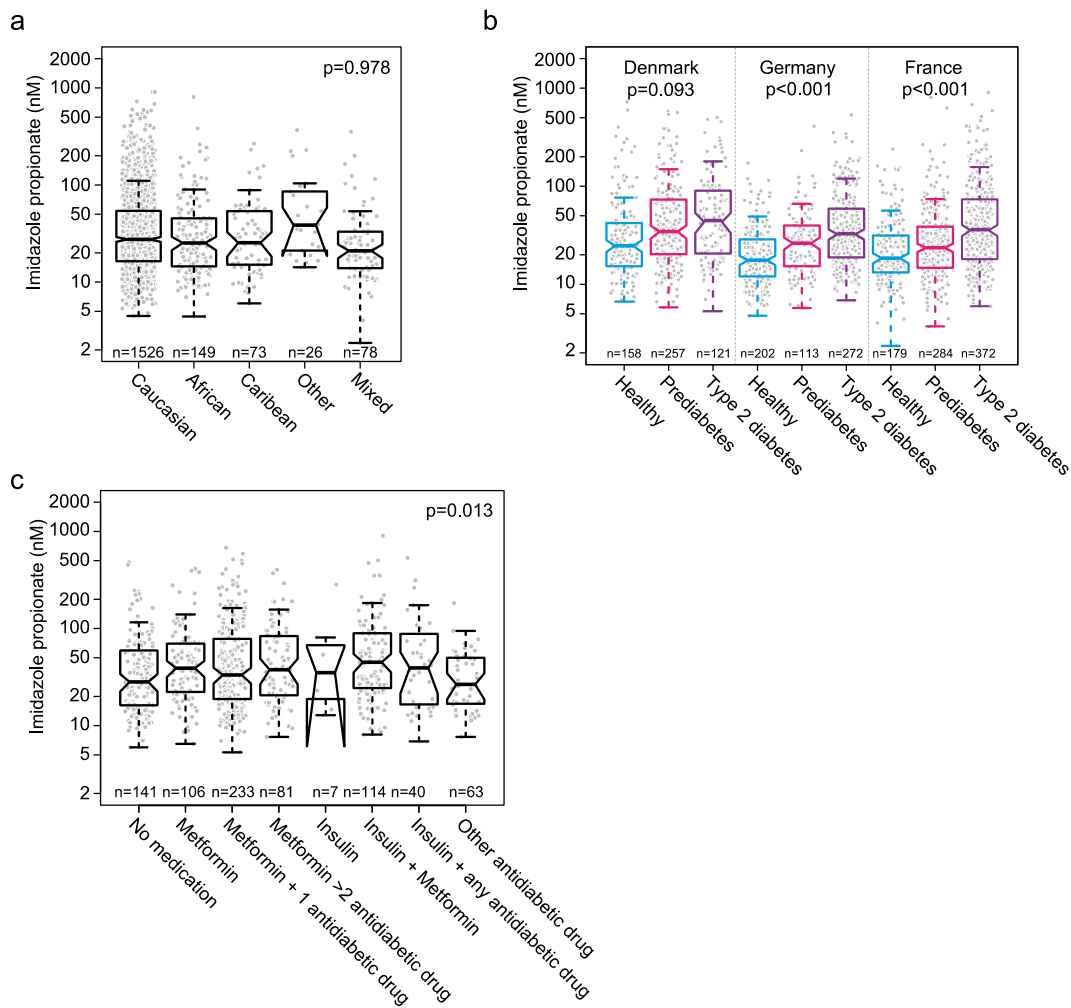


Supplementary information for

Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology

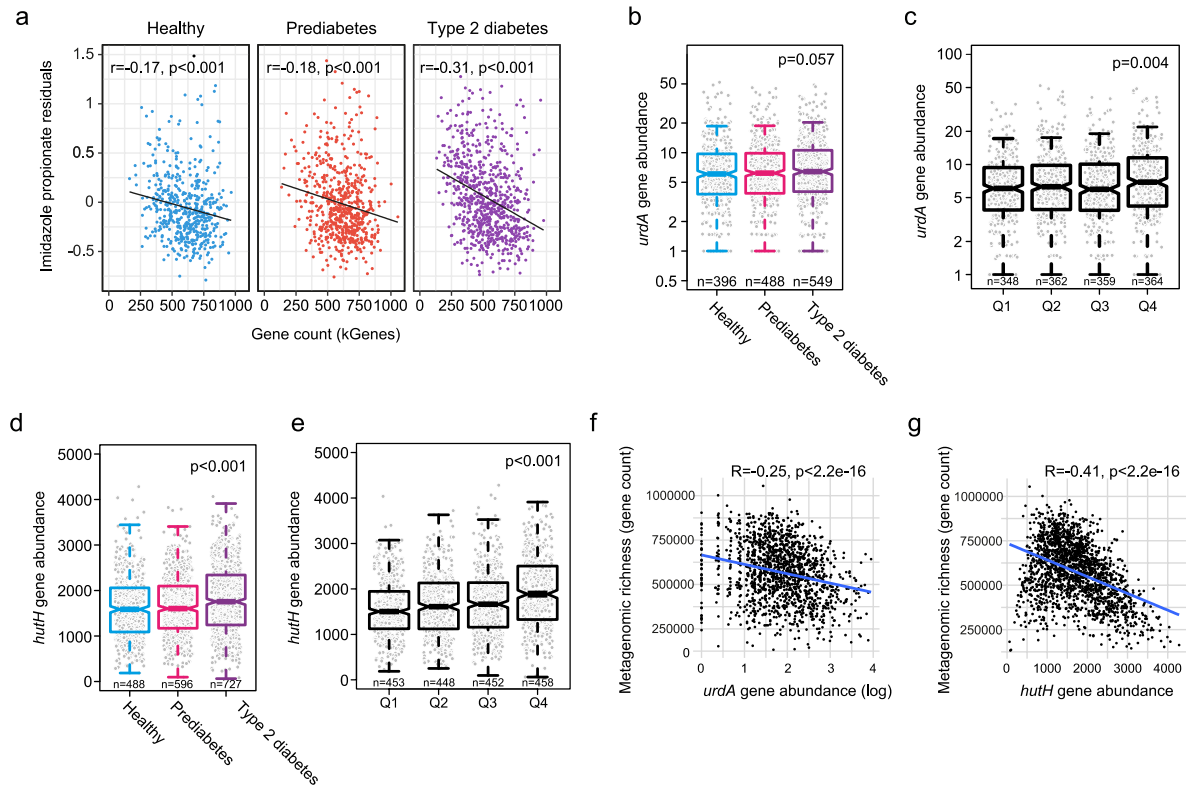
Molinaro A, Bel Lassen P, et al.

