COMPOSITIONS AND METHODS FOR MODIFYING BILE ACIDS TO REGULATE LIPID AND STEROID METABOLISM

CROSS-REFERENCE TO RELATED APPLICATION

This application claims the benefit of U.S. Provisional Patent Application No. 63/288,980, filed on December 13, 2021, U.S. Provisional Patent Application No. 63/289,412, filed on December 14, 2021, U.S. Provisional Patent Application No. 63/355,381, filed on June 24, 2022, the entire contents of each of which are incorporated herein by reference.

BACKGROUND

Metabolic disorders represent a growing worldwide health challenge due to their dramatically increasing prevalence. Metabolic disorders are associated with alterations in the composition and function of the gut microbiota. The gut microbiota can interact with the host by the production of a diverse reservoir of metabolites, from exogenous dietary substrates or endogenous host compounds. Specific classes of microbiota-derived metabolites, notably bile acids, short-chain fatty acids, branched-chain amino acids, trimethylamine N-oxide, tryptophan and indole derivatives, have been implicated in the pathogenesis of metabolic disorders. Considerable efforts have been made to understand the mechanism of metabolic disorders. Presently, it remains unclear which bacterial strains regulate bile acids and salts in the gut and by what mechanism. There remains an unmet need to identify gut bacterial strains that regulate bile acids and salts and develop microbial therapeutics to treat metabolic disorders.

SUMMARY

Provided herein are methods and compositions for regulating bile salts or bile acids by administering compositions (e.g., the composition disclosed herein) to a subject. In certain embodiments, the methods and compositions are for the treatment or prevention of a metabolic disorder in a subject (e.g., a subject with a lipid metabolic disorder, such as hyperlipidemia, hypercholeresterolemia, acid lipase disease, Barth syndrome, Fabry disease, Farber's disease, Gaucher disease, Niemann-Pick disease, or Tay-Sachs disease; or a steroid metabolic disorder such as cytochrome p450 oxidoreductase deficiency, apparent mineralocorticoid excess, lipoid congenital adrenal hyperplasia, congenital bile acid

synthesis defect, 3-beta-hydroxysteroid dehydrogenase deficiency, aldosterone-producing adenoma, polyendocrinopathy, adrenal hyperplasia).

In some aspects, provided herein are methods for preventing or treating a metabolic disorder (e.g., a lipid metabolic disorder and/or a steroid metabolic disorder) in a subject, comprising administering to the subject a composition comprising a bacterial strain (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) that expresses a bile salt-regulating gene or bile acid-regulating gene.

Also provided herein are methods of treating or preventing a metabolic disorder in a subject by depleting the gut microbiota of the subject (e.g., by administering antibiotics to the subject) and administering a composition comprising a bacterial strain (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) that expresses a bile salt-regulating gene or bile acid-regulating gene.

Provided herein are bacterial strains (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) comprising a bile salt-regulating gene or bile acid-regulating gene, wherein the bacterial strain is genetically engineered to express the bile salt-regulating gene or bile acid-regulating gene. Similarly, provided herein are bacterial strains (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) that express a bile salt-regulating gene or bile acid-regulating gene encoded by an exogenous nucleic acid, e.g., a plasmid or other vector in which the bile salt-regulating gene or bile acid-regulating gene is operably coupled to a promoter that promotes expression (e.g., constitutively or inducibly) of the bile salt-regulating gene or bile acid-regulating gene in the bacterial strain.

Also provided herein are compositions (e.g., compositions comprising bacterial strains described herein and a pharmaceutically acceptable carrier; or compositions comprising a bacterial strain (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) that expresses a bile salt-regulating gene or bile acid-regulating gene (e.g., as described herein) and a pharmaceutically acceptable carrier).

The composition may be formulated for oral or rectal delivery. The composition may be self-administered. The composition may be a food or beverage product. In some embodiments, the food product is a dairy product (e.g., yogurt or kefir). In some embodiments, the composition comprises probiotics. In some embodiments, the composition comprises a fecal sample (e.g., a fecal sample from a fecal bank) comprising a

bacterial straina strain (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) that expresses a bile salt-regulating gene or bile acid-regulating gene.

Provided herein are methods of making a bacterial strain described herein, comprising : transforming a bacterial strain with a gene expression construct encoding a bile salt-regulating gene or bile acid-regulating gene operably coupled to a promoter that promotes expression (e.g., constitutively or inducibly) of the bile salt-regulating gene or bile acid-regulating gene in the bacterial strain. In certain embodiments, the method further comprises formulating the bacterial strain for administration to a subject, e.g., in a pharmaceutical composition or in a food or beverage product. In some embodiments, the method further comprises culturing the bacterial strain to allow expression of the bile salt-regulating gene or bile acid-regulating gene.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1A & Figure 1B show genomic comparison reveal distinct sub groups of *Turicibacter sanguinis*. A: Phylogenetic tree comparing full-length 16S rRNA sequences from noted *T. sanguinis* isolates. Circles indicate human-derived isolated, triangles indicate mouse-derived isolates, and squares indicate mouse-derived contaminating isolate. B: Full shotgun-assembled genome comparisons of *T. sanguinis* isolates listed in A.

Figure 2A & Figure 2B show *T. sanguinis* isolates differ in their bile-modifying abilities. A: Liquid chromatograms of individual *T. sanguinis* isolates grown for 24 hours in media with sub-inhibitory concentrations of five bile salts/acids: taurocholic acid (TCA), cholic acid (CA), glycochenodeoxycholic acid (GCDCA), chenodeoxycholic acid (CDCA), and deoxycholic acid (DCA). Shaded regions indicate expected retention time of each bile species. B: Relative amounts of remaining conjugated bile salts (taurichолic acid, taurochenodeoxycholic acid, glycocholic acid, glycochenodeoxycholic acid) after 24 growth with noted *T. sanguinis* isolate. Magenta=glycine-conjugated bile salts, blue=taurine-conjugated bile salts.

Figure 3A-Figure 3D show *T. sanguinis* isolates differ in their genetic capacity to modify bile species. A: Liquid chromatograms of media after 24 hour cultures of *E. coli* expressing individual predicted bile salt hydrolases (BSH) from each sequence grouping and isolate and grown in with TCA and TCDCA. Control is *E. coli* with same expression vector but expressing non-bile modifying gene. B: same as A, but with GCA and GCDCA instead of taurine-conjugated bile salts. C. Remaining amounts of TCA, TCDCA, GCA,

and GCDCA after 24 hour growths of *E. coli* expressing noted BSH homologs. D: Phylogenetic tree of each predicted BSH gene from *T. sanguinis* isolates, with bile salt specificity noted in boxes. The study did not detect bile salt hydrolase activity in sequences without boxes.

Figures 4A-Figure 4D show *T. sanguinis* BSH expression is sufficient to alter host lipidome and health-associated lipid markers. A: Heatmap of plasma lipid species significantly altered by expression of at least one *T. sanguinis* BSH in *Bacteroides thetaiotaomicron*. Colors on left correspond to lipid class, cyan-magenta colorscale represents Z-score. B. Relative white adipose tissue weight of mice monocolonized with BSH-expression *B. thetatiotaomicron*. C. Relative combined plasma triglycerides (TG) of mice monocolonized with BSH-expression *B. thetatiotaomicron.* D. Relative cholesterol esters (CE) of mice monocolonized with BSH-expression *B. thetatiotaomicron.* All values normalized to sex-matched littermates, *= $p<0.05$ two-tailed t-test. BSH3 corresponds to BSH-IV-MOL361; BSH4 corresponds to BSH-I-MOL361; BSH5 corresponds to BSH-III-1E2; BSH7 corresponds to BSH-II-H121

Figure 5A-Figure 5B show *T. sanguinis* isolates differ in their effects on host lipid biology and bile acids. A: Sex and littermatched relative abdominal fat pad mass from mice monocolonized with individual *T. sanguinis* isolates. B: top: Example image of adipose tissue histology section. bottom: Sex and litter matched relative adipocyte size of mice monocolonized with individual *T. sanguinis* isolates.

Figure 6 shows levels of circulating serum bile acids and cholesterol in mice monocolonzed by individual T. sanguinis isolates. #=$p<0.1$, *=$p<0.05$.

Figure 7 shows genomic comparisons reveal distinct subgroups of *Turicibacter*. **a**, Phylogenetic tree comparing full-length 16S rRNA gene sequences from noted *Turicibacter* isolates. Circles indicate human-derived isolates, triangles indicate mouse-derived isolates, and square indicates a mouse-derived contaminating isolate. **b**, Association between guanine-cytosine % (GC%) and calculated genome size in megabases (Mb) for shotgun-assembled genomes of *Turicibacter* isolates from **a**. **c**, Full genome sequence comparisons across *Turicibacter* strains. Position of predicted bile-modification gene homologs are noted outside of rings, with the color of the gene name denoting the genome family that gene is found in. Each ring represents sequence blocks in one genome. **d**, Average nucleotide identity (ANI) between noted *Turicibacter* genomes. Number denotes ANI, white to blue scale represents 100%-75% ANI scale.

Figure 8 shows *Turicibacter* colonization alters host lipids in a strain-dependent manner. **a**, Heatmap of relative abundance of serum lipids from gnotobiotic mice monocolonized with noted *Turicibacter* strains. Heatmap values represent mean abundance of each detected lipid species from labeled lipid categories scaled across all the means of that individual lipid species. Black ($p<0.05$) and grey ($p<0.1$) rectangles indicate statistically significant differences of that metabolite between i) GF and MOL361 monocolonized mice, ii) CONV and MOL361 monocolonized mice, and iii) between mice colonized by different *Turicibacter* strains. **b**, Serum cholesterol concentrations of mice colonized by noted *Turicibacter* strains. **c**, Sex and litter-matched relative epididymal/gonadal white adipose tissue (e/g WAT) mass of mice monocolonized with noted *Turicibacter* strains. Shapes indicate value for individual mouse, dotted bar represents combined ANOVA statistic for each group versus the experimental mean. Metabolite and cholesterol analysis n=6-10. WAT analysis n=6-26, Mann-Whitney test for MOL361-GF and MOL361-CONV comparisons, Kruskal-Wallis for intra-*Turicibacter* comparison. *$p<0.05$, ***$p<0.0005$.

Figure 9 shows *Turicibacter* colonization alters circulating host bile species in a strain-specific manner. **a-c**,: Serum concentrations of **a-d**) primary unconjugated bile acids, **e-f**) secondary unconjugated bile acids, or **g-l**) primary conjugated bile acids, Serum levels of individual bile species from mice colonized by noted *Turicibacter* strains. Points indicate log-transformed value for individual mouse with shapes and colors matching **Fig. 1**, error bars represent mean +/- SEM. Kruskal-Wallis test across all noted colonizations with Dunn's multiple comparisons to GF for **a-f.** Kruskal-Wallis test between noted *Turicibacter* strains and multiple comparisons to H121 for **g-l**. Mann-Whitney test used to compare GF and MOL361 in g-l, and p-values are noted above GF data points. n=6-10 for each group. Dotted bar represents ANOVA statistic for each group versus the combined experimental mean. *$p<0.05$, **$p<0.005$, ***$p<0.0005$.

Figure 10 shows *Turicibacter* isolates differ in their bile-modifying abilities. a, Schematic for types of bile transformations found to be performed by *Turicibacter* isolates. b, inset: 16S rRNA-based phylogenic tree from Fig. 7a. Liquid chromatograms of individual *Turicibacter* isolates grown for 24 hours in media with sub-inhibitory concentrations of five bile acids: taurocholic acid (TCA), cholic acid (CA), glycochenodeoxycholic acid (GCDCA), chenodeoxycholic acid (CDCA), and deoxycholic acid (DCA). Shaded regions indicate expected retention time of each bile species. c, Percent

remaining (compared to cultures at time=0) of conjugated bile acids (TCA, taurochenodeoxycholic acid [TCDCA], glycocholic acid [GCA], GCDCA) after 24 growth with noted *Turicibacter* isolate. Yellow=glycine-conjugated bile acids, orange=taurine-conjugated bile acids. n=4 independent cultures. Values not shown were below 0.1% remaining. Statistical analysis performed by one sample t-test, annotations of legend denotes strains with significant difference from 100% remaining for each bile acid.

Figure 11 shows *Turicibacter* isolates differ in their genetic capacity to modify bile species. **a**, Phylogenetic tree of amino acid sequences for each predicted bile salt hydrolase (BSH) sequence from *Turicibacter* strains, with observed bile species specificity noted in boxes. We did not detect bile salt hydrolase activity in sequences without boxes, representing groups V-VIII. **b**, Presence or absence of sequence homologs with potential BSH activity in *Turicibacter* strains. **c**, Liquid chromatograms of media after 24 hour cultures of *E. coli* expressing individual predicted *bsh* genes from each sequence grouping and grown in with TCA and TCDCA. Control is *E. coli* with same expression vector but expressing non-bile-modifying gene. **d**, same as **c**, but with GCA and GCDCA instead of tauro- bile acids. **e**, Quantification of percent remaining (compared to media controls) of conjugated bile acid (TCA, TCDCA, GCA, GCDCA) after 24h growth with *E. coli* expressing the noted *Turicibacter bsh* gene. n=3 independent cultures, *$p<0.05$, **$p<0.005$, ***$p<0.0005$ using one sample t-test comparison with 100% remaining. BSH nomenclature indicates homolog group (*e.g.* III) and isolate of origin (*e.g.* MOL361).

Figure 12 shows *Turicibacter bsh* expression is sufficient to alter host lipidome and health-associated lipid markers**.** **a**, Percent remaining of noted bile acids after 24 hour growth with *Bacteroides thetaiotaomicron* expressing noted *bsh* genes. n=4 cultures per strain. **b**, Same as **a**, but with 48 hour growth with noted *B. thetaiotaomicron* strains. n=3 cultures strain^{-1}. For **a** and **b**, points represent individual comparison with media control, legend annotations denote strains with statistical significance for each bile acid using one sample t-test comparison with 100% remaining. **c**, Quantification of colonic bile acids (BA) from mice colonized with *bsh*-expressing *B. thetaiotaomicron.* Values are normalized to sex-matched littermates colonized with wild-type *B. thetatiotaomicron.* Statistical analysis was performed with Kruskal-Wallis test with Dunn's multiple comparisons test. n=3-4. **d**, Heatmap of circulating lipid species significantly altered by expression of at least one *Turicibacter bsh* in *B. thetaiotaomicron.* Colors on left correspond to lipid class, cyan-magenta color scale represents Z-score, each column represents one animal. **e-i**, Relative

combined circulating concentrations of **e**, triglycerides (TG), **f**, cholesterol esters (CE), **g**, diacylglycerides (DG), **h**, phosphotidylglycines (PG), or **i**, phosphotidylserines (PS) of mice monocolonized with *bsh*-expressing *B. thetatiotaomicron.* **j**, Relative white adipose tissue weight of mice monocolonized with *bsh*-expressing *B. thetatiotaomicron.* All values normalized to sex-matched littermates, animal n=4-6 colonization^{-1}, statistical analysis performed by Welch's ANOVA with Dunnet's multiple comparisons to GF, dotted bar in **c-j** represents ANOVA statistic for each group versus the combined experimental mean. *p<0.05, **p<0.005, ***p<0.0005.

Figure 13 shows strain-dependent variation in colonization and adipocyte size. **a-e**, Representative images of adipose tissue from *Turicibacter* monocolonized mice. **f**, Sex- and litter- matched relative adipocyte area of mice monocolonized with individual *Turicibacter* strains. Each point represents mean of 10 images of adipocyte area per animal. **g, h**, Colony-forming units (CFU) equivalents per gram of contents for distal small intestine (**g**) or proximal colon **(h).** Each dot represents sample from one animal, per colonization n=10-15 for qPCR, n=10-14 for adipocyte area calculation. Statistics for adipocyte area performed by Welch's ANOVA with Dunnet's multiple comparisons, dotted bar represents ANOVA statistic for each group versus the combined experimental mean.

Figure 14 shows host effects of *Turicibacter* colonization varies with sex. **a-c**, Heatmap of mean relative **a**) bile species, **b**) sterols, or **c**) lipids. Column labels represent colonization state and sex, blue=male, red=female. n=3-6 group^{-1}, except female T129 (n=1).

Figure 15 shows summary table of bile transformations performed by *Turicibacter* isolates. Table indicating presence/absence of noted bile species after growth in mixture of bile acids described in **Fig. 10b**.

Figure 16 shows some strains of *Turicibacter* encode a functional 7alpha-HSDH gene. **a**, Table depicting amino acid similarity and sequence coverage between closest predicted 7alpha-HSDH homolog in noted isolate genome and 7alpha-HSDH gene from *Clostridium absonum*. **b**, Chromatograms of cholic acid (CA) or cholic acid with 2 hydrogens removed (CA-2H) from *E. coli* cultures expressing the MOL361 HSDH homolog (7alpha-HSDH) or non-bile modifying gene sequence in the same plasmid (cell control). Chromatograms from independent triplicate cultures are shown, dotted boxes indicate each bile species. **c**, Quantification of CA/CA-2H ratios determined from reconstructed areas under the curve in **b**. Statistical comparison performed with Welch's t-

test, n=3 cultures, bars indicate mean +/- SEM. **d**, Same as **b**, but with CDCA instead of CA. **e**, same as **b**, but with DCA instead of CA. **d** and **e** triplicate chromatograms are stacked on the same axis.

Figure 17 shows bile transformations performed by *B. thetaiotaomicron* expressing *Turicibacter bsh* genes. Table indicating presence/absence of noted bile species after growth in mixture of bile acids described in **Fig. 11c-e**.

Figure 18 shows expressing *bsh* genes from *Turicibacter* does not impart significant *in vitro* growth defect of *B. thetaiotaomicron*. OD_{600} readings of noted *B. thetaiotaomicron* strains in BHI-S medium. Each point represents mean +/- SEM for 6 independent cultures.

Figure 19 shows sex differences in lipidomic response to *Turicibacter bsh* expression in *B. thetaiotaomicron*. Similar to **Fig. 12d**, but animal lipidome analysis separated into **a**) males and **b**) females. Note that lipid species presented were found to be significantly altered by expression of at least one *bsh* in males and females combined (i.e. all lipid species shown across the three analyses are the same). Each column represents one animal.

Figure 20 shows *Turicibacter bsh* expression by *B. thetaiotaomicron* is sufficient to drive broad scale changes in circulating host lipids in male and female mice. Related to **Fig. 12e-j**, circulating concentrations of specific lipid categories in mice colonized by *B. thetaiotaomicron* expressing the noted *Turicibacter bsh* homologs. Each point represents one animal, red points indicate female, blue represent male. n=4-5 per colonization, error bars represent mean +/- SEM. Statistical comparison done with Welch's ANOVA with Dunnet's multiple comparisons, dotted bar represents combined ANOVA statistic for each group versus the experimental mean, *$p<0.05$.

Figure 21 shows *Turicibacter* strains MOL361 and 1E2 can deconjugate at least six taurine-conjugated bile acids. Chromatograms (left) and unconjugated/conjugated bile acid ratios (right) of *Turicibacter* MOL361 or 1E2 grown for 24 hours in YCFA + 0.5mM of individual taurine-conjugated bile acids: **a**, TCA; **b**, TCDCA; **c**, tauroursodeoxycholic acid (TUDCA); **d**, taurolithocholic acid (TLCA); **e**, taurohyodeoxycholic acid (THDCA); **f**, taurodeoxycholic acid (TDCA). Chromatograms are concatenated reconstructed chromatograms for conjugated and unconjugated bile acid. Each trace and each point represents one biological replicate, n=3 cultures. Statistics were performed by Mann-

Whitney test, # = p≤0.1 (Note: this p-value is the minimum for this test and our experimental parameters).

Figure 22 shows *bsh* expression does not alter *B. thetaiotaomicron* colonization of the murine gut. CFU/mL quantifications of the noted *B. thetaiotaomicron* strains in the **a,** distal small intestine; **b,** cecum; and **c,** proximal colon of gnotobiotic mice.

Figure 23 shows *Turicibacter* colonization and *bsh* expression induce similar gene expression patterns in the liver. qRT-PCR analysis of liver transcript levels of **a,** Fxr; **b,** Cyp7a1; and **c,** G6pase after colonization with the noted *Turicibacter* strains of *B. thetaiotaomicron* expressing the noted *bsh* gene. Data are displayed as fold change relative to appropriate control (GF for *Turicibacter* colonizations, *Bt*-WT for *bsh* colonizations). Each point represent data from a single animal, statistics performed with Kruskal-Wallis test with Dunn's multiple comparisons. Dotted horizontal line represents total ANOVA statistic for that comparison, *=p<0.05.

DETAILED DESCRIPTION

Provided herein are methods and compositions for regulating bile salts and/or bile acids by administering compositions provided herein.

In some aspects, provided herein are methods for preventing or treating a metabolic disorder (e.g., a lipid metabolic disorder and/or a steroid metabolic disorder) in a subject, comprising administering to the subject a composition comprising a bacterial strain (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) that expresses a bile salt-regulating gene or bile acid-regulating gene.

Also provided herein are methods of treating or preventing a metabolic disorder in a subject by depleting the gut microbiota of the subject (e.g., by administering antibiotics to the subject) and administering a composition comprising a bacterial strain (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) that expresses a bile salt-regulating gene or bile acid-regulating gene.

Provided herein are bacterial strains (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) comprising a bile salt-regulating gene or bile acid-regulating gene, wherein the bacterial strain is genetically engineered to express the bile salt-regulating gene or bile acid-regulating gene. Similarly, provided herein are bacterial strains (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) that express a bile salt-regulating gene or bile acid-regulating gene encoded by an exogenous

nucleic acid, e.g., a plasmid or other vector in which the bile salt-regulating gene or bile acid-regulating gene is operably coupled to a promoter that promotes expression (e.g., constitutively or inducibly) of the bile salt-regulating gene or bile acid-regulating gene in the bacterial strain.

Also provided herein are compositions (e.g., compositions comprising bacterial strains described herein and a pharmaceutically acceptable carrier; or compositions comprising a bacterial strain (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) that expresses a bile salt-regulating gene or bile acid-regulating gene (e.g., as described herein) and a pharmaceutically acceptable carrier).

Provided herein are methods of making a bacterial strain described herein, comprising : transforming a bacterial strain with a gene expression construct encoding a bile salt-regulating gene or bile acid-regulating gene operably coupled to a promoter that promotes expression (e.g., constitutively or inducibly) of the bile salt-regulating gene or bile acid-regulating gene in the bacterial strain. In certain embodiments, the method further comprises formulating the bacterial strain for administration to a subject, e.g., in a pharmaceutical composition or in a food or beverage product. In some embodiments, the method further comprises culturing the bacterial strain to allow expression of the bile salt-regulating gene or bile acid-regulating gene.

In certain embodiments, the methods and compositions are for the treatment or prevention of a metabolic disorder in a subject (e.g., a subject with a lipid metabolic disorder, such as hyperlipidemia, hypercholeresterolemia, acid lipase disease, Barth syndrome, Fabry disease, Farber's disease, Gaucher disease, Niemann-Pick disease, or Tay-Sachs disease; or a steroid metabolic disorder such as cytochrome p450 oxidoreductase deficiency, apparent mineralocorticoid excess, lipoid congenital adrenal hyperplasia, congenital bile acid synthesis defect, 3-beta-hydroxysteroid dehydrogenase deficiency, aldosterone-producing adenoma, polyendocrinopathy, adrenal hyperplasia).

Definitions

As used herein in the specification, "*a*" or "*an*" may mean one or more. As used herein in the claim(s), when used in conjunction with the word "comprising", the words "a" or "an" may mean one or more than one. As used herein "another" may mean at least a second or more.

The phrase "*pharmaceutically-acceptable carrier*" as used herein means a pharmaceutically-acceptable material, composition or vehicle, such as a liquid or solid filler, diluent, excipient, solvent or encapsulating material. Each carrier must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not injurious to the subject. Some examples of materials which can serve as pharmaceutically-acceptable carriers include: (1) sugars, such as lactose, glucose and sucrose; (2) starches, such as corn starch and potato starch; (3) cellulose, and its derivatives, such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; (4) powdered tragacanth; (5) malt; (6) gelatin; (7) talc; (8) excipients, such as cocoa butter and suppository waxes; (9) oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; (10) glycols, such as propylene glycol; (11) polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol; (12) esters, such as ethyl oleate and ethyl laurate; (13) agar; (14) buffering agents, such as magnesium hydroxide and aluminum hydroxide; (15) alginic acid; (16) pyrogen-free water; (17) isotonic saline; (18) Ringer's solution; (19) ethyl alcohol; (20) phosphate buffer solutions; and (21) other non-toxic compatible substances employed in pharmaceutical formulations.

The term "*preventing*" is art-recognized, and when used in relation to a condition, such as a local recurrence, is well understood in the art, and includes administration of a composition which reduces the frequency of, or delays the onset of, symptoms of a medical condition in a subject relative to a subject which does not receive the composition.

The term "*prophylactic*" or "*therapeutic*" treatment is art-recognized and includes administration to the host of one or more of the subject compositions. If it is administered prior to clinical manifestation of the unwanted condition (e.g., disease or other unwanted state of the host animal) then the treatment is prophylactic (i.e., it protects the host against developing the unwanted condition), whereas if it is administered after manifestation of the unwanted condition, the treatment is therapeutic (i.e., it is intended to diminish, ameliorate, or stabilize the existing unwanted condition or side effects thereof).

The term "*subject*" refers to a mammal, including, but not limited to, a human or non-human mammal, such as a bovine, equine, canine, ovine, or feline.

A "*therapeutically effective amount*" of a compound with respect to the subject method of treatment refers to an amount of the compound(s) in a preparation which, when administered as part of a desired dosage regimen (to a mammal, preferably a human) alleviates a symptom, ameliorates a condition, or slows the onset of disease conditions

according to clinically acceptable standards for the disorder or condition to be treated or the cosmetic purpose, e.g., at a reasonable benefit/risk ratio applicable to any medical treatment.

As used herein, the term "*treating*" or "*treatment*" includes reversing, reducing, or arresting the symptoms, clinical signs, and underlying pathology of a condition in a manner to improve or stabilize a subject's condition.

As used herein, the terms "*modulate*" or "*modulation*," or "*regulate*" or "*regulation*" and "differentially regulated" can refer to both up regulation (i.e., activation or stimulation, e.g., by agonizing or potentiating) and down regulation (i.e., inhibition or suppression, e.g., by antagonizing, decreasing or inhibiting), unless otherwise specified or clear from the context of a specific usage.

Therapeutic Methods

The disclosure herein, relates, in part, to the discovery that different strains of *Turicibacter sanguinis* differentially deconjugate and dehydrogenate bile acids and differentially affect host metabolites, including fat tissue mass, lipid composition, bile acids, and tryptophan-related metabolites. Whole genomes of different strains of *Turicibacter* were sequenced and genes were identified that are potentially responsible for different bile acid modifications (e.g., genes encoding bile salt hydrolase or 7-alpha hydroxysteroid dehydrogenase). Additionally, strains of *Escherichia coli* and *Bacteroides thetaiotaomicron* were developed to express *Turicibacter sanguinis* bile-modifying genes (e.g., genes encoding bile salt hydrolase or -alpha hydroxysteroid dehydrogenase).

In some aspects, provided herein are methods of preventing or treating a metabolic disorder (e.g., a lipid metabolic disorder and/or a steroid metabolic disorder), comprising administering to the subject a composition comprising a bacterial strain (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) that that expresses a bile salt-regulating gene or bile acid-regulating gene.

Also provided herein are methods of treating or preventing a metabolic disorder in a subject by depleting the gut microbiota of the subject and administering a composition comprising a bacterial strain (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) that expresses a bile salt-regulating gene or bile acid-regulating gene.

In other aspects, provided herein are methods of treating or preventing a metabolic disorder in a subject by depleting the gut microbiota of the subject and administering a composition comprising a bacterial strain (e.g., *Turicibacter sanguinis, Escherichia coli,* or

Bacteroides thetaiotaomicron) that expresses a bile salt-regulating gene or bile acid-regulating gene.

In some aspects, the methods comprise depleting the gut microbiota of the subject prior to administration with a composition described herein (e.g., by administering antibiotics to the subject).

In some embodiments, the bacterial strain expresses a bile salt-regulating gene or bile acid-regulating gene encoded by an exogenous nucleic acid, e.g., a plasmid or other vector in which the bile salt-regulating gene or bile acid-regulating gene is operably coupled to a promoter that promotes expression (e.g., constitutively or inducibly) of the bile salt-regulating gene or bile acid-regulating gene in the bacterial strain.

Provided herein are methods of making a bacterial strain described herein, comprising : transforming a bacterial strain with a gene expression construct encoding a bile salt-regulating gene or bile acid-regulating gene operably coupled to a promoter that promotes expression (e.g., constitutively or inducibly) of the bile salt-regulating gene or bile acid-regulating gene in the bacterial strain. In certain embodiments, the method further comprises formulating the bacterial strain for administration to a subject, e.g., in a pharmaceutical composition or in a food or beverage product. In some embodiments, the method further comprises culturing the bacterial strain to allow expression of the bile salt-regulating gene or bile acid-regulating gene.In some embodiments, the bacterial strain (e.g., *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*) regulates the bile salt by glycine conjugation or taurine conjugation. In some embodiments, the bile salt-regulating gene encodes a bile salt hydrolase (BSH), such as any one of the bile salt hydrolases shown in Table 1. In some embodiments, the BSH is encoded by a nucleic acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to any one of the nucleic acid sequences in Table 1.

Table 1: Exemplary Bile Salt Hydrolases (BSH)

BSH Type	Bacterial Strain	Nucleic Acid Sequence
BSH Group I	*Turicibacter sanguinis* MOL361	ATGTGTACAGGACTTAGCTTAGTTACAAAAGATAATAAGCATTTATTTGGACGAAATTTAGA TGTACCCGCTACATATGGACAAGCTGTTCATATTGTTCCAAGAAATTATGATTGGTTCAATAT TGTGAGTGATGAAACATATACGTCAAAGTATGCTTGTATTGGGATGGGAATTGTTGTGGATC GTCTTCCCCTTCTTTTTGATGCAGTTAATGAAAAAGGATTAGCAGGTGCCGGGTTAAATTTTA CGCATTTTGCTAAGTTTAACGAAAAAAGCTGTTGATGGAAAAACGAATATTTCAGGTTCAACT TTCTTATACTGGGCATTAAGTAATTTCTCAAATTTAGATGAATTAAAAGAAGCCTTAAAACA GTTAATTATTACGAATATTCCAGTTAAAGAAGGGCTTCCTGTTGCAGGACTTCACTGGATGTT TACAGATTTAAGTGGAAAAAGTATTGTCATTGAGTACATGGAAGATGGAATGCACGTATACG ACAATCCAGTAGGAGCCTTAACAAATGATCCAACTTTCCCTTGGCATTTAACAAATCTATGC CAATATGTAACATTAGATACAAAAACTCCAGCACCAAAACAATTTGGAGAATATGTTGCTAA ACCATTTGGTCATGGGCTTAATATGTGTGGAAATCCCAGGAGATGCTTCTCCAGCTGCACGAT TTGTTCGAACAGTCTATTTCCGTGATACAGTTGTCGAAGCAGATGATGAAGTCAGTGGTGTTT CAGCATTCTTCCAAGTGCTAACAGGTGTTACCGTCATAAAAGGAAGCGAAATTGATCCAAAT GGAGATATGAATTACACCGTCTATAAATCTTGTATGTGCCAAGAATCAGGAACATACTACTA CACAGATTATAAAAACCGTCGTATTAGTGCCGTTTGCTTATCAAAAGCCGACCTAGATGGAA AAGAAATCATCAGCTTTGAATATCAAGGTAAACAAGATATTTTATTCCAAAACTAA

BSH Group II	*Turicibacter sanguinis* H121	ATGTGTACAGGGTTAAGTTTAACTACTAAAGATGGAAAACACTTCTTTGGT AGAAATTTAGATGTTCCCGCTTCATACGGACAATCTGTTCATATCATTCCAA GAAATTTCAATTGGCTAAATGTCGTAAATGGTGAAACATTAGCTTCTAAAT ATGCGTGTATTGGAATGGGAATCGTTGTAGATAATCATCCACTTCTTTTTGA TGCAGTCAATGAAAAAGGATTAGCTGGTGGTGGATTAAACTTTACGCACTT TGCTAAATTTAATGAAAATGCCATCGATGGAAAAATAAATATCTCCGCATC TGACTTTGTATACTGGGCACTTAGTAACTTTGCGGATTTTAAATGAGTTACGT CAAGCGTTAGAAAATTTAGTACTGACTAATATTCCATTTGAGCATGAGCTT CCAGTTGCAGGTCTTCACTGGATGTTCACTGATTTATCTGGGCGTAGTATCG TGATTGAAAATATGGCCGACGGTATGCATATTCATGAAAATCCAGTTGGTG TTTTAACGAATGACCCAACTTTTGATTGGCACTTAACTAATTTAAGACAGTA TGTTACCCTTGAAAAAGCAACACCGGCTCCAAAACAAATGGGAGATTTACT GCTTCATCCATATGGTCATGGTTTAGGAATGTGTGGAATTCCAGGAGATGC TTCACCTGCTGCACGATTTGTTAGAACGGTCTTCTTTAGAGATTCAATCGTT GAAGCGAATGATGAAATCAGTGGCGTTACTGCTTTCCTCAACGTGTTAACA GGGGTAACAGTTATTAAAGGGTCTGAAGTTGATCCCGATGGCTCAATGAAT TATACCGTGTATAAATCAGCGATGTGTCAAGAAAGTGGAACTTACTATTAT ACCGATTATTACAATCGACGTATCAATGCCGTTAAATTATCAAATGCTAAT TTAGACTCAAAAGAAATTACAAGTTTCCCTTATCAAGGAGAGCAAGATATC TTGTTCCAAAACTAA

BSH Group III	*Turicibacter sanguinis* 1E2	ATGTGCACAGGATTATGCTTATCTACAAAGGATGGAAAACATCTTTTTGGA CGAAACCTTGATGTTCCTGCTTCTTATAACCAGGCCGTTCAAATTGTTCCAA GGAATTTTAAGTGGCTAAACGTTGCGACCCAAGAAACAATCACCTCTAAAT ACGCTTGCATAGCCATGGGAATCGTCATTGACAATCACCCTCTTCTCTTTGA CGGGGTTAATGAAAAGGGATTAGCTGGTGGAGGATTAAATTTCACACACTT CGCAAAATTCTCTTCAACTGCTGTAAAAGATAAAATCTCTTTATCAGCTTCT GATTTCGTCTATTGGGTGCTGAGTACGTTTTCATCTTTAAGCGAGTTAAAAG AGACCTTACCCTCTGTTATCTTAACAAGTATTCCCTTCAAACCGGATTTACC AGTTGCGGGATTACATTGGATTTTTACAGATAAAACAGGTGAAAGTATTGT TATTGAATATATGGAAGACGGAATGCATATCCACGATAATCCAGTCGGTGT TCTAACAAACGACCCAACCTTCGACTGGCAATTAACAAATTTAAGCCAATA TGTAACCCTTTCTTGTAAAACTCCACAACCAGAAGAAATGGGGAATCTACT CGTTAAACCATTTGGTCATGGACTTGGCATGTGCGGAATTCCAGGAGACGG TTCTCCCGCTGCAAGATTTGTCCGCACCGTCTTTTTCCGTGATGCCGTTGTT GGAGCCGACGATGAAATAAGTGGGGTTACAGCCTTCTTTAATGTTCTATCA GAAGTTACGGTGATGAAAGGATCTGAAATTGACCCCGATGGATCCATGAA CTTTACCGTTTATAAATCAGCCATGTGTCAAGAATCTCAAACTTATTACTAC ACAGATTACTATAACCGTCGAATCAACGCGGTTAAATTAACACCTGATACA ATGAATGCTGACCACATTACAACGTTCCCTTACCTAGGAAAACAAGATATT TGTTATCAAAATTAA

BSH Group IV	*Turicibacter sanguinis* MOL361	ATGTGTACAGCATTATCATTAACAGCAAAAGATGGTTCACATTTATTCGGT AGAAATATGGATATTGAATATTCATTTAATCAATCAATTTTATTAACACCAC GTCGTTTTGATTATAAAAATCGTGCAACAGGTGAAATGAATCAAACAAAGT ATGCGATTATTGGAATGGGAACCATTATTGATGAACATCCATGTTATGCAG AGCTTTTTAATGAAAAAGGATTAGCGGCAGGATTAAACTTCCCTAACT ACGCACACTGGGATGAAAAAGCAATCGAAGGAAAAACAAATATCCCTCCT TATGATTTAGTTTTATGGGTCACTTCAAATTTTGAAACAGTTAAAGAAGTA AAAGAAGCTTTAAAAGATGTTGTTTTAGTTGATGTTCCAGTCAATGAACAA ACTCCAATTGCTCCTTTTACACTGGATGATTTGTGATAAAACAGGTGAAAGT ATCGTTGTAGAAAAAACAGTAAATGGTTTAAGTGTTATGGATAATAAAGTA GGAGTTTTAACGAATGCGCCAACTTTTGATTGGCATTTAACAAACTTAACT CAATACATGGGATTAACGTCGACACAACCAAAAGATATAACACTCGGAGA ACAAGAATTACATCCATTAGGGCAAGGGCTTGGTGCTTTCTCATTACCAGG AGATTATTCATCACCATCACGATTTGTTAAAGCTGCTTTCTTACGTAATAAT ATCGATTATGCAAATGTTAATTACTCTGGAATCAGTGAATTCTTCCACATCT TAAACGGAGTTGCAATGGTTCGAGGATCAGTCGTTACTCCTCAACATTTAA ATGACATTACGTTATATACATCTTGTATGGATCAAGAACGTGGAATTTATT ATTACAATACTTATACAAATCATACGATTTCATCTATTAATATGCATAATGA AGATTTAGACGCAAAAGAAATTAAATCATTTAAATTTAATGATGAATTTGC TGTAAATTTACAAAATTAA

BSH Group V	*Turicibacter sanguinis* MOL361	ATGTGTACAGCTATTACATTAAAGACACAAGATGGATTGCATGCATTAGGG
		AGAAATTTAGATATTGTGGCTTTATTAGATGTTGCTGTTATTTTGATTCCGA
		GGTCATATGCATTTACTCATACTATCATGAGTCTAAAAAAGAAAAATAAAT
		ACGCGATGGTTGGAATGTCTACGACGTTTGAAAATCATGTCTTATTAGTTG
		ACGGGATGAATGAAAAGGGATTAGCTTGCGCTGTATTAGAGTTACCTAAAT
		ATGCTTCATGGAGTAAAGCATTGGATAAAGATAAAATAAATATGGCTCCTT
		ATGATTTTGTTTATTGGATTTTTAGCAAATTTTCAATCTCTTGAGGAAGTAAA
		AGACGGATTAAAAAATGTAAATCTAGTTAATGAGTCGCTTGAAGGGAAAG
		AGGTATCAGTAGATGTTCATTGGATTGTAACTGATCGTACAGGACAGTCTA
		TTGTAATAGAAAAAACGAAGGGGAATTTTCGAATTTATAATAATAAGGTGG
		GAGTTTTAACTAATGCTCCAACATTCGATTGGCATCTCATAAATTTAAATCG
		GTATATGAATATACAAGTGACGAATCCGCATAAGGTGAAGTGGGGACATC
		AGGAGTTAAGTTTTGACTCAGAAGGTTTTGGGGGAATCGGACTACCAGGAG
		ATGTTTCATCTTCATCTCGTTTTGTAAAAGCAGCTTTTCTAAGAAATCATAT
		TAGAGTAGAAAAAGGAGAAGATGCTTTAATAACAAGTACTTTTCATATTTT
		AAGTAATGTGGCTGTTATCAAAGGAACTGCTGTTACTTGCCACCAACAATA
		TTTGAAAACGCAGTGTACTAGTTGTATGTGTTTAGAGACAGGCGTTTATTA
		CTATAACACTTATAATAATCAAATTAATGCTATTCATTTATTTGACGAG
		AATTTAGATGCCTCTGAAGTTAAAGTGTTTCCTTATCAAGATAAACTGGTA
		GTACAGAAACAAAATTAA

BSH Group VI	*Turicibacter sanguinis* H121	GTGTGTACAGCCATTACATTAAAAACAAGCGAAAATCATCATCTTGTTGGA CGGAATTTTGATATTCACCCAATGAATGATTTATCAGTTGCTTTAGTTCCAC GAGAATTTGAATATGTAAATCGTGTGACGAATGAAGAAATGAAAACGAAA TATGCAGTTTTAGGAATGGGATTATTTATGAAAATCATATTCTTTTTTGTG ATGGAGTAAATGAAAAAGGATTATCTTGTCTGATGTTACAATTATCTAAGT TTTCTACTTGGAGTCATAAAATCAGGAAGGATAAGGTCAATATAGCCCCAT ATGATGTAGCTTTTTGGGTTTTATCTAATTTTTTCAACGATTTCTGAATTAAT GGAAGGTCTTAAACAGTTAAATATTGTGGCTCTTCCTGATGATCAAACGGC ATTATCGACAGAAATTCATTGGCTTGTTAGTGATACGAGTGGTCAATCGAT CGTCATTGAGCGAACAAGAGATAAGTTAACAGTTTATAATAATAAGGTAG GCGTTTTAGCAAATTCTCCAACCTTTGATTGGCATTTAAATAACTTAGATTG TTATATTAATGTCAAATCAGAGCAGCCAGAGGAAACTAAATGGGGACAAC AAATGTTATCGCCTTATTCTAATGGCTTTGGTACGATTGGACTTCCTGGCGA TTTTTCTTCTCCGTCACGATTTGTAAAGGCTGCTTTTTTTACGAAATCATGTG AACGTTGGGGAAGGTGATGAATCAGCAATTAGTGAATGCTTTCATATACTA GATAACTTTGTTGTACCACGTGGGGTGGTTGAGACTCCAAAAAGAAAAGA GTGTCATTTGACTAAGTATAGTGCATGTCTTTGTTTAGAGACTCAATTATAT TATTATAAGACCAGCAGTAATCAGCAAATTCAAGTCATTGATTTAAACAAA GAAAATTTAGATGCTAAAGGATTAAAACTATTTCCTTATCCAACAAGATTA ACAGTCCATGATCAGAATTAG

BSH Group VII	*Turicibacter sanguinis* 1E2	ATGTGTACAGCAATCTCAATCAAGCATCAAACAGACCACGCATTTTTAGCA AGAAACTTTGATTATGATTCGACCAGTCAATTAAAGTTAGCTAAAATTCCA AGAAATTATAGCTCCCCGCTTGAACCAACGCTCAACACCTTTAAAACCCGA TATTCGATCATTGGCATGATGCTATGGCATGAAGGAACCCATGTCCTAGTA GATGGCATGAATGAAAAGGGGCTATCAGGTGCCATTTTAAATTTACCTGAC GCCTGCGTGTGGAATAAAGCCCTCATTTCCGATGGCATCAATCTCTTACCTA CCGATGTCTCCTTCTATTGTTTATCGCAGTTTTCTTCTGTCACCGAAATTAAA GGCGGCCATTCATCAACTCAATATTGTGGCCCCCGAGGATCATCCCTTTGCT AAAACCACTCAAATTCACTGGATGTTTTTGCGATAAAACTGGTGAGTCAATC GTCGTCGAACAAACGGAATCAGGCCTATGTATTTATGATAACCCTATTGGG GTTCTAACTAATGGGCCAACCTTCGATCAACAATTAATCAACATTTCCCCCT ATCTCAAAGATAGCCAAACGGCTCCTCCCCTCCCAGGAGATGATTCCTCTC CCTCACGCTTTATCCGGGCGGGGTATTTAAAACACCATCTTCAATGGACTC AACAGCCGCTATCGACGGTAACTCATTGCTTTCACATTCTAGGAAATGTCG CCCTCCTTCCTGGGATTTTAAAGCAAACACAAGGAGAAGAGTTTGAGACGC GTTATACAGCTTGTATGGACCTTAAACACTTGCGCTATTACCTGAAATGGT ATCATCATCTAAAGACTCAAATCATTGACTTAAAACAAGAGCAGGATGAA AGCAAGACGCTGACTTTTTTTGAGTAA

BSH Group VIII	*Turicibacter sanguinis* MOL361	GTGAAGGAAGGAACCATCCCCTTACAACCTATCTTTGCCGTTACTTACTTCT TAAGTATGTGTGCTACCGTCGAAGAAGTCATTTCAAAATTAGAAAATGATG TTACACTTATCGCAAAGCCTGTCTTCGGGGATATCCGTAATACTCACTGGAT GTTTAGTGACCGTACAGGAGAAACCATCATCATTGAACCTGATGTAGATAA ACTGAAGATTCACCGACATTCAATGGGCGTCTTAACAAATAGTCCAAATTA CGATTGGCATCGTACCAATTTATTAAATTACTGCAATATACGAAGTCTCGA TTATTCAAGCGTTACACTGAATGACGATACGATTGAAGCCTGTTTCTCAGG GAGCGGAGCAGCTGGACTGCCAGGAGATTTTAGCTCGCCATCTCGATTTAC ACGTTTAGCCTTCCTCAAAAATTACGCCTGCAAAGGAAAAAATGAAACCGA AGCTGTTACCTATATGTTCCAAACATTTAAAAACGTTCAATTTCCAATGGG GATCGTTGAAGTTGGCGAAGATAAAACCATTACGGAGCATGATAGTGGCG TCGTTTTATTTGATTACACGATTTACACTGCCGTTATGTGCTCTGAATCTCTT CGCTATTACTGGGTAAGCTACCAAAACATGCGTATTCAATGTGTGGATATG AACCCATTAATTGAGAAAAAACAAGCTGTTCAATTCGAATTAAATCCTATA AATGACATCAAATATCTTAATTAA

In certain embodiments, the bile acid-regulating gene encodes a 7-alpha hydroxysteroid dehydrogenase, such as a 7-alpha hydroxysteroid dehydrogenase encoded by the exemplary nucleic acid sequence shown below. In some embodiments, the 7-alpha hydroxysteroid dehydrogenase is encoded by a nucleic acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to the exemplary 7-alpha hydroxysteroid dehydrogenase nucleic acid sequence shown below.

Exemplary 7-alpha hydroxysteroid dehydrogenase nucleic acid sequence:

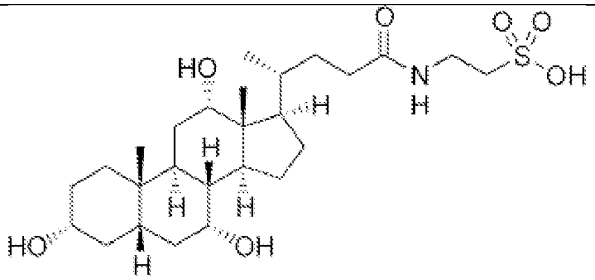
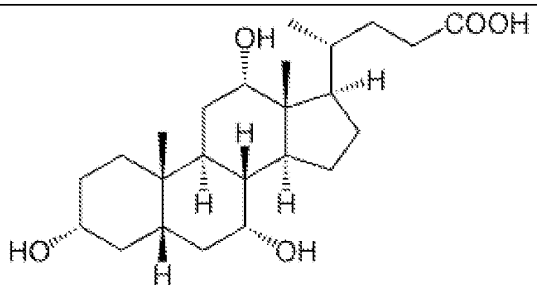
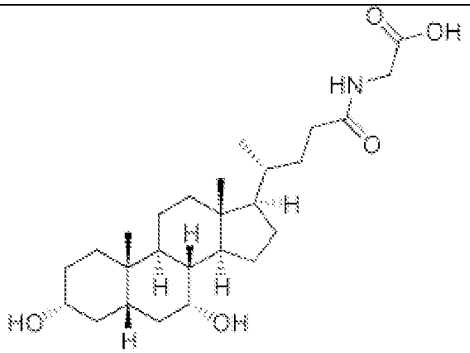
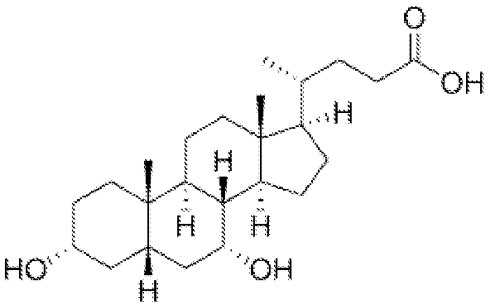
>MOL361_HSDH (locus tag: HLK68_RS02750)

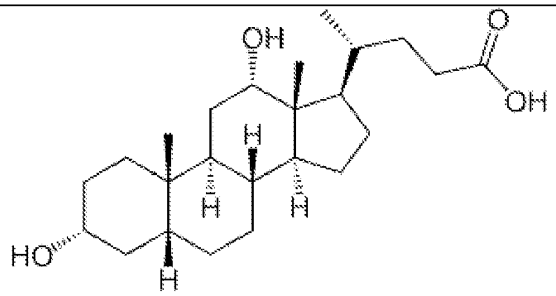
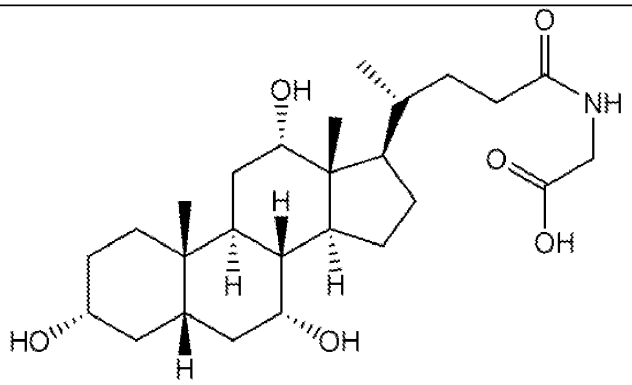
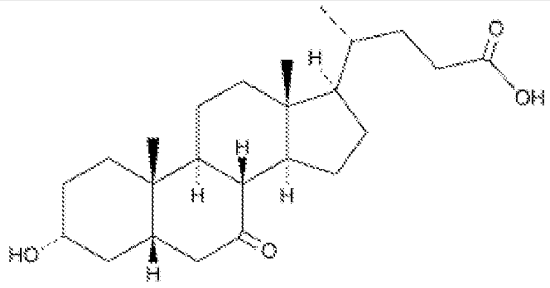
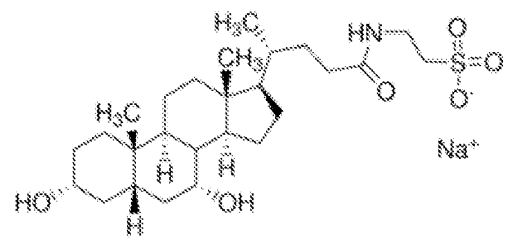
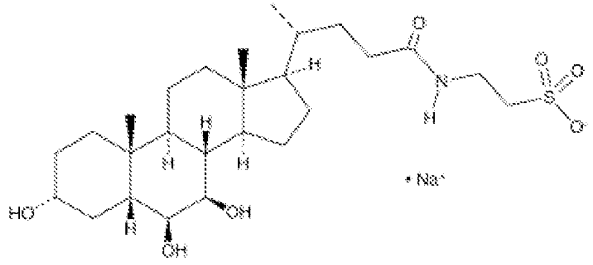
ATGCGAAAATTAGAGAATGCAATAGCTCTTGTCACGTCTTCAACAAGAGGTATT
GGGTTAGCGTGTGCTAAAAAATTAGCGAGTGAGGGTGCCATTGTTTATATGGG
AGTTCGTCGTTTAGAGGTCACTCAAGAAATTTGTGATGAAGTGGCTAAAGAGG
GTTTGAAAATGAAGCCTGTCTTTTTTGACGCCTACAACATTGATTCTTATGAAA
CGATGGTAGAAGAAGTGATTAGGGAACAAGGTAAGATTGATATTTTAGTTAAT
AATTTTGGAACTGGAAGACCGGAAGTAGATTTAGATTTAGTTAGTGGAGATGA
GAAAGCTTTTTTTGATATTTTAGAAGCGAATATCGGATCAGTTTATCGTATCTCT
AAACTGGTGATTCCTCATATGATTAAACAAGGAAAAGGAAGCATTGTTAATATT
TCATCGATTGGTGGAACGGTCCCAGATATTTCTCGTATTGGTTATGGTGTTTCAA
AAGCAGGCGTTAACAATATAACTCAACAAATCGCTATGCAGTATGCGCGCTAT
AATATAAGATGTAATGCGGTATTACCAGGTTTAACAGCAACCGATGCAGCTCTT
GATAATATGCCAGAACAATTTATTAAGTCTTTCTTATCGCATGTTCCTTTAAATC
GCATGGGAACACCTGAAGACATGGCGAATGCGGTTCTATTTTTCGCTAGCGATG
ATTCTTCTTATGTAACGGGGGATATTATGGAGGTATCAGGTGGTTATCATTTAG
GAACACCACAATATGCTGATTTTGTTGGTCGTAAAGTAGTTGAGGAAAAG

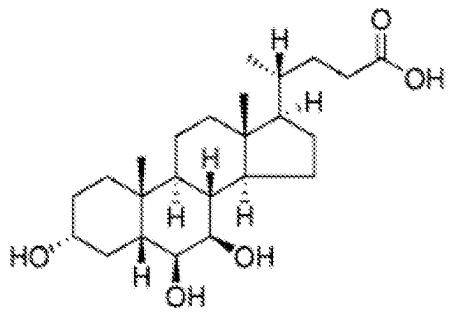
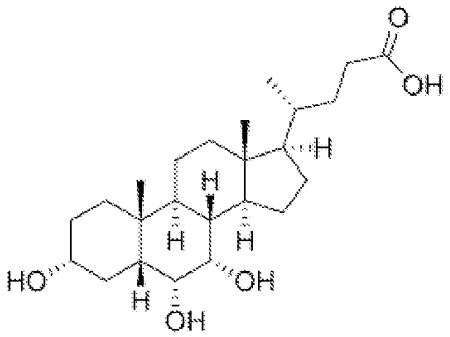
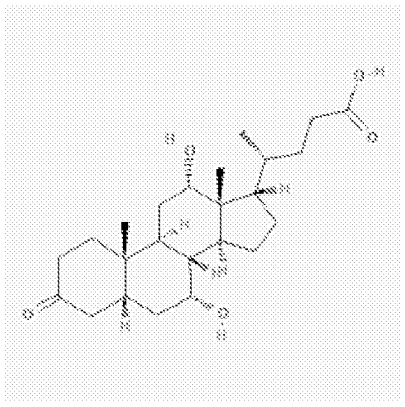
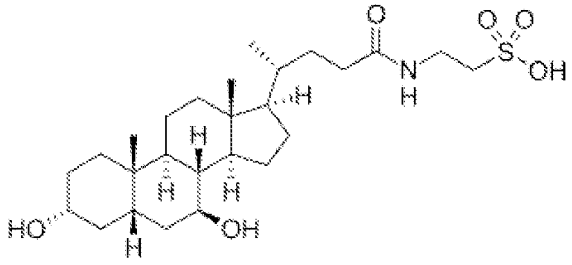
In some embodiments, the 7-alpha hydroxysteroid dehydrogenase is at least 40%, at least 41%, at least 42%, at least 43%, at least 44%, at least 45%, at least 46%, at least 47%, at least 48%, at least 49%, at least 50%, at least 51%, at least 52%, at least 53%, at least 54%, at least 55%, at least 56%, at least 57%, at least 58%, at least 59%, at least 60%, at least 61%, at least 62%, at least 63%, at least 64%, at least 65%, at least 66%, at least 67%, at least 68%, at least 69%, or at least 70% homologous to an amino acid sequence of a *Clostridium absonum* 7-alpha hydroxysteroid dehydrogenase.

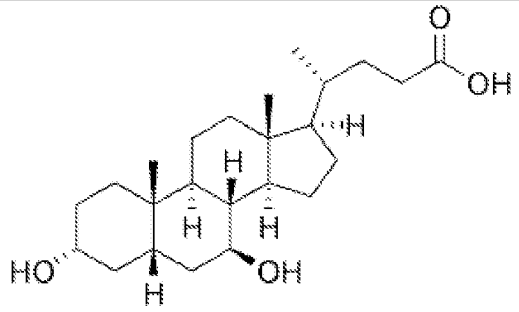
In certain embodiments, the bile salt or bile acid is any one of the bile salts or bile acids listed in Table 3. In some embodiments, administration of the composition increases a bile acid in the subject.

Table 3: Exemplary Bile Salts and Bile Acids

Bile Salt or Bile Acid	Chemical Structure
Taurocholic acid (TCA)	
Cholic acid (CA)	
Glycochenodeoxycholic acid (GCDCA)	
Chenodeoxycholic acid (CDCA)	

Deoxycholic acid (DCA)	
Glycocholic acid	
7-keto deoxycholic acid	
Taurochenodeoxycholate	
Tauro-beta-muricholic acid	

Beta-muricholic acid	
Hyocholic acid	
3-dehydrocholic acid	
Tauroursodeoxycholic	

Ursodeoxycholic acid	

In certain embodiments, administration of the composition alters the subject's lipidome.

In some embodiments, administration of the composition decreases white adipose tissue weight in the subject.

In certain embodiments, administration of the composition alters health-associated lipid biomarkers in the subject (e.g., decreases triglycerides (TG) levels in the subject, decreases cholesterol levels and/or cholesterol ester (CE) levels in the subject).

In some embodiments, administration of the composition decreases abdominal fat pad mass in the subject.

In some embodiments, the bacterial strain is *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron.*

In certain embodiments, the *T. sanguinis* bacterial strain is any one of the *T. sanguinis* bacterial strains listed in Table 4.

Table 4: Exemplary *T. sanguinis* bacterial strains

Isolate of *T. saunginis*
MOL361
18F6
T46
GALT-E2
H121
T129
GALT-G1
1E2
TA25

In some embodiments, the *T. sanguinis* bacterial strain comprises a 16S nucleic acid sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identical to any one of the exemplary *Turicibacter sanguinis strain* 16S nucleic acid sequences shown below.

Exemplary *Turicibacter sanguinis* strain 16S nucleic acid sequences:

>MOL361
AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCAA
GTCGAGC
GAACCACTTCGGTGGTGAGCGGCGAACGGGTGAGTAACACGTAGGTTATCTGC
CCATCAG
ACGGGGACAACGATTGGAAACGATCGCTAATACCGGATAGGACGAAAGTTTAA
AGGTGCT
TCGGCACCACTGATGGATGAGCCTGCGGCGCATTAGCTAGTTGGTAGGGTAAA
GGCCTAC
CAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTG
AGACACG
GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGCGAAAG
CCTGACC
GAGCAACGCCGCGTGAATGATGAAGGCCTTCGGGTTGTAAAATTCTGTTATAA
GGGAAGA
ATGGCTCTAGTAGGAAATGGCTAGAGTGTGACGGTACCTTATGAGAAAGCCAC
GGCTAAC

TACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCGAGCGTTATCCGGAATTATT
GGGCGT
AAAGAGCGCGCAGGTGGTTGATTAAGTCTGATGTGAAAGCCCACGGCTTAACC
GTGGAGG
GTCATTGGAAACTGGTCAACTTGAGTGCAGAAGAGGGAAGTGGAATTCCATGT
GTAGCGG
TGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCTTCCTGGTC
TGTAACT
GACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGT
CCACGCC
GTAAACGATGAGTGCTAAGTGTTGGGGGTCGAACCTCAGTGCTGAAGTTAACG
CATTAAG
CACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGG
GACCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAG
GTCTTGA
CATACCAGTGACCGTCCTAGAGATAGGATTTTCCCTTCGGGGACAATGGATACA
GGTGGT
GCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG
CGCAAC
CCCTGTCGTTAGTTGCCAGCATTCAGTTGGGGACTCTAACGAGACTGCCAGTGA
CAAACT
GGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTAC
ACACGTG
CTACAATGGTTGGTACAAAGAGAAGCGAAGCGGTGACGTGGAGCAAACCTCAT
AAAGCCA
ATCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGTTGGAATCGCTAG
TAATCG
CGAATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC
ACACCA
CGAGAGTTTACAACACCCGAAGTCAGTGGCCTAACCGCAAGGAGGGAGCTGCC
TAAGGTG
GGGTAGATGATTGGGGTGAAGTCGTAACAAGGTATCCCTACCGGAAGGTGGGG
ATGGATC
ACCTCCTT

>1E2
AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCAA
GTCGAGC
GAACCACTTCGGTGGGAAGCGGCGAACGGGTGAGTAACACGTAGGTGATCTGC
CCATCAG
ACGGGGACAACGATTGGAAACGATCGCTAATACCGGATAGGACGAAAGTTTAA
AGATGCT
CCTGGCATCACTGATGGATGAGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAA
AGGCCTA
CCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACT
GAGACAC
GGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGCGAAA
GCCTGAC
CGAGCAACGCCGCGTGAATGAAGAAGGCCTTCGGGTTGTAAAATTCTGTTATA

AGGGAAG
AAAGGTGATAGGAGGAAATGACTATCAATTGACGGTACCTTATGAGAAAGCCA
CGGCTAA
CTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTA
TTGGGCG
TAAAGAGCGCGCAGGTGGTTAATTAAGTCTGATGTGAAAGCCCACGGCTTAAC
CGTGGAG
GGTCATTGGAAACTGGTTGACTTGAGTGCAGAAGAGGGAAGTGGAATTCCATG
TGTAGCG
GTGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCTTCCTGGT
CTGCAAC
TGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG
TCCACGC
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In some embodiments, the subject has a metabolic disorder (e.g., a lipid metabolic disorder and/or a steroid metabolic disorder). The lipid metabolic disorder may be hyperlipidemia, hypercholeresterolemia, acid lipase disease, Barth syndrome, Fabry disease, Farber's disease, Gaucher disease, Niemann-Pick disease, or Tay-Sachs disease. The steroid metabolic disorder may be cytochrome p450 oxidoreductase deficiency, apparent mineralocorticoid excess, lipoid congenital adrenal hyperplasia, congenital bile acid synthesis defect, 3-beta-hydroxysteroid dehydrogenase deficiency, aldosterone-producing adenoma, polyendocrinopathy, adrenal hyperplasia.

The composition may be formulated for oral delivery. In some embodiments, the composition may comprise probiotics. In some embodiments, the compositions disclosed herein are food products. The composition may be in the form of a pill, tablet, or capsule. In some embodiments, the subject may be a mammal (e.g., a human). In some embodiments, the composition is self-administered. While it is preferred for a single composition to comprise all the bacteria to be administered, it will be recognized that for any of the various embodiments described herein, the combination of bacteria can similarly be administered in multiple compositions that together comprise the combination of bacteria. For example, the invention further provides kits comprising multiple compositions that together that comprise a *Turicibacter sanguinis* bacterial strain (e.g., a bacterial strain listed in Table 4) and/or a *Turicibacter sanguinis* bacterial strain that regulates a bile salt and/or a bile acid (e.g., a bacterial strain listed in Table 4).

In some embodiments, the composition is formulated for rectal delivery (e.g., a fecal sample). In some embodiments, the subject undergoes fecal microbiota transplant, wherein the transplant comprises a composition disclosed herein. Fecal microbiota transplantation (FMT), also commonly known as 'fecal bacteriotherapy' represents a therapeutic protocol that allows the reconstitution of colon microbial communities. The process involves the transplantation of fecal bacteria from a healthy individual into a recipient. FMT restores colonic microflora by introducing healthy bacterial flora through infusion of a fecal sample, e.g., by enema, orogastric tube or by mouth in the form of a capsule containing freeze-

dried material, obtained from a healthy donor. In some embodiments, the fecal sample is from a fecal bank.

In some embodiments, the bacterial DNA in subject's gut microbiota is sequenced. The subject's gut bacterial DNA may be sequenced prior to administration of the composition. For example, a sample comprising bacterial DNA may be obtained from the subject, and the bacterial DNA is then sequenced for any one of the bacteria listed in Table 4, therefore measuring the presence or level of any one of such bacteria (e.g., one or more, two or more, five or more, or ten or more of the bacteria of interest) in the subject's gut microbiota. The composition disclosed herein may then be administered to the subject if the level of the bacteria is low. In some embodiments, the subject is deemed to have low levels of any one of the bacteria listed in Table 4 if less than 0.0001%, less than 0.001%, less than 0.01%, less than 0.02%, less than 0.03%, less than 0.04%, less than 0.05%, less than 0.06% less than 0.07%, less than 0.08%, less than 0.09%, less than 0.1%, less than 0.2%, less than 0.3% less than 0.4%, less than 0.5%, less than 0.6%, less than 0.7%, less than 0.8%, less than 0.9%, less than 1%, less than 2%, less than 3%, less than 5%, less than 7%, less than 10%, less than 20%, less than 30%, less than 40%, or less than 50% of the bacteria in the sample is the bacteria of interest. Bacterial DNA to be sequenced may be obtained through any means known in the art, including, but not limited to, obtaining a fecal sample from the subject and isolating the bacterial DNA. Bacterial DNA sequencing by any known technique in the art, including, but not limited to, Maxam Gilbert sequencing, Sanger sequencing, shotgun sequencing, bridge PCR, or next generation sequencing methods, such as massively parallel signature sequencing (MPSS), polony sequencing, 454 pyrosequencing, Illumina (Solexa) sequencing, SOLiD sequencing, Ion torrent semiconductor sequencing, DNA nanoball sequencing, heliscope single molecule sequencing, single molecule real time (SMRT) sequencing, or nanopore DNA sequencing.

In some embodiments, the above methods directly act to reduce the amount of pathogenic bacteria in a subject (i.e., in the gastrointestinal tract of the subject). In some embodiments, this includes any such therapy that achieves the same goal of reducing the number of pathogenic organisms, when used in combination with the compositions described herein, would lead to replacement of the pathogenic microflora involved in the diseased state with microflora associated with a non-diseased state, or less pathogenic species occupying the same ecological niche as the type causing a disease state. For example, a subject may undergo treatment with antibiotics (e.g., antimicrobial compounds)

or a composition comprising antibiotics to target and decrease the prevalence of pathogenic organisms, and subsequently be treated with a composition described herein. The treatment may also comprise an antifungal or anti-viral compound.

Suitable antimicrobial compounds include capreomycins, including capreomycin IA, capreomycin IB, capreomycin IIA and capreomycin IIB; carbomycins, including carbomycin A; carumonam; cefaclor, cefadroxil, cefamandole, cefatrizine, cefazedone, cefazolin, cefbuperazone, cefcapene pivoxil, cefclidin, cefdinir, cefditoren, cefime, ceftamet, cefmenoxime, cefmetzole, cefminox, cefodizime, cefonicid, cefoperazone, ceforanide, cefotaxime, cefotetan, cefotiam, cefoxitin, cefpimizole, cefpiramide, cefpirome, cefprozil, cefroxadine, cefsulodin, ceftazidime, cefteram, ceftezole, ceftibuten, ceftiofur, ceftizoxime, ceftriaxone, cefuroxime, cefuzonam, cephalexin, cephalogycin, cephaloridine, cephalosporin C, cephalothin, cephapirin, cephamycins, such as cephamycin C, cephradine, chlortetracycline; chlarithromycin, clindamycin, clometocillin, clomocycline, cloxacillin, cyclacillin, danofloxacin, demeclocyclin, destomycin A, dicloxacillin, dirithromycin, doxycyclin, epicillin, erythromycin A, ethanbutol, fenbenicillin, flomoxef, florfenicol, floxacillin, flumequine, fortimicin A, fortimicin B, forfomycin, foraltadone, fusidic acid, gentamycin, glyconiazide, guamecycline, hetacillin, idarubicin, imipenem, isepamicin, josamycin, kanamycin, leumycins such as leumycin A1, lincomycin, lomefloxacin, loracarbef, lymecycline, meropenam, metampicillin, methacycline, methicillin, mezlocillin, micronomicin, midecamycins such as midecamycin A1, mikamycin, minocycline, mitomycins such as mitomycin C, moxalactam, mupirocin, nafcillin, netilicin, norcardians such as norcardian A, oleandomycin, oxytetracycline, panipenam, pazufloxacin, penamecillin, penicillins such as penicillin G, penicillin N and penicillin O, penillic acid, pentylpenicillin, peplomycin, phenethicillin, pipacyclin, piperacilin, pirlimycin, pivampicillin, pivcefalexin, porfiromycin, propiallin, quinacillin, ribostamycin, rifabutin, rifamide, rifampin, rifamycin SV, rifapentine, rifaximin, ritipenem, rekitamycin, rolitetracycline, rosaramicin, roxithromycin, sancycline, sisomicin, sparfloxacin, spectinomycin, streptozocin, sulbenicillin, sultamicillin, talampicillin, teicoplanin, temocillin, tetracyclin, thostrepton, tiamulin, ticarcillin, tigemonam, tilmicosin, tobramycin, tropospectromycin, trovafloxacin, tylosin, and vancomycin, and analogs, derivatives, pharmaceutically acceptable salts, esters, prodrugs, and protected forms thereof.

Suitable anti-fungal compounds include ketoconazole, miconazole, fluconazole, clotrimazole, undecylenic acid, sertaconazole, terbinafine, butenafine, clioquinol,

haloprogin, nystatin, naftifine, tolnaftate, ciclopirox, amphotericin B, or tea tree oil and analogs, derivatives, pharmaceutically acceptable salts, esters, prodrugs, and protected forms thereof.

Compositions

In some aspects, the invention relates to a composition (e.g., a food product or a pharmaceutical composition). Provided herein are compositions (e.g., compositions comprising a *Turicibacter sanguinis* bacterial strain, such as any bacteria listed in Table 4, and a pharmaceutically acceptable carrier; or compositions comprising a *Turicibacter sanguinis* bacterial strain that regulates a bile salt and/or a bile acid, such as any bacteria listed in Table 4, and a pharmaceutically acceptable carrier). composition may comprise at least one, at least two, at least three, at least four, at least five, at least six at least seven, at least eight, at least nine, at least ten, at least fifteen, or at least twenty bacteria that regulate a bile salt and/or a bile acid, such as any bacteria listed in Table 4. Any combination of the bacteria listed in Table 4 may be include in the composition.

The composition may comprise a pharmaceutically acceptable carrier. The composition may comprise probiotics. The pharmaceutical compositions disclosed herein may be delivered by any suitable route of administration, including orally, bucally, sublingually, parenterally, and rectally, as by powders, ointments, drops, liquids, gels, tablets, capsules, pills, or creams. In certain embodiments, the pharmaceutical compositions are delivered generally (e.g., via oral administration). In certain other embodiments, the compositions disclosed herein are delivered rectally.

In certain embodiments, the invention provides kits comprising multiple compositions (e.g., compositions comprising a *Turicibacter sanguinis* bacterial strain, such as any bacteria listed in Table 4, and a pharmaceutically acceptable carrier; or compositions comprising a *Turicibacter sanguinis* bacterial strain that regulates a bile salt and/or a bile acid, such as any bacteria listed in Table 4, and a pharmaceutically acceptable carrier). The kits disclosed herein may comprise at least one, at least two, at least three, at least four, at least five, at least six at least seven, at least eight, at least nine, at least ten, at least fifteen, or at least twenty of the compounds listed in Table 1. The kits provided herein may comprise at least one, at least two, at least three, at least four, at least five, at least six at least seven, at least eight, at least nine, at least ten, at least fifteen, or at least twenty

bacteria that regulate a bile salt and/or a bile acid, such as any bacteria listed in Table 4. Any combination of the bacteria listed in Table 4 may be include in the composition.

In some embodiments, at least 1%, at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35% , at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95%, of the bacteria in the composition that regulate a bile salt and/or a bile acid, such as any bacteria listed in Table 4.

Compositions described herein may be used for oral administration to the gastrointestinal tract, directed at the objective of introducing the bacteria (e.g., the bacteria disclosed herein) to tissues of the gastrointestinal tract. The formulation for a composition (e.g., a probiotic composition) of the present invention may also include other probiotic agents or nutrients which promote spore germination and/or bacterial growth. An exemplary material is a bifidogenic oligosaccharide, which promotes the growth of beneficial probiotic bacteria. In some embodiments, the probiotic bacterial composition is administered with a therapeutically-effective dose of an (preferably, broad spectrum) antibiotic, or an anti-fungal agent. In some embodiments, the compositions described herein are encapsulated into an enterically-coated, time-released capsule or tablet. The enteric coating allows the capsule/tablet to remain intact (i.e., undissolved) as it passes through the gastrointestinal tract, until after a certain time and/or until it reaches a certain part of the GI tract (e.g., the small intestine). The time-released component prevents the "release" of the probiotic bacterial strain in the compositions described herein for a pre-determined time period.

The composition may be a food product, such as, but not limited to, a dairy product. The dairy product may be cultured or a non-cultured (e.g., milk) dairy product. Non-limiting examples of cultured dairy products include yogurt, cottage cheese, sour cream, kefir, buttermilk, etc. Dairy products also often contain various specialty dairy ingredients, e.g. whey, non-fat dry milk, whey protein concentrate solids, etc. The dairy product may be processed in any way known in the art to achieve desirable qualities such as flavor, thickening power, nutrition, specific microorganisms and other properties such as mold growth control. The compositions of the present invention may also include known antioxidants, buffering agents, and other agents such as coloring agents, flavorings, vitamins, or minerals.

In some embodiments, the compositions of the present invention are combined with a carrier (e.g., a pharmaceutically acceptable carrier) which is physiologically compatible with the gastrointestinal tissue of the subject(s) to which it is administered. Carriers can be comprised of solid-based, dry materials for formulation into tablet, capsule or powdered form; or the carrier can be comprised of liquid or gel-based materials for formulations into liquid or gel forms. The specific type of carrier, as well as the final formulation depends, in part, upon the selected route(s) of administration. The therapeutic composition of the present invention may also include a variety of carriers and/or binders. In some embodiments, the carrier is micro-crystalline cellulose (MCC) added in an amount sufficient to complete the one gram dosage total weight. Carriers can be solid-based dry materials for formulations in tablet, capsule or powdered form, and can be liquid or gel-based materials for formulations in liquid or gel forms, which forms depend, in part, upon the routes of administration. Typical carriers for dry formulations include, but are not limited to: trehalose, malto-dextrin, rice flour, microcrystalline cellulose (MCC) magnesium sterate, inositol, FOS, GOS, dextrose, sucrose, and like carriers. Suitable liquid or gel-based carriers include but are not limited to: water and physiological salt solutions; urea; alcohols and derivatives (e.g., methanol, ethanol, propanol, butanol); glycols (e.g., ethylene glycol, propylene glycol, and the like). Preferably, water-based carriers possess a neutral pH value (i.e., pH 7.0). Other carriers or agents for administering the compositions described herein are known in the art, e.g., in U.S. Patent No. 6,461,607.

In some embodiments, the composition further comprises other bacteria or microorganisms known to colonize the gastrointestinal tract. For example, the composition may comprise species belonging to the Firmicutes phylum, the Proteobacteria phylum, the Tenericutes phylum, the Actinobacteria phylum, or a combination thereof. Examples of additional bacteria and microorganisms that may be included in the subject compositions include, but are not limited to, Saccharomyces, Bacteroides, Eubacterium, Clostridium, Lactobacillus, Fusobacterium, Propionibacterium, Streptococcus, Enteroccus, Lactococcus and Staphylococcus, Peptostreptococcus. In certain embodiments, the composition is substantially free of bacteria that increase the risk of metabolic disorder. Such bacteria include Bifidobacterium bacteria. Thus, in some embodiments, the composition is substantially free of Bacteroides bacteria. A composition is substantially free of a bacterial type if that type makes up less than 10% of the bacteria in a composition, preferably less

than 5%, even more preferably less than 1%, most preferably less than 0.5%, or even 0% of the bacteria in the composition.

In some embodiments, the composition comprises a fecal sample comprising at least one bacteria that regulate a bile salt and/or a bile acid, such as any bacteria listed in Table 4. In some embodiments, the fecal sample is from a fecal bank. In some embodiments, the compositions may be added to a fecal sample prior to administration to the subject.

