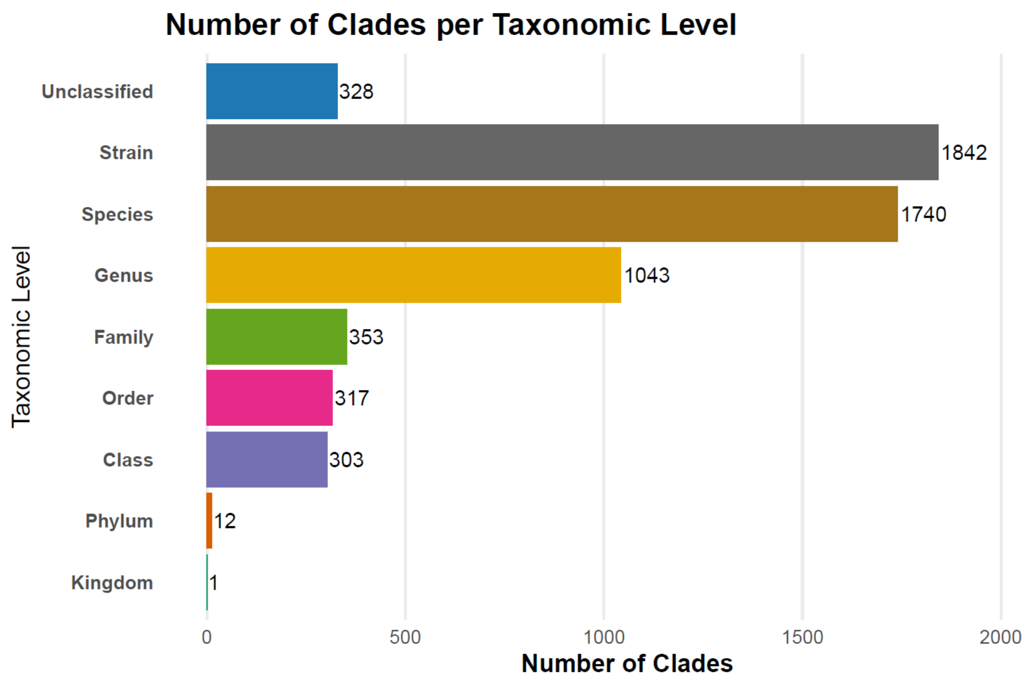
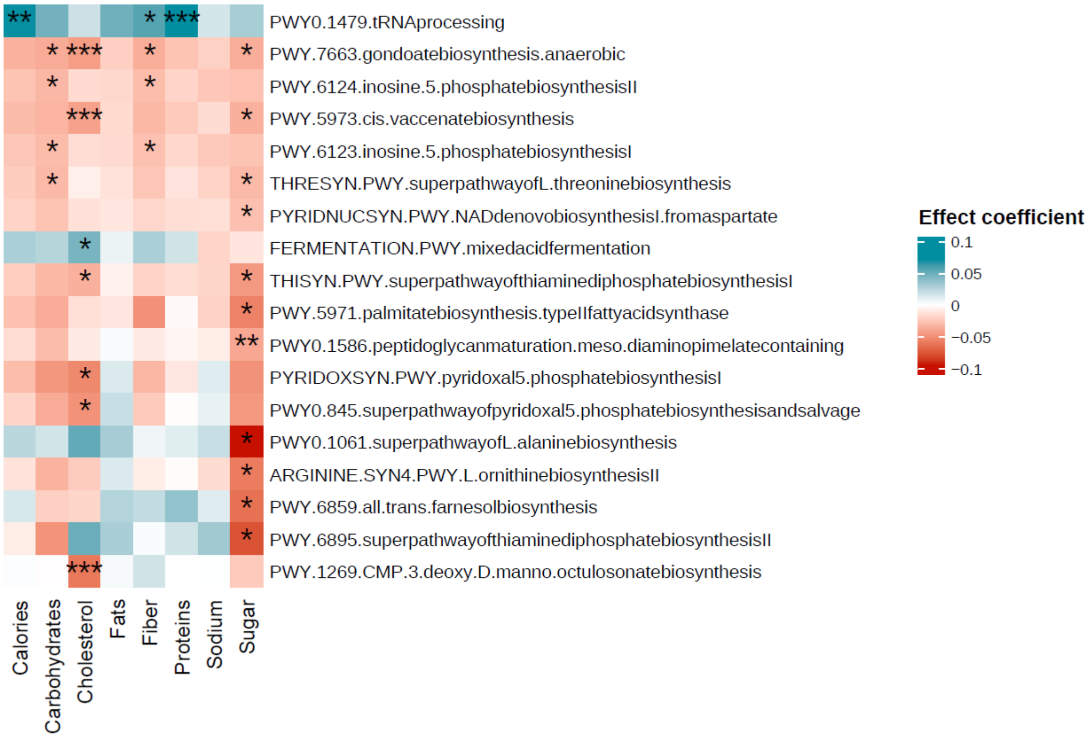


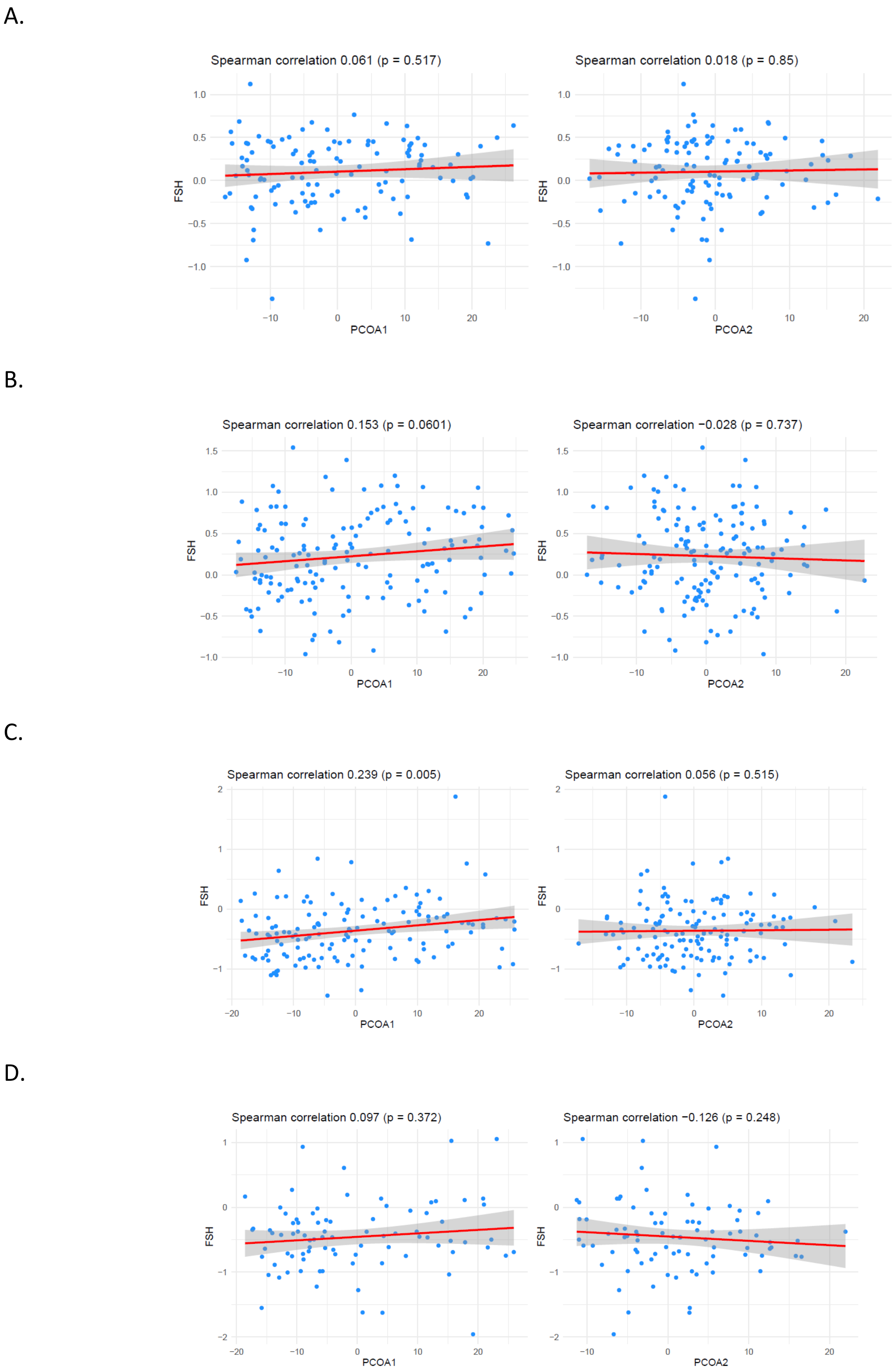
Supplementary Figure 1: Bar plots of microbial clades across taxonomic levels. Bars represent the number of microbial taxa at the phylum, class, order, family, and genus, species, strains, and unclassified levels. Each color corresponds to a distinct clade.



