

Supplementary data

Supplementary materials and methods

Analysis of the gut microbiome

DNA was extracted from the fecal samples using the QIAamp DNA Stool Mini Kit (Qiagen, Inc., Valencia, CA, USA) with the following protocol modifications: Approximately 200 mg of fecal sample was mixed with 1.3-mL ASL buffer in a 0.7-mm garnet bead tube (MO BIO Laboratories, Carlsbad, CA, USA), vortexed for 30 s, and subsequently heated at 95°C for 10 min followed by centrifugation. The supernatant was transferred into a 0.1-mm glass bead tube (MO BIO Laboratories, Carlsbad, CA, USA), homogenized twice by bead-beating for 2 min each, and centrifuged. The supernatant was transferred into a new tube, vortexed with an inhibitEX tablet (Qiagen, Inc., Valencia, CA, USA) for 1 min, and incubated for 1 min. The samples were centrifuged, and the supernatant was placed in a new sample tube. The remaining steps of the DNA extraction process were carried out using automated QIAcube instrument (Qiagen, Inc., Valencia, CA, USA) and eluted in 200 µL of AE buffer. The extracted DNA samples were stored at –20°C until use.

PCR amplification of the fecal DNA samples was performed with the Illumina-adapted universal primers 515F/806R targeting the V4 region of the 16S rRNA gene.[1] PCR mixtures (50 µL) contained 35.5 µL of PCR water, 5 µL 10× Takara Ex Taq buffer, 0.1 mM Takara dNTP mix, 0.25 µM of each primer, 0.05 units Ex Taq polymerase (TaKaRa, Shiga, Japan), and 5.0 µL of genomic DNA. Reactions were held at 94°C for 3 min for denaturation, followed by 35-cycle amplification at 94°C for 45 s, 50°C for 60 s, and 72°C for 90 s; a final extension at 72°C for 10 min was added to ensure complete amplification. The amplicons were purified using the MO BIO UltraClean PCR Clean-Up Kit (MO BIO Laboratories, Carlsbad, CA, USA) and quantified using the KAPA Library Quantification Kit (KAPA Biosystems, Woburn, MA, USA). The amplicons for each sample were normalized, pooled, and

sequenced on the MiSeq platform using a paired-end 2×300 bp reagent kit (Illumina, San Diego, CA, USA).

Sequence data were processed using QIIME (v 1.7.0).[2] Sequences were clustered into operational taxonomic units (OTUs) at 97% identity using an open-reference OTU picking protocol against the 13_5 revision of the Greengenes database.[3] The taxonomy assignments for OTUs were based on the Greengenes reference sequence using the RDP classifier.[4] The relative abundances of microbial taxa at each level from genus to kingdom were generated from a non-rarefied OTU table.

Statistical analysis

Alpha-diversity indexes (Chao1 richness, observed species, and Shannon diversity index) were estimated and tested for significant differences between the healthy and metabolic syndrome (MetS) groups by two-sample t-test using Monte Carlo permutations in QIIME.

Beta-diversity distances (unweighted/weighted UniFrac and Bray-Curtis distances) were calculated on an OTU table rarefied to an even sequence depth of 8,000 sequences per sample. Analysis of similarities (ANOSIM) analysis[5] on beta-diversity matrices was performed in QIIME to test for significant differences between the microbial communities of the healthy and MetS groups. Additionally, two-dimensional nonparametric multi-dimensional scaling (NMDS) plots were generated from Bray-Curtis distances using the Vegan package in R to visually represent microbiota compositional differences among samples.

Multivariate analysis was performed using multivariate association with linear models (MaAsLin)[6] to identify associations of microbial abundances (at all taxonomic levels from kingdom to genus) with MetS status after accounting for confounding variables. In the analysis, age and sex were treated as fixed effects, and monozygotic (MZ) twin and family relationships were treated as random variables. Associations with a Benjamini and Hochberg false discovery rate (FDR)-corrected p value (q value) of

<0.25 were considered to be significant. Correlations between each MetS component and MetS-related microbes were assessed by Spearman's rank correlation test. Univariate analysis for identifying differentially abundant taxa between the MetS and healthy groups was performed using the linear discriminant analysis effect size (LEfSe).[7] The G-test of independence was used to determine whether the presence/absence of taxa was associated with MetS status.

Beta-diversity distances between MZ twin pairs, dizygotic (DZ) twin pairs, family members, and unrelated individuals were compared by two-sample t-test with 1000 Monte Carlo permutations. Heritability estimates (H2r) for each microbial taxon were obtained using a variance component method in Sequential Oligogenic Linkage Analysis Routines (SOLAR),[8] which can estimate the heritability of traits within diverse family structures. All MZ/DZ twin pairs and their parents and siblings were included in this analysis. Because the traits with high residual kurtosis (above 0.8) and low standard deviation (below 0.5) are not suitable for SOLAR analysis, we used the filtered set of taxa excluding low-abundance taxa (<0.1% of mean relative abundance) to meet the analytic conditions of SOLAR. The relative abundances of the taxa were transformed using the inverse normal command in SOLAR. H2r values were calculated after adjustment for covariates including age, sex, and MetS. q values of <0.05 were considered significant. H2r values for metabolic traits were calculated in the same manner, except that only age and sex were included as covariates. Heritability of MetS was analyzed using a threshold model with adjustment for age and sex in SOLAR. Additionally, the heritability of each taxon was assessed using another heritability measure, intraclass correlation coefficients (ICCs), for a gut microbial profile generated by combining the two OTU tables from 190 twin pairs in the present study and 382 twin pairs of the study by Goodrich *et al.*[9] The MZ/DZ ICCs for the relative abundance of each taxon were calculated using the irr package in R. Heritability estimates were obtained by multiplying the difference between the MZ and DZ ICCs by two.

The associations between host genotype and specific gut microbial taxa were tested using the family-based association tests for quantitative traits (QFAM) module implemented in PLINK

(<http://pngu.mgh.harvard.edu/purcell/plink/>).[10] QFAM performs a simple linear regression of quantitative phenotype on genotype while accounting for family structure. This analysis was conducted for 351 twins, parents, and siblings whose *APOA5* SNP rs651821 genotype data were available. In the case of MZ twins, genotyping was performed for only one member of each pair. Because QFAM do not accept covariates, the gut microbial abundances, which were transformed with the arcsine square-root transformation, were regressed on MetS status and/or triglyceride in addition to age and sex, and the standardized residual values were used as quantitative phenotypes in QFAM analysis. A total of 100,000 permutations were carried out to correct for the dependence between related individuals, and the results were reported as pointwise empirical p value (EMP1). The resulting EMP1 values were adjusted for multiple testing with the FDR correction. q values of <0.05 were considered significant. The effects of host genotype on each MetS trait were also examined with QFAM. The association of host genotype with MetS status was assessed by chi-square test.

Supplementary tables

Supplementary table S1. Significant associations between MetS status and filtered set of taxa.

| Taxon | Coefficient | p value | q value |
|---|-------------|---------|---------|
| Bacteria Proteobacteria Betaproteobacteria Burkholderiales Alcaligenaceae Sutterella | 0.0095 | 0.0125 | 0.0735 |
| Bacteria Proteobacteria Betaproteobacteria Burkholderiales Alcaligenaceae | 0.0094 | 0.0125 | 0.0735 |
| Bacteria Proteobacteria Betaproteobacteria Burkholderiales | 0.0086 | 0.0206 | 0.1020 |
| Bacteria Proteobacteria Betaproteobacteria | 0.0084 | 0.0258 | 0.1129 |
| Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae | 0.0080 | 0.0077 | 0.0526 |
| Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae Lactobacillus | 0.0077 | 0.0084 | 0.0556 |
| Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Dorea | 0.0034 | 0.0915 | 0.2374 |
| Archaea Euryarchaeota Methanobacteria Methanobacteriales Methanobacteriaceae Methanobrevibacter | 0.0008 | 0.0112 | 0.0706 |
| Bacteria Verrucomicrobia | -0.0025 | 0.0267 | 0.1129 |
| Bacteria Verrucomicrobia Verrucomicrobiae Verrucomicrobiales Verrucomicrobiaceae | -0.0025 | 0.0283 | 0.1129 |
| Bacteria Verrucomicrobia Verrucomicrobiae Verrucomicrobiales Verrucomicrobiaceae Akkermansia | -0.0025 | 0.0282 | 0.1129 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales [Odoribacteraceae] Odoribacter | -0.0043 | 0.0475 | 0.1659 |
| Bacteria Firmicutes Clostridia Clostridiales Christensenellaceae | -0.0054 | 0.0381 | 0.1371 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales [Odoribacteraceae] | -0.0078 | 0.0097 | 0.0628 |
| Bacteria Actinobacteria Actinobacteria Bifidobacteriales Bifidobacteriaceae Bifidobacterium | -0.0102 | 0.0874 | 0.2369 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales [Paraprevotellaceae] Paraprevotella | -0.0105 | 0.0803 | 0.2223 |
| Bacteria Actinobacteria Actinobacteria Bifidobacteriales Bifidobacteriaceae | -0.0108 | 0.0792 | 0.2218 |
| Bacteria Actinobacteria Actinobacteria Bifidobacteriales | -0.0108 | 0.0792 | 0.2218 |
| Bacteria Actinobacteria Actinobacteria | -0.0118 | 0.0537 | 0.1757 |
| Bacteria Actinobacteria | -0.0122 | 0.0481 | 0.1659 |

| | | | |
|---|---------|--------|--------|
| Bacteria Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Parabacteroides | -0.0135 | 0.0352 | 0.1321 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae | -0.0141 | 0.0287 | 0.1129 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales [Paraprevotellaceae] | -0.0176 | 0.0707 | 0.2109 |
| Bacteria Proteobacteria Gammaproteobacteria | -0.0177 | 0.0788 | 0.2218 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales Rikenellaceae | -0.0253 | 0.0037 | 0.0289 |
| Bacteria Tenericutes Mollicutes | -0.0272 | 0.0075 | 0.0523 |
| Bacteria Tenericutes | -0.0274 | 0.0071 | 0.0514 |

Supplementary table S2. Associations between MetS status and full set of taxa.

| Rank | Taxon | Coefficient | p value | q value |
|------|---|-------------|---------|---------|
| 1 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales Other Other | -0.0120 | 0.0036 | 0.0285 |
| 2 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Rikenellaceae g__ | -0.0253 | 0.0037 | 0.0285 |
| 3 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Rikenellaceae | -0.0253 | 0.0037 | 0.0285 |
| 4 | k__Bacteria p__Actinobacteria c__Coriobacteriia o__Coriobacteriales f__Coriobacteriaceae g__ | -0.0038 | 0.0042 | 0.0319 |
| 5 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Peptococcaceae | -0.0017 | 0.0061 | 0.0449 |
| 6 | k__Bacteria p__Tenericutes | -0.0274 | 0.0071 | 0.0504 |
| 7 | k__Bacteria p__Tenericutes c__Mollicutes | -0.0272 | 0.0075 | 0.0520 |
| 8 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Lactobacillaceae | 0.0080 | 0.0077 | 0.0525 |
| 9 | k__Bacteria p__Tenericutes c__Mollicutes o__RF39 f__ g__ | -0.0269 | 0.0080 | 0.0533 |
| 10 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Lactobacillaceae g__Lactobacillus | 0.0077 | 0.0084 | 0.0542 |
| 11 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__[Paraprevotellaceae] Other | -0.0021 | 0.0097 | 0.0607 |
| 12 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__[Odoribacteraceae] | -0.0078 | 0.0097 | 0.0607 |
| 13 | k__Archaea p__Euryarchaeota c__Methanobacteria o__Methanobacteriales f__Methanobacteriaceae g__Methanobrevibacter | 0.0008 | 0.0112 | 0.0684 |
| 14 | k__Bacteria p__Proteobacteria c__Betaproteobacteria o__Burkholderiales f__Alcaligenaceae g__Sutterella | 0.0095 | 0.0125 | 0.0732 |
| 15 | k__Bacteria p__Proteobacteria c__Betaproteobacteria o__Burkholderiales f__Alcaligenaceae | 0.0094 | 0.0125 | 0.0732 |
| 16 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Veillonellaceae Other | 0.0065 | 0.0136 | 0.0784 |
| 17 | k__Bacteria p__Tenericutes Other Other Other Other | -0.0011 | 0.0157 | 0.0877 |
| 18 | k__Bacteria p__Proteobacteria c__Betaproteobacteria o__Burkholderiales | 0.0086 | 0.0206 | 0.1053 |
| 19 | k__Bacteria p__Actinobacteria c__Coriobacteriia o__Coriobacteriales f__Coriobacteriaceae | -0.0032 | 0.0232 | 0.1081 |
| 20 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales Other Other | 0.0012 | 0.0240 | 0.1103 |
| 21 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Leuconostocaceae g__ | 0.0024 | 0.0242 | 0.1103 |
| 22 | k__Bacteria p__Proteobacteria c__Betaproteobacteria | 0.0084 | 0.0258 | 0.1146 |

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|----|--|---------|--------|--------|
| 23 | k__Bacteria p__Verrucomicrobia | -0.0025 | 0.0267 | 0.1150 |
| 24 | k__Bacteria p__Verrucomicrobia c__Verrucomicrobiae o__Verrucomicrobiales f__Verrucomicrobiaceae g__Akkermansia | -0.0025 | 0.0282 | 0.1180 |
| 25 | k__Bacteria p__Verrucomicrobia c__Verrucomicrobiae o__Verrucomicrobiales f__Verrucomicrobiaceae | -0.0025 | 0.0283 | 0.1180 |
| 26 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Porphyromonadaceae | -0.0141 | 0.0287 | 0.1180 |
| 27 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Ruminococcaceae Other | -0.0204 | 0.0288 | 0.1180 |
| 28 | k__Bacteria p__Actinobacteria c__Actinobacteria o__Actinomycetales f__Micrococcaceae | -0.0016 | 0.0290 | 0.1180 |
| 29 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Clostridiaceae g__ | 0.0056 | 0.0297 | 0.1190 |
| 30 | k__Bacteria p__Actinobacteria c__Actinobacteria o__Actinomycetales f__Micrococcaceae g__Rothia | -0.0016 | 0.0298 | 0.1190 |
| 31 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Porphyromonadaceae g__Parabacteroides | -0.0135 | 0.0352 | 0.1376 |
| 32 | k__Bacteria p__Tenericutes c__Mollicutes Other Other Other | -0.0010 | 0.0372 | 0.1424 |
| 33 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Christensenellaceae | -0.0054 | 0.0381 | 0.1446 |
| 34 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Christensenellaceae g__ | -0.0054 | 0.0446 | 0.1658 |
| 35 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__[Odoribacteraceae] g__Odoribacter | -0.0043 | 0.0475 | 0.1743 |
| 36 | k__Bacteria p__Actinobacteria | -0.0122 | 0.0481 | 0.1751 |
| 37 | k__Bacteria p__Actinobacteria c__Actinobacteria o__Actinomycetales | -0.0019 | 0.0517 | 0.1804 |
| 38 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Prevotellaceae | -0.0031 | 0.0527 | 0.1807 |
| 39 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__[Mogibacteriaceae] g__ | -0.0027 | 0.0529 | 0.1807 |
| 40 | k__Bacteria p__Actinobacteria c__Actinobacteria | -0.0118 | 0.0537 | 0.1822 |
| 41 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Peptococcaceae Other | -0.0011 | 0.0570 | 0.1887 |
| 42 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__[Paraprevotellaceae] | -0.0176 | 0.0707 | 0.2229 |
| 43 | k__Bacteria p__Actinobacteria c__Coriobacteriia o__Coriobacteriales f__Coriobacteriaceae g__Eggerthella | 0.0007 | 0.0751 | 0.2303 |
| 44 | k__Bacteria p__Proteobacteria c__Gammaproteobacteria | -0.0177 | 0.0788 | 0.2376 |
| 45 | k__Bacteria p__Actinobacteria c__Actinobacteria o__Bifidobacteriales | -0.0108 | 0.0792 | 0.2376 |
| 46 | k__Bacteria p__Actinobacteria c__Actinobacteria o__Bifidobacteriales f__Bifidobacteriaceae | -0.0108 | 0.0792 | 0.2376 |
| 47 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__[Paraprevotellaceae] g__Paraprevotella | -0.0105 | 0.0803 | 0.2395 |

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|----|---|---------|--------|--------|
| 48 | k__Bacteria p__Actinobacteria c__Actinobacteria o__Bifidobacteriales f__Bifidobacteriaceae g__Bifidobacterium | -0.0102 | 0.0874 | 0.2539 |
| 49 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Clostridiaceae Other | 0.0009 | 0.0882 | 0.2548 |
| 50 | k__Bacteria p__Synergistetes c__Synergistia o__Synergistales f__Synergistaceae | -0.0005 | 0.0900 | 0.2571 |
| 51 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__Dorea | 0.0034 | 0.0915 | 0.2575 |
| 52 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Ruminococcaceae g__ | -0.0183 | 0.0944 | 0.2608 |
| 53 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__[Mogibacteriaceae] | -0.0024 | 0.0958 | 0.2615 |
| 54 | k__Bacteria p__Cyanobacteria c__Chloroplast o__Streptophyta f__ g__ | 0.0011 | 0.1028 | 0.2710 |
| 55 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Clostridiaceae | 0.0050 | 0.1110 | 0.2871 |
| 56 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Ruminococcaceae g__Oscillospira | -0.0060 | 0.1119 | 0.2880 |
| 57 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Christensenellaceae g__Christensenella | -0.0009 | 0.1155 | 0.2953 |
| 58 | k__Bacteria p__Firmicutes c__Bacilli | 0.0066 | 0.1184 | 0.2975 |
| 59 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__[Odoribacteraceae] g__Butyricimonas | -0.0039 | 0.1185 | 0.2975 |
| 60 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Leuconostocaceae | 0.0018 | 0.1189 | 0.2975 |
| 61 | k__Bacteria p__Proteobacteria c__Deltaproteobacteria | -0.0059 | 0.1213 | 0.3020 |
| 62 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales | 0.0065 | 0.1256 | 0.3076 |
| 63 | k__Bacteria p__Fusobacteria c__Fusobacteriia o__Fusobacteriales f__Fusobacteriaceae Other | 0.0003 | 0.1258 | 0.3076 |
| 64 | k__Bacteria p__Proteobacteria c__Deltaproteobacteria o__Desulfovibrionales | -0.0058 | 0.1287 | 0.3080 |
| 65 | k__Bacteria p__Proteobacteria c__Deltaproteobacteria o__Desulfovibrionales f__Desulfovibrionaceae | -0.0058 | 0.1290 | 0.3080 |
| 66 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Veillonellaceae g__Veillonella | -0.0057 | 0.1299 | 0.3080 |
| 67 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__ g__ | -0.0010 | 0.1308 | 0.3080 |
| 68 | k__Bacteria p__Proteobacteria c__Gammaproteobacteria Other Other Other | -0.0014 | 0.1325 | 0.3087 |
| 69 | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Pasteurellales f__Pasteurellaceae g__Actinobacillus | -0.0004 | 0.1453 | 0.3300 |
| 70 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__ g__ | -0.0141 | 0.1472 | 0.3300 |
| 71 | k__Bacteria p__Bacteroidetes Other Other Other Other | -0.0012 | 0.1531 | 0.3406 |
| 72 | k__Bacteria p__Cyanobacteria c__Chloroplast | 0.0010 | 0.1578 | 0.3497 |

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|----|--|---------|--------|--------|
| 73 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Leuconostocaceae g__Leuconostoc | 0.0007 | 0.1631 | 0.3572 |
| 74 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Prevotellaceae Other | -0.0010 | 0.1645 | 0.3574 |
| 75 | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Pasteurellales f__Pasteurellaceae Other | -0.0016 | 0.1750 | 0.3771 |
| 76 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__[Tissierellaceae] g__WAL_1855D | -0.0007 | 0.1785 | 0.3817 |
| 77 | k__Bacteria p__Proteobacteria c__Betaproteobacteria Other Other Other | 0.0007 | 0.1820 | 0.3861 |
| 78 | k__Bacteria p__Actinobacteria c__Actinobacteria o__Actinomycetales f__Actinomycetaceae g__Actinomyces | -0.0009 | 0.1883 | 0.3930 |
| 79 | k__Bacteria Other Other Other Other Other | -0.0026 | 0.1887 | 0.3930 |
| 80 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__[Tissierellaceae] | -0.0012 | 0.1889 | 0.3930 |
| 81 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Veillonellaceae | 0.0202 | 0.1981 | 0.4065 |
| 82 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__Lachnospira | -0.0075 | 0.1982 | 0.4065 |
| 83 | k__Bacteria p__Actinobacteria c__Actinobacteria o__Actinomycetales f__Actinomycetaceae g__ | -0.0008 | 0.2076 | 0.4145 |
| 84 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__[Barnesiellaceae] g__ | -0.0049 | 0.2329 | 0.4484 |
| 85 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__Anaerostipes | -0.0026 | 0.2391 | 0.4540 |
| 86 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__S24-7 g__ | -0.0069 | 0.2400 | 0.4540 |
| 87 | k__Bacteria p__Proteobacteria c__Deltaproteobacteria o__Desulfovibrionales f__Desulfovibrionaceae g__ | -0.0008 | 0.2570 | 0.4747 |
| 88 | k__Bacteria p__Proteobacteria c__Deltaproteobacteria o__Desulfovibrionales f__Desulfovibrionaceae g__Bilophila | -0.0027 | 0.2700 | 0.4937 |
| 89 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Dehalobacteriaceae g__Dehalobacterium | -0.0009 | 0.2889 | 0.5247 |
| 90 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__Roseburia | 0.0072 | 0.2908 | 0.5249 |
| 91 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Ruminococcaceae | -0.0148 | 0.2924 | 0.5249 |
| 92 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Dehalobacteriaceae | -0.0009 | 0.2929 | 0.5249 |
| 93 | k__Bacteria p__Proteobacteria | -0.0095 | 0.2965 | 0.5297 |
| 94 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Enterococcaceae g__Enterococcus | -0.0006 | 0.2983 | 0.5311 |
| 95 | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacteriales f__Enterobacteriaceae | -0.0098 | 0.3013 | 0.5347 |
| 96 | k__Bacteria p__Proteobacteria Other Other Other Other | 0.0005 | 0.3065 | 0.5420 |
| 97 | k__Bacteria p__Fusobacteria c__Fusobacteriia o__Fusobacteriales f__Fusobacteriaceae | -0.0005 | 0.3364 | 0.5742 |

