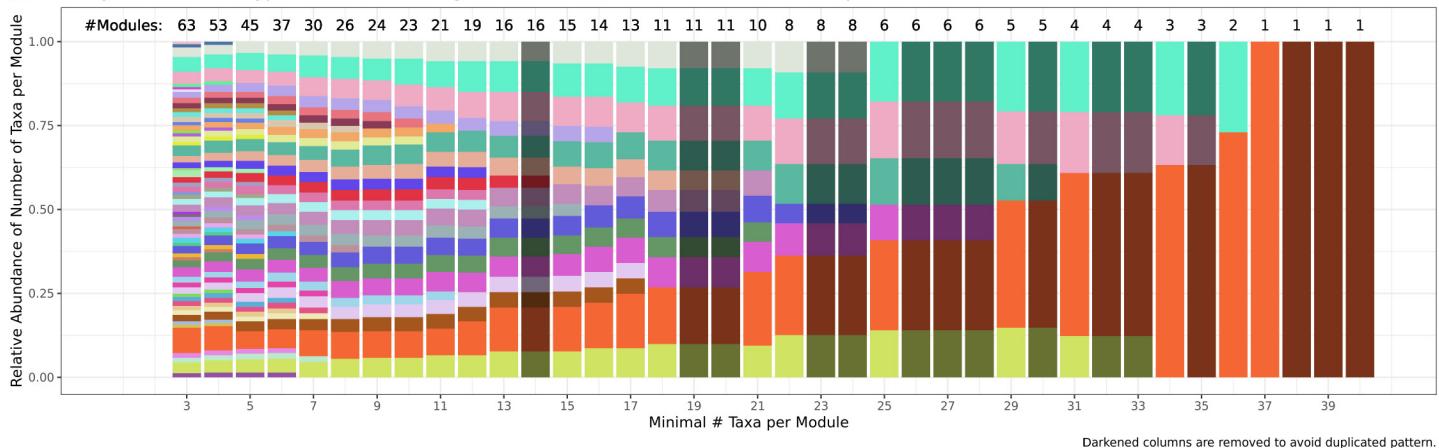
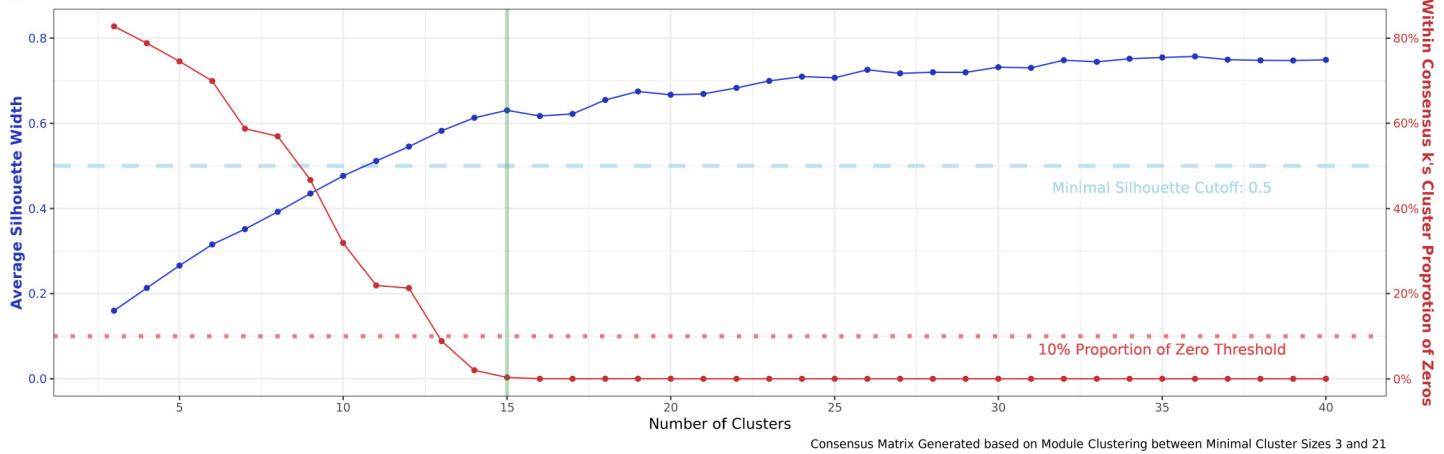


A Study: cancer; Phenotype: Cancer; Clustering Method: dada2; Maximum Minimal # Taxa per Module: 21



B Best Estimated Number of Clusters: 15

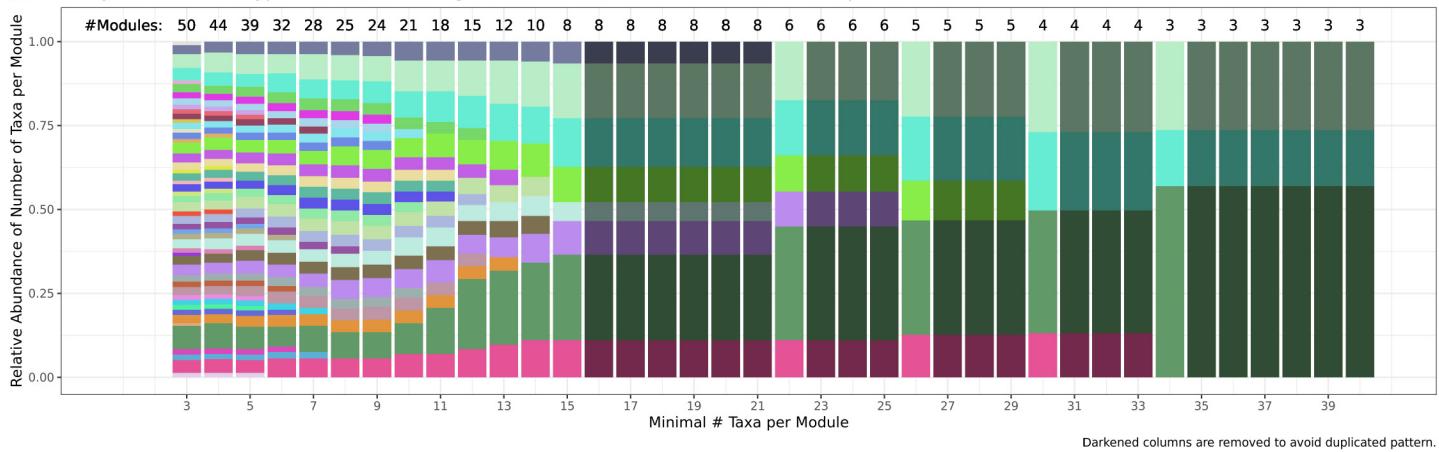


Supplementary Figure 12

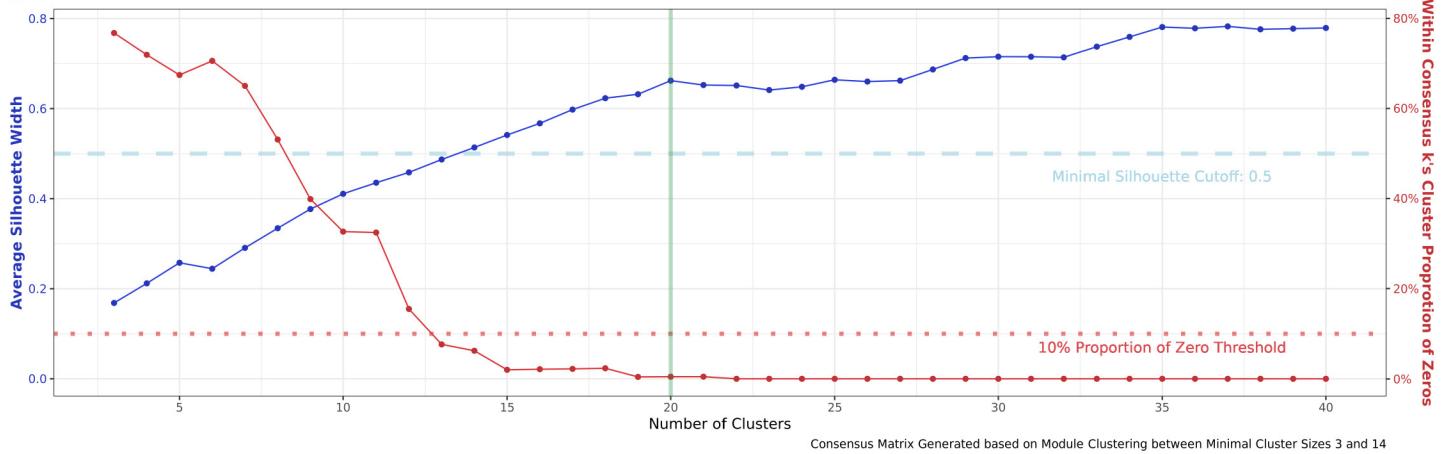
Baxter et al. Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Cancer

A. Module Patterns are generated based on different minimal module sizes. Darkened columns represent the replicated patterns. **B.** The average silhouette width was calculated for different numbers of clusters with the consensus matrix generated from patterns in A. The unique patterns including all the minimal number of taxa per module until the unique modules drop below 10.

A Study: cancer; Phenotype: Normal; Clustering Method: dada2; Maximum Minimal # Taxa per Module: 14



B Best Estimated Number of Clusters: 20

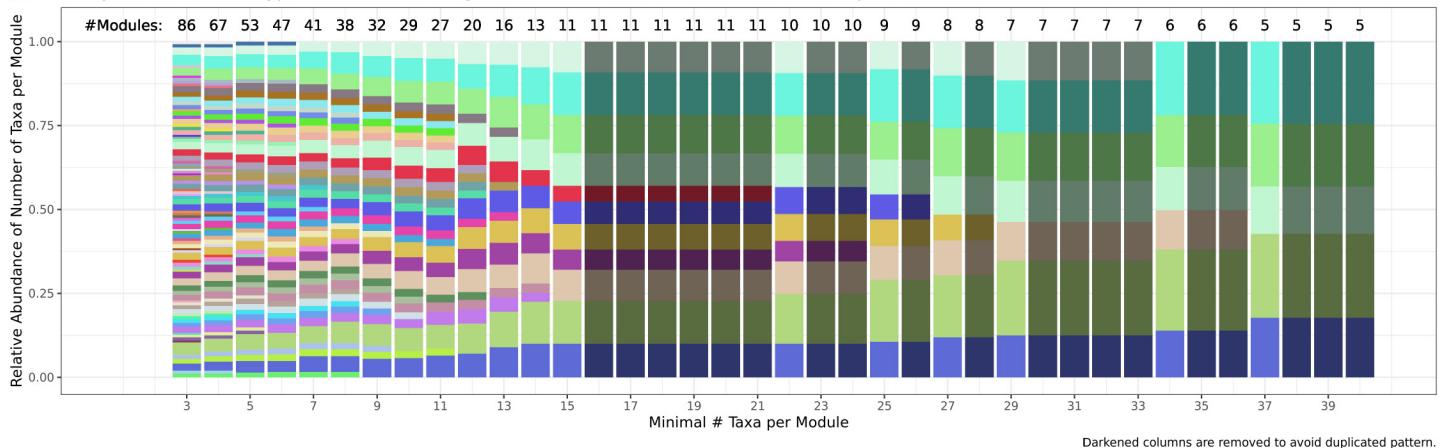


Supplementary Figure 13

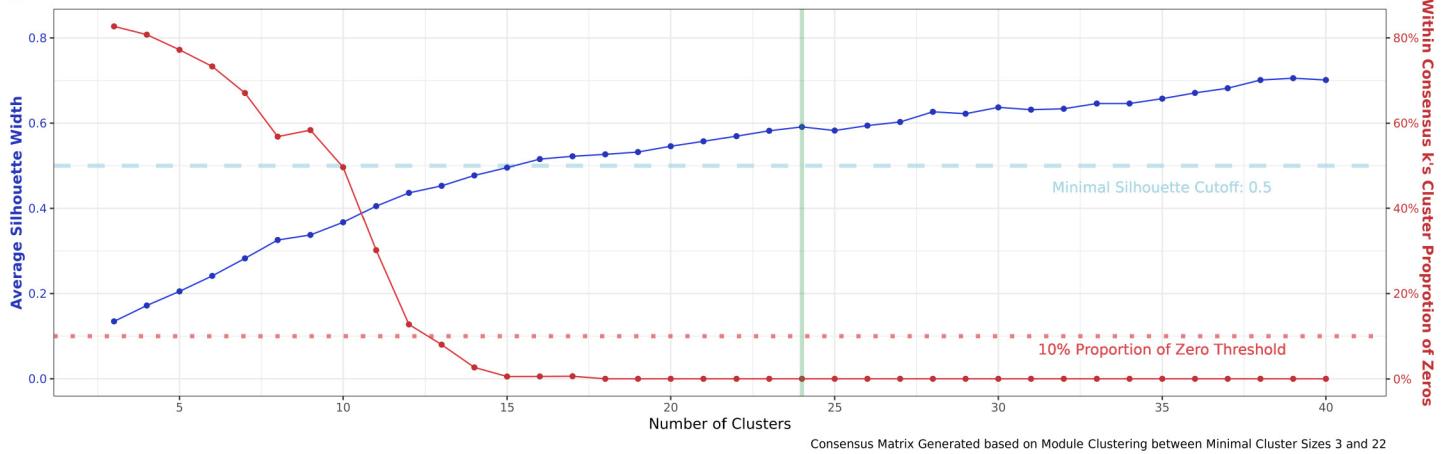
Baxter et al. Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Normal

A. Module Patterns are generated based on different minimal module sizes. Darkened columns represent the replicated patterns. **B.** The average silhouette width was calculated for different numbers of clusters with the consensus matrix generated from patterns in A. The unique patterns including all the minimal number of taxa per module until the unique modules drop below 10.