In some embodiments, provided herein are methods of treating or preventing a metabolic condition, by administering a composition (e.g., a fecal sample) that regulate a bile salt and/or a bile acid, such as any bacteria listed in Table 4. The fecal sample is enriched if at least 0.01%, at least 0.02%, at least 0.03%, at least 0.04%, at least 0.05%, at least 0.06%, at least 0.07%, at least 0.08%, at least .09%, at least 0.1%, at least 0.2%, at least 0.3%, at least 0.4%, at least 0.5%, at least 0.6%, at least 0.7%, at least 0.8%, at least 0.9%, at least 1%, or at least 2%, at least 3%, at least 4%, at least 5%, at least 6%, at least 7%, at least 8%, at least 9%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, or at least 50% of the bacteria in the fecal sample is bacteria that regulate a bile salt and/or a bile acid, such as any bacteria listed in Table 4. In some embodiments, the fecal sample is from a fecal bank. In some embodiments, the fecal sample is from a donor.

The composition may further comprise a nutrient. In some embodiments, the nutrient aids in the growth of bacteria (e.g., bacteria disclosed herein). In some embodiments, the nutrient is a lipid (e.g., lineoleic acid, stearic acid, or palmitic acid). In some embodiments, the nutrient may be conjointly administered with a composition disclosed herein. As used herein, the phrase “conjoint administration” refers to any form of administration of two or more different agents (e.g., a composition disclosed herein and a nutrient disclosed herein) such that the second agent is administered while the previously administered agent is still effective in the body. For example, the compositions disclosed herein and the nutrients disclosed herein can be administered either in the same formulation or in a separate formulation, either concomitantly or sequentially.

Actual dosage levels of the active ingredients in the pharmaceutical compositions may be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient.

The selected dosage level will depend upon a variety of factors including the

activity of the particular agent employed, the route of administration, the time of administration, the rate of excretion or metabolism of the particular compound being employed, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular compound employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts.

A physician or veterinarian having ordinary skill in the art can readily determine and prescribe the effective amount of the pharmaceutical composition required. For example, the physician or veterinarian could prescribe and/or administer doses of the compounds employed in the pharmaceutical composition at levels lower than that required in order to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect is achieved.

EXEMPLIFICATION

Example 1: Genomic comparison reveal distinct sub groups of *Turicibacter sanguinis*

Figure 1A & Figure 1B show genomic comparison reveal distinct sub groups of *Turicibacter sanguinis*. A: Phylogenetic tree comparing full-length 16S rRNA sequences from noted *T. sanguinis* isolates. Circles indicate human-derived isolated, triangles indicate mouse-derived isolates, and squares indicate mouse-derived contaminating isolate. B: Full shotgun-assembled genome comparisons of *T. sanguinis* isolates listed in A.

Example 2: *T. sanguinis* isolates differ in their bile-modifying abilities

Figure 2A & Figure 2B show *T. sanguinis* isolates differ in their bile-modifying abilities. A: Liquid chromatograms of individual *T. sanguinis* isolates grown for 24 hours in media with sub-inhibitory concentrations of five bile salts/acids: taurocholic acid (TCA), cholic acid (CA), glycochenodeoxycholic acid (GCDCA), chenodeoxycholic acid (CDCA), and deoxycholic acid (DCA). Shaded regions indicate expected retention time of each bile species. B: Relative amounts of remaining conjugated bile salts (taurocholic acid, taurochenodeoxycholic acid, glycocholic acid, glycochenodeoxycholic acid) after 24

growth with noted *T. sanguinis* isolate. Magenta=glycine-conjugated bile salts, blue=taurine-conjugated bile salts.

Example 3: *T. sanguinis* isolates differ in their genetic capacity to modify bile species

Table 2 shows presence (+) or absence (-) of sequence homologs with potential bile modifying activity in *T. sanguinis* isolates. For 7-alpha hydroxysteroid dehydrogenase homologs (far right column), percent amino acid identify with *Clostridium absonum* is also shown.

Table 2

Isolate	BSH Group I	BSH Group II	BSH Group III	BSH Group IV	BSH Group V	BSH Group VI	BSH Group VII	BSH Group VIII	7α-HSDH
MOL361	+	-	-	+	+	-	-	+	57%
18F6	+	-	-	-	+	-	-	+	57%
T46	+	-	-	-	+	-	-	+	57%
GALT-E2	+	-	-	-	+	-	-	+	?
H121	-	+	-	-	-	+	-	-	64%
T129	-	+	-	-	-	+	-	-	64%
GALT-G1	-	+	-	-	-	+	-	-	?
1E2	-	-	+	+	-	-	+	-	-
TA25	-	-	+	+	-	-	+	-	-

Figure 3A-Figure 3D show *T. sanguinis* isolates differ in their genetic capacity to modify bile species. A: Liquid chromatograms of media after 24 hour cultures of *E. coli* expressing individual predicted bile salt hydrolases (BSH) from each sequence grouping and isolate and grown in with TCA and TCDCA. Control is *E. coli* with same expression vector but expressing non-bile modifying gene. B: same as A, but with GCA and GCDCA instead of taurine-conjugated bile salts. C. Remaining amounts of TCA, TCDCA, GCA, and GCDCA after 24 hour growths of *E. coli* expressing noted BSH homologs. D: Phylogenetic tree of each predicted BSH gene from *T. sanguinis* isolates, with bile salt specificity noted in boxes. We did not detect bile salt hydrolase activity in sequences without boxes.

Example 4: *T. sanguinis* BSH expression is sufficient to alter host lipidome and health-associated lipid markers

Figures 4A-Figure 4D show *T. sanguinis* BSH expression is sufficient to alter host lipidome and health-associated lipid markers. A: Heatmap of plasma lipid species significantly altered by expression of at least one *T. sanguinis* BSH in *Bacteroides thetaiotaomicron*. Colors on left correspond to lipid class, cyan-magenta colorscale represents Z-score. B. Relative white adipose tissue weight of mice monocolonized with BSH-expression *B. thetatiotaomicron*. C. Relative combined plasma triglycerides (TG) of mice monocolonized with BSH-expression *B. thetatiotaomicron.* D. Relative cholesterol esters (CE) of mice monocolonized with BSH-expression *B. thetatiotaomicron.* All values normalized to sex-matched littermates, *= $p<0.05$ two-tailed t-test.

Example 5: *T. sanguinis* isolates differ in their effects on host lipid biology and bile acids

Figure 5A-Figure 5B show *T. sanguinis* isolates differ in their effects on host lipid biology and bile acids. A: Sex and littermatched relative abdominal fat pad mass from mice monocolonized with individual *T. sanguinis* isolates. B: top: Example image of adipose

tissue histology section. bottom: Sex and litter matched relative adipocyte size of mice monocolonized with individual *T. sanguinis* isolates.

Example 6: *T. sanguinis* isolates differ in their effects on host lipid biology and bile acids

Figure 6 shows levels of circulating serum bile acids and cholesterol in mice monocolonzed by individual *T. sanguinis* isolates. #=p<0.1, *=p<0.05.

Example 7: *Turicibacter* modifies host bile acids and lipids in a strain-specific manner

Bacteria from the *Turicibacter* genus are prominent members of the mammalian gut microbiota and are associated with alterations in dietary fat and body weight, but the specific connections between these symbionts and host physiology are poorly understood. A a diverse set of mouse- and human-derived *Turicibacter* strains were genomically and phenotypically characterized, and found they group into three clades that differ in their transformations of bile acids. *Turicibacter* bile salt hydrolases that confer strain-specific differences in bile deconjugation were identified. Colonization with individual *Turicibacter* strains led to changes in host bile acid profiles, generally aligning with those produced *in vitro*. Further, colonizing mice with another bacterium expressing bile-modifying genes from these strains decreased serum cholesterol, and triglycerides, and as well as adipose tissue mass. This work identifies genes that enable diverse *Turicibacter* strains to differentially modify host bile acids and lipid metabolism, and positions multiple *Turicibacter* strains as candidates for altering host fat biology.

Introduction

The gut microbiota forms complex relationships with its host organism, modulating broad aspects of host physiology including metabolism[1,2] and neurobiology[3,4]. Often, the connections between the gut microbiota and host physiology are easiest to decipher through presence/absence of large sectors of the microbial community (examples in [5–7]), but in some cases, specific microbial features and/or taxa serve important roles in host physiology[8–10].

The mammalian gut microbiota has long been associated with obesity[25,26], but studies often provide strong correlations rather than mechanistic determinants of these relationships, indicating a further need for fundamental interrogation into connections between the microbiota and host fat[27]. Numerous microbiota community profiling studies

reveal correlations between *Turicibacter* and features of host fat metabolism, such as adiposity and dietary lipids[28–33], but the nature of these correlations varies [34,35]. It was recently observed that the type strain of *T. sanguinis,* MOL361[36,37], broadly alters the host serum lipidome while decreasing serum cholesterol and triglycerides in mice[38]. This same strain was also reported to modify bile species through deconjugation and dehydrogenation *in vitro*[21], suggesting at least one potential means by which *Turicibacter* can influence host lipid status. Based on these findings, it is hypothesized that there may be variations in the functional activity of *Turicibacter* strains that account for differences in host bile and lipid biology, providing a mechanism to connect this taxon to aspects of host physiology.

Results

Turicibacter *isolates separate into genetically distinguishable strains*

To better understand the diversity within the *Turicibacter* genus, nine isolates were gathered from the fecal microbiotas of mice and humans that had been identified as *T. sanguinis* based on their 16S rRNA gene sequence (97% full length 16S rRNA gene sequence similarity cutoff, **Table 5**). Two of these isolates had been previously identified (human-derived type strain MOL361 and H121, which was derived from contaminated germ-free mice[36,39]); five had been isolated but not published (human isolates 18F6, T46, and T129, and mouse isolates 1E2 and TA25); and two were isolated from a human fecal sample specifically for this study (GALT-E2 and GALT-G1) using an array-based isolation and cultivation platform (see Methods). Shotgun short read sequencing was performed and draft assemblies of each isolate genome were created. Comparisons of the 16S rRNA gene phylogeny (**Fig. 7a**), general genome characteristics (**Fig. 7b**), or specific genome sequence (**Fig. 7c, d**) revealed that even with this fairly small sample of the 16S rRNA gene-based "*T. sanguinis*" species designation, there were at least three distinct subgroups: two from humans (exemplar isolates MOL361 and H121, with 99.3% full length 16S rRNA gene similarity), and one from mice (exemplar strain 1E2, 97.5% and 97.8% 16S rRNA gene similarity with MOL361 and H121, respectively). Genomic alignments indicated a substantial amount of shared DNA sequences within members of the same subgroups (all within group average nucleotide identity [ANI] >98.3%) with the remaining amount of genetic variation indicating smaller genetic differences between related isolates. These within-subgroup shared sequences were distinct from members of the other two subgroups (intergroup ANI: MOL361-H121=76.80%, MOL361-1E2=74.95%, H121-1E2=77.43%). It

is important to note that the H121-group genomically resembles the newly described species *Turicibacter bilis*[13] (98.8% ANI), currently the only other named species from this genus. Overall, these genomic differences suggest distinct evolutionary histories that correspond at least partially with host origin.

Table 5

Isolate	Derived from	Source	Reference	Notes
MOL361	human	DMSZ	Bosshard, 2002	*Turicibacter sanguinis* type strain
18F6	human	Kenya Honda	N/A	
T46	human	Thomas Auchtung	N/A	
GALT-G1	human	this work	N/A	
H121	contaminated germ-free mouse	Thomas Auchtung	Auchtung, 2016	
T129	human	Thomas Auchtung	N/A	
GALT-E2	human	this work	N/A	
1E2 (also known as 80E2)	mouse	Kenya Honda	N/A	
TA25	mouse	Thomas Auchtung	N/A	
Bacteroides thetaiotaomicron VPI-5482	human	Justin Sonnenburg/ Fatima Enam	Xu, 2003	background strain
B. thetaiotaomicron pWW3837	N/A	rederived for this work	Whitaker, 2017	referred to as "WT" in this work
Bt-BSH-IV:MOL361	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-IV from MOL361 in place of GFP
Bt-BSH-I:MOL361	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-I from MOL361 in place of GFP

Bt-BSH-II:H121	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-II from H121 in place of GFP
Bt-BSH-III:1E2	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-III from 1E2 in place of GFP
Escherichia coli C41-pLys	N/A	Lucigen	N/A	expression strain
Escherichia coli WM3064	N/A	Brittany Bennett	Lynch, 2019	conjugation donor

Turicibacter *isolates differ in their impact on host fat biology and circulating metabolome*

Previous findings revealed that monocolonizing mice with *T. sanguinis* MOL361 altered host fat tissue and circulating lipids[38]. Due to the large genomic variation between our *Turicibacter* strains, it was predicted that they would vary in their effects on host lipid biology. Representative isolates from each of the distinct phylogenetic subgroups (MOL361, H121 and T129, and 1E2) were chosedn and measured their effects on circulating metabolites and adipose tissue in monocolonized mice relative to germ-free (GF) and conventionalized controls (*i. e.* gavaged with complete microbiota, CONV). Compared to GF littermates, CONV mice had decreased levels of several dicarboxylate fatty acids, long-chain fatty acids, and long-chain acyl carnitines, with a broad increase in short- and medium-chain acyl carnitines (**Fig. 8a**). Consistent with a previous report[38], colonization with individual *Turicibacter* strains also induced widespread alterations in host serum lipids, with many strain-level differences in host lipid alterations (**Fig. 8a, Table 6**). Compared to GF controls, MOL361 increased a subset of long-chain acyl carnitines, and decreased many long-chain saturated fatty acids and dicarboxylic acids. In addition, colonization with MOL361 elicited significant decreases in host cholesterol to levels below those seen in both GF and CONV animals (**Fig. 8b**). Compared to GF, H121 colonization significantly increased serum levels of several medium-chain fatty acids, dicarboxylic acids, and short-, medium- and long-chain acyl carnitines. 1E2 colonization had a smaller overall effect on host lipids, but led to a decrease in several dicarboxlyate fatty acids (**Fig. 8a**), In addition to differences between GF or CONV mice and *Turicibacter*-monocolonized animals, there were also broad alterations in host lipids in response to colonization with

different *Turicibacter* strains, with sizeable discrepancies in dicarboxylate and long chain saturated fatty acids (**Fig. 8a**) At the tissue level, two of the four *Turicibacter* strains stimulated statistically significant increases in epididymal/gonadal white adipose tissue (e/gWAT) mass in comparison to GF controls, and a third strain elicited similar increases that were not statistically significant. In contrast, there was no noticeable effect of H121 (**Fig. 8c**). Consistent with this, H121 showed the smallest e/gWAT adipocyte size within fat pads (**Fig. 13a-f**). This may be due to lower colonization of H121 in both the small intestine and the colon (**Fig. 13g, h**) These results indicate that there is not necessarily a connection between changes in specific lipid species and mass of adipose tissue.

Table 6

Sub Pathway	Biochemical Name	Fold Change Welch's Two-Sample t-Test (bold indicates p<0.1) MOL361 GF	1E2_ GF	H121 GF	T129 GF	CONV GF
Fatty Acid, Branched	(14 or 15)-methylpalmitate (a17:0 or i17:0)	**0.66**	1.07	1.14	1.06	**0.57**
Fatty Acid, Branched	(16 or 17)-methylstearate (a19:0 or i19:0)	**0.66**	1.13	1.01	1.08	**0.36**
Medium Chain Fatty Acid	(2 or 3)-decenoate (10:1n7 or n8)	0.82	0.93	**1.78**	1.05	**0.39**
Polyamine Metabolism	(N(1) + N(8))-acetylspermidine	1.00	1.10	0.79	1.18	1.04
Fatty Acid Metabolism (Acyl Carnitine, Hydroxy)	(R)-3-hydroxybutyrylcarnitine	1.55	**1.76**	1.93	1.47	**2.63**
Fatty Acid Metabolism (Acyl Carnitine, Hydroxy)	(S)-3-hydroxybutyrylcarnitine	1.27	1.32	**1.44**	1.11	**1.56**
Lysoplasmalogen	1-(1-enyl-oleoyl)-GPE (P-18:1)*	1.08	1.17	**1.58**	1.02	0.92
Plasmalogen	1-(1-enyl-palmitoyl)-2-arachidonoyl-GPC (P-16:0/20:4)*	0.94	1.08	1.20	1.02	1.36
Plasmalogen	1-(1-enyl-palmitoyl)-2-arachidonoyl-GPE (P-16:0/20:4)*	1.06	**1.39**	**1.26**	1.16	1.17
Plasmalogen	1-(1-enyl-palmitoyl)-2-linoleoyl-GPC (P-16:0/18:2)*	**0.82**	0.98	0.95	0.99	**1.38**
Plasmalogen	1-(1-enyl-palmitoyl)-2-linoleoyl-GPE (P-16:0/18:2)*	1.04	**1.60**	1.26	**1.38**	**1.41**
Plasmalogen	1-(1-enyl-palmitoyl)-2-oleoyl-GPC (P-16:0/18:1)*	1.02	**1.22**	**1.33**	1.18	**1.14**
Plasmalogen	1-(1-enyl-palmitoyl)-2-oleoyl-GPE (P-16:0/18:1)*	**1.21**	**1.37**	**1.20**	**1.39**	**1.42**

Plasmalogen	1-(1-enyl-palmitoyl)-2-palmitoyl-GPC (P-16:0/16:0)*	**0.90**	0.96	**1.12**	1.02	0.99
Lysoplasmalogen	1-(1-enyl-palmitoyl)-GPC (P-16:0)*	0.96	1.02	0.96	0.98	0.93
Lysoplasmalogen	1-(1-enyl-palmitoyl)-GPE (P-16:0)*	0.94	1.09	1.20	0.96	**0.87**
Plasmalogen	1-(1-enyl-stearoyl)-2-arachidonoyl-GPE (P-18:0/20:4)*	1.04	**1.19**	**1.24**	0.92	1.20
Plasmalogen	1-(1-enyl-stearoyl)-2-linoleoyl-GPE (P-18:0/18:2)*	1.03	**1.25**	1.17	1.00	**1.42**
Plasmalogen	1-(1-enyl-stearoyl)-2-oleoyl-GPE (P-18:0/18:1)	1.22	**1.40**	**1.29**	**1.22**	**1.95**
Lysoplasmalogen	1-(1-enyl-stearoyl)-GPE (P-18:0)*	1.05	**1.10**	1.10	0.97	1.00
Lysophospholipid	1-arachidonoyl-GPA (20:4)	1.08	1.23	1.13	1.12	**0.63**
Lysophospholipid	1-arachidonoyl-GPC (20:4n6)*	0.93	0.97	0.98	1.06	**0.69**
Lysophospholipid	1-arachidonoyl-GPE (20:4n6)*	1.01	0.97	0.94	0.98	**0.53**
Lysophospholipid	1-arachidonoyl-GPI (20:4)*	**0.61**	0.84	**0.62**	**0.63**	**0.43**
Monoacylglycerol	1-arachidonylglycerol (20:4)	0.84	1.25	0.93	**1.21**	**0.71**
Monoacylglycerol	1-dihomo-linolenylglycerol (20:3)	0.89	1.32	0.96	1.14	**0.54**
Monoacylglycerol	1-docosahexaenoylglycerol (22:6)	0.95	1.30	0.84	1.14	**0.64**
Monoacylglycerol	1-eicosapentaenoylglycerol (20:5)*	**0.71**	1.09	**0.80**	1.09	**0.70**
Monoacylglycerol	1-heptadecenoylglycerol (17:1)*	0.78	1.23	0.98	1.03	**0.59**
Lysophospholipid	1-lignoceroyl-GPC (24:0)	0.89	0.93	**0.86**	1.04	**0.78**
Lysophospholipid	1-linolenoyl-GPC (18:3)*	**0.71**	0.85	0.89	0.89	**0.79**
Monoacylglycerol	1-linolenoylglycerol (18:3)	**0.71**	1.14	**0.72**	1.07	**0.57**
Phosphatidylcholine (PC)	1-linoleoyl-2-arachidonoyl-GPC (18:2/20:4n6)*	0.90	1.05	0.98	1.01	**0.85**
Phosphatidylcholine (PC)	1-linoleoyl-2-linolenoyl-GPC (18:2/18:3)*	0.85	0.99	0.94	1.16	**1.24**
Lysophospholipid	1-linoleoyl-GPA (18:2)*	**0.78**	1.10	0.97	0.91	**0.65**
Lysophospholipid	1-linoleoyl-GPC (18:2)	**0.84**	0.98	0.97	1.04	**0.83**
Lysophospholipid	1-linoleoyl-GPE (18:2)*	**0.79**	0.90	0.85	1.02	**0.58**
Lysophospholipid	1-linoleoyl-GPG (18:2)*	**0.63**	0.98	0.85	1.05	**0.54**

Lysophospholipid	1-linoleoyl-GPI (18:2)*	**0.52**	0.81	**0.60**	**0.63**	**0.40**
Lysophospholipid	1-linoleoyl-GPS (18:2)*	1.13	1.40	1.02	1.30	**0.41**
Monoacylglycerol	1-linoleoylglycerol (18:2)	0.79	1.16	0.84	1.02	**0.48**
Histidine Metabolism	1-methyl-4-imidazoleacetate	1.19	1.05	1.20	0.93	0.95
Histidine Metabolism	1-methyl-5-imidazoleacetate	0.96	1.41	1.11	1.14	1.04
Histidine Metabolism	1-methyl-5-imidazolelactate	0.96	1.28	1.08	1.05	1.01
Guanidino and Acetamido Metabolism	1-methylguanidine	0.85	0.89	0.85	0.97	1.32
Histidine Metabolism	1-methylhistamine	1.50	1.27	1.16	0.87	0.66
Histidine Metabolism	1-methylhistidine	1.22	1.46	1.32	1.13	**1.28**
Nicotinate and Nicotinamide Metabolism	1-methylnicotinamide	0.87	0.95	0.91	0.75	0.79
Phosphatidylcholine (PC)	1-myristoyl-2-arachidonoyl-GPC (14:0/20:4)*	0.97	1.01	0.99	1.01	1.13
Phosphatidylcholine (PC)	1-myristoyl-2-palmitoyl-GPC (14:0/16:0)	0.93	1.03	1.04	**1.15**	1.09
Monoacylglycerol	1-myristoylglycerol (14:0)	**0.65**	1.05	**0.69**	0.96	**0.43**
Phosphatidylethanolamine (PE)	1-oleoyl-2-arachidonoyl-GPE (18:1/20:4)*	**1.23**	1.16	1.05	**1.23**	1.14
Phosphatidylinositol (PI)	1-oleoyl-2-arachidonoyl-GPI (18:1/20:4)*	0.89	1.14	0.99	1.01	0.82
Phosphatidylcholine (PC)	1-oleoyl-2-docosahexaenoyl-GPC (18:1/22:6)*	**1.18**	**1.48**	**1.21**	1.22	0.90
Phosphatidylethanolamine (PE)	1-oleoyl-2-docosahexaenoyl-GPE (18:1/22:6)*	1.17	0.98	1.16	1.07	1.44
Phosphatidylcholine (PC)	1-oleoyl-2-linoleoyl-GPC (18:1/18:2)*	0.87	1.10	1.05	1.01	**0.70**
Phosphatidylethanolamine (PE)	1-oleoyl-2-linoleoyl-GPE (18:1/18:2)*	0.95	1.13	1.03	1.13	1.15
Lysophospholipid	1-oleoyl-GPC (18:1)	0.92	1.08	0.99	1.04	0.90
Lysophospholipid	1-oleoyl-GPE (18:1)	0.91	1.12	1.04	1.04	**0.79**
Lysophospholipid	1-oleoyl-GPI (18:1)	**0.51**	0.93	**0.48**	**0.45**	**0.36**
Monoacylglycerol	1-oleoylglycerol (18:1)	1.12	**1.74**	0.74	**1.59**	**0.54**
Phosphatidylcholine (PC)	1-palmitoleoyl-2-linolenoyl-GPC (16:1/18:3)*	0.84	0.96	1.01	1.08	1.33
Phosphatidylcholine (PC)	1-palmitoleoyl-2-linoleoyl-GPC (16:1/18:2)*	0.99	1.18	1.09	1.15	1.22
Lysophospholipid	1-palmitoleoyl-GPC (16:1)*	0.87	1.13	1.03	0.99	1.02
Monoacylglycerol	1-palmitoleoylglycerol (16:1)*	**0.65**	1.04	**0.68**	0.87	**0.52**

Phosphatidylcholine (PC)	1-palmitoyl-2-arachidonoyl-GPC (16:0/20:4n6)	1.02	1.06	1.04	1.13	0.98
Phosphatidylethanolamine (PE)	1-palmitoyl-2-arachidonoyl-GPE (16:0/20:4)*	1.00	0.94	**0.85**	1.03	1.08
Phosphatidylinositol (PI)	1-palmitoyl-2-arachidonoyl-GPI (16:0/20:4)*	**0.79**	**0.79**	**0.80**	0.94	0.90
Phosphatidylcholine (PC)	1-palmitoyl-2-dihomo-linolenoyl-GPC (16:0/20:3n3 or 6)*	0.99	1.18	1.10	1.17	0.93
Phosphatidylcholine (PC)	1-palmitoyl-2-docosahexaenoyl-GPC (16:0/22:6)	1.04	1.04	1.01	1.15	1.09
Phosphatidylethanolamine (PE)	1-palmitoyl-2-docosahexaenoyl-GPE (16:0/22:6)*	0.94	**0.74**	0.83	0.85	1.44
Phosphatidylcholine (PC)	1-palmitoyl-2-gamma-linolenoyl-GPC (16:0/18:3n6)*	**0.74**	**0.62**	**0.82**	0.91	0.85
Phosphatidylcholine (PC)	1-palmitoyl-2-linoleoyl-GPC (16:0/18:2)	**0.96**	1.08	1.04	1.18	1.01
Phosphatidylethanolamine (PE)	1-palmitoyl-2-linoleoyl-GPE (16:0/18:2)	**0.84**	0.95	**0.84**	1.09	1.18
Phosphatidylinositol (PI)	1-palmitoyl-2-linoleoyl-GPI (16:0/18:2)	**0.69**	**0.77**	**0.81**	0.94	0.89
Phosphatidylcholine (PC)	1-palmitoyl-2-oleoyl-GPC (16:0/18:1)	0.97	1.02	1.02	1.10	1.15
Phosphatidylethanolamine (PE)	1-palmitoyl-2-oleoyl-GPE (16:0/18:1)	1.19	1.08	1.09	1.22	**1.38**
Phosphatidylinositol (PI)	1-palmitoyl-2-oleoyl-GPI (16:0/18:1)*	0.80	0.88	0.89	0.99	0.99
Phosphatidylcholine (PC)	1-palmitoyl-2-palmitoleoyl-GPC (16:0/16:1)*	0.82	0.95	0.99	1.01	1.22
Phosphatidylcholine (PC)	1-palmitoyl-2-stearoyl-GPC (16:0/18:0)	1.00	**0.87**	0.98	1.12	1.07
Lysophospholipid	1-palmitoyl-GPA (16:0)	0.84	1.06	0.88	0.83	0.84
Lysophospholipid	1-palmitoyl-GPC (16:0)	0.94	0.99	0.94	1.01	0.95
Lysophospholipid	1-palmitoyl-GPE (16:0)	0.91	0.91	**0.85**	0.98	1.07
Lysophospholipid	1-palmitoyl-GPG (16:0)*	**0.44**	0.80	**0.60**	0.84	**0.65**
Lysophospholipid	1-palmitoyl-GPI (16:0)	**0.50**	0.75	**0.41**	**0.49**	**0.41**
Monoacylglycerol	1-palmitoylglycerol (16:0)	**0.78**	1.14	1.01	1.13	**0.57**
Monoacylglycerol	1-pentadecanoylglycerol (15:0)	**0.74**	1.14	0.92	1.06	**0.57**
Histidine Metabolism	1-ribosyl-imidazoleacetate*	0.90	1.42	0.74	0.96	1.02
Phosphatidylcholine (PC)	1-stearoyl-2-arachidonoyl-GPC (18:0/20:4)	1.01	0.94	0.99	1.07	0.91

Phosphatidylethanolamine (PE)	1-stearoyl-2-arachidonoyl-GPE (18:0/20:4)	1.00	0.84	**0.85**	0.97	1.05
Phosphatidylinositol (PI)	1-stearoyl-2-arachidonoyl-GPI (18:0/20:4)	0.95	**0.94**	0.96	1.03	0.99
Phosphatidylserine (PS)	1-stearoyl-2-arachidonoyl-GPS (18:0/20:4)	**2.43**	1.21	2.07	2.74	1.63
Phosphatidylcholine (PC)	1-stearoyl-2-docosahexaenoyl-GPC (18:0/22:6)	1.04	0.88	0.94	1.11	**1.15**
Phosphatidylethanolamine (PE)	1-stearoyl-2-docosahexaenoyl-GPE (18:0/22:6)*	0.88	**0.66**	0.85	0.90	**1.44**
Phosphatidylcholine (PC)	1-stearoyl-2-linoleoyl-GPC (18:0/18:2)*	**0.91**	0.98	0.98	1.10	**0.88**
Phosphatidylethanolamine (PE)	1-stearoyl-2-linoleoyl-GPE (18:0/18:2)*	**0.82**	**0.81**	**0.79**	0.97	0.98
Phosphatidylinositol (PI)	1-stearoyl-2-linoleoyl-GPI (18:0/18:2)	**0.75**	**0.81**	**0.83**	0.90	0.89
Phosphatidylcholine (PC)	1-stearoyl-2-oleoyl-GPC (18:0/18:1)	0.95	0.94	0.96	1.04	1.04
Phosphatidylethanolamine (PE)	1-stearoyl-2-oleoyl-GPE (18:0/18:1)	0.86	**0.75**	**0.83**	0.87	1.27
Phosphatidylinositol (PI)	1-stearoyl-2-oleoyl-GPI (18:0/18:1)*	0.83	0.90	0.84	1.00	1.00
Lysophospholipid	1-stearoyl-GPC (18:0)	0.96	**0.89**	**0.87**	0.97	**0.84**
Lysophospholipid	1-stearoyl-GPE (18:0)	0.93	**0.88**	**0.85**	0.92	0.99
Lysophospholipid	1-stearoyl-GPI (18:0)	**0.56**	0.78	**0.47**	**0.46**	**0.43**
Phosphatidylcholine (PC)	1,2-dilinoleoyl-GPC (18:2/18:2)	**0.83**	0.96	0.95	1.05	0.94
Phosphatidylethanolamine (PE)	1,2-dilinoleoyl-GPE (18:2/18:2)*	**0.75**	0.86	0.94	1.13	1.08
Phosphatidylcholine (PC)	1,2-dioleoyl-GPC (18:1/18:1)	1.00	1.19	1.02	1.04	**0.88**
Phosphatidylcholine (PC)	1,2-dipalmitoyl-GPC (16:0/16:0)	1.10	1.14	**1.16**	**1.33**	1.11
Phosphatidylethanolamine (PE)	1,2-dipalmitoyl-GPE (16:0/16:0)*	**1.67**	**1.24**	1.31	1.61	1.33
Glycolysis, Gluconeogenesis, and Pyruvate Metabolism	1,5-anhydroglucitol (1,5-AG)	0.98	1.01	1.03	1.18	**0.59**
Long Chain Monounsaturated Fatty Acid	10-heptadecenoate (17:1n7)	0.82	1.27	1.28	1.21	**0.55**
Long Chain Monounsaturated Fatty Acid	10-nonadecenoate (19:1n9)	0.78	1.31	1.20	1.18	**0.44**
Medium Chain Fatty Acid	10-undecenoate (11:1n1)	0.74	0.61	1.17	0.73	0.90
Eicosanoid	12-HEPE	1.19	1.14	**1.61**	1.65	**0.45**
Eicosanoid	12-HETE	1.03	1.39	**3.43**	1.48	**0.21**
Eicosanoid	12-HHTrE	0.53	1.91	6.01	1.07	**0.18**
Fatty Acid, Dihydroxy	12,13-DiHOME	1.14	0.95	**1.54**	**1.52**	0.77

Fatty Acid, Monohydroxy	13-HODE + 9-HODE	0.93	1.04	**1.22**	**1.38**	**0.60**
Docosanoid	14-HDoHE/17-HDoHE	1.22	1.17	**1.57**	1.78	**0.43**
Fatty Acid, Monohydroxy	16-hydroxypalmitate	0.91	0.91	1.26	1.01	**0.74**
Fatty Acid, Branched	18-methylnonadecanoate (i20:0)	**0.71**	1.02	1.16	1.45	**0.42**
Benzoate Metabolism	2-(4-hydroxyphenyl)propionate	1.00	1.00	1.00	1.00	**1.66**
Benzoate Metabolism	2-amino-p-cresol sulfate	0.85	0.77	0.81	0.77	**35.50**
Lysine Metabolism	2-aminoadipate	1.00	**0.84**	0.98	1.27	1.03
Glutathione Metabolism	2-aminobutyrate	1.01	0.96	1.04	1.06	1.20
Fatty Acid, Amino	2-aminoheptanoate	0.96	1.09	1.14	0.86	1.02
Fatty Acid, Amino	2-aminooctanoate	1.21	**1.31**	**1.53**	1.17	**0.75**
Food Component/Plant	2-aminophenol sulfate	0.78	1.36	0.77	0.67	**16.52**
Monoacylglycerol	2-arachidonoylglycerol (20:4)	**0.75**	1.09	0.80	0.96	**0.62**
Fatty Acid Metabolism (Acyl Glycine)	2-butenoylglycine	0.89	0.79	**0.62**	1.02	1.29
Monoacylglycerol	2-docosahexaenoylglycerol (22:6)*	0.85	1.12	0.81	1.02	**0.58**
Leucine, Isoleucine and Valine Metabolism	2-hydroxy-3-methylvalerate	0.31	0.27	0.31	0.47	0.28
Methionine, Cysteine, SAM and Taurine Metabolism	2-hydroxy-4-(methylthio)butanoic acid	**0.68**	**0.62**	0.89	0.90	**4.06**
Fatty Acid, Dicarboxylate	2-hydroxyadipate	0.90	0.82	0.96	1.04	0.91
Fatty Acid, Monohydroxy	2-hydroxyarachidate*	0.74	1.30	0.85	**1.43**	0.67
Fatty Acid, Monohydroxy	2-hydroxybehenate	**0.76**	1.08	0.97	**1.19**	0.94
Glutathione Metabolism	2-hydroxybutyrate/2-hydroxyisobutyrate	0.93	0.90	0.99	0.95	1.17
Fatty Acid, Monohydroxy	2-hydroxydecanoate	0.89	0.83	**1.43**	1.06	0.88
Fatty Acid, Dicarboxylate	2-hydroxyglutarate	0.89	1.01	1.27	1.28	1.28
Benzoate Metabolism	2-hydroxyhippurate (salicylurate)	0.85	1.10	0.96	1.12	0.91
Fatty Acid, Monohydroxy	2-hydroxyoctanoate	0.99	1.07	**1.38**	1.04	0.81
Fatty Acid, Monohydroxy	2-hydroxypalmitate	**0.66**	1.03	0.80	0.90	**0.56**
Phenylalanine Metabolism	2-hydroxyphenylacetate	0.84	**0.58**	1.00	0.86	0.94
Fatty Acid, Dicarboxylate	2-hydroxysebacate	0.81	1.09	1.06	0.98	**0.42**

Fatty Acid, Monohydroxy	2-hydroxystearate	**0.64**	1.07	**0.71**	0.85	**0.63**
Food Component/Plant	2-isopropylmalate	0.55	0.46	0.71	0.51	**1.62**
Food Component/Plant	2-keto-3-deoxy-gluconate	0.71	0.71	0.90	0.52	0.48
Fructose, Mannose and Galactose Metabolism	2-ketogulonate	0.96	0.89	0.87	0.80	**2.69**
Monoacylglycerol	2-linoleoylglycerol (18:2)	0.81	1.08	**0.79**	1.00	**0.51**
Benzoate Metabolism	2-methoxyhydroquinone sulfate (1)	1.08	0.99	1.07	1.16	0.86
Benzoate Metabolism	2-methoxyhydroquinone sulfate (2)	1.24	1.26	1.31	**1.34**	1.03
Leucine, Isoleucine and Valine Metabolism	2-methylbutyrylcarnitine (C5)	1.26	1.15	1.21	1.02	1.47
Leucine, Isoleucine and Valine Metabolism	2-methylbutyrylglycine	0.75	**0.47**	**0.50**	1.06	0.92
TCA Cycle	2-methylcitrate/homocitrate	0.93	1.04	0.99	1.23	1.01
Glycine, Serine and Threonine Metabolism	2-methylserine	1.45	**1.62**	**2.21**	**1.84**	0.99
Ascorbate and Aldarate Metabolism	2-O-methylascorbic acid	1.01	0.86	0.84	0.89	**1.23**
Monoacylglycerol	2-oleoylglycerol (18:1)	0.82	1.16	**0.71**	0.97	**0.41**
Food Component/Plant	2-oxindole-3-acetate	0.89	1.09	0.97	0.96	1.19
Lysine Metabolism	2-oxoadipate	1.01	1.26	1.47	1.20	1.16
Urea cycle; Arginine and Proline Metabolism	2-oxoarginine*	**0.77**	0.93	0.84	**1.16**	0.97
Lysophospholipid	2-palmitoleoyl-GPC (16:1)*	**0.57**	0.94	0.84	0.79	0.69
Monoacylglycerol	2-palmitoleoylglycerol (16:1)*	0.64	0.93	0.65	0.81	**0.52**
Lysophospholipid	2-palmitoyl-GPC (16:0)*	**0.68**	1.03	**0.76**	0.93	0.74
Monoacylglycerol	2-palmitoylglycerol (16:0)	**0.59**	1.19	0.97	0.75	**0.55**
Food Component/Plant	2-piperidinone	1.04	0.77	1.00	0.86	1.15
Lysophospholipid	2-stearoyl-GPE (18:0)*	**0.67**	0.99	**0.70**	0.83	**0.67**
Chemical	2,2'-Methylenebis(6-tert-butyl-p-cresol)	0.63	0.96	0.54	1.41	1.30
Leucine, Isoleucine and Valine Metabolism	2,3-dihydroxy-2-methylbutyrate	1.04	1.23	1.18	**1.50**	1.28
Methionine, Cysteine, SAM and Taurine Metabolism	2,3-dihydroxy-5-methylthio-4-pentenoate (DMTPA)*	0.91	0.94	1.10	0.86	0.90
Food Component/Plant	2,3-dihydroxyisovalerate	**0.45**	0.52	0.72	0.66	**0.48**
Chemical	2,4-di-tert-butylphenol	**0.71**	1.14	**0.83**	1.09	0.80

Drug - Topical Agents	2,6-dihydroxybenzoic acid	0.83	1.31	1.10	0.97	1.12
Food Component/Plant	2,8-quinolinediol sulfate	1.00	1.00	1.00	1.00	**2.27**
Pyrimidine Metabolism, Cytidine containing	2'-deoxycytidine	**1.18**	1.18	1.07	1.14	1.01
Purine Metabolism, (Hypo)Xanthine/Inosine containing	2'-deoxyinosine	0.98	2.67	**5.68**	1.41	**0.37**
Pyrimidine Metabolism, Uracil containing	2'-deoxyuridine	1.14	**0.80**	0.88	1.05	1.44
Pyrimidine Metabolism, Cytidine containing	2'-O-methylcytidine	0.95	0.79	0.90	0.93	0.84
Pyrimidine Metabolism, Uracil containing	2'-O-methyluridine	0.87	**0.75**	0.81	0.95	0.94
Fatty Acid, Dihydroxy	2R,3R-dihydroxybutyrate	0.90	1.03	0.98	1.10	**0.84**
Fatty Acid, Dihydroxy	2S,3R-dihydroxybutyrate	0.98	0.99	0.93	1.05	1.13
Benzoate Metabolism	3-(2-hydroxyphenyl)propionate	0.88	1.12	1.59	1.30	**2.05**
Benzoate Metabolism	3-(3-hydroxyphenyl)propionate sulfate	1.00	1.00	1.00	1.00	**3.63**
Tyrosine Metabolism	3-(4-hydroxyphenyl)lactate	0.97	0.95	0.88	0.91	0.93
Benzoate Metabolism	3-(4-hydroxyphenyl)propionate	1.29	1.38	1.40	3.59	**2.25**
Chemical	3-acetylphenol sulfate	0.74	0.74	0.97	0.74	**6.01**
Urea cycle; Arginine and Proline Metabolism	3-amino-2-piperidone	1.02	1.13	1.13	1.14	0.94
Pyrimidine Metabolism, Thymine containing	3-aminoisobutyrate	**0.79**	**0.78**	0.93	1.15	0.92
Chemical	3-bromo-5-chloro-2,6-dihydroxybenzoic acid*	**0.65**	1.45	1.00	1.05	1.08
Fatty Acid, Dicarboxylate	3-carboxy-4-methyl-5-pentyl-2-furanpropionate (3-CMPFP)**	**0.76**	1.08	0.94	0.91	**0.66**
Fatty Acid, Dicarboxylate	3-carboxy-4-methyl-5-propyl-2-furanpropanoate (CMPF)	**0.80**	0.86	0.92	0.98	**1.21**
Fatty Acid Metabolism (Acyl Carnitine, Monounsaturated)	3-decenoylcarnitine	1.11	1.05	**1.60**	1.39	**0.72**
Secondary Bile Acid Metabolism	3-dehydrocholate	**6.49**	**8.20**	**12.43**	10.88	1.00
Food Component/Plant	3-formylindole	0.77	1.20	1.30	0.99	0.89
Leucine, Isoleucine and Valine Metabolism	3-hydroxy-2-ethylpropionate	0.96	0.94	1.28	1.08	**1.26**
Chemical	3-hydroxy-2-methylpyridine sulfate	0.95	0.76	0.87	0.79	1.32

Mevalonate Metabolism	3-hydroxy-3-methylglutarate	1.08	0.93	0.90	1.05	1.11
Fatty Acid, Dicarboxylate	3-hydroxyadipate	0.83	**0.71**	0.85	0.82	**0.66**
Ketone Bodies	3-hydroxybutyrate (BHBA)	**0.80**	1.03	1.13	0.86	**1.91**
Fatty Acid Metabolism (Acyl Glycine)	3-hydroxybutyroylglycine**	1.42	1.46	1.23	**3.02**	**2.83**
Fatty Acid, Monohydroxy	3-hydroxydecanoate	1.05	1.07	**1.88**	1.20	**0.49**
Fatty Acid Metabolism (Acyl Carnitine, Hydroxy)	3-hydroxydecanoylcarnitine	**1.43**	1.31	**1.78**	1.59	1.00
Fatty Acid, Dicarboxylate	3-hydroxydodecanedioate*	0.94	**0.68**	**1.69**	1.07	**0.68**
Fatty Acid, Monohydroxy	3-hydroxyhexanoate	1.08	0.83	**1.90**	0.91	**2.74**
Fatty Acid Metabolism (Acyl Carnitine, Hydroxy)	3-hydroxyhexanoylcarnitine (1)	**1.30**	1.34	**1.74**	1.43	1.39
Fatty Acid Metabolism (Acyl Carnitine, Hydroxy)	3-hydroxyhexanoylcarnitine (2)	1.94	1.50	**2.32**	1.27	**1.80**
Leucine, Isoleucine and Valine Metabolism	3-hydroxyisobutyrate	**0.65**	0.78	1.00	0.94	0.88
Fatty Acid, Monohydroxy	3-hydroxylaurate	1.04	0.97	**1.87**	1.16	**0.36**
Fatty Acid, Monohydroxy	3-hydroxymyristate	0.91	0.83	1.46	1.04	**0.38**
Fatty Acid, Monohydroxy	3-hydroxyoctanoate	1.03	1.02	**2.27**	1.09	0.89
Fatty Acid Metabolism (Acyl Carnitine, Hydroxy)	3-hydroxyoctanoylcarnitine (1)	**1.28**	1.25	**1.50**	**1.59**	**1.50**
Fatty Acid Metabolism (Acyl Carnitine, Hydroxy)	3-hydroxyoctanoylcarnitine (2)	**1.55**	**1.58**	**1.82**	1.59	**2.30**
Fatty Acid Metabolism (Acyl Glycine)	3-hydroxyoctanoylglycine	1.41	0.70	0.97	2.44	1.07
Fatty Acid Metabolism (Acyl Carnitine, Hydroxy)	3-hydroxyoleoylcarnitine	**1.40**	**1.38**	**2.17**	**1.73**	0.88
Fatty Acid, Monohydroxy	3-hydroxypalmitate	**0.67**	0.83	1.13	0.86	**0.45**
Fatty Acid Metabolism (Acyl Carnitine, Hydroxy)	3-hydroxypalmitoylcarnitine	**1.25**	**1.20**	**1.56**	**1.48**	0.98
Chemical	3-hydroxypyridine sulfate	0.95	0.93	0.89	0.85	1.21
Fatty Acid, Monohydroxy	3-hydroxysebacate	0.78	**0.73**	**1.42**	1.08	0.92

Fatty Acid, Monohydroxy	3-hydroxystearate	**0.52**	**0.53**	0.69	**0.54**	**0.35**
Fatty Acid, Monohydroxy	3-hydroxysuberate	0.68	0.55	0.61	0.86	0.73
Food Component/Plant	3-indoleglyoxylic acid	**0.64**	**0.72**	0.96	**0.62**	**0.75**
Tryptophan Metabolism	3-indoxyl sulfate	0.68	1.24	0.95	0.94	**316.97**
Benzoate Metabolism	3-methoxycatechol sulfate (1)	2.57	0.55	1.80	0.93	**1.77**
Benzoate Metabolism	3-methoxycatechol sulfate (2)	2.10	0.73	1.32	0.65	**5.73**
Tyrosine Metabolism	3-methoxytyrosine	**0.75**	**0.75**	0.90	0.91	0.94
Benzoate Metabolism	3-methyl catechol sulfate (1)	1.01	0.94	1.14	0.65	**5.72**
Leucine, Isoleucine and Valine Metabolism	3-methyl-2-oxobutyrate	0.92	0.96	1.08	1.05	0.97
Leucine, Isoleucine and Valine Metabolism	3-methyl-2-oxovalerate	0.93	0.98	**1.14**	1.11	1.03
Leucine, Isoleucine and Valine Metabolism	3-methylcrotonylglycine	**0.68**	0.70	**0.57**	1.11	**0.66**
Pyrimidine Metabolism, Cytidine containing	3-methylcytidine	1.09	0.96	0.99	0.85	**0.64**
Leucine, Isoleucine and Valine Metabolism	3-methylglutaconate	**0.77**	**0.84**	0.91	0.94	0.95
Fatty Acid, Dicarboxylate	3-methylglutarate/2-methylglutarate	1.17	0.77	0.76	0.87	1.15
Histidine Metabolism	3-methylhistidine	**1.26**	**1.37**	**1.31**	1.05	1.23
Benzoate Metabolism	3-phenylpropionate (hydrocinnamate)	1.29	0.93	1.53	3.48	**109.01**
Glycolysis, Gluconeogenesis, and Pyruvate Metabolism	3-phosphoglycerate	1.57	1.18	1.55	**3.61**	0.62
Pyrimidine Metabolism, Uracil containing	3-ureidopropionate	1.29	1.44	1.08	**1.31**	**1.99**
Fatty Acid, Dihydroxy	3,4-dihydroxybutyrate	1.11	1.07	1.14	1.02	**1.16**
Tyrosine Metabolism	3,4-dihydroxyphenylacetate sulfate	1.05	0.84	1.17	0.99	0.84
Chemical	3,5-dichloro-2,6-dihydroxybenzoic acid	0.70	1.45	1.10	1.06	1.11
Chemical	4-acetamidobenzoate	0.84	0.96	1.07	0.66	**2.84**
Polyamine Metabolism	4-acetamidobutanoate	1.13	1.19	1.23	0.98	0.98
Food Component/Plant	4-acetylcatechol sulfate (1)	0.76	1.52	0.70	0.83	**10.96**
Benzoate Metabolism	4-acetylphenol sulfate	1.01	0.94	0.98	0.99	**2.81**
Benzoate Metabolism	4-allylcatechol sulfate	1.00	1.20	1.00	1.00	**13.74**
Food Component/Plant	4-allylphenol sulfate	0.41	1.17	0.79	0.59	1.58

Chemical	4-chlorobenzoic acid	0.98	1.23	1.19	**1.61**	1.09
Sterol	4-cholesten-3-one	0.96	1.00	1.17	0.87	0.96
Benzoate Metabolism	4-ethylcatechol sulfate	0.92	0.92	0.92	0.92	**196.36**
Benzoate Metabolism	4-ethylphenylsulfate	0.98	0.98	0.98	0.98	**58.21**
Guanidino and Acetamido Metabolism	4-guanidinobutanoate	**0.74**	**0.68**	**0.76**	0.99	**1.53**
Fatty Acid, Monohydroxy	4-hydroxybutyrate (GHB)	1.03	0.96	1.17	**1.63**	0.87
Food Component/Plant	4-hydroxycinnamate	0.64	0.93	0.95	0.73	0.83
Tyrosine Metabolism	4-hydroxycinnamate sulfate	0.79	0.75	0.77	0.85	0.96
Glutamate Metabolism	4-hydroxyglutamate	0.73	**0.62**	**0.64**	0.90	1.31
Benzoate Metabolism	4-hydroxyhippurate	1.05	0.87	0.84	1.08	1.00
Phenylalanine Metabolism	4-hydroxyphenylacetate	1.02	2.54	1.22	1.01	**1.91**
Tyrosine Metabolism	4-hydroxyphenylacetate sulfate	0.97	2.73	0.88	0.74	1.54
Tyrosine Metabolism	4-hydroxyphenylpyruvate	0.94	1.49	1.70	1.16	**2.16**
Histidine Metabolism	4-imidazoleacetate	0.89	1.23	0.78	0.91	1.10
Leucine, Isoleucine and Valine Metabolism	4-methyl-2-oxopentanoate	0.91	0.96	1.10	1.08	1.09
Chemical	4-methylbenzenesulfonate	1.25	0.81	0.49	0.40	0.39
Benzoate Metabolism	4-methylcatechol sulfate	4.58	1.20	4.94	0.64	**24.63**
Fatty Acid Metabolism (Acyl Glycine)	4-methylhexanoylglycine	0.84	**0.60**	**0.55**	1.51	1.24
Benzoate Metabolism	4-vinylcatechol sulfate	**0.49**	0.61	0.69	0.52	**1.93**
Food Component/Plant	4-vinylguaiacol glucuronide	0.83	0.95	0.99	0.86	1.12
Food Component/Plant	4-vinylguaiacol sulfate	1.11	**0.64**	0.79	0.75	**1.66**
Benzoate Metabolism	4-vinylphenol sulfate	0.84	1.16	1.31	0.71	**1.94**
Lysine Metabolism	5-(galactosylhydroxy)-L-lysine	0.79	0.80	0.85	0.87	**0.68**
Lysine Metabolism	5-aminovalerate	1.95	**3.23**	1.42	1.63	**1.73**
Medium Chain Fatty Acid	5-dodecenoate (12:1n7)	1.04	0.82	**1.56**	1.11	**0.53**
Fatty Acid Metabolism (Acyl Carnitine, Monounsaturated)	5-dodecenoylcarnitine (C12:1)	1.25	1.05	**1.89**	1.19	1.83
Eicosanoid	5-HETE	0.78	0.85	0.82	0.61	**0.34**

Chemical	5-hydroxy-2-methylpyridine sulfate	1.29	0.86	1.24	0.79	**2.17**
Fatty Acid, Monohydroxy	5-hydroxyhexanoate	1.02	1.07	**1.35**	1.29	0.95
Tryptophan Metabolism	5-hydroxyindoleacetate	1.02	1.18	1.18	0.97	0.81
Lysine Metabolism	5-hydroxylysine	0.96	1.00	0.91	1.10	**1.21**
Pyrimidine Metabolism, Cytidine containing	5-methyl-2'-deoxycytidine	1.10	0.90	1.06	1.04	**2.02**
Pyrimidine Metabolism, Cytidine containing	5-methylcytidine	1.06	1.00	0.99	1.04	1.29
Polyamine Metabolism	5-methylthioadenosine (MTA)	1.08	**1.20**	1.11	1.27	**0.66**
Methionine, Cysteine, SAM and Taurine Metabolism	5-methylthioribose**	0.97	1.11	**1.15**	1.11	0.87
Pyrimidine Metabolism, Uracil containing	5-methyluridine (ribothymidine)	0.94	**0.62**	0.84	0.98	0.93
Glutathione Metabolism	5-oxoproline	**0.84**	0.90	0.86	0.95	**0.73**
Pyrimidine Metabolism, Thymine containing	5,6-dihydrothymine	0.76	0.71	0.87	1.20	**0.64**
Pyrimidine Metabolism, Uracil containing	5,6-dihydrouracil	1.26	0.99	1.08	1.12	1.13
Pyrimidine Metabolism, Uracil containing	5,6-dihydrouridine	**1.43**	**1.87**	**1.66**	**1.49**	1.37
Chemical	6-hydroxyindole sulfate	1.00	1.00	1.00	1.00	**2.91**
Lysine Metabolism	6-oxopiperidine-2-carboxylate	0.98	0.73	1.07	0.99	1.23
Sterol	7-alpha-hydroxy-3-oxo-4-cholestenoate (7-Hoca)	1.18	**2.31**	**1.93**	1.19	0.90
Secondary Bile Acid Metabolism	7-ketodeoxycholate	**4.89**	**5.30**	**32.93**	83.25	**2.94**
Purine Metabolism, Guanine containing	7-methylguanine	1.12	1.06	1.11	1.09	1.02
Fatty Acid, Monohydroxy	8-hydroxyoctanoate	1.08	1.18	**2.08**	1.43	0.77
Fatty Acid, Dihydroxy	9,10-DiHOME	1.23	0.99	**1.74**	**1.74**	0.98
Fatty Acid Metabolism (Acyl Carnitine, Short Chain)	acetylcarnitine (C2)	1.15	**1.23**	**1.18**	1.05	**1.24**
TCA Cycle	aconitate [cis or trans]	1.05	1.23	**1.20**	**1.27**	1.12
Purine Metabolism, Adenine containing	adenine	**0.68**	**0.48**	**0.66**	0.86	**0.63**
Purine Metabolism, Adenine containing	adenosine	2.73	0.56	1.29	**2.68**	1.10

Purine Metabolism, Adenine containing	adenosine 5'-monophosphate (AMP)	1.01	0.11	0.67	**3.14**	0.63
Fatty Acid, Dicarboxylate	adipate (C6-DC)	0.99	0.99	1.51	1.12	**0.64**
Fatty Acid Metabolism (Acyl Carnitine, Dicarboxylate)	adipoylcarnitine (C6-DC)	1.07	**0.75**	1.00	0.92	0.74
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	adrenate (22:4n6)	0.81	1.24	0.88	1.12	**0.44**
Alanine and Aspartate Metabolism	alanine	0.98	0.96	1.17	1.07	1.02
Purine Metabolism, (Hypo)Xanthine/Inosine containing	allantoic acid	0.75	0.85	**0.69**	**0.68**	**0.57**
Purine Metabolism, (Hypo)Xanthine/Inosine containing	allantoin	0.99	1.00	1.05	1.00	1.04
Fatty Acid, Monohydroxy	alpha-hydroxycaproate	0.80	0.87	**1.78**	2.25	0.78
Leucine, Isoleucine and Valine Metabolism	alpha-hydroxyisocaproate	0.41	0.34	0.64	0.54	0.43
Leucine, Isoleucine and Valine Metabolism	alpha-hydroxyisovalerate	0.33	0.30	0.34	0.63	0.29
Glutamate Metabolism	alpha-ketoglutaramate*	0.85	1.01	1.23	0.93	0.79
TCA Cycle	alpha-ketoglutarate	0.97	1.30	0.98	1.02	1.18
Tocopherol Metabolism	alpha-tocopherol	0.85	0.74	0.78	0.78	0.98
Histidine Metabolism	anserine	1.03	1.04	1.15	1.11	1.21
Tryptophan Metabolism	anthranilate	**0.61**	1.15	0.98	0.79	1.27
Pentose Metabolism	arabitol/xylitol	**0.80**	0.87	0.87	0.95	0.97
Pentose Metabolism	arabonate/xylonate	0.89	0.82	0.87	**0.76**	**0.75**
Long Chain Saturated Fatty Acid	arachidate (20:0)	**0.71**	1.04	0.94	**1.31**	**0.58**
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	arachidonate (20:4n6)	**0.67**	0.95	0.83	0.78	**0.41**
Endocannabinoid	arachidonoyl ethanolamide	0.90	0.85	0.98	1.06	0.93
Fatty Acid Metabolism (Acyl Carnitine, Polyunsaturated)	arachidonoylcarnitine (C20:4)	**1.33**	1.22	**1.74**	1.44	**0.77**
Fatty Acid Metabolism (Acyl Choline)	arachidonoylcholine	0.94	0.89	0.81	0.72	0.85
Urea cycle; Arginine and Proline Metabolism	argininate*	**0.66**	**0.64**	**0.64**	0.93	0.78

Urea cycle; Arginine and Proline Metabolism	arginine	1.01	1.09	0.97	1.20	**0.90**
Urea cycle; Arginine and Proline Metabolism	argininosuccinate	0.99	1.15	1.21	**1.41**	0.74
Ascorbate and Aldarate Metabolism	ascorbate (Vitamin C)	0.26	0.32	0.58	0.34	1.17
Ascorbate and Aldarate Metabolism	ascorbic acid 2-sulfate	1.12	1.21	1.14	0.82	**0.70**
Ascorbate and Aldarate Metabolism	ascorbic acid 3-sulfate*	0.92	0.83	0.85	**0.66**	**0.67**
Alanine and Aspartate Metabolism	asparagine	0.98	1.02	1.10	1.14	1.10
Alanine and Aspartate Metabolism	aspartate	**0.77**	0.77	0.84	0.76	**1.47**
Fatty Acid, Dicarboxylate	azelate (C9-DC)	1.16	1.15	**1.99**	1.46	0.76
Dihydrosphingomyelins	behenoyl dihydrosphingomyelin (d18:0/22:0)*	1.25	1.06	0.76	1.40	1.50
Sphingomyelins	behenoyl sphingomyelin (d18:1/22:0)*	1.00	0.81	0.76	1.19	1.16
Fatty Acid Metabolism (Acyl Carnitine, Long Chain Saturated)	behenoylcarnitine (C22)*	1.17	1.01	1.01	1.32	0.96
Benzoate Metabolism	benzoate	0.93	1.21	1.04	**1.76**	1.56
Pyrimidine Metabolism, Uracil containing	beta-alanine	1.29	1.21	0.95	**1.38**	1.12
Leucine, Isoleucine and Valine Metabolism	beta-hydroxyisovalerate	1.01	0.97	1.21	1.24	0.76
Leucine, Isoleucine and Valine Metabolism	beta-hydroxyisovaleroylcarnitine	1.05	1.02	1.06	0.95	0.90
Primary Bile Acid Metabolism	beta-muricholate	3.85	**5.20**	**15.92**	53.03	0.47
Sterol	beta-sitosterol	0.91	0.75	0.77	0.91	1.41
Glycine, Serine and Threonine Metabolism	betaine	**1.21**	1.29	**1.23**	1.12	1.10
Food Component/Plant	betonicine	0.84	1.02	1.01	1.03	1.10
Hemoglobin and Porphyrin Metabolism	bilirubin (Z,Z)	0.45	0.54	1.04	0.56	**2.10**
Partially Characterized Molecules	bilirubin degradation product, C17H18N2O4 (1)**	0.89	0.93	1.19	1.04	0.95
Partially Characterized Molecules	bilirubin degradation product, C17H18N2O4 (2)**	0.87	0.88	1.10	1.03	1.02
Partially Characterized Molecules	bilirubin degradation product, C17H18N2O4 (3)**	0.83	0.82	1.07	0.86	0.98

Partially Characterized Molecules	bilirubin degradation product, C17H20N2O5 (1)**	0.86	0.78	1.11	0.77	0.98
Partially Characterized Molecules	bilirubin degradation product, C17H20N2O5 (2)**	0.90	0.78	1.11	0.74	0.96
Hemoglobin and Porphyrin Metabolism	biliverdin	1.01	1.05	1.06	1.02	0.98
Tetrahydrobiopterin Metabolism	biopterin	0.96	0.99	1.07	1.07	**1.25**
Fatty Acid, Dicarboxylate	branched chain 14:0 dicarboxylic acid**	0.84	1.04	1.08	1.16	**3.75**
Partially Characterized Molecules	branched-chain, straight-chain, or cyclopropyl 10:1 fatty acid (1)*	0.66	1.01	1.21	1.35	0.53
Partially Characterized Molecules	branched-chain, straight-chain, or cyclopropyl 10:1 fatty acid (3)*	1.28	1.35	**1.80**	**1.57**	0.58
Partially Characterized Molecules	branched-chain, straight-chain, or cyclopropyl 12:1 fatty acid*	1.00	0.79	1.41	0.84	1.34
Short Chain Fatty Acid	butyrate/isobutyrate (4:0)	1.00	**1.24**	**1.45**	1.13	2.41
Fatty Acid Metabolism (also BCAA Metabolism)	butyrylcarnitine (C4)	1.25	1.38	1.04	0.80	**5.44**
Fatty Acid Metabolism (also BCAA Metabolism)	butyrylglycine	**0.72**	**0.58**	**0.42**	0.79	**4.62**
Tryptophan Metabolism	C-glycosyltryptophan	**1.28**	**1.30**	1.33	1.28	1.10
Food Component/Plant	caffeic acid sulfate	0.68	1.20	0.88	0.68	0.76
Sterol	campesterol	0.92	0.79	0.85	0.92	1.14
Medium Chain Fatty Acid	caprate (10:0)	1.10	1.04	**1.57**	1.21	0.87
Medium Chain Fatty Acid	caproate (6:0)	0.96	0.99	**1.34**	1.16	**3.62**
Medium Chain Fatty Acid	caprylate (8:0)	1.05	1.05	**1.54**	1.28	**2.49**
Glutamate Metabolism	carboxyethyl-GABA	0.94	1.03	1.07	1.17	**0.21**
Carnitine Metabolism	carnitine	**1.23**	**1.35**	**1.27**	1.08	0.93
Histidine Metabolism	carnosine	1.14	0.77	1.14	**0.63**	1.18
Vitamin A Metabolism	carotene diol (1)	1.17	1.28	1.53	0.82	1.12
Vitamin A Metabolism	carotene diol (2)	0.86	1.30	1.56	**0.56**	0.99

Tyrosine Metabolism	catechol glucuronide	1.00	1.00	1.00	1.00	**1.26**
Benzoate Metabolism	catechol sulfate	1.16	0.83	1.19	0.74	**167.54**
Ceramides	ceramide (d16:1/24:1, d18:1/22:1)*	1.19	1.04	0.93	**1.58**	1.44
Ceramides	ceramide (d18:1/20:0, d16:1/22:0, d20:1/18:0)*	1.03	**0.64**	0.81	0.87	1.34
Ceramides	ceramide (d18:2/24:1, d18:1/24:2)*	1.12	1.08	0.94	1.13	1.15
Primary Bile Acid Metabolism	chenodeoxycholate	2.99	**5.14**	**6.81**	6.61	**0.52**
Inositol Metabolism	chiro-inositol	**1.63**	**2.10**	**2.08**	**1.81**	1.09
Primary Bile Acid Metabolism	cholate	**16.37**	**27.62**	**35.33**	28.37	1.70
Sterol	cholesterol	**0.88**	0.89	0.92	0.96	0.99
Sterol	cholesterol sulfate	0.97	1.13	1.08	1.10	**0.43**
Phospholipid Metabolism	choline	0.91	0.87	0.90	1.09	1.08
Phospholipid Metabolism	choline phosphate	0.99	0.77	0.87	0.88	0.79
Food Component/Plant	cinnamate	0.91	0.95	**0.89**	1.35	**9.54**
Food Component/Plant	cinnamoylglycine	1.03	0.73	0.68	7.87	**75.87**
Fatty Acid, Branched	cis-3,4-methyleneheptanoate	1.21	1.23	**3.26**	1.67	1.01
Fatty Acid Metabolism (Acyl Carnitine, Medium Chain)	cis-3,4-methyleneheptanoylcarnitine	**1.31**	1.05	**1.81**	1.17	1.13
Medium Chain Fatty Acid	cis-4-decenoate (10:1n6)*	0.89	1.01	**1.78**	1.22	**0.58**
Fatty Acid Metabolism (Acyl Carnitine, Monounsaturated)	cis-4-decenoylcarnitine (C10:1)	**1.37**	1.21	**1.81**	1.34	1.15
TCA Cycle	citrate	0.99	**1.34**	1.21	**1.38**	1.07
Fatty Acid, Branched	citronellic acid	0.82	0.88	**0.76**	1.13	0.76
Urea cycle; Arginine and Proline Metabolism	citrulline	0.96	**1.27**	1.10	**1.17**	**0.79**
Corticosteroids	corticosterone	1.26	**2.29**	1.80	1.33	1.21
Creatine Metabolism	creatine	1.02	1.25	1.16	1.23	**1.10**
Creatine Metabolism	creatinine	0.96	1.10	1.03	1.17	1.02

Methionine, Cysteine, SAM and Taurine Metabolism	cystathionine	1.04	1.09	1.33	1.02	**1.28**
Methionine, Cysteine, SAM and Taurine Metabolism	cysteine	1.00	1.26	1.11	**1.41**	**1.34**
Methionine, Cysteine, SAM and Taurine Metabolism	cysteine s-sulfate	1.13	1.02	1.02	0.89	1.23
Methionine, Cysteine, SAM and Taurine Metabolism	cysteine sulfinic acid	0.85	0.88	0.87	0.83	1.48
Glutathione Metabolism	cysteine-glutathione disulfide	1.09	1.02	0.92	0.88	**2.87**
Glutathione Metabolism	cysteinylglycine disulfide*	**1.49**	1.24	1.00	0.82	**2.11**
Methionine, Cysteine, SAM and Taurine Metabolism	cystine	1.16	1.23	1.09	0.98	**2.14**
Pyrimidine Metabolism, Cytidine containing	cytidine	1.03	1.06	0.98	1.08	0.97
Pyrimidine Metabolism, Cytidine containing	cytidine 5'-monophosphate (5'-CMP)	**1.35**	1.05	1.34	**1.68**	0.74
Pyrimidine Metabolism, Cytidine containing	cytosine	0.93	1.04	0.86	1.06	1.25
Food Component/Plant	daidzein	0.81	1.01	0.87	0.96	0.93
Food Component/Plant	daidzein 7-O-glucuronide	0.94	1.23	1.23	1.10	**1.63**
Food Component/Plant	daidzein sulfate (1)	**0.41**	0.55	0.85	0.87	0.77
Food Component/Plant	daidzein sulfate (2)	0.66	1.02	1.05	1.16	0.79
Fatty Acid, Dicarboxylate	decadienedioic acid (C10:2-DC)**	1.26	1.11	**3.05**	0.97	0.88
Fatty Acid Metabolism (Acyl Carnitine, Medium Chain)	decanoylcarnitine (C10)	1.25	1.05	1.73	1.48	2.19
Carnitine Metabolism	deoxycarnitine	**0.84**	**0.77**	**0.84**	0.92	**0.68**
Secondary Bile Acid Metabolism	deoxycholate	1.00	1.00	1.00	1.00	**4.29**
Chemical	dibutyl sulfosuccinate	0.91	0.50	0.85	1.17	1.33
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	dihomo-linoleate (20:2n6)	0.80	1.47	1.09	1.18	**0.46**
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	dihomo-linolenate (20:3n3 or n6)	0.77	1.26	0.90	0.99	**0.42**

Fatty Acid Metabolism (Acyl Carnitine, Polyunsaturated)	dihomo-linolenoylcarnitine (C20:3n3 or 6)*	1.21	1.08	**1.68**	1.42	0.84
Fatty Acid Metabolism (Acyl Carnitine, Polyunsaturated)	dihomo-linoleoylcarnitine (C20:2)*	**1.36**	1.06	1.46	1.64	1.06
Tetrahydrobiopterin Metabolism	dihydrobiopterin	0.99	0.82	0.97	**0.76**	1.27
Food Component/Plant	dihydrocaffeate sulfate (2)	0.68	15.80	0.30	0.63	**1.31**
Food Component/Plant	dihydroferulate	0.38	0.26	0.26	0.78	0.62
Food Component/Plant	dihydroferulic acid sulfate	0.16	0.10	0.08	0.55	0.29
Pyrimidine Metabolism, Orotate containing	dihydroorotate	1.29	0.95	0.78	0.83	1.26
Glycolysis, Gluconeogenesis, and Pyruvate Metabolism	dihydroxyacetone phosphate (DHAP)	1.45	1.56	**2.08**	1.73	0.90
Chemical	dimethyl sulfone	0.84	**0.79**	**0.80**	**0.65**	**4.06**
Urea cycle; Arginine and Proline Metabolism	dimethylarginine (SDMA + ADMA)	0.98	0.98	0.98	1.05	**0.67**
Glycine, Serine and Threonine Metabolism	dimethylglycine	0.94	0.94	0.94	0.88	**0.81**
Fatty Acid, Dicarboxylate	dimethylmalonic acid	0.77	1.14	1.06	1.23	0.77
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	docosadienoate (22:2n6)	0.80	1.86	1.01	**1.67**	**0.58**
Fatty Acid, Dicarboxylate	docosadioate (C22-DC)	**0.74**	0.91	1.20	**1.49**	0.84
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	docosahexaenoate (DHA; 22:6n3)	0.83	1.10	0.92	0.98	**0.51**
Fatty Acid Metabolism (Acyl Choline)	docosahexaenoylcholine	0.96	0.81	0.75	0.68	1.18
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	docosapentaenoate (n3 DPA; 22:5n3)	0.77	1.33	0.95	1.19	0.69
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	docosapentaenoate (n6 DPA; 22:5n6)	0.79	0.86	0.84	1.03	**0.31**
Fatty Acid Metabolism (Acyl Carnitine, Polyunsaturated)	docosapentaenoylcarnitine (C22:5n3)*	1.32	0.89	**1.94**	1.55	1.08
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	docosatrienoate (22:3n3)	0.77	1.90	1.07	1.40	**0.49**

Long Chain Polyunsaturated Fatty Acid (n3 and n6)	docosatrienoate (22:3n6)*	0.95	1.75	0.81	1.70	**0.38**
Fatty Acid, Dicarboxylate	dodecadienoate (12:2)*	1.00	0.97	**1.85**	1.27	**0.55**
Fatty Acid, Dicarboxylate	dodecanedioate (C12-DC)	1.22	1.22	**2.24**	1.46	0.82
Fatty Acid, Dicarboxylate	dodecenedioate (C12:1-DC)*	0.83	1.42	**1.84**	**1.87**	**1.36**
Tyrosine Metabolism	dopamine 3-O-sulfate	0.97	1.05	1.26	0.86	0.82
Chemical	ectoine	0.90	1.31	0.99	**1.28**	1.00
Fatty Acid, Dicarboxylate	eicosanedioate (C20-DC)	0.76	**0.75**	1.04	1.47	0.85
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	eicosapentaenoate (EPA; 20:5n3)	**0.68**	0.80	0.95	0.83	**0.43**
Fatty Acid, Dicarboxylate	eicosenedioate (C20:1-DC)*	1.07	1.19	**1.90**	1.03	1.38
Long Chain Monounsaturated Fatty Acid	eicosenoate (20:1)	0.77	1.09	1.09	**1.63**	**0.56**
Fatty Acid Metabolism (Acyl Carnitine, Monounsaturated)	eicosenoylcarnitine (C20:1)*	**1.34**	1.11	**1.46**	**2.11**	1.25
Food Component/Plant	enterolactone sulfate	1.00	1.00	1.00	1.00	**1.83**
Food Component/Plant	equol glucuronide	1.00	1.00	1.00	1.00	**1.46**
Food Component/Plant	equol sulfate	1.00	1.00	1.00	1.00	**1.36**
Food Component/Plant	ergothioneine	1.06	1.09	0.95	1.24	**0.81**
Long Chain Monounsaturated Fatty Acid	erucate (22:1n9)	0.80	1.32	1.27	**2.02**	0.71
Food Component/Plant	erythritol	1.08	1.18	1.01	**1.22**	1.22
Aminosugar Metabolism	erythronate*	1.01	0.95	0.97	0.99	1.00
Food Component/Plant	ethyl alpha-glucopyranoside	0.82	**1.39**	1.00	**1.55**	0.91
Food Component/Plant	ethyl beta-glucopyranoside	1.08	**1.64**	1.35	**1.44**	0.81
Leucine, Isoleucine and Valine Metabolism	ethylmalonate	1.08	1.29	1.15	0.83	**4.92**
Food Component/Plant	ferulate	0.77	1.29	0.83	0.75	0.84
Food Component/Plant	ferulic acid 4-sulfate	0.83	0.89	0.75	0.80	0.99
Histidine Metabolism	formiminoglutamate	**0.64**	0.69	1.16	0.73	1.49
Fructose, Mannose and Galactose Metabolism	fructose	0.93	0.73	**0.69**	0.70	0.95

Lysine Metabolism	fructosyllysine	**0.77**	0.90	**0.72**	1.13	**0.47**
TCA Cycle	fumarate	1.02	1.04	0.96	1.11	1.04
Fructose, Mannose and Galactose Metabolism	galactonate	**1.65**	**1.84**	**2.10**	**1.49**	0.95
Gamma-glutamyl Amino Acid	gamma-glutamyl-alpha-lysine	0.95	0.92	1.00	1.00	**1.68**
Gamma-glutamyl Amino Acid	gamma-glutamyl-epsilon-lysine	0.69	0.74	1.01	0.91	0.83
Gamma-glutamyl Amino Acid	gamma-glutamylalanine	0.95	0.96	1.37	2.42	**1.53**
Gamma-glutamyl Amino Acid	gamma-glutamylcitrulline*	0.76	0.93	1.08	0.77	1.12
Gamma-glutamyl Amino Acid	gamma-glutamylglutamate	1.01	1.05	0.87	0.97	**2.89**
Gamma-glutamyl Amino Acid	gamma-glutamylglutamine	0.99	1.05	0.96	1.11	**2.16**
Gamma-glutamyl Amino Acid	gamma-glutamylglycine	0.90	0.91	0.86	0.96	**2.07**
Gamma-glutamyl Amino Acid	gamma-glutamylhistidine	0.94	0.98	1.00	0.81	1.85
Gamma-glutamyl Amino Acid	gamma-glutamylisoleucine*	0.80	0.96	0.89	0.96	1.57
Gamma-glutamyl Amino Acid	gamma-glutamylleucine	**0.80**	0.91	0.93	0.92	**1.87**
Gamma-glutamyl Amino Acid	gamma-glutamylmethionine	0.84	0.86	0.94	0.76	**2.57**
Gamma-glutamyl Amino Acid	gamma-glutamylphenylalanine	0.83	1.07	1.06	1.02	**1.62**
Gamma-glutamyl Amino Acid	gamma-glutamylserine	1.01	0.96	1.05	0.90	**1.73**
Gamma-glutamyl Amino Acid	gamma-glutamylthreonine	0.97	1.12	1.09	1.06	**1.88**
Gamma-glutamyl Amino Acid	gamma-glutamyltryptophan	0.91	1.04	1.14	0.91	**2.07**
Gamma-glutamyl Amino Acid	gamma-glutamyltyrosine	0.85	0.94	0.96	0.88	**1.82**
Gamma-glutamyl Amino Acid	gamma-glutamylvaline	0.80	0.91	0.90	0.95	1.71
Tocopherol Metabolism	gamma-tocopherol/beta-tocopherol	0.90	**0.75**	0.79	0.95	1.11
Food Component/Plant	genistein	**0.71**	1.05	0.95	1.17	1.03
Food Component/Plant	genistein glucuronide*	0.85	1.50	1.55	1.37	**1.65**
Food Component/Plant	genistein sulfate*	**0.59**	1.18	1.22	1.28	0.68
Tyrosine Metabolism	gentisate	0.88	1.04	0.91	0.82	**2.25**
Food Component/Plant	gluconate	**1.19**	1.04	1.13	1.04	1.22
Glycolysis, Gluconeogenesis, and Pyruvate Metabolism	glucose	0.95	0.88	**0.83**	0.87	0.97

