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| **Analysis** | **Corresponding document(s)** | **Summary of Results** |
| Statistical analysis of differential taxa by treatment group | /taxon differences, between and within groups   * alpha\_diversity.txt * alpha-diversity-by-timepoint-beeswarm.pdf | At Timepoint 2, Group B has significantly  lower   * Coriobacteriaceae * Christensenellaceae 🡨 ASSOCIATED WITH LOW BMI * Dehalobacterium * Anaerofustis * Ruminococcaceae 🡨 active plant degraders * Mogibacteriaceae   and higher   * Roseburia 🡨 butyrate producer (this bug is also associated with increased butyrate in Group B at Timepoint 2) * Erysipelotrichaceae 🡨 (this bug is also associated with a decrease in acetate, butyrate, propionate and increase in ADJREE in group B at timepoint 2), also increases in mice with high fat diets?? But another study found lower abundances associated with high BMI |
| Comparison of beta diversity between groups | /beta diversity, between groups | Using Unweighted Unifrac, there is a significant difference between Group A and Group B at Timepoint 1 |
| Comparison of alpha diversity between groups | /alpha diversity, between groups | * Alpha diversity is higher in Group A than in Group B at Timepoint 1 * This difference does not appear to be driven by outliers (alpha-diversity-by-timepoint-beeswarm.pdf). * The two treatments are also not inducing significantly different changes in alpha diversity (within group). |
| **Clinical Variables Analyses** | | |
| **Statistical analysis of associations between taxa and metadata**   * **Selected outcomes for association with pre-intervention microbes** * **Clinical outcomes that changed post-intervention to be analyzed against changes in microbes** | /clinical variables/taxon output/   * BOXPLOT-pvalues-v-covariate-all-groups.pdf * BOXPLOT-pvalues-v-covariate.pdf | * Each bubble represents the adjusted p-value of whether a specific taxa is correlated with a clinical variable change. Bubbles above the horizontal dotted line are significant as identified by linear association only (note that we also test for spearman’s correlation separately). These two PDFs correspond to testing for both treatment groups together (all-groups.pdf) and with the treatment groups separately. Corresponding adjusted p-values plotted here can be found in delta-taxon-v-delta-covariate-within-group.txt and delta-taxon-v-delta-covariate-all-groups.txt. |
| *Significant associations between change in taxa and change in clinical variables within groups* | /clinical variables/taxon output/significant-delta-taxon-v-delta-covariate-within-group.txt | Associations with FM in Group A  Positive change in  f\_\_[Odoribacteraceae];g\_\_Butyricimonas  f\_\_[Paraprevotellaceae];g\_\_  c\_\_Bacilli;o\_\_Lactobacillales;Other;Other    Associations with CD4NAIVE in Group A  Negative change in  o\_\_Bacteroidales;f\_\_S24-7;g\_\_  Positive change in  f\_\_Clostridiaceae;g\_\_Clostridium  f\_\_Clostridiaceae;g\_\_SMB53  f\_\_Eubacteriaceae;g\_\_Anaerofustis  f\_\_[Tissierellaceae];g\_\_Parvimonas  Associations with CONA\_5UG\_PER\_ML in Group B  Positive change in  f\_\_Coriobacteriaceae;g\_\_Atopobium  f\_\_Peptococcaceae;g\_\_rc4-4  Associations with ACETATE in Group A  Negative change in  f\_\_Coriobacteriaceae;g\_\_Slackia  Associations with PROPIONATE in Group B  Positive change in  f\_\_Actinomycetaceae;g\_\_Actinomyces  f\_\_Lachnospiraceae;g\_\_[Ruminococcus]  f\_\_Oxalobacteraceae;g\_\_Oxalobacter  Associations with ADJREE in Group B  Positive change in  f\_\_Pseudomonadaceae;Other |
