

**“Plant-based diet index and metabolic risk in older men: exploring the role of the gut microbiome” Y Li et al. Online Supplemental Material**

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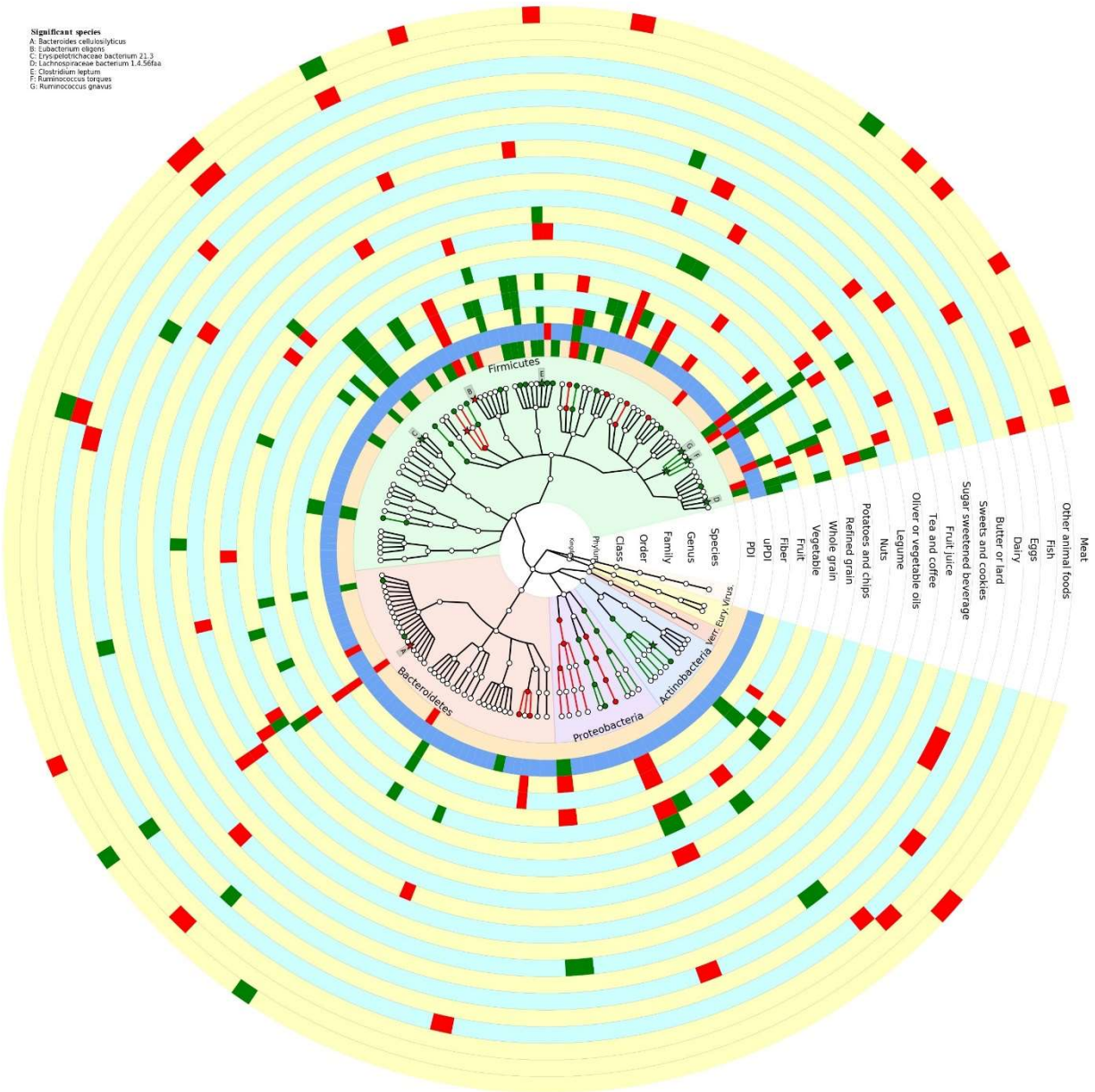
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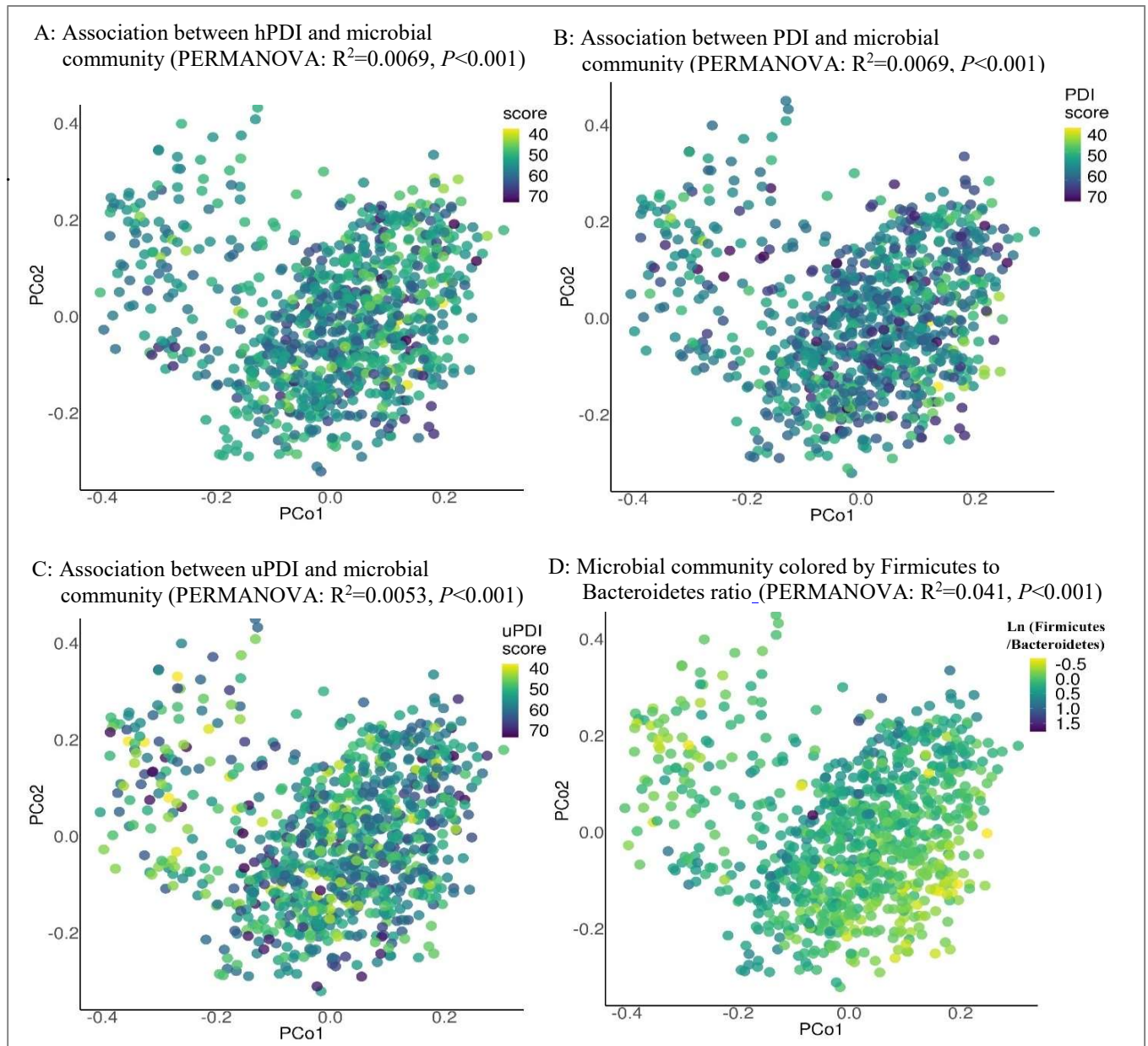
**Supplemental Figure 1: Flowchart of participant enrollment.**