A Study: cancer2; Phenotype: Cancer; Clustering Method: dada2; Maximum Minimal # Taxa per Module: 22



B Best Estimated Number of Clusters: 24

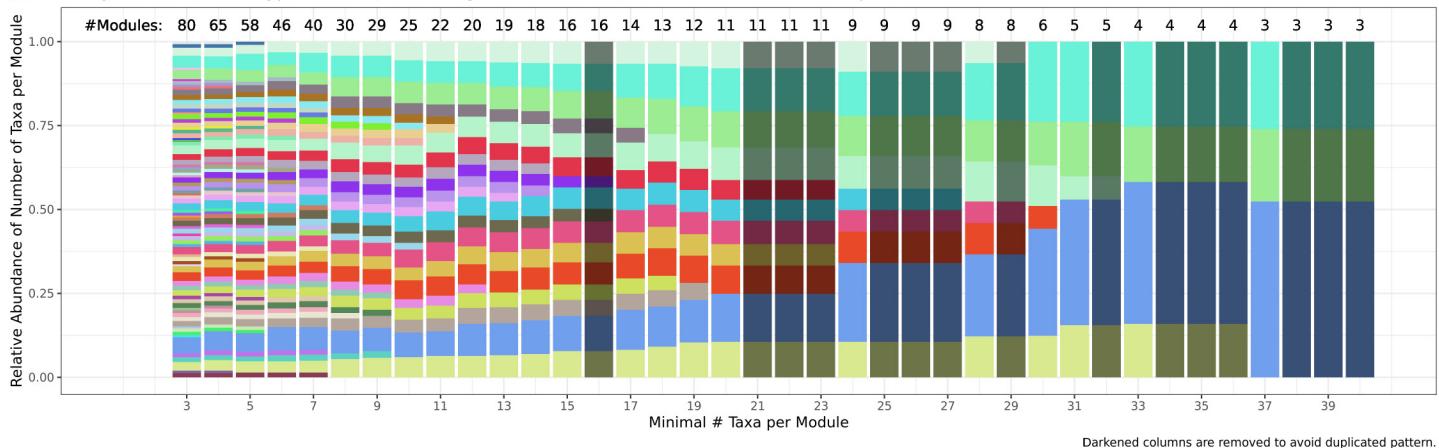


Supplementary Figure 14

Zeller et al. Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Cancer

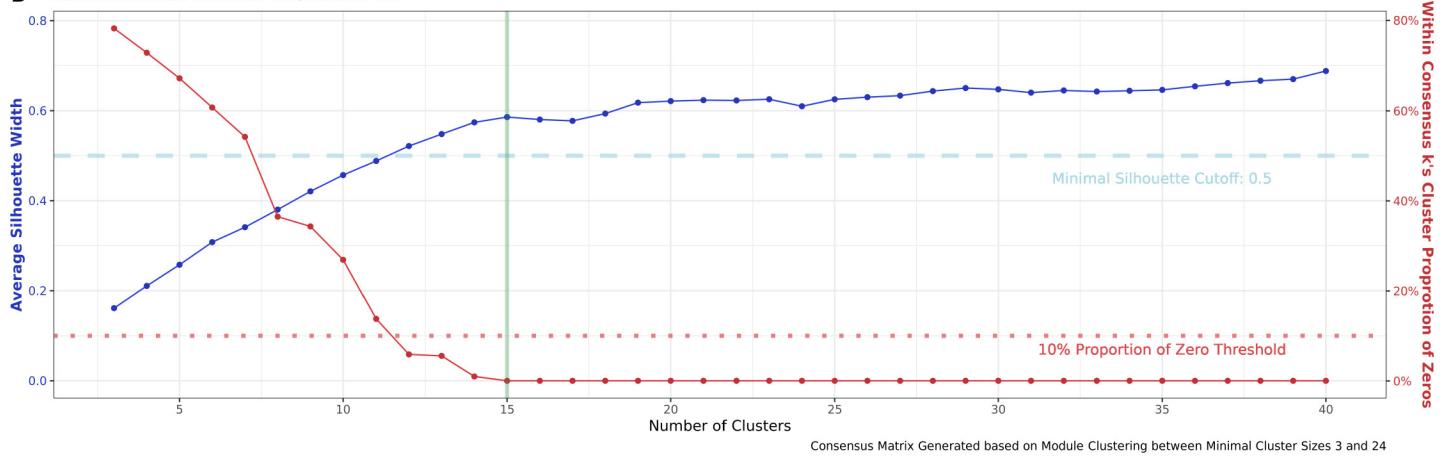
A. Module Patterns are generated based on different minimal module sizes. Darkened columns represent the replicated patterns. **B.** The average silhouette width was calculated for different numbers of clusters with the consensus matrix generated from patterns in A. The unique patterns including all the minimal number of taxa per module until the unique modules drop below 10.

A Study: cancer2; Phenotype: Normal; Clustering Method: dada2; Maximum Minimal # Taxa per Module: 24



Darkened columns are removed to avoid duplicated pattern.

B Best Estimated Number of Clusters: 15

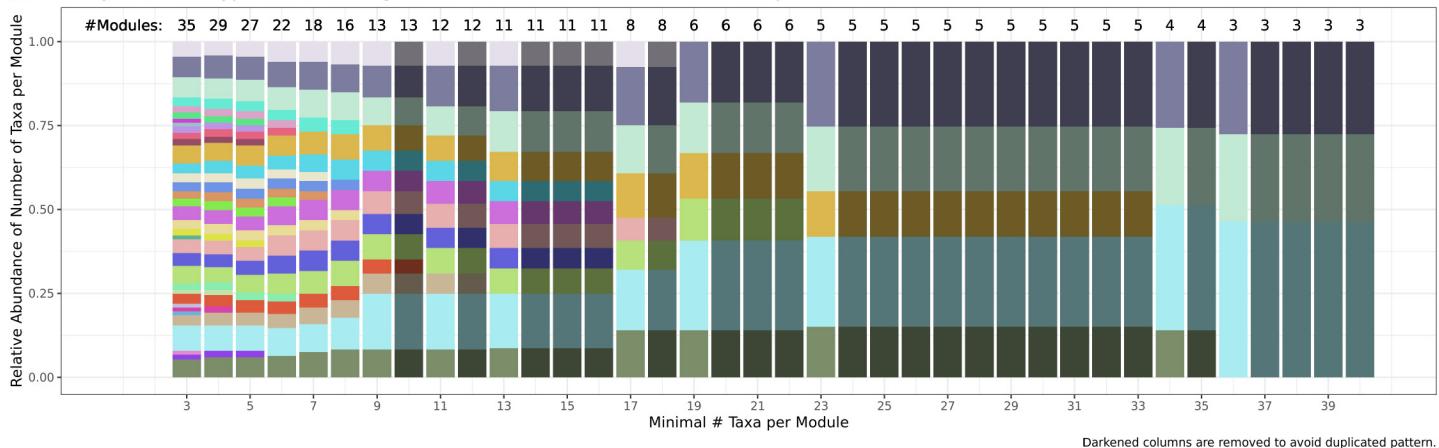


Supplementary Figure 15

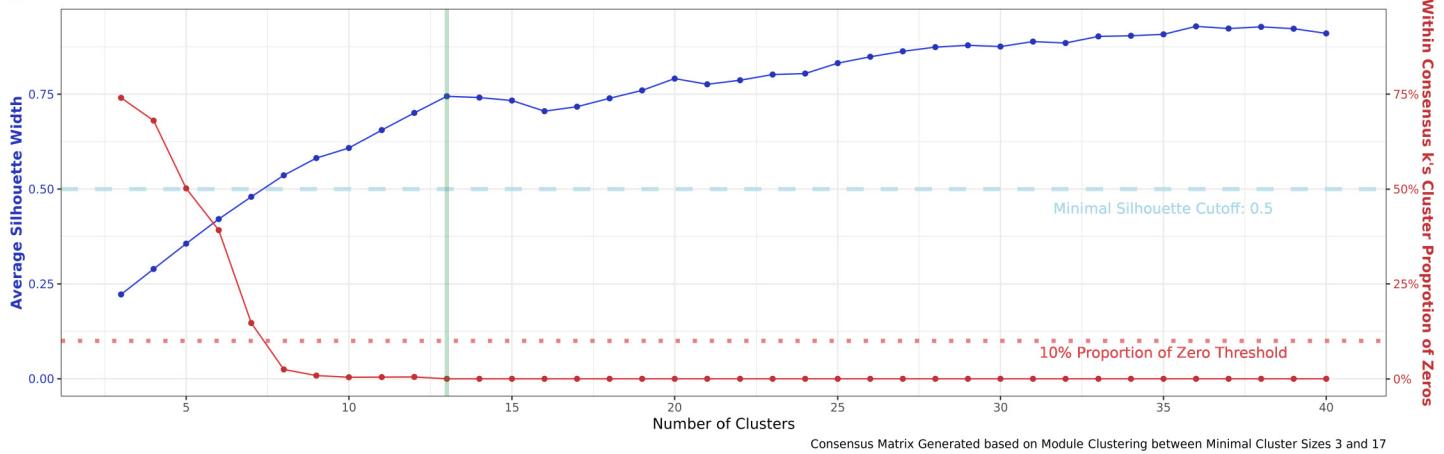
Zeller et al. Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Normal

A. Module Patterns are generated based on different minimal module sizes. Darkened columns represent the replicated patterns. **B.** The average silhouette width was calculated for different numbers of clusters with the consensus matrix generated from patterns in A. The unique patterns including all the minimal number of taxa per module until the unique modules drop below 10.

A Study: CD; Phenotype: CD; Clustering Method: dada2; Maximum Minimal # Taxa per Module: 17



B Best Estimated Number of Clusters: 13

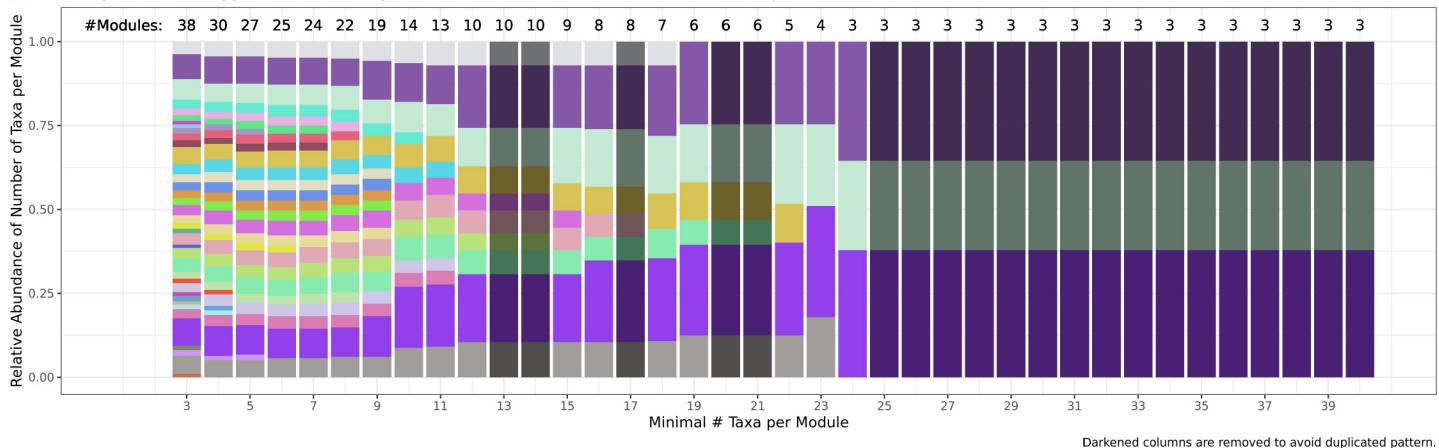


Supplementary Figure 16

Gevers et al. Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Crohn's Disease

