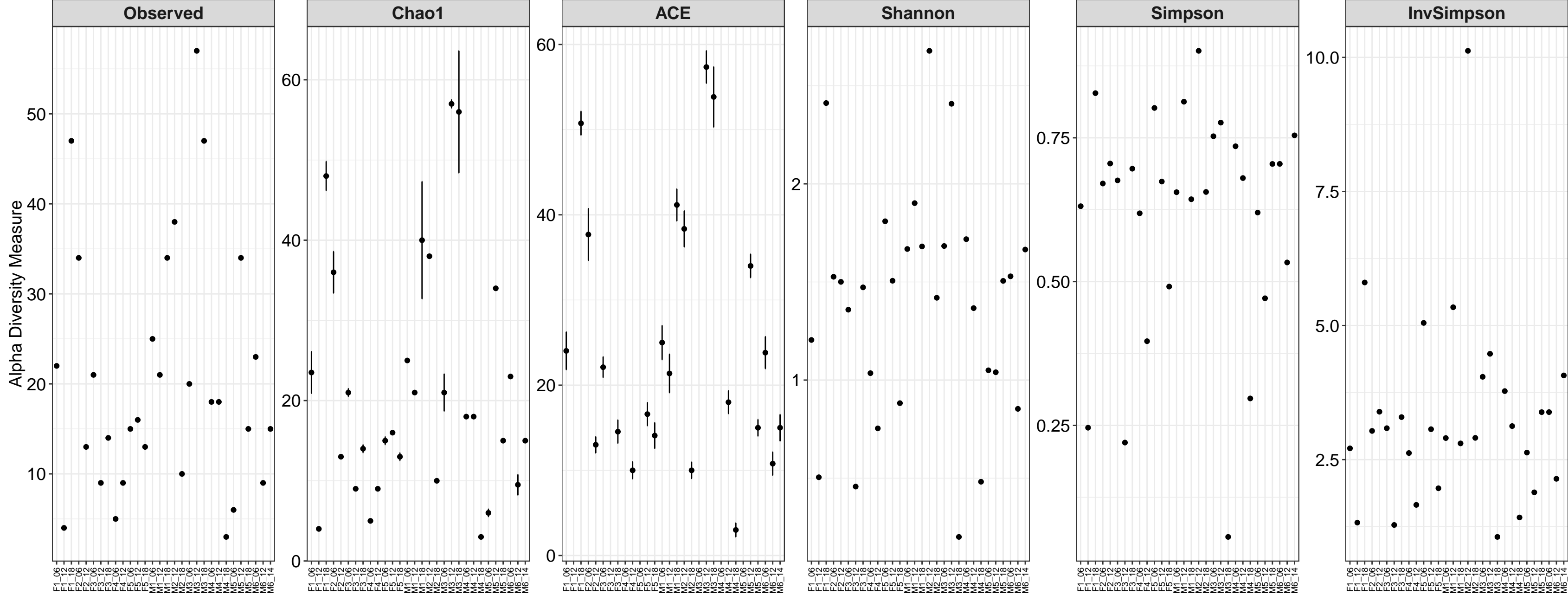
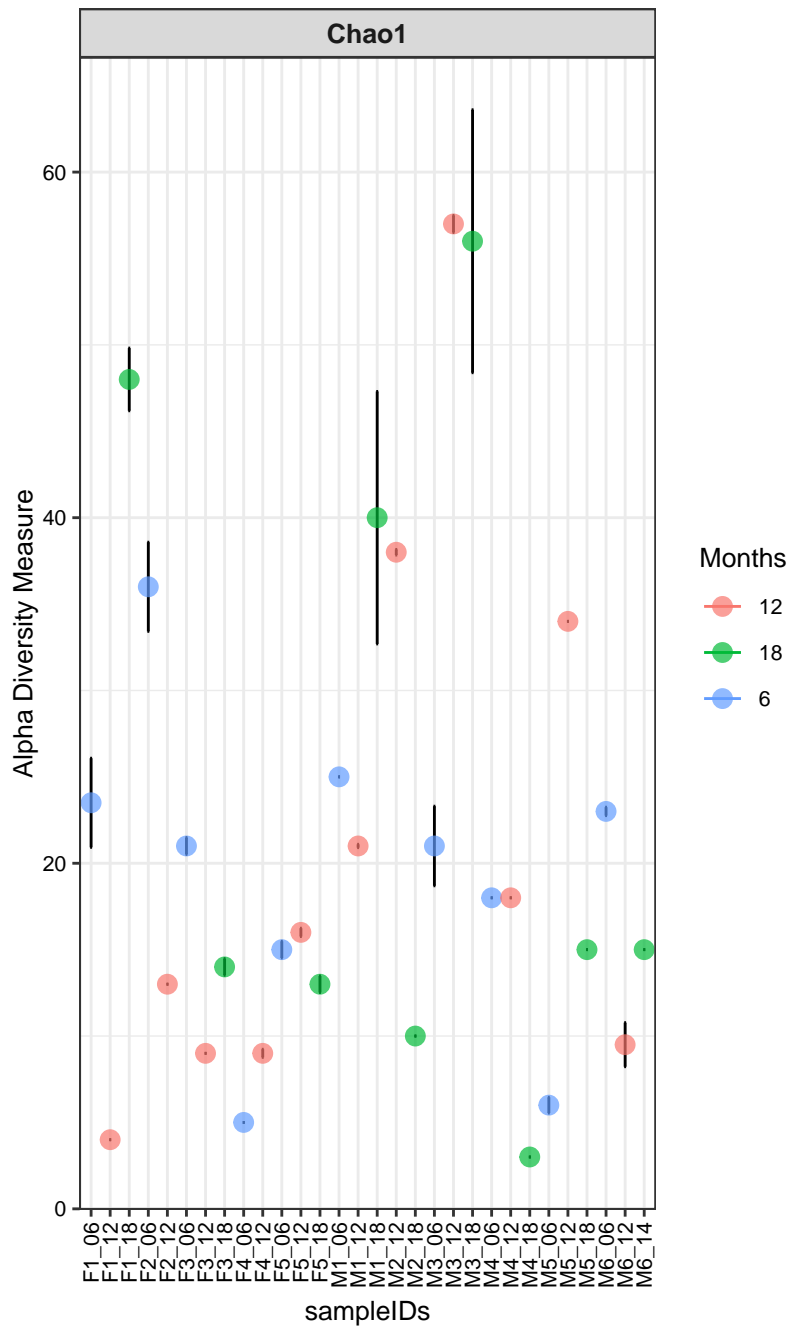


Figure | alpha diversity – overview all measures



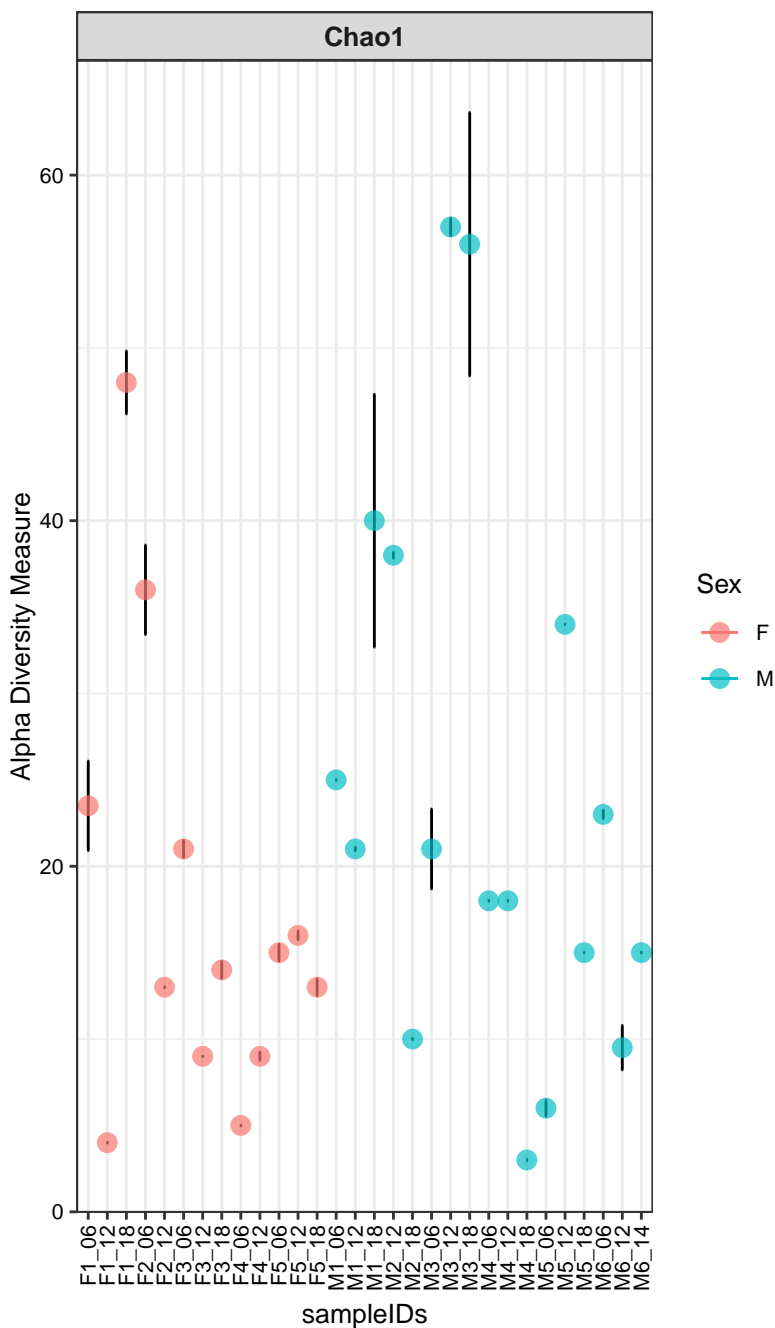
alpha diversity calculated on unfiltered data (only OTUs with 0 counts in all samples were removed)

Figure | alpha diversity\* according to the Chao1 measure



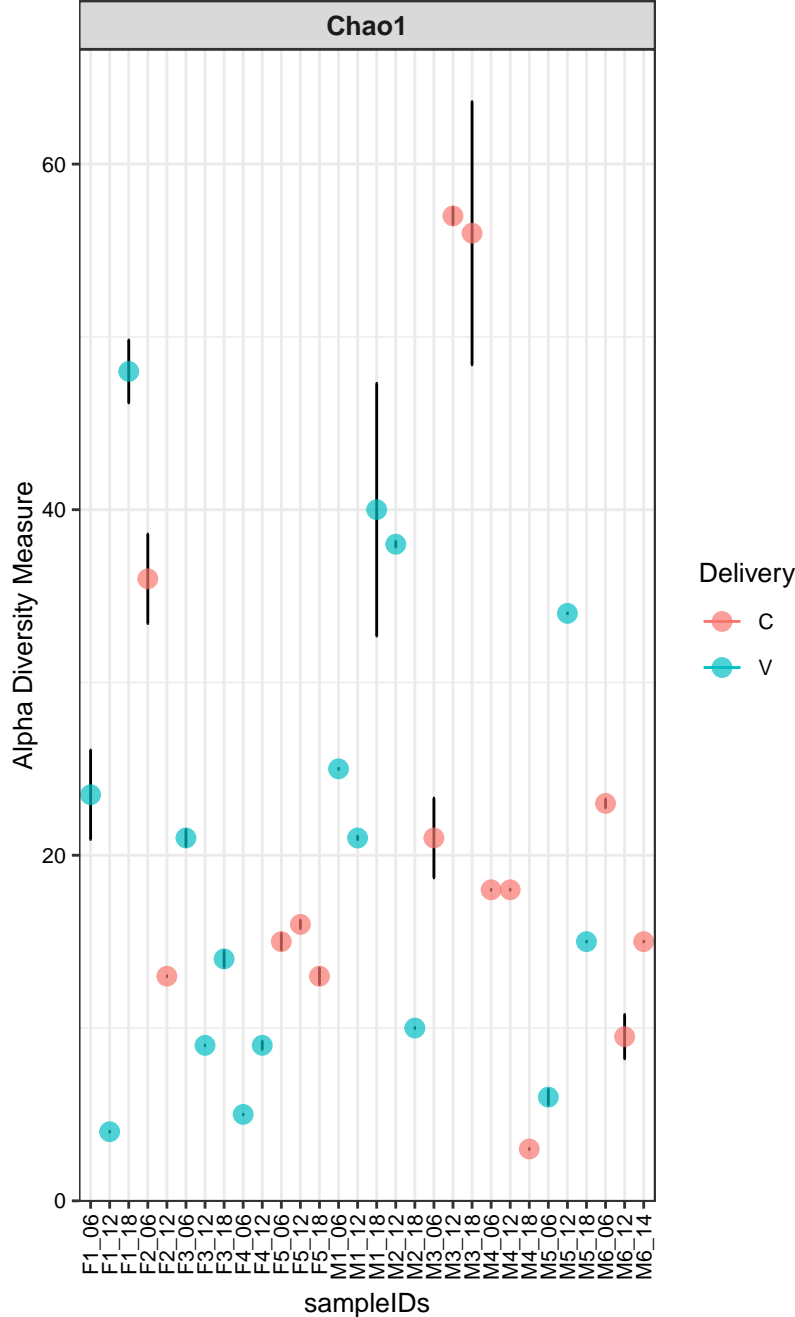
\*calculated on unfiltered data; OTUs with 0 counts in all samples were removed

Figure | alpha diversity\* according to the Chao1 measure

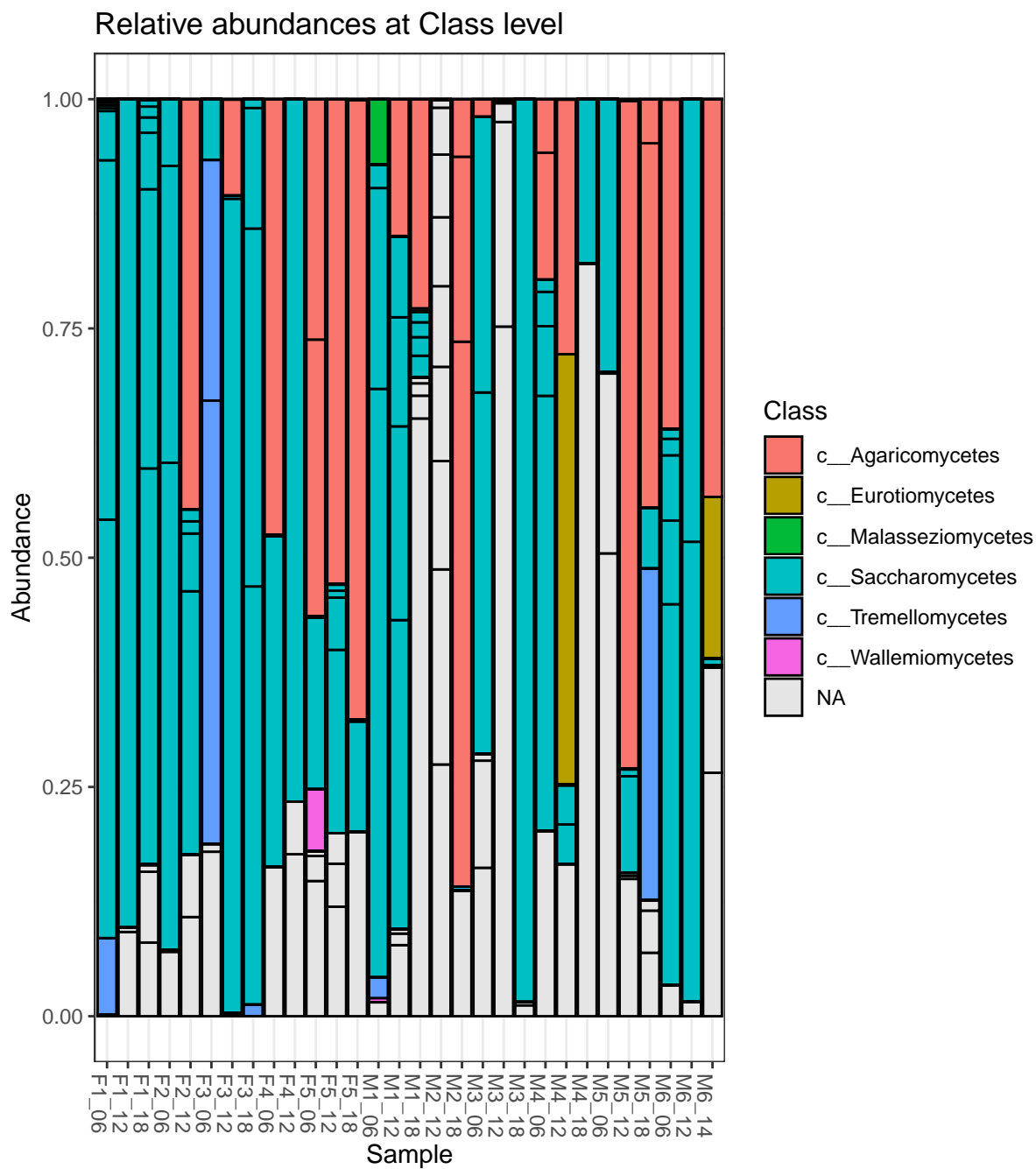


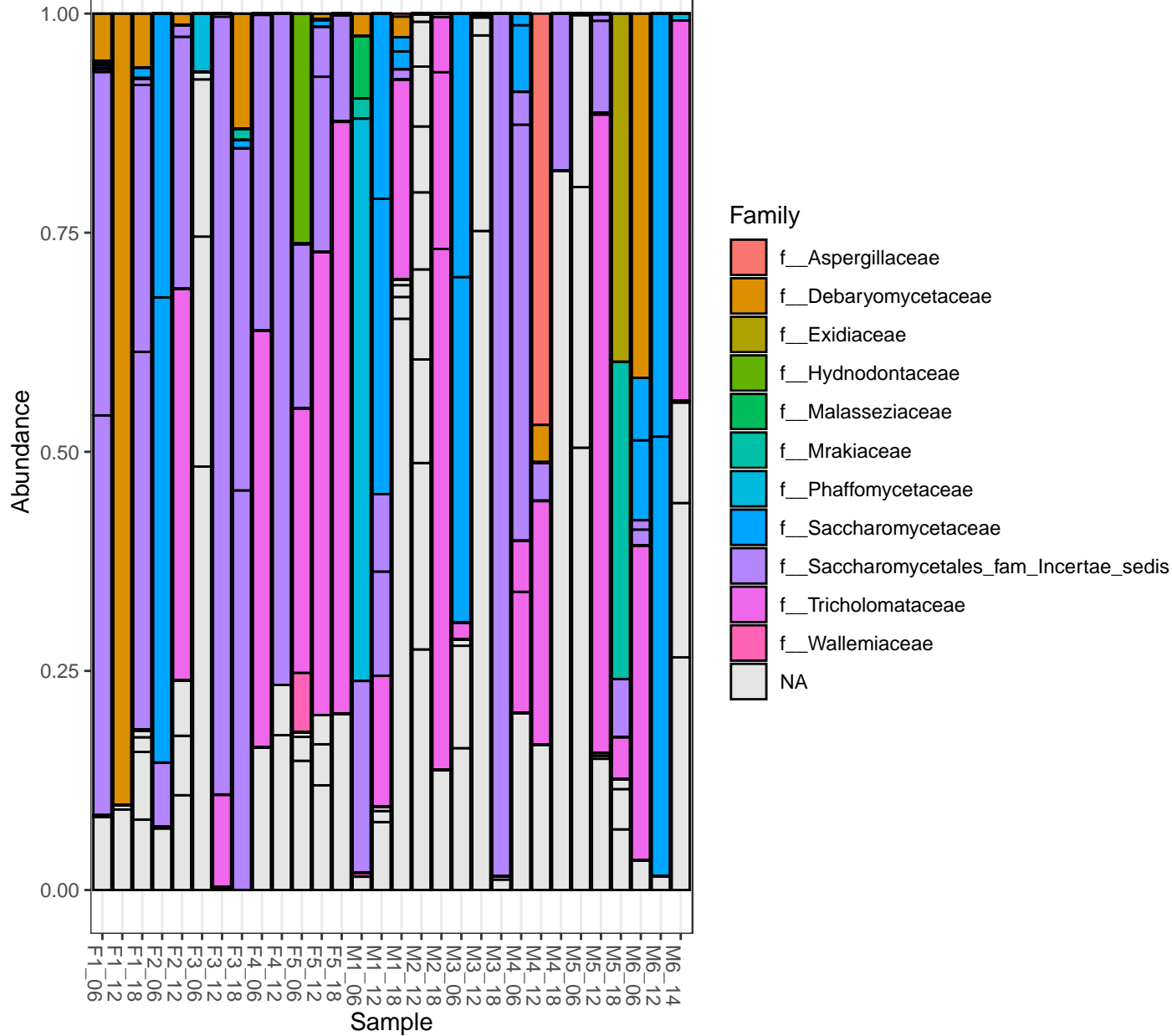
\*calculated on unfiltered data; OTUs with 0 counts in all samples were removed

Figure | alpha diversity\* according to the Chao1 measure

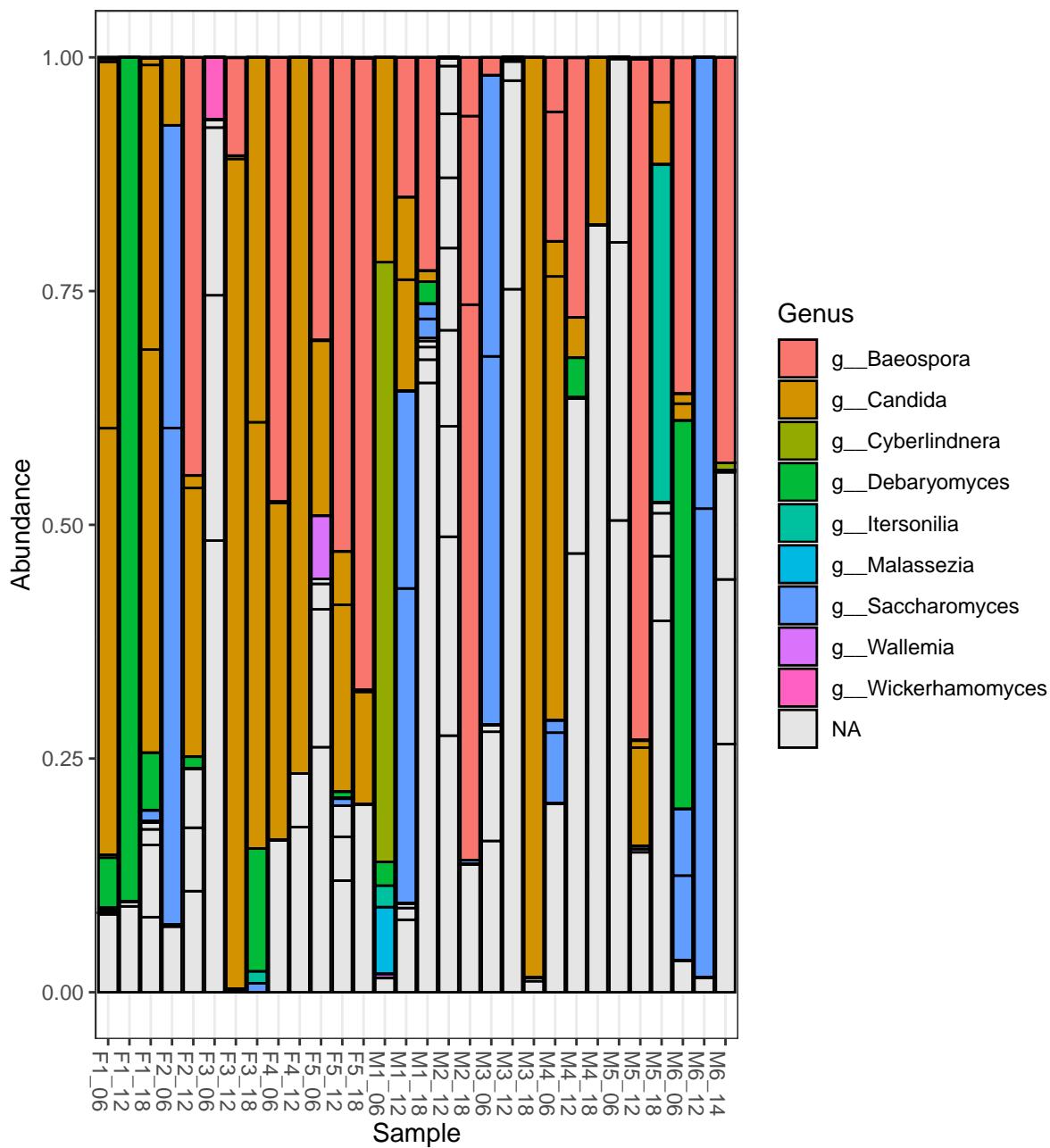


\*calculated on unfiltered data; OTUs with 0 counts in all samples were removed

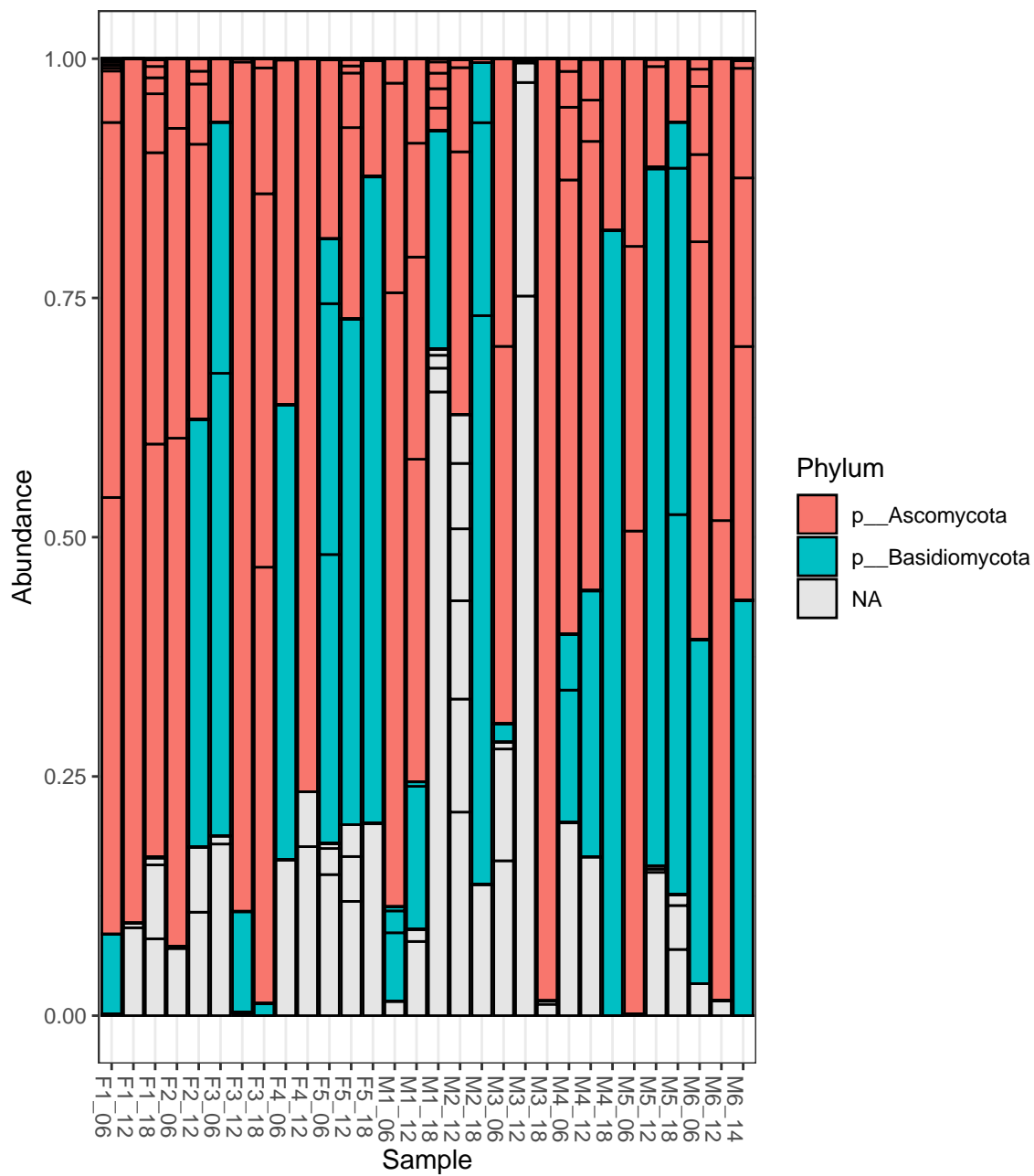


[illegible]