Supplementary Figure 1



Supplementary Figure 1: Imidazole propionate levels according to ethnicity, enrolment center and antidiabetic treatment. Imidazole propionate according to (a) ethnicity (b) enrolment center and (c) type of antidiabetic drugs. p values were calculated with linear regression after adjustment for age, gender, BMI, ethnicity and creatinine clearance when applicable. Data are represented as boxplots: middle line is the median, the lower and upper hinges are the first and third quartiles, the upper whisker extends from the hinge to the largest value no further than $1.5 \times$ the inter-quartile range (IQR) from the hinge and the lower whisker extends from the hinge to the smallest value at most $1.5 \times$ IQR of the hinge. Grey dots are single data points. Source data are provided as a Source Data file.

Supplementary Figure 2



Supplementary Figure 2: Abundances of *hutH* and *urdA* are negatively correlated with metagenomic richness. a. Correlation analysis of gene count with imidazole propionate (ImP) residuals according to diabetes status. ImP residuals were calculated using a linear regression adjusted for age, gender, creatinine clearance, BMI and ethnicity. b-e. Relative abundance of *urdA* and *hutH* according to diabetes status and quartiles of serum ImP concentration. p values were calculated with linear regression after adjustment for age, gender, BMI, ethnicity, and creatinine clearance. Data are represented as boxplots: middle line is the median, the lower and upper hinges are the first and third quartiles, the upper whisker extends from the hinge to the largest value no further than $1.5 \times$ the inter-quartile range (IQR) from the hinge and the lower whisker extends from the hinge to the smallest value at most $1.5 \times$ IQR of the hinge. Grey dots are single data points. Source data are provided as a Source Data file. Log transformed relative abundance of (f) *urdA* and (g) *hutH* correlations with gene count. Correlations coefficients and p values were determined according to Spearman's method. Source data are provided as a Source Data file.

Supplementary Table 1

| | Quartiles ImP | Prediabetes | p value | Type 2 diabetes | p value |
|------------|-----------------|---------------------|---------|---------------------|---------|
| | | Odds ratio (95% CI) | | Odds ratio (95% CI) | |
| Unadjusted | Q1 (<16.2) | reference | - | reference | - |
| | Q2 (13.3-27.2) | 1.36 (1-1.84) | 0.048 | 1.45 (1.07-1.97) | 0.018 |
| | Q3 (27.3-52.5) | 2.40 (1.74-3.30) | <0.001 | 2.82 (2.05-3.89) | <0.001 |
| | Q4 (52.7-901.2) | 2.78 (1.96-3.93) | <0.001 | 5.08 (3.62-7.11) | <0.001 |
| Model 1 | Q1 (<16.2) | reference | - | reference | - |
| | Q2 (13.3-27.2) | 1.04 (0.75-1.44) | 0.832 | 1.03 (0.75-1.47) | 0.873 |
| | Q3 (27.3-52.5) | 1.59 (1.12-2.25) | 0.009 | 1.63 (1.13-2.37) | 0.010 |
| | Q4 (52.7-901.2) | 1.70 (1.16-2.49) | 0.006 | 2.50 (1.69-3.69) | <0.001 |
| Model 2 | Q1 (<16.2) | reference | - | reference | - |
| | Q2 (13.3-27.2) | 1.05 (0.75-1.46) | 0.986 | 1.07 (0.74-1.52) | 0.697 |
| | Q3 (27.3-52.5) | 1.64 (1.15-2.32) | 0.007 | 1.74 (1.19-2.53) | 0.002 |
| | Q4 (52.7-901.2) | 1.75 (1.18-2.57) | 0.006 | 2.76 (1.86-4.12) | <0.001 |

Supplementary Table 1: Multinomial logistic regression according to quartiles (Q) of imidazole propionate (ImP) for pre- and type 2 diabetes. p values were calculated using multinomial logistic regression model: unadjusted; Model 1 adjusted for age, gender, BMI, ethnicity; Model 2 adjusted for model 1 plus creatinine clearance.