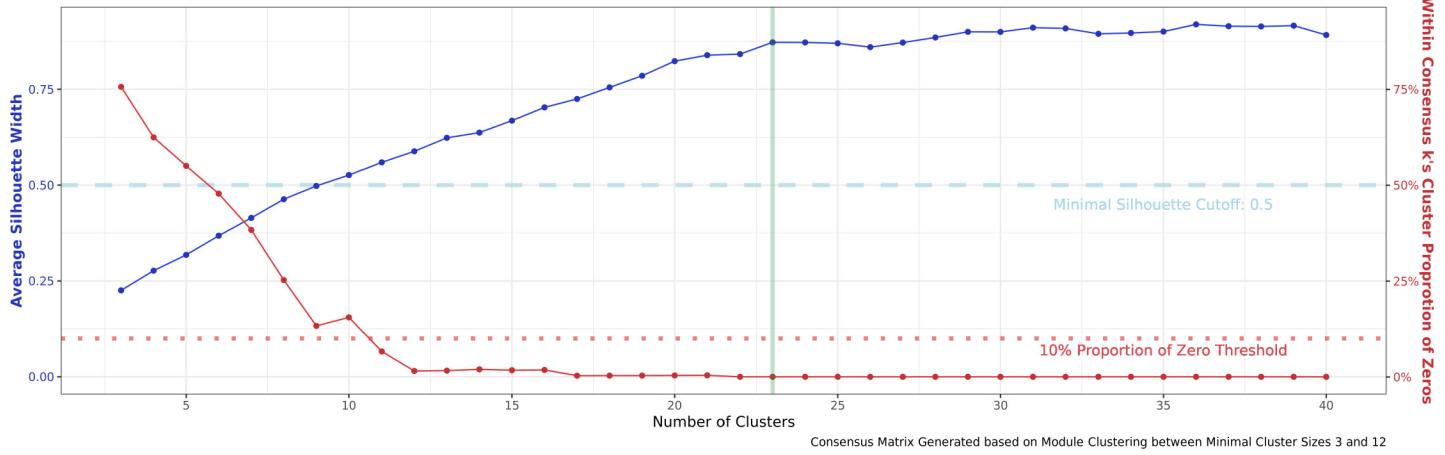
A. Module Patterns are generated based on different minimal module sizes. Darkened columns represent the replicated patterns. **B.** The average silhouette width was calculated for different numbers of clusters with the consensus matrix generated from patterns in A. The unique patterns including all the minimal number of taxa per module until the unique modules drop below 10.

A Study: CD; Phenotype: no; Clustering Method: dada2; Maximum Minimal # Taxa per Module: 12



Darkened columns are removed to avoid duplicated pattern.

B Best Estimated Number of Clusters: 23

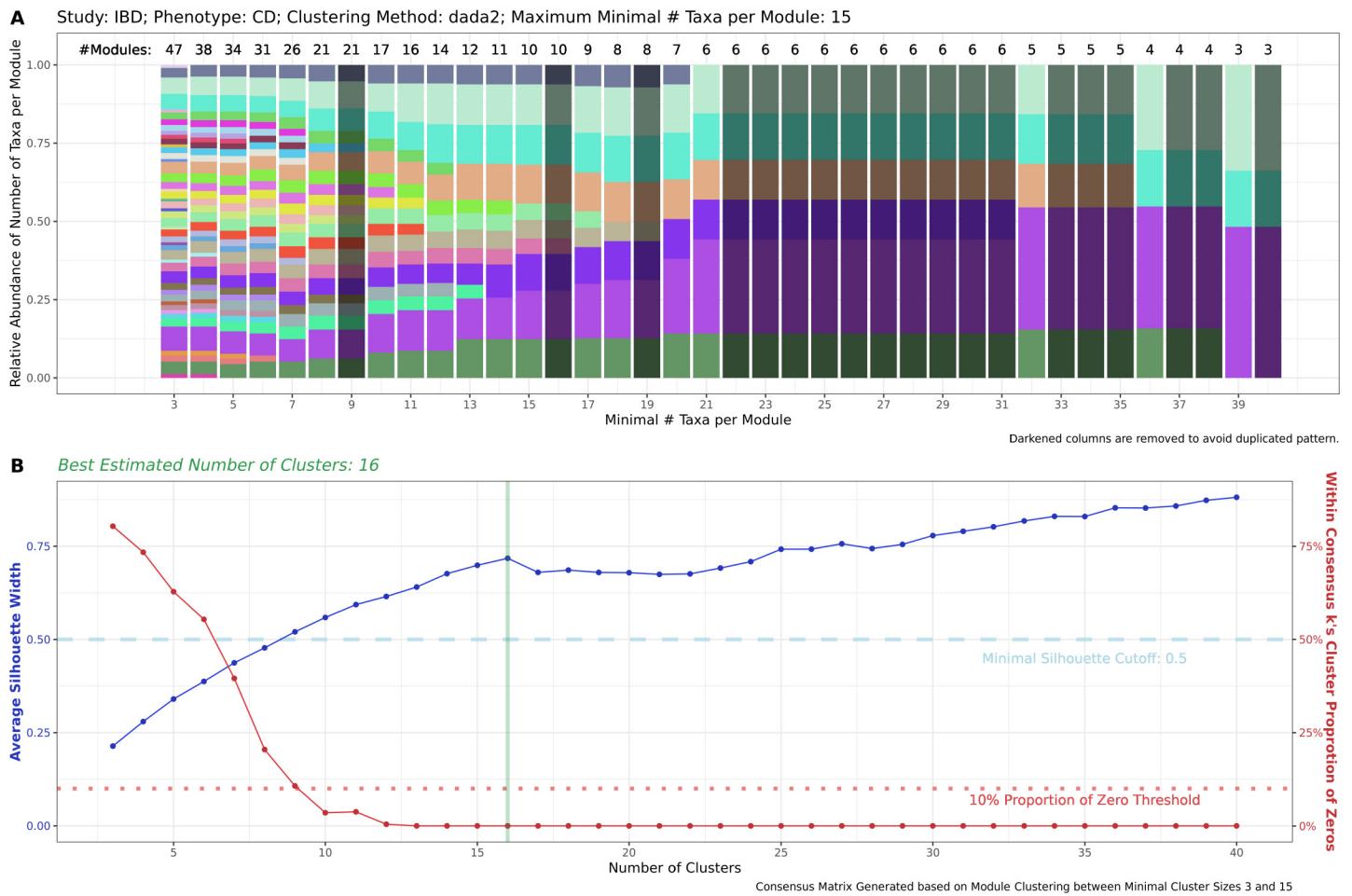


Consensus Matrix Generated based on Module Clustering between Minimal Cluster Sizes 3 and 12

Supplementary Figure 17

Gevers et al. Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Normal

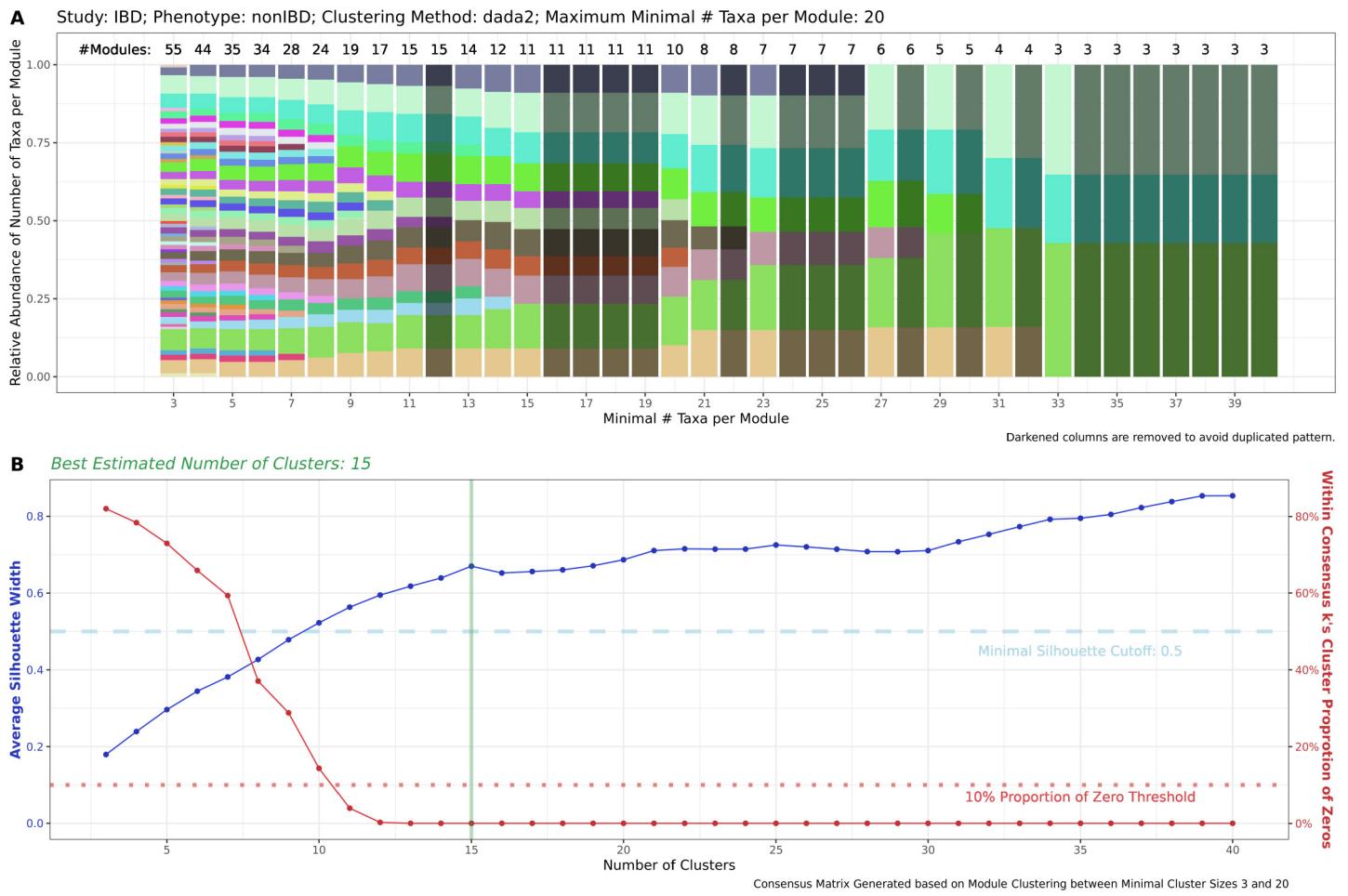
A. Module Patterns are generated based on different minimal module sizes. Darkened columns represent the replicated patterns. **B.** The average silhouette width was calculated for different numbers of clusters with the consensus matrix generated from patterns in A. The unique patterns including all the minimal number of taxa per module until the unique modules drop below 10.