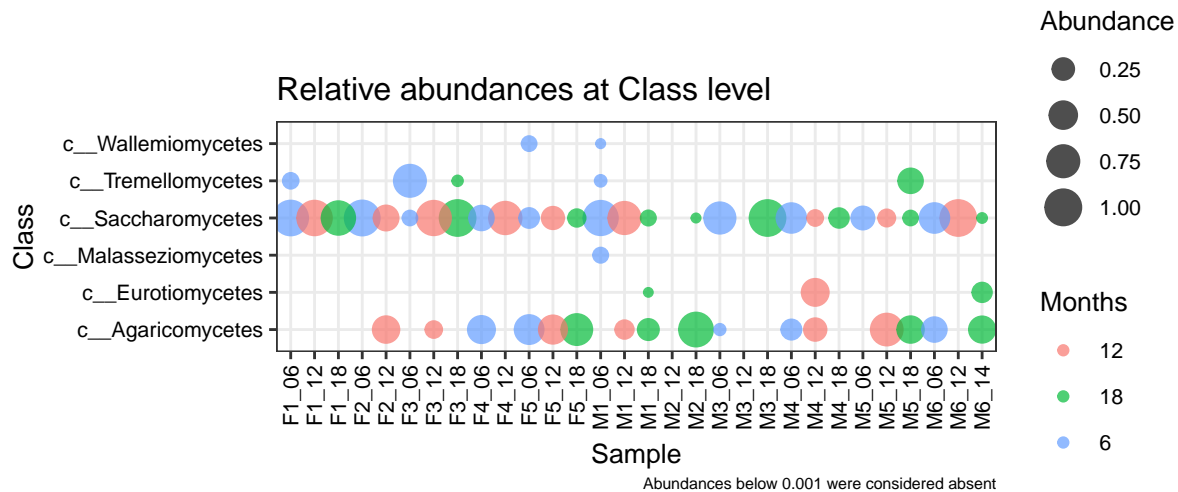
Relative abundances at Genus level

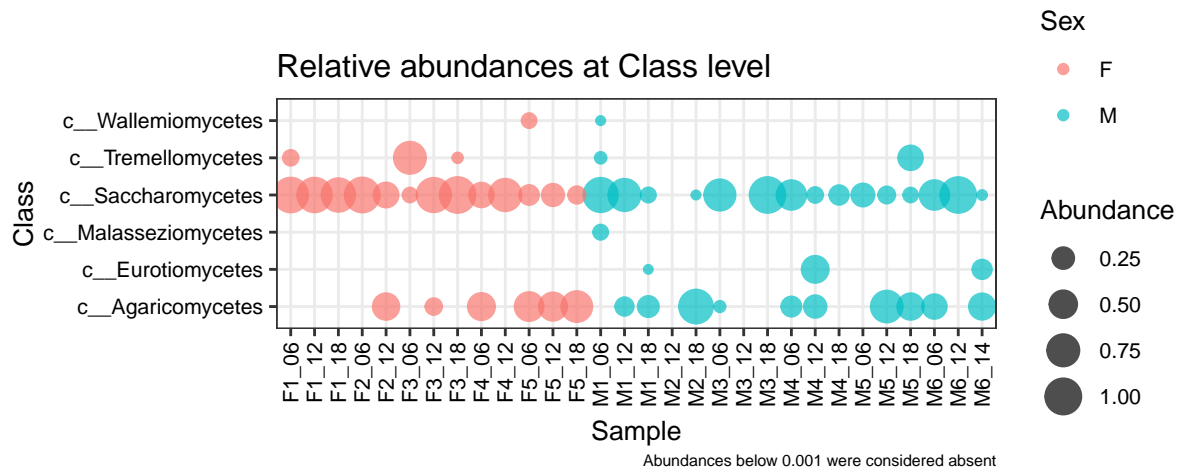


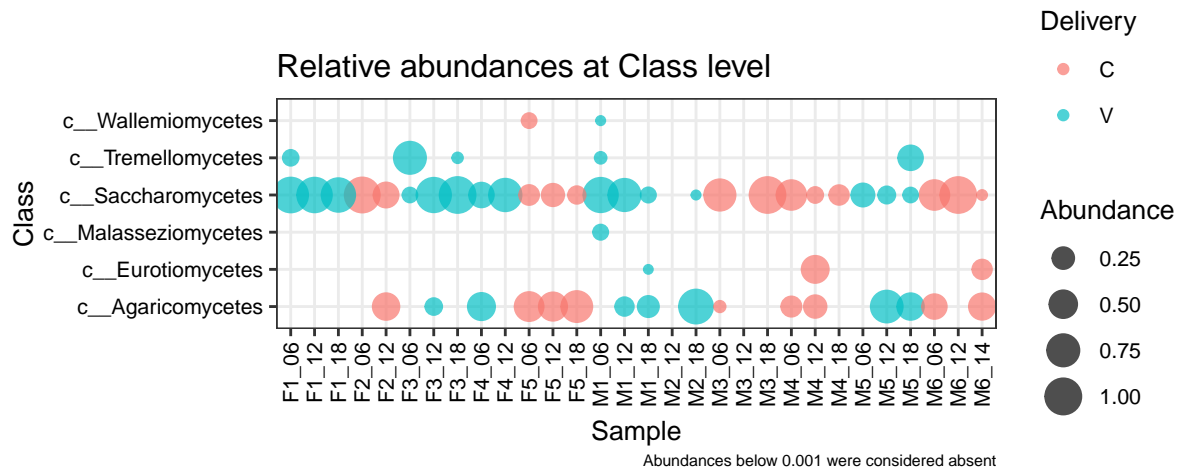
Relative abundances at Phylum level



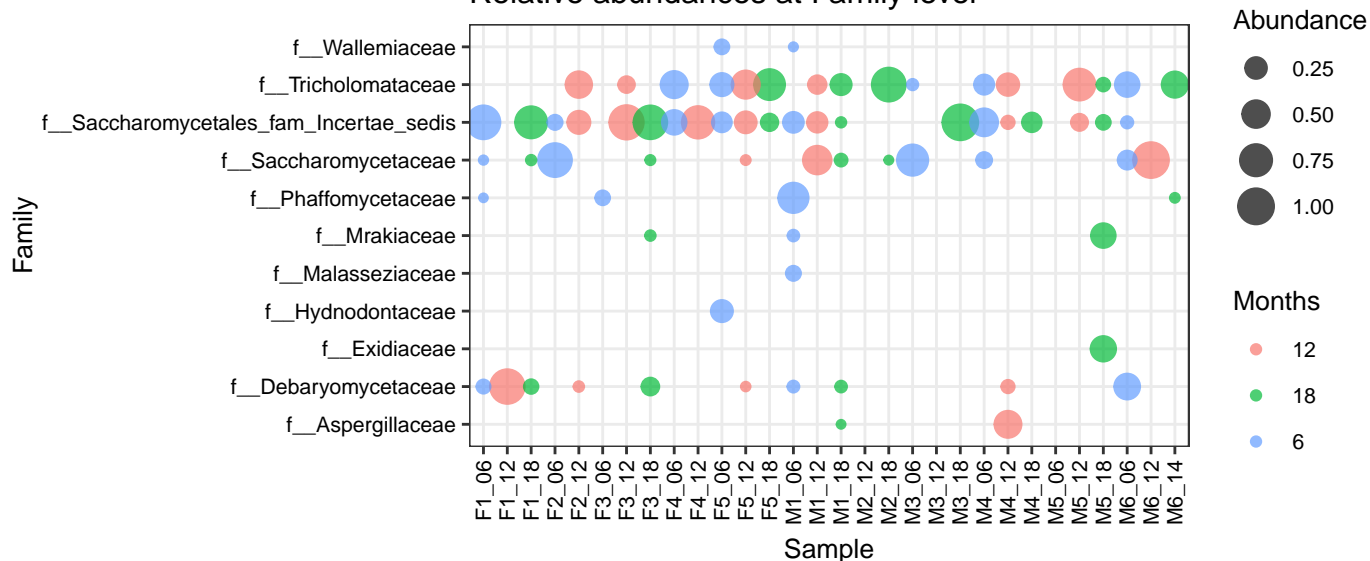






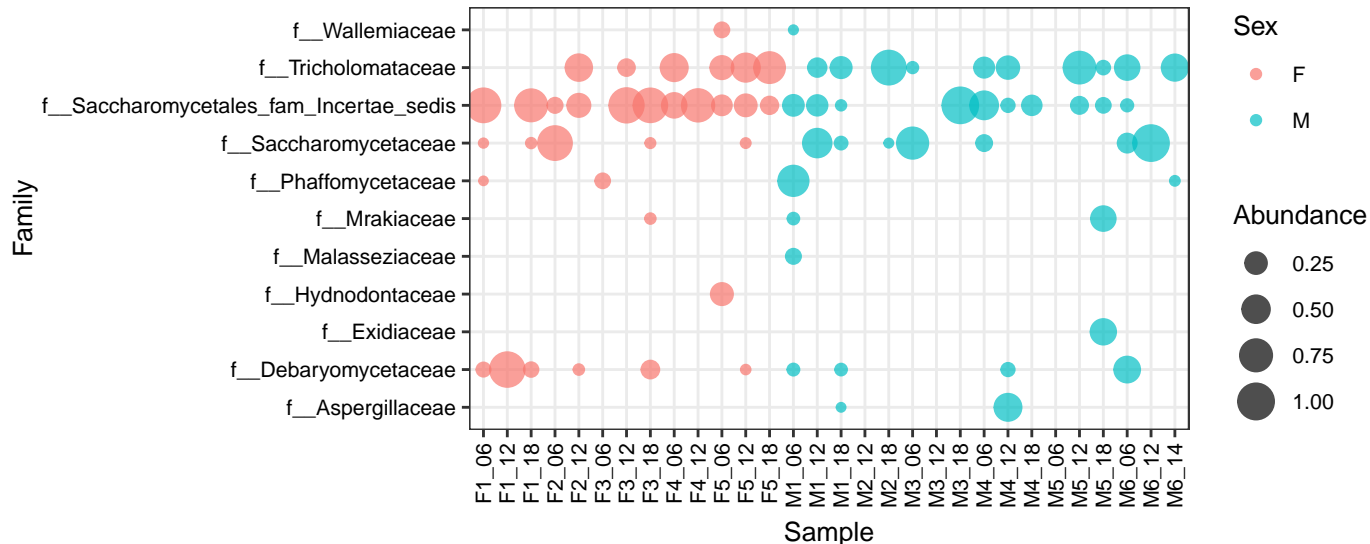


# Relative abundances at Family level

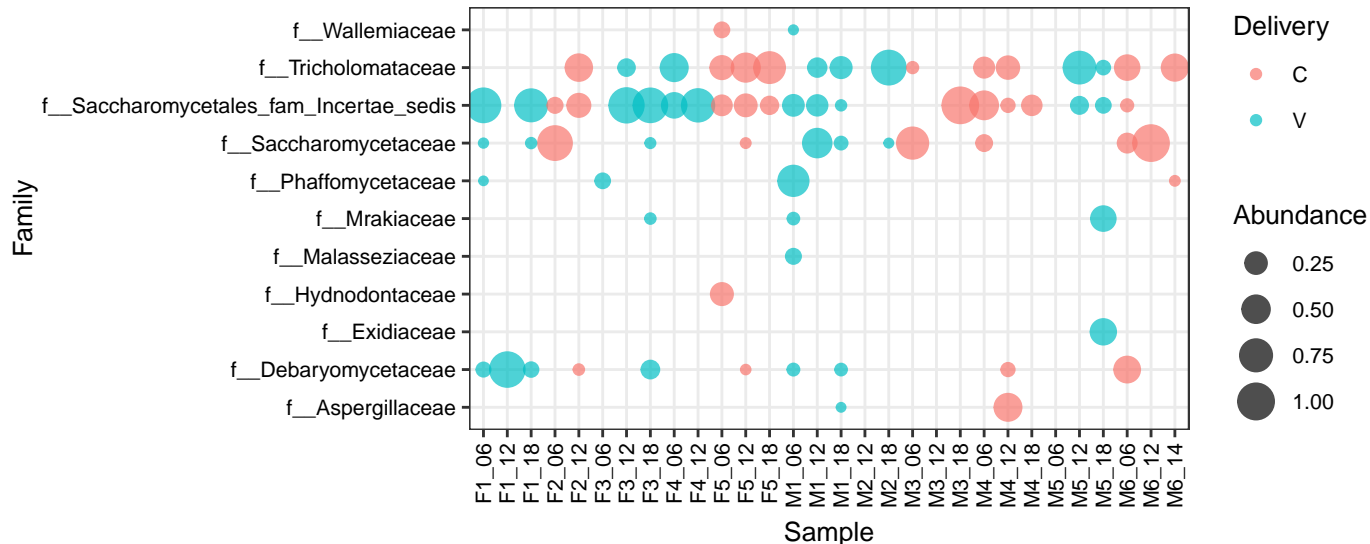


Abundances below 0.001 were considered absent

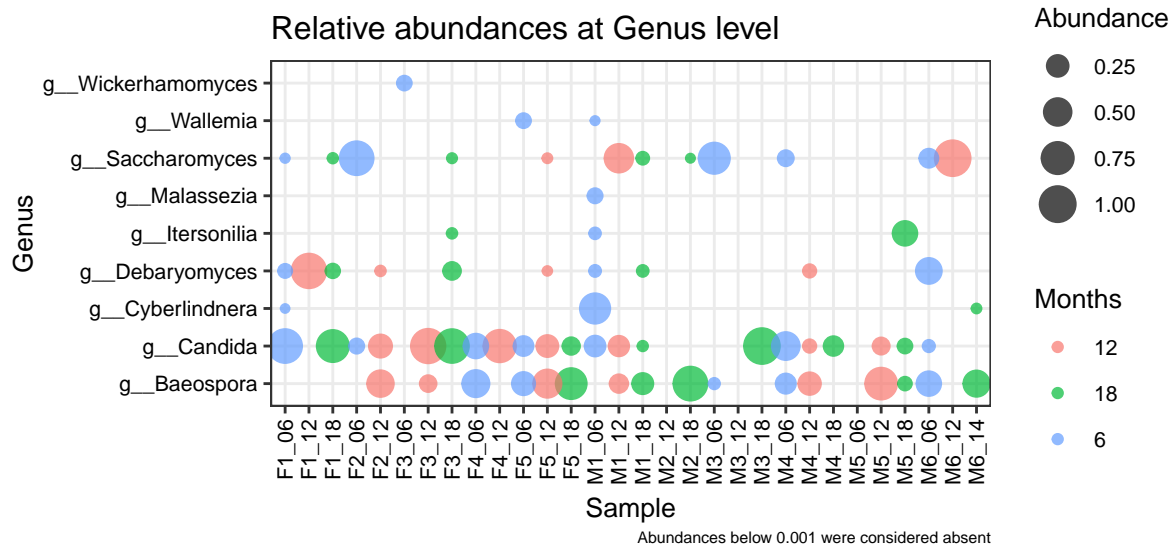
## Relative abundances at Family level

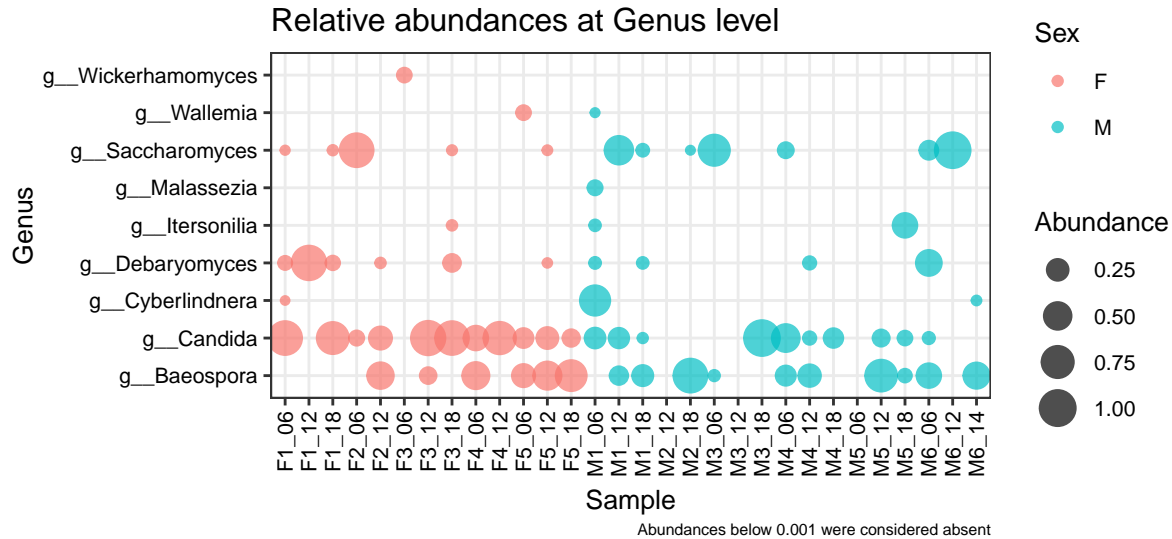


## Relative abundances at Family level

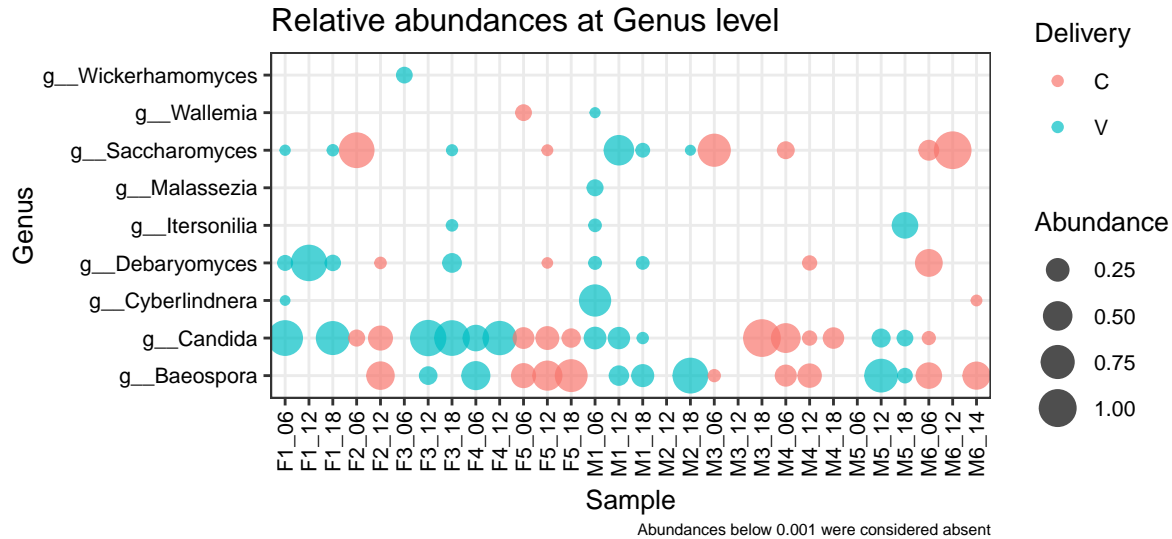


Abundances below 0.001 were considered absent

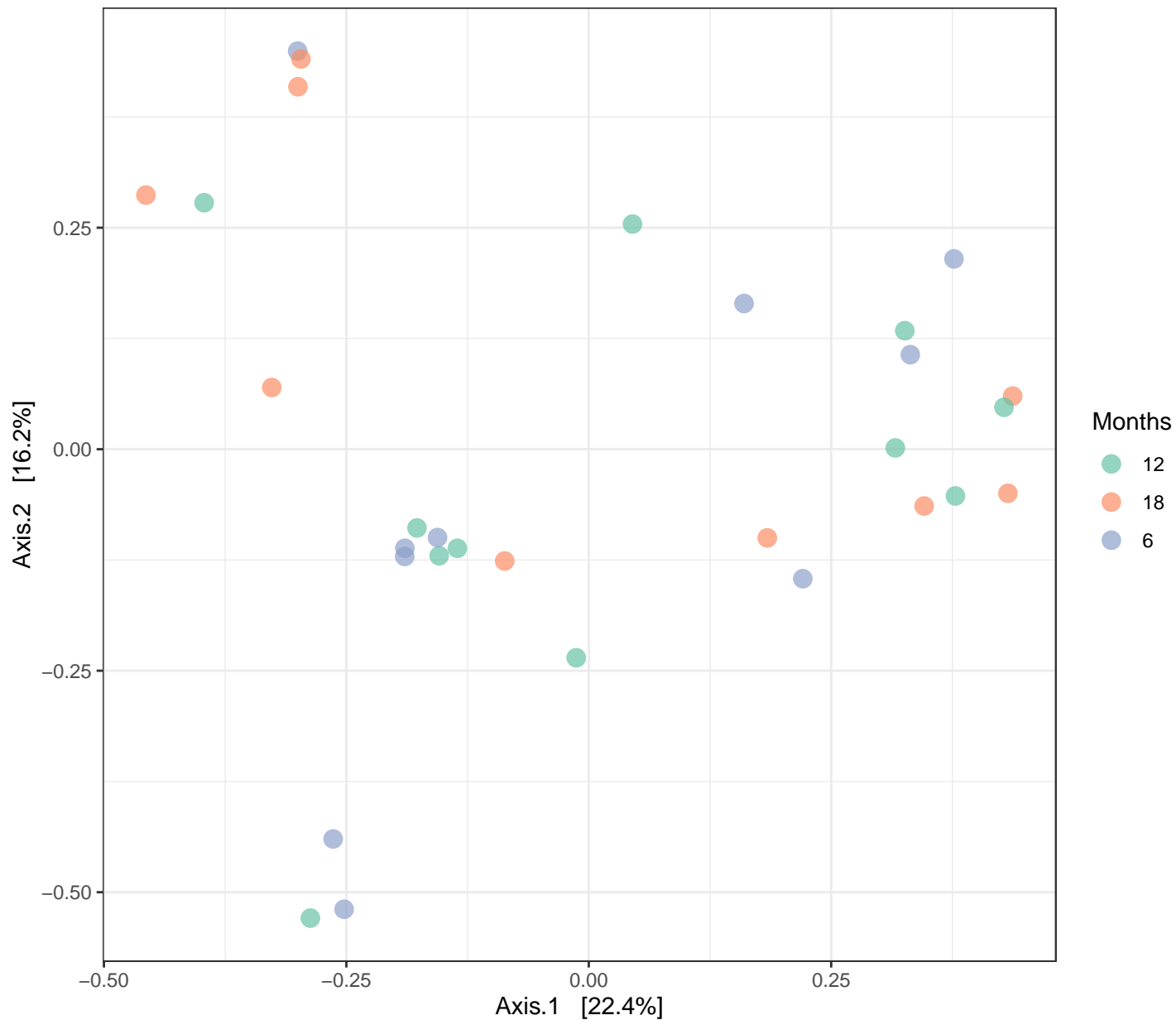