Supplementary Table 2

| Variables | Beta | p.value | q.value | Symbol | Partial correlation coefficient | Group |
|------------------|-------------|----------------|----------------|---------------|--|--------------|
| HbA1c | 0.193264802 | 1.01E-17 | 6.08E-17 | ** | 0.193264802 | univariate |
| Glycemia | 0.182722316 | 5.75E-16 | 1.72E-15 | ** | 0.182722316 | univariate |
| Insulinemia | 0.150734631 | 3.21E-11 | 4.81E-11 | ** | 0.150734631 | univariate |
| HOMA B | -0.07630798 | 0.001710028 | 0.001710028 | ** | -0.07630798 | univariate |
| HOMA IR | 0.126928962 | 1.69E-07 | 2.03E-07 | ** | 0.126928962 | univariate |
| Tyg index | 0.180890715 | 1.21E-15 | 2.41E-15 | ** | 0.180890715 | univariate |
| HbA1c | 0.120266692 | 1.28E-07 | 7.69E-07 | ** | 0.120266692 | model1 |
| Glycemia | 0.074464563 | 0.001103456 | 0.001324147 | ** | 0.074464563 | model1 |
| Insulinemia | 0.10397807 | 5.49E-06 | 1.65E-05 | ** | 0.10397807 | model1 |
| HOMA B | 0.013925987 | 0.569215607 | 0.569215607 | NA | -0.013925987 | model1 |
| HOMA IR | 0.101783013 | 3.03E-05 | 6.07E-05 | ** | 0.101783013 | model1 |
| Tyg index | 0.082762463 | 0.000290413 | 0.00043562 | ** | 0.082762463 | model1 |
| HbA1c | 0.132472173 | 6.20E-09 | 3.72E-08 | ** | 0.132472173 | model2 |
| Glycemia | 0.088460231 | 0.000108352 | 0.000162528 | ** | 0.088460231 | model2 |
| Insulinemia | 0.108929562 | 2.02E-06 | 6.05E-06 | ** | 0.108929562 | model2 |
| HOMA B | 0.027212008 | 0.266966584 | 0.266966584 | NA | -0.027212008 | model2 |
| HOMA IR | 0.104699459 | 1.85E-05 | 3.70E-05 | ** | 0.104699459 | model2 |
| Tyg index | 0.086233494 | 0.000163049 | 0.000195658 | ** | 0.086233494 | model2 |
| HbA1c | 0.063645177 | 0.005405987 | 0.010811974 | ** | 0.063645177 | model3 |
| Glycemia | 0.017017798 | 0.457414966 | 0.457414966 | NA | 0.017017798 | model3 |
| Insulinemia | 0.073162097 | 0.001445797 | 0.004337391 | ** | 0.073162097 | model3 |
| HOMA B | 0.019927996 | 0.416435872 | 0.457414966 | NA | 0.019927996 | model3 |
| HOMA IR | 0.082409663 | 0.000763002 | 0.004337391 | ** | 0.082409663 | model3 |
| Tyg index | 0.034619375 | 0.130822661 | 0.196233991 | NA | 0.034619375 | model3 |

Supplementary Table 2: Pearson partial correlation coefficients for imidazole propionate and markers of impaired glucose metabolism. *p< 0.05, ** False discovery rate (FDR) adjustment for p< 0.05

Supplementary Table 3

| | Q1 (<16.2) | Q2 (13.3-27.2) | Q3 (27.3-52.5) | Q4 (52.7-901.2) | p value |
|----------------------------|------------------------|------------------------|------------------------|------------------------|---------|
| n | 135 | 145 | 149 | 157 | |
| Glucose (nM) | 6.3 (5.3-7.8) | 6.2(5.3-7.7) | 6.6(5.5-8.0) | 6.6(5.5-8.5) | 0.053 |
| Insulin (mUI) | 30.4 (21.4-55.4) | 32 (18.5-62.10) | 39.5 (22.4-64.9) | 38.5 (23.8-62.8) | 0.020 |
| C-Peptide (ug/L) | 7.1 (5.4-9.2) | 7.3 (5.47-10.1) | 8.1 (6.2-10.1) | 8.3 (6.4-10.9) | 0.00014 |
| Stumvoll Sensitivity index | 0.095 (0.076-0.104) | 0.092 (0.072-0.107) | 0.088 (0.058-0.103) | 0.083 (0.064-0.102) | 0.004 |

Supplementary Table 3: 2-hours serum glucose, insulin, C-peptide levels and Stumvoll Sensitivity Index after oral glucose tolerance according to quartiles levels of imidazole propionate according to imidazole propionate quartiles (Q). Data obtained from a subset of MetaCardis cohort (n=586). p values were calculated using linear regression model.

