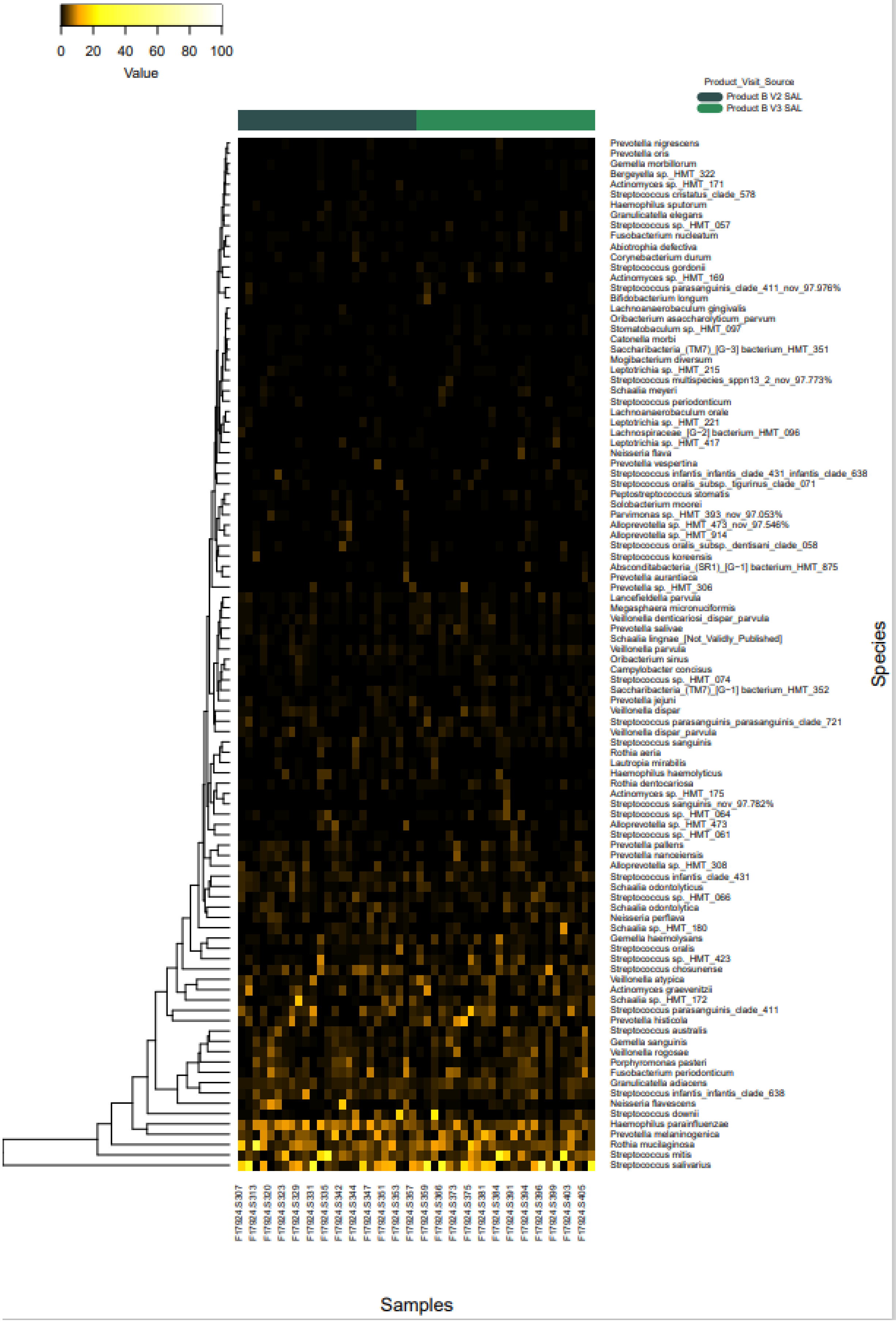
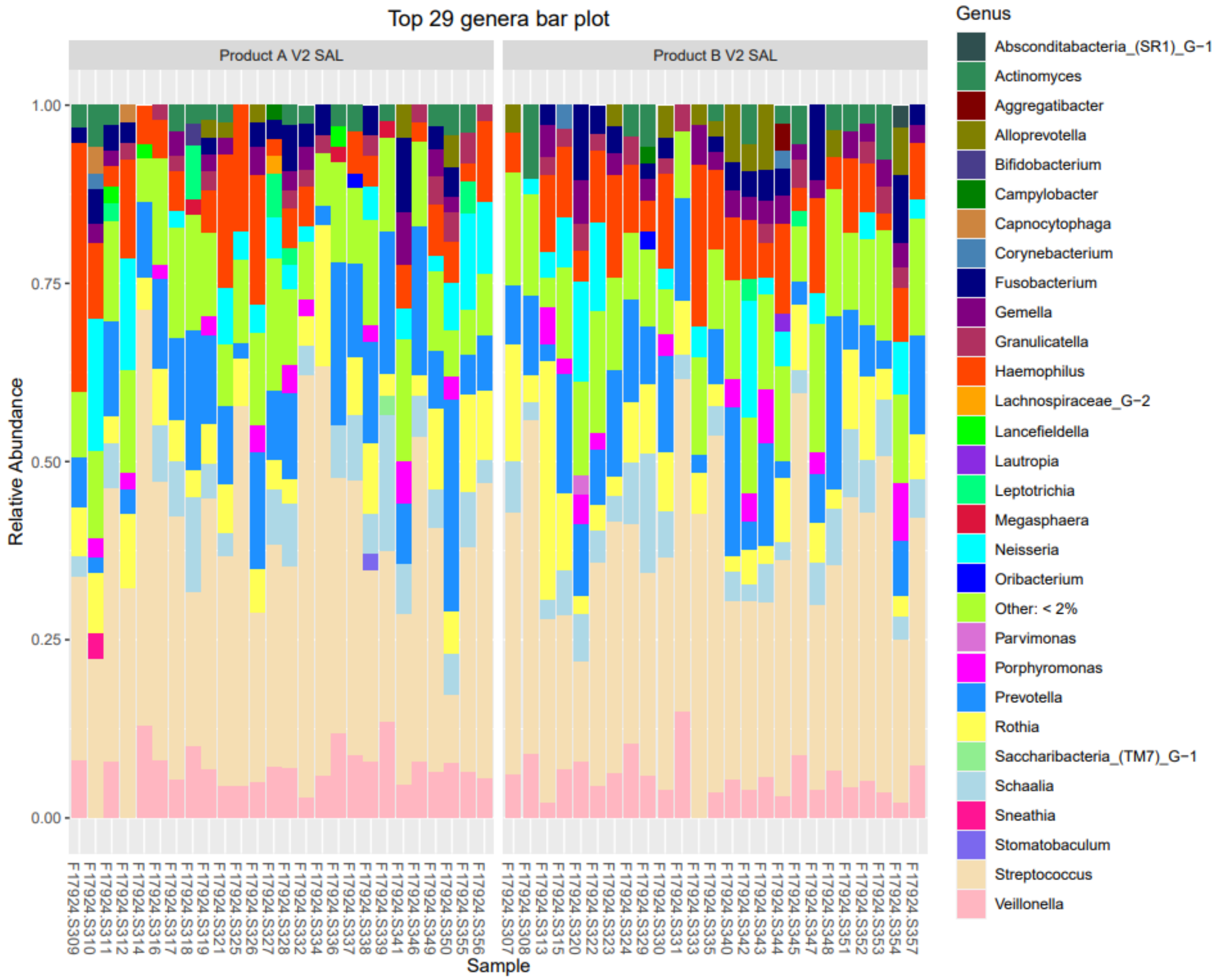
F17924.S394
F17924.S396
F17924.S399
F17924.S403
F17924.S405
Samples


0
20
40
60
80
100
Value
Product_Visit_Source
Product B V2 SAL
Product B V3 SAL
Prevotella nigrescens
Prevotella oris
Gemella morbillorum
Bergeyella sp._HMT_322
Actinomyces sp._HMT_171
Streptococcus cristatus_clade_578
Haemophilus sputorum
Granulicatella elegans
Streptococcus sp._HMT_057
Fusobacterium nucleatum
Abiotrophia defectiva
Corynebacterium durum
Streptococcus gordonii
Actinomyces sp._HMT_169
Streptococcus parasanguinis_clade_411_nov_97.976%
Bifidobacterium longum
Lachnoanaerobaculum gingivalis
Oribacterium asaccharolyticum_parvum
Stomatobaculum sp._HMT_097
Catonella morbi
Saccharibacteria_(TM7)_[G-3] bacterium_HMT_351
Mogibacterium diversum
Leptotrichia sp._HMT_215
Streptococcus multispecies_sppn13_2_nov_97.773%
Schaalia meyeri
Streptococcus periodonticum
Lachnoanaerobaculum orale
Leptotrichia sp._HMT_221
Lachnospiraceae_[G-2] bacterium_HMT_096
Leptotrichia sp._HMT_417
Neisseria flava
Prevotella vespertina
Streptococcus infantis_infantis_clade_431_infantis_clade_638
Streptococcus oralis_subsp._tigurinus_clade_071
Peptostreptococcus stomatis
Solobacterium moorei
Parvimonas sp._HMT_393_nov_97.053%
Alloprevotella sp._HMT_473_nov_97.546%
Alloprevotella sp._HMT_914
Streptococcus oralis_subsp._dentisani_clade_058
Streptococcus koreensis
Absconditabacteria_(SR1)_[G-1] bacterium_HMT_875
Prevotella aurantiaca
Prevotella sp._HMT_306
Lancefieldella parvula
Megasphaera micronuciformis
Veillonella denticariosi_dispar_parvula
Prevotella salivae
Schaalia lingnae_[Not_Validly_Published]
Veillonella parvula
Oribacterium sinus
Campylobacter concisus
Streptococcus sp._HMT_074
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_352
Prevotella jejuni
Veillonella dispar
Streptococcus parasanguinis_parasanguinis_clade_721
Veillonella dispar_parvula
Streptococcus sanguinis
Rothia aeria
Lautropia mirabilis
Haemophilus haemolyticus
Rothia dentocariosa
Actinomyces sp._HMT_175
Streptococcus sanguinis_nov_97.782%
Streptococcus sp._HMT_064
Alloprevotella sp._HMT_473
Streptococcus sp._HMT_061
Prevotella pallens
Prevotella nanceiensis
Alloprevotella sp._HMT_308
Streptococcus infantis_clade_431
Schaalia odontolyticus
Streptococcus sp._HMT_066
Schaalia odontolytica
Neisseria perflava
Schaalia sp._HMT_180
Gemella haemolysans
Streptococcus oralis
Streptococcus sp._HMT_423
Streptococcus cheonanense
Veillonella atypica
Actinomyces graevenitzii
Schaalia sp._HMT_172
Streptococcus parasanguinis_clade_411
Prevotella histicola
Streptococcus australis
Gemella sanguinis
Veillonella rogosae
Porphyromonas pasteri
Fusobacterium periodonticum
Granulicatella adiacens
Streptococcus infantis_infantis_clade_638
Neisseria flavescens
Streptococcus downii
Haemophilus parainfluenzae
Prevotella melaninogenica
Rothia mucilaginosa
Streptococcus mitis
Streptococcus salivarius
Species
F17924.S307
F17924.S313
F17924.S320
F17924.S323
F17924.S329
F17924.S331
F17924.S335
F17924.S342
F17924.S344
F17924.S347
F17924.S351
F17924.S353
F17924.S357
F17924.S359
F17924.S366
F17924.S373
F17924.S375
F17924.S381
F17924.S384
F17924.S391
F17924.S394
F17924.S396
F17924.S399
F17924.S403
F17924.S405
Samples

Comparison 7. Product A V2 SAL vs Product B V2 SAL

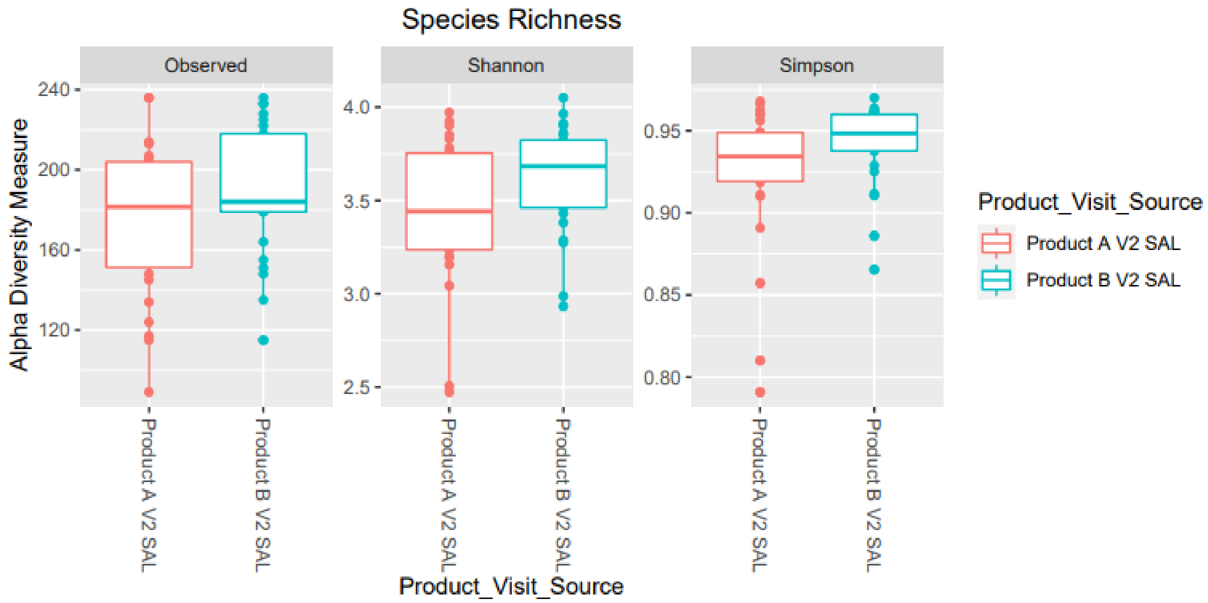
1) Taxonomy Barplots



17)

2) Alpha diversity

18)



19)

20)

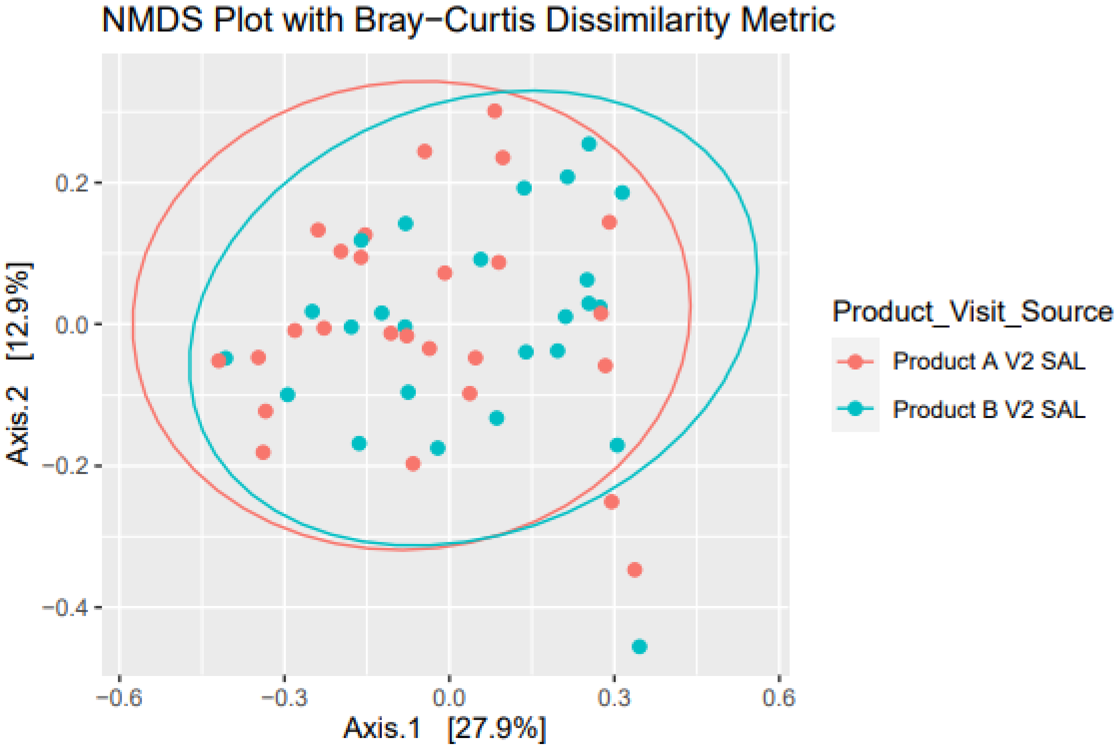
No significant differences in observed and Shannon

Simpson

No Significant difference but close to significance

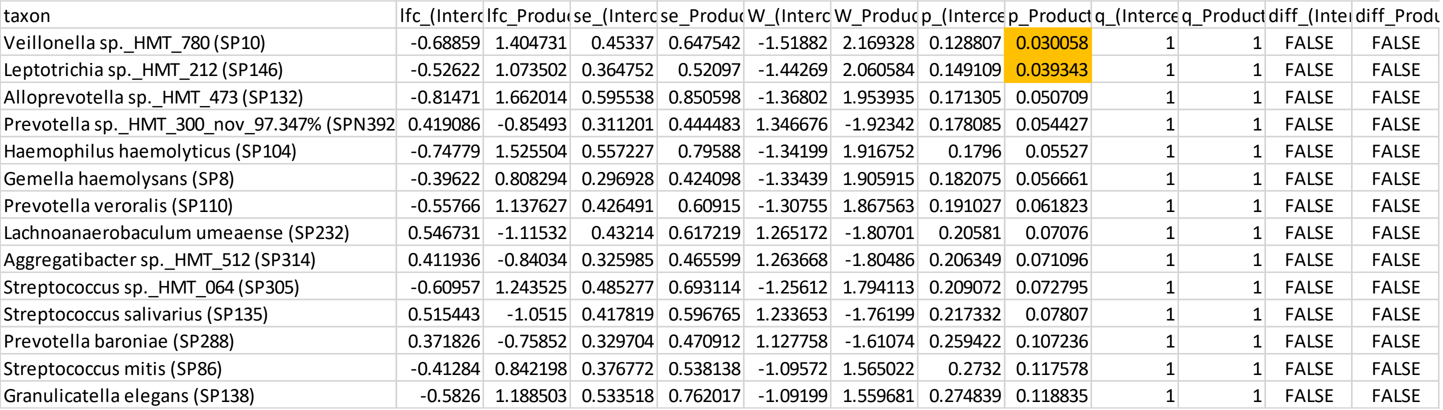
Group 1	Group 2	H	p-value	q-value
Product A V2 SAL (n=26)	Product B V2 SAL (n=25)	3.479645	0.062128	0.062128

3) Beta diversity



No Statistically significant differences

4) Differential abundance



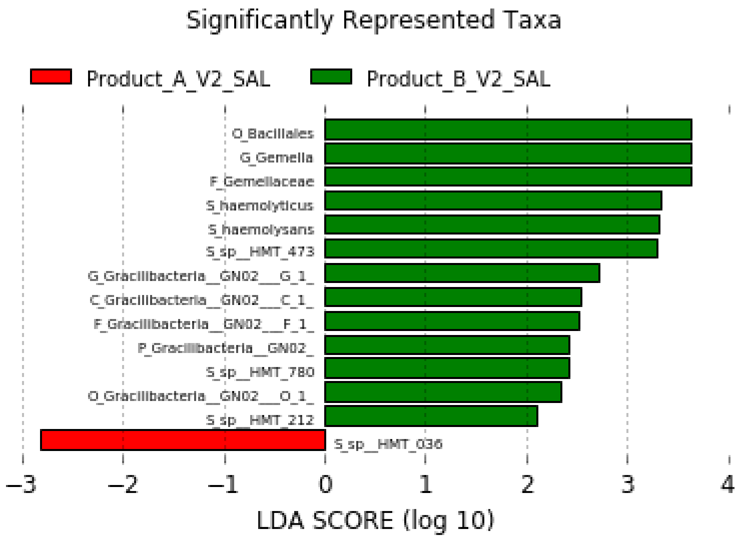
taxon	lfc_(Interc	lfc_Produc	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inter	diff_Produ
Veillonella sp._HMT_780 (SP10)	-0.68859	1.404731	0.45337	0.647542	-1.51882	2.169328	0.128807	0.030058	1	1	FALSE	FALSE
Leptotrichia sp._HMT_212 (SP146)	-0.52622	1.073502	0.364752	0.52097	-1.44269	2.060584	0.149109	0.039343	1	1	FALSE	FALSE
Alloprevotella sp._HMT_473 (SP132)	-0.81471	1.662014	0.595538	0.850598	-1.36802	1.953935	0.171305	0.050709	1	1	FALSE	FALSE
Prevotella sp._HMT_300_nov_97.347% (SPN392	0.419086	-0.85493	0.311201	0.444483	1.346676	-1.92342	0.178085	0.054427	1	1	FALSE	FALSE
Haemophilus haemolyticus (SP104)	-0.74779	1.525504	0.557227	0.79588	-1.34199	1.916752	0.1796	0.05527	1	1	FALSE	FALSE
Gemella haemolysans (SP8)	-0.39622	0.808294	0.296928	0.424098	-1.33439	1.905915	0.182075	0.056661	1	1	FALSE	FALSE
Prevotella veroralis (SP110)	-0.55766	1.137627	0.426491	0.60915	-1.30755	1.867563	0.191027	0.061823	1	1	FALSE	FALSE
Lachnoanaerobaculum umeaense (SP232)	0.546731	-1.11532	0.43214	0.617219	1.265172	-1.80701	0.20581	0.07076	1	1	FALSE	FALSE
Aggregatibacter sp._HMT_512 (SP314)	0.411936	-0.84034	0.325985	0.465599	1.263668	-1.80486	0.206349	0.071096	1	1	FALSE	FALSE
Streptococcus sp._HMT_064 (SP305)	-0.60957	1.243525	0.485277	0.693114	-1.25612	1.794113	0.209072	0.072795	1	1	FALSE	FALSE
Streptococcus salivarius (SP135)	0.515443	-1.0515	0.417819	0.596765	1.233653	-1.76199	0.217332	0.07807	1	1	FALSE	FALSE
Prevotella baroniae (SP288)	0.371826	-0.75852	0.329704	0.470912	1.127758	-1.61074	0.259422	0.107236	1	1	FALSE	FALSE
Streptococcus mitis (SP86)	-0.41284	0.842198	0.376772	0.538138	-1.09572	1.565022	0.2732	0.117578	1	1	FALSE	FALSE
Granulicatella elegans (SP138)	-0.5826	1.188503	0.533518	0.762017	-1.09199	1.559681	0.274839	0.118835	1	1	FALSE	FALSE

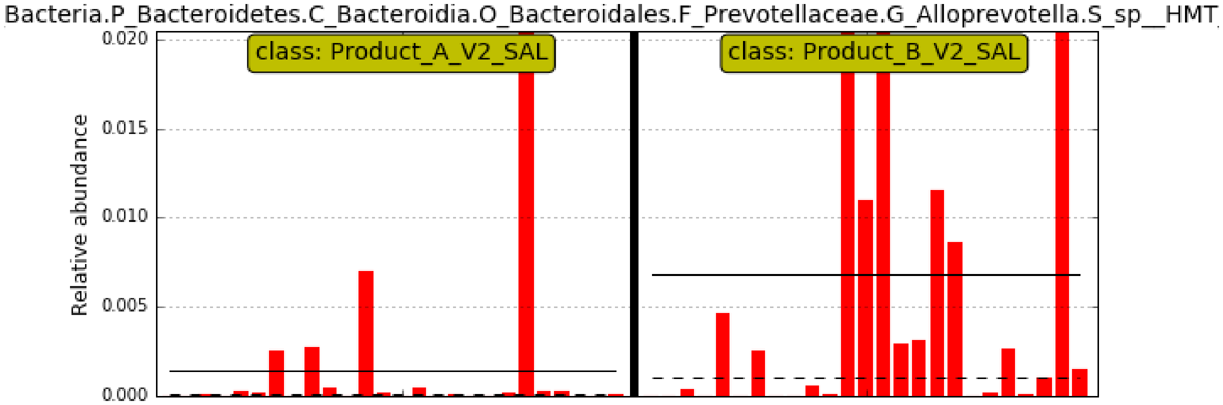
No statistically significant differences. Similar results with Lefse

Lefse will show better.

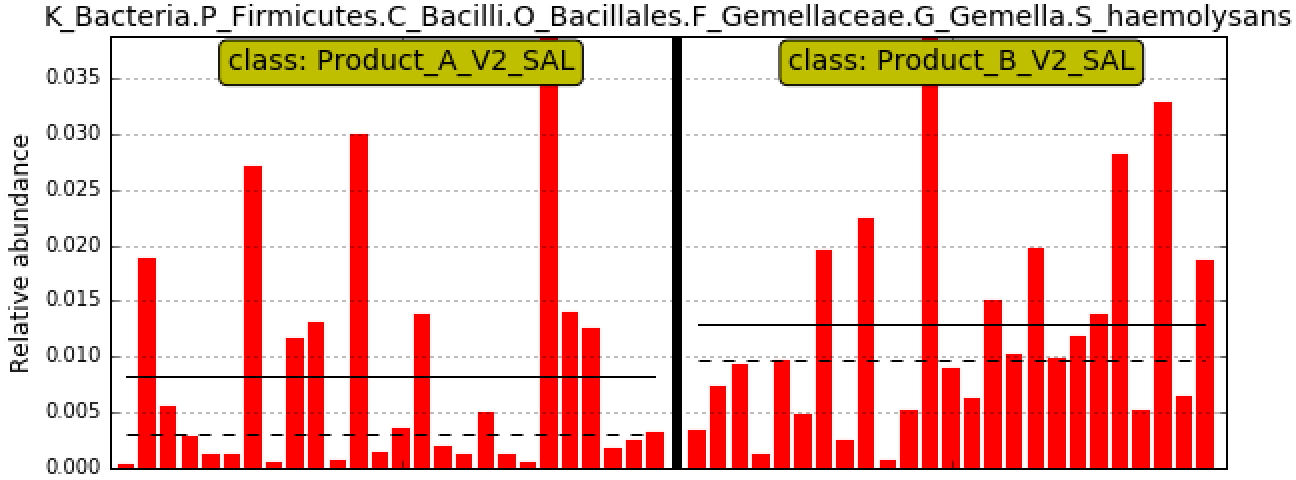
5) LefSe -Individual plots will show better

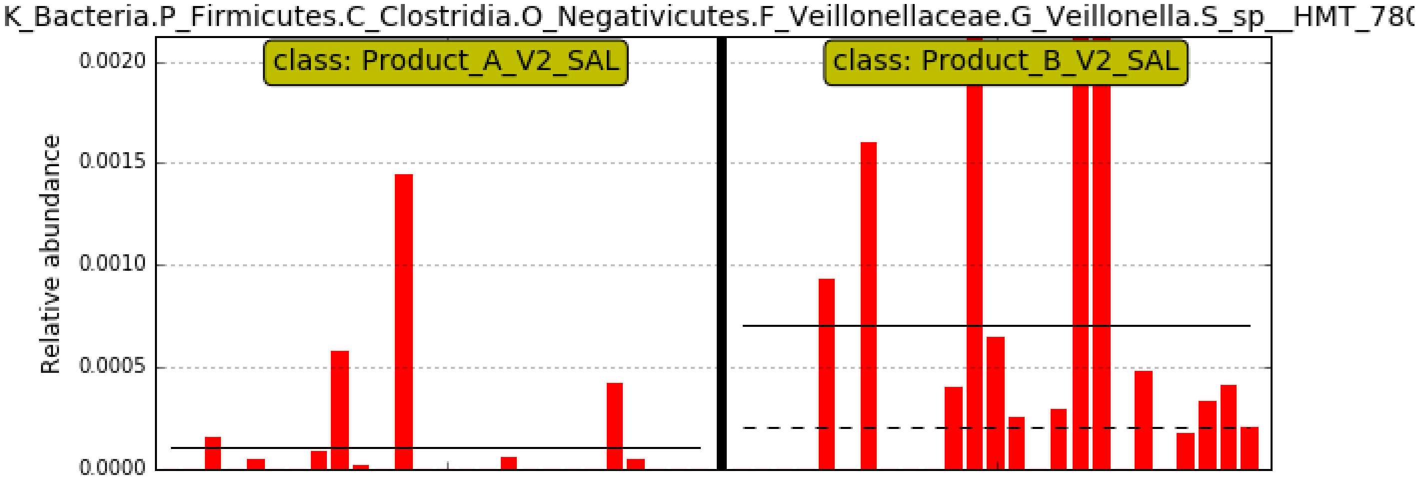
Overall, only minor differences

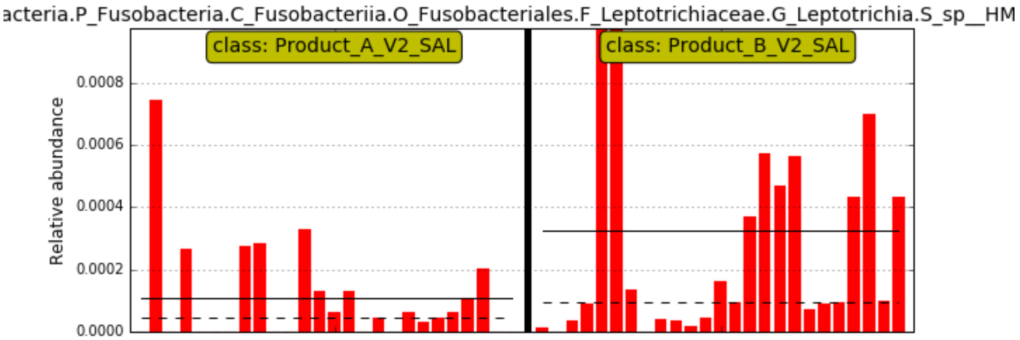




HMT473

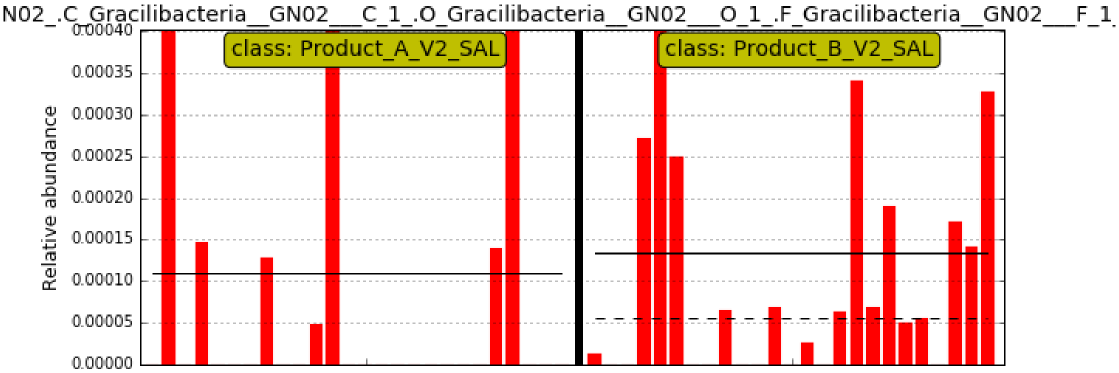

K_Bacteria.P_Firmicutes.C_Bacilli.O_Bacillales.F_Gemellaceae.G_Gemella.S_haemolysans
class: Product_A_V2_SAL
class: Product_B_V2_SAL
Relative abundance
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000


K_Bacteria.P_Firmicutes.C_Clostridia.O_Negativicutes.F_Veillonellaceae.G_Veillonella.S_sp__HMT_780
class: Product_A_V2_SAL
class: Product_B_V2_SAL
Relative abundance
0.0020
0.0015
0.0010
0.0005
0.0000

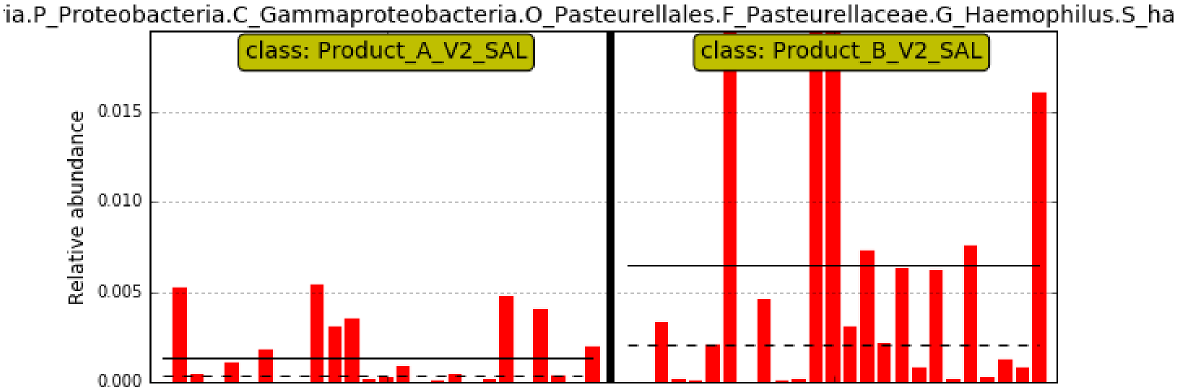


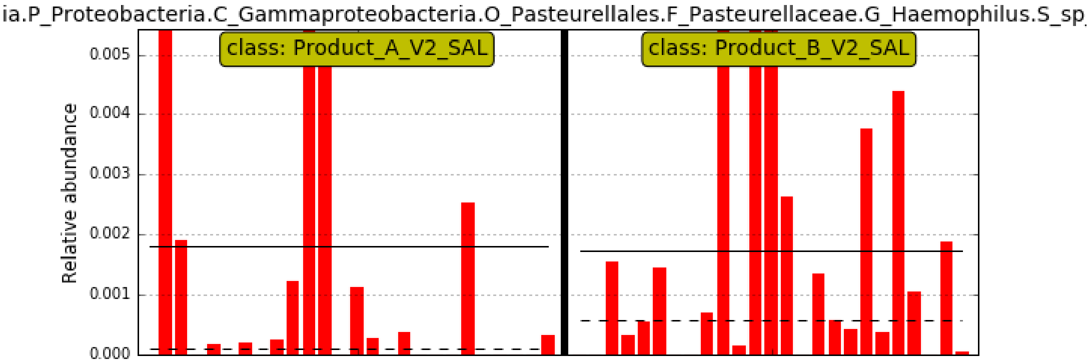
21)

HMT212

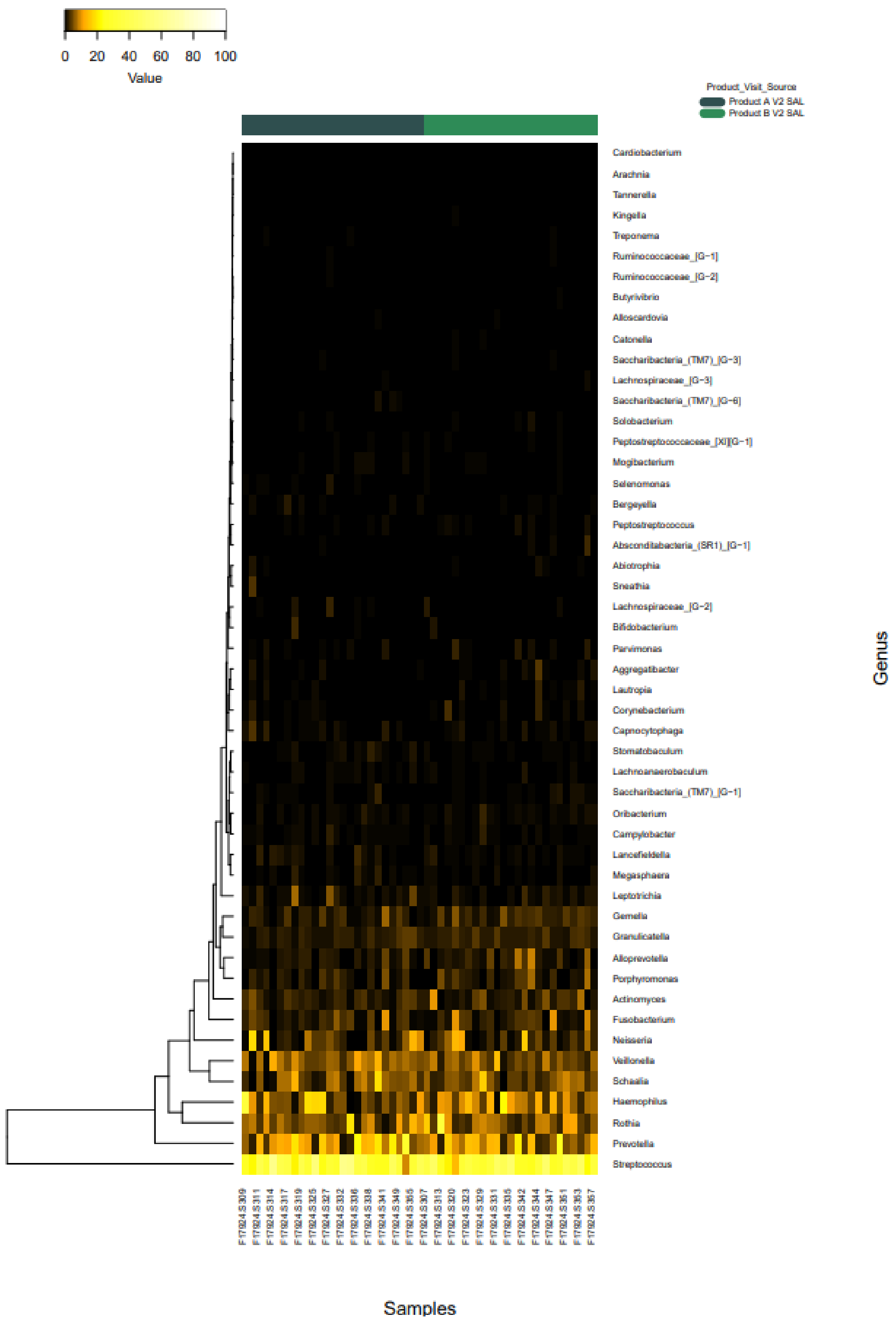


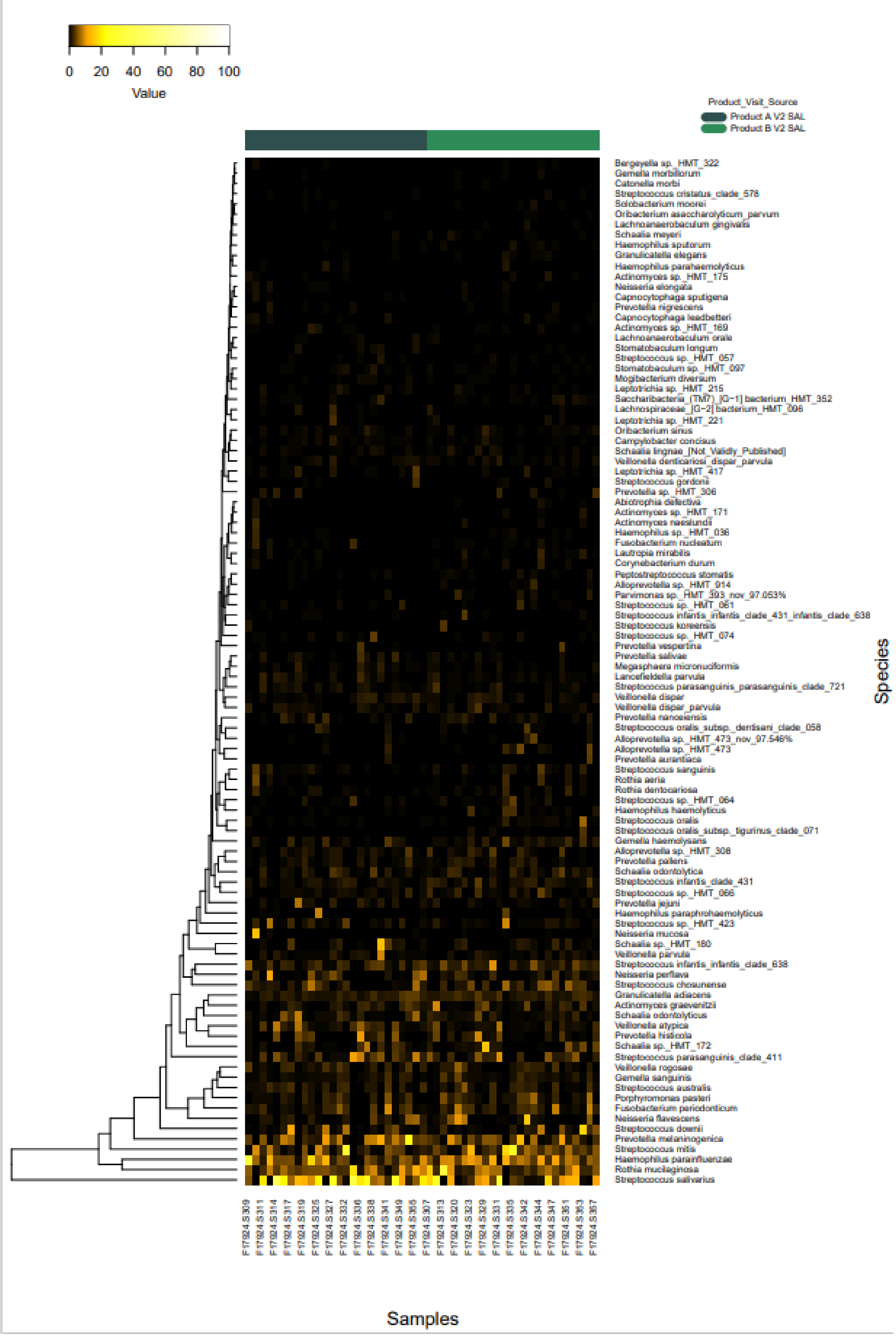
very low levels





6) Heat maps


0
20
40
60
80
100
Value
Product_Visit_Source
Product A V2 SAL
Product B V2 SAL
Cardiobacterium
Arachnia
Tannerella
Kingella
Treponema
Ruminococcaceae_[G-1]
Ruminococcaceae_[G-2]
Butyrivibrio
Alloscardovia
Catonella
Saccharibacteria_(TM7)_[G-3]
Lachnospiraceae_[G-3]
Saccharibacteria_(TM7)_[G-6]
Solobacterium
Peptostreptococcaceae_[XI][G-1]
Mogibacterium
Selenomonas
Bergeyella
Peptostreptococcus
Absconditabacteria_(SR1)_[G-1]
Abiotrophia
Sneathia
Lachnospiraceae_[G-2]
Bifidobacterium
Parvimonas
Aggregatibacter
Lautropia
Corynebacterium
Capnocytophaga
Stomatobaculum
Lachnoanaerobaculum
Saccharibacteria_(TM7)_[G-1]
Oribacterium
Campylobacter
Lancefieldella
Megasphaera
Leptotrichia
Gemella
Granulicatella
Alloprevotella
Porphyromonas
Actinomyces
Fusobacterium
Neisseria
Veillonella
Schaalia
Haemophilus
Rothia
Prevotella
Streptococcus
Genus
F17924.S309
F17924.S311
F17924.S314
F17924.S317
F17924.S319
F17924.S325
F17924.S327
F17924.S332
F17924.S336
F17924.S338
F17924.S341
F17924.S349
F17924.S365
F17924.S307
F17924.S313
F17924.S320
F17924.S323
F17924.S329
F17924.S331
F17924.S335
F17924.S342
F17924.S344
F17924.S347
F17924.S351
F17924.S353
F17924.S357
Samples


0
20
40
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80
100
Value
Product_Visit_Source
Product A V2 SAL
Product B V2 SAL
Bergeyella sp._HMT_322
Gemella morbillorum
Catonella morbi
Streptococcus cristatus_clade_578
Solobacterium moorei
Oribacterium asaccharolyticum_parvum
Lachnoanaerobaculum gingivalis
Schaalia meyeri
Haemophilus sputorum
Granulicatella elegans
Haemophilus parahaemolyticus
Actinomyces sp._HMT_175
Neisseria elongata
Capnocytophaga sputigena
Prevotella nigrescens
Capnocytophaga leadbetteri
Actinomyces sp._HMT_169
Lachnoanaerobaculum orale
Stomatobaculum longum
Streptococcus sp._HMT_057
Stomatobaculum sp._HMT_097
Mogibacterium diversum
Leptotrichia sp._HMT_215
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_352
Lachnospiraceae_[G−2] bacterium_HMT_096
Leptotrichia sp._HMT_221
Oribacterium sinus
Campylobacter concisus
Schaalia lingnae_[Not_Validly_Published]
Veillonella denticariosi_dispar_parvula
Leptotrichia sp._HMT_417
Streptococcus gordonii
Prevotella sp._HMT_306
Abiotrophia defectiva
Actinomyces sp._HMT_171
Actinomyces naeslundii
Haemophilus sp._HMT_036
Fusobacterium nucleatum
Lautropia mirabilis
Corynebacterium durum
Peptostreptococcus stomatis
Alloprevotella sp._HMT_914
Parvimonas sp._HMT_393_nov_97.053%
Streptococcus sp._HMT_061
Streptococcus infantis_infantis_clade_431_infantis_clade_638
Streptococcus koreensis
Streptococcus sp._HMT_074
Prevotella vespertina
Prevotella salivae
Megasphaera micronuciformis
Lancefieldella parvula
Streptococcus parasanguinis_parasanguinis_clade_721
Veillonella dispar
Veillonella dispar_parvula
Prevotella nanceiensis
Streptococcus oralis_subsp._dentisani_clade_058
Alloprevotella sp._HMT_473_nov_97.546%
Alloprevotella sp._HMT_473
Prevotella aurantiaca
Streptococcus sanguinis
Rothia aeria
Rothia dentocariosa
Streptococcus sp._HMT_064
Haemophilus haemolyticus
Streptococcus oralis
Streptococcus oralis_subsp._tigurinus_clade_071
Gemella haemolysans
Alloprevotella sp._HMT_308
Prevotella pallens
Schaalia odontolytica
Streptococcus infantis_clade_431
Streptococcus sp._HMT_066
Prevotella jejuni
Haemophilus paraphrohaemolyticus
Streptococcus sp._HMT_423
Neisseria mucosa
Schaalia sp._HMT_180
Veillonella parvula
Streptococcus infantis_infantis_clade_638
Neisseria perflava
Streptococcus chosunense
Granulicatella adiacens
Actinomyces graevenitzii
Schaalia odontolyticus
Veillonella atypica
Prevotella histicola
Schaalia sp._HMT_172
Streptococcus parasanguinis_clade_411
Veillonella rogosae
Gemella sanguinis
Streptococcus australis
Porphyromonas pasteri
Fusobacterium periodonticum
Neisseria flavescens
Streptococcus downii
Prevotella melaninogenica
Streptococcus mitis
Haemophilus parainfluenzae
Rothia mucilaginosa
Streptococcus salivarius
Species
FIT924 S309
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FIT924 S319
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FIT924 S336
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FIT924 S335
FIT924 S342
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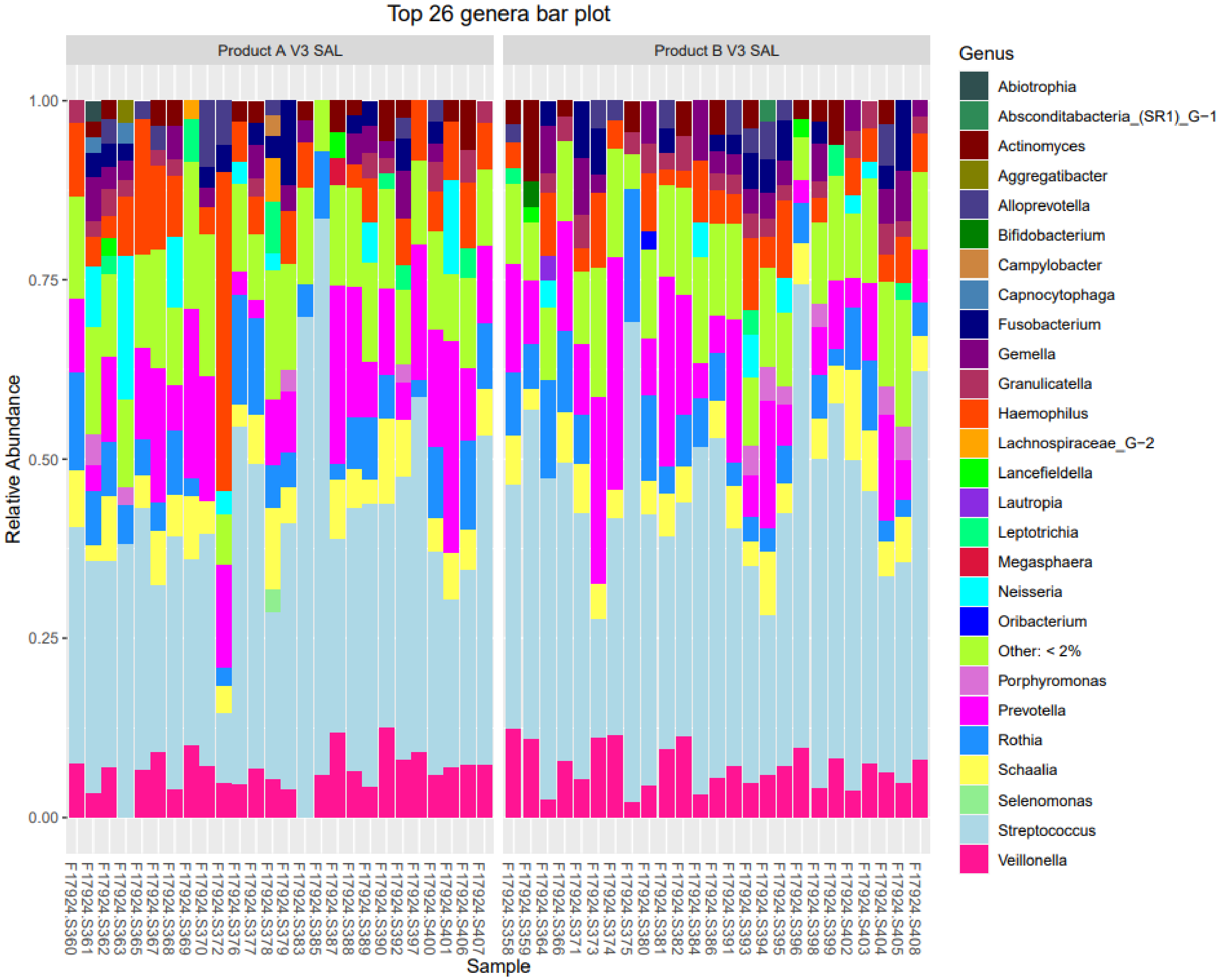
FIT924 S361
FIT924 S363
FIT924 S367
Samples

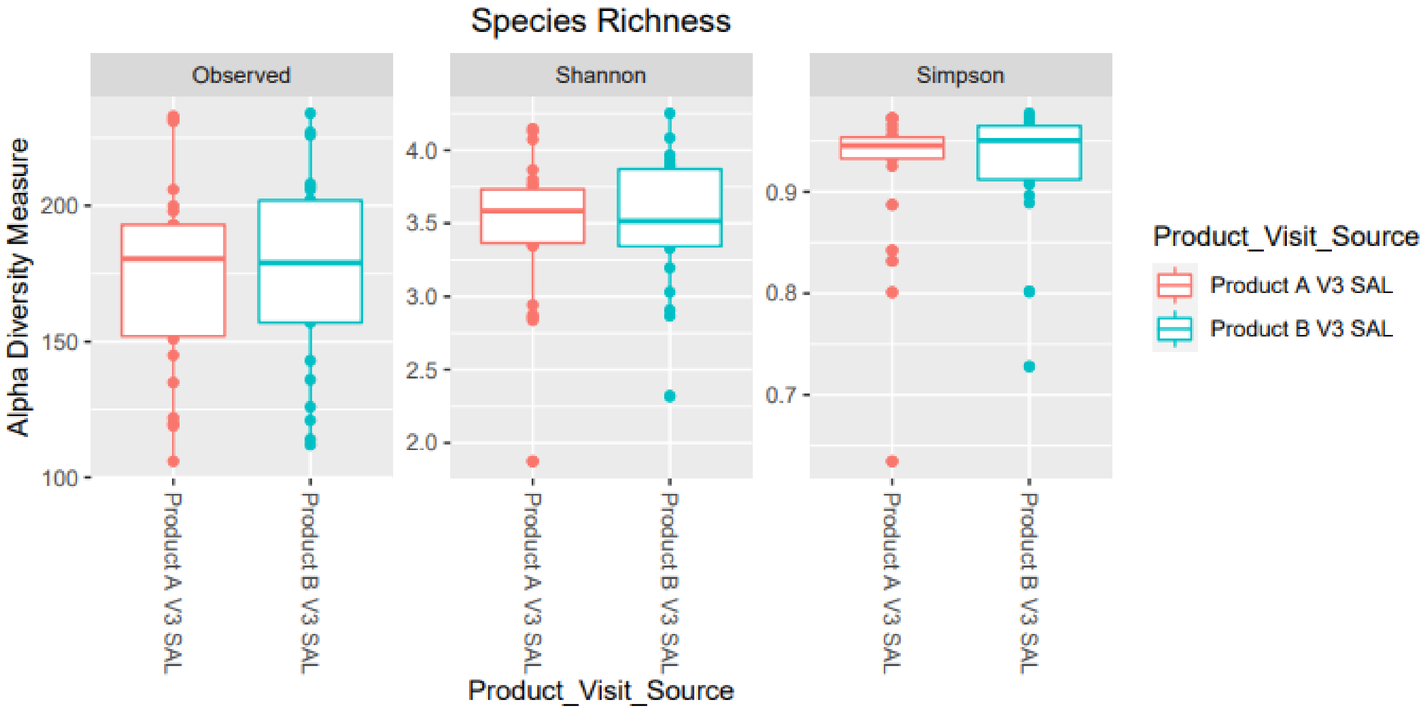
Comparison 8. Product A V3 SAL vs Product B V3 SAL

1) Taxonomy bar graphs



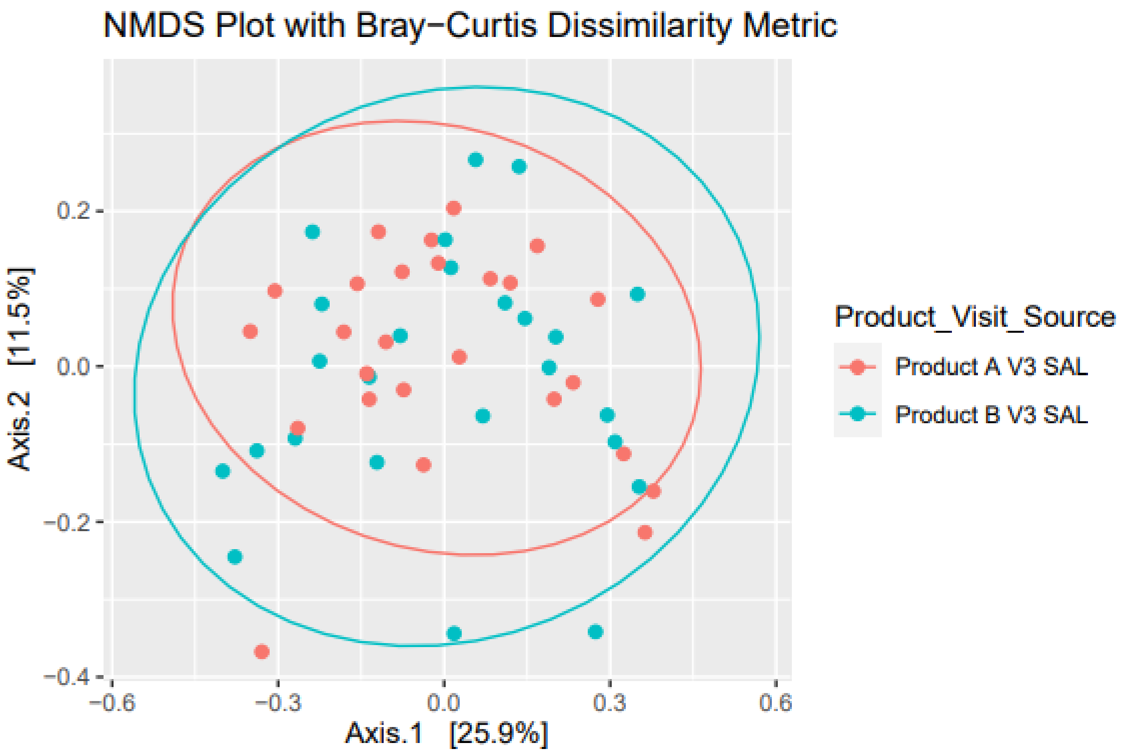
Difficult to see major differences. These will be ID'd in subsequently analyses

2) Alpha diversity



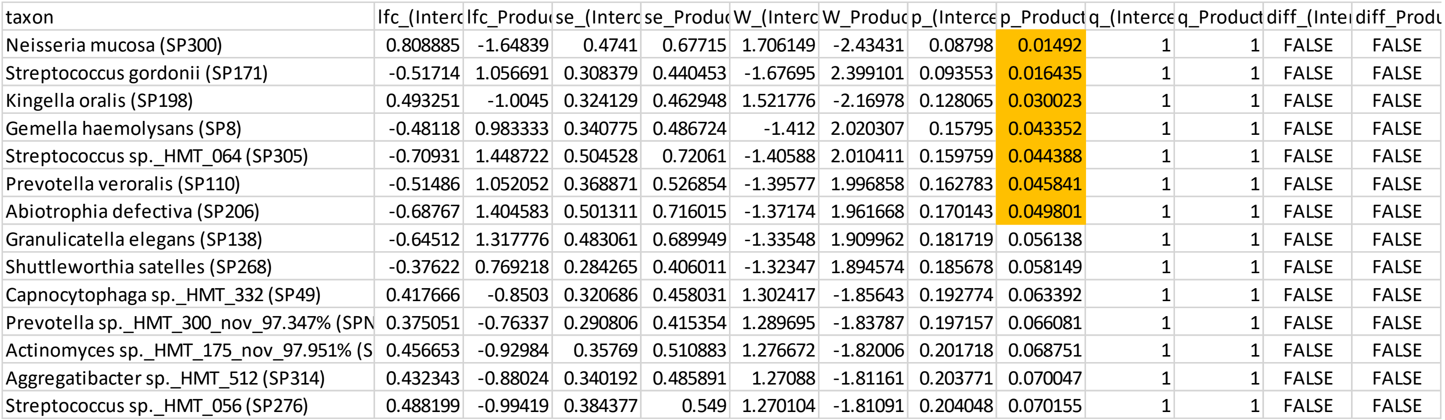
No significant differences

3) Beta diversity



No Significant differences.

4) Differential abundance

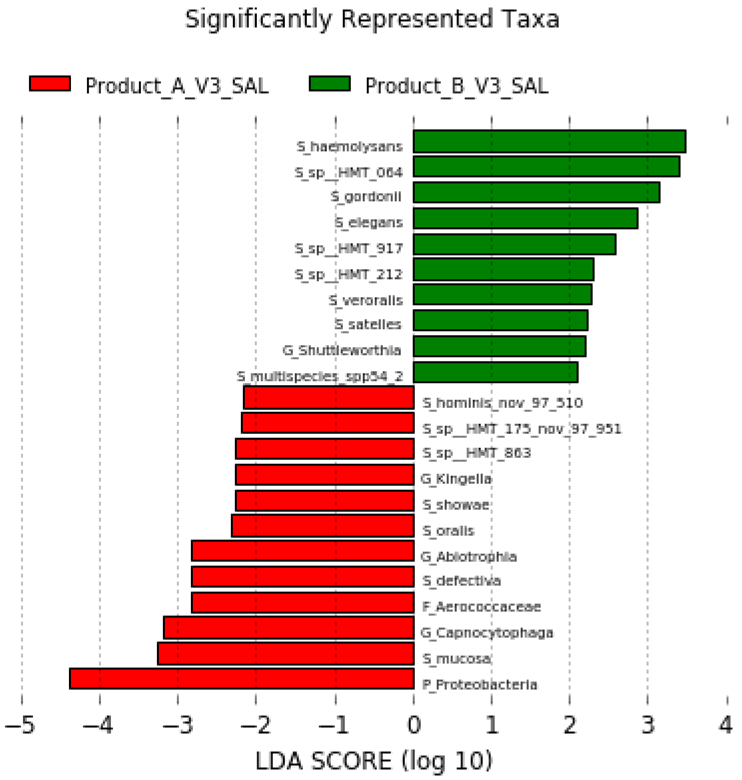


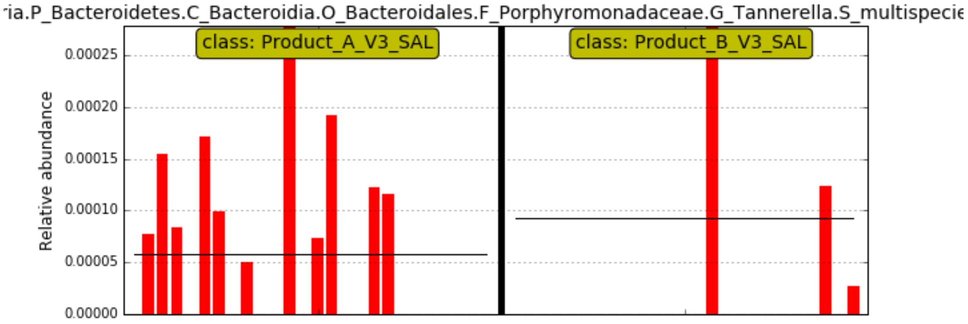
taxon	lfc_(Interc	lfc_Produc	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inter	diff_Produ
Neisseria mucosa (SP300)	0.808885	-1.64839	0.4741	0.67715	1.706149	-2.43431	0.08798	0.01492	1	1	FALSE	FALSE
Streptococcus gordonii (SP171)	-0.51714	1.056691	0.308379	0.440453	-1.67695	2.399101	0.093553	0.016435	1	1	FALSE	FALSE
Kingella oralis (SP198)	0.493251	-1.0045	0.324129	0.462948	1.521776	-2.16978	0.128065	0.030023	1	1	FALSE	FALSE
Gemella haemolysans (SP8)	-0.48118	0.983333	0.340775	0.486724	-1.412	2.020307	0.15795	0.043352	1	1	FALSE	FALSE
Streptococcus sp._HMT_064 (SP305)	-0.70931	1.448722	0.504528	0.72061	-1.40588	2.010411	0.159759	0.044388	1	1	FALSE	FALSE
Prevotella veroralis (SP110)	-0.51486	1.052052	0.368871	0.526854	-1.39577	1.996858	0.162783	0.045841	1	1	FALSE	FALSE
Abiotrophia defectiva (SP206)	-0.68767	1.404583	0.501311	0.716015	-1.37174	1.961668	0.170143	0.049801	1	1	FALSE	FALSE
Granulicatella elegans (SP138)	-0.64512	1.317776	0.483061	0.689949	-1.33548	1.909962	0.181719	0.056138	1	1	FALSE	FALSE
Shuttleworthia satelles (SP268)	-0.37622	0.769218	0.284265	0.406011	-1.32347	1.894574	0.185678	0.058149	1	1	FALSE	FALSE
Capnocytophaga sp._HMT_332 (SP49)	0.417666	-0.8503	0.320686	0.458031	1.302417	-1.85643	0.192774	0.063392	1	1	FALSE	FALSE
Prevotella sp._HMT_300_nov_97.347% (SPN	0.375051	-0.76337	0.290806	0.415354	1.289695	-1.83787	0.197157	0.066081	1	1	FALSE	FALSE
Actinomyces sp._HMT_175_nov_97.951% (S	0.456653	-0.92984	0.35769	0.510883	1.276672	-1.82006	0.201718	0.068751	1	1	FALSE	FALSE
Aggregatibacter sp._HMT_512 (SP314)	0.432343	-0.88024	0.340192	0.485891	1.27088	-1.81161	0.203771	0.070047	1	1	FALSE	FALSE
Streptococcus sp._HMT_056 (SP276)	0.488199	-0.99419	0.384377	0.549	1.270104	-1.81091	0.204048	0.070155	1	1	FALSE	FALSE

No significant differences, but lost after multiple comparisons.

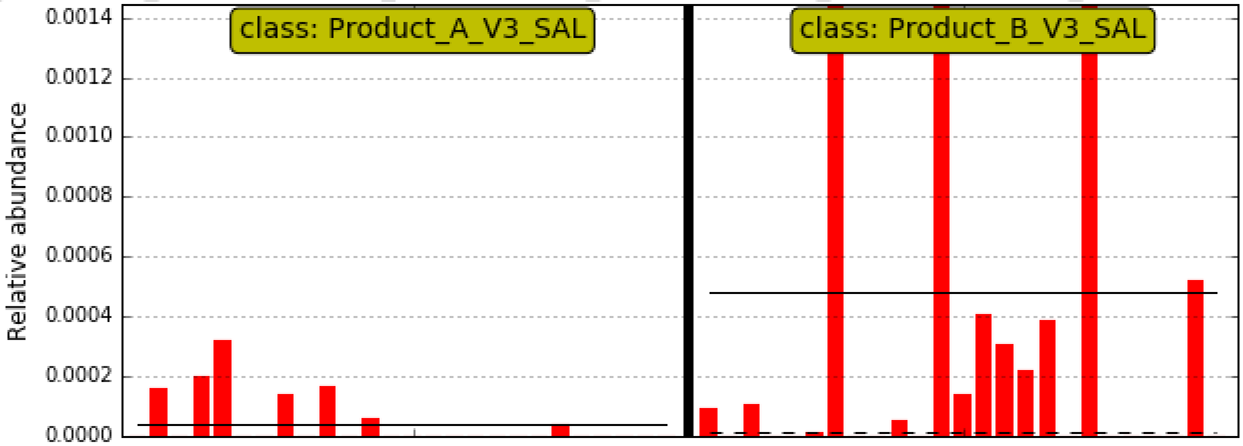
Similar results in Lefse

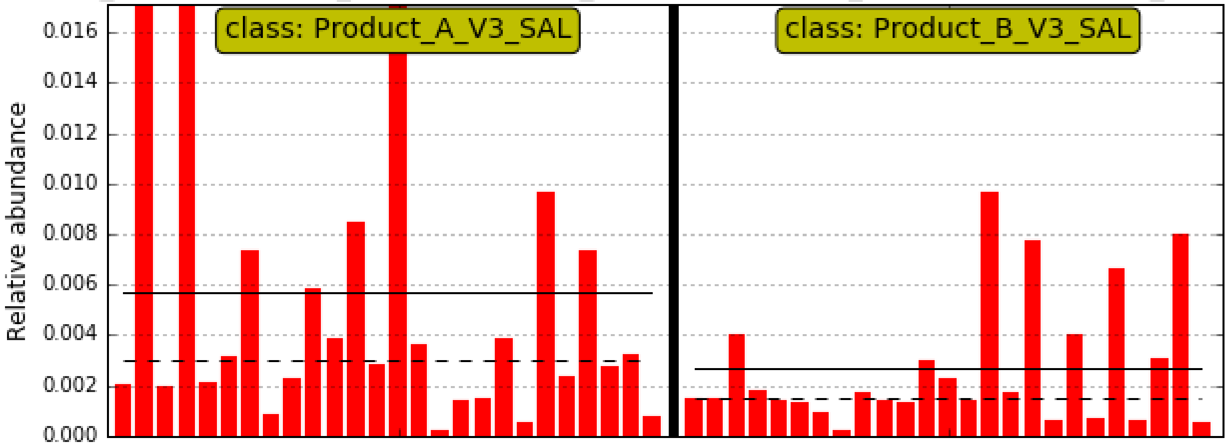
5) Lefse





very low levels


K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_veroralis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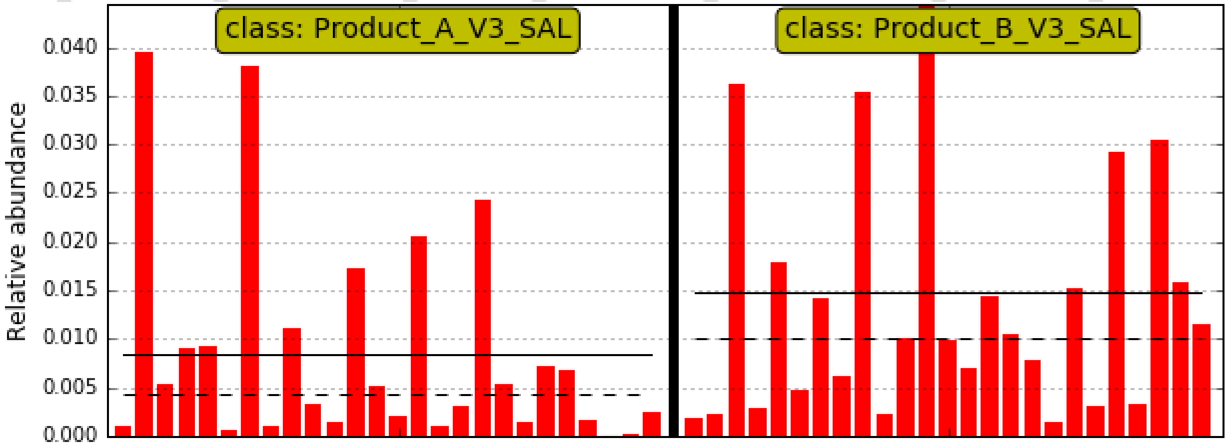
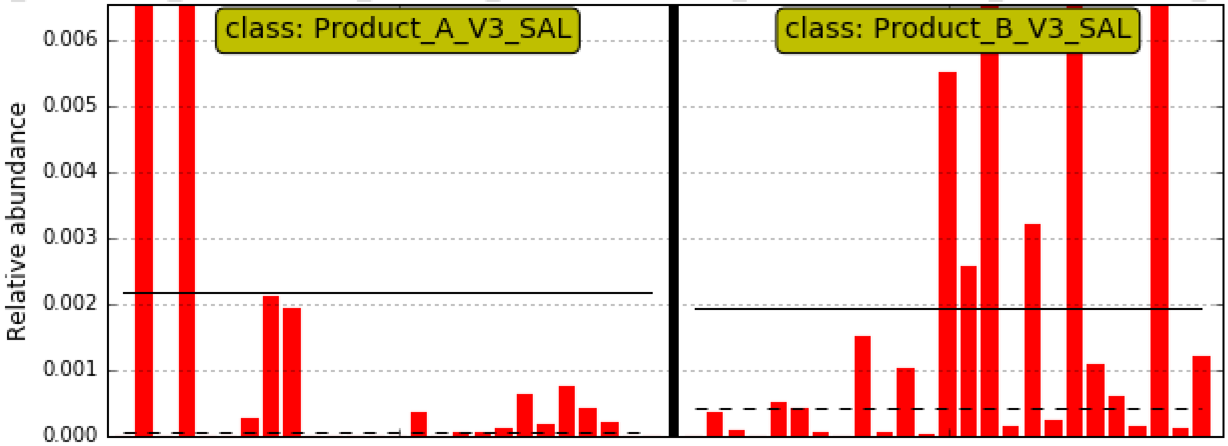
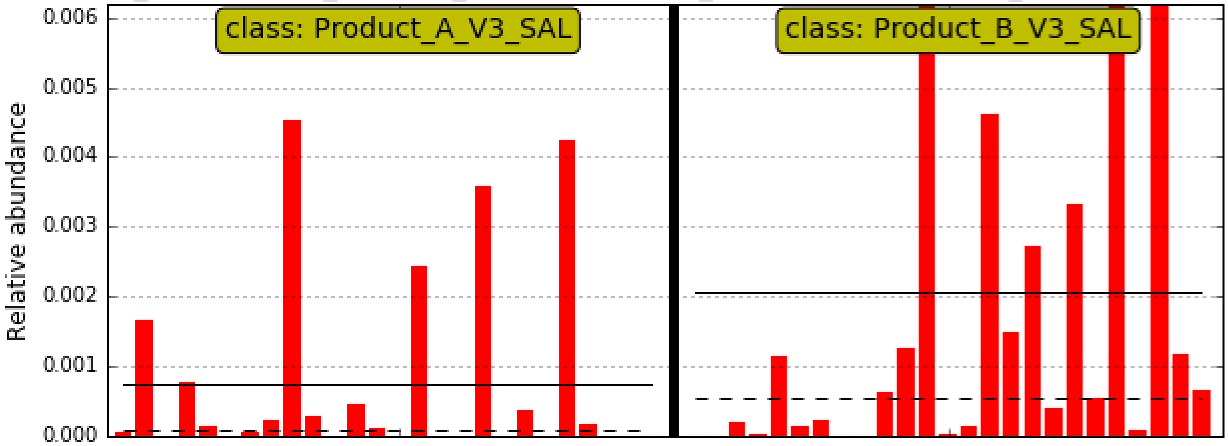
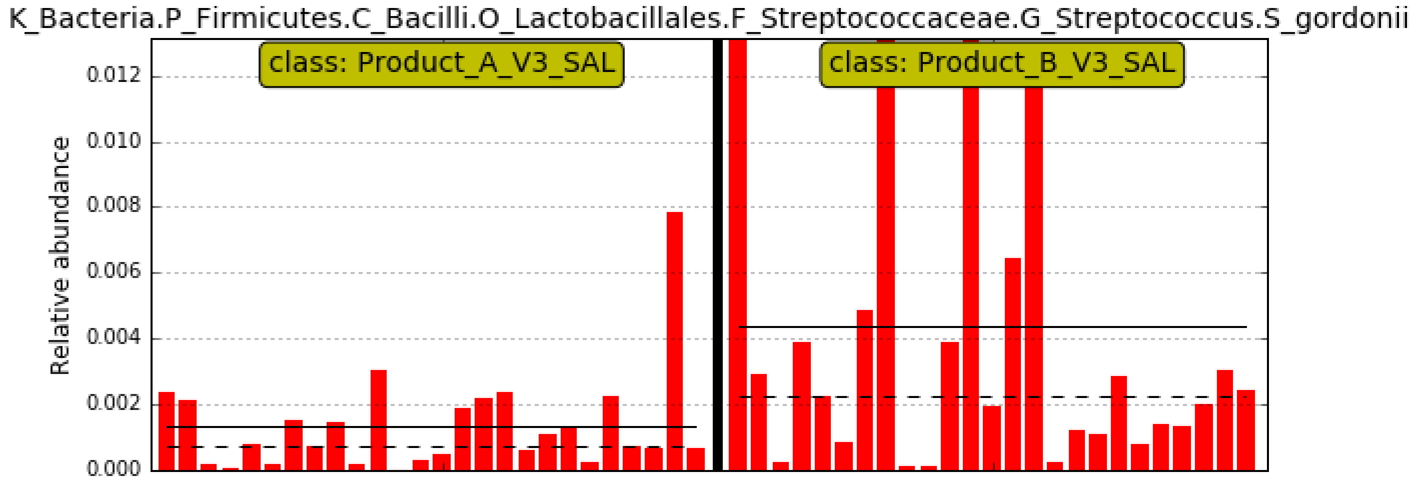

K_Bacteria.P_Firmicutes.C_Bacilli.O_Bacillales.F_Gemellaceae.G_Gemella.S_haemolysans


K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Aerococcaceae.G_Abiotrophia.S_defectiva


K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Carnobacteriaceae.G_Granulicatella.S_elegans


K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_gordonii
class: Product_A_V3_SAL
class: Product_B_V3_SAL
Relative abundance
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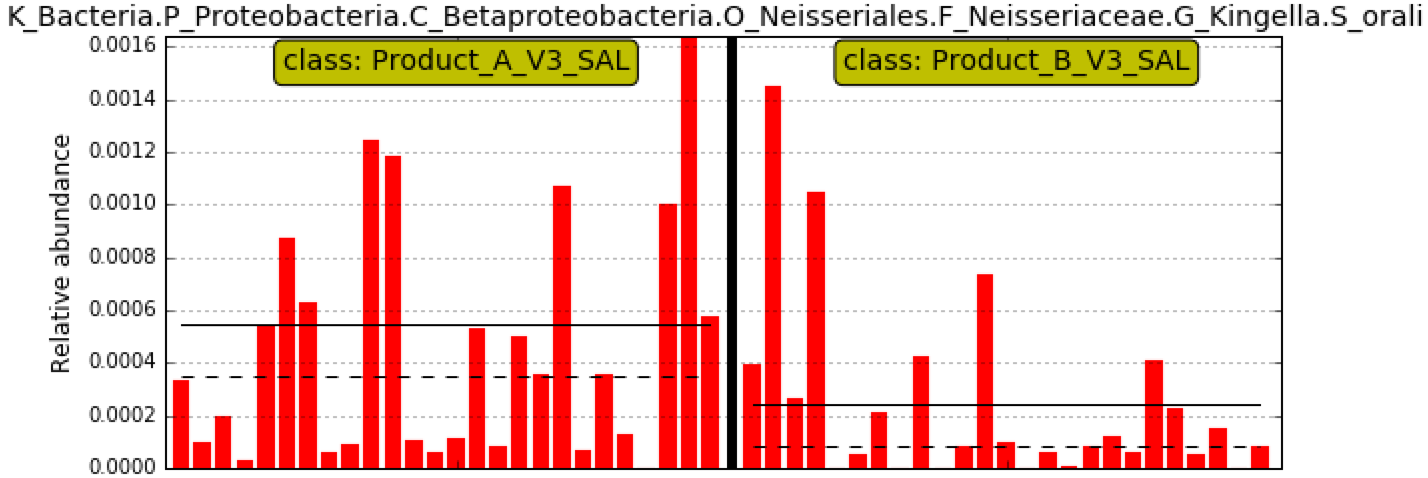
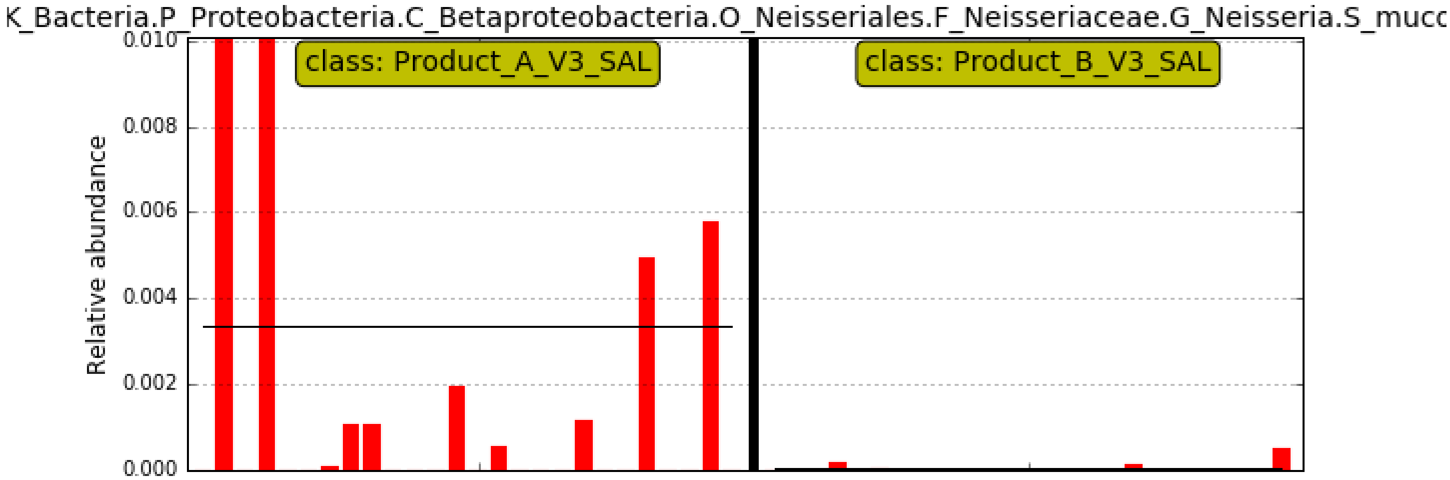
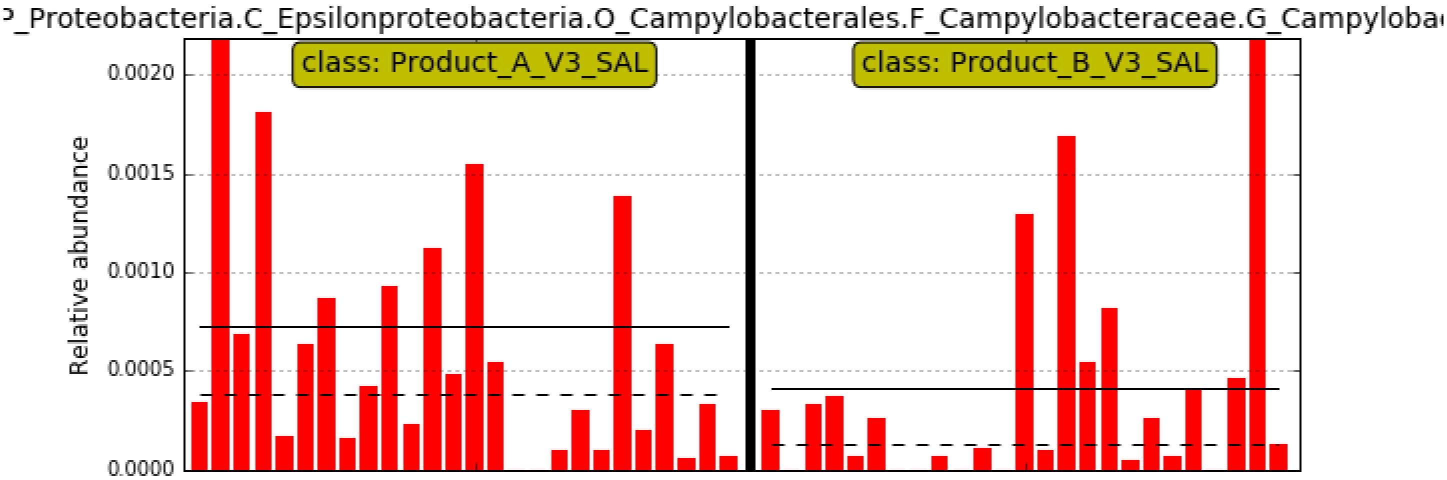
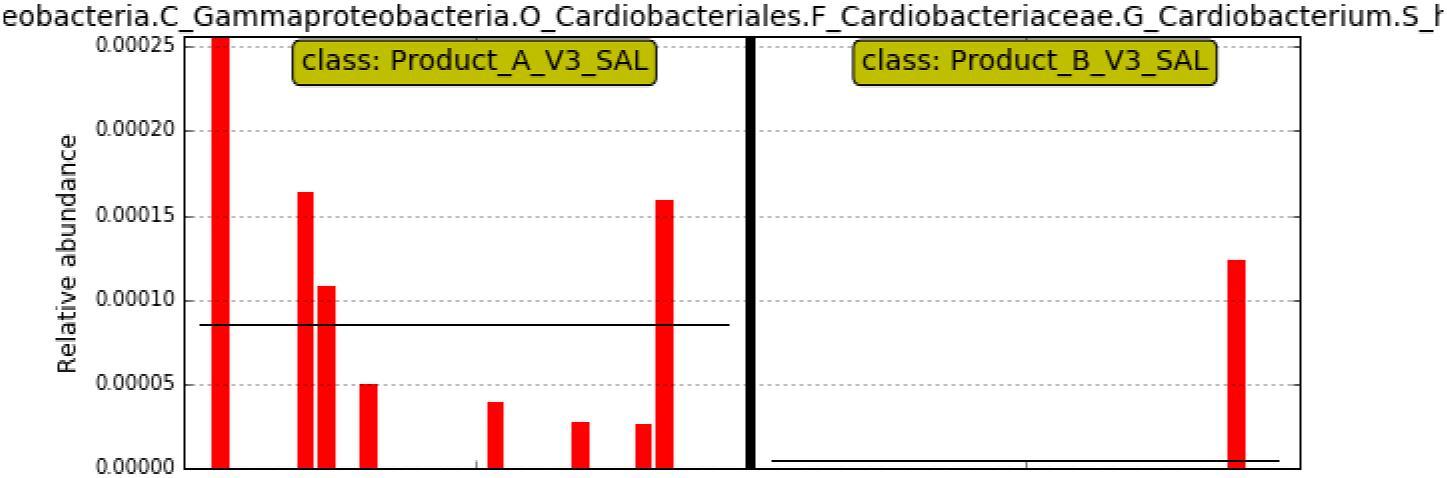
0.002
0.004
0.006
0.008
0.010
0.012


K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Kingella.S_orali
class: Product_A_V3_SAL
class: Product_B_V3_SAL
Relative abundance
0.0000
0.0002
0.0004
0.0006
0.0008
0.0010
0.0012
0.0014
0.0016


K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Neisseria.S_muco
class: Product_A_V3_SAL
class: Product_B_V3_SAL
Relative abundance
0.000
0.002
0.004
0.006
0.008
0.010

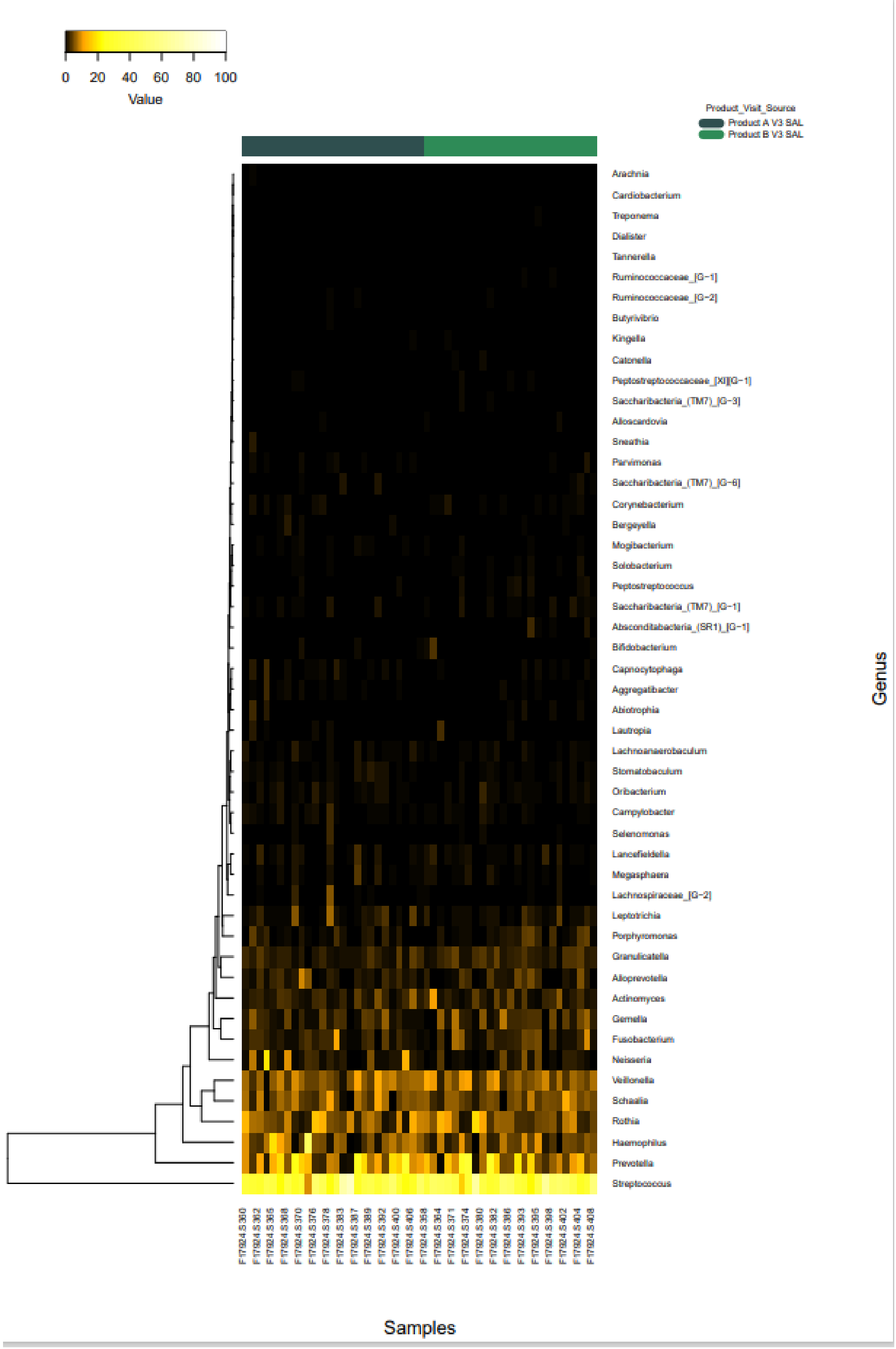


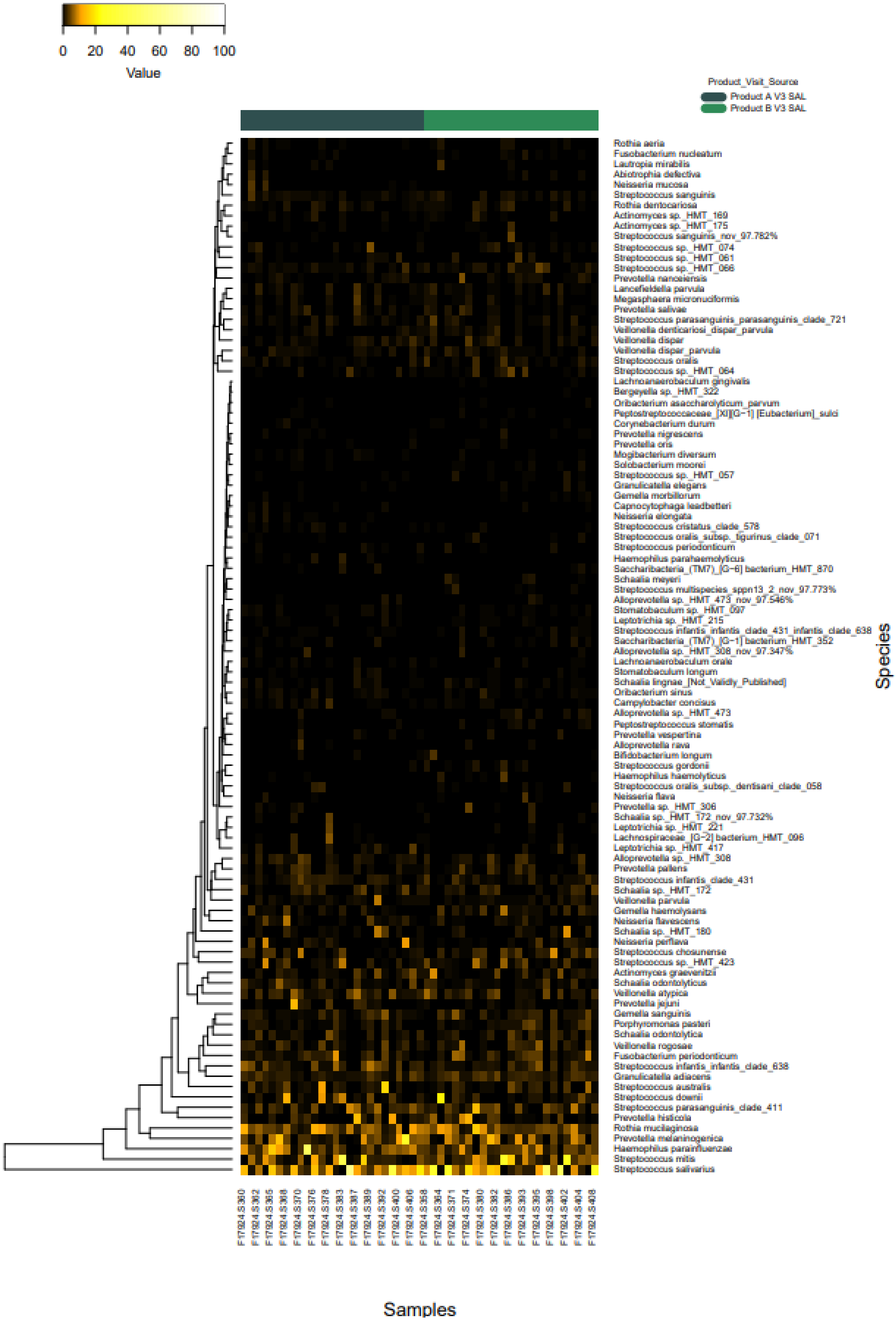
P_Proteobacteria.C_Epsilonproteobacteria.O_Campylobacterales.F_Campylobacteraceae.G_Campyloba
class: Product_A_V3_SAL
class: Product_B_V3_SAL
Relative abundance
0.0020
0.0015
0.0010
0.0005
0.0000



eobacteria.C_Gammaproteobacteria.O_Cardiobacteriales.F_Cardiobacteriaceae.G_Cardiobacterium.S_
class: Product_A_V3_SAL
class: Product_B_V3_SAL
Relative abundance
0.00025
0.00020
0.00015
0.00010
0.00005
0.00000

6) heat maps –difficult to see consistent differences



0
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40
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Value
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Product B V3 SAL
Rothia aeria
Fusobacterium nucleatum
Lautropia mirabilis
Abiotrophia defectiva
Neisseria mucosa
Streptococcus sanguinis
Rothia dentocariosa
Actinomyces sp._HMT_169
Actinomyces sp._HMT_175
Streptococcus sanguinis_nov_97.782%
Streptococcus sp._HMT_074
Streptococcus sp._HMT_061
Streptococcus sp._HMT_066
Prevotella nanceiensis
Lancefieldella parvula
Megasphaera micronuciformis
Prevotella salivae
Streptococcus parasanguinis_parasanguinis_clade_721
Veillonella denticariosi_dispar_parvula
Veillonella dispar
Veillonella dispar_parvula
Streptococcus oralis
Streptococcus sp._HMT_064
Lachnoanaerobaculum gingivalis
Bergeyella sp._HMT_322
Oribacterium asaccharolyticum_parvum
Peptostreptococcaceae_[XI][G−1] [Eubacterium]_sulci
Corynebacterium durum
Prevotella nigrescens
Prevotella oris
Mogibacterium diversum
Solobacterium moorei
Streptococcus sp._HMT_057
Granulicatella elegans
Gemella morbillorum
Capnocytophaga leadbetteri
Neisseria elongata
Streptococcus cristatus_clade_578
Streptococcus oralis_subsp._tigurinus_clade_071
Streptococcus periodonticum
Haemophilus parahaemolyticus
Saccharibacteria_(TM7)_[G−6] bacterium_HMT_870
Schaalia meyeri
Streptococcus multispecies_sppn13_2_nov_97.773%
Alloprevotella sp._HMT_473_nov_97.546%
Stomatobaculum sp._HMT_097
Leptotrichia sp._HMT_215
Streptococcus infantis_infantis_clade_431_infantis_clade_638
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_352
Alloprevotella sp._HMT_308_nov_97.347%
Lachnoanaerobaculum orale
Stomatobaculum longum
Schaalia lingnae_[Not_Validly_Published]
Oribacterium sinus
Campylobacter concisus
Alloprevotella sp._HMT_473
Peptostreptococcus stomatis
Prevotella vespertina
Alloprevotella rava
Bifidobacterium longum
Streptococcus gordonii
Haemophilus haemolyticus
Streptococcus oralis_subsp._dentisani_clade_058
Neisseria flava
Prevotella sp._HMT_306
Schaalia sp._HMT_172_nov_97.732%
Leptotrichia sp._HMT_221
Lachnospiraceae_[G−2] bacterium_HMT_096
Leptotrichia sp._HMT_417
Alloprevotella sp._HMT_308
Prevotella pallens
Streptococcus infantis_clade_431
Schaalia sp._HMT_172
Veillonella parvula
Gemella haemolysans
Neisseria flavescens
Schaalia sp._HMT_180
Neisseria perflava
Streptococcus chosunense
Streptococcus sp._HMT_423
Actinomyces graevenitzii
Schaalia odontolyticus
Veillonella atypica
Prevotella jejuni
Gemella sanguinis
Porphyromonas pasteri
Schaalia odontolytica
Veillonella rogosae
Fusobacterium periodonticum
Streptococcus infantis_infantis_clade_638
Granulicatella adiacens
Streptococcus australis
Streptococcus downii
Streptococcus parasanguinis_clade_411
Prevotella histicola
Rothia mucilaginosa
Prevotella melaninogenica
Haemophilus parainfluenzae
Streptococcus mitis
Streptococcus salivarius
Species
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FIT924.S395
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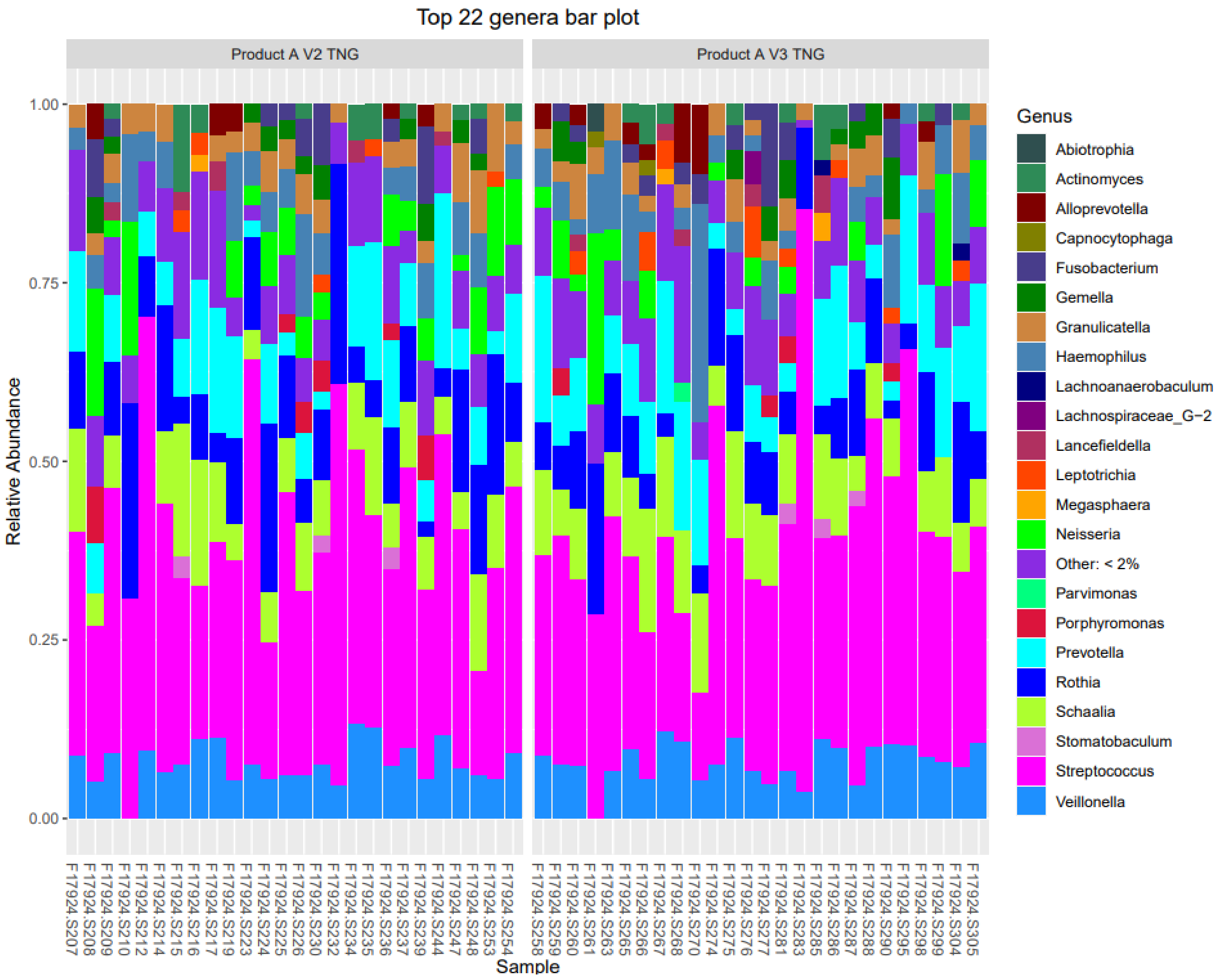
FIT924.S404
FIT924.S408
Samples

Comparison 9. Product A V2 TNG vs Product A V3 TNG

1) Taxonomy bar graphs

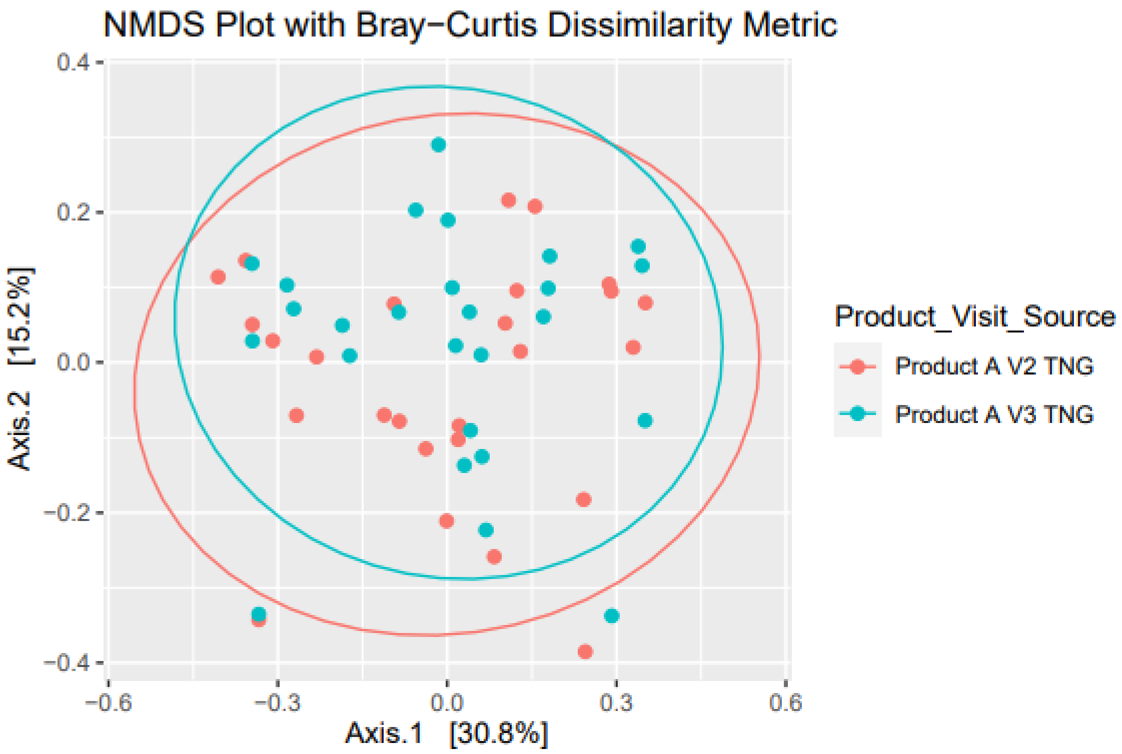


Some differences can be seen, but analyses below will be more informative.

2) Alpha

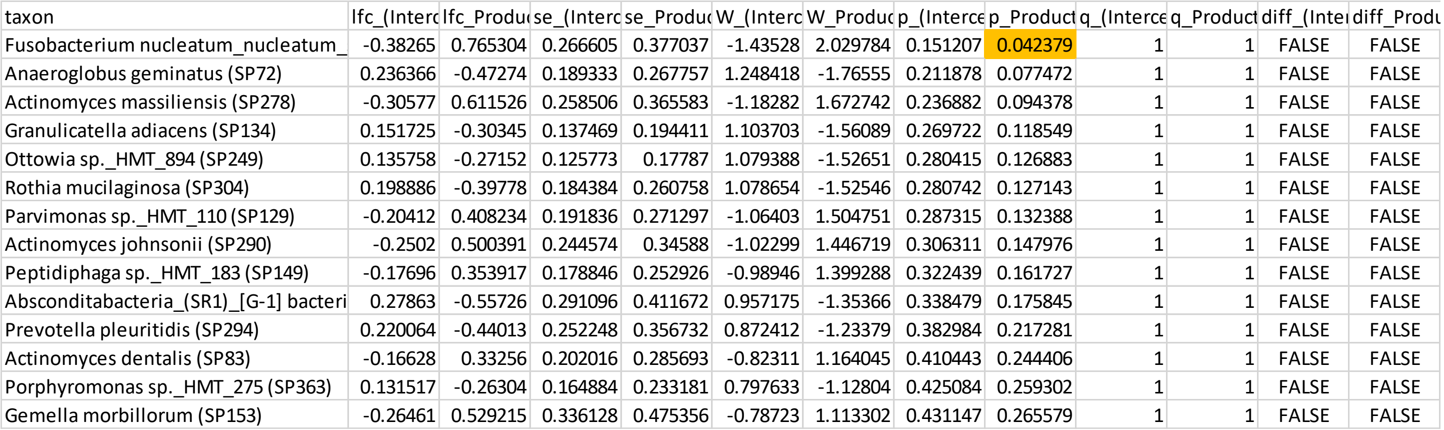
No significant differences

3) Beta



No significant differences

4) Differential abundance



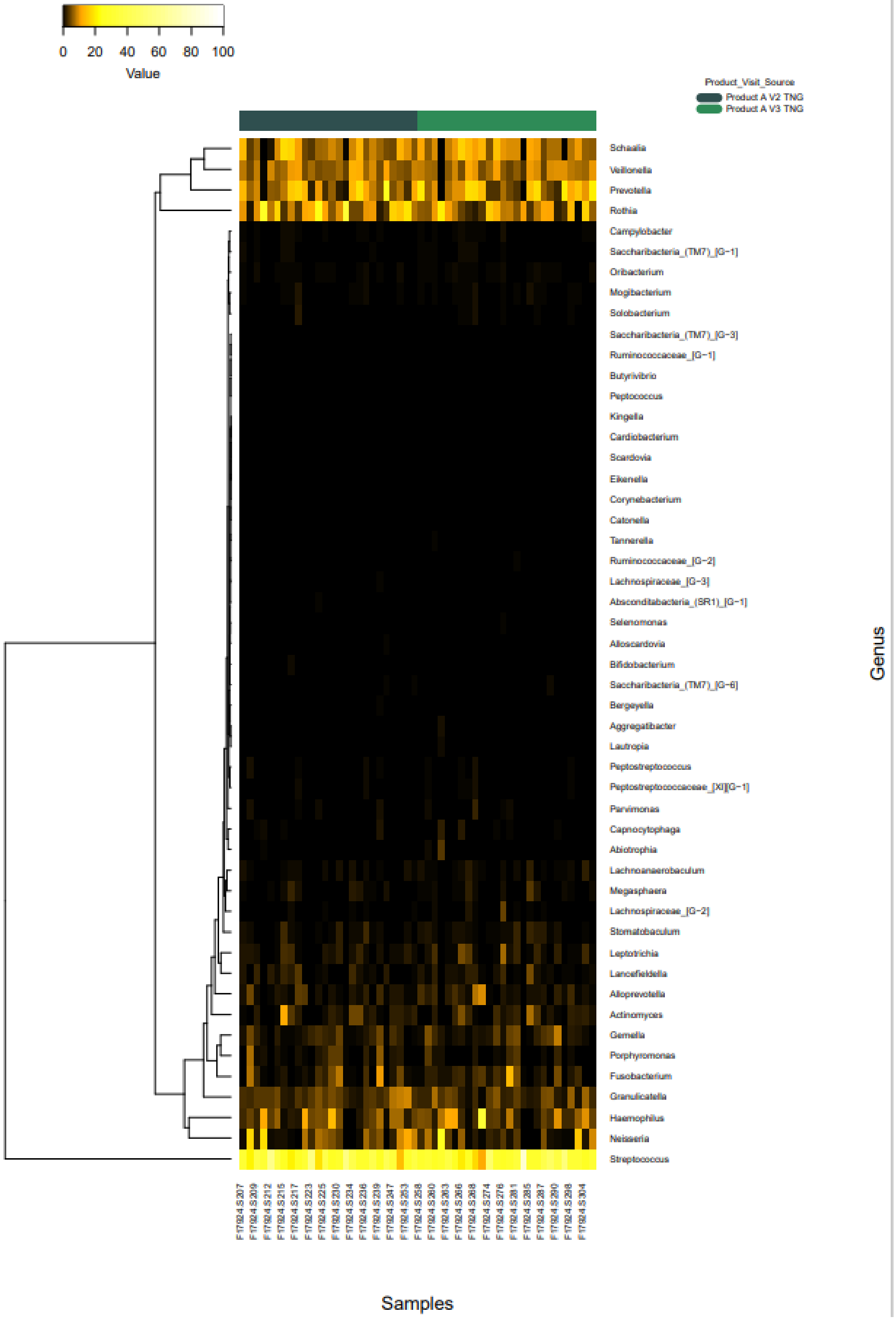
taxon	lfc_(Interc	lfc_Produc	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inte	diff_Produ
Fusobacterium nucleatum_nucleatum_	-0.38265	0.765304	0.266605	0.377037	-1.43528	2.029784	0.151207	0.042379	1	1	FALSE	FALSE
Anaeroglobus geminatus (SP72)	0.236366	-0.47274	0.189333	0.267757	1.248418	-1.76555	0.211878	0.077472	1	1	FALSE	FALSE
Actinomyces massiliensis (SP278)	-0.30577	0.611526	0.258506	0.365583	-1.18282	1.672742	0.236882	0.094378	1	1	FALSE	FALSE
Granulicatella adiacens (SP134)	0.151725	-0.30345	0.137469	0.194411	1.103703	-1.56089	0.269722	0.118549	1	1	FALSE	FALSE
Ottowia sp._HMT_894 (SP249)	0.135758	-0.27152	0.125773	0.17787	1.079388	-1.52651	0.280415	0.126883	1	1	FALSE	FALSE
Rothia mucilaginosa (SP304)	0.198886	-0.39778	0.184384	0.260758	1.078654	-1.52546	0.280742	0.127143	1	1	FALSE	FALSE
Parvimonas sp._HMT_110 (SP129)	-0.20412	0.408234	0.191836	0.271297	-1.06403	1.504751	0.287315	0.132388	1	1	FALSE	FALSE
Actinomyces johnsonii (SP290)	-0.2502	0.500391	0.244574	0.34588	-1.02299	1.446719	0.306311	0.147976	1	1	FALSE	FALSE
Peptidiphaga sp._HMT_183 (SP149)	-0.17696	0.353917	0.178846	0.252926	-0.98946	1.399288	0.322439	0.161727	1	1	FALSE	FALSE
Absconditabacteria_(SR1)_[G-1] bacteri	0.27863	-0.55726	0.291096	0.411672	0.957175	-1.35366	0.338479	0.175845	1	1	FALSE	FALSE
Prevotella pleuritidis (SP294)	0.220064	-0.44013	0.252248	0.356732	0.872412	-1.23379	0.382984	0.217281	1	1	FALSE	FALSE
Actinomyces dentalis (SP83)	-0.16628	0.33256	0.202016	0.285693	-0.82311	1.164045	0.410443	0.244406	1	1	FALSE	FALSE
Porphyromonas sp._HMT_275 (SP363)	0.131517	-0.26304	0.164884	0.233181	0.797633	-1.12804	0.425084	0.259302	1	1	FALSE	FALSE
Gemella morbillorum (SP153)	-0.26461	0.529215	0.336128	0.475356	-0.78723	1.113302	0.431147	0.265579	1	1	FALSE	FALSE

No differences

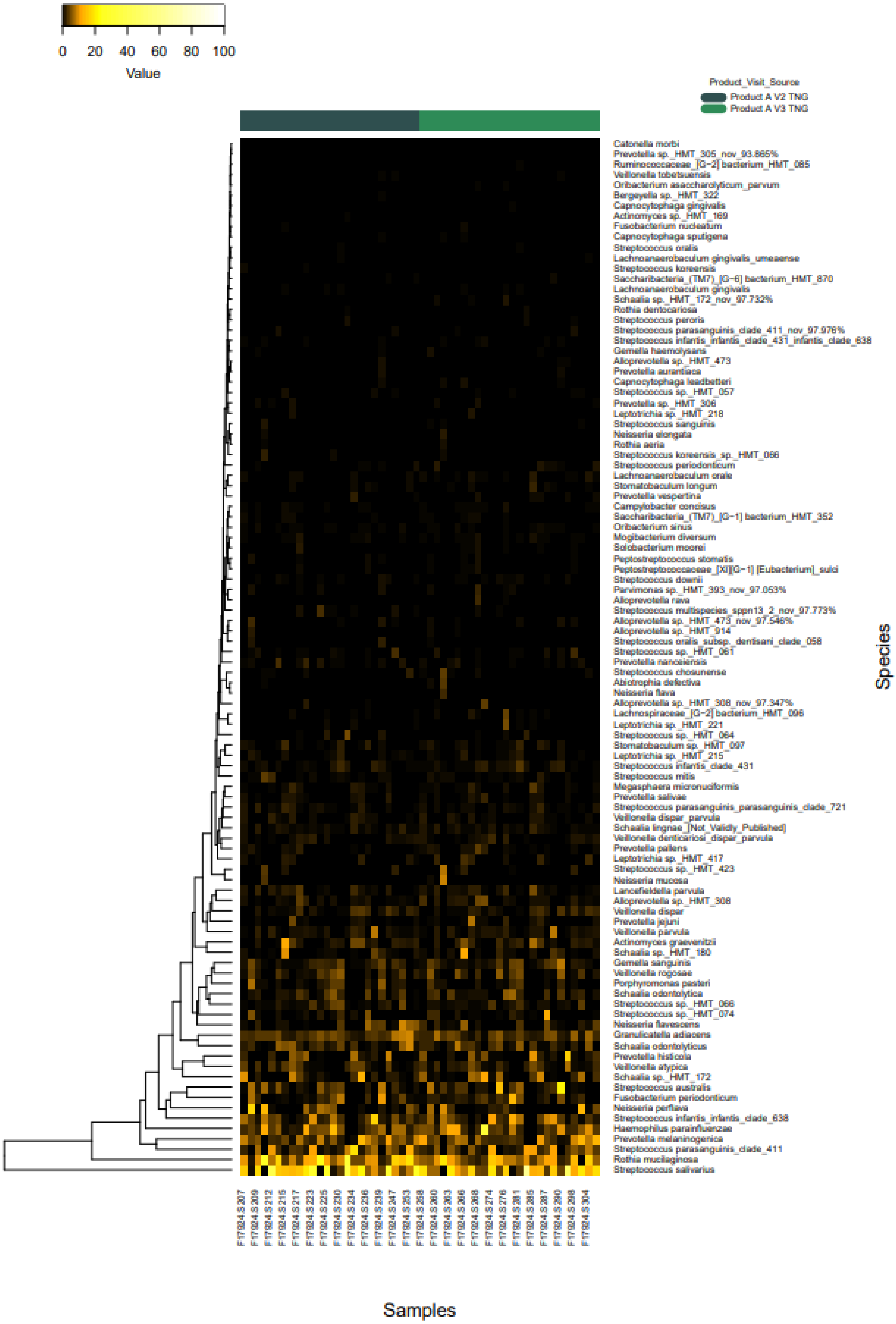
5) Lefse

. NO differences –graph was not produced

6) Heat maps



0
20
40
60
80
100
Value
Product_Visit_Source
Product A V2 TNG
Product A V3 TNG
Schaalia
Veillonella
Prevotella
Rothia
Campylobacter
Saccharibacteria_(TM7)_[G-1]
Oribacterium
Mogibacterium
Solobacterium
Saccharibacteria_(TM7)_[G-3]
Ruminococcaceae_[G-1]
Butyrivibrio
Peptococcus
Kingella
Cardiobacterium
Scardovia
Eikenella
Corynebacterium
Catonella
Tannerella
Ruminococcaceae_[G-2]
Lachnospiraceae_[G-3]
Absconditabacteria_(SR1)_[G-1]
Selenomonas
Alloscardovia
Bifidobacterium
Saccharibacteria_(TM7)_[G-6]
Bergeyella
Aggregatibacter
Lautropia
Peptostreptococcus
Peptostreptococcaceae_[XI][G-1]
Parvimonas
Capnocytophaga
Abiotrophia
Lachnoanaerobaculum
Megasphaera
Lachnospiraceae_[G-2]
Stomatobaculum
Leptotrichia
Lancefieldella
Alloprevotella
Actinomyces
Gemella
Porphyromonas
Fusobacterium
Granulicatella
Haemophilus
Neisseria
Streptococcus
F17924.S207
F17924.S209
F17924.S212
F17924.S215
F17924.S217
F17924.S223
F17924.S225
F17924.S230
F17924.S234
F17924.S236
F17924.S239
F17924.S247
F17924.S253
F17924.S258
F17924.S260
F17924.S263
F17924.S266
F17924.S268
F17924.S274
F17924.S276
F17924.S281
F17924.S285
F17924.S287
F17924.S290
F17924.S298
F17924.S304
Samples
Genus


0
20
40
60
80
100
Value
Product_Visit_Source
Product A V2 TNG
Product A V3 TNG
Catonella morbi
Prevotella sp._HMT_305_nov_93.865%
Ruminococcaceae_[G-2] bacterium_HMT_085
Veillonella tobetsuensis
Oribacterium asaccharolyticum_parvum
Bergeyella sp._HMT_322
Capnocytophaga gingivalis
Actinomyces sp._HMT_169
Fusobacterium nucleatum
Capnocytophaga sputigena
Streptococcus oralis
Lachnoanaerobaculum gingivalis_umeaense
Streptococcus koreensis
Saccharibacteria_(TM7)_[G-6] bacterium_HMT_870
Lachnoanaerobaculum gingivalis
Schaalia sp._HMT_172_nov_97.732%
Rothia dentocariosa
Streptococcus peroris
Streptococcus parasanguinis_clade_411_nov_97.976%
Streptococcus infantis_infantis_clade_431_infantis_clade_638
Gemella haemolysans
Alloprevotella sp._HMT_473
Prevotella aurantiaca
Capnocytophaga leadbetteri
Streptococcus sp._HMT_057
Prevotella sp._HMT_306
Leptotrichia sp._HMT_218
Streptococcus sanguinis
Neisseria elongata
Rothia aeria
Streptococcus koreensis_sp._HMT_066
Streptococcus periodonticum
Lachnoanaerobaculum orale
Stomatobaculum longum
Prevotella vespertina
Campylobacter concisus
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_352
Oribacterium sinus
Mogibacterium diversum
Solobacterium moorei
Peptostreptococcus stomatis
Peptostreptococcaceae_[XI][G-1] [Eubacterium]_sulci
Streptococcus downii
Parvimonas sp._HMT_393_nov_97.053%
Alloprevotella rava
Streptococcus multispecies_sppn13_2_nov_97.773%
Alloprevotella sp._HMT_473_nov_97.546%
Alloprevotella sp._HMT_914
Streptococcus oralis_subsp._dentisani_clade_058
Streptococcus sp._HMT_061
Prevotella nanceiensis
Streptococcus chosunense
Abiotrophia defectiva
Neisseria flava
Alloprevotella sp._HMT_308_nov_97.347%
Lachnospiraceae_[G-2] bacterium_HMT_096
Leptotrichia sp._HMT_221
Streptococcus sp._HMT_064
Stomatobaculum sp._HMT_097
Leptotrichia sp._HMT_215
Streptococcus infantis_clade_431
Streptococcus mitis
Megasphaera micronuciformis
Prevotella salivae
Streptococcus parasanguinis_parasanguinis_clade_721
Veillonella dispar_parvula
Schaalia lingnae_[Not_Validly_Published]
Veillonella denticariosi_dispar_parvula
Prevotella pallens
Leptotrichia sp._HMT_417
Streptococcus sp._HMT_423
Neisseria mucosa
Lancefieldella parvula
Alloprevotella sp._HMT_308
Veillonella dispar
Prevotella jejuni
Veillonella parvula
Actinomyces graevenitzii
Schaalia sp._HMT_180
Gemella sanguinis
Veillonella rogosae
Porphyromonas pasteri
Schaalia odontolytica
Streptococcus sp._HMT_066
Streptococcus sp._HMT_074
Neisseria flavescens
Granulicatella adiacens
Schaalia odontolyticus
Prevotella histicola
Veillonella atypica
Schaalia sp._HMT_172
Streptococcus australis
Fusobacterium periodonticum
Neisseria perflava
Streptococcus infantis_infantis_clade_638
Haemophilus parainfluenzae
Prevotella melaninogenica
Streptococcus parasanguinis_clade_411
Rothia mucilaginosa
Streptococcus salivarius
Species
F17924-S207
F17924-S209
F17924-S212
F17924-S215
F17924-S217
F17924-S223
F17924-S225
F17924-S230
F17924-S234
F17924-S236
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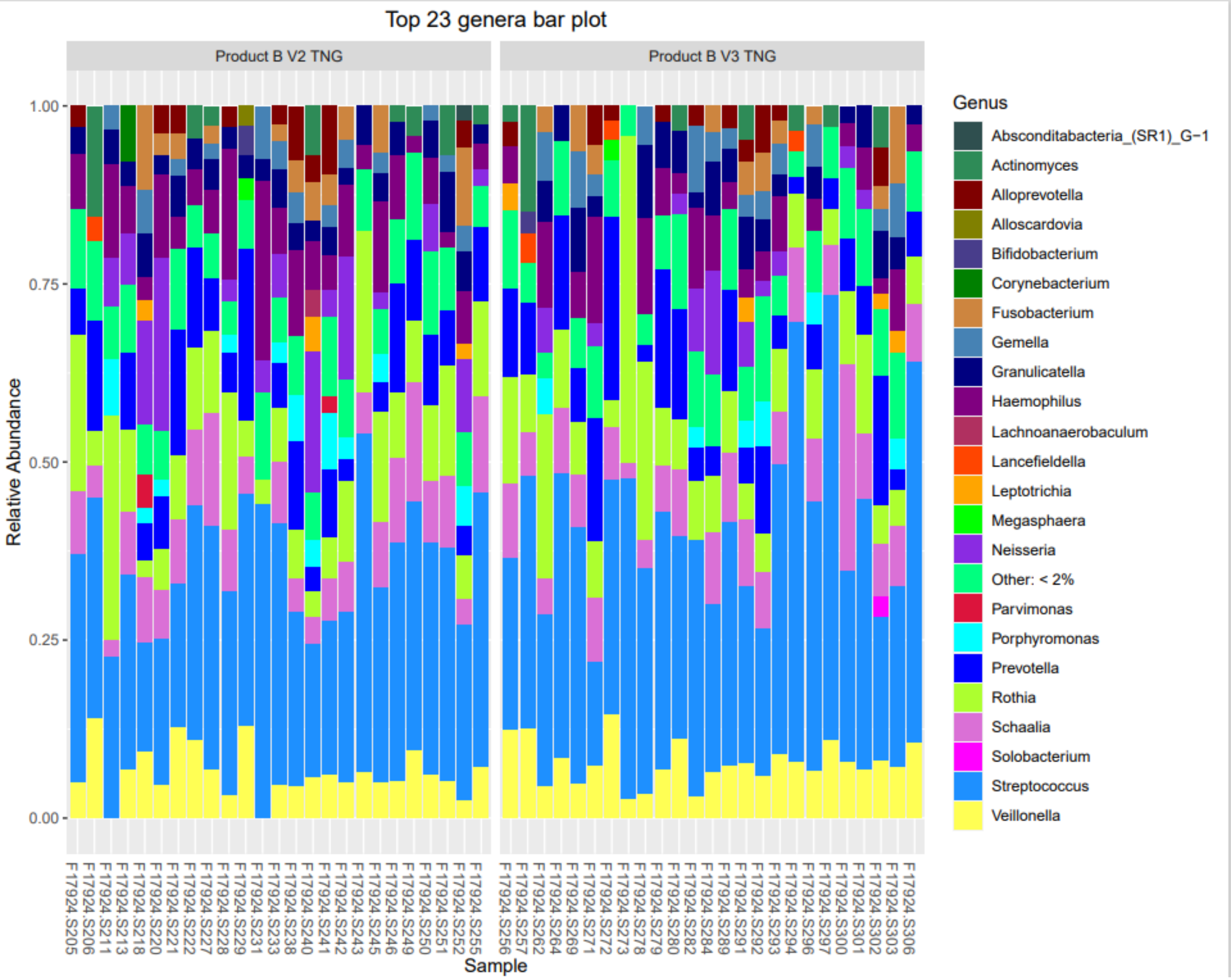
F17924-S268
F17924-S274
F17924-S276
F17924-S281
F17924-S285
F17924-S287
F17924-S290
F17924-S298
F17924-S304
Samples

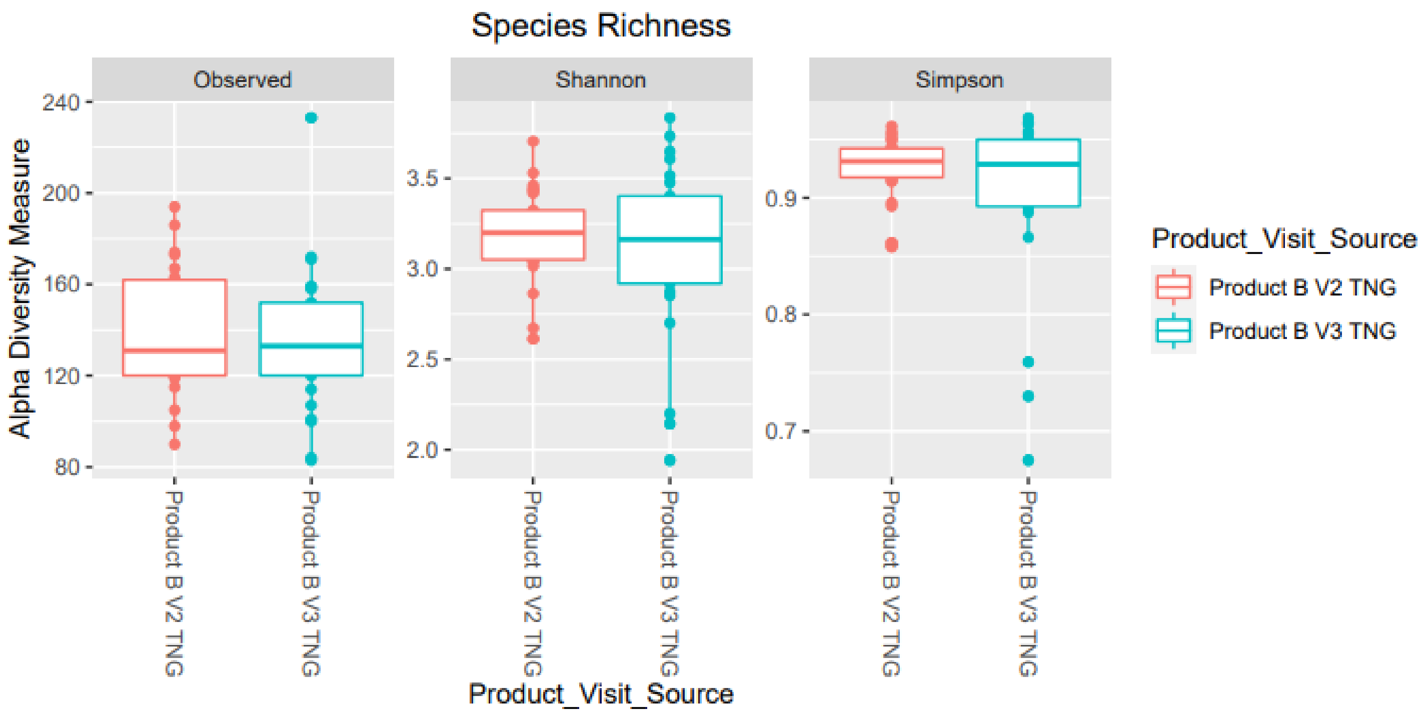
7)

Comparison 10. Product B V2 TNG vs Product B V3 TNG

1) Taxonomy bar graphs

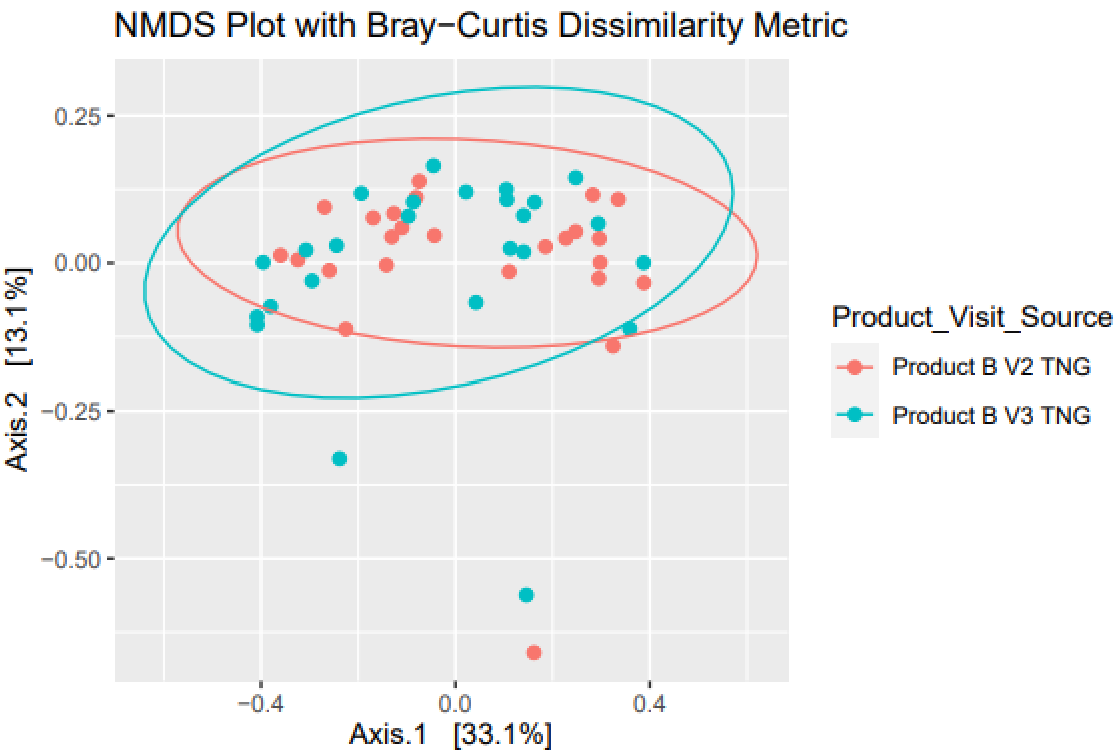


2) Alpha



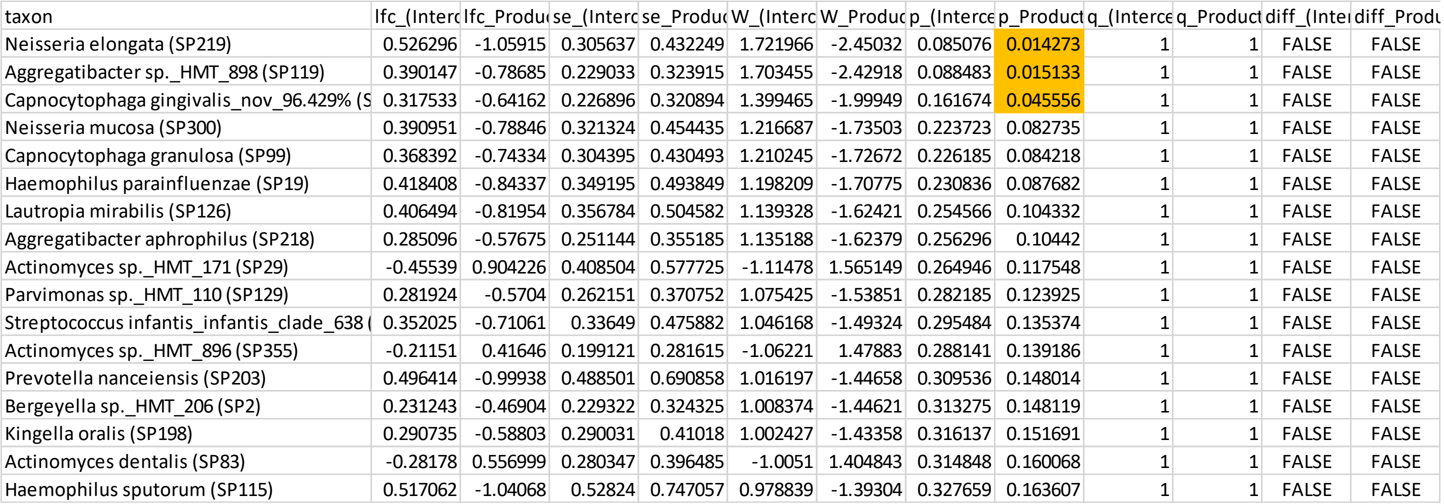
No significance

3) Beta diversity



Not significant

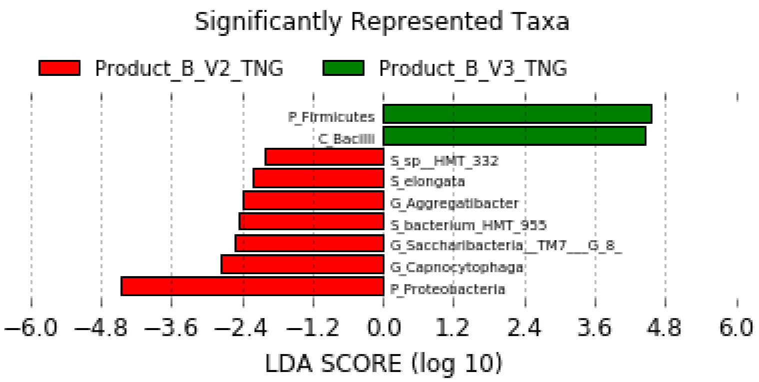
4) Differential abundance



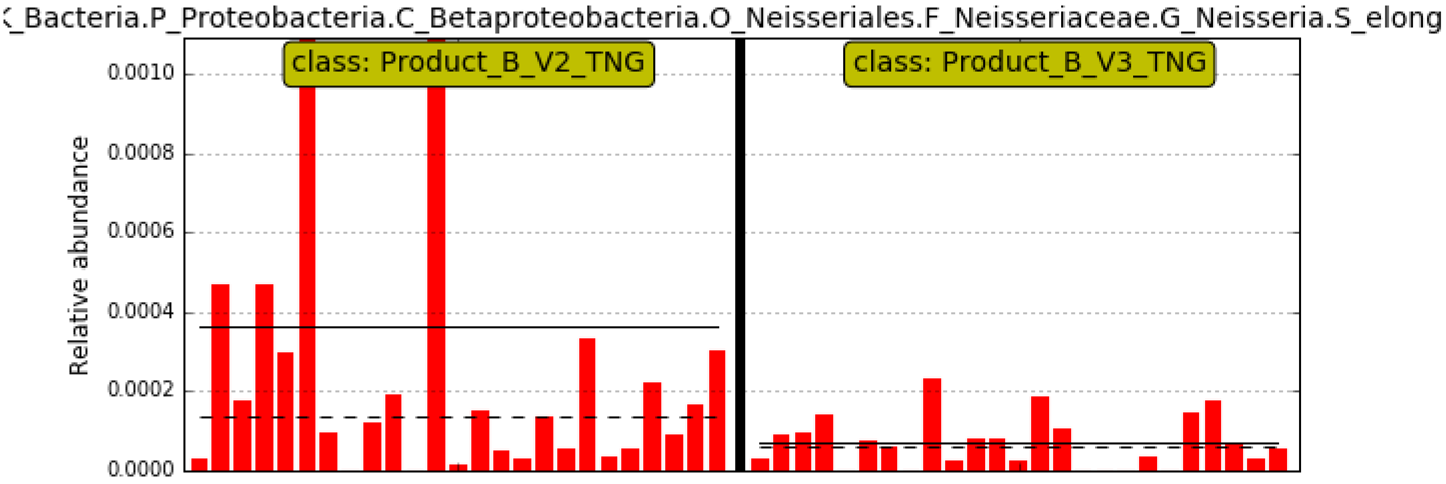
taxon	lfc_(Interc	lfc_Produc	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inter	diff_Produ
Neisseria elongata (SP219)	0.526296	-1.05915	0.305637	0.432249	1.721966	-2.45032	0.085076	0.014273	1	1	FALSE	FALSE
Aggregatibacter sp._HMT_898 (SP119)	0.390147	-0.78685	0.229033	0.323915	1.703455	-2.42918	0.088483	0.015133	1	1	FALSE	FALSE
Capnocytophaga gingivalis_nov_96.429% (S	0.317533	-0.64162	0.226896	0.320894	1.399465	-1.99949	0.161674	0.045556	1	1	FALSE	FALSE
Neisseria mucosa (SP300)	0.390951	-0.78846	0.321324	0.454435	1.216687	-1.73503	0.223723	0.082735	1	1	FALSE	FALSE
Capnocytophaga granulosa (SP99)	0.368392	-0.74334	0.304395	0.430493	1.210245	-1.72672	0.226185	0.084218	1	1	FALSE	FALSE
Haemophilus parainfluenzae (SP19)	0.418408	-0.84337	0.349195	0.493849	1.198209	-1.70775	0.230836	0.087682	1	1	FALSE	FALSE
Lautropia mirabilis (SP126)	0.406494	-0.81954	0.356784	0.504582	1.139328	-1.62421	0.254566	0.104332	1	1	FALSE	FALSE
Aggregatibacter aphrophilus (SP218)	0.285096	-0.57675	0.251144	0.355185	1.135188	-1.62379	0.256296	0.10442	1	1	FALSE	FALSE
Actinomyces sp._HMT_171 (SP29)	-0.45539	0.904226	0.408504	0.577725	-1.11478	1.565149	0.264946	0.117548	1	1	FALSE	FALSE
Parvimonas sp._HMT_110 (SP129)	0.281924	-0.5704	0.262151	0.370752	1.075425	-1.53851	0.282185	0.123925	1	1	FALSE	FALSE
Streptococcus infantis_infantis_clade_638 (	0.352025	-0.71061	0.33649	0.475882	1.046168	-1.49324	0.295484	0.135374	1	1	FALSE	FALSE
Actinomyces sp._HMT_896 (SP355)	-0.21151	0.41646	0.199121	0.281615	-1.06221	1.47883	0.288141	0.139186	1	1	FALSE	FALSE
Prevotella nanceiensis (SP203)	0.496414	-0.99938	0.488501	0.690858	1.016197	-1.44658	0.309536	0.148014	1	1	FALSE	FALSE
Bergeyella sp._HMT_206 (SP2)	0.231243	-0.46904	0.229322	0.324325	1.008374	-1.44621	0.313275	0.148119	1	1	FALSE	FALSE
Kingella oralis (SP198)	0.290735	-0.58803	0.290031	0.41018	1.002427	-1.43358	0.316137	0.151691	1	1	FALSE	FALSE
Actinomyces dentalis (SP83)	-0.28178	0.556999	0.280347	0.396485	-1.0051	1.404843	0.314848	0.160068	1	1	FALSE	FALSE
Haemophilus sputorum (SP115)	0.517062	-1.04068	0.52824	0.747057	0.978839	-1.39304	0.327659	0.163607	1	1	FALSE	FALSE

Nothing significant but some trends as also shown in Lefse

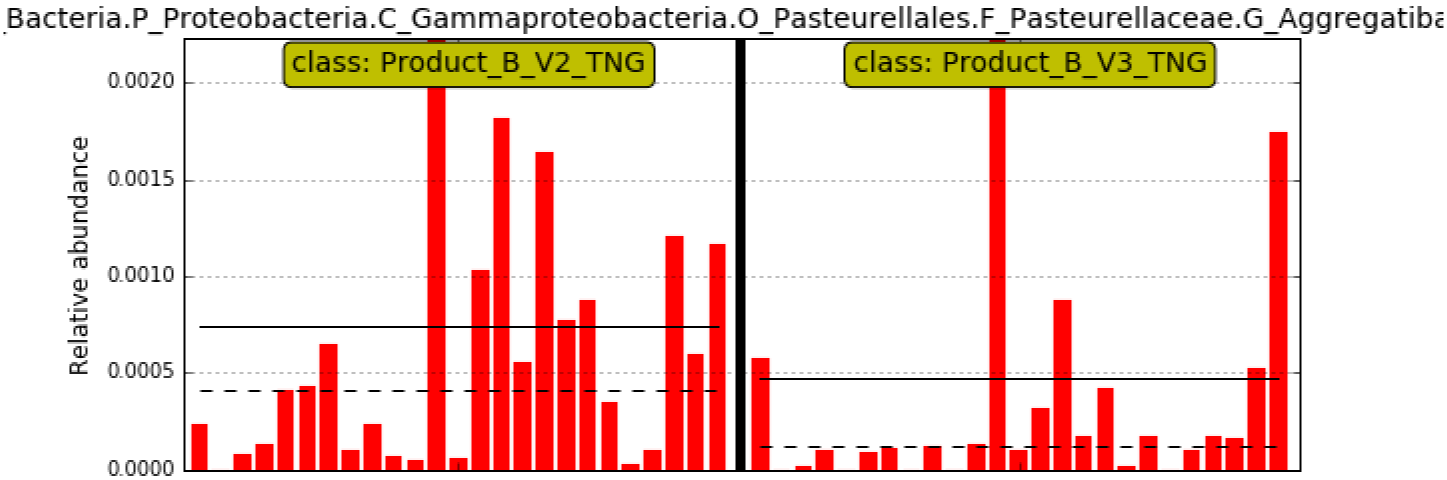
5) Lefse

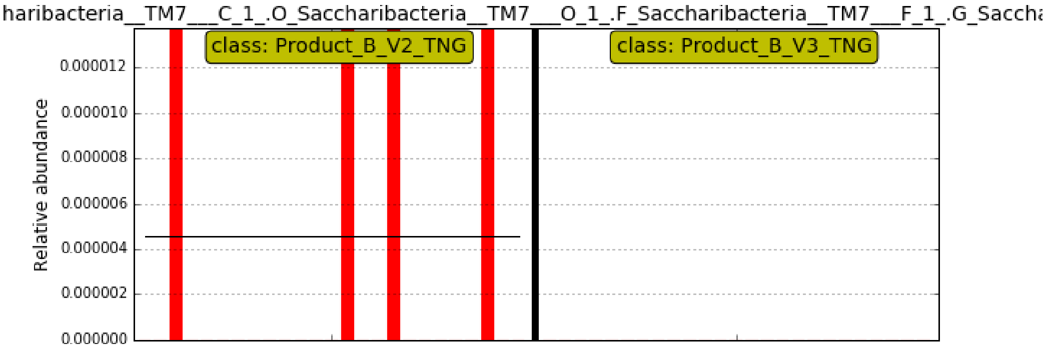


Significantly Represented Taxa
Product_B_V2_TNG
Product_B_V3_TNG
P_Firmicutes
C_Bacilli
S_sp__HMT_332
S_elongata
G_Aggregatibacter
S_bacterium_HMT_955
G_Saccharibacteria__TM7___G_8_
G_Capnocytophaga
P_Proteobacteria
−6.0
−4.8
−3.6
−2.4
−1.2
0.0
1.2
2.4
3.6
4.8
6.0
LDA SCORE (log 10)



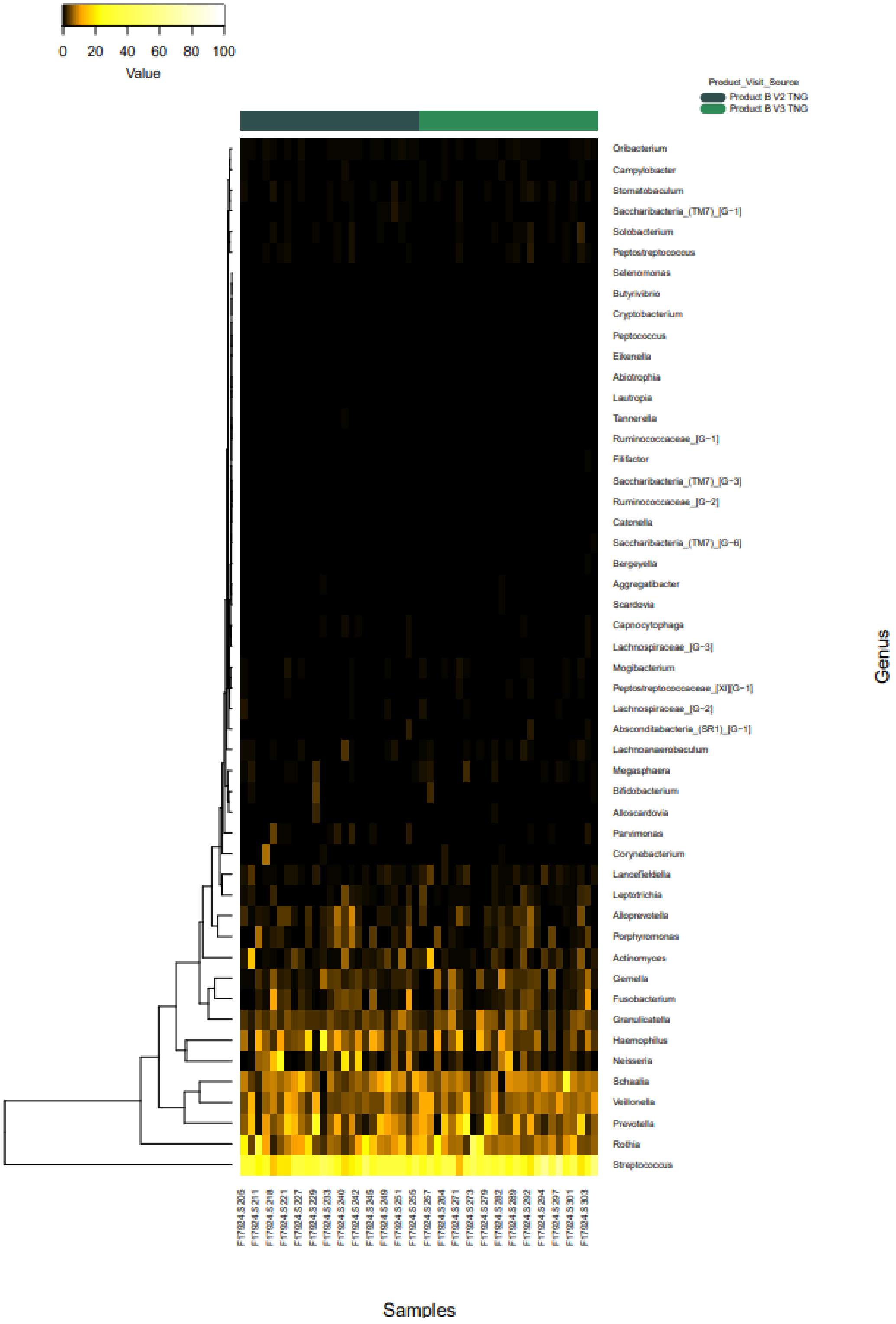
_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Neisseria.S_elong
class: Product_B_V2_TNG
class: Product_B_V3_TNG
Relative abundance
0.0010
0.0008
0.0006
0.0004
0.0002
0.0000

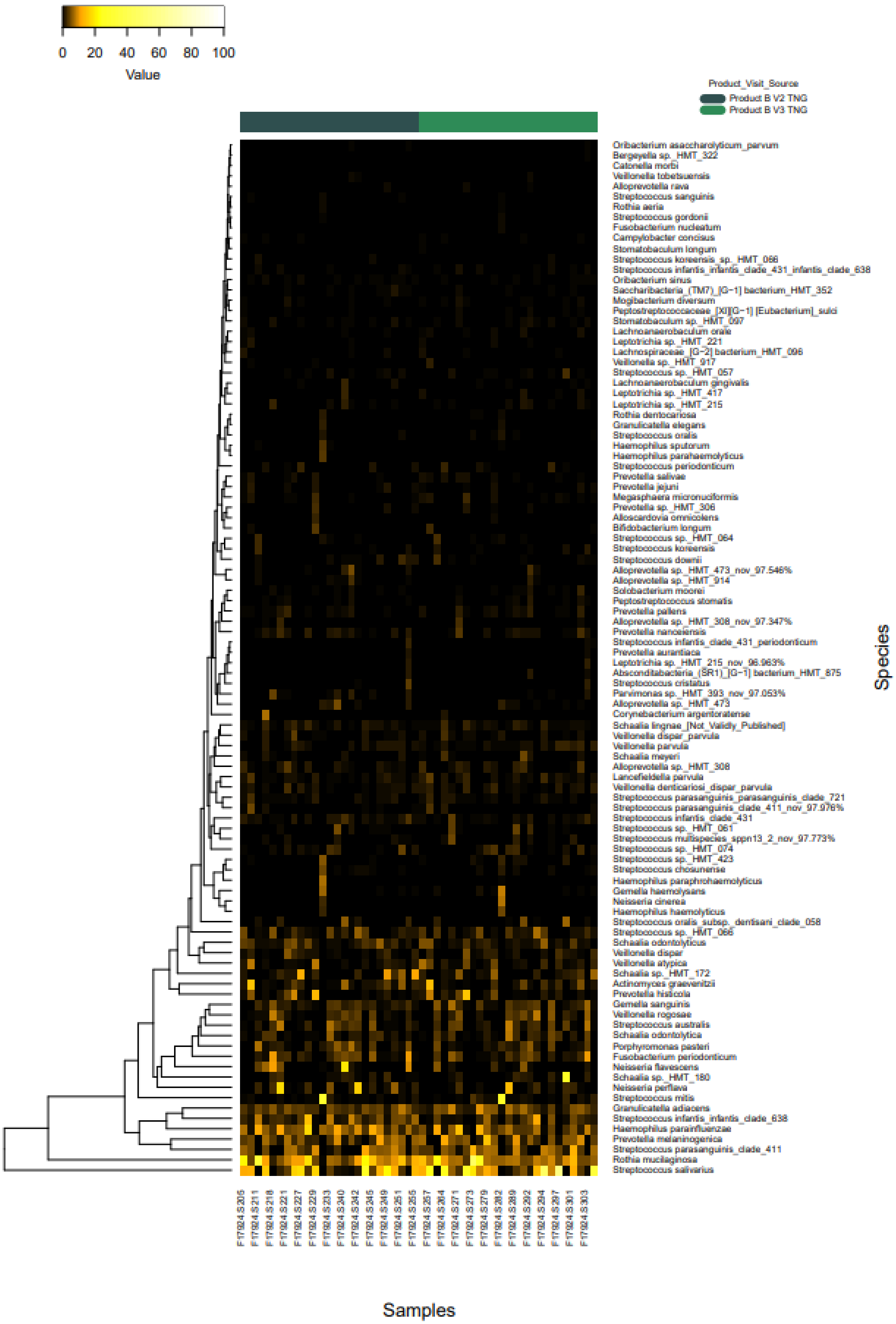




very low levels

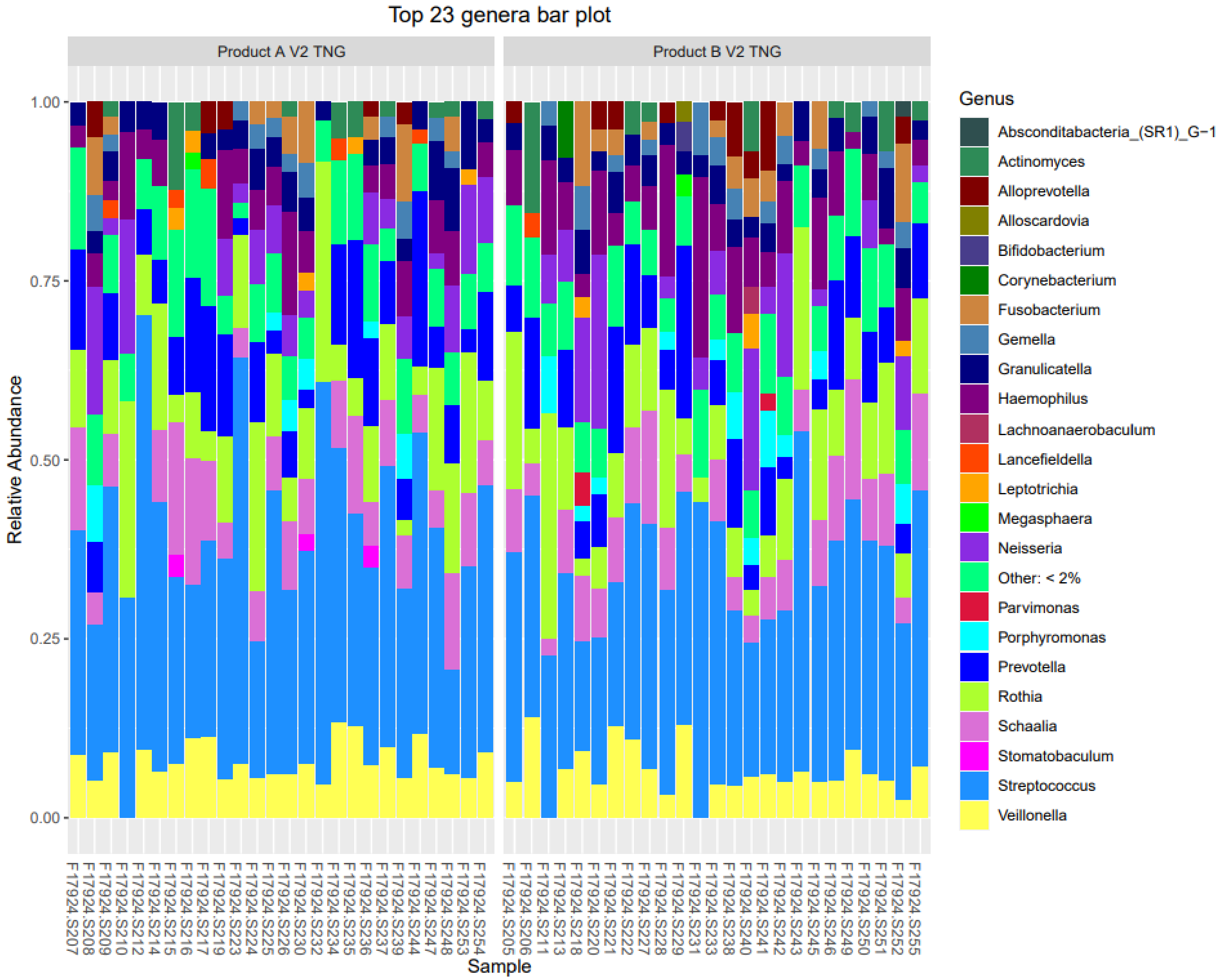
6) Heat map. Difficult to see differences



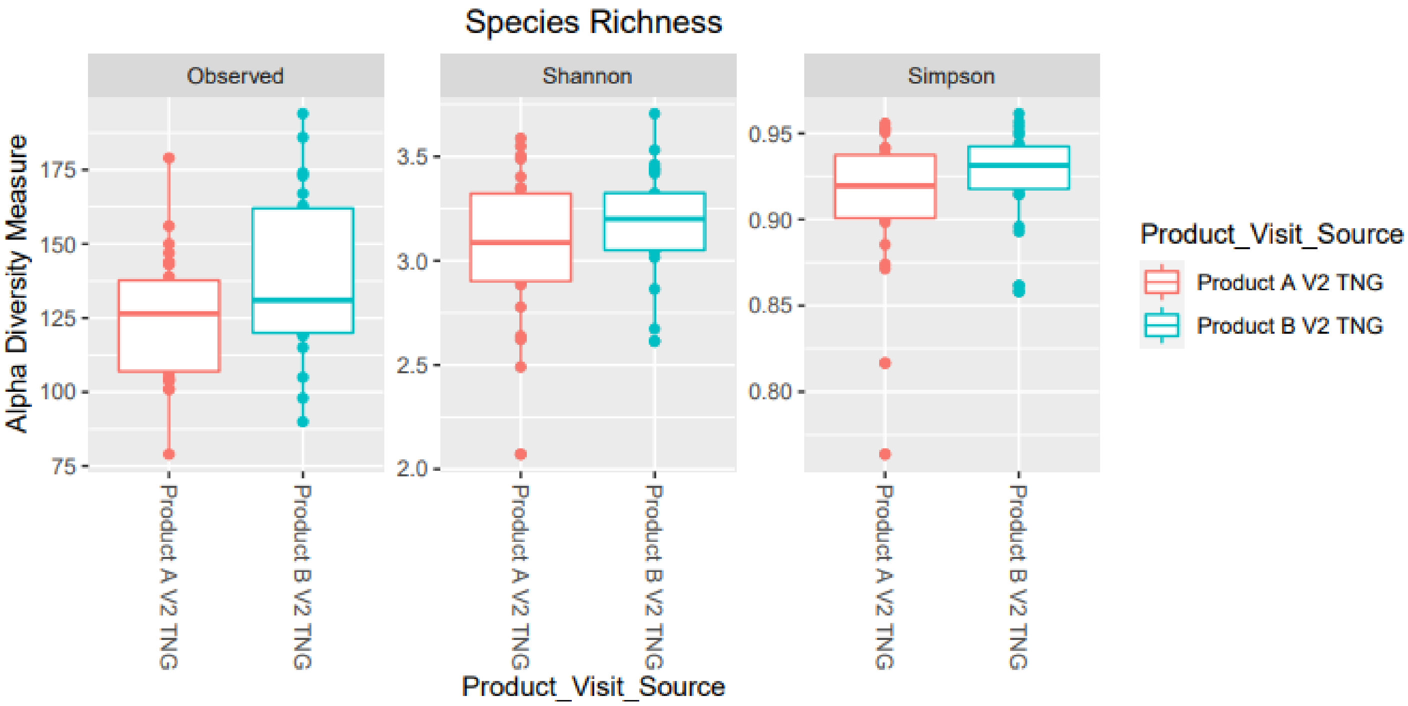

0
20
40
60
80
100
Value
Product_Visit_Source
Product B V2 TNG
Product B V3 TNG
Oribacterium asaccharolyticum_parvum
Bergeyella sp._HMT_322
Catonella morbi
Veillonella tobetsuensis
Alloprevotella rava
Streptococcus sanguinis
Rothia aeria
Streptococcus gordonii
Fusobacterium nucleatum
Campylobacter concisus
Stomatobaculum longum
Streptococcus koreensis_sp._HMT_066
Streptococcus infantis_infantis_clade_431_infantis_clade_638
Oribacterium sinus
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_352
Mogibacterium diversum
Peptostreptococcaceae_[XI][G-1] [Eubacterium]_sulci
Stomatobaculum sp._HMT_097
Lachnoanaerobaculum orale
Leptotrichia sp._HMT_221
Lachnospiraceae_[G-2] bacterium_HMT_096
Veillonella sp._HMT_917
Streptococcus sp._HMT_057
Lachnoanaerobaculum gingivalis
Leptotrichia sp._HMT_417
Leptotrichia sp._HMT_215
Rothia dentocariosa
Granulicatella elegans
Streptococcus oralis
Haemophilus sputorum
Haemophilus parahaemolyticus
Streptococcus periodonticum
Prevotella salivae
Prevotella jejuni
Megasphaera micronuciformis
Prevotella sp._HMT_306
Alloscardovia omnicolens
Bifidobacterium longum
Streptococcus sp._HMT_064
Streptococcus koreensis
Streptococcus downii
Alloprevotella sp._HMT_473_nov_97.546%
Alloprevotella sp._HMT_914
Solobacterium moorei
Peptostreptococcus stomatis
Prevotella pallens
Alloprevotella sp._HMT_308_nov_97.347%
Prevotella nanceiensis
Streptococcus infantis_clade_431_periodonticum
Prevotella aurantiaca
Leptotrichia sp._HMT_215_nov_96.963%
Absconditabacteria_(SR1)_[G-1] bacterium_HMT_875
Streptococcus cristatus
Parvimonas sp._HMT_393_nov_97.053%
Alloprevotella sp._HMT_473
Corynebacterium argentoratense
Schaalia lingnae_[Not_Validly_Published]
Veillonella dispar_parvula
Veillonella parvula
Schaalia meyeri
Alloprevotella sp._HMT_308
Lancefieldella parvula
Veillonella denticariosi_dispar_parvula
Streptococcus parasanguinis_parasanguinis_clade_721
Streptococcus parasanguinis_clade_411_nov_97.976%
Streptococcus infantis_clade_431
Streptococcus sp._HMT_061
Streptococcus multispecies_sppn13_2_nov_97.773%
Streptococcus sp._HMT_074
Streptococcus sp._HMT_423
Streptococcus chosunense
Haemophilus paraphrohaemolyticus
Gemella haemolysans
Neisseria cinerea
Haemophilus haemolyticus
Streptococcus oralis_subsp._dentisani_clade_058
Streptococcus sp._HMT_066
Schaalia odontolyticus
Veillonella dispar
Veillonella atypica
Schaalia sp._HMT_172
Actinomyces graevenitzii
Prevotella histicola
Gemella sanguinis
Veillonella rogosae
Streptococcus australis
Schaalia odontolytica
Porphyromonas pasteri
Fusobacterium periodonticum
Neisseria flavescens
Schaalia sp._HMT_180
Neisseria perflava
Streptococcus mitis
Granulicatella adiacens
Streptococcus infantis_infantis_clade_638
Haemophilus parainfluenzae
Prevotella melaninogenica
Streptococcus parasanguinis_clade_411
Rothia mucilaginosa
Streptococcus salivarius
Species
F17924.S205
F17924.S211
F17924.S218
F17924.S221
F17924.S227
F17924.S229
F17924.S233
F17924.S240
F17924.S242
F17924.S245
F17924.S249
F17924.S251
F17924.S255
F17924.S257
F17924.S264
F17924.S271
F17924.S273
F17924.S279
F17924.S282
F17924.S289
F17924.S292
F17924.S294
F17924.S297
F17924.S301
F17924.S303
Samples

Comparison 11. Product A V2 TNG vs Product B V2 TNG

1) Taxonomy bar graphs

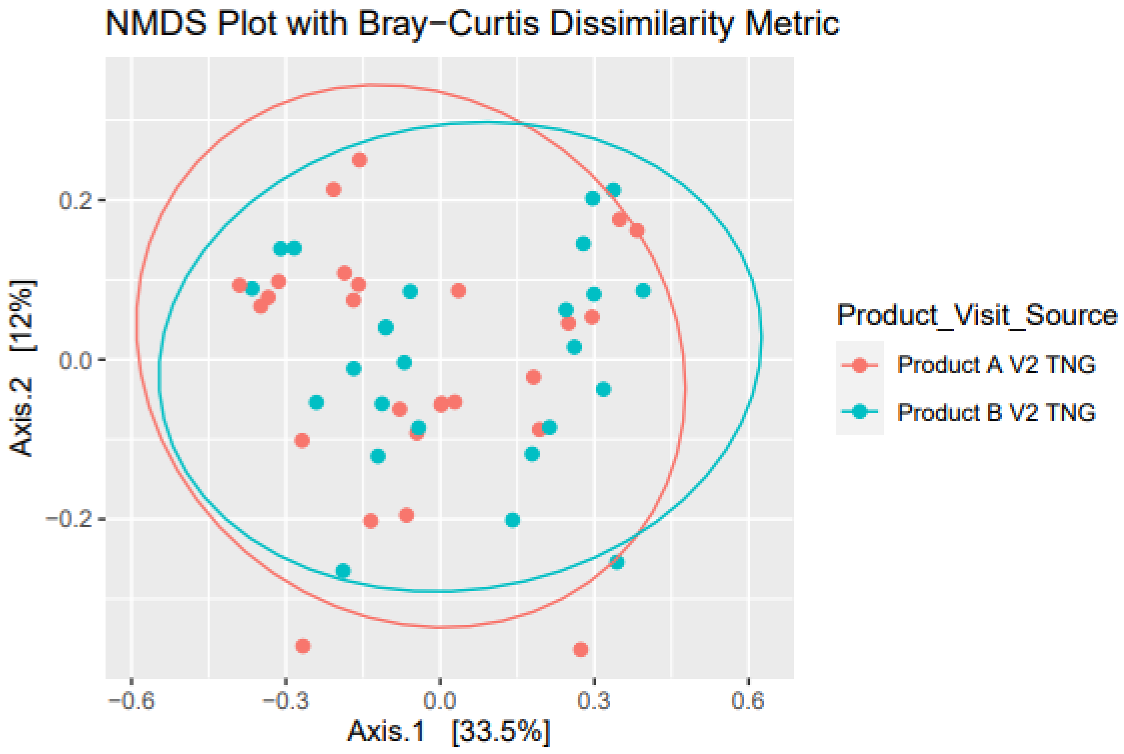


2) Alpha



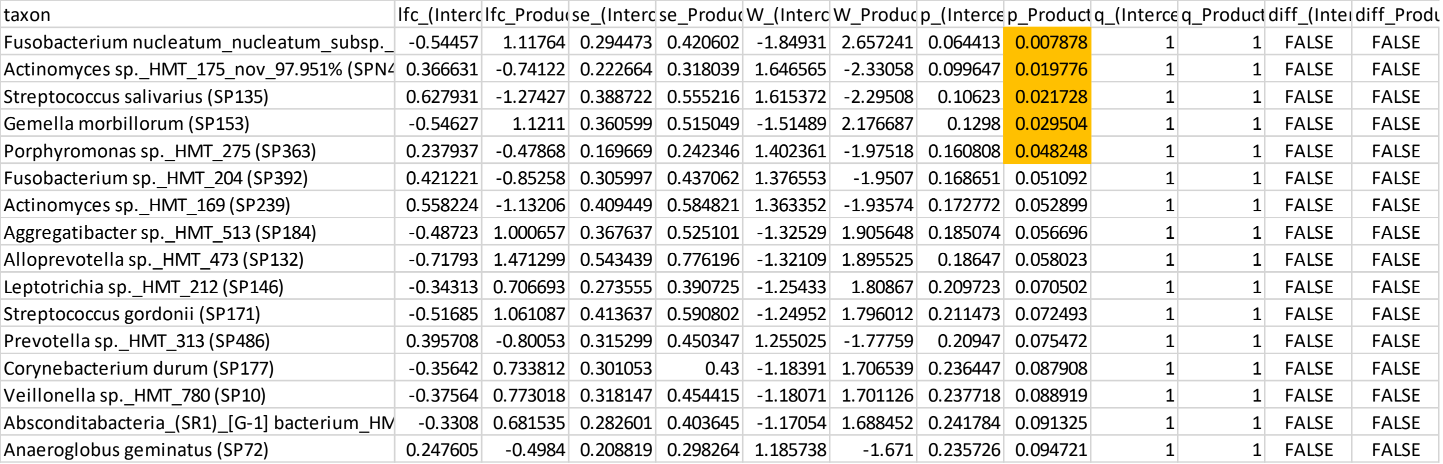
No significant differences

3) Beta diversity



No significant differences

4) Differential abundance

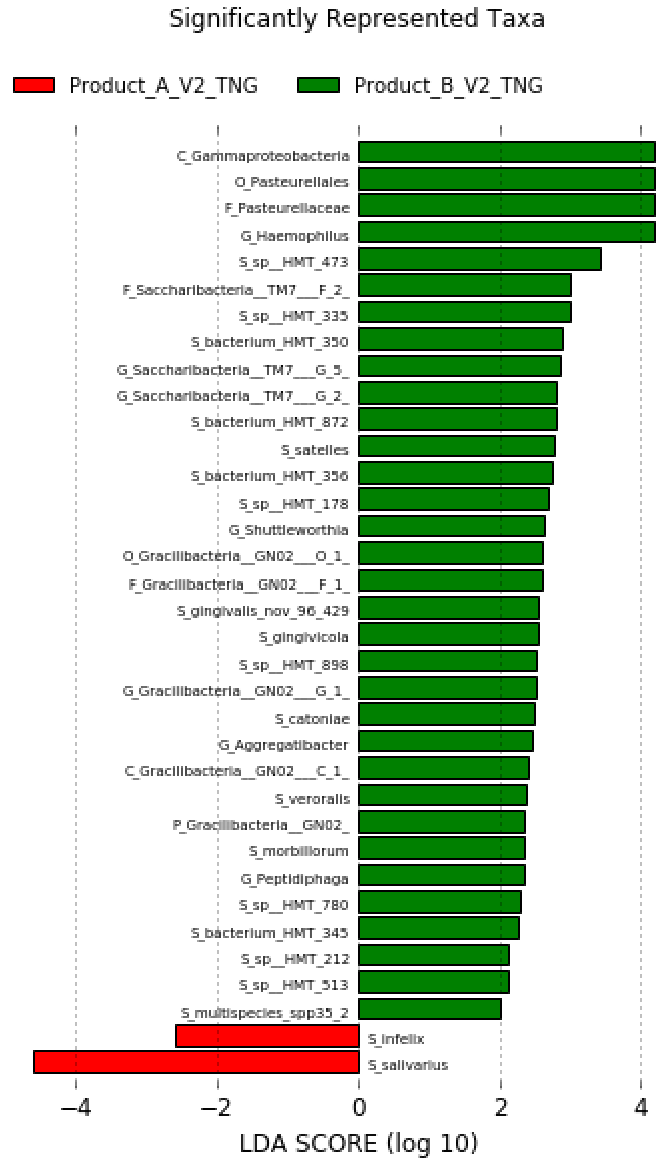


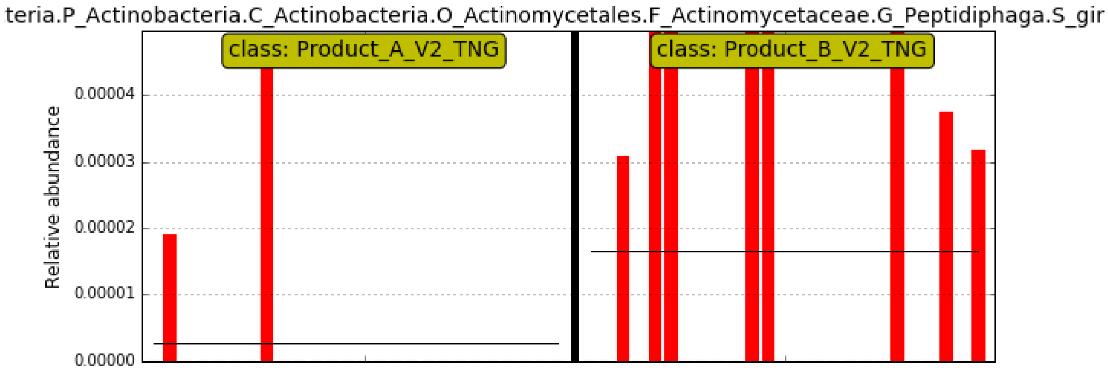
taxon	lfc_(Interc	lfc_Produ	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inte	diff_Produ
Fusobacterium nucleatum_nucleatum_subsp._	-0.54457	1.11764	0.294473	0.420602	-1.84931	2.657241	0.064413	0.007878	1	1	FALSE	FALSE
Actinomyces sp._HMT_175_nov_97.951% (SPN4	0.366631	-0.74122	0.222664	0.318039	1.646565	-2.33058	0.099647	0.019776	1	1	FALSE	FALSE
Streptococcus salivarius (SP135)	0.627931	-1.27427	0.388722	0.555216	1.615372	-2.29508	0.10623	0.021728	1	1	FALSE	FALSE
Gemella morbillorum (SP153)	-0.54627	1.1211	0.360599	0.515049	-1.51489	2.176687	0.1298	0.029504	1	1	FALSE	FALSE
Porphyromonas sp._HMT_275 (SP363)	0.237937	-0.47868	0.169669	0.242346	1.402361	-1.97518	0.160808	0.048248	1	1	FALSE	FALSE
Fusobacterium sp._HMT_204 (SP392)	0.421221	-0.85258	0.305997	0.437062	1.376553	-1.9507	0.168651	0.051092	1	1	FALSE	FALSE
Actinomyces sp._HMT_169 (SP239)	0.558224	-1.13206	0.409449	0.584821	1.363352	-1.93574	0.172772	0.052899	1	1	FALSE	FALSE
Aggregatibacter sp._HMT_513 (SP184)	-0.48723	1.000657	0.367637	0.525101	-1.32529	1.905648	0.185074	0.056696	1	1	FALSE	FALSE
Alloprevotella sp._HMT_473 (SP132)	-0.71793	1.471299	0.543439	0.776196	-1.32109	1.895525	0.18647	0.058023	1	1	FALSE	FALSE
Leptotrichia sp._HMT_212 (SP146)	-0.34313	0.706693	0.273555	0.390725	-1.25433	1.80867	0.209723	0.070502	1	1	FALSE	FALSE
Streptococcus gordonii (SP171)	-0.51685	1.061087	0.413637	0.590802	-1.24952	1.796012	0.211473	0.072493	1	1	FALSE	FALSE
Prevotella sp._HMT_313 (SP486)	0.395708	-0.80053	0.315299	0.450347	1.255025	-1.77759	0.20947	0.075472	1	1	FALSE	FALSE
Corynebacterium durum (SP177)	-0.35642	0.733812	0.301053	0.43	-1.18391	1.706539	0.236447	0.087908	1	1	FALSE	FALSE
Veillonella sp._HMT_780 (SP10)	-0.37564	0.773018	0.318147	0.454415	-1.18071	1.701126	0.237718	0.088919	1	1	FALSE	FALSE
Absconditabacteria_(SR1)_[G-1] bacterium_HM	-0.3308	0.681535	0.282601	0.403645	-1.17054	1.688452	0.241784	0.091325	1	1	FALSE	FALSE
Anaeroglobus geminatus (SP72)	0.247605	-0.4984	0.208819	0.298264	1.185738	-1.671	0.235726	0.094721	1	1	FALSE	FALSE

No statistical differences.

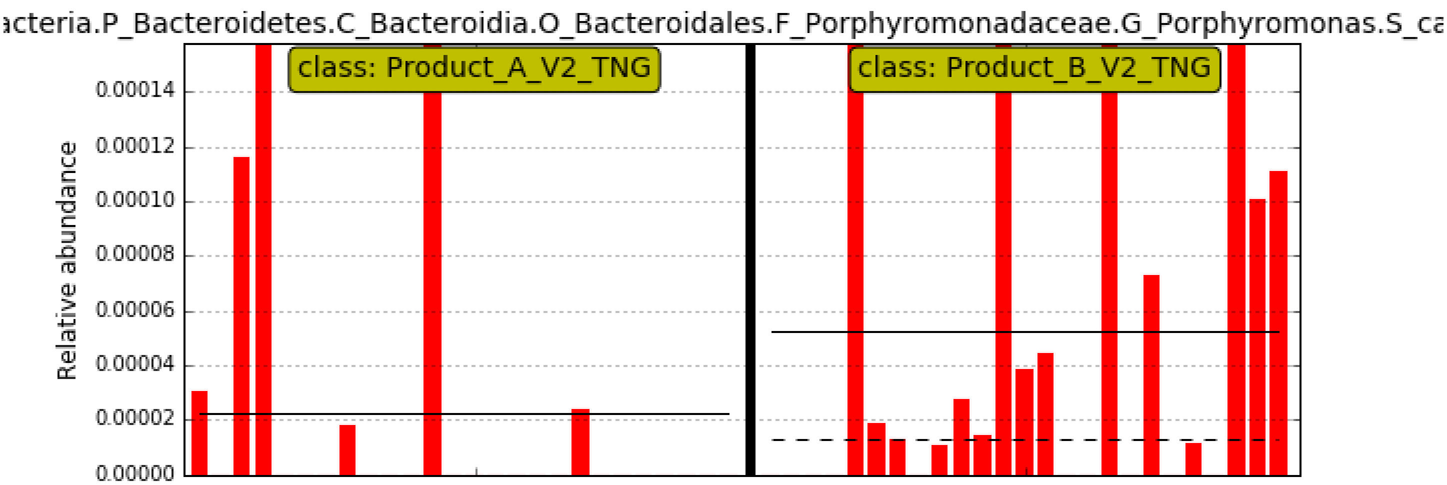
Data indicates that baseline subjects differ a little bit.

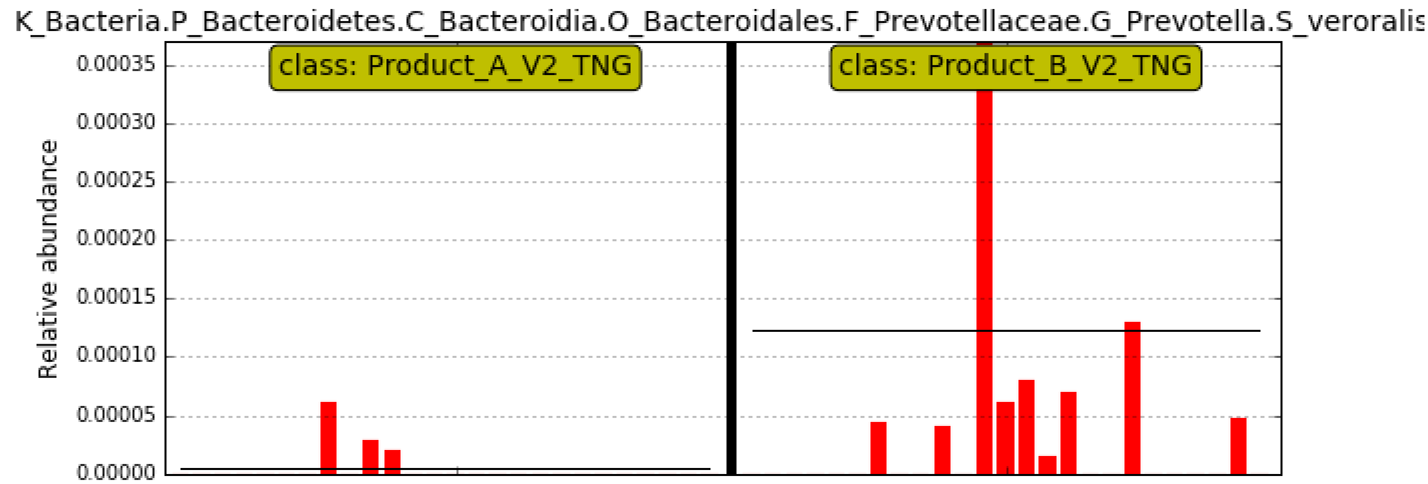
5) Lefse

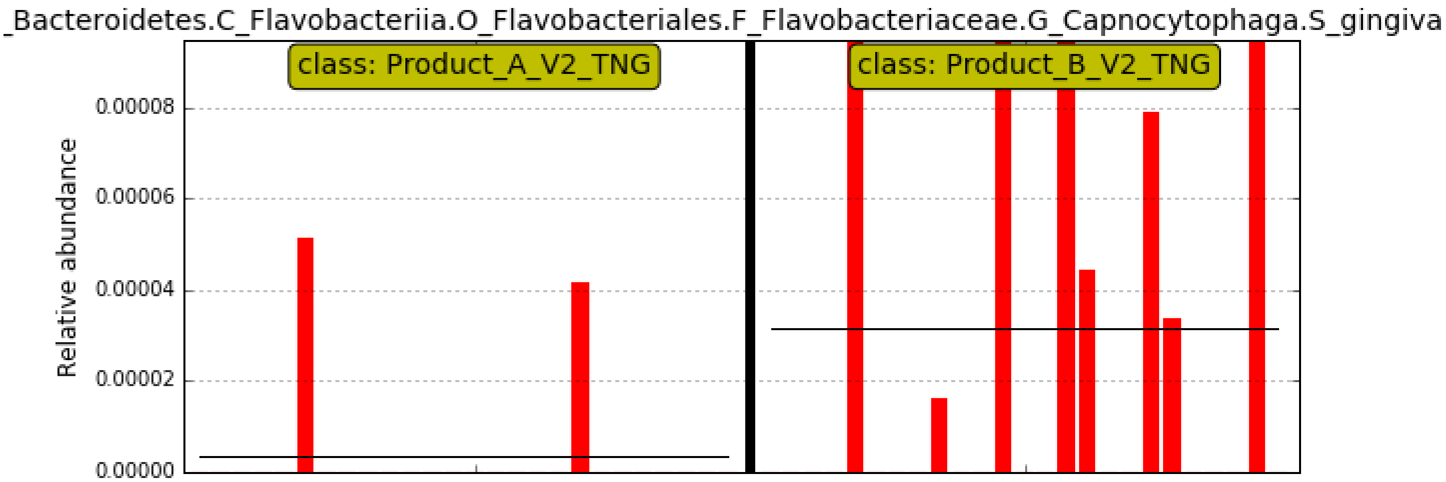


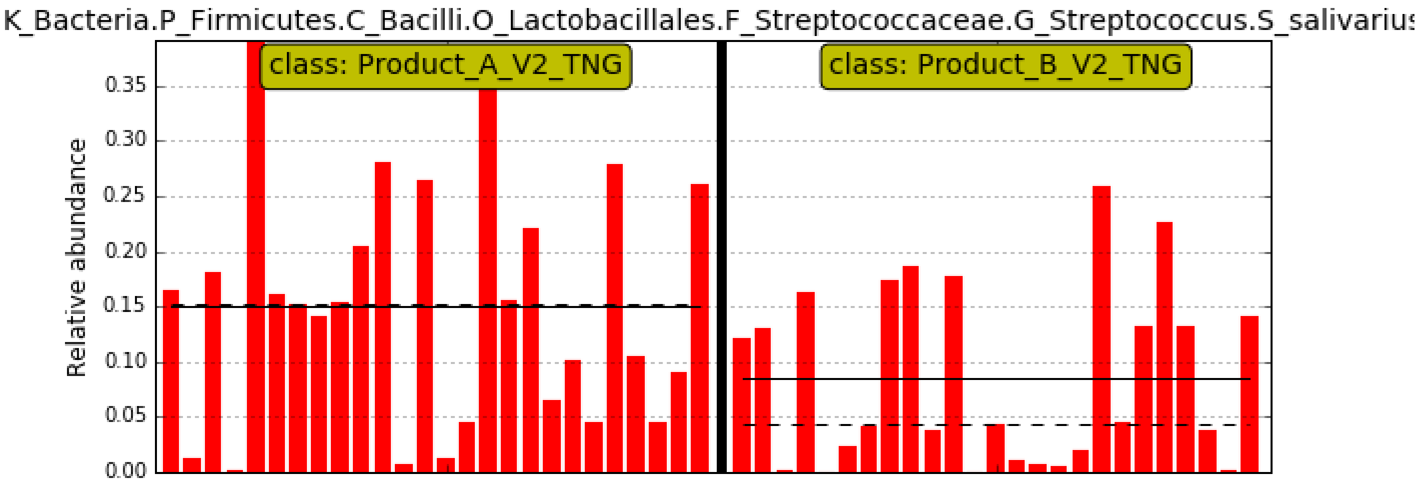


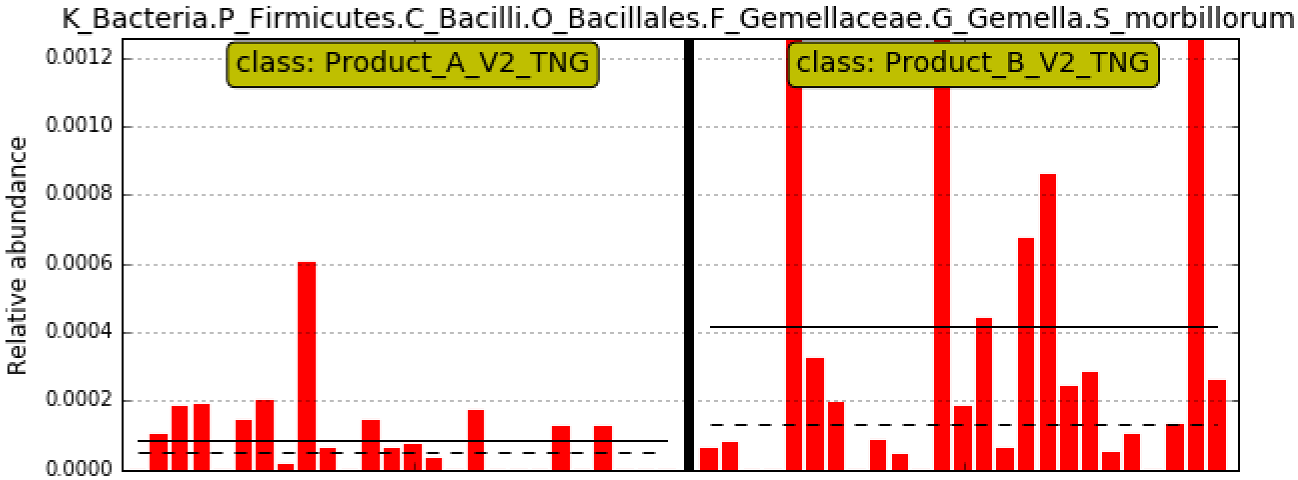
very low levels

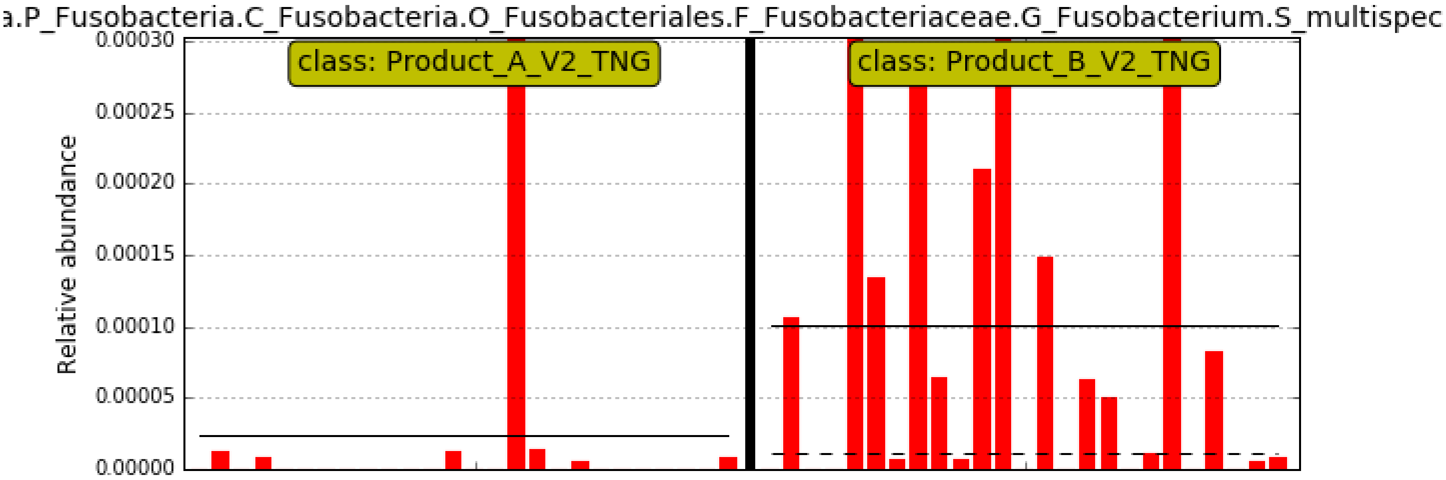

acteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Porphyromonadaceae.G_Porphyromonas.S_ca
class: Product_A_V2_TNG
class: Product_B_V2_TNG
Relative abundance
0.00014
0.00012
0.00010
0.00008
0.00006
0.00004
0.00002
0.00000

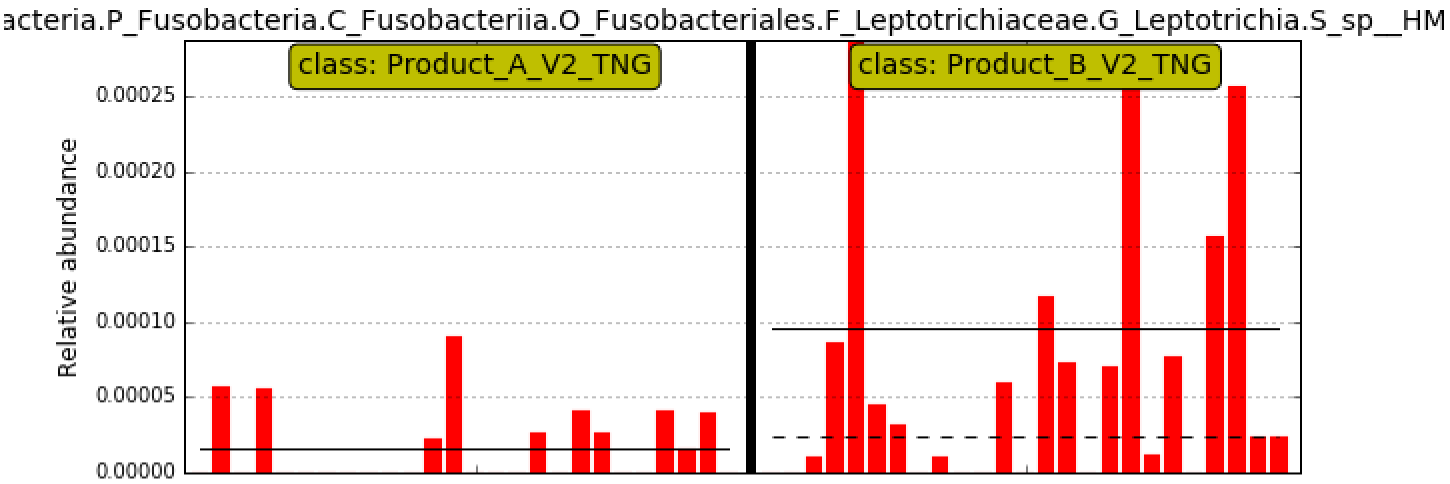

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_veroralis
class: Product_A_V2_TNG
class: Product_B_V2_TNG
Relative abundance
0.00035
0.00030
0.00025
0.00020
0.00015
0.00010
0.00005
0.00000

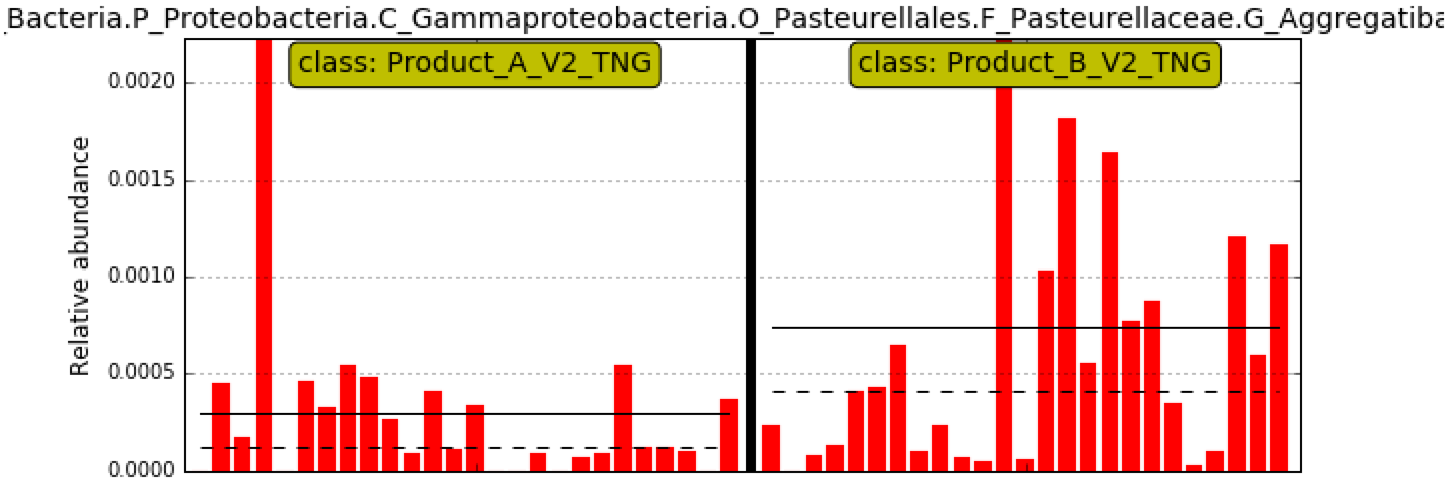

_Bacteroidetes.C_Flavobacteriia.O_Flavobacteriales.F_Flavobacteriaceae.G_Capnocytophaga.S_gingiva
class: Product_A_V2_TNG
class: Product_B_V2_TNG
Relative abundance
0.00008
0.00006
0.00004
0.00002
0.00000

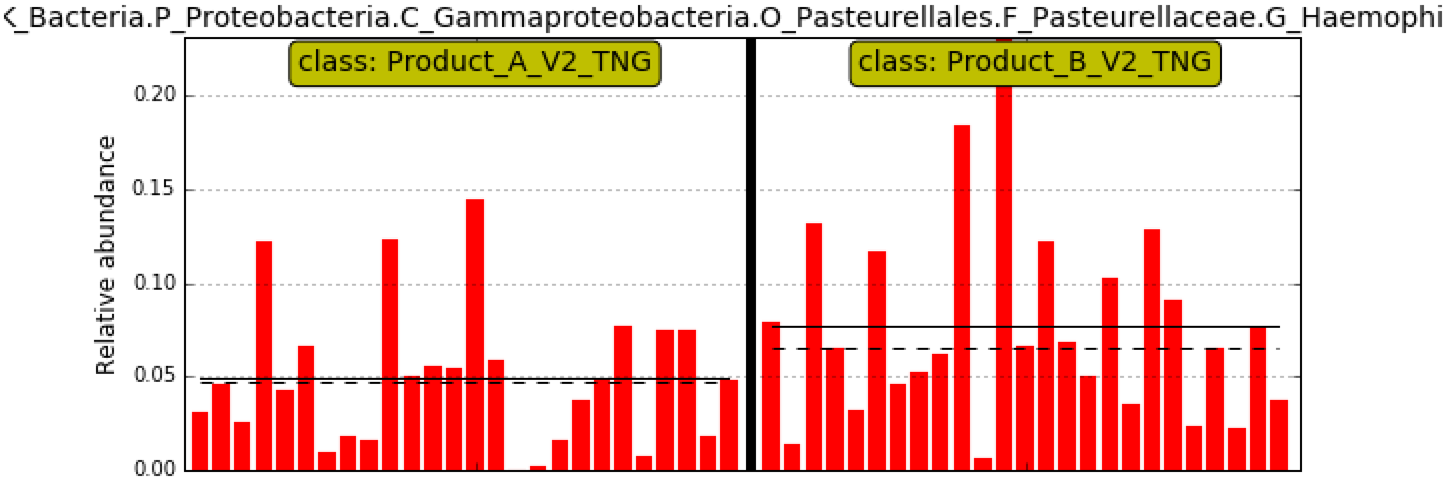

K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_salivarius
class: Product_A_V2_TNG
class: Product_B_V2_TNG
Relative abundance
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00


K_Bacteria.P_Firmicutes.C_Bacilli.O_Bacillales.F_Gemellaceae.G_Gemella.S_morbillorum
class: Product_A_V2_TNG
class: Product_B_V2_TNG
Relative abundance
0.0012
0.0010
0.0008
0.0006
0.0004
0.0002
0.0000

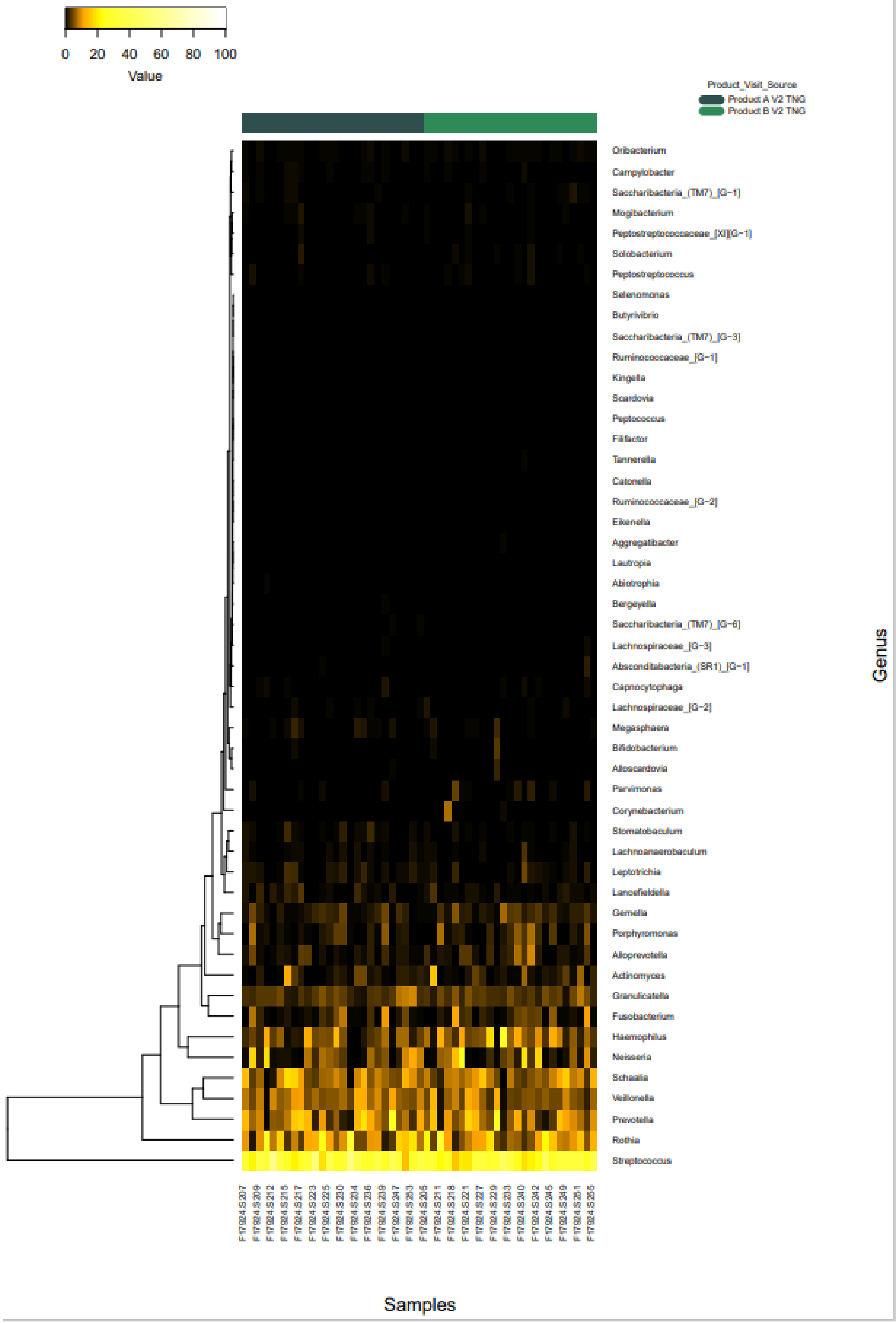

a.P_Fusobacteria.C_Fusobacteria.O_Fusobacteriales.F_Fusobacteriaceae.G_Fusobacterium.S_multispec
class: Product_A_V2_TNG
class: Product_B_V2_TNG
Relative abundance
0.00030
0.00025
0.00020
0.00015
0.00010
0.00005
0.00000

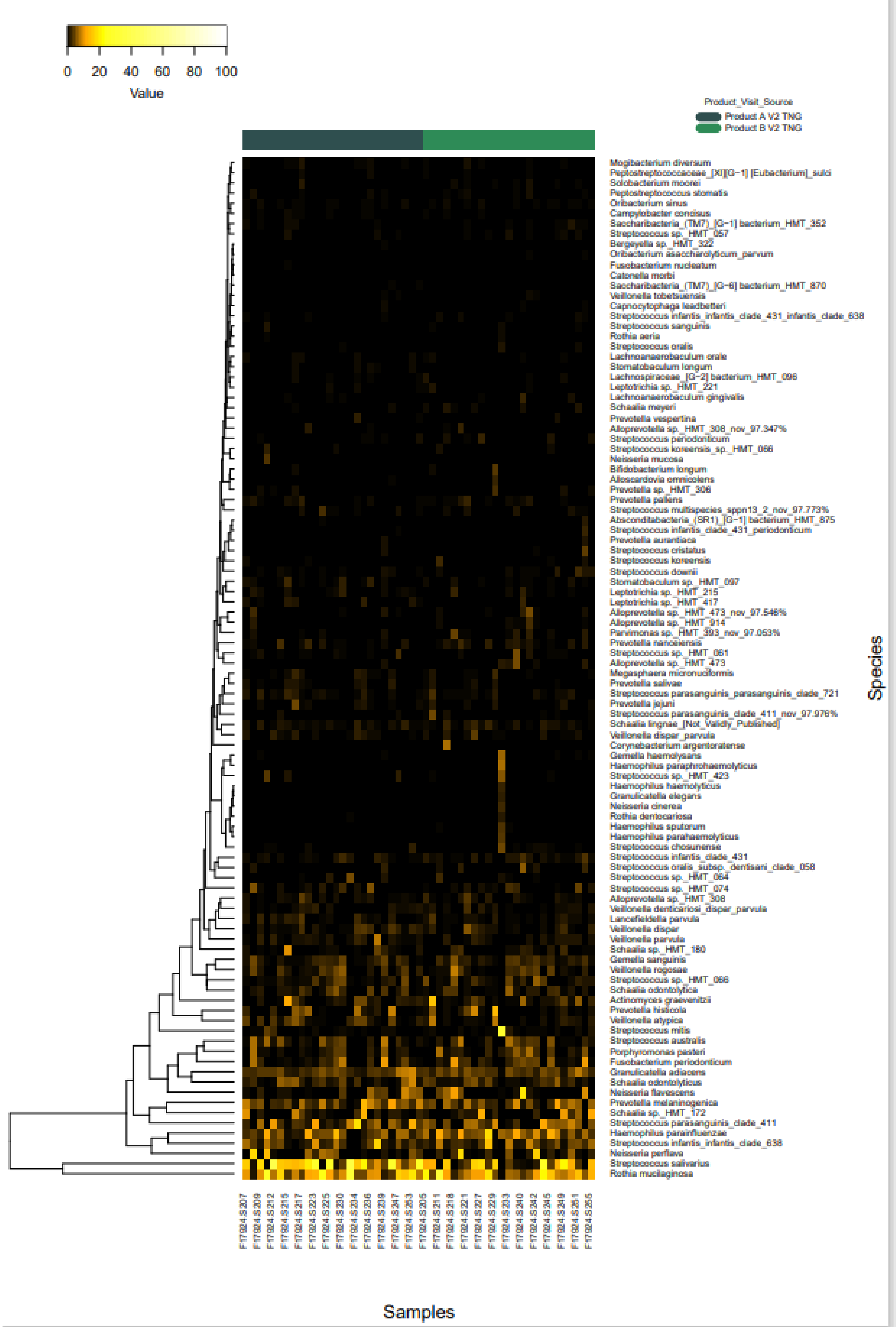

acteria.P_Fusobacteria.C_Fusobacteriia.O_Fusobacteriales.F_Leptotrichiaceae.G_Leptotrichia.S_sp__HM
class: Product_A_V2_TNG
class: Product_B_V2_TNG
Relative abundance
0.00025
0.00020
0.00015
0.00010
0.00005
0.00000


Bacteria.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Aggregatiba
class: Product_A_V2_TNG
class: Product_B_V2_TNG
Relative abundance
0.0020
0.0015
0.0010
0.0005
0.0000


(_Bacteria.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophi
class: Product_A_V2_TNG
class: Product_B_V2_TNG
Relative abundance
0.20
0.15
0.10
0.05
0.00

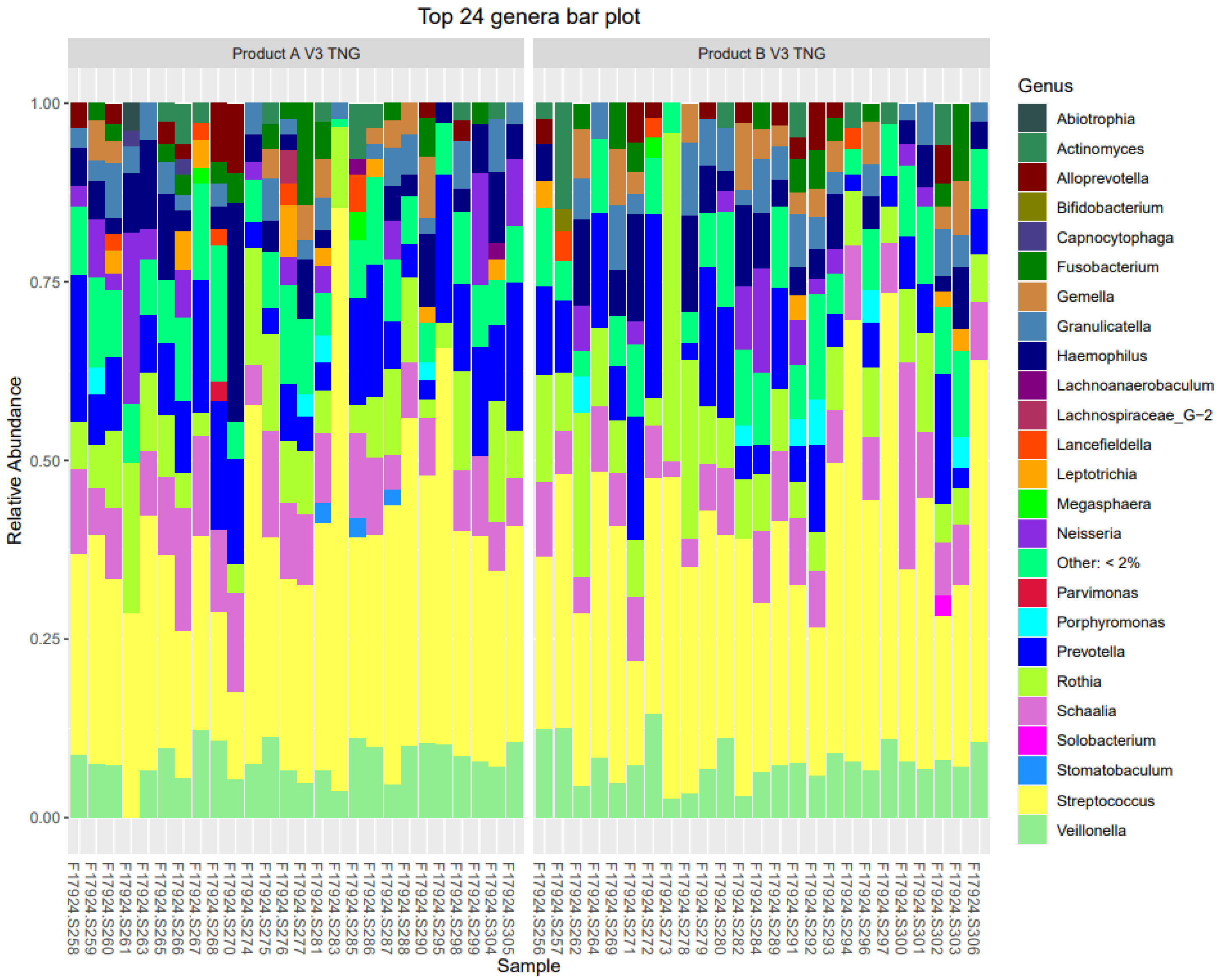
6) Heat map.


