Table S1 Identifying specific microbiota function responsing to isomalt consumption via PICRUSt

KEGG pathway	pvalue	KEGG pathway	pvalue
Biosynthesis of secondary metabolites	0.03619	Glutamatergic synapse	0.006423
Microbial metabolism in diverse environments	0.01927	AMPK signaling pathway	0.02881
Biosynthesis of amino acids	0.04883	Peroxisome	0.03091
Carbon metabolism	0.007137	Chloroalkane and chloroalkene degradation	0.001383
ABC transporters	0.0211	PPAR signaling pathway	0.001915
Glycolysis / Gluconeogenesis	0.04956	Nitrotoluene degradation	0.01639
Pyruvate metabolism	0.03012	Various types of N-glycan biosynthesis	0.008102
Galactose metabolism	0.008011	Epithelial cell signaling in Helicobacter pylori infection	0.01006
Cysteine and methionine metabolism	0.008807	Aminobenzoate degradation	0.03944
Carbon fixation pathways in prokaryotes	0.0272	RNA transport	0.01958
Peptidoglycan biosynthesis	0.02544	Longevity regulating pathway - multiple species	0.00024
Fructose and mannose metabolism	0.0168	Protein processing in endoplasmic reticulum	0.0116
Pentose phosphate pathway	0.01635	Biosynthesis of vancomycin group antibiotics	0.0125
Propanoate metabolism	0.1191	Glucosinolate biosynthesis	0.023
Pantothenate and CoA biosynthesis	0.002181	Carbapenem biosynthesis	0.02447
Terpenoid backbone biosynthesis	0.02582	Platinum drug resistance	0.03354
Thiamine metabolism	0.01447	Cushing syndrome	0.03271
Nucleotide excision repair	0.01636	Renal cell carcinoma	0.006392
Fatty acid metabolism	0.007157	Shigellosis	0.02714
Glycerolipid metabolism	0.005833	Ether lipid metabolism	0.02614
Valine, leucine and isoleucine biosynthesis	0.003387	Choline metabolism in cancer	0.003087

Pentose and glucuronate interconversions	0.007035	Axon regeneration	0.02506
Folate biosynthesis	0.02866	Phospholipase D signaling pathway	0.02506
Arginine and proline metabolism	0.02729	Arachidonic acid metabolism	0.02215
Selenocompound metabolism	0.02079	Protein digestion and absorption	0.01042
Biotin metabolism	0.0243	Non-alcoholic fatty liver disease (NAFLD)	0.02739
Lysosome	0.007904	Parkinson disease	0.0128
C5-Branched dibasic acid metabolism	0.005031	Bacterial invasion of epithelial cells	0.0128
Sulfur relay system	0.004265	Retrograde endocannabinoid signaling	0.01829
Antifolate resistance	0.01478	Bile secretion	0.01626
Polyketide sugar unit biosynthesis	0.001628	Gastric cancer	0.01626
Biofilm formation - Escherichia coli	0.01843	Ethylbenzene degradation	0.01624
Monobactam biosynthesis	0.007887	Renin-angiotensin system	0.000313
Salmonella infection	0.000954	Toxoplasmosis	0.01752
Tuberculosis	0.001417	Mineral absorption	0.0264
Fluid shear stress and atherosclerosis	0.01124	Meiosis - yeast	0.04357
Vitamin B6 metabolism	0.04969	Proteasome	0.005432
Taurine and hypotaurine metabolism	0.005766	Polycyclic aromatic hydrocarbon degradation	0.005951
Riboflavin metabolism	0.02865	Chagas disease (American trypanosomiasis)	0.002724
Legionellosis	0.006732	Bladder cancer	0.005002
Degradation of aromatic compounds	0.000921	cAMP signaling pathway	0.004872
NOD-like receptor signaling pathway	0.001104	Basal transcription factors	0.003986
Cocaine addiction	0.001308	Alcoholism	0.001308
Dopaminergic synapse	0.001308	Amphetamine addiction	0.001308
Serotonergic synapse	0.001308		