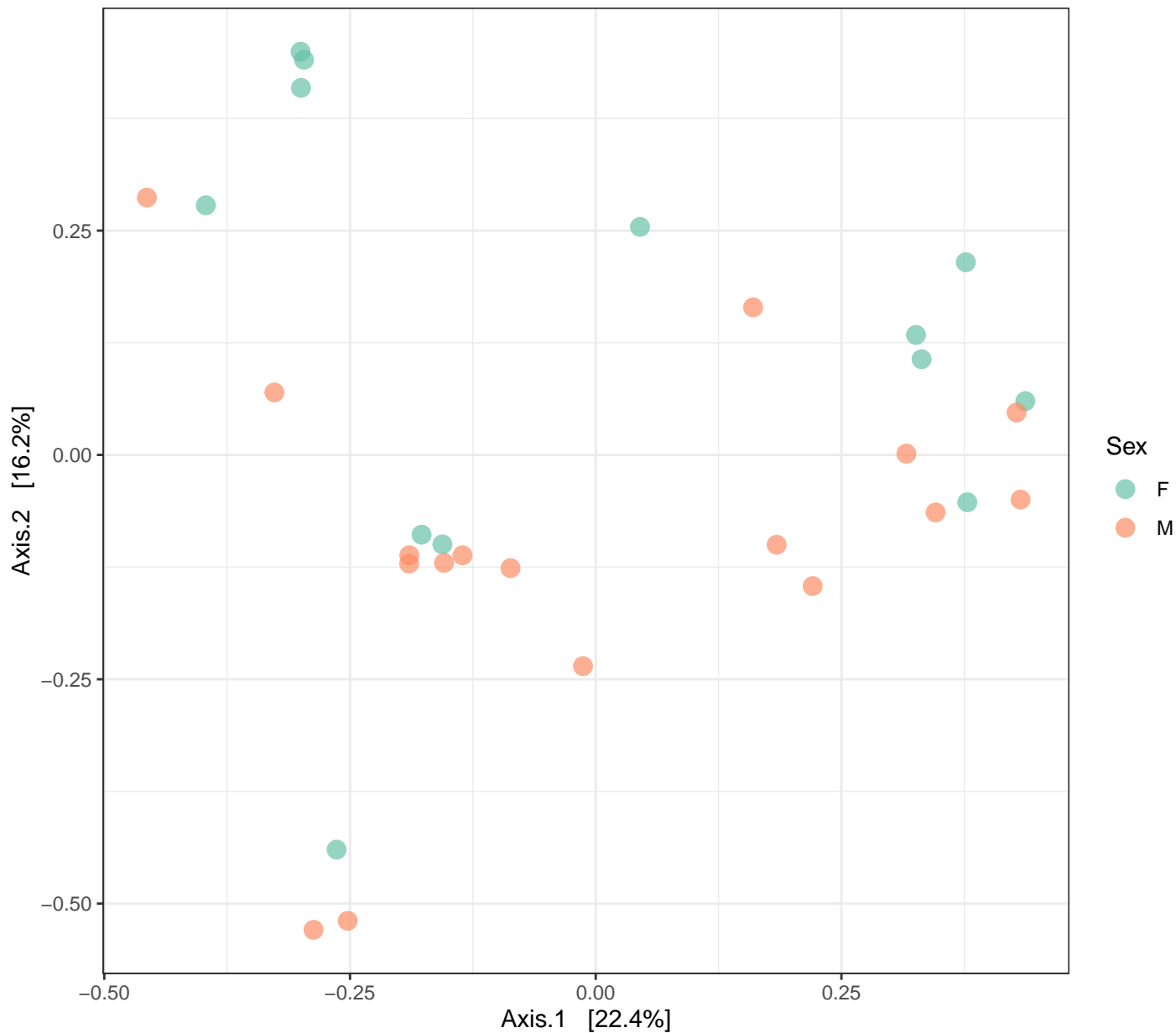




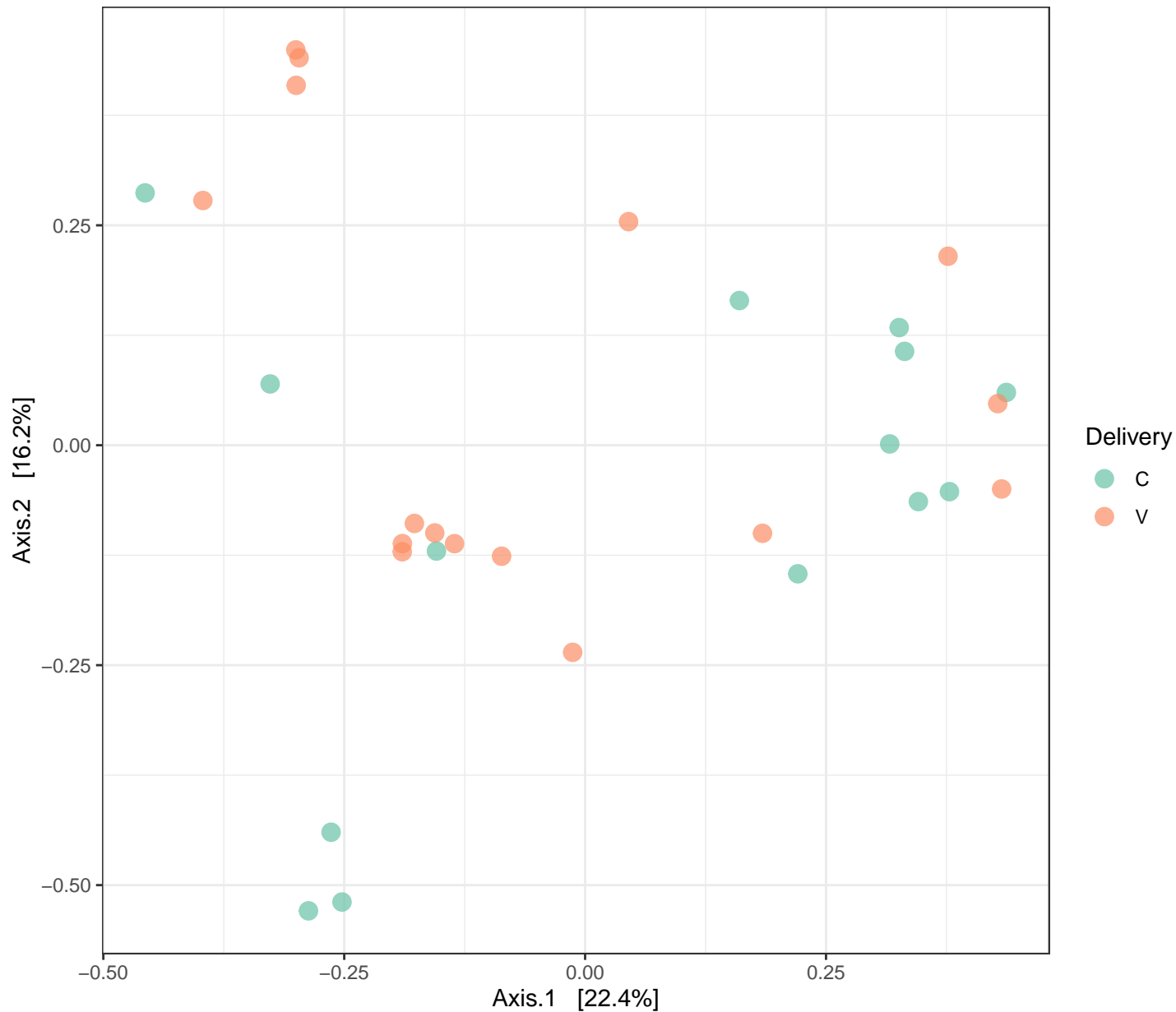
MDS using distance method bray



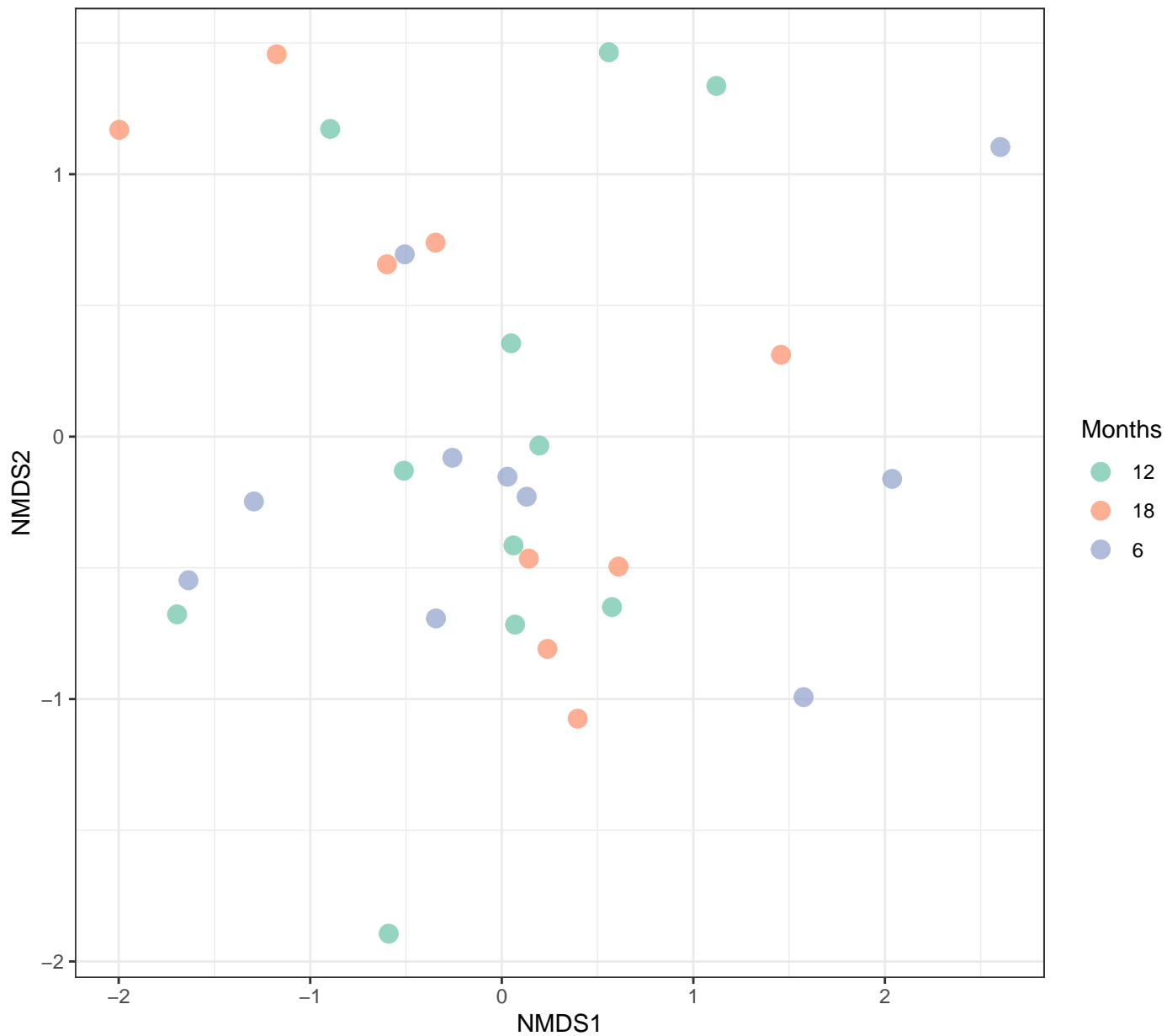
MDS using distance method bray



MDS using distance method bray

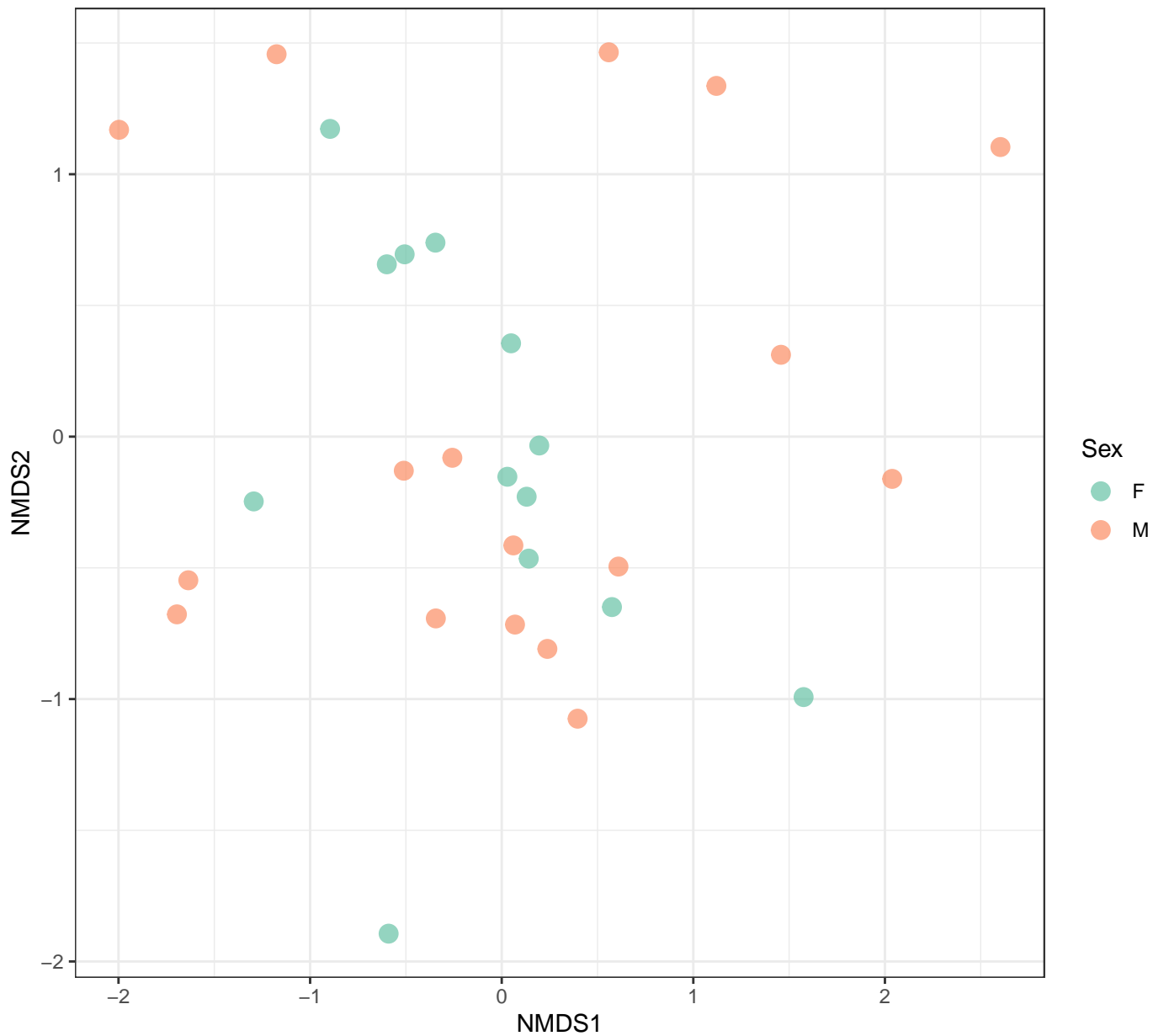


# NDMS on bray



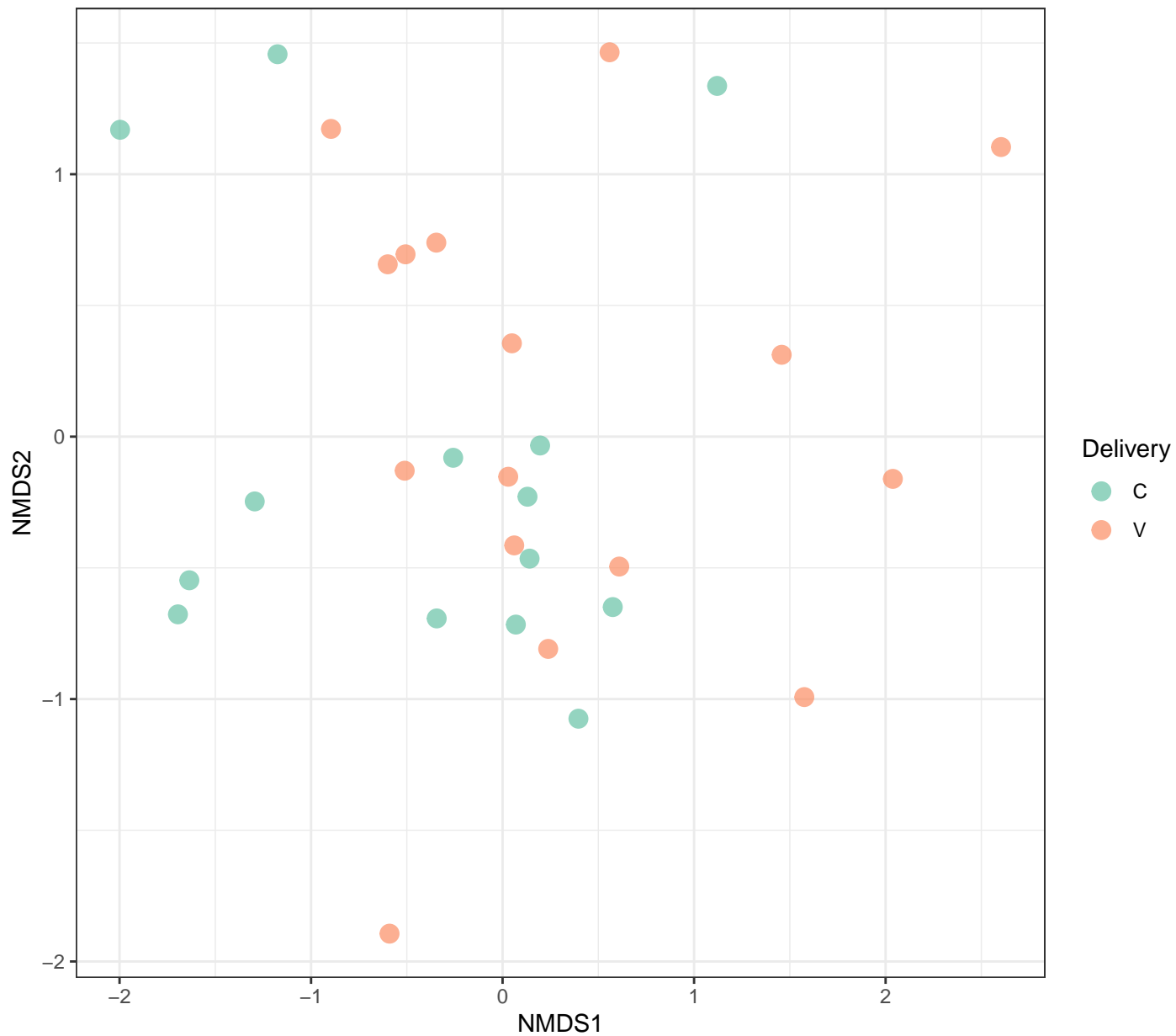
Stress 0.1836

NDMS on bray



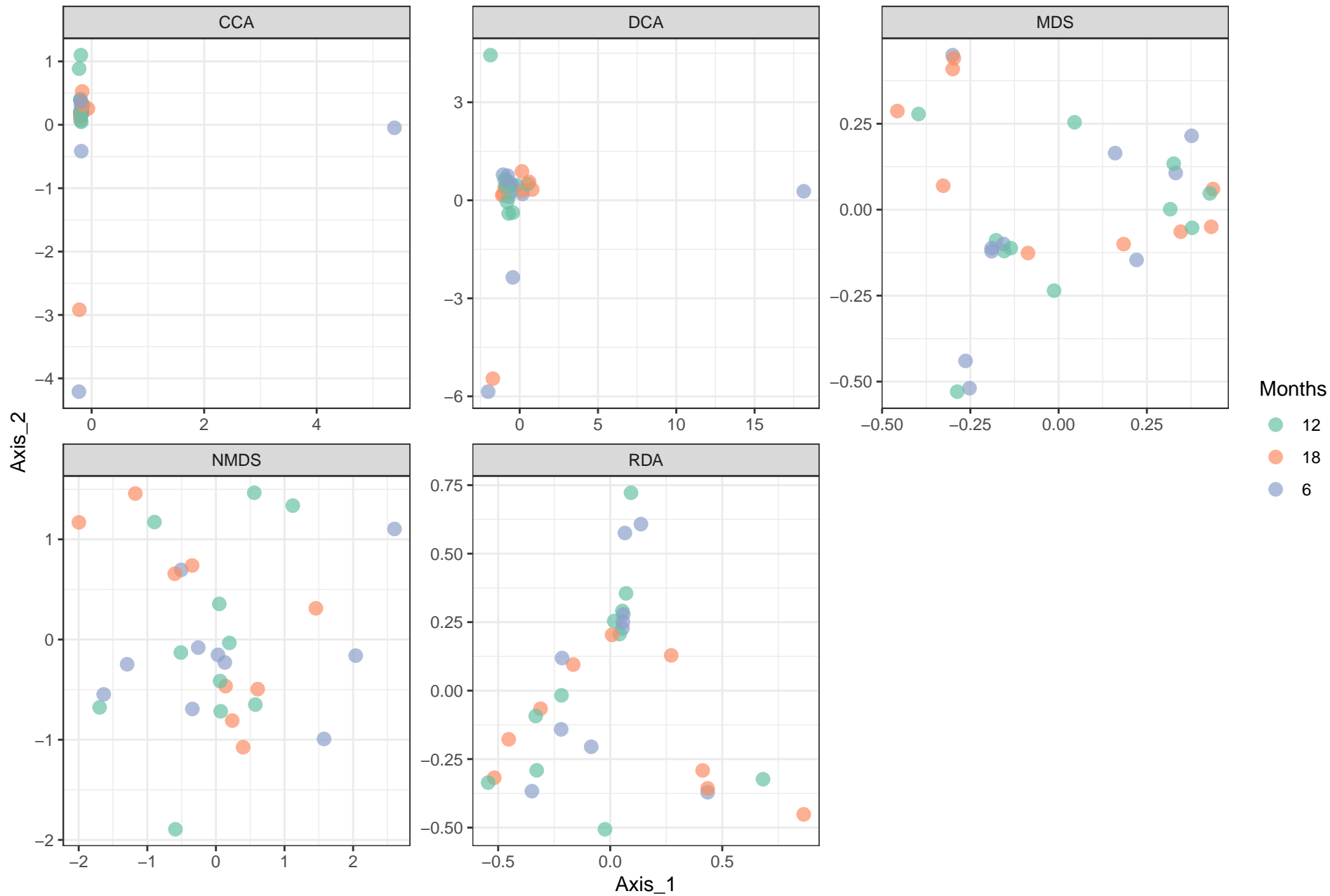
Stress 0.1836

# NDMS on bray



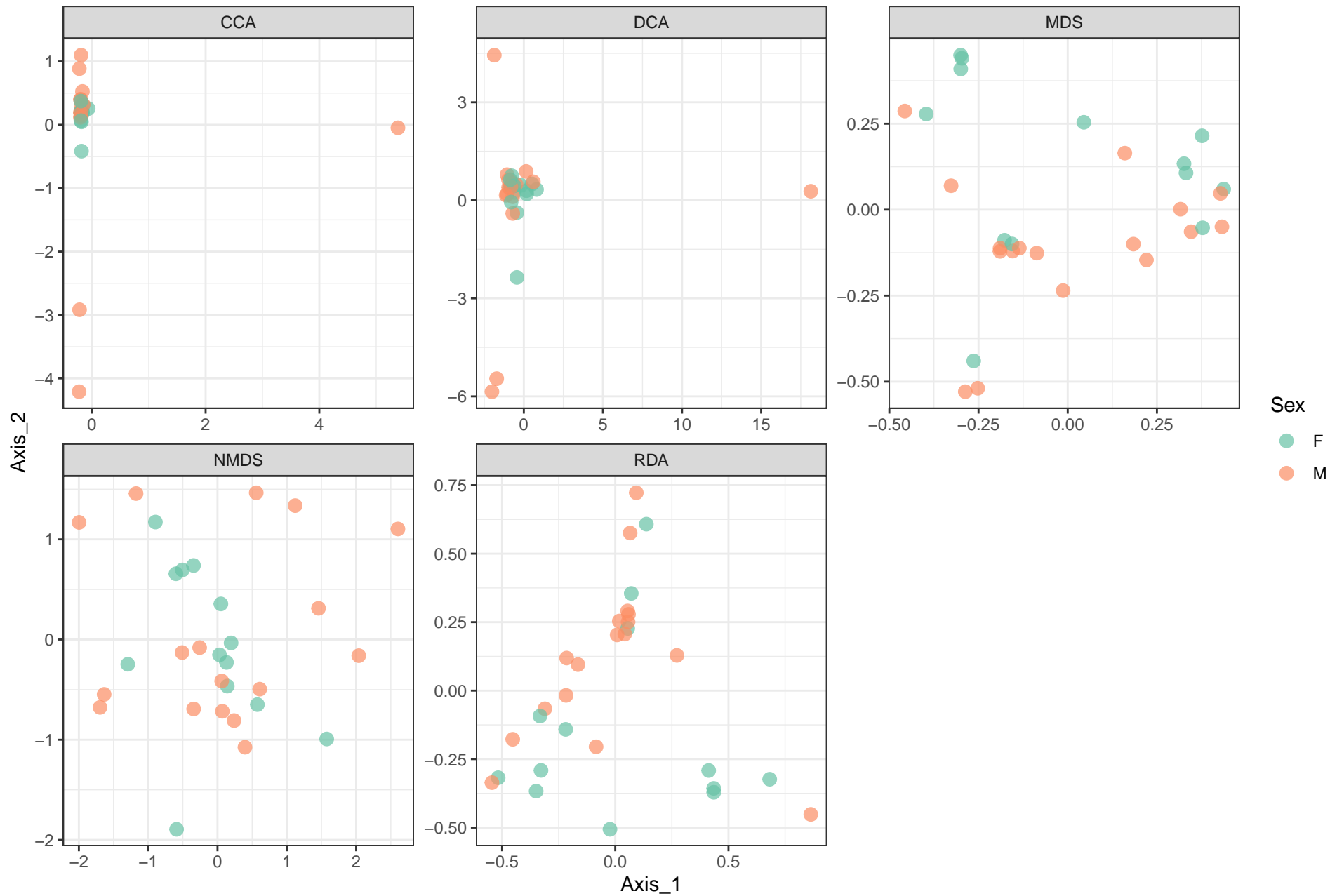
Stress 0.1836

bray

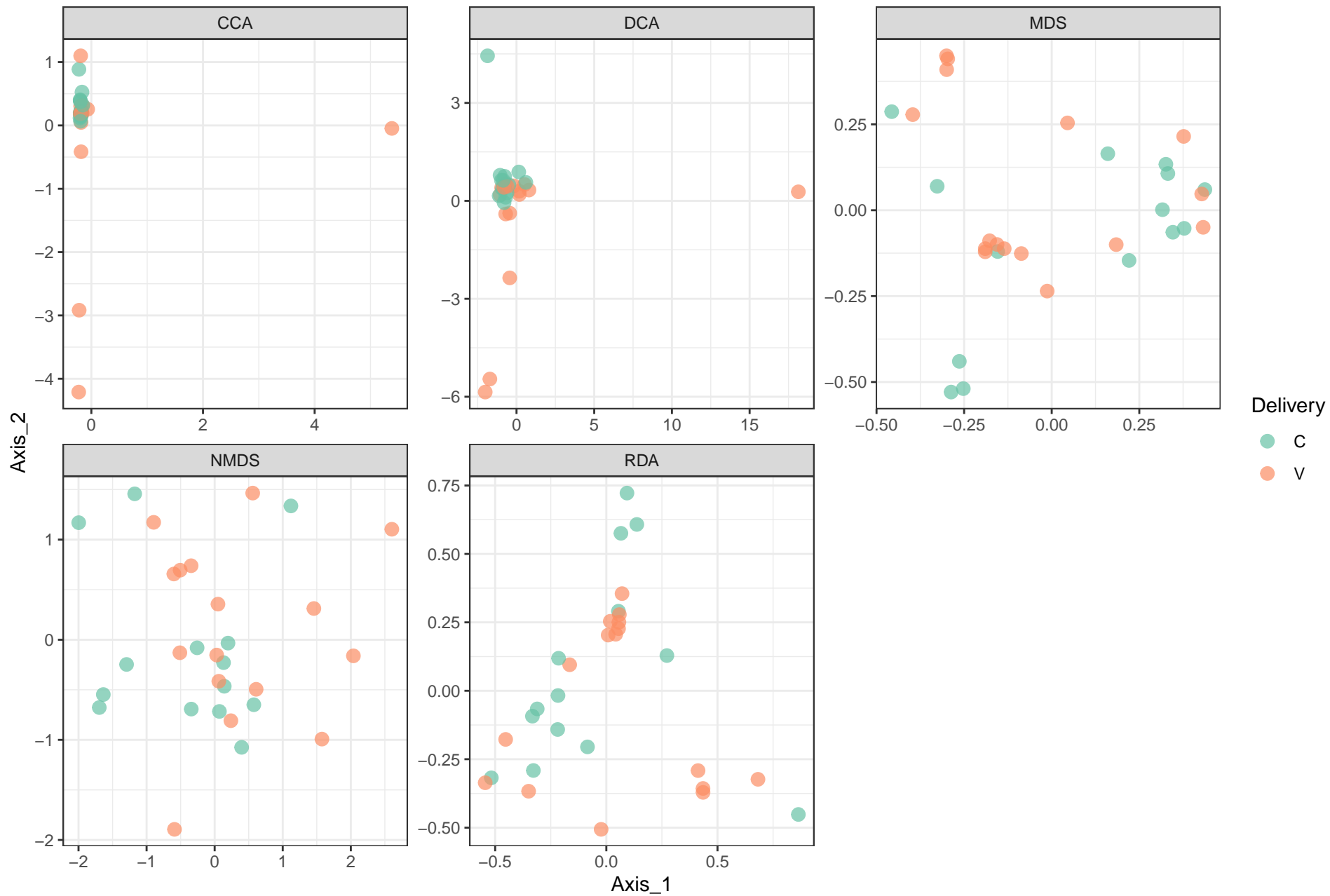




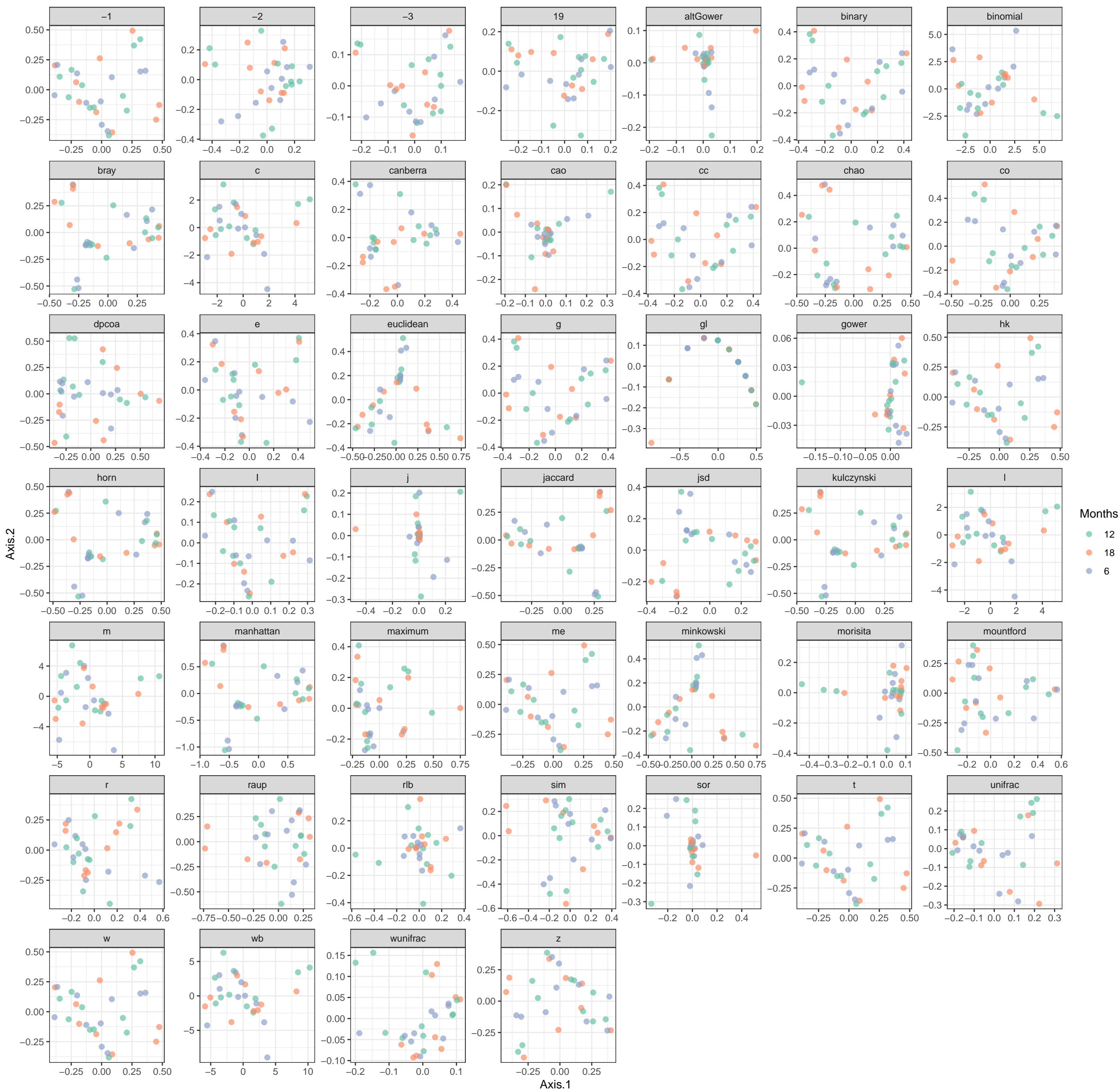
bray



bray



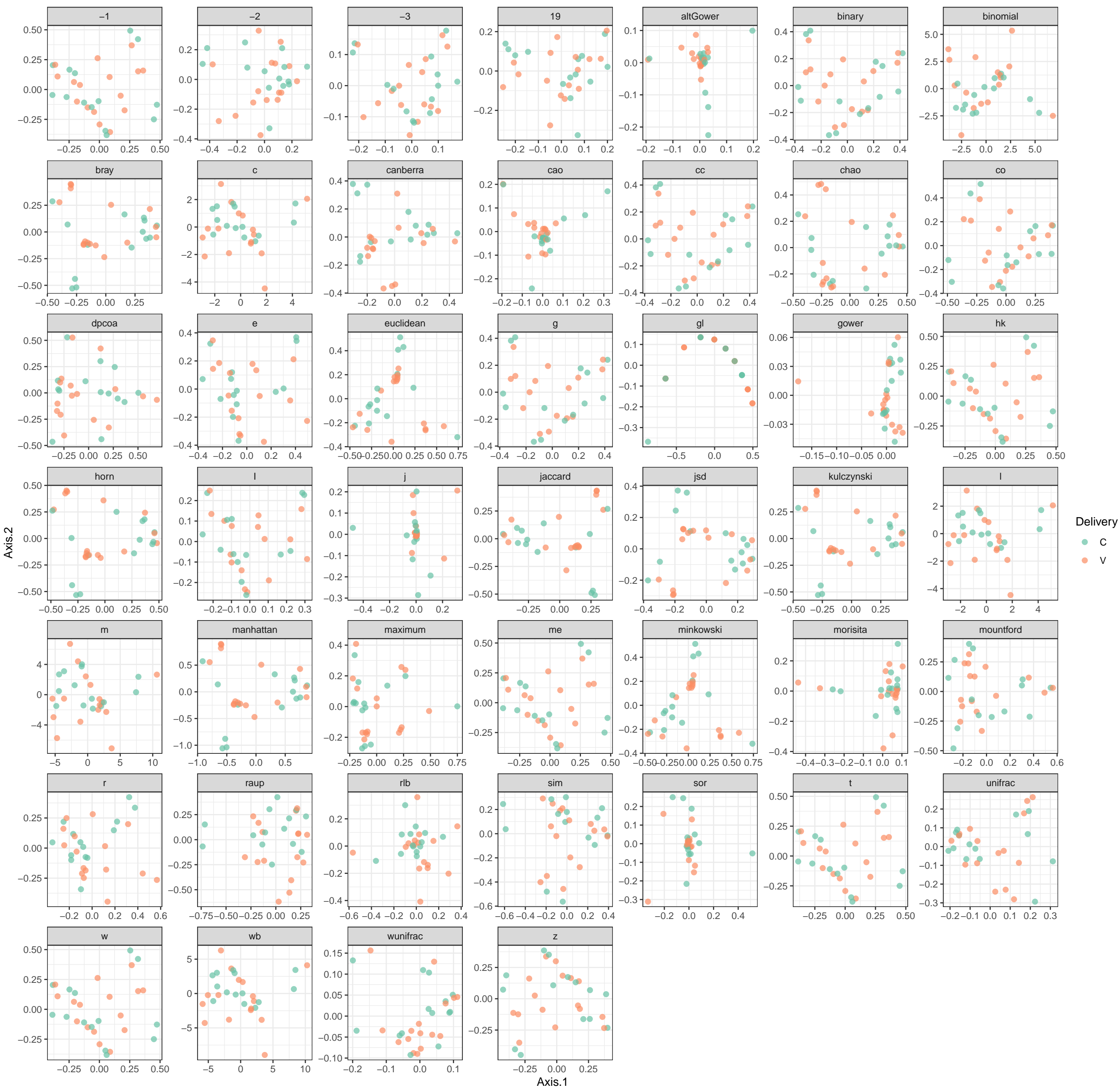
MDS on various distance metrics