Supplementary Figure 18

IBDMDB Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Crohn's Disease

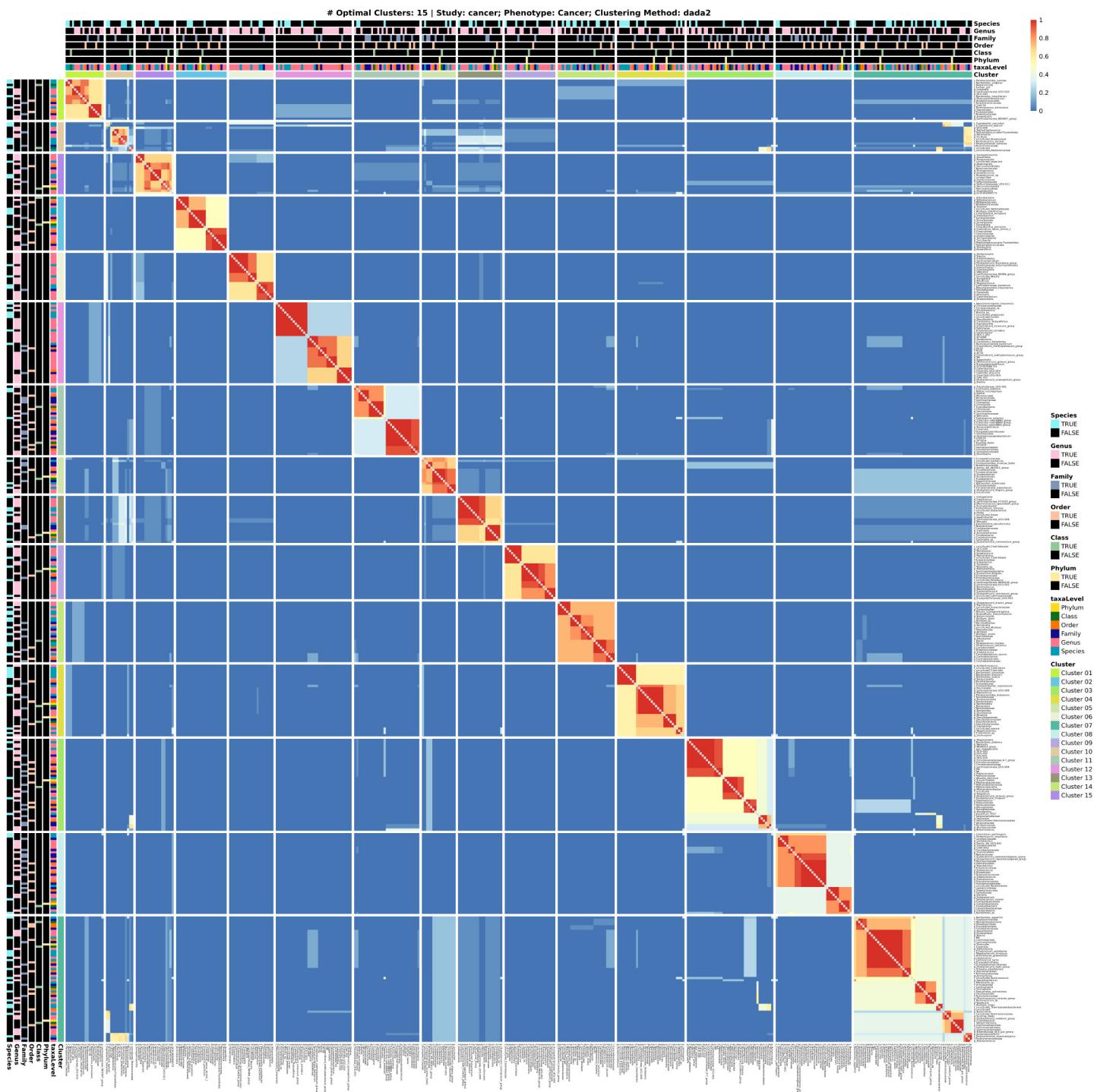
A. Module Patterns are generated based on different minimal module sizes. Darkened columns represent the replicated patterns. **B.** The average silhouette width was calculated for different numbers of clusters with the consensus matrix generated from patterns in A. The unique patterns including all the minimal number of taxa per module until the unique modules drop below 10.



Supplementary Figure 19

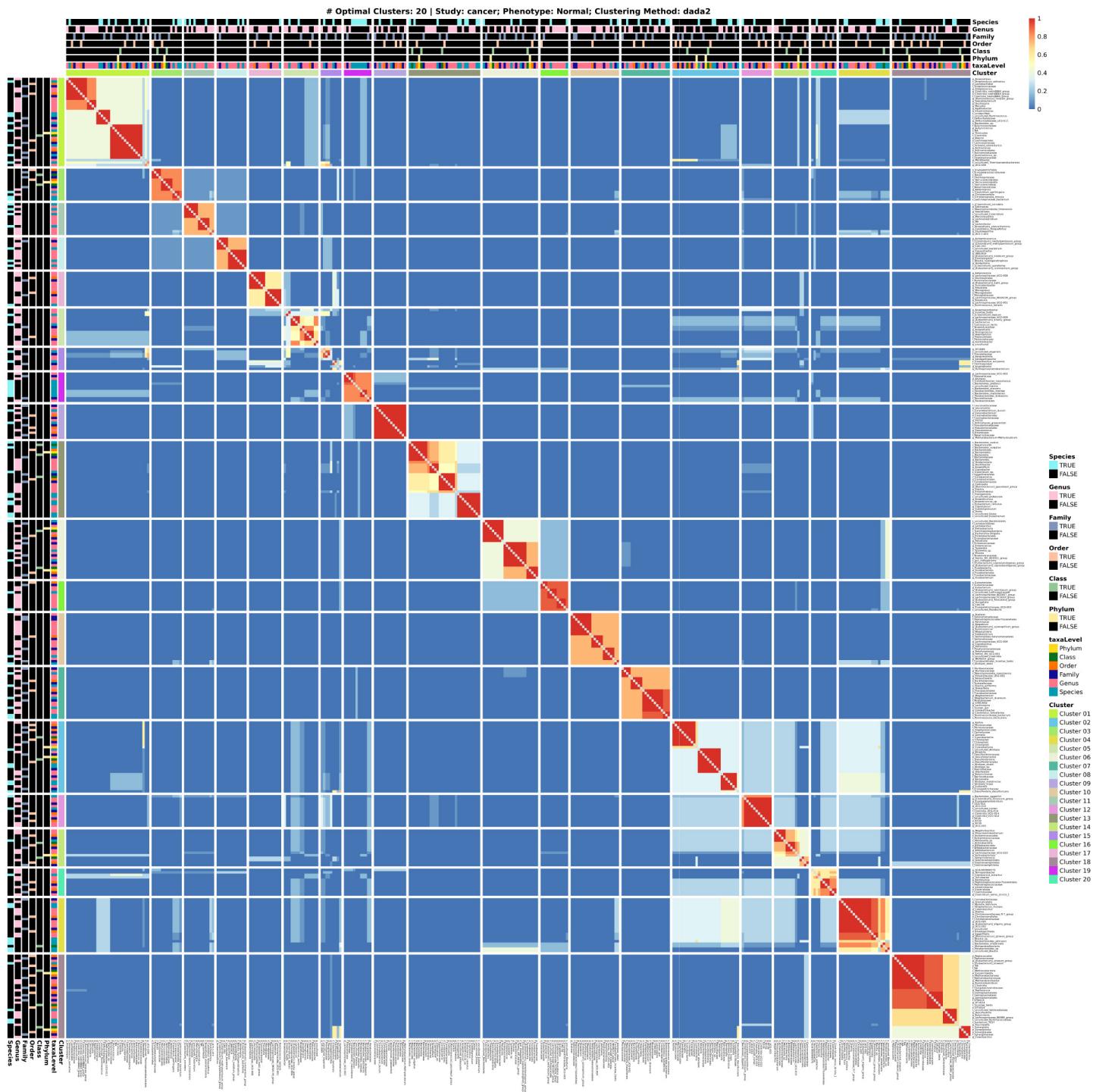
IBDMDB Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Normal

A. Module Patterns are generated based on different minimal module sizes. Darkened columns represent the replicated patterns. **B.** The average silhouette width was calculated for different numbers of clusters with the consensus matrix generated from patterns in A. The unique patterns including all the minimal number of taxa per module until the unique modules drop below 10.



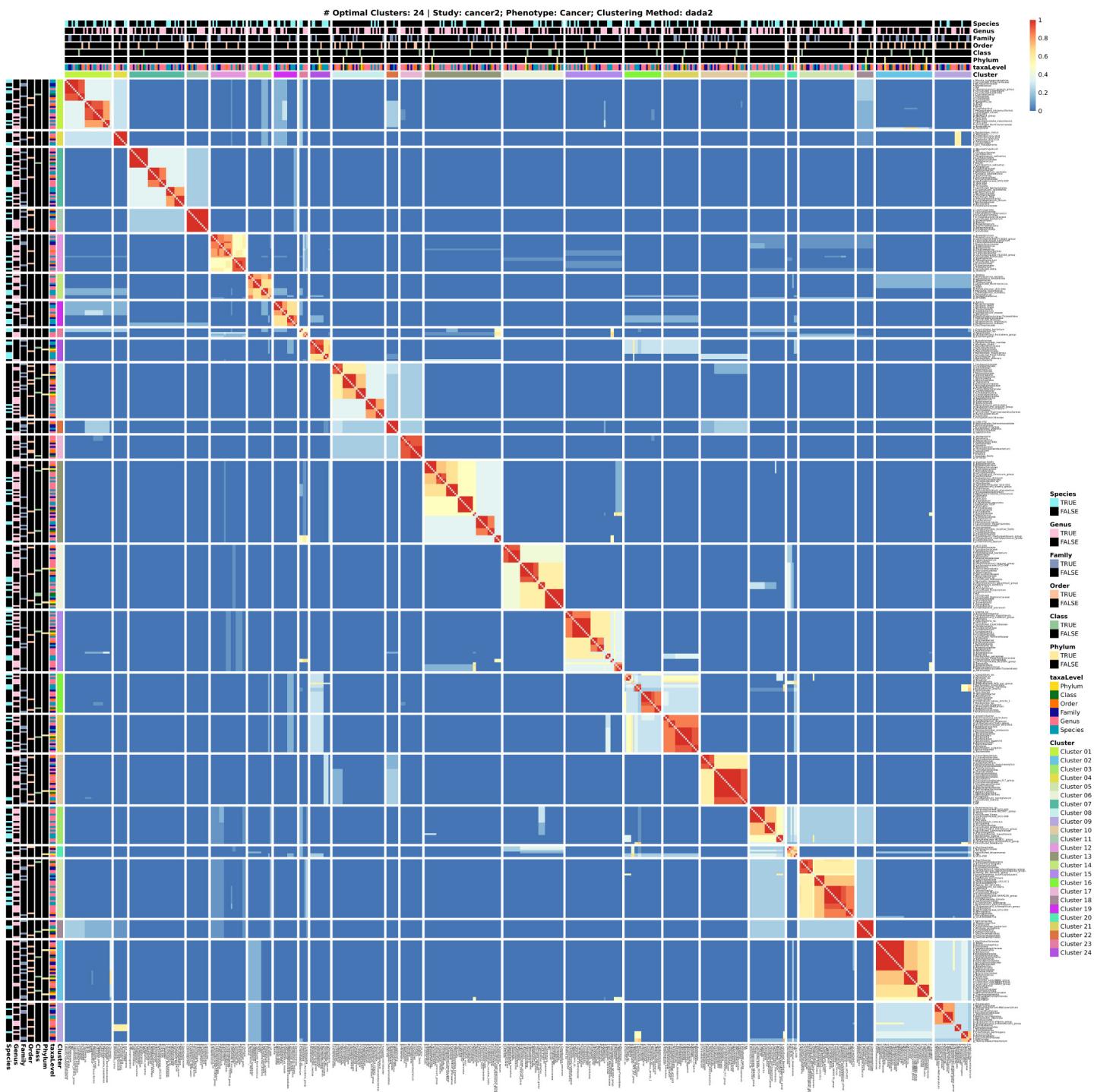
Supplementary Figure 20

Baxter et al. Consensus Plot from DADA2 ASVs Assignment Method with Phenotype: Cancer
Consensus plot based on the best estimated number of clusters obtained.