0
20
40
60
80
100
Value
Product_Visit_Source
Product A V2 TNG
Product B V2 TNG
Oribacterium
Campylobacter
Saccharibacteria_(TM7)_[G-1]
Mogibacterium
Peptostreptococcaceae_[XI][G-1]
Solobacterium
Peptostreptococcus
Selenomonas
Butyrivibrio
Saccharibacteria_(TM7)_[G-3]
Ruminococcaceae_[G-1]
Kingella
Scardovia
Peptococcus
Filifactor
Tannerella
Catonella
Ruminococcaceae_[G-2]
Eikenella
Aggregatibacter
Lautropia
Abiotrophia
Bergeyella
Saccharibacteria_(TM7)_[G-6]
Lachnospiraceae_[G-3]
Absconditabacteria_(SR1)_[G-1]
Capnocytophaga
Lachnospiraceae_[G-2]
Megasphaera
Bifidobacterium
Alloscardovia
Parvimonas
Corynebacterium
Stomatobaculum
Lachnoanaerobaculum
Leptotrichia
Lancefieldella
Gemella
Porphyromonas
Alloprevotella
Actinomyces
Granulicatella
Fusobacterium
Haemophilus
Neisseria
Schaalia
Veillonella
Prevotella
Rothia
Streptococcus
Genus
FIT924.S207
FIT924.S209
FIT924.S212
FIT924.S215
FIT924.S217
FIT924.S223
FIT924.S225
FIT924.S230
FIT924.S234
FIT924.S236
FIT924.S239
FIT924.S247
FIT924.S253
FIT924.S205
FIT924.S211
FIT924.S218
FIT924.S221
FIT924.S227
FIT924.S229
FIT924.S233
FIT924.S240
FIT924.S242
FIT924.S245
FIT924.S249
FIT924.S251
FIT924.S255
Samples

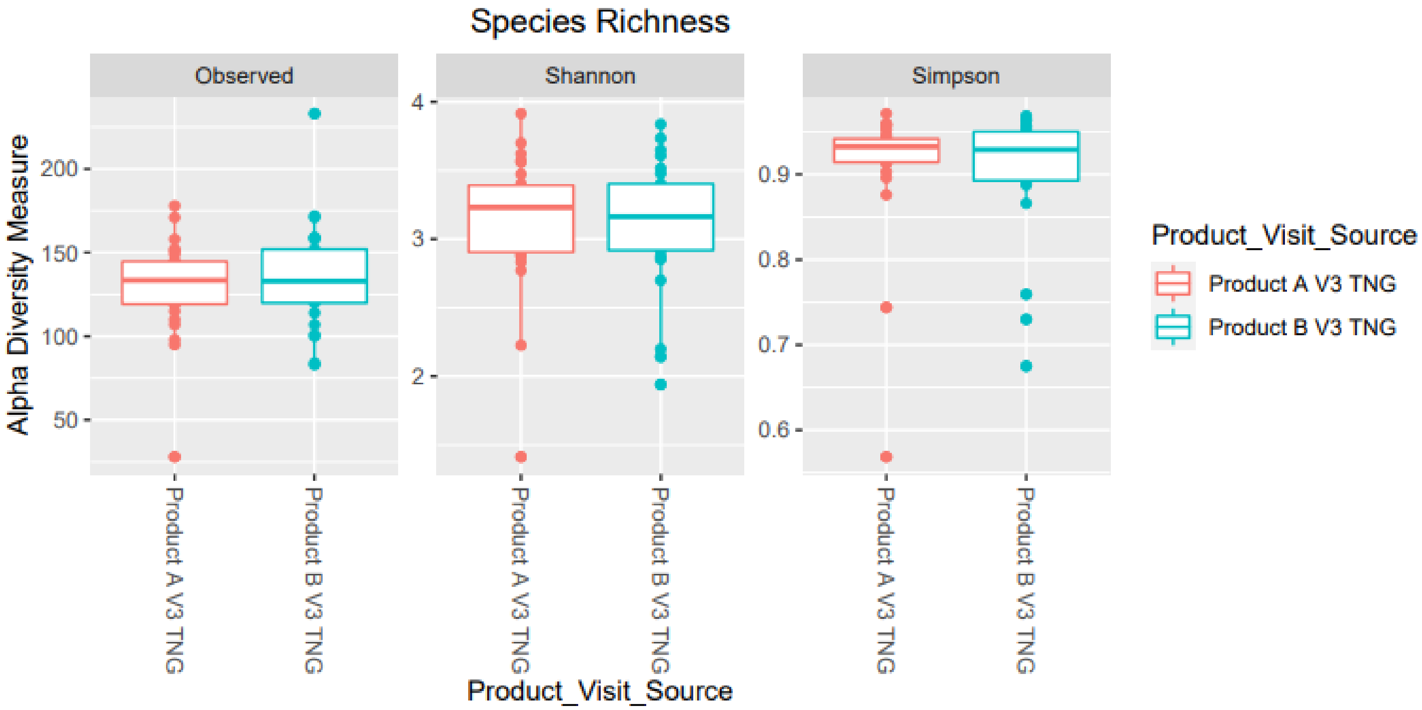

0
20
40
60
80
100
Value
Product_Visit_Source
Product A V2 TNG
Product B V2 TNG
Mogibacterium diversum
Peptostreptococcaceae_[XI][G−1] [Eubacterium]_sulci
Solobacterium moorei
Peptostreptococcus stomatis
Oribacterium sinus
Campylobacter concisus
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_352
Streptococcus sp._HMT_057
Bergeyella sp._HMT_322
Oribacterium asaccharolyticum_parvum
Fusobacterium nucleatum
Catonella morbi
Saccharibacteria_(TM7)_[G−6] bacterium_HMT_870
Veillonella tobetsuensis
Capnocytophaga leadbetteri
Streptococcus infantis_infantis_clade_431_infantis_clade_638
Streptococcus sanguinis
Rothia aeria
Streptococcus oralis
Lachnoanaerobaculum orale
Stomatobaculum longum
Lachnospiraceae_[G−2] bacterium_HMT_096
Leptotrichia sp._HMT_221
Lachnoanaerobaculum gingivalis
Schaalia meyeri
Prevotella vespertina
Alloprevotella sp._HMT_308_nov_97.347%
Streptococcus periodonticum
Streptococcus koreensis_sp._HMT_066
Neisseria mucosa
Bifidobacterium longum
Alloscardovia omnicolens
Prevotella sp._HMT_306
Prevotella pallens
Streptococcus multispecies_sppn13_2_nov_97.773%
Absconditabacteria_(SR1)_[G−1] bacterium_HMT_875
Streptococcus infantis_clade_431_periodonticum
Prevotella aurantiaca
Streptococcus cristatus
Streptococcus koreensis
Streptococcus downii
Stomatobaculum sp._HMT_097
Leptotrichia sp._HMT_215
Leptotrichia sp._HMT_417
Alloprevotella sp._HMT_473_nov_97.546%
Alloprevotella sp._HMT_914
Parvimonas sp._HMT_393_nov_97.053%
Prevotella nanceiensis
Streptococcus sp._HMT_061
Alloprevotella sp._HMT_473
Megasphaera micronuciformis
Prevotella salivae
Streptococcus parasanguinis_parasanguinis_clade_721
Prevotella jejuni
Streptococcus parasanguinis_clade_411_nov_97.976%
Schaalia lingnae_[Not_Validly_Published]
Veillonella dispar_parvula
Corynebacterium argentoratense
Gemella haemolysans
Haemophilus paraphrohaemolyticus
Streptococcus sp._HMT_423
Haemophilus haemolyticus
Granulicatella elegans
Neisseria cinerea
Rothia dentocariosa
Haemophilus sputorum
Haemophilus parahaemolyticus
Streptococcus chosunense
Streptococcus infantis_clade_431
Streptococcus oralis_subsp._dentisani_clade_058
Streptococcus sp._HMT_064
Streptococcus sp._HMT_074
Alloprevotella sp._HMT_308
Veillonella denticariosi_dispar_parvula
Lancefieldella parvula
Veillonella dispar
Veillonella parvula
Schaalia sp._HMT_180
Gemella sanguinis
Veillonella rogosae
Streptococcus sp._HMT_066
Schaalia odontolytica
Actinomyces graevenitzii
Prevotella histicola
Veillonella atypica
Streptococcus mitis
Streptococcus australis
Porphyromonas pasteri
Fusobacterium periodonticum
Granulicatella adiacens
Schaalia odontolyticus
Neisseria flavescens
Prevotella melaninogenica
Schaalia sp._HMT_172
Streptococcus parasanguinis_clade_411
Haemophilus parainfluenzae
Streptococcus infantis_infantis_clade_638
Neisseria perflava
Streptococcus salivarius
Rothia mucilaginosa
Species
F17924.S207
F17924.S209
F17924.S212
F17924.S215
F17924.S217
F17924.S223
F17924.S225
F17924.S230
F17924.S234
F17924.S236
F17924.S239
F17924.S247
F17924.S253
F17924.S205
F17924.S211
F17924.S218
F17924.S221
F17924.S227
F17924.S229
F17924.S233
F17924.S240
F17924.S242
F17924.S245
F17924.S249
F17924.S251
F17924.S255
Samples

Comparison 12. Product A V3 TNG vs Product B V3 TNG

1) Taxonomy bar graphs

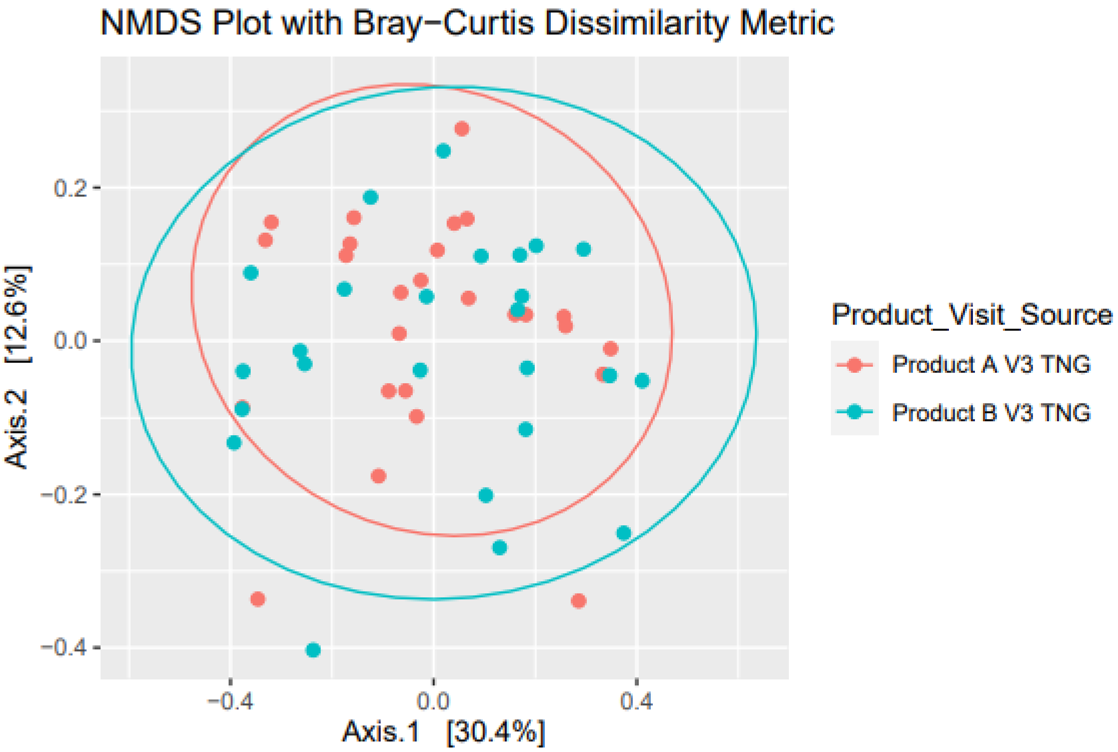


2) Alpha



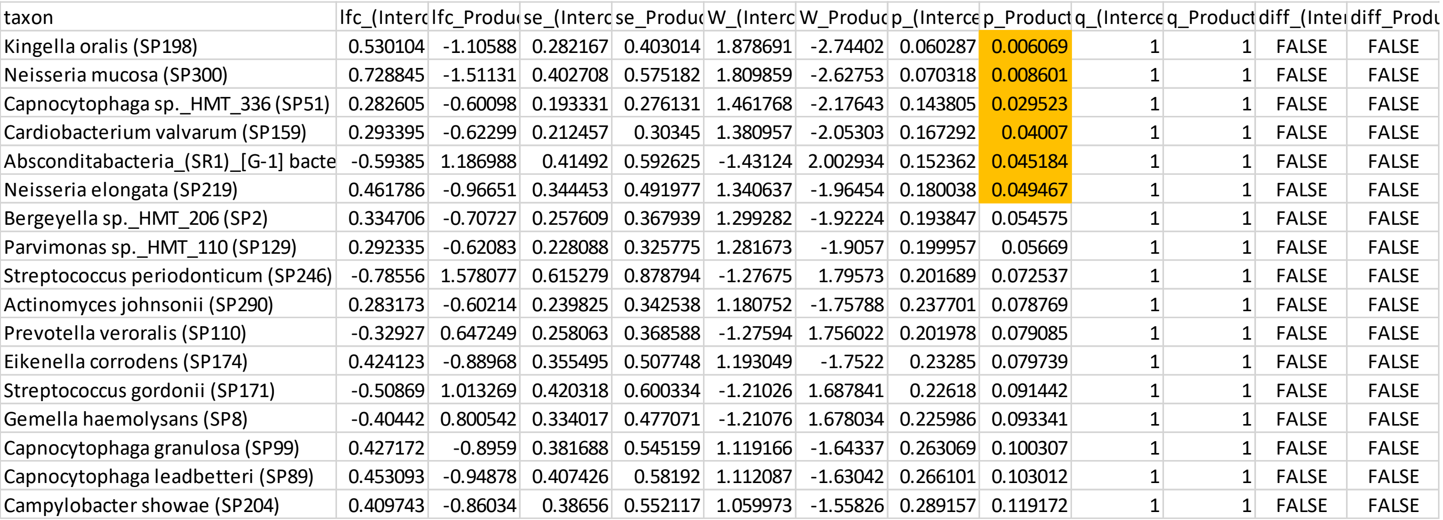
No significant differences

3) Beta diversity



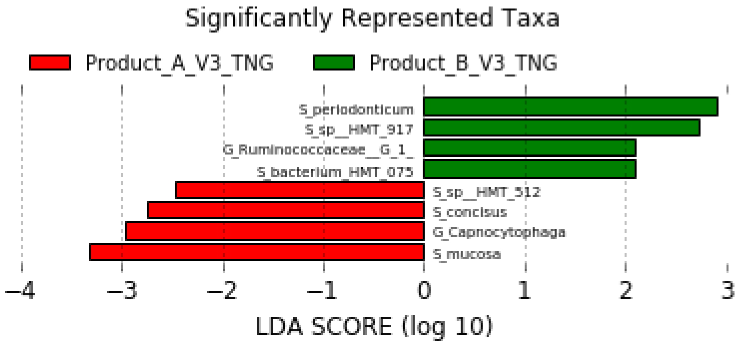
No significant differences

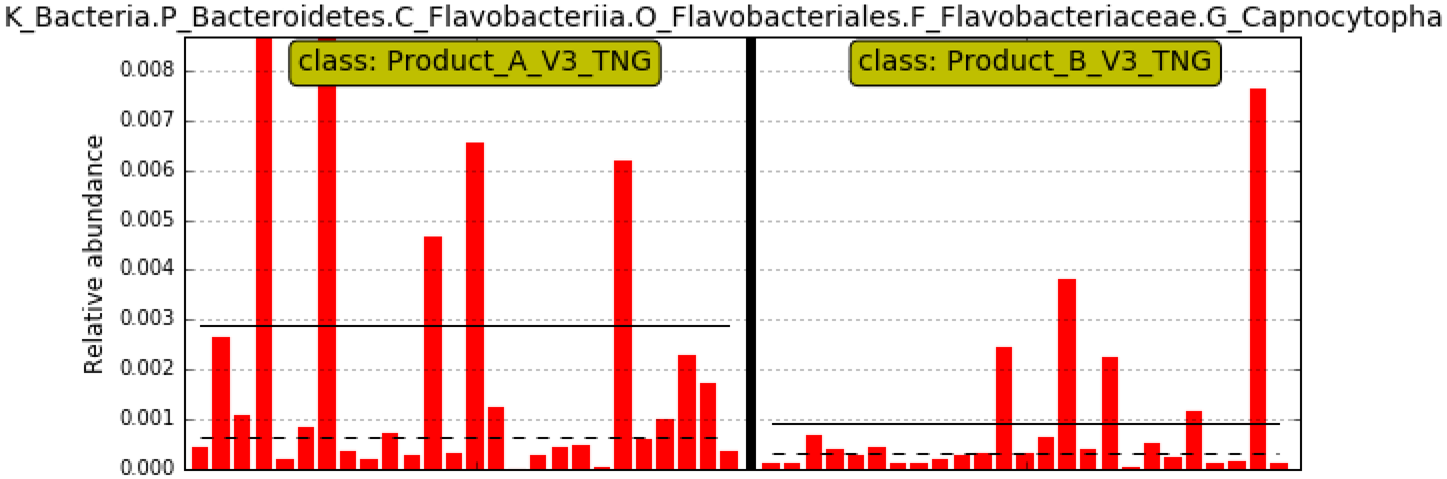
4) Differential abundance

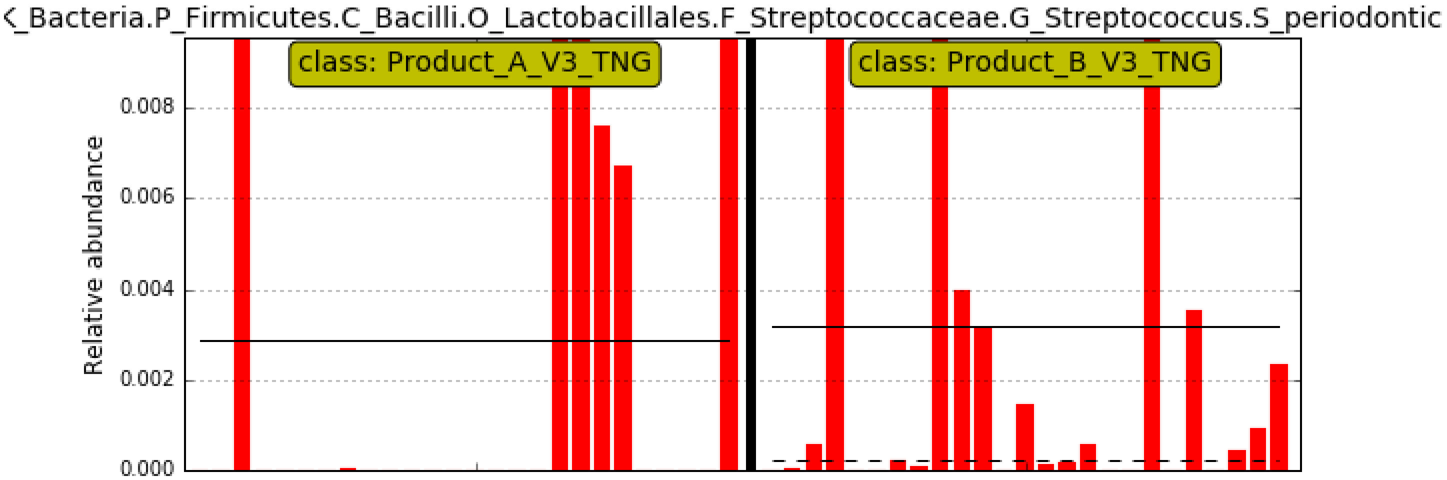


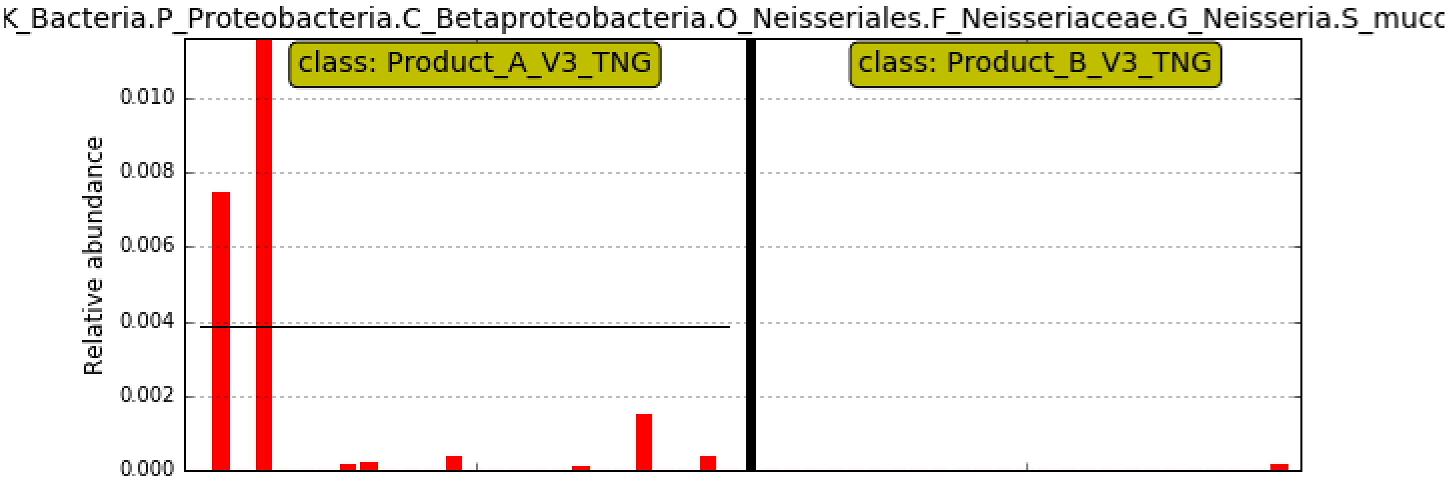
taxon	lfc_(Interc	lfc_Produ	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inte	diff_Produ
Kingella oralis (SP198)	0.530104	-1.10588	0.282167	0.403014	1.878691	-2.74402	0.060287	0.006069	1	1	FALSE	FALSE
Neisseria mucosa (SP300)	0.728845	-1.51131	0.402708	0.575182	1.809859	-2.62753	0.070318	0.008601	1	1	FALSE	FALSE
Capnocytophaga sp._HMT_336 (SP51)	0.282605	-0.60098	0.193331	0.276131	1.461768	-2.17643	0.143805	0.029523	1	1	FALSE	FALSE
Cardiobacterium valvarum (SP159)	0.293395	-0.62299	0.212457	0.30345	1.380957	-2.05303	0.167292	0.04007	1	1	FALSE	FALSE
Absconditabacteria_(SR1)_[G-1] bacte	-0.59385	1.186988	0.41492	0.592625	-1.43124	2.002934	0.152362	0.045184	1	1	FALSE	FALSE
Neisseria elongata (SP219)	0.461786	-0.96651	0.344453	0.491977	1.340637	-1.96454	0.180038	0.049467	1	1	FALSE	FALSE
Bergeyella sp._HMT_206 (SP2)	0.334706	-0.70727	0.257609	0.367939	1.299282	-1.92224	0.193847	0.054575	1	1	FALSE	FALSE
Parvimonas sp._HMT_110 (SP129)	0.292335	-0.62083	0.228088	0.325775	1.281673	-1.9057	0.199957	0.05669	1	1	FALSE	FALSE
Streptococcus periodonticum (SP246)	-0.78556	1.578077	0.615279	0.878794	-1.27675	1.79573	0.201689	0.072537	1	1	FALSE	FALSE
Actinomyces johnsonii (SP290)	0.283173	-0.60214	0.239825	0.342538	1.180752	-1.75788	0.237701	0.078769	1	1	FALSE	FALSE
Prevotella veroralis (SP110)	-0.32927	0.647249	0.258063	0.368588	-1.27594	1.756022	0.201978	0.079085	1	1	FALSE	FALSE
Eikenella corrodens (SP174)	0.424123	-0.88968	0.355495	0.507748	1.193049	-1.7522	0.23285	0.079739	1	1	FALSE	FALSE
Streptococcus gordonii (SP171)	-0.50869	1.013269	0.420318	0.600334	-1.21026	1.687841	0.22618	0.091442	1	1	FALSE	FALSE
Gemella haemolysans (SP8)	-0.40442	0.800542	0.334017	0.477071	-1.21076	1.678034	0.225986	0.093341	1	1	FALSE	FALSE
Capnocytophaga granulosa (SP99)	0.427172	-0.8959	0.381688	0.545159	1.119166	-1.64337	0.263069	0.100307	1	1	FALSE	FALSE
Capnocytophaga leadbetteri (SP89)	0.453093	-0.94878	0.407426	0.58192	1.112087	-1.63042	0.266101	0.103012	1	1	FALSE	FALSE
Campylobacter showae (SP204)	0.409743	-0.86034	0.38656	0.552117	1.059973	-1.55826	0.289157	0.119172	1	1	FALSE	FALSE

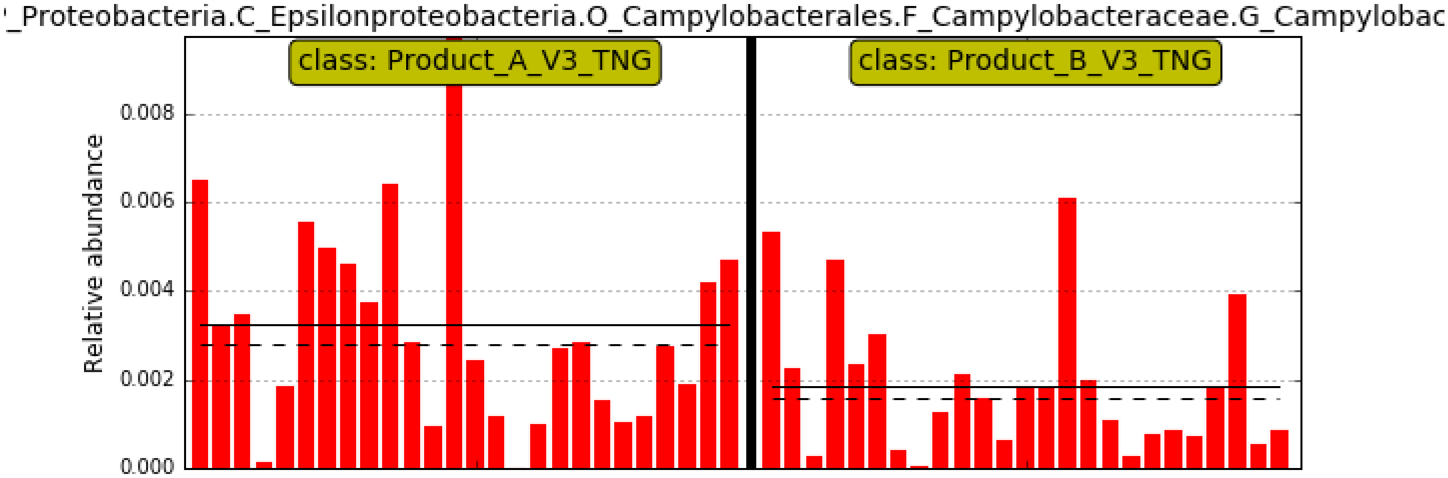
5) Lefse


Significantly Represented Taxa
🟥 Product_A_V3_TNG
🟩 Product_B_V3_TNG
S_periodonticum
S_sp__HMT_917
G_Ruminococcaceae__G_1_
S_bacterium_HMT_075
S_sp__HMT_512
S_concisus
G_Capnocytophaga
S_mucosa
−4
−3
−2
−1
0
1
2
3
LDA SCORE (log 10)

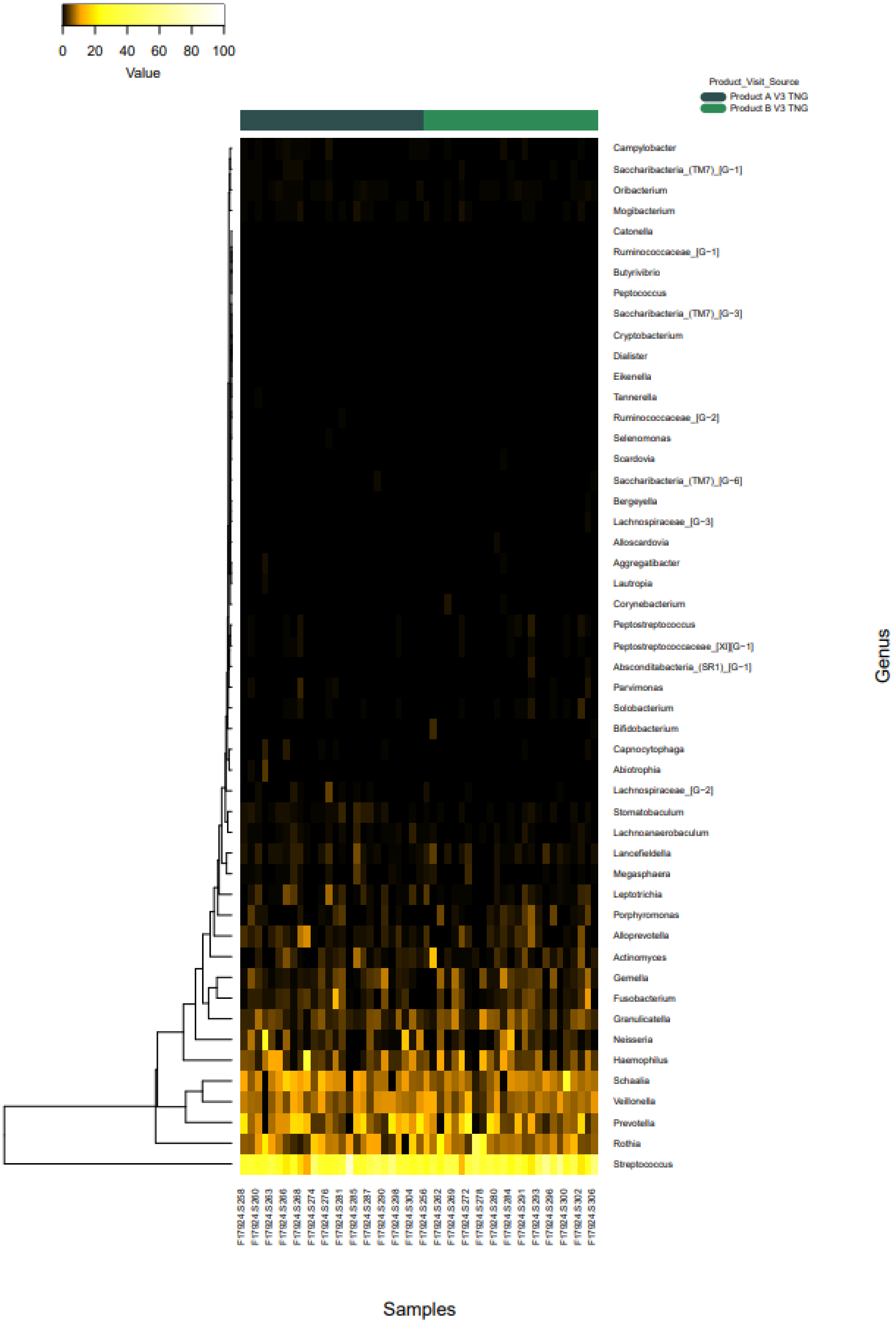

K_Bacteria.P_Bacteroidetes.C_Flavobacteriia.O_Flavobacteriales.F_Flavobacteriaceae.G_Capnocytopha
class: Product_A_V3_TNG
class: Product_B_V3_TNG
Relative abundance
0.000
0.001
0.002
0.003
0.004
0.005
0.006
0.007
0.008

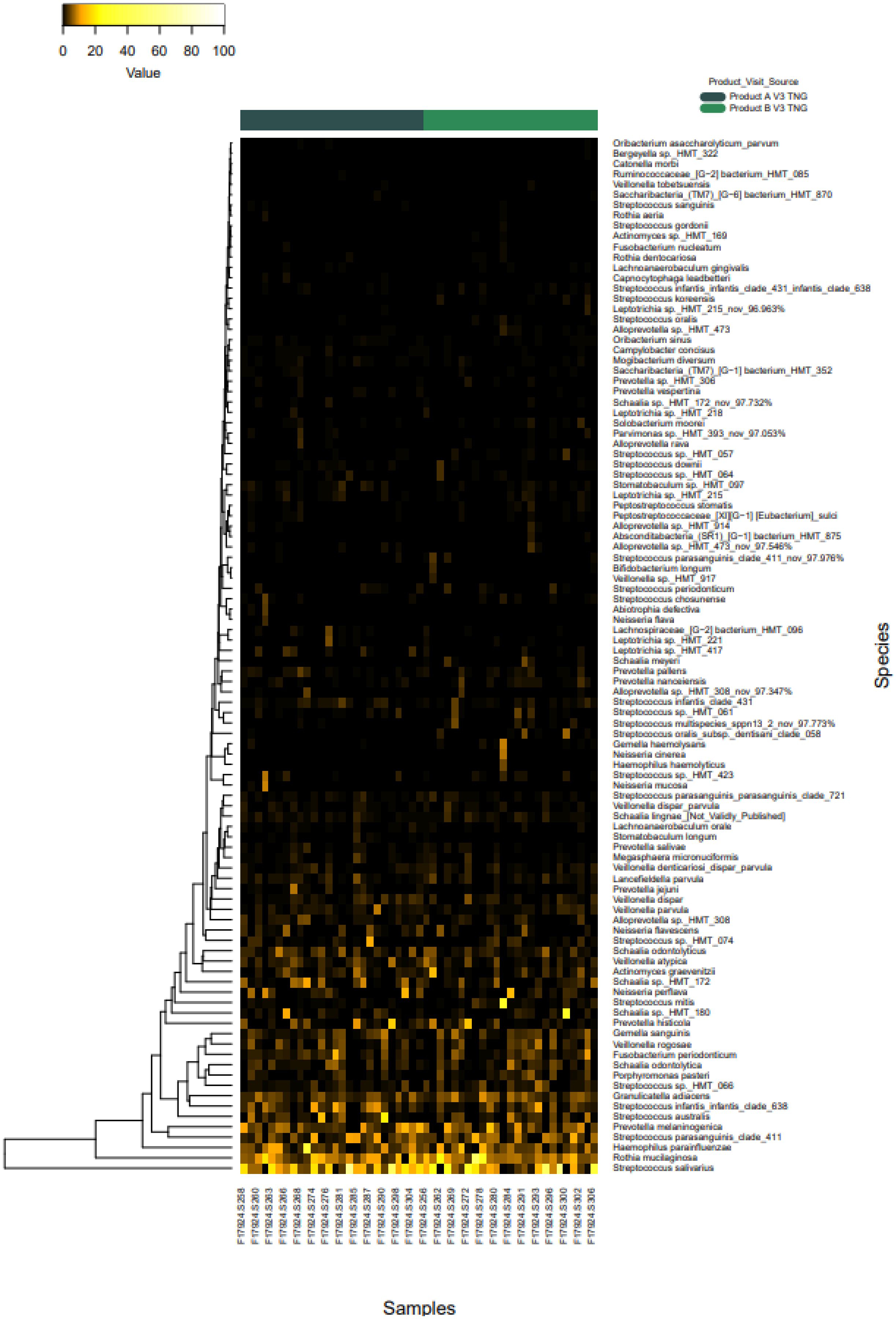

_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_periodontic
class: Product_A_V3_TNG
class: Product_B_V3_TNG
Relative abundance
0.000
0.002
0.004
0.006
0.008


K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Neisseria.S_muco
class: Product_A_V3_TNG
class: Product_B_V3_TNG
Relative abundance
0.010
0.008
0.006
0.004
0.002
0.000


_Proteobacteria.C_Epsilonproteobacteria.O_Campylobacterales.F_Campylobacteraceae.G_Campylobac
class: Product_A_V3_TNG
class: Product_B_V3_TNG
Relative abundance
0.008
0.006
0.004
0.002
0.000

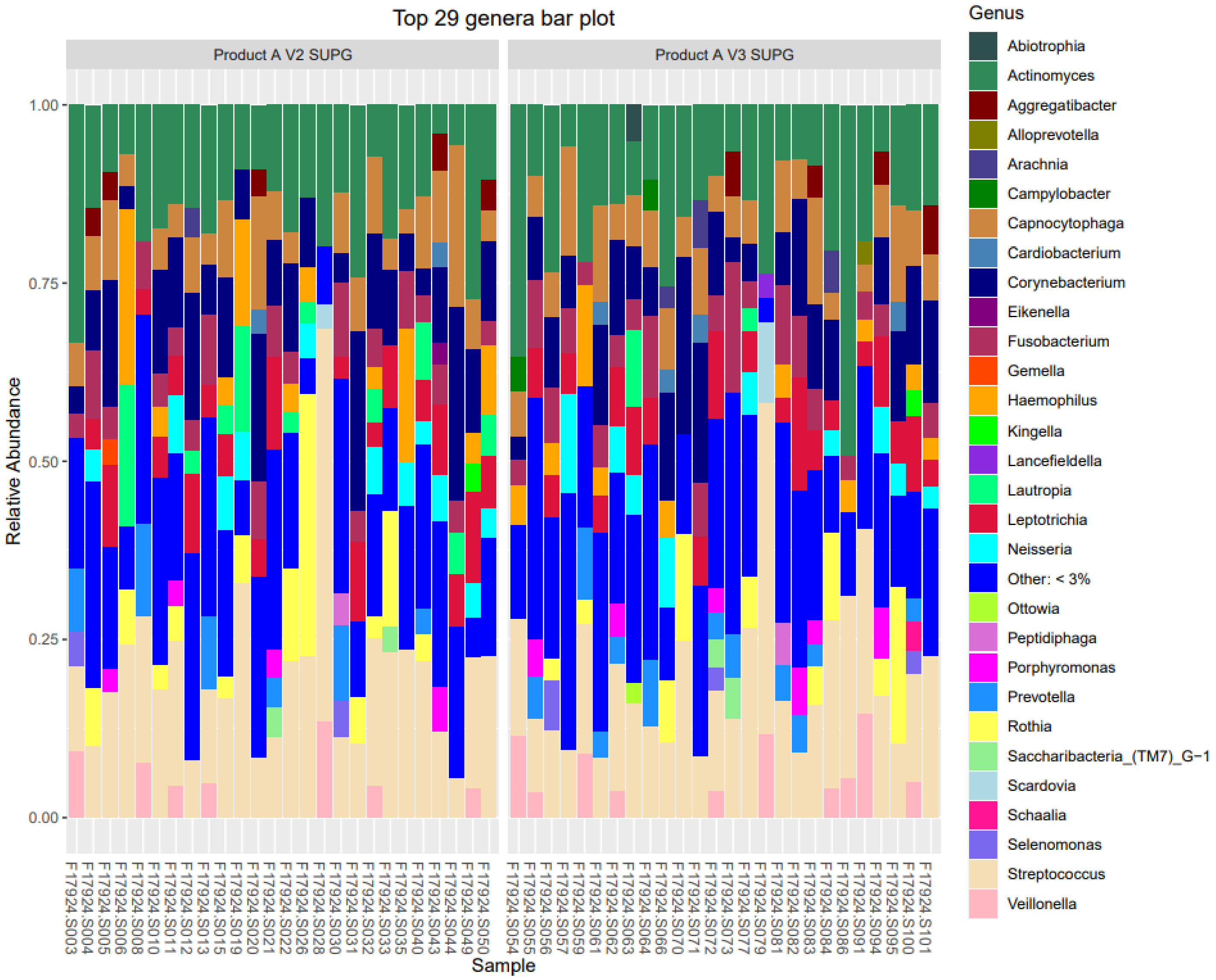
6) Heat map.


0
20
40
60
80
100
Value
Product_Visit_Source
Product A V3 TNG
Product B V3 TNG
Campylobacter
Saccharibacteria_(TM7)_[G-1]
Oribacterium
Mogibacterium
Catonella
Ruminococcaceae_[G-1]
Butyrivibrio
Peptococcus
Saccharibacteria_(TM7)_[G-3]
Cryptobacterium
Dialister
Eikenella
Tannerella
Ruminococcaceae_[G-2]
Selenomonas
Scardovia
Saccharibacteria_(TM7)_[G-6]
Bergeyella
Lachnospiraceae_[G-3]
Alloscardovia
Aggregatibacter
Lautropia
Corynebacterium
Peptostreptococcus
Peptostreptococcaceae_[XI][G-1]
Absconditabacteria_(SR1)_[G-1]
Parvimonas
Solobacterium
Bifidobacterium
Capnocytophaga
Abiotrophia
Lachnospiraceae_[G-2]
Stomatobaculum
Lachnoanaerobaculum
Lancefieldella
Megasphaera
Leptotrichia
Porphyromonas
Alloprevotella
Actinomyces
Gemella
Fusobacterium
Granulicatella
Neisseria
Haemophilus
Schaalia
Veillonella
Prevotella
Rothia
Streptococcus
Genus
F17924.S258
F17924.S260
F17924.S263
F17924.S266
F17924.S268
F17924.S274
F17924.S276
F17924.S281
F17924.S285
F17924.S287
F17924.S290
F17924.S298
F17924.S304
F17924.S256
F17924.S262
F17924.S269
F17924.S272
F17924.S278
F17924.S280
F17924.S284
F17924.S291
F17924.S293
F17924.S296
F17924.S300
F17924.S302
F17924.S306
Samples

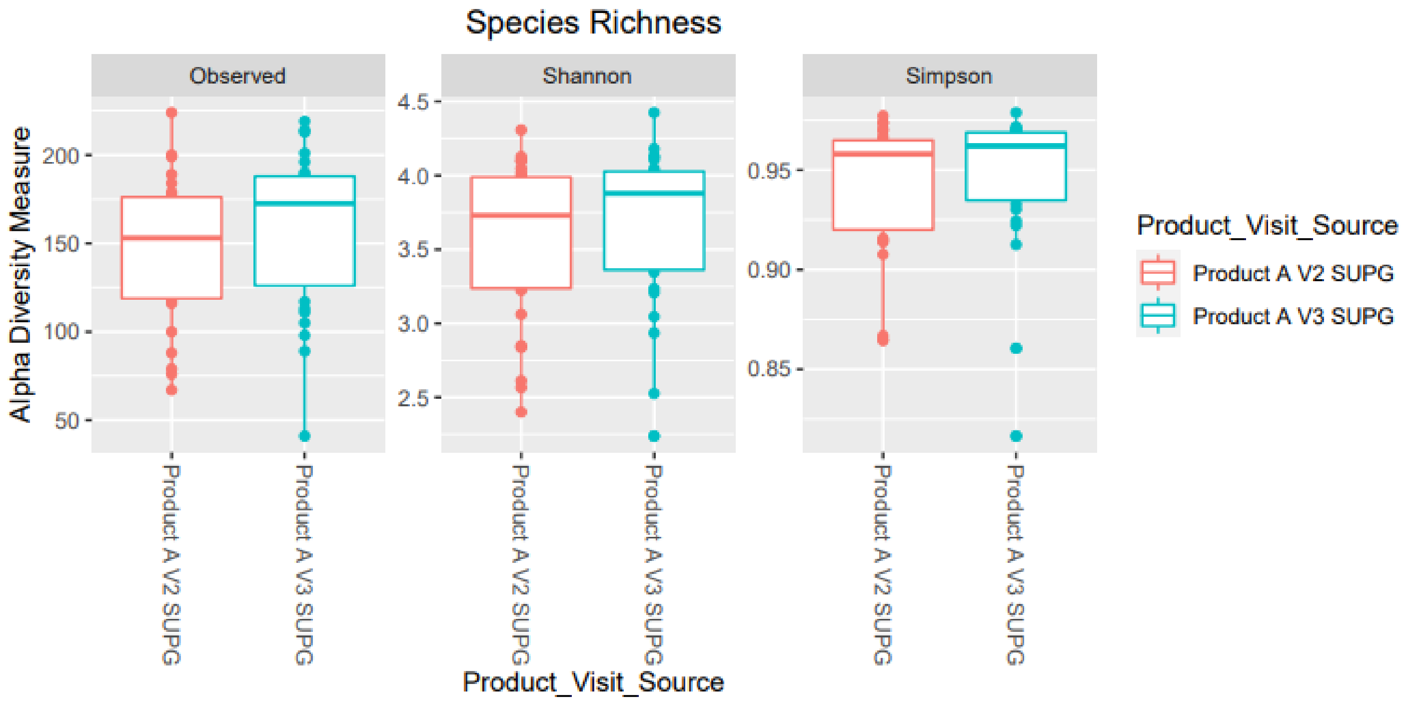

0
20
40
60
80
100
Value
Product_Visit_Source
Product A V3 TNG
Product B V3 TNG
Oribacterium asaccharolyticum_parvum
Bergeyella sp._HMT_322
Catonella morbi
Ruminococcaceae_[G-2] bacterium_HMT_085
Veillonella tobetsuensis
Saccharibacteria_(TM7)_[G-6] bacterium_HMT_870
Streptococcus sanguinis
Rothia aeria
Streptococcus gordonii
Actinomyces sp._HMT_169
Fusobacterium nucleatum
Rothia dentocariosa
Lachnoanaerobaculum gingivalis
Capnocytophaga leadbetteri
Streptococcus infantis_infantis_clade_431_infantis_clade_638
Streptococcus koreensis
Leptotrichia sp._HMT_215_nov_96.963%
Streptococcus oralis
Alloprevotella sp._HMT_473
Oribacterium sinus
Campylobacter concisus
Mogibacterium diversum
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_352
Prevotella sp._HMT_306
Prevotella vespertina
Schaalia sp._HMT_172_nov_97.732%
Leptotrichia sp._HMT_218
Solobacterium moorei
Parvimonas sp._HMT_393_nov_97.053%
Alloprevotella rava
Streptococcus sp._HMT_057
Streptococcus downii
Streptococcus sp._HMT_064
Stomatobaculum sp._HMT_097
Leptotrichia sp._HMT_215
Peptostreptococcus stomatis
Peptostreptococcaceae_[XI][G-1] [Eubacterium]_sulci
Alloprevotella sp._HMT_914
Absconditabacteria_(SR1)_[G-1] bacterium_HMT_875
Alloprevotella sp._HMT_473_nov_97.546%
Streptococcus parasanguinis_clade_411_nov_97.976%
Bifidobacterium longum
Veillonella sp._HMT_917
Streptococcus periodonticum
Streptococcus chosunense
Abiotrophia defectiva
Neisseria flava
Lachnospiraceae_[G-2] bacterium_HMT_096
Leptotrichia sp._HMT_221
Leptotrichia sp._HMT_417
Schaalia meyeri
Prevotella pallens
Prevotella nanceiensis
Alloprevotella sp._HMT_308_nov_97.347%
Streptococcus infantis_clade_431
Streptococcus sp._HMT_061
Streptococcus multispecies_sppn13_2_nov_97.773%
Streptococcus oralis_subsp._dentisani_clade_058
Gemella haemolysans
Neisseria cinerea
Haemophilus haemolyticus
Streptococcus sp._HMT_423
Neisseria mucosa
Streptococcus parasanguinis_parasanguinis_clade_721
Veillonella dispar_parvula
Schaalia lingnae_[Not_Validly_Published]
Lachnoanaerobaculum orale
Stomatobaculum longum
Prevotella salivae
Megasphaera micronuciformis
Veillonella denticariosi_dispar_parvula
Lancefieldella parvula
Prevotella jejuni
Veillonella dispar
Veillonella parvula
Alloprevotella sp._HMT_308
Neisseria flavescens
Streptococcus sp._HMT_074
Schaalia odontolyticus
Veillonella atypica
Actinomyces graevenitzii
Schaalia sp._HMT_172
Neisseria perflava
Streptococcus mitis
Schaalia sp._HMT_180
Prevotella histicola
Gemella sanguinis
Veillonella rogosae
Fusobacterium periodonticum
Schaalia odontolytica
Porphyromonas pasteri
Streptococcus sp._HMT_066
Granulicatella adiacens
Streptococcus infantis_infantis_clade_638
Streptococcus australis
Prevotella melaninogenica
Streptococcus parasanguinis_clade_411
Haemophilus parainfluenzae
Rothia mucilaginosa
Streptococcus salivarius
Species
FIT924.S258
FIT924.S260
FIT924.S263
FIT924.S266
FIT924.S268
FIT924.S274
FIT924.S276
FIT924.S281
FIT924.S285
FIT924.S287
FIT924.S290
FIT924.S298
FIT924.S304
FIT924.S256
FIT924.S262
FIT924.S269
FIT924.S272
FIT924.S278
FIT924.S280
FIT924.S284
FIT924.S291
FIT924.S293
FIT924.S296
FIT924.S300
FIT924.S302
FIT924.S306
Samples

Comparison 13. Product A V2 SUPG vs Product A V3 SUPG

1) Taxonomy bar graphs

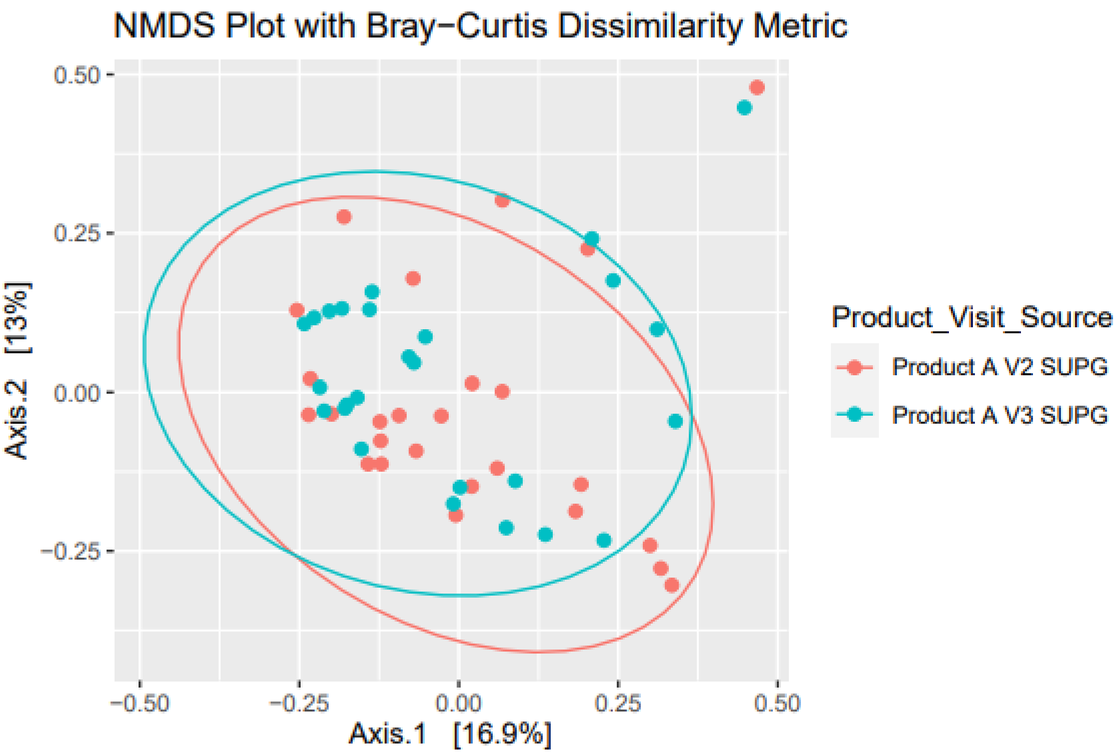


2) Alpha



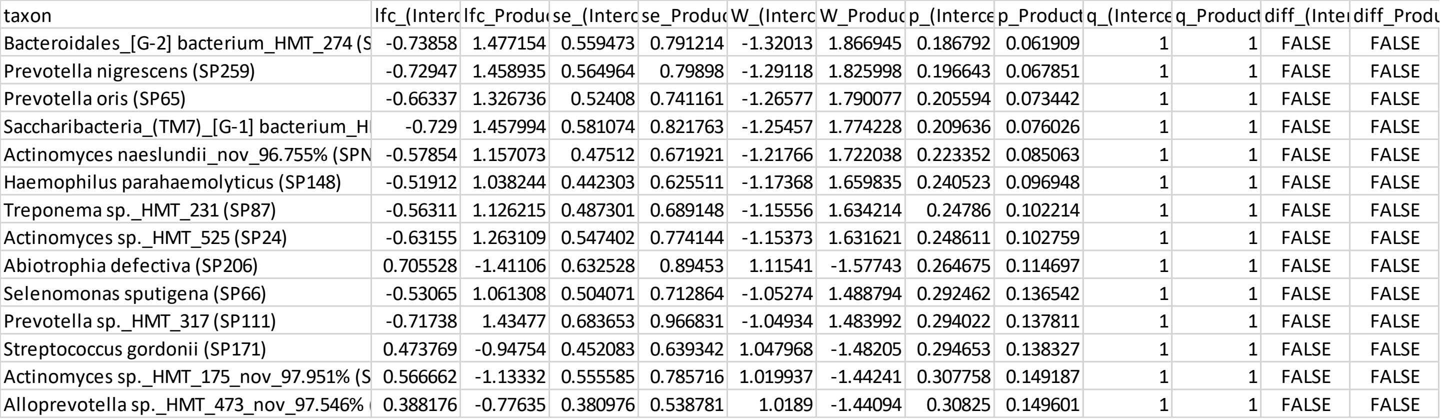
No significant differences

3) Beta diversity



No significant differences

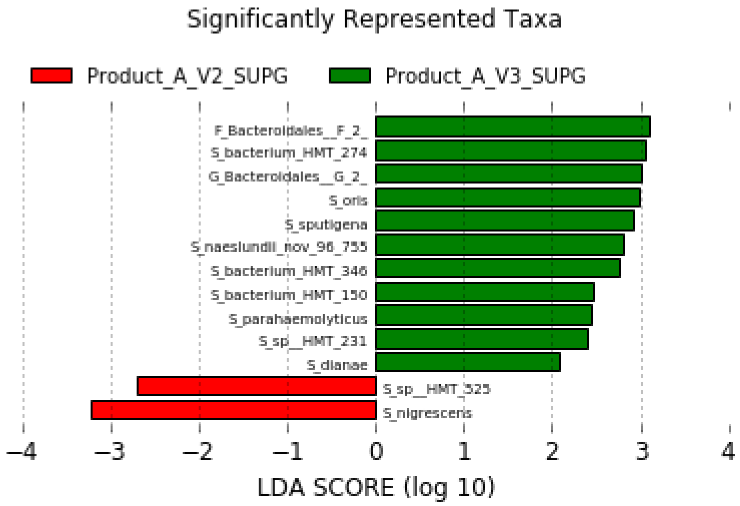
4) Differential abundance



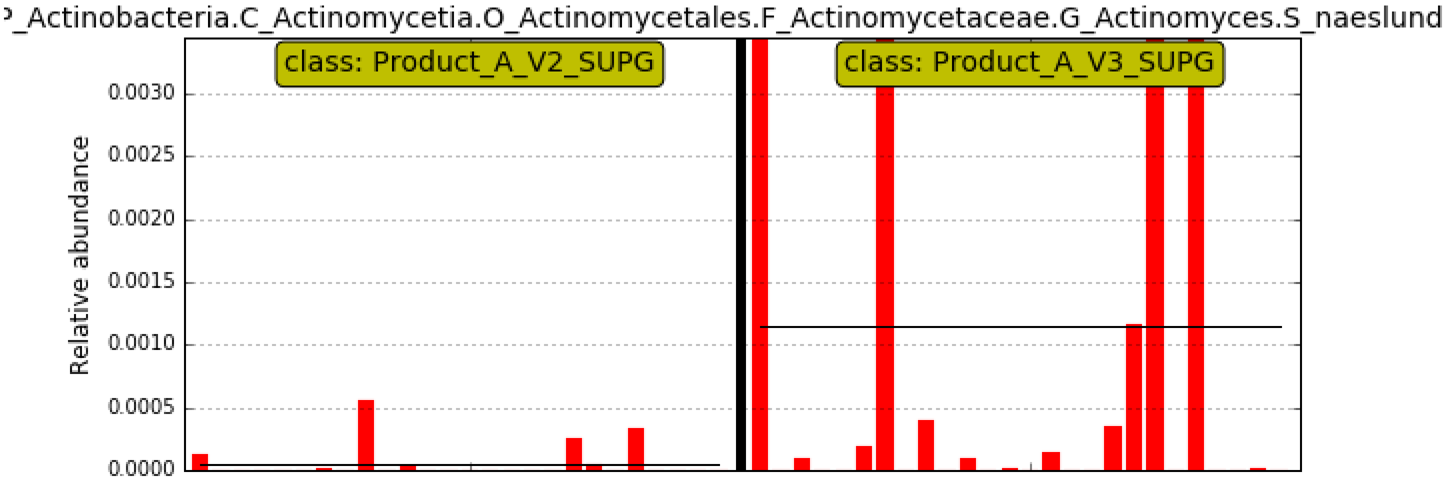
taxon	lfc_(Interc	lfc_Produc	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inte	diff_Produ
Bacteroidales_[G-2] bacterium_HMT_274 (S	-0.73858	1.477154	0.559473	0.791214	-1.32013	1.866945	0.186792	0.061909	1	1	FALSE	FALSE
Prevotella nigrescens (SP259)	-0.72947	1.458935	0.564964	0.79898	-1.29118	1.825998	0.196643	0.067851	1	1	FALSE	FALSE
Prevotella oris (SP65)	-0.66337	1.326736	0.52408	0.741161	-1.26577	1.790077	0.205594	0.073442	1	1	FALSE	FALSE
Saccharibacteria_(TM7)_[G-1] bacterium_H	-0.729	1.457994	0.581074	0.821763	-1.25457	1.774228	0.209636	0.076026	1	1	FALSE	FALSE
Actinomyces naeslundii_nov_96.755% (SPN	-0.57854	1.157073	0.47512	0.671921	-1.21766	1.722038	0.223352	0.085063	1	1	FALSE	FALSE
Haemophilus parahaemolyticus (SP148)	-0.51912	1.038244	0.442303	0.625511	-1.17368	1.659835	0.240523	0.096948	1	1	FALSE	FALSE
Treponema sp._HMT_231 (SP87)	-0.56311	1.126215	0.487301	0.689148	-1.15556	1.634214	0.24786	0.102214	1	1	FALSE	FALSE
Actinomyces sp._HMT_525 (SP24)	-0.63155	1.263109	0.547402	0.774144	-1.15373	1.631621	0.248611	0.102759	1	1	FALSE	FALSE
Abiotrophia defectiva (SP206)	0.705528	-1.41106	0.632528	0.89453	1.11541	-1.57743	0.264675	0.114697	1	1	FALSE	FALSE
Selenomonas sputigena (SP66)	-0.53065	1.061308	0.504071	0.712864	-1.05274	1.488794	0.292462	0.136542	1	1	FALSE	FALSE
Prevotella sp._HMT_317 (SP111)	-0.71738	1.43477	0.683653	0.966831	-1.04934	1.483992	0.294022	0.137811	1	1	FALSE	FALSE
Streptococcus gordonii (SP171)	0.473769	-0.94754	0.452083	0.639342	1.047968	-1.48205	0.294653	0.138327	1	1	FALSE	FALSE
Actinomyces sp._HMT_175_nov_97.951% (S	0.566662	-1.13332	0.555585	0.785716	1.019937	-1.44241	0.307758	0.149187	1	1	FALSE	FALSE
Alloprevotella sp._HMT_473_nov_97.546% (	0.388176	-0.77635	0.380976	0.538781	1.0189	-1.44094	0.30825	0.149601	1	1	FALSE	FALSE

NO significant differences

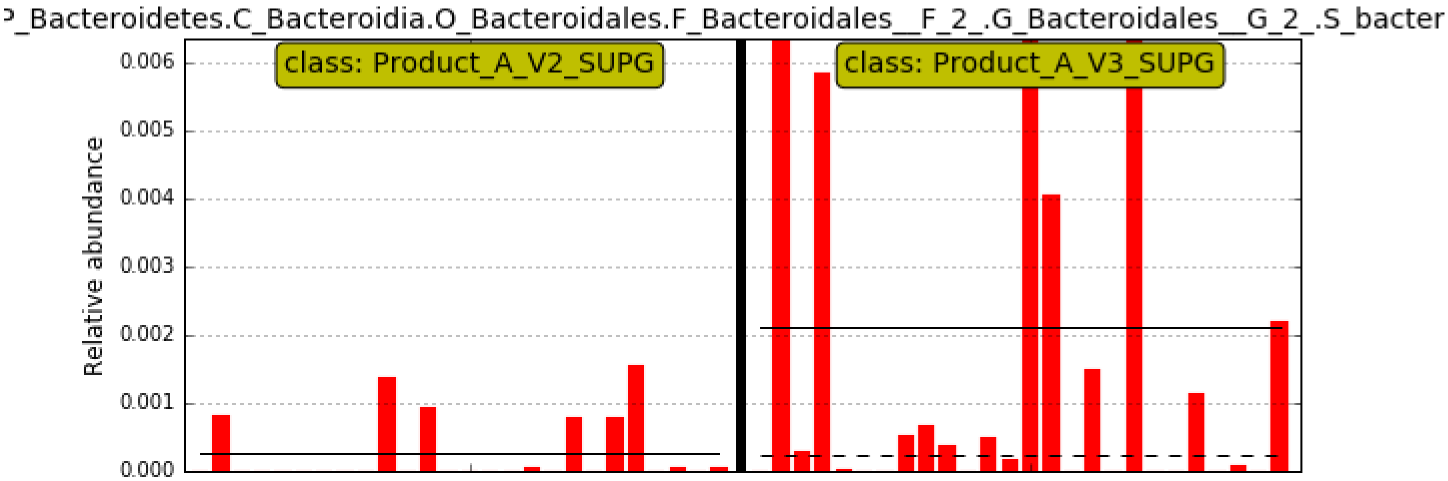
5) Lefse



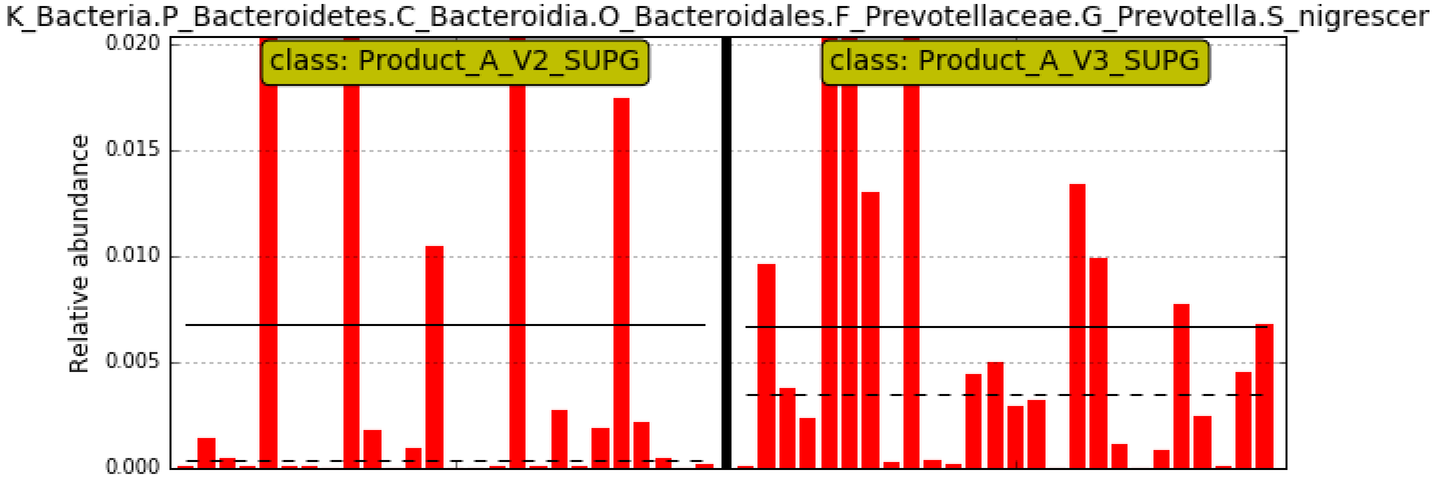
Significantly Represented Taxa
Product_A_V2_SUPG
Product_A_V3_SUPG
F_Bacteroidales__F_2_
S_bacterium_HMT_274
G_Bacteroidales__G_2_
S_oris
S_sputigena
S_naeslundii_nov_96_755
S_bacterium_HMT_346
S_bacterium_HMT_150
S_parahaemolyticus
S_sp__HMT_231
S_dianae
S_sp__HMT_525
S_nigrescens
−4
−3
−2
−1
0
1
2
3
4
LDA SCORE (log 10)

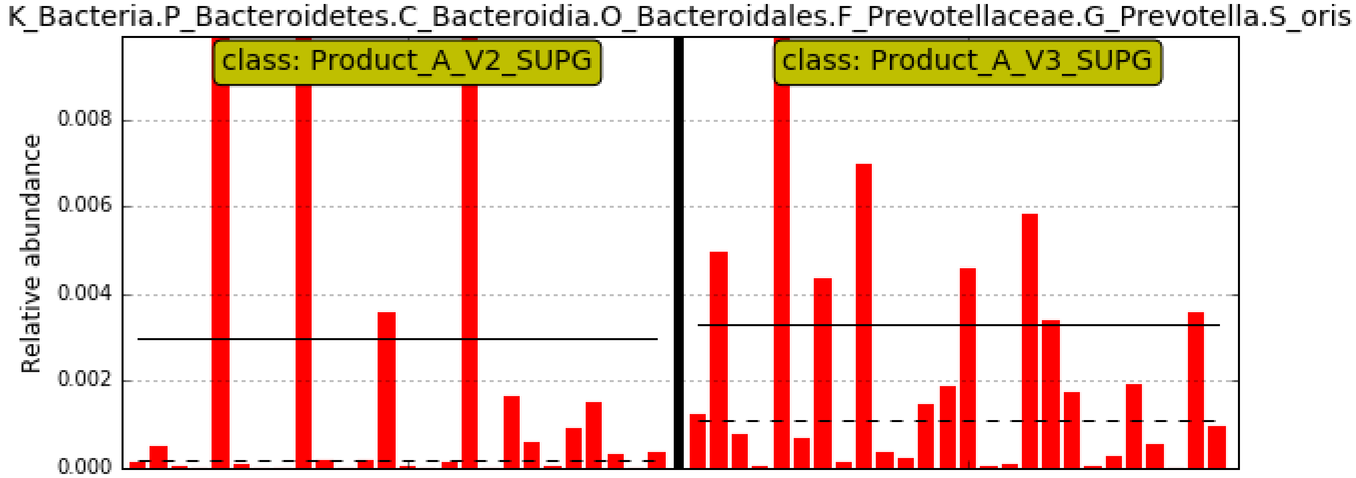


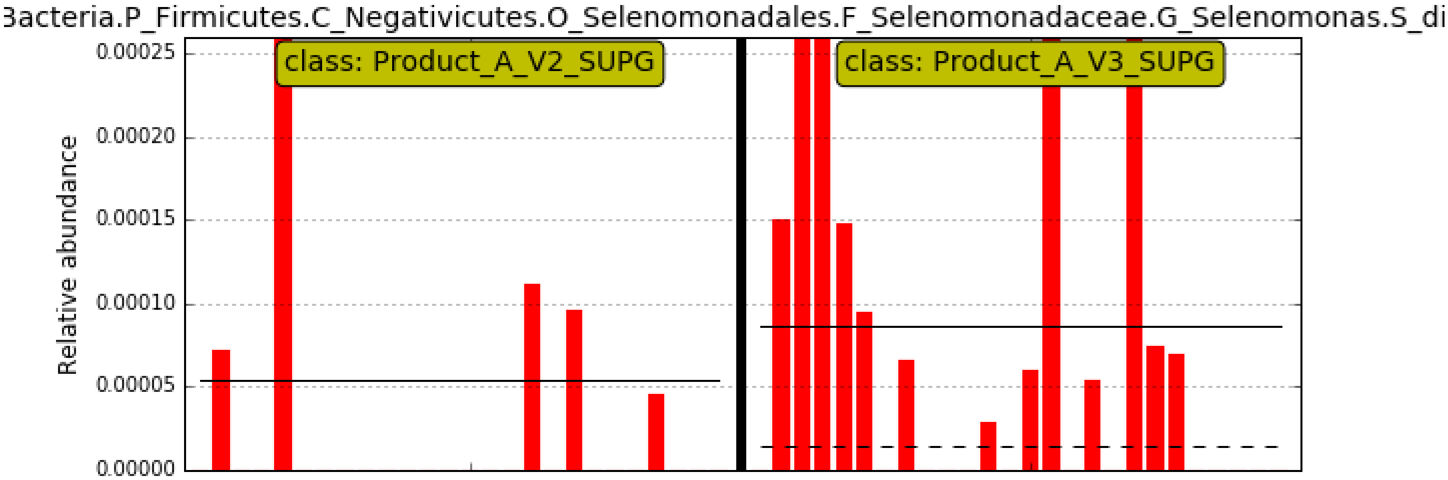
P_Actinobacteria.C_Actinomycetia.O_Actinomycetales.F_Actinomycetaceae.G_Actinomyces.S_naeslund
class: Product_A_V2_SUPG
class: Product_A_V3_SUPG
Relative abundance
0.0030
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000

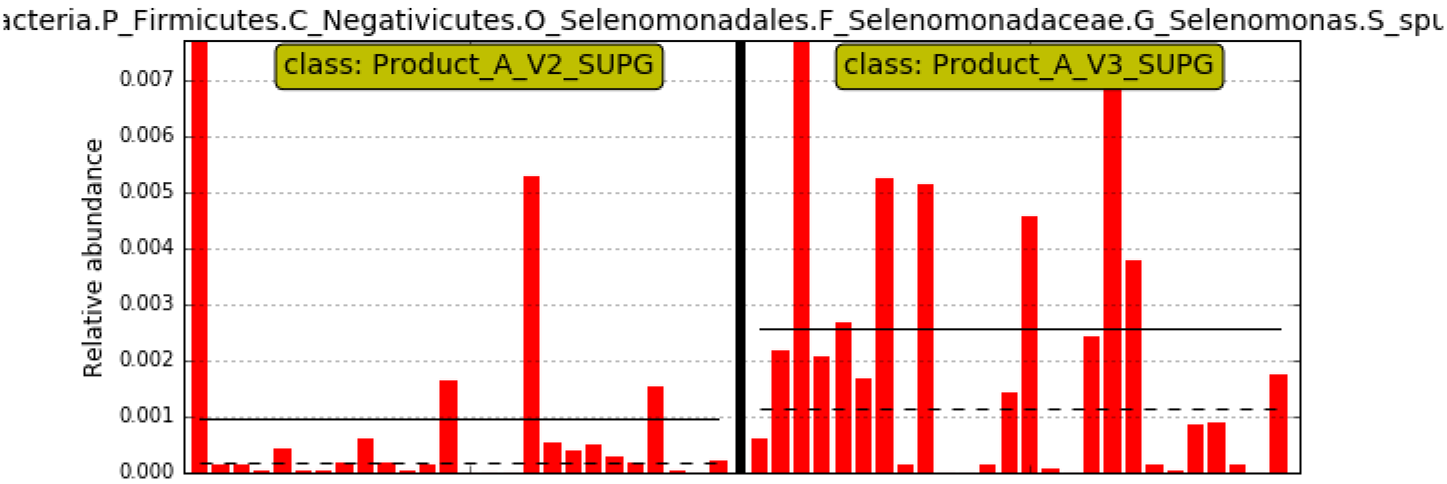


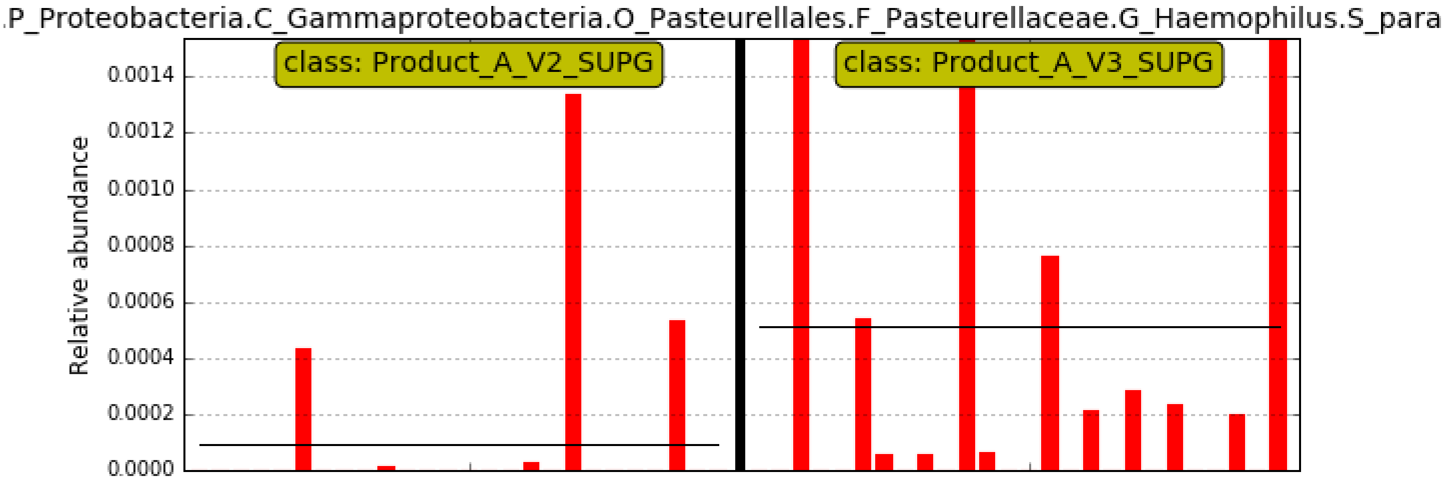
P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Bacteroidales__F_2_.G_Bacteroidales__G_2_.S_bacter
class: Product_A_V2_SUPG
class: Product_A_V3_SUPG
Relative abundance
0.006
0.005
0.004
0.003
0.002
0.001
0.000

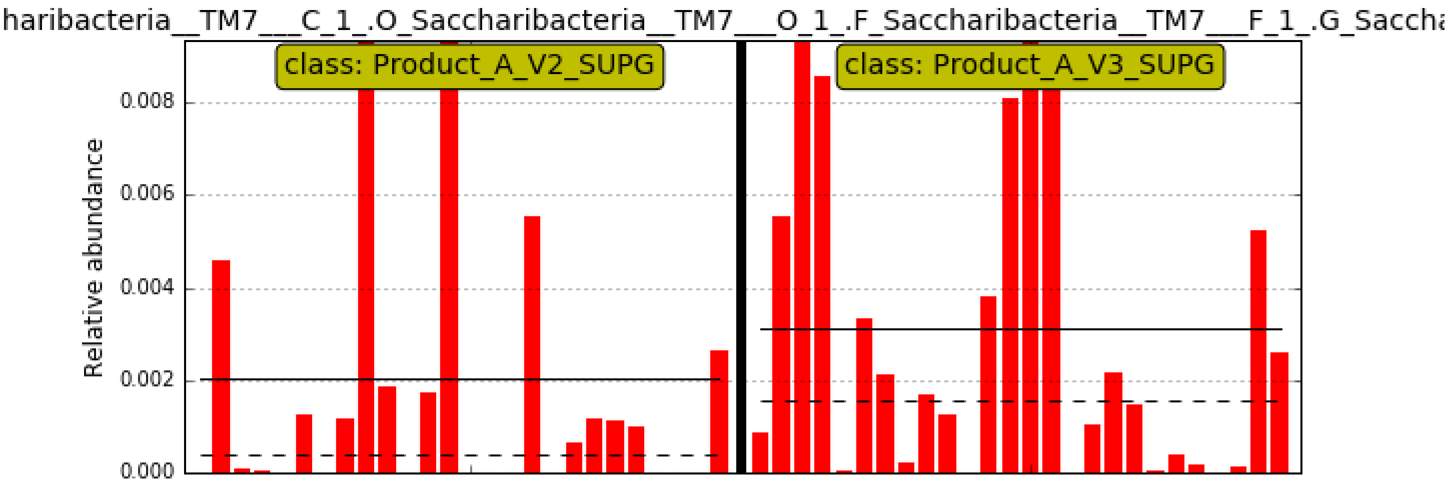

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_nigrescer
class: Product_A_V2_SUPG
class: Product_A_V3_SUPG
Relative abundance
0.020
0.015
0.010
0.005
0.000

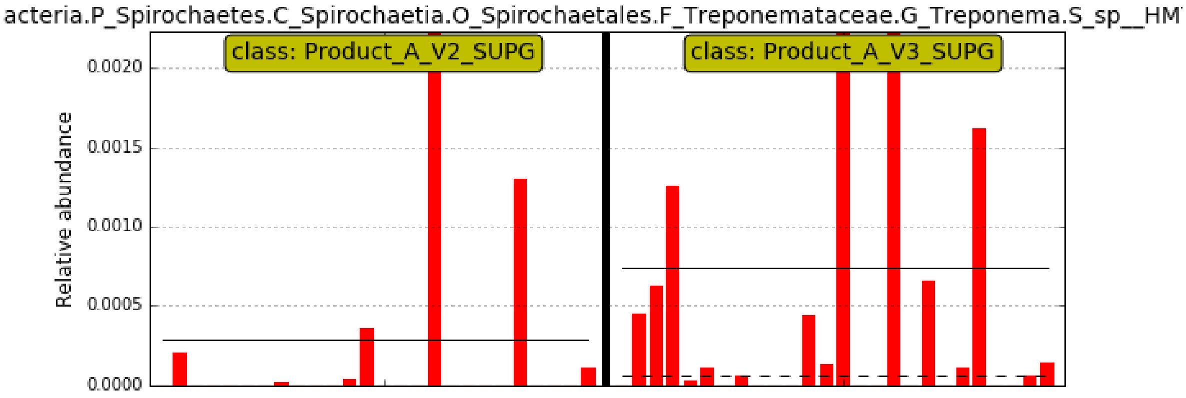

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_oris
class: Product_A_V2_SUPG
class: Product_A_V3_SUPG
Relative abundance
0.008
0.006
0.004
0.002
0.000


3acteria.P_Firmicutes.C_Negativicutes.O_Selenomonadales.F_Selenomonadaceae.G_Selenomonas.S_di
class: Product_A_V2_SUPG
class: Product_A_V3_SUPG
Relative abundance
0.00025
0.00020
0.00015
0.00010
0.00005
0.00000


acteria.P_Firmicutes.C_Negativicutes.O_Selenomonadales.F_Selenomonadaceae.G_Selenomonas.S_spu
Relative abundance
0.000
0.001
0.002
0.003
0.004
0.005
0.006
0.007
class: Product_A_V2_SUPG
class: Product_A_V3_SUPG

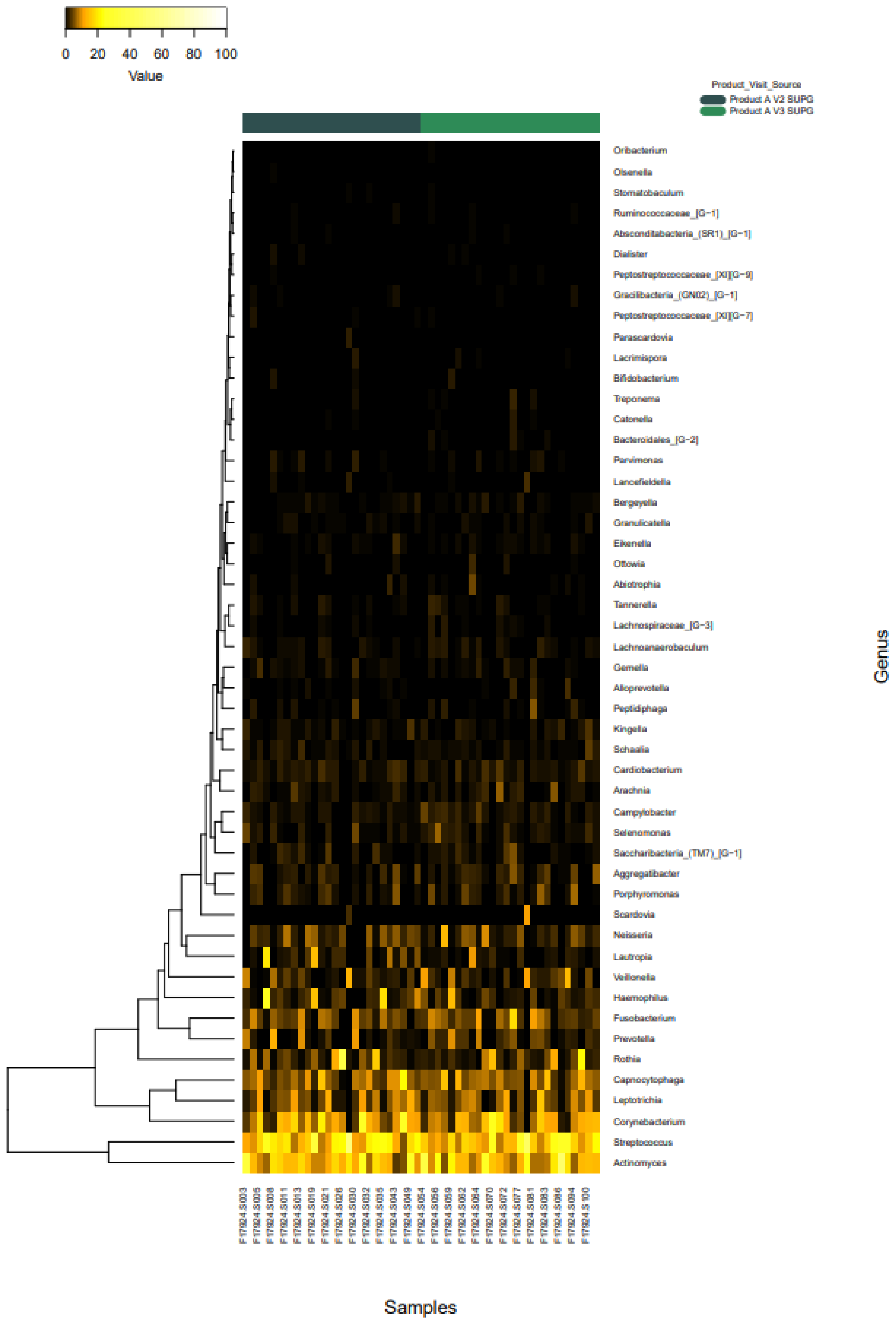

.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophilus.S_para
Relative abundance
0.0000
0.0002
0.0004
0.0006
0.0008
0.0010
0.0012
0.0014
class: Product_A_V2_SUPG
class: Product_A_V3_SUPG

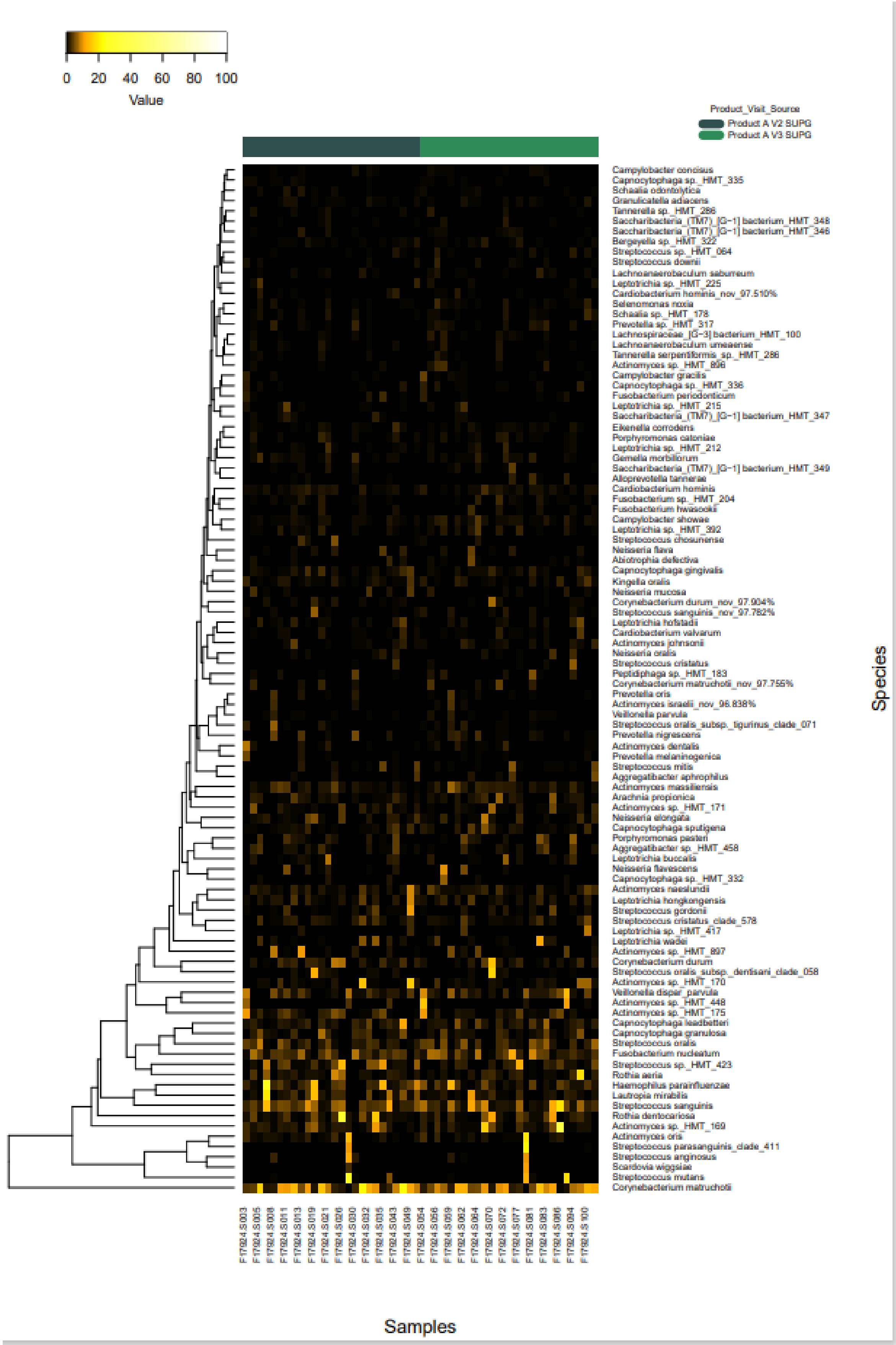




Treponema sp. HMT-231

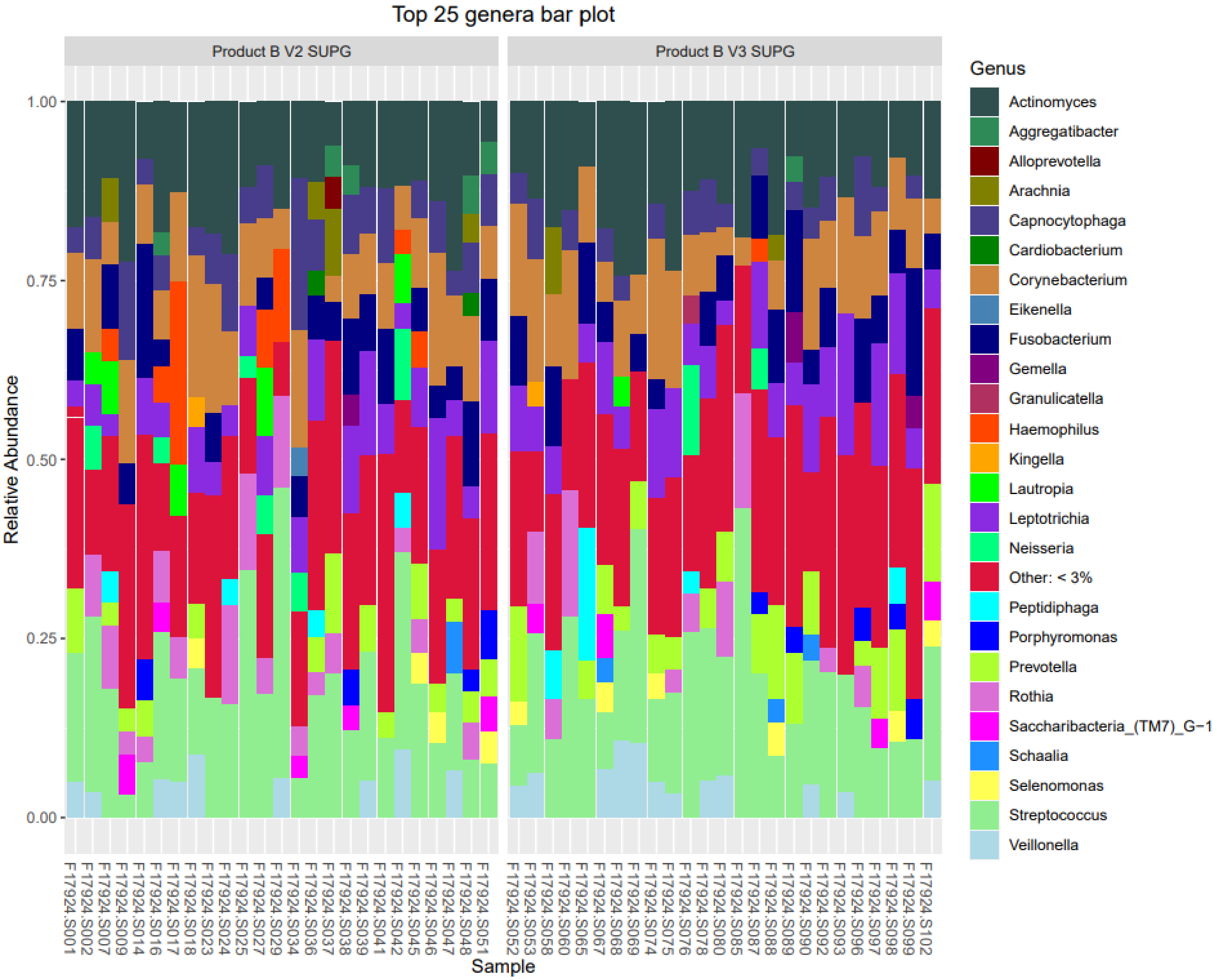
6) Heat map.


0
20
40
60
80
100
Value
Product_Visit_Source
Product A V2 SUPG
Product A V3 SUPG
Oribacterium
Olsenella
Stomatobaculum
Ruminococcaceae_[G-1]
Absconditabacteria_(SR1)_[G-1]
Dialister
Peptostreptococcaceae_[XI][G-9]
Gracilibacteria_(GN02)_[G-1]
Peptostreptococcaceae_[XI][G-7]
Parascardovia
Lacrimispora
Bifidobacterium
Treponema
Catonella
Bacteroidales_[G-2]
Parvimonas
Lancefieldella
Bergeyella
Granulicatella
Eikenella
Ottowia
Abiotrophia
Tannerella
Lachnospiraceae_[G-3]
Lachnoanaerobaculum
Gemella
Alloprevotella
Peptidiphaga
Kingella
Schaalia
Cardiobacterium
Arachnia
Campylobacter
Selenomonas
Saccharibacteria_(TM7)_[G-1]
Aggregatibacter
Porphyromonas
Scardovia
Neisseria
Lautropia
Veillonella
Haemophilus
Fusobacterium
Prevotella
Rothia
Capnocytophaga
Leptotrichia
Corynebacterium
Streptococcus
Actinomyces
Genus
FIT924.S003
FIT924.S005
FIT924.S008
FIT924.S011
FIT924.S013
FIT924.S019
FIT924.S021
FIT924.S026
FIT924.S030
FIT924.S032
FIT924.S035
FIT924.S043
FIT924.S049
FIT924.S054
FIT924.S056
FIT924.S059
FIT924.S062
FIT924.S064
FIT924.S070
FIT924.S072
FIT924.S077
FIT924.S081
FIT924.S083
FIT924.S086
FIT924.S094
FIT924.S100
Samples

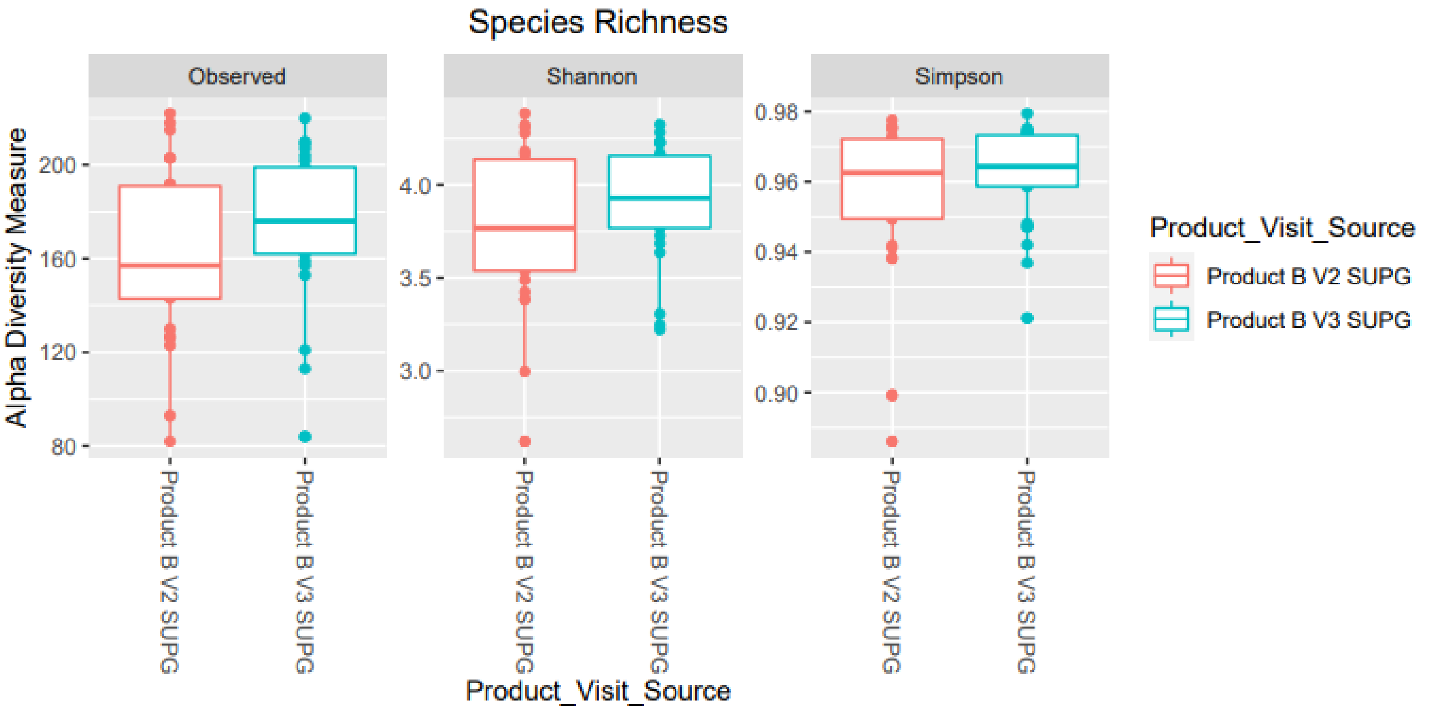

0
20
40
60
80
100
Value
Product_Visit_Source
Product A V2 SUPG
Product A V3 SUPG
Campylobacter concisus
Capnocytophaga sp._HMT_335
Schaalia odontolytica
Granulicatella adiacens
Tannerella sp._HMT_286
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_348
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346
Bergeyella sp._HMT_322
Streptococcus sp._HMT_064
Streptococcus downii
Lachnoanaerobaculum saburreum
Leptotrichia sp._HMT_225
Cardiobacterium hominis_nov_97.510%
Selenomonas noxia
Schaalia sp._HMT_178
Prevotella sp._HMT_317
Lachnospiraceae_[G-3] bacterium_HMT_100
Lachnoanaerobaculum umeaense
Tannerella serpentiformis_sp._HMT_286
Actinomyces sp._HMT_896
Campylobacter gracilis
Capnocytophaga sp._HMT_336
Fusobacterium periodonticum
Leptotrichia sp._HMT_215
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_347
Eikenella corrodens
Porphyromonas catoniae
Leptotrichia sp._HMT_212
Gemella morbillorum
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_349
Alloprevotella tannerae
Cardiobacterium hominis
Fusobacterium sp._HMT_204
Fusobacterium hwasookii
Campylobacter showae
Leptotrichia sp._HMT_392
Streptococcus chosunense
Neisseria flava
Abiotrophia defectiva
Capnocytophaga gingivalis
Kingella oralis
Neisseria mucosa
Corynebacterium durum_nov_97.904%
Streptococcus sanguinis_nov_97.782%
Leptotrichia hofstadii
Cardiobacterium valvarum
Actinomyces johnsonii
Neisseria oralis
Streptococcus cristatus
Peptidiphaga sp._HMT_183
Corynebacterium matruchotii_nov_97.755%
Prevotella oris
Actinomyces israelii_nov_96.838%
Veillonella parvula
Streptococcus oralis_subsp._tigurinus_clade_071
Prevotella nigrescens
Actinomyces dentalis
Prevotella melaninogenica
Streptococcus mitis
Aggregatibacter aphrophilus
Actinomyces massiliensis
Arachnia propionica
Actinomyces sp._HMT_171
Neisseria elongata
Capnocytophaga sputigena
Porphyromonas pasteri
Aggregatibacter sp._HMT_458
Leptotrichia buccalis
Neisseria flavescens
Capnocytophaga sp._HMT_332
Actinomyces naeslundii
Leptotrichia hongkongensis
Streptococcus gordonii
Streptococcus cristatus_clade_578
Leptotrichia sp._HMT_417
Leptotrichia wadei
Actinomyces sp._HMT_897
Corynebacterium durum
Streptococcus oralis_subsp._dentisani_clade_058
Actinomyces sp._HMT_170
Veillonella dispar_parvula
Actinomyces sp._HMT_448
Actinomyces sp._HMT_175
Capnocytophaga leadbetteri
Capnocytophaga granulosa
Streptococcus oralis
Fusobacterium nucleatum
Streptococcus sp._HMT_423
Rothia aeria
Haemophilus parainfluenzae
Lautropia mirabilis
Streptococcus sanguinis
Rothia dentocariosa
Actinomyces sp._HMT_169
Actinomyces oris
Streptococcus parasanguinis_clade_411
Streptococcus anginosus
Scardovia wiggsiae
Streptococcus mutans
Corynebacterium matruchotii
F17924.S003
F17924.S005
F17924.S008
F17924.S011
F17924.S013
F17924.S019
F17924.S021
F17924.S026
F17924.S030
F17924.S032
F17924.S035
F17924.S043
F17924.S049
F17924.S054
F17924.S056
F17924.S059
F17924.S062
F17924.S064
F17924.S070
F17924.S072
F17924.S077
F17924.S081
F17924.S083
F17924.S086
F17924.S094
F17924.S100
Samples
Species

Comparison 14. Product B V2 SUPG vs Product B V3 SUPG

1) Taxonomy bar graphs



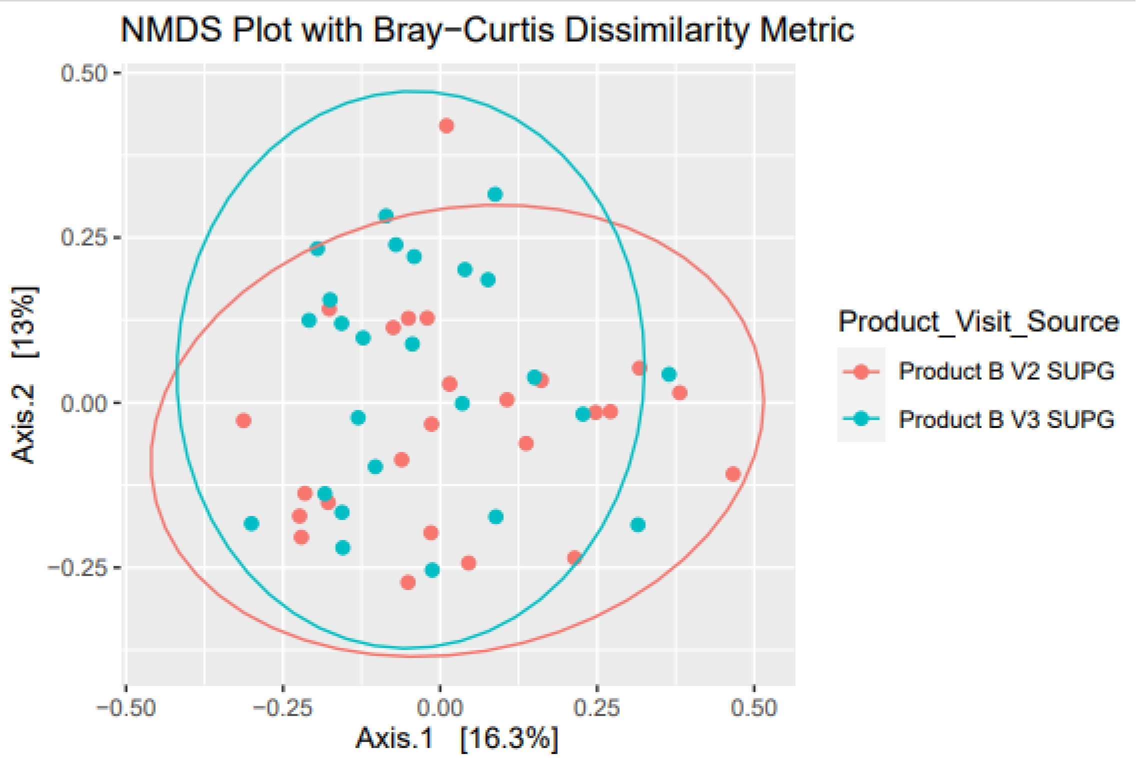
2) Alpha



No significant differences

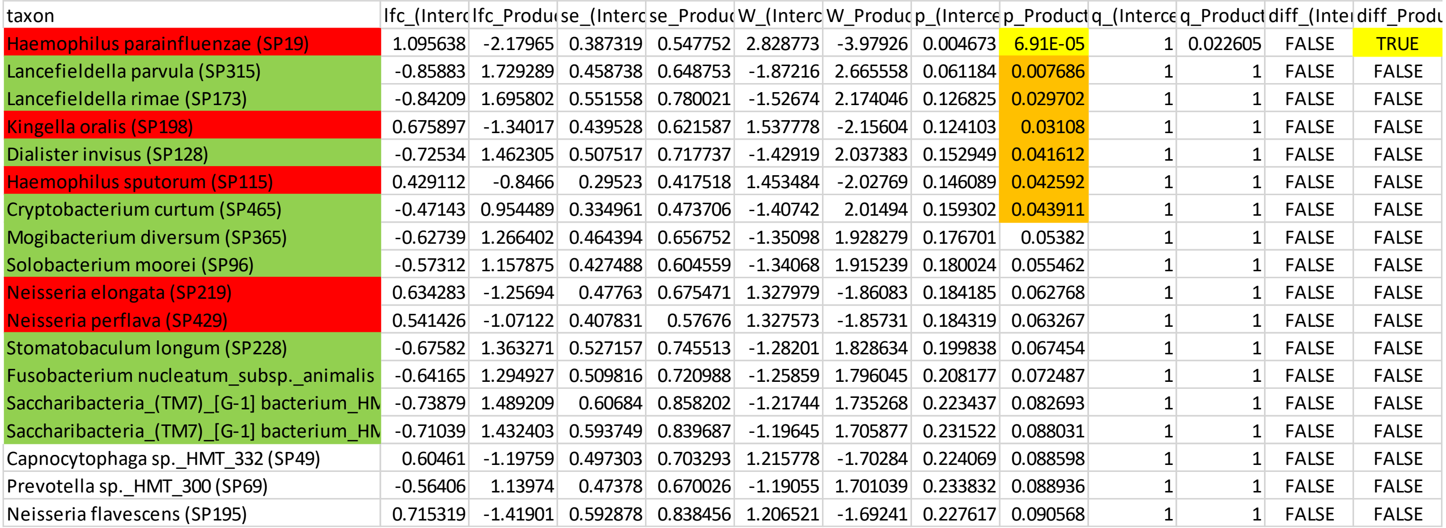
P value for Observed is 0.099

3) Beta diversity



No significant differences but P = 0.09

4) Differential abundance



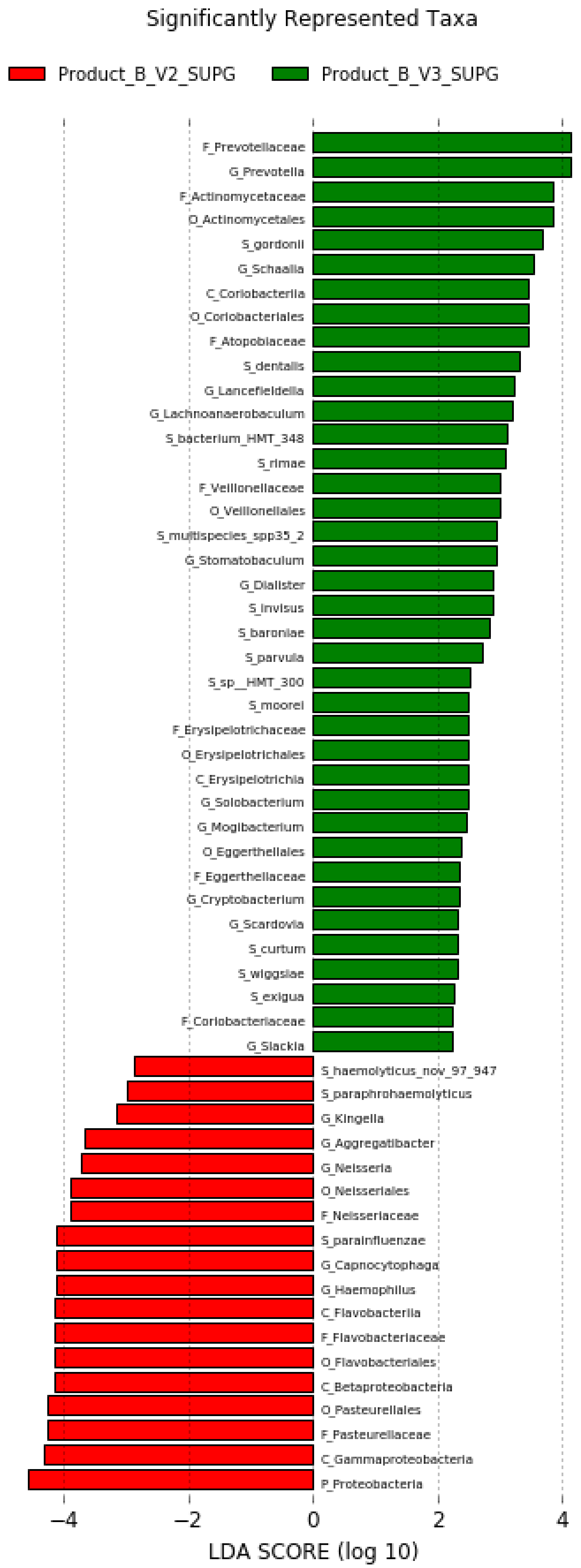
taxon	lfc_(Interc	lfc_Produ	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inter	diff_Produ
Haemophilus parainfluenzae (SP19)	1.095638	-2.17965	0.387319	0.547752	2.828773	-3.97926	0.004673	6.91E-05	1	0.022605	FALSE	TRUE
Lancefieldella parvula (SP315)	-0.85883	1.729289	0.458738	0.648753	-1.87216	2.665558	0.061184	0.007686	1	1	FALSE	FALSE
Lancefieldella rimae (SP173)	-0.84209	1.695802	0.551558	0.780021	-1.52674	2.174046	0.126825	0.029702	1	1	FALSE	FALSE
Kingella oralis (SP198)	0.675897	-1.34017	0.439528	0.621587	1.537778	-2.15604	0.124103	0.03108	1	1	FALSE	FALSE
Dialister invisus (SP128)	-0.72534	1.462305	0.507517	0.717737	-1.42919	2.037383	0.152949	0.041612	1	1	FALSE	FALSE
Haemophilus sputorum (SP115)	0.429112	-0.8466	0.29523	0.417518	1.453484	-2.02769	0.146089	0.042592	1	1	FALSE	FALSE
Cryptobacterium curtum (SP465)	-0.47143	0.954489	0.334961	0.473706	-1.40742	2.01494	0.159302	0.043911	1	1	FALSE	FALSE
Mogibacterium diversum (SP365)	-0.62739	1.266402	0.464394	0.656752	-1.35098	1.928279	0.176701	0.05382	1	1	FALSE	FALSE
Solobacterium moorei (SP96)	-0.57312	1.157875	0.427488	0.604559	-1.34068	1.915239	0.180024	0.055462	1	1	FALSE	FALSE
Neisseria elongata (SP219)	0.634283	-1.25694	0.47763	0.675471	1.327979	-1.86083	0.184185	0.062768	1	1	FALSE	FALSE
Neisseria perflava (SP429)	0.541426	-1.07122	0.407831	0.57676	1.327573	-1.85731	0.184319	0.063267	1	1	FALSE	FALSE
Stomatobaculum longum (SP228)	-0.67582	1.363271	0.527157	0.745513	-1.28201	1.828634	0.199838	0.067454	1	1	FALSE	FALSE
Fusobacterium nucleatum_subsp._animalis	-0.64165	1.294927	0.509816	0.720988	-1.25859	1.796045	0.208177	0.072487	1	1	FALSE	FALSE
Saccharibacteria_(TM7)_[G-1] bacterium_HM	-0.73879	1.489209	0.60684	0.858202	-1.21744	1.735268	0.223437	0.082693	1	1	FALSE	FALSE
Saccharibacteria_(TM7)_[G-1] bacterium_HM	-0.71039	1.432403	0.593749	0.839687	-1.19645	1.705877	0.231522	0.088031	1	1	FALSE	FALSE
Capnocytophaga sp._HMT_332 (SP49)	0.60461	-1.19759	0.497303	0.703293	1.215778	-1.70284	0.224069	0.088598	1	1	FALSE	FALSE
Prevotella sp._HMT_300 (SP69)	-0.56406	1.13974	0.47378	0.670026	-1.19055	1.701039	0.233832	0.088936	1	1	FALSE	FALSE
Neisseria flavescens (SP195)	0.715319	-1.41901	0.592878	0.838456	1.206521	-1.69241	0.227617	0.090568	1	1	FALSE	FALSE

H. influenzae is statistically different

Green, more prevalent in V3

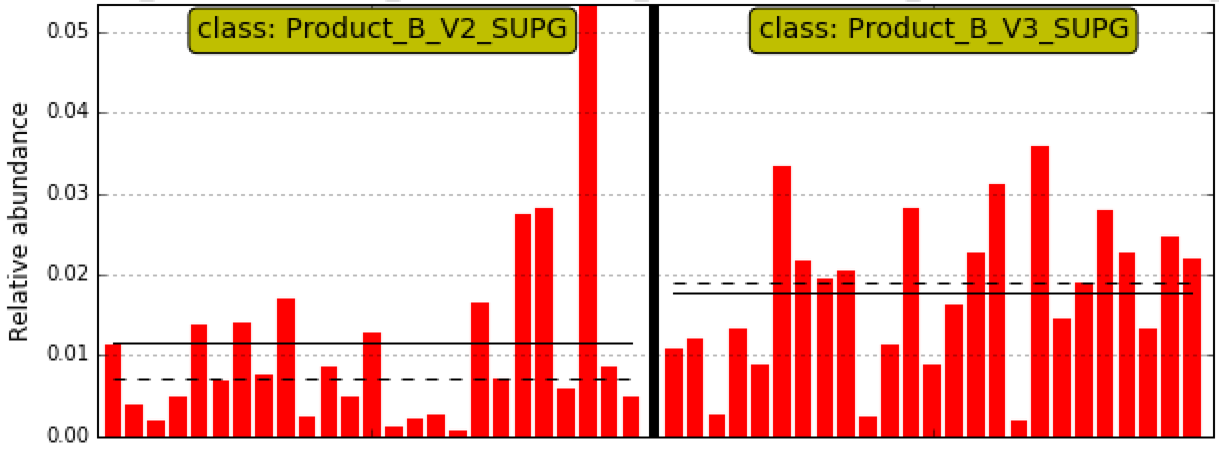
Red, more prevalent in V2

5) Lefse Many differences

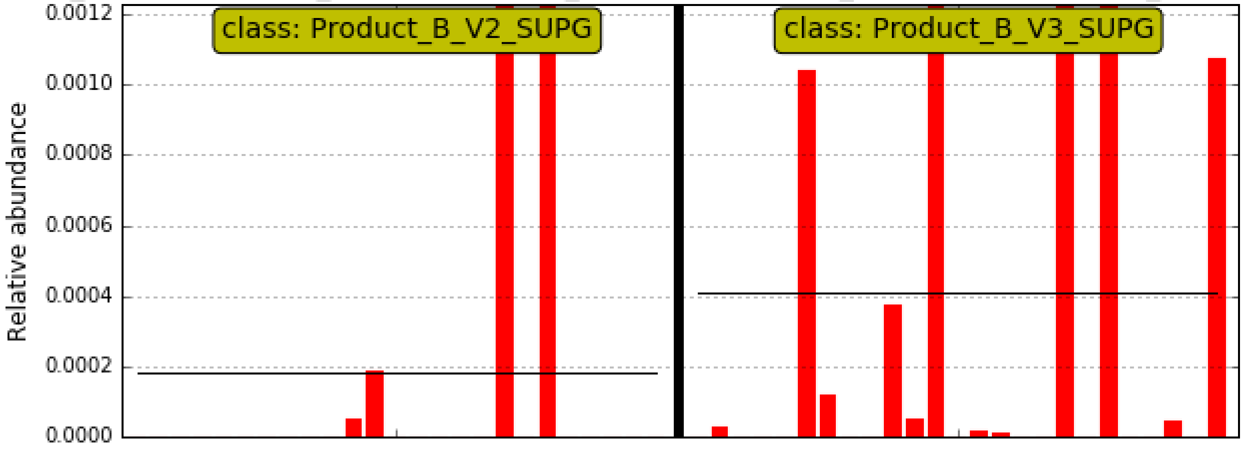


Significantly Represented Taxa
Product_B_V2_SUPG
Product_B_V3_SUPG
F_Prevotellaceae
G_Prevotella
F_Actinomycetaceae
O_Actinomycetales
S_gordonii
G_Schaalia
C_Coriobacteriia
O_Coriobacteriales
F_Atopobiaceae
S_dentalis
G_Lancefieldella
G_Lachnoanaerobaculum
S_bacterium_HMT_348
S_rimae
F_Veillonellaceae
O_Veillonellales
S_multispecies_spp35_2
G_Stomatobaculum
G_Dialister
S_invisus
S_baroniae
S_parvula
S_sp__HMT_300
S_moorei
F_Erysipelotrichaceae
O_Erysipelotrichales
C_Erysipelotrichia
G_Solobacterium
G_Mogibacterium
O_Eggerthellales
F_Eggerthellaceae
G_Cryptobacterium
G_Scardovia
S_curtum
S_wiggsiae
S_exigua
F_Coriobacteriaceae
G_Slackia
S_haemolyticus_nov_97_947
S_paraphrohaemolyticus
G_Kingella
G_Aggregatibacter
G_Neisseria
O_Neisseriales
F_Neisseriaceae
S_parainfluenzae
G_Capnocytophaga
G_Haemophilus
C_Flavobacteriia
F_Flavobacteriaceae
O_Flavobacteriales
C_Betaproteobacteria
O_Pasteurellales
F_Pasteurellaceae
C_Gammaproteobacteria
P_Proteobacteria
−4
−2
0
2
4
LDA SCORE (log 10)

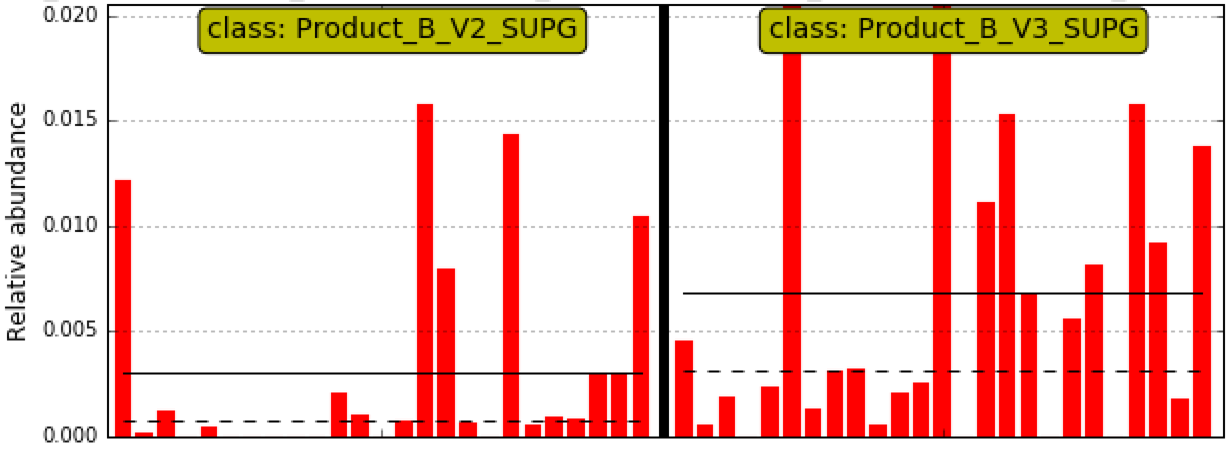
K_Bacteria.P_Actinobacteria.C_Actinobacteria.O_Actinomycetales.F_Actinomycetaceae.G_Schaalia



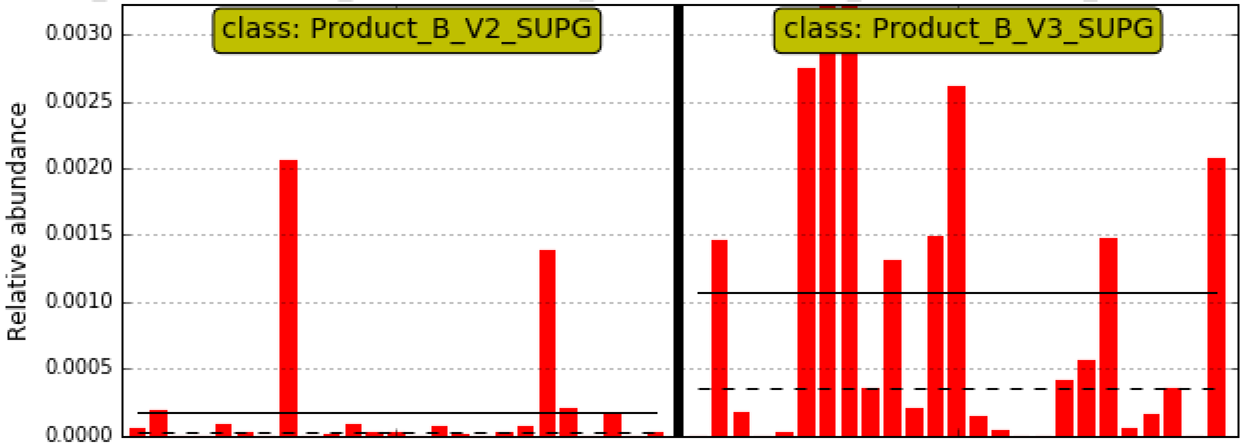
acteria.P_Actinobacteria.C_Actinobacteria.O_Bifidobacteriales.F_Bifidobacteriaceae.G_Scardovia.S_wig



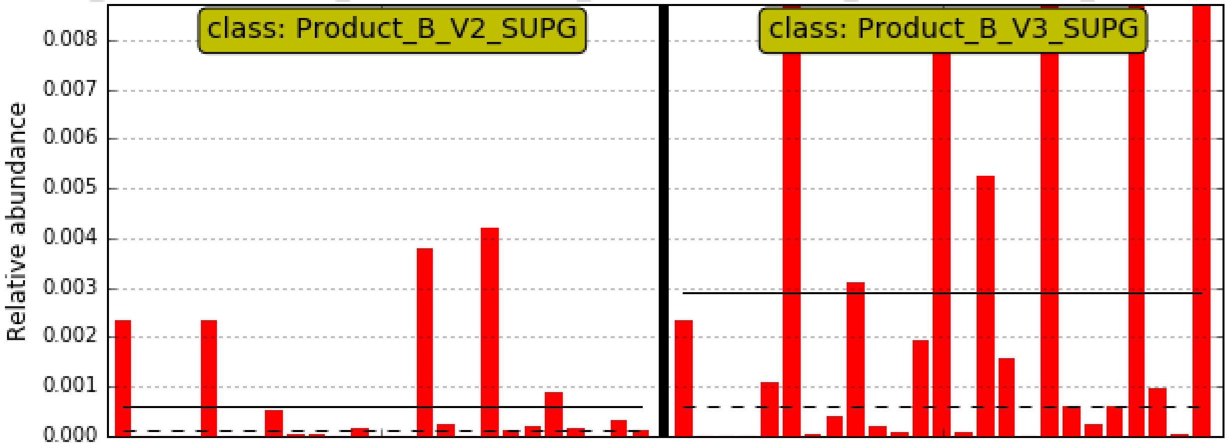
acteria.P_Actinobacteria.C_Actinomycetia.O_Actinomycetales.F_Actinomycetaceae.G_Actinomyces.S_d



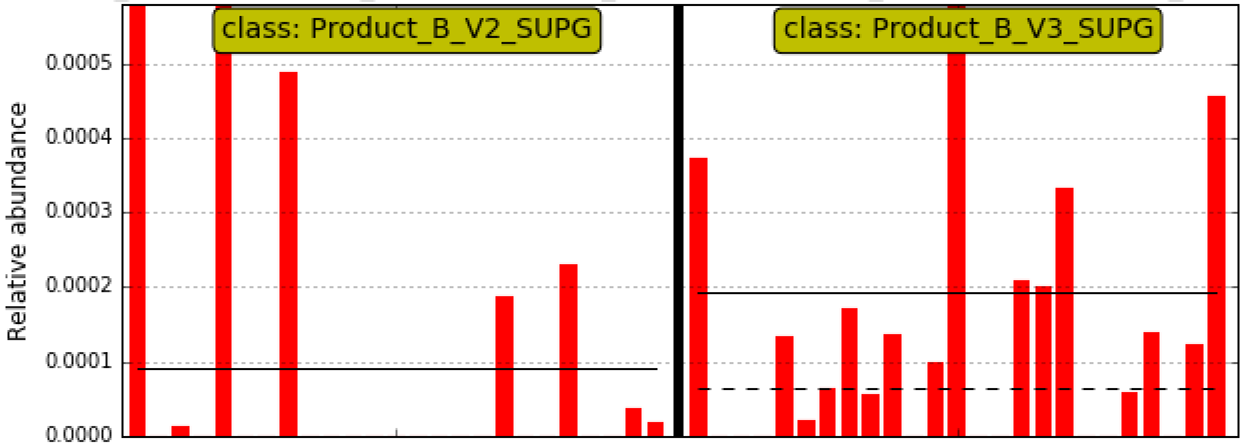
_Bacteria.P_Actinobacteria.C_Coriobacteriia.O_Coriobacteriales.F_Atopobiaceae.G_Lancefieldella.S_par

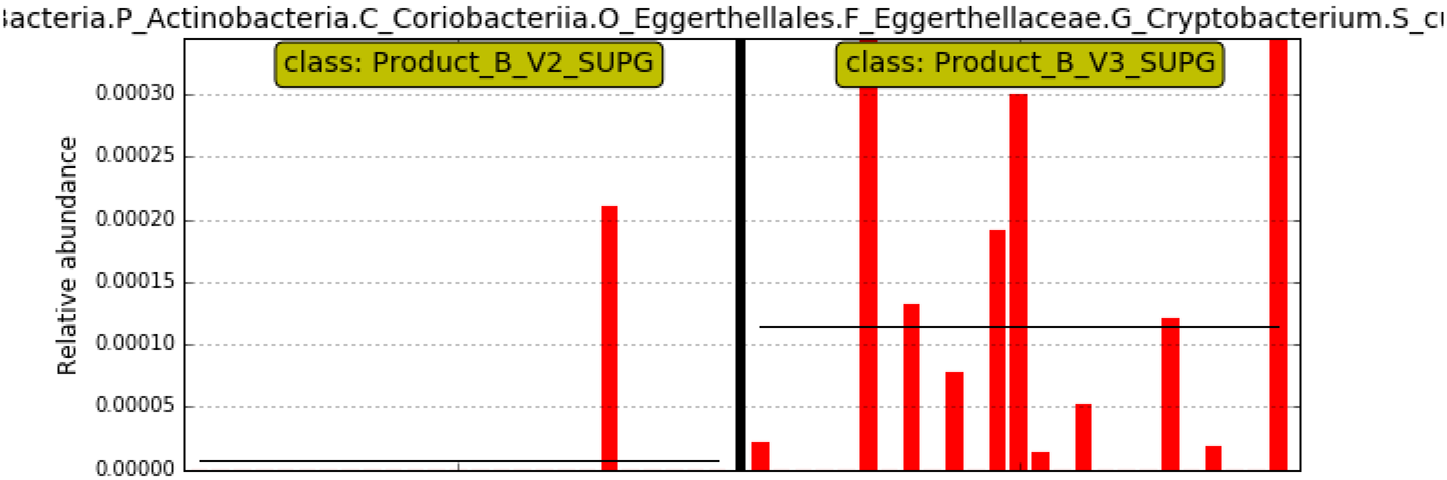


<_Bacteria.P_Actinobacteria.C_Coriobacteriia.O_Coriobacteriales.F_Atopobiaceae.G_Lancefieldella.S_rim

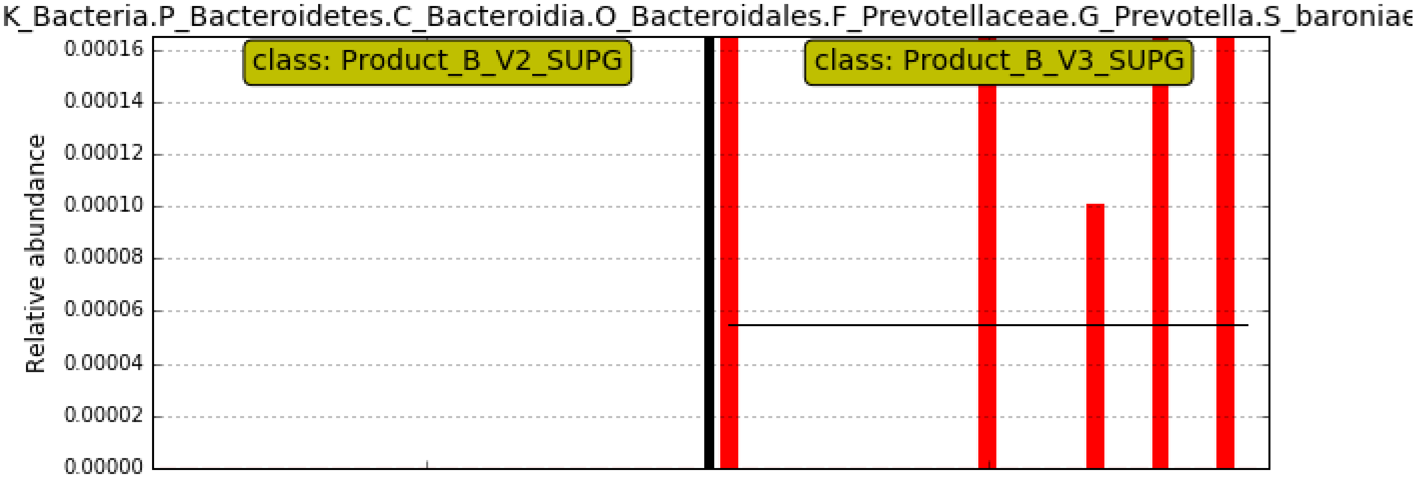


K_Bacteria.P_Actinobacteria.C_Coriobacteriia.O_Coriobacteriales.F_Coriobacteriaceae.G_Slackia.S_exig

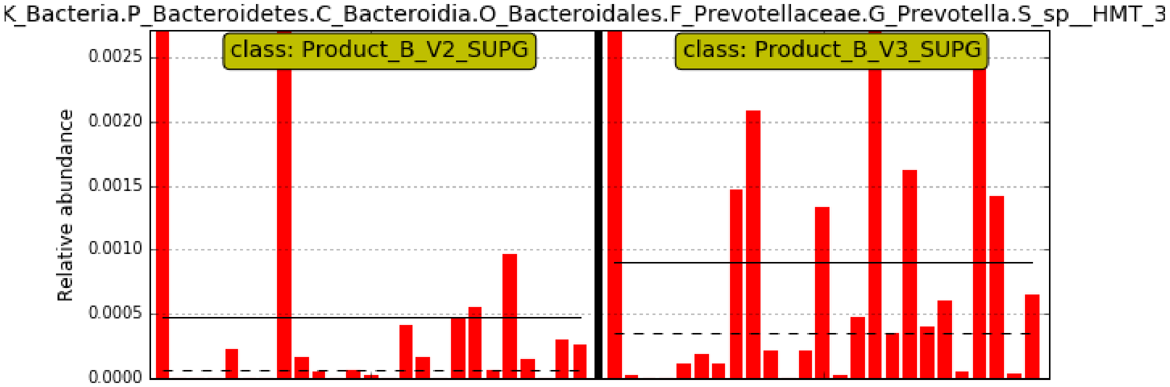




;acteria.P_Actinobacteria.C_Coriobacteriia.O_Eggerthellales.F_Eggerthellaceae.G_Cryptobacterium.S_cu
class: Product_B_V2_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.00030
0.00025
0.00020
0.00015
0.00010
0.00005
0.00000

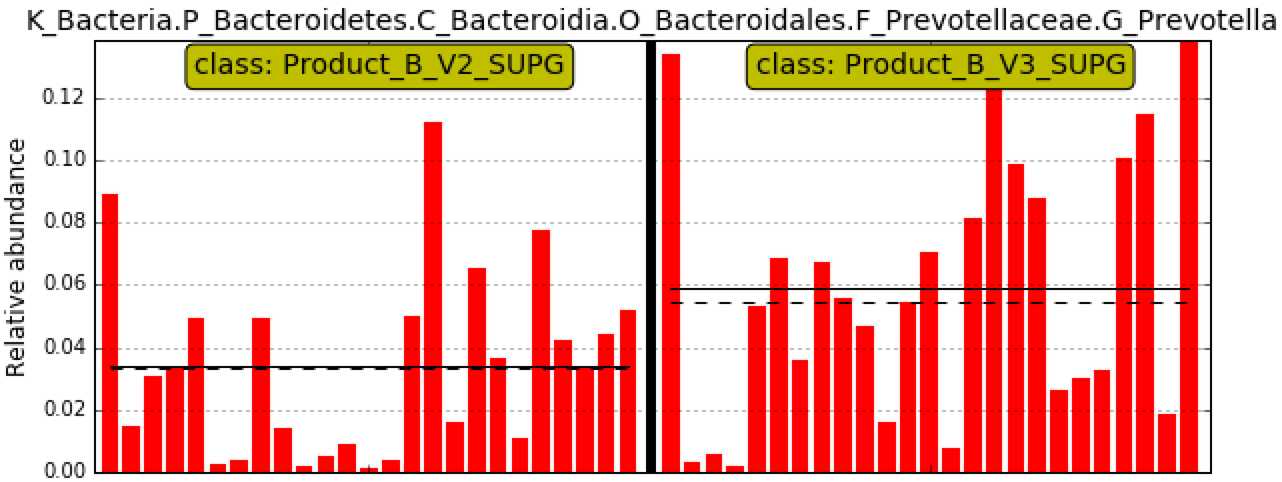


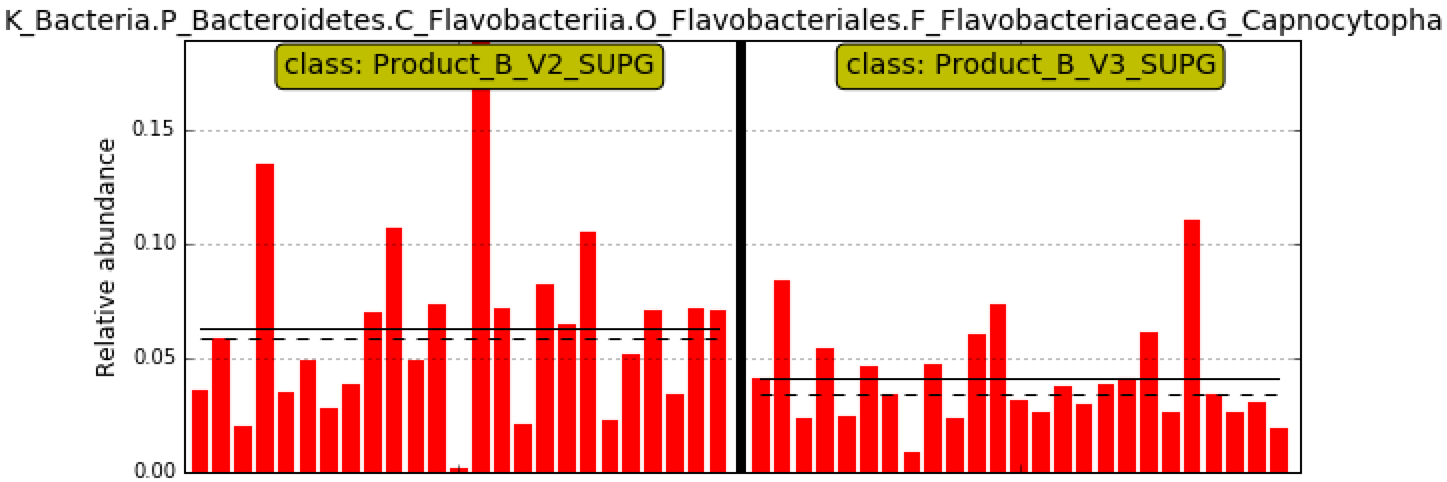
K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_baroniae
class: Product_B_V2_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.00016
0.00014
0.00012
0.00010
0.00008
0.00006
0.00004
0.00002
0.00000

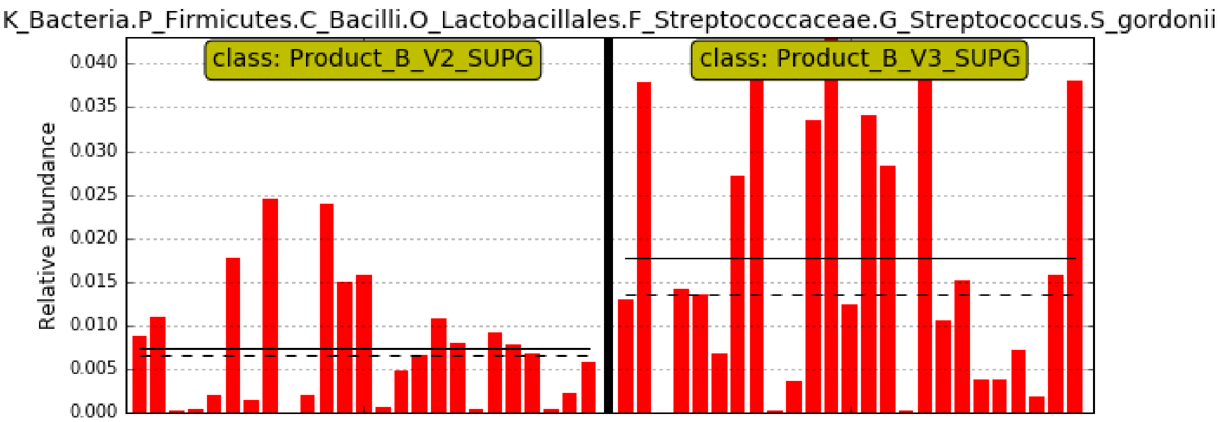


K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_sp__HMT_3
class: Product_B_V2_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000

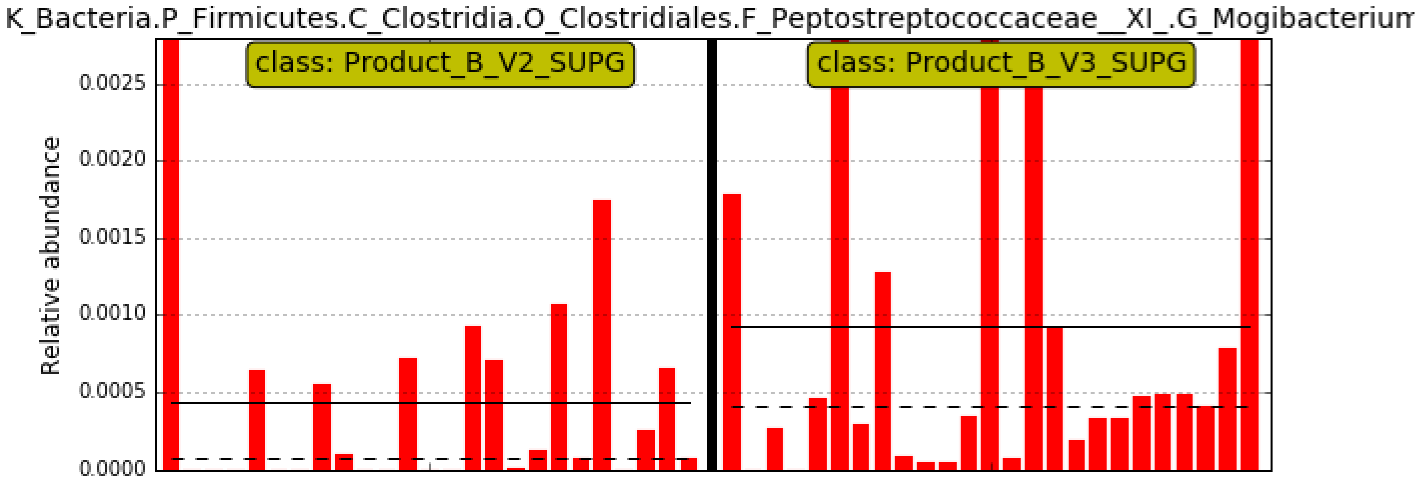
HMT300

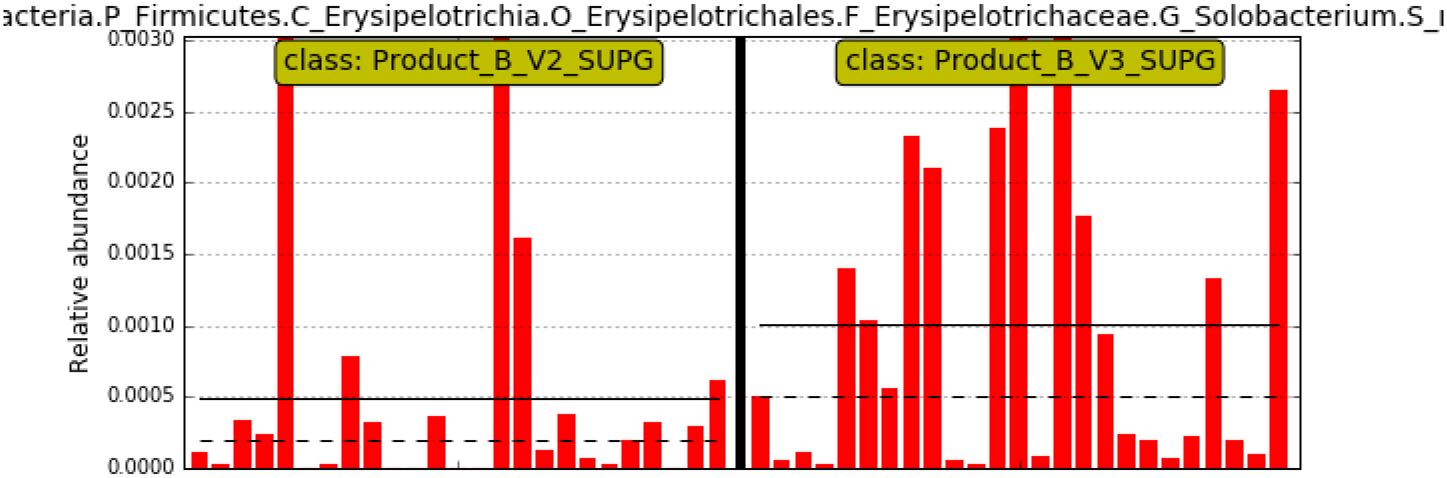

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella
class: Product_B_V2_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.12
0.10
0.08
0.06
0.04
0.02
0.00

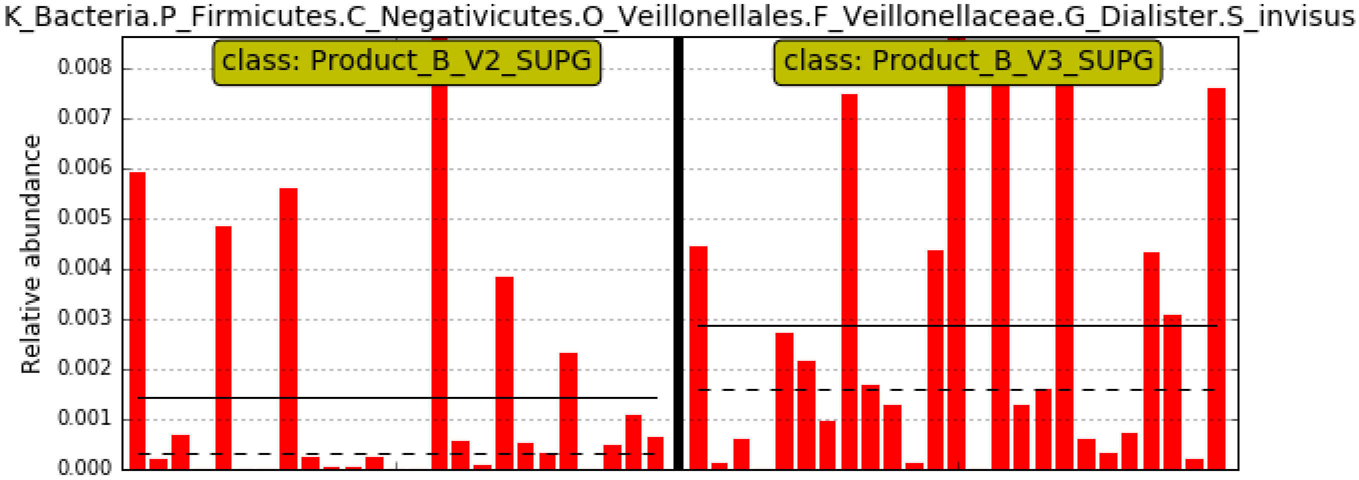

K_Bacteria.P_Bacteroidetes.C_Flavobacteriia.O_Flavobacteriales.F_Flavobacteriaceae.G_Capnocytopha
class: Product_B_V2_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.15
0.10
0.05
0.00

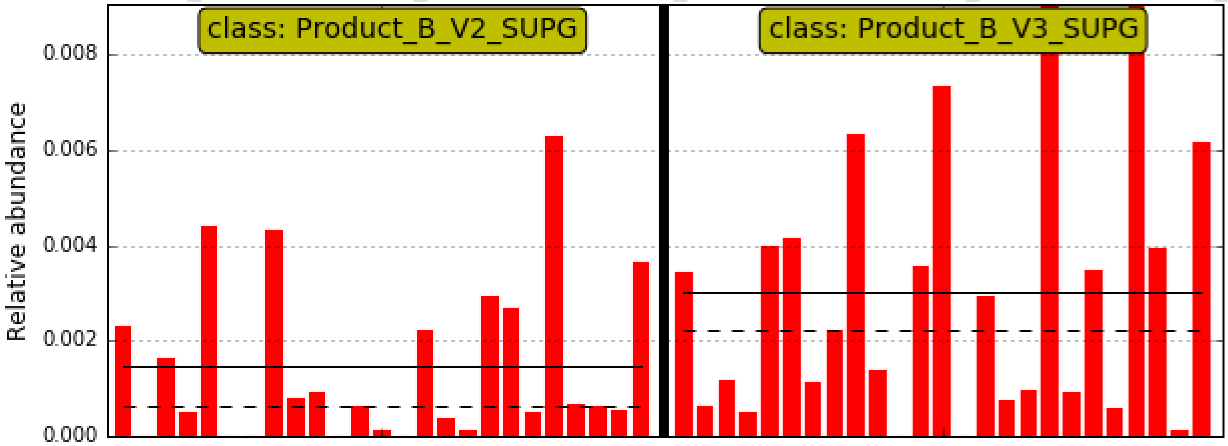

K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_gordonii
class: Product_B_V2_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.040
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000

#####

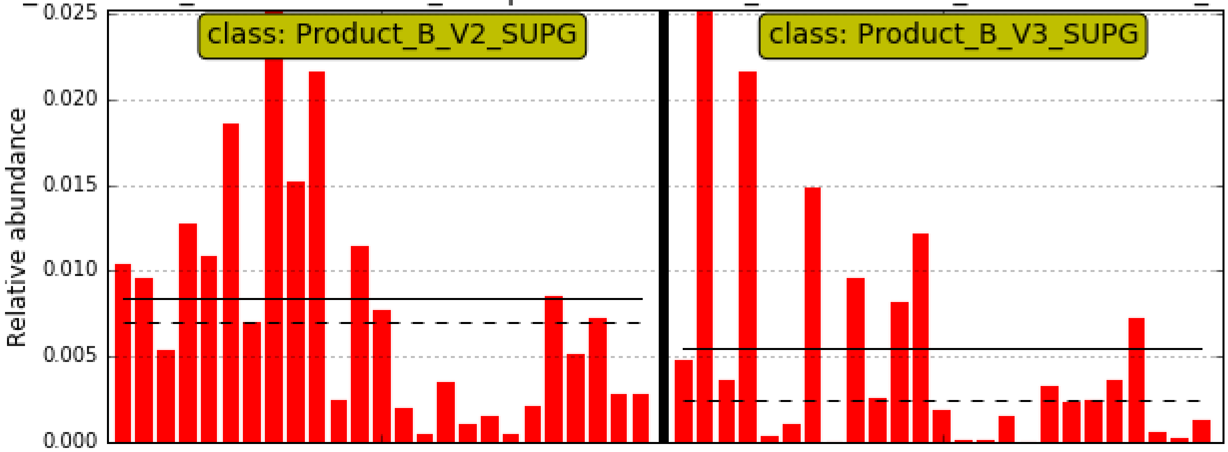

K_Bacteria.P_Firmicutes.C_Clostridia.O_Clostridiales.F_Peptostreptococcaceae__XI_.G_Mogibacterium
class: Product_B_V2_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000


acteria.P_Firmicutes.C_Erysipelotrichia.O_Erysipelotrichales.F_Erysipelotrichaceae.G_Solobacterium.S_
class: Product_B_V2_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.0030
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000

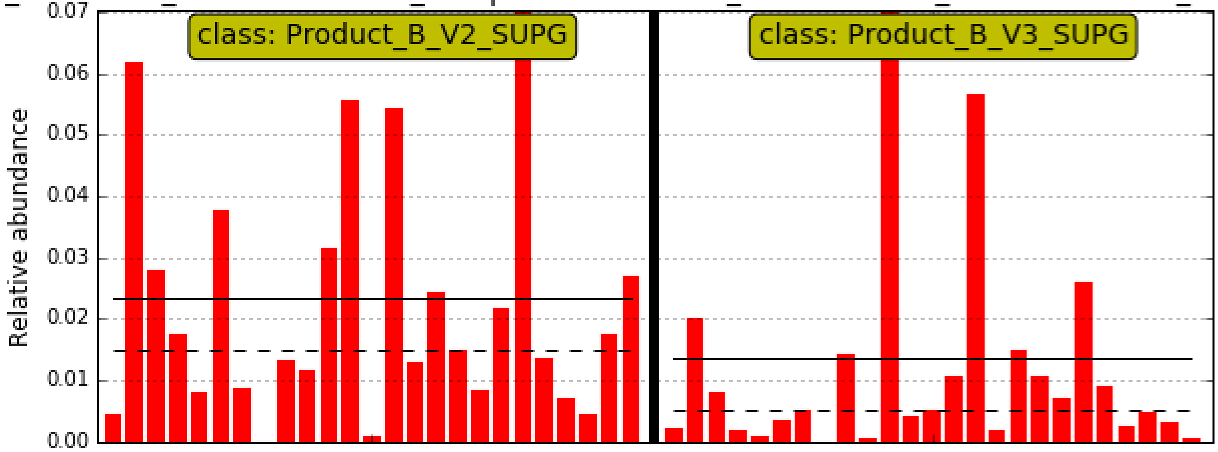

K_Bacteria.P_Firmicutes.C_Negativicutes.O_Veillonellales.F_Veillonellaceae.G_Dialister.S_invisus
class: Product_B_V2_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.008
0.007
0.006
0.005
0.004
0.003
0.002
0.001
0.000



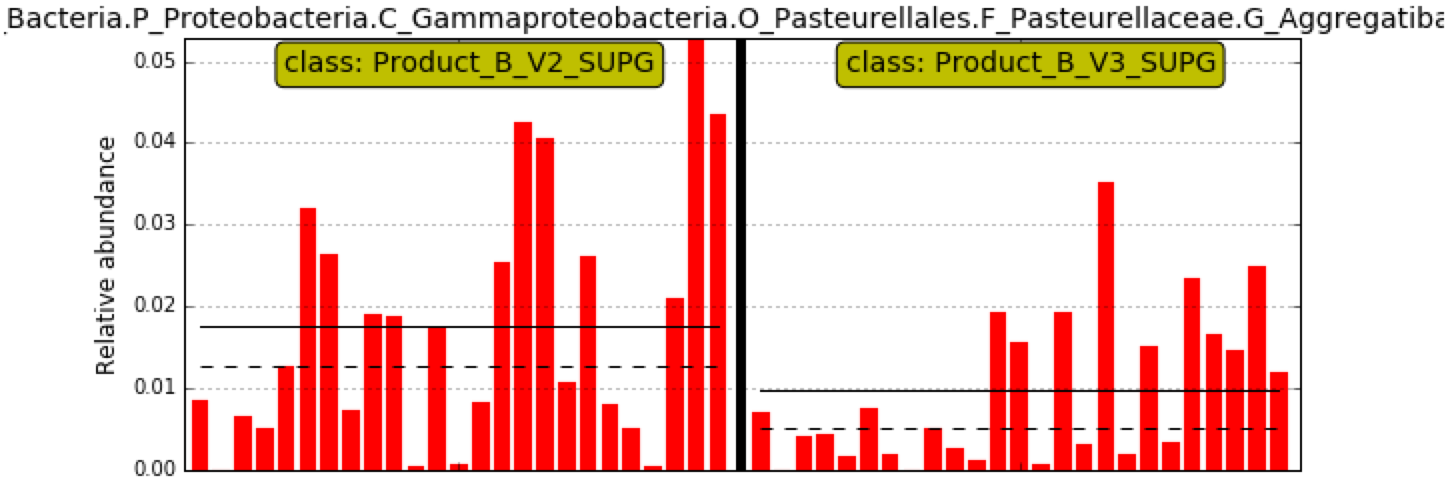
a.P_Fusobacteria.C_Fusobacteria.O_Fusobacteriales.F_Fusobacteriaceae.G_Fusobacterium.S_multispec

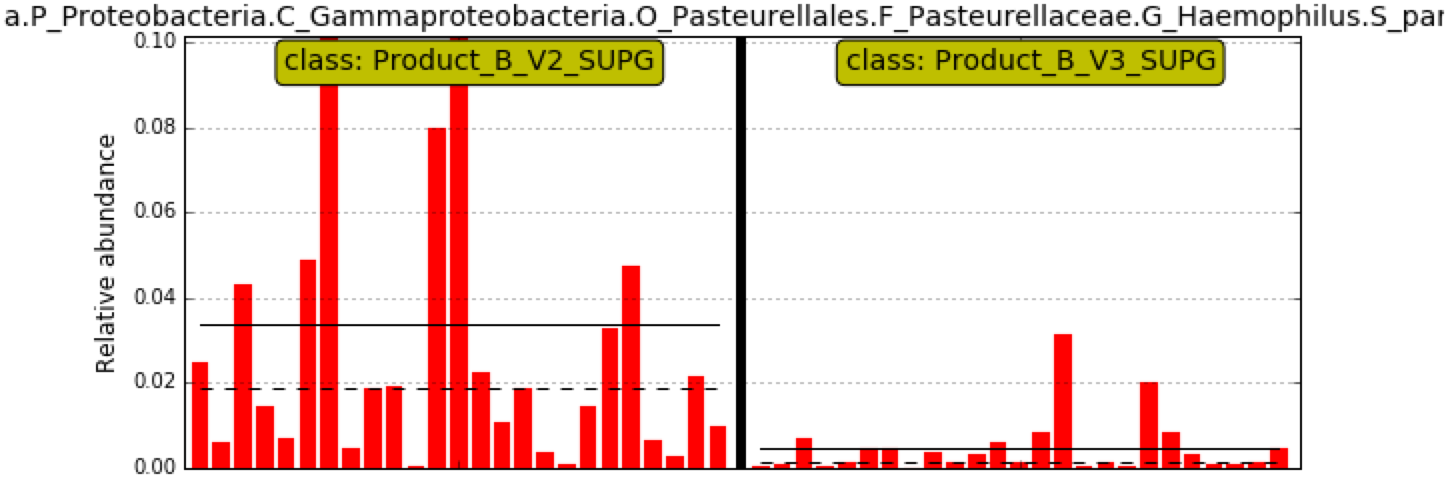


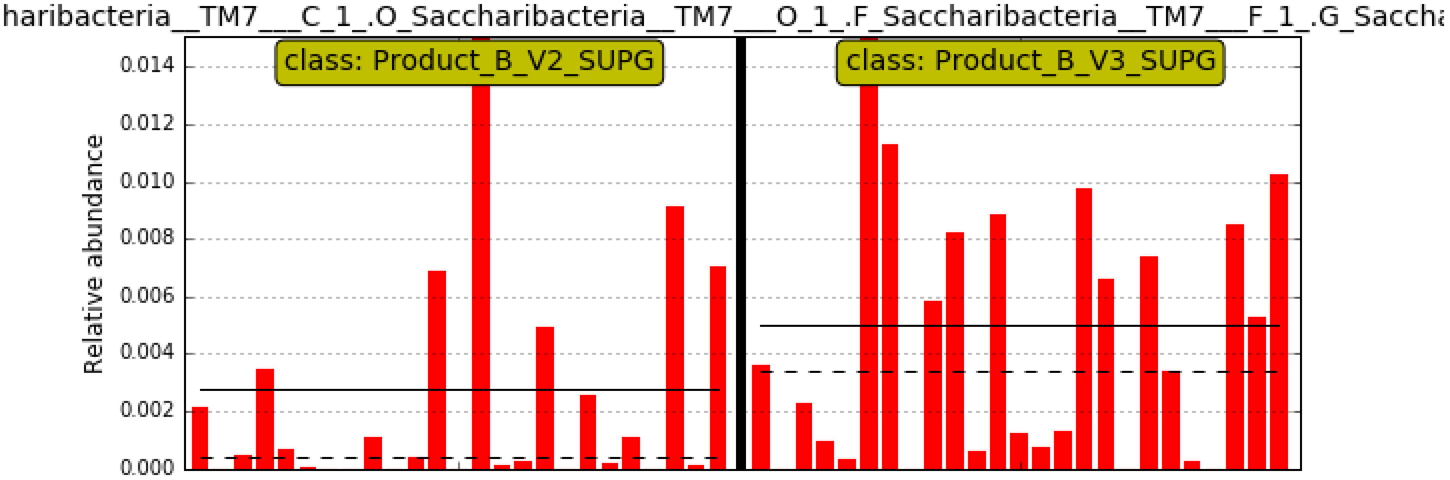
K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Kingella



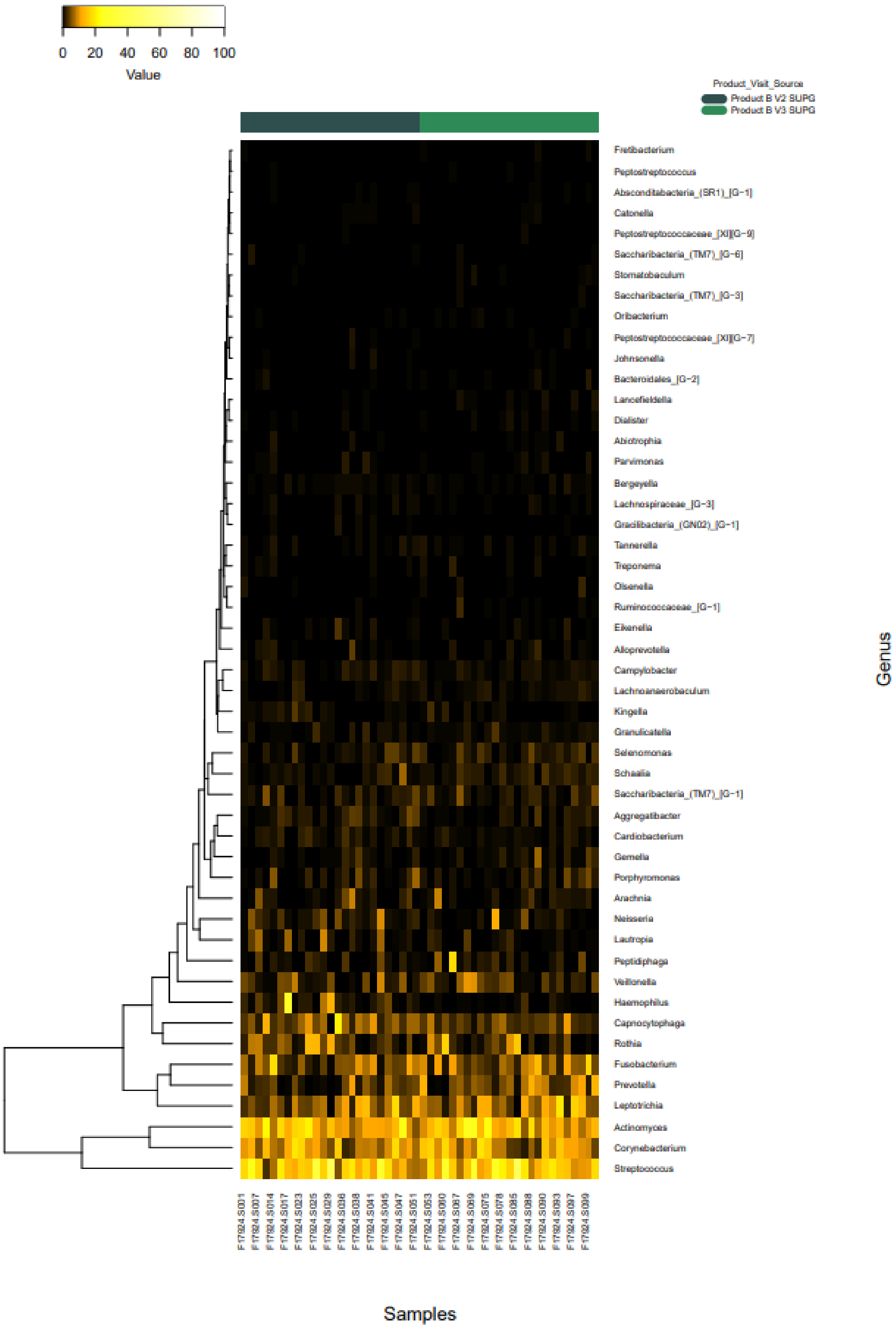
K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Neisseria

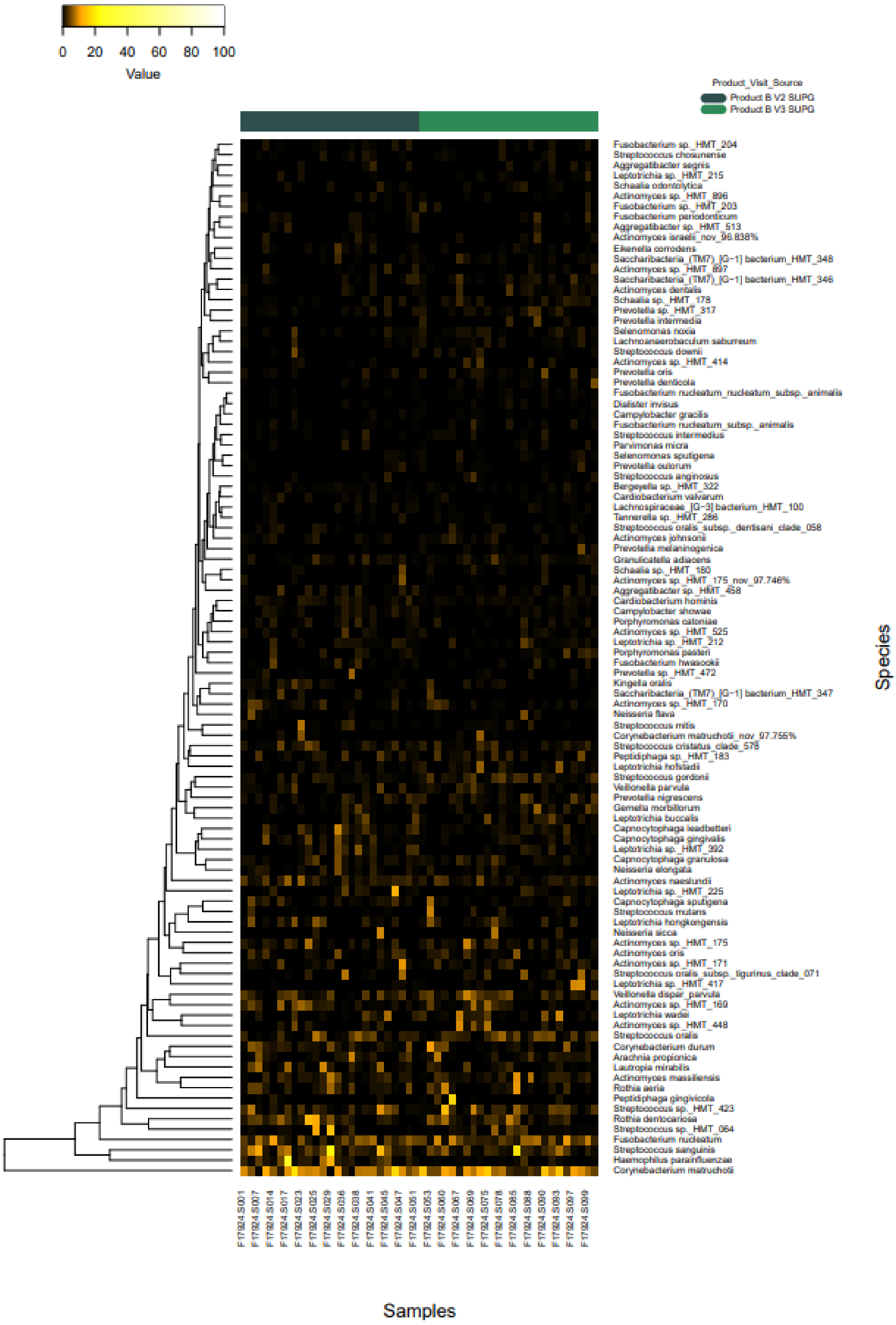

Bacteria.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Aggregatiba
class: Product_B_V2_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.05
0.04
0.03
0.02
0.01
0.00


a.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophilus.S_par
class: Product_B_V2_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.10
0.08
0.06
0.04
0.02
0.00


haribacteria__TM7___C_1_.O_Saccharibacteria__TM7___O_1_.F_Saccharibacteria__TM7___F_1_.G_Saccha
class: Product_B_V2_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000

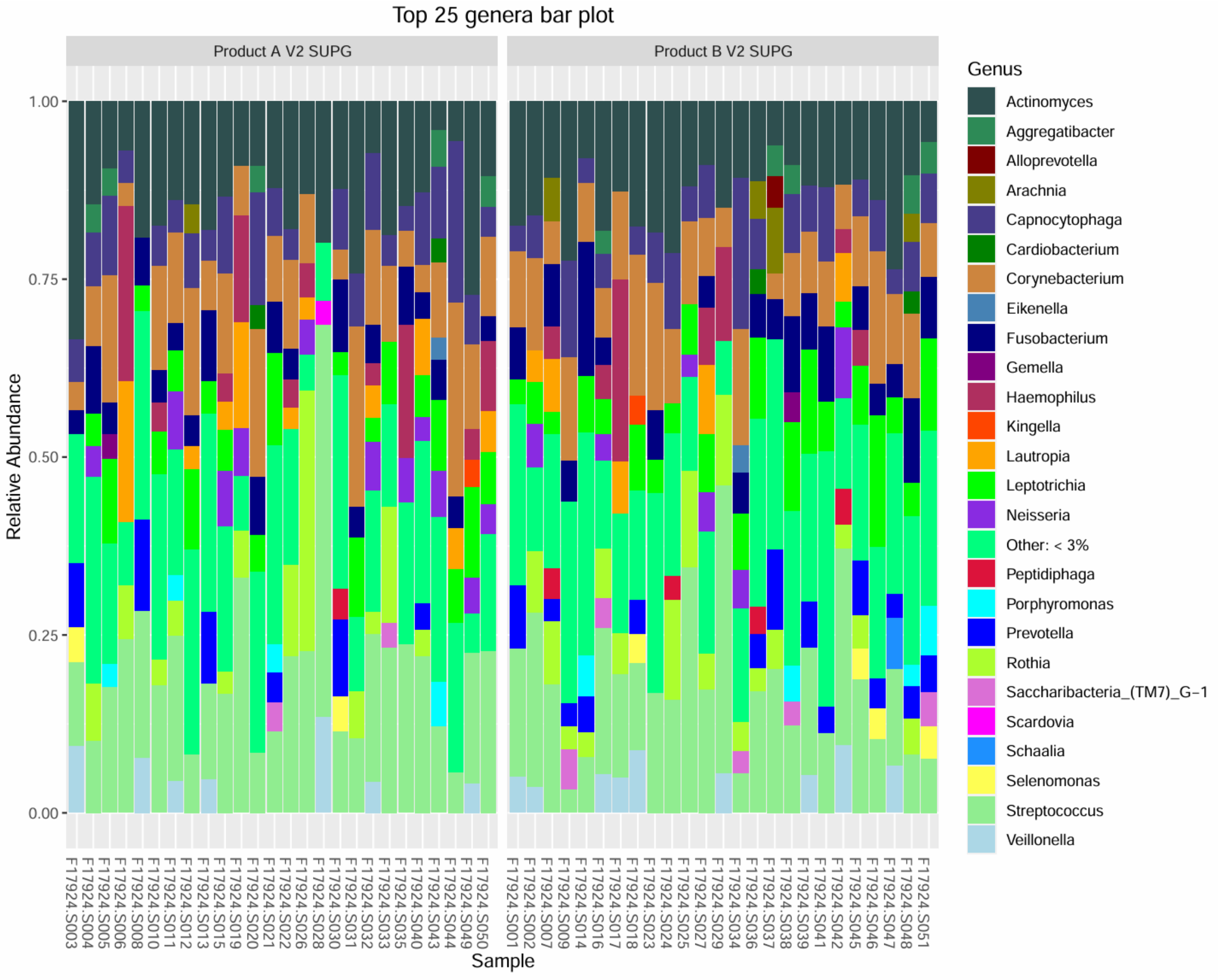
6) Heat map.


0
20
40
60
80
100
Value
Product_Visit_Source
Product B V2 SUPG
Product B V3 SUPG
Fretibacterium
Peptostreptococcus
Absconditabacteria_(SR1)_[G-1]
Catonella
Peptostreptococcaceae_[XI][G-9]
Saccharibacteria_(TM7)_[G-6]
Stomatobaculum
Saccharibacteria_(TM7)_[G-3]
Oribacterium
Peptostreptococcaceae_[XI][G-7]
Johnsonella
Bacteroidales_[G-2]
Lancefieldella
Dialister
Abiotrophia
Parvimonas
Bergeyella
Lachnospiraceae_[G-3]
Gracilibacteria_(GN02)_[G-1]
Tannerella
Treponema
Olsenella
Ruminococcaceae_[G-1]
Eikenella
Alloprevotella
Campylobacter
Lachnoanaerobaculum
Kingella
Granulicatella
Selenomonas
Schaalia
Saccharibacteria_(TM7)_[G-1]
Aggregatibacter
Cardiobacterium
Gemella
Porphyromonas
Arachnia
Neisseria
Lautropia
Peptidiphaga
Veillonella
Haemophilus
Capnocytophaga
Rothia
Fusobacterium
Prevotella
Leptotrichia
Actinomyces
Corynebacterium
Streptococcus
Genus
F17924.S001
F17924.S007
F17924.S014
F17924.S017
F17924.S023
F17924.S025
F17924.S029
F17924.S036
F17924.S038
F17924.S041
F17924.S045
F17924.S047
F17924.S051
F17924.S053
F17924.S060
F17924.S067
F17924.S069
F17924.S075
F17924.S078
F17924.S085
F17924.S088
F17924.S090
F17924.S093
F17924.S097
F17924.S099
Samples

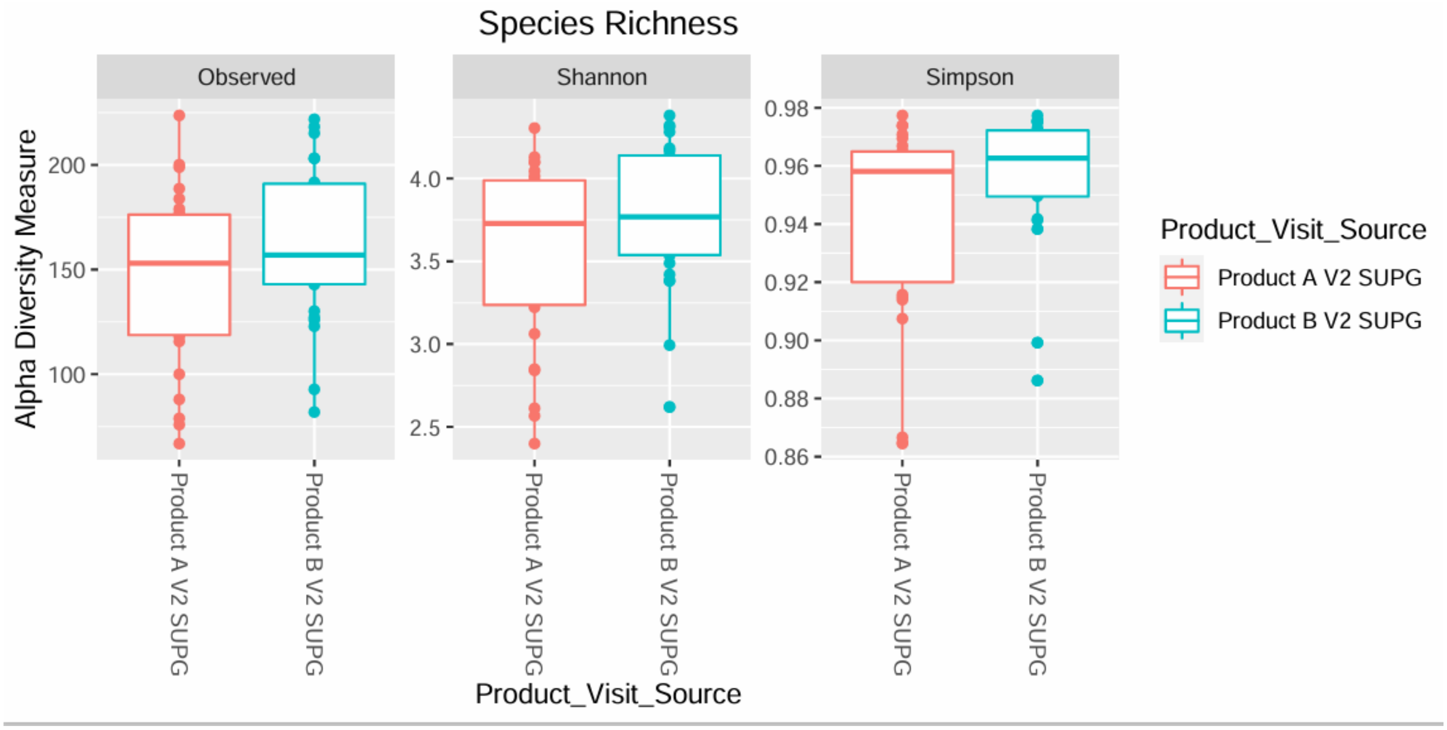

0
20
40
60
80
100
Value
Product_Visit_Source
Product B V2 SUPG
Product B V3 SUPG
Fusobacterium sp._HMT_204
Streptococcus chosunense
Aggregatibacter segnis
Leptotrichia sp._HMT_215
Schaalia odontolytica
Actinomyces sp._HMT_896
Fusobacterium sp._HMT_203
Fusobacterium periodonticum
Aggregatibacter sp._HMT_513
Actinomyces israelii_nov_96.838%
Eikenella corrodens
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_348
Actinomyces sp._HMT_897
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346
Actinomyces dentalis
Schaalia sp._HMT_178
Prevotella sp._HMT_317
Prevotella intermedia
Selenomonas noxia
Lachnoanaerobaculum saburreum
Streptococcus downii
Actinomyces sp._HMT_414
Prevotella oris
Prevotella denticola
Fusobacterium nucleatum_nucleatum_subsp._animalis
Dialister invisus
Campylobacter gracilis
Fusobacterium nucleatum_subsp._animalis
Streptococcus intermedius
Parvimonas micra
Selenomonas sputigena
Prevotella oulorum
Streptococcus anginosus
Bergeyella sp._HMT_322
Cardiobacterium valvarum
Lachnospiraceae_[G-3] bacterium_HMT_100
Tannerella sp._HMT_286
Streptococcus oralis_subsp._dentisani_clade_058
Actinomyces johnsonii
Prevotella melaninogenica
Granulicatella adiacens
Schaalia sp._HMT_180
Actinomyces sp._HMT_175_nov_97.746%
Aggregatibacter sp._HMT_458
Cardiobacterium hominis
Campylobacter showae
Porphyromonas catoniae
Actinomyces sp._HMT_525
Leptotrichia sp._HMT_212
Porphyromonas pasteri
Fusobacterium hwasookii
Prevotella sp._HMT_472
Kingella oralis
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_347
Actinomyces sp._HMT_170
Neisseria flava
Streptococcus mitis
Corynebacterium matruchotii_nov_97.755%
Streptococcus cristatus_clade_578
Peptidiphaga sp._HMT_183
Leptotrichia hofstadii
Streptococcus gordonii
Veillonella parvula
Prevotella nigrescens
Gemella morbillorum
Leptotrichia buccalis
Capnocytophaga leadbetteri
Capnocytophaga gingivalis
Leptotrichia sp._HMT_392
Capnocytophaga granulosa
Neisseria elongata
Actinomyces naeslundii
Leptotrichia sp._HMT_225
Capnocytophaga sputigena
Streptococcus mutans
Leptotrichia hongkongensis
Neisseria sicca
Actinomyces sp._HMT_175
Actinomyces oris
Actinomyces sp._HMT_171
Streptococcus oralis_subsp._tigurinus_clade_071
Leptotrichia sp._HMT_417
Veillonella dispar_parvula
Actinomyces sp._HMT_169
Leptotrichia wadei
Actinomyces sp._HMT_448
Streptococcus oralis
Corynebacterium durum
Arachnia propionica
Lautropia mirabilis
Actinomyces massiliensis
Rothia aeria
Peptidiphaga gingivicola
Streptococcus sp._HMT_423
Rothia dentocariosa
Streptococcus sp._HMT_064
Fusobacterium nucleatum
Streptococcus sanguinis
Haemophilus parainfluenzae
Corynebacterium matruchotii
Species
FIT924.S001
FIT924.S007
FIT924.S014
FIT924.S017
FIT924.S023
FIT924.S025
FIT924.S029
FIT924.S036
FIT924.S038
FIT924.S041
FIT924.S045
FIT924.S047
FIT924.S051
FIT924.S053
FIT924.S060
FIT924.S067
FIT924.S069
FIT924.S075
FIT924.S078
FIT924.S085
FIT924.S088
FIT924.S090
FIT924.S093
FIT924.S097
FIT924.S099
Samples

Comparison 15. Product A V2 SUPG vs Product B V2 SUPG

1) Taxonomy bar graphs

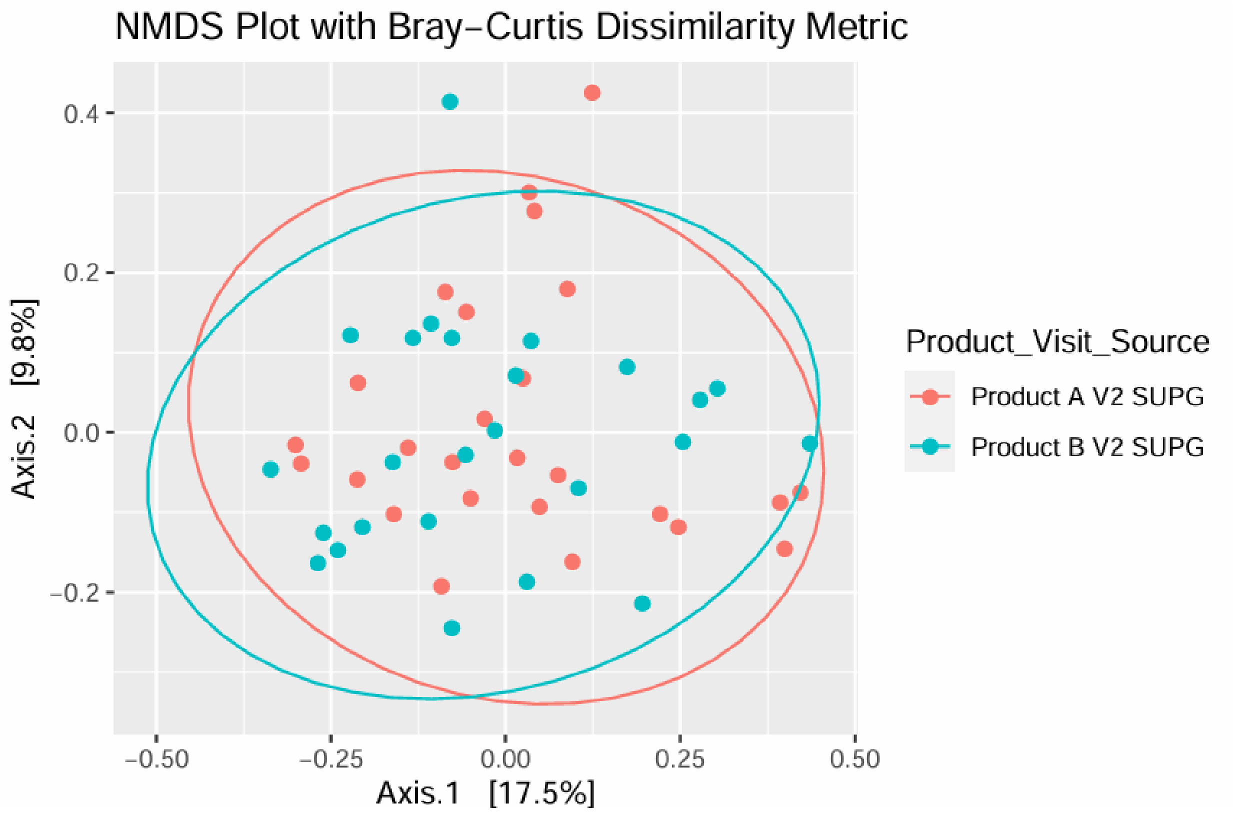


2) Alpha



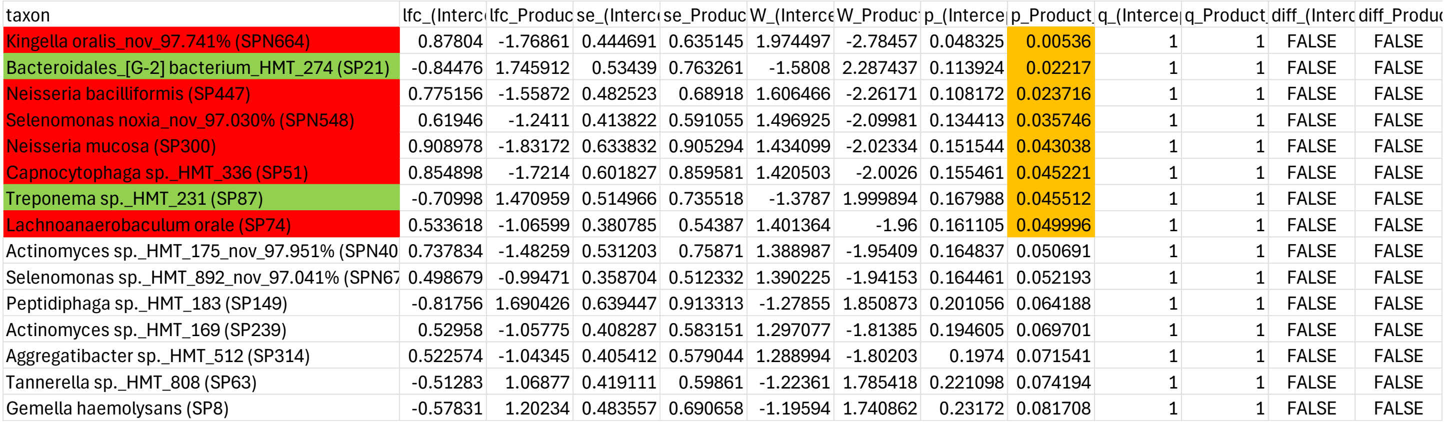
No significant differences

3) Beta diversity



No significant differences

4) Differential abundance



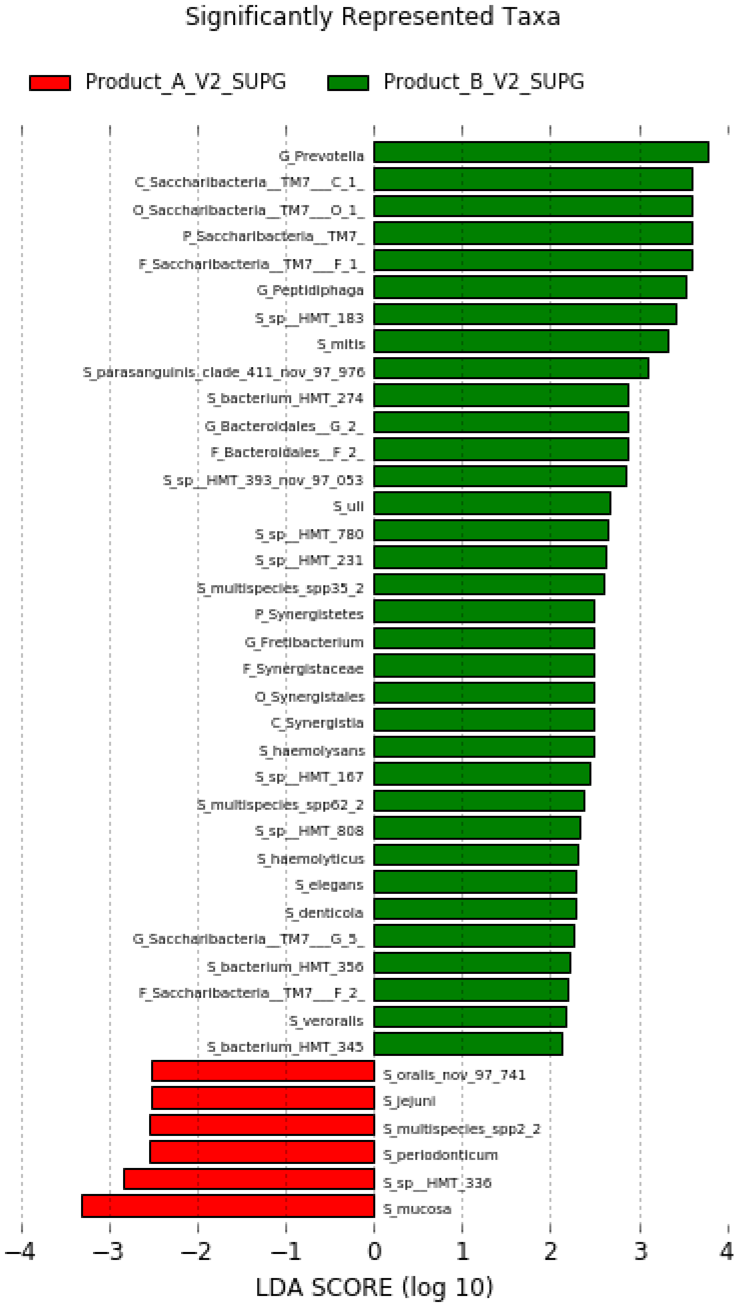
taxon	lfc_(Interc	lfc_Produc	se_(Interc	se_Produc	W_(Interce	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Interc	diff_Produc
Kingella oralis_nov_97.741% (SPN664)	0.87804	-1.76861	0.444691	0.635145	1.974497	-2.78457	0.048325	0.00536	1	1	FALSE	FALSE
Bacteroidales_[G-2] bacterium_HMT_274 (SP21)	-0.84476	1.745912	0.53439	0.763261	-1.5808	2.287437	0.113924	0.02217	1	1	FALSE	FALSE
Neisseria bacilliformis (SP447)	0.775156	-1.55872	0.482523	0.68918	1.606466	-2.26171	0.108172	0.023716	1	1	FALSE	FALSE
Selenomonas noxia_nov_97.030% (SPN548)	0.61946	-1.2411	0.413822	0.591055	1.496925	-2.09981	0.134413	0.035746	1	1	FALSE	FALSE
Neisseria mucosa (SP300)	0.908978	-1.83172	0.633832	0.905294	1.434099	-2.02334	0.151544	0.043038	1	1	FALSE	FALSE
Capnocytophaga sp._HMT_336 (SP51)	0.854898	-1.7214	0.601827	0.859581	1.420503	-2.0026	0.155461	0.045221	1	1	FALSE	FALSE
Treponema sp._HMT_231 (SP87)	-0.70998	1.470959	0.514966	0.735518	-1.3787	1.999894	0.167988	0.045512	1	1	FALSE	FALSE
Lachnoanaerobaculum orale (SP74)	0.533618	-1.06599	0.380785	0.54387	1.401364	-1.96	0.161105	0.049996	1	1	FALSE	FALSE
Actinomyces sp._HMT_175_nov_97.951% (SPN40	0.737834	-1.48259	0.531203	0.75871	1.388987	-1.95409	0.164837	0.050691	1	1	FALSE	FALSE
Selenomonas sp._HMT_892_nov_97.041% (SPN67	0.498679	-0.99471	0.358704	0.512332	1.390225	-1.94153	0.164461	0.052193	1	1	FALSE	FALSE
Peptidiphaga sp._HMT_183 (SP149)	-0.81756	1.690426	0.639447	0.913313	-1.27855	1.850873	0.201056	0.064188	1	1	FALSE	FALSE
Actinomyces sp._HMT_169 (SP239)	0.52958	-1.05775	0.408287	0.583151	1.297077	-1.81385	0.194605	0.069701	1	1	FALSE	FALSE
Aggregatibacter sp._HMT_512 (SP314)	0.522574	-1.04345	0.405412	0.579044	1.288994	-1.80203	0.1974	0.071541	1	1	FALSE	FALSE
Tannerella sp._HMT_808 (SP63)	-0.51283	1.06877	0.419111	0.59861	-1.22361	1.785418	0.221098	0.074194	1	1	FALSE	FALSE
Gemella haemolysans (SP8)	-0.57831	1.20234	0.483557	0.690658	-1.19594	1.740862	0.23172	0.081708	1	1	FALSE	FALSE

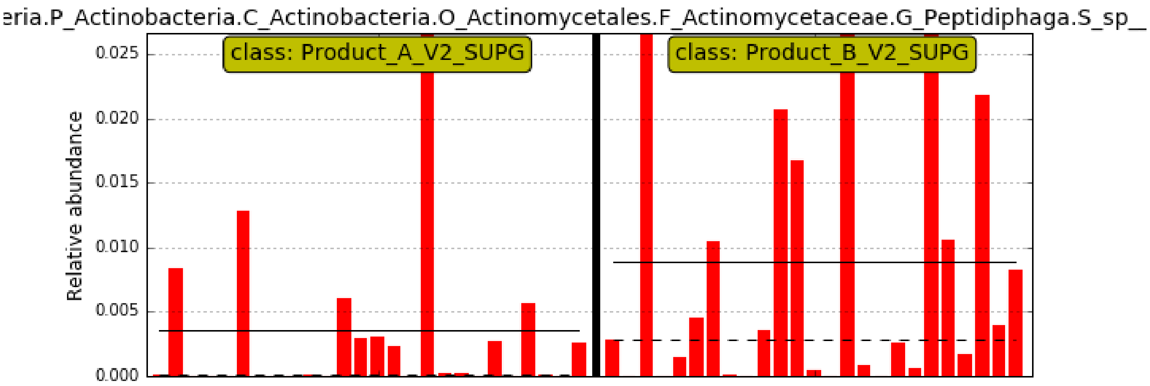
Red, more prevalent in A

Green, more prevalent in B

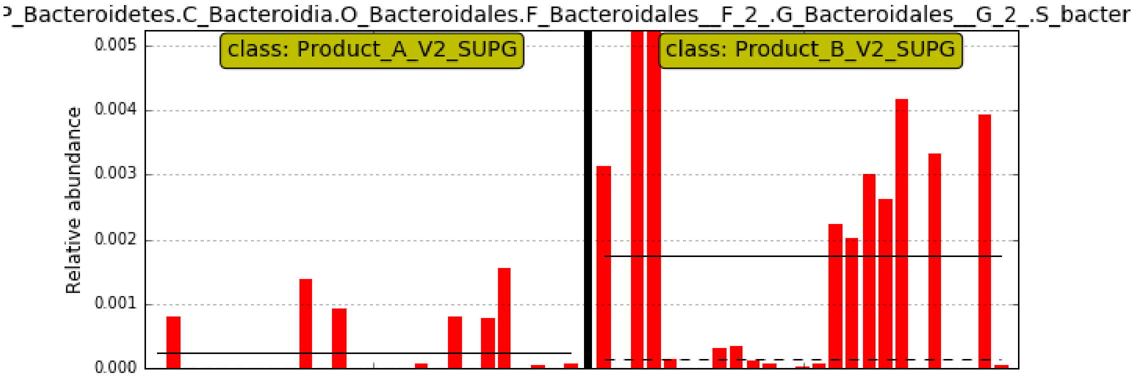
No statistical significance, lost after multiple comparisons.