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|-----|--|---------|--------|--------|
| 98 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Ruminococcaceae g__Ruminococcus | 0.0075 | 0.3364 | 0.5742 |
| 99 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Porphyromonadaceae g__Porphyromonas | -0.0004 | 0.3412 | 0.5742 |
| 100 | k__Archaea | 0.0004 | 0.3414 | 0.5742 |
| 101 | k__Archaea p__Euryarchaeota | 0.0004 | 0.3414 | 0.5742 |
| 102 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Clostridiaceae g__02d06 | -0.0017 | 0.3426 | 0.5742 |
| 103 | k__Bacteria p__Firmicutes Other Other Other Other | 0.0006 | 0.3449 | 0.5763 |
| 104 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Veillonellaceae g__Phascolarctobacterium | -0.0073 | 0.3508 | 0.5843 |
| 105 | k__Archaea p__Euryarchaeota c__Methanobacteria o__Methanobacteriales f__Methanobacteriaceae g__Methanosphaera | -0.0008 | 0.3614 | 0.5964 |
| 106 | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacteriales f__Enterobacteriaceae g__ | -0.0029 | 0.3653 | 0.5993 |
| 107 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales Other Other | -0.0021 | 0.3692 | 0.6038 |
| 108 | k__Bacteria p__Firmicutes c__Erysipelotrichi o__Erysipelotrichales f__Erysipelotrichaceae | 0.0042 | 0.3719 | 0.6046 |
| 109 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__[Paraprevotellaceae] g__[Prevotella] | -0.0074 | 0.3826 | 0.6105 |
| 110 | k__Archaea p__Euryarchaeota c__Methanobacteria o__Methanobacteriales | 0.0003 | 0.3830 | 0.6105 |
| 111 | k__Archaea p__Euryarchaeota c__Methanobacteria o__Methanobacteriales f__Methanobacteriaceae | 0.0003 | 0.3830 | 0.6105 |
| 112 | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacteriales f__Enterobacteriaceae g__Citrobacter | 0.0005 | 0.3845 | 0.6105 |
| 113 | k__Bacteria p__Synergistetes c__Synergistia o__Synergistales | -0.0004 | 0.3929 | 0.6173 |
| 114 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__[Tissierellaceae] g__Peptoniphilus | -0.0003 | 0.3968 | 0.6173 |
| 115 | k__Bacteria | 0.0007 | 0.4090 | 0.6277 |
| 116 | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Pasteurellales f__Pasteurellaceae g__Haemophilus | -0.0024 | 0.4104 | 0.6277 |
| 117 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Ruminococcaceae g__Anaerotruncus | -0.0004 | 0.4184 | 0.6329 |
| 118 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Streptococcaceae | 0.0025 | 0.4197 | 0.6331 |
| 119 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Veillonellaceae g__Megasphaera | -0.0034 | 0.4392 | 0.6498 |
| 120 | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacteriales f__Enterobacteriaceae Other | -0.0062 | 0.4422 | 0.6525 |
| 121 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales | 0.0135 | 0.4484 | 0.6591 |
| 122 | k__Bacteria p__Firmicutes c__Clostridia | 0.0133 | 0.4539 | 0.6630 |

| | | | | |
|-----|---|---------|--------|--------|
| 123 | k__Bacteria p__Firmicutes c__Erysipelotrichi o__Erysipelotrichales f__Erysipelotrichaceae g__Catenibacterium | 0.0024 | 0.4605 | 0.6678 |
| 124 | k__Bacteria p__Firmicutes | 0.0139 | 0.4612 | 0.6678 |
| 125 | k__Bacteria p__Cyanobacteria c__4C0d-2 o__YS2 f__ g__ | 0.0002 | 0.4661 | 0.6731 |
| 126 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae Other | 0.0025 | 0.4680 | 0.6741 |
| 127 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Streptococcaceae g__Lactococcus | 0.0003 | 0.4711 | 0.6742 |
| 128 | k__Bacteria p__Cyanobacteria c__4C0d-2 | 0.0002 | 0.4718 | 0.6742 |
| 129 | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Enterobacteriales f__Enterobacteriaceae g__Klebsiella | -0.0019 | 0.4792 | 0.6794 |
| 130 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Veillonellaceae g__Dialister | 0.0115 | 0.4908 | 0.6904 |
| 131 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Porphyromonadaceae Other | -0.0003 | 0.5341 | 0.7380 |
| 132 | k__Bacteria p__Proteobacteria c__Alphaproteobacteria | 0.0002 | 0.5640 | 0.7599 |
| 133 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Veillonellaceae g__Megamonas | 0.0006 | 0.5829 | 0.7796 |
| 134 | k__Bacteria p__Firmicutes c__Bacilli o__Gemellales f__Gemellaceae | 0.0003 | 0.6071 | 0.8001 |
| 135 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Prevotellaceae g__Prevotella | 0.0144 | 0.6093 | 0.8011 |
| 136 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__ g__ | -0.0002 | 0.6108 | 0.8011 |
| 137 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Prevotellaceae g__ | 0.0140 | 0.6189 | 0.8034 |
| 138 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Streptococcaceae g__Streptococcus | 0.0015 | 0.6252 | 0.8034 |
| 139 | k__Bacteria p__Firmicutes c__Erysipelotrichi o__Erysipelotrichales f__Erysipelotrichaceae g__Holdemania | -0.0004 | 0.6383 | 0.8136 |
| 140 | k__Bacteria p__Firmicutes c__Erysipelotrichi o__Erysipelotrichales f__Erysipelotrichaceae g__[Eubacterium] | 0.0020 | 0.6481 | 0.8204 |
| 141 | k__Bacteria p__Cyanobacteria | -0.0004 | 0.6576 | 0.8265 |
| 142 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Veillonellaceae g__Acidaminococcus | -0.0001 | 0.6609 | 0.8288 |
| 143 | k__Bacteria p__Firmicutes c__Bacilli o__Gemellales | 0.0002 | 0.6878 | 0.8547 |
| 144 | k__Bacteria p__Firmicutes c__Erysipelotrichi o__Erysipelotrichales f__Erysipelotrichaceae Other | -0.0002 | 0.6895 | 0.8548 |
| 145 | k__Bacteria p__Fusobacteria c__Fusobacteriia o__Fusobacteriales f__Fusobacteriaceae g__Fusobacterium | -0.0002 | 0.7085 | 0.8561 |
| 146 | k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Pasteurellales f__Pasteurellaceae | -0.0011 | 0.7162 | 0.8623 |
| 147 | k__Bacteria p__Firmicutes c__Erysipelotrichi o__Erysipelotrichales f__Erysipelotrichaceae g__Bulleidia | 0.0001 | 0.7237 | 0.8675 |

| | | | | |
|-----|--|---------|--------|--------|
| 148 | k__Bacteria p__Firmicutes c__Erysipelotrichi o__Erysipelotrichales f__Erysipelotrichaceae g__Coprobacillus | -0.0001 | 0.7271 | 0.8696 |
| 149 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__Coprococcus | -0.0013 | 0.7717 | 0.9050 |
| 150 | k__Bacteria p__Firmicutes c__Erysipelotrichi o__Erysipelotrichales f__Erysipelotrichaceae g__ | 0.0006 | 0.7802 | 0.9091 |
| 151 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__[Paraprevotellaceae] g__ | -0.0001 | 0.7881 | 0.9144 |
| 152 | k__Bacteria p__Proteobacteria c__Betaproteobacteria o__Burkholderiales f__Oxalobacteraceae | -0.0002 | 0.8153 | 0.9377 |
| 153 | k__Bacteria p__Firmicutes c__Bacilli o__Gemellales f__Gemellaceae g__Gemella | 0.0001 | 0.8212 | 0.9382 |
| 154 | k__Bacteria p__Fusobacteria c__Fusobacteriia o__Fusobacteriales | -0.0002 | 0.8224 | 0.9382 |
| 155 | k__Bacteria p__Proteobacteria c__Betaproteobacteria o__Burkholderiales f__Oxalobacteraceae g__Oxalobacter | 0.0002 | 0.8299 | 0.9417 |
| 156 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales | 0.0047 | 0.8353 | 0.9417 |
| 157 | k__Bacteria p__Bacteroidetes | 0.0046 | 0.8376 | 0.9417 |
| 158 | k__Bacteria p__Firmicutes c__Bacilli o__Turicibacterales f__Turicibacteraceae g__Turicibacter | -0.0001 | 0.8434 | 0.9417 |
| 159 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__[Tissierellaceae] g__Parvimonas | -0.0001 | 0.8473 | 0.9417 |
| 160 | k__Bacteria p__Firmicutes c__Clostridia Other Other Other | -0.0002 | 0.8521 | 0.9417 |
| 161 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Clostridiaceae g__Clostridium | 0.0004 | 0.8617 | 0.9430 |
| 162 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__[Ruminococcus] | -0.0006 | 0.8657 | 0.9430 |
| 163 | k__Bacteria p__Proteobacteria c__Deltaproteobacteria o__Desulfovibrionales f__Desulfovibrionaceae g__Desulfovibrio | -0.0004 | 0.8666 | 0.9430 |
| 164 | k__Bacteria p__Actinobacteria c__Actinobacteria o__Bifidobacteriales f__Bifidobacteriaceae Other | -0.0002 | 0.8778 | 0.9445 |
| 165 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Peptostreptococcaceae g__ | 0.0002 | 0.8991 | 0.9578 |
| 166 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__Pseudobutyrvibrio | 0.0001 | 0.9054 | 0.9582 |
| 167 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Bacteroidaceae g__Bacteroides | 0.0025 | 0.9057 | 0.9582 |
| 168 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Carnobacteriaceae | -0.0001 | 0.9070 | 0.9582 |
| 169 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__ | 0.0005 | 0.9171 | 0.9629 |
| 170 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Veillonellaceae g__Mitsuokella | -0.0001 | 0.9178 | 0.9629 |
| 171 | k__Bacteria p__Bacteroidetes c__Bacteroidia o__Bacteroidales f__Bacteroidaceae | 0.0022 | 0.9190 | 0.9629 |
| 172 | k__Bacteria p__Actinobacteria c__Actinobacteria Other Other Other | 0.0000 | 0.9305 | 0.9679 |

| | | | | |
|-----|---|---------|--------|--------|
| 173 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Peptostreptococcaceae | -0.0001 | 0.9354 | 0.9693 |
| 174 | k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Carnobacteriaceae g__Granulicatella | 0.0000 | 0.9425 | 0.9748 |
| 175 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae | 0.0006 | 0.9512 | 0.9805 |
| 176 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Lachnospiraceae g__Blautia | 0.0001 | 0.9676 | 0.9932 |
| 177 | k__Bacteria p__Firmicutes c__Clostridia o__Clostridiales f__Ruminococcaceae g__Faecalibacterium | -0.0003 | 0.9801 | 0.9993 |
| 178 | Unclassified Other Other Other Other Other | 0.0000 | 0.9809 | 0.9993 |

Rank: rank of the q values

Gray-colored taxa are those previously identified as significant features in the filtered set (supplementary table S1).

Supplementary table S3. Heritability of the gut microbiota.

| Taxon | H2r | | | | C2 | | | | Covariates | | | Group |
|--|-----------------|-----------------|---------|---------|-----------------|------------|---------|---------|---------------|---------------|----------------|---------|
| | H2r ± SE | 95% CI | p value | q value | C2 ± SE | 95% CI | p value | q value | p value (sex) | p value (age) | p value (MetS) | |
| Archaea | 0.2222 ± 0.0576 | (0.1093–0.3351) | 0.0000 | 0.0001 | 0.0000 ± NA | NA | NA | NA | 0.7592 | 0.0332 | 0.1594 | |
| Archaea Euryarchaeota | 0.2222 ± 0.0576 | (0.1093–0.3351) | 0.0000 | 0.0001 | 0.0000 ± NA | NA | NA | NA | 0.7592 | 0.0332 | 0.1594 | |
| Archaea Euryarchaeota Methanobacteria Methanobacteriales | 0.2254 ± 0.0577 | (0.1123–0.3385) | 0.0000 | 0.0001 | 0.0000 ± NA | NA | NA | NA | 0.7327 | 0.0299 | 0.1590 | |
| Archaea Euryarchaeota ... Methanobacteriales Methanobacteriaceae | 0.2254 ± 0.0577 | (0.1123–0.3385) | 0.0000 | 0.0001 | 0.0000 ± NA | NA | NA | NA | 0.7327 | 0.0299 | 0.1590 | |
| Archaea Euryarchaeota ... Methanobacteriaceae Methanobrevibacter | 0.2085 ± 0.0595 | (0.0919–0.3251) | 0.0001 | 0.0004 | 0.0000 ± NA | NA | NA | NA | 0.5688 | 0.1840 | 0.3873 | MetS |
| Bacteria | 0.2452 ± 0.0563 | (0.1349–0.3555) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.4470 | 0.1263 | 0.3435 | |
| Bacteria Actinobacteria | 0.4569 ± 0.0548 | (0.3495–0.5643) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.2051 | 0.0000 | 0.1054 | Healthy |
| Bacteria Actinobacteria Actinobacteria | 0.4112 ± 0.0561 | (0.3012–0.5212) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.2319 | 0.0000 | 0.1294 | Healthy |
| Bacteria Actinobacteria Actinobacteria Bifidobacteriales | 0.3724 ± 0.0953 | (0.1856–0.5592) | 0.0002 | 0.0005 | 0.0286 ± 0.0737 | (0–0.1731) | 0.3464 | 0.4606 | 0.1456 | 0.0000 | 0.3518 | Healthy |
| Bacteria Actinobacteria ... Bifidobacteriales Bifidobacteriaceae | 0.3724 ± 0.0953 | (0.1856–0.5592) | 0.0002 | 0.0005 | 0.0286 ± 0.0737 | (0–0.1731) | 0.3464 | 0.4606 | 0.1456 | 0.0000 | 0.3518 | Healthy |
| Bacteria Actinobacteria ... Bifidobacteriaceae Bifidobacterium | 0.3740 ± 0.0941 | (0.1896–0.5584) | 0.0001 | 0.0005 | 0.0198 ± 0.0727 | (0–0.1623) | 0.3911 | 0.4620 | 0.2077 | 0.0000 | 0.3585 | Healthy |
| Bacteria Bacteroidetes | 0.2520 ± 0.1005 | (0.0550–0.4490) | 0.0084 | 0.0164 | 0.0455 ± 0.0874 | (0–0.2168) | 0.2962 | 0.4606 | 0.3769 | 0.8094 | 0.5422 | |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales | 0.2527 ± 0.1005 | (0.0557–0.4497) | 0.0083 | 0.0164 | 0.0451 ± 0.0874 | (0–0.2164) | 0.2978 | 0.4606 | 0.3785 | 0.8079 | 0.5363 | |
| Bacteria Bacteroidetes ... Bacteroidales [Odoribacteraceae] | 0.1917 ± 0.0975 | (0.0006–0.3828) | 0.0276 | 0.0470 | 0.0580 ± 0.0787 | (0–0.2123) | 0.2239 | 0.4606 | 0.0498 | 0.1234 | 0.0029 | Healthy |
| Bacteria Bacteroidetes ... [Odoribacteraceae] Butyrivibrio | 0.1438 ± 0.1058 | (0–0.3512) | 0.0906 | 0.1262 | 0.0640 ± 0.0828 | (0–0.2263) | 0.2124 | 0.4606 | 0.3988 | 0.2535 | 0.0190 | |
| Bacteria Bacteroidetes ... [Odoribacteraceae] Odoribacter | 0.1916 ± 0.0575 | (0.0789–0.3043) | 0.0002 | 0.0006 | 0.0000 ± NA | NA | NA | NA | 0.0020 | 0.2504 | 0.0350 | Healthy |
| Bacteria Bacteroidetes ... Bacteroidales [Paraprevotellaceae] | 0.0830 ± 0.1067 | (0–0.2921) | 0.2209 | 0.2572 | 0.0968 ± 0.0863 | (0–0.2659) | 0.1188 | 0.4606 | 0.3476 | 0.0009 | 0.0664 | Healthy |
| Bacteria Bacteroidetes ... [Paraprevotellaceae] Prevotella | 0.0439 ± 0.1086 | (0–0.2568) | 0.3435 | 0.3605 | 0.0723 ± 0.0880 | (0–0.2448) | 0.1949 | 0.4606 | 0.1594 | 0.0008 | 0.9142 | |

| | | | | | | | | | | | | |
|---|-----------------|-----------------|--------|--------|-----------------|------------|--------|--------|--------|--------|--------|---------|
| Bacteria Bacteroidetes ... Paraprevotellaceae Paraprevotella | 0.1412 ± 0.0561 | (0.0312–0.2512) | 0.0043 | 0.0091 | 0.0000 ± NA | NA | NA | NA | 0.6257 | 0.0565 | 0.0589 | Healthy |
| Bacteria Bacteroidetes ... Bacteroidales Bacteroidaceae | 0.2383 ± 0.0595 | (0.1217–0.3549) | 0.0000 | 0.0001 | 0.0000 ± NA | NA | NA | NA | 0.0000 | 0.0053 | 0.9052 | |
| Bacteria Bacteroidetes ... Bacteroidaceae Bacteroides | 0.2381 ± 0.0595 | (0.1215–0.3547) | 0.0000 | 0.0001 | 0.0000 ± NA | NA | NA | NA | 0.0000 | 0.0048 | 0.9243 | |
| Bacteria Bacteroidetes ... Bacteroidales Porphyromonadaceae | 0.1527 ± 0.0583 | (0.0384–0.2670) | 0.0027 | 0.0061 | 0.0000 ± NA | NA | NA | NA | 0.0172 | 0.1113 | 0.0595 | Healthy |
| Bacteria Bacteroidetes ... Porphyromonadaceae Parabacteroides | 0.1567 ± 0.0591 | (0.0409–0.2725) | 0.0024 | 0.0059 | 0.0000 ± NA | NA | NA | NA | 0.0165 | 0.1186 | 0.0772 | Healthy |
| Bacteria Bacteroidetes ... Bacteroidales Prevotellaceae | 0.1487 ± 0.0959 | (0–0.3367) | 0.0628 | 0.1007 | 0.0737 ± 0.0812 | (0–0.2329) | 0.1739 | 0.4606 | 0.0028 | 0.0123 | 0.9730 | |
| Bacteria Bacteroidetes ... Prevotellaceae Prevotella | 0.1545 ± 0.0962 | (0–0.3431) | 0.0567 | 0.0927 | 0.0714 ± 0.0814 | (0–0.2309) | 0.1826 | 0.4606 | 0.0034 | 0.0145 | 0.9815 | |
| Bacteria Bacteroidetes ... Bacteroidales Rikenellaceae | 0.1299 ± 0.0911 | (0–0.3085) | 0.0804 | 0.1139 | 0.0704 ± 0.0759 | (0–0.2192) | 0.1678 | 0.4606 | 0.0000 | 0.1564 | 0.0051 | Healthy |
| Bacteria Cyanobacteria | 0.2749 ± 0.0654 | (0.1467–0.4031) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.0792 | 0.0098 | 0.2204 | |
| Bacteria Firmicutes | 0.1019 ± 0.1052 | (0–0.3081) | 0.1678 | 0.2067 | 0.0718 ± 0.0859 | (0–0.2402) | 0.1937 | 0.4606 | 0.1613 | 0.1159 | 0.5854 | |
| Bacteria Firmicutes Bacilli | 0.3528 ± 0.0569 | (0.2413–0.4643) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.9759 | 0.0019 | 0.1732 | |
| Bacteria Firmicutes Bacilli Lactobacillales | 0.3283 ± 0.0570 | (0.2166–0.4400) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.8378 | 0.0015 | 0.1546 | |
| Bacteria Firmicutes ... Lactobacillales Lactobacillaceae | 0.1708 ± 0.0591 | (0.0550–0.2866) | 0.0010 | 0.0029 | 0.0000 ± NA | NA | NA | NA | 0.8529 | 0.0023 | 0.0835 | MetS |
| Bacteria Firmicutes ... Lactobacillaceae Lactobacillus | 0.1481 ± 0.0594 | (0.0317–0.2645) | 0.0040 | 0.0086 | 0.0000 ± NA | NA | NA | NA | 0.8830 | 0.0037 | 0.0882 | MetS |
| Bacteria Firmicutes ... Lactobacillales Leuconostocaceae | 0.1366 ± 0.0951 | (0–0.3230) | 0.0779 | 0.1122 | 0.1438 ± 0.0812 | (0–0.3030) | 0.0293 | 0.4489 | 0.3517 | 0.0004 | 0.0994 | |
| Bacteria Firmicutes ... Lactobacillales Streptococcaceae | 0.2909 ± 0.0937 | (0.1072–0.4746) | 0.0017 | 0.0043 | 0.0412 ± 0.0737 | (0–0.1857) | 0.2829 | 0.4606 | 0.8866 | 0.0794 | 0.9084 | |
| Bacteria Firmicutes ... Streptococcaceae Streptococcus | 0.3186 ± 0.0949 | (0.1326–0.5046) | 0.0008 | 0.0025 | 0.0242 ± 0.0739 | (0–0.1690) | 0.3697 | 0.4620 | 0.8755 | 0.2575 | 0.9764 | |
| Bacteria Firmicutes Clostridia | 0.0719 ± 0.1040 | (0–0.2757) | 0.2454 | 0.2818 | 0.0923 ± 0.0852 | (0–0.2593) | 0.1287 | 0.4606 | 0.3155 | 0.0189 | 0.4784 | |
| Bacteria Firmicutes Clostridia Clostridiales | 0.0693 ± 0.1040 | (0–0.2731) | 0.2530 | 0.2858 | 0.0945 ± 0.0853 | (0–0.2617) | 0.1231 | 0.4606 | 0.3128 | 0.0185 | 0.4730 | |
| Bacteria Firmicutes ... Clostridiales Christensenellaceae | 0.3065 ± 0.0593 | (0.1903–0.4227) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.0018 | 0.0196 | 0.0310 | Healthy |
| Bacteria Firmicutes ... Clostridiales Clostridiaceae | 0.3365 ± 0.0572 | (0.2244–0.4486) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.0678 | 0.0079 | 0.7332 | |
| Bacteria Firmicutes ... Clostridiaceae Clostridium | 0.1427 ± 0.0973 | (0–0.3334) | 0.0764 | 0.1120 | 0.0470 ± 0.0765 | (0–0.1969) | 0.2629 | 0.4606 | 0.0088 | 0.6926 | 0.6667 | |