Glycolysis, Gluconeogenesis, and Pyruvate Metabolism	glucose 6-phosphate	1.37	1.05	1.61	3.27	0.62
Aminosugar Metabolism	glucuronate	0.98	1.02	0.99	0.89	**2.07**
Partially Characterized Molecules	glucuronide of C14H22O4 (1)*	0.87	0.88	1.64	1.01	**3.44**
Glutamate Metabolism	glutamate	1.01	0.99	1.05	1.11	1.40
Glutamate Metabolism	glutamine	0.95	0.95	0.93	1.07	1.03
Partially Characterized Molecules	glutamine_degradant*	0.88	1.28	1.98	1.07	0.98
Fatty Acid, Dicarboxylate	glutarate (C5-DC)	0.80	**0.75**	0.81	**0.74**	0.87
Lysine Metabolism	glutarylcarnitine (C5-DC)	1.26	0.99	1.15	0.80	**0.37**
Glutathione Metabolism	glutathione, oxidized (GSSG)	1.00	1.00	1.04	0.99	2.40
Glycolysis, Gluconeogenesis, and Pyruvate Metabolism	glycerate	1.00	0.98	1.04	1.00	1.12
Glycerolipid Metabolism	glycerol	0.97	0.91	1.06	1.14	0.89
Glycerolipid Metabolism	glycerol 3-phosphate	0.87	**0.74**	0.91	1.01	1.83
Phospholipid Metabolism	glycerophosphoethanolamine	0.92	0.90	**0.79**	0.88	**0.58**
Glycerolipid Metabolism	glycerophosphoglycerol	**0.81**	**0.72**	0.94	0.93	**1.57**
Phospholipid Metabolism	glycerophosphoinositol*	0.70	0.66	**0.64**	**0.45**	**0.57**
Phospholipid Metabolism	glycerophosphorylcholine (GPC)	0.93	0.91	**0.91**	0.96	**0.87**
Phospholipid Metabolism	glycerophosphoserine*	1.15	1.14	1.10	1.16	1.07
Glycine, Serine and Threonine Metabolism	glycine	0.90	0.93	0.84	1.07	1.04
Partially Characterized Molecules	glycine conjugate of C6H10O2 (2)*	1.24	0.90	0.75	1.44	1.09
Partially Characterized Molecules	glycine conjugate of C6H10O2 (3)*	0.96	0.63	0.92	1.31	1.76
Food Component/Plant	glycitein sulfate (2)	0.70	0.98	1.25	0.90	0.64
Primary Bile Acid Metabolism	glyco-beta-muricholate**	4.41	3.13	**9.47**	3.13	0.79
Primary Bile Acid Metabolism	glycocholate	**6.63**	**6.25**	**15.63**	3.56	0.87
Chemical	glycolate (hydroxyacetate)	0.95	0.80	1.17	0.90	1.55
Hexosylceramides (HCER)	glycosyl ceramide (d16:1/24:1, d18:1/22:1)*	1.56	1.26	0.97	1.56	0.89
Hexosylceramides (HCER)	glycosyl ceramide (d18:1/20:0, d16:1/22:0)*	1.24	0.79	0.90	0.93	1.14

Hexosylceramides (HCER)	glycosyl ceramide (d18:1/23:1, d17:1/24:1)*	1.35	1.20	1.11	0.77	0.82
Hexosylceramides (HCER)	glycosyl ceramide (d18:2/24:1, d18:1/24:2)*	1.38	1.13	0.96	1.02	1.00
Hexosylceramides (HCER)	glycosyl-N-behenoyl-sphingadienine (d18:2/22:0)*	0.99	0.87	0.64	1.10	0.85
Hexosylceramides (HCER)	glycosyl-N-behenoyl-sphingosine (d18:1/22:0)*	1.35	0.99	0.72	1.14	1.15
Hexosylceramides (HCER)	glycosyl-N-nervonoyl-sphingosine (d18:1/24:1)*	1.36	1.09	0.97	0.97	1.08
Hexosylceramides (HCER)	glycosyl-N-palmitoyl-sphingosine (d18:1/16:0)	1.27	0.88	1.01	**0.76**	1.21
Hexosylceramides (HCER)	glycosyl-N-stearoyl-sphingosine (d18:1/18:0)	1.75	0.69	1.18	**0.39**	1.66
Dipeptide	glycylvaline	1.06	1.12	**0.71**	1.13	1.22
Benzoate Metabolism	guaiacol sulfate	0.44	0.37	0.61	0.58	**2.95**
Creatine Metabolism	guanidinoacetate	1.03	1.05	1.38	2.32	**0.73**
Guanidino and Acetamido Metabolism	guanidinosuccinate	0.64	**0.48**	0.69	0.68	0.86
Purine Metabolism, Guanine containing	guanosine	0.80	0.96	**1.43**	**0.30**	**0.32**
Purine Metabolism, Guanine containing	guanosine 5'-monophosphate (5'-GMP)	1.29	0.48	1.12	2.02	0.62
Ascorbate and Aldarate Metabolism	gulonate*	0.95	0.92	0.85	0.89	**2.62**
Hemoglobin and Porphyrin Metabolism	heme	1.22	**1.40**	1.14	**1.56**	**0.53**
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	heneicosapentaenoate (21:5n3)	0.88	1.23	0.98	1.09	**0.42**
Fatty Acid, Dicarboxylate	heptadecanedioate (C17-DC)	0.97	0.79	**1.28**	1.42	1.01
Medium Chain Fatty Acid	heptanoate (7:0)	1.01	1.03	**1.52**	1.11	**1.68**
Fatty Acid Metabolism (Acyl Glycine)	heptanoyl glycine	**0.53**	**0.41**	**0.37**	1.13	1.48
Fatty Acid, Dicarboxylate	heptenedioate (C7:1-DC)*	1.24	0.84	1.35	0.65	0.73
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	hexadecadienoate (16:2n6)	0.98	1.10	**1.47**	**1.38**	**0.55**
Fatty Acid, Dicarboxylate	hexadecanedioate (C16-DC)	0.91	**0.70**	1.29	1.29	1.06
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	hexadecatrienoate (16:3n3)	1.07	0.96	**1.61**	**1.38**	**0.43**
Fatty Acid, Dicarboxylate	hexadecenedioate (C16:1-DC)*	0.94	0.83	1.33	1.56	1.07

Fatty Acid Metabolism (Acyl Carnitine, Medium Chain)	hexanoylcarnitine (C6)	1.30	1.38	1.12	0.74	**16.67**
Fatty Acid Metabolism (Acyl Glycine)	hexanoylglycine	0.73	0.69	**0.42**	1.06	**3.04**
Endocannabinoid	hexanoyltaurine	0.72	**0.43**	0.89	0.91	**7.84**
Benzoate Metabolism	hippurate	1.32	0.95	1.04	1.91	**17.41**
Histidine Metabolism	histamine	0.74	1.80	1.03	0.83	0.53
Histidine Metabolism	histidine	1.08	1.10	1.09	1.08	1.09
Food Component/Plant	histidine betaine (hercynine)*	0.94	1.06	1.20	1.08	**0.57**
Urea cycle; Arginine and Proline Metabolism	homoarginine	0.92	0.98	0.99	0.97	**0.43**
Urea cycle; Arginine and Proline Metabolism	homocitrulline	1.03	1.18	1.05	0.82	1.14
Food Component/Plant	homostachydrine*	1.10	**1.57**	1.25	1.08	0.74
Tyrosine Metabolism	homovanillate sulfate	0.89	0.70	1.07	0.93	1.01
Histidine Metabolism	hydantoin-5-propionate	0.65	0.53	0.46	0.92	0.68
Food Component/Plant	hydroquinone beta-D-glucopyranoside	1.12	0.83	0.98	0.89	1.29
Drug - Topical Agents	hydroquinone sulfate	0.80	0.89	0.86	0.68	**5.84**
Lysine Metabolism	hydroxy-N6,N6,N6-trimethyllysine*	0.95	1.10	1.00	1.20	**0.68**
Fatty Acid, Monohydroxy	hydroxy-undecanedioate (OH-C11:0-DC)*	1.14	1.04	**1.88**	1.26	**0.64**
Alanine and Aspartate Metabolism	hydroxyasparagine**	1.07	1.10	1.12	0.96	0.97
Thiamine Metabolism	hydroxymethylpyrimidine	0.83	1.01	0.90	0.90	0.85
Sphingomyelins	hydroxypalmitoyl sphingomyelin (d18:1/16:0(OH))**	**0.85**	0.94	1.00	1.02	**0.85**
Secondary Bile Acid Metabolism	hyocholate	1.43	1.66	**3.05**	3.40	0.99
Methionine, Cysteine, SAM and Taurine Metabolism	hypotaurine	1.23	**1.82**	**1.49**	**1.79**	**2.24**
Purine Metabolism, (Hypo)Xanthine/Inosine containing	hypoxanthine	1.12	1.55	**2.27**	1.21	0.71
Histidine Metabolism	imidazole lactate	0.83	1.00	0.75	1.17	1.23
Histidine Metabolism	imidazole propionate	0.98	0.81	0.93	1.00	**1.73**

Tryptophan Metabolism	indole-3-carboxylate	0.91	0.83	1.14	0.99	1.02
Tryptophan Metabolism	indoleacetate	1.20	2.94	1.87	0.77	1.31
Tryptophan Metabolism	indoleacetylglycine	1.25	3.10	1.13	0.85	1.05
Tryptophan Metabolism	indoleacrylate	0.91	1.14	1.07	40.93	**55.13**
Tryptophan Metabolism	indolelactate	**0.73**	0.93	1.08	0.87	1.00
Tryptophan Metabolism	indolepropionate	1.22	1.11	1.37	29.57	**171.90**
Tryptophan Metabolism	indolepropionylglycine	1.00	1.00	1.00	1.36	**2.24**
Food Component/Plant	indolin-2-one	1.00	1.00	1.00	1.00	**3.82**
Tryptophan Metabolism	indoxyl glucuronide	1.00	1.00	1.00	1.00	**2.31**
Purine Metabolism, (Hypo)Xanthine/Inosine containing	inosine	1.07	1.50	**2.50**	0.86	0.55
Leucine, Isoleucine and Valine Metabolism	isobutyrylcarnitine (C4)	1.41	1.22	1.29	0.97	**1.70**
Fatty Acid Metabolism (Acyl Carnitine, Short Chain)	isocaproylcarnitine	2.88	1.38	1.59	0.77	**4.62**
Fatty Acid Metabolism (Acyl Glycine)	isocaproylglycine	1.26	0.61	**0.52**	1.26	1.14
TCA Cycle	isocitrate	0.81	1.09	1.17	1.15	**1.96**
TCA Cycle	isocitric lactone	1.68	1.62	**1.97**	1.19	1.23
Leucine, Isoleucine and Valine Metabolism	isoleucine	**0.87**	0.99	0.93	1.02	0.91
Dipeptide Derivative	isoleucylhydroxyproline*	0.85	0.82	**0.60**	0.89	0.99
Leucine, Isoleucine and Valine Metabolism	isovalerate (i5:0)	**0.81**	**0.78**	1.08	**1.14**	**3.58**
Leucine, Isoleucine and Valine Metabolism	isovalerylcarnitine (C5)	0.81	1.00	0.92	0.74	**2.08**
Leucine, Isoleucine and Valine Metabolism	isovalerylglycine	**0.58**	**0.52**	**0.44**	0.83	1.36
TCA Cycle	itaconate	**1.59**	1.39	1.12	0.91	**2.63**
Tryptophan Metabolism	kynurenate	**0.74**	0.87	0.87	0.83	**0.45**
Tryptophan Metabolism	kynurenine	0.74	1.08	1.28	0.76	1.36
Glycolysis, Gluconeogenesis, and Pyruvate Metabolism	lactate	1.06	1.13	0.96	1.05	1.01

Lactosylceramides (LCER)	lactosyl-N-palmitoyl-sphingosine (d18:1/16:0)	**0.69**	**0.73**	0.92	0.93	1.13
Methionine, Cysteine, SAM and Taurine Metabolism	lanthionine	0.85	1.28	0.98	1.04	0.94
Fatty Acid Metabolism (Acyl Carnitine, Medium Chain)	laurylcarnitine (C12)	1.23	1.09	**1.75**	1.43	1.13
Leucine, Isoleucine and Valine Metabolism	leucine	**0.86**	0.92	0.91	0.99	**0.89**
Dipeptide Derivative	leucylhydroxyproline*	0.97	0.84	0.81	0.92	**0.63**
Sphingomyelins	lignoceroyl sphingomyelin (d18:1/24:0)	0.93	**0.79**	**0.80**	0.96	1.05
Fatty Acid Metabolism (Acyl Carnitine, Long Chain Saturated)	lignoceroylcarnitine (C24)*	**1.24**	1.00	1.00	1.03	0.96
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	linoleate (18:2n6)	**0.78**	1.08	1.12	1.07	**0.51**
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	linolenate [alpha or gamma; (18:3n3 or 6)]	0.79	1.03	1.28	1.13	**0.53**
Fatty Acid Metabolism (Acyl Carnitine, Polyunsaturated)	linolenoylcarnitine (C18:3)*	**1.30**	**1.26**	**1.77**	1.72	1.00
Endocannabinoid	linoleoyl ethanolamide	**0.61**	0.96	0.81	0.94	**0.58**
Diacylglycerol	linoleoyl-arachidonoyl-glycerol (18:2/20:4) [1]*	1.27	0.89	0.98	1.09	1.22
Diacylglycerol	linoleoyl-arachidonoyl-glycerol (18:2/20:4) [2]*	1.30	0.91	0.91	**1.54**	1.39
Diacylglycerol	linoleoyl-docosahexaenoyl-glycerol (18:2/22:6) [1]*	0.88	**0.41**	1.00	**0.59**	0.89
Diacylglycerol	linoleoyl-docosahexaenoyl-glycerol (18:2/22:6) [2]*	**1.70**	1.70	0.96	**2.10**	1.46
Diacylglycerol	linoleoyl-linolenoyl-glycerol (18:2/18:3) [2]*	1.02	1.45	0.74	**1.67**	1.32
Diacylglycerol	linoleoyl-linoleoyl-glycerol (18:2/18:2) [1]*	0.60	**0.28**	0.82	**0.39**	0.74
Diacylglycerol	linoleoyl-linoleoyl-glycerol (18:2/18:2) [2]*	1.14	1.36	0.83	**1.50**	1.07
Fatty Acid Metabolism (Acyl Carnitine, Polyunsaturated)	linoleoylcarnitine (C18:2)*	1.21	1.06	**1.64**	1.57	0.90
Fatty Acid Metabolism (Acyl Choline)	linoleoylcholine*	0.75	0.84	**0.72**	**0.64**	0.89
Lysine Metabolism	lysine	1.00	0.99	1.02	1.14	0.99

Pentose Metabolism	lyxonate	0.89	0.97	0.98	1.00	**0.67**
TCA Cycle	malate	1.03	1.05	1.00	1.10	1.05
Fatty Acid, Dicarboxylate	maleate	**0.78**	0.90	1.05	1.02	0.89
Fatty Acid Synthesis	malonate	0.94	1.09	1.03	**1.24**	**1.39**
Fatty Acid Synthesis	malonylcarnitine	1.12	**1.62**	1.32	1.70	0.82
Food Component/Plant	maltol sulfate	1.11	0.80	0.90	0.99	1.45
Glycogen Metabolism	maltose	1.24	0.63	0.68	0.80	0.80
Fructose, Mannose and Galactose Metabolism	mannitol/sorbitol	0.93	**0.81**	0.86	0.98	**1.39**
Food Component/Plant	mannonate*	1.07	**0.77**	**0.79**	**0.75**	**0.73**
Fructose, Mannose and Galactose Metabolism	mannose	1.00	0.86	0.87	0.81	0.98
Long Chain Saturated Fatty Acid	margarate (17:0)	**0.73**	1.16	0.95	1.07	**0.54**
Fatty Acid Metabolism (Acyl Carnitine, Long Chain Saturated)	margaroylcarnitine (C17)*	**1.22**	1.11	1.38	1.22	**1.38**
Methionine, Cysteine, SAM and Taurine Metabolism	methionine	0.87	1.10	1.14	0.93	0.95
Methionine, Cysteine, SAM and Taurine Metabolism	methionine sulfone	0.80	1.18	1.02	0.90	0.80
Methionine, Cysteine, SAM and Taurine Metabolism	methionine sulfoxide	0.86	1.18	1.14	1.09	1.00
Food Component/Plant	methyl glucopyranoside (alpha + beta)	1.18	**1.81**	**1.36**	1.47	**0.49**
Food Component/Plant	methyl indole-3-acetate	0.94	**1.57**	1.10	1.15	**0.46**
Food Component/Plant	methyl vanillate sulfate	0.34	1.01	0.68	1.27	0.31
Benzoate Metabolism	methyl-4-hydroxybenzoate sulfate	0.38	1.30	0.61	0.81	0.55
Fatty Acid Metabolism (also BCAA Metabolism)	methylmalonate (MMA)	0.83	0.85	0.89	0.83	1.07
Purine and Pyrimidine Metabolism	methylphosphate	1.00	1.06	1.01	**1.26**	1.11
Leucine, Isoleucine and Valine Metabolism	methylsuccinate	1.42	**0.58**	**0.72**	**0.71**	**3.60**
Mevalonate Metabolism	mevalonate	1.12	1.16	1.20	1.12	**1.19**
Inositol Metabolism	myo-inositol	**1.21**	**1.53**	1.28	1.17	1.08

Long Chain Saturated Fatty Acid	myristate (14:0)	0.79	0.94	**1.46**	1.01	**0.49**
Fatty Acid Metabolism (Acyl Carnitine, Monounsaturated)	myristoleoylcarnitine (C14:1)*	1.31	1.18	**2.41**	1.51	0.97
Fatty Acid Metabolism (Acyl Carnitine, Long Chain Saturated)	myristoylcarnitine (C14)	1.15	1.09	**1.63**	1.31	0.92
Food Component/Plant	N-(2-furoyl)glycine	1.09	0.76	0.92	1.19	1.37
Histidine Metabolism	N-acetyl-1-methylhistidine*	1.08	1.38	1.17	1.18	**0.42**
Fatty Acid, Amino	N-acetyl-2-aminooctanoate*	1.05	1.12	1.30	1.22	0.93
Histidine Metabolism	N-acetyl-3-methylhistidine*	1.10	1.34	0.94	1.07	**0.54**
Glutamate Metabolism	N-acetyl-aspartyl-glutamate (NAAG)	**1.18**	**1.28**	**1.27**	1.08	1.06
Pyrimidine Metabolism, Uracil containing	N-acetyl-beta-alanine	0.94	1.27	1.15	1.32	0.77
Polyamine Metabolism	N-acetyl-isoputreanine	0.81	1.01	0.99	0.82	**0.16**
Alanine and Aspartate Metabolism	N-acetylalanine	0.96	0.87	0.97	0.93	**1.34**
Urea cycle; Arginine and Proline Metabolism	N-acetylarginine	**0.70**	0.89	1.02	1.03	1.00
Alanine and Aspartate Metabolism	N-acetylasparagine	**0.79**	**0.61**	0.85	0.82	1.40
Alanine and Aspartate Metabolism	N-acetylaspartate (NAA)	**1.27**	1.16	1.24	1.14	1.09
Urea cycle; Arginine and Proline Metabolism	N-acetylcitrulline	**0.75**	0.95	0.92	0.98	**0.76**
Aminosugar Metabolism	N-acetylglucosamine/N-acetylgalactosamine	1.01	0.95	1.00	1.06	0.90
Aminosugar Metabolism	N-acetylglucosaminylasparagine	1.06	1.04	0.94	1.21	0.78
Glutamate Metabolism	N-acetylglutamate	0.98	0.77	1.05	0.93	**2.05**
Glutamate Metabolism	N-acetylglutamine	0.99	1.10	1.03	**1.25**	**2.08**
Glycine, Serine and Threonine Metabolism	N-acetylglycine	0.84	**0.72**	**0.74**	0.89	1.24
Histidine Metabolism	N-acetylhistamine	0.97	0.92	0.89	0.81	0.97
Histidine Metabolism	N-acetylhistidine	0.91	**0.71**	0.83	**0.72**	1.16
Urea cycle; Arginine and Proline Metabolism	N-acetylhomocitrulline	0.97	0.95	1.00	0.83	**0.68**
Leucine, Isoleucine and Valine Metabolism	N-acetylisoleucine	**0.68**	**0.69**	**0.76**	0.88	0.86
Tryptophan Metabolism	N-acetylkynurenine (2)	0.65	1.11	1.32	0.82	**1.29**
Leucine, Isoleucine and Valine Metabolism	N-acetylleucine	**0.70**	**0.70**	0.78	0.86	1.23

Methionine, Cysteine, SAM and Taurine Metabolism	N-acetylmethionine	0.81	0.85	0.91	0.84	**1.63**
Methionine, Cysteine, SAM and Taurine Metabolism	N-acetylmethionine sulfoxide	0.92	1.14	1.12	0.97	**1.38**
Aminosugar Metabolism	N-acetylneuraminate	**1.16**	1.19	1.15	0.97	1.08
Phenylalanine Metabolism	N-acetylphenylalanine	0.75	0.91	0.98	0.90	**0.61**
Urea cycle; Arginine and Proline Metabolism	N-acetylproline	0.87	0.86	0.97	1.01	1.02
Polyamine Metabolism	N-acetylputrescine	1.28	1.16	1.24	1.22	1.24
Food Component/Plant	N-acetylpyrraline	0.84	1.12	1.08	0.98	1.16
Glycine, Serine and Threonine Metabolism	N-acetylserine	0.96	0.82	0.92	0.89	**1.85**
Methionine, Cysteine, SAM and Taurine Metabolism	N-acetyltaurine	0.93	1.05	1.18	1.02	**2.57**
Glycine, Serine and Threonine Metabolism	N-acetylthreonine	**0.81**	**0.74**	0.92	0.85	1.22
Tryptophan Metabolism	N-acetyltryptophan	**0.64**	0.82	0.86	0.91	0.79
Tyrosine Metabolism	N-acetyltyrosine	0.78	0.83	0.99	0.84	**0.49**
Leucine, Isoleucine and Valine Metabolism	N-acetylvaline	**0.74**	0.79	0.87	0.95	1.19
Ceramides	N-behenoyl-sphingadienine (d18:2/22:0)*	0.82	0.60	**0.59**	1.13	1.25
Pyrimidine Metabolism, Orotate containing	N-carbamoylaspartate	1.02	1.06	0.99	1.14	1.29
Urea cycle; Arginine and Proline Metabolism	N-delta-acetylornithine	1.03	1.38	1.15	1.20	**1.39**
Tryptophan Metabolism	N-formylanthranilic acid	**0.79**	1.20	1.05	0.98	**2.53**
Methionine, Cysteine, SAM and Taurine Metabolism	N-formylmethionine	0.78	0.81	0.67	0.99	1.18
Tyrosine Metabolism	N-formylphenylalanine	0.88	1.04	1.20	**1.53**	1.22
Aminosugar Metabolism	N-glycolylneuraminate	1.14	1.25	1.25	1.34	1.39
Endocannabinoid	N-linoleoyltaurine*	0.89	1.20	1.18	**1.47**	0.79
Glutamate Metabolism	N-methyl-GABA	**0.75**	**0.64**	**0.65**	0.90	**0.57**
Bacterial/Fungal	N-methylpipecolate	0.92	0.97	0.99	0.83	1.16
Urea cycle; Arginine and Proline Metabolism	N-methylproline	0.90	1.10	1.10	1.00	**1.61**

Urea cycle; Arginine and Proline Metabolism	N-monomethylarginine	**0.87**	0.91	0.86	1.11	**0.85**
Fatty Acid Metabolism (Acyl Glycine)	N-octanoylglycine	0.90	0.75	0.75	1.86	**3.71**
Endocannabinoid	N-oleoyltaurine	0.79	1.14	**1.27**	1.46	0.70
Dihydroceramides	N-palmitoyl-phytosphingosine (t18:0/16:0)	**0.74**	0.80	**0.76**	0.81	1.04
Dihydroceramides	N-palmitoyl-sphinganine (d18:0/16:0)	**0.65**	0.71	**0.69**	0.92	**1.39**
Ceramides	N-palmitoyl-sphingosine (d18:1/16:0)	0.87	**0.77**	**0.77**	**0.74**	1.12
Fatty Acid Metabolism (Acyl Glycine)	N-palmitoylglycine	**0.61**	0.97	0.88	0.85	0.71
Endocannabinoid	N-palmitoyltaurine	**0.64**	1.18	1.42	1.42	0.77
Ceramides	N-stearoyl-sphingosine (d18:1/18:0)*	1.26	0.74	0.78	0.69	1.49
Endocannabinoid	N-stearoylserine*	**0.62**	1.01	0.87	1.11	**0.52**
Endocannabinoid	N-stearoyltaurine	0.75	1.23	1.08	1.29	**0.60**
Modified Peptides	N,N-dimethyl-pro-pro	1.10	**1.24**	**1.35**	**1.36**	**0.76**
Alanine and Aspartate Metabolism	N,N-dimethylalanine	0.94	1.18	1.10	0.96	**3.02**
Lysine Metabolism	N,N,N-trimethyl-5-aminovalerate	1.04	1.32	1.17	1.00	**5.89**
Urea cycle; Arginine and Proline Metabolism	N,N,N-trimethyl-alanylproline betaine (TMAP)	1.03	1.19	**1.39**	**1.25**	**0.70**
Nicotinate and Nicotinamide Metabolism	N1-Methyl-2-pyridone-5-carboxamide	0.91	0.92	0.87	0.88	0.84
Nicotinate and Nicotinamide Metabolism	N1-Methyl-4-pyridone-3-carboxamide	1.17	1.35	0.89	**1.33**	0.89
Purine Metabolism, Adenine containing	N1-methyladenosine	1.03	0.99	1.04	0.86	0.86
Purine Metabolism, (Hypo)Xanthine/Inosine containing	N1-methylinosine	1.12	1.03	1.07	0.97	1.03
Lysine Metabolism	N2-acetyl,N6,N6-dimethyllysine	0.89	0.99	0.89	0.91	0.82
Lysine Metabolism	N2-acetyllysine	**0.66**	**0.74**	0.86	**0.60**	**0.59**
Purine Metabolism, Guanine containing	N2,N2-dimethylguanosine	1.14	1.03	0.84	1.37	**0.63**
Urea cycle; Arginine and Proline Metabolism	N2,N5-diacetylornithine	0.95	1.07	0.93	**1.27**	0.93
Lysine Metabolism	N2,N6-diacetyllysine	**0.77**	0.94	0.93	1.00	**0.64**
Pyrimidine Metabolism, Cytidine containing	N4-acetylcytidine	1.38	2.45	1.86	0.89	1.35
Lysine Metabolism	N6-acetyllysine	1.00	1.14	1.18	0.93	1.12
Purine Metabolism, Adenine containing	N6-carbamoylthreonyladenosine	0.91	0.92	1.07	0.92	0.88

Lysine Metabolism	N6-carboxyethyllysine	0.96	1.07	1.03	0.96	**0.65**
Advanced Glycation End-product	N6-carboxymethyllysine	1.13	**0.69**	1.16	0.92	**0.50**
Lysine Metabolism	N6-methyllysine	0.92	1.04	0.93	0.88	1.21
Purine Metabolism, Adenine containing	N6-succinyladenosine	1.12	1.43	1.30	**1.49**	**0.48**
Lysine Metabolism	N6,N6-dimethyllysine	1.04	1.12	1.03	0.91	**1.53**
Lysine Metabolism	N6,N6,N6-trimethyllysine	1.10	1.15	1.08	1.30	0.97
Chemical	neopentyl glycol adipate**	1.35	1.55	**2.64**	1.82	0.98
Chemical	neopentyl glycol azelate**	0.84	1.19	**2.18**	0.88	1.14
Chemical	neopentyl glycol glutarate**	1.14	1.22	**2.12**	1.72	0.94
Chemical	neopentyl glycol sebacate**	0.94	1.43	**2.44**	1.19	1.27
Chemical	neopentyl glycol suberate**	1.00	1.43	**2.64**	1.35	1.14
Chemical	neopentyl glycol undecanedioate**	0.67	1.43	**2.50**	1.16	1.55
Fatty Acid Metabolism (Acyl Carnitine, Monounsaturated)	nervonoylcarnitine (C24:1)*	**1.45**	1.34	1.41	1.35	1.10
Nicotinate and Nicotinamide Metabolism	nicotinamide	0.94	1.08	0.87	1.24	0.97
Nicotinate and Nicotinamide Metabolism	nicotinamide N-oxide	0.94	1.13	0.97	1.20	0.91
Nicotinate and Nicotinamide Metabolism	nicotinamide ribonucleotide (NMN)	1.30	0.98	0.92	1.82	0.57
Nicotinate and Nicotinamide Metabolism	nicotinamide riboside	1.21	1.20	1.13	1.34	**0.65**
Nicotinate and Nicotinamide Metabolism	nicotinate ribonucleoside	1.02	**1.60**	1.03	1.17	0.80
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	nisinate (24:6n3)	0.92	1.62	0.94	1.34	**0.36**
Fatty Acid, Dicarboxylate	nonadecanedioate (C19-DC)	0.97	0.99	**1.75**	2.11	0.97
Long Chain Saturated Fatty Acid	nonadecanoate (19:0)	**0.70**	1.14	0.85	1.09	**0.41**
Fatty Acid Metabolism (Acyl Carnitine, Medium Chain)	nonanoylcarnitine (C9)	1.28	1.22	1.46	1.05	**7.20**
Benzoate Metabolism	o-cresol sulfate	0.80	**0.69**	1.03	**0.64**	1.74
Chemical	O-sulfo-L-tyrosine	0.92	0.97	1.01	1.07	**0.81**
Fatty Acid, Dicarboxylate	octadecadienedioate (C18:2-DC)*	1.05	1.00	1.53	1.58	1.28

Fatty Acid, Dicarboxylate	octadecanedioate (C18-DC)	0.82	**0.67**	1.10	1.34	0.96
Fatty Acid, Dicarboxylate	octadecenedioate (C18:1-DC)	0.98	0.98	1.57	1.40	1.13
Fatty Acid Metabolism (Acyl Carnitine, Medium Chain)	octanoylcarnitine (C8)	**1.38**	1.21	**1.45**	1.10	**13.88**
Long Chain Monounsaturated Fatty Acid	oleate/vaccenate (18:1)	0.80	1.22	1.21	1.14	**0.47**
Endocannabinoid	oleoyl ethanolamide	0.89	0.84	1.06	0.81	0.73
Diacylglycerol	oleoyl-arachidonoyl-glycerol (18:1/20:4) [2]*	1.20	0.94	0.75	1.28	1.49
Diacylglycerol	oleoyl-linoleoyl-glycerol (18:1/18:2) [1]	0.93	0.87	**0.80**	**0.84**	0.94
Diacylglycerol	oleoyl-linoleoyl-glycerol (18:1/18:2) [2]	0.97	0.85	**0.82**	0.98	0.92
Fatty Acid Metabolism (Acyl Carnitine, Monounsaturated)	oleoylcarnitine (C18:1)	1.24	1.09	**1.62**	1.42	0.93
Fatty Acid Metabolism (Acyl Choline)	oleoylcholine	0.87	0.90	0.83	**0.63**	1.40
Glutathione Metabolism	ophthalmate	1.79	1.13	1.95	0.88	**4.39**
Urea cycle; Arginine and Proline Metabolism	ornithine	**0.88**	0.97	0.99	1.13	1.02
Pyrimidine Metabolism, Orotate containing	orotate	0.95	0.96	0.88	1.27	1.10
Pyrimidine Metabolism, Orotate containing	orotidine	1.09	1.00	0.98	1.17	1.08
Ascorbate and Aldarate Metabolism	oxalate (ethanedioate)	0.99	1.01	1.08	1.01	**1.32**
Tryptophan Metabolism	oxindolylalanine	0.99	0.95	1.32	0.94	1.43
Tyrosine Metabolism	p-cresol glucuronide*	142.38	0.88	115.91	0.75	**72.80**
Benzoate Metabolism	p-cresol sulfate	53.54	**2.52**	75.15	0.62	**56.31**
Benzoate Metabolism	p-hydroxybenzaldehyde	0.85	1.24	0.96	0.84	0.84
Long Chain Saturated Fatty Acid	palmitate (16:0)	**0.83**	1.11	1.03	1.15	**0.67**
Long Chain Monounsaturated Fatty Acid	palmitoleate (16:1n7)	0.79	1.06	**1.84**	1.13	**0.50**
Diacylglycerol	palmitoleoyl-linoleoyl-glycerol (16:1/18:2) [1]*	0.73	**0.61**	0.88	**0.55**	0.72
Fatty Acid Metabolism (Acyl Carnitine, Monounsaturated)	palmitoleoylcarnitine (C16:1)*	1.30	1.07	**2.11**	1.65	0.92
Dihydrosphingomyelins	palmitoyl dihydrosphingomyelin (d18:0/16:0)*	**0.87**	0.88	0.92	0.94	1.04

Endocannabinoid	palmitoyl ethanolamide	0.93	0.95	1.00	1.04	0.97
Sphingomyelins	palmitoyl sphingomyelin (d18:1/16:0)	1.00	1.08	0.96	1.09	1.02
Diacylglycerol	palmitoyl-docosahexaenoyl-glycerol (16:0/22:6) [1]*	0.80	0.90	1.00	1.08	0.94
Diacylglycerol	palmitoyl-linoleoyl-glycerol (16:0/18:2) [1]*	1.07	0.87	0.84	0.90	0.77
Diacylglycerol	palmitoyl-linoleoyl-glycerol (16:0/18:2) [2]*	0.92	0.81	**0.71**	1.14	0.89
Ceramide PEs	palmitoyl-sphingosine-phosphoethanolamine (d18:1/16:0)	**0.75**	**0.63**	0.94	**0.56**	**0.48**
Fatty Acid Metabolism (Acyl Carnitine, Long Chain Saturated)	palmitoylcarnitine (C16)	1.12	1.07	**1.26**	1.22	0.98
Fatty Acid Metabolism (Acyl Choline)	palmitoylcholine	0.94	0.92	0.80	0.70	1.20
Pantothenate and CoA Metabolism	pantothenate	1.03	1.25	1.26	0.87	0.97
Medium Chain Fatty Acid	pelargonate (9:0)	1.21	1.18	**2.01**	1.28	0.99
Long Chain Saturated Fatty Acid	pentadecanoate (15:0)	**0.85**	1.15	**1.14**	**1.22**	**0.70**
Fatty Acid Metabolism (Acyl Carnitine, Long Chain Saturated)	pentadecanoylcarnitine (C15)*	1.11	1.13	**1.62**	**1.51**	**1.30**
Partially Characterized Molecules	pentose acid*	**0.78**	0.87	0.82	0.94	**0.76**
Chemical	perfluorohexanesulfonate (PFHxS)	0.89	1.06	1.07	1.03	**0.69**
Chemical	perfluorooctanesulfonate (PFOS)	0.78	0.77	0.96	1.14	0.84
Tyrosine Metabolism	phenol glucuronide	0.86	0.86	0.86	0.86	**37.21**
Tyrosine Metabolism	phenol sulfate	0.54	0.54	0.70	0.76	**73.48**
Phenylalanine Metabolism	phenylacetate	2.16	1.99	2.98	0.64	**4.25**
Acetylated Peptides	phenylacetylcarnitine	8.86	**3.82**	11.61	0.87	**5.99**
Acetylated Peptides	phenylacetylglutamine	2.64	3.91	1.99	0.97	**2.74**
Acetylated Peptides	phenylacetylglycine	1.98	2.90	1.30	0.98	**2.05**
Acetylated Peptides	phenylacetyltaurine	2.91	1.87	1.58	**0.53**	**3.01**
Phenylalanine Metabolism	phenylalanine	**0.91**	1.03	0.98	1.03	**0.87**
Dipeptide	phenylalanylhydroxyproline*	0.84	0.70	**0.56**	0.60	**0.47**

Phenylalanine Metabolism	phenyllactate (PLA)	**0.71**	0.78	0.89	0.80	1.40
Benzoate Metabolism	phenylpropionylglycine	1.52	**0.55**	**0.54**	8.20	**65.21**
Phenylalanine Metabolism	phenylpyruvate	**0.76**	1.25	1.13	0.98	1.06
Oxidative Phosphorylation	phosphate	1.08	1.07	1.15	**1.71**	1.17
Glycolysis, Gluconeogenesis, and Pyruvate Metabolism	phosphoenolpyruvate (PEP)	1.45	1.27	1.60	2.90	**0.36**
Phospholipid Metabolism	phosphoethanolamine	1.08	1.22	1.34	1.35	0.99
Tryptophan Metabolism	picolinate	0.68	1.07	1.18	0.71	0.69
Fatty Acid Metabolism (Acyl Glycine)	picolinoylglycine	0.85	0.98	1.02	1.13	**0.68**
Fatty Acid, Dicarboxylate	pimelate (C7-DC)	1.04	1.01	1.67	1.13	**0.64**
Fatty Acid Metabolism (Acyl Carnitine, Dicarboxylate)	pimeloylcarnitine/3-methyladipoylcarnitine (C7-DC)	**1.36**	1.32	1.26	1.22	**0.58**
Lysine Metabolism	pipecolate	1.03	1.27	1.00	**1.36**	**1.65**
Urea cycle; Arginine and Proline Metabolism	pro-hydroxy-pro	0.91	1.02	0.88	0.99	**0.61**
Urea cycle; Arginine and Proline Metabolism	proline	0.93	1.03	1.05	1.08	1.08
Dipeptide	prolylglycine	0.90	0.96	0.91	0.84	1.05
Fatty Acid Metabolism (also BCAA Metabolism)	propionylcarnitine (C3)	0.98	0.93	1.19	0.81	**1.59**
Fatty Acid Metabolism (also BCAA Metabolism)	propionylglycine	**0.61**	**0.57**	**0.59**	0.94	0.97
Chemical	propylene azelate (2)**	1.23	1.61	**2.72**	1.40	1.12
Chemical	propylene glutarate (1)**	1.43	1.69	**3.24**	**3.15**	**1.76**
Chemical	propylene glutarate (2)**	1.44	1.71	**3.07**	**3.13**	1.70
Chemical	propylene suberate (1)**	1.36	1.48	**3.08**	2.55	1.29
Chemical	propylene suberate (2)**	1.40	1.48	**3.00**	2.52	1.30
Pyrimidine Metabolism, Uracil containing	pseudouridine	1.06	1.15	**1.40**	0.99	0.97
Polyamine Metabolism	putrescine	1.18	1.10	0.78	1.18	0.85
Vitamin B6 Metabolism	pyridoxal	0.79	0.95	1.00	0.71	0.89

Vitamin B6 Metabolism	pyridoxamine	0.75	1.09	1.13	0.98	0.94
Vitamin B6 Metabolism	pyridoxate	0.91	0.88	0.96	0.91	0.86
Food Component/Plant	pyrraline	0.97	1.31	1.11	1.08	**1.91**
Glycolysis, Gluconeogenesis, and Pyruvate Metabolism	pyruvate	0.98	**1.30**	0.99	0.85	**1.32**
Food Component/Plant	quinate	0.81	1.02	0.93	1.00	0.68
Nicotinate and Nicotinamide Metabolism	quinolinate	1.05	**1.36**	1.69	1.12	**2.12**
Vitamin A Metabolism	retinal	1.06	1.16	**1.36**	**1.36**	1.07
Vitamin A Metabolism	retinol (Vitamin A)	0.91	1.00	0.89	0.90	**1.45**
Pentose Metabolism	ribitol	0.94	0.93	0.98	1.04	0.91
Riboflavin Metabolism	riboflavin (Vitamin B2)	0.98	1.17	1.24	**1.39**	0.91
Pentose Metabolism	ribonate	0.84	0.86	0.86	0.83	**0.76**
Pentose Metabolism	ribose	0.87	1.48	1.46	**0.56**	**0.36**
Chemical	S-(3-hydroxypropyl)mercapturic acid (HPMA)	0.88	0.99	1.01	1.10	1.13
Glutamate Metabolism	S-1-pyrroline-5-carboxylate	0.95	1.09	1.49	1.17	**1.76**
Methionine, Cysteine, SAM and Taurine Metabolism	S-adenosylhomocysteine (SAH)	**0.48**	**0.27**	**0.41**	0.63	0.92
Drug - Other	S-carboxymethyl-L-cysteine	1.05	**1.29**	1.07	**1.27**	0.83
Methionine, Cysteine, SAM and Taurine Metabolism	S-methylcysteine	**1.24**	1.08	**1.27**	0.98	**1.66**
Methionine, Cysteine, SAM and Taurine Metabolism	S-methylcysteine sulfoxide	1.06	0.58	1.91	0.43	1.05
Glutathione Metabolism	S-methylglutathione	0.76	**0.43**	0.72	**0.52**	**1.85**
Drug - Topical Agents	salicylate	0.73	1.03	1.19	0.65	1.52
Glycine, Serine and Threonine Metabolism	sarcosine	**0.71**	**0.71**	**0.76**	0.87	**0.73**
Fatty Acid, Dicarboxylate	sebacate (C10-DC)	1.11	1.12	**1.97**	1.39	0.77
Pentose Metabolism	sedoheptulose	0.97	1.17	0.94	1.36	0.83
Pentose Phosphate Pathway	sedoheptulose-7-phosphate	1.24	1.45	1.56	2.67	**0.24**

Glycine, Serine and Threonine Metabolism	serine	1.05	0.98	1.09	1.04	0.95
Tryptophan Metabolism	serotonin	0.91	0.82	0.95	0.72	**0.31**
Polyamine Metabolism	spermidine	1.24	1.06	0.98	1.20	**0.62**
Polyamine Metabolism	spermine	1.56	1.10	1.70	1.16	0.89
Sphingolipid Synthesis	sphinganine	**1.56**	**1.22**	1.18	1.32	1.33
Sphingolipid Synthesis	sphinganine-1-phosphate	1.03	0.95	0.94	**0.84**	**0.71**
Sphingomyelins	sphingomyelin (d17:1/14:0, d16:1/15:0)*	0.84	0.94	0.89	0.86	**0.77**
Sphingomyelins	sphingomyelin (d17:1/16:0, d18:1/15:0, d16:1/17:0)*	0.81	0.85	1.05	0.85	**0.69**
Sphingomyelins	sphingomyelin (d17:2/16:0, d18:2/15:0)*	0.93	0.89	**0.75**	0.86	0.89
Dihydrosphingomyelins	sphingomyelin (d18:0/18:0, d19:0/17:0)*	1.21	**0.85**	1.07	0.98	1.14
Dihydrosphingomyelins	sphingomyelin (d18:0/20:0, d16:0/22:0)*	0.87	**0.52**	0.79	**0.59**	1.05
Sphingomyelins	sphingomyelin (d18:1/14:0, d16:1/16:0)*	**0.89**	0.91	**0.90**	0.95	**0.81**
Sphingomyelins	sphingomyelin (d18:1/17:0, d17:1/18:0, d19:1/16:0)	**0.84**	**0.85**	0.95	0.88	1.08
Sphingomyelins	sphingomyelin (d18:1/18:1, d18:2/18:0)	0.97	1.01	0.98	**1.17**	0.90
Sphingomyelins	sphingomyelin (d18:1/19:0, d19:1/18:0)*	0.92	**0.77**	0.95	0.89	0.91
Sphingomyelins	sphingomyelin (d18:1/20:0, d16:1/22:0)*	0.92	**0.73**	0.90	0.92	1.02
Sphingomyelins	sphingomyelin (d18:1/20:1, d18:2/20:0)*	1.04	1.01	1.03	1.24	0.89
Sphingomyelins	sphingomyelin (d18:1/21:0, d17:1/22:0, d16:1/23:0)*	0.91	**0.71**	**0.77**	1.07	0.92
Sphingomyelins	sphingomyelin (d18:1/22:1, d18:2/22:0, d16:1/24:1)*	0.98	0.84	0.87	**1.18**	0.95
Sphingomyelins	sphingomyelin (d18:1/22:2, d18:2/22:1, d16:1/24:2)*	1.15	1.14	1.00	**1.41**	0.91
Sphingomyelins	sphingomyelin (d18:1/24:1, d18:2/24:0)*	1.35	**1.55**	0.91	**1.52**	1.29
Sphingomyelins	sphingomyelin (d18:1/25:0, d19:0/24:1, d20:1/23:0, d19:1/24:0)*	1.16	**1.16**	1.14	1.11	0.97
Sphingomyelins	sphingomyelin (d18:2/14:0, d18:1/14:1)*	0.89	**0.88**	0.86	0.90	**0.84**

Sphingomyelins	sphingomyelin (d18:2/16:0, d18:1/16:1)*	1.00	1.01	0.91	1.12	0.99
Sphingomyelins	sphingomyelin (d18:2/18:1)*	1.13	1.04	1.11	1.01	0.84
Sphingomyelins	sphingomyelin (d18:2/21:0, d16:2/23:0)*	1.06	0.87	0.93	**1.21**	0.81
Sphingomyelins	sphingomyelin (d18:2/23:0, d18:1/23:1, d17:1/24:1)*	0.85	**0.80**	0.88	0.82	**0.74**
Sphingomyelins	sphingomyelin (d18:2/23:1)*	0.97	0.97	0.99	0.98	**0.77**
Sphingomyelins	sphingomyelin (d18:2/24:1, d18:1/24:2)*	1.01	1.04	0.99	1.01	0.91
Sphingomyelins	sphingomyelin (d18:2/24:2)*	1.05	1.16	1.04	**1.18**	0.93
Sphingosines	sphingosine	**1.27**	1.12	1.12	1.21	1.19
Sphingosines	sphingosine 1-phosphate	1.06	1.03	0.89	0.95	**0.72**
Food Component/Plant	stachydrine	1.07	**1.25**	1.21	1.01	**1.26**
Long Chain Saturated Fatty Acid	stearate (18:0)	**0.78**	1.05	0.93	1.09	**0.65**
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	stearidonate (18:4n3)	0.87	0.91	1.24	1.14	**0.60**
Endocannabinoid	stearoyl ethanolamide	0.95	0.88	0.99	1.11	0.80
Sphingomyelins	stearoyl sphingomyelin (d18:1/18:0)	0.99	1.02	1.03	1.18	1.04
Fatty Acid Metabolism (Acyl Carnitine, Long Chain Saturated)	stearoylcarnitine (C18)	**1.41**	1.18	1.21	**1.52**	**1.23**
Fatty Acid Metabolism (Acyl Choline)	stearoylcholine*	0.99	0.77	0.81	0.67	1.10
Fatty Acid, Dicarboxylate	suberate (C8-DC)	1.13	1.09	**1.92**	1.36	**0.70**
Fatty Acid Metabolism (Acyl Carnitine, Dicarboxylate)	suberoylcarnitine (C8-DC)	**1.58**	1.10	**1.97**	1.30	**1.55**
TCA Cycle	succinate	0.95	0.83	**0.77**	0.92	0.98
Methionine, Cysteine, SAM and Taurine Metabolism	succinoyltaurine	0.73	**0.42**	**0.68**	**0.59**	0.75
TCA Cycle	succinylcarnitine (C4-DC)	1.15	1.29	1.24	**1.70**	**0.38**
Chemical	sulfate*	0.92	0.99	0.98	1.02	0.96
Food Component/Plant	tartarate	0.84	0.96	0.87	**0.69**	**0.68**
Food Component/Plant	tartronate (hydroxymalonate)	0.98	1.02	0.92	0.91	**0.85**

Methionine, Cysteine, SAM and Taurine Metabolism	taurine	1.02	1.04	1.19	1.18	**1.09**
Primary Bile Acid Metabolism	tauro-beta-muricholate	**0.32**	0.35	6.75	0.61	**0.24**
Primary Bile Acid Metabolism	taurochenodeoxycholate	**0.45**	0.64	4.70	0.93	0.73
Primary Bile Acid Metabolism	taurocholate	**0.33**	0.47	2.23	0.61	0.45
Methionine, Cysteine, SAM and Taurine Metabolism	taurocyamine	1.03	0.72	1.24	0.94	1.08
Secondary Bile Acid Metabolism	taurodeoxycholate	1.11	3.25	0.71	1.09	**367.34**
Secondary Bile Acid Metabolism	taurohyodeoxycholic acid	**0.66**	**0.66**	2.11	0.67	**5.04**
Secondary Bile Acid Metabolism	taurolithocholate 3-sulfate	2.90	7.50	**3.30**	0.87	0.89
Secondary Bile Acid Metabolism	tauroursodeoxycholate	0.63	0.70	12.94	1.05	0.56
Fatty Acid, Dicarboxylate	tetradecadienedioate (C14:2-DC)*	1.07	1.09	**1.71**	**1.66**	**0.75**
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	tetradecadienoate (14:2)*	1.14	0.96	**1.87**	1.21	**0.51**
Fatty Acid, Dicarboxylate	tetradecanedioate (C14-DC)	1.03	0.98	**1.52**	1.34	0.89
Thiamine Metabolism	thiamin (Vitamin B1)	0.81	0.95	0.75	1.12	0.98
Thiamine Metabolism	thiamin monophosphate	0.72	0.77	0.67	0.77	1.02
Chemical	thioproline	1.10	0.97	1.12	0.99	1.10
Ascorbate and Aldarate Metabolism	threonate	0.98	0.99	1.06	0.96	**1.48**
Glycine, Serine and Threonine Metabolism	threonine	0.95	1.02	1.04	1.07	1.07
Pyrimidine Metabolism, Thymine containing	thymidine	1.11	0.86	1.09	0.99	1.25
Pyrimidine Metabolism, Thymine containing	thymine	1.11	1.66	1.24	**1.80**	1.23
Tyrosine Metabolism	thyroxine	0.73	1.10	1.11	0.88	**0.65**
Leucine, Isoleucine and Valine Metabolism	tigloylglycine	0.92	0.74	**0.65**	1.30	0.78
Leucine, Isoleucine and Valine Metabolism	tiglylcarnitine (C5:1-DC)	0.95	1.06	**1.37**	1.09	1.06
Fatty Acid Metabolism (Acyl Glycine)	trans-2-hexenoylglycine	1.13	0.76	0.67	1.48	**2.66**
Fatty Acid Metabolism (Acyl Glycine)	trans-3,4-methyleneheptanoylglycine	0.79	0.68	0.88	1.28	0.92
Urea cycle; Arginine and Proline Metabolism	trans-4-hydroxyproline	0.99	1.11	1.06	**1.22**	0.94

Histidine Metabolism	trans-urocanate	0.86	1.34	1.15	1.18	0.77
Sphingomyelins	tricosanoyl sphingomyelin (d18:1/23:0)*	0.75	**0.53**	0.92	**0.54**	0.84
Fatty Acid, Dicarboxylate	tridecanedioate (C13-DC)	1.25	1.17	**2.26**	1.45	0.81
Nicotinate and Nicotinamide Metabolism	trigonelline (N'-methylnicotinate)	0.92	1.08	1.04	1.07	**1.12**
Phospholipid Metabolism	trimethylamine N-oxide	2.53	0.56	1.25	1.31	**96.73**
Tryptophan Metabolism	tryptophan	**0.84**	0.96	**0.93**	0.94	**0.83**
Tyrosine Metabolism	tyrosine	**0.87**	0.92	0.92	0.97	**0.90**
Fatty Acid, Dicarboxylate	undecanedioate (C11-DC)	1.20	1.15	**2.02**	1.40	0.82
Medium Chain Fatty Acid	undecanoate (11:0)	1.18	1.23	**1.89**	1.36	0.98
Fatty Acid Metabolism (Acyl Carnitine, Monounsaturated)	undecenoylcarnitine (C11:1)	1.09	0.80	1.81	0.87	1.10
Pyrimidine Metabolism, Uracil containing	uracil	1.15	1.08	0.97	1.33	**1.26**
Purine Metabolism, (Hypo)Xanthine/Inosine containing	urate	1.03	0.85	0.86	0.93	0.92
Urea cycle; Arginine and Proline Metabolism	urea	**0.83**	1.04	1.07	1.07	0.97
Pyrimidine Metabolism, Uracil containing	uridine	0.89	**0.72**	**0.78**	0.99	0.95
Pyrimidine Metabolism, Uracil containing	uridine 5'-monophosphate (UMP)	1.21	0.43	0.96	**2.60**	0.58
Secondary Bile Acid Metabolism	ursodeoxycholate	**11.99**	**14.60**	**45.21**	82.94	0.85
Short Chain Fatty Acid	valerate (5:0)	1.04	0.87	**1.55**	1.32	**4.82**
Fatty Acid Metabolism (Acyl Carnitine, Short Chain)	valerylcarnitine (C5)	1.21	1.08	1.39	0.76	**4.00**
Fatty Acid Metabolism (Acyl Glycine)	valerylglycine	**0.55**	**0.37**	**0.43**	0.84	**1.61**
Leucine, Isoleucine and Valine Metabolism	valine	**0.80**	0.87	**0.86**	0.93	**0.85**
Tyrosine Metabolism	vanillactate	1.27	1.04	1.01	0.93	1.36
Food Component/Plant	vanillic acid glycine	0.98	0.66	0.79	0.86	1.05
Purine Metabolism, (Hypo)Xanthine/Inosine containing	xanthine	1.12	**1.63**	**1.55**	1.06	0.62

Purine Metabolism, (Hypo)Xanthine/Inosine containing	xanthosine	1.00	0.81	0.83	0.92	0.88
Tryptophan Metabolism	xanthurenate	**0.64**	**0.66**	0.79	0.94	0.84

Bile acids can affect circulating host lipids by altering fat digestion and systemic hormonal signaling[40]. They are produced by the host and released into the small intestine, where they promote digestion of fats by facilitating micelle formation, and can also act through receptors like the farnesoid X receptor (FXR)[40] and GPBAR1/TGR5[41]. Gut bacteria can modify bile acids, primarily through transformations like deconjugation. Previous reports found that MOL361 can broadly modify bile acids *in vitro*[21], so to determine if these abilities allowed MOL361 and other *Turicibacter* strains to modify host bile acids *in vivo*, the studyprofiled serum bile acids in *Turicibacter*-monocolonized mice. Though each strain uniquely impacted host serum metabolites, the study noted some patterns in bile acids across monocolonized mice in comparison to either their GF or CONV controls. (Note: bile species with amino acid conjugants are typically referred to as "bile salts," but for simplicity, the study will herein refer to both conjugated and unconjugated bile species as "bile acids"). Colonization with all of the *Turicibacter* strains led to a general increase in serum levels of unconjugated primary bile acids like cholate (CA), chenodeoxycholate (CDCA), and β-muricholate (βMCA) (**Fig. 9a-d**), and a similar rise in unconjugated secondary bile acids 3-dehydrocholate and 7-ketodeoxycholate (**Fig. 9e,f**). These responses were highly variable in the case of T129 colonization, leading us to de-emphasize this strain for subsequent experiments. In all, these results suggest that these *Turicibacter* strains are able to impact host bile acids, potentially by deconjugating them in the gut.

To determine potential explanations for increases in unconjugated bile species, it was observed that the levels of conjugated bile acids differed between animals colonized by different *Turicibacter* strains, with the clearest delineation separating H121 from MOL361 and 1E2. MOL361- and 1E2-colonized animals generally had lower levels of taurine-conjugated primary bile acids in comparison to H121-colonized animals (**Fig. 9g-j**), whereas H121 colonization led to an increase in glyco-beta-muricholic acid (GβMCA) (**Fig. 9k**). Female mice displayed the most significant *Turicibacter*-associated changes in circulating bile species, lipids, and cholesterol, indicating sex-dependent responses to *Turicibacter* colonization (**Fig. 14a-c**). This sex difference has also been reported in C57BL/6 mice monocolonized with *T. sanguinis* MOL361, albeit with a directionally different change in adipocyte size[38]. Overall, these data demonstrate that colonization with *Turicibacter* alters serum bile acids, lipids, and cholesterol, as well as host fat mass. Further, while some changes like increased unconjugated bile acids were conserved across *Turicibacter* colonizations, changes to specific conjugated bile acids differed between

Turicibacter strains, with MOL361 and 1E2 leading to lower levels of taurine-conjugated bile acids than H121 colonization.

Turicibacter *strains differ in their ability to modify host bile acids*

Based on the large genetic variation between the *Turicibacter* strains (**Fig. 7**) and the differences in serum lipid and bile acid profiles seen in response to colonization with different strains (**Fig. 8**), the study posited that these strains differ in their ability to modify bile acids. To test this, the study grew each of our nine isolates to stationary phase in rich medium supplemented with a sub-inhibitory concentration of five bile species[21]: cholic acid, chenodeoxycholic acid deoxycholic acid (DCA), taurocholic acid (TCA) and glycochenodeoxycholic acid (GCDCA). The study then used liquid chromatography-mass spectrometry (LC-MS) to characterize the resulting bile transformations performed by each isolate (**Fig. 10a**). The study discovered that the strains not only differed in their ability to modify this combination of bile species, but also that these capabilities generally mirrored the groupings identified in genomic comparisons (**Fig. 10b**). MOL361, 18F6, and GALT-E2 deconjugated both tauro- and glyco- bile acids, and also dehydrogenated CA and CDCA (**Fig. 10b**). 1E2 and TA25 deconjugated tauro- bile acids, but did not detectably deconjugate glyco- bile acids or perform dehydrogenation (**Fig. 10b**). H121 and T129 deconjugated glyco- bile acids, but did not readily deconjugate tauro- bile acids nor perform detectable dehydrogenation (**Fig. 10b**). T46 and GALT-G1 did not have bile-modifying capacity that mirrored their genetic phylogeny; T46 genomically resembled the MOL361 group but performed modifications similar to the H121 group (*i.e.* glyco- but not tauro-deconjugation, minimal dehydrogenation), whereas GALT-G1, which genomically resembled the H121 group, performed more MOL361-like transformations (*i.e.* glyco- and tauro-deconjugation, dehydrogenation of CDCA) (**Fig. 7, 10b, Fig. 15**). Overall, each strain performed at least one of three bile transformations, with some showing capacity for all three (**Fig. 10b, Fig. 15**).

To confirm these intragroup distinctions, the study chose one isolate from each of the subgroups (MOL361, H121, 1E2), and grew them in the presence of four primary conjugated bile acids: TCA, taurochenodeoxycholic acid (TCDCA), glycocholic acid (GCA), and GCDCA. This supported the same pattern seen above; MOL361 deconjugated both groups of bile acids, 1E2 preferentially deconjugated tauro-conjugates, and H121

preferentially deconjugated glyco-conjugates (**Fig. 10c**). MOL361 and 1E2 displayed broad deconjugation of tauro-conjugates and were able to process at least six taurine-conjugated bile acids (**Fig. 21**). These data reveal that while all tested strains are efficient modifiers of bile species, their specific transformations differ in a strain-dependent manner, potentially reflecting functions that influence their differential effects on host lipid biology.

Turicibacter *genomes have different repertoires of bile salt hydrolases*

The different bile modification abilities across strain subgroups suggested that each contained unique repertoires of bile-modifying genes.

Certain bacteria from the gut microbiota dehydrogenate hydroxyl groups from the steroid core of bile acids[42], increasing their polarity and modulating their affinity for host bile acid receptors[43]. The study searched the *Turicibacter* genomes for homologs of the characterized 7α-hydroxysteroid dehydrogenase (7α-HSDH[21]) from *Clostridium absolum*[44]. This revealed genes with 57% amino acid identity in MOL361, 18F6, T46, and GALT-E2, and homologs with 59% amino acid identity in H121 and T129 (**Fig. 16a**). Though the H121-derived putative homolog had higher overall sequence identity than the MOL361-derived homolog, it lacked certain features predicted to be critical for dehydrogenase activity, such as the analogous Asp38 that is catalytically critical for this reaction[44]. Because *in vitro* experiments showed only isolates from the MOL361 group performed bile dehydrogenation, the study cloned the putative 7α-HSDH homolog from MOL361 into *E. coli* C41-pLys and then grew these cells in individual unconjugated bile acids that can be dehydrogenated: CA, CDCA, and DCA. Indeed, the protein encoded by the gene removed the mass equivalent of two hydrogens from CA (**Fig. 16b, c**). Background transformation by *E. coli* prevented clear evidence of CDCA dehydrogenation by this putative 7α-HSDH homolog (**Fig. 16d**), but this homolog did not act on DCA (**Fig. 16e**), supporting its annotation as a 7α-HSDH.

Conjugation increases bile acid solubility and emulsification ability[45], while deconjugation reverses these effects, leading to decreased dietary lipid absorption. To identify *Turicibacter* bile salt hydrolase (*bsh*) genes responsible for the strain-specific differences in bile deconjugation, the study first searched our assembled genomes for annotations of "choloylglycine hydrolase," the broad category that includes these genes. Of these annotated genes, the study identified eight groups of potentially homologous sequences, and found that each *Turicibacter* strain encodes putative choloylglycine

hydrolases from at least two of the eight groups **(Fig. 11a, b)**. Isolates within the same phylogenetic and phenotypic subgroups largely shared similar sequences (**Fig. 11a, b**). To assay the function of the strain-specific putative *bsh* genes, the study cloned and individually expressed one representative sequence from each of the eight putative choloylglycine hydrolase groups in *E. coli* C41-pLys and measured the ability of these engineered bacteria to perform the deconjugations the study observed in the native *Turicibacter*. The study cultured the individual *E. coli* strains to stationary phase in the presence of two tauro- (TCA, TCDCA) or glyco- (GCA, GCDCA) bile acids, then measured their ability to deconjugate these bile acid pools. The study found that *E. coli* expressing four of the eight putative *bsh* gene groups showed deconjugation activity against at least one of the bile acids (**Fig. 11c-e**). From MOL361, one BSH (group IV) is tauro-specific, and one (group I) deconjugates both glyco- and tauro-conjugates (**Fig. 11c, d**). 1E2 shares a tauro-specific BSH with MOL361 (group IV), and has another BSH (group III) with moderate activity on TCDCA (**Fig. 11c, d**). H121 has a BSH (group II) with activity on TCDCA and GCDCA (**Fig. 11c, d**), although this was blunted when presented with the combined four bile acids (**Fig. 11e**), potentially because of competitive inhibition. Collectively, these findings reveal that *Turicibacter* strains contain a range of bile salt hydrolases with deconjugation preferences for different bile acids.

Strain- and substrate-specific bile salt hydrolases from Turicibacter *differentially alter host lipid composition*

Given that *Turicibacter* colonization broadly modified host lipid and bile pools (**Fig. 8**), and that bile transformations have been previously shown to alter host lipids[46,47], the study predicted that expressing *Turicibacter* bile-modifying genes outside the context of *Turicibacter* colonization would be sufficient to impact host lipid biology. To measure the individual effects of these bile acid transformations, the study expressed *Turicibacter bsh* genes off of a genomically- integrated high expression vector[48] in the common gut bacterium *Bacteroides thetaiotaomicron*. This bacterium was chosen because it stably colonizes the murine gut, and unlike *E. coli* C41-pLys, contains a homolog of a characterized 7α-HSDH similar to that of *T. sanguinis* MOL361[49,50], allowing the engineered bacteria to more completely mimic *Turicibacter* bile transformations. These strains generally transformed tauro- and glyco- conjugated bile acids as predicted based on

the BSH characterization in *E. coli*, including preferential TCDCA transformation, indicating they were capable of performing *Turicibacter*-like bile transformations (**Fig. 12a, Fig. 17**). However, the *B. thetaiotaomicron* strain that expressed *bsh* (group III) from strain 1E2 more completely transformed glyco-conjugated bile acids than the strain expressing *bsh* (group II) from H121, counter to the *E. coli* findings. This observation led us to not use the *bsh* (group II)-expressing strain further. Additionally, although a signficiant *in vitro* growth defect in the engineered *B. thetaiotaomicron* strains was not noticed (**Fig. 22**), we observed a bile transformation delay in *B. thetaiotaomicron* expressing *bsh* (group I) from MOL361, that the study could compensate for by extending the growth period (**Fig. 12b,**).

The study monocolonized mice with the *bsh*-expressing *B. thetaiotaomicron* strains and assessed their circulating lipid profiles and abdominal WAT mass. It was found that the engineered strains colonized the gnotobiotic mouse gut at least as well as the parental strain (**Supplemental Fig. 8**), and that expressing individual *Turicibacter bsh* genes in the *B. thetaiotaomicron* background was sufficient to significantly alter host colonic bile levels (**Fig. 12c**) and the absolute abundance of 346 circulating lipid species (**Fig. 12d, Table 7**). In particular, expression of either the group I or group IV *bsh* led to a decrease in triglycerides (**Fig. 12d, e**). Expressing the tauro-specific *bsh* (group IV) from MOL361 also decreased diacylglycerides (**Fig. 12g**). Expressing the broader specificity *bsh* (group I) from MOL361 also led to a decrease of phosphatidylglycine, phosphatidylserine, and cholesterol (**Fig. 12d-f, h, i**). Despite having broad capacity for transformation, *B. thetaiotaomicron* expressing *bsh* (group III) from 1E2 did not alter host lipid profiles as much as the other strains **(Fig. 12d-i)**. On a tissue-level, *bsh*-expression also altered WAT storage in the colonized mice, with the broad tauro-deconjugating BSHs (group I and IV) significantly reducing WAT mass (**Fig. 12j**). Similar to our findings with *Turicibacter* monocolonization, we also observed a sex difference in BSH responses, with male mice showing more consistent decrease in triglycerides in response to the tauro-specific BSH from MOL361, and females showing more consistent triglyceride responses to the broadly deconjugating BSH (**Supplementary Fig. 9**).

To further explore potential factors that may drive the cholesterol and WAT alterations in response to *Turicibacter* colonization and *bsh* expression, liver transcript levels were measured of farnesoid X receptor, (Fxr), a key nuclear receptor for bile acids; cytochrome P450 Family A Subfamily A Member 1/Cholesterol 7α Hydroxylase (Cyp7a1), the rate-limiting enzyme for conversion of cholesterol into bile acids; and glucose-6-

phosphatase (G6pase), a key enzyme for gluconeogenesis. There were no differences in Fxr transcript levels across any of the native and engineered bacterial colonization conditions (**Fig. 23a**). However, similar increases in Cyp7a1 expression (**Fig. 23b**) and decreases in G6pase expression (**Fig. 23c**) were found between the *Turicibacter* and *bsh* colonizations. In all, these results demonstrate that expressing strain-specific *bsh* genes from *Turicibacter*, especially those able to process the abundant taurine-conjugated bile acids present in the murine intestine, is sufficient to drastically alter host cholesterol, bile, and lipid biology.

Discussion

Results from this study show that *Turicibacter* bacteria from the mammalian gut microbiota modulate host bile and lipid compositions in a strain-dependent manner. The study identified and characterized five novel *Turicibacter* genes capable of performing bile transformations (four *bsh*, one 7α-HSDH), and revealed that expression of individual *bsh* genes is sufficient to broadly and differentially alter host lipid profiles. Further, the study found that while bile-transforming genes are present in all our surveyed *Turicibacter* strains, the specific transformation capacity of BSH variants differed by strain in a manner consistent with host environment co-evolution: bile acids in the human gut are a mix of taurine- and glycine-conjugants, whereas murine bile acids are predominantly taurine-conjugants[51,52], providing different bile environments that are preferentially processed by *Turicibacter* strains isolated from their respective gastrointestinal tracts. This close connection between host-specific bile composition and bacterial modifications may be due in part to the bile sensitivity previously exhibited by MOL361 and/or the high abundance of *Turicibacter* in the small intestine, causing these bacteria to more strongly associate with host genes for bile reabsorption and lumenal bile levels than other bile-modifying gut bacteria[21,53–57].

This work displays metabolic consequences of colonization by specific gut bacteria and improves the resolution of our understanding connecting specific taxa—in this case, at the strain level—with host physiology. In rodent and human studies, *Turicibacter* relative abundance often negatively correlates with dietary fats[29,31,58–62] and host adiposity[28,33,63], but some studies have shown opposite relationships[30,64,65]. This could be a result of the phenotypic diversity identified here among *Turicibacter* isolates wherein the host may experience different lipid outcomes depending on their own specific *Turicibacter* strains,

but could also vary with other features such as host genetics and sex[21,38]. Importantly, effects of *Turicibacter* colonization could also be influenced by biogeographic organization of an individual's microbiota; in addition to the specific taxonomic membership, *Turicibacter* positioning in the small and large intestine may affect host consequences from their respective bile modifications by transforming bile pools in either section of the gut tract. Despite genomic and localization differences between them, the study found that MOL361 and H121 induced lipid metabolite changes that indicate increases in fatty acid oxidation, suggesting that these strains at least share features that alter host fatty acid metabolism.

Further research into *bsh* gene regulation in the *Turicibacter* genus, the relationship between bile and *Turicibacter* colonization and transmission behaviors, as well as the native functionality of the putative BSH and 7α-HSDH homologs the study tested, will further explain how these bacteria wields their bile modifications in the intestine. Interestingly, several of the *in vitro* bile transformations, specifically increases in unconjugated bile acids, were generalizable between our *in vitro* characterizations and *Turicibacter* colonization, whereas concurrent *in vivo* increases in certain conjugated bile acids seen during 1E2 and H121 colonization indicate the possibility of more complex interactions between host bile production and *Turicibacter* colonization. The fact that the specificity and activity of the individual BSH homologs differed when expressed in different bacterial backgrounds indicates that other unknown cellular or environmental factors influence the way individual BSH act *in vivo.* This may also include mechanisms that modify the functionality of proteins encoded by the other putative BSH homologs the study identified from *Turicibacter* which did not deconjugate the specific tauro- or glyco-conjugated bile acids used in our experiments. These findings may influence the ways that bile-modifying genes can be employed to shape host lipid profiles through microbiota engineering, positioning certain microbial species as more appropriate vectors to impart specific host effects. It will also be informative to determine what other activities performed by *Turicibacter* lead to WAT gain in colonized animals, which contrasted findings from colonizing mice with specific *bsh*-overexpressing strains of *B. thetaiotaomicron*. Given this finding, it is likely that *Turicibacter* also influences host lipids through other mechanisms in addition to the bile transformations the study characterized.

Our work also connects specific *Turicibacter* members and BSH activity with specific host outcomes. Though some host responses such as broadly decreased

triglycerides were consistent across our BSH-recipient mice, the exact lipid and cholesterol responses differed, indicating that the type of deconjugations might have differing connections with host physiology. Further work will continue strengthening the exciting prospect of utilizing *Turicibacter* and/or its bile modifications to intentionally alter host lipid biology to improve host metabolic and lipid-associated health[66,67], as has been proposed with other bacteria[54,68]. Beyond lipid biology, *Turicibacter* abundance has been positively correlated with diseases such as Parkinson's disease[69] and depression[70], and selective serotonin reuptake inhibitors (SSRIs) have been found to negatively affect *Turicibacter* growth and colonization[71], potentially because they inhibit activity of its unique serotonin transporter[38]. SSRI use is frequently associated with metabolic side effects like weight gain[72,73], and our findings suggests a hypothesis that connects SSRI use and these side effects: SSRI use could diminish gut colonization of bacteria like *Turicibacter*, thus unintentionally altering their impact on host physiology. Future work may develop strategies to reduce interactions between SSRIs and activity of the microbiota, and minimizing the side effects of these drugs and improving host outcomes. In all, these associations further emphasize the importance of understanding mechanisms connecting members of the diverse *Turicibacter* genus to host physiology.

Methods

Mouse husbandry

Adult (6-8 week old) germ-free Swiss Webster mice were used for all animal experiments according to UCLA Institutional Animal Care and Use Committee-approved protocols. Mice were reared in flexible gnotobiotic isolators on a 12h:12h light dark schedule on standard chow (Labdiet 5K52, 22.1%: 16.6%: 61.3% protein: fat: carbohydrate by calories), then were exited to autoclaved filter top cages with autoclaved chow (Labdiet 5010, 28.7%: 13.1%: 58.2% protein: fat: carbohydrate by calories) and water. After one day of cage acclimation, the noted *Turicibacter* or *Bacteroides thetaiotaomicron* strain was grown in YCFA medium (see below) overnight, pelleted by centrifugation, and resuspended in 1X PBS. Mice were colonized by a 200μL gavage containing ~10^6 colony-forming units (CFU) of *Turicibacter* or ~10^8 CFU of *B. thetaiotaomicron*. Alternatively, mice were gavaged with the same volume of PBS alone (referred to as germ-free [GF]) or PBS-suspended fecal slurry from a specific pathogen-free adult mouse (referred to as conventionalized [CONV]). Colonization was quantified using strain-specific TuriSERT

primers (Table 7) and quantitative PCR (qPCR) from weight-normalized contents from the distal small intestine and proximal colon after addition of Low Abundance Microbiota Standard (Zymo) and extraction using the Zymo DNA Mini kit (Zymo).

Bacterial culturing

Turicibacter isolates and *Bacteroides thetaiotaomicron* strains (**Table 5**) were cultured in a flexible vinyl chamber (Coy) in an anaerobic 85%/10%/5% nitrogen/carbon dioxide/hydrogen mixture (Airgas). *Turicibacter* was grown on Schaedler's agar (BD Biosciences) or modified YCFA[74] (pH 7.4, per liter: 100mM MOPS, 10g casitone, 2.5g yeast extract, 2g glucose, 2g maltose monohydrate, 2g cellobiose, 44mg $MgSO_4$, 68mg $CaCl_2$, 0.9g NaCl, 10mg hemin, 0.45g K_2HPO_4, 0.45g KH_2PO_4, 4g $NaHCO_3$, 1g cysteine, 1mg resazurin, 1.9mL glacial acetic acid, 0.7mL propionic acid, 90µL isobutyric acid, 100uL isovaleric acid, 100uL valeric acid, 10mL ATCC vitamin mixture, 0.2% Tween-80) at 37°C. Cells were normally grown without shaking, but when appropriate, *Turicibacter* cultures were anaerobically transferred to sealed Hungate tubes or 1.7mL microcentrifuge tubes and shaken at 225 RPM at 37°C.

For *B. thetaiotaomicron* growth curves, overnight cultures were grown anaerobically in BHI-S for ~48 hours at 37 °C to ensure culture saturation, then were subcultured 1:50 for 6 hours at 37 °C (final OD_{600}=0.41-0.51). Subcultures were all then diluted to OD_{600}=0.1, and then six replicates were further diluted 1:10 in 100µL BHI-S in a 96 well plate. Plates were anaerobically sealed with parafilm and incubated at 37 °C. OD_{600} readings were taken every 15 minutes in a Biotek Synergy H1 microplate reader (Agilent).

Escherichia coli C41-pLys (Lucigen) was used for characterizing putative bile modification genes, which were expressed off the pET21+ plasmid. *E. coli* was grown aerobically shaking at 37°C C in Luria Broth (LB, 1% NaCl, 1% tryptone, 0.5% yeast extract) supplemented with 100µg mL^{-1} ampicillin. Expression of genes was induced by addition of 100µM IPTG.

Bacterial isolation and identification

The frozen stool sample was thawed on ice and diluted 1:10 with PRAS anaerobic dilution blank medium (Anaerobe Systems). 100µL of the diluted stool was further diluted to 1:1000 with modified YCFA media containing 0.05% bovine bile, 0.2% Tween-80, and 50mM resorufin and loaded on Prospector® system arrays (Isolation Bio, San Carlos, CA,

USA) following manufacturer's instructions. The fluorescent green signal of the arrays at time 0 was read on the Prospector® instrument in a Coy anaerobic chamber and the arrays incubated at 37°C in an Anaerobic Systems AS-580 anaerobic chamber (Anaerobe Systems). At 17 and 41 hours of incubation the arrays were scanned again and the decrease in green fluorescence from time 0 was used as an indicator for bacterial growth in the array nanowells. Bacteria from the array were transferred to 96-well transfer plates containing 200µL per well of modified YCFA media, without the addition of 50mM resorufin. The transfer plates were sealed with a gas permeable film and incubated at 37°C in a Mitsubishi AnaeroPack jar with a gas-generating sachet (Remel) for seven days. After incubation, the contents of 538 wells from the transfer plates with visible turbidity were consolidated into secondary 96-well plates, preserved with reduced glycerol, and stored at -80°C until needed. Unless stated otherwise, all stool and isolate manipulations were conducted anaerobically with a 5% CO_2/5% H_2/90% N_2 atmosphere.

