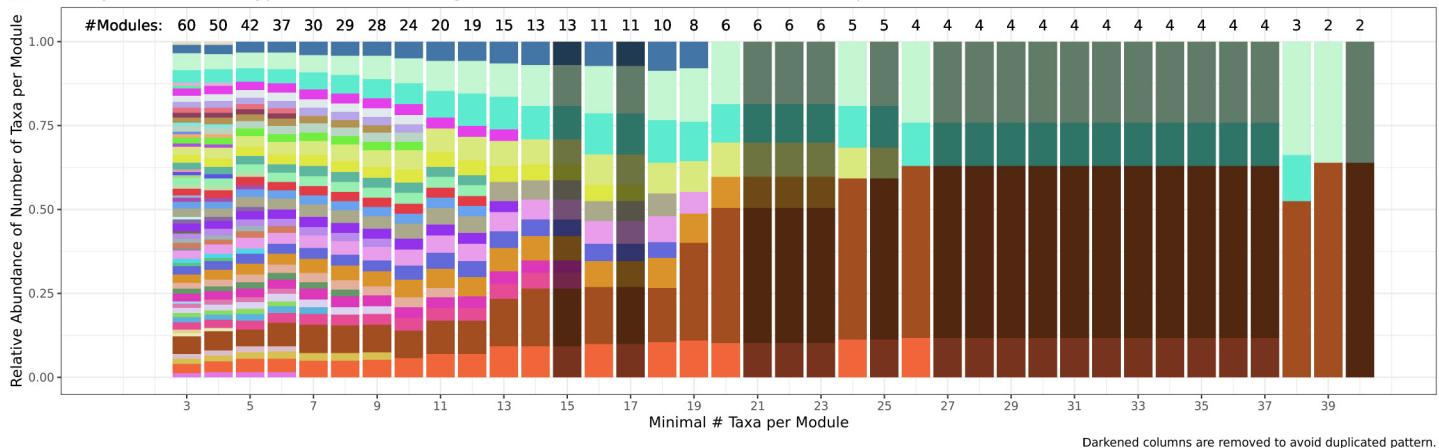
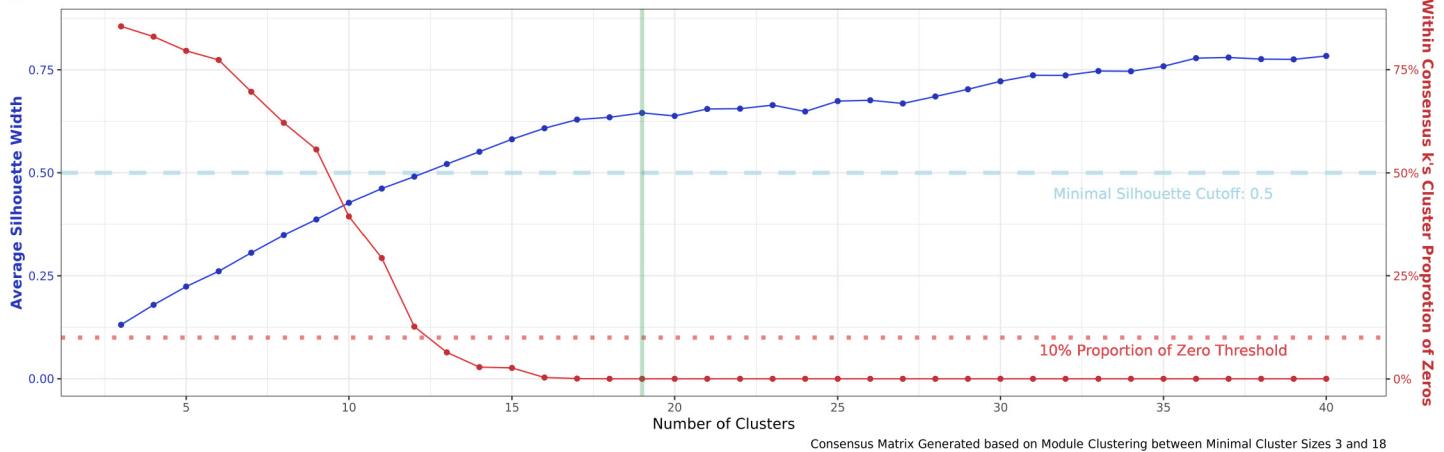


A Study: cancer; Phenotype: Cancer; Clustering Method: denovo; Maximum Minimal # Taxa per Module: 18



B Best Estimated Number of Clusters: 19

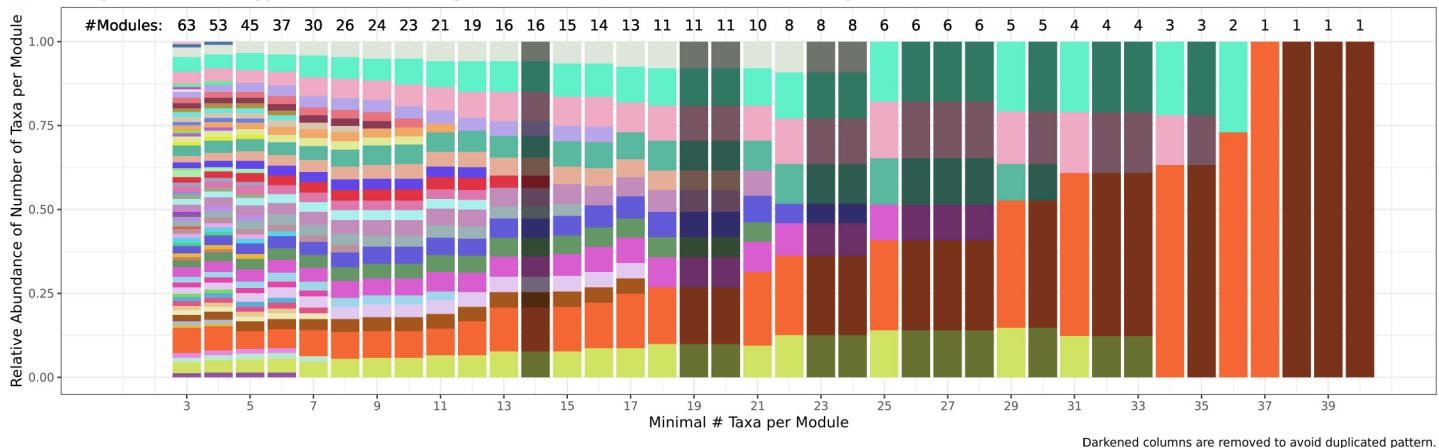


Supplementary Figure 11

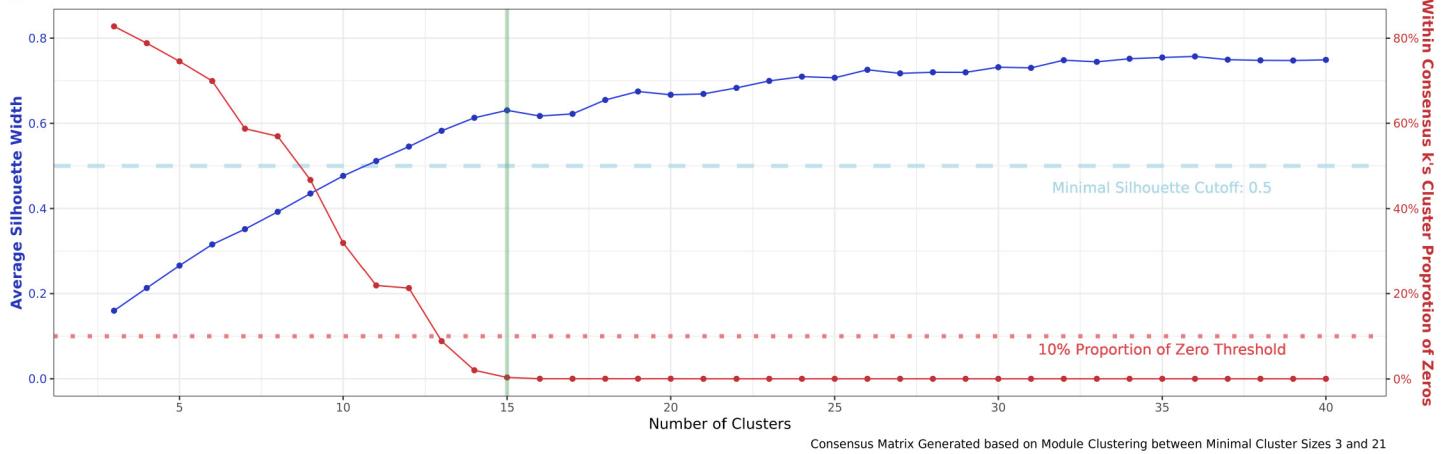
Baxter et al. Module Patterns Plot from *de novo* OTUs Assignment Method with Phenotype: Cancer

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: Cancer; Clustering Method: dada2; Maximum Minimal # Taxa per Module: 21



B Best Estimated Number of Clusters: 15

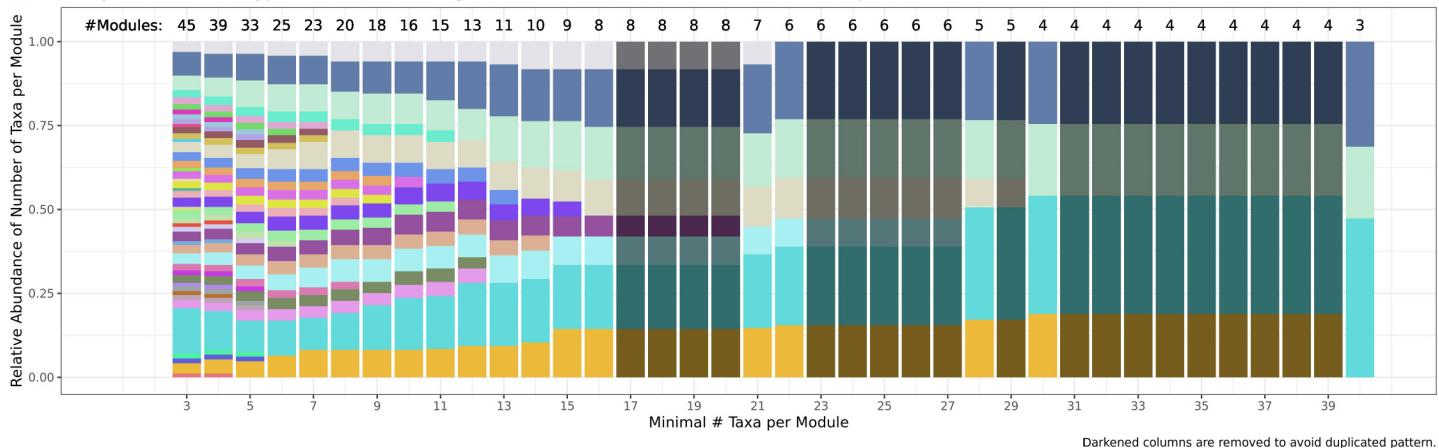


Supplementary Figure 12

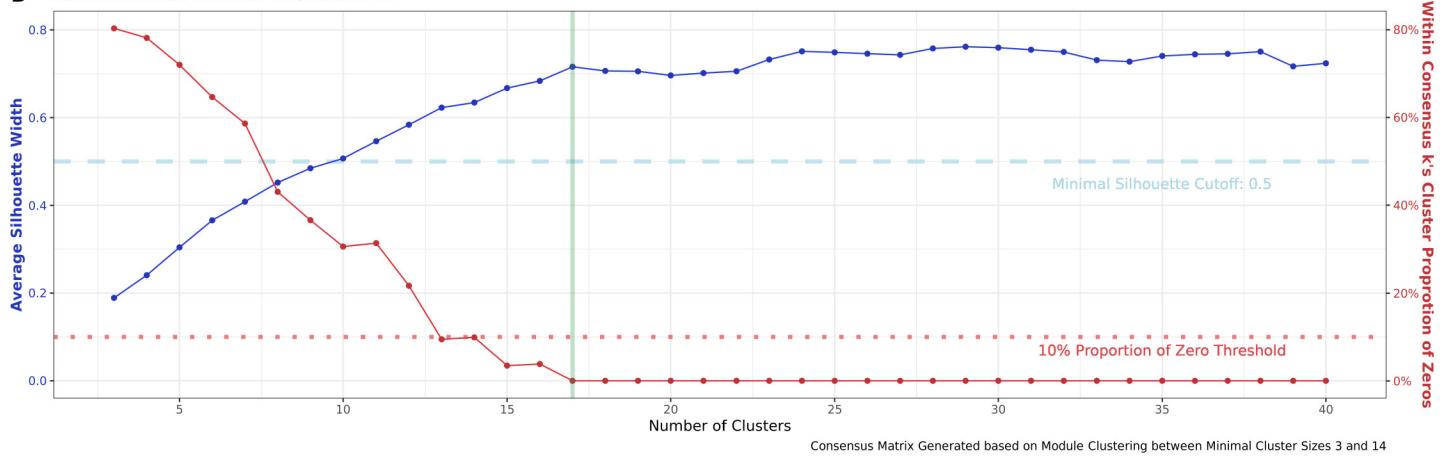
Baxter et al. Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Cancer

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: denovo; Maximum Minimal # Taxa per Module: 14



B Best Estimated Number of Clusters: 17

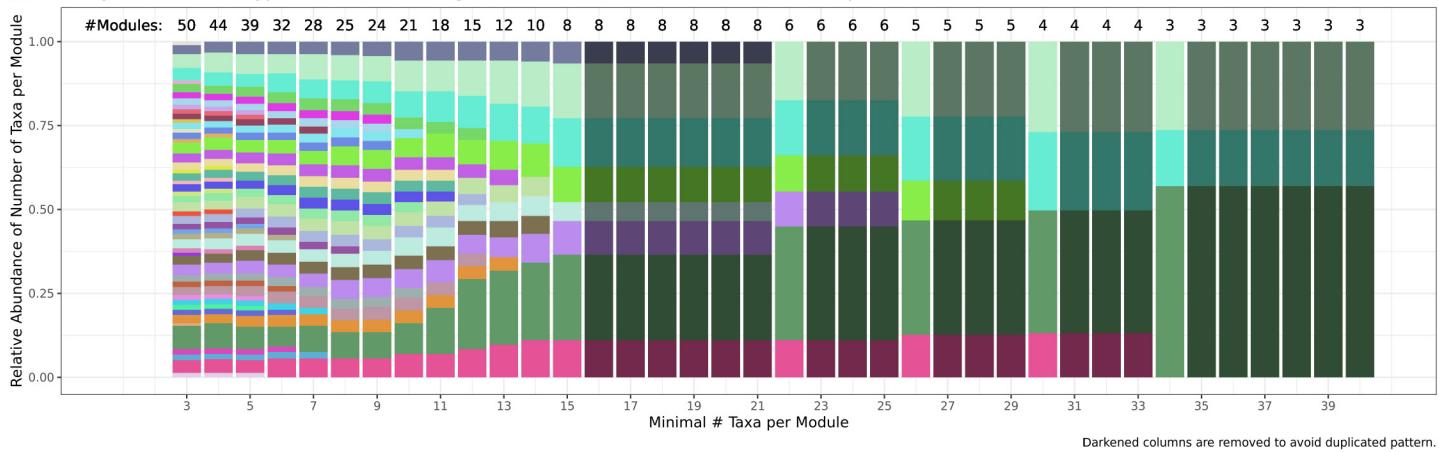


Supplementary Figure 13

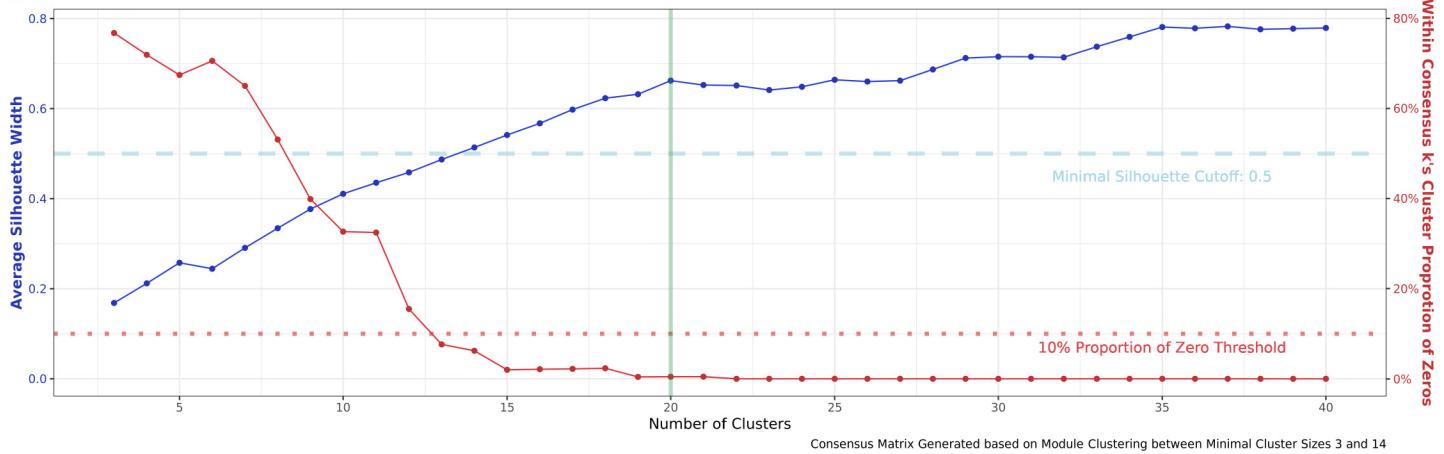
Baxter et al. Module Patterns Plot from *de novo* OTUs Assignment Method with Phenotype: Normal

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



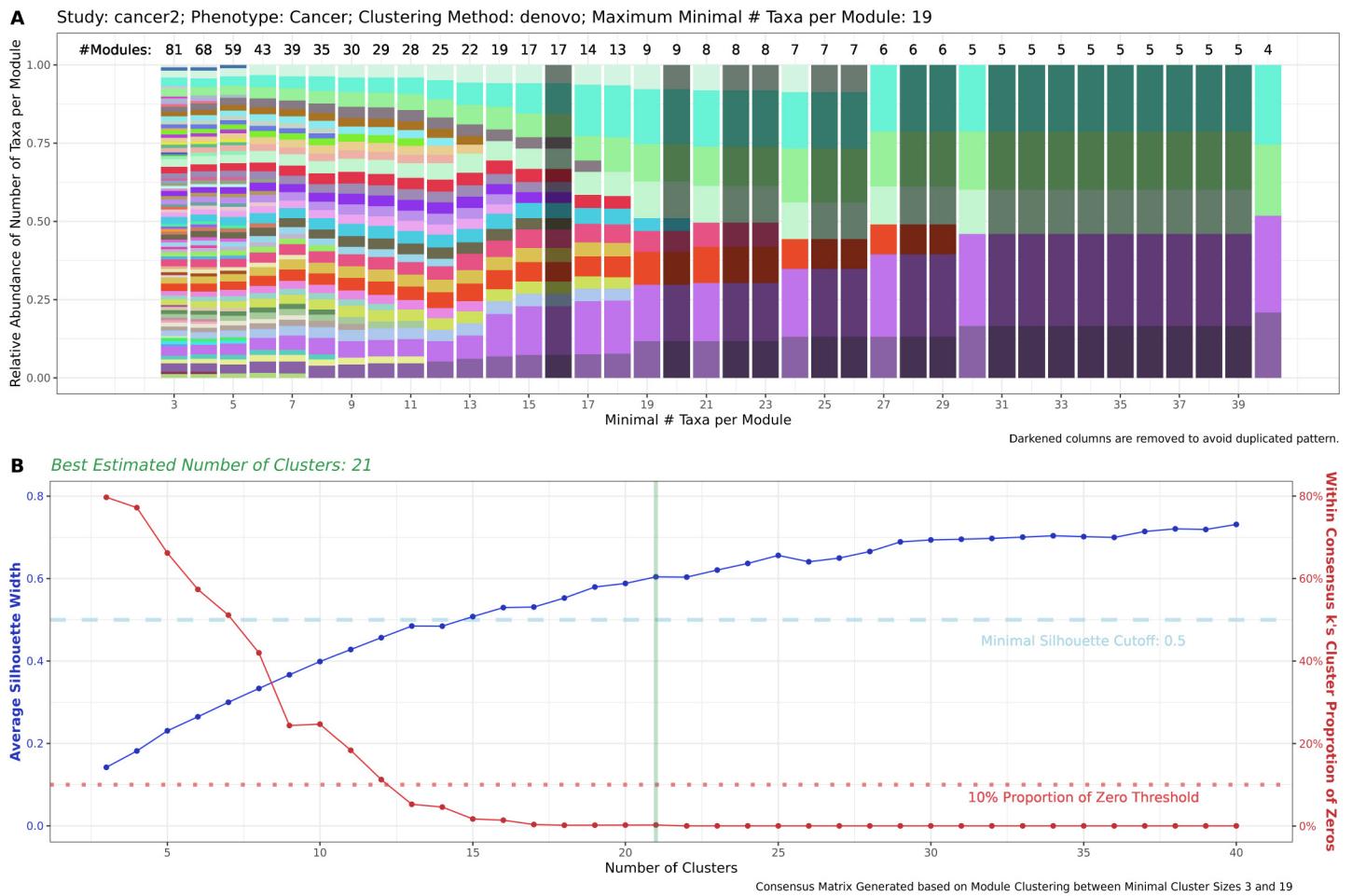
B Best Estimated Number of Clusters: 20



Supplementary Figure 14

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.

