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| Chart  Description automatically generated |
| **Supplementary Figure 12** |
| Baxter et al. Module Patterns Plot from DADA2ASVs 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. |
| |  | | --- | | Chart  Description automatically generated | | **Supplementary Figure 13** | | Baxter et al. Module Patterns Plot from DADA2ASVs 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. | |
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| Chart  Description automatically generated |
| **Supplementary Figure 14** |
| Zeller et al. Module Patterns Plot from DADA2ASVs 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. |

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| Chart  Description automatically generated |
| **Supplementary Figure 15** |
| Zeller et al. Module Patterns Plot from DADA2ASVs 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. |

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| Chart  Description automatically generated |
| **Supplementary Figure 16** |
| Gevers et al. Module Patterns Plot from DADA2ASVs 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. |

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| Chart  Description automatically generated |
| **Supplementary Figure 17** |
| Gevers et al. Module Patterns Plot from DADA2ASVs 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. |

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| Chart  Description automatically generated |
| **Supplementary Figure 18** |
| IBDMDB Module Patterns Plot from DADA2ASVs 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. |

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| Chart  Description automatically generated |
| **Supplementary Figure 19** |
| IBDMDB Module Patterns Plot from DADA2ASVs 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. |

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| **Chart  Description automatically generated** |
| **Supplementary Figure 20** |
| Baxter et al. Consensus Plot from DADA2ASVs Assignment Method with Phenotype: Cancer |
| Consensus plot based on the best estimated number of clusters obtained. |

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| Chart  Description automatically generated |
| **Supplementary Figure 21** |
| Baxter et al. Consensus Plot from DADA2ASVs Assignment Method with Phenotype: Normal |
| Consensus plot based on the best estimated number of clusters obtained. |

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| Chart  Description automatically generated |
| **Supplementary Figure 22** |
| Zeller et al. Consensus Plot from DADA2ASVs Assignment Method with Phenotype: Cancer |
| Consensus plot based on the best estimated number of clusters obtained. |

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| Chart  Description automatically generated |
| **Supplementary Figure 23** |
| Zeller et al. Consensus Plot from DADA2ASVs Assignment Method with Phenotype: Normal |
| Consensus plot based on the best estimated number of clusters obtained. |

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| Chart  Description automatically generated |
| **Supplementary Figure 24** |
| Gevers et al. Consensus Plot from DADA2ASVs Assignment Method with Phenotype: Crohn's Disease |
| Consensus plot based on the best estimated number of clusters obtained. |
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| Chart  Description automatically generated |
| **Supplementary Figure 25** |
| Gevers et al. Consensus Plot from DADA2ASVs Assignment Method with Phenotype: Normal |
| Consensus plot based on the best estimated number of clusters obtained. |
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| Chart  Description automatically generated |
| **Supplementary Figure 26** |
| IBDMDB Consensus Plot from DADA2ASVs Assignment Method with Phenotype: Crohn's Disease |
| Consensus plot based on the best estimated number of clusters obtained. |
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| Chart  Description automatically generated |
| **Supplementary Figure 27** |
| IBDMDB Consensus Plot from DADA2ASVs Assignment Method with Phenotype: Normal |
| Consensus plot based on the best estimated number of clusters obtained. |

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| Chart, scatter chart  Description automatically generated |
| **Supplementary Figure 28** |
| Baxter et al. Correlation Plot from DADA2ASVs Assignment Method with Phenotype: Cancer |
| Correlation plot based on the best estimated number of clusters obtained. |

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| Chart, scatter chart  Description automatically generated |
| **Supplementary Figure 29** |
| Baxter et al. Correlation Plot from DADA2ASVs Assignment Method with Phenotype: Normal |
| Correlation plot based on the best estimated number of clusters obtained. |

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| Scatter chart  Description automatically generated |
| **Supplementary Figure 30** |
| Zeller et al. Correlation Plot from DADA2ASVs Assignment Method with Phenotype: Cancer |
| Correlation plot based on the best estimated number of clusters obtained. |

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| Chart, scatter chart  Description automatically generated |
| **Supplementary Figure 31** |
| Zeller et al. Correlation Plot from DADA2ASVs Assignment Method with Phenotype: Normal |
| Correlation plot based on the best estimated number of clusters obtained. |

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| Chart, scatter chart  Description automatically generated |
| **Supplementary Figure 32** |
| Gevers et al. Correlation Plot from DADA2ASVs Assignment Method with Phenotype: Crohn's Disease |
| Correlation plot based on the best estimated number of clusters obtained. |
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| Chart, scatter chart  Description automatically generated |
| **Supplementary Figure 33** |
| Gevers et al. Correlation Plot from DADA2ASVs Assignment Method with Phenotype: Normal |
| Correlation plot based on the best estimated number of clusters obtained. |
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| Chart  Description automatically generated |
| **Supplementary Figure 34** |
| IBDMDB Correlation Plot from DADA2ASVs Assignment Method with Phenotype: Crohn's Disease |
| Correlation plot based on the best estimated number of clusters obtained. |

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| Chart  Description automatically generated |
| **Supplementary Figure 35** |
| IBDMDB Correlation Plot from DADA2ASVs Assignment Method with Phenotype: Normal |
| Correlation plot based on the best estimated number of clusters obtained. |