Genomic DNA was extracted in a 96-well format from the consolidated Prospector® culture plates using the Extract All Kit (Applied Biosystems). 20µL of culture was combined with 20µL of Lysis Solution and incubated for 10 minutes at 95°C, followed by three minutes at room temperature. The DNA was stabilized with the addition of 20µL of DNA Stabilizing Solution and the resulting DNA lysate stored at -20°C until needed.

qPCR screening of novel Turicibacter *isolates*

Genomic DNA from 538 isolates was screened for *Turicibacter* 16S and the *Turicibacter* TuriSERT[38] gene using a multiplexed primer set (**Table 7**). Each 25µL qPCR reaction mixture had 1µL Extract All lysate, 10µL SYBR Power master mix (Applied Biosystems), 0.5µL of each of the 10µM primers, and 12µL molecular grade water. The reactions were run in a QuantStudio 6 Flex (Thermo Fisher) with a 95°C hold followed by 40 cycles of 95°C for 15s, 50°C for 30s, 72°C for 30s. *Turicibacter sanguinis* MOL361 gDNA and water were used as positive and negative controls, respectively.

Molecular cloning

Turicibacter genes were amplified from template culture lysates with Phusion or Q5 DNA polymerase (NEB) and primers designed to amplify denoted *Turicibacter* genes. pET21- or pWW3837[48] derived expression plasmids were assembled using Gibson assembly (see **Table 7** for oligos) for expression in *E. coli* or *Bacteroides thetaiotaomicron*,

respectively. Cloned constructs were confirmed through Sanger sequencing prior to functional characterization. pWW3837-derived constructs were cloned into *B. thetaiotaomicron* VPI-5482 as previously described[48]. *bsh*-expressing *B. thetaiotaomicron* was compared to *B. thetaiotaomicron* containing the original pWW3837 construct (referred to as wild-type *B. thetaiotaomicron*).

Genome assemblies

Each strain was streaked on Schaedler agar plates and incubated anaerobically, then an individual colony from each isolate was picked into YCFA medium and grown overnight at 37°C. DNA was extracted using the Zymo DNA mini kit (Zymo), with bead beating used to lyse cells. Purified genomic DNA was sequenced by MiGS (migscenter.org), and 151bp paired-end sequences were assembled using CLC Genomics Workbench (Qiagen). Genome assemblies have been deposited at NCBI at BioProject PRJNA846348.

Whole genome and gene comparisons

anvi'o[75] was used to profile and visualize the different *Turicibacter* strain DNA sequences to locate putative bile salt hydrolase and 7α-HSDH homologs in contig groups, generate variability profiles, and measure gene coverage and detection statistics. Average nucleotide identity (ANI) was calculated using OrthoANIu[76] (available https://www.ezbiocloud.net/tools/ani).

Sequences comparisons between 16S rRNA and *bsh* genes/BSH amino acid sequences were performed in CLC Genomics Workbench (Qiagen). 7α-HSDH sequence comparisons were performed using tblastn[77] using the translated amino acid sequence from *Clostridium absonum*[44].

Assessment of bile transformations

In vitro characterization of bile transformations by engineered *E. coli* or *B. thetaiotaomicron* strains were performed by growing cells in respective media conditions described above supplemented with 0.5mM (total combined concentration) of the noted bile species. Cells were grown to stationary phase (shaking at 37°C), then frozen at -80°C until further processing. Cells were then thawed, pelleted (5 minutes at 16,000 x g), and the supernatant was removed to a new microcentrifuge tube. Three volumes of methanol was

added, then the mixture was vigorously mixed for 30-60 seconds and incubated (room temperature, 15 minutes). Mixtures were centrifuged (5 minutes, 16,000 x g), the supernatant removed to a clean microcentrifuge tube and dried in a vacuum concentrator. The dried residue was treated with methanol/water/formic acid (50/50/0.1, all by volume) then vigorously mixed and centrifuged as described above. Supernatants were transferred to polypropylene HPLC vials, capped, and maintained at 4°C while aliquots (typically 5µL) were injected onto a reversed phase HPLC column (Cadenza CD-C18, 3.0µm, 250 x 2mm, Imtakt) equilibrated in solution A (water/formic acid, 100/0.1, vol./vol.) and eluted (0.2mL $minute^{-1}$) with an increasing concentration of solution B (acetonitrile/formic acid, 100/0.1, vol./vol.); minute/% B: 0/30, 45/70, 48/100, 50/30, 67/30). The effluent from the column was passed through an electrospray ion source (capillary voltage 42V, capillary temperature 275°C, sheath gas flow 15L min^{-1}, spray voltage 5kV, and -15kV conversion dynode with -1.2kV multipliers) connected to a linear ion trap mass spectrometer (Thermo LTQ) scanning from m/z 95-1000 in the positive ion mode. Spectra were recorded and analyzed with instrument-manufacturer supplied software. Confirmation of proposed elemental compositions was achieved using the same chromatography and ion source configuration with the spectra recorded by scanning on an orbitrap mass spectrometer (Thermo LTQ XL).

For bile species quantification, an internal spike-in standard of 100mM chenodeoxycholic acid-D4 (CDCA-D4, Sigma) was added to initial culture supernatants as a normalization reference. Area under the curve from reconstructed ion chromatograms was used to quantify the abundances of each species.

Serum metabolite analysis

Mice were euthanized with isoflurane and whole blood was collected via cardiac puncture. Blood was allowed to clot in SST Vacutainer tubes (BD) on ice, then centrifuged (4°C, 1 minute, 1500 x g). The supernatant was removed and snap frozen in liquid nitrogen. Serum metabolites were analyzed using global metabolomics platform by Metabolon (Morrisville, NC, USA). Unless otherwise noted, values presented are in arbitrary units (a.u.) for that particular metabolite, determined by the log-transform of the volume-corrected quantification.

Circulating lipid analysis

Mice were fasted for 4-6 hours, then euthanized as described above. Blood was collected via cardiac puncture and deposited into anticoagulatory K_2EDTA Vacutainer tubes (BD) on ice. Blood was centrifuged (4°C, 15 minutes, 2000 x g), then plasma was collected from supernatant and snap frozen in liquid nitrogen. Shotgun lipidomics was performed by the UCLA Lipidomics Core (Los Angeles, CA, USA) with the following protocol. Thawed plasma was pipetted into glass tubes, a mixture of 70 internal standard lipids (Sciex and Avanti) was added, and lipids were extracted using a modified Bligh and Dyer extraction[79]. The pooled organic layers from two extractions were dried in a vacuum concentrator and resuspended in 50/50 (vol./vol.) methanol/dichloromethane plus 10mM ammonium acetate. After transfer to robovials, samples were analyzed with a Sciex 5500 with DMS Device (Lipidyzer Platform) using a targeted acquisition list of 1450 lipid species. The Lipidyzer Differential Mobility device was tuned using the EquiSPLASH LIPIDOMIX standard mixture (Avanti). Data was analyzed using an in-house platform using previously described parameters[80], and quantitative values were normalized to input volume. Statistical significance identification for species to include in heatmap was performed with two-tailed Welch's t-test (p-value cutoff <0.05).

Total colonic bile concentration measurement

Mice were colonized and fasted as described above, then upon sacrifice contents from ~1 cm of proximal colon were collected into microcentrifuge tubes and snap frozen in liquid nitrogen. Thawed contents were weighed and suspended into water, then total bile levels were measured using the Bile Acid Assay Kit (Sigma). Total bile values were normalized by sample mass, and each sample value was compared to sex-matched littermate controls. Values shown at "0" were below limit of detection.

Adipocyte area calculation

After sacrifice, mice epididymal or gonadal white adipose tissue (e/g WAT) pads were weighed and placed into 4% paraformaldehyde in 1X PBS for 48 hours at 4°C. Fat pads were washed twice in 70% ethanol, then submitted to the UCLA Translational Pathology Core Laboratory (Los Angeles, CA, USA) for paraffin embedding, sectioning, and H&E staining. Ten adipocyte images from each animal (five from each fat pad) were visualized with a 20X objective on an EVOS microscope (Thermo). Adipocyte area for all

cells contained entirely within the field of view was automatically measured using the Fiji[78] Adiposoft[79] plug-in (version 1.1.16).

qRT-PCR measurement of liver transcripts

Gnotobiotic mice were colonized with single as described above, and upon sacrifice, the median lobe of the liver was dissected and either directly snap frozen in liquid nitrogen (all *Turicibacter* colonized animals) or placed in Trizol, bead bead for one minute, then frozen in liquid nitrogen (all *B. thetaiotaomicron* colonized animals). All livers were then transferred to -80°C until further processing. Directly snap frozen livers were thawed overnight at -20°C in RNALater-ICE (ThermoFisher), then bead beat in Trizol for one minute, after which all samples were processed in the same manner. RNA was extracted from thawed Trizol samples using the Direct-Zol RNA Miniprep Kit (Zymo), then cDNA was generated using the qScript cDNA Synthesis Kit (Quantabio). qPCR was performed using the PowerUp SYBR Green Master Mix (ThermoFisher) on a QuantStudio5 Real-Time PCR System (ThermoFisher) (primers[83,84] available in **Table 7**) (cycling conditions: 50°C for 2 min, 95°C for 2 min, 50 cycles of 95°C for 15 sec, 55°C for 15 sec, 72°C for 1 min, followed by melt curve. Fold changes in comparison with sex-matched controls (GF for *Turicibacter* colonizations, *Bt*-WT for *B. thetaiotaomicron* colonizations) were calculated using the ΔΔCt method with auto-thresholded Ct values with *ppia* as the house-keeping gene.

Statistical analysis

Statistical calculations were performed in in Prism 9.3.1 (Graphpad). Unless otherwise noted, *** = $p<0.0005$, ** = $p<0.005$, * = $p<0.05$, written p-value = $0.05 < 0.2$. Heatmaps were created using the *pheatmap*[80] package in R (version 3.6.3)[81].

Table 7 shows a list of oligos used in the work.

Table 8 shows a list of strains used in this work.

Table 9 shows serum metabolomics from GF, CONV, and *Turicibacter* monocolonized mice. Volume-adjusted log-transformed levels of listed serum metabolites from mice from different colonization states. Note that statistics on far right of sheet are generated automatically as part of analysis pipeline, but were not used for this work because data analyzed did not have normal distribution.

Table 10 shows absolute quantification of lipid species from plasma of mice colonized with *B. thetaiotaomicron* engineered to express *Turicibacter bsh* genes.

Table 7

Name	sequence	purpose	Reference
TuriSERT-H121_F	GGTTTAGCTGATGCTGGAATTAG	Turicibacter discovery/qPCR	this study
TuriSERT-H121_R	TCCAAATTTATCAACAAATGCTGTAATAAT	Turicibacter discovery/qPCR	this study
TuriSERT-MOL361_F	GGGTTTGCAGATGCGGG	Turicibacter discovery/qPCR	this study
TuriSERT-MOL361_R	AATTTATCAACCACCGCTGTAATAAT	Turicibacter discovery/qPCR	this study
TuriSERT-1E2_F	GGGTTTGCTGATGCCGC	Turicibacter discovery/qPCR	this study
TuriSERT-1E2_R	CCCAAATTTATCAACTACTGCTGTAATAAT	Turicibacter discovery/qPCR	this study
pET21_F	CTCGAGCACCACCACCAC	linearize pET21 *E. coli* expression vector	this study
pET21_R	GAATACCTCCTTAAGTTGTTCTAGAAGG	linearize pET21 *E. coli* expression vector	this study
BSHIMOL361_F	aacaacttaaggaggtattcATGTGTACAGGACTTAGC	insert into pET21	this study
BSHIMOL361_R	tggtggtggtggtgctcgagGTTTTGGAATAAAATATCTTGTTTACCTTG	insert into pET21	this study
BSHIIH121_F	aacaacttaaggaggtattcATGTGTACAGGGTTAAGTTTAAC	insert into pET21	this study
BSHIIH121_R	tggtggtggtggtgctcgagGTTTTGGAACAAGATATCTTGCTCTCC	insert into pET21	this study
BSHIII1E2_F	aacaacttaaggaggtattcATGTGCACAGGATTATGC	insert into pET21	this study
BSHIII1E2_R	tggtggtggtggtgctcgagATTTTGATAACAAATATCTTGTTTTCCTAGG	insert into pET21	this study
BSHIVMOL361_F	aacaacttaaggaggtattcATGTGTACAGCATTATCATTAAC	insert into pET21	this study
BSHIVMOL361_R	tggtggtggtggtgctcgagATTTTGTAAATTTACAGCAAATTCATCATTA	insert into pET21	this study

BSHVMOL361_F	aacaacttaaggaggtattcATGTGTACAGCTATTACATTAA AG	insert into pET21	this study
BSHVMOL361_R	tggtggtggtggctcgagATTTTGTTTCTGTACTACCAGTT TATCT	insert into pET21	this study
BSHVIH121_F	aacaacttaaggaggtattcATGTGTACAGCCATTACATTAA AAAC	insert into pET21	this study
BSHVIH121_R	tggtggtggtggctcgagATTCTGATCATGGACTGTTAAT CTTGT	insert into pET21	this study
BSHVIII1E2_F	aacaacttaaggaggtattcATGTGTACAGCAATCTCAATC	insert into pET21	this study
BSHVIII1E2_R	tggtggtggtggctcgagCTCAAAAAAAAGTCAGCGTCTTG C	insert into pET21	this study
BSHVIIIMOL361_F	aacaacttaaggaggtattcATGAAGGAAGGAACCATC	insert into pET21	this study
BSHVIIIMOL361_R	tggtggtggtggctcgagATTAAGATATTTGATGTCATTT ATAGGATTTAATTCG	insert into pET21	this study
7A_HSDS_F	aacaacttaaggaggtattcATGCGAAAATTAGAGAATGCAA TAGC	insert into pET21	this study
7A_HSDS_R	tggtggtggtggctcgagCTTTTCCTCAACTACTTTACGAC C	insert into pET21	this study
pWW3837_fwd	GGATCTGATTACAAGGAC	linearize pWW3837 *B. thetaiotaomicron* overexpression vector	this study
pWW3837_rev	TATTTTAAATTTTTTTTGAATCCATAGATC	linearize pWW3837 *B. thetaiotaomicron* overexpression vector	this study
pWW_BSHIVMOL361_F	tggattcaaaaaaatttaaaataATGTGTACAGCATTATCATTA AC	insert into pWW3837	this study
pWW_BSHIVMOL361_R	tcgtccttgtaatcagatccATTTTGTAAATTTACAGCAAATT C	insert into pWW3837	this study
pWW_BSHIMOL361_F	tggattcaaaaaaatttaaaataATGTGTACAGGACTTAGC	insert into pWW3837	this study

pWW_BSHIMOL361_R	tcgtccttgtaatcagatccGTTTTGGAATAAAATATCTTGTTTAC	insert into pWW3837	this study
pWW_BSHIII1E2_F	tggattcaaaaaaatttaaaataATGTGCACAGGATTATGC	insert into pWW3837	this study
pWW_BSHIII1E2_R	tcgtccttgtaatcagatccATTTTGATAACAAATATCTTGTTTTC	insert into pWW3837	this study
pWW_BSHIIH121_F	tggattcaaaaaaatttaaaataATGTGTACAGGGTTAAGTTTAAC	insert into pWW3837	this study
pWW_BSHIIH121_R	tcgtccttgtaatcagatccGTTTTGGAACAAGATATCTTG	insert into pWW3837	this study
ppia_F	CAGTGCTCAGAGCTCGAAAGT	baseline qRT-PCR control	Takahashi, 2016
ppia_R	GTGTTCTTCGACATCACGGC	baseline qRT-PCR control	Takahashi, 2016
Fxr_F	TCCAGGGTTTCAGACACTGG	fxr transcript measurement	Sayin, 2013
Fxr_R	GCCGAACGAAGAAACATGG	fxr transcript measurement	Sayin, 2013
Cyp7a1_F	AGCAACTAAACAACCTGCCAGTACTA	Cyp7a1 transcript measurement	Sayin, 2013
Cyp7a1_R	GTCCGGATATTCAAGGATGCA	Cyp7a1 transcript measurement	Sayin, 2013

Table 8

Isolate	Derived from	Source	Reference	Notes
MOL361	human	DMSZ	Bosshard, 2002	*Turicibacter sanguinis* type strain
18F6	human	Kenya Honda	N/A	
T46	human	Thomas Auchtung	N/A	
GALT-G1	human	this work	N/A	
H121	contaminated germ-free mouse	Thomas Auchtung	Auchtung, 2016	
T129	human	Thomas Auchtung	N/A	
GALT-E2	human	this work	N/A	
1E2 (also known as 80E2)	mouse	Kenya Honda	N/A	
TA25	mouse	Thomas Auchtung	N/A	
Bacteroides thetaiotaomicron VPI-5482	human	Justin Sonnenburg/Fatima Enam	Xu, 2003	background strain
B. thetaiotaomicron pWW3837	N/A	rederived for this work	Whitaker, 2017	referred to as "WT" in this work
Bt-BSH-IV:MOL361	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-IV from MOL361 in place of GFP
Bt-BSH-I:MOL361	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-I from MOL361 in place of GFP
Bt-BSH-II:H121	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-II from H121 in place of GFP
Bt-BSH-III:1E2	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-III from 1E2 in place of GFP

Escherichia coli C41-pLys	N/A	Lucigen	N/A	expression strain
Escherichia coli S17λ-*pir*	N/A	Justin Sonnenburg	Lynch, 2012/Whitaker, 2017	conjugation donor

Table 9

Fold Change				
Welch's Two-Sample t-Test (bold indicates p<0.1)				
MOL361	**1E2**	**H121**	**T129**	**CONV**
GF	**GF**	**GF**	**GF**	**GF**
0.66	1.07	1.14	1.06	**0.57**
0.66	1.13	1.01	1.08	**0.36**
0.82	0.93	**1.78**	1.05	**0.39**
1.00	1.10	0.79	1.18	1.04
1.55	**1.76**	1.93	1.47	**2.63**
1.27	1.32	**1.44**	1.11	**1.56**
1.08	1.17	**1.58**	1.02	0.92
0.94	1.08	1.20	1.02	1.36
1.06	**1.39**	**1.26**	1.16	1.17
0.82	0.98	0.95	0.99	**1.38**
1.04	**1.60**	1.26	**1.38**	**1.41**
1.02	**1.22**	**1.33**	1.18	**1.14**
1.21	**1.37**	**1.20**	**1.39**	**1.42**
0.90	0.96	**1.12**	1.02	0.99
0.96	1.02	0.96	0.98	0.93

0.94	1.09	1.20	0.96	**0.87**
1.04	**1.19**	**1.24**	0.92	1.20
1.03	**1.25**	1.17	1.00	**1.42**
1.22	**1.40**	**1.29**	**1.22**	**1.95**
1.05	**1.10**	1.10	0.97	1.00
1.08	1.23	1.13	1.12	**0.63**
0.93	0.97	0.98	1.06	**0.69**
1.01	0.97	0.94	0.98	**0.53**
0.61	0.84	**0.62**	**0.63**	**0.43**
0.84	1.25	0.93	**1.21**	**0.71**
0.89	1.32	0.96	1.14	**0.54**
0.95	1.30	0.84	1.14	**0.64**
0.71	1.09	**0.80**	1.09	**0.70**
0.78	1.23	0.98	1.03	**0.59**
0.89	0.93	**0.86**	1.04	**0.78**
0.71	0.85	0.89	0.89	**0.79**
0.71	1.14	**0.72**	1.07	**0.57**
0.90	1.05	0.98	1.01	**0.85**
0.85	0.99	0.94	1.16	**1.24**
0.78	1.10	0.97	0.91	**0.65**
0.84	0.98	0.97	1.04	**0.83**
0.79	0.90	0.85	1.02	**0.58**
0.63	0.98	0.85	1.05	**0.54**
0.52	0.81	**0.60**	**0.63**	**0.40**
1.13	1.40	1.02	1.30	**0.41**
0.79	1.16	0.84	1.02	**0.48**
1.19	1.05	1.20	0.93	0.95

0.96	1.41	1.11	1.14	1.04	
0.96	1.28	1.08	1.05	1.01	
0.85	0.89	0.85	0.97	1.32	
1.50	1.27	1.16	0.87	0.66	
1.22	1.46	1.32	1.13	**1.28**	
0.87	0.95	0.91	0.75	0.79	
0.97	1.01	0.99	1.01	1.13	
0.93	1.03	1.04	**1.15**	1.09	
0.65	1.05	**0.69**	0.96	**0.43**	
1.23	1.16	1.05	**1.23**	1.14	
0.89	1.14	0.99	1.01	0.82	
1.18	**1.48**	**1.21**	1.22	0.90	
1.17	0.98	1.16	1.07	1.44	
0.87	1.10	1.05	1.01	**0.70**	
0.95	1.13	1.03	1.13	1.15	
0.92	1.08	0.99	1.04	0.90	
0.91	1.12	1.04	1.04	**0.79**	
0.51	0.93	**0.48**	**0.45**	**0.36**	
1.12	**1.74**	0.74	**1.59**	**0.54**	
0.84	0.96	1.01	1.08	1.33	
0.99	1.18	1.09	1.15	1.22	
0.87	1.13	1.03	0.99	1.02	
0.65	1.04	**0.68**	0.87	**0.52**	
1.02	1.06	1.04	1.13	0.98	
1.00	0.94	**0.85**	1.03	1.08	
0.79	**0.79**	**0.80**	0.94	0.90	
0.99	1.18	1.10	1.17	0.93	

1.04	1.04	1.01	1.15	1.09	
0.94	**0.74**	0.83	0.85	1.44	
0.74	**0.62**	**0.82**	0.91	0.85	
0.96	1.08	1.04	1.18	1.01	
0.84	0.95	**0.84**	1.09	1.18	
0.69	**0.77**	**0.81**	0.94	0.89	
0.97	1.02	1.02	1.10	1.15	
1.19	1.08	1.09	1.22	**1.38**	
0.80	0.88	0.89	0.99	0.99	
0.82	0.95	0.99	1.01	1.22	
1.00	**0.87**	0.98	1.12	1.07	
0.84	1.06	0.88	0.83	0.84	
0.94	0.99	0.94	1.01	0.95	
0.91	0.91	**0.85**	0.98	1.07	
0.44	0.80	**0.60**	0.84	**0.65**	
0.50	0.75	**0.41**	**0.49**	**0.41**	
0.78	1.14	1.01	1.13	**0.57**	
0.74	1.14	0.92	1.06	**0.57**	
0.90	1.42	0.74	0.96	1.02	
1.01	0.94	0.99	1.07	0.91	
1.00	0.84	**0.85**	0.97	1.05	
0.95	**0.94**	0.96	1.03	0.99	
2.43	1.21	2.07	2.74	1.63	
1.04	0.88	0.94	1.11	**1.15**	
0.88	**0.66**	0.85	0.90	**1.44**	
0.91	0.98	0.98	1.10	**0.88**	
0.82	**0.81**	**0.79**	0.97	0.98	

0.75	**0.81**	**0.83**	0.90	0.89	
0.95	0.94	0.96	1.04	1.04	
0.86	**0.75**	**0.83**	0.87	1.27	
0.83	0.90	0.84	1.00	1.00	
0.96	**0.89**	**0.87**	0.97	**0.84**	
0.93	**0.88**	**0.85**	0.92	0.99	
0.56	0.78	**0.47**	**0.46**	**0.43**	
0.83	0.96	0.95	1.05	0.94	
0.75	0.86	0.94	1.13	1.08	
1.00	1.19	1.02	1.04	**0.88**	
1.10	1.14	**1.16**	**1.33**	1.11	
1.67	**1.24**	1.31	1.61	1.33	
0.98	1.01	1.03	1.18	**0.59**	
0.82	1.27	1.28	1.21	**0.55**	
0.78	1.31	1.20	1.18	**0.44**	
0.74	0.61	1.17	0.73	0.90	
1.19	1.14	**1.61**	1.65	**0.45**	
1.03	1.39	**3.43**	1.48	**0.21**	
0.53	1.91	6.01	1.07	**0.18**	
1.14	0.95	**1.54**	**1.52**	0.77	
0.93	1.04	**1.22**	**1.38**	**0.60**	
1.22	1.17	**1.57**	1.78	**0.43**	
0.91	0.91	1.26	1.01	**0.74**	
0.71	1.02	1.16	1.45	**0.42**	
1.00	1.00	1.00	1.00	**1.66**	
0.85	0.77	0.81	0.77	**35.50**	
1.00	**0.84**	0.98	1.27	1.03	

1.01	0.96	1.04	1.06	1.20
0.96	1.09	1.14	0.86	1.02
1.21	**1.31**	**1.53**	1.17	**0.75**
0.78	1.36	0.77	0.67	**16.52**
0.75	1.09	0.80	0.96	**0.62**
0.89	0.79	**0.62**	1.02	1.29
0.85	1.12	0.81	1.02	**0.58**
0.31	0.27	0.31	0.47	0.28
0.68	**0.62**	0.89	0.90	**4.06**
0.90	0.82	0.96	1.04	0.91
0.74	1.30	0.85	**1.43**	0.67
0.76	1.08	0.97	**1.19**	0.94
0.93	0.90	0.99	0.95	1.17
0.89	0.83	**1.43**	1.06	0.88
0.89	1.01	1.27	1.28	1.28
0.85	1.10	0.96	1.12	0.91
0.99	1.07	**1.38**	1.04	0.81
0.66	1.03	0.80	0.90	**0.56**
0.84	**0.58**	1.00	0.86	0.94
0.81	1.09	1.06	0.98	**0.42**
0.64	1.07	**0.71**	0.85	**0.63**
0.55	0.46	0.71	0.51	**1.62**
0.71	0.71	0.90	0.52	0.48
0.96	0.89	0.87	0.80	**2.69**
0.81	1.08	**0.79**	1.00	**0.51**
1.08	0.99	1.07	1.16	0.86
1.24	1.26	1.31	**1.34**	1.03

1.26	1.15	1.21	1.02	1.47	
0.75	**0.47**	**0.50**	1.06	0.92	
0.93	1.04	0.99	1.23	1.01	
1.45	**1.62**	**2.21**	**1.84**	0.99	
1.01	0.86	0.84	0.89	**1.23**	
0.82	1.16	**0.71**	0.97	**0.41**	
0.89	1.09	0.97	0.96	1.19	
1.01	1.26	1.47	1.20	1.16	
0.77	0.93	0.84	**1.16**	0.97	
0.57	0.94	0.84	0.79	0.69	
0.64	0.93	0.65	0.81	**0.52**	
0.68	1.03	**0.76**	0.93	0.74	
0.59	1.19	0.97	0.75	**0.55**	
1.04	0.77	1.00	0.86	1.15	
0.67	0.99	**0.70**	0.83	**0.67**	
0.63	0.96	0.54	1.41	1.30	
1.04	1.23	1.18	**1.50**	1.28	
0.91	0.94	1.10	0.86	0.90	
0.45	0.52	0.72	0.66	**0.48**	
0.71	1.14	**0.83**	1.09	0.80	
0.83	1.31	1.10	0.97	1.12	
1.00	1.00	1.00	1.00	**2.27**	
1.18	1.18	1.07	1.14	1.01	
0.98	2.67	**5.68**	1.41	**0.37**	
1.14	**0.80**	0.88	1.05	1.44	
0.95	0.79	0.90	0.93	0.84	
0.87	**0.75**	0.81	0.95	0.94	

0.90	1.03	0.98	1.10	**0.84**
0.98	0.99	0.93	1.05	1.13
0.88	1.12	1.59	1.30	**2.05**
1.00	1.00	1.00	1.00	**3.63**
0.97	0.95	0.88	0.91	0.93
1.29	1.38	1.40	3.59	**2.25**
0.74	0.74	0.97	0.74	**6.01**
1.02	1.13	1.13	1.14	0.94
0.79	**0.78**	0.93	1.15	0.92
0.65	1.45	1.00	1.05	1.08
0.76	1.08	0.94	0.91	**0.66**
0.80	0.86	0.92	0.98	**1.21**
1.11	1.05	**1.60**	1.39	**0.72**
6.49	**8.20**	**12.43**	10.88	1.00
0.77	1.20	1.30	0.99	0.89
0.96	0.94	1.28	1.08	**1.26**
0.95	0.76	0.87	0.79	1.32
1.08	0.93	0.90	1.05	1.11
0.83	**0.71**	0.85	0.82	**0.66**
0.80	1.03	1.13	0.86	**1.91**
1.42	1.46	1.23	**3.02**	**2.83**
1.05	1.07	**1.88**	1.20	**0.49**
1.43	1.31	**1.78**	1.59	1.00
0.94	**0.68**	**1.69**	1.07	**0.68**
1.08	0.83	**1.90**	0.91	**2.74**
1.30	1.34	**1.74**	1.43	1.39
1.94	1.50	**2.32**	1.27	**1.80**

0.65	0.78	1.00	0.94	0.88	
1.04	0.97	**1.87**	1.16	**0.36**	
0.91	0.83	1.46	1.04	**0.38**	
1.03	1.02	**2.27**	1.09	0.89	
1.28	1.25	**1.50**	**1.59**	**1.50**	
1.55	**1.58**	**1.82**	1.59	**2.30**	
1.41	0.70	0.97	2.44	1.07	
1.40	**1.38**	**2.17**	**1.73**	0.88	
0.67	0.83	1.13	0.86	**0.45**	
1.25	**1.20**	**1.56**	**1.48**	0.98	
0.95	0.93	0.89	0.85	1.21	
0.78	**0.73**	**1.42**	1.08	0.92	
0.52	**0.53**	0.69	**0.54**	**0.35**	
0.68	0.55	0.61	0.86	0.73	
0.64	**0.72**	0.96	**0.62**	**0.75**	
0.68	1.24	0.95	0.94	**316.97**	
2.57	0.55	1.80	0.93	**1.77**	
2.10	0.73	1.32	0.65	**5.73**	
0.75	**0.75**	0.90	0.91	0.94	
1.01	0.94	1.14	0.65	**5.72**	
0.92	0.96	1.08	1.05	0.97	
0.93	0.98	**1.14**	1.11	1.03	
0.68	0.70	**0.57**	1.11	**0.66**	
1.09	0.96	0.99	0.85	**0.64**	
0.77	**0.84**	0.91	0.94	0.95	
1.17	0.77	0.76	0.87	1.15	
1.26	**1.37**	**1.31**	1.05	1.23	

1.29	0.93	1.53	3.48	**109.01**	
1.57	1.18	1.55	**3.61**	0.62	
1.29	1.44	1.08	**1.31**	**1.99**	
1.11	1.07	1.14	1.02	**1.16**	
1.05	0.84	1.17	0.99	0.84	
0.70	1.45	1.10	1.06	1.11	
0.84	0.96	1.07	0.66	**2.84**	
1.13	1.19	1.23	0.98	0.98	
0.76	1.52	0.70	0.83	**10.96**	
1.01	0.94	0.98	0.99	**2.81**	
1.00	1.20	1.00	1.00	**13.74**	
0.41	1.17	0.79	0.59	1.58	
0.98	1.23	1.19	**1.61**	1.09	
0.96	1.00	1.17	0.87	0.96	
0.92	0.92	0.92	0.92	**196.36**	
0.98	0.98	0.98	0.98	**58.21**	
0.74	**0.68**	**0.76**	0.99	**1.53**	
1.03	0.96	1.17	**1.63**	0.87	
0.64	0.93	0.95	0.73	0.83	
0.79	0.75	0.77	0.85	0.96	
0.73	**0.62**	**0.64**	0.90	1.31	
1.05	0.87	0.84	1.08	1.00	
1.02	2.54	1.22	1.01	**1.91**	
0.97	2.73	0.88	0.74	1.54	
0.94	1.49	1.70	1.16	**2.16**	
0.89	1.23	0.78	0.91	1.10	
0.91	0.96	1.10	1.08	1.09	

1.25	0.81	0.49	0.40	0.39	
4.58	1.20	4.94	0.64	**24.63**	
0.84	**0.60**	**0.55**	1.51	1.24	
0.49	0.61	0.69	0.52	**1.93**	
0.83	0.95	0.99	0.86	1.12	
1.11	**0.64**	0.79	0.75	**1.66**	
0.84	1.16	1.31	0.71	**1.94**	
0.79	0.80	0.85	0.87	**0.68**	
1.95	**3.23**	1.42	1.63	**1.73**	
1.04	0.82	**1.56**	1.11	**0.53**	
1.25	1.05	**1.89**	1.19	1.83	
0.78	0.85	0.82	0.61	**0.34**	
1.29	0.86	1.24	0.79	**2.17**	
1.02	1.07	**1.35**	1.29	0.95	
1.02	1.18	1.18	0.97	0.81	
0.96	1.00	0.91	1.10	**1.21**	
1.10	0.90	1.06	1.04	**2.02**	
1.06	1.00	0.99	1.04	1.29	
1.08	**1.20**	1.11	1.27	**0.66**	
0.97	1.11	**1.15**	1.11	0.87	
0.94	**0.62**	0.84	0.98	0.93	
0.84	0.90	0.86	0.95	**0.73**	
0.76	0.71	0.87	1.20	**0.64**	
1.26	0.99	1.08	1.12	1.13	
1.43	**1.87**	**1.66**	**1.49**	1.37	
1.00	1.00	1.00	1.00	**2.91**	
0.98	0.73	1.07	0.99	1.23	

1.18	**2.31**	**1.93**	1.19	0.90	
4.89	**5.30**	**32.93**	83.25	**2.94**	
1.12	1.06	1.11	1.09	1.02	
1.08	1.18	**2.08**	1.43	0.77	
1.23	0.99	**1.74**	**1.74**	0.98	
1.15	**1.23**	**1.18**	1.05	**1.24**	
1.05	1.23	**1.20**	**1.27**	1.12	
0.68	**0.48**	**0.66**	0.86	**0.63**	
2.73	0.56	1.29	**2.68**	1.10	
1.01	0.11	0.67	**3.14**	0.63	
0.99	0.99	1.51	1.12	**0.64**	
1.07	**0.75**	1.00	0.92	0.74	
0.81	1.24	0.88	1.12	**0.44**	
0.98	0.96	1.17	1.07	1.02	
0.75	0.85	**0.69**	**0.68**	**0.57**	
0.99	1.00	1.05	1.00	1.04	
0.80	0.87	**1.78**	2.25	0.78	
0.41	0.34	0.64	0.54	0.43	
0.33	0.30	0.34	0.63	0.29	
0.85	1.01	1.23	0.93	0.79	
0.97	1.30	0.98	1.02	1.18	
0.85	0.74	0.78	0.78	0.98	
1.03	1.04	1.15	1.11	1.21	
0.61	1.15	0.98	0.79	1.27	
0.80	0.87	0.87	0.95	0.97	
0.89	0.82	0.87	**0.76**	**0.75**	
0.71	1.04	0.94	**1.31**	**0.58**	

0.67	0.95	0.83	0.78	**0.41**
0.90	0.85	0.98	1.06	0.93
1.33	1.22	**1.74**	1.44	**0.77**
0.94	0.89	0.81	0.72	0.85
0.66	**0.64**	**0.64**	0.93	0.78
1.01	1.09	0.97	1.20	**0.90**
0.99	1.15	1.21	**1.41**	0.74
0.26	0.32	0.58	0.34	1.17
1.12	1.21	1.14	0.82	**0.70**
0.92	0.83	0.85	**0.66**	**0.67**
0.98	1.02	1.10	1.14	1.10
0.77	0.77	0.84	0.76	**1.47**
1.16	1.15	**1.99**	1.46	0.76
1.25	1.06	0.76	1.40	1.50
1.00	0.81	0.76	1.19	1.16
1.17	1.01	1.01	1.32	0.96
0.93	1.21	1.04	**1.76**	1.56
1.29	1.21	0.95	**1.38**	1.12
1.01	0.97	1.21	1.24	0.76
1.05	1.02	1.06	0.95	0.90
3.85	**5.20**	**15.92**	53.03	0.47
0.91	0.75	0.77	0.91	1.41
1.21	1.29	**1.23**	1.12	1.10
0.84	1.02	1.01	1.03	1.10
0.45	0.54	1.04	0.56	**2.10**
0.89	0.93	1.19	1.04	0.95
0.87	0.88	1.10	1.03	1.02

0.83	0.82	1.07	0.86	0.98
0.86	0.78	1.11	0.77	0.98
0.90	0.78	1.11	0.74	0.96
1.01	1.05	1.06	1.02	0.98
0.96	0.99	1.07	1.07	**1.25**
0.84	1.04	1.08	1.16	**3.75**
0.66	1.01	1.21	1.35	0.53
1.28	1.35	**1.80**	**1.57**	0.58
1.00	0.79	1.41	0.84	1.34
1.00	**1.24**	**1.45**	1.13	2.41
1.25	1.38	1.04	0.80	**5.44**
0.72	**0.58**	**0.42**	0.79	**4.62**
1.28	**1.30**	1.33	1.28	1.10
0.68	1.20	0.88	0.68	0.76
0.92	0.79	0.85	0.92	1.14
1.10	1.04	**1.57**	1.21	0.87
0.96	0.99	**1.34**	1.16	**3.62**
1.05	1.05	**1.54**	1.28	**2.49**
0.94	1.03	1.07	1.17	**0.21**
1.23	**1.35**	**1.27**	1.08	0.93
1.14	0.77	1.14	**0.63**	1.18
1.17	1.28	1.53	0.82	1.12
0.86	1.30	1.56	**0.56**	0.99
1.00	1.00	1.00	1.00	**1.26**
1.16	0.83	1.19	0.74	**167.54**
1.19	1.04	0.93	**1.58**	1.44
1.03	**0.64**	0.81	0.87	1.34

1.12	1.08	0.94	1.13	1.15	
2.99	**5.14**	**6.81**	6.61	**0.52**	
1.63	**2.10**	**2.08**	**1.81**	1.09	
16.37	**27.62**	**35.33**	28.37	1.70	
0.88	0.89	0.92	0.96	0.99	
0.97	1.13	1.08	1.10	**0.43**	
0.91	0.87	0.90	1.09	1.08	
0.99	0.77	0.87	0.88	0.79	
0.91	0.95	**0.89**	1.35	**9.54**	
1.03	0.73	0.68	7.87	**75.87**	
1.21	1.23	**3.26**	1.67	1.01	
1.31	1.05	**1.81**	1.17	1.13	
0.89	1.01	**1.78**	1.22	**0.58**	
1.37	1.21	**1.81**	1.34	1.15	
0.99	**1.34**	1.21	**1.38**	1.07	
0.82	0.88	**0.76**	1.13	0.76	
0.96	**1.27**	1.10	**1.17**	**0.79**	
1.26	**2.29**	1.80	1.33	1.21	
1.02	1.25	1.16	1.23	**1.10**	
0.96	1.10	1.03	1.17	1.02	
1.04	1.09	1.33	1.02	**1.28**	
1.00	1.26	1.11	**1.41**	**1.34**	
1.13	1.02	1.02	0.89	1.23	
0.85	0.88	0.87	0.83	1.48	
1.09	1.02	0.92	0.88	**2.87**	
1.49	1.24	1.00	0.82	**2.11**	
1.16	1.23	1.09	0.98	**2.14**	

1.03	1.06	0.98	1.08	0.97
1.35	1.05	1.34	**1.68**	0.74
0.93	1.04	0.86	1.06	1.25
0.81	1.01	0.87	0.96	0.93
0.94	1.23	1.23	1.10	**1.63**
0.41	0.55	0.85	0.87	0.77
0.66	1.02	1.05	1.16	0.79
1.26	1.11	**3.05**	0.97	0.88
1.25	1.05	1.73	1.48	2.19
0.84	**0.77**	**0.84**	0.92	**0.68**
1.00	1.00	1.00	1.00	**4.29**
0.91	0.50	0.85	1.17	1.33
0.80	1.47	1.09	1.18	**0.46**
0.77	1.26	0.90	0.99	**0.42**
1.21	1.08	**1.68**	1.42	0.84
1.36	1.06	1.46	1.64	1.06
0.99	0.82	0.97	**0.76**	1.27
0.68	15.80	0.30	0.63	**1.31**
0.38	0.26	0.26	0.78	0.62
0.16	0.10	0.08	0.55	0.29
1.29	0.95	0.78	0.83	1.26
1.45	1.56	**2.08**	1.73	0.90
0.84	**0.79**	**0.80**	**0.65**	**4.06**
0.98	0.98	0.98	1.05	**0.67**
0.94	0.94	0.94	0.88	**0.81**
0.77	1.14	1.06	1.23	0.77
0.80	1.86	1.01	**1.67**	**0.58**

0.74	0.91	1.20	**1.49**	0.84	
0.83	1.10	0.92	0.98	**0.51**	
0.96	0.81	0.75	0.68	1.18	
0.77	1.33	0.95	1.19	0.69	
0.79	0.86	0.84	1.03	**0.31**	
1.32	0.89	**1.94**	1.55	1.08	
0.77	1.90	1.07	1.40	**0.49**	
0.95	1.75	0.81	1.70	**0.38**	
1.00	0.97	**1.85**	1.27	**0.55**	
1.22	1.22	**2.24**	1.46	0.82	
0.83	1.42	**1.84**	**1.87**	**1.36**	
0.97	1.05	1.26	0.86	0.82	
0.90	1.31	0.99	**1.28**	1.00	
0.76	**0.75**	1.04	1.47	0.85	
0.68	0.80	0.95	0.83	**0.43**	
1.07	1.19	**1.90**	1.03	1.38	
0.77	1.09	1.09	**1.63**	**0.56**	
1.34	1.11	**1.46**	**2.11**	1.25	
1.00	1.00	1.00	1.00	**1.83**	
1.00	1.00	1.00	1.00	**1.46**	
1.00	1.00	1.00	1.00	**1.36**	
1.06	1.09	0.95	1.24	**0.81**	
0.80	1.32	1.27	**2.02**	0.71	
1.08	1.18	1.01	**1.22**	1.22	
1.01	0.95	0.97	0.99	1.00	
0.82	**1.39**	1.00	**1.55**	0.91	
1.08	**1.64**	1.35	**1.44**	0.81	

1.08	1.29	1.15	0.83	**4.92**
0.77	1.29	0.83	0.75	0.84
0.83	0.89	0.75	0.80	0.99
0.64	0.69	1.16	0.73	1.49
0.93	0.73	**0.69**	0.70	0.95
0.77	0.90	**0.72**	1.13	**0.47**
1.02	1.04	0.96	1.11	1.04
1.65	**1.84**	**2.10**	**1.49**	0.95
0.95	0.92	1.00	1.00	**1.68**
0.69	0.74	1.01	0.91	0.83
0.95	0.96	1.37	2.42	**1.53**
0.76	0.93	1.08	0.77	1.12
1.01	1.05	0.87	0.97	**2.89**
0.99	1.05	0.96	1.11	**2.16**
0.90	0.91	0.86	0.96	**2.07**
0.94	0.98	1.00	0.81	1.85
0.80	0.96	0.89	0.96	1.57
0.80	0.91	0.93	0.92	**1.87**
0.84	0.86	0.94	0.76	**2.57**
0.83	1.07	1.06	1.02	**1.62**
1.01	0.96	1.05	0.90	**1.73**
0.97	1.12	1.09	1.06	**1.88**
0.91	1.04	1.14	0.91	**2.07**
0.85	0.94	0.96	0.88	**1.82**
0.80	0.91	0.90	0.95	1.71
0.90	**0.75**	0.79	0.95	1.11
0.71	1.05	0.95	1.17	1.03

0.85	1.50	1.55	1.37	**1.65**	
0.59	1.18	1.22	1.28	0.68	
0.88	1.04	0.91	0.82	**2.25**	
1.19	1.04	1.13	1.04	1.22	
0.95	0.88	**0.83**	0.87	0.97	
1.37	1.05	1.61	3.27	0.62	
0.98	1.02	0.99	0.89	**2.07**	
0.87	0.88	1.64	1.01	**3.44**	
1.01	0.99	1.05	1.11	1.40	
0.95	0.95	0.93	1.07	1.03	
0.88	1.28	1.98	1.07	0.98	
0.80	**0.75**	0.81	**0.74**	0.87	
1.26	0.99	1.15	0.80	**0.37**	
1.00	1.00	1.04	0.99	2.40	
1.00	0.98	1.04	1.00	1.12	
0.97	0.91	1.06	1.14	0.89	
0.87	**0.74**	0.91	1.01	1.83	
0.92	0.90	**0.79**	0.88	**0.58**	
0.81	**0.72**	0.94	0.93	**1.57**	
0.70	0.66	**0.64**	**0.45**	**0.57**	
0.93	0.91	**0.91**	0.96	**0.87**	
1.15	1.14	1.10	1.16	1.07	
0.90	0.93	0.84	1.07	1.04	
1.24	0.90	0.75	1.44	1.09	
0.96	0.63	0.92	1.31	1.76	
0.70	0.98	1.25	0.90	0.64	
4.41	3.13	**9.47**	3.13	0.79	

6.63	**6.25**	**15.63**	3.56	0.87
0.95	0.80	1.17	0.90	1.55
1.56	1.26	0.97	1.56	0.89
1.24	0.79	0.90	0.93	1.14
1.35	1.20	1.11	0.77	0.82
1.38	1.13	0.96	1.02	1.00
0.99	0.87	0.64	1.10	0.85
1.35	0.99	0.72	1.14	1.15
1.36	1.09	0.97	0.97	1.08
1.27	0.88	1.01	**0.76**	1.21
1.75	0.69	1.18	**0.39**	1.66
1.06	1.12	**0,71**	1.13	1.22
0.44	0.37	0.61	0.58	**2.95**
1.03	1.05	1.38	2.32	**0.73**
0.64	**0.48**	0.69	0.68	0.86
0.80	0.96	**1.43**	**0.30**	**0.32**
1.29	0.48	1.12	2.02	0.62
0.95	0.92	0.85	0.89	**2.62**
1.22	**1.40**	1.14	**1.56**	**0.53**
0.88	1.23	0.98	1.09	**0.42**
0.97	0.79	**1.28**	1.42	1.01
1.01	1.03	**1.52**	1.11	**1.68**
0.53	**0.41**	**0.37**	1.13	1.48
1.24	0.84	1.35	0.65	0.73
0.98	1.10	**1.47**	**1.38**	**0.55**
0.91	**0.70**	1.29	1.29	1.06
1.07	0.96	**1.61**	**1.38**	**0.43**

0.94	0.83	1.33	1.56	1.07	
1.30	1.38	1.12	0.74	**16.67**	
0.73	0.69	**0.42**	1.06	**3.04**	
0.72	**0.43**	0.89	0.91	**7.84**	
1.32	0.95	1.04	1.91	**17.41**	
0.74	1.80	1.03	0.83	0.53	
1.08	1.10	1.09	1.08	1.09	
0.94	1.06	1.20	1.08	**0.57**	
0.92	0.98	0.99	0.97	**0.43**	
1.03	1.18	1.05	0.82	1.14	
1.10	**1.57**	1.25	1.08	0.74	
0.89	0.70	1.07	0.93	1.01	
0.65	0.53	0.46	0.92	0.68	
1.12	0.83	0.98	0.89	1.29	
0.80	0.89	0.86	0.68	**5.84**	
0.95	1.10	1.00	1.20	**0.68**	
1.14	1.04	**1.88**	1.26	**0.64**	
1.07	1.10	1.12	0.96	0.97	
0.83	1.01	0.90	0.90	0.85	
0.85	0.94	1.00	1.02	**0.85**	
1.43	1.66	**3.05**	3.40	0.99	
1.23	**1.82**	**1.49**	**1.79**	**2.24**	
1.12	1.55	**2.27**	1.21	0.71	
0.83	1.00	0.75	1.17	1.23	
0.98	0.81	0.93	1.00	**1.73**	
0.91	0.83	1.14	0.99	1.02	
1.20	2.94	1.87	0.77	1.31	

1.25	3.10	1.13	0.85	1.05
0.91	1.14	1.07	40.93	**55.13**
0.73	0.93	1.08	0.87	1.00
1.22	1.11	1.37	29.57	**171.90**
1.00	1.00	1.00	1.36	**2.24**
1.00	1.00	1.00	1.00	**3.82**
1.00	1.00	1.00	1.00	**2.31**
1.07	1.50	**2.50**	0.86	0.55
1.41	1.22	1.29	0.97	**1.70**
2.88	1.38	1.59	0.77	**4.62**
1.26	0.61	**0.52**	1.26	1.14
0.81	1.09	1.17	1.15	**1.96**
1.68	1.62	**1.97**	1.19	1.23
0.87	0.99	0.93	1.02	0.91
0.85	0.82	**0.60**	0.89	0.99
0.81	**0.78**	1.08	**1.14**	**3.58**
0.81	1.00	0.92	0.74	**2.08**
0.58	**0.52**	**0.44**	0.83	1.36
1.59	1.39	1.12	0.91	**2.63**
0.74	0.87	0.87	0.83	**0.45**
0.74	1.08	1.28	0.76	1.36
1.06	1.13	0.96	1.05	1.01
0.69	**0.73**	0.92	0.93	1.13
0.85	1.28	0.98	1.04	0.94
1.23	1.09	**1.75**	1.43	1.13
0.86	0.92	0.91	0.99	**0.89**
0.97	0.84	0.81	0.92	**0.63**

0.93	**0.79**	**0.80**	0.96	1.05
1.24	1.00	1.00	1.03	0.96
0.78	1.08	1.12	1.07	**0.51**
0.79	1.03	1.28	1.13	**0.53**
1.30	**1.26**	**1.77**	1.72	1.00
0.61	0.96	0.81	0.94	**0.58**
1.27	0.89	0.98	1.09	1.22
1.30	0.91	0.91	**1.54**	1.39
0.88	**0.41**	1.00	**0.59**	0.89
1.70	1.70	0.96	**2.10**	1.46
1.02	1.45	0.74	**1.67**	1.32
0.60	**0.28**	0.82	**0.39**	0.74
1.14	1.36	0.83	**1.50**	1.07
1.21	1.06	**1.64**	1.57	0.90
0.75	0.84	**0.72**	**0.64**	0.89
1.00	0.99	1.02	1.14	0.99
0.89	0.97	0.98	1.00	**0.67**
1.03	1.05	1.00	1.10	1.05
0.78	0.90	1.05	1.02	0.89
0.94	1.09	1.03	**1.24**	**1.39**
1.12	**1.62**	1.32	1.70	0.82
1.11	0.80	0.90	0.99	1.45
1.24	0.63	0.68	0.80	0.80
0.93	**0.81**	0.86	0.98	**1.39**
1.07	**0.77**	**0.79**	**0.75**	**0.73**
1.00	0.86	0.87	0.81	0.98
0.73	1.16	0.95	1.07	**0.54**

1.22	1.11	1.38	1.22	**1.38**
0.87	1.10	1.14	0.93	0.95
0.80	1.18	1.02	0.90	0.80
0.86	1.18	1.14	1.09	1.00
1.18	**1.81**	**1.36**	1.47	**0.49**
0.94	**1.57**	1.10	1.15	**0.46**
0.34	1.01	0.68	1.27	0.31
0.38	1.30	0.61	0.81	0.55
0.83	0.85	0.89	0.83	1.07
1.00	1.06	1.01	**1.26**	1.11
1.42	**0.58**	**0.72**	**0.71**	**3.60**
1.12	1.16	1.20	1.12	**1.19**
1.21	**1.53**	1.28	1.17	1.08
0.79	0.94	**1.46**	1.01	**0.49**
1.31	1.18	**2.41**	1.51	0.97
1.15	1.09	**1.63**	1.31	0.92
1.09	0.76	0.92	1.19	1.37
1.08	1.38	1.17	1.18	**0.42**
1.05	1.12	1.30	1.22	0.93
1.10	1.34	0.94	1.07	**0.54**
1.18	**1.28**	**1.27**	1.08	1.06
0.94	1.27	1.15	1.32	0.77
0.81	1.01	0.99	0.82	**0.16**
0.96	0.87	0.97	0.93	**1.34**
0.70	0.89	1.02	1.03	1.00
0.79	**0.61**	0.85	0.82	1.40
1.27	1.16	1.24	1.14	1.09

0.75	0.95	0.92	0.98	**0.76**
1.01	0.95	1.00	1.06	0.90
1.06	1.04	0.94	1.21	0.78
0.98	0.77	1.05	0.93	**2.05**
0.99	1.10	1.03	**1.25**	**2.08**
0.84	**0.72**	**0.74**	0.89	1.24
0.97	0.92	0.89	0.81	0.97
0.91	**0.71**	0.83	**0.72**	1.16
0.97	0.95	1.00	0.83	**0.68**
0.68	**0.69**	**0.76**	0.88	0.86
0.65	1.11	1.32	0.82	**1.29**
0.70	**0.70**	0.78	0.86	1.23
0.81	0.85	0.91	0.84	**1.63**
0.92	1.14	1.12	0.97	**1.38**
1.16	1.19	1.15	0.97	1.08
0.75	0.91	0.98	0.90	**0.61**
0.87	0.86	0.97	1.01	1.02
1.28	1.16	1.24	1.22	1.24
0.84	1.12	1.08	0.98	1.16
0.96	0.82	0.92	0.89	**1.85**
0.93	1.05	1.18	1.02	**2.57**
0.81	**0.74**	0.92	0.85	1.22
0.64	0.82	0.86	0.91	0.79
0.78	0.83	0.99	0.84	**0.49**
0.74	0.79	0.87	0.95	1.19
0.82	0.60	**0.59**	1.13	1.25
1.02	1.06	0.99	1.14	1.29

1.03	1.38	1.15	1.20	**1.39**
0.79	1.20	1.05	0.98	**2.53**
0.78	0.81	0.67	0.99	1.18
0.88	1.04	1.20	**1.53**	1.22
1.14	1.25	1.25	1.34	1.39
0.89	1.20	1.18	**1.47**	0.79
0.75	**0.64**	**0.65**	0.90	**0.57**
0.92	0.97	0.99	0.83	1.16
0.90	1.10	1.10	1.00	**1.61**
0.87	0.91	0.86	1.11	**0.85**
0.90	0.75	0.75	1.86	**3.71**
0.79	1.14	**1.27**	1.46	0.70
0.74	0.80	**0.76**	0.81	1.04
0.65	0.71	**0.69**	0.92	**1.39**
0.87	**0.77**	**0.77**	**0.74**	1.12
0.61	0.97	0.88	0.85	0.71
0.64	1.18	1.42	1.42	0.77
1.26	0.74	0.78	0.69	1.49
0.62	1.01	0.87	1.11	**0.52**
0.75	1.23	1.08	1.29	**0.60**
1.10	**1.24**	**1.35**	**1.36**	**0.76**
0.94	1.18	1.10	0.96	**3.02**
1.04	1.32	1.17	1.00	**5.89**
1.03	1.19	**1.39**	**1.25**	**0.70**
0.91	0.92	0.87	0.88	0.84
1.17	1.35	0.89	**1.33**	0.89
1.03	0.99	1.04	0.86	0.86

1.12	1.03	1.07	0.97	1.03	
0.89	0.99	0.89	0.91	0.82	
0.66	**0.74**	0.86	**0.60**	**0.59**	
1.14	1.03	0.84	1.37	**0.63**	
0.95	1.07	0.93	**1.27**	0.93	
0.77	0.94	0.93	1.00	**0.64**	
1.38	2.45	1.86	0.89	1.35	
1.00	1.14	1.18	0.93	1.12	
0.91	0.92	1.07	0.92	0.88	
0.96	1.07	1.03	0.96	**0.65**	
1.13	**0.69**	1.16	0.92	**0.50**	
0.92	1.04	0.93	0.88	1.21	
1.12	1.43	1.30	**1.49**	**0.48**	
1.04	1.12	1.03	0.91	**1.53**	
1.10	1.15	1.08	1.30	0.97	
1.35	1.55	**2.64**	1.82	0.98	
0.84	1.19	**2.18**	0.88	1.14	
1.14	1.22	**2.12**	1.72	0.94	
0.94	1.43	**2.44**	1.19	1.27	
1.00	1.43	**2.64**	1.35	1.14	
0.67	1.43	**2.50**	1.16	1.55	
1.45	1.34	1.41	1.35	1.10	
0.94	1.08	0.87	1.24	0.97	
0.94	1.13	0.97	1.20	0.91	
1.30	0.98	0.92	1.82	0.57	
1.21	1.20	1.13	1.34	**0.65**	
1.02	**1.60**	1.03	1.17	0.80	

0.92	1.62	0.94	1.34	**0.36**
0.97	0.99	**1.75**	2.11	0.97
0.70	1.14	0.85	1.09	**0.41**
1.28	1.22	1.46	1.05	**7.20**
0.80	**0.69**	1.03	**0.64**	1.74
0.92	0.97	1.01	1.07	**0.81**
1.05	1.00	1.53	1.58	1.28
0.82	**0.67**	1.10	1.34	0.96
0.98	0.98	1.57	1.40	1.13
1.38	1.21	**1.45**	1.10	**13.88**
0.80	1.22	1.21	1.14	**0.47**
0.89	0.84	1.06	0.81	0.73
1.20	0.94	0.75	1.28	1.49
0.93	0.87	**0.80**	**0.84**	0.94
0.97	0.85	**0.82**	0.98	0.92
1.24	1.09	**1.62**	1.42	0.93
0.87	0.90	0.83	**0.63**	1.40
1.79	1.13	1.95	0.88	**4.39**
0.88	0.97	0.99	1.13	1.02
0.95	0.96	0.88	1.27	1.10
1.09	1.00	0.98	1.17	1.08
0.99	1.01	1.08	1.01	**1.32**
0.99	0.95	1.32	0.94	1.43
142.38	0.88	115.91	0.75	**72.80**
53.54	**2.52**	75.15	0.62	**56.31**
0.85	1.24	0.96	0.84	0.84
0.83	1.11	1.03	1.15	**0.67**

0.79	1.06	**1.84**	1.13	**0.50**	
0.73	**0.61**	0.88	**0.55**	0.72	
1.30	1.07	**2.11**	1.65	0.92	
0.87	0.88	0.92	0.94	1.04	
0.93	0.95	1.00	1.04	0.97	
1.00	1.08	0.96	1.09	1.02	
0.80	0.90	1.00	1.08	0.94	
1.07	0.87	0.84	0.90	0.77	
0.92	0.81	**0.71**	1.14	0.89	
0.75	**0.63**	0.94	**0.56**	**0.48**	
1.12	1.07	**1.26**	1.22	0.98	
0.94	0.92	0.80	0.70	1.20	
1.03	1.25	1.26	0.87	0.97	
1.21	1.18	**2.01**	1.28	0.99	
0.85	1.15	**1.14**	**1.22**	**0.70**	
1.11	1.13	**1.62**	**1.51**	**1.30**	
0.78	0.87	0.82	0.94	**0.76**	
0.89	1.06	1.07	1.03	**0.69**	
0.78	0.77	0.96	1.14	0.84	
0.86	0.86	0.86	0.86	**37.21**	
0.54	0.54	0.70	0.76	**73.48**	
2.16	1.99	2.98	0.64	**4.25**	
8.86	**3.82**	11.61	0.87	**5.99**	
2.64	3.91	1.99	0.97	**2.74**	
1.98	2.90	1.30	0.98	**2.05**	
2.91	1.87	1.58	**0.53**	**3.01**	
0.91	1.03	0.98	1.03	**0.87**	

0.84	0.70	**0.56**	0.60	**0.47**	
0.71	0.78	0.89	0.80	1.40	
1.52	**0.55**	**0.54**	8.20	**65.21**	
0.76	1.25	1.13	0.98	1.06	
1.08	1.07	1.15	**1.71**	1.17	
1.45	1.27	1.60	2.90	**0.36**	
1.08	1.22	1.34	1.35	0.99	
0.68	1.07	1.18	0.71	0.69	
0.85	0.98	1.02	1.13	**0.68**	
1.04	1.01	1.67	1.13	**0.64**	
1.36	1.32	1.26	1.22	**0.58**	
1.03	1.27	1.00	**1.36**	**1.65**	
0.91	1.02	0.88	0.99	**0.61**	
0.93	1.03	1.05	1.08	1.08	
0.90	0.96	0.91	0.84	1.05	
0.98	0.93	1.19	0.81	**1.59**	
0.61	**0.57**	**0.59**	0.94	0.97	
1.23	1.61	**2.72**	1.40	1.12	
1.43	1.69	**3.24**	**3.15**	**1.76**	
1.44	1.71	**3.07**	**3.13**	1.70	
1.36	1.48	**3.08**	2.55	1.29	
1.40	1.48	**3.00**	2.52	1.30	
1.06	1.15	**1.40**	0.99	0.97	
1.18	1.10	0.78	1.18	0.85	
0.79	0.95	1.00	0.71	0.89	
0.75	1.09	1.13	0.98	0.94	
0.91	0.88	0.96	0.91	0.86	

0.97	1.31	1.11	1.08	**1.91**
0.98	**1.30**	0.99	0.85	**1.32**
0.81	1.02	0.93	1.00	0.68
1.05	**1.36**	1.69	1.12	**2.12**
1.06	1.16	**1.36**	**1.36**	1.07
0.91	1.00	0.89	0.90	**1.45**
0.94	0.93	0.98	1.04	0.91
0.98	1.17	1.24	**1.39**	0.91
0.84	0.86	0.86	0.83	**0.76**
0.87	1.48	1.46	**0.56**	**0.36**
0.88	0.99	1.01	1.10	1.13
0.95	1.09	1.49	1.17	**1.76**
0.48	**0.27**	**0.41**	0.63	0.92
1.05	**1.29**	1.07	**1.27**	0.83
1.24	1.08	**1.27**	0.98	**1.66**
1.06	0.58	1.91	0.43	1.05
0.76	**0.43**	0.72	**0.52**	**1.85**
0.73	1.03	1.19	0.65	1.52
0.71	**0.71**	**0.76**	0.87	**0.73**
1.11	1.12	**1.97**	1.39	0.77
0.97	1.17	0.94	1.36	0.83
1.24	1.45	1.56	2.67	**0.24**
1.05	0.98	1.09	1.04	0.95
0.91	0.82	0.95	0.72	**0.31**
1.24	1.06	0.98	1.20	**0.62**
1.56	1.10	1.70	1.16	0.89
1.56	**1.22**	1.18	1.32	1.33

1.03	0.95	0.94	**0.84**	**0.71**
0.84	0.94	0.89	0.86	**0.77**
0.81	0.85	1.05	0.85	**0.69**
0.93	0.89	**0.75**	0.86	0.89
1.21	**0.85**	1.07	0.98	1.14
0.87	**0.52**	0.79	**0.59**	1.05
0.89	0.91	**0.90**	0.95	**0.81**
0.84	**0.85**	0.95	0.88	1.08
0.97	1.01	0.98	**1.17**	0.90
0.92	**0.77**	0.95	0.89	0.91
0.92	**0.73**	0.90	0.92	1.02
1.04	1.01	1.03	1.24	0.89
0.91	**0.71**	**0.77**	1.07	0.92
0.98	0.84	0.87	**1.18**	0.95
1.15	1.14	1.00	**1.41**	0.91
1.35	**1.55**	0.91	**1.52**	1.29
1.16	**1.16**	1.14	1.11	0.97
0.89	**0.88**	0.86	0.90	**0.84**
1.00	1.01	0.91	1.12	0.99
1.13	1.04	1.11	1.01	0.84
1.06	0.87	0.93	**1.21**	0.81
0.85	**0.80**	0.88	0.82	**0.74**
0.97	0.97	0.99	0.98	**0.77**
1.01	1.04	0.99	1.01	0.91
1.05	1.16	1.04	**1.18**	0.93
1.27	1.12	1.12	1.21	1.19
1.06	1.03	0.89	0.95	**0.72**

1.07	**1.25**	1.21	1.01	**1.26**	
0.78	1.05	0.93	1.09	**0.65**	
0.87	0.91	1.24	1.14	**0.60**	
0.95	0.88	0.99	1.11	0.80	
0.99	1.02	1.03	1.18	1.04	
1.41	1.18	1.21	**1.52**	**1.23**	
0.99	0.77	0.81	0.67	1.10	
1.13	1.09	**1.92**	1.36	**0.70**	
1.58	1.10	**1.97**	1.30	**1.55**	
0.95	0.83	**0.77**	0.92	0.98	
0.73	**0.42**	**0.68**	**0.59**	0.75	
1.15	1.29	1.24	**1.70**	**0.38**	
0.92	0.99	0.98	1.02	0.96	
0.84	0.96	0.87	**0.69**	**0.68**	
0.98	1.02	0.92	0.91	**0.85**	
1.02	1.04	1.19	1.18	**1.09**	
0.32	0.35	6.75	0.61	**0.24**	
0.45	0.64	4.70	0.93	0.73	
0.33	0.47	2.23	0.61	0.45	
1.03	0.72	1.24	0.94	1.08	
1.11	3.25	0.71	1.09	**367.34**	
0.66	**0.66**	2.11	0.67	**5.04**	
2.90	7.50	**3.30**	0.87	0.89	
0.63	0.70	12.94	1.05	0.56	
1.07	1.09	**1.71**	**1.66**	**0.75**	
1.14	0.96	**1.87**	1.21	**0.51**	
1.03	0.98	**1.52**	1.34	0.89	

0.81	0.95	0.75	1.12	0.98	
0.72	0.77	0.67	0.77	1.02	
1.10	0.97	1.12	0.99	1.10	
0.98	0.99	1.06	0.96	**1.48**	
0.95	1.02	1.04	1.07	1.07	
1.11	0.86	1.09	0.99	1.25	
1.11	1.66	1.24	**1.80**	1.23	
0.73	1.10	1.11	0.88	**0.65**	
0.92	0.74	**0.65**	1.30	0.78	
0.95	1.06	**1.37**	1.09	1.06	
1.13	0.76	0.67	1.48	**2.66**	
0.79	0.68	0.88	1.28	0.92	
0.99	1.11	1.06	**1.22**	0.94	
0.86	1.34	1.15	1.18	0.77	
0.75	**0.53**	0.92	**0.54**	0.84	
1.25	1.17	**2.26**	1.45	0.81	
0.92	1.08	1.04	1.07	**1.12**	
2.53	0.56	1.25	1.31	**96.73**	
0.84	0.96	**0.93**	0.94	**0.83**	
0.87	0.92	0.92	0.97	**0.90**	
1.20	1.15	**2.02**	1.40	0.82	
1.18	1.23	**1.89**	1.36	0.98	
1.09	0.80	1.81	0.87	1.10	
1.15	1.08	0.97	1.33	**1.26**	
1.03	0.85	0.86	0.93	0.92	
0.83	1.04	1.07	1.07	0.97	
0.89	**0.72**	**0.78**	0.99	0.95	

1.21	0.43	0.96	**2.60**	0.58
11.99	**14.60**	**45.21**	82.94	0.85
1.04	0.87	**1.55**	1.32	**4.82**
1.21	1.08	1.39	0.76	**4.00**
0.55	**0.37**	**0.43**	0.84	**1.61**
0.80	0.87	**0.86**	0.93	**0.85**
1.27	1.04	1.01	0.93	1.36
0.98	0.66	0.79	0.86	1.05
1.12	**1.63**	**1.55**	1.06	0.62
1.00	0.81	0.83	0.92	0.88
0.64	**0.66**	0.79	0.94	0.84

Statistical Values (p-value is t-test statistic, q-value is false discovery statistic)									
Welch's Two-Sample t-Test (comparison between noted conditions)									
MOL361		**1E2**		**H121**		**T129**		**CONV**	
GF		**GF**		**GF**		**GF**		**GF**	
p-value	**q-value**	**p-value**	**q-value**	**p-value**	**q-value**	**p-value**	**q-value**	**p-value**	**q-value**
0.0158	0.2237	0.6126	0.7739	0.1165	0.2991	0.4947	0.7056	0.0071	0.0192
0.0272	0.2533	0.6074	0.7706	0.8195	0.6467	0.4013	0.6735	0.0039	0.0141
0.7797	0.6954	0.8165	0.8179	0.0875	0.2629	0.5929	0.7490	0.0084	0.0216
0.9376	0.7324	0.5875	0.7627	0.1569	0.3276	0.6290	0.7630	0.7148	0.4158
0.2310	0.4709	0.0894	0.4917	0.3076	0.4471	0.4305	0.6821	0.0040	0.0141
0.1219	0.3802	0.3461	0.6614	0.0389	0.1920	0.9316	0.8246	0.0193	0.0395
0.3166	0.5349	0.1210	0.5031	0.0992	0.2799	0.8608	0.8201	0.4795	0.3275
0.4588	0.6004	0.3055	0.6550	0.1398	0.3151	0.5718	0.7389	0.2544	0.2190
0.4772	0.6122	0.0032	0.1565	0.0477	0.2104	0.3150	0.6635	0.1582	0.1645

0.0264	0.2518	0.7987	0.8177	0.5191	0.5510	0.8096	0.8090	0.0290	0.0511
0.6267	0.6579	0.0090	0.2084	0.1657	0.3370	0.0496	0.5116	0.0046	0.0148
0.6525	0.6642	0.0621	0.4455	0.0020	0.0487	0.1017	0.5714	0.0800	0.1009
0.0639	0.3199	0.0018	0.1565	0.0435	0.2004	0.0525	0.5116	0.0057	0.0168
0.0278	0.2533	0.4968	0.7261	0.0384	0.1918	0.9522	0.8303	0.8798	0.4643
0.5818	0.6459	0.8386	0.8280	0.6043	0.5870	0.8558	0.8188	0.4068	0.2963
0.3231	0.5407	0.1916	0.5973	0.1625	0.3342	0.5224	0.7144	0.0627	0.0847
0.6829	0.6642	0.0232	0.2968	0.0029	0.0549	0.2306	0.6375	0.1066	0.1233
0.9273	0.7294	0.0403	0.3763	0.1467	0.3169	0.9112	0.8246	0.0045	0.0147
0.1779	0.4322	0.0090	0.2084	0.0012	0.0375	0.0665	0.5225	0.0010	0.0057
0.3162	0.5349	0.0730	0.4701	0.1637	0.3342	0.5423	0.7285	0.9945	0.4951
0.5426	0.6273	0.1757	0.5741	0.3826	0.4833	0.4141	0.6821	0.0015	0.0077
0.3444	0.5504	0.7411	0.8059	0.7265	0.6254	0.3764	0.6648	0.0000	0.0007
0.9473	0.7353	0.8362	0.8269	0.4738	0.5264	0.8531	0.8177	0.0001	0.0010
0.0063	0.2237	0.3214	0.6550	0.0045	0.0637	0.0104	0.3368	0.0032	0.0126
0.2292	0.4709	0.3835	0.6811	0.5071	0.5459	0.0720	0.5234	0.0383	0.0612
0.3821	0.5570	0.3709	0.6705	0.5163	0.5510	0.1483	0.6116	0.0015	0.0076
0.5004	0.6198	0.7096	0.8004	0.1811	0.3581	0.2329	0.6380	0.0382	0.0612
0.0079	0.2237	0.5845	0.7622	0.0631	0.2352	0.6087	0.7535	0.0658	0.0879
0.2207	0.4709	0.2246	0.6090	0.5368	0.5578	0.6136	0.7548	0.0386	0.0615
0.2220	0.4709	0.2841	0.6498	0.0386	0.1918	0.6287	0.7630	0.0035	0.0133
0.0093	0.2237	0.2008	0.5977	0.3613	0.4796	0.3719	0.6648	0.0521	0.0761
0.0788	0.3430	0.7990	0.8177	0.0768	0.2530	0.5689	0.7388	0.0382	0.0612
0.1178	0.3750	0.4445	0.7041	0.7228	0.6254	0.9461	0.8288	0.0333	0.0562
0.1848	0.4361	0.9684	0.8488	0.5925	0.5837	0.1143	0.5856	0.0770	0.0976
0.0806	0.3442	0.4329	0.7007	0.7726	0.6352	0.4560	0.6890	0.0018	0.0089
0.0252	0.2518	0.8018	0.8177	0.6275	0.5966	0.5779	0.7402	0.0028	0.0114

0.0308	0.2635	0.2939	0.6533	0.1113	0.2946	0.8152	0.8113	0.0002	0.0020
0.0159	0.2237	0.7783	0.8174	0.3989	0.4941	0.4999	0.7056	0.0105	0.0258
0.0023	0.1952	0.3156	0.6550	0.0108	0.0965	0.0216	0.3996	0.0017	0.0086
0.9827	0.7411	0.4637	0.7101	0.7705	0.6352	0.5723	0.7389	0.0073	0.0194
0.1711	0.4288	0.8128	0.8177	0.2415	0.3993	0.7053	0.7879	0.0036	0.0136
0.9179	0.7281	0.9159	0.8444	0.5495	0.5654	0.5115	0.7070	0.7464	0.4272
0.5739	0.6410	0.1601	0.5502	0.6561	0.6121	0.8155	0.8113	0.7607	0.4320
0.5666	0.6393	0.2408	0.6241	0.8573	0.6565	0.9676	0.8347	0.8777	0.4643
0.2731	0.5009	0.4819	0.7227	0.2330	0.3956	0.9977	0.8421	0.1982	0.1884
0.3374	0.5484	0.3343	0.6550	0.5255	0.5525	0.6978	0.7879	0.2398	0.2129
0.1443	0.4142	0.1411	0.5147	0.2904	0.4354	0.5006	0.7056	0.0543	0.0771
0.7569	0.6906	0.7912	0.8177	0.9873	0.6904	0.3752	0.6648	0.5296	0.3439
0.7763	0.6952	0.8653	0.8352	0.9484	0.6745	0.7940	0.8058	0.4593	0.3224
0.3122	0.5330	0.6021	0.7706	0.8315	0.6518	0.0406	0.5116	0.1879	0.1828
0.0183	0.2422	0.9671	0.8487	0.0377	0.1918	0.9226	0.8246	0.0004	0.0031
0.0225	0.2518	0.1800	0.5796	0.7575	0.6335	0.0685	0.5225	0.5296	0.3439
0.3764	0.5570	0.3546	0.6631	0.9317	0.6736	0.8696	0.8201	0.2005	0.1899
0.0687	0.3270	0.0075	0.2084	0.0399	0.1921	0.1801	0.6258	0.2976	0.2403
0.3667	0.5570	0.8038	0.8177	0.2520	0.4091	0.6113	0.7543	0.1396	0.1499
0.1844	0.4361	0.5385	0.7501	0.6820	0.6153	0.8342	0.8170	0.0058	0.0169
0.5201	0.6257	0.1914	0.5973	0.8473	0.6538	0.2587	0.6561	0.1069	0.1233
0.3560	0.5539	0.5110	0.7340	0.8756	0.6657	0.7367	0.7941	0.3221	0.2516
0.5025	0.6204	0.2889	0.6500	0.6241	0.5957	0.7009	0.7879	0.0866	0.1047
0.0081	0.2237	0.6918	0.7890	0.0032	0.0549	0.0033	0.2605	0.0066	0.0181
0.6664	0.6642	0.0272	0.3156	0.1194	0.3042	0.0168	0.3996	0.0321	0.0545
0.1341	0.4035	0.7966	0.8177	0.7851	0.6389	0.4268	0.6821	0.1943	0.1869
0.7982	0.7024	0.2099	0.5977	0.3115	0.4486	0.2034	0.6258	0.1842	0.1811