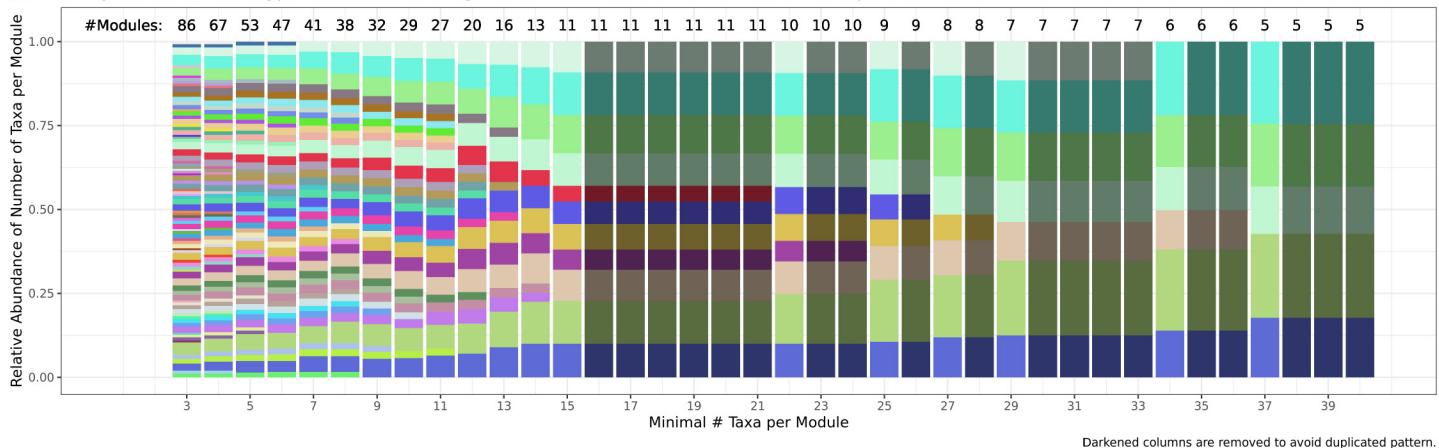


Supplementary Figure 15

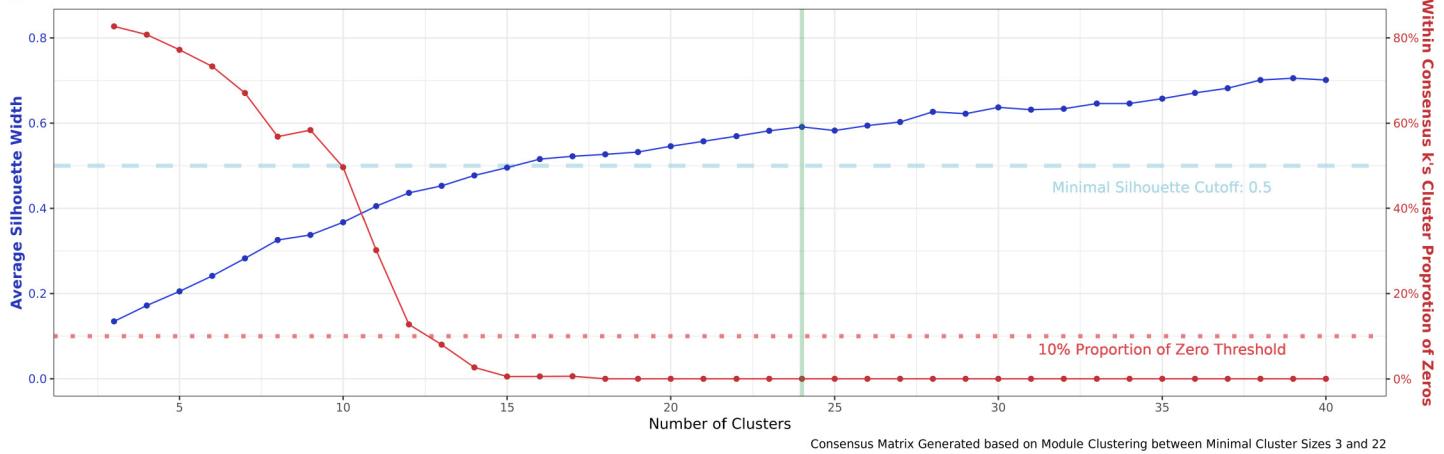
Zeller et al. Module Patterns Plot from *de novo* OTUs Assignment Method with Phenotype: Cancer

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: Cancer; Clustering Method: dada2; Maximum Minimal # Taxa per Module: 22



B Best Estimated Number of Clusters: 24

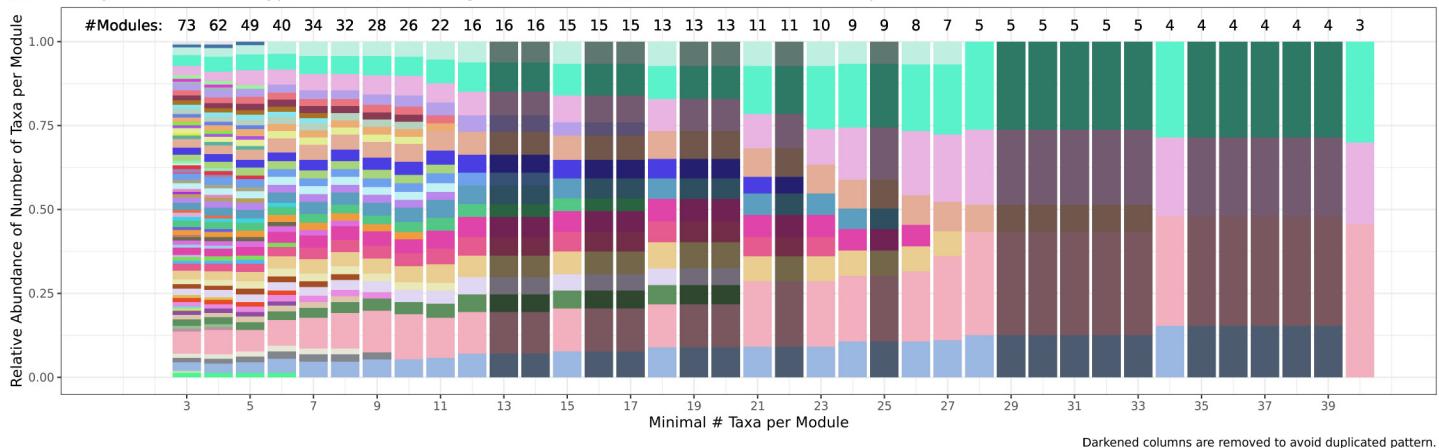


Supplementary Figure 16

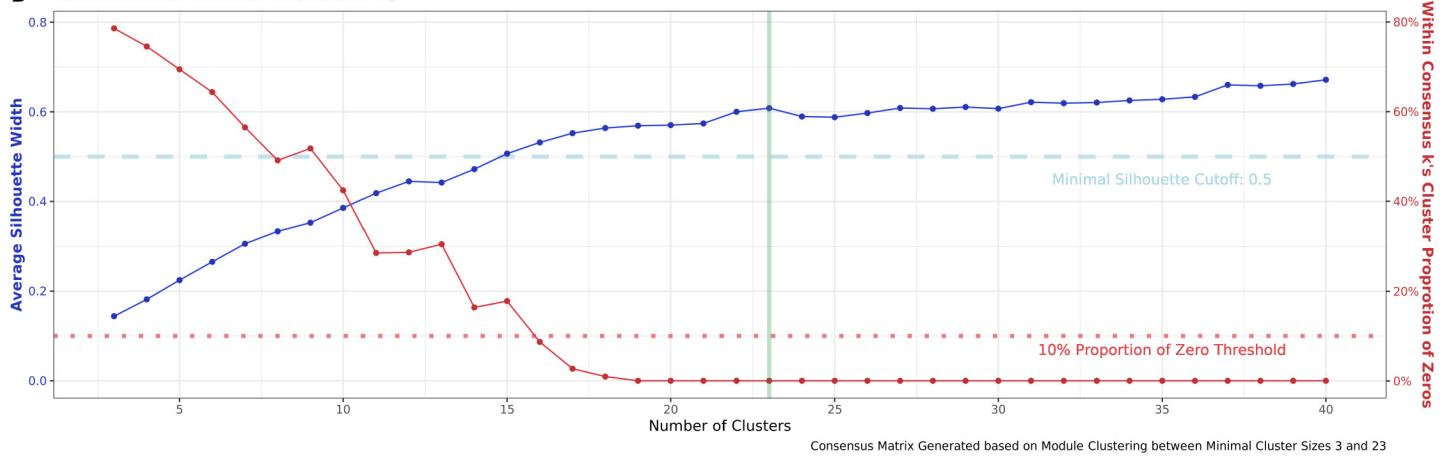
Zeller et al. Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Cancer

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: denovo; Maximum Minimal # Taxa per Module: 23



B Best Estimated Number of Clusters: 23

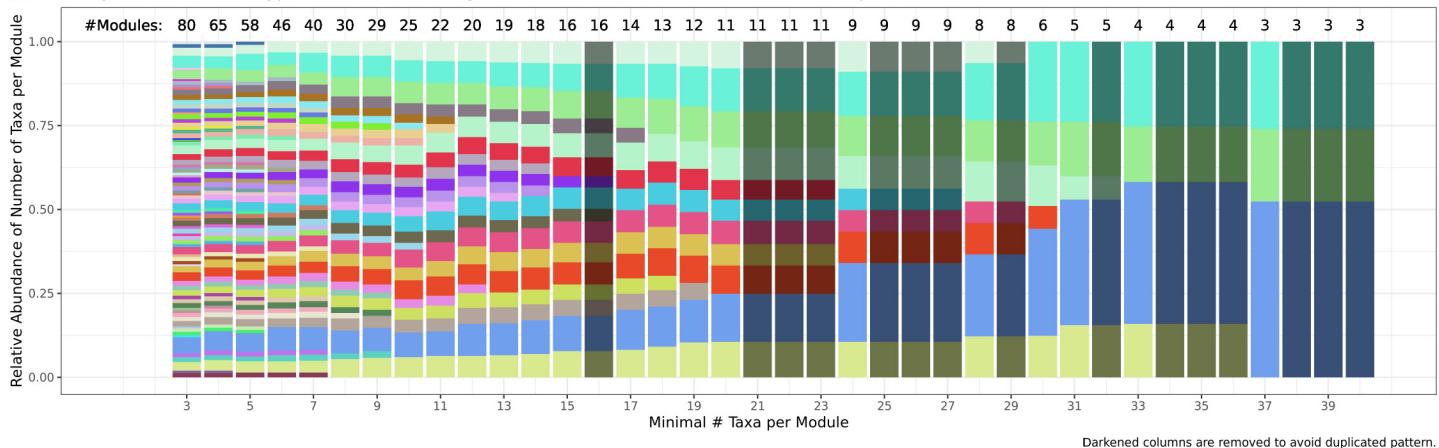


Supplementary Figure 17

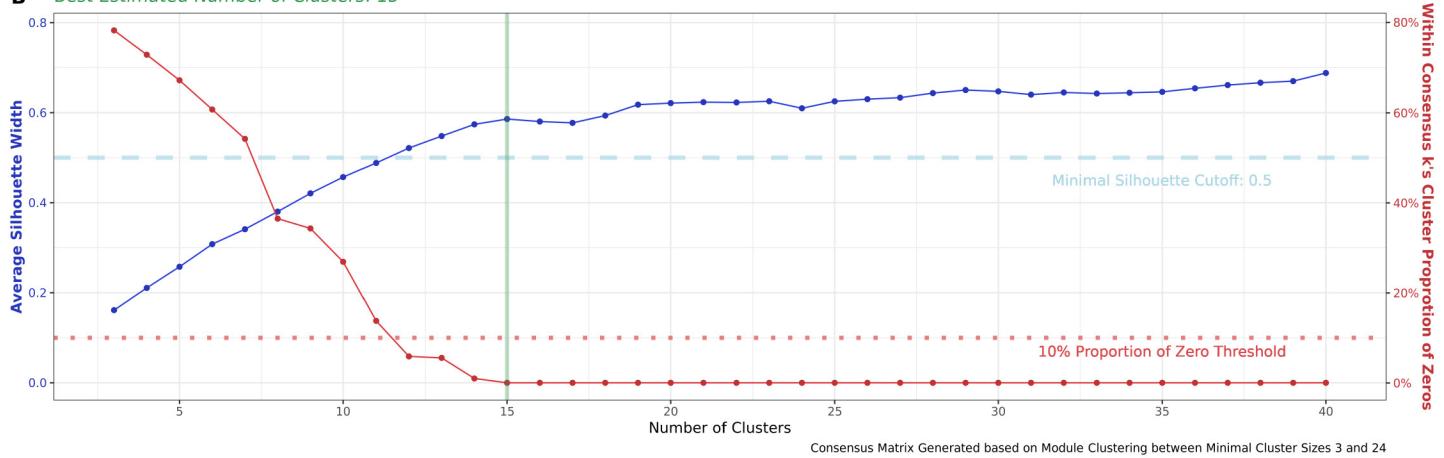
Zeller et al. Module Patterns Plot from *de novo* OTUs Assignment Method with Phenotype: Normal

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: Normal; Clustering Method: dada2; Maximum Minimal # Taxa per Module: 24



B Best Estimated Number of Clusters: 15

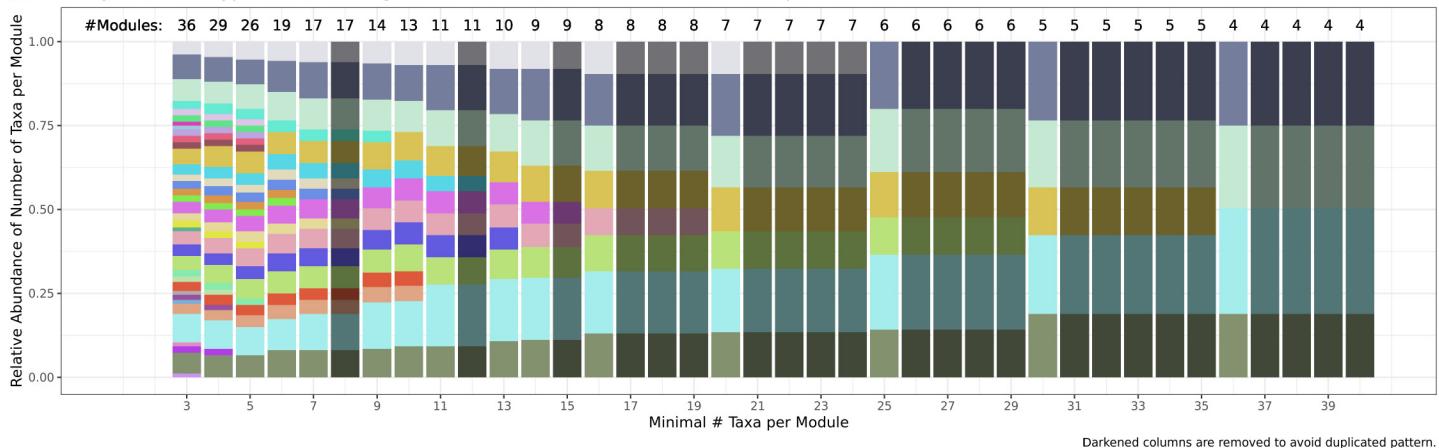


Supplementary Figure 18

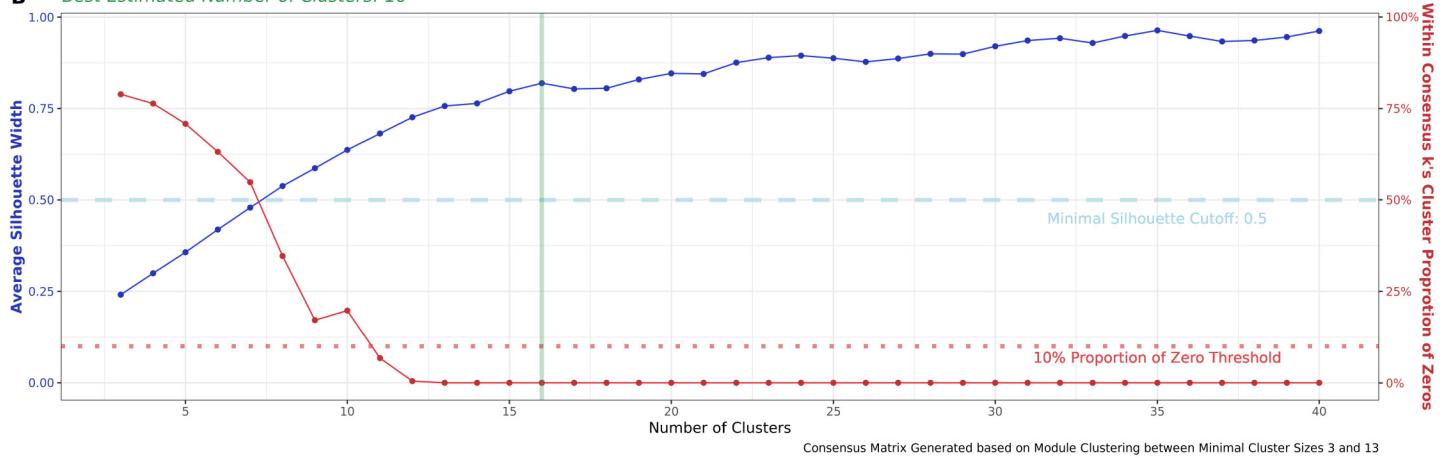
Zeller et al. Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Normal

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: *denovo*; Maximum Minimal # Taxa per Module: 13



B Best Estimated Number of Clusters: 16

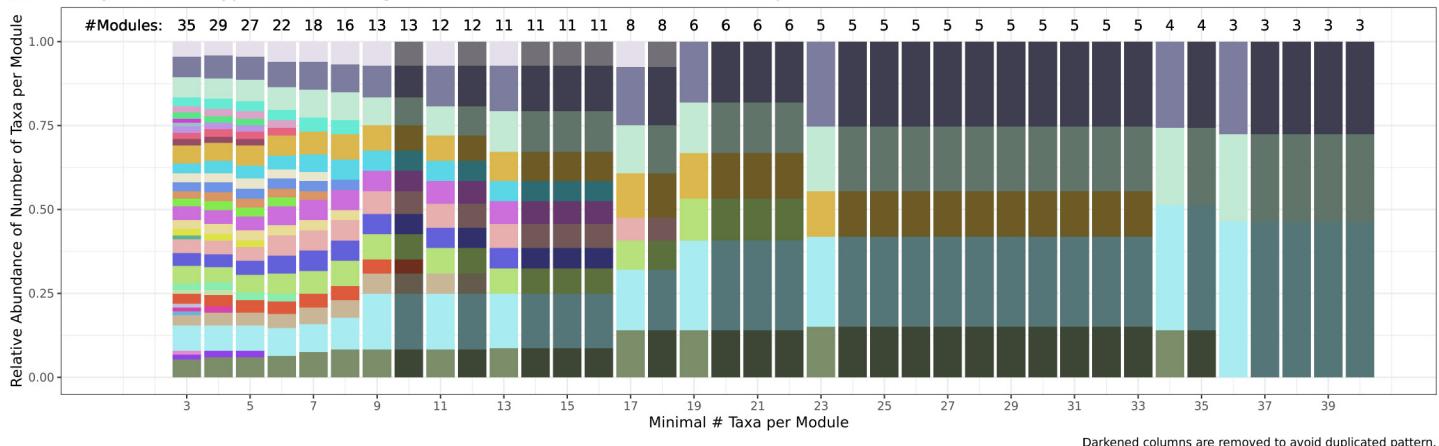


Supplementary Figure 19

Gevers et al. Module Patterns Plot from *de novo* OTUs Assignment Method with Phenotype: Crohn's Disease

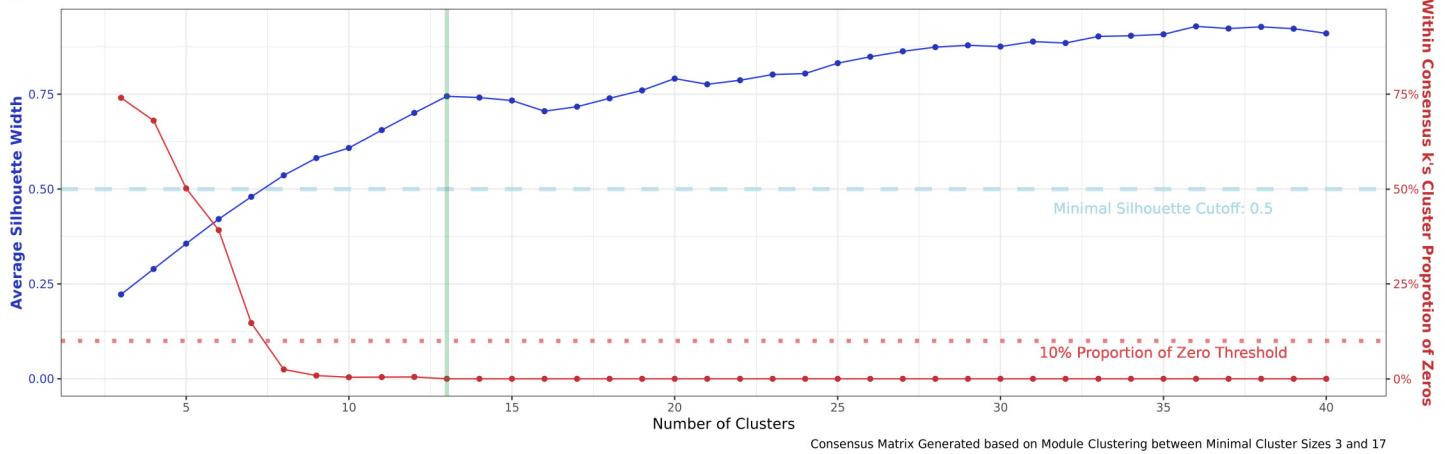
A. Module Patterns are generated based on different minimal module sizes. Darkened columns represent the replicated patterns. **B.** The average silhouette width was calculated for different numbers of clusters with the consensus matrix generated from patterns in A. The unique patterns including all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

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



Darkened columns are removed to avoid duplicated pattern.

B Best Estimated Number of Clusters: 13



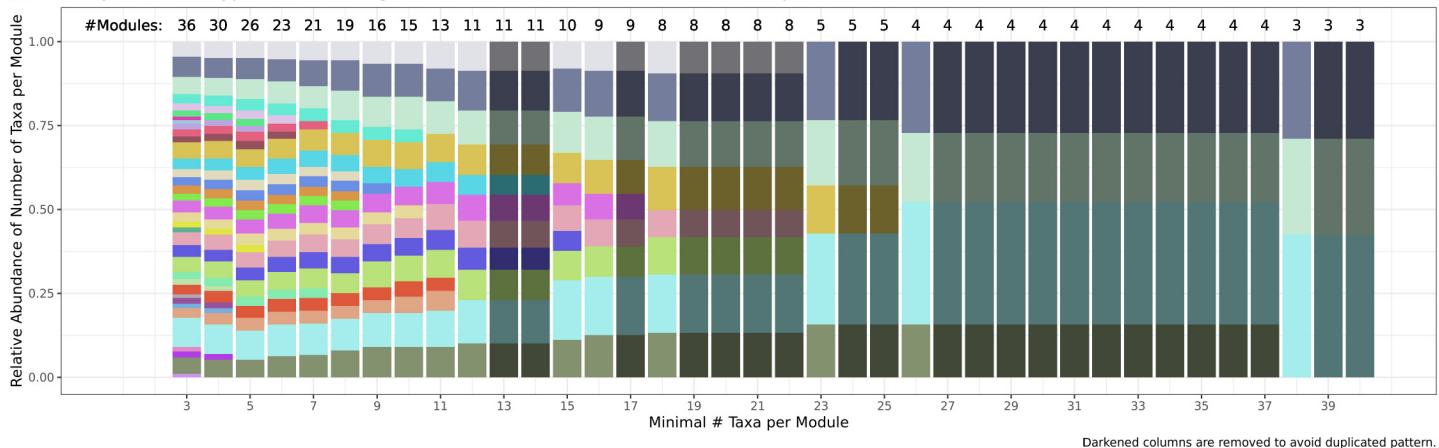
Consensus Matrix Generated based on Module Clustering between Minimal Cluster Sizes 3 and 17

Supplementary Figure 20

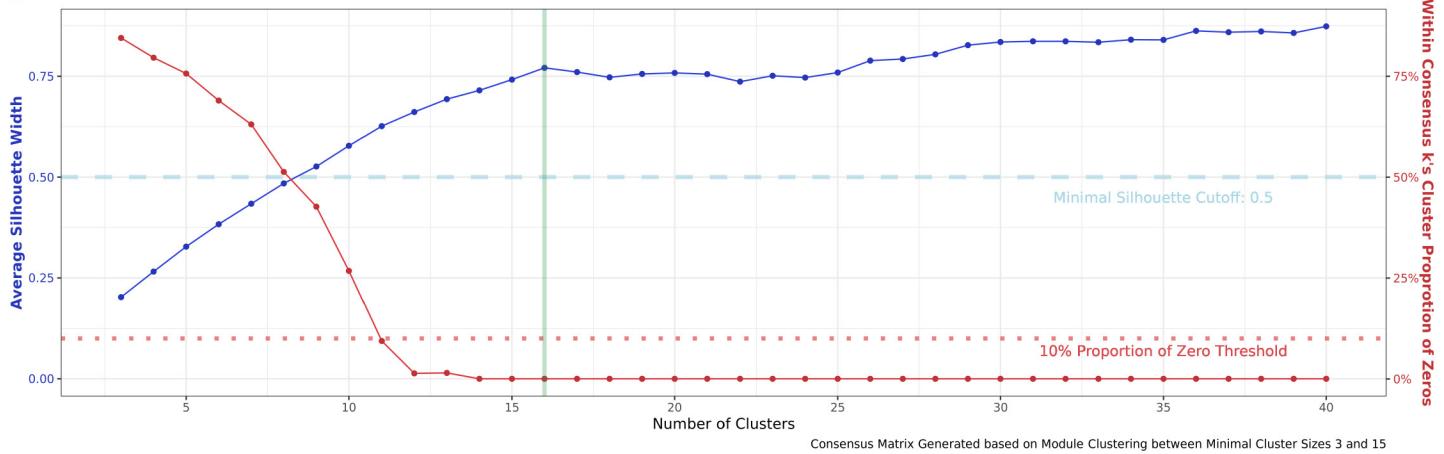
Gevers et al. Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Crohn's Disease

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: denovo; Maximum Minimal # Taxa per Module: 15