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|--|--------------------|---------------------|--------|--------|--------------------|---------------------|--------|--------|--------|--------|--------|------|
| Bacteria Firmicutes ... Clostridiales Lachnospiraceae | 0.1542 ± 0.0564 | (0.0437– 0.2647) | 0.0014 | 0.0037 | 0.0000 ± NA | NA | NA | NA | 0.2964 | 0.3846 | 0.9963 | |
| Bacteria Firmicutes ... Lachnospiraceae [Ruminococcus] | 0.2084 ± 0.0984 | (0.0155– 0.4013) | 0.0193 | 0.0342 | 0.1036 ± 0.0809 | (0–0.2622) | 0.0884 | 0.4606 | 0.0002 | 0.0000 | 0.8004 | |
| Bacteria Firmicutes ... Lachnospiraceae Anaerostipes | 0.0120 ± 0.0919 | (0–0.1921) | 0.4482 | 0.4535 | 0.0543 ± 0.0751 | (0–0.2015) | 0.2288 | 0.4606 | 0.6073 | 0.8601 | 0.0984 | |
| Bacteria Firmicutes ... Lachnospiraceae Blautia | 0.1946 ± 0.0969 | (0.0047– 0.3845) | 0.0235 | 0.0408 | 0.0365 ± 0.0719 | (0–0.1774) | 0.3030 | 0.4606 | 0.7673 | 0.0000 | 0.5957 | |
| Bacteria Firmicutes ... Lachnospiraceae Coprococcus | 0.1628 ± 0.0571 | (0.0509– 0.2747) | 0.0011 | 0.0029 | 0.0000 ± NA | NA | NA | NA | 0.1723 | 0.1506 | 0.7319 | |
| Bacteria Firmicutes ... Lachnospiraceae Dorea | 0.0278 ± 0.1025 | (0–0.2287) | 0.3933 | 0.4077 | 0.1635 ± 0.0848 | (0–0.3297) | 0.0200 | 0.4489 | 0.0299 | 0.0018 | 0.3575 | MetS |
| Bacteria Firmicutes ... Lachnospiraceae Lachnospira | 0.1533 ± 0.0584 | (0.0388– 0.2678) | 0.0025 | 0.0059 | 0.0000 ± NA | NA | NA | NA | 0.4834 | 0.1164 | 0.2724 | |
| Bacteria Firmicutes ... Lachnospiraceae Roseburia | 0.0000 ± NA | NA | 0.5000 | 0.5000 | 0.0679 ± 0.0418 | (0–0.1498) | 0.1574 | 0.4606 | 0.0779 | 0.4169 | 0.4605 | |
| Bacteria Firmicutes ... Clostridiales Ruminococcaceae | 0.0546 ± 0.0992 | (0–0.2490) | 0.2915 | 0.3137 | 0.1731 ± 0.0851 | (0.0063– 0.3399) | 0.0149 | 0.4489 | 0.0034 | 0.1575 | 0.3533 | |
| Bacteria Firmicutes ... Ruminococcaceae Faecalibacterium | 0.2631 ± 0.0572 | (0.1510– 0.3752) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.1092 | 0.1204 | 0.6208 | |
| Bacteria Firmicutes ... Ruminococcaceae Oscillospira | 0.1434 ± 0.0969 | (0–0.3333) | 0.0750 | 0.1120 | 0.0088 ± 0.0751 | (0–0.156) | 0.4534 | 0.4733 | 0.0000 | 0.1641 | 0.0566 | |
| Bacteria Firmicutes ... Ruminococcaceae Ruminococcus | 0.0562 ± 0.0581 | (0–0.1701) | 0.1575 | 0.1984 | 0.0000 ± NA | NA | NA | NA | 0.0010 | 0.5001 | 0.6916 | |
| Bacteria Firmicutes ... Clostridiales Veillonellaceae | 0.1343 ± 0.0589 | (0.0189– 0.2497) | 0.0085 | 0.0164 | 0.0000 ± NA | NA | NA | NA | 0.0000 | 0.0172 | 0.0773 | |
| Bacteria Firmicutes ... Veillonellaceae Acidaminococcus | 0.1312 ± 0.0562 | (0.0210– 0.2414) | 0.0067 | 0.0140 | 0.0000 ± NA | NA | NA | NA | 0.0156 | 0.2438 | 0.9763 | |
| Bacteria Firmicutes ... Veillonellaceae Dialister | 0.1636 ± 0.0628 | (0.0405– 0.2867) | 0.0028 | 0.0064 | 0.0000 ± NA | NA | NA | NA | 0.3238 | 0.0089 | 0.2050 | |
| Bacteria Firmicutes ... Veillonellaceae Megasphaera | 0.2177 ± 0.0633 | (0.0936– 0.3418) | 0.0001 | 0.0005 | 0.0000 ± NA | NA | NA | NA | 0.0007 | 0.0023 | 0.5567 | |
| Bacteria Firmicutes ... Veillonellaceae Megasphaera | 0.1375 ± 0.0619 | (0.0162– 0.2588) | 0.0089 | 0.0169 | 0.0000 ± NA | NA | NA | NA | 0.0001 | 0.4755 | 0.0332 | |
| Bacteria Firmicutes ... Veillonellaceae Phascolarctobacterium | 0.3549 ± 0.0929 | (0.1728– 0.5370) | 0.0002 | 0.0006 | 0.0045 ± 0.0669 | (0–0.1356) | 0.4733 | 0.4733 | 0.0270 | 0.4549 | 0.3422 | |
| Bacteria Firmicutes ... Veillonellaceae Succiniclasticum | 0.0139 ± 0.0543 | (0–0.1203) | 0.3983 | 0.4079 | 0.0000 ± NA | NA | NA | NA | 0.6973 | 0.5403 | 0.8166 | |
| Bacteria Firmicutes ... Veillonellaceae Veillonella | 0.2168 ± 0.0998 | (0.0212– 0.4124) | 0.0171 | 0.0310 | 0.0531 ± 0.0911 | (0–0.2317) | 0.2745 | 0.4606 | 0.3765 | 0.0001 | 0.6574 | |
| Bacteria Firmicutes ... Erysipelotrichales Erysipelotrichaceae | 0.1402 ± 0.0955 | (0–0.3274) | 0.0744 | 0.1120 | 0.0843 ± 0.0781 | (0–0.2374) | 0.1287 | 0.4606 | 0.0127 | 0.2363 | 0.9147 | |
| Bacteria Firmicutes ... Erysipelotrichaceae [Eubacterium] | 0.2831 ± 0.0592 | (0.1671– 0.3991) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.0053 | 0.5167 | 0.6889 | |

| | | | | | | | | | | | | |
|---|--------------------|---------------------|--------|--------|--------------------|------------|--------|--------|--------|--------|--------|---------|
| Bacteria Firmicutes ... Erysipelotrichaceae Catenibacterium | 0.1208 ± 0.1025 | (0–0.3217) | 0.1216 | 0.1656 | 0.0212 ± 0.0781 | (0–0.1743) | 0.3917 | 0.4620 | 0.0793 | 0.5195 | 0.9312 | |
| Bacteria Fusobacteria Fusobacteriia Fusobacteriales | 0.1037 ± 0.1024 | (0–0.3044) | 0.1587 | 0.1984 | 0.0582 ± 0.0847 | (0–0.2242) | 0.2402 | 0.4606 | 0.6478 | 0.6521 | 0.3197 | |
| Bacteria Fusobacteria ... Fusobacteriales Fusobacteriaceae | 0.0946 ± 0.0997 | (0–0.2900) | 0.1732 | 0.2103 | 0.0908 ± 0.0827 | (0–0.2529) | 0.1267 | 0.4606 | 0.4860 | 0.5261 | 0.6087 | |
| Bacteria Proteobacteria | 0.1385 ± 0.0527 | (0.0352– 0.2418) | 0.0025 | 0.0059 | 0.0000 ± NA | NA | NA | NA | 0.6985 | 0.0000 | 0.2652 | |
| Bacteria Proteobacteria Betaproteobacteria | 0.0730 ± 0.0899 | (0–0.2492) | 0.2111 | 0.2492 | 0.0290 ± 0.0702 | (0–0.1666) | 0.3365 | 0.4606 | 0.8894 | 0.8047 | 0.0633 | MetS |
| Bacteria Proteobacteria Betaproteobacteria Burkholderiales | 0.0759 ± 0.0929 | (0–0.2580) | 0.2098 | 0.2492 | 0.0272 ± 0.0721 | (0–0.1685) | 0.3505 | 0.4606 | 0.9092 | 0.7426 | 0.0605 | MetS |
| Bacteria Proteobacteria ... Burkholderiales Alcaligenaceae | 0.1344 ± 0.0912 | (0–0.3132) | 0.0761 | 0.1120 | 0.0064 ± 0.0706 | (0–0.1448) | 0.4635 | 0.4733 | 0.6601 | 0.7359 | 0.0387 | MetS |
| Bacteria Proteobacteria ... Alcaligenaceae Sutterella | 0.1361 ± 0.0912 | (0–0.3149) | 0.0735 | 0.1120 | 0.0051 ± 0.0705 | (0–0.1433) | 0.4710 | 0.4733 | 0.6684 | 0.7389 | 0.0383 | MetS |
| Bacteria Proteobacteria Deltaproteobacteria | 0.0987 ± 0.0971 | (0–0.2890) | 0.1569 | 0.1984 | 0.0088 ± 0.0777 | (0–0.1611) | 0.4548 | 0.4733 | 0.5910 | 0.0234 | 0.0664 | |
| Bacteria Proteobacteria Deltaproteobacteria Desulfovibrionales | 0.1010 ± 0.0967 | (0–0.2905) | 0.1506 | 0.1969 | 0.0063 ± 0.0776 | (0–0.1584) | 0.4677 | 0.4733 | 0.5961 | 0.0211 | 0.0696 | |
| Bacteria Proteobacteria ... Desulfovibrionales Desulfovibrionaceae | 0.1012 ± 0.0967 | (0–0.2907) | 0.1500 | 0.1969 | 0.0061 ± 0.0776 | (0–0.1582) | 0.4686 | 0.4733 | 0.5958 | 0.0210 | 0.0697 | |
| Bacteria Proteobacteria ... Desulfovibrionaceae Bilophila | 0.0501 ± 0.0944 | (0–0.2351) | 0.2982 | 0.3168 | 0.0360 ± 0.0792 | (0–0.1912) | 0.3222 | 0.4606 | 0.1134 | 0.0001 | 0.1482 | |
| Bacteria Proteobacteria ... Desulfovibrionaceae Desulfovibrio | 0.1095 ± 0.0934 | (0–0.2926) | 0.1227 | 0.1656 | 0.0296 ± 0.0732 | (0–0.1731) | 0.3404 | 0.4606 | 0.0069 | 0.2838 | 0.8967 | |
| Bacteria Proteobacteria Gammaproteobacteria | 0.2350 ± 0.0979 | (0.0431– 0.4269) | 0.0103 | 0.0190 | 0.0257 ± 0.0813 | (0–0.1850) | 0.3738 | 0.4620 | 0.2903 | 0.0000 | 0.2628 | Healthy |
| Bacteria Proteobacteria ... Enterobacteriales Enterobacteriaceae | 0.2592 ± 0.0558 | (0.1498– 0.3686) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.3321 | 0.0000 | 0.2650 | |
| Bacteria Proteobacteria ... Enterobacteriaceae Klebsiella | 0.1875 ± 0.1060 | (0–0.3953) | 0.0423 | 0.0705 | 0.0490 ± 0.0780 | (0–0.2019) | 0.2593 | 0.4606 | 0.8134 | 0.0000 | 0.2318 | |
| Bacteria Proteobacteria ... Pasteurellales Pasteurellaceae | 0.2899 ± 0.0633 | (0.1658– 0.4140) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.1870 | 0.0001 | 0.3285 | |
| Bacteria Proteobacteria ... Pasteurellaceae Haemophilus | 0.2727 ± 0.0644 | (0.1465– 0.3989) | 0.0000 | 0.0000 | 0.0000 ± NA | NA | NA | NA | 0.1931 | 0.0002 | 0.2614 | |
| Bacteria Tenericutes | 0.2294 ± 0.0575 | (0.1167– 0.3421) | 0.0000 | 0.0001 | 0.0000 ± NA | NA | NA | NA | 0.0531 | 0.0000 | 0.0660 | Healthy |
| Bacteria Tenericutes Mollicutes | 0.2287 ± 0.0576 | (0.1158– 0.3416) | 0.0000 | 0.0001 | 0.0000 ± NA | NA | NA | NA | 0.0609 | 0.0000 | 0.0684 | Healthy |
| Bacteria Verrucomicrobia | 0.0533 ± 0.0949 | (0–0.2393) | 0.2883 | 0.3137 | 0.1150 ± 0.0839 | (0–0.2794) | 0.0737 | 0.4606 | 0.0011 | 0.7012 | 0.0260 | Healthy |
| Bacteria Verrucomicrobia ... Verrucomicrobiales Verrucomicrobiaceae | 0.0635 ± 0.0961 | (0–0.2519) | 0.2556 | 0.2858 | 0.0973 ± 0.0825 | (0–0.2590) | 0.1085 | 0.4606 | 0.0025 | 0.5685 | 0.0354 | Healthy |

| | | | | | | | | | | | | |
|--|--------------------|------------|--------|--------|--------------------|------------|--------|--------|--------|--------|--------|---------|
| Bacteria Verrucomicrobia ... Verrucomicrobiaceae Akkermansia | 0.0614 ± 0.0963 | (0–0.2501) | 0.2629 | 0.2903 | 0.1012 ± 0.0828 | (0–0.2635) | 0.1002 | 0.4606 | 0.0025 | 0.5742 | 0.0360 | Healthy |
|--|--------------------|------------|--------|--------|--------------------|------------|--------|--------|--------|--------|--------|---------|

H2r: total additive genetic heritability; C2: common/shared environment; SE: standard error; CI: confidence interval;

Group: association with MetS status (obtained from MaAsLin). "Healthy"-enriched in healthy individuals, "MetS"-enriched in MetS individuals

Supplementary Table S4. Associations of *APOA5* SNP rs651821 with gut microbial taxa using the QFAM procedure in PLINK (adjusted for age and sex).

| Taxon | BETA | EMP1 | q.EMP1 |
|---|-------------|-------------|---------------|
| Bacteria Actinobacteria | -0.2713 | 0.002 | 0.0102 |
| Bacteria Actinobacteria Actinobacteria Bifidobacteriales Bifidobacteriaceae Bifidobacterium | -0.2632 | 0.0026 | 0.0102 |
| Bacteria Actinobacteria Actinobacteria Bifidobacteriales Bifidobacteriaceae | -0.2586 | 0.0029 | 0.0102 |
| Bacteria Actinobacteria Actinobacteria Bifidobacteriales | -0.2586 | 0.0029 | 0.0102 |
| Bacteria Actinobacteria Actinobacteria | -0.2583 | 0.003 | 0.0102 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales [Paraprevotellaceae] Paraprevotella | 0.0961 | 0.2058 | 0.5759 |
| Bacteria Tenericutes | -0.0907 | 0.303 | 0.5759 |
| Bacteria Tenericutes Mollicutes | -0.0901 | 0.309 | 0.5759 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales [Odoribacteraceae] Odoribacter | 0.0802 | 0.342 | 0.5759 |
| Bacteria Proteobacteria Gammaproteobacteria | -0.0748 | 0.3961 | 0.5759 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Parabacteroides | 0.0739 | 0.4022 | 0.5759 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae | 0.0732 | 0.4065 | 0.5759 |
| Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae | -0.0445 | 0.6479 | 0.7709 |
| Bacteria Firmicutes Clostridia Clostridiales Christensenellaceae | 0.0428 | 0.6751 | 0.7709 |
| Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae Lactobacillus | -0.041 | 0.6802 | 0.7709 |
| Archaea Euryarchaeota Methanobacteria Methanobacteriales Methanobacteriaceae Methanobrevibacter | 0.0286 | 0.7331 | 0.7789 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales [Odoribacteraceae] | 0.0055 | 0.9462 | 0.9462 |

The standardized residuals of the arcsine square-root-transformed microbial abundances regressed against age and sex were used as quantitative phenotypes in this analysis.

BETA: the effect size (regression coefficient); EMP1: pointwise empirical p value; q.EMP1: FDR-corrected EMP1

Supplementary table S5. Associations of *APOA5* SNP rs651821 with gut microbial taxa using the QFAM procedure in PLINK (adjusted for MetS status, age, and sex).

| Taxon | BETA | EMP1 | q.EMP1 |
|---|-------------|-------------|---------------|
| Bacteria Actinobacteria | -0.2541 | 0.0037 | 0.016 |
| Bacteria Actinobacteria Actinobacteria Bifidobacteriales Bifidobacteriaceae Bifidobacterium | -0.2477 | 0.0038 | 0.016 |
| Bacteria Actinobacteria Actinobacteria Bifidobacteriales Bifidobacteriaceae | -0.2429 | 0.0045 | 0.016 |
| Bacteria Actinobacteria Actinobacteria | -0.2418 | 0.0047 | 0.016 |
| Bacteria Actinobacteria Actinobacteria Bifidobacteriales | -0.2429 | 0.0047 | 0.016 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales [Paraprevotellaceae] Paraprevotella | 0.1108 | 0.1441 | 0.4083 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae Parabacteroides | 0.0948 | 0.2795 | 0.5527 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales Porphyromonadaceae | 0.0943 | 0.2806 | 0.5527 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales [Odoribacteraceae] Odoribacter | 0.0899 | 0.2926 | 0.5527 |
| Bacteria Tenericutes | -0.0653 | 0.4605 | 0.7194 |
| Bacteria Tenericutes Mollicutes | -0.0649 | 0.4655 | 0.7194 |
| Bacteria Proteobacteria Gammaproteobacteria | -0.0566 | 0.5219 | 0.7394 |
| Bacteria Firmicutes Clostridia Clostridiales Christensenellaceae | 0.055 | 0.5903 | 0.7396 |
| Archaea Euryarchaeota Methanobacteria Methanobacteriales Methanobacteriaceae Methanobrevibacter | 0.0421 | 0.6091 | 0.7396 |
| Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae | -0.0412 | 0.6694 | 0.749 |
| Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae Lactobacillus | -0.0375 | 0.7049 | 0.749 |
| Bacteria Bacteroidetes Bacteroidia Bacteroidales [Odoribacteraceae] | 0.0226 | 0.7895 | 0.7895 |

The standardized residuals of the arcsine square-root-transformed microbial abundances regressed against age, sex, and MetS status were used as quantitative phenotypes in this analysis.

BETA: the effect size (regression coefficient); EMP1: pointwise empirical p value; q.EMP1: FDR-corrected EMP1

Supplementary table S6. Comparison between MetS-related gut microbes identified in this study and previously reported obesity- or type 2 diabetes-related gut microbes.

| Kingdom | Phylum | Class | Order | Family | Genus | Species | MetS* | T2D [11] | Obesity [12] |
|----------|----------------|-----------------|--------------------|----------------------|---------------------------|-----------------------------|-------|----------|--------------|
| Archaea | Euryarchaeota | Methanobacteria | Methanobacteriales | Methanobacteriaceae | <i>Methanobrevibacter</i> | | | | |
| Archaea | Euryarchaeota | Methanobacteria | Methanobacteriales | Methanobacteriaceae | <i>Methanobrevibacter</i> | <i>M. smithii</i> | | | |
| Bacteria | Actinobacteria | | | | | | | | |
| Bacteria | Actinobacteria | Actinobacteria | | | | | | | |
| Bacteria | Actinobacteria | Actinobacteria | Bifidobacteriales | | | | | | |
| Bacteria | Actinobacteria | Actinobacteria | Bifidobacteriales | Bifidobacteriaceae | | | | | |
| Bacteria | Actinobacteria | Actinobacteria | Bifidobacteriales | Bifidobacteriaceae | <i>Bifidobacterium</i> | | | | |
| Bacteria | Actinobacteria | Actinobacteria | Bifidobacteriales | Bifidobacteriaceae | <i>Bifidobacterium</i> | <i>Bifidobacterium spp.</i> | | | |
| Bacteria | Actinobacteria | Actinobacteria | Bifidobacteriales | Bifidobacteriaceae | <i>Bifidobacterium</i> | <i>B. animalis</i> | | | |
| Bacteria | Bacteroidetes | Bacteroidia | Bacteroidales | [Odoribacteraceae] | | | | | |
| Bacteria | Bacteroidetes | Bacteroidia | Bacteroidales | [Odoribacteraceae] | <i>Odoribacter</i> | | | | |
| Bacteria | Bacteroidetes | Bacteroidia | Bacteroidales | [Paraprevotellaceae] | | | | | |
| Bacteria | Bacteroidetes | Bacteroidia | Bacteroidales | [Paraprevotellaceae] | <i>Paraprevotella</i> | | | | |
| Bacteria | Bacteroidetes | Bacteroidia | Bacteroidales | Porphyromonadaceae | | | | | |
| Bacteria | Bacteroidetes | Bacteroidia | Bacteroidales | Porphyromonadaceae | <i>Parabacteroides</i> | | | | |
| Bacteria | Bacteroidetes | Bacteroidia | Bacteroidales | Rikenellaceae | | | | | |
| Bacteria | Firmicutes | Bacilli | Lactobacillales | Lactobacillaceae | | | | | |
| Bacteria | Firmicutes | Bacilli | Lactobacillales | Lactobacillaceae | <i>Lactobacillus</i> | | | | |
| Bacteria | Firmicutes | Bacilli | Lactobacillales | Lactobacillaceae | <i>Lactobacillus</i> | <i>Lactobacillus spp.</i> | | | |

| | | | | | | | | | | |
|----------|-----------------|---------------------|--------------------|---------------------|----------------------|-----------------------|------|-------|--|------|
| Bacteria | Firmicutes | Bacilli | Lactobacillales | Lactobacillaceae | <i>Lactobacillus</i> | <i>L. paracasei</i> | | | | Blue |
| Bacteria | Firmicutes | Bacilli | Lactobacillales | Lactobacillaceae | <i>Lactobacillus</i> | <i>L. plantarum</i> | | | | Blue |
| Bacteria | Firmicutes | Bacilli | Lactobacillales | Lactobacillaceae | <i>Lactobacillus</i> | <i>L. reuteri</i> | | | | Red |
| Bacteria | Firmicutes | Clostridia | Clostridiales | Christensenellaceae | | | Blue | | | |
| Bacteria | Firmicutes | Clostridia | Clostridiales | Lachnospiraceae | <i>Dorea</i> | | Red | | | |
| Bacteria | Proteobacteria | Betaproteobacteria | | | | | Red | Red | | |
| Bacteria | Proteobacteria | Betaproteobacteria | Burkholderiales | | | | Red | | | |
| Bacteria | Proteobacteria | Betaproteobacteria | Burkholderiales | Alcaligenaceae | | | Red | | | Red |
| Bacteria | Proteobacteria | Betaproteobacteria | Burkholderiales | Alcaligenaceae | <i>Sutterella</i> | | Red | | | |
| Bacteria | Proteobacteria | Gammaproteobacteria | | | | | Blue | | | |
| Bacteria | Tenericutes | | | | | | Blue | | | |
| Bacteria | Tenericutes | Mollicutes | | | | | Blue | | | |
| Bacteria | Verrucomicrobia | | | | | | Blue | | | |
| Bacteria | Verrucomicrobia | Verrucomicrobiae | Verrucomicrobiales | Verrucomicrobiaceae | <i>Akkermansia</i> | | Blue | | | |
| Bacteria | Verrucomicrobia | Verrucomicrobiae | Verrucomicrobiales | Verrucomicrobiaceae | <i>Akkermansia</i> | <i>A. muciniphila</i> | | Green | | |

*This study

The taxa enriched and depleted in the individuals with a designated disease in each column compared to the healthy individuals are denoted by red and blue, respectively. Green indicates that inconsistent results concerning the association between a taxon and a disease were reported in the referenced paper.