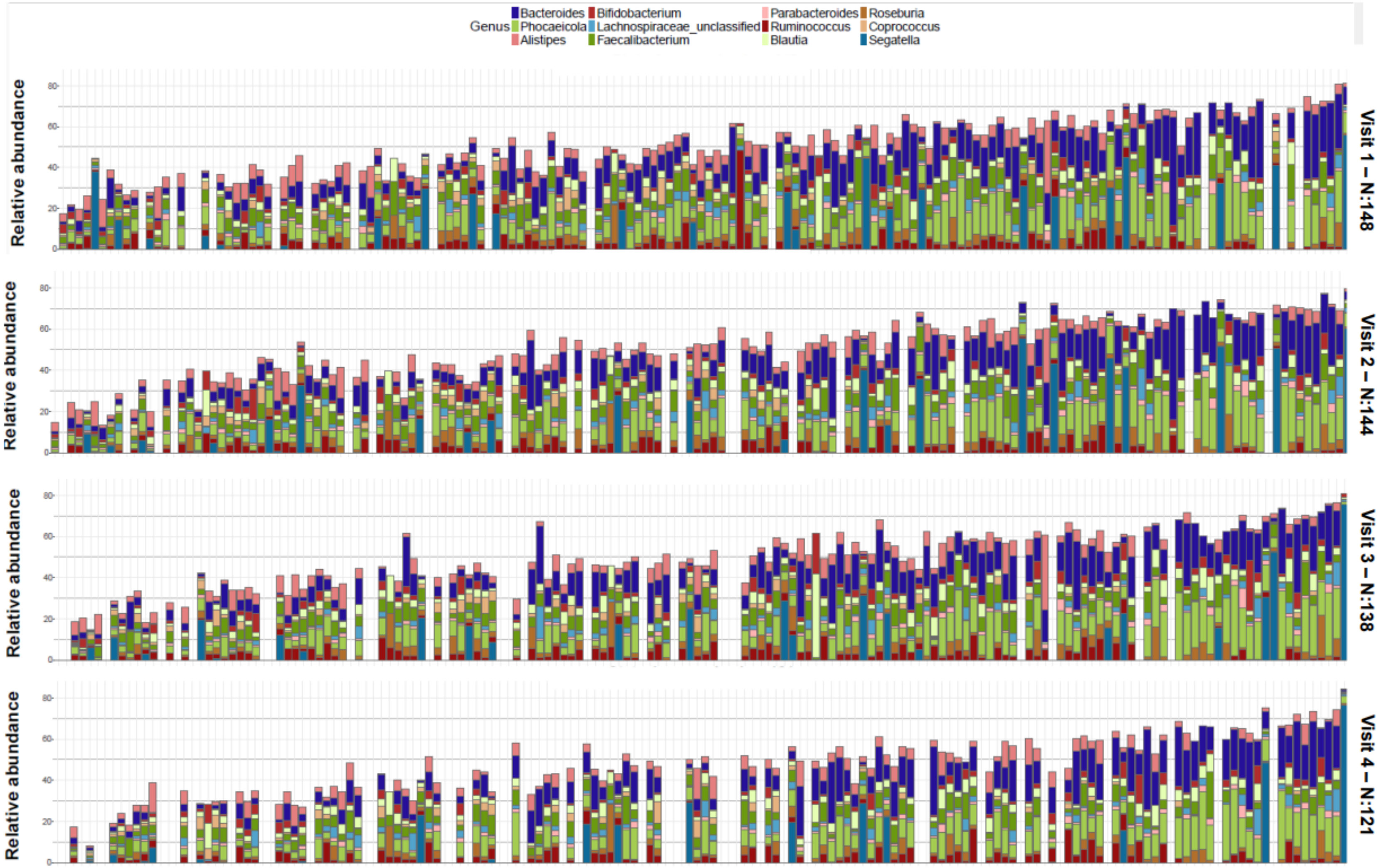
Supplementary Figure 2: Heatmap showing associations between pathways and nutrient intake (Nutrients $_{3days}$). Heatmap of associations between microbial pathways and nutrient intake, calculated as the 3-days average prior to fecal sample collection.Squares are colored according to the effect size of the association, as in the side legend. Asterisks mark level of significance (* q<0.25, **q<0.1, ***q<0.05).


Effect coefficient
0.2
0.1
0
−0.1
−0.2
PWY.7977.L.methioninebiosynthesisIV
PWY.6969.TCAcycleV.2.oxoglutaratesynthase.
PWY.5103.L.isoleucinebiosynthesisIII
PWY0.1586.peptidoglycanmaturation.meso.diaminopimelatecontaining.
PWY.5154.L.argininebiosynthesisIII.viaN.acetyl.L.citrulline.
PWY.6147.6.hydroxymethyl.dihydropterindiphosphatebiosynthesisI
BRANCHED.CHAIN.AA.SYN.PWY.superpathwayofbranchedchainaminoacidbiosynthesis
PWY.1269.CMP.3.deoxy.D.manno.octulosonatebiosynthesis
ILEUSYN.PWY.L.isoleucinebiosynthesisI.fromthreonine.
FERMENTATION.PWY.mixedacidfermentation
PWY.5505.L.glutamateandL.glutaminebiosynthesis
PWY.5097.L.lysinebiosynthesisVI
THISYN.PWY.superpathwayofthiaminediphosphatebiosynthesisI
PHOSLIPSYN.PWY.superpathwayofphospholipidbiosynthesisI.bacteria.
PWY.2942.L.lysinebiosynthesisIII
PWY.5100.pyruvatefermentationtoacetateandlactateII
PWY.7221.guanosineribonucleotidesdenovobiosynthesis
ANAGLYCOLYSIS.PWY.glycolysisIII.fromglucose.
PWY0.1061.superpathwayofL.alaninebiosynthesis
PWY.6122.5.aminoimidazoleribonucleotidebiosynthesisII
PWY.6277.superpathwayof5.aminoimidazoleribonucleotidebiosynthesis
PWY.6703.preQ0biosynthesis
ASPASN.PWY.superpathwayofL.aspartateandL.asparaginebiosynthesis
PWY.7663.gondoatebiosynthesis.anaerobic.
CALVIN.PWY.Calvin.Benson.Basshamcycle
PWY.1042.glycolysisIV
PWY.6897.thiaminediphosphatesalvageII
DTDPRHAMSYN.PWY.dTDP..beta..L.rhamnosebiosynthesis
PWY.7560.methylerythritolphosphatepathwayII
DAPLYSINESYN.PWY.L.lysinebiosynthesisI
PWY.6317.D.galactosedegradationI.Leloirpathway.