Table S2 Identifying specific microbiota function responsing to erythritol consumption via PICRUSt

KEGG pathway	pvalue	KEGG pathway	pvalue
Pentose and glucuronate interconversions	0.005794	Salmonella infection	0.02173
Fatty acid biosynthesis	0.01839	Pertussis	0.01565
Synthesis and degradation of ketone bodies	0.002151	Tuberculosis	0.01517
Primary bile acid biosynthesis	0.01659	Human papillomavirus infection	0.004085
Secondary bile acid biosynthesis	0.01018	Viral carcinogenesis	0.004085
Steroid hormone biosynthesis	0.003281	Renal cell carcinoma	0.01176
Photosynthesis	0.00513	Hepatocellular carcinoma	0.002671
Arginine biosynthesis	0.02083	Fluid shear stress and atherosclerosis	0.01381
Glycine, serine and threonine metabolism	0.008518	Pyrimidine metabolism	0.02325
Monobactam biosynthesis	0.009689	D-Arginine and D-ornithine metabolism	0.02294
Cysteine and methionine metabolism	0.01741	C5-Branched dibasic acid metabolism	0.02271
Lysine biosynthesis	0.009042	Amoebiasis	0.02369
Carbapenem biosynthesis	0.009691	Central carbon metabolism in cancer	0.02431
D-Glutamine and D-glutamate metabolism	0.0131	Starch and sucrose metabolism	0.02516
Lipopolysaccharide biosynthesis	0.01523	Nonribosomal peptide structures	0.02541
Glycerophospholipid metabolism	0.0197	Antifolate resistance	0.02574
Arabinogalactan biosynthesis - Mycobacterium	0.01907	Citrate cycle (TCA cycle)	0.02718
Glycosphingolipid biosynthesis - globo and isoglobo series	0.01716	Fructose and mannose metabolism	0.02693
Carbon fixation in photosynthetic organisms	0.01973	Longevity regulating pathway - multiple species	0.02716
Vitamin B6 metabolism	0.01496	Proteoglycans in cancer	0.02625
Biotin metabolism	0.01466	Other glycan degradation	0.02909
Lipoic acid metabolism	0.01448	Polycyclic aromatic hydrocarbon degradation	0.02764

Terpenoid backbone biosynthesis	0.005852	Fatty acid metabolism	0.02844
Caprolactam degradation	0.01636	Biosynthesis of amino acids	0.02891
Flavone and flavonol biosynthesis	0.02031	RNA polymerase	0.02934
Glucosinolate biosynthesis	0.02145	Longevity regulating pathway - worm	0.0288
Aminoacyl-tRNA biosynthesis	0.01858	Benzoate degradation	0.03027
Drug metabolism - other enzymes	0.01443	Glucagon signaling pathway	0.02998
Metabolic pathways	0.01039	Valine, leucine and isoleucine biosynthesis	0.03069
Biosynthesis of secondary metabolites	0.01848	2-Oxocarboxylic acid metabolism	0.03184
beta-Lactam resistance	0.004874	Ferroptosis	0.03177
ABC transporters	0.01758	Necroptosis	0.03207
Phosphotransferase system (PTS)	0.01893	Various types of N-glycan biosynthesis	0.03339
Ribosome biogenesis in eukaryotes	0.01873	Peptidoglycan biosynthesis	0.03363
Ribosome	0.01746	Glycosphingolipid biosynthesis - ganglio series	0.03338
DNA replication	0.01497	Lysosome	0.03278
PPAR signaling pathway	0.006694	Sphingolipid metabolism	0.03505
Base excision repair	0.02176	Pentose phosphate pathway	0.0362
Nucleotide excision repair	0.01284	Alanine, aspartate and glutamate metabolism	0.04235
Mismatch repair	0.008279	Histidine metabolism	0.04074
Homologous recombination	0.01862	D-Alanine metabolism	0.0394
HIF-1 signaling pathway	0.02075	Amino sugar and nucleotide sugar metabolism	0.03998
Cell cycle - Caulobacter	0.01311	Lipoarabinomannan (LAM) biosynthesis	0.0397
Sulfur relay system	0.002572	Zeatin biosynthesis	0.04078
Autophagy - yeast	0.009513	AMPK signaling pathway	0.04046
Apoptosis - fly	0.01919	Antigen processing and presentation	0.04228
Renin-angiotensin system	0.00739	IL-17 signaling pathway	0.04228
NOD-like receptor signaling pathway	0.01608	Th17 cell differentiation	0.04228
Plant-pathogen interaction	0.01681	Progesterone-mediated oocyte maturation	0.04228
Glutamatergic	0.01416	Estrogen signaling	0.04228