Supplementary Table 4

| Variables | Increase in node purity | Correlation coefficient | p.value | q.value | Correlation with ImP |
|---------------------------------|-------------------------|-------------------------|-------------|-------------|----------------------|
| Coprococcus_comes | 1.642573604 | -0.111181168 | 1.82E-06 | 2.79E-06 | negative |
| Dorea_formicigenerans | 1.463595845 | -0.086671259 | 0.000202257 | 0.00022473 | negative |
| Dorea_longicatena | 0.971225794 | -0.048780758 | 0.036719761 | 0.03865238 | negative |
| Eubacterium_eligens | 1.037167562 | -0.176461943 | 2.71E-14 | 7.74E-14 | negative |
| Faecalibacterium_prausnitzii | 1.483652523 | -0.094512417 | 5.04E-05 | 5.93E-05 | negative |
| Subdoligranulum_variabile | 0.870215223 | -0.047930151 | 0.040130833 | 0.040130833 | negative |
| Bacteroides_dorei_vulgatus | 0.9239209 | 0.144232609 | 5.47E-10 | 1.37E-09 | positive |
| Bacteroides_ovatus | 1.065662996 | 0.096007322 | 3.82E-05 | 5.09E-05 | positive |
| Bacteroides_xylanisolvens | 1.073375974 | 0.122428856 | 1.45E-07 | 2.41E-07 | positive |
| Bifidobacterium_longum | 1.198733 | 0.13406643 | 8.24E-09 | 1.65E-08 | positive |
| Clostridium_bartlettii | 1.032897892 | 0.095581541 | 4.13E-05 | 5.17E-05 | positive |
| Clostridium_bolteae | 2.755278513 | 0.200779801 | <1E-16 | <1E-16 | positive |
| Clostridium_ramosum | 1.319685722 | 0.209217719 | <1E-16 | <1E-16 | positive |
| Clostridium_scindens | 1.223055998 | 0.18799422 | 4.44E-16 | 2.22E-15 | positive |
| Clostridium_symbiosum | 1.513025804 | 0.179593848 | 9.33E-15 | 3.11E-14 | positive |
| Eggerthella_lenta | 0.908292124 | 0.181936489 | 4.00E-15 | 1.60E-14 | positive |
| Pseudoflavonifractor_capillosus | 1.127715688 | 0.13260629 | 1.20E-08 | 2.18E-08 | positive |
| Ruminococcus_gnavus | 2.150152475 | 0.229083504 | <1E-16 | <1E-16 | positive |
| Veillonella_atypica | 0.982732567 | 0.135342806 | 5.92E-09 | 1.32E-08 | positive |
| Veillonella_parvula | 1.071466862 | 0.109192132 | 2.77E-06 | 3.96E-06 | positive |

Supplementary Table 4: 20 most significant mOTUs correlated with imidazole propionate (ImP) residuals. p values were calculated using random forest models using ImP residuals adjusted for age, gender, BMI, diabetes status, ethnicity and creatinine clearance.

Supplementary Table 5

| Variable | p.value | q.value | Symbol | Correlation coefficient | Model |
|------------------|----------------|----------------|---------------|--------------------------------|--------------|
| Leucocytes | 3.08E-06 | 3.08E-05 | ** | 0.10555127 | univariate |
| Neutrophiles (%) | 0.00884815 | 0.01313202 | ** | 0.05943668 | univariate |
| Monocytes (%) | 0.0210675 | 0.02633438 | ** | 0.05238389 | univariate |
| Lymphocytes (%) | 6.44E-06 | 3.22E-05 | ** | -0.102249 | univariate |
| CRP | 0.00919241 | 0.01313202 | ** | 0.05895879 | univariate |
| IL6 | 0.00111824 | 0.00223648 | ** | 0.07369097 | univariate |
| IL7 | 0.33594449 | 0.37327166 | NA | 0.02201118 | univariate |
| CXCL5 | 0.00100789 | 0.00223648 | ** | -0.0751252 | univariate |
| CCL2 | 0.88309579 | 0.88309579 | NA | 0.00336417 | univariate |
| IP10 | 0.00013878 | 0.00046259 | ** | 0.08700918 | univariate |
| Leucocytes | 1.76E-05 | 0.00017647 | ** | 0.09756958 | model1 |
| Neutrophiles (%) | 0.41655824 | 0.41655824 | NA | 0.01853656 | model1 |
| Monocytes (%) | 0.39312409 | 0.41655824 | NA | -0.0194846 | model1 |
| Lymphocytes (%) | 0.12307443 | 0.30768607 | NA | -0.0351756 | model1 |
| CRP | 0.01876555 | 0.06255185 | * | 0.0534228 | model1 |
| IL6 | 0.19412404 | 0.35365525 | NA | 0.02951581 | model1 |
| IL7 | 0.40102096 | 0.41655824 | NA | 0.01929247 | model1 |
| CXCL5 | 0.21219315 | 0.35365525 | NA | -0.0286566 | model1 |
| CCL2 | 0.35167293 | 0.41655824 | NA | 0.02139516 | model1 |
| IP10 | 0.00937464 | 0.0468732 | ** | 0.05963739 | model1 |
| Leucocytes | 8.42E-06 | 8.42E-05 | ** | 0.10140385 | model2 |
| Neutrophiles (%) | 0.40779257 | 0.40779257 | NA | 0.01892187 | model2 |
| Monocytes (%) | 0.40487431 | 0.40779257 | NA | -0.0190399 | model2 |
| Lymphocytes (%) | 0.1210296 | 0.30257399 | NA | -0.0354333 | model2 |
| CRP | 0.03197909 | 0.10659695 | * | 0.04887145 | model2 |
| IL6 | 0.40652149 | 0.40779257 | NA | 0.018914 | model2 |
| IL7 | 0.37371592 | 0.40779257 | NA | 0.02047806 | model2 |
| CXCL5 | 0.22959003 | 0.40779257 | NA | -0.0276555 | model2 |
| CCL2 | 0.3250122 | 0.40779257 | NA | 0.02265707 | model2 |
| IP10 | 0.00835926 | 0.04179628 | ** | 0.06066178 | model2 |
| Leucocytes | 0.00018792 | 0.00187916 | ** | 0.08511174 | model3 |
| Neutrophiles (%) | 0.35921965 | 0.39894512 | NA | 0.0209629 | model3 |
| Monocytes (%) | 0.39894512 | 0.39894512 | NA | -0.0192862 | model3 |
| Lymphocytes (%) | 0.07156601 | 0.14313202 | NA | -0.0411849 | model3 |
| CRP | 0.04675287 | 0.14313202 | * | 0.045329 | model3 |
| IL6 | 0.34379238 | 0.39894512 | NA | 0.02157755 | model3 |
| IL7 | 0.29801169 | 0.39894512 | NA | 0.02396364 | model3 |
| CXCL5 | 0.06806751 | 0.14313202 | NA | -0.0420004 | model3 |
| CCL2 | 0.32574169 | 0.39894512 | NA | 0.02262894 | model3 |
| IP10 | 0.00584179 | 0.02920893 | ** | 0.06341798 | model3 |