**Supplemental Figure 2: Taxonomic tree with highlighted species that were significantly associated with plant-based diet indices (PDIs) and individual food items based on 911 repeated measurements of the 303 participants.**

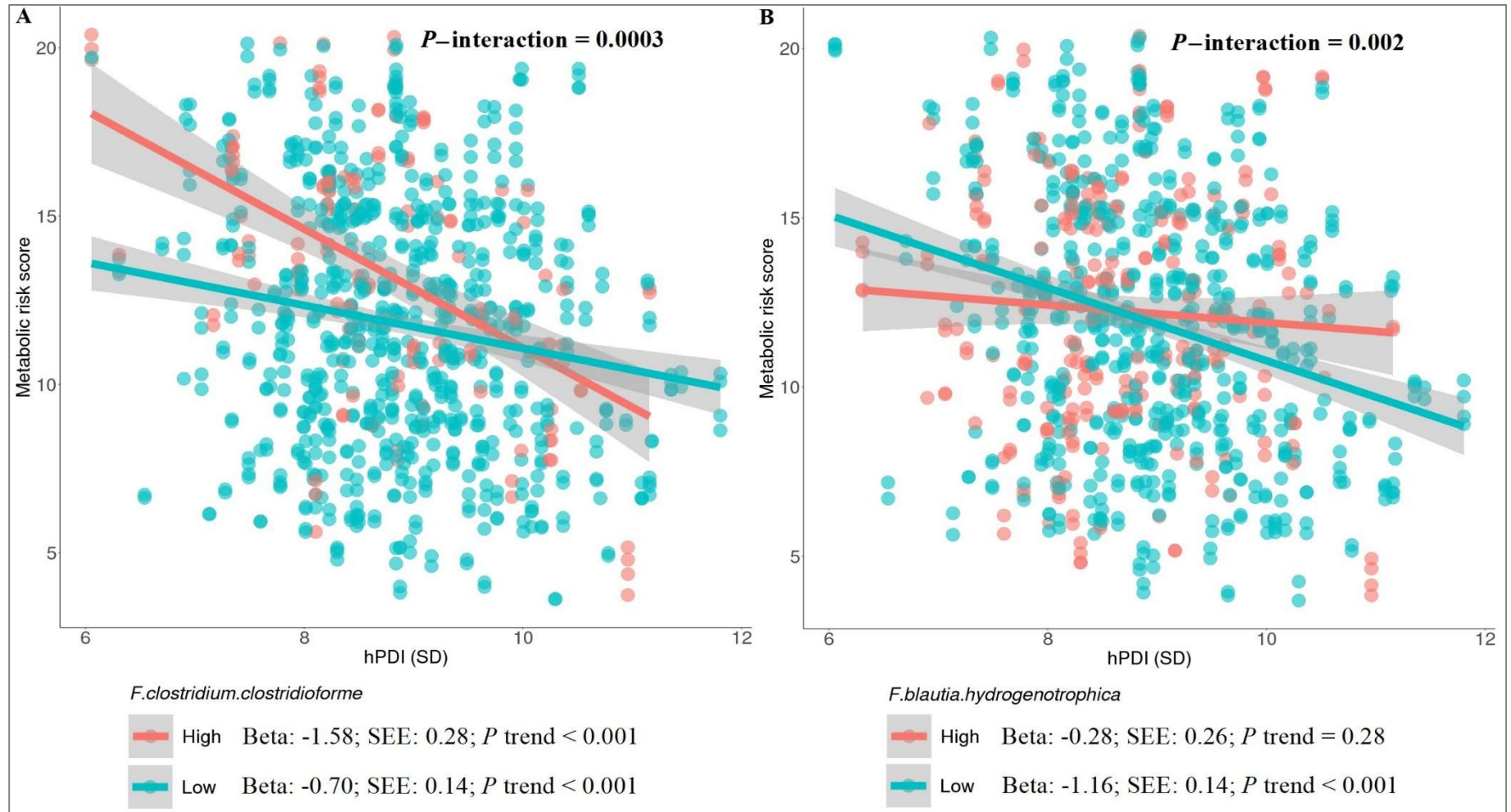


### Supplemental Figure 3. Associations between PDIs and microbial communities based on 911 repeated measurements of the 303 participants.

Principal coordinates analysis based on Bray-Curtis dissimilarity were performed using taxonomic data at species level; the first 2 principal coordinates (PCo) were plotted by healthy plant-based diet index (hPDI) (A), PDI (B), unhealthy PDI (uPDI) (C), Firmicutes to Bacteroidetes ratio (D). A PERMANOVA test was used to evaluate the association of overall microbial compositions and PDIs, with multivariable models adjusted for repeated measurements (participants ID as random intercept), age, energy intake, alcohol, smoking, physical activity, using of antibiotics, consumed any probiotics and fecal sample characteristics (the Bristol stool chart).



**Supplemental Figure 4. Interactions between healthy plant-based diet index (hPDI) and species on metabolic risk based on 911 repeated measurements of the 303 participants.**



(SD: standard deviation;  $FDR$  for interaction: 0.01 (5A) and 0.036 (5B) after false discovery rate correction following the Benjamini–Hochberg).

**Supplemental Table 1: List of enzymes that were significantly associated with hPDI**

| Enzymes      | beta coefficients | SEM      | N.not.0 | P-value  | Q-value     | NAME of enzymes                                    |
|--------------|-------------------|----------|---------|----------|-------------|----------------------------------------------------|
| ecd1_17_99_5 | -0.001339601      | 0.000169 | 629     | 6.00E-15 | 3.31E-11    | transferred entry: 1.17.98.1                       |
| ecd2_9_1_1   | -0.001627706      | 0.000213 | 892     | 5.12E-14 | 1.42E-10    | l-seryl-trna(sec) selenium transferase             |
| ecd5_5_1_1   | 0.002007925       | 0.000276 | 852     | 8.06E-13 | 1.48E-09    | muconate cycloisomerase                            |
| ecd3_6_3_2   | -0.001072414      | 0.000154 | 705     | 5.97E-12 | 8.25E-09    | magnesium-importing atpase                         |
| ecd1_1_1_2   | -0.001642922      | 0.000253 | 809     | 1.33E-10 | 1.47E-07    | alcohol dehydrogenase (nadp(+))                    |
| ecd5_4_99_62 | -0.002074804      | 0.000325 | 838     | 2.91E-10 | 2.51E-07    | d-ribose pyranase                                  |
| ecd6_2_1_26  | -0.002083701      | 0.000327 | 856     | 3.18E-10 | 2.51E-07    | o-succinylbenzoate--coa ligase                     |
| ecd3_5_4_10  | 0.001829211       | 0.00029  | 895     | 4.55E-10 | 3.14E-07    | Imp cyclohydrolase                                 |
| ecd2_4_1_1   | 0.00294311        | 0.000486 | 895     | 2.04E-09 | 1.03E-06    | glycogen phosphorylase                             |
| ecd3_2_1_49  | -0.001009516      | 0.00017  | 661     | 4.34E-09 | 1.60E-06    | alpha-n-acetylgalactosaminidase                    |
| ecd2_3_1_48  | -0.000939905      | 0.00016  | 757     | 6.43E-09 | 2.22E-06    | histone acetyltransferase                          |
| ecd3_6_5_3   | 0.001630807       | 0.000282 | 895     | 9.66E-09 | 3.14E-06    | protein-synthesizing gtpase                        |
| ecd2_7_9_1   | 0.001076647       | 0.000189 | 894     | 1.80E-08 | 4.79E-06    | pyruvate, phosphate dikinase                       |
| ecd4_4_1_8   | -0.001453846      | 0.000267 | 810     | 6.60E-08 | 1.46E-05    | cystathionine beta-lyase                           |
| ecd3_1_21_3  | 0.002178838       | 0.000405 | 894     | 9.69E-08 | 1.91E-05    | type I site-specific deoxyribonuclease             |
| ecd2_7_7_85  | -0.001027477      | 0.000192 | 771     | 1.14E-07 | 2.17E-05    | diadenylate cyclase                                |
| ecd3_1_4_16  | -0.001044992      | 0.000207 | 589     | 5.67E-07 | 7.46E-05    | 2',3'-cyclic-nucleotide 2'-phosphodiesterase       |
| ecd4_3_1_18  | -0.001186432      | 0.000236 | 892     | 5.87E-07 | 7.55E-05    | d-serine ammonia-lyase                             |
| ecd1_2_1_16  | -0.00100538       | 0.000203 | 599     | 8.69E-07 | 0.000101552 | succinate-semialdehyde dehydrogenase (nad(p)(+))   |
| ecd2_1_2_3   | 0.001499589       | 0.000304 | 895     | 9.51E-07 | 0.000103212 | phosphoribosylaminoimidazolecarboxamide formyltran |
| ecd1_1_1_157 | 0.001251811       | 0.000254 | 894     | 1.03E-06 | 0.000109746 | 3-hydroxybutyryl-coa dehydrogenase                 |
| ecd2_7_1_12  | -0.001405965      | 0.000287 | 363     | 1.18E-06 | 0.00011494  | gluconokinase                                      |
| ecd3_1_1_1   | 0.000971876       | 0.000199 | 789     | 1.21E-06 | 0.00011494  | carboxylesterase                                   |
| ecd1_3_99_2  | 0.001294741       | 0.000267 | 895     | 1.44E-06 | 0.000130029 | transferred entry: 1.3.8.1                         |
| ecd3_6_3_12  | -0.00199246       | 0.000412 | 888     | 1.54E-06 | 0.000134952 | potassium-transporting atpase                      |
| ecd4_3_1_15  | -0.001015337      | 0.00021  | 869     | 1.62E-06 | 0.000140058 | diaminopropionate ammonia-lyase                    |
| ecd2_4_1_281 | 0.001657555       | 0.000348 | 895     | 2.19E-06 | 0.000182986 | 4-o-beta-d-mannosyl-d-glucose phosphorylase        |