PWY.3841.folatetransformationsII.plants.
PWY.6151.S.adenosyl.L.methioninesalvageI
PWY.8178.pentosephosphatepathway.non.oxidativebranch.II
PWY.7345.superpathwayofanaerobicsucrosedegradation
NONOXIPENT.PWY.pentosephosphatepathway.non.oxidativebranch.I
PWY.6121.5.aminoimidazoleribonucleotidebiosynthesisI
PWY0.162.superpathwayofpyrimidineribonucleotidesdenovobiosynthesis
PWY.7761.NADsalvagepathwayII.PNCIVcycle.
PWY.6527.stachyosedegradation
PWY.7198.pyrimidinedeoxyribonucleotidesdenovobiosynthesisIV
PWY.5941.glycogendegradationII
PWY4FS.7.phosphatidylglycerolbiosynthesisI.plastidic.
PWY4FS.8.phosphatidylglycerolbiosynthesisII.non.plastidic.
PWY.724.superpathwayofL.lysine.L.threonineandL.methioninebiosynthesisII
ARO.PWY.chorismatebiosynthesisI
GLCMANNANAUT.PWY.superpathwayofN.acetylglucosamine.N.acetylmannosamineandN.acetylneuraminatedegradation
GLYCOLYSIS.E.D.PWY.superpathwayofglycolysisandtheEntner.Doudoroffpathway
PWY.5188.tetrapyrrolebiosynthesisI.fromglutamate.
PWY.7237.myo..chiro.andscyllo.inositoldegradation
PWY.3001.superpathwayofL.isoleucinebiosynthesisI
PWY.6892.thiazolecomponentofthiaminediphosphatebiosynthesisI
PWY.6936.seleno.aminoacidbiosynthesis.plants.
PWY.6282.palmitoleatebiosynthesisI.from.5Z..dodec.5.enoate.
FASYN.ELONG.PWY.fattyacidelongation..saturated
COA.PWY.coenzymeAbiosynthesisI.prokaryotic.
GLUCONEO.PWY.gluconeogenesisI
PWY.6123.inosine.5..phosphatebiosynthesisI
PWY.7117.C4photosyntheticcarbonassimilationcycle.PEPCKtype
PWY.7664.oleatebiosynthesisIV.anaerobic.
COA.PWY.1.superpathwayofcoenzymeAbiosynthesisIII.mammals.
PWY.621.sucrosedegradationIII.sucroseinvertase.
ANAEROFRUCAT.PWY.homolacticfermentation
GLUCOSE1PMETAB.PWY.glucoseandglucose.1.phosphatedegradation
PWY.5384.sucrosedegradationIV.sucrosephosphorylase.
PWY.5989.stearatebiosynthesisII.bacteriaandplants.
COMPLETE.ARO.PWY.superpathwayofaromaticaminoacidbiosynthesis
PWY0.1261.anhydromuropeptidesrecyclingI
PWY.7242.D.fructuronatedegradation
PWY.6124.inosine.5..phosphatebiosynthesisII
PWY.7220.adenosinedeoxyribonucleotidesdenovobiosynthesisII
PWY.7222.guanosinedeoxyribonucleotidesdenovobiosynthesisII
RIBOSYN2.PWY.flavinbiosynthesisI.bacteriaandplants.
PWY.6823.molybdopterinbiosynthesis
PWY.6901.superpathwayofglucoseandxylosedegradation
PWY.7357.thiaminephosphateformationfrompyrithiamineandoxythiamine.yeast.
PWY.6292.superpathwayofL.cysteinebiosynthesis.mammalian.
GLYCOLYSIS.PWY.glycolysisI.fromglucose6.phosphate.
PWY.6628.superpathwayofL.phenylalaninebiosynthesis
PWY.5484.glycolysisII.fromfructose6.phosphate.
GLUTORN.PWY.L.ornithinebiosynthesisI
PWY.5659.GDP.mannosebiosynthesis
PWY.841.superpathwayofpurinenucleotidesdenovobiosynthesisI
THISYNARA.PWY.superpathwayofthiaminediphosphatebiosynthesisIII.eukaryotes.
HISDEG.PWY.L.histidinedegradationI
PWY.6519.8.amino.7.oxononanoatebiosynthesisI
GLUCUROCAT.PWY.superpathwayof.beta..D.glucuronosidesdegradation
PWY.4041..gamma..glutamylcycle
BIOTIN.BIOSYNTHESIS.PWY.biotinbiosynthesisI
PWY.7111.pyruvatefermentationtoisobutanol.engineered.
PWY0.862..5Z..dodecenoatebiosynthesisI
PWY.6125.superpathwayofguanosinenucleotidesdenovobiosynthesisII
PWY.7229.superpathwayofadenosinenucleotidesdenovobiosynthesisI
NAGLIPASYN.PWY.lipidIVAbiosynthesis.E.coli.
PWY.6126.superpathwayofadenosinenucleotidesdenovobiosynthesisII
PWY.8073.lipidIVAbiosynthesis.P.putida.