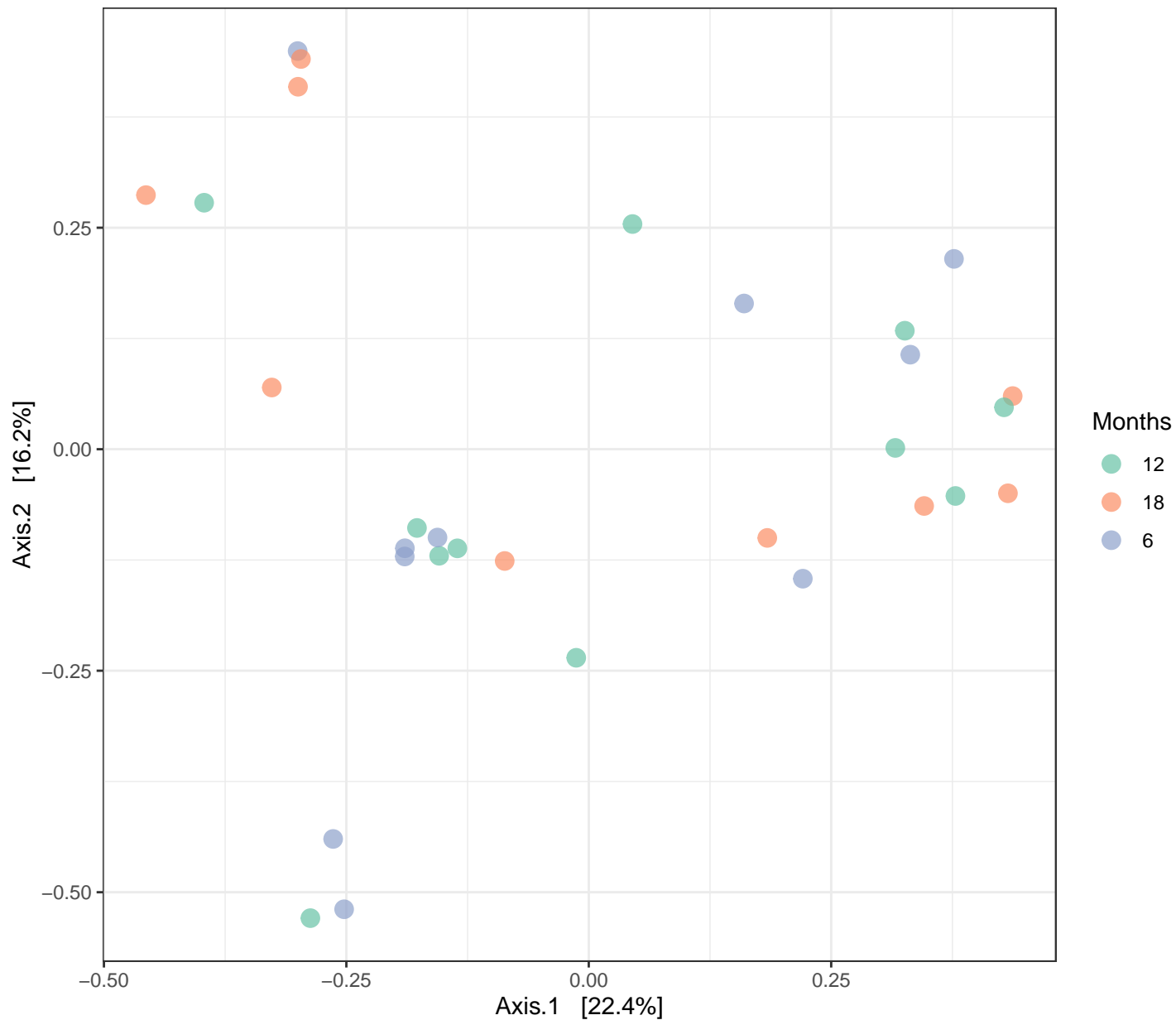
MDS on various distance metrics



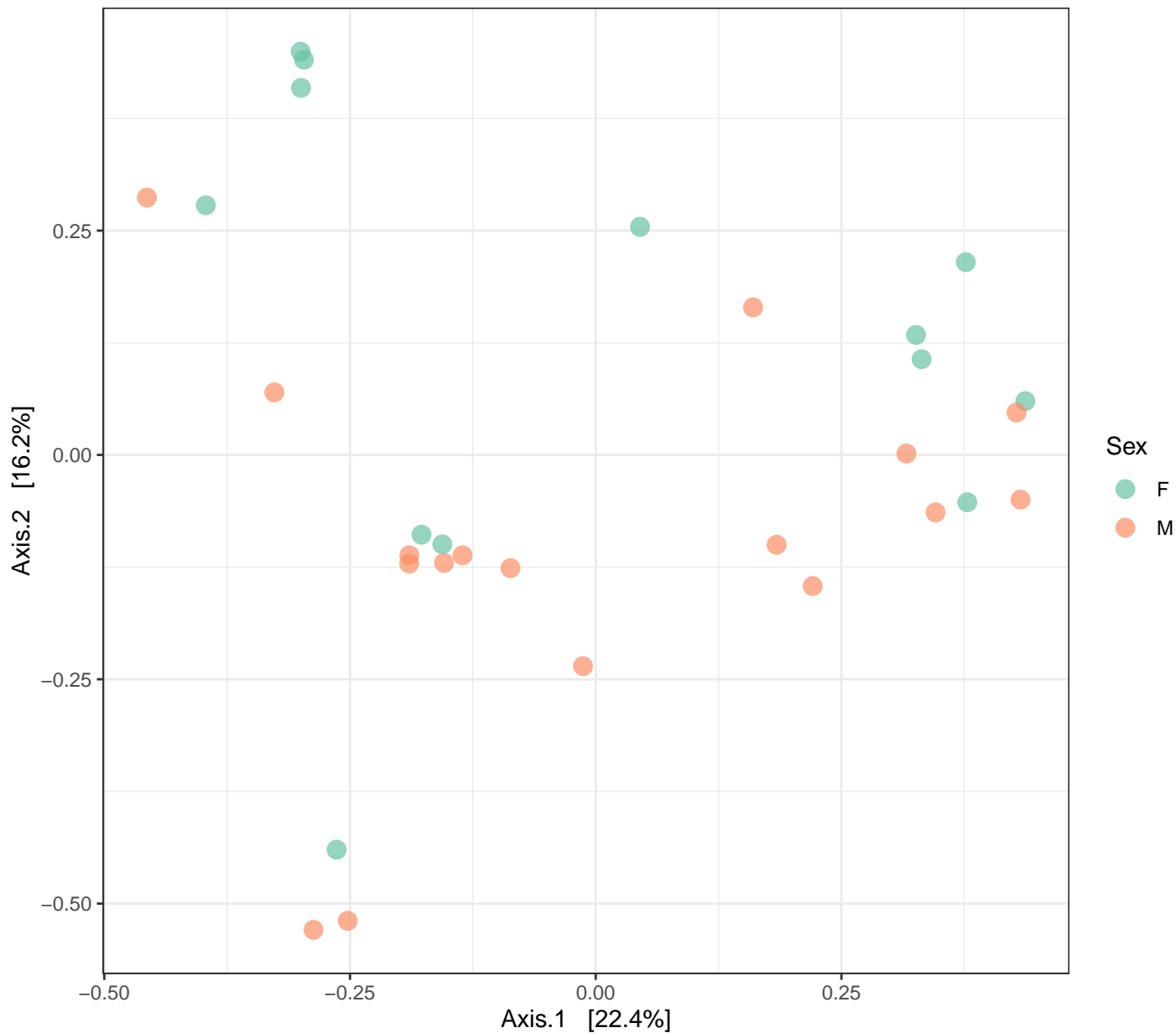
MDS on various distance metrics



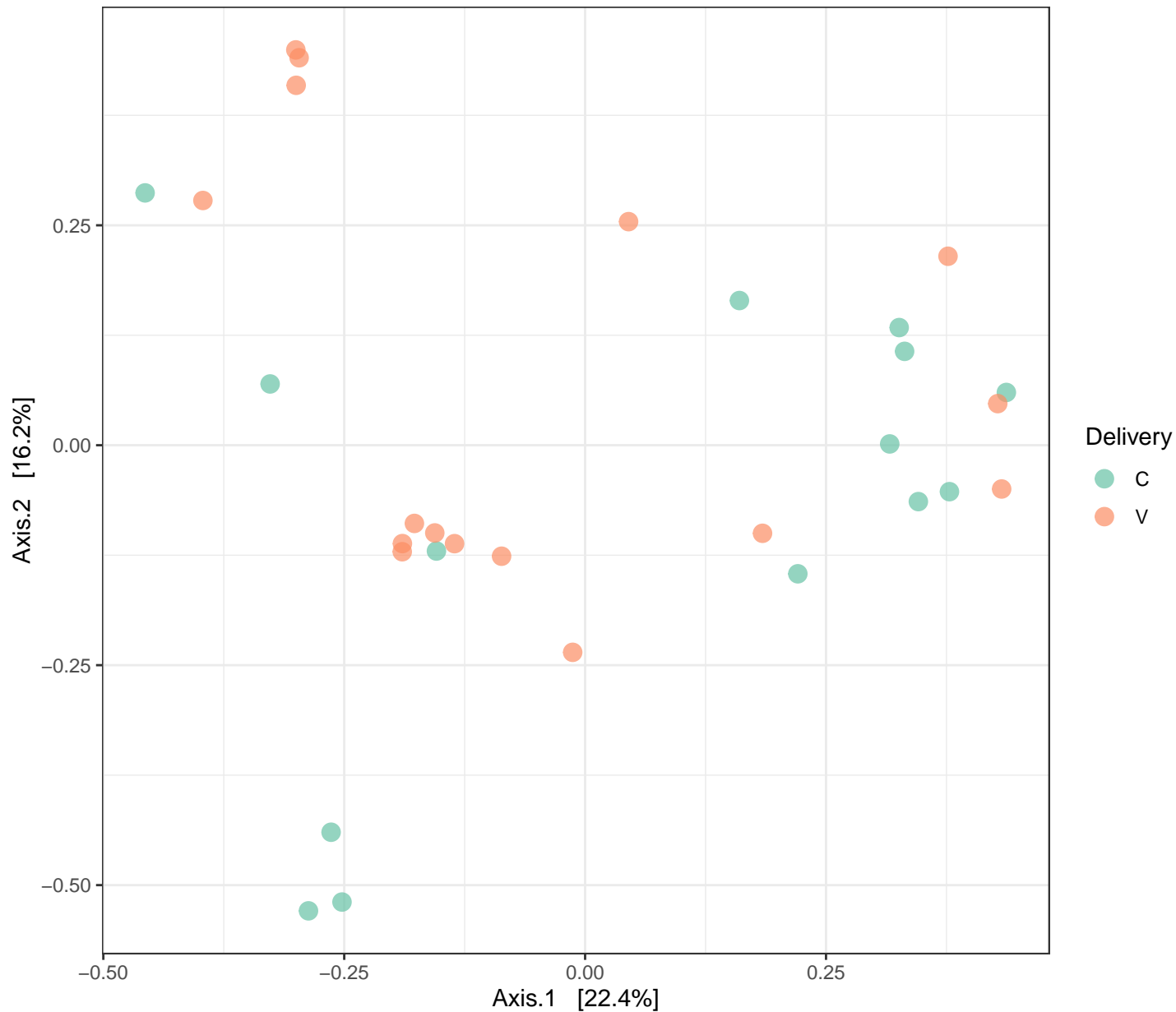
MDS using distance method bray



MDS using distance method bray

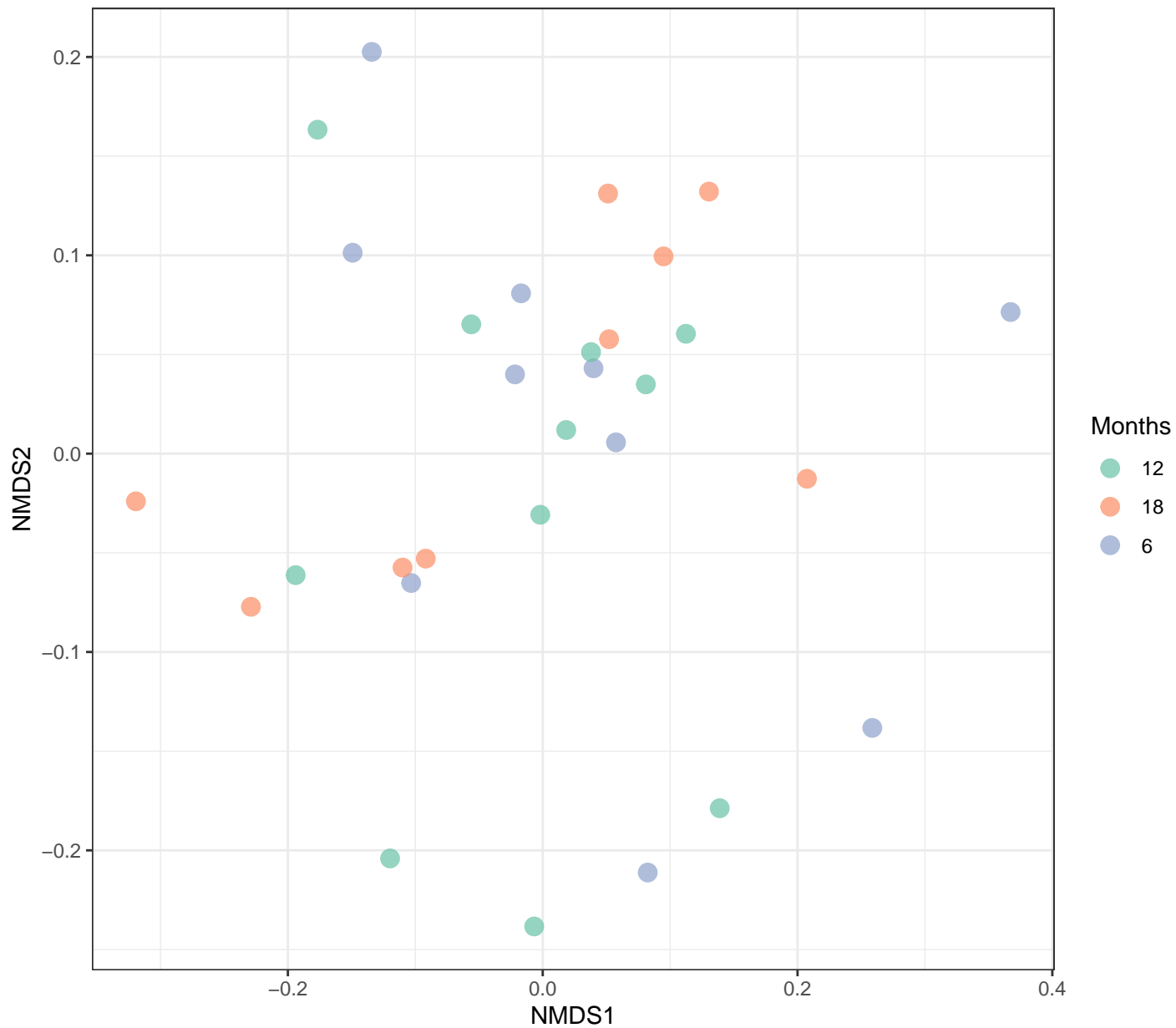


MDS using distance method bray



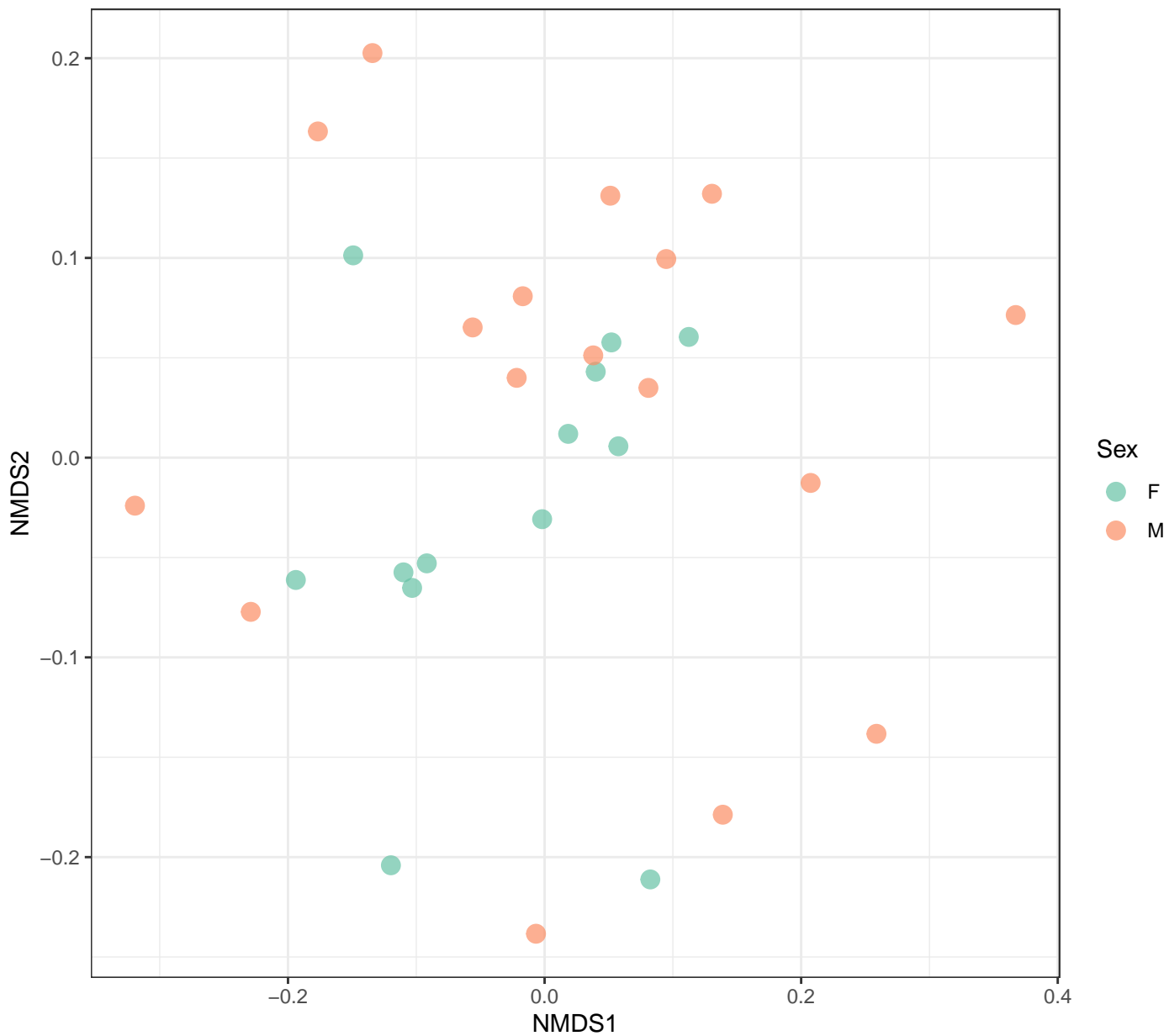


# NDMS on jsd



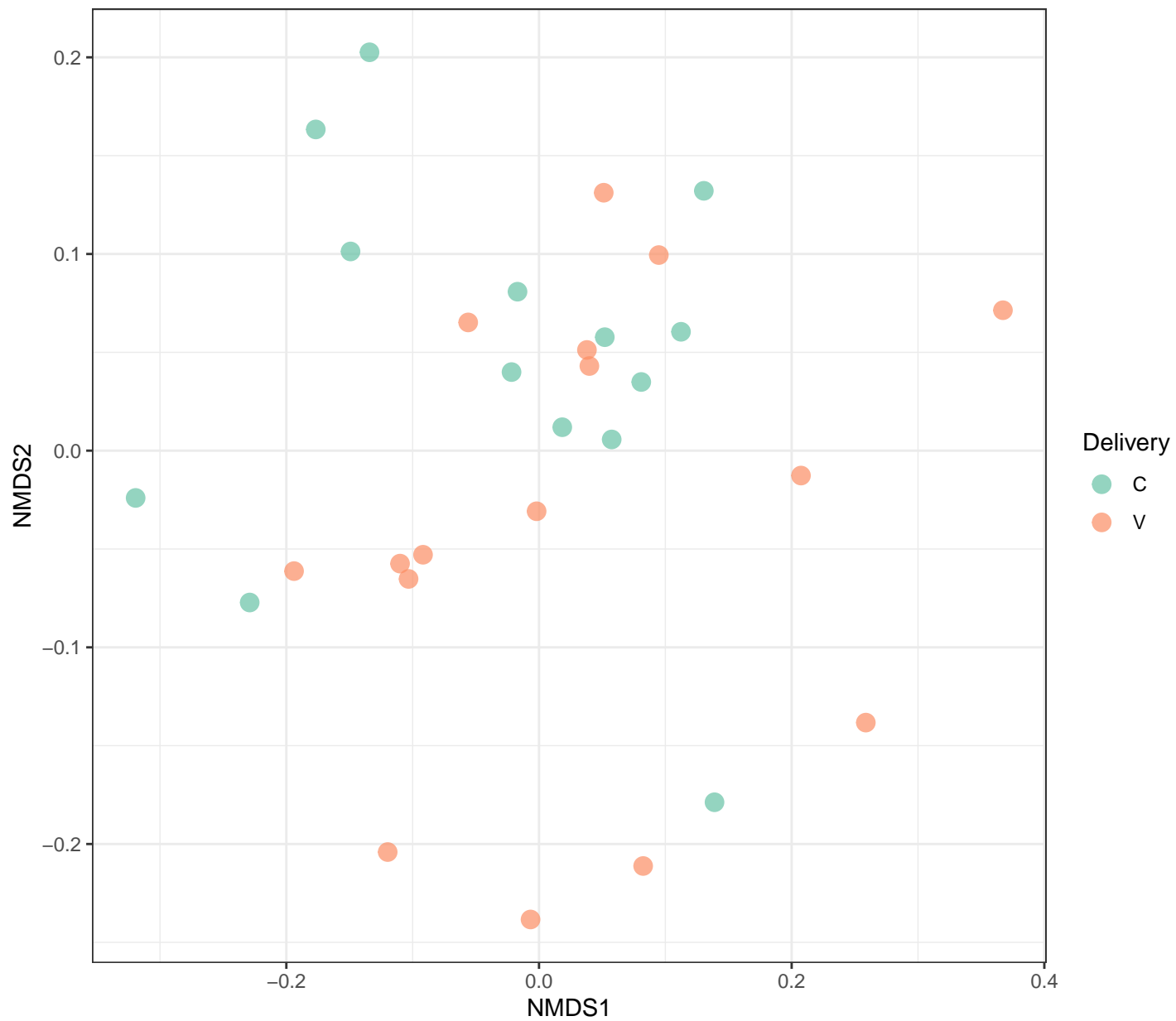
Stress 0.1781

# NDMS on jsd



Stress 0.1781

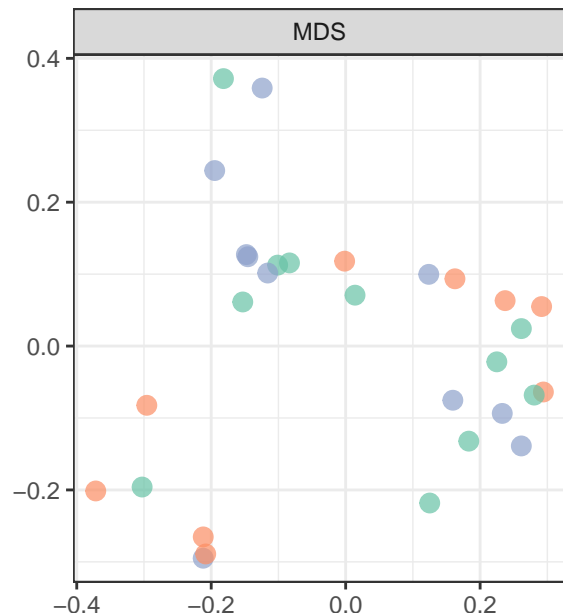
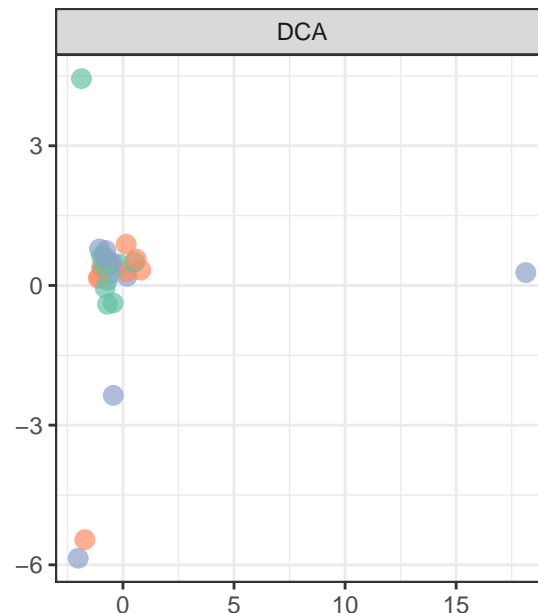
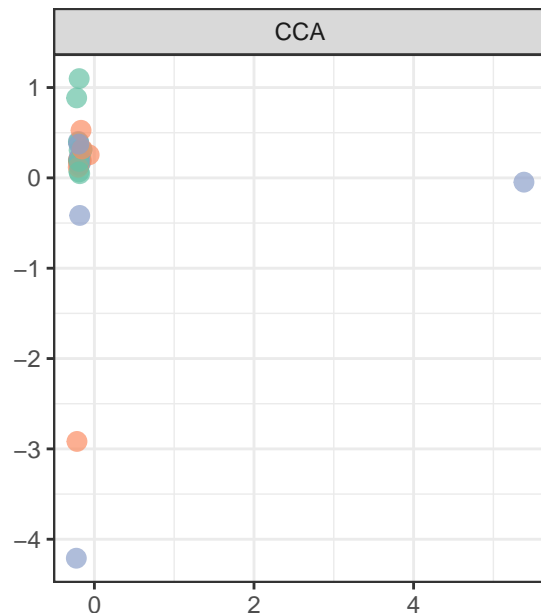
NDMS on jsd



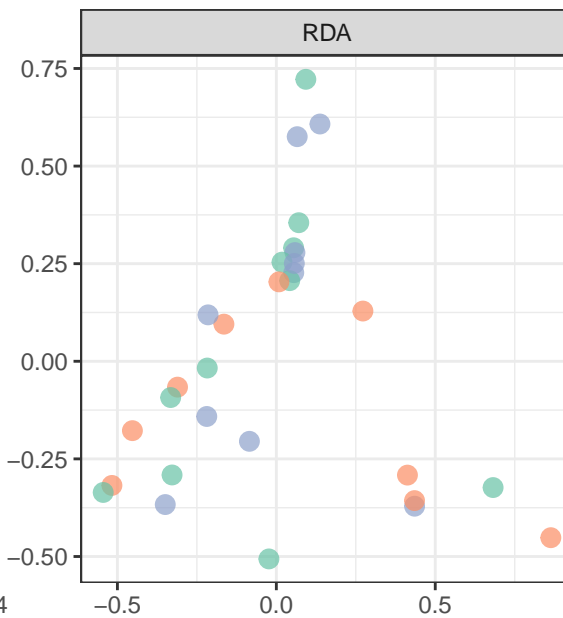
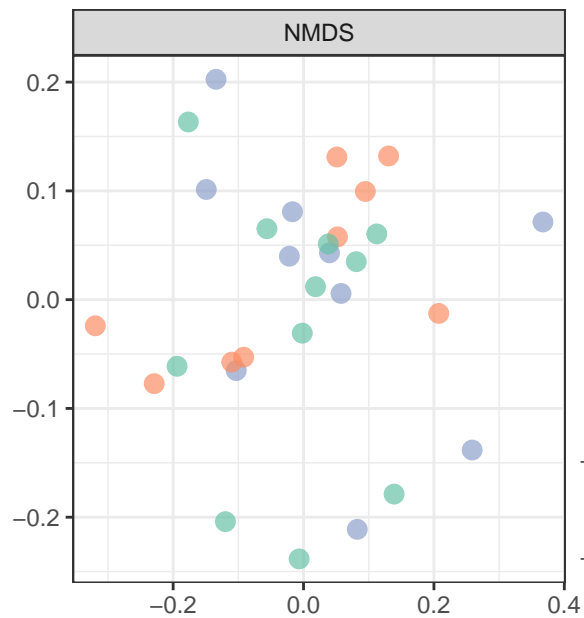
Stress 0.1781