|              |              |          |     |          |             |                                                    |
|--------------|--------------|----------|-----|----------|-------------|----------------------------------------------------|
| ecd2_1_1_79  | -0.001462186 | 0.000307 | 780 | 2.26E-06 | 0.00018361  | cyclopropane-fatty-acyl-phospholipid synthase      |
| ecd4_1_99_18 | -0.001506866 | 0.000317 | 895 | 2.39E-06 | 0.00018368  | cyclic pyranopterin phosphate synthase             |
| ecd3_1_3_3   | -0.000847365 | 0.000179 | 894 | 2.50E-06 | 0.000186766 | phosphoserine phosphatase                          |
| ecd1_11_1_6  | -0.00165279  | 0.000357 | 895 | 4.28E-06 | 0.00027378  | catalase                                           |
| ecd2_6_1_42  | 0.001346271  | 0.000291 | 895 | 4.22E-06 | 0.00027378  | branched-chain-amino-acid transaminase             |
| ecd3_5_1_25  | -0.001714207 | 0.00037  | 895 | 4.21E-06 | 0.00027378  | n-acetylglucosamine-6-phosphate deacetylase        |
| ecd2_1_1_176 | -0.001049875 | 0.000228 | 315 | 4.80E-06 | 0.000298072 | 16s rrna (cytosine(967)-c(5))-methyltransferase    |
| ecd3_6_3_30  | 0.001427097  | 0.000312 | 881 | 5.53E-06 | 0.000338382 | fe(3+)-transporting atpase                         |
| ecd2_7_6_5   | 0.001374286  | 0.000303 | 895 | 6.47E-06 | 0.000376459 | gtp diphosphokinase                                |
| ecd6_2_1_13  | -0.001070014 | 0.000241 | 672 | 1.01E-05 | 0.000538135 | acetate--coa ligase (adp-forming)                  |
| ecd2_3_1_89  | -0.001166636 | 0.000265 | 877 | 1.19E-05 | 0.000618525 | tetrahydrodipicolinate n-acetyltransferase         |
| ecd4_1_3_6   | 0.001396489  | 0.000317 | 890 | 1.20E-05 | 0.000618525 | citrate (pro-3s)-lyase                             |
| ecd1_2_1_12  | -0.001304921 | 0.000301 | 882 | 1.66E-05 | 0.000779253 | glyceraldehyde-3-phosphate dehydrogenase (phosphor |
| ecd2_7_1_107 | -0.001728432 | 0.0004   | 888 | 1.71E-05 | 0.000779253 | diacylglycerol kinase (atp)                        |
| ecd6_1_1_4   | 0.001911903  | 0.000441 | 895 | 1.60E-05 | 0.000779253 | leucine--trna ligase                               |
| ecd6_3_4_6   | 0.000678436  | 0.000157 | 885 | 1.64E-05 | 0.000779253 | urea carboxylase                                   |
| ecd3_6_1_7   | -0.001785306 | 0.000414 | 893 | 1.79E-05 | 0.000783982 | cylphosphatase                                     |
| ecd2_4_1_18  | 0.002161944  | 0.000506 | 895 | 2.12E-05 | 0.0009016   | 1,4-alpha-glucan branching enzyme                  |
| ecd4_3_1_7   | -0.001240355 | 0.000291 | 887 | 2.19E-05 | 0.000908875 | ethanolamine ammonia-lyase                         |
| ecd1_1_1_31  | -0.000714563 | 0.000169 | 726 | 2.59E-05 | 0.001028541 | 3-hydroxyisobutyrate dehydrogenase                 |
| ecd3_4_19_3  | -0.00108473  | 0.000257 | 876 | 2.61E-05 | 0.001028541 | pyroglutamyl-peptidase I                           |
| ecd3_1_13_5  | -0.000930905 | 0.00022  | 885 | 2.67E-05 | 0.001037379 | ribonuclease d                                     |
| ecd3_1_3_45  | -0.001316062 | 0.000312 | 782 | 2.69E-05 | 0.001041083 | 3-deoxy-manno-octulosonate-8-phosphatase           |
| ecd4_2_1_52  | -0.000722193 | 0.000173 | 612 | 3.22E-05 | 0.001211667 | transferred entry: 4.3.3.7                         |
| ecd1_1_99_33 | -0.000960083 | 0.00023  | 282 | 3.31E-05 | 0.001235873 | formate dehydrogenase (acceptor)                   |
| ecd2_4_2_3   | -0.001316639 | 0.000318 | 894 | 3.78E-05 | 0.001370968 | uridine phosphorylase                              |
| ecd1_16_3_1  | -0.0016048   | 0.000391 | 881 | 4.52E-05 | 0.001562436 | ferroxidase                                        |
| ecd3_4_11_19 | 0.000994408  | 0.000244 | 850 | 4.94E-05 | 0.001667995 | d-stereospecific aminopeptidase                    |
| ecd3_6_3_24  | -0.001093757 | 0.000271 | 490 | 5.79E-05 | 0.001828481 | nickel-transporting atpase                         |
| ecd3_5_3_6   | -0.001037761 | 0.000258 | 891 | 6.17E-05 | 0.001915256 | arginine deiminase                                 |