B Best Estimated Number of Clusters: 16

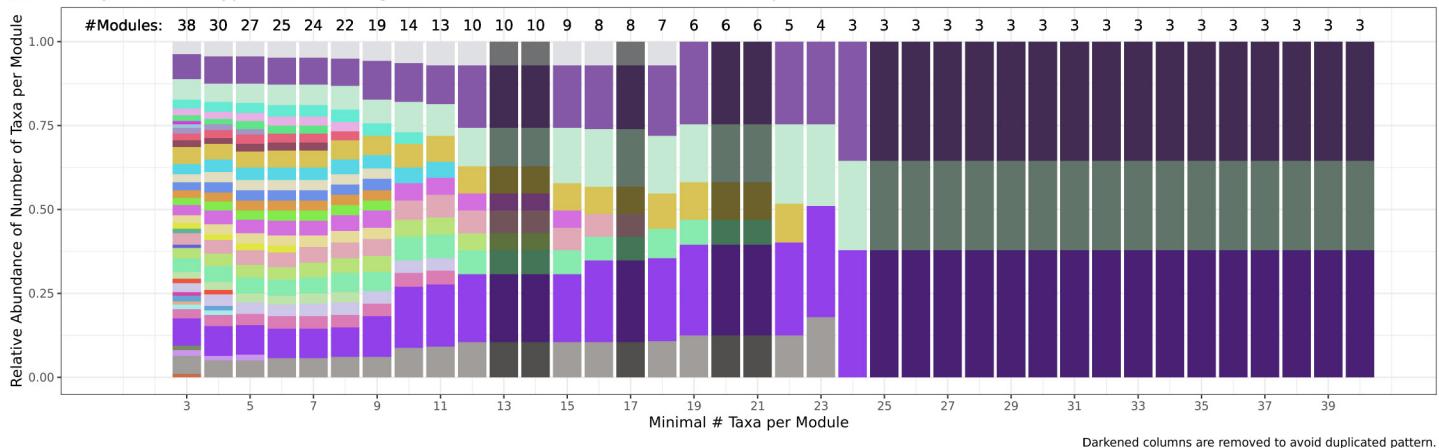


Supplementary Figure 21

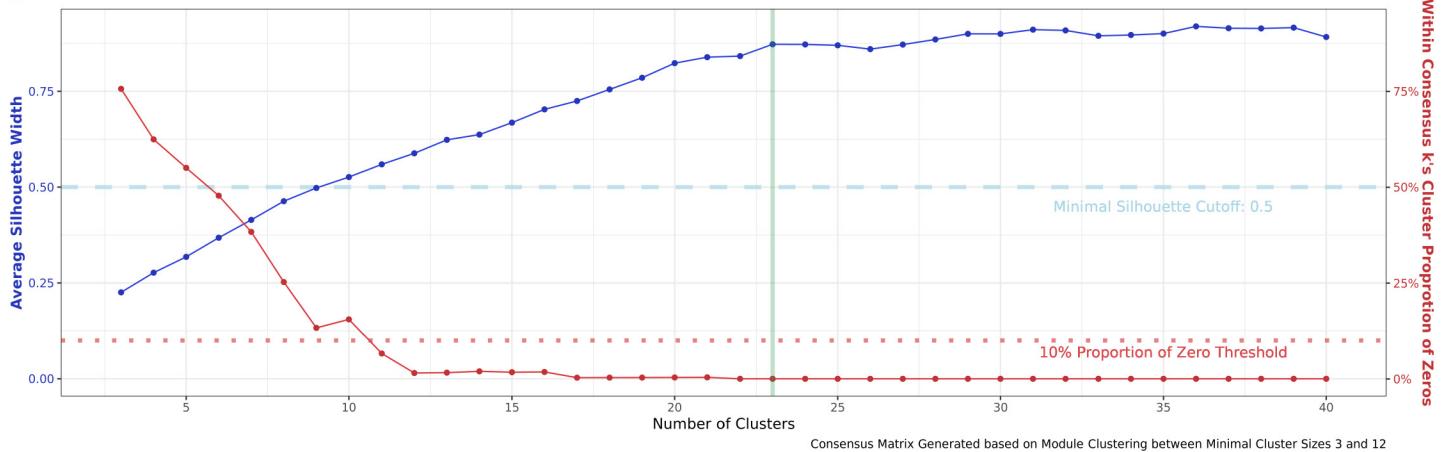
Gevers et al. Module Patterns Plot from *de novo* OTUs Assignment Method with Phenotype: Normal

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: no; Clustering Method: dada2; Maximum Minimal # Taxa per Module: 12



B Best Estimated Number of Clusters: 23

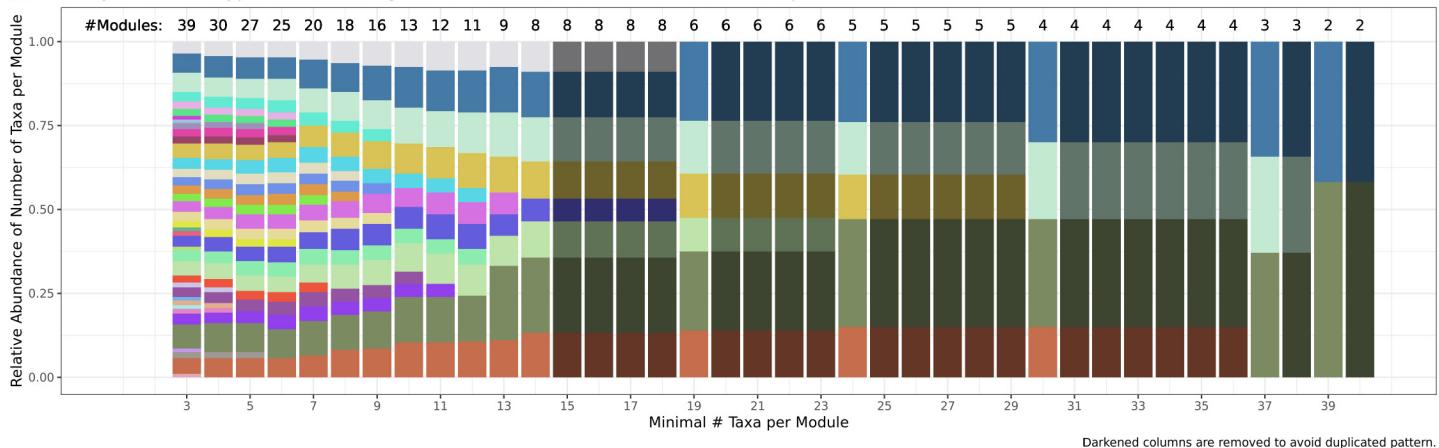


Supplementary Figure 22

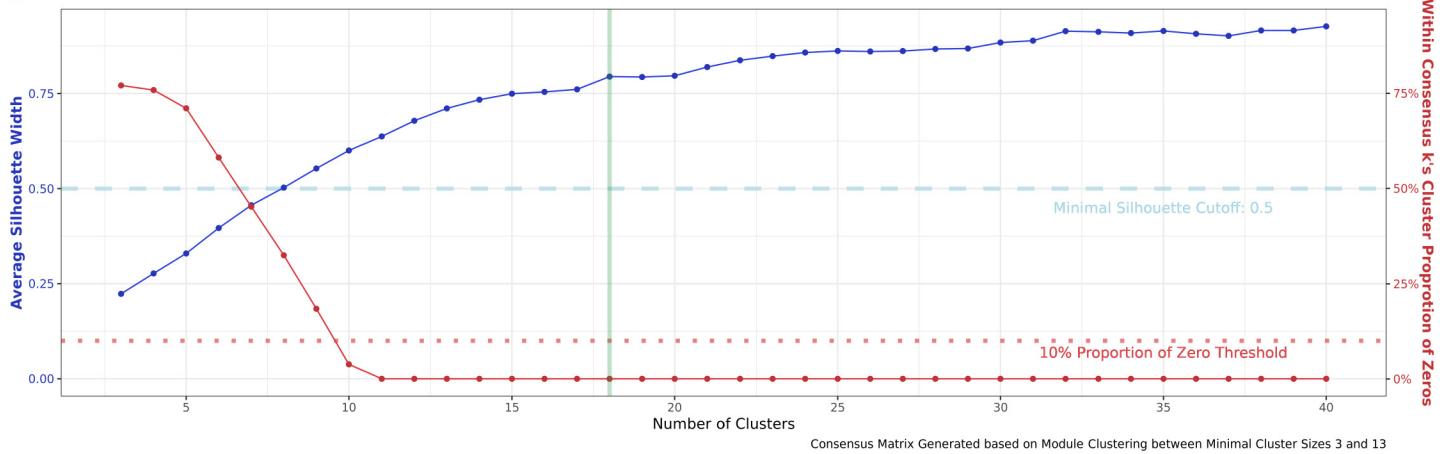
Gevers et al. Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Normal

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.

A Study: IBD; Phenotype: CD; Clustering Method: denovo; Maximum Minimal # Taxa per Module: 13



B Best Estimated Number of Clusters: 18

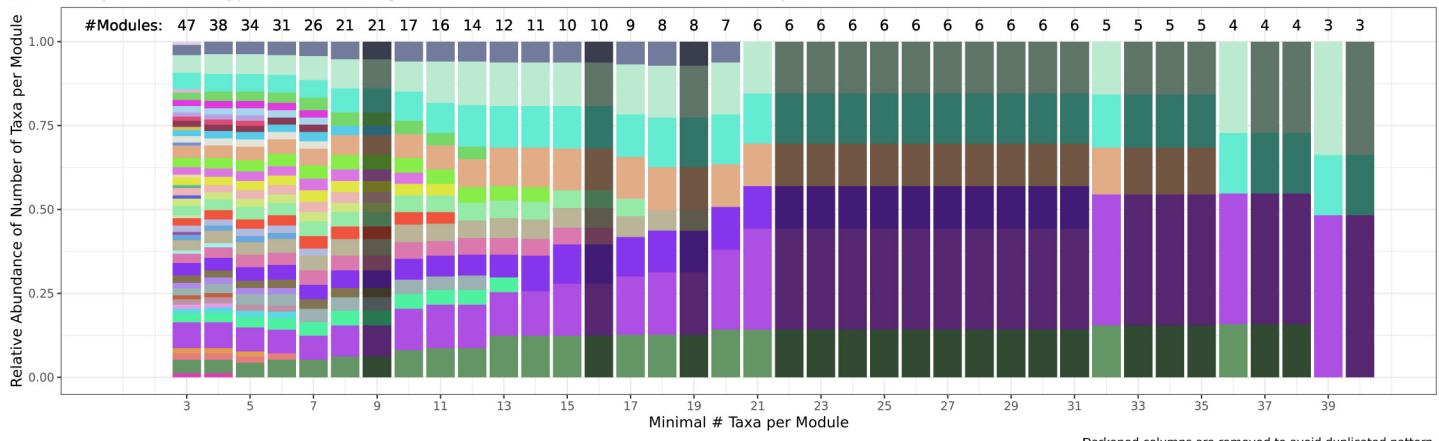


Supplementary Figure 23

IBDMDB Module Patterns Plot from *de novo* OTUs Assignment Method with Phenotype: Crohn's Disease

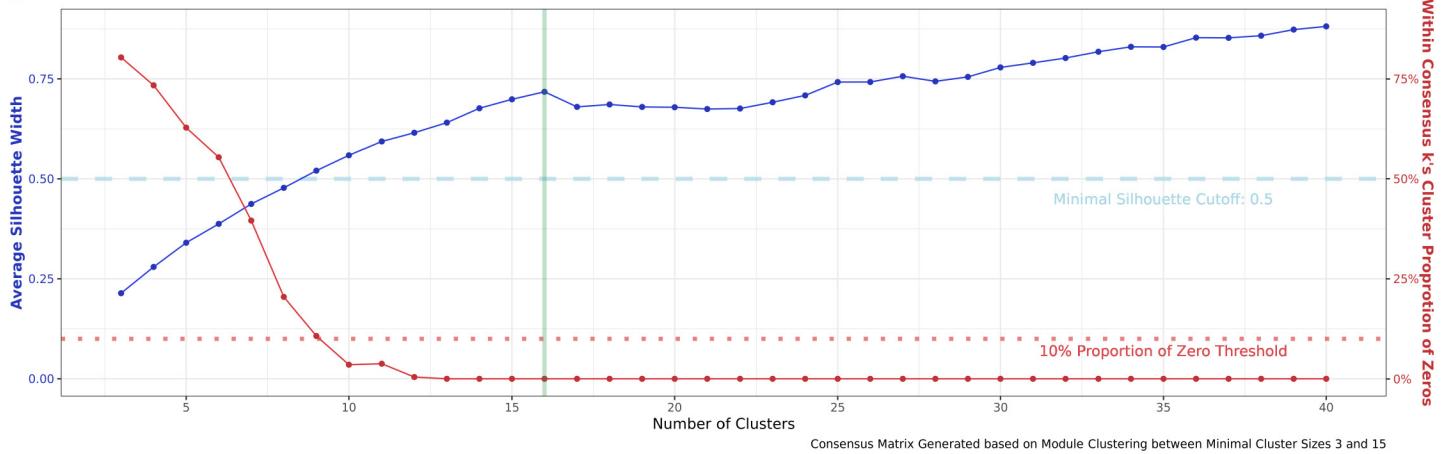
A. Module Patterns are generated based on different minimal module sizes. Darkened columns represent the replicated patterns. **B.** The average silhouette width was calculated for different numbers of clusters with the consensus matrix generated from patterns in A. The unique patterns including all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

A Study: IBD; Phenotype: CD; Clustering Method: dada2; Maximum Minimal # Taxa per Module: 15



Darkened columns are removed to avoid duplicated pattern.

B Best Estimated Number of Clusters: 16

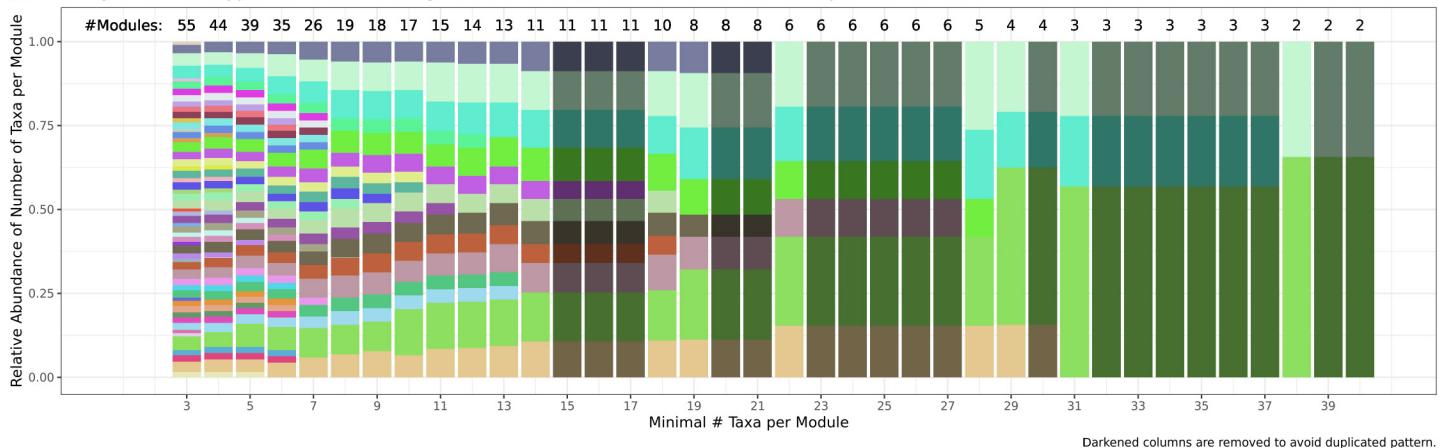


Supplementary Figure 24

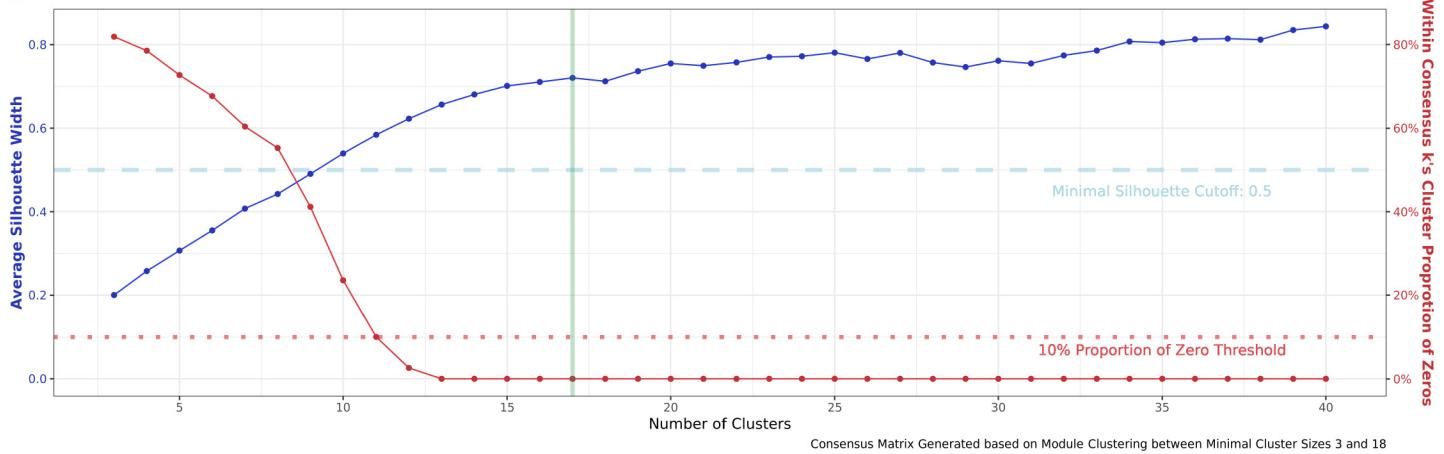
IBDMDB Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Crohn's Disease

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.

A Study: IBD; Phenotype: nonIBD; Clustering Method: denovo; Maximum Minimal # Taxa per Module: 18



B Best Estimated Number of Clusters: 17

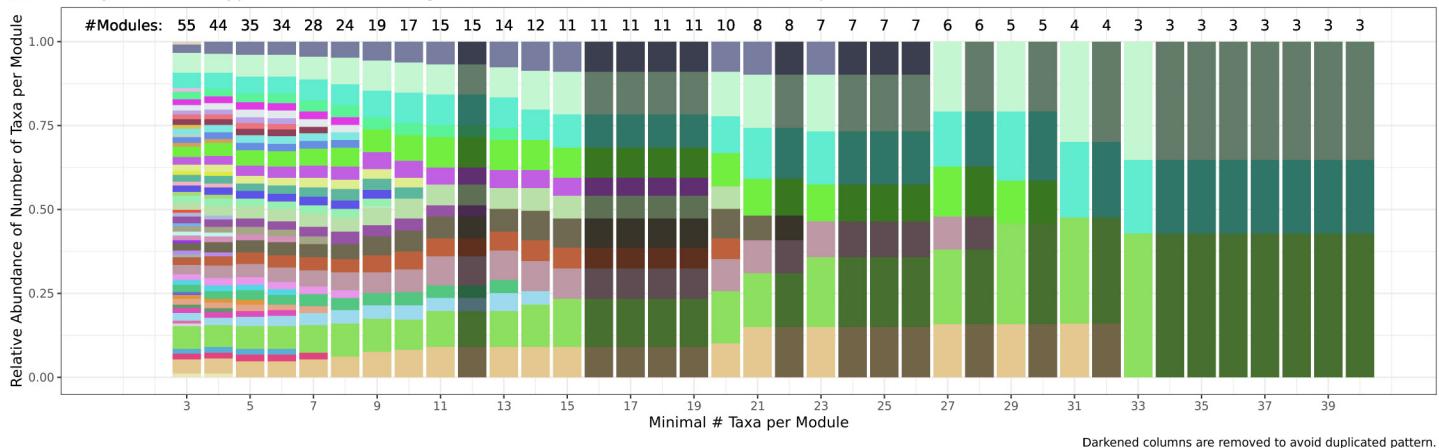


Supplementary Figure 25

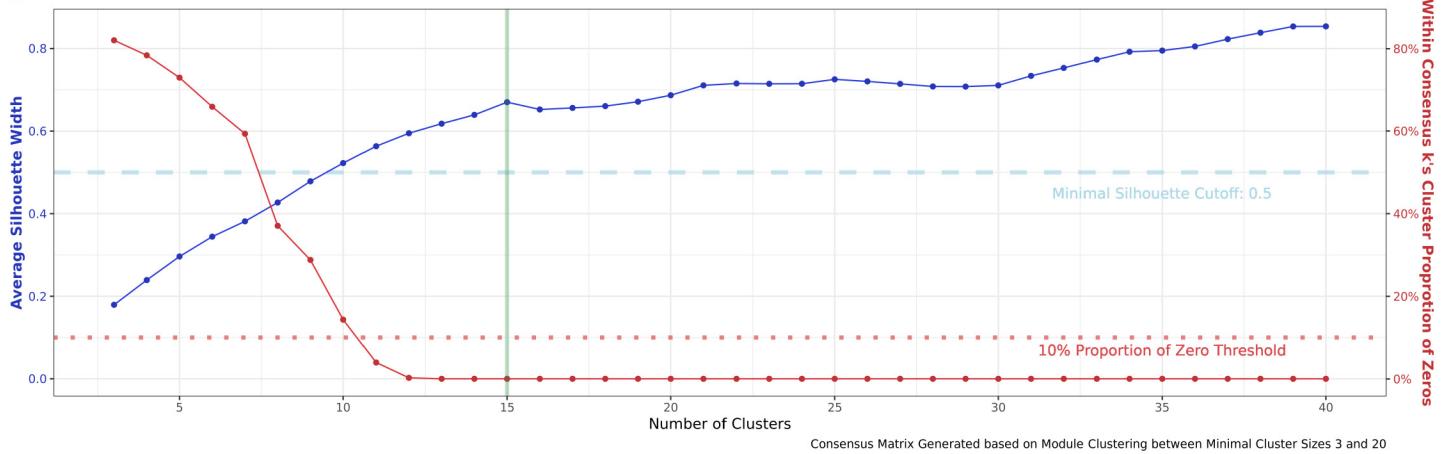
IBDMDB Module Patterns Plot from *de novo* OTUs Assignment Method with Phenotype: Normal

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: IBD; Phenotype: nonIBD; Clustering Method: dada2; Maximum Minimal # Taxa per Module: 20