synapse		pathway	
Insulin signaling pathway	0.0175	Prolactin signaling pathway	0.03931
Thyroid hormone synthesis	0.009768	Epithelial cell signaling in Helicobacter pylori infection	0.0378
Adipocytokine signaling pathway	0.02118	Staphylococcus aureus infection	0.03961
Type II diabetes mellitus	0.004399	Pathways in cancer	0.03984
Cushing syndrome	0.01176	Prostate cancer	0.04228
Mineral absorption	0.003102	Glycosaminoglycan degradation	0.0435
Alzheimer disease	0.0121	Glyoxylate and dicarboxylate metabolism	0.04361
Bacterial invasion of epithelial cells	0.0007122	Phenylpropanoid biosynthesis	0.0447
Pathogenic Escherichia coli infection	0.01234	Linoleic acid metabolism	0.04546
Aminobenzoate degradation	0.04666	RNA transport	0.04601
One carbon pool by folate	0.04757	Penicillin and cephalosporin biosynthesis	0.04802
Apoptosis	0.04728	Prodigiosin biosynthesis	0.04806
Thyroid hormone signaling pathway	0.04844		

Table S3 Identifying specific microbiota function responsing to eylitol consumption via PICRUSt

KEGG pathway	pvalue	KEGG pathway	pvalue
ABC transporters	0.0064887	Metabolic pathways	0.0061129
Alanine, aspartate and glutamate metabolism	0.0090603	MicroRNAs in cancer	0.0099905
Amino sugar and nucleotide sugar metabolism	0.0445786	Microbial metabolism in diverse environments	0.0056212
Aminoacyl-tRNA biosynthesis	0.0447904	Mismatch repair	0.0128221
Amoebiasis	0.049086	Neomycin, kanamycin and gentamicin biosynthesis	0.0006868
Autophagy - yeast	0.0001114	Nicotinate and nicotinamide metabolism	0.0185625
Bacterial invasion of epithelial cells	0.0246079	Nitrogen metabolism	0.0475809
Basal transcription factors	0.0104633	Nucleotide excision repair	0.0257944
Biosynthesis of amino acids	0.0396475	Oxidative phosphorylation	0.0321354
Biosynthesis of ansamycins	0.0012312	Pathways in cancer	0.0007925
Biosynthesis of secondary metabolites	0.0067511	Pentose and glucuronate interconversions	0.0368738
Biosynthesis of various secondary metabolites - part 2	0.0007559	Pentose phosphate pathway	0.0154762
Bladder cancer	0.0122155	Peptidoglycan biosynthesis	0.0411856
Butanoate metabolism	0.0428755	Pertussis	0.0305444
Carbon fixation in photosynthetic organisms	0.0097389	Photosynthesis	0.021938
Carbon metabolism	0.0229893	Polycyclic aromatic hydrocarbon degradation	0.0135013
Cell cycle - Caulobacter	0.0146054	Polyketide sugar unit biosynthesis	0.0310148
Chagas disease (American trypanosomiasis)	0.011617	Prion diseases	0.0023246
Cyanoamino acid metabolism	0.0228137	Prolactin signaling pathway	0.0477923
DNA replication	0.0343789	Proteasome	0.0122992
Drug metabolism - other enzymes	0.0257192	Purine metabolism	0.0425457
Flavone and flavonol biosynthesis	0.0227242	Pyrimidine metabolism	0.0493156
Folate biosynthesis	0.009976	Pyruvate metabolism	0.0403185
Fructose and mannose metabolism	0.0222391	RNA degradation	0.0129427
GABAergic synapse	0.0052768	RNA transport	0.0377808
Galactose metabolism	0.0229488	Renin-angiotensin system	0.0116358
Glutamatergic synapse	0.0027024	Riboflavin metabolism	0.0083532