jsd

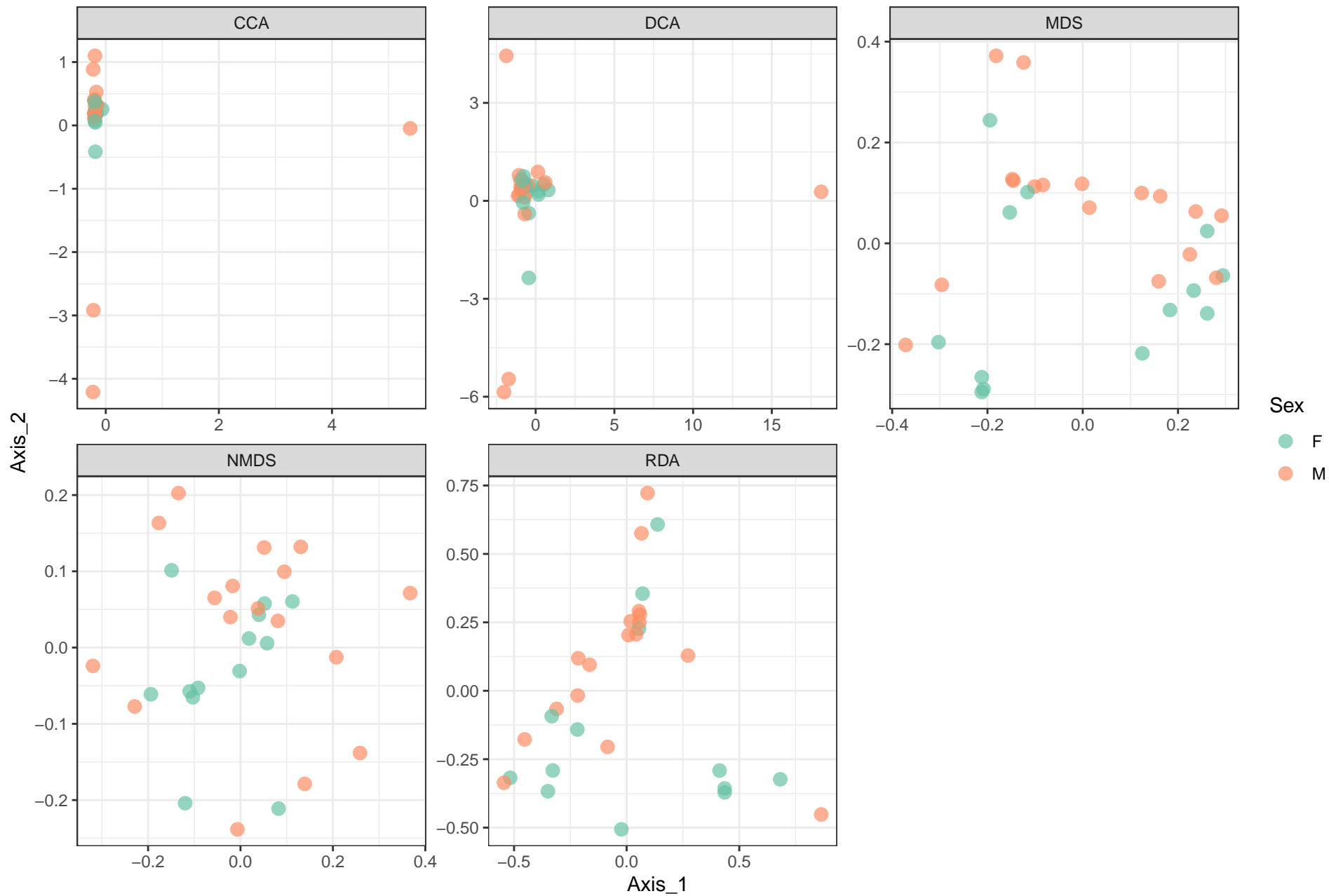
Axis\_2



Months



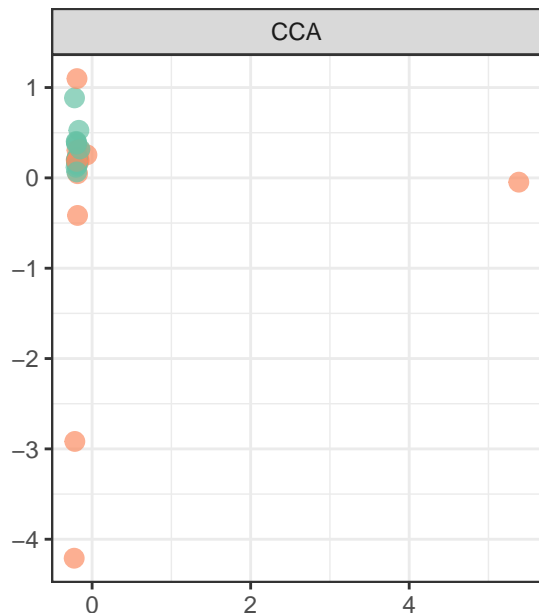
jsd



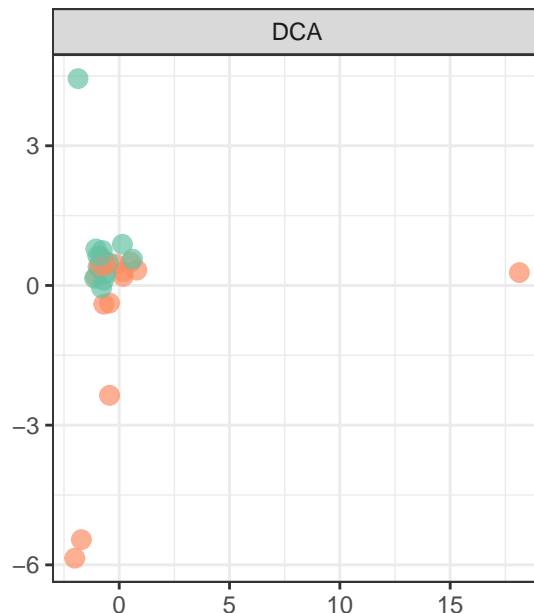
jsd

Axis\_2

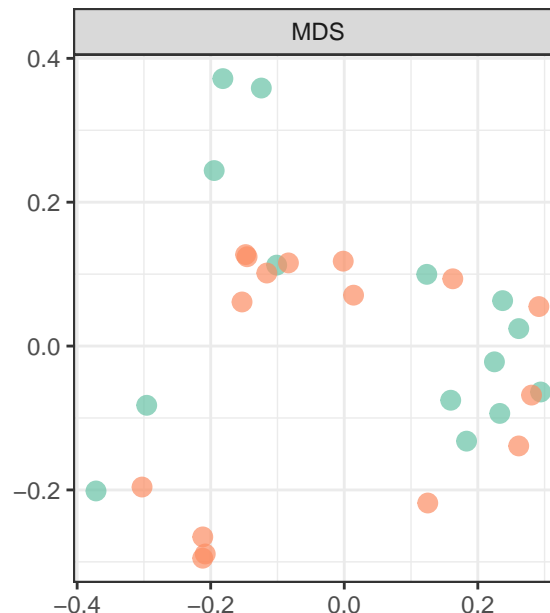
CCA



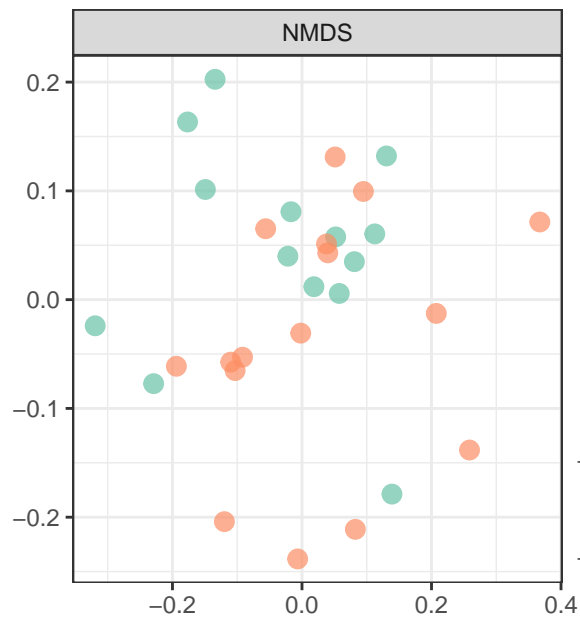
DCA



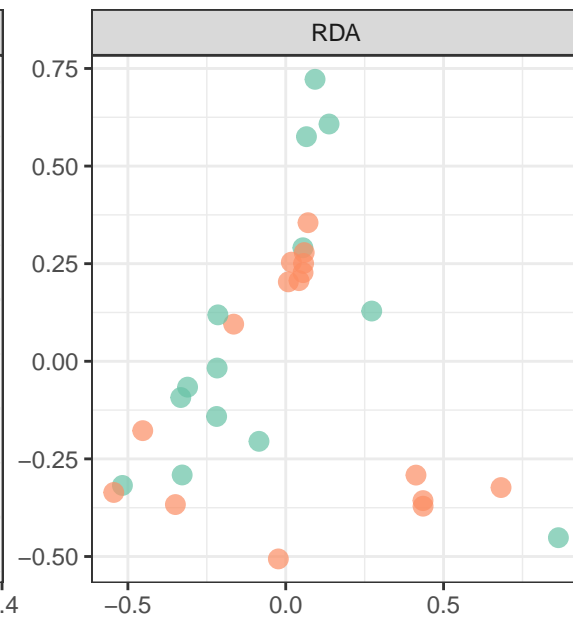
MDS



NMDS



RDA

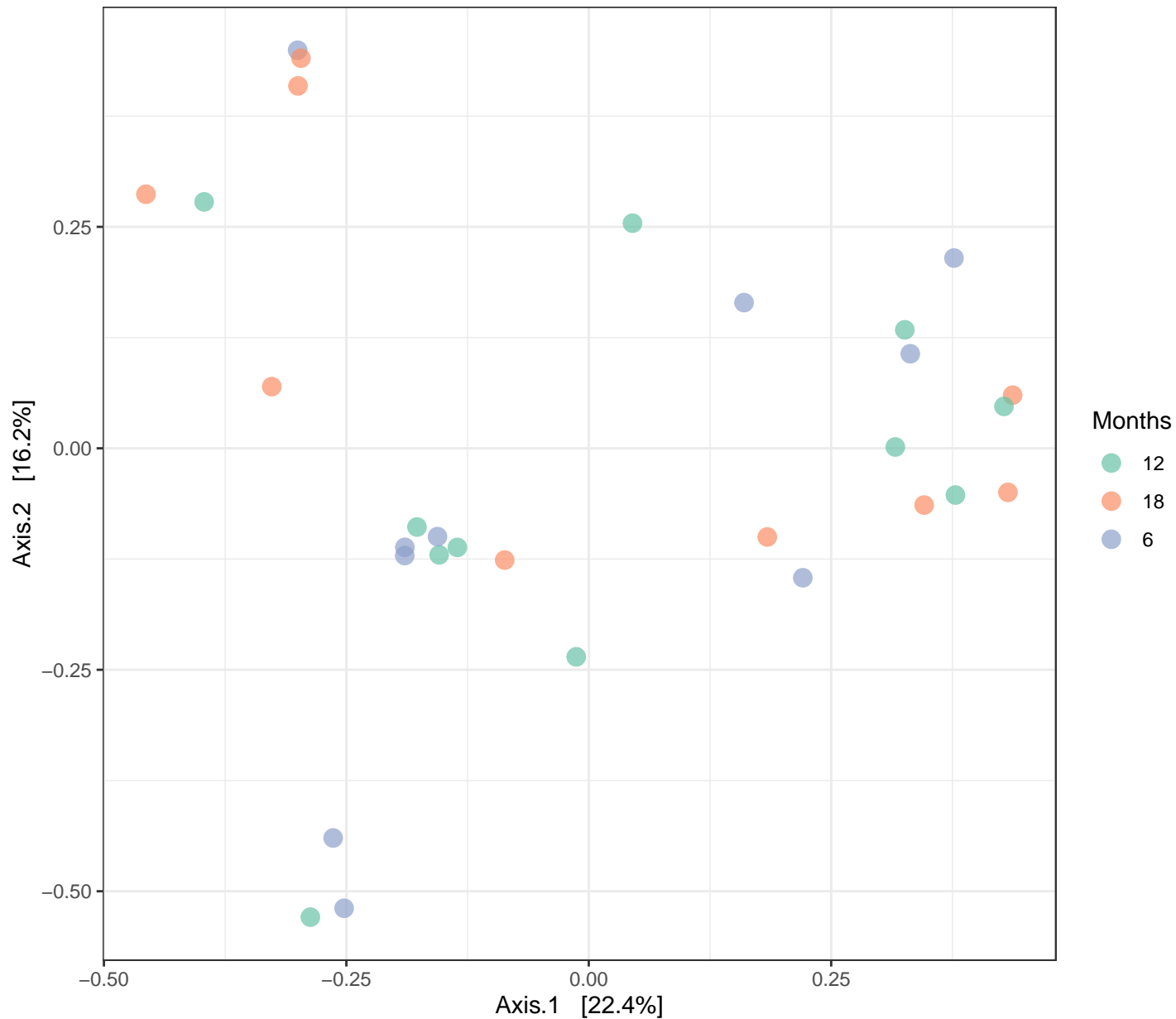


Axis\_1

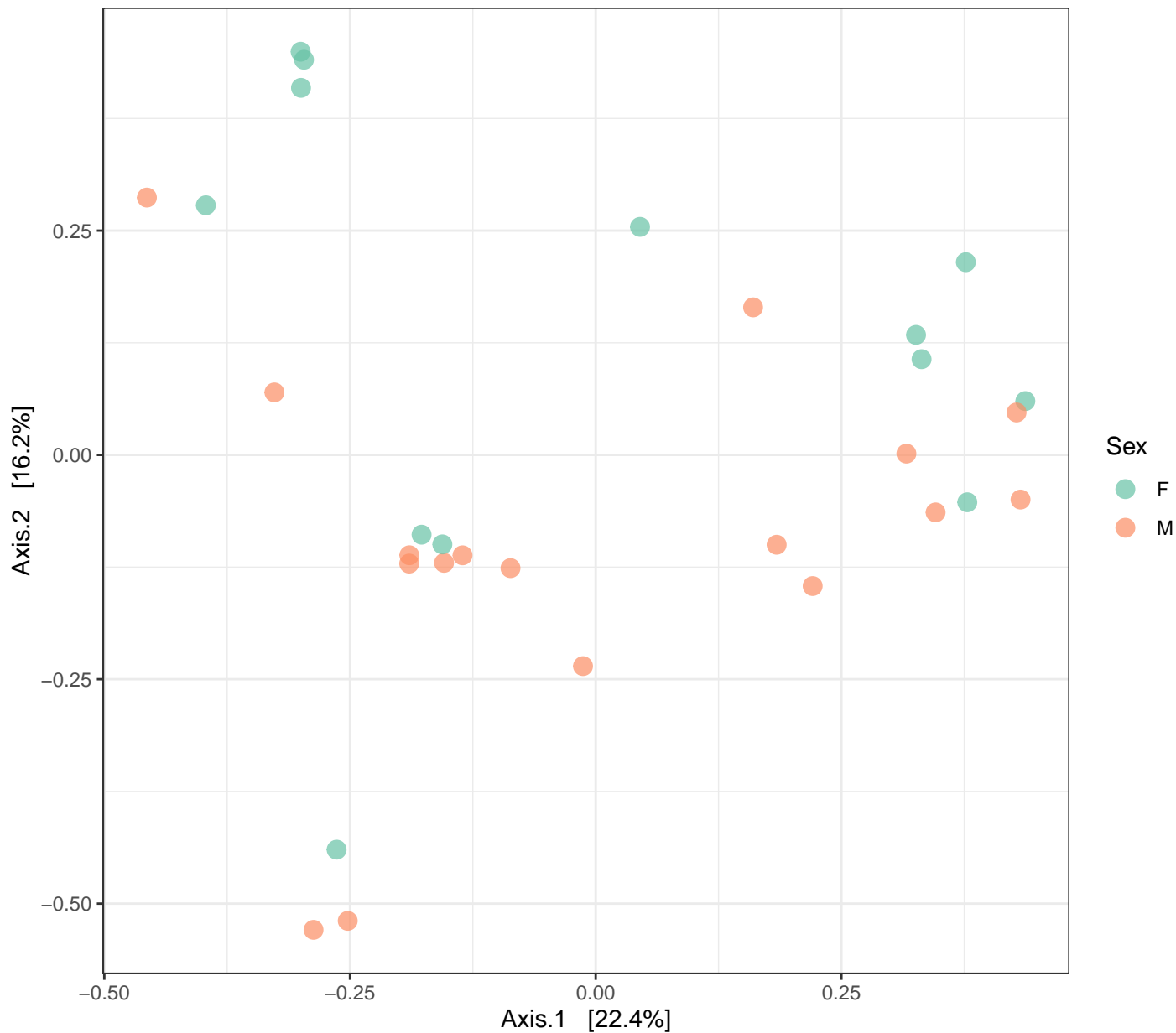
Delivery

C  
V

## MDS using distance method bray

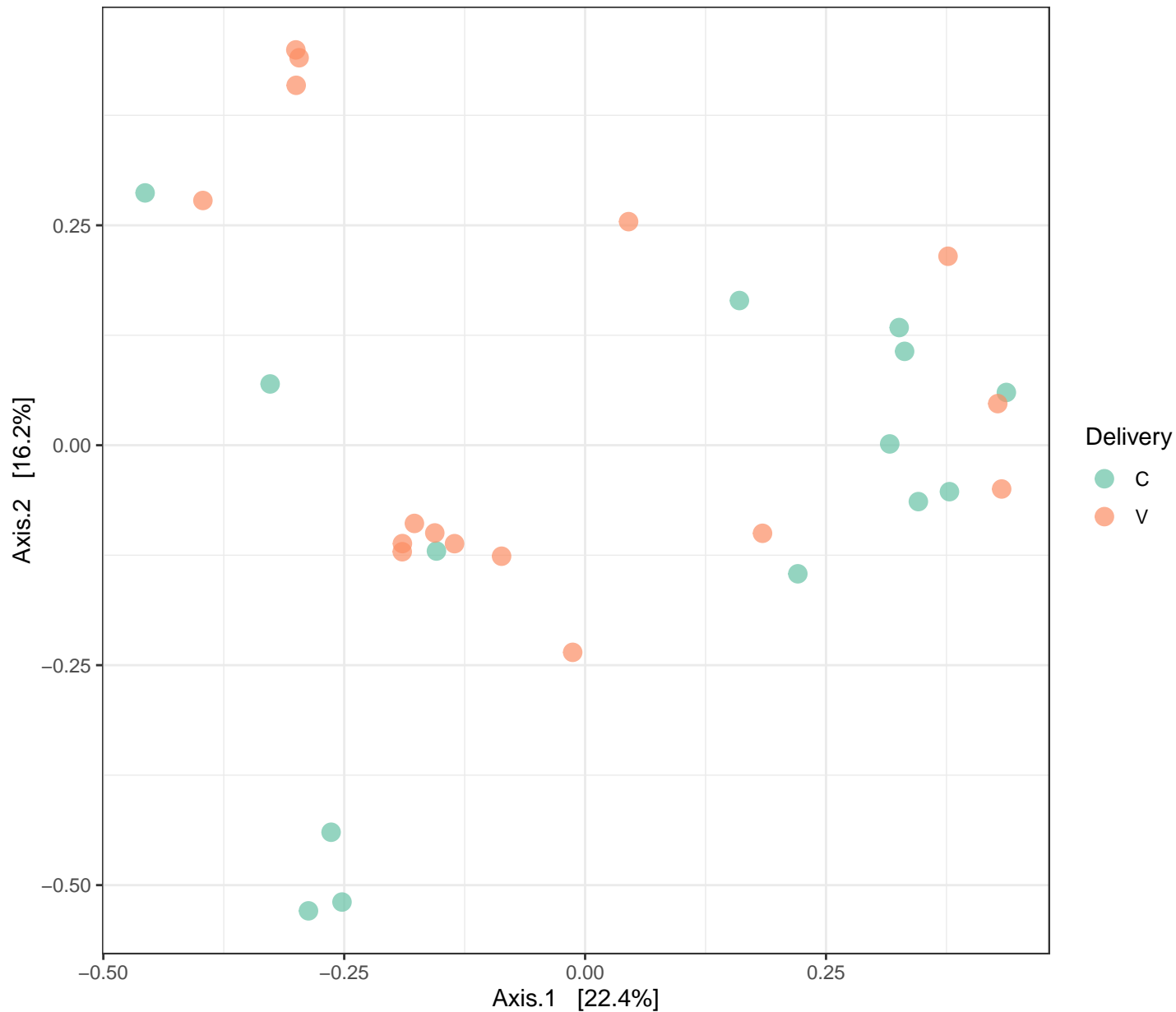


MDS using distance method bray

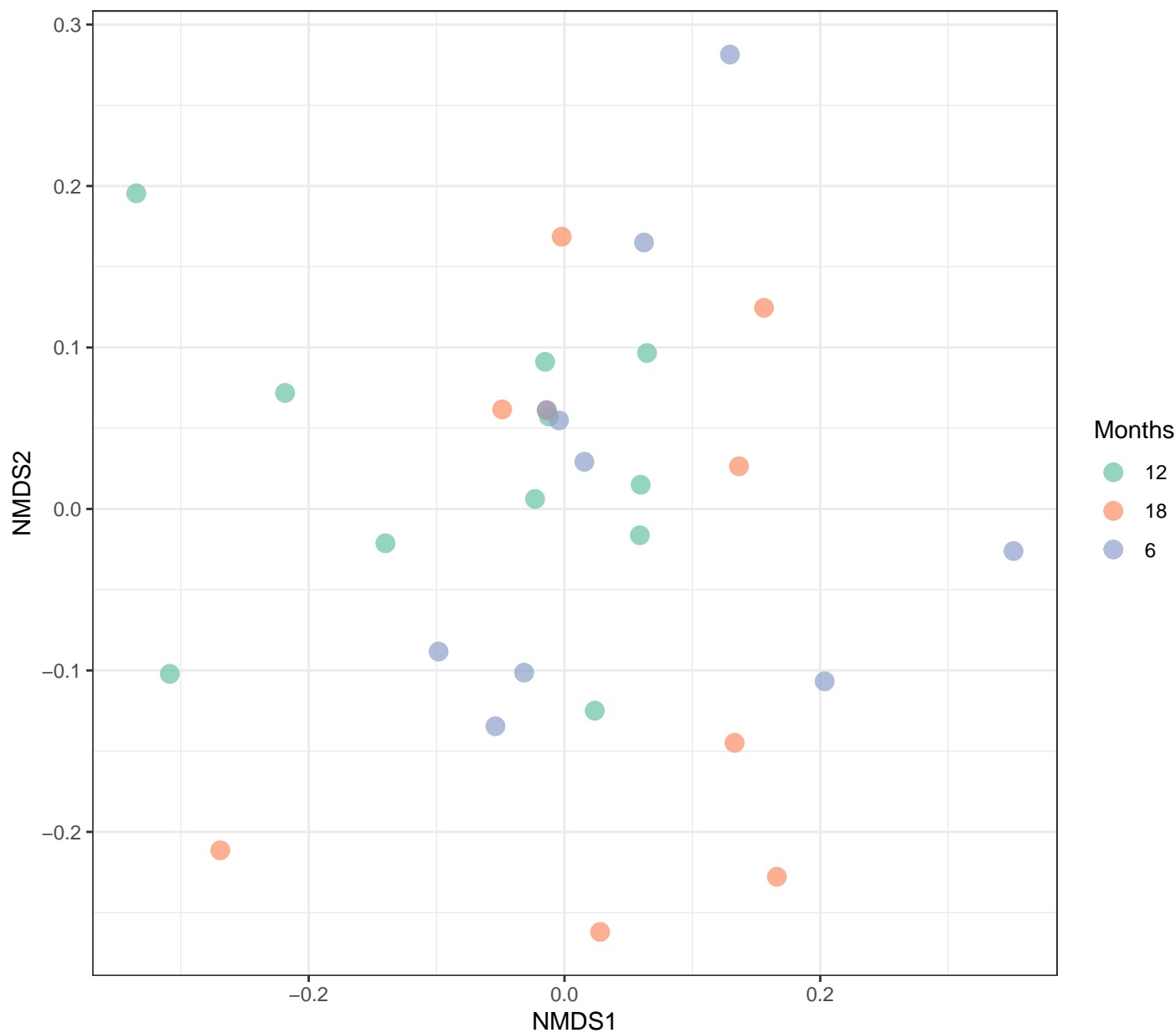




MDS using distance method bray

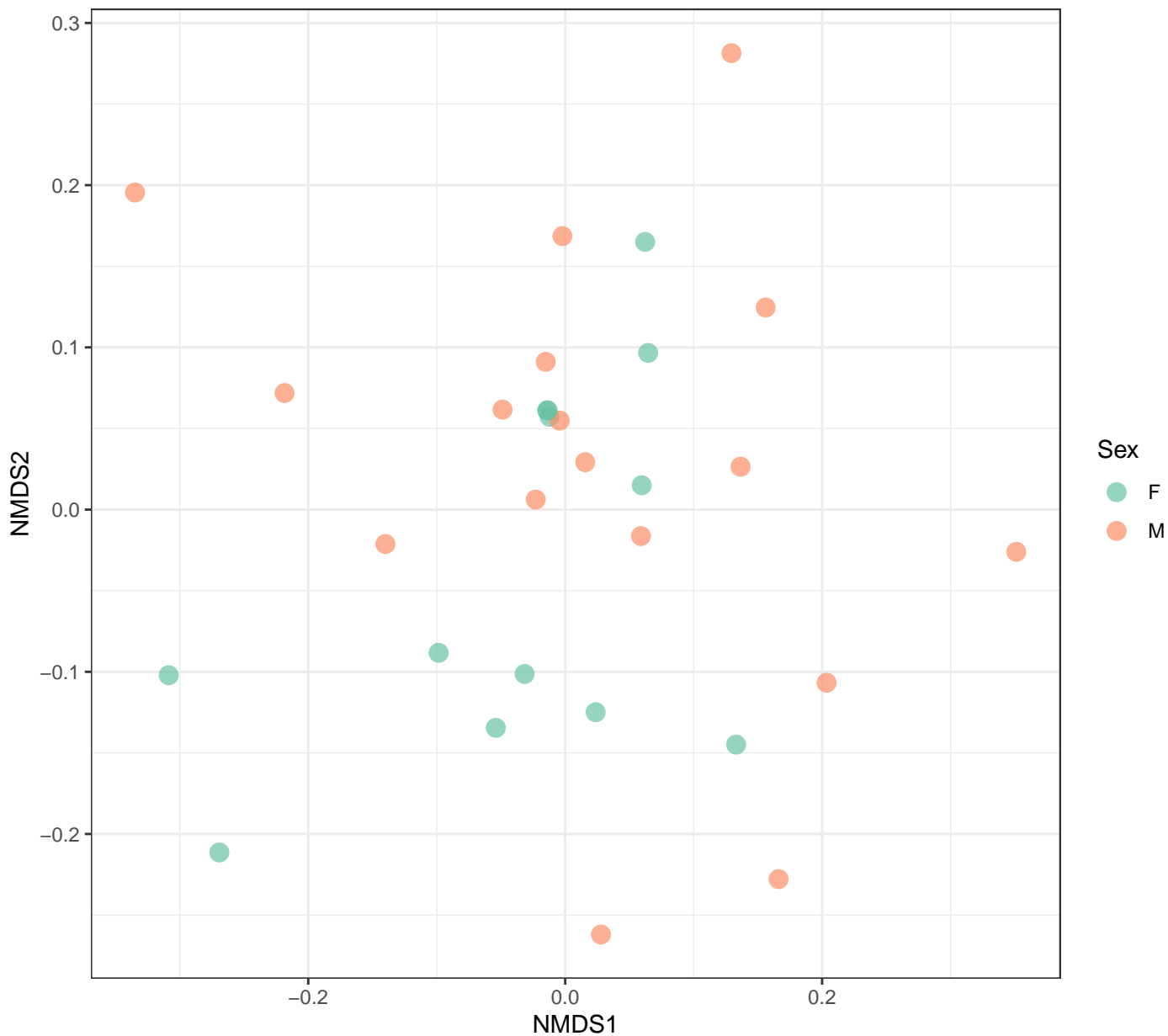


# NDMS on unifrac



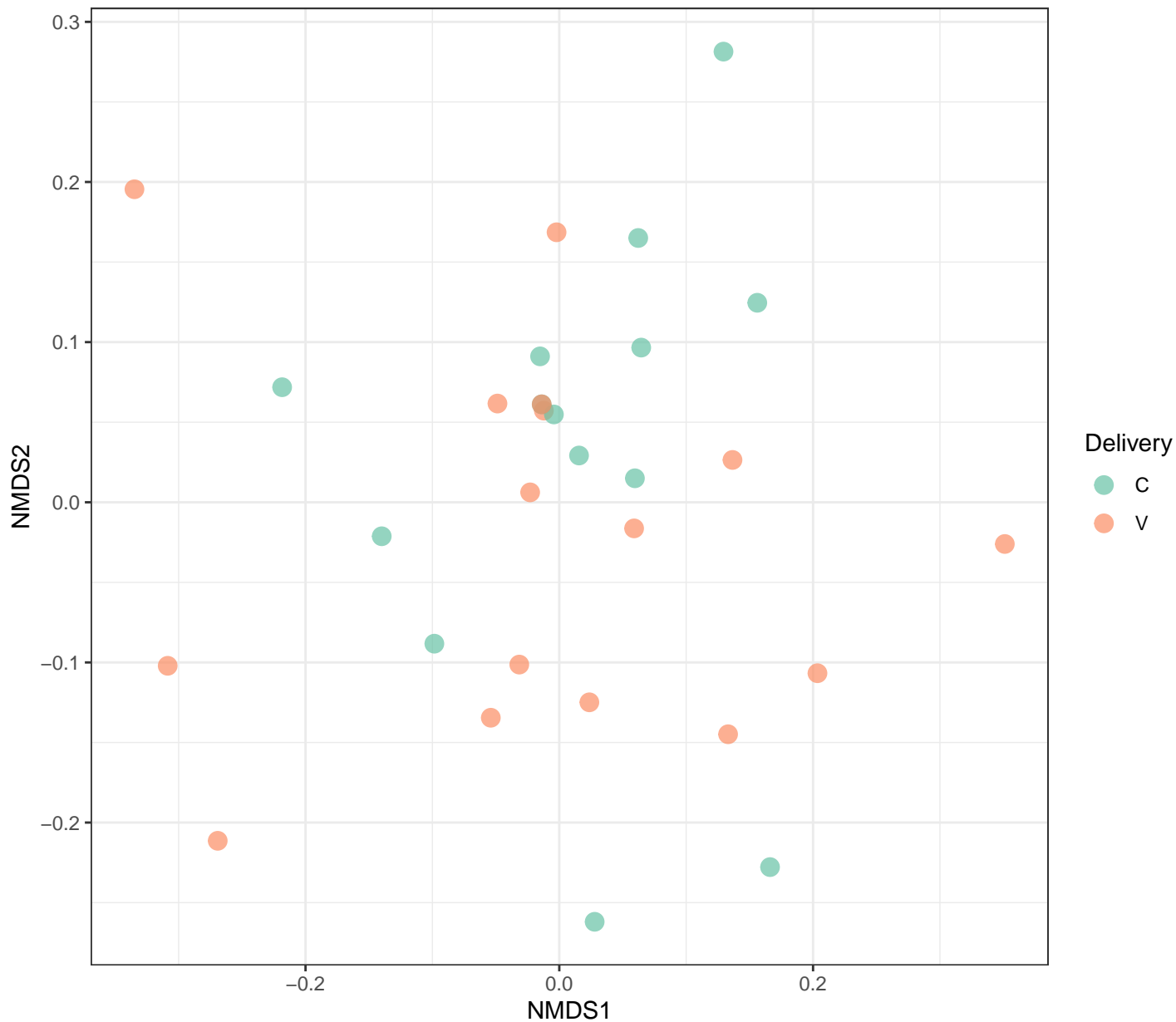