|              |              |          |     |             |             |                                                    |
|--------------|--------------|----------|-----|-------------|-------------|----------------------------------------------------|
| ecd3_1_1_31  | -0.001150826 | 0.000286 | 881 | 6.22E-05    | 0.001920455 | 6-phosphogluconolactonase                          |
| ecd3_2_2_8   | -0.000746684 | 0.000187 | 384 | 7.05E-05    | 0.002128083 | ribosylpyrimidine nucleosidase                     |
| ecd1_1_1_272 | -0.000812296 | 0.000204 | 869 | 7.26E-05    | 0.002157804 | d-2-hydroxyacid dehydrogenase (nadp(+))            |
| ecd3_1_1_61  | 0.001416032  | 0.000361 | 895 | 9.33E-05    | 0.002630463 | protein-glutamate methylesterase                   |
| ecd2_1_1_151 | -0.000796347 | 0.000203 | 827 | 9.49E-05    | 0.002642209 | cobalt-factor II c(20)-methyltransferase           |
| ecd2_1_1_166 | -0.001239135 | 0.000317 | 831 | 0.000101433 | 0.002761169 | 23s rrna (uridine(2552)-2'-o)-methyltransferase    |
| ecd1_1_5_3   | -0.001791144 | 0.000459 | 844 | 0.000103566 | 0.002805427 | glycerol-3-phosphate dehydrogenase                 |
| ecd2_7_1_5   | -0.001076914 | 0.000276 | 895 | 0.000104697 | 0.002815351 | rhamnukinase                                       |
| ecd3_2_2_23  | -0.00117051  | 0.000302 | 882 | 0.000112882 | 0.002998983 | dna-formamidopyrimidine glycosylase                |
| ecd2_7_7_6   | 0.002685797  | 0.000698 | 895 | 0.00012742  | 0.003274992 | dna-directed rna polymerase                        |
| ecd5_4_99_16 | 0.001158048  | 0.000301 | 891 | 0.000131285 | 0.00331271  | maltose alpha-d-glucosyltransferase                |
| ecd3_6_3_34  | -0.001386165 | 0.000362 | 895 | 0.000135725 | 0.003342299 | Iron-chelate-transporting atpase                   |
| ecd3_5_1_44  | 0.001336545  | 0.000349 | 893 | 0.000138319 | 0.003382093 | protein-glutamine glutaminase                      |
| ecd1_1_1_159 | -0.001766627 | 0.000463 | 893 | 0.000144669 | 0.003496755 | 7-alpha-hydroxysteroid dehydrogenase               |
| ecd6_1_1_13  | -0.001526742 | 0.000401 | 889 | 0.000148704 | 0.003546755 | d-alanine--poly(phosphoribitol) ligase             |
| ecd1_1_1_6   | -0.001164777 | 0.000306 | 887 | 0.000149829 | 0.003553466 | glycerol dehydrogenase                             |
| ecd1_17_4_2  | 0.000787679  | 0.000207 | 894 | 0.000152103 | 0.003591965 | ribonucleoside-triphosphate reductase              |
| ecd1_21_4_2  | -0.000597738 | 0.000157 | 700 | 0.000153966 | 0.003620492 | glycine reductase                                  |
| ecd2_7_1_45  | 0.001276593  | 0.000337 | 895 | 0.000159651 | 0.003691355 | 2-dehydro-3-deoxygluconokinase                     |
| ecd3_6_3_44  | -0.001435626 | 0.000381 | 836 | 0.000176106 | 0.003988366 | xenobiotic-transporting atpase                     |
| ecd3_5_3_9   | 0.000735776  | 0.000195 | 835 | 0.000177496 | 0.004003439 | allantoate deiminase                               |
| ecd3_1_3_25  | -0.001110089 | 0.000298 | 893 | 0.000205089 | 0.004497316 | Inositol-phosphate phosphatase                     |
| ecd5_1_3_14  | -0.00103064  | 0.000277 | 895 | 0.000215434 | 0.004705486 | udp-n-acetylglucosamine 2-epimerase (non-hydrolyzi |
| ecd1_21_4_4  | -0.00055115  | 0.000149 | 653 | 0.000219078 | 0.004733685 | betaine reductase                                  |
| ecd1_4_1_21  | 0.000840911  | 0.000227 | 892 | 0.000218561 | 0.004733685 | aspartate dehydrogenase                            |
| ecd3_1_6_1   | -0.001158808 | 0.000315 | 633 | 0.000248262 | 0.005157505 | arylsulfatase                                      |
| ecd2_7_7_87  | 0.001194134  | 0.000325 | 895 | 0.000253147 | 0.00521975  | l-threonylcarbamoyladenylate synthase              |
| ecd5_3_1_25  | -0.001230989 | 0.000336 | 895 | 0.0002647   | 0.00529975  | l-fucose Isomerase                                 |
| ecd2_1_1_107 | -0.001002465 | 0.000277 | 893 | 0.000307926 | 0.005867587 | uroporphyrinogen-iii c-methyltransferase           |
| ecd2_4_1_7   | -0.000964774 | 0.000267 | 665 | 0.000313028 | 0.00594431  | sucrose phosphorylase                              |



|              |              |          |     |             |             |                                                     |
|--------------|--------------|----------|-----|-------------|-------------|-----------------------------------------------------|
| ecd1_15_1_2  | 0.001048577  | 0.00029  | 874 | 0.000318269 | 0.006019838 | superoxide reductase                                |
| ecd1_1_1_251 | -0.000747083 | 0.000209 | 868 | 0.000367481 | 0.006724166 | galactitol-1-phosphate 5-dehydrogenase              |
| ecd1_3_1_74  | 0.001254806  | 0.000354 | 895 | 0.000416699 | 0.007306555 | 2-alkenal reductase (nad(p)(+))                     |
| ecd3_4_15_5  | -0.000623856 | 0.000176 | 521 | 0.00041782  | 0.007306555 | peptidyl-dipeptidase dcp                            |
| ecd3_6_1_3   | 0.001238454  | 0.000351 | 894 | 0.000437682 | 0.007629742 | adenosinetriphosphatase                             |
| ecd4_3_1_1   | -0.001417611 | 0.000405 | 880 | 0.000487744 | 0.008293147 | aspartate ammonia-lyase                             |
| ecd2_1_1_74  | 0.001407353  | 0.000404 | 894 | 0.000511295 | 0.008614082 | (fadh(2)-oxidizing)                                 |
| ecd2_7_7_77  | -0.000927916 | 0.000266 | 890 | 0.00051889  | 0.008689046 | molybdenum cofactor guanylyltransferase             |
| ecd2_8_3_12  | -0.000605121 | 0.000175 | 842 | 0.000587527 | 0.009577213 | glutaconate coa-transferase                         |
| ecd5_3_1_13  | -0.001165274 | 0.000339 | 895 | 0.000616179 | 0.00984105  | arabinose-5-phosphate Isomerase                     |
| ecd3_5_2_17  | -0.001366408 | 0.000399 | 374 | 0.000636749 | 0.00996792  | hydroxyisourate hydrolase                           |
| ecd1_1_1_38  | 0.000904787  | 0.000265 | 894 | 0.000653691 | 0.010204222 | malate dehydrogenase (oxaloacetate-decarboxylating) |
| ecd1_3_99_1  | 0.002018226  | 0.00059  | 895 | 0.000655826 | 0.01020872  | deleted entry                                       |
| ecd3_1_2_6   | -0.001165853 | 0.000342 | 563 | 0.00068703  | 0.010516698 | hydroxyacylglutathione hydrolase                    |
| ecd1_3_8_1   | -0.001155643 | 0.000341 | 711 | 0.000726418 | 0.010917572 | short-chain acyl-coa dehydrogenase                  |
| ecd3_2_1_86  | -0.001460251 | 0.000432 | 895 | 0.000757458 | 0.011044093 | 6-phospho-beta-glucosidase                          |
| ecd3_2_1_4   | 0.001924385  | 0.00057  | 895 | 0.000767712 | 0.011150023 | cellulase                                           |
| ecd1_1_1_26  | -0.000638398 | 0.000191 | 492 | 0.000855731 | 0.012001954 | glyoxylate reductase                                |
| ecd2_8_3_8   | -0.000871462 | 0.000261 | 895 | 0.000862767 | 0.012070006 | acetate coa-transferase                             |
| ecd3_6_3_21  | 0.000979711  | 0.000294 | 894 | 0.000912893 | 0.012674985 | polar-amino-acid-transporting atpase                |
| ecd3_8_1_2   | 0.000854311  | 0.00026  | 893 | 0.001042334 | 0.014082978 | (s)-2-haloacid dehalogenase                         |
| ecd3_1_1_11  | 0.002007398  | 0.000613 | 895 | 0.001096514 | 0.014565717 | pectinesterase                                      |
| ecd3_6_3_8   | -0.000798854 | 0.000246 | 886 | 0.001222071 | 0.015680244 | calcium-transporting atpase                         |
| ecd6_3_2_5   | 0.000857183  | 0.000264 | 895 | 0.001231779 | 0.015720117 | phosphopantothenate--cysteine ligase                |
| ecd3_2_1_8   | 0.00178968   | 0.000556 | 895 | 0.001330327 | 0.016557177 | endo-1,4-beta-xylanase                              |
| ecd2_7_13_3  | -0.002015436 | 0.000627 | 895 | 0.001365132 | 0.016672229 | histidine kinase                                    |
| ecd2_4_1_211 | 0.000896546  | 0.000282 | 875 | 0.001517642 | 0.018163874 | 1,3-beta-galactosyl-n-acetylhexosamine phosphoryla  |
| ecd3_4_17_19 | 0.000792474  | 0.00025  | 890 | 0.00158763  | 0.018666471 | carboxypeptidase taq                                |
| ecd5_1_3_11  | 0.00157484   | 0.000502 | 895 | 0.001753665 | 0.020220525 | cellobiose epimerase                                |
| ecd2_3_1_128 | -0.001216767 | 0.000391 | 895 | 0.001919876 | 0.021389582 | ribosomal-protein-alanine n-acetyltransferase       |