Glycerolipid metabolism	0.0253752	Secondary bile acid biosynthesis	0.0020085
Glycerophospholipid metabolism	0.0214289	Starch and sucrose metabolism	0.0198505
HIF-1 signaling pathway	0.0376902	Steroid hormone biosynthesis	0.0023164
Homologous recombination	0.036604	Streptomycin biosynthesis	0.0210548
Human papillomavirus infection	0.0031168	Sulfur relay system	0.0066912
Inositol phosphate metabolism	0.0412234	Terpenoid backbone biosynthesis	0.025495
Lipoic acid metabolism	0.0215529	Thiamine metabolism	0.0040972
Lipopolysaccharide biosynthesis	0.0394751	Two-component system	0.0474213
Longevity regulating pathway - worm	0.000708	Type II diabetes mellitus	0.0034107
Lysine biosynthesis	0.041022	Viral carcinogenesis	0.0031168
Meiosis - yeast	0.0192279	cAMP signaling pathway	0.0124321

Table S4 Identifying specific microbiota function responsing to sorbitol consumption via PICRUSt

KEGG pathway	pvalue	KEGG pathway	pvalue
Citrate cycle (TCA cycle)	0.03389	Biosynthesis of ansamycins	0.006053
Pentose phosphate pathway	0.02409	Biosynthesis of siderophore group nonribosomal peptides	0.01801
Ascorbate and aldarate metabolism	0.03353	Biosynthesis of vancomycin group antibiotics	0.02067
Ubiquinone and other terpenoid-quinone biosynthesis	0.006369	Metabolic pathways	0.02586
Steroid hormone biosynthesis	0.0009929	Carbon metabolism	0.001861
Oxidative phosphorylation	0.02209	beta-Lactam resistance	0.000592
Photosynthesis	0.005129	Vancomycin resistance	0.01948
Glycine, serine and threonine metabolism	0.003066	Antifolate resistance	0.00479
Valine, leucine and isoleucine degradation	0.01955	ABC transporters	0.005786
Benzoate degradation	0.01	Two-component system	0.009185
Tryptophan metabolism	0.0242	Basal transcription factors	0.003662
Other glycan degradation	0.005457	Proteasome	0.003579
Various types of N-glycan biosynthesis	0.01139	PPAR signaling pathway	0.0005664
Glycosaminoglycan degradation	0.02885	MAPK signaling pathway - yeast	0.02598
Lipopolysaccharide biosynthesis	0.003729	MAPK signaling pathway - fly	0.00242
Inositol phosphate metabolism	0.01943	cAMP signaling pathway	0.003442
Ether lipid metabolism	0.01277	FoxO signaling pathway	0.02337
Arabinogalactan biosynthesis - Mycobacterium	0.0001506	Phosphatidylinositol signaling system	0.01125
Arachidonic acid metabolism	0.0014	Meiosis - yeast	0.005441
Linoleic acid metabolism	0.04386	Sulfur relay system	7.06E-05
alpha-Linolenic acid metabolism	0.04557	Lysosome	0.01369
Sphingolipid metabolism	0.003756	Peroxisome	0.0003227
Glycosphingolipid biosynthesis - globo and isoglobo series	0.004342	Apoptosis	0.00476
Glycosphingolipid biosynthesis - ganglio series	0.01139	Longevity regulating pathway	0.007433
Polycyclic aromatic hydrocarbon degradation	0.003571	Longevity regulating pathway - multiple species	0.0008084