PWY.2941.L.lysinebiosynthesisII
PWY.7197.pyrimidinedeoxyribonucleotidephosphorylation
PWY.702.L.methioninebiosynthesisII
PWY.7228.superpathwayofguanosinenucleotidesdenovobiosynthesisI
METH.ACETATE.PWY.methanogenesisfromacetate
PWY.7238.sucrosebiosynthesisII
Beer
Bread
Butter
Cheese
Coffee
Cold cuts
Eggs
Fish
Fruit
Olive oil
Pasta or rice
Red meat
Semi skimmed milk
Spirits
Vegetables
White meat
Whole milk
Wine
Yogurt

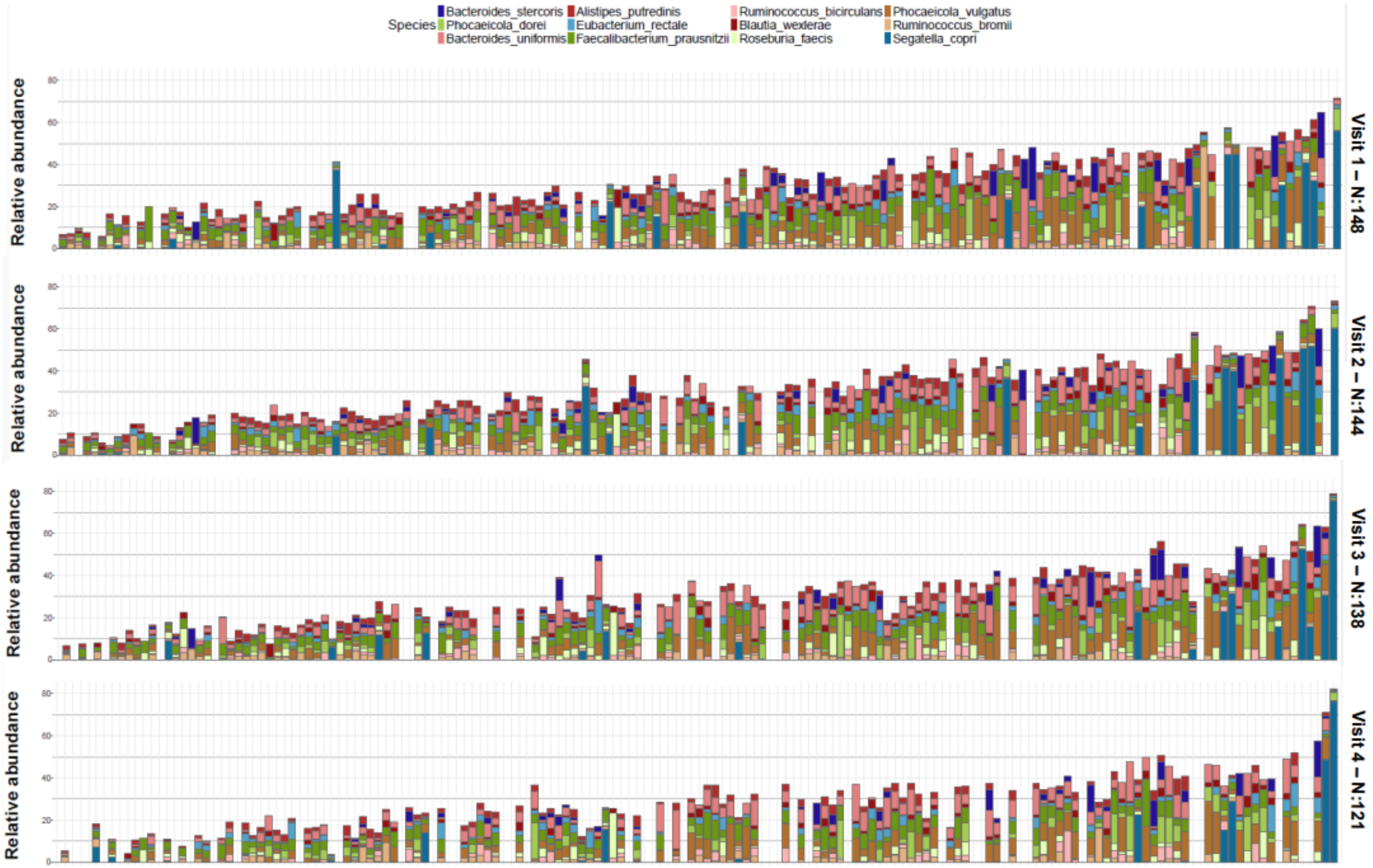
Supplementary Figure 3: Heatmap showing associations between pathways and food habits. Heatmap of associations between microbial pathways and food habits from frequency food questionaries. Squares are colored according to the effect size of the association, as in the side legend. Asterisks mark level of significance (* q<0.25, **q<0.1).