|               |              |          |     |             |             |                                                    |
|---------------|--------------|----------|-----|-------------|-------------|----------------------------------------------------|
| ecd4_1_2_17   | -0.000944583 | 0.000305 | 882 | 0.002034481 | 0.02200106  | l-fuculose-phosphate aldolase                      |
| ecd1_3_1_12   | 0.000850127  | 0.000276 | 894 | 0.002101027 | 0.022544227 | prephenate dehydrogenase                           |
| ecd5_1_3_6    | -0.000520925 | 0.00017  | 467 | 0.002216643 | 0.023556098 | udp-glucuronate 4-epimerase                        |
| ecd6_3_4_14   | -0.000805112 | 0.000263 | 895 | 0.002287875 | 0.02417361  | biotin carboxylase                                 |
| ecd3_2_1_89   | 0.00158396   | 0.000519 | 895 | 0.002336418 | 0.024535055 | arabinogalactan endo-beta-1,4-galactanase          |
| ecd3_4_13_19  | 0.000797005  | 0.000262 | 882 | 0.002415001 | 0.024944478 | membrane dipeptidase                               |
| ecd2_7_1_31   | -0.001026607 | 0.000338 | 895 | 0.00242778  | 0.025029686 | glycerate 3-kinase                                 |
| ecd2_5_1_30   | 0.000999697  | 0.000333 | 735 | 0.002748099 | 0.027461455 | heptaprenyl diphosphate synthase                   |
| ecd2_4_99_16  | 0.000897152  | 0.0003   | 521 | 0.002875358 | 0.028424378 | starch synthase (maltosyl-transferring)            |
| ecd3_5_4_3    | -0.000573124 | 0.000193 | 841 | 0.002991511 | 0.029104028 | guanine deaminase                                  |
| ecd1_1_1_58   | 0.000827581  | 0.000278 | 895 | 0.003011873 | 0.029235752 | tagaturonate reductase                             |
| ecd3_5_3_1    | -0.000643433 | 0.000218 | 881 | 0.003242734 | 0.030895424 | arginase                                           |
| ecd1_1_1_103  | -0.001024031 | 0.000348 | 895 | 0.003303649 | 0.031367637 | l-threonine 3-dehydrogenase                        |
| ecd1_5_3_1    | -0.001071485 | 0.000364 | 887 | 0.00334612  | 0.031500275 | sarcosine oxidase                                  |
| ecd4_1_2_13   | 0.000914837  | 0.000313 | 895 | 0.003526845 | 0.032589746 | fructose-bisphosphate aldolase                     |
| ecd3_5_1_47   | -0.000755935 | 0.000259 | 788 | 0.003665186 | 0.033467475 | n-acetyldiaminopimelate deacetylase                |
| ecd2_7_1_51   | -0.001010822 | 0.000348 | 853 | 0.00372115  | 0.033724276 | l-fuculokinase                                     |
| ecd2_3_1_8    | 0.000705309  | 0.000243 | 895 | 0.003808391 | 0.034376741 | phosphate acetyltransferase                        |
| ecd3_1_3_11   | -0.001084264 | 0.000375 | 895 | 0.003898333 | 0.034797809 | fructose-bisphosphatase                            |
| ecd3_2_1_96   | -0.00054227  | 0.000189 | 418 | 0.004143279 | 0.036445559 | mannosyl-glycoprotein endo-beta-n-acetylglucosamin |
| ecd6_3_2_2    | -0.001466335 | 0.000511 | 859 | 0.004243456 | 0.03704477  | glutamate--cysteine ligase                         |
| ecd2_1_1_63   | -0.001148331 | 0.000401 | 895 | 0.004329591 | 0.037626999 | methylated-dna--[protein]-cysteine s-methyltransfe |
| ecd2_7_1_60   | -0.000632056 | 0.000222 | 812 | 0.004432509 | 0.038071475 | n-acylmannosamine kinase                           |
| ecd5_3_1_5    | 0.001080138  | 0.000379 | 895 | 0.004427119 | 0.038071475 | xylose Isomerase                                   |
| ecd1_14_13_81 | 0.000428179  | 0.000151 | 890 | 0.004565698 | 0.038935257 | magnesium-protoporphyrin IX monomethyl ester (oxid |
| ecd3_2_1_85   | -0.000825607 | 0.000291 | 807 | 0.00460722  | 0.039168462 | 6-phospho-beta-galactosidase                       |
| ecd4_2_2_n2   | -0.000754545 | 0.000267 | 246 | 0.004759672 | 0.040278632 | peptidoglycan lytic endotransglycosylase           |
| ecd2_8_3_11   | 0.000506325  | 0.00018  | 369 | 0.004951548 | 0.041084466 | citramalate coa-transferase                        |
| ecd5_3_1_4    | 0.001018079  | 0.000362 | 895 | 0.00507678  | 0.041749888 | l-arabinose Isomerase                              |
| ecd1_2_99_7   | -0.000799985 | 0.000285 | 871 | 0.005140411 | 0.042074045 | aldehyde dehydrogenase (fad-independent)           |