Supplementary table S7. Metadata for the samples.

| Sample_ID | Age | Sex | Family_ID | Family_relations | rs651821 | MetS_status | DBP | SBP | Waist | Triglyceride | FBS | HDL | Accession |
|-----------|-----|--------|-----------|------------------|----------|-------------|-----|-----|-------|--------------|-----|-----|-----------|
| F001 | 50 | Male | Family001 | MZ | TT | Healthy | 52 | 84 | 86 | 140 | 147 | 34 | ERS714176 |
| F002 | 38 | Male | Family002 | DZ | TT | Healthy | 89 | 134 | 80.7 | 178 | 98 | 47 | ERS714177 |
| F003 | 38 | Male | Family002 | DZ | TT | Healthy | 73 | 110 | 79 | 107 | 92 | 45 | ERS714179 |
| F004 | 75 | Male | Family002 | DZ_FA | TT | Healthy | 60 | 125 | 89 | 59 | 132 | 53 | ERS714181 |
| F005 | 72 | Female | Family002 | DZ_MO | CT | MetS | 75 | 126 | 85.2 | 119 | 119 | 46 | ERS714182 |
| F006 | 40 | Male | Family002 | DZ_sibling | CT | MetS | 82 | 126 | 96.1 | 387 | 95 | 37 | ERS714183 |
| F007 | 46 | Male | Family003 | MZ | TT | Healthy | 74 | 111 | 76.3 | 53 | 140 | 40 | ERS714191 |
| F008 | 46 | Male | Family003 | MZ | NA | Healthy | 73 | 121 | 84 | 141 | 147 | 43 | ERS714193 |
| F009 | 73 | Female | Family003 | MZ_MO | TT | Healthy | 81 | 129 | 80 | 131 | 109 | 42 | ERS714195 |
| F010 | 38 | Male | Family003 | MZ | TT | Healthy | 71 | 112 | 85.1 | 57 | 88 | 43 | ERS714197 |
| F011 | 38 | Male | Family003 | MZ | NA | Healthy | 72 | 110 | 75.9 | 72 | 101 | 40 | ERS714198 |
| F012 | 53 | Male | Family003 | MZ_sibling | TT | Healthy | 72 | 99 | 85.2 | 147 | 108 | 35 | ERS714199 |
| F013 | 35 | Female | Family004 | DZ | TT | MetS | 62 | 93 | 86 | 135 | 185 | 31 | ERS714201 |
| F014 | 35 | Female | Family004 | DZ | CT | Healthy | 53 | 88 | 70 | 184 | 96 | 32 | ERS714202 |
| F015 | 54 | Male | Family005 | DZ_sibling | TT | MetS | 88 | 142 | 96.2 | 148 | 101 | 36 | ERS714209 |
| F016 | 48 | Male | Family001 | MZ_sibling | TT | Healthy | 70 | 103 | 84.9 | 127 | 87 | 35 | ERS714220 |
| F017 | 45 | Female | Family006 | MZ | CT | Healthy | 72 | 111 | 71.9 | 50 | 96 | 36 | ERS714224 |
| F018 | 45 | Female | Family006 | MZ | NA | Healthy | 71 | 110 | 78.2 | 74 | 97 | 38 | ERS714226 |
| F019 | 56 | Female | Family006 | MZ_sibling | TT | Healthy | 61 | 124 | 82.5 | 75 | 93 | 46 | ERS714228 |
| F020 | 53 | Female | Family006 | MZ_sibling | TT | Healthy | 63 | 111 | 84.6 | 102 | 92 | 47 | ERS714230 |
| F021 | 46 | Female | Family006 | MZ_sibling | CT | MetS | 63 | 132 | 91.3 | 127 | 85 | 48 | ERS714232 |
| F022 | 76 | Female | Family006 | MZ_MO | CT | MetS | 74 | 130 | 91.5 | 84 | 114 | 35 | ERS714234 |

| | | | | | | | | | | | | | |
|------|----|--------|-----------|------------|----|---------|----|-----|------|-----|-----|----|-----------|
| F023 | 28 | Female | Family007 | DZ_sibling | CT | Healthy | 64 | 106 | 65 | 85 | 92 | 56 | ERS714236 |
| F024 | 69 | Male | Family007 | DZ_FA | TT | Healthy | 62 | 118 | 83 | 132 | 88 | 27 | ERS714237 |
| F025 | 64 | Female | Family007 | DZ_MO | CT | Healthy | 51 | 97 | 82.4 | 103 | 87 | 45 | ERS714238 |
| F026 | 39 | Female | Family007 | DZ | TT | Healthy | 77 | 110 | 83 | 90 | 82 | 48 | ERS714240 |
| F027 | 39 | Female | Family007 | DZ | CT | Healthy | 63 | 102 | 74 | 90 | 85 | 42 | ERS714241 |
| F028 | 36 | Female | Family007 | DZ_sibling | TT | Healthy | 77 | 110 | 76 | 112 | 81 | 35 | ERS714242 |
| F029 | 55 | Male | Family008 | DZ_sibling | CC | MetS | 80 | 126 | 95.1 | 110 | 114 | 29 | ERS714243 |
| F030 | 52 | Male | Family008 | DZ | CT | Healthy | 80 | 120 | 85.2 | 169 | 87 | 42 | ERS714244 |
| F031 | 52 | Male | Family008 | DZ | NA | MetS | 80 | 120 | 96.8 | 204 | 101 | 28 | ERS714245 |
| F032 | 48 | Male | Family008 | DZ_sibling | CC | MetS | 80 | 122 | 97.4 | 196 | 92 | 39 | ERS714246 |
| F033 | 47 | Female | Family001 | MZ_sibling | TT | Healthy | 61 | 90 | 79.9 | 84 | 91 | 32 | ERS714247 |
| F034 | 45 | Female | Family001 | MZ_sibling | TT | Healthy | 71 | 118 | 76 | 77 | 91 | 54 | ERS714248 |
| F035 | 74 | Female | Family009 | MZ_MO | CT | MetS | 71 | 134 | 82.7 | 61 | 109 | 49 | ERS714249 |
| F036 | 54 | Female | Family009 | MZ_sibling | NA | MetS | 71 | 138 | 74.4 | 73 | 107 | 44 | ERS714250 |
| F037 | 52 | Male | Family009 | MZ_sibling | NA | Healthy | 75 | 112 | 91.1 | 58 | 100 | 42 | ERS714252 |
| F038 | 50 | Female | Family009 | MZ_sibling | TT | Healthy | 69 | 110 | 74.1 | 94 | 101 | 44 | ERS714253 |
| F039 | 46 | Female | Family009 | MZ | CT | Healthy | 81 | 122 | 79.8 | 102 | 92 | 48 | ERS714254 |
| F040 | 42 | Female | Family009 | MZ_sibling | CT | Healthy | 61 | 101 | 77 | 69 | 88 | 38 | ERS714256 |
| F041 | 33 | Male | Family010 | MZ | CT | Healthy | 71 | 110 | 86.1 | 144 | 95 | 38 | ERS714264 |
| F042 | 33 | Male | Family010 | MZ | NA | Healthy | 71 | 114 | 83 | 179 | 95 | 33 | ERS714265 |
| F043 | 63 | Female | Family010 | MZ_MO | NA | Healthy | 61 | 101 | 73.1 | 109 | 87 | 42 | ERS714266 |
| F044 | 51 | Male | Family011 | MZ | TT | MetS | 72 | 118 | 76.5 | 165 | 109 | 33 | ERS714273 |
| F045 | 45 | Male | Family011 | MZ_sibling | TT | Healthy | 80 | 116 | 82 | 203 | 97 | 38 | ERS714274 |
| F046 | 48 | Male | Family011 | MZ_sibling | TT | MetS | 92 | 142 | 96 | 199 | 96 | 29 | ERS714276 |
| F047 | 36 | Female | Family012 | MZ | TT | Healthy | 52 | 89 | 70 | 40 | 82 | 68 | ERS714277 |

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|------|----|--------|-----------|------------|----|---------|----|-----|-------|-----|-----|----|-----------|
| F048 | 36 | Female | Family012 | MZ | NA | Healthy | 61 | 98 | 70.7 | 45 | 84 | 59 | ERS714279 |
| F049 | 46 | Female | Family009 | MZ | NA | Healthy | 73 | 111 | 83.2 | 137 | 102 | 42 | ERS714281 |
| F050 | 51 | Male | Family011 | MZ | NA | Healthy | 68 | 117 | 77 | 110 | 108 | 35 | ERS714283 |
| F051 | 60 | Female | Family011 | MZ_sibling | TT | MetS | 80 | 110 | 90 | 142 | 105 | 39 | ERS714284 |
| F052 | 47 | Female | Family013 | MZ | TT | Healthy | 53 | 94 | 68.1 | 54 | 96 | 50 | ERS714285 |
| F053 | 47 | Female | Family013 | MZ | NA | Healthy | 70 | 104 | 74.5 | 61 | 101 | 58 | ERS714287 |
| F054 | 50 | Male | Family014 | MZ | CT | Healthy | 64 | 110 | 88.5 | 54 | 89 | 47 | ERS714289 |
| F055 | 50 | Male | Family014 | MZ | NA | Healthy | 63 | 123 | 93.5 | 130 | 92 | 38 | ERS714291 |
| F056 | 55 | Female | Family014 | MZ_sibling | TT | Healthy | 61 | 98 | 80 | 157 | 97 | 42 | ERS714293 |
| F057 | 66 | Male | Family015 | MZ_sibling | CT | Healthy | 78 | 128 | 80.3 | 228 | 96 | 33 | ERS714297 |
| F058 | 53 | Female | Family015 | MZ | CT | Healthy | 75 | 119 | 76.1 | 164 | 91 | 52 | ERS714298 |
| F059 | 53 | Female | Family015 | MZ | NA | Healthy | 68 | 102 | 69.7 | 85 | 88 | 57 | ERS714299 |
| F060 | 67 | Male | Family016 | MZ_FA | TT | Healthy | 77 | 138 | 98.3 | 69 | 84 | 45 | ERS714300 |
| F061 | 38 | Male | Family016 | MZ_sibling | TT | Healthy | 69 | 110 | 103.2 | 87 | 87 | 45 | ERS714301 |
| F062 | 37 | Female | Family016 | MZ | TT | Healthy | 57 | 100 | 73.5 | 34 | 80 | 42 | ERS714302 |
| F063 | 37 | Female | Family016 | MZ | NA | Healthy | 66 | 102 | 72.4 | 59 | 86 | 49 | ERS714303 |
| F064 | 50 | Male | Family015 | MZ_sibling | CT | Healthy | 70 | 110 | 70.1 | 171 | 99 | 43 | ERS714308 |
| F065 | 70 | Male | Family017 | MZ_FA | TT | Healthy | 77 | 121 | 83.6 | 124 | 218 | 44 | ERS714310 |
| F066 | 61 | Female | Family017 | MZ_MO | TT | Healthy | 63 | 100 | 71 | 80 | 87 | 75 | ERS714311 |
| F067 | 37 | Male | Family017 | MZ | TT | Healthy | 71 | 120 | 75.1 | 138 | 91 | 53 | ERS714312 |
| F068 | 37 | Male | Family017 | MZ | NA | Healthy | 73 | 113 | 77 | 126 | 84 | 44 | ERS714313 |
| F069 | 67 | Female | Family018 | MZ_MO | CT | MetS | 81 | 137 | 87 | 131 | 91 | 37 | ERS714314 |
| F070 | 42 | Female | Family018 | MZ | CT | Healthy | 61 | 99 | 85.5 | 86 | 92 | 45 | ERS714315 |
| F071 | 42 | Female | Family018 | MZ | NA | Healthy | 69 | 99 | 78 | 71 | 90 | 46 | ERS714316 |
| F072 | 40 | Male | Family018 | MZ_sibling | TT | Healthy | 85 | 132 | 78.4 | 140 | 89 | 34 | ERS714317 |

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|------|----|--------|-----------|------------|----|---------|----|-----|------|-----|-----|----|-----------|
| F073 | 51 | Male | Family013 | MZ_sibling | TT | Healthy | 62 | 110 | 78 | 104 | 102 | 35 | ERS714318 |
| F074 | 59 | Female | Family019 | MZ | CT | MetS | 84 | 126 | 85.2 | 219 | 90 | 31 | ERS714334 |
| F075 | 67 | Male | Family020 | MZ_FA | TT | Healthy | 79 | 140 | 89 | 132 | 122 | 41 | ERS714336 |
| F076 | 40 | Female | Family020 | MZ | TT | Healthy | 67 | 124 | 72.5 | 66 | 88 | 38 | ERS714337 |
| F077 | 40 | Female | Family020 | MZ | NA | Healthy | 70 | 108 | 75.2 | 89 | 95 | 34 | ERS714339 |
| F078 | 38 | Male | Family020 | MZ_sibling | CT | Healthy | 65 | 102 | 69.7 | 60 | 87 | 48 | ERS714341 |
| F079 | 59 | Female | Family019 | MZ | NA | MetS | 57 | 89 | 88.1 | 252 | 98 | 32 | ERS714345 |
| F080 | 50 | Female | Family021 | DZ_sibling | TT | Healthy | 80 | 121 | 70.4 | 63 | 86 | 70 | ERS714374 |
| F081 | 38 | Female | Family021 | DZ | TT | Healthy | 68 | 103 | 74.3 | 123 | 88 | 58 | ERS714375 |
| F082 | 38 | Female | Family021 | DZ | TT | Healthy | 57 | 88 | 68.2 | 65 | 72 | 47 | ERS714376 |
| F083 | 43 | Female | Family022 | MZ | TT | Healthy | 53 | 90 | 80.4 | 60 | 97 | 46 | ERS714379 |
| F084 | 56 | Female | Family023 | MZ | CT | Healthy | 51 | 78 | 60.5 | 74 | 83 | 61 | ERS714380 |
| F085 | 56 | Female | Family023 | MZ | NA | Healthy | 51 | 78 | 63.5 | 105 | 85 | 57 | ERS714382 |
| F086 | 67 | Female | Family024 | DZ_sibling | TT | Healthy | 52 | 87 | 91 | 111 | 87 | 43 | ERS714386 |
| F087 | 64 | Female | Family024 | DZ_sibling | CT | Healthy | 61 | 101 | 79.3 | 147 | 93 | 33 | ERS714387 |
| F088 | 52 | Female | Family024 | DZ_sibling | CT | Healthy | 57 | 97 | 82 | 78 | 89 | 37 | ERS714388 |
| F089 | 51 | Male | Family024 | DZ | CT | Healthy | 63 | 106 | 82 | 114 | 89 | 35 | ERS714389 |
| F090 | 51 | Male | Family024 | DZ | CT | Healthy | 68 | 104 | 84.2 | 193 | 95 | 35 | ERS714390 |
| F091 | 62 | Female | Family025 | DZ_MO | NA | Healthy | 73 | 113 | 81.6 | 113 | 89 | 54 | ERS714391 |
| F092 | 38 | Female | Family025 | DZ | TT | Healthy | 67 | 103 | 84.5 | 81 | 85 | 38 | ERS714392 |
| F093 | 38 | Female | Family025 | DZ | CT | Healthy | 54 | 88 | 76.3 | 119 | 84 | 46 | ERS714393 |
| F094 | 60 | Female | Family026 | DZ | NA | Healthy | 71 | 110 | 78.5 | 88 | 105 | 43 | ERS714398 |
| F095 | 60 | Female | Family026 | DZ | NA | MetS | 71 | 111 | 93.5 | 95 | 135 | 48 | ERS714399 |
| F096 | 51 | Female | Family027 | MZ | NA | Healthy | 61 | 99 | 75.4 | 110 | 95 | 48 | ERS714400 |
| F097 | 51 | Female | Family027 | MZ | NA | Healthy | 61 | 107 | 71 | 107 | 97 | 65 | ERS714401 |

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|------|----|--------|-----------|------------|----|---------|----|-----|------|------|----|----|-----------|
| F098 | 39 | Male | Family028 | DZ_sibling | CT | Healthy | 61 | 106 | 90.2 | 99 | 83 | 46 | ERS714406 |
| F099 | 34 | Male | Family028 | DZ | NA | Healthy | 72 | 108 | 96.5 | 307 | 98 | 46 | ERS714407 |
| F100 | 34 | Male | Family028 | DZ | TT | Healthy | 71 | 108 | 88 | 144 | 94 | 35 | ERS714408 |
| F101 | 67 | Male | Family029 | MZ_FA | TT | Healthy | 73 | 111 | 84.5 | 108 | 86 | 44 | ERS714414 |
| F102 | 63 | Female | Family029 | MZ_MO | CT | Healthy | 70 | 102 | 73 | 73 | 96 | 44 | ERS714415 |
| F103 | 37 | Female | Family029 | MZ | TT | Healthy | 53 | 84 | 71.1 | 71 | 85 | 50 | ERS714416 |
| F104 | 37 | Female | Family029 | MZ | NA | Healthy | 53 | 80 | 71.7 | 78 | 81 | 46 | ERS714417 |
| F105 | 32 | Male | Family029 | MZ_sibling | TT | Healthy | 70 | 107 | 89 | 124 | 96 | 30 | ERS714418 |
| F106 | 45 | Female | Family030 | MZ_sibling | CT | Healthy | 52 | 93 | 72 | 89 | 83 | 42 | ERS714423 |
| F107 | 35 | Female | Family030 | MZ | CT | Healthy | 68 | 108 | 69 | 83 | 77 | 53 | ERS714425 |
| F108 | 42 | Female | Family030 | MZ_sibling | CT | Healthy | 62 | 99 | 80 | 64 | 90 | 46 | ERS714427 |
| F109 | 35 | Female | Family030 | MZ | NA | Healthy | 67 | 106 | 73.5 | 68 | 83 | 40 | ERS714429 |
| F110 | 74 | Male | Family031 | MZ_FA | TT | Healthy | 71 | 100 | 90.2 | 77 | 83 | 65 | ERS714431 |
| F111 | 75 | Female | Family031 | MZ_MO | CT | MetS | 79 | 120 | 99 | 1110 | 95 | 24 | ERS714432 |
| F112 | 48 | Female | Family031 | MZ_sibling | CT | Healthy | 62 | 108 | 80 | 68 | 85 | 52 | ERS714433 |
| F113 | 41 | Female | Family031 | MZ | TT | Healthy | 53 | 90 | 73.4 | 59 | 88 | 54 | ERS714435 |
| F114 | 41 | Female | Family031 | MZ | NA | Healthy | 68 | 108 | 79.5 | 79 | 94 | 46 | ERS714437 |
| F115 | 64 | Male | Family025 | DZ_FA | TT | MetS | 93 | 133 | 91.8 | 260 | 92 | 26 | ERS714441 |
| F116 | 73 | Male | Family032 | MZ_FA | CT | Healthy | 63 | 118 | 72.1 | 46 | 89 | 51 | ERS714445 |
| F117 | 71 | Female | Family032 | MZ_MO | CT | Healthy | 72 | 145 | 68.3 | 60 | 95 | 62 | ERS714446 |
| F118 | 39 | Male | Family032 | MZ | CT | Healthy | 74 | 116 | 74.3 | 65 | 97 | 51 | ERS714447 |
| F119 | 62 | Female | Family033 | MZ_MO | CT | MetS | 81 | 148 | 92.6 | 215 | 92 | 37 | ERS714451 |
| F120 | 38 | Female | Family033 | MZ | TT | Healthy | 67 | 110 | 74.3 | 79 | 86 | 40 | ERS714452 |
| F121 | 38 | Female | Family033 | MZ | NA | Healthy | 67 | 114 | 75 | 79 | 85 | 38 | ERS714453 |
| F122 | 36 | Female | Family033 | MZ_sibling | CC | Healthy | 73 | 109 | 71.1 | 91 | 86 | 36 | ERS714454 |

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|------|----|--------|-----------|------------|----|---------|-----|-----|-------|-----|-----|----|-----------|
| F123 | 44 | Male | Family034 | MZ_sibling | NA | MetS | 70 | 112 | 99.6 | 162 | 105 | 31 | ERS714455 |
| F124 | 47 | Female | Family034 | MZ | TT | Healthy | 61 | 91 | 78 | 52 | 97 | 49 | ERS714458 |
| F125 | 47 | Female | Family034 | MZ | NA | Healthy | 71 | 109 | 68 | 59 | 93 | 56 | ERS714459 |
| F126 | 46 | Female | Family035 | MZ_sibling | TT | Healthy | 80 | 121 | 105.5 | 93 | 90 | 37 | ERS714462 |
| F127 | 44 | Male | Family035 | MZ | CT | MetS | 100 | 139 | 94.2 | 172 | 101 | 46 | ERS714463 |
| F128 | 49 | Male | Family036 | MZ | CT | Healthy | 54 | 98 | 79 | 81 | 100 | 31 | ERS714466 |
| F129 | 49 | Male | Family036 | MZ | NA | Healthy | 53 | 82 | 75.5 | 88 | 88 | 33 | ERS714467 |
| F130 | 65 | Male | Family037 | MZ_FA | TT | MetS | 83 | 141 | 93.3 | 152 | 117 | 42 | ERS714468 |
| F131 | 58 | Female | Family037 | MZ_MO | TT | MetS | 93 | 131 | 96.6 | 236 | 114 | 27 | ERS714469 |
| F132 | 35 | Male | Family037 | MZ | TT | Healthy | 79 | 121 | 104.1 | 173 | 97 | 43 | ERS714470 |
| F133 | 35 | Male | Family037 | MZ | NA | MetS | 81 | 108 | 99.4 | 155 | 109 | 55 | ERS714471 |
| F134 | 54 | Male | Family038 | MZ | TT | MetS | 84 | 134 | 84 | 113 | 104 | 33 | ERS714472 |
| F138 | 37 | Female | Family039 | MZ | TT | Healthy | 61 | 88 | 76.6 | 114 | 87 | 54 | ERS714478 |
| F139 | 36 | Female | Family039 | MZ_sibling | CT | Healthy | 71 | 101 | 69.1 | 78 | 93 | 48 | ERS714479 |
| F140 | 44 | Male | Family035 | MZ | NA | MetS | 71 | 138 | 108 | 166 | 107 | 36 | ERS714480 |
| F141 | 37 | Female | Family039 | MZ | NA | Healthy | 67 | 92 | 67.6 | 55 | 87 | 57 | ERS714489 |
| F142 | 75 | Female | Family040 | MZ_MO | CT | Healthy | 61 | 95 | 69.6 | 128 | 91 | 37 | ERS714490 |
| F143 | 43 | Male | Family040 | MZ | TT | Healthy | 62 | 100 | 75.4 | 150 | 89 | 27 | ERS714491 |
| F144 | 43 | Male | Family040 | MZ | NA | MetS | 61 | 93 | 69.4 | 162 | 103 | 33 | ERS714492 |
| F145 | 66 | Male | Family041 | MZ_FA | CT | Healthy | 60 | 93 | 70.5 | 44 | 96 | 51 | ERS714506 |
| F146 | 66 | Female | Family041 | MZ_MO | CT | MetS | 70 | 128 | 95.6 | 248 | 102 | 29 | ERS714507 |
| F147 | 38 | Male | Family041 | MZ | CT | Healthy | 62 | 104 | 79.1 | 111 | 93 | 34 | ERS714508 |
| F148 | 38 | Male | Family041 | MZ | NA | Healthy | 69 | 108 | 74.2 | 81 | 100 | 43 | ERS714509 |
| F149 | 70 | Male | Family042 | MZ_FA | CT | MetS | 63 | 116 | 96.8 | 215 | 193 | 29 | ERS714515 |
| F150 | 70 | Female | Family042 | MZ_MO | TT | MetS | 72 | 123 | 105.6 | 78 | 100 | 39 | ERS714516 |