0.3210	0.5392	0.5027	0.7316	0.8124	0.6465	0.9257	0.8246	0.8578	0.4604
0.0644	0.3199	0.7121	0.8004	0.0902	0.2629	0.7448	0.7941	0.0354	0.0594
0.7256	0.6785	0.2508	0.6323	0.6641	0.6129	0.2005	0.6258	0.5599	0.3561
0.8583	0.7196	0.4525	0.7097	0.0684	0.2437	0.5631	0.7370	0.7688	0.4346
0.0302	0.2616	0.0043	0.1828	0.0272	0.1652	0.4454	0.6869	0.3493	0.2670
0.9594	0.7367	0.1083	0.4999	0.3046	0.4468	0.3674	0.6648	0.4037	0.2951
0.4413	0.5969	0.4004	0.6946	0.9775	0.6851	0.1991	0.6258	0.4355	0.3094
0.5719	0.6402	0.0627	0.4455	0.1121	0.2946	0.1746	0.6256	0.2013	0.1902
0.0023	0.1952	0.0026	0.1565	0.0572	0.2296	0.3511	0.6648	0.1767	0.1765
0.0203	0.2497	0.3162	0.6550	0.7188	0.6238	0.2374	0.6397	0.8339	0.4532
0.0209	0.2497	0.5486	0.7501	0.0755	0.2530	0.3918	0.6735	0.1891	0.1833
0.0294	0.2612	0.0181	0.2862	0.0829	0.2629	0.5782	0.7402	0.3764	0.2801
0.5775	0.6422	0.9375	0.8447	0.9324	0.6736	0.5343	0.7215	0.2420	0.2136
0.3278	0.5435	0.4234	0.7007	0.4417	0.5163	0.1165	0.5885	0.0847	0.1042
0.1104	0.3672	0.3662	0.6705	0.3763	0.4819	0.8840	0.8246	0.9995	0.4964
0.1405	0.4089	0.7186	0.8004	0.9174	0.6736	0.8199	0.8124	0.3796	0.2811
0.8801	0.7219	0.0246	0.2968	0.5805	0.5786	0.2977	0.6604	0.3277	0.2545
0.1124	0.3697	0.6828	0.7859	0.1870	0.3581	0.1341	0.6069	0.1707	0.1720
0.1676	0.4260	0.7736	0.8159	0.1199	0.3042	0.8954	0.8246	0.3775	0.2805
0.1071	0.3668	0.1613	0.5502	0.0114	0.1002	0.7390	0.7941	0.3515	0.2677
0.0001	0.0401	0.2289	0.6110	0.0040	0.0591	0.3224	0.6635	0.0623	0.0847
0.0100	0.2237	0.2422	0.6241	0.0005	0.0255	0.0114	0.3368	0.0234	0.0444
0.0532	0.3182	0.6831	0.7859	0.7551	0.6335	0.4273	0.6821	0.0059	0.0171
0.0236	0.2518	0.4714	0.7161	0.4089	0.4992	0.3891	0.6718	0.0008	0.0053
0.8545	0.7193	0.2485	0.6323	0.2071	0.3713	0.9296	0.8246	0.6776	0.4034
0.8757	0.7219	0.1822	0.5796	0.7563	0.6335	0.6793	0.7844	0.1320	0.1442
0.8314	0.7149	0.1459	0.5270	0.0974	0.2773	0.7071	0.7879	0.6965	0.4104

0.2923	0.5154	0.0670	0.4509	0.3679	0.4812	0.7798	0.8048	0.7217	0.4176
0.0068	0.2237	0.3272	0.6550	0.1018	0.2849	0.1066	0.5768	0.4284	0.3054
0.5601	0.6343	0.1212	0.5031	0.4155	0.4992	0.5258	0.7177	0.0849	0.1042
0.4616	0.6004	0.0614	0.4455	0.3111	0.4486	0.5423	0.7285	0.0590	0.0819
0.0003	0.0868	0.6469	0.7782	0.5824	0.5786	0.5513	0.7345	0.0023	0.0104
0.0382	0.2966	0.0631	0.4455	0.0228	0.1506	0.7928	0.8058	0.8964	0.4668
0.0111	0.2237	0.0126	0.2491	0.0560	0.2294	0.1574	0.6131	0.1614	0.1670
0.2076	0.4610	0.3181	0.6550	0.3910	0.4880	0.7163	0.7887	0.6509	0.3926
0.2011	0.4548	0.0439	0.3767	0.0900	0.2629	0.2144	0.6280	0.1969	0.1881
0.1681	0.4260	0.3964	0.6946	0.1887	0.3581	0.8712	0.8201	0.9353	0.4787
0.3480	0.5514	0.0132	0.2491	0.0099	0.0944	0.5733	0.7390	0.0062	0.0176
0.2511	0.4761	0.0367	0.3731	0.0086	0.0901	0.1577	0.6131	0.8495	0.4589
0.0098	0.2237	0.2317	0.6142	0.0005	0.0255	0.0027	0.2605	0.0115	0.0278
0.0096	0.2237	0.4580	0.7101	0.3604	0.4796	0.5103	0.7066	0.2081	0.1938
0.0288	0.2596	0.3093	0.6550	0.4873	0.5338	0.1975	0.6258	0.3983	0.2916
0.8728	0.7219	0.2978	0.6533	0.8851	0.6670	0.9474	0.8290	0.0879	0.1054
0.1943	0.4446	0.1048	0.4999	0.0785	0.2550	0.0271	0.4503	0.2582	0.2194
0.0489	0.3055	0.0675	0.4509	0.2585	0.4111	0.1456	0.6069	0.2894	0.2353
0.8286	0.7149	0.9202	0.8444	0.8846	0.6670	0.2090	0.6280	0.0042	0.0141
0.1510	0.4183	0.2711	0.6469	0.1504	0.3199	0.2325	0.6380	0.0224	0.0436
0.1062	0.3668	0.1144	0.5031	0.2085	0.3713	0.2030	0.6258	0.0037	0.0137
0.3289	0.5435	0.1201	0.5031	0.3996	0.4941	0.2766	0.6595	0.7069	0.4130
0.2293	0.4709	0.4103	0.6997	0.0283	0.1690	0.1733	0.6256	0.0118	0.0283
0.5174	0.6257	0.2600	0.6342	0.0404	0.1928	0.3198	0.6635	0.0037	0.0137
0.3988	0.5691	0.3217	0.6550	0.3091	0.4473	0.4053	0.6753	0.0196	0.0397
0.6201	0.6579	0.7752	0.8165	0.0224	0.1493	0.0090	0.3368	0.1216	0.1344
0.6724	0.6642	0.8558	0.8302	0.0987	0.2797	0.0481	0.5116	0.0066	0.0181

0.2376	0.4709	0.6365	0.7782	0.0362	0.1918	0.2685	0.6561	0.0235	0.0444
0.4955	0.6198	0.6066	0.7706	0.1623	0.3342	0.8459	0.8170	0.0681	0.0891
0.0818	0.3452	0.5721	0.7622	0.4978	0.5425	0.1144	0.5856	0.0915	0.1092
								0.0246	0.0461
0.6949	0.6653	0.3466	0.6614	0.5191	0.5510	0.3466	0.6648	0.0001	0.0012
0.6363	0.6641	0.0842	0.4917	0.5154	0.5510	0.2692	0.6561	0.9305	0.4787
0.9234	0.7286	0.5390	0.7501	0.9653	0.6811	0.7068	0.7879	0.1704	0.1720
0.6550	0.6642	0.5664	0.7622	0.5830	0.5786	0.3252	0.6635	0.9211	0.4756
0.1213	0.3802	0.0443	0.3767	0.0010	0.0358	0.4844	0.7017	0.0684	0.0891
0.9771	0.7411	0.2022	0.5977	0.8889	0.6670	0.6008	0.7506	0.0000	0.0000
0.0818	0.3452	0.6496	0.7782	0.1461	0.3167	0.8622	0.8201	0.0133	0.0305
0.5000	0.6198	0.2253	0.6090	0.0148	0.1169	0.8874	0.8246	0.1570	0.1640
0.2198	0.4709	0.7204	0.8004	0.1031	0.2871	0.8821	0.8246	0.0361	0.0604
0.2273	0.4709	0.2093	0.5977	0.2070	0.3713	0.8564	0.8188	0.3126	0.2476
0.0860	0.3518	0.0436	0.3767	0.5945	0.5837	0.6807	0.7844	0.0038	0.0139
0.5097	0.6224	0.2968	0.6533	0.8335	0.6518	0.8819	0.8246	0.7234	0.4181
0.1572	0.4185	0.7256	0.8004	0.4520	0.5216	0.0837	0.5601	0.1488	0.1568
0.0083	0.2237	0.6083	0.7706	0.7642	0.6352	0.0622	0.5225	0.6124	0.3754
0.4919	0.6198	0.3719	0.6705	0.7508	0.6335	0.6879	0.7844	0.1860	0.1822
0.4612	0.6004	0.2799	0.6478	0.0385	0.1918	0.6341	0.7663	0.5037	0.3359
0.5156	0.6257	0.8996	0.8441	0.2121	0.3734	0.5907	0.7484	0.1061	0.1233
0.3876	0.5639	0.4141	0.7007	0.4506	0.5216	0.3188	0.6635	0.7207	0.4176
0.9596	0.7367	0.6976	0.7941	0.0665	0.2396	0.6991	0.7879	0.2923	0.2373
0.0120	0.2237	0.8020	0.8177	0.1438	0.3151	0.6093	0.7535	0.0083	0.0216
0.5456	0.6273	0.0756	0.4788	0.7108	0.6211	0.3336	0.6648	0.8647	0.4604
0.1760	0.4322	0.9975	0.8533	0.5836	0.5786	0.9832	0.8347	0.0001	0.0009
0.0056	0.2237	0.5786	0.7622	0.0235	0.1525	0.3251	0.6635	0.0514	0.0756

0.1166	0.3746	0.1234	0.5031	0.2752	0.4248	0.2024	0.6258	0.0526	0.0763
0.3461	0.5504	0.8167	0.8179	0.9497	0.6745	0.1512	0.6131	0.1065	0.1233
0.5528	0.6286	0.9198	0.8444	0.9351	0.6736	0.7604	0.8010	0.0926	0.1101
0.1572	0.4185	0.9908	0.8533	0.0900	0.2629	0.8642	0.8201	0.0039	0.0141
0.4589	0.6004	0.9246	0.8444	0.9237	0.6736	0.2455	0.6504	0.6543	0.3942
0.1657	0.4260	0.3302	0.6550	0.2579	0.4111	0.0766	0.5375	0.8151	0.4478
0.3816	0.5570	0.4897	0.7234	0.3886	0.4870	0.6676	0.7801	0.1980	0.1884
0.2306	0.4709	0.0041	0.1828	0.0064	0.0739	0.9043	0.8246	0.8276	0.4515
0.6167	0.6579	0.7890	0.8177	0.5982	0.5856	0.1275	0.5967	0.7689	0.4346
0.2458	0.4740	0.0951	0.4999	0.0501	0.2160	0.0498	0.5116	0.7712	0.4347
0.8771	0.7219	0.3830	0.6811	0.2855	0.4338	0.5040	0.7056	0.0495	0.0742
0.2667	0.4945	0.5133	0.7350	0.0623	0.2338	0.9278	0.8246	0.0007	0.0046
0.8614	0.7201	0.5975	0.7700	0.9883	0.6904	0.7222	0.7918	0.5724	0.3593
0.7268	0.6785	0.1287	0.5071	0.2728	0.4242	0.5143	0.7071	0.5834	0.3630
0.0090	0.2237	0.4960	0.7261	0.1243	0.3083	0.0727	0.5234	0.7911	0.4415
0.0100	0.2237	0.9137	0.8444	0.3613	0.4796	0.2746	0.6595	0.1444	0.1533
0.1097	0.3672	0.9880	0.8533	0.1192	0.3042	0.6460	0.7736	0.0536	0.0771
0.0019	0.1952	0.9144	0.8444	0.0239	0.1525	0.5577	0.7350	0.1148	0.1298
0.0205	0.2497	0.6489	0.7782	0.3695	0.4814	0.1579	0.6131	0.0311	0.0531
0.7794	0.6954	0.4915	0.7234	0.9168	0.6736	0.8477	0.8177	0.3012	0.2411
0.0055	0.2237	0.6697	0.7821	0.0078	0.0824	0.1688	0.6229	0.0548	0.0774
0.2015	0.4548	0.6272	0.7782	0.1220	0.3058	0.7816	0.8048	0.1205	0.1344
0.5711	0.6402	0.2536	0.6326	0.3360	0.4727	0.0464	0.5116	0.1012	0.1185
0.5092	0.6224	0.6372	0.7782	0.6847	0.6155	0.3039	0.6607	0.4960	0.3322
0.0521	0.3182	0.1335	0.5071	0.4355	0.5107	0.3868	0.6693	0.0862	0.1047
0.0008	0.1857	0.3507	0.6627	0.0593	0.2308	0.4274	0.6821	0.1641	0.1683
0.1611	0.4185	0.2095	0.5977	0.8339	0.6518	0.9090	0.8246	0.3006	0.2411

									0.0544	0.0771
0.0595	0.3182	0.2455	0.6307	0.3760	0.4819	0.1454	0.6069	0.9622	0.4866	
0.6891	0.6642	0.1228	0.5031	0.0831	0.2629	0.8397	0.8170	0.0005	0.0040	
0.4613	0.6004	0.0383	0.3763	0.1867	0.3581	0.8139	0.8113	0.2069	0.1931	
0.9811	0.7411	0.1933	0.5977	0.6178	0.5944	0.8426	0.8170	0.3908	0.2880	
0.3495	0.5524	0.0518	0.4026	0.1420	0.3151	0.7987	0.8058	0.7329	0.4231	
0.2063	0.4610	0.9304	0.8444	0.6767	0.6152	0.2173	0.6280	0.0916	0.1092	
0.7422	0.6844	0.6273	0.7782	0.9992	0.6926	0.5131	0.7071	0.2528	0.2188	
0.6251	0.6579	0.8702	0.8353	0.1336	0.3151	0.8048	0.8058	0.0164	0.0353	
								0.0056	0.0168	
0.8022	0.7040	0.5856	0.7622	0.1402	0.3151	0.3365	0.6648	0.4864	0.3293	
0.3170	0.5349	0.3137	0.6550	0.5254	0.5525	0.1455	0.6069	0.0087	0.0224	
0.1228	0.3802	0.1228	0.5031	0.8302	0.6518	0.1228	0.5944	0.0013	0.0072	
0.8442	0.7175	0.3908	0.6899	0.3998	0.4941	0.2480	0.6526	0.6562	0.3948	
0.0764	0.3417	0.0947	0.4999	0.3297	0.4663	0.4308	0.6821	0.5592	0.3561	
0.0428	0.3026	0.1711	0.5676	0.7479	0.6335	0.9862	0.8349	0.7927	0.4419	
0.0793	0.3430	0.5459	0.7501	0.6359	0.6001	0.5564	0.7345	0.0041	0.0141	
0.0896	0.3523	0.2679	0.6441	0.5388	0.5589	0.8906	0.8246	0.0506	0.0749	
0.6480	0.6641	0.8038	0.8177	0.0448	0.2035	0.2103	0.6280	0.0587	0.0818	
0.0348	0.2863	0.0075	0.2084	0.0068	0.0760	0.1257	0.5944	0.3466	0.2653	
0.1431	0.4142	0.1848	0.5832	0.3566	0.4796	0.7403	0.7941	0.6428	0.3883	
0.8763	0.7219	0.8270	0.8229	0.1484	0.3185	0.5562	0.7345	0.0515	0.0756	
0.8278	0.7149	0.7364	0.8037	0.6087	0.5883	0.9733	0.8347	0.2145	0.1985	
0.5471	0.6273	0.4767	0.7213	0.2903	0.4354	0.5993	0.7506	0.4686	0.3248	
0.3325	0.5448	0.0709	0.4642	0.4003	0.4941	0.3346	0.6648	0.0371	0.0612	
0.0178	0.2407	0.7925	0.8177	0.3845	0.4847	0.1801	0.6258	0.0002	0.0020	
0.3463	0.5504	0.3281	0.6550	0.9308	0.6736	0.0908	0.5648	0.0029	0.0117	

0.6513	0.6641	0.5911	0.7629	0.0558	0.2294	0.2946	0.6604	0.0268	0.0490
0.0696	0.3270	0.1222	0.5031	0.0071	0.0766	0.1172	0.5885	0.8579	0.4604
0.6615	0.6642	0.0221	0.2928	0.0470	0.2088	0.9420	0.8280	0.0221	0.0435
0.9862	0.7417	0.4391	0.7007	0.0514	0.2160	0.7371	0.7941	0.0057	0.0168
0.0526	0.3182	0.1819	0.5796	0.0000	0.0046	0.3305	0.6648	0.1132	0.1288
0.1101	0.3672	0.3107	0.6550	0.0511	0.2160	0.7913	0.8058	0.0467	0.0713
0.0109	0.2237	0.1744	0.5741	0.8237	0.6484	0.7466	0.7941	0.4654	0.3239
0.5924	0.6522	0.7315	0.8011	0.0733	0.2484	0.3983	0.6735	0.0221	0.0435
0.9282	0.7294	0.8265	0.8229	0.1254	0.3083	0.6533	0.7778	0.0077	0.0202
0.7230	0.6785	0.7451	0.8088	0.0534	0.2215	0.5502	0.7345	0.9780	0.4911
0.0632	0.3199	0.1059	0.4999	0.0056	0.0722	0.0137	0.3604	0.0381	0.0612
0.0968	0.3626	0.0216	0.2928	0.0421	0.1982	0.1612	0.6166	0.0007	0.0046
0.7683	0.6924	0.8059	0.8177	0.9206	0.6736	0.1861	0.6258	0.7052	0.4130
0.0711	0.3285	0.0412	0.3763	0.0022	0.0498	0.0924	0.5648	0.4850	0.3292
0.0668	0.3242	0.4639	0.7101	0.5253	0.5525	0.4553	0.6890	0.0011	0.0059
0.0755	0.3417	0.0641	0.4455	0.0030	0.0549	0.0945	0.5648	0.9948	0.4951
0.8055	0.7040	0.9817	0.8530	0.6569	0.6121	0.9974	0.8421	0.2347	0.2112
0.2197	0.4709	0.0993	0.4999	0.0166	0.1257	0.7111	0.7885	0.6577	0.3952
0.0232	0.2518	0.0323	0.3518	0.2181	0.3764	0.0543	0.5116	0.0009	0.0055
0.3637	0.5570	0.1063	0.4999	0.1882	0.3581	0.8422	0.8170	0.3594	0.2714
0.0213	0.2497	0.0764	0.4788	0.7076	0.6201	0.0201	0.3996	0.0934	0.1108
0.7024	0.6696	0.4473	0.7043	0.8987	0.6704	0.9775	0.8347	0.0000	0.0000
0.3797	0.5570	0.2511	0.6323	0.7758	0.6352	0.7297	0.7936	0.0138	0.0312
0.4563	0.6004	0.3352	0.6550	0.7118	0.6211	0.1850	0.6258	0.0000	0.0006
0.0159	0.2237	0.0111	0.2328	0.2752	0.4248	0.3249	0.6635	0.5681	0.3584
0.4662	0.6028	0.5646	0.7617	0.9178	0.6736	0.7648	0.8016	0.0001	0.0013
0.3679	0.5570	0.6085	0.7706	0.1918	0.3598	0.4763	0.7017	0.7745	0.4358

0.4500	0.5999	0.8830	0.8408	0.0717	0.2465	0.1447	0.6069	0.8282	0.4515
0.0806	0.3442	0.1102	0.5011	0.0098	0.0944	0.3601	0.6648	0.0687	0.0891
0.4834	0.6133	0.9320	0.8444	0.9165	0.6736	0.3202	0.6635	0.0061	0.0176
0.0150	0.2237	0.0879	0.4917	0.2898	0.4354	0.4773	0.7017	0.5915	0.3665
0.7087	0.6724	0.2292	0.6110	0.1853	0.3581	0.4933	0.7056	0.6879	0.4064
0.0676	0.3260	0.0332	0.3519	0.0771	0.2530	0.9791	0.8347	0.1817	0.1800
0.2865	0.5116	0.6650	0.7800	0.1440	0.3151	0.1832	0.6258	0.0000	0.0000
0.3436	0.5504	0.5034	0.7316	0.3328	0.4696	0.0599	0.5136	0.2553	0.2192
0.2477	0.4741	0.1000	0.4999	0.8714	0.6635	0.0542	0.5116	0.0027	0.0111
0.5532	0.6286	0.4922	0.7234	0.6494	0.6073	0.7603	0.8010	0.0506	0.0749
0.9124	0.7281	0.7840	0.8177	0.5660	0.5730	0.9308	0.8246	0.5380	0.3462
0.1081	0.3668	0.2063	0.5977	0.7829	0.6379	0.8026	0.8058	0.4898	0.3298
0.5291	0.6262	0.8001	0.8177	0.8819	0.6670	0.1262	0.5944	0.0046	0.0148
0.3646	0.5570	0.2519	0.6323	0.1891	0.3581	0.7908	0.8058	0.9063	0.4712
0.8934	0.7230	0.3005	0.6544	0.4146	0.4992	0.9750	0.8347	0.0000	0.0001
0.8408	0.7175	0.9427	0.8465	0.7582	0.6335	0.7609	0.8010	0.0014	0.0072
		0.3559	0.6631					0.0001	0.0009
0.1239	0.3805	0.2803	0.6478	0.9427	0.6736	0.3456	0.6648	0.1518	0.1593
0.7142	0.6724	0.2989	0.6533	0.1152	0.2984	0.0471	0.5116	0.2812	0.2328
0.9429	0.7349	0.9921	0.8533	0.5938	0.5837	0.4362	0.6835	0.8647	0.4604
0.3466	0.5504	0.3466	0.6614	0.3466	0.4742	0.3466	0.6648	0.0000	0.0000
0.3466	0.5504	0.3466	0.6614	0.5560	0.5684	0.3466	0.6648	0.0003	0.0022
0.0480	0.3055	0.0201	0.2928	0.0673	0.2410	0.9351	0.8268	0.0048	0.0152
0.8115	0.7058	0.6800	0.7857	0.4683	0.5264	0.0701	0.5225	0.3960	0.2912
0.1662	0.4260	0.9532	0.8469	0.6446	0.6046	0.3799	0.6652	0.7064	0.4130
0.4315	0.5919	0.3280	0.6550	0.2364	0.3980	0.8510	0.8177	0.7079	0.4130
0.1021	0.3666	0.0168	0.2839	0.0262	0.1623	0.7131	0.7885	0.5068	0.3370

0.9212	0.7281	0.6022	0.7706	0.2872	0.4338	0.6237	0.7619	0.7584	0.4315
0.8495	0.7193	0.1465	0.5270	0.8424	0.6536	0.9486	0.8291	0.0040	0.0141
0.9309	0.7298	0.2832	0.6496	0.4231	0.5059	0.1546	0.6131	0.3210	0.2512
0.9305	0.7298	0.5276	0.7446	0.1545	0.3248	0.4063	0.6753	0.0025	0.0107
0.6614	0.6642	0.9340	0.8446	0.2276	0.3886	0.9260	0.8246	0.6213	0.3782
0.3523	0.5537	0.6625	0.7800	0.1760	0.3535	0.2196	0.6280	0.5298	0.3439
0.7810	0.6954	0.9574	0.8469	0.4325	0.5107	0.5807	0.7422	0.5597	0.3561
0.4215	0.5830	0.4005	0.6946	0.9671	0.6817	0.7125	0.7885	0.0000	0.0000
0.5685	0.6395	0.0826	0.4917	0.0213	0.1450	0.8429	0.8170	0.3887	0.2874
0.0975	0.3626	0.3299	0.6550	0.3074	0.4471	0.1937	0.6258	0.0224	0.0436
0.8852	0.7219	0.8762	0.8353	0.8126	0.6465	0.9457	0.8288	0.3905	0.2880
0.7865	0.6966	0.0783	0.4804	0.2718	0.4242	0.2717	0.6595	0.0866	0.1047
0.6784	0.6642	0.5771	0.7622	0.2539	0.4095	0.2806	0.6595	0.0123	0.0291
0.1059	0.3668	0.2087	0.5977	0.2003	0.3664	0.2975	0.6604	0.0831	0.1036
0.2320	0.4709	0.0642	0.4455	0.7535	0.6335	0.9135	0.8246	0.0275	0.0498
0.6824	0.6642	0.5436	0.7501	0.0377	0.1918	0.3641	0.6648	0.0670	0.0887
0.2224	0.4709	0.6688	0.7821	0.0394	0.1921	0.6624	0.7801	0.1410	0.1507
0.4354	0.5938	0.4337	0.7007	0.5002	0.5441	0.1439	0.6069	0.0021	0.0096
0.5358	0.6273	0.9301	0.8444	0.8080	0.6465	0.9007	0.8246	0.0310	0.0531
0.9197	0.7281	0.8755	0.8353	0.0321	0.1796	0.3107	0.6635	0.8579	0.4604
0.7448	0.6849	0.4442	0.7041	0.4077	0.4992	0.9803	0.8347	0.3578	0.2707
0.6258	0.6579	0.9313	0.8444	0.2965	0.4402	0.3041	0.6607	0.0867	0.1047
0.4034	0.5710	0.3975	0.6946	0.6784	0.6152	0.4869	0.7023	0.0002	0.0015
0.5419	0.6273	0.9715	0.8497	0.9762	0.6850	0.5491	0.7345	0.4215	0.3023
0.5855	0.6479	0.0897	0.4917	0.3765	0.4819	0.2189	0.6280	0.0007	0.0046
0.6785	0.6642	0.4613	0.7101	0.0653	0.2365	0.5401	0.7281	0.1726	0.1728
0.6243	0.6579	0.0087	0.2084	0.1437	0.3151	0.6910	0.7857	0.5681	0.3584

0.0697	0.3270	0.1055	0.4999	0.1075	0.2942	0.4142	0.6821	0.0031	0.0122
0.2070	0.4610	0.1694	0.5645	0.5035	0.5447	0.3606	0.6648	0.0754	0.0969
0.1223	0.3802	0.8249	0.8229	0.3820	0.4833	0.5976	0.7506	0.7084	0.4130
0.0461	0.3055	0.0809	0.4884	0.0319	0.1796	0.0214	0.3996	0.2742	0.2279
								0.0285	0.0506
0.9853	0.7417	0.2418	0.6241	0.7555	0.6335	0.7229	0.7918	0.2199	0.2023
0.8605	0.7201	0.0432	0.3767	0.0354	0.1918	0.2652	0.6561	0.3515	0.2677
0.0870	0.3518	0.0788	0.4804	0.0091	0.0921	0.2218	0.6290	0.0208	0.0418
0.2233	0.4709	0.6425	0.7782	0.1957	0.3624	0.3391	0.6648	0.9666	0.4880
0.7205	0.6773	0.6143	0.7747	0.0068	0.0760	0.9202	0.8246	0.1667	0.1703
0.5250	0.6262	0.9989	0.8533	0.0132	0.1128	0.0124	0.3368	0.9722	0.4898
0.1133	0.3697	0.0400	0.3763	0.0164	0.1257	0.8028	0.8058	0.0006	0.0040
0.7243	0.6785	0.1290	0.5071	0.0858	0.2629	0.0124	0.3368	0.1715	0.1725
0.0633	0.3199	0.0155	0.2839	0.0610	0.2329	0.3245	0.6635	0.0436	0.0679
0.1240	0.3805	0.7233	0.8004	0.4586	0.5239	0.0283	0.4590	0.9957	0.4951
0.2251	0.4709	0.5424	0.7501	0.9875	0.6904	0.0778	0.5395	0.9617	0.4866
0.9931	0.7431	0.9957	0.8533	0.2191	0.3772	0.9632	0.8347	0.0117	0.0281
0.8812	0.7219	0.0986	0.4999	0.9325	0.6736	0.7005	0.7879	0.1664	0.1703
0.1854	0.4361	0.5729	0.7622	0.3794	0.4819	0.5068	0.7061	0.0062	0.0176
0.8427	0.7175	0.6984	0.7941	0.1632	0.3342	0.6839	0.7844	0.9756	0.4907
0.1098	0.3672	0.2575	0.6326	0.0108	0.0965	0.0401	0.5116	0.0038	0.0138
0.9149	0.7281	0.9748	0.8504	0.6671	0.6147	0.9710	0.8347	0.5745	0.3594
0.9947	0.7431	0.8108	0.8177	0.0430	0.1995	0.3626	0.6648	0.9900	0.4951
0.2486	0.4741	0.2100	0.5977	0.3613	0.4796	0.8266	0.8167	0.5784	0.3613
0.1690	0.4260	0.1224	0.5031	0.1480	0.3185	0.9698	0.8347	0.1587	0.1646
0.4587	0.6004	0.8131	0.8177	0.3783	0.4819	0.9016	0.8246	0.2366	0.2123
0.8453	0.7175	0.1232	0.5031	0.8838	0.6670	0.7388	0.7941	0.2831	0.2328

0.5297	0.6262	0.2198	0.6071	0.2396	0.3982	0.3169	0.6635	0.8146	0.4478
0.8748	0.7219	0.6640	0.7800	0.5197	0.5510	0.3656	0.6648	0.2843	0.2328
0.0428	0.3026	0.9327	0.8444	0.7428	0.6307	0.3998	0.6735	0.3689	0.2768
0.0579	0.3182	0.2585	0.6326	0.2172	0.3760	0.6667	0.7801	0.8627	0.4604
0.3767	0.5570	0.1152	0.5031	0.2452	0.4043	0.0695	0.5225	0.0322	0.0545
0.0469	0.3055	0.9454	0.8469	0.7032	0.6196	0.0490	0.5116	0.0311	0.0531
0.0125	0.2237	0.6075	0.7706	0.2379	0.3980	0.1534	0.6131	0.0023	0.0102
0.6196	0.6579	0.3575	0.6644	0.9564	0.6771	0.7826	0.8048	0.6930	0.4088
0.0231	0.2518	0.3556	0.6631	0.0006	0.0255	0.2381	0.6397	0.0470	0.0715
0.6230	0.6579	0.4471	0.7043	0.1629	0.3342	0.1950	0.6258	0.4237	0.3029
0.0320	0.2669	0.0400	0.3763	0.0279	0.1678	0.6702	0.7805	0.2465	0.2167
0.7478	0.6849	0.1362	0.5085	0.3750	0.4819	0.1035	0.5714	0.0127	0.0295
0.8989	0.7249	0.4334	0.7007	0.6233	0.5957	0.0395	0.5116	0.1212	0.1344
0.5181	0.6257	0.6630	0.7800	0.6841	0.6155	0.9115	0.8246	0.9337	0.4787
0.3812	0.5570	0.5101	0.7340	0.5481	0.5654	0.1389	0.6069	0.0536	0.0771
0.6690	0.6642	0.2787	0.6478	0.3082	0.4471	0.0462	0.5116	0.0972	0.1150
0.7137	0.6724	0.9106	0.8444	0.2354	0.3976	0.3854	0.6693	0.3191	0.2510
0.0625	0.3199	0.1348	0.5071	0.2112	0.3734	0.1015	0.5714	0.0984	0.1161
0.4805	0.6122	0.6751	0.7856	0.0184	0.1354	0.7703	0.8025	0.1330	0.1449
0.4660	0.6028	0.6367	0.7782	0.2342	0.3967	0.1338	0.6069	0.1567	0.1640
0.8946	0.7230	0.2686	0.6441	0.1111	0.2946	0.2977	0.6604	0.6225	0.3782
0.1715	0.4288	0.9380	0.8447	0.7488	0.6335	0.2683	0.6561	0.8921	0.4665
0.6748	0.6642	0.2763	0.6478	0.6935	0.6181	0.0463	0.5116	0.1908	0.1841
0.1843	0.4361	0.4912	0.7234	0.7909	0.6398	0.0598	0.5136	0.3982	0.2916
0.7328	0.6803	0.6320	0.7782	0.4460	0.5191	0.2280	0.6375	0.1189	0.1337
0.6663	0.6642	0.8062	0.8177	0.6914	0.6181	0.5622	0.7370	0.2732	0.2275
0.1028	0.3668	0.0090	0.2084	0.0014	0.0375	0.2165	0.6280	0.7465	0.4272

0.6447	0.6641	0.1624	0.5502	0.1383	0.3151	0.6654	0.7801	0.5128	0.3375
0.0663	0.3241	0.1625	0.5502	0.0576	0.2296	0.5083	0.7061	0.5326	0.3444
0.1057	0.3668	0.9263	0.8444	0.6982	0.6188	0.6622	0.7801	0.4091	0.2963
0.1498	0.4179	0.1557	0.5448	0.5766	0.5780	0.2541	0.6561	0.0795	0.1006
0.8048	0.7040	0.9878	0.8533	0.7280	0.6254	0.8880	0.8246	0.8660	0.4604
0.4935	0.6198	0.6529	0.7782	0.8227	0.6484	0.6862	0.7844	0.8451	0.4577
0.4193	0.5824	0.5086	0.7340	0.8528	0.6554	0.4818	0.7017	0.9676	0.4880
0.4153	0.5792	0.2498	0.6323	0.9457	0.6745	0.2785	0.6595	0.8768	0.4643
0.5076	0.6224	0.2137	0.6009	0.9335	0.6736	0.2285	0.6375	0.7751	0.4358
0.8799	0.7219	0.9948	0.8533	0.9476	0.6745	0.7007	0.7879	0.8642	0.4604
0.5673	0.6393	0.8332	0.8269	0.6376	0.6008	0.7893	0.8058	0.0569	0.0798
0.3685	0.5570	0.5840	0.7622	0.8418	0.6536	0.9440	0.8288	0.0126	0.0295
0.4656	0.6028	0.8752	0.8353	0.3441	0.4742	0.5554	0.7345	0.2536	0.2188
0.3785	0.5570	0.3788	0.6779	0.0212	0.1450	0.0530	0.5116	0.1080	0.1236
0.9203	0.7281	0.3515	0.6627	0.4147	0.4992	0.4053	0.6753	0.8797	0.4643
0.9867	0.7417	0.0586	0.4396	0.0889	0.2629	0.6183	0.7573	0.1072	0.1233
0.5449	0.6273	0.3473	0.6614	0.6584	0.6121	0.1866	0.6258	0.0000	0.0007
0.0432	0.3026	0.0250	0.2973	0.0006	0.0255	0.2171	0.6280	0.0000	0.0001
0.0646	0.3199	0.0521	0.4026	0.2206	0.3787	0.2161	0.6280	0.6742	0.4030
0.1344	0.4035	0.3669	0.6705	0.6288	0.5970	0.1634	0.6171	0.3370	0.2593
0.6222	0.6579	0.1092	0.4999	0.2411	0.3993	0.6341	0.7663	0.8367	0.4542
0.3402	0.5493	0.7356	0.8037	0.0010	0.0358	0.2206	0.6280	0.1189	0.1337
0.5344	0.6273	0.8421	0.8286	0.0104	0.0958	0.3157	0.6635	0.0130	0.0298
0.6626	0.6642	0.7612	0.8135	0.0011	0.0358	0.1419	0.6069	0.0169	0.0360
0.6398	0.6641	0.7629	0.8135	0.7337	0.6280	0.7957	0.8058	0.0001	0.0013
0.0417	0.3026	0.0070	0.2084	0.0214	0.1450	0.8669	0.8201	0.2729	0.2275
0.6051	0.6577	0.4337	0.7007	0.6921	0.6181	0.0935	0.5648	0.3537	0.2685

0.6511	0.6641	0.7844	0.8177	0.3881	0.4870	0.2974	0.6604	0.2309	0.2103
0.6892	0.6642	0.9302	0.8444	0.3734	0.4819	0.0910	0.5648	0.8298	0.4515
								0.0157	0.0342
0.6367	0.6641	0.6495	0.7782	0.9927	0.6909	0.6354	0.7663	0.0000	0.0000
0.2758	0.5031	0.8918	0.8427	0.6811	0.6153	0.0390	0.5116	0.8148	0.4478
0.9551	0.7367	0.0238	0.2968	0.2006	0.3664	0.4307	0.6821	0.1008	0.1183
0.5986	0.6550	0.6453	0.7782	0.4846	0.5327	0.1384	0.6069	0.4087	0.2963
0.2560	0.4813	0.0223	0.2928	0.0193	0.1407	0.3205	0.6635	0.0043	0.0141
0.0354	0.2879	0.0032	0.1565	0.0004	0.0255	0.0048	0.2636	0.3282	0.2545
0.0254	0.2518	0.0014	0.1535	0.0029	0.0549	0.2887	0.6600	0.2965	0.2403
0.0301	0.2616	0.1240	0.5031	0.1722	0.3493	0.5671	0.7388	0.8462	0.4577
0.6165	0.6579	0.5168	0.7372	0.2992	0.4421	0.5692	0.7388	0.0000	0.0005
0.1943	0.4446	0.1342	0.5071	0.1317	0.3137	0.2807	0.6595	0.2639	0.2219
0.8025	0.7040	0.1277	0.5071	0.3687	0.4813	0.4840	0.7017	0.1971	0.1881
0.1544	0.4185	0.4848	0.7227	0.0859	0.2629	0.6241	0.7619	0.0001	0.0010
0.5472	0.6273	0.5168	0.7372	0.1537	0.3243	0.1480	0.6116	0.0000	0.0000
0.2881	0.5130	0.5256	0.7446	0.0060	0.0737	0.3599	0.6648	0.7170	0.4165
0.0484	0.3055	0.9987	0.8533	0.0005	0.0255	0.9279	0.8246	0.3964	0.2912
0.7622	0.6915	0.9537	0.8469	0.0839	0.2629	0.4316	0.6821	0.0565	0.0795
0.0374	0.2966	0.1185	0.5031	0.0008	0.0324	0.1304	0.6031	0.2328	0.2112
0.9175	0.7281	0.0903	0.4917	0.1393	0.3151	0.0259	0.4387	0.6118	0.3754
0.1609	0.4185	0.3659	0.6705	0.0450	0.2035	0.5915	0.7484	0.1313	0.1437
0.6644	0.6642	0.0386	0.3763	0.3582	0.4796	0.0768	0.5375	0.0186	0.0383
0.8127	0.7060	0.0367	0.3731	0.2537	0.4095	0.3011	0.6607	0.8664	0.4604
0.8703	0.7219	0.2008	0.5977	0.2018	0.3675	0.1105	0.5853	0.0819	0.1026
0.7090	0.6724	0.4570	0.7101	0.9539	0.6762	0.1253	0.5944	0.7809	0.4374
0.8461	0.7175	0.3245	0.6550	0.2867	0.4338	0.7381	0.7941	0.0185	0.0382

0.8938	0.7230	0.2227	0.6085	0.4134	0.4992	0.0514	0.5116	0.0444	0.0688
0.9344	0.7310	0.9385	0.8447	0.9328	0.6736	0.8313	0.8170	0.2487	0.2179
0.2805	0.5062	0.4362	0.7007	0.3411	0.4742	0.2525	0.6561	0.4903	0.3298
0.5227	0.6260	0.8583	0.8316	0.3907	0.4880	0.3643	0.6648	0.0026	0.0110
0.0894	0.3523	0.4332	0.7007	0.9318	0.6736	0.3196	0.6635	0.0001	0.0014
0.1069	0.3668	0.4105	0.6997	0.5594	0.5709	0.8584	0.8197	0.0001	0.0010
0.6262	0.6579	0.6919	0.7890	0.8621	0.6588	0.3710	0.6648	0.6358	0.3851
0.0649	0.3199	0.7154	0.8004	0.2936	0.4391	0.0726	0.5234	0.3698	0.2770
0.6175	0.6579	0.7685	0.8147	0.2151	0.3760	0.7271	0.7936	0.4897	0.3298
0.1536	0.4185	0.7529	0.8130	0.3076	0.4471	0.7388	0.7941	0.7036	0.4130
0.9592	0.7367	0.5886	0.7627	0.5481	0.5654	0.6851	0.7844	0.0256	0.0473
0.0573	0.3182	0.2136	0.6009	0.6701	0.6152	0.8802	0.8246	0.6834	0.4053
0.1469	0.4179	0.9480	0.8469	0.9301	0.6736	0.4605	0.6929	0.4285	0.3054
0.8437	0.7175	0.7528	0.8130	0.0378	0.1918	0.7312	0.7936	0.8513	0.4594
0.3592	0.5547	0.7628	0.8135	0.1378	0.3151	0.6077	0.7535	0.1808	0.1800
0.0447	0.3046	0.0132	0.2491	0.0513	0.2160	0.4190	0.6821	0.0021	0.0096
								0.0146	0.0325
0.7766	0.6952	0.6486	0.7782	0.7545	0.6335	0.7016	0.7879	0.2398	0.2129
0.1345	0.4035	0.2320	0.6142	0.4729	0.5264	0.2821	0.6595	0.0033	0.0127
0.1001	0.3640	0.4890	0.7234	0.4719	0.5264	0.9819	0.8347	0.0021	0.0096
0.3016	0.5249	0.6332	0.7782	0.0238	0.1525	0.4428	0.6869	0.1946	0.1869
0.0484	0.3055	0.6579	0.7800	0.1122	0.2946	0.1938	0.6258	0.4796	0.3275
0.6836	0.6642	0.1604	0.5502	0.6195	0.5944	0.0527	0.5116	0.1063	0.1233
0.6221	0.6579	0.1503	0.5306	0.9282	0.6736	0.5331	0.7215	0.0053	0.0162
0.7261	0.6785	0.3466	0.6614	0.3466	0.4742	0.9673	0.8347	0.7457	0.4272
0.9633	0.7367	0.6411	0.7782	0.5264	0.5525	0.9162	0.8246	0.2866	0.2335
0.8062	0.7040	0.7894	0.8177	0.1401	0.3151	0.3486	0.6648	0.3163	0.2497

0.2803	0.5062	0.3323	0.6550	0.0648	0.2361	0.1121	0.5856	0.5061	0.3370
0.1787	0.4322	0.0856	0.4917	0.0877	0.2629	0.0025	0.2605	0.0000	0.0000
0.6499	0.6641	0.7623	0.8135	0.6955	0.6188	0.2909	0.6600	0.0008	0.0053
0.4986	0.6198	0.5464	0.7501	0.4609	0.5240	0.2168	0.6280	0.0672	0.0887
0.1003	0.3640	0.4362	0.7007	0.9428	0.6736	0.2673	0.6561	0.1892	0.1833
0.3211	0.5392	0.3841	0.6811	0.8843	0.6670	0.0945	0.5648	0.0992	0.1167
0.0588	0.3182	0.4199	0.7007	0.1157	0.2984	0.0804	0.5451	0.1871	0.1828
0.1867	0.4375	0.8704	0.8353	0.5127	0.5492	0.8339	0.8170	0.0230	0.0442
0.6447	0.6641	0.3117	0.6550	0.1233	0.3078	0.1944	0.6258	0.9544	0.4841
0.1215	0.3802	0.7298	0.8004	0.7775	0.6352	0.3967	0.6735	0.1256	0.1382
0.1903	0.4413	0.3332	0.6550	0.3585	0.4796	0.7956	0.8058	0.0001	0.0013
0.4403	0.5967	0.4860	0.7227	0.0397	0.1921	0.6636	0.7801	0.7990	0.4432
0.2244	0.4709	0.7713	0.8147	0.7767	0.6352	0.7647	0.8016	0.0379	0.0612
0.7629	0.6915	0.1987	0.5977	0.4159	0.4992	0.6008	0.7506	0.0177	0.0375
0.8752	0.7219	0.9319	0.8444	0.0367	0.1918	0.1875	0.6258	0.0523	0.0761
0.3089	0.5330	0.6206	0.7782	0.0138	0.1128	0.7611	0.8010	0.2373	0.2123
0.2381	0.4709	0.1060	0.4999	0.0003	0.0255	0.0011	0.2465	0.0252	0.0468
0.7127	0.6724	0.8937	0.8427	0.4094	0.4992	0.3859	0.6693	0.3107	0.2465
0.4877	0.6173	0.1021	0.4999	0.5108	0.5480	0.0441	0.5116	0.9307	0.4787
0.1144	0.3701	0.0789	0.4804	0.7394	0.6304	0.2306	0.6375	0.3101	0.2465
0.0317	0.2669	0.2251	0.6090	0.6486	0.6073	0.3152	0.6635	0.0043	0.0142
0.9039	0.7281	0.8251	0.8229	0.0762	0.2530	0.9404	0.8276	0.4849	0.3292
0.2041	0.4576	0.9503	0.8469	0.5042	0.5447	0.0229	0.4066	0.0541	0.0771
0.0928	0.3558	0.6915	0.7890	0.0600	0.2308	0.0790	0.5427	0.2344	0.2112
								0.0197	0.0397
								0.0440	0.0683
								0.0183	0.0381

0.6865	0.6642	0.5454	0.7501	0.5539	0.5673	0.1216	0.5944	0.0767	0.0976
0.2453	0.4740	0.9173	0.8444	0.4616	0.5240	0.0087	0.3368	0.1833	0.1807
0.4252	0.5863	0.1328	0.5071	0.7754	0.6352	0.0637	0.5225	0.2508	0.2180
0.9478	0.7353	0.3990	0.6946	0.5315	0.5551	0.8971	0.8246	0.9469	0.4817
0.2114	0.4679	0.0121	0.2468	0.5691	0.5733	0.0901	0.5648	0.5309	0.3439
0.3416	0.5504	0.0360	0.3731	0.1884	0.3581	0.0541	0.5116	0.5095	0.3375
0.5218	0.6260	0.4627	0.7101	0.4680	0.5264	0.2617	0.6561	0.0000	0.0006
0.7813	0.6954	0.4054	0.6950	0.9688	0.6820	0.6669	0.7801	0.9761	0.4907
0.7731	0.6952	0.6269	0.7782	0.4553	0.5225	0.7578	0.8010	0.9949	0.4951
0.0389	0.2985	0.1119	0.5031	0.5287	0.5530	0.1591	0.6131	0.2111	0.1962
0.5420	0.6273	0.1026	0.4999	0.0258	0.1623	0.1029	0.5714	0.7437	0.4272
0.0058	0.2237	0.2744	0.6478	0.0025	0.0531	0.4528	0.6869	0.0005	0.0036
0.8580	0.7196	0.8325	0.8269	0.8035	0.6446	0.3755	0.6648	0.7552	0.4315
0.0865	0.3518	0.0172	0.2839	0.0039	0.0591	0.0701	0.5225	0.9354	0.4787
0.5196	0.6257	0.4364	0.7007	0.8433	0.6536	0.9856	0.8349	0.0278	0.0500
0.1358	0.4035	0.2947	0.6533	0.7170	0.6238	0.8531	0.8177	0.4508	0.3188
0.5987	0.6550	0.6553	0.7782	0.4796	0.5291	0.8337	0.8170	0.0489	0.0740
0.1559	0.4185	0.7865	0.8177	0.6317	0.5988	0.1935	0.6258	0.8293	0.4515
0.9940	0.7431	0.6530	0.7782	0.3780	0.4819	0.9796	0.8347	0.0209	0.0418
0.6511	0.6641	0.4614	0.7101	0.4768	0.5269	0.2967	0.6604	0.0012	0.0063
0.3533	0.5537	0.4349	0.7007	0.1875	0.3581	0.7731	0.8037	0.0243	0.0458
0.4782	0.6122	0.6046	0.7706	0.9590	0.6782	0.1657	0.6172	0.1471	0.1559
0.1369	0.4035	0.9290	0.8444	0.4846	0.5327	0.9709	0.8347	0.1813	0.1800
0.0774	0.3417	0.4293	0.7007	0.5024	0.5447	0.5336	0.7215	0.0535	0.0771
0.2487	0.4741	0.4054	0.6950	0.5743	0.5767	0.2087	0.6280	0.0028	0.0114
0.1691	0.4260	0.5059	0.7338	0.9941	0.6909	0.7473	0.7941	0.0101	0.0254
0.9726	0.7393	0.7706	0.8147	0.6629	0.6129	0.3549	0.6648	0.0054	0.0162

0.6151	0.6579	0.1093	0.4999	0.4537	0.5216	0.6644	0.7801	0.0226	0.0438
0.3142	0.5343	0.6242	0.7782	0.5953	0.5837	0.3973	0.6735	0.0181	0.0381
0.2909	0.5154	0.8105	0.8177	0.6721	0.6152	0.4507	0.6869	0.0763	0.0976
0.1794	0.4325	0.6809	0.7857	0.5906	0.5837	0.9310	0.8246	0.1818	0.1800
0.3587	0.5547	0.0678	0.4509	0.1102	0.2946	0.5034	0.7056	0.2373	0.2123
0.0775	0.3417	0.4383	0.7007	0.7914	0.6398	0.2479	0.6526	0.6018	0.3704
0.6714	0.6642	0.4303	0.7007	0.2382	0.3980	0.5952	0.7506	0.0623	0.0847
0.0942	0.3584	0.7282	0.8004	0.6754	0.6152	0.4215	0.6821	0.2793	0.2317
0.7762	0.6952	0.6803	0.7857	0.7101	0.6211	0.6828	0.7844	0.0031	0.0124
0.0458	0.3055	0.5233	0.7446	0.2962	0.4402	0.6811	0.7844	0.1635	0.1680
0.5288	0.6262	0.2103	0.5977	0.0455	0.2035	0.2637	0.6561	0.7691	0.4346
0.3967	0.5681	0.6525	0.7782	0.1254	0.3083	0.2029	0.6258	0.2641	0.2219
0.8556	0.7193	0.8904	0.8427	0.9398	0.6736	0.2527	0.6561	0.0159	0.0344
0.4827	0.6133	0.7382	0.8038	0.2484	0.4053	0.8020	0.8058	0.0000	0.0007
0.9347	0.7310	0.9698	0.8492	0.8560	0.6565	0.2571	0.6561	0.3162	0.2497
0.3008	0.5249	0.3672	0.6705	0.1966	0.3624	0.3597	0.6648	0.4121	0.2975
0.4487	0.5997	0.2199	0.6071	0.1385	0.3151	0.4418	0.6869	0.8607	0.4604
0.1590	0.4185	0.0768	0.4788	0.1859	0.3581	0.0992	0.5714	0.4639	0.3236
0.2186	0.4709	0.9641	0.8486	0.6187	0.5944	0.2908	0.6600	0.0006	0.0040
0.7678	0.6924	0.6739	0.7856	0.7346	0.6280	0.5300	0.7209	0.3011	0.2411
0.9446	0.7353	0.7968	0.8177	0.7889	0.6398	0.9538	0.8308	0.1726	0.1728
0.7571	0.6906	0.4025	0.6946	0.4897	0.5355	0.4835	0.7017	0.3370	0.2593
0.2382	0.4709	0.0082	0.2084	0.4092	0.4992	0.7837	0.8048	0.2532	0.2188
0.4017	0.5708	0.3112	0.6550	0.0500	0.2160	0.2796	0.6595	0.0010	0.0057
0.0868	0.3518	0.0058	0.2084	0.4727	0.5264	0.5611	0.7370	0.0629	0.0847
0.1448	0.4142	0.1303	0.5071	0.0579	0.2296	0.0030	0.2605	0.0522	0.0761
0.1882	0.4380	0.1834	0.5810	0.0811	0.2607	0.4714	0.7014	0.0088	0.0226

0.1759	0.4322	0.4109	0.6997	0.3247	0.4614	0.3443	0.6648	0.4231	0.3029
0.3121	0.5330	0.5424	0.7501	0.1095	0.2946	0.3508	0.6648	0.5160	0.3386
0.3236	0.5407	0.9574	0.8469	0.3464	0.4742	0.3453	0.6648	0.4901	0.3298
0.8849	0.7219	0.1351	0.5071	0.8919	0.6685	0.2733	0.6595	0.1146	0.1298
0.6540	0.6642	0.7791	0.8174	0.5079	0.5459	0.8973	0.8246	0.4173	0.2998
0.2973	0.5226	0.1813	0.5796	0.0031	0.0549	0.5673	0.7388	0.2034	0.1914
0.0857	0.3518	0.0169	0.2839	0.0022	0.0498	0.3129	0.6635	0.3750	0.2800
0.6655	0.6642	0.2065	0.5977	0.7776	0.6352	0.4006	0.6735	0.1832	0.1807
0.1830	0.4361	0.8436	0.8286	0.8463	0.6538	0.3499	0.6648	0.4866	0.3293
0.5399	0.6273	0.1144	0.5031	0.4355	0.5107	0.4750	0.7017	0.3707	0.2772
0.3311	0.5439	0.7216	0.8004	0.8535	0.6554	0.3036	0.6607	0.4741	0.3261
0.3795	0.5570	0.8713	0.8353	0.7284	0.6254	0.8397	0.8170	0.9347	0.4787
0.9821	0.7411	0.5350	0.7501	0.2559	0.4101	0.8182	0.8124	0.8952	0.4668
0.2600	0.4862	0.7370	0.8037	0.3799	0.4819	0.3383	0.6648	0.3204	0.2512
0.3923	0.5655	0.7296	0.8004	0.8960	0.6700	0.9087	0.8246	0.8279	0.4515
0.6290	0.6592	0.2412	0.6241	0.8871	0.6670	0.0336	0.4937	0.3002	0.2411
0.6495	0.6641	0.3661	0.6705	0.7803	0.6366	0.0093	0.3368	0.5969	0.3679
0.6968	0.6662	0.5474	0.7501	0.0303	0.1756	0.3932	0.6735	0.1874	0.1828
0.7622	0.6915	0.4957	0.7261	0.8765	0.6657	0.6174	0.7573	0.0022	0.0099
0.9814	0.7411	0.9120	0.8444	0.9068	0.6736	0.2598	0.6561	0.0678	0.0891
0.1014	0.3659	0.0110	0.2328	0.1574	0.3277	0.1698	0.6229	0.6689	0.4004
0.9199	0.7281	0.6792	0.7857	0.0872	0.2629	0.0432	0.5116	0.0598	0.0827
0.3127	0.5330	0.5849	0.7622	0.8841	0.6670	0.1398	0.6069	0.5024	0.3355
0.9246	0.7286	0.7576	0.8135	0.3652	0.4812	0.6043	0.7510	0.0625	0.0847
0.2240	0.4709	0.0518	0.4026	0.4265	0.5082	0.0880	0.5648	0.0040	0.0141
0.4047	0.5715	0.7588	0.8135	0.8462	0.6538	0.6389	0.7665	0.0073	0.0194
0.6175	0.6579	0.1341	0.5071	0.0962	0.2751	0.2675	0.6561	0.7765	0.4360

0.8858	0.7219	0.9270	0.8444	0.0424	0.1982	0.7640	0.8016	0.0194	0.0395
0.0369	0.2961	0.0102	0.2244	0.0029	0.0549	0.9246	0.8246	0.1208	0.1344
0.9936	0.7431	0.4048	0.6950	0.5631	0.5718	0.1261	0.5944	0.3286	0.2545
0.9143	0.7281	0.7234	0.8004	0.0782	0.2550	0.0466	0.5116	0.0108	0.0264
0.4205	0.5828	0.0500	0.4026	0.1892	0.3581	0.3446	0.6648	0.4740	0.3261
0.7637	0.6915	0.8101	0.8177	0.0070	0.0766	0.0362	0.5116	0.0000	0.0007
0.3545	0.5538	0.2030	0.5977	0.3461	0.4742	0.4647	0.6953	0.8054	0.4446
0.3901	0.5655	0.7107	0.8004	0.7055	0.6200	0.1429	0.6069	0.0000	0.0006
0.4431	0.5982	0.3110	0.6550	0.0138	0.1128	0.9108	0.8246	0.0042	0.0141
0.1612	0.4185	0.0025	0.1565	0.6035	0.5870	0.5029	0.7056	0.0000	0.0006
0.5306	0.6262	0.9268	0.8444	0.7601	0.6341	0.3321	0.6648	0.0000	0.0000
0.3707	0.5570	0.6377	0.7782	0.8322	0.6518	0.6652	0.7801	0.1907	0.1841
0.2698	0.4963	0.4384	0.7007	0.1817	0.3581	0.5703	0.7388	0.1239	0.1366
0.8111	0.7058	0.6896	0.7890	0.2085	0.3713	0.6018	0.7506	0.0844	0.1041
0.7345	0.6810	0.8936	0.8427	0.9106	0.6736	0.9715	0.8347	0.0001	0.0010
0.5851	0.6479	0.2170	0.6056	0.6774	0.6152	0.2006	0.6258	0.1624	0.1673
0.3127	0.5330	0.0065	0.2084	0.1246	0.3083	0.4330	0.6821	0.1204	0.1344
0.6893	0.6642	0.2011	0.5977	0.5828	0.5786	0.7780	0.8048	0.8459	0.4577
0.3742	0.5570	0.2126	0.6009	0.1084	0.2946	0.7754	0.8048	0.5304	0.3439
0.5493	0.6273	0.5796	0.7622	0.4153	0.4992	0.9203	0.8246	0.2185	0.2015
0.5048	0.6218	0.8093	0.8177	0.6146	0.5925	0.2672	0.6561	0.0026	0.0111
0.6435	0.6641	0.6457	0.7782	0.8343	0.6518	0.8699	0.8201	0.0660	0.0879
0.5307	0.6262	0.9593	0.8476	0.0292	0.1728	0.9564	0.8312	0.0122	0.0291
0.7738	0.6952	0.5406	0.7501	0.4276	0.5084	0.6143	0.7548	0.7209	0.4176
0.5656	0.6393	0.7164	0.8004	0.7760	0.6352	0.6502	0.7764	0.6282	0.3810
0.0400	0.3026	0.4015	0.6946	0.8528	0.6554	0.8665	0.8201	0.0266	0.0489
0.1823	0.4361	0.3523	0.6627	0.0406	0.1928	0.3646	0.6648	0.3466	0.2653

0.1768	0.4322	0.0430	0.3767	0.0303	0.1756	0.0989	0.5714	0.0156	0.0342
0.7118	0.6724	0.1019	0.4999	0.0589	0.2308	0.3854	0.6693	0.2832	0.2328
0.4441	0.5983	0.8549	0.8302	0.2544	0.4095	0.2202	0.6280	0.9451	0.4815
0.7033	0.6696	0.2289	0.6110	0.3186	0.4548	0.7607	0.8010	0.0015	0.0076
0.4342	0.5933	0.1789	0.5787	0.5941	0.5837	0.9564	0.8312	0.8018	0.4441
0.9496	0.7359	0.1771	0.5752	0.4330	0.5107	0.3446	0.6648	0.2388	0.2129
0.8517	0.7193	0.2553	0.6326	0.3884	0.4870	0.2100	0.6280	0.7467	0.4272
0.6875	0.6642	0.6901	0.7890	0.6868	0.6165	0.4798	0.7017	0.0000	0.0000
0.0115	0.2237	0.5698	0.7622	0.9088	0.6736	0.2371	0.6397	0.8939	0.4668
0.5430	0.6273	0.5408	0.7501	0.2663	0.4184	0.4517	0.6869	0.0000	0.0000
						0.3559	0.6648	0.0128	0.0295
								0.0387	0.0615
								0.0272	0.0494
0.7611	0.6915	0.1957	0.5977	0.0046	0.0647	0.3200	0.6635	0.1213	0.1344
0.3756	0.5570	0.3372	0.6550	0.4466	0.5191	0.6468	0.7736	0.0450	0.0692
0.3053	0.5297	0.8917	0.8427	0.5438	0.5632	0.2298	0.6375	0.0001	0.0013
0.6021	0.6554	0.1154	0.5031	0.0207	0.1450	0.7977	0.8058	0.5188	0.3390
0.4067	0.5723	0.9151	0.8444	0.3272	0.4638	0.5910	0.7484	0.0603	0.0831
0.4465	0.5992	0.7095	0.8004	0.0889	0.2629	0.4320	0.6821	0.5957	0.3679
0.0074	0.2237	0.7607	0.8135	0.2260	0.3869	0.8516	0.8177	0.1440	0.1532
0.3709	0.5570	0.2880	0.6500	0.0127	0.1101	0.4975	0.7056	0.8825	0.4647
0.0215	0.2497	0.0474	0.3955	0.4756	0.5265	0.0667	0.5225	0.0051	0.0160
0.3009	0.5249	0.8474	0.8286	0.6431	0.6046	0.1577	0.6131	0.0014	0.0072
0.0274	0.2533	0.0092	0.2084	0.0014	0.0375	0.5555	0.7345	0.2638	0.2219
0.0698	0.3270	0.2285	0.6110	0.5823	0.5786	0.8448	0.8170	0.0006	0.0046
0.0858	0.3518	0.4636	0.7101	0.4312	0.5107	0.3296	0.6648	0.0002	0.0021
0.1348	0.4035	0.8472	0.8286	0.2726	0.4242	0.1932	0.6258	0.1695	0.1716

0.2647	0.4921	0.1630	0.5502	0.5683	0.5733	0.4972	0.7056	0.9626	0.4866
0.0141	0.2237	0.0547	0.4144	0.6226	0.5957	0.5465	0.7328	0.5702	0.3592
0.3068	0.5309	0.1183	0.5031	0.8875	0.6670	0.9642	0.8347	0.7774	0.4360
0.1599	0.4185	0.4890	0.7234	0.0041	0.0591	0.2381	0.6397	0.3426	0.2632
0.0026	0.1976	0.2368	0.6235	0.1124	0.2946	0.7933	0.8058	0.0579	0.0808
0.9952	0.7431	0.5368	0.7501	0.3501	0.4770	0.8218	0.8133	0.0376	0.0612
0.4802	0.6122	0.0173	0.2839	0.0367	0.1918	0.7052	0.7879	0.9163	0.4742
0.0611	0.3199	0.8043	0.8177	0.8149	0.6465	0.9097	0.8246	0.8808	0.4643
0.0578	0.3182	0.9974	0.8533	0.3704	0.4815	0.5291	0.7209	0.0059	0.0171
0.1785	0.4322	0.8615	0.8326	0.2057	0.3713	0.3634	0.6648	0.0145	0.0324
0.0917	0.3547	0.0313	0.3457	0.0009	0.0358	0.1296	0.6029	0.9443	0.4815
0.0087	0.2237	0.8676	0.8353	0.2664	0.4184	0.8918	0.8246	0.0298	0.0518
0.3536	0.5537	0.8844	0.8410	0.8014	0.6445	0.3383	0.6648	0.2316	0.2105
0.2436	0.4738	0.5501	0.7501	0.5217	0.5517	0.0218	0.3996	0.4601	0.3224
0.4883	0.6173	0.0191	0.2914	0.9167	0.6736	0.0856	0.5648	0.5625	0.3572
0.0774	0.3417	0.1267	0.5071	0.9085	0.6736	0.0013	0.2465	0.2976	0.2403
0.9093	0.7281	0.2585	0.6326	0.1963	0.3624	0.0070	0.3316	0.2536	0.2188
0.1080	0.3668	0.0046	0.1882	0.5174	0.5510	0.0167	0.3996	0.3069	0.2448
0.4328	0.5925	0.4360	0.7007	0.3649	0.4812	0.0326	0.4878	0.9280	0.4787
0.1649	0.4260	0.5629	0.7608	0.0023	0.0498	0.1649	0.6172	0.4726	0.3261
0.2187	0.4709	0.3222	0.6550	0.0825	0.2629	0.0761	0.5375	0.4783	0.3275
0.9711	0.7390	0.8396	0.8280	0.8438	0.6536	0.2732	0.6595	0.9086	0.4719
0.1483	0.4179	0.6225	0.7782	0.6701	0.6152	0.9130	0.8246	0.0008	0.0051
0.7861	0.6966	0.7922	0.8177	0.9270	0.6736	0.3263	0.6640	0.6853	0.4056
0.0625	0.3199	0.4333	0.7007	0.9099	0.6736	0.8334	0.8170	0.4110	0.2971
0.7299	0.6795	0.3212	0.6550	0.6614	0.6129	0.0312	0.4825	0.0616	0.0843
0.5257	0.6262	0.0641	0.4455	0.1376	0.3151	0.4622	0.6929	0.2418	0.2136

0.8389	0.7175	0.5259	0.7446	0.4029	0.4960	0.7244	0.7918	0.6146	0.3757
0.2306	0.4709	0.1067	0.4999	0.1299	0.3130	0.4247	0.6821	0.5265	0.3436
0.4616	0.6004	0.0609	0.4455	0.1356	0.3151	0.7692	0.8025	0.0146	0.0325
0.6096	0.6579	0.0496	0.4026	0.0877	0.2629	0.0807	0.5451	0.0373	0.0612
0.6870	0.6642	0.4395	0.7007	0.4186	0.5015	0.2835	0.6595	0.8784	0.4643
0.0218	0.2497	0.4413	0.7020	0.7415	0.6307	0.3999	0.6735	0.0019	0.0090
0.0595	0.3182	0.6889	0.7890	0.1066	0.2930	0.1989	0.6258	0.0281	0.0502
0.4122	0.5760	0.7055	0.8004	0.4144	0.4992	0.6697	0.7805	0.7713	0.4347
0.4768	0.6122	0.7700	0.8147	0.8438	0.6536	0.5972	0.7506	0.4451	0.3153
0.2164	0.4709	0.2963	0.6533	0.6023	0.5870	0.5178	0.7106	0.9900	0.4951
0.2326	0.4709	0.0192	0.2914	0.0881	0.2629	0.1409	0.6069	0.0066	0.0181
0.8947	0.7230	0.0514	0.4026	0.7041	0.6196	0.4247	0.6821	0.0099	0.0250
0.1940	0.4446	0.6767	0.7856	0.8428	0.6536	0.6869	0.7844	0.1617	0.1670
0.1364	0.4035	0.2166	0.6056	0.6339	0.5991	0.9990	0.8423	0.5680	0.3584
0.2289	0.4709	0.3033	0.6550	0.4713	0.5264	0.2572	0.6561	0.4808	0.3278
0.8836	0.7219	0.6166	0.7764	0.9601	0.6782	0.0654	0.5225	0.2592	0.2198
0.6910	0.6644	0.0061	0.2084	0.0760	0.2530	0.0917	0.5648	0.0000	0.0004
0.3256	0.5421	0.3075	0.6550	0.1309	0.3131	0.1928	0.6258	0.0871	0.1049
0.0199	0.2497	0.0374	0.3757	0.3568	0.4796	0.2188	0.6280	0.5810	0.3621
0.2843	0.5094	0.8454	0.8286	0.0703	0.2448	0.7390	0.7941	0.0049	0.0156
0.1560	0.4185	0.2634	0.6395	0.0048	0.0656	0.3016	0.6607	0.9127	0.4729
0.2890	0.5133	0.3436	0.6614	0.0063	0.0739	0.2032	0.6258	0.5643	0.3575
0.6506	0.6641	0.5699	0.7622	0.5041	0.5447	0.7455	0.7941	0.1475	0.1559
0.5141	0.6257	0.1235	0.5031	0.1745	0.3524	0.3732	0.6648	0.0000	0.0002
0.7975	0.7024	0.4312	0.7007	0.1205	0.3046	0.3554	0.6648	0.4734	0.3261
0.6853	0.6642	0.1970	0.5977	0.6981	0.6188	0.8933	0.8246	0.0071	0.0193
0.0435	0.3026	0.0235	0.2968	0.0310	0.1784	0.4478	0.6869	0.5581	0.3561

0.8886	0.7227	0.3687	0.6705	0.2821	0.4322	0.2003	0.6258	0.2561	0.2192
0.3388	0.5484	0.9235	0.8444	0.8152	0.6465	0.4406	0.6869	0.0000	0.0002
0.6689	0.6642	0.1252	0.5043	0.8114	0.6465	0.4846	0.7017	0.0156	0.0342
0.0119	0.2237	0.4648	0.7101	0.9407	0.6736	0.6267	0.7630	0.6188	0.3773
0.0752	0.3417	0.0009	0.1535	0.2086	0.3713	0.2367	0.6397	0.2847	0.2328
0.0791	0.3430	0.1490	0.5300	0.2290	0.3899	0.3955	0.6735	0.5874	0.3645
0.0257	0.2518	0.6090	0.7706	0.4529	0.5216	0.9075	0.8246	0.0449	0.0692
0.9525	0.7367	0.5251	0.7446	0.9917	0.6909	0.3695	0.6648	0.1582	0.1645
0.5749	0.6410	0.5890	0.7627	0.9957	0.6909	0.5090	0.7061	0.3763	0.2801
0.8435	0.7175	0.2821	0.6490	0.7898	0.6398	0.9374	0.8269	0.0832	0.1036
0.7643	0.6915	0.6077	0.7706	0.7933	0.6402	0.0703	0.5225	0.0839	0.1038
0.2696	0.4963	0.0682	0.4509	0.0600	0.2308	0.4939	0.7056	0.1433	0.1528
0.9785	0.7411	0.9025	0.8444	0.5490	0.5654	0.6628	0.7801	0.8852	0.4655
0.4515	0.5999	0.0056	0.2084	0.1345	0.3151	0.0234	0.4066	0.5077	0.3370
0.8860	0.7219	0.7681	0.8147	0.8674	0.6620	0.2170	0.6280	0.0109	0.0264
0.0078	0.2237	0.0176	0.2839	0.0613	0.2329	0.3649	0.6648	0.3637	0.2742
0.1588	0.4185	0.9494	0.8469	0.4153	0.4992	0.6843	0.7844	0.0820	0.1026
0.0582	0.3182	0.0859	0.4917	0.1889	0.3581	0.4787	0.7017	0.4928	0.3306
0.2395	0.4709	0.4022	0.6946	0.5798	0.5786	0.3759	0.6648	0.0406	0.0639
0.5230	0.6260	0.5474	0.7501	0.5729	0.5762	0.8685	0.8201	0.0549	0.0774
0.0884	0.3523	0.1953	0.5977	0.1419	0.3151	0.8032	0.8058	0.3642	0.2742
0.1689	0.4260	0.6316	0.7782	0.8192	0.6467	0.7472	0.7941	0.0756	0.0969
0.9140	0.7281	0.5529	0.7526	0.7726	0.6352	0.7030	0.7879	0.5631	0.3572
0.1512	0.4183	0.2065	0.5977	0.2660	0.4184	0.4025	0.6735	0.1387	0.1497
0.4371	0.5949	0.3307	0.6550	0.7685	0.6352	0.9176	0.8246	0.2438	0.2148
0.9647	0.7367	0.1754	0.5741	0.6335	0.5991	0.4987	0.7056	0.0683	0.0891
0.6165	0.6579	0.8895	0.8427	0.1891	0.3581	0.8101	0.8090	0.0000	0.0002

0.0998	0.3640	0.0173	0.2839	0.4325	0.5107	0.2922	0.6600	0.1349	0.1463
0.0265	0.2518	0.3690	0.6705	0.4663	0.5264	0.7828	0.8048	0.2852	0.2328
0.2540	0.4788	0.4332	0.7007	0.9395	0.6736	0.4784	0.7017	0.0283	0.0503
0.0423	0.3026	0.1382	0.5119	0.3583	0.4796	0.8707	0.8201	0.3301	0.2552
0.4580	0.6004	0.1336	0.5071	0.0896	0.2629	0.4325	0.6821	0.9404	0.4807
0.8313	0.7149	0.7570	0.8135	0.8704	0.6634	0.3774	0.6649	0.4174	0.2998
0.6203	0.6579	0.1525	0.5361	0.3409	0.4742	0.3043	0.6607	0.0024	0.0104
0.0547	0.3182	0.2552	0.6326	0.6813	0.6153	0.6559	0.7795	0.0500	0.0747
0.4512	0.5999	0.5456	0.7501	0.1459	0.3167	0.7068	0.7879	0.5381	0.3462
0.1957	0.4463	0.9479	0.8469	0.4590	0.5239	0.0148	0.3753	0.3066	0.2448
0.3711	0.5570	0.1613	0.5502	0.3596	0.4796	0.1624	0.6166	0.1684	0.1712
0.3971	0.5681	0.3605	0.6684	0.1960	0.3624	0.0385	0.5116	0.2167	0.2002
0.0250	0.2518	0.0032	0.1565	0.0060	0.0737	0.4607	0.6929	0.0540	0.0771
0.5028	0.6204	0.9756	0.8504	0.4107	0.4992	0.3225	0.6635	0.2629	0.2219
0.4010	0.5708	0.4713	0.7161	0.9484	0.6745	0.9145	0.8246	0.0018	0.0089
0.0960	0.3622	0.3346	0.6550	0.1443	0.3151	0.2556	0.6561	0.0484	0.0735
0.6128	0.6579	0.3366	0.6550	0.2382	0.3980	0.5024	0.7056	0.0009	0.0056
0.1573	0.4185	0.3110	0.6550	0.0836	0.2629	0.1212	0.5944	0.1141	0.1296
0.0134	0.2237	0.1243	0.5031	0.0323	0.1796	0.1066	0.5768	0.5440	0.3490
0.0412	0.3026	0.1314	0.5071	0.0689	0.2439	0.7428	0.7941	0.0293	0.0513
0.2349	0.4709	0.0906	0.4917	0.0262	0.1623	0.0468	0.5116	0.4392	0.3116
0.0599	0.3182	0.8916	0.8427	0.6607	0.6129	0.7241	0.7918	0.2721	0.2274
0.0379	0.2966	0.8347	0.8269	0.1272	0.3101	0.1359	0.6069	0.2569	0.2193
0.9413	0.7345	0.3324	0.6550	0.3012	0.4441	0.1947	0.6258	0.2498	0.2179
0.0576	0.3182	0.8605	0.8326	0.5606	0.5711	0.5030	0.7056	0.0234	0.0444
0.1172	0.3748	0.4852	0.7227	0.7731	0.6352	0.1556	0.6131	0.0297	0.0518
0.2823	0.5081	0.0866	0.4917	0.0040	0.0591	0.0055	0.2791	0.0057	0.0168

0.3929	0.5655	0.4119	0.6999	0.7768	0.6352	0.6021	0.7506	0.0007	0.0046
0.5407	0.6273	0.1153	0.5031	0.1809	0.3581	0.8526	0.8177	0.0001	0.0013
0.7682	0.6924	0.3510	0.6627	0.0091	0.0921	0.0297	0.4724	0.0002	0.0021
0.3973	0.5681	0.5089	0.7340	0.2051	0.3713	0.3076	0.6635	0.2066	0.1931
0.3376	0.5484	0.2807	0.6478	0.3673	0.4812	0.0504	0.5116	0.4632	0.3236
0.8773	0.7219	0.9819	0.8530	0.6246	0.5957	0.1235	0.5944	0.2340	0.2112
0.4256	0.5863	0.9961	0.8533	0.4696	0.5264	0.8669	0.8201	0.8274	0.4515
0.2484	0.4741	0.9137	0.8444	0.2745	0.4248	0.3698	0.6648	0.2032	0.1914
0.0018	0.1952	0.0276	0.3156	0.2172	0.3760	0.0005	0.2465	0.0014	0.0072
0.3381	0.5484	0.9637	0.8486	0.2116	0.3734	0.1621	0.6166	0.0057	0.0168
0.6942	0.6653	0.6635	0.7800	0.4860	0.5333	0.0581	0.5136	0.5709	0.3592
0.0176	0.2407	0.5715	0.7622	0.4266	0.5082	0.9099	0.8246	0.0104	0.0258
0.5174	0.6257	0.2882	0.6500	0.2797	0.4296	0.6638	0.7801	0.6796	0.4040
0.9682	0.7383	0.2047	0.5977	0.4753	0.5265	0.4243	0.6821	0.2138	0.1983
0.2630	0.4903	0.3368	0.6550	0.2477	0.4052	0.4018	0.6735	0.1353	0.1464
0.6774	0.6642	0.6659	0.7800	0.7418	0.6307	0.6119	0.7543	0.0042	0.0141
0.6007	0.6551	0.0414	0.3763	0.7252	0.6254	0.3863	0.6693	0.0001	0.0010
0.2445	0.4740	0.9052	0.8444	0.2956	0.4402	0.1916	0.6258	0.2649	0.2222
0.9529	0.7367	0.3120	0.6550	0.9236	0.6736	0.0947	0.5648	0.0029	0.0117
0.5913	0.6522	0.2207	0.6071	0.8166	0.6465	0.1759	0.6258	0.0001	0.0013
0.4035	0.5710	0.1167	0.5031	0.6025	0.5870	0.1331	0.6069	0.8147	0.4478
0.1608	0.4185	0.3827	0.6811	0.0003	0.0255	0.3801	0.6652	0.8047	0.4446
0.8558	0.7193	0.8727	0.8353	0.0199	0.1425	0.8033	0.8058	0.7579	0.4315
0.4968	0.6198	0.5448	0.7501	0.0019	0.0485	0.4422	0.6869	0.7949	0.4426
0.8918	0.7230	0.6422	0.7782	0.0033	0.0549	0.9835	0.8347	0.8968	0.4668
0.7384	0.6827	0.5278	0.7446	0.0135	0.1128	0.5134	0.7071	0.5591	0.3561
0.9120	0.7281	0.5491	0.7501	0.0572	0.2296	0.9114	0.8246	0.5185	0.3390