|               |              |          |     |             |             |                                                     |
|---------------|--------------|----------|-----|-------------|-------------|-----------------------------------------------------|
| ecd1_6_99_5   | -0.001120732 | 0.0004   | 866 | 0.005171311 | 0.042210728 | transferred entry: 1.6.5.11                         |
| ecd1_2_1_2    | -0.000955516 | 0.000342 | 795 | 0.005305527 | 0.042738104 | formate dehydrogenase                               |
| ecd1_3_5_2    | -0.001017997 | 0.000367 | 893 | 0.00559278  | 0.044214163 | dihydroorotate dehydrogenase (quinone)              |
| ecd1_13_12_16 | 0.000629111  | 0.000227 | 738 | 0.005799846 | 0.045396525 | nitronate monooxygenase                             |
| ecd3_6_3_41   | -0.000605352 | 0.00022  | 782 | 0.00596647  | 0.046242232 | heme-transporting atpase                            |
| ecd2_3_1_12   | -0.000555552 | 0.000202 | 501 | 0.00616655  | 0.047022603 | dihydrolipoyllysine-residue acetyltransferase       |
| ecd3_6_1_1    | 0.001016092  | 0.000371 | 895 | 0.006234823 | 0.047196757 | Inorganic diphosphatase                             |
| ecd5_3_1_26   | -0.000718956 | 0.000264 | 539 | 0.006599837 | 0.049218214 | galactose-6-phosphate Isomerase                     |
| ecd1_1_1_57   | 0.000781443  | 0.000289 | 894 | 0.007006703 | 0.051106777 | fructuronate reductase                              |
| ecd4_1_3_27   | -0.001027838 | 0.000381 | 894 | 0.007150324 | 0.051785965 | anthranilate synthase                               |
| ecd2_5_1_17   | -0.000776686 | 0.000289 | 893 | 0.007247655 | 0.052285305 | cob(i)yrinic acid a,c-diamide adenosyltransferase   |
| ecd4_1_1_3    | 0.001021565  | 0.00038  | 895 | 0.007280813 | 0.052456027 | oxaloacetate decarboxylase                          |
| ecd3_6_4_12   | 0.001503723  | 0.000563 | 895 | 0.007666712 | 0.054315708 | dna helicase                                        |
| ecd3_1_1_47   | -0.000581331 | 0.000218 | 742 | 0.007827627 | 0.054892724 | 1-alkyl-2-acetyl-glycerophosphocholine esterase     |
| ecd2_1_1_242  | -0.000720949 | 0.000272 | 870 | 0.008095847 | 0.056132559 | 16s rrna (guanine(1516)-n(2))-methyltransferase     |
| ecd1_3_1_44   | 0.000856328  | 0.000323 | 873 | 0.008128052 | 0.056227332 | trans-2-enoyl-coa reductase (nad(+))                |
| ecd2_1_2_5    | -0.001122688 | 0.000423 | 794 | 0.008129866 | 0.056227332 | glutamate formimidoyltransferase                    |
| ecd3_2_1_21   | 0.001131331  | 0.000427 | 895 | 0.008222824 | 0.056672081 | beta-glucosidase                                    |
| ecd4_1_1_17   | -0.000703879 | 0.000266 | 536 | 0.008267347 | 0.056822588 | ornithine decarboxylase                             |
| ecd1_1_1_40   | -0.000735    | 0.000278 | 793 | 0.008312493 | 0.057049174 | malate dehydrogenase (oxaloacetate-decarboxylating) |
| ecd3_5_4_5    | -0.00065621  | 0.000249 | 895 | 0.008446963 | 0.057414409 | cytidine deaminase                                  |
| ecd3_4_23_43  | 0.000947807  | 0.000361 | 876 | 0.008772226 | 0.058910665 | prepilin peptidase                                  |
| ecd1_8_1_2    | -0.001055718 | 0.000406 | 588 | 0.009542513 | 0.06270146  | assimilatory sulfite reductase (nadph)              |
| ecd2_3_1_117  | -0.000816453 | 0.000318 | 881 | 0.010355782 | 0.066598981 | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n-suc  |
| ecd3_2_1_94   | -0.000574652 | 0.000224 | 298 | 0.010508324 | 0.067131788 | glucan 1,6-alpha-isomaltosidase                     |
| ecd2_7_1_4    | 0.000945242  | 0.000369 | 895 | 0.010600035 | 0.067405974 | fructokinase                                        |
| ecd3_2_1_18   | -0.000853757 | 0.000335 | 811 | 0.01096525  | 0.069250254 | exo-alpha-sialidase                                 |
| ecd1_8_1_4    | -0.001266765 | 0.000498 | 895 | 0.011094033 | 0.069903792 | dihydrolipoyl dehydrogenase                         |
| ecd4_2_2_8    | -0.000794777 | 0.000314 | 234 | 0.011572977 | 0.071725735 | heparin-sulfate lyase                               |
| ecd5_3_3_3    | -0.000420878 | 0.000166 | 613 | 0.011643626 | 0.071971672 | vinylacetyl-coa delta-isomerase                     |

|              |              |          |     |             |             |                                                    |
|--------------|--------------|----------|-----|-------------|-------------|----------------------------------------------------|
| ecd4_2_1_32  | 0.000932529  | 0.00037  | 895 | 0.011821459 | 0.072826512 | l(+)-tartrate dehydratase                          |
| ecd3_5_4_12  | 0.000761737  | 0.000303 | 894 | 0.012063129 | 0.073821539 | dcmp deaminase                                     |
| ecd3_1_4_53  | -0.000622453 | 0.000248 | 570 | 0.012097218 | 0.073880369 | 3',5'-cyclic-amp phosphodiesterase                 |
| ecd6_6_1_2   | -0.000470946 | 0.000188 | 607 | 0.012258303 | 0.074520775 | cobaltochelataase                                  |
| ecd5_3_3_10  | -0.000640285 | 0.000256 | 174 | 0.012484643 | 0.075316744 | 5-carboxymethyl-2-hydroxymuconate delta-isomerase  |
| ecd5_1_99_1  | -0.00093288  | 0.000374 | 870 | 0.01278776  | 0.076477451 | methylmalonyl-coa epimerase                        |
| ecd4_1_1_70  | 0.000709224  | 0.000285 | 895 | 0.012903607 | 0.076906123 | glutaconyl-coa decarboxylase                       |
| ecd1_1_1_21  | -0.000445408 | 0.000179 | 786 | 0.013079991 | 0.07755368  | ldehyde reductase                                  |
| ecd6_2_1_22  | 0.000637262  | 0.000257 | 868 | 0.013227157 | 0.078091099 | [citrate (pro-3s)-lyase] ligase                    |
| ecd1_8_98_1  | -0.000651324 | 0.000262 | 882 | 0.013242161 | 0.078096247 | cob--com heterodisulfide reductase                 |
| ecd3_6_4_13  | -0.001404777 | 0.000567 | 811 | 0.013343513 | 0.07833068  | rna helicase                                       |
| ecd3_2_1_25  | 0.000522769  | 0.000212 | 831 | 0.013966777 | 0.080506911 | beta-mannosidase                                   |
| ecd3_2_2_1   | -0.000515195 | 0.000209 | 831 | 0.014024818 | 0.080562521 | purine nucleosidase                                |
| ecd4_1_99_12 | -0.000866351 | 0.000353 | 895 | 0.014175614 | 0.081089135 | 3,4-dihydroxy-2-butanone-4-phosphate synthase      |
| ecd1_1_1_100 | -0.001076763 | 0.000443 | 895 | 0.015265502 | 0.085295412 | 3-oxoacyl-[acyl-carrier-protein] reductase         |
| ecd3_5_4_25  | -0.000610163 | 0.000251 | 852 | 0.015333165 | 0.085586938 | gtp cyclohydrolase II                              |
| ecd6_3_5_11  | -0.000610376 | 0.000253 | 894 | 0.015836201 | 0.087862298 | cobyrinate a,c-diamide synthase (glutamine-hydroly |
| ecd1_2_7_1   | 0.001034533  | 0.00043  | 890 | 0.016296427 | 0.089606024 | pyruvate synthase                                  |
| ecd1_2_4_1   | -0.000483295 | 0.000201 | 481 | 0.016520266 | 0.090420998 | pyruvate dehydrogenase (acetyl-transferring)       |
| ecd5_1_1_11  | 0.000458182  | 0.000191 | 583 | 0.016526458 | 0.090420998 | phenylalanine racemase (atp-hydrolyzing)           |
| ecd4_1_1_31  | -0.001129794 | 0.000472 | 557 | 0.016823638 | 0.091503372 | phosphoenolpyruvate carboxylase                    |
| ecd2_5_1_1   | -0.000483488 | 0.000203 | 381 | 0.017208067 | 0.092961207 | dimethylallyltranstransferase                      |
| ecd2_3_1_222 | -0.000804125 | 0.000338 | 895 | 0.017452867 | 0.093726477 | phosphate propanoyltransferase                     |
| ecd3_2_1_n1  | -0.000987846 | 0.000415 | 892 | 0.017584969 | 0.09434421  | blood group b branched chain alpha-1,3-galactosida |
| ecd1_17_1_4  | -0.000597617 | 0.000253 | 890 | 0.018408609 | 0.096789697 | xanthine dehydrogenase                             |
| ecd1_6_5_5   | -0.000616136 | 0.000261 | 624 | 0.018636273 | 0.097652587 | nadph:quinone reductase                            |
| ecd3_1_3_27  | -0.001052837 | 0.000447 | 880 | 0.018747824 | 0.098106511 | phosphatidylglycerophosphatase                     |
| ecd3_4_25_2  | -0.000885943 | 0.000378 | 750 | 0.019218849 | 0.100108567 | hslu--hslv peptidase                               |
| ecd3_4_19_5  | -0.000638517 | 0.000274 | 496 | 0.019795991 | 0.102331753 | beta-aspartyl-peptidase                            |
| ecd2_1_1_113 | -0.000664962 | 0.000287 | 762 | 0.020711638 | 0.105974546 | site-specific dna-methyltransferase (cytosine-n(4) |