| *Significant associations between change in taxa and change in clinical variables in all groups* | /clinical variables/taxon output/significant-delta-taxon-v-delta-covariate-all-groups.txt | Associations with LPS\_TNF\_A in all groups  Positive change in  f\_\_Alcaligenaceae;g\_\_Sutterella  Negative change in  o\_\_Clostridiales;f\_\_Peptostreptococcaceae;g\_\_ |
| *Significant associations between taxa and clinical variables at timepoint 1 (baseline)* | /clinical variables/taxon output/significant-taxon-v-covariate-timepoint-1.txt | Associations with STOOLWT at Timepoint 1  NEGATIVE  f\_\_Ruminococcaceae;g\_\_  k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;  o\_\_Bacteroidales;f\_\_Rikenellaceae;g\_\_  o\_\_Bacteroidales;Other;Other  f\_\_Christensenellaceae;g\_\_  f\_\_Methanobacteriaceae;g\_\_Methanobrevibacter  f\_\_Ruminococcaceae;g\_\_Oscillospira  f\_\_Desulfovibrionaceae;g\_\_Bilophila  f\_\_Ruminococcaceae;Other  o\_\_Bacteroidales;f\_\_[Odoribacteraceae];g\_\_Odoribacter  f\_\_Oxalobacteraceae;g\_\_Oxalobacter  f\_\_Dehalobacteriaceae;g\_\_Dehalobacterium  f\_\_Christensenellaceae;g\_\_Christensenella  POSITIVE  f\_\_Actinomycetaceae;g\_\_Actinomyces  o\_\_Lactobacillales;Other;Other  f\_\_Streptococcaceae;g\_\_Streptococcus  f\_\_Lachnospiraceae;Other  f\_\_Lachnospiraceae;g\_\_Roseburia  f\_\_Lachnospiraceae;g\_\_Coprococcus  f\_\_Lachnospiraceae;g\_\_  f\_\_Ruminococcaceae;g\_\_Faecalibacterium  f\_\_Lachnospiraceae;g\_\_Blautia  Associations with STOOLEN at Timepoint 1  NEGATIVE  f\_\_Lachnospiraceae;g\_\_Blautia  f\_\_Streptococcaceae;g\_\_Streptococcus  f\_\_Veillonellaceae;g\_\_Veillonella  f\_\_Erysipelotrichaceae;g\_\_Holdemania  o\_\_Lactobacillales;Other;Other  f\_\_[Tissierellaceae];g\_\_Parvimonas  POSITIVE  f\_\_Dehalobacteriaceae;g\_\_Dehalobacterium  f\_\_Ruminococcaceae;Other  f\_\_[Mogibacteriaceae];g\_\_  f\_\_Lachnospiraceae;g\_\_Dorea  f\_\_Christensenellaceae;g\_\_  f\_\_Erysipelotrichaceae;g\_\_[Eubacterium]  k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;  c\_\_Mollicutes;o\_\_RF39;f\_\_;g\_\_  f\_\_Ruminococcaceae;g\_\_  f\_\_Ruminococcaceae;g\_\_Ruminococcus  Associations with ACETATE at Timepoint 1  NEGATIVE  f\_\_Ruminococcaceae;g\_\_Ruminococcus  o\_\_Bacteroidales;f\_\_Rikenellaceae;g\_\_  k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;  f\_\_Ruminococcaceae;g\_\_  o\_\_Bacteroidales;f\_\_[Barnesiellaceae];g\_\_  o\_\_Bacteroidales;Other;Other  f\_\_Verrucomicrobiaceae;g\_\_Akkermansia  f\_\_Ruminococcaceae;g\_\_Oscillospira  f\_\_Christensenellaceae;g\_\_  f\_\_Desulfovibrionaceae;g\_\_Bilophila  f\_\_Ruminococcaceae;Other  o\_\_Bacteroidales;f\_\_[Odoribacteraceae];g\_\_Odoribacter  f\_\_[Mogibacteriaceae];g\_\_  f\_\_Victivallaceae;g\_\_  f\_\_Dehalobacteriaceae;g\_\_Dehalobacterium  f\_\_Ruminococcaceae;g\_\_Anaerotruncus  f\_\_Christensenellaceae;g\_\_Christensenella  POSITIVE  k\_\_Bacteria;p\_\_Firmicutes;Other;Other;Other;Other  o\_\_Gemellales;f\_\_Gemellaceae;g\_\_  f\_\_Lachnospiraceae;Other  f\_\_Lachnospiraceae;g\_\_Blautia  f\_\_Ruminococcaceae;g\_\_Faecalibacterium  Associations with PROPIONATE at Timepoint 1  NEGATIVE  f\_\_Ruminococcaceae;g\_\_Ruminococcus  f\_\_Ruminococcaceae;g\_\_  k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;  o\_\_Bacteroidales;f\_\_Rikenellaceae;g\_\_  f\_\_Ruminococcaceae;g\_\_Oscillospira  f\_\_Christensenellaceae;g\_\_  f\_\_Verrucomicrobiaceae;g\_\_Akkermansia  f\_\_Desulfovibrionaceae;g\_\_Bilophila  o\_\_Bacteroidales;f\_\_[Odoribacteraceae];g\_\_Odoribacter  f\_\_[Mogibacteriaceae];g\_\_  f\_\_Ruminococcaceae;Other  f\_\_Dehalobacteriaceae;g\_\_Dehalobacterium  o\_\_Burkholderiales;Other;Other  POSITIVE  o\_\_Gemellales;f\_\_Gemellaceae;g\_\_  Associations with ADJREE at Timepoint 1  POSITIVE  f\_\_Erysipelotrichaceae;g\_\_Coprobacillus |