5) Lefse

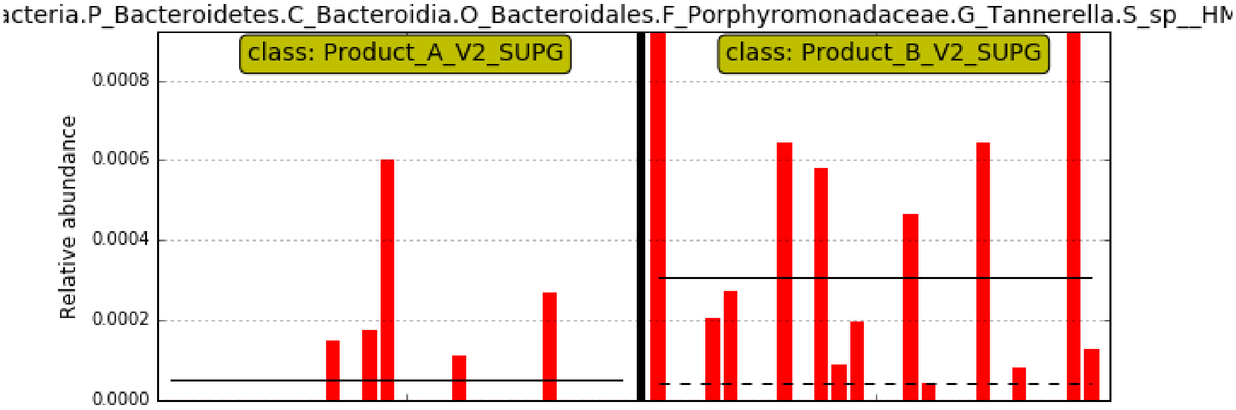

Significantly Represented Taxa
Product_A_V2_SUPG
Product_B_V2_SUPG
G_Prevotella
C_Saccharibacteria__TM7___C_1_
O_Saccharibacteria__TM7___O_1_
P_Saccharibacteria__TM7_
F_Saccharibacteria__TM7___F_1_
G_Peptidiphaga
S_sp__HMT_183
S_mitis
S_parasanguinis_clade_411_nov_97_976
S_bacterium_HMT_274
G_Bacteroidales__G_2_
F_Bacteroidales__F_2_
S_sp__HMT_393_nov_97_053
S_ulI
S_sp__HMT_780
S_sp__HMT_231
S_multispecies_spp35_2
P_Synergistetes
G_Fretibacterium
F_Synergistaceae
O_Synergistales
C_Synergistia
S_haemolysans
S_sp__HMT_167
S_multispecies_spp62_2
S_sp__HMT_808
S_haemolyticus
S_elegans
S_denticola
G_Saccharibacteria__TM7___G_5_
S_bacterium_HMT_356
F_Saccharibacteria__TM7___F_2_
S_veroralis
S_bacterium_HMT_345
S_oralis_nov_97_741
S_jejuni
S_multispecies_spp2_2
S_periodonticum
S_sp__HMT_336
S_mucosa
−4
−3
−2
−1
0
1
2
3
4
LDA SCORE (log 10)



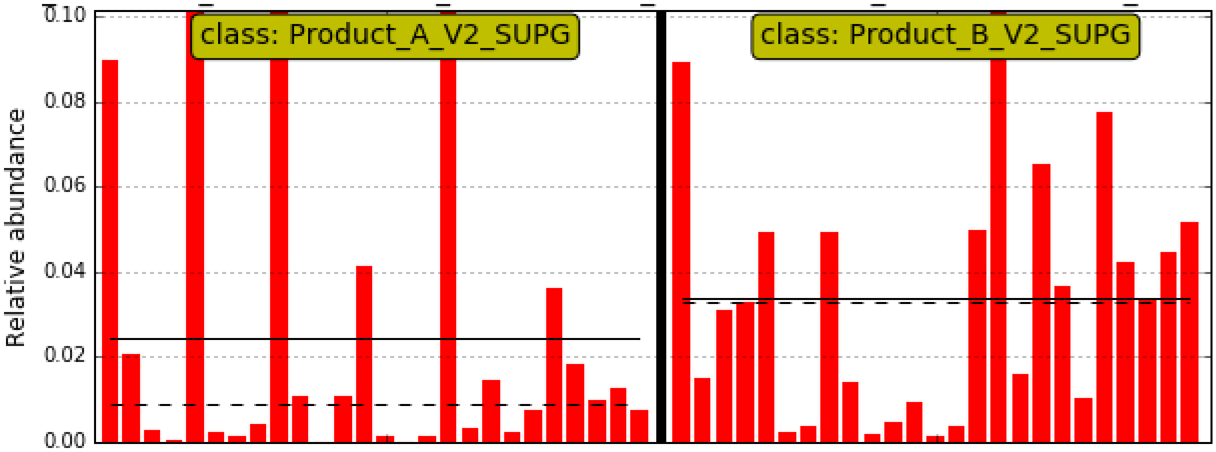
HMT183

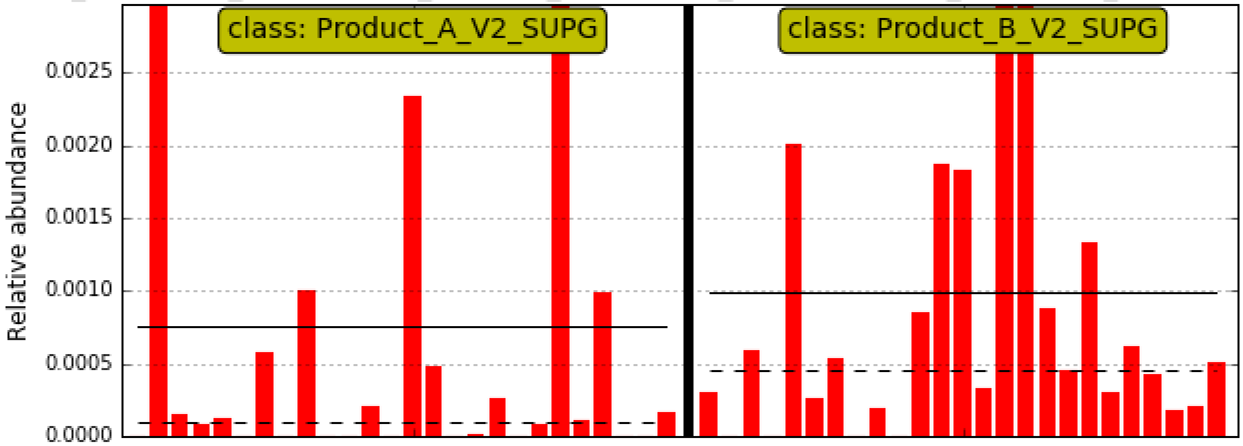


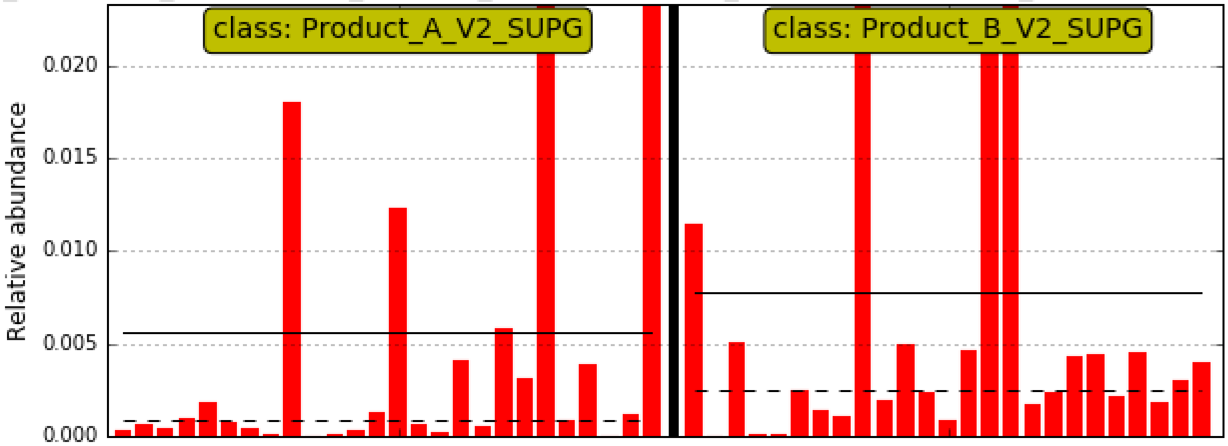
HMT274

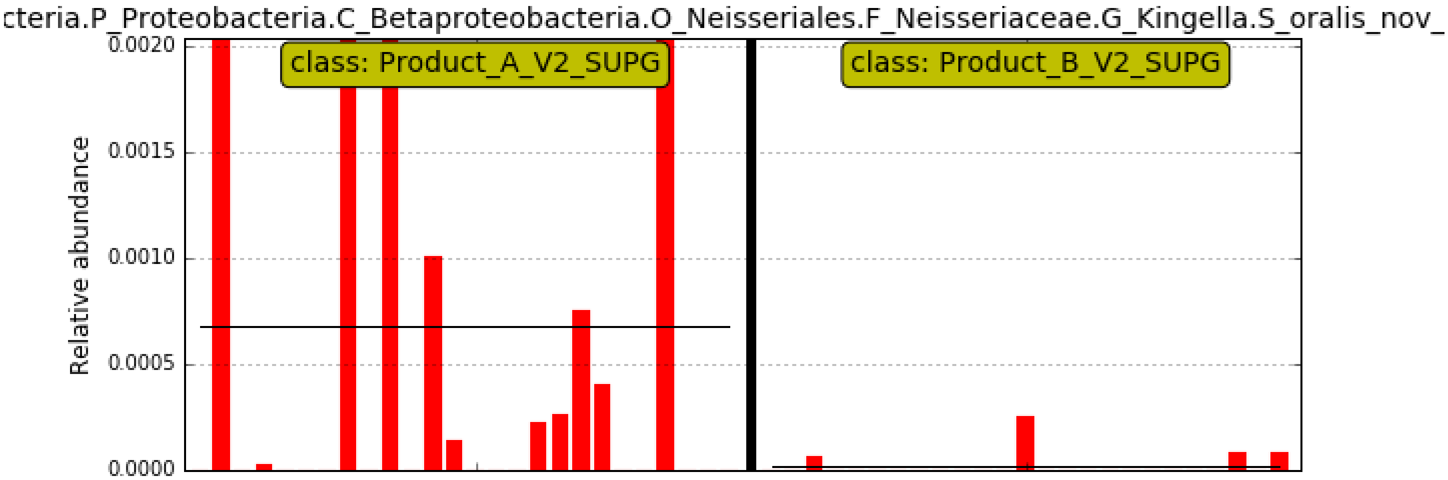


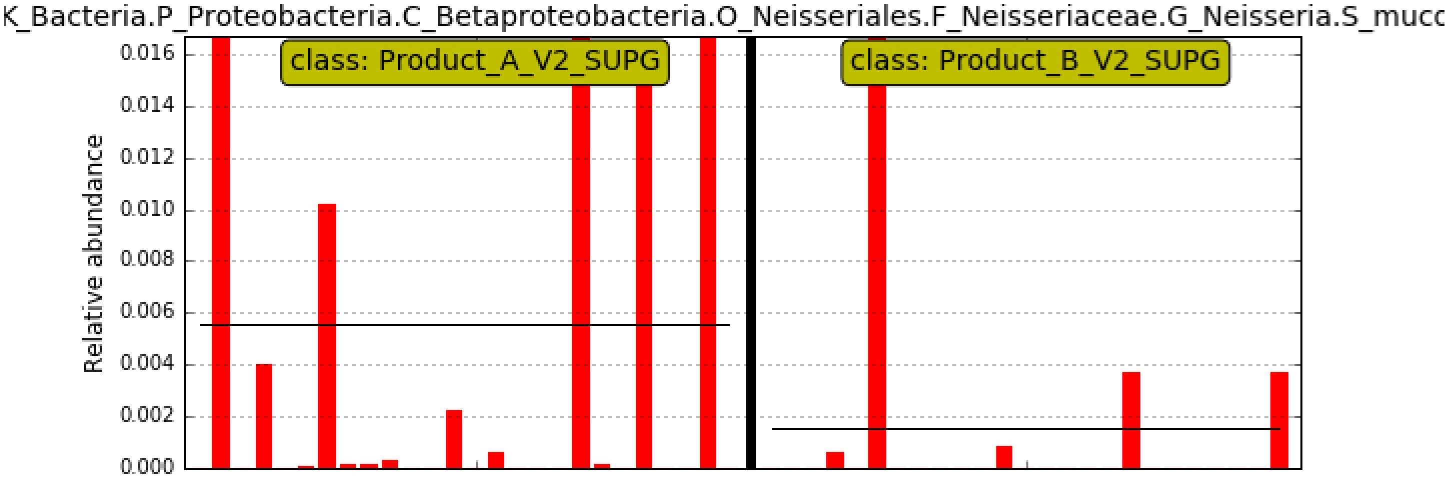
HMT808

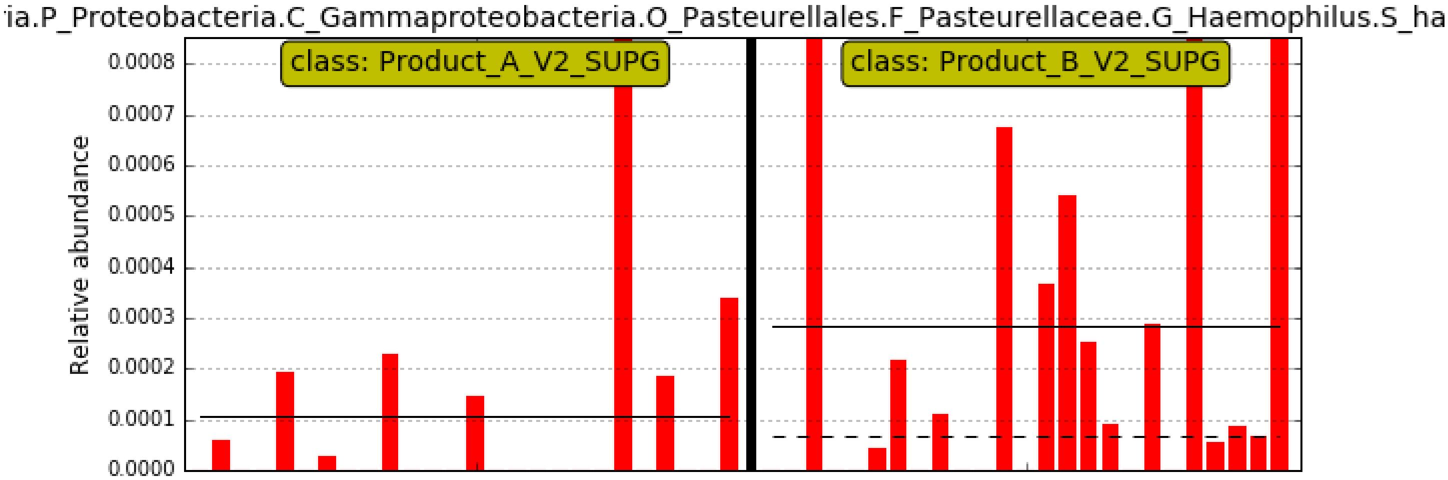

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella

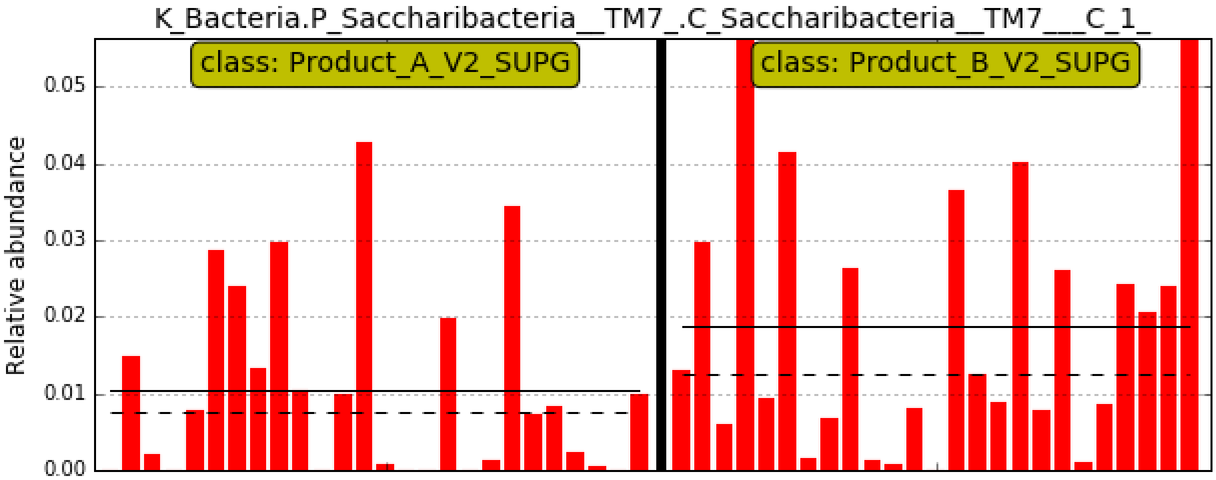

K_Bacteria.P_Firmicutes.C_Bacilli.O_Bacillales.F_Gemellaceae.G_Gemella.S_haemolysans

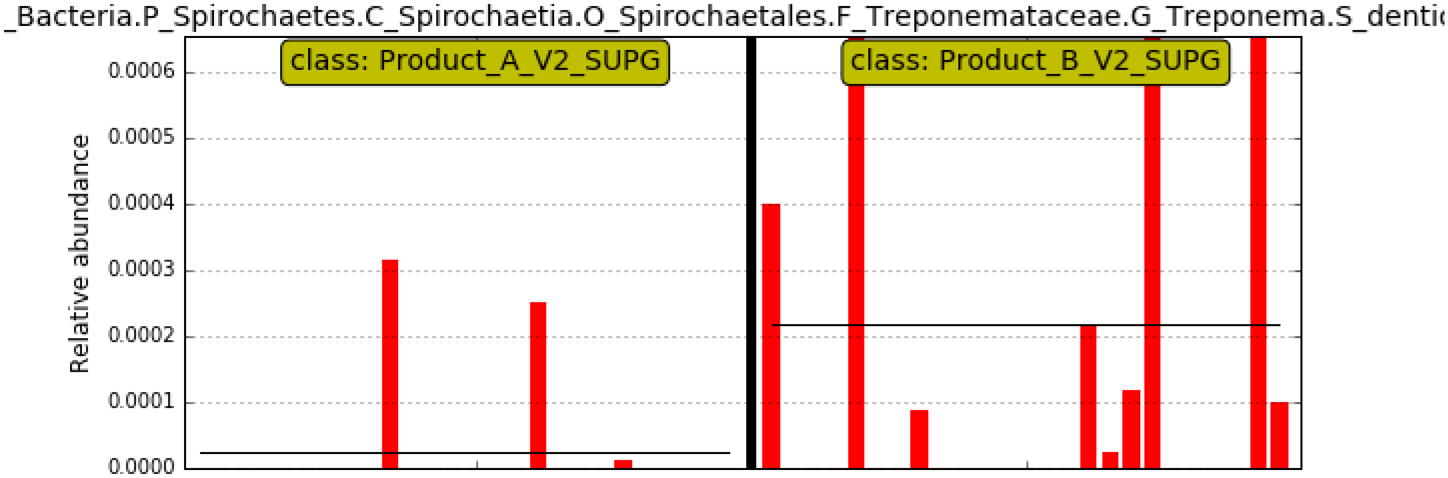

K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_mitis

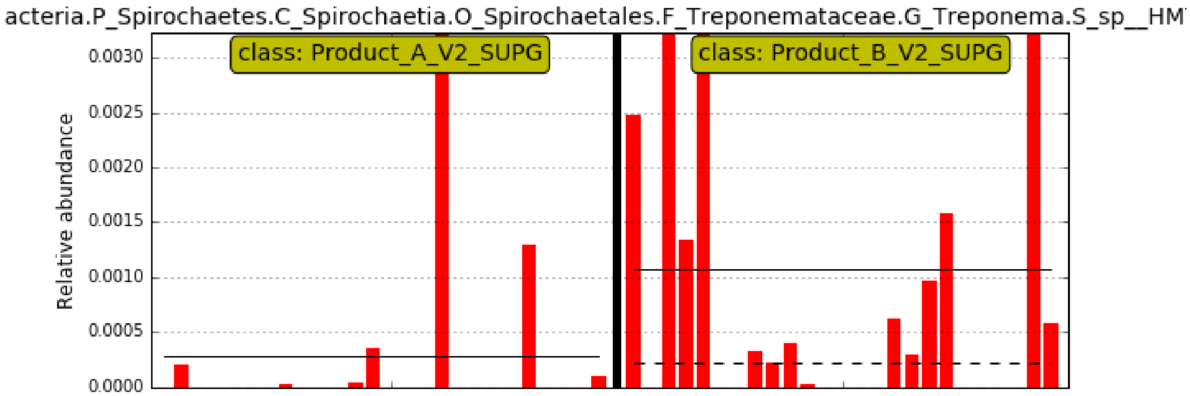

cteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Kingella.S_oralis_nov_
class: Product_A_V2_SUPG
class: Product_B_V2_SUPG
Relative abundance
0.0020
0.0015
0.0010
0.0005
0.0000


K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Neisseria.S_mucc
class: Product_A_V2_SUPG
class: Product_B_V2_SUPG
Relative abundance
0.016
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000

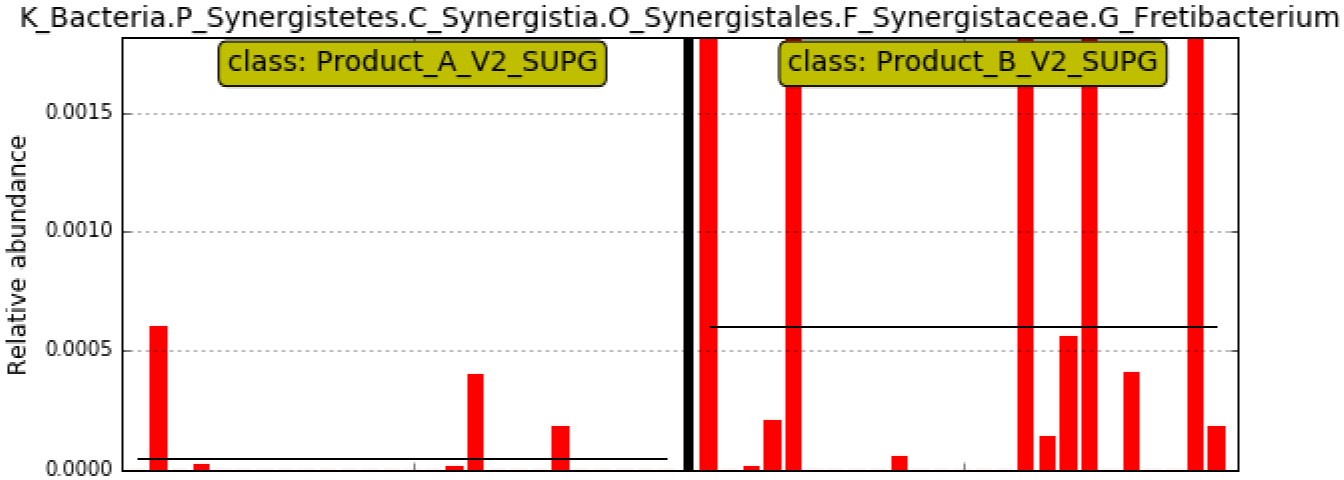

ia.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophilus.S_ha
class: Product_A_V2_SUPG
class: Product_B_V2_SUPG
Relative abundance
0.0008
0.0007
0.0006
0.0005
0.0004
0.0003
0.0002
0.0001
0.0000


K_Bacteria.P_Saccharibacteria__TM7_.C_Saccharibacteria__TM7___C_1_
class: Product_A_V2_SUPG
class: Product_B_V2_SUPG
Relative abundance
0.05
0.04
0.03
0.02
0.01
0.00

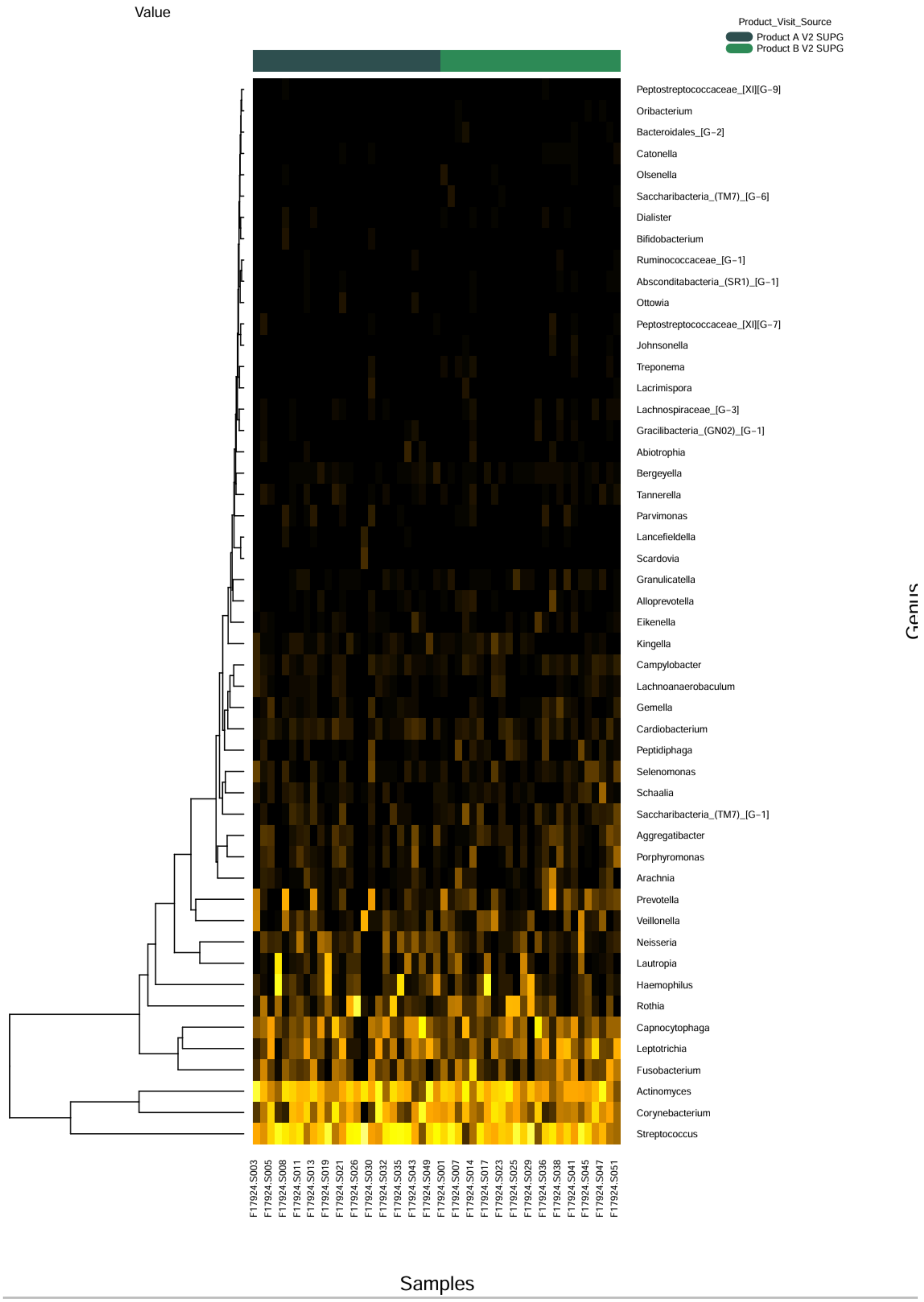

_Bacteria.P_Spirochaetes.C_Spirochaetia.O_Spirochaetales.F_Treponemataceae.G_Treponema.S_dentic
class: Product_A_V2_SUPG
class: Product_B_V2_SUPG
Relative abundance
0.0006
0.0005
0.0004
0.0003
0.0002
0.0001
0.0000

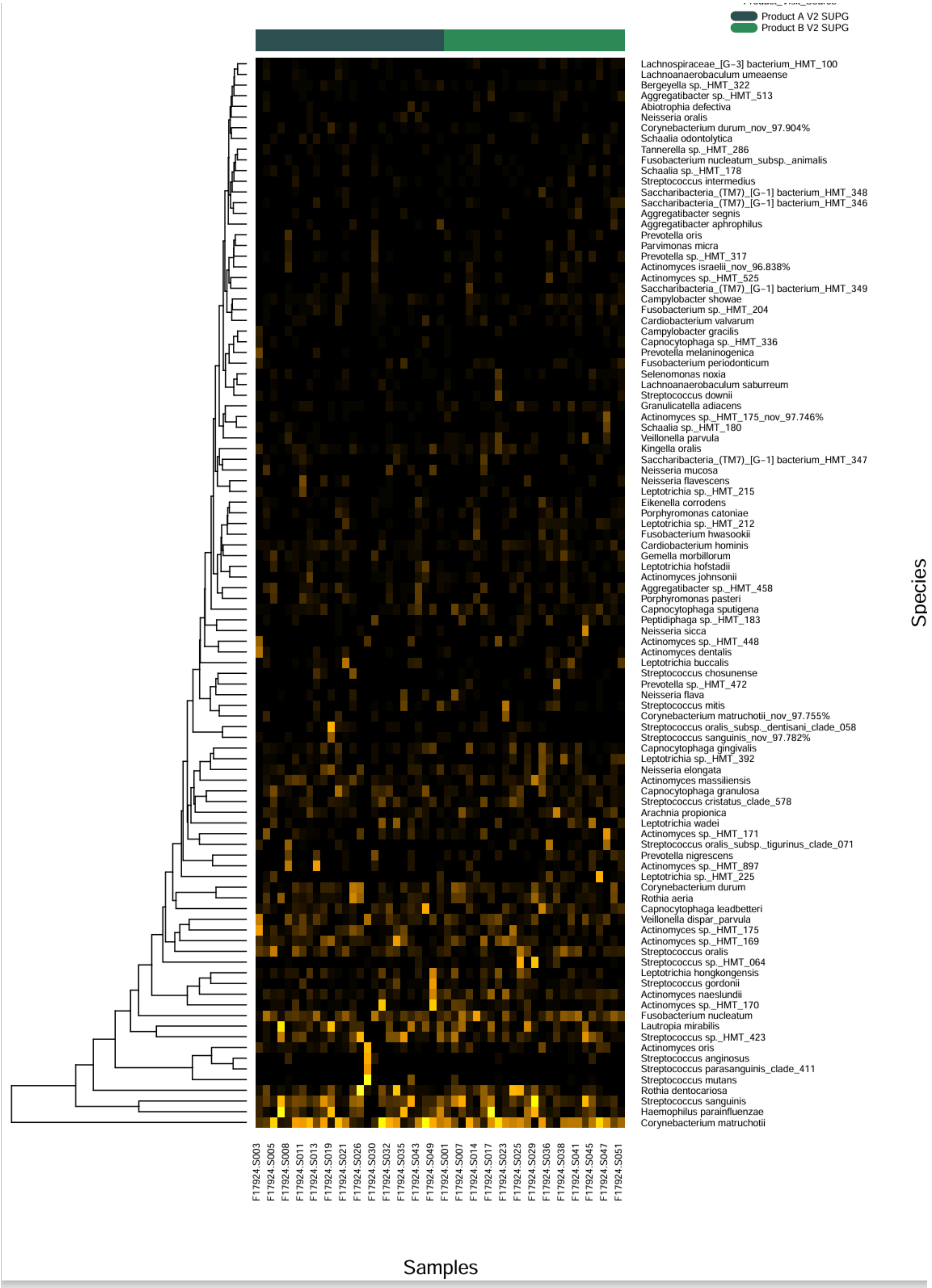

acteria.P_Spirochaetes.C_Spirochaetia.O_Spirochaetales.F_Treponemataceae.G_Treponema.S_sp__HM
Relative abundance
0.0030
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000
class: Product_A_V2_SUPG
class: Product_B_V2_SUPG

HMT231


K_Bacteria.P_Synergistetes.C_Synergistia.O_Synergistales.F_Synergistaceae.G_Fretibacterium
Relative abundance
0.0015
0.0010
0.0005
0.0000
class: Product_A_V2_SUPG
class: Product_B_V2_SUPG

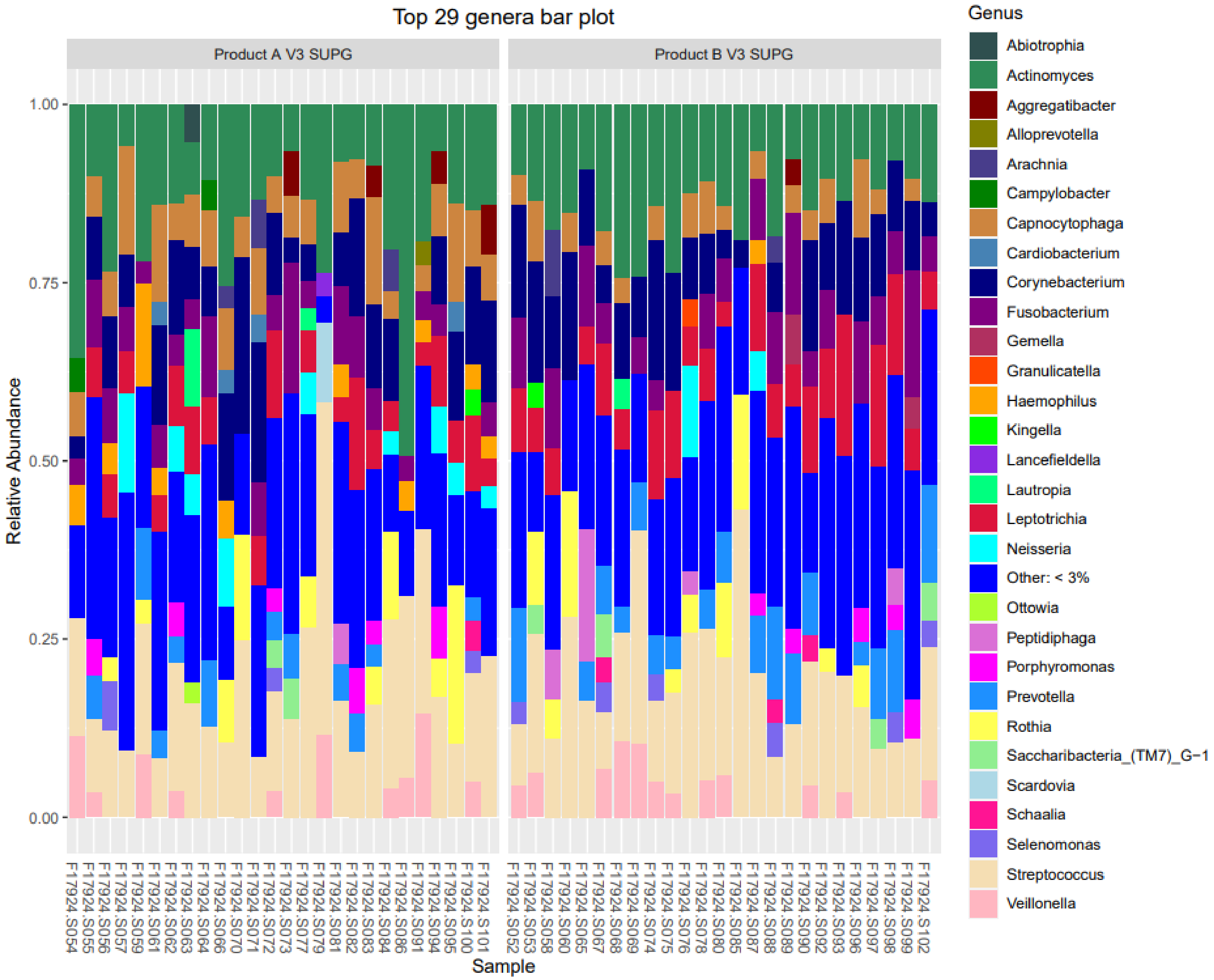
6) Heat map.


Value
Product_Visit_Source
Product A V2 SUPG
Product B V2 SUPG
Peptostreptococcaceae_[XI][G-9]
Oribacterium
Bacteroidales_[G-2]
Catonella
Olsenella
Saccharibacteria_(TM7)_[G-6]
Dialister
Bifidobacterium
Ruminococcaceae_[G-1]
Absconditabacteria_(SR1)_[G-1]
Ottowia
Peptostreptococcaceae_[XI][G-7]
Johnsonella
Treponema
Lacrimispora
Lachnospiraceae_[G-3]
Gracilibacteria_(GN02)_[G-1]
Abiotrophia
Bergeyella
Tannerella
Parvimonas
Lancefieldella
Scardovia
Granulicatella
Alloprevotella
Eikenella
Kingella
Campylobacter
Lachnoanaerobaculum
Gemella
Cardiobacterium
Peptidiphaga
Selenomonas
Schaalia
Saccharibacteria_(TM7)_[G-1]
Aggregatibacter
Porphyromonas
Arachnia
Prevotella
Veillonella
Neisseria
Lautropia
Haemophilus
Rothia
Capnocytophaga
Leptotrichia
Fusobacterium
Actinomyces
Corynebacterium
Streptococcus
Genus
F17924.S003
F17924.S005
F17924.S008
F17924.S011
F17924.S013
F17924.S019
F17924.S021
F17924.S026
F17924.S030
F17924.S032
F17924.S035
F17924.S043
F17924.S049
F17924.S001
F17924.S007
F17924.S014
F17924.S017
F17924.S023
F17924.S025
F17924.S029
F17924.S036
F17924.S038
F17924.S041
F17924.S045
F17924.S047
F17924.S051
Samples


Product A V2 SUPG
Product B V2 SUPG
Lachnospiraceae_[G−3] bacterium_HMT_100
Lachnoanaerobaculum umeaense
Bergeyella sp._HMT_322
Aggregatibacter sp._HMT_513
Abiotrophia defectiva
Neisseria oralis
Corynebacterium durum_nov_97.904%
Schaalia odontolytica
Tannerella sp._HMT_286
Fusobacterium nucleatum_subsp._animalis
Schaalia sp._HMT_178
Streptococcus intermedius
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_348
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_346
Aggregatibacter segnis
Aggregatibacter aphrophilus
Prevotella oris
Parvimonas micra
Prevotella sp._HMT_317
Actinomyces israelii_nov_96.838%
Actinomyces sp._HMT_525
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_349
Campylobacter showae
Fusobacterium sp._HMT_204
Cardiobacterium valvarum
Campylobacter gracilis
Capnocytophaga sp._HMT_336
Prevotella melaninogenica
Fusobacterium periodonticum
Selenomonas noxia
Lachnoanaerobaculum saburreum
Streptococcus downii
Granulicatella adiacens
Actinomyces sp._HMT_175_nov_97.746%
Schaalia sp._HMT_180
Veillonella parvula
Kingella oralis
Saccharibacteria_(TM7)_[G−1] bacterium_HMT_347
Neisseria mucosa
Neisseria flavescens
Leptotrichia sp._HMT_215
Eikenella corrodens
Porphyromonas catoniae
Leptotrichia sp._HMT_212
Fusobacterium hwasookii
Cardiobacterium hominis
Gemella morbillorum
Leptotrichia hofstadii
Actinomyces johnsonii
Aggregatibacter sp._HMT_458
Porphyromonas pasteri
Capnocytophaga sputigena
Peptidiphaga sp._HMT_183
Neisseria sicca
Actinomyces sp._HMT_448
Actinomyces dentalis
Leptotrichia buccalis
Streptococcus chosunense
Prevotella sp._HMT_472
Neisseria flava
Streptococcus mitis
Corynebacterium matruchotii_nov_97.755%
Streptococcus oralis_subsp._dentisani_clade_058
Streptococcus sanguinis_nov_97.782%
Capnocytophaga gingivalis
Leptotrichia sp._HMT_392
Neisseria elongata
Actinomyces massiliensis
Capnocytophaga granulosa
Streptococcus cristatus_clade_578
Arachnia propionica
Leptotrichia wadei
Actinomyces sp._HMT_171
Streptococcus oralis_subsp._tigurinus_clade_071
Prevotella nigrescens
Actinomyces sp._HMT_897
Leptotrichia sp._HMT_225
Corynebacterium durum
Rothia aeria
Capnocytophaga leadbetteri
Veillonella dispar_parvula
Actinomyces sp._HMT_175
Actinomyces sp._HMT_169
Streptococcus oralis
Streptococcus sp._HMT_064
Leptotrichia hongkongensis
Streptococcus gordonii
Actinomyces naeslundii
Actinomyces sp._HMT_170
Fusobacterium nucleatum
Lautropia mirabilis
Streptococcus sp._HMT_423
Actinomyces oris
Streptococcus anginosus
Streptococcus parasanguinis_clade_411
Streptococcus mutans
Rothia dentocariosa
Streptococcus sanguinis
Haemophilus parainfluenzae
Corynebacterium matruchotii
Species
F17924.S003
F17924.S005
F17924.S008
F17924.S011
F17924.S013
F17924.S019
F17924.S021
F17924.S026
F17924.S030
F17924.S032
F17924.S035
F17924.S043
F17924.S049
F17924.S001
F17924.S007
F17924.S014
F17924.S017
F17924.S023
F17924.S025
F17924.S029
F17924.S036
F17924.S038
F17924.S041
F17924.S045
F17924.S047
F17924.S051
Samples

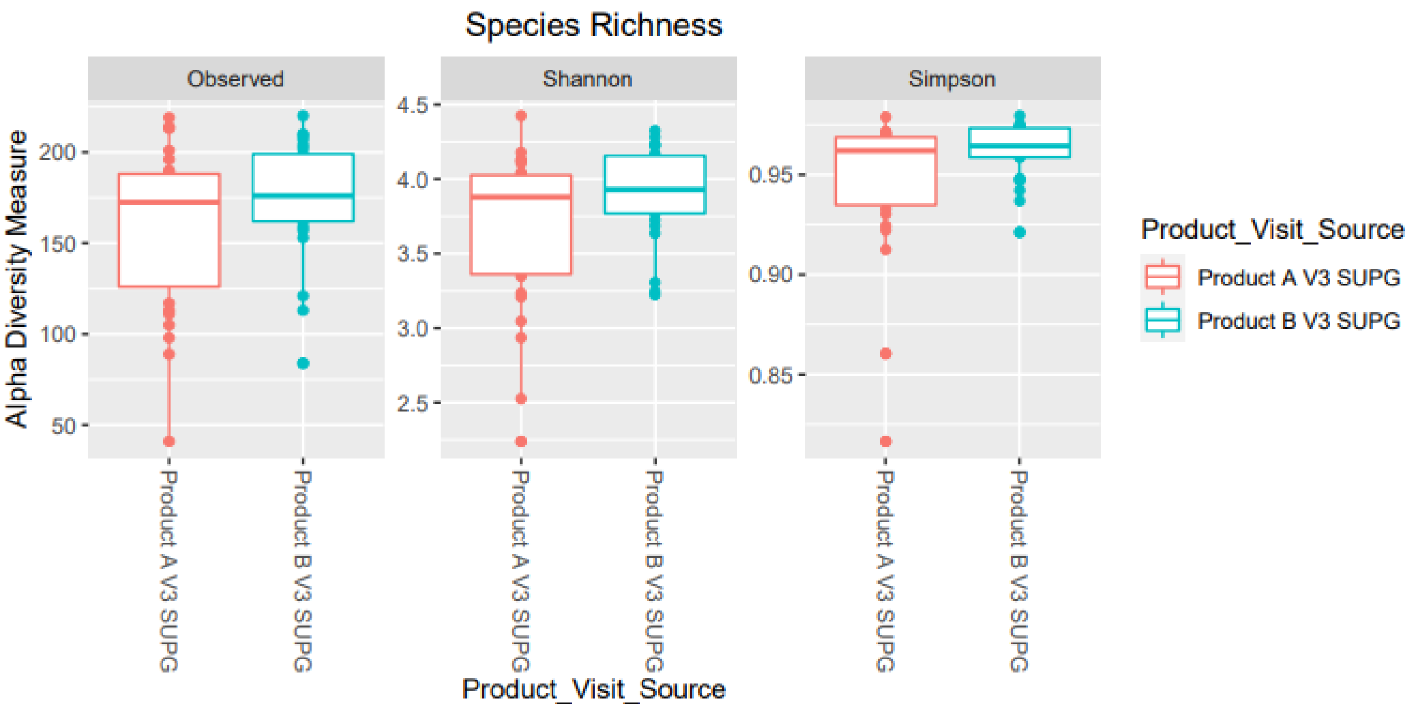
Comparison 16. Product A V3 SUPG vs Product B V3 SUPG

1) Taxonomy bar graphs



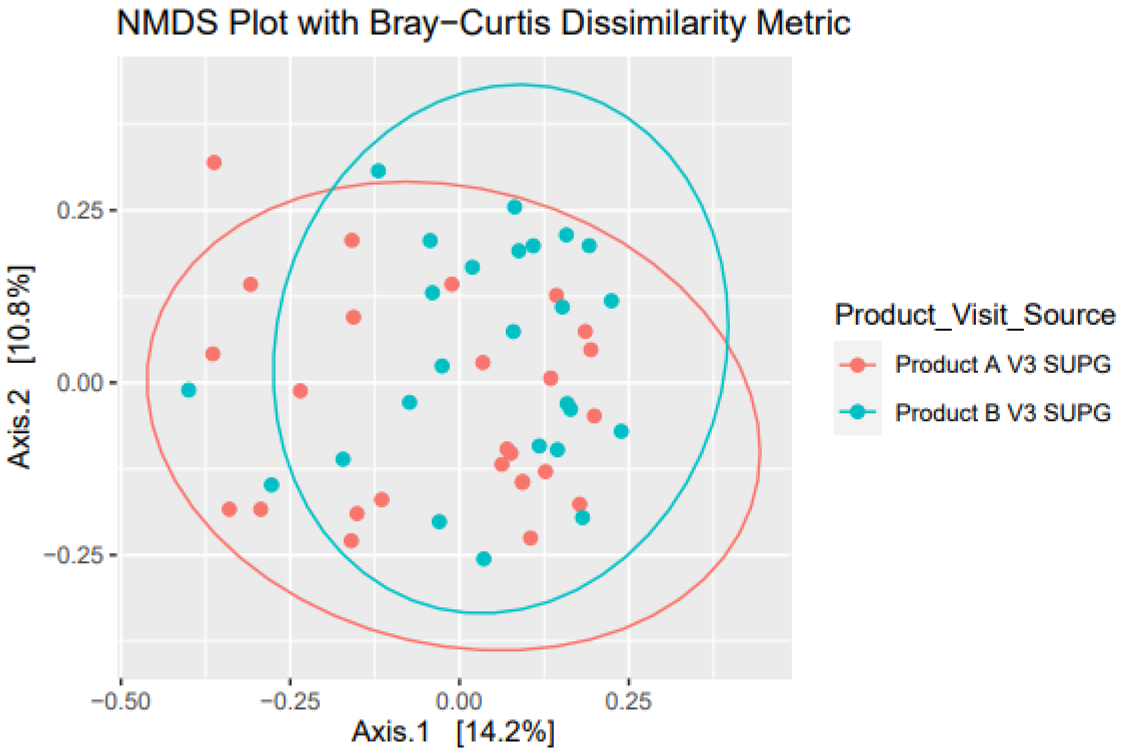
23)

2) Alpha



No significant differences

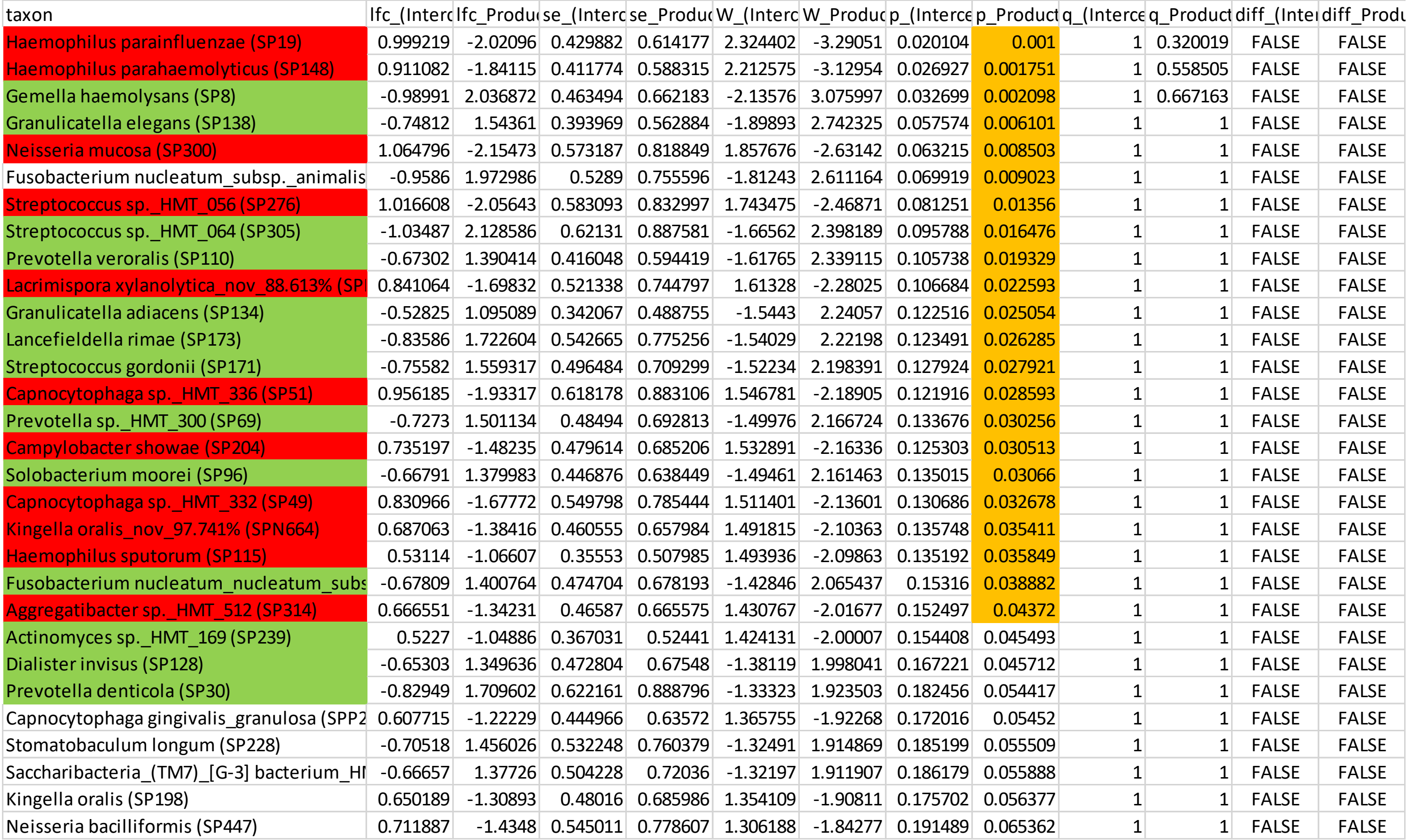
3) Beta diversity



Group 1	Group 2	Sample si	Permutati	pseudo-F	p-value
Product A V3 SUPG	Product B V3 SUPG	51	999	1.669907	0.023

significant difference

4) Differential abundance

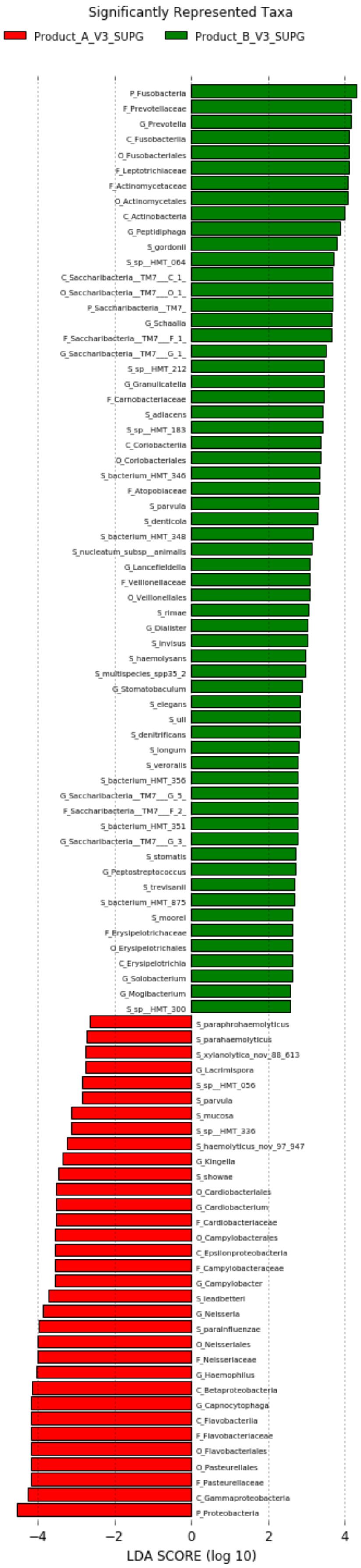


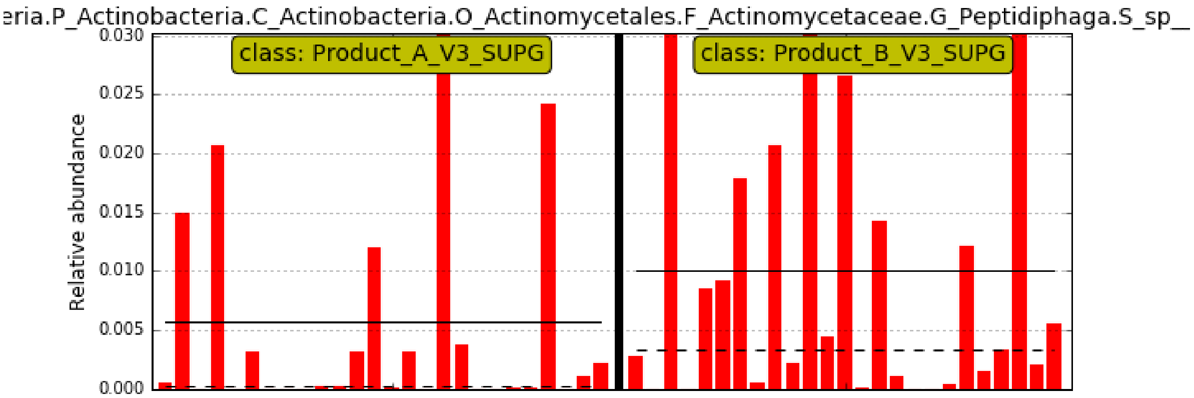
taxon	lfc_(Interc	lfc_Produ	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inte	diff_Produ
🟥 Haemophilus parainfluenzae (SP19)	0.999219	-2.02096	0.429882	0.614177	2.324402	-3.29051	0.020104	0.001	1	0.320019	FALSE	FALSE
🟥 Haemophilus parahaemolyticus (SP148)	0.911082	-1.84115	0.411774	0.588315	2.212575	-3.12954	0.026927	0.001751	1	0.558505	FALSE	FALSE
🟩 Gemella haemolysans (SP8)	-0.98991	2.036872	0.463494	0.662183	-2.13576	3.075997	0.032699	0.002098	1	0.667163	FALSE	FALSE
🟩 Granulicatella elegans (SP138)	-0.74812	1.54361	0.393969	0.562884	-1.89893	2.742325	0.057574	0.006101	1	1	FALSE	FALSE
🟥 Neisseria mucosa (SP300)	1.064796	-2.15473	0.573187	0.818849	1.857676	-2.63142	0.063215	0.008503	1	1	FALSE	FALSE
Fusobacterium nucleatum_subsp._animalis	-0.9586	1.972986	0.5289	0.755596	-1.81243	2.611164	0.069919	0.009023	1	1	FALSE	FALSE
🟥 Streptococcus sp._HMT_056 (SP276)	1.016608	-2.05643	0.583093	0.832997	1.743475	-2.46871	0.081251	0.01356	1	1	FALSE	FALSE
🟩 Streptococcus sp._HMT_064 (SP305)	-1.03487	2.128586	0.62131	0.887581	-1.66562	2.398189	0.095788	0.016476	1	1	FALSE	FALSE
🟩 Prevotella veroralis (SP110)	-0.67302	1.390414	0.416048	0.594419	-1.61765	2.339115	0.105738	0.019329	1	1	FALSE	FALSE
🟥 Lacrimispora xylanolytica_nov_88.613% (SP	0.841064	-1.69832	0.521338	0.744797	1.61328	-2.28025	0.106684	0.022593	1	1	FALSE	FALSE
🟩 Granulicatella adiacens (SP134)	-0.52825	1.095089	0.342067	0.488755	-1.5443	2.24057	0.122516	0.025054	1	1	FALSE	FALSE
🟩 Lancefieldella rimae (SP173)	-0.83586	1.722604	0.542665	0.775256	-1.54029	2.22198	0.123491	0.026285	1	1	FALSE	FALSE
🟩 Streptococcus gordonii (SP171)	-0.75582	1.559317	0.496484	0.709299	-1.52234	2.198391	0.127924	0.027921	1	1	FALSE	FALSE
🟥 Capnocytophaga sp._HMT_336 (SP51)	0.956185	-1.93317	0.618178	0.883106	1.546781	-2.18905	0.121916	0.028593	1	1	FALSE	FALSE
🟩 Prevotella sp._HMT_300 (SP69)	-0.7273	1.501134	0.48494	0.692813	-1.49976	2.166724	0.133676	0.030256	1	1	FALSE	FALSE
🟥 Campylobacter showae (SP204)	0.735197	-1.48235	0.479614	0.685206	1.532891	-2.16336	0.125303	0.030513	1	1	FALSE	FALSE
🟩 Solobacterium moorei (SP96)	-0.66791	1.379983	0.446876	0.638449	-1.49461	2.161463	0.135015	0.03066	1	1	FALSE	FALSE
🟥 Capnocytophaga sp._HMT_332 (SP49)	0.830966	-1.67772	0.549798	0.785444	1.511401	-2.13601	0.130686	0.032678	1	1	FALSE	FALSE
🟥 Kingella oralis_nov_97.741% (SPN664)	0.687063	-1.38416	0.460555	0.657984	1.491815	-2.10363	0.135748	0.035411	1	1	FALSE	FALSE
🟥 Haemophilus sputorum (SP115)	0.53114	-1.06607	0.35553	0.507985	1.493936	-2.09863	0.135192	0.035849	1	1	FALSE	FALSE
🟩 Fusobacterium nucleatum_nucleatum_subs	-0.67809	1.400764	0.474704	0.678193	-1.42846	2.065437	0.15316	0.038882	1	1	FALSE	FALSE
🟥 Aggregatibacter sp._HMT_512 (SP314)	0.666551	-1.34231	0.46587	0.665575	1.430767	-2.01677	0.152497	0.04372	1	1	FALSE	FALSE
🟩 Actinomyces sp._HMT_169 (SP239)	0.5227	-1.04886	0.367031	0.52441	1.424131	-2.00007	0.154408	0.045493	1	1	FALSE	FALSE
🟩 Dialister invisus (SP128)	-0.65303	1.349636	0.472804	0.67548	-1.38119	1.998041	0.167221	0.045712	1	1	FALSE	FALSE
🟩 Prevotella denticola (SP30)	-0.82949	1.709602	0.622161	0.888796	-1.33323	1.923503	0.182456	0.054417	1	1	FALSE	FALSE
Capnocytophaga gingivalis_granulosa (SPP2	0.607715	-1.22229	0.444966	0.63572	1.365755	-1.92268	0.172016	0.05452	1	1	FALSE	FALSE
Stomatobaculum longum (SP228)	-0.70518	1.456026	0.532248	0.760379	-1.32491	1.914869	0.185199	0.055509	1	1	FALSE	FALSE
Saccharibacteria_(TM7)_[G-3] bacterium_HI	-0.66657	1.37726	0.504228	0.72036	-1.32197	1.911907	0.186179	0.055888	1	1	FALSE	FALSE
Kingella oralis (SP198)	0.650189	-1.30893	0.48016	0.685986	1.354109	-1.90811	0.175702	0.056377	1	1	FALSE	FALSE
Neisseria bacilliformis (SP447)	0.711887	-1.4348	0.545011	0.778607	1.306188	-1.84277	0.191489	0.065362	1	1	FALSE	FALSE

Red, more prevalent in A

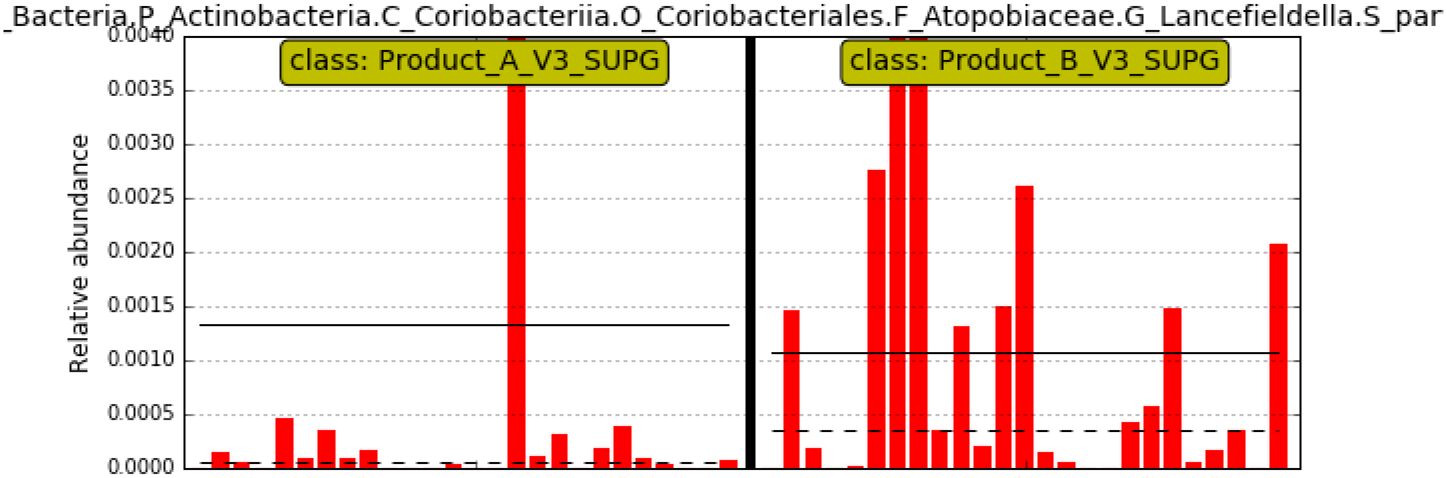
Green, more prevalent in B

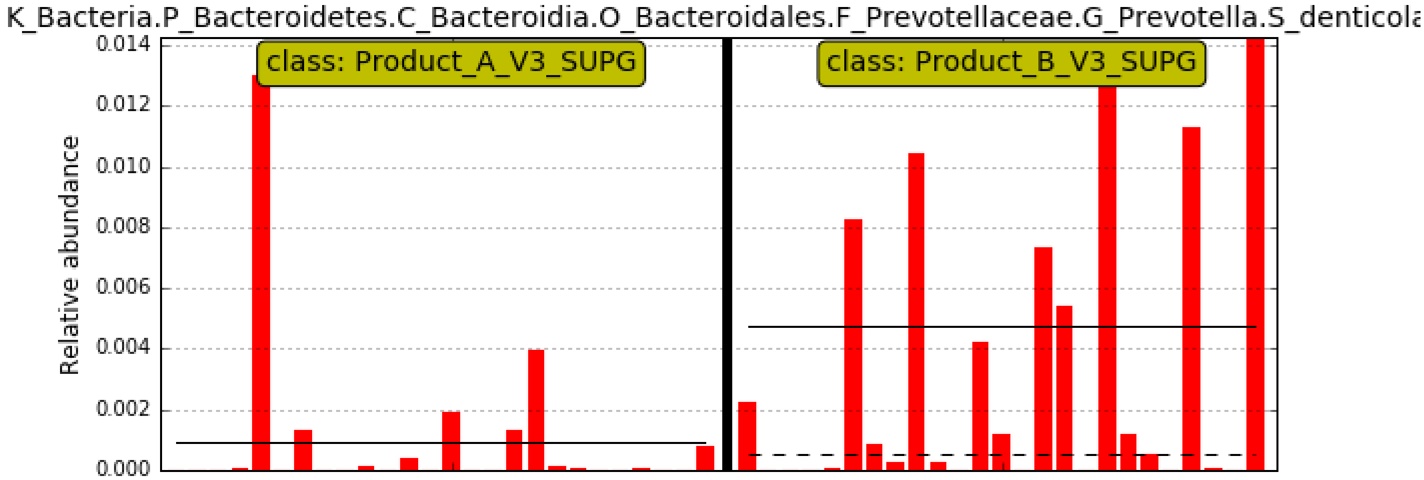
5) Lefse

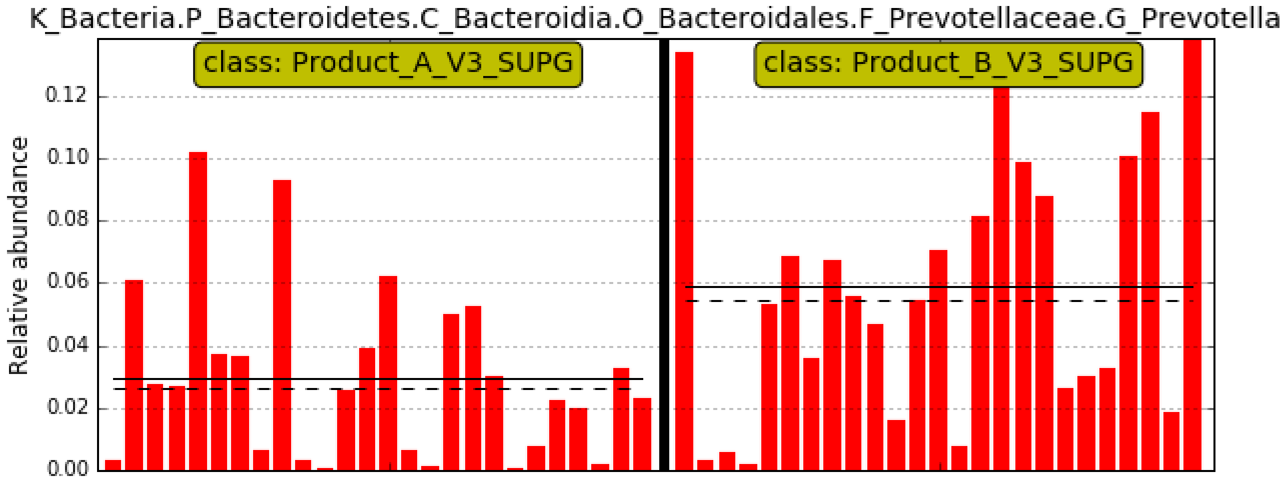

Significantly Represented Taxa
Product_A_V3_SUPG
Product_B_V3_SUPG
P_Fusobacteria
F_Prevotellaceae
G_Prevotella
C_Fusobacteriia
O_Fusobacteriales
F_Leptotrichiaceae
F_Actinomycetaceae
O_Actinomycetales
C_Actinobacteria
G_Peptidiphaga
S_gordonii
S_sp__HMT_064
C_Saccharibacteria__TM7___C_1_
O_Saccharibacteria__TM7___O_1_
P_Saccharibacteria__TM7_
G_Schaalia
F_Saccharibacteria__TM7___F_1_
G_Saccharibacteria__TM7___G_1_
S_sp__HMT_212
G_Granulicatella
F_Carnobacteriaceae
S_adiacens
S_sp__HMT_183
C_Coriobacteriia
O_Coriobacteriales
S_bacterium_HMT_346
F_Atopobiaceae
S_parvula
S_denticola
S_bacterium_HMT_348
S_nucleatum_subsp__animalis
G_Lancefieldella
F_Veillonellaceae
O_Veillonellales
S_rimae
G_Dialister
S_invisus
S_haemolysans
S_multispecies_spp35_2
G_Stomatobaculum
S_elegans
S_uli
S_denitrificans
S_longum
S_veroralis
S_bacterium_HMT_356
G_Saccharibacteria__TM7___G_5_
F_Saccharibacteria__TM7___F_2_
S_bacterium_HMT_351
G_Saccharibacteria__TM7___G_3_
S_stomatis
G_Peptostreptococcus
S_trevisanii
S_bacterium_HMT_875
S_moorei
F_Erysipelotrichaceae
O_Erysipelotrichales
C_Erysipelotrichia
G_Solobacterium
G_Mogibacterium
S_sp__HMT_300
S_paraphrohaemolyticus
S_parahaemolyticus
S_xylanolytica_nov_88_613
G_Lacrimispora
S_sp__HMT_056
S_parvula
S_mucosa
S_sp__HMT_336
S_haemolyticus_nov_97_947
G_Kingella
S_showae
O_Cardiobacteriales
G_Cardiobacterium
F_Cardiobacteriaceae
O_Campylobacterales
C_Epsilonproteobacteria
F_Campylobacteraceae
G_Campylobacter
S_leadbetteri
G_Neisseria
S_parainfluenzae
O_Neisseriales
F_Neisseriaceae
G_Haemophilus
C_Betaproteobacteria
G_Capnocytophaga
C_Flavobacteriia
F_Flavobacteriaceae
O_Flavobacteriales
O_Pasteurellales
F_Pasteurellaceae
C_Gammaproteobacteria
P_Proteobacteria
−4
−2
0
2
4
LDA SCORE (log 10)

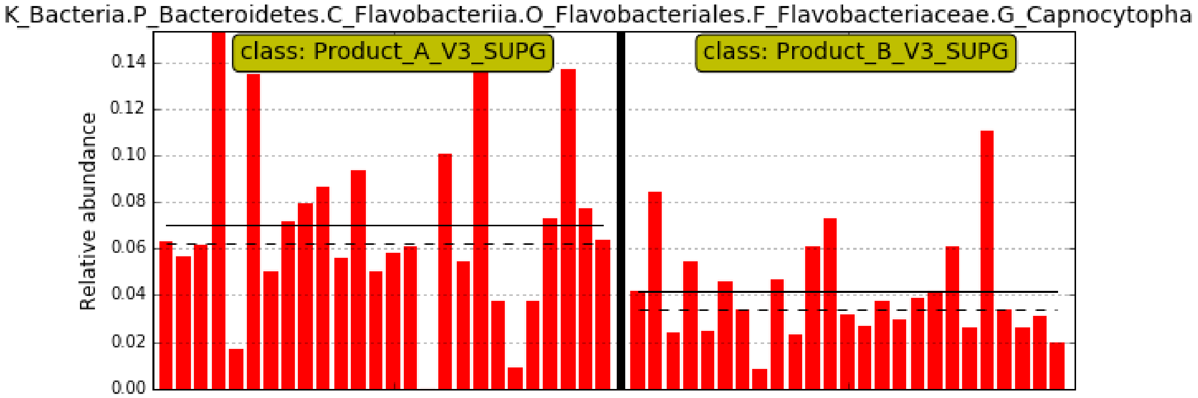

eria.P_Actinobacteria.C_Actinobacteria.O_Actinomycetales.F_Actinomycetaceae.G_Peptidiphaga.S_sp_
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.030
0.025
0.020
0.015
0.010
0.005
0.000

HMT183

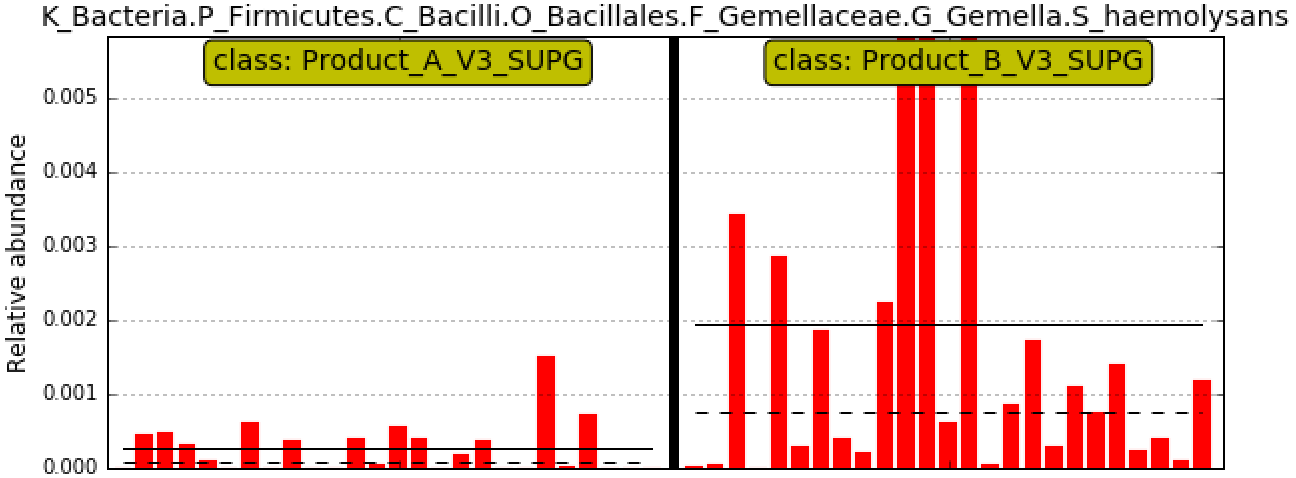

_Bacteria.P_Actinobacteria.C_Coriobacteriia.O_Coriobacteriales.F_Atopobiaceae.G_Lancefieldella.S_par
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.0040
0.0035
0.0030
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000


K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_denticola
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000

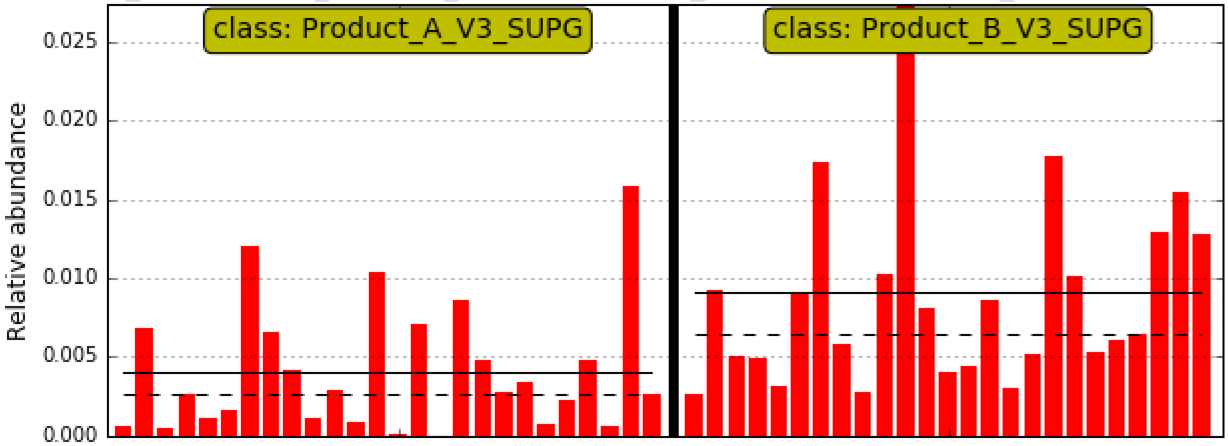

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.12
0.10
0.08
0.06
0.04
0.02
0.00


K_Bacteria.P_Bacteroidetes.C_Flavobacteriia.O_Flavobacteriales.F_Flavobacteriaceae.G_Capnocytopha
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00

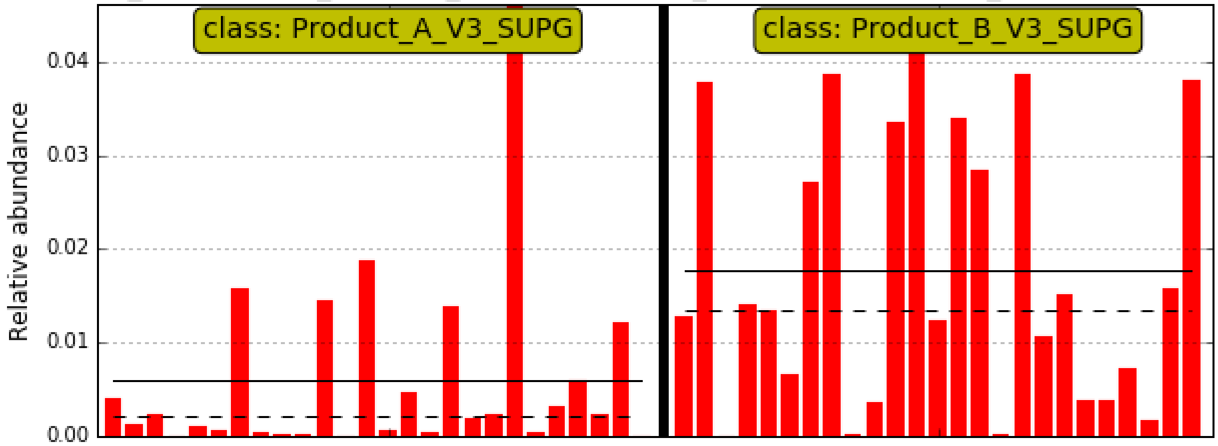
High levels


K_Bacteria.P_Firmicutes.C_Bacilli.O_Bacillales.F_Gemellaceae.G_Gemella.S_haemolysans
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.005
0.004
0.003
0.002
0.001
0.000

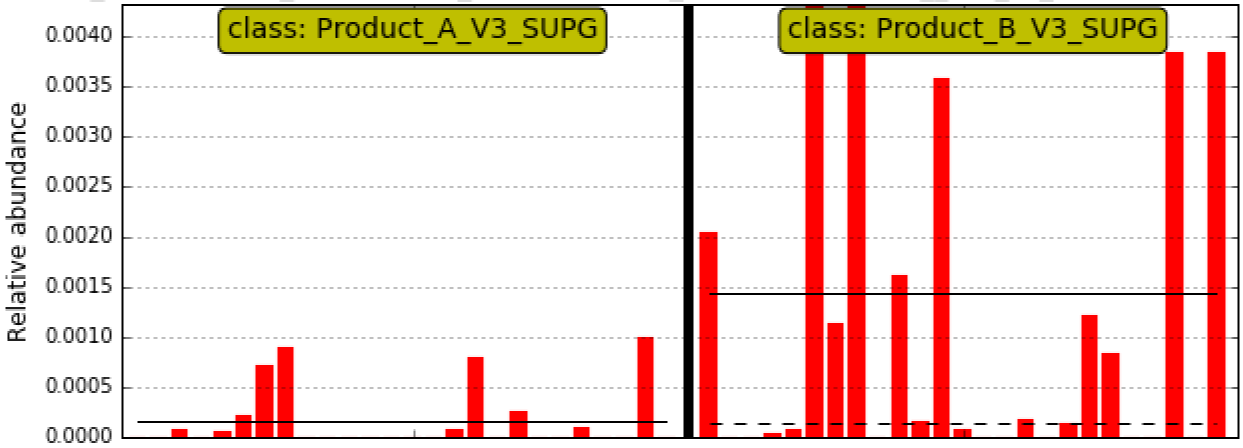
K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Carnobacteriaceae.G_Granulicatella.S_adiacens

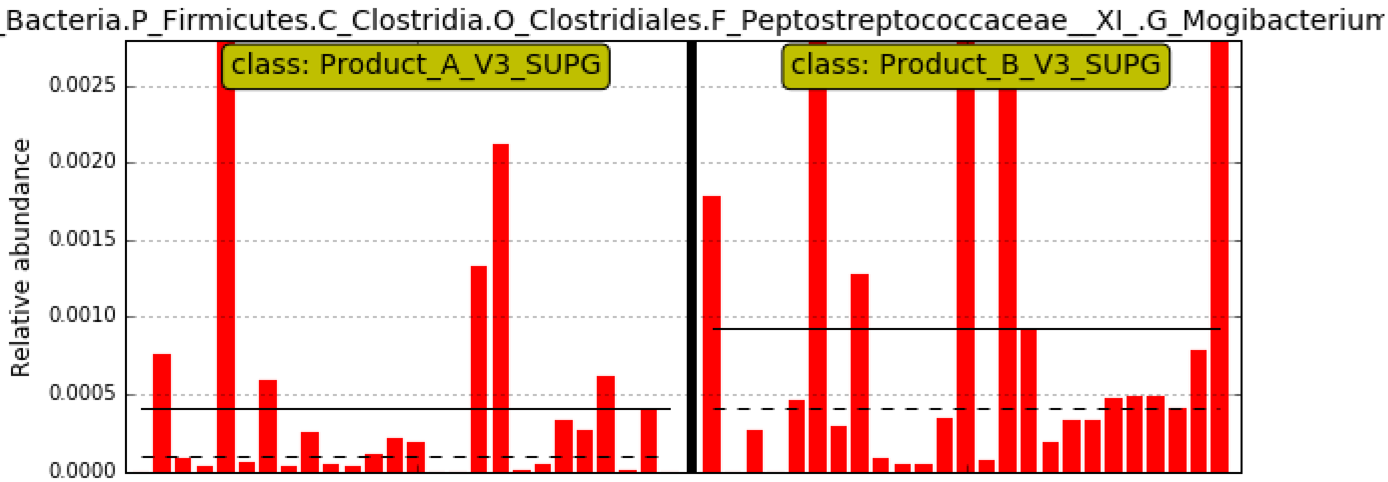


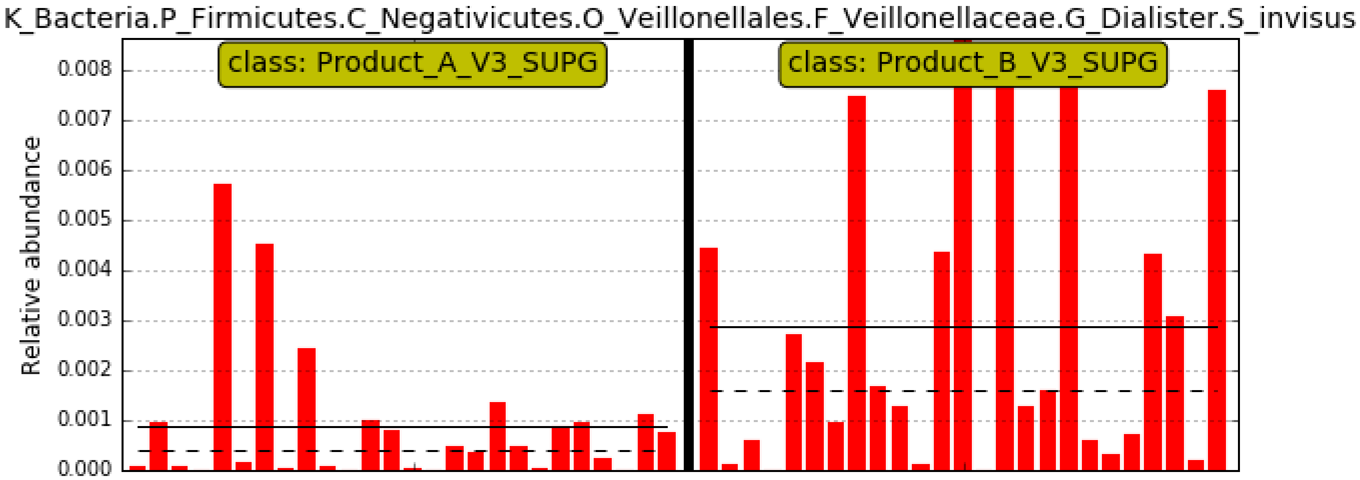
K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_gordonii

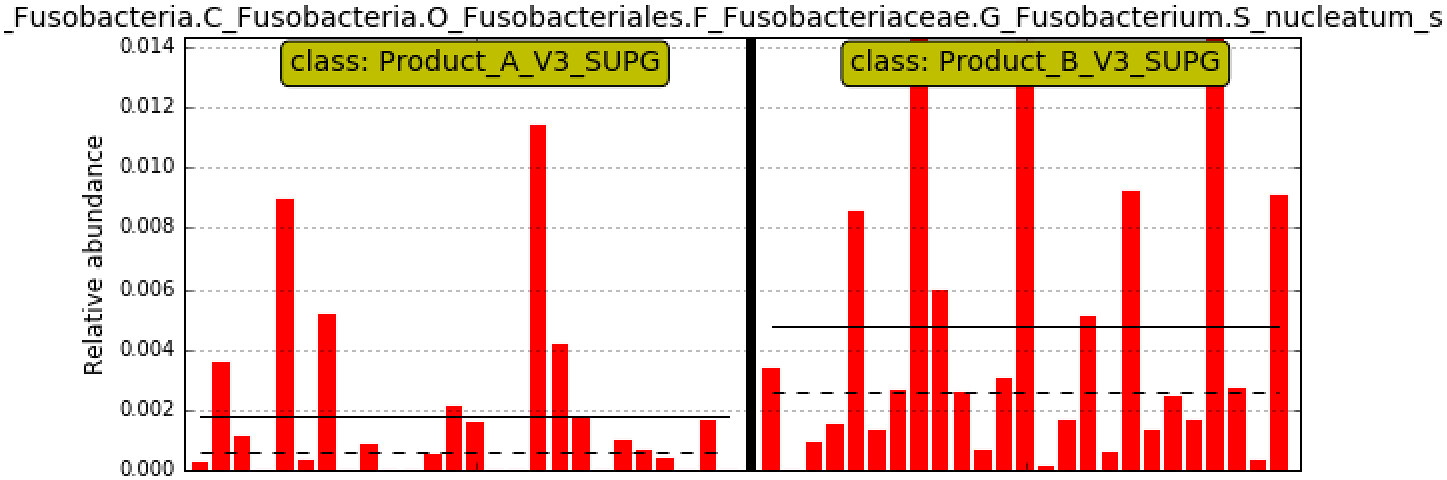


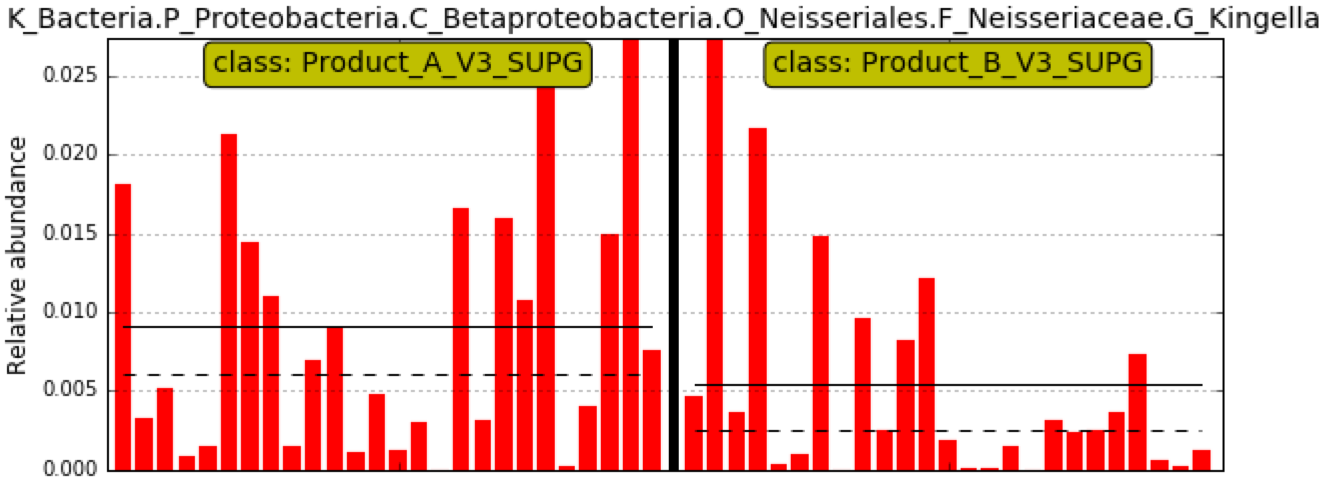
_Bacteria.P_Firmicutes.C_Clostridia.O_Clostridiales.F_Lachnospiraceae__XIV_.G_Stomatobaculum.S_lon

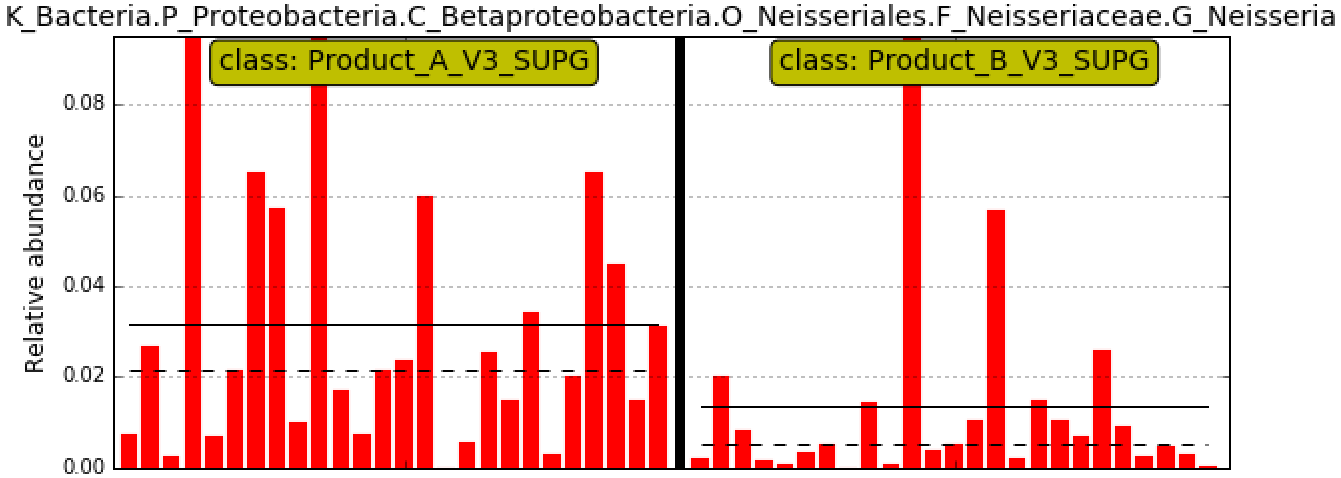


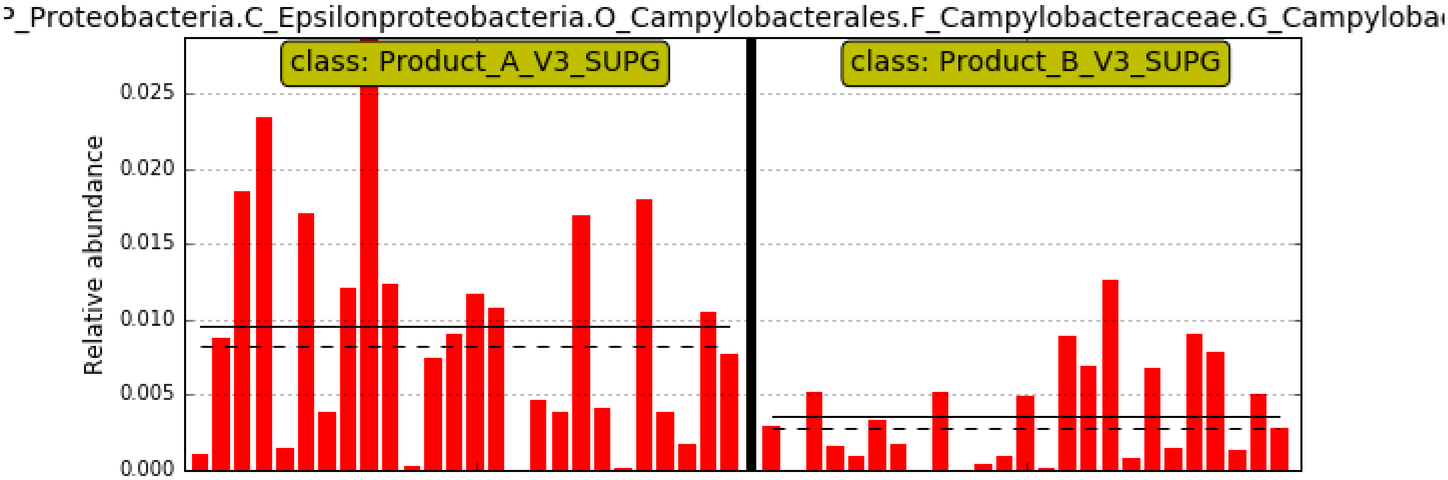

K_Bacteria.P_Firmicutes.C_Clostridia.O_Clostridiales.F_Peptostreptococcaceae__XI_.G_Mogibacterium
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000

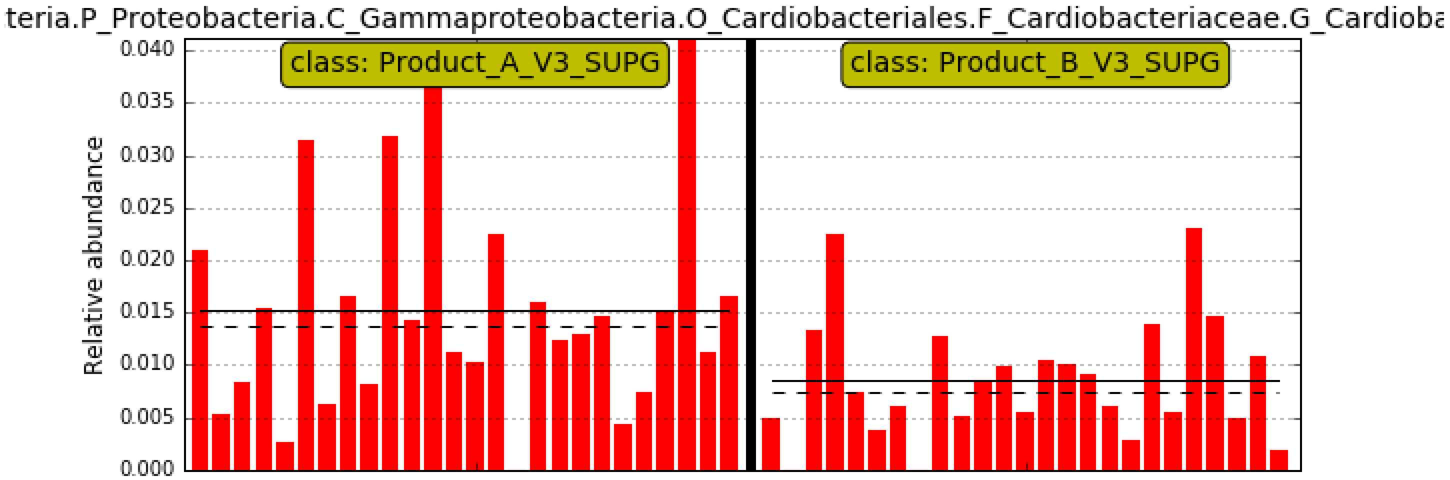

K_Bacteria.P_Firmicutes.C_Negativicutes.O_Veillonellales.F_Veillonellaceae.G_Dialister.S_invisus
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.008
0.007
0.006
0.005
0.004
0.003
0.002
0.001
0.000

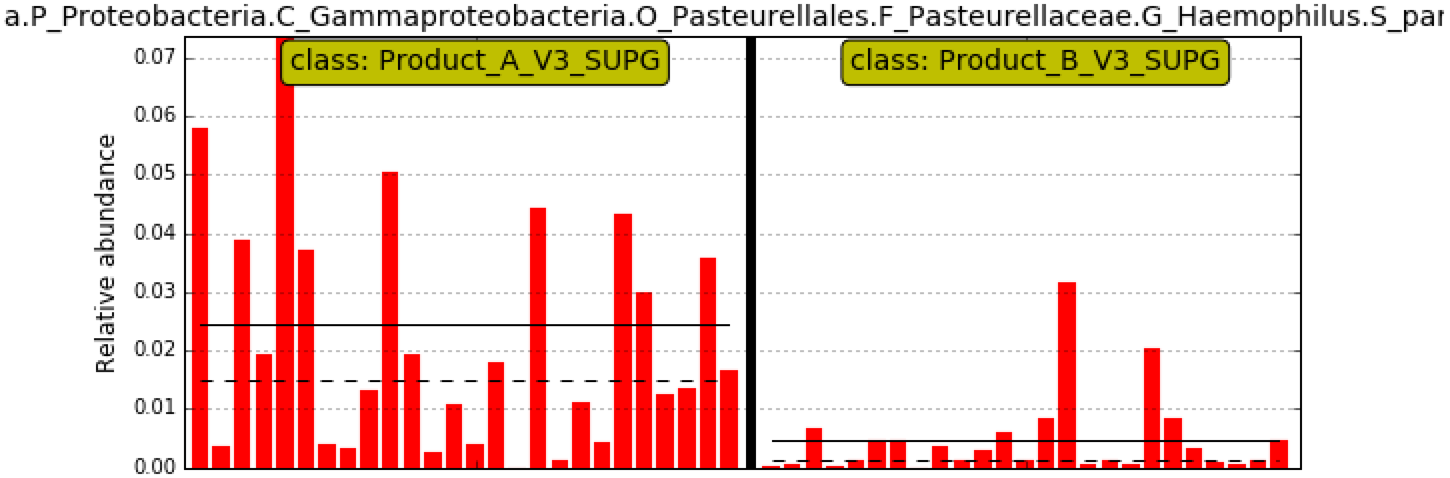

_Fusobacteria.C_Fusobacteria.O_Fusobacteriales.F_Fusobacteriaceae.G_Fusobacterium.S_nucleatum_s
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000

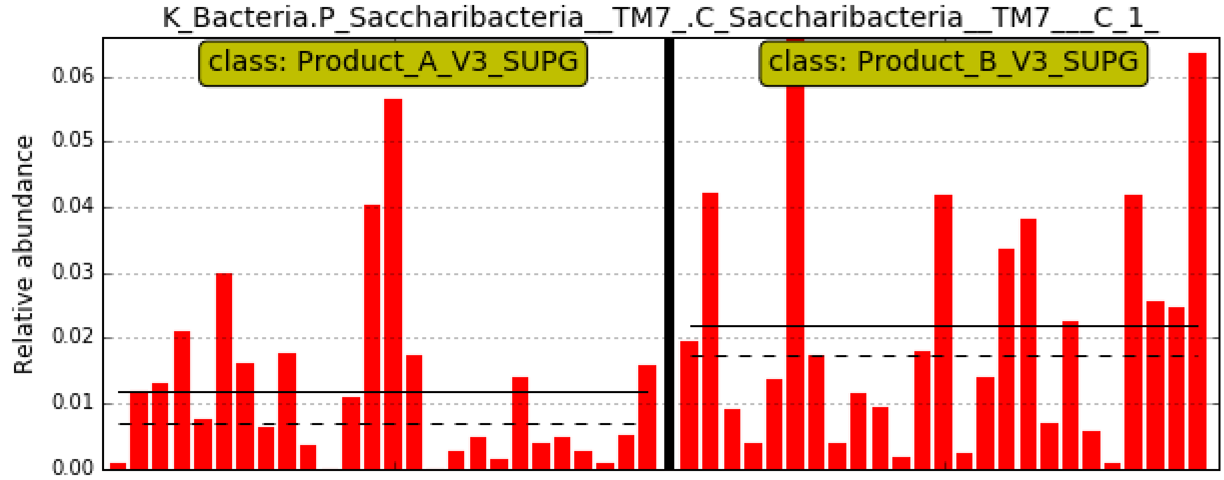

K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Kingella
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.025
0.020
0.015
0.010
0.005
0.000


K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Neisseria
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.08
0.06
0.04
0.02
0.00

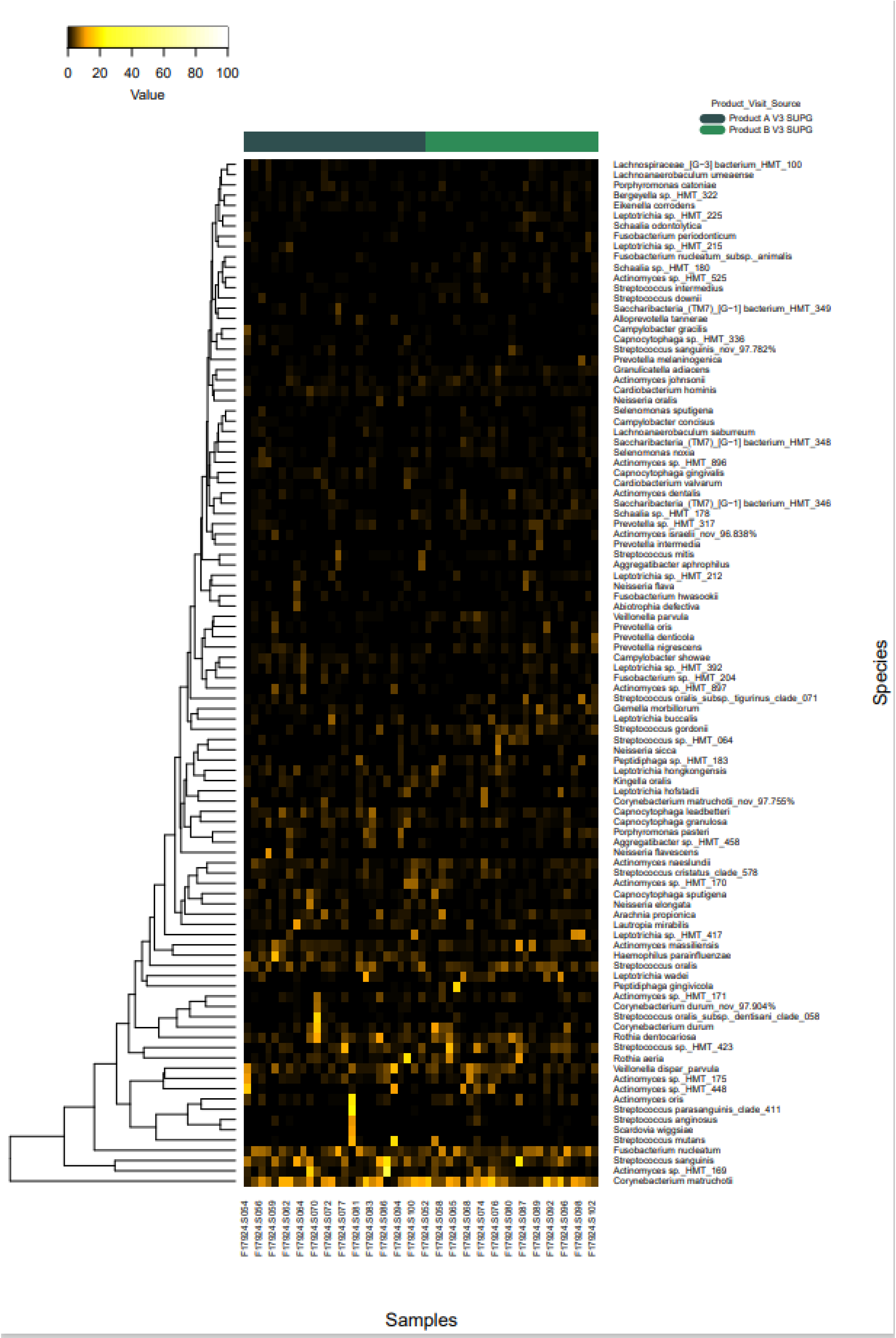

_Proteobacteria.C_Epsilonproteobacteria.O_Campylobacterales.F_Campylobacteraceae.G_Campyloba
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG
Relative abundance
0.025
0.020
0.015
0.010
0.005
0.000


teria.P_Proteobacteria.C_Gammaproteobacteria.O_Cardiobacteriales.F_Cardiobacteriaceae.G_Cardioba
Relative abundance
0.000
0.005
0.010
0.015
0.020
0.025
0.030
0.035
0.040
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG


a.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophilus.S_par
Relative abundance
0.00
0.01
0.02
0.03
0.04
0.05
0.06
0.07
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG


K_Bacteria.P_Saccharibacteria__TM7_.C_Saccharibacteria__TM7___C_1_
Relative abundance
0.00
0.01
0.02
0.03
0.04
0.05
0.06
class: Product_A_V3_SUPG
class: Product_B_V3_SUPG

6) Heat map.


0
20
40
60
80
100
Value
Product_Visit_Source
Product A V3 SUPG
Product B V3 SUPG
Lachnospiraceae_[G-3] bacterium_HMT_100
Lachnoanaerobaculum umeaense
Porphyromonas catoniae
Bergeyella sp._HMT_322
Eikenella corrodens
Leptotrichia sp._HMT_225
Schaalia odontolytica
Fusobacterium periodonticum
Leptotrichia sp._HMT_215
Fusobacterium nucleatum_subsp._animalis
Schaalia sp._HMT_180
Actinomyces sp._HMT_525
Streptococcus intermedius
Streptococcus downii
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_349
Alloprevotella tannerae
Campylobacter gracilis
Capnocytophaga sp._HMT_336
Streptococcus sanguinis_nov_97.782%
Prevotella melaninogenica
Granulicatella adiacens
Actinomyces johnsonii
Cardiobacterium hominis
Neisseria oralis
Selenomonas sputigena
Campylobacter concisus
Lachnoanaerobaculum saburreum
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_348
Selenomonas noxia
Actinomyces sp._HMT_896
Capnocytophaga gingivalis
Cardiobacterium valvarum
Actinomyces dentalis
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346
Schaalia sp._HMT_178
Prevotella sp._HMT_317
Actinomyces israelii_nov_96.838%
Prevotella intermedia
Streptococcus mitis
Aggregatibacter aphrophilus
Leptotrichia sp._HMT_212
Neisseria flava
Fusobacterium hwasookii
Abiotrophia defectiva
Veillonella parvula
Prevotella oris
Prevotella denticola
Prevotella nigrescens
Campylobacter showae
Leptotrichia sp._HMT_392
Fusobacterium sp._HMT_204
Actinomyces sp._HMT_897
Streptococcus oralis_subsp._tigurinus_clade_071
Gemella morbillorum
Leptotrichia buccalis
Streptococcus gordonii
Streptococcus sp._HMT_064
Neisseria sicca
Peptidiphaga sp._HMT_183
Leptotrichia hongkongensis
Kingella oralis
Leptotrichia hofstadii
Corynebacterium matruchotii_nov_97.755%
Capnocytophaga leadbetteri
Capnocytophaga granulosa
Porphyromonas pasteri
Aggregatibacter sp._HMT_458
Neisseria flavescens
Actinomyces naeslundii
Streptococcus cristatus_clade_578
Actinomyces sp._HMT_170
Capnocytophaga sputigena
Neisseria elongata
Arachnia propionica
Lautropia mirabilis
Leptotrichia sp._HMT_417
Actinomyces massiliensis
Haemophilus parainfluenzae
Streptococcus oralis
Leptotrichia wadei
Peptidiphaga gingivicola
Actinomyces sp._HMT_171
Corynebacterium durum_nov_97.904%
Streptococcus oralis_subsp._dentisani_clade_058
Corynebacterium durum
Rothia dentocariosa
Streptococcus sp._HMT_423
Rothia aeria
Veillonella dispar_parvula
Actinomyces sp._HMT_175
Actinomyces sp._HMT_448
Actinomyces oris
Streptococcus parasanguinis_clade_411
Streptococcus anginosus
Scardovia wiggsiae
Streptococcus mutans
Fusobacterium nucleatum
Streptococcus sanguinis
Actinomyces sp._HMT_169
Corynebacterium matruchotii
Species
F17924S054
F17924S056
F17924S059
F17924S062
F17924S064
F17924S070
F17924S072
F17924S077
F17924S081
F17924S083
F17924S086
F17924S094
F17924S100
F17924S052
F17924S058
F17924S065
F17924S068
F17924S074
F17924S076
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F17924S087
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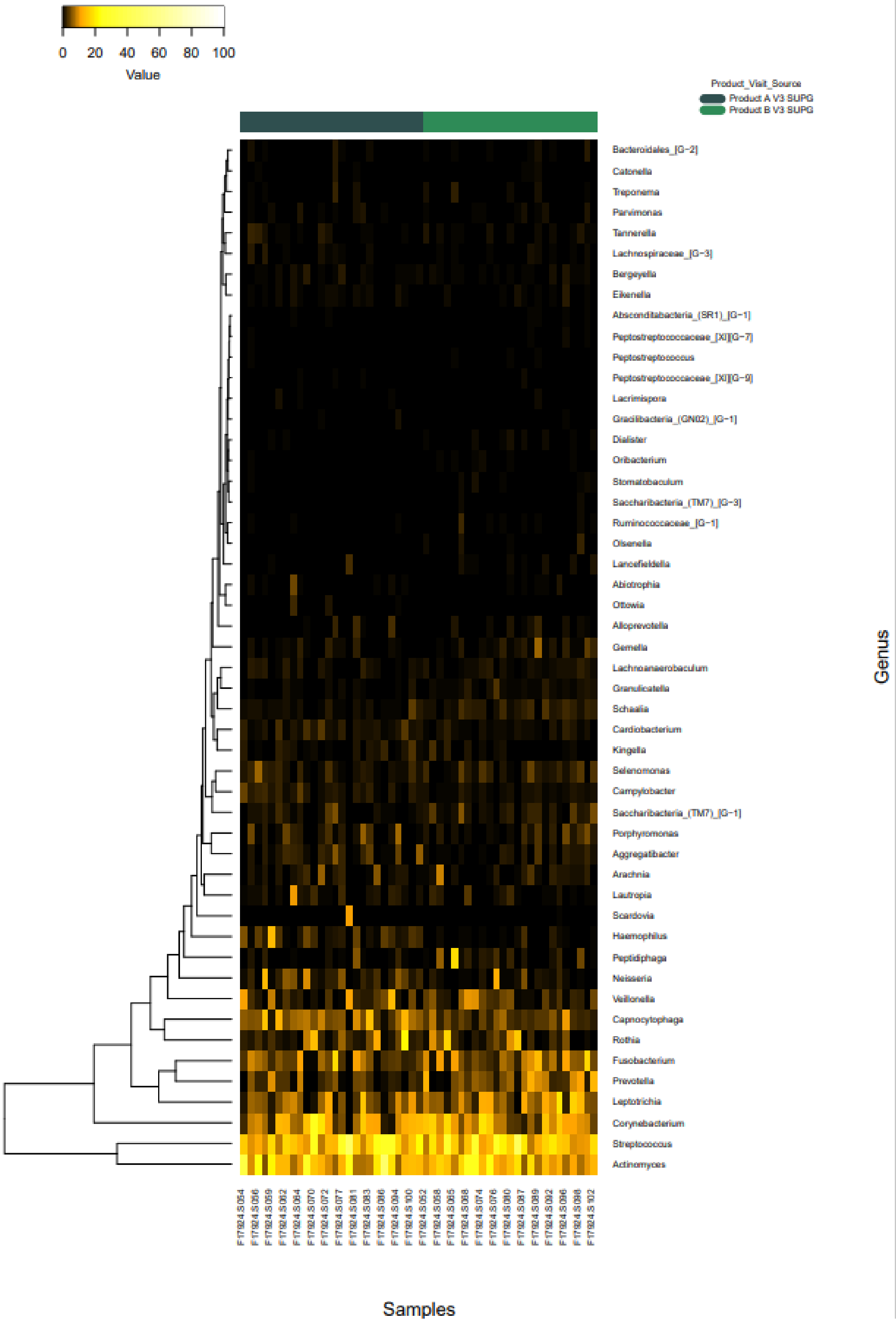
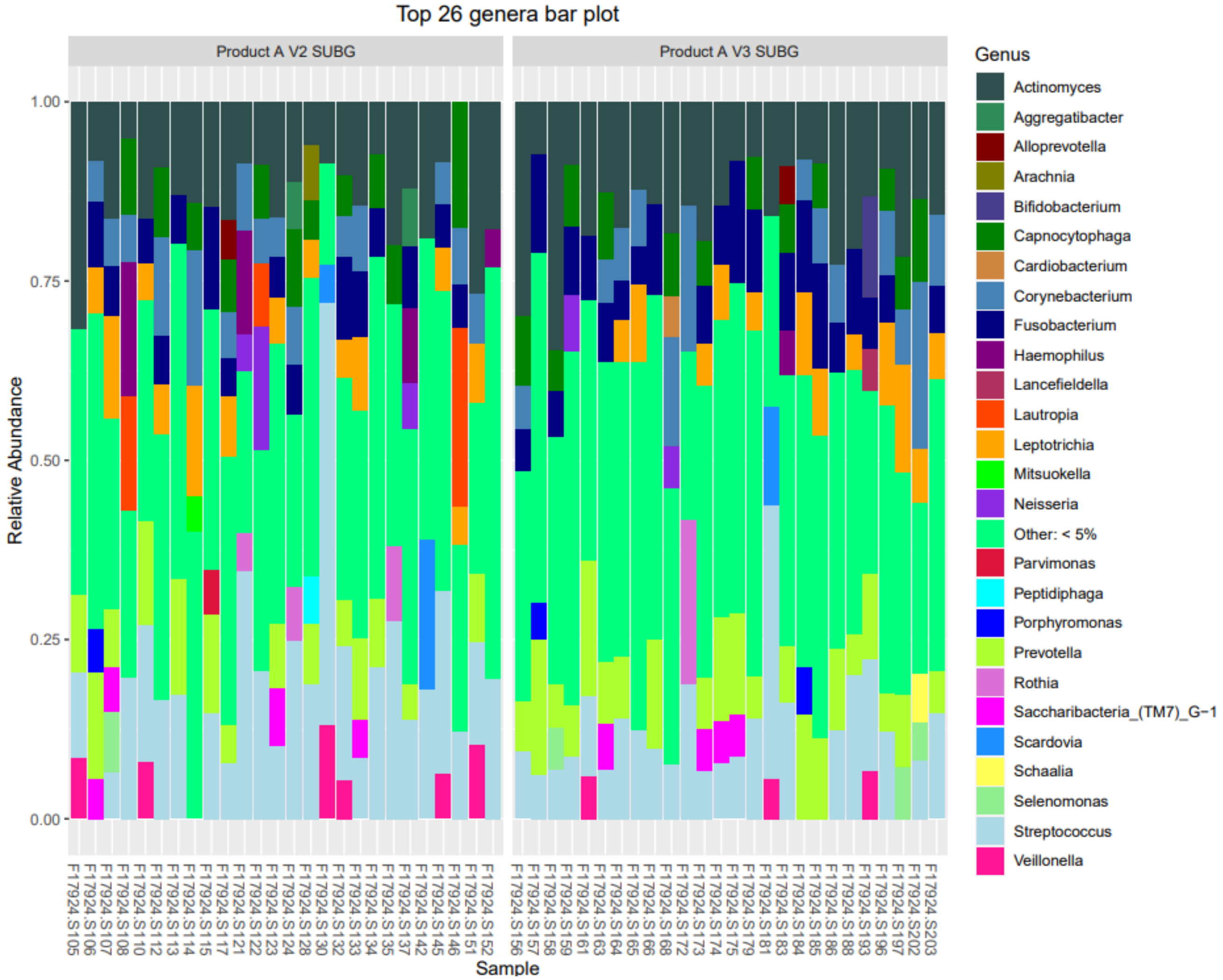
F17924S092
F17924S096
F17924S098
F17924S102
Samples

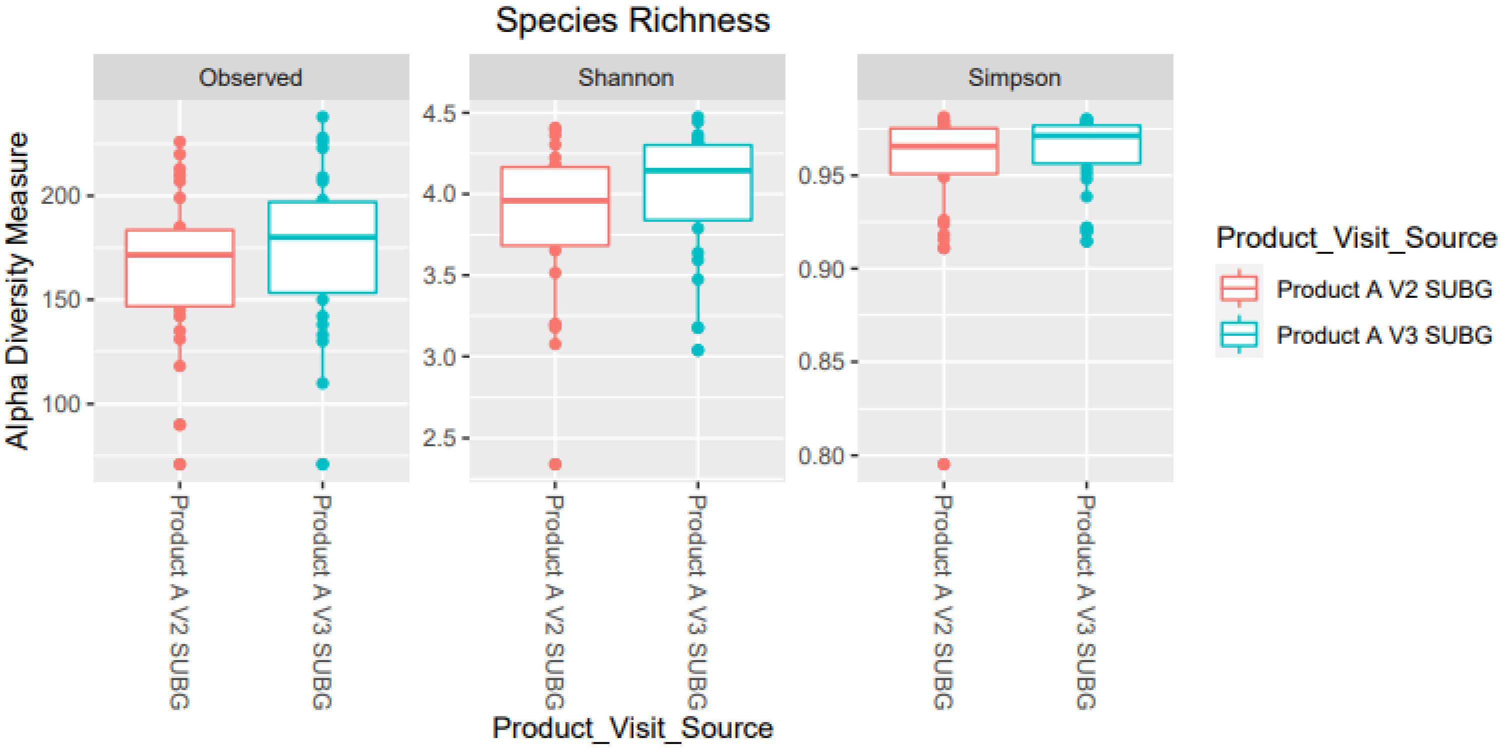

0
20
40
60
80
100
Value
Product_Visit_Source
Product A V3 SUPG
Product B V3 SUPG
Bacteroidales_[G-2]
Catonella
Treponema
Parvimonas
Tannerella
Lachnospiraceae_[G-3]
Bergeyella
Eikenella
Absconditabacteria_(SR1)_[G-1]
Peptostreptococcaceae_[XI][G-7]
Peptostreptococcus
Peptostreptococcaceae_[XI][G-9]
Lacrimispora
Gracilibacteria_(GN02)_[G-1]
Dialister
Oribacterium
Stomatobaculum
Saccharibacteria_(TM7)_[G-3]
Ruminococcaceae_[G-1]
Olsenella
Lancefieldella
Abiotrophia
Ottowia
Alloprevotella
Gemella
Lachnoanaerobaculum
Granulicatella
Schaalia
Cardiobacterium
Kingella
Selenomonas
Campylobacter
Saccharibacteria_(TM7)_[G-1]
Porphyromonas
Aggregatibacter
Arachnia
Lautropia
Scardovia
Haemophilus
Peptidiphaga
Neisseria
Veillonella
Capnocytophaga
Rothia
Fusobacterium
Prevotella
Leptotrichia
Corynebacterium
Streptococcus
Actinomyces
Genus
FIT924.S054
FIT924.S056
FIT924.S059
FIT924.S062
FIT924.S064
FIT924.S070
FIT924.S072
FIT924.S077
FIT924.S081
FIT924.S083
FIT924.S086
FIT924.S094
FIT924.S100
FIT924.S052
FIT924.S058
FIT924.S065
FIT924.S068
FIT924.S074
FIT924.S076
FIT924.S080
FIT924.S087
FIT924.S089
FIT924.S092
FIT924.S096
FIT924.S098
FIT924.S102
Samples

Comparison 17. Product A V2 SUBG vs Product A V3 SUBG

1) Taxonomy bar graphs

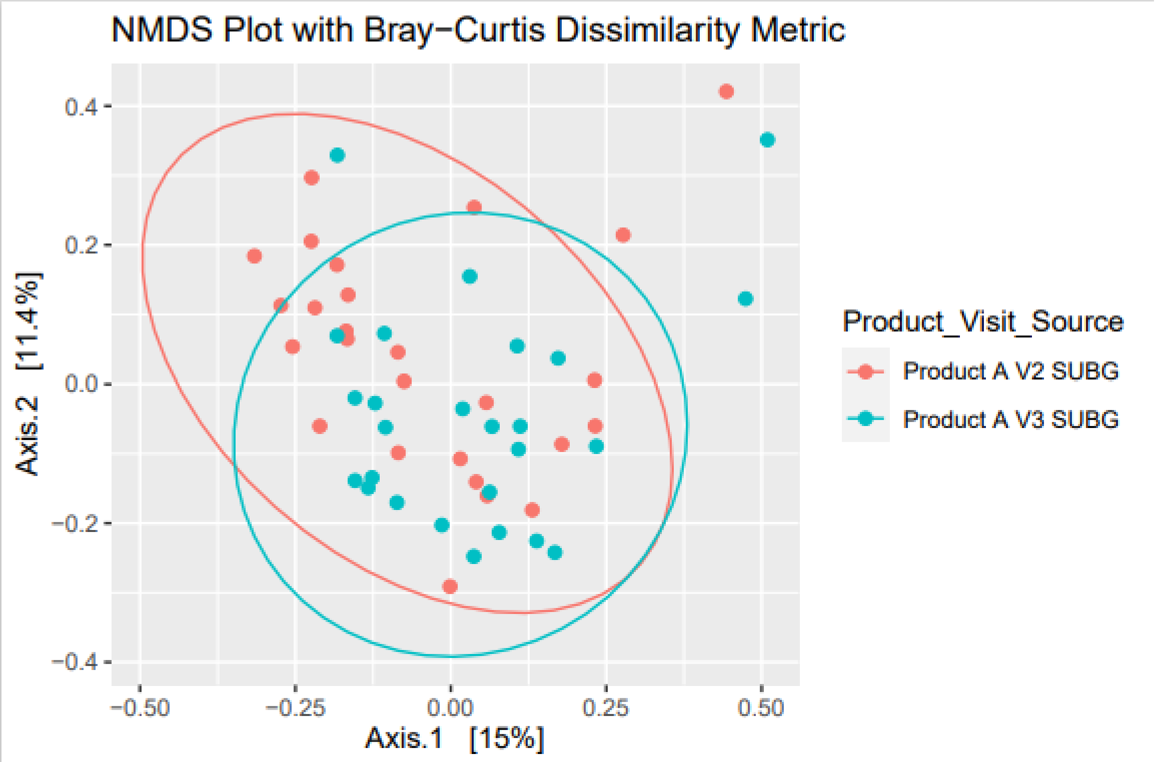


2) Alpha



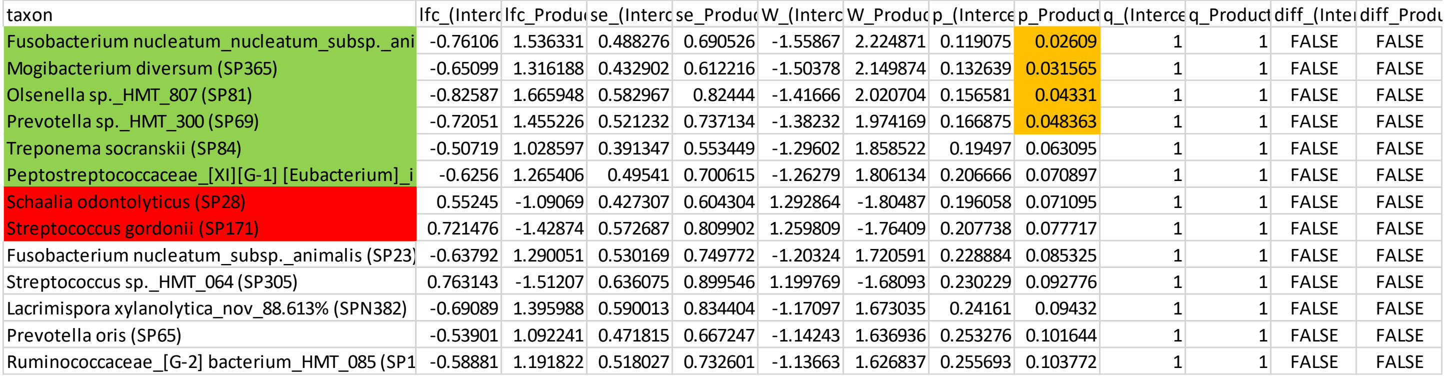
No significant differences

3) Beta diversity



No significant differences

4) Differential abundance



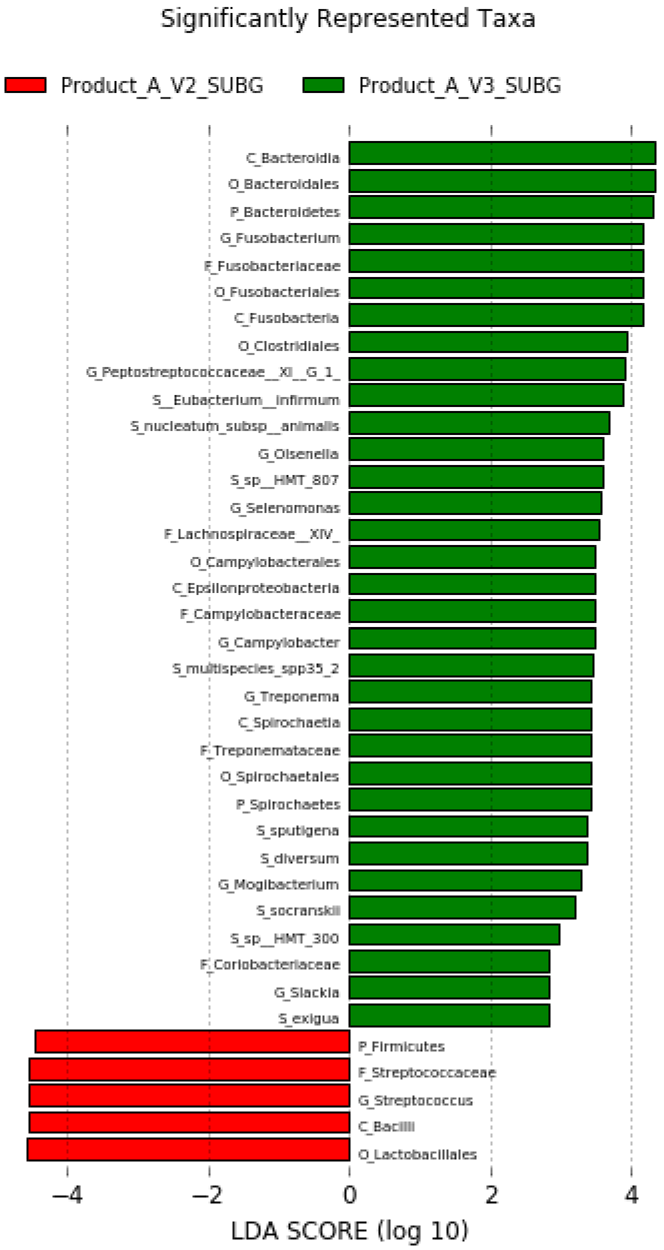
taxon	lfc_(Interc	lfc_Produ	se_(Interc	se_Produ	W_(Interc	W_Produ	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inte	diff_Produ
Fusobacterium nucleatum_nucleatum_subsp._ani	-0.76106	1.536331	0.488276	0.690526	-1.55867	2.224871	0.119075	0.02609	1	1	FALSE	FALSE
Mogibacterium diversum (SP365)	-0.65099	1.316188	0.432902	0.612216	-1.50378	2.149874	0.132639	0.031565	1	1	FALSE	FALSE
Olsenella sp._HMT_807 (SP81)	-0.82587	1.665948	0.582967	0.82444	-1.41666	2.020704	0.156581	0.04331	1	1	FALSE	FALSE
Prevotella sp._HMT_300 (SP69)	-0.72051	1.455226	0.521232	0.737134	-1.38232	1.974169	0.166875	0.048363	1	1	FALSE	FALSE
Treponema socranskii (SP84)	-0.50719	1.028597	0.391347	0.553449	-1.29602	1.858522	0.19497	0.063095	1	1	FALSE	FALSE
Peptostreptococcaceae_[XI][G-1] [Eubacterium]_i	-0.6256	1.265406	0.49541	0.700615	-1.26279	1.806134	0.206666	0.070897	1	1	FALSE	FALSE
Schaalia odontolyticus (SP28)	0.55245	-1.09069	0.427307	0.604304	1.292864	-1.80487	0.196058	0.071095	1	1	FALSE	FALSE
Streptococcus gordonii (SP171)	0.721476	-1.42874	0.572687	0.809902	1.259809	-1.76409	0.207738	0.077717	1	1	FALSE	FALSE
Fusobacterium nucleatum_subsp._animalis (SP23)	-0.63792	1.290051	0.530169	0.749772	-1.20324	1.720591	0.228884	0.085325	1	1	FALSE	FALSE
Streptococcus sp._HMT_064 (SP305)	0.763143	-1.51207	0.636075	0.899546	1.199769	-1.68093	0.230229	0.092776	1	1	FALSE	FALSE
Lacrimispora xylanolytica_nov_88.613% (SPN382)	-0.69089	1.395988	0.590013	0.834404	-1.17097	1.673035	0.24161	0.09432	1	1	FALSE	FALSE
Prevotella oris (SP65)	-0.53901	1.092241	0.471815	0.667247	-1.14243	1.636936	0.253276	0.101644	1	1	FALSE	FALSE
Ruminococcaceae_[G-2] bacterium_HMT_085 (SP1	-0.58881	1.191822	0.518027	0.732601	-1.13663	1.626837	0.255693	0.103772	1	1	FALSE	FALSE

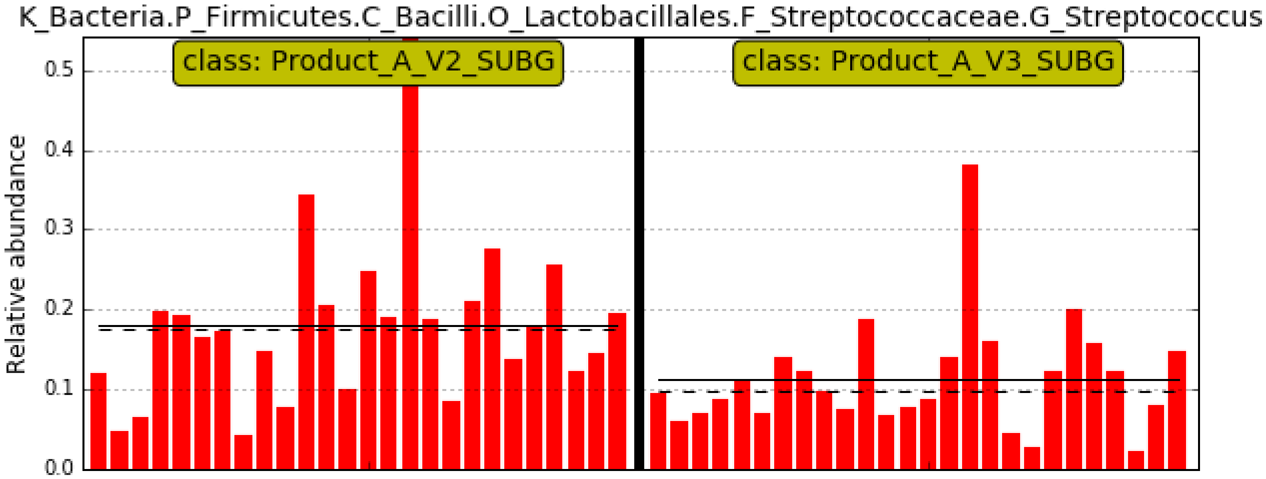
Green, more prevalent in V3

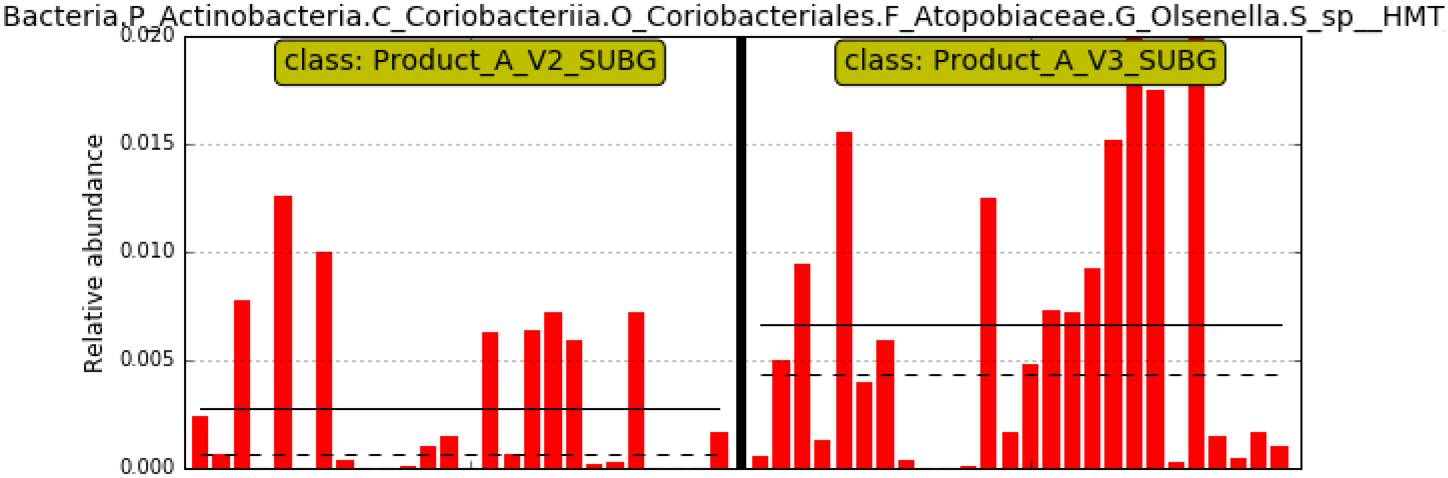
Red more prevalent in V2

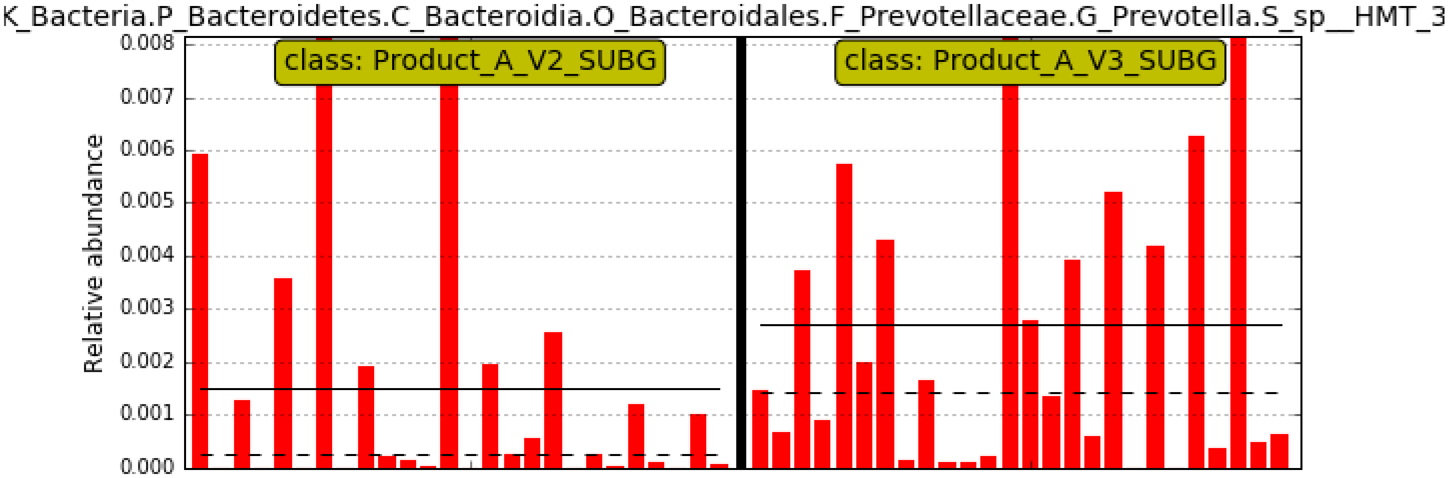
Not much difference of baseline as compared to visit 3. No statistical difference.

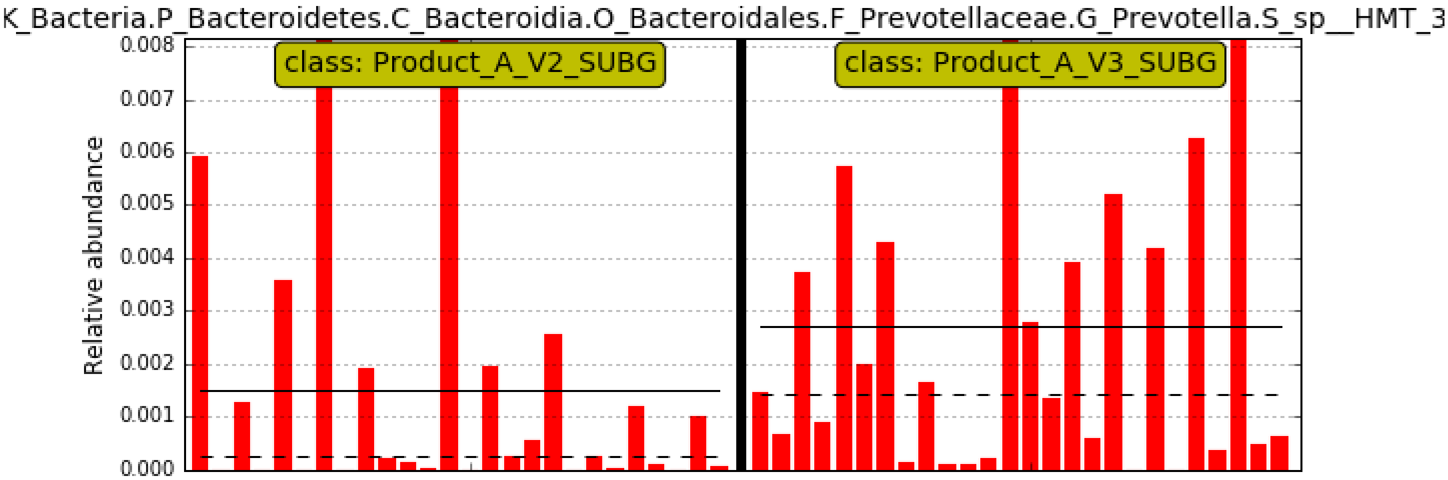
5) Lefse

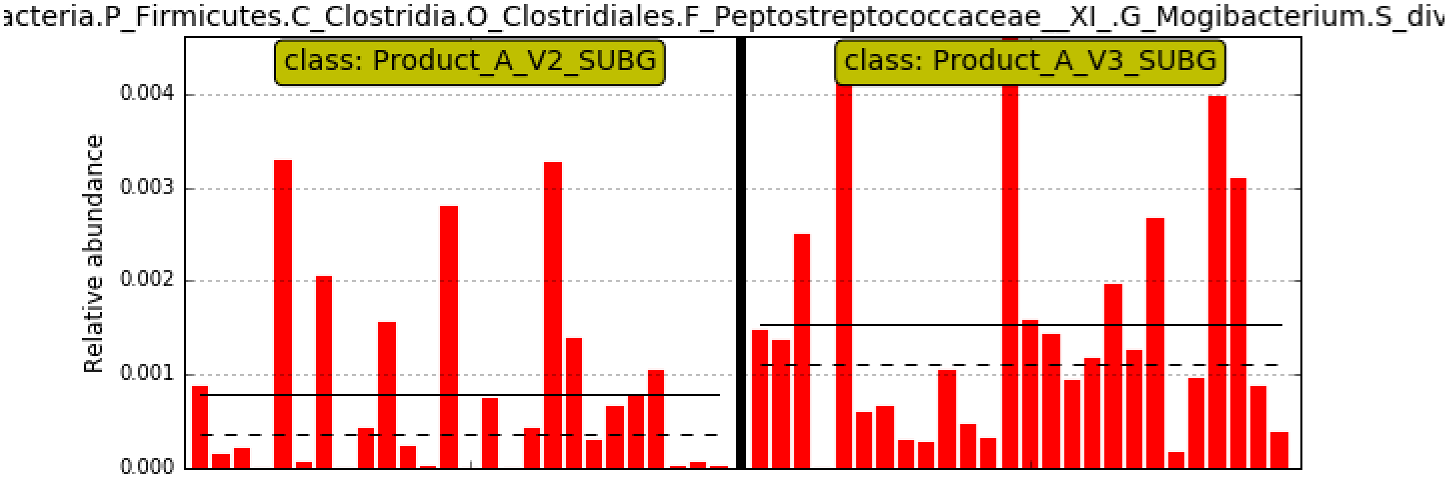

Significantly Represented Taxa
Product_A_V2_SUBG
Product_A_V3_SUBG
C_Bacteroidia
O_Bacteroidales
P_Bacteroidetes
G_Fusobacterium
F_Fusobacteriaceae
O_Fusobacteriales
C_Fusobacteria
O_Clostridiales
G_Peptostreptococcaceae__XI__G_1_
S__Eubacterium__infirmum
S_nucleatum_subsp__animalis
G_Olsenella
S_sp__HMT_807
G_Selenomonas
F_Lachnospiraceae__XIV_
O_Campylobacterales
C_Epsilonproteobacteria
F_Campylobacteraceae
G_Campylobacter
S_multispecies_spp35_2
G_Treponema
C_Spirochaetia
F_Treponemataceae
O_Spirochaetales
P_Spirochaetes
S_sputigena
S_diversum
G_Mogibacterium
S_socranskii
S_sp__HMT_300
F_Coriobacteriaceae
G_Slackia
S_exigua
P_Firmicutes
F_Streptococcaceae
G_Streptococcus
C_Bacilli
O_Lactobacillales
−4
−2
0
2
4
LDA SCORE (log 10)

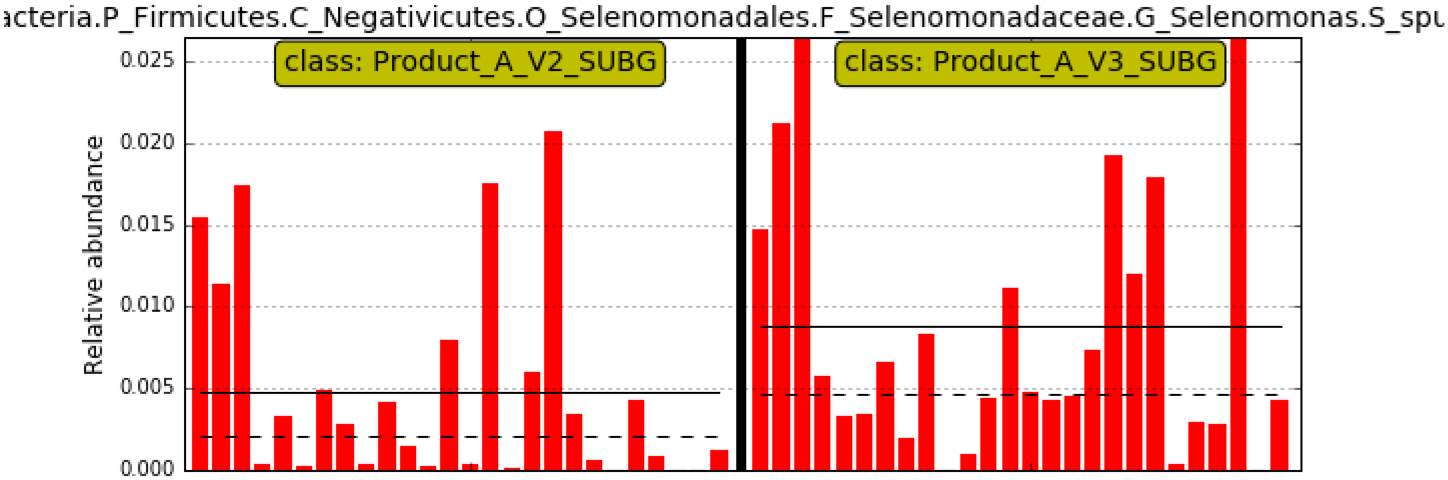

K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus

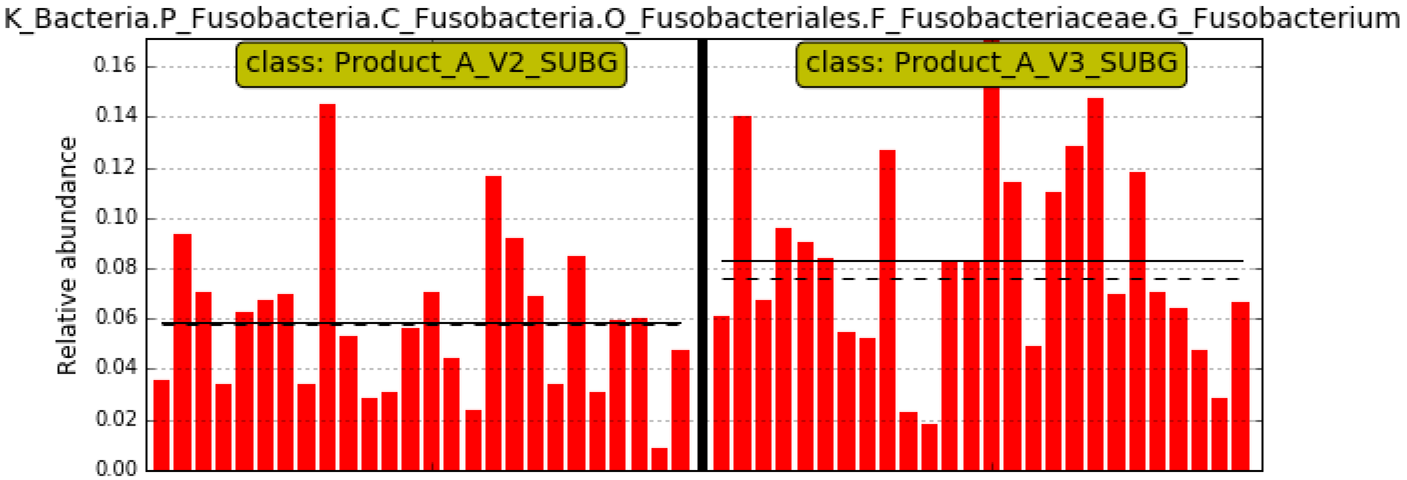

Bacteria.P_Actinobacteria.C_Coriobacteriia.O_Coriobacteriales.F_Atopobiaceae.G_Olsenella.S_sp__HMT

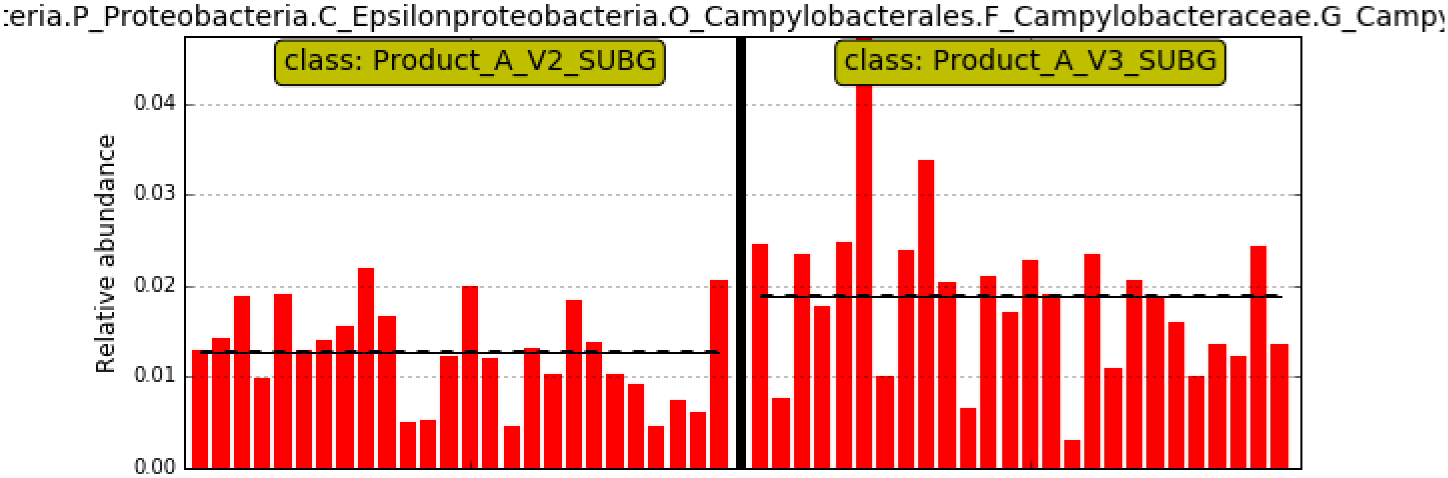

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_sp__HMT_3

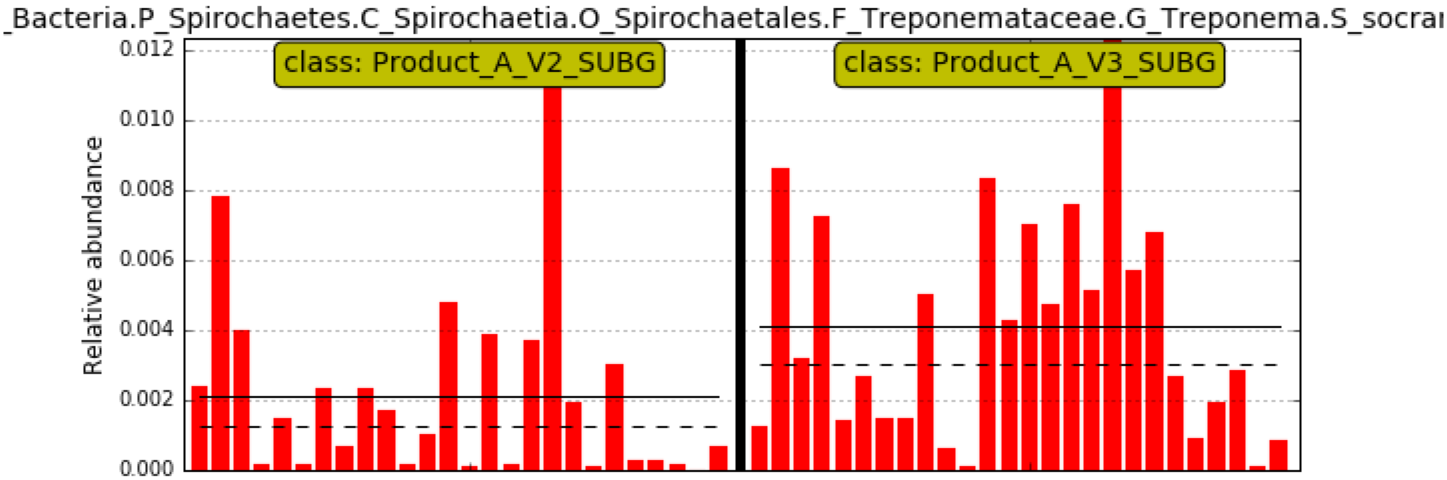

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_sp__HMT_3

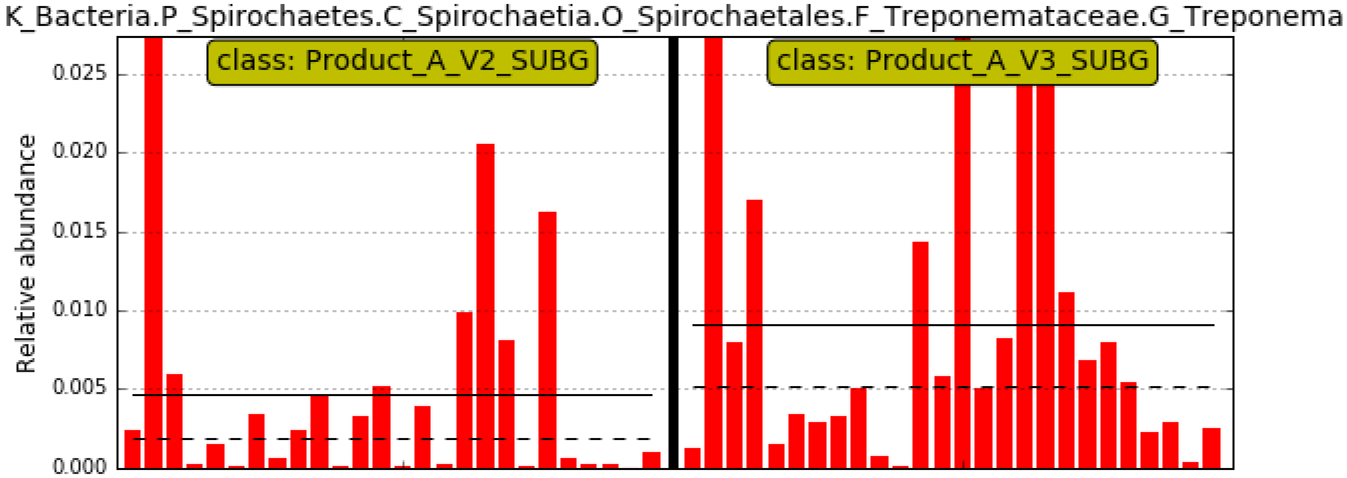

acteria.P_Firmicutes.C_Clostridia.O_Clostridiales.F_Peptostreptococcaceae__XI_.G_Mogibacterium.S_div


acteria.P_Firmicutes.C_Negativicutes.O_Selenomonadales.F_Selenomonadaceae.G_Selenomonas.S_spu

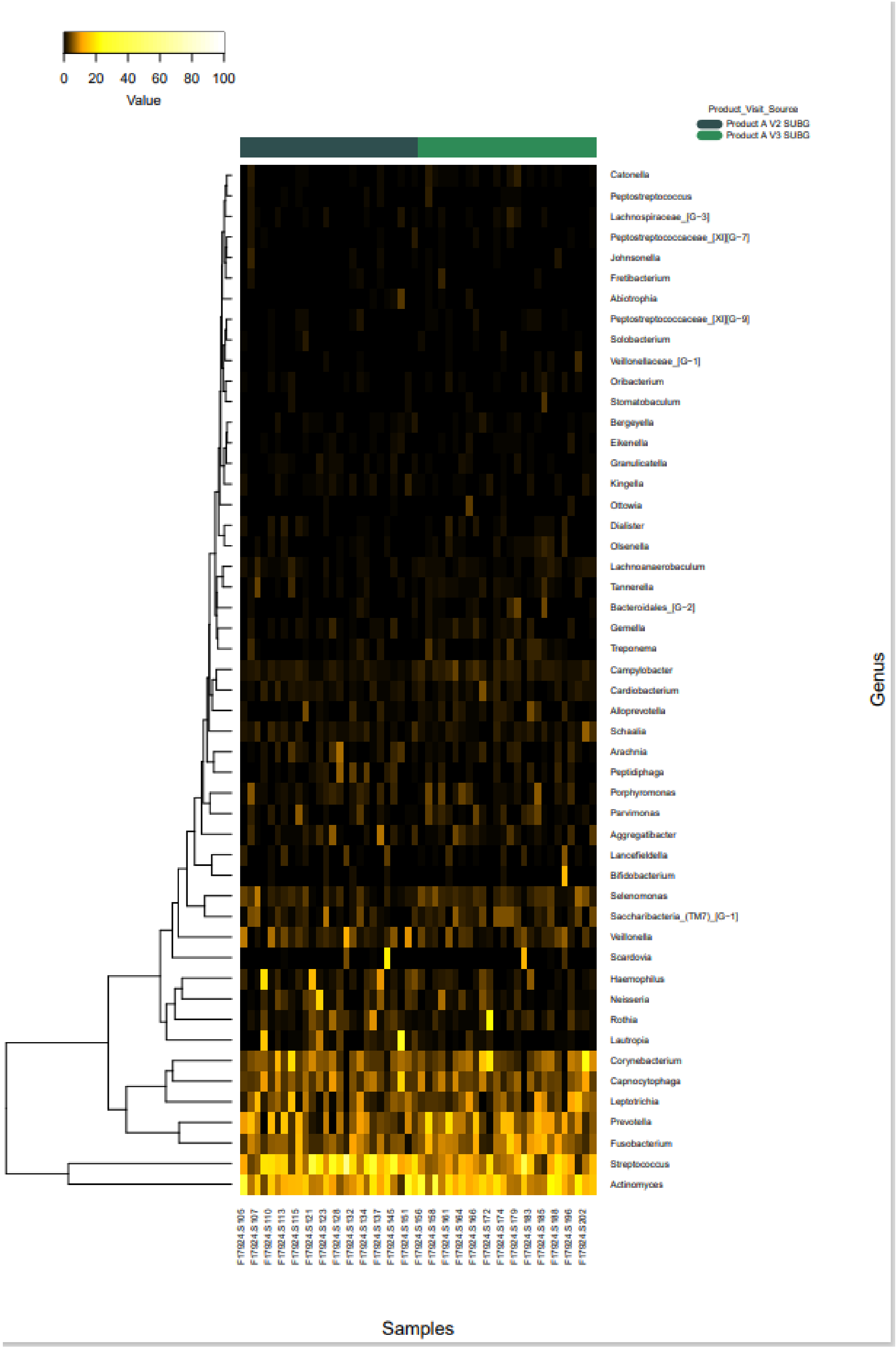

K_Bacteria.P_Fusobacteria.C_Fusobacteria.O_Fusobacteriales.F_Fusobacteriaceae.G_Fusobacterium
class: Product_A_V2_SUBG
class: Product_A_V3_SUBG
Relative abundance
0.16
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0.00

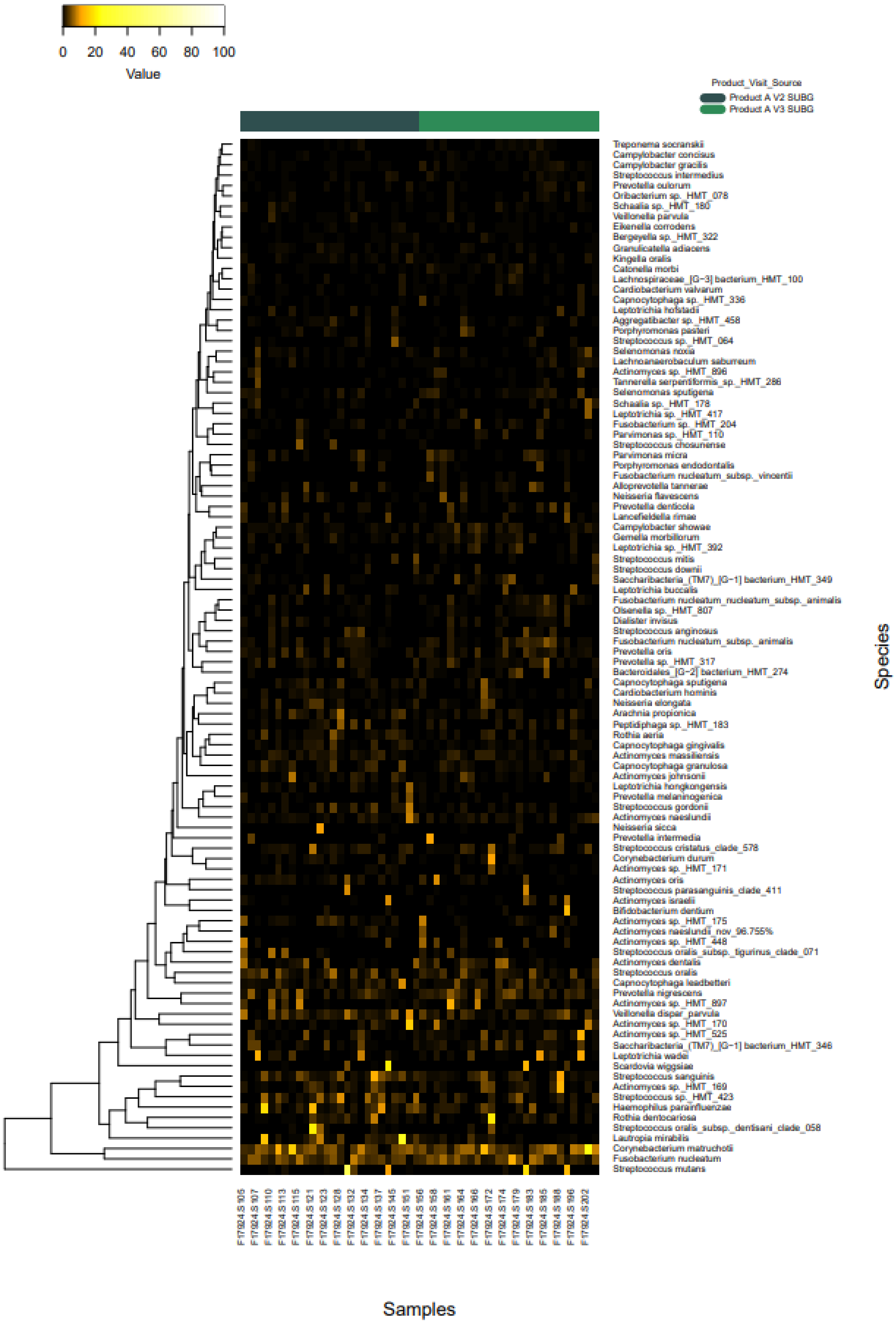

eria.P_Proteobacteria.C_Epsilonproteobacteria.O_Campylobacterales.F_Campylobacteraceae.G_Campy
class: Product_A_V2_SUBG
class: Product_A_V3_SUBG
Relative abundance
0.04
0.03
0.02
0.01
0.00


_Bacteria.P_Spirochaetes.C_Spirochaetia.O_Spirochaetales.F_Treponemataceae.G_Treponema.S_socrai


K_Bacteria.P_Spirochaetes.C_Spirochaetia.O_Spirochaetales.F_Treponemataceae.G_Treponema

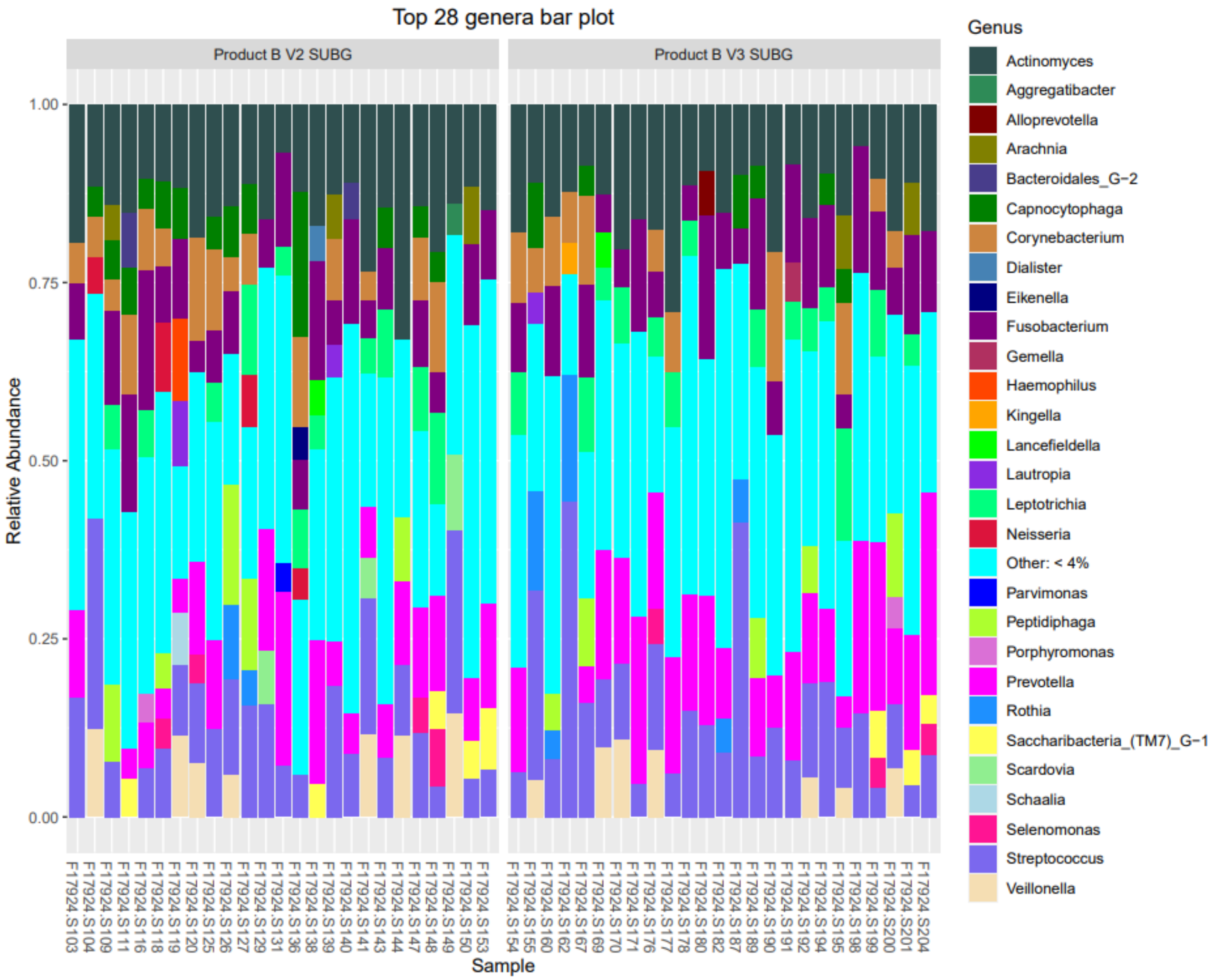
6) Heat map.


0
20
40
60
80
100
Value
Product_Visit_Source
Product A V2 SUBG
Product A V3 SUBG
Catonella
Peptostreptococcus
Lachnospiraceae_[G-3]
Peptostreptococcaceae_[XI][G-7]
Johnsonella
Filifactor
Abiotrophia
Peptostreptococcaceae_[XI][G-9]
Solobacterium
Veillonellaceae_[G-1]
Oribacterium
Stomatobaculum
Bergeyella
Eikenella
Granulicatella
Kingella
Ottowia
Dialister
Olsenella
Lachnoanaerobaculum
Tannerella
Bacteroidales_[G-2]
Gemella
Treponema
Campylobacter
Cardiobacterium
Alloprevotella
Schaalia
Arachnia
Peptidiphaga
Porphyromonas
Parvimonas
Aggregatibacter
Lancefieldella
Bifidobacterium
Selenomonas
Saccharibacteria_(TM7)_[G-1]
Veillonella
Scardovia
Haemophilus
Neisseria
Rothia
Lautropia
Corynebacterium
Capnocytophaga
Leptotrichia
Prevotella
Fusobacterium
Streptococcus
Actinomyces
Genus
F17924.S105
F17924.S107
F17924.S110
F17924.S113
F17924.S115
F17924.S121
F17924.S123
F17924.S128
F17924.S132
F17924.S134
F17924.S137
F17924.S145
F17924.S151
F17924.S156
F17924.S158
F17924.S161
F17924.S164
F17924.S166
F17924.S172
F17924.S174
F17924.S179
F17924.S183
F17924.S185
F17924.S188
F17924.S196
F17924.S202
Samples

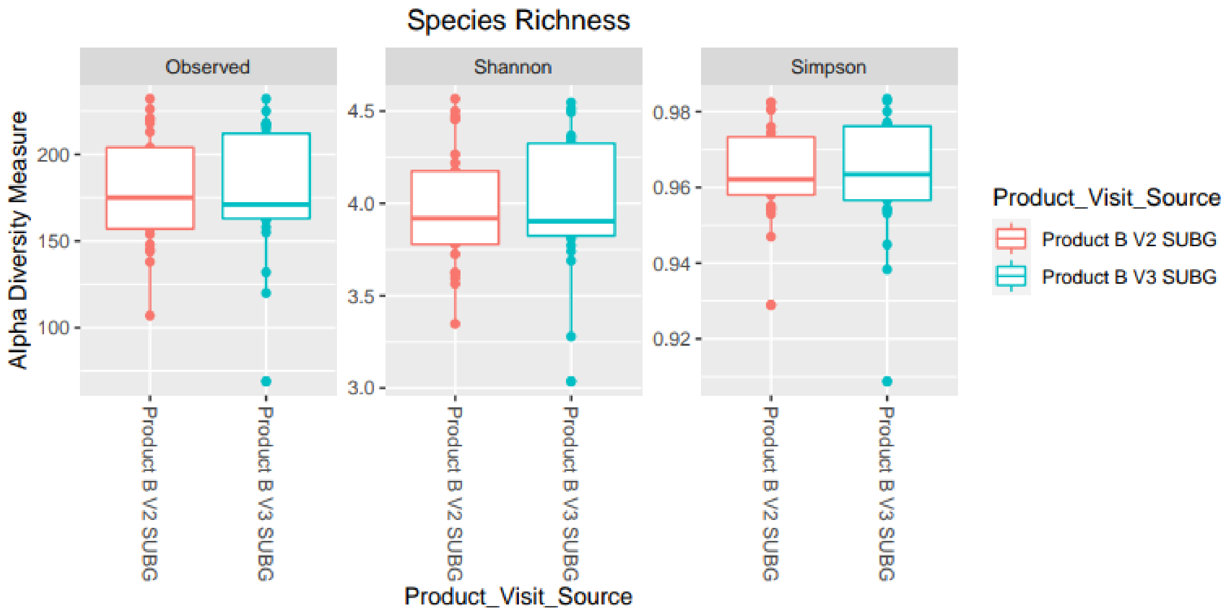

0
20
40
60
80
100
Value
Product_Visit_Source
Product A V2 SUBG
Product A V3 SUBG
Treponema socranskii
Campylobacter concisus
Campylobacter gracilis
Streptococcus intermedius
Prevotella oulorum
Oribacterium sp._HMT_078
Schaalia sp._HMT_180
Veillonella parvula
Eikenella corrodens
Bergeyella sp._HMT_322
Granulicatella adiacens
Kingella oralis
Catonella morbi
Lachnospiraceae_[G-3] bacterium_HMT_100
Cardiobacterium valvarum
Capnocytophaga sp._HMT_336
Leptotrichia hofstadii
Aggregatibacter sp._HMT_458
Porphyromonas pasteri
Streptococcus sp._HMT_064
Selenomonas noxia
Lachnoanaerobaculum saburreum
Actinomyces sp._HMT_896
Tannerella serpentiformis_sp._HMT_286
Selenomonas sputigena
Schaalia sp._HMT_178
Leptotrichia sp._HMT_417
Fusobacterium sp._HMT_204
Parvimonas sp._HMT_110
Streptococcus chosunense
Parvimonas micra
Porphyromonas endodontalis
Fusobacterium nucleatum_subsp._vincentii
Alloprevotella tannerae
Neisseria flavescens
Prevotella denticola
Lancefieldella rimae
Campylobacter showae
Gemella morbillorum
Leptotrichia sp._HMT_392
Streptococcus mitis
Streptococcus downii
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_349
Leptotrichia buccalis
Fusobacterium nucleatum_nucleatum_subsp._animalis
Olsenella sp._HMT_807
Dialister invisus
Streptococcus anginosus
Fusobacterium nucleatum_subsp._animalis
Prevotella oris
Prevotella sp._HMT_317
Bacteroidales_[G-2] bacterium_HMT_274
Capnocytophaga sputigena
Cardiobacterium hominis
Neisseria elongata
Arachnia propionica
Peptidiphaga sp._HMT_183
Rothia aeria
Capnocytophaga gingivalis
Actinomyces massiliensis
Capnocytophaga granulosa
Actinomyces johnsonii
Leptotrichia hongkongensis
Prevotella melaninogenica
Streptococcus gordonii
Actinomyces naeslundii
Neisseria sicca
Prevotella intermedia
Streptococcus cristatus_clade_578
Corynebacterium durum
Actinomyces sp._HMT_171
Actinomyces oris
Streptococcus parasanguinis_clade_411
Actinomyces israelii
Bifidobacterium dentium
Actinomyces sp._HMT_175
Actinomyces naeslundii_nov_96.755%
Actinomyces sp._HMT_448
Streptococcus oralis_subsp._tigurinus_clade_071
Actinomyces dentalis
Streptococcus oralis
Capnocytophaga leadbetteri
Prevotella nigrescens
Actinomyces sp._HMT_897
Veillonella dispar_parvula
Actinomyces sp._HMT_170
Actinomyces sp._HMT_525
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346
Leptotrichia wadei
Scardovia wiggsiae
Streptococcus sanguinis
Actinomyces sp._HMT_169
Streptococcus sp._HMT_423
Haemophilus parainfluenzae
Rothia dentocariosa
Streptococcus oralis_subsp._dentisani_clade_058
Lautropia mirabilis
Corynebacterium matruchotii
Fusobacterium nucleatum
Streptococcus mutans
Species
FI7924.S105
FI7924.S107
FI7924.S110
FI7924.S113
FI7924.S115
FI7924.S121
FI7924.S123
FI7924.S128
FI7924.S132
FI7924.S134
FI7924.S137
FI7924.S145
FI7924.S151
FI7924.S156
FI7924.S158
FI7924.S161
FI7924.S164
FI7924.S166
FI7924.S172
FI7924.S174
FI7924.S179
FI7924.S183
FI7924.S185
FI7924.S188
FI7924.S196
FI7924.S202
Samples

Comparison 18. Product B V2 SUBG vs Product B V3 SUBG

1) Taxonomy bar graphs
24)

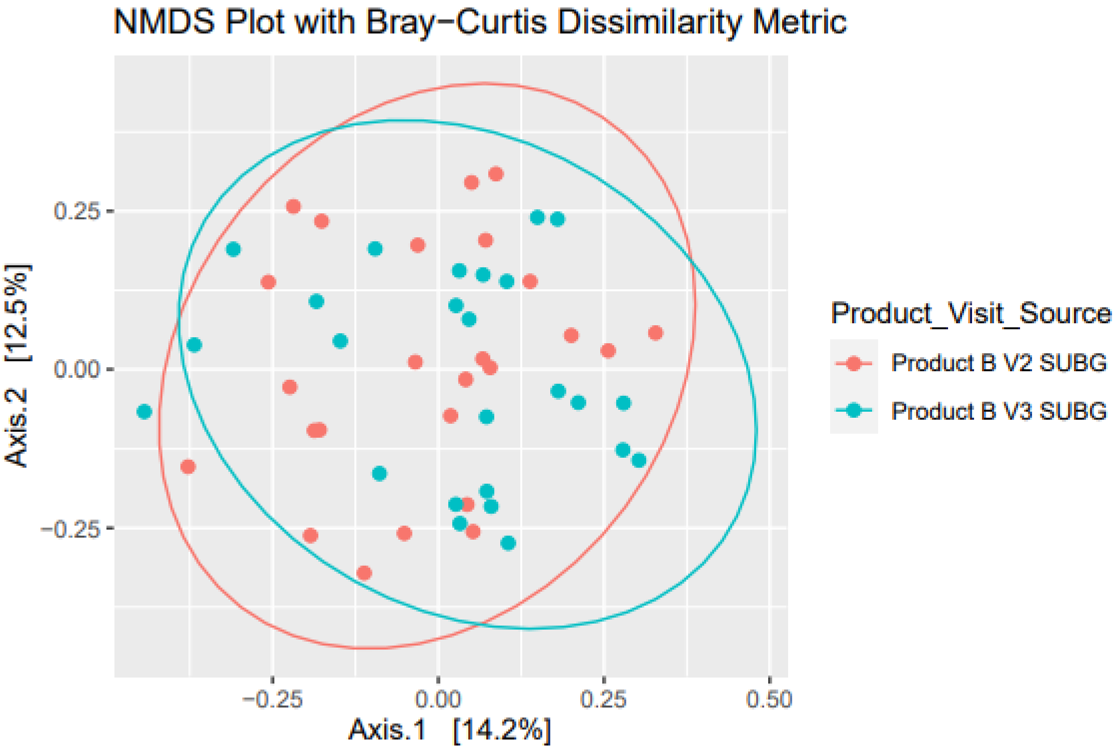


2) Alpha



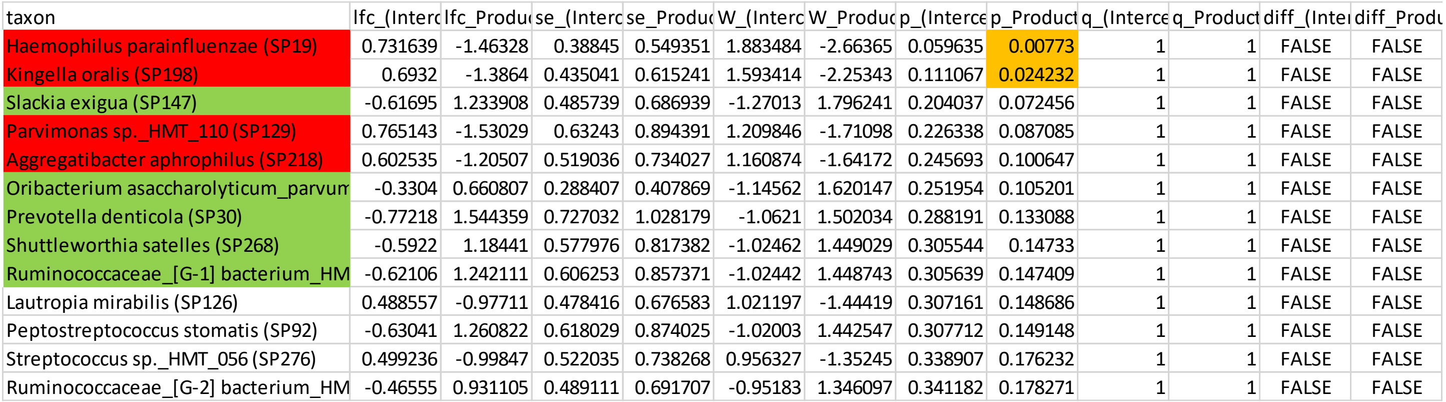
No significant differences

3) Beta diversity



No significant differences

4) Differential abundance

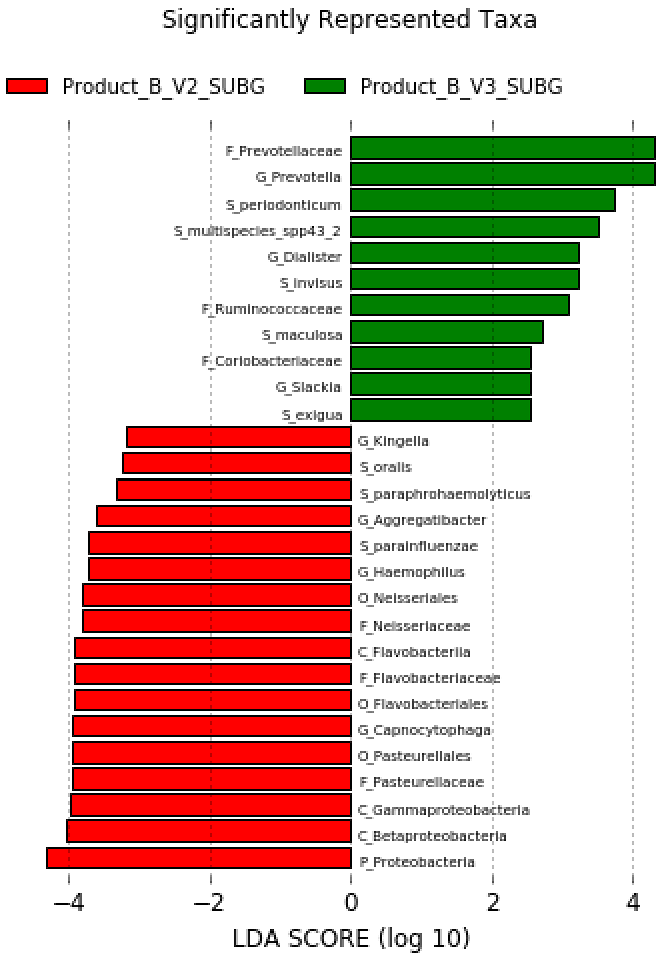


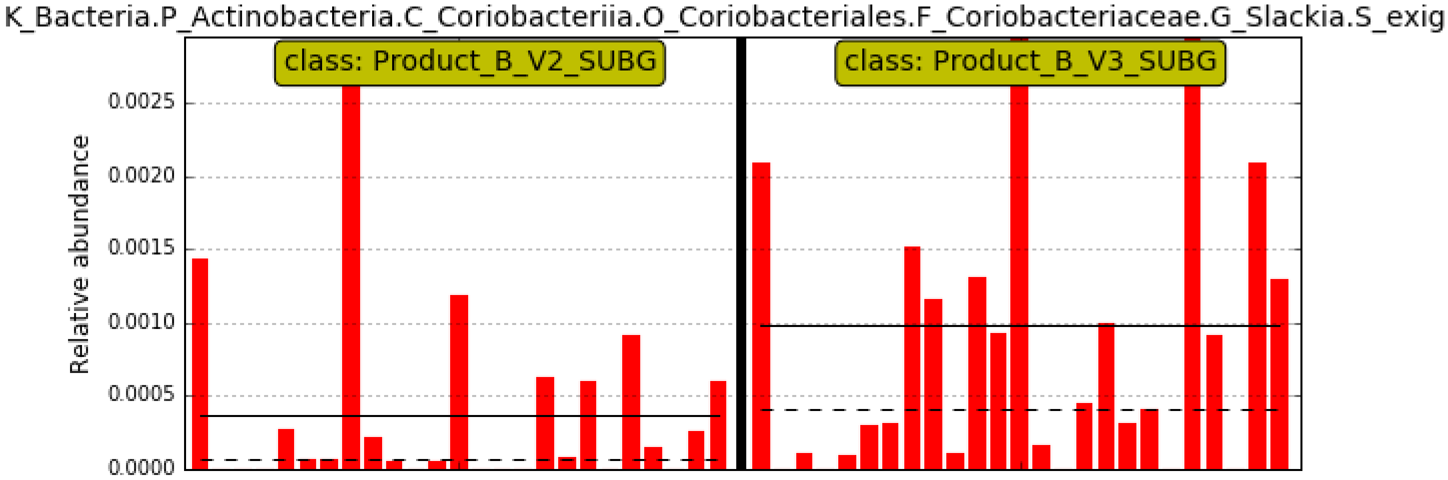
taxon	lfc_(Interc	lfc_Produ	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inte	diff_Produ
Haemophilus parainfluenzae (SP19)	0.731639	-1.46328	0.38845	0.549351	1.883484	-2.66365	0.059635	0.00773	1	1	FALSE	FALSE
Kingella oralis (SP198)	0.6932	-1.3864	0.435041	0.615241	1.593414	-2.25343	0.111067	0.024232	1	1	FALSE	FALSE
Slackia exigua (SP147)	-0.61695	1.233908	0.485739	0.686939	-1.27013	1.796241	0.204037	0.072456	1	1	FALSE	FALSE
Parvimonas sp._HMT_110 (SP129)	0.765143	-1.53029	0.63243	0.894391	1.209846	-1.71098	0.226338	0.087085	1	1	FALSE	FALSE
Aggregatibacter aphrophilus (SP218)	0.602535	-1.20507	0.519036	0.734027	1.160874	-1.64172	0.245693	0.100647	1	1	FALSE	FALSE
Oribacterium asaccharolyticum_parvum	-0.3304	0.660807	0.288407	0.407869	-1.14562	1.620147	0.251954	0.105201	1	1	FALSE	FALSE
Prevotella denticola (SP30)	-0.77218	1.544359	0.727032	1.028179	-1.0621	1.502034	0.288191	0.133088	1	1	FALSE	FALSE
Shuttleworthia satelles (SP268)	-0.5922	1.18441	0.577976	0.817382	-1.02462	1.449029	0.305544	0.14733	1	1	FALSE	FALSE
Ruminococcaceae_[G-1] bacterium_HM	-0.62106	1.242111	0.606253	0.857371	-1.02442	1.448743	0.305639	0.147409	1	1	FALSE	FALSE
Lautropia mirabilis (SP126)	0.488557	-0.97711	0.478416	0.676583	1.021197	-1.44419	0.307161	0.148686	1	1	FALSE	FALSE
Peptostreptococcus stomatis (SP92)	-0.63041	1.260822	0.618029	0.874025	-1.02003	1.442547	0.307712	0.149148	1	1	FALSE	FALSE
Streptococcus sp._HMT_056 (SP276)	0.499236	-0.99847	0.522035	0.738268	0.956327	-1.35245	0.338907	0.176232	1	1	FALSE	FALSE
Ruminococcaceae_[G-2] bacterium_HM	-0.46555	0.931105	0.489111	0.691707	-0.95183	1.346097	0.341182	0.178271	1	1	FALSE	FALSE

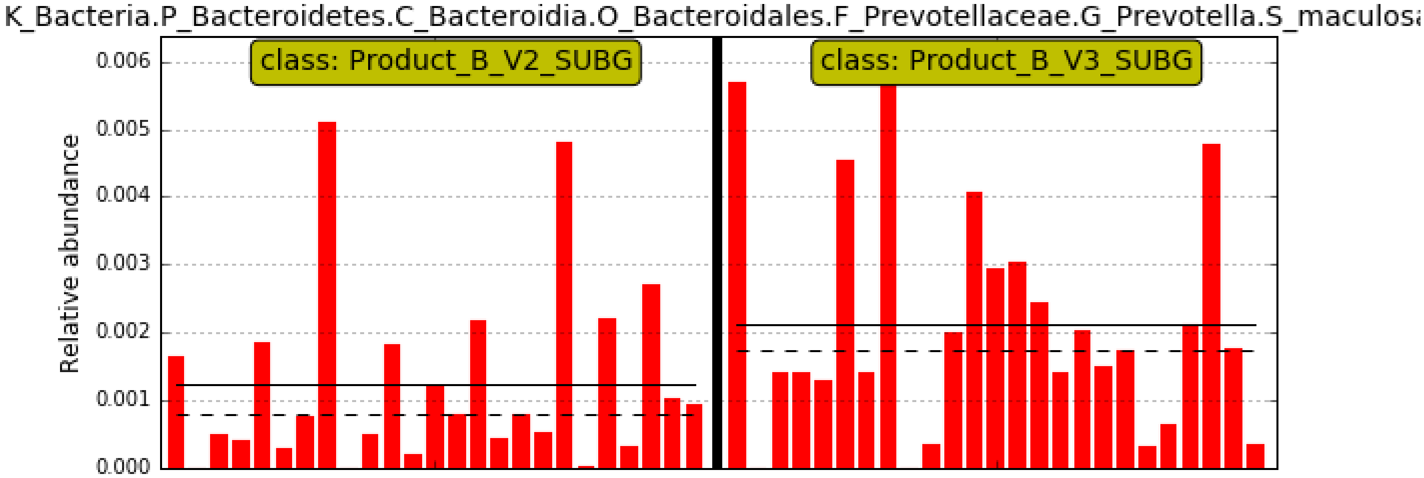
Red, more prevalent in baseline (V2)

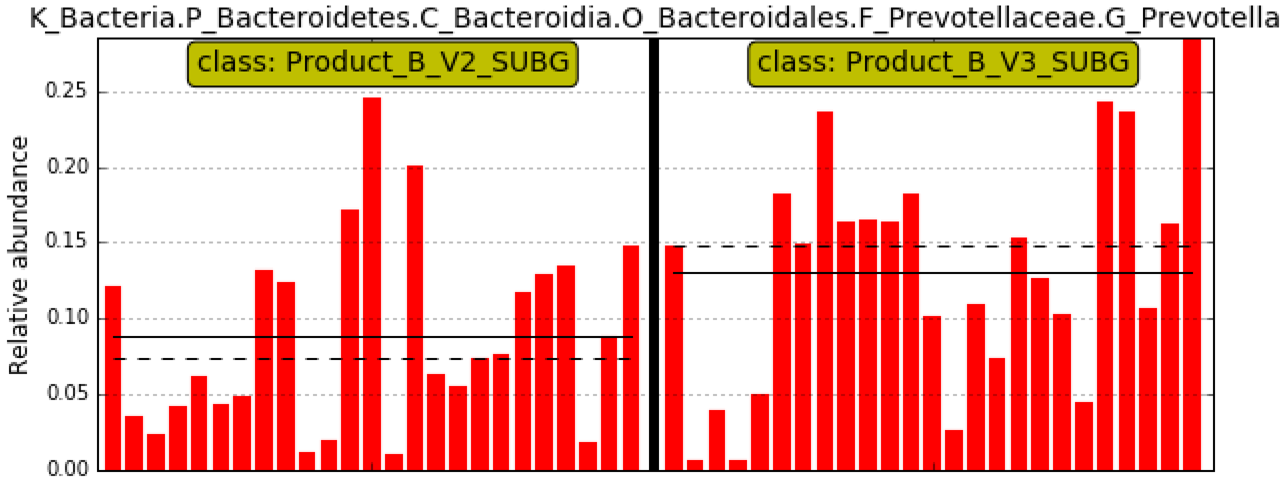
Green, more prevalent in visit 3, after treatment.