|              |              |          |     |             |             |                                                    |
|--------------|--------------|----------|-----|-------------|-------------|----------------------------------------------------|
| ecd3_4_14_11 | -0.00045004  | 0.000194 | 854 | 0.020862095 | 0.106214416 | xaa-pro dipeptidyl-peptidase                       |
| ecd2_2_1_1   | 0.000895921  | 0.000387 | 895 | 0.02099664  | 0.106642859 | transketolase                                      |
| ecd1_1_1_69  | 0.000953466  | 0.000413 | 895 | 0.021037688 | 0.106704199 | gluconate 5-dehydrogenase                          |
| ecd3_2_1_131 | 0.000606475  | 0.000263 | 871 | 0.021479347 | 0.107513472 | xylan alpha-1,2-glucuronosidase                    |
| ecd3_5_2_10  | -0.000571831 | 0.00025  | 602 | 0.022238646 | 0.110314863 | creatininase                                       |
| ecd1_2_7_8   | 0.001019056  | 0.000445 | 895 | 0.022314504 | 0.110591883 | Indolepyruvate ferredoxin oxidoreductase           |
| ecd1_1_1_67  | 0.000552144  | 0.000242 | 828 | 0.02274159  | 0.112000844 | mannitol 2-dehydrogenase                           |
| ecd3_4_17_11 | 0.00033585   | 0.000147 | 583 | 0.022760939 | 0.112000844 | glutamate carboxypeptidase                         |
| ecd3_2_1_151 | 0.000694082  | 0.000305 | 599 | 0.023136236 | 0.113055273 | xyloglucan-specific endo-beta-1,4-glucanase        |
| ecd3_2_1_54  | 0.000465379  | 0.000205 | 311 | 0.023389883 | 0.113485486 | cyclomaltodextrinase                               |
| ecd1_3_3_4   | 0.000709256  | 0.000313 | 578 | 0.023736808 | 0.114859543 | protoporphyrinogen oxidase                         |
| ecd3_4_13_21 | -0.000581494 | 0.000257 | 803 | 0.02380187  | 0.115073606 | dipeptidase e                                      |
| ecd4_2_1_7   | 0.000582399  | 0.000258 | 895 | 0.023968279 | 0.115574792 | altronate dehydratase                              |
| ecd6_3_1_2   | 0.000601705  | 0.000267 | 895 | 0.024218891 | 0.116174991 | glutamate--ammonia ligase                          |
| ecd1_10_3_10 | -0.000821538 | 0.000365 | 831 | 0.02468751  | 0.117403768 | ubiquinol oxidase (h(+)-transporting)              |
| ecd5_4_99_1  | -0.000814173 | 0.000364 | 529 | 0.025538877 | 0.120420446 | methylo-aspartate mutase                           |
| ecd3_2_1_78  | 0.001421238  | 0.00064  | 798 | 0.026732902 | 0.12393122  | mannan endo-1,4-beta-mannosidase                   |
| ecd1_7_1_7   | -0.000504605 | 0.000228 | 823 | 0.027182113 | 0.125592269 | gmp reductase                                      |
| ecd2_4_1_83  | -0.00041385  | 0.000188 | 842 | 0.028081858 | 0.128383687 | dolichyl-phosphate beta-d-mannosyltransferase      |
| ecd3_5_4_2   | -0.000638665 | 0.000291 | 895 | 0.028252063 | 0.128730089 | adenine deaminase                                  |
| ecd3_2_1_20  | 0.000627507  | 0.000287 | 895 | 0.029123418 | 0.131269173 | alpha-glucosidase                                  |
| ecd3_5_4_28  | -0.000649842 | 0.000297 | 895 | 0.029116867 | 0.131269173 | s-adenosylhomocysteine deaminase                   |
| ecd6_3_4_18  | -0.000682081 | 0.000315 | 894 | 0.030846522 | 0.137456025 | 5-(carboxyamino)imidazole ribonucleotide synthase  |
| ecd2_2_1_2   | -0.000757022 | 0.00035  | 895 | 0.030998913 | 0.137684878 | transaldolase                                      |
| ecd2_6_1_62  | -0.000685641 | 0.000318 | 895 | 0.031204972 | 0.138393802 | adenosylmethionine--8-amino-7-oxononanoate transam |
| ecd4_2_1_75  | -0.000639491 | 0.000299 | 753 | 0.032617749 | 0.142478094 | uroporphyrinogen-iii synthase                      |
| ecd2_8_3_9   | 0.000393853  | 0.000185 | 802 | 0.033557047 | 0.145668688 | butyrate--acetoacetate coa-transferase             |
| ecd2_1_1_77  | -0.000614657 | 0.000289 | 658 | 0.033855103 | 0.146387557 | protein-l-isoaspartate(d-aspartate) o-methyltransf |
| ecd2_7_1_53  | -0.000596498 | 0.000284 | 791 | 0.035946086 | 0.152643213 | l-xylulokinase                                     |
| ecd3_2_1_31  | 0.000851799  | 0.000408 | 895 | 0.037267662 | 0.155779954 | beta-glucuronidase                                 |