| *Significant associations between taxa and clinical variables at timepoint 2 (post-intervention)* | /clinical variables/taxon output/significant-taxon-v-covariate-timepoint-2.txt | Associations with STOOLWT at Timepoint 2  NEGATIVE  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_Ruminococcus  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_  o\_\_Clostridiales;f\_\_;g\_\_  o\_\_Bacteroidales;f\_\_Rikenellaceae;g\_\_  o\_\_Bacteroidales;Other;Other  o\_\_Clostridiales;f\_\_Christensenellaceae;g\_\_  o\_\_Bacteroidales;f\_\_Porphyromonadaceae;g\_\_Parabacteroides  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_Oscillospira  o\_\_RF39;f\_\_;g\_\_  o\_\_Desulfovibrionales;f\_\_Desulfovibrionaceae;g\_\_Bilophila  o\_\_Coriobacteriales;f\_\_Coriobacteriaceae;g\_\_  o\_\_Clostridiales;f\_\_Ruminococcaceae;Other  o\_\_Clostridiales;f\_\_[Mogibacteriaceae];g\_\_  o\_\_Bacteroidales;f\_\_Rikenellaceae;Other  o\_\_Bacteroidales;f\_\_[Odoribacteraceae];g\_\_Odoribacter  o\_\_Desulfovibrionales;f\_\_Desulfovibrionaceae;g\_\_  o\_\_Clostridiales;f\_\_Dehalobacteriaceae;g\_\_Dehalobacterium  o\_\_SHA-98;f\_\_;g\_\_  o\_\_Burkholderiales;f\_\_Oxalobacteraceae;g\_\_Oxalobacter  o\_\_Campylobacterales;f\_\_Campylobacteraceae;g\_\_Campylobacter  o\_\_Clostridiales;f\_\_EtOH8;g\_\_  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_Anaerotruncus  o\_\_Clostridiales;f\_\_Christensenellaceae;g\_\_Christensenella  o\_\_Clostridiales;f\_\_Eubacteriaceae;g\_\_Anaerofustis  POSITIVE  o\_\_Clostridiales;f\_\_Lachnospiraceae;Other  o\_\_Clostridiales;f\_\_Lachnospiraceae;g\_\_Roseburia  Associations with ISO at Timepoint 2  POSITIVE  f\_\_Veillonellaceae;g\_\_Megasphaera  Associations with ACETATE at Timepoint 2  NEGATIVE  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_Ruminococcus  o\_\_Bacteroidales;f\_\_Rikenellaceae;g\_\_  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_  o\_\_Clostridiales;f\_\_;g\_\_  o\_\_Clostridiales;f\_\_Christensenellaceae;g\_\_  o\_\_RF39;f\_\_;g\_\_  o\_\_Erysipelotrichales;f\_\_Erysipelotrichaceae;g\_\_[Eubacterium]  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_Oscillospira  o\_\_Bacteroidales;Other;Other  o\_\_Desulfovibrionales;f\_\_Desulfovibrionaceae;g\_\_Bilophila  o\_\_Coriobacteriales;f\_\_Coriobacteriaceae;g\_\_  o\_\_Coriobacteriales;f\_\_Coriobacteriaceae;g\_\_Collinsella  o\_\_Clostridiales;f\_\_Ruminococcaceae;Other  o\_\_Clostridiales;f\_\_[Mogibacteriaceae];g\_\_  o\_\_Bacteroidales;f\_\_[Odoribacteraceae];g\_\_Odoribacter  o\_\_Coriobacteriales;f\_\_Coriobacteriaceae;g\_\_Adlercreutzia  o\_\_Clostridiales;f\_\_Dehalobacteriaceae;g\_\_Dehalobacterium  o\_\_Clostridiales;f\_\_Peptococcaceae;g\_\_  o\_\_Bacteroidales;f\_\_Rikenellaceae;Other  o\_\_SHA-98;f\_\_;g\_\_  o\_\_Burkholderiales;f\_\_Oxalobacteraceae;g\_\_Oxalobacter  o\_\_Synergistales;f\_\_Synergistaceae;g\_\_  o\_\_Clostridiales;f\_\_EtOH8;g\_\_  o\_\_Clostridiales;f\_\_Christensenellaceae;g\_\_Christensenella  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_Anaerotruncus  o\_\_Desulfovibrionales;f\_\_Desulfovibrionaceae;Other  POSITIVE  o\_\_Clostridiales;f\_\_Veillonellaceae;g\_\_Veillonella  o\_\_Clostridiales;f\_\_Lachnospiraceae;g\_\_Roseburia  