One carbon pool by folate	0.03676	Renin-angiotensin system	0.0001049
Thiamine metabolism	0.003357	Thermogenesis	0.007097
Lipoic acid metabolism	0.003765	Glutamatergic synapse	0.002827
Carotenoid biosynthesis	0.04864	Insulin signaling pathway	0.04309
Sulfur metabolism	0.041	Prolactin signaling pathway	0.04754
Caprolactam degradation	0.0004116	Adipocytokine signaling pathway	0.01112
Phenylpropanoid biosynthesis	0.003113	Protein digestion and absorption	0.001335
Flavone and flavonol biosynthesis	0.03079	Huntington disease	0.001127
Biosynthesis of various secondary metabolites - part 3	0.01225	Bacterial invasion of epithelial cells	1.34E-05
Biosynthesis of various secondary metabolites - part 2	0.01182	Pertussis	0.002831
Biosynthesis of unsaturated fatty acids	0.04663	Bladder cancer	0.003073

Table S5 Identifying specific microbiota function responsing to mannitol consumption via PICRUSt

KEGG pathway	pvalue	KEGG pathway	pvalue
Metabolic pathways	0.005293	Phosphonate and phosphinate metabolism	0.03729
Carbon metabolism	0.0006981	Glucosinolate biosynthesis	0.006744
ABC transporters	0.00017	Insulin signaling pathway	0.02715
Two-component system	0.004289	Synthesis and degradation of ketone bodies	0.003594
Peptidoglycan biosynthesis	0.01388	Zeatin biosynthesis	6.18E-05
Alanine, aspartate and glutamate metabolism	0.02728	Longevity regulating pathway - multiple species	0.0002218
Mismatch repair	0.002362	Type II diabetes mellitus	0.0002218
Glycine, serine and threonine metabolism	0.00161	Biosynthesis of vancomycin group antibiotics	0.002754
Carbon fixation pathways in prokaryotes	0.02575	Ascorbate and aldarate metabolism	0.01339
Pentose phosphate pathway	0.0008918	Platinum drug resistance	0.0004888
Lysine biosynthesis	0.03088	Phenazine biosynthesis	0.02693
Thiamine metabolism	0.00163	Drug metabolism - cytochrome P450	0.04189
Carbon fixation in photosynthetic organisms	0.01629	Proximal tubule bicarbonate reclamation	0.00316
Cell cycle - Caulobacter	0.01922	Prolactin signaling pathway	0.0001121
One carbon pool by folate	0.04408	Adipocytokine signaling pathway	7.22E-05
Fatty acid metabolism	0.001377	Lipoic acid metabolism	0.01123
Fatty acid biosynthesis	4.74E-06	Amoebiasis	0.0006357
Photosynthesis	0.007632	Huntington disease	0.0001478
Bacterial chemotaxis	0.02422	Xylene degradation	7.79E-05
Vancomycin resistance	0.007284	Limonene and pinene degradation	0.0001469
Folate biosynthesis	0.008139	MAPK signaling pathway - fly	5.41E-05
Sulfur relay system	1.03E-06	Steroid hormone biosynthesis	1.88E-05
Sulfur metabolism	0.001871	Atrazine degradation	0.001122
C5-Branched dibasic acid metabolism	0.0001378	Biosynthesis of siderophore group nonribosomal peptides	0.0005789
RNA polymerase	0.0009791	Pertussis	0.006171
Cyanoamino acid metabolism	0.001457	Apoptosis	0.01894
Longevity regulating pathway - worm	0.0001705	Arachidonic acid metabolism	0.005294