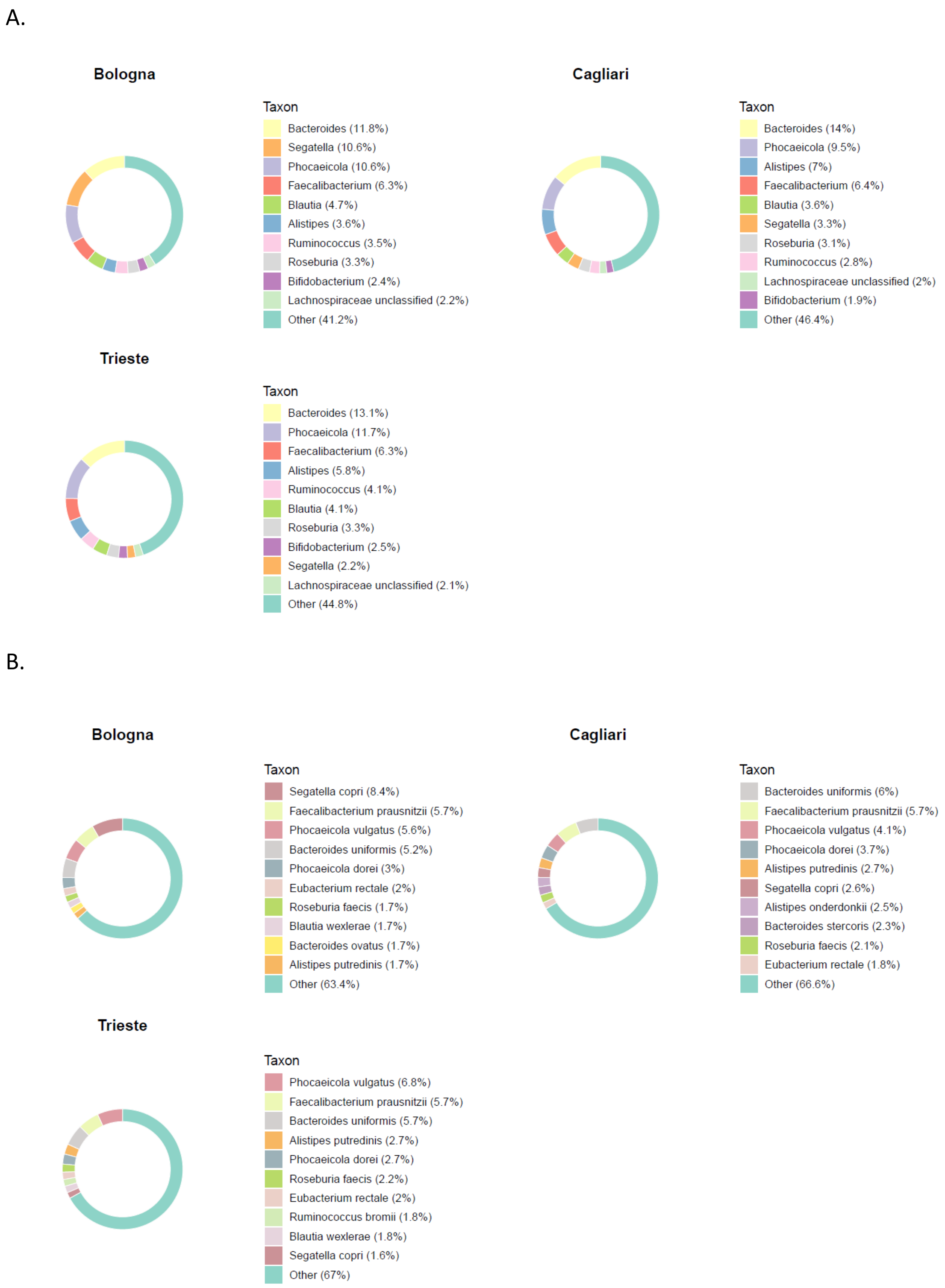
Supplementary Figure 4: Spearman correlation between FSH and gut microbial beta diversity PCs. Spearman correlations were calculated between circulating FSH levels and the first two principal coordinates (PCoA1 and PCoA2) of beta diversity, based on CLR-transformed species abundances. Panel A, B, C, D refer to beta-diversity calculated for phases F, O, EL and LL, respectively. Correlation coefficients (ρ) and corresponding p-values are reported.