WARNING: stress 0.2025 is > 0.20 – representation may be random!

# NDMS on unifrac



WARNING: stress 0.2025 is > 0.20 – representation may be random!

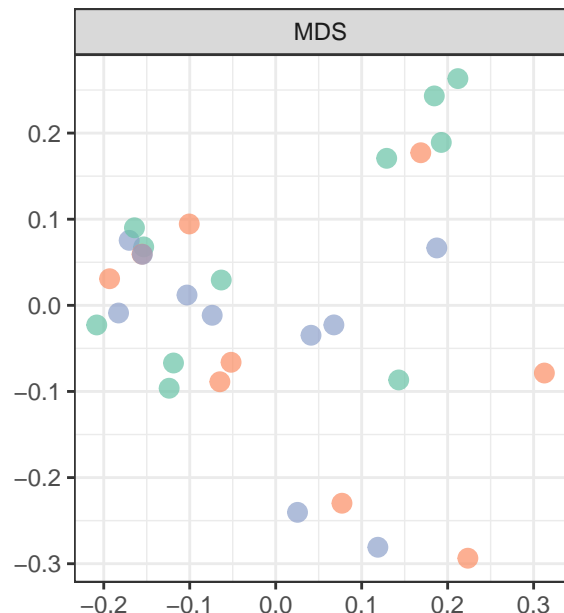
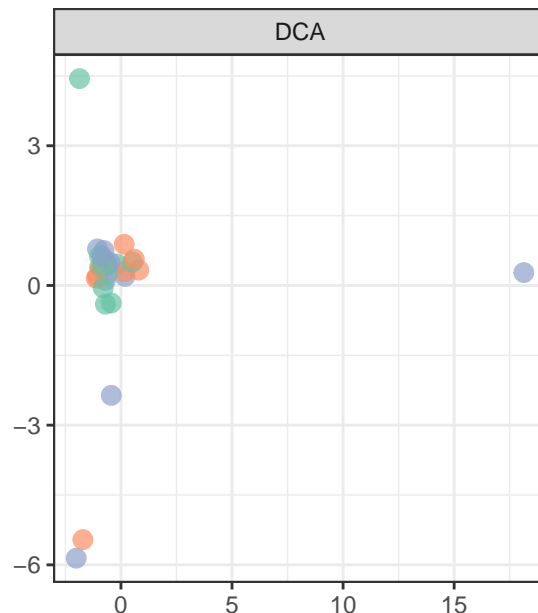
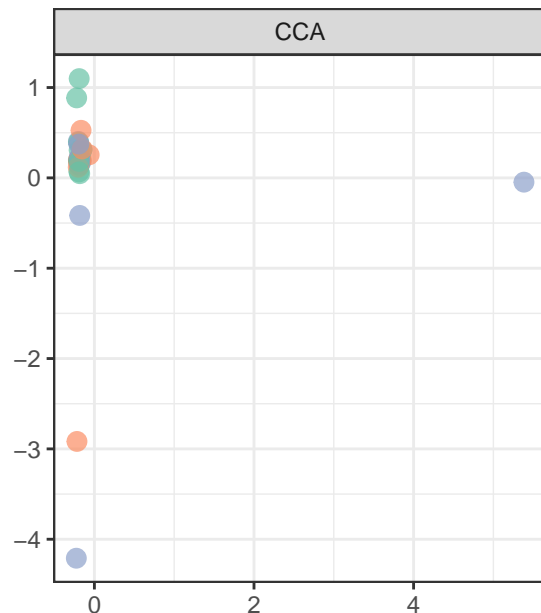
# NDMS on unifrac



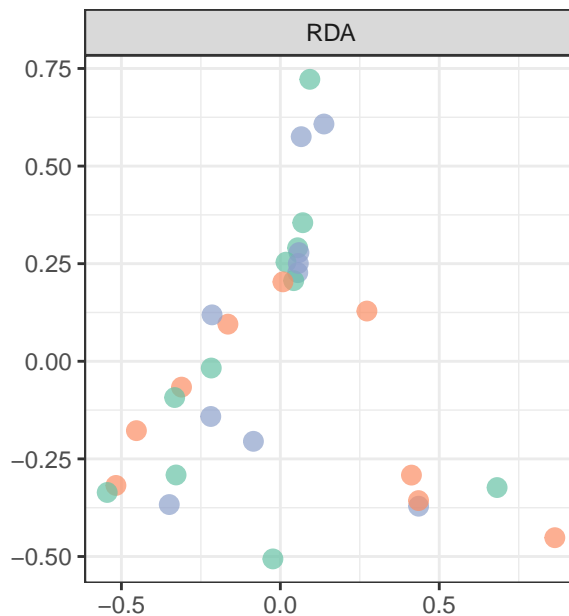
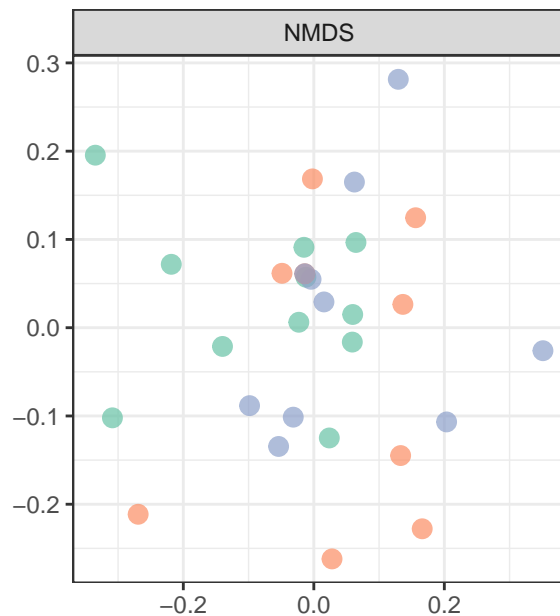
WARNING: stress 0.2025 is > 0.20 – representation may be random!

# unifrac

Axis\_2



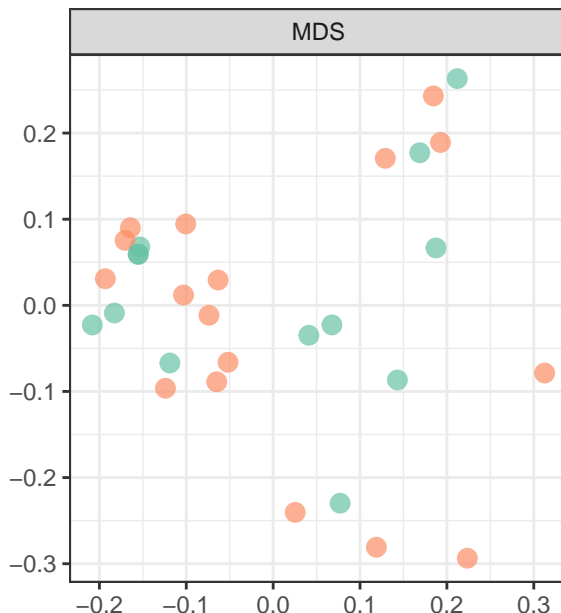
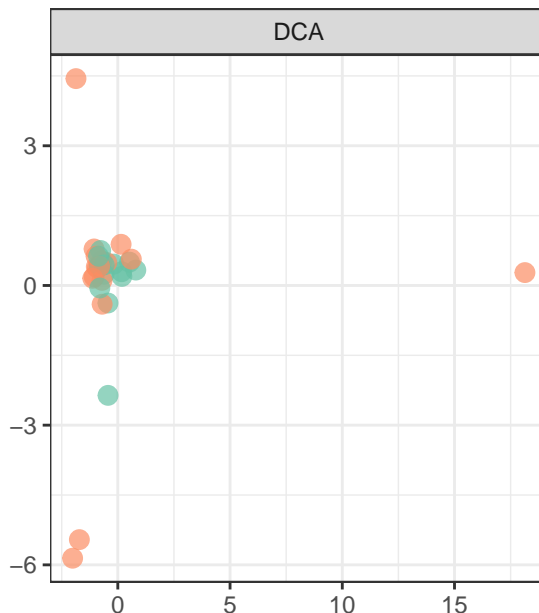
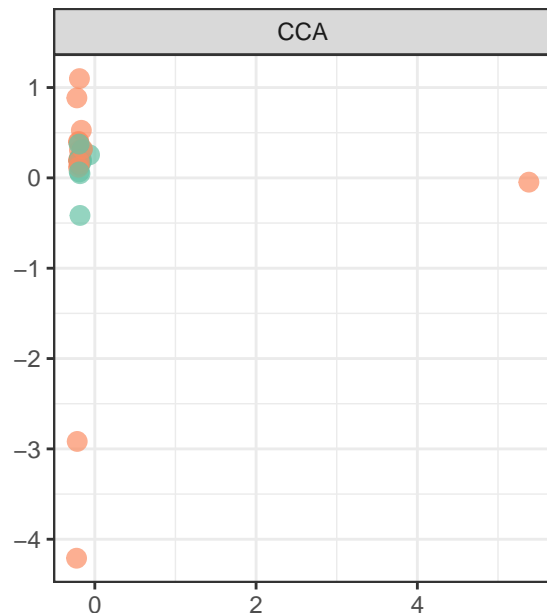
Months



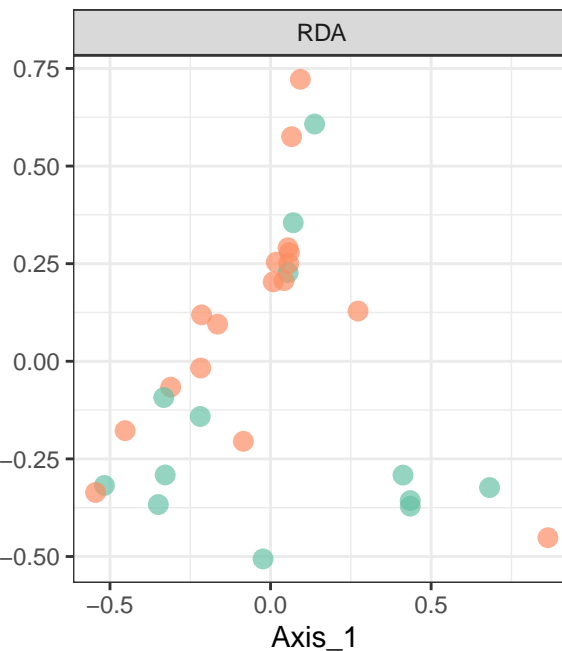
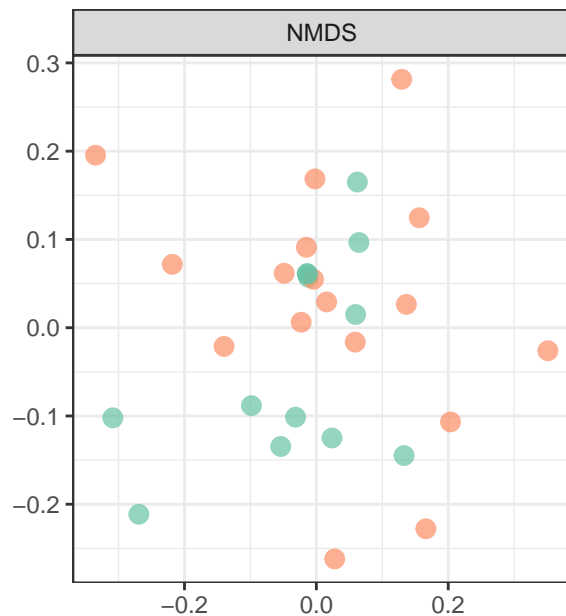
Axis\_1