Supplementary Table 5: Partial correlation matrix for imidazole propionate serum levels and serum inflammatory markers. * $p < 0.05$, ** $p < 0.01$. C-reactive protein (CRP), Interleukin 6 (IL6), Interleukin 7 (IL7), Interferon gamma-induced protein 10 (IP10), C-X-C motif chemokine 5 (CXCL5), chemokine (C-C motif) ligand 2 (CCL2)

Supplementary Table 6

| Variable | p.value | q.value | Symbol | Correlation coefficient | Model |
|-------------------|-------------|-------------|--------|-------------------------|------------|
| B Lymphocytes (%) | 0.120215493 | 0.160287324 | NA | -0.067514351 | univariate |
| T Lymphocytes (%) | 0.033761353 | 0.067522706 | * | -0.092147541 | univariate |
| TREG (%) | 0.178289621 | 0.178289621 | NA | 0.068123836 | univariate |
| MAIT (%) | 0.001171391 | 0.004685563 | ** | -0.163354602 | univariate |
| B Lymphocytes (%) | 0.472175061 | 0.472175061 | NA | -0.031565502 | model1 |
| T Lymphocytes (%) | 0.157643112 | 0.236464668 | NA | -0.06199588 | model1 |
| TREG (%) | 0.121887816 | 0.236464668 | NA | 0.079281388 | model1 |
| MAIT (%) | 0.00011929 | 0.00011929 | ** | -0.195595633 | model1 |
| B Lymphocytes (%) | 0.929908301 | 0.929908301 | NA | -0.003881631 | model2 |
| T Lymphocytes (%) | 0.383894415 | 0.575841623 | NA | -0.038411337 | model2 |
| TREG (%) | 0.076412368 | 0.229237103 | NA | 0.091248324 | model2 |
| MAIT (%) | 0.000276514 | 0.000276514 | ** | -0.186015512 | model2 |
| B Lymphocytes (%) | 0.231749669 | 0.231749669 | NA | -0.052787583 | model3 |
| T Lymphocytes (%) | 0.167892937 | 0.231749669 | NA | -0.060857804 | model3 |
| TREG (%) | 0.050515821 | 0.151547462 | NA | 0.100795064 | model3 |
| MAIT (%) | 0.002220664 | 0.002220664 | ** | -0.157089648 | model3 |

Supplementary Table 6: Partial correlation matrix in a subgroup of patients (n=439) between serum imidazole propionate levels and white blood cells subtype. * p<0.05, ** p<0.01. Regulatory T cells (TREG, %) and mucosal associated invariant T cell (MAIT, %).

Supplementary Table 7

| Co-abundance group | Species | Genus | Family | Order | Class | Phylum | Superkingdom |
|--------------------|---------------------------------|------------------------------|------------------------|------------------------|------------------------|------------------------|--------------|
| CAG00001 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00002 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00003 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00004 | Blastocystis sp. ST4 (obsolete) | Blastocystis | unclassified Eukaryota | unclassified Eukaryota | unclassified Eukaryota | unclassified Eukaryota | Eukaryota |
| CAG00012 | Klebsiella pneumoniae 1 | Klebsiella | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG00024 | Bacteroides fragilis 1 | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00028 | Klebsiella oxytoca | Klebsiella | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG01028 | Ruminococcaceae bacterium LM158 | unclassified Ruminococcaceae | Ruminococcaceae | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00030 | Enterobacter aerogenes | Enterobacter | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG00034 | Enterobacter cloacae 2 | Enterobacter | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG00062 | Bacteroides salyersiae | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00043 | Enterobacter cloacae 3 | Enterobacter | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG00044 | Clostridium symbiosum | Lachnoclostridium | Lachnospiraceae | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00046 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00050 | Bacteroides thetaiotaomicron | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00052 | Parabacteroides goldsteinii | Parabacteroides | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00054 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Firmicutes | Bacteria |
| CAG00058 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00059 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00061 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00066 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00146 | Unclassified | Butyrivimonas | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00071 | Bacteroides cellulosilyticus | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00072 | Odoribacter laneus | Odoribacter | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00073 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00074 | Unclassified | Parabacteroides | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00075 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00076 | Unclassified | Blautia | Lachnospiraceae | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00081 | Bacteroides fragilis 2 | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |

| | | | | | | | |
|----------|---------------------------------|-------------------------------|----------------------------|-------------------------|-------------------------|----------------|----------|
| CAG00083 | Odoribacter sp. CAG:788 | Odoribacter | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00085 | Unclassified | Unclassified | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00086 | Bacteroides massiliensis | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00087 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00089 | Unclassified | Blautia | Lachnospiraceae | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00093 | Klebsiella pneumoniae 2 | Klebsiella | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG00098 | Bacteroides fluxus | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00105 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00106 | Unclassified | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00109 | Unclassified | Fusobacterium | Fusobacteriaceae | Fusobacteriales | Fusobacteriia | Fusobacteria | Bacteria |
| CAG00111 | Unclassified | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00116 | Bacteroides nordii | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00117 | Parabacteroides merdae | Parabacteroides | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00118 | Bacteroides vulgatus | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00124 | Klebsiella variicola | Klebsiella | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG00267 | Clostridium sp. CAG:58 | unclassified Clostridiales | unclassified Clostridiales | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00126 | Parabacteroides gordonii | Parabacteroides | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00128 | Unclassified | Blautia | Lachnospiraceae | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00129 | Unclassified | Unclassified | Desulfovibrionaceae | Desulfovibrionales | Deltaproteobacteria | Proteobacteria | Bacteria |
| CAG00131 | Bacteroides sp. CAG:754 | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00133 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00134 | Unclassified | Cloacibacillus | Synergistaceae | Synergistales | Synergistia | Synergistetes | Bacteria |
| CAG00135 | Bacteroides eggerthii | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00384 | Alistipes shahii | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00138 | Unclassified | Parabacteroides | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00141 | Parabacteroides distasonis | Parabacteroides | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00142 | Bacteroides stercoris | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00143 | Unclassified | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | Firmicutes | Bacteria |
| CAG00144 | Fusobacterium ulcerans | Fusobacterium | Fusobacteriaceae | Fusobacteriales | Fusobacteriia | Fusobacteria | Bacteria |
| CAG00260 | Acidaminococcus intestinalis | Acidaminococcus | Acidaminococcaceae | Selenomonadales | Negativicutes | Firmicutes | Bacteria |
| CAG00153 | Hafnia paralvei | Hafnia | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |

| | | | | | | | |
|------------|---------------------------------|-------------------------|-------------------------|-------------------------|-------------------------|----------------|--------------|
| CAG00155 | Firmicutes bacterium CAG:424 | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | Firmicutes | Bacteria |
| CAG00158 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00159 | Bacteroides uniformis | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00163 | Prevotella sp. CAG:255 | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00172 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00175 | Bacteroides clarus | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00005_1 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Firmicutes | Bacteria |
| CAG00180 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00181 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00182 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00184 | Bacteroides sp. CAG:462 | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00185 | Veillonella sp. CAG:933 | Veillonella | Veillonellaceae | Selenomonadales | Negativicutes | Firmicutes | Bacteria |
| CAG00191 | Fusobacterium varium | Fusobacterium | Fusobacteriaceae | Fusobacteriales | Fusobacteriia | Fusobacteria | Bacteria |
| CAG00192 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Firmicutes | Bacteria |
| CAG00193 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Firmicutes | Bacteria |
| CAG00199 | uncultured Alistipes sp. | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00202 | Parabacteroides johnsonii | Parabacteroides | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00206 | Pyramidobacter piscolens | Pyramidobacter | Synergistaceae | Synergistales | Synergistia | Synergistetes | Bacteria |
| CAG00211 | Firmicutes bacterium CAG:227 | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | Firmicutes | Bacteria |
| CAG00213 | Unclassified | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00214 | Prevotella corporis | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00220 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00945 | Bacteroides xylanisolvens | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00231 | Odoribacter splanchnicus | Odoribacter | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00237 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00238 | Clostridium saccharolyticum | Lachnoclostridium | Lachnospiraceae | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00252 | Unclassified | Sutterella | Sutterellaceae | Burkholderiales | Betaproteobacteria | Proteobacteria | Bacteria |
| CAG00263 | Klebsiella oxytoca | Klebsiella | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG00280 | Prevotella sp. CAG:485 | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00287 | Prevotella sp. CAG:1124 | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |

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|------------|---------------------------------|-------------------------------|----------------------------|-------------------------|-------------------------|----------------|--------------|
| CAG00292 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00293 | Firmicutes bacterium CAG:145 | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | Firmicutes | Bacteria |
| CAG00298 | Bacteroides intestinalis 1 | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00299 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Proteobacteria | Bacteria |
| CAG00309 | Alistipes onderdonkii | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00310 | Sutterella parvirubra | Sutterella | Sutterellaceae | Burkholderiales | Betaproteobacteria | Proteobacteria | Bacteria |
| CAG00312 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Bacteroidetes | Bacteria |
| CAG00314 | Unclassified | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00315 | Citrobacter freundii | Citrobacter | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG00319 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00321 | Clostridium sp. CAG:138 | unclassified Clostridiales | unclassified Clostridiales | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00325 | Unclassified | Parasutterella | Sutterellaceae | Burkholderiales | Betaproteobacteria | Proteobacteria | Bacteria |
| CAG00332 | Unclassified | Parabacteroides | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00334 | Prevotella sp. CAG:1092 | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00019_1 | Intestinibacter bartlettii | Intestinibacter | Peptostreptococcaceae | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00340 | Unclassified | unclassified Clostridiales | unclassified Clostridiales | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00344 | Unclassified | Unclassified | Unclassified | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00352 | Unclassified | Acidaminococcus | Acidaminococcaceae | Selenomonadales | Negativicutes | Firmicutes | Bacteria |
| CAG00355 | Bacteroides sp. CAG:661 | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00357 | Bacteroides ovatus | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00360 | Alistipes finegoldii | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00361 | Unclassified | Acidaminococcus | Acidaminococcaceae | Selenomonadales | Negativicutes | Firmicutes | Bacteria |
| CAG00364 | Blautia hansenii | Blautia | Lachnospiraceae | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00367 | Firmicutes bacterium CAG:170 | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | Firmicutes | Bacteria |
| CAG00368 | Unclassified | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00370 | Unclassified | Unclassified | Unclassified | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00371 | Bacteroides dorei | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00373 | Unclassified | Unclassified | Unclassified | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00375 | Unclassified | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00381 | Clostridium sp. CAG:242 | unclassified Clostridiales | unclassified Clostridiales | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00401 | Prevotella sp. CAG:592 | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |

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|------------|---------------------------------|-------------------------------|----------------------------|-------------------------|-------------------------|----------------|--------------|
| CAG00405 | Unclassified | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | Firmicutes | Bacteria |
| CAG00412 | Unclassified | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00416 | Lelliottia amnigena | Lelliottia | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG00421 | Unclassified | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00424 | Firmicutes bacterium CAG:137 | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | Firmicutes | Bacteria |
| CAG00436 | Clostridium sp. CAG:299 | unclassified Clostridiales | unclassified Clostridiales | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00016_2 | Unclassified | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00458 | Fusobacterium nucleatum | Fusobacterium | Fusobacteriaceae | Fusobacteriales | Fusobacteriia | Fusobacteria | Bacteria |
| CAG00467 | Prevotella sp. CAG:873 | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00479 | Unclassified | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00489 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00497 | Unclassified | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | Firmicutes | Bacteria |
| CAG00499 | Prevotella sp. CAG:891 | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00505 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Firmicutes | Bacteria |
| CAG00510 | Unclassified | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00521 | Prevotella sp. CAG:1058 | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00529 | Prevotella sp. CAG:1185 | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00533 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Firmicutes | Bacteria |
| CAG00549 | Bifidobacterium longum | Bifidobacterium | Bifidobacteriaceae | Bifidobacteriales | Actinobacteria | Actinobacteria | Bacteria |
| CAG00578 | Alistipes putredinis | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00586 | Unclassified | Blautia | Lachnospiraceae | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00596 | Unclassified | unclassified Clostridiales | unclassified Clostridiales | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00600 | Prevotella sp. CAG:1031 | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00608 | Unclassified | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00609 | Bacteroides sp. CAG:770 | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00629 | Firmicutes bacterium CAG:124 | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | Firmicutes | Bacteria |
| CAG00634 | Unclassified | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00642 | Unclassified | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00647 | Unclassified | Sutterella | Sutterellaceae | Burkholderiales | Betaproteobacteria | Proteobacteria | Bacteria |
| CAG00655 | Unclassified | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00660 | Alistipes timonensis | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |

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|----------|------------------------------------|---------------------------------|------------------------------|-------------------------|-------------------------|----------------|--------------|
| CAG00664 | Alistipes sp. CAG:268 | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00672 | Clostridium sp. CAG:169 | unclassified Clostridiales | unclassified Clostridiales | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00694 | Unclassified | Unclassified | Unclassified | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00699 | Veillonella ratti | Veillonella | Veillonellaceae | Selenomonadales | Negativicutes | Firmicutes | Bacteria |
| CAG00701 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00705 | Prevotella sp. CAG:520 | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00712 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Proteobacteria | Bacteria |
| CAG00731 | Parasutterella excrementihominis 2 | Parasutterella | Sutterellaceae | Burkholderiales | Betaproteobacteria | Proteobacteria | Bacteria |
| CAG00734 | Bacteroides sp. CAG:545 | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00737 | Unclassified | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00739 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00751 | Firmicutes bacterium CAG:238 | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | Firmicutes | Bacteria |
| CAG00961 | Unclassified | Ruminococcaceae bacterium LM158 | unclassified Ruminococcaceae | Ruminococcaceae | Clostridiales | Clostridia | Firmicutes |
| CAG00757 | Bacteroides sp. CAG:709 | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00798 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00802 | Unclassified | Cloacibacillus | Synergistaceae | Synergistales | Synergistia | Synergistetes | Bacteria |
| CAG00810 | Unclassified | Unclassified | Unclassified | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00819 | Acidaminococcus sp. CAG:542 | Acidaminococcus | Acidaminococcaceae | Selenomonadales | Negativicutes | Firmicutes | Bacteria |
| CAG00836 | Fusobacterium gonidiaformans | Fusobacterium | Fusobacteriaceae | Fusobacteriales | Fusobacteriia | Fusobacteria | Bacteria |
| CAG00849 | Unclassified | Unclassified | Unclassified | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG00853 | Unclassified | Unclassified | Unclassified | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00858 | Streptococcus thermophilus | Streptococcus | Streptococcaceae | Lactobacillales | Bacilli | Firmicutes | Bacteria |
| CAG00860 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00862 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG00873 | Unclassified | Butyrivimonas | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00878 | Citrobacter koseri | Citrobacter | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG00883 | Escherichia coli | Escherichia | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG00887 | Alistipes sp. CAG:435 | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00899 | Unclassified | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00908 | Unclassified | Intestinibacter | Peptostreptococcaceae | Clostridiales | Clostridia | Firmicutes | Bacteria |