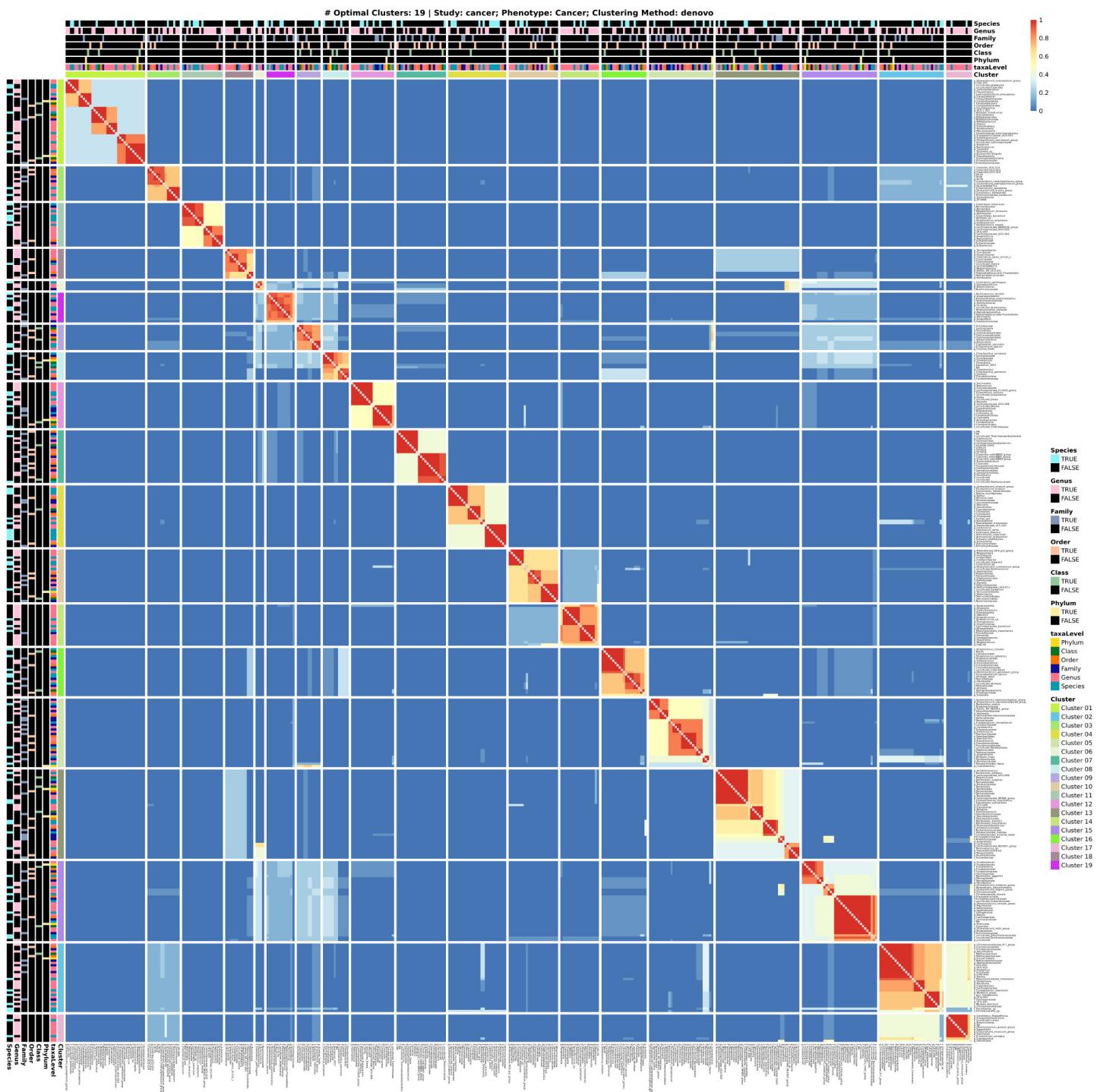
B Best Estimated Number of Clusters: 15



Supplementary Figure 26

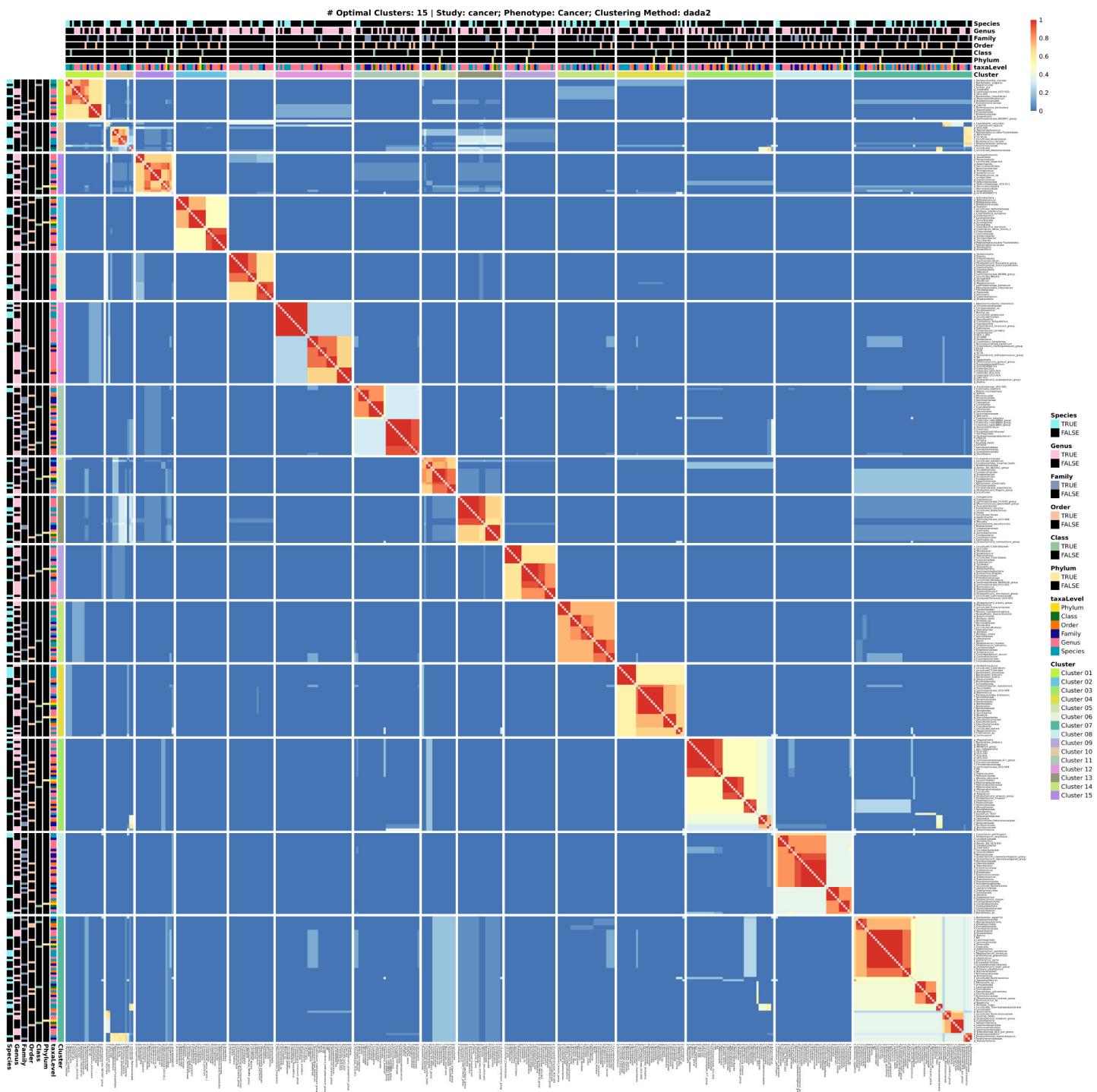
IBDMDB Module Patterns Plot from DADA2 ASVs Assignment Method with Phenotype: Normal

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.



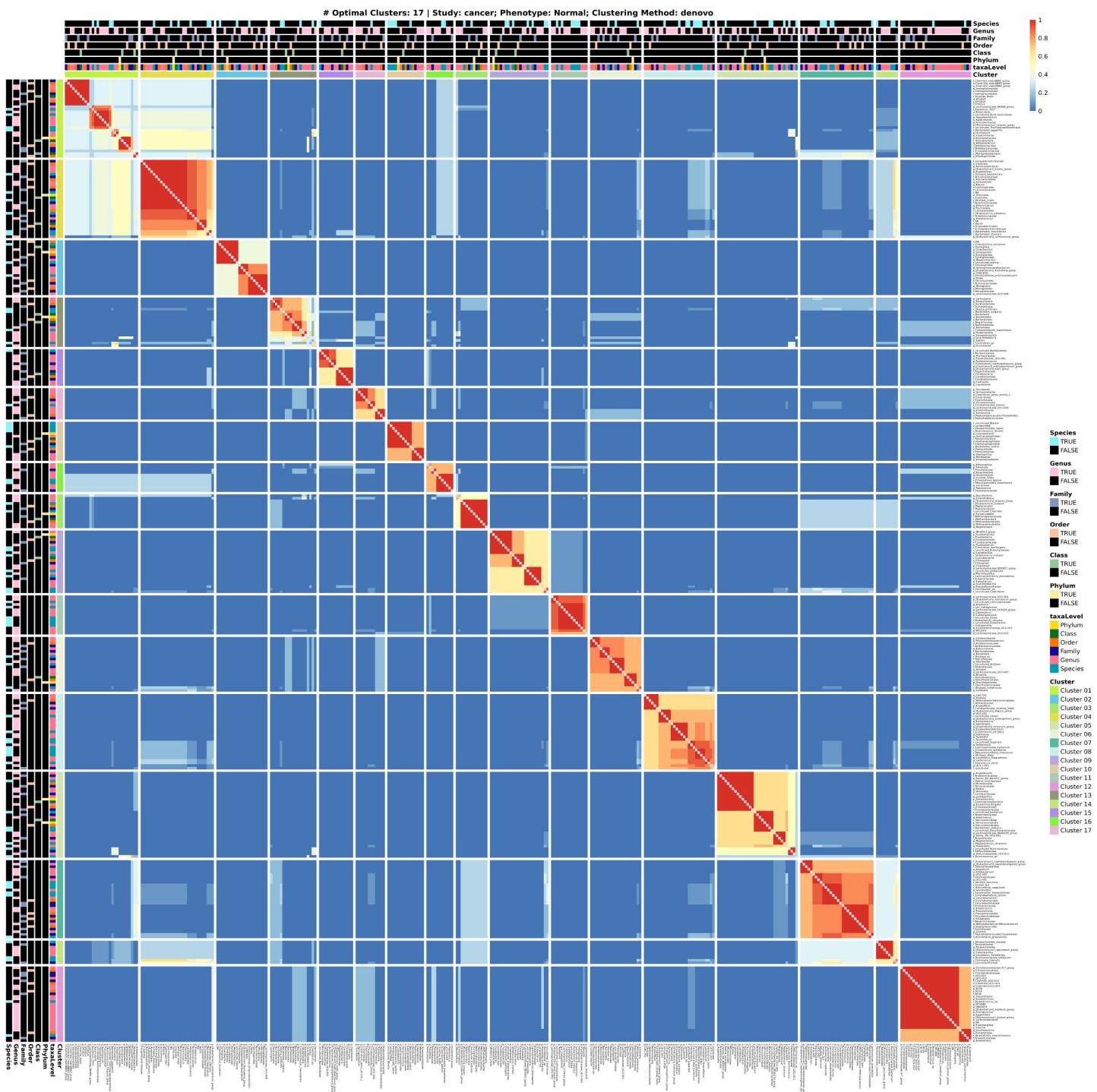
Supplementary Figure 27

Baxter et al. Consensus Plot from *de novo* OTUs Assignment Method with Phenotype: Cancer
Consensus plot based on the best estimated number of clusters obtained.



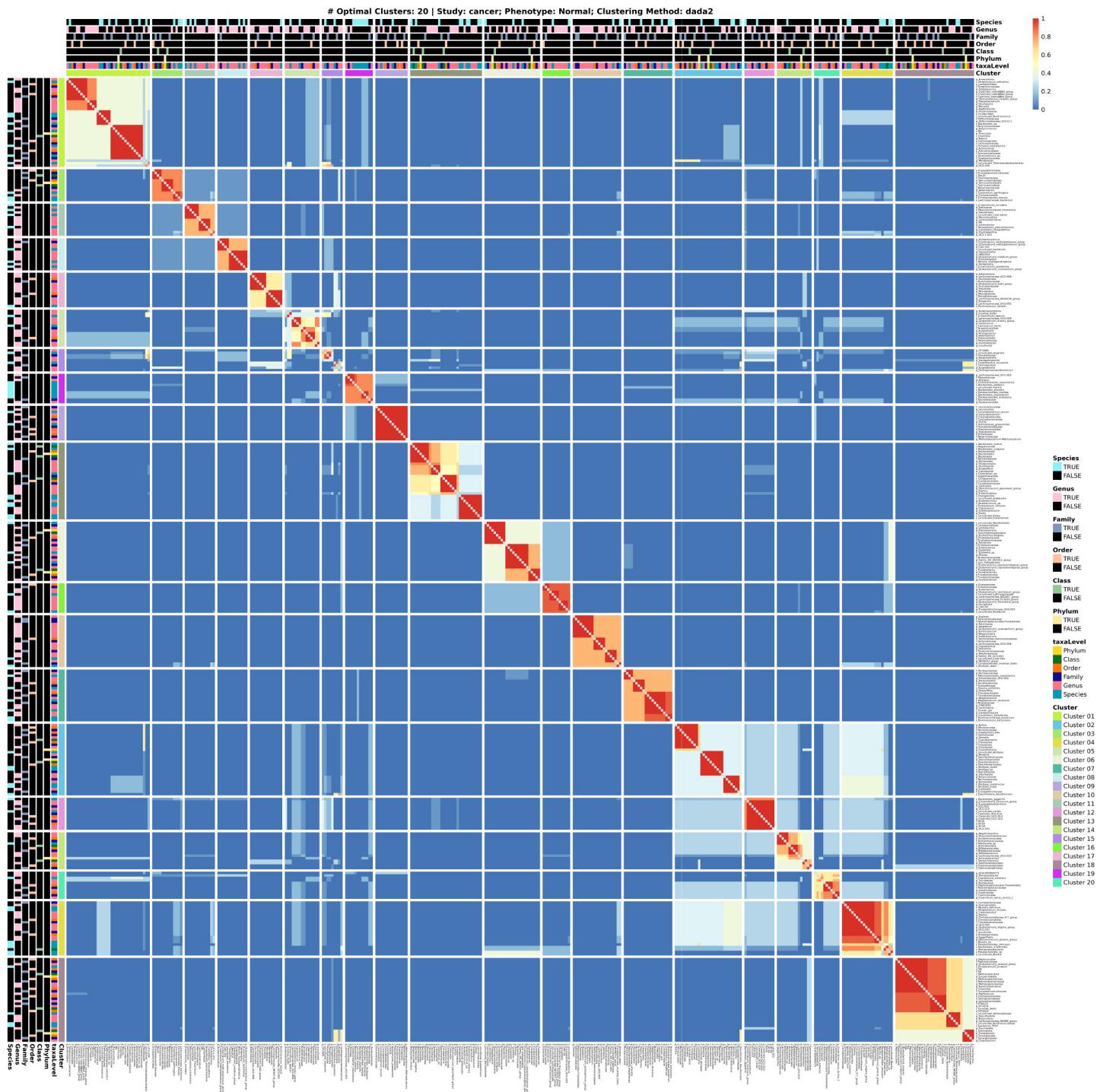
Supplementary Figure 28

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



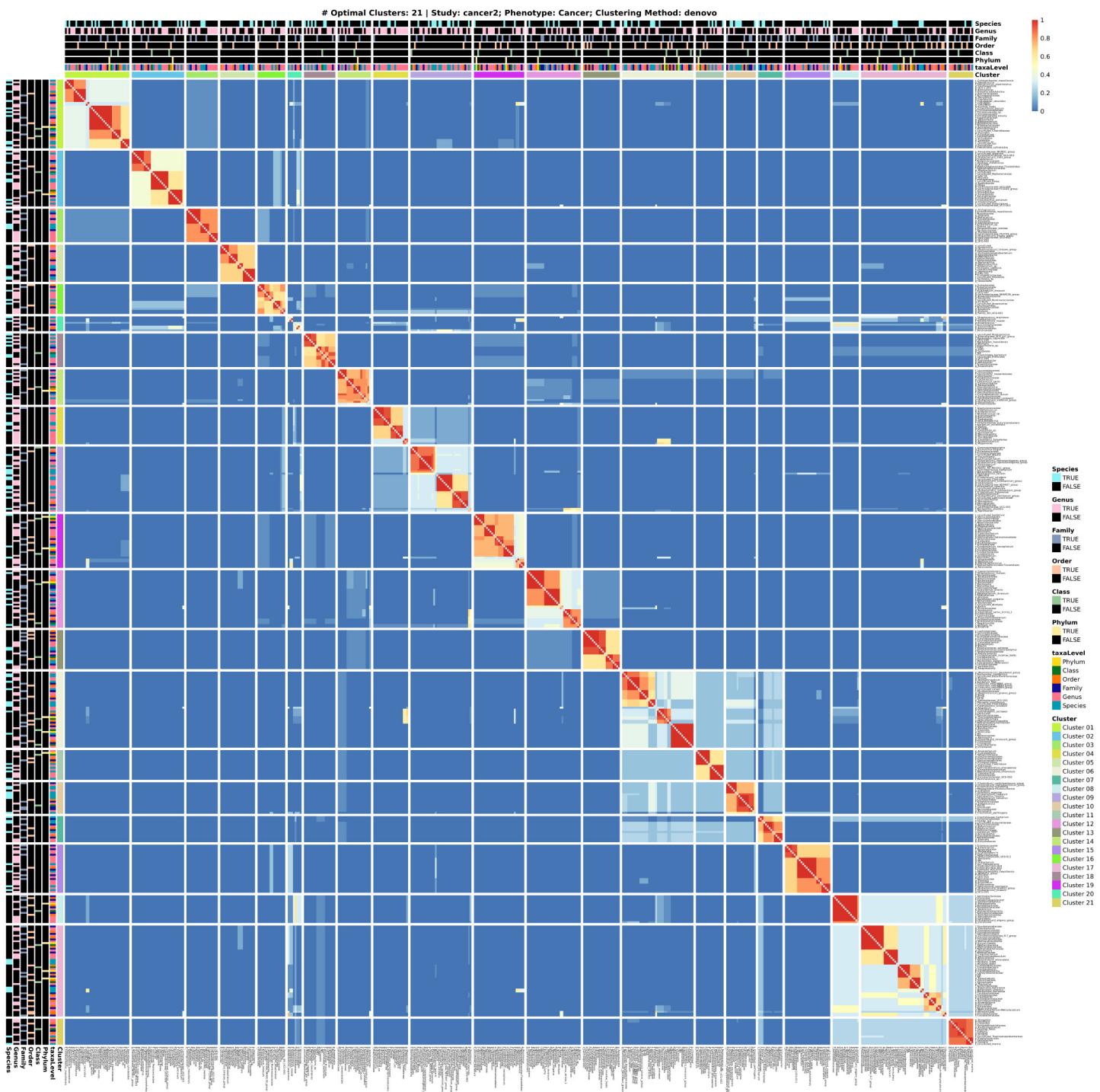
Supplementary Figure 29

Baxter et al. Consensus Plot from *de novo* OTUs Assignment Method with Phenotype: Normal
Consensus plot based on the best estimated number of clusters obtained.



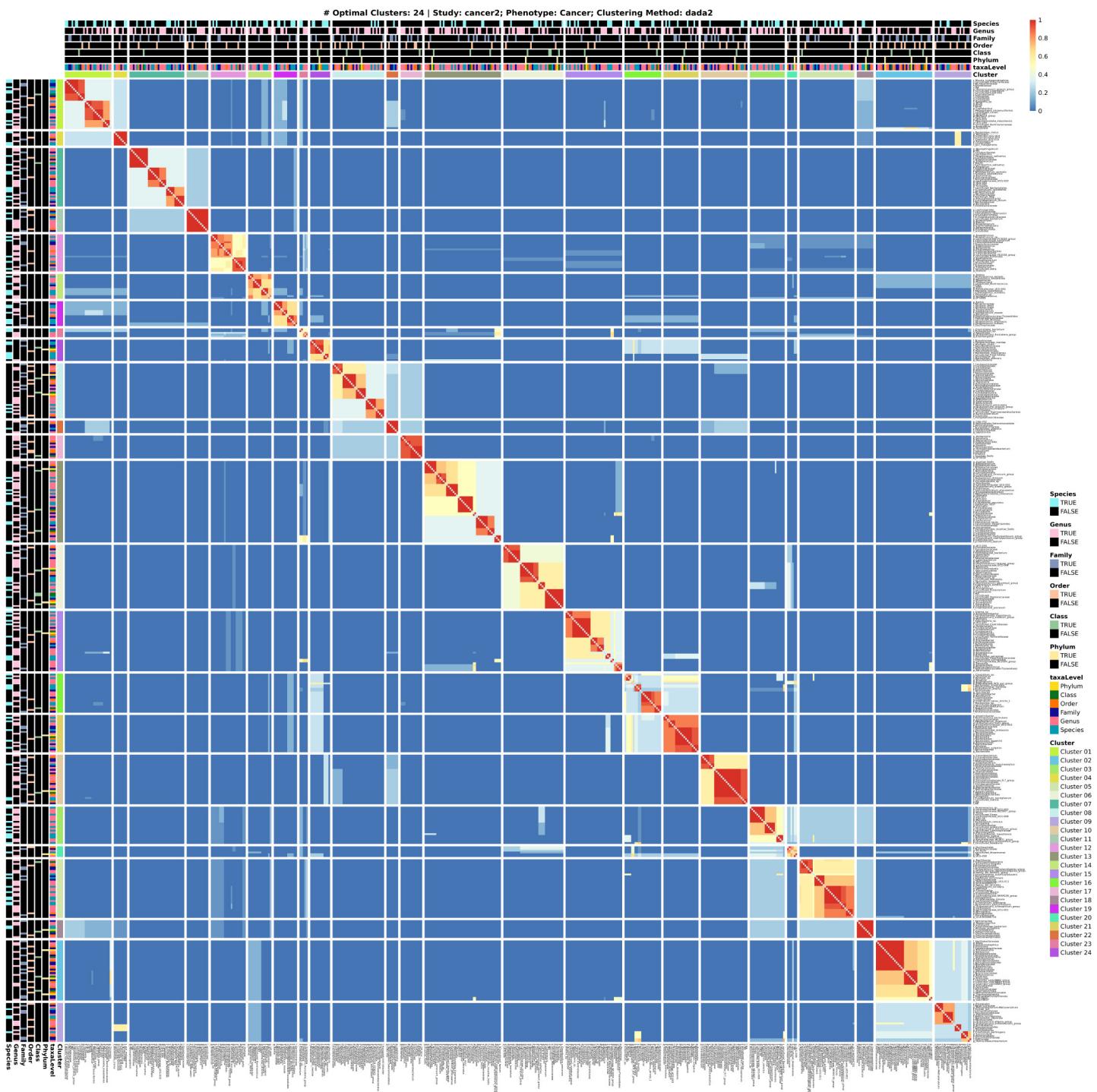
Supplementary Figure 30

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



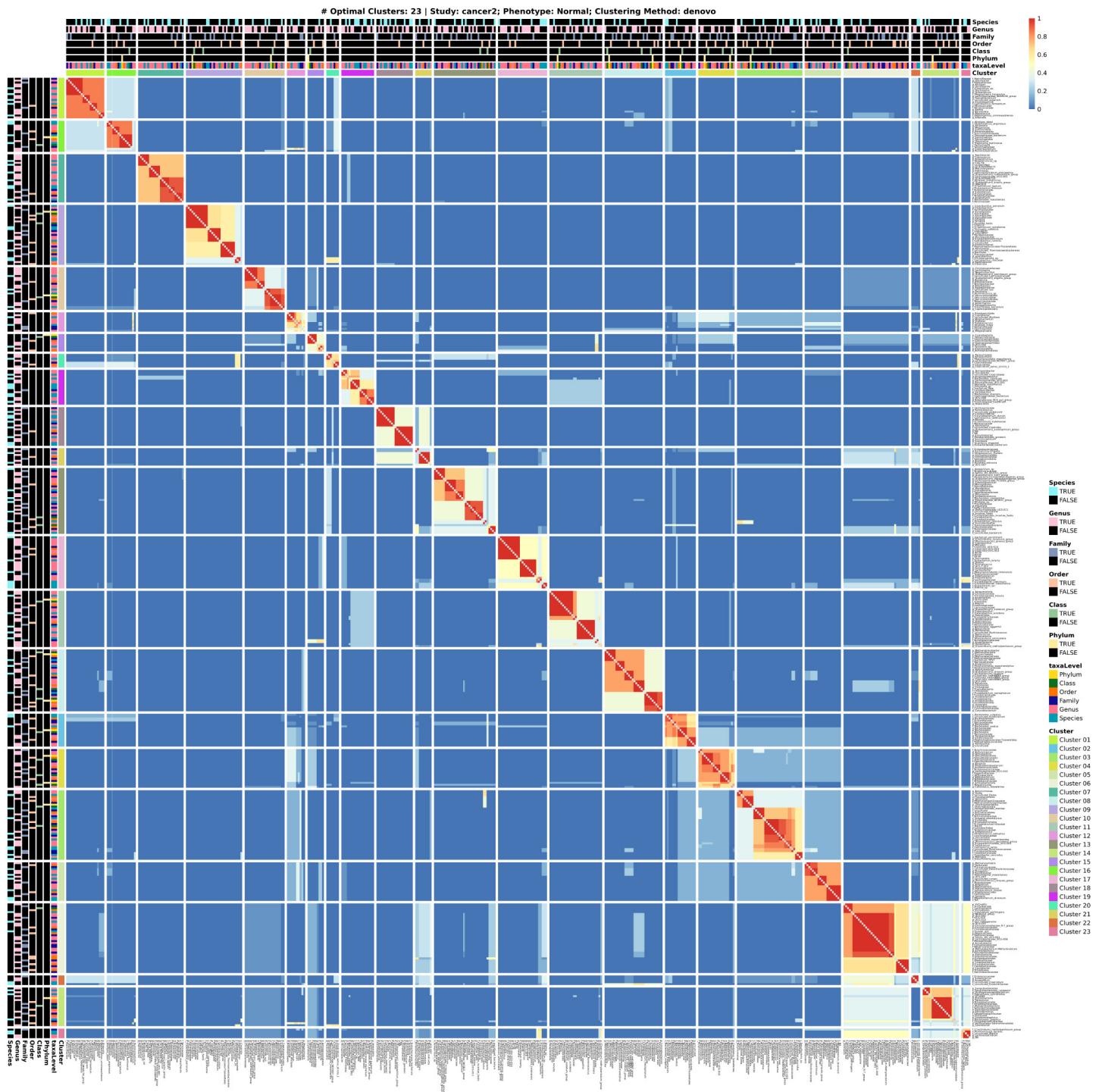
Supplementary Figure 31

Zeller et al. Consensus Plot from *de novo* OTUs Assignment Method with Phenotype: Cancer
Consensus plot based on the best estimated number of clusters obtained.