# unifrac

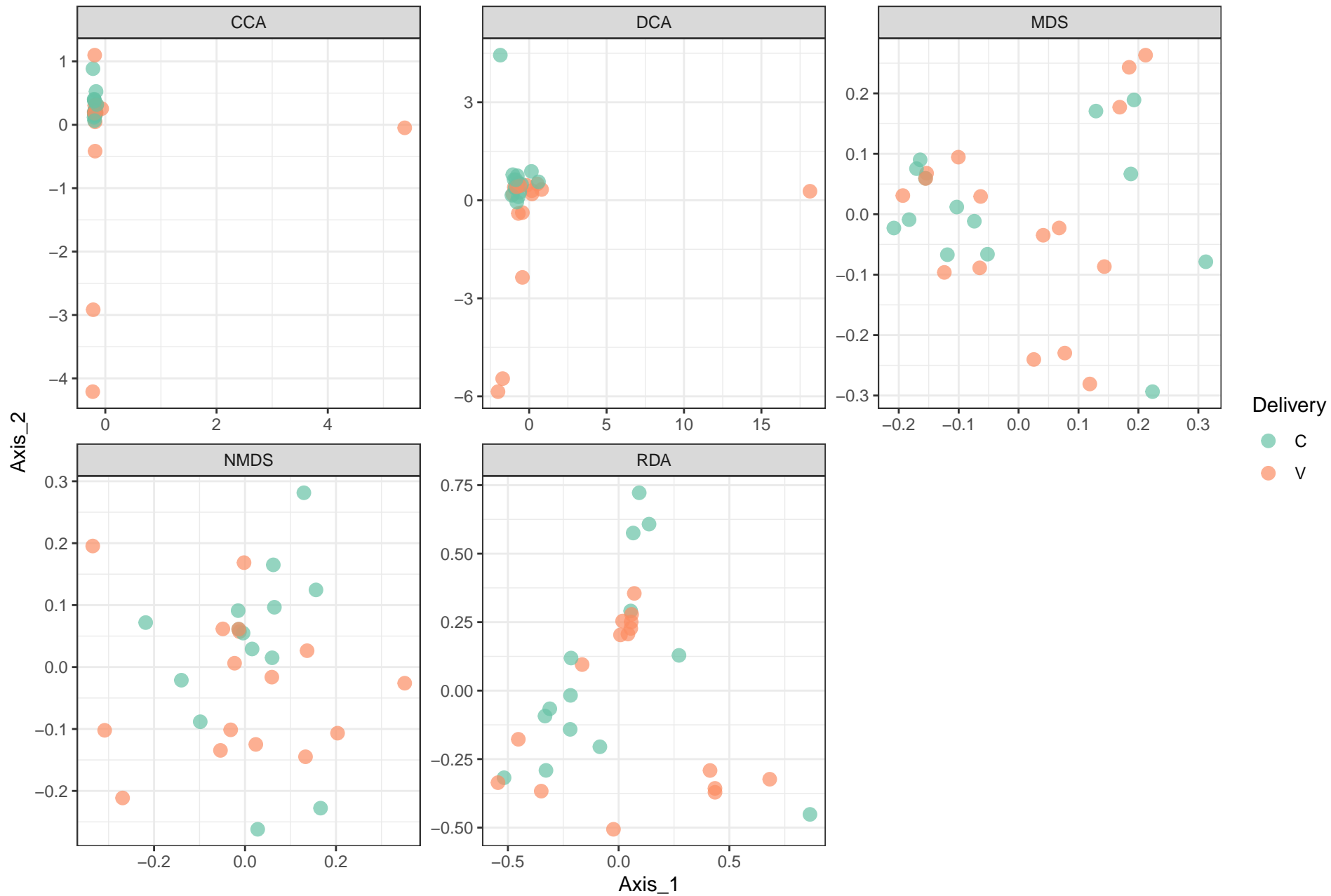
Axis\_2



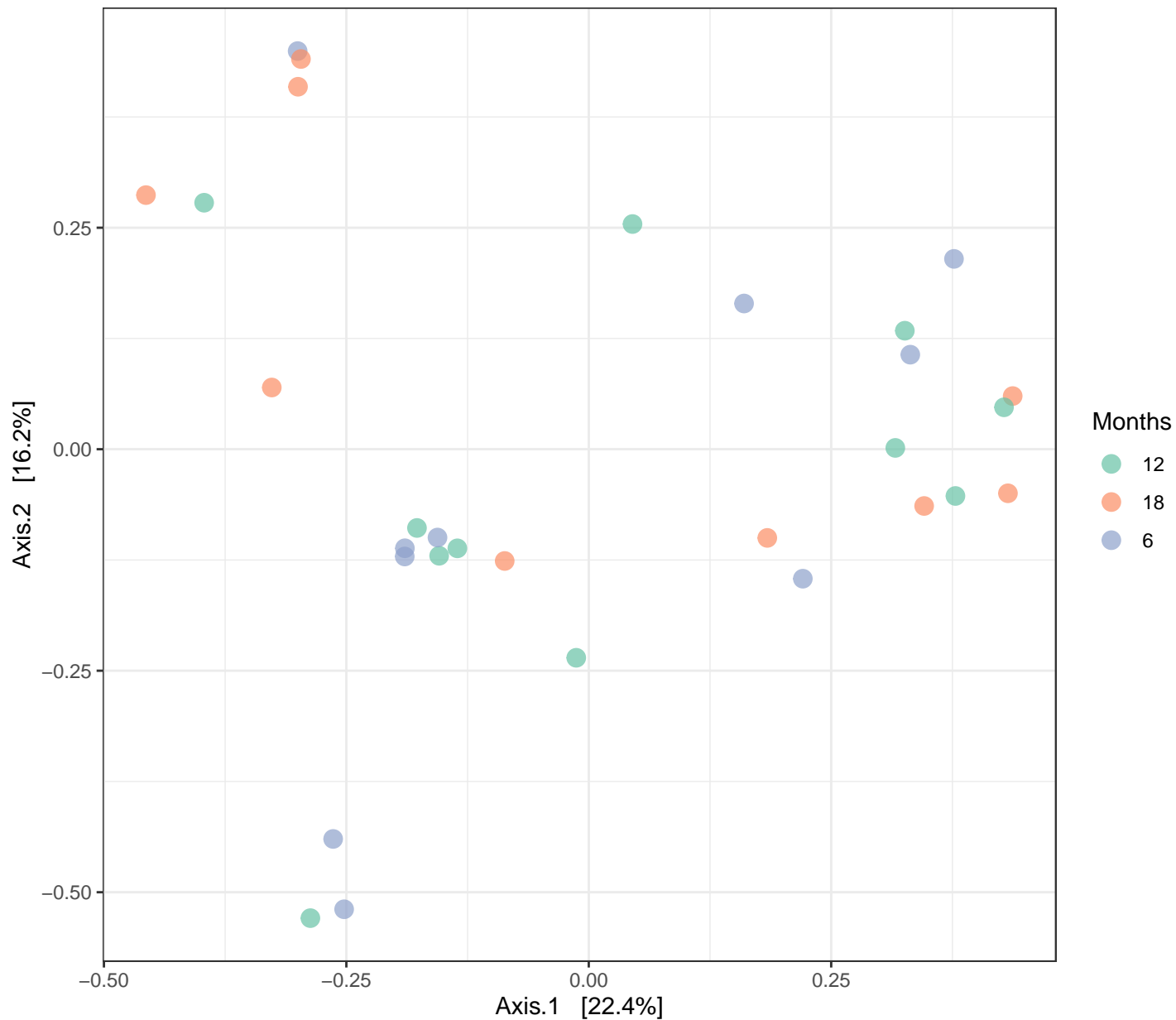
Sex  
F  
M



# unifrac

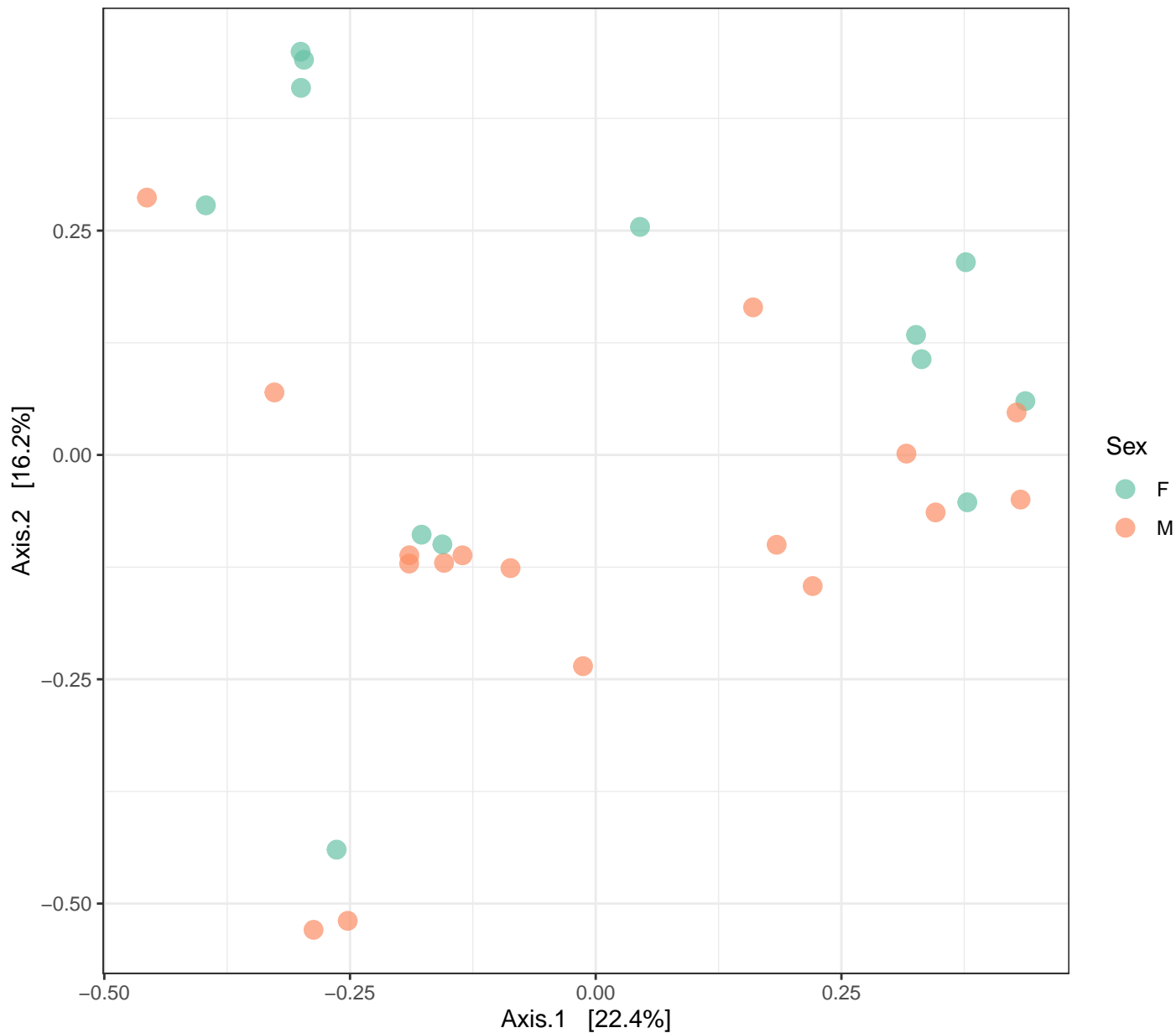


MDS using distance method bray

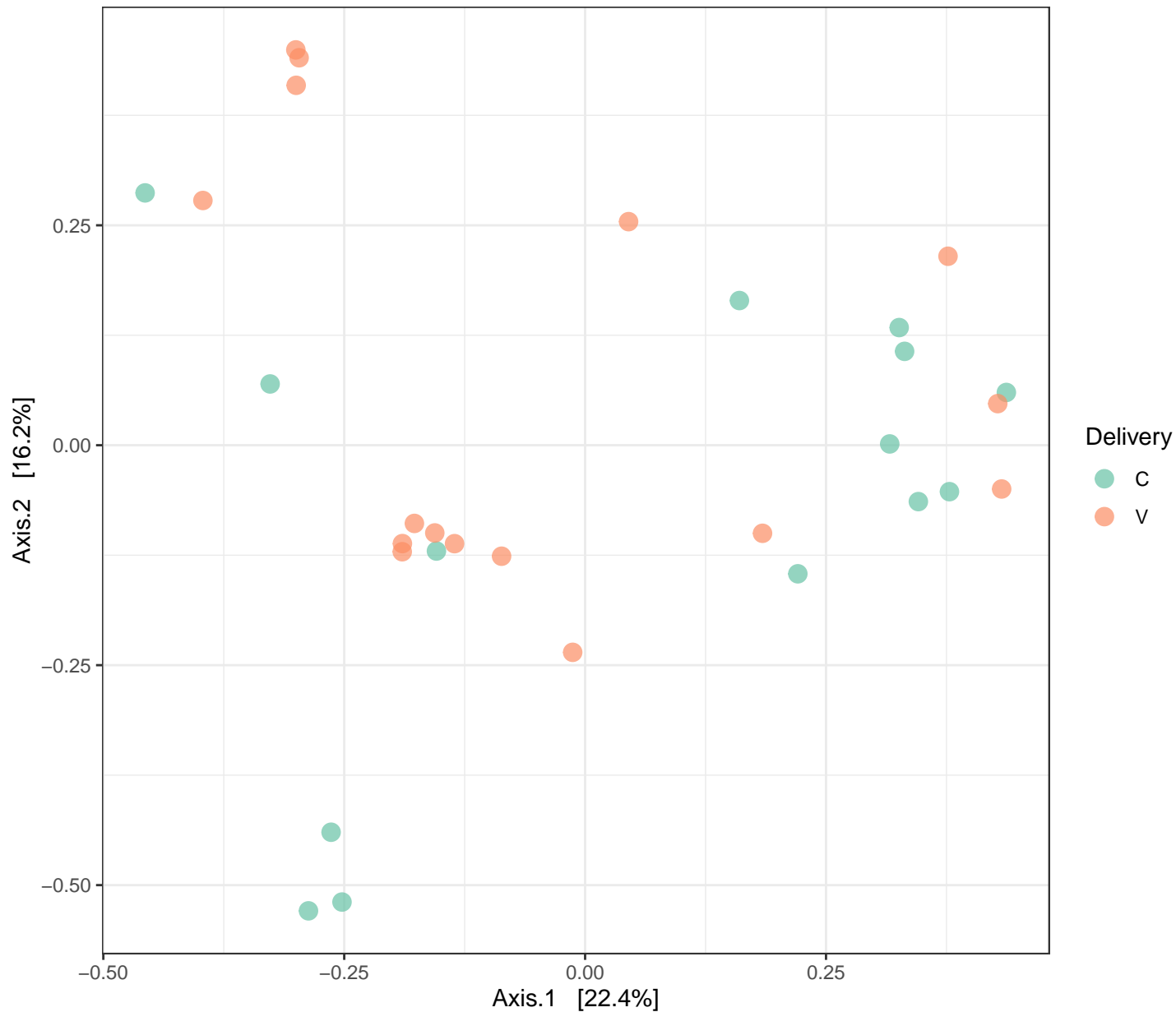




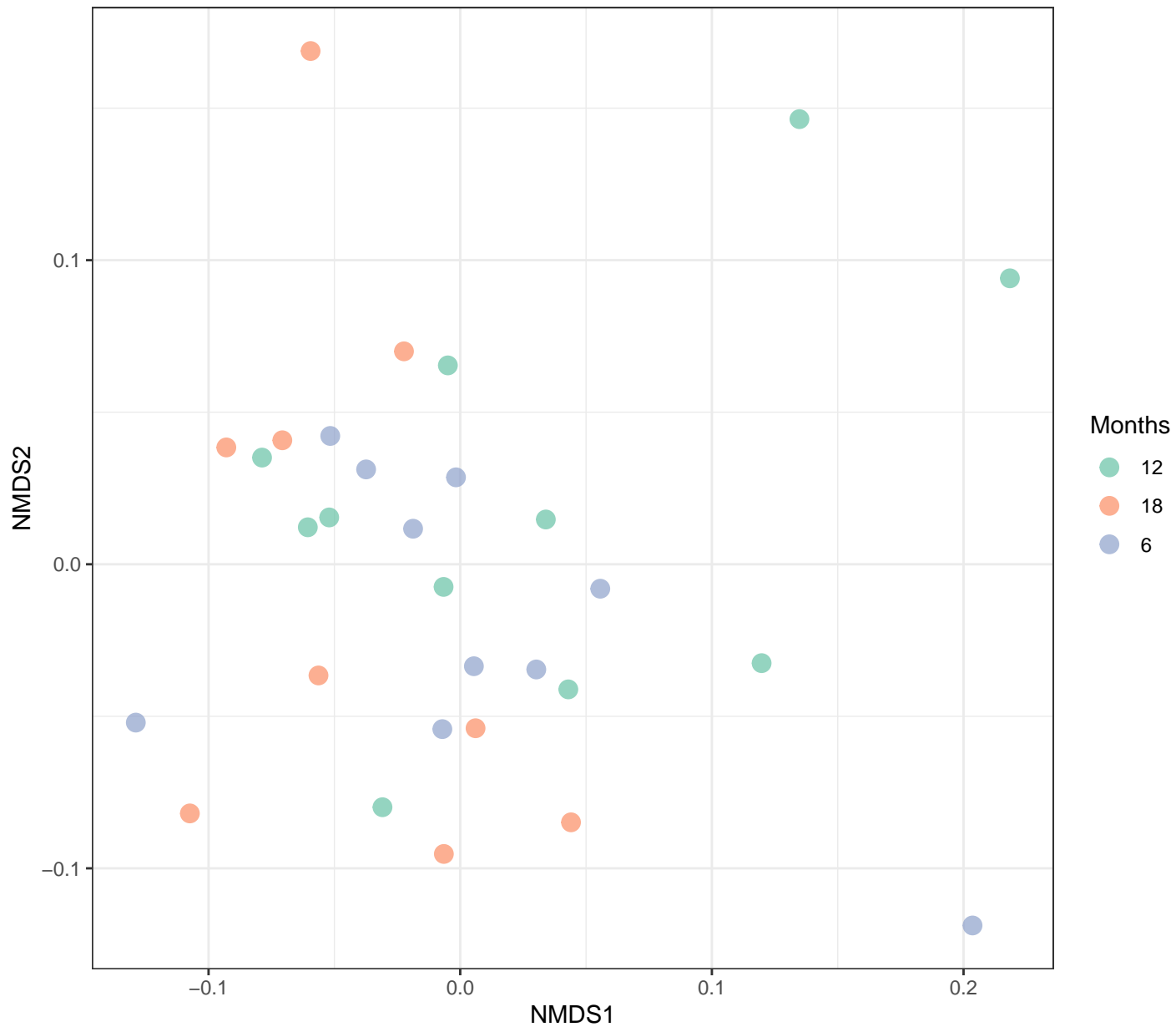
MDS using distance method bray



MDS using distance method bray

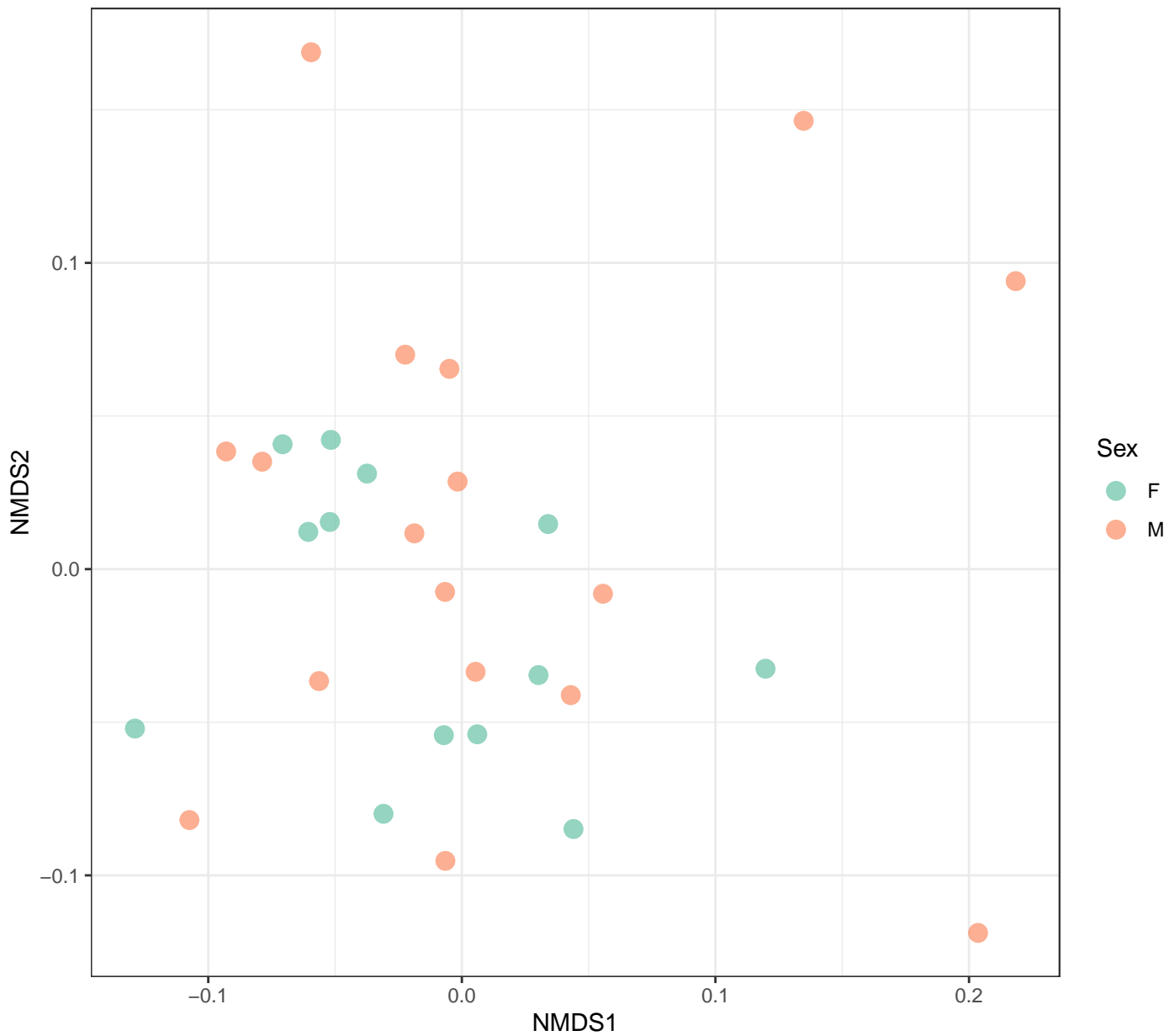


# NDMS on wunifrac



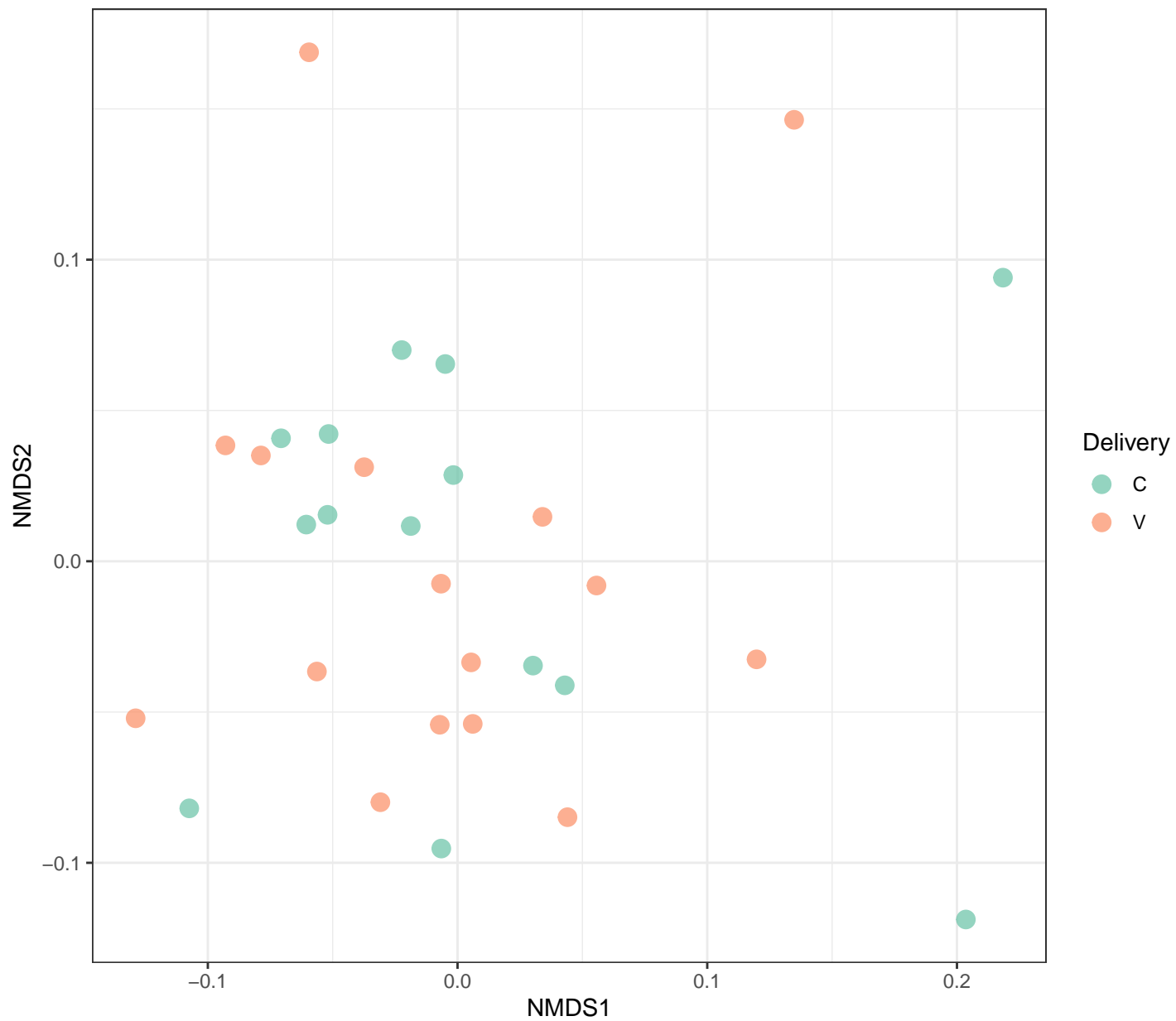
Stress 0.143

# NDMS on wunifrac



Stress 0.143

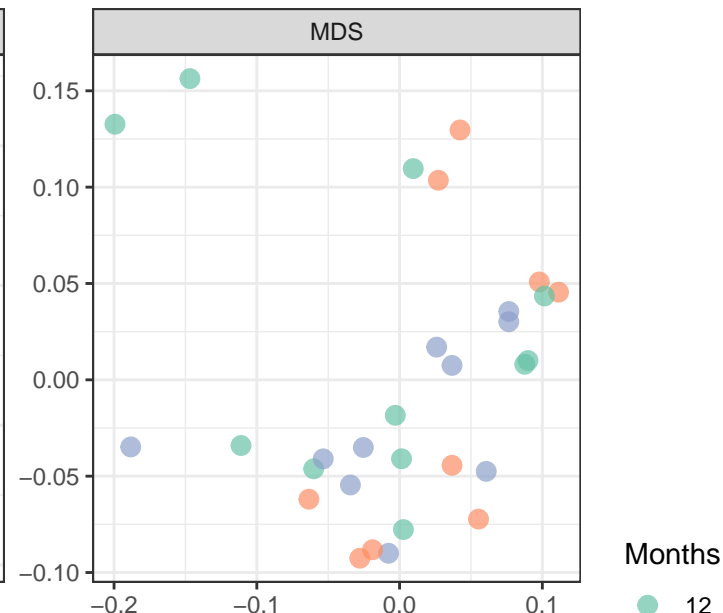
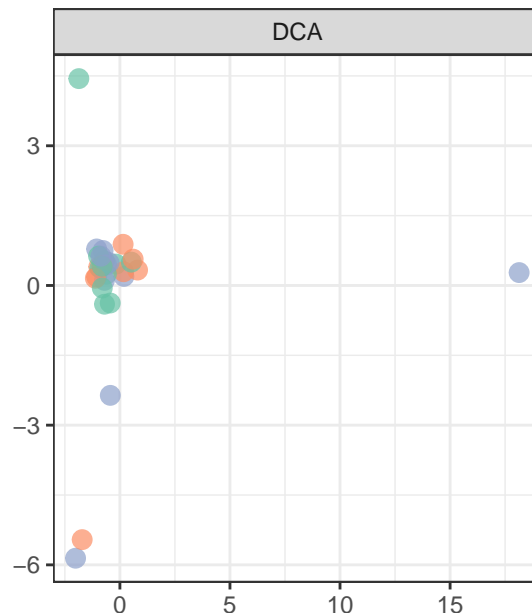
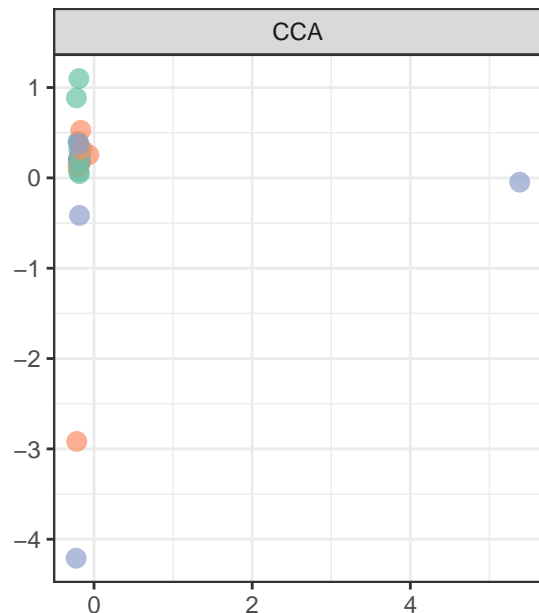
NDMS on wunifrac



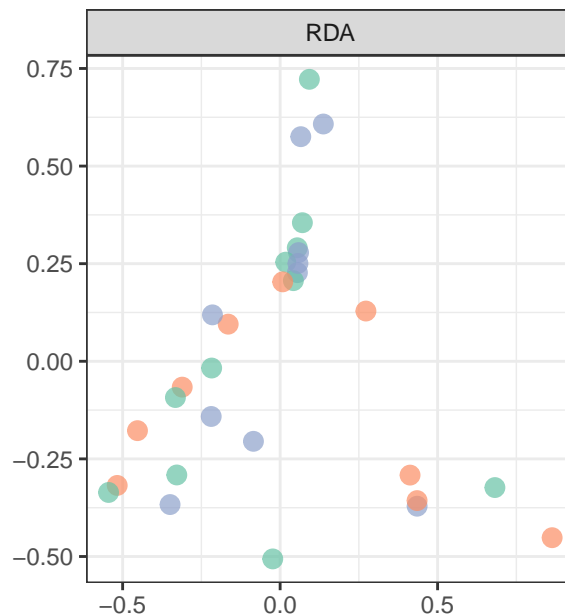
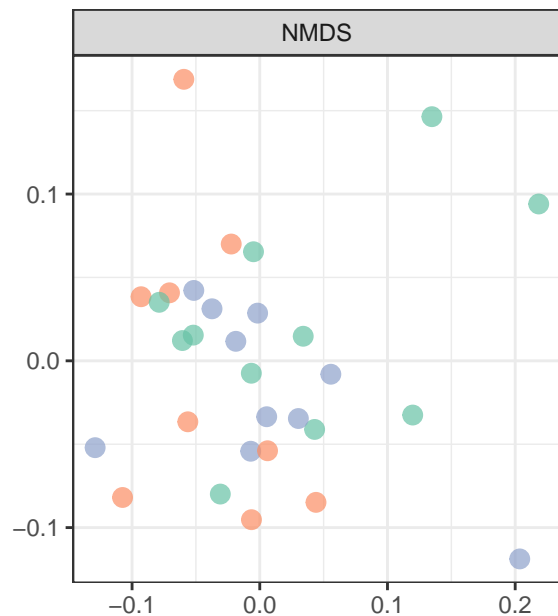
Stress 0.143