o\_\_Clostridiales;f\_\_Lachnospiraceae;g\_\_Lachnospira  o\_\_Burkholderiales;f\_\_Alcaligenaceae;g\_\_Sutterella  Associations with PROPIONATE at Timepoint 2  NEGATIVE  o\_\_Clostridiales;f\_\_;g\_\_  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_Ruminococcus  o\_\_Erysipelotrichales;f\_\_Erysipelotrichaceae;g\_\_[Eubacterium]  o\_\_RF39;f\_\_;g\_\_  o\_\_Clostridiales;f\_\_Christensenellaceae;g\_\_  o\_\_Methanobacteriales;f\_\_Methanobacteriaceae;g\_\_Methanobrevibacter  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_Oscillospira  o\_\_Coriobacteriales;f\_\_Coriobacteriaceae;g\_\_Collinsella  o\_\_Coriobacteriales;f\_\_Coriobacteriaceae;g\_\_  o\_\_Clostridiales;Other;Other  o\_\_Clostridiales;f\_\_Lachnospiraceae;g\_\_Dorea  o\_\_Clostridiales;f\_\_[Mogibacteriaceae];g\_\_  o\_\_Clostridiales;f\_\_Ruminococcaceae;Other  o\_\_Clostridiales;f\_\_Peptococcaceae;g\_\_Peptococcus  o\_\_Bacteroidales;f\_\_[Odoribacteraceae];g\_\_Odoribacter  o\_\_YS2;f\_\_;g\_\_  o\_\_Victivallales;f\_\_Victivallaceae;g\_\_  o\_\_Coriobacteriales;f\_\_Coriobacteriaceae;g\_\_Slackia  o\_\_Coriobacteriales;f\_\_Coriobacteriaceae;g\_\_Adlercreutzia  o\_\_ML615J-28;f\_\_;g\_\_  o\_\_Clostridiales;f\_\_Dehalobacteriaceae;g\_\_Dehalobacterium  o\_\_Burkholderiales;f\_\_Oxalobacteraceae;g\_\_Oxalobacter  o\_\_SHA-98;f\_\_;g\_\_  o\_\_Clostridiales;f\_\_EtOH8;g\_\_  o\_\_Clostridiales;f\_\_Christensenellaceae;g\_\_Christensenella  o\_\_Burkholderiales;Other;Other  o\_\_Clostridiales;f\_\_Eubacteriaceae;g\_\_Anaerofustis  o\_\_Bacteroidales;f\_\_Rikenellaceae;g\_\_Alistipes  o\_\_Streptophyta;f\_\_;g\_\_  POSITIVE  o\_\_Pasteurellales;f\_\_Pasteurellaceae;g\_\_Aggregatibacter  Associations with BUTYRATE at Timepoint 2  NEGATIVE  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_  o\_\_RF39;f\_\_;g\_\_  o\_\_Clostridiales;f\_\_Christensenellaceae;g\_\_  o\_\_Erysipelotrichales;f\_\_Erysipelotrichaceae;g\_\_[Eubacterium]  o\_\_Erysipelotrichales;f\_\_Erysipelotrichaceae;g\_\_Catenibacterium  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_Oscillospira  o\_\_Coriobacteriales;f\_\_Coriobacteriaceae;g\_\_  o\_\_Clostridiales;f\_\_[Mogibacteriaceae];g\_\_  o\_\_Coriobacteriales;f\_\_Coriobacteriaceae;g\_\_Collinsella  o\_\_Clostridiales;f\_\_Ruminococcaceae;Other  o\_\_Victivallales;f\_\_Victivallaceae;g\_\_  o\_\_Bacteroidales;f\_\_[Odoribacteraceae];g\_\_Odoribacter  o\_\_ML615J-28;f\_\_;g\_\_  o\_\_Coriobacteriales;f\_\_Coriobacteriaceae;g\_\_Slackia  o\_\_Clostridiales;f\_\_Dehalobacteriaceae;g\_\_Dehalobacterium  o\_\_SHA-98;f\_\_;g\_\_  o\_\_Burkholderiales;f\_\_Oxalobacteraceae;g\_\_Oxalobacter  o\_\_Clostridiales;f\_\_EtOH8;g\_\_  o\_\_Clostridiales;f\_\_Christensenellaceae;g\_\_Christensenella  o\_\_Burkholderiales;Other;Other  POSITIVE  o\_\_Clostridiales;f\_\_Peptococcaceae;Other  o\_\_Clostridiales;f\_\_Veillonellaceae;g\_\_Veillonella  o\_\_Pasteurellales;f\_\_Pasteurellaceae;g\_\_Haemophilus  o\_\_Clostridiales;f\_\_Lachnospiraceae;Other  o\_\_Clostridiales;f\_\_Lachnospiraceae;g\_\_Lachnospira  o\_\_Clostridiales;f\_\_Lachnospiraceae;g\_\_Roseburia  o\_\_Clostridiales;f\_\_Ruminococcaceae;g\_\_Faecalibacterium  o\_\_Bacteroidales;f\_\_Bacteroidaceae;g\_\_Bacteroides  Associations with ADJREE at Timepoint 2  NEGATIVE  f\_\_Pasteurellaceae;Other  POSITIVE  f\_\_Erysipelotrichaceae;g\_\_Coprobacillus  f\_\_Erysipelotrichaceae;g\_\_cc\_115 |