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|------------|--|------------------------------------|---------------------------------|-------------------------|-------------------------|----------------|--------------|
| CAG00909 | Parasutterella excrementihominis 1 | Parasutterella | Sutterellaceae | Burkholderiales | Betaproteobacteria | Proteobacteria | Bacteria |
| CAG00942 | Prevotella disiens | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG00977 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG01026 | Peptoniphilus harei | Peptoniphilus | Peptoniphilaceae | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG01069 | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified | Unclassified |
| CAG01127 | Unclassified | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG01130 | Prevotella bivia | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG01145 | Unclassified | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG01165 | common Bacteroides xylanisolvens & ovatus | Bacteroides | Bacteroidaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG01190 | Butyricimonas virosa | Butyricimonas | Porphyromonadaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG01195 | Unclassified | Ruminococcaceae bacterium LM158 | unclassified Ruminococcaceae | Ruminococcaceae | Clostridiales | Clostridia | Firmicutes |
| CAG00006_3 | Unclassified | Oscillibacter | Oscillospiraceae | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG01273 | Enterobacter hormaechei | Enterobacter | Enterobacteriaceae | Enterobacteriales | Gammaproteobacteria | Proteobacteria | Bacteria |
| CAG01278 | Unclassified | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | unclassified Firmicutes | Firmicutes | Bacteria |
| CAG01289 | Unclassified | Alistipes | Rikenellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG01339 | Peptoniphilus lacrimalis | Peptoniphilus | Peptoniphilaceae | Clostridiales | Clostridia | Firmicutes | Bacteria |
| CAG01342 | Unclassified | Ruminococcaceae bacterium LM158 | unclassified Ruminococcaceae | Ruminococcaceae | Clostridiales | Clostridia | Firmicutes |
| CAG01368 | Unclassified | Unclassified | Unclassified | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG01383 | Unclassified | Prevotella | Prevotellaceae | Bacteroidales | Bacteroidia | Bacteroidetes | Bacteria |
| CAG01394 | Unclassified | Blautia | Lachnospiraceae | Clostridiales | Clostridia | Firmicutes | Bacteria |

Supplementary Table 7: List of metagenomic species with *hutH* gene

Supplementary Table 8

| Variable | Beta | p.value | q.value | Symbol | Partial correlation coefficient |
|-----------------|--------------|-------------|-------------|--------|---------------------------------|
| Red meat | -0.048231823 | 0.054272277 | 0.090453795 | NA | -0.048231823 |
| Poultry | -0.053262171 | 0.033531458 | 0.083828644 | * | -0.053262171 |
| Fish | -0.030800834 | 0.219198624 | 0.27399828 | NA | -0.030800834 |
| Milk | 0.045786356 | 0.067704697 | 0.101557046 | NA | 0.045786356 |
| Cheese | 0.063674572 | 0.011022329 | 0.055111643 | * | 0.063674572 |
| Yogurt | 0.012433233 | 0.619986229 | 0.66427096 | NA | 0.012433233 |
| Eggs | 0.015007503 | 0.549473646 | 0.634008053 | NA | 0.015007503 |
| Starch | -0.001099461 | 0.965025799 | 0.965025799 | NA | -0.001099461 |
| Vegetables | -0.055208206 | 0.027563531 | 0.082690593 | * | -0.055208206 |
| Fruits | -0.05057615 | 0.043557643 | 0.089518713 | * | -0.05057615 |
| Nuts | -0.090414244 | 0.000302418 | 0.004536277 | ** | -0.090414244 |
| Energy intake | -0.020608008 | 0.410954473 | 0.513693091 | NA | -0.020608008 |
| Carbohydrate | 0.031437497 | 0.209816158 | 0.349693597 | NA | 0.031437497 |
| Sugar | 0.005947827 | 0.812495558 | 0.812495558 | NA | 0.005947827 |
| Fibre | -0.054125575 | 0.030759543 | 0.117435205 | * | -0.054125575 |
| Fat | -0.008905001 | 0.722478691 | 0.802754101 | NA | -0.008905001 |
| Unsaturated fat | -0.063547293 | 0.011183934 | 0.111839337 | * | -0.063547293 |
| Saturated fat | 0.052762661 | 0.035230561 | 0.117435205 | * | 0.052762661 |
| Protein | -0.043095393 | 0.085525298 | 0.213813244 | NA | -0.043095393 |
| Animal protein | -0.024239688 | 0.333620594 | 0.476600849 | NA | -0.024239688 |
| Vegetal protein | -0.033820829 | 0.177273707 | 0.349693597 | NA | -0.033820829 |
| aHEI score | -0.079267542 | 0.001544139 | 0.011581041 | ** | -0.079267542 |
| DASH score | -0.04442065 | 0.076325173 | 0.104079782 | NA | -0.04442065 |
| DDS score | -0.049608171 | 0.047743314 | 0.089518713 | * | -0.049608171 |
| Med Diet Score | -0.060186549 | 0.016284221 | 0.06106583 | * | -0.060186549 |

Supplementary Table 8: Pearson partial correlation coefficients for imidazole propionate and dietary nutrients and scores. p values were calculated using partial correlations adjusted for: age, gender, body mass index, ethnicity, diabetes status, creatinine clearance, daily energy intake (kcal/day) and enrolment center. * $p < 0.05$, ** False discovery rate (FDR) adjusted $p < 0.05$.