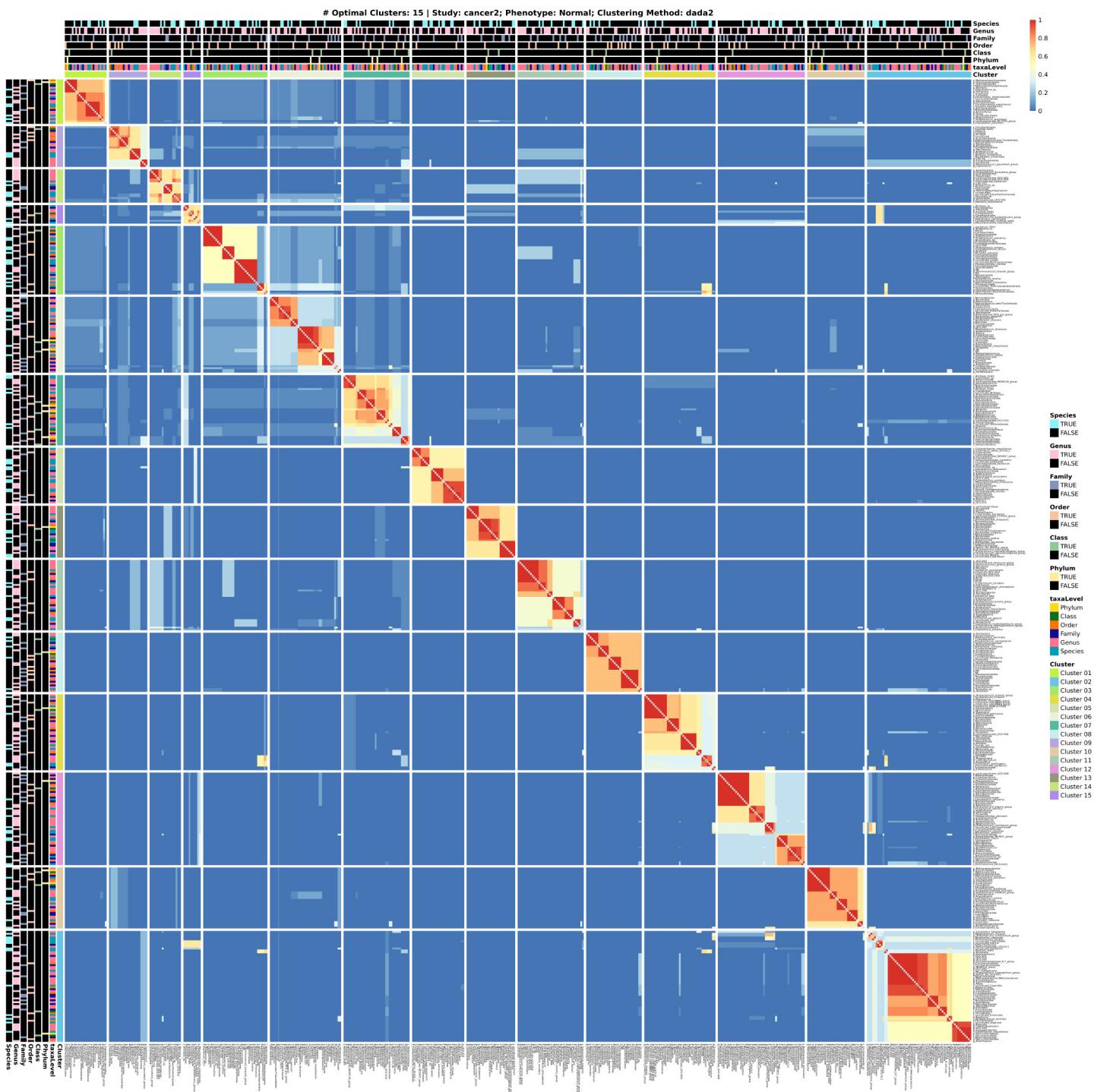
Supplementary Figure 32

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



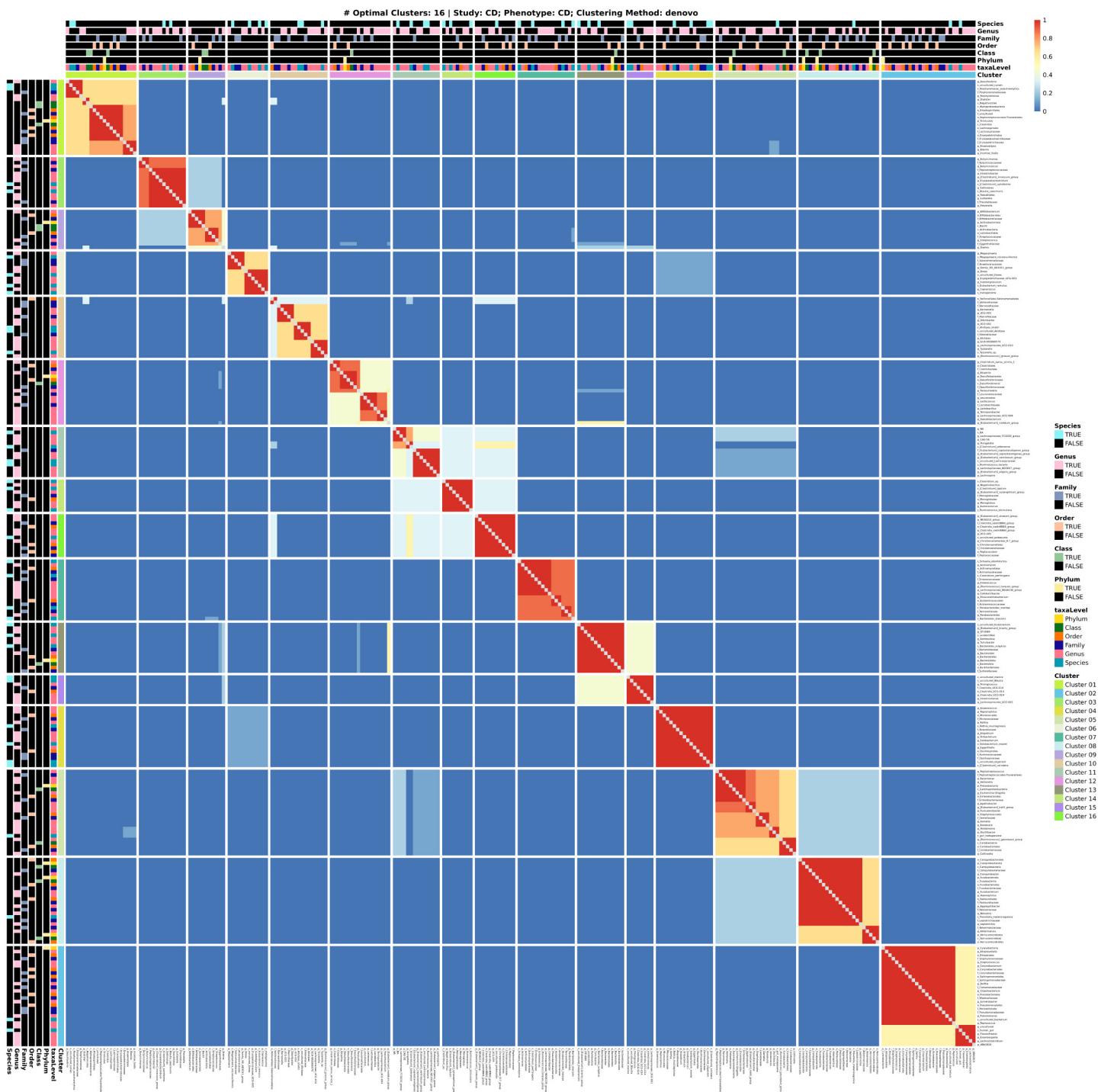
Supplementary Figure 33

Zeller et al. Consensus Plot from *de novo* OTUs Assignment Method with Phenotype: Normal
Consensus plot based on the best estimated number of clusters obtained.



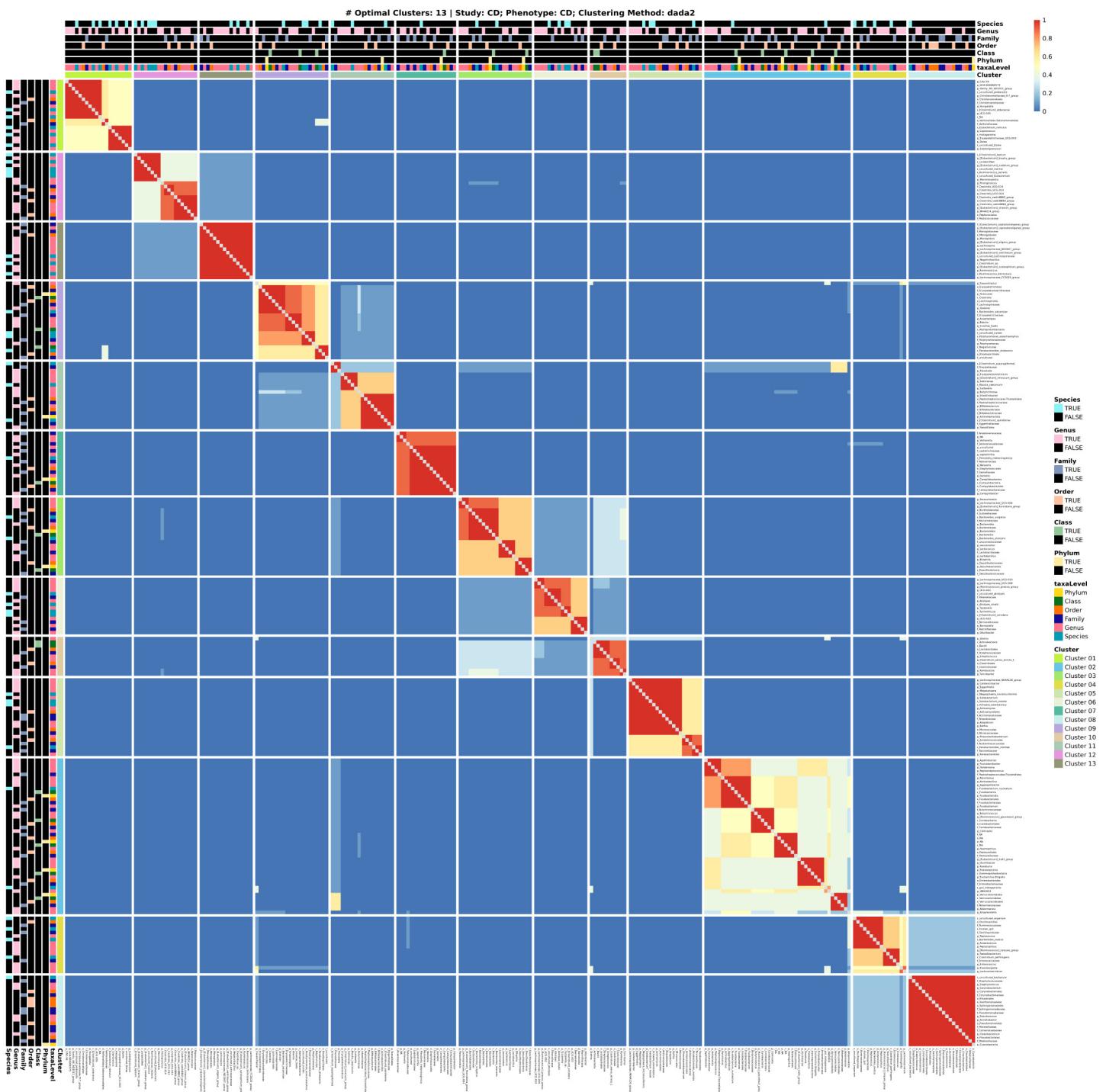
Supplementary Figure 34

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



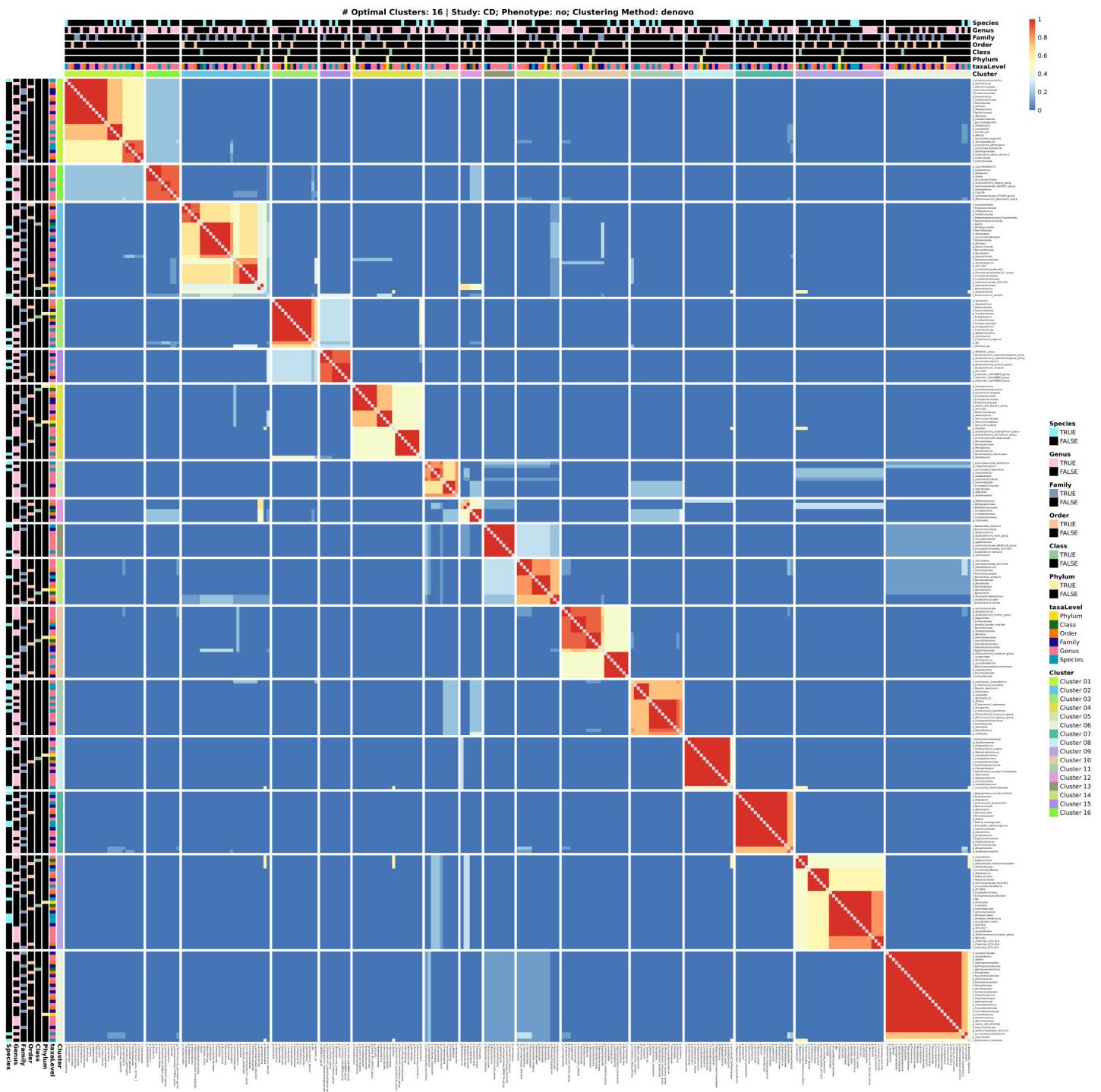
Supplementary Figure 35

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



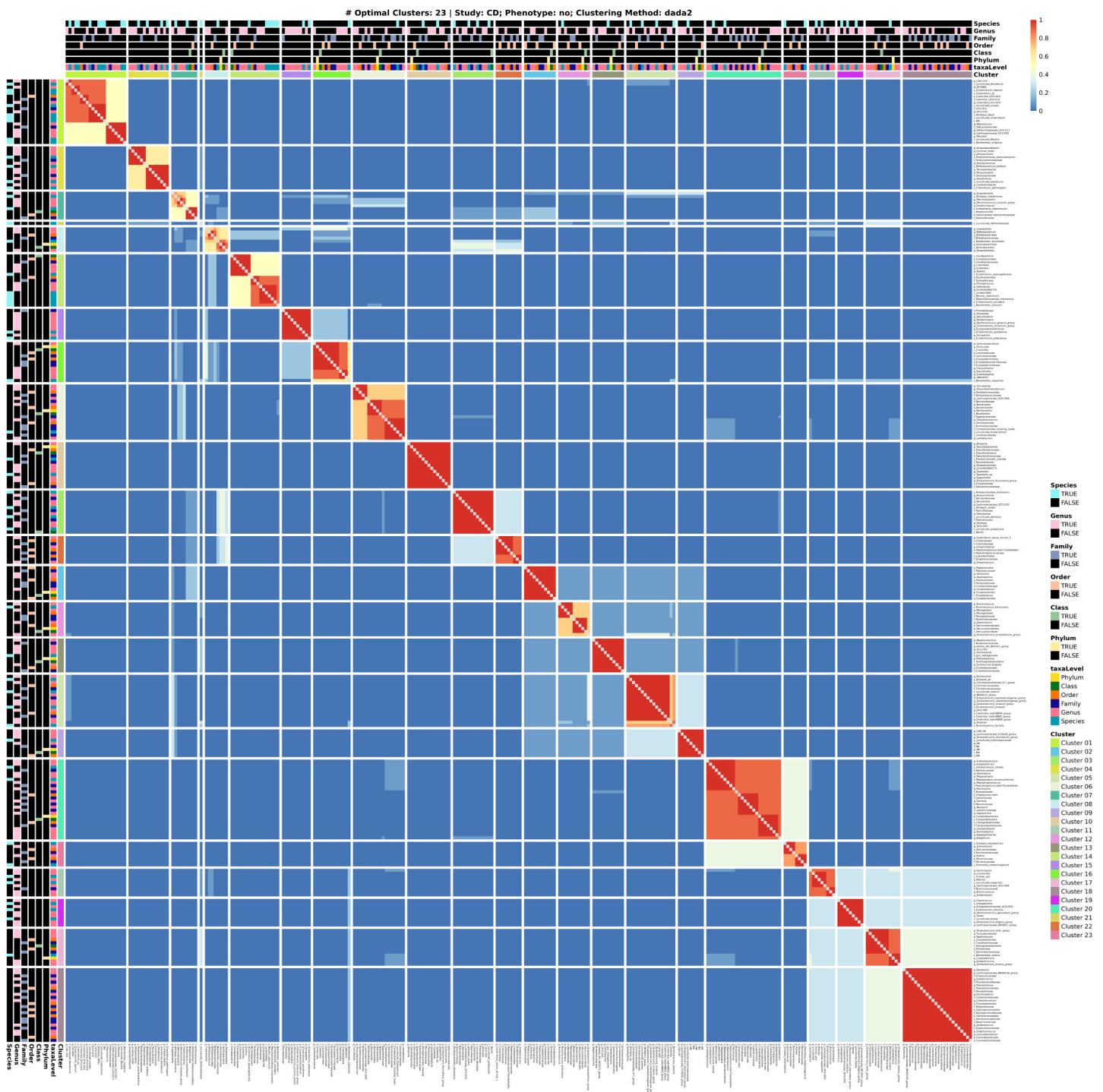
Supplementary Figure 36

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.



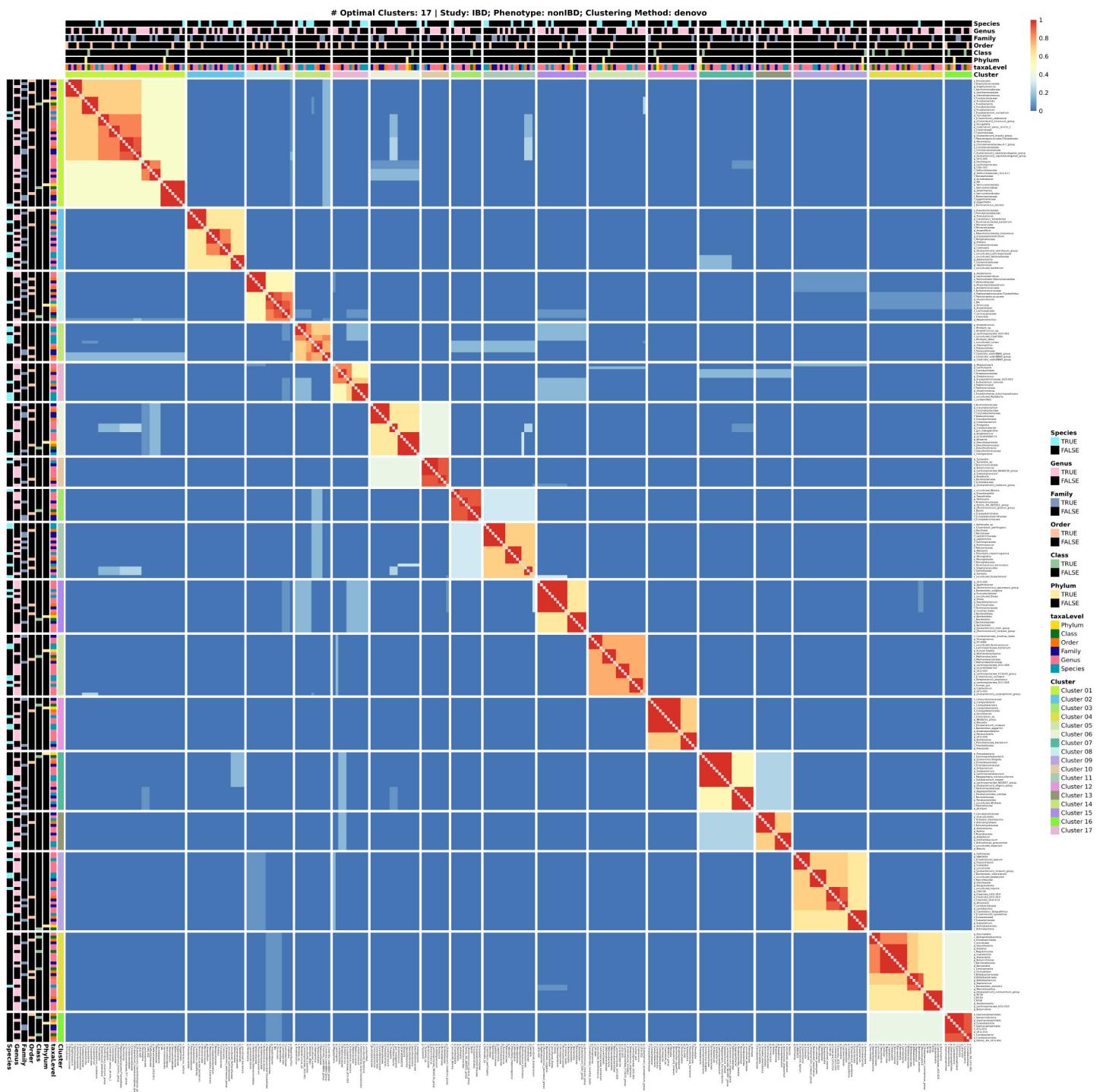
Supplementary Figure 37

Gevens et al. Consensus Plot from *de novo* OTUs Assignment Method with Phenotype: Normal
Consensus plot based on the best estimated number of clusters obtained.