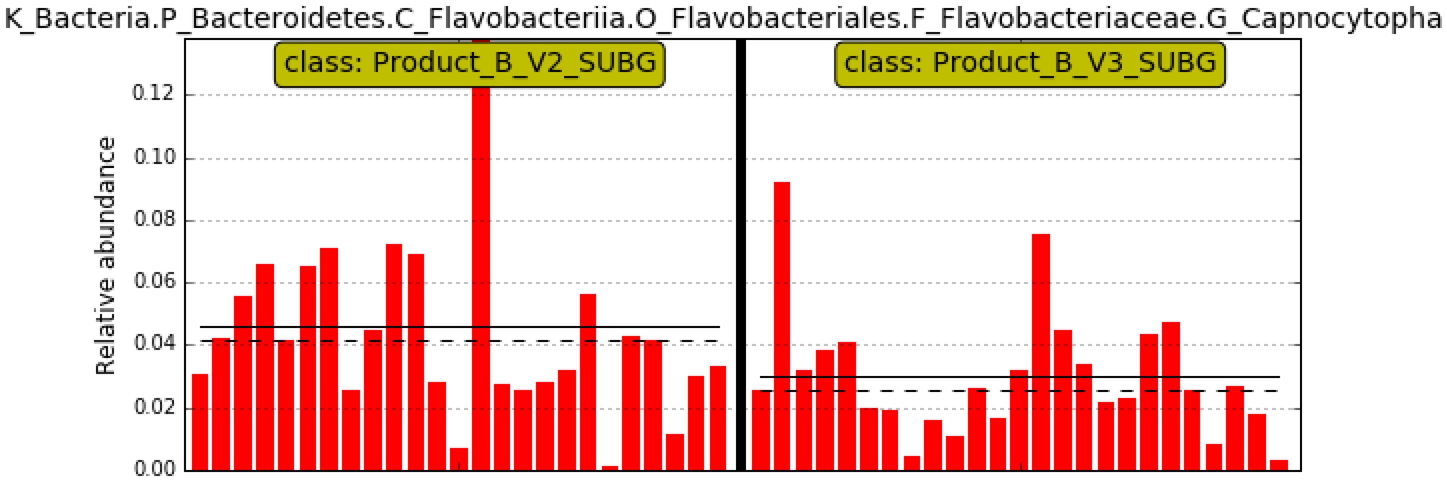
5) Lefse

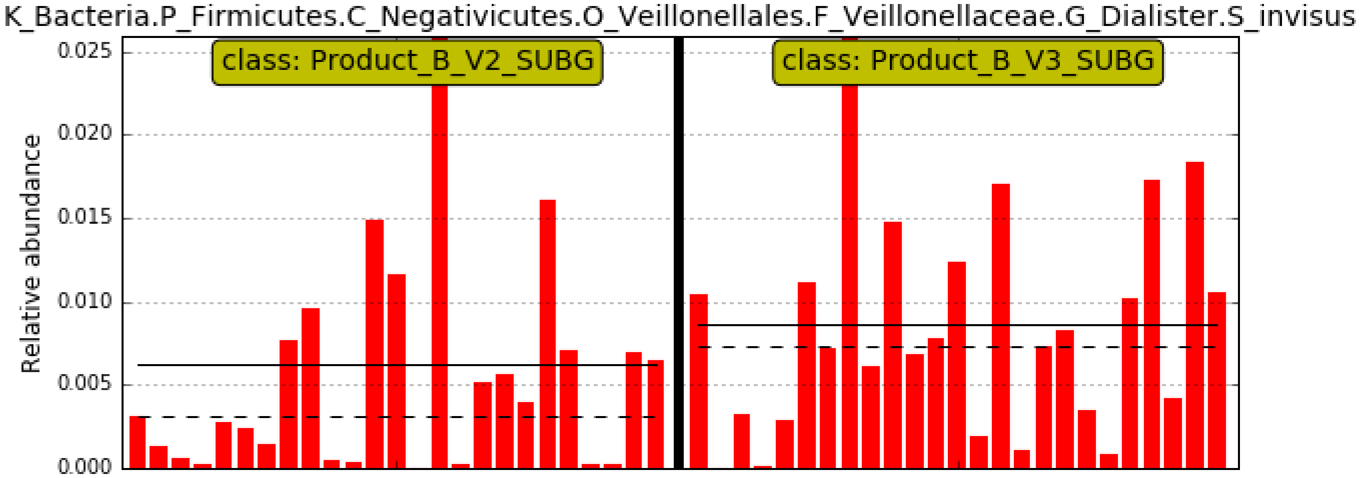

Significantly Represented Taxa
Product_B_V2_SUBG
Product_B_V3_SUBG
F_Prevotellaceae
G_Prevotella
S_periodonticum
S_multispecies_spp43_2
G_Dialister
S_invisus
F_Ruminococcaceae
S_maculosa
F_Coriobacteriaceae
G_Slackia
S_exigua
G_Kingella
S_oralis
S_paraphrohaemolyticus
G_Aggregatibacter
S_parainfluenzae
G_Haemophilus
O_Neisseriales
F_Neisseriaceae
C_Flavobacteriia
F_Flavobacteriaceae
O_Flavobacteriales
G_Capnocytophaga
O_Pasteurellales
F_Pasteurellaceae
C_Gammaproteobacteria
C_Betaproteobacteria
P_Proteobacteria
−4
−2
0
2
4
LDA SCORE (log 10)

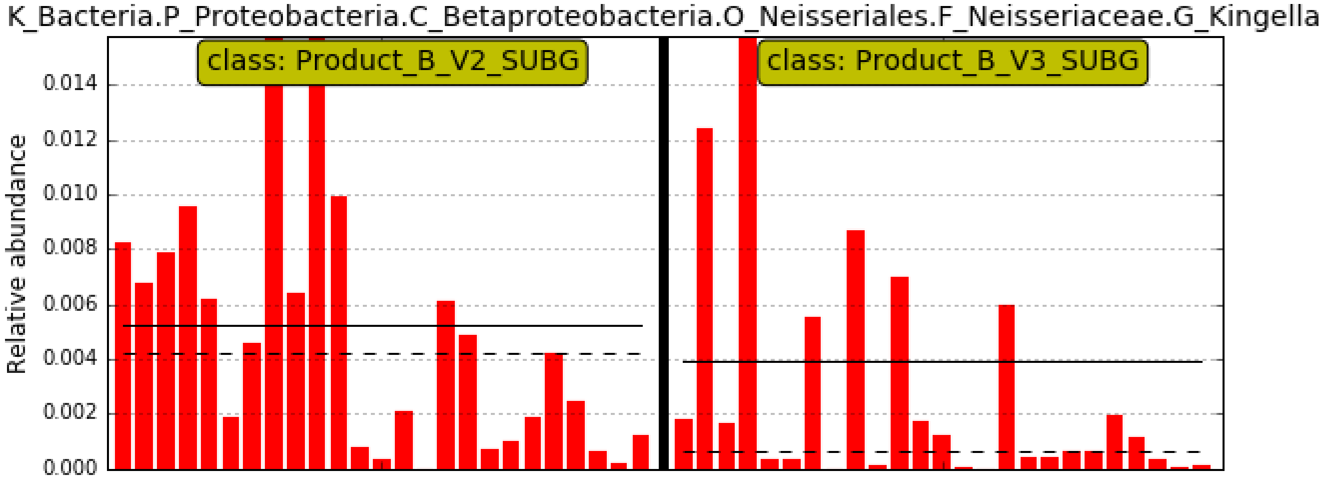

K_Bacteria.P_Actinobacteria.C_Coriobacteriia.O_Coriobacteriales.F_Coriobacteriaceae.G_Slackia.S_exig
class: Product_B_V2_SUBG
class: Product_B_V3_SUBG
Relative abundance
0.0000
0.0005
0.0010
0.0015
0.0020
0.0025

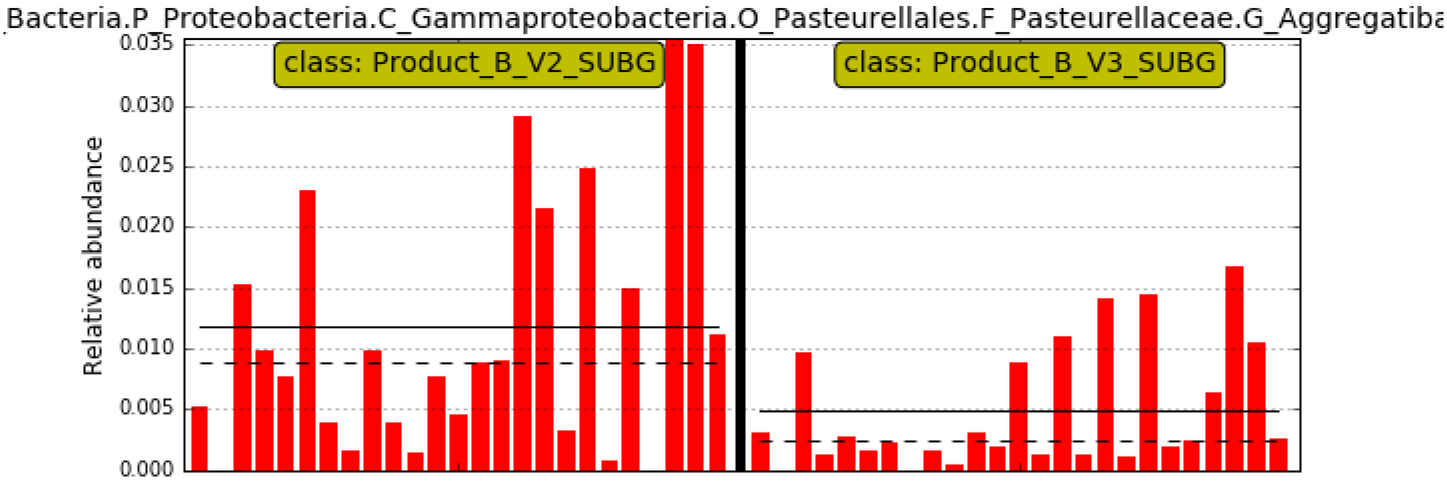

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_maculosa
class: Product_B_V2_SUBG
class: Product_B_V3_SUBG
Relative abundance
0.000
0.001
0.002
0.003
0.004
0.005
0.006

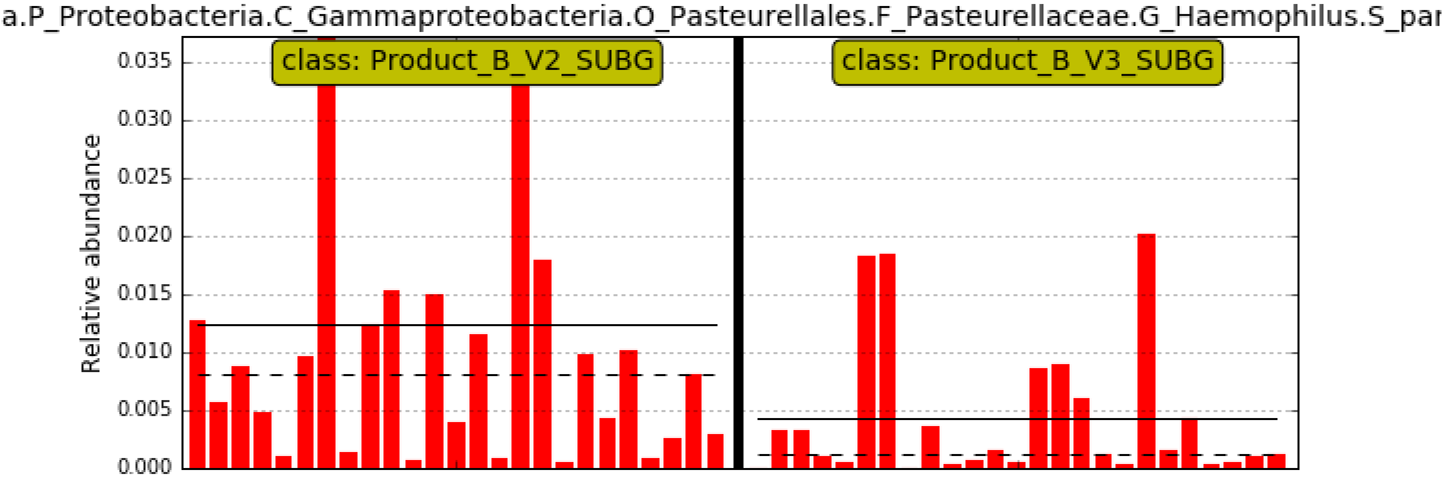

K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella
class: Product_B_V2_SUBG
class: Product_B_V3_SUBG
Relative abundance
0.00
0.05
0.10
0.15
0.20
0.25


K_Bacteria.P_Bacteroidetes.C_Flavobacteriia.O_Flavobacteriales.F_Flavobacteriaceae.G_Capnocytopha
class: Product_B_V2_SUBG
class: Product_B_V3_SUBG
Relative abundance
0.12
0.10
0.08
0.06
0.04
0.02
0.00

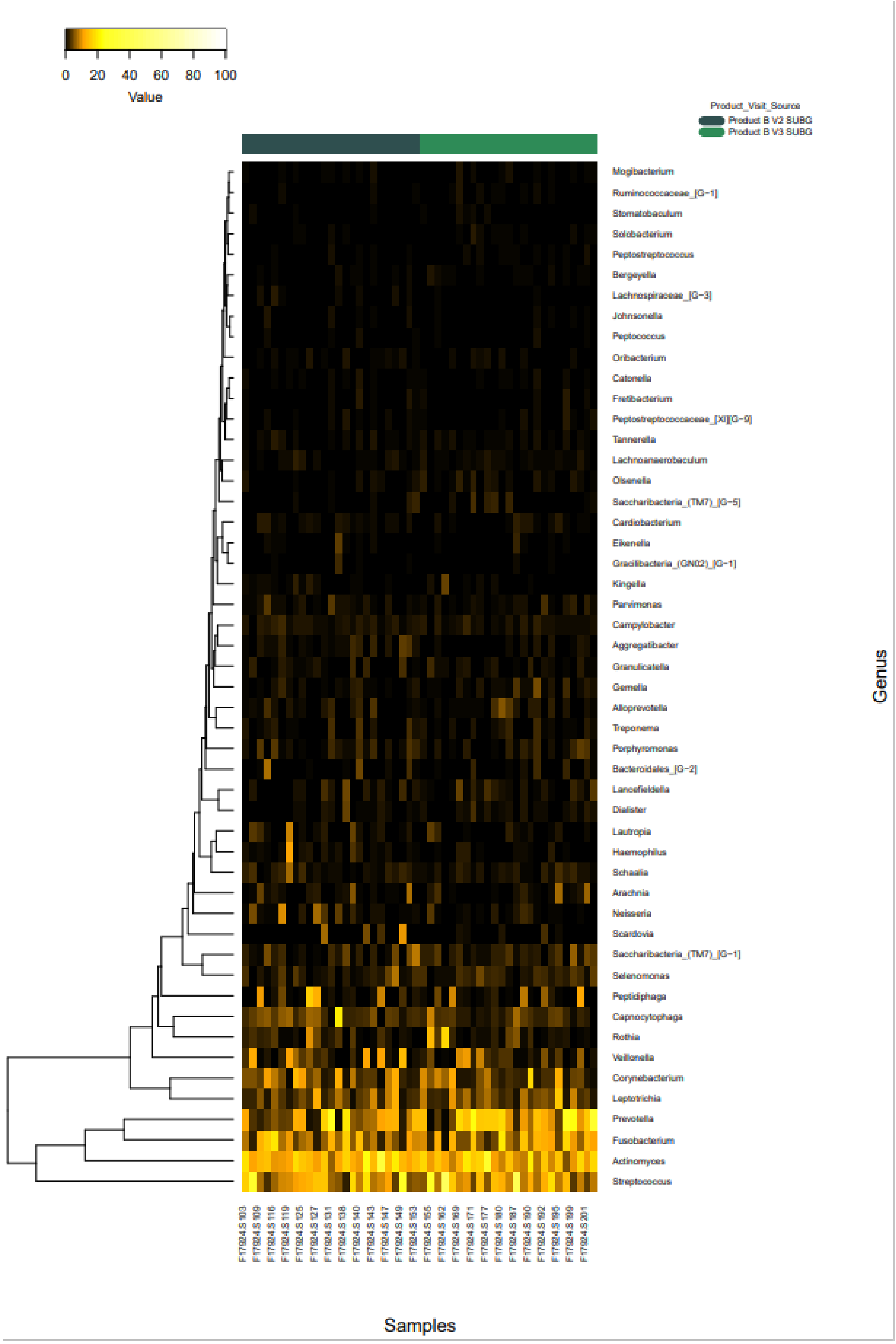

K_Bacteria.P_Firmicutes.C_Negativicutes.O_Veillonellales.F_Veillonellaceae.G_Dialister.S_invisus
class: Product_B_V2_SUBG
class: Product_B_V3_SUBG
Relative abundance
0.025
0.020
0.015
0.010
0.005
0.000


K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Kingella
class: Product_B_V2_SUBG
class: Product_B_V3_SUBG
Relative abundance
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000

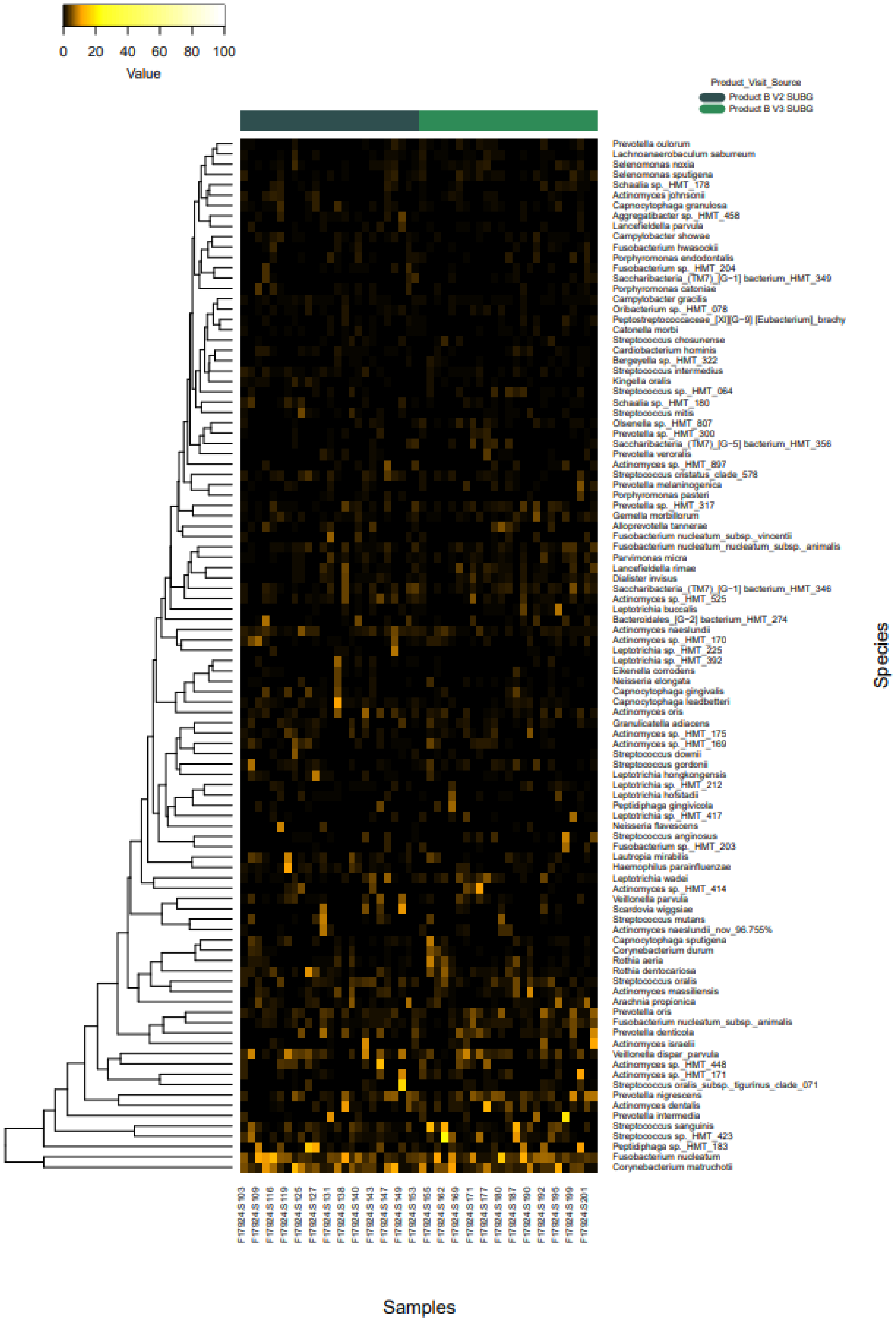

Bacteria.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Aggregatiba
class: Product_B_V2_SUBG
class: Product_B_V3_SUBG
Relative abundance
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000


a.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophilus.S_par
class: Product_B_V2_SUBG
class: Product_B_V3_SUBG
Relative abundance
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000

6) Heat map.

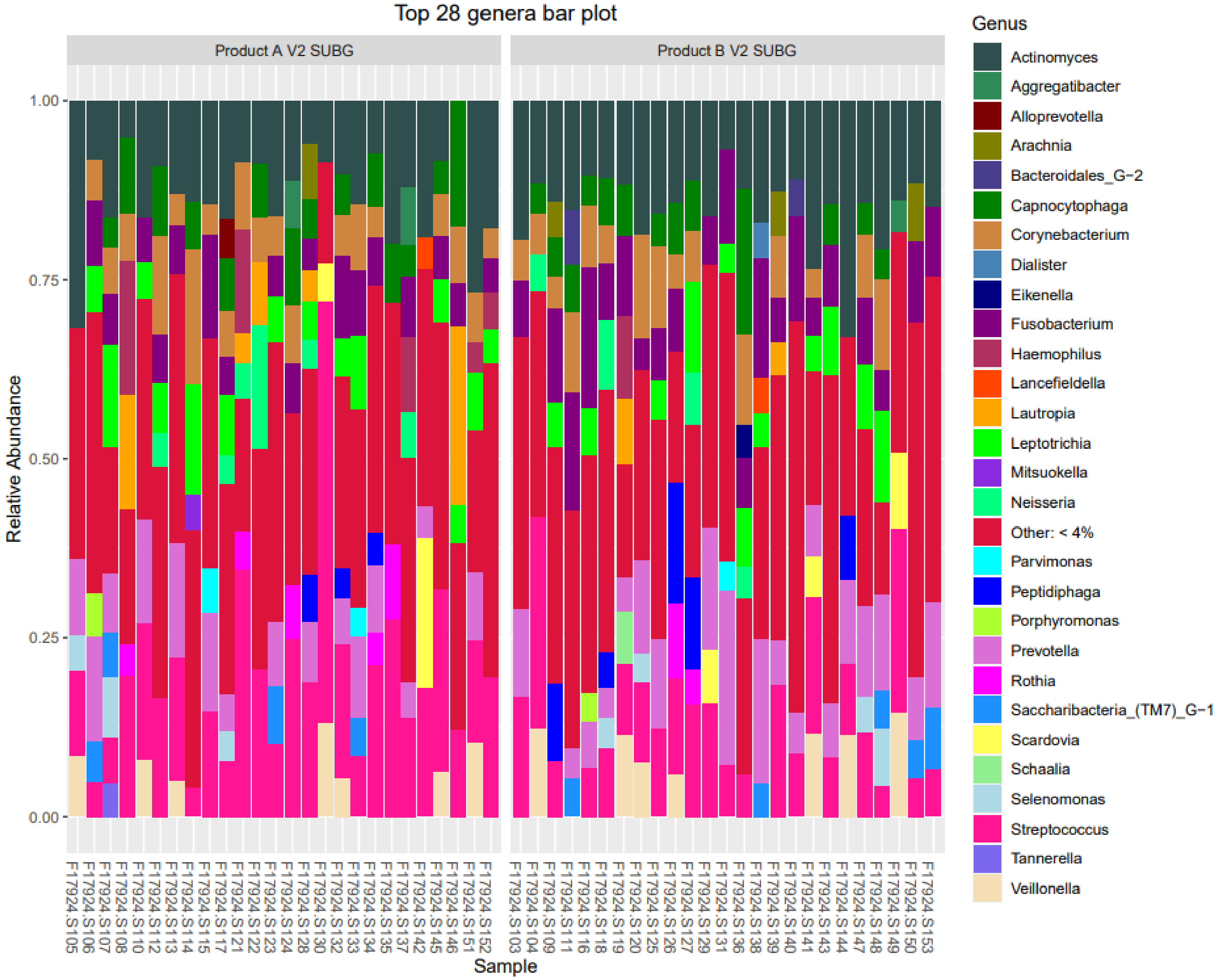


0
20
40
60
80
100
Value
Product_Visit_Source
Product B V2 SUBG
Product B V3 SUBG
Mogibacterium
Ruminococcaceae_[G−1]
Stomatobaculum
Solobacterium
Peptostreptococcus
Bergeyella
Lachnospiraceae_[G−3]
Johnsonella
Peptococcus
Oribacterium
Catonella
Filifactor
Peptostreptococcaceae_[XI][G−9]
Tannerella
Lachnoanaerobaculum
Olsenella
Saccharibacteria_(TM7)_[G−5]
Cardiobacterium
Eikenella
Gracilibacteria_(GN02)_[G−1]
Kingella
Parvimonas
Campylobacter
Aggregatibacter
Granulicatella
Gemella
Alloprevotella
Treponema
Porphyromonas
Bacteroidales_[G−2]
Lancefieldella
Dialister
Lautropia
Haemophilus
Schaalia
Arachnia
Neisseria
Scardovia
Saccharibacteria_(TM7)_[G−1]
Selenomonas
Peptidiphaga
Capnocytophaga
Rothia
Veillonella
Corynebacterium
Leptotrichia
Prevotella
Fusobacterium
Actinomyces
Streptococcus
Genus
F17924 S 103
F17924 S 109
F17924 S 116
F17924 S 119
F17924 S 125
F17924 S 127
F17924 S 131
F17924 S 138
F17924 S 140
F17924 S 143
F17924 S 147
F17924 S 149
F17924 S 153
F17924 S 155
F17924 S 162
F17924 S 169
F17924 S 171
F17924 S 177
F17924 S 180
F17924 S 187
F17924 S 190
F17924 S 192
F17924 S 195
F17924 S 199
F17924 S 201
Samples

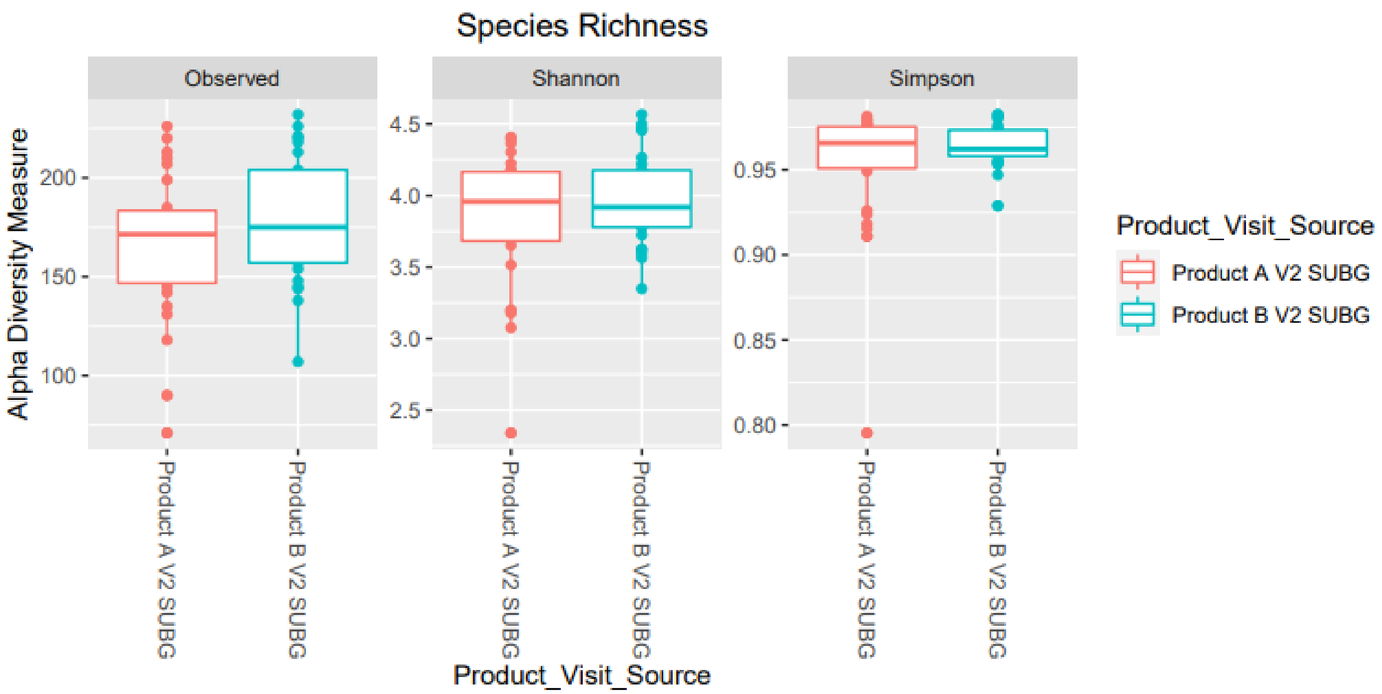

0
20
40
60
80
100
Value
Product_Visit_Source
Product B V2 SUBG
Product B V3 SUBG
Prevotella oulorum
Lachnoanaerobaculum saburreum
Selenomonas noxia
Selenomonas sputigena
Schaalia sp._HMT_178
Actinomyces johnsonii
Capnocytophaga granulosa
Aggregatibacter sp._HMT_458
Lancefieldella parvula
Campylobacter showae
Fusobacterium hwasookii
Porphyromonas endodontalis
Fusobacterium sp._HMT_204
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_349
Porphyromonas catoniae
Campylobacter gracilis
Oribacterium sp._HMT_078
Peptostreptococcaceae_[XI][G-9] [Eubacterium]_brachy
Catonella morbi
Streptococcus cheosunense
Cardiobacterium hominis
Bergeyella sp._HMT_322
Streptococcus intermedius
Kingella oralis
Streptococcus sp._HMT_064
Schaalia sp._HMT_180
Streptococcus mitis
Olsenella sp._HMT_807
Prevotella sp._HMT_300
Saccharibacteria_(TM7)_[G-5] bacterium_HMT_356
Prevotella veroralis
Actinomyces sp._HMT_897
Streptococcus cristatus_clade_578
Prevotella melaninogenica
Porphyromonas pasteri
Prevotella sp._HMT_317
Gemella morbillorum
Alloprevotella tannerae
Fusobacterium nucleatum_subsp._vincentii
Fusobacterium nucleatum_nucleatum_subsp._animalis
Parvimonas micra
Lancefieldella rimae
Dialister invisus
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346
Actinomyces sp._HMT_525
Leptotrichia buccalis
Bacteroidales_[G-2] bacterium_HMT_274
Actinomyces naeslundii
Actinomyces sp._HMT_170
Leptotrichia sp._HMT_225
Leptotrichia sp._HMT_392
Eikenella corrodens
Neisseria elongata
Capnocytophaga gingivalis
Capnocytophaga leadbetteri
Actinomyces oris
Granulicatella adiacens
Actinomyces sp._HMT_175
Actinomyces sp._HMT_169
Streptococcus downii
Streptococcus gordonii
Leptotrichia hongkongensis
Leptotrichia sp._HMT_212
Leptotrichia hofstadii
Peptidiphaga gingivicola
Leptotrichia sp._HMT_417
Neisseria flavescens
Streptococcus anginosus
Fusobacterium sp._HMT_203
Lautropia mirabilis
Haemophilus parainfluenzae
Leptotrichia wadei
Actinomyces sp._HMT_414
Veillonella parvula
Scardovia wiggsiae
Streptococcus mutans
Actinomyces naeslundii_nov_98.755%
Capnocytophaga sputigena
Corynebacterium durum
Rothia aeria
Rothia dentocariosa
Streptococcus oralis
Actinomyces massiliensis
Arachnia propionica
Prevotella oris
Fusobacterium nucleatum_subsp._animalis
Prevotella denticola
Actinomyces israelii
Veillonella dispar_parvula
Actinomyces sp._HMT_448
Actinomyces sp._HMT_171
Streptococcus oralis_subsp._tigurinus_clade_071
Prevotella nigrescens
Actinomyces dentalis
Prevotella intermedia
Streptococcus sanguinis
Streptococcus sp._HMT_423
Peptidiphaga sp._HMT_183
Fusobacterium nucleatum
Corynebacterium matruchotii
Species
F17924-S103
F17924-S109
F17924-S116
F17924-S119
F17924-S125
F17924-S127
F17924-S131
F17924-S138
F17924-S140
F17924-S143
F17924-S147
F17924-S149
F17924-S153
F17924-S155
F17924-S162
F17924-S169
F17924-S171
F17924-S177
F17924-S180
F17924-S187
F17924-S190
F17924-S192
F17924-S195
F17924-S199
F17924-S201
Samples

Comparison 19. Product A V2 SUBG vs Product B V2 SUBG

1) Taxonomy bar graphs

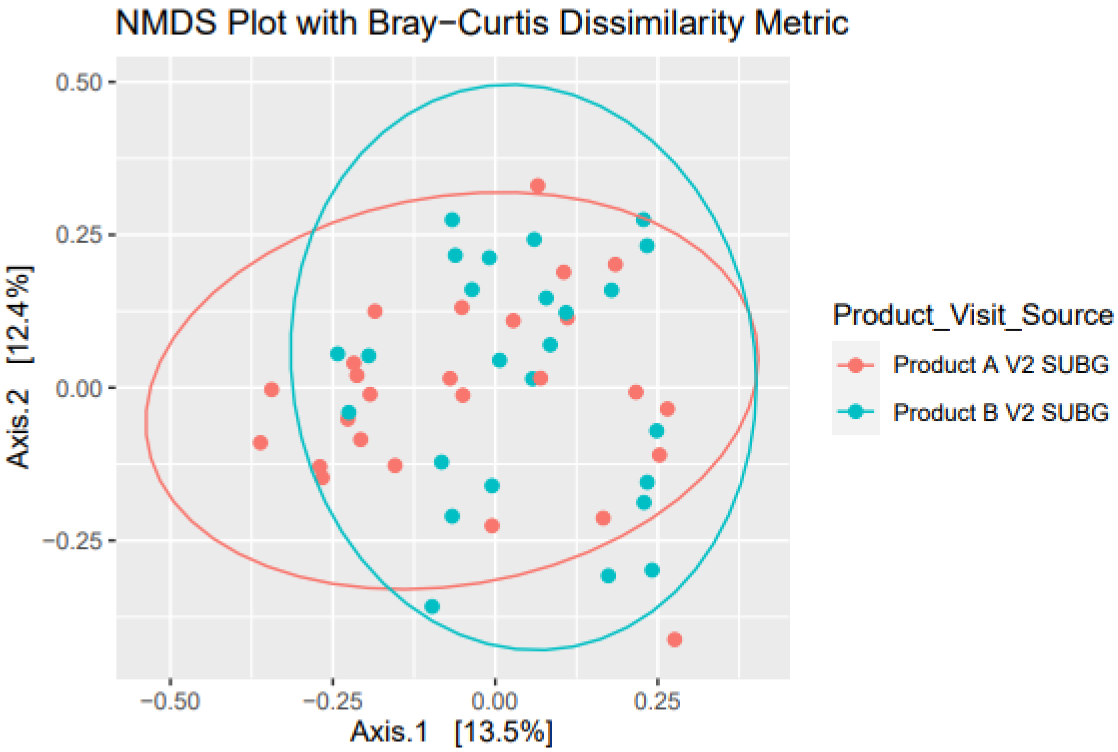


2) Alpha



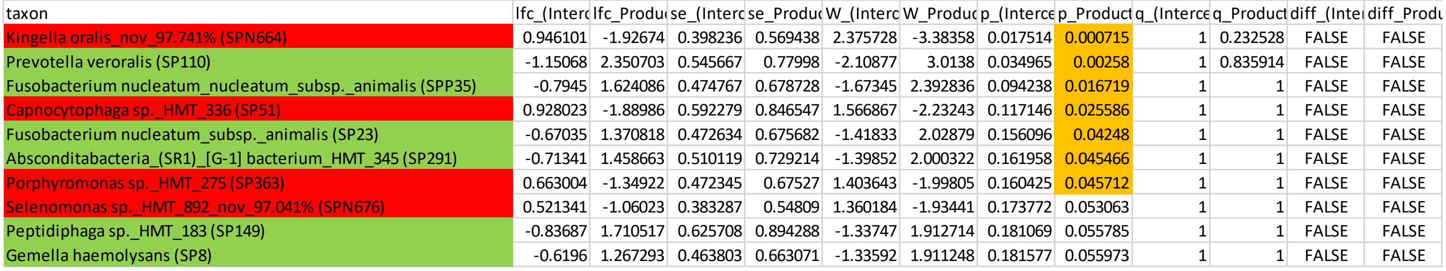
No significant differences

3) Beta diversity



No significant differences

4) Differential abundance

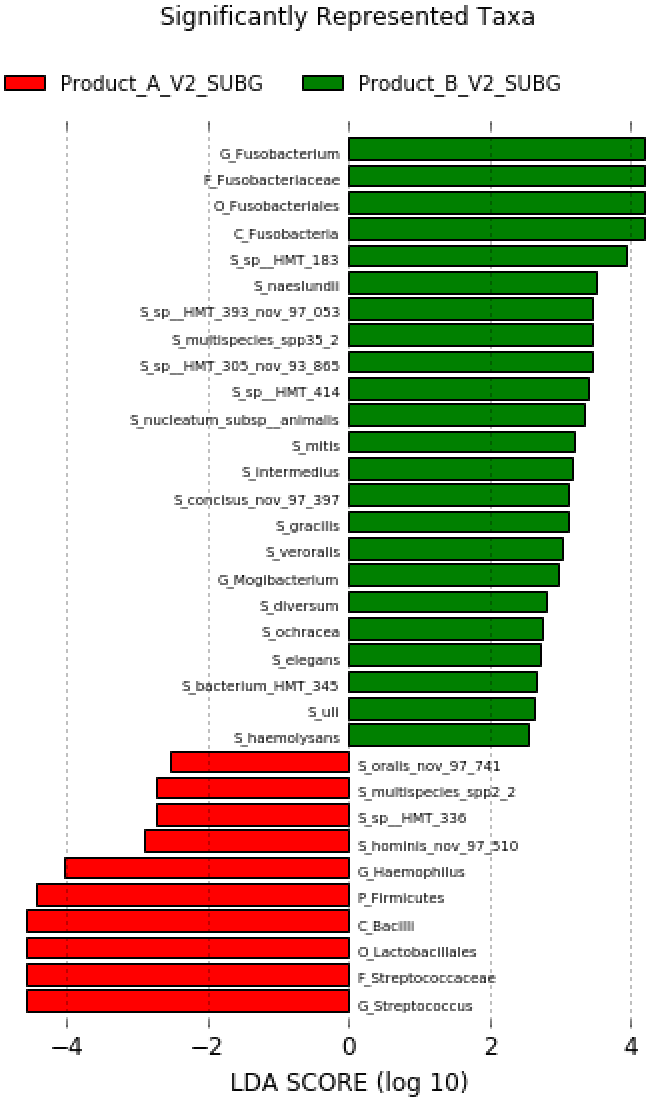


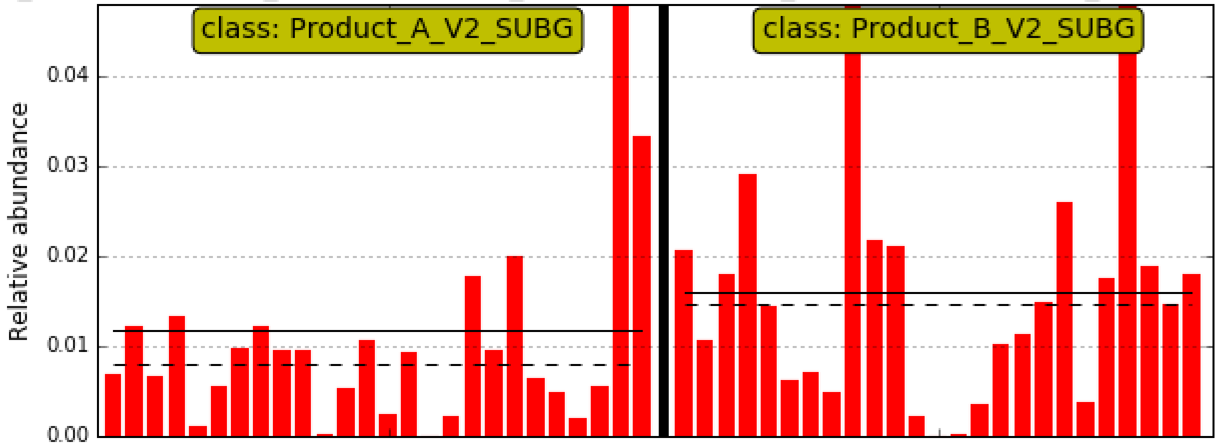
taxon	lfc_(Interc	lfc_Produ	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inte	diff_Produ
Kingella oralis_nov_97.741% (SPN664)	0.946101	-1.92674	0.398236	0.569438	2.375728	-3.38358	0.017514	0.000715	1	0.232528	FALSE	FALSE
Prevotella veroralis (SP110)	-1.15068	2.350703	0.545667	0.77998	-2.10877	3.0138	0.034965	0.00258	1	0.835914	FALSE	FALSE
Fusobacterium nucleatum_nucleatum_subsp._animalis (SPP35)	-0.7945	1.624086	0.474767	0.678728	-1.67345	2.392836	0.094238	0.016719	1	1	FALSE	FALSE
Capnocytophaga sp._HMT_336 (SP51)	0.928023	-1.88986	0.592279	0.846547	1.566867	-2.23243	0.117146	0.025586	1	1	FALSE	FALSE
Fusobacterium nucleatum_subsp._animalis (SP23)	-0.67035	1.370818	0.472634	0.675682	-1.41833	2.02879	0.156096	0.04248	1	1	FALSE	FALSE
Absconditabacteria_(SR1)_[G-1] bacterium_HMT_345 (SP291)	-0.71341	1.458663	0.510119	0.729214	-1.39852	2.000322	0.161958	0.045466	1	1	FALSE	FALSE
Porphyromonas sp._HMT_275 (SP363)	0.663004	-1.34922	0.472345	0.67527	1.403643	-1.99805	0.160425	0.045712	1	1	FALSE	FALSE
Selenomonas sp._HMT_892_nov_97.041% (SPN676)	0.521341	-1.06023	0.383287	0.54809	1.360184	-1.93441	0.173772	0.053063	1	1	FALSE	FALSE
Peptidiphaga sp._HMT_183 (SP149)	-0.83687	1.710517	0.625708	0.894288	-1.33747	1.912714	0.181069	0.055785	1	1	FALSE	FALSE
Gemella haemolysans (SP8)	-0.6196	1.267293	0.463803	0.663071	-1.33592	1.911248	0.181577	0.055973	1	1	FALSE	FALSE

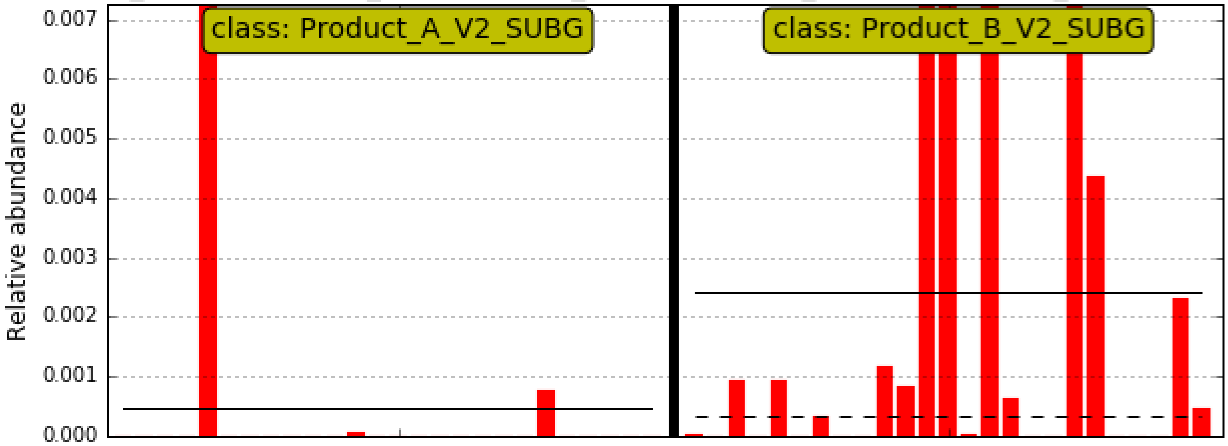
Red more prevalent in A

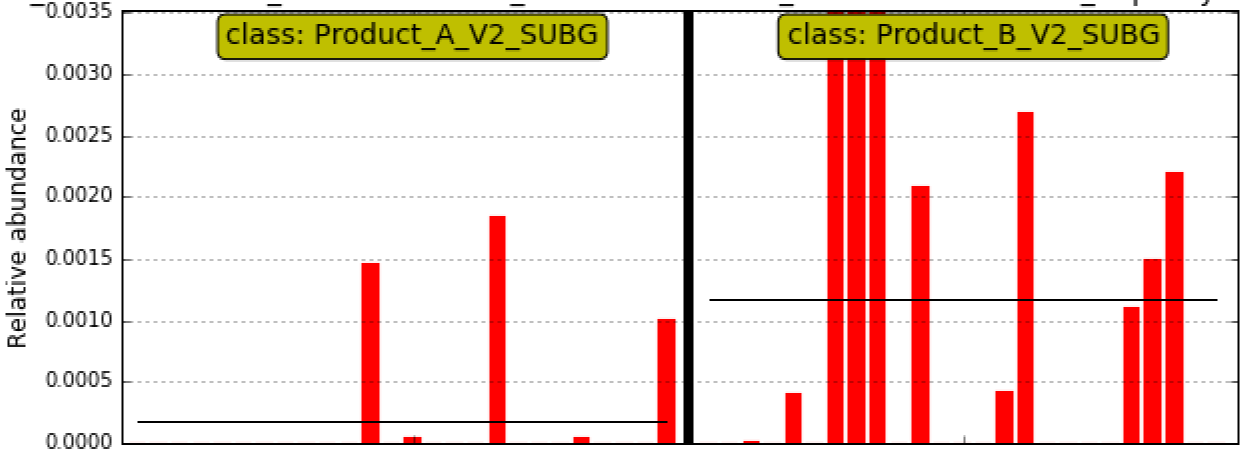
Green, more prevalent in B

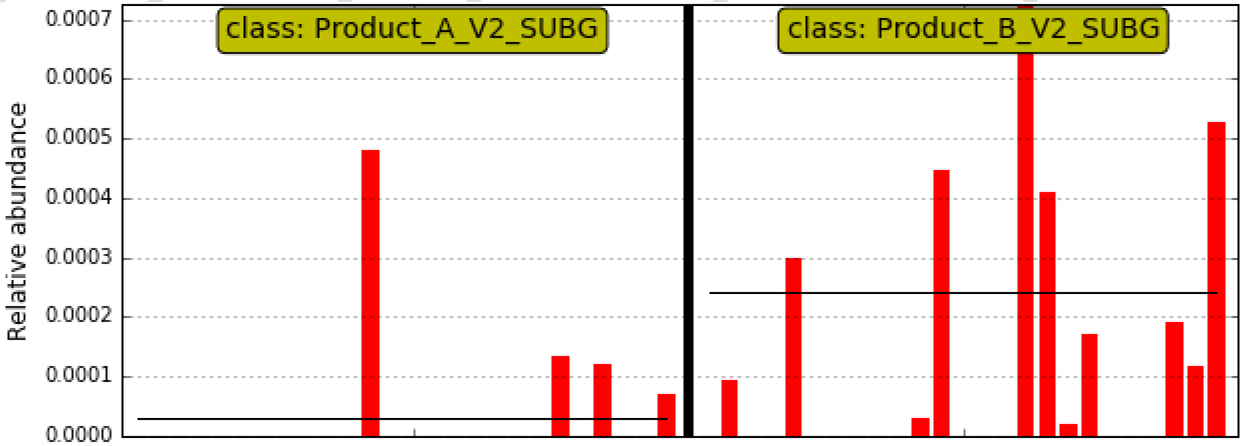
5) Lefse


Significantly Represented Taxa
🟥 Product_A_V2_SUBG
🟩 Product_B_V2_SUBG
G_Fusobacterium
F_Fusobacteriaceae
O_Fusobacteriales
C_Fusobacteria
S_sp__HMT_183
S_naeslundii
S_sp__HMT_393_nov_97_053
S_multispecies_spp35_2
S_sp__HMT_305_nov_93_865
S_sp__HMT_414
S_nucleatum_subsp__animalis
S_mitis
S_intermedius
S_concisus_nov_97_397
S_gracilis
S_veroralis
G_Mogibacterium
S_diversum
S_ochracea
S_elegans
S_bacterium_HMT_345
S_uli
S_haemolysans
S_oralis_nov_97_741
S_multispecies_spp2_2
S_sp__HMT_336
S_hominis_nov_97_510
G_Haemophilus
P_Firmicutes
C_Bacilli
O_Lactobacillales
F_Streptococcaceae
G_Streptococcus
−4
−2
0
2
4
LDA SCORE (log 10)

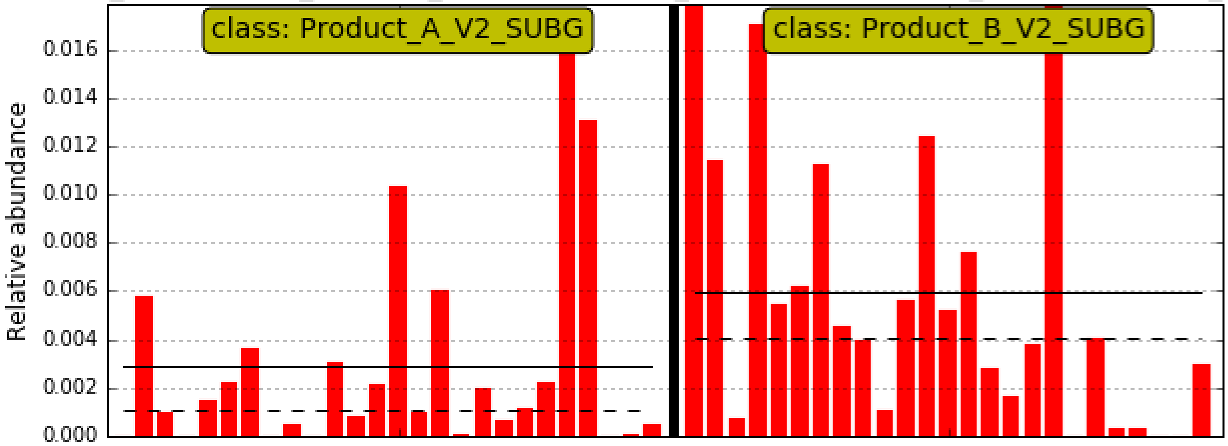

cteria.P_Actinobacteria.C_Actinomycetia.O_Actinomycetales.F_Actinomycetaceae.G_Actinomyces.S_na


K_Bacteria.P_Bacteroidetes.C_Bacteroidia.O_Bacteroidales.F_Prevotellaceae.G_Prevotella.S_veroralis

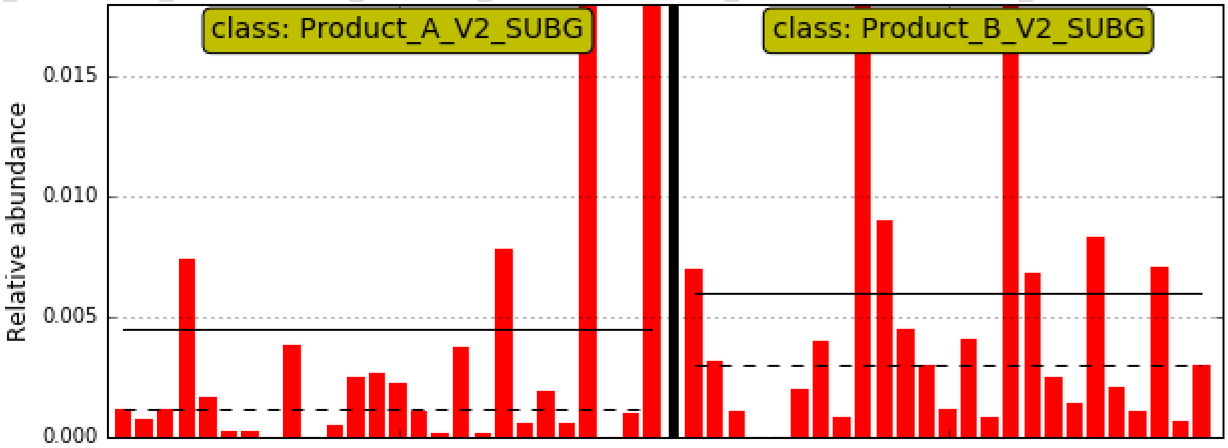

teria.P_Bacteroidetes.C_Flavobacteriia.O_Flavobacteriales.F_Flavobacteriaceae.G_Capnocytophaga.S_c



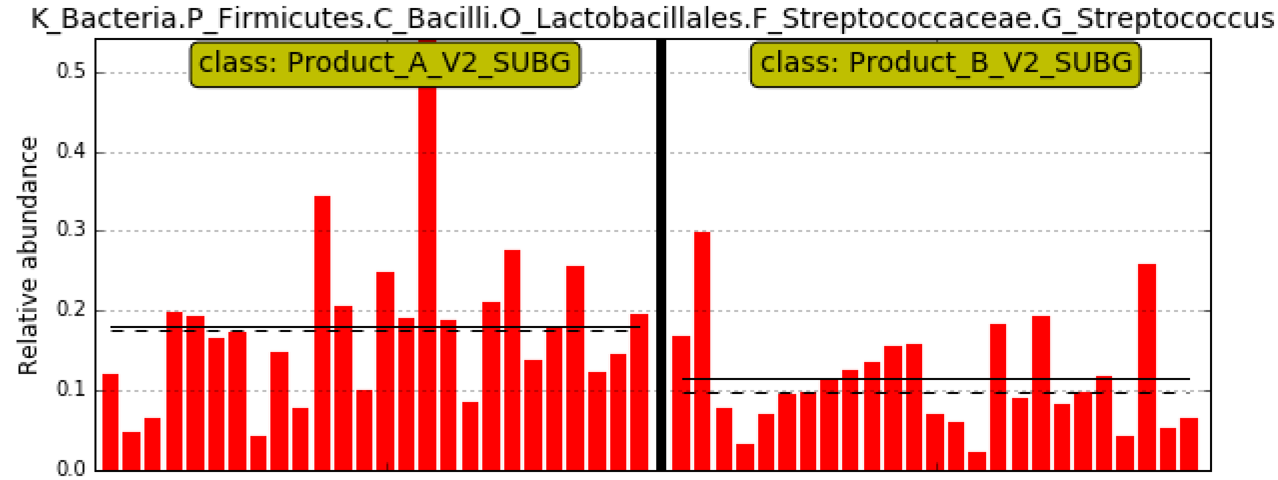
K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Carnobacteriaceae.G_Granulicatella.S_elegans

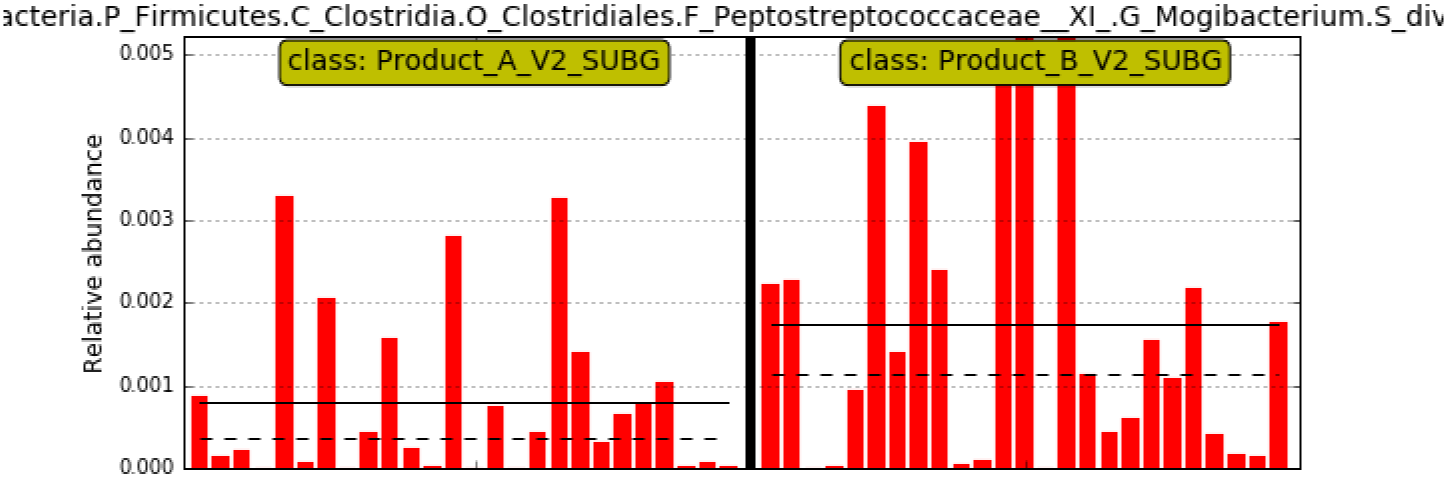


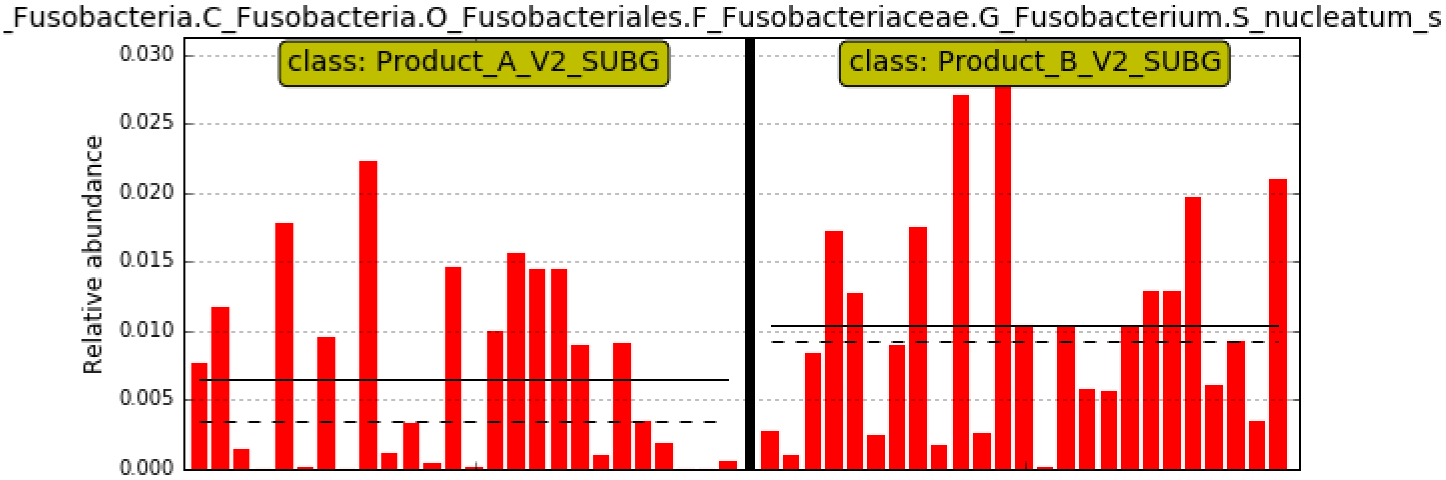
K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_intermediu

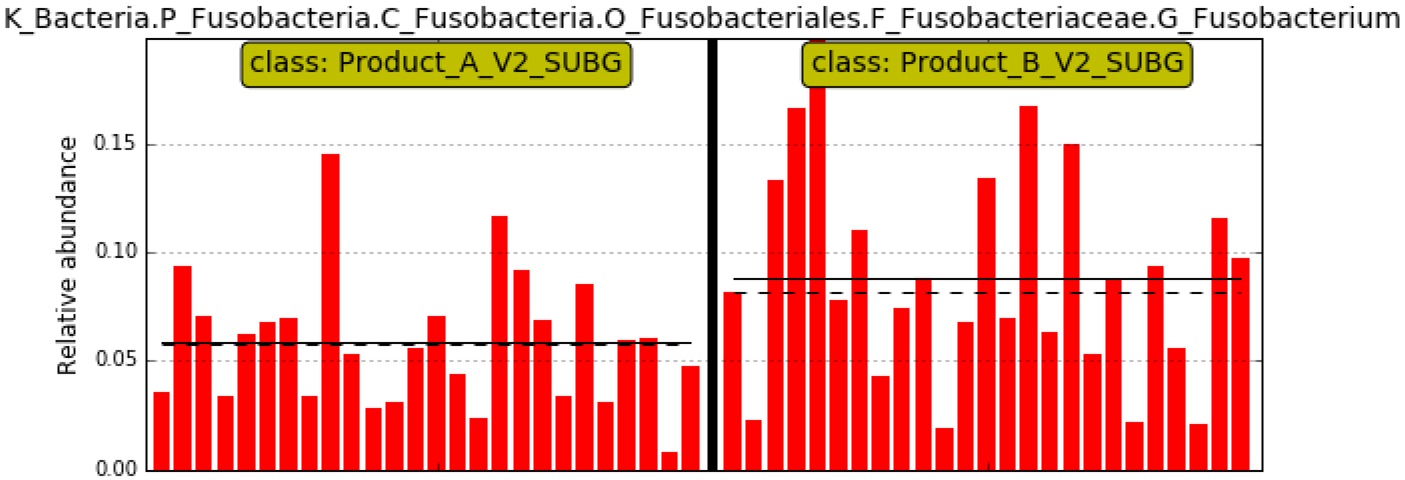


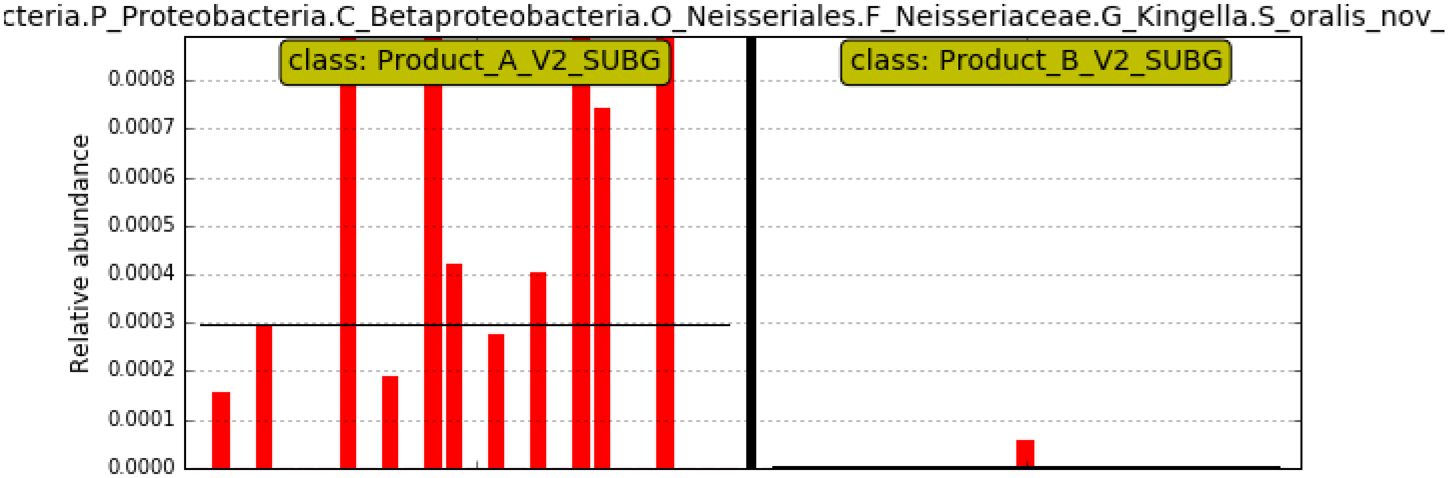
K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_mitis

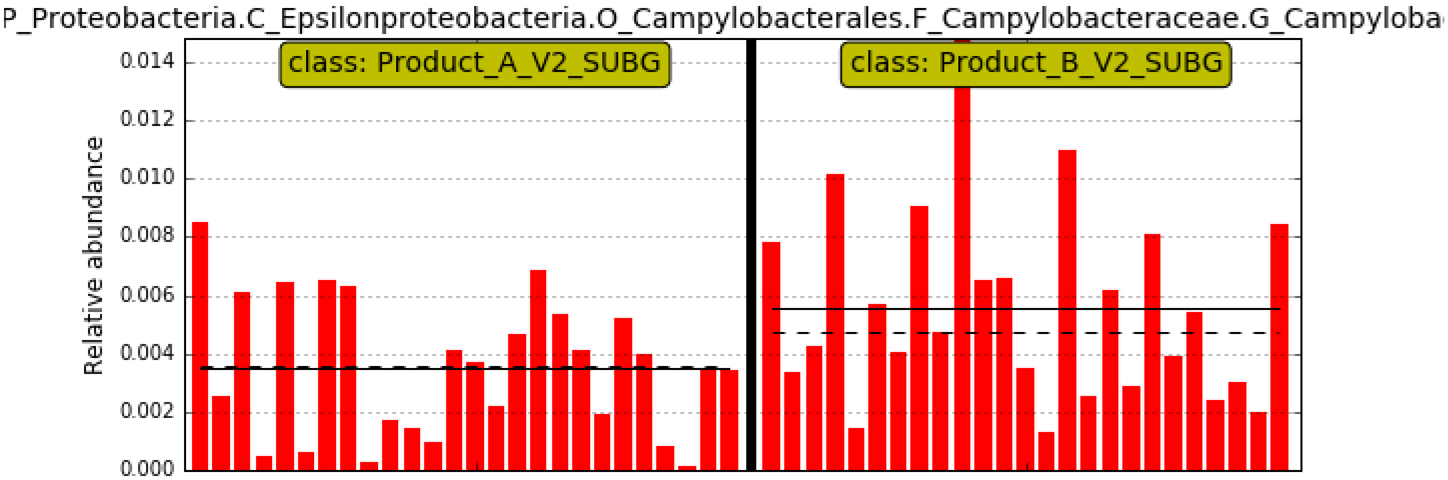

K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus

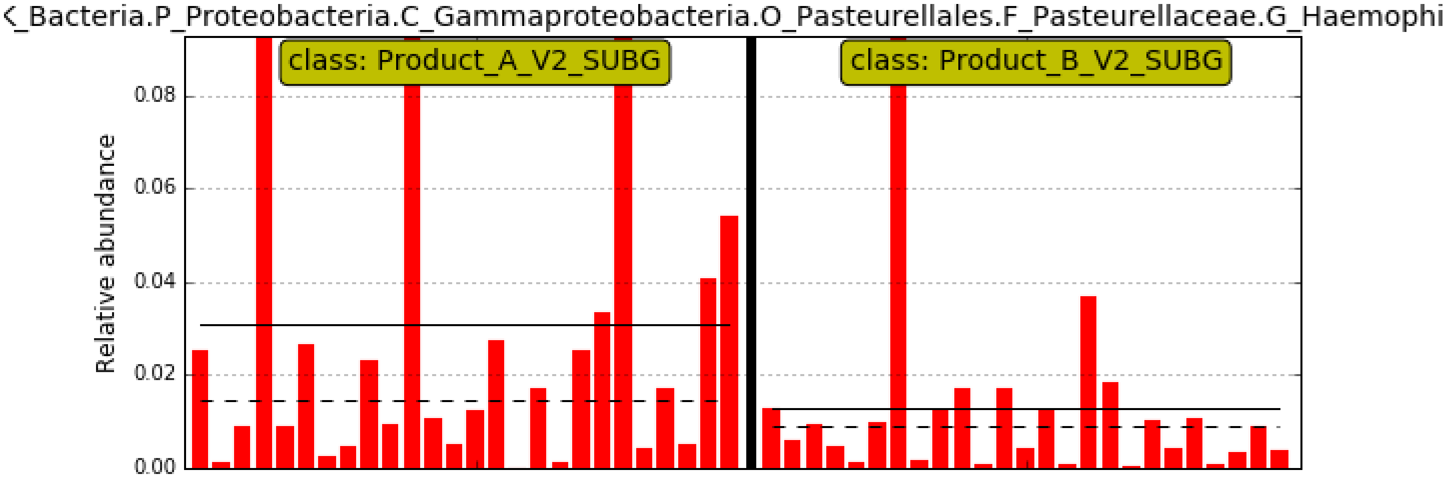

acteria.P_Firmicutes.C_Clostridia.O_Clostridiales.F_Peptostreptococcaceae__XI_.G_Mogibacterium.S_div


_Fusobacteria.C_Fusobacteria.O_Fusobacteriales.F_Fusobacteriaceae.G_Fusobacterium.S_nucleatum_s

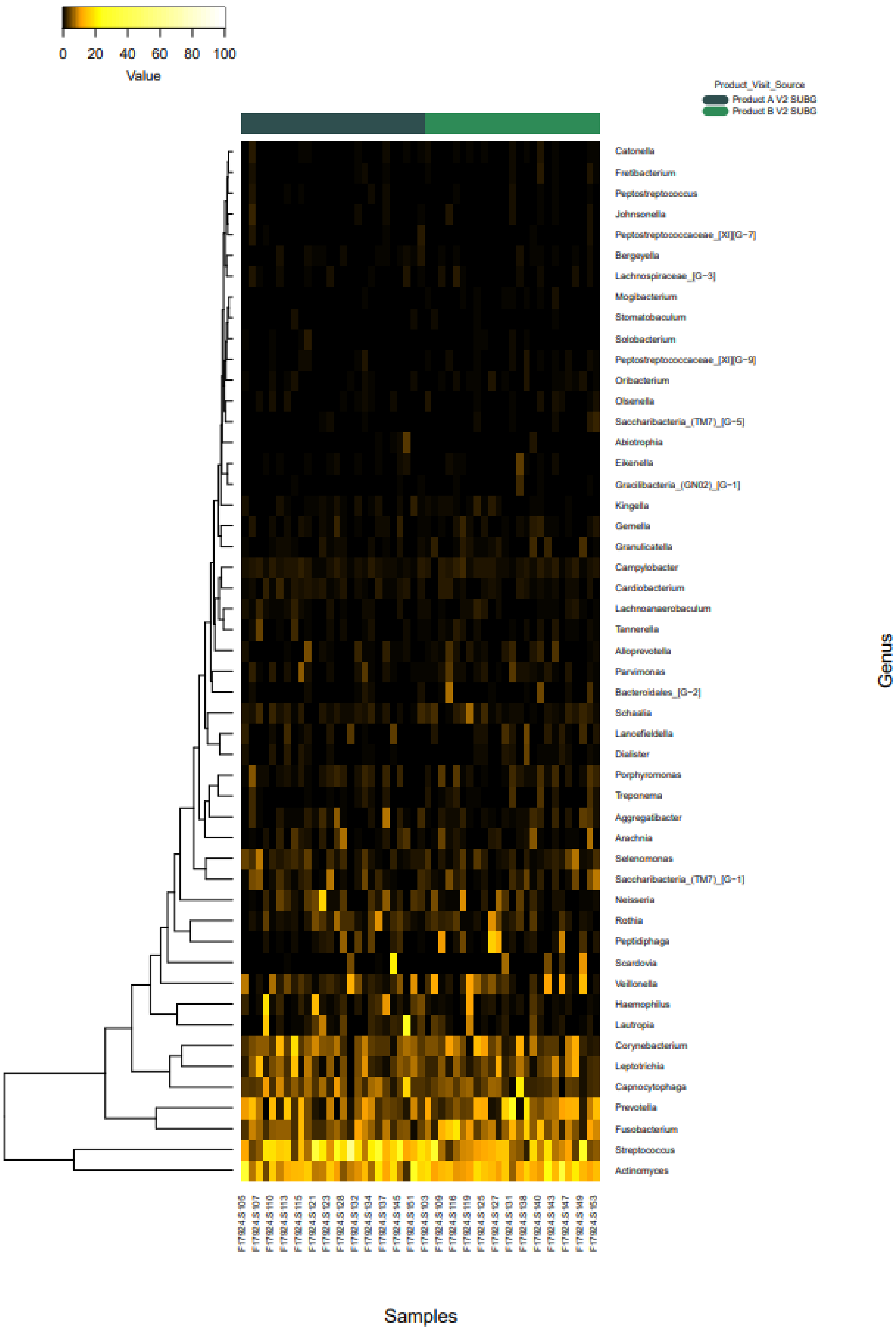

K_Bacteria.P_Fusobacteria.C_Fusobacteria.O_Fusobacteriales.F_Fusobacteriaceae.G_Fusobacterium
class: Product_A_V2_SUBG
class: Product_B_V2_SUBG
Relative abundance
0.15
0.10
0.05
0.00


cteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Kingella.S_oralis_nov_
class: Product_A_V2_SUBG
class: Product_B_V2_SUBG
Relative abundance
0.0008
0.0007
0.0006
0.0005
0.0004
0.0003
0.0002
0.0001
0.0000


P_Proteobacteria.C_Epsilonproteobacteria.O_Campylobacterales.F_Campylobacteraceae.G_Campyloba
class: Product_A_V2_SUBG
class: Product_B_V2_SUBG
Relative abundance
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000


_Bacteria.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophi
class: Product_A_V2_SUBG
class: Product_B_V2_SUBG
Relative abundance
0.08
0.06
0.04
0.02
0.00

6) Heat map.


0
20
40
60
80
100
Value
Product_Visit_Source
Product A V2 SUBG
Product B V2 SUBG
Catonella
Fretibacterium
Peptostreptococcus
Johnsonella
Peptostreptococcaceae_[XI][G-7]
Bergeyella
Lachnospiraceae_[G-3]
Mogibacterium
Stomatobaculum
Solobacterium
Peptostreptococcaceae_[XI][G-9]
Oribacterium
Olsenella
Saccharibacteria_(TM7)_[G-5]
Abiotrophia
Eikenella
Gracilibacteria_(GN02)_[G-1]
Kingella
Gemella
Granulicatella
Campylobacter
Cardiobacterium
Lachnoanaerobaculum
Tannerella
Alloprevotella
Parvimonas
Bacteroidales_[G-2]
Schaalia
Lancefieldella
Dialister
Porphyromonas
Treponema
Aggregatibacter
Arachnia
Selenomonas
Saccharibacteria_(TM7)_[G-1]
Neisseria
Rothia
Peptidiphaga
Scardovia
Veillonella
Haemophilus
Lautropia
Corynebacterium
Leptotrichia
Capnocytophaga
Prevotella
Fusobacterium
Streptococcus
Actinomyces
Genus
F17924.S105
F17924.S107
F17924.S110
F17924.S113
F17924.S115
F17924.S121
F17924.S123
F17924.S128
F17924.S132
F17924.S134
F17924.S137
F17924.S145
F17924.S151
F17924.S103
F17924.S109
F17924.S116
F17924.S119
F17924.S125
F17924.S127
F17924.S131
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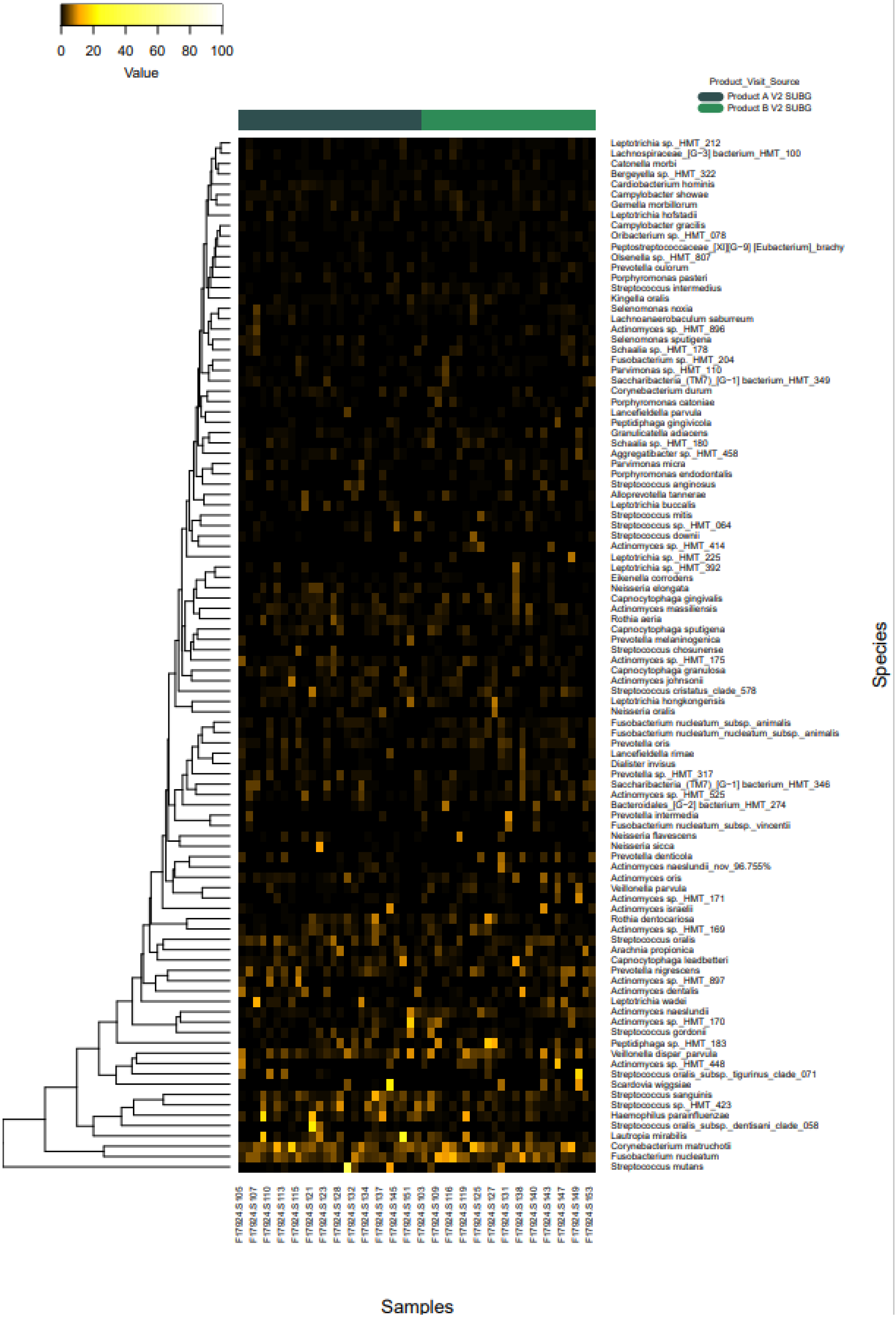
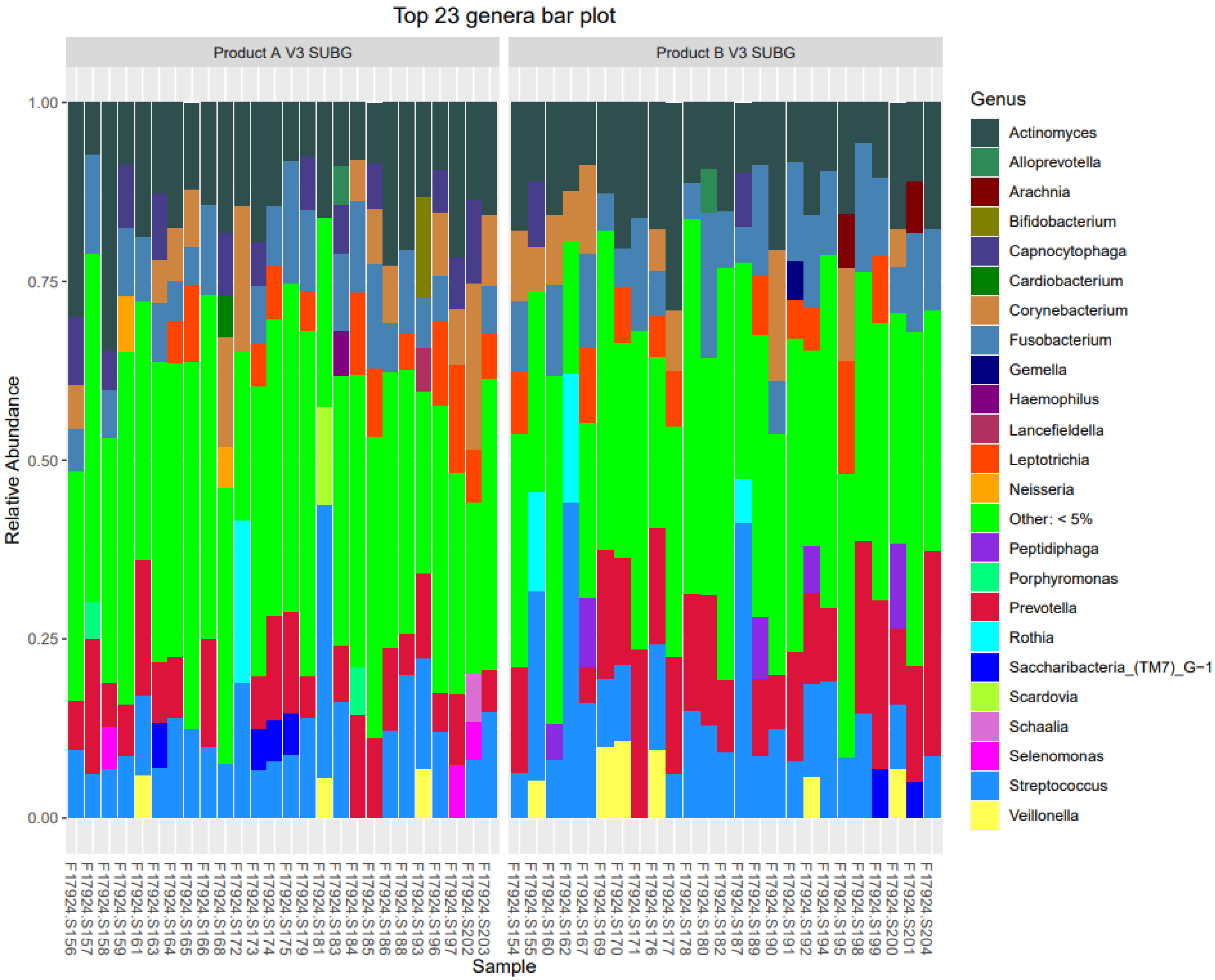
F17924.S147
F17924.S149
F17924.S153
Samples

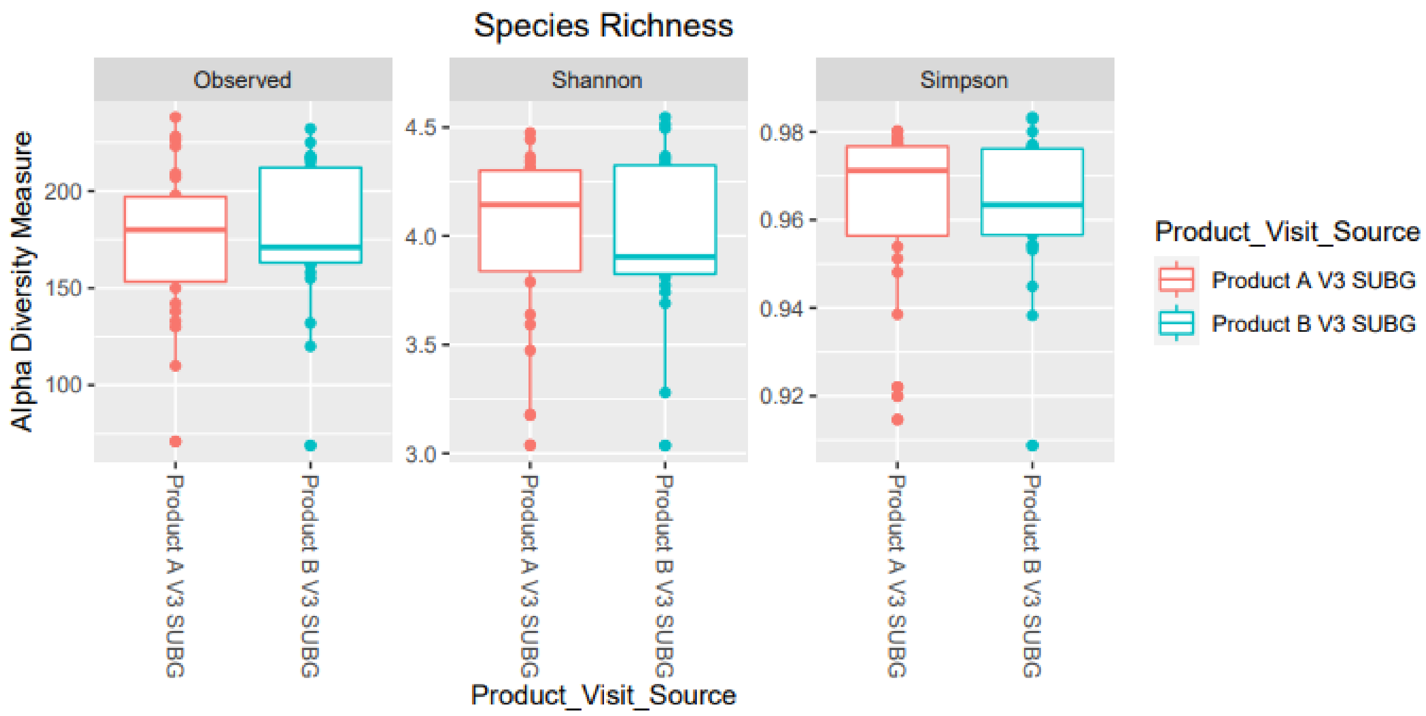

0
20
40
60
80
100
Value
Product_Visit_Source
Product A V2 SUBG
Product B V2 SUBG
Leptotrichia sp._HMT_212
Lachnospiraceae_[G-3] bacterium_HMT_100
Catonella morbi
Bergeyella sp._HMT_322
Cardiobacterium hominis
Campylobacter showae
Gemella morbillorum
Leptotrichia hofstadii
Campylobacter gracilis
Oribacterium sp._HMT_078
Peptostreptococcaceae_[XI][G-9] [Eubacterium]_brachy
Olsenella sp._HMT_807
Prevotella oulorum
Porphyromonas pasteri
Streptococcus intermedius
Kingella oralis
Selenomonas noxia
Lachnoanaerobaculum saburreum
Actinomyces sp._HMT_896
Selenomonas sputigena
Schaalia sp._HMT_178
Fusobacterium sp._HMT_204
Parvimonas sp._HMT_110
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_349
Corynebacterium durum
Porphyromonas catoniae
Lancefieldella parvula
Peptidiphaga gingivicola
Granulicatella adiacens
Schaalia sp._HMT_180
Aggregatibacter sp._HMT_458
Parvimonas micra
Porphyromonas endodontalis
Streptococcus anginosus
Alloprevotella tannerae
Leptotrichia buccalis
Streptococcus mitis
Streptococcus sp._HMT_064
Streptococcus downii
Actinomyces sp._HMT_414
Leptotrichia sp._HMT_225
Leptotrichia sp._HMT_392
Eikenella corrodens
Neisseria elongata
Capnocytophaga gingivalis
Actinomyces massiliensis
Rothia aeria
Capnocytophaga sputigena
Prevotella melaninogenica
Streptococcus chosunense
Actinomyces sp._HMT_175
Capnocytophaga granulosa
Actinomyces johnsonii
Streptococcus cristatus_clade_578
Leptotrichia hongkongensis
Neisseria oralis
Fusobacterium nucleatum_subsp._animalis
Fusobacterium nucleatum_nucleatum_subsp._animalis
Prevotella oris
Lancefieldella rimae
Dialister invisus
Prevotella sp._HMT_317
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346
Actinomyces sp._HMT_525
Bacteroidales_[G-2] bacterium_HMT_274
Prevotella intermedia
Fusobacterium nucleatum_subsp._vincentii
Neisseria flavescens
Neisseria sicca
Prevotella denticola
Actinomyces naeslundii_nov_96.755%
Actinomyces oris
Veillonella parvula
Actinomyces sp._HMT_171
Actinomyces israelii
Rothia dentocariosa
Actinomyces sp._HMT_169
Streptococcus oralis
Arachnia propionica
Capnocytophaga leadbetteri
Prevotella nigrescens
Actinomyces sp._HMT_897
Actinomyces dentalis
Leptotrichia wadei
Actinomyces naeslundii
Actinomyces sp._HMT_170
Streptococcus gordonii
Peptidiphaga sp._HMT_183
Veillonella dispar_parvula
Actinomyces sp._HMT_448
Streptococcus oralis_subsp._tigurinus_clade_071
Scardovia wiggsiae
Streptococcus sanguinis
Streptococcus sp._HMT_423
Haemophilus parainfluenzae
Streptococcus oralis_subsp._dentisani_clade_058
Lautropia mirabilis
Corynebacterium matruchotii
Fusobacterium nucleatum
Streptococcus mutans
Species
F17924.S105
F17924.S107
F17924.S110
F17924.S113
F17924.S115
F17924.S121
F17924.S123
F17924.S128
F17924.S132
F17924.S134
F17924.S137
F17924.S145
F17924.S151
F17924.S103
F17924.S109
F17924.S116
F17924.S119
F17924.S125
F17924.S127
F17924.S131
F17924.S138
F17924.S140
F17924.S143
F17924.S147
F17924.S149
F17924.S153
Samples

Comparison 20. Product A V3 SUBG vs Product B V3 SUBG

1) Taxonomy bar graphs

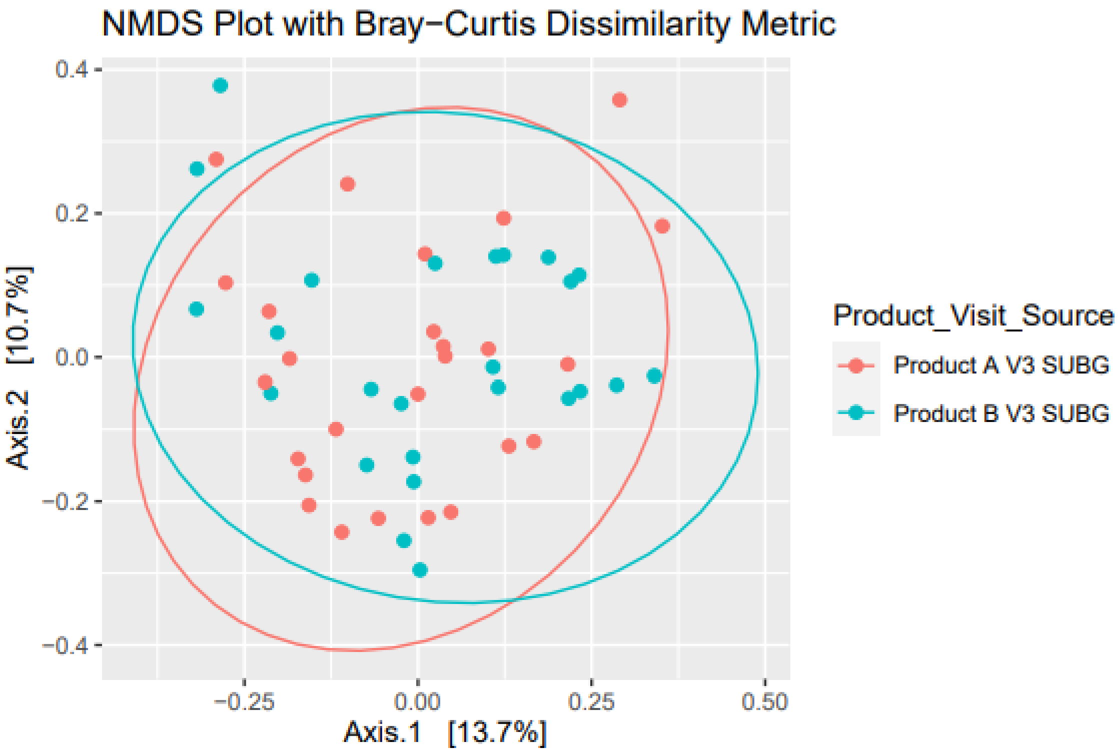


2) Alpha



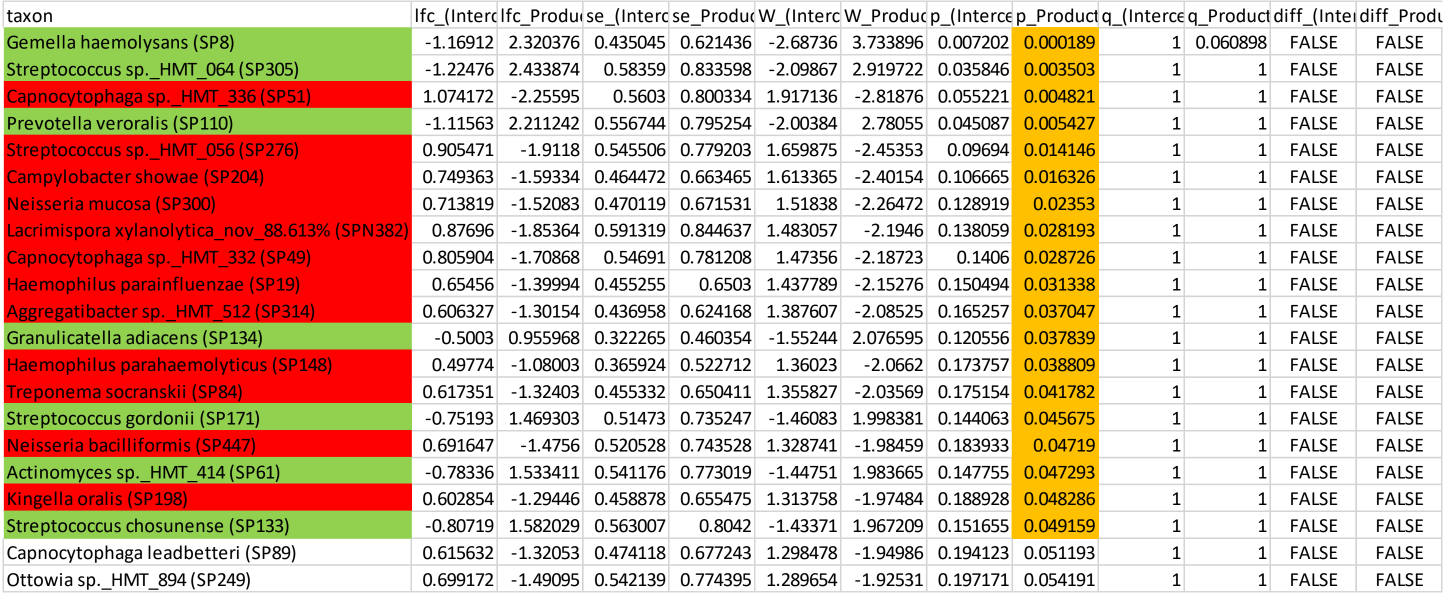
No significant differences

3) Beta diversity



No significant differences

4) Differential abundance

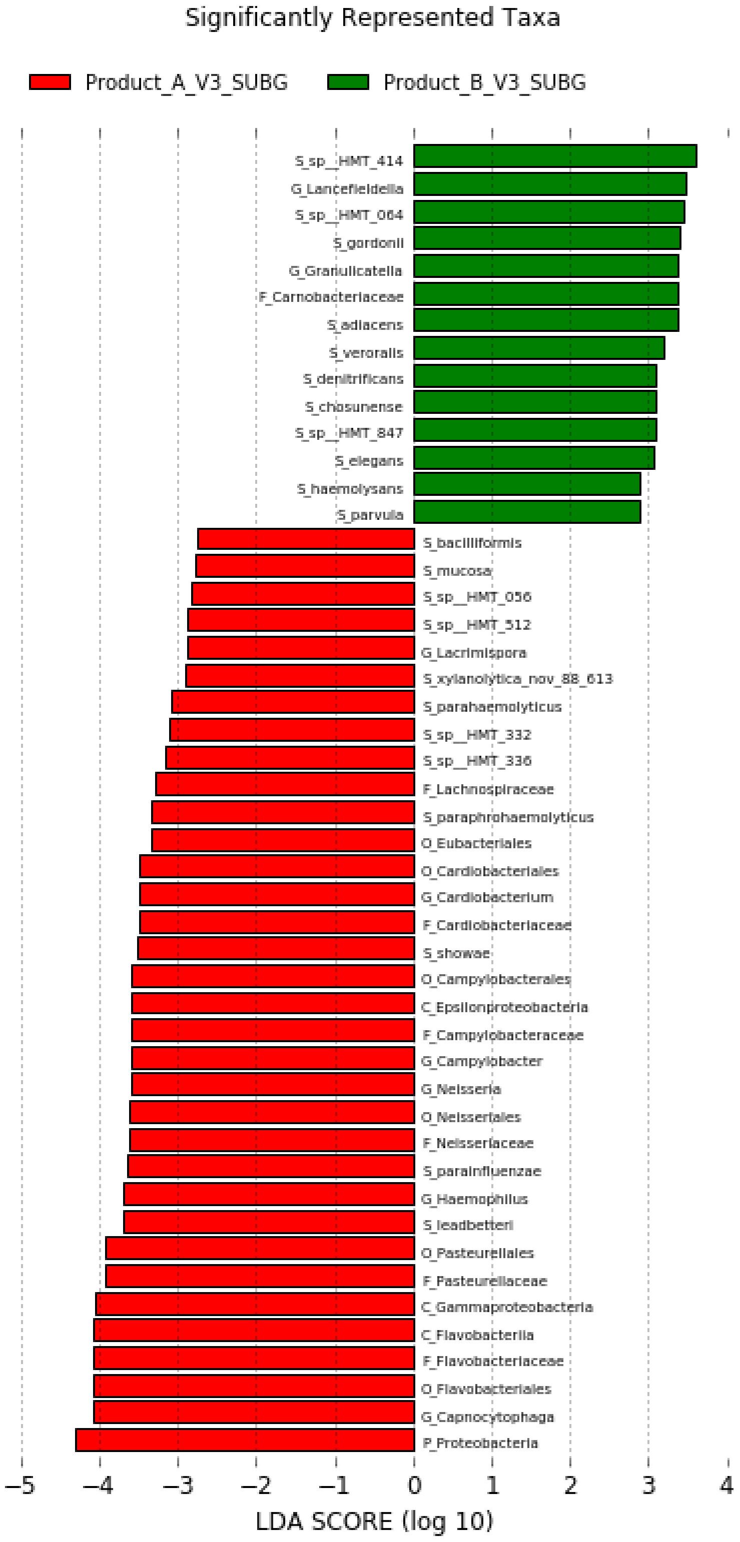


taxon	lfc_(Interc	lfc_Produ	se_(Interc	se_Produc	W_(Interc	W_Produc	p_(Interce	p_Product	q_(Interce	q_Product	diff_(Inter	diff_Produ
Gemella haemolysans (SP8)	-1.16912	2.320376	0.435045	0.621436	-2.68736	3.733896	0.007202	0.000189	1	0.060898	FALSE	FALSE
Streptococcus sp._HMT_064 (SP305)	-1.22476	2.433874	0.58359	0.833598	-2.09867	2.919722	0.035846	0.003503	1	1	FALSE	FALSE
Capnocytophaga sp._HMT_336 (SP51)	1.074172	-2.25595	0.5603	0.800334	1.917136	-2.81876	0.055221	0.004821	1	1	FALSE	FALSE
Prevotella veroralis (SP110)	-1.11563	2.211242	0.556744	0.795254	-2.00384	2.78055	0.045087	0.005427	1	1	FALSE	FALSE
Streptococcus sp._HMT_056 (SP276)	0.905471	-1.9118	0.545506	0.779203	1.659875	-2.45353	0.09694	0.014146	1	1	FALSE	FALSE
Campylobacter showae (SP204)	0.749363	-1.59334	0.464472	0.663465	1.613365	-2.40154	0.106665	0.016326	1	1	FALSE	FALSE
Neisseria mucosa (SP300)	0.713819	-1.52083	0.470119	0.671531	1.51838	-2.26472	0.128919	0.02353	1	1	FALSE	FALSE
Lacrimispora xylanolytica_nov_88.613% (SPN382)	0.87696	-1.85364	0.591319	0.844637	1.483057	-2.1946	0.138059	0.028193	1	1	FALSE	FALSE
Capnocytophaga sp._HMT_332 (SP49)	0.805904	-1.70868	0.54691	0.781208	1.47356	-2.18723	0.1406	0.028726	1	1	FALSE	FALSE
Haemophilus parainfluenzae (SP19)	0.65456	-1.39994	0.455255	0.6503	1.437789	-2.15276	0.150494	0.031338	1	1	FALSE	FALSE
Aggregatibacter sp._HMT_512 (SP314)	0.606327	-1.30154	0.436958	0.624168	1.387607	-2.08525	0.165257	0.037047	1	1	FALSE	FALSE
Granulicatella adiacens (SP134)	-0.5003	0.955968	0.322265	0.460354	-1.55244	2.076595	0.120556	0.037839	1	1	FALSE	FALSE
Haemophilus parahaemolyticus (SP148)	0.49774	-1.08003	0.365924	0.522712	1.36023	-2.0662	0.173757	0.038809	1	1	FALSE	FALSE
Treponema socranskii (SP84)	0.617351	-1.32403	0.455332	0.650411	1.355827	-2.03569	0.175154	0.041782	1	1	FALSE	FALSE
Streptococcus gordonii (SP171)	-0.75193	1.469303	0.51473	0.735247	-1.46083	1.998381	0.144063	0.045675	1	1	FALSE	FALSE
Neisseria bacilliformis (SP447)	0.691647	-1.4756	0.520528	0.743528	1.328741	-1.98459	0.183933	0.04719	1	1	FALSE	FALSE
Actinomyces sp._HMT_414 (SP61)	-0.78336	1.533411	0.541176	0.773019	-1.44751	1.983665	0.147755	0.047293	1	1	FALSE	FALSE
Kingella oralis (SP198)	0.602854	-1.29446	0.458878	0.655475	1.313758	-1.97484	0.188928	0.048286	1	1	FALSE	FALSE
Streptococcus chosunense (SP133)	-0.80719	1.582029	0.563007	0.8042	-1.43371	1.967209	0.151655	0.049159	1	1	FALSE	FALSE
Capnocytophaga leadbetteri (SP89)	0.615632	-1.32053	0.474118	0.677243	1.298478	-1.94986	0.194123	0.051193	1	1	FALSE	FALSE
Ottowia sp._HMT_894 (SP249)	0.699172	-1.49095	0.542139	0.774395	1.289654	-1.92531	0.197171	0.054191	1	1	FALSE	FALSE

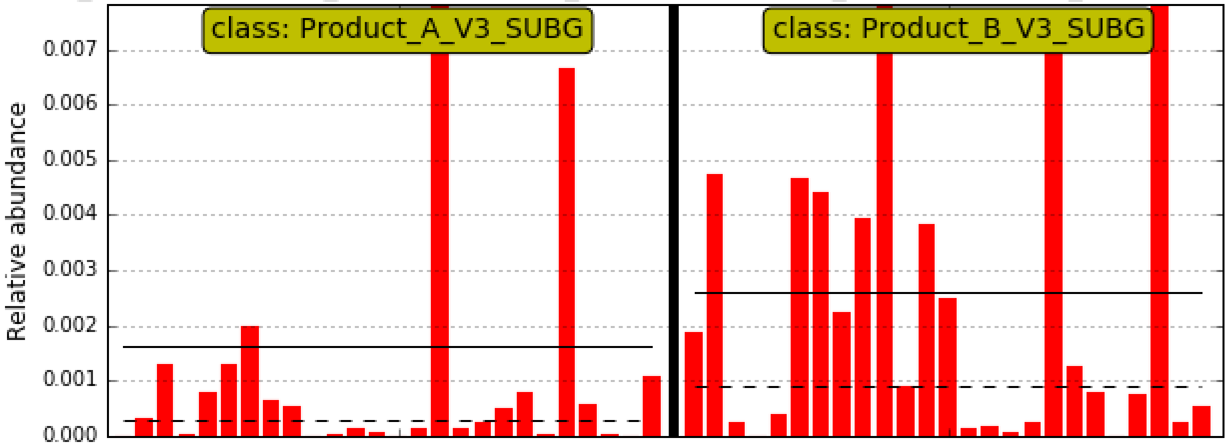
Green, more abundant in B

Red, more abundant in A

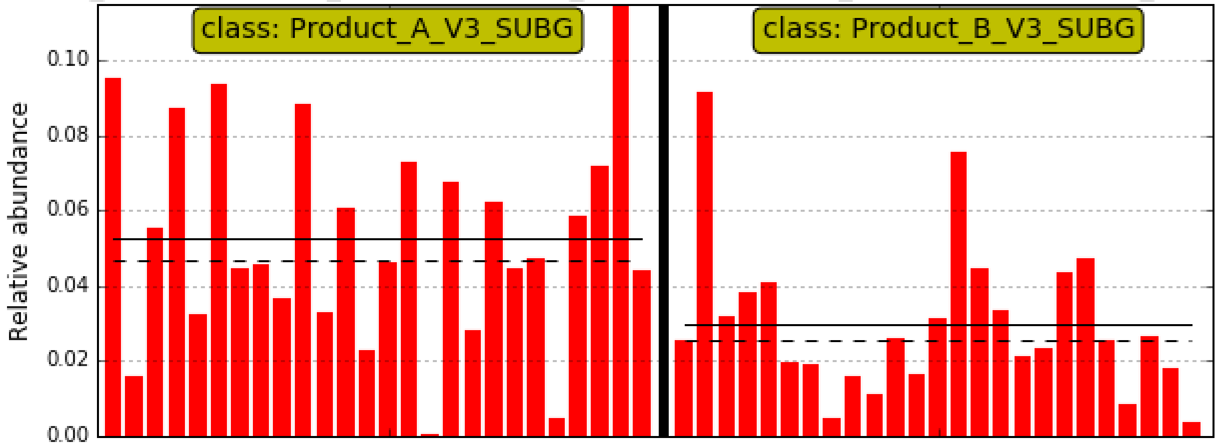
5) Lefse


Significantly Represented Taxa
🟥 Product_A_V3_SUBG
🟩 Product_B_V3_SUBG
S_sp__HMT_414
G_Lancefieldella
S_sp__HMT_064
S_gordonii
G_Granulicatella
F_Carnobacteriaceae
S_adiacens
S_veroralis
S_denitrificans
S_chosunense
S_sp__HMT_847
S_elegans
S_haemolysans
S_parvula
S_bacilliformis
S_mucosa
S_sp__HMT_056
S_sp__HMT_512
G_Lacrimispora
S_xylanolytica_nov_88_613
S_parahaemolyticus
S_sp__HMT_332
S_sp__HMT_336
F_Lachnospiraceae
S_paraphrohaemolyticus
O_Eubacteriales
O_Cardiobacteriales
G_Cardiobacterium
F_Cardiobacteriaceae
S_showae
O_Campylobacterales
C_Epsilonproteobacteria
F_Campylobacteraceae
G_Campylobacter
G_Neisseria
O_Neisseriales
F_Neisseriaceae
S_parainfluenzae
G_Haemophilus
S_leadbetteri
O_Pasteurellales
F_Pasteurellaceae
C_Gammaproteobacteria
C_Flavobacteriia
F_Flavobacteriaceae
O_Flavobacteriales
G_Capnocytophaga
P_Proteobacteria
−5
−4
−3
−2
−1
0
1
2
3
4
LDA SCORE (log 10)

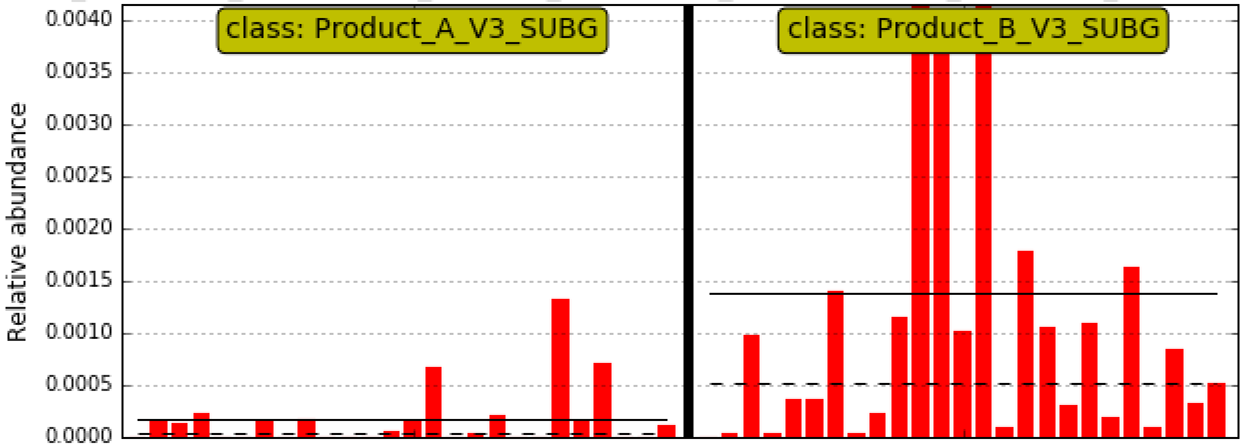
_Bacteria.P_Actinobacteria.C_Coriobacteriia.O_Coriobacteriales.F_Atopobiaceae.G_Lancefieldella.S_par

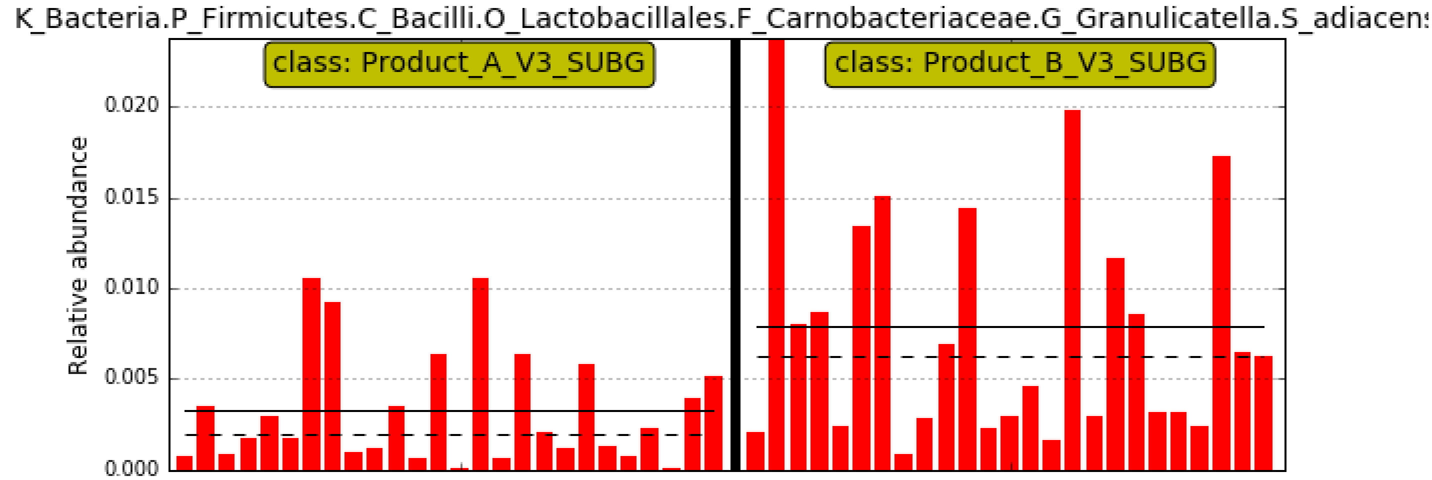


K_Bacteria.P_Bacteroidetes.C_Flavobacteriia.O_Flavobacteriales.F_Flavobacteriaceae.G_Capnocytopha

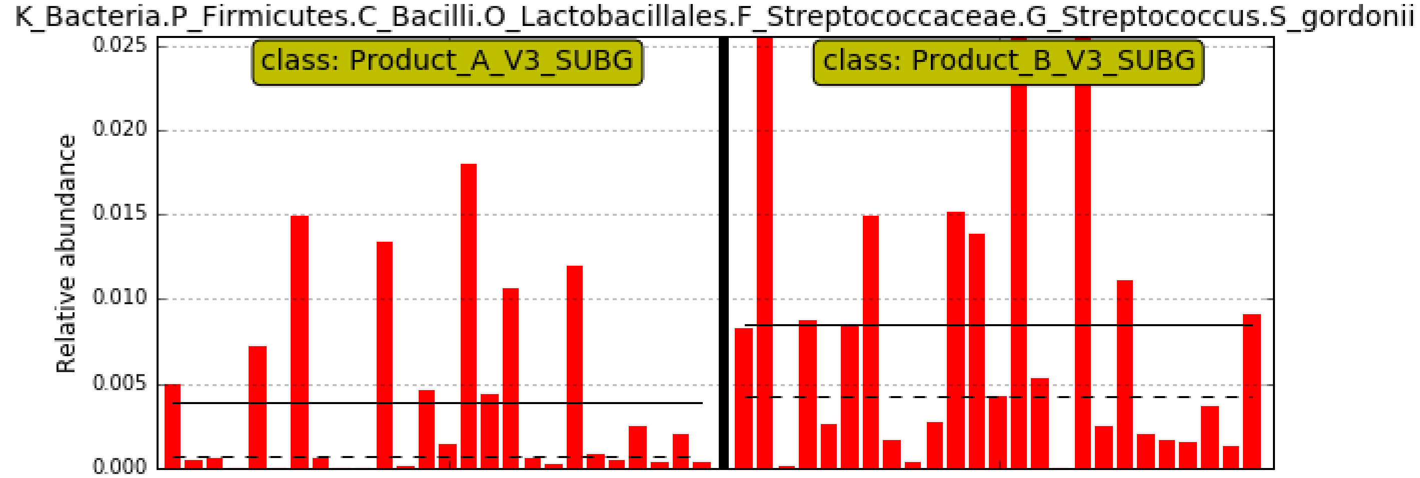


K_Bacteria.P_Firmicutes.C_Bacilli.O_Bacillales.F_Gemellaceae.G_Gemella.S_haemolysans

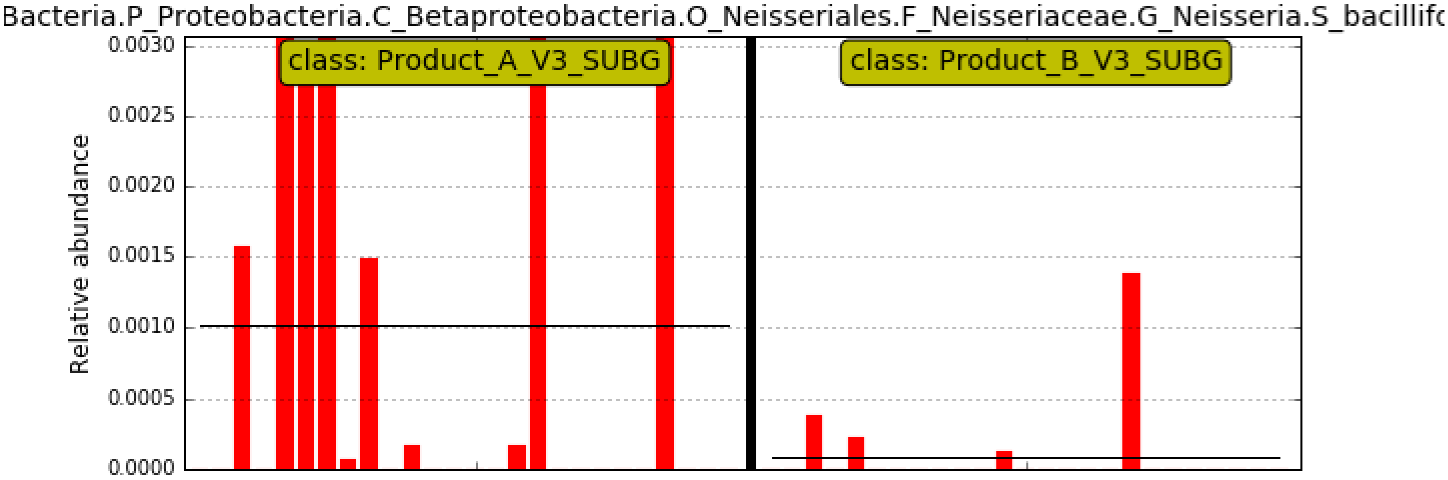




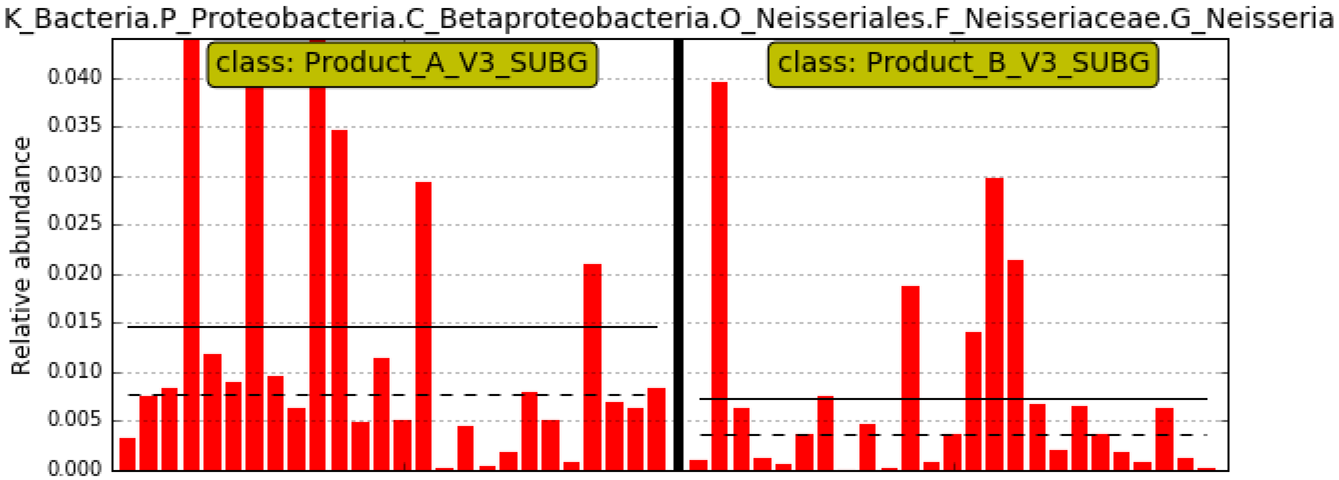
K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Carnobacteriaceae.G_Granulicatella.S_adiacen

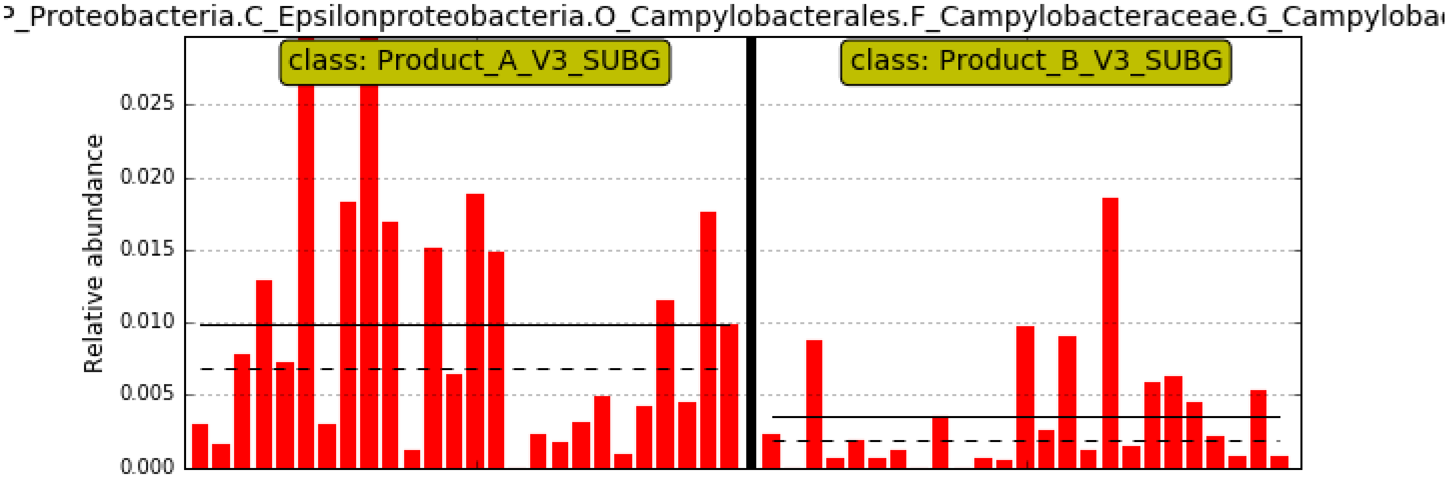


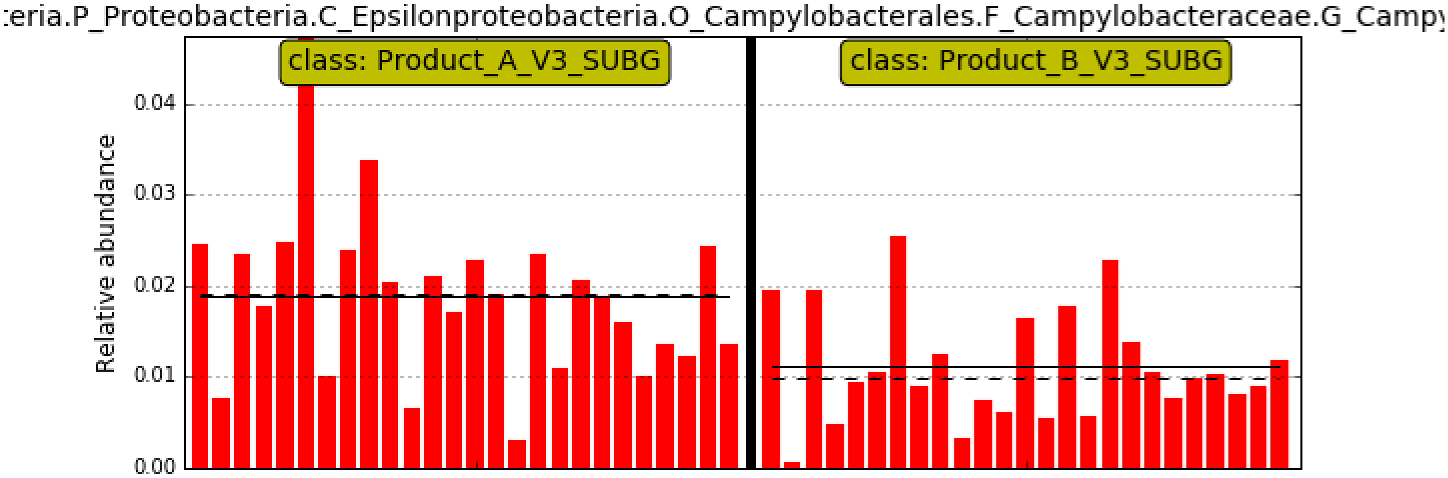
K_Bacteria.P_Firmicutes.C_Bacilli.O_Lactobacillales.F_Streptococcaceae.G_Streptococcus.S_gordonii

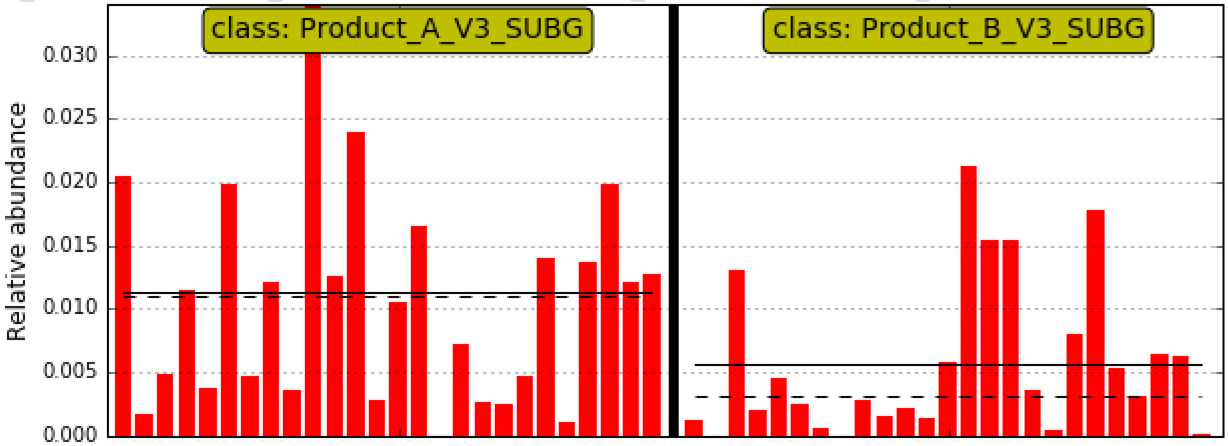


Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Neisseria.S_bacillif

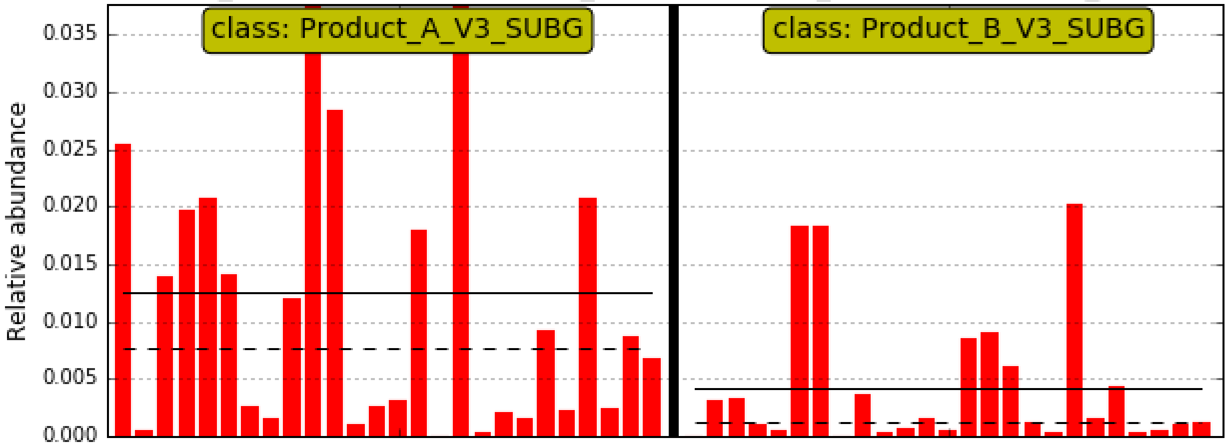

K_Bacteria.P_Proteobacteria.C_Betaproteobacteria.O_Neisseriales.F_Neisseriaceae.G_Neisseria


_Proteobacteria.C_Epsilonproteobacteria.O_Campylobacterales.F_Campylobacteraceae.G_Campyloba


eria.P_Proteobacteria.C_Epsilonproteobacteria.O_Campylobacterales.F_Campylobacteraceae.G_Campy

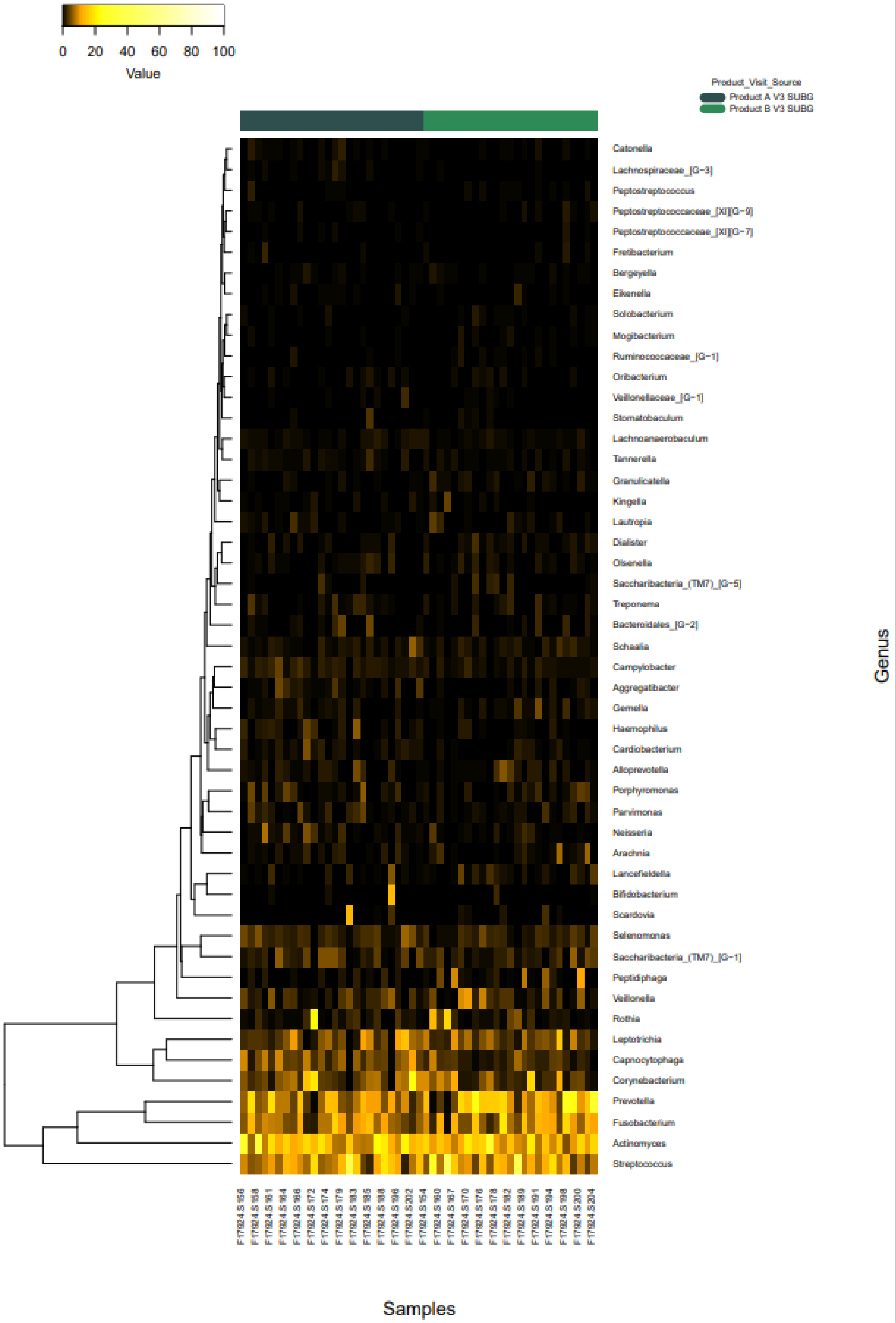


teria.P_Proteobacteria.C_Gammaproteobacteria.O_Cardiobacteriales.F_Cardiobacteriaceae.G_Cardioba



a.P_Proteobacteria.C_Gammaproteobacteria.O_Pasteurellales.F_Pasteurellaceae.G_Haemophilus.S_par

6) Heat map


0
20
40
60
80
100
Value
Product_Visit_Source
Product A V3 SUBG
Product B V3 SUBG
Catonella
Lachnospiraceae_[G-3]
Peptostreptococcus
Peptostreptococcaceae_[XI][G-9]
Peptostreptococcaceae_[XI][G-7]
Fretibacterium
Bergeyella
Eikenella
Solobacterium
Mogibacterium
Ruminococcaceae_[G-1]
Oribacterium
Veillonellaceae_[G-1]
Stomatobaculum
Lachnoanaerobaculum
Tannerella
Granulicatella
Kingella
Lautropia
Dialister
Olsenella
Saccharibacteria_(TM7)_[G-5]
Treponema
Bacteroidales_[G-2]
Schaalia
Campylobacter
Aggregatibacter
Gemella
Haemophilus
Cardiobacterium
Alloprevotella
Porphyromonas
Parvimonas
Neisseria
Arachnia
Lancefieldella
Bifidobacterium
Scardovia
Selenomonas
Saccharibacteria_(TM7)_[G-1]
Peptidiphaga
Veillonella
Rothia
Leptotrichia
Capnocytophaga
Corynebacterium
Prevotella
Fusobacterium
Actinomyces
Streptococcus
Genus
F17924.S156
F17924.S158
F17924.S161
F17924.S164
F17924.S166
F17924.S172
F17924.S174
F17924.S179
F17924.S183
F17924.S185
F17924.S188
F17924.S196
F17924.S202
F17924.S154
F17924.S160
F17924.S167
F17924.S170
F17924.S176
F17924.S178
F17924.S182
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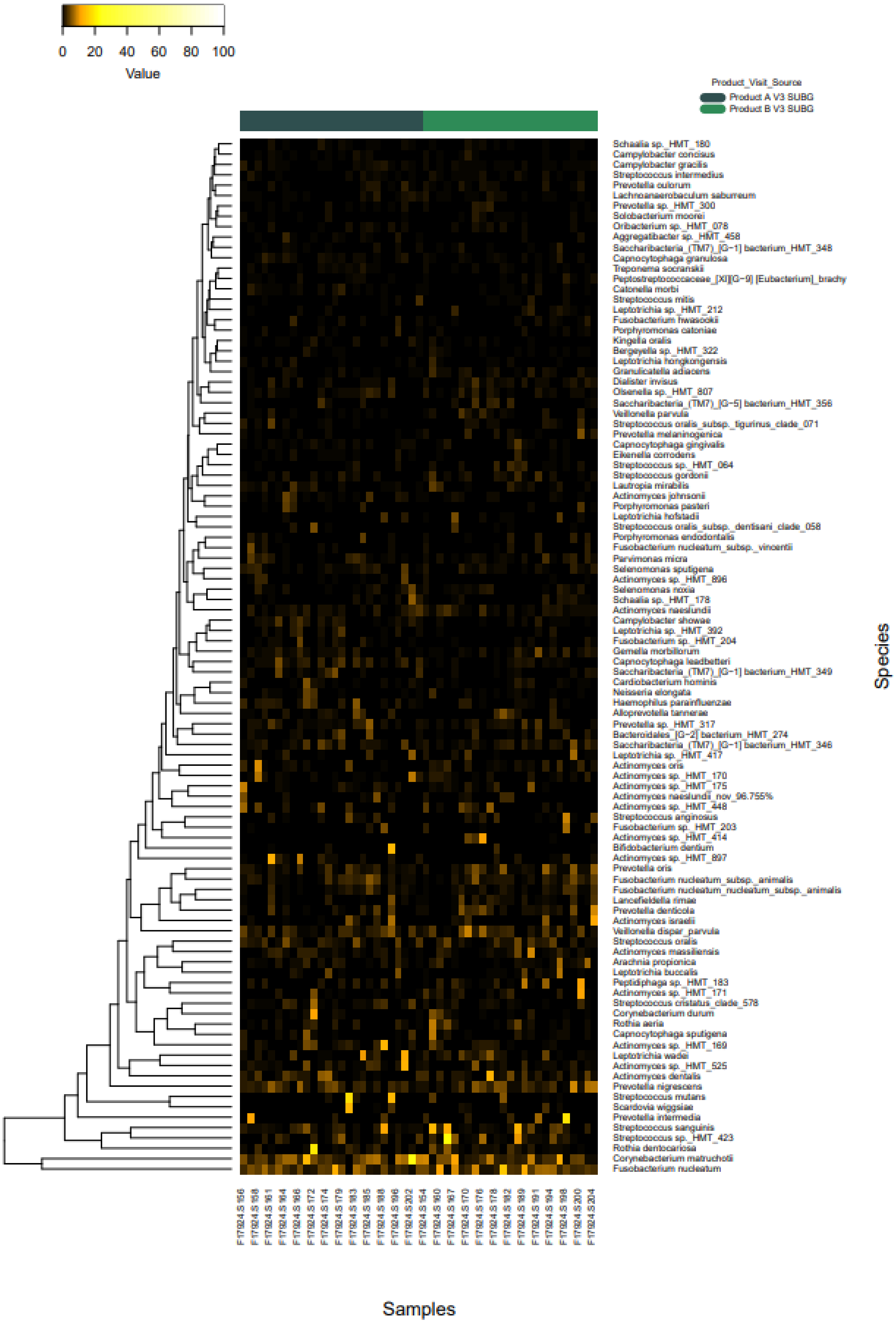
F17924.S191
F17924.S194
F17924.S198
F17924.S200
F17924.S204
Samples

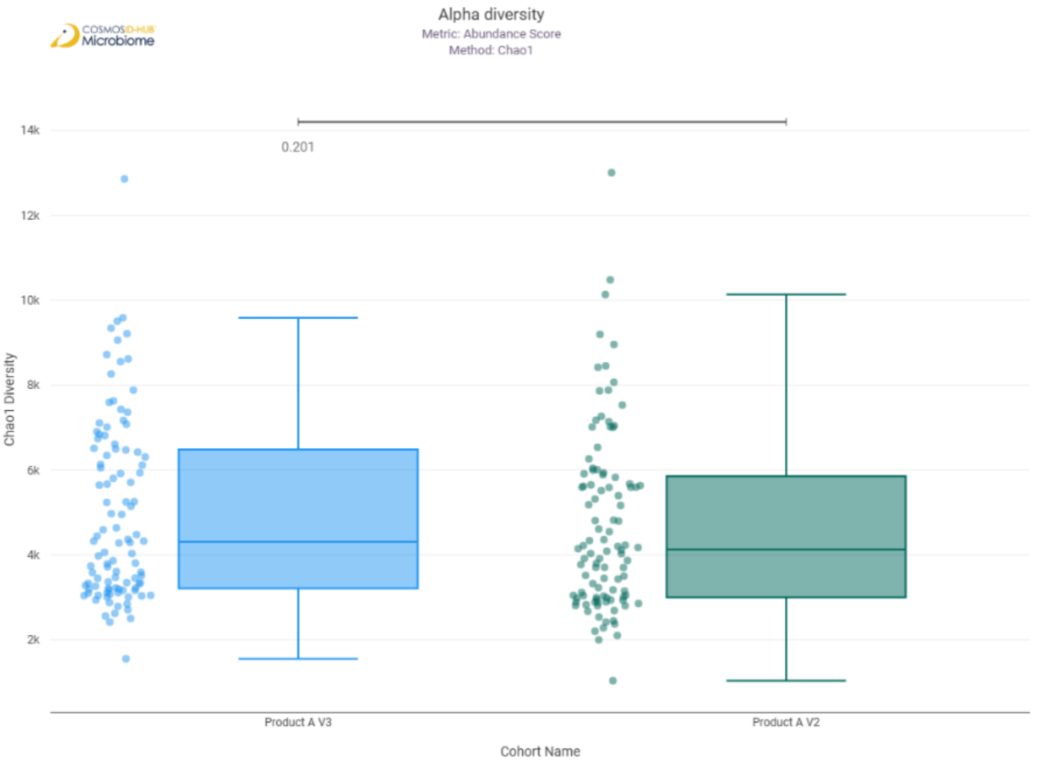

0
20
40
60
80
100
Value
Product_Visit_Source
Product A V3 SUBG
Product B V3 SUBG
Schaalia sp._HMT_180
Campylobacter concisus
Campylobacter gracilis
Streptococcus intermedius
Prevotella oulorum
Lachnoanaerobaculum saburreum
Prevotella sp._HMT_300
Solobacterium moorei
Oribacterium sp._HMT_078
Aggregatibacter sp._HMT_458
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_348
Capnocytophaga granulosa
Treponema socranskii
Peptostreptococcaceae_[XI][G-9] [Eubacterium]_brachy
Catonella morbi
Streptococcus mitis
Leptotrichia sp._HMT_212
Fusobacterium hwasookii
Porphyromonas catoniae
Kingella oralis
Bergeyella sp._HMT_322
Leptotrichia hongkongensis
Granulicatella adiacens
Dialister invisus
Olsenella sp._HMT_807
Saccharibacteria_(TM7)_[G-5] bacterium_HMT_356
Veillonella parvula
Streptococcus oralis_subsp._tigurinus_clade_071
Prevotella melaninogenica
Capnocytophaga gingivalis
Eikenella corrodens
Streptococcus sp._HMT_064
Streptococcus gordonii
Lautropia mirabilis
Actinomyces johnsonii
Porphyromonas pasteri
Leptotrichia hofstadii
Streptococcus oralis_subsp._dentisani_clade_058
Porphyromonas endodontalis
Fusobacterium nucleatum_subsp._vincentii
Parvimonas micra
Selenomonas sputigena
Actinomyces sp._HMT_896
Selenomonas noxia
Schaalia sp._HMT_178
Actinomyces naeslundii
Campylobacter showae
Leptotrichia sp._HMT_392
Fusobacterium sp._HMT_204
Gemella morbillorum
Capnocytophaga leadbetteri
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_349
Cardiobacterium hominis
Neisseria elongata
Haemophilus parainfluenzae
Alloprevotella tannerae
Prevotella sp._HMT_317
Bacteroidales_[G-2] bacterium_HMT_274
Saccharibacteria_(TM7)_[G-1] bacterium_HMT_346
Leptotrichia sp._HMT_417
Actinomyces oris
Actinomyces sp._HMT_170
Actinomyces sp._HMT_175
Actinomyces naeslundii_nov_96.755%
Actinomyces sp._HMT_448
Streptococcus anginosus
Fusobacterium sp._HMT_203
Actinomyces sp._HMT_414
Bifidobacterium dentium
Actinomyces sp._HMT_897
Prevotella oris
Fusobacterium nucleatum_subsp._animalis
Fusobacterium nucleatum_nucleatum_subsp._animalis
Lancefieldella rimae
Prevotella denticola
Actinomyces israelii
Veillonella dispar_parvula
Streptococcus oralis
Actinomyces massiliensis
Arachnia propionica
Leptotrichia buccalis
Peptidiphaga sp._HMT_183
Actinomyces sp._HMT_171
Streptococcus cristatus_clade_578
Corynebacterium durum
Rothia aeria
Capnocytophaga sputigena
Actinomyces sp._HMT_169
Leptotrichia wadei
Actinomyces sp._HMT_525
Actinomyces dentalis
Prevotella nigrescens
Streptococcus mutans
Scardovia wiggsiae
Prevotella intermedia
Streptococcus sanguinis
Streptococcus sp._HMT_423
Rothia dentocariosa
Corynebacterium matruchotii
Fusobacterium nucleatum
Species
FIT924.S156
FIT924.S158
FIT924.S161
FIT924.S164
FIT924.S166
FIT924.S172
FIT924.S174
FIT924.S179
FIT924.S183
FIT924.S185
FIT924.S188
FIT924.S196
FIT924.S202
FIT924.S154
FIT924.S160
FIT924.S167
FIT924.S170
FIT924.S176
FIT924.S178
FIT924.S182
FIT924.S189
FIT924.S191
FIT924.S194
FIT924.S198
FIT924.S200
FIT924.S204
Samples

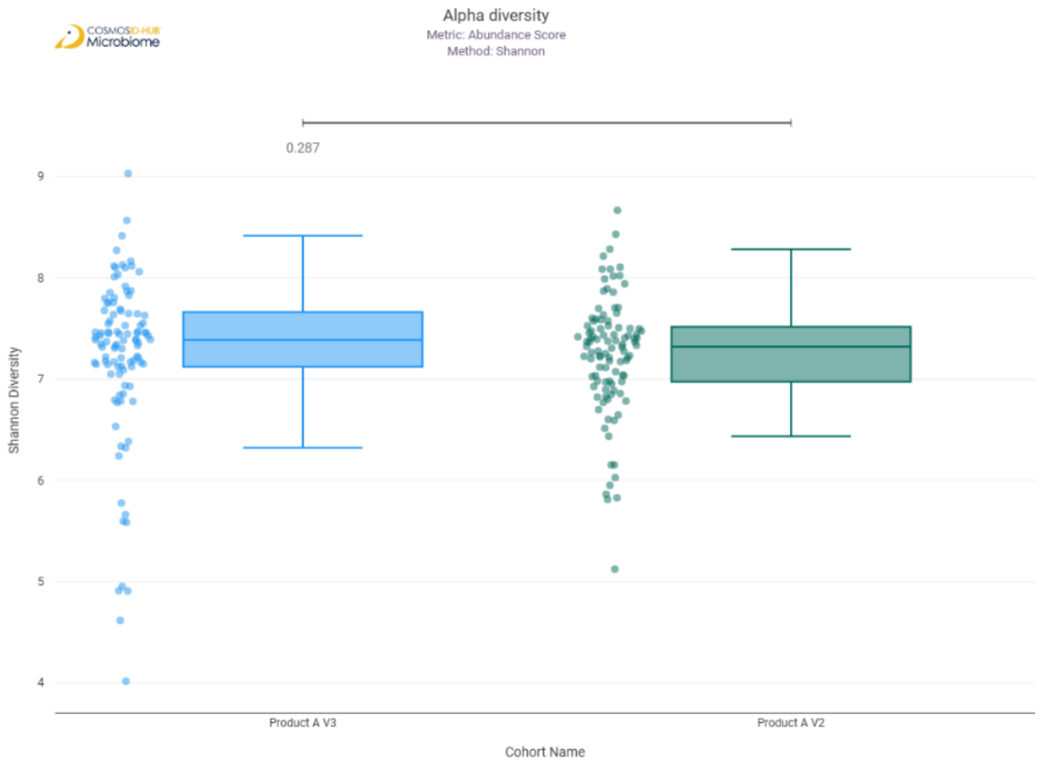
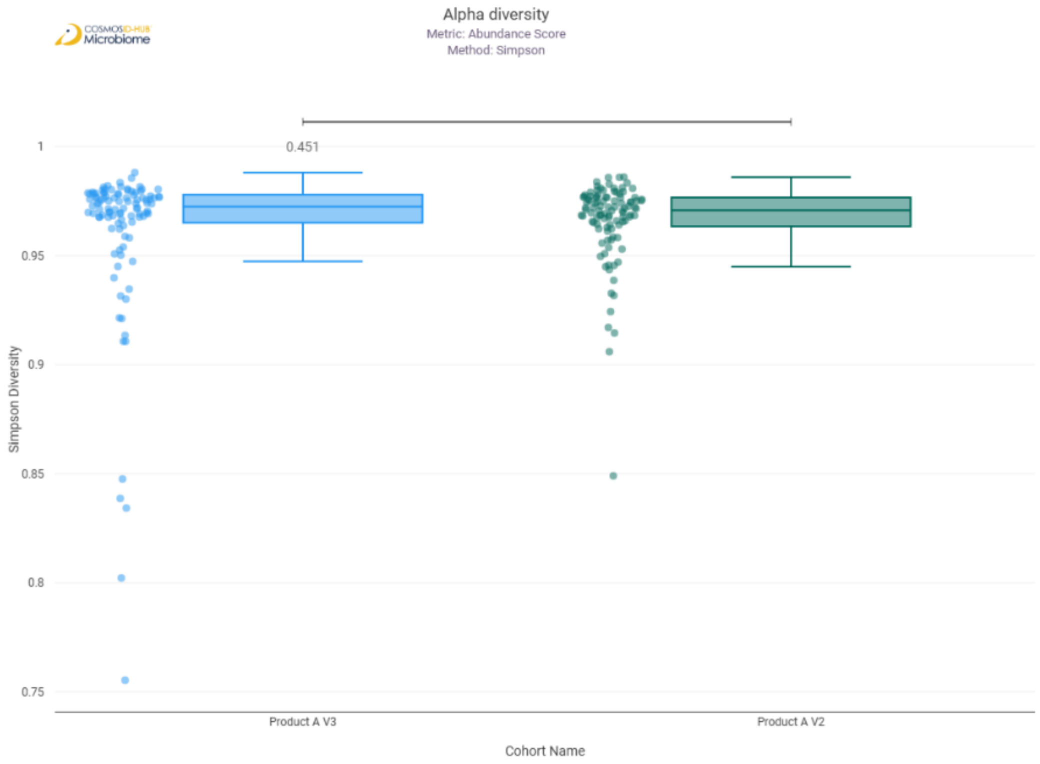
Appendix B. CosmosID-HUB Metatranscriptomic Analysis

Comparison 1: Product A V2 vs Product A V3

Gene Ontology

Alpha Diversity

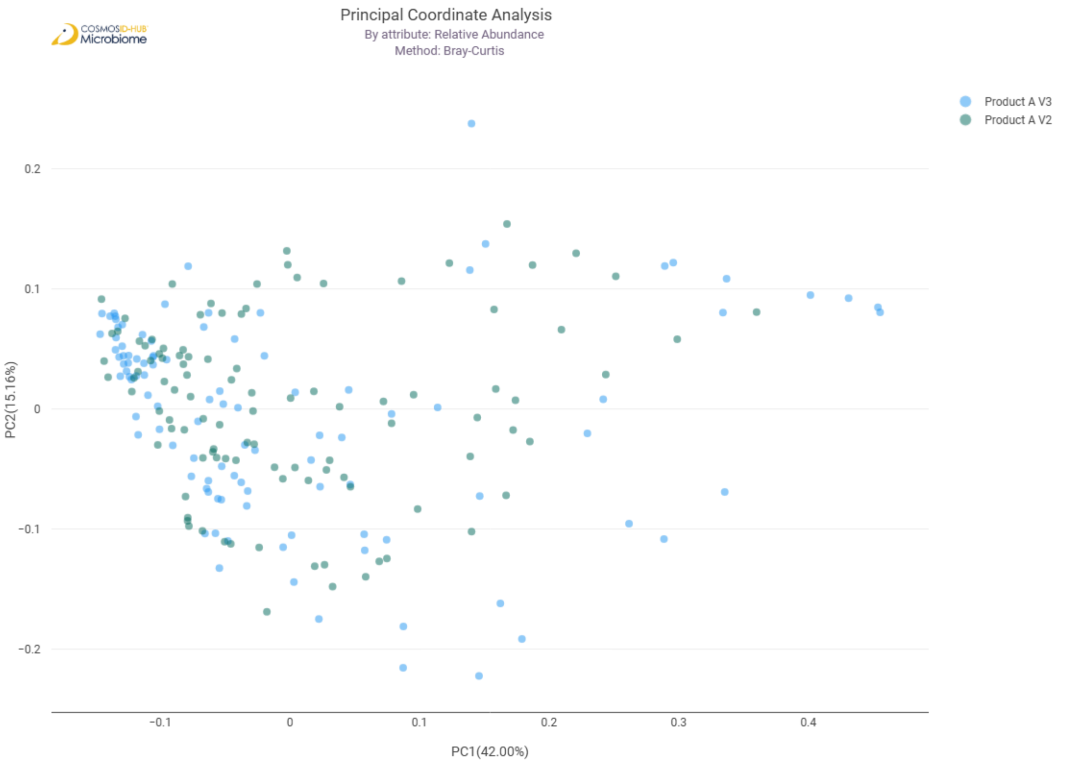
Chao1	

Shannon	
Simpson	

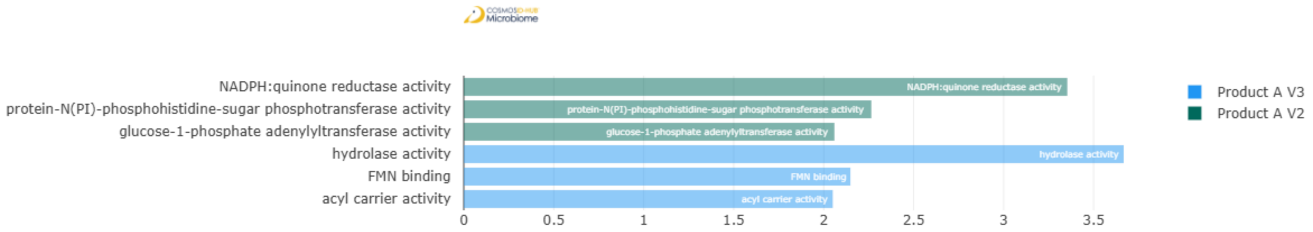
Beta Diversity

Bray-Curtis

PERMNOVA
p = 0.542



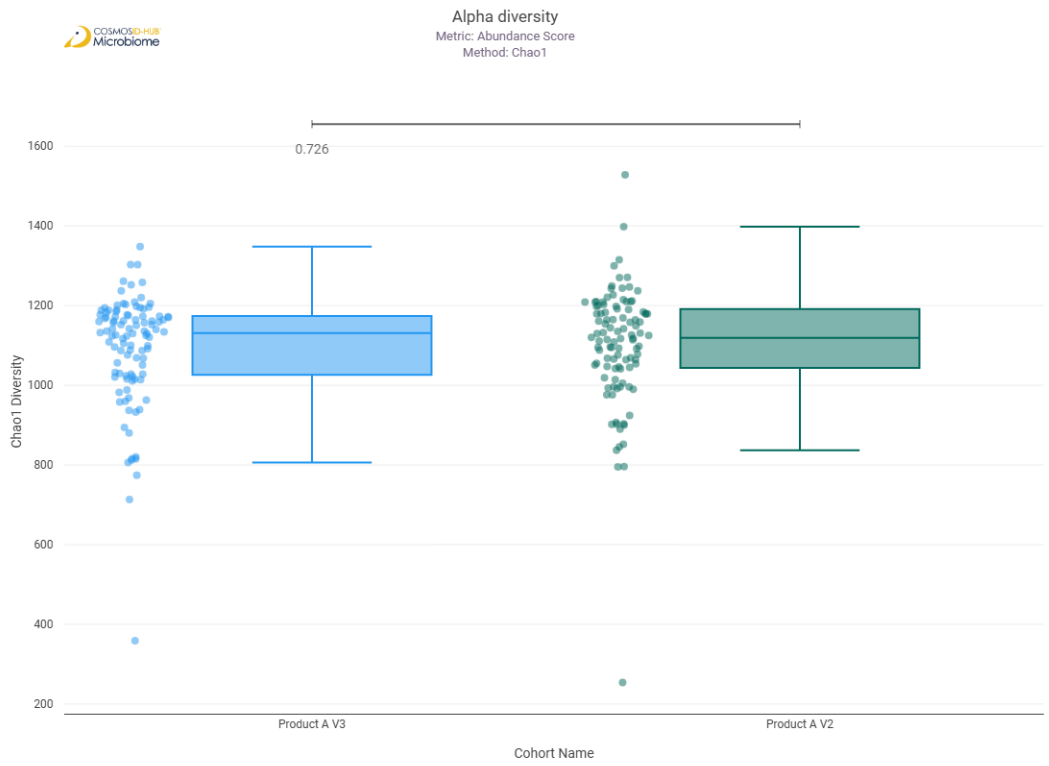
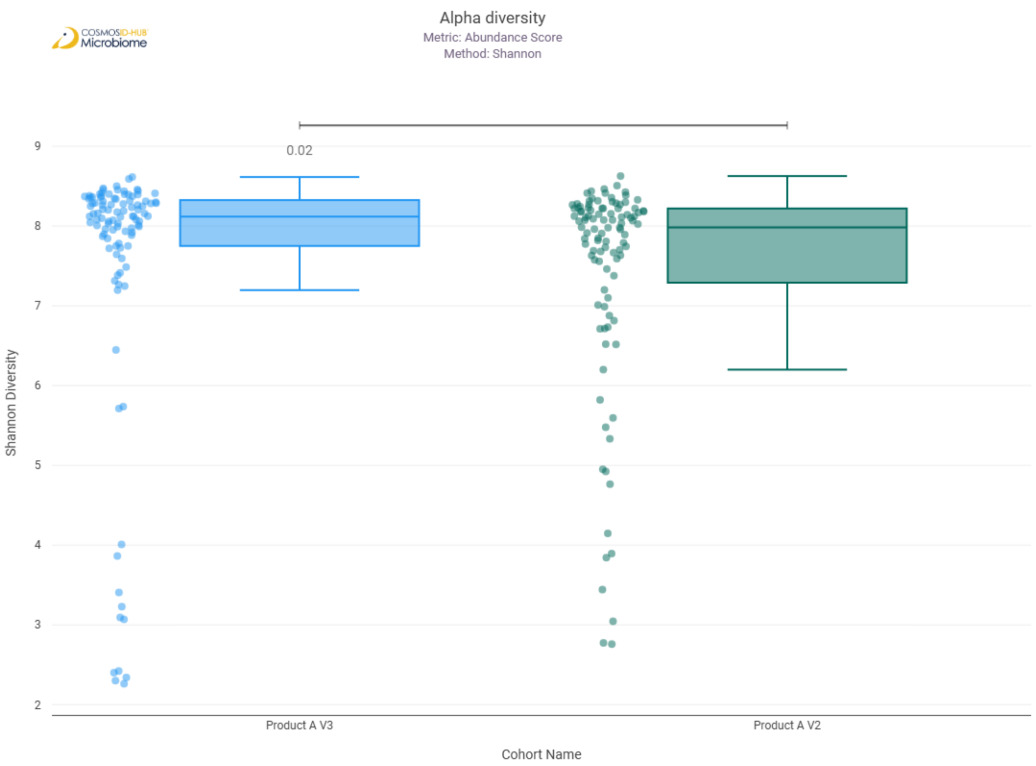
Differential Abundance (LEfSe)

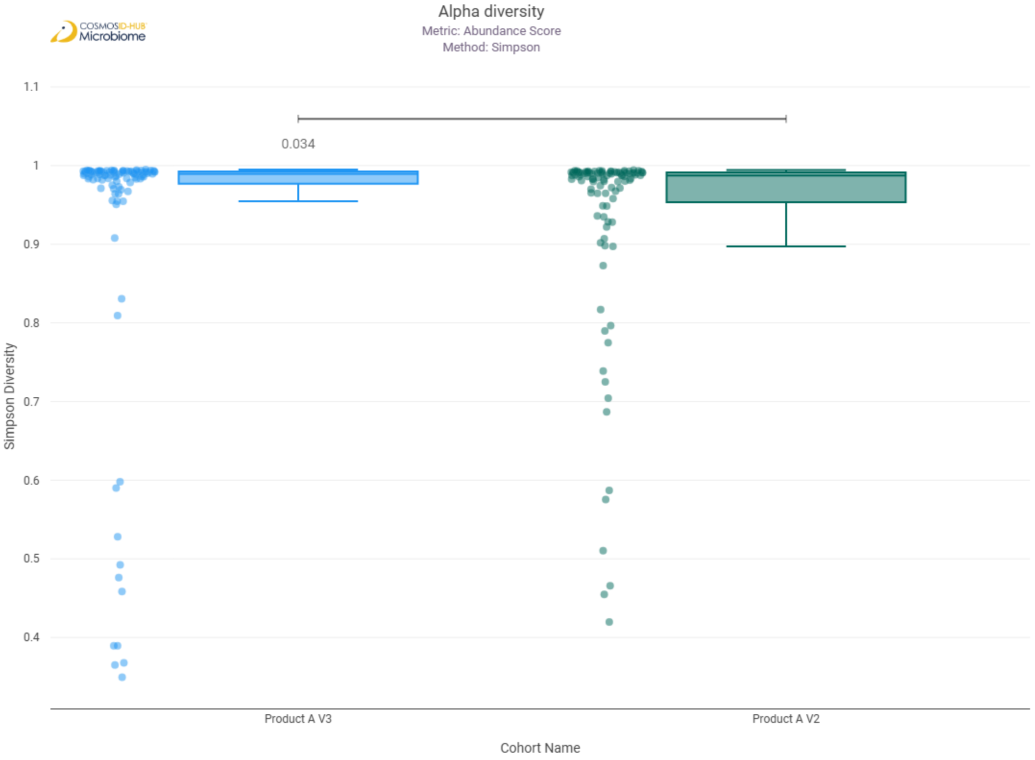


Feature	Enriched Cohort	LDA Score	P-value
NADPH:quinone reductase activity	Product A V2	3.354002146	2.53E-02
protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	Product A V2	2.264785233	0.047799842
glucose-1-phosphate adenylyltransferase activity	Product A V2	2.059758242	0.048846674
hydrolase activity	Product A V3	3.667079616	0.024094148
FMN binding	Product A V3	2.148514318	0.004766408
acyl carrier activity	Product A V3	2.050417129	0.017748428

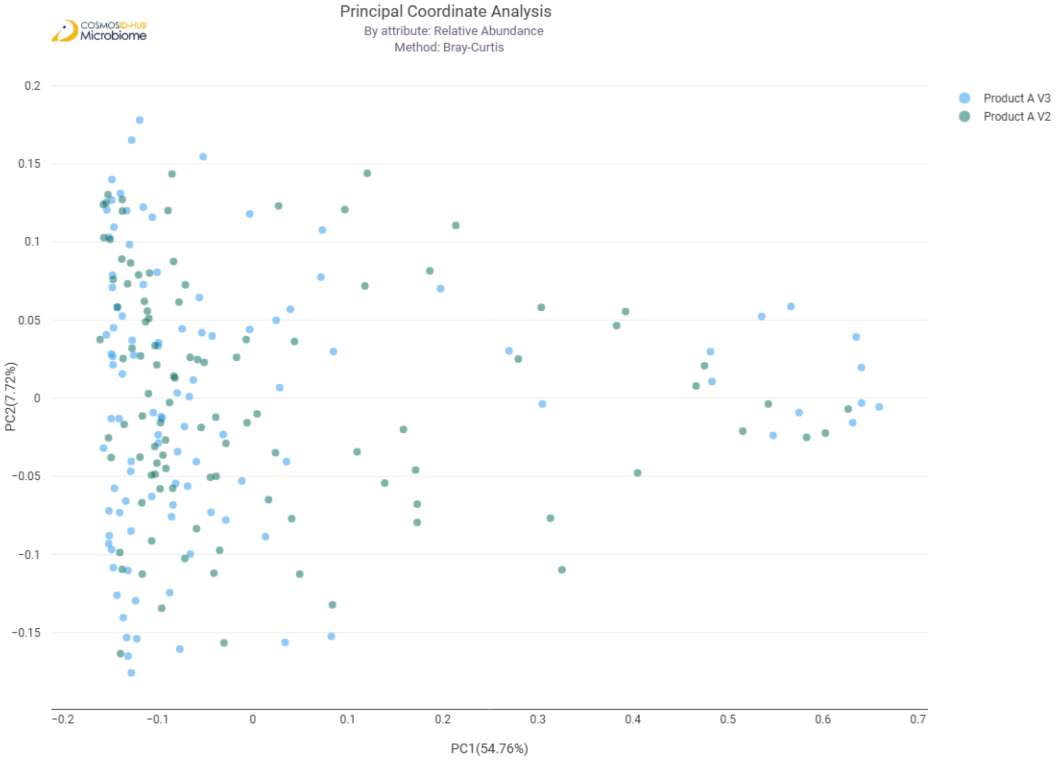
Enzyme Commission

Alpha Diversity (EC)

Chao1	
Shannon	

Simpson	

Beta Diversity (EC)

Bray-Curtis PERMNOVA p = 0.280	

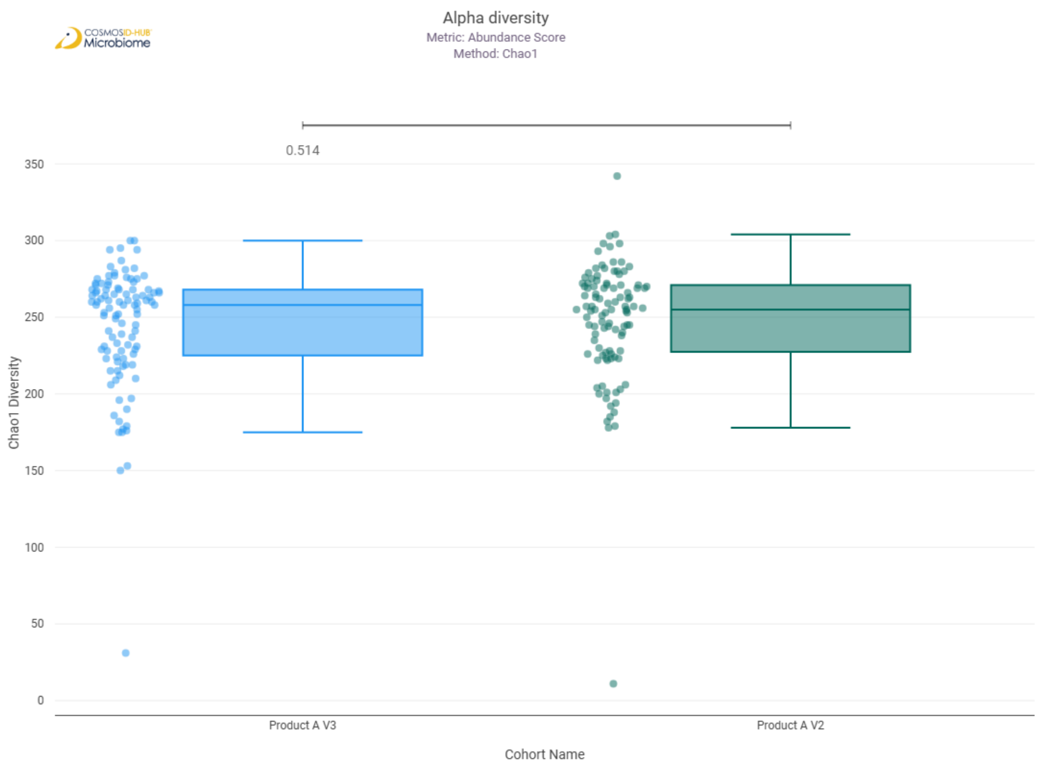
Differential Abundance (LEfSe) (EC)

Feature	Enriched Cohort	LDA Score	P-value
1,4-alpha-glucan branching enzyme	Product A V2	2.684260612	2.44E-02
Glycerol kinase	Product A V2	2.440527929	0.013515178
Phosphoglucomutase (alpha-D-glucose-1,6-bisphosphate-dependent)	Product A V2	2.39543707	0.00904253
Glycerol-3-phosphate oxidase	Product A V2	2.390435287	0.031040567
Phosphomannomutase	Product A V2	2.199521301	0.007681948
Pyridoxal 5'-phosphate synthase	Product A V3	2.579541329	0.002826568
Ribonucleoside-triphosphate reductase (thioredoxin)	Product A V3	2.571583891	0.013256264
3-hydroxybutyryl-CoA dehydrogenase	Product A V3	2.486837375	0.029804167
DNA helicase	Product A V3	2.464351655	0.002198431
[Formate-C-acetyltransferase]-activating enzyme	Product A V3	2.343710979	0.036849101
Thioredoxin-disulfide reductase	Product A V3	2.311700333	0.037902094
Ribonuclease P	Product A V3	2.241667448	0.0029349
Orotidine-5'-phosphate decarboxylase	Product A V3	2.23363033	0.001957618
Cysteine desulfurase	Product A V3	2.221119485	0.042608467
Short-chain acyl-CoA dehydrogenase	Product A V3	2.220517395	0.011677397
Pyruvate, phosphate dikinase	Product A V3	2.140426457	0.019839554
Asparagine--tRNA ligase	Product A V3	2.118204505	0.007122062
Phenylalanine--tRNA ligase	Product A V3	2.110783168	0.00345801
Signal peptidase I	Product A V3	2.096427343	0.005695585
Beta-ketoacyl-[acyl-carrier-protein] synthase III	Product A V3	2.09399442	0.036849101
Transferred entry 2.3.1.274	Product A V3	2.092424107	0.000331128
Citrate (pro-3S)-lyase	Product A V3	2.08887282	0.000953333

[Acyl-carrier-protein] S-malonyltransferase	Product A V3	2.076345774	0.023241053
Adenine phosphoribosyltransferase	Product A V3	2.074820233	0.011715972
Peptide-methionine (S)-S-oxide reductase	Product A V3	2.047296647	0.027783601
Tyrosine--tRNA ligase	Product A V3	2.024258503	0.034817712
Alanine--tRNA ligase	Product A V3	2.00263877	0.01535833

MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1	

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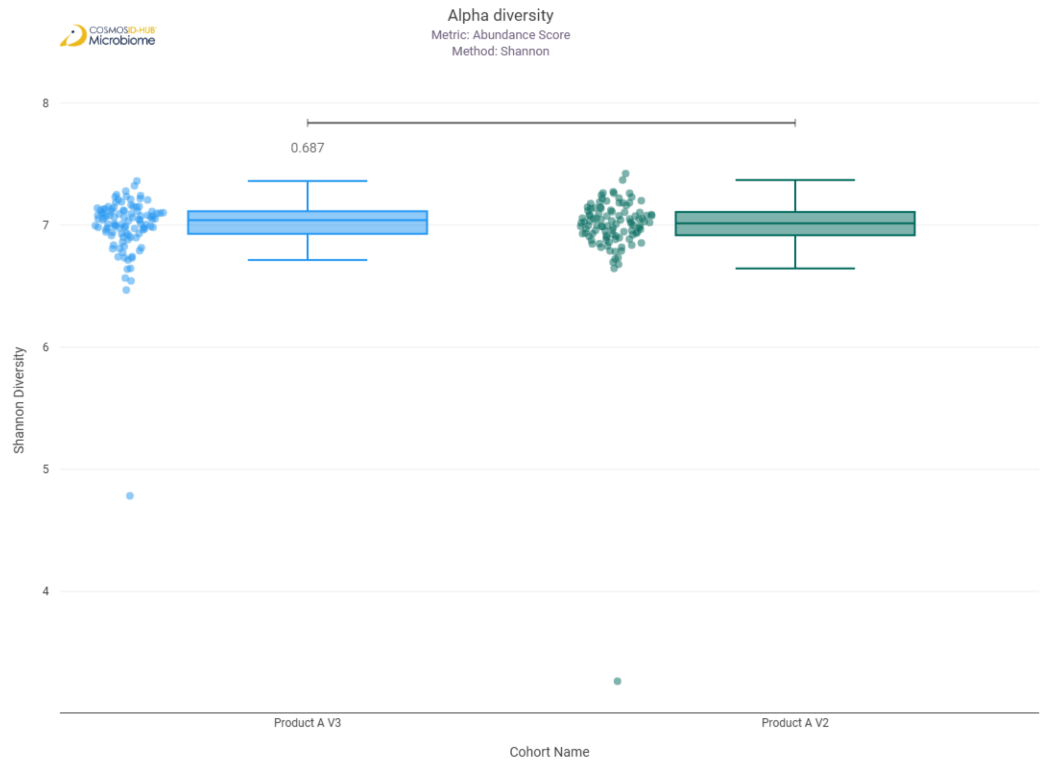

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Beta Diversity (MetaCyc)

Bray-Curtis

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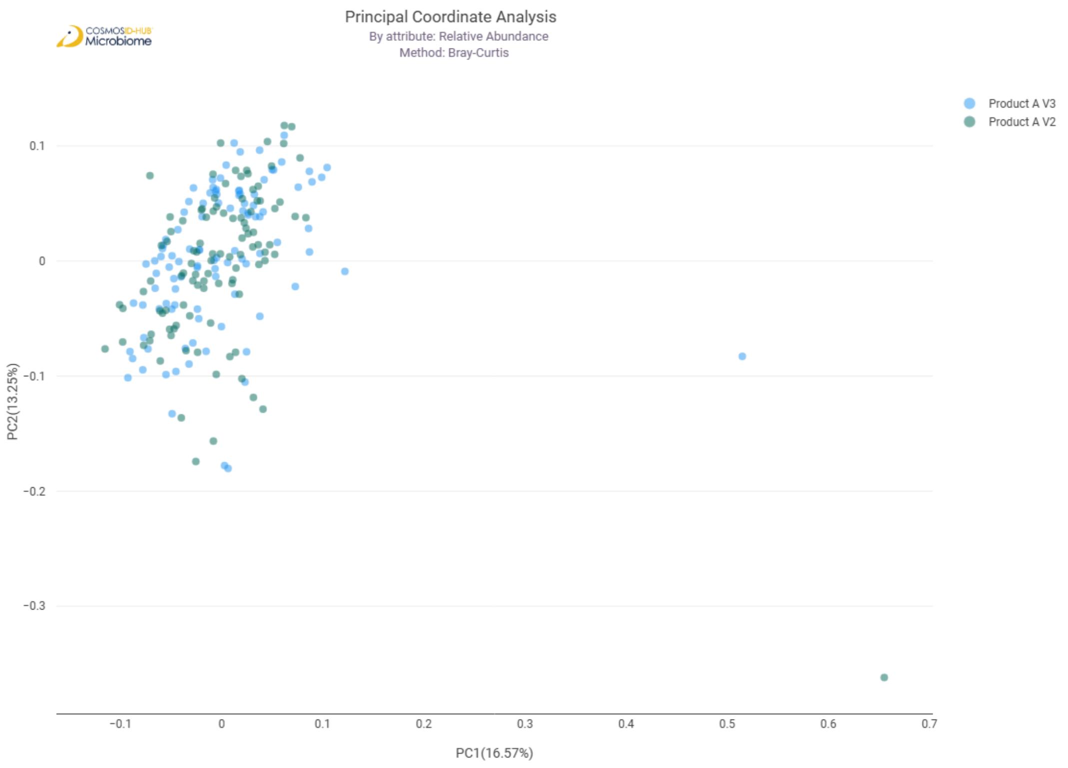
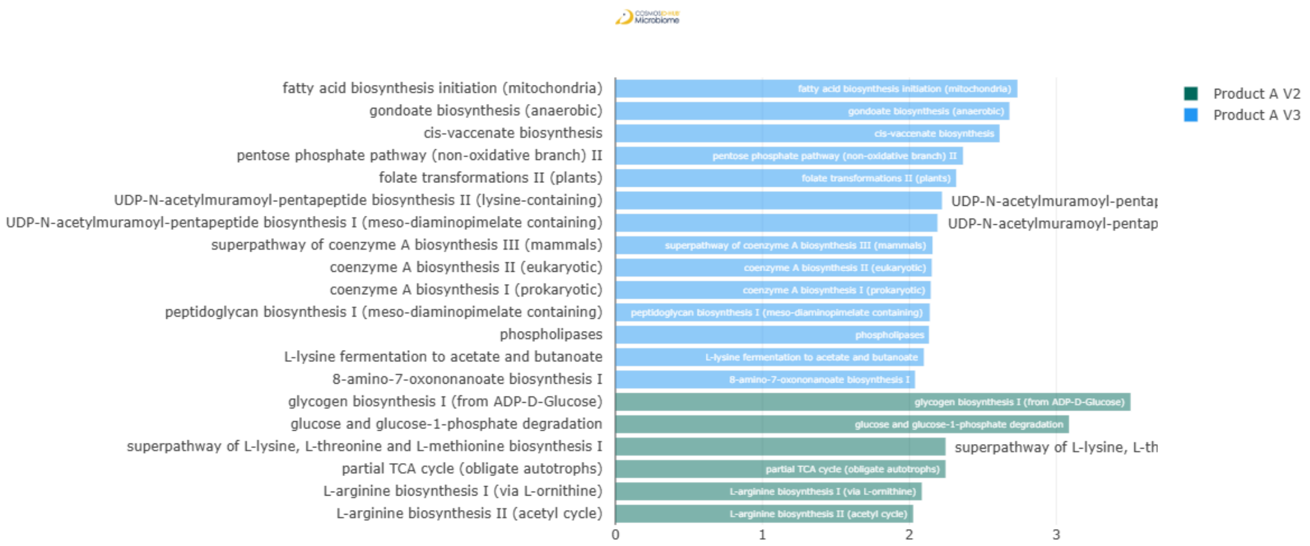


Differential Abundance (LEfSe) (MetaCyc)



Feature	Enriched Cohort	LDA Score	P-value
fatty acid biosynthesis initiation (mitochondria)	Product A V3	2.735008255	0.039973314
gondoate biosynthesis (anaerobic)	Product A V3	2.68021462	0.015554288
cis-vaccenate biosynthesis	Product A V3	2.613361453	0.034227261

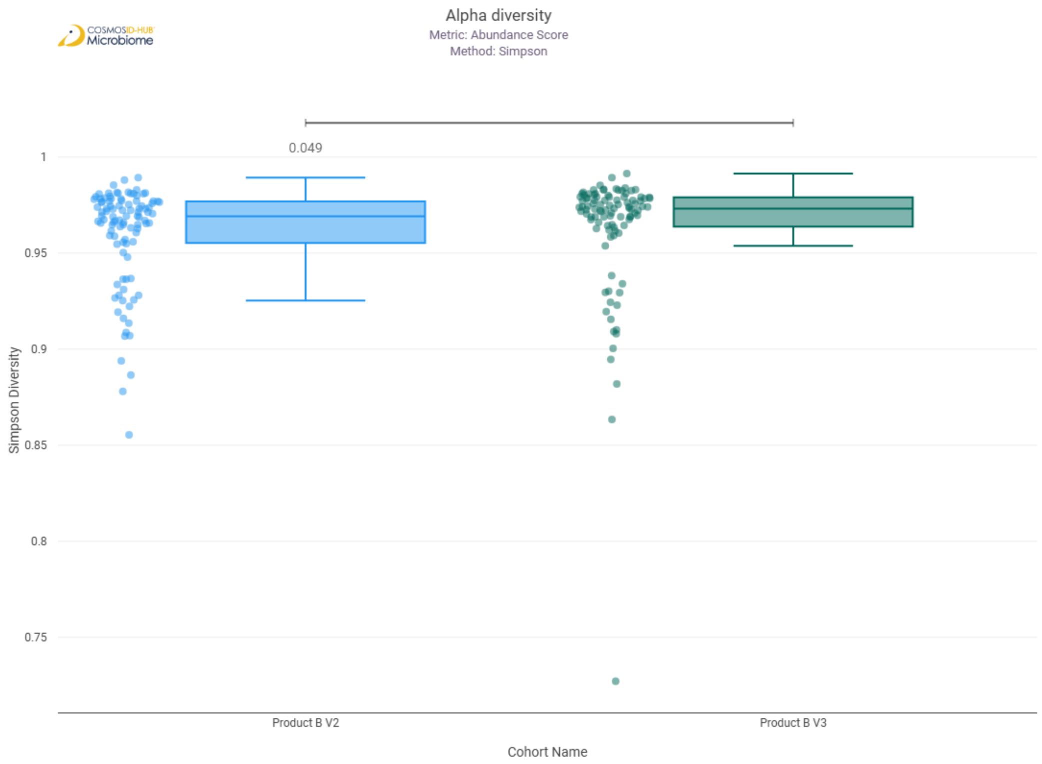
pentose phosphate pathway (non-oxidative branch) II	Product A V3	2.364544919	0.01871087
folate transformations II (plants)	Product A V3	2.31833131	0.038762815
UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)	Product A V3	2.221900027	0.024021987
UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)	Product A V3	2.191038313	0.020773626
superpathway of coenzyme A biosynthesis III (mammals)	Product A V3	2.157245055	0.001492812
coenzyme A biosynthesis II (eukaryotic)	Product A V3	2.151990248	0.001980554
coenzyme A biosynthesis I (prokaryotic)	Product A V3	2.145034758	0.006262567
peptidoglycan biosynthesis I (meso-diaminopimelate containing)	Product A V3	2.138440512	0.045141198
phospholipases	Product A V3	2.132849146	0.014251091
L-lysine fermentation to acetate and butanoate	Product A V3	2.098199076	0.02972225
Transferred entry 2.3.1.274	Product A V3	2.092424107	0.000331128
Citrate (pro-3S)-lyase	Product A V3	2.08887282	0.000953333
[Acyl-carrier-protein] S-malonyltransferase	Product A V3	2.076345774	0.023241053
Adenine phosphoribosyltransferase	Product A V3	2.074820233	0.011715972
Peptide-methionine (S)-S-oxide reductase	Product A V3	2.047296647	0.027783601
8-amino-7-oxononanoate biosynthesis I	Product A V3	2.03838881	0.023770185
Tyrosine--tRNA ligase	Product A V3	2.024258503	0.034817712
Alanine--tRNA ligase	Product A V3	2.00263877	0.01535833
glycogen biosynthesis I (from ADP-D-Glucose)	Product A V2	3.504241049	7.47E-03
glucose and glucose-1-phosphate degradation	Product A V2	3.085696443	0.001014125
superpathway of L-lysine, L-threonine and L-methionine biosynthesis I	Product A V2	2.246128695	0.000192166
partial TCA cycle (obligate autotrophs)	Product A V2	2.245865551	0.012144606
L-arginine biosynthesis I (via L-ornithine)	Product A V2	2.084419907	0.008864648
L-arginine biosynthesis II (acetyl cycle)	Product A V2	2.025666773	0.007998331

Comparison 2: Product B V2 vs Product B V3

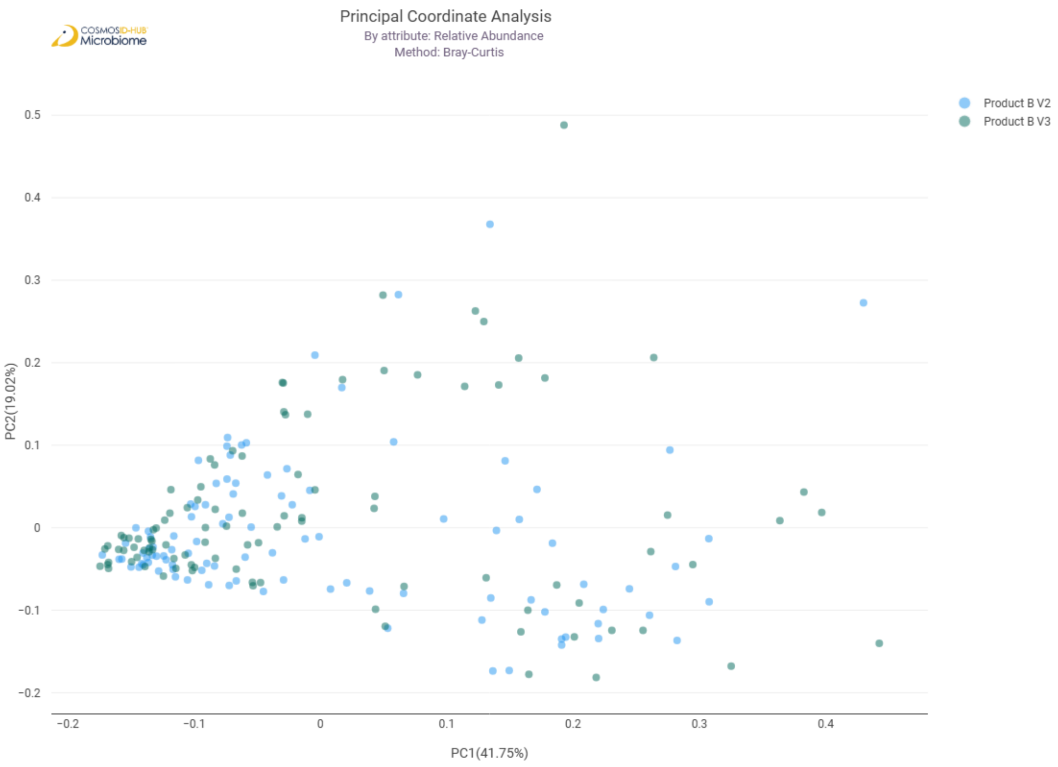
Gene Ontology

Alpha Diversity (GO)

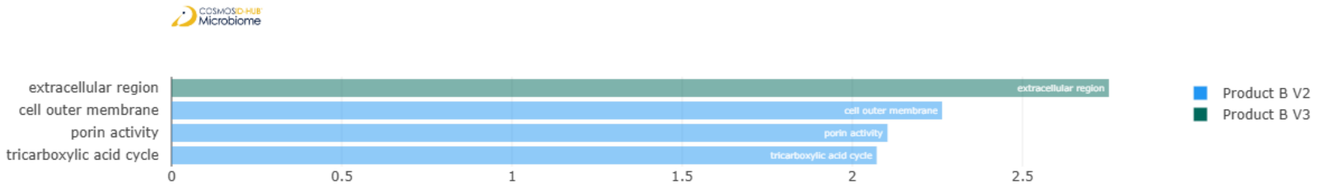
Chao1	
Shannon	

Simpson	

Beta Diversity (GO)

Bray-Curtis PERMNOVA p = 0.271	

Differential Abundance (LEfSe) (GO)

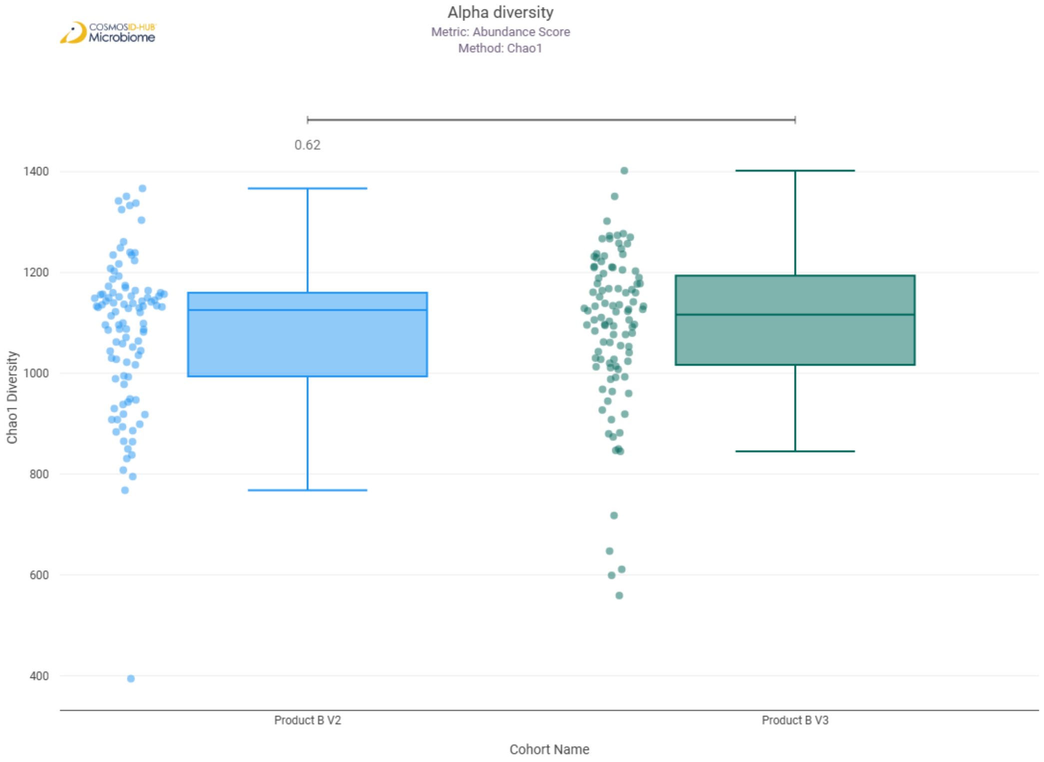


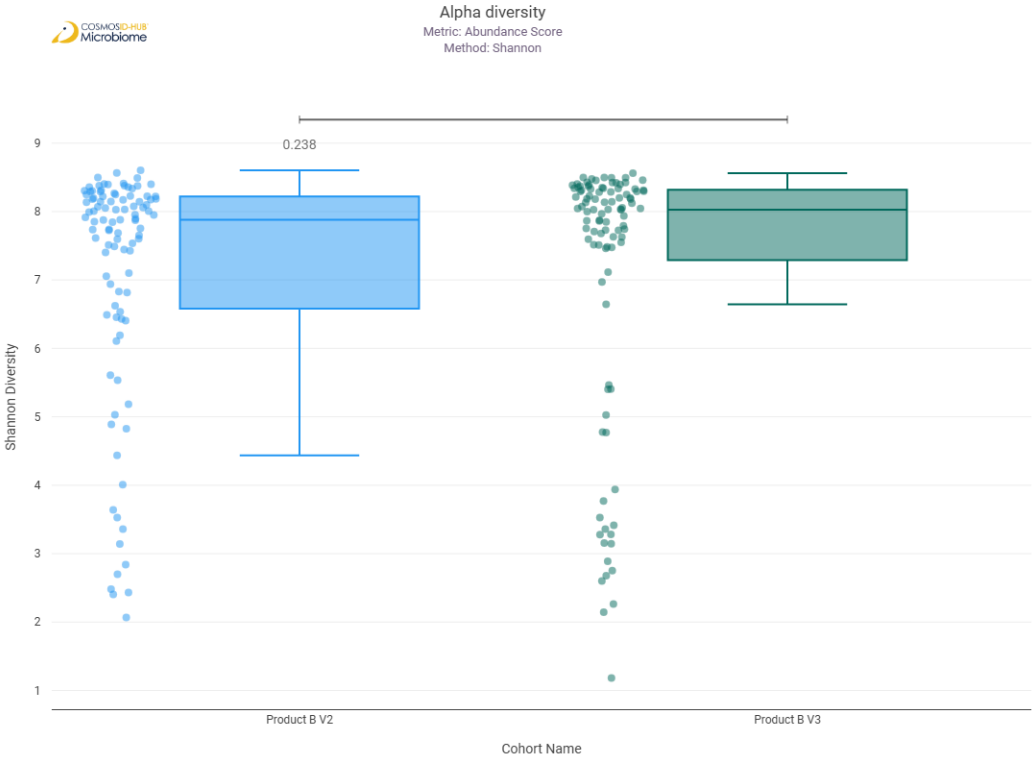
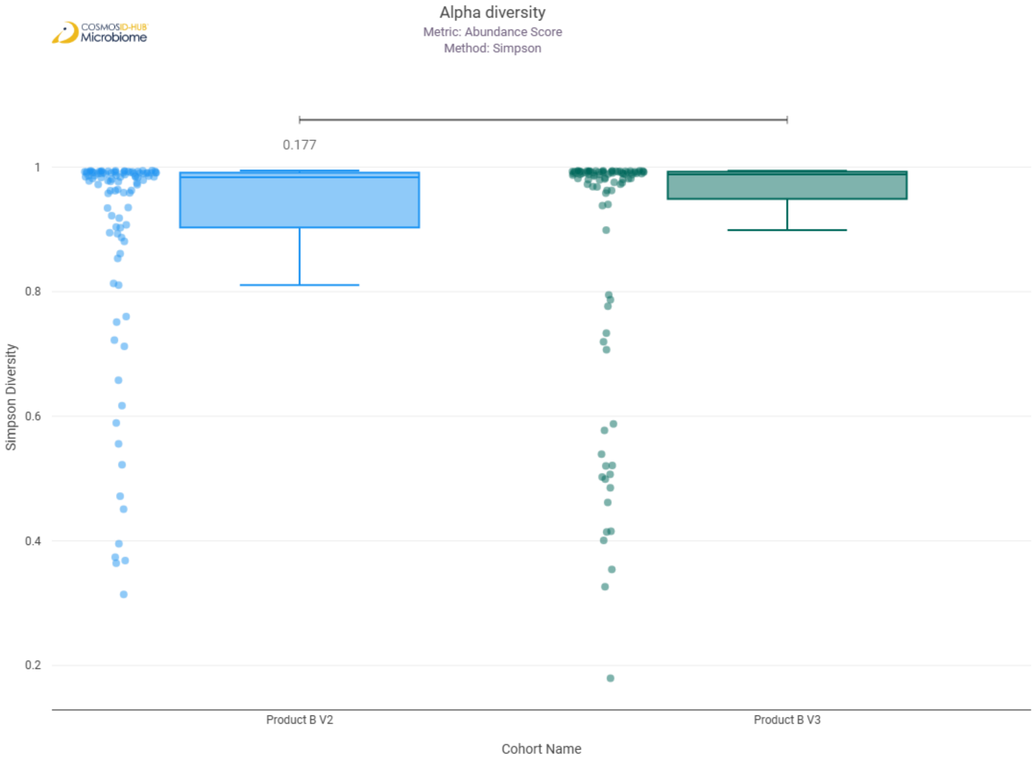
Feature	Enriched Cohort	LDA Score	P-value
extracellular region	Product B V3	2.753697521	0.026348219
cell outer membrane	Product B V2	2.263677165	0.043566353
porin activity	Product B V2	2.103296471	8.17E-08
tricarboxylic acid cycle	Product B V2	2.071505025	0.011602109

Enzyme Commission

Alpha Diversity (EC)

Chao1



Shannon	
Simpson	

Beta Diversity (EC)

Bray-Curtis

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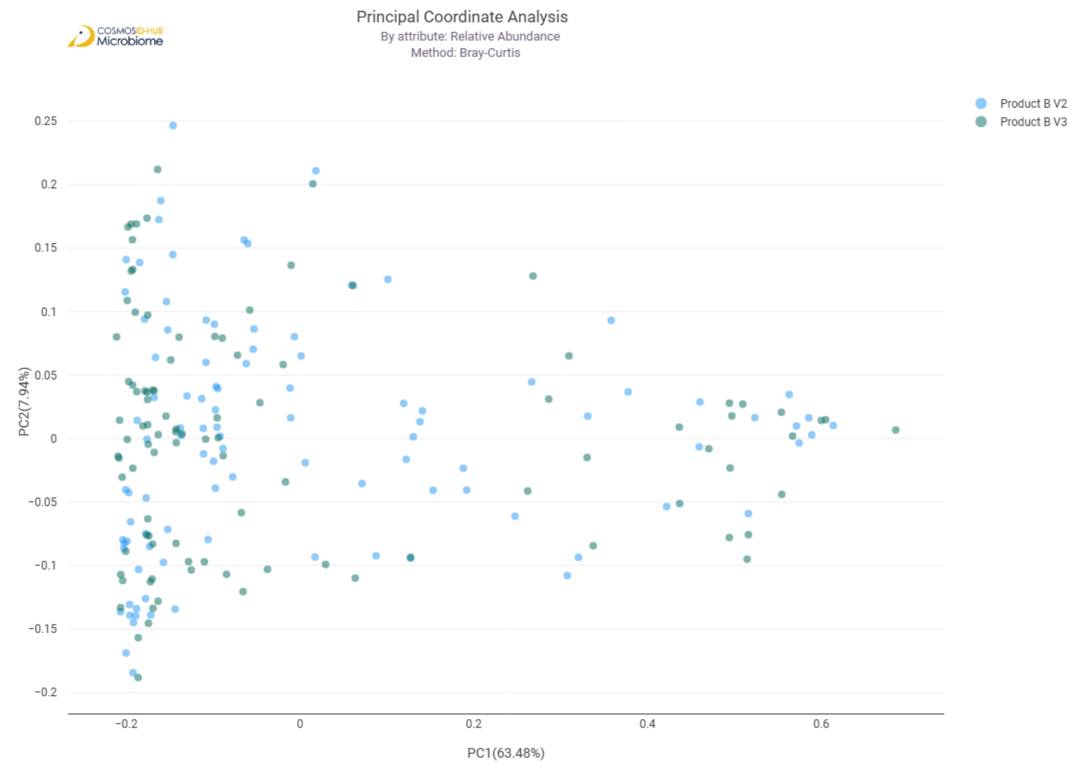
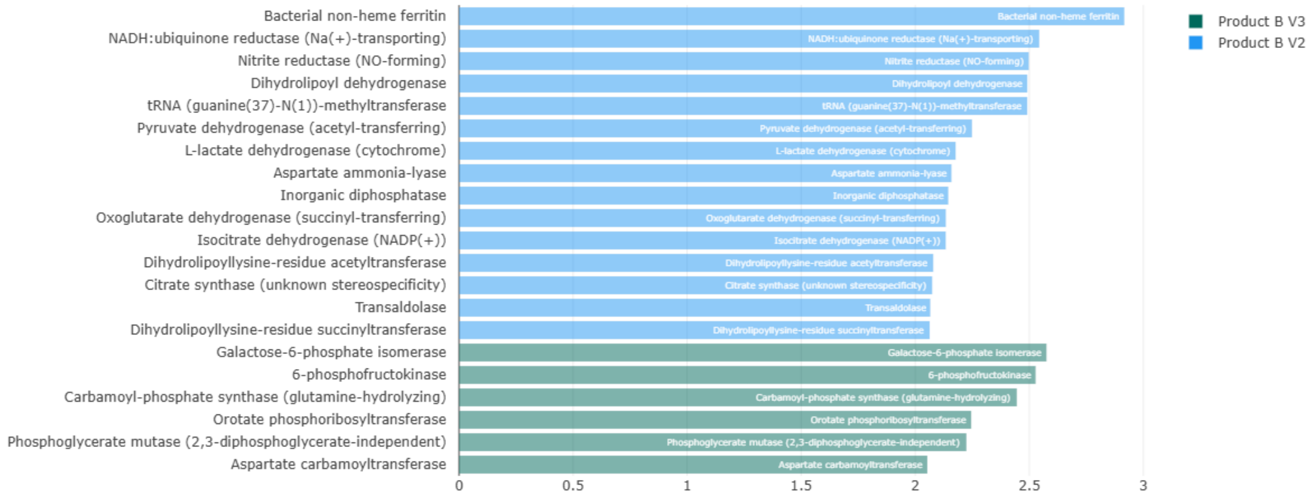


Differential Abundance (LEfSe) (EC)