|              |              |          |     |             |             |                                                    |
|--------------|--------------|----------|-----|-------------|-------------|----------------------------------------------------|
| ecd1_1_1_271 | 0.001021403  | 0.000494 | 895 | 0.038902868 | 0.159662824 | gdp-l-fucose synthase                              |
| ecd1_7_7_1   | 0.00034679   | 0.000169 | 738 | 0.040282066 | 0.162855846 | ferredoxin--nitrite reductase                      |
| ecd3_4_24_70 | -0.000683111 | 0.000336 | 629 | 0.042063573 | 0.167105179 | oligopeptidase a                                   |
| ecd4_1_99_1  | -0.000720409 | 0.000355 | 889 | 0.042730685 | 0.169023777 | tryptophanase                                      |
| ecd2_7_7_63  | -0.00052477  | 0.000268 | 895 | 0.050705631 | 0.190054343 | lipoate--protein ligase                            |
| ecd5_1_3_20  | -0.000690992 | 0.000353 | 879 | 0.050698177 | 0.190054343 | adp-glyceromanno-heptose 6-epimerase               |
| ecd3_1_4_37  | 0.000587661  | 0.000301 | 306 | 0.051274307 | 0.190850715 | 2',3'-cyclic-nucleotide 3'-phosphodiesterase       |
| ecd5_1_3_4   | -0.000800633 | 0.000411 | 894 | 0.051519397 | 0.191134319 | l-ribulose-5-phosphate 4-epimerase                 |
| ecd5_4_2_2   | -0.000707494 | 0.000364 | 895 | 0.052005026 | 0.192098781 | phosphoglucomutase (alpha-d-glucose-1,6-bisphospha |
| ecd1_4_3_16  | -0.000683831 | 0.000354 | 895 | 0.053754255 | 0.197110826 | l-aspartate oxidase                                |
| ecd3_1_6_12  | 0.000456797  | 0.000237 | 830 | 0.054156682 | 0.197988106 | n-acetylgalactosamine-4-sulfatase                  |
| ecd4_2_2_2   | -0.000398867 | 0.000207 | 564 | 0.054353562 | 0.198009362 | pectate lyase                                      |
| ecd3_2_1_156 | 0.000497168  | 0.000263 | 350 | 0.058993    | 0.208037854 | oligosaccharide reducing-end xylanase              |
| ecd3_6_3_16  | -0.000498778 | 0.000266 | 796 | 0.061509614 | 0.21408857  | arsenite-transporting atpase                       |
| ecd3_5_1_5   | -0.00096094  | 0.000514 | 887 | 0.061742065 | 0.2145828   | urease                                             |
| ecd3_4_13_3  | 0.000480765  | 0.000257 | 892 | 0.062155312 | 0.215476948 | transferred entry: 3.4.13.18 and 3.4.13.20         |
| ecd3_5_4_9   | -0.000457086 | 0.000245 | 869 | 0.062382313 | 0.216128315 | methenyltetrahydrofolate cyclohydrolase            |
| ecd2_6_1_1   | 0.000534957  | 0.000287 | 895 | 0.062662506 | 0.216420629 | aspartate transaminase                             |
| ecd1_11_1_5  | -0.000598585 | 0.000324 | 800 | 0.064623371 | 0.220965568 | cytochrome-c peroxidase                            |
| ecd3_3_1_1   | 0.000683149  | 0.000369 | 895 | 0.064738193 | 0.220965568 | adenosylhomocysteinase                             |
| ecd2_7_1_21  | 0.000699974  | 0.000379 | 895 | 0.064987868 | 0.220998743 | thymidine kinase                                   |
| ecd3_1_26_12 | -0.000308783 | 0.000167 | 555 | 0.065586534 | 0.221806112 | ribonuclease e                                     |
| ecd4_1_1_50  | 0.000685801  | 0.000372 | 886 | 0.065662136 | 0.221816372 | adenosylmethionine decarboxylase                   |
| ecd4_2_1_59  | -0.000636738 | 0.000347 | 895 | 0.066823079 | 0.223932282 | 3-hydroxyacyl-[acyl-carrier-protein] dehydratase   |
| ecd2_1_1_14  | 0.000559672  | 0.000305 | 893 | 0.066992561 | 0.224364178 | 5-methyltetrahydropteroyltriglutamate--homocystein |
| ecd4_2_99_20 | -0.000399461 | 0.000218 | 504 | 0.067068729 | 0.224483219 | 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxyl |
| ecd2_7_7_58  | -0.000678631 | 0.000371 | 753 | 0.067755714 | 0.225825136 | (2,3-dihydroxybenzoyl)adenylate synthase           |
| ecd3_6_1_22  | 0.000495261  | 0.000271 | 895 | 0.067996574 | 0.2264913   | nad(+) diphosphatase                               |
| ecd5_1_3_9   | -0.000507802 | 0.000278 | 894 | 0.068202377 | 0.226494192 | n-acylglucosamine-6-phosphate 2-epimerase          |
| ecd2_3_1_47  | -0.000553581 | 0.000303 | 895 | 0.068394353 | 0.226632739 | 8-amino-7-oxononanoate synthase                    |

|              |              |          |     |             |             |                                                     |
|--------------|--------------|----------|-----|-------------|-------------|-----------------------------------------------------|
| ecd2_7_1_2   | 0.000576834  | 0.000316 | 895 | 0.068521223 | 0.226788136 | glucokinase                                         |
| ecd2_7_8_6   | -0.000781949 | 0.000429 | 894 | 0.068658727 | 0.227054533 | undecaprenyl-phosphate galactose phosphotransferase |
| ecd3_5_3_11  | 0.000474008  | 0.000261 | 894 | 0.069743109 | 0.229132236 | agmatinase                                          |
| ecd3_4_11_7  | -0.000583068 | 0.000322 | 663 | 0.070117602 | 0.229407857 | glutamyl aminopeptidase                             |
| ecd2_4_1_187 | -0.000524659 | 0.00029  | 761 | 0.07044963  | 0.230085493 | mannosaminyltransferase                             |
| ecd3_5_3_12  | 0.000632947  | 0.00035  | 894 | 0.071160816 | 0.231437146 | agmatine deiminase                                  |
| ecd5_4_99_5  | 0.000647154  | 0.000359 | 894 | 0.071398872 | 0.231522339 | chorismate mutase                                   |
| ecd3_4_14_5  | -0.000371525 | 0.000206 | 684 | 0.071932856 | 0.232368565 | dipeptidyl-peptidase Iv                             |
| ecd1_3_3_1   | 0.000540662  | 0.000301 | 891 | 0.07247512  | 0.233526248 | transferred entry: 1.3.98.1                         |
| ecd4_1_1_18  | -0.000543244 | 0.000303 | 894 | 0.073530508 | 0.235433774 | lysine decarboxylase                                |
| ecd5_4_2_6   | -0.000461863 | 0.000258 | 886 | 0.074186641 | 0.23673917  | beta-phosphoglucomutase                             |
| ecd2_4_1_129 | -0.000621959 | 0.00035  | 895 | 0.076205532 | 0.240772882 | peptidoglycan glycosyltransferase                   |
| ecd1_1_1_140 | -0.000494767 | 0.00028  | 812 | 0.077091182 | 0.242791824 | sorbitol-6-phosphate 2-dehydrogenase                |
| ecd6_4_1_2   | 0.000725197  | 0.000412 | 895 | 0.078887477 | 0.245944162 | acetyl-coa carboxylase                              |
| ecd3_5_1_11  | 0.000389148  | 0.000223 | 892 | 0.080697338 | 0.249543084 | penicillin amidase                                  |

**Supplemental Table 2: List of species that were significantly associated with metabolic risk (METscore).**

| <b>Species</b>                      | <b>beta coefficients</b> | <b>SEM</b>      | <b>N</b>   | <b>N.not.0</b> | <b>P-value</b>  | <b>Q-value</b>  |
|-------------------------------------|--------------------------|-----------------|------------|----------------|-----------------|-----------------|
| <b>Coprococcus_sp_art55_1</b>       | <b>-0.01421</b>          | <b>0.004108</b> | <b>911</b> | <b>148</b>     | <b>0.000586</b> | <b>0.037377</b> |
| <b>Faecalibacterium_prausnitzii</b> | <b>-0.01388</b>          | <b>0.004157</b> | <b>911</b> | <b>901</b>     | <b>0.000919</b> | <b>0.044591</b> |
| Acidaminococcus_unclassified        | 0.004625                 | 0.001507        | 911        | 116            | 0.002217        | 0.067882        |
| Eubacterium_ventriosum              | 0.004583                 | 0.001522        | 911        | 530            | 0.002728        | 0.080408        |
| Subdoligranulum_unclassified        | -0.01346                 | 0.00461         | 911        | 910            | 0.003648        | 0.098012        |
| Butyrivibrio_crossotus              | -0.01102                 | 0.003807        | 911        | 121            | 0.00392         | 0.098339        |
| Barnesiella_intestinihominis        | -0.00868                 | 0.003272        | 911        | 482            | 0.008141        | 0.142258        |
| Bacteroides_xylanisolvens           | 0.0041                   | 0.001561        | 911        | 639            | 0.008861        | 0.14569         |
| Clostridium_bolteae                 | 0.004291                 | 0.001786        | 911        | 454            | 0.016651        | 0.211992        |
| Eubacterium_rectale                 | 0.017374                 | 0.007155        | 911        | 868            | 0.015593        | 0.211992        |
| Paraprevotella_unclassified         | 0.004809                 | 0.002           | 911        | 255            | 0.016409        | 0.211992        |
| Roseburia_inulinivorans             | 0.005544                 | 0.002337        | 911        | 761            | 0.018104        | 0.218347        |
| Streptococcus_vestibularis          | 0.001555                 | 0.000665        | 911        | 137            | 0.019922        | 0.230273        |
| Burkholderiales_bacterium_1_1_47    | 0.002128                 | 0.000932        | 911        | 406            | 0.022708        | 0.236928        |

Analyzed using MaAsLin2 adjusted for repeated measurements (participants ID as random intercept), age, energy intake, alcohol, smoking, physical activity, using of antibiotics, consumed any probiotics and fecal sample characteristics)