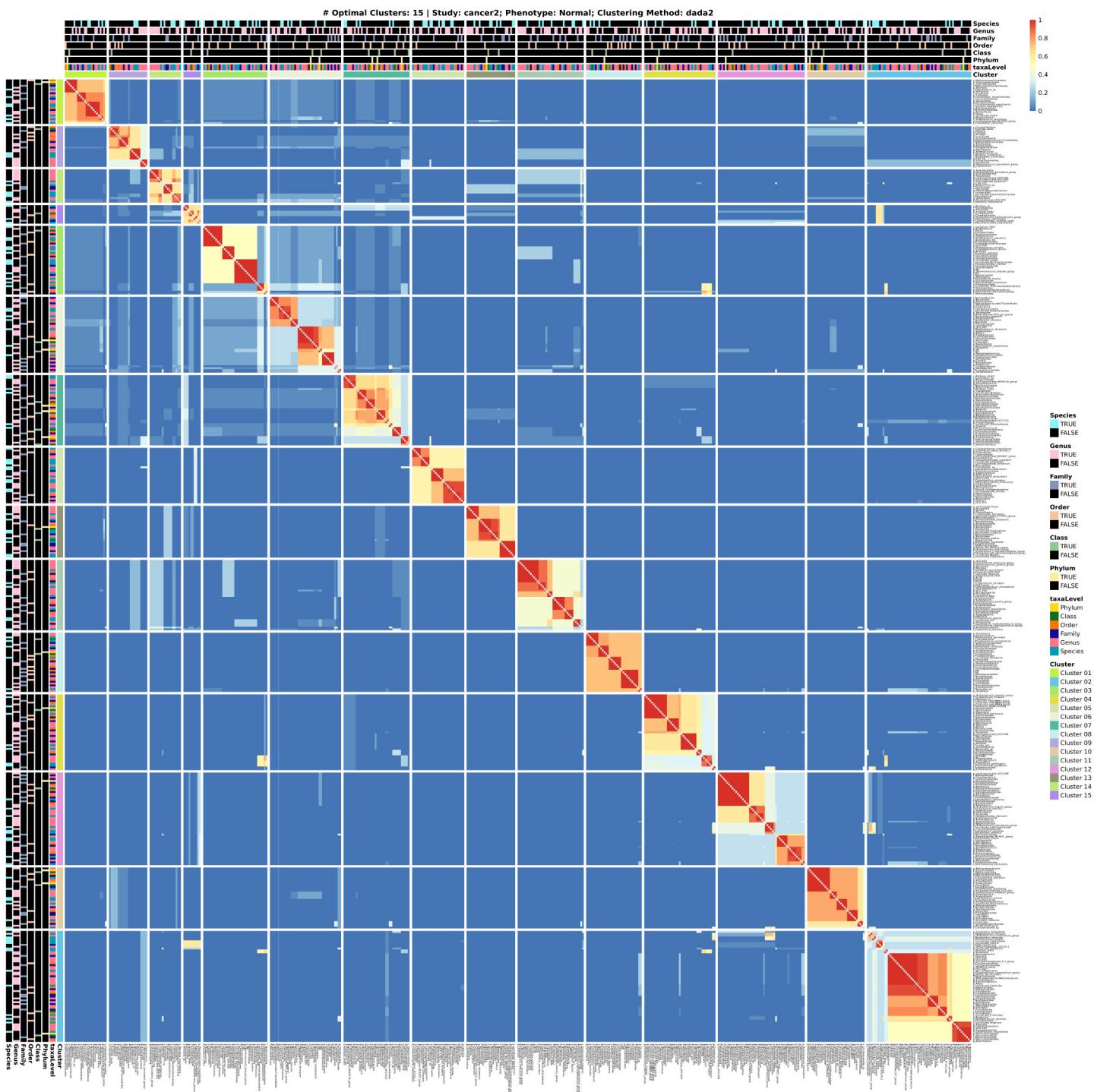
Supplementary Figure 21

Baxter et al. Consensus Plot from DADA2 ASVs Assignment Method with Phenotype: Normal
Consensus plot based on the best estimated number of clusters obtained.



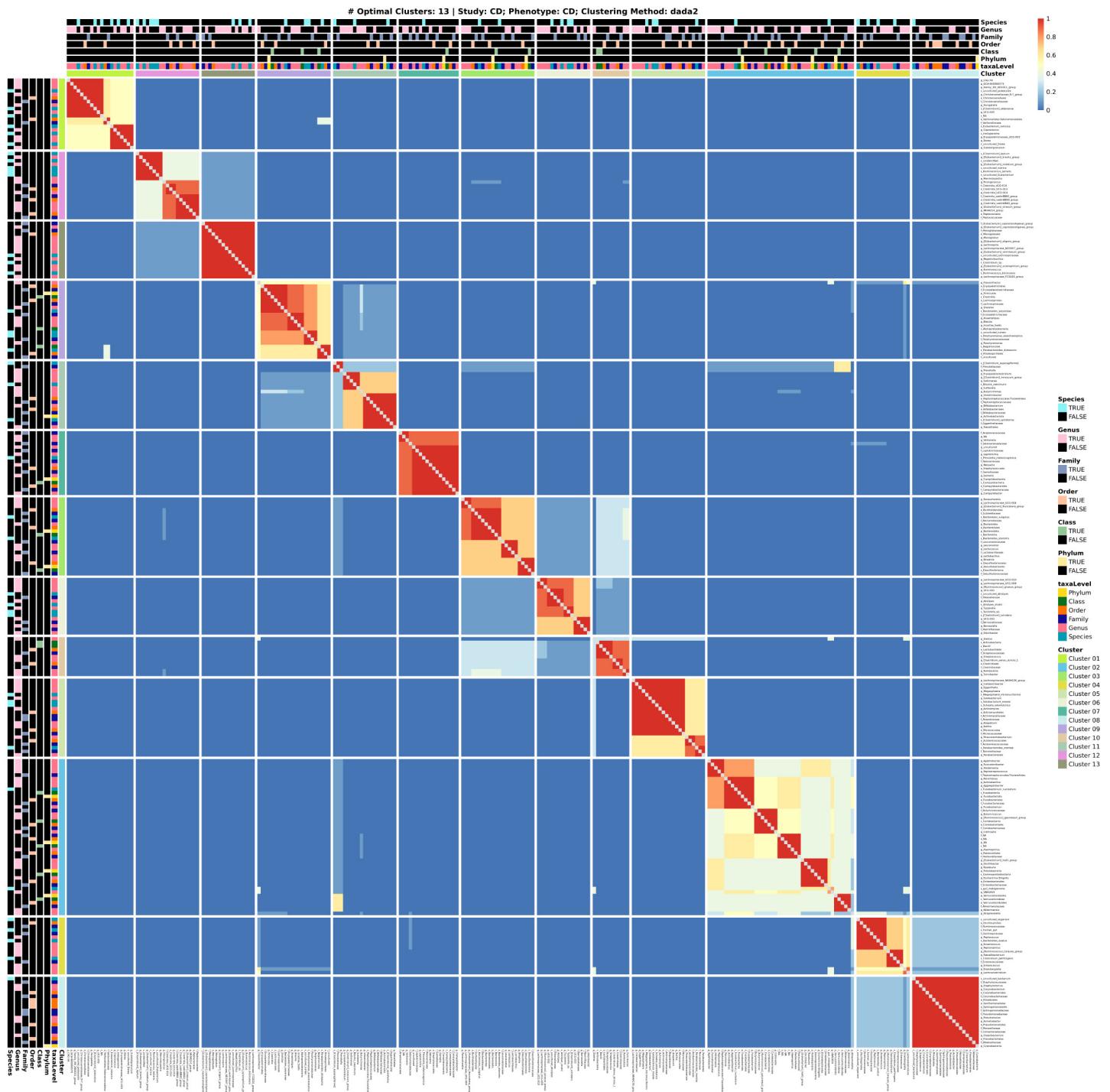
Supplementary Figure 22

Zeller et al. Consensus Plot from DADA2 ASVs Assignment Method with Phenotype: Cancer
Consensus plot based on the best estimated number of clusters obtained.



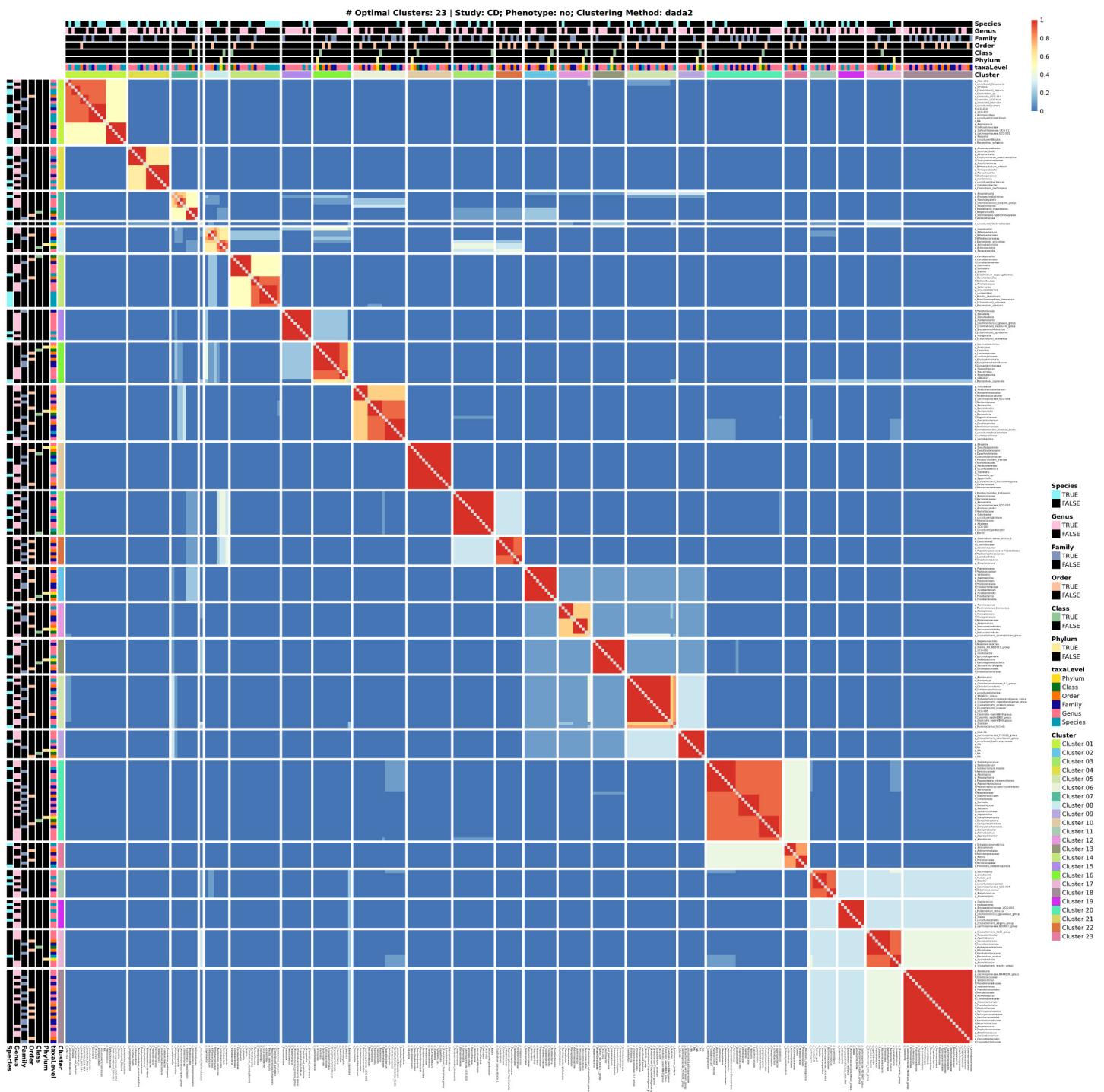
Supplementary Figure 23

Zeller et al. Consensus Plot from DADA2 ASVs Assignment Method with Phenotype: Normal
Consensus plot based on the best estimated number of clusters obtained.



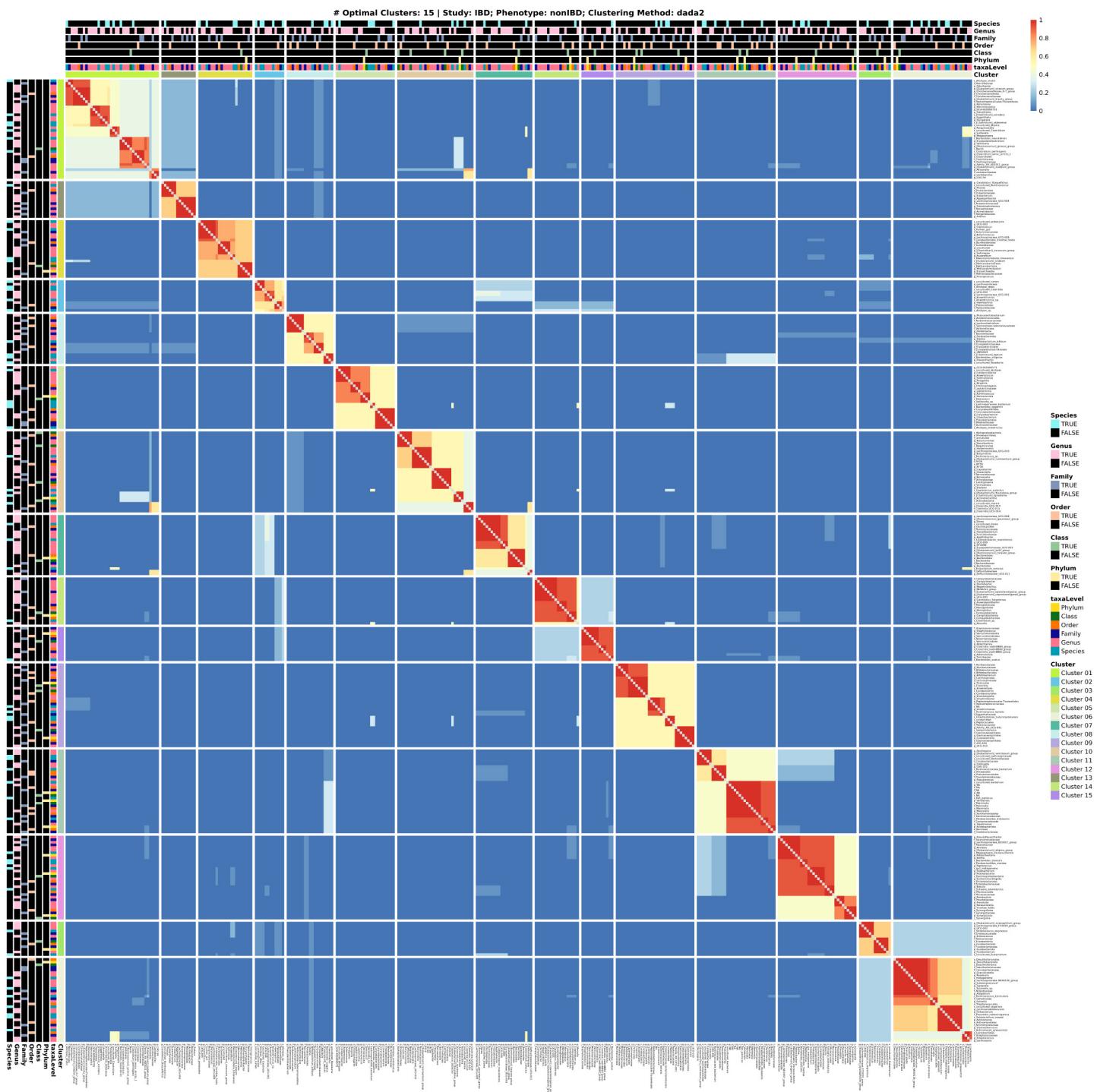
Supplementary Figure 24

Gevvers et al. Consensus Plot from DADA2 ASVs Assignment Method with Phenotype: Crohn's Disease
 Consensus plot based on the best estimated number of clusters obtained.