Supplementary Figure 38

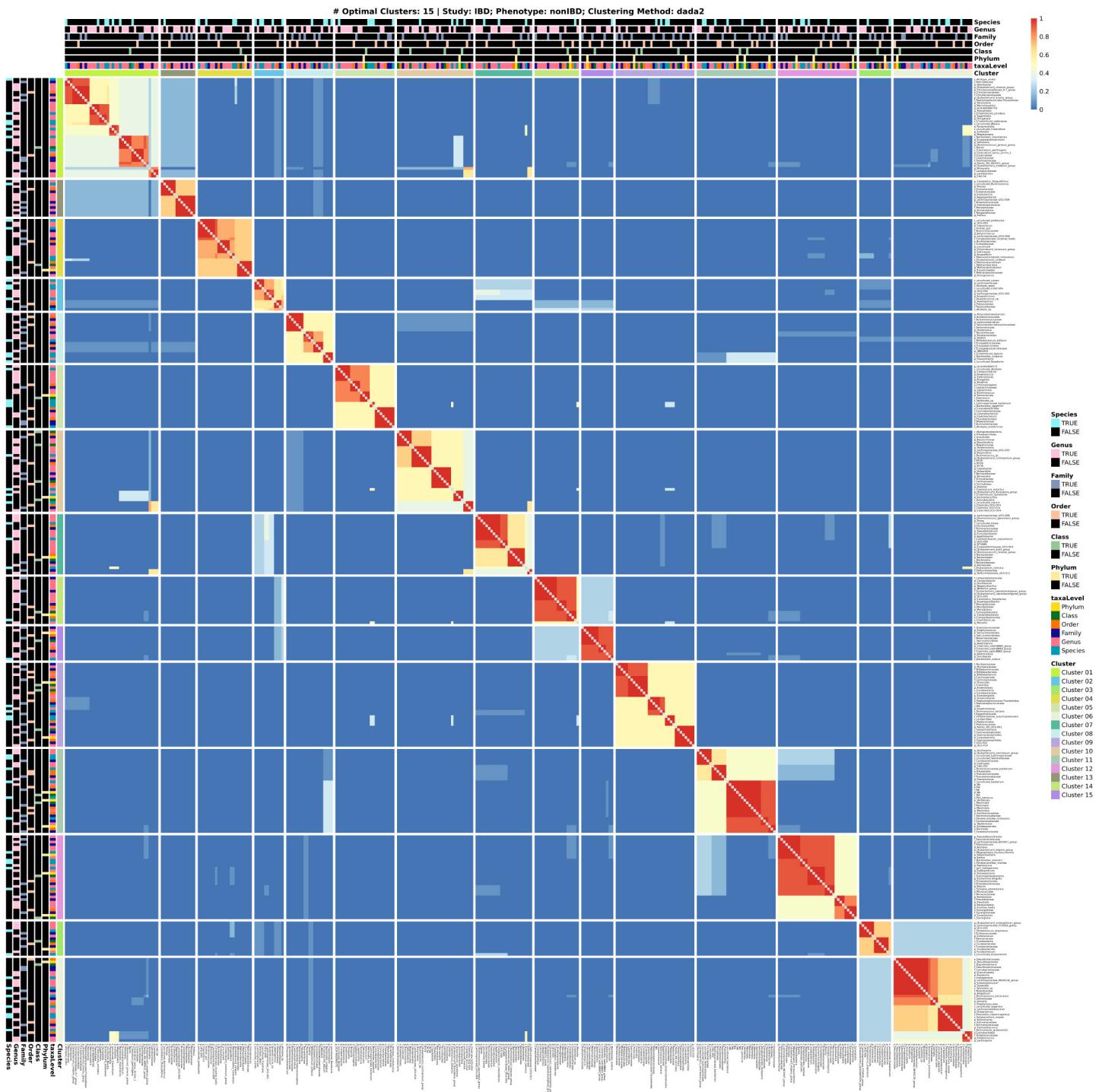
Gevers et al. Consensus Plot from DADA2 ASVs Assignment Method with Phenotype: Normal
Consensus plot based on the best estimated number of clusters obtained.



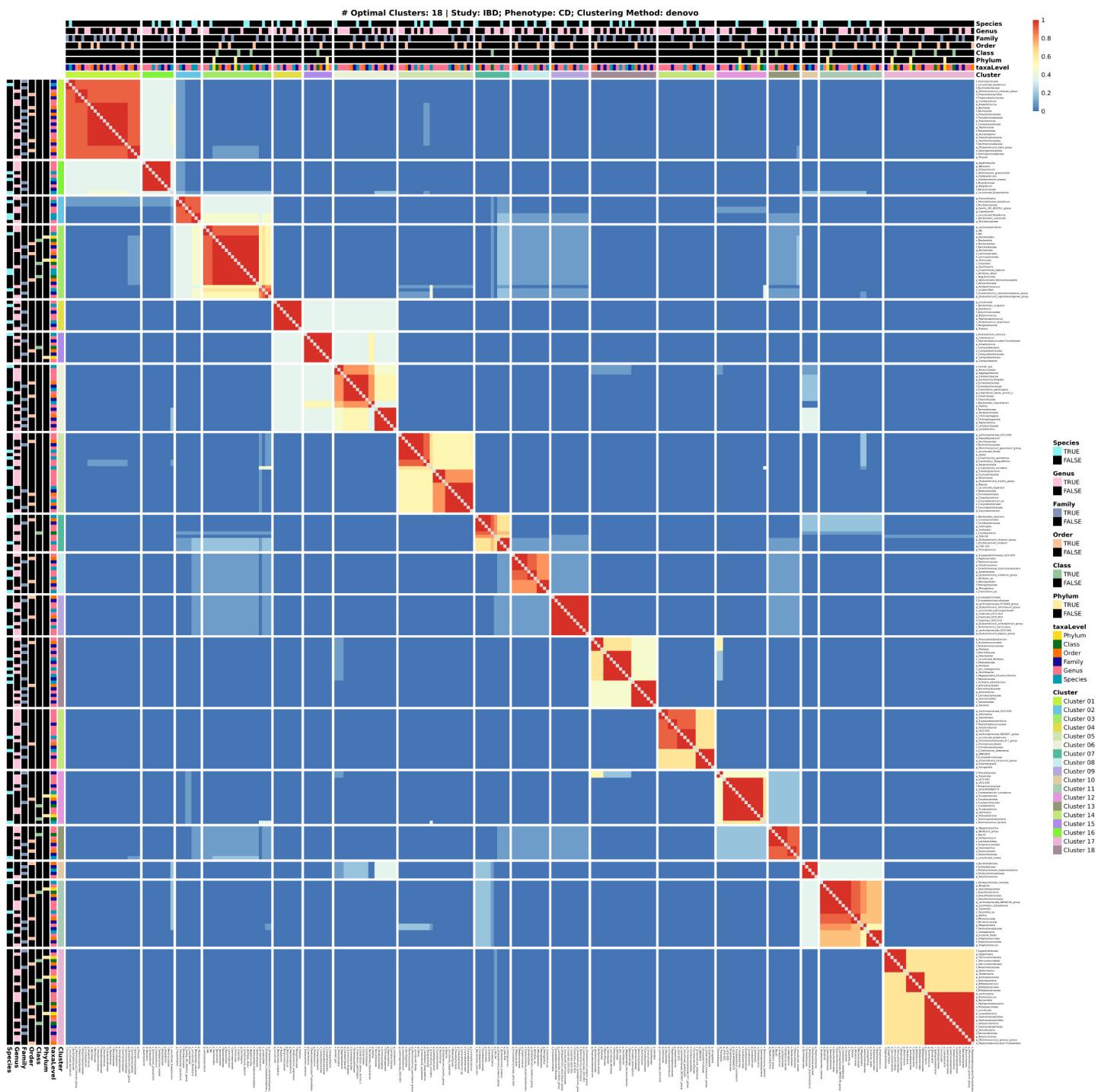
Supplementary Figure 39

IBDMDB Consensus Plot from *de novo* OTUs Assignment Method with Phenotype: Crohn's Disease

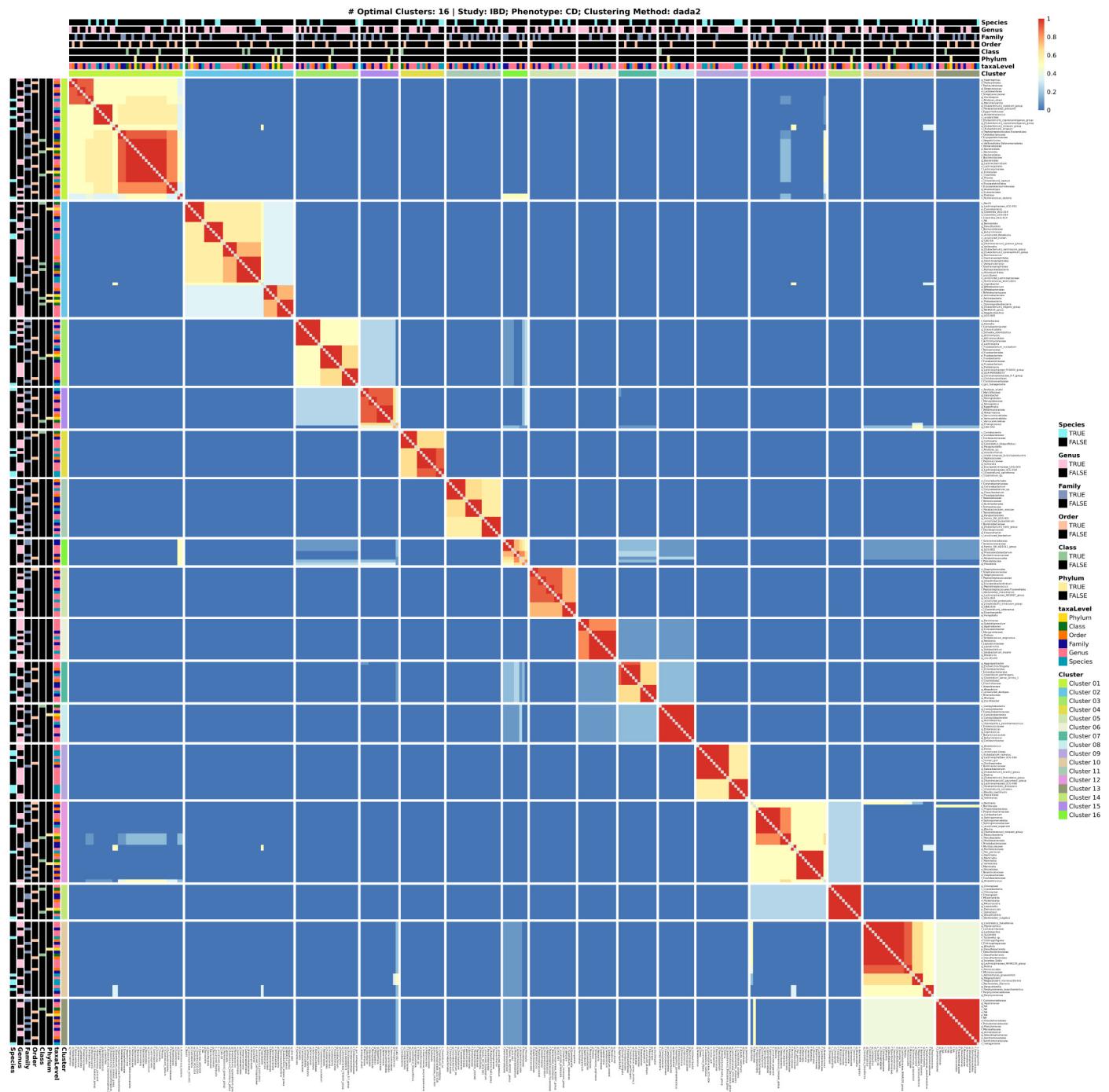
Consensus plot based on the best estimated number of clusters obtained.



Supplementary Figure 40
IBDMDB Consensus Plot from DADA2 ASVs Assignment Method with Phenotype: Crohn's Disease
Consensus plot based on the best estimated number of clusters obtained.

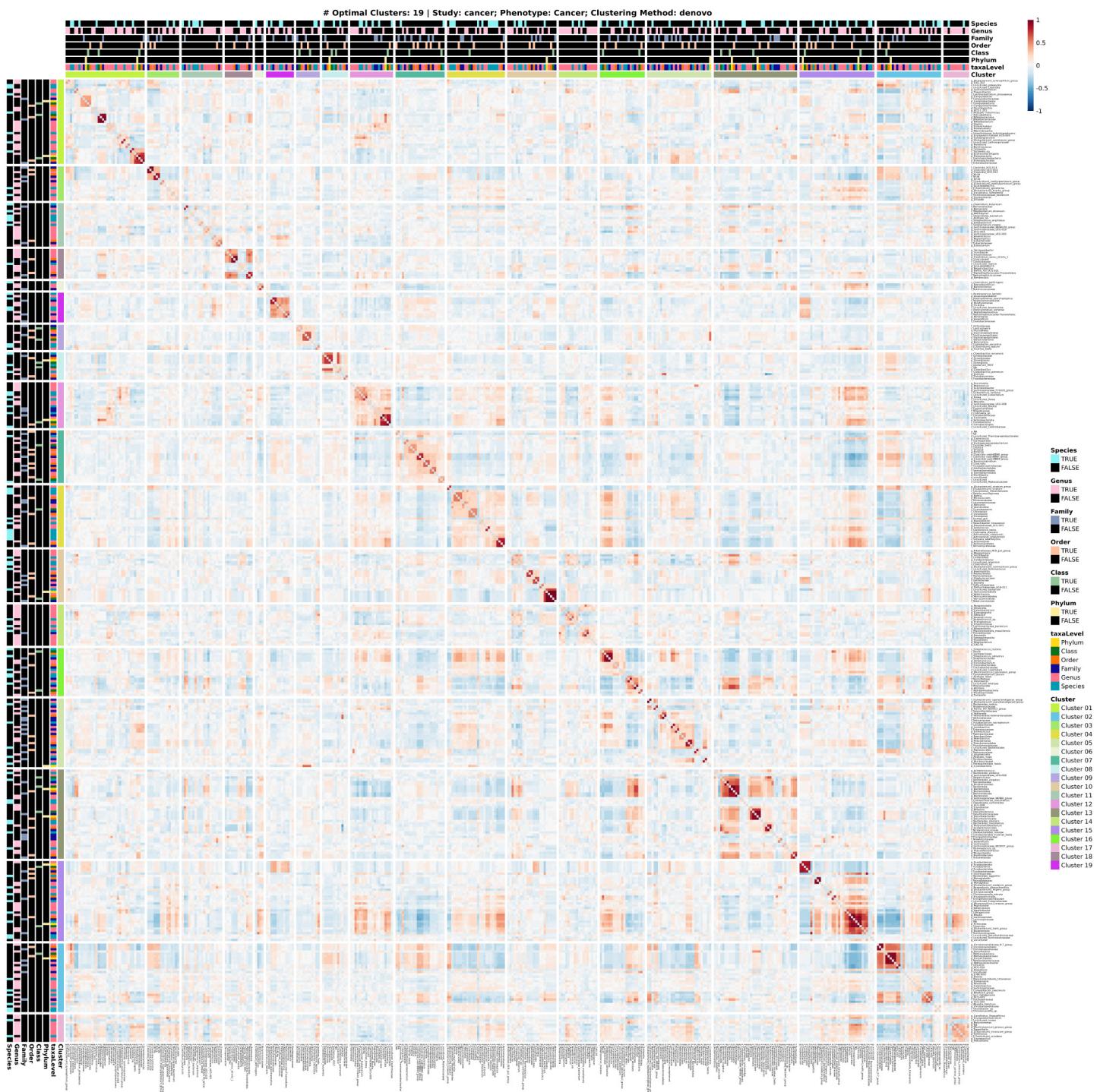


Supplementary Figure 41
IBDMDB Consensus Plot from *de novo* OTUs Assignment Method with Phenotype: Normal
Consensus plot based on the best estimated number of clusters obtained.



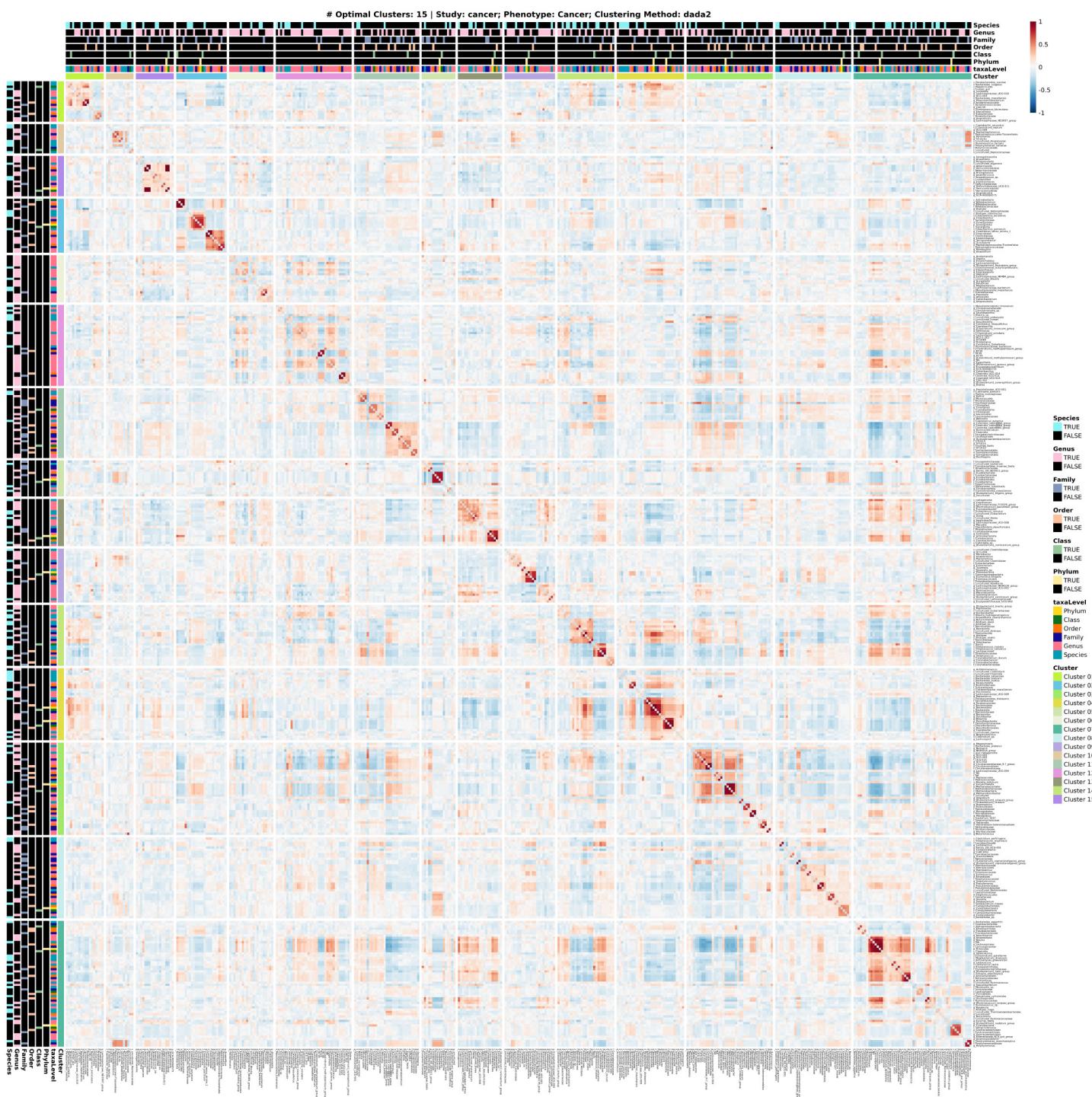
Supplementary Figure 42

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



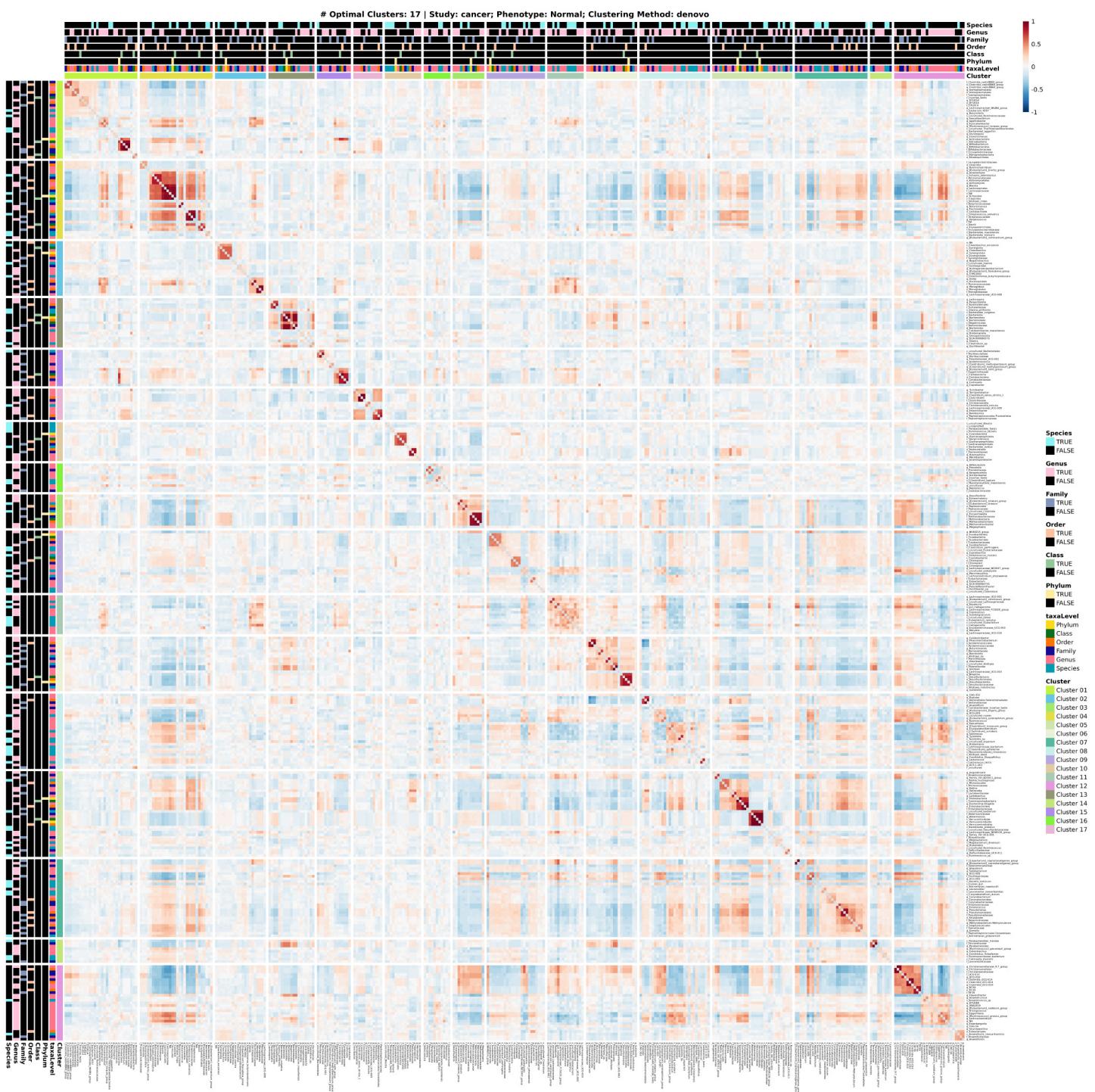
Supplementary Figure 43

Baxter et al. Correlation Plot from *de novo* OTUs Assignment Method with Phenotype: Cancer
Correlation plot based on the best estimated number of clusters obtained.