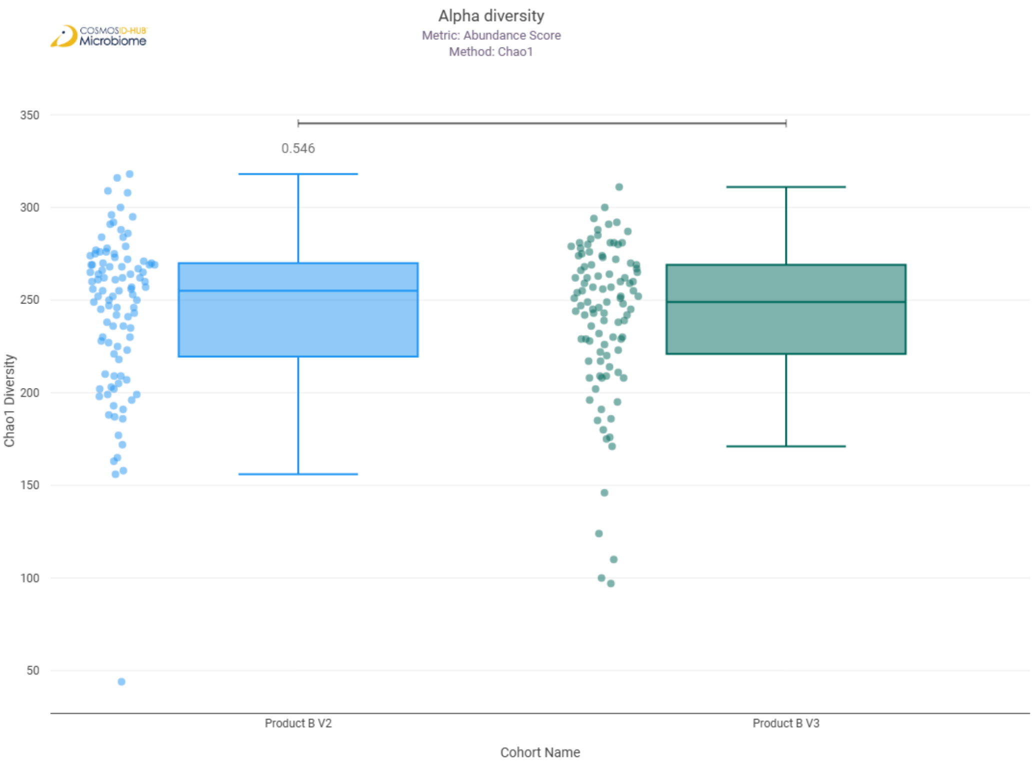


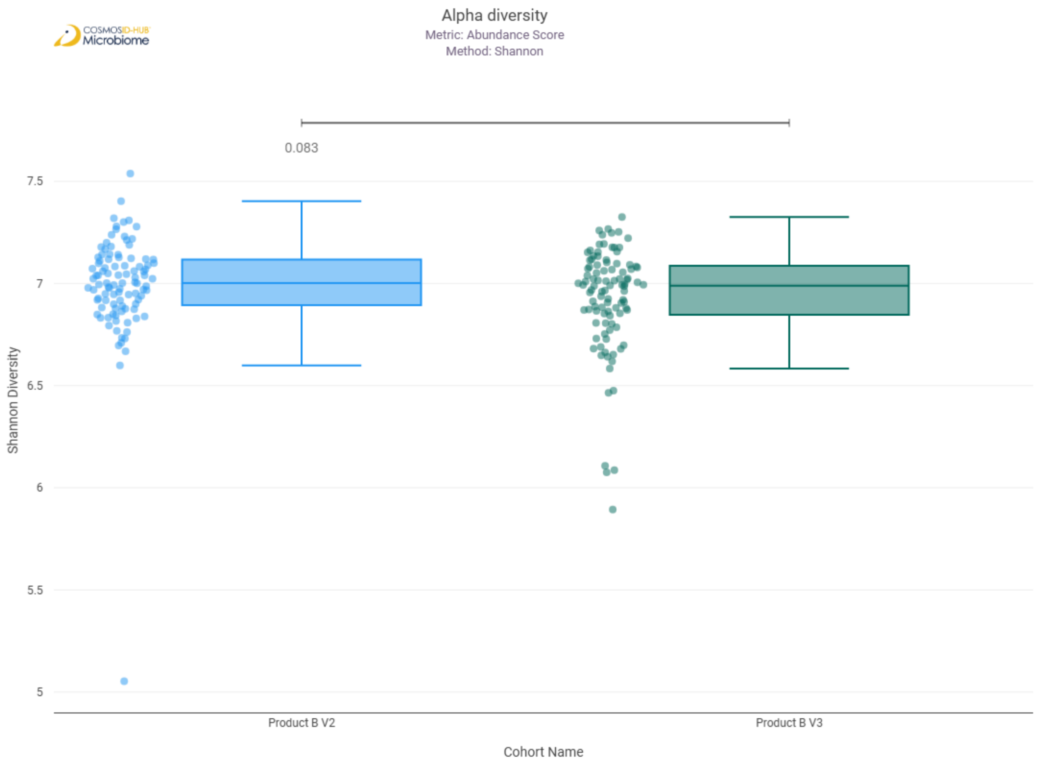
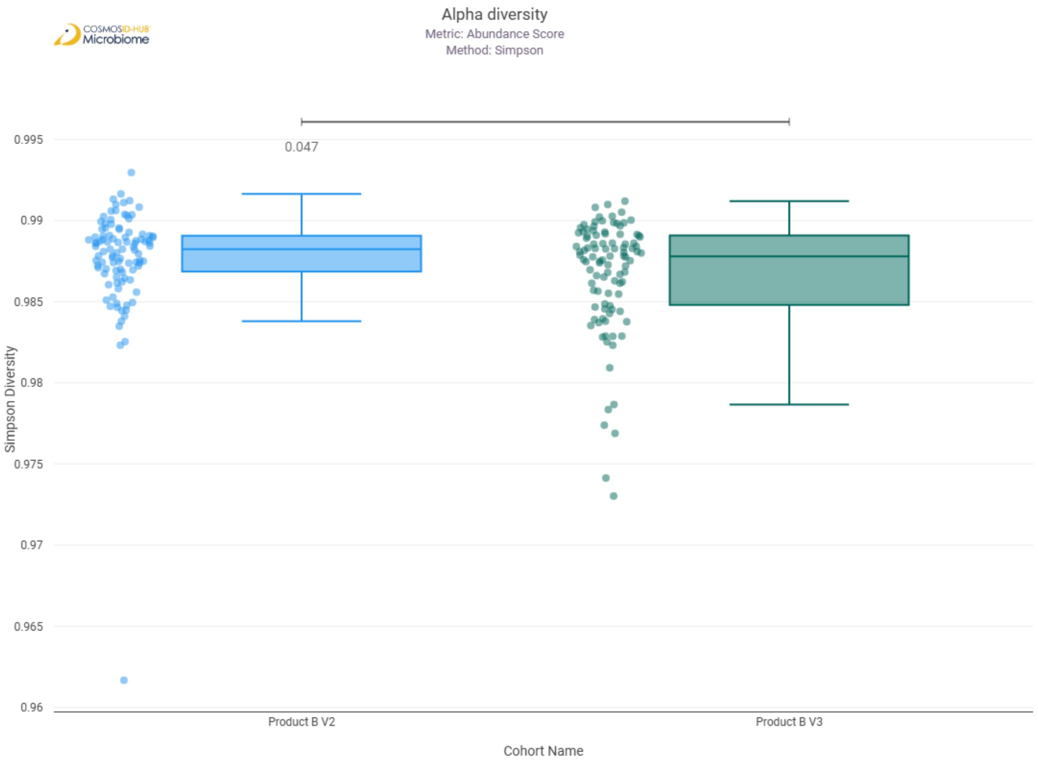
Feature	Enriched Cohort	LDA Score	P-value
Bacterial non-heme ferritin	Product B V2	2.916370778	0.008140404
NADH:ubiquinone reductase (Na(+)-transporting)	Product B V2	2.543316962	3.35E-02
Nitrite reductase (NO-forming)	Product B V2	2.497728264	0.000588206

Dihydrolipoyl dehydrogenase	Product B V2	2.491221448	0.007299969
tRNA (guanine(37)-N(1))-methyltransferase	Product B V2	2.491026824	0.001868126
Pyruvate dehydrogenase (acetyl-transferring)	Product B V2	2.248619249	0.023812891
L-lactate dehydrogenase (cytochrome)	Product B V2	2.176913806	3.15038E-05
Aspartate ammonia-lyase	Product B V2	2.158608668	0.006538231
Inorganic diphosphatase	Product B V2	2.144704717	0.047525328
Oxoglutarate dehydrogenase (succinyl-transferring)	Product B V2	2.133982099	0.000116559
Isocitrate dehydrogenase (NADP(+))	Product B V2	2.13357857	0.007737888
Dihydrolipoyllysine-residue acetyltransferase	Product B V2	2.078756294	1.59585E-05
Citrate synthase (unknown stereospecificity)	Product B V2	2.074165128	0.014096561
Transaldolase	Product B V2	2.065814207	0.013686825
Dihydrolipoyllysine-residue succinyltransferase	Product B V2	2.063232884	0.001962993
Galactose-6-phosphate isomerase	Product B V3	2.575276965	0.040843374
6-phosphofructokinase	Product B V3	2.527683882	0.011764389
Carbamoyl-phosphate synthase (glutamine-hydrolyzing)	Product B V3	2.445328101	0.035613373
Orotate phosphoribosyltransferase	Product B V3	2.24538852	0.004285808
Phosphoglycerate mutase (2,3-diphosphoglycerate-independent)	Product B V3	2.224097039	0.038266022
Aspartate carbamoyltransferase	Product B V3	2.052876435	0.006116265

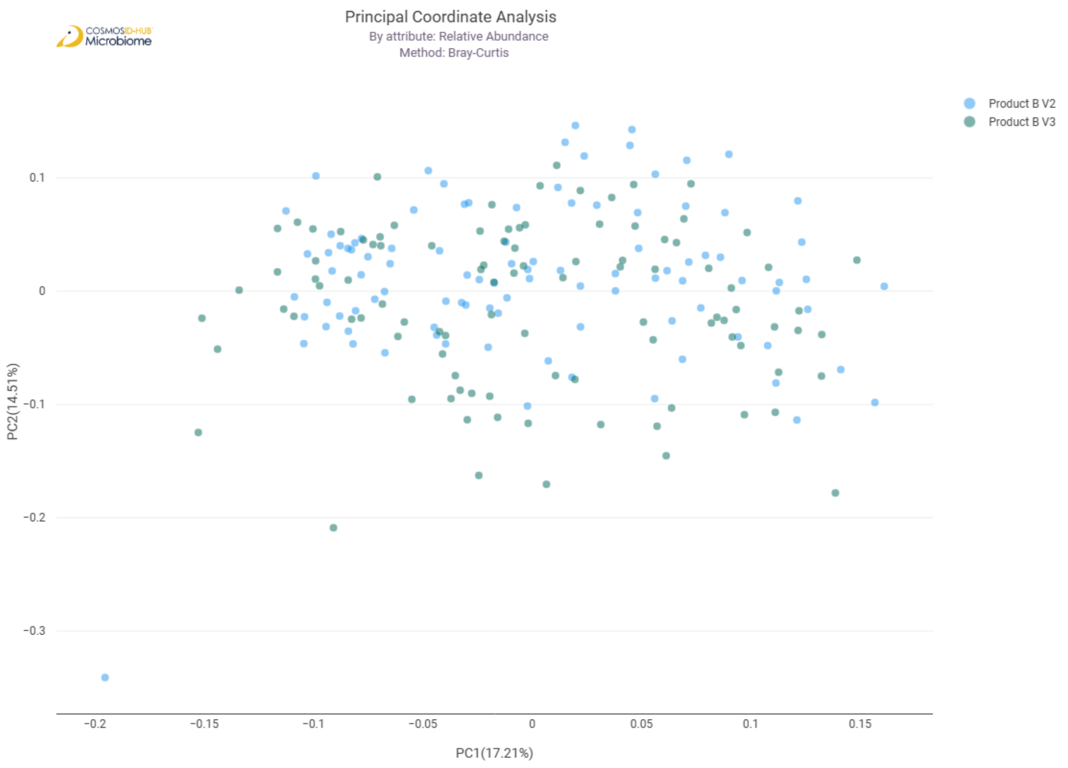
MetaCyc Pathways

Alpha Diversity (MetaCyc)

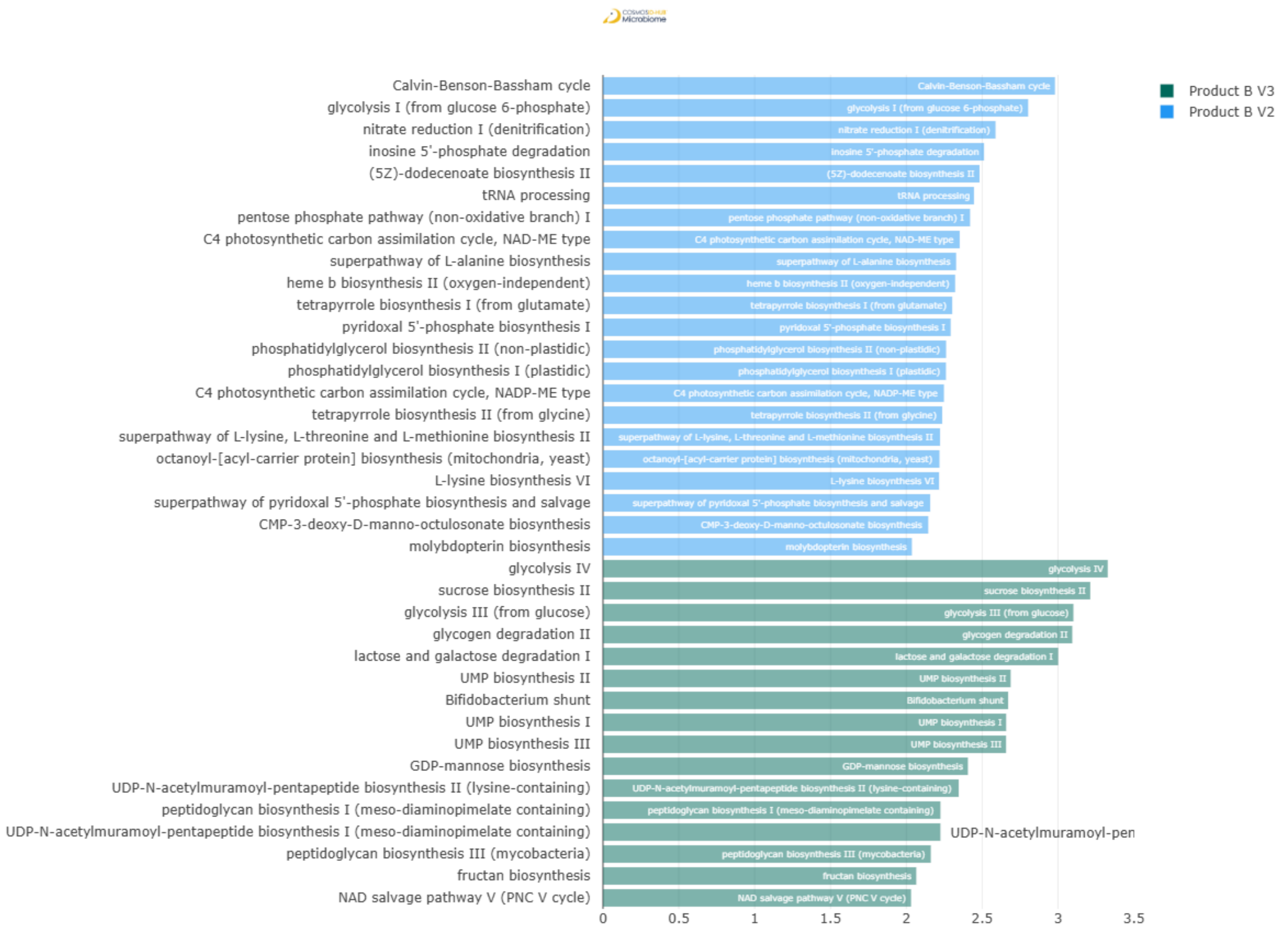
Chao1	

Shannon	
Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis PERMNOVA p = 0.007	

Differential Abundance (LEfSe) (MetaCyc)



Feature	Enriched Cohort	LDA Score	P-value
Calvin-Benson-Bassham cycle	Product B V2	2.980017469	0.002293376
glycolysis I (from glucose 6-phosphate)	Product B V2	2.803147252	0.049050725
nitrate reduction I (denitrification)	Product B V2	2.588156927	0.00033841
inosine 5'-phosphate degradation	Product B V2	2.512470778	0.040843374
(5Z)-dodecenoate biosynthesis II	Product B V2	2.482703129	0.002215853
tRNA processing	Product B V2	2.446113576	0.000101039
pentose phosphate pathway (non-oxidative branch) I	Product B V2	2.420285883	0.014160637
C4 photosynthetic carbon assimilation cycle, NAD-ME type	Product B V2	2.352117478	0.002962847
superpathway of L-alanine biosynthesis	Product B V2	2.328429283	0.001134473
heme b biosynthesis II (oxygen-independent)	Product B V2	2.32188526	5.35921E-06
tetrapyrrole biosynthesis I (from glutamate)	Product B V2	2.302670791	2.31E-02
pyridoxal 5'-phosphate biosynthesis I	Product B V2	2.292538957	0.019224991
phosphatidylglycerol biosynthesis II (non-plastidic)	Product B V2	2.262213821	0.012475606
phosphatidylglycerol biosynthesis I (plastidic)	Product B V2	2.261336783	0.011763758
C4 photosynthetic carbon assimilation cycle, NADP-ME type	Product B V2	2.248031239	0.036917997
tetrapyrrole biosynthesis II (from glycine)	Product B V2	2.236665884	0.014840025

superpathway of L-lysine, L-threonine and L-methionine biosynthesis II	Product B V2	2.222294134	0.010593229
octanoyl-[acyl-carrier protein] biosynthesis (mitochondria, yeast)	Product B V2	2.218678927	0.02610799
L-lysine biosynthesis VI	Product B V2	2.215637736	0.011047972
superpathway of pyridoxal 5'-phosphate biosynthesis and salvage	Product B V2	2.157495637	0.01350269
CMP-3-deoxy-D-manno-octulosonate biosynthesis	Product B V2	2.144607845	0.004222717
molybdopterin biosynthesis	Product B V2	2.036690834	0.003881927
glycolysis IV	Product B V3	3.327911078	0.007851099
sucrose biosynthesis II	Product B V3	3.212667295	3.12E-02
glycolysis III (from glucose)	Product B V3	3.101708701	0.02351136
glycogen degradation II	Product B V3	3.09417983	0.035613373
lactose and galactose degradation I	Product B V3	3.001224899	0.038038729
UMP biosynthesis II	Product B V3	2.687935173	0.000363989
Bifidobacterium shunt	Product B V3	2.671196279	0.038942744
UMP biosynthesis I	Product B V3	2.658158059	0.000570683
UMP biosynthesis III	Product B V3	2.657607009	0.000565546
GDP-mannose biosynthesis	Product B V3	2.406080835	0.030213058
UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)	Product B V3	2.345372582	0.014748123
peptidoglycan biosynthesis I (meso-diaminopimelate containing)	Product B V3	2.224909222	0.031156435
UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)	Product B V3	2.224695184	0.040603143
peptidoglycan biosynthesis III (mycobacteria)	Product B V3	2.161540068	0.046039851
fructan biosynthesis	Product B V3	2.065573749	0.031928973
NAD salvage pathway V (PNC V cycle)	Product B V3	2.031437871	0.002049925

Comparison 3: Product A V2 vs Product B V2

Gene Ontology

Alpha Diversity (GO)

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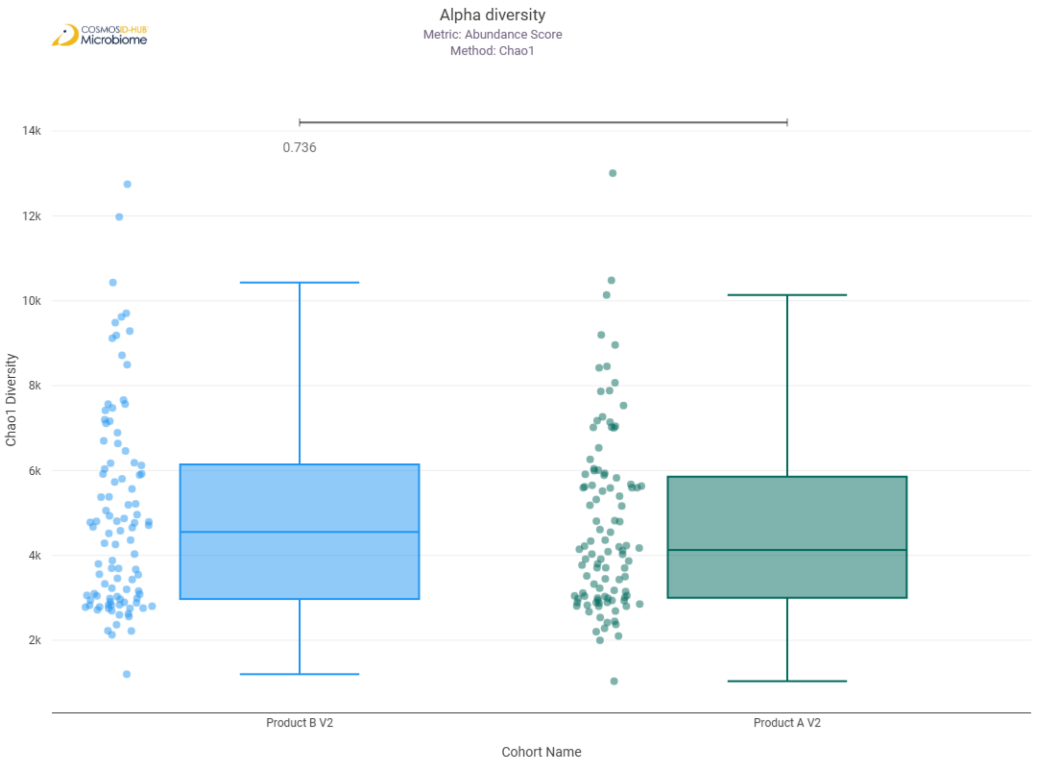
<td> </td>
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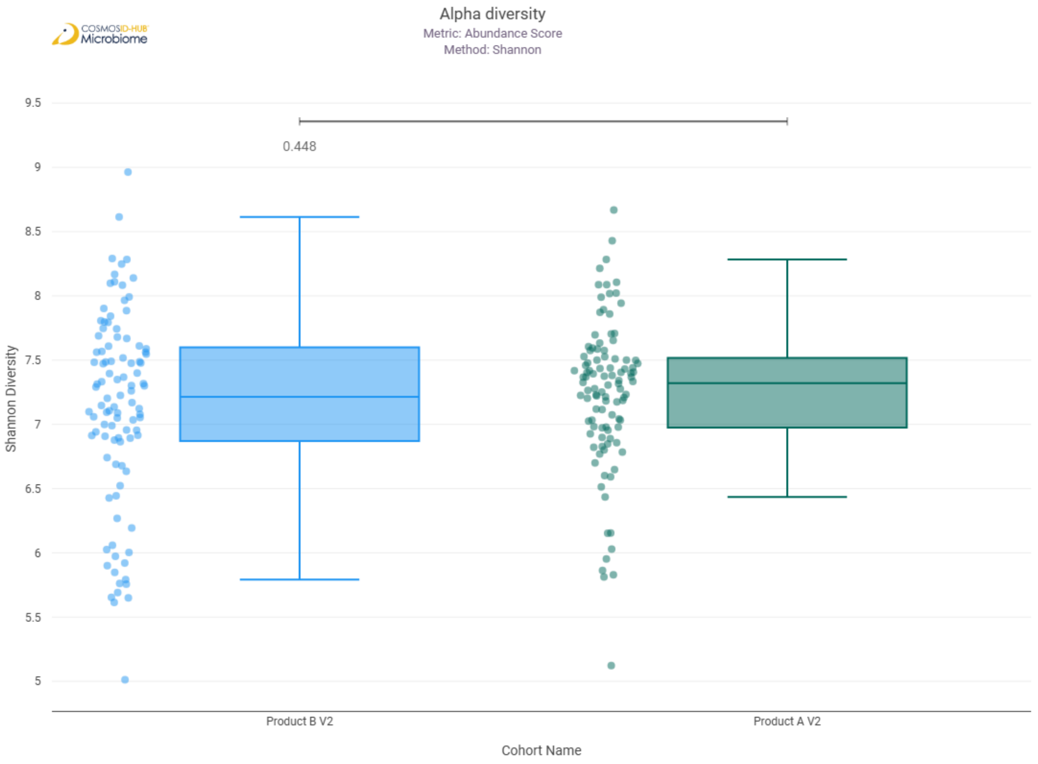
<td> </td>
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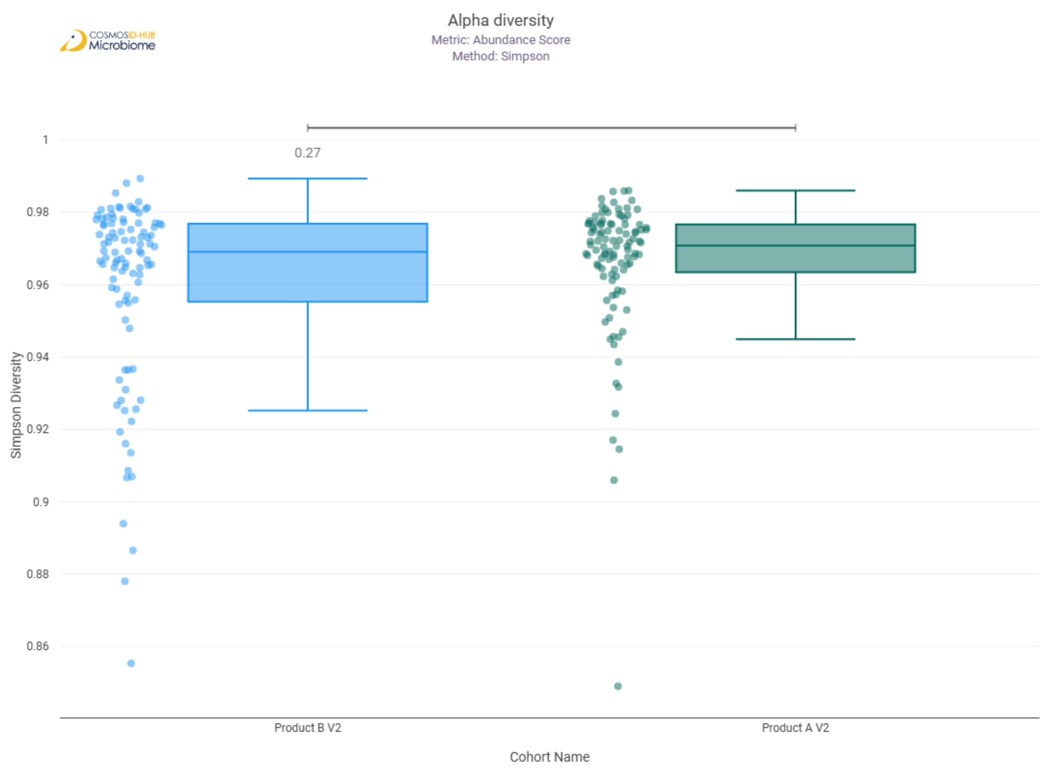
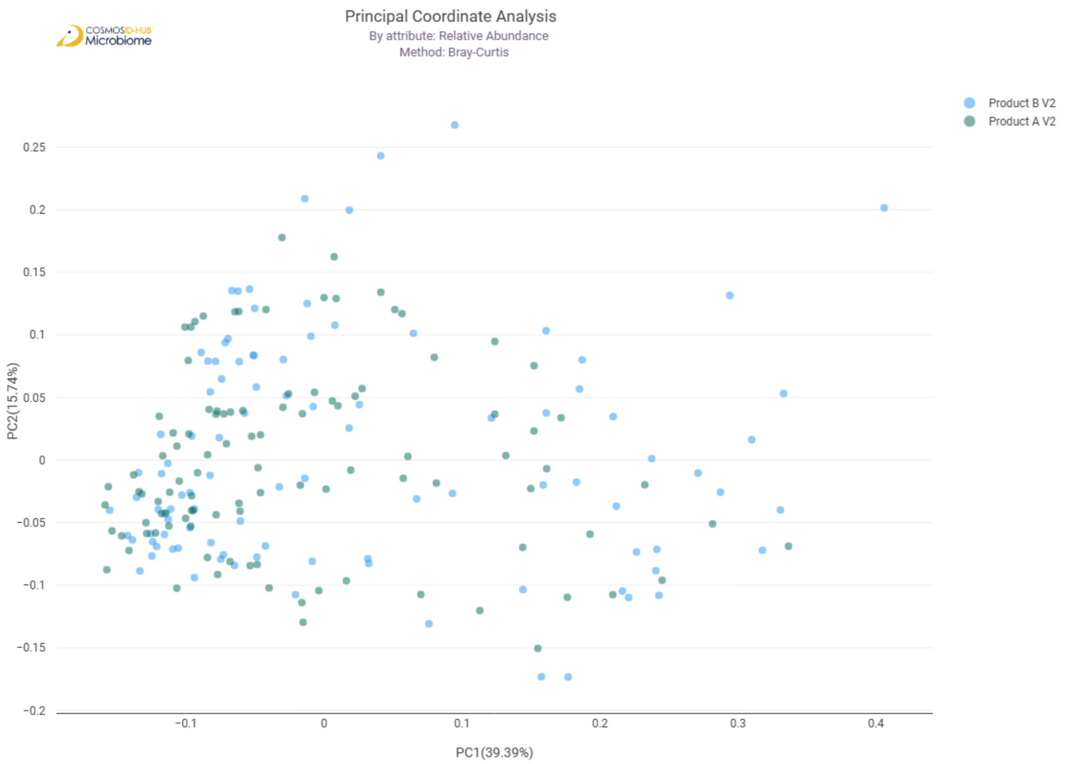
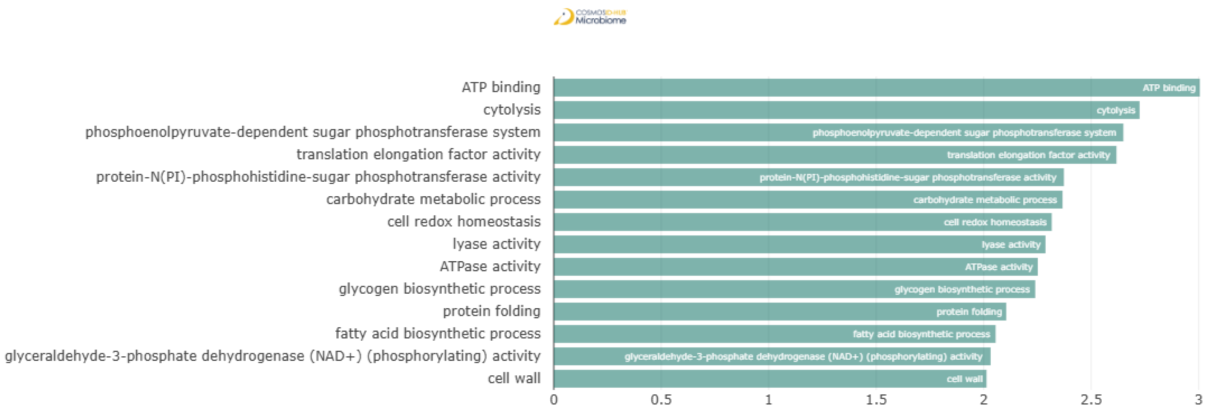
Simpson	

Beta Diversity (GO)

Bray-Curtis PERMNOVA p = 0.044	

Differential Abundance (LEfSe) (GO)



Feature	Enriched Cohort	LDA Score	P-value
ATP binding	Product A V2	3.005226801	0.031977275
cytolysis	Product A V2	2.725138877	0.000880468
phosphoenolpyruvate-dependent sugar phosphotransferase system	Product A V2	2.649451853	0.042757398
translation elongation factor activity	Product A V2	2.617507076	0.043739123
protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	Product A V2	2.372987284	0.047591773
carbohydrate metabolic process	Product A V2	2.366604496	0.047858458
cell redox homeostasis	Product A V2	2.316574729	0.048395595
lyase activity	Product A V2	2.287508955	0.008162299
ATPase activity	Product A V2	2.251478935	0.040616459
glycogen biosynthetic process	Product A V2	2.2397374	0.035346801
protein folding	Product A V2	2.104787498	1.88E-02
fatty acid biosynthetic process	Product A V2	2.055382736	0.002140946
glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity	Product A V2	2.032207372	0.010614864
cell wall	Product A V2	2.013176421	0.042273563

Enzyme Commission

Alpha Diversity (EC)

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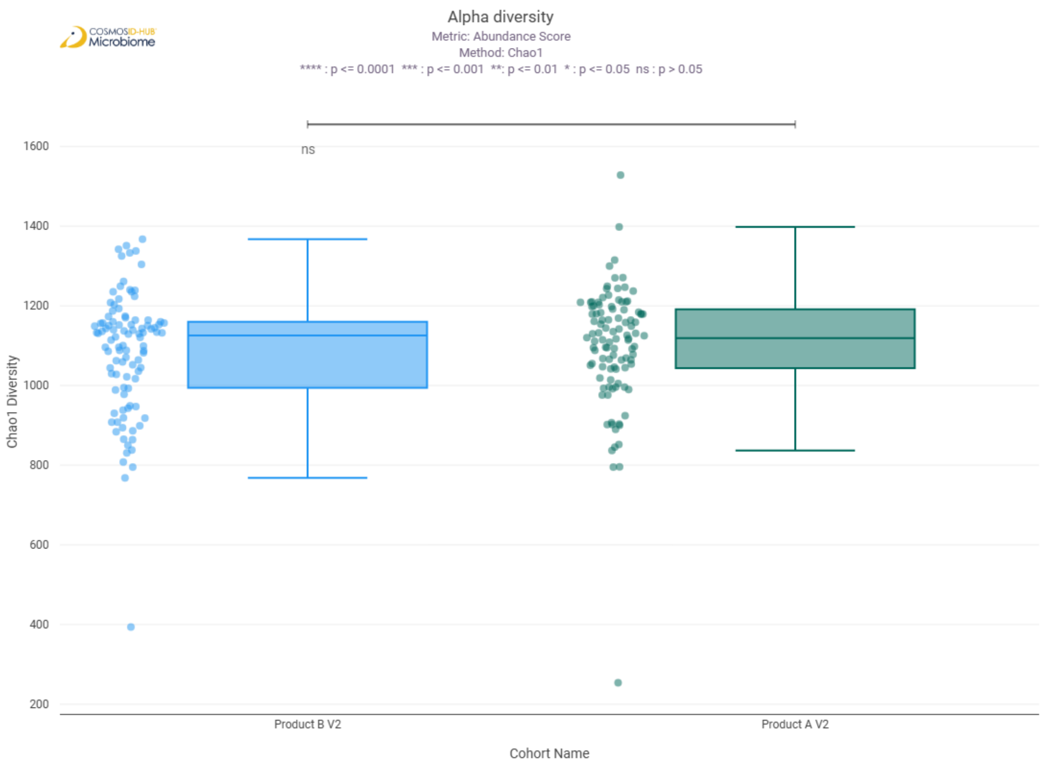
<tr><td>Chao1</td><td>
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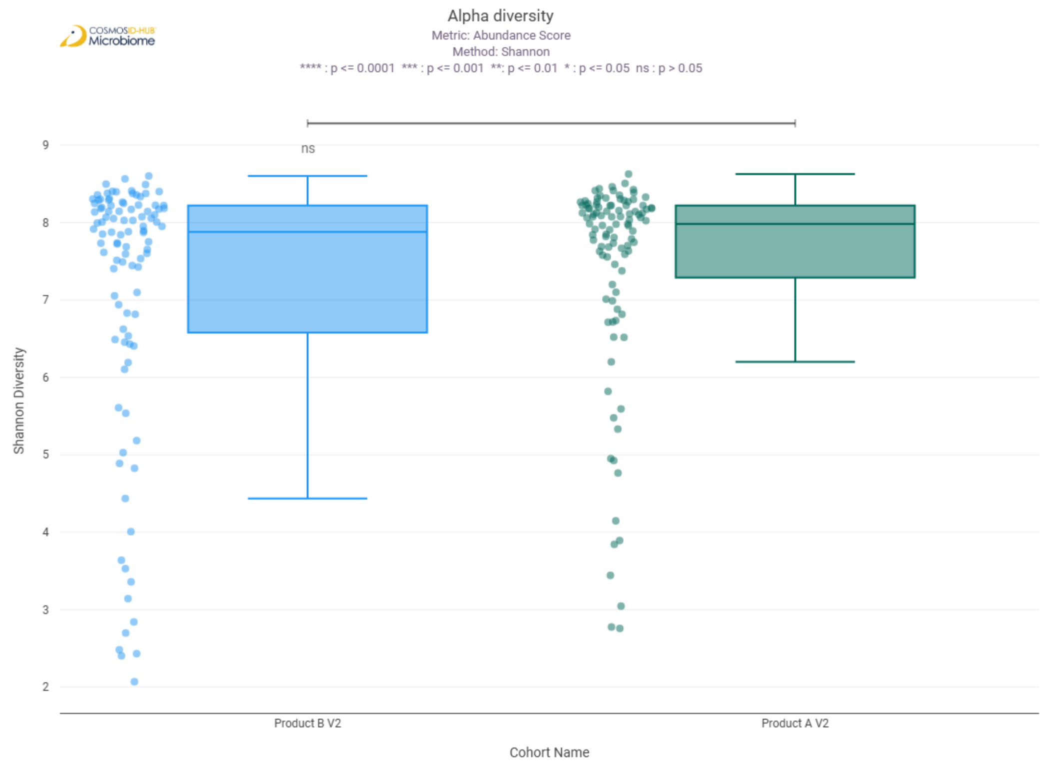
<tr><td>Shannon</td><td>
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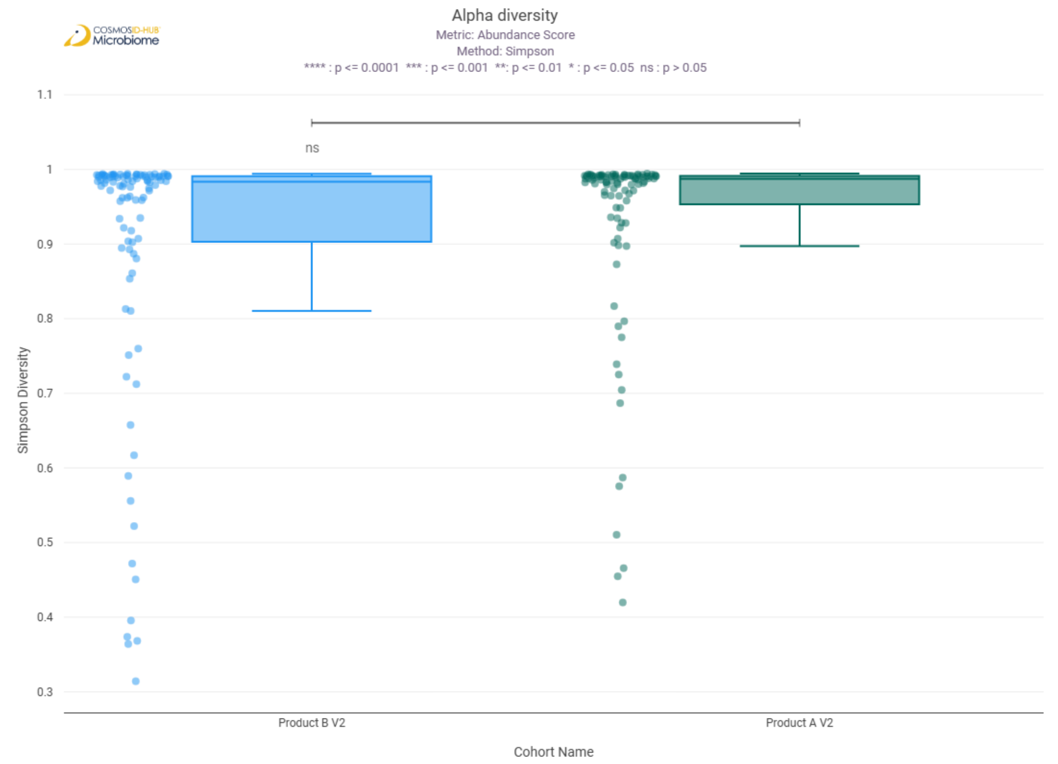
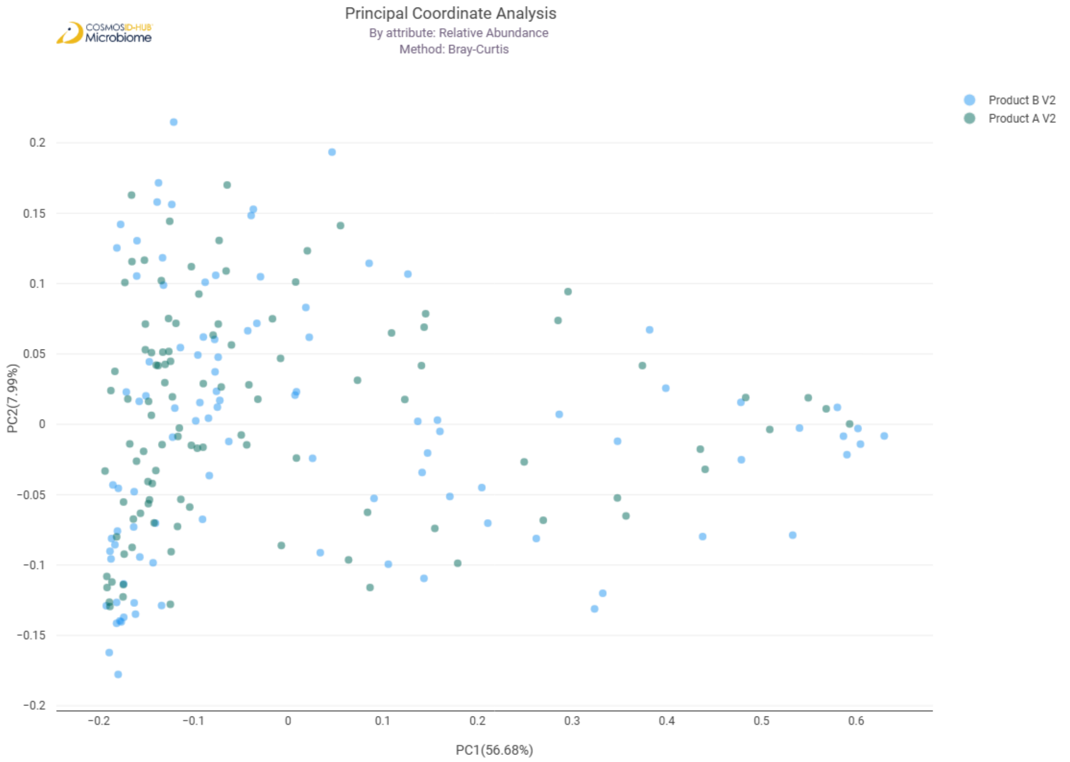
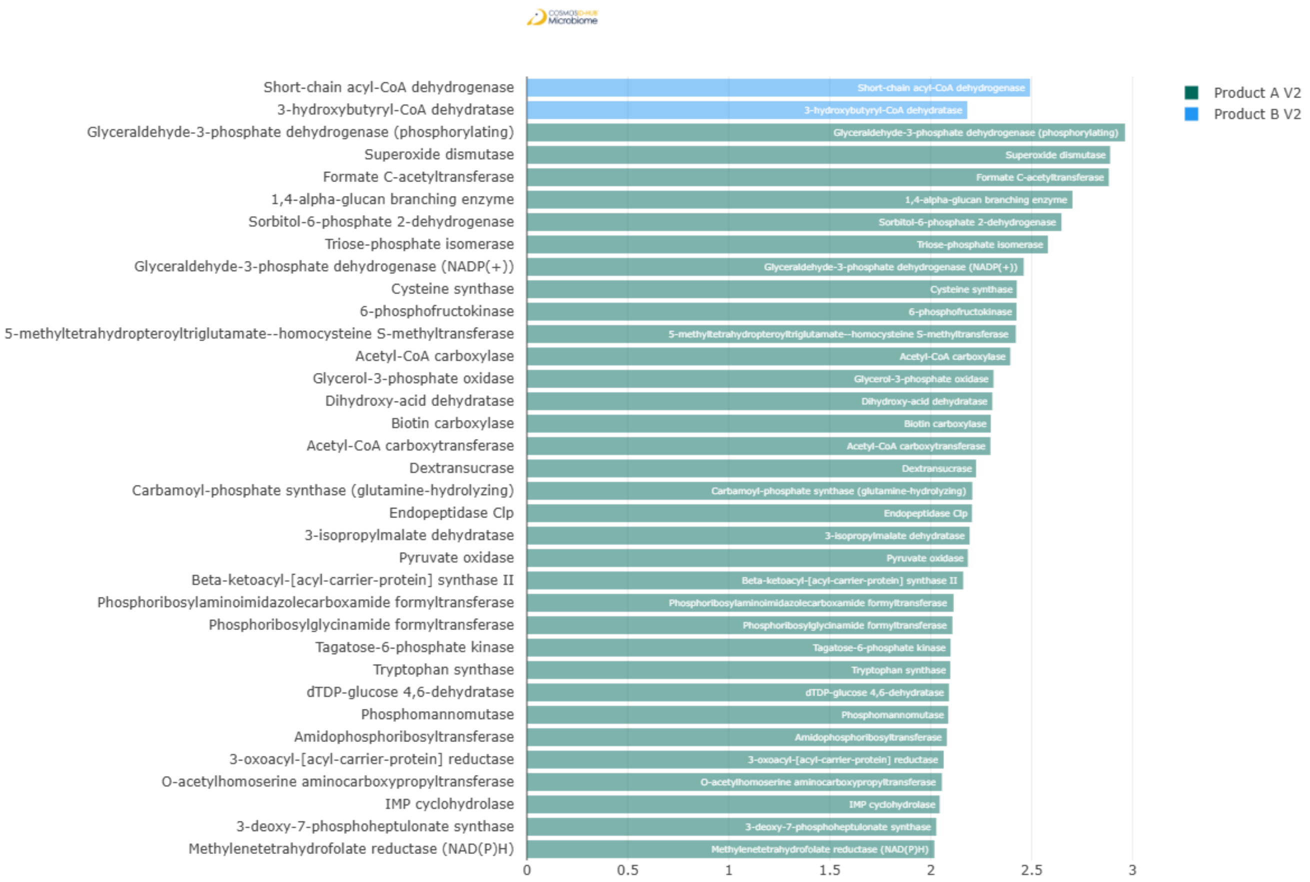
Simpson	

Beta Diversity (EC)

Bray-Curtis PERMNOVA p = 0.091	

Differential Abundance (LEfSe) (EC)

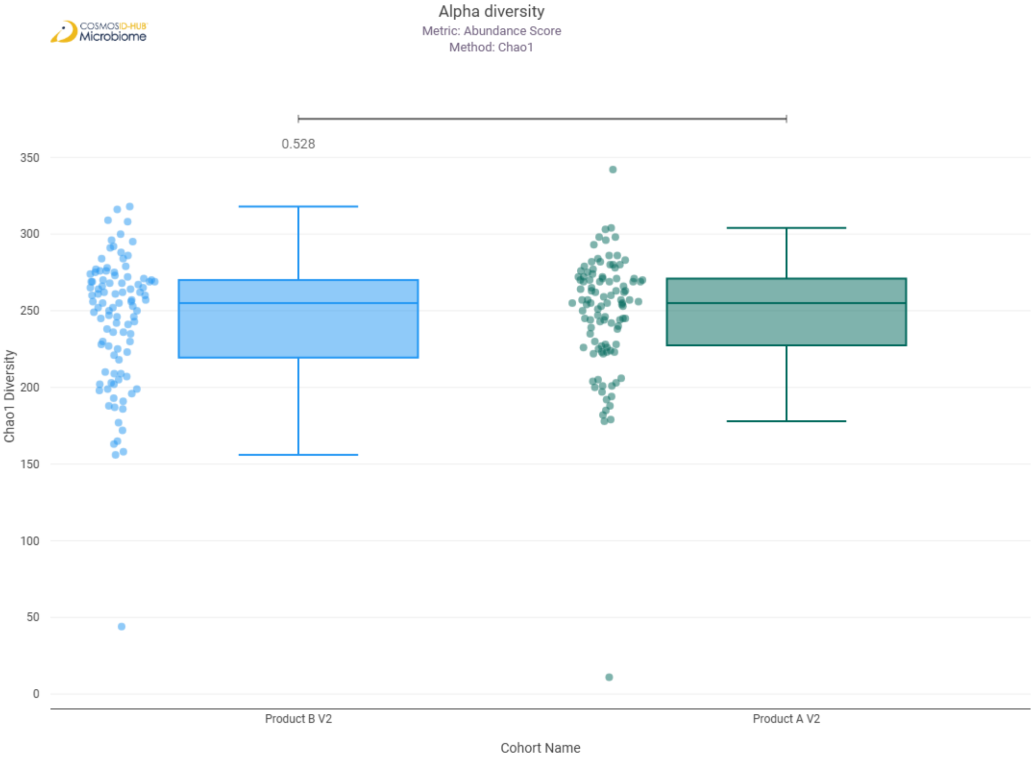


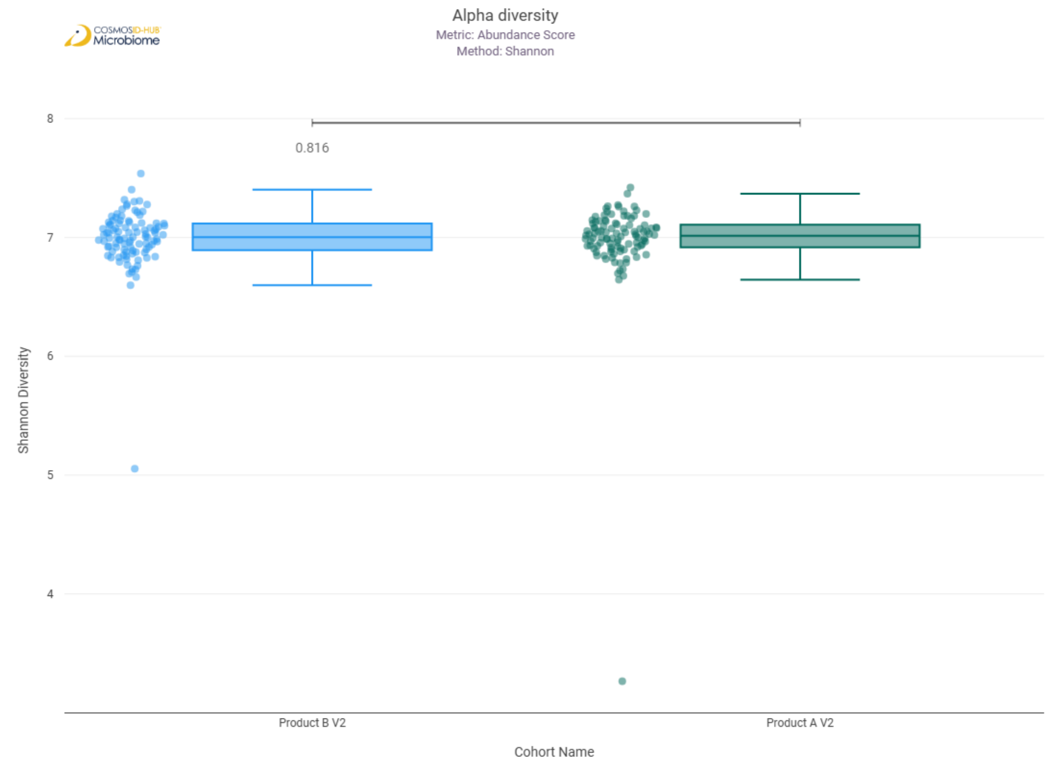
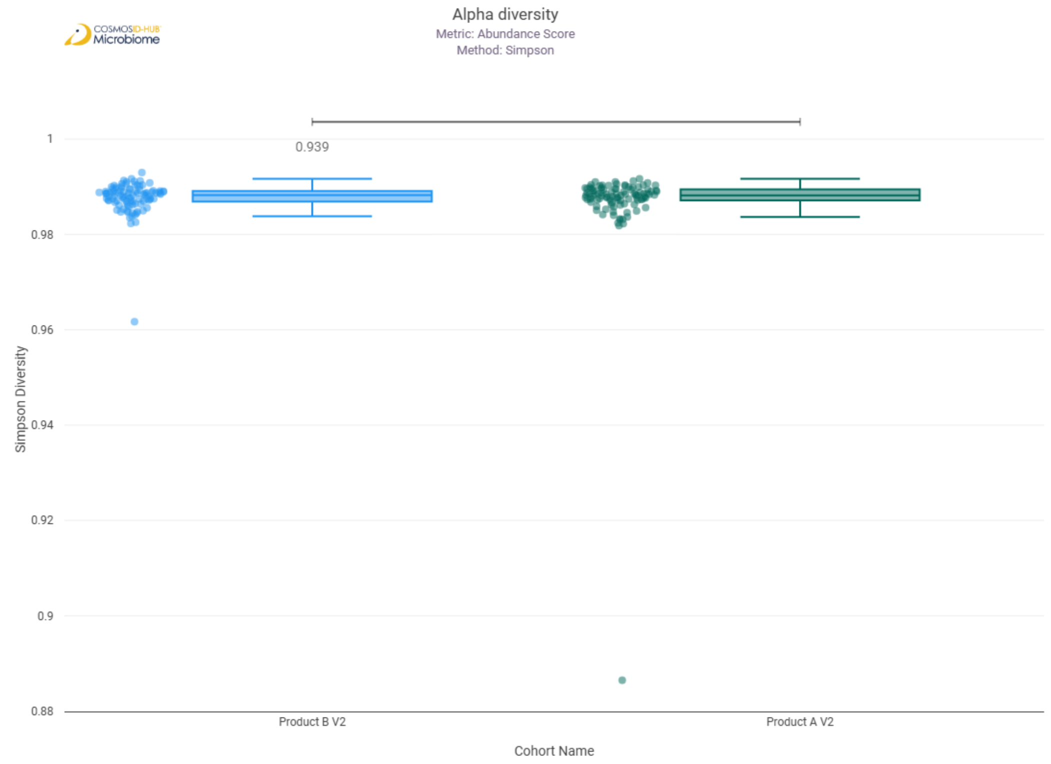
Feature	Enriched Cohort	LDA Score	P-value
Short-chain acyl-CoA dehydrogenase	Product B V2	2.49235307	0.047858458
3-hydroxybutyryl-CoA dehydratase	Product B V2	2.181214019	0.007008368
Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	Product A V2	2.96240361	0.023181239
Superoxide dismutase	Product A V2	2.888470105	0.008512232
Formate C-acetyltransferase	Product A V2	2.882169725	0.049210789
1,4-alpha-glucan branching enzyme	Product A V2	2.702278422	0.01532342
Sorbitol-6-phosphate 2-dehydrogenase	Product A V2	2.647440049	0.009739743
Triose-phosphate isomerase	Product A V2	2.580449029	0.019446308
Glyceraldehyde-3-phosphate dehydrogenase (NADP(+))	Product A V2	2.460621406	0.000147279
Cysteine synthase	Product A V2	2.426220942	0.000177076
6-phosphofructokinase	Product A V2	2.42502775	0.046277021
5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	Product A V2	2.421501802	5.84E-03
Acetyl-CoA carboxylase	Product A V2	2.393966755	0.001383544
Glycerol-3-phosphate oxidase	Product A V2	2.311155395	0.047591773
Dihydroxy-acid dehydratase	Product A V2	2.305025521	0.004189269
Biotin carboxylase	Product A V2	2.297534048	0.006551378
Acetyl-CoA carboxytransferase	Product A V2	2.295974089	0.012071344
Dextransucrase	Product A V2	2.224701535	0.001199349

Carbamoyl-phosphate synthase (glutamine-hydrolyzing)	Product A V2	2.206170018	0.010399771
Endopeptidase Clp	Product A V2	2.204536759	0.026538437
3-isopropylmalate dehydratase	Product A V2	2.192743488	0.037794131
Pyruvate oxidase	Product A V2	2.184095944	0.041794368
Beta-ketoacyl-[acyl-carrier-protein] synthase II	Product A V2	2.161147246	0.032744287
Phosphoribosylaminoimidazolecarboxamide formyltransferase	Product A V2	2.11335053	3.97E-03
Phosphoribosylglycinamide formyltransferase	Product A V2	2.107677905	0.014829928
Tagatose-6-phosphate kinase	Product A V2	2.098303951	0.00984503
Tryptophan synthase	Product A V2	2.096956912	0.003188504
dTDP-glucose 4,6-dehydratase	Product A V2	2.090506399	0.010833904
Phosphomannomutase	Product A V2	2.086978462	0.027859375
Amidophosphoribosyltransferase	Product A V2	2.079994467	0.01522358
3-oxoacyl-[acyl-carrier-protein] reductase	Product A V2	2.064298956	0.010471034
O-acetylhomoserine aminocarboxypropyltransferase	Product A V2	2.055559479	0.000623736
IMP cyclohydrolase	Product A V2	2.044081157	0.009381425
3-deoxy-7-phosphoheptulonate synthase	Product A V2	2.027555519	0.044992985
Methylenetetrahydrofolate reductase (NAD(P)H)	Product A V2	2.018412166	0.040616459

MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1	

Shannon	
Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis

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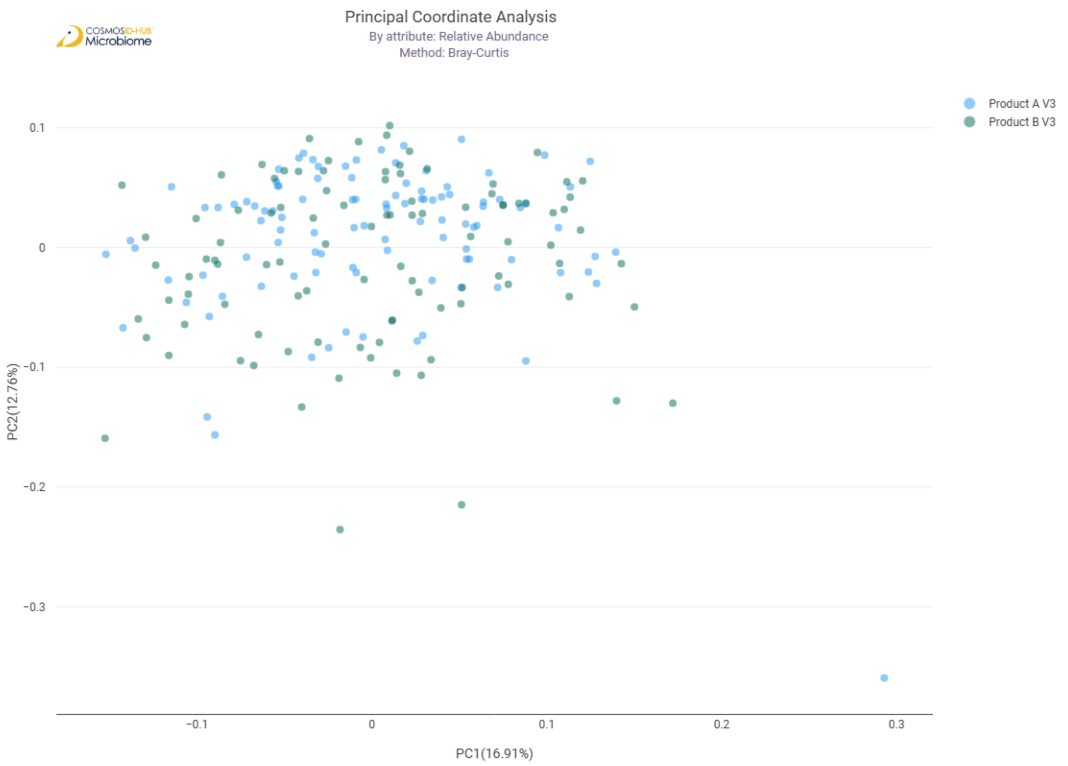
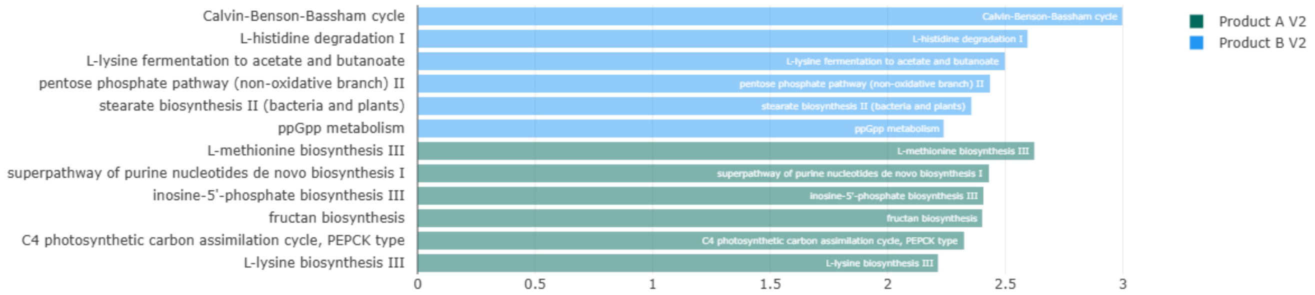


Differential Abundance (LEfSe) (MetaCyc)



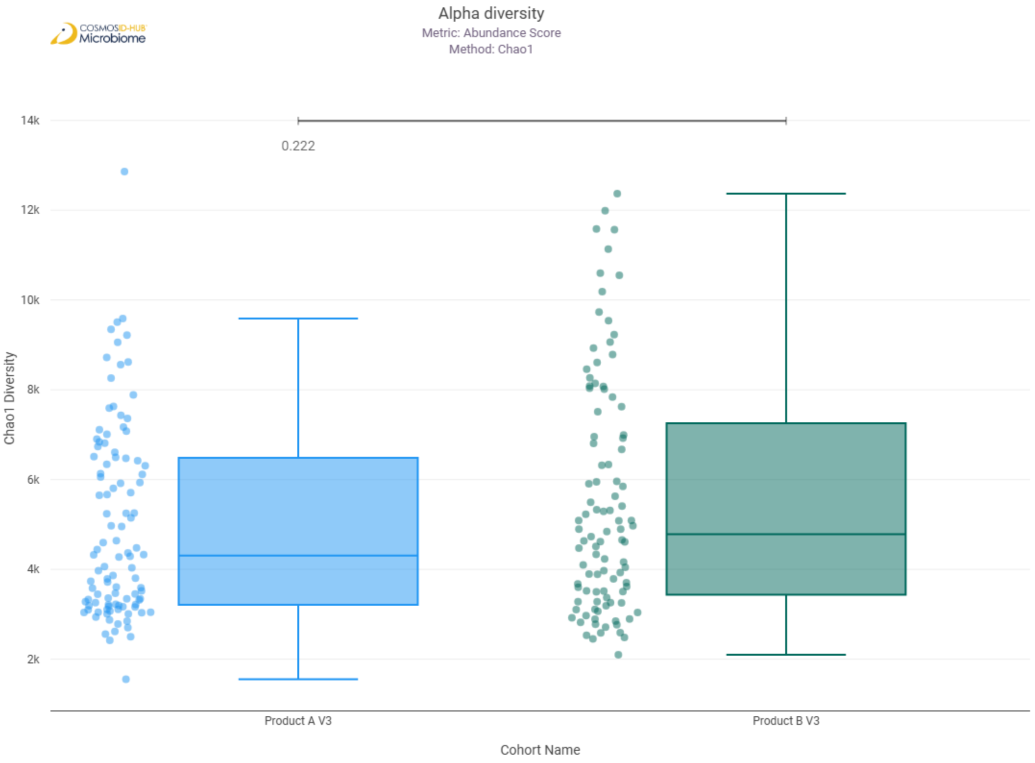
Feature	Enriched Cohort	LDA Score	P-value
Calvin-Benson-Bassham cycle	Product B V2	2.997196461	0.006693692
L-histidine degradation I	Product B V2	2.594507344	0.034935275
L-lysine fermentation to acetate and butanoate	Product B V2	2.498148123	0.033803124
pentose phosphate pathway (non-oxidative branch) II	Product B V2	2.434816755	0.002668748
stearate biosynthesis II (bacteria and plants)	Product B V2	2.355737355	0.018897851
ppGpp metabolism	Product B V2	2.23788823	0.032550826
L-methionine biosynthesis III	Product A V2	2.623137255	0.002918071
superpathway of purine nucleotides de novo biosynthesis I	Product A V2	2.430450703	0.037903528

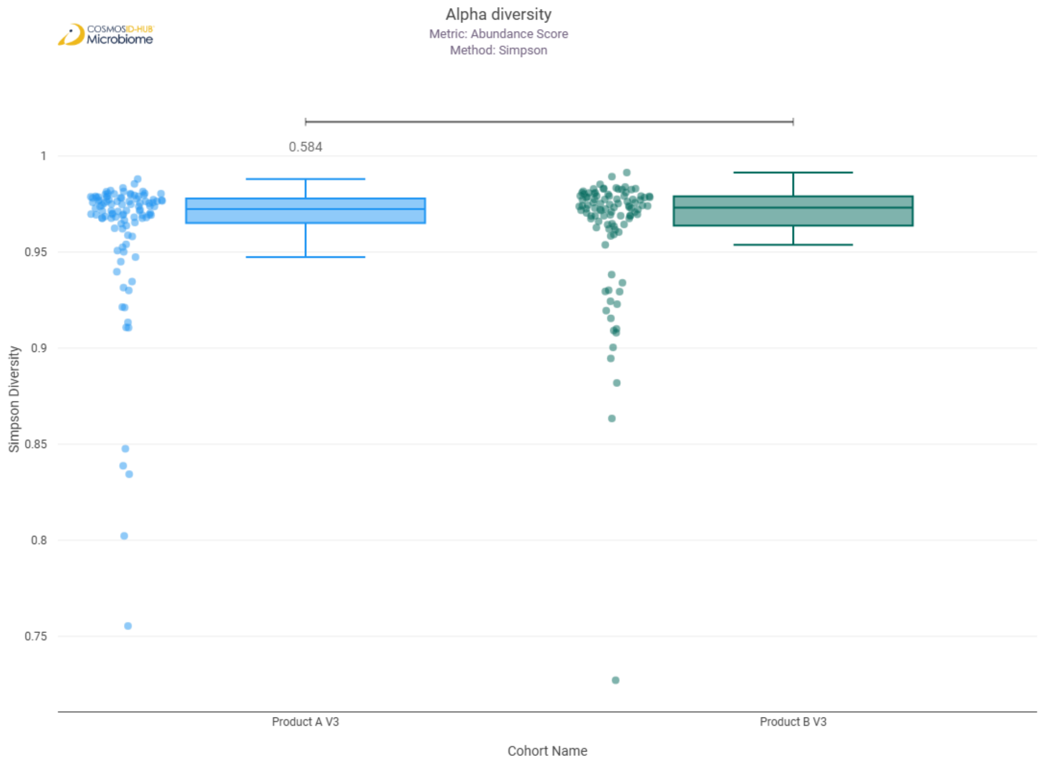
inosine-5'-phosphate biosynthesis III	Product A V2	2.406751294	0.014349805
fructan biosynthesis	Product A V2	2.401680055	0.021736476
C4 photosynthetic carbon assimilation cycle, PEPCK type	Product A V2	2.324662591	0.029148795
L-lysine biosynthesis III	Product A V2	2.213631989	4.16E-02

Comparison 4: Product A V2 SAL vs Product A V3 SAL

Gene Ontology

Alpha Diversity (GO)

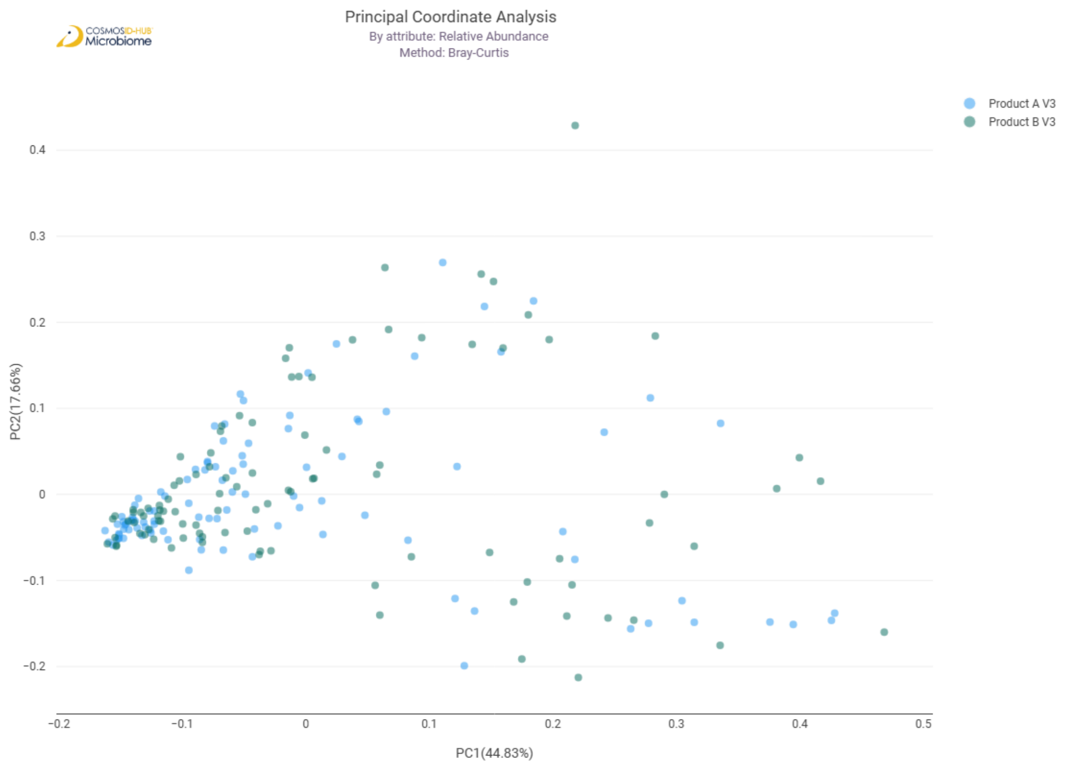
Chao1	

Shannon	
Simpson	

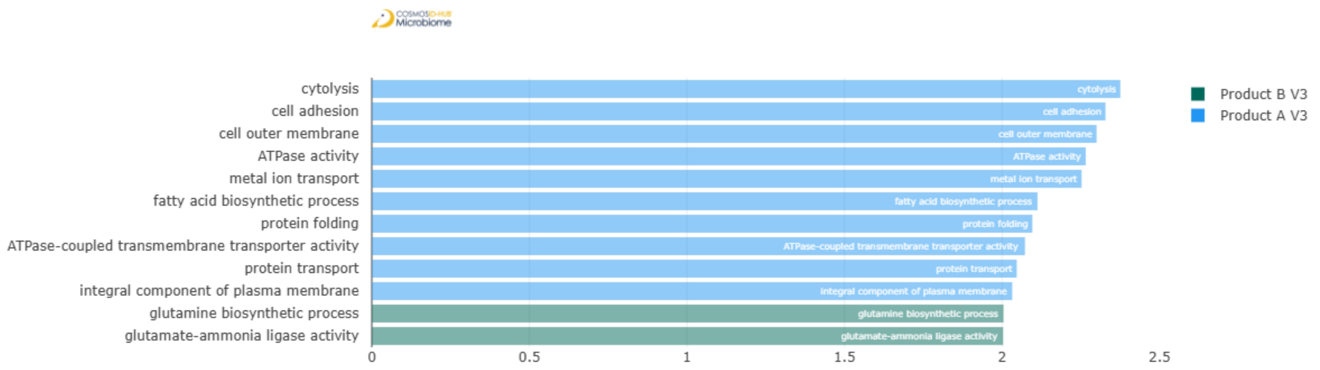
Beta Diversity (GO)

Bray-Curtis

PERMNOVA
p = 0.107



Differential Abundance (LEfSe) (GO)

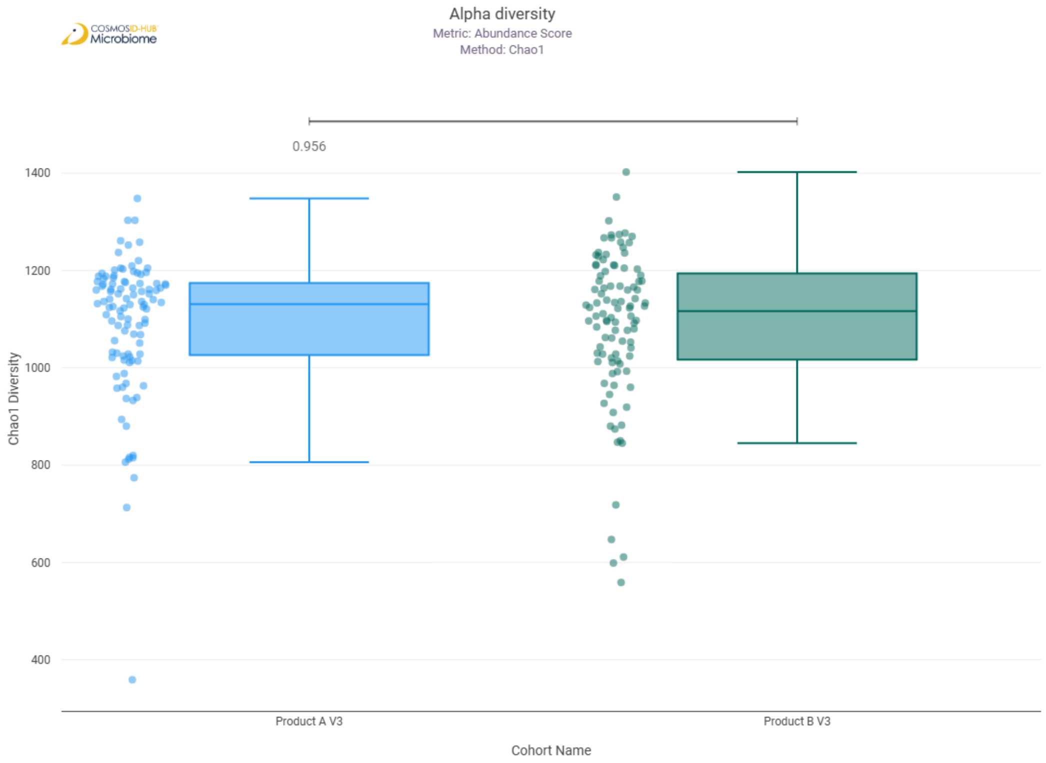


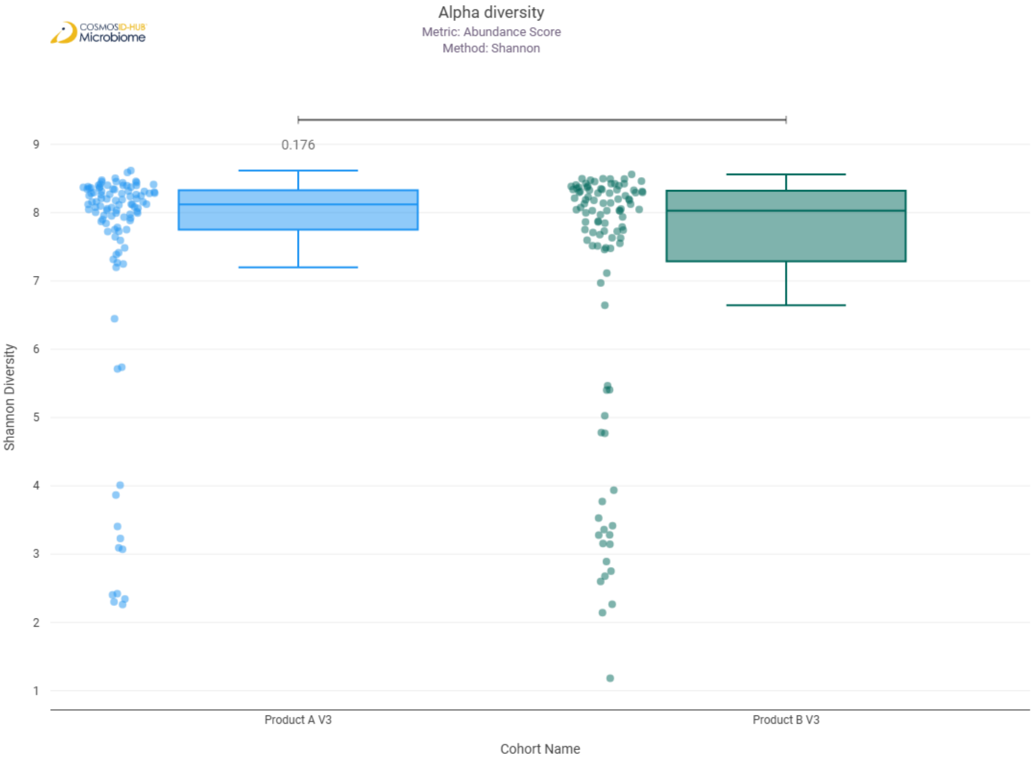
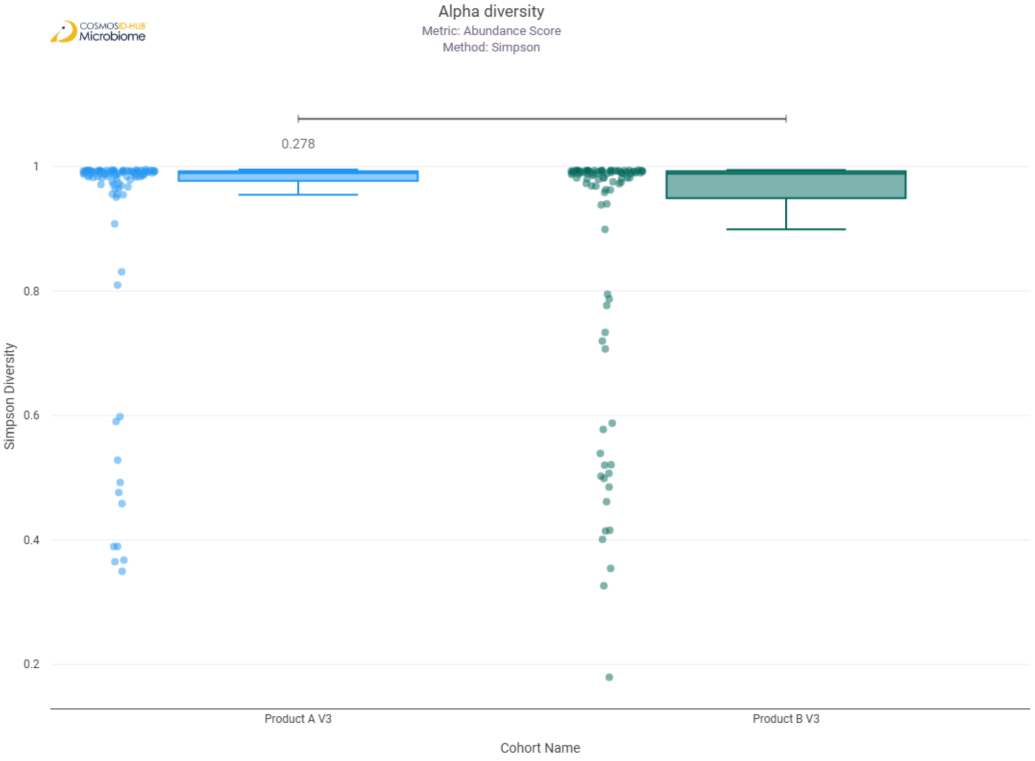
Feature	Enriched Cohort	LDA Score	P-value
cytolysis	Product A V3	2.375326591	0.014445134
cell adhesion	Product A V3	2.328189792	0.01744488
cell outer membrane	Product A V3	2.299945816	0.044739816
ATPase activity	Product A V3	2.265544054	0.025898504
metal ion transport	Product A V3	2.252289492	0.000698338
fatty acid biosynthetic process	Product A V3	2.112486859	0.001839284
protein folding	Product A V3	2.096102407	0.000359491
ATPase-coupled transmembrane transporter activity	Product A V3	2.072667654	0.004581458

protein transport	Product A V3	2.046545024	0.008571841
integral component of plasma membrane	Product A V3	2.032254996	0.008105245
glutamine biosynthetic process	Product B V3	2.004671978	2.19E-02
glutamate-ammonia ligase activity	Product B V3	2.00334107	0.025271957

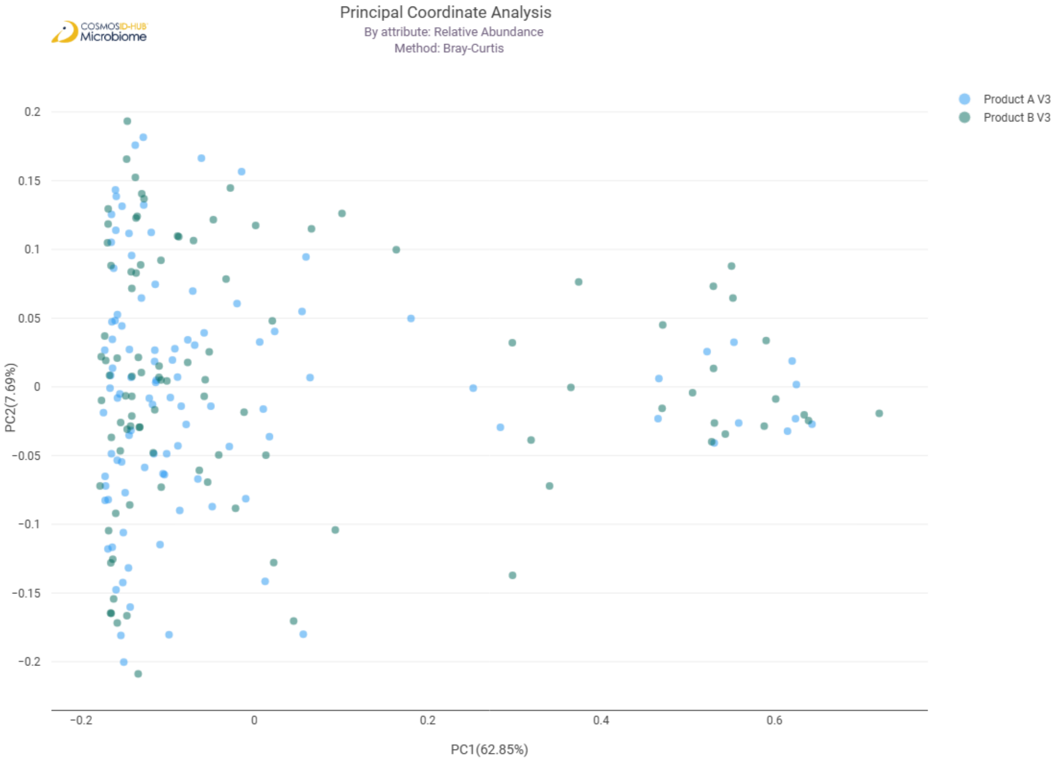
Enzyme Commission

Alpha Diversity (EC)

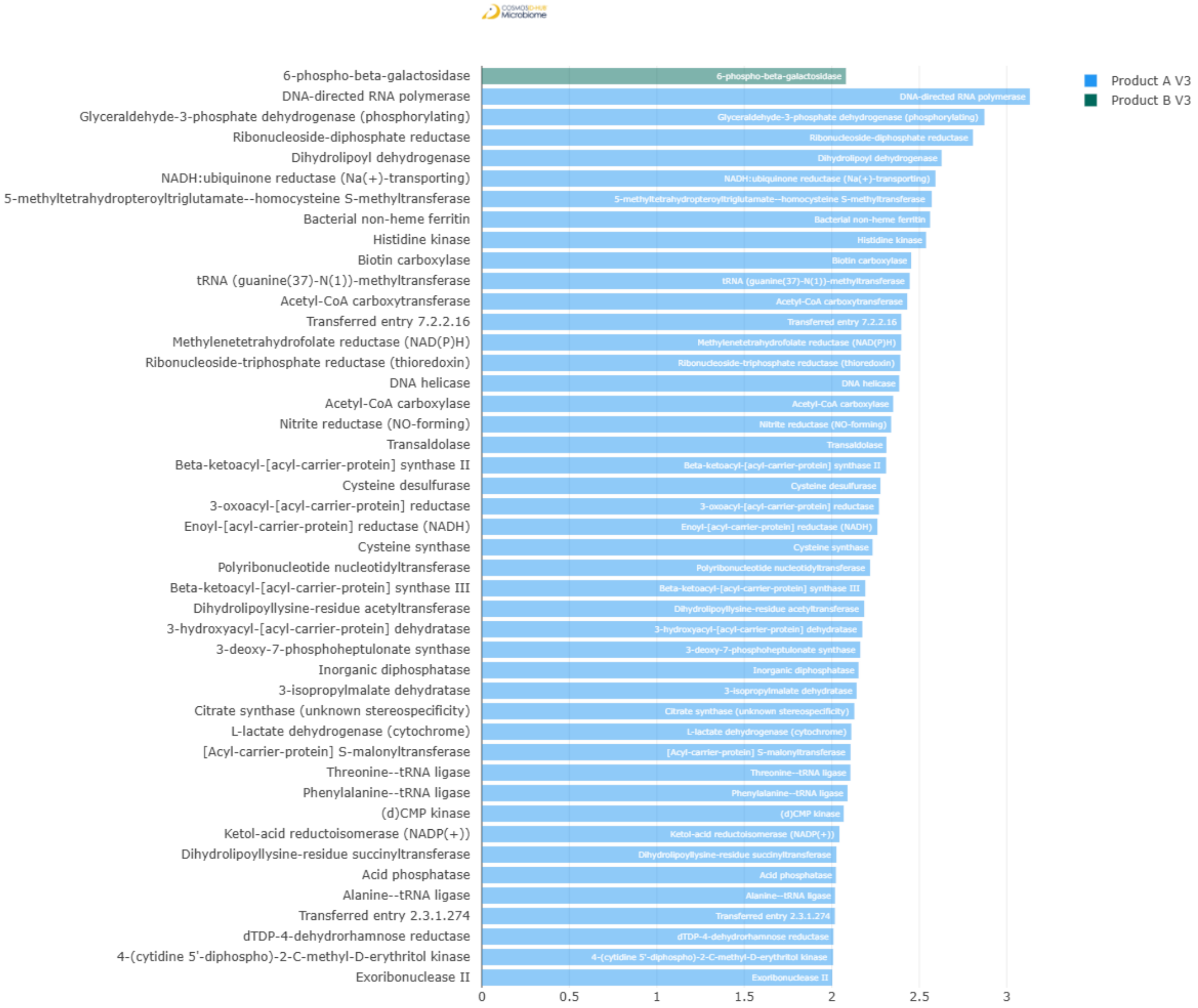
Chao1	

Shannon	
Simpson	

Beta Diversity (EC)

Bray-Curtis PERMNOVA p = 0.072	

Differential Abundance (LEfSe) (EC)

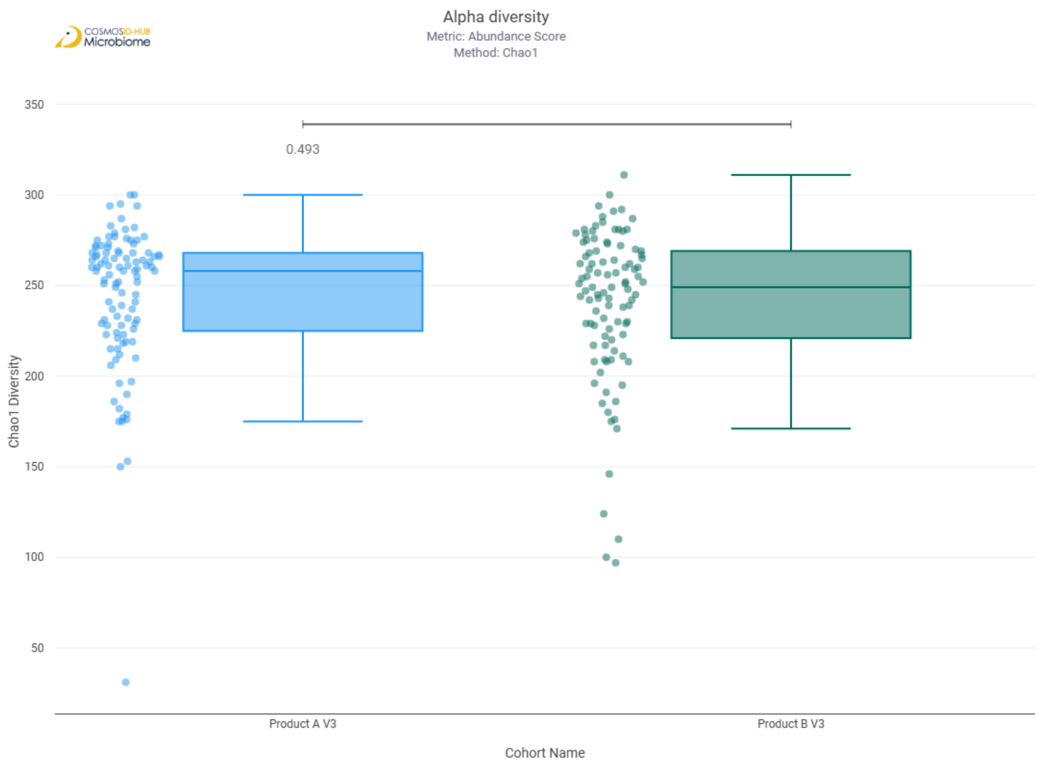
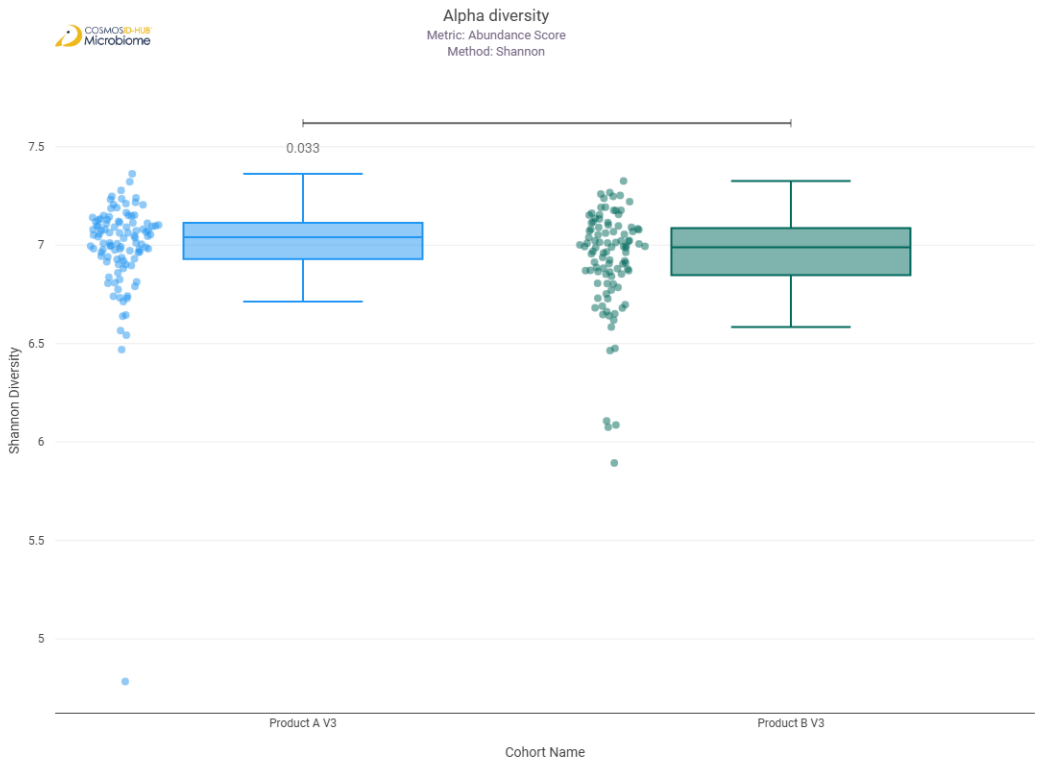


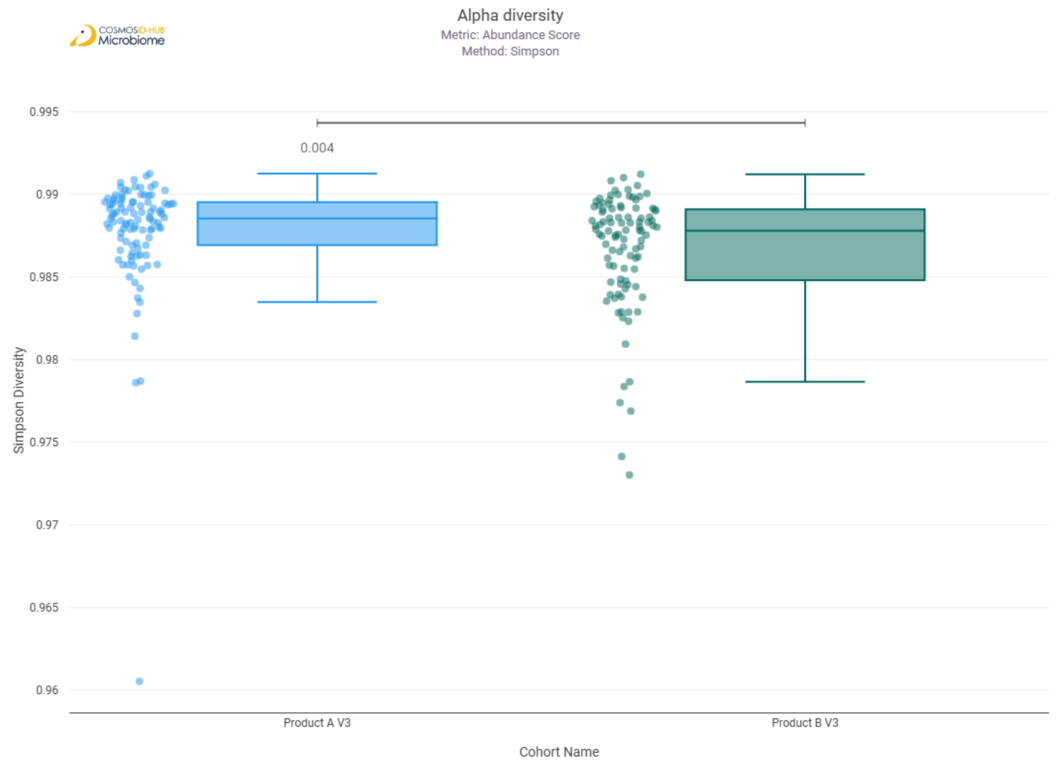
Feature	Enriched Cohort	LDA Score	P-value
6-phospho-beta-galactosidase	Product B V3	2.080727545	0.046385006
DNA-directed RNA polymerase	Product A V3	3.131684191	0.026538437
Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	Product A V3	2.872341567	0.028198334
Ribonucleoside-diphosphate reductase	Product A V3	2.806603682	0.007770359
Dihydrolipoyl dehydrogenase	Product A V3	2.627544199	0.008937395
NADH:ubiquinone reductase (Na(+)-transporting)	Product A V3	2.59253101	0.013431321
5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	Product A V3	2.571096295	0.012993227
Bacterial non-heme ferritin	Product A V3	2.561732858	0.022612184
Histidine kinase	Product A V3	2.53874264	0.017670566
Biotin carboxylase	Product A V3	2.453594887	0.002648014
tRNA (guanine(37)-N(1))-methyltransferase	Product A V3	2.445456033	0.000781151
Acetyl-CoA carboxytransferase	Product A V3	2.430837617	1.91E-03

Transferred entry 7.2.2.16	Product A V3	2.397074415	0.03216757
Methylenetetrahydrofolate reductase (NAD(P)H)	Product A V3	2.397041877	0.027691217
Ribonucleoside-triphosphate reductase (thioredoxin)	Product A V3	2.391476364	0.009252593
DNA helicase	Product A V3	2.385246652	0.040384285
Acetyl-CoA carboxylase	Product A V3	2.350690765	0.014069443
Nitrite reductase (NO-forming)	Product A V3	2.339275293	0.006125811
Transaldolase	Product A V3	2.312003861	0.000815362
Beta-ketoacyl-[acyl-carrier-protein] synthase II	Product A V3	2.310457827	0.017001077
Cysteine desulfurase	Product A V3	2.277719109	0.003091956
3-oxoacyl-[acyl-carrier-protein] reductase	Product A V3	2.269677866	7.19E-03
Enoyl-[acyl-carrier-protein] reductase (NADH)	Product A V3	2.260621834	5.44775E-05
Cysteine synthase	Product A V3	2.232785492	0.011056954
Polyribonucleotide nucleotidyltransferase	Product A V3	2.218940509	0.00760761
Beta-ketoacyl-[acyl-carrier-protein] synthase III	Product A V3	2.191178527	0.016782914
Dihydrolipoyllysine-residue acetyltransferase	Product A V3	2.184992934	2.21596E-05
3-hydroxyacyl-[acyl-carrier-protein] dehydratase	Product A V3	2.174872472	0.006645961
3-deoxy-7-phosphoheptulonate synthase	Product A V3	2.162273672	0.000597086
Inorganic diphosphatase	Product A V3	2.152950641	0.028369142
3-isopropylmalate dehydratase	Product A V3	2.142110454	0.006693711
Citrate synthase (unknown stereospecificity)	Product A V3	2.128832033	0.047502293
L-lactate dehydrogenase (cytochrome)	Product A V3	2.111713408	0.000198287
[Acyl-carrier-protein] S-malonyltransferase	Product A V3	2.107247626	0.033133665
Threonine--tRNA ligase	Product A V3	2.106387094	0.01004989
Phenylalanine--tRNA ligase	Product A V3	2.090165423	0.01744488
(d)CMP kinase	Product A V3	2.068001372	0.007661517
Ketol-acid reductoisomerase (NADP(+))	Product A V3	2.043610854	0.047858458
Dihydrolipoyllysine-residue succinyltransferase	Product A V3	2.026340003	0.028886698
Acid phosphatase	Product A V3	2.023639908	0.002648014
Alanine--tRNA ligase	Product A V3	2.018798405	0.02332543
Transferred entry 2.3.1.274	Product A V3	2.017852023	0.003915394
dTDP-4-dehydrorhamnose reductase	Product A V3	2.009516698	0.005965544
4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	Product A V3	2.007683828	0.000111216
Exoribonuclease II	Product A V3	2.002632022	0.000131097

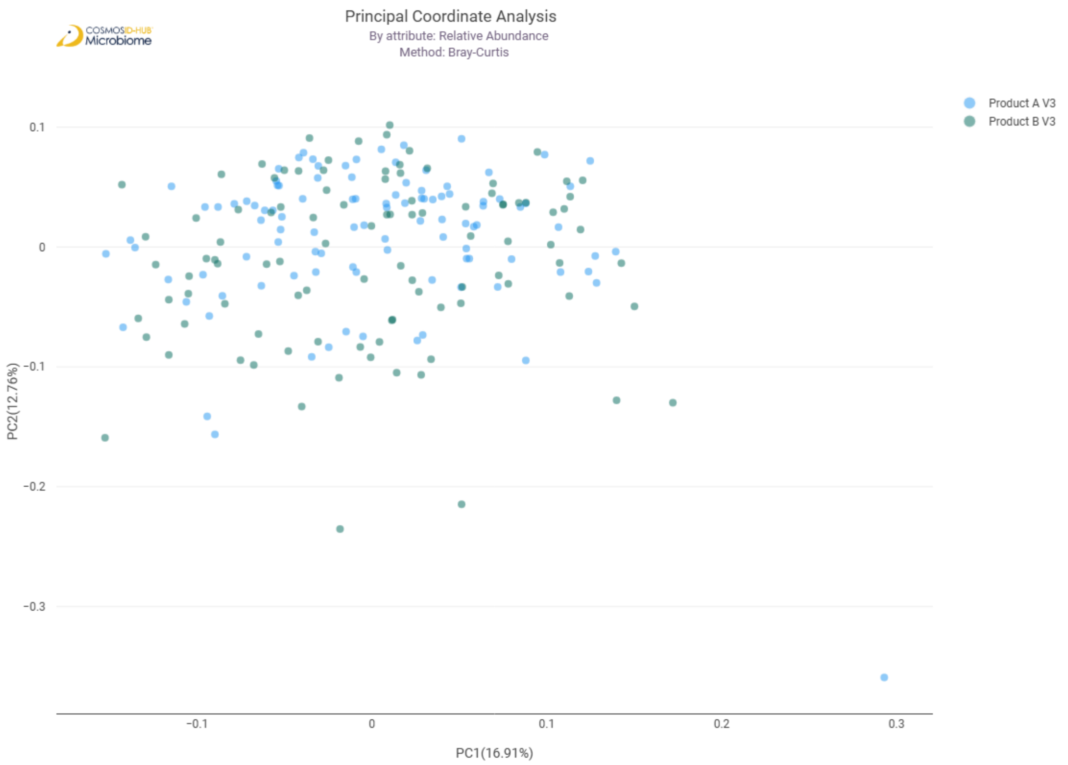
MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1	
Shannon	

Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis PERMNOVA p = 0.003	

Differential Abundance (LEfSe) (MetaCyc)

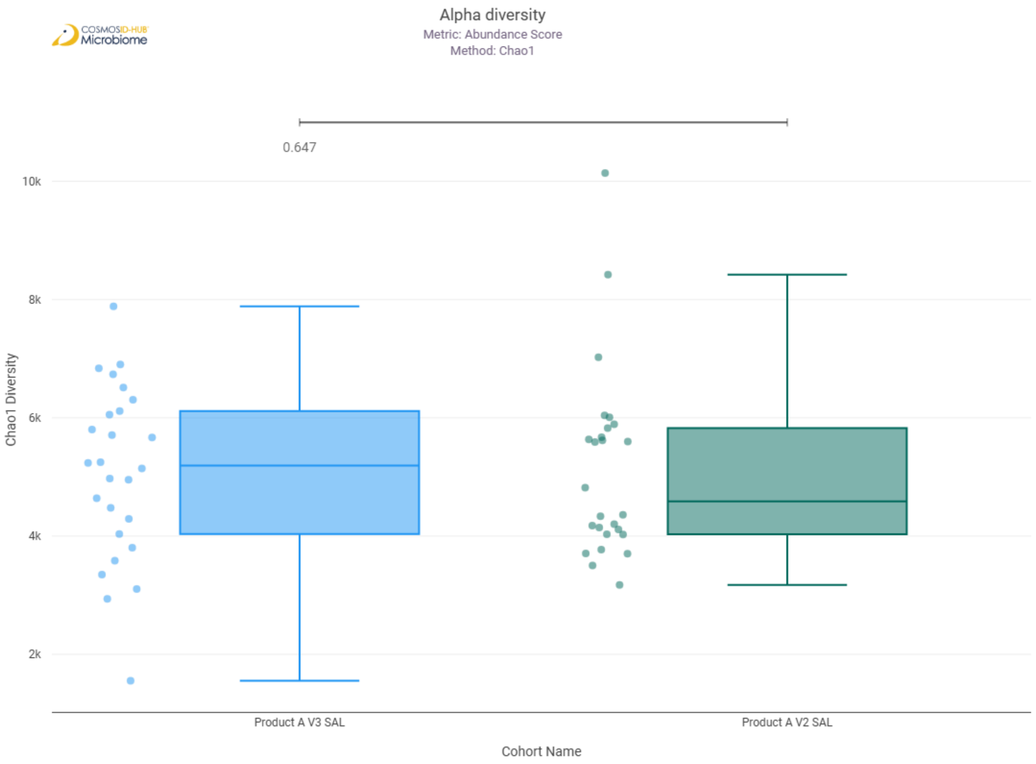
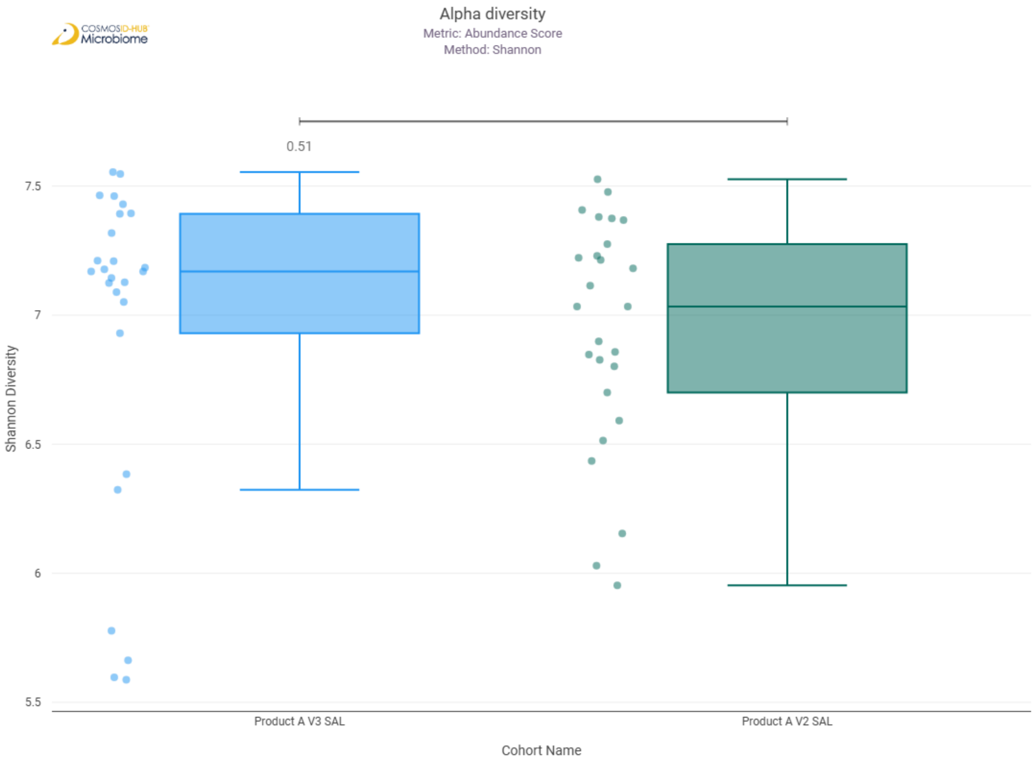
Feature	Enriched Cohort	LDA Score	P-value
gondoate biosynthesis (anaerobic)	Product A V3	2.924054289	1.71664E-05
Calvin-Benson-Bassham cycle	Product A V3	2.90518626	0.037034519
cis-vaccenate biosynthesis	Product A V3	2.873686051	0.000100888
(5Z)-dodecenoate biosynthesis I	Product A V3	2.860646941	0.000168085
fatty acid biosynthesis initiation (mitochondria)	Product A V3	2.798040194	0.014350494
fatty acid elongation -- saturated	Product A V3	2.734390918	0.000250374
oleate biosynthesis IV (anaerobic)	Product A V3	2.717536982	0.000364402
palmitate biosynthesis (type II fatty acid synthase)	Product A V3	2.714526789	0.007301725
palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate)	Product A V3	2.708135225	0.000464298
(5Z)-dodecenoate biosynthesis II	Product A V3	2.545755648	0.000414729
tRNA processing	Product A V3	2.525229504	0.0003883
nitrate reduction I (denitrification)	Product A V3	2.489917921	0.001492854
inosine 5'-phosphate degradation	Product A V3	2.427780228	0.008219712
C4 photosynthetic carbon assimilation cycle, NADP-ME type	Product A V3	2.409347733	0.000732058

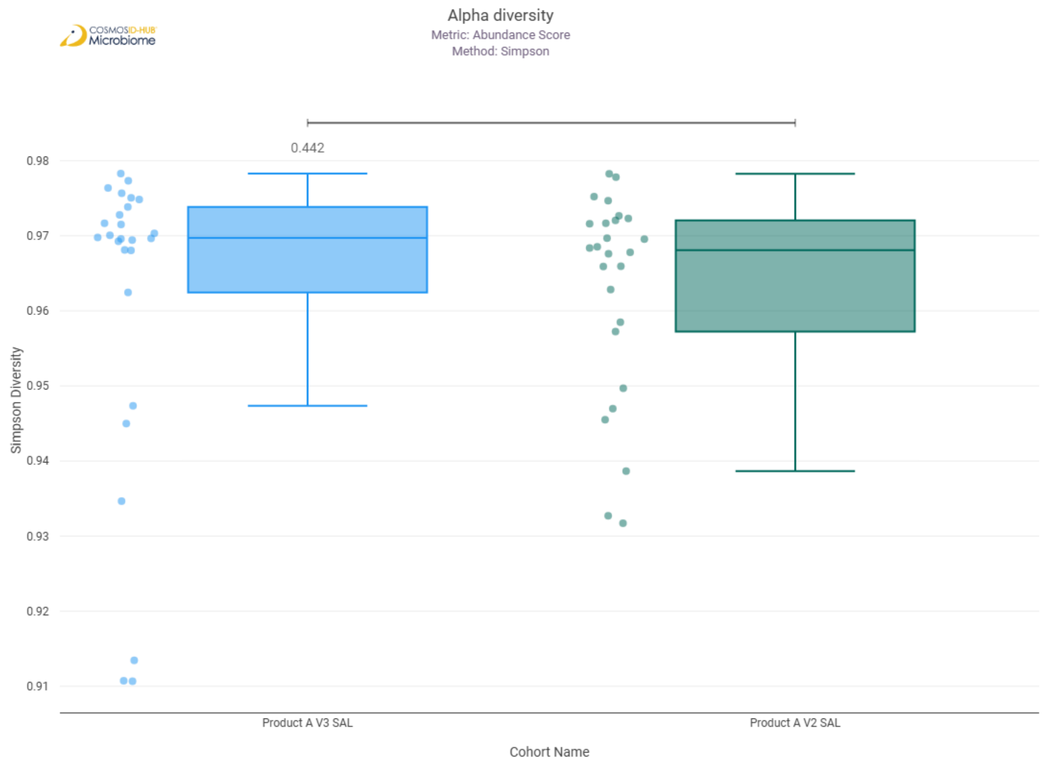
C4 photosynthetic carbon assimilation cycle, PEPCK type	Product A V3	2.394946465	0.012152566
molybdopterin biosynthesis	Product A V3	2.266745981	7.60264E-06
heme b biosynthesis II (oxygen-independent)	Product A V3	2.264050701	1.53555E-06
C4 photosynthetic carbon assimilation cycle, NAD-ME type	Product A V3	2.254910685	1.72E-03
tetrapyrrole biosynthesis I (from glutamate)	Product A V3	2.248434275	0.003468115
superpathway of L-alanine biosynthesis	Product A V3	2.226385681	0.004459743
tetrapyrrole biosynthesis II (from glycine)	Product A V3	2.210751712	0.011432973
L-lysine biosynthesis I	Product A V3	2.204168356	0.006050982
L-ornithine biosynthesis II	Product A V3	2.187087921	9.90522E-05
octanoyl-[acyl-carrier protein] biosynthesis (mitochondria, yeast)	Product A V3	2.079495823	0.004954342
superpathway of L-lysine, L-threonine and L-methionine biosynthesis II	Product A V3	2.070683632	0.014539384
myristate biosynthesis (mitochondria)	Product A V3	2.045732729	0.007144376
L-lysine biosynthesis VI	Product A V3	2.04325135	0.017109717
biotin biosynthesis I	Product A V3	2.038724205	0.00151055
8-amino-7-oxononanoate biosynthesis I	Product A V3	2.034984754	0.0141078
glycogen biosynthesis I (from ADP-D-Glucose)	Product B V3	3.424674828	0.041084202
sucrose biosynthesis II	Product B V3	3.34606056	0.011750774
glycogen degradation II	Product B V3	3.296799534	0.00049628
glucose and glucose-1-phosphate degradation	Product B V3	3.28145505	0.000621487
glycolysis IV	Product B V3	3.163269183	0.041319779
Bifidobacterium shunt	Product B V3	2.587848076	0.031218555
UDP-N-acetyl-D-glucosamine biosynthesis I	Product B V3	2.468183133	1.29E-02
adenosine nucleotides degradation II	Product B V3	2.282555947	0.031371437
guanosine nucleotides degradation III	Product B V3	2.280018501	0.0383138
pyrimidine deoxyribonucleotides de novo biosynthesis IV	Product B V3	2.232203919	0.020694587
superpathway of L-lysine, L-threonine and L-methionine biosynthesis I	Product B V3	2.079988259	0.003202322
nitrate reduction V (assimilatory)	Product B V3	2.025191349	0.026585987

Comparison 5: Product A V3 vs Product B V3

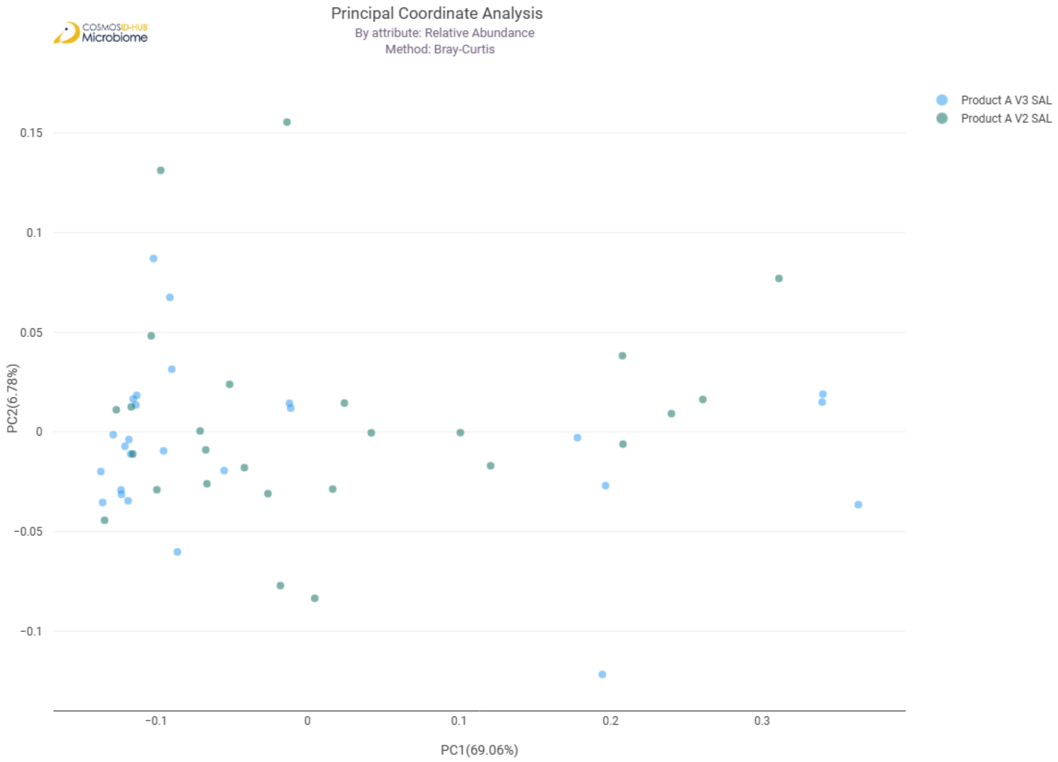
Gene Ontology

Alpha Diversity (GO)

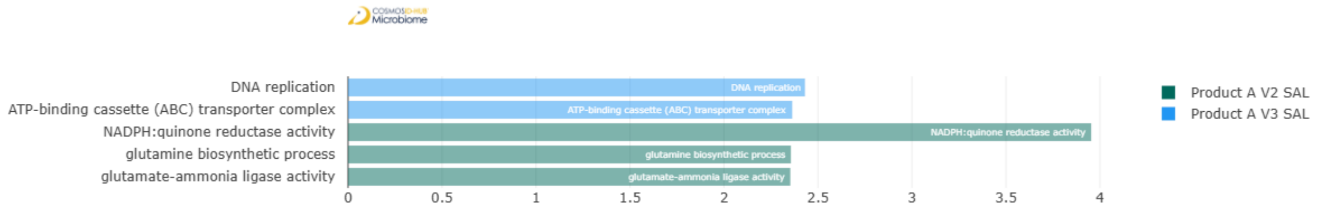
Chao1	
Shannon	

Simpson	

Beta Diversity (GO)

Bray-Curtis PERMNOVA p = 0.473	

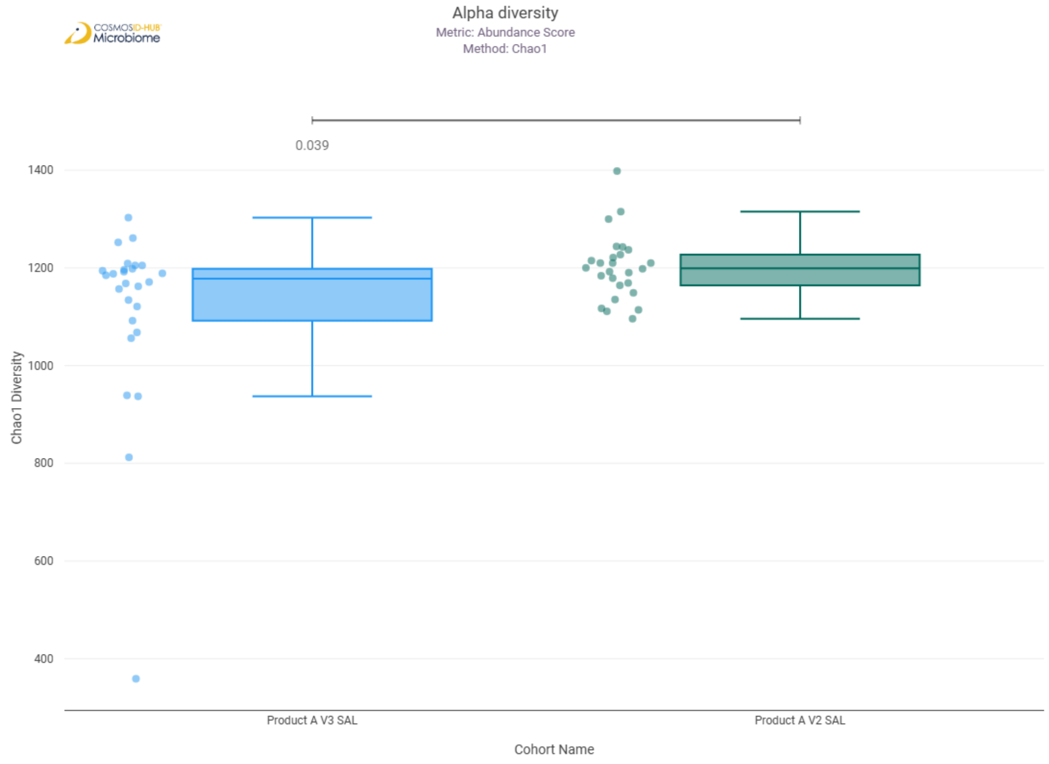
Differential Abundance (LEfSe) (GO)

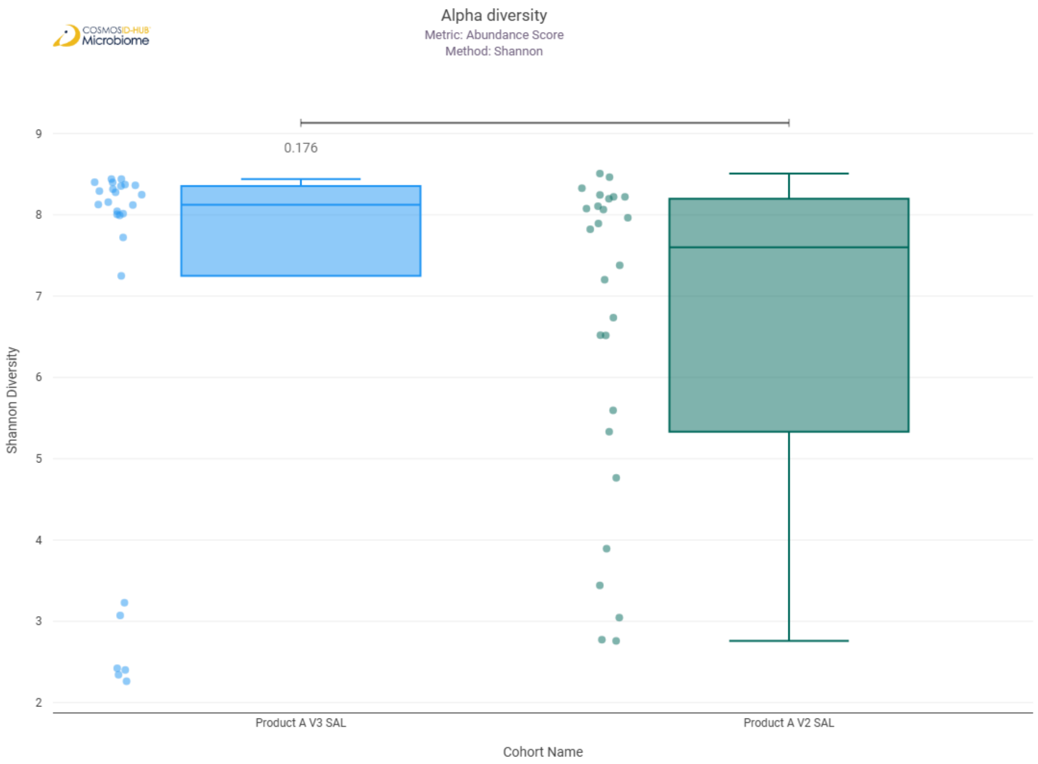
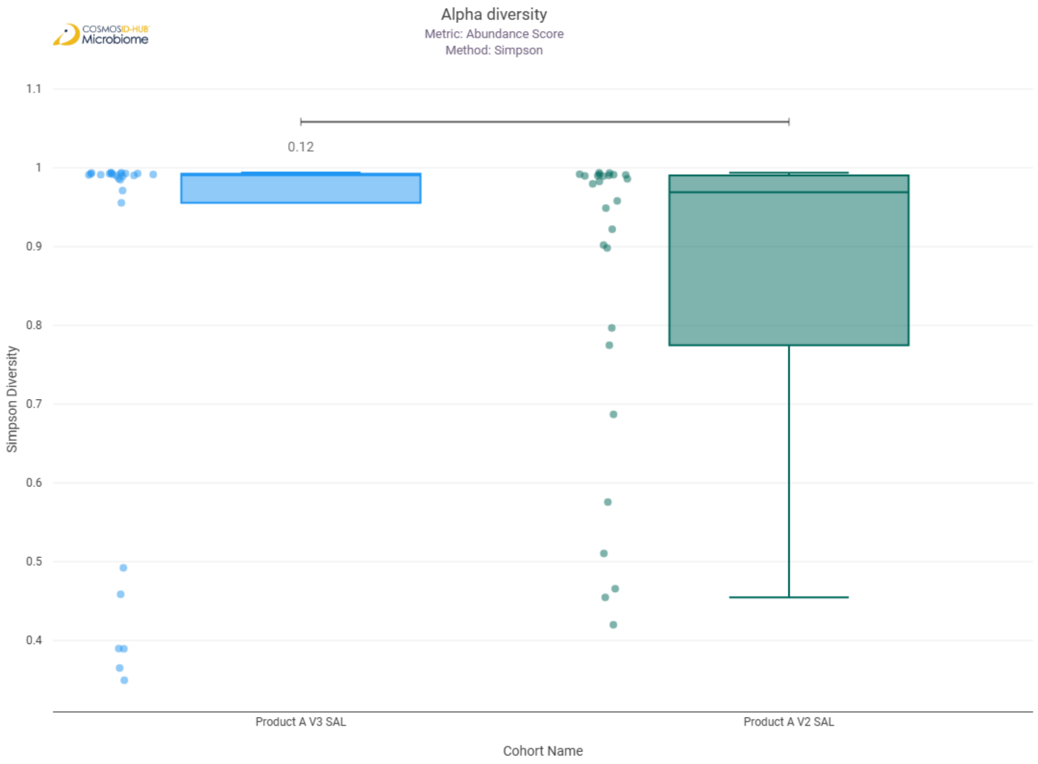


Feature	Enriched Cohort	LDA Score	P-value
DNA replication	Product A V3 SAL	2.430760658	0.035322927
ATP-binding cassette (ABC) transporter complex	Product A V3 SAL	2.362960966	0.032254747
NADPH:quinone reductase activity	Product A V2 SAL	3.953508756	0.040390461
glutamine biosynthetic process	Product A V2 SAL	2.355947932	0.007139316
glutamate-ammonia ligase activity	Product A V2 SAL	2.353037259	0.02556575

Enzyme Commission

Alpha Diversity (EC)

Chao1	

Shannon	
Simpson	

Beta Diversity (EC)

Bray-Curtis

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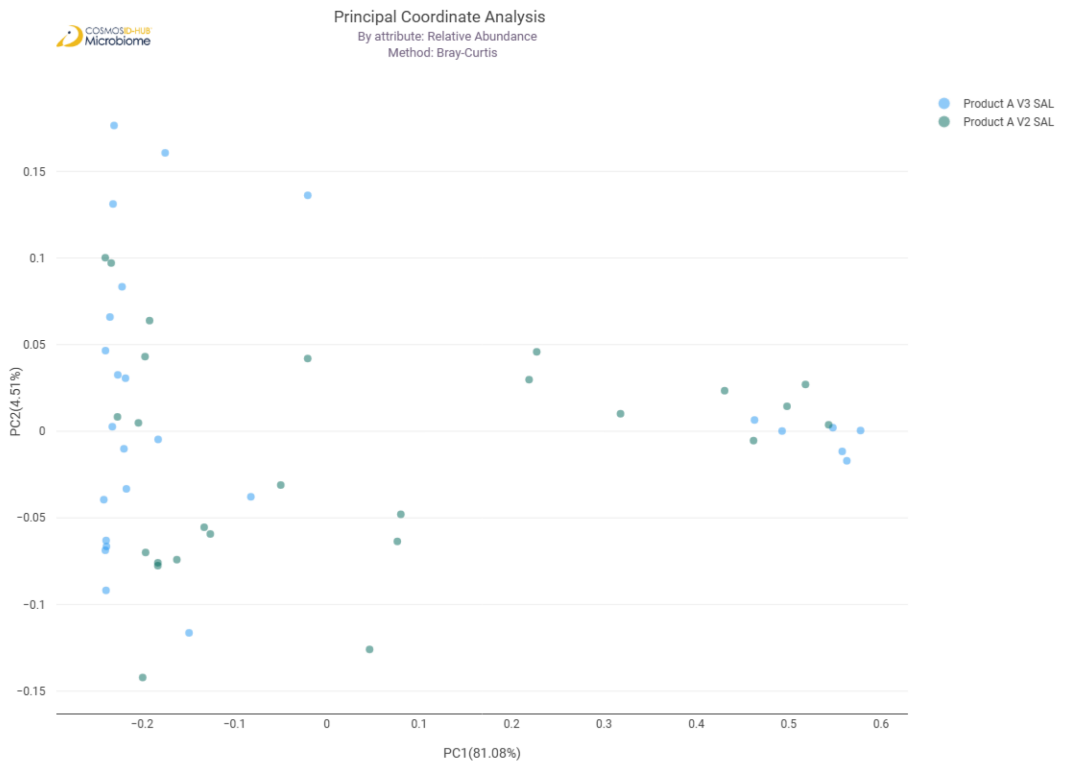
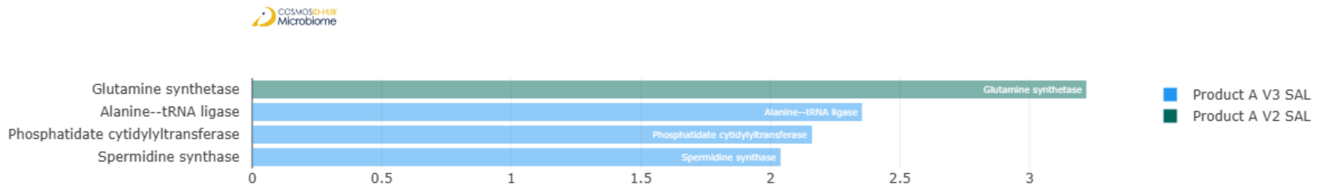


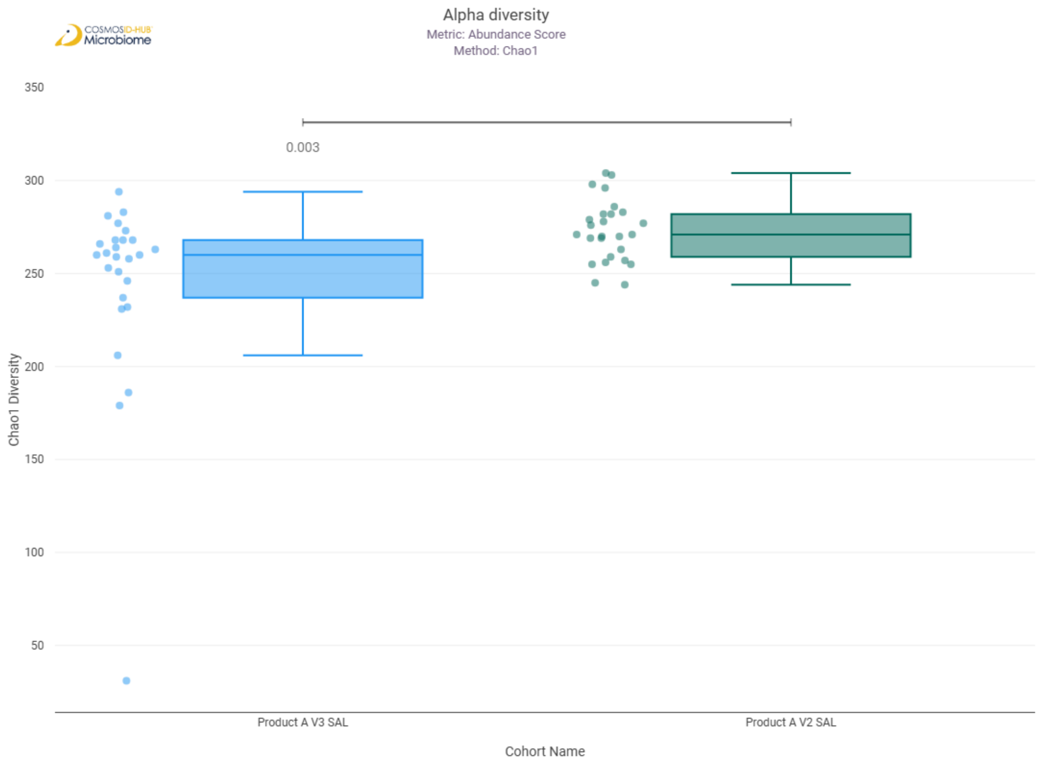
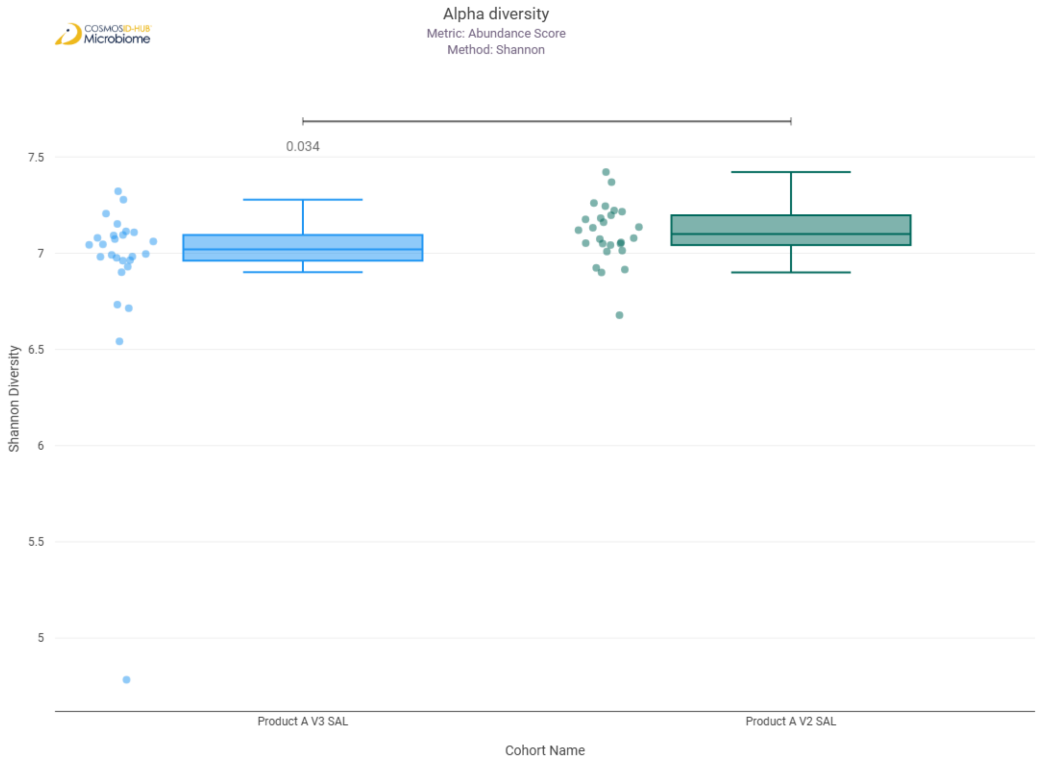
Differential Abundance (LEfSe) (EC)



Feature	Enriched Cohort	LDA Score	P-value
Glutamine synthetase	Product A V2 SAL	3.219463934	0.006393679
Alanine--tRNA ligase	Product A V3 SAL	2.353669717	0.014192278
Phosphatidate cytidylyltransferase	Product A V3 SAL	2.160690623	0.038636777
Spermidine synthase	Product A V3 SAL	2.039315636	0.040390461

MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1	
Shannon	

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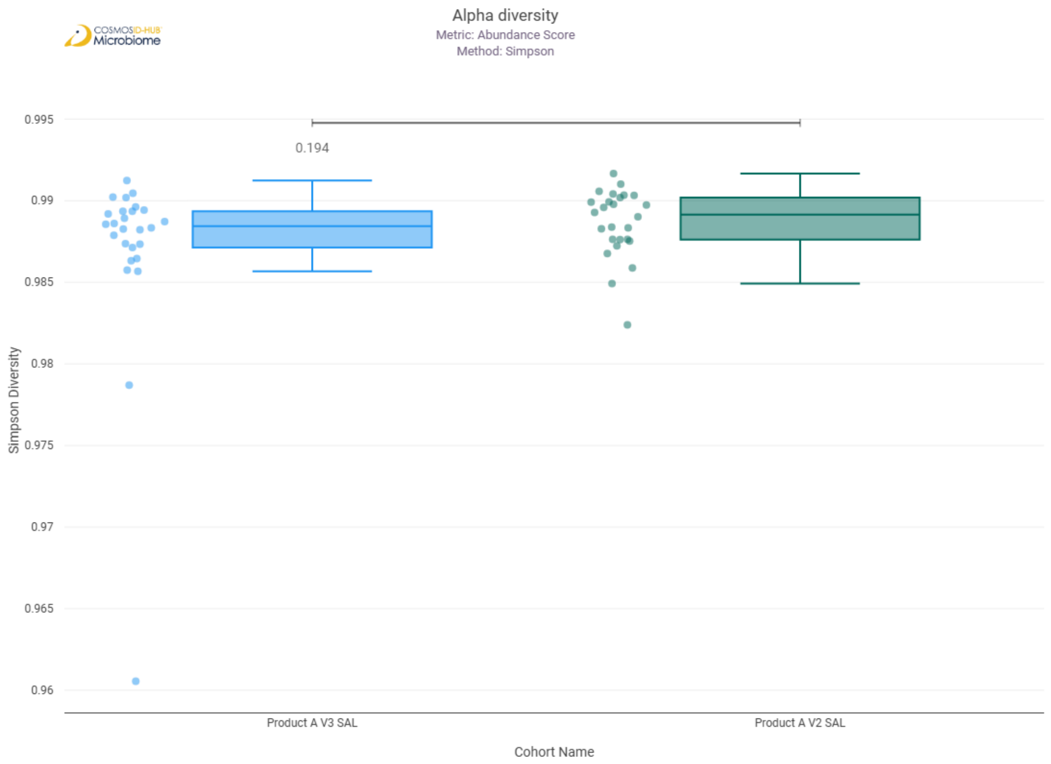

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Beta Diversity (MetaCyc)

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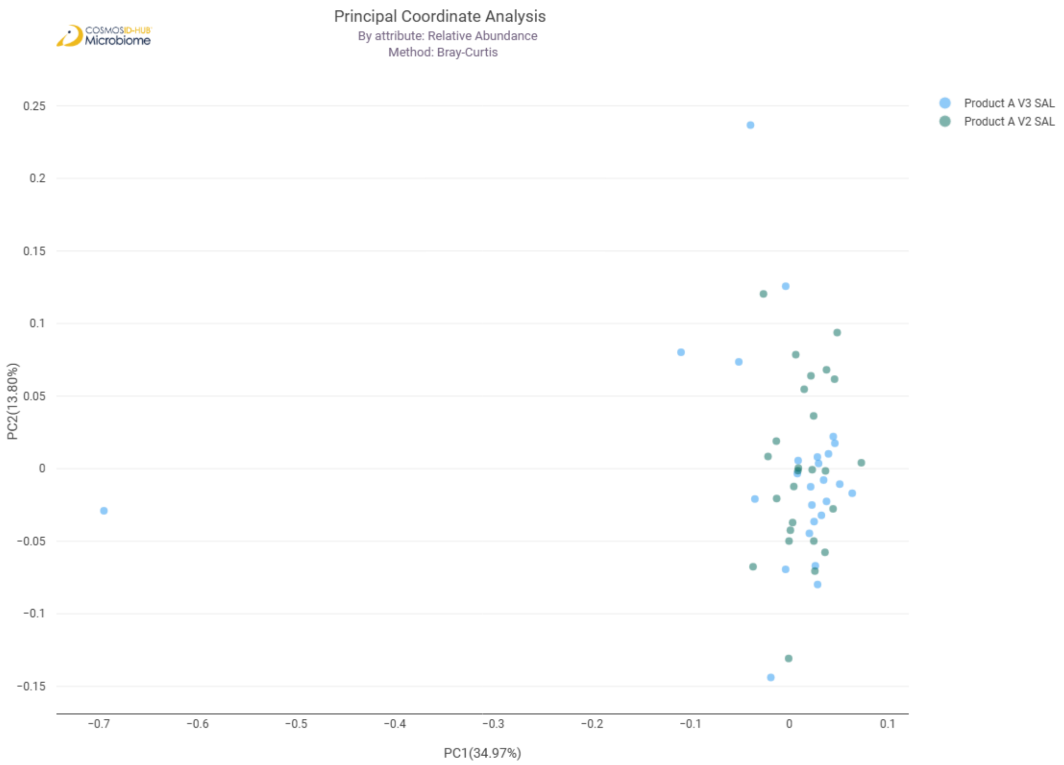

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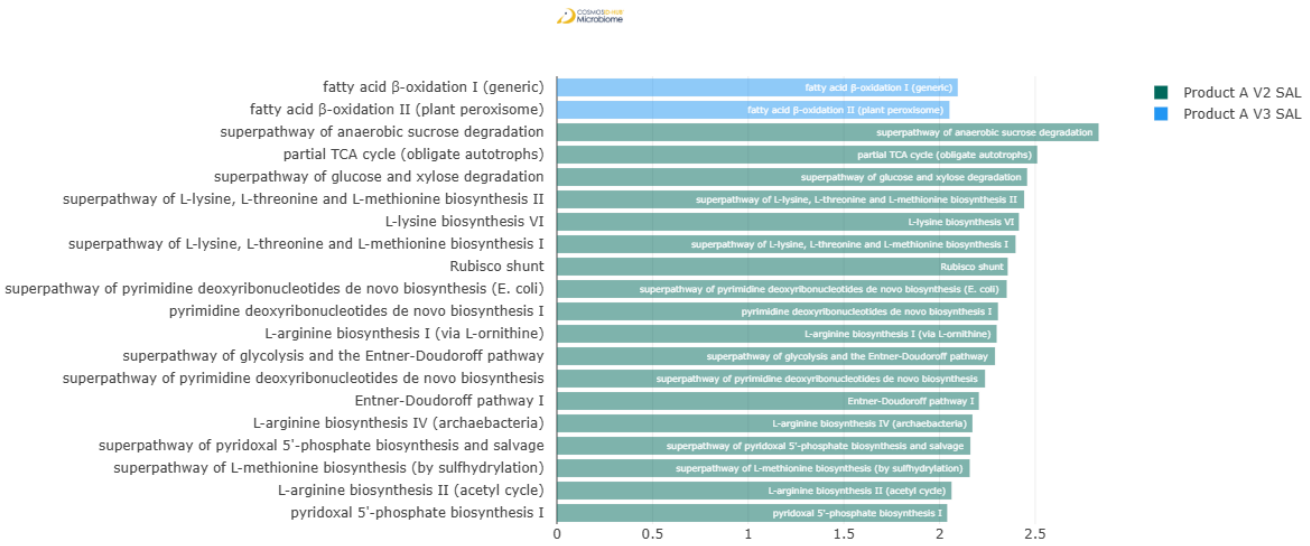
Differential Abundance (LEfSe) (MetaCyc)

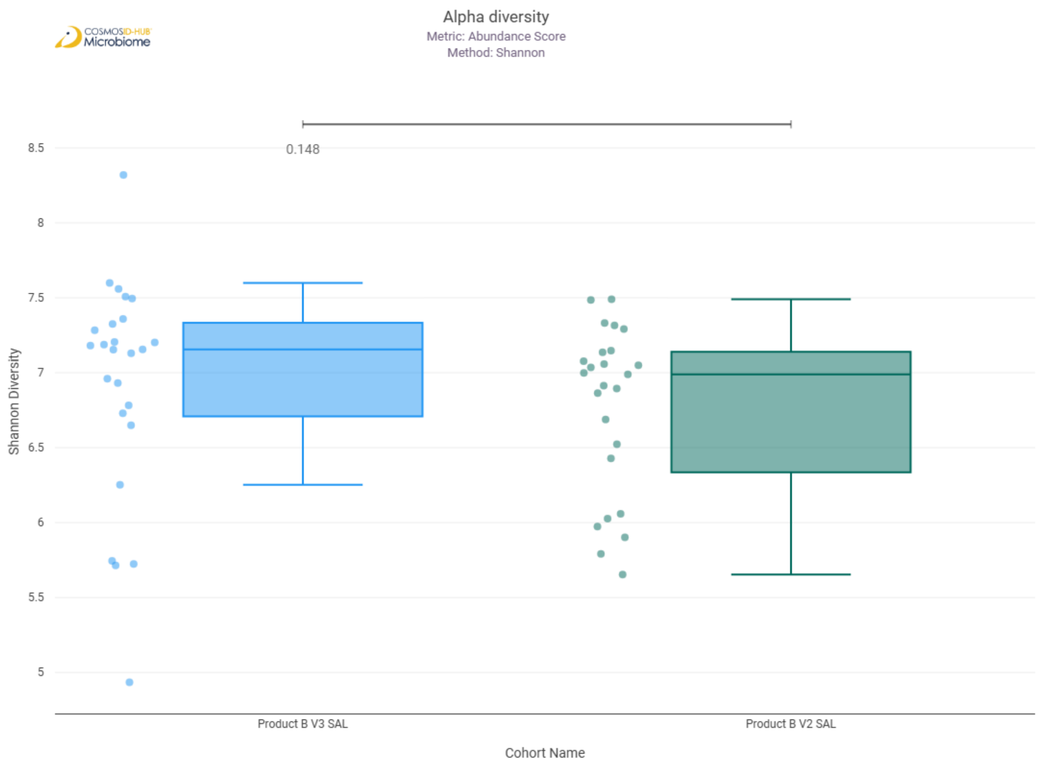


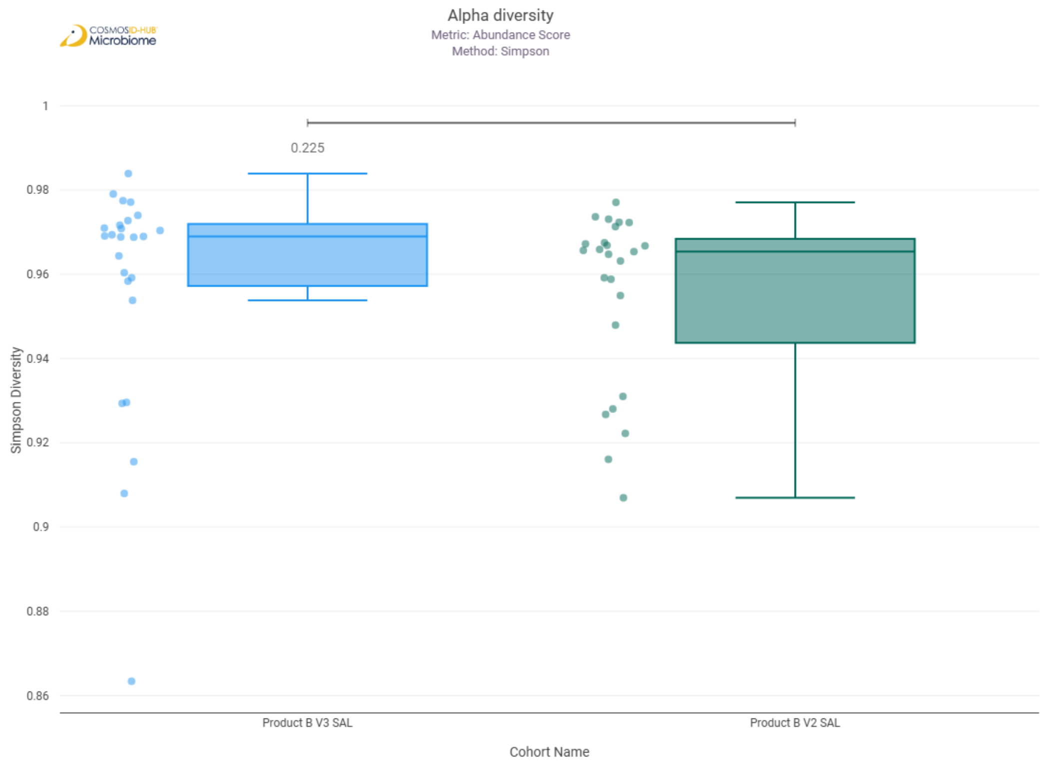
Feature	Enriched Cohort	LDA Score	P-value
fatty acid β-oxidation I (generic)	Product A V3 SAL	2.095429545	0.022553634
fatty acid β-oxidation II (plant peroxisome)	Product A V3 SAL	2.051853376	0.033983438
superpathway of anaerobic sucrose degradation	Product A V2 SAL	2.831636712	0.046061451
partial TCA cycle (obligate autotrophs)	Product A V2 SAL	2.510981802	0.014192278
superpathway of glucose and xylose degradation	Product A V2 SAL	2.458074599	0.001825689
superpathway of L-lysine, L-threonine and L-methionine biosynthesis II	Product A V2 SAL	2.442438549	0.02808172
L-lysine biosynthesis VI	Product A V2 SAL	2.415101559	0.030808261
superpathway of L-lysine, L-threonine and L-methionine biosynthesis I	Product A V2 SAL	2.397506712	0.002163783
Rubisco shunt	Product A V2 SAL	2.356421973	0.030608442
superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli)	Product A V2 SAL	2.351444885	0.004756827
pyrimidine deoxyribonucleotides de novo biosynthesis I	Product A V2 SAL	2.305719888	0.013266719
L-arginine biosynthesis I (via L-ornithine)	Product A V2 SAL	2.29886903	0.000911585
superpathway of glycolysis and the Entner-Doudoroff pathway	Product A V2 SAL	2.290181726	0.004455412
superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis	Product A V2 SAL	2.237994675	2.09E-02
Entner-Doudoroff pathway I	Product A V2 SAL	2.205795946	0.004718777
L-arginine biosynthesis IV (archaebacteria)	Product A V2 SAL	2.17211688	0.004825811
superpathway of pyridoxal 5'-phosphate biosynthesis and salvage	Product A V2 SAL	2.161332919	0.033683115
superpathway of L-methionine biosynthesis (by sulfhydrylation)	Product A V2 SAL	2.158067819	0.002046016
L-arginine biosynthesis II (acetyl cycle)	Product A V2 SAL	2.062786375	0.007905304
pyridoxal 5'-phosphate biosynthesis I	Product A V2 SAL	2.040191452	0.013446627

Comparison 6: Product B V2 SAL vs Product B V3 SAL

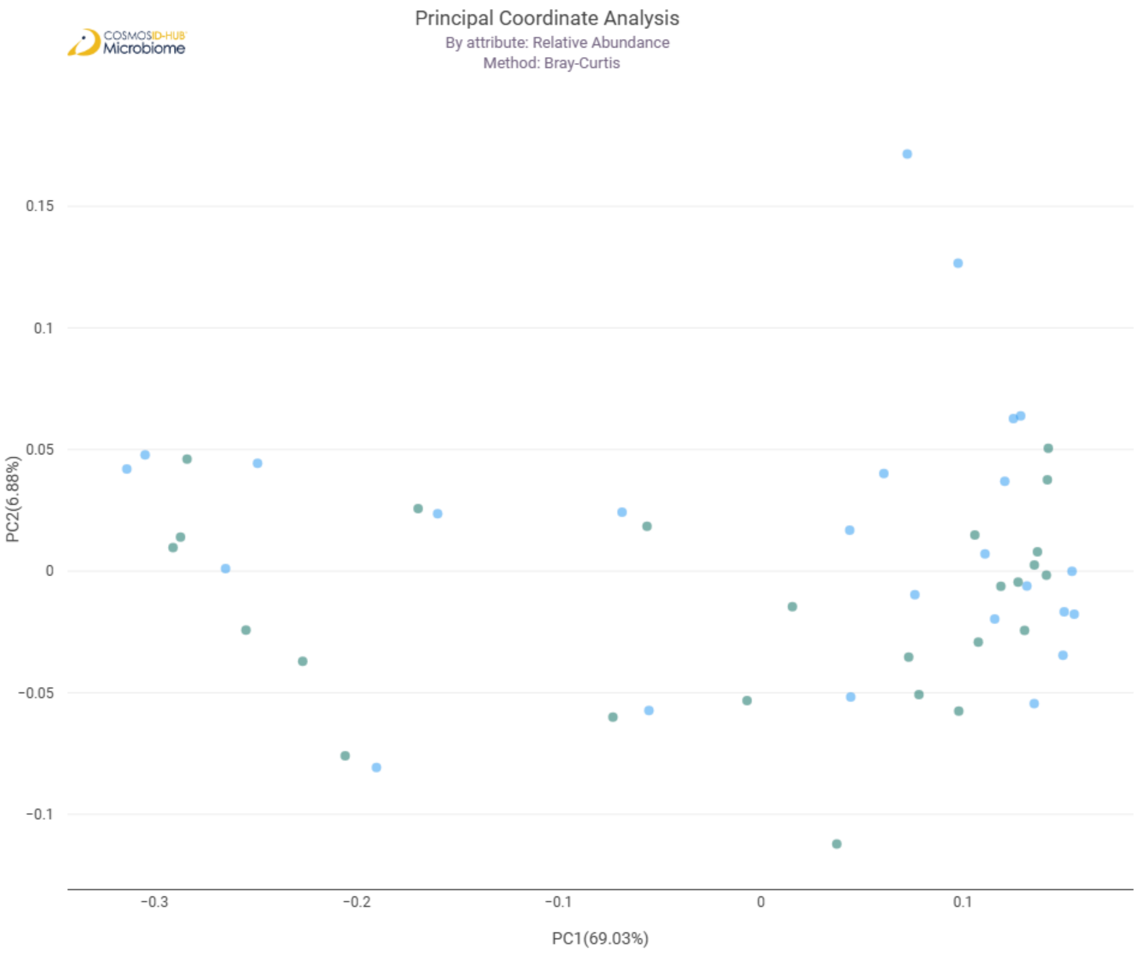
Gene Ontology

Alpha Diversity (GO)

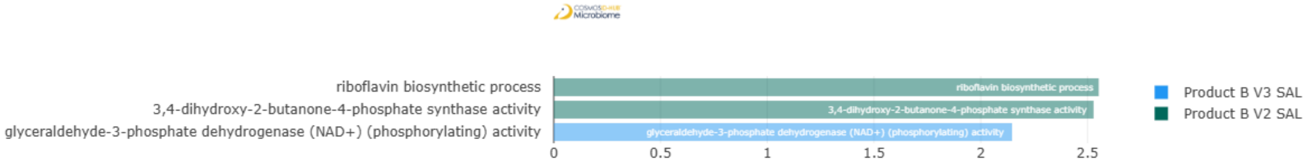
Chao1	
Shannon	

Simpson	Alpha diversity Metric: Abundance Score Method: Simpson COSMOSID-HUB Microbiome 1 0.98 0.96 0.94 0.92 0.9 0.88 0.86 Simpson Diversity 0.225 Product B V3 SAL Product B V2 SAL Cohort Name

Beta Diversity (GO)

Bray-Curtis PERMNOVA p = 0.526	

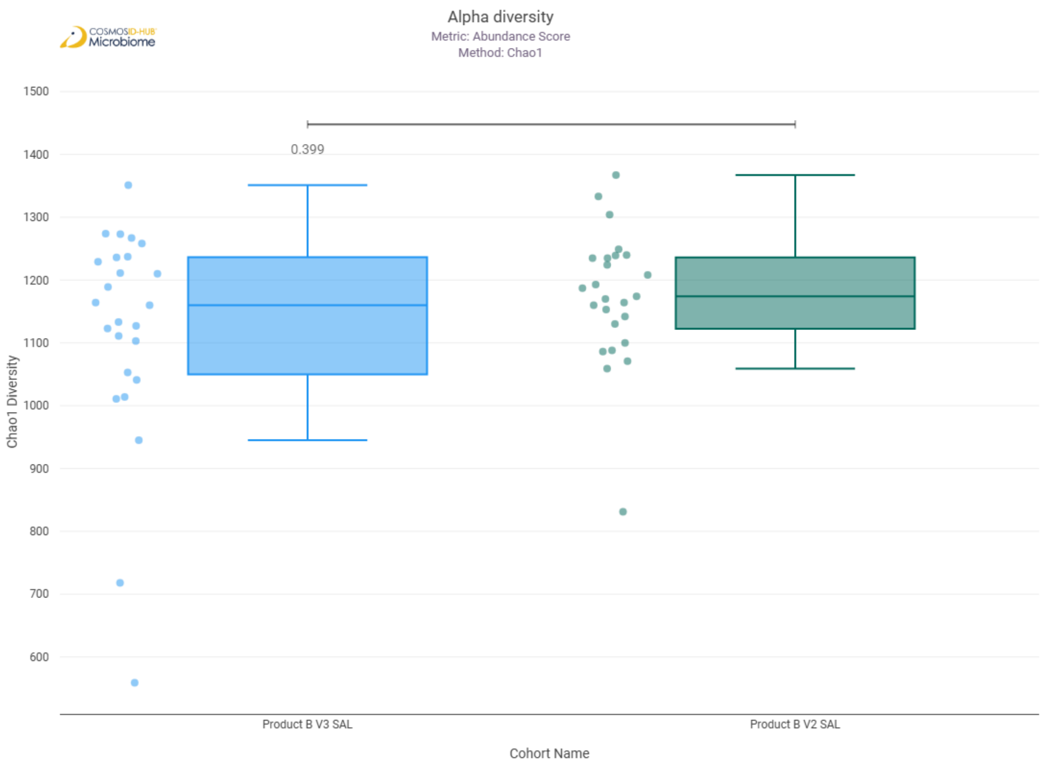
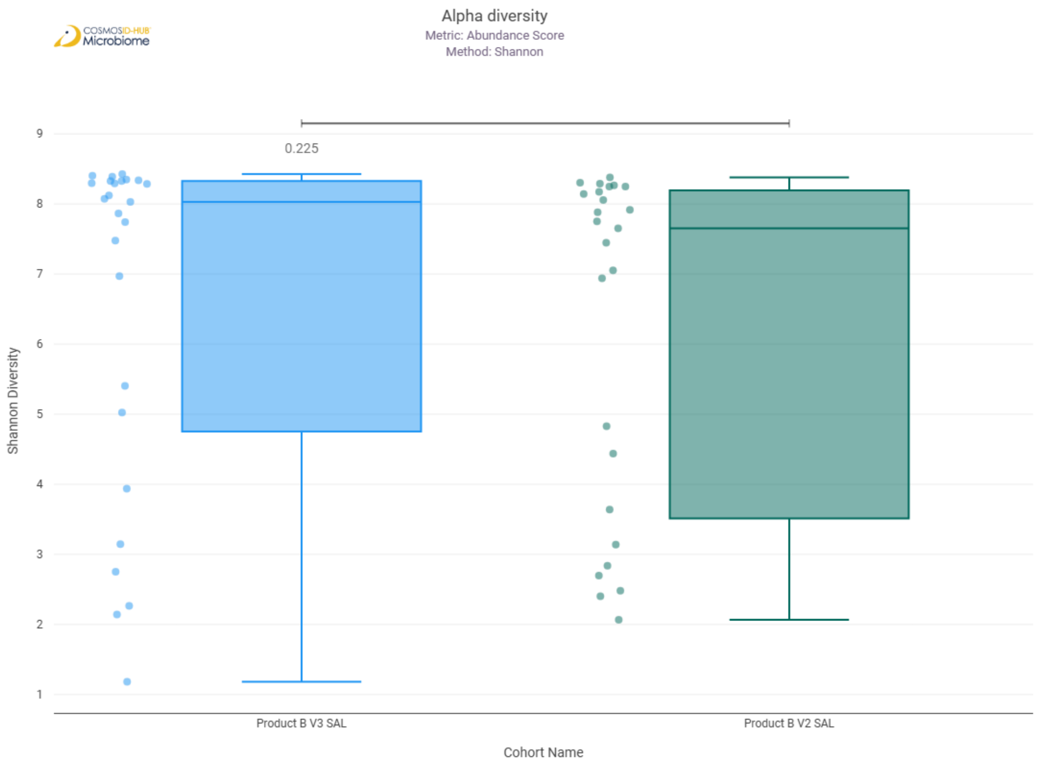
Differential Abundance (LEfSe) (GO)

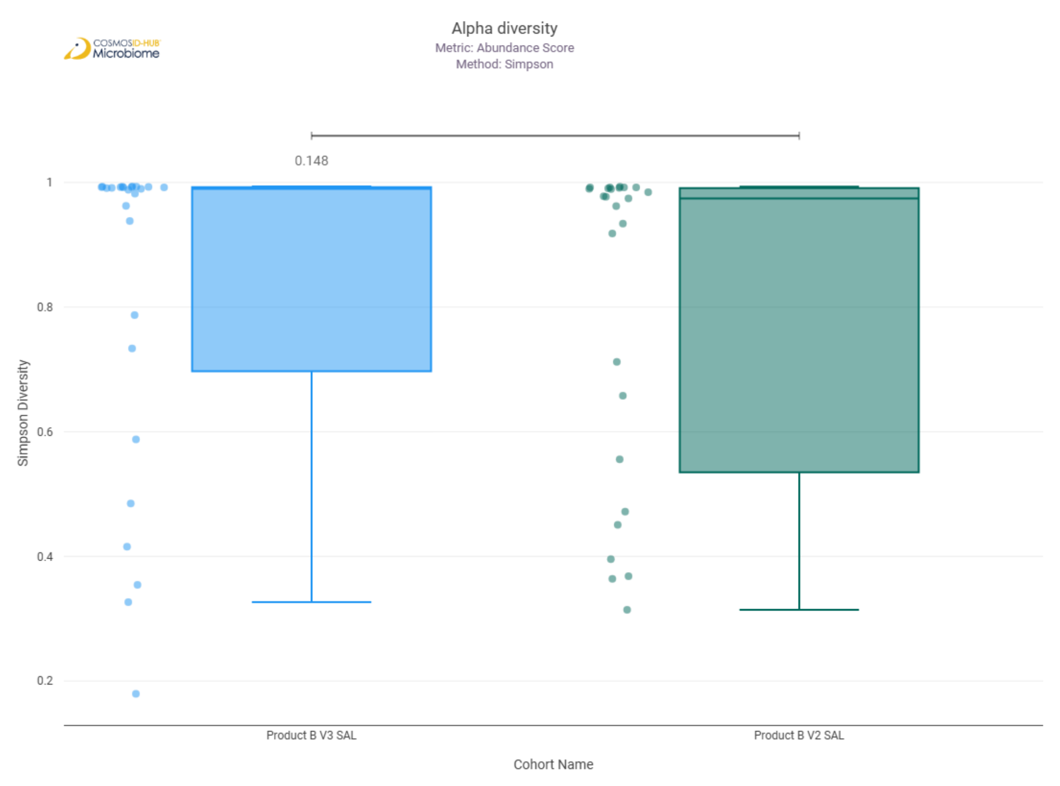


Feature	Enriched Cohort	LDA Score	P-value
glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity	Product B V3 SAL	2.14674601	0.026308569
riboflavin biosynthetic process	Product B V2 SAL	2.552661472	0.0352731
3,4-dihydroxy-2-butanone-4-phosphate synthase activity	Product B V2 SAL	2.528684256	0.0250207

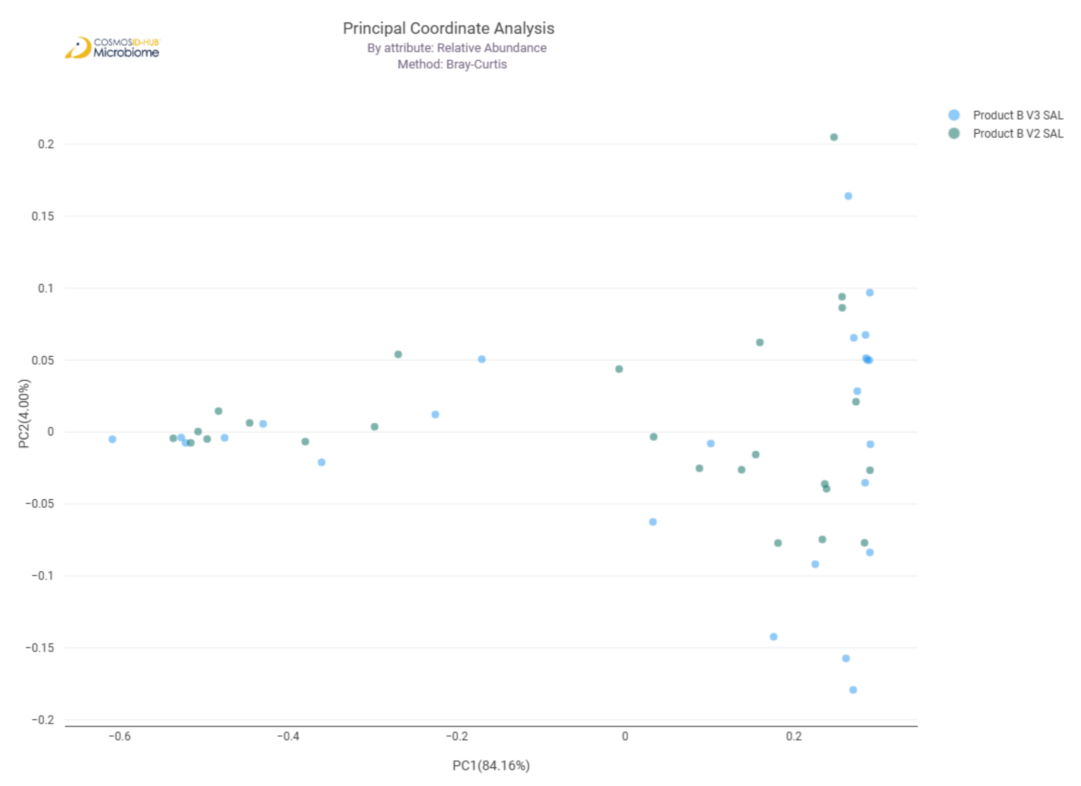
Enzyme Commission

Alpha Diversity (EC)

Chao1	
Shannon	

Simpson	

Beta Diversity (EC)

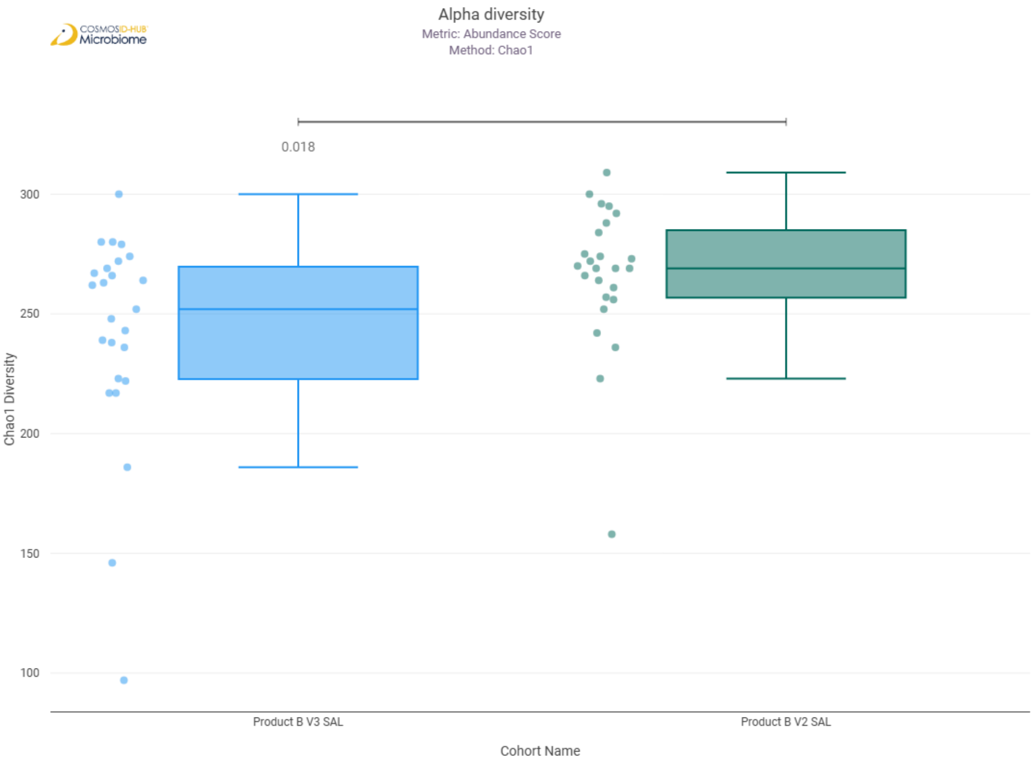
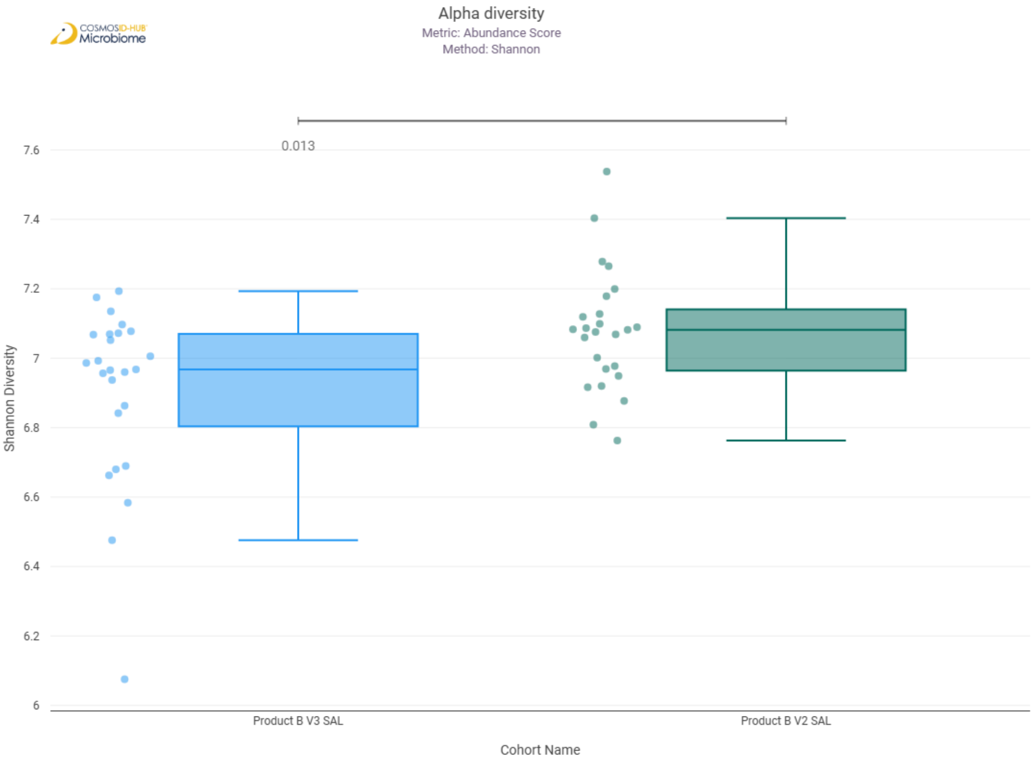
Bray-Curtis PERMNOVA p = 0.440	

Differential Abundance (LEfSe) (EC)

No differentially abundant features detected

MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1	
Shannon	

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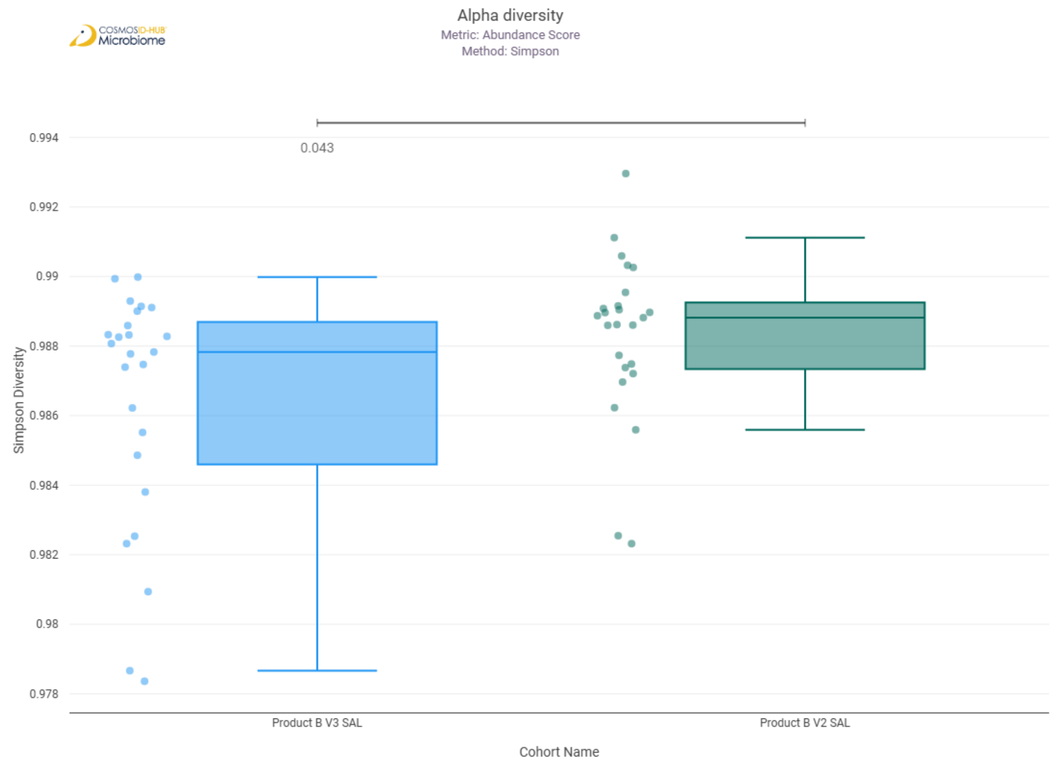

Beta Diversity (MetaCyc)

Bray-Curtis

PERMNOVA
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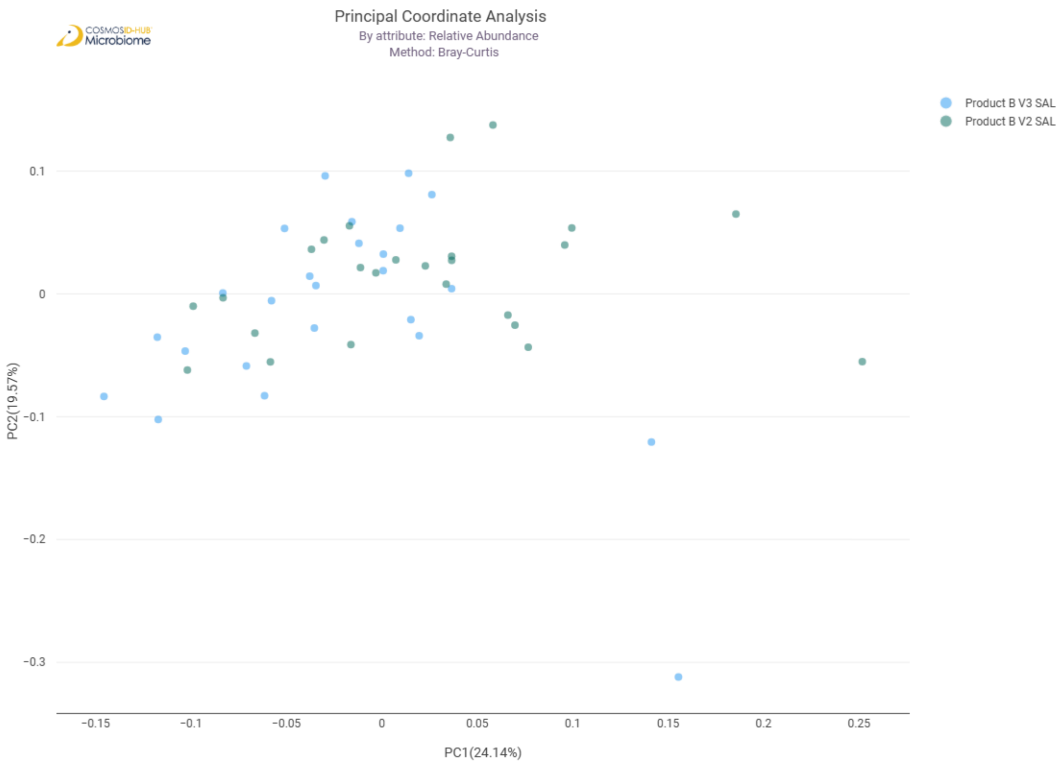
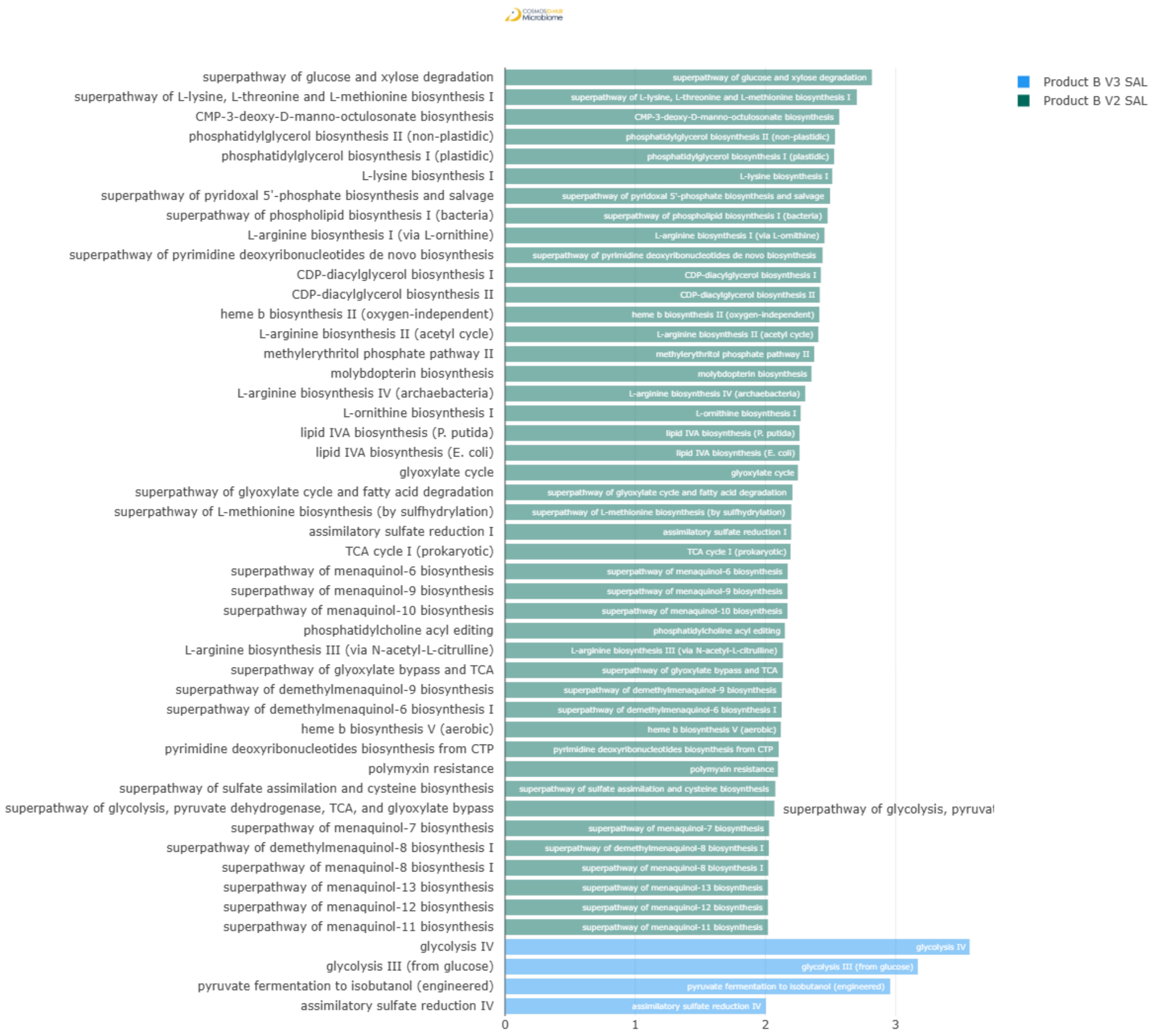


Differential Abundance (LEfSe) (MetaCyc)



Feature	Enriched Cohort	LDA Score	P-value
superpathway of glucose and xylose degradation	Product B V2 SAL	2.818172394	0.003199335
superpathway of L-lysine, L-threonine and L-methionine biosynthesis I	Product B V2 SAL	2.702332952	0.001268472
CMP-3-deoxy-D-manno-octulosonate biosynthesis	Product B V2 SAL	2.567217917	0.021478913
phosphatidylglycerol biosynthesis II (non-plastidic)	Product B V2 SAL	2.534565735	0.011339073
phosphatidylglycerol biosynthesis I (plastidic)	Product B V2 SAL	2.527633184	0.011339073
L-lysine biosynthesis I	Product B V2 SAL	2.513475321	0.044617455
superpathway of pyridoxal 5'-phosphate biosynthesis and salvage	Product B V2 SAL	2.496575918	0.045855823
superpathway of phospholipid biosynthesis I (bacteria)	Product B V2 SAL	2.47795577	0.040658018
L-arginine biosynthesis I (via L-ornithine)	Product B V2 SAL	2.453409033	0.028209048
superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis	Product B V2 SAL	2.43911832	0.035179233

CDP-diacylglycerol biosynthesis I	Product B V2 SAL	2.425530852	4.07E-02
CDP-diacylglycerol biosynthesis II	Product B V2 SAL	2.417219654	0.0352731
heme b biosynthesis II (oxygen-independent)	Product B V2 SAL	2.414277056	0.009055969
L-arginine biosynthesis II (acetyl cycle)	Product B V2 SAL	2.406610684	0.012881271
methylerythritol phosphate pathway II	Product B V2 SAL	2.374746616	0.038785713
molybdopterin biosynthesis	Product B V2 SAL	2.353869718	0.004474919
L-arginine biosynthesis IV (archaebacteria)	Product B V2 SAL	2.30565784	0.046662482
L-ornithine biosynthesis I	Product B V2 SAL	2.270426756	0.034286155
lipid IVA biosynthesis (E. coli)	Product B V2 SAL	2.262174403	0.013543566
lipid IVA biosynthesis (P. putida)	Product B V2 SAL	2.262174403	0.013543566
glyoxylate cycle	Product B V2 SAL	2.249728953	1.84E-03
superpathway of glyoxylate cycle and fatty acid degradation	Product B V2 SAL	2.20753772	0.030301371
superpathway of L-methionine biosynthesis (by sulfhydrylation)	Product B V2 SAL	2.19885117	0.011392734
assimilatory sulfate reduction I	Product B V2 SAL	2.197446182	0.010334085
TCA cycle I (prokaryotic)	Product B V2 SAL	2.192838295	0.027140444
superpathway of menaquinol-6 biosynthesis	Product B V2 SAL	2.171045532	6.09421E-05
superpathway of menaquinol-9 biosynthesis	Product B V2 SAL	2.170593917	6.09421E-05
superpathway of menaquinol-10 biosynthesis	Product B V2 SAL	2.169649613	6.09421E-05
phosphatidylcholine acyl editing	Product B V2 SAL	2.149186255	0.043498937
L-arginine biosynthesis III (via N-acetyl-L-citrulline)	Product B V2 SAL	2.134965514	0.031737021
superpathway of glyoxylate bypass and TCA	Product B V2 SAL	2.134203058	0.044486372
superpathway of demethylmenaquinol-9 biosynthesis	Product B V2 SAL	2.1257968	6.09421E-05
superpathway of demethylmenaquinol-6 biosynthesis I	Product B V2 SAL	2.124841397	6.09421E-05
heme b biosynthesis V (aerobic)	Product B V2 SAL	2.118223752	0.031887431
pyrimidine deoxyribonucleotides biosynthesis from CTP	Product B V2 SAL	2.102099596	0.044416899
polymyxin resistance	Product B V2 SAL	2.095875541	0.00741426
superpathway of sulfate assimilation and cysteine biosynthesis	Product B V2 SAL	2.076167827	0.004912845
superpathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass	Product B V2 SAL	2.068575031	0.002366655
superpathway of menaquinol-7 biosynthesis	Product B V2 SAL	2.028076494	0.030318736
superpathway of demethylmenaquinol-8 biosynthesis I	Product B V2 SAL	2.026100386	0.013730328
superpathway of menaquinol-8 biosynthesis I	Product B V2 SAL	2.021614503	0.009305995
superpathway of menaquinol-11 biosynthesis	Product B V2 SAL	2.019480361	0.016137021
superpathway of menaquinol-12 biosynthesis	Product B V2 SAL	2.019480361	0.016137021
superpathway of menaquinol-13 biosynthesis	Product B V2 SAL	2.019480361	0.016137021
glycolysis IV	Product B V3 SAL	3.567908932	0.002551693
glycolysis III (from glucose)	Product B V3 SAL	3.170717244	0.011339073
pyruvate fermentation to isobutanol (engineered)	Product B V3 SAL	2.958214564	0.036996166
assimilatory sulfate reduction IV	Product B V3 SAL	2.00338347	0.006173676

Comparison 7: Product A V2 SAL vs Product B V2 SAL

Gene Ontology

Alpha Diversity (GO)

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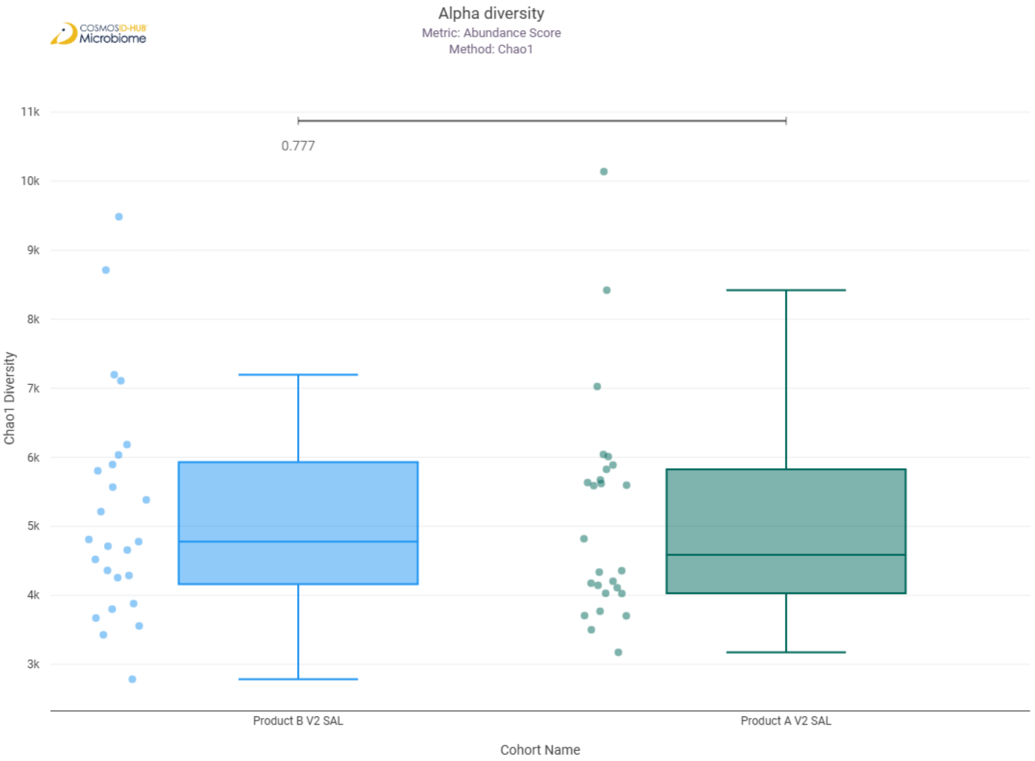
<tr><td>Chao1</td><td>
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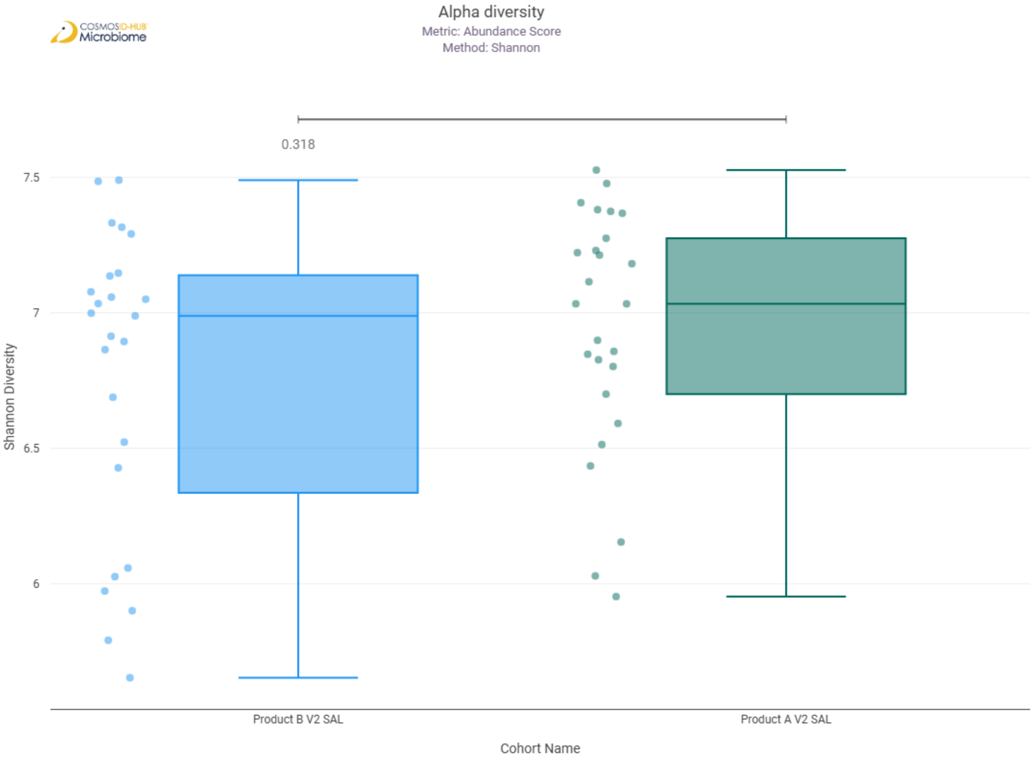
<tr><td>Shannon</td><td>
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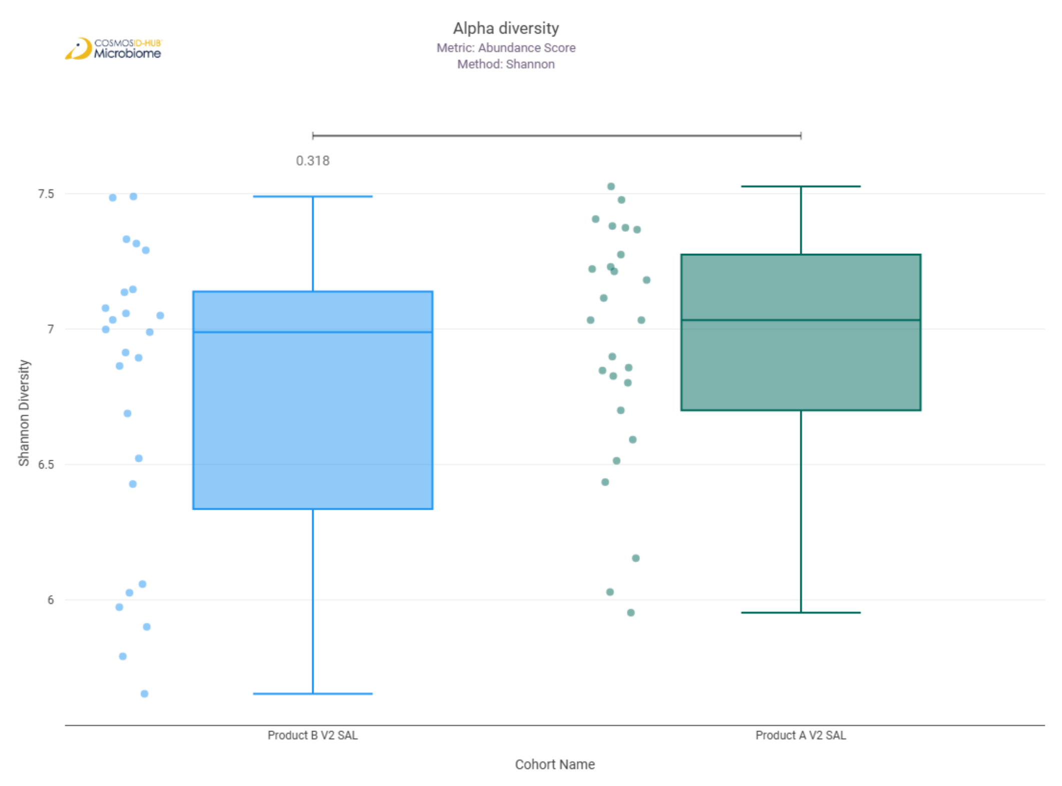
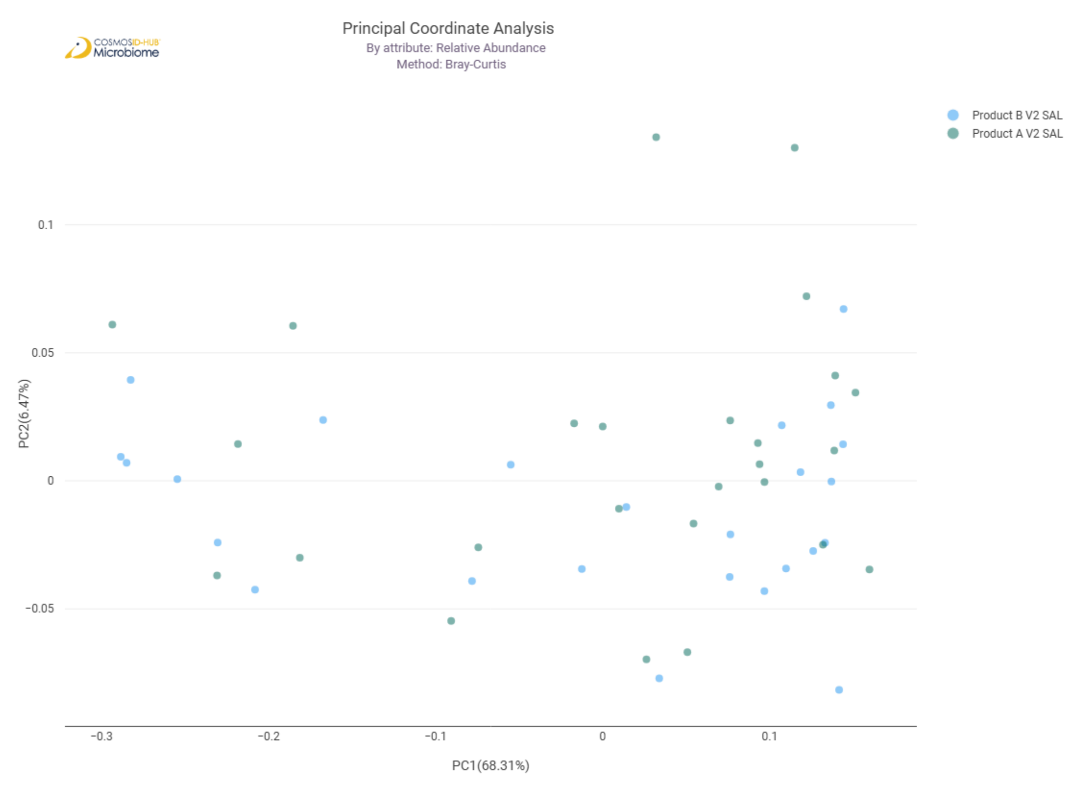
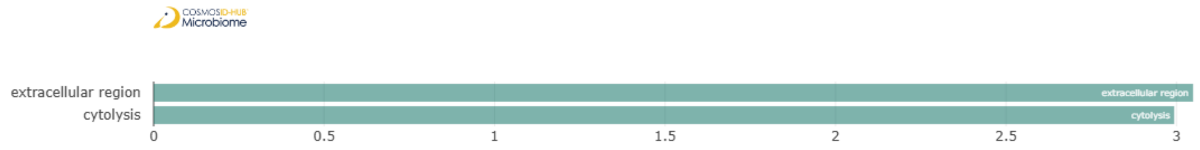
Simpson	

Beta Diversity (GO)

Bray-Curtis PERMNOVA p = 0.573	

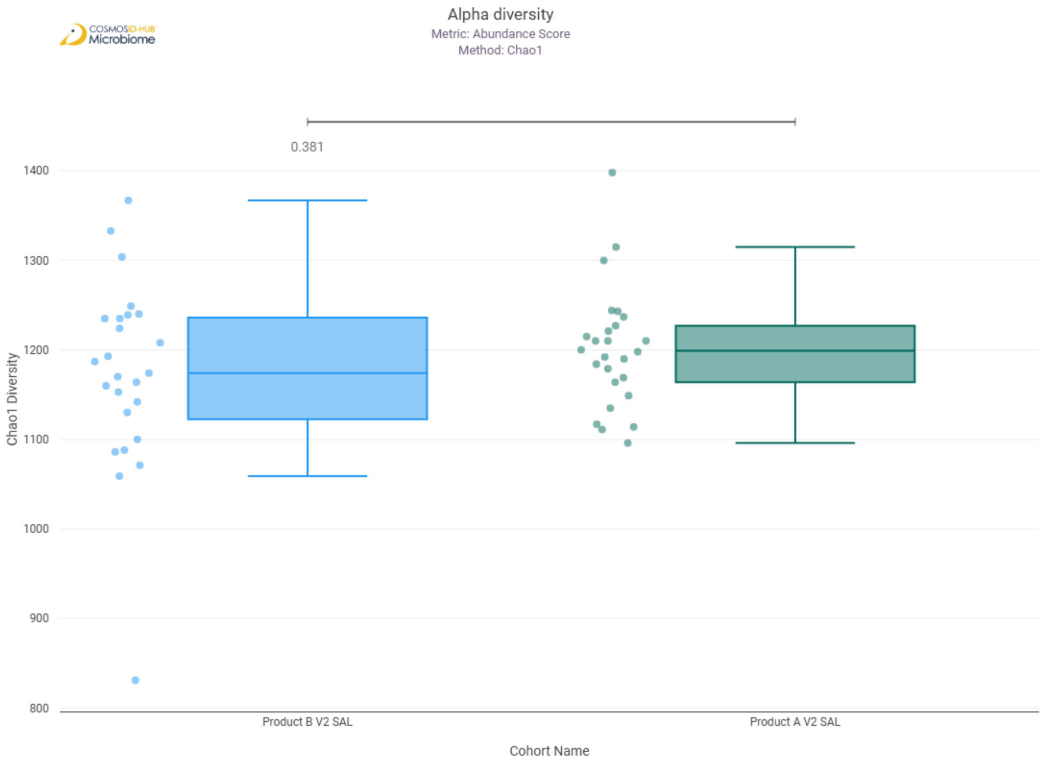
Differential Abundance (LEfSe) (GO)