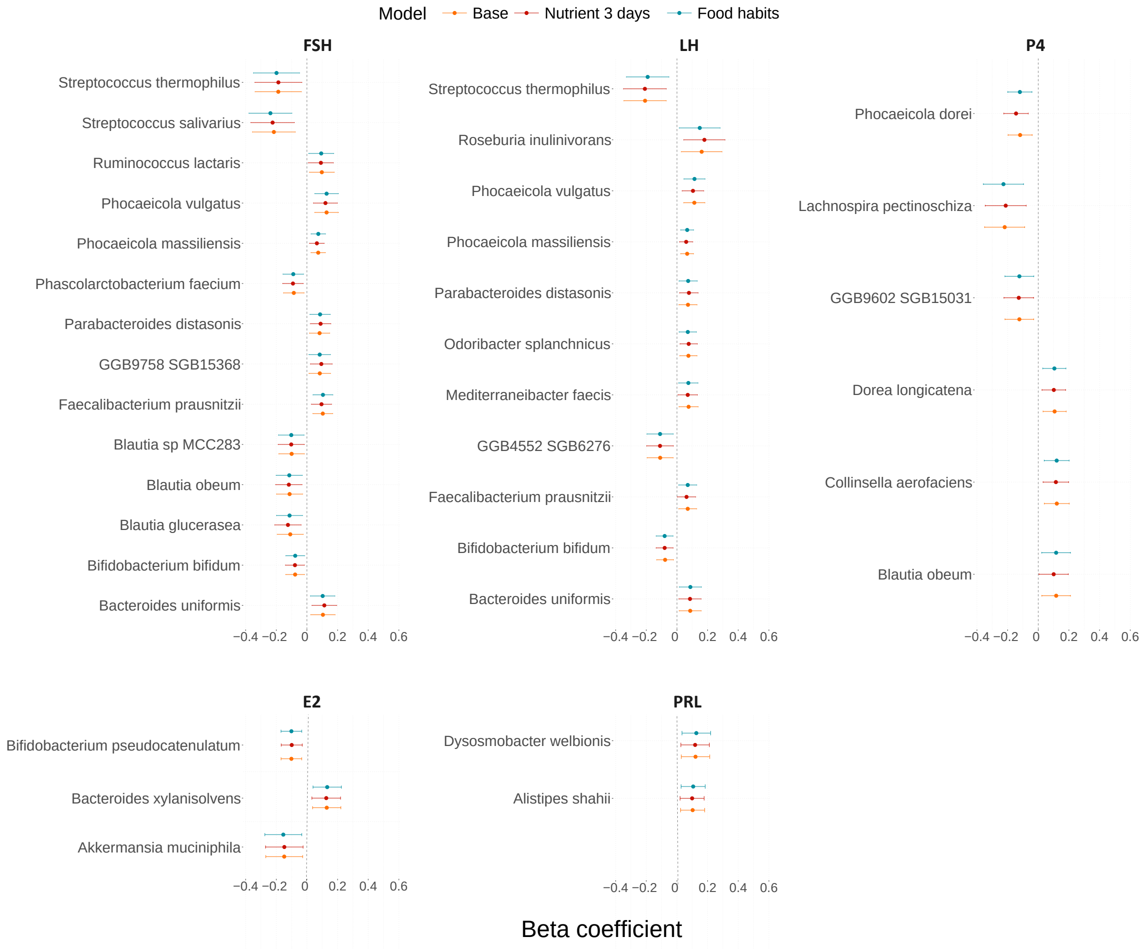
Supplementary Figure 5: Relative abundance of the most abundant genera across visits. The figure shows the distribution of the most prevalent gut microbial genera within each visit. Genera are represented as percentages of total community composition.



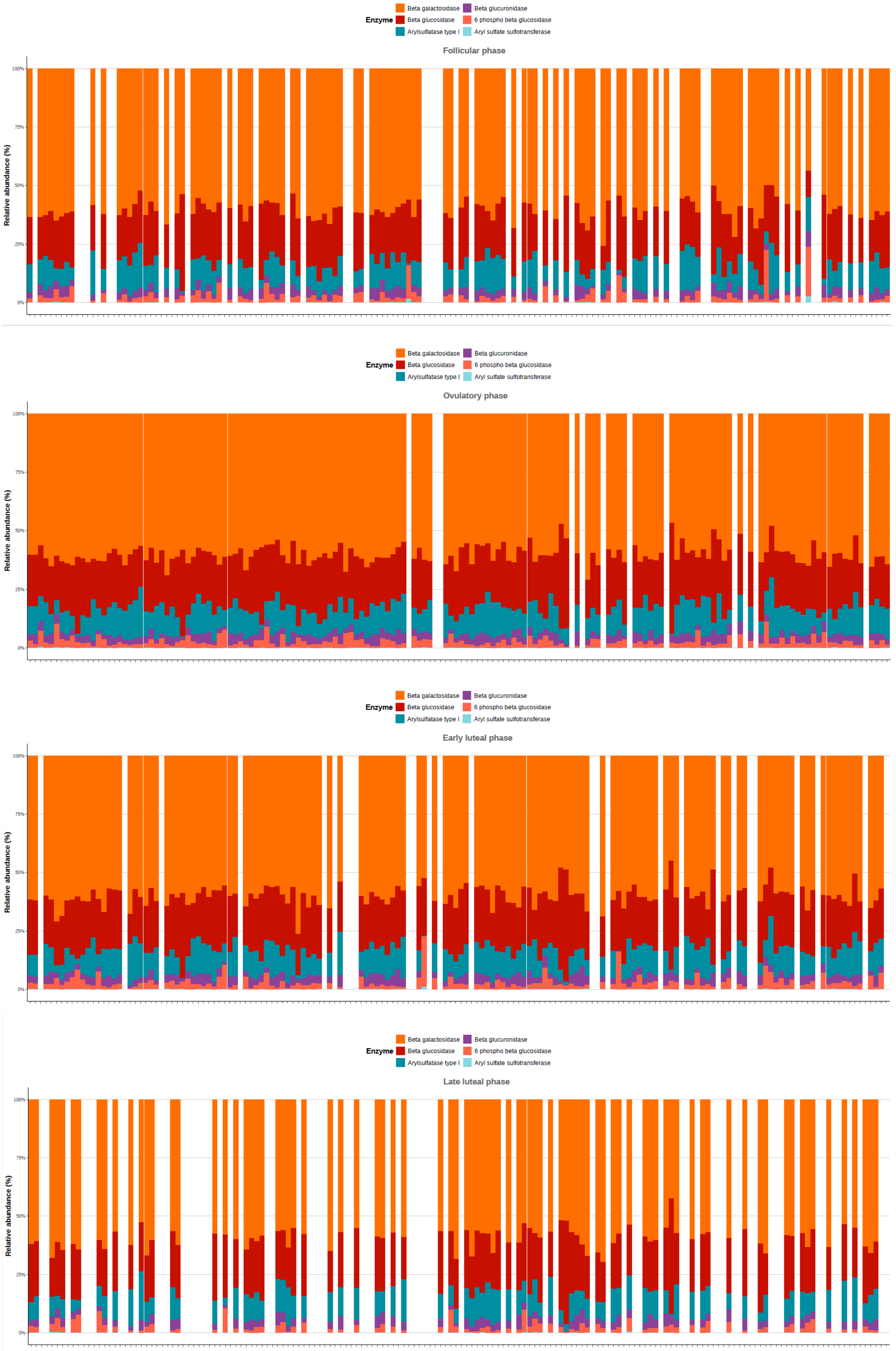
Supplementary Figure 6. Relative abundance of the most abundant species across visits. The figure shows the distribution of the most prevalent gut microbial species within each visit. Species are represented as percentages of total community composition.



