**Supplementary Table S3. Permutation based MANCOVA with stepwise variable selection results for Sanger, 454 V1-V3 and 454 V3-V5 sequencing.** Samples with Crohn’s colitis and indeterminate colitis were excluded in this analysis. The dependent variable was the vector generated by the centered log ratio of the relative frequencies of six phyla/subphyla categories (see text). The significant main effects and first order interactions selected by analysis of each of the three data sets as well as the R2, P values are listed below. To address multiple comparison issues, the Benjamini-Hochberg method was applied to adjust P-values to the false discovery rate (FDR). The number of samples (around 150 samples) that yielded results suitable for analysis is listed for each method.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sequencing** | **Sanger** (*n = 155*) | **R2** | **P value** | **FDR** |
| **Main effects** | Disease phenotype | 0.132 | 0.001 | 0.008 |
| *C. difficile* | 0.024 | 0.011 | 0.025 |
| NOD2 | 0.024 | 0.013 | 0.027 |
| Steroids | 0.017 | 0.029 | 0.048 |
| **Interactions** | Disease phenotype \* Age | 0.040 | 0.005 | 0.023 |
|  | | | | |
| **Sequencing** | **454 V1-V3** (*n = 153*) | **R2** | **P value** | **FDR** |
| **Main effects** | Disease phenotype | 0.134 | 0.001 | 0.008 |
| Sex | 0.022 | 0.015 | 0.029 |
| NOD2 | 0.025 | 0.011 | 0.025 |
| **Interactions** | BMI \* 5-ASA | 0.018 | 0.029 | 0.048 |
| Steroids \* Immunomodulators | 0.023 | 0.011 | 0.025 |
|  | | | | |
| **Sequencing** | **454 V3-V5** (*n=159*) | **R2** | **P value** | **FDR** |
| **Main effects** | Disease phenotype | 0.141 | 0.001 | 0.008 |
| *C. difficile* | 0.027 | 0.006 | 0.023 |
| NOD2 | 0.035 | 0.002 | 0.012 |
| **Interactions** | Steroids \* Immunomodulators | 0.025 | 0.010 | 0.025 |
| NOD2 \* ATG16L1 | 0.028 | 0.031 | 0.048 |