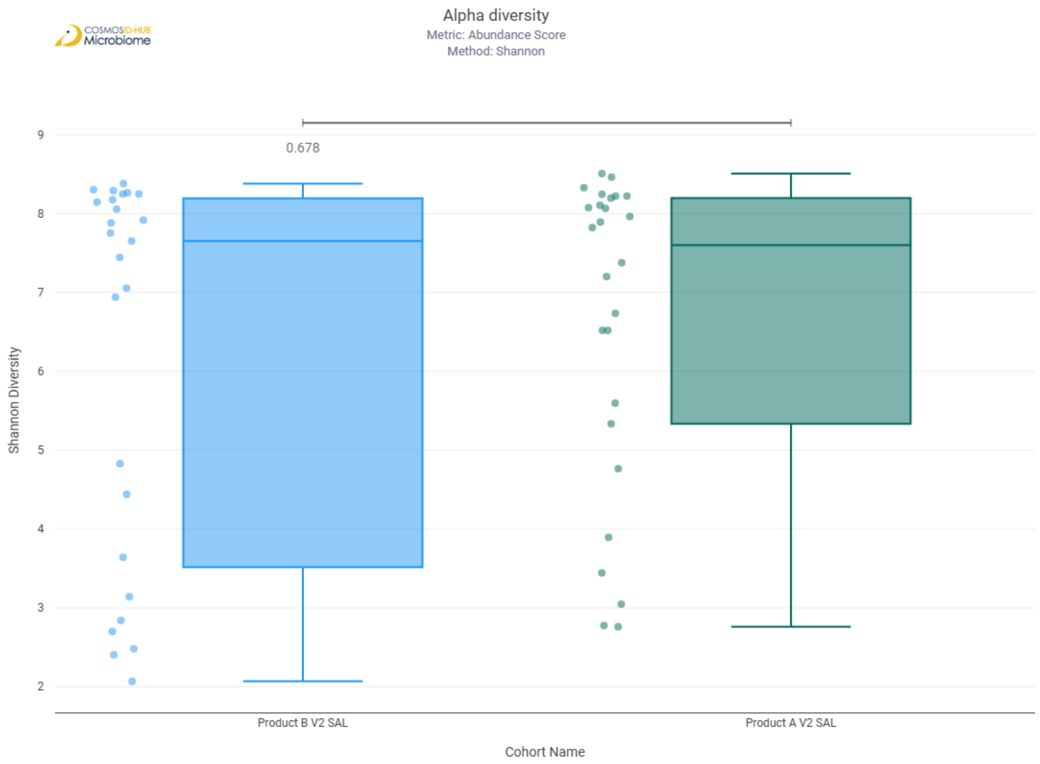
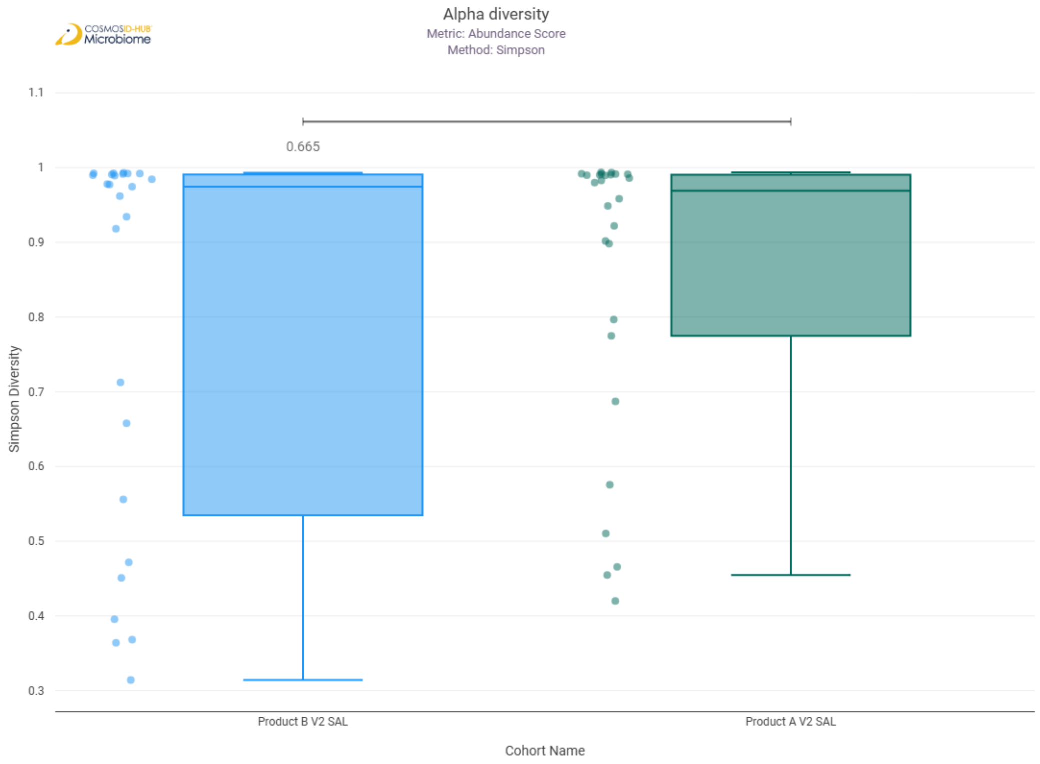


Feature	Enriched Cohort	LDA Score	P-value
extracellular region	Product A V2 SAL	3.048793763	0.028837668
cytolysis	Product A V2 SAL	2.99327891	0.021519031

Enzyme Commission

Alpha Diversity (EC)

Chao1	

Shannon	
Simpson	

Beta Diversity (EC)

Bray-Curtis

PERMNOVA
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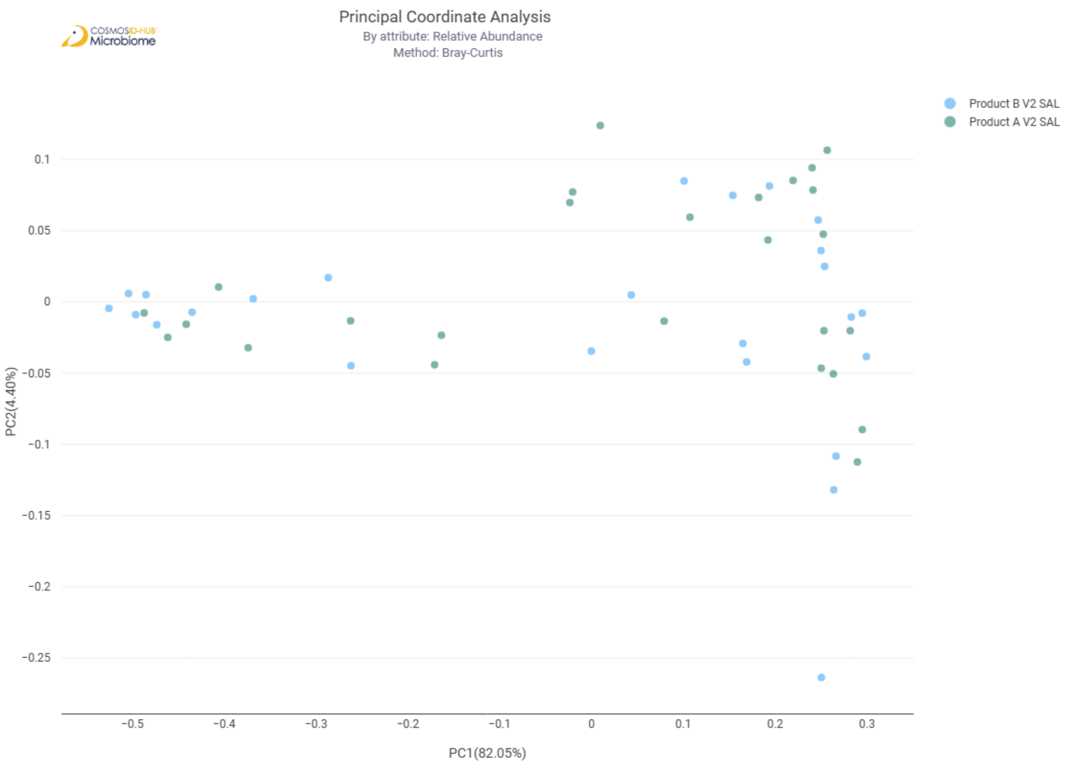
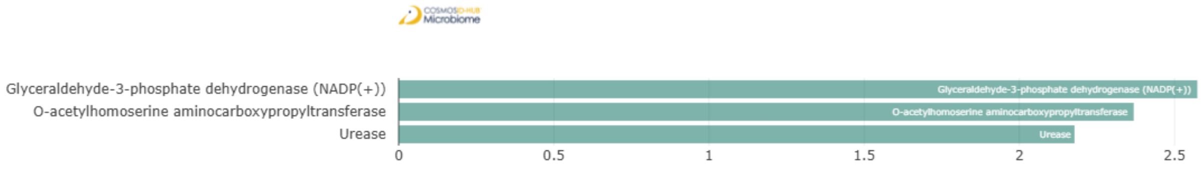


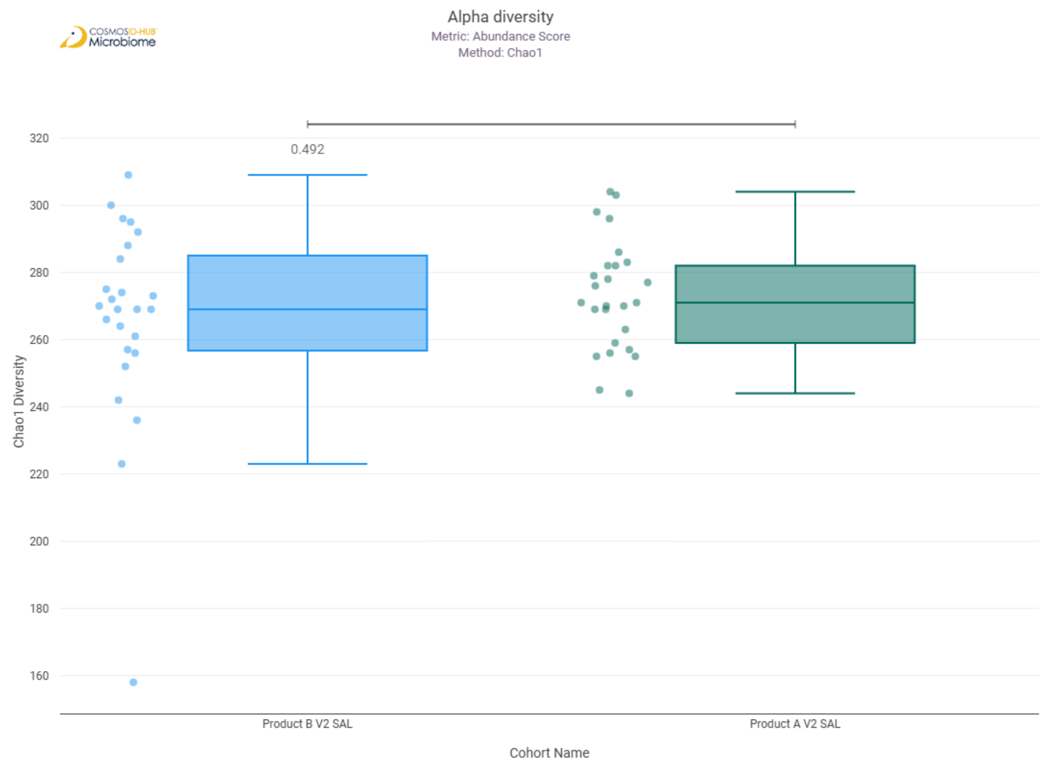
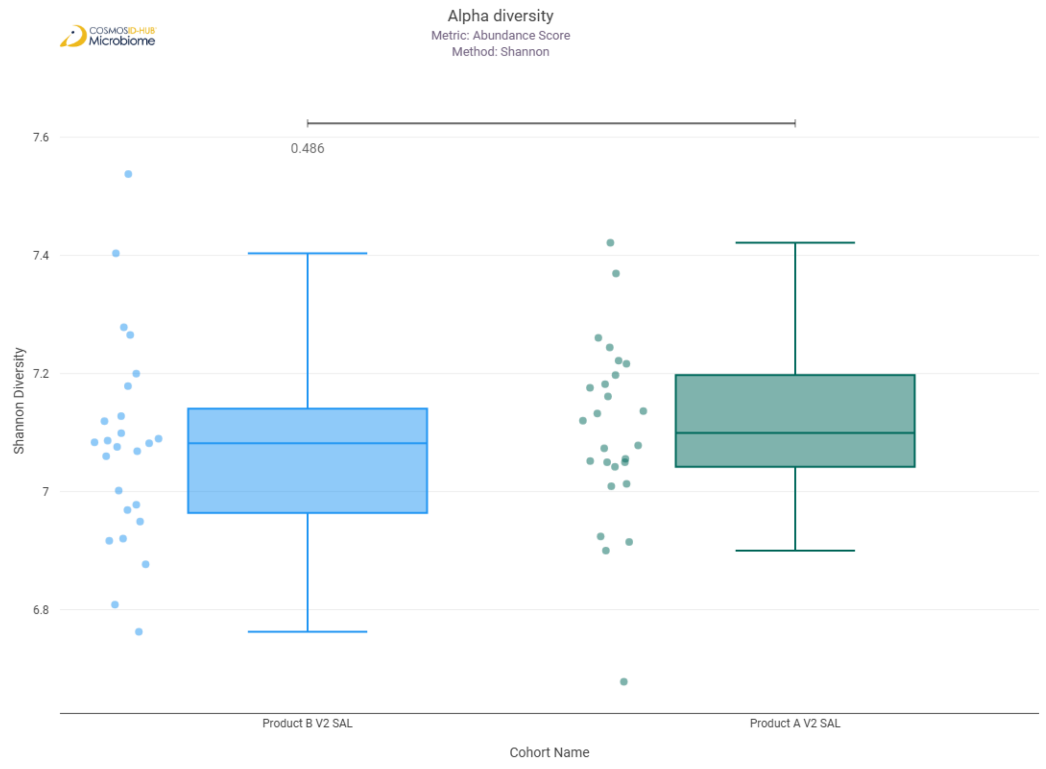
Differential Abundance (LEfSe) (EC)

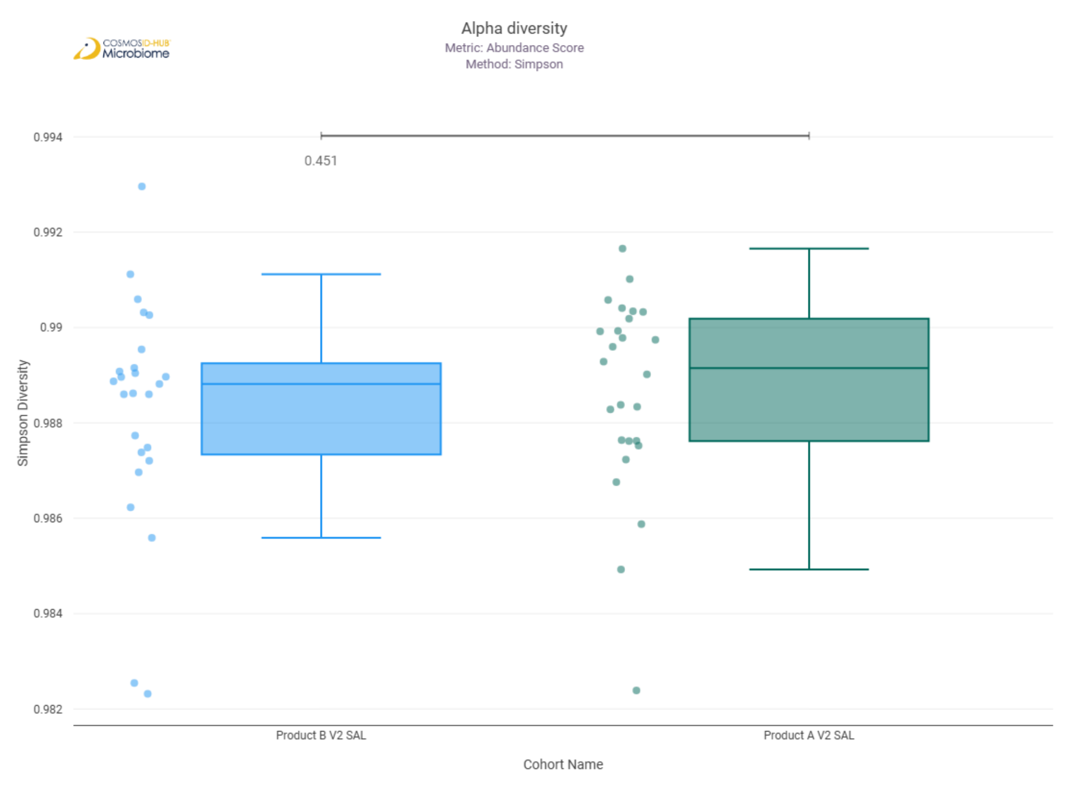


Feature	Enriched Cohort	LDA Score	P-value
Glyceraldehyde-3-phosphate dehydrogenase (NADP(+))	Product A V2 SAL	2.573441142	0.034813536
O-acetylhomoserine aminocarboxypropyltransferase	Product A V2 SAL	2.368534336	0.039994768
Urease	Product A V2 SAL	2.177716688	0.041854827

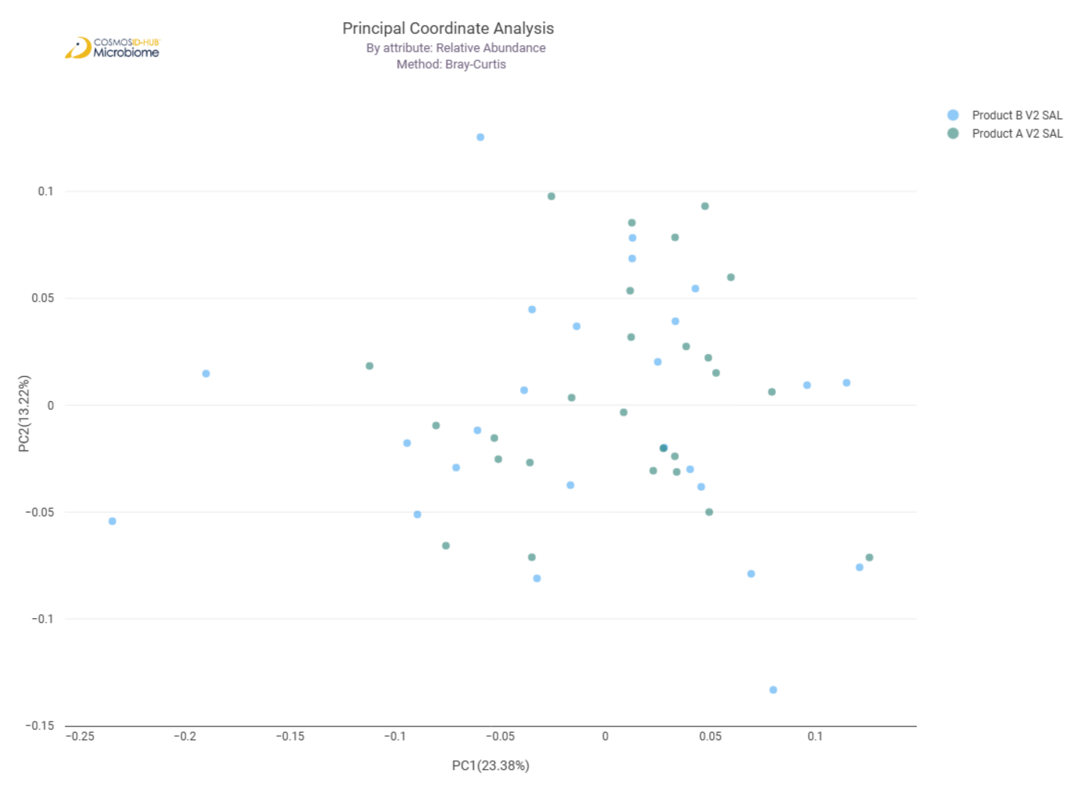
MetaCyc Pathways

Alpha Diversity (MetaCyc)

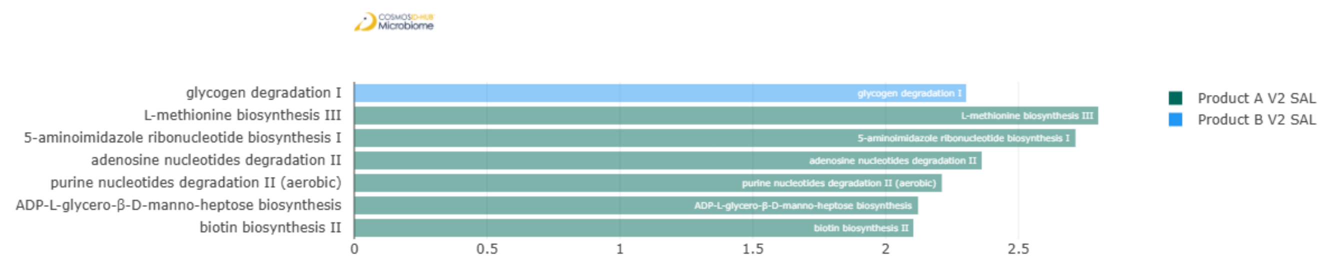
Chao1	
Shannon	

Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis PERMNOVA p = 0.588	

Differential Abundance (LEfSe) (MetaCyc)

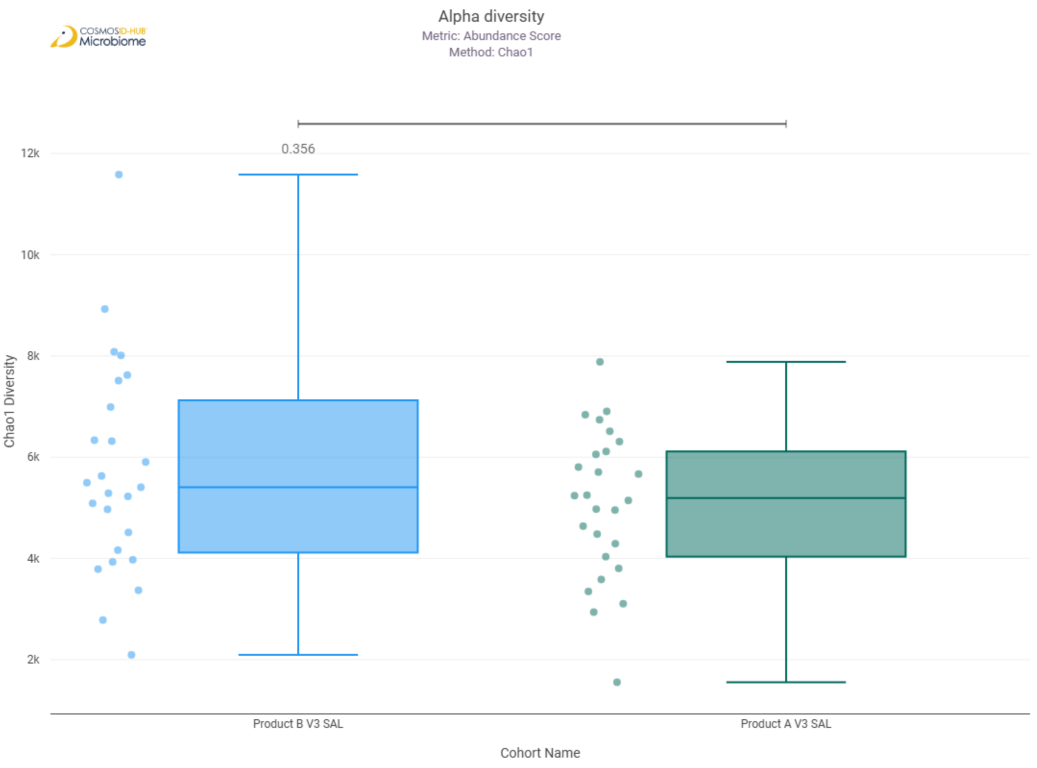
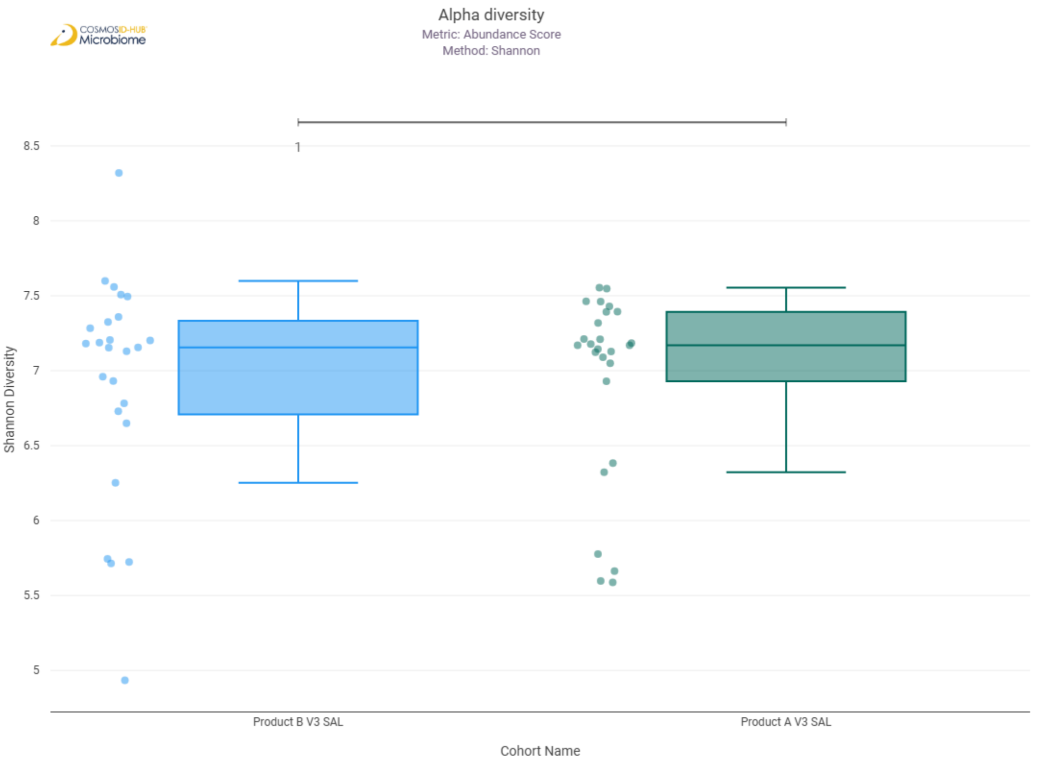


Feature	Enriched Cohort	LDA Score	P-value
glycogen degradation I	Product B V2 SAL	2.302816818	0.038205314
L-methionine biosynthesis III	Product A V2 SAL	2.800174369	0.028837668
5-aminoimidazole ribonucleotide biosynthesis I	Product A V2 SAL	2.714616828	0.041854827
adenosine nucleotides degradation II	Product A V2 SAL	2.361586069	0.033160392
purine nucleotides degradation II (aerobic)	Product A V2 SAL	2.211547707	0.020887991
ADP-L-glycero-β-D-manno-heptose biosynthesis	Product A V2 SAL	2.122101305	0.026186596
biotin biosynthesis II	Product A V2 SAL	2.104231519	0.018951173

Comparison 8: Product A V3 SAL vs Product B V3 SAL

Gene Ontology

Alpha Diversity (GO)

Chao1	
Shannon	

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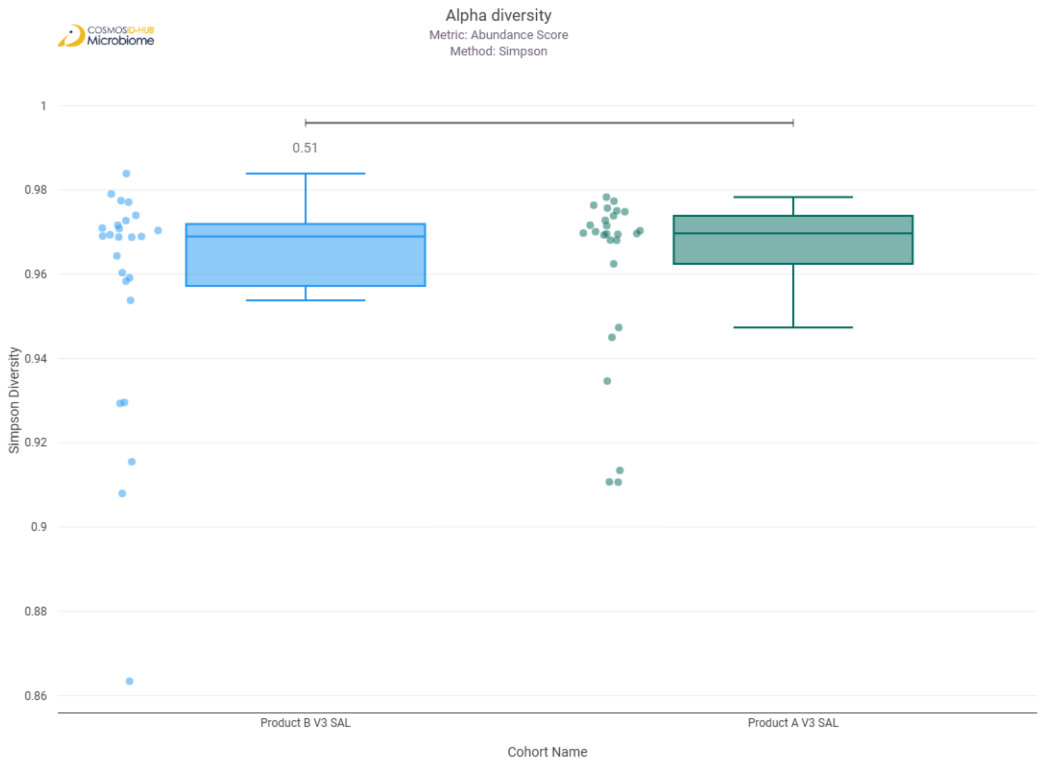
<tr><td>Simpson</td><td>
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Beta Diversity (GO)

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PERMNOVA
p = 0.505</td><td>
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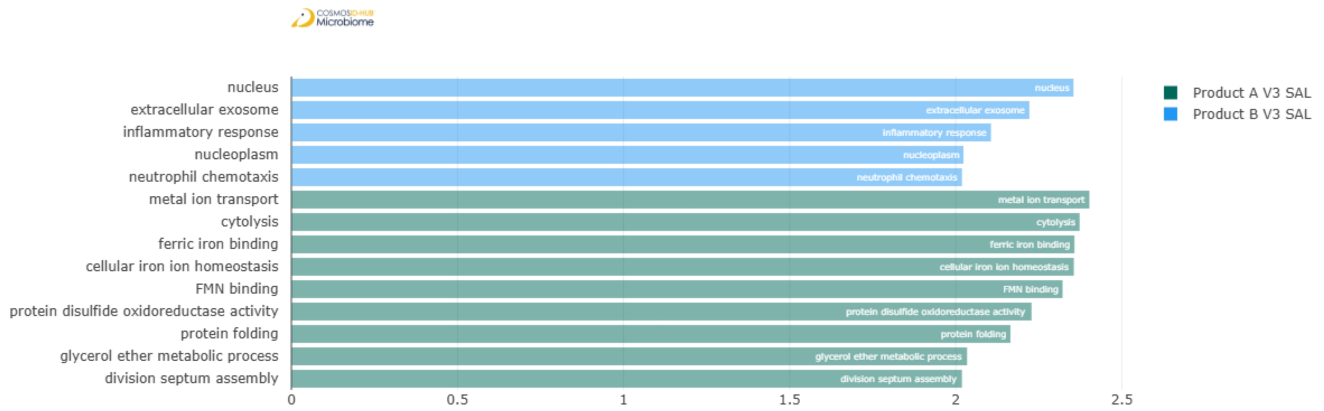
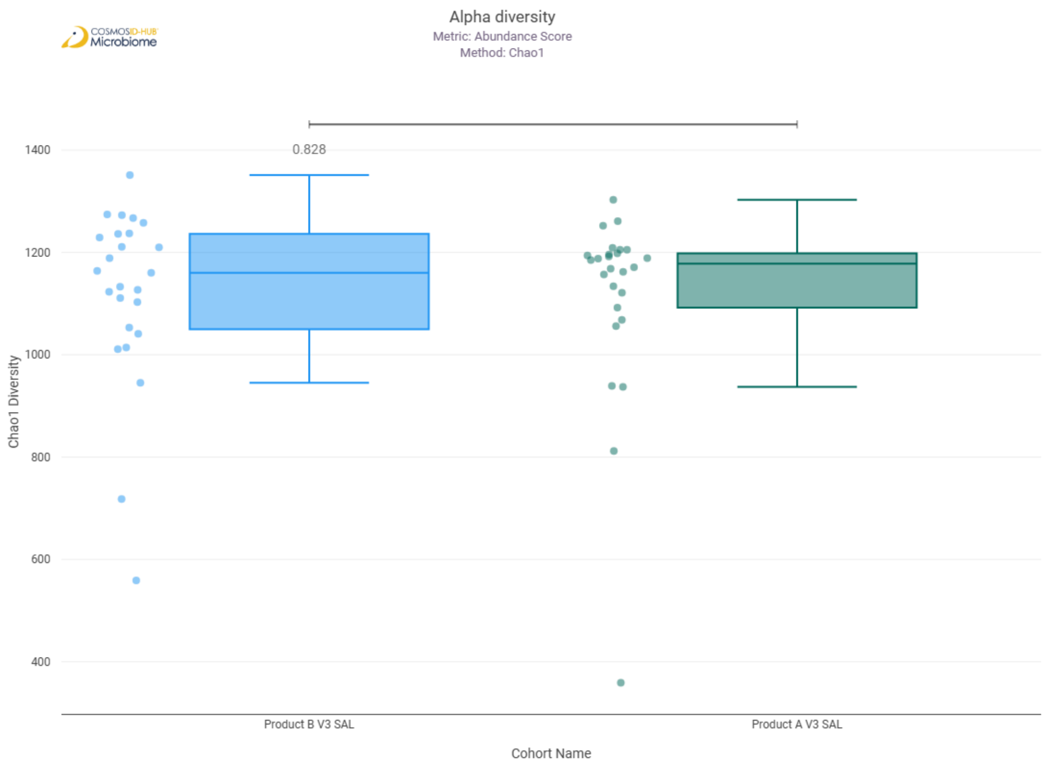
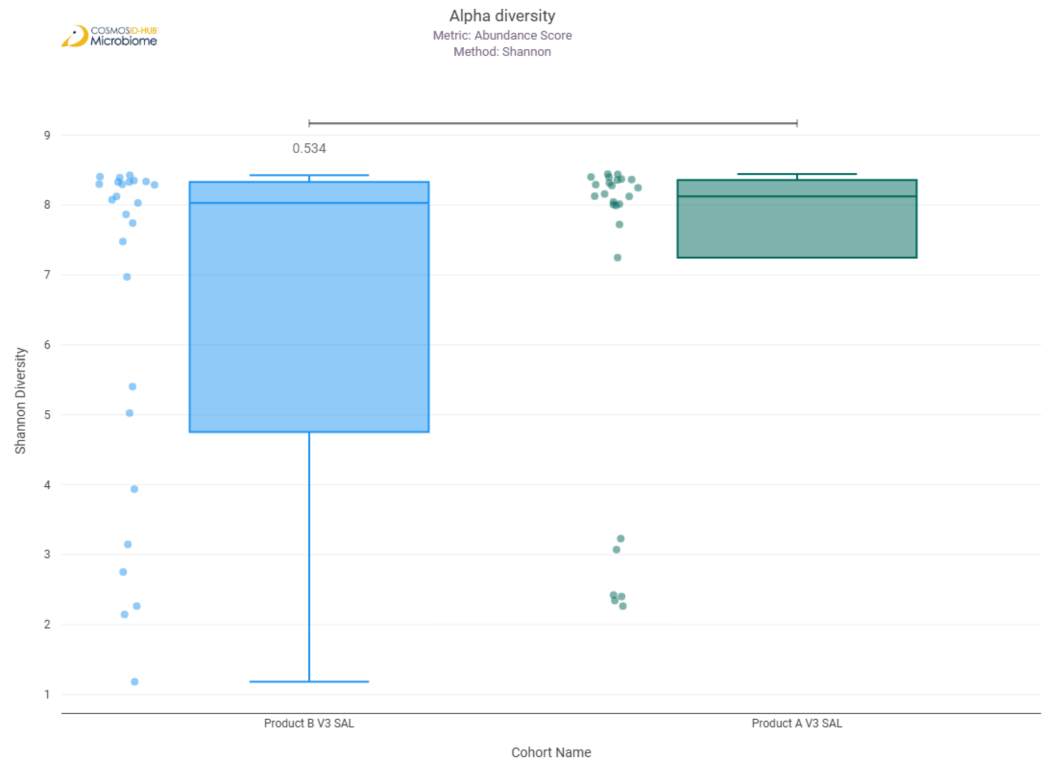
Differential Abundance (LEfSe) (GO)

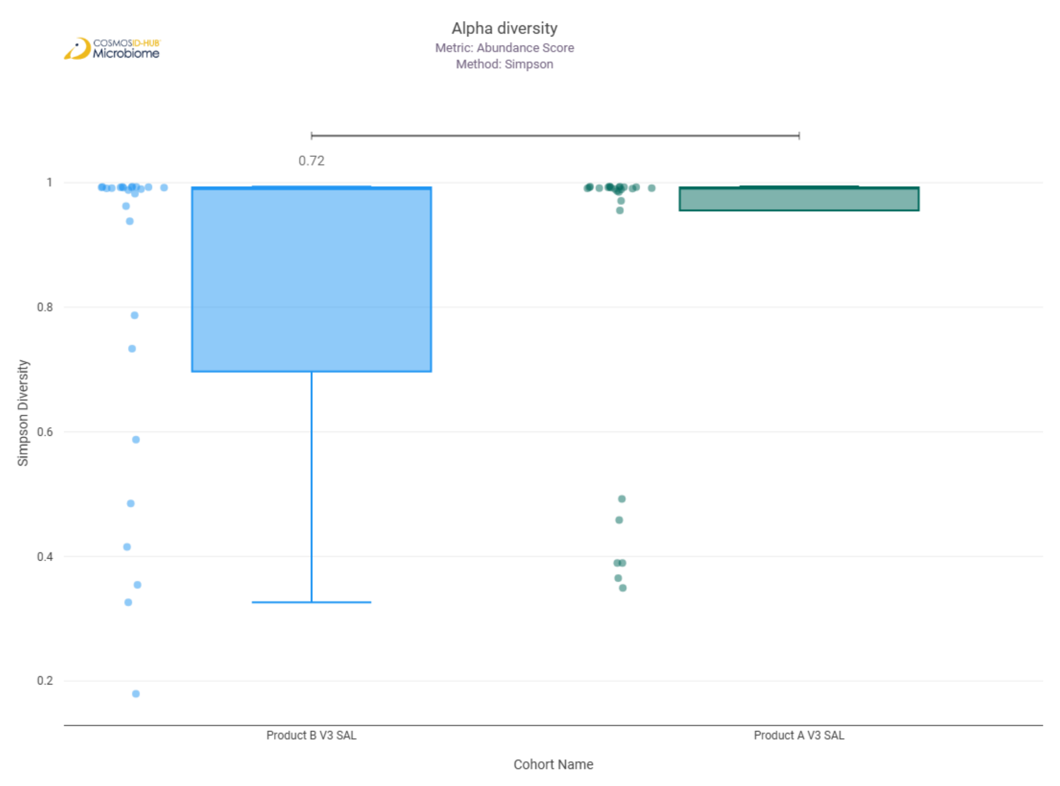


Feature	Enriched Cohort	LDA Score	P-value
nucleus	Product B V3 SAL	2.354393027	0.030245812
extracellular exosome	Product B V3 SAL	2.221604406	0.047879765
inflammatory response	Product B V3 SAL	2.106087975	0.033240045
nucleoplasm	Product B V3 SAL	2.023113821	0.038205314
neutrophil chemotaxis	Product B V3 SAL	2.01875955	0.045795182
metal ion transport	Product A V3 SAL	2.402291309	0.010390869
cytolysis	Product A V3 SAL	2.372871937	0.024341408
ferric iron binding	Product A V3 SAL	2.357375209	0.00745964
cellular iron ion homeostasis	Product A V3 SAL	2.355615079	0.00881699
FMN binding	Product A V3 SAL	2.321558848	0.028837668
protein disulfide oxidoreductase activity	Product A V3 SAL	2.228239528	0.030245812
protein folding	Product A V3 SAL	2.164657961	0.039994768
glycerol ether metabolic process	Product A V3 SAL	2.034126856	0.045795182
division septum assembly	Product A V3 SAL	2.018707201	0.009840467

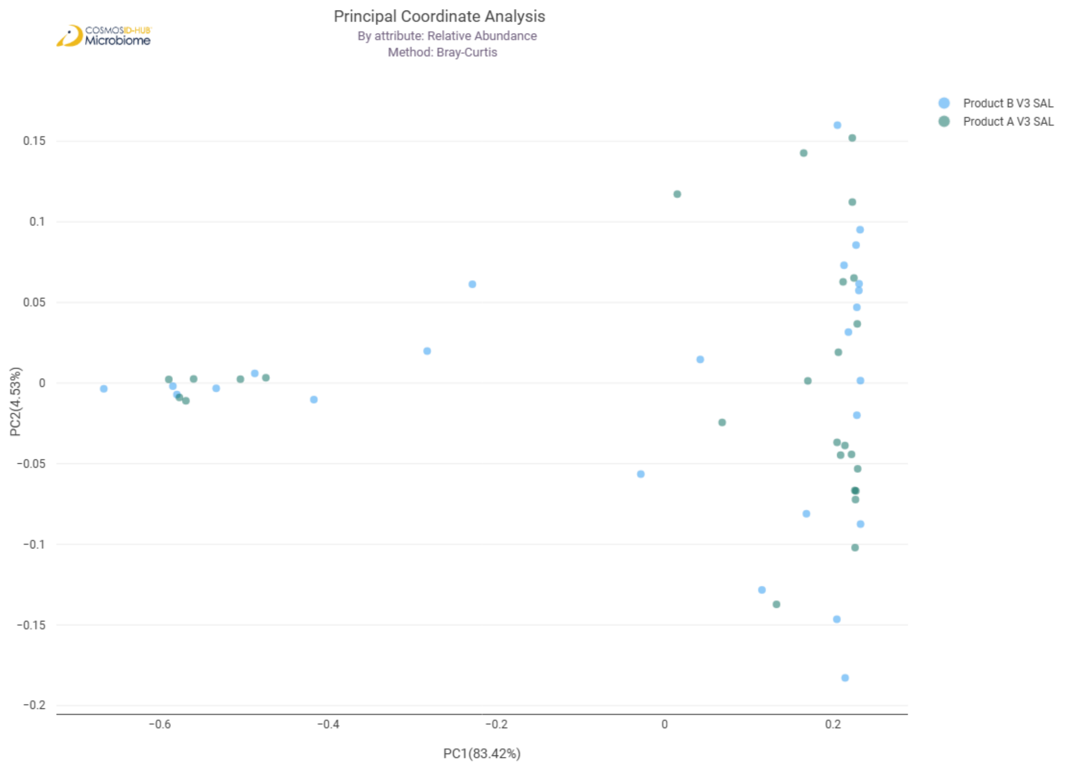
Enzyme Commission

Alpha Diversity (EC)

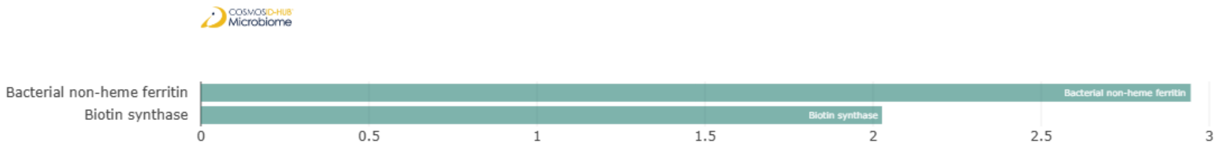
Chao1	
Shannon	

Simpson	 Alpha diversity Metric: Abundance Score Method: Simpson

Beta Diversity (EC)

Bray-Curtis PERMNOVA p = 0.676	 Principal Coordinate Analysis By attribute: Relative Abundance Method: Bray-Curtis

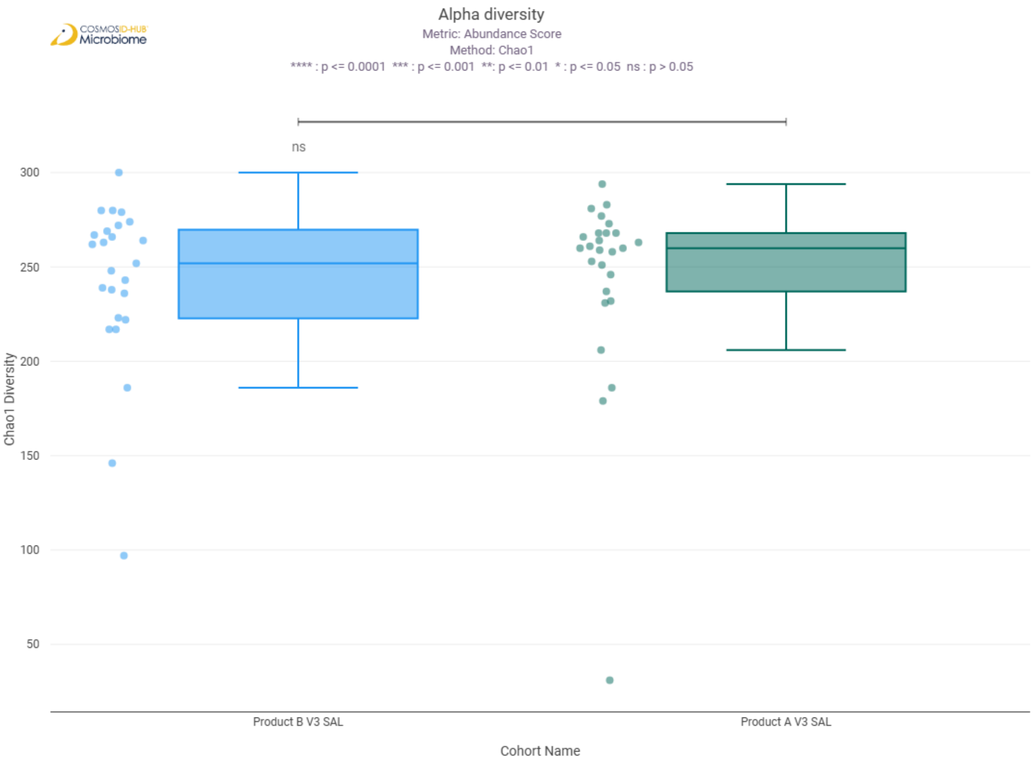
Differential Abundance (LEfSe) (EC)



Feature	Enriched Cohort	LDA Score	P-value
Bacterial non-heme ferritin	Product A V3 SAL	2.945043561	0.047879765
Biotin synthase	Product A V3 SAL	2.02663125	0.01946851

MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1	

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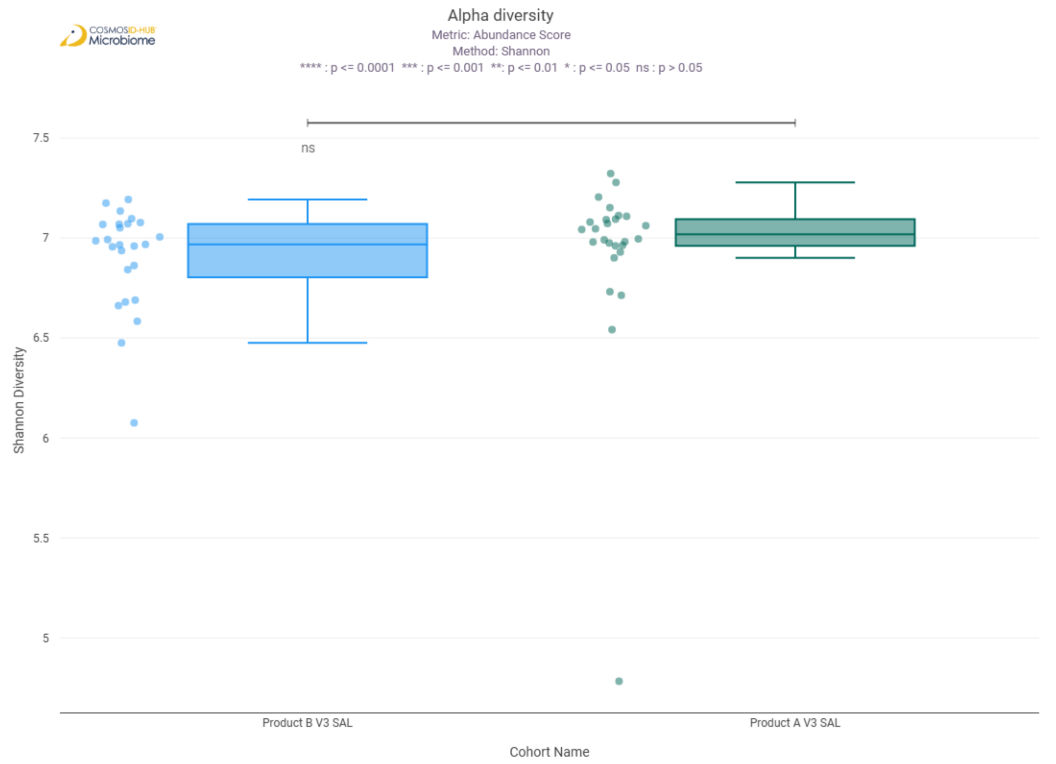
<tr><td>Shannon</td><td>
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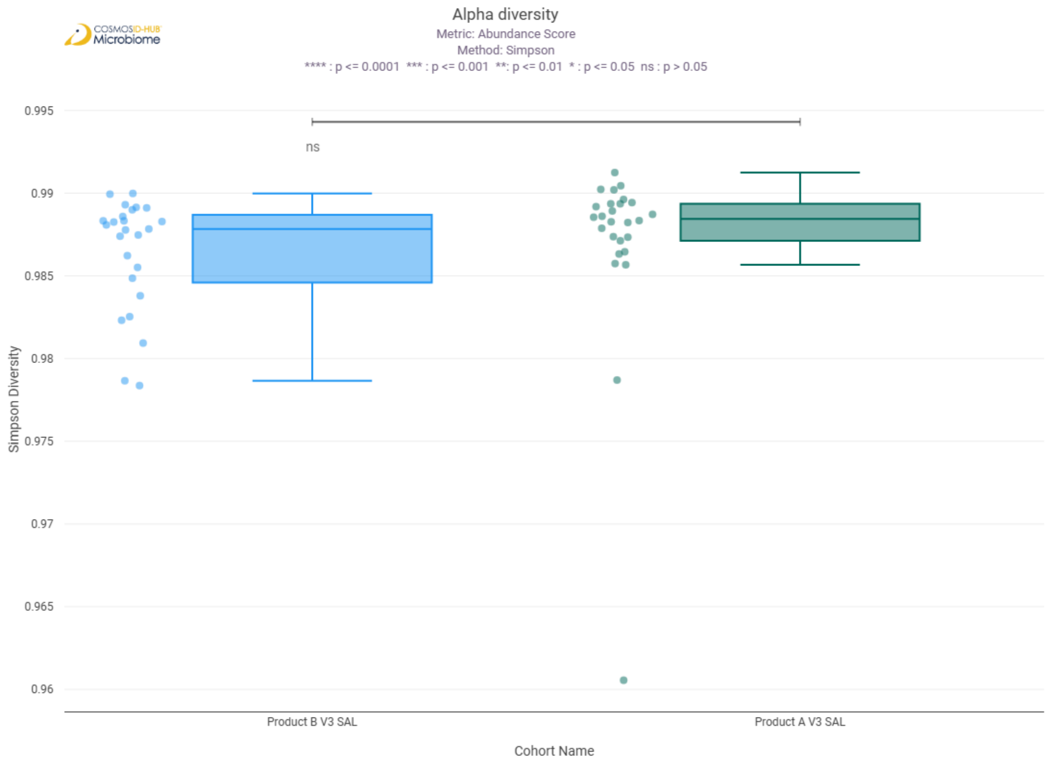
<tr><td>Simpson</td><td>
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Beta Diversity (MetaCyc)

Bray-Curtis

PERMNOVA
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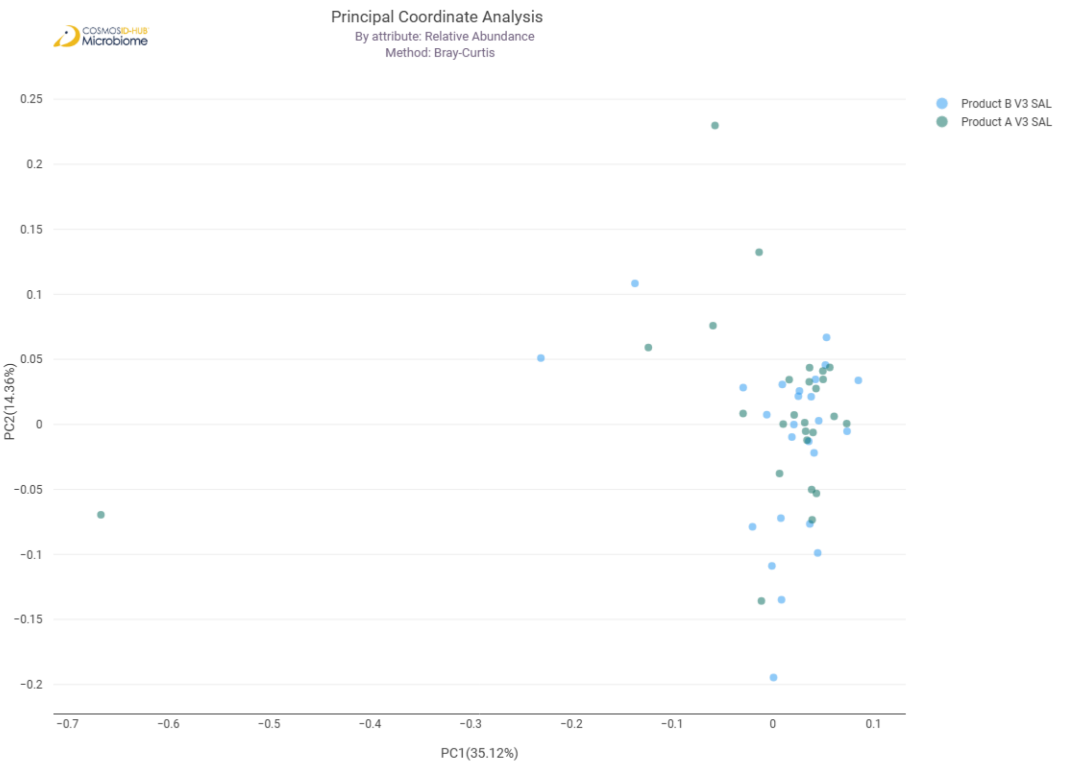
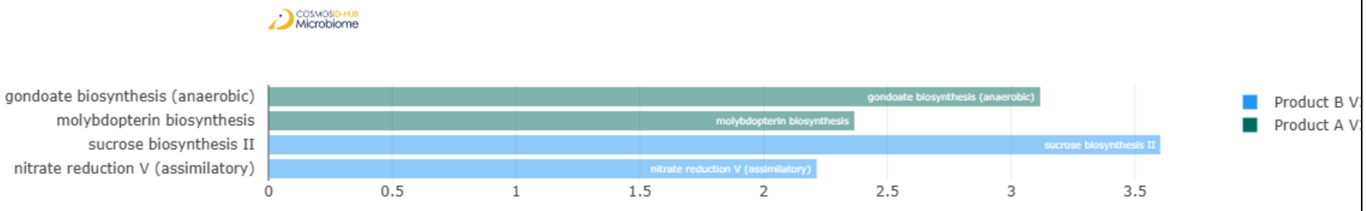


Differential Abundance (LEfSe) (MetaCyc)

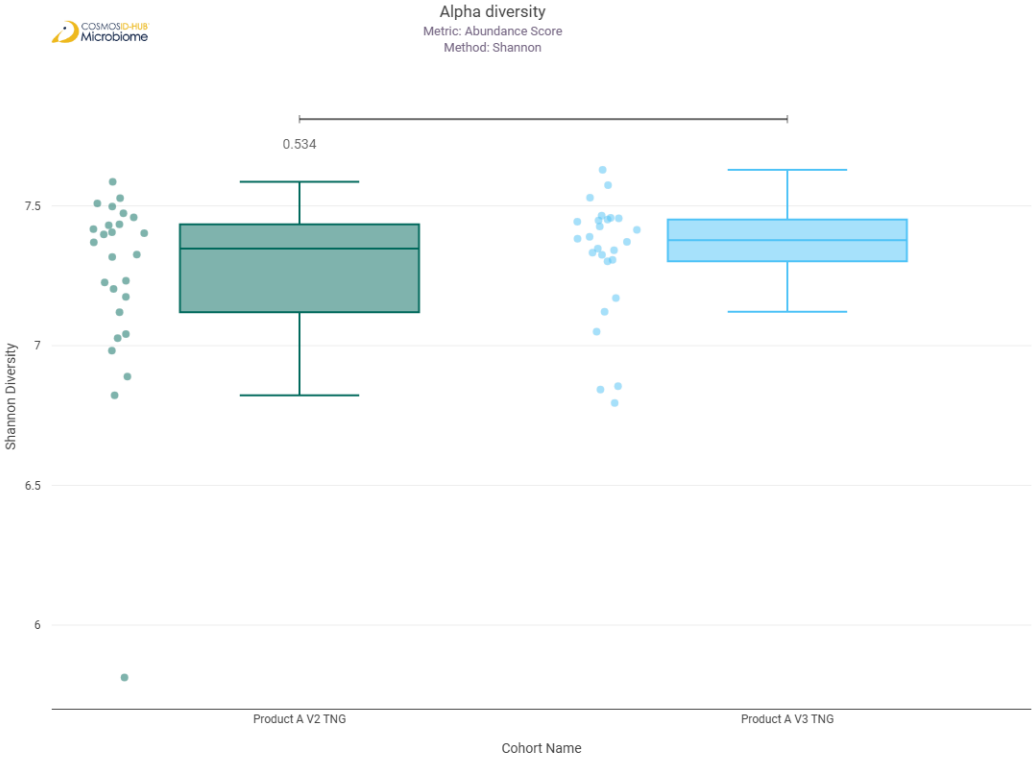


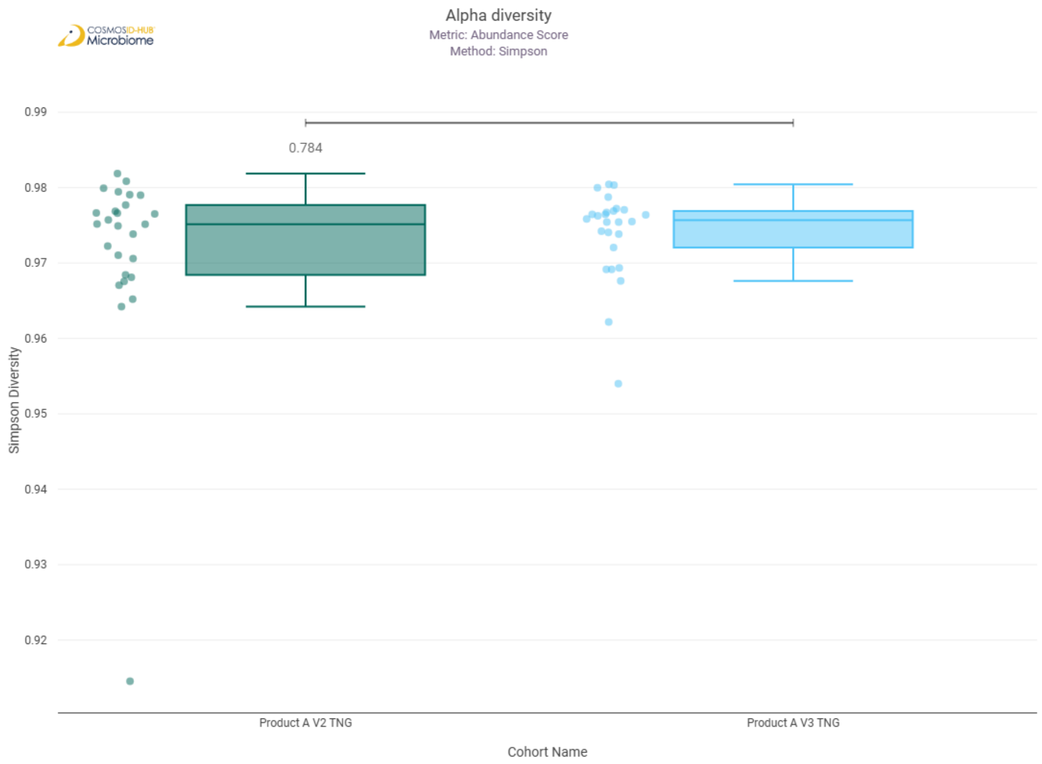
Feature	Enriched Cohort	LDA Score	P-value
gondoate biosynthesis (anaerobic)	Product A V3 SAL	3.117262564	0.047879765
molybdopterin biosynthesis	Product A V3 SAL	2.366346684	0.016703061
sucrose biosynthesis II	Product B V3 SAL	3.602180306	0.02494682
nitrate reduction V (assimilatory)	Product B V3 SAL	2.214455356	0.01756521

Comparison 9: Product A V2 TNG vs Product A V3 TNG

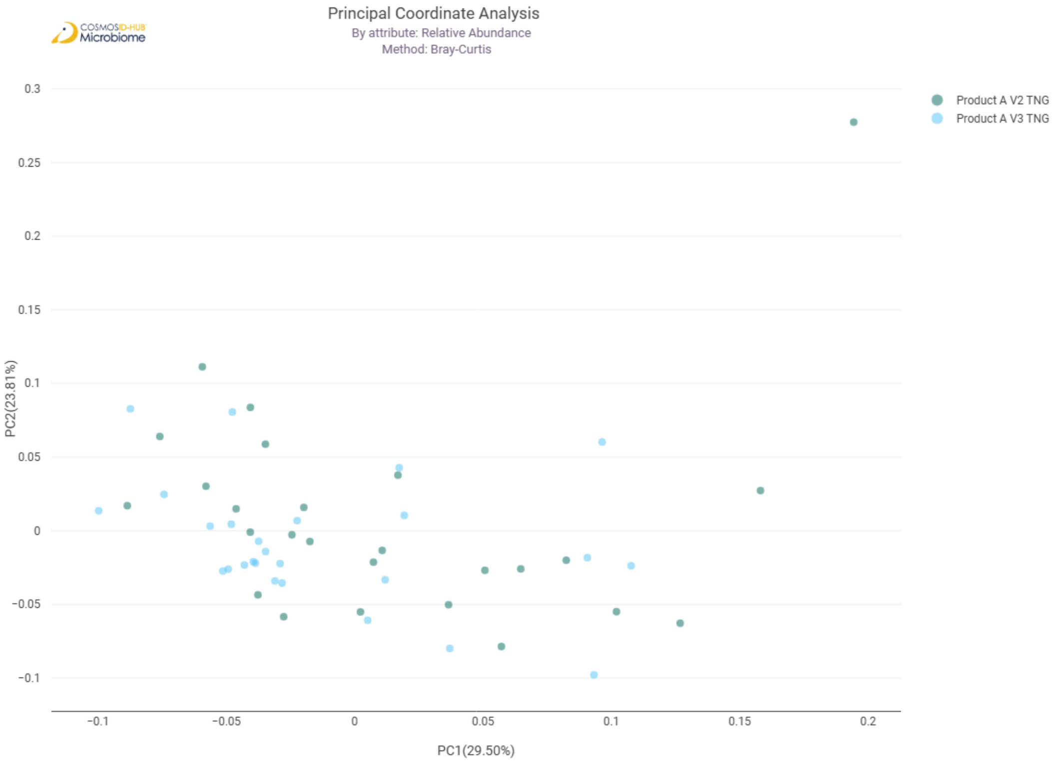
Gene Ontology

Alpha Diversity (GO)

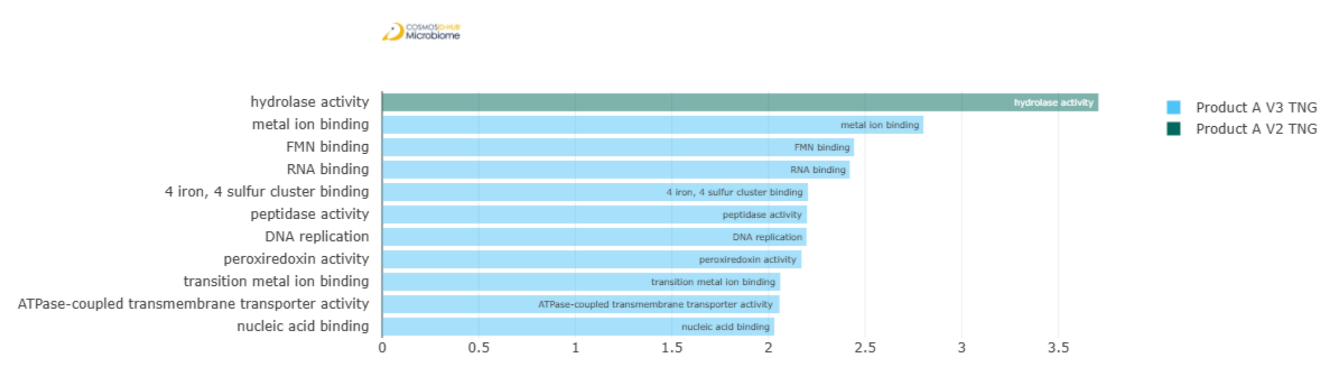
Chao1	
Shannon	

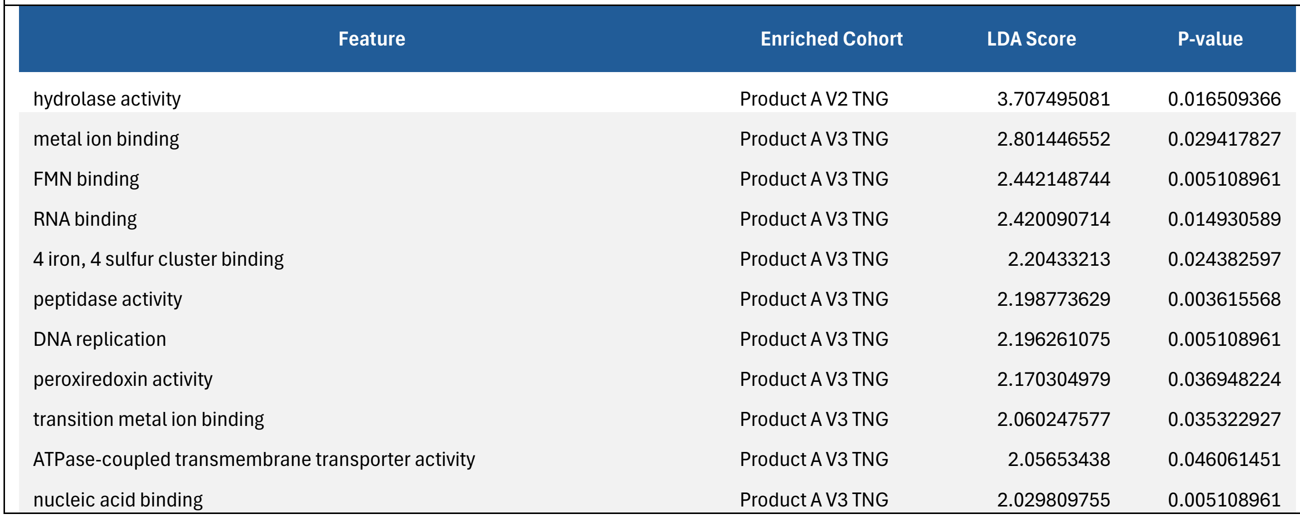
Simpson	

Beta Diversity (GO)

Bray-Curtis PERMNOVA p = 0.170	

Differential Abundance (LEfSe) (GO)

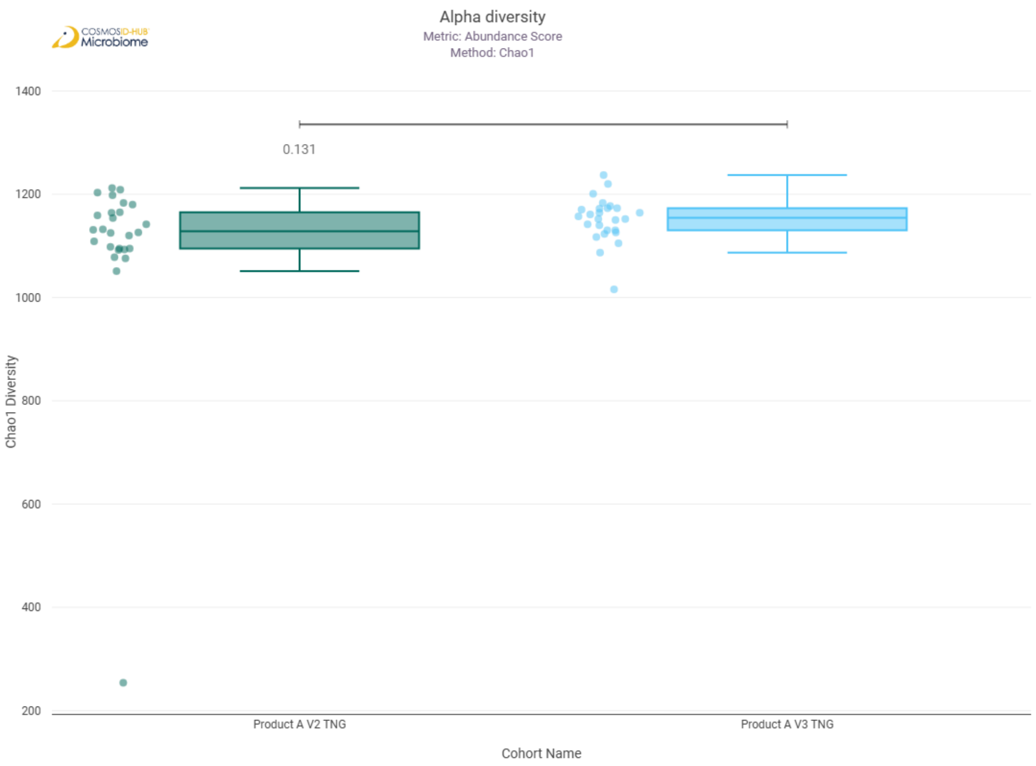
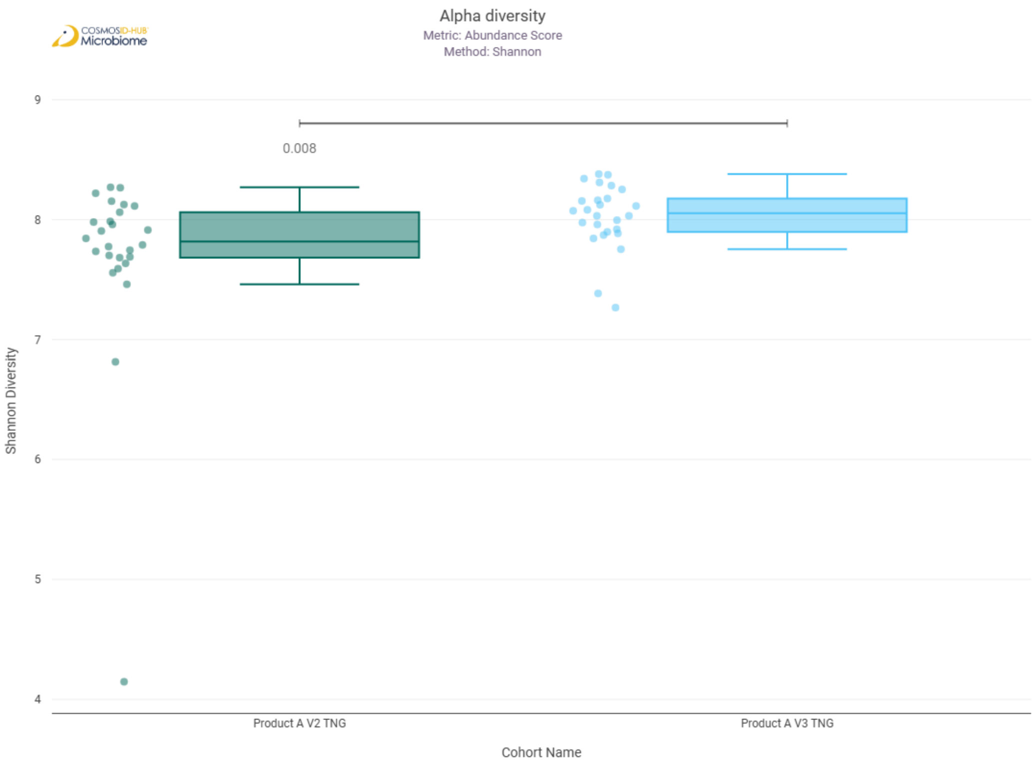


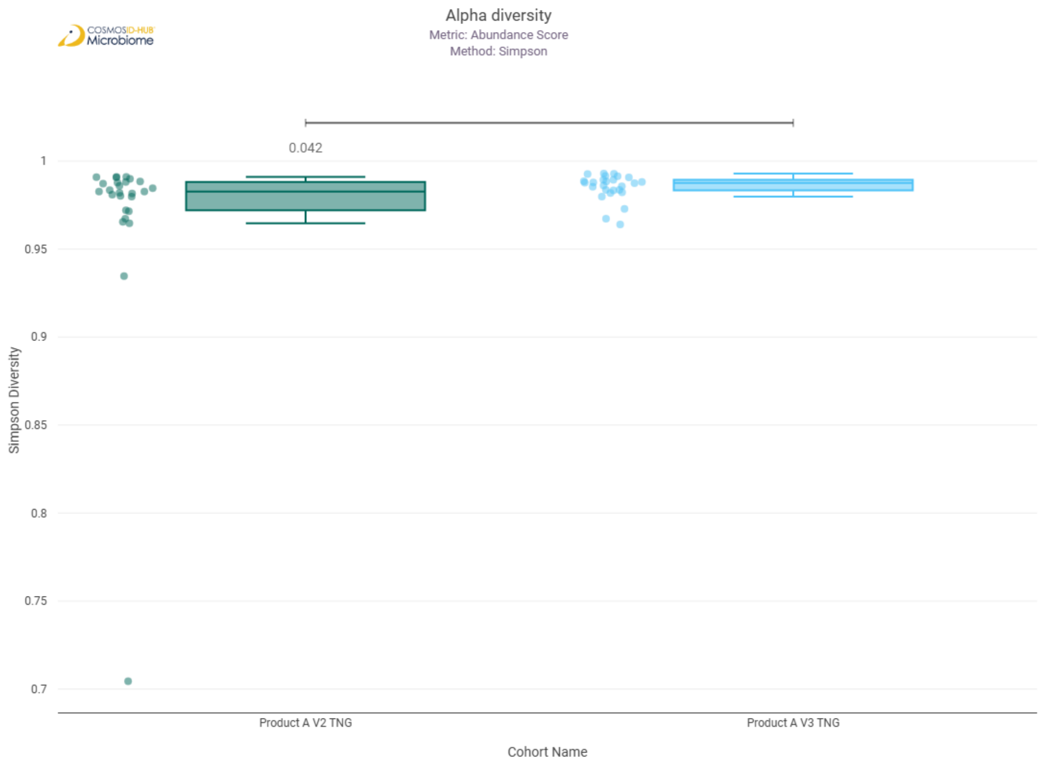


Feature	Enriched Cohort	LDA Score	P-value
hydrolase activity	Product A V2 TNG	3.707495081	0.016509366
metal ion binding	Product A V3 TNG	2.801446552	0.029417827
FMN binding	Product A V3 TNG	2.442148744	0.005108961
RNA binding	Product A V3 TNG	2.420090714	0.014930589
4 iron, 4 sulfur cluster binding	Product A V3 TNG	2.20433213	0.024382597
peptidase activity	Product A V3 TNG	2.198773629	0.003615568
DNA replication	Product A V3 TNG	2.196261075	0.005108961
peroxiredoxin activity	Product A V3 TNG	2.170304979	0.036948224
transition metal ion binding	Product A V3 TNG	2.060247577	0.035322927
ATPase-coupled transmembrane transporter activity	Product A V3 TNG	2.05653438	0.046061451
nucleic acid binding	Product A V3 TNG	2.029809755	0.005108961

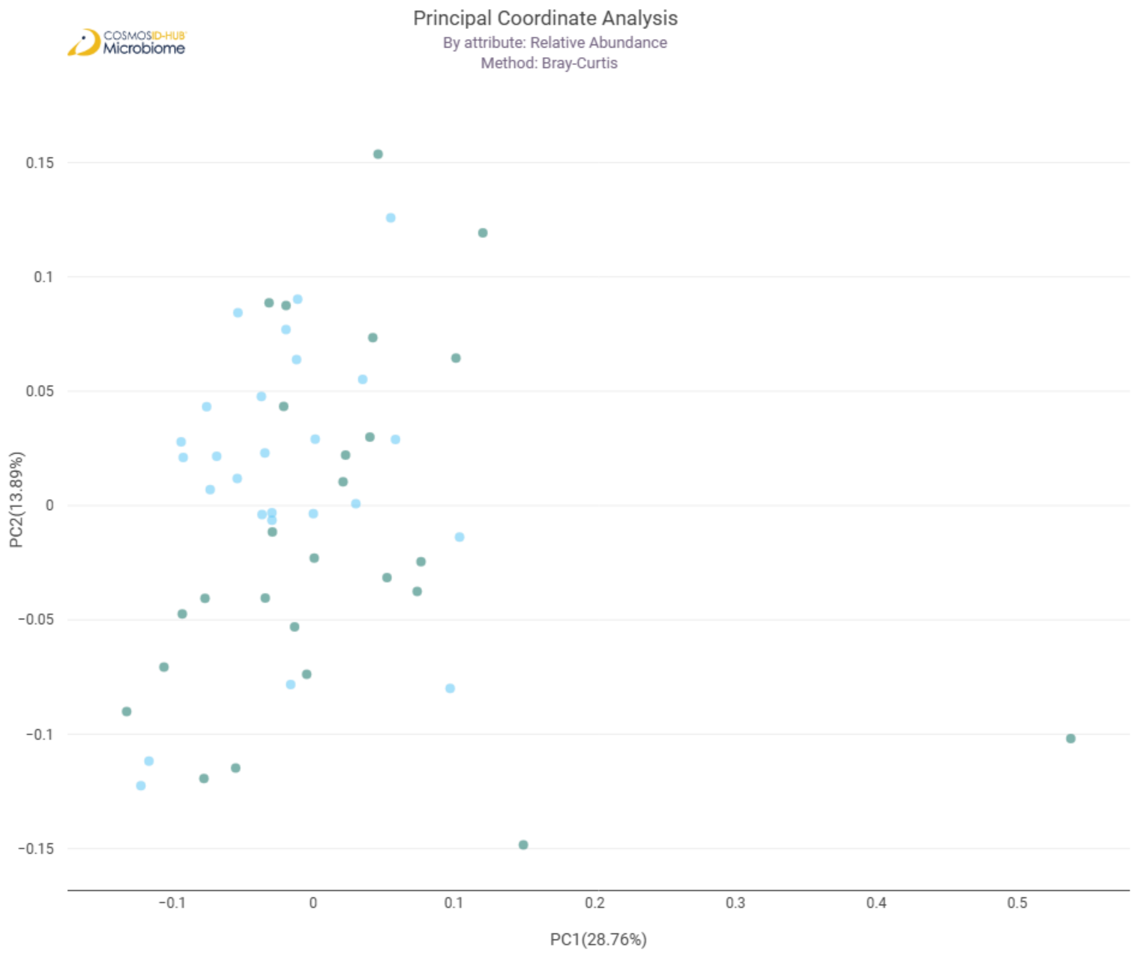
Enzyme Commission

Alpha Diversity (EC)

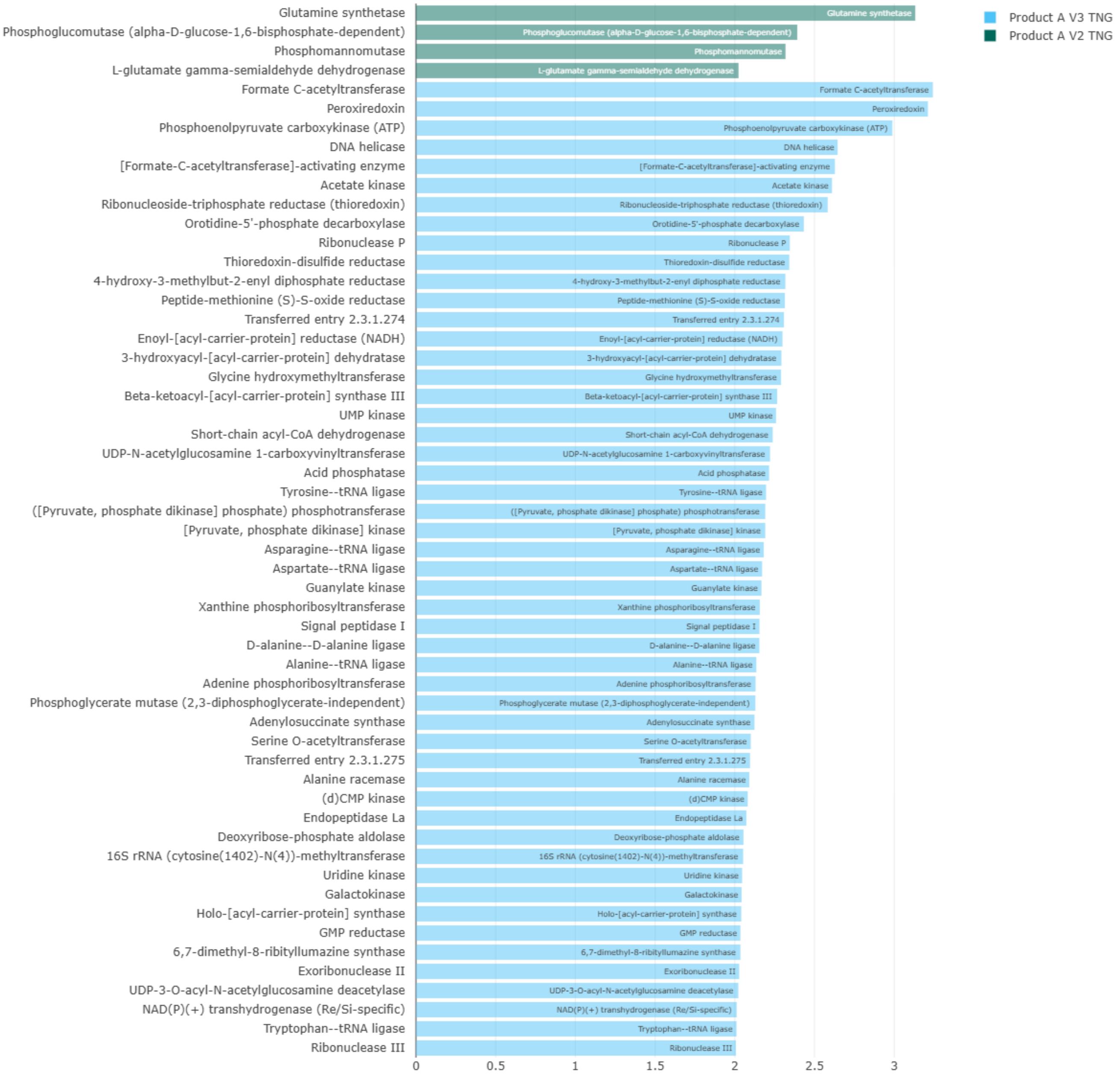
Chao1	
Shannon	

Simpson	COSMOSID-HUB Microbiome Alpha diversity Metric: Abundance Score Method: Simpson 0.042 1 0.95 0.9 0.85 0.8 0.75 0.7 Simpson Diversity Product A V2 TNG Product A V3 TNG Cohort Name

Beta Diversity (EC)

Bray-Curtis PERMNOVA p = 0.053	

Differential Abundance (LEfSe) (EC)



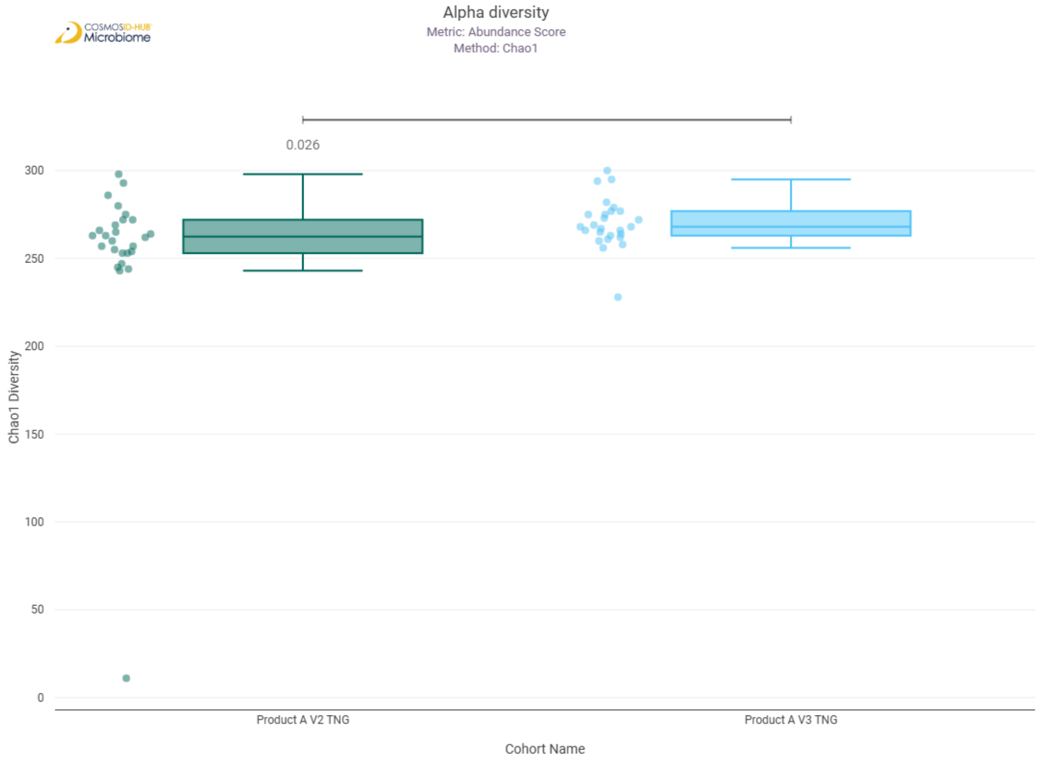
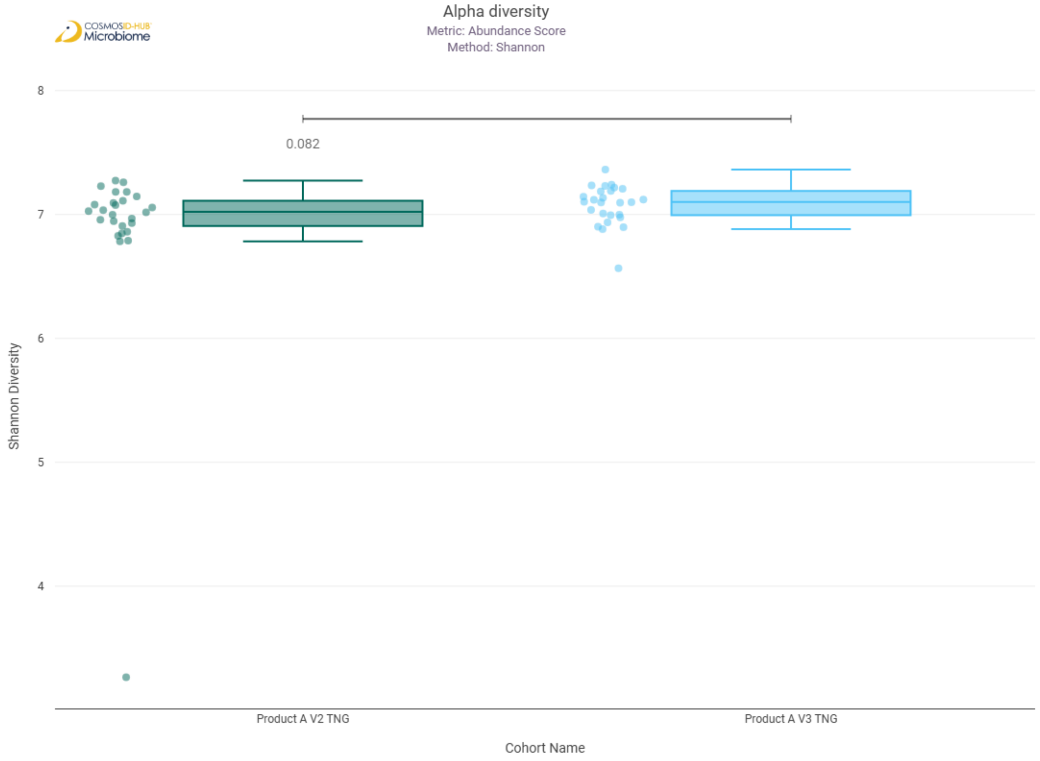
Feature	Enriched Cohort	LDA Score	P-value
Glutamine synthetase	Product A V2 TNG	3.131773587	0.019152346
Phosphoglucomutase (alpha-D-glucose-1,6-bisphosphate-dependent)	Product A V2 TNG	2.391780049	0.008404526
Phosphomannomutase	Product A V2 TNG	2.318057666	0.013486371
L-glutamate gamma-semialdehyde dehydrogenase	Product A V2 TNG	2.023541115	0.030808261
Formate C-acetyltransferase	Product A V3 TNG	3.242142189	0.02808172
Peroxiredoxin	Product A V3 TNG	3.210994816	0.036948224

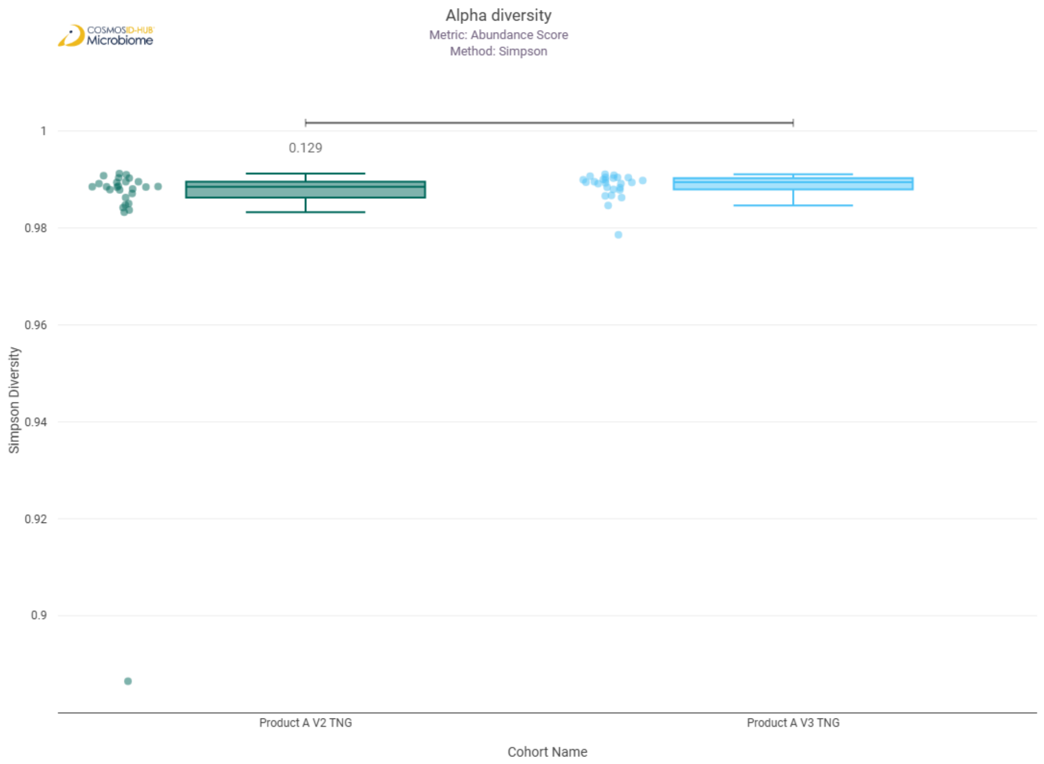
Phosphoenolpyruvate carboxykinase (ATP)	Product A V3 TNG	2.988111427	0.006393679
DNA helicase	Product A V3 TNG	2.644863609	0.004826615
[Formate-C-acetyltransferase]-activating enzyme	Product A V3 TNG	2.627544174	0.012167011
Acetate kinase	Product A V3 TNG	2.609351455	0.036948224
Ribonucleoside-triphosphate reductase (thioredoxin)	Product A V3 TNG	2.58250405	0.008404526
Orotidine-5'-phosphate decarboxylase	Product A V3 TNG	2.432550553	0.020112035
Ribonuclease P	Product A V3 TNG	2.344650231	0.006393679
Thioredoxin-disulfide reductase	Product A V3 TNG	2.341433821	0.029417827
4-hydroxy-3-methylbut-2-enyl diphosphate reductase	Product A V3 TNG	2.317067874	0.013486371
Peptide-methionine (S)-S-oxide reductase	Product A V3 TNG	2.313771424	0.015702531
Transferred entry 2.3.1.274	Product A V3 TNG	2.307913789	2.77761E-05
Enoyl-[acyl-carrier-protein] reductase (NADH)	Product A V3 TNG	2.299102917	0.024382597
3-hydroxyacyl-[acyl-carrier-protein] dehydratase	Product A V3 TNG	2.29215255	8.40E-03
Glycine hydroxymethyltransferase	Product A V3 TNG	2.289754924	0.020112035
Beta-ketoacyl-[acyl-carrier-protein] synthase III	Product A V3 TNG	2.265318101	0.038636777
UMP kinase	Product A V3 TNG	2.258348794	0.038636777
Short-chain acyl-CoA dehydrogenase	Product A V3 TNG	2.237427668	0.046061451
UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Product A V3 TNG	2.221010504	0.012811669
Acid phosphatase	Product A V3 TNG	2.214868777	0.003833001
Tyrosine--tRNA ligase	Product A V3 TNG	2.195780873	0.038636777
[Pyruvate, phosphate dikinase] kinase	Product A V3 TNG	2.190769448	0.048090171
([Pyruvate, phosphate dikinase] phosphate) phosphotransferase	Product A V3 TNG	2.190769448	0.048090171
Asparagine--tRNA ligase	Product A V3 TNG	2.18153077	0.013486371
Aspartate--tRNA ligase	Product A V3 TNG	2.171000903	0.00675726
Guanylate kinase	Product A V3 TNG	2.167070883	0.002853503
Xanthine phosphoribosyltransferase	Product A V3 TNG	2.156672978	0.036948224
Signal peptidase I	Product A V3 TNG	2.154503472	0.010402139
D-alanine--D-alanine ligase	Product A V3 TNG	2.154118252	0.002381558
Alanine--tRNA ligase	Product A V3 TNG	2.134582965	0.046061451
Adenine phosphoribosyltransferase	Product A V3 TNG	2.130121973	0.026798248
Phosphoglycerate mutase (2,3-diphosphoglycerate-independent)	Product A V3 TNG	2.128669083	1.92E-02
Adenylosuccinate synthase	Product A V3 TNG	2.122998977	0.022157981
Serine O-acetyltransferase	Product A V3 TNG	2.100032319	0.022157981
Transferred entry 2.3.1.275	Product A V3 TNG	2.09535326	0.003615568
Alanine racemase	Product A V3 TNG	2.090745674	0.03375904
(d)CMP kinase	Product A V3 TNG	2.080791026	0.014192278
Endopeptidase La	Product A V3 TNG	2.072431	0.015702531
Deoxyribose-phosphate aldolase	Product A V3 TNG	2.054306578	0.01096333
16S rRNA (cytosine(1402)-N(4))-methyltransferase	Product A V3 TNG	2.05217557	0.042211177
Uridine kinase	Product A V3 TNG	2.046121636	0.000865916
Galactokinase	Product A V3 TNG	2.042511013	0.02808172
Holo-[acyl-carrier-protein] synthase	Product A V3 TNG	2.040422943	0.036948224
GMP reductase	Product A V3 TNG	2.035067493	0.029417827
6,7-dimethyl-8-ribityllumazine synthase	Product A V3 TNG	2.035018511	0.038636777
Exoribonuclease II	Product A V3 TNG	2.027495812	0.023247195
UDP-3-O-acyl-N-acetylglucosamine deacetylase	Product A V3 TNG	2.022030905	0.008868809

NAD(P)(+) transhydrogenase (Re/Si-specific)	Product A V3 TNG	2.011575686	0.01096333
Tryptophan--tRNA ligase	Product A V3 TNG	2.010476434	0.016509366
Ribonuclease III	Product A V3 TNG	2.006528818	0.024382597

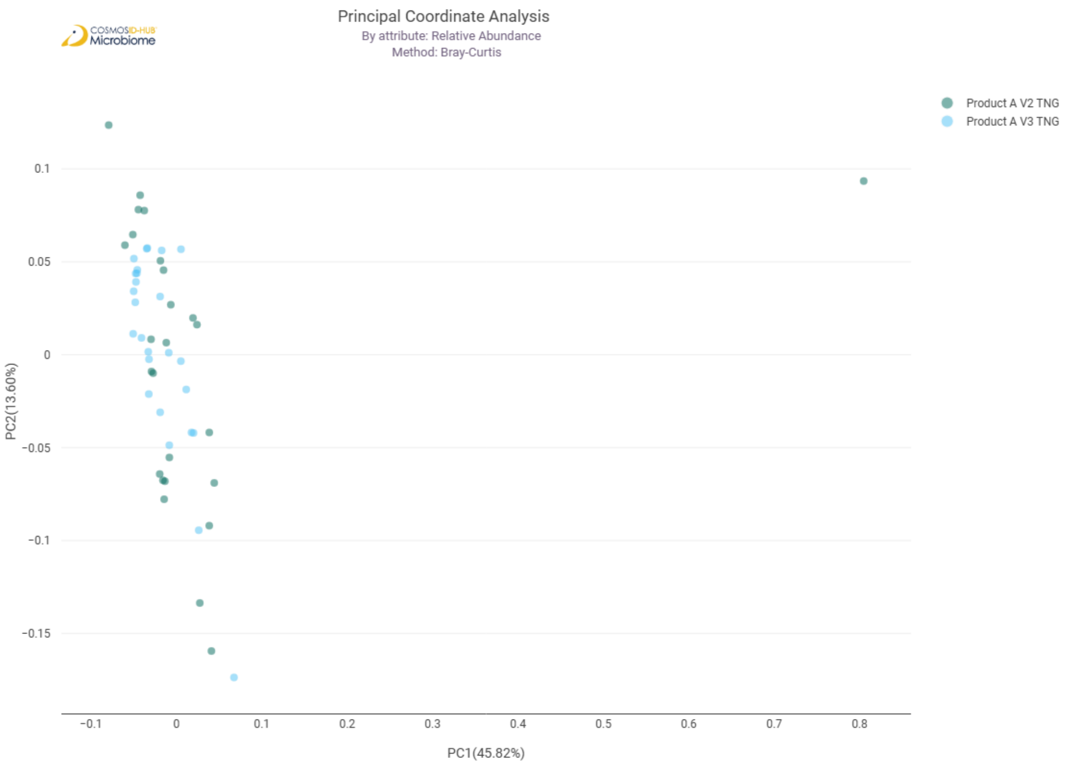
MetaCyc Pathways

Alpha Diversity (MetaCyc)

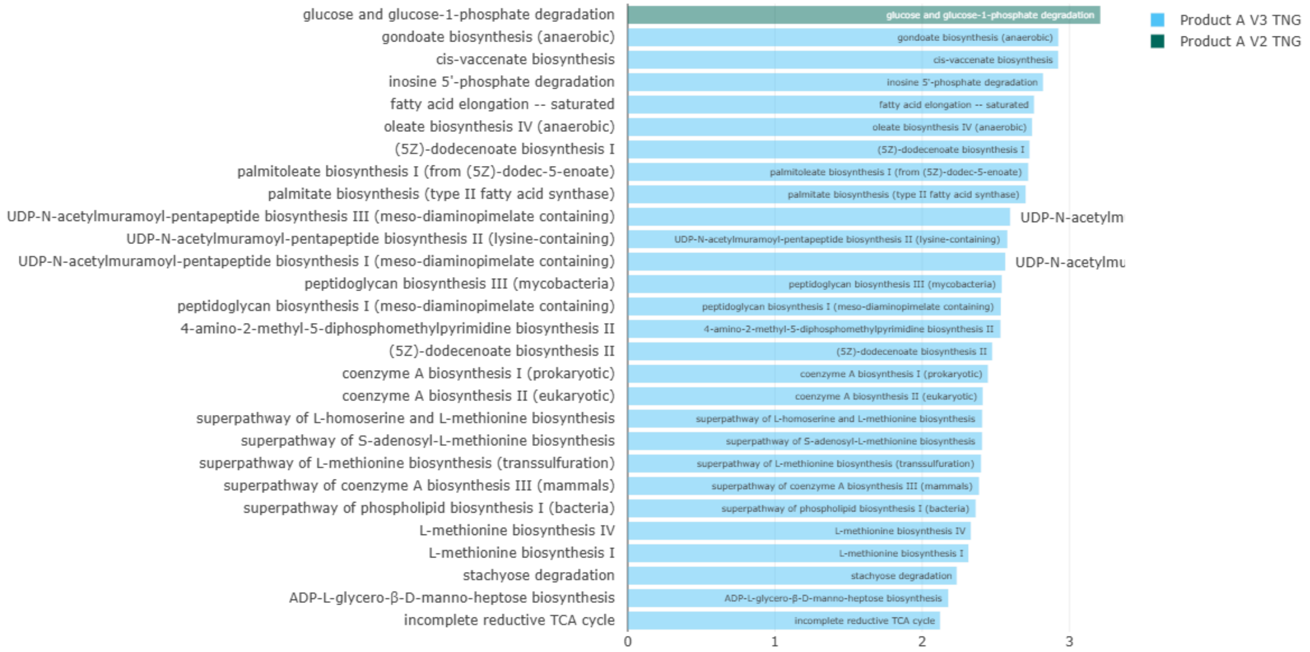
Chao1	
Shannon	

Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis PERMNOVA p = 0.164	

Differential Abundance (LEfSe) (MetaCyc)



Feature	Enriched Cohort	LDA Score	P-value
glucose and glucose-1-phosphate degradation	Product A V2 TNG	3.209559052	0.00340667
gondoate biosynthesis (anaerobic)	Product A V3 TNG	2.924765578	0.012811669
cis-vaccenate biosynthesis	Product A V3 TNG	2.923502255	0.024382597
inosine 5'-phosphate degradation	Product A V3 TNG	2.820503146	0.007962104
fatty acid elongation -- saturated	Product A V3 TNG	2.759343308	0.02808172
oleate biosynthesis IV (anaerobic)	Product A V3 TNG	2.746062827	0.022157981
(5Z)-dodecenoate biosynthesis I	Product A V3 TNG	2.728547812	0.024382597
palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate)	Product A V3 TNG	2.720034844	0.03375904
palmitate biosynthesis (type II fatty acid synthase)	Product A V3 TNG	2.702281934	0.032254747
UDP-N-acetylmuramoyl-pentapeptide biosynthesis III (meso-diaminopimelate containing)	Product A V3 TNG	2.597049045	0.008868809
UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)	Product A V3 TNG	2.578363977	0.02556575
UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)	Product A V3 TNG	2.563990058	0.019152346
peptidoglycan biosynthesis III (mycobacteria)	Product A V3 TNG	2.540069927	0.036948224
peptidoglycan biosynthesis I (meso-diaminopimelate containing)	Product A V3 TNG	2.533524177	0.026798248
4-amino-2-methyl-5-diphosphomethylpyrimidine biosynthesis II	Product A V3 TNG	2.531429766	0.003615568
(5Z)-dodecenoate biosynthesis II	Product A V3 TNG	2.475232712	0.030736851
coenzyme A biosynthesis I (prokaryotic)	Product A V3 TNG	2.446066864	0.02808172
coenzyme A biosynthesis II (eukaryotic)	Product A V3 TNG	2.410665002	0.00210785
superpathway of L-homoserine and L-methionine biosynthesis	Product A V3 TNG	2.407228434	3.08E-02
superpathway of S-adenosyl-L-methionine biosynthesis	Product A V3 TNG	2.406586807	0.014930589
superpathway of L-methionine biosynthesis (transsulfuration)	Product A V3 TNG	2.399360615	0.038636777

superpathway of coenzyme A biosynthesis III (mammals)	Product A V3 TNG	2.385903102	0.00406225
superpathway of phospholipid biosynthesis I (bacteria)	Product A V3 TNG	2.363206689	0.000664015
L-methionine biosynthesis IV	Product A V3 TNG	2.330041224	0.006393679
L-methionine biosynthesis I	Product A V3 TNG	2.313741316	0.029417827
stachyose degradation	Product A V3 TNG	2.234251147	0.044100855
ADP-L-glycero-β-D-manno-heptose biosynthesis	Product A V3 TNG	2.177105902	0.011551265
incomplete reductive TCA cycle	Product A V3 TNG	2.121158237	0.012466883

Comparison 10: Product B V2 TNG vs Product B V3 TNG

Gene Ontology

Alpha Diversity (GO)

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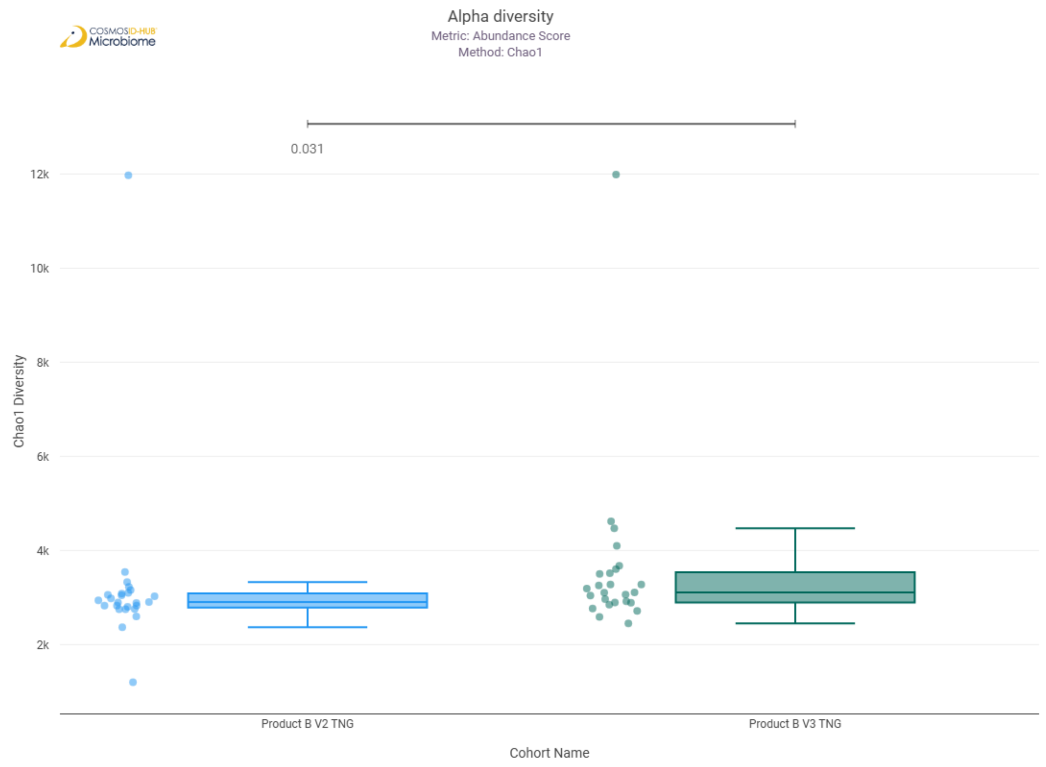
<tr><td>Chao1</td><td>
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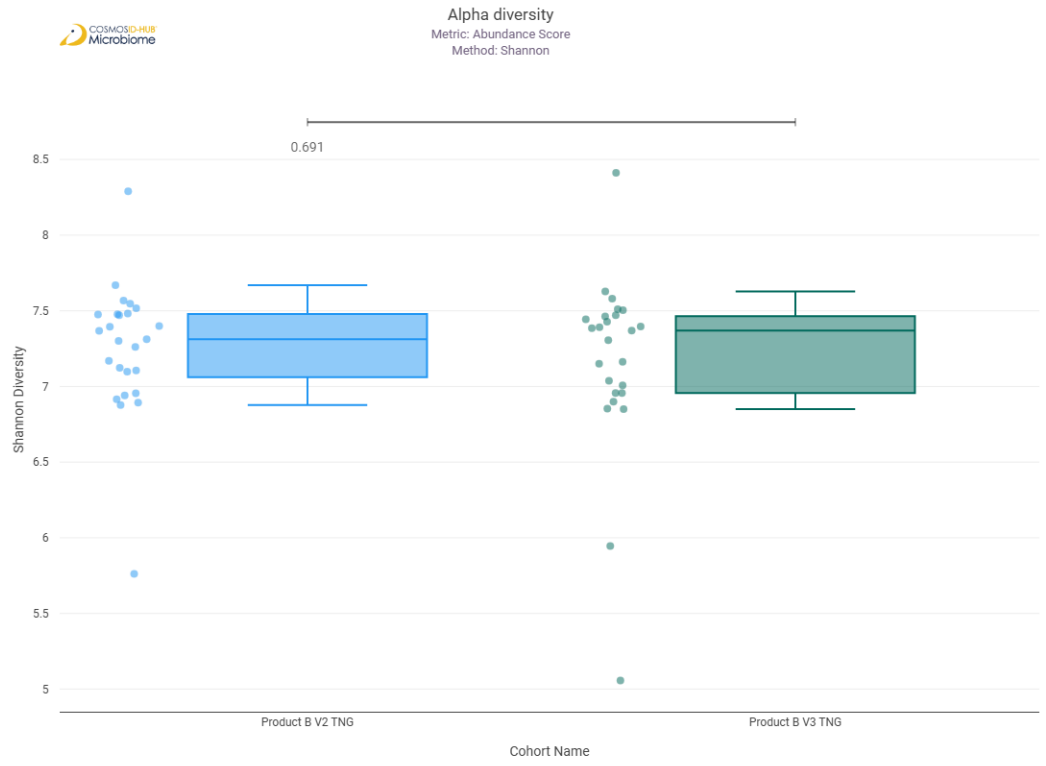
<tr><td>Shannon</td><td>
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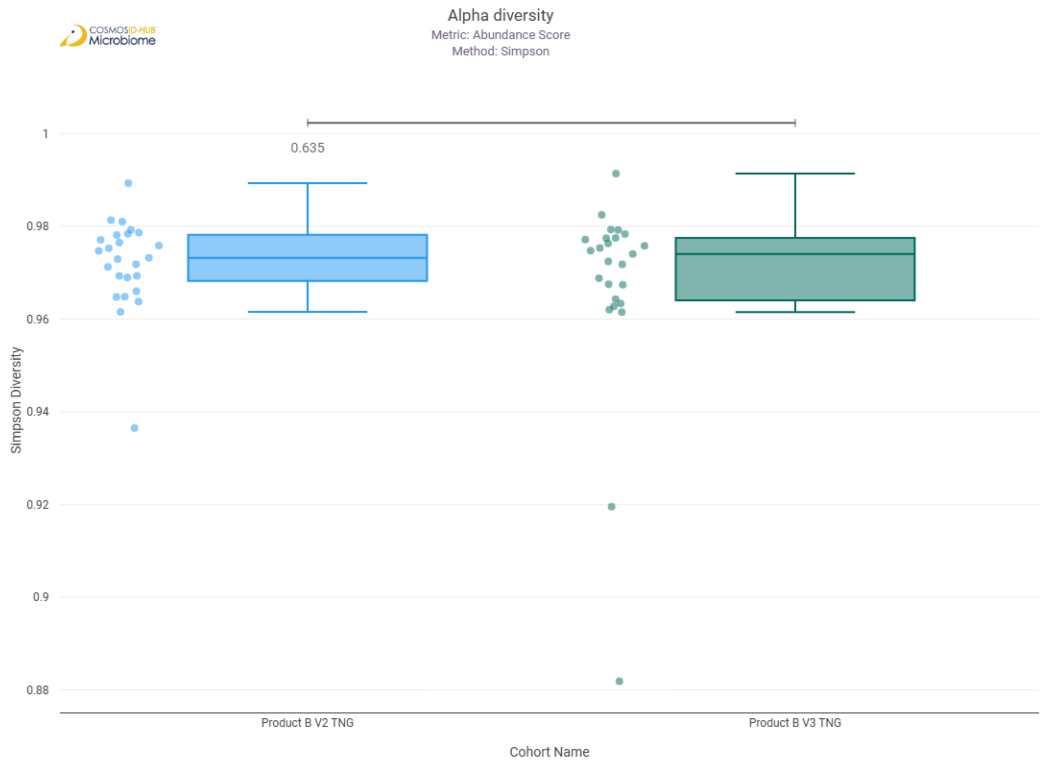
Simpson



Beta Diversity (GO)

Bray-Curtis

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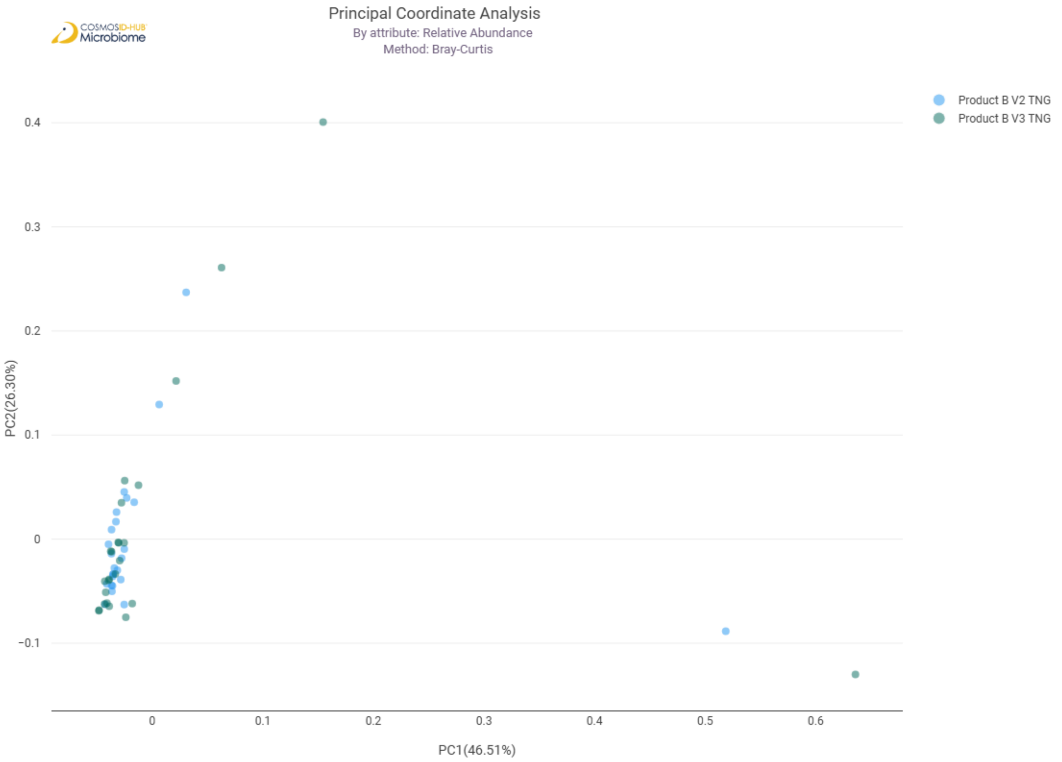
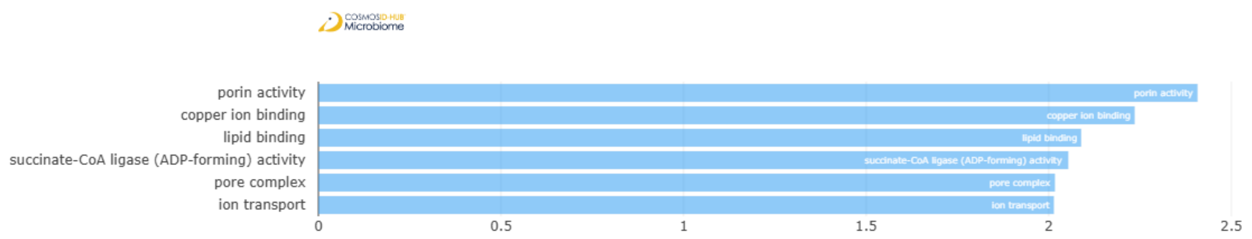


Differential Abundance (LEfSe) (GO)

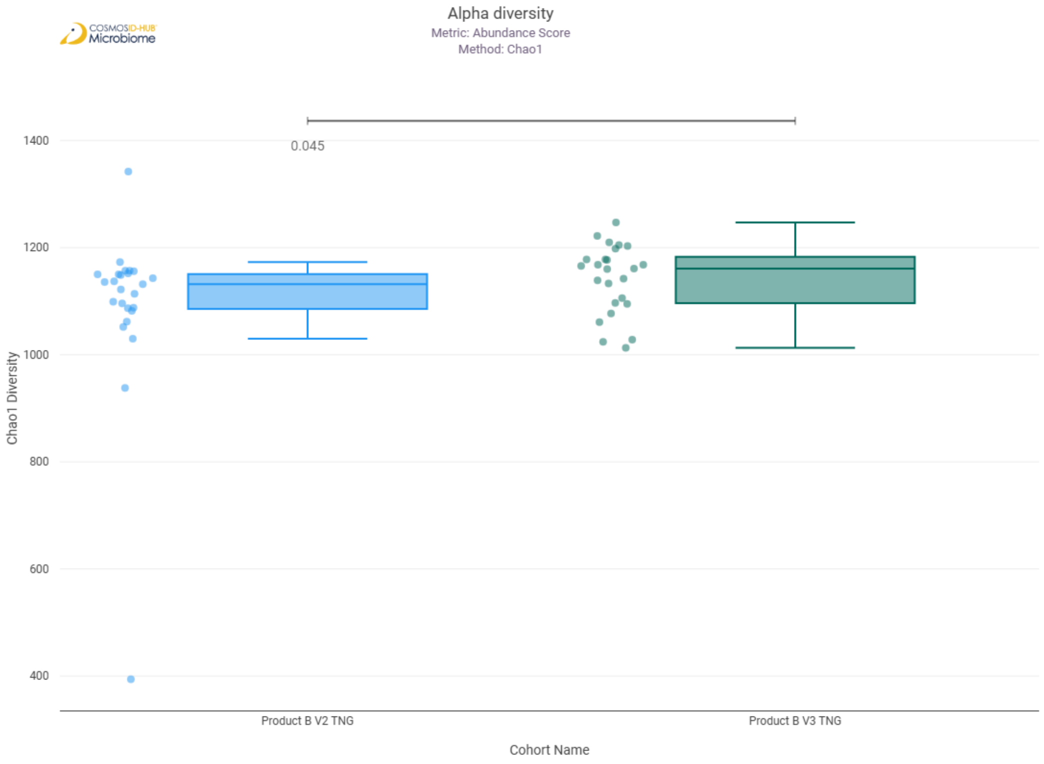


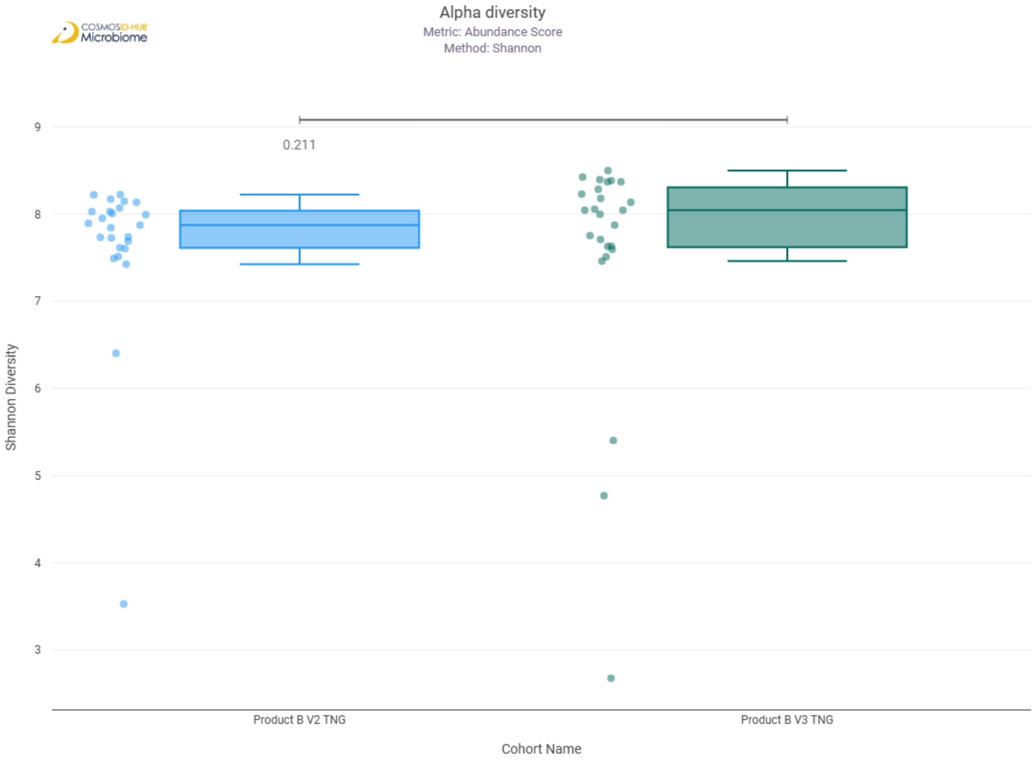
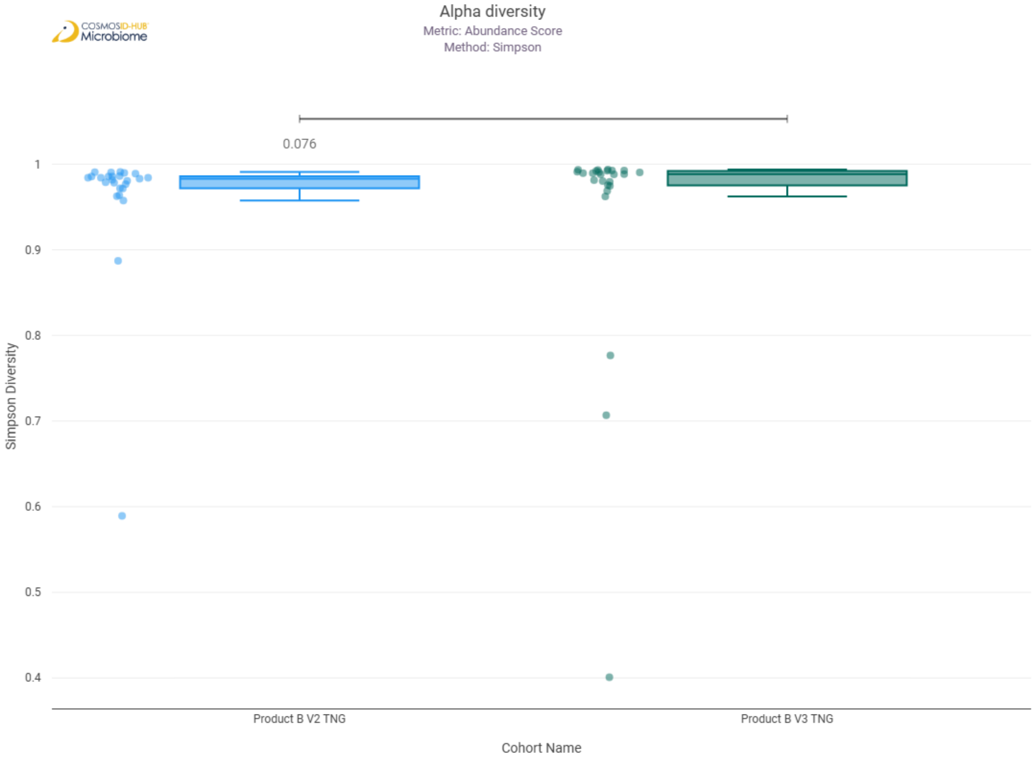
Feature	Enriched Cohort	LDA Score	P-value
porin activity	Product B V2 TNG	2.40751192	0.019384996
copper ion binding	Product B V2 TNG	2.2353981	0.010726809
lipid binding	Product B V2 TNG	2.088755697	0.021491444
succinate-CoA ligase (ADP-forming) activity	Product B V2 TNG	2.053577679	0.046724152
pore complex	Product B V2 TNG	2.016987317	0.008561466
ion transport	Product B V2 TNG	2.014120892	0.007632882

Enzyme Commission

Alpha Diversity (EC)

Chao1



Shannon	
Simpson	

Beta Diversity (EC)

Bray-Curtis

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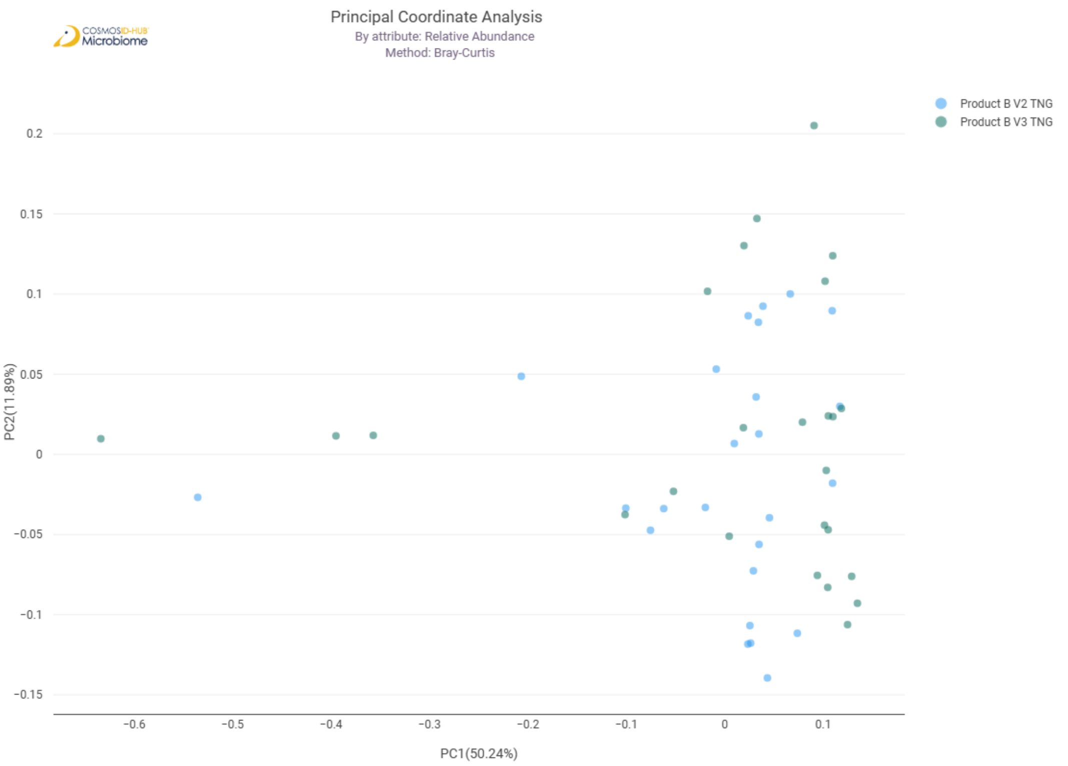
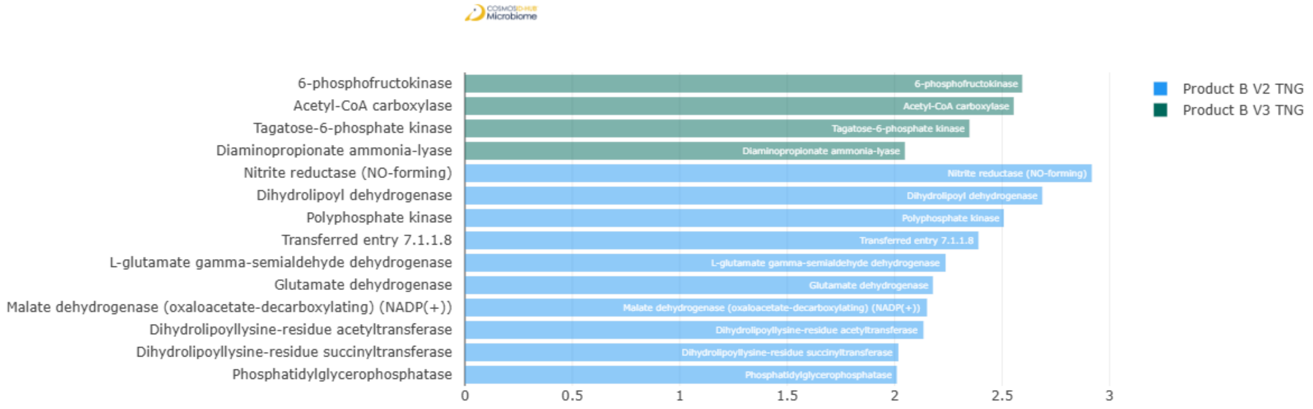


Differential Abundance (LEfSe) (EC)

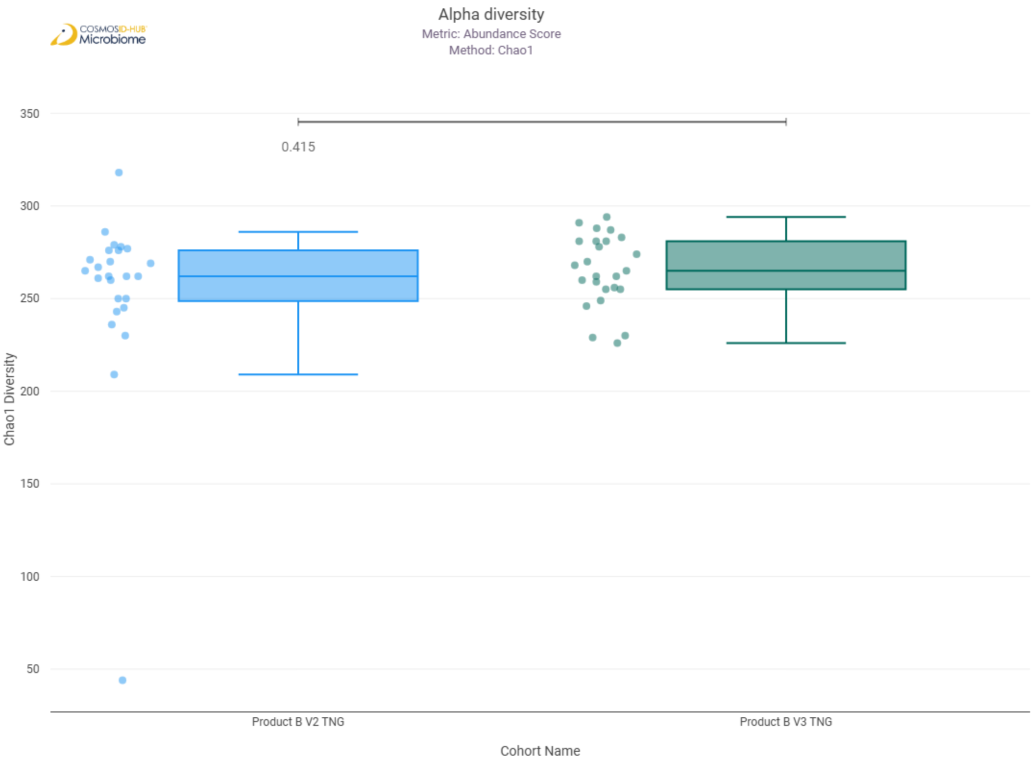


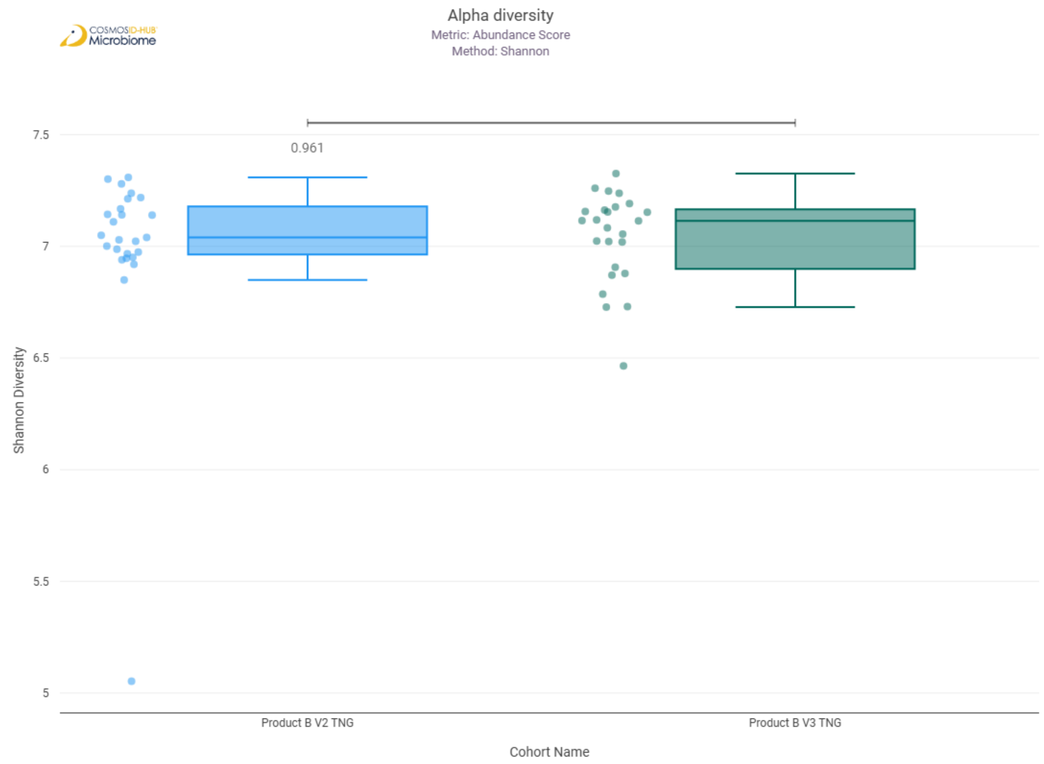
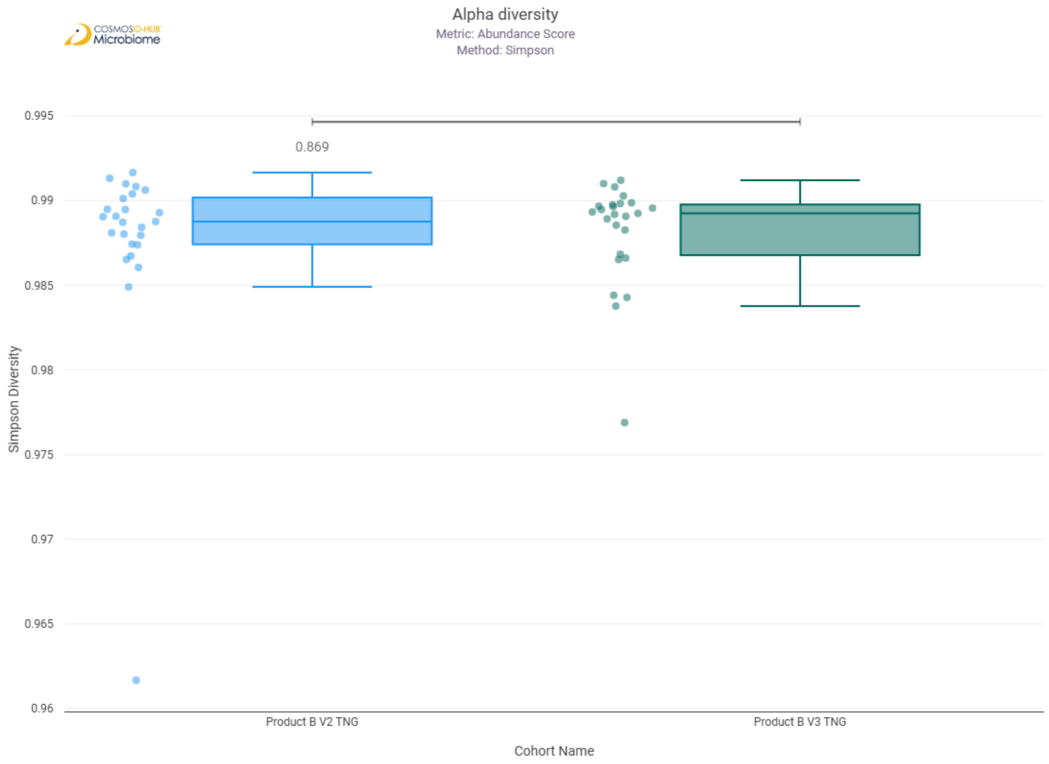
Feature	Enriched Cohort	LDA Score	P-value
6-phosphofructokinase	Product B V3 TNG	2.593878204	0.046724152
Acetyl-CoA carboxylase	Product B V3 TNG	2.554255826	0.023794451
Tagatose-6-phosphate kinase	Product B V3 TNG	2.348108235	0.048908406
Diaminopropionate ammonia-lyase	Product B V3 TNG	2.047738576	0.0250207
Nitrite reductase (NO-forming)	Product B V2 TNG	2.917501423	0.011973973
Dihydrolipoyl dehydrogenase	Product B V2 TNG	2.687051774	0.044622577

Polyphosphate kinase	Product B V2 TNG	2.50802902	0.019384996
Transferred entry 7.1.1.8	Product B V2 TNG	2.390039535	0.0352731
L-glutamate gamma-semialdehyde dehydrogenase	Product B V2 TNG	2.237146802	0.0352731
Glutamate dehydrogenase	Product B V2 TNG	2.178088537	0.016563699
Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP(+))	Product B V2 TNG	2.150718273	0.044622577
Dihydrolipoyllysine-residue acetyltransferase	Product B V2 TNG	2.134159792	0.010726809
Dihydrolipoyllysine-residue succinyltransferase	Product B V2 TNG	2.017575362	0.019384996
Phosphatidylglycerophosphatase	Product B V2 TNG	2.010237144	0.001321949

MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1	

Shannon	
Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis

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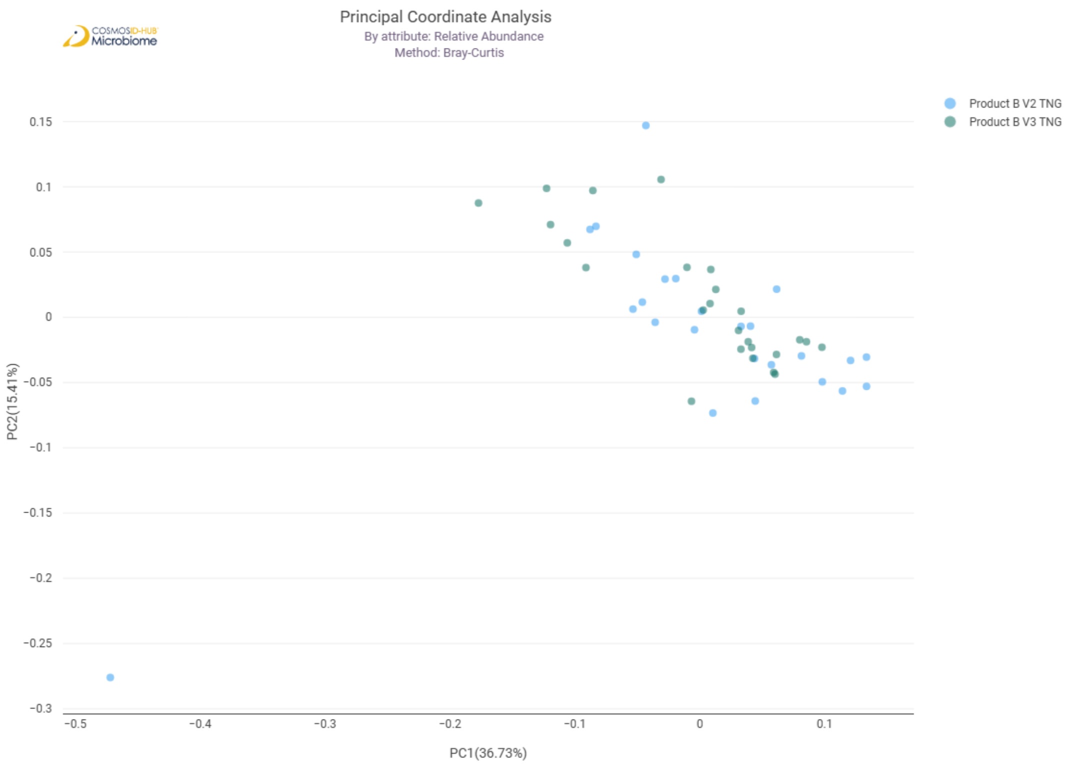
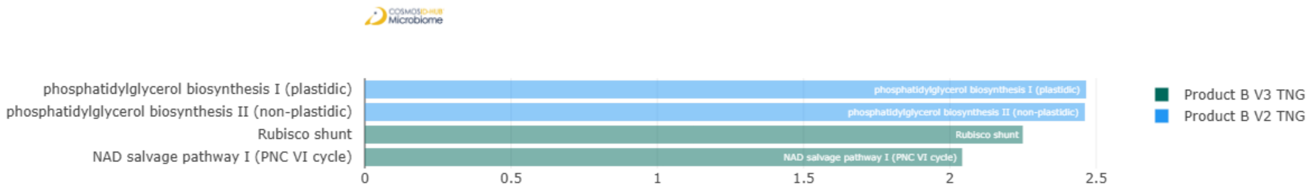


Differential Abundance (LEfSe) (MetaCyc)

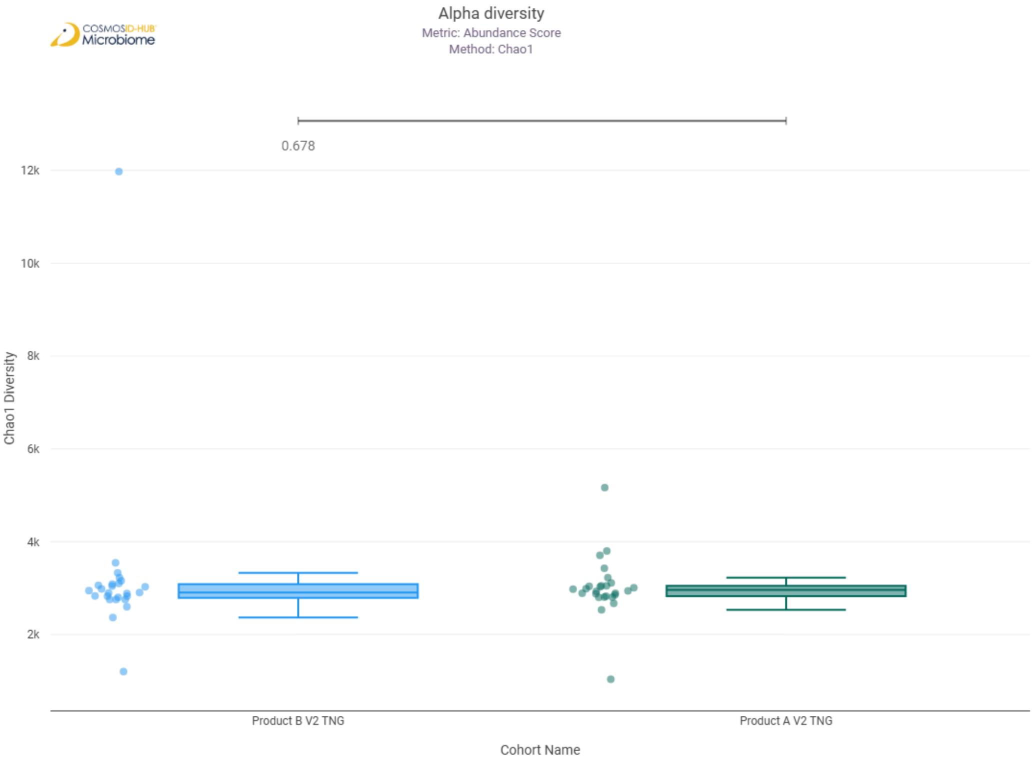
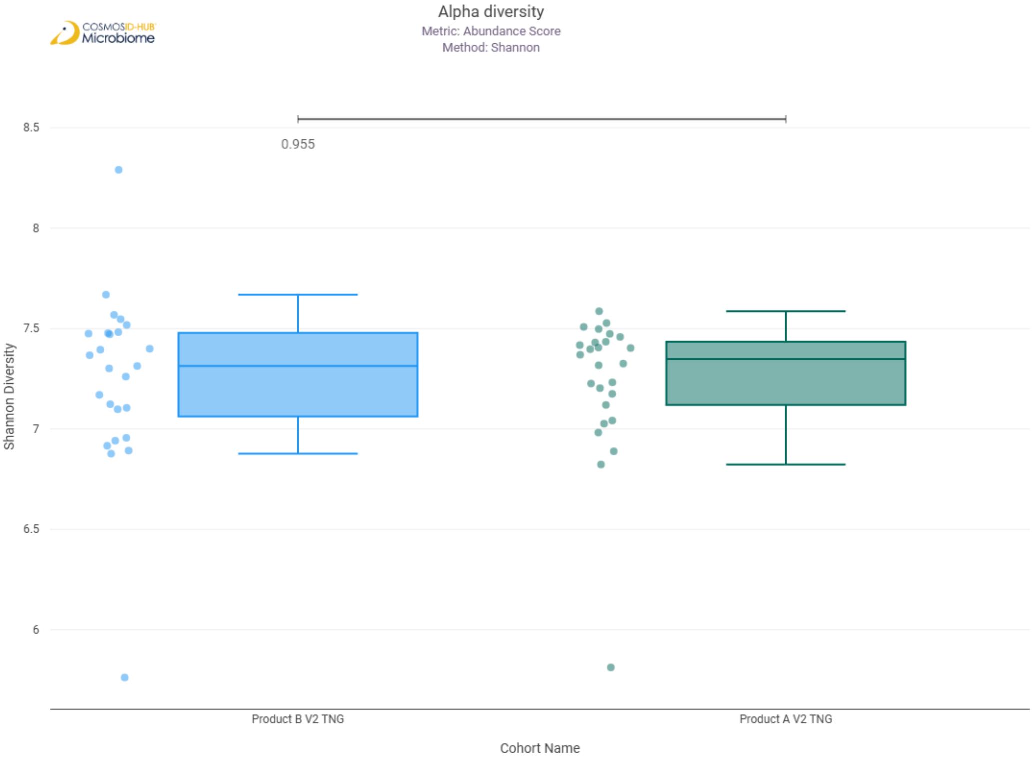


Feature	Enriched Cohort	LDA Score	P-value
phosphatidylglycerol biosynthesis I (plastidic)	Product B V2 TNG	2.46589043	0.022617484
phosphatidylglycerol biosynthesis II (non-plastidic)	Product B V2 TNG	2.461496298	0.022617484
Rubisco shunt	Product B V3 TNG	2.249336154	0.038590299
NAD salvage pathway I (PNC VI cycle)	Product B V3 TNG	2.04217463	0.042581422

Comparison 11: Product A V2 TNG vs Product B V2 TNG

Gene Ontology

Alpha Diversity (GO)

Chao1	
Shannon	

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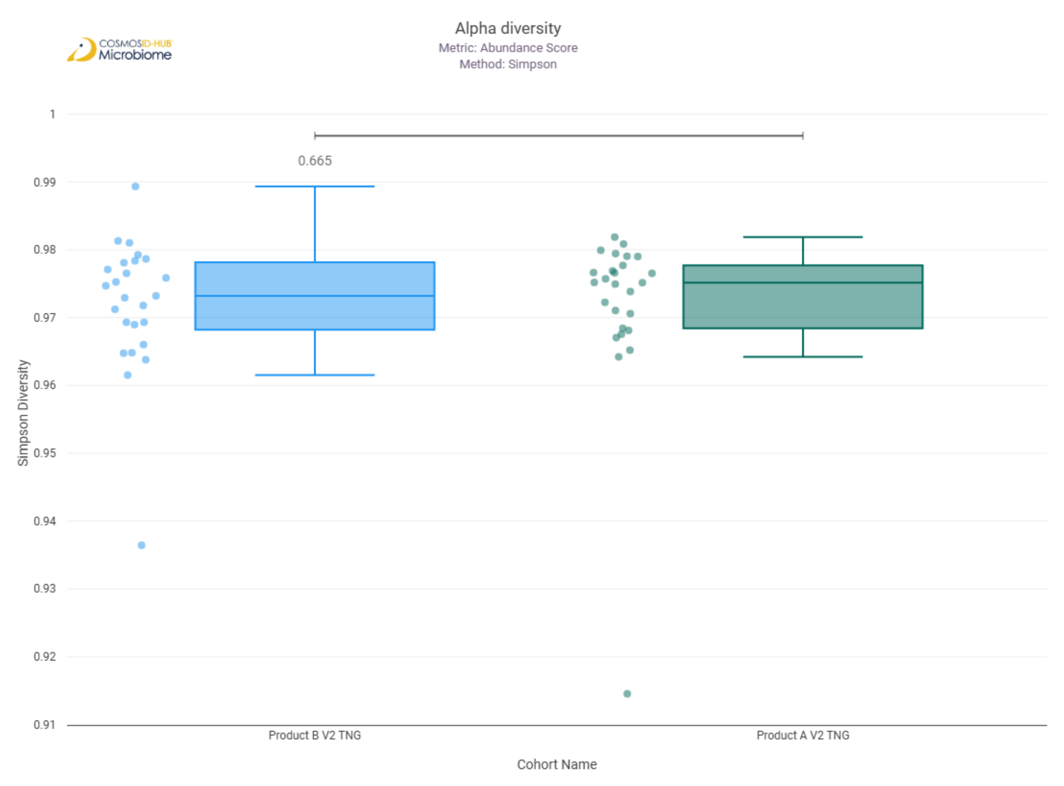

Beta Diversity (GO)

Bray-Curtis

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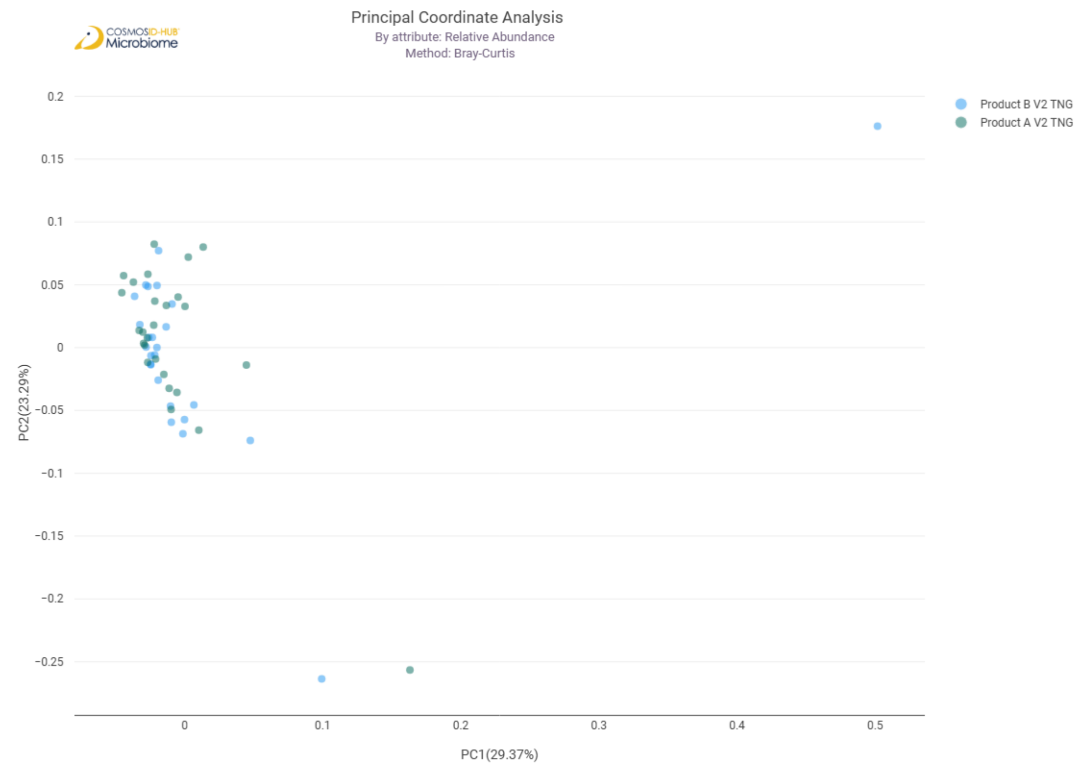
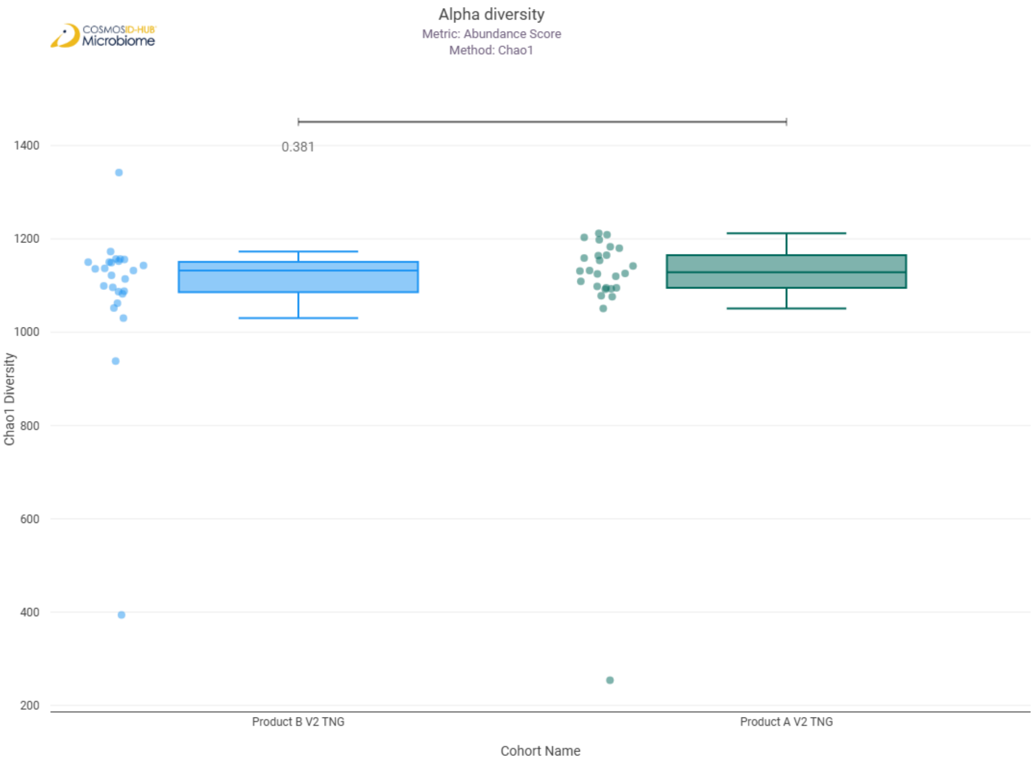


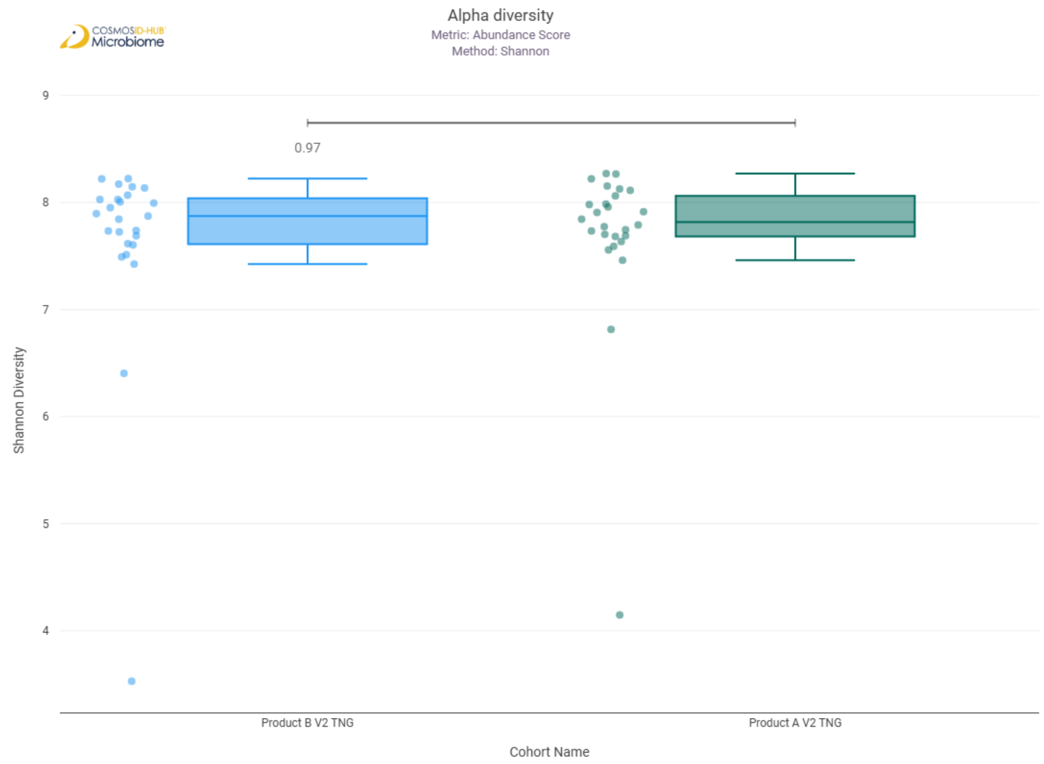
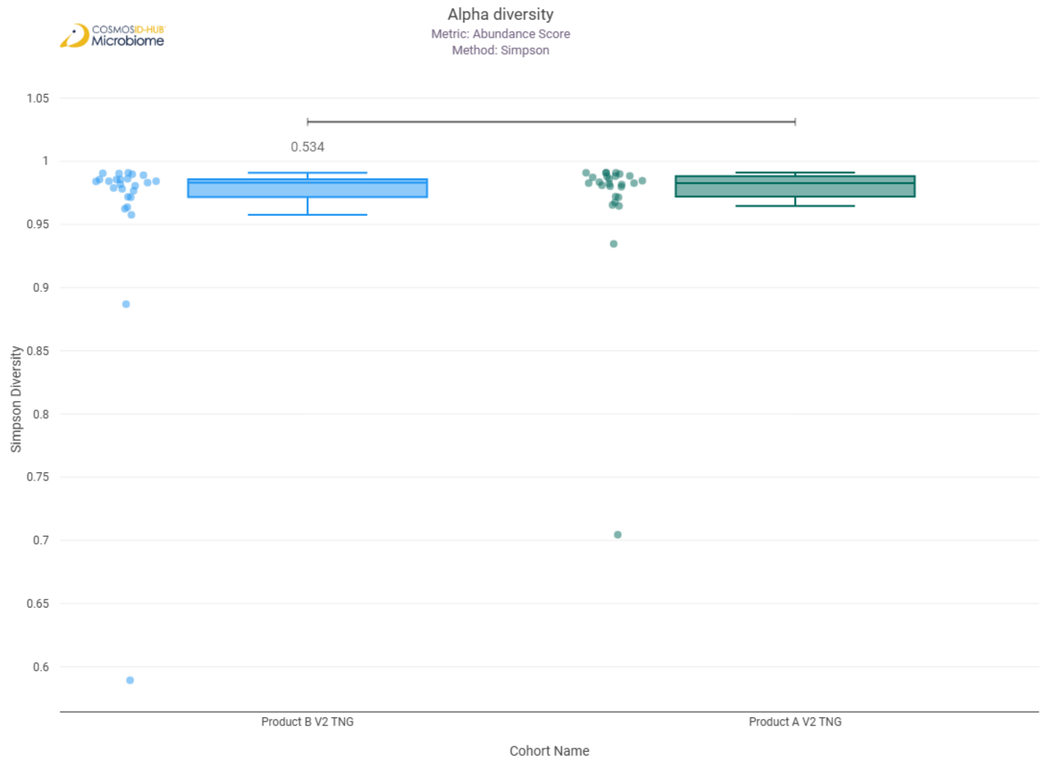
Differential Abundance (LEfSe) (GO)

Feature	Enriched Cohort	LDA Score	P-value
cytolysis	Product A V2 TNG	3.06689764	0.015071869
ATPase activity	Product A V2 TNG	2.355539921	0.031712637
regulation of transcription, DNA-templated	Product A V2 TNG	2.222731989	0.027486336

Enzyme Commission

Alpha Diversity (EC)

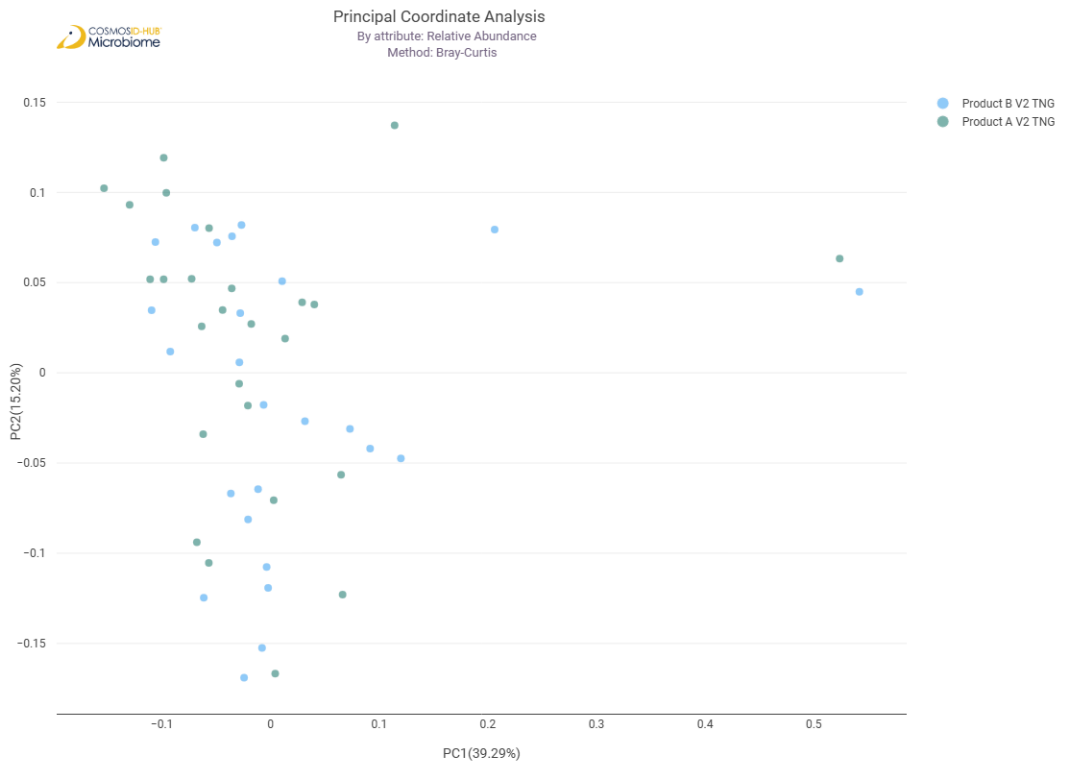
Chao1	

Shannon	
Simpson	

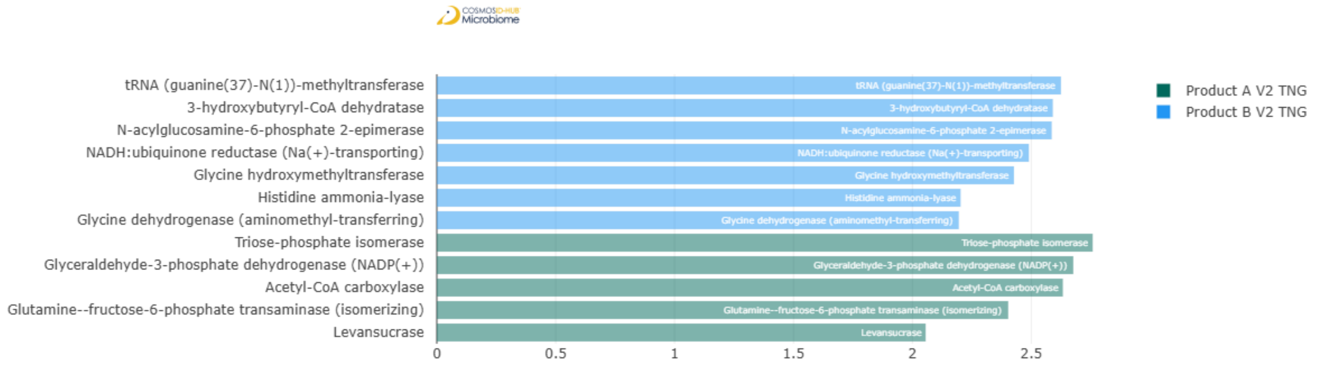
Beta Diversity (EC)

Bray-Curtis

PERMNOVA
p = 0.494



Differential Abundance (LEfSe) (EC)

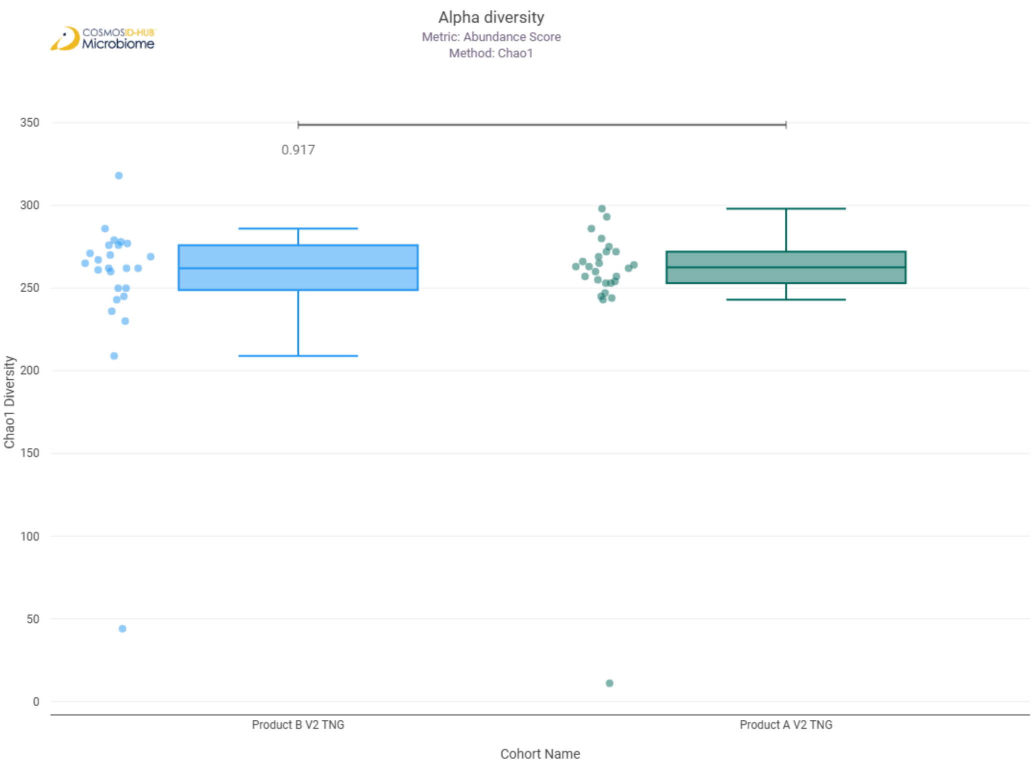
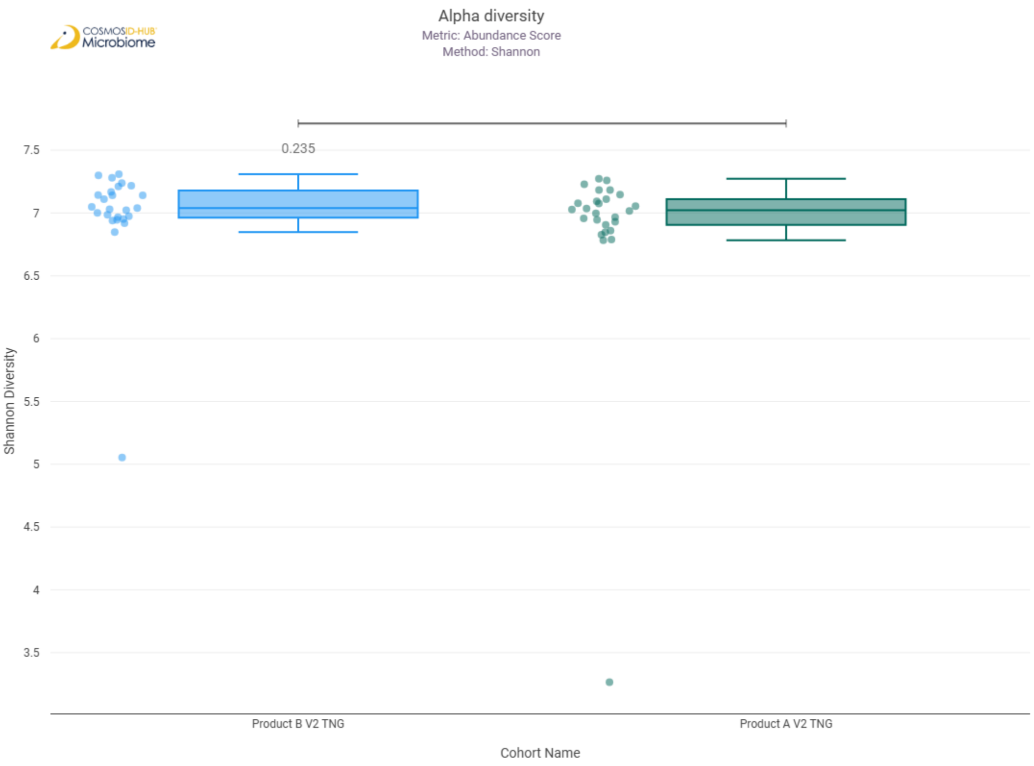


Feature	Enriched Cohort	LDA Score	P-value
tRNA (guanine(37)-N(1))-methyltransferase	Product B V2 TNG	2.624857402	0.010968497
3-hydroxybutyryl-CoA dehydratase	Product B V2 TNG	2.590594741	0.041854827
N-acylglucosamine-6-phosphate 2-epimerase	Product B V2 TNG	2.585952682	0.017590793
NADH:ubiquinone reductase (Na(+)-transporting)	Product B V2 TNG	2.489874734	0.026189985
Glycine hydroxymethyltransferase	Product B V2 TNG	2.427217585	0.031712637
Histidine ammonia-lyase	Product B V2 TNG	2.202715444	0.021519031
Glycine dehydrogenase (aminomethyl-transferring)	Product B V2 TNG	2.195190326	0.036484395
Triose-phosphate isomerase	Product A V2 TNG	2.758297723	0.030245812
Glyceraldehyde-3-phosphate dehydrogenase (NADP(+))	Product A V2 TNG	2.676691408	0.045697083

Acetyl-CoA carboxylase	Product A V2 TNG	2.63288439	0.00745964
Glutamine--fructose-6-phosphate transaminase (isomerizing)	Product A V2 TNG	2.403033073	0.045795182
Levansucrase	Product A V2 TNG	2.055940637	0.017552852

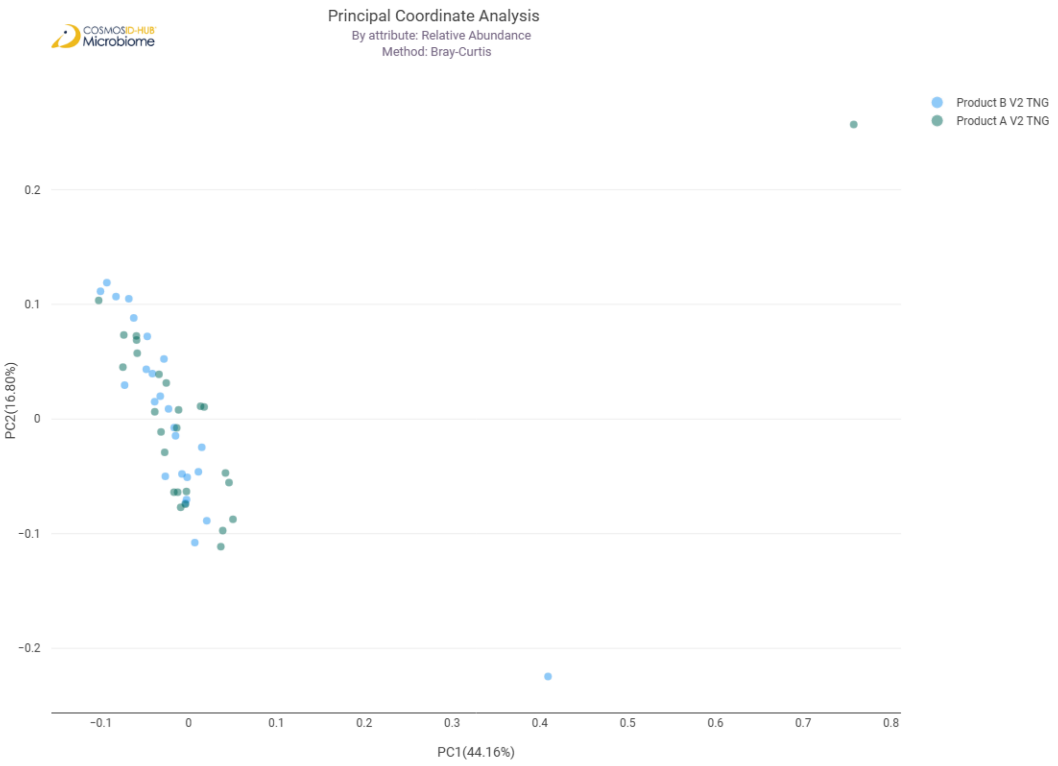
MetaCyc Pathways

Alpha Diversity (MetaCyc)

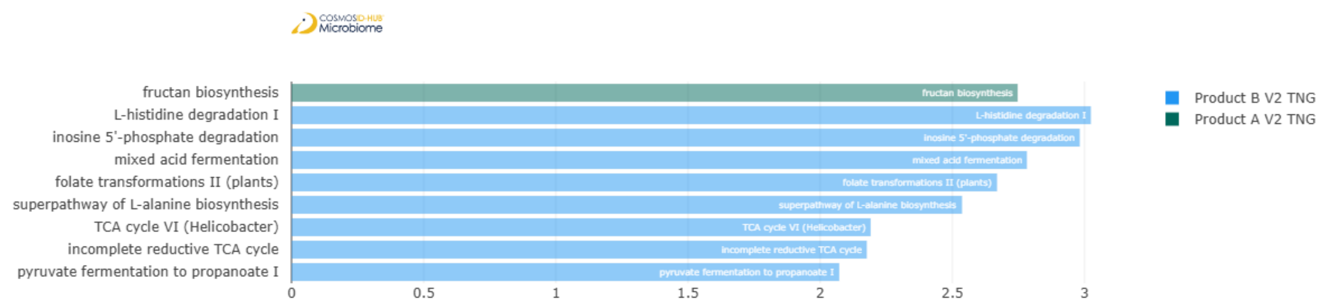
Chao1	
Shannon	

Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis PERMNOVA p = 0.666	

Differential Abundance (LEfSe) (MetaCyc)



Feature	Enriched Cohort	LDA Score	P-value
fructan biosynthesis	Product A V2 TNG	2.746991997	0.019443383
L-histidine degradation I	Product B V2 TNG	3.02380233	0.021519031
inosine 5'-phosphate degradation	Product B V2 TNG	2.981940294	0.002269883
mixed acid fermentation	Product B V2 TNG	2.781796134	0.030967972
folate transformations II (plants)	Product B V2 TNG	2.668838629	0.026189985
superpathway of L-alanine biosynthesis	Product B V2 TNG	2.536575601	0.048946493
TCA cycle VI (Helicobacter)	Product B V2 TNG	2.190843266	0.00083361
incomplete reductive TCA cycle	Product B V2 TNG	2.17615078	0.018956342
pyruvate fermentation to propanoate I	Product B V2 TNG	2.071955954	0.010899265

Comparison 12: Product A V3 TNG vs Product B V3 TNG

Gene Ontology

Alpha Diversity (GO)

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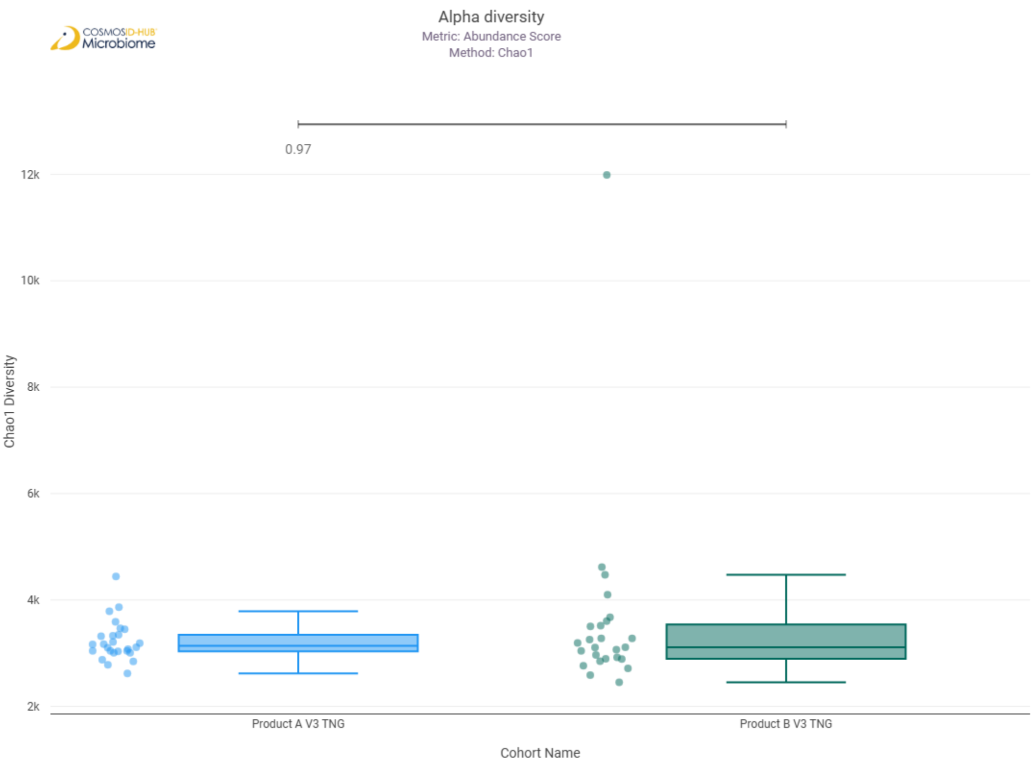
<tr><td>Chao1</td><td>
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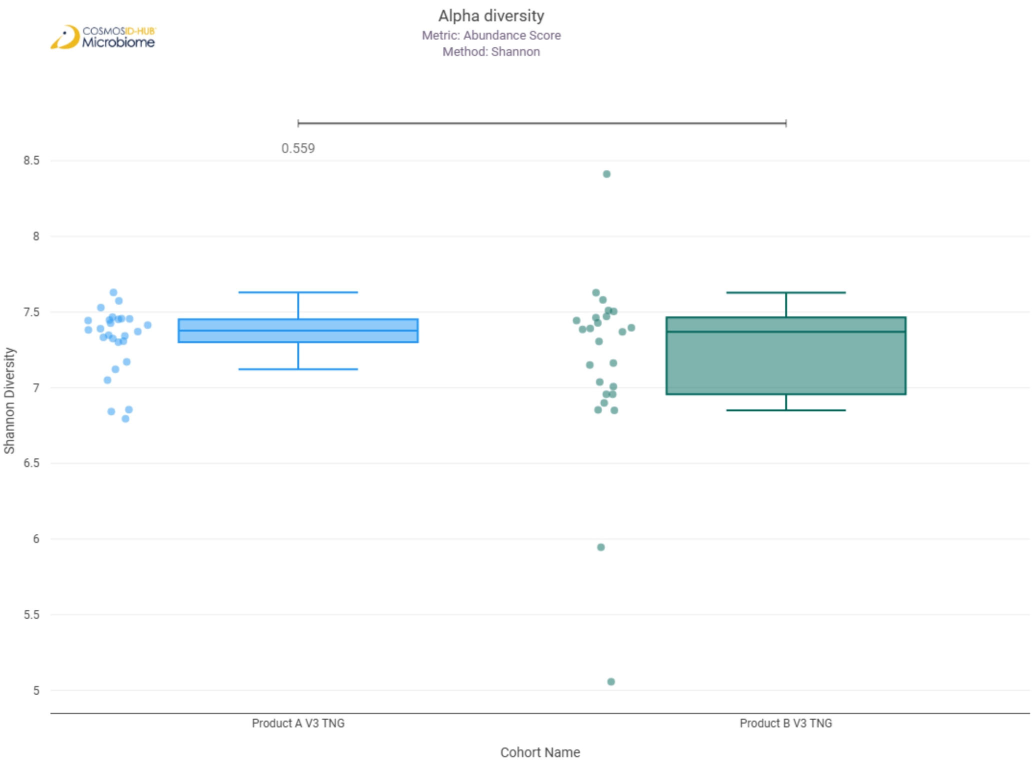
<tr><td>Shannon</td><td>
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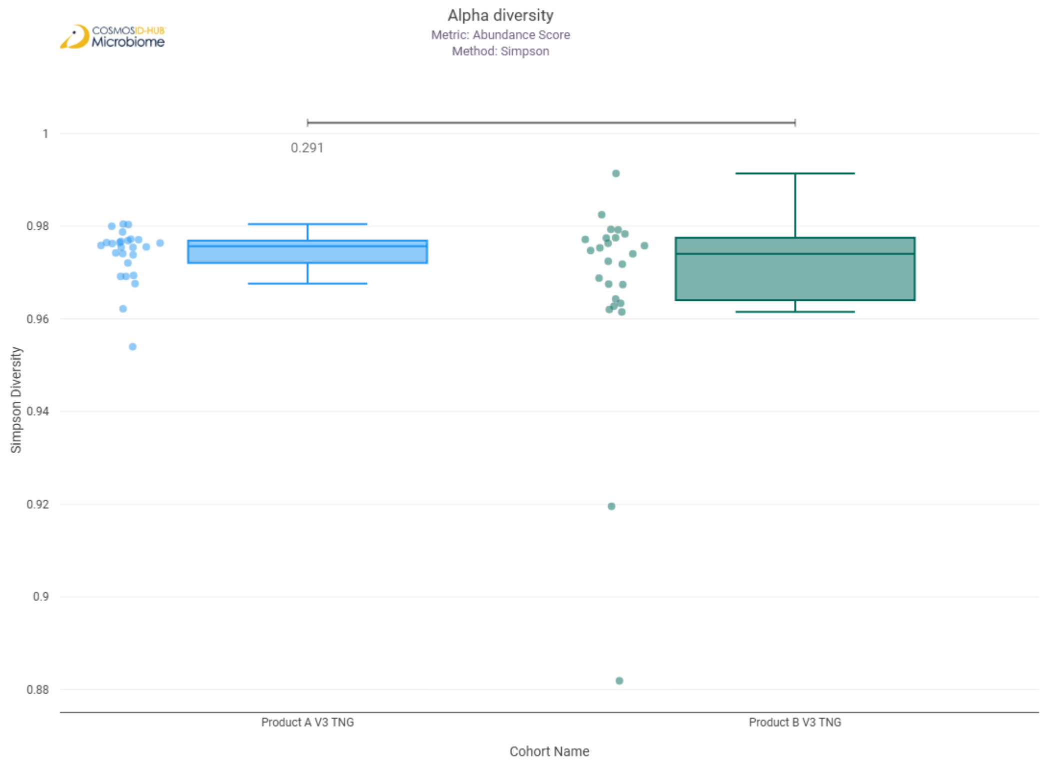
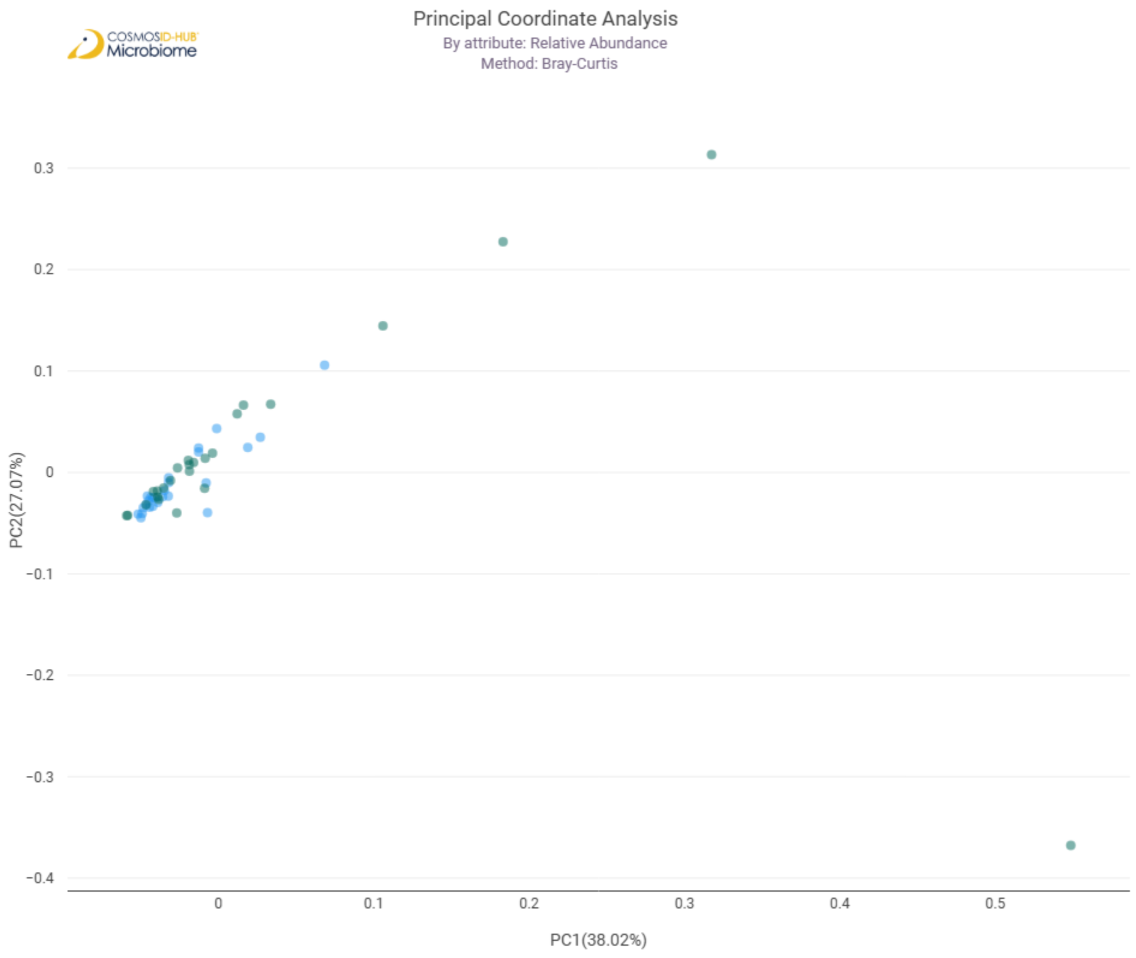
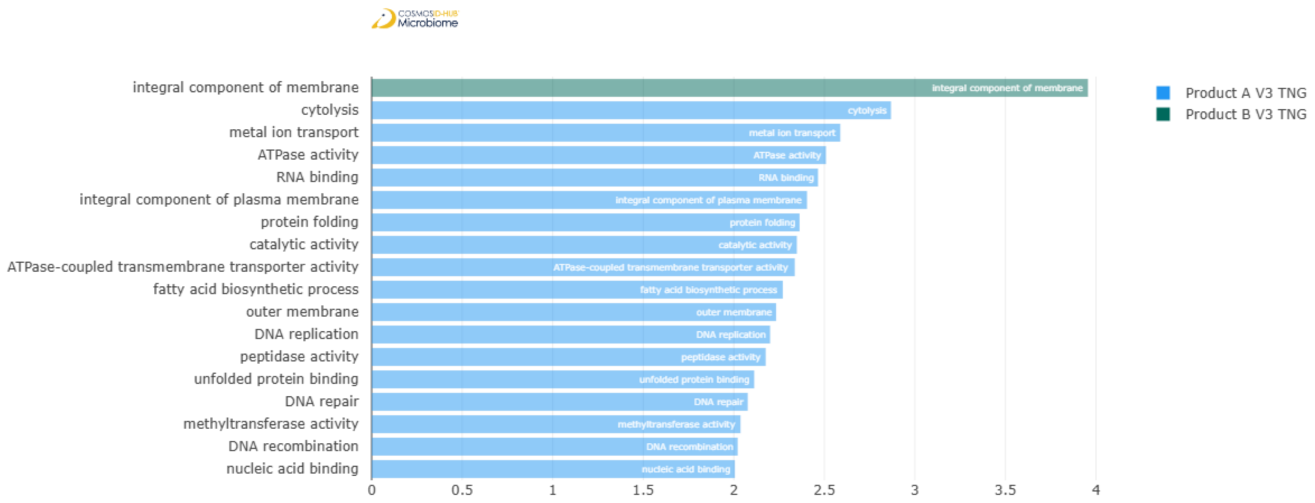
Simpson	

Beta Diversity (GO)

Bray-Curtis PERMNOVA p = 0.053	

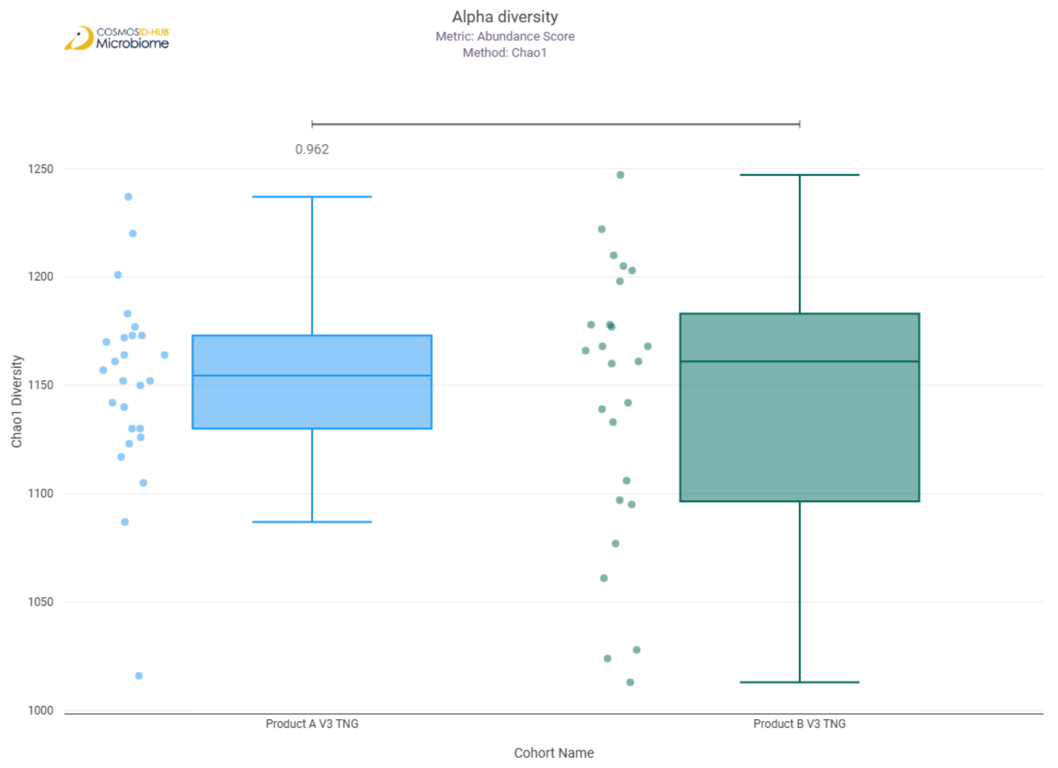
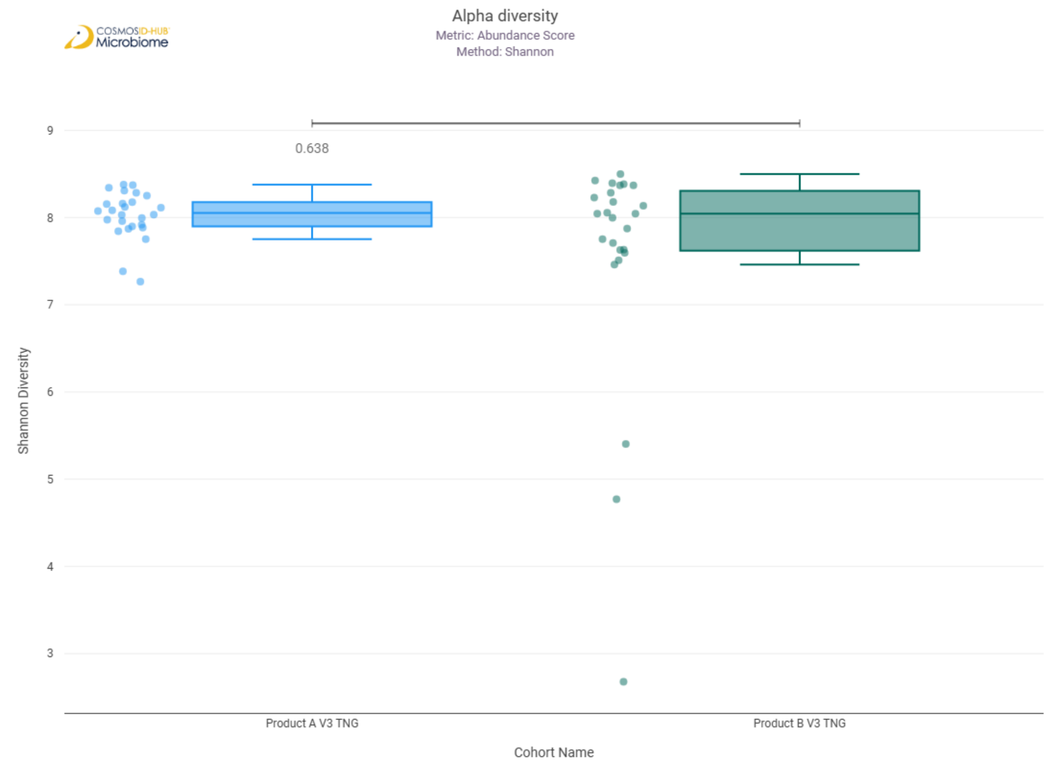
Differential Abundance (LEfSe) (GO)



Feature	Enriched Cohort	LDA Score	P-value
integral component of membrane	Product B V3 TNG	3.95594467	0.030245812
cytolysis	Product A V3 TNG	2.86819902	0.043787588
metal ion transport	Product A V3 TNG	2.588053047	0.000121136
ATPase activity	Product A V3 TNG	2.509036589	0.031712637
RNA binding	Product A V3 TNG	2.46499143	0.026189985
integral component of plasma membrane	Product A V3 TNG	2.404445655	0.004992891
protein folding	Product A V3 TNG	2.363291849	0.008341822
catalytic activity	Product A V3 TNG	2.348315829	0.045795182
ATPase-coupled transmembrane transporter activity	Product A V3 TNG	2.336885912	0.004438681
fatty acid biosynthetic process	Product A V3 TNG	2.27062913	0.045795182
outer membrane	Product A V3 TNG	2.233829492	0.030245812
DNA replication	Product A V3 TNG	2.200445561	0.036484395
peptidase activity	Product A V3 TNG	2.176299275	0.012209995
unfolded protein binding	Product A V3 TNG	2.112611698	0.033240045
DNA repair	Product A V3 TNG	2.07714937	0.026189985
methyltransferase activity	Product A V3 TNG	2.037014259	0.027486336
DNA recombination	Product A V3 TNG	2.02153966	0.00666206
nucleic acid binding	Product A V3 TNG	2.005813652	0.041854827

Enzyme Commission

Alpha Diversity (EC)

Chao1	
Shannon	

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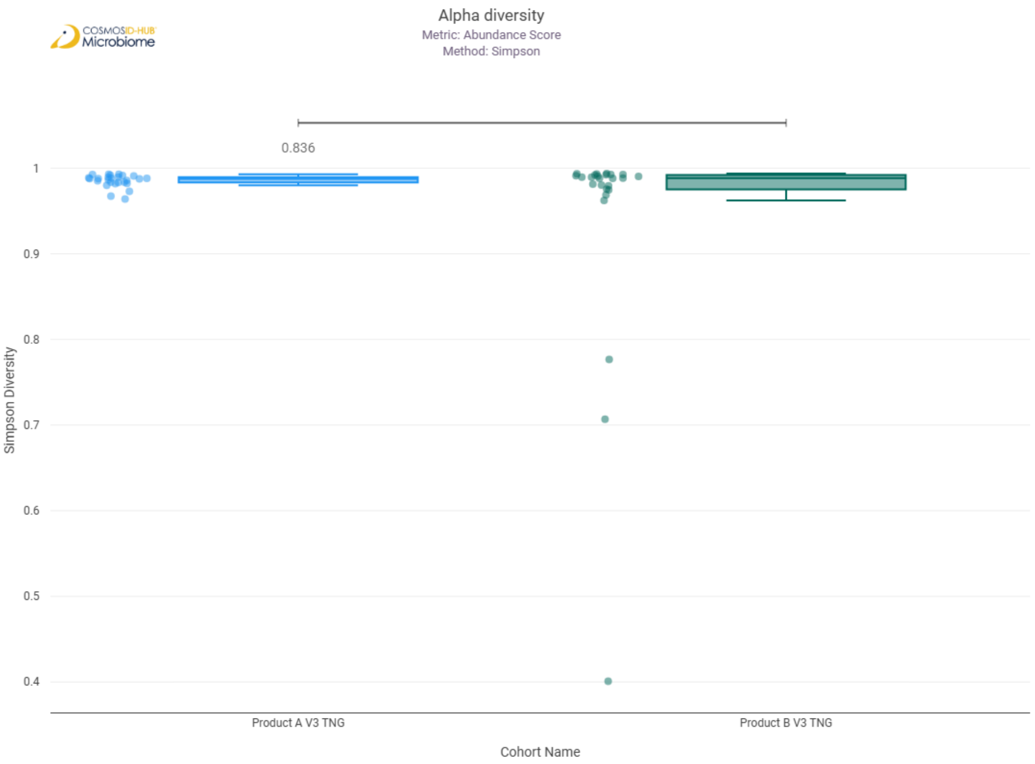