Monobactam biosynthesis	0.0132	Chlorocyclohexane and chlorobenzene degradation	0.0004603
Plant-pathogen interaction	0.0003739	Carotenoid biosynthesis	0.000265
Vitamin B6 metabolism	0.03269	MAPK signaling pathway - yeast	0.0009477
Legionellosis	0.02951	Prion diseases	0.001122
Benzoate degradation	0.001284	Biosynthesis of unsaturated fatty acids	0.04137
Degradation of aromatic compounds	0.0008387	Steroid biosynthesis	0.007375
Glutamatergic synapse	5.36E-05	Ether lipid metabolism	0.02788
Glycosaminoglycan degradation	0.0001554	Linoleic acid metabolism	0.01772
Lipopolysaccharide biosynthesis	0.0005664	Ethylbenzene degradation	0.02113
Inositol phosphate metabolism	0.0001147	Renin-angiotensin system	6.86E-05
Peroxisome	6.00E-05	Caprolactam degradation	0.0002884
beta-Alanine metabolism	0.001537	Proteasome	0.005377
Tryptophan metabolism	0.01572	Meiosis - yeast	0.006111
PPAR signaling pathway	8.02E-05	Polycyclic aromatic hydrocarbon degradation	0.005651
Biosynthesis of ansamycins	0.01641	Chagas disease (American trypanosomiasis)	0.0036
Biosynthesis of various secondary metabolites - part 2	0.003756	Bacterial invasion of epithelial cells	0.00752
Secondary bile acid biosynthesis	0.03199	Bladder cancer	0.00501
MicroRNAs in cancer	0.03184	cAMP signaling pathway	0.005367
Phosphatidylinositol signaling system	0.005088	Basal transcription factors	0.004424

Table S6 Identifying specific microbiota function responsing to maltitol consumption via PICRUSt

KEGG pathway	pvalue	KEGG pathway	pvalue
Phenylpropanoid biosynthesis	0.0003839	Pyruvate metabolism	0.0009152
ABC transporters	4.81E-05	Glycine, serine and threonine metabolism	0.0001831
Degradation of aromatic compounds	0.03324	Tuberculosis	0.01919
Photosynthesis	4.15E-06	Vancomycin resistance	0.001448
Galactose metabolism	0.005876	Terpenoid backbone biosynthesis	0.01239
Starch and sucrose metabolism	0.03775	Bacterial secretion system	0.00379
C5-Branched dibasic acid metabolism	0.01665	Peroxisome	0.004046
Cyanoamino acid metabolism	0.002134	Antifolate resistance	9.48E-05
Pentose and glucuronate interconversions	0.008286	Plant-pathogen interaction	0.002037
Polyketide sugar unit biosynthesis	0.01049	Longevity regulating pathway - worm	0.0002029
Sulfur relay system	9.08E-05	Vitamin B6 metabolism	0.002155
Selenocompound metabolism	0.0003059	Biofilm formation - Vibrio cholerae	0.0003437
Methane metabolism	0.0272	Citrate cycle (TCA cycle)	0.002036
Streptomycin biosynthesis	0.004588	Glycosphingolipid biosynthesis - globo and isoglobo series	0.03151
Glutamatergic synapse	0.008654	Phenylalanine metabolism	0.04216
Thiamine metabolism	0.01333	Lysosome	0.03177
Peptidoglycan biosynthesis	0.04713	Lysine degradation	0.005072
Microbial metabolism in diverse environments	0.006231	Valine, leucine and isoleucine degradation	0.000128
Carbon metabolism	0.003195	Ubiquinone and other terpenoid-quinone biosynthesis	0.002876
RNA degradation	0.009059	Lipopolysaccharide biosynthesis	0.001415
One carbon pool by folate	0.001654	Flagellar assembly	0.005846
Butanoate metabolism	0.04161	Glycosaminoglycan degradation	0.004017
Propanoate metabolism	0.02564		