# wunifrac

Axis\_2



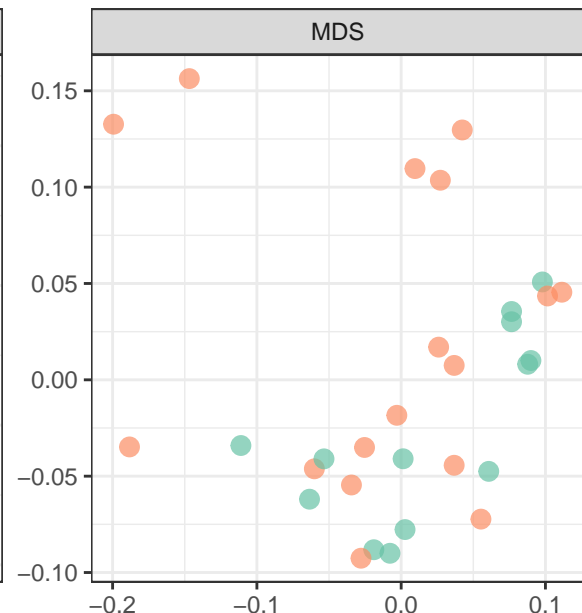
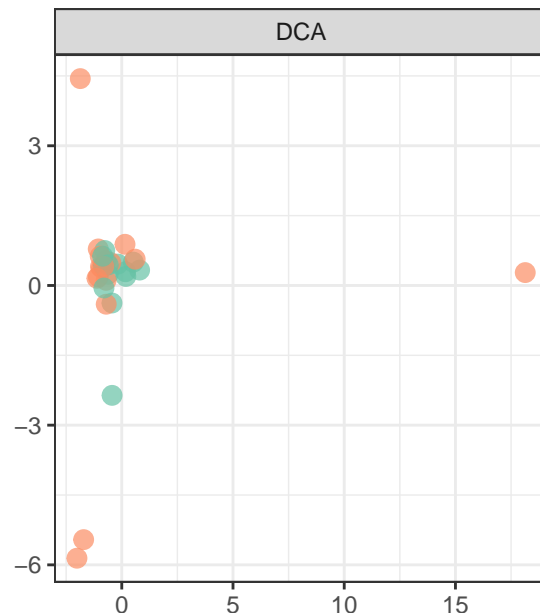
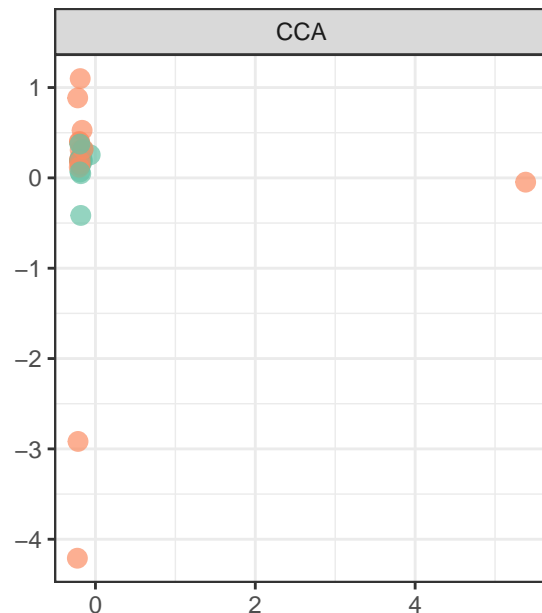
Months



Axis\_1

wunifrac

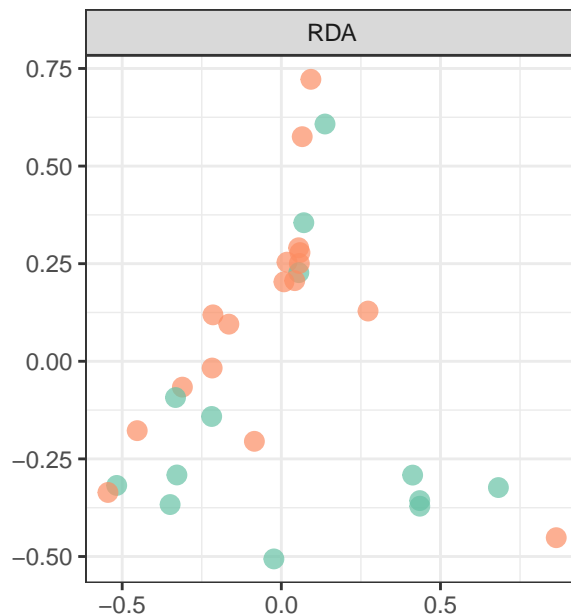
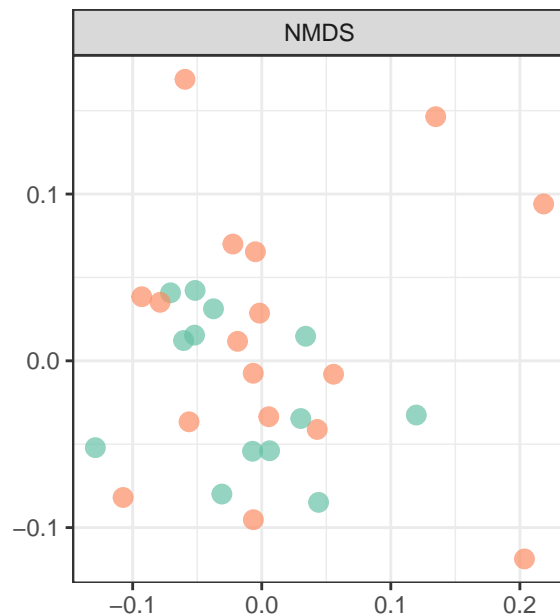
Axis\_2



Sex

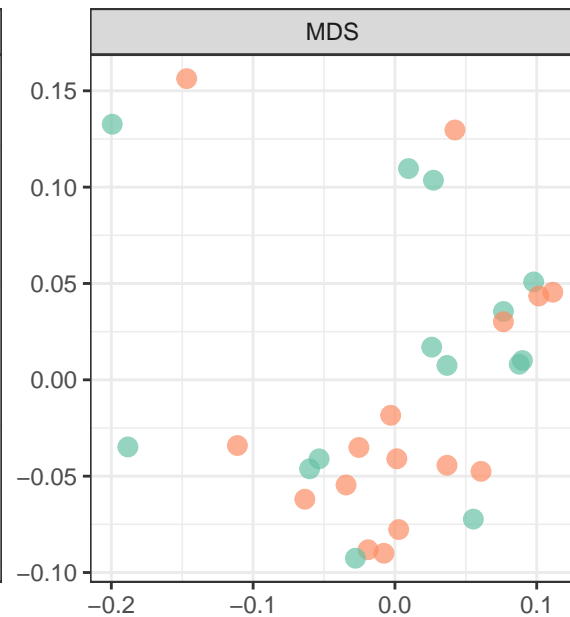
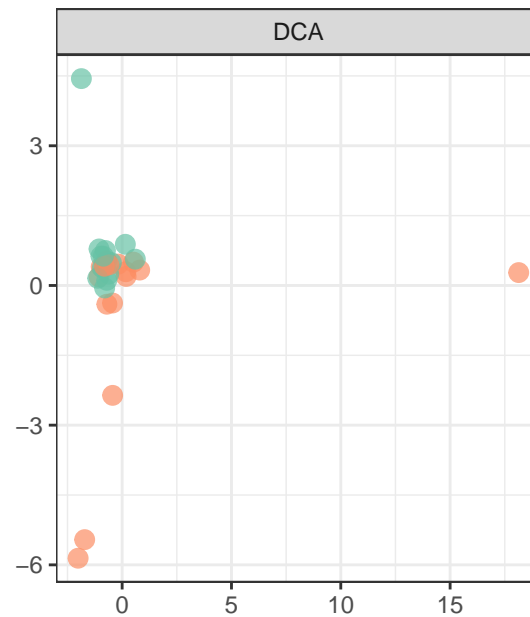
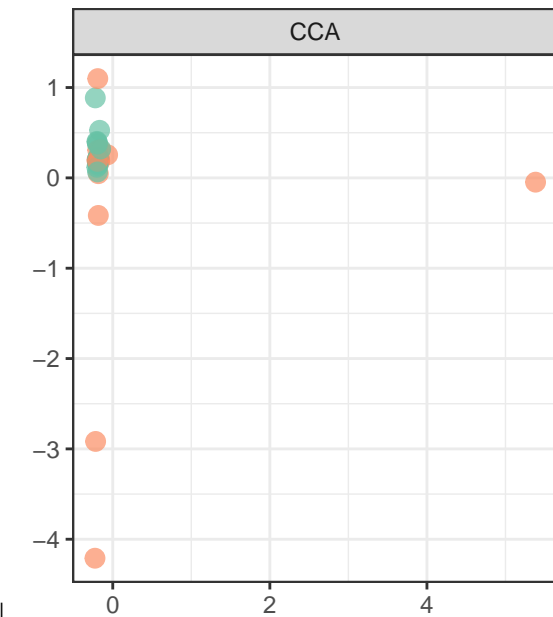
F

M



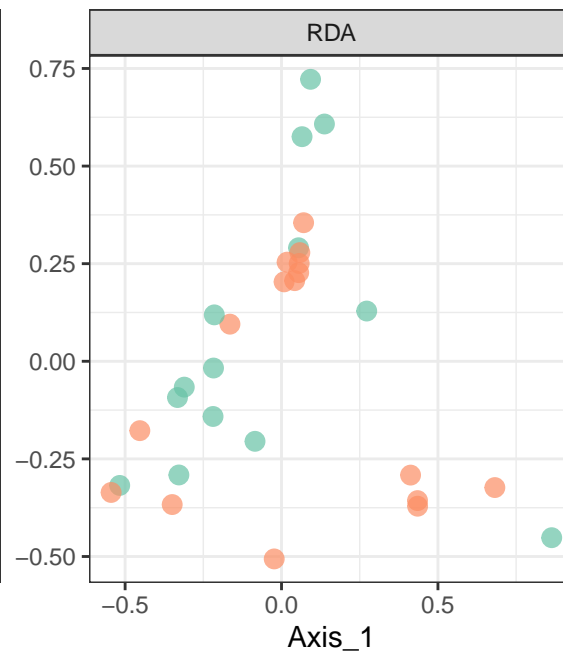
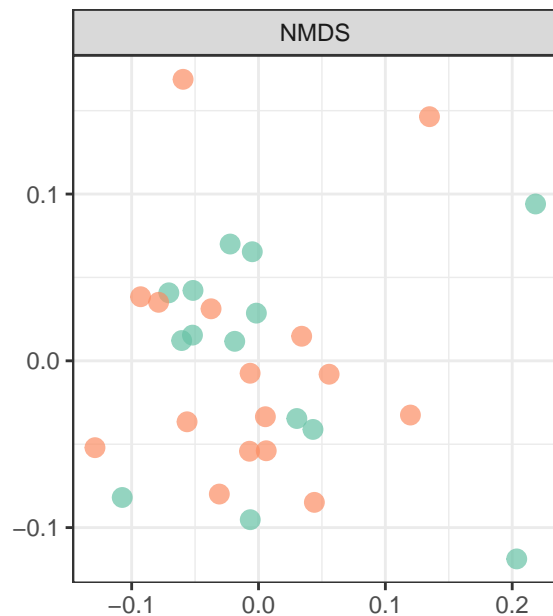
# wunifrac

Axis\_2



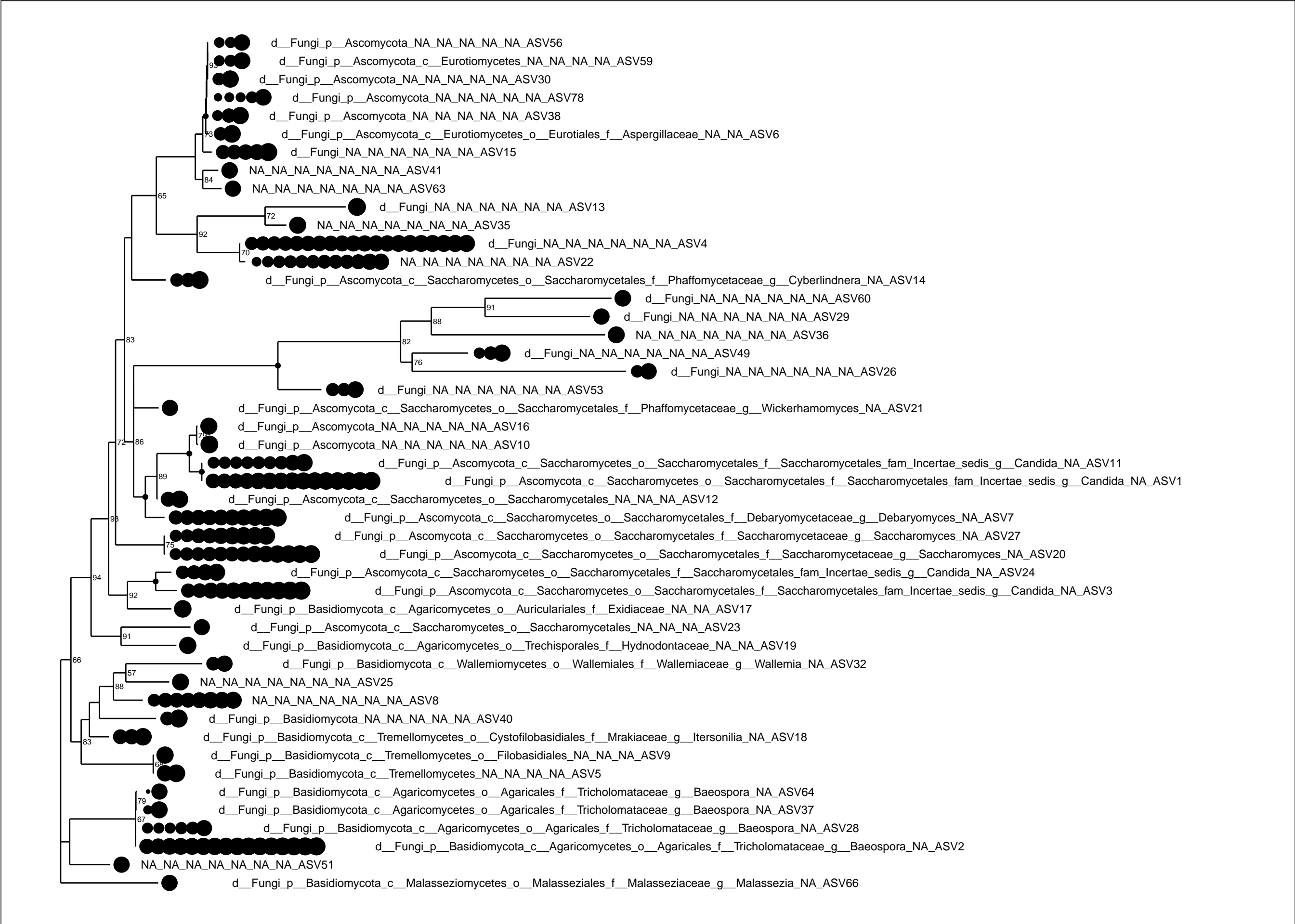
Delivery

- C
- V

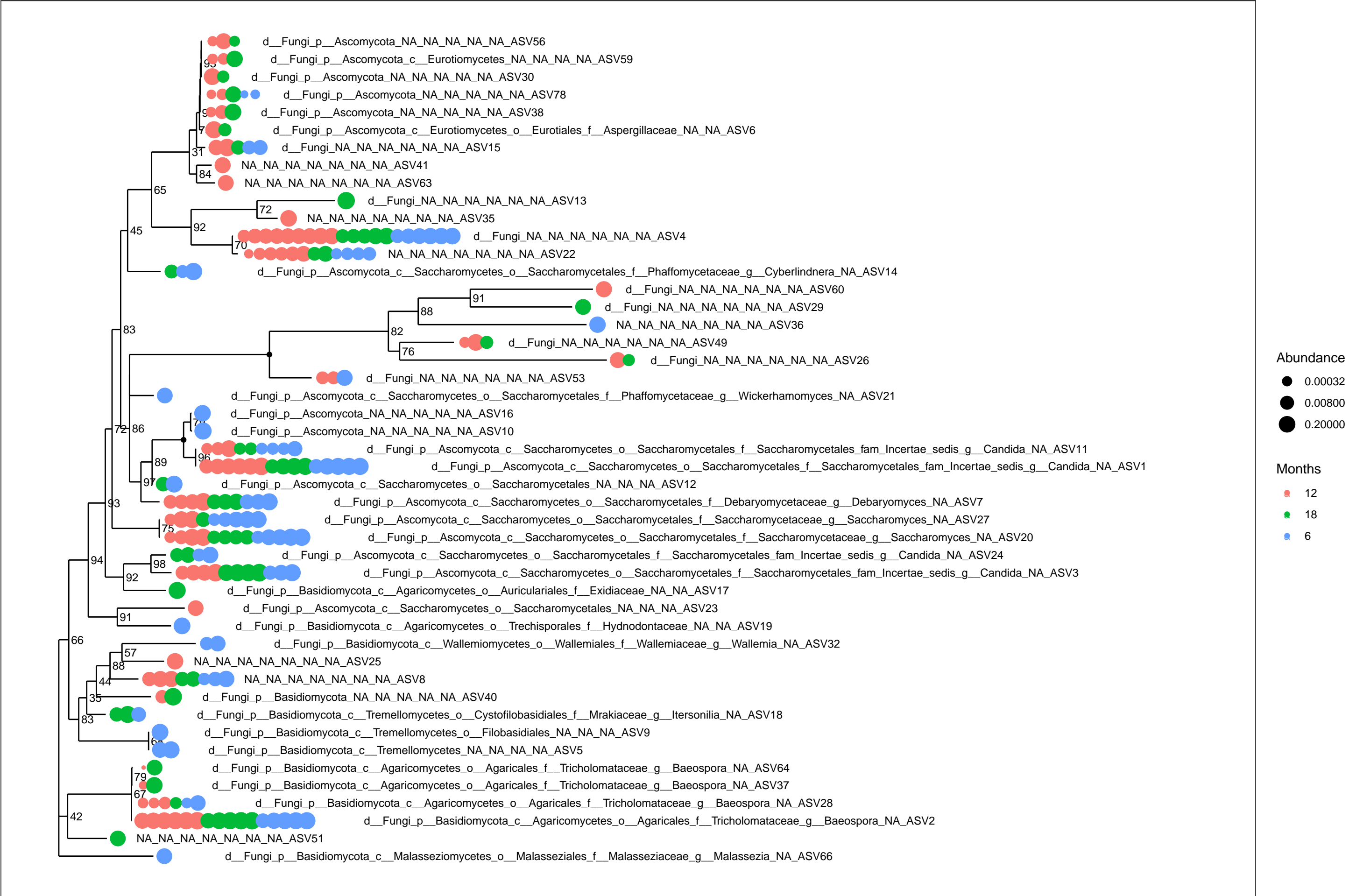




Full tree



Full tree with colored according to variable



A detailed phylogenetic tree showing the relationships between various Ascomycota and Basidiomycota lineages. The tree is rooted on the left and branches out to the right. Each terminal node is labeled with a specific ASV (Assembled Sequence Variant) and its corresponding taxonomic classification. The labels are color-coded: red for Ascomycota and blue for Basidiomycota. Support values (bootstrap percentages) are provided at the nodes. The tree is divided into two main sections: the top section for Ascomycota and the bottom section for Basidiomycota. The Ascomycota section includes lineages such as d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_NA\_ASV56, d\_Fungi\_p\_Ascomycota\_c\_Eurotiomycetes\_NA\_NA\_NA\_NA\_NA\_ASV59, and d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Phaffomycetaceae\_g\_Cyberlindnera\_NA\_ASV14. The Basidiomycota section includes lineages such as d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Auriculariales\_f\_Exidiaceae\_NA\_NA\_ASV17, d\_Fungi\_p\_Basidiomycota\_c\_Tremellomycetes\_o\_Filobasidiales\_NA\_NA\_NA\_ASV9, and d\_Fungi\_p\_Basidiomycota\_c\_Malasseziomycetes\_o\_Malasseziales\_f\_Malasseziaceae\_g\_Malassezia\_NA\_ASV66.

Phylogenetic tree showing relationships between various Ascomycota and Basidiomycota lineages, with support values indicated at the nodes. The tree is rooted on the left and branches out to the right. The labels represent different ASVs (Assembled Sequence Variants) and their corresponding taxonomic classifications. The tree is divided into two main sections: the top section for Ascomycota and the bottom section for Basidiomycota.

**Ascomycota Lineages (Top Section):**

- d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_NA\_ASV56
- d\_Fungi\_p\_Ascomycota\_c\_Eurotiomycetes\_NA\_NA\_NA\_NA\_NA\_ASV59
- d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_NA\_ASV30
- d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_NA\_ASV78
- d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_NA\_ASV38
- d\_Fungi\_p\_Ascomycota\_c\_Eurotiomycetes\_o\_Eurotiales\_f\_Aspergillaceae\_NA\_NA\_ASV6
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV15
- NA\_NA\_NA\_NA\_NA\_NA\_ASV41
- NA\_NA\_NA\_NA\_NA\_NA\_ASV63
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV13
- NA\_NA\_NA\_NA\_NA\_NA\_ASV35
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV4
- NA\_NA\_NA\_NA\_NA\_NA\_ASV22
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Phaffomycetaceae\_g\_Cyberlindnera\_NA\_ASV14
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV60
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV29
- NA\_NA\_NA\_NA\_NA\_NA\_ASV36
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV49
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV26
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV53
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Phaffomycetaceae\_g\_Wickerhamomyces\_NA\_ASV21
- d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_NA\_ASV16
- d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_NA\_ASV10
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Saccharomycetales\_fam\_Incertae\_sedis\_g\_Candida\_NA\_ASV11
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Saccharomycetales\_fam\_Incertae\_sedis\_g\_Candida\_NA\_ASV1
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_NA\_NA\_NA\_ASV12
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Debaryomycetaceae\_g\_Debaryomyces\_NA\_ASV7
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Saccharomycetaceae\_g\_Saccharomyces\_NA\_ASV27
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Saccharomycetaceae\_g\_Saccharomyces\_NA\_ASV20
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Saccharomycetales\_fam\_Incertae\_sedis\_g\_Candida\_NA\_ASV24
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Saccharomycetales\_fam\_Incertae\_sedis\_g\_Candida\_NA\_ASV3
- d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Auriculariales\_f\_Exidiaceae\_NA\_NA\_ASV17
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_NA\_NA\_NA\_ASV23
- d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Trechisporales\_f\_Hydnotontaceae\_NA\_NA\_ASV19
- d\_Fungi\_p\_Basidiomycota\_c\_Walleimomycetes\_o\_Walleimiales\_f\_Walleimiaceae\_g\_Walleimia\_NA\_ASV32
- NA\_NA\_NA\_NA\_NA\_NA\_ASV25
- NA\_NA\_NA\_NA\_NA\_NA\_ASV8
- d\_Fungi\_p\_Basidiomycota\_NA\_NA\_NA\_NA\_NA\_NA\_ASV40
- d\_Fungi\_p\_Basidiomycota\_c\_Tremellomycetes\_o\_Cystofilobasidiales\_f\_Mrakiaceae\_g\_Itersonilia\_NA\_ASV18
- d\_Fungi\_p\_Basidiomycota\_c\_Tremellomycetes\_o\_Filobasidiales\_NA\_NA\_NA\_ASV9
- d\_Fungi\_p\_Basidiomycota\_c\_Tremellomycetes\_NA\_NA\_NA\_NA\_ASV5
- d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Agaricales\_f\_Tricholomataceae\_g\_Baeospora\_NA\_ASV64
- d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Agaricales\_f\_Tricholomataceae\_g\_Baeospora\_NA\_ASV37
- d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Agaricales\_f\_Tricholomataceae\_g\_Baeospora\_NA\_ASV28
- d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Agaricales\_f\_Tricholomataceae\_g\_Baeospora\_NA\_ASV2
- NA\_NA\_NA\_NA\_NA\_NA\_ASV51
- d\_Fungi\_p\_Basidiomycota\_c\_Malasseziomycetes\_o\_Malasseziales\_f\_Malasseziaceae\_g\_Malassezia\_NA\_ASV66

A phylogenetic tree illustrating the evolutionary relationships among various fungal taxa, primarily focusing on Ascomycota and Basidiomycota. The tree is rooted on the left and branches out to the right. Bootstrap values are provided at many of the internal nodes, indicating the confidence in the branching order. Taxa names are listed to the right of the branches, often followed by a unique identifier (e.g., ASV56, ASV59). Colored circles (red and blue) are placed along the branches and next to some taxon names, likely representing different phenotypic or genetic traits associated with those groups.

**Taxa and Identifiers:**

- d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_ASV56
- d\_Fungi\_p\_Ascomycota\_c\_Eurotiomycetes\_NA\_NA\_NA\_NA\_ASV59
- d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_ASV30
- d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_ASV78
- d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_ASV38
- d\_Fungi\_p\_Ascomycota\_c\_Eurotiomycetes\_o\_Eurotiales\_f\_Aspergillaceae\_NA\_NA\_ASV6
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV15
- NA\_NA\_NA\_NA\_NA\_NA\_NA\_ASV41
- NA\_NA\_NA\_NA\_NA\_NA\_NA\_ASV63
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV13
- NA\_NA\_NA\_NA\_NA\_NA\_NA\_ASV35
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV4
- NA\_NA\_NA\_NA\_NA\_NA\_NA\_ASV22
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Phaffomycetaceae\_g\_Cyberlindnera\_NA\_ASV14
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV60
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV29
- NA\_NA\_NA\_NA\_NA\_NA\_NA\_ASV36
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV49
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV26
- d\_Fungi\_NA\_NA\_NA\_NA\_NA\_NA\_ASV53
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Phaffomycetaceae\_g\_Wickerhamomyces\_NA\_ASV21
- d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_ASV16
- d\_Fungi\_p\_Ascomycota\_NA\_NA\_NA\_NA\_NA\_ASV10
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Saccharomycetales\_fam\_Incertae\_sedis\_g\_Candida\_NA\_ASV11
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Saccharomycetales\_fam\_Incertae\_sedis\_g\_Candida\_NA\_ASV1
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_NA\_NA\_NA\_ASV12
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Deбaryomycetaceae\_g\_Deбaryomyces\_NA\_ASV7
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Saccharomycetaceae\_g\_Saccharomyces\_NA\_ASV27
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Saccharomycetaceae\_g\_Saccharomyces\_NA\_ASV20
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Saccharomycetales\_fam\_Incertae\_sedis\_g\_Candida\_NA\_ASV24
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_f\_Saccharomycetales\_fam\_Incertae\_sedis\_g\_Candida\_NA\_ASV3
- d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Auriculariales\_f\_Exidiaceae\_NA\_NA\_ASV17
- d\_Fungi\_p\_Ascomycota\_c\_Saccharomycetes\_o\_Saccharomycetales\_NA\_NA\_NA\_ASV23
- d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Trechisporales\_f\_Hydnotontaceae\_NA\_NA\_ASV19
- d\_Fungi\_p\_Basidiomycota\_c\_Walleimomycetes\_o\_Walleimiaes\_f\_Walleimiaceae\_g\_Walleimia\_NA\_ASV32
- NA\_NA\_NA\_NA\_NA\_NA\_NA\_ASV25
- NA\_NA\_NA\_NA\_NA\_NA\_NA\_ASV8
- d\_Fungi\_p\_Basidiomycota\_NA\_NA\_NA\_NA\_NA\_ASV40
- d\_Fungi\_p\_Basidiomycota\_c\_Tremellomycetes\_o\_Cystofilobasidiales\_f\_Mrakiaceae\_g\_Itersonilia\_NA\_ASV18
- d\_Fungi\_p\_Basidiomycota\_c\_Tremellomycetes\_o\_Filobasidiales\_NA\_NA\_NA\_ASV9
- d\_Fungi\_p\_Basidiomycota\_c\_Tremellomycetes\_NA\_NA\_NA\_NA\_ASV5
- d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Agaricales\_f\_Tricholomataceae\_g\_Baeospora\_NA\_ASV64
- d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Agaricales\_f\_Tricholomataceae\_g\_Baeospora\_NA\_ASV37
- d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Agaricales\_f\_Tricholomataceae\_g\_Baeospora\_NA\_ASV28
- d\_Fungi\_p\_Basidiomycota\_c\_Agaricomycetes\_o\_Agaricales\_f\_Tricholomataceae\_g\_Baeospora\_NA\_ASV2
- NA\_NA\_NA\_NA\_NA\_NA\_NA\_ASV51
- d\_Fungi\_p\_Basidiomycota\_c\_Malasseziomycetes\_o\_Malasseziales\_f\_Malasseziaceae\_g\_Malassezia\_NA\_ASV66