Beta Diversity (EC)

Bray-Curtis

PERMNOVA
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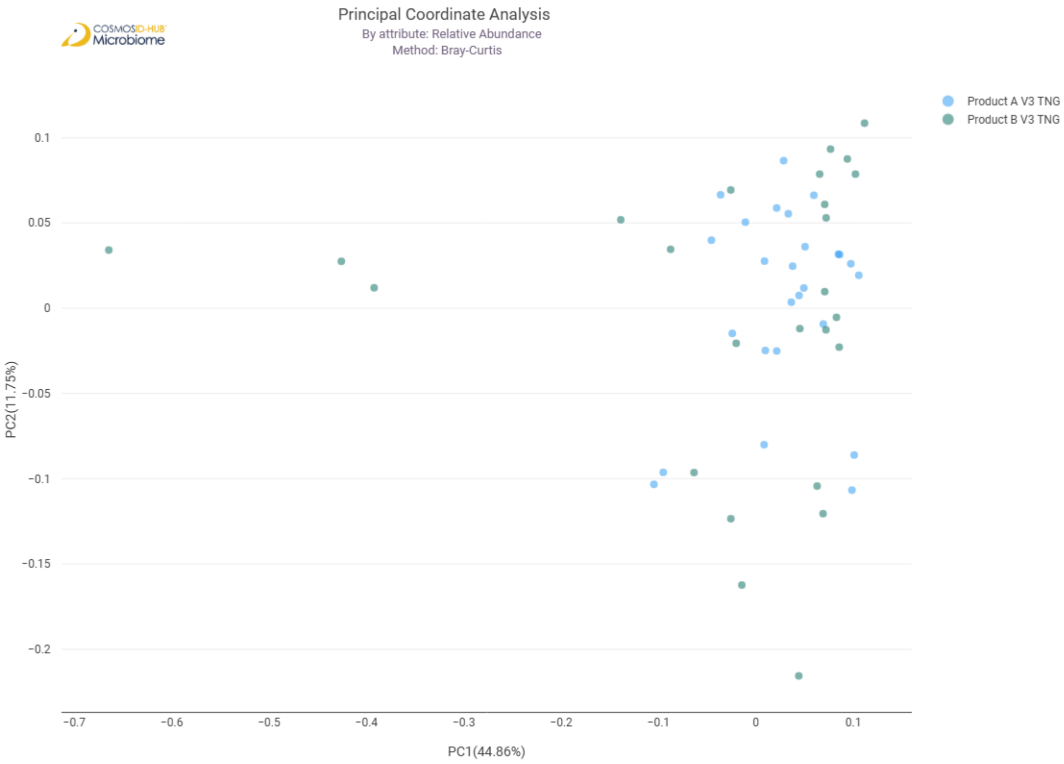
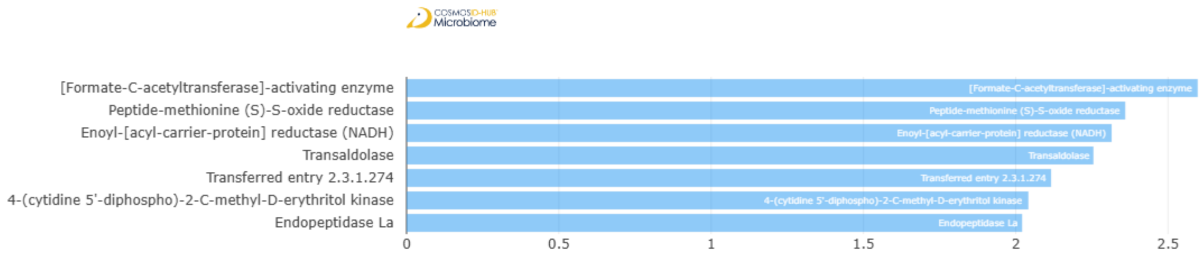


Differential Abundance (LEfSe) (EC)

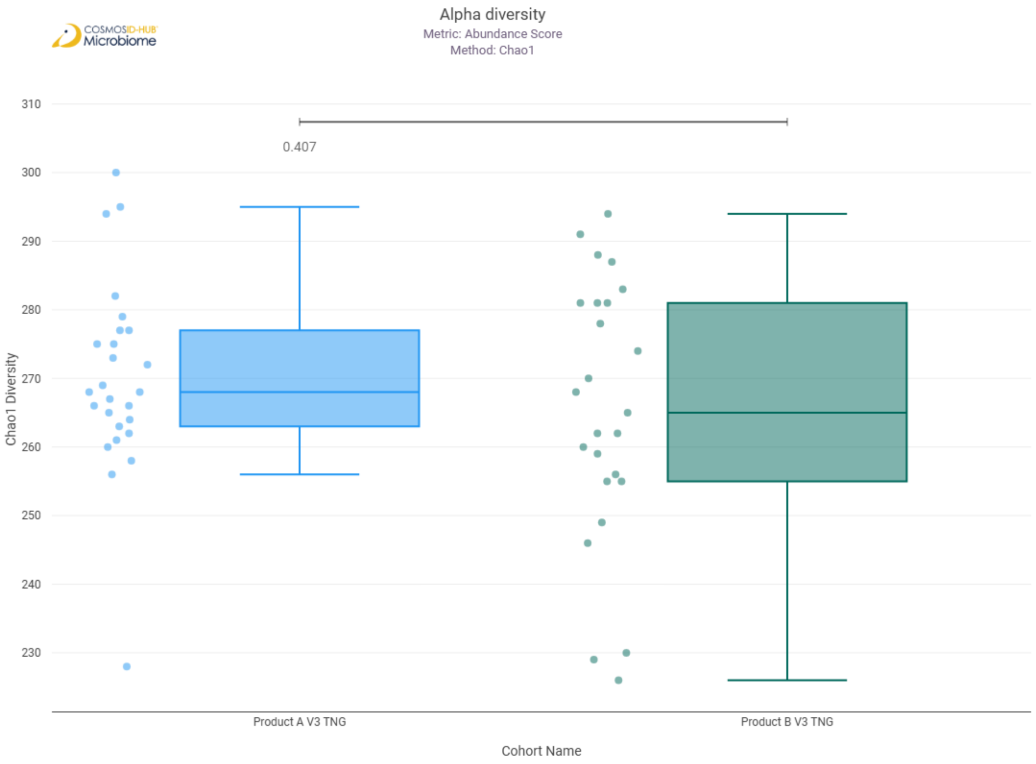


Feature	Enriched Cohort	LDA Score	P-value
[Formate-C-acetyltransferase]-activating enzyme	Product A V3 TNG	2.597387363	0.021519031
Peptide-methionine (S)-S-oxide reductase	Product A V3 TNG	2.359536073	0.009840467
Enoyl-[acyl-carrier-protein] reductase (NADH)	Product A V3 TNG	2.31483187	0.033240045
Transaldolase	Product A V3 TNG	2.254985266	0.033240045
Transferred entry 2.3.1.274	Product A V3 TNG	2.116157133	0.043787588
4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	Product A V3 TNG	2.041454779	0.008341822
Endopeptidase La	Product A V3 TNG	2.020895553	0.045795182

MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1



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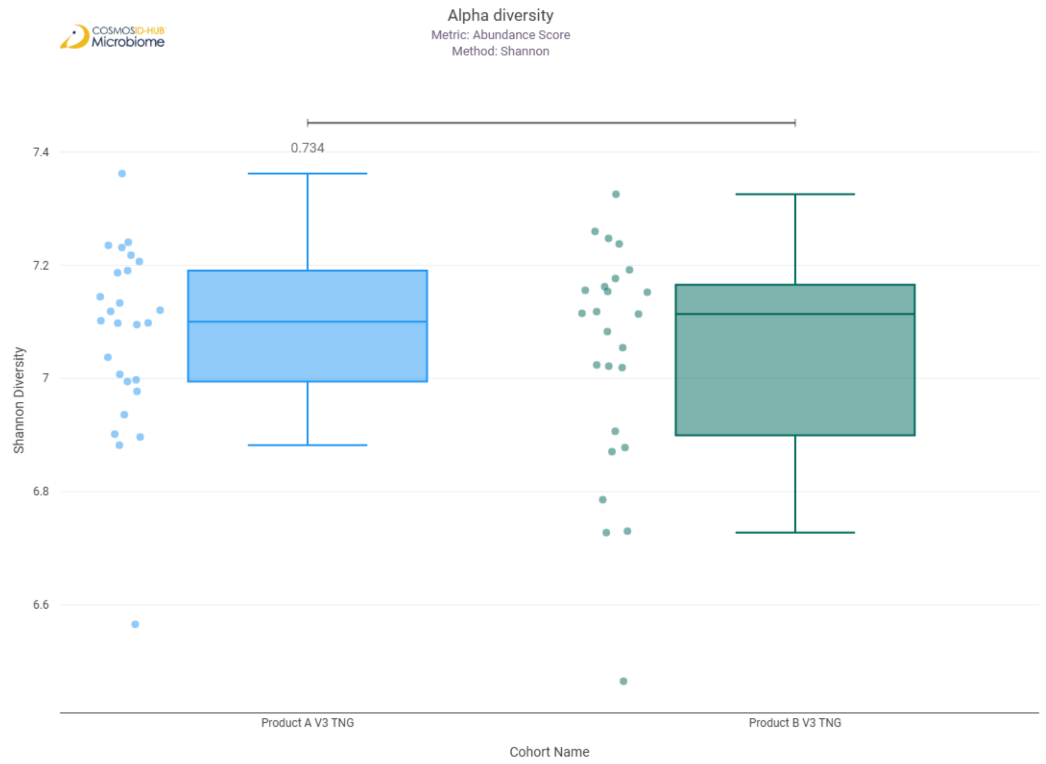
<tr><td>Shannon</td><td>
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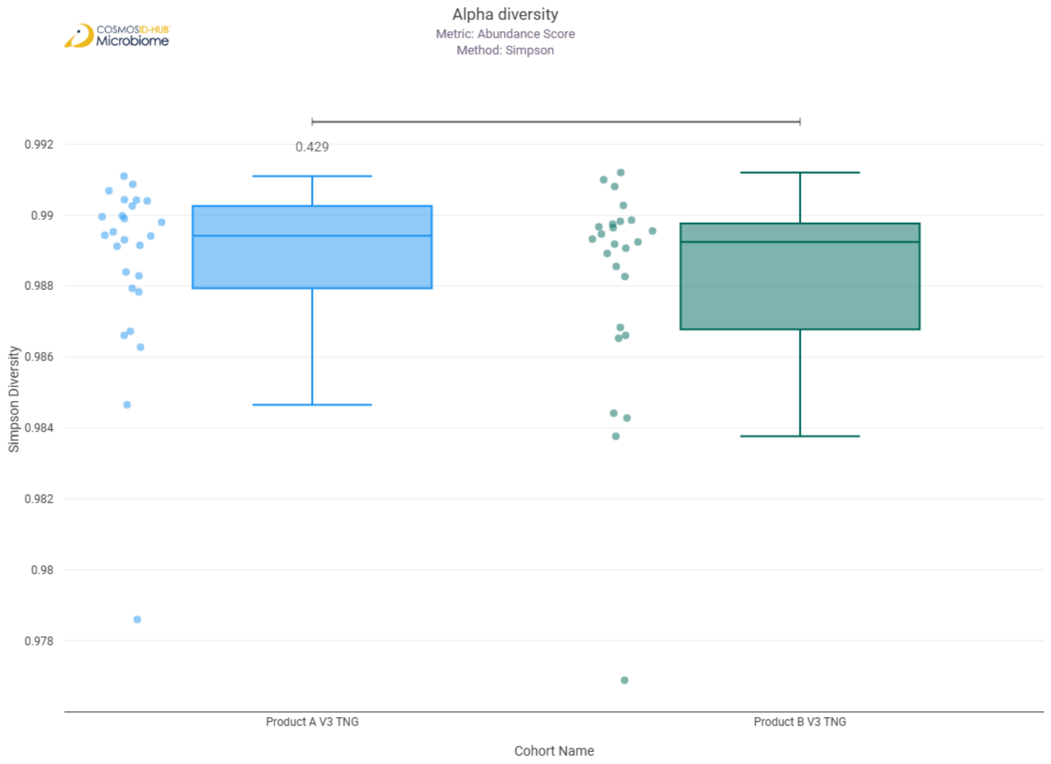
<tr><td>Simpson</td><td>
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Beta Diversity (MetaCyc)

Bray-Curtis

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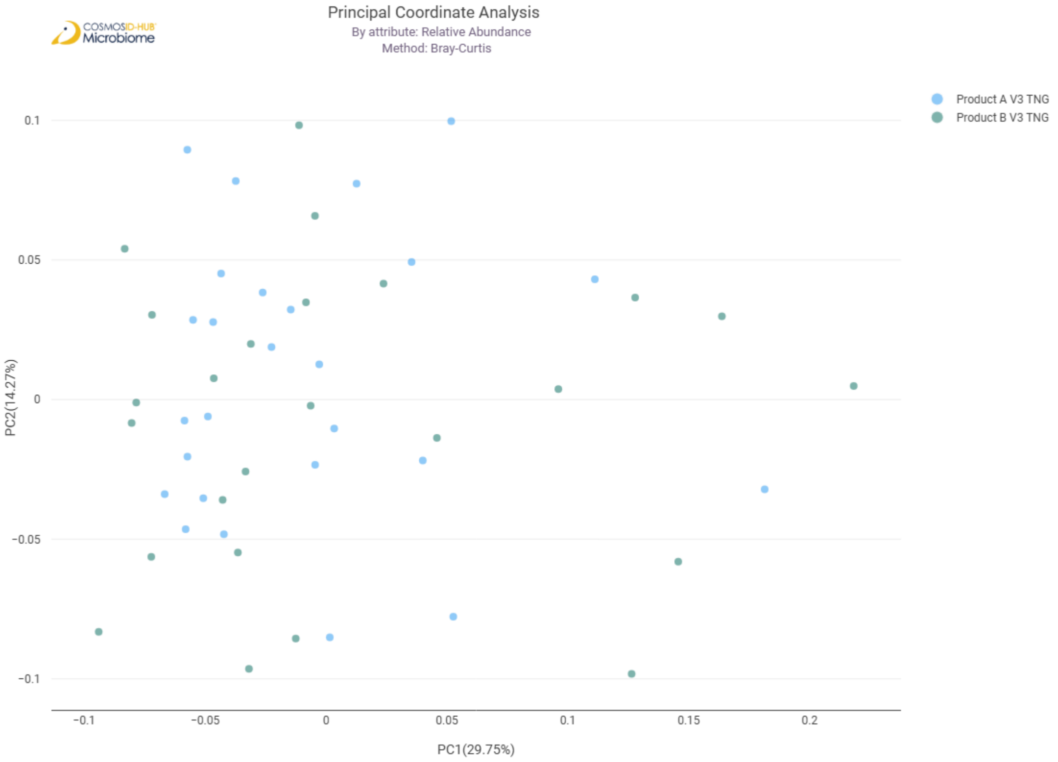
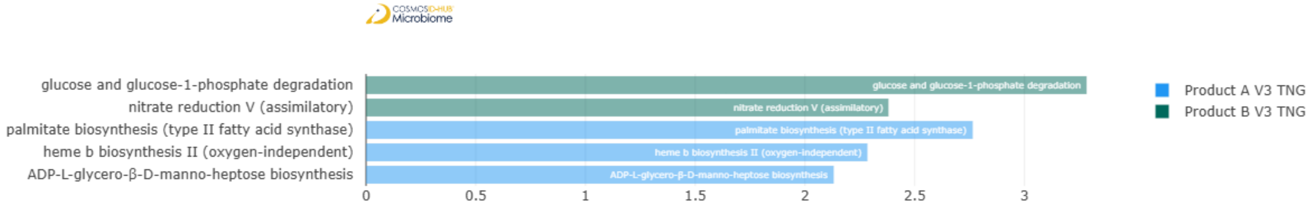


Differential Abundance (LEfSe) (MetaCyc)



Feature	Enriched Cohort	LDA Score	P-value
glucose and glucose-1-phosphate degradation	Product B V3 TNG	3.28329517	0.039994768
nitrate reduction V (assimilatory)	Product B V3 TNG	2.380513641	0.027486336
palmitate biosynthesis (type II fatty acid synthase)	Product A V3 TNG	2.764475862	0.038200947
heme b biosynthesis II (oxygen-independent)	Product A V3 TNG	2.284637925	0.013574437
ADP-L-glycero-β-D-manno-heptose biosynthesis	Product A V3 TNG	2.130957279	0.045795182

Comparison 13: Product A V2 SUPG vs Product A V3 SUPG

Gene Ontology

Alpha Diversity (GO)

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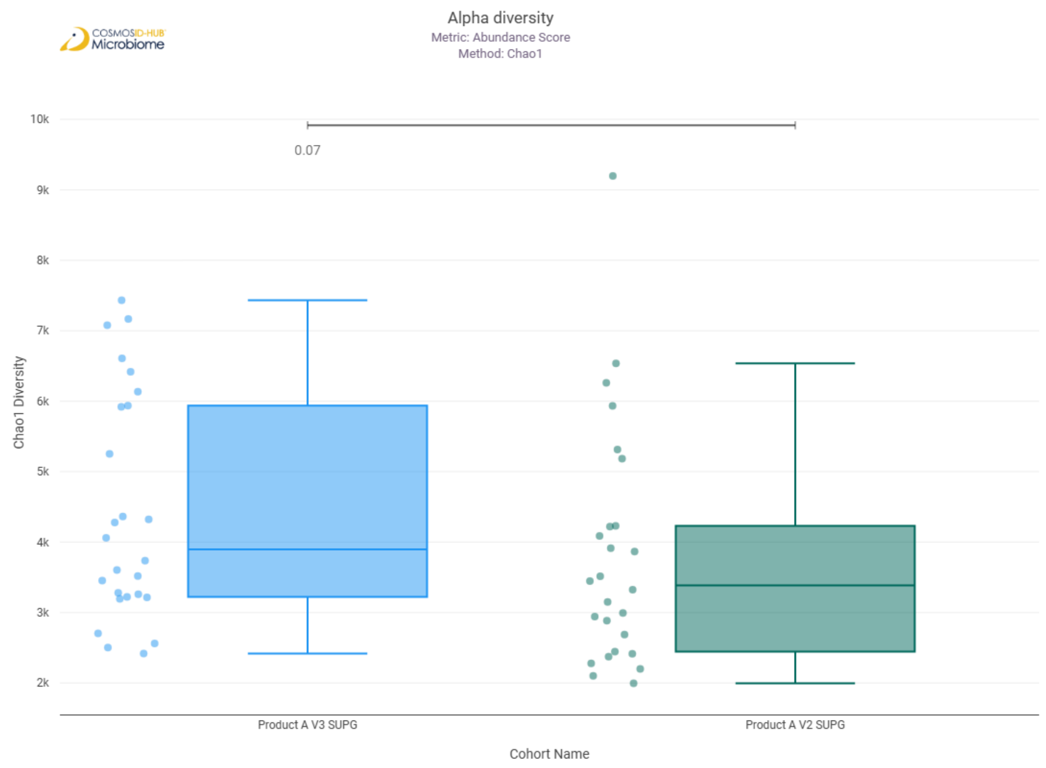

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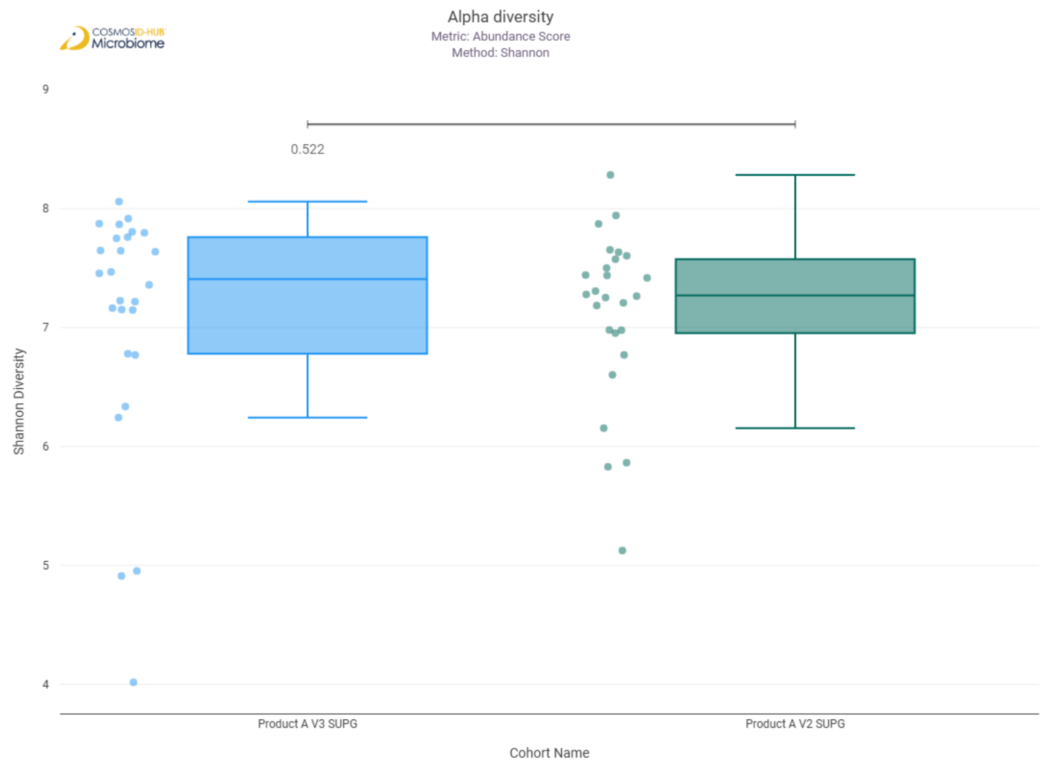

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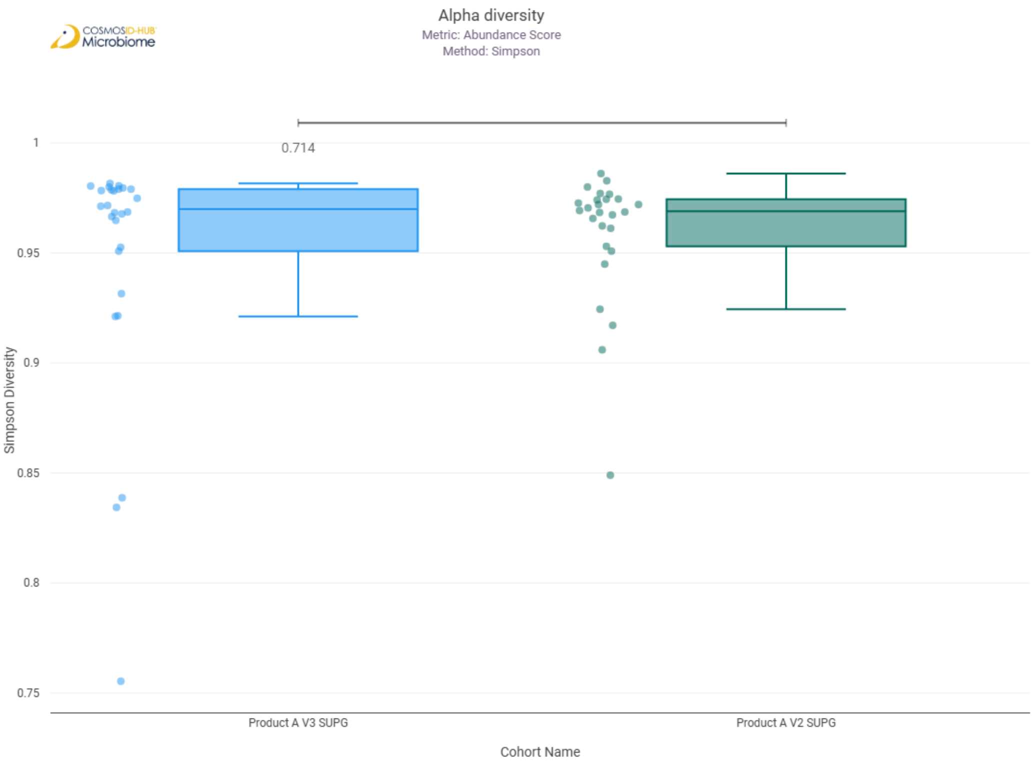

Beta Diversity (GO)

Bray-Curtis

PERMNOVA
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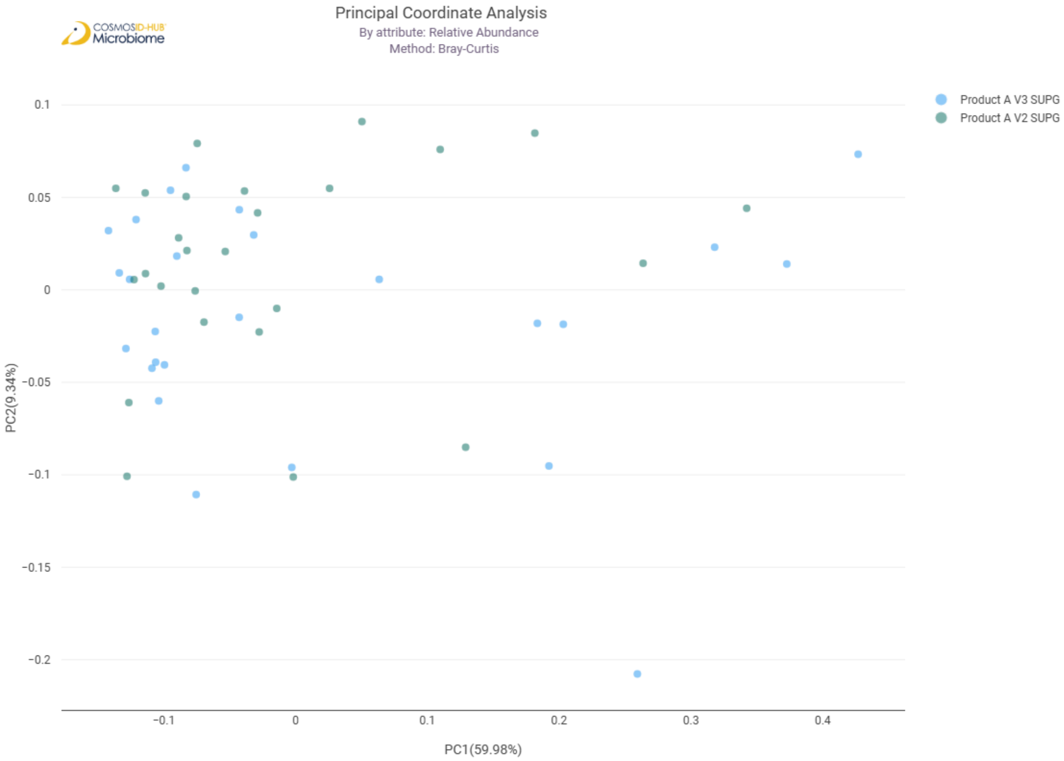
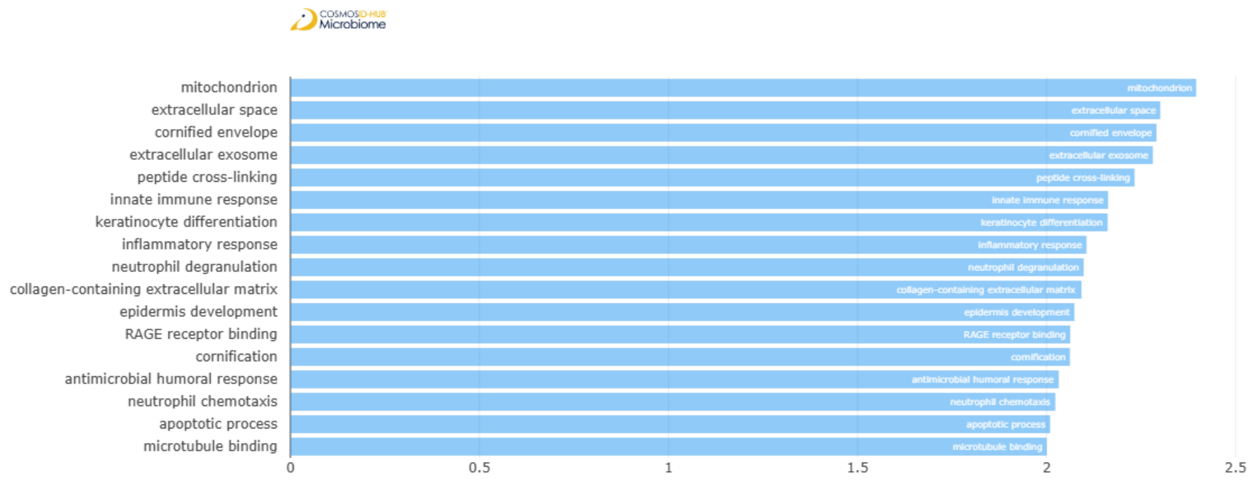


Differential Abundance (LEfSe) (GO)



Feature	Enriched Cohort	LDA Score	P-value
mitochondrion	Product A V3 SUPG	2.395593333	0.044100855
extracellular space	Product A V3 SUPG	2.30062659	0.044100855
cornified envelope	Product A V3 SUPG	2.290652157	0.036807215
extracellular exosome	Product A V3 SUPG	2.280967867	0.035244686
peptide cross-linking	Product A V3 SUPG	2.232724206	0.042057434
innate immune response	Product A V3 SUPG	2.162582759	0.03077255
keratinocyte differentiation	Product A V3 SUPG	2.161426341	0.042057434
inflammatory response	Product A V3 SUPG	2.105579409	0.022101093
neutrophil degranulation	Product A V3 SUPG	2.098179782	0.028014666
collagen-containing extracellular matrix	Product A V3 SUPG	2.092271978	0.038553793
epidermis development	Product A V3 SUPG	2.073464904	0.03686763
RAGE receptor binding	Product A V3 SUPG	2.062537534	0.030683327
cornification	Product A V3 SUPG	2.06157641	0.036807215
antimicrobial humoral response	Product A V3 SUPG	2.032144347	0.033626203
neutrophil chemotaxis	Product A V3 SUPG	2.023076006	0.026684643
apoptotic process	Product A V3 SUPG	2.009510989	0.026684643
microtubule binding	Product A V3 SUPG	2.000388259	0.026684643

Enzyme Commission

Alpha Diversity (EC)

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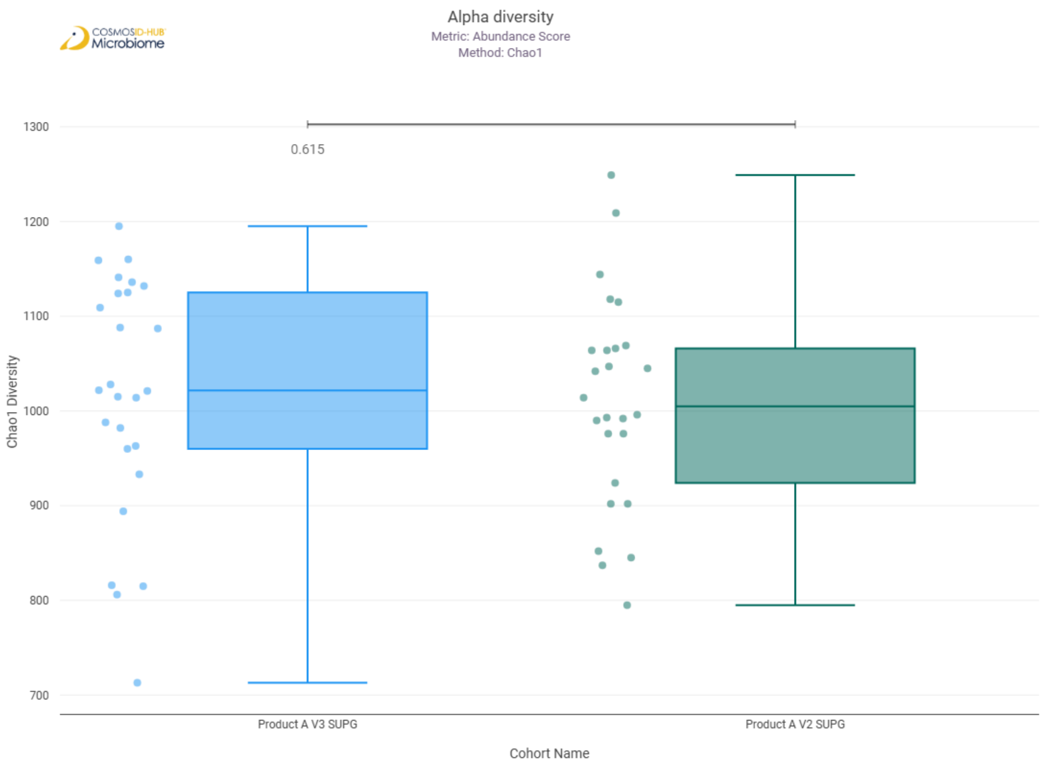

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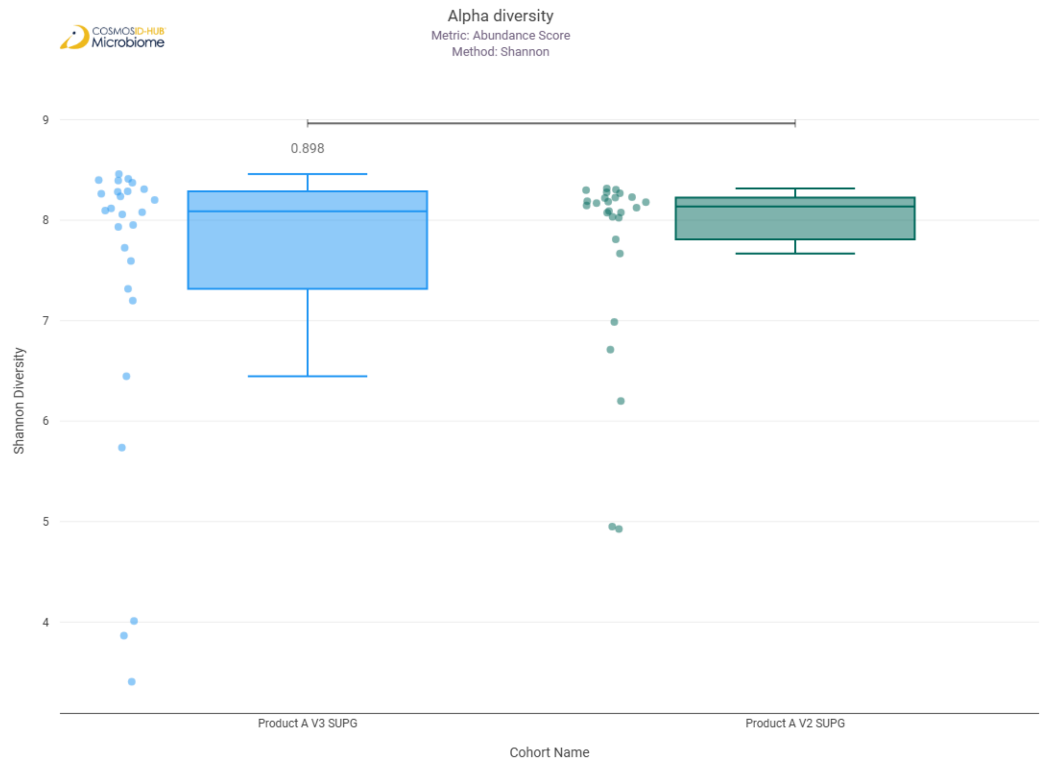

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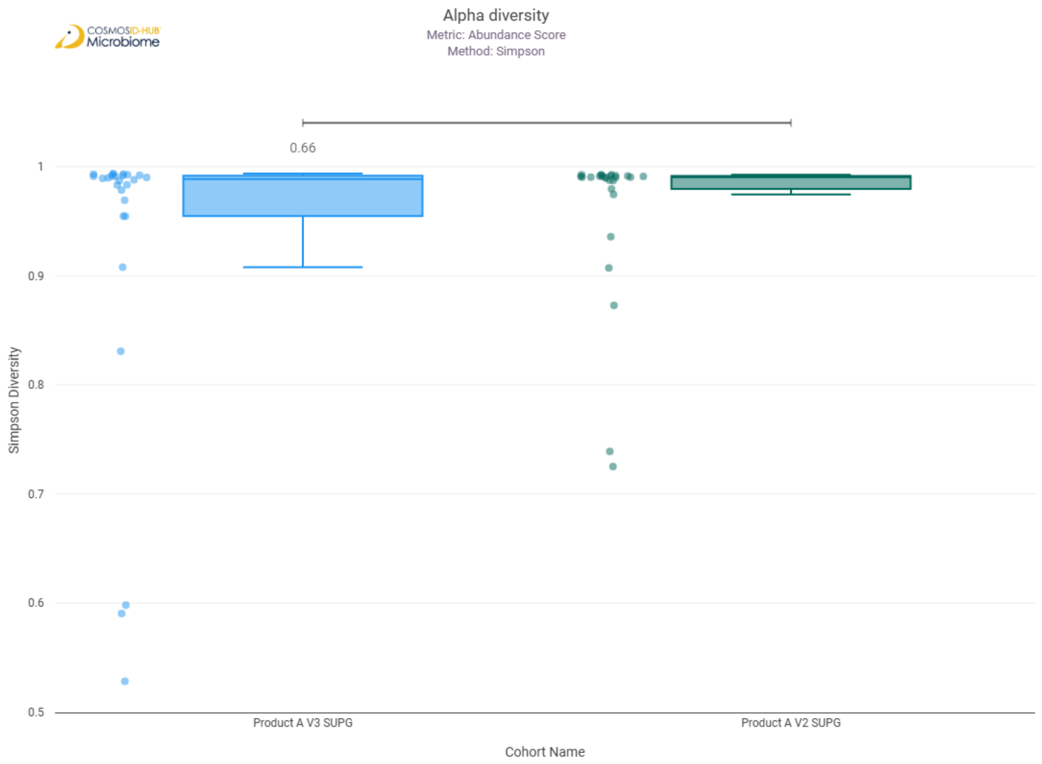

Beta Diversity (EC)

Bray-Curtis

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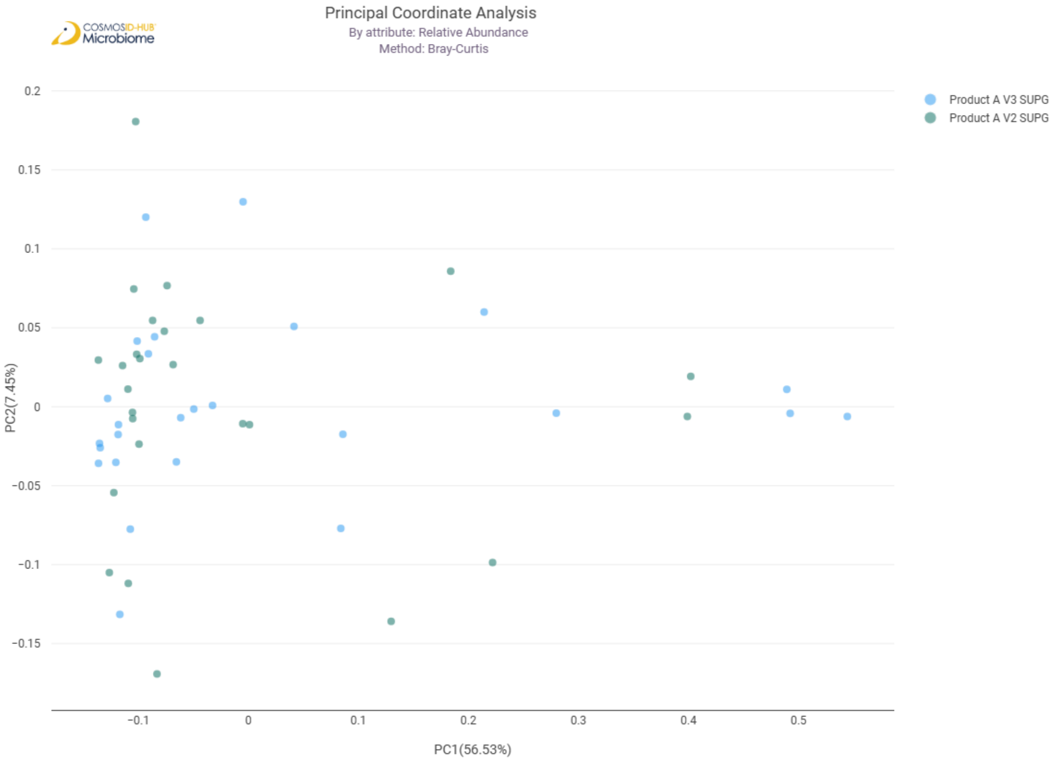
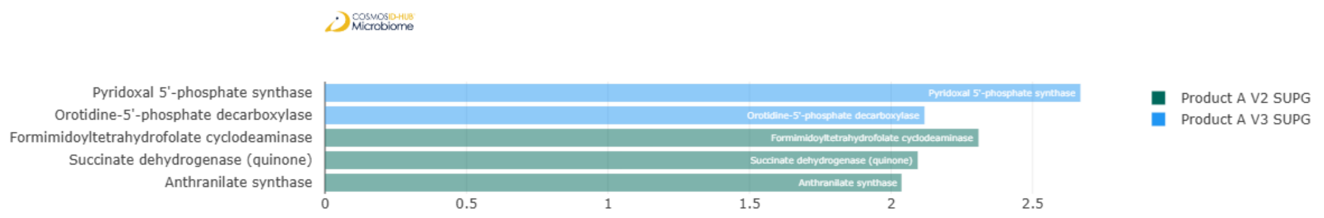


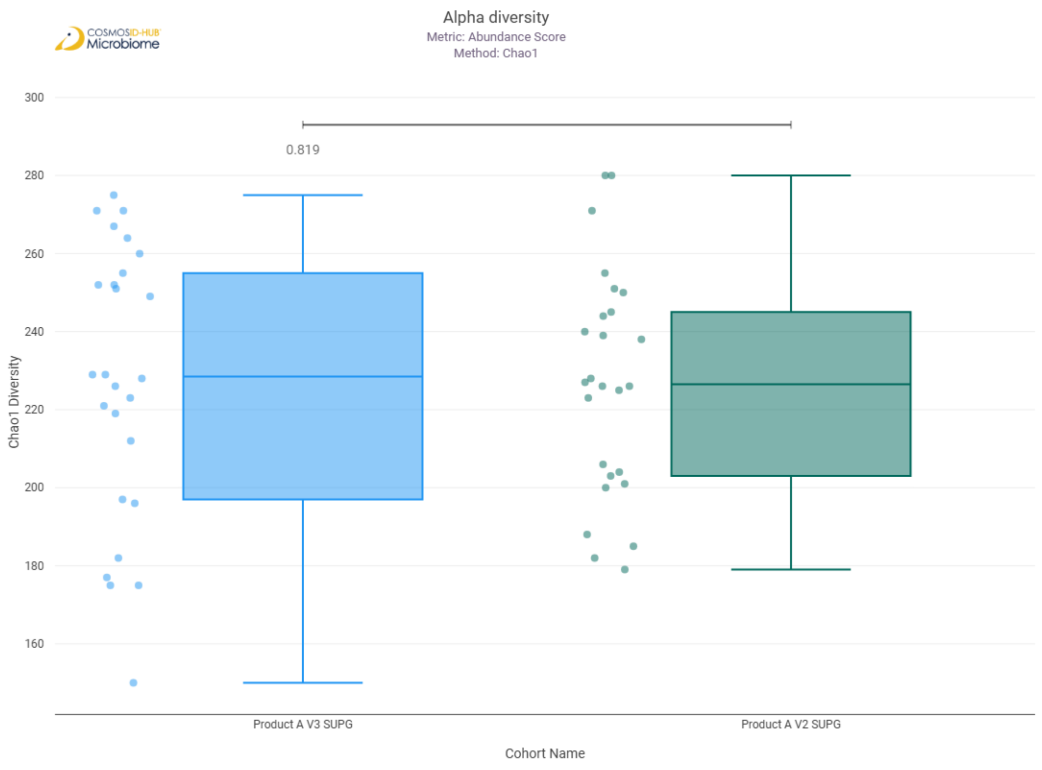
Differential Abundance (LEfSe) (EC)



Feature	Enriched Cohort	LDA Score	P-value
Pyridoxal 5'-phosphate synthase	Product A V3 SUPG	2.668823124	0.042211177
Orotidine-5'-phosphate decarboxylase	Product A V3 SUPG	2.117963651	0.035322927
Formimidoyltetrahydrofolate cyclodeaminase	Product A V2 SUPG	2.308922282	0.042211177
Succinate dehydrogenase (quinone)	Product A V2 SUPG	2.094121479	0.035322927
Anthranilate synthase	Product A V2 SUPG	2.036878376	0.030808261

MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1	

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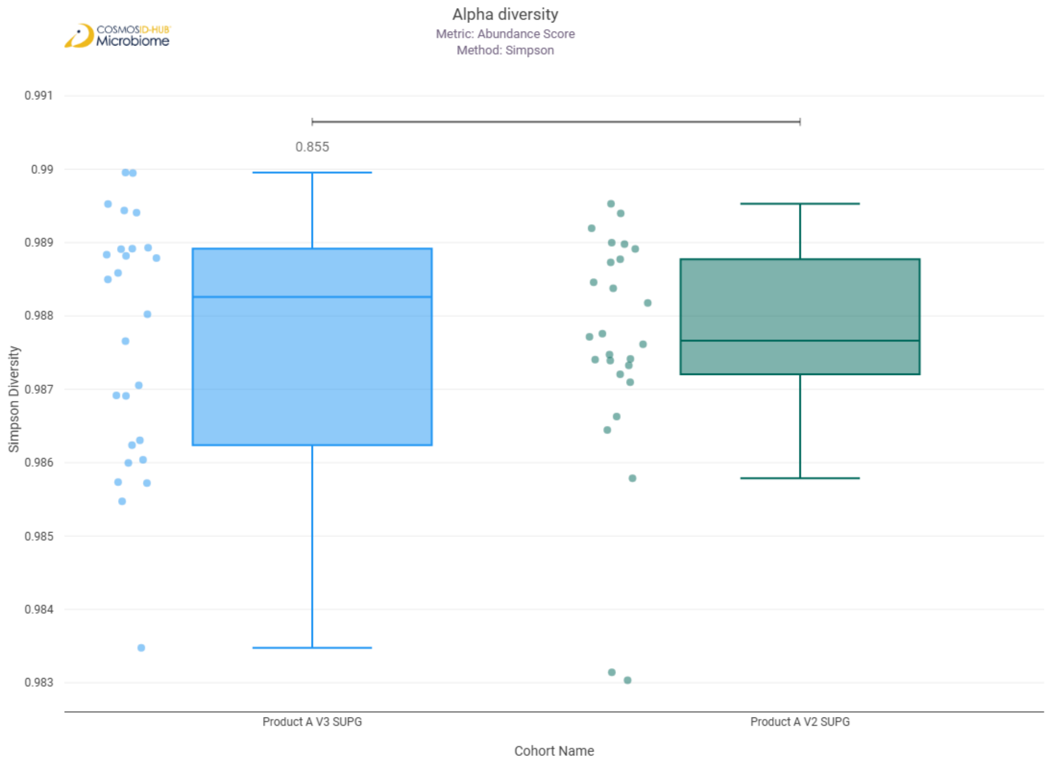

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Beta Diversity (MetaCyc)

Bray-Curtis

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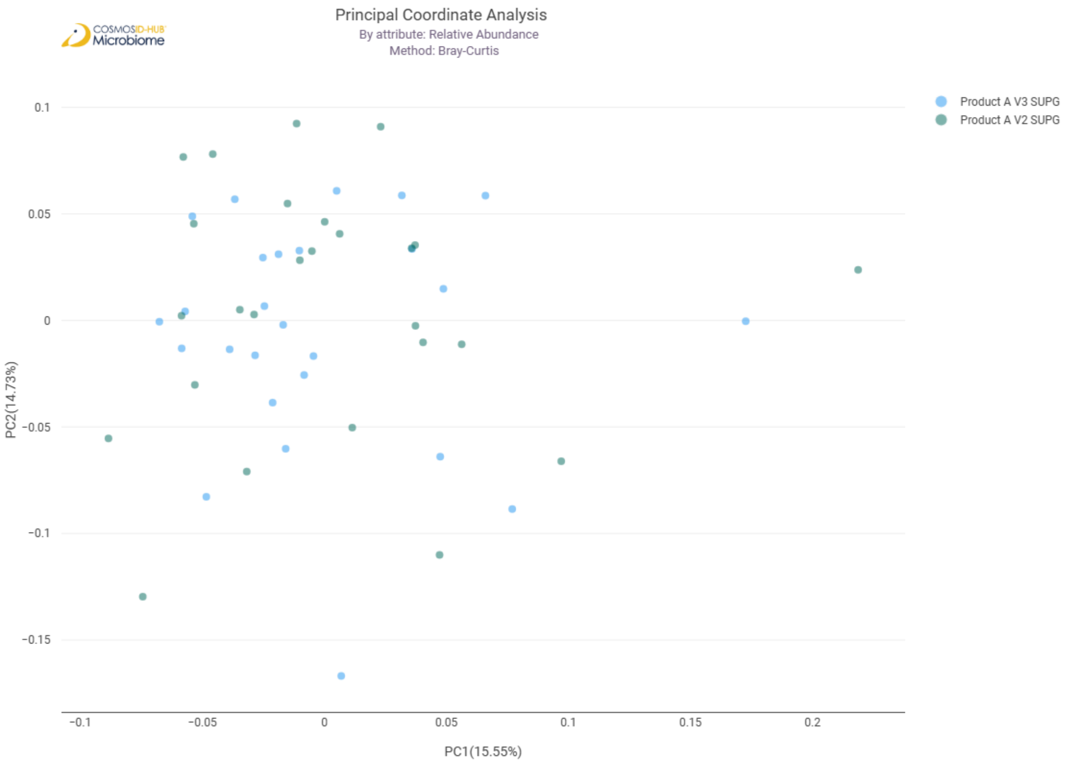
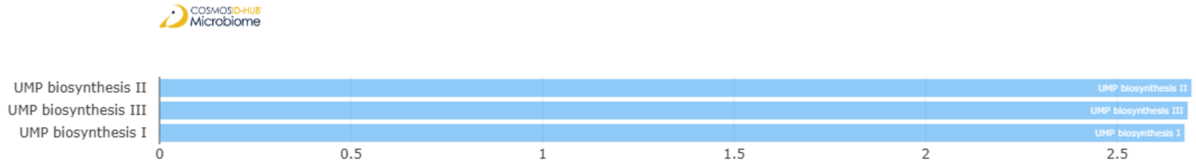


Differential Abundance (LEfSe) (MetaCyc)

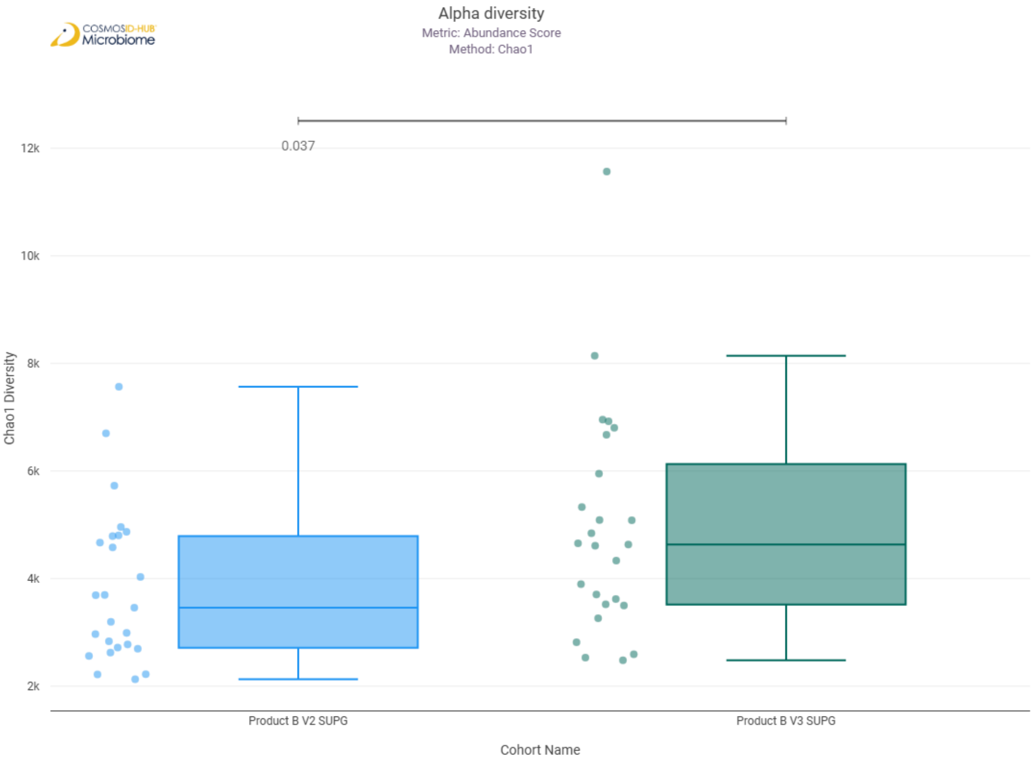
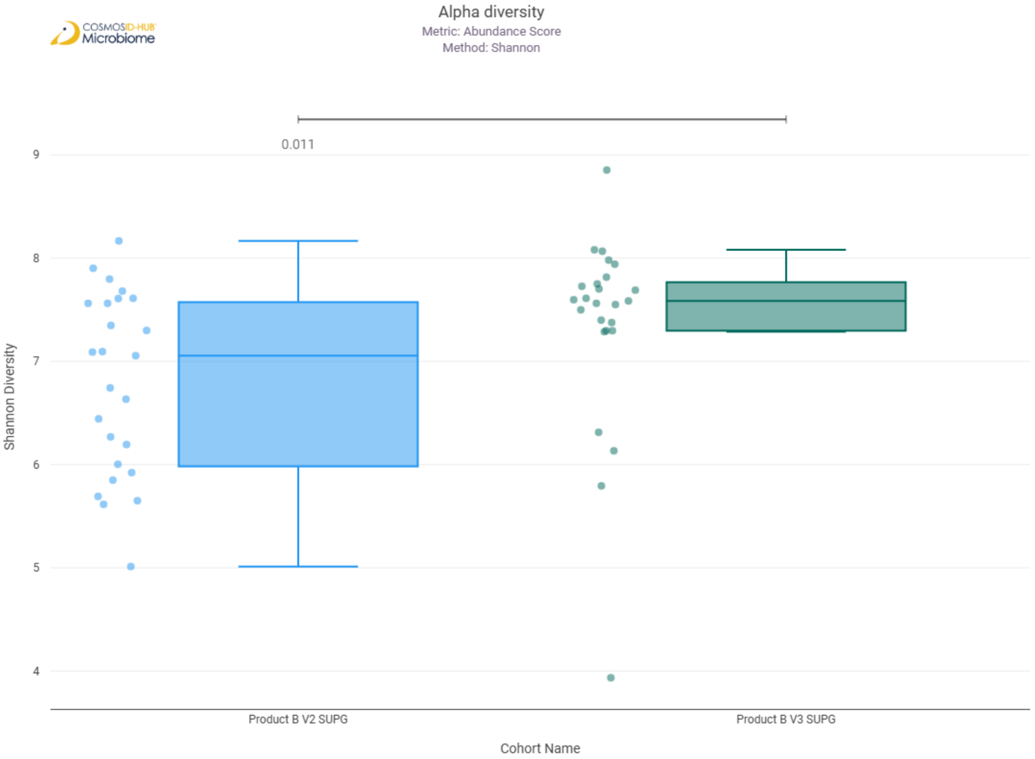


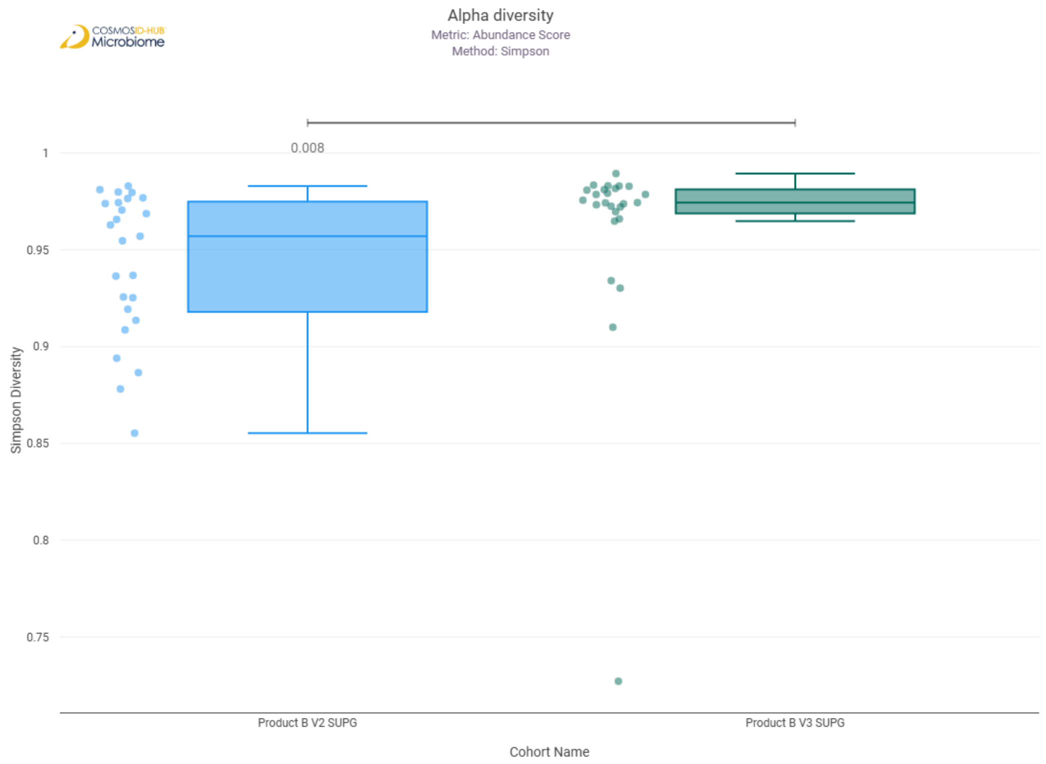
Feature	Enriched Cohort	LDA Score	P-value
UMP biosynthesis II	Product A V3 SUPG	2.693855617	0.014192278
UMP biosynthesis III	Product A V3 SUPG	2.684091372	0.016509366
UMP biosynthesis I	Product A V3 SUPG	2.675675228	0.022157981

Comparison 14: Product B V2 SUPG vs Product B V3 SUPG

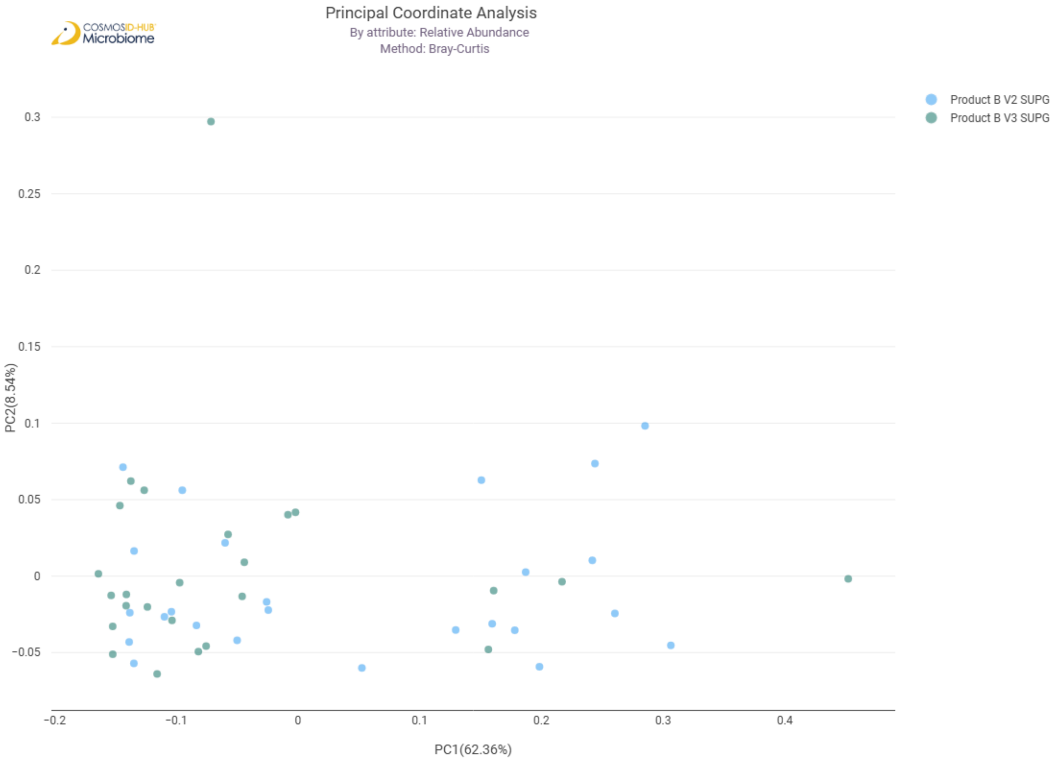
Gene Ontology

Alpha Diversity (GO)

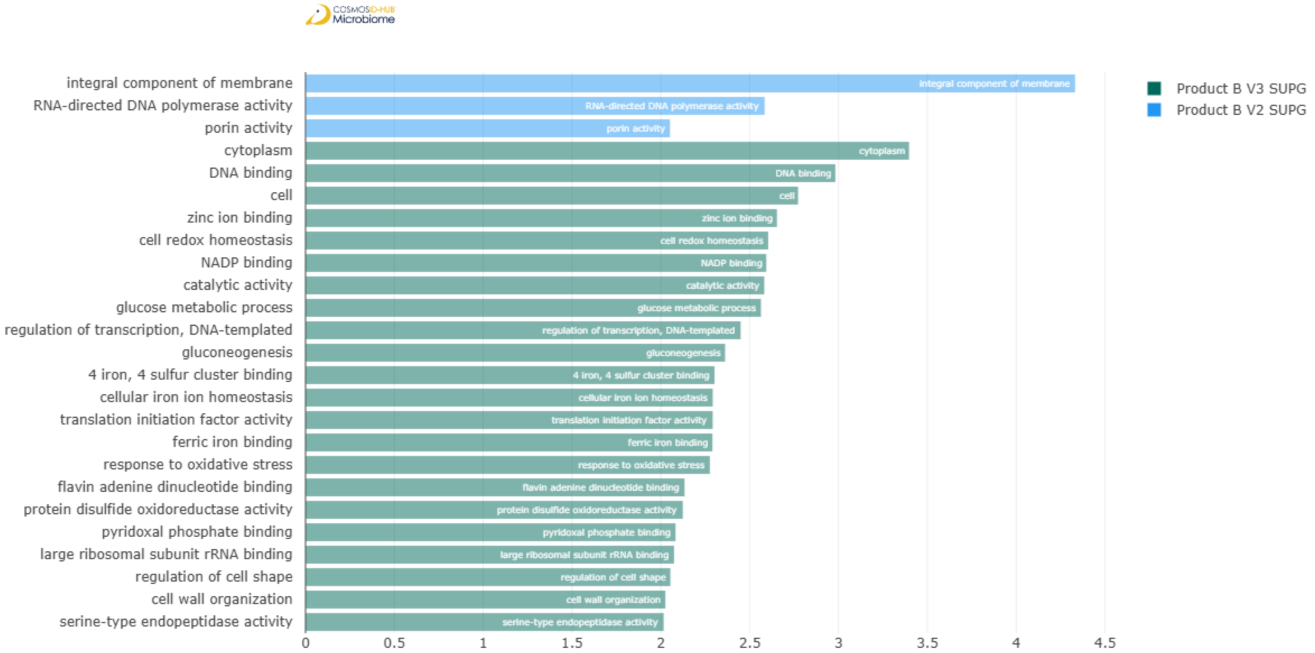
Chao1	
Shannon	

Simpson	

Beta Diversity (GO)

Bray-Curtis PERMNOVA p = 0.031	

Differential Abundance (LEfSe) (GO)



Feature	Enriched Cohort	LDA Score	P-value
integral component of membrane	Product B V2 SUPG	4.331239388	0.000876011
RNA-directed DNA polymerase activity	Product B V2 SUPG	2.583794457	0.021491444
porin activity	Product B V2 SUPG	2.051060432	0.000370258
cytoplasm	Product B V3 SUPG	3.396749929	0.009589776
DNA binding	Product B V3 SUPG	2.981994326	0.048908406
cell	Product B V3 SUPG	2.772339093	0.004210827
zinc ion binding	Product B V3 SUPG	2.653236004	0.033618995
cell redox homeostasis	Product B V3 SUPG	2.604058534	0.011982167
NADP binding	Product B V3 SUPG	2.593277033	0.044622577
catalytic activity	Product B V3 SUPG	2.581800698	0.014109615
glucose metabolic process	Product B V3 SUPG	2.563245358	0.048908406
regulation of transcription, DNA-templated	Product B V3 SUPG	2.448756977	0.029049022
gluconeogenesis	Product B V3 SUPG	2.361417944	0.046724152
4 iron, 4 sulfur cluster binding	Product B V3 SUPG	2.301918482	0.005364191
cellular iron ion homeostasis	Product B V3 SUPG	2.291981249	0.01265739
translation initiation factor activity	Product B V3 SUPG	2.291727599	0.010144117
ferric iron binding	Product B V3 SUPG	2.290111	0.010726809
response to oxidative stress	Product B V3 SUPG	2.275933055	0.019384996
flavin adenine dinucleotide binding	Product B V3 SUPG	2.133201392	0.038790393
protein disulfide oxidoreductase activity	Product B V3 SUPG	2.12366867	6.80E-03
pyridoxal phosphate binding	Product B V3 SUPG	2.082319369	0.0352731
large ribosomal subunit rRNA binding	Product B V3 SUPG	2.074326848	0.027649527
regulation of cell shape	Product B V3 SUPG	2.053444527	0.015706943

cell wall organization	Product B V3 SUPG	2.025283891	0.021491444
serine-type endopeptidase activity	Product B V3 SUPG	2.015887339	0.006795613

Enzyme Commission

Alpha Diversity (EC)

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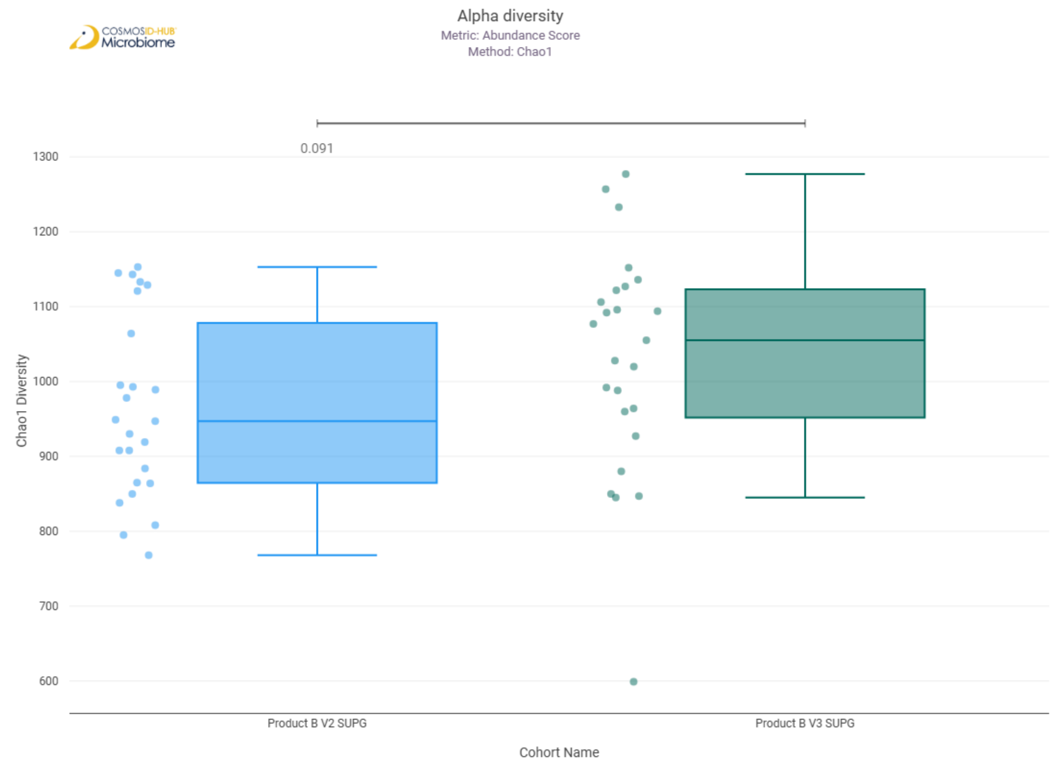

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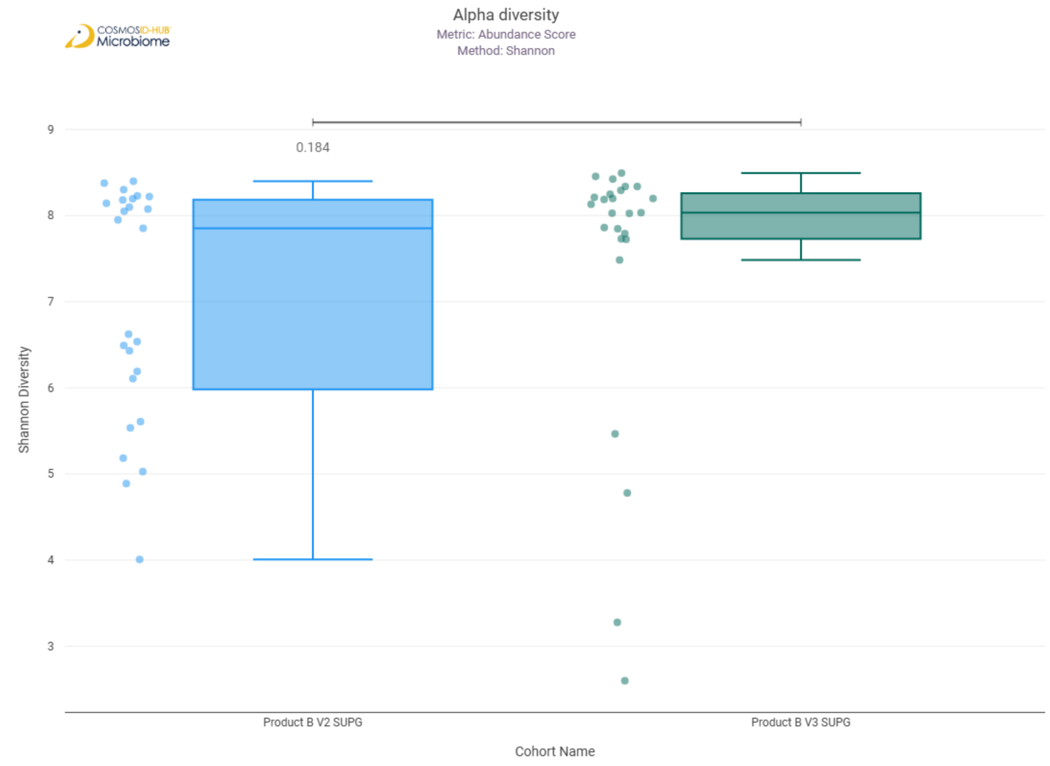

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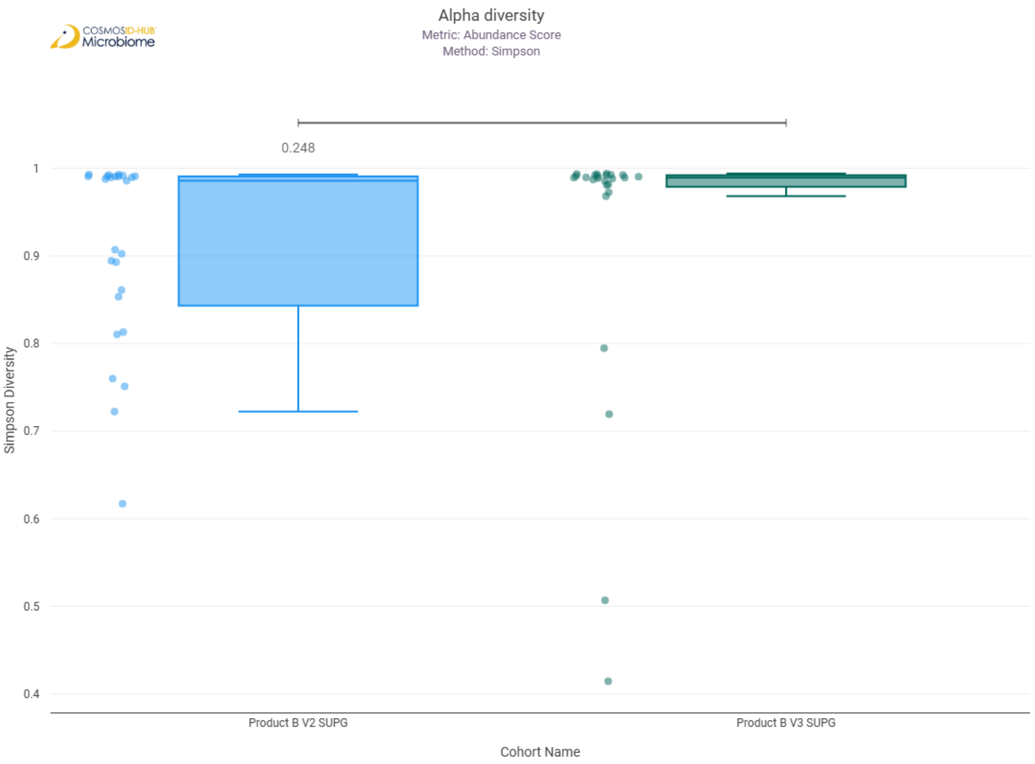
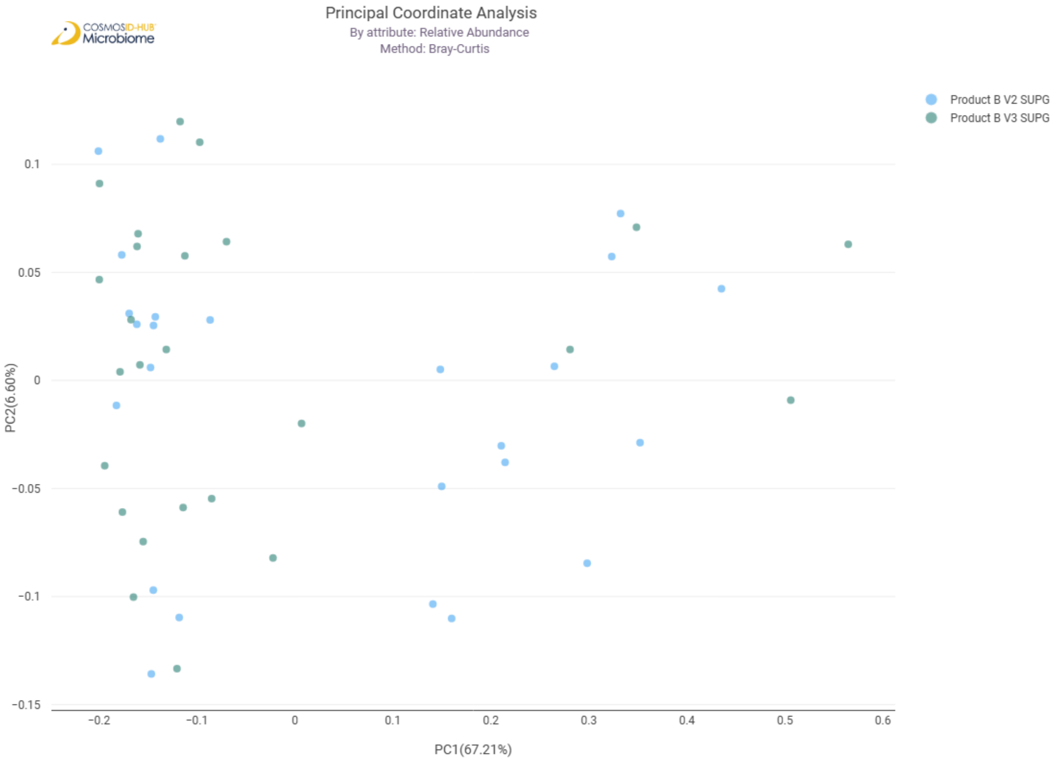
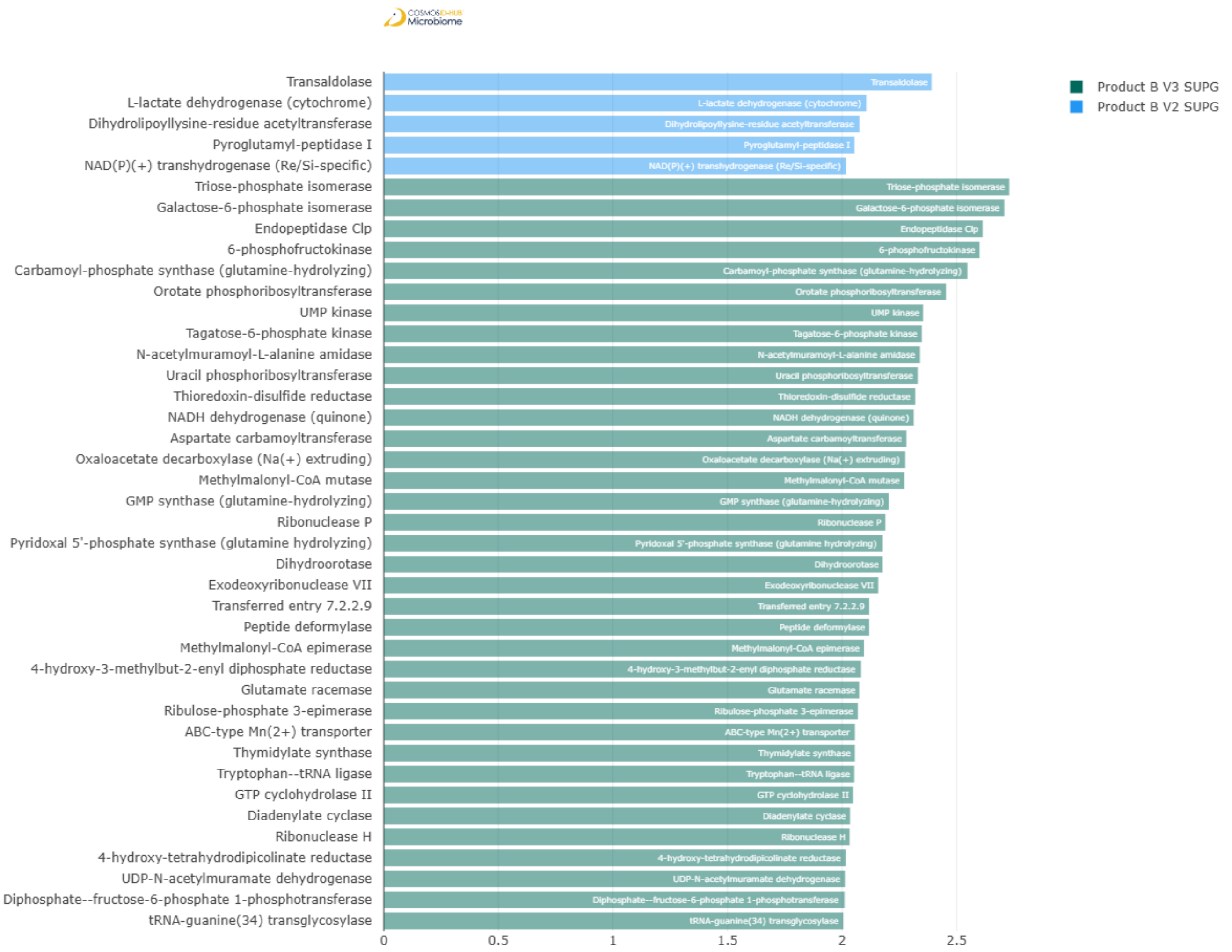
Simpson	

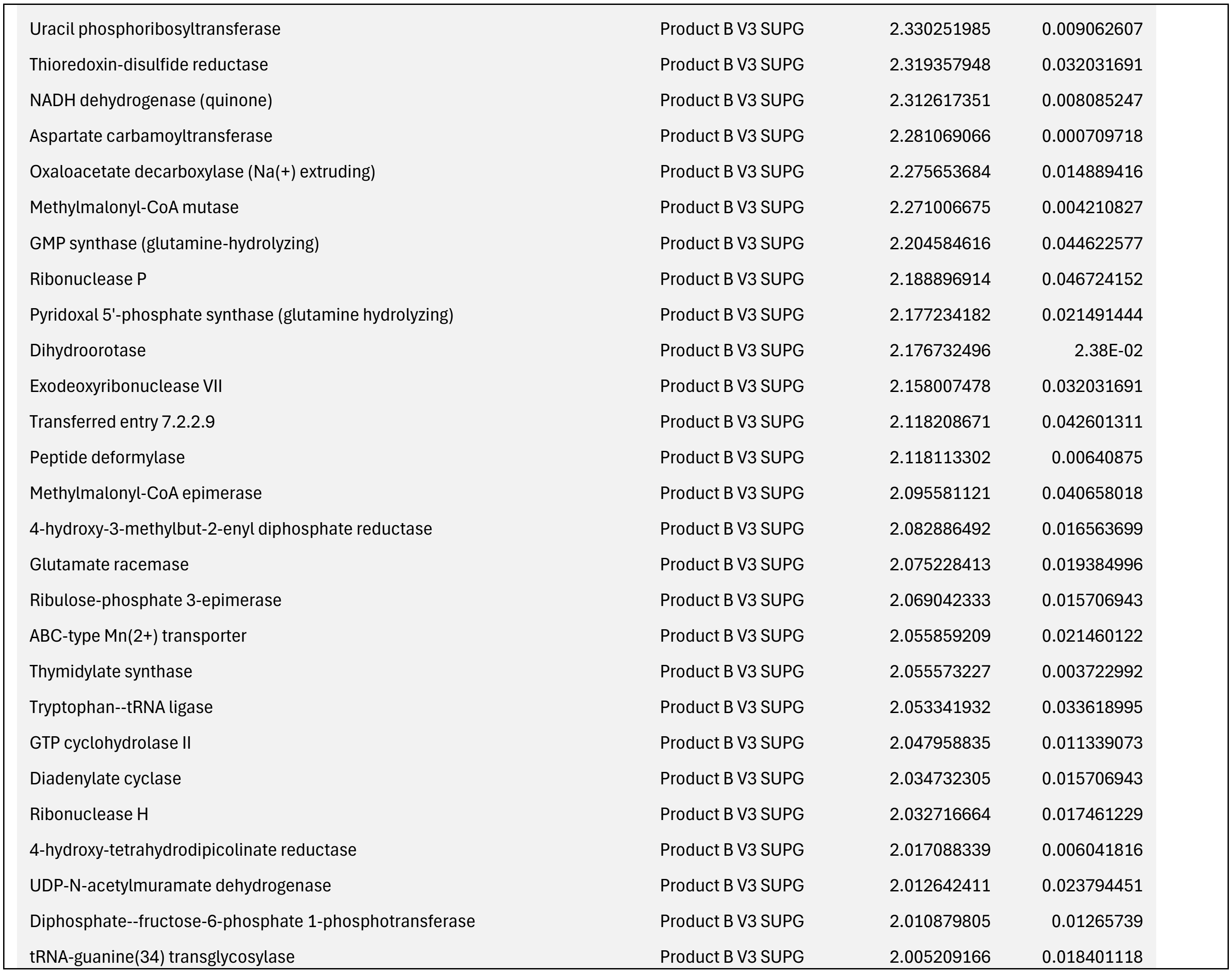
Beta Diversity (EC)

Bray-Curtis PERMNOVA p = 0.166	

Differential Abundance (LEfSe) (EC)



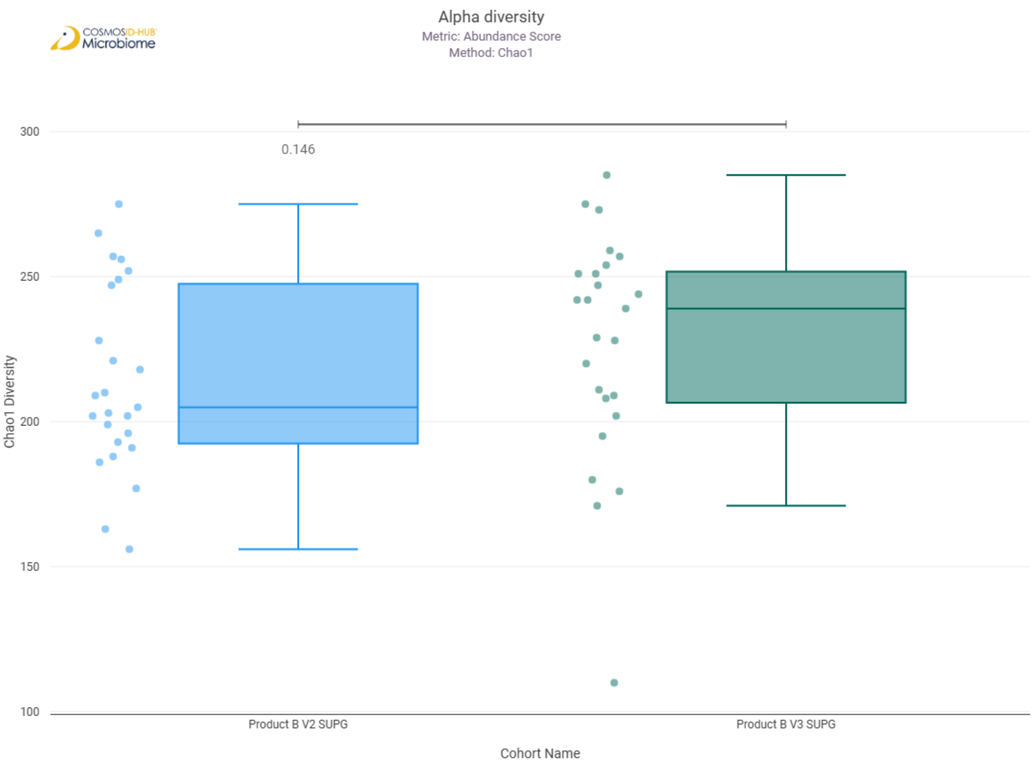
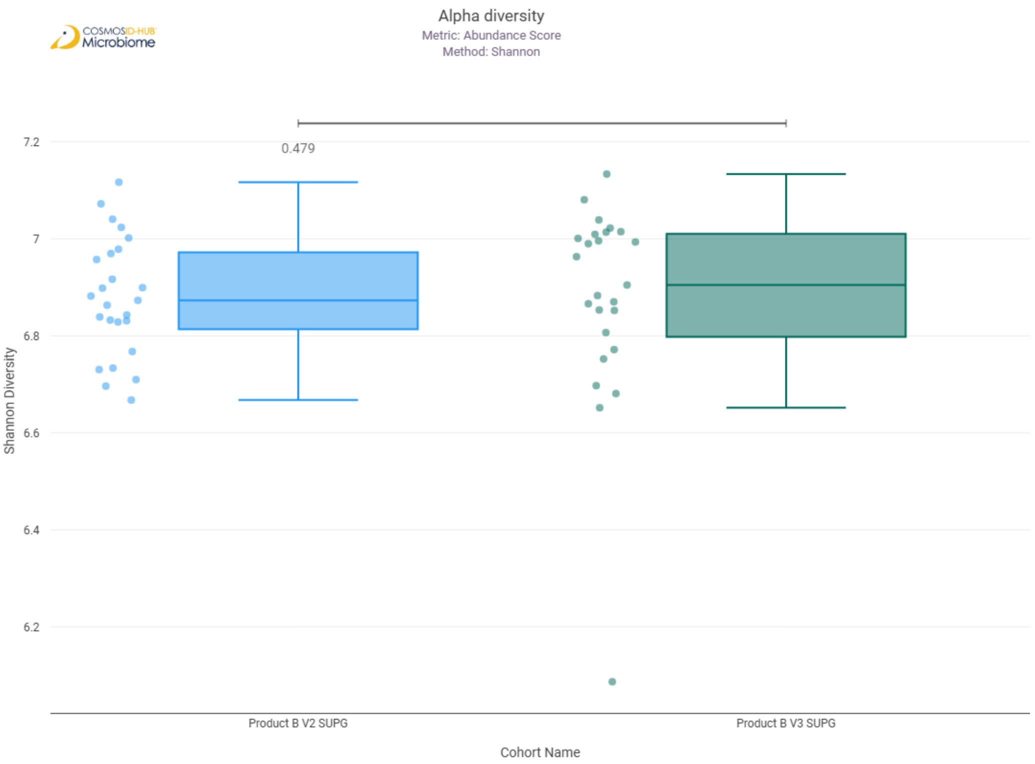
Feature	Enriched Cohort	LDA Score	P-value
Transaldolase	Product B V2 SUPG	2.390769552	0.042601311
L-lactate dehydrogenase (cytochrome)	Product B V2 SUPG	2.105776673	0.005364191
Dihydrolipoyllysine-residue acetyltransferase	Product B V2 SUPG	2.07600155	0.0352731
Pyroglutamyl-peptidase I	Product B V2 SUPG	2.053847965	0.033618995
NAD(P)(+) transhydrogenase (Re/Si-specific)	Product B V2 SUPG	2.017837527	1.72E-04
Triose-phosphate isomerase	Product B V3 SUPG	2.729787667	0.042601311
Galactose-6-phosphate isomerase	Product B V3 SUPG	2.708214701	0.048908406
Endopeptidase Clp	Product B V3 SUPG	2.613478253	0.000428923
6-phosphofructokinase	Product B V3 SUPG	2.599739158	0.033618995
Carbamoyl-phosphate synthase (glutamine-hydrolyzing)	Product B V3 SUPG	2.547124164	0.010726809
Orotate phosphoribosyltransferase	Product B V3 SUPG	2.453677511	0.003722992
UMP kinase	Product B V3 SUPG	2.353643566	0.006795613
Tagatose-6-phosphate kinase	Product B V3 SUPG	2.348135378	0.040658018
N-acetylmuramoyl-L-alanine amidase	Product B V3 SUPG	2.34005959	0.008085247

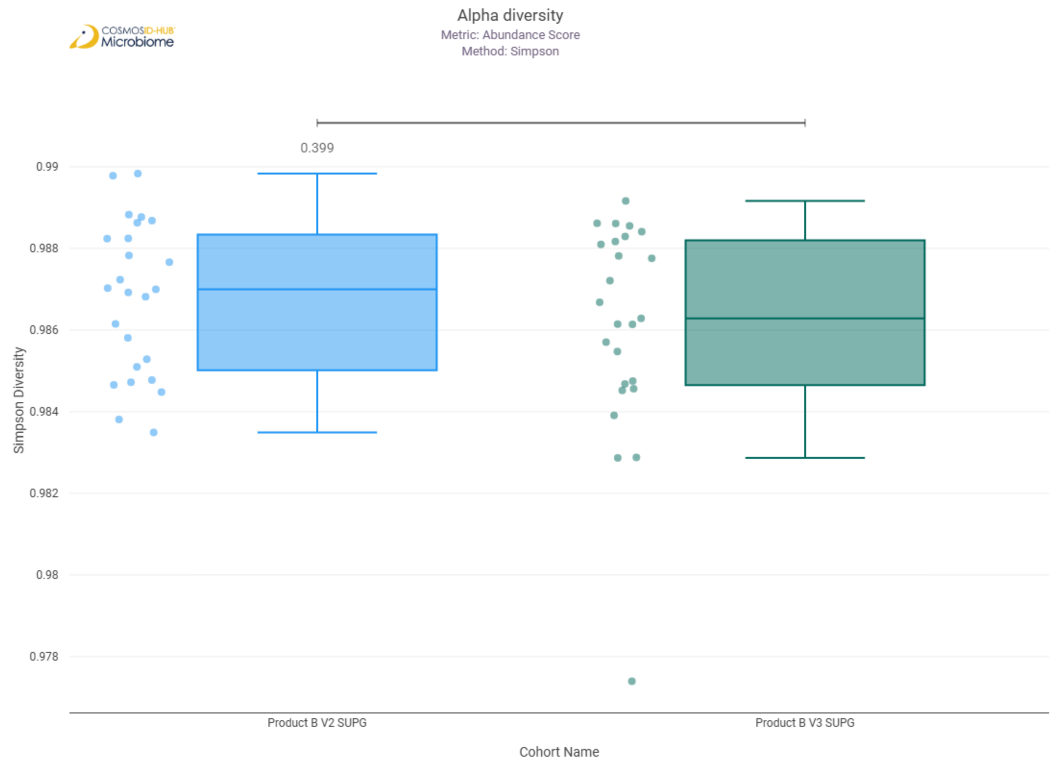


Uracil phosphoribosyltransferase	Product B V3 SUPG	2.330251985	0.009062607
Thioredoxin-disulfide reductase	Product B V3 SUPG	2.319357948	0.032031691
NADH dehydrogenase (quinone)	Product B V3 SUPG	2.312617351	0.008085247
Aspartate carbamoyltransferase	Product B V3 SUPG	2.281069066	0.000709718
Oxaloacetate decarboxylase (Na(+) extruding)	Product B V3 SUPG	2.275653684	0.014889416
Methylmalonyl-CoA mutase	Product B V3 SUPG	2.271006675	0.004210827
GMP synthase (glutamine-hydrolyzing)	Product B V3 SUPG	2.204584616	0.044622577
Ribonuclease P	Product B V3 SUPG	2.188896914	0.046724152
Pyridoxal 5'-phosphate synthase (glutamine hydrolyzing)	Product B V3 SUPG	2.177234182	0.021491444
Dihydroorotase	Product B V3 SUPG	2.176732496	2.38E-02
Exodeoxyribonuclease VII	Product B V3 SUPG	2.158007478	0.032031691
Transferred entry 7.2.2.9	Product B V3 SUPG	2.118208671	0.042601311
Peptide deformylase	Product B V3 SUPG	2.118113302	0.00640875
Methylmalonyl-CoA epimerase	Product B V3 SUPG	2.095581121	0.040658018
4-hydroxy-3-methylbut-2-enyl diphosphate reductase	Product B V3 SUPG	2.082886492	0.016563699
Glutamate racemase	Product B V3 SUPG	2.075228413	0.019384996
Ribulose-phosphate 3-epimerase	Product B V3 SUPG	2.069042333	0.015706943
ABC-type Mn(2+) transporter	Product B V3 SUPG	2.055859209	0.021460122
Thymidylate synthase	Product B V3 SUPG	2.055573227	0.003722992
Tryptophan--tRNA ligase	Product B V3 SUPG	2.053341932	0.033618995
GTP cyclohydrolase II	Product B V3 SUPG	2.047958835	0.011339073
Diadenylate cyclase	Product B V3 SUPG	2.034732305	0.015706943
Ribonuclease H	Product B V3 SUPG	2.032716664	0.017461229
4-hydroxy-tetrahydrodipicolinate reductase	Product B V3 SUPG	2.017088339	0.006041816
UDP-N-acetylmuramate dehydrogenase	Product B V3 SUPG	2.012642411	0.023794451
Diphosphate--fructose-6-phosphate 1-phosphotransferase	Product B V3 SUPG	2.010879805	0.01265739
tRNA-guanine(34) transglycosylase	Product B V3 SUPG	2.005209166	0.018401118

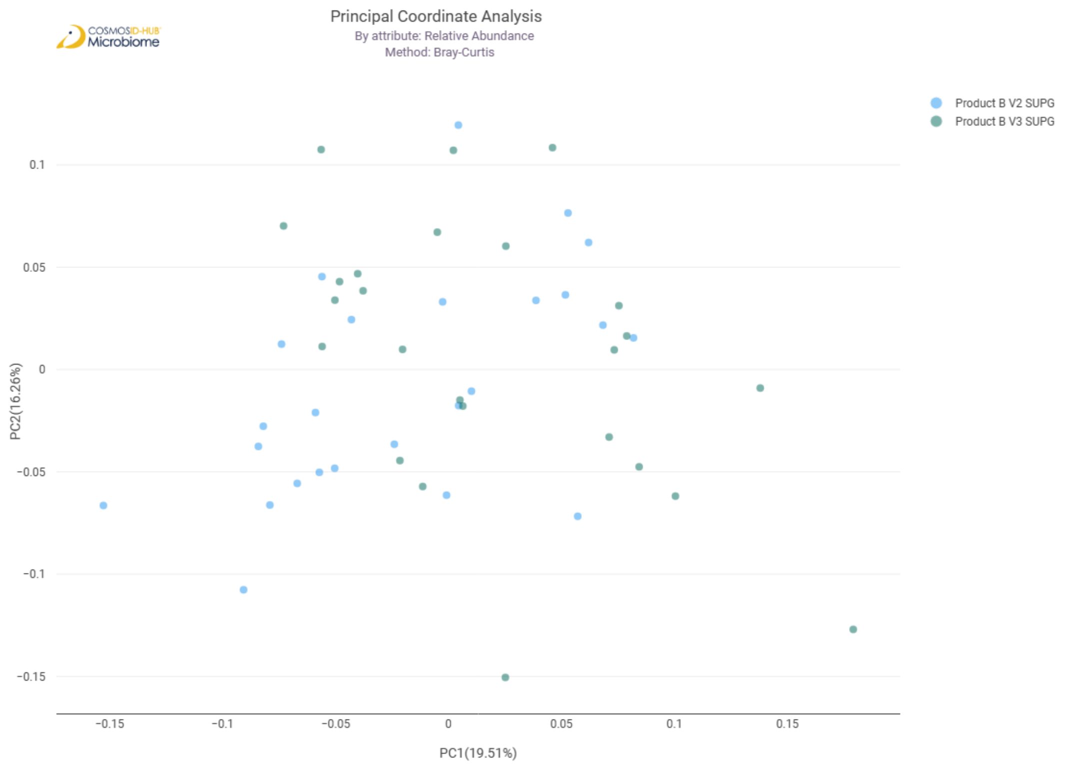
MetaCyc Pathways

Alpha Diversity (MetaCyc)

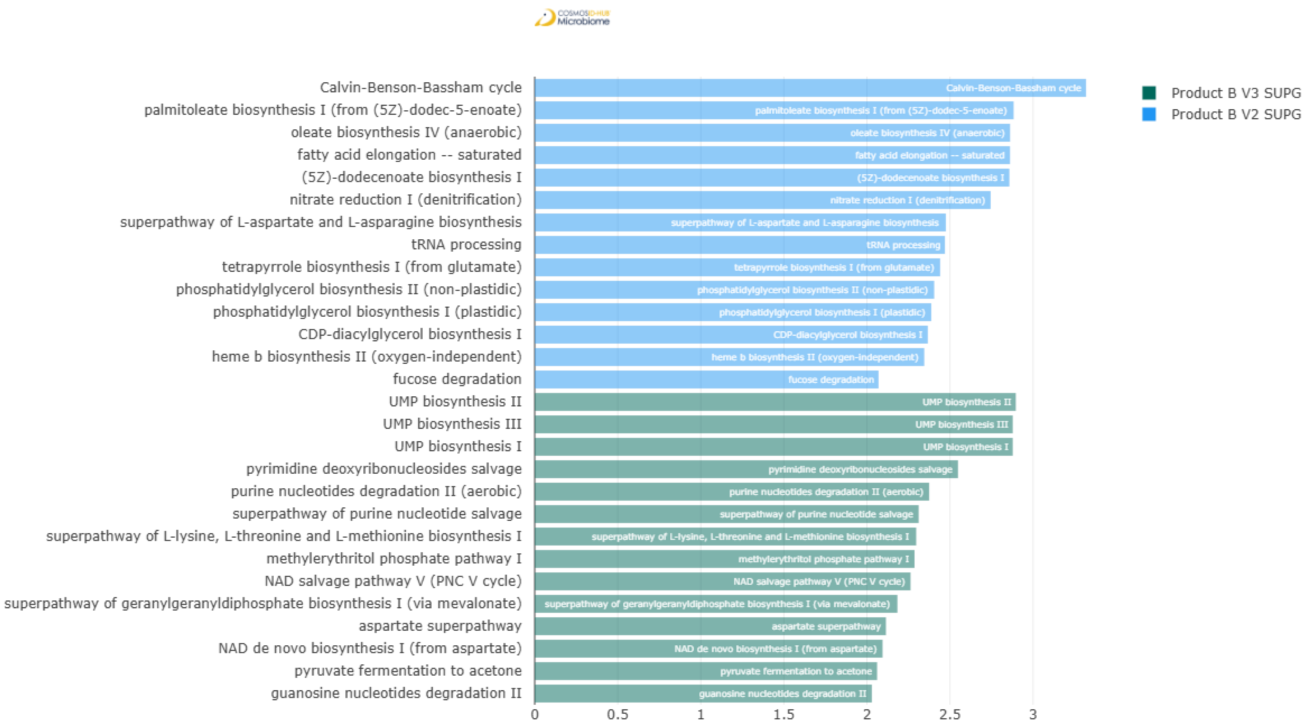
Chao1	
Shannon	

Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis PERMNOVA p = 0.044	

Differential Abundance (LEfSe) (MetaCyc)



Feature	Enriched Cohort	LDA Score	P-value
Calvin-Benson-Bassham cycle	Product B V2 SUPG	3.318964082	0.002102544
palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate)	Product B V2 SUPG	2.883013913	0.018401118
oleate biosynthesis IV (anaerobic)	Product B V2 SUPG	2.86144877	0.020414533
fatty acid elongation -- saturated	Product B V2 SUPG	2.861077094	0.022617484
(5Z)-dodecenoate biosynthesis I	Product B V2 SUPG	2.857405063	0.025024185
nitrate reduction I (denitrification)	Product B V2 SUPG	2.744568111	0.022585015
superpathway of L-aspartate and L-asparagine biosynthesis	Product B V2 SUPG	2.474947946	0.026308569
tRNA processing	Product B V2 SUPG	2.469238055	0.029067013
tetrapyrrole biosynthesis I (from glutamate)	Product B V2 SUPG	2.440540879	0.039710137
phosphatidylglycerol biosynthesis II (non-plastidic)	Product B V2 SUPG	2.404869686	0.044602091
phosphatidylglycerol biosynthesis I (plastidic)	Product B V2 SUPG	2.387244196	0.048902981
CDP-diacylglycerol biosynthesis I	Product B V2 SUPG	2.366479671	0.048902981
heme b biosynthesis II (oxygen-independent)	Product B V2 SUPG	2.344926162	0.013357193
fucose degradation	Product B V2 SUPG	2.069795282	0.032608192
UMP biosynthesis II	Product B V3 SUPG	2.896161476	0.001077834
UMP biosynthesis I	Product B V3 SUPG	2.877911888	0.002243495
UMP biosynthesis III	Product B V3 SUPG	2.877911888	2.24E-03
pyrimidine deoxyribonucleosides salvage	Product B V3 SUPG	2.548343874	0.020414533
purine nucleotides degradation II (aerobic)	Product B V3 SUPG	2.374685324	0.012279495
superpathway of purine nucleotide salvage	Product B V3 SUPG	2.311473792	0.021218334
superpathway of L-lysine, L-threonine and L-methionine biosynthesis I	Product B V3 SUPG	2.296487754	0.042729021
methylerythritol phosphate pathway I	Product B V3 SUPG	2.286396655	0.033576403

NAD salvage pathway V (PNC V cycle)	Product B V3 SUPG	2.262555783	0.007877552
superpathway of geranylgeranyldiphosphate biosynthesis I (via mevalonate)	Product B V3 SUPG	2.183446506	0.037096259
aspartate superpathway	Product B V3 SUPG	2.114483365	1.29E-02
NAD de novo biosynthesis I (from aspartate)	Product B V3 SUPG	2.094212339	0.018497446
pyruvate fermentation to acetone	Product B V3 SUPG	2.061285087	0.040706043
guanosine nucleotides degradation II	Product B V3 SUPG	2.029587133	0.011292706

Comparison 15: Product A V2 SUPG vs Product B V2 SUPG

Gene Ontology

Alpha Diversity (GO)

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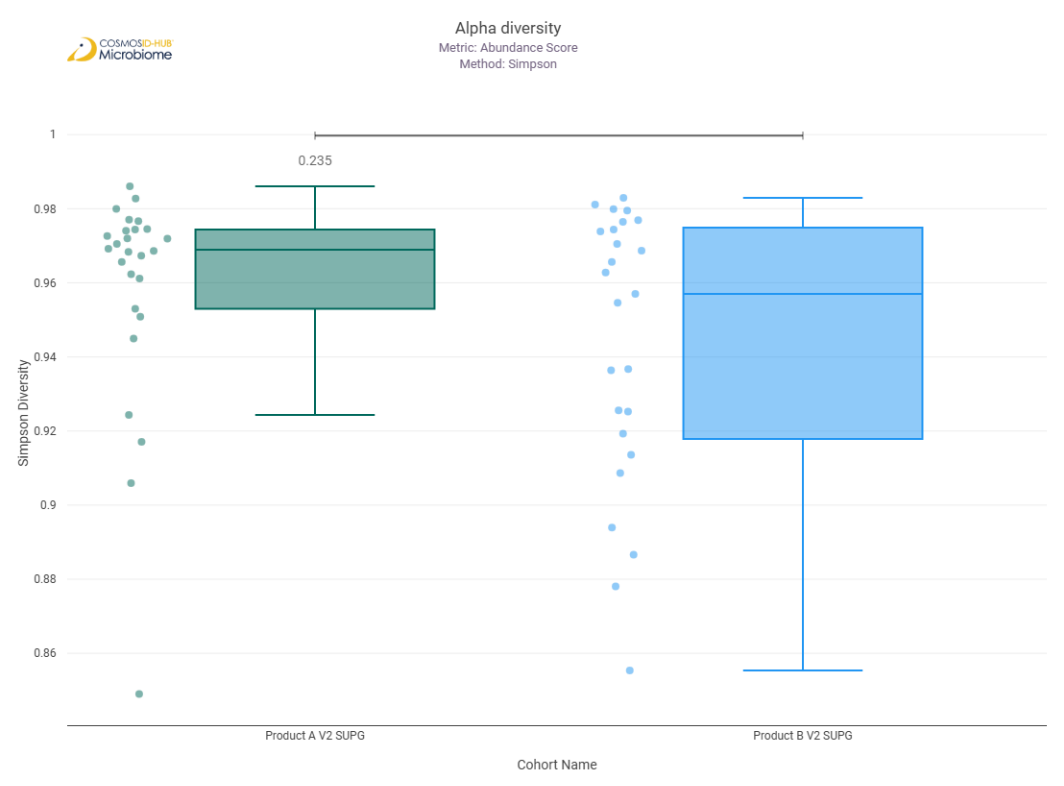
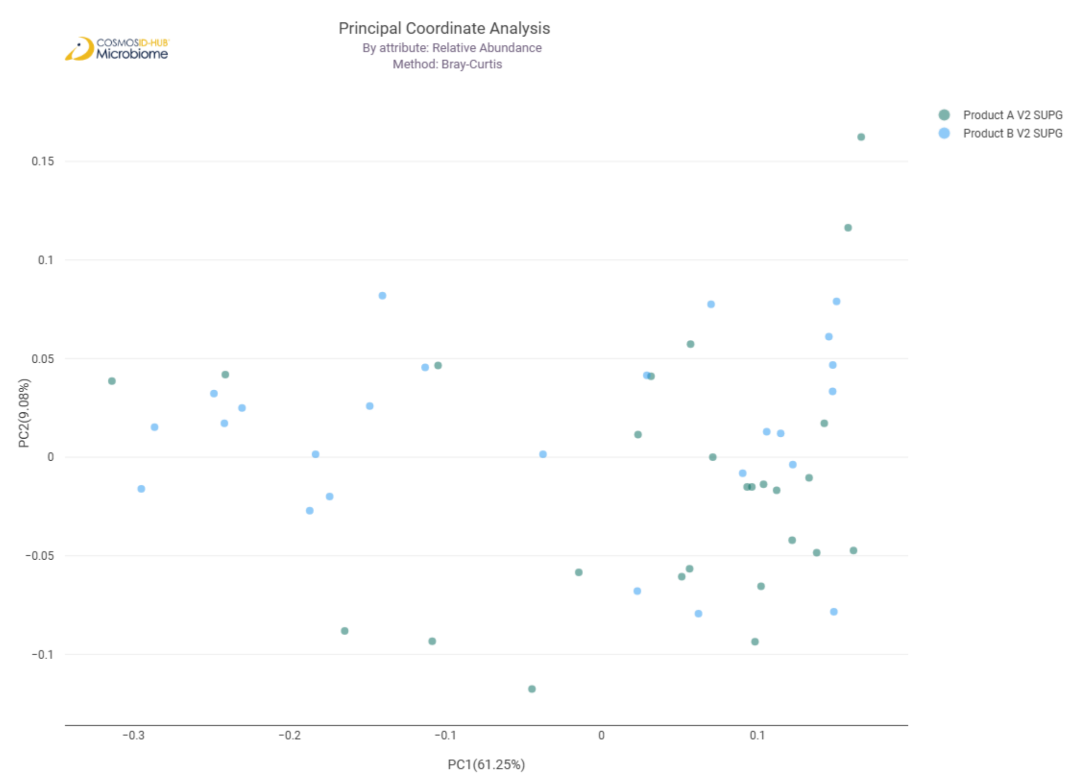
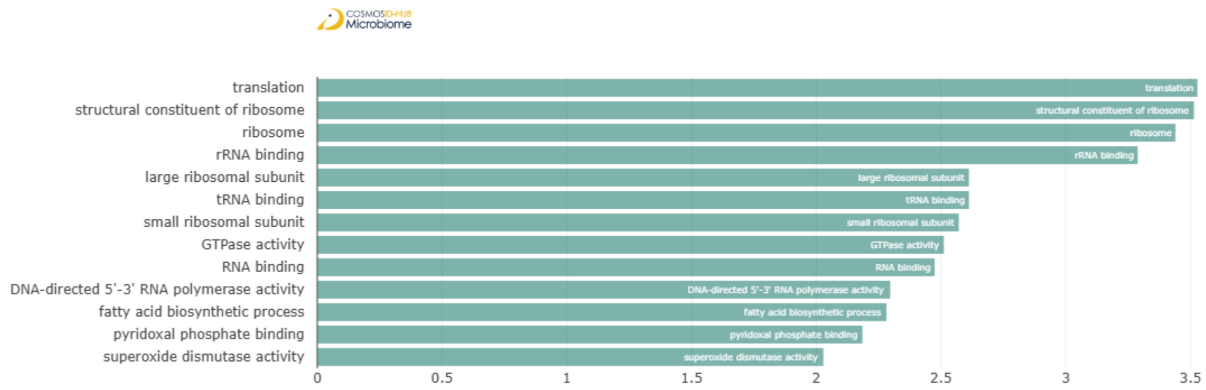
Simpson	

Beta Diversity (GO)

Bray-Curtis PERMNOVA p = 0.067	

Differential Abundance (LEfSe) (GO)



Feature	Enriched Cohort	LDA Score	P-value
translation	Product A V2 SUPG	3.528322109	0.020471389
structural constituent of ribosome	Product A V2 SUPG	3.514165407	0.022613046
ribosome	Product A V2 SUPG	3.439853578	0.017590793
rRNA binding	Product A V2 SUPG	3.288581331	0.033240045
large ribosomal subunit	Product A V2 SUPG	2.612173486	0.02494682
tRNA binding	Product A V2 SUPG	2.612099379	0.047879765
small ribosomal subunit	Product A V2 SUPG	2.571517429	0.034829974
GTPase activity	Product A V2 SUPG	2.511887932	0.036484395
RNA binding	Product A V2 SUPG	2.474828575	0.022613046
DNA-directed 5'-3' RNA polymerase activity	Product A V2 SUPG	2.296592301	0.038205314
fatty acid biosynthetic process	Product A V2 SUPG	2.281471017	0.009840467
pyridoxal phosphate binding	Product A V2 SUPG	2.185362531	0.036484395
superoxide dismutase activity	Product A V2 SUPG	2.028763107	0.020471389

Enzyme Commission

Alpha Diversity (EC)

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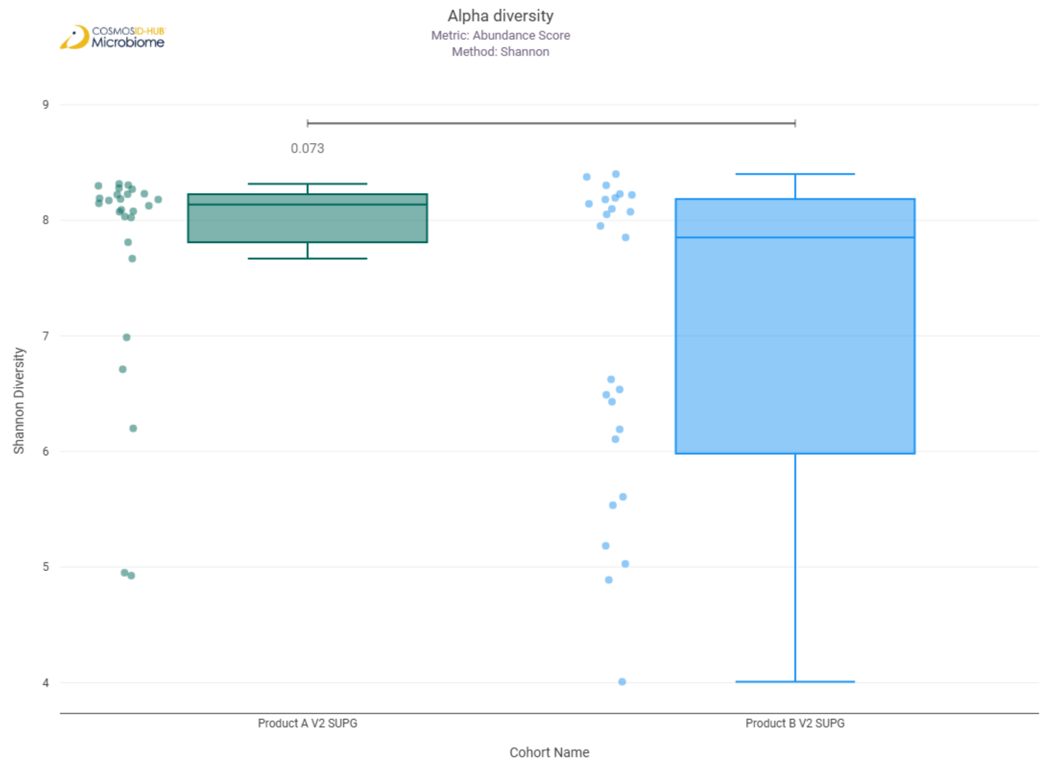

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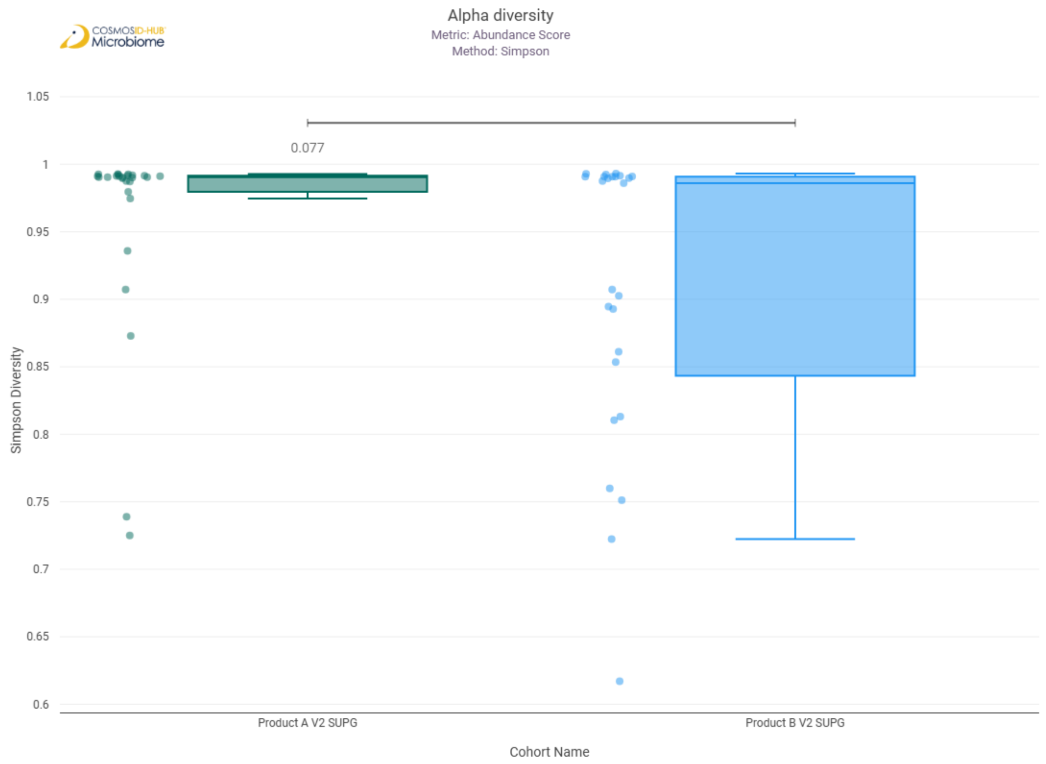
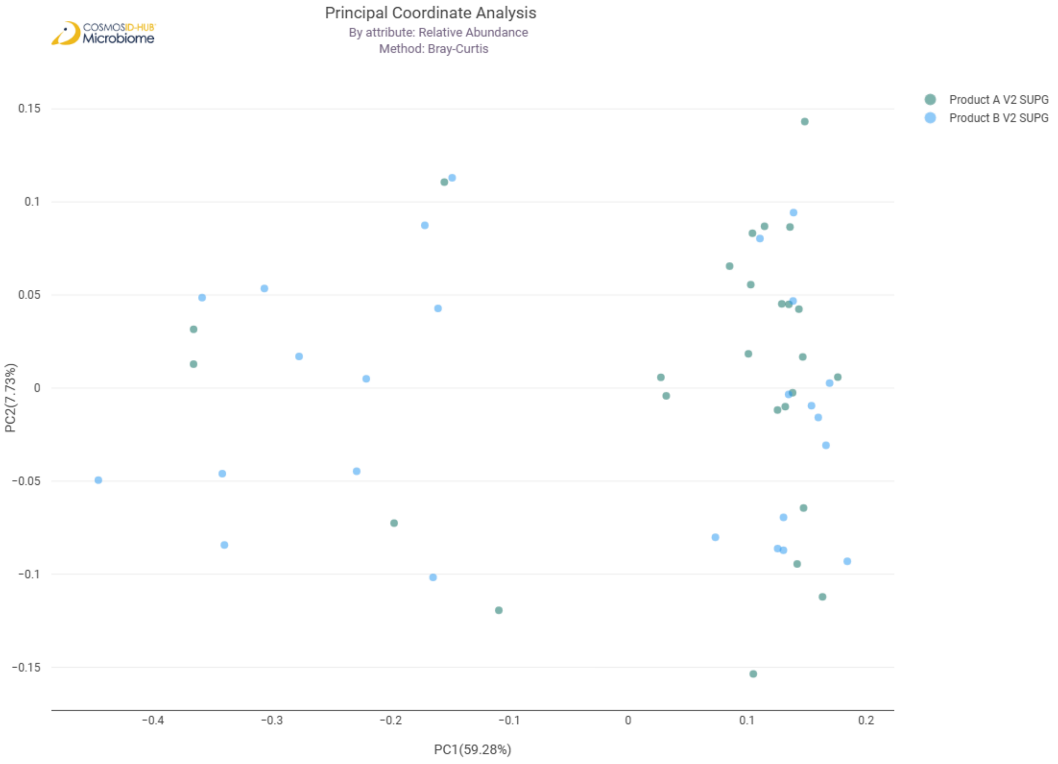
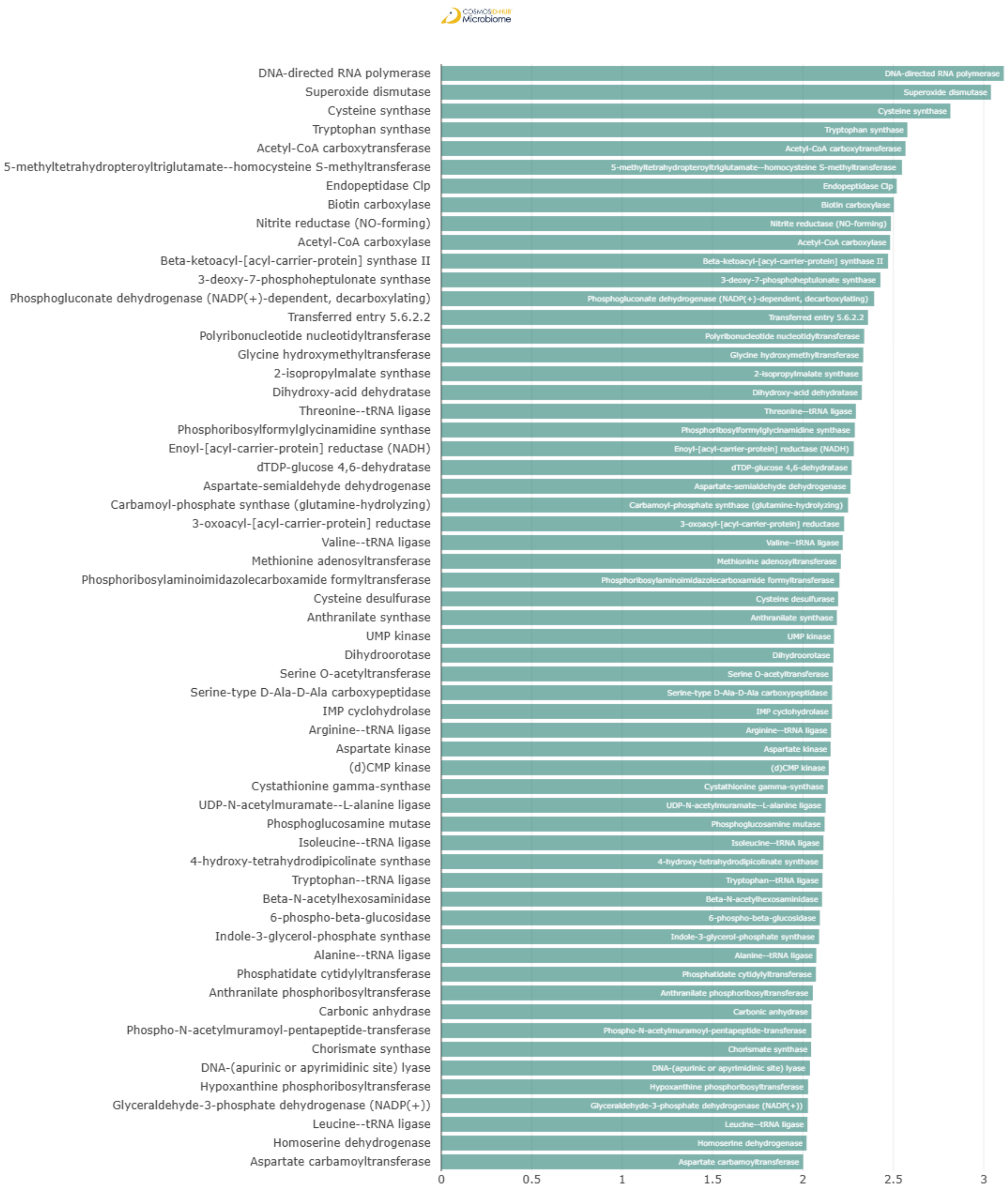
Simpson	

Beta Diversity (EC)

Bray-Curtis PERMNOVA p = 0.036	

Differential Abundance (LEfSe) (EC)



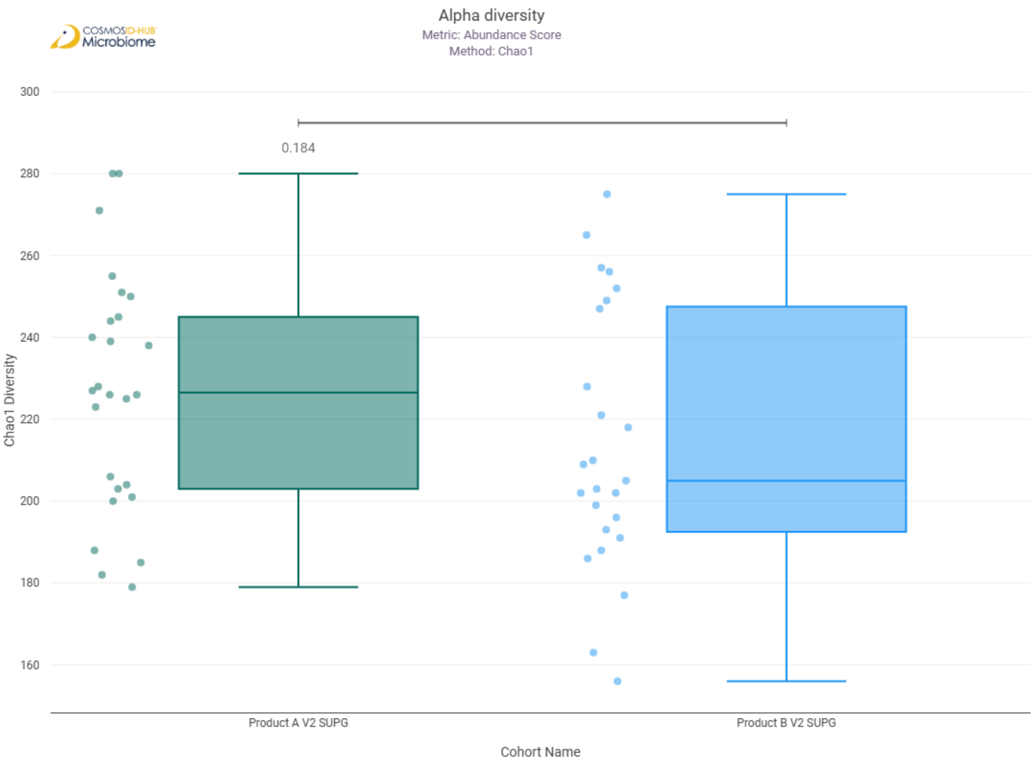
Feature	Enriched Cohort	LDA Score	P-value
DNA-directed RNA polymerase	Product A V2 SUPG	3.111020333	0.02375508
Superoxide dismutase	Product A V2 SUPG	3.040013385	0.011574483
Cysteine synthase	Product A V2 SUPG	2.815737109	0.001548196
Tryptophan synthase	Product A V2 SUPG	2.577744157	0.000276314

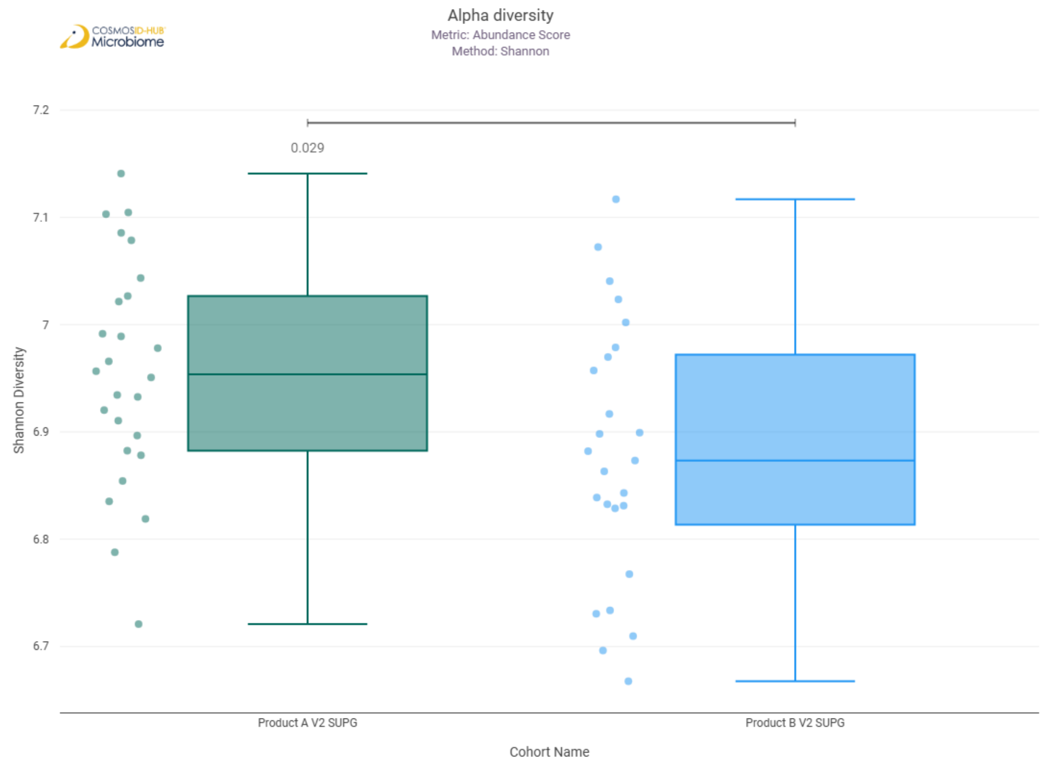
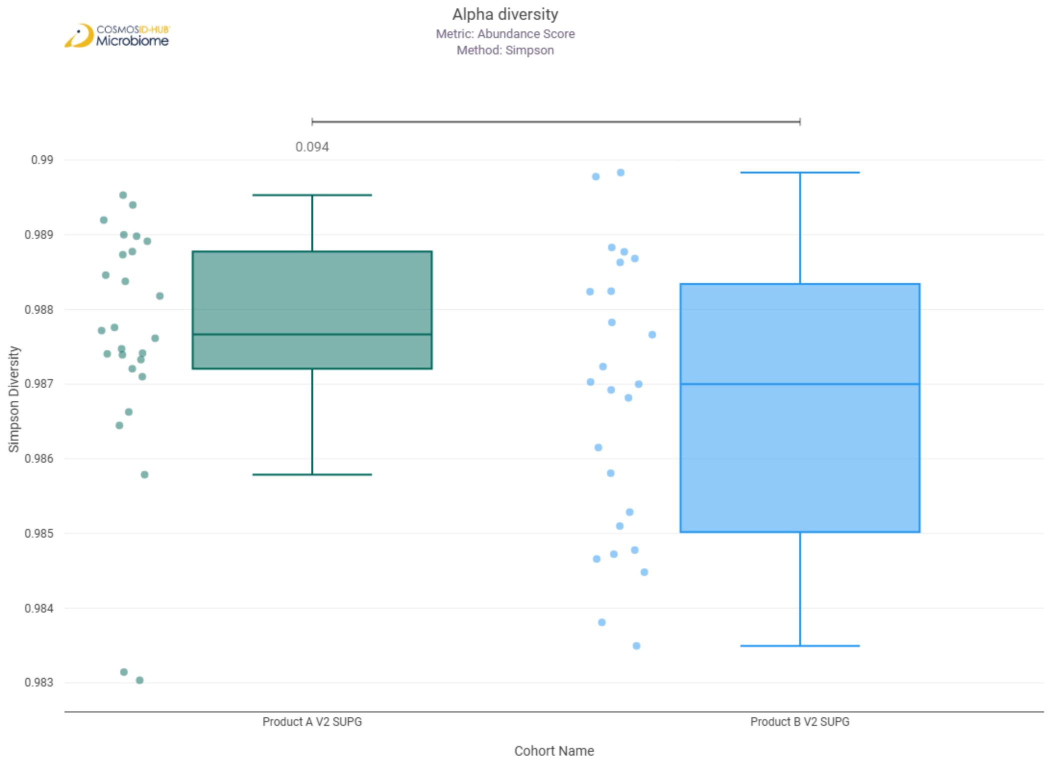
Acetyl-CoA carboxytransferase	Product A V2 SUPG	2.567719746	0.007889693
5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	Product A V2 SUPG	2.547962006	0.036484395
Endopeptidase Clp	Product A V2 SUPG	2.518826283	0.006292761
Biotin carboxylase	Product A V2 SUPG	2.502821472	0.015873756
Nitrite reductase (NO-forming)	Product A V2 SUPG	2.486578655	0.030245812
Acetyl-CoA carboxylase	Product A V2 SUPG	2.482112113	0.038205314
Beta-ketoacyl-[acyl-carrier-protein] synthase II	Product A V2 SUPG	2.471132956	0.016712924
3-deoxy-7-phosphoheptulonate synthase	Product A V2 SUPG	2.428626553	0.020471389
Phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating)	Product A V2 SUPG	2.393945069	0.039994768
Transferred entry 5.6.2.2	Product A V2 SUPG	2.360090893	0.010968497
Polyribonucleotide nucleotidyltransferase	Product A V2 SUPG	2.339073295	0.034829974
Glycine hydroxymethyltransferase	Product A V2 SUPG	2.334029314	0.038205314
2-isopropylmalate synthase	Product A V2 SUPG	2.328902169	1.43E-02
Dihydroxy-acid dehydratase	Product A V2 SUPG	2.325621312	0.015873756
Threonine--tRNA ligase	Product A V2 SUPG	2.293236056	0.016712924
Phosphoribosylformylglycinamidine synthase	Product A V2 SUPG	2.287096387	0.02375508
Enoyl-[acyl-carrier-protein] reductase (NADH)	Product A V2 SUPG	2.281565459	0.013574437
dTDP-glucose 4,6-dehydratase	Product A V2 SUPG	2.269477405	0.005941992
Aspartate-semialdehyde dehydrogenase	Product A V2 SUPG	2.263052348	0.012209995
Carbamoyl-phosphate synthase (glutamine-hydrolyzing)	Product A V2 SUPG	2.249725795	0.010968497
3-oxoacyl-[acyl-carrier-protein] reductase	Product A V2 SUPG	2.228019455	4.58E-02
Valine--tRNA ligase	Product A V2 SUPG	2.220189052	0.005608941
Methionine adenosyltransferase	Product A V2 SUPG	2.210159621	0.002416555
Phosphoribosylaminoimidazolecarboxamide formyltransferase	Product A V2 SUPG	2.202152483	0.00881699
Cysteine desulfurase	Product A V2 SUPG	2.194846541	0.015873756
Anthranilate synthase	Product A V2 SUPG	2.188027235	0.000177114
UMP kinase	Product A V2 SUPG	2.17234657	0.038205314
Dihydroorotase	Product A V2 SUPG	2.169410392	0.02375508
Serine O-acetyltransferase	Product A V2 SUPG	2.164156919	0.031712637
Serine-type D-Ala-D-Ala carboxypeptidase	Product A V2 SUPG	2.161571218	0.026189985
IMP cyclohydrolase	Product A V2 SUPG	2.161164207	0.012209995
Arginine--tRNA ligase	Product A V2 SUPG	2.15520944	0.038205314
Aspartate kinase	Product A V2 SUPG	2.15326488	0.014305878
(d)CMP kinase	Product A V2 SUPG	2.143007637	0.017590793
Cystathionine gamma-synthase	Product A V2 SUPG	2.137563453	0.007889693
UDP-N-acetylmuramate--L-alanine ligase	Product A V2 SUPG	2.125778796	0.02375508
Phosphoglucosamine mutase	Product A V2 SUPG	2.120102518	0.028837668
Isoleucine--tRNA ligase	Product A V2 SUPG	2.113675052	0.002000719
4-hydroxy-tetrahydrodipicolinate synthase	Product A V2 SUPG	2.111127915	0.015071869
Tryptophan--tRNA ligase	Product A V2 SUPG	2.108140128	0.003711399
Beta-N-acetylhexosaminidase	Product A V2 SUPG	2.106142229	0.011574483
6-phospho-beta-glucosidase	Product A V2 SUPG	2.093597012	0.015873756
Indole-3-glycerol-phosphate synthase	Product A V2 SUPG	2.089718618	0.004183032
Alanine--tRNA ligase	Product A V2 SUPG	2.074156106	0.007050729
Phosphatidate cytidylyltransferase	Product A V2 SUPG	2.071961346	0.003711399
Anthranilate phosphoribosyltransferase	Product A V2 SUPG	2.055331504	0.002910155

Carbonic anhydrase	Product A V2 SUPG	2.047193511	0.01946851
Phospho-N-acetylmuramoyl-pentapeptide-transferase	Product A V2 SUPG	2.04715419	0.045795182
Chorismate synthase	Product A V2 SUPG	2.045269032	0.034829974
DNA-(apurinic or apyrimidinic site) lyase	Product A V2 SUPG	2.039280143	0.015071869
Hypoxanthine phosphoribosyltransferase	Product A V2 SUPG	2.028740275	0.039994768
Glyceraldehyde-3-phosphate dehydrogenase (NADP(+))	Product A V2 SUPG	2.027884467	0.012762404
Leucine--tRNA ligase	Product A V2 SUPG	2.025092427	0.028837668
Homoserine dehydrogenase	Product A V2 SUPG	2.020459585	0.010390869
Aspartate carbamoyltransferase	Product A V2 SUPG	2.001420241	0.00745964

MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1	

Shannon	
Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis

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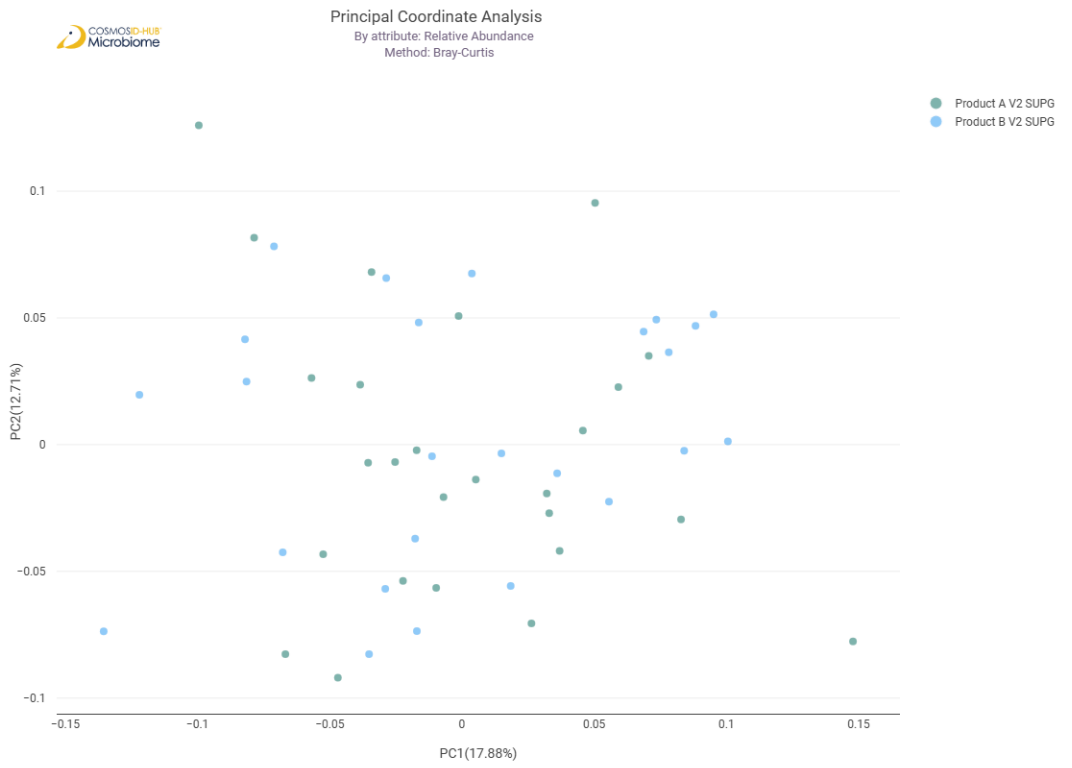
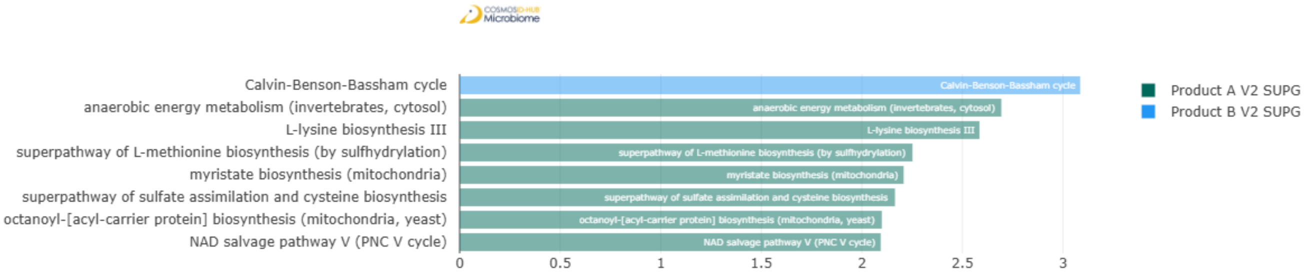


Differential Abundance (LEfSe) (MetaCyc)

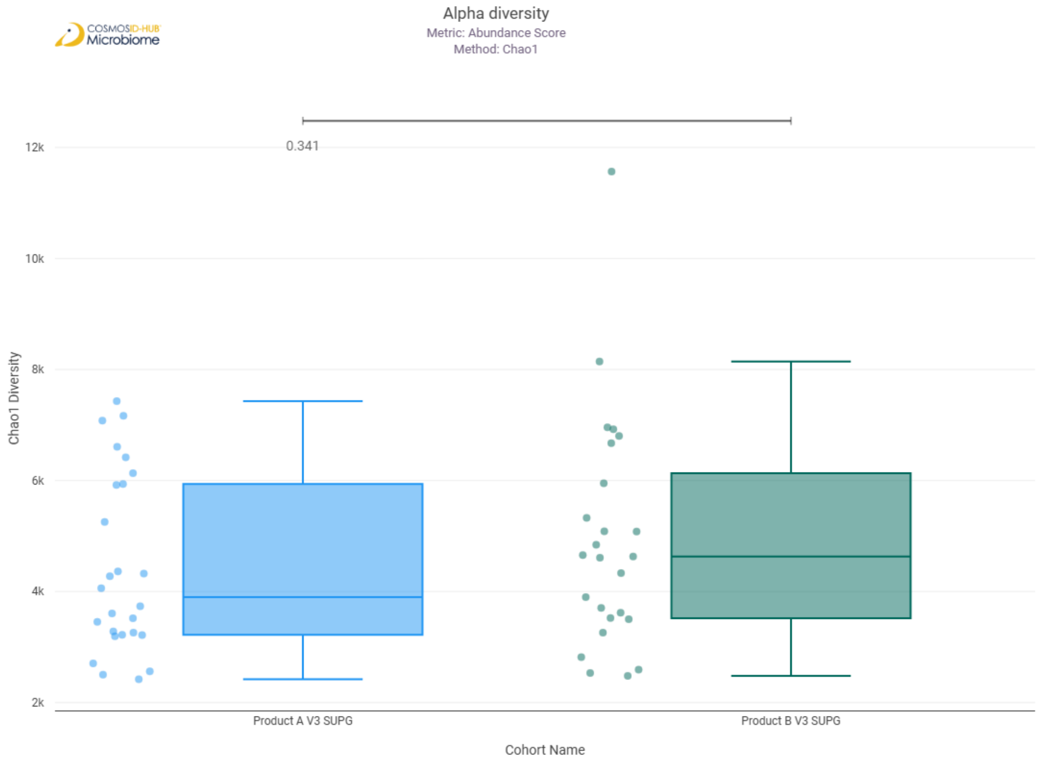
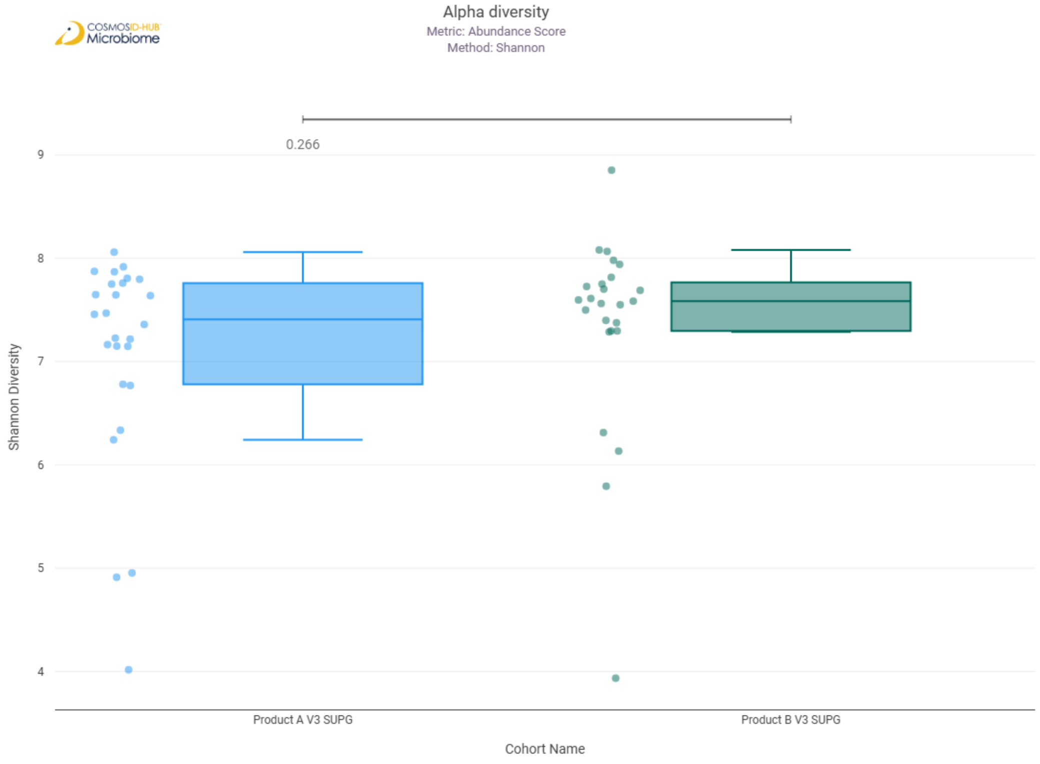


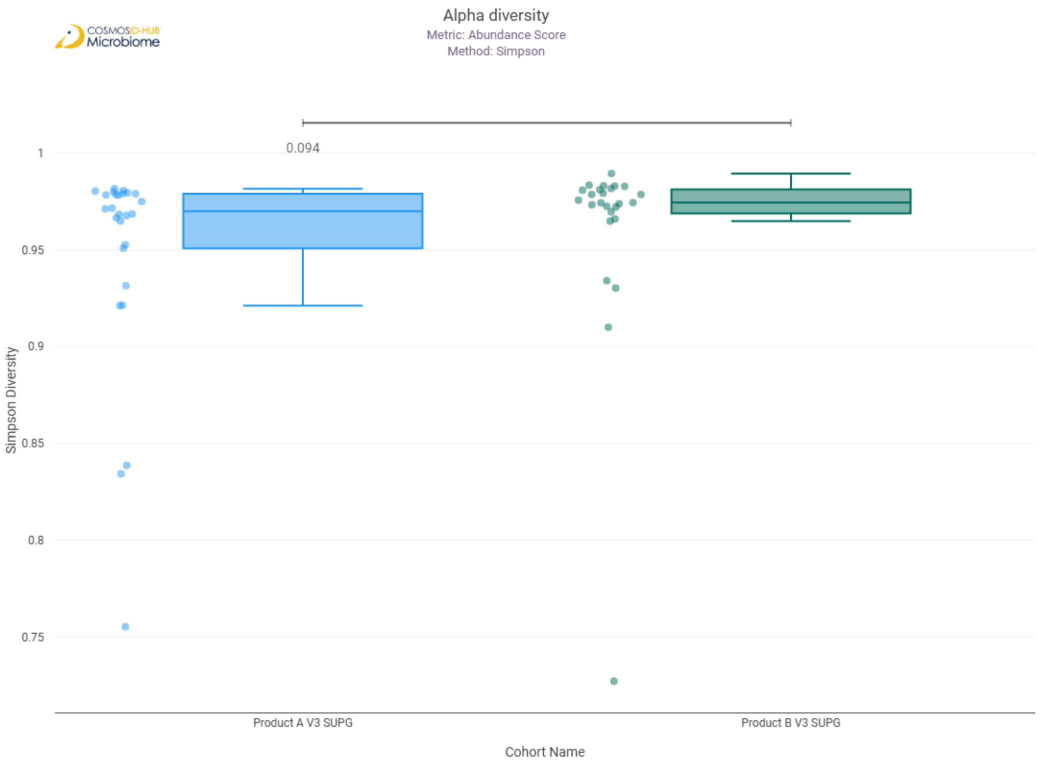
Feature	Enriched Cohort	LDA Score	P-value
Calvin-Benson-Bassham cycle	Product B V2 SUPG	3.085510466	0.047879765
anaerobic energy metabolism (invertebrates, cytosol)	Product A V2 SUPG	2.693616266	0.018508823
L-lysine biosynthesis III	Product A V2 SUPG	2.584864736	0.012209995
superpathway of L-methionine biosynthesis (by sulfhydrylation)	Product A V2 SUPG	2.251777445	0.005206458
myristate biosynthesis (mitochondria)	Product A V2 SUPG	2.207702327	0.001041621
superpathway of sulfate assimilation and cysteine biosynthesis	Product A V2 SUPG	2.164724922	0.003030685
octanoyl-[acyl-carrier protein] biosynthesis (mitochondria, yeast)	Product A V2 SUPG	2.099384673	0.005433155
NAD salvage pathway V (PNC V cycle)	Product A V2 SUPG	2.093878625	0.03882039

Comparison 16: Product A V3 SUPG vs Product B V3 SUPG

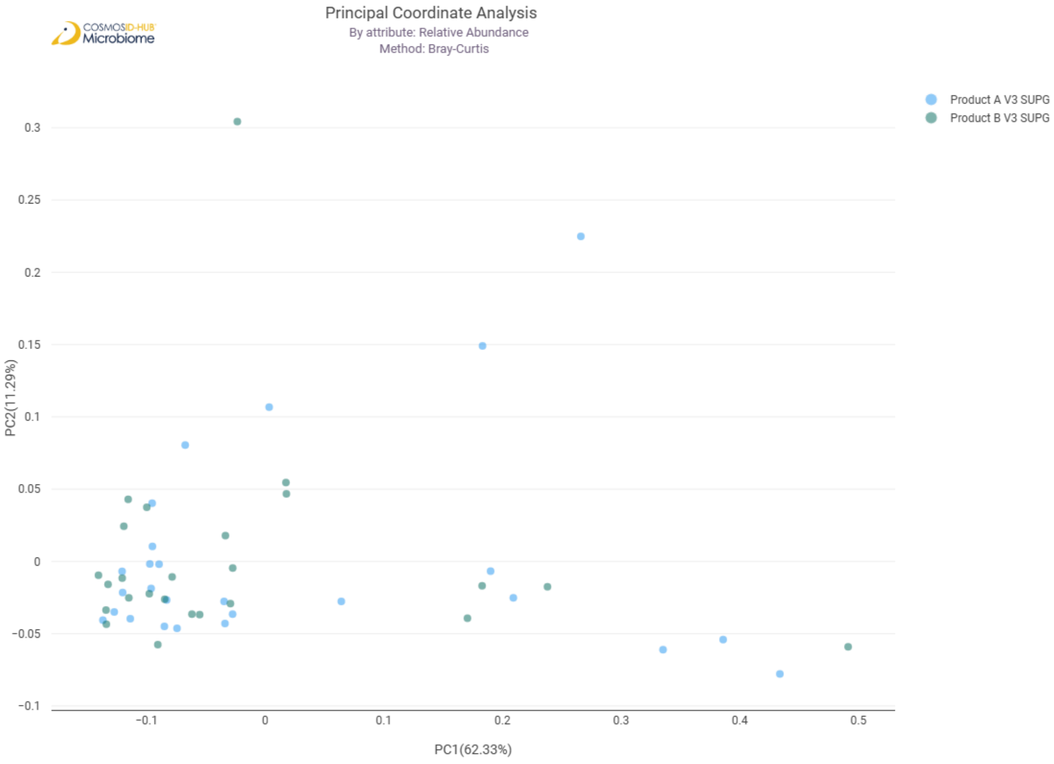
Gene Ontology

Alpha Diversity (GO)

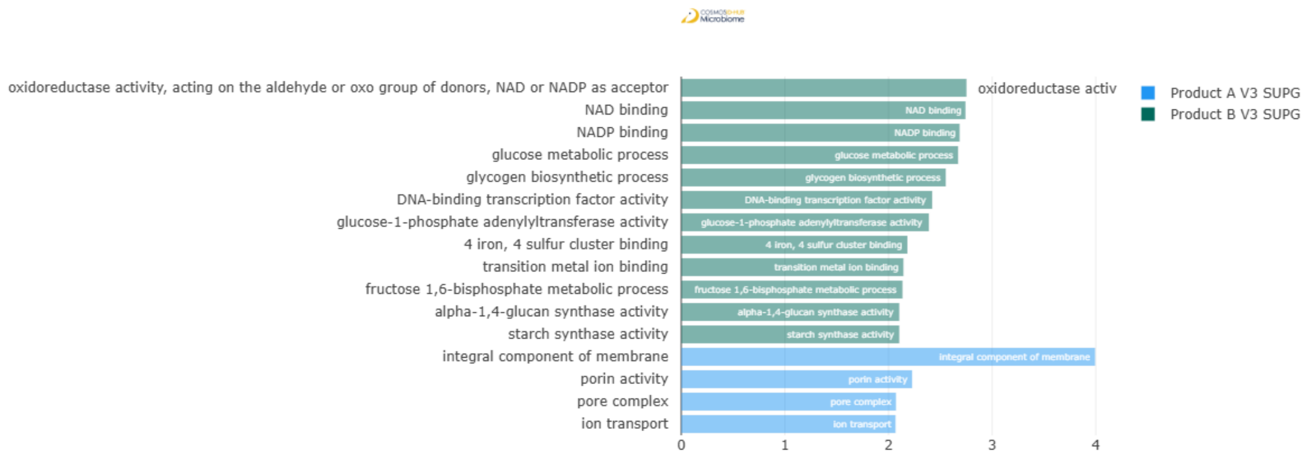
Chao1	
Shannon	

Simpson	

Beta Diversity (GO)

Bray-Curtis PERMNOVA p = 0.323	

Differential Abundance (LEfSe) (GO)



Feature	Enriched Cohort	LDA Score	P-value
oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	Product B V3 SUPG	2.752474797	0.012209995
NAD binding	Product B V3 SUPG	2.742648085	0.027486336
NADP binding	Product B V3 SUPG	2.686305478	0.013574437
glucose metabolic process	Product B V3 SUPG	2.671540978	0.015071869
glycogen biosynthetic process	Product B V3 SUPG	2.552404183	0.015873756
DNA-binding transcription factor activity	Product B V3 SUPG	2.42153675	0.020471389
glucose-1-phosphate adenylyltransferase activity	Product B V3 SUPG	2.389556209	0.011574483
4 iron, 4 sulfur cluster binding	Product B V3 SUPG	2.182217095	0.031712637
transition metal ion binding	Product B V3 SUPG	2.143807206	0.022613046
fructose 1,6-bisphosphate metabolic process	Product B V3 SUPG	2.135242629	0.02494682
starch synthase activity	Product B V3 SUPG	2.103901259	0.010390869
alpha-1,4-glucan synthase activity	Product B V3 SUPG	2.103901259	0.010390869
integral component of membrane	Product A V3 SUPG	3.993290893	0.030245812
porin activity	Product A V3 SUPG	2.227729313	0.000425892
pore complex	Product A V3 SUPG	2.071930111	0.004438681
ion transport	Product A V3 SUPG	2.067516171	0.004438681

Enzyme Commission

Alpha Diversity (EC)

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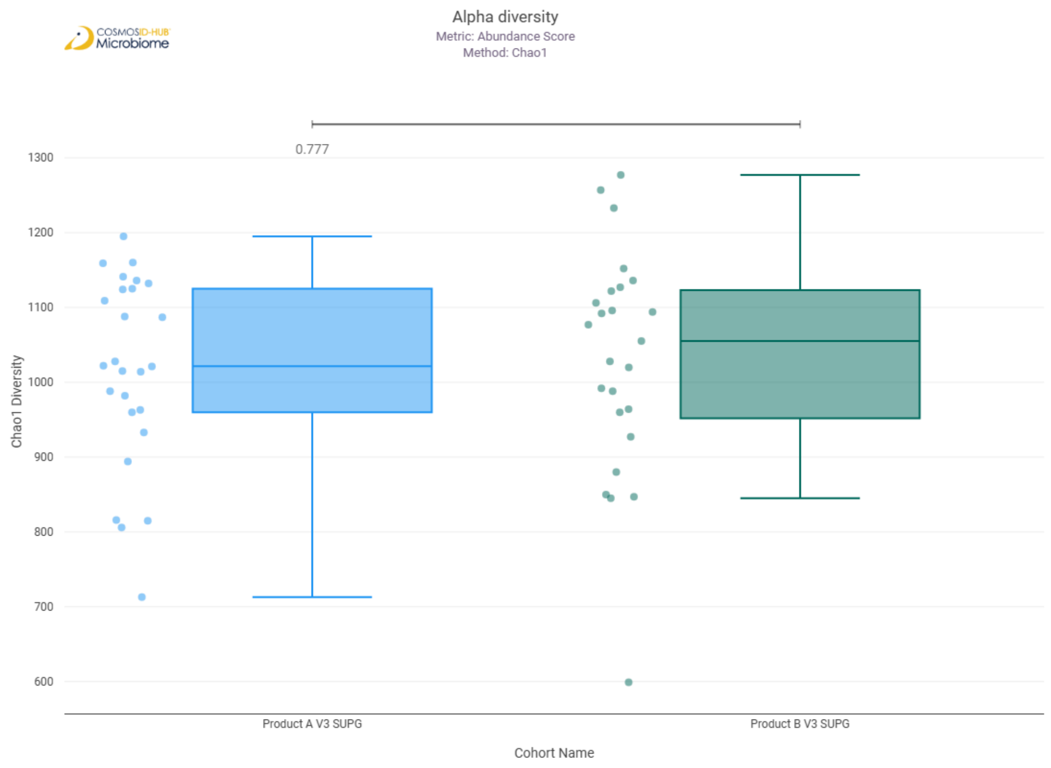

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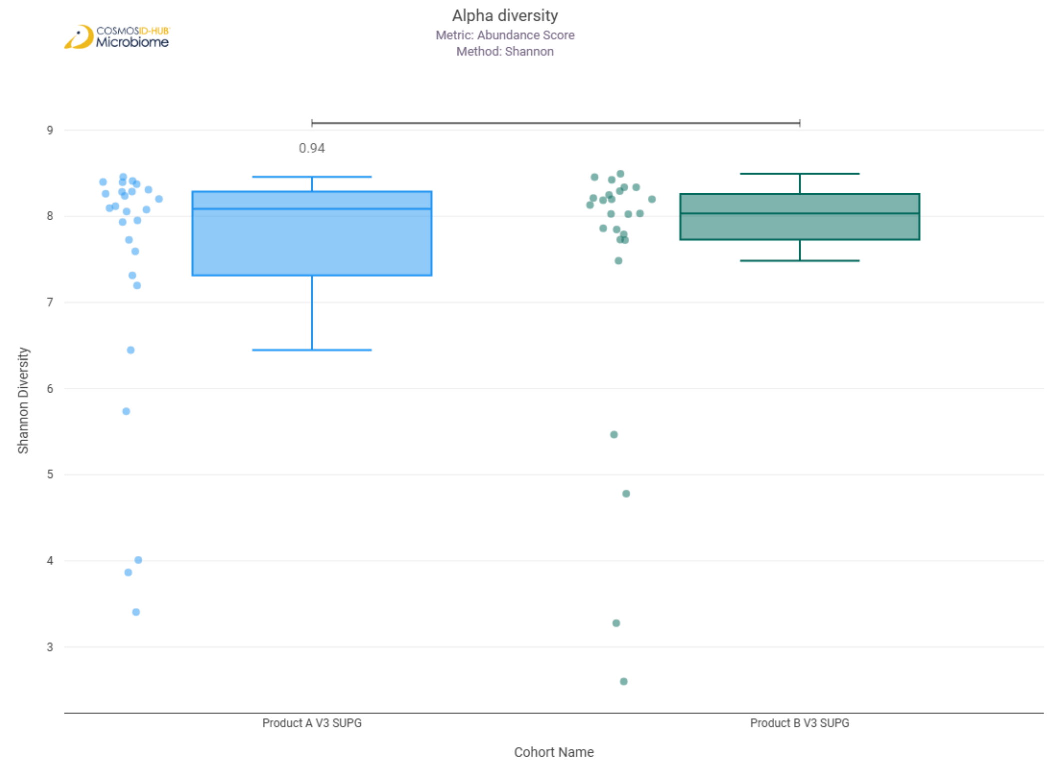

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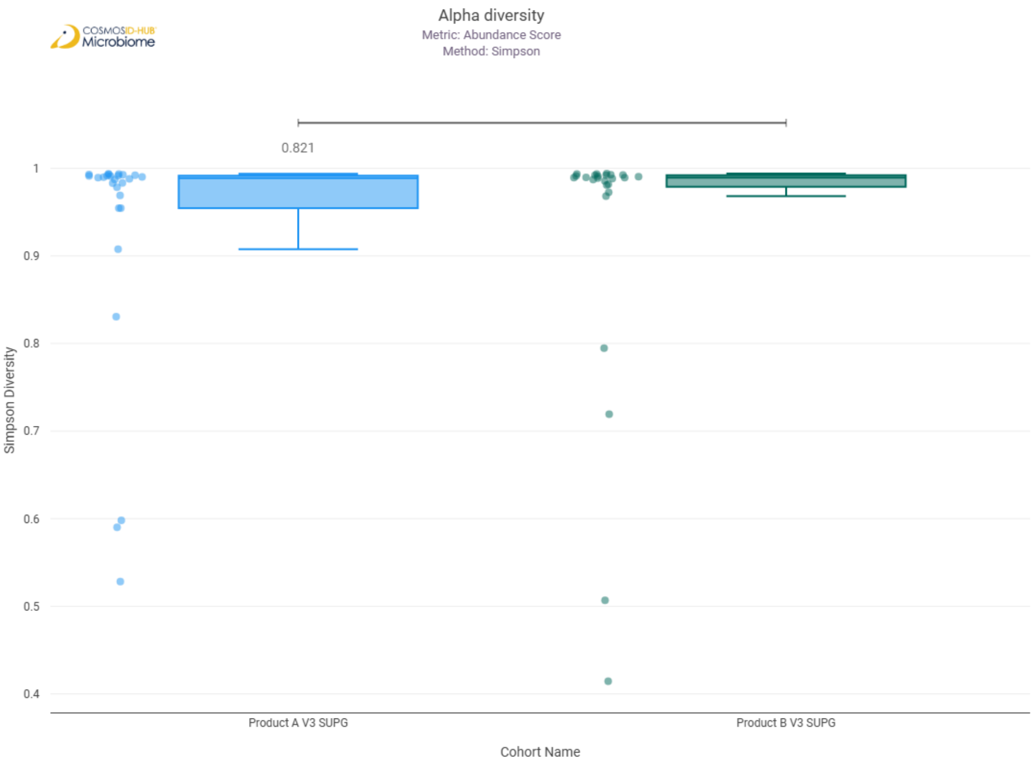
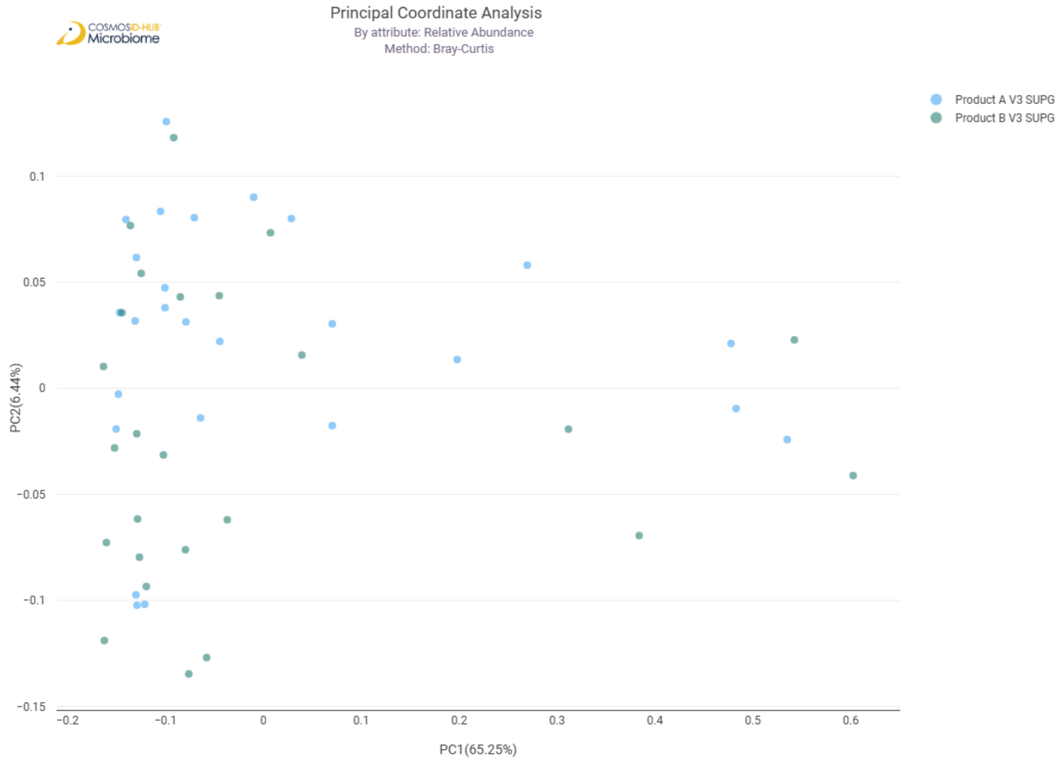
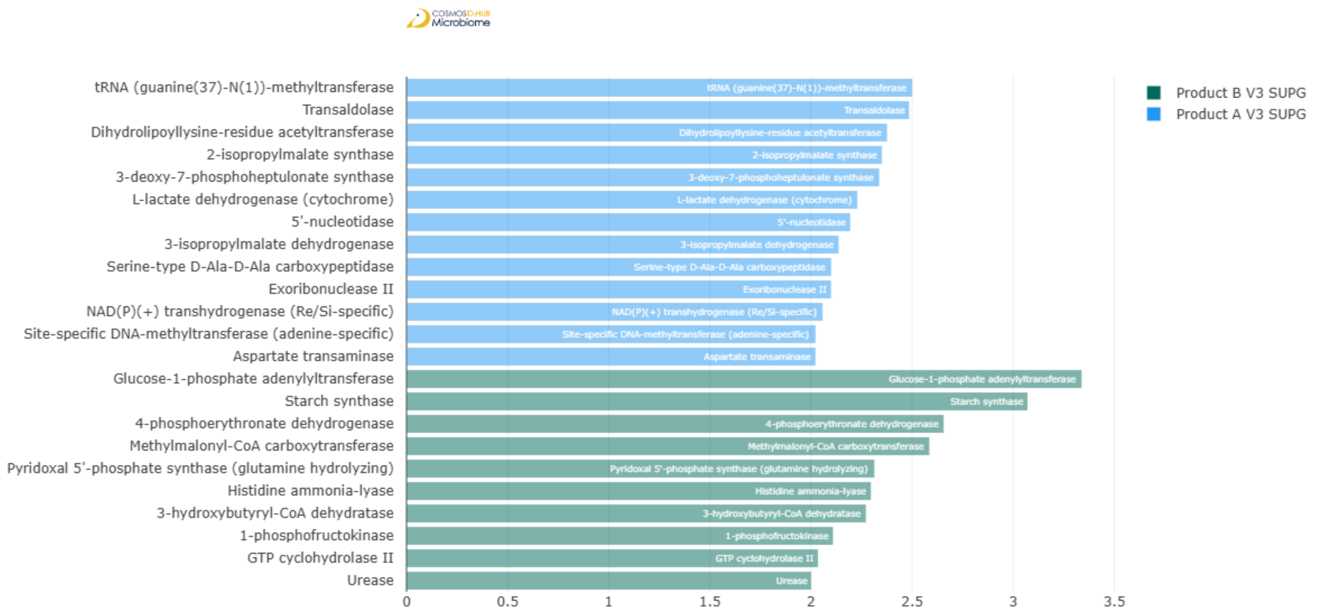
Simpson	

Beta Diversity (EC)

Bray-Curtis PERMNOVA p = 0.444	

Differential Abundance (LEfSe) (EC)



Feature	Enriched Cohort	LDA Score	P-value
tRNA (guanine(37)-N(1))-methyltransferase	Product A V3 SUPG	2.500264278	0.01946851
Transaldolase	Product A V3 SUPG	2.484762088	0.018508823
Dihydrolipoyllysine-residue acetyltransferase	Product A V3 SUPG	2.375737852	0.002269883
2-isopropylmalate synthase	Product A V3 SUPG	2.350585213	0.009316196
3-deoxy-7-phosphoheptulonate synthase	Product A V3 SUPG	2.337189254	0.012209995
L-lactate dehydrogenase (cytochrome)	Product A V3 SUPG	2.228905441	0.000975879
5'-nucleotidase	Product A V3 SUPG	2.193891563	0.017590793
3-isopropylmalate dehydrogenase	Product A V3 SUPG	2.136461137	0.034829974
Serine-type D-Ala-D-Ala carboxypeptidase	Product A V3 SUPG	2.099533029	3.65E-02
Exoribonuclease II	Product A V3 SUPG	2.098730123	0.00666206
NAD(P)(+) transhydrogenase (Re/Si-specific)	Product A V3 SUPG	2.057129937	9.12086E-05
Site-specific DNA-methyltransferase (adenine-specific)	Product A V3 SUPG	2.022241583	0.004708409
Aspartate transaminase	Product A V3 SUPG	2.022013886	0.007889693
Glucose-1-phosphate adenylyltransferase	Product B V3 SUPG	3.338057083	0.014305878
Starch synthase	Product B V3 SUPG	3.070387876	0.010390869
4-phosphoerythronate dehydrogenase	Product B V3 SUPG	2.655965123	0.02375508
Methylmalonyl-CoA carboxytransferase	Product B V3 SUPG	2.585105624	0.030245812
Pyridoxal 5'-phosphate synthase (glutamine hydrolyzing)	Product B V3 SUPG	2.3131954	0.009840467
Histidine ammonia-lyase	Product B V3 SUPG	2.295994799	0.041854827
3-hydroxybutyryl-CoA dehydratase	Product B V3 SUPG	2.271443172	0.027416296
1-phosphofructokinase	Product B V3 SUPG	2.108726986	0.026189985
GTP cyclohydrolase II	Product B V3 SUPG	2.034218049	0.032464726
Urease	Product B V3 SUPG	2.000448337	0.036484395

MetaCyc Pathways

Alpha Diversity (MetaCyc)

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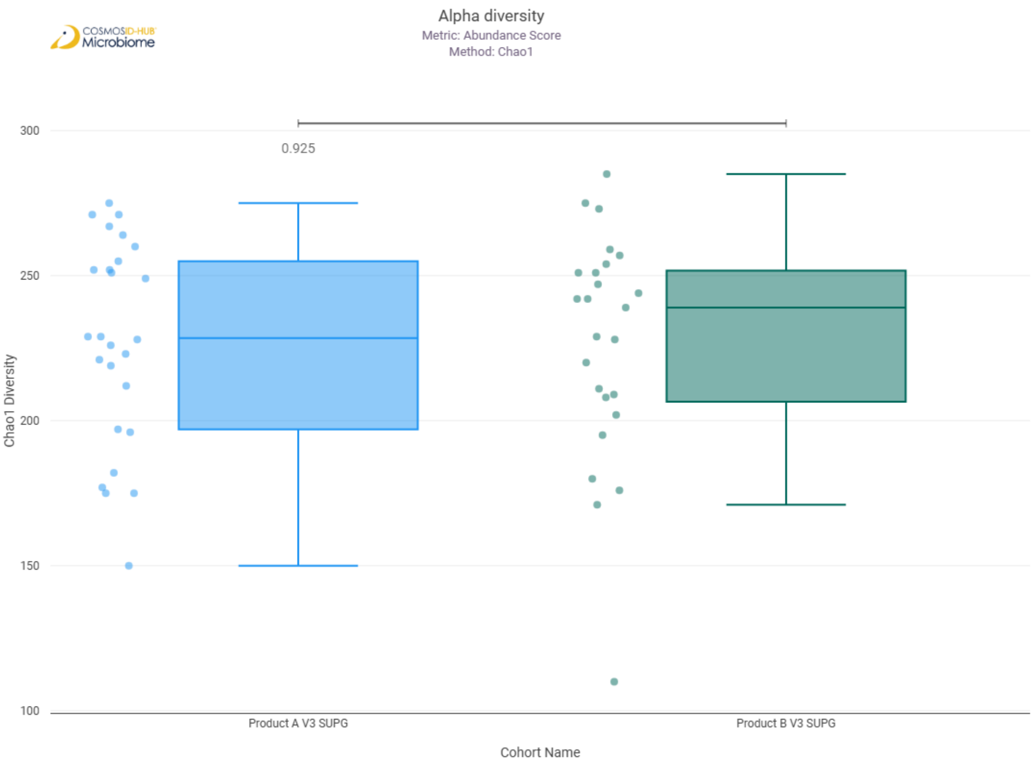
<tr><td>Chao1</td><td>
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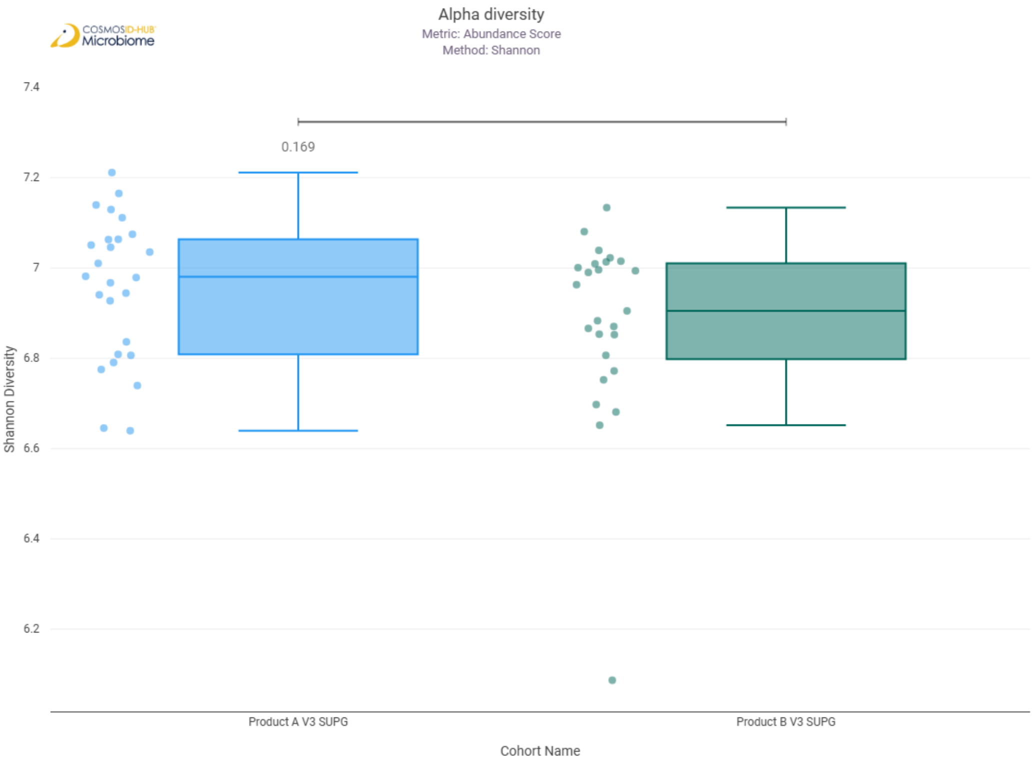
<tr><td>Shannon</td><td>
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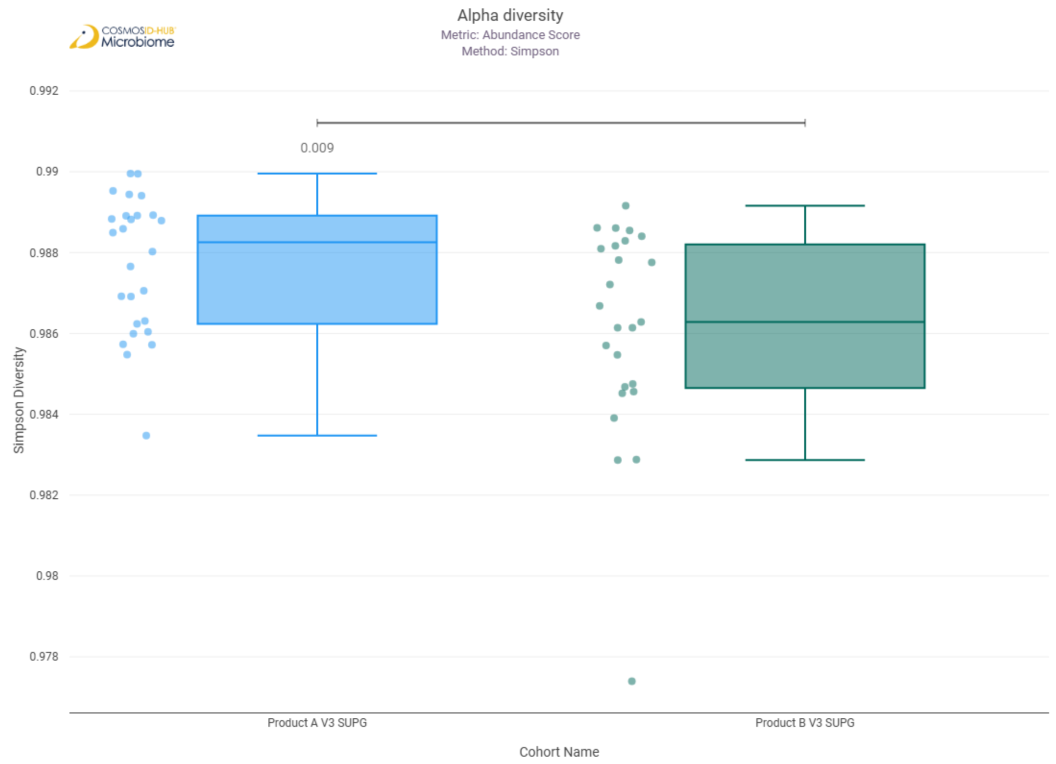
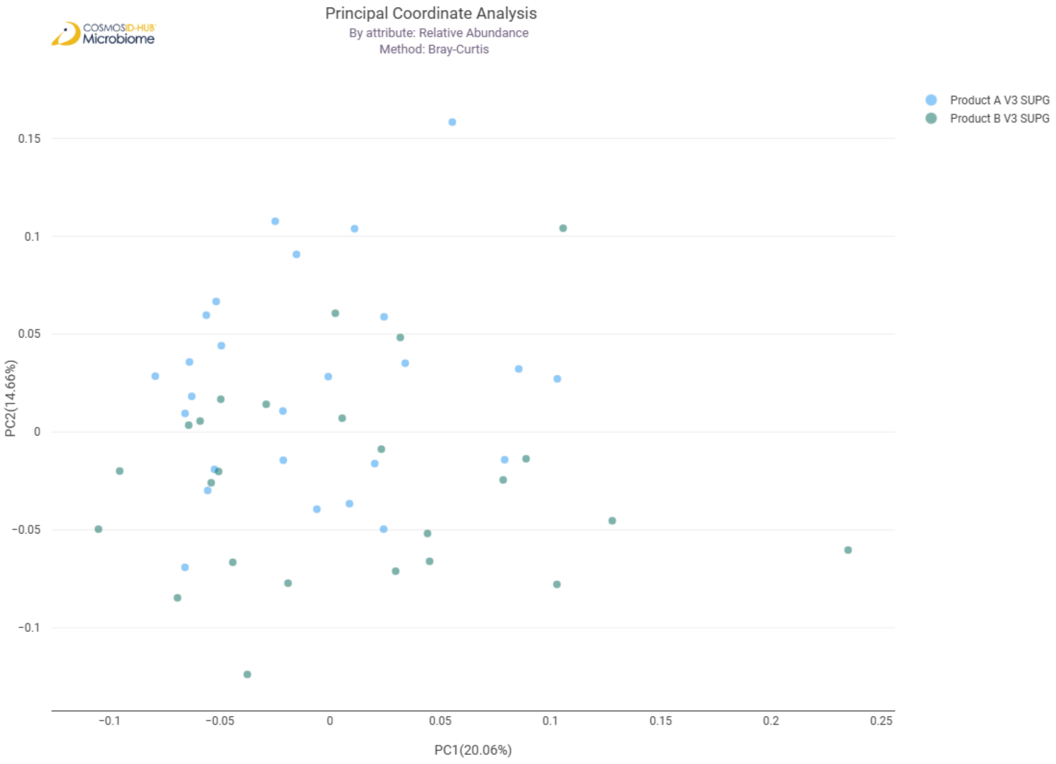
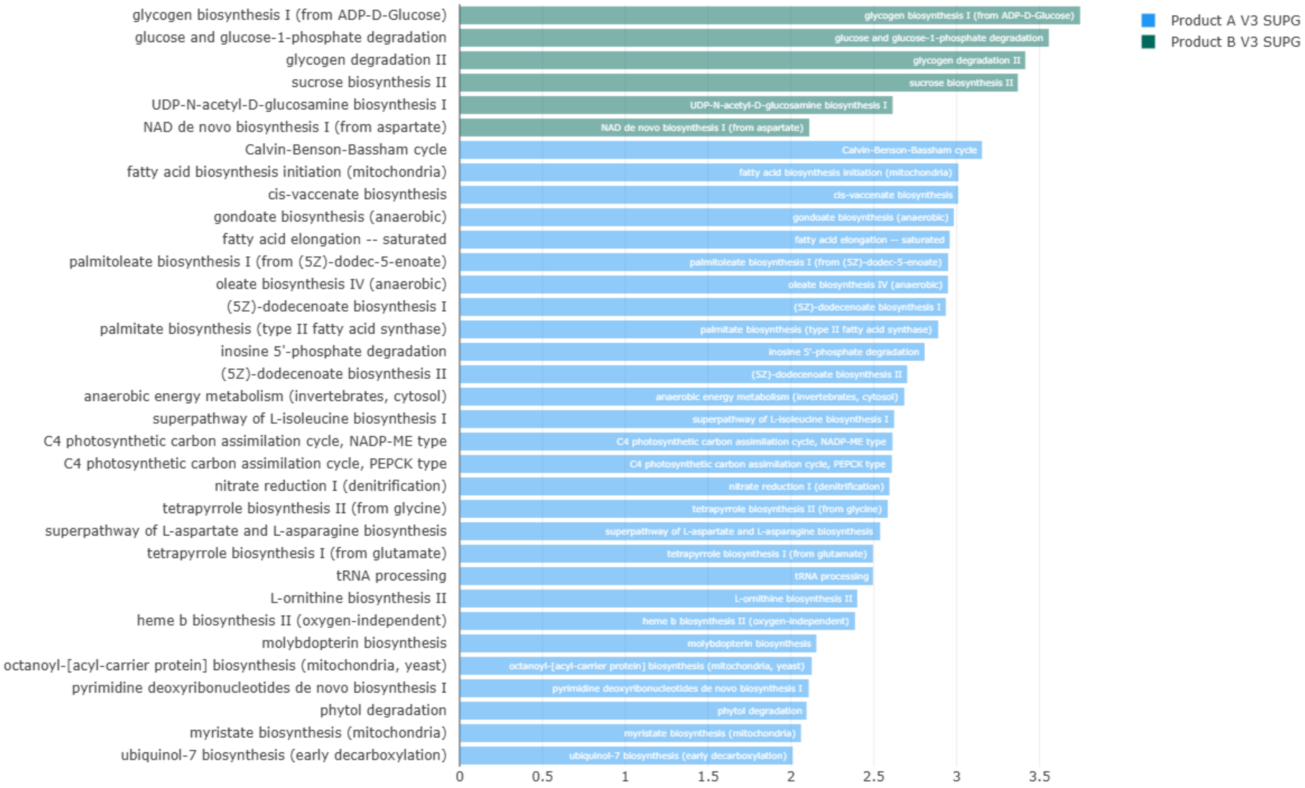
Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis PERMNOVA p = 0.003	

Differential Abundance (LEfSe) (MetaCyc)



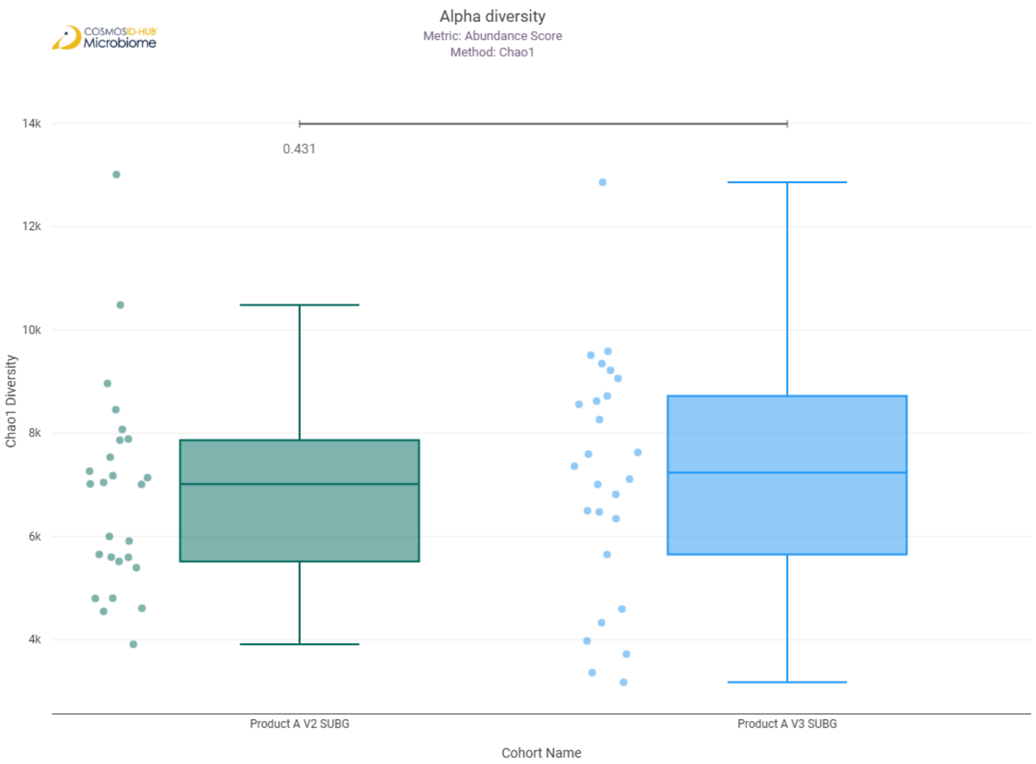
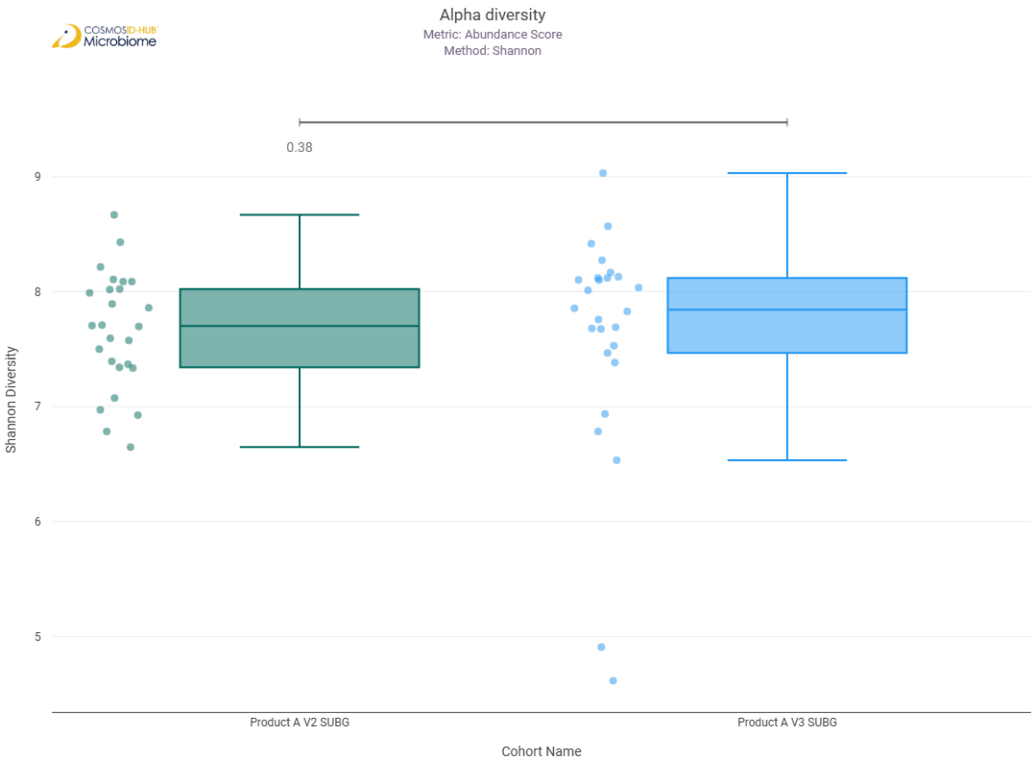
Feature	Enriched Cohort	LDA Score	P-value
glycogen biosynthesis I (from ADP-D-Glucose)	Product B V3 SUPG	3.745453908	0.004992891
glucose and glucose-1-phosphate degradation	Product B V3 SUPG	3.556342772	0.001185563
glycogen degradation II	Product B V3 SUPG	3.414064751	0.002416555
sucrose biosynthesis II	Product B V3 SUPG	3.369416045	0.043787588
UDP-N-acetyl-D-glucosamine biosynthesis I	Product B V3 SUPG	2.613767033	0.038205314
NAD de novo biosynthesis I (from aspartate)	Product B V3 SUPG	2.11061315	0.022998367
Calvin-Benson-Bassham cycle	Product A V3 SUPG	3.152784189	0.014305878
fatty acid biosynthesis initiation (mitochondria)	Product A V3 SUPG	3.01039182	0.045795182
cis-vaccenate biosynthesis	Product A V3 SUPG	3.009160863	0.002131408
gondoate biosynthesis (anaerobic)	Product A V3 SUPG	2.982772569	0.001651513
fatty acid elongation -- saturated	Product A V3 SUPG	2.957467752	1.55E-03
palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate)	Product A V3 SUPG	2.9484708	0.001548196
oleate biosynthesis IV (anaerobic)	Product A V3 SUPG	2.947646008	0.001548196
(5Z)-dodecenoate biosynthesis I	Product A V3 SUPG	2.934424036	0.001450862
palmitate biosynthesis (type II fatty acid synthase)	Product A V3 SUPG	2.888494581	0.031388853
inosine 5'-phosphate degradation	Product A V3 SUPG	2.80641503	0.005608941
(5Z)-dodecenoate biosynthesis II	Product A V3 SUPG	2.70155732	0.001546672
anaerobic energy metabolism (invertebrates, cytosol)	Product A V3 SUPG	2.683835359	0.00176114

superpathway of L-isoleucine biosynthesis I	Product A V3 SUPG	2.622456465	0.00745964
C4 photosynthetic carbon assimilation cycle, NADP-ME type	Product A V3 SUPG	2.612696215	0.005608941
C4 photosynthetic carbon assimilation cycle, PEPCK type	Product A V3 SUPG	2.609269035	0.003940813
nitrate reduction I (denitrification)	Product A V3 SUPG	2.594250369	0.038117995
tetrapyrrole biosynthesis II (from glycine)	Product A V3 SUPG	2.583988202	0.002736233
superpathway of L-aspartate and L-asparagine biosynthesis	Product A V3 SUPG	2.537954679	0.01946851
tetrapyrrole biosynthesis I (from glutamate)	Product A V3 SUPG	2.494703731	0.021519031
tRNA processing	Product A V3 SUPG	2.494482922	3.04E-03
L-ornithine biosynthesis II	Product A V3 SUPG	2.400005683	0.001710728
heme b biosynthesis II (oxygen-independent)	Product A V3 SUPG	2.386491358	0.01038393
molybdopterin biosynthesis	Product A V3 SUPG	2.153352631	0.042764988
octanoyl-[acyl-carrier protein] biosynthesis (mitochondria, yeast)	Product A V3 SUPG	2.125495299	0.007588752
pyrimidine deoxyribonucleotides de novo biosynthesis I	Product A V3 SUPG	2.107076766	0.022483275
phytol degradation	Product A V3 SUPG	2.093939151	0.020872668
myristate biosynthesis (mitochondria)	Product A V3 SUPG	2.060356177	0.015762918
ubiquinol-7 biosynthesis (early decarboxylation)	Product A V3 SUPG	2.010244202	0.034572268

Comparison 17: Product A V2 SUBG vs Product A V3 SUBG

Gene Ontology

Alpha Diversity (GO)

Chao1	
Shannon	

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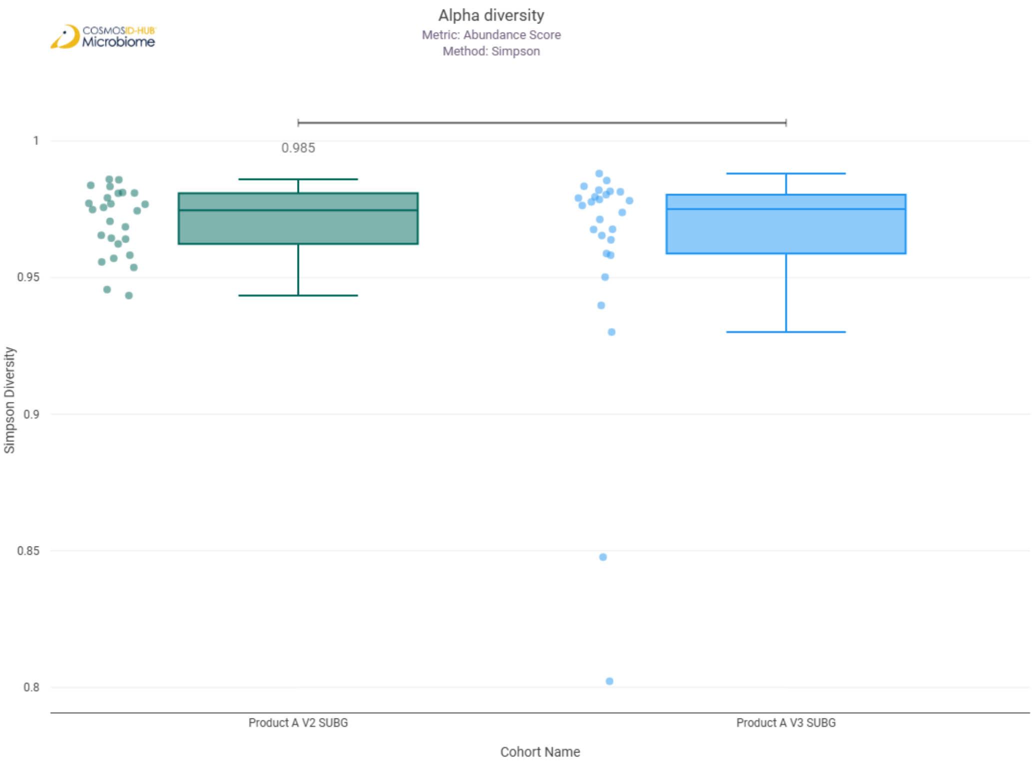

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Beta Diversity (GO)