Table S7 Shared microbiota species in type 2

p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Rikenellaceae	p__Bacteroidota
p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Aerococcaceae	p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Butyricicoccaceae
p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae	p__Firmicutes
p__Actinobacteriota	p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales
p__Bacteroidota.c__Bacteroidia	p__Actinobacteriota.c__Actinobacteria.o__Micrococcales
p__Actinobacteriota.c__Coriobacteriia	p__Bacteroidota.c__Bacteroidia.o__Bacteroidales

Table S8 Shared stool metabolites in type 2

Val-Glu-Arg-Gln-Val	Glu-Lys-Arg
Thr-Ser-Arg-Ile-Ile	Ethephon
Thr-Glu-Lys-Asp-Glu	3-Cysteinylacetaminophen
Ser-Glu-Gln-Lys	(Aminomethyl)phosphonic acid
PGF2 dimethyl amide	TG(20:0/20:0/o-18:0)
Lys-Leu-Gln	Sandosapogenol
Lys-Gln-Ile	Promazine
Leu-Phe-Thr	Priverogenin A
JWH182	Masticadienonic acid
Ile-Glu-Tyr-Cys-Lys	Maslinic acid
Ile-Asn-Val	Lucidenic acid M
Hederagenin	L-Palmitoylcarnitine
Gly-Gly-Lys-Pro-Asn	Glycerol trilaurate
Endomorphin-1	Eplerenone
Asn-Gly-Arg-Ile-Leu	Cortol
Acetoxy-10-gingerol	5alpha-Androstan-17beta-ol-3-one sulfate
3,4,6-Trichlorocatechol	2-Octenoic acid
17-U-46619	1-Behenoyl-2-hydroxy-sn-glycero-3-phosphocholine
Hesperetin dihydrochalcone	(2S)-3-Hydroxypropane-1,2-diyl didecanoate
N6DTC	(+)-Ecdysterone
NI3C	Bis(4-Chlorophenyl)Acetic Acid
1,6-Dibromo-1,6-dideoxy-D-mannitol	5BNDB
Cyanate	2-Fluoromethamphetamine
Melperone	Bisphenol E
Leucomycin A1	Carnitine C15:1
Galegine	Carnitine C16:1
Ticarcillin	Cytarabine
Oleanolic acid	LPC(O-16:0/2:0)
N-Acetyl-L-Glutamic Acid	Metanephrine
N-Acetylhistamine	Estriol
N-3-Hydroxyoctanoyl-L-homoserine lactone	Goshonoside F7
Leukotriene C4 methyl ester	

Table S9 Shared global metabolites in type 2

Ser-Arg-Ile-Lys	Lasalocid
Leu-His-OH	Isovaleric acid
Ile-Met-Gln	DG(18:0/20:4(5Z,8Z,11Z,14Z)/0:0)[iso2]
Glu-Lys-Leu-Thr-His	3-methoxy Limaprost
Ala-Ala-Ile	1-(1Z-Octadecenyl)-2-(4Z,7Z,10Z,13Z,16Z,19Z-docosahexaenoyl)-sn-glycero-3-phosphocholine
trans-Zeatin	Pholedrine
Pyridine	N-Desmethyltapentadol
Mangiferdesmethylursanone	d-Benzphetamine
3-Phosphoglyceraldehyde	Isoproturon
1-Phenylicosane-1,3-dione	2-Acetylaminofluorene
Rimantadine	3-Hydroxydodecanoic acid
Palmyramide A	Bis(2-ethylhexyl) adipate
2-Methylpropyl formate	Carnitine C13:1
N-Methylene-ethenamine	1,3-Diaminopropane
Tuberonic acid	Ephedrine
PC(18:0/20:4(5Z,8Z,11Z,14Z))	PC(18:3/18:3)
N,N-Bis(2-hydroxyethyl)dodecanamide	