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|------|----|--------|-----------|------------|----|---------|----|-----|------|-----|-----|----|-----------|
| F151 | 50 | Female | Family042 | MZ_sibling | TT | MetS | 97 | 147 | 85.5 | 44 | 79 | 43 | ERS714518 |
| F152 | 45 | Female | Family042 | MZ_sibling | CT | Healthy | 63 | 112 | 82.2 | 88 | 83 | 45 | ERS714520 |
| F153 | 43 | Female | Family042 | MZ | TT | Healthy | 72 | 112 | 97 | 127 | 86 | 42 | ERS714522 |
| F154 | 43 | Female | Family042 | MZ | NA | Healthy | 53 | 95 | 96.5 | 61 | 88 | 42 | ERS714524 |
| F155 | 41 | Male | Family041 | MZ_sibling | CT | MetS | 70 | 109 | 91.4 | 138 | 104 | 32 | ERS714526 |
| F156 | 71 | Male | Family043 | MZ_FA | CT | Healthy | 81 | 136 | 84.9 | 64 | 86 | 43 | ERS714529 |
| F157 | 63 | Female | Family043 | MZ_MO | CT | MetS | 81 | 133 | 90.5 | 117 | 107 | 40 | ERS714530 |
| F158 | 50 | Female | Family043 | MZ_sibling | TT | MetS | 62 | 102 | 85 | 77 | 102 | 48 | ERS714531 |
| F159 | 45 | Male | Family043 | MZ_sibling | CT | Healthy | 71 | 107 | 80.4 | 174 | 90 | 43 | ERS714532 |
| F160 | 41 | Female | Family043 | MZ_sibling | CC | Healthy | 53 | 91 | 63 | 76 | 86 | 52 | ERS714533 |
| F161 | 38 | Male | Family043 | MZ | TT | Healthy | 66 | 104 | 87.8 | 192 | 91 | 36 | ERS714534 |
| F162 | 38 | Male | Family043 | MZ | NA | Healthy | 60 | 100 | 73.4 | 85 | 92 | 39 | ERS714535 |
| F163 | 70 | Male | Family044 | DZ_FA | CT | Healthy | 77 | 123 | 91.4 | 90 | 99 | 35 | ERS714536 |
| F164 | 67 | Female | Family044 | DZ_MO | CT | Healthy | 72 | 109 | 66.9 | 140 | 86 | 58 | ERS714537 |
| F165 | 37 | Male | Family045 | MZ | TT | Healthy | 73 | 118 | 91.4 | 91 | 88 | 39 | ERS714540 |
| F166 | 37 | Male | Family045 | MZ | NA | MetS | 90 | 127 | 95.9 | 133 | 82 | 34 | ERS714541 |
| F168 | 55 | Male | Family046 | DZ | TT | Healthy | 80 | 128 | 77.4 | 58 | 84 | 47 | ERS714542 |
| F169 | 55 | Male | Family046 | DZ | TT | Healthy | 88 | 131 | 81.7 | 99 | 93 | 43 | ERS714543 |
| F170 | 49 | Male | Family046 | DZ_sibling | TT | Healthy | 60 | 100 | 88.6 | 189 | 92 | 43 | ERS714544 |
| F171 | 50 | Male | Family047 | DZ | CT | MetS | 84 | 163 | 80.4 | 164 | 102 | 39 | ERS714547 |
| F172 | 50 | Male | Family047 | DZ | CT | MetS | 74 | 140 | 88.5 | 193 | 113 | 73 | ERS714548 |
| F174 | 62 | Female | Family048 | MZ_MO | CT | Healthy | 69 | 120 | 77 | 222 | 90 | 48 | ERS714549 |
| F176 | 33 | Male | Family048 | MZ | TT | Healthy | 78 | 138 | 83.7 | 257 | 96 | 62 | ERS714551 |
| F177 | 33 | Male | Family048 | MZ | NA | Healthy | 70 | 130 | 78.7 | 117 | 87 | 67 | ERS714553 |
| F178 | 64 | Female | Family049 | DZ_MO | TT | Healthy | 70 | 111 | 69.9 | 36 | 87 | 82 | ERS714555 |

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|------|----|--------|-----------|------------|----|---------|-----|-----|------|-----|-----|----|-----------|
| F179 | 36 | Female | Family049 | DZ | CT | Healthy | 70 | 118 | 70.7 | 89 | 94 | 73 | ERS714556 |
| F180 | 36 | Female | Family049 | DZ | TT | Healthy | 60 | 99 | 65.4 | 36 | 90 | 70 | ERS714557 |
| F182 | 42 | Female | Family050 | MZ | TT | Healthy | 60 | 90 | 74.5 | 79 | 88 | 70 | ERS714558 |
| F184 | 42 | Female | Family050 | MZ | NA | Healthy | 61 | 102 | 82.1 | 205 | 95 | 52 | ERS714560 |
| F185 | 42 | Female | Family043 | MZ_sibling | TT | Healthy | 61 | 93 | 71 | 104 | 98 | 70 | ERS714562 |
| F186 | 65 | Male | Family051 | MZ_FA | TT | Healthy | 74 | 123 | 79.5 | 100 | 109 | 74 | ERS714563 |
| F187 | 60 | Female | Family051 | MZ_MO | CC | Healthy | 72 | 119 | 84 | 311 | 96 | 41 | ERS714564 |
| F188 | 33 | Female | Family051 | MZ | CT | Healthy | 73 | 121 | 78.2 | 75 | 91 | 70 | ERS714569 |
| F189 | 33 | Female | Family051 | MZ | NA | Healthy | 71 | 100 | 75.4 | 70 | 93 | 69 | ERS714570 |
| F190 | 46 | Female | Family047 | DZ_sibling | CC | Healthy | 89 | 120 | 85.3 | 65 | 93 | 70 | ERS714571 |
| F191 | 43 | Female | Family047 | DZ_sibling | CC | Healthy | 100 | 170 | 83.1 | 85 | 90 | 53 | ERS714572 |
| F192 | 36 | Male | Family044 | DZ | CT | Healthy | 75 | 114 | 74 | 100 | 81 | 47 | ERS714573 |
| F193 | 36 | Male | Family044 | DZ | CT | Healthy | 78 | 125 | 76.7 | 125 | 88 | 44 | ERS714574 |
| F194 | 34 | Male | Family052 | MZ | TT | Healthy | 70 | 120 | 91.5 | 102 | 92 | 65 | ERS714575 |
| F195 | 34 | Male | Family052 | MZ | NA | Healthy | 68 | 122 | 89.3 | 83 | 97 | 76 | ERS714576 |
| F196 | 59 | Male | Family053 | DZ | TT | Healthy | 88 | 128 | 85.7 | 200 | 87 | 54 | ERS714577 |
| F197 | 59 | Male | Family053 | DZ | TT | MetS | 72 | 140 | 92.5 | 120 | 104 | 57 | ERS714579 |
| F202 | 49 | Female | Family054 | MZ | CC | Healthy | 73 | 112 | 88.9 | 72 | 89 | 33 | ERS714623 |
| F203 | 38 | Male | Family055 | MZ_sibling | TT | Healthy | 65 | 98 | 73.4 | 72 | 96 | 38 | ERS714624 |
| F204 | 58 | Female | Family056 | MZ_MO | CT | Healthy | 70 | 118 | 82.9 | 119 | 147 | 43 | ERS714625 |
| F205 | 36 | Male | Family056 | MZ_sibling | TT | MetS | 75 | 120 | 87 | 271 | 108 | 32 | ERS714628 |
| F206 | 34 | Female | Family056 | MZ | CT | Healthy | 65 | 100 | 74.6 | 113 | 99 | 36 | ERS714630 |
| F207 | 63 | Male | Family056 | MZ_FA | TT | MetS | 79 | 140 | 81.5 | 60 | 118 | 31 | ERS714632 |
| F208 | 34 | Female | Family056 | MZ | NA | Healthy | 69 | 110 | 73.4 | 90 | 89 | 42 | ERS714634 |
| F213 | 47 | Female | Family057 | MZ | CT | Healthy | 50 | 79 | 67.1 | 94 | 100 | 40 | ERS714636 |

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|------|----|--------|-----------|------------|----|---------|----|-----|------|-----|-----|----|-----------|
| F214 | 47 | Female | Family057 | MZ | NA | Healthy | 52 | 80 | 65.5 | 153 | 93 | 38 | ERS714638 |
| F215 | 66 | Female | Family058 | MZ_MO | NA | MetS | 91 | 160 | 90.6 | 106 | 96 | 39 | ERS714640 |
| F216 | 42 | Female | Family058 | MZ | NA | Healthy | 61 | 98 | 65 | 95 | 95 | 49 | ERS714641 |
| F217 | 42 | Female | Family058 | MZ | NA | Healthy | 61 | 92 | 66.4 | 93 | 95 | 53 | ERS714642 |
| F218 | 28 | Male | Family058 | MZ_sibling | NA | Healthy | 71 | 110 | 91.6 | 105 | 99 | 33 | ERS714643 |
| F219 | 30 | Male | Family059 | DZ | NA | Healthy | 71 | 111 | 77.7 | 122 | 94 | 52 | ERS714644 |
| F220 | 30 | Male | Family059 | DZ | NA | Healthy | 69 | 129 | 82.6 | 201 | 96 | 58 | ERS714645 |
| F221 | 49 | Female | Family060 | MZ | TT | Healthy | 72 | 100 | 79 | 100 | 86 | 39 | ERS714646 |
| F222 | 49 | Female | Family060 | MZ | NA | MetS | 71 | 100 | 74.8 | 173 | 103 | 42 | ERS714647 |
| F223 | 44 | Female | Family060 | MZ | TT | Healthy | 71 | 101 | 87.6 | 148 | 96 | 43 | ERS714648 |
| F224 | 44 | Female | Family060 | MZ | NA | Healthy | 61 | 100 | 86 | 116 | 98 | 37 | ERS714649 |
| F225 | 59 | Male | Family060 | MZ_sibling | CT | Healthy | 62 | 94 | 80.1 | 53 | 110 | 46 | ERS714650 |
| F226 | 60 | Female | Family061 | MZ_MO | CC | MetS | 81 | 135 | 89 | 404 | 123 | 30 | ERS714652 |
| F227 | 39 | Female | Family061 | MZ_sibling | CC | MetS | 71 | 102 | 92.2 | 312 | 93 | 43 | ERS714654 |
| F228 | 37 | Male | Family061 | MZ_sibling | CC | MetS | 71 | 101 | 109 | 463 | 285 | 36 | ERS714655 |
| F229 | 34 | Male | Family061 | MZ | CC | Healthy | 61 | 107 | 81.3 | 104 | 93 | 49 | ERS714657 |
| F230 | 34 | Male | Family061 | MZ | NA | Healthy | 72 | 102 | 83.5 | 140 | 94 | 53 | ERS714659 |
| F231 | 72 | Female | Family062 | MZ_MO | CT | MetS | 90 | 159 | 83.1 | 245 | 99 | 32 | ERS714661 |
| F232 | 37 | Female | Family062 | MZ_sibling | CT | Healthy | 59 | 96 | 78.5 | 173 | 89 | 51 | ERS714664 |
| F233 | 35 | Male | Family062 | MZ | CT | Healthy | 70 | 120 | 85.5 | 435 | 94 | 32 | ERS714666 |
| F234 | 35 | Male | Family062 | MZ | NA | Healthy | 71 | 119 | 85.3 | 217 | 99 | 34 | ERS714668 |
| F235 | 38 | Female | Family063 | DZ | CT | Healthy | 60 | 98 | 75.6 | 66 | 95 | 49 | ERS714670 |
| F236 | 38 | Female | Family063 | DZ | CT | Healthy | 69 | 100 | 80 | 53 | 90 | 54 | ERS714671 |
| F237 | 65 | Male | Family064 | MZ_FA | CT | Healthy | 71 | 111 | 97.5 | 147 | 95 | 46 | ERS714672 |
| F238 | 56 | Female | Family064 | MZ_MO | TT | Healthy | 71 | 123 | 77.3 | 164 | 93 | 39 | ERS714673 |

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|------|----|--------|-----------|------------|----|---------|----|-----|------|-----|-----|----|-----------|
| F239 | 38 | Female | Family064 | MZ_sibling | TT | Healthy | 71 | 100 | 72 | 80 | 89 | 38 | ERS714674 |
| F240 | 36 | Male | Family064 | MZ_sibling | TT | MetS | 62 | 113 | 92.4 | 189 | 102 | 44 | ERS714675 |
| F241 | 33 | Female | Family064 | MZ | NA | Healthy | 61 | 98 | 70 | 47 | 80 | 47 | ERS714676 |
| F242 | 33 | Female | Family064 | MZ | CT | Healthy | 51 | 80 | 68.5 | 85 | 89 | 50 | ERS714677 |
| F243 | 55 | Female | Family065 | MZ_sibling | CC | Healthy | 71 | 111 | 80 | 96 | 95 | 68 | ERS714678 |
| F244 | 64 | Female | Family065 | MZ_sibling | CT | Healthy | 82 | 130 | 84.1 | 116 | 106 | 67 | ERS714679 |
| F245 | 45 | Female | Family065 | MZ | CC | Healthy | 72 | 102 | 78.3 | 109 | 93 | 43 | ERS714680 |
| F246 | 45 | Female | Family065 | MZ | NA | Healthy | 71 | 99 | 71.3 | 85 | 80 | 57 | ERS714681 |
| F247 | 47 | Female | Family066 | MZ_sibling | NA | Healthy | 70 | 122 | 65.7 | 106 | 90 | 51 | ERS714682 |
| F250 | 63 | Female | Family067 | MZ_MO | CT | MetS | 74 | 130 | 94.4 | 195 | 99 | 39 | ERS714686 |
| F251 | 42 | Male | Family067 | MZ_sibling | CC | MetS | 71 | 108 | 90 | 288 | 92 | 36 | ERS714687 |
| F252 | 36 | Male | Family067 | MZ | TT | MetS | 73 | 130 | 86.2 | 217 | 112 | 46 | ERS714688 |
| F253 | 36 | Male | Family067 | MZ | NA | MetS | 70 | 108 | 83 | 492 | 107 | 39 | ERS714690 |
| F254 | 65 | Male | Family063 | DZ_FA | CC | MetS | 62 | 106 | 90 | 280 | 98 | 25 | ERS714692 |
| F255 | 35 | Male | Family063 | DZ_sibling | CC | Healthy | 61 | 90 | 73.4 | 58 | 99 | 40 | ERS714693 |
| F256 | 33 | Female | Family063 | DZ_sibling | CT | Healthy | 62 | 96 | 70.1 | 54 | 87 | 53 | ERS714694 |
| F257 | 46 | Female | Family068 | DZ | NA | Healthy | 62 | 91 | 75.5 | 231 | 89 | 39 | ERS714695 |
| F258 | 45 | Female | Family068 | DZ | NA | Healthy | 61 | 91 | 70.3 | 144 | 88 | 38 | ERS714696 |
| F259 | 71 | Male | Family018 | MZ_FA | NA | Healthy | 71 | 120 | 83 | 191 | 81 | 27 | ERS714697 |
| F260 | 49 | Female | Family003 | MZ_sibling | NA | Healthy | 62 | 97 | 77.3 | 36 | 82 | 28 | ERS714700 |
| F262 | 74 | Female | Family069 | MZ_MO | NA | MetS | 80 | 128 | 95.9 | 201 | 110 | 39 | ERS714701 |
| F263 | 52 | Female | Family069 | MZ | NA | Healthy | 51 | 88 | 91 | 99 | 86 | 43 | ERS714702 |
| F264 | 52 | Female | Family069 | MZ | NA | Healthy | 72 | 107 | 86 | 65 | 85 | 35 | ERS714703 |
| F267 | 34 | Female | Family070 | DZ | NA | Healthy | 66 | 110 | 83.5 | 172 | 78 | 74 | ERS714704 |
| F268 | 34 | Female | Family070 | DZ | NA | Healthy | 70 | 111 | 67 | 52 | 88 | 46 | ERS714706 |

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|------|----|--------|-----------|------------|----|---------|----|-----|-------|------|-----|----|-----------|
| F269 | 62 | Male | Family070 | DZ_FA | NA | MetS | 80 | 126 | 84 | 180 | 119 | 31 | ERS714708 |
| F271 | 31 | Male | Family070 | DZ_sibling | NA | MetS | 99 | 139 | 91 | 261 | 99 | 49 | ERS714710 |
| F272 | 55 | Female | Family036 | MZ_sibling | NA | Healthy | 64 | 119 | 82.3 | 92 | 97 | 88 | ERS714711 |
| F273 | 64 | Male | Family011 | MZ_sibling | NA | Healthy | 82 | 114 | 87 | 170 | 91 | 32 | ERS714712 |
| F274 | 55 | Male | Family071 | MZ_FA | NA | Healthy | 79 | 122 | 76.2 | 74 | 100 | 59 | ERS714714 |
| F275 | 53 | Female | Family071 | MZ_MO | NA | MetS | 73 | 116 | 85 | 62 | 108 | 37 | ERS714715 |
| F276 | 28 | Male | Family071 | MZ_sibling | NA | Healthy | 63 | 128 | 87.3 | 152 | 111 | 50 | ERS714716 |
| F277 | 25 | Male | Family071 | MZ | NA | Healthy | 52 | 94 | 75 | 45 | 87 | 40 | ERS714717 |
| F278 | 25 | Male | Family071 | MZ | NA | Healthy | 53 | 102 | 78 | 81 | 84 | 35 | ERS714718 |
| F280 | 71 | Male | Family024 | DZ_sibling | NA | Healthy | 51 | 96 | 83 | 83 | 88 | 37 | ERS714720 |
| F281 | 32 | Female | Family072 | MZ | NA | Healthy | 60 | 92 | 76 | 58 | 80 | 45 | ERS714724 |
| F282 | 57 | Female | Family072 | MZ_MO | NA | Healthy | 60 | 90 | 76.2 | 88 | 77 | 69 | ERS714725 |
| F283 | 45 | Female | Family073 | MZ | NA | Healthy | 60 | 100 | 65.5 | 45 | 88 | 68 | ERS714726 |
| F284 | 45 | Female | Family073 | MZ | NA | Healthy | 61 | 100 | 68 | 66 | 82 | 61 | ERS714727 |
| F285 | 27 | Female | Family074 | MZ | NA | Healthy | 66 | 93 | 71 | 48 | 87 | 51 | ERS714728 |
| F286 | 27 | Female | Family074 | MZ | NA | Healthy | 63 | 92 | 82.4 | 66 | 82 | 45 | ERS714729 |
| F287 | 38 | Female | Family075 | MZ | NA | Healthy | 64 | 100 | 101.4 | 69 | 92 | 42 | ERS714730 |
| F288 | 38 | Female | Family075 | MZ | NA | Healthy | 62 | 100 | 107.5 | 109 | 97 | 43 | ERS714731 |
| F289 | 71 | Male | Family075 | MZ_FA | NA | MetS | 91 | 130 | 95 | 70 | 125 | 42 | ERS714732 |
| F291 | 29 | Male | Family076 | MZ | NA | MetS | 79 | 120 | 90 | 1579 | 90 | 22 | ERS714733 |
| F292 | 29 | Male | Family076 | MZ | NA | Healthy | 71 | 110 | 84 | 389 | 96 | 28 | ERS714734 |
| F293 | 55 | Male | Family076 | MZ_FA | NA | Healthy | 66 | 98 | 89 | 102 | 269 | 37 | ERS714735 |
| F294 | 51 | Female | Family076 | MZ_MO | NA | Healthy | 74 | 110 | 81 | 111 | 93 | 58 | ERS714736 |
| F295 | 63 | Female | Family077 | MZ_sibling | NA | Healthy | 71 | 111 | 79.3 | 175 | 93 | 39 | ERS714737 |
| F296 | 57 | Female | Family077 | MZ_sibling | NA | Healthy | 71 | 114 | 73 | 157 | 94 | 40 | ERS714738 |

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|------|----|--------|-----------|------------|----|---------|----|-----|-------|-----|-----|----|-----------|
| F297 | 53 | Female | Family077 | MZ | NA | Healthy | 72 | 114 | 74.5 | 82 | 92 | 52 | ERS714739 |
| F298 | 53 | Female | Family077 | MZ | NA | Healthy | 71 | 112 | 75.5 | 116 | 93 | 46 | ERS714740 |
| F299 | 28 | Male | Family072 | MZ_sibling | NA | Healthy | 81 | 119 | 92.5 | 112 | 97 | 40 | ERS714741 |
| F300 | 20 | Female | Family078 | MZ | NA | Healthy | 70 | 106 | 73.1 | 61 | 98 | 56 | ERS714742 |
| F301 | 20 | Female | Family078 | MZ | NA | Healthy | 60 | 98 | 78.2 | 75 | 88 | 61 | ERS714743 |
| F302 | 46 | Male | Family078 | MZ_FA | NA | Healthy | 79 | 118 | 90.9 | 90 | 178 | 68 | ERS714744 |
| F303 | 47 | Female | Family078 | MZ_MO | NA | Healthy | 69 | 103 | 84.6 | 92 | 107 | 45 | ERS714745 |
| F304 | 29 | Female | Family079 | MZ | NA | Healthy | 65 | 98 | 61 | 56 | 80 | 40 | ERS714746 |
| F305 | 29 | Female | Family079 | MZ | NA | Healthy | 71 | 100 | 68 | 56 | 86 | 65 | ERS714747 |
| F306 | 26 | Female | Family079 | MZ_sibling | NA | Healthy | 65 | 98 | 66.6 | 40 | 87 | 53 | ERS714748 |
| F307 | 24 | Female | Family079 | MZ_sibling | NA | Healthy | 60 | 92 | 68 | 48 | 83 | 67 | ERS714749 |
| F308 | 32 | Female | Family072 | MZ | NA | Healthy | 60 | 90 | 85.3 | 41 | 86 | 49 | ERS714750 |
| F309 | 39 | Female | Family080 | MZ | NA | Healthy | 60 | 97 | 87.1 | 68 | 80 | 55 | ERS714751 |
| F310 | 39 | Female | Family080 | MZ | NA | Healthy | 69 | 111 | 79.3 | 109 | 75 | 59 | ERS714752 |
| F311 | 38 | Female | Family081 | DZ | TT | Healthy | 60 | 100 | 75.9 | 123 | 96 | 65 | ERS714801 |
| F312 | 38 | Female | Family081 | DZ | TT | Healthy | 60 | 100 | 73.1 | 68 | 73 | 50 | ERS714802 |
| F313 | 44 | Female | Family082 | MZ | NA | Healthy | 80 | 120 | 76.05 | 81 | 99 | 68 | ERS714803 |
| F314 | 44 | Female | Family082 | MZ | NA | Healthy | 80 | 120 | 63.4 | 91 | 99 | 70 | ERS714804 |
| F315 | 38 | Female | Family082 | MZ_sibling | NA | Healthy | 80 | 110 | 72 | 107 | 93 | 45 | ERS714807 |
| F316 | 46 | Male | Family083 | DZ | TT | Healthy | 80 | 110 | 73.8 | 47 | 82 | 57 | ERS714809 |
| F317 | 49 | Female | Family082 | MZ_sibling | NA | Healthy | 80 | 120 | 73.75 | 130 | 102 | 47 | ERS714812 |
| F318 | 46 | Male | Family083 | DZ | CT | Healthy | 80 | 110 | 71.7 | 103 | 96 | 42 | ERS714824 |
| F319 | 35 | Female | Family084 | MZ | TT | Healthy | 80 | 110 | 83.1 | 77 | 102 | 47 | ERS714828 |
| F320 | 35 | Female | Family084 | MZ | NA | MetS | 80 | 120 | 85.4 | 93 | 104 | 47 | ERS714829 |
| F321 | 43 | Female | Family022 | MZ | NA | Healthy | 77 | 108 | 85.6 | 78 | 81 | 42 | ERS714830 |