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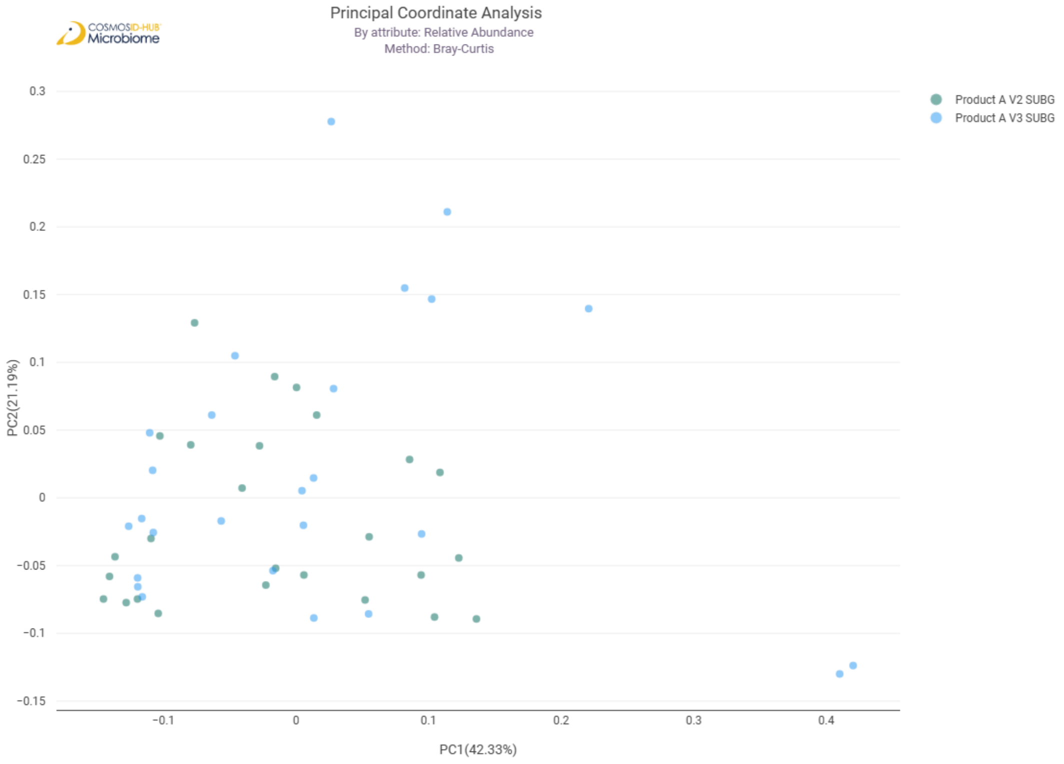

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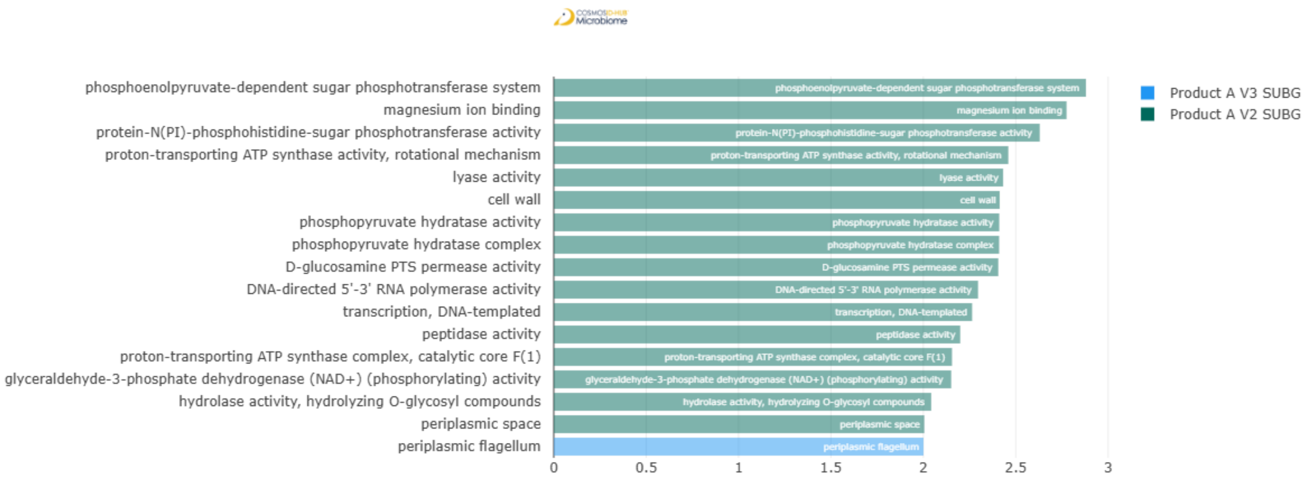
Differential Abundance (LEfSe) (GO)



Feature	Enriched Cohort	LDA Score	P-value
phosphoenolpyruvate-dependent sugar phosphotransferase system	Product A V2 SUBG	2.879797903	0.032254747
magnesium ion binding	Product A V2 SUBG	2.774888442	0.036948224
protein-N(PI)-phosphohistidine-sugar phosphotransferase activity	Product A V2 SUBG	2.629946921	0.019152346
proton-transporting ATP synthase activity, rotational mechanism	Product A V2 SUBG	2.459822872	0.035322927
lyase activity	Product A V2 SUBG	2.431775521	0.020112035
cell wall	Product A V2 SUBG	2.413162378	0.00935587
phosphopyruvate hydratase activity	Product A V2 SUBG	2.410854956	0.029417827
phosphopyruvate hydratase complex	Product A V2 SUBG	2.410229337	0.032254747
D-glucosamine PTS permease activity	Product A V2 SUBG	2.405537558	0.030808261
DNA-directed 5'-3' RNA polymerase activity	Product A V2 SUBG	2.295963259	0.019152346
transcription, DNA-templated	Product A V2 SUBG	2.26404028	1.65E-02
peptidase activity	Product A V2 SUBG	2.199570388	0.044100855
proton-transporting ATP synthase complex, catalytic core F(1)	Product A V2 SUBG	2.155169223	0.030808261
glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity	Product A V2 SUBG	2.150756046	0.01096333
hydrolase activity, hydrolyzing O-glycosyl compounds	Product A V2 SUBG	2.042624495	0.044100855
periplasmic space	Product A V2 SUBG	2.005080067	0.046061451
periplasmic flagellum	Product A V3 SUBG	2.000494506	0.029983145

Enzyme Commission

Alpha Diversity (EC)

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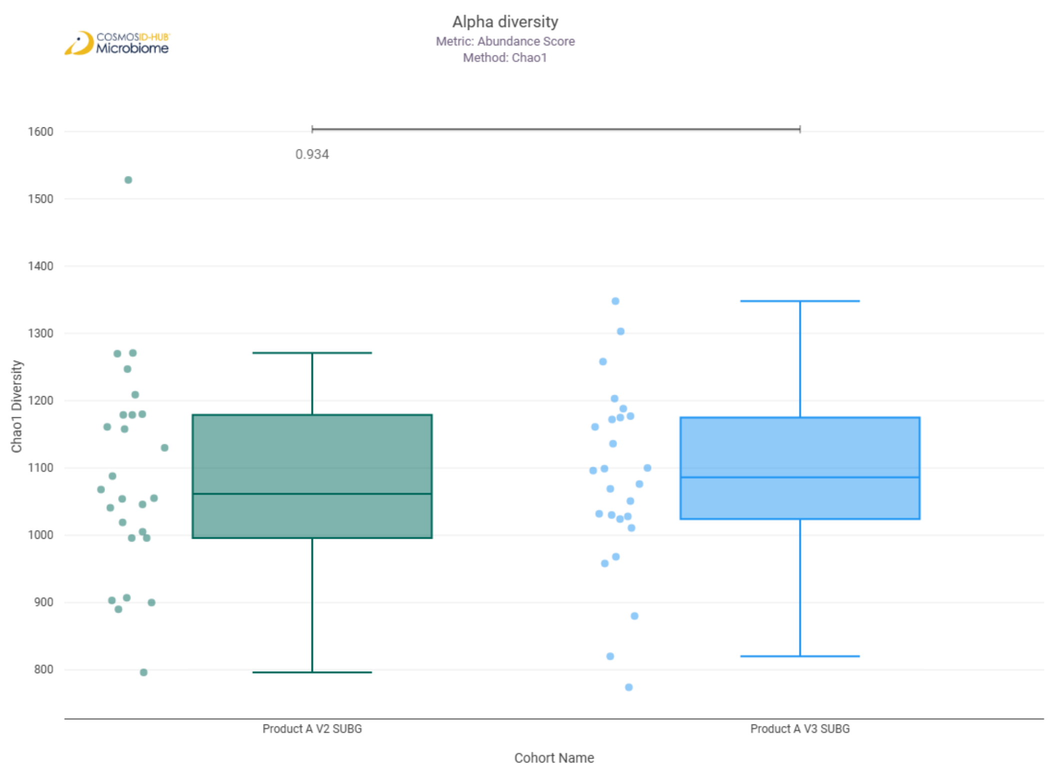
<td>
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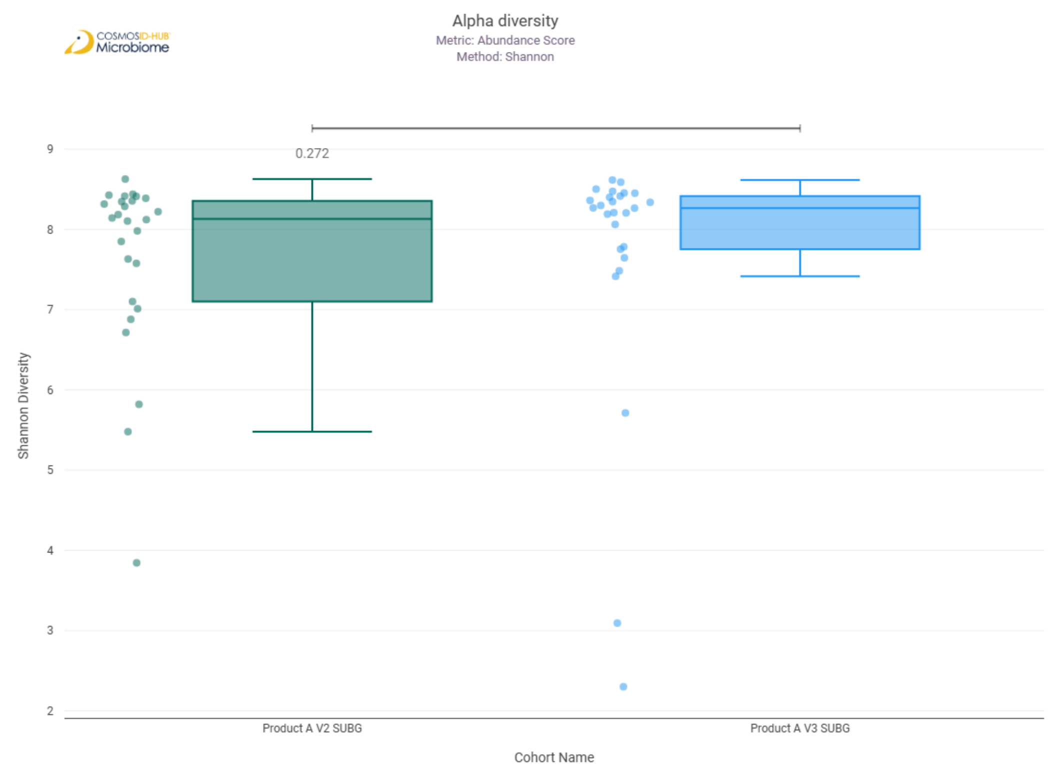
<td>
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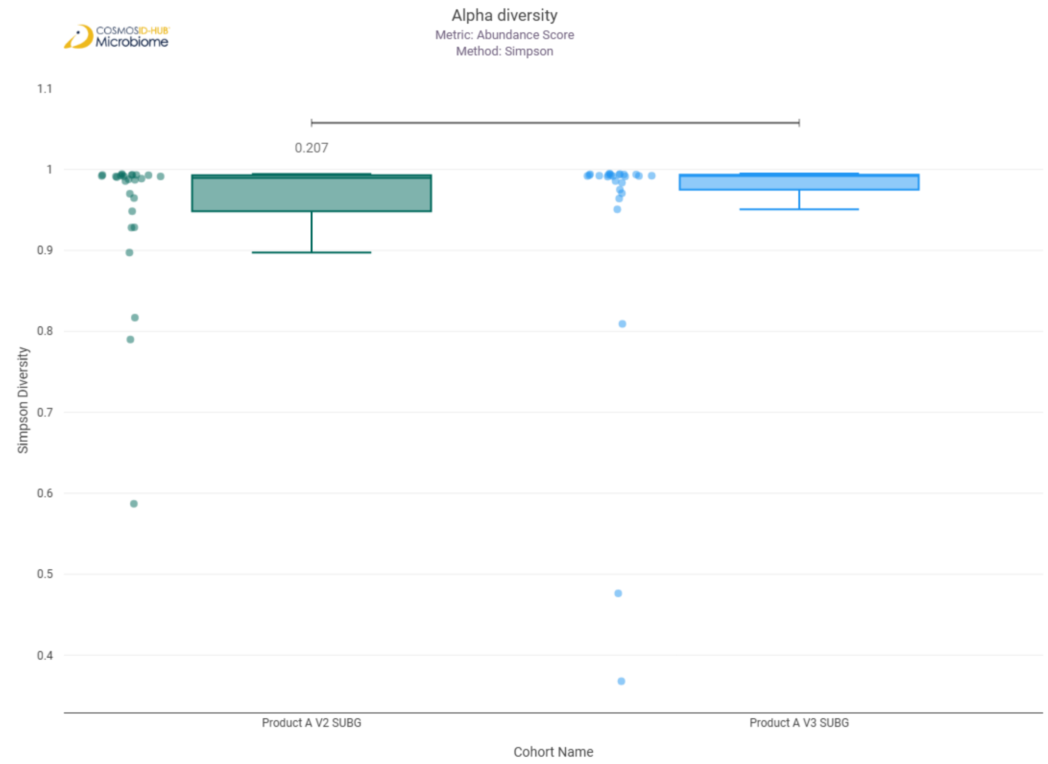
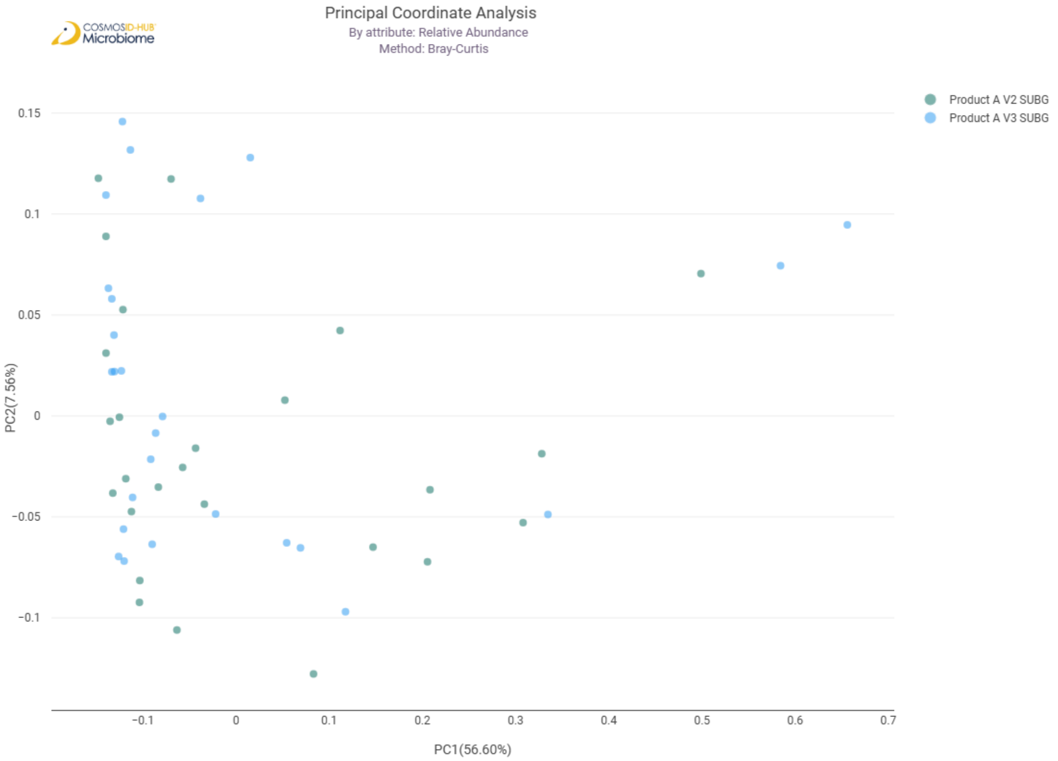
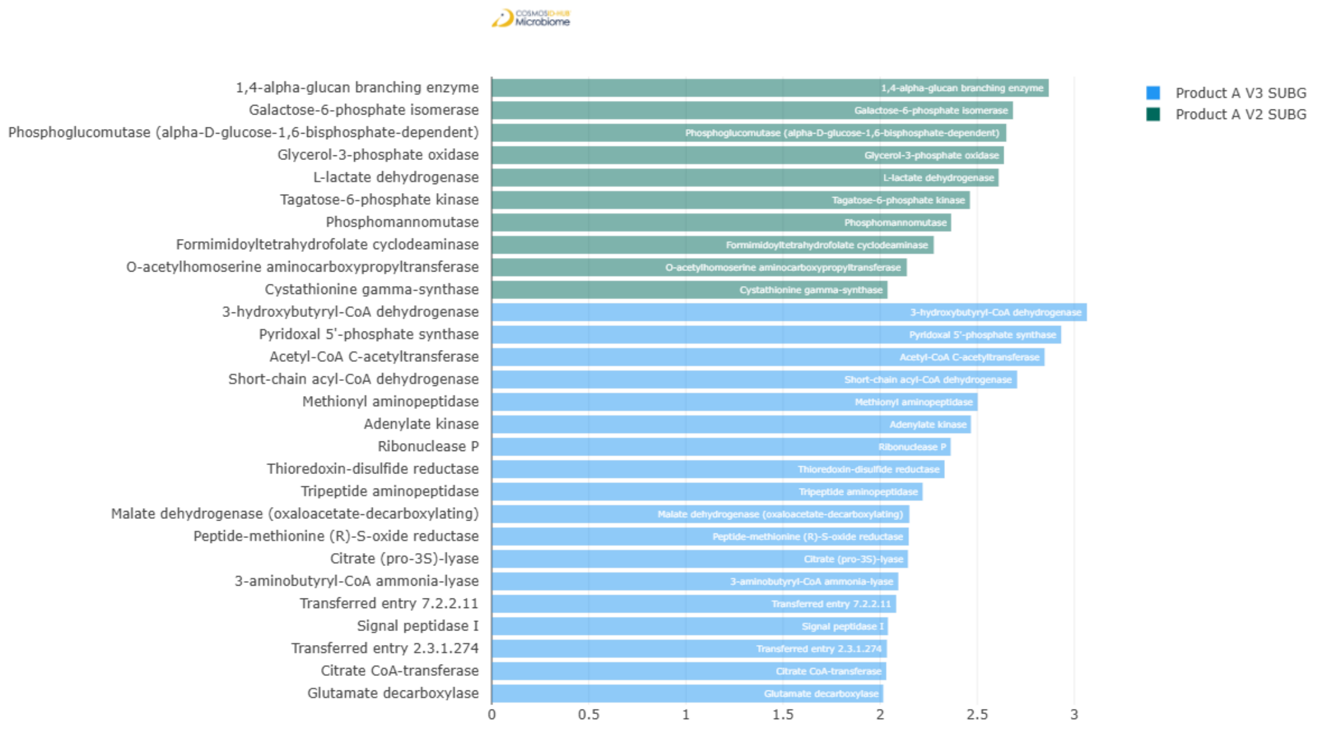
Simpson	

Beta Diversity (EC)

Bray-Curtis PERMNOVA p = 0.477	

Differential Abundance (LEfSe) (EC)

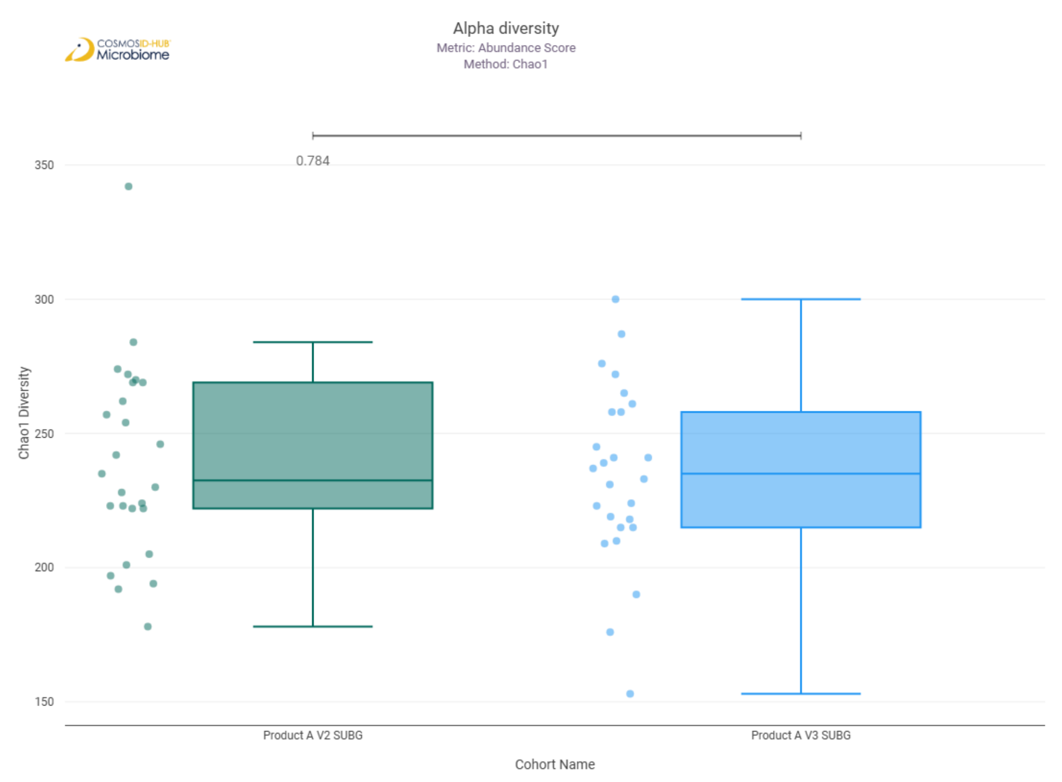


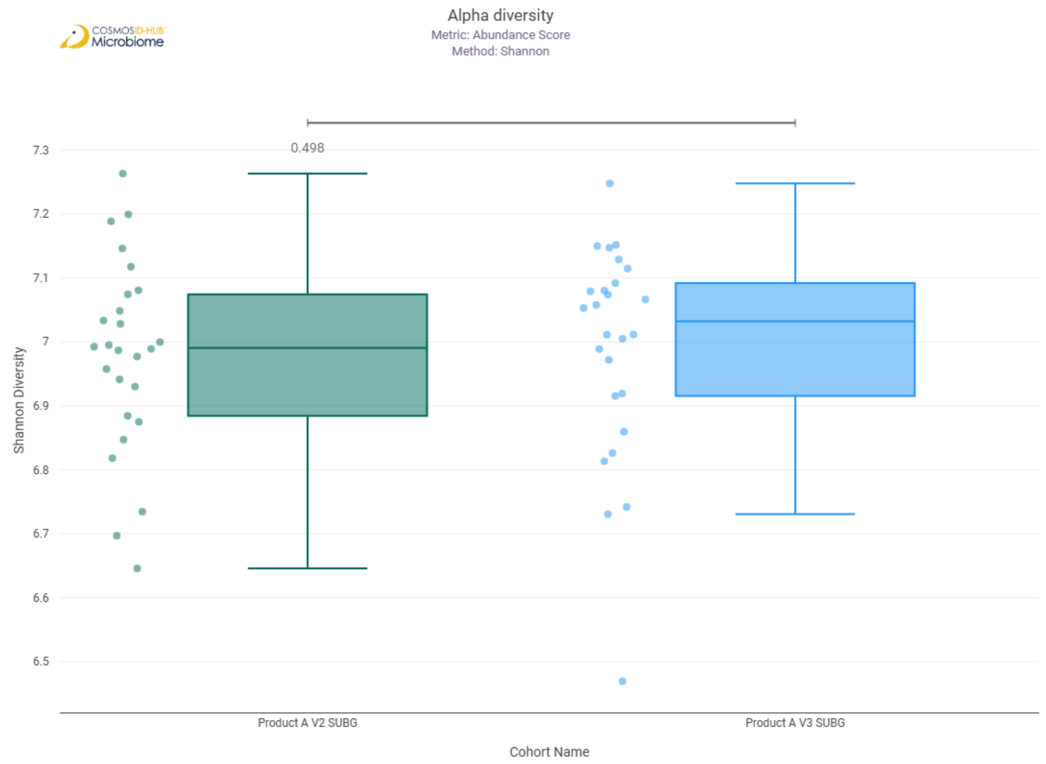
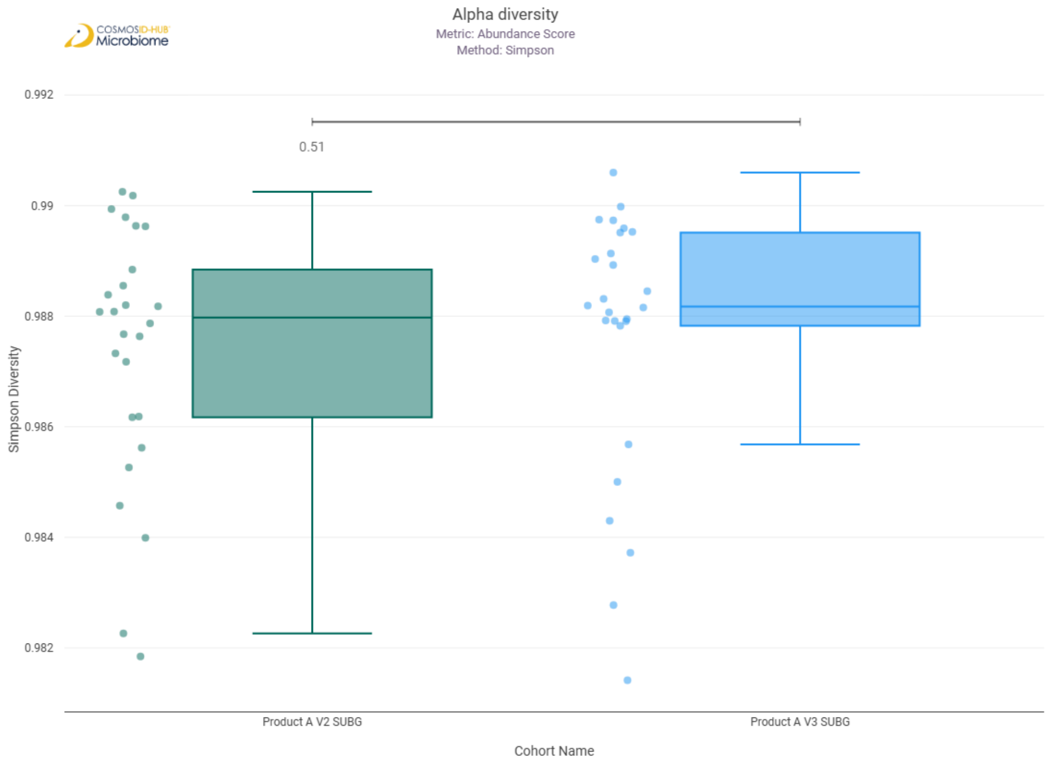
Feature	Enriched Cohort	LDA Score	P-value
1,4-alpha-glucan branching enzyme	Product A V2 SUBG	2.868316426	0.03375904
Galactose-6-phosphate isomerase	Product A V2 SUBG	2.684149527	0.030808261
Phosphoglucomutase (alpha-D-glucose-1,6-bisphosphate-dependent)	Product A V2 SUBG	2.649842397	0.02808172
Glycerol-3-phosphate oxidase	Product A V2 SUBG	2.637420912	0.016509366
L-lactate dehydrogenase	Product A V2 SUBG	2.610313421	0.040390461
Tagatose-6-phosphate kinase	Product A V2 SUBG	2.462341427	0.008404526
Phosphomannomutase	Product A V2 SUBG	2.365644114	0.026798248
Formimidoyltetrahydrofolate cyclodeaminase	Product A V2 SUBG	2.27631209	0.041248997
O-acetylhomoserine aminocarboxypropyltransferase	Product A V2 SUBG	2.137713911	0.004826615
Cystathionine gamma-synthase	Product A V2 SUBG	2.038346401	0.044100855
3-hydroxybutyryl-CoA dehydrogenase	Product A V3 SUBG	3.064708375	0.040390461
Pyridoxal 5'-phosphate synthase	Product A V3 SUBG	2.932292833	0.001450508
Acetyl-CoA C-acetyltransferase	Product A V3 SUBG	2.846871144	0.040390461
Short-chain acyl-CoA dehydrogenase	Product A V3 SUBG	2.705416934	0.023247195
Methionyl aminopeptidase	Product A V3 SUBG	2.502082155	0.03375904
Adenylate kinase	Product A V3 SUBG	2.467441243	4.04E-02
Ribonuclease P	Product A V3 SUBG	2.363351826	0.013486371
Thioredoxin-disulfide reductase	Product A V3 SUBG	2.331473944	0.029417827
Tripeptide aminopeptidase	Product A V3 SUBG	2.218866344	0.008404526
Malate dehydrogenase (oxaloacetate-decarboxylating)	Product A V3 SUBG	2.150705321	0.044100855
Peptide-methionine (R)-S-oxide reductase	Product A V3 SUBG	2.147252427	0.046061451
Citrate (pro-3S)-lyase	Product A V3 SUBG	2.143123658	0.019152346

3-aminobutyryl-CoA ammonia-lyase	Product A V3 SUBG	2.093593451	0.004825711
Transferred entry 7.2.2.11	Product A V3 SUBG	2.082564986	0.046061451
Signal peptidase I	Product A V3 SUBG	2.040245909	0.036948224
Transferred entry 2.3.1.274	Product A V3 SUBG	2.034991023	6.05E-03
Citrate CoA-transferase	Product A V3 SUBG	2.031605498	0.036948224
Glutamate decarboxylase	Product A V3 SUBG	2.016312006	0.042211177

MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1	

Shannon	
Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis

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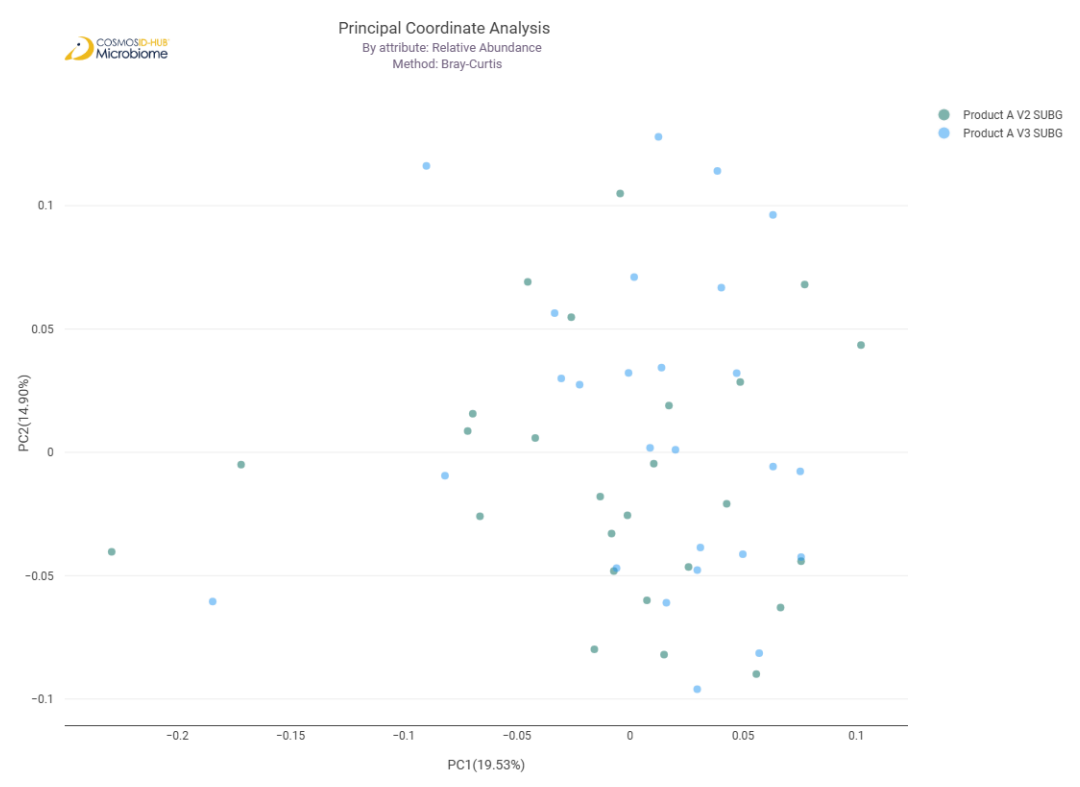
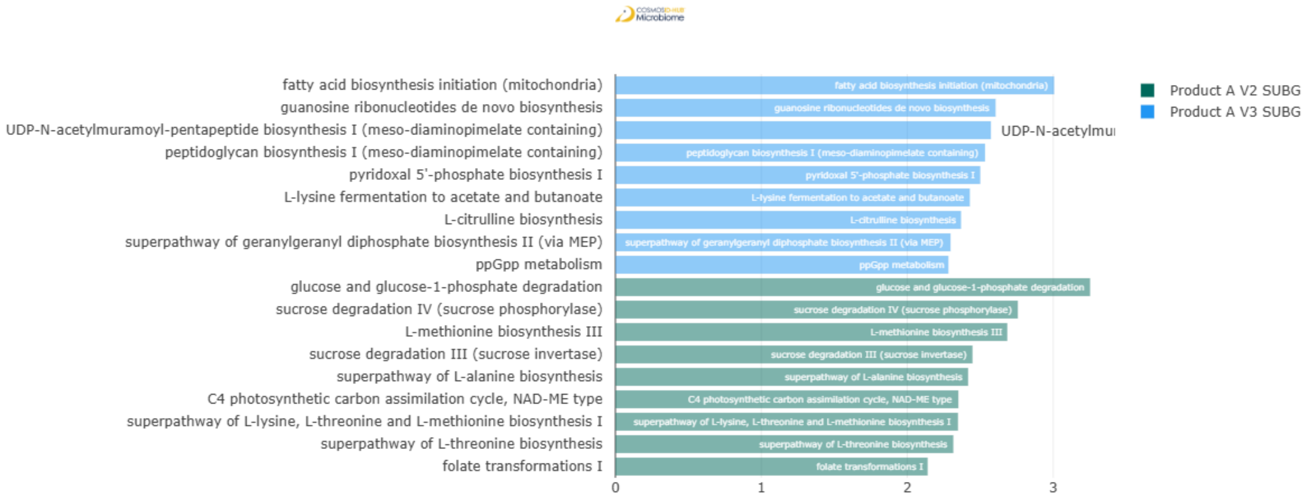


Differential Abundance (LEfSe) (MetaCyc)



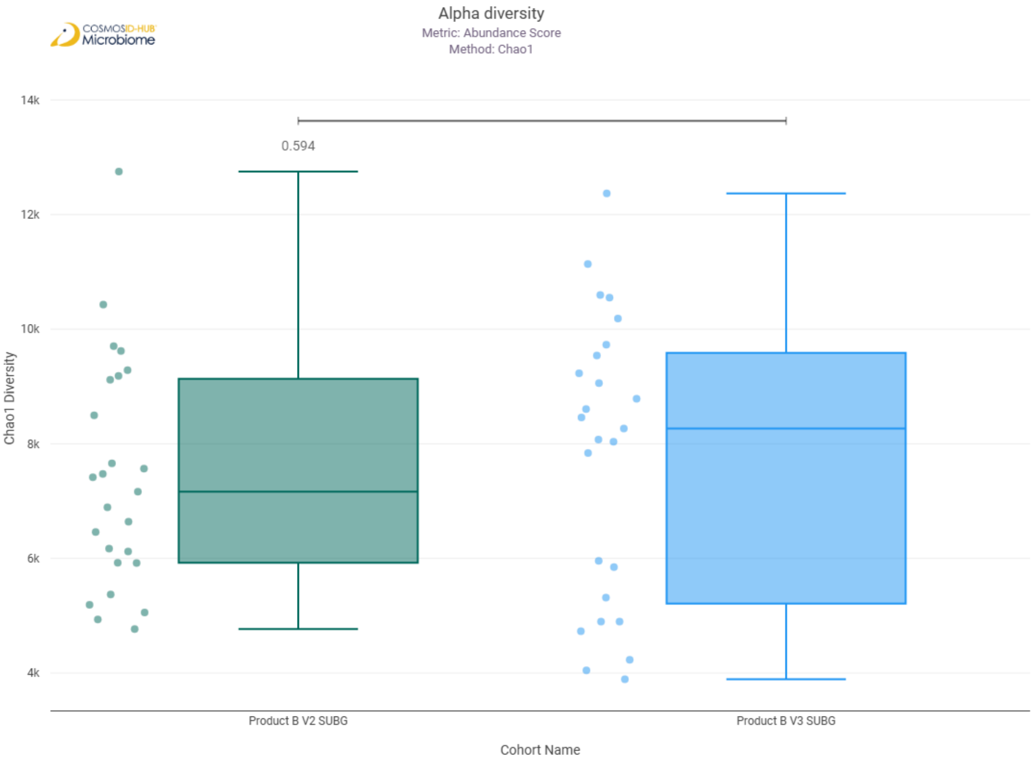
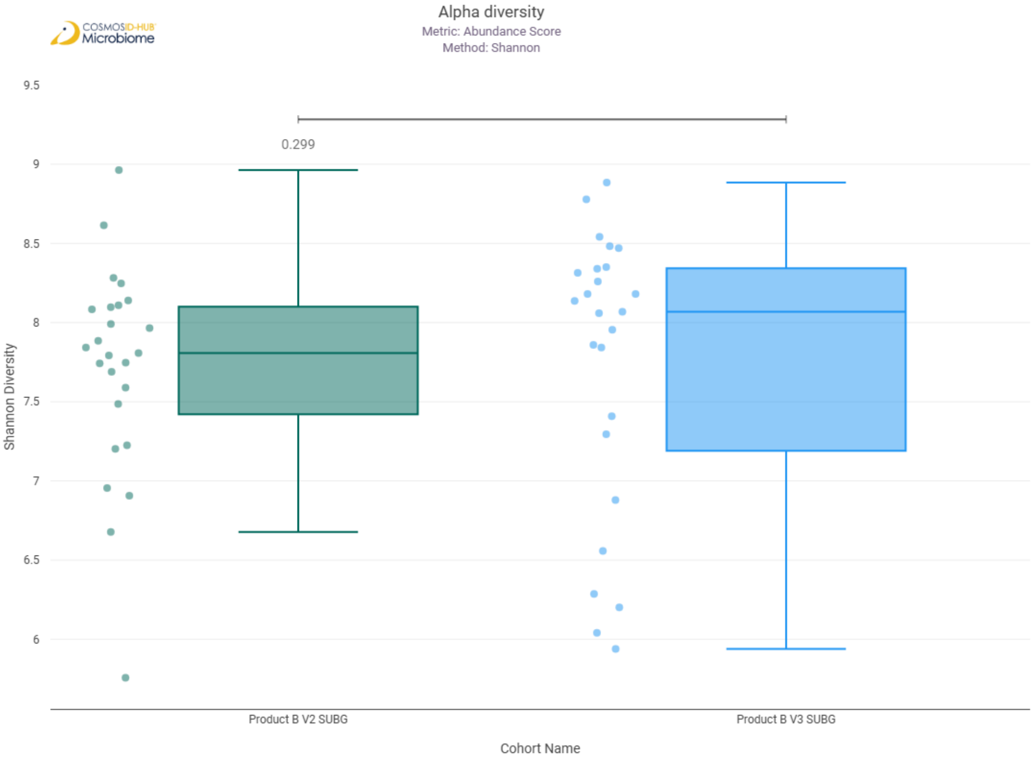
Feature	Enriched Cohort	LDA Score	P-value
fatty acid biosynthesis initiation (mitochondria)	Product A V3 SUBG	3.005949407	0.019152346
guanosine ribonucleotides de novo biosynthesis	Product A V3 SUBG	2.605116224	0.020112035
UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)	Product A V3 SUBG	2.572950032	0.023247195
peptidoglycan biosynthesis I (meso-diaminopimelate containing)	Product A V3 SUBG	2.53279651	0.032254747
pyridoxal 5'-phosphate biosynthesis I	Product A V3 SUBG	2.500028395	0.048970397
L-lysine fermentation to acetate and butanoate	Product A V3 SUBG	2.42853662	0.025907733

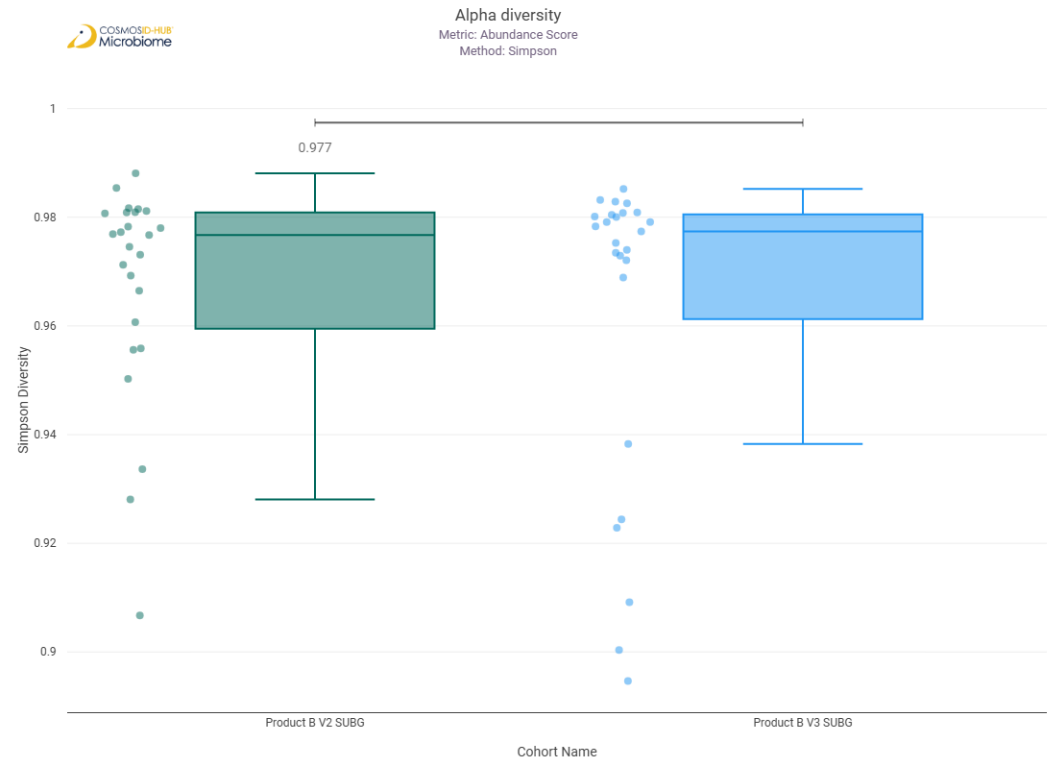
L-citrulline biosynthesis	Product A V3 SUBG	2.368319134	0.011551265
superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP)	Product A V3 SUBG	2.29634489	4.91E-02
ppGpp metabolism	Product A V3 SUBG	2.281827361	0.044100855
glucose and glucose-1-phosphate degradation	Product A V2 SUBG	3.252312629	0.022595697
sucrose degradation IV (sucrose phosphorylase)	Product A V2 SUBG	2.757431708	0.015702531
L-methionine biosynthesis III	Product A V2 SUBG	2.685167724	0.026798248
sucrose degradation III (sucrose invertase)	Product A V2 SUBG	2.446760597	0.019152346
superpathway of L-alanine biosynthesis	Product A V2 SUBG	2.416704919	0.046061451
C4 photosynthetic carbon assimilation cycle, NAD-ME type	Product A V2 SUBG	2.350104694	0.026798248
superpathway of L-lysine, L-threonine and L-methionine biosynthesis I	Product A V2 SUBG	2.347295262	0.013505326
superpathway of L-threonine biosynthesis	Product A V2 SUBG	2.315420543	0.046061451
folate transformations I	Product A V2 SUBG	2.139570387	0.03927407

Comparison 18: Product B V2 SUBG vs Product B V3 SUBG

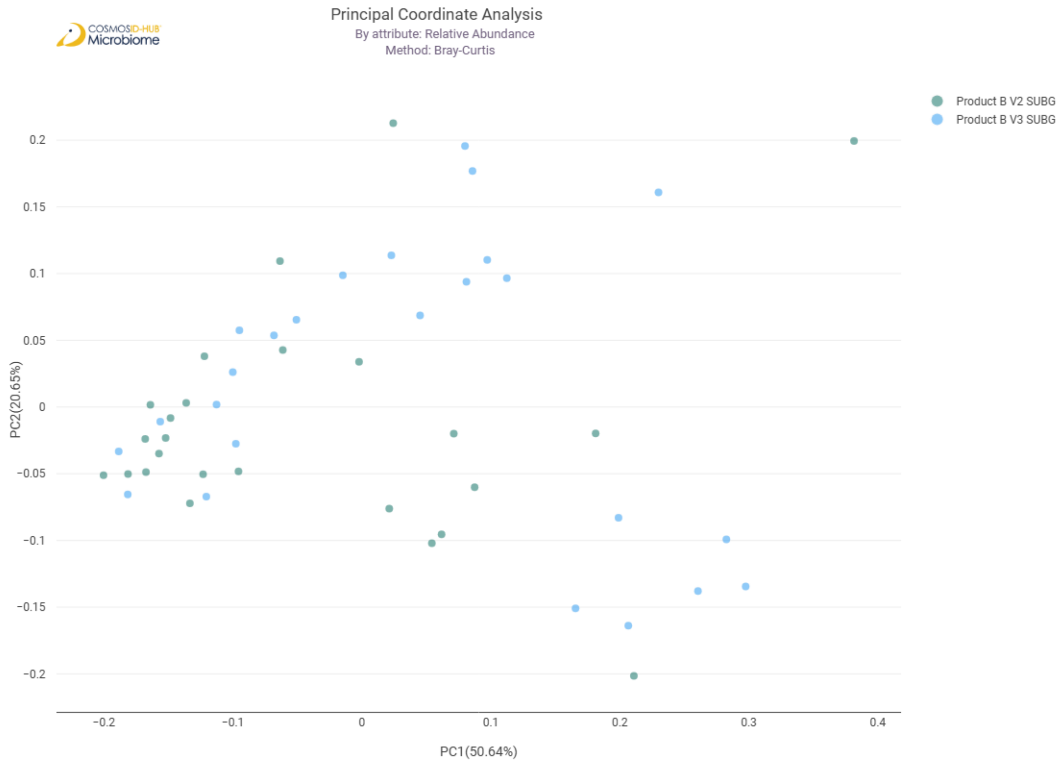
Gene Ontology

Alpha Diversity (GO)

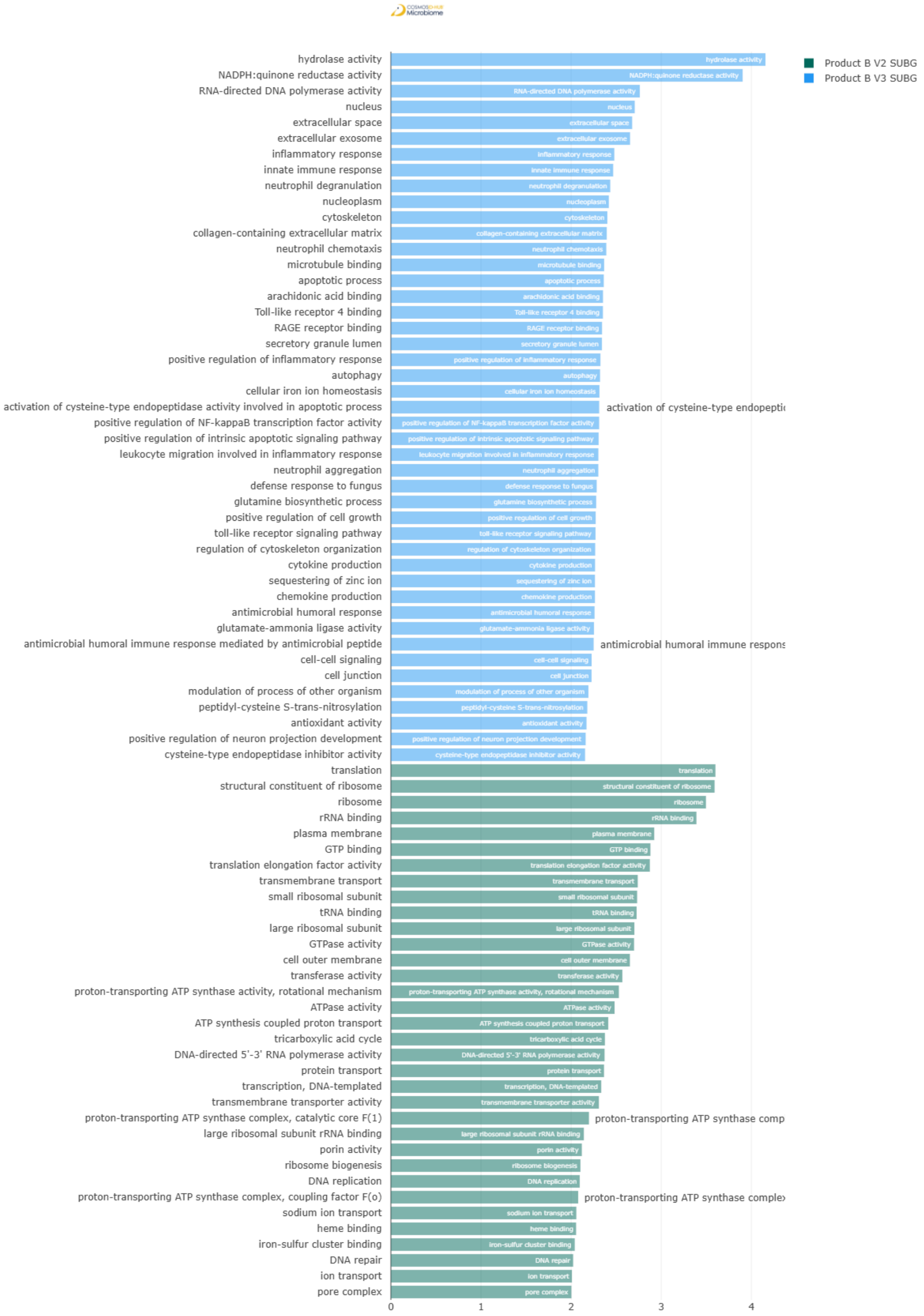
Chao1	
Shannon	

Simpson	

Beta Diversity (GO)

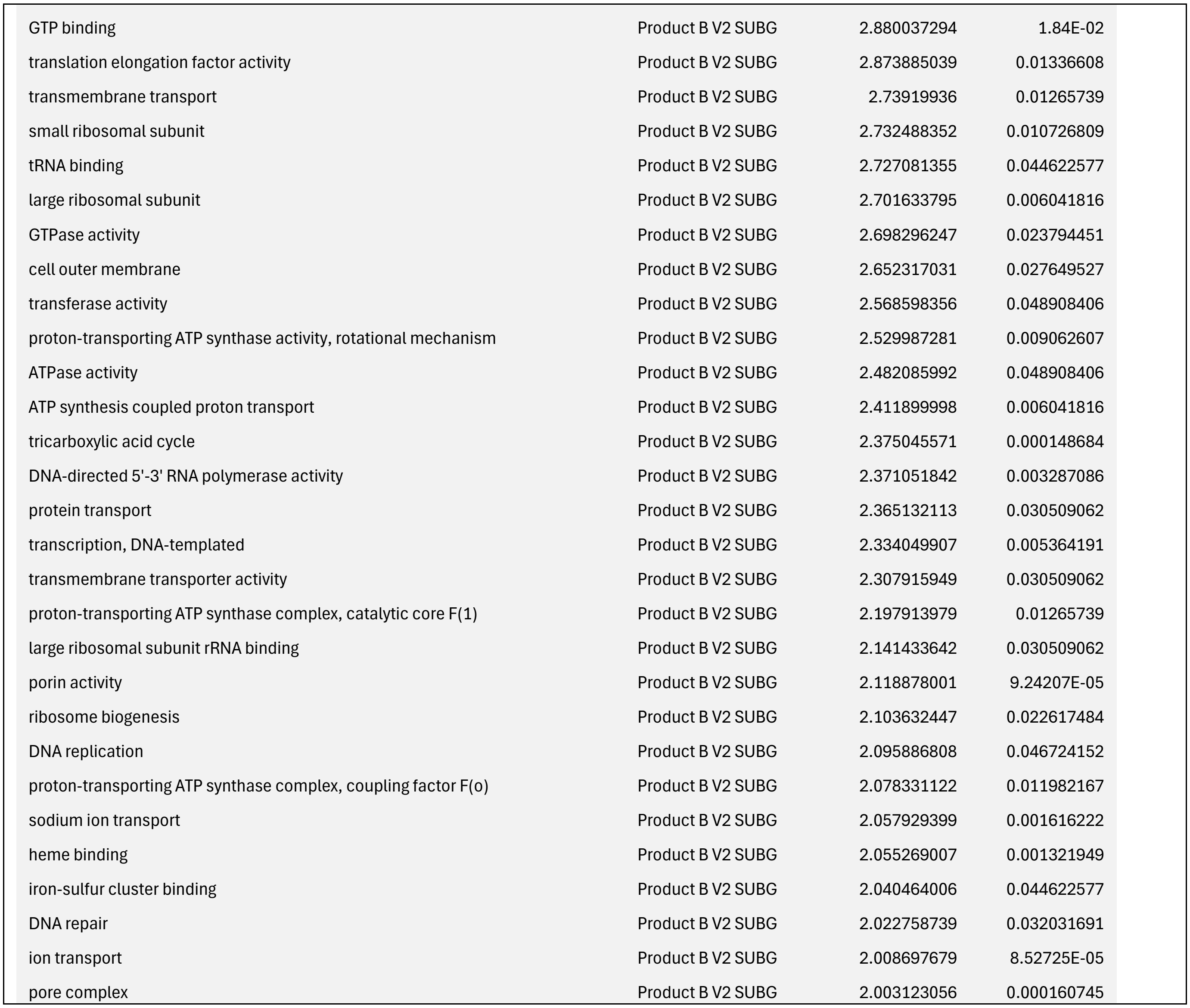
Bray-Curtis PERMNOVA p = 0.052	

Differential Abundance (LEfSe) (GO)



Feature	Enriched Cohort	LDA Score	P-value
hydrolase activity	Product B V3 SUBG	4.156534105	0.046724152
NADPH:quinone reductase activity	Product B V3 SUBG	3.903411192	0.038790393
RNA-directed DNA polymerase activity	Product B V3 SUBG	2.762516384	0.010144117
nucleus	Product B V3 SUBG	2.705824935	0.044622577

extracellular space	Product B V3 SUBG	2.677161463	0.032031691
extracellular exosome	Product B V3 SUBG	2.654055757	0.030509062
inflammatory response	Product B V3 SUBG	2.479045769	0.022617484
innate immune response	Product B V3 SUBG	2.466561032	0.025024185
neutrophil degranulation	Product B V3 SUBG	2.434546953	0.022617484
nucleoplasm	Product B V3 SUBG	2.418583258	1.84E-02
cytoskeleton	Product B V3 SUBG	2.402056268	0.007632882
collagen-containing extracellular matrix	Product B V3 SUBG	2.395453748	0.027649527
neutrophil chemotaxis	Product B V3 SUBG	2.390410925	0.020414533
microtubule binding	Product B V3 SUBG	2.366393497	0.014109615
apoptotic process	Product B V3 SUBG	2.362287574	0.014889416
arachidonic acid binding	Product B V3 SUBG	2.35381107	0.01265739
Toll-like receptor 4 binding	Product B V3 SUBG	2.352803461	0.01265739
RAGE receptor binding	Product B V3 SUBG	2.342847827	0.022617484
secretory granule lumen	Product B V3 SUBG	2.341644066	0.014109615
positive regulation of inflammatory response	Product B V3 SUBG	2.325368311	0.010144117
autophagy	Product B V3 SUBG	2.321122165	0.010144117
cellular iron ion homeostasis	Product B V3 SUBG	2.314227493	0.040658018
activation of cysteine-type endopeptidase activity involved in apoptotic process	Product B V3 SUBG	2.311541194	0.009589776
positive regulation of NF-kappaB transcription factor activity	Product B V3 SUBG	2.3110923	0.01265739
positive regulation of intrinsic apoptotic signaling pathway	Product B V3 SUBG	2.305115842	0.009062607
leukocyte migration involved in inflammatory response	Product B V3 SUBG	2.302179173	0.009062607
neutrophil aggregation	Product B V3 SUBG	2.301823987	0.009062607
defense response to fungus	Product B V3 SUBG	2.283744629	0.009589776
glutamine biosynthetic process	Product B V3 SUBG	2.27825556	0.014889416
positive regulation of cell growth	Product B V3 SUBG	2.272313134	0.009589776
toll-like receptor signaling pathway	Product B V3 SUBG	2.270650056	0.009062607
regulation of cytoskeleton organization	Product B V3 SUBG	2.267159509	0.010144117
cytokine production	Product B V3 SUBG	2.265455874	0.009589776
sequestering of zinc ion	Product B V3 SUBG	2.264105441	0.009062607
chemokine production	Product B V3 SUBG	2.264080101	0.009062607
antimicrobial humoral response	Product B V3 SUBG	2.260004794	0.027649527
glutamate-ammonia ligase activity	Product B V3 SUBG	2.253778074	0.019384996
antimicrobial humoral immune response mediated by antimicrobial peptide	Product B V3 SUBG	2.25017464	0.017461229
cell-cell signaling	Product B V3 SUBG	2.227194438	0.011339073
cell junction	Product B V3 SUBG	2.226507863	0.01336608
modulation of process of other organism	Product B V3 SUBG	2.191713031	0.007632882
peptidyl-cysteine S-trans-nitrosylation	Product B V3 SUBG	2.179649634	0.00640875
antioxidant activity	Product B V3 SUBG	2.170911949	0.003722992
positive regulation of neuron projection development	Product B V3 SUBG	2.161135069	0.007203336
cysteine-type endopeptidase inhibitor activity	Product B V3 SUBG	2.154679366	0.042601311
translation	Product B V2 SUBG	3.601581062	0.010726809
structural constituent of ribosome	Product B V2 SUBG	3.592047496	0.011339073
ribosome	Product B V2 SUBG	3.496305651	0.005051804
rRNA binding	Product B V2 SUBG	3.390564483	0.018401118
plasma membrane	Product B V2 SUBG	2.921973878	0.042601311

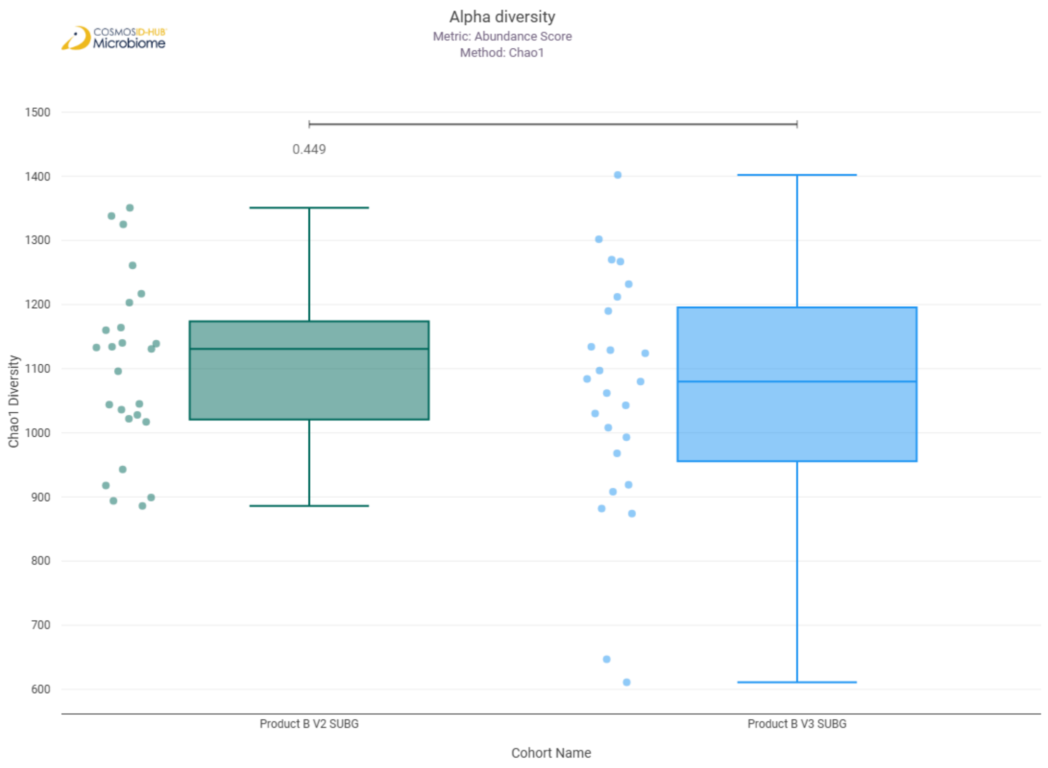


GTP binding	Product B V2 SUBG	2.880037294	1.84E-02
translation elongation factor activity	Product B V2 SUBG	2.873885039	0.01336608
transmembrane transport	Product B V2 SUBG	2.73919936	0.01265739
small ribosomal subunit	Product B V2 SUBG	2.732488352	0.010726809
tRNA binding	Product B V2 SUBG	2.727081355	0.044622577
large ribosomal subunit	Product B V2 SUBG	2.701633795	0.006041816
GTPase activity	Product B V2 SUBG	2.698296247	0.023794451
cell outer membrane	Product B V2 SUBG	2.652317031	0.027649527
transferase activity	Product B V2 SUBG	2.568598356	0.048908406
proton-transporting ATP synthase activity, rotational mechanism	Product B V2 SUBG	2.529987281	0.009062607
ATPase activity	Product B V2 SUBG	2.482085992	0.048908406
ATP synthesis coupled proton transport	Product B V2 SUBG	2.411899998	0.006041816
tricarboxylic acid cycle	Product B V2 SUBG	2.375045571	0.000148684
DNA-directed 5'-3' RNA polymerase activity	Product B V2 SUBG	2.371051842	0.003287086
protein transport	Product B V2 SUBG	2.365132113	0.030509062
transcription, DNA-templated	Product B V2 SUBG	2.334049907	0.005364191
transmembrane transporter activity	Product B V2 SUBG	2.307915949	0.030509062
proton-transporting ATP synthase complex, catalytic core F(1)	Product B V2 SUBG	2.197913979	0.01265739
large ribosomal subunit rRNA binding	Product B V2 SUBG	2.141433642	0.030509062
porin activity	Product B V2 SUBG	2.118878001	9.24207E-05
ribosome biogenesis	Product B V2 SUBG	2.103632447	0.022617484
DNA replication	Product B V2 SUBG	2.095886808	0.046724152
proton-transporting ATP synthase complex, coupling factor F(o)	Product B V2 SUBG	2.078331122	0.011982167
sodium ion transport	Product B V2 SUBG	2.057929399	0.001616222
heme binding	Product B V2 SUBG	2.055269007	0.001321949
iron-sulfur cluster binding	Product B V2 SUBG	2.040464006	0.044622577
DNA repair	Product B V2 SUBG	2.022758739	0.032031691
ion transport	Product B V2 SUBG	2.008697679	8.52725E-05
pore complex	Product B V2 SUBG	2.003123056	0.000160745

Enzyme Commission

Alpha Diversity (EC)

Chao1



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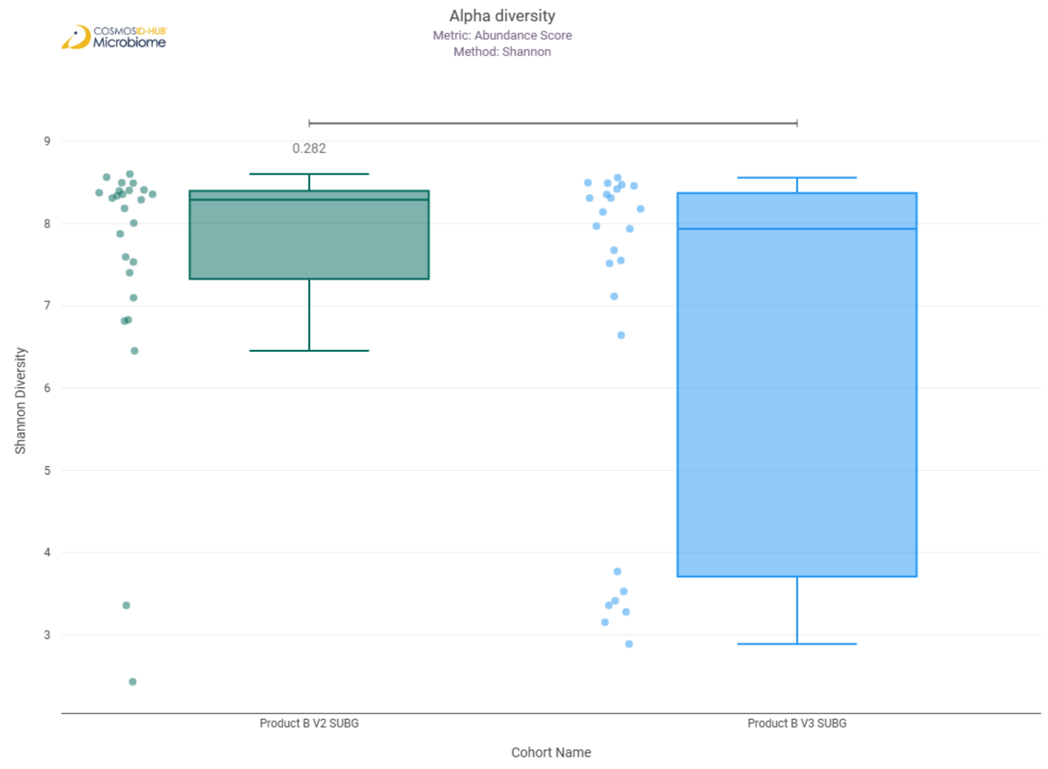
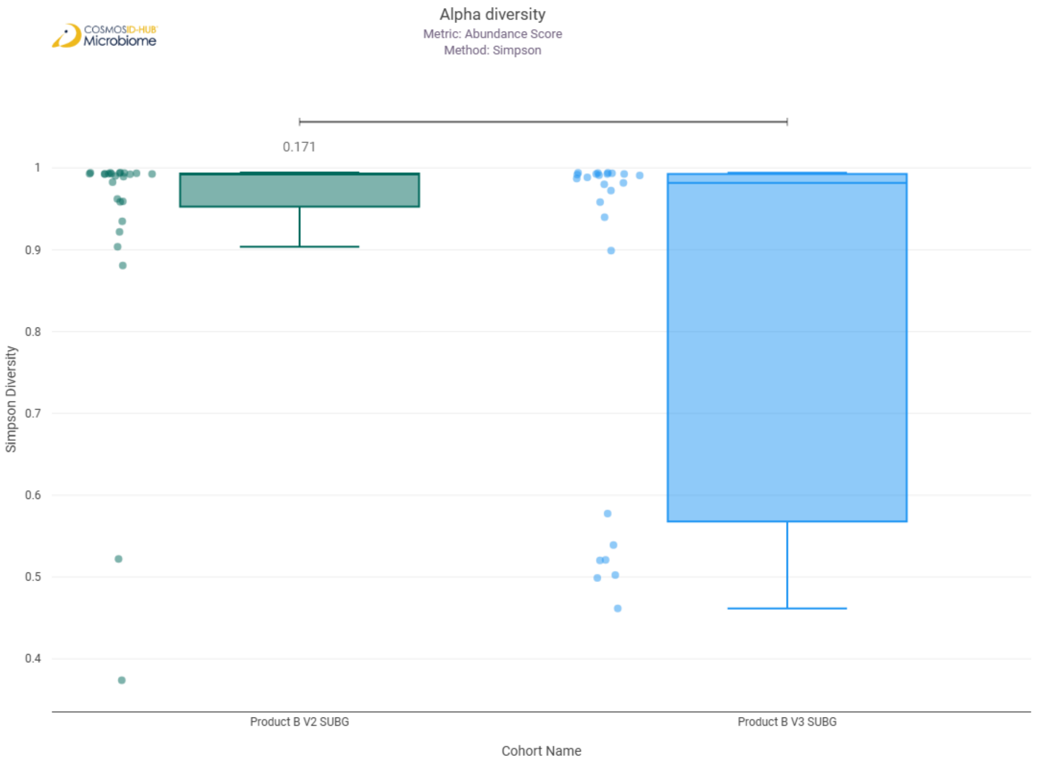
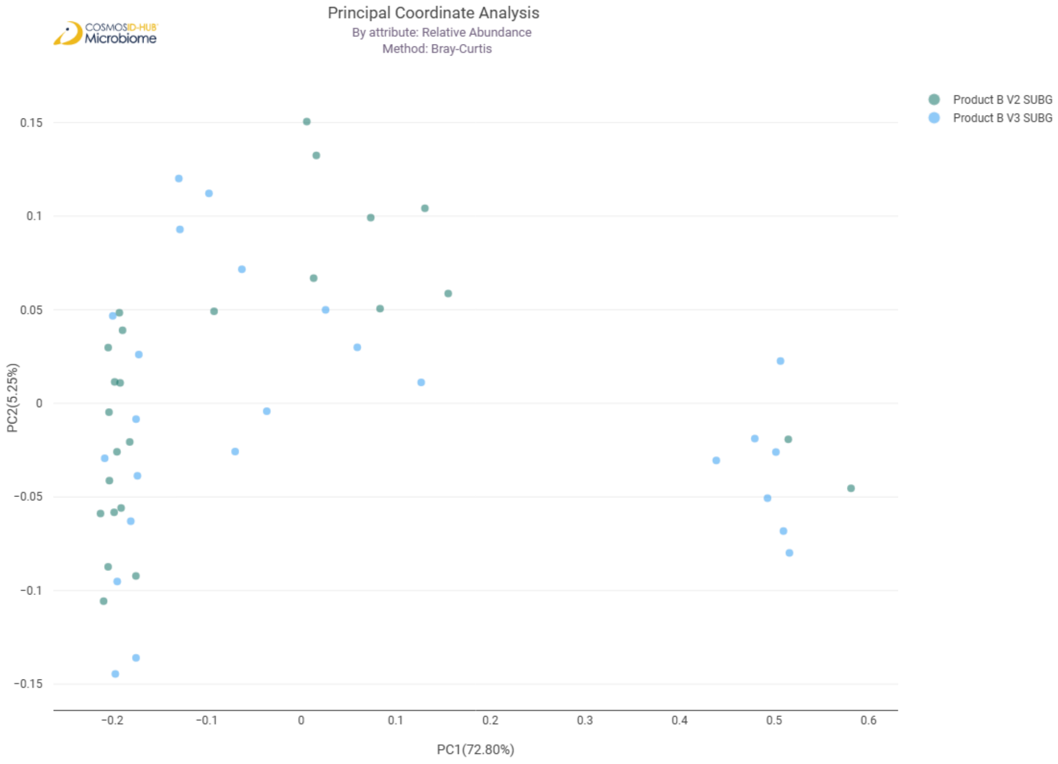
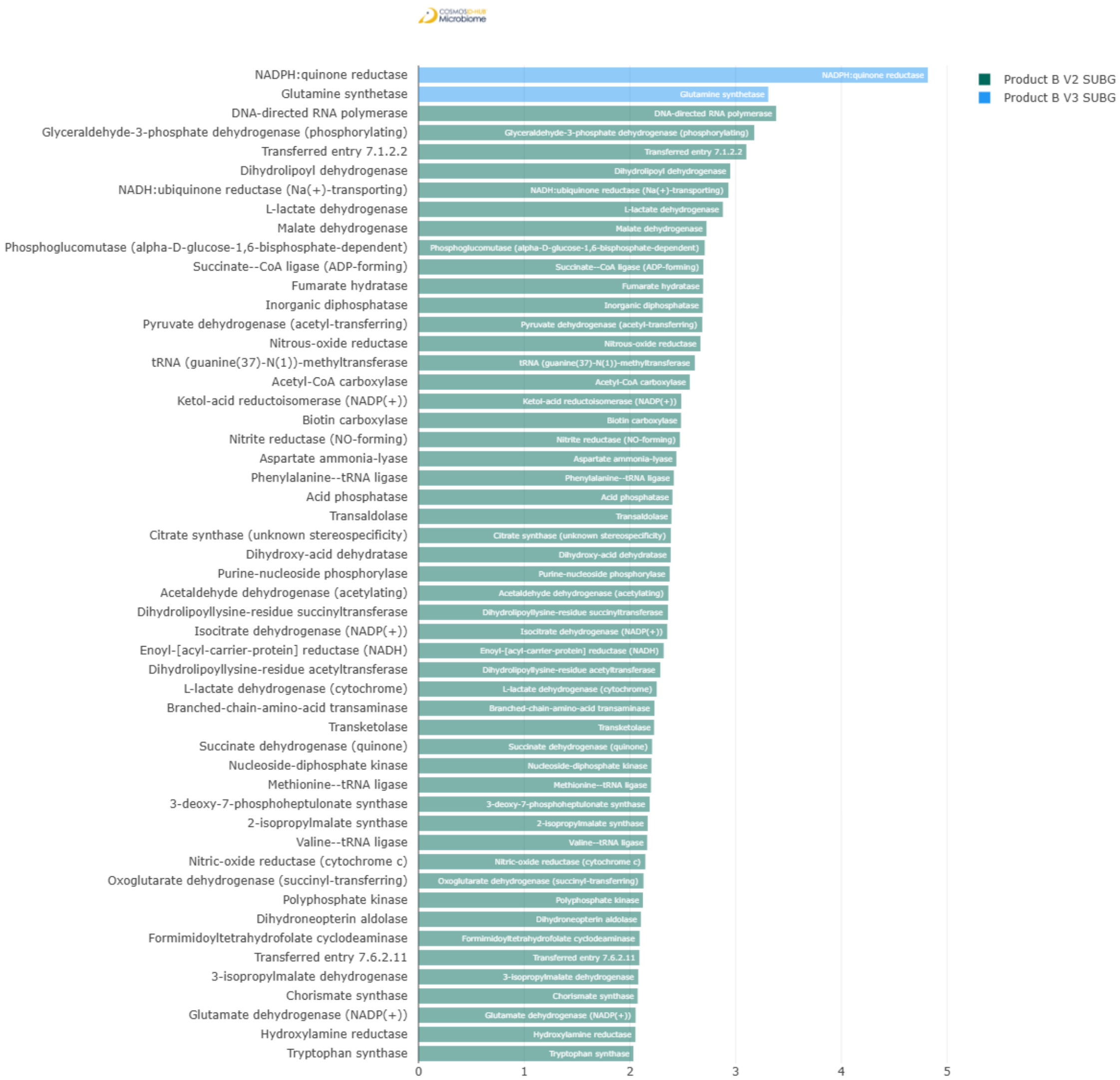


Simpson	

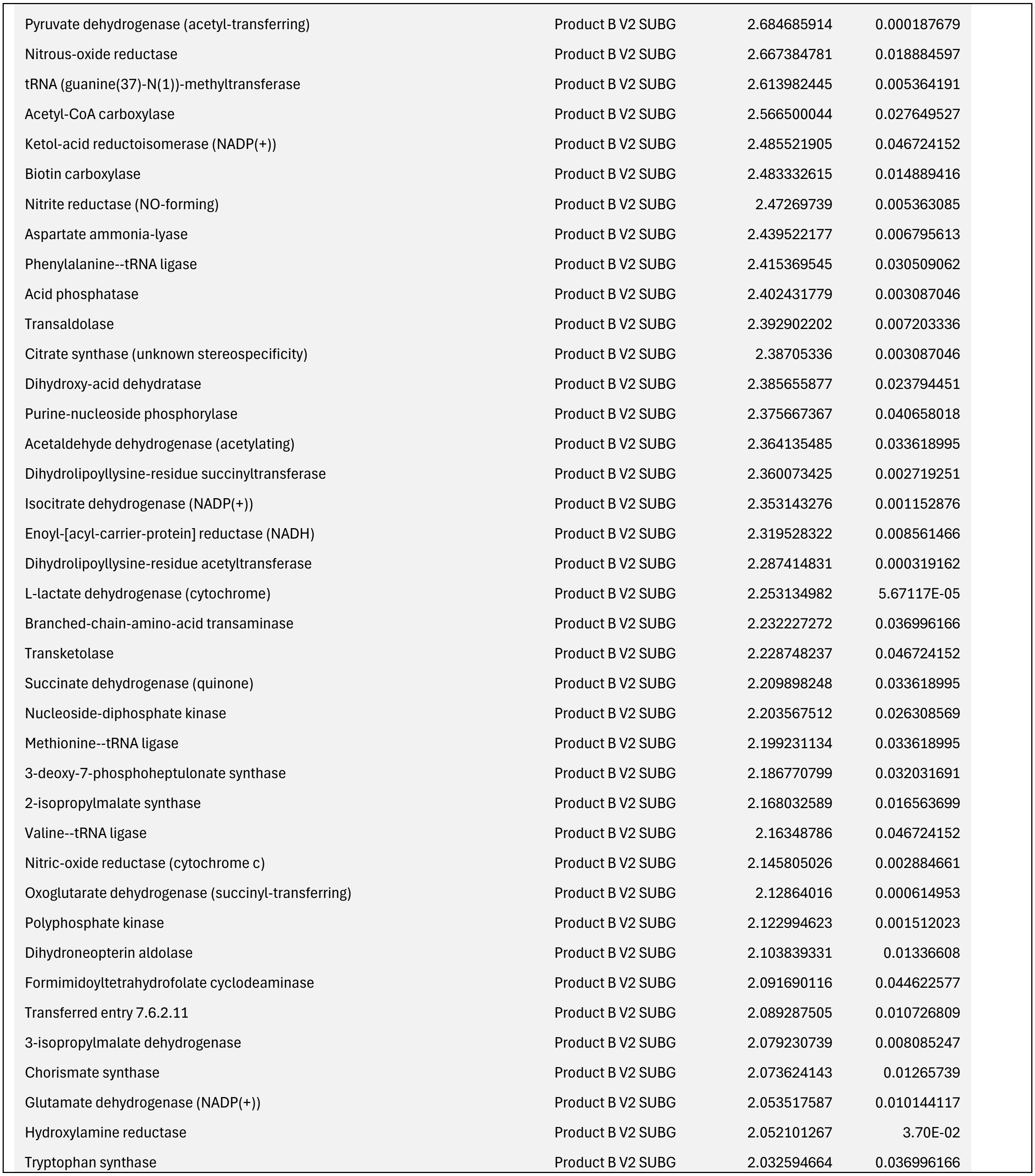
Beta Diversity (EC)

Bray-Curtis PERMNOVA p = 0.093	

Differential Abundance (LEfSe) (EC)



Feature	Enriched Cohort	LDA Score	P-value
NADPH:quinone reductase	Product B V3 SUBG	4.817843052	0.032031691
Glutamine synthetase	Product B V3 SUBG	3.308540704	0.022617484
DNA-directed RNA polymerase	Product B V2 SUBG	3.383240925	0.019384996
Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	Product B V2 SUBG	3.176211311	0.025024185
Transferred entry 7.1.2.2	Product B V2 SUBG	3.10148784	0.004210827
Dihydrolipoyl dehydrogenase	Product B V2 SUBG	2.948469076	5.22129E-05
NADH:ubiquinone reductase (Na(+)-transporting)	Product B V2 SUBG	2.931691645	0.004210827
L-lactate dehydrogenase	Product B V2 SUBG	2.879235232	0.048908406
Malate dehydrogenase	Product B V2 SUBG	2.724100617	0.005051804
Phosphoglucomutase (alpha-D-glucose-1,6-bisphosphate-dependent)	Product B V2 SUBG	2.707465232	1.27E-02
Succinate--CoA ligase (ADP-forming)	Product B V2 SUBG	2.694617006	0.023794451
Fumarate hydratase	Product B V2 SUBG	2.692816588	0.000160745
Inorganic diphosphatase	Product B V2 SUBG	2.690026587	0.003960093



Pyruvate dehydrogenase (acetyl-transferring)	Product B V2 SUBG	2.684685914	0.000187679
Nitrous-oxide reductase	Product B V2 SUBG	2.667384781	0.018884597
tRNA (guanine(37)-N(1))-methyltransferase	Product B V2 SUBG	2.613982445	0.005364191
Acetyl-CoA carboxylase	Product B V2 SUBG	2.566500044	0.027649527
Ketol-acid reductoisomerase (NADP(+))	Product B V2 SUBG	2.485521905	0.046724152
Biotin carboxylase	Product B V2 SUBG	2.483332615	0.014889416
Nitrite reductase (NO-forming)	Product B V2 SUBG	2.47269739	0.005363085
Aspartate ammonia-lyase	Product B V2 SUBG	2.439522177	0.006795613
Phenylalanine--tRNA ligase	Product B V2 SUBG	2.415369545	0.030509062
Acid phosphatase	Product B V2 SUBG	2.402431779	0.003087046
Transaldolase	Product B V2 SUBG	2.392902202	0.007203336
Citrate synthase (unknown stereospecificity)	Product B V2 SUBG	2.38705336	0.003087046
Dihydroxy-acid dehydratase	Product B V2 SUBG	2.385655877	0.023794451
Purine-nucleoside phosphorylase	Product B V2 SUBG	2.375667367	0.040658018
Acetaldehyde dehydrogenase (acetylating)	Product B V2 SUBG	2.364135485	0.033618995
Dihydrolipoyllysine-residue succinyltransferase	Product B V2 SUBG	2.360073425	0.002719251
Isocitrate dehydrogenase (NADP(+))	Product B V2 SUBG	2.353143276	0.001152876
Enoyl-[acyl-carrier-protein] reductase (NADH)	Product B V2 SUBG	2.319528322	0.008561466
Dihydrolipoyllysine-residue acetyltransferase	Product B V2 SUBG	2.287414831	0.000319162
L-lactate dehydrogenase (cytochrome)	Product B V2 SUBG	2.253134982	5.67117E-05
Branched-chain-amino-acid transaminase	Product B V2 SUBG	2.232227272	0.036996166
Transketolase	Product B V2 SUBG	2.228748237	0.046724152
Succinate dehydrogenase (quinone)	Product B V2 SUBG	2.209898248	0.033618995
Nucleoside-diphosphate kinase	Product B V2 SUBG	2.203567512	0.026308569
Methionine--tRNA ligase	Product B V2 SUBG	2.199231134	0.033618995
3-deoxy-7-phosphoheptulonate synthase	Product B V2 SUBG	2.186770799	0.032031691
2-isopropylmalate synthase	Product B V2 SUBG	2.168032589	0.016563699
Valine--tRNA ligase	Product B V2 SUBG	2.16348786	0.046724152
Nitric-oxide reductase (cytochrome c)	Product B V2 SUBG	2.145805026	0.002884661
Oxoglutarate dehydrogenase (succinyl-transferring)	Product B V2 SUBG	2.12864016	0.000614953
Polyphosphate kinase	Product B V2 SUBG	2.122994623	0.001512023
Dihydroneopterin aldolase	Product B V2 SUBG	2.103839331	0.01336608
Formimidoyltetrahydrofolate cyclodeaminase	Product B V2 SUBG	2.091690116	0.044622577
Transferred entry 7.6.2.11	Product B V2 SUBG	2.089287505	0.010726809
3-isopropylmalate dehydrogenase	Product B V2 SUBG	2.079230739	0.008085247
Chorismate synthase	Product B V2 SUBG	2.073624143	0.01265739
Glutamate dehydrogenase (NADP(+))	Product B V2 SUBG	2.053517587	0.010144117
Hydroxylamine reductase	Product B V2 SUBG	2.052101267	3.70E-02
Tryptophan synthase	Product B V2 SUBG	2.032594664	0.036996166

MetaCyc Pathway

Alpha Diversity (MetaCyc)

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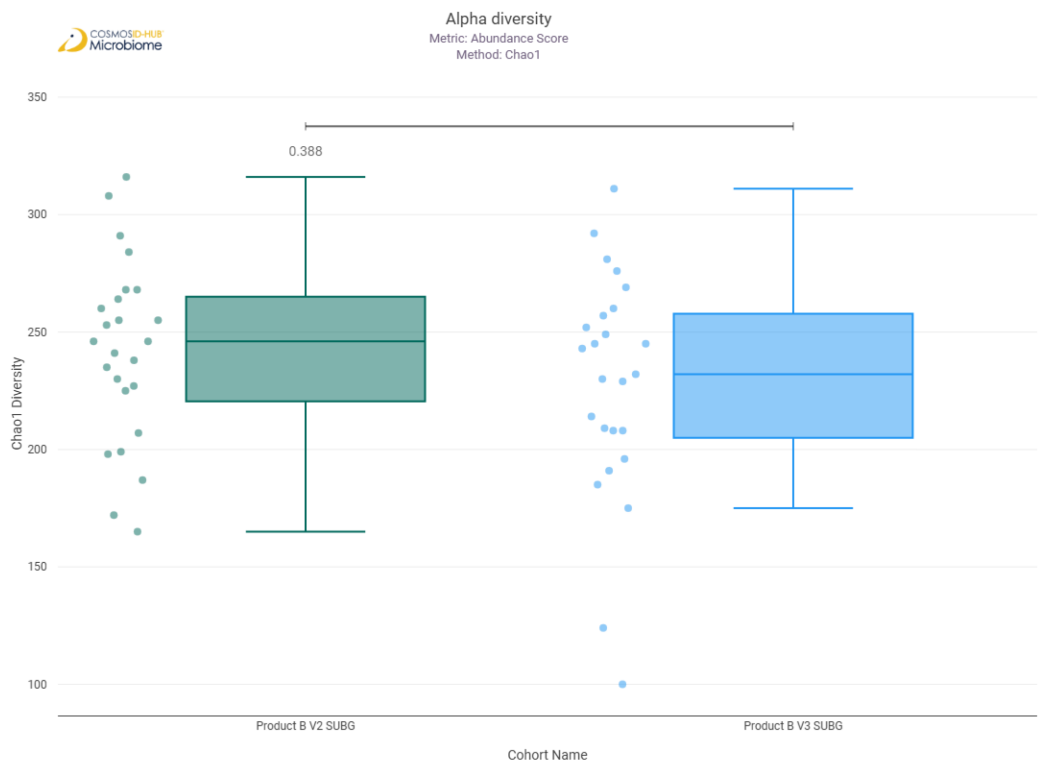

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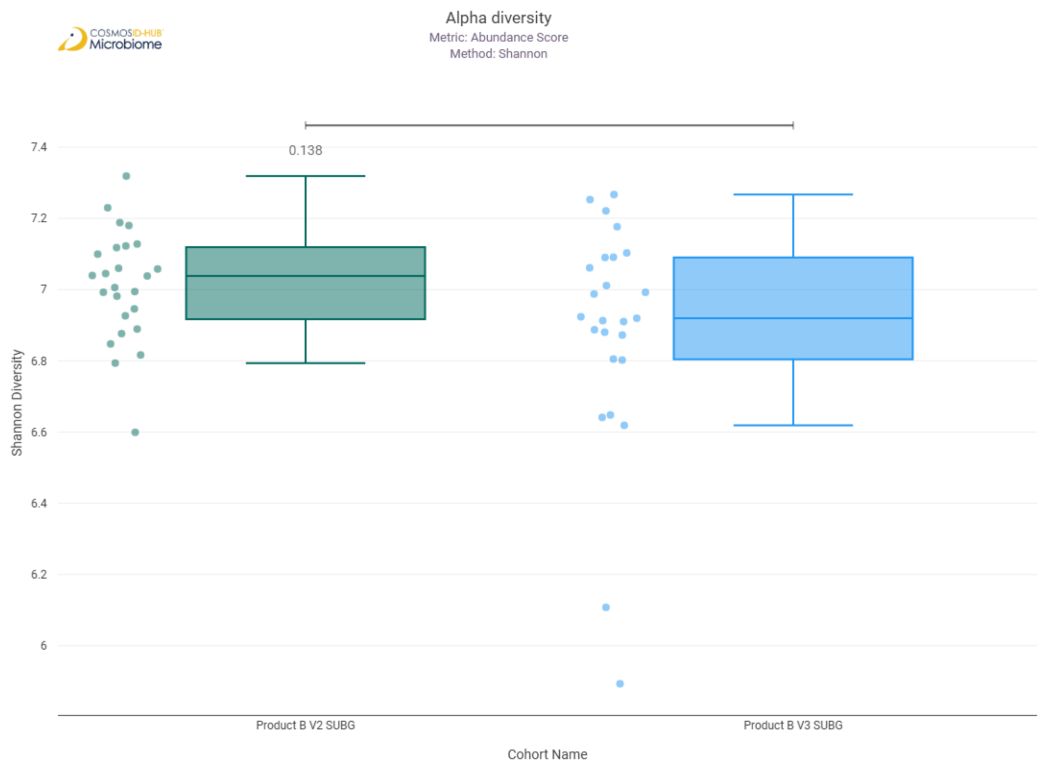

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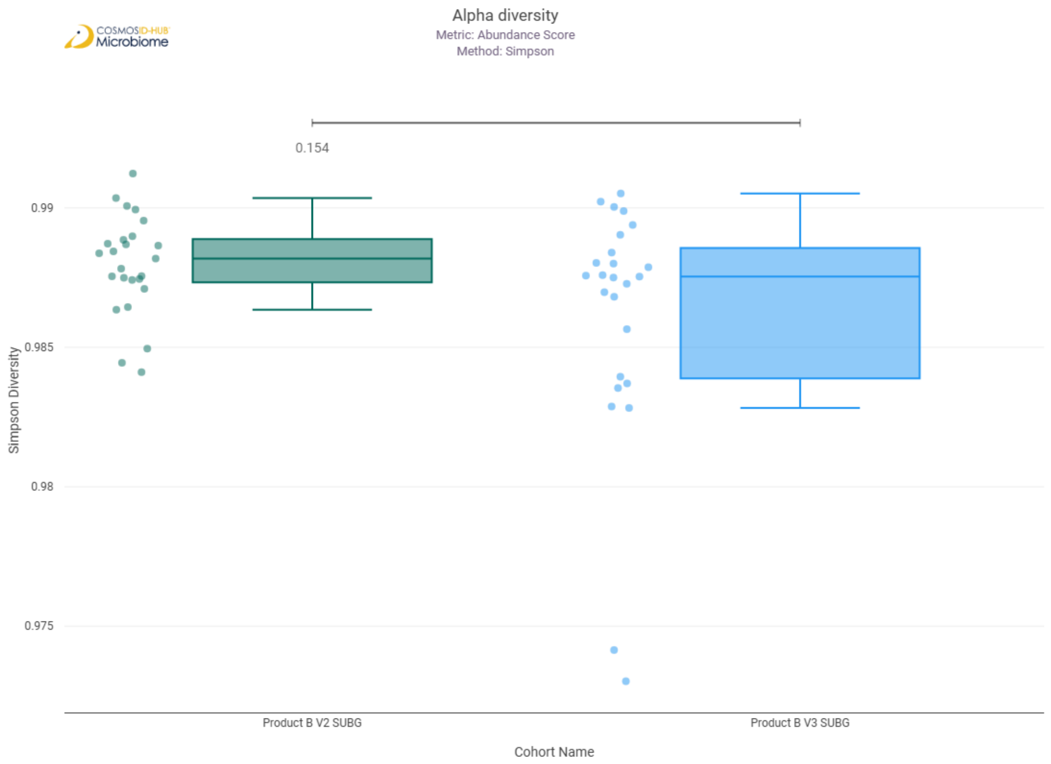
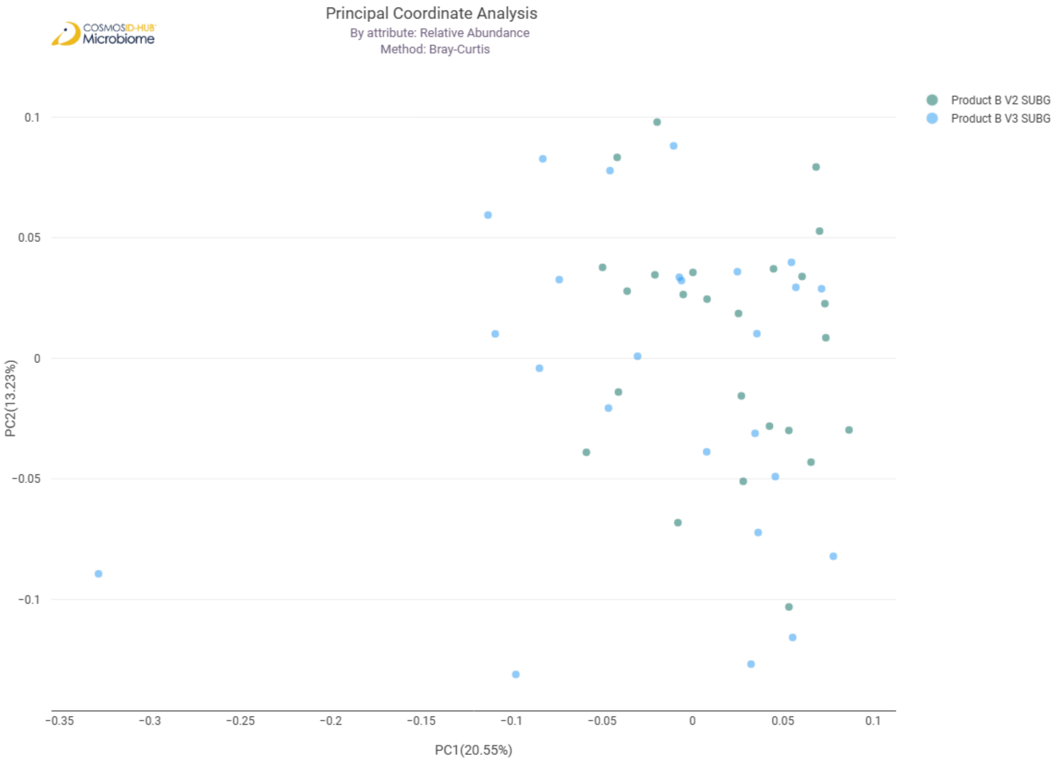
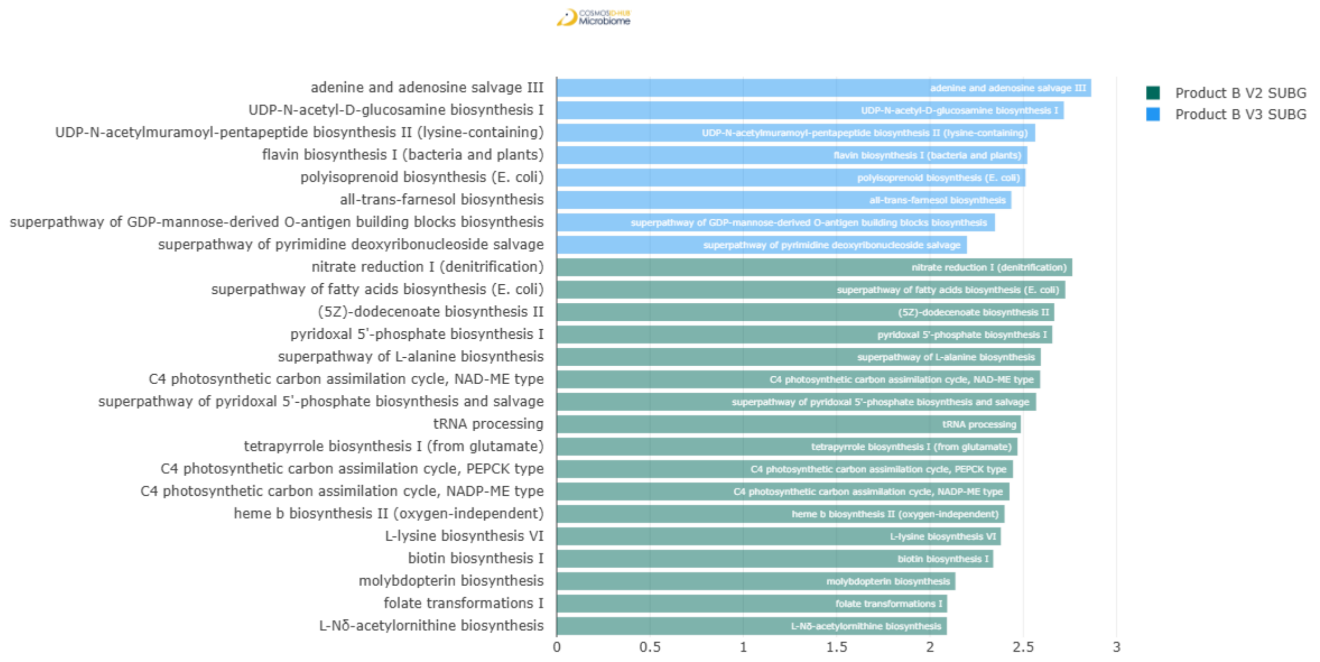
Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis PERMNOVA p = 0.107	

Differential Abundance (LEfSe) (MetaCyc)



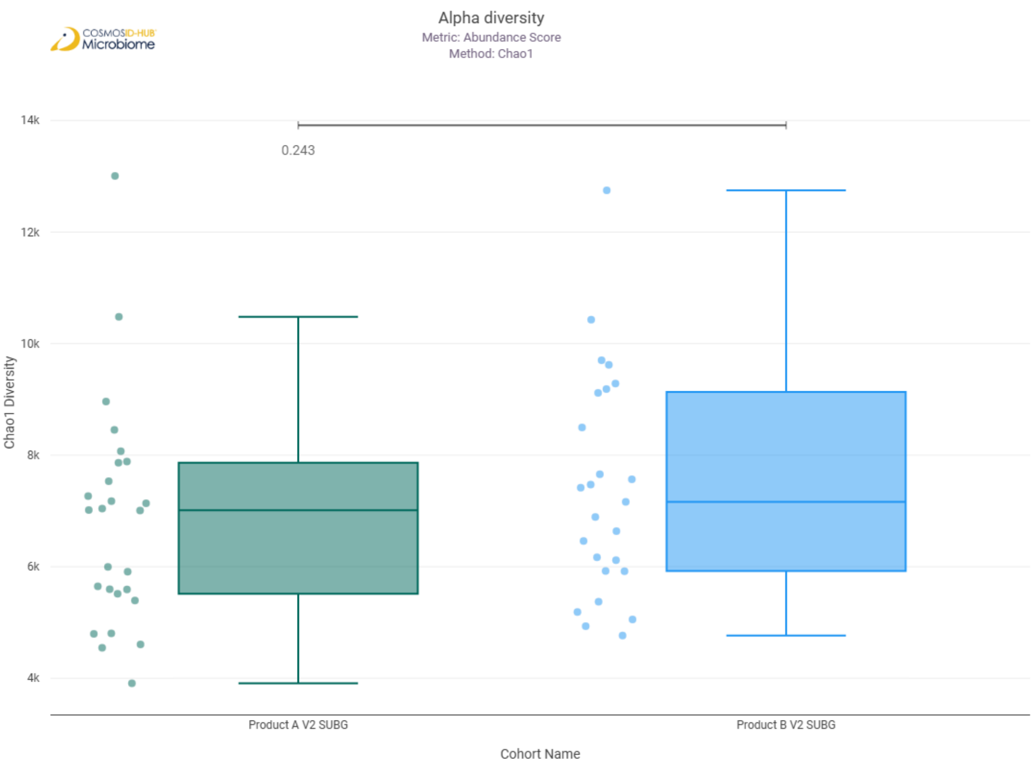
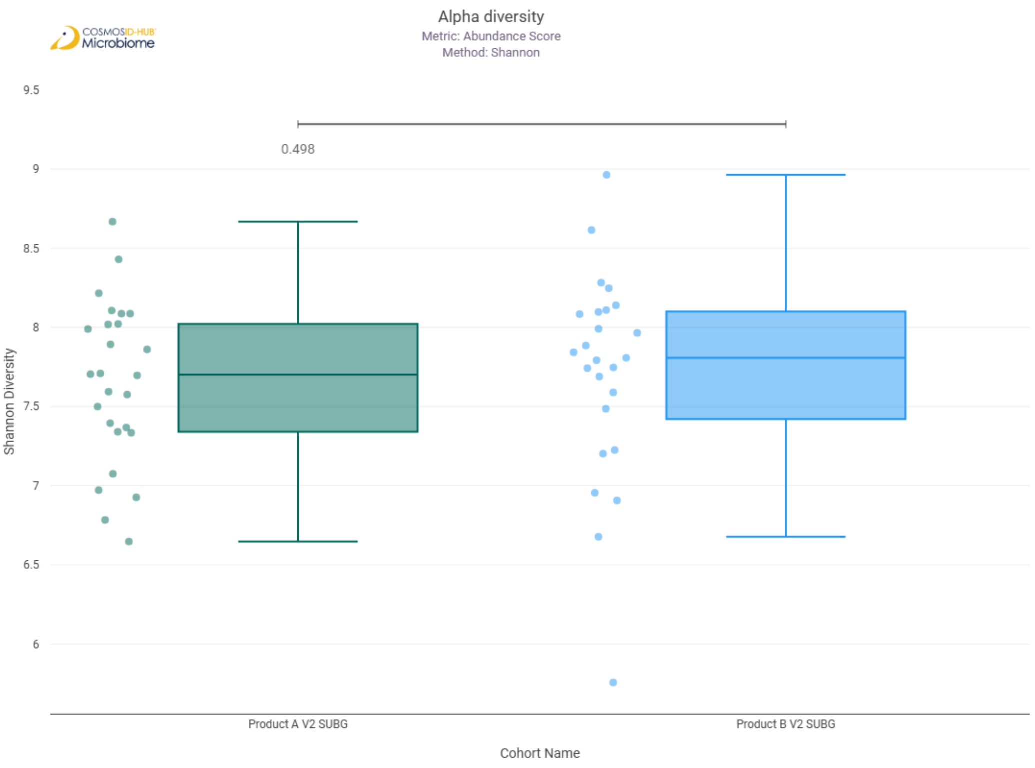
Feature	Enriched Cohort	LDA Score	P-value
adenine and adenosine salvage III	Product B V3 SUBG	2.863969812	0.048908406
UDP-N-acetyl-D-glucosamine biosynthesis I	Product B V3 SUBG	2.717396176	0.036996166
UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)	Product B V3 SUBG	2.564005299	2.15E-02
flavin biosynthesis I (bacteria and plants)	Product B V3 SUBG	2.521691982	0.021478913
polyisoprenoid biosynthesis (E. coli)	Product B V3 SUBG	2.511972274	0.009321172
all-trans-farnesol biosynthesis	Product B V3 SUBG	2.435974793	0.009321172
superpathway of GDP-mannose-derived O-antigen building blocks biosynthesis	Product B V3 SUBG	2.348650203	0.007288006
superpathway of pyrimidine deoxyribonucleoside salvage	Product B V3 SUBG	2.198461861	0.042804512
nitrate reduction I (denitrification)	Product B V2 SUBG	2.76268097	0.028209048
superpathway of fatty acids biosynthesis (E. coli)	Product B V2 SUBG	2.725110183	0.015664854
(5Z)-dodecenoate biosynthesis II	Product B V2 SUBG	2.666038782	0.000376802
pyridoxal 5'-phosphate biosynthesis I	Product B V2 SUBG	2.655506221	0.007401096
superpathway of L-alanine biosynthesis	Product B V2 SUBG	2.593947019	0.001489919
C4 photosynthetic carbon assimilation cycle, NAD-ME type	Product B V2 SUBG	2.590401904	0.000990491
superpathway of pyridoxal 5'-phosphate biosynthesis and salvage	Product B V2 SUBG	2.56884596	0.002984314
tRNA processing	Product B V2 SUBG	2.486859617	0.000545225
tetrapyrrole biosynthesis I (from glutamate)	Product B V2 SUBG	2.469081125	0.026304962
C4 photosynthetic carbon assimilation cycle, PEPCK type	Product B V2 SUBG	2.445053069	0.044617455
C4 photosynthetic carbon assimilation cycle, NADP-ME type	Product B V2 SUBG	2.426092745	0.018401118
heme b biosynthesis II (oxygen-independent)	Product B V2 SUBG	2.399730809	0.011910559
L-lysine biosynthesis VI	Product B V2 SUBG	2.379651672	0.046703062
biotin biosynthesis I	Product B V2 SUBG	2.338785942	0.02096431
molybdopterin biosynthesis	Product B V2 SUBG	2.136102637	0.02751897

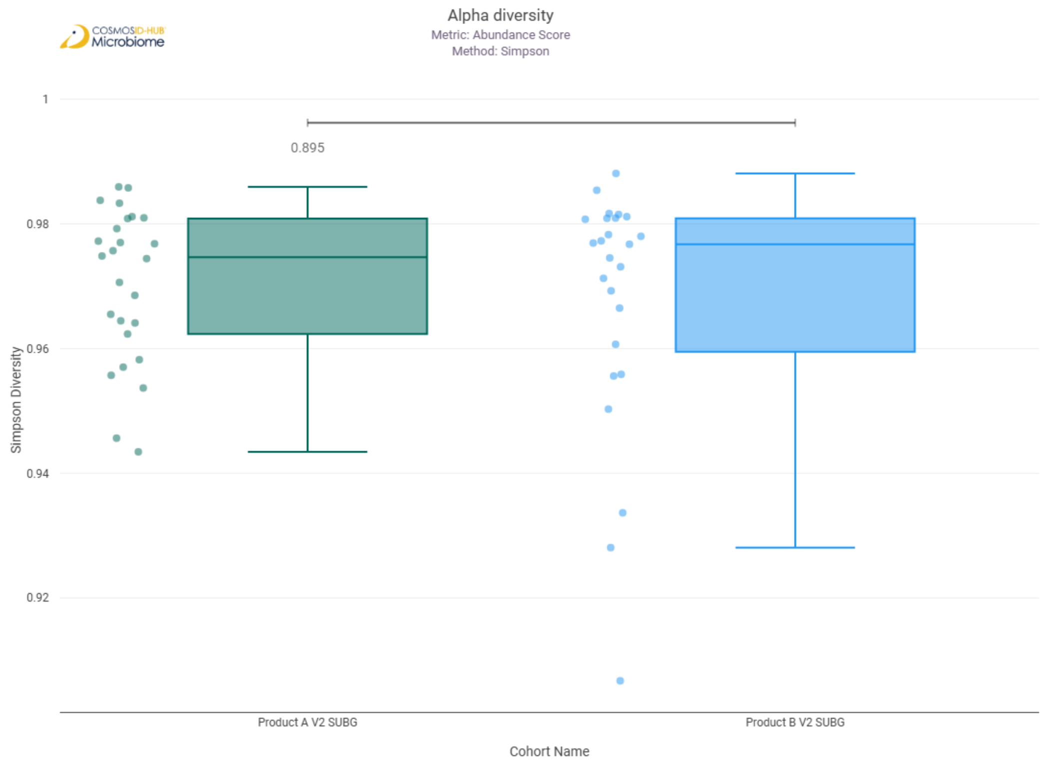
folate transformations I	Product B V2 SUBG	2.092205713	0.011137717
L-Nδ-acetylornithine biosynthesis	Product B V2 SUBG	2.090649307	0.006724272

Comparison 19: Product A V2 SUBG vs Product B V2 SUBG

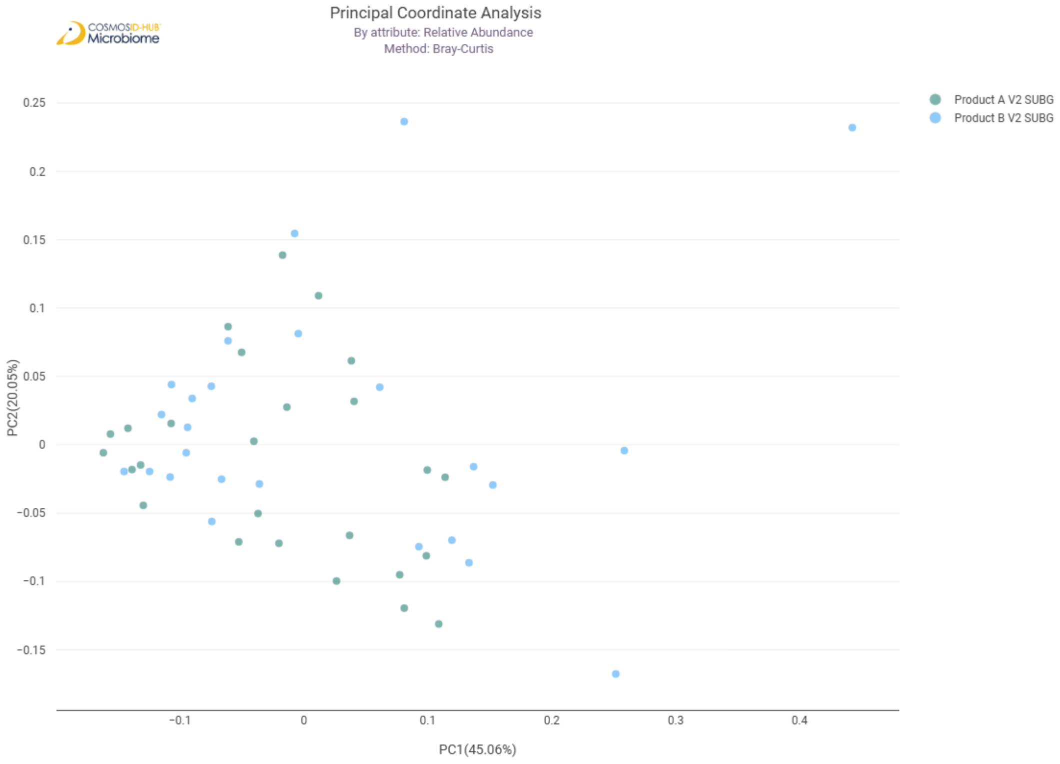
Gene Ontology

Alpha Diversity (GO)

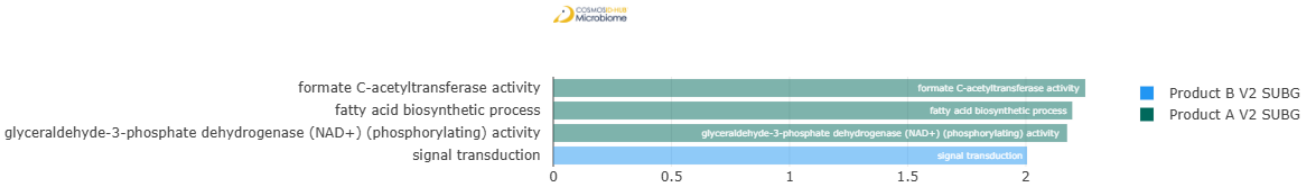
Chao1	
Shannon	

Simpson	

Beta Diversity (GO)

Bray-Curtis PERMNOVA p = 0.224	

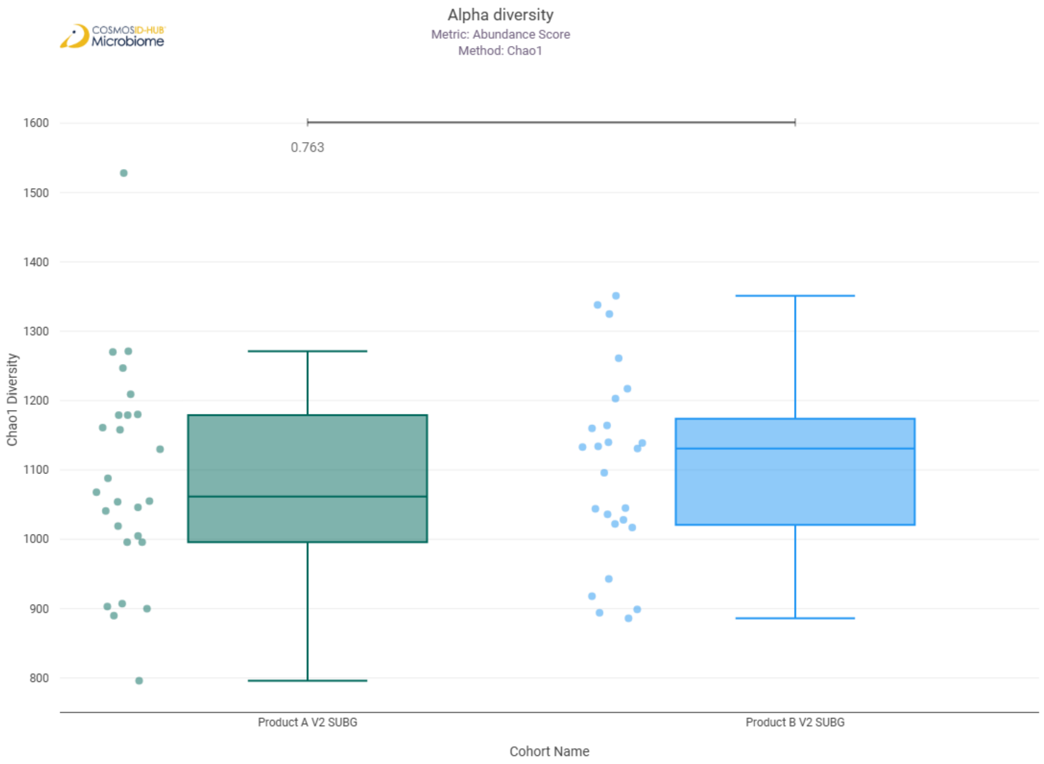
Differential Abundance (LEfSe) (GO)

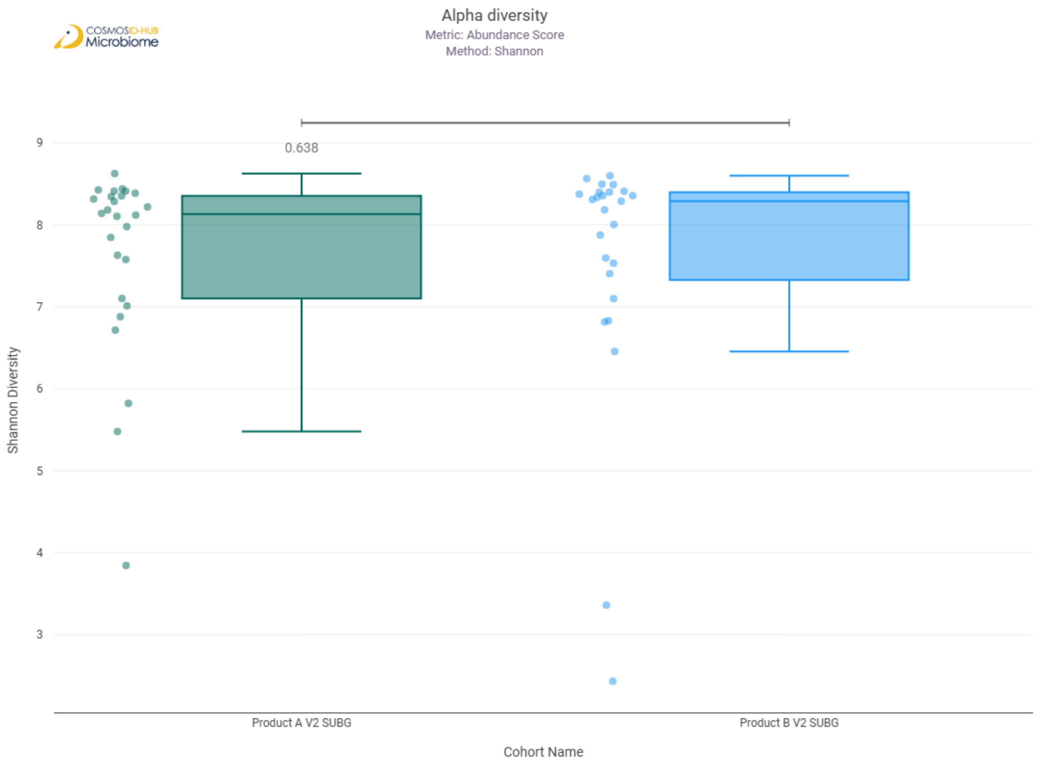
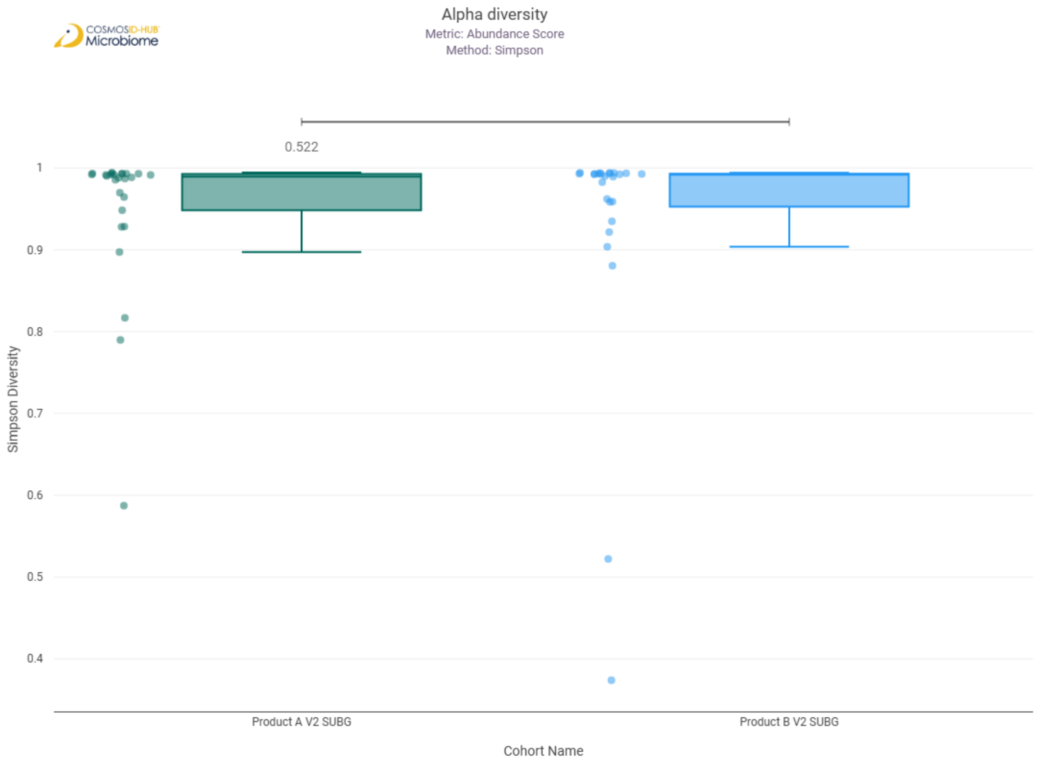


Feature	Enriched Cohort	LDA Score	P-value
formate C-acetyltransferase activity	Product A V2 SUBG	2.251730741	0.02494682
fatty acid biosynthetic process	Product A V2 SUBG	2.196641523	0.016712924
glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity	Product A V2 SUBG	2.175052685	1.36E-02
signal transduction	Product B V2 SUBG	2.005231571	0.045795182

Enzyme Commission

Alpha Diversity (EC)

Chao1	

Shannon	
Simpson	

Beta Diversity (EC)

Bray-Curtis

PERMNOVA
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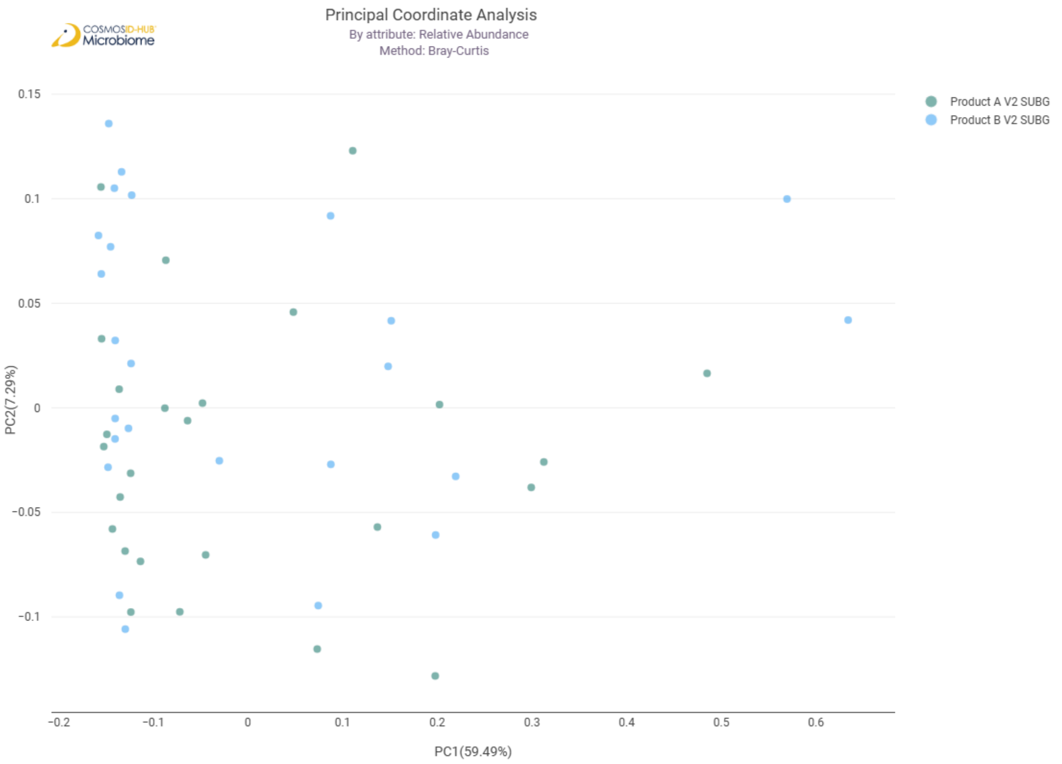
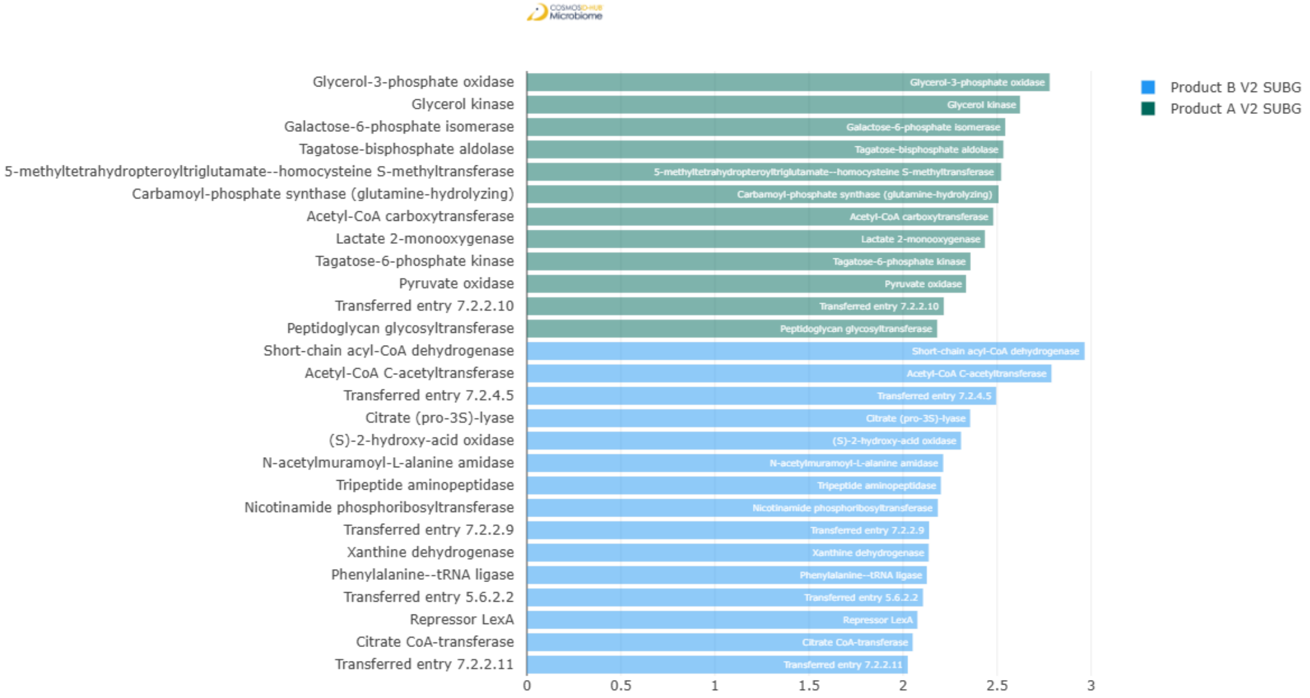
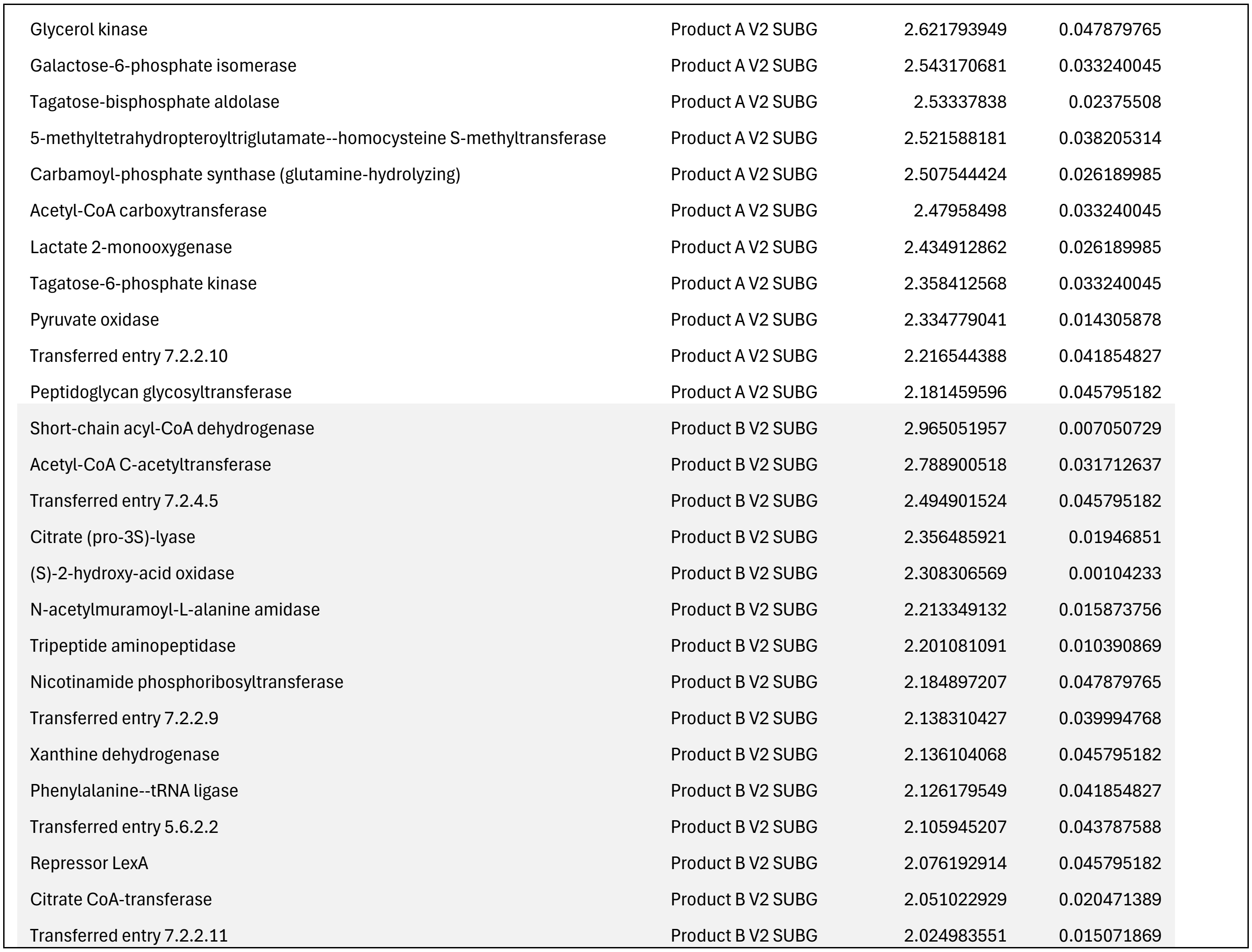


Differential Abundance (LEfSe) (EC)



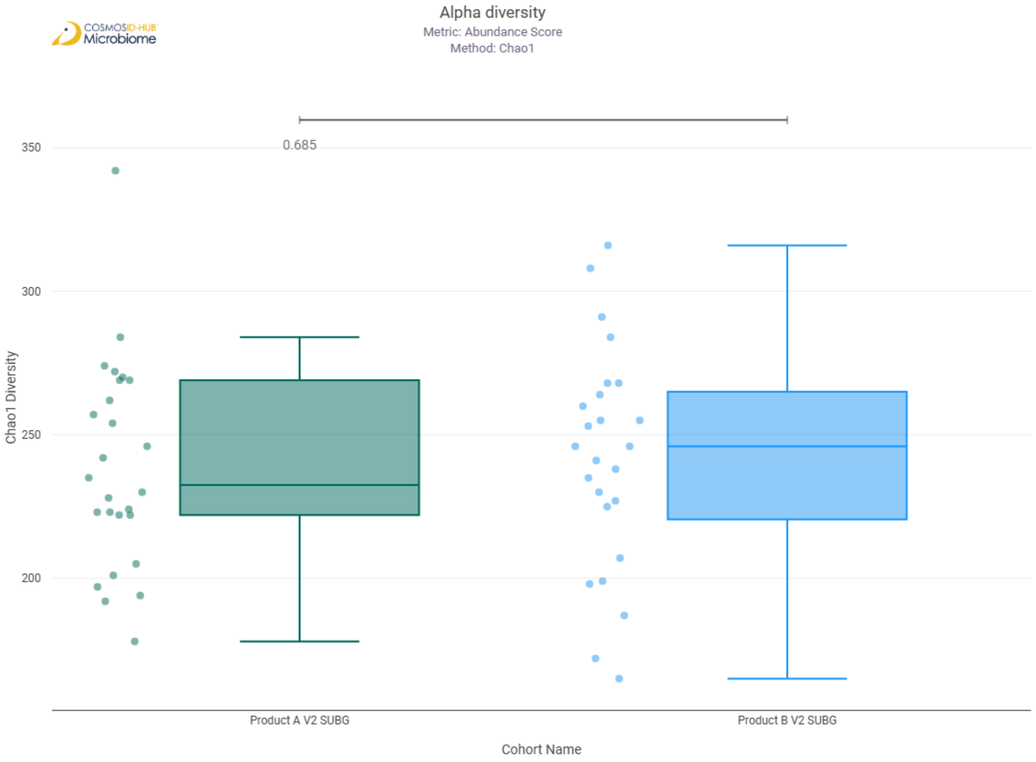
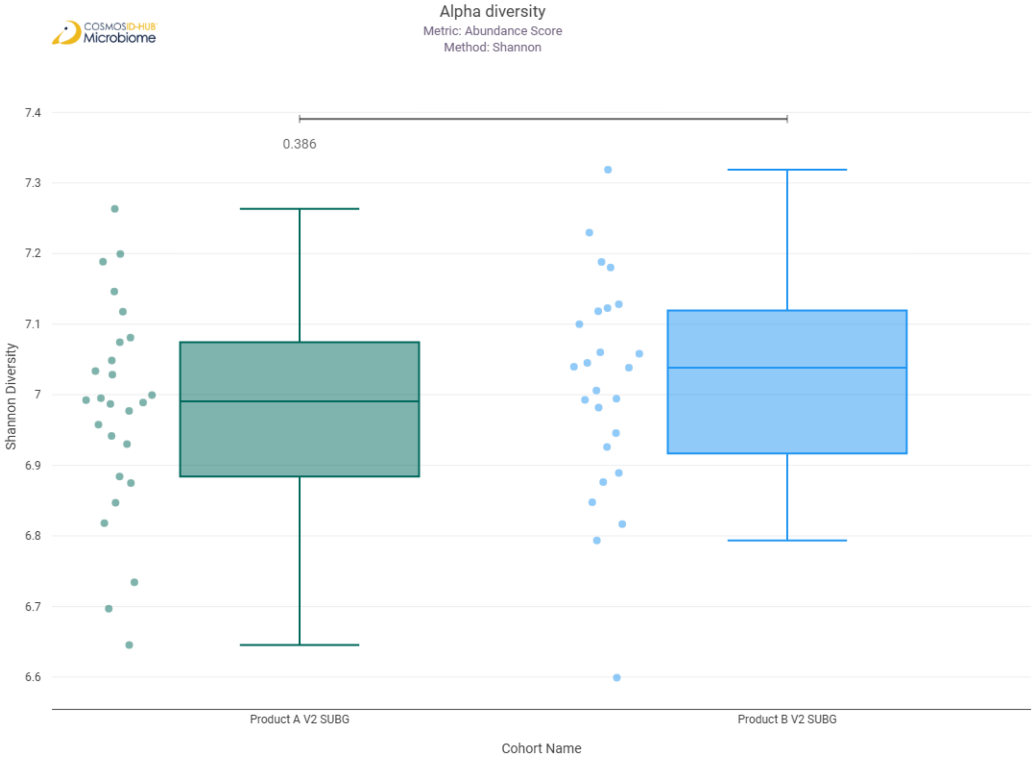
Feature	Enriched Cohort	LDA Score	P-value
Glycerol-3-phosphate oxidase	Product A V2 SUBG	2.779339307	7.46E-03



Glycerol kinase	Product A V2 SUBG	2.621793949	0.047879765
Galactose-6-phosphate isomerase	Product A V2 SUBG	2.543170681	0.033240045
Tagatose-bisphosphate aldolase	Product A V2 SUBG	2.53337838	0.02375508
5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	Product A V2 SUBG	2.521588181	0.038205314
Carbamoyl-phosphate synthase (glutamine-hydrolyzing)	Product A V2 SUBG	2.507544424	0.026189985
Acetyl-CoA carboxytransferase	Product A V2 SUBG	2.47958498	0.033240045
Lactate 2-monooxygenase	Product A V2 SUBG	2.434912862	0.026189985
Tagatose-6-phosphate kinase	Product A V2 SUBG	2.358412568	0.033240045
Pyruvate oxidase	Product A V2 SUBG	2.334779041	0.014305878
Transferred entry 7.2.2.10	Product A V2 SUBG	2.216544388	0.041854827
Peptidoglycan glycosyltransferase	Product A V2 SUBG	2.181459596	0.045795182
Short-chain acyl-CoA dehydrogenase	Product B V2 SUBG	2.965051957	0.007050729
Acetyl-CoA C-acetyltransferase	Product B V2 SUBG	2.788900518	0.031712637
Transferred entry 7.2.4.5	Product B V2 SUBG	2.494901524	0.045795182
Citrate (pro-3S)-lyase	Product B V2 SUBG	2.356485921	0.01946851
(S)-2-hydroxy-acid oxidase	Product B V2 SUBG	2.308306569	0.00104233
N-acetylmuramoyl-L-alanine amidase	Product B V2 SUBG	2.213349132	0.015873756
Tripeptide aminopeptidase	Product B V2 SUBG	2.201081091	0.010390869
Nicotinamide phosphoribosyltransferase	Product B V2 SUBG	2.184897207	0.047879765
Transferred entry 7.2.2.9	Product B V2 SUBG	2.138310427	0.039994768
Xanthine dehydrogenase	Product B V2 SUBG	2.136104068	0.045795182
Phenylalanine--tRNA ligase	Product B V2 SUBG	2.126179549	0.041854827
Transferred entry 5.6.2.2	Product B V2 SUBG	2.105945207	0.043787588
Repressor LexA	Product B V2 SUBG	2.076192914	0.045795182
Citrate CoA-transferase	Product B V2 SUBG	2.051022929	0.020471389
Transferred entry 7.2.2.11	Product B V2 SUBG	2.024983551	0.015071869

MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1	
Shannon	

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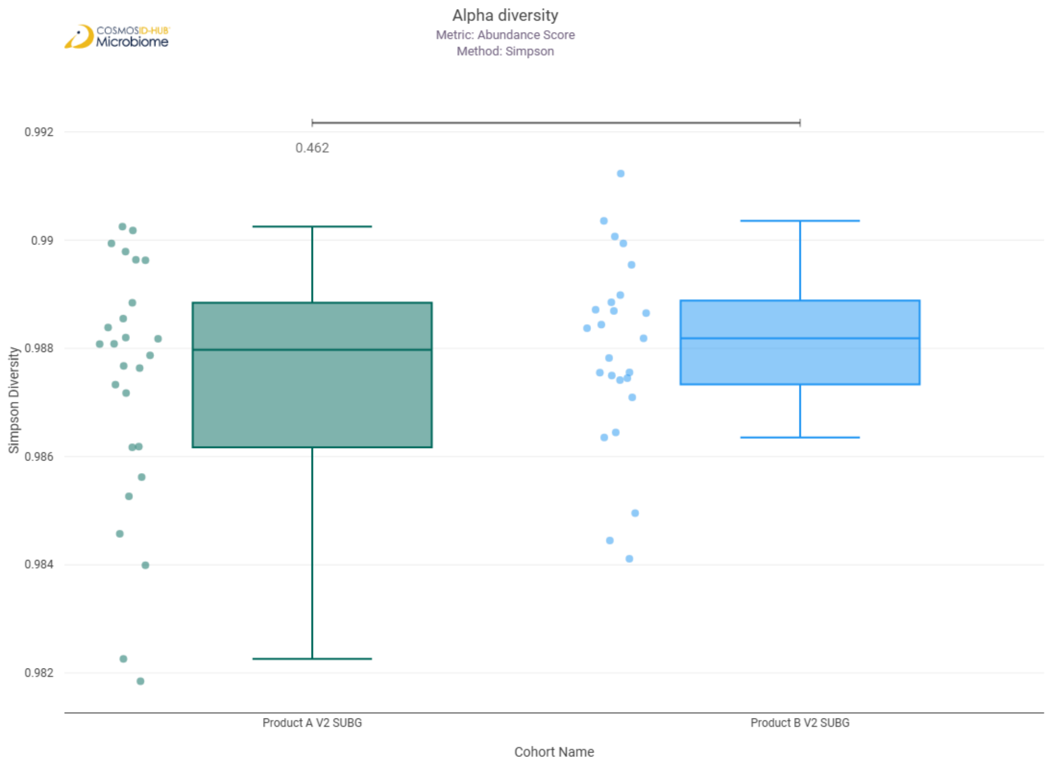
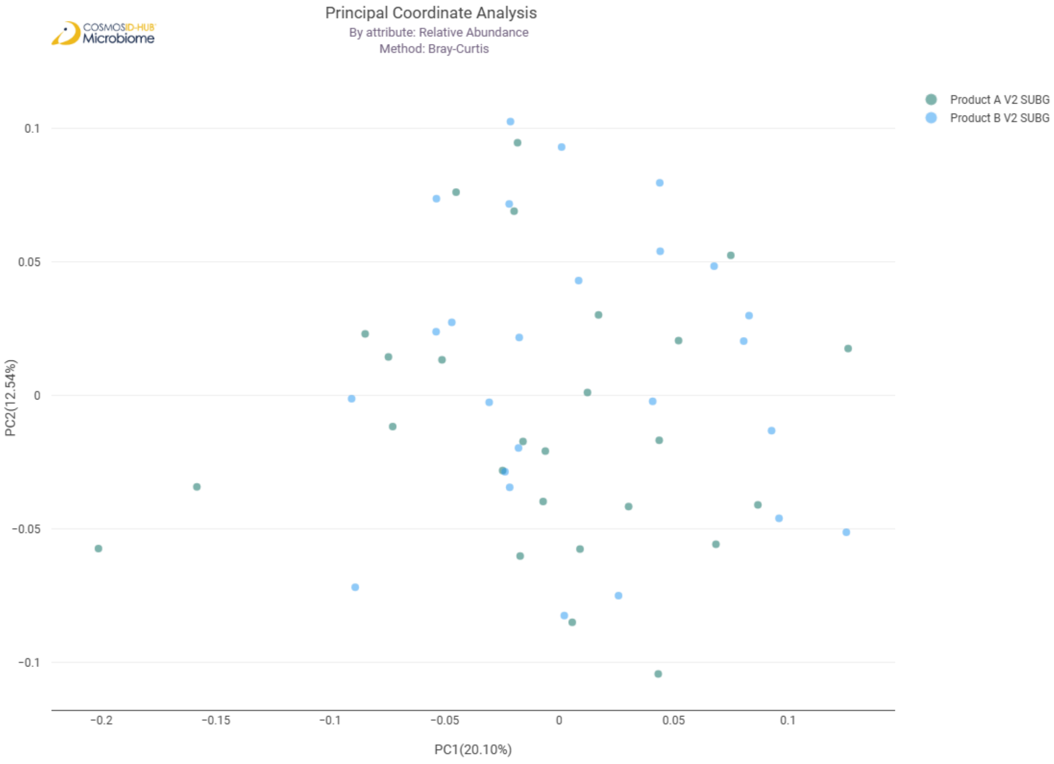


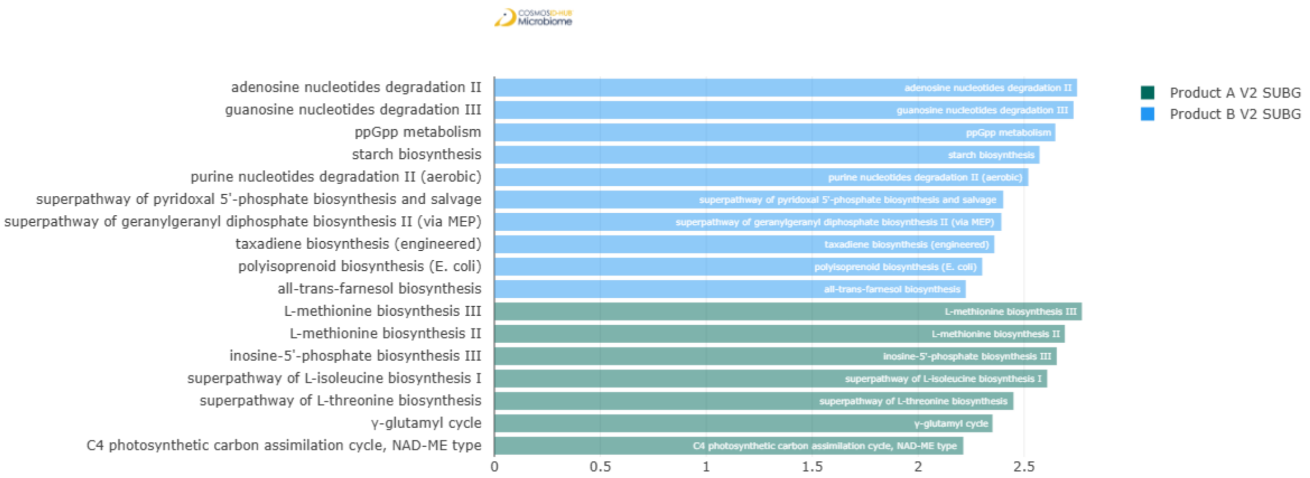
Beta Diversity (MetaCyc)

Bray-Curtis

PERMNOVA
p = 0.374



Differential Abundance (LEfSe) (MetaCyc)

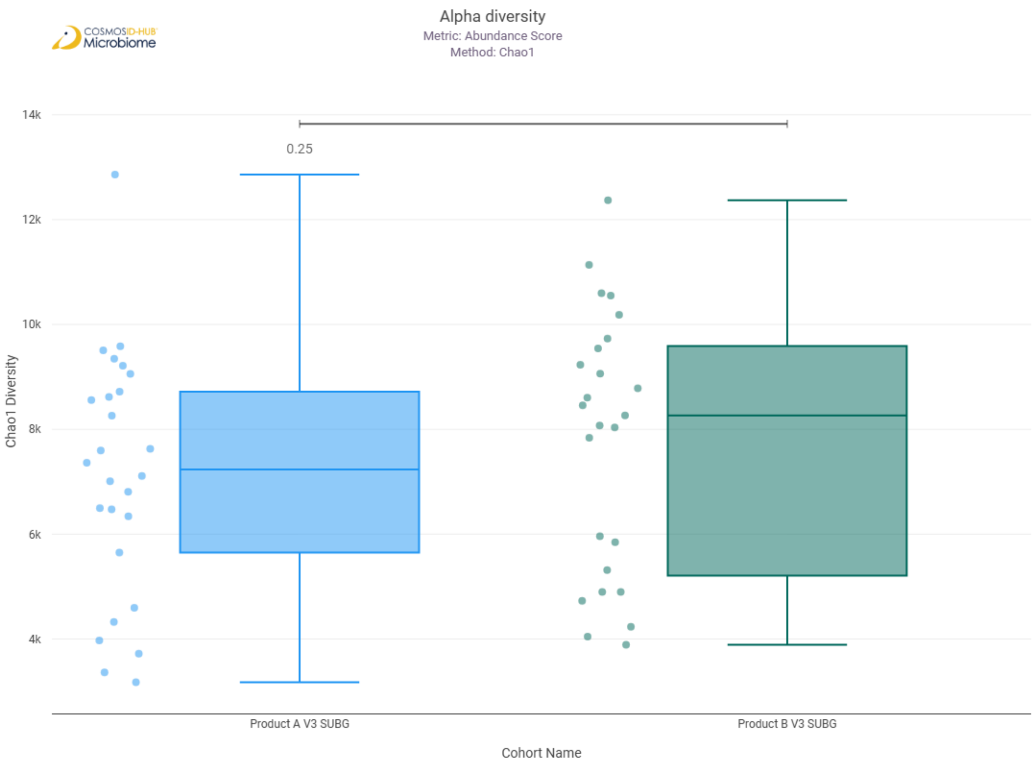
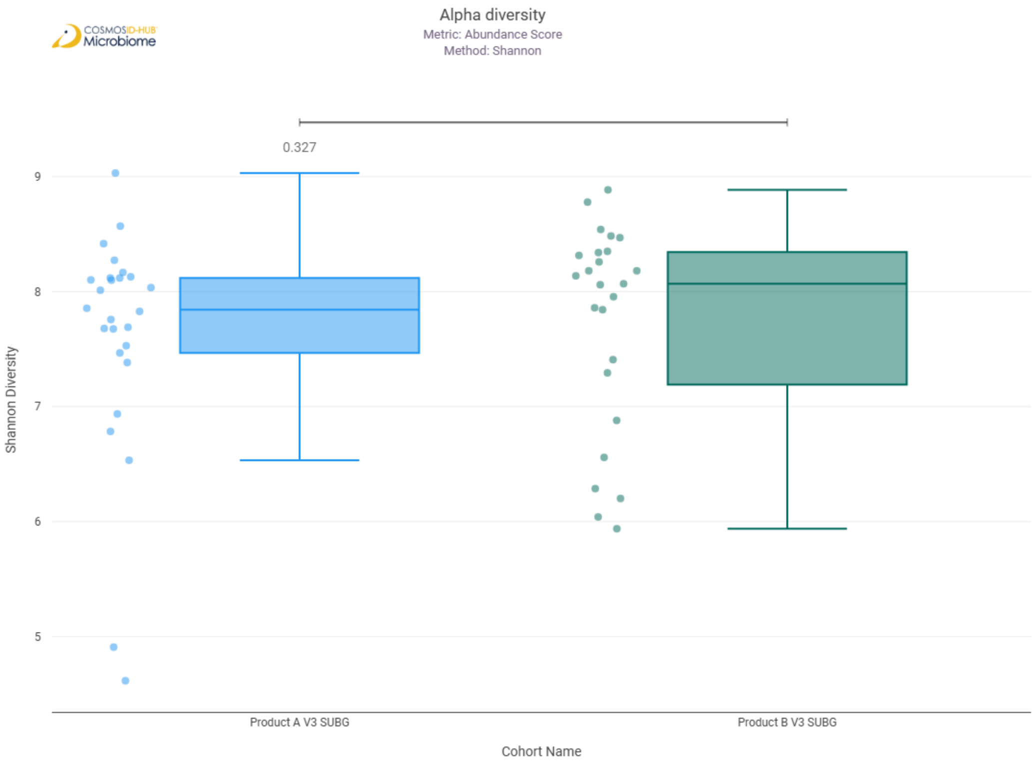


Feature	Enriched Cohort	LDA Score	P-value
adenosine nucleotides degradation II	Product B V2 SUBG	2.750057755	0.038205314
guanosine nucleotides degradation III	Product B V2 SUBG	2.733312194	0.047879765
ppGpp metabolism	Product B V2 SUBG	2.647451783	0.021519031
starch biosynthesis	Product B V2 SUBG	2.572844723	0.034763054
purine nucleotides degradation II (aerobic)	Product B V2 SUBG	2.520017744	0.018888853
superpathway of pyridoxal 5'-phosphate biosynthesis and salvage	Product B V2 SUBG	2.401578989	0.032429435
superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP)	Product B V2 SUBG	2.392576475	0.003816582
taxadiene biosynthesis (engineered)	Product B V2 SUBG	2.359588815	0.005256809
polyisoprenoid biosynthesis (E. coli)	Product B V2 SUBG	2.302252108	0.015864256
all-trans-farnesol biosynthesis	Product B V2 SUBG	2.224778884	0.031697196
L-methionine biosynthesis III	Product A V2 SUBG	2.772698362	1.36E-02
L-methionine biosynthesis II	Product A V2 SUBG	2.692264645	0.039994768
inosine-5'-phosphate biosynthesis III	Product A V2 SUBG	2.65398707	0.008340354
superpathway of L-isoleucine biosynthesis I	Product A V2 SUBG	2.608969913	0.009840467
superpathway of L-threonine biosynthesis	Product A V2 SUBG	2.449856176	0.028837668
γ-glutamyl cycle	Product A V2 SUBG	2.35086058	0.03174462
C4 photosynthetic carbon assimilation cycle, NAD-ME type	Product A V2 SUBG	2.213100244	0.022057133

Comparison 20: Product A V3 SUBG vs Product B V3 SUBG

Gene Ontology

Alpha Diversity (GO)

Chao1	
Shannon	

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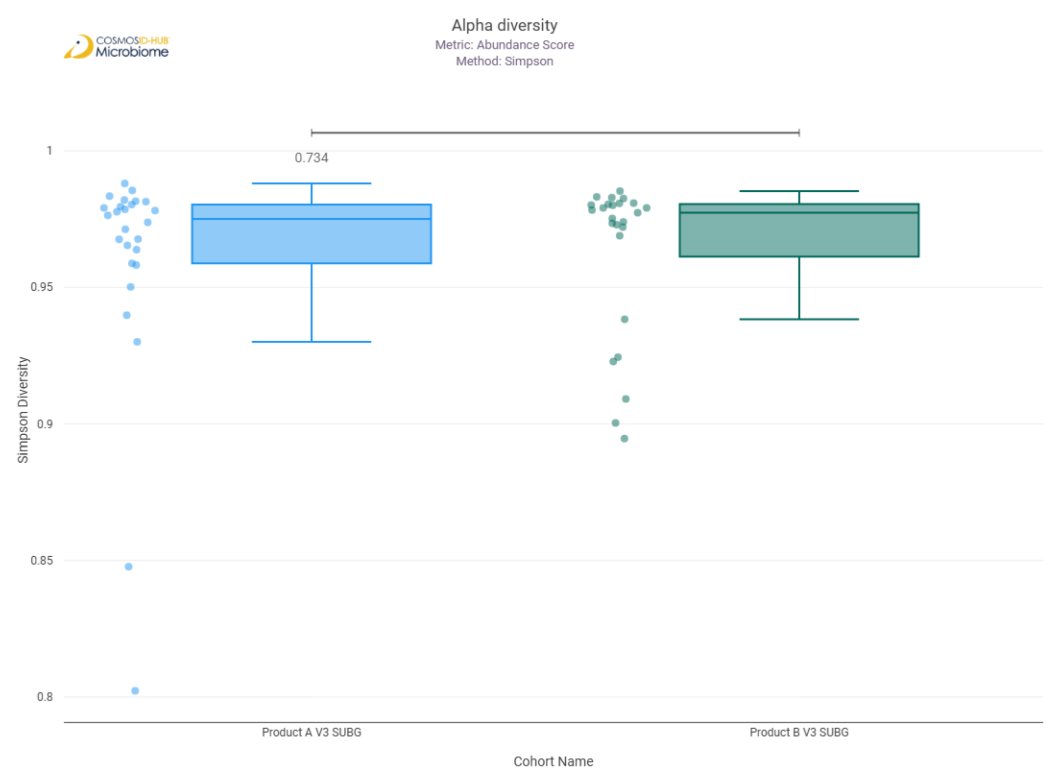

Beta Diversity (GO)

Bray-Curtis

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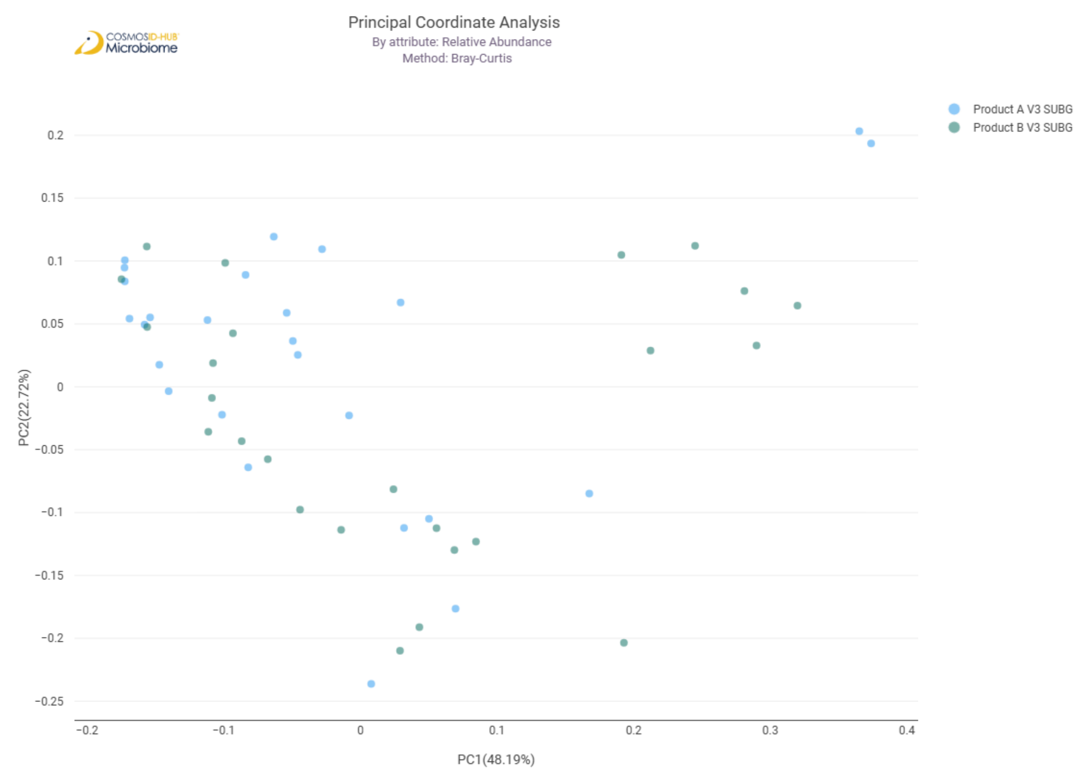
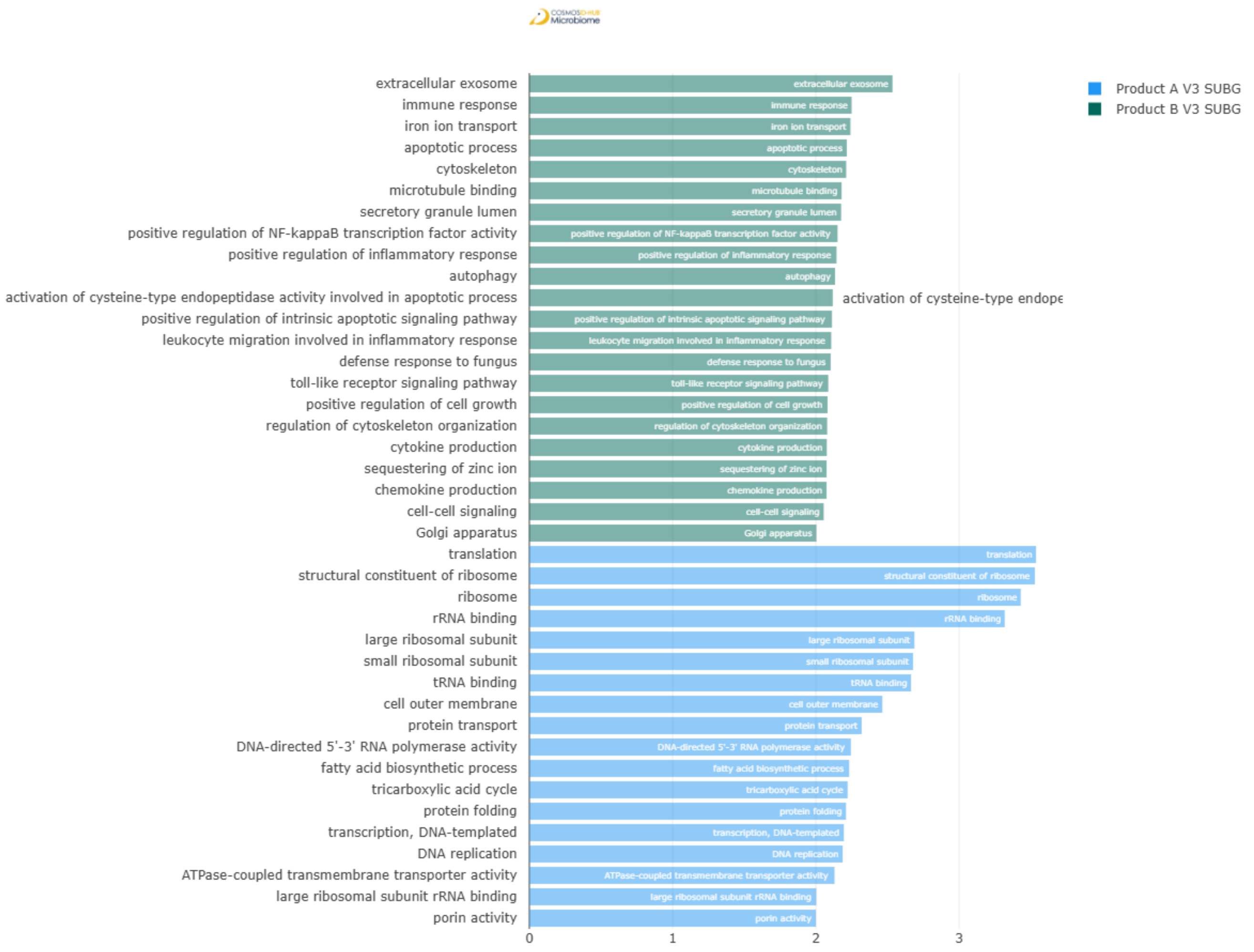


Differential Abundance (LEfSe) (GO)

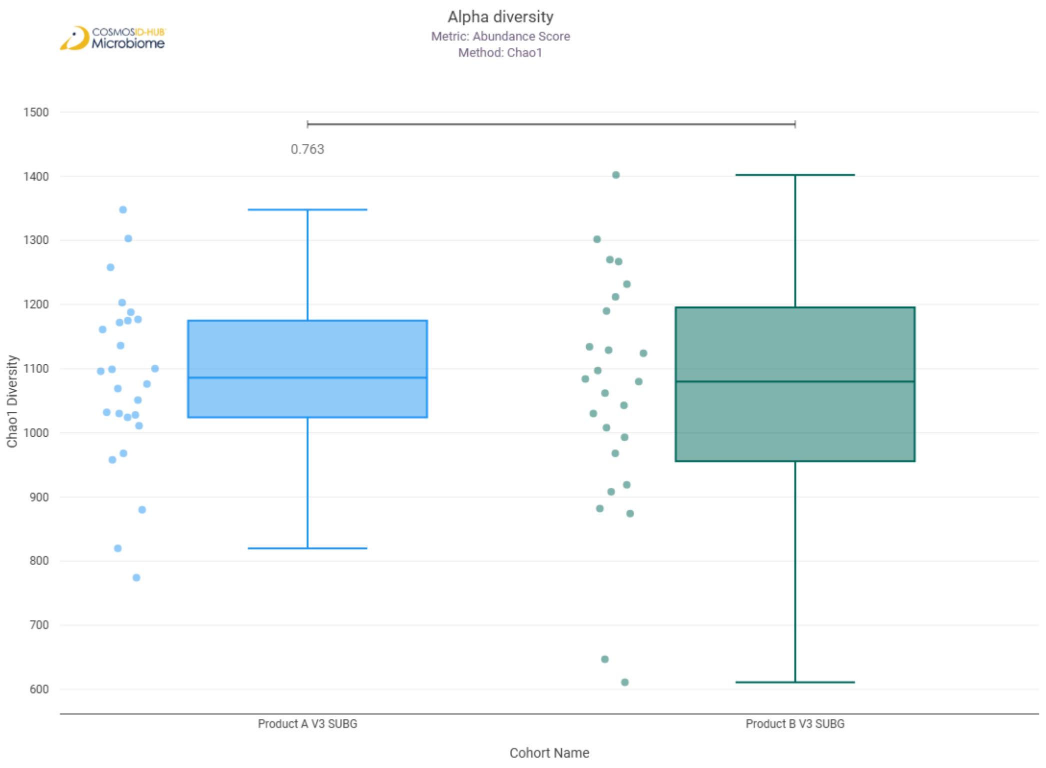
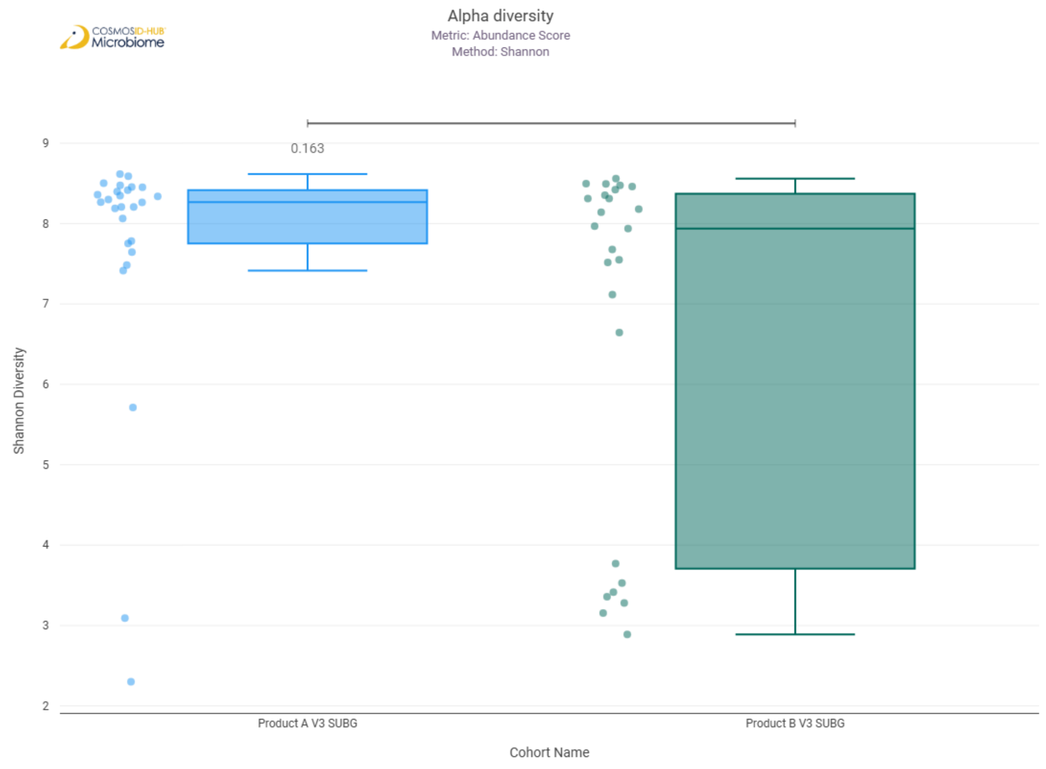


Feature	Enriched Cohort	LDA Score	P-value
translation	Product A V3 SUBG	3.536687332	0.020471389
structural constituent of ribosome	Product A V3 SUBG	3.528572939	0.022613046
ribosome	Product A V3 SUBG	3.430131346	0.012876233
rRNA binding	Product A V3 SUBG	3.318350314	0.01946851
large ribosomal subunit	Product A V3 SUBG	2.688003944	0.008341822
small ribosomal subunit	Product A V3 SUBG	2.678502093	0.012876233
tRNA binding	Product A V3 SUBG	2.664213181	0.041854827
cell outer membrane	Product A V3 SUBG	2.463894606	0.041854827
protein transport	Product A V3 SUBG	2.319737363	0.016712924
DNA-directed 5'-3' RNA polymerase activity	Product A V3 SUBG	2.244648568	0.021519031
fatty acid biosynthetic process	Product A V3 SUBG	2.23219525	0.004183032
tricarboxylic acid cycle	Product A V3 SUBG	2.221672233	0.002000719
protein folding	Product A V3 SUBG	2.210436333	0.028837668
transcription, DNA-templated	Product A V3 SUBG	2.195364258	0.036484395
DNA replication	Product A V3 SUBG	2.187269297	0.033240045

ATPase-coupled transmembrane transporter activity	Product A V3 SUBG	2.130170003	0.028837668
large ribosomal subunit rRNA binding	Product A V3 SUBG	2.003191729	0.041854827
porin activity	Product A V3 SUBG	2.000393644	0.000744191
extracellular exosome	Product B V3 SUBG	2.535130566	0.039994768
immune response	Product B V3 SUBG	2.249850104	4.38E-02
iron ion transport	Product B V3 SUBG	2.241435289	0.012209995
apoptotic process	Product B V3 SUBG	2.216215889	0.045795182
cytoskeleton	Product B V3 SUBG	2.212010433	0.039994768
microtubule binding	Product B V3 SUBG	2.179482504	0.045795182
secretory granule lumen	Product B V3 SUBG	2.176539587	0.034829974
positive regulation of NF-kappaB transcription factor activity	Product B V3 SUBG	2.151381348	0.038205314
positive regulation of inflammatory response	Product B V3 SUBG	2.144302779	0.039994768
autophagy	Product B V3 SUBG	2.133749546	0.039994768
activation of cysteine-type endopeptidase activity involved in apoptotic process	Product B V3 SUBG	2.1181929	0.043787588
positive regulation of intrinsic apoptotic signaling pathway	Product B V3 SUBG	2.112289442	0.043787588
leukocyte migration involved in inflammatory response	Product B V3 SUBG	2.107427716	0.047879765
defense response to fungus	Product B V3 SUBG	2.103586985	0.039994768
toll-like receptor signaling pathway	Product B V3 SUBG	2.086746471	0.043787588
positive regulation of cell growth	Product B V3 SUBG	2.081484217	0.047879765
regulation of cytoskeleton organization	Product B V3 SUBG	2.079085603	0.047879765
cytokine production	Product B V3 SUBG	2.076455901	0.047879765
sequestering of zinc ion	Product B V3 SUBG	2.074832793	0.045795182
chemokine production	Product B V3 SUBG	2.074720372	0.045795182
cell-cell signaling	Product B V3 SUBG	2.054731602	0.038205314
Golgi apparatus	Product B V3 SUBG	2.003938769	0.038205314

Enzyme Commission

Alpha Diversity (EC)

Chao1	
Shannon	

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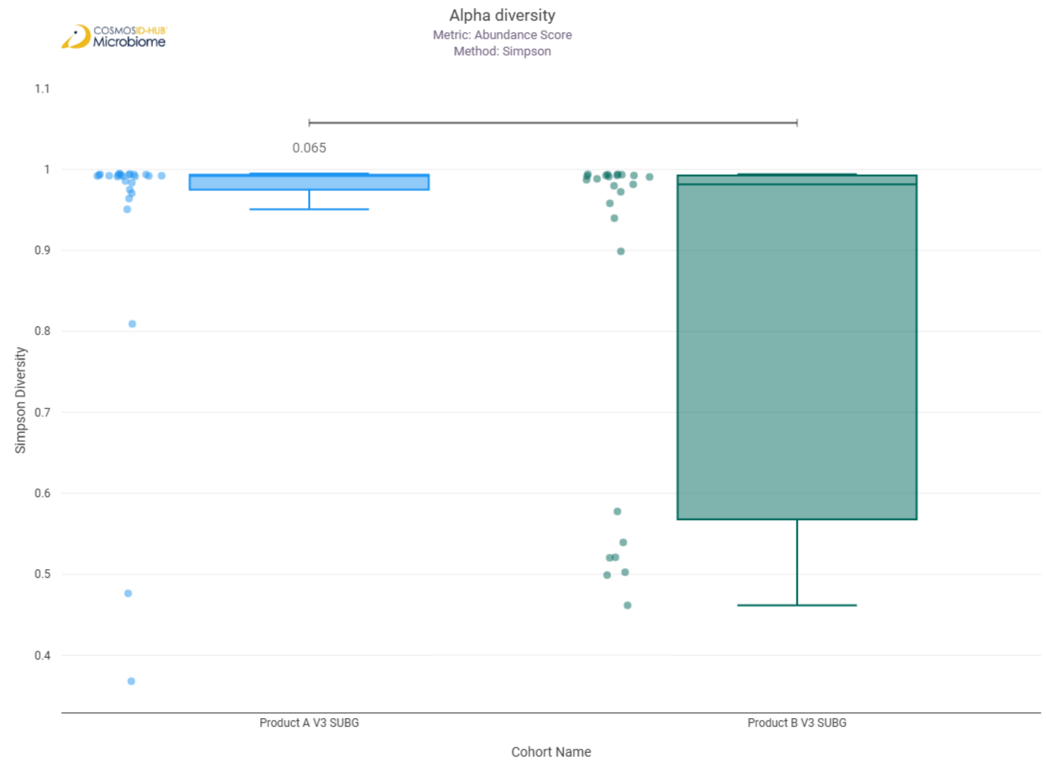
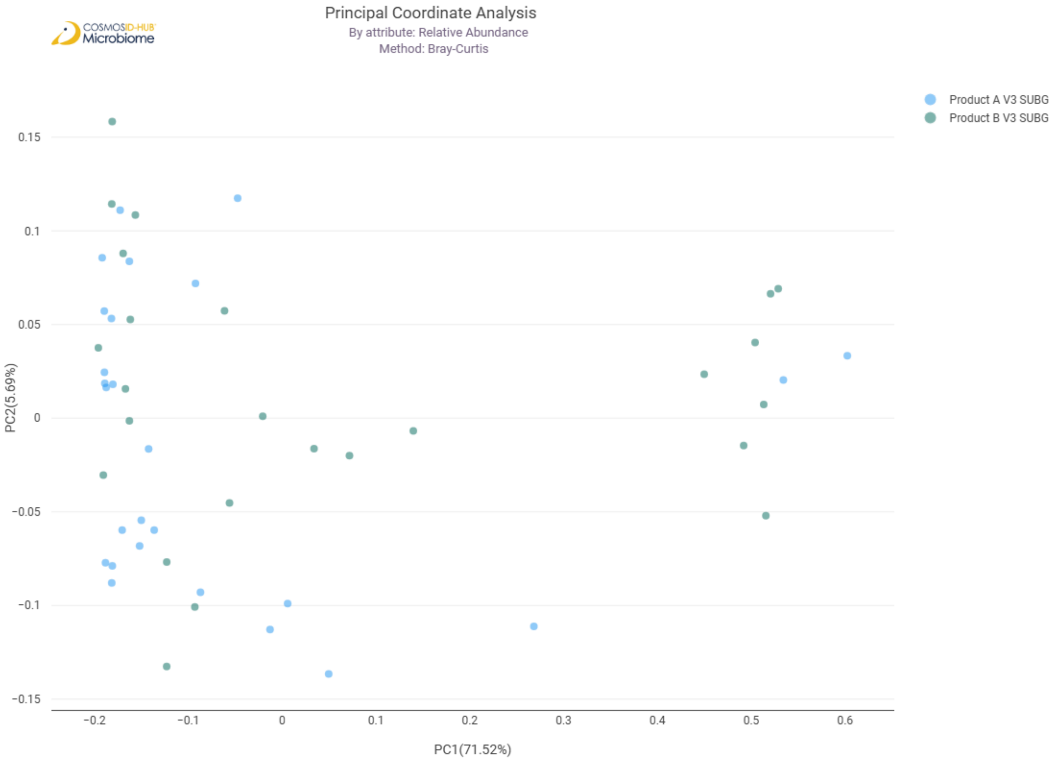


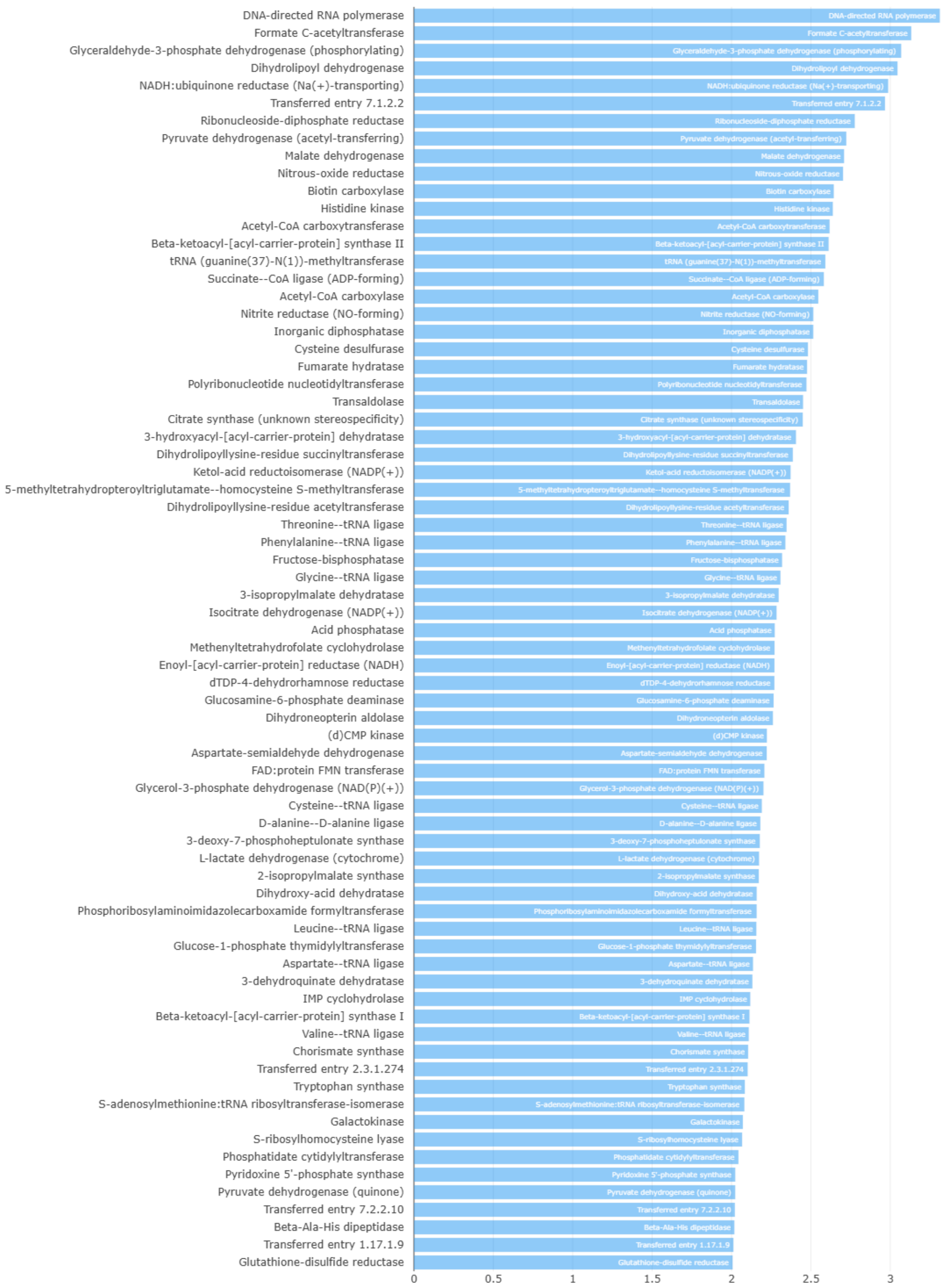
Beta Diversity (EC)

Bray-Curtis

PERMNOVA
p = 0.073



Differential Abundance (LEfSe) (EC)



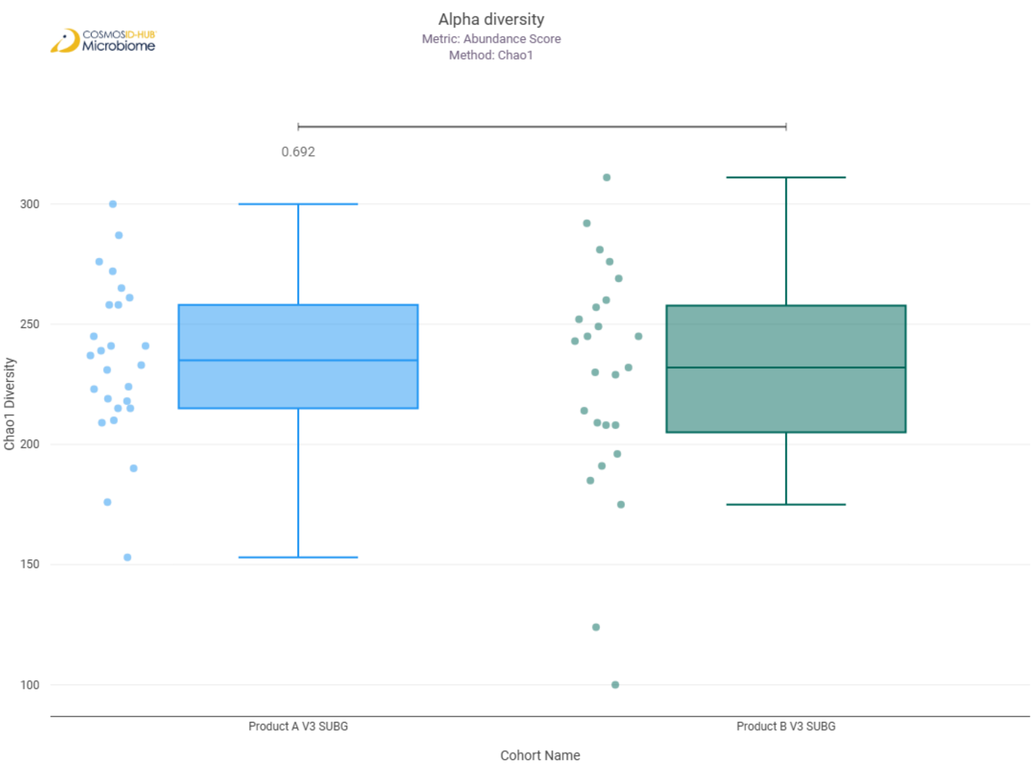
Feature	Enriched Cohort	LDA Score	P-value
DNA-directed RNA polymerase	Product A V3 SUBG	3.312199282	0.007889693
Formate C-acetyltransferase	Product A V3 SUBG	3.13215656	0.039994768
Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	Product A V3 SUBG	3.068813313	0.031712637

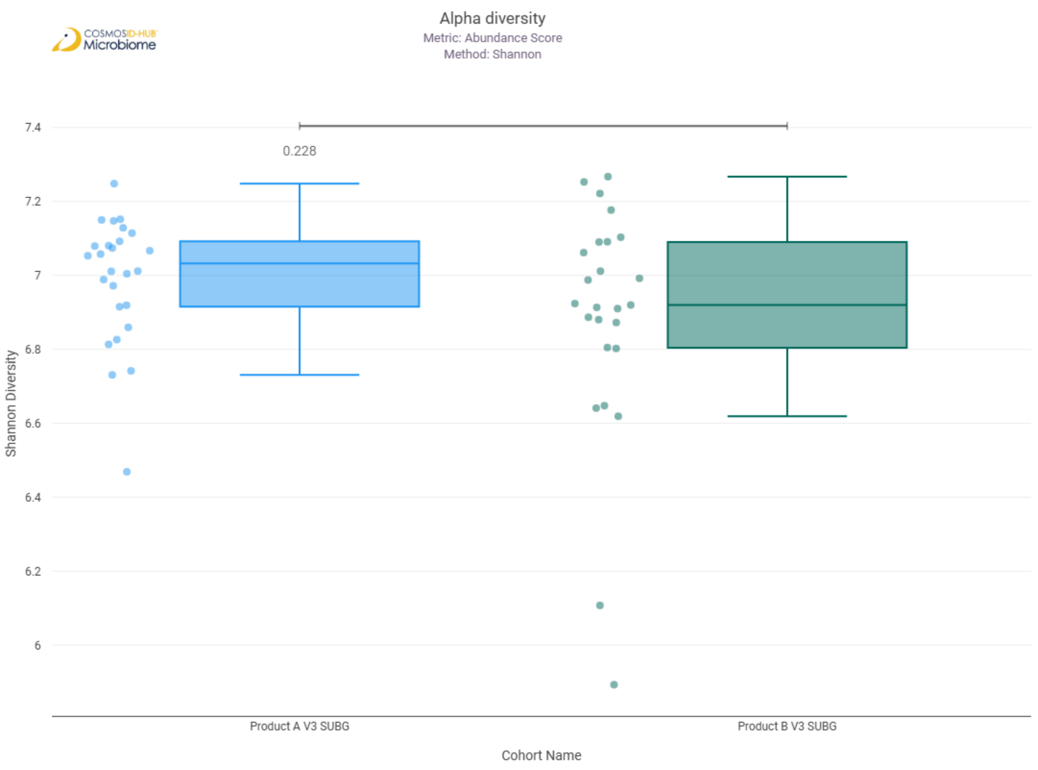
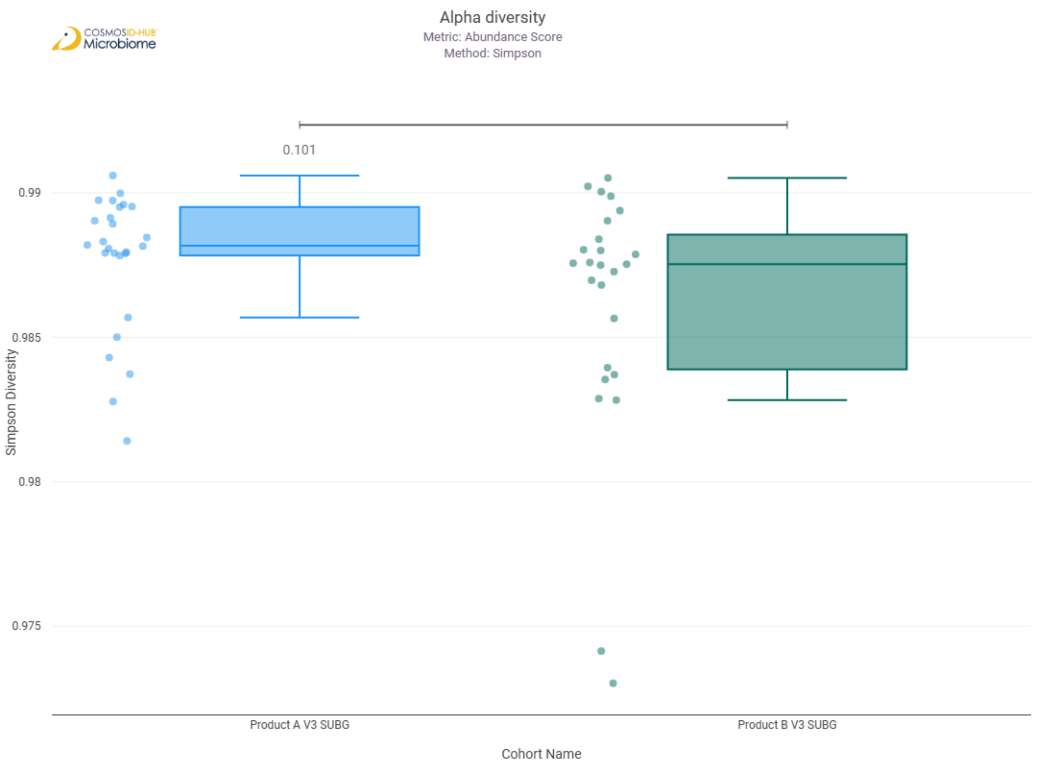
Dihydrolipoyl dehydrogenase	Product A V3 SUBG	3.045630912	1.46616E-05
NADH:ubiquinone reductase (Na(+)-transporting)	Product A V3 SUBG	2.986963277	0.000605172
Transferred entry 7.1.2.2	Product A V3 SUBG	2.966871817	0.020471389
Ribonucleoside-diphosphate reductase	Product A V3 SUBG	2.776516943	0.016712924
Pyruvate dehydrogenase (acetyl-transferring)	Product A V3 SUBG	2.723062614	0.000605172
Malate dehydrogenase	Product A V3 SUBG	2.709053579	0.005941992
Nitrous-oxide reductase	Product A V3 SUBG	2.702720573	0.021507212
Biotin carboxylase	Product A V3 SUBG	2.644235086	0.000852766
Histidine kinase	Product A V3 SUBG	2.638292954	0.041854827
Acetyl-CoA carboxytransferase	Product A V3 SUBG	2.617952144	0.002736233
Beta-ketoacyl-[acyl-carrier-protein] synthase II	Product A V3 SUBG	2.611822632	0.015071869
tRNA (guanine(37)-N(1))-methyltransferase	Product A V3 SUBG	2.591202435	0.000694855
Succinate--CoA ligase (ADP-forming)	Product A V3 SUBG	2.581609521	0.02494682
Acetyl-CoA carboxylase	Product A V3 SUBG	2.546806449	0.004438681
Nitrite reductase (NO-forming)	Product A V3 SUBG	2.515556565	0.00628096
Inorganic diphosphatase	Product A V3 SUBG	2.515254374	0.020471389
Cysteine desulfurase	Product A V3 SUBG	2.48170098	1.88E-03
Fumarate hydratase	Product A V3 SUBG	2.475987752	0.008341822
Polyribonucleotide nucleotidyltransferase	Product A V3 SUBG	2.472260598	0.012876233
Transaldolase	Product A V3 SUBG	2.450906966	0.005292825
Citrate synthase (unknown stereospecificity)	Product A V3 SUBG	2.448881882	0.002269883
3-hydroxyacyl-[acyl-carrier-protein] dehydratase	Product A V3 SUBG	2.406150454	0.02494682
Dihydrolipoyllysine-residue succinyltransferase	Product A V3 SUBG	2.386412108	0.00097562
Ketol-acid reductoisomerase (NADP(+))	Product A V3 SUBG	2.372178573	0.047879765
5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	Product A V3 SUBG	2.369261081	0.028837668
Dihydrolipoyllysine-residue acetyltransferase	Product A V3 SUBG	2.360242064	0.000319608
Threonine--tRNA ligase	Product A V3 SUBG	2.347096758	0.02494682
Phenylalanine--tRNA ligase	Product A V3 SUBG	2.339465697	0.028837668
Fructose-bisphosphatase	Product A V3 SUBG	2.318793495	0.016712924
Glycine--tRNA ligase	Product A V3 SUBG	2.308480299	0.038205314
3-isopropylmalate dehydratase	Product A V3 SUBG	2.297290891	0.01946851
Isocitrate dehydrogenase (NADP(+))	Product A V3 SUBG	2.28378722	0.000852534
Acid phosphatase	Product A V3 SUBG	2.272511228	0.009316196
Methenyltetrahydrofolate cyclohydrolase	Product A V3 SUBG	2.271222446	0.043787588
Enoyl-[acyl-carrier-protein] reductase (NADH)	Product A V3 SUBG	2.27078058	0.00881699
dTDP-4-dehydrorhamnose reductase	Product A V3 SUBG	2.270338236	0.004708409
Glucosamine-6-phosphate deaminase	Product A V3 SUBG	2.26535543	0.013574437
Dihydroneopterin aldolase	Product A V3 SUBG	2.260965749	0.001043427
(d)CMP kinase	Product A V3 SUBG	2.222871162	0.010390869
Aspartate-semialdehyde dehydrogenase	Product A V3 SUBG	2.222116087	0.036484395
FAD:protein FMN transferase	Product A V3 SUBG	2.207303025	0.021519031
Glycerol-3-phosphate dehydrogenase (NAD(P)(+))	Product A V3 SUBG	2.201487687	0.015071869
Cysteine--tRNA ligase	Product A V3 SUBG	2.191170276	0.004992891
D-alanine--D-alanine ligase	Product A V3 SUBG	2.181747657	0.027486336
3-deoxy-7-phosphoheptulonate synthase	Product A V3 SUBG	2.178294885	0.002571856
L-lactate dehydrogenase (cytochrome)	Product A V3 SUBG	2.173648975	0.000975879

2-isopropylmalate synthase	Product A V3 SUBG	2.172001333	0.010390869
Dihydroxy-acid dehydratase	Product A V3 SUBG	2.15868405	2.49E-02
Phosphoribosylaminoimidazolecarboxamide formyltransferase	Product A V3 SUBG	2.158625201	0.022613046
Leucine--tRNA ligase	Product A V3 SUBG	2.156558873	0.021519031
Glucose-1-phosphate thymidylyltransferase	Product A V3 SUBG	2.154769362	0.018508823
Aspartate--tRNA ligase	Product A V3 SUBG	2.135805728	0.031712637
3-dehydroquinate dehydratase	Product A V3 SUBG	2.131724086	0.013574437
IMP cyclohydrolase	Product A V3 SUBG	2.118278512	0.028837668
Beta-ketoacyl-[acyl-carrier-protein] synthase I	Product A V3 SUBG	2.113359831	0.018508823
Valine--tRNA ligase	Product A V3 SUBG	2.108822781	0.033240045
Chorismate synthase	Product A V3 SUBG	2.104886081	0.00176114
Transferred entry 2.3.1.274	Product A V3 SUBG	2.101880318	0.030245812
Tryptophan synthase	Product A V3 SUBG	2.084119262	0.018508823
S-adenosylmethionine:tRNA ribosyltransferase-isomerase	Product A V3 SUBG	2.081182245	0.020471389
Galactokinase	Product A V3 SUBG	2.071628618	0.014305878
S-ribosylhomocysteine lyase	Product A V3 SUBG	2.06704668	0.030245812
Phosphatidate cytidylyltransferase	Product A V3 SUBG	2.043892086	0.016712924
Pyridoxine 5'-phosphate synthase	Product A V3 SUBG	2.023792626	0.000275433
Pyruvate dehydrogenase (quinone)	Product A V3 SUBG	2.023536332	0.003703627
Transferred entry 7.2.2.10	Product A V3 SUBG	2.021427948	0.018506169
Beta-Ala-His dipeptidase	Product A V3 SUBG	2.018269524	0.015850009
Transferred entry 1.17.1.9	Product A V3 SUBG	2.012359892	0.008810865
Glutathione-disulfide reductase	Product A V3 SUBG	2.007145806	0.009316196

MetaCyc Pathways

Alpha Diversity (MetaCyc)

Chao1	

Shannon	
Simpson	

Beta Diversity (MetaCyc)

Bray-Curtis

PERMNOVA
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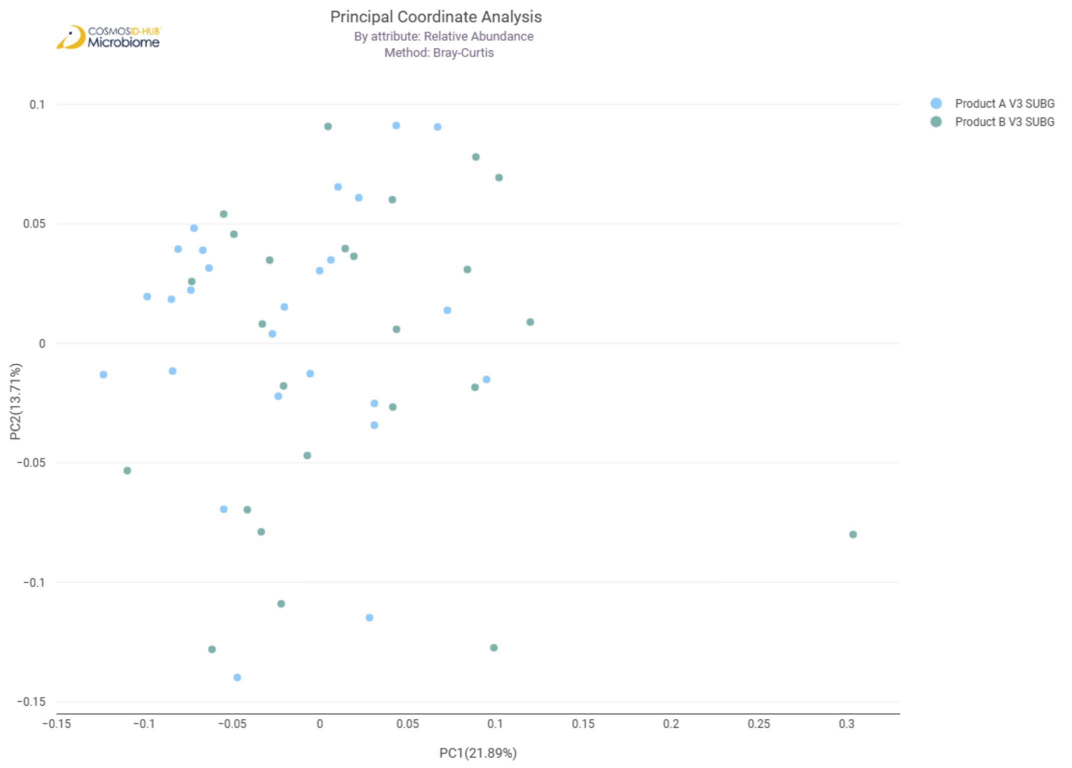

Differential Abundance (LEfSe) (MetaCyc)

Feature	Enriched Cohort	LDA Score	P-value
glycolysis III (from glucose)	Product B V3 SUBG	3.398008161	0.038205314
glycogen degradation II	Product B V3 SUBG	3.135718597	0.043787588
pyrimidine deoxyribonucleotides de novo biosynthesis IV	Product B V3 SUBG	2.620523396	0.008561476
polyisoprenoid biosynthesis (E. coli)	Product B V3 SUBG	2.590644283	0.002064632
flavin biosynthesis I (bacteria and plants)	Product B V3 SUBG	2.527895481	0.020459981
all-trans-farnesol biosynthesis	Product B V3 SUBG	2.512006003	0.002199138
superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP)	Product B V3 SUBG	2.412732939	0.022030076
superpathway of L-methionine biosynthesis (by sulfhydrylation)	Product B V3 SUBG	2.072286136	0.038070937
aspartate superpathway	Product B V3 SUBG	2.044846563	0.035123508
fatty acid biosynthesis initiation (mitochondria)	Product A V3 SUBG	3.03335721	0.043787588
nitrate reduction I (denitrification)	Product A V3 SUBG	2.770074976	0.017447725
(5Z)-dodecenoate biosynthesis II	Product A V3 SUBG	2.768822004	0.000357175
gondoate biosynthesis (anaerobic)	Product A V3 SUBG	2.745818707	0.039994768
inosine-5'-phosphate biosynthesis III	Product A V3 SUBG	2.685496558	0.004437784
D-galactose degradation I (Leloir pathway)	Product A V3 SUBG	2.670583482	0.026189985
pyridoxal 5'-phosphate biosynthesis I	Product A V3 SUBG	2.621986388	0.00336473
superpathway of L-alanine biosynthesis	Product A V3 SUBG	2.562183598	0.003070652
C4 photosynthetic carbon assimilation cycle, NAD-ME type	Product A V3 SUBG	2.513144729	0.00186182
C4 photosynthetic carbon assimilation cycle, PEPCK type	Product A V3 SUBG	2.506672461	0.023751913
C4 photosynthetic carbon assimilation cycle, NADP-ME type	Product A V3 SUBG	2.496833971	0.034829974
tRNA processing	Product A V3 SUBG	2.456212513	0.000875251
superpathway of pyridoxal 5'-phosphate biosynthesis and salvage	Product A V3 SUBG	2.403555807	3.55E-02
L-lysine biosynthesis VI	Product A V3 SUBG	2.38774424	0.036480158
L-lysine biosynthesis I	Product A V3 SUBG	2.379557703	0.012835527
superpathway of L-lysine, L-threonine and L-methionine biosynthesis II	Product A V3 SUBG	2.373267579	0.039990269
chorismate biosynthesis I	Product A V3 SUBG	2.350578747	0.041854827
molybdopterin biosynthesis	Product A V3 SUBG	2.322613992	0.003924514
L-ornithine biosynthesis II	Product A V3 SUBG	2.302634401	0.002370652
heme b biosynthesis II (oxygen-independent)	Product A V3 SUBG	2.292271137	0.014121484
phytol degradation	Product A V3 SUBG	2.196476941	0.005851078
superpathway of methylglyoxal degradation	Product A V3 SUBG	2.190473884	0.033160392
L-Nδ-acetylornithine biosynthesis	Product A V3 SUBG	2.016218191	0.006620791