0.0553	0.3182	0.1494	0.5300	0.2611	0.4138	0.1719	0.6245	0.3203	0.2512
0.6949	0.6653	0.5117	0.7340	0.3440	0.4742	0.2615	0.6561	0.9438	0.4815
0.5487	0.6273	0.2768	0.6478	0.6443	0.6046	0.3500	0.6648	0.8722	0.4630
0.5491	0.6273	0.8550	0.8302	0.6767	0.6152	0.1040	0.5714	0.2608	0.2208
0.7455	0.6849	0.4695	0.7159	0.6270	0.5966	0.5888	0.7484	0.0051	0.0159
0.8766	0.7219	0.0070	0.2084	0.7759	0.6352	0.5848	0.7462	0.2276	0.2081
0.5585	0.6336	0.3776	0.6774	0.7039	0.6196	0.2116	0.6280	0.0021	0.0098
0.6898	0.6642	0.9569	0.8469	0.0693	0.2439	0.1350	0.6069	0.8220	0.4505
0.0445	0.3046	0.7102	0.8004	0.2718	0.4242	0.4525	0.6869	0.0066	0.0181
0.1146	0.3701	0.6532	0.7782	0.1511	0.3199	0.9393	0.8275	0.0003	0.0028
0.3312	0.5439	0.0891	0.4917	0.9390	0.6736	0.0414	0.5116	0.1079	0.1236
0.3924	0.5655	0.7600	0.8135	0.9261	0.6736	0.4486	0.6869	0.0647	0.0867
0.7830	0.6954	0.8994	0.8441	0.1094	0.2946	0.2807	0.6595	0.4739	0.3261
0.2407	0.4709	0.0301	0.3374	0.4537	0.5216	0.2204	0.6280	0.9546	0.4841
0.4557	0.6004	0.7184	0.8004	0.1281	0.3111	0.4286	0.6821	0.5927	0.3668
0.0205	0.2497	0.7145	0.8004	0.0913	0.2637	0.9264	0.8246	0.0001	0.0012
0.1213	0.3802	0.3905	0.6899	0.1749	0.3524	0.2872	0.6600	0.0042	0.0141
0.5374	0.6273	0.3754	0.6750	0.7230	0.6254	0.3048	0.6607	0.1343	0.1460
0.6990	0.6674	0.8675	0.8353	0.3149	0.4505	0.2588	0.6561	0.2575	0.2193
0.4997	0.6198	0.3034	0.6550	0.0642	0.2359	0.0957	0.5660	0.6117	0.3754
0.7824	0.6954	0.2376	0.6235	0.0928	0.2667	0.9153	0.8246	0.4771	0.3275
0.1438	0.4142	0.4372	0.7007	0.0099	0.0944	0.1496	0.6131	0.6396	0.3869
0.4716	0.6075	0.2892	0.6500	0.2475	0.4052	0.0935	0.5648	0.9120	0.4729
0.7376	0.6827	0.9053	0.8444	0.5653	0.5730	0.4023	0.6735	0.0292	0.0513
0.0488	0.3055	0.6538	0.7782	0.6919	0.6181	0.1012	0.5714	0.7347	0.4235
0.9584	0.7367	0.9357	0.8447	0.4725	0.5264	0.3177	0.6635	0.4571	0.3218
0.2925	0.5154	0.9124	0.8444	0.8973	0.6701	0.5088	0.7061	0.3786	0.2808

0.8731	0.7219	0.9753	0.8504	0.5348	0.5566	0.9701	0.8347	0.0066	0.0181
0.7548	0.6904	0.6652	0.7800	0.1821	0.3581	0.5628	0.7370	0.2402	0.2129
0.2157	0.4709	0.8364	0.8269	0.2768	0.4261	0.3466	0.6648	0.0005	0.0037
0.4544	0.6004	0.0992	0.4999	0.1427	0.3151	0.6534	0.7778	0.0001	0.0008
0.2188	0.4709	0.2019	0.5977	0.6753	0.6152	0.2026	0.6258	0.2059	0.1930
0.0472	0.3055	0.2970	0.6533	0.7036	0.6196	0.1039	0.5714	0.0053	0.0162
0.2171	0.4709	0.9234	0.8444	0.0703	0.2448	0.7084	0.7879	0.0233	0.0444
0.2399	0.4709	0.0891	0.4917	0.5683	0.5733	0.0359	0.5116	0.2396	0.2129
0.2498	0.4750	0.7167	0.8004	0.0098	0.0944	0.2924	0.6600	0.6824	0.4052
0.0557	0.3182	0.1031	0.4999	0.2063	0.3713	0.4519	0.6869	0.7014	0.4127
0.4450	0.5983	0.5779	0.7622	0.9421	0.6736	0.7079	0.7879	0.7426	0.4272
0.8955	0.7230	0.4644	0.7101	0.4705	0.5264	0.2173	0.6280	0.8024	0.4441
0.1494	0.4179	0.4861	0.7227	0.9247	0.6736	0.9762	0.8347	0.7631	0.4328
0.6373	0.6641	0.4850	0.7227	0.3451	0.4742	0.4900	0.7055	0.3169	0.2497
0.6457	0.6641	0.2582	0.6326	0.0453	0.2035	0.3642	0.6648	0.4851	0.3292
0.0572	0.3182	0.0246	0.2968	0.5531	0.5673	0.0044	0.2605	0.0004	0.0029
0.2358	0.4709	0.3334	0.6550	0.0644	0.2359	0.1243	0.5944	0.7883	0.4405
0.6067	0.6579	0.4279	0.7007	0.1504	0.3199	0.1743	0.6256	0.9350	0.4787
0.8388	0.7175	0.6371	0.7782	0.3671	0.4812	0.4835	0.7017	0.8582	0.4604
0.2418	0.4717	0.6542	0.7782	0.0035	0.0562	0.8717	0.8201	0.9909	0.4951
0.0979	0.3626	0.2379	0.6235	0.0799	0.2581	0.0116	0.3368	0.0143	0.0322
0.4397	0.5967	0.3108	0.6550	0.0167	0.1257	0.0567	0.5136	0.0137	0.0312
0.0919	0.3547	0.2736	0.6478	0.1265	0.3097	0.6710	0.7805	0.0860	0.1047
0.3562	0.5539	0.4623	0.7101	0.4360	0.5107	0.7163	0.7887	0.0306	0.0528
0.1067	0.3668	0.1043	0.4999	0.7017	0.6196	0.6276	0.7630	0.3078	0.2451
0.1384	0.4044	0.1384	0.5119	0.1384	0.3151	0.1384	0.6069	0.0000	0.0001
0.4675	0.6034	0.4462	0.7043	0.7669	0.6352	0.8898	0.8246	0.0000	0.0000

0.8035	0.7040	0.4022	0.6946	0.3993	0.4941	0.1041	0.5714	0.0494	0.0742
0.1360	0.4035	0.0331	0.3519	0.1216	0.3058	0.2889	0.6600	0.0769	0.0976
0.1608	0.4185	0.1873	0.5888	0.2845	0.4337	0.3466	0.6648	0.0410	0.0641
0.2741	0.5014	0.1301	0.5071	0.7335	0.6280	0.8045	0.8058	0.0303	0.0524
0.7282	0.6789	0.9955	0.8533	0.5619	0.5716	0.0109	0.3368	0.0002	0.0021
0.0150	0.2237	0.7701	0.8147	0.6093	0.5883	0.6370	0.7663	0.0021	0.0096
0.6199	0.6579	0.2555	0.6326	0.0598	0.2308	0.1159	0.5885	0.0379	0.0612
0.0731	0.3355	0.2395	0.6241	0.4581	0.5239	0.2827	0.6595	0.2040	0.1915
0.5099	0.6224	0.0476	0.3955	0.0200	0.1425	0.2455	0.6504	0.0000	0.0000
0.0983	0.3626	0.2881	0.6500	0.7070	0.6201	0.9133	0.8246	0.5331	0.3444
0.6778	0.6642	0.7900	0.8177	0.3670	0.4812	0.0085	0.3368	0.1845	0.1811
0.3125	0.5330	0.3469	0.6614	0.3766	0.4819	0.1081	0.5768	0.0218	0.0433
0.6767	0.6642	0.5073	0.7340	0.1842	0.3581	0.1708	0.6234	0.9476	0.4817
0.1049	0.3668	0.9631	0.8486	0.6934	0.6181	0.1695	0.6229	0.1507	0.1586
0.3573	0.5543	0.7261	0.8004	0.7583	0.6335	0.4682	0.6992	0.0492	0.0742
0.9251	0.7286	0.9878	0.8533	0.1913	0.3598	0.8388	0.8170	0.0100	0.0251
0.0945	0.3584	0.3305	0.6550	0.3149	0.4505	0.9649	0.8347	0.0731	0.0943
0.9468	0.7353	0.4583	0.7101	0.6000	0.5865	0.0185	0.3996	0.0221	0.0435
0.5697	0.6398	0.8019	0.8177	0.4610	0.5240	0.9299	0.8246	0.0266	0.0489
0.3018	0.5249	0.7824	0.8177	0.7287	0.6254	0.4090	0.6770	0.4171	0.2998
0.2845	0.5094	0.5619	0.7608	0.2518	0.4091	0.1519	0.6131	0.3660	0.2750
0.6742	0.6642	0.6761	0.7856	0.6743	0.6152	0.2611	0.6561	0.0182	0.0381
0.0123	0.2237	0.0028	0.1565	0.0053	0.0694	0.7710	0.8025	0.9922	0.4951
0.5456	0.6273	0.3558	0.6631	0.0014	0.0375	0.2886	0.6600	0.6228	0.3782
0.1828	0.4361	0.1997	0.5977	0.0001	0.0242	0.0497	0.5116	0.0687	0.0891
0.1481	0.4179	0.2465	0.6309	0.0002	0.0255	0.0585	0.5136	0.1114	0.1272
0.2001	0.4548	0.4284	0.7007	0.0001	0.0203	0.1965	0.6258	0.2841	0.2328

0.1543	0.4185	0.4516	0.7097	0.0002	0.0255	0.1770	0.6258	0.2505	0.2180
0.7958	0.7021	0.4858	0.7227	0.0324	0.1796	0.7923	0.8058	0.8897	0.4660
0.5755	0.6410	0.5837	0.7622	0.1506	0.3199	0.7009	0.7879	0.4347	0.3093
0.4078	0.5723	0.8446	0.8286	0.9955	0.6909	0.1862	0.6258	0.7959	0.4426
0.4163	0.5794	0.9669	0.8487	0.4738	0.5264	0.8855	0.8246	0.7589	0.4315
0.6888	0.6642	0.4310	0.7007	0.6729	0.6152	0.5531	0.7345	0.4598	0.3224
0.9560	0.7367	0.1485	0.5300	0.7182	0.6238	0.6817	0.7844	0.0009	0.0054
0.8659	0.7219	0.0909	0.4917	0.8023	0.6445	0.3048	0.6607	0.0073	0.0194
0.3777	0.5570	0.6525	0.7782	0.4441	0.5182	0.7681	0.8025	0.1394	0.1499
0.8549	0.7193	0.0939	0.4999	0.1014	0.2848	0.5744	0.7391	0.0010	0.0057
0.8442	0.7175	0.2739	0.6478	0.0382	0.1918	0.0207	0.3996	0.8867	0.4658
0.4479	0.5997	0.9573	0.8469	0.3567	0.4796	0.4618	0.6929	0.0376	0.0612
0.6446	0.6641	0.6031	0.7706	0.8887	0.6670	0.6823	0.7844	0.4552	0.3209
0.8723	0.7219	0.6181	0.7771	0.1380	0.3151	0.0177	0.3996	0.5846	0.3632
0.1909	0.4413	0.2954	0.6533	0.2476	0.4052	0.2333	0.6380	0.0271	0.0494
0.5430	0.6273	0.1404	0.5144	0.3389	0.4742	0.0591	0.5136	0.0018	0.0087
0.4807	0.6122	0.9213	0.8444	0.8152	0.6465	0.3742	0.6648	0.2981	0.2403
0.4962	0.6198	0.9230	0.8444	0.1550	0.3248	0.4237	0.6821	0.0052	0.0160
0.0552	0.3182	0.0011	0.1535	0.0149	0.1169	0.3135	0.6635	0.8535	0.4600
0.8077	0.7043	0.0658	0.4504	0.7758	0.6352	0.0584	0.5136	0.2472	0.2169
0.0621	0.3199	0.4817	0.7227	0.0885	0.2629	0.9214	0.8246	0.0010	0.0057
0.8620	0.7201	0.4764	0.7213	0.1381	0.3151	0.1588	0.6131	0.7875	0.4405
0.2031	0.4570	0.0009	0.1535	0.1054	0.2908	0.0038	0.2605	0.0605	0.0831
0.4960	0.6198	0.7272	0.8004	0.9934	0.6909	0.4467	0.6869	0.2696	0.2257
0.0148	0.2237	0.0215	0.2928	0.0727	0.2474	0.3632	0.6648	0.0506	0.0749
0.7402	0.6835	0.8095	0.8177	0.0357	0.1918	0.8775	0.8246	0.1285	0.1411
0.9936	0.7431	0.8548	0.8302	0.8959	0.6700	0.5191	0.7111	0.7091	0.4130

0.4315	0.5919	0.2647	0.6395	0.5068	0.5459	0.2498	0.6549	0.0083	0.0216
0.6429	0.6641	0.8989	0.8441	0.2135	0.3747	0.7462	0.7941	0.6143	0.3757
0.9181	0.7281	0.5819	0.7622	0.7375	0.6296	0.3699	0.6648	0.0183	0.0381
0.3293	0.5435	0.5596	0.7591	0.9101	0.6736	0.8422	0.8170	0.0839	0.1038
0.1072	0.3668	0.8134	0.8177	0.1042	0.2888	0.5762	0.7401	0.5811	0.3621
0.0089	0.2237	0.0933	0.4999	0.3793	0.4819	0.1513	0.6131	0.1199	0.1344
0.7469	0.6849	0.5852	0.7622	0.4519	0.5216	0.0705	0.5225	0.0194	0.0395
0.1489	0.4179	0.5909	0.7629	0.2975	0.4407	0.2577	0.6561	0.0467	0.0713
0.1383	0.4044	0.3214	0.6550	0.5284	0.5530	0.2772	0.6595	0.0363	0.0606
0.5431	0.6273	0.4554	0.7101	0.0720	0.2465	0.3750	0.6648	0.5111	0.3375
0.3658	0.5570	0.0411	0.3763	0.3497	0.4770	0.7832	0.8048	0.2237	0.2050
0.3677	0.5570	0.0004	0.1535	0.1418	0.3151	0.0041	0.2605	0.4785	0.3275
0.0411	0.3026	0.2691	0.6441	0.0766	0.2530	0.4934	0.7056	0.0042	0.0141
0.0250	0.2518	0.0767	0.4788	0.4923	0.5374	0.2424	0.6488	0.4526	0.3196
0.6633	0.6642	0.9520	0.8469	0.7176	0.6238	0.0677	0.5225	0.3230	0.2519
0.5513	0.6285	0.0441	0.3767	0.7912	0.6398	0.3685	0.6648	0.5167	0.3386
0.3600	0.5547	0.0090	0.2084	0.2549	0.4095	0.4152	0.6821	0.6678	0.4002
0.8153	0.7074	0.9648	0.8486	0.9283	0.6736	0.2162	0.6280	0.2557	0.2192
0.4076	0.5723	0.0512	0.4026	0.0907	0.2632	0.7910	0.8058	0.5118	0.3375
0.6762	0.6642	0.2198	0.6071	0.2159	0.3760	0.0655	0.5225	0.5728	0.3593
0.6008	0.6551	0.4372	0.7007	0.7578	0.6335	0.0038	0.2605	0.5107	0.3375
0.2163	0.4709	0.0197	0.2928	0.6585	0.6121	0.0220	0.3996	0.4058	0.2962
0.3261	0.5421	0.0531	0.4065	0.1913	0.3598	0.1867	0.6258	0.5520	0.3536
0.1769	0.4322	0.0720	0.4676	0.1135	0.2962	0.2244	0.6317	0.0711	0.0920
0.8866	0.7219	0.9803	0.8530	0.3052	0.4468	0.1209	0.5944	0.8892	0.4660
0.2347	0.4709	0.6476	0.7782	0.1966	0.3624	0.9368	0.8269	0.1026	0.1198
0.9182	0.7281	0.2786	0.6478	0.4006	0.4941	0.0192	0.3996	0.2337	0.2112

0.2169	0.4709	0.0645	0.4455	0.3039	0.4468	0.1130	0.5856	0.0395	0.0625
0.7309	0.6795	0.8522	0.8302	0.9366	0.6736	0.9869	0.8349	0.0162	0.0350
0.8551	0.7193	0.5852	0.7622	0.9739	0.6846	0.7663	0.8020	0.2826	0.2328
0.5199	0.6257	0.1392	0.5126	0.8431	0.6536	0.0115	0.3368	0.4658	0.3239
0.0257	0.2518	0.1662	0.5588	0.8157	0.6465	0.4336	0.6821	0.3360	0.2593
0.3816	0.5570	0.8485	0.8286	0.1153	0.2984	0.4237	0.6821	0.0043	0.0142
0.5961	0.6550	0.0864	0.4917	0.3655	0.4812	0.8274	0.8167	0.0229	0.0442
0.0133	0.2237	0.5016	0.7316	0.4361	0.5107	0.4354	0.6835	0.0009	0.0054
0.4105	0.5748	0.5814	0.7622	0.2873	0.4338	0.2904	0.6600	0.0171	0.0365
0.7113	0.6724	0.3645	0.6705	0.9505	0.6745	0.2684	0.6561	0.1405	0.1506
0.8270	0.7149	0.8739	0.8353	0.7997	0.6441	0.3438	0.6648	0.9177	0.4744
0.0157	0.2237	0.1424	0.5169	0.3744	0.4819	0.0016	0.2465	0.0877	0.1054
0.6815	0.6642	0.1980	0.5977	0.1291	0.3124	0.1424	0.6069	0.7092	0.4130
0.5987	0.6550	0.8152	0.8179	0.0579	0.2296	0.8199	0.8124	0.0279	0.0500
0.0920	0.3547	0.6649	0.7800	0.0032	0.0549	0.4317	0.6821	0.0099	0.0250
0.6625	0.6642	0.1760	0.5741	0.0355	0.1918	0.4716	0.7014	0.8212	0.4505
0.1134	0.3697	0.0027	0.1565	0.0507	0.2160	0.0558	0.5136	0.2204	0.2023
0.3752	0.5570	0.2783	0.6478	0.3219	0.4585	0.0940	0.5648	0.0103	0.0257
0.1744	0.4322	0.7529	0.8130	0.6642	0.6129	0.9089	0.8246	0.5743	0.3594
0.1881	0.4380	0.5775	0.7622	0.2116	0.3734	0.0316	0.4825	0.0368	0.0612
0.7950	0.7021	0.9412	0.8461	0.3452	0.4742	0.2864	0.6600	0.0636	0.0854
0.8308	0.7149	0.8488	0.8286	0.1952	0.3624	0.1080	0.5768	0.0860	0.1047
0.0520	0.3182	0.1014	0.4999	0.5541	0.5673	0.4512	0.6869	0.0250	0.0466
0.0705	0.3281	0.3233	0.6550	0.2834	0.4331	0.7113	0.7885	0.6766	0.4034
0.0898	0.3523	0.3720	0.6705	0.3558	0.4796	0.3782	0.6649	0.4092	0.2963
0.9124	0.7281	0.2877	0.6500	0.6969	0.6188	0.9015	0.8246	0.4685	0.3248
0.9691	0.7383	0.3318	0.6550	0.1979	0.3636	0.6888	0.7844	0.0000	0.0004

0.0896	0.3523	0.0896	0.4917	0.8171	0.6465	0.1134	0.5856	0.0008	0.0052
0.2695	0.4963	0.1990	0.5977	0.0140	0.1128	0.1891	0.6258	0.2818	0.2328
0.2589	0.4855	0.3302	0.6550	0.1413	0.3151	0.8427	0.8170	0.1678	0.1710
0.7124	0.6724	0.6503	0.7782	0.0063	0.0739	0.0688	0.5225	0.0155	0.0342
0.4993	0.6198	0.9976	0.8533	0.0529	0.2209	0.5532	0.7345	0.0407	0.0640
0.9086	0.7281	0.7298	0.8004	0.0019	0.0485	0.2227	0.6293	0.3524	0.2679
0.2539	0.4788	0.5596	0.7591	0.1768	0.3536	0.7302	0.7936	0.7982	0.4432
0.2341	0.4709	0.3709	0.6705	0.1343	0.3151	0.3936	0.6735	0.7564	0.4315
0.6742	0.6642	0.7148	0.8004	0.3427	0.4742	0.9759	0.8347	0.5125	0.3375
0.8336	0.7158	0.9975	0.8533	0.7939	0.6402	0.7510	0.7970	0.0011	0.0059
0.3926	0.5655	0.7650	0.8146	0.6094	0.5883	0.4466	0.6869	0.5022	0.3355
0.3359	0.5484	0.4010	0.6946	0.3364	0.4727	0.9498	0.8292	0.4913	0.3300
0.3505	0.5527	0.3075	0.6550	0.3148	0.4505	0.0217	0.3996	0.5377	0.3462
0.1123	0.3697	0.2989	0.6533	0.2615	0.4138	0.4434	0.6869	0.0378	0.0612
0.6565	0.6642	0.1065	0.4999	0.0215	0.1450	0.2830	0.6595	0.1992	0.1891
0.5306	0.6262	0.8189	0.8191	0.0617	0.2329	0.6377	0.7663	0.6162	0.3762
0.9648	0.7367	0.4243	0.7007	0.1305	0.3131	0.4820	0.7017	0.0026	0.0110
0.2355	0.4709	0.1048	0.4999	0.5344	0.5566	0.3235	0.6635	0.6657	0.3994
0.8213	0.7117	0.2647	0.6395	0.5869	0.5809	0.0014	0.2465	0.3560	0.2698
0.5061	0.6222	0.4219	0.7007	0.5221	0.5517	0.5058	0.7061	0.2495	0.2179
0.1336	0.4035	0.0028	0.1565	0.6825	0.6153	0.0094	0.3368	0.4090	0.2963
0.2403	0.4709	0.7771	0.8174	0.0178	0.1327	0.7288	0.7936	0.2284	0.2085
0.2795	0.5062	0.6368	0.7782	0.9367	0.6736	0.4955	0.7056	0.0804	0.1011
0.5879	0.6494	0.1693	0.5645	0.6060	0.5877	0.5703	0.7388	0.0000	0.0001
0.0115	0.2237	0.4360	0.7007	0.0861	0.2629	0.3434	0.6648	0.0035	0.0133
0.0867	0.3518	0.2487	0.6323	0.1627	0.3342	0.6038	0.7510	0.0606	0.0831
0.3818	0.5570	0.7089	0.8004	0.0140	0.1128	0.8457	0.8170	0.2577	0.2193

0.1750	0.4322	0.3500	0.6627	0.0104	0.0958	0.4330	0.6821	0.8901	0.4660
0.9794	0.7411	0.6376	0.7782	0.2161	0.3760	0.6846	0.7844	0.9868	0.4950
0.2391	0.4709	0.9468	0.8469	0.8487	0.6541	0.1787	0.6258	0.0127	0.0295
0.6179	0.6579	0.2216	0.6076	0.1772	0.3536	0.5315	0.7215	0.4621	0.3233
0.0096	0.2237	0.7459	0.8088	0.8072	0.6465	0.4859	0.7022	0.5148	0.3383
0.2347	0.4709	0.0221	0.2928	0.0265	0.1631	0.8308	0.8170	0.5969	0.3679
0.2772	0.5043	0.5690	0.7622	0.9746	0.6846	0.0890	0.5648	0.6857	0.4056
0.0546	0.3182	0.0222	0.2928	0.0052	0.0694	0.1658	0.6172	0.8634	0.4604
0.6380	0.6641	0.4782	0.7221	0.0501	0.2160	0.6364	0.7663	0.0127	0.0295
0.9639	0.7367	0.8949	0.8427	0.7244	0.6254	0.2440	0.6504	0.0064	0.0179
0.0016	0.1952	0.0001	0.0630	0.0003	0.0255	0.3357	0.6648	0.0032	0.0126
0.0126	0.2237	0.1090	0.4999	0.0639	0.2359	0.4078	0.6765	0.0668	0.0886
0.3674	0.5570	0.7912	0.8177	0.8582	0.6565	0.7148	0.7887	0.1688	0.1712
0.9605	0.7367	0.1617	0.5502	0.2395	0.3982	0.7798	0.8048	0.6769	0.4034
0.7466	0.6849	0.0013	0.1535	0.0715	0.2465	0.4734	0.7017	0.1963	0.1881
0.7927	0.7012	0.2991	0.6533	0.2568	0.4104	0.5901	0.7484	0.5397	0.3467
0.0046	0.2237	0.0278	0.3156	0.1120	0.2946	0.7239	0.7918	0.3254	0.2534

Table 10

Lipid species	Bt:WT-M1	Bt:WT-M2	Bt:WT-F3	Bt:WT-M18	Bt:WT-F19	Bt:BSHIVMOL361-M4	Bt:BSHIVMOL361-M5	Bt:BSHIVMOL361-M6	Bt:BSHIVMOL361-F7
CE 12:0	2.8205287	2.6197959	2.6684662	1.5551072	0.7086725	3.7873036	2.3219351	1.5967224	3.7409552
CE 14:0	6.4658433	6.141865	4.746562	5.1077041	3.1688251	7.0848343	5.9334441	4.6227474	6.7166259
CE 14:1	4.6458692	3.9346624	3.9778745	2.9961049	1.1777462	5.5002478	3.4343202	2.7790632	5.9470227
CE 15:0	7.7324218	8.0865727	5.9072193	6.2898184	4.351373	8.9020616	7.8689673	5.5831207	8.2884003

CE 16:0	94.824119	110.6156	66.643962	92.883835	102.39789	102.64703	117.33327	91.306014	104.91616
CE 16:1	39.880856	36.488747	37.473816	34.90033	40.866078	48.55576	36.965479	35.164076	59.936962
CE 17:0	5.4668457	6.77396	4.7752674	4.1449322	5.7486699	6.0347891	5.1248054	4.8563874	8.8076864
CE 18:0	6.3159394	10.467799	6.5826592	5.9566261	10.532525	7.9967056	7.6187395	8.9330937	9.8273594
CE 18:1	111.49877	117.22932	93.758816	106.76781	161.71018	133.15325	124.77739	113.8683	174.19722
CE 18:2	1269.2477	1336.769	630.02152	1305.4159	845.00891	1211.9108	1551.6136	1238.8906	1009.6038
CE 18:3	32.711933	27.695203	22.682603	24.039716	14.99627	33.995486	28.873226	22.52118	35.130521
CE 18:4	2.8879007	2.5508695	2.452469	1.6979054	0.7861928	3.3322451	2.0003131	1.6622857	3.5794448
CE 20:0	182.01825	206.57895	141.48872	142.84837	74.568354	280.55408	246.67964	170.17931	214.65787
CE 20:1	64.637982	45.724015	48.898568	24.266267	7.8449479	99.456283	35.5104	22.627029	76.698798
CE 20:2	3.0316554	2.7334719	2.4809102	1.6285987	1.1665434	4.4698197	2.5348995	1.6221844	3.5719475
CE 20:3	30.37984	29.895242	18.384904	26.915497	21.643408	33.240605	36.125895	26.328802	28.329695
CE 20:4	651.39374	675.67728	451.34758	639.29292	566.06875	621.61545	727.91604	609.21378	643.76897
CE 20:5	138.16244	138.97544	89.619751	136.96998	65.986675	137.7666	131.93953	128.62414	187.31013
CE 22:0	4.0863535	4.5512026	3.2621362	3.6505116	1.8772393	6.3029716	5.1685927	3.7459906	5.2218917
CE 22:1	3.4158462	4.1205707	2.7336285	2.5159311	1.7572223	5.8519202	4.1874624	3.4442345	4.8870524

CE 22:2	33.929538	36.256921	27.897029	25.602958	18.493493	44.610371	40.249936	28.660134	43.033129
CE 22:4	4.0442349	4.5442532	4.5200824	3.0909189	1.6703763	6.1336069	3.9351662	2.9722126	6.7771842
CE 22:5	7.9402796	7.9242285	5.4879236	10.043453	3.6377331	10.895008	8.142855	6.667991	9.0509172
CE 22:6	191.60182	202.29939	109.88072	212.12826	119.57823	214.21908	249.06159	221.67861	200.00841
CE 24:0	65.758526	88.389117	58.183396	61.384361	52.491947	87.666522	101.2581	72.096024	88.924235
CE 24:1	15.800786	16.026549	12.423203	12.508993	5.8238023	19.861932	16.142133	13.267948	23.308043
Cer d18:0/24:1	0.2097789								
Cer d18:1/14:0									
Cer d18:1/16:0	0.2015476	0.1917517	0.1776299	0.1197856	0.1842449		0.1398755	0.1102742	0.1898528
Cer d18:1/18:0									
Cer d18:1/20:0									
Cer d18:1/22:0	0.6920071	0.7539929	0.358754	0.7713594	0.2184741	0.4934352	0.9425068	0.7410147	0.3199908
Cer d18:1/24:0	1.1543339	1.2065794	0.850807	1.1765779	0.5977065	0.9571946	1.194078	1.0892943	0.8309422
Cer d18:1/24:1	0.4964801	0.4353349	0.7819596	0.4677449	0.6711591	0.4986169	0.5404877	0.4433059	0.9395859
DG 12:0_18:1									0.3027643
DG 12:0_18:2		0.6651082							

DG 14:1_18:1	0.456045								
DG 15:0_18:2		0.7340456							
DG 16:0_16:0	0.9471072	0.9409531	0.4918631	0.4860837	0.4500826	0.4012716	0.2158316	0.2490216	0.6046182
DG 16:0_16:1		0.2748631							
DG 16:0_18:0	0.9738081							0.9041611	
DG 16:0_18:1	1.5573628	2.0883877	1.5003807	1.5245318	2.3672274	1.4156923	0.662902	0.9337346	1.1646436
DG 16:0_18:2	5.3085512	6.3134349	4.353147	5.5242757	4.3865361	4.1342065	3.1455864	1.9398901	
DG 16:0_22:6				0.4334409	0.2647662		0.318549	0.3027901	
DG 16:1_18:1					0.5843421				
DG 16:1_18:2	1.082268	1.0611898	0.9882861	1.0769515	1.1685925				
DG 18:0_18:1		0.2192722							
DG 18:0_18:2	0.7351349	0.9163166	0.9143003	0.4729591	0.5063285	0.6612901		0.4194545	
DG 18:1_18:1	0.7258495	0.9077485	0.7681729	0.647318	2.2191516	0.530076	0.2434069	0.4676261	0.54863
DG 18:1_18:2	10.92136	8.4705773	7.0087817	10.752033	11.018153	5.5386408	4.9573222	3.6461888	
DG 18:1_20:1	0.4435185	0.3636486			0.2413693	0.2941025			0.3090783
DG 18:1_20:2									

DG 18:1_20:4					0.43733 1				
DG 18:1_22:6				1.30121 75	1.16809 51		0.9143947	0.7912277	
DG 18:2_20:4					0.60117 54				
DG 18:2_22:6				4.55189 66	1.60598 74		2.9375232	1.7543331	
FA 12:0	3.8664 393	2.4251 07	3.0372 257	2.81026 77	2.64691 53	3.1337673	3.071337	2.8736802	3.1119497
FA 14:0	22.789 277	17.023 753	20.371 688	20.4358 94	17.0837 31	24.006095	23.82572	26.167148	23.098382
FA 14:1	5.1422 294	4.6537 343	6.0306 435	5.26225 9	4.59058 57	5.8453821	5.6866108	5.7011175	5.9285047
FA 15:0	11.112 662	10.752 546	11.578 02	10.7725 17	9.54599 17	10.684604	11.402378	11.029248	11.556327
FA 16:0	190.51 149	141.67 621	190.61 66	177.075 67	153.527 23	204.10549	210.7934	224.47445	206.90803
FA 16:1	27.559 952	18.759 798	24.397 578	23.2211 52	22.1367 46	28.126886	28.750823	31.412525	28.447076
FA 17:0	11.797 738	11.277 556	12.632 838	11.3029 34	10.2206 94	12.898102	12.757234	12.249012	12.817524
FA 18:0	71.268 227	51.802 427	66.497 146	58.2875 57	53.2724 44	67.020288	67.497201	65.564339	66.379066
FA 18:1	68.773 249	46.989 814	67.078 934	62.4175 72	52.2121 83	73.767482	83.11243	81.538768	80.801151
FA 18:2	82.315 519	46.598 776	67.119 004	79.8674 46	51.2003 58	73.657692	101.01527	90.735966	90.956178
FA 18:3	8.3099 989	5.0763 046	6.5436 243	9.61774 7	5.39612 24	6.3801073	8.7722811	7.7268575	8.05871
FA 18:4	1.4123 905	1.2080 058	1.3789 627	1.49706 08	0.93798 9	1.3001726	1.4456597	1.2679334	1.6099313

FA 20:0	7.6508198	4.1567734	8.2689331	5.1085877	3.3380586	9.3832301	7.2763555	6.0817505	10.114626
FA 20:1	6.677309	4.2147559	6.1757319	4.9204843	3.1416636	6.2157708	6.0971532	5.4506142	6.203513
FA 20:2	1.9556585	1.5324989	2.0890886	1.8813294	1.4941689	2.2402655	2.2237762	1.912577	2.1586639
FA 20:3	2.3588725	2.1457153	2.4215541	2.4011064	2.0361405	2.4758157	2.5757548	2.2433928	2.5411972
FA 20:4	5.4373061	4.2648726	5.1055686	6.1167605	5.5972358	4.4885234	6.1759078	5.2897709	5.3080196
FA 20:5	2.5039149	1.8907828	2.3896583	3.6140289	1.8608491	2.37195	3.1090194	2.6273052	2.6906945
FA 22:0	3.3066335	3.0522546	3.7980334	3.1399232	3.1113403	3.5722035	3.7896794	3.8039068	4.1189881
FA 22:1	3.4596428	3.2855745	4.9224876	3.8567565	3.0882855	4.4863584	4.5281177	5.121508	4.5193462
FA 22:2	2.0614965	1.356067	2.0523042	1.52323	1.284399	1.7711761	1.6673192	1.6389668	1.8223979
FA 22:4	1.4336785	1.4403398	1.5714955	1.3619841	1.2601264	1.5491645	1.5374407	1.2704374	1.6345007
FA 22:5	7.4855619	3.7617243	6.0325457	6.0396357	4.7023034	4.9595861	5.4321507	3.99973	4.820024
FA 22:6	7.4607314	5.6343261	6.4215594	10.25385	7.232963	8.0006422	9.8147395	7.991949	6.6864033
FA 24:0	2.3304737	2.4191614	2.8331303	2.1684547	1.9525979	2.4602981	2.242451	2.2197227	2.5833424
FA 24:1	2.9466557	3.4732579	3.9699698	2.9700243	2.4850425	3.5519963	3.281878	3.4335373	3.4138354
HexCER d18:1/16:0	0.1545452	0.1698333	0.2656102	0.1507009	0.2100413		0.2174336	0.2246891	0.3402799
HexCER d18:1/18:0			0.1072293						

HexCER d18:1/20:0										0.1222956
HexCER d18:1/22:0	0.4882548	0.4343526	0.3409506	0.64993 28	0.30682 34	0.3811911	0.5850652	0.474579	0.3983126	
HexCER d18:1/22:1				0.12515 82		0.117292	0.1278583			
HexCER d18:1/24:0	0.2087666	0.1823239	0.2380 17	0.23694 01	0.19836 29	0.2221398	0.2038733	0.1976629	0.2386303	
HexCER d18:1/24:1	0.2168038	0.1301556	0.4398575	0.19903 56	0.34239 25	0.2887701	0.2537457	0.1719567	0.5675677	
LPC 15:0	0.7977903	0.7663533	0.9784 13	0.90261 24	0.62676 01	0.9883396	0.8026829	0.8219836	0.8653324	
LPC 16:0	155.20821	146.18904	210.58537	170.526 5	154.209 05	201.82997	219.51394	189.80873	191.94905	
LPC 16:1	2.0435477	1.6442511	2.9678857	2.45401 87	2.41970 06	3.0336872	2.5164388	2.1179704	3.4295186	
LPC 17:0	4.7879 34	4.8567631	4.8473287	5.58117 57	4.16340 45	4.5587688	5.2119209	4.7192896	5.2006645	
LPC 18:0	62.861994	64.297769	84.879009	83.6653 51	78.2864 89	60.123954	83.017364	74.249905	74.349691	
LPC 18:1	28.944221	23.131147	36.022812	32.8133 04	28.4660 6	46.962533	33.797436	27.357464	37.601073	
LPC 18:2	88.183061	65.210465	96.386285	102.630 06	77.0448 1	108.1754	108.41232	87.290313	108.35115	
LPC 18:3	0.5743598		0.5058941	0.72026 16	0.49551 3		0.5252252	0.4732598	0.6305416	
LPC 20:0	4.1813382	2.5060327	4.3893157	2.51570 39	0.82467 64	5.8938146	3.2044787	2.1014239	5.1302532	
LPC 20:1	1.408284	0.9094796	0.9315268	1.10370 19	0.67860 12	1.6092104	1.1354659	0.9569684	1.3161824	
LPC 20:2	0.8083987	0.6957641	0.6303142	0.73321 58	0.65951 8	1.1835994	0.9032079	0.66905	0.8508304	

LPC 20:3	5.1385759	3.9881821	3.7485552	5.113636	5.5004993	5.8982847	5.2630298	3.9399311	4.2257873
LPC 20:4	11.03309	8.4130512	9.7060455	12.856152	14.071344	9.0718493	12.048316	10.636414	11.881264
LPC 20:5	0.5423802	0.5136143	0.7691267	1.2719164	0.534266	0.5104891	0.6059468	0.7952598	0.9635305
LPC 22:5				0.5832807					
LPC 22:6	2.0886178	1.6363887	1.0574953	2.6557129	1.9706744	1.583261	2.2732971	2.5065484	1.7118868
LPE 16:0	4.6524 31	4.9927175	6.6616515	4.7867155	4.1998727	4.9320033	5.1685804	4.8439743	5.4025164
LPE 18:0	1.5216276	1.9123469	2.0088568	2.0816376	1.6796216	1.7326299	2.2097112	1.8207728	2.0085508
LPE 18:1	0.8676029	0.9684716	1.1917729	0.9703606	0.9152206	1.071815	0.8754013	0.8200818	1.3734043
LPE 18:2	2.2288526	1.5618217	1.8576233	2.2817746	1.1870492	1.7280446	2.5053641	1.8663292	2.5472963
LPE 20:4	0.3769819				0.4103775				
LacCER d18:1/16:0									
LacCER d18:1/18:1									
LacCER d18:1/22:0				0.2105764	0.1884532				
PA 34:1	0.3623669	0.3614799	0.3400997	0.3103798		0.41597	0.2350231	0.2030481	0.2546081
PA 34:2	1.1125444	1.1475055	1.4342789	1.2677031	0.480573	1.4632951	1.0787222	1.0872302	1.1572885
PA 34:3				0					

PA 34:4	2.1722584	2.2957797	2.3042 85	2.35354 6	2.34589 93	2.2302908	2.1824796	2.2253009	2.3108795
PA 34:5	0.5879593	0.5911502	0.5300 71	0.51195 79	0.58517 14	0.7286388	0.5623052	0.4593841	0.6883496
PA 36:1	0.1399251	0.1033 33	0.1803 42	0.15705 04		0.2375611	0.1119514	0.1530752	0.137257
PA 36:2	0.7181603	0.8546272	0.7649 533	0.86478 34	0.34045 28	0.8092042	0.7135106	0.7199199	0.8171991
PA 36:3	0.2750549	0.3330728	0.3369 643		0.15950 41	0.3155845	0.1959801		0.2897679
PA 36:4	0.1699153		0.1630 779	0.24090 78		0.2268551	0.2015395		
PA 36:5	0.1874 25	0.3398 523	0.3450 296	0.25307 76		0.3858581	0.3409478	0.2951038	0.4955441
PA 38:3									
PA 38:4		0.2413801	0.2797 085	0.36049 08		0.2997618	0.3310787	0.2694869	0.3173505
PA 38:6							0.1675676		0.1860859
PA 38:7				0.21194 45			0.2011904		
PA 40:6									
PA 40:8									0.1710954
PC 12:0_16:0	0.5312391		0.3901 075	0.43216 36		0.6136904		0.3990097	0.5658538
PC 12:0_18:0									
PC 12:0_18:3	0.9516506	0.9515332	1.3564 576	0.71364 13		1.4204447	0.7939776	0.6976693	1.1425444
PC 14:0_18:1	0.9826846	0.8275452	0.6261 948	1.03673 3	1.00260 43	1.1598772	1.0163837	0.7421172	0.7698949
PC 14:0_18:2	1.5941643	1.4554149	1.5548 906	2.01402	1.10524 36	1.8644396	1.8186553	1.5738887	1.5625056

PC 14:0_18:3											
PC 14:0_20:4											
PC 14:1_20:0				0.41028 16							
PC 15:0_18:1		0.4706 937						0.4712798			
PC 15:0_18:2	1.5695 751	1.2999 576	0.7124 156	1.41656 94	0.84817 45	1.3999062	1.6911621	1.083718	1.045663		
PC 16:0_16:0	45.161 806	42.148 13	34.057 428	41.2867 72	27.7070 05	38.755767	49.285155	43.10041	31.878298		
PC 16:0_16:1	3.1279 784	2.9346 373	3.9416 696	2.92403 87	2.41239 67	3.5178683	3.0718615	2.5641246	2.8675079		
PC 16:0_18:0	52.313 624	49.694 056	36.031 068	49.9745 47	36.1895 49	33.071971	43.333871	44.431305	39.172708		
PC 16:0_18:1	150.37 293	122.29 494	132.50 178	136.437 79	101.995 67	186.85611	168.53326	135.02074	130.54623		
PC 16:0_18:2	717.07 671	613.57 614	570.53 201	648.355 76	409.960 71	701.48124	854.80333	654.95543	571.26295		
PC 16:0_18:3	3.7210 975	2.8220 964	4.4649 71	4.37497 83	2.18878 37	3.2385628	4.5134929	2.9192946	3.8395465		
PC 16:0_20:1	4.2156 887	2.6642 052	3.0919 691	2.90654 28	1.23798 2	4.0133297	2.4271812	2.0966712	3.0936625		
PC 16:0_20:2	4.2605 379	3.4048 572	3.0943 559	3.46301 76	2.64539 12	7.7781901	5.4577187	3.9151987	4.2172382		
PC 16:0_20:3	58.758 251	55.061 849	50.002 818	49.2553 81	39.3867 75	75.411998	64.925099	53.338884	49.826803		
PC 16:0_20:4	195.12 794	155.59 508	202.39 709	200.242 18	139.087	193.42372	198.7081	172.6518	185.99668		
PC 16:0_20:5	20.512 649	21.645 695	27.765 623	32.0433 52	13.7517 03	27.444764	22.670805	22.905607	39.464144		

PC 16:0_22:1	0.4661571					0.4811686					
PC 16:0_22:2	0.5365972										
PC 16:0_22:4	2.1515552	1.9825612			1.3133325						
PC 16:0_22:5	18.856182	14.883168	13.36853	26.074011	6.1145466	26.096301	15.516014	14.769679	16.7086		
PC 16:0_22:6	261.55015	243.20883	199.09218	245.91159	114.30303	341.39018	293.78849	295.33079	280.01678		
PC 16:1_17:0				0.847999							
PC 16:1_18:0		0.4287625	0.6602891		0.3255653		0.3742509		0.5864761		
PC 16:1_18:1	4.7338655	3.2700366	4.0289137	4.5557039	4.2481329	5.163692	3.7844677	3.4015024	4.5517931		
PC 16:1_18:2	9.7178348	7.288176	8.6191036	12.306719	5.8060033	11.049385	11.117694	8.0805665	9.968546		
PC 16:1_20:0			0.3829046						0.4077208		
PC 17:0_18:1	1.1949968	0.9936145	0.7784824	1.3111342	0.6758588	0.9719682	1.2057371	0.9717043	1.2166262		
PC 17:0_18:2	6.5548207	5.8891959	4.3938884	5.9458917	3.643436	5.3814728	6.5466363	5.3323982	4.6167551		
PC 17:0_20:3	1.1478307	1.2387562	1.8389309	1.2652836	1.0588994	1.8622108		1.6838527	1.5903021		
PC 17:0_20:4	7.3487346	5.8982442	5.6766055	5.6844708	4.3195064	6.1059494	5.6725041	5.0926687	6.2811532		
PC 17:0_22:6				7.7349388		7.3941676	4.9454498		6.2410566		
PC 18:0_18:0	1.0165327	0.934812	0.864578	0.945357	0.8968441	0.7552522	0.7453348	0.8010022	0.7201723		

PC 18:0_18:1	21.409108	19.282087	18.947198	23.375787	14.593385	21.284393	20.859985	18.264372	18.603444
PC 18:0_18:2	316.10263	289.52771	249.29724	321.00108	210.26652	249.23208	325.60727	282.99265	259.35498
PC 18:0_18:3	0.9656271	0.9971363	1.0104403	0.986848	0.7432077	0.8496963	0.9000294		1.0960125
PC 18:0_20:0	5.5726356	5.3516609	5.3626152	5.4256627	2.8863949	5.4951477	5.7611424	4.8107611	5.8982747
PC 18:0_20:1	1.1205816	0.7241698	1.135101	0.7220003		1.0527433	0.4859271	0.6747496	0.8406792
PC 18:0_20:2	1.4943641	1.2228866	1.0019389	1.2344191	0.9365066	1.9716078	1.4342582	1.2016526	1.4273453
PC 18:0_20:3	23.348929	22.279982	21.405096	23.98217	19.53175	23.335819	24.89359	23.793304	22.215929
PC 18:0_20:4	99.44627	82.690822	125.14022	125.91229	87.56829	77.669151	100.70658	95.962686	114.3578
PC 18:0_20:5	10.210375	12.921765	13.123048	17.257322	7.3455388	11.340938	10.114149	12.615384	22.421087
PC 18:0_22:4									
PC 18:0_22:5	3.7815329	4.1919711	4.9857778	8.884615	2.4696612	5.6029272	4.3147222	3.5984808	5.0716102
PC 18:0_22:6	64.546072	63.386773	55.412251	76.386949	40.656311	71.295631	72.643411	79.013509	63.536882
PC 18:1_18:1	5.9198401	5.3350813	4.2002282	5.6473619	4.6586815	6.091454	5.0068441	3.8849068	5.5629563
PC 18:1_18:2	70.823563	60.86387	46.617588	60.221491	47.9215	61.238711	62.581128	45.59193	57.787173
PC 18:1_18:3									
PC 18:1_20:0	2.1610547	1.8750072	1.5194017	2.0120436	1.2968441	2.6378534	1.9286398	1.6780902	2.2270545

PC 18:1_20:1		0.4718633	0.4332295			0.7337087			
PC 18:1_20:2			0.5384662	0.3761319	0.3069766	0.8245082			0.4562686
PC 18:1_20:3	4.4822126	4.2987855	3.8056748	3.9522085	4.8178336	6.4704668	4.1484012	3.6547625	6.2330707
PC 18:1_20:4	17.009433	14.391104	21.609525	18.593684	17.741196	22.745374	15.719424	15.139215	24.583303
PC 18:1_20:5			3.5063687	3.3348126	1.825129	3.5122328		2.6963802	5.8428591
PC 18:1_22:5									
PC 18:1_22:6	16.596759	18.282796	15.188555	18.457246	12.387177	24.759821	16.417923	18.772914	26.836021
PC 18:2_18:2	13.904155	11.477931	6.1220212	15.983529	7.2586799	11.714548	12.660191	9.952324	8.4140665
PC 18:2_18:3	1.0345669			1.9130952					
PC 18:2_20:0	10.610847	9.7997463	5.2704961	10.695468	4.7410739	9.0988478	11.196696	8.2020042	6.2650265
PC 18:2_20:1	2.1477282	1.9306927	1.1216934	2.0422742	0.9715457	1.4104702	2.1906743	1.3961018	1.0852024
PC 18:2_20:2	1.0604397	0.806984	0.44922	0.8303167	0.5005576	0.9773994		0.7913684	0.7127922
PC 18:2_20:3	2.1369208	1.811133	1.2668275	1.9786685	1.1834923	2.6199001	2.0755734	1.6922532	2.1042944
PC 18:2_20:4	6.2442814	4.7554584	4.5617017	9.4998349	4.0369491	6.1711988	6.9933756	5.7628693	5.0029924
PC 18:2_20:5		1.7966727							
PC 18:2_22:6				5.2301277				4.6286618	

PC 20:0_20:3				0.9212872			0.8158567		
PC 20:0_20:4	3.7840642	2.8148862	2.6339747	3.9682591	2.232221	3.5966626	3.3142215	2.8090413	2.1184958
PC 20:0_22:6				3.5644498			4.0009885		
PE 16:0_18:1	1.1417238				0.8169335				
PE 16:0_18:2	5.3968251				5.736519				
PE 16:0_20:4	5.3622307				5.2177041				
PE 18:0_18:0	0.8095919				0.8044152			1.8901686	1.145921
PE 18:0_18:1	29.51101				30.83376			107.0333	76.636298
PE 18:0_18:2	109.70253				191.16627				
PE 18:0_20:1	1.5702127							3.1961115	4.6203976
PE 18:0_20:2	2.4810922				3.1289758				
PE 18:0_20:4	42.689284				58.757719				
PE 18:0_22:2									
PE 18:0_22:4	1.1253272								
PE 18:1_18:1	0.5278017				0.5965006				1.042178
PE 18:1_18:2	3.4680553				5.0700923				

PE 18:1_20:4	3.3713824		4.5249556					
PE 18:1_22:0	1.7109477		1.0034041			4.850343		4.540962
PE 18:2_18:2	0.2482566							
PE O-16:0/18:1								
PE O-16:0/18:2	0.7526089							
PE O-16:0/20:4								
PE O-18:0/16:0	0.7979952							1.5469198
PE O-18:0/18:1	1.0921612		0.70847			1.7676861		
PE O-18:0/18:2	3.4293909		4.9686699					
PE O-18:0/20:4	3.1922201		4.0932839					
PE P-16:0/16:0	0.3613248							
PE P-16:0/18:1	0.4907919							
PE P-16:0/18:2	0.9410121		1.5459661					
PE P-16:0/20:4	2.4403893		2.6842913					
PE P-18:0/16:0	0.847506		0.6704668					1.8016999
PE P-18:0/18:1	0.7186229					1.6609995		

PE P-18:0/18:2	2.0318167				2.4634018					
PE P-18:0/20:4	3.6852475				4.9816537					
PE P-18:1/18:1	0.2215604									
PE P-18:1/18:2	0.3486617									
PE P-18:1/20:4	0.6580275									
PG 16:0_18:1	0.1693643	0.2076305		0.1485438	0.1257579	0.1584124	0.1436004	0.1103193		0.1063306
PG 16:0_18:2	0.1667104	0.2485909	0.1008355	0.2222246	0.1591537		0.136307	0.1145947		0.1339546
PG 16:1_18:1	0.1669876	0.1154631	0.1525019	0.1584127	0.0913123	0.1876074	0.127165			
PG 16:1_18:2	0.8902 2	0.6049412	0.4659629	0.6796558	0.3768401	0.552141	0.6018899	0.4583627		0.4270092
PG 17:0_20:0	0.6620726	0.6560983	0.5360821	0.5001487	0.6118173	0.5162376	0.6540045	0.5901231		0.5908622
PG 17:0_22:1										
PG 18:0_18:0	0.1412476									
PG 18:0_18:1		0.2361327	0.1329718	0.1984617		0.1440503	0.1263403	0.1448448		0.1783942
PG 18:0_18:2	0.4766788	1.0065034	0.7426733	1.2034721	0.4691767	0.5468217	0.9249107	0.7326062		0.7064147
PG 18:0_20:0	0.3574497	0.5695422	0.4418251	0.7591724	0.3609737	0.3635171	0.6173787	0.8075624		0.3965746
PG 18:0_20:4	0.6585933	1.9340681	0.9280979	1.8932769	0.8481446	1.3606769	1.2296107	1.1475034		0.8619081

PG 18:0_22:5										
PG 18:0_22:6	0.5980578	1.6406873	0.6072998	1.98718 8	0.79555 85	1.1248437	0.8485643	1.2654647		0.5976936
PG 18:1_18:1		0.0771 6	0.0698412	0.06860 65			0.0584884			0.063299
PG 18:1_18:2	0.6778 49	1.0660 835	0.6199 986	0.96843 84	0.42896 34	0.6668506	0.7417731	0.6582767		0.6091889
PG 18:1_20:0	0.1318 641	0.1905 125	0.1590 766	0.17342 77		0.1507497		0.1272672		0.1321904
PG 18:1_20:3						0.1750502	0.1705753			
PG 18:1_20:4	0.9744 638	1.7990 793	0.8227 09	2.01174 35	0.97045	1.2002853	1.1208615	1.352681		0.8327936
PG 18:1_22:6		0.5853 597		0.84683 39			0.4530363			
PG 18:2_18:2	0.1028 302	0.1038 43	0.0828 01	0.13468 42		0.0861313	0.0774255	0.0721479		0.1044453
PG 18:2_20:0	0.6499 151	1.9118 394	0.9730 957	1.71260 21	0.84931 49	0.7254455	1.1853477	1.0700593		0.7306178
PG 18:2_20:4	0.3462 478	0.5626 845		0.68299 57			0.3453305			
PG 20:0_20:3		0.2651 261		0.27530 35	0.12478 89		0.2740811	0.2407703		0.1407383
PG 20:0_20:4	1.3724 666	5.2870 069	2.5965 476	6.07282 23	2.18752 82	2.6985337	3.5471405	3.7045555		2.3304141
PG 20:0_20:5										
PG 20:0_22:6		0.9771 695	0.4357 807	1.36835 72			0.7867443	0.8571132		
PI 14:0_18:1	0.4482 252	1.2756 011	1.2364 706	1.39501 49	0.81959 86	1.1826703	1.2221545	1.1886726		1.2613442

PI 14:0_18:2		0.5266699	0.4218556	0.64009 44	0.35947 88	0.3387243	0.3915612	0.5107716	
PI 15:0_18:1			0.1938417						
PI 15:0_20:1		0.2791117							
PI 15:0_20:2	0.5740008	0.5286127	0.2876439	0.47029 41		0.4454927	0.5750447	0.3525391	0.319505
PI 15:0_22:0	0.9820666	0.9041702	0.6961 68	1.01529 11	0.89683 55	0.8241674	0.9291576	0.9915339	0.8212537
PI 15:0_22:1	0.3761289	0.2795974	0.3317 28			0.4128059	0.3352466		
PI 15:0_22:2	0.826305	0.531656	0.4874384			0.696532			
PI 15:0_22:4	0.982108	0.906059	0.6675 53	0.80532 08	0.66932 2	0.9731621	1.0075072	1.0675877	0.8831955
PI 15:0_22:6						0.4940149			
PI 16:0_16:0	0.1444704	0.1570128			0.12053 82				
PI 16:0_18:0		0.2409552							
PI 16:0_18:1	2.1493831	1.8736974	1.2283 189	1.77465 2	1.09219 82	1.3733989	1.7975194	1.2234567	1.0993522
PI 16:0_18:2	10.479836	8.4896564	5.2439 698	9.00328 99	4.72326 12	8.0333692	14.100062	7.9239609	5.677306
PI 16:0_20:2							0.4249905		
PI 16:0_20:3	3.1130446	2.643188	2.2393 512	2.45091 49	1.29519 27	3.9908452	4.6399219	2.7629671	2.2355459
PI 16:0_20:4	11.878469	8.9718084	8.4299 02	10.7137 73	6.63514 48	9.6144432	15.833689	12.577918	9.1086581
PI 16:0_20:5									

PI 16:0_22:5				1.01921 46		0.9946676				
PI 16:0_22:6							0.9102115			
PI 17:0_18:1	0.4220 351					0.2616165	0.2042025			0.2404196
PI 17:0_18:2	0.8673 851	0.7736 641		0.55475 64	0.37248 1	0.483138	0.7784413	0.5781269		0.4136156
PI 17:0_20:0	1.2929 791	1.3631 242	1.4172 554	1.60057 26	1.57015 38	1.3015584	1.5081555	1.4538939		0.9434704
PI 17:0_20:1			0.3174 437						0.3503346	
PI 17:0_20:3										
PI 17:0_20:4	1.2258 442	1.5370 822	1.4577 843	1.97657 38	1.12127 75	1.6352356	2.0678273	1.6909443		1.9039578
PI 17:0_22:1	0.8752 914	0.9453 257	0.9792 074	1.06783 15	0.84046 09	1.2229358	1.0465978	1.1893788		1.0004493
PI 17:0_22:2						0.7007332				
PI 18:0_18:0	0.0878 502	0.1047 747		0.10769 35						0.07867
PI 18:0_18:1	2.2844 416	2.0660 663	0.9676 869	1.75772 8	1.14831 75	1.2821469	1.6515716	1.1471548		1.2429826
PI 18:0_18:2	16.695 923	14.857 465	7.0892 136	13.4623 18	7.96331 42	11.366838	17.066721	10.596106		7.7683361
PI 18:0_20:0	0.8575 562	0.7046 491	0.6382 353	0.51903 82		0.803704	0.8243041	0.4993139		0.6241641
PI 18:0_20:2	0.3609 01	0.3741 344		0.29398 12		0.4504558	0.5179457	0.261804		0.1947127
PI 18:0_20:3	9.9148 02	7.1818 413	8.9432 577	8.70483 66	4.88223 96	12.502167	13.319612	9.0781611		10.266198
PI 18:0_20:4	95.968 014	89.879 59	114.18 543	112.124 07	71.7303 13	101.70869	159.02277	154.06226		148.82018

PI 18:0_20:5	1.5031693	1.1322582	1.1923019	1.6284172		1.050388	1.8063181	1.884107	2.2659987
PI 18:0_22:4									
PI 18:0_22:5	1.3738957			1.444313		1.8532739	1.1957084	0.8709617	1.2361753
PI 18:0_22:6	1.6814039	1.2623365	1.2317289	2.4328763	0.7169748	1.6104206	2.6667573	1.6048492	2.3750762
PI 18:1_18:1	0.5491862	0.4843313	0.2500876	0.5201405	0.2941515	0.3880064	0.6036555	0.4267206	0.3183867
PI 18:1_18:2	2.1644557	1.7254539	0.9383775	2.6739068	1.2818394	2.1455805	2.5172453	1.7032011	1.5549687
PI 18:1_20:0									
PI 18:1_20:3	0.5448613			0.384919		0.8656771	0.6811497	0.4512296	
PI 18:1_20:4	3.5896363	2.5445041	2.0676146	3.9527436	1.9346434	4.4410561	4.370778	3.7303713	6.1309085
PI 18:2_18:2	0.2171772			0.2699076		0.1925706	0.3400813		
PI 18:2_20:0									
PI 20:0_20:4	1.1764133			0.9768478			0.8542495	0.9136481	
PS 16:0_18:2								0.9707876	
PS 16:0_22:6									
PS 16:1_18:1				1.9924702					
PS 16:1_18:2	1.5124787	4.8231702	2.7012247	4.1971221	1.0142315	4.0212022	2.911965	3.8071667	
PS 17:0_20:0	1.3133503	0.9197031	0.7848314	1.3257164	1.1983263	1.1586325	1.2849639	1.338248	1.1721793
PS 17:0_20:3	0.9616992	1.6396155	2.5181126	2.103111	1.0171948	2.8804058	1.8831001	1.720817	2.1162176

PS 17:0_22:1					0.68069 8					
PS 18:0_18:0	0.2423 458	0.4776 671		0.66017 52			0.39919			
PS 18:0_18:1	0.6252 377	2.9668 132	1.8563 58	2.45326 66		2.1723169	1.8217894	2.5118505		1.7084713
PS 18:0_18:2	1.3639 859	7.8814 894	5.6443 717	8.62989 99	1.77375 74	4.6626889	5.5173604	6.7734019		4.3249796
PS 18:0_20:0	0.5754 09	2.5796 642	1.2964 207	3.12341 63	0.54515 07	1.1057392	1.7594381	2.2343676		1.1086999
PS 18:0_20:4					3.47812 61					
PS 18:0_22:5										
PS 18:0_22:6	3.3400 542				6.54390 21					
PS 18:1_18:1		1.4338 673		1.07821 54		0.83822	0.7743528	1.1349326		0.880352
PS 18:1_18:2	2.0754 907	9.7754 247	5.4270 699	7.17236 33	1.82656 95	4.9343449	5.0908436	9.3346547		4.1991042
PS 18:1_20:0	0.8990 573	4.4432 149	3.5763 001	5.22269 95	1.18521 59	4.182646	3.1324792	5.6846814		3.0396276
PS 18:1_20:4					4.66294 14					
PS 18:1_22:5										
PS 18:1_22:6	3.3881 406				7.01054 77					
PS 18:2_18:2	0.3737 647		0.7724 896	1.37729 76						
PS 18:2_20:0	1.8509 246	11.399 639	6.0486 942	10.6356 4	2.90752 63	6.2183357	8.6595042	10.769662		7.2129034

PS 20:0_20:4	1.7598494				4.1127409				
PS 20:0_22:6					4.045929				
SM d18:1/14:0	0.9993765	1.0398783	1.1385214	0.9328712	0.6592949	1.0906381	1.0205519	0.8668596	1.3147461
SM d18:1/16:0	34.869876	38.191305	29.739705	34.497489	31.143308	28.386125	38.519616	34.478444	39.957699
SM d18:1/18:0	3.7939545	4.01767	4.1169515	3.5291281	4.0380513	3.2350868	3.3389482	2.7969878	5.2054917
SM d18:1/18:1	1.8001195	1.8276435	1.7695944	1.5144783	1.6220462	1.5588204	1.4544809	1.1748554	2.0878258
SM d18:1/20:0	37.65012	34.622669	28.980684	35.70145	25.910534	36.282235	44.835776	36.61861	32.114441
SM d18:1/20:1	1.8660219	1.9115481	2.0143407	2.0464032	1.1826062	2.1776245	1.9143468	1.7028057	1.8904184
SM d18:1/22:0	44.227358	45.098631	30.438054	48.911633	29.587371	36.580506	52.779384	45.550604	34.741739
SM d18:1/22:1	14.008544	14.273929	9.1861414	15.077161	8.8151413	13.802555	14.825387	12.220575	10.217126
SM d18:1/24:0	13.475545	13.549401	10.226827	15.186201	7.9832295	15.069362	16.356129	13.810742	11.636069
SM d18:1/24:1	23.760403	24.693226	35.476848	26.706506	32.492031	33.130793	30.726971	24.512321	41.862909
SM d18:1/26:0	2.0671055	2.008818	2.7703769	1.7248993	1.2274737	2.9296086	2.0599659	1.6178563	2.8122598
SM d18:1/26:1	3.4291923	2.9535914	3.9041673	2.9277254	2.0687725	3.7602491	3.373527	2.7283356	3.9898355
TG 36:0-FA12:0				0.0654359					
TG 38:0-FA12:0		0.0525861							

TG 40:0-FA12:0		0.1139181	0.0685049								
TG 40:0-FA16:0						0.0763857			0.0396226		
TG 42:0-FA16:0	0.1297091	0.1178644	0.1113497		0.10070 35	0.074922			0.044709	0.0768393	
TG 42:1-FA16:0	0.2194 44	0.2723216	0.2214168	0.14078 11	0.14453 29	0.1847786			0.065495	0.1571259	
TG 42:1-FA16:1		0.0436 88									
TG 42:1-FA18:1	0.1294847	0.161164	0.0920238	0.09546 78	0.08377 31	0.0945976					
TG 42:2-FA18:2	0.1504308	0.1761552	0.1319307	0.14445 96	0.07891 14	0.1555128			0.0494406	0.1136016	
TG 44:0-FA12:0		0.0759014									
TG 44:0-FA14:0											
TG 44:0-FA16:0	0.1373076	0.1123753	0.0992517	0.07809 75	0.12166 46	0.0928709			0.0420655	0.091487	
TG 44:0-FA18:0											
TG 44:1-FA14:0											
TG 44:1-FA16:0	0.3917805	0.3258881	0.3314145	0.24487 64	0.20230 17	0.1949871	0.0718364		0.0971629	0.2177894	
TG 44:1-FA18:1	0.2330254	0.1734814	0.2119021	0.12013 53	0.14488 9	0.1076196				0.1194862	
TG 44:2-FA16:0	0.5321959	0.4438073	0.4183844	0.40560 77	0.25303 1	0.290443	0.1313924		0.1340969	0.3027262	
TG 44:2-FA16:1											

TG 44:2-FA18:1	0.1002235	0.1426105	0.1151046	0.0983322	0.1190082	0.1139609				
TG 44:2-FA18:2	0.3113861	0.2196385	0.1821682	0.2378834	0.0852946	0.1492738	0.0753891	0.072418		0.1546914
TG 44:3-FA18:2	0.1762771	0.1339955	0.1349222	0.1713102	0.1001802	0.1123487		0.0628604		0.1211179
TG 45:0-FA16:0	0.1764751	0.1891155	0.1723448	0.1051783	0.0946664	0.0945794		0.0393235		0.1008726
TG 45:1-FA16:0	0.3422002	0.3405265	0.3519845	0.3022069	0.1470092	0.2214947				0.2685366
TG 45:1-FA18:1	0.1427185	0.1747835	0.1244083	0.1054794	0.0867114	0.1103588				0.1001569
TG 46:0-FA12:0		0.0188204								
TG 46:0-FA14:0	0.1441458	0.3416178	0.1174405	0.0959742	0.2505749	0.0785441				0.079324
TG 46:0-FA16:0	0.3583508	0.6770417	0.2391886	0.2161433	0.5690048	0.2046641	0.1022079	0.1386451		0.2064385
TG 46:1-FA12:0	0.1812865	0.3353912	0.2269384	0.1862389	0.2089272	0.134479	0.0808734	0.0938203		0.1479049
TG 46:1-FA14:0	0.1042023	0.2251789	0.0979177	0.0741635	0.4163679					
TG 46:1-FA14:1	0.0671574	0.1084214	0.0918377							
TG 46:1-FA16:0	0.459347	0.4077429	0.3216662	0.3290226	0.4733926	0.1807162	0.0955533	0.1465118		0.1784064
TG 46:1-FA16:1	0.0760867	0.1620882			0.2288306			0.0553183		0.0738789
TG 46:1-FA18:0	0.0757591	0.0631355								
TG 46:1-FA18:1	0.1268022	0.1267111	0.0987503	0.0899712	0.1355713					0.066477

TG 46:2-FA12:0	0.4043214	0.4626078	0.3722513	0.5443101	0.269167	0.297199	0.186059	0.310203	0.2659397
TG 46:2-FA14:0	0.0915075	0.1860228	0.0557306	0.0924357	0.2392594				
TG 46:2-FA14:1					0.0861406				
TG 46:2-FA16:0	0.2975112	0.3449468	0.3267521	0.2874364	0.2804474	0.2192219	0.1130917	0.1939097	0.2220612
TG 46:2-FA16:1		0.071748			0.1736609				
TG 46:2-FA18:1	0.2158867	0.2517339	0.1674785	0.1460454	0.210925	0.1456551		0.0737394	0.1603307
TG 46:2-FA18:2	0.1714222	0.2040687	0.1297138	0.1808282	0.19879	0.0906908	0.0943251	0.1199915	0.0954149
TG 46:3-FA12:0	0.0765029	0.1170348	0.1022393	0.1107576		0.0776156	0.0724944		0.0586901
TG 46:3-FA14:1									
TG 46:3-FA16:0	0.4229518	0.3914254	0.3373896	0.385865	0.2152134	0.2567284	0.1021225	0.1811726	0.2435641
TG 46:3-FA16:1					0.0742999	0.0663381			
TG 46:3-FA18:1	0.2720723	0.2370481	0.201871	0.1544879	0.1731438	0.144012	0.0634237	0.0618317	0.1519463
TG 46:3-FA18:2	0.3226704	0.2466315	0.2307267	0.2945007	0.1500583	0.1672243	0.0862868	0.124388	0.2131068
TG 46:3-FA18:3				0.0589516					
TG 46:4-FA18:2	0.2654947	0.2664548	0.1456473	0.2523443	0.1459939	0.1507081	0.0910469	0.0936337	0.1437477
TG 47:0-FA14:0		0.0551229							

TG 47:0-FA15:0	0.2895062	0.7072061	0.1731099	0.12386 03	0.30698 52	0.1393496	0.1274257	0.1246439	0.2063207
TG 47:0-FA16:0	0.7308895	1.6623 77	0.3646042	0.40374 51	0.72944 04	0.3785637	0.2800475	0.2555864	0.3750349
TG 47:0-FA17:0	0.0689932								
TG 47:1-FA14:0		0.0911324							
TG 47:1-FA15:0	0.1256706	0.2386102	0.0810789		0.12473 02	0.0662982			0.0706723
TG 47:1-FA16:0	0.3633394	0.5626882	0.2624998	0.29667 51	0.25909 86	0.1936208	0.1063523	0.1304063	0.1712996
TG 47:1-FA16:1	0.1383728	0.2269611	0.1015693	0.08354 77	0.13929 8			0.0600491	0.0790713
TG 47:1-FA17:0		0.0565174							
TG 47:1-FA18:1	0.1261135	0.1575263	0.0908777	0.08062 31	0.09947 35	0.0705052	0.0553943		0.1076564
TG 47:2-FA14:0	0.0746359	0.1340601			0.07367 06				
TG 47:2-FA15:0	0.0820559	0.1648785			0.08731 34				
TG 47:2-FA16:1		0.0708823	0.0655 11		0.07230 64				
TG 47:2-FA18:1	0.1857605	0.1494693	0.1241262	0.09922 44	0.13479	0.1144508		0.0523303	0.1053969
TG 47:2-FA18:2	0.2106392	0.2912339	0.1846377	0.19519 55		0.1080924	0.0845058	0.0947603	0.1375082
TG 48:0-FA14:0	0.0552307	0.2054076	0.0674788	0.04747 66	0.05587 11	0.0420689	0.0541532	0.0483308	0.0507646
TG 48:0-FA16:0	3.9485906	8.2115884	2.4008179	2.10537 26	7.67179 47	2.272737	0.8635929	1.1643249	2.1744401

TG 48:0-FA18:0	0.0862898	0.1758155	0.0455301		0.1091294	0.0657765		0.052545	
TG 48:1-FA12:0		0.099729	0.063419	0.0424967	0.0592004	0.0559639		0.0389622	0.053434
TG 48:1-FA14:0	0.7162274	1.6485116	0.6205012	0.600609	2.4734004	0.4256515	0.177728	0.3652272	0.4404299
TG 48:1-FA14:1		0.0414524	0.0311841		0.0409787	0.0320124			0.0314268
TG 48:1-FA16:0	1.9452686	4.0433162	1.7451253	1.502836	6.2062051	1.1208809	0.4403927	1.1175672	1.260267
TG 48:1-FA16:1	0.71905	1.3725688	0.6386837	0.4377349	1.8270001	0.4261376	0.1582044	0.3430394	0.5396712
TG 48:1-FA18:0		0.1079671	0.0651113	0.0415149	0.057967				
TG 48:1-FA18:1	0.8307162	1.5543967	0.6223605	0.6475122	2.4873715	0.3643414	0.2000306	0.3570876	0.4422836
TG 48:2-FA12:0	0.1732923	0.36279	0.245643	0.3316936	0.2227908	0.1714558	0.1901899	0.1739268	0.1632616
TG 48:2-FA14:0	1.5957487	3.0673988	1.2734297	1.9851866	4.2413878	0.9064424	0.5070281	0.9250909	0.8359406
TG 48:2-FA14:1	0.3602779	0.4806583	0.4179452	0.4074977	0.4385837	0.3556391	0.1144468	0.1520788	0.3353055
TG 48:2-FA16:0	1.852795	3.2039314	1.4770517	2.0594949	4.8651635	0.9501145	0.4974965	1.0969339	0.8813328
TG 48:2-FA16:1	0.5552692	1.0425732	0.6406021	0.4972223	3.6958512	0.2143962	0.0848409	0.2487348	0.3954042
TG 48:2-FA18:0					0.0469238				
TG 48:2-FA18:1	0.3845697	0.5588091	0.3943248	0.3832979	1.5124208	0.2249108	0.0822211	0.1691922	0.2462326
TG 48:2-FA18:2	1.4962061	2.453902	0.9516671	1.6199818	2.8868355	0.6219341	0.4568661	0.8041091	0.5925804

TG 48:3-FA12:0	0.2349571	0.2557866	0.2463052	0.36669 06	0.26286 66	0.156383	0.1654355	0.1583307	0.189753
TG 48:3-FA14:0	0.3589712	0.6660057	0.3195223	0.55599 95	1.53615 32	0.1770942	0.0909576	0.1447732	0.178992
TG 48:3-FA14:1	0.7436727	0.8604336	0.7688 73	1.00705 61	0.62504 56	0.595707	0.3221858	0.4442867	0.5307333
TG 48:3-FA16:0	0.5028334	0.6069152	0.4300581	0.62279 49	0.71225 61	0.2510869	0.1496551	0.2571958	0.2877473
TG 48:3-FA16:1	0.3901132	0.7441 17	0.3247397	0.45495 09	1.71673 65	0.1355435	0.0971634	0.1766788	0.1859249
TG 48:3-FA18:1	0.2685913	0.2393855	0.2571535	0.30088 49	0.33714 38	0.1389921	0.1078954	0.1418549	0.1995268
TG 48:3-FA18:2	0.5645921	0.7872708	0.5083136	0.78554 89	1.44024 71	0.2892041	0.2102336	0.3654474	0.3457185
TG 48:3-FA18:3	0.139047	0.2153217	0.0962672	0.15963 2	0.25305 07	0.071502	0.0596925		0.0914637
TG 48:4-FA12:0	0.1743581	0.2056021	0.1646782	0.36173	0.16769 02	0.1541717	0.2074258	0.183994	0.1658474
TG 48:4-FA14:0				0.09692 29	0.09039 55				
TG 48:4-FA14:1	0.1154936	0.110589	0.1139127	0.13318 24	0.09694 59	0.0780187			0.1010879
TG 48:4-FA16:0	0.2565076	0.2756937	0.2180025	0.31240 32	0.19651 2	0.1404336	0.1058887	0.1428206	0.1845644
TG 48:4-FA16:1	0.0855025	0.0981283	0.0731903	0.08403 83	0.16769 02				
TG 48:4-FA18:1	0.179982	0.1551928	0.1491224	0.17114 48	0.14323 63	0.0966586	0.0547356		0.1076921
TG 48:4-FA18:2	0.3744723	0.2923325	0.2994386	0.66234 28	0.27885 2	0.1893407	0.1589458	0.2235882	0.2129653
TG 48:4-FA18:3			0.0791365	0.08497 45	0.13389 23				

TG 48:5-FA18:2	0.2452278	0.2102118	0.1207278	0.2580663	0.14013 65	0.1188669	0.0671623	0.0744692	0.1152688
TG 48:5-FA18:3				0.0706806					
TG 49:0-FA15:0	0.1823326	0.3637087	0.0612 99	0.0701439	0.15029 33	0.1001131	0.0826393	0.0440121	0.1190868
TG 49:0-FA16:0	0.8264445	2.1964449	0.5057289	0.7335947	1.22178 91	0.4807038	0.3715407	0.3350866	0.5306922
TG 49:0-FA17:0	0.2810993	0.7796322	0.2190268	0.2098807	0.44218 93	0.2275348	0.1591298	0.1280073	0.2790563
TG 49:0-FA18:0	0.19965	0.5100091	0.1562 04	0.1706235	0.19623 23	0.1607143	0.1354145	0.1230254	0.1679639
TG 49:1-FA14:0	0.1089882	0.1256527	0.0680693	0.0655194	0.09335 03	0.0597432			
TG 49:1-FA15:0	0.989536	1.8586152	0.4895318	0.5562993	1.10855 65	0.4088797	0.300707	0.3444821	0.5197119
TG 49:1-FA16:0	1.3687916	2.701363	0.6487933	0.7714647	1.84979 34	0.5934146	0.44824	0.5215411	0.6761129
TG 49:1-FA16:1	0.1723497	0.3174026	0.1176754	0.1124368	0.16721 65		0.0987966	0.0965095	0.1029511
TG 49:1-FA17:0	0.1266779	0.2328488	0.112335	0.0864908	0.18003 49				
TG 49:1-FA18:1	1.250259	2.3768939	0.4224691	0.5680281	1.33180 16	0.3729231	0.4003544	0.447332	0.5145094
TG 49:2-FA14:0	0.1357355	0.2569424	0.1380895	0.1331211	0.23334 85	0.1064209		0.0723419	0.0799252
TG 49:2-FA15:0	2.1015253	3.9108146	0.8945485	1.3591402	2.41032 55	0.6391225	0.5890924	0.8002866	0.9705412
TG 49:2-FA16:0	2.1492294	4.1342668	0.7775787	1.4222534	2.62415 71	0.7821387	0.677355	0.7913746	0.9627218
TG 49:2-FA16:1	0.2330277	0.412197	0.1555394	0.1734692	0.58379 31	0.0862098		0.0999663	0.111738