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|------|----|--------|-----------|------------|----|---------|-----|-----|-------|-----|-----|----|-----------|
| F322 | 81 | Female | Family022 | MZ_MO | TT | MetS | 63 | 142 | 91.7 | 131 | 144 | 39 | ERS714831 |
| F323 | 38 | Female | Family085 | MZ | CT | Healthy | 70 | 110 | 68.4 | 86 | 76 | 63 | ERS714836 |
| F324 | 38 | Female | Family085 | MZ | NA | Healthy | 80 | 120 | 66.2 | 91 | 91 | 49 | ERS714837 |
| F325 | 34 | Male | Family086 | MZ | CT | Healthy | 80 | 120 | 86 | 62 | 109 | 54 | ERS714838 |
| F326 | 34 | Male | Family086 | MZ | NA | Healthy | 70 | 110 | 87 | 101 | 94 | 42 | ERS714839 |
| F331 | 43 | Female | Family087 | MZ | CT | Healthy | 60 | 90 | 68.05 | 55 | 96 | 53 | ERS714844 |
| F332 | 43 | Female | Family087 | MZ | NA | Healthy | 60 | 90 | 63.1 | 82 | 91 | 54 | ERS714846 |
| F333 | 35 | Male | Family088 | DZ | CT | Healthy | 70 | 110 | 87 | 155 | 81 | 31 | ERS714848 |
| F334 | 35 | Male | Family088 | DZ | CT | Healthy | 70 | 110 | 76.2 | 113 | 100 | 35 | ERS714849 |
| F336 | 38 | Male | Family089 | DZ_sibling | CT | MetS | 80 | 130 | 90.6 | 216 | 104 | 30 | ERS714853 |
| F337 | 54 | Male | Family038 | MZ | NA | MetS | 80 | 140 | 88.25 | 135 | 113 | 36 | ERS714854 |
| F338 | 65 | Female | Family038 | MZ_sibling | TT | MetS | 80 | 140 | 92.05 | 115 | 110 | 48 | ERS714855 |
| F342 | 67 | Male | Family038 | MZ_sibling | TT | Healthy | 80 | 120 | 87 | 119 | 113 | 31 | ERS714857 |
| F343 | 51 | Female | Family038 | MZ_sibling | TT | Healthy | 60 | 110 | 73 | 106 | 100 | 42 | ERS714858 |
| F344 | 63 | Female | Family038 | MZ_sibling | TT | MetS | 80 | 130 | 75.4 | 167 | 126 | 33 | ERS714859 |
| F345 | 47 | Male | Family090 | MZ | CT | Healthy | 90 | 140 | 68 | 79 | 103 | 40 | ERS714861 |
| F346 | 47 | Male | Family090 | MZ | NA | Healthy | 90 | 150 | 71.5 | 58 | 102 | 50 | ERS714862 |
| F347 | 34 | Male | Family091 | MZ | CC | MetS | 100 | 150 | 89.75 | 182 | 109 | 45 | ERS714870 |
| F350 | 28 | Male | Family092 | MZ | NA | Healthy | 80 | 120 | 85.1 | 102 | 87 | 45 | ERS714879 |
| F351 | 28 | Male | Family092 | MZ | NA | Healthy | 80 | 120 | 84 | 142 | 85 | 39 | ERS714881 |
| F352 | 68 | Male | Family085 | MZ_FA | CT | Healthy | 80 | 120 | 70.5 | 76 | 89 | 42 | ERS714885 |
| F353 | 40 | Female | Family085 | MZ_sibling | TT | Healthy | 70 | 110 | 69 | 65 | 76 | 56 | ERS714886 |
| F354 | 69 | Male | Family086 | MZ_FA | NA | MetS | 90 | 130 | 96.8 | 154 | 129 | 50 | ERS714887 |
| F355 | 55 | Female | Family086 | MZ_MO | NA | Healthy | 80 | 120 | 81.3 | 90 | 162 | 52 | ERS714888 |
| F356 | 34 | Male | Family093 | MZ | CT | MetS | 70 | 110 | 83.8 | 160 | 102 | 30 | ERS714889 |

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|------|----|--------|-----------|------------|----|---------|----|-----|-------|-----|-----|----|-----------|
| F357 | 34 | Male | Family093 | MZ | NA | Healthy | 70 | 110 | 83.9 | 100 | 99 | 41 | ERS714891 |
| F358 | 54 | Female | Family059 | DZ_MO | NA | Healthy | 80 | 120 | 82.7 | 101 | 106 | 53 | ERS714893 |
| F359 | 33 | Male | Family094 | MZ | NA | Healthy | 70 | 100 | 77 | 90 | 103 | 41 | ERS714894 |
| F360 | 33 | Male | Family094 | MZ | NA | Healthy | 70 | 100 | 72.25 | 91 | 102 | 41 | ERS714895 |
| F361 | 50 | Male | Family001 | MZ | NA | MetS | 71 | 101 | 87.1 | 175 | 178 | 29 | ERS714910 |
| F362 | 73 | Female | Family001 | MZ_MO | TT | MetS | 91 | 141 | 95.4 | 261 | 89 | 36 | ERS714911 |
| F364 | 50 | Female | Family055 | MZ | TT | Healthy | 80 | 120 | 64.9 | 42 | 86 | 70 | ERS714161 |
| F365 | 50 | Female | Family055 | MZ | NA | Healthy | 69 | 109 | 72.8 | 58 | 94 | 48 | ERS714162 |
| F366 | 75 | Female | Family055 | MZ_MO | CT | MetS | 80 | 131 | 84.3 | 169 | 100 | 28 | ERS714163 |
| F367 | 47 | Female | Family055 | MZ_sibling | CT | Healthy | 80 | 99 | 72.2 | 150 | 90 | 37 | ERS714164 |
| F368 | 37 | Female | Family095 | MZ | TT | Healthy | 71 | 104 | 75 | 72 | 90 | 53 | ERS714170 |
| F369 | 68 | Male | Family095 | MZ_FA | TT | Healthy | 80 | 126 | 87.8 | 131 | 97 | 35 | ERS714172 |
| F370 | 34 | Female | Family096 | MZ | NA | Healthy | 61 | 90 | 81.8 | 55 | 92 | 32 | ERS714203 |
| F371 | 34 | Female | Family096 | MZ | NA | Healthy | 60 | 90 | 73 | 65 | 90 | 41 | ERS714204 |
| F372 | 48 | Male | Family097 | DZ | NA | Healthy | 51 | 98 | 87.5 | 243 | 92 | 46 | ERS714217 |
| F373 | 55 | Male | Family097 | DZ_sibling | NA | Healthy | 70 | 101 | 88.8 | 211 | 96 | 53 | ERS714219 |
| F374 | 48 | Male | Family097 | DZ | NA | Healthy | 75 | 114 | 86.4 | 162 | 94 | 42 | ERS714218 |
| F375 | 34 | Male | Family098 | MZ | NA | Healthy | 65 | 104 | 83.5 | 147 | 86 | 42 | ERS714260 |
| F376 | 34 | Male | Family098 | MZ | NA | Healthy | 79 | 112 | 81.2 | 85 | 91 | 45 | ERS714261 |
| F377 | 66 | Male | Family098 | MZ_FA | NA | Healthy | 61 | 90 | 83.2 | 91 | 86 | 59 | ERS714262 |
| F378 | 62 | Female | Family098 | MZ_MO | NA | Healthy | 72 | 110 | 77.4 | 93 | 93 | 75 | ERS714263 |
| F379 | 50 | Female | Family099 | MZ | TT | Healthy | 70 | 125 | 75.2 | 69 | 86 | 70 | ERS714328 |
| F380 | 50 | Female | Family099 | MZ | NA | Healthy | 81 | 138 | 75.5 | 78 | 85 | 73 | ERS714329 |
| F381 | 70 | Female | Family099 | MZ_MO | TT | Healthy | 71 | 128 | 72.5 | 151 | 100 | 54 | ERS714330 |
| F382 | 40 | Female | Family099 | MZ_sibling | TT | Healthy | 57 | 90 | 70 | 68 | 88 | 55 | ERS714331 |

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|------|----|--------|-----------|------------|----|---------|-----|-----|------|-----|-----|----|-----------|
| F383 | 66 | Female | Family100 | MZ_MO | CT | MetS | 70 | 114 | 87.3 | 106 | 106 | 44 | ERS714342 |
| F384 | 48 | Female | Family100 | MZ_sibling | CC | Healthy | 90 | 134 | 82.7 | 103 | 110 | 61 | ERS714343 |
| F385 | 37 | Male | Family100 | MZ | TT | Healthy | 78 | 118 | 87 | 135 | 96 | 56 | ERS714344 |
| F386 | 53 | Female | Family101 | MZ | CT | Healthy | 51 | 88 | 61.1 | 102 | 84 | 41 | ERS714348 |
| F387 | 53 | Female | Family101 | MZ | NA | Healthy | 51 | 90 | 64.3 | 96 | 87 | 40 | ERS714349 |
| F388 | 49 | Female | Family101 | MZ_sibling | TT | Healthy | 61 | 104 | 77.7 | 118 | 89 | 57 | ERS714350 |
| F389 | 48 | Female | Family102 | MZ | TT | Healthy | 66 | 104 | 68 | 109 | 84 | 67 | ERS714360 |
| F390 | 48 | Female | Family102 | MZ | NA | Healthy | 61 | 93 | 68.3 | 62 | 90 | 65 | ERS714362 |
| F391 | 37 | Male | Family100 | MZ | NA | Healthy | 59 | 110 | 86.2 | 110 | 101 | 57 | ERS714373 |
| F392 | 54 | Male | Family103 | MZ_FA | TT | Healthy | 78 | 117 | 80.8 | 47 | 80 | 43 | ERS714394 |
| F393 | 57 | Female | Family103 | MZ_MO | CC | Healthy | 59 | 96 | 80.5 | 208 | 86 | 35 | ERS714395 |
| F394 | 34 | Male | Family103 | MZ | CT | Healthy | 88 | 128 | 83 | 145 | 89 | 43 | ERS714396 |
| F395 | 34 | Male | Family103 | MZ | NA | Healthy | 102 | 144 | 83.5 | 102 | 86 | 51 | ERS714397 |
| F396 | 47 | Female | Family104 | MZ | TT | Healthy | 60 | 108 | 79.9 | 142 | 74 | 39 | ERS714402 |
| F397 | 47 | Female | Family104 | MZ | NA | Healthy | 60 | 98 | 84.5 | 84 | 78 | 51 | ERS714404 |
| F398 | 66 | Female | Family105 | MZ_MO | TT | Healthy | 62 | 118 | 84 | 130 | 85 | 39 | ERS714409 |
| F399 | 34 | Female | Family105 | MZ | TT | MetS | 63 | 108 | 89 | 175 | 83 | 38 | ERS714410 |
| F400 | 34 | Female | Family105 | MZ | NA | MetS | 61 | 100 | 93 | 193 | 86 | 37 | ERS714411 |
| F401 | 35 | Female | Family106 | MZ | TT | Healthy | 78 | 111 | 78.8 | 168 | 87 | 47 | ERS714412 |
| F402 | 35 | Female | Family106 | MZ | NA | Healthy | 79 | 118 | 77.6 | 114 | 86 | 32 | ERS714413 |
| F403 | 46 | Male | Family107 | DZ | TT | Healthy | 74 | 118 | 75 | 110 | 94 | 58 | ERS714439 |
| F404 | 46 | Male | Family107 | DZ | CT | Healthy | 97 | 147 | 86.8 | 251 | 92 | 53 | ERS714440 |
| F405 | 63 | Female | Family108 | MZ_MO | TT | Healthy | 79 | 129 | 82.2 | 60 | 88 | 62 | ERS714442 |
| F406 | 40 | Male | Family108 | MZ | TT | Healthy | 82 | 115 | 81.4 | 97 | 85 | 47 | ERS714443 |
| F407 | 40 | Male | Family108 | MZ | NA | Healthy | 79 | 121 | 85.5 | 165 | 85 | 49 | ERS714444 |

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|------|----|--------|-----------|------------|----|---------|----|-----|------|-----|-----|----|-----------|
| F410 | 42 | Female | Family109 | MZ | TT | Healthy | 68 | 103 | 70.6 | 59 | 84 | 55 | ERS714499 |
| F411 | 42 | Female | Family109 | MZ | NA | Healthy | 70 | 107 | 64.5 | 61 | 83 | 51 | ERS714500 |
| F413 | 39 | Female | Family110 | MZ_sibling | TT | Healthy | 71 | 98 | 73.3 | 69 | 85 | 64 | ERS714503 |
| F414 | 31 | Female | Family110 | MZ | TT | Healthy | 62 | 92 | 63.5 | 51 | 80 | 65 | ERS714504 |
| F415 | 31 | Female | Family110 | MZ | NA | Healthy | 62 | 90 | 66 | 51 | 76 | 61 | ERS714505 |
| F417 | 34 | Male | Family111 | DZ | CT | Healthy | 86 | 126 | 79.4 | 73 | 96 | 45 | ERS714527 |
| F418 | 34 | Male | Family111 | DZ | CT | Healthy | 77 | 108 | 85.8 | 105 | 97 | 43 | ERS714528 |
| F422 | 67 | Male | Family112 | MZ_FA | NA | Healthy | 80 | 129 | 84.5 | 65 | 86 | 74 | ERS714581 |
| F423 | 61 | Female | Family112 | MZ_MO | NA | Healthy | 80 | 110 | 89.2 | 139 | 88 | 44 | ERS714582 |
| F424 | 35 | Female | Family112 | MZ | NA | Healthy | 60 | 92 | 81.1 | 101 | 85 | 62 | ERS714584 |
| F425 | 35 | Female | Family112 | MZ | NA | Healthy | 80 | 100 | 71.3 | 75 | 76 | 68 | ERS714586 |
| F426 | 30 | Female | Family112 | MZ_sibling | NA | Healthy | 68 | 110 | 75.4 | 76 | 103 | 49 | ERS714588 |
| F427 | 34 | Male | Family113 | MZ | CT | Healthy | 74 | 100 | 80.1 | 53 | 96 | 45 | ERS714589 |
| F430 | 29 | Female | Family114 | MZ | NA | Healthy | 60 | 102 | 73.5 | 60 | 94 | 60 | ERS714591 |
| F431 | 29 | Female | Family114 | MZ | NA | Healthy | 54 | 96 | 67 | 77 | 91 | 66 | ERS714593 |
| F435 | 34 | Male | Family113 | MZ | NA | Healthy | 66 | 110 | 76.5 | 47 | 101 | 50 | ERS714595 |
| F436 | 52 | Male | Family115 | MZ | TT | Healthy | 60 | 92 | 88.9 | 85 | 82 | 43 | ERS714597 |
| F437 | 52 | Male | Family115 | MZ | NA | Healthy | 61 | 90 | 76.5 | 51 | 88 | 67 | ERS714598 |
| F438 | 33 | Male | Family116 | MZ | CT | Healthy | 80 | 120 | 77.5 | 76 | 86 | 47 | ERS714599 |
| F439 | 33 | Male | Family116 | MZ | NA | Healthy | 70 | 110 | 77 | 70 | 87 | 56 | ERS714600 |
| F440 | 31 | Male | Family116 | MZ_sibling | NA | Healthy | 84 | 120 | 87.8 | 179 | 76 | 34 | ERS714601 |
| F441 | 46 | Male | Family117 | MZ | CT | Healthy | 70 | 110 | 82.6 | 80 | 79 | 48 | ERS714603 |
| F442 | 53 | Female | Family118 | MZ_sibling | CT | Healthy | 54 | 88 | 67 | 92 | 82 | 50 | ERS714604 |
| F443 | 50 | Female | Family104 | MZ_sibling | TT | Healthy | 68 | 110 | 78.3 | 52 | 97 | 48 | ERS714602 |
| F444 | 41 | Female | Family104 | MZ_sibling | TT | Healthy | 70 | 102 | 77.1 | 98 | 80 | 48 | ERS714605 |

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|------|----|--------|-----------|------------|----|---------|----|-----|-------|-----|-----|----|-----------|
| F445 | 69 | Female | Family119 | MZ_MO | TT | Healthy | 64 | 120 | 86.1 | 94 | 87 | 37 | ERS714606 |
| F446 | 46 | Female | Family119 | MZ | TT | Healthy | 76 | 108 | 75 | 47 | 79 | 50 | ERS714607 |
| F447 | 43 | Male | Family119 | MZ_sibling | TT | Healthy | 80 | 108 | 87.1 | 100 | 89 | 42 | ERS714608 |
| F448 | 46 | Male | Family117 | MZ | NA | Healthy | 70 | 110 | 86.3 | 87 | 83 | 52 | ERS714609 |
| F449 | 45 | Male | Family066 | MZ | TT | Healthy | 68 | 120 | 84.3 | 88 | 97 | 39 | ERS714612 |
| F450 | 46 | Female | Family119 | MZ | NA | Healthy | 60 | 101 | 75 | 61 | 87 | 49 | ERS714611 |
| F451 | 50 | Male | Family119 | MZ_sibling | TT | Healthy | 60 | 109 | 89 | 125 | 88 | 30 | ERS714610 |
| F452 | 45 | Male | Family066 | MZ | NA | Healthy | 69 | 130 | 83.2 | 125 | 91 | 36 | ERS714613 |
| F453 | 49 | Female | Family120 | MZ | CT | Healthy | 59 | 90 | 71.8 | 95 | 81 | 68 | ERS714614 |
| F454 | 49 | Female | Family120 | MZ | NA | Healthy | 60 | 100 | 83.3 | 258 | 92 | 54 | ERS714616 |
| F455 | 43 | Female | Family120 | MZ_sibling | TT | MetS | 69 | 120 | 97 | 191 | 132 | 54 | ERS714618 |
| F456 | 36 | Male | Family098 | MZ_sibling | NA | Healthy | 74 | 104 | 79.6 | 101 | 92 | 50 | ERS714721 |
| F457 | 50 | Female | Family107 | DZ_sibling | NA | Healthy | 60 | 92 | 65.1 | 132 | 84 | 48 | ERS714722 |
| F458 | 46 | Female | Family099 | MZ_sibling | NA | MetS | 70 | 121 | 86 | 209 | 104 | 37 | ERS714723 |
| F459 | 37 | Female | Family095 | MZ | NA | Healthy | 70 | 110 | 86.9 | 83 | 85 | 38 | ERS714171 |
| F460 | 48 | Female | Family121 | DZ | TT | Healthy | 70 | 100 | 75.25 | 70 | 96 | 70 | ERS714799 |
| F461 | 50 | Male | Family122 | MZ | TT | MetS | 80 | 130 | 88.85 | 279 | 107 | 40 | ERS714805 |
| F462 | 50 | Male | Family122 | MZ | NA | Healthy | 80 | 120 | 83.95 | 209 | 90 | 40 | ERS714806 |
| F463 | 48 | Female | Family121 | DZ | NA | Healthy | 80 | 120 | 74.7 | 104 | 91 | 58 | ERS714808 |
| F467 | 43 | Female | Family055 | MZ_sibling | TT | Healthy | 80 | 110 | 60.9 | 51 | 93 | 40 | ERS714815 |
| F468 | 35 | Male | Family121 | DZ_sibling | CT | Healthy | 80 | 130 | 81.95 | 139 | 89 | 43 | ERS714800 |
| F470 | 42 | Female | Family123 | MZ | CT | Healthy | 80 | 120 | 69 | 40 | 83 | 71 | ERS714832 |
| F471 | 42 | Female | Family123 | MZ | NA | Healthy | 80 | 120 | 78 | 55 | 88 | 54 | ERS714834 |
| F472 | 68 | Male | Family089 | DZ_FA | CC | Healthy | 70 | 110 | 77 | 123 | 106 | 31 | ERS714840 |
| F477 | 36 | Female | Family089 | DZ | CT | Healthy | 60 | 100 | 77.9 | 74 | 94 | 41 | ERS714851 |

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|------|----|--------|-----------|------------|----|---------|----|-----|-------|-----|-----|----|-----------|
| F478 | 36 | Female | Family089 | DZ | CT | Healthy | 70 | 110 | 68.5 | 64 | 90 | 68 | ERS714852 |
| F480 | 46 | Male | Family040 | MZ_sibling | CT | Healthy | 80 | 110 | 82 | 173 | 99 | 33 | ERS714860 |
| F481 | 36 | Female | Family124 | MZ | CC | Healthy | 70 | 110 | 75 | 91 | 82 | 58 | ERS714865 |
| F482 | 36 | Female | Family124 | MZ | NA | Healthy | 70 | 125 | 74.8 | 100 | 85 | 56 | ERS714866 |
| F483 | 54 | Female | Family124 | MZ_MO | CT | Healthy | 70 | 110 | 78.5 | 39 | 91 | 39 | ERS714867 |
| F484 | 35 | Male | Family091 | MZ | NA | Healthy | 70 | 140 | 87 | 79 | 89 | 43 | ERS714871 |
| F488 | 51 | Female | Family118 | MZ | TT | Healthy | 80 | 130 | 64.3 | 124 | 84 | 46 | ERS714874 |
| F489 | 51 | Female | Family118 | MZ | NA | Healthy | 90 | 140 | 71.7 | 128 | 96 | 55 | ERS714875 |
| F490 | 48 | Female | Family118 | MZ_sibling | CT | Healthy | 80 | 120 | 70.7 | 108 | 92 | 42 | ERS714876 |
| F491 | 80 | Female | Family118 | MZ_MO | CT | Healthy | 70 | 140 | 70.8 | 134 | 94 | 42 | ERS714877 |
| F492 | 40 | Female | Family121 | DZ_sibling | CC | Healthy | 80 | 120 | 73.5 | 81 | 102 | 54 | ERS714878 |
| F496 | 49 | Female | Family054 | MZ | NA | MetS | 80 | 130 | 81.55 | 92 | 101 | 36 | ERS714884 |
| F499 | 41 | Male | Family125 | MZ_sibling | NA | Healthy | 73 | 120 | 83 | 490 | 99 | 40 | ERS714768 |
| F500 | 56 | Female | Family126 | MZ | NA | MetS | 71 | 121 | 79.6 | 469 | 106 | 37 | ERS714449 |
| F501 | 44 | Female | Family125 | MZ | NA | Healthy | 79 | 120 | 88.1 | 103 | 102 | 66 | ERS714913 |
| F502 | 39 | Male | Family127 | MZ | NA | Healthy | 79 | 122 | 91.7 | 149 | 118 | 54 | ERS714332 |
| F503 | 39 | Male | Family127 | MZ | NA | MetS | 66 | 126 | 98.6 | 178 | 125 | 55 | ERS714333 |
| F504 | 56 | Male | Family125 | MZ_sibling | NA | MetS | 59 | 102 | 94.5 | 223 | 103 | 41 | ERS714766 |
| F505 | 38 | Female | Family128 | DZ | NA | Healthy | 71 | 107 | 69.5 | 79 | 101 | 64 | ERS714173 |
| F506 | 50 | Female | Family129 | MZ | TT | Healthy | 63 | 101 | 67.5 | 131 | 79 | 51 | ERS714268 |
| F507 | 44 | Female | Family125 | MZ | CC | Healthy | 79 | 135 | 86.5 | 83 | 93 | 53 | ERS714211 |
| F508 | 50 | Female | Family129 | MZ | NA | Healthy | 71 | 115 | 74.3 | 94 | 88 | 63 | ERS714269 |
| F509 | 80 | Female | Family125 | MZ_MO | NA | MetS | 59 | 99 | 96.1 | 240 | 91 | 34 | ERS714765 |
| F510 | 39 | Female | Family125 | MZ_sibling | NA | Healthy | 59 | 100 | 73.6 | 88 | 94 | 46 | ERS714767 |
| F511 | 48 | Female | Family125 | MZ_sibling | NA | Healthy | 68 | 102 | 83.1 | 103 | 95 | 56 | ERS714212 |