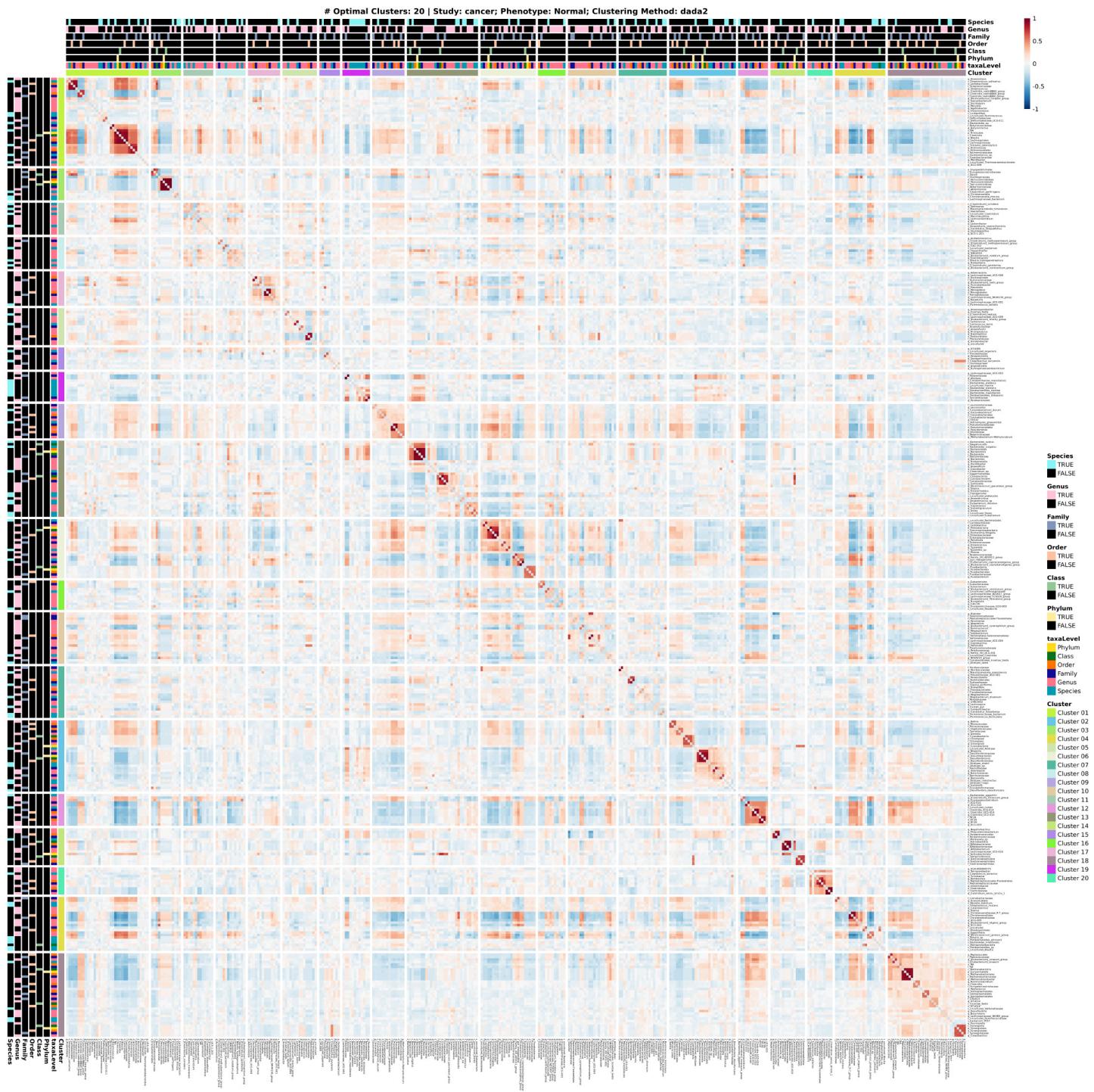
Supplementary Figure 44

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



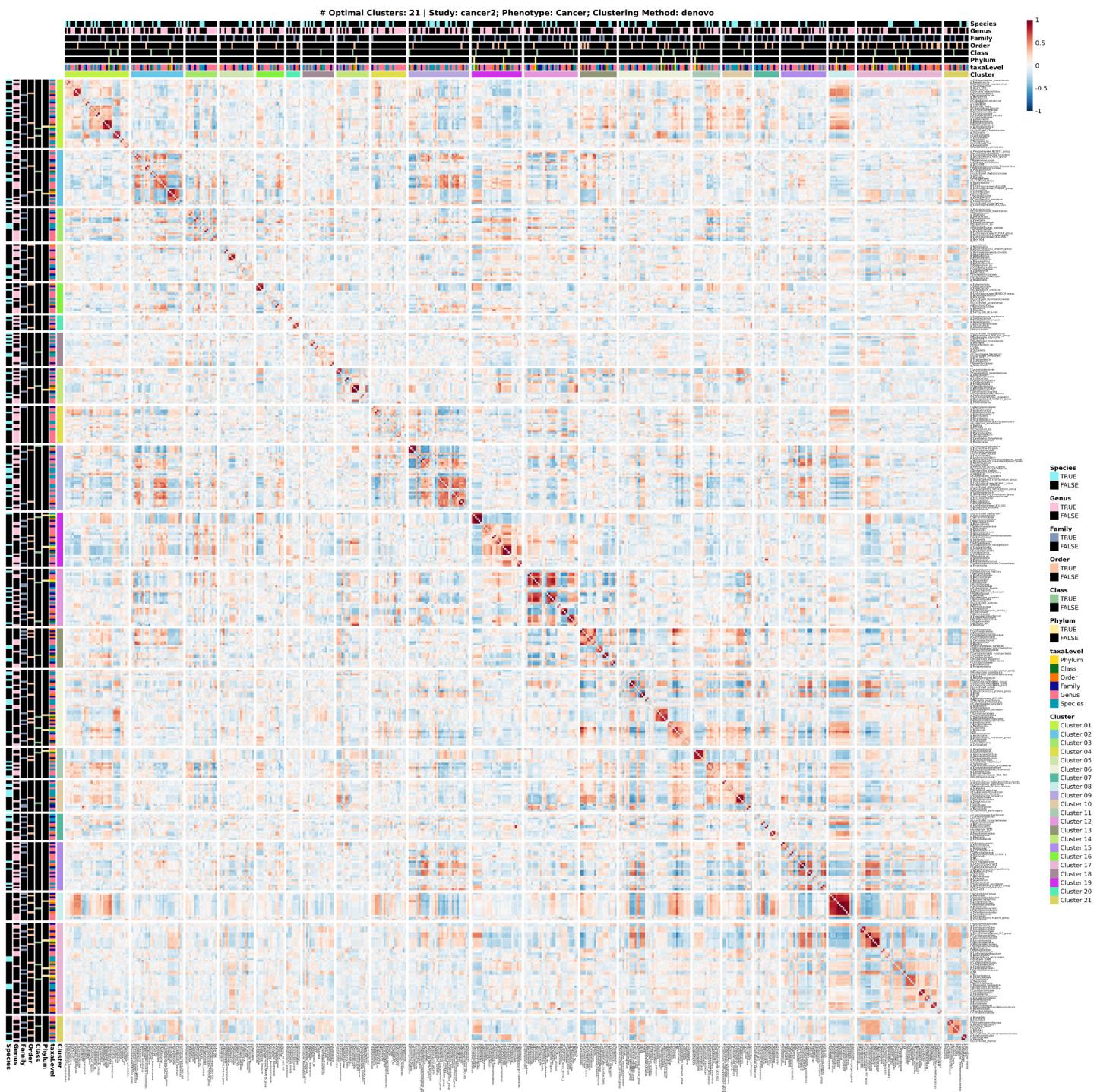
Supplementary Figure 45

Baxter et al. Correlation Plot from *de novo* OTUs Assignment Method with Phenotype: Normal
Correlation plot based on the best estimated number of clusters obtained.



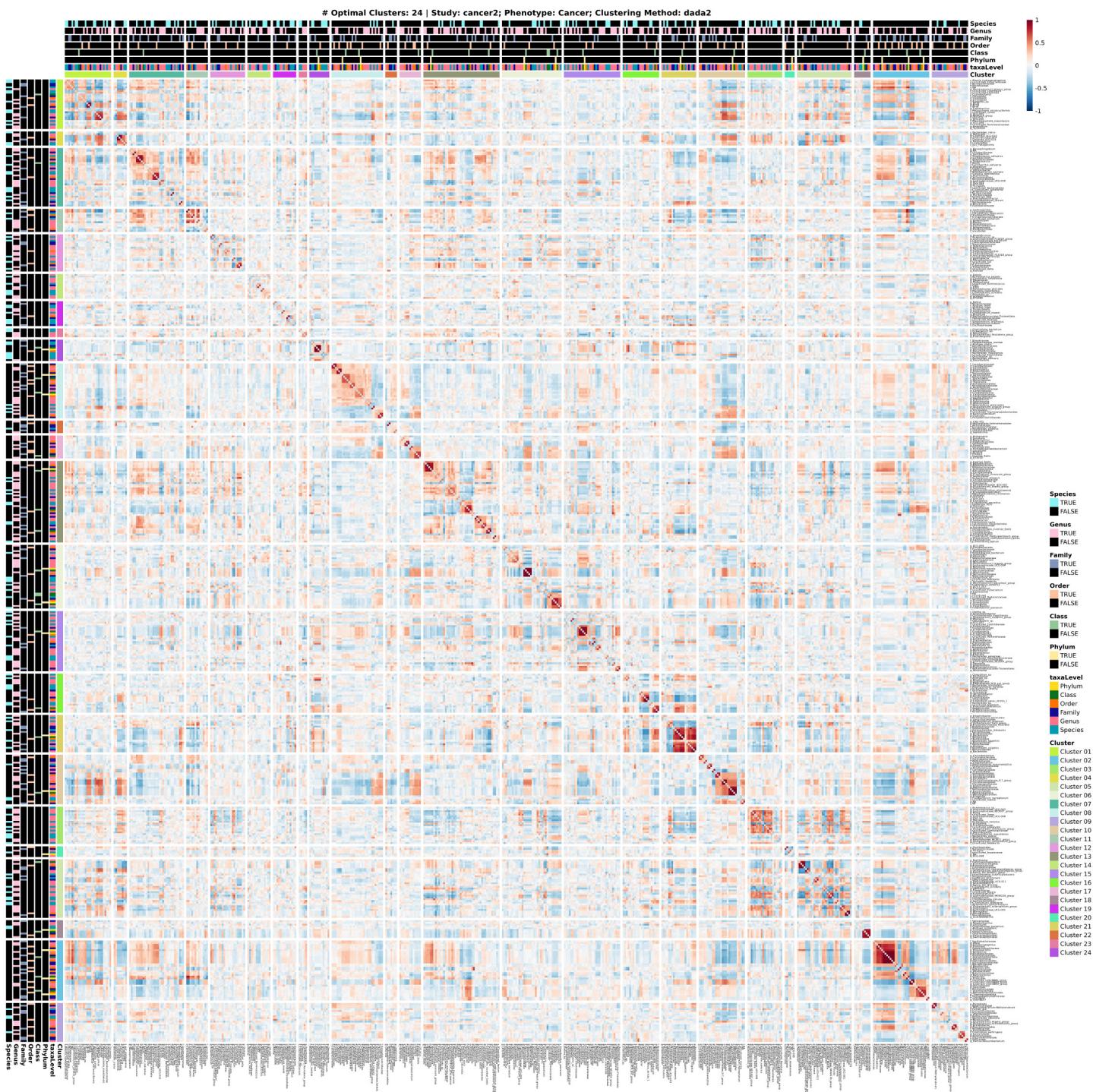
Supplementary Figure 46

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



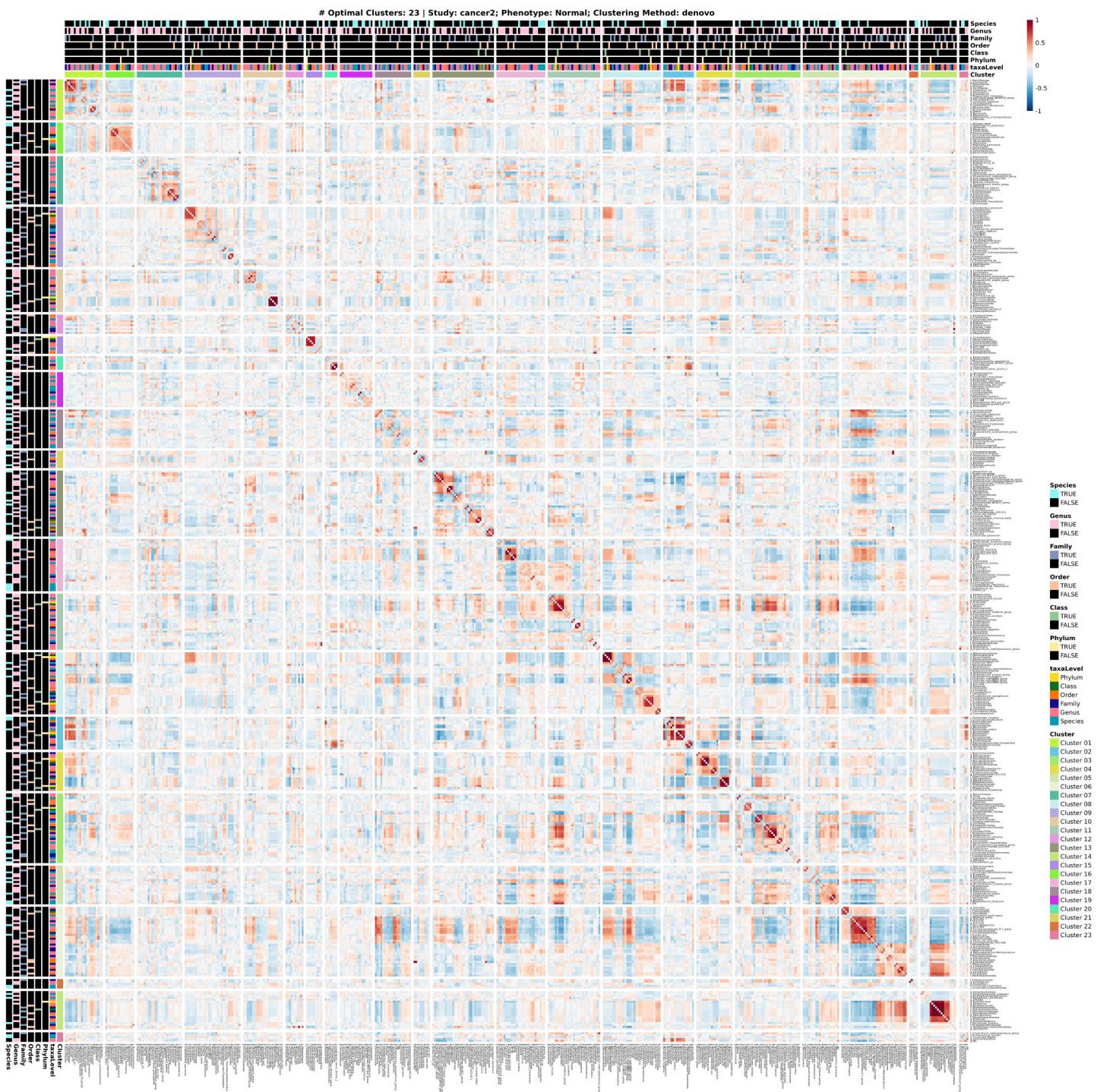
Supplementary Figure 47

Zeller et al. Correlation Plot from *de novo* OTUs Assignment Method with Phenotype: Cancer
Correlation plot based on the best estimated number of clusters obtained.



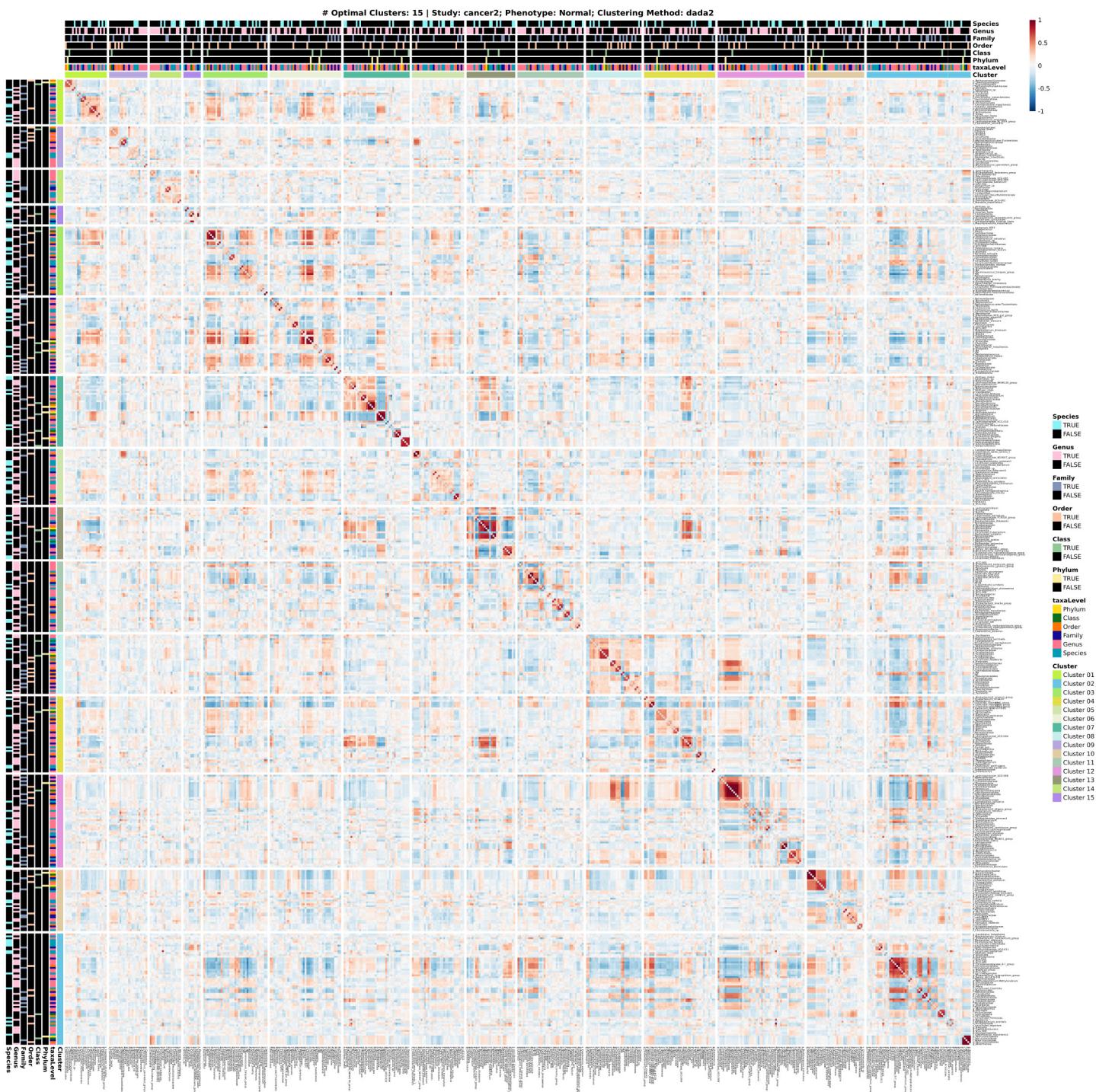
Supplementary Figure 48

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



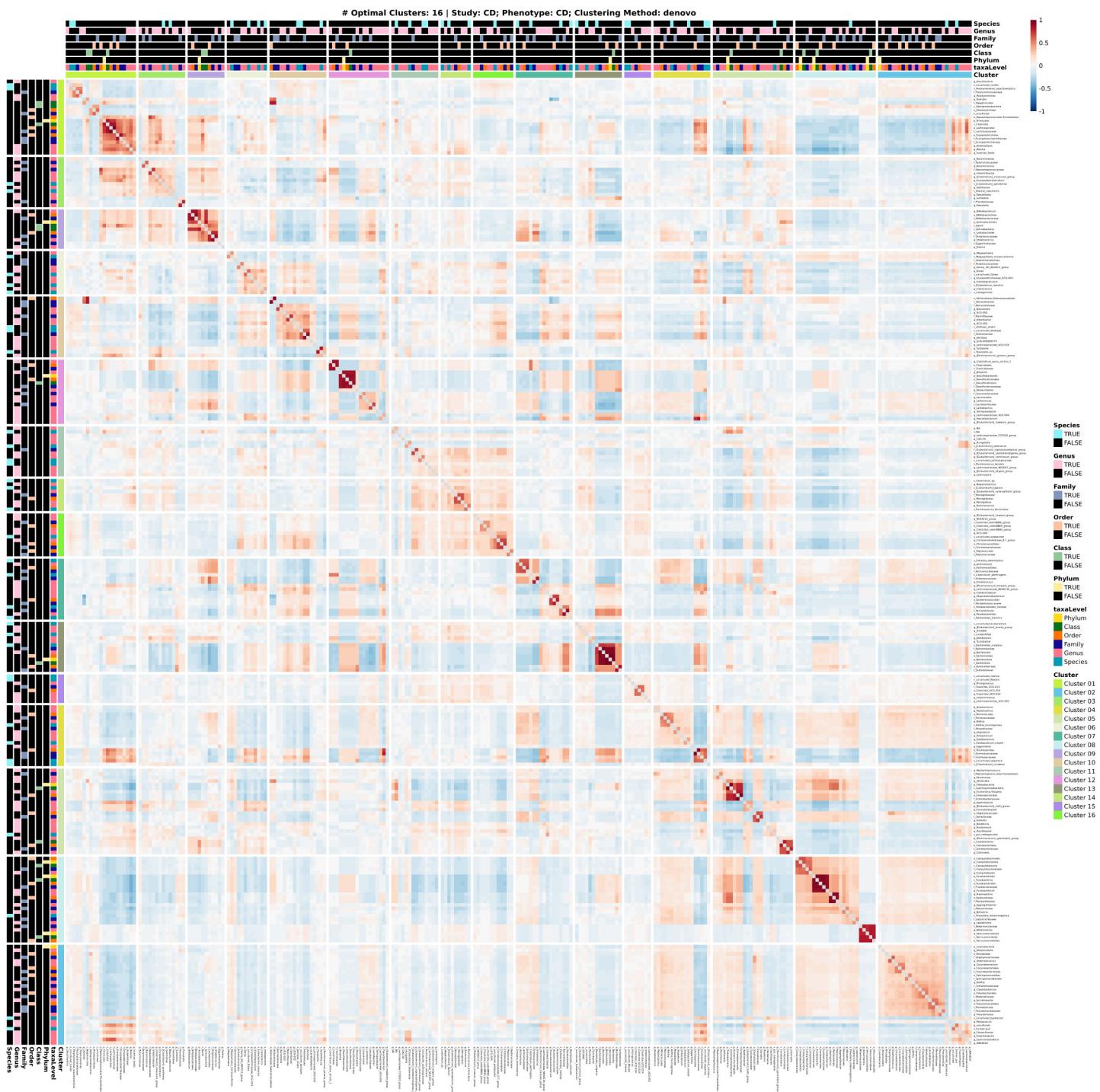
Supplementary Figure 49

Zeller et al. Correlation Plot from *de novo* OTUs Assignment Method with Phenotype: Normal
Correlation plot based on the best estimated number of clusters obtained.