TG 49:2-FA17:0	0.1255553	0.1344032		0.0910828	0.127281				
TG 49:2-FA18:1	0.3717967	0.5486727	0.2378246	0.2795934	0.5678498	0.1427549	0.0929981	0.124992	0.1989166
TG 49:2-FA18:2	2.5505657	4.376715	0.6168179	1.5378502	2.5993322	0.6898973	0.776944	0.8223751	0.8898396
TG 49:3-FA15:0	0.3816416	0.6303444	0.1570056	0.3010958	0.5301784		0.0880526	0.1562116	0.1897655
TG 49:3-FA16:0	0.4596661	0.5814927	0.2427742	0.3626458	0.2982254	0.2100325	0.1513887	0.1718328	0.1700299
TG 49:3-FA16:1	0.312098	0.5310651	0.1753786	0.2894513	0.478486	0.1056665	0.0895974	0.1470993	0.1411855
TG 49:3-FA18:2	0.6038418	0.8178718	0.2015184	0.4657836	0.6759775	0.1606131	0.1746377	0.2095839	0.244418
TG 49:3-FA18:3	0.183188	0.3246273	0.0652334	0.13133	0.1524263			0.0685139	0.0543329
TG 50:0-FA14:0		0.1157022			0.0648073				
TG 50:0-FA16:0	1.7385367	4.2037095	1.2334604	1.0231822	2.9272643	1.3540954	0.4953029	0.5971833	1.2372507
TG 50:0-FA18:0	0.8952633	2.3917683	0.7721041	0.6122121	1.7408396	0.7612028	0.2798814	0.3849983	0.6119434
TG 50:1-FA14:0	0.2132421	0.4620856	0.1428993	0.1069784	0.2484355	0.1223472	0.0550094	0.0945309	0.111029
TG 50:1-FA16:0	20.206055	32.806106	12.624205	13.738692	47.559194	9.4640128	4.854393	9.5963082	10.790049
TG 50:1-FA16:1	0.1661512	0.5638205	0.2682506	0.1793012	0.2782505	0.1085254	0.0657543	0.1407601	0.1647485
TG 50:1-FA18:0	0.4426579	1.0055325	0.3352642	0.2186019	0.7266469	0.228732	0.135257	0.1710866	0.2008469
TG 50:1-FA18:1	10.475148	17.141351	6.1954016	6.9612948	23.788846	4.6625948	2.6620547	4.8351493	5.8782542

TG 50:1-FA20:1	0.2131727	0.3757233	0.0804013	0.11185 41	0.11754 38	0.0852865				
TG 50:2-FA14:0	1.2172966	2.7123375	0.8400772	1.22360 28	6.42479	0.5991186	0.2398934	0.4930645		0.5797633
TG 50:2-FA14:1	0.1303884	0.1494 73	0.1008407	0.10998	0.04339 73					0.0999695
TG 50:2-FA16:0	51.014507	76.707291	28.266371	45.8020 92	107.171 85	22.235409	13.746652	28.447751		26.279952
TG 50:2-FA16:1	5.9961049	9.5039403	5.1336 41	5.03856 75	26.7816 73	2.8437069	0.992189	3.1233334		4.0710917
TG 50:2-FA18:0	0.3049174	0.7307 76	0.1772087	0.20658 86	0.61808 77	0.1710956	0.0942212	0.1448557		0.1496846
TG 50:2-FA18:1	7.0665506	12.389412	6.0243903	6.17203 82	35.4151 19	3.2052179	1.1576572	3.6213712		4.6669085
TG 50:2-FA18:2	23.71183	35.450136	10.307431	20.6969 22	39.2548 41	9.3566721	6.2274702	11.902799		11.061987
TG 50:2-FA20:2					0.06164					
TG 50:3-FA14:0	3.623682	5.7764403	2.3403926	5.25748 5	11.5484 97	1.2332112	0.7154104	1.5647695		1.6117622
TG 50:3-FA14:1	0.2126432	0.2465451	0.166075	0.21869 82	0.25869 33	0.162391	0.0771609	0.0748739		0.1302865
TG 50:3-FA16:0	14.719169	18.612614	10.081868	17.6750 96	35.8533 47	5.4036603	3.0962856	8.8005992		8.4620613
TG 50:3-FA16:1	12.73435	16.450715	9.2212885	14.9502 69	36.8725 61	4.7890362	2.676799	7.1959101		7.7457749
TG 50:3-FA18:0		0.1131776	0.077899	0.07357 1	0.11814 43					
TG 50:3-FA18:1	4.2126352	6.60748	2.92012 48	5.89378 59	14.9479 95	1.4942199	0.8464165	1.8974084		2.1132737
TG 50:3-FA18:2	13.845912	18.027907	9.272558	17.1976 72	36.6916 74	4.726714	2.8172297	7.6350893		7.5313793

TG 50:3-FA18:3	1.3018442	1.9548396	0.5221239	1.33547 26	2.00317 87	0.4490515	0.320034	0.6493627	0.5351026
TG 50:3-FA20:3	0.0699712	0.1108695		0.07041 34	0.11052 78				
TG 50:4-FA14:0	2.5079 66	3.0932 905	1.3464 545	4.93067 91	4.95044 36	0.7538583	0.6453794	1.2036131	0.9146527
TG 50:4-FA14:1	0.2624 027	0.2326 347	0.2679 361	0.41377 57	0.28143 95	0.1791654	0.1290964	0.1368892	0.2655566
TG 50:4-FA16:0	1.4708 135	1.4087 594	0.7432 73	2.07730 7	1.95918 48	0.4239849	0.3444892	0.6185209	0.6505588
TG 50:4-FA16:1	1.4816 865	1.8886 702	1.0163 863	1.84556 21	5.25983 66	0.3618434	0.2122738	0.5899408	0.7978607
TG 50:4-FA18:1	0.3690 337	0.4460 105	0.2629 019	0.55711 59	0.79790 76	0.1712636	0.0942686	0.174553	0.1909426
TG 50:4-FA18:2	4.5425 678	5.3339 688	2.2806 199	8.54781 92	8.42274 17	1.1895423	1.0901854	2.1403263	1.9109972
TG 50:4-FA18:3	0.6606 496	0.9907 924	0.4597 716	1.00179 5	1.83332 24	0.1544803	0.1101395	0.3333869	0.3121793
TG 50:4-FA20:3									
TG 50:4-FA20:4	0.0646 801	0.1261 448			0.19858 48				
TG 50:5-FA14:0	0.3223 328	0.4364 574	0.1652 044	0.68437 48	0.56538 97	0.0780532	0.0860384	0.1329006	0.1193538
TG 50:5-FA16:0	0.2571 804	0.3584 048	0.1539 769	0.40019 95	0.34700 46	0.1701561	0.1093047	0.1671126	0.1626621
TG 50:5-FA16:1	0.1817 408	0.1959 28	0.1267 102	0.27913 07	0.42739 18	0.0867258		0.0664849	0.0844002
TG 50:5-FA18:1	0.1560 228	0.1656 627	0.1202 945	0.19824 12	0.20900 66	0.087091	0.0671443	0.0747955	0.1082261
TG 50:5-FA18:2	0.4834 991	0.5224 745	0.3031 421	0.99040 97	0.65917 47	0.1592286	0.1542758	0.1855344	0.2194404

TG 50:5-FA18:3	0.3549089	0.4667227	0.2133222	0.8491628	0.7020479	0.0921028	0.0824123	0.1486907	0.1718694
TG 50:5-FA20:4					0.0720192				
TG 50:5-FA20:5	0.0762016	0.1162824		0.1309808	0.1205807				
TG 51:0-FA16:0	1.0147801	2.0203258	0.6167036	0.8232608	1.1532156	0.5438967	0.5148612	0.4024885	0.4786144
TG 51:0-FA17:0	0.1364161	0.3671694	0.0874393	0.0709661	0.1458347	0.0911394	0.0623271	0.0555239	0.1452181
TG 51:0-FA18:0	0.2197797	0.5421866	0.1618422	0.1937852	0.2894602	0.1668634	0.1463227	0.1140164	0.2000654
TG 51:1-FA15:0	0.4281813	1.0258313	0.1893054	0.2059613	0.2735381	0.1736771	0.1622362	0.1605917	0.2157684
TG 51:1-FA16:0	1.8936352	3.7927685	1.0097799	1.2289803	2.4305617	0.9312853	0.5728276	0.7071291	1.0107052
TG 51:1-FA17:0	1.137013	2.257139	0.684332	0.738063	1.544197	0.619349	0.291744	0.447501	0.612309
TG 51:1-FA18:0	0.3552161	0.8276 26	0.1869367	0.2257725	0.2900804	0.1732907	0.178494	0.1457966	0.2001548
TG 51:1-FA18:1	1.3835332	2.8066154	0.5820797	0.9003731	1.7015496	0.5403002	0.5322165	0.4021909	0.5359637
TG 51:2-FA15:0	1.2621304	2.2112927	0.4706515	0.8758101	2.1742203	0.3931735	0.3431045	0.4752969	0.5493983
TG 51:2-FA16:0	4.8165395	7.4225009	2.8506277	3.3984852	6.7275964	2.2361548	1.2539938	1.9430639	2.878816
TG 51:2-FA16:1	0.3058574	0.5537085	0.2843025	0.2028671	0.6015535	0.1746657	0.0805017	0.1515742	0.2370841
TG 51:2-FA17:0	2.3531 48	4.3125352	1.1705 69	2.0832028	3.2444468	1.098569	0.7219494	1.0092894	1.2391149
TG 51:2-FA18:1	3.0857243	4.9010568	1.3589471	2.2085953	6.5262532	1.0361716	0.8522748	1.0976505	1.5048024

TG 51:2-FA18:2	3.1321982	5.1468995	0.8307908	2.15952 7	3.51812 62	0.9368534	1.0398585	1.0405638	1.0774503
TG 51:3-FA15:0	3.1564492	4.3443 25	0.9305341	2.89554 95	4.22597 18	0.7711559	0.6658132	1.0814273	1.1893901
TG 51:3-FA16:1	0.7591537	1.0249801	0.5824078	0.54117 4	1.23946 67	0.3074452	0.143291	0.2157391	0.5180954
TG 51:3-FA17:0	0.406029	0.6722363	0.2061497	0.37948 89	0.61151 43	0.1469259		0.1305047	0.234505
TG 51:3-FA18:2	4.8184627	6.5154981	1.6327827	4.27200 53	6.65258 82	1.2256326	1.1127957	1.6562258	1.8284447
TG 51:3-FA18:3	0.186385	0.3792968	0.0751343	0.12291 86	0.18146 75	0.0538236	0.0820977	0.0586404	0.105916
TG 51:4-FA15:0	3.1605252	3.6937731	0.6929097	3.80736 03	2.83706 31	0.55594	0.7233956	1.0663561	1.0541799
TG 51:4-FA16:1	0.3209095	0.3738898	0.198145	0.34024 67	0.55439 98	0.1168737	0.0533625	0.1198153	0.1769904
TG 51:4-FA18:2	5.7316934	6.7045284	1.3817138	6.49891 42	5.24845 8	1.1092437	1.4094339	1.9270331	1.9091655
TG 51:4-FA18:3	0.4129971	0.5638143	0.1324107	0.46481 69	0.49589 72	0.1033318	0.1054104	0.1202322	0.1449943
TG 51:4-FA20:4	0.1231599	0.2965333		0.11460 94	0.24534 56				0.0800788
TG 51:5-FA18:2	0.5757298	0.6025553	0.1605176	0.69899 72	0.41330 37	0.1294699	0.1590393	0.1889852	0.1800415
TG 51:5-FA18:3	0.4005831	0.5187775		0.59695 38	0.40652 82	0.0797761	0.0789669	0.1424043	0.113302
TG 52:0-FA16:0	0.7667196	1.8660358	0.4970621	0.60895 55	1.00932 48	0.4829108	0.2772335	0.3613799	0.4128438
TG 52:0-FA18:0	0.5552973	1.2997236	0.5615337	0.36839 41	1.05647 46	0.5374302	0.198423	0.2986512	0.5714714
TG 52:0-FA20:0	1.5642292	2.7501728	1.0154325	1.10549 36	1.89849 71	0.8362214	0.4311252	0.682129	0.974878

TG 52:1-FA16:0	6.6736361	12.911136	3.2718375	3.7852997	9.0933697	2.7545041	1.4604231	2.2041307	2.7537787
TG 52:1-FA16:1	0.1549066	0.2577941	0.0831889	0.1135259	0.1148525	0.0671226	0.0361242	0.0607646	0.0864084
TG 52:1-FA18:0	3.9345866	8.1756393	2.1515479	2.5624653	7.7301599	1.9965096	1.2917519	1.7120894	1.7012358
TG 52:1-FA18:1	3.3887241	6.7729238	1.8663996	2.2937059	7.8622235	1.6569039	1.2384972	1.6358227	1.6538934
TG 52:1-FA20:0	0.7973263	1.3744222	0.7153314	0.7888438	1.4533446	0.3864153	0.1690192	0.4418918	0.5898947
TG 52:1-FA20:1	2.3136221	4.1605576	0.8004408	1.0860512	1.7306041	0.7130532	0.3428215	0.4859449	0.6624744
TG 52:2-FA14:0	0.23131	0.4331976	0.1362914	0.1752187	0.2115223	0.1176631		0.0838903	0.1394508
TG 52:2-FA16:0	51.347742	72.601579	32.698586	41.531911	156.48854	25.763981	11.036686	24.918562	33.087643
TG 52:2-FA16:1	1.04801	1.7831668	0.6319507	0.6070308	1.6604339	0.3954152	0.1861579	0.379815	0.4524465
TG 52:2-FA18:0	8.8777699	18.15017	4.3728922	7.1789971	15.421554	4.291041	3.3170591	4.3863876	4.1429678
TG 52:2-FA18:1	78.840597	105.45099	52.709204	62.862329	253.78758	39.265478	14.277924	35.306177	52.050357
TG 52:2-FA18:2	7.2875589	15.50435	3.3030745	6.0993638	12.108616	3.2718052	2.9500625	3.6872417	3.3148391
TG 52:2-FA20:0	0.4149579	0.5146112	0.2873244	0.5373785	0.4940052	0.1783756	0.1241431	0.1943127	0.1878847
TG 52:2-FA20:1	0.976173	1.4958016	0.5223072	0.4680225	0.7762603	0.3593247	0.1385536	0.2575165	0.3360672
TG 52:2-FA20:2	0.2128131	0.3757847	0.1302183	0.1724958	0.3733905	0.1431585	0.0767898	0.1343119	0.1099008
TG 52:3-FA14:0	0.353947	0.6282222	0.185375	0.2573695	0.3666779	0.1301628	0.0685963	0.0787219	0.1533257

TG 52:3-FA16:0	181.04128	180.14552	95.709051	196.77608	323.61873	65.853039	42.294144	89.2412	99.862297
TG 52:3-FA16:1	4.8456081	7.4150673	3.4103961	4.3492524	23.221432	2.0021662	0.9314868	1.706596	3.3652718
TG 52:3-FA18:0	1.3141802	2.4687484	0.8346093	1.2972385	3.1247535	0.6062168	0.4008462	0.6970274	0.8490305
TG 52:3-FA18:1	169.58836	174.78669	90.370866	182.09429	322.53208	61.303354	38.844853	83.368946	93.812569
TG 52:3-FA18:2	155.66159	157.90813	78.432066	164.18036	269.5879	55.053324	34.817633	74.977729	83.461188
TG 52:3-FA18:3	0.4461283	0.7340743	0.191644	0.3321944	0.5919066	0.1554355	0.1240236	0.1951167	0.2011448
TG 52:3-FA20:0	0.4609591	0.3994232	0.2261416	0.5026327	0.5923641	0.1598806	0.0953997	0.2047656	0.268778
TG 52:3-FA20:1	0.5327219	0.8965884	0.286492	0.5070502	0.4956281	0.150281	0.0951005	0.1677819	0.1960536
TG 52:3-FA20:2	0.3439007	0.4708301	0.1606374	0.2791688	0.7843106	0.112975	0.0709968	0.142475	0.1254268
TG 52:3-FA20:3	0.2892428	0.5333645	0.1260413	0.2164418	0.8098528	0.1204244	0.1152723	0.1449751	0.167794
TG 52:3-FA22:1	0.0987505	0.0727133		0.1083324	0.2058698			0.0714696	0.0734819
TG 52:4-FA14:0	0.1573287	0.2790948	0.1010939	0.1864421	0.4482268	0.063036	0.0705714	0.0766724	
TG 52:4-FA16:0	185.92391	142.83765	69.920523	257.26482	187.13792	47.397475	48.273845	89.631471	77.960762
TG 52:4-FA16:1	14.264977	16.070153	7.6150828	17.092676	40.883483	3.7306677	2.2217436	4.7611071	7.7469231
TG 52:4-FA18:0	0.2580136	0.3936901	0.1255007	0.2344724	0.3148492	0.1457625	0.1098372	0.1285969	0.1111383
TG 52:4-FA18:1	24.106637	24.206976	11.852289	30.81756	52.179465	6.3919623	4.5055092	9.564145	11.551861

TG 52:4-FA18:2	295.97564	231.66394	111.6886	403.78464	307.82381	74.914788	76.726134	141.66353	121.63261
TG 52:4-FA18:3	16.038892	15.533379	6.9577627	21.128513	24.344823	4.1830855	3.7935009	7.4287721	6.9313628
TG 52:4-FA20:0	1.1737376	0.9894146	0.4644823	1.7258333	1.184534	0.3530299	0.3749383	0.5964959	0.5841467
TG 52:4-FA20:2	0.2617765	0.3338533	0.1373847	0.3116947	0.3948818	0.1044135	0.08033	0.1096558	0.1149723
TG 52:4-FA20:3	0.4842615	0.636611	0.2183272	0.5335679	1.3507033	0.1437358	0.1212525	0.2360233	0.1755522
TG 52:4-FA20:4	0.970309	1.880009	0.4297368	0.8431304	3.2612035	0.3705178	0.3952276	0.6016983	0.4521094
TG 52:4-FA22:1	0.2526431	0.1988609	0.1116071	0.3338102	0.3180693	0.0672598	0.0865242	0.1211843	0.1334744
TG 52:4-FA22:4	0.1501178	0.0961093		0.1289064	0.1405898				
TG 52:5-FA14:0	0.1423183	0.2945493	0.0771618	0.1742816	0.4657855		0.0671772	0.0727901	0.067626
TG 52:5-FA16:0	17.281363	14.385162	6.9020845	32.478984	19.03565	3.7027739	4.2187874	8.335151	6.3216119
TG 52:5-FA16:1	12.812018	10.794593	5.1566616	20.165798	19.407056	2.4168817	2.2503708	4.1506541	5.4321902
TG 52:5-FA18:1	2.3129102	2.1837065	1.020457	3.6314217	4.0795454	0.4955626	0.4642747	0.8350168	1.0427918
TG 52:5-FA18:2	30.945092	25.564074	11.890553	50.901901	39.746181	6.0951991	5.9580736	11.94356	12.246739
TG 52:5-FA18:3	21.349343	16.945245	8.0589736	35.975041	23.009627	3.8960544	4.8429374	9.4114437	7.7788574
TG 52:5-FA20:3	0.1645813	0.2836253	0.0713106	0.2225641	0.4590222	0.0698689		0.0777417	
TG 52:5-FA20:4	0.4674603	0.9588979	0.2895049	0.5087024	1.8919094	0.1752022	0.1622974	0.3057629	0.2017303

TG 52:5-FA20:5	0.8289374	1.3730434	0.441899	1.3083937	1.2697554	0.4099726	0.4315259	0.6623686	0.5309
TG 52:5-FA22:5	0.4219201	0.3734419	0.197869	0.7888478	0.5648389	0.1358156	0.1337204	0.1797918	0.149192
TG 52:6-FA14:0	0.1963823	0.4007413	0.185353	0.3697224	0.6343868	0.1660321	0.1638423	0.1345684	0.1553651
TG 52:6-FA16:0	1.3458147	1.2868228	0.667860	3.2633647	1.6720362	0.2917484	0.4675045	0.8310068	0.6163659
TG 52:6-FA16:1	1.6973041	1.4726429	0.708607	3.2827911	2.8444645	0.3288712	0.3489234	0.6109406	0.6089058
TG 52:6-FA18:1	0.3379649	0.3225115	0.137940	0.5467655	0.5188611	0.1229481	0.1122953	0.1499241	0.156928
TG 52:6-FA18:2	3.1684179	2.3620931	1.125242	6.3317111	3.4404867	0.4725528	0.7327391	1.1397945	1.1487604
TG 52:6-FA18:3	2.4109433	2.1079644	0.989098	4.8304662	3.4678901	0.3911332	0.3610599	0.8531638	0.9525923
TG 52:6-FA20:4	0.2458125	0.4905146	0.115638	0.3828444	0.7881337	0.0812222	0.1182392	0.1494284	0.1218505
TG 52:6-FA20:5	0.557853	0.915862	0.470286	1.2261468	1.4415624	0.2647841	0.2227082	0.4679251	0.3611298
TG 52:6-FA22:6	0.4731978	1.1556833	0.317525	0.7571761	1.4831907	0.2979659	0.2412914	0.3627604	0.2225201
TG 52:7-FA16:0	0.8033576	1.7231856	0.561768	0.6555697	0.9242378	0.454794	0.4134891	0.2986108	0.3810906
TG 52:7-FA18:1	0.0416918	0.1035322	0.067600	0.1278802	0.0913156	0.0334788	0.0316713	0.0651681	0.0663145
TG 52:7-FA20:5	0.3435659	0.4885623	0.234491	1.2394879	0.6835077	0.1511984	0.1622765	0.2704014	0.1804205
TG 52:7-FA22:6	0.2296282	0.454363	0.157421	0.3266334	0.6999448	0.193198	0.0970626	0.1466356	0.1056926
TG 52:8-FA16:1	0.1197606	0.180051	0.089268	0.1118095	0.1157884				0.0701193

TG 52:8-FA18:2	0.06165252	0.0964738	0.0451666	0.18017 17	0.08151 8	0.0401817	0.0851179	0.0444989	0.0894594
TG 53:0-FA16:0	4.24765129	5.1425623	2.1415798	11.3514 71	5.94991 75	1.827885	2.3442901	3.3086784	2.3822572
TG 53:1-FA16:0	1.50096644	2.9096 95	0.8206321	1.42529 11	1.52664 34	0.6893881	0.7095471	0.487203	0.646575
TG 53:1-FA17:0	0.37030054	0.8000 83	0.1756088	0.24850 67	0.31872 49	0.1705199	0.1276866	0.1615272	0.204384
TG 53:1-FA18:0	0.54385577	1.1340122	0.2694021	0.38447 99	0.50010 03	0.2783192	0.2921021	0.2387557	0.3247772
TG 53:1-FA18:1	0.96728017	1.9274277	0.4139237	0.74687 37	0.96869 57	0.3124664	0.4938602	0.2628047	0.3173841
TG 53:2-FA16:0	3.86778747	5.0276666	2.8066304	2.44690 59	4.33408 31	2.4028008	0.8405893	1.1701859	2.6587353
TG 53:2-FA17:0	1.09042512	2.1222605	0.6374168	0.81789 88	2.28986 47	0.4702452	0.3789151	0.3956845	0.6570506
TG 53:2-FA18:1	4.6769155	6.5228307	3.0495456	3.15637 86	6.53634 22	2.3230368	1.1633427	1.5735761	2.7798894
TG 53:2-FA18:2	2.027812	3.3584349	0.6606684	1.85932 76	2.22698 92	0.7000443	0.8472252	0.6284516	0.7055888
TG 53:3-FA16:0	11.580927	9.7332919	8.126143	7.75223 58	7.41834 39	5.608197	1.8544451	3.0499146	7.9576612
TG 53:3-FA17:0	2.9251069	4.4721229	1.3177721	2.66032 13	4.83435 03	1.0032557	0.7077917	1.2678076	1.4621251
TG 53:3-FA18:2	6.6950003	8.1320557	3.0699424	5.06019 34	6.79591 32	2.3382821	1.6476802	2.0911642	3.0441914
TG 53:4-FA16:0	14.015095	8.7773144	7.8768571	10.7065 18	4.80613 91	4.8518635	2.1171963	3.20041	7.5043792
TG 53:4-FA17:0	2.8977778	3.7951498	0.9096981	3.21961 28	3.22535 47	0.7900637	0.9104404	1.2134321	1.2229359
TG 53:4-FA18:2	14.918321	13.766074	6.869217	13.5397 77	10.6370 15	4.977886	3.1627442	4.2776544	7.134322

TG 53:4-FA18:3	0.6388243	0.7468301	0.2755655	0.60911 59	0.60596 73	0.1858023	0.1842375	0.198834	0.2763517
TG 53:4-FA20:4	0.1272693	0.3075362		0.11117 62	0.31078 57	0.0720811		0.1023619	0.1187515
TG 53:5-FA20:4	0.1424439	0.335604		0.13660 11	0.38034 94		0.0793691	0.1026881	0.1100391
TG 53:6-FA20:4	0.2003996	0.3525955	0.0681078	0.27828 6	0.37694 33	0.0917831	0.0839878	0.0988559	0.0952365
TG 54:0-FA16:0	1.0569358	1.5632636	0.5856054	1.70420 69	1.31549 56	0.4472048	0.3518319	0.5610114	0.5156977
TG 54:0-FA18:0	0.204024	0.5755823	0.1462488	0.14970 92	0.17866 09	0.1883626	0.1113161	0.1572485	0.1544483
TG 54:1-FA16:0	1.4279457	3.0577171	0.4893788	0.96064 05	1.07139 97	0.5899687	0.3996565	0.4917901	0.4085917
TG 54:1-FA18:0	1.1947155	2.4174192	0.6927467	0.59983 05	1.32238 64	0.7293486	0.3538761	0.4091904	0.6501827
TG 54:1-FA18:1	1.11571	2.1308895	0.4470423	0.72242 98	1.21883 66	0.4564969	0.4016515	0.4283797	0.414358
TG 54:1-FA20:0	8.5050865	10.121475	6.3978143	7.12412 36	10.0875 58	4.2284494	1.9543683	3.7736812	5.8397347
TG 54:1-FA20:1	0.6691468	1.4731525	0.3438378	0.39689 18	0.52976 47	0.2844958	0.195814	0.1940972	0.283856
TG 54:2-FA16:0	8.9526236	11.771103	5.1812491	4.56085 36	5.78736 75	3.8451957	1.5200884	2.1897501	4.2476905
TG 54:2-FA18:0	3.2069326	6.1000954	1.7009314	2.33091 77	7.90135 34	1.7052811	1.1611859	1.3806223	1.6555262
TG 54:2-FA18:1	10.091905	13.593951	5.4094737	5.25472 66	13.0651 87	4.0934337	1.9170657	2.2060795	4.4030024
TG 54:2-FA18:2	2.0825833	4.4412165	0.5619782	1.70814 27	1.83380 2	0.6957843	0.7368398	0.7157369	0.4633475
TG 54:2-FA20:0	13.894576	14.092234	7.4701326	14.9704 68	10.4972 37	5.0828516	3.7198724	5.752682	7.3380866

TG 54:2-FA20:1	7.9622434	10.546174	3.9009402	3.8762914	6.2155318	2.9347702	1.2237901	1.9495844	3.2305137
TG 54:2-FA20:2	0.1020482	0.1422435	0.0542521	0.0496907	0.1049736	0.0491535	0.0470432	0.060971	0.0422958
TG 54:3-FA16:0	16.014394	18.164054	7.3646433	9.9761803	11.515439	5.8636621	2.8155022	3.7949985	6.4413979
TG 54:3-FA16:1	0.8785092	1.3130753	0.4638668	0.4821963	0.9017489	0.3206534	0.1387181	0.259015	0.4233693
TG 54:3-FA18:0	11.736116	18.745361	4.8054504	9.6818502	21.786265	4.4475018	4.294082	4.099525	5.3136594
TG 54:3-FA18:1	28.354089	37.656194	14.751021	22.466815	97.473811	12.149628	7.1306348	8.8347273	14.931585
TG 54:3-FA18:2	21.296271	27.450957	8.1920195	14.290893	22.681314	7.0078536	5.1124369	5.5779731	7.907672
TG 54:3-FA18:3	0.1276077	0.2167008	0.0331631	0.1086509	0.0500511	0.0380713	0.0387601	0.0510111	0.0742547
TG 54:3-FA20:1	15.063265	18.275388	5.8672089	10.252127	10.307558	4.722779	2.6443797	3.4605367	5.2440971
TG 54:3-FA20:2	1.7010212	2.5510648	0.693238	1.2166526	3.9090036	0.8761056	0.377318	0.6594668	0.6102231
TG 54:3-FA20:3	0.1098026	0.218013	0.0758284	0.1118528	0.2582083	0.1002751	0.0675749	0.0517904	0.0793337
TG 54:4-FA16:0	5.067734	6.8801603	2.0502311	4.4960171	10.018572	2.1214478	1.3467354	2.0334153	1.7303775
TG 54:4-FA16:1	1.3967218	1.9647968	0.6091993	1.0409467	1.5486684	0.3522361	0.1980524	0.3229507	0.4952425
TG 54:4-FA18:0	14.611005	21.996436	4.2657841	14.794077	21.806684	5.0536298	5.0809828	5.3803371	5.9356057
TG 54:4-FA18:1	60.789947	58.575622	26.589805	59.242975	154.05339	19.179928	12.354518	17.505698	28.617981
TG 54:4-FA18:2	49.524948	60.41503	18.23993	48.702055	99.605313	16.201881	13.324545	16.076401	21.640582

TG 54:4-FA18:3	1.5515854	2.3160286	0.6248832	1.5111608	1.9645666	0.554016	0.3993388	0.4842895	0.564307
TG 54:4-FA20:1	1.7223785	2.3979807	0.6522999	1.3500837	1.4302019	0.4167508	0.2539765	0.4100528	0.5611465
TG 54:4-FA20:2	2.7935661	3.8854658	1.0480813	3.0335924	4.8757397	1.2333806	0.7824843	1.2062879	0.8719666
TG 54:4-FA20:3	2.3682542	3.7875632	0.9465084	1.8252945	7.4214488	0.9960642	0.5788144	0.8315327	0.7844698
TG 54:4-FA20:4	0.6648643	1.4413825	0.3442315	0.6271232	1.8090936	0.304051	0.363295	0.4099971	0.4470534
TG 54:4-FA22:1	0.1391211	0.1500239	0.0980523	0.1580665	0.2986907			0.0626116	0.0701874
TG 54:4-FA22:4	0.0839699	0.1598012		0.0959767	0.2108604	0.0595553		0.0567502	
TG 54:5-FA16:0	5.4849618	7.2358832	1.9172768	5.6786241	11.712665	1.881555	1.7428546	2.6757354	1.9395094
TG 54:5-FA16:1	0.5268087	0.8066427	0.2941134	0.4988614	1.8003871	0.1909366	0.1275973	0.1620395	0.2330602
TG 54:5-FA18:0	1.3585911	1.9107719	0.4378629	1.5489353	1.8060995	0.4298074	0.5093921	0.5418039	0.50865
TG 54:5-FA18:1	50.495387	42.947529	16.398558	62.290234	82.049093	12.617612	11.53721	14.98279	19.211858
TG 54:5-FA18:2	80.086869	65.378237	24.367219	94.890687	117.91932	18.995343	18.463668	23.550998	27.864324
TG 54:5-FA18:3	5.3209883	5.6346057	2.0585598	6.4244574	10.494697	1.4148556	1.2242321	1.7489764	2.1359098
TG 54:5-FA20:2	0.4414614	0.6089485	0.1965479	0.5306645	1.0449836	0.1626243	0.1271871	0.1525872	0.1439411
TG 54:5-FA20:3	4.8872562	5.6034911	1.6703 62	4.7805456	9.4471424	1.5783771	1.3714596	1.8364554	1.4916157
TG 54:5-FA20:4	5.5003029	8.4962377	2.2312399	4.5192968	15.135327	2.0042557	2.0442396	3.2588527	2.1185717

TG 54:5-FA20:5	0.2553351	0.5361597	0.1817917	0.34471 66	0.36145 81	0.1068589	0.1816636	0.1700497	0.2108606
TG 54:5-FA22:1	0.303228	0.3117231	0.1183782	0.45575 91	0.50755 14	0.1288762	0.0745147	0.1087124	0.1477422
TG 54:5-FA22:4	0.1272727	0.2235992		0.08665 34	0.38751 51	0.0671353		0.0653657	
TG 54:5-FA22:5	0.4660031	0.9325174	0.1970533	0.56374 16	0.99396 37	0.2950298	0.2029493	0.3710758	0.240676
TG 54:6-FA16:0	6.0335258	8.9822801	2.6365311	8.53083 95	12.5604 96	2.5825391	2.9072743	4.2750503	2.844582
TG 54:6-FA16:1	0.599089	0.9293616	0.2740962	0.78827 46	1.93783 89	0.214861	0.1693474	0.2913428	0.2216829
TG 54:6-FA18:1	10.326884	8.7227667	3.7709438	17.3790 91	15.1980 16	2.4781498	2.4147458	3.7222572	4.0015923
TG 54:6-FA18:2	61.815759	51.262882	14.954941	92.0545 33	74.2406 11	12.625314	16.212122	19.255297	18.095346
TG 54:6-FA18:3	9.6676737	7.590768	3.3041114	16.4685 92	13.5465 61	2.1316227	2.0472388	3.3053318	3.4731654
TG 54:6-FA20:3	0.5998054	0.7665343	0.2762541	0.73447 15	1.58572 57	0.1893737	0.1600041	0.2399598	0.1815231
TG 54:6-FA20:4	10.949542	15.132435	3.9644147	12.5884 59	22.1482 27	3.3973996	5.2627358	7.774596	3.9128609
TG 54:6-FA20:5	5.9378846	7.555447	3.5489331	11.8262 96	10.3649 55	2.9214052	2.7336194	4.6699597	3.934164
TG 54:6-FA22:5	0.5148296	0.9914072	0.3051514	0.74016 07	1.78298 21	0.3111672	0.1901904	0.4046401	0.2141926
TG 54:6-FA22:6	4.1298577	8.0659232	2.1072532	5.19869 55	10.8375 31	2.6602073	2.2491477	3.4703786	2.3692195
TG 54:7-FA16:1	0.812307	1.2961233	0.4478898	1.22400 8	2.49559 9	0.3902063	0.3227032	0.507817	0.4461705
TG 54:7-FA18:1	1.218722	1.2654578	0.4700027	2.25536 95	2.07795 31	0.2601168	0.2732722	0.4515718	0.5387502

TG 54:7-FA18:2	13.580665	9.9183941	4.1356057	32.664689	12.098132	2.5521404	3.8994476	5.7322653	4.5318738
TG 54:7-FA18:3	7.4319229	4.8019905	1.999982	16.187294	6.4370905	1.102961	1.6560765	2.3634659	2.1995242
TG 54:7-FA20:4	1.2437929	1.5154882	0.528879	1.7455687	2.4845769	0.3321628	0.5169868	0.6340835	0.4284314
TG 54:7-FA20:5	14.678852	14.33	7.0986064	42.107727	15.643035	5.694712	8.3335617	11.540528	8.2479426
TG 54:7-FA22:5	0.2979901	0.5651939	0.2502103	0.8693312	0.75681	0.1812628	0.168748	0.2236787	0.1451852
TG 54:7-FA22:6	3.3662908	8.1844578	1.9329091	4.5108846	14.635593	1.9559613	1.1127317	2.1270857	1.4586173
TG 54:8-FA18:2	1.5621241	1.6183 88	0.5938083	4.1295588	2.025519	0.4122099	0.474086	0.691645	0.5334023
TG 54:8-FA18:3	1.3265494	0.9326624	0.3806759	3.7219076	1.1262548	0.2252398	0.2900356	0.5076647	0.4219699
TG 54:8-FA20:4	0.1603936	0.1507687		0.2531671	0.211523		0.0848964	0.0868917	0.0689913
TG 54:8-FA20:5	1.5649698	1.6704649	0.8519091	4.9086282	1.9625409	0.4978126	0.7103545	0.9864379	1.026847
TG 54:8-FA22:6	2.1421981	4.9847472	0.9508513	4.8066582	6.8808002	1.0250043	0.808067	1.158411	0.7123751
TG 55:1-FA16:0	16.673952	24.692637	6.1206674	26.322681	25.046664	7.8413438	8.2687812	9.897663	5.8282728
TG 55:1-FA18:1	2.0046261	2.5714038	0.871321	3.6608967	3.9512601	0.722358	1.0148536	0.9345371	1.0589913
TG 55:2-FA18:1	1.4513383	2.0114547	0.6122664	1.0660506	1.1849339	0.4661685	0.5534987	0.4696796	0.4406161
TG 55:2-FA18:2	3.0314747	3.6066674	1.13463	7.8327739	4.2706904	1.0128494	1.9291381	1.8269053	1.4291506
TG 55:3-FA18:1	2.0585485	2.8143 77	1.1647276	1.3363087	2.6337419	0.987048	0.5904453	0.5790182	1.0890547

TG 55:3-FA18:2	2.5112201	3.5595945	0.796842	2.5099295	2.0181837	0.8022635	0.8599273	0.7517182	0.7587058
TG 55:4-FA18:1	3.7527697	3.3832971	2.3590823	2.1735324	3.6367018	1.8041542	0.6854039	0.714954	2.2224567
TG 55:4-FA18:2	3.3466396	4.1347751	1.2629397	2.5961986	3.0098183	1.121758	0.8933873	0.8423278	1.4628901
TG 55:5-FA18:1	4.0614087	2.9353514	1.9421398	2.8067344	2.4972663	1.4028093	0.5887973	0.6420612	2.0839022
TG 55:5-FA18:2	4.9397474	4.0363189	2.2579073	3.9920769	3.2899817	1.8671078	0.8447279	0.9038996	2.3567748
TG 55:5-FA20:4	0.3302844	0.574931	0.190139	0.2651892	0.5856735	0.1189662	0.1322212	0.1392757	0.1591757
TG 55:7-FA15:0	0.2212666	0.3976608		0.3468516	0.3599802	0.1129848	0.0988586	0.1336245	
TG 55:7-FA22:6	1.1081466	2.3657445	0.402107	1.1792953	2.5595443	0.5102569	0.4393716	0.5066596	0.4626312
TG 56:1-FA16:0	1.4873978	1.8928984	0.740494	1.2350537	0.8903044	0.7946212	0.3936575	0.4270701	0.6429287
TG 56:1-FA18:1	0.624814	1.0397617	0.204576	0.5154551	0.7582189	0.2576718	0.1892068	0.2059129	0.2302682
TG 56:10-FA18:2	1.9609387	2.6477014	0.651665	2.2223259	1.7419379	0.5544194	0.7490015	0.6138365	0.6935899
TG 56:2-FA16:0	1.2170983	2.1679236	0.289537	0.6242908	0.6258222	0.3457348	0.1941037	0.3596159	0.2359092
TG 56:2-FA18:0	0.8870827	1.5418278	0.362613	0.5020211	0.5744879	0.3405267	0.2340222	0.2490558	0.2767513
TG 56:2-FA20:0	2.5500408	3.5914546	1.302252	2.0165246	3.3445771	1.2001435	0.6545728	0.7506793	1.2848604
TG 56:2-FA20:1	2.648985	4.2210498	0.550577	1.1996765	1.1608777	0.4969401	0.3514387	0.7798893	0.5338758
TG 56:3-FA16:0	0.9105823	1.4461297	0.211639	0.4644866	0.5244347	0.2693551	0.1623947	0.222974	0.202465

TG 56:3-FA18:0	1.9318735	3.2811222	0.5479222	1.1180007	1.17985 6	0.6370235	0.4687881	0.4471762	0.7172069
TG 56:3-FA18:1	4.6274989	6.0861956	1.6000769	2.6573695	4.42968 19	1.5079489	0.940014	1.0045348	1.4092503
TG 56:3-FA18:2	2.8018919	4.8026342	0.6145379	1.9227805	1.72741 61	0.7416043	0.5998386	0.6294855	0.6358615
TG 56:3-FA20:0	4.5001211	5.2312658	1.7088 34	4.3856973	4.34434 22	1.3589295	1.0566043	1.1668834	1.7635889
TG 56:3-FA20:1	3.7385964	5.6570308	1.3166761	2.2495731	3.43866 52	1.1320697	0.7665379	0.835448	1.0458875
TG 56:3-FA20:2	0.2011395	0.2684299	0.1232722	0.1190946	0.22509 82	0.1007324		0.0757416	0.0814904
TG 56:4-FA16:0	0.4111705	0.7109103	0.1475606	0.2735038	0.45099 5	0.2113663	0.1236598	0.1321409	0.1152383
TG 56:4-FA18:0	0.5871103	0.8438946	0.2338903	0.4161466	1.07713 13	0.3109006	0.2125589	0.2517296	0.2422069
TG 56:4-FA18:1	7.7412695	9.7747716	2.1603457	4.7368933	8.70151 54	2.1178558	1.3726487	1.4207798	2.0212608
TG 56:4-FA18:2	7.8525148	9.7788444	1.776414	5.5333034	6.19782 63	1.7606943	1.5216976	1.4217773	1.7117776
TG 56:4-FA20:1	7.4709342	9.1312534	1.974633	4.8233346	6.75801 06	1.6391703	1.3305679	1.3724387	1.7641541
TG 56:4-FA20:2	0.5233219	0.974561	0.2324376	0.4265846	1.77100 51	0.2876604	0.1987003	0.1937036	0.2263198
TG 56:4-FA20:3	0.3417373	0.5540104	0.1751238	0.2752604	0.69838 81	0.2068783	0.1161093	0.1389206	0.1448813
TG 56:4-FA20:4	0.254579	0.3559325	0.0791209	0.1824253	0.33731 5	0.0584988	0.0696787	0.1244396	0.1026317
TG 56:4-FA22:4	0.0854179	0.0907876	0.0493122	0.0844349	0.09646 1	0.0348786		0.0400482	0.0293549
TG 56:5-FA16:0	0.7159145	1.3184153	0.2469534	0.4739002	1.98043 56	0.3662251	0.2166153	0.2601047	0.2204028

TG 56:5-FA18:0	0.8850524	1.4439586	0.4258863	1.10803092	1.8825102	0.4342828	0.4192741	0.5873421	0.458429
TG 56:5-FA18:1	2.6310314	3.6829088	1.052909	2.5325898	8.348018	1.0136317	0.8166999	0.8700802	0.8900812
TG 56:5-FA18:2	9.9259854	12.258039	2.1123649	8.1252094	9.686219	2.0995214	1.9581978	1.6748736	2.0862145
TG 56:5-FA20:1	6.2969411	7.8934648	1.2681884	5.0557746	5.1305765	1.1025066	1.1656037	1.050095	1.2334813
TG 56:5-FA20:2	1.0147257	1.3101541	0.4005251	1.0919399	2.8311847	0.4105291	0.2924457	0.3261276	0.3734059
TG 56:5-FA20:3	0.9847249	1.3787611	0.2999353	0.9346859	3.4458898	0.4013768	0.2985394	0.2954675	0.3548246
TG 56:5-FA20:4	1.5766593	2.5997172	0.7336081	1.6720431	3.42153	0.6197983	0.7570365	1.0137477	0.7270278
TG 56:5-FA22:4	0.7154601	1.5275287	0.3168577	0.5934767	2.6199819	0.3939148	0.2040218	0.3546272	0.2892052
TG 56:5-FA22:5	0.1729507	0.5033897	0.1263558	0.1883194	0.5140197	0.1416765	0.0670676	0.1349828	0.1025994
TG 56:6-FA16:0	3.0376066	5.2635223	1.4508586	4.2939154	7.0451538	2.1127163	1.2713407	2.1002805	1.3182833
TG 56:6-FA18:0	1.2032618	1.6741384	0.4518471	1.5089974	2.323855	0.4586946	0.5863147	0.7211207	0.5787229
TG 56:6-FA18:1	3.8587114	5.1529436	1.5634172	4.8416067	10.53049	1.7801753	1.2448844	1.9318219	1.4788141
TG 56:6-FA18:2	4.2610113	5.0500682	1.2477612	4.7572033	8.319542	1.2733473	1.3760635	1.5069401	1.2980081
TG 56:6-FA18:3	0.8806479	1.0833858	0.2854349	0.8758409	0.864574	0.2003903	0.2030821	0.2196675	0.272856
TG 56:6-FA20:2	0.9424119	0.9800017	0.2544168	1.2925352	1.774417	0.2958325	0.2671841	0.3089898	0.2288498
TG 56:6-FA20:3	1.8086511	2.0310587	0.5886076	2.0038986	5.461795	0.5496306	0.597933	0.4018371	0.5571395

TG 56:6-FA20:4	3.7740665	5.1926423	1.4647051	4.721942	9.9381432	1.2547935	1.8971065	2.0533189	1.6818709
TG 56:6-FA20:5	0.6789722	1.0089568	0.2969792	0.7613673	0.6995549	0.2950887	0.2559368	0.3419274	0.3809835
TG 56:6-FA22:4	1.5850258	2.6599075	0.7115769	1.5189651	3.2724433	0.7350663	0.604392	0.7748068	0.56615
TG 56:6-FA22:5	4.0254463	6.6417263	1.8592347	5.4353449	9.6477808	2.8290148	1.4608326	2.4836942	1.7384518
TG 56:6-FA22:6	0.9734636	2.5949511	0.6436185	1.0467279	2.2521113	0.751504	0.726655	0.8444883	0.5912649
TG 56:7-FA16:0	9.1512296	16.267969	3.9150124	13.524038	21.564334	5.9515874	3.744312	5.9906689	4.0714884
TG 56:7-FA16:1	0.2327158	0.4763302	0.1272221	0.3246365	0.9056304	0.1054186	0.0911294	0.1134666	0.0907182
TG 56:7-FA18:0	0.5086872	0.7465524	0.2060841	0.7236606	0.6320384	0.1752225	0.2967104	0.2837779	0.2464262
TG 56:7-FA18:1	6.9363519	11.785773	3.0229165	8.5243438	18.866143	3.7722426	3.0024018	3.8786903	2.9844859
TG 56:7-FA18:2	6.4038259	7.4156788	2.1337841	11.454706	10.868246	3.0951475	2.7829435	3.4420409	2.2313845
TG 56:7-FA18:3	0.5589286	0.5848945	0.2194043	0.7708499	0.8847701	0.1894647	0.2355703	0.2203618	0.2262362
TG 56:7-FA20:3	1.6266421	1.4388493	0.5063054	2.3417753	3.2009773	0.3885511	0.5172406	0.4531918	0.4219786
TG 56:7-FA20:4	4.0392485	4.8270857	1.5702726	4.6683317	10.320893	1.2728565	2.2024008	2.223826	1.7037889
TG 56:7-FA20:5	2.427005	3.2150413	1.2578101	4.605896	4.7233667	1.1825602	1.4171166	1.5305505	1.719644
TG 56:7-FA22:4	0.2545218	0.3589297	0.1285301	0.3841944	0.6163499	0.0966987	0.0932897	0.1157834	0.0759457
TG 56:7-FA22:5	8.4207674	11.647462	3.490571	15.831353	12.419049	5.2629013	3.4261964	6.0206173	3.4113526

TG 56:7-FA22:6	37.480199	71.838507	16.484036	44.396131	104.54731	23.699321	15.249527	22.207844	16.165728
TG 56:8-FA16:0	17.481928	25.755504	6.2479496	28.29595	26.653948	8.6189046	8.501203	10.524562	6.2041971
TG 56:8-FA16:1	1.0104419	1.8127 84	0.4082954	1.613263	3.2686912	0.4641719	0.2729016	0.4531839	0.4152545
TG 56:8-FA18:1	1.9921016	2.7214048	1.0372561	4.1355918	4.2201693	0.8142325	1.075068	1.1093055	1.1591166
TG 56:8-FA18:2	14.965107	20.456987	5.3367469	25.06630 4	23.442156	6.7880597	7.4691835	8.8421565	5.4891481
TG 56:8-FA18:3	0.6749341	0.8419695	0.3749543	1.291242	0.9819533	0.3422449	0.3253952	0.3853738	0.4598481
TG 56:8-FA20:4	3.2869421	3.6549752	1.0353387	4.862900 7	6.8458501	0.9195011	2.0882289	1.851915	1.15913
TG 56:8-FA20:5	4.8410429	4.3609643	2.2408186	12.18622 1	6.7871713	1.8137547	2.8601747	3.0162354	3.0602105
TG 56:8-FA22:5	1.7908295	2.4965627	0.7386527	3.304832	2.9426763	0.7515887	0.7695251	0.9132317	0.7367458
TG 56:8-FA22:6	87.438101	133.21554	32.156357	144.0220 2	141.88085	43.66055	42.260405	52.23143	31.447729
TG 56:9-FA18:3	0.7498126	0.8873845	0.3052722	1.754818 7	1.1575231	0.2620616	0.4409529	0.4924434	0.3691867
TG 56:9-FA20:4	0.7186468	0.7340935	0.269257	1.389830 8	0.9583947	0.1852792	0.4948824	0.4277223	0.2969902
TG 56:9-FA20:5	4.5520409	3.4848153	1.7973331	14.45381	4.2891388	1.3336767	3.1691505	2.912451	2.4825752
TG 56:9-FA22:6	8.1434416	12.735075	3.4025847	15.64233 9	17.786809	3.1414011	3.0819116	3.7439769	3.0535839
TG 57:10-FA22:6	0.5412725	0.6251503	0.2947949	0.749002 7	0.6923886	0.2936681	0.4346307	0.4908074	0.3616793
TG 57:2-FA18:1	3.721137	5.2119906	1.3624439	6.057984	9.4264082	1.7629437	1.7015253	1.6903471	1.5500499

TG 57:3-FA18:2	5.5987165	6.2801785	1.4527449	11.510067	8.641119	1.8316734	3.103455	2.4948367	1.8371371
TG 58:10-FA18:2	6.0407753	6.8646482	1.6451588	12.198196	9.0335727	2.1901212	3.3529384	2.7756086	1.9817602
TG 58:10-FA20:4	0.7443165	0.9841477	0.3279794	0.9892417	1.5983827	0.382375	1.2165959	0.9712472	0.5319373
TG 58:10-FA20:5	0.547457	0.5556516	0.299917	1.2429878	0.5962803	0.271418	0.8662163	0.699298	0.422865
TG 58:10-FA22:5	0.7161937	0.6897743	0.2315149	1.6530266	0.7501118	0.2526406	0.3163149	0.3223102	0.2215007
TG 58:10-FA22:6	16.464956	18.660486	4.5373411	35.369989	28.606802	6.1555549	8.9849664	7.8462384	5.4737525
TG 58:2-FA18:1	0.4915727	0.7846022	0.2048294	0.3793516	0.4265745	0.203343	0.1272409	0.1648197	0.1879674
TG 58:3-FA18:1	0.8698818	1.2812091	0.1740012	0.4698643	0.4947639	0.2326443	0.1641794	0.271079	0.1765642
TG 58:5-FA18:1	0.2233735	0.332688	0.146642	0.1777312	0.3957667	0.1246785	0.0999417	0.0819212	0.0939933
TG 58:6-FA16:0	0.2724846	0.4475274	0.181177	0.2171949	0.3068598	0.2176481	0.0778283	0.1127896	0.1340095
TG 58:6-FA18:0	0.1739864	0.3068491	0.0757111	0.2073615	0.3826111	0.0870918	0.0857966	0.1096973	0.0767768
TG 58:6-FA18:1	0.3438223	0.5448021	0.1530345	0.3291334	1.1694083	0.1776263	0.1238625	0.1277343	0.1211596
TG 58:6-FA20:4	0.3262422	0.4873101		0.3405548	0.3343586	0.1316785	0.1939291	0.1074326	0.0710855
TG 58:6-FA22:4	0.2136403	0.3791287	0.104951	0.2020688	0.8792251	0.1456562	0.1212736	0.0755035	0.0956114
TG 58:6-FA22:5	0.3578078	0.5692669	0.187464	0.4442618	0.5157728	0.2438624	0.1525418	0.140801	0.1789106
TG 58:7-FA16:0	0.8481965	1.4958569	0.3826946	0.6459787	1.4341209	0.5826218	0.2857516	0.3758871	0.3711798

TG 58:7-FA18:0	0.4396 61	1.0509 923	0.2562 622	0.81147 76	1.36123 26	0.2670475	0.3420364	0.3282548	0.2999611
TG 58:7-FA18:1	0.9701 299	1.7734 423	0.4172 027	1.18154 69	3.44478 34	0.6450355	0.4585327	0.4182805	0.4260302
TG 58:7-FA18:2	0.5189 167	0.8269 952	0.2110 786	0.70651 78	1.21547 03	0.2498218	0.2773006	0.2802349	0.2034666
TG 58:7-FA20:4	0.4429 659	0.6592 516	0.1037 578	0.31962 35	0.71334 05	0.1686659	0.2196896	0.1678079	0.1266462
TG 58:7-FA22:4	0.4029 53	0.6260 496	0.1364 911	0.39993 61	1.21429 33	0.2147379	0.2023283	0.1914459	0.1987583
TG 58:7-FA22:5	0.8913 796	1.5873 407	0.4543 144	1.43990 28	2.74780 45	0.5646335	0.4284176	0.4690189	0.4608296
TG 58:7-FA22:6	2.3855 442	4.3810 055	1.2570 878	2.49777 23	5.00908 73	1.5916641	1.0836651	1.0310987	1.1848672
TG 58:8-FA18:1	2.6066 086	4.1284 678	1.1256 56	4.27758 86	9.78370 14	1.5523221	1.1263048	1.1570483	1.3043005
TG 58:8-FA18:2	1.9334 659	3.0474 374	0.7650 057	3.12111 06	4.31897 05	0.9896138	1.0104506	1.0821059	0.800028
TG 58:8-FA20:3	0.1677 901	0.2541 841		0.19637 6	0.39759 89	0.0941494	0.1171342	0.0950124	
TG 58:8-FA20:4	0.3088 312	0.4068 403	0.1051 43	0.35697 14	0.80933 61	0.0815241	0.2635819	0.2542554	0.1253996
TG 58:8-FA22:5	1.8864 812	2.1820 051	0.7797	3.55097 29	4.05073 75	0.9407732	0.7581512	0.7417205	0.7975655
TG 58:8-FA22:6	9.5148 151	18.038 359	4.0917 72	13.4135 97	35.4071 43	5.7470057	5.0613691	4.94878	4.9797705
TG 58:9-FA18:1	3.7857 645	5.2360 887	1.3365 225	6.29827 55	10.0592 76	1.7878836	1.8925984	1.7305422	1.70379
TG 58:9-FA18:2	3.4280 722	4.5201 578	1.0638 803	6.70777 86	8.33680 96	1.6414707	1.7516986	1.7138305	1.2109481
TG 58:9-FA20:4	0.4140 332	0.4785 991	0.1692 385	0.51169 16	0.82755 01	0.1080121	0.4885221	0.3556605	0.1798363

TG 58:9-FA22:5	1.4697584	1.5501169	0.5380027	3.2422222	2.082629	0.65112	0.8806829	0.7063165	0.4935449
TG 58:9-FA22:6	18.61141	25.434474	6.8474466	32.810368	51.1683	9.2347201	8.7648203	8.7361836	8.0187712
TG 60:10-FA22:5	0.2183027	0.2841845	0.0983874	0.3200879	0.380738	0.1137942	0.1528195	0.1360617	0.0888765
TG 60:10-FA22:6	1.0561734	2.0894851	0.3015817	1.8203787	3.0572719	0.5322239	0.8369942	0.611418	0.3864341
TG 60:11-FA22:5	0.2662207	0.5024728	0.1331586	0.5776475	0.5082359	0.276021	0.2841996	0.2693696	0.131211
TG 60:11-FA22:6	1.6567391	2.5009244	0.5292205	2.5558195	3.7683435	1.0816952	1.4808636	1.3265684	0.6103937
TG 60:12-FA22:6	3.0208612	5.4920393	1.2175371	5.6302075	5.7262161	2.4380652	4.4395697	3.6967996	1.6932683

Lipid species	**Bt:BSHIVMOL361-F16**	**Bt:BSHIVMOL361-F17**	**Bt:BSHIMOL361-M12**	**Bt:BSHIMOL361-M13**	**Bt:BSHIMOL361-F14**	**Bt:BSHIMOL361-F15**	**Bt:BSHIII1E2-M8**	**Bt:BSHIII1E2-M9**	**Bt:BSHIII1E2-M10**	**Bt:BSHIII1E2-F11**
CE 12:0	3.6580931	0.7926343	1.7960596	2.57589	2.04201	1.040752	1.9176849	2.1969315	2.6354707	2.1786693
CE 14:0	6.3043649	4.3469295	5.194435	5.7531597	4.6540089	3.0124468	4.6318943	4.631584	6.5477518	5.6069791
CE 14:1	5.4931365	1.428596	3.8780368	4.8809786	3.8167046	1.5069648	3.7409554	3.3142005	5.4648106	4.1912094
CE 15:0	8.4737029	4.2921358	6.5285139	7.1218766	5.6132151	3.1488501	5.1701132	5.5277658	7.8536281	6.618575
CE 16:0	86.697314	93.028925	82.522357	72.835394	66.546174	57.003381	75.191678	77.980515	96.991981	93.958926
CE 16:1	37.124467	75.36668	35.297183	28.753677	32.103473	31.435352	28.824514	31.737744	43.024515	54.315762

CE 17:0	4.9121194	6.4055141	4.478475	4.2361353	5.1113337	3.2368795	4.987988 9	3.362495 1	5.521928 5	5.569789 7
CE 18:0	5.8917728	10.750232	7.091118	5.0185987	6.7592949	5.354442	7.124857 8	5.067250 2	7.670267 3	6.818766 5
CE 18:1	101.1598	287.62788	95.288424	80.549954	109.17137	102.33843	92.20022 8	83.87814 6	110.2383	146.7972
CE 18:2	1267.6847	830.43583	1060.3564	1069.6102	758.08954	637.5834	1003.655	1204.186 4	1387.679	1031.601 9
CE 18:3	33.27735	18.729852	28.037208	29.596903	25.519152	14.943774	24.96446 7	25.14094 9	31.87926 8	27.35684
CE 18:4	3.5372114	1.3513208	2.6915035	2.9628196	2.8185187	1.1186722	2.084367 4	2.196639 1	2.914918 5	2.456080 4
CE 20:0	293.25724	70.894211	168.41202	230.76558	157.76391	87.485047	191.0914 3	213.1740 6	221.9022 1	152.6048 5
CE 20:1	98.611196	9.2536879	37.123673	78.339815	68.591309	14.818806	45.50554 8	38.82843 7	62.66917 8	47.78733 8
CE 20:2	3.7363241	1.8069044	2.2422702	2.8965331	3.1747882	1.16447	2.004927 8	1.900807 4	3.070411 6	2.368630 9
CE 20:3	24.546141	26.273581	25.433467	21.885898	16.139361	17.026909	18.85225 4	26.52799 2	24.46377 3	26.22415 1
CE 20:4	607.89027	450.80356	629.0342	531.03167	448.06024	412.74661	471.1181 3	634.8184 1	545.1693 6	606.3297 9
CE 20:5	125.27131	113.09258	106.38496	93.912109	80.836746	80.43222	102.3348 9	126.7141 6	171.6604 3	110.7497 2
CE 22:0	5.3044209	2.1318532	3.4036909	3.9051104	2.8243329	1.8267582	3.190891 7	3.280439	5.272459 4	4.106103
CE 22:1	4.6923709	1.8849572	3.647789	3.4210455	2.6266453	1.8244574	3.138641 8	3.787423 1	3.606403 8	3.353757 8
CE 22:2	42.29661	15.099143	30.864415	34.258432	25.547622	20.318353	30.25066 7	39.95915 1	26.64864 5	28.25968 1
CE 22:4	6.8902838	1.6640183	4.6080697	5.6176147	4.5479532	2.4437434	4.002070 5	4.245413 8	4.818501 7	4.748683 5

CE 22:5	11.422316	7.5240562	8.3235345	6.7000833	6.145526	4.7610453	7.220776 6	6.900821 3	12.19584 6	8.153773 4
CE 22:6	194.24443	137.73733	159.81215	147.82835	98.604478	96.396379	162.3962 5	197.6468 9	232.0580 9	170.2550 7
CE 24:0	84.897984	36.092907	73.169007	69.870603	42.816916	49.410016	69.30800 5	90.26042 1	60.25439 9	62.77110 4
CE 24:1	19.021779	8.597845	12.596927	14.395107	9.8927974	9.1992214	13.54771 8	16.33936 8	17.47962 2	12.19381 3
Cer d18:0/24:1						0.2680448				
Cer d18:1/14:0										
Cer d18:1/16:0	0.1676792	0.1681277	0.2002354	0.1778481	0.1908725	0.14377	0.148897 7	0.117715 1	0.223032 3	0.232063 6
Cer d18:1/18:0						0.0625459				
Cer d18:1/20:0										
Cer d18:1/22:0	1.0440365	0.3318669	0.8721007	0.8962401	0.3683281	0.4566125	0.779169 3	0.941416 4	0.943917 7	0.322307 7
Cer d18:1/24:0	1.370194	0.7730831	1.0973682	1.1094032	0.7398598	0.8220561	0.767014 4	0.816998 5	1.229748 2	0.775851 8
Cer d18:1/24:1	0.4898566	0.9129086	0.3556753	0.4892119	0.7715835	0.8537345	0.265146 2	0.360965 5	0.409509 8	0.698685

DG 12:0_18:1			0.2684882								
DG 12:0_18:2				0.5764418							
DG 14:1_18:1											
DG 15:0_18:2											
DG 16:0_16:0	0.5712101	0.3870702	0.557242	0.556452	0.7600047	0.318855	0.4864776	0.3954026	0.4706918	0.5476047	
DG 16:0_16:1											
DG 16:0_18:0							1.7650747				
DG 16:0_18:1	2.5817944	1.8087951	1.6630539	1.7503957	2.6014169	1.4336315	1.3563894	1.6105319	1.6506871	3.0576643	
DG 16:0_18:2		2.763573		6.7373682	6.1725741	4.461057	7.4621215	5.6226368		4.3826092	
DG 16:0_22:6								0.4194765			

DG 16:1_18:1	0.3497686			0.3725159						
DG 16:1_18:2	0.8462362		0.8885846	1.2487553	0.9681309	0.992130 4	0.628669 3			1.008602 1
DG 18:0_18:1	0.1628333			0.2658465		0.198918 3				0.233913
DG 18:0_18:2			1.021402	1.0614685	0.6156215		0.724487 1			0.604445 5
DG 18:1_18:1	2.571286	0.67396	0.8076498	1.4789625	1.1393391	0.325585 6	0.588289 4	0.495302 1		2.204155 7
DG 18:1_18:2	11.767728		12.888031	14.264311	10.309941	7.868521 8	6.625662 9			11.59995 8
DG 18:1_20:1	0.3272946	0.3971991	0.461825	0.6434222		0.304779		0.372877 7		0.400346 3
DG 18:1_20:2				0.3575817						
DG 18:1_20:4										
DG 18:1_22:6							1.647196 2			

DG 18:2_20:4												
DG 18:2_22:6										4.568211 7		
FA 12:0	3.0765737	2.4071725	2.4313353	2.9397414	2.9532835	2.5286224	3.063783 1	3.079023 8	2.863747 7	2.785455 8
FA 14:0	20.523373	17.065264	12.865227	15.38645	20.804251	17.778222	26.60544 6	28.01927 3	21.24504 6	19.52665 7
FA 14:1	5.1995161	4.7730261	3.7864972	4.289778	5.7932388	4.8873679	5.535154 7	5.332656 4	5.222874	5.048798 7
FA 15:0	10.36534	9.2947429	8.2764875	10.374332	11.79886	9.3556365	10.03036 8	10.33425	10.27370 1	10.15997 4
FA 16:0	183.30583	166.71131	125.55464	163.86842	203.49007	173.56772	211.8108 1	221.5085 6	176.5782 7	170.2960 9
FA 16:1	23.762066	26.20237	10.661124	13.60639	31.521746	24.331187	28.12080 1	39.62638 8	29.85031 2	20.03358
FA 17:0	11.9777	10.570495	9.9958562	11.396243	12.170755	10.933287	12.04026	11.95734 5	11.75394 5	11.35847 7
FA 18:0	59.354454	52.000069	47.370458	53.153872	55.126953	59.505681	65.13087 5	57.41500 2	54.76407 4	62.44226 4
FA 18:1	62.360039	81.528129	35.037085	60.372756	81.12321	62.800084	68.79200 3	81.29269 4	60.59426 4	60.10512 6
FA 18:2	72.014212	76.806012	32.442462	77.954509	89.945888	69.455117	78.50959 4	91.85981 6	66.50918 2	57.71827 2
FA 18:3	6.4524666	7.0145897	2.9971291	4.4400662	7.2872924	6.7761397	7.861547 2	8.677073 6	6.864098 3	4.822104 6
FA 18:4	1.3262884	1.105855	0.9890403	1.2108543	1.3623268	1.1234179	1.312191 1	1.312934 7	1.398335 4	1.157651 4
FA 20:0	8.5679416	4.0696908	3.5603511	9.4290572	10.879333	5.0637638	7.627892 3	7.483067 9	5.867372 7	5.343793 4

FA 20:1	6.2749069	4.2482637	3.4668308	6.0933355	7.5439132	3.9293807	5.708688 6	4.632843 7	5.542287 4	4.825195 9
FA 20:2	1.9387879	1.8942474	1.4136163	1.7169535	2.2545173	1.7535352	1.825034 9	1.839732 5	1.778190 8	1.935492 1
FA 20:3	2.4150942	2.6064308	1.7434604	2.0979238	2.4409672	2.3088563	2.226610 6	2.166047 6	2.116831 3	2.288637 2
FA 20:4	4.2194122	6.0761332	3.9807248	4.0208655	4.8814364	6.3522878	4.751864 6	4.813850 1	4.263552 9	5.004244 4
FA 20:5	2.3163202	3.1105616	1.6617986	1.9873641	2.1368415	2.8682399	2.764051	2.893924	2.998751 9	2.089280 9
FA 22:0	3.7878699	3.3429245	3.0516841	3.7086984	3.9577341	3.2151873	3.573179 8	3.518808 1	3.351363	3.294252 3
FA 22:1	4.0289646	3.716404	2.5125756	3.0888851	3.9459404	3.1873578	4.201535	3.850906	4.155162 3	3.652044 1
FA 22:2	1.8244959	1.3700622	1.2897676	1.3666671	1.9659668	1.5385183	1.667369 7	1.614153 4	1.761671 1	1.405580 6
FA 22:4	1.5564871	1.24563	1.3398408	1.489889	1.641898	1.3696849	1.452071 5	1.315562 5	1.340550 5	1.351749 5
FA 22:5	5.1259684	4.5422486	4.2625721	3.8419076	5.6282373	5.1572067	5.474812 7	4.344300 7	5.079085 3	4.808412 3
FA 22:6	5.1956156	8.6815076	2.9251658	4.4252042	5.4100177	7.4263467	7.417499 9	7.830875 9	7.446235	6.090558 6
FA 24:0	2.6152097	1.9277048	2.3511709	2.6651778	2.576732	2.2230309	2.425781 6	2.254860 9	2.349903 7	2.20717
FA 24:1	3.3949594	2.9015713	2.6833271	2.9730252	3.158639	2.9076692	3.567935 6	3.083510 2	3.156549	3.024465 8
HexCER d18:1/16:0	0.1433926	0.4157281	0.1797717	0.1588118	0.3290385	0.3568915	0.116281 6	0.157454 3	0.137549	0.384687 5
HexCER d18:1/18:0		0.1216031	0.0800932			0.1508864				0.131651 1

HexCER d18:1/20:0	0.1436785				0.1372593					
HexCER d18:1/22:0	0.4974887	0.6039758	0.8844851	0.4631636	0.4193398	0.4873431	0.530522 2	0.635124 5	0.666759 1	0.467369 7
HexCER d18:1/22:1		0.1258802				0.1314413				0.134374 6
HexCER d18:1/24:0	0.1662418	0.4039145	0.2681605	0.1043351	0.2077278	0.2821018		0.185500 5	0.195769 6	0.296240 5
HexCER d18:1/24:1		0.9458165	0.2405544	0.1718748	0.3624886	0.5879752	0.137491 7	0.146759 1	0.165650 1	0.558040 5
LPC 15:0	0.8087539	0.7161131	1.0909031	1.0480987	0.7366124	0.7166251	0.821337 9	0.864651 3	0.807274 7	0.705963 6
LPC 16:0	210.459	183.4655	209.70943	186.96787	158.78731	163.28073	176.6920 8	214.0228 7	190.7792 9	210.2876 6
LPC 16:1	2.853036	3.9458268	2.537378	2.4032262	2.4513495	2.3295413	1.853734 6	2.513521 2	2.252859 7	3.925985 7
LPC 17:0	6.1866704	4.4280282	5.6189308	5.3609307	4.3822451	4.186176	4.538655 7	5.315034	5.417428 8	4.202520 1
LPC 18:0	90.941607	69.197745	90.956311	80.701393	67.07233	82.882357	66.00092 1	85.91209 8	71.79039 5	77.98156 2
LPC 18:1	38.544393	53.290049	34.502286	35.7588	34.257174	38.648738	25.02775 8	29.33897 5	30.86156 3	45.96687 9
LPC 18:2	109.09439	115.00295	95.853595	132.43065	111.98777	116.41582	91.65961 7	98.94883 1	100.7437 9	110.4307 1
LPC 18:3		0.7728139	0.5323706		0.4509649	0.6380145	0.507081 1	0.668231 8	0.500707 1	0.707354 2

LPC 20:0	6.5794707	1.2656131	3.6700002	8.128901	7.518903	2.6582383	4.476228 2	4.030775 2	4.233519 4	4.180483 2
LPC 20:1	1.7262188	1.1088566	1.5165859	1.9311471	1.489279	0.7380089	1.157198 1	1.049474	1.339639	1.126343 6
LPC 20:2	0.8086499	1.3216116	0.9173786	0.863341	0.8374407	0.7021	0.502570 3	0.997961 3	0.642155	0.898538 4
LPC 20:3	4.5962309	8.2018881	4.0352509	4.5771997	4.017997	6.8606782	3.827286 6	5.044932 1	4.091004 6	6.314246 5
LPC 20:4	9.0365704	14.45263	9.1306783	8.3590659	9.1345309	15.604274	7.953548 2	10.24033 3	7.956345 7	12.42462 1
LPC 20:5	0.5898218	1.7461221	0.6180554	0.5784075	0.740707	1.0192701	0.565777	0.652726 9	1.109132 1	0.865166 1
LPC 22:5	0.5780179	0.7191528	0.4485606		0.2725554	0.4918117	0.301301 4		0.467556 6	0.499928 1
LPC 22:6	1.3500348	2.8765376	1.1681292	1.1684927	1.0821467	2.1281971	1.450478 2	1.985894 6	1.910828 6	1.485462 9
LPE 16:0	4.6810324	6.0972489	5.4476681	5.0501378	4.3173204	4.4096701	4.227348 3	5.470822 3	4.451358 9	7.784990 8
LPE 18:0	2.3215119	1.8722487	2.1558606	2.5681785	1.9079489	2.0958027	2.016408 3	2.758533 7	1.959529 6	2.993284 2
LPE 18:1	0.9989941	1.9322763	0.6914244	1.4038919	0.850875	0.7954878	0.621274	0.848489 1	0.739534 1	1.742964 9
LPE 18:2	2.6138725	2.7180759	2.5490386	4.5987372	2.4704308	1.9425891	2.387143	2.570496 5	3.303024 8	3.592820 5
LPE 20:4				0.4598686	0.3397829	0.4447572		0.600673 3		
LacCER d18:1/16:0						0.1363377				
LacCER d18:1/18:1				0.1583014						

LacCER d18:1/22:0		0.17865						0.156313 9			
PA 34:1	0.5082822	0.2244102	0.4256072	0.3772869	0.3177437	0.2075854		0.235140 2	0.254221 5	0.326656 9	0.587836 2
PA 34:2	2.1810296	0.5588633	1.4115386	1.8964838	1.065994	0.4538898		1.149650 7	1.210065 2	1.939763 3	1.410242 8
PA 34:3		0									
PA 34:4	2.2356091	2.4075688	2.3462308	2.3469755	2.1112698	2.14805		2.14579	2.208177 6	2.452611 8	2.098898
PA 34:5	0.642644	0.5347679	0.5970138	0.6346145	0.4332346	0.5295902		0.594249 5	0.653271 6	0.689892 3	0.692465 1
PA 36:1	0.3005941		0.1112379	0.2236133	0.1082432			0.154072 3	0.112556 5		0.156808 4
PA 36:2	1.2816894	0.4109072	1.1866467	1.4274852	0.8590781	0.4976402	0.736643		0.812492 8	1.182638 7	1.024041 3
PA 36:3	0.5293344		0.3423167	0.4357083	0.2678005	0.1775614			0.245740 7	0.343124 8	0.423186 9
PA 36:4	0.2241544			0.2959157	0.1950945			0.162951 3	0.228309 3	0.212199 5	0.213795 1
PA 36:5	0.525146	0.2958845		0.3531749	0.4106895	0.2197822		0.290106 1	0.307055 5	0.375342 3	0.431766 2
PA 38:3								0.122654 5			
PA 38:4	0.2529423		0.255327	0.2688831	0.228907	0.172656		0.345318 9	0.263303 3	0.386874 8	0.273889
PA 38:6	0.2971872										
PA 38:7	0.1927222	0.2034586		0.2119445		0.1510916			0.207040 5	0.299874 1	0.256496 2
PA 40:6					0.1340125			0.152318 8			

PA 40:8												
PC 12:0_16:0	0.5669536		0.4697966	0.5441006	0.4819114		0.3928159	0.4829269	0.450916			
PC 12:0_18:0												
PC 12:0_18:3	1.7131735	0.4304301	1.2992569	1.7165296	1.0448838		0.6094429	0.759002	1.321282	1.123461		
PC 14:0_18:1	0.8203231	1.5195327	1.021673	0.6846992	0.598696	0.6273024	0.6189559	0.7151603	0.727501	1.163954		
PC 14:0_18:2	2.0085938	1.0233983	2.1206339	1.990674	1.271514	1.1451204	1.6843172	1.696496	2.153633	1.808088		
PC 14:0_18:3												
PC 14:0_20:4										1.182067		
PC 14:1_20:0		0.3844417					0.43322			0.349796		
PC 15:0_18:1	0.5388297	0.4496185	0.4652028	0.5147186	0.3380268				0.545735			
PC 15:0_18:2	1.4274936	0.8699278	1.1976567	1.586999	0.7767495	0.7107978	1.0799792	1.259276	1.414807	0.883935		

PC 16:0_16:0	43.167206	31.562768	39.929913	45.595307	29.693213	23.943789	36.31242 6	36.79968 8	37.97764	31.86414 9
PC 16:0_16:1	3.4740522	3.8748756	3.0128359	3.0755207	2.325096	2.2843595	2.153119 6	2.566495 1	3.567837 6	3.585222 4
PC 16:0_18:0	48.844967	38.189124	54.668454	55.072242	40.462256	38.582564	38.67800 6	45.07867 1	41.51642 8	36.47189 6
PC 16:0_18:1	161.93172	180.4279	152.5388	127.75653	97.66697	113.86026	109.1259 3	125.3246 7	147.6723 8	163.4551 5
PC 16:0_18:2	817.4712	468.12402	699.93785	861.73325	485.27417	384.75664	664.8790 7	708.0315 6	775.8676 7	613.8447
PC 16:0_18:3	3.5342902	2.6688289	3.9679569	3.3311706	2.513969	2.5774221	3.512719	3.687216 9	4.318770 8	3.340638 2
PC 16:0_20:1	4.6441487	1.8988296	3.3212738	5.3127415	3.6342264	1.186076	2.574066 3	2.958578 3	3.577314 4	3.071856 3
PC 16:0_20:2	4.1199859	4.9482236	4.6628536	3.4443442	2.8413294	2.4554849	2.948109 9	3.917577 8	3.357410 4	4.435833 8
PC 16:0_20:3	54.987463	54.906432	48.204426	46.503377	32.91804	34.480044	44.26731 7	59.14997 6	49.10771 5	46.05237
PC 16:0_20:4	187.21102	140.93722	168.66929	182.77861	138.60484	120.71013	164.1239 6	194.5961 4	183.5514 3	188.3371 1