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|------|----|--------|-----------|------------|----|---------|-----|-----|------|-----|-----|----|-----------|
| F512 | 39 | Male | Family130 | MZ | NA | Healthy | 82 | 121 | 85.4 | 101 | 98 | 49 | ERS714216 |
| F513 | 61 | Female | Family131 | DZ_MO | CT | Healthy | 79 | 121 | 90.9 | 116 | 99 | 38 | ERS714566 |
| F514 | 38 | Female | Family128 | DZ | CT | Healthy | 63 | 92 | 74.5 | 84 | 92 | 64 | ERS714174 |
| F515 | 35 | Female | Family131 | DZ_sibling | TT | Healthy | 67 | 102 | 87.1 | 41 | 95 | 52 | ERS714567 |
| F516 | 38 | Female | Family131 | DZ | CT | Healthy | 62 | 109 | 84.1 | 99 | 102 | 33 | ERS714545 |
| F517 | 68 | Male | Family128 | DZ_FA | TT | Healthy | 81 | 142 | 85.6 | 148 | 96 | 40 | ERS714214 |
| F518 | 38 | Female | Family131 | DZ | TT | Healthy | 64 | 101 | 72.1 | 86 | 98 | 35 | ERS714546 |
| F519 | 66 | Female | Family128 | DZ_MO | CT | Healthy | 74 | 129 | 84.3 | 222 | 183 | 60 | ERS714215 |
| F520 | 53 | Male | Family019 | MZ_sibling | TT | Healthy | 109 | 151 | 83.1 | 139 | 89 | 34 | ERS714335 |
| F521 | 62 | Female | Family019 | MZ_sibling | CT | MetS | 87 | 160 | 84.4 | 232 | 96 | 39 | ERS714347 |
| F522 | 68 | Female | Family019 | MZ_sibling | CT | MetS | 97 | 166 | 78.4 | 156 | 97 | 41 | ERS714346 |
| F523 | 66 | Male | Family130 | MZ_FA | TT | Healthy | 75 | 142 | 84.7 | 133 | 89 | 34 | ERS714189 |
| F524 | 57 | Female | Family005 | DZ_sibling | CT | Healthy | 77 | 124 | 83 | 71 | 95 | 46 | ERS714210 |
| F525 | 39 | Male | Family130 | MZ | TT | Healthy | 83 | 121 | 92.1 | 206 | 93 | 41 | ERS714206 |
| F526 | 47 | Female | Family019 | MZ_sibling | CT | Healthy | 73 | 111 | 82.6 | 180 | 84 | 29 | ERS714351 |
| F527 | 65 | Female | Family130 | MZ_MO | TT | MetS | 79 | 132 | 97.9 | 135 | 100 | 54 | ERS714190 |
| F528 | 50 | Female | Family005 | DZ | TT | Healthy | 83 | 122 | 79.1 | 115 | 82 | 31 | ERS714207 |
| F529 | 50 | Female | Family005 | DZ | TT | MetS | 83 | 133 | 94.3 | 144 | 86 | 32 | ERS714208 |
| F530 | 58 | Male | Family132 | MZ_sibling | NA | MetS | 100 | 151 | 94.4 | 100 | 183 | 62 | ERS714760 |
| F531 | 76 | Male | Family015 | MZ_sibling | TT | Healthy | 66 | 129 | 88.4 | 102 | 94 | 28 | ERS714307 |
| F532 | 46 | Male | Family132 | MZ | NA | Healthy | 80 | 118 | 76.4 | 128 | 92 | 57 | ERS714758 |
| F533 | 55 | Male | Family132 | MZ_sibling | NA | MetS | 92 | 139 | 91.2 | 164 | 180 | 46 | ERS714761 |
| F534 | 46 | Male | Family132 | MZ | NA | MetS | 92 | 137 | 83 | 140 | 110 | 35 | ERS714759 |
| F535 | 41 | Female | Family132 | MZ_sibling | NA | Healthy | 86 | 123 | 77.1 | 109 | 99 | 50 | ERS714763 |
| F536 | 49 | Female | Family132 | MZ_sibling | NA | MetS | 101 | 159 | 77.1 | 344 | 242 | 53 | ERS714762 |

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|------|----|--------|-----------|------------|----|---------|----|-----|------|-----|-----|----|-----------|
| F537 | 69 | Male | Family133 | DZ_FA | NA | Healthy | 79 | 129 | 99.5 | 157 | 88 | 40 | ERS714764 |
| F538 | 37 | Male | Family133 | DZ | CT | MetS | 80 | 130 | 105 | 504 | 108 | 33 | ERS714539 |
| F539 | 63 | Female | Family134 | MZ | TT | Healthy | 70 | 121 | 67.4 | 94 | 89 | 69 | ERS714483 |
| F540 | 72 | Male | Family134 | MZ_sibling | TT | Healthy | 72 | 119 | 85.1 | 84 | 96 | 60 | ERS714481 |
| F541 | 63 | Female | Family134 | MZ | NA | Healthy | 69 | 110 | 72.5 | 74 | 89 | 68 | ERS714484 |
| F542 | 68 | Female | Family134 | MZ_sibling | CT | Healthy | 79 | 133 | 79.5 | 91 | 102 | 54 | ERS714482 |
| F543 | 37 | Male | Family133 | DZ | CT | Healthy | 77 | 115 | 80.3 | 120 | 91 | 40 | ERS714565 |
| F544 | 62 | Female | Family133 | DZ_MO | TT | MetS | 85 | 123 | 89.5 | 181 | 94 | 35 | ERS714538 |
| F550 | 35 | Male | Family135 | MZ | NA | Healthy | 51 | 91 | 79 | 83 | 90 | 42 | ERS714355 |
| F551 | 35 | Male | Family135 | MZ | NA | Healthy | 51 | 93 | 87.1 | 62 | 97 | 35 | ERS714354 |
| F552 | 51 | Female | Family136 | MZ | CT | Healthy | 60 | 91 | 71 | 166 | 92 | 56 | ERS714621 |
| F553 | 37 | Female | Family137 | MZ | NA | MetS | 51 | 95 | 84.8 | 210 | 109 | 44 | ERS714320 |
| F554 | 56 | Male | Family138 | MZ | CT | Healthy | 71 | 111 | 90.9 | 67 | 95 | 33 | ERS714352 |
| F555 | 40 | Male | Family032 | MZ | NA | Healthy | 67 | 105 | 76.1 | 183 | 97 | 53 | ERS714450 |
| F557 | 56 | Female | Family126 | MZ | CT | MetS | 61 | 107 | 72.8 | 199 | 105 | 33 | ERS714448 |
| F558 | 49 | Male | Family139 | MZ | NA | Healthy | 69 | 111 | 85.6 | 175 | 119 | 42 | ERS714184 |
| F559 | 37 | Female | Family137 | MZ | NA | Healthy | 79 | 117 | 82.1 | 44 | 97 | 56 | ERS714319 |
| F560 | 56 | Male | Family138 | MZ | NA | MetS | 83 | 126 | 97.9 | 180 | 103 | 29 | ERS714353 |
| F561 | 59 | Male | Family140 | MZ_FA | NA | Healthy | 75 | 111 | 87.9 | 120 | 114 | 35 | ERS714754 |
| F562 | 51 | Female | Family141 | MZ_sibling | NA | Healthy | 82 | 113 | 80.4 | 117 | 99 | 47 | ERS714769 |
| F563 | 56 | Female | Family141 | MZ | TT | Healthy | 79 | 121 | 75.8 | 134 | 90 | 47 | ERS714456 |
| F564 | 40 | Male | Family128 | DZ_sibling | NA | Healthy | 71 | 111 | 77.9 | 157 | 94 | 52 | ERS714200 |
| F565 | 38 | Female | Family142 | MZ | TT | Healthy | 79 | 110 | 67.5 | 58 | 95 | 59 | ERS714326 |
| F566 | 38 | Female | Family142 | MZ | NA | Healthy | 50 | 91 | 59.9 | 70 | 84 | 56 | ERS714327 |
| F567 | 67 | Female | Family142 | MZ_MO | NA | Healthy | 79 | 128 | 83.3 | 277 | 96 | 64 | ERS714770 |

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|------|----|--------|-----------|------------|----|---------|----|-----|------|-----|-----|----|-----------|
| F568 | 41 | Male | Family142 | MZ_sibling | NA | Healthy | 79 | 120 | 79.9 | 105 | 87 | 56 | ERS714771 |
| F569 | 34 | Male | Family039 | MZ_sibling | NA | Healthy | 71 | 103 | 87.1 | 118 | 93 | 45 | ERS714753 |
| F570 | 53 | Female | Family143 | MZ | NA | Healthy | 73 | 125 | 82.9 | 55 | 109 | 48 | ERS714296 |
| F571 | 44 | Female | Family144 | MZ | NA | Healthy | 60 | 100 | 80.7 | 164 | 81 | 32 | ERS714221 |
| F572 | 27 | Female | Family140 | MZ_sibling | NA | Healthy | 71 | 94 | 65 | 99 | 91 | 54 | ERS714757 |
| F573 | 56 | Female | Family141 | MZ | NA | MetS | 78 | 139 | 79.1 | 232 | 93 | 45 | ERS714457 |
| F574 | 44 | Female | Family144 | MZ | TT | Healthy | 66 | 100 | 81.2 | 127 | 84 | 38 | ERS714213 |
| F575 | 29 | Female | Family140 | MZ | NA | Healthy | 67 | 91 | 74.7 | 119 | 91 | 44 | ERS714756 |
| F576 | 29 | Female | Family140 | MZ | NA | Healthy | 68 | 95 | 77.9 | 135 | 74 | 57 | ERS714755 |
| F577 | 49 | Male | Family139 | MZ | CT | Healthy | 71 | 113 | 91.9 | 130 | 117 | 48 | ERS714175 |
| F578 | 44 | Male | Family145 | MZ | NA | Healthy | 70 | 102 | 78.4 | 38 | 91 | 50 | ERS714914 |
| F581 | 44 | Male | Family145 | MZ | NA | Healthy | 71 | 112 | 86.1 | 46 | 90 | 68 | ERS714915 |
| F582 | 51 | Male | Family146 | MZ | NA | MetS | 79 | 135 | 90.4 | 517 | 101 | 50 | ERS714684 |
| F583 | 51 | Male | Family146 | MZ | CT | MetS | 79 | 131 | 94.7 | 171 | 101 | 38 | ERS714683 |
| F584 | 71 | Female | Family145 | MZ_MO | NA | Healthy | 71 | 122 | 86.5 | 78 | 77 | 59 | ERS714916 |
| F589 | 36 | Female | Family147 | MZ | NA | Healthy | 59 | 100 | 70.4 | 74 | 90 | 43 | ERS714165 |
| F599 | 36 | Female | Family147 | MZ | NA | Healthy | 59 | 100 | 75.8 | 76 | 94 | 44 | ERS714166 |
| F603 | 41 | Female | Family148 | MZ | CT | Healthy | 53 | 108 | 71.5 | 78 | 87 | 51 | ERS714898 |
| F604 | 79 | Female | Family148 | MZ_MO | TT | MetS | 71 | 113 | 98.5 | 237 | 100 | 48 | ERS714902 |
| F606 | 41 | Female | Family148 | MZ | NA | Healthy | 55 | 118 | 77.5 | 74 | 94 | 51 | ERS714899 |
| F607 | 42 | Female | Family148 | MZ_sibling | CT | Healthy | 79 | 131 | 83.7 | 147 | 104 | 51 | ERS714903 |
| F608 | 80 | Male | Family148 | MZ_FA | CC | Healthy | 52 | 111 | 89.6 | 119 | 119 | 57 | ERS714901 |
| F609 | 39 | Female | Family149 | MZ | TT | Healthy | 61 | 116 | 71.1 | 38 | 93 | 90 | ERS714464 |
| F610 | 39 | Female | Family149 | MZ | NA | Healthy | 69 | 100 | 78.2 | 67 | 103 | 80 | ERS714465 |
| F614 | 53 | Female | Family143 | MZ | CT | MetS | 70 | 111 | 86.2 | 162 | 118 | 38 | ERS714295 |

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|------|----|--------|-----------|------------|----|---------|-----|-----|------|-----|-----|----|-----------|
| F616 | 43 | Female | Family143 | MZ_sibling | NA | MetS | 100 | 161 | 86.9 | 139 | 118 | 42 | ERS714772 |
| F617 | 38 | Female | Family150 | MZ | CT | Healthy | 64 | 101 | 82.1 | 107 | 83 | 44 | ERS714485 |
| F618 | 30 | Female | Family150 | MZ_sibling | CT | Healthy | 53 | 93 | 64.6 | 61 | 76 | 69 | ERS714488 |
| F619 | 73 | Male | Family136 | MZ_FA | CT | Healthy | 80 | 123 | 90.7 | 77 | 94 | 64 | ERS714619 |
| F620 | 73 | Female | Family136 | MZ_MO | CT | Healthy | 70 | 123 | 89.1 | 154 | 81 | 53 | ERS714620 |
| F621 | 38 | Female | Family150 | MZ | NA | Healthy | 61 | 99 | 80.3 | 105 | 79 | 48 | ERS714487 |
| F622 | 33 | Female | Family151 | MZ | NA | Healthy | 71 | 106 | 81.7 | 64 | 97 | 48 | ERS714186 |
| F623 | 63 | Female | Family150 | MZ_MO | CT | Healthy | 80 | 121 | 68.5 | 111 | 81 | 49 | ERS714486 |
| F624 | 51 | Female | Family136 | MZ | NA | Healthy | 51 | 94 | 68.8 | 62 | 81 | 84 | ERS714622 |
| F625 | 33 | Female | Family151 | MZ | NA | Healthy | 63 | 109 | 68.1 | 57 | 99 | 53 | ERS714185 |
| F627 | 41 | Female | Family152 | MZ | NA | Healthy | 61 | 97 | 72.5 | 66 | 74 | 60 | ERS714502 |
| F629 | 41 | Female | Family152 | MZ | CT | Healthy | 53 | 97 | 67.9 | 43 | 85 | 60 | ERS714501 |
| F630 | 70 | Male | Family153 | MZ_FA | CC | MetS | 72 | 136 | 80.2 | 162 | 140 | 42 | ERS714369 |
| F631 | 72 | Female | Family153 | MZ_MO | TT | Healthy | 71 | 124 | 81.9 | 154 | 114 | 57 | ERS714370 |
| F632 | 40 | Male | Family153 | MZ | CT | Healthy | 84 | 127 | 82.8 | 159 | 284 | 51 | ERS714371 |
| F633 | 40 | Male | Family153 | MZ | NA | Healthy | 83 | 126 | 85 | 259 | 167 | 49 | ERS714372 |
| F634 | 65 | Male | Family154 | MZ_FA | NA | Healthy | 71 | 118 | 85.7 | 166 | 107 | 47 | ERS714774 |
| F635 | 38 | Male | Family155 | MZ | TT | Healthy | 74 | 105 | 86.3 | 106 | 79 | 44 | ERS714460 |
| F636 | 39 | Male | Family154 | MZ | NA | Healthy | 68 | 104 | 84.5 | 333 | 93 | 59 | ERS714498 |
| F637 | 38 | Male | Family155 | MZ | NA | Healthy | 80 | 110 | 91.9 | 118 | 104 | 44 | ERS714461 |
| F638 | 40 | Female | Family155 | MZ_sibling | NA | Healthy | 74 | 122 | 88.1 | 121 | 96 | 53 | ERS714773 |
| F639 | 39 | Male | Family154 | MZ | CT | Healthy | 68 | 99 | 76.6 | 225 | 94 | 65 | ERS714497 |
| F640 | 56 | Male | Family156 | MZ | NA | Healthy | 81 | 119 | 80 | 69 | 74 | 54 | ERS714474 |
| F641 | 56 | Male | Family156 | MZ | CT | Healthy | 69 | 103 | 67.1 | 62 | 77 | 52 | ERS714473 |
| F642 | 46 | Male | Family157 | MZ | CC | Healthy | 70 | 121 | 82.4 | 85 | 91 | 40 | ERS714377 |

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|------|----|--------|-----------|------------|----|---------|----|-----|-------|-----|-----|----|-----------|
| F644 | 38 | Male | Family158 | MZ | NA | MetS | 88 | 137 | 97.9 | 318 | 107 | 35 | ERS714258 |
| F645 | 68 | Female | Family158 | MZ_MO | NA | MetS | 61 | 111 | 96.1 | 233 | 120 | 44 | ERS714257 |
| F646 | 38 | Male | Family158 | MZ | NA | MetS | 64 | 118 | 100.5 | 350 | 310 | 40 | ERS714259 |
| F647 | 46 | Male | Family157 | MZ | NA | Healthy | 52 | 97 | 85.2 | 75 | 96 | 43 | ERS714378 |
| F648 | 38 | Female | Family159 | DZ_sibling | NA | Healthy | 63 | 108 | 78.4 | 71 | 81 | 54 | ERS714912 |
| F649 | 59 | Female | Family159 | DZ_MO | NA | Healthy | 61 | 126 | 81.1 | 95 | 91 | 42 | ERS714897 |
| F650 | 34 | Female | Family159 | DZ | NA | Healthy | 62 | 101 | 75.9 | 88 | 90 | 52 | ERS714896 |
| F651 | 34 | Female | Family159 | DZ | NA | Healthy | 70 | 110 | 66.1 | 50 | 90 | 59 | ERS714900 |
| F655 | 36 | Female | Family160 | DZ | NA | Healthy | 71 | 104 | 69.6 | 69 | 91 | 45 | ERS714205 |
| F656 | 36 | Female | Family160 | DZ | NA | Healthy | 57 | 98 | 74.4 | 79 | 92 | 50 | ERS714187 |
| F657 | 41 | Female | Family161 | DZ | NA | Healthy | 58 | 103 | 78.1 | 60 | 78 | 49 | ERS714309 |
| F658 | 40 | Male | Family162 | DZ | NA | MetS | 80 | 135 | 84.3 | 292 | 112 | 60 | ERS714908 |
| F660 | 40 | Male | Family162 | DZ | NA | Healthy | 63 | 104 | 69.1 | 49 | 97 | 93 | ERS714907 |
| F661 | 37 | Female | Family162 | DZ_sibling | NA | Healthy | 71 | 111 | 76.1 | 72 | 110 | 86 | ERS714909 |
| F662 | 65 | Female | Family162 | DZ_MO | NA | Healthy | 83 | 140 | 82.2 | 99 | 102 | 80 | ERS714906 |
| F666 | 41 | Male | Family163 | MZ | NA | Healthy | 73 | 111 | 88.3 | 61 | 100 | 45 | ERS714367 |
| F667 | 41 | Male | Family163 | MZ | NA | Healthy | 63 | 109 | 86.8 | 97 | 90 | 47 | ERS714368 |
| F668 | 39 | Male | Family164 | DZ | NA | Healthy | 73 | 125 | 73.1 | 72 | 67 | 93 | ERS714305 |
| F670 | 37 | Male | Family165 | DZ_sibling | NA | MetS | 89 | 119 | 117.2 | 163 | 83 | 41 | ERS714776 |
| F671 | 40 | Female | Family166 | MZ | NA | Healthy | 57 | 100 | 62 | 92 | 85 | 77 | ERS714325 |
| F672 | 49 | Female | Family163 | MZ_sibling | TT | Healthy | 79 | 122 | 91.9 | 100 | 99 | 47 | ERS714365 |
| F673 | 40 | Male | Family165 | DZ | CT | Healthy | 82 | 123 | 88.6 | 89 | 83 | 60 | ERS714476 |
| F674 | 40 | Male | Family165 | DZ | CT | MetS | 88 | 127 | 91.1 | 180 | 83 | 48 | ERS714477 |
| F675 | 40 | Female | Family166 | MZ | NA | Healthy | 79 | 117 | 68.1 | 108 | 88 | 64 | ERS714267 |
| F676 | 56 | Female | Family167 | MZ_MO | NA | Healthy | 73 | 123 | 76.6 | 120 | 80 | 77 | ERS714777 |

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|------|----|--------|-----------|------------|----|---------|-----|-----|-------|-----|-----|----|-----------|
| F677 | 29 | Female | Family167 | MZ_sibling | NA | Healthy | 56 | 107 | 71 | 32 | 75 | 52 | ERS714780 |
| F678 | 66 | Male | Family167 | MZ_FA | NA | Healthy | 77 | 123 | 99.5 | 145 | 92 | 53 | ERS714781 |
| F679 | 35 | Female | Family167 | MZ | NA | Healthy | 51 | 94 | 66.7 | 52 | 75 | 65 | ERS714779 |
| F680 | 35 | Female | Family167 | MZ | NA | Healthy | 52 | 94 | 65.1 | 55 | 81 | 66 | ERS714778 |
| F681 | 64 | Female | Family165 | DZ_MO | CC | MetS | 79 | 140 | 103.5 | 311 | 131 | 50 | ERS714475 |
| F682 | 68 | Male | Family164 | DZ_FA | NA | Healthy | 62 | 111 | 74.3 | 86 | 72 | 55 | ERS714306 |
| F683 | 61 | Female | Family160 | DZ_MO | NA | Healthy | 72 | 117 | 98.9 | 146 | 103 | 58 | ERS714188 |
| F684 | 39 | Male | Family164 | DZ | NA | Healthy | 71 | 116 | 77.1 | 92 | 74 | 65 | ERS714304 |
| F687 | 50 | Male | Family163 | MZ_sibling | TT | MetS | 79 | 131 | 94.2 | 90 | 146 | 39 | ERS714364 |
| F688 | 46 | Male | Family163 | MZ_sibling | TT | MetS | 83 | 123 | 108.1 | 467 | 209 | 44 | ERS714366 |
| F689 | 50 | Female | Family168 | MZ | NA | Healthy | 60 | 90 | 87 | 61 | 76 | 73 | ERS714811 |
| F690 | 49 | Female | Family168 | MZ | CT | Healthy | 80 | 120 | 85 | 66 | 52 | 63 | ERS714810 |
| F691 | 53 | Male | Family169 | MZ | TT | Healthy | 80 | 110 | 67.5 | 152 | 75 | 51 | ERS714816 |
| F693 | 63 | Male | Family170 | MZ | CT | MetS | 90 | 130 | 95 | 122 | 102 | 44 | ERS714863 |
| F694 | 53 | Male | Family169 | MZ | NA | Healthy | 80 | 110 | 71.5 | 147 | 70 | 43 | ERS714817 |
| F696 | 39 | Female | Family171 | MZ | NA | Healthy | 70 | 100 | 79 | 151 | 91 | 41 | ERS714868 |
| F697 | 43 | Female | Family161 | DZ | NA | Healthy | 60 | 100 | 78 | 53 | 69 | 47 | ERS714825 |
| F698 | 39 | Female | Family171 | MZ | NA | Healthy | 60 | 90 | 72 | 87 | 90 | 45 | ERS714869 |
| F699 | 46 | Female | Family172 | MZ | NA | MetS | 101 | 151 | 84 | 156 | 94 | 42 | ERS714821 |
| F700 | 46 | Female | Family172 | MZ | CC | MetS | 110 | 159 | 87 | 195 | 92 | 38 | ERS714820 |
| F701 | 48 | Female | Family172 | MZ_sibling | CT | MetS | 100 | 160 | 82 | 130 | 106 | 36 | ERS714822 |
| F702 | 64 | Female | Family161 | DZ_MO | NA | Healthy | 80 | 110 | 81.5 | 109 | 98 | 48 | ERS714826 |
| F703 | 45 | Female | Family172 | MZ_sibling | CT | MetS | 102 | 143 | 104 | 185 | 196 | 49 | ERS714823 |
| F704 | 53 | Female | Family173 | MZ | NA | Healthy | 76 | 119 | 68.2 | 69 | 89 | 78 | ERS714223 |
| F707 | 49 | Female | Family174 | MZ | CT | Healthy | 70 | 120 | 76.3 | 126 | 90 | 76 | ERS714167 |