| *Associations between alpha diversity and change in clinical variable*  *Association between change in alpha diversity and change in clinical variable* | /clinical variables/taxon output/alpha.div.result.txt | Significant associations between alpha diversity at timepoint 1 and change in clinical variables:  CD4NAIVE (negative association)  STOOLEN (positive assocation)  Significant associations between change in alpha diversity and change in clinical variables:  CD4NAIVE (positive association) |
| *Significant associations between change in metagenome and change in clinical variables within groups* | /clinical variables/metagenome output/significant-delta-mg-v-delta-covariate-within-group.txt | Associations with ISO in Group B  NEGATIVE  alpha-Linolenic acid metabolism  Taurine and hypotaurine metabolism  Alanine, aspartate and glutamate metabolism  Amino sugar and nucleotide sugar metabolism  Steroid hormone biosynthesis  Other glycan degradation  POSITIVE  Ether lipid metabolism  Associations with PROPIONATE in Group B  NEGATIVE  alpha-Linolenic acid metabolism |
| *Significant associations between change in metagenome and change in clinical variables in all groups* | /clinical variables/metagenome output/significant-delta-mg-v-delta-covariate-all-groups.txt | Associations with STOOLEN in ALL GROUPS  NEGATIVE  Lysine biosynthesis  Phenylalanine, tyrosine and tryptophan biosynthesis  Synthesis and degradation of ketone bodies  Associations with ISO in ALL GROUPS  NEGATIVE  alpha-Linolenic acid metabolism  Associations with PROPIONATE in ALL GROUPS  NEGATIVE  Alanine, aspartate and glutamate metabolism  D-Glutamine and D-glutamate metabolism  Lipid biosynthesis proteins  Lipopolysaccharide biosynthesis proteins  Other glycan degradation  Steroid hormone biosynthesis  POSITIVE  Ether lipid metabolism |
| *Significant associations between metagenome and clinical variables at timepoint 1 (baseline)* | /clinical variables/metagenome output/significant-mg-v-covariate-timepoint-1.txt | Associations with STOOLWT at Timepoint 1  NEGATIVE  Valine, leucine and isoleucine degradation  Associations with AR at Timepoint 1  POSITIVE  Tyrosine metabolism  Associations with ACETATE at Timepoint 1  NEGATIVE  Phosphonate and phosphinate metabolism  Butanoate metabolism  Steroid biosynthesis  Lipid biosynthesis proteins  Phenylalanine metabolism  Tyrosine metabolism  Fatty acid metabolism  Biosynthesis of unsaturated fatty acids  Lysine degradation  alpha-Linolenic acid metabolism  Tryptophan metabolism  POSITIVE  Selenocompound metabolism  beta-Alanine metabolism |
| *Significant associations between metagenome and clinical variables at timepoint 2 (post-intervention)* | /clinical variables/metagenome output/significant-mg-v-covariate-timepoint-2.txt | Associations with STOOLWT at Timepoint 2  NEGATIVE  Tyrosine metabolism  Various types of N-glycan biosynthesis  POSITIVE  Selenocompound metabolism  Glycine, serine and threonine metabolism  beta-Alanine metabolism  Associations with ACETATE at Timepoint 2  NEGATIVE  Pyruvate metabolism  Histidine metabolism  Glycerolipid metabolism  Glycolysis / Gluconeogenesis  Propanoate metabolism  Fatty acid biosynthesis  Steroid biosynthesis  Lysine degradation  Tryptophan metabolism  Fatty acid metabolism  Tyrosine metabolism  Various types of N-glycan biosynthesis  POSITIVE  N-Glycan biosynthesis  Glycine, serine and threonine metabolism  Glycosyltransferases  Purine metabolism  Associations with PROPIONATE at Timepoint 2  NEGATIVE  Valine, leucine and isoleucine biosynthesis  Glycerolipid metabolism  Pyruvate metabolism  Propanoate metabolism  Butanoate metabolism  Glycolysis / Gluconeogenesis  