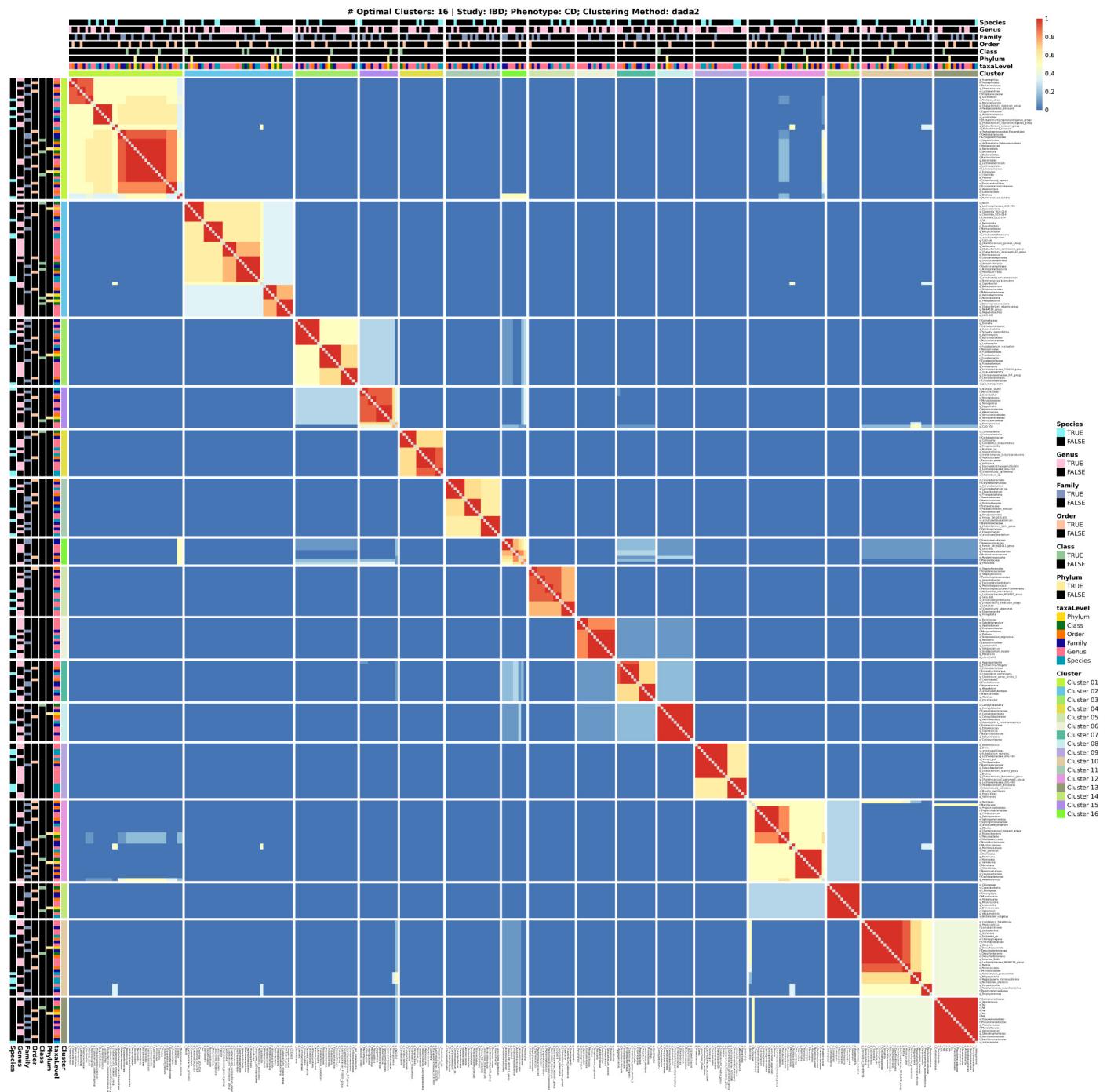
Supplementary Figure 25

Gevers et al. Consensus Plot from DADA2 ASVs Assignment Method with Phenotype: Normal
Consensus plot based on the best estimated number of clusters obtained.



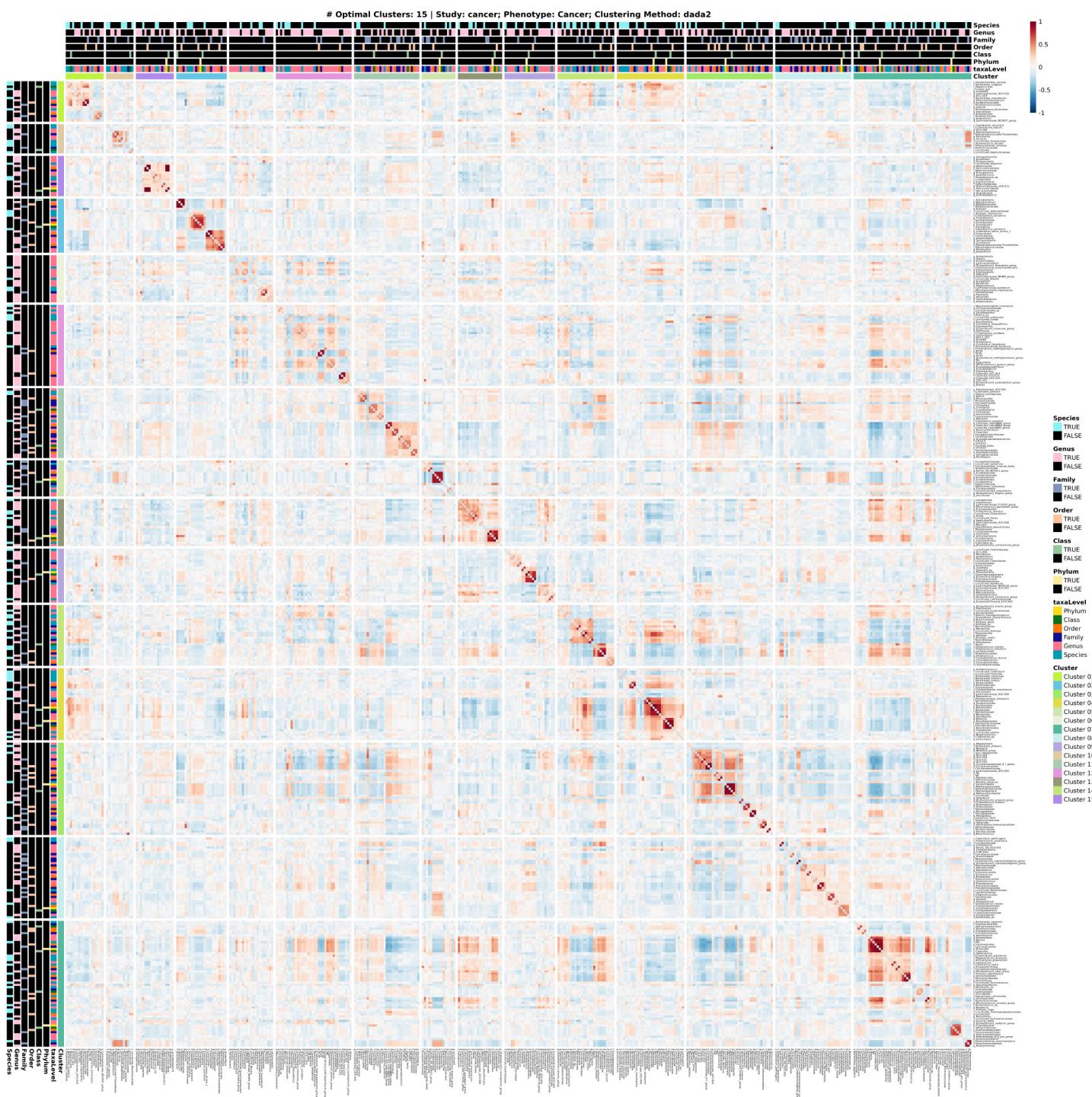
Supplementary Figure 26

IBDMDB Consensus Plot from DADA2 ASVs Assignment Method with Phenotype: Crohn's Disease
Consensus plot based on the best estimated number of clusters obtained.



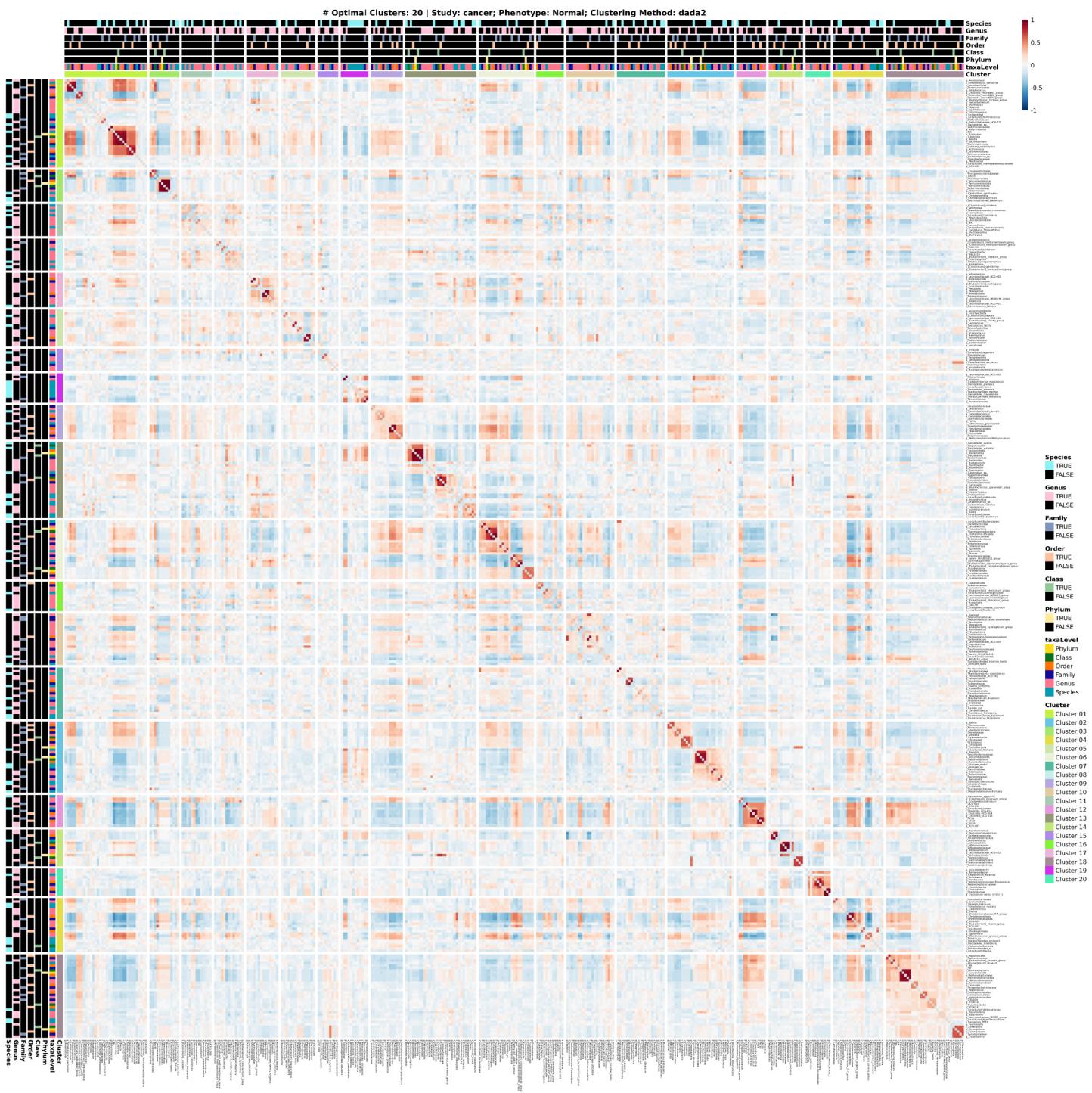
Supplementary Figure 27

IBDMDB Consensus Plot from DADA2 ASVs Assignment Method with Phenotype: Normal
 Consensus plot based on the best estimated number of clusters obtained.