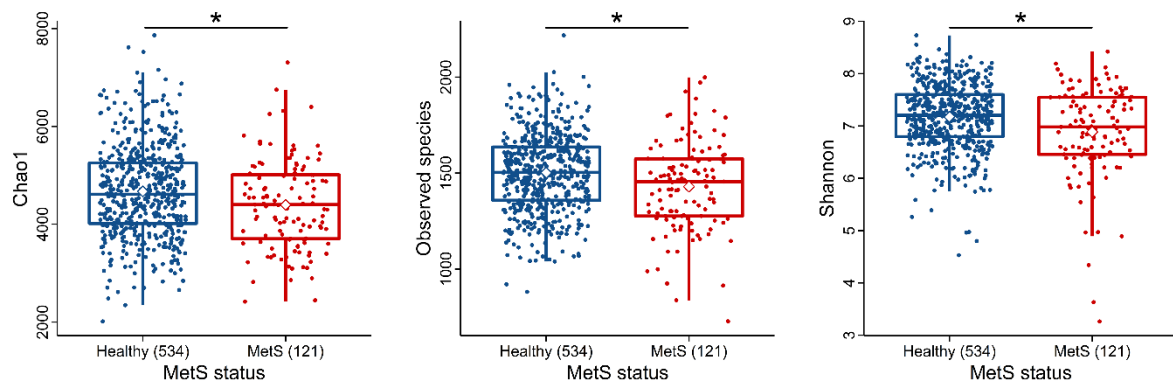
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|------|----|--------|-----------|------------|----|---------|-----|-----|------|-----|-----|----|-----------|
| F708 | 53 | Female | Family173 | MZ | TT | Healthy | 80 | 128 | 71.1 | 55 | 82 | 87 | ERS714222 |
| F709 | 49 | Female | Family174 | MZ | NA | Healthy | 80 | 118 | 78.7 | 99 | 88 | 76 | ERS714168 |
| F711 | 57 | Male | Family174 | MZ_sibling | TT | Healthy | 60 | 110 | 93 | 96 | 83 | 48 | ERS714169 |
| F713 | 37 | Female | Family175 | MZ | NA | Healthy | 60 | 90 | 77.3 | 98 | 54 | 63 | ERS714783 |
| F714 | 37 | Female | Family175 | MZ | NA | Healthy | 60 | 100 | 76.1 | 64 | 69 | 61 | ERS714782 |
| F716 | 43 | Female | Family176 | MZ_sibling | NA | Healthy | 60 | 85 | 78.9 | 72 | 87 | 62 | ERS714787 |
| F717 | 64 | Female | Family175 | MZ_MO | NA | Healthy | 60 | 100 | 77.5 | 125 | 62 | 71 | ERS714784 |
| F719 | 72 | Male | Family176 | MZ_FA | CT | Healthy | 60 | 100 | 99.9 | 65 | 85 | 62 | ERS714270 |
| F721 | 41 | Female | Family176 | MZ | NA | Healthy | 60 | 100 | 70 | 115 | 83 | 69 | ERS714272 |
| F722 | 33 | Female | Family175 | MZ_sibling | NA | Healthy | 60 | 110 | 80 | 95 | 75 | 43 | ERS714786 |
| F723 | 41 | Female | Family176 | MZ | CC | Healthy | 60 | 103 | 80 | 114 | 85 | 57 | ERS714271 |
| F727 | 63 | Male | Family170 | MZ | NA | Healthy | 100 | 140 | 95.8 | 118 | 93 | 48 | ERS714864 |
| F729 | 41 | Female | Family177 | MZ_sibling | CC | Healthy | 100 | 130 | 74 | 74 | 81 | 57 | ERS714856 |
| F730 | 37 | Male | Family177 | MZ | CC | MetS | 80 | 120 | 97 | 310 | 99 | 36 | ERS714842 |
| F731 | 37 | Male | Family177 | MZ | NA | MetS | 90 | 120 | 90 | 120 | 102 | 37 | ERS714843 |
| F732 | 44 | Female | Family178 | MZ | NA | Healthy | 80 | 120 | 76 | 88 | 87 | 49 | ERS714819 |
| F733 | 31 | Male | Family175 | MZ_sibling | NA | Healthy | 70 | 110 | 87.5 | 53 | 66 | 55 | ERS714785 |
| F735 | 44 | Female | Family178 | MZ | CT | Healthy | 90 | 130 | 81 | 37 | 88 | 60 | ERS714818 |
| F741 | 29 | Male | Family179 | MZ | NA | Healthy | 74 | 106 | 87.1 | 66 | 88 | 63 | ERS714798 |
| F743 | 38 | Female | Family180 | MZ | NA | Healthy | 55 | 90 | 83.3 | 61 | 77 | 47 | ERS714514 |
| F747 | 35 | Male | Family181 | MZ_sibling | CC | Healthy | 72 | 108 | 86.6 | 418 | 92 | 49 | ERS714324 |
| F749 | 62 | Female | Family180 | MZ_MO | TT | Healthy | 63 | 104 | 82.9 | 173 | 80 | 45 | ERS714511 |
| F750 | 40 | Female | Family181 | MZ | NA | Healthy | 55 | 98 | 80.9 | 52 | 85 | 45 | ERS714322 |
| F751 | 64 | Male | Family180 | MZ_FA | TT | Healthy | 70 | 114 | 95.7 | 119 | 88 | 33 | ERS714510 |
| F753 | 32 | Male | Family182 | DZ | NA | Healthy | 80 | 120 | 94.5 | 125 | 90 | 46 | ERS714792 |

| | | | | | | | | | | | | | |
|------|----|--------|-----------|------------|----|---------|----|-----|------|-----|-----|----|-----------|
| F756 | 51 | Female | Family183 | MZ | NA | Healthy | 60 | 93 | 70.2 | 155 | 96 | 54 | ERS714789 |
| F757 | 32 | Male | Family182 | DZ | NA | Healthy | 80 | 123 | 89.9 | 172 | 87 | 41 | ERS714791 |
| F759 | 51 | Female | Family183 | MZ | NA | Healthy | 73 | 118 | 72.4 | 152 | 85 | 50 | ERS714788 |
| F760 | 54 | Female | Family183 | MZ_sibling | NA | Healthy | 65 | 111 | 82.6 | 153 | 90 | 35 | ERS714790 |
| F763 | 40 | Male | Family184 | MZ | NA | Healthy | 75 | 113 | 84.3 | 208 | 95 | 45 | ERS714385 |
| F769 | 56 | Male | Family179 | MZ_FA | NA | Healthy | 70 | 100 | 69 | 67 | 79 | 62 | ERS714793 |
| F770 | 42 | Female | Family185 | MZ | NA | Healthy | 56 | 91 | 70.6 | 40 | 79 | 59 | ERS714904 |
| F773 | 42 | Female | Family185 | MZ | NA | Healthy | 50 | 89 | 71.1 | 84 | 79 | 45 | ERS714905 |
| F774 | 54 | Female | Family179 | MZ_MO | NA | Healthy | 80 | 111 | 91.1 | 261 | 91 | 58 | ERS714794 |
| F776 | 29 | Male | Family179 | MZ | NA | Healthy | 78 | 119 | 90.2 | 215 | 83 | 53 | ERS714795 |
| F777 | 63 | Male | Family182 | DZ_FA | NA | Healthy | 77 | 116 | 90.6 | 142 | 114 | 41 | ERS714796 |
| F783 | 40 | Male | Family184 | MZ | CC | Healthy | 72 | 113 | 85.6 | 205 | 89 | 41 | ERS714384 |
| F784 | 73 | Male | Family186 | MZ_FA | CT | Healthy | 69 | 128 | 89.1 | 57 | 84 | 60 | ERS714420 |
| F787 | 41 | Male | Family186 | MZ_sibling | CT | Healthy | 72 | 113 | 93.5 | 156 | 90 | 45 | ERS714421 |
| F788 | 38 | Female | Family180 | MZ | TT | Healthy | 59 | 100 | 71.5 | 63 | 82 | 50 | ERS714513 |
| F789 | 38 | Female | Family186 | MZ | CT | Healthy | 60 | 100 | 72.5 | 57 | 89 | 66 | ERS714419 |
| F790 | 60 | Male | Family187 | MZ_sibling | TT | Healthy | 81 | 125 | 91.6 | 72 | 92 | 63 | ERS714493 |
| F791 | 66 | Female | Family181 | MZ_MO | CT | Healthy | 69 | 109 | 94.7 | 89 | 98 | 47 | ERS714323 |
| F792 | 40 | Female | Family181 | MZ | CT | Healthy | 70 | 110 | 72 | 89 | 87 | 40 | ERS714321 |
| F793 | 58 | Male | Family187 | MZ | TT | Healthy | 71 | 108 | 90.1 | 91 | 94 | 40 | ERS714494 |
| F794 | 38 | Female | Family186 | MZ | NA | Healthy | 62 | 96 | 72.4 | 45 | 87 | 66 | ERS714422 |
| F795 | 58 | Male | Family187 | MZ | NA | Healthy | 81 | 127 | 99.7 | 163 | 95 | 57 | ERS714495 |
| F796 | 50 | Male | Family187 | MZ_sibling | TT | Healthy | 70 | 116 | 93.1 | 105 | 100 | 57 | ERS714496 |
| F801 | 39 | Female | Family180 | MZ_sibling | TT | Healthy | 60 | 89 | 65 | 66 | 80 | 57 | ERS714512 |
| F803 | 52 | Male | Family014 | MZ_sibling | CT | Healthy | 72 | 120 | 94 | 48 | 101 | 40 | ERS714827 |

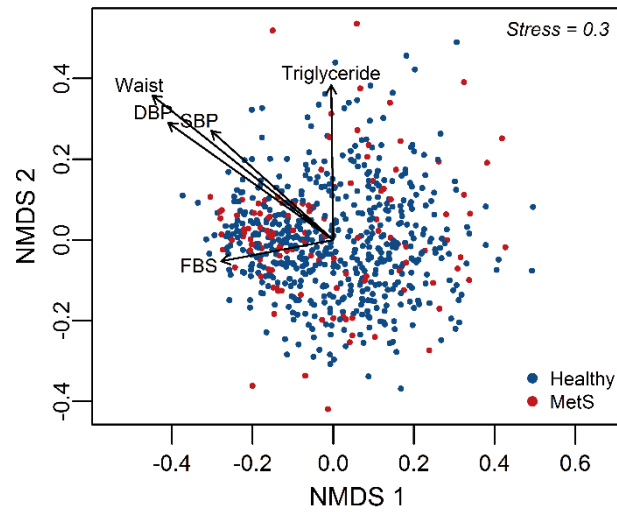
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|------|----|--------|-----------|------------|----|---------|----|-----|------|-----|-----|----|-----------|
| F804 | 45 | Female | Family069 | MZ_sibling | NA | Healthy | 80 | 111 | 71.5 | 57 | 85 | 44 | ERS714713 |
| F805 | 54 | Male | Family188 | MZ_sibling | CT | MetS | 62 | 98 | 92.2 | 156 | 89 | 37 | ERS714357 |
| F806 | 44 | Female | Family003 | MZ_sibling | NA | Healthy | 63 | 120 | 73.6 | 62 | 73 | 49 | ERS714698 |
| F807 | 34 | Female | Family007 | DZ_sibling | CT | Healthy | 56 | 92 | 70 | 106 | 74 | 45 | ERS714239 |
| F808 | 61 | Male | Family188 | MZ_sibling | CC | MetS | 73 | 106 | 93.1 | 205 | 90 | 31 | ERS714356 |
| F809 | 52 | Male | Family188 | MZ | NA | Healthy | 61 | 91 | 86.1 | 105 | 96 | 46 | ERS714359 |
| F810 | 52 | Male | Family188 | MZ | CT | Healthy | 64 | 99 | 91 | 58 | 105 | 48 | ERS714358 |
| F811 | 57 | Male | Family011 | MZ_sibling | TT | Healthy | 63 | 110 | 81.5 | 137 | 99 | 46 | ERS714275 |

Units: DBP (mm Hg); SBP (mm Hg); Waist (cm); Triglyceride (mg/dL); FBS (mg/dL); HDL (mg/dL)

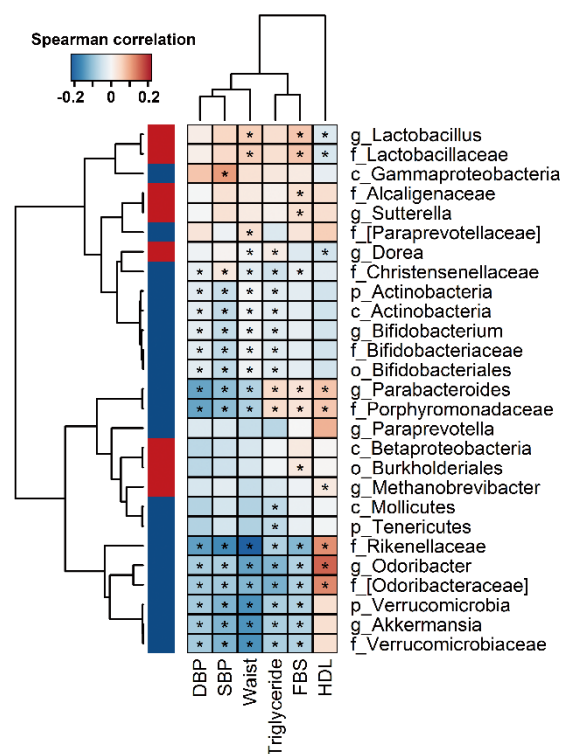
Supplementary figures



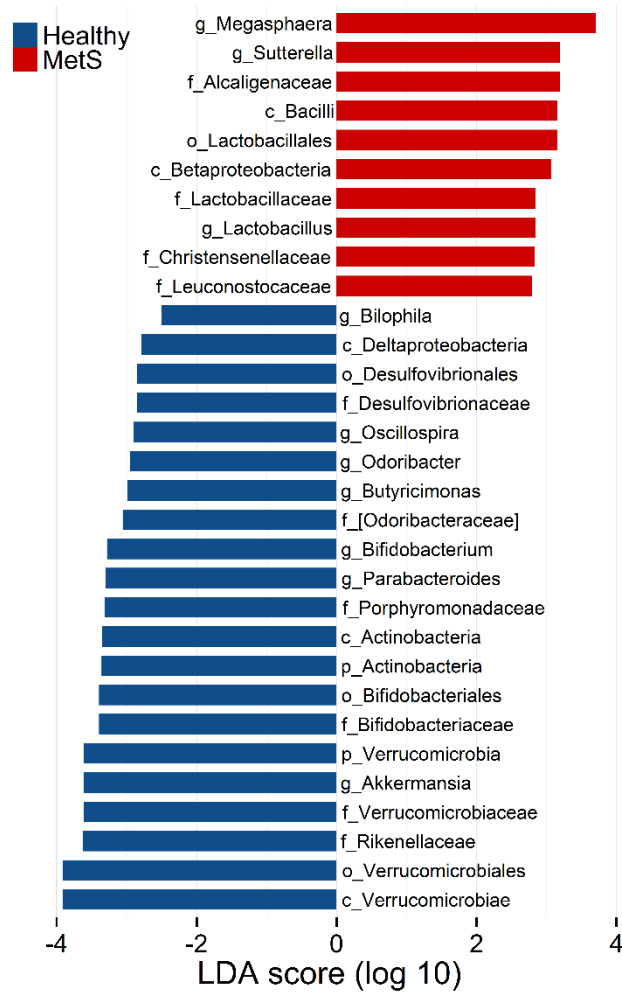
Supplementary figure S1. Alpha-diversity indexes (Chao1 richness, observed species, and Shannon diversity index) according to MetS status. Asterisks indicate significant differences (two-sample t-test using Monte Carlo permutations; $p < 0.05$).



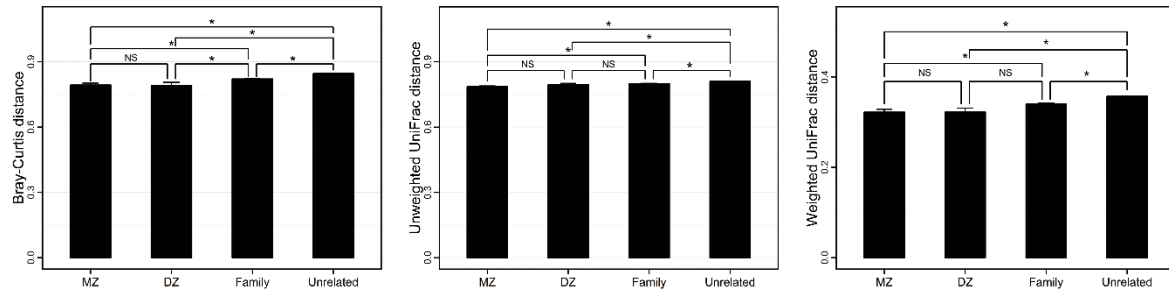
Supplementary figure S2. Nonparametric multi-dimensional scaling (NMDS) plots of gut microbiota. Bray-Curtis distances generated from a rarefied OTU table were used in this NMDS analysis. Red and blue dots represent MetS individuals and healthy individuals, respectively. Arrows indicate MetS components that had significant correlations with the ordination (DBP: diastolic blood pressure; SBP: systolic blood pressure; FBS: fasting blood sugar; HDL: high-density lipoprotein cholesterol; waist: waist circumference).



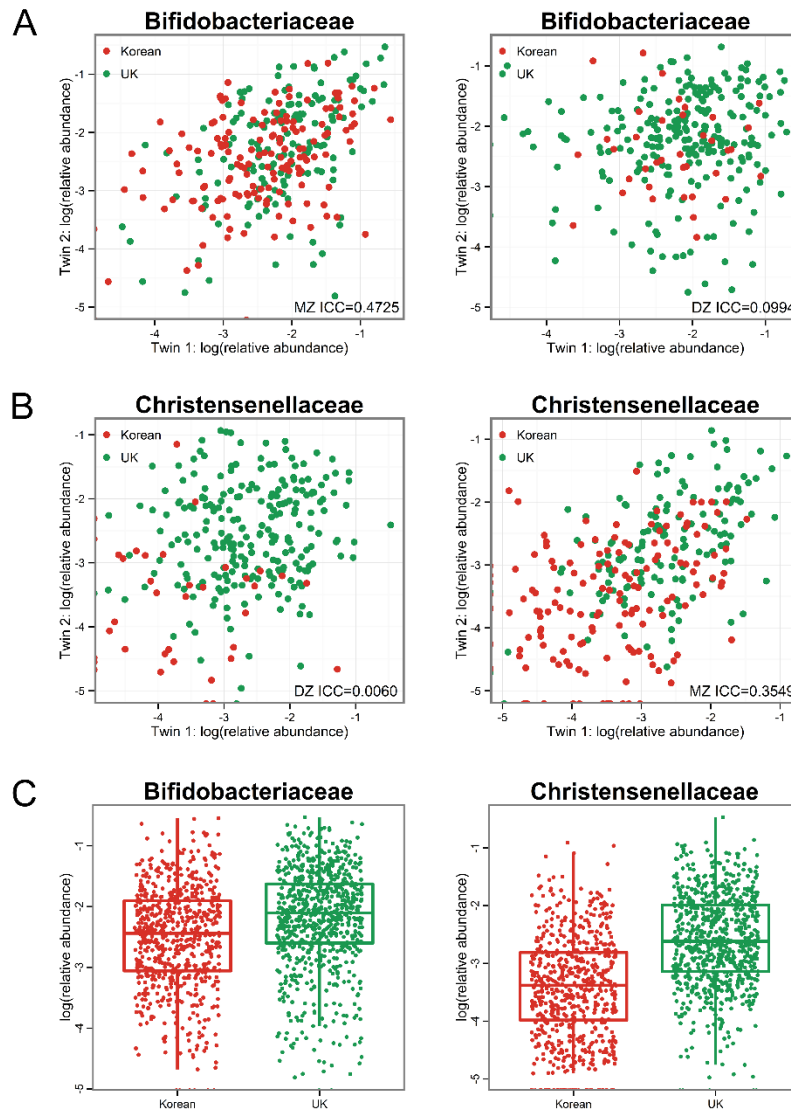
Supplementary figure S3. Spearman's rank correlation coefficients between MetS-associated gut microbial taxa and each MetS component. Red and blue in the row-side color bar on left-hand side indicate taxa that were enriched in MetS individuals and healthy individuals, respectively, in MaAsLin analysis. Asterisks indicate significant associations at q values of <0.25. (DBP: diastolic blood pressure; SBP: systolic blood pressure; FBS: fasting blood sugar; HDL: high-density lipoprotein cholesterol; waist: waist circumference)



Supplementary figure S4. Univariate analysis of associations between microbial taxa and MetS status. This analysis was conducted using LEfSe. Features with LDA scores (log 10) greater than 2 are presented.



Supplementary figure S5. Differences in the gut microbiota between family members. Bar graph of Bray-Curtis and unweighted/weighted UniFrac distances generated from a rarefied OTU table between monozygotic (MZ) twin pairs, dizygotic (DZ) twin pairs, family members, and unrelated individuals (mean \pm standard error of the mean; * p <0.05 for two-sample t-test with 1000 Monte Carlo permutations).



Supplementary figure S6. Heritability estimation of microbial taxa using a merged dataset of Korean and UK twin pairs. Correlations of (A) Bifidobacteriaceae and (B) Christensenellaceae between MZ twin pairs (left panel) and DZ twin pairs (right panel). The intraclass correlation coefficient (ICC) for the relative abundance of the taxon is shown in the bottom right corner of each panel. (C) Box plots of the relative abundances of Bifidobacteriaceae and Christensenellaceae, which showed significant differences between Korean and UK twin pairs in LEfSe analysis. Red and green dots represent the samples from Korean twin pairs (this study) and UK twin pairs[9], respectively.

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