Synthesis and degradation of ketone bodies  Fatty acid metabolism  Tryptophan metabolism  Fatty acid biosynthesis  Lysine degradation  Tyrosine metabolism  Various types of N-glycan biosynthesis  POSITIVE  Selenocompound metabolism  N-Glycan biosynthesis  Glycine, serine and threonine metabolism  beta-Alanine metabolism  Alanine, aspartate and glutamate metabolism  Amino sugar and nucleotide sugar metabolism  Glycosyltransferases  Other glycan degradation  Lipopolysaccharide biosynthesis proteins  Associations with BUTYRATE at Timepoint 2  NEGATIVE  Tryptophan metabolism |
| **Predictive modeling of clinical covariates by microbiome composition** | /clinical variables/taxon output/initial-mb-predict-delta-covariate.txt  /clinical variables/taxon output/delta-mb-predict-delta-covariate.txt | Large positive R2 values indicates a stronger capability of the initial microbiome predicting the change in clinical covariate, stratified by treatment group. Unfortunately mostly all change in clinical covariates were not predictable by the initial or delta microbiomes. These covariates might be worth looking into further due to their positive R2 values:  FM for Group B  CONA\_5UG\_PER\_ML for Group A  LPS\_TNF\_A for Group B  FM for Group A  STOOLWT for Group A  CONA\_5UG\_PER\_ML for Group A  LPS\_TNF\_A for Group B  ISO for Group B  PROPIONATE for Group B |
| **PiCRUSt** | / metagenome differences, between and within groups | At TimePoint 2, Group B has significantly  higher   * Cyanoamino acid metabolism   and lower   * Tyrosine metabolism |

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| Clinical Variable Tests | Corresponding Document | Results |
| Significant associations between change in taxa and change in clinical variables within groups | /clinical variables - per lab/EML/taxon output/significant-delta-taxon-v-delta-covariate-within-group.txt |  |
| Significant associations between change in taxa and change in clinical variables in all groups | /clinical variables - per lab/EML/taxon output/significant-delta-taxon-v-delta-covariate-all-groups.txt |  |
| Significant associations between taxa and clinical variables at timepoint 1 (baseline) | /clinical variables - per lab/EML/taxon output/significant-taxon-v-covariate-timepoint-1.txt |  |
| Significant associations between taxa and clinical variables at timepoint 2 (post-intervention) | /clinical variables - per lab/EML/taxon output/significant-taxon-v-covariate-timepoint-2.txt |  |
| * Associations between alpha diversity and change in clinical variable * Association between change in alpha diversity and change in clinical variable | /clinical variables - per lab/EML/taxon output/alpha.div.result.txt |  |
| Significant associations between change in metagenome and change in clinical variables within groups | /clinical variables - per lab/EML/metagenome output/significant-delta-mg-v-delta-covariate-within-group.txt |  |
| Significant associations between change in metagenome and change in clinical variables in all groups | /clinical variables - per lab/EML/metagenome output/significant-delta-mg-v-delta-covariate-all-groups.txt |  |
| Significant associations between metagenome and clinical variables at timepoint 1 (baseline) | /clinical variables - per lab/EML/metagenome output/significant-mg-v-covariate-timepoint-1.txt |  |
| Significant associations between metagenome and clinical variables at timepoint 2 (post-intervention) | /clinical variables - per lab/EML/metagenome output/significant-mg-v-covariate-timepoint-2.txt |  |