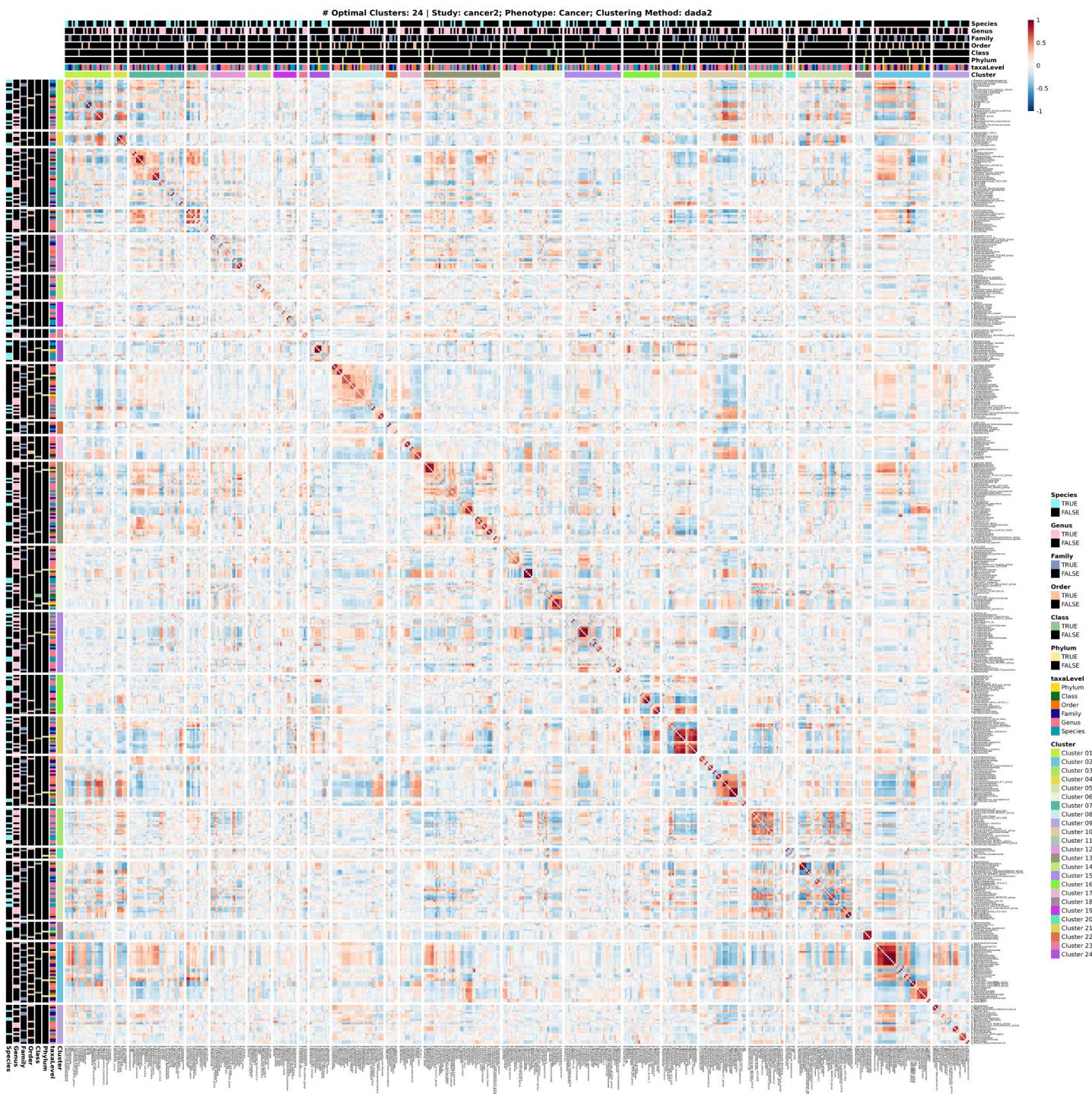
Supplementary Figure 28

Baxter et al. Correlation Plot from DADA2 ASVs Assignment Method with Phenotype: Cancer
Correlation plot based on the best estimated number of clusters obtained.



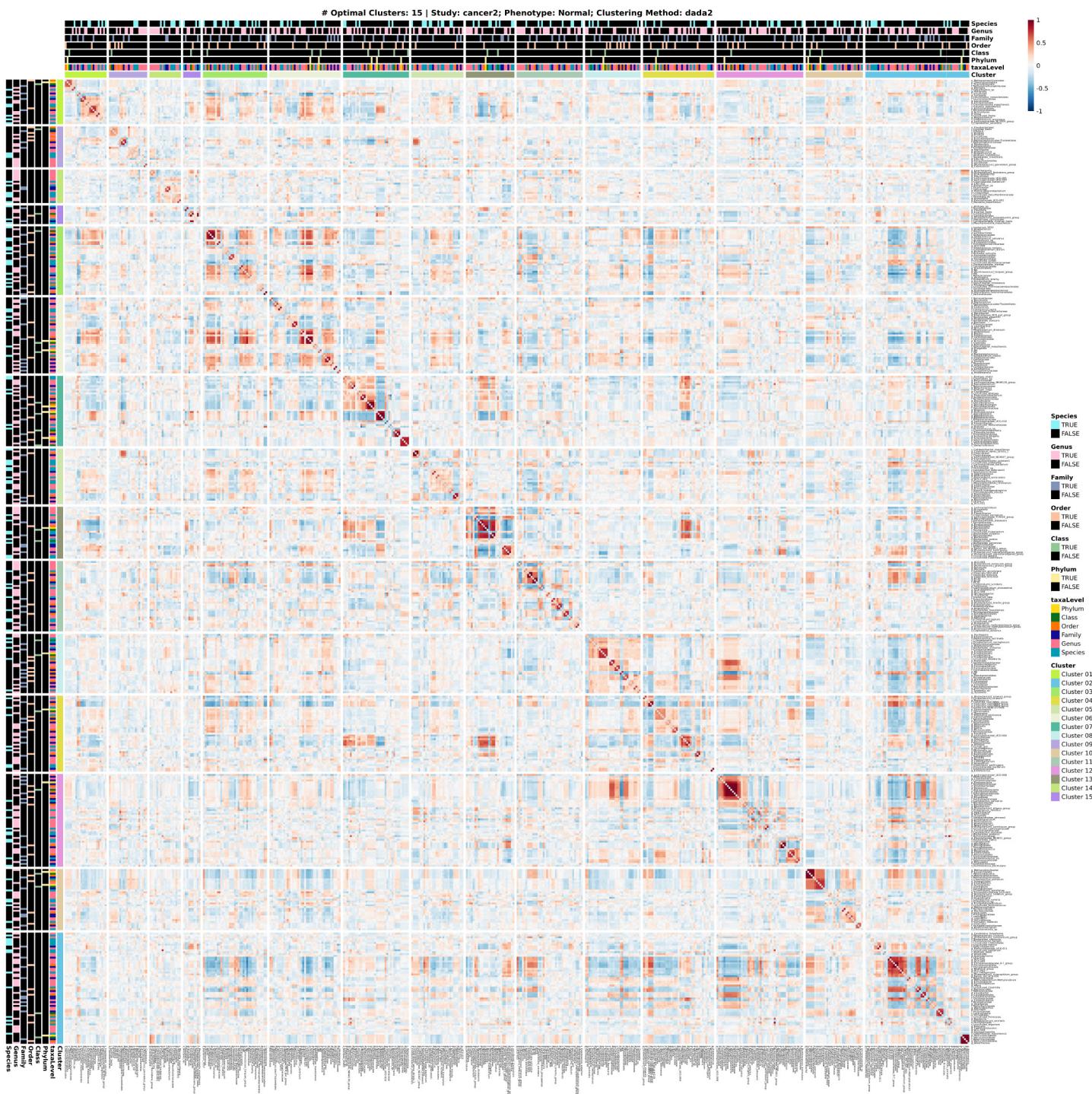
Supplementary Figure 29

Baxter et al. Correlation Plot from DADA2 ASVs Assignment Method with Phenotype: Normal
Correlation plot based on the best estimated number of clusters obtained.



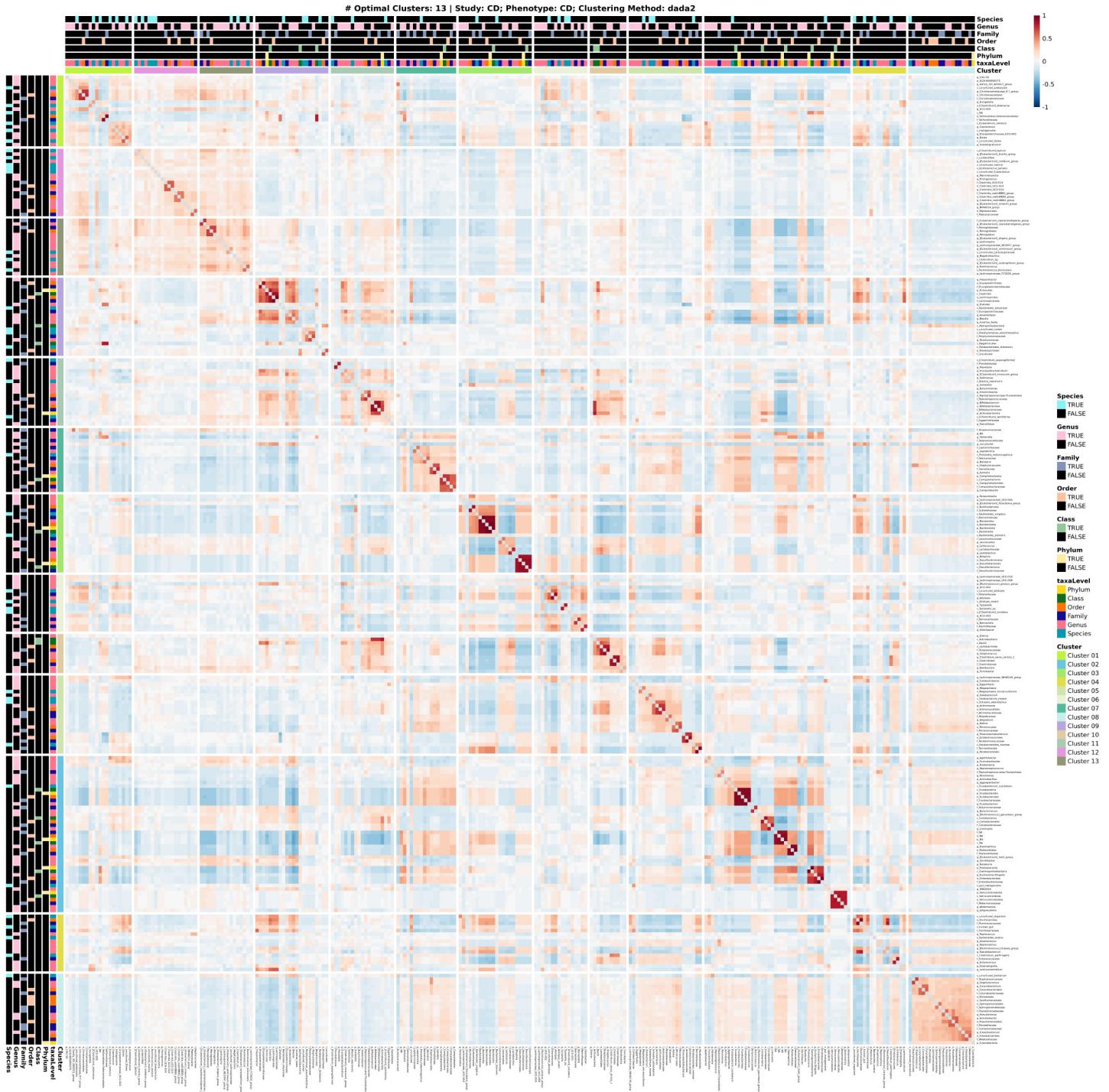
Supplementary Figure 30

Zeller et al. Correlation Plot from DADA2 ASVs Assignment Method with Phenotype: Cancer
Correlation plot based on the best estimated number of clusters obtained.