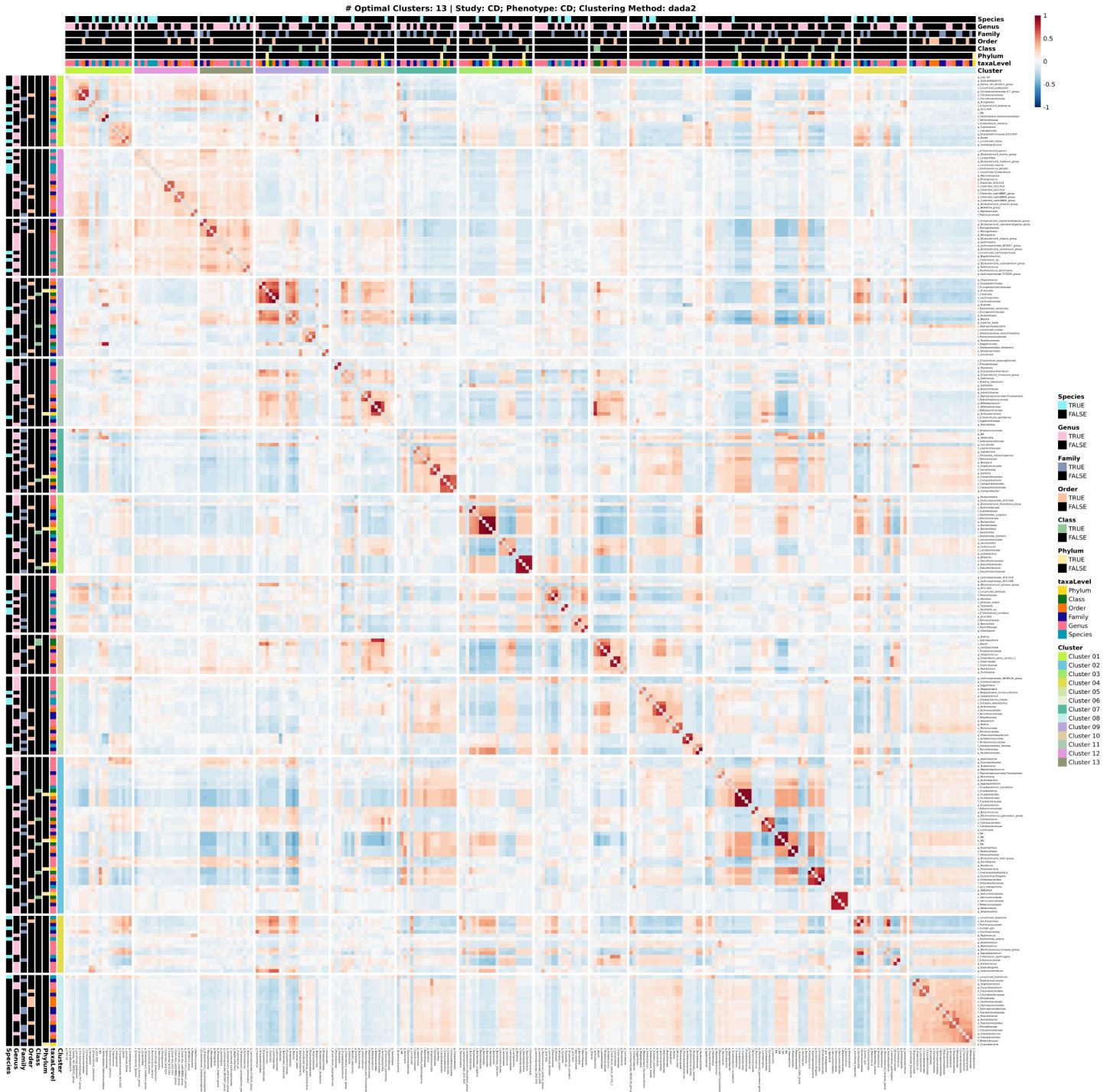
Supplementary Figure 50

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



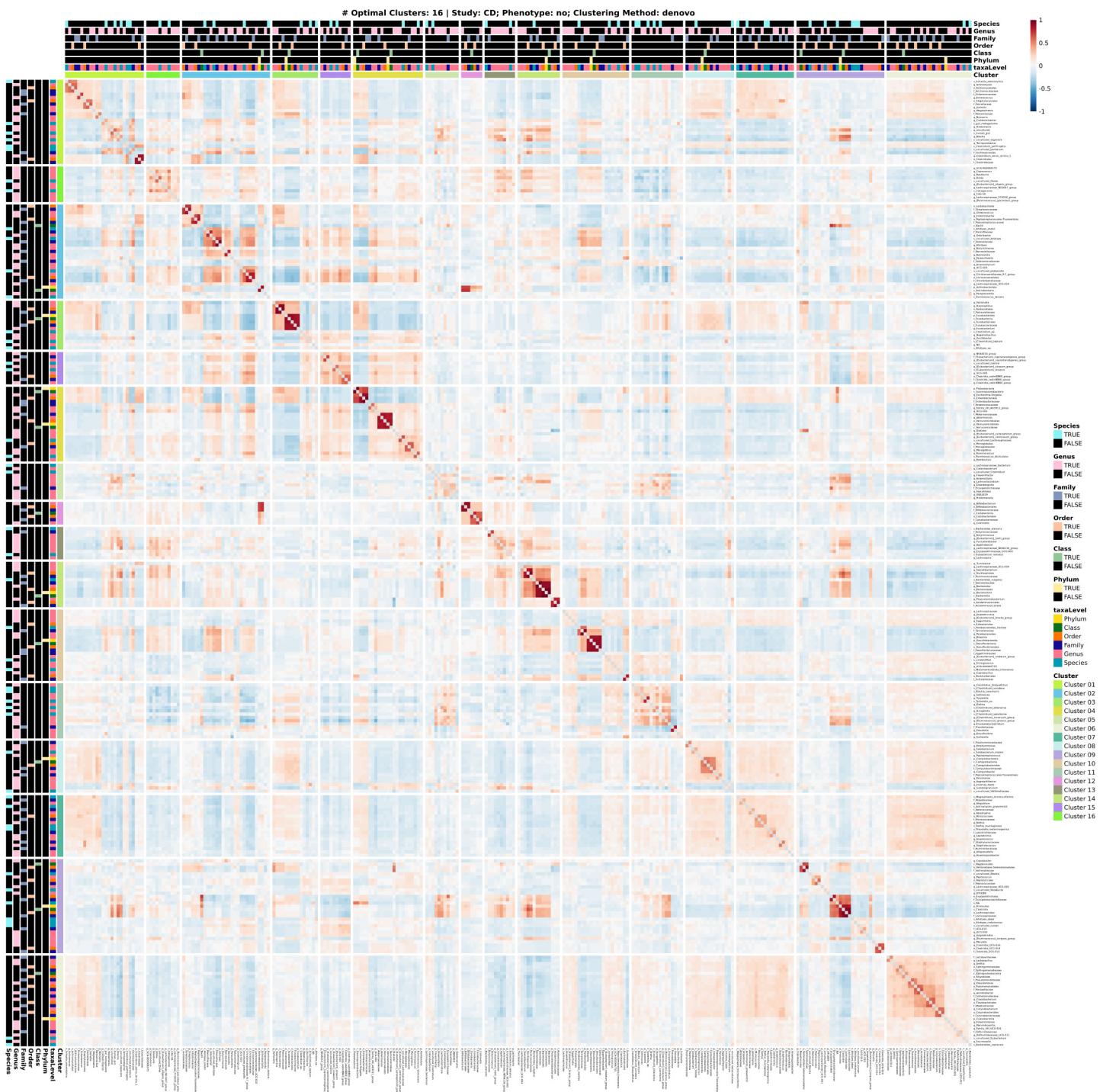
Supplementary Figure 51

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



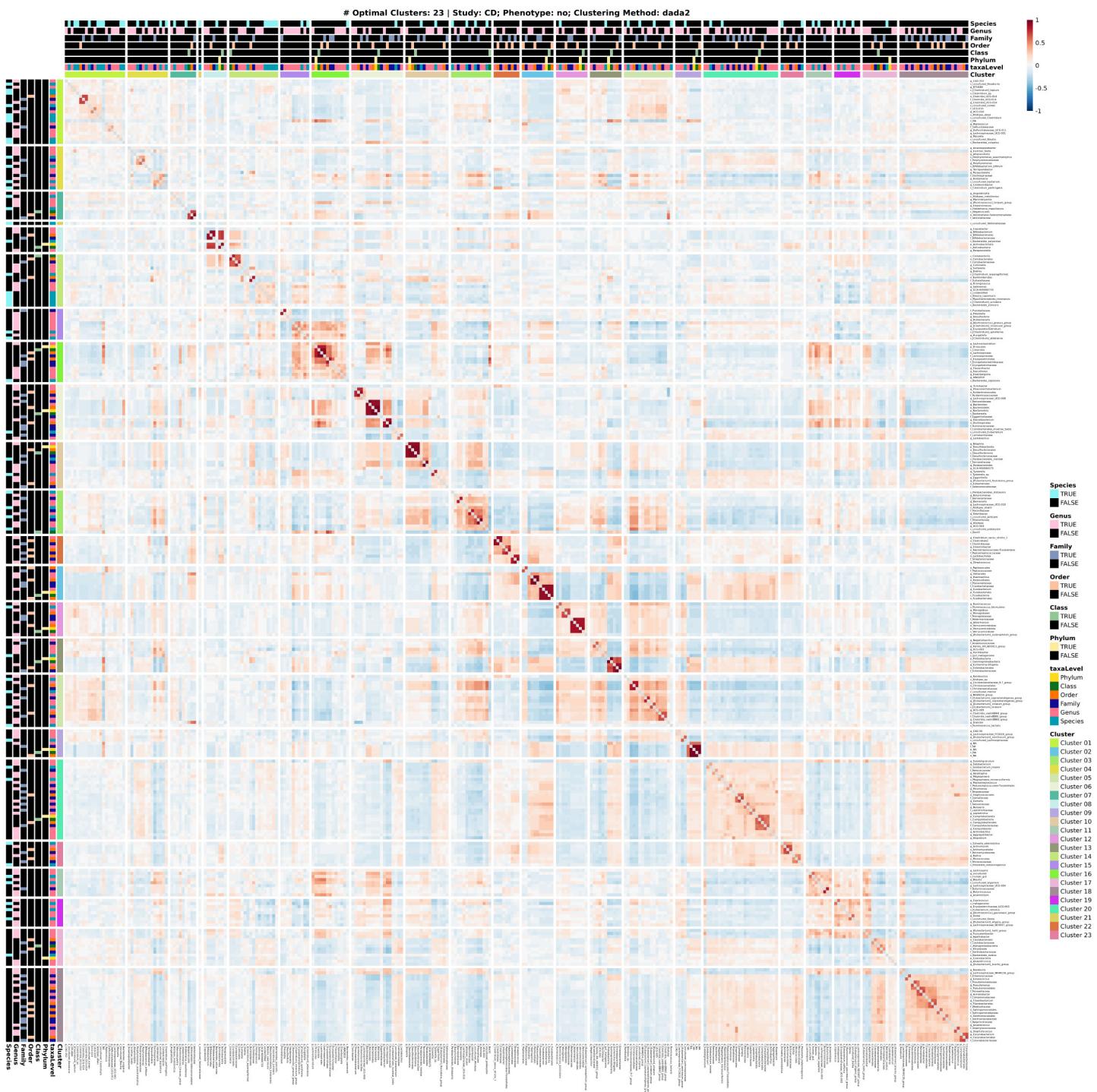
Supplementary Figure 52

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.



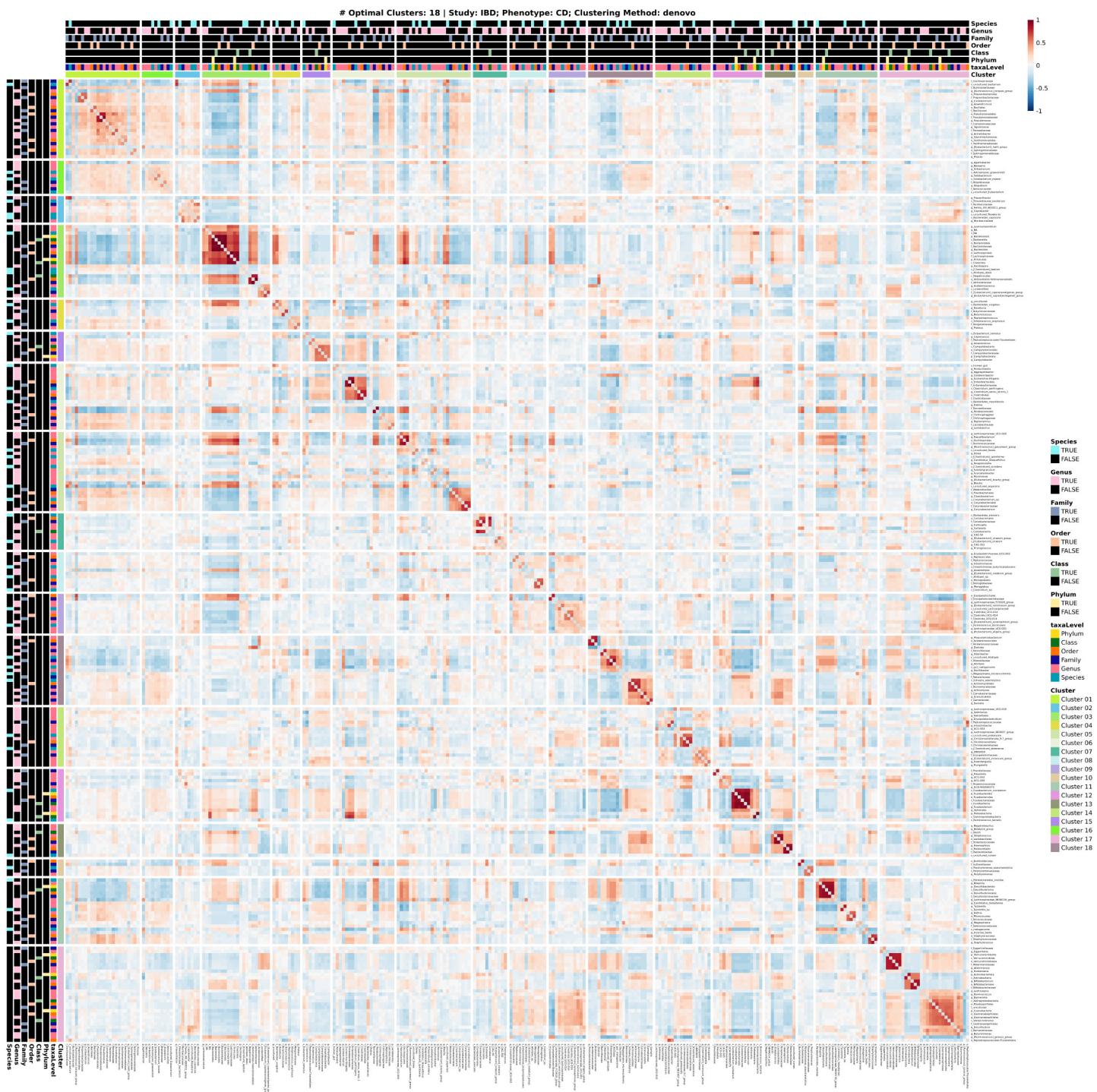
Supplementary Figure 53

Gevvers et al. Correlation Plot from *de novo* OTUs Assignment Method with Phenotype: Normal
Correlation plot based on the best estimated number of clusters obtained.



Supplementary Figure 54

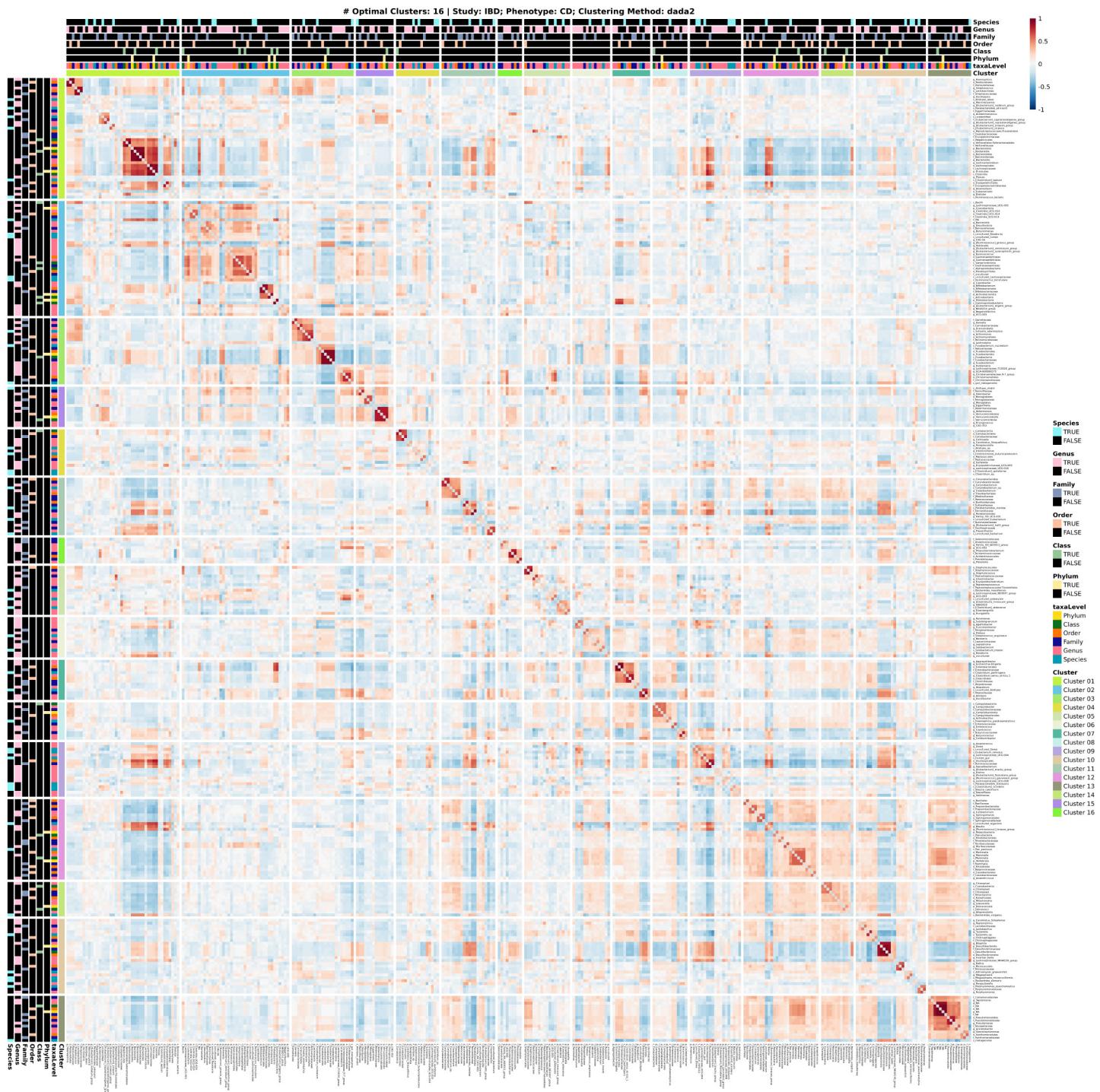
Gevers et al. Correlation Plot from DADA2 ASVs Assignment Method with Phenotype: Normal
Correlation plot based on the best estimated number of clusters obtained.



Supplementary Figure 55

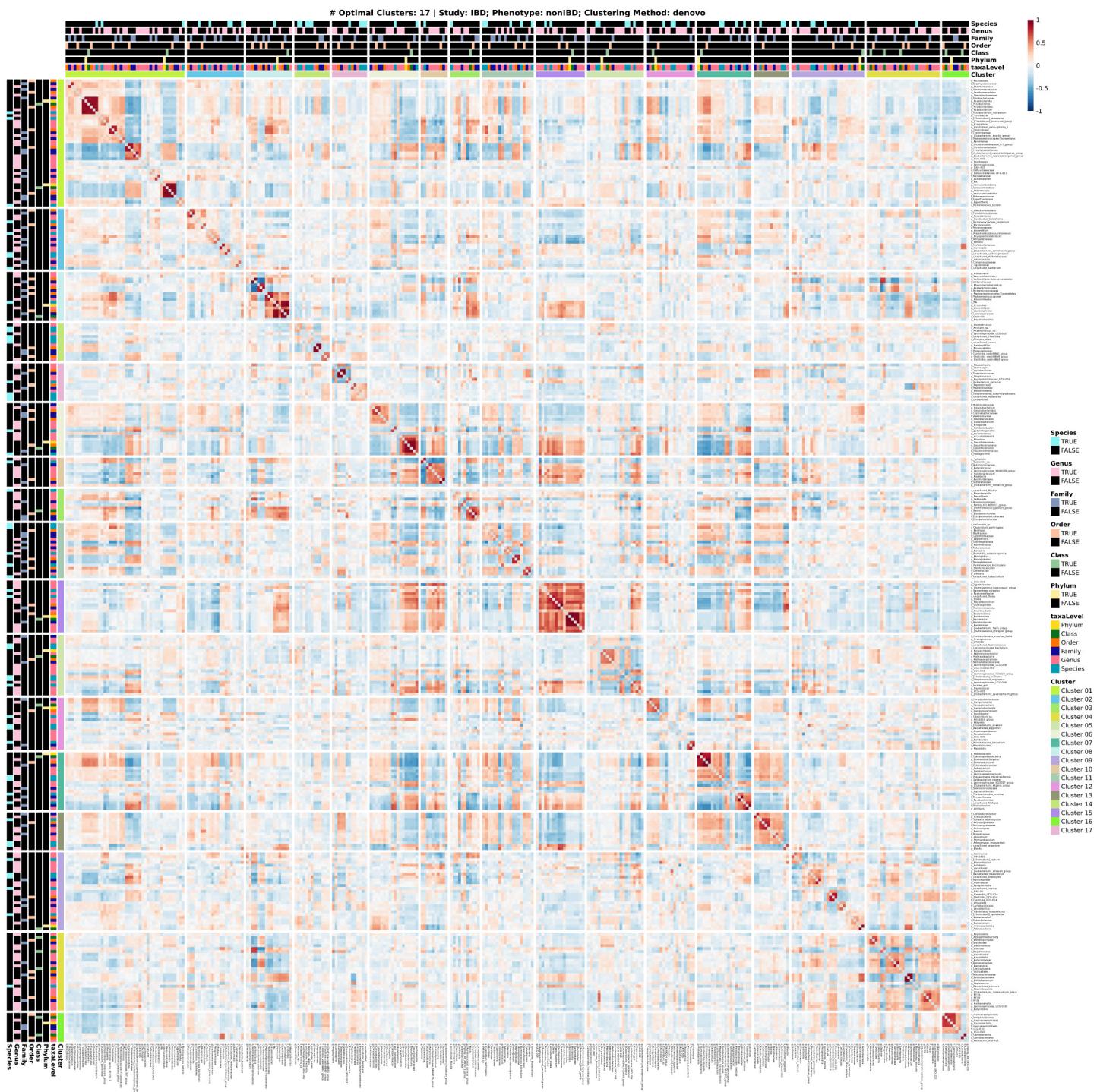
IBDMDB Correlation Plot from *de novo* OTUs Assignment Method with Phenotype: Crohn's Disease

Correlation plot based on the best estimated number of clusters obtained.



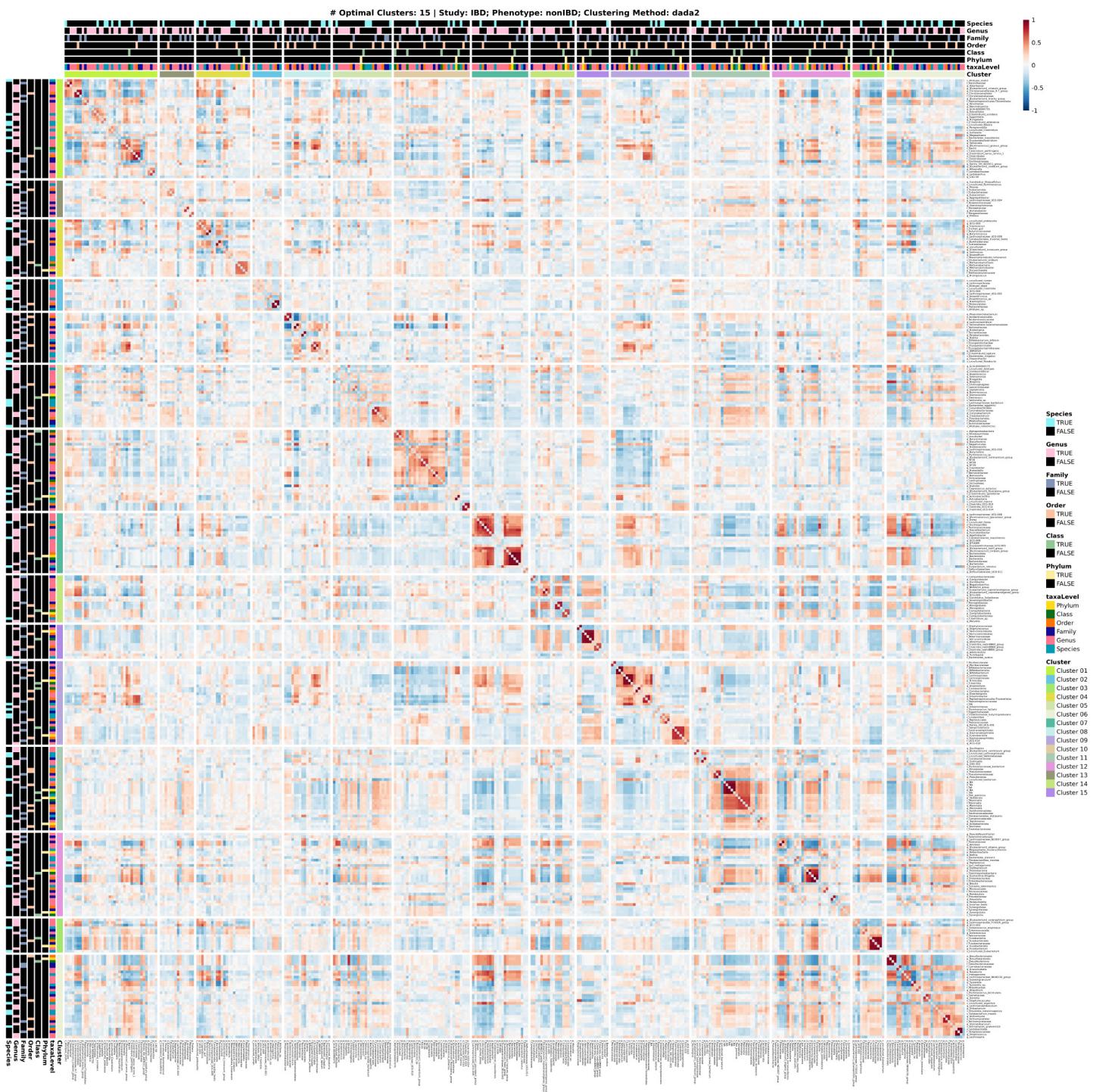
Supplementary Figure 56

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 57

IBDMDB Correlation Plot from *de novo* OTUs Assignment Method with Phenotype: Normal
Correlation plot based on the best estimated number of clusters obtained.



Supplementary Figure 58

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