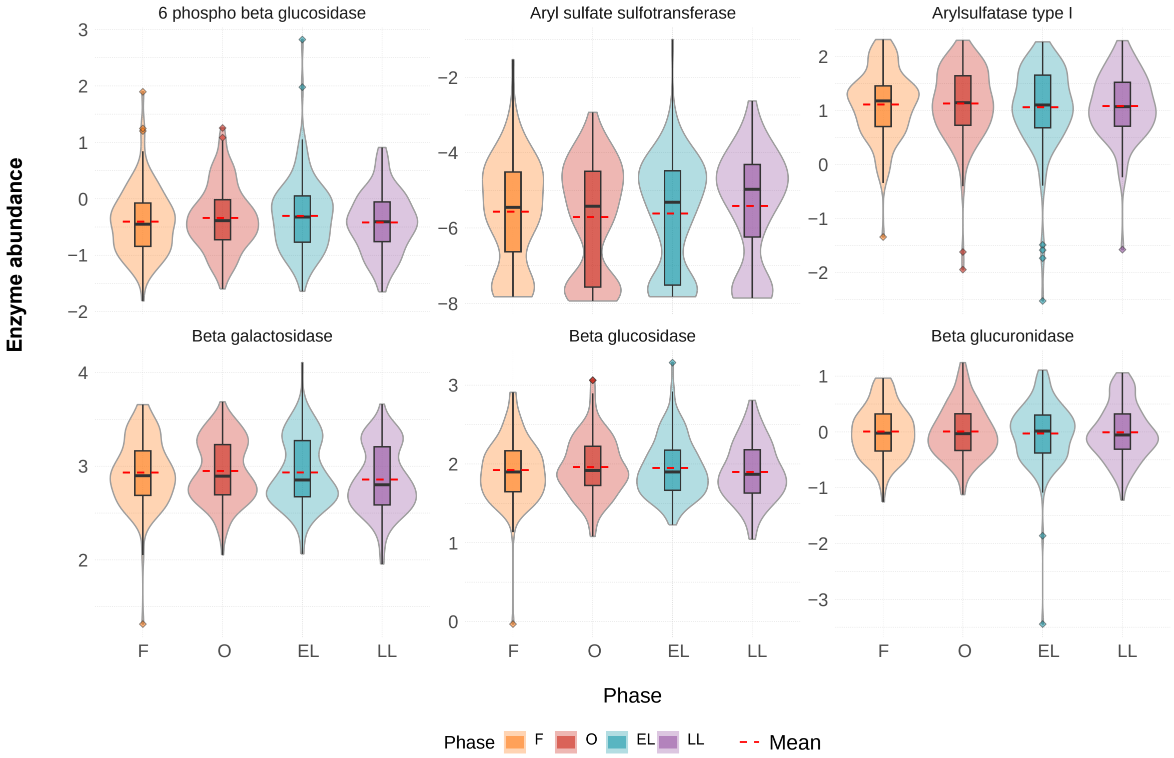
Supplementary Figure 7. Relative abundance of dominant gut microbial taxa across cities. Microbial species are represented as proportions (%) in circular plots. Panel A shows genus level abundances, and panel B – species level abundances.



Supplementary Figure 8: Forest plot showing associations between microbial species and sex hormone levels across models (Base, Nutrient 3-day intake, and Food habits). Beta coefficients are presented on the x-axis and microbial species on the y-axis. The Base model (in orange) excludes dietary variables. The Food habits model (in blue) includes coffee, fruits, whole milk, yogurt, vegetables, pasta and rice, and spirits, while the Nutrient 3-day intake model (in red) includes carbohydrate, fat, sugar, cholesterol, protein, sodium, and fiber. All models were adjusted for age, BMI, Bristol Stool Scale, city of sampling, time of fecal collection, DNA concentration, reads left after quality control, and batch effect.



Supplementary Figure 9: Relative abundance of estrobolome enzymes across menstrual phases. The abundances of the six estrobolome enzymes investigated in the study are shown as the relative abundance for each participant, separated by menstrual phase.



Supplementary Figure 10. Functional gene family abundances across menstrual cycle phases. Abundances are shown as centered log-ratio transformed values for each gene family and mean in each phase is reported.