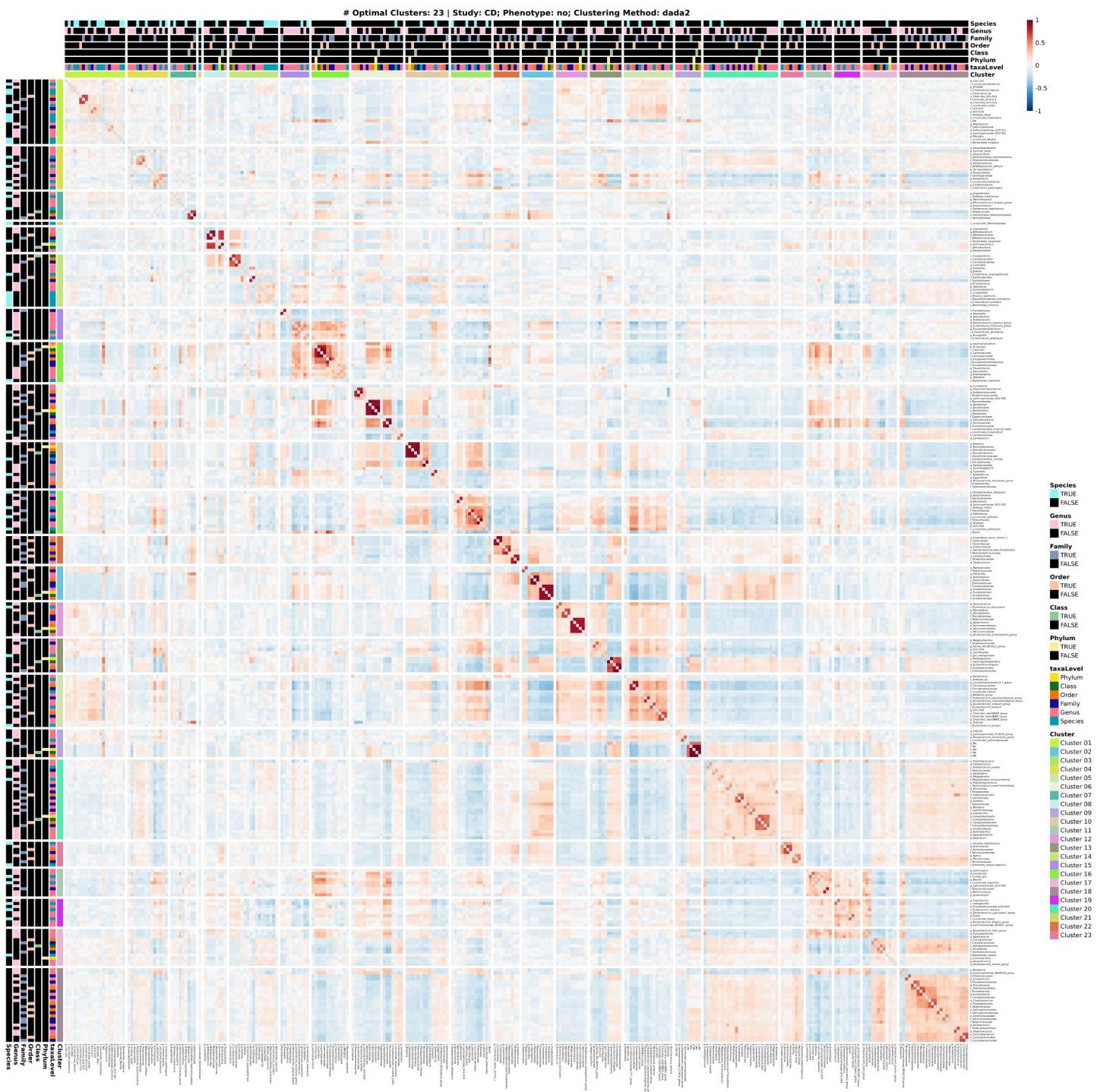
Supplementary Figure 31

Zeller et al. Correlation Plot from DADA2 ASVs Assignment Method with Phenotype: Normal
 Correlation plot based on the best estimated number of clusters obtained.



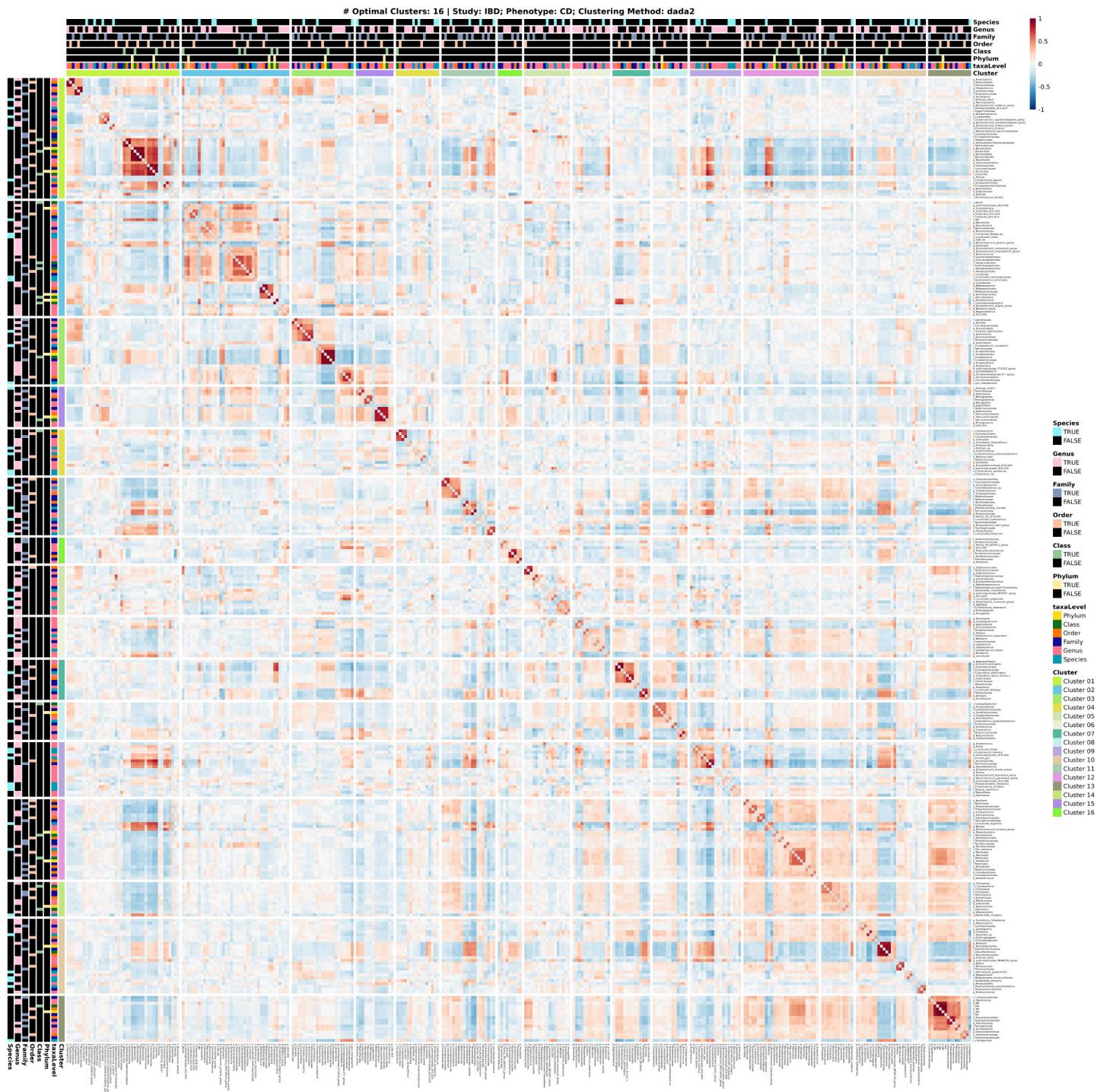
Supplementary Figure 32

Gevvers et al. Correlation Plot from DADA2 ASVs Assignment Method with Phenotype: Crohn's Disease
Correlation plot based on the best estimated number of clusters obtained.



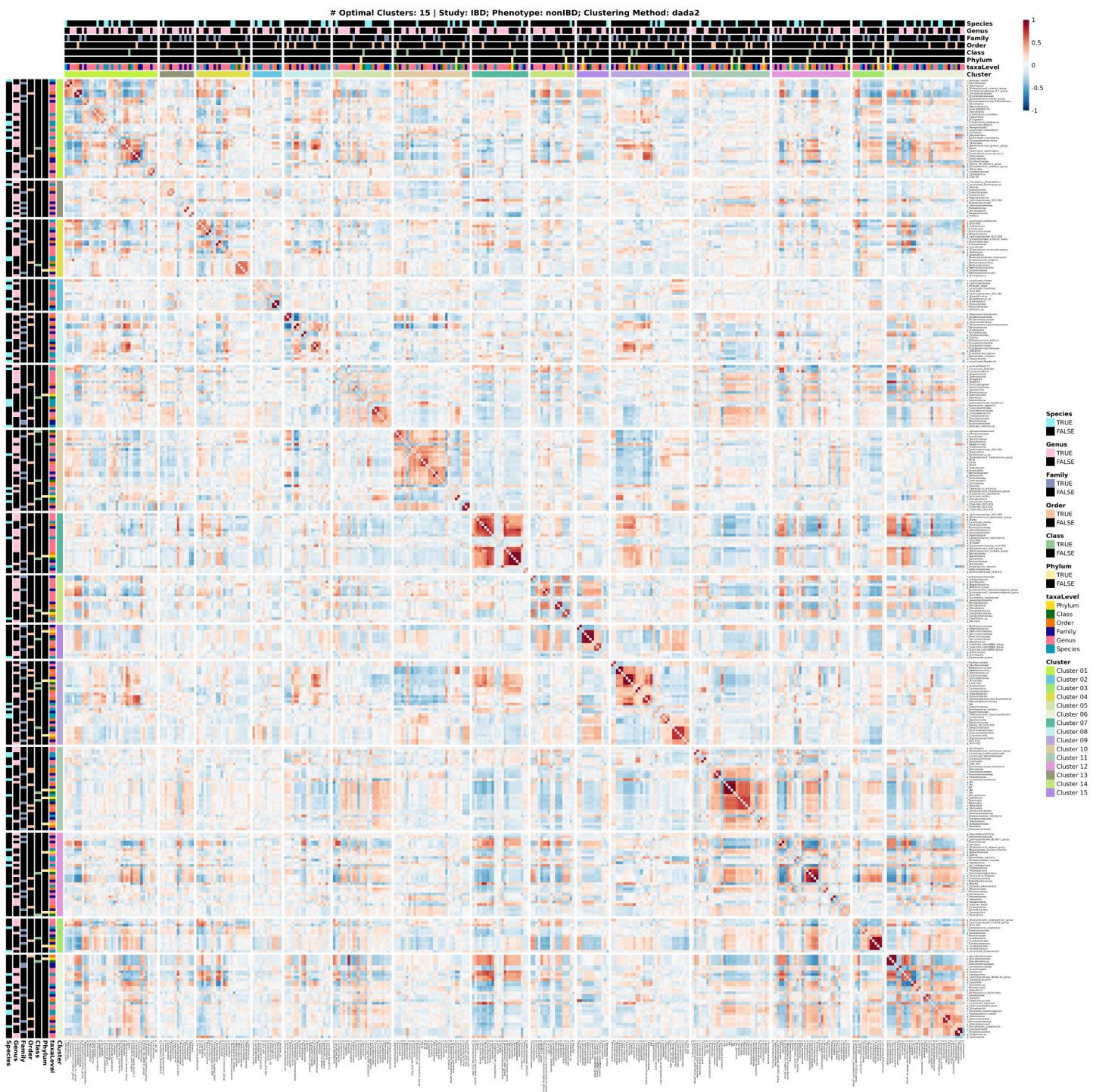
Supplementary Figure 33

Gevers et al. Correlation Plot from DADA2 ASVs Assignment Method with Phenotype: Normal
Correlation plot based on the best estimated number of clusters obtained.



Supplementary Figure 34

IBDMDB Correlation Plot from DADA2 ASVs Assignment Method with Phenotype: Crohn's Disease
 Correlation plot based on the best estimated number of clusters obtained.



Supplementary Figure 35
IBDMDB Correlation Plot from DADA2 ASVs Assignment Method with Phenotype: Normal
Correlation plot based on the best estimated number of clusters obtained.