PC 16:0_20:5	25.280392	27.57052	23.478688	19.025419	19.856503	17.061245	33.06258 2	27.48516 2	41.35212 2		22.49174
PC 16:0_22:1											
PC 16:0_22:2								0.407212 2	0.346500 7		
PC 16:0_22:4	1.9748346	2.1995301	1.9494395			1.184073	1.441792 6	1.986890 9	1.547835 8		2.653345 5
PC 16:0_22:5	22.080952	14.49043	21.093556	16.154777	7.8923238	12.424314	11.86118	14.39411 9	18.86702		14.84085 2
PC 16:0_22:6	299.1005	213.35375	213.45982	204.03926	122.5536	131.22938	212.4657 6	279.6372 8	290.3411 9		225.1088 6
PC 16:1_17:0											
PC 16:1_18:0	0.528965	0.8642824	0.4946834	0.6483476	0.5259313	0.4187057	0.360165 9		0.547364 3		0.616307 7
PC 16:1_18:1	4.0820855	6.5929836	4.0611002	2.7940755	2.2093952	3.4389896	2.382943 3	3.084368 3	4.069300 1		5.249796 8
PC 16:1_18:2	10.385903	8.1106863	9.8104437	10.227015	6.4156956	5.8865438	8.170820 3	9.143890 8	10.66947 3		9.156314

PC 16:1_20:0				0.4448345					0.298389 1		
PC 17:0_18:1	1.083673	1.1026991	0.8940908	0.8963162	0.6005345	0.7603994	0.933585 9	1.030004 5	1.183626 9	0.881071 6	
PC 17:0_18:2	7.002754	3.9542138	5.9944021	6.8601169	4.7674382	3.2772304	5.231799 6	5.674174 9	6.471312 6	4.088190 7	
PC 17:0_20:3	1.7577833	0.8891505				1.0357808		1.295338 9			
PC 17:0_20:4	6.9983955	4.2628553	4.6100506	5.3522357	5.325811	3.0600442	5.541066 1	6.081091 8	5.640550 5	3.958225 8	
PC 17:0_22:6	7.1090841	3.2525098		6.7053171				5.577368 4	6.181812 2		
PC 18:0_18:0	0.7479356	0.9692622	0.6955262	0.7333491	0.5605608	0.9067738	0.628990 7	0.683678 9	0.536070 7	0.733576 1	
PC 18:0_18:1	23.654044	23.44038	24.915802	23.443111	17.6499	21.743457	15.52092 2	20.15638	22.56208 6	22.09075 8	
PC 18:0_18:2	372.14137	225.4161	373.47486	397.37334	267.93304	242.45421	254.6241 4	326.0974 9	334.2943 6	264.1580 8	
PC 18:0_18:3	0.9792107	1.0155499	1.3515215	1.165032	0.8554777	0.942482		1.062154 1	1.130545 7	1.151870 7	

PC 18:0_20:0	9.0535902	3.1912543	7.6210682	9.7109339	5.6861071	4.3941474	5.081013 4	6.182133 8	5.356686 2	4.251604 6
PC 18:0_20:1	1.1302071	0.4812811	0.8853684	1.3502431	1.4912075	0.4658764	0.601095	0.599453 1	0.979544	0.971338 4
PC 18:0_20:2	1.2520299	1.4915213	1.6657764	1.0886702	0.7737213	1.1861746	0.916915 1	1.309116 1	0.951995	1.265995 7
PC 18:0_20:3	22.650418	22.459644	22.292757	21.365768	17.221063	20.745188	16.21905 4	24.4659	17.68023 2	19.19019 3
PC 18:0_20:4	102.0124	72.091813	93.137015	108.86861	93.443215	101.57106	77.97959 5	110.6140 4	91.92778 9	92.92894 4
PC 18:0_20:5	14.223972	14.482841	12.254711	12.700982	12.584212	13.33748	13.39253 9	15.05041 5	17.36095 2	10.62425 3
PC 18:0_22:4						0.9616638				
PC 18:0_22:5	5.5270933	4.5474763	6.1754039	5.6205162	3.6307815	5.8497701	2.723808 1	4.438226 1	6.279328 2	4.339106 3
PC 18:0_22:6	87.459867	53.820475	53.577325	57.76706	41.580656	57.891791	61.65660 5	79.58322 6	77.93978 9	59.67149 7
PC 18:1_18:1	5.6857443	9.9056319	5.5313309	6.7704455	5.2418374	5.3879231	3.276502 9	3.978328 2	4.811894 2	7.303551 2

PC 18:1_18:2	75.627277	66.224007	71.047656	89.522914	62.612301	46.75846	44.39452 8	54.62043 4	63.33991 5	68.39368 5
PC 18:1_18:3		0.7987698								
PC 18:1_20:0	3.2542191	1.6956043	2.7111211	3.906608	2.1882358	1.5225333	1.811442 9	2.452233 2	2.734717 1	2.138703 2
PC 18:1_20:1	0.8280098	0.4875746	0.3898633	0.6147217	0.4980139		0.338650 1	0.396129 4	0.370112 5	0.430461 9
PC 18:1_20:2	0.574024	0.974024	0.4753937					0.358646 7		
PC 18:1_20:3	3.6273863	8.2923432	3.4604682	3.3093855	3.6874566	3.6534161	2.652944 9	3.464720 4	3.496065 7	5.205973 6
PC 18:1_20:4	18.242911	20.476811	14.100282	14.825372	16.41188	15.855229	12.37862 2	14.00923 5	14.2733	19.74505 5
PC 18:1_20:5	2.3076368	4.4898715	2.545595		3.0041419	2.0604305	3.260465 1		3.592488 9	3.657301 4
PC 18:1_22:5										1.516872 8
PC 18:1_22:6	16.988382	27.749422	11.491965	15.314126	9.8042012	13.230019	12.26635 8	18.85225 1	16.99718 4	21.23446 9

PC 18:2_18:2	15.427156	9.5132622	17.561162	22.781532	11.209402	8.0954037	12.82060 2	13.27013 4	16.00753 3	10.56908 9
PC 18:2_18:3			1.0152365	1.2659148			1.645928 6	1.153102 4	1.484065	
PC 18:2_20:0	13.560004	4.6144591	12.815477	15.621142	7.2747336	4.9900188	9.844936 5	12.72133 8	12.40464 7	6.756266
PC 18:2_20:1	2.2026961	1.4672662	2.4188516	2.7374401	1.3479191	0.9831883	1.399436 8	1.720171 5	1.827944 3	1.184929 1
PC 18:2_20:2		0.6730044		0.9414668	0.7053637	0.5120823	0.741574 8	0.893928 9	0.943206 2	0.649322
PC 18:2_20:3	1.5370104	1.6650689	1.6854773	1.3340607	1.2182682	1.2756396	1.352194 1	1.878078 3	1.942360 6	1.147879 2
PC 18:2_20:4	6.6944154	4.6085332	7.4458475	6.8119782	4.9196566	4.3635804	5.707795 4	7.335737 5	7.427928 5	4.651419 4
PC 18:2_20:5									2.647928 9	
PC 18:2_22:6									5.794243	
PC 20:0_20:3								0.996701 8		

PC 20:0_20:4	3.8482551	1.5391541	3.0217981	4.3658937	2.292245	1.7055152	3.560092 7	4.170261 6	3.691939 8	2.680252 5
PC 20:0_22:6										
PE 16:0_18:1				0.9949391	1.041372	0.696802			1.218149	
PE 16:0_18:2		4.0718708	5.8585092	8.0354332	3.9030563	3.3112781	4.905419 8	4.597200 6		
PE 16:0_20:4				4.8195863		3.7747217				
PE 18:0_18:0		1.0559308	0.6475951	0.5945533	0.5433193	0.6348792	0.623826 9	0.820383 2	1.190368 5	1.256121 1
PE 18:0_18:1		110.30449	54.239152	26.125876	27.636462	38.667659	36.55403 9	42.94824	72.20560 1	81.04575 1
PE 18:0_18:2		287.55866	241.73055	209.26901	132.1946	126.95901	208.6406 2	212.4293 3		
PE 18:0_20:1		2.0529367	2.1277013	2.2075721	2.0437195	1.027735	1.943738 6	1.879790 1	3.234705 7	3.274147 9
PE 18:0_20:2		7.2030632	5.2783317	4.3110605	3.0016255	2.2233026	3.559244 4	4.482643 5		

PE 18:0_20:4				49.62598		44.852753					
PE 18:0_22:2				0.7178923							
PE 18:0_22:4				1.4407335		1.0135854					
PE 18:1_18:1		1.8016724	0.8534802	0.6121147	0.5554721	0.5547941	0.442294 7	0.635286 2	0.951975	1.375775 8
PE 18:1_18:2		6.4909376	5.0754322	5.9381083	3.672898	3.1061143	3.355848	3.365728 3		
PE 18:1_20:4				3.2653964		2.5007644				
PE 18:1_22:0		6.9273345	2.5739804	2.5523807	2.7017753	2.1317785	1.749791 9	2.955695 8	4.314640 8	3.866601 5
PE 18:2_18:2				0.7231908						
PE O-16:0/18:1								0.268291 9		
PE O-16:0/18:2			1.1322022	1.979693	1.0104494		1.112388 4	1.006937		
PE O-16:0/20:4				1.2990187						
PE O-18:0/16:0		1.4045735	1.0067857	0.8181271	0.9745635	0.7513622	0.786681 7	0.998596 7	1.504651 3	1.208453 7

PE O-18:0/18:1		1.5966002	1.1639424	0.9519813	0.8295993	0.5877857	1.0846036	1.1713362	1.8784337	1.2539744
PE O-18:0/18:2		4.9357352	5.3828136	6.2532496	3.7666863	2.9382706	4.4954246	3.897373		
PE O-18:0/20:4				4.5345952		2.5131171				
PE P-16:0/16:0										
PE P-16:0/18:1					0.4648096					
PE P-16:0/18:2		1.7357857	1.1228675	1.6315885	1.2007808	1.0508686	1.5141801	1.3109976		
PE P-16:0/20:4				2.7395697		1.4728988				
PE P-18:0/16:0			1.1932711	0.8183499	0.8701454		0.943309	0.848404	1.6645531	1.2487854
PE P-18:0/18:1				0.5606779		0.5503419	0.6512092	0.7853492	1.5567653	
PE P-18:0/18:2		3.6272203	2.4450253	2.9784499	2.3383754	2.1379844	2.4702643	3.1503254		
PE P-18:0/20:4				4.8734093		3.7174043				
PE P-18:1/18:1										
PE P-18:1/18:2				0.4983263						
PE P-18:1/20:4										
PG 16:0_18:1	0.1761487		0.1494805	0.2366119	0.1640523		0.130722	0.136832	0.1635018	0.1959548

PG 16:0_18:2	0.2359194	0.1061032	0.2038487	0.2517634	0.1466308	0.0711554	0.1110195	0.1670975	0.2095305	0.1628394
PG 16:1_18:1	0.1576093	0.1442568	0.1457008	0.1572669	0.1310393	0.1077339	0.1070474	0.1187739	0.1739101	0.1293814
PG 16:1_18:2	0.5542768	0.3689965	0.6042037	1.1875482	0.4447837	0.3712546	0.6053019	0.6545529	0.7040491	0.4488559
PG 17:0_20:0	0.467738	0.5670793	0.6132529	0.5347422	0.4900898	0.442292	0.4360757	0.4849129	0.647665	0.5460415
PG 17:0_22:1										
PG 18:0_18:0										
PG 18:0_18:1	0.2235385	0.276952	0.1286475	0.1381606	0.1071337		0.1191739	0.1268965	0.2253356	0.3527854
PG 18:0_18:2	0.9696397	0.7280405	0.6252484	0.5438926	0.3050322	0.2736724	0.5768867	0.5574558	1.046397	0.8288163
PG 18:0_20:0	0.4145912	0.6195734	0.3515381	0.3098329		0.2719803		0.4602176	0.6075589	0.3945654
PG 18:0_20:4	1.7485047	1.4473444	0.6714176		0.4459039	0.3674997	0.4372762	0.8752752	1.306328	1.8506688

PG 18:0_22:5	0.2208722					0.330373	0.048195 7	0.734004 9	1.227555 2		1.076625 2
PG 18:0_22:6	0.9846528						0.737283 7	0.806275 4	1.078865 6		0.893541 6
PG 18:1_18:1	0.0619913	0.0729047	0.0777824	0.089682	0.071527	0.0622067	0.117620 6	0.073153 4	0.228169 3		0.184880 3
PG 18:1_18:2	0.9168816	0.6554303	1.1012863	1.4213901	0.6340742	0.5626757		0.154806 9			0.186305 3
PG 18:1_20:0	0.1908533	0.1539914	0.1811683	0.1647266	0.1180515		0.1310949		1.142903 6	1.327495	1.5058		1.242864 5
PG 18:1_20:3				0.1786161									0.479228 1
PG 18:1_20:4	1.4191404	0.9096994	1.5170754	1.7203575	0.9787871	1.1490735							0.119335 5
PG 18:1_22:6							0.066924 7	0.076302 4	0.125129 8		1.797726 4		1.203907 9
PG 18:2_18:2	0.0922467	0.1022836	0.1111314	0.1537448	0.0882444	0.0667472							
PG 18:2_20:0	1.7006949	1.222014	1.1984745	1.0055525	0.4190705	0.5096117	0.631791	0.710008 2					

PG 18:2_20:4								0.3763649	0.4605017		0.5085905
PG 20:0_20:3			0.2650942					0.1074838	0.2598940		
PG 20:0_20:4	4.7759966	2.7187217	1.8225779	1.7312005	1.3111222	1.3275227	1.6878148	2.1852791	4.0748784	4.2114128	
PG 20:0_20:5									0.4921385		
PG 20:0_22:6	0.8167606	0.4842224							0.8108987		
PI 14:0_18:1	1.1309429	1.0915381	0.7710926	0.7941733	0.4876113	0.6780326	0.7251083	0.9313474	1.1691011	1.1367509	
PI 14:0_18:2	0.4426838	0.5685919							0.3597836		
PI 15:0_18:1											
PI 15:0_20:1											
PI 15:0_20:2	0.4975283		0.467021	0.5546574	0.3623424		0.3613672		0.6070998		

PI 15:0_22:0	0.8757225	0.9009402	0.9355593	0.7818073	0.6272747	0.8423484	0.9052533	0.7469465	0.9197045		0.819529
PI 15:0_22:1	0.4444977			0.3958806	0.5060992		0.2730592		0.4966012		0.4060676
PI 15:0_22:2	0.7825777		0.6445555	0.8750171	0.6547906				1.0045958		
PI 15:0_22:4	1.0217005	0.8280067	1.0498038	0.635493	0.7637511	0.4939061	0.6369775	1.0471492	1.2011856		0.716057 2
PI 15:0_22:6											
PI 16:0_16:0	0.1362584			0.2039762	0.1264624		0.1252819		0.1321386		0.176616 2
PI 16:0_18:0											0.306458 4
PI 16:0_18:1	1.9163619	0.9935966	2.0677261	2.6755612	1.4211594	1.0525629	1.2687231	1.6077157	1.8293261		1.429813 4
PI 16:0_18:2	8.6646599	3.9655445	9.5059483	10.977548	6.0424375	3.5245792	7.4588597	8.8346425	10.115388		6.566403 1
PI 16:0_20:2		0.3035381									0.482897 6

PI 16:0_20:3	2.9692179	2.2060199	2.8983237	2.4843982	1.9223721	1.8314661	2.100303	2.390327 7	2.875716 8	2.411047
PI 16:0_20:4	10.827474	8.7567714	12.287867	9.3359156	6.4944626	6.8196213	8.117371 8	11.19488 2	12.17150 8	10.54912 1
PI 16:0_20:5										
PI 16:0_22:5			0.9127854							
PI 16:0_22:6										
PI 17:0_18:1	0.423407		0.2697544	0.4230512	0.4269942	0.1551736			0.378263 1	0.317173 2
PI 17:0_18:2	0.7823669	0.2888283	0.6493472	0.6997495	0.5504162	0.3323178	0.460425 3	0.565526 2	0.694923 5	0.383443 6
PI 17:0_20:0	1.0865609	1.4984063	1.2571197	1.0781931	1.2171117	1.3463188	1.158443 9	1.802290 7	1.392027 5	1.326917 5
PI 17:0_20:1	0.3750268				0.2933161	0.1956449			0.401296 8	
PI 17:0_20:3							0.285404 2	0.281342 5	0.532605 4	

PI 17:0_20:4	1.5902868	1.1644723	1.3157149	1.363299	1.1029578	1.1191993	1.275208 9	1.381391 5	1.972915 5	1.254948 7
PI 17:0_22:1	1.1014702	0.9024178	1.145905	1.1904034	1.0436124	1.2207169	1.000440 6	1.147087 5	1.023191 9	1.501734 7
PI 17:0_22:2										
PI 18:0_18:0	0.1385094								0.109578	0.097918 3
PI 18:0_18:1	1.9641593	0.9463752	1.8329866	2.5446068	1.4901186	1.0588186	1.255413 2	1.496436 7	2.121163 7	1.314746 1
PI 18:0_18:2	13.369677	6.1358874	12.709085	15.660284	8.6112529	6.6165602	10.88285 6	12.03464 1	14.81203 2	8.897044 5
PI 18:0_20:0	1.0014582		0.6871868	1.1010986	0.7142023	0.3729661	0.669256 2	0.544072 6	0.913128 4	0.464469 3
PI 18:0_20:2	0.6723991	0.5362494		0.5442348			0.427957 6	0.382759 4	0.513395 7	0.431820 8
PI 18:0_20:3	8.6202954	9.5533211	7.2000584	7.6197606	5.4866262	6.9179271	7.764279 5	8.938987 9	8.020605 7	6.932348 5
PI 18:0_20:4	110.38479	79.911595	88.257844	75.488279	74.083092	82.637993	85.87572 3	134.3504 1	137.1463 9	110.7616 9

PI 18:0_20:5	1.4242024	1.2266055	0.9744058			1.0704381	1.247193 3	1.524901 3	2.017581 3	1.588280 2
PI 18:0_22:4						0.4533228				
PI 18:0_22:5	1.388912	1.2738397				0.7760433	1.186506 7	1.103358 2	1.368904 8	
PI 18:0_22:6	1.3245604	1.1558342	1.40753			0.7632066	1.611508 8	1.594002 8	2.021999 3	
PI 18:1_18:1	0.5849974	0.4021422	0.5044583	0.7965933	0.4898565	0.3488562	0.429158 1	0.487241 8	0.664889 8	0.411948 5
PI 18:1_18:2	2.4464823	1.2488564	2.0073137	2.9155707	1.4360818	1.0035188	1.672323 1	1.977178 7	2.740522	1.455959 7
PI 18:1_20:0				0.4387128			0.306454 2			
PI 18:1_20:3		0.5431935		0.4351619					0.497660 4	
PI 18:1_20:4	2.0595559	2.8078943	2.2759392	2.3496857	2.3277623	2.0091264	2.622051 9	3.608687 5	3.216398 9	4.348667 7
PI 18:2_18:2	0.2589539		0.2313626	0.3950855			0.239406	0.254208	0.344321 9	

PI 18:2_20:0								0.2855301	0.3768582		
PI 20:0_20:4	0.9007487							0.8634438	1.4850009	1.2173638	
PS 16:0_18:2											
PS 16:0_22:6											3.5044173
PS 16:1_18:1										1.8312588	1.6652522
PS 16:1_18:2	3.8032818	2.7214689	2.3847824	2.261621	1.2009138			1.4488058	1.8248114	4.5254436	2.4681468
PS 17:0_20:0	1.0023878	1.0558551	1.355176	1.1191074	1.1292857	0.9124057		1.2307517	1.3318971	1.0502747	0.8391593
PS 17:0_20:3	3.0189494	1.5220105	1.0212647	1.7820961	1.0044666	0.8729661		1.5059751	0.9299645	2.0869526	1.7756404
PS 17:0_22:1			1.3649461	1.2272117							
PS 18:0_18:0	0.3933844	0.3433014	0.4019972	0.1766817				0.2673609	0.230922	0.5208584	0.3787603

PS 18:0_18:1	2.1176971	2.3519556		1.0921704					2.415818	1.808199
PS 18:0_18:2	6.226063	6.8683771	2.2290277	2.1696814	1.0573213		1.203483 5	2.363976 9	7.389319 8	4.552289 9
PS 18:0_20:0	1.8091467	1.2680543	1.2468963	0.9430938		0.5985349	1.059790 2	1.137507	2.687574 1	0.873404 7
PS 18:0_20:4										5.114449 3
PS 18:0_22:5										3.331588
PS 18:0_22:6						3.5231176				9.982341 8
PS 18:1_18:1	1.0539394	0.8636383	0.579814	0.6745249					1.220131 4	1.202502 9
PS 18:1_18:2	5.3129279	6.2237857	4.128748	4.1499537	1.8926088	1.6272505	2.528792 5	3.467957 8	9.527237	5.588753
PS 18:1_20:0	2.8588336	3.8470748	1.793762	1.7387756		1.1236628		1.762288 2	3.944923 8	3.040013 5
PS 18:1_20:4						3.3775909				10.41545 4

PS 18:1_22:5											2.6859036
PS 18:1_22:6							3.8564014				10.0995
PS 18:2_18:2			0.6237426	0.6095888						0.9584827	1.0281513
PS 18:2_20:0	7.0368964	8.0118501	3.6630166	2.995906	1.5836721	1.8109518	1.8177794	2.5542022		9.8274707	7.2142447
PS 20:0_20:4						3.2790714					8.4010022
PS 20:0_22:6											7.4907486
SM d18:1/14:0	1.3645945	0.8189513	1.097563	1.1369479	1.2414398	0.8727753	0.953672	1.0804701	1.4073389		1.2813371
SM d18:1/16:0	43.135907	30.866814	33.421169	33.203014	36.249114	31.771178	26.01942	29.876879	37.93242		33.10269
SM d18:1/18:0	4.1364207	3.7907079	3.6279233	3.5692287	4.9993558	4.5783296	2.631503	3.0475759	3.9469829		3.9096655
SM d18:1/18:1	1.8290578	1.4191548	1.6242797	1.4645048	1.7789071	1.4197729	1.190624	1.4524335	1.68684		1.7426575

SM d18:1/20:0	44.824624	32.397826	38.915101	46.389793	27.115741	25.951286	36.05417 1	42.05259 1	46.78689 9	36.99947 8
SM d18:1/20:1	2.2859626	1.2780207	1.9228553	2.1174295	1.8103136	1.368468	1.755397 4	1.962341 4	2.425266 1	2.031628 2
SM d18:1/22:0	55.361639	32.709295	49.739521	53.537556	33.52259	35.060193	46.14043 3	57.30509 5	56.76286	36.27124 8
SM d18:1/22:1	15.796273	10.65971	13.832997	14.071083	8.862012	8.2579307	12.47762 9	14.81595	16.40500 4	11.51489 5
SM d18:1/24:0	15.106196	8.6367449	11.898698	13.177158	9.1830666	8.8481208	11.43428 6	13.52867 8	14.02887 5	9.532497
SM d18:1/24:1	24.682396	30.988794	21.548572	21.54478	27.019513	32.097821	17.31023 4	22.68667 1	21.25131 1	30.43021
SM d18:1/26:0	2.8693271	1.2019357	2.2093295	2.758016	2.6541148	1.843797	2.081307 1	2.548165 5	2.182854 1	2.363411 6
SM d18:1/26:1	4.064774	1.8110092	3.8674829	3.9754689	3.1862104	2.5928136	3.127562 8	3.593136	3.680308 8	3.514530 5
TG 36:0-FA12:0						0.0421423				
TG 38:0-FA12:0										
TG 40:0-FA12:0										
TG 40:0-FA16:0	0.1174668			0.1005944	0.140555			0.061140 1	0.085682 1	0.129409 1

TG 42:0-FA16:0	0.1734713		0.1340947	0.1816362	0.1728721	0.0704887	0.1102615	0.0655638	0.1092053	0.1768161
TG 42:1-FA16:0	0.3532192	0.0663032	0.2111702	0.2865689	0.3470531	0.1262844	0.1941843	0.1295606	0.2865506	0.3564254
TG 42:1-FA16:1										
TG 42:1-FA18:1	0.1836688	0.0693574	0.1330502	0.1387798	0.1614376	0.0554884	0.0882908	0.0508021	0.1036931	0.2144738
TG 42:2-FA18:2	0.2563208	0.0524743	0.1220686	0.2384598	0.2252579	0.1070841	0.1908233	0.1203637	0.2072046	0.2044694
TG 44:0-FA12:0									0.0747944	
TG 44:0-FA14:0									0.0853352	
TG 44:0-FA16:0	0.1489813	0.0768734	0.1473583	0.1177972	0.1552815	0.0762094	0.1227034	0.0822556	0.1614901	0.1287157
TG 44:0-FA18:0	0.0875478				0.0728069					
TG 44:1-FA14:0										
TG 44:1-FA16:0	0.5642972	0.1504893	0.2608048	0.491767	0.6178757	0.2045989	0.2318351	0.1952998	0.3542057	0.6168534
TG 44:1-FA18:1	0.3308591	0.0917967	0.2147673	0.2981831	0.3798459	0.1025641	0.1391209	0.0956362	0.1723165	0.3469197
TG 44:2-FA16:0	0.8563132	0.1243121	0.3525854	0.6555889	0.7058721	0.2790517	0.4624744	0.2997945	0.4714965	0.6244296
TG 44:2-FA16:1	0.1018693				0.1178661					0.0784382
TG 44:2-FA18:1	0.2038794	0.0961852	0.1099243	0.1619264	0.2040979	0.0783651	0.0946035	0.0651552	0.1450641	0.2729373
TG 44:2-FA18:2	0.4265327		0.1924986	0.4194344	0.3621141	0.1250179	0.2320619	0.1384683	0.2195585	0.2849755

TG 44:3-FA18:2	0.2804639	0.0686336	0.1189619	0.2320123	0.2065347	0.1187343	0.146690 1	0.099009 5	0.157118 4	0.218331 1
TG 45:0-FA16:0	0.2336689		0.1745118	0.1495975	0.2460511	0.0860783	0.150679 7	0.121581 2	0.126139 1	0.193714 6
TG 45:1-FA16:0	0.636318	0.1221972	0.2972674	0.5330223	0.6123212	0.1952572	0.278353 5	0.189569 3	0.359426 5	0.501046 1
TG 45:1-FA18:1	0.2819835	0.0649913	0.1605244	0.2210928	0.31219	0.0871903	0.09411		0.144101 8	0.301872 5
TG 46:0-FA12:0									0.035114 2	0.019236 5
TG 46:0-FA14:0	0.1361691	0.1981686	0.3308466	0.1623113	0.1804284	0.1105493	0.210554 8	0.147007 2	0.354421 7	0.168364 7
TG 46:0-FA16:0	0.3464727	0.3951392	0.7858345	0.3160399	0.4559042	0.2642235	0.415312 4	0.318781	0.714623 2	0.421656 1
TG 46:1-FA12:0	0.3414086	0.1769308	0.2452723	0.2484961	0.2639001	0.1532531	0.193055 2	0.141442	0.256505 2	0.366791 3
TG 46:1-FA14:0	0.0968551	0.2151986	0.2267973	0.0891519	0.1238777	0.1444096	0.111668 7	0.079851 3	0.224349 7	0.239847 3
TG 46:1-FA14:1		0.03789		0.1006868	0.083904		0.066091 1		0.098008 4	0.088394 8
TG 46:1-FA16:0	0.5195409	0.2509648	0.3454351	0.4660782	0.6149436	0.2719879	0.345176 6	0.201661 7	0.494937 5	0.433765 4
TG 46:1-FA16:1		0.1552724	0.1944506		0.105703	0.0758109	0.091312 9	0.061319 5	0.221220 8	0.141927 6
TG 46:1-FA18:0	0.0844099		0.0603395	0.0914052	0.1040349	0.0472514			0.078888 8	0.068949 6
TG 46:1-FA18:1	0.1123859	0.1084171	0.1498065	0.1633013	0.1770966	0.0929974	0.100545 4	0.063425 8	0.160725 9	0.172346 9
TG 46:2-FA12:0	0.6508832	0.2048748	0.3289597	0.4485211	0.3736369	0.311139	0.393997 5	0.384166 8	0.525571 3	0.428577 9
TG 46:2-FA14:0	0.0991126	0.0906001	0.2318025		0.0893532	0.0910819	0.076767 2	0.07732	0.182834 2	0.139926 7

TG 46:2-FA14:1	0.076704						0.238886 5	0.247463 8	0.070086	0.090395 8
TG 46:2-FA16:0	0.4430956	0.1705867	0.3111197	0.3887908	0.5246875	0.2480102			0.423305 5	0.419309 1
TG 46:2-FA16:1			0.0904431			0.0724963			0.085547 3	0.138791 5
TG 46:2-FA18:1	0.4160415	0.1678214	0.2450614	0.5044297	0.4036486	0.1552966	0.145094 8	0.114191 3	0.269591 4	0.515858 1
TG 46:2-FA18:2	0.2017807	0.091523	0.2465481	0.2567875	0.2034066	0.1464549	0.189594 8	0.146419 9	0.264963 2	0.179757 6
TG 46:3-FA12:0	0.1381745			0.1126086	0.0883903	0.0773066	0.084856 1	0.092208 2	0.108827 1	
TG 46:3-FA14:1									0.061389 6	
TG 46:3-FA16:0	0.6788316	0.1339208	0.3350392	0.4920131	0.5295577	0.2877378	0.412668 6	0.258687 3	0.418565 8	0.512758 4
TG 46:3-FA16:1				0.0638268					0.079307 2	0.104306 7
TG 46:3-FA18:1	0.3528204	0.16746	0.2820308	0.5718503	0.3835205	0.1651995	0.177786 5	0.138883 4	0.221484 2	0.436385 5
TG 46:3-FA18:2	0.468874	0.1087361	0.3010553	0.6367655	0.4091612	0.221904	0.300540 1	0.197662 3	0.262398 9	0.378469 1
TG 46:3-FA18:3	0.0875105			0.1000966	0.0541747		0.056273		0.065110 2	
TG 46:4-FA18:2	0.5155323	0.0903027	0.3184171	0.6893045	0.3709854	0.1850872	0.285298 9	0.150513 6	0.249390 4	0.350646 7
TG 47:0-FA14:0									0.076229 5	
TG 47:0-FA15:0	0.2005785	0.1985321	0.2690262	0.2076032	0.2345931	0.1406018	0.179851 5	0.210491 1	0.260989 8	0.259859 6
TG 47:0-FA16:0	0.5426101	0.5741733	0.7551568	0.6541993	0.6351872	0.2968109	0.569174 3	0.488073 8	0.639214 6	0.592253 8

TG 47:0-FA17:0									0.047620 6		
TG 47:1-FA14:0		0.0543014	0.0862871		0.0533864					0.084077 8	
TG 47:1-FA15:0	0.0957115	0.0942826	0.161099		0.0939273	0.0862872	0.100843 4				0.107269 5
TG 47:1-FA16:0	0.4446984	0.2015583	0.3698241	0.4264801	0.5230658	0.2388746	0.344824 9	0.241430 9	0.450463 6		0.440958
TG 47:1-FA16:1	0.0961255	0.08158	0.1215286	0.0962584	0.104857	0.0600698	0.106086 1	0.102782 6	0.095830 9		0.111082 8
TG 47:1-FA17:0			0.0641987		0.0589386						
TG 47:1-FA18:1	0.1643729	0.1140772	0.1802719	0.2337445	0.2222174	0.0923914	0.091925 8	0.084337 6	0.147246 6		0.213609 5
TG 47:2-FA14:0	0.088537	0.0623109	0.1292034		0.0764457		0.084345 2	0.081547 6	0.111044 6		0.065421 2
TG 47:2-FA15:0			0.1246433	0.083743			0.057234 3		0.103516 2		
TG 47:2-FA16:1					0.0923118	0.0489793			0.094501 8		0.076030 1
TG 47:2-FA18:1	0.275097	0.1144444	0.1930451	0.4206626	0.3151582	0.1336255	0.116577 2	0.088916 8	0.176165 7		0.300760 8
TG 47:2-FA18:2	0.2921719	0.1026053	0.2918477	0.3610687	0.2781614	0.1348186	0.207398 9	0.157863 8	0.230370 5		0.254612 4
TG 48:0-FA14:0	0.0493751	0.0666487	0.1134888	0.0825247	0.0779115	0.0428282	0.092696	0.068035 5	0.181682 2		0.019149 9
TG 48:0-FA16:0	2.7534405	4.3955647	6.1607697	4.5736306	3.8933574	2.1086492	3.138093	2.704390 6	4.853563		5.061071 6
TG 48:0-FA18:0		0.1055756	0.1653604	0.1127306	0.1261562	0.051056	0.067727 6	0.069467 8	0.245779 4		0.084875 3
TG 48:1-FA12:0	0.1252709	0.0517724	0.0758893	0.0854853	0.0947891	0.0406114		0.043926 8	0.101949 6		0.091352 7

TG 48:1-FA14:0	0.9995412	1.8083961	1.865916	0.8449367	1.1480614	1.0003608	0.721802 3	0.558047 3	1.572062	2.018514
TG 48:1-FA14:1	0.0477201		0.047941	0.0713331	0.0700983			0.039320 4	0.055516 3	0.052870 1
TG 48:1-FA16:0	2.0405402	4.6370009	3.8916214	1.6118365	2.8622109	2.73839	1.919131 4	1.599626 5	3.192569 4	4.265484 1
TG 48:1-FA16:1	0.6952877	1.4461225	1.2221604	0.4657715	0.9930134	0.8423256	0.672043 4	0.544306 1	1.283588	1.280736 9
TG 48:1-FA18:0			0.0795692		0.1158598	0.0548862	0.052446 1		0.087737 2	0.070581 6
TG 48:1-FA18:1	0.7787915	1.7589387	1.8166574	0.8112683	1.2524199	1.0620822	0.750795 1	0.594407 9	1.418205 6	1.734407 6
TG 48:2-FA12:0	0.3970947	0.3376209	0.2437396	0.2523404	0.167279	0.1623675	0.165420 9	0.171432 7	0.334552 6	0.325747 3
TG 48:2-FA14:0	2.0010805	1.9062539	3.2025255	1.6771903	1.9059767	1.7990259	1.704798 8	1.396243 7	2.494911 7	2.865243 6
TG 48:2-FA14:1	0.6847022	0.3794672	0.3968431	0.4708732	0.5731153	0.3816639	0.351423 5	0.314414 6	0.513913 7	0.745333 3
TG 48:2-FA16:0	2.0433743	2.3304346	3.49249	1.6984654	2.3393499	2.3918109	1.661476 8	1.452569 2	2.718653	3.099865 6
TG 48:2-FA16:1	0.5968203	1.8302724	0.987529	0.2336536	0.8969549	1.2922653	0.365954 2	0.414774 1	0.975583 8	2.197230 2
TG 48:2-FA18:0			0.0635851		0.0720191		0.065012 5			0.062243 8
TG 48:2-FA18:1	0.5720919	0.8976441	0.5710451	0.4941951	0.6333573	0.5884974	0.242268 1	0.266068 3	0.591777 1	1.255900 2
TG 48:2-FA18:2	1.4801931	1.2392369	2.9619746	1.4915418	1.7387954	1.5701288	1.42477	1.239128 2	2.183921 3	1.834467 8
TG 48:3-FA12:0	0.3851228	0.2566412	0.2118588	0.2814318	0.2020692	0.2696239	0.200500 7	0.194861 9	0.289416 8	0.40815
TG 48:3-FA14:0	0.424881	0.4116128	0.5789764	0.29361	0.4324918	0.5527731	0.291723 6	0.292442 7	0.563703 2	0.874928 2

TG 48:3-FA14:1	1.3934521	0.3043166	0.5628195	0.974886	0.8360624	0.6930933	0.930863	0.860256 4	0.971794 2	0.877168 5
TG 48:3-FA16:0	0.6997185	0.3138557	0.5369865	0.4485177	0.5874734	0.595448	0.460432 5	0.401561 4	0.704992 4	0.673170 4
TG 48:3-FA16:1	0.3565774	0.5934982	0.5483294	0.1896847	0.4481633	0.6190132	0.288331	0.290895 9	0.569220 8	1.026647 4
TG 48:3-FA18:1	0.4213388	0.2953098	0.3050195	0.4474203	0.3872825	0.334037	0.263591	0.191685 3	0.403349 3	0.560161 7
TG 48:3-FA18:2	0.6859165	0.5437107	0.6937216	0.6219475	0.7464646	0.8685957	0.519830 4	0.475605 4	0.784293 5	1.021958 5
TG 48:3-FA18:3	0.1528386	0.1058676	0.2165618	0.1080445	0.1518134	0.1057038	0.137167 8	0.113916 8	0.198330 3	0.137819 5
TG 48:4-FA12:0	0.2972507	0.1529137	0.1705499	0.2232372	0.160669	0.2014008	0.205532 1	0.184767 2	0.196455 6	0.220116 5
TG 48:4-FA14:0			0.0853603			0.0672817	0.071555 6		0.117953 4	
TG 48:4-FA14:1	0.1534197	0.0587861	0.0938065	0.1102406	0.124657	0.1073334	0.098655 4	0.082511 7	0.136978 2	0.149594 6
TG 48:4-FA16:0	0.40848	0.1688699	0.2796404	0.288791	0.2853261	0.2532585	0.306928	0.202964	0.320186 5	0.271843 9
TG 48:4-FA16:1	0.0920518	0.0741824			0.0892606	0.0825153		0.052879 5		0.167627 2
TG 48:4-FA18:1	0.2540828	0.1369334	0.2189343	0.3624007	0.2510331	0.174761	0.150275 3	0.119167 5	0.187807 8	0.311678 5
TG 48:4-FA18:2	0.4732039	0.1621455	0.4044328	0.5528509	0.4170708	0.3839331	0.397697 2	0.311024 5	0.415470 4	0.447201 5
TG 48:4-FA18:3	0.1073336		0.0814066		0.0547873	0.0682865		0.065919 6	0.093085	0.090425 6
TG 48:5-FA18:2	0.347008	0.1076721	0.2780205	0.4587389	0.2644705	0.1494983	0.220538 3	0.160923 2	0.227657 9	0.273370 4
TG 48:5-FA18:3	0.1001189								0.075675 8	

TG 49:0-FA15:0	0.0734338	0.1323398	0.0864855	0.0582296	0.122115	0.056152	0.123842 8	0.122821 3	0.155971 8	0.115491 8
TG 49:0-FA16:0	0.7378114	1.0592385	1.1274284	0.7544857	0.943906	0.6194326	0.870606 9	0.632984 6	1.156419 2	0.720393 8
TG 49:0-FA17:0	0.2227925	0.3188869	0.3191595	0.20126	0.3034836	0.1848609	0.270453 1	0.212838 6	0.356882	0.340909 7
TG 49:0-FA18:0	0.1430964	0.2005765	0.2070365	0.1262717	0.1817314	0.1166648	0.219418 3	0.188957 7	0.248535	0.138845 7
TG 49:1-FA14:0	0.0993252	0.0799749	0.1600365	0.0831909	0.1253416	0.0378389	0.081828 8	0.058230 3	0.151652 3	0.109898 9
TG 49:1-FA15:0	0.8588206	0.9840467	1.0832613	0.950621	0.9694726	0.563558	0.592672 2	0.584706 8	0.727847 3	1.145718 5
TG 49:1-FA16:0	1.1468523	1.5986094	1.782591	1.2496827	1.3228839	0.8766652	0.969156 9	0.889207 1	1.456832 2	1.404648
TG 49:1-FA16:1	0.1436305	0.1750164	0.1887086	0.1136821	0.1019682	0.1001402	0.149217 2	0.175391 9	0.240159 9	0.121707 6
TG 49:1-FA17:0	0.1189985	0.1277979	0.1783993	0.0796472	0.1405099	0.0798273	0.114152 9	0.096198	0.204804	0.164750 6
TG 49:1-FA18:1	1.0348428	1.1337239	1.6772912	1.1442075	1.0907673	0.5606192	0.714401 3	0.663245 9	1.017234 5	1.027412
TG 49:2-FA14:0	0.2145119	0.1722476	0.2503508	0.168546	0.1626023	0.1098454	0.152537 2	0.126076 9	0.216603 8	0.236045 4
TG 49:2-FA15:0	1.6227538	1.4547832	2.050169	1.7318549	1.7307272	1.004687	1.233730 9	1.254933 2	1.202541 4	1.853053 1
TG 49:2-FA16:0	1.8221277	1.7183657	2.6825768	2.240119	1.8641581	1.1740291	1.323495 9	1.367417 5	1.731809 5	2.133887
TG 49:2-FA16:1	0.2144577	0.4450461	0.2860778	0.0996509	0.2826227	0.2285567	0.128895 3	0.144148 6	0.257044 7	0.453575 5
TG 49:2-FA17:0	0.1062345	0.0956931	0.1321728	0.1056952	0.0944333	0.0655218	0.075903 7	0.100735 6	0.117832 5	0.110335 4
TG 49:2-FA18:1	0.4145115	0.4928587	0.4467175	0.402673	0.4422208	0.2923459	0.250196 6	0.216520 7	0.466184 1	0.592031 5

TG 49:2-FA18:2	1.75486	1.6671669	3.1336815	2.1389839	1.6501953	0.9920389	1.2381624	1.334219 3	1.681628 2	1.657954 4
TG 49:3-FA15:0	0.3240201	0.2677109	0.3684182	0.2473657	0.3138966	0.2928332	0.223192	0.254910 6	0.310083 6	0.302698 4
TG 49:3-FA16:0	0.5316258	0.2596392	0.5021059	0.4158612	0.4175945	0.3184561	0.433907 5	0.305892 7	0.517960 8	0.428009 1
TG 49:3-FA16:1	0.2250679	0.3013429	0.2751478	0.1469854	0.2844688	0.2659902	0.153877 7	0.219506 3	0.299689 7	0.348265 9
TG 49:3-FA18:2	0.5781916	0.4183823	0.6062579	0.5341665	0.4792528	0.414847	0.421430 9	0.349793 9	0.623631 8	0.543555 2
TG 49:3-FA18:3	0.1164144	0.0928244	0.2440577	0.1254754	0.103698	0.0704969	0.128413 8		0.150711	
TG 50:0-FA14:0			0.079764		0.0465159				0.086226 7	0.043365 1
TG 50:0-FA16:0	1.2972365	2.1006183	2.5195502	1.5092982	1.7411295	1.009738	1.727020 4	1.338690 7	2.513370 4	1.894015 3
TG 50:0-FA18:0	0.7447903	1.261576	1.4977706	0.7415518	1.0337665	0.7611723	1.018577 7	0.806925	1.630502	1.168782 3
TG 50:1-FA14:0	0.2280428	0.2565366	0.5431906	0.1961602	0.3369443	0.0929006	0.267926 6	0.178689 5	0.531472 8	0.266393 6
TG 50:1-FA16:0	19.816593	43.176568	34.193209	25.874947	24.238998	22.263958	13.95356 3	13.08588	21.23673 8	40.00827 3
TG 50:1-FA16:1	0.2037979	0.2816164	0.4777937	0.1795971	0.2574264	0.2461513	0.267766	0.244756 3	0.478865 6	0.224737 9
TG 50:1-FA18:0	0.2760351	0.6167014	0.7007921	0.2868548	0.4281455	0.3638359	0.439205 5	0.359804 9	0.831125 5	0.557852 7
TG 50:1-FA18:1	10.039643	21.238661	18.44746	13.634336	13.30252	10.994402	7.484504 2	6.39995	11.75163 2	19.41251 9
TG 50:1-FA20:1	0.1674062	0.1171634	0.3961039	0.1829244	0.225437	0.0716336	0.191005 2	0.103558 4	0.329326 1	0.111492 6
TG 50:2-FA14:0	1.203957	5.1946356	2.4170656	1.0327405	1.5328692	1.8196346	0.745521 5	0.811844 1	1.678144 3	4.842762 1

TG 50:2-FA14:1	0.1696579		0.1221657	0.1143741	0.1568221	0.0690482	0.1005386	0.0691437	0.1337592	0.1290277
TG 50:2-FA16:0	47.883399	59.126346	67.806945	53.292937	48.993033	49.597634	38.48015	36.99280	44.48445	77.76653
TG 50:2-FA16:1	6.8589073	20.754029	8.5147053	3.5180885	8.6447868	11.373878	3.296534	4.014876	6.503251	19.46754
TG 50:2-FA18:0	0.287905	0.331645	0.7693579	0.3300469	0.3525628	0.2116461	0.352045	0.310438	0.730449	0.391134
TG 50:2-FA18:1	8.2372625	28.448226	11.553806	4.8811066	10.428295	13.71995	3.895134	4.779739	8.707671	26.68779
TG 50:2-FA18:2	20.475887	18.193844	31.47809	26.819297	21.390551	18.316129	18.07997	15.77876	19.57016	27.89812
TG 50:2-FA20:2			0.0642689							
TG 50:3-FA14:0	3.6889518	6.1528072	5.3660273	3.2609404	3.7074949	4.6631756	2.159903	2.182527	3.641135	8.501660
TG 50:3-FA14:1	0.290925	0.3272196	0.1994229	0.3095209	0.2885874	0.1887497	0.155515	0.131403	0.261561	0.386045
TG 50:3-FA16:0	14.889003	16.524843	13.660646	8.0592916	15.239049	21.081459	10.27662	11.24919	14.13045	21.66018
TG 50:3-FA16:1	13.494582	17.966866	11.986707	7.0451952	14.458107	19.945893	8.386018	9.623125	12.38929	23.37384
TG 50:3-FA18:0	0.1073664	0.0912536	0.1187388	0.0831952	0.1068622	0.071576	0.074352	0.073997	0.143089	
TG 50:3-FA18:1	4.685391	8.4202589	6.9450188	3.8519058	4.5877537	6.1545663	2.607058	2.803912	4.995441	10.62217
TG 50:3-FA18:2	14.532261	17.723644	15.083549	8.7231867	14.864219	20.114322	9.059648	10.39084	13.26143	23.48463
TG 50:3-FA18:3	0.8410076	0.89652	1.7351193	0.8310877	1.0103353	0.970943	1.241551	0.799892	1.362301	0.926549
TG 50:3-FA20:3	0.0748795	0.0572235					0.061813			

TG 50:4-FA14:0	2.5080082	1.8298458	2.6978107	2.2317083	1.9764272	2.866054	2.009460 5	1.867977 1	2.263592 1	3.182843 4
TG 50:4-FA14:1	0.5002642	0.2530053	0.2121926	0.4712349	0.3428922	0.3651779	0.281742 6	0.221947 7	0.362576 6	0.524918 2
TG 50:4-FA16:0	1.3148989	0.8659715	1.1473959	0.9412467	1.1071217	1.554895	1.149770 7	0.995423 9	1.287034 2	1.243138 5
TG 50:4-FA16:1	1.4533781	2.1652245	1.1596593	0.6486202	1.71457	2.6128276	0.870488 5	0.927187 5	1.563559 1	3.281211 5
TG 50:4-FA18:1	0.4939	0.4865104	0.4805803	0.5160117	0.4402639	0.493933	0.335116 8	0.248708 8	0.514204 9	0.620143 5
TG 50:4-FA18:2	4.5526197	3.433856	4.8297907	4.0694295	3.8921967	5.1725273	3.382043 3	2.961550 6	4.055671 9	5.768501 2
TG 50:4-FA18:3	0.6482225	0.6654522	0.7198889	0.3283022	0.5952086	1.0208481	0.464463 2	0.508259 2	0.782961 8	0.862023
TG 50:4-FA20:3	0.0752281				0.0883016	0.0536468	0.062522		0.080111 4	
TG 50:4-FA20:4		0.0592924	0.1454063	0.0701606	0.0791335		0.063914 7		0.087253 1	
TG 50:5-FA14:0	0.2922235	0.1658999	0.3095511	0.1848136	0.2181387	0.3404016	0.246626	0.239059 1	0.295927 9	0.263202 9
TG 50:5-FA16:0	0.3098746	0.1998958	0.3409777	0.2591014	0.2280541	0.2639346	0.325097 9	0.274846 3	0.371223 1	0.286233 1
TG 50:5-FA16:1	0.1686659	0.1604606	0.1854164	0.0978425	0.1628958	0.2614679	0.117707 9		0.264408 9	0.241817 6
TG 50:5-FA18:1	0.2549601	0.1591007	0.1869877	0.2192397	0.2124727	0.1726675	0.156943 8	0.134560 2	0.210126 3	0.231947 5
TG 50:5-FA18:2	0.558951	0.2896449	0.5075382	0.5761836	0.4787719	0.5759693	0.468028 9	0.359304 3	0.572594 1	0.597141 5
TG 50:5-FA18:3	0.3098746	0.2338917	0.347263	0.250042	0.2294705	0.4094686	0.255033 7	0.300613 2	0.386982 6	0.347098 8
TG 50:5-FA20:4										0.060004 5

TG 50:5-FA20:5	0.0915241	0.0758645	0.0909715			0.07263	0.0910835	0.1065666	0.1478666	0.0806059
TG 51:0-FA16:0	0.7243584	1.2868787	1.0428648	0.8096233	1.2495329	0.8192845	1.0887807	0.8049975	1.4443089	0.8151671
TG 51:0-FA17:0	0.0531412	0.1412124	0.115521	0.1032015	0.119835	0.1276689	0.1465288	0.0785276	0.2239563	0.1221499
TG 51:0-FA18:0	0.1397367	0.3006806	0.2500178	0.1576755	0.1878507	0.1863272	0.2778127	0.1636837	0.3529247	0.1625417
TG 51:1-FA15:0	0.3027866	0.2957578	0.3129546	0.2076588	0.3297437	0.1606357	0.2397332	0.1903689	0.3228311	0.2434766
TG 51:1-FA16:0	2.0243127	2.2431716	3.0356763	2.2168965	2.5230582	1.3866922	1.5037301	1.0479966	2.1507307	2.4854733
TG 51:1-FA17:0	1.1714539	1.4942409	1.4586588	1.0152967	1.2556514	0.8880425	0.8149463	0.6968515	1.2966664	1.6017105
TG 51:1-FA18:0	0.2560935	0.3910887	0.4811509	0.2832377	0.2687661	0.2491109	0.3221217	0.2644555	0.4162983	0.2048469
TG 51:1-FA18:1	1.2698643	1.8172131	2.134536	1.4026611	1.4408459	0.9886625	1.0054248	0.7879597	1.614459	1.1541782
TG 51:2-FA15:0	1.0309176	2.1259843	1.3980832	1.1494139	1.2165676	0.9792222	0.7029982	0.7818795	0.9777499	1.7731044
TG 51:2-FA16:0	5.3401864	5.6277642	6.2577672	5.6602063	6.0690508	3.9367435	3.2469066	2.7850408	4.6752402	6.7205942
TG 51:2-FA16:1	0.3431458	0.5281028	0.4264111	0.2623433	0.4516151	0.3133023	0.2230474	0.1911445	0.4436216	0.6552935
TG 51:2-FA17:0	2.4214159	2.1808581	2.5603341	2.0924809	2.1171157	1.6775066	1.8721471	1.6931947	2.3589542	2.5788342
TG 51:2-FA18:1	3.0245913	6.6679931	4.2422801	2.8367542	3.1934187	3.0261265	1.5897922	1.5991999	2.6418212	5.2688449
TG 51:2-FA18:2	2.5097916	2.8300374	4.4536591	2.8212391	2.5674984	1.8376409	1.8137788	1.4763277	2.6616358	1.9594622
TG 51:3-FA15:0	2.795581	2.9600152	2.6390398	2.8729273	2.5089022	2.2929344	1.5198829	1.6358459	1.8146893	3.3686523

TG 51:3-FA16:1	0.9950146	0.9952898	0.7776376	0.5492535	1.0895043	0.7866247	0.492673 1	0.363346 5	0.739170 4	1.405802 1
TG 51:3-FA17:0	0.3632241	0.3440495	0.375295	0.2933921	0.3555152	0.3469939	0.302065	0.268012 5	0.451891 2	0.462817 8
TG 51:3-FA18:2	4.4295434	5.0940595	4.9203296	4.2283928	3.9703195	3.7720452	2.464578 3	2.352406 4	3.320175 3	5.153097 6
TG 51:3-FA18:3	0.12607	0.1459891	0.2375521		0.1398841	0.1116161	0.162980 5	0.119037 5	0.260644	0.118011 1
TG 51:4-FA15:0	2.3394136	1.5381279	1.8886302	2.559078	1.8443986	1.7980873	1.681416	1.587316 7	1.4031	2.216864 5
TG 51:4-FA16:1	0.3313673	0.409984	0.2384634	0.2103299	0.3869368	0.384324	0.164455 5	0.147724 7	0.317114 8	0.609138 4
TG 51:4-FA18:2	5.0051211	3.1802032	4.3800944	5.1123882	3.6002654	3.3675184	3.170063 5	2.977898 8	2.975968	4.389241 9
TG 51:4-FA18:3	0.3147024	0.2871095	0.4141751	0.2645782	0.2279521	0.283227	0.267028 3	0.236958 9	0.311108 5	0.263955 3
TG 51:4-FA20:4		0.1004323	0.1351293		0.089003	0.0577931		0.076225 4	0.099209 1	0.105114 5
TG 51:5-FA18:2	0.4800409	0.3204618	0.5626048	0.5552779	0.4068781	0.3804664	0.420936 5	0.325765 6	0.508294 1	0.429263 9
TG 51:5-FA18:3	0.2935788	0.1870507	0.3067309	0.2767227	0.2363904	0.234517	0.291962 7	0.262060 4	0.301080 1	0.227942 4
TG 52:0-FA16:0	0.6703541	1.0702272	1.0959145	0.6976987	0.6404262	0.5658004	0.846837 9	0.629978 3	1.019196 8	0.817063 4
TG 52:0-FA18:0	0.3805651	1.0869889	0.6793818	0.3873852	0.5550019	0.5856261	0.619705 3	0.484634 1	0.744473 7	0.804010 8
TG 52:0-FA20:0	2.2696139	0.8995301	2.4487278	2.5714265	2.1142652	1.2671858	1.722248 6	1.374	1.471742 5	1.895561 7
TG 52:1-FA16:0	6.364895	7.2614496	10.133321	6.3603217	6.950468	4.6697157	4.329632	3.638713 8	7.083526 8	6.548752 6
TG 52:1-FA16:1	0.1093266	0.166672	0.2365615	0.0617874	0.1287012	0.0874592	0.129273 2	0.101555 9	0.216211 2	0.114800 5

TG 52:1-FA18:0	3.7813277	6.4658367	7.035373	4.4787565	4.0990403	3.7687078	2.929094 3	3.093033 8	5.177542 9	6.083144
TG 52:1-FA18:1	3.464447	5.7459677	6.1917171	4.2467868	3.8402123	3.085785	2.741630 2	2.838971 2	4.861406 1	5.101303 3
TG 52:1-FA20:0	1.3456449	0.7170765	1.2608085	0.8729395	1.2279953	1.1725646	0.762968 6	0.735281 9	0.969442 1	1.384581 8
TG 52:1-FA20:1	1.7988817	1.2110345	2.9305055	1.6303721	2.0002133	0.8125525	1.324202 1	0.733338 9	1.804114 4	1.043829 6
TG 52:2-FA14:0	0.2799451	0.2600406	0.5855801	0.3328903	0.3031729	0.1308327	0.200965 9	0.131717 4	0.343000 5	0.330456 8
TG 52:2-FA16:0	56.054757	174.83084	63.6901	47.360342	59.48941	77.015167	27.64825 3	31.83717 1	41.00248 9	141.9745 7
TG 52:2-FA16:1	1.0992731	1.3414475	1.438104	0.6474591	1.1761214	0.8736725	0.708391 9	0.539783 3	1.320191	1.246959 3
TG 52:2-FA18:0	7.5815775	8.7109799	13.819821	8.1669343	8.0720155	6.8806264	7.411041 7	7.791116 9	9.953970 5	9.878729 5
TG 52:2-FA18:1	87.948614	294.689	96.708595	77.415744	96.127098	127.38318	39.53018 5	44.25131 7	62.11208 8	231.4204 2
TG 52:2-FA18:2	6.3399089	6.0114256	11.330015	7.0094283	6.5998209	5.7577779	6.122628 5	6.089227 7	8.176958	7.345561 2
TG 52:2-FA20:0	0.6288012	0.2566581	0.7027177	0.5656459	0.4911072	0.4193806	0.407699 2	0.349937 7	0.438670 8	0.483888 4
TG 52:2-FA20:1	0.8847236	0.7583296	1.3465042	0.5208319	1.0401125	0.5573363	0.621894 9	0.390575 1	1.044081 8	0.873763 2
TG 52:2-FA20:2	0.1707533	0.3077088	0.3803919	0.1423676	0.2212559	0.1591218	0.194053 4	0.141538 6	0.235825 5	0.214819 6
TG 52:3-FA14:0	0.5155855	0.2927594	0.7682097	0.2988149	0.4148074	0.2125143	0.285471 7	0.230604 4	0.492961 2	0.406348 4
TG 52:3-FA16:0	182.19591	239.06705	138.53593	153.70884	160.38476	216.97523	111.2117 5	113.6937 2	120.2261 6	265.1335
TG 52:3-FA16:1	5.7447127	27.742405	6.3109452	3.6373486	6.8475049	9.2803092	2.447996 3	2.688448 1	4.618451 6	19.79234 2

TG 52:3-FA18:0	1.2763495	1.7133461	2.0910342	0.9627955	1.3336419	1.4781271	1.141075 9	1.302994 1	1.893879 2	1.545605 2
TG 52:3-FA18:1	174.88873	258.65103	141.06041	148.60866	156.60496	209.1406	104.0543 8	107.8093 3	117.9426 1	271.0379 9
TG 52:3-FA18:2	156.7565	199.49521	125.7156	138.38149	137.71787	179.6046	94.96816 2	96.54881	104.4503 3	223.2091 4
TG 52:3-FA18:3	0.2698081	0.3688867	0.5193326	0.2492442	0.2585446	0.1682275	0.268599 6	0.345277 3	0.428300 6	0.300750 8
TG 52:3-FA20:0	0.44056	0.4847855	0.3386824	0.431655	0.4327753	0.4525288	0.281827 3	0.289368 2	0.370814 5	0.585154 4
TG 52:3-FA20:1	0.6060734	0.4079722	0.975902	0.4417718	0.5701668	0.3431968	0.430528 7	0.308500 8	0.693276 8	0.500019 6
TG 52:3-FA20:2	0.3682176	0.5671792	0.4811317	0.2352016	0.2938532	0.3083392	0.180536 3	0.217346 6	0.265003	0.548224 9
TG 52:3-FA20:3	0.21439	0.37042	0.3683485	0.2083149	0.2921846	0.2531652	0.188640 8	0.229572 5	0.225187 4	0.363921 4
TG 52:3-FA22:1	0.1153103	0.1205317	0.110085	0.1091036	0.0903327	0.1055136	0.073715 7			0.172996 2
TG 52:4-FA14:0	0.1425002	0.2015919	0.2707345	0.1431221	0.1373838	0.1279126	0.124283	0.096987 1	0.170752 3	0.243929 4
TG 52:4-FA16:0	164.97308	96.126707	95.17048	141.50997	117.40282	166.11036	139.8034 6	118.9951 2	101.9318 4	141.8608
TG 52:4-FA16:1	14.661369	32.417835	12.281169	10.459327	15.478799	22.122878	6.783780 1	7.012593 5	10.56028 2	31.94233
TG 52:4-FA18:0	0.2172855	0.2005063	0.320214	0.1750467	0.2235736	0.2535724	0.210512 5	0.176492 1	0.317652 3	0.222374
TG 52:4-FA18:1	23.053441	39.407592	18.411478	16.323286	21.559979	31.430631	14.03696 3	13.09534	17.89991 1	39.73011 5
TG 52:4-FA18:2	265.26164	166.67548	163.00083	234.56763	190.23737	264.65094	217.1566	187.9727 3	167.9457 8	237.5731 6
TG 52:4-FA18:3	14.133623	12.927781	10.202724	10.821798	11.121105	17.028967	11.19806 6	10.03585 2	10.78590 6	14.95778

TG 52:4-FA20:0	1.1599922	0.612262	0.6833661	1.0438558	0.8711335	1.1711938	0.962159 4	0.777824 4	0.713149 4	1.050397 1
TG 52:4-FA20:2	0.275465	0.2284454	0.2827026	0.236264	0.1824336	0.2599723	0.184661 1	0.169704 3	0.192509 3	0.284636 9
TG 52:4-FA20:3	0.4570581	0.5331551	0.4725284	0.3256205	0.3656192	0.5532387	0.292013	0.330057 6	0.295724 2	0.671811 6
TG 52:4-FA20:4	0.5811536	0.8383606	1.3904036	0.5212737	0.720565	0.6683005	0.625259 5	0.588195 5	0.672951 1	1.106080 3
TG 52:4-FA22:1	0.2749462	0.1878531	0.1784791	0.2206374	0.1942294	0.2852261	0.140524	0.172849 9	0.154097 6	0.311415 8
TG 52:4-FA22:4	0.1129025	0.054013	0.091529	0.092067	0.0840044	0.076018	0.092691 7	0.095378 8	0.080512 9	0.134506 9
TG 52:5-FA14:0	0.1570072	0.1467619	0.2324862	0.1131724	0.0909958	0.1168779	0.110768 5	0.111979 5	0.151248 3	0.191659 1
TG 52:5-FA16:0	14.077899	8.0531359	8.07947	8.3175507	9.0251984	17.194059	14.76907 1	11.94202 6	11.87232 3	9.530088 3
TG 52:5-FA16:1	11.231824	10.967428	7.8563827	8.6119833	9.6824379	14.65347	6.513433 9	6.187399 6	7.889151 3	13.78584 8
TG 52:5-FA18:1	1.9864408	2.5566195	1.9210699	1.6762429	1.7841619	2.6306562	1.388282 9	1.202631 9	1.988055	2.687852
TG 52:5-FA18:2	26.243446	20.898261	17.870329	18.984724	21.093778	33.460633	19.95162 3	17.64141 6	20.19249	26.42063 3
TG 52:5-FA18:3	16.674266	9.7059837	10.020762	10.710157	11.114387	19.540953	16.58081 6	13.38951 2	13.28874	12.10676 2
TG 52:5-FA20:3	0.1847129	0.1788521	0.2257053	0.1600864	0.1527014	0.1698999	0.106833 1	0.105602 8	0.154172 5	0.220870 1
TG 52:5-FA20:4	0.3608894	0.5056436	0.9769243	0.2466869	0.3755288	0.5972979	0.238713 1	0.368701 2	0.455957 8	0.714932 6
TG 52:5-FA20:5	0.7405614	0.9024403	1.0285746	0.5251315	0.6634814	0.7968871	1.142234 2	0.779789 2	1.240450 3	0.644553 4
TG 52:5-FA22:5	0.442946	0.2557103	0.2857228	0.229579	0.2222095	0.3873289	0.412595	0.329332 3	0.339429 7	0.324426 4

TG 52:6-FA14:0	0.222633	0.1877404	0.2571129	0.1443376	0.1506548	0.2081154	0.196329	0.210808 9	0.273985 9	0.353287
TG 52:6-FA16:0	1.0799661	0.589091	0.6736925	0.6524702	0.6633147	1.3420845	1.224938 5	1.147738 3	1.242744 3	0.727590 9
TG 52:6-FA16:1	1.3558552	1.3280897	0.9288204	0.7041337	1.038649	2.1429576	1.030369	0.934000 5	1.366348 2	1.525863 3
TG 52:6-FA18:1	0.3145821	0.4096499	0.4559209	0.2554782	0.2582942	0.3375333	0.255840 2	0.203706 8	0.439699 5	0.333534 9
TG 52:6-FA18:2	2.4168721	1.6298651	2.3847222	2.1994912	1.9078113	2.9148764	2.105162 8	1.736245 5	2.290379 2	2.158415 2
TG 52:6-FA18:3	1.9415205	1.3266991	1.1489733	1.106231	1.5050995	2.784962	1.570632	1.379041 6	1.797920 8	1.621755 5
TG 52:6-FA20:4	0.1980712	0.1605634	0.4644788	0.2265417	0.1764592	0.2266663	0.167548	0.191502 4	0.237038 1	0.325630 9
TG 52:6-FA20:5	0.7196177	0.7313897	0.6182325	0.3377007	0.5069501	0.8996269	0.552381 7	0.739812 8	1.092477 3	0.937766 7
TG 52:6-FA22:6	0.4139716	0.5634738	0.4706491	0.2721707	0.4408626	0.5048169	0.498528 6	0.506431 1	0.589060 2	0.683259 2
TG 52:7-FA16:0	0.6909957	0.9012393	0.8469388	0.596717	0.9396648	0.7146845	0.937023 5	0.663208 9	1.103282 8	0.731933 3
TG 52:7-FA18:1	0.109138	0.1530672	0.1404644	0.1002381	0.0717649	0.071793	0.067640 5	0.105848 4	0.122115 2	0.101923 6
TG 52:7-FA20:5	0.3549029	0.2599773	0.3229012	0.2963884	0.2534296	0.4804131	0.342398 2	0.453688 6	0.581821 7	0.422135 4
TG 52:7-FA22:6	0.2490547	0.1765621	0.1686797	0.1945049	0.1810212	0.240837	0.169050 2	0.247333 5	0.256001 5	0.388499 1
TG 52:8-FA16:1	0.1214252	0.1022354	0.1270967	0.0722262	0.1323832	0.1195702	0.122162 6	0.099171 5	0.189569	0.1052
TG 52:8-FA18:2	0.122768	0.1172708	0.1796123	0.1303247	0.0730547	0.1114209	0.141688 8	0.136825 1	0.153369 2	0.101192 8
TG 53:0-FA16:0	4.3931528	3.2693566	2.6320047	2.730951	2.2367062	4.8607764	5.505302 6	5.081736 1	5.743922 4	3.691995 8

TG 53:1-FA16:0	1.5716854	1.7477187	2.0153529	1.4205112	1.9313646	1.2932301	1.495168	0.902830 1	1.980512 2	1.624238 2
TG 53:1-FA17:0	0.358956	0.3715663	0.3781522	0.2530069	0.3848284	0.2372725	0.284562 6	0.209433 2	0.374005 4	0.240988 1
TG 53:1-FA18:0	0.4158121	0.6765245	0.8164335	0.4686207	0.5741599	0.4138225	0.477067 4	0.383877 2	0.651774 2	0.450025 3
TG 53:1-FA18:1	0.8717256	1.4820837	1.5594556	0.9655506	1.2182393	0.9709256	0.872281 9	0.597134 3	1.324343 9	0.900259 5
TG 53:2-FA16:0	5.3185278	4.2107109	4.6523746	4.9269062	6.2303314	3.685392	2.542874	2.182860 6	3.822644 1	7.453365 4
TG 53:2-FA17:0	1.1276637	2.8587178	1.54431	1.0754771	1.323073	1.1829786	0.731766 6	0.660046 1	1.222551 9	2.150288 7
TG 53:2-FA18:1	5.9629887	8.3858975	6.216979	5.7340677	6.5604733	4.658409	2.867231 7	2.263041 7	4.333064 3	8.792309 4
TG 53:2-FA18:2	1.6908351	2.3279832	3.0129431	1.9859103	2.2744602	1.8758906	1.811964 5	1.211057 7	2.363381 2	1.473495 7
TG 53:3-FA16:0	17.284598	5.3237064	8.2225	14.602336	16.794678	9.304698	7.605969 7	5.948756 6	7.531474 1	17.10646 6
TG 53:3-FA17:0	3.208832	4.2140843	3.3026786	3.2515396	3.034224	2.8214378	1.752690 9	1.677745 6	2.623567 7	3.941435 2
TG 53:3-FA18:2	7.9940151	5.8853162	7.4105931	7.4626818	7.222252	5.1646589	4.261986 9	3.476727 5	5.422211 2	7.309368 7
TG 53:4-FA16:0	19.220529	2.4531045	6.6840598	17.14756	15.887418	8.6660385	10.25943 8	7.093738 9	7.332588 9	11.55358 6
TG 53:4-FA17:0	2.569774	1.9971057	2.3873965	2.6422694	2.2239747	1.9900359	1.963709 1	1.653427 9	2.124022 3	2.530007 2
TG 53:4-FA18:2	18.680593	7.9630895	11.245809	18.147084	15.3875	10.201647	10.19127 3	7.742664 8	9.394992 8	13.81969 6
TG 53:4-FA18:3	0.6495479	0.4165915	0.629375	0.549457	0.5145782	0.4837868	0.465547	0.361502 1	0.527381	0.468204 6
TG 53:4-FA20:4	0.0968208	0.1443208	0.1414927	0.0808969	0.0928656	0.1125823	0.106025 6	0.091008 9	0.094504 9	0.113049 1

TG 53:5-FA20:4	0.1509951	0.1622791	0.215149	0.1189154	0.1161022	0.1379873	0.093424 4	0.131458 8	0.116989 6	0.176299 5
TG 53:6-FA20:4	0.1724327	0.1378428	0.2633013	0.168674	0.1421201	0.1390531	0.124651 2	0.151185	0.128596 5	0.158243 3
TG 54:0-FA16:0	1.1493524	0.7092794	0.845747	1.0432742	0.7479309	1.0179924	1.132230 8	1.026838 7	1.262803 8	1.044382 7
TG 54:0-FA18:0	0.2039207	0.1852787	0.2837192	0.1830644	0.1800029	0.1648427	0.376046 9	0.213711 1	0.284665 8	0.169731 2
TG 54:1-FA16:0	1.616058	1.0401875	3.1278605	1.6372369	1.1075205	0.7323029	1.233718 4	0.955373	1.745687 5	1.077942 5
TG 54:1-FA18:0	0.9960683	1.6120721	1.5859	1.0027806	1.2880305	0.8675356	1.000451 5	0.773253 6	1.519816 3	1.065767 5
TG 54:1-FA18:1	1.1361895	1.4828711	2.3337895	1.2953693	0.9787507	0.8207831	0.898180 8	0.680363 3	1.378061 9	1.070811 7
TG 54:1-FA20:0	14.194076	7.2855118	9.9333831	12.283018	11.208704	10.38505	7.266240 3	6.715081 6	6.814930 2	13.06548
TG 54:1-FA20:1	0.6071943	0.4576811	0.8178075	0.4044375	0.6036383	0.2901206	0.556705 8	0.321768	0.684179 1	0.242621 5
TG 54:2-FA16:0	12.225185	6.1722617	12.271117	10.817681	11.211388	5.0760385	5.327047 9	4.159273 1	7.082685 8	9.687061
TG 54:2-FA18:0	3.2593531	8.6873	4.8095988	4.4070098	4.081495	4.071097	2.578342	2.693930 2	4.281083 4	5.644639 7
TG 54:2-FA18:1	12.22165	14.875966	14.217257	12.982229	12.661759	8.1006557	5.586047 6	4.665378 5	9.136760 3	14.10966 2
TG 54:2-FA18:2	1.8431459	1.701861	3.9594703	2.3015066	1.3672126	1.1576146	1.765250 6	1.572354 7	2.498757	1.416199
TG 54:2-FA20:0	21.387194	5.4704476	12.818606	18.693617	13.790443	13.176905	14.16930 8	11.82541 8	9.485324	11.70722 6
TG 54:2-FA20:1	9.6797972	6.3198372	10.105694	7.8519305	8.7466237	4.7514415	4.145817 8	3.392782 8	6.003724 4	7.684087 3
TG 54:2-FA20:2	0.0791538	0.0779797	0.094847	0.0897675	0.1031214	0.0751323	0.071661 3	0.134563 2	0.118006 1	0.054747 7

TG 54:3-FA16:0	20.669429	9.2656615	16.19026	16.944247	15.609173	8.2299069	10.172962	7.367374 8	10.35044 1	12.36797 7
TG 54:3-FA16:1	1.0153726	1.0243691	1.2372643	0.7355545	1.0034918	0.6545711	0.482136 7	0.415413 2	0.884618 6	1.141883 7
TG 54:3-FA18:0	11.494742	17.305797	17.509318	15.201138	12.354841	12.448251	7.821425 8	8.570728 1	11.09653 7	16.32741 1
TG 54:3-FA18:1	32.819714	184.28887	43.237543	56.463766	36.82944	46.347719	15.10550 5	15.21137 6	25.83695 6	94.10809 4
TG 54:3-FA18:2	22.825376	17.610447	26.054251	23.945148	19.630115	14.497941	12.76769 5	11.10202 5	16.06500 1	18.63280 7
TG 54:3-FA18:3	0.0668652	0.0804363	0.1898828	0.1471322	0.0926299	0.0632462	0.126990 8	0.082218 5	0.156928 7	0.097694
TG 54:3-FA20:1	17.838339	7.8677587	16.69769	14.274079	13.04956	7.6799101	9.184331	6.673691 1	10.07482 5	9.299522 3
TG 54:3-FA20:2	1.9745251	3.6609291	3.0561036	1.2204351	1.4339753	1.6708669	0.800473 1	0.964707 3	1.372158	2.8423
TG 54:3-FA20:3	0.1226568	0.146679	0.1792068	0.0864432	0.1145	0.0633277	0.106021 3	0.094606 2	0.141261 2	0.165948
TG 54:4-FA16:0	5.3827175	5.859939	5.9641155	3.7862155	3.875265	4.5775899	3.238246 8	3.098332 6	3.620606 1	5.568266 7
TG 54:4-FA16:1	1.6494845	1.5268975	1.585022	1.239682	1.3311601	0.9653195	0.705469 9	0.583441 4	1.042643 8	1.570560 5
TG 54:4-FA18:0	12.617725	12.153319	18.269923	15.143984	12.480964	12.563349	9.472481 8	10.66364 3	11.53553 8	14.90592 9
TG 54:4-FA18:1	66.809049	204.34812	78.2769	135.94956	67.401406	87.688549	30.06629 2	28.35010 4	44.37845 9	146.2460 1
TG 54:4-FA18:2	49.438253	108.02652	64.587267	86.953016	49.028126	56.524523	28.14658 3	29.42267 1	37.59600 2	88.32911 2
TG 54:4-FA18:3	1.5702321	1.373901	1.7609458	1.5049541	1.2624941	1.2033384	1.066307 5	1.084955 5	1.471189 1	1.314504 5
TG 54:4-FA20:1	1.7816731	1.1583197	2.1458937	1.2781627	1.52025	1.0546378	1.122210 7	0.758786 9	1.570732 7	1.282187 5

TG 54:4-FA20:2	3.3208802	3.3456587	3.8363309	2.3795199	2.2066624	2.4912292	2.012624 9	1.986968 7	2.077416 6	3.313361 2
TG 54:4-FA20:3	2.239067	4.451676	3.1750876	1.6091587	1.6670006	2.7074016	1.073546 8	1.163784 1	1.336287 4	3.798288 4
TG 54:4-FA20:4	0.4331668	0.6591145	0.7753412	0.3531731	0.3579099	0.5207677	0.441986 7	0.59629	0.520544 9	0.597830 1
TG 54:4-FA22:1	0.1461164	0.3831198	0.1993109	0.3063438	0.1606063	0.1766911	0.125522	0.102760 3	0.123142 2	0.331708 2
TG 54:4-FA22:4	0.074536	0.0813867	0.2345241		0.0956812	0.0829547	0.074414 3			0.131079 4
TG 54:5-FA16:0	4.7430051	4.793812	5.7889723	3.6233809	3.312278	5.0060141	3.226939 1	3.603620 3	3.400159 1	5.216221 9
TG 54:5-FA16:1	0.6520293	0.9812208	0.6770883	0.5668264	0.4798904	0.6651573	0.319391 8	0.281795 1	0.401029 2	1.016470 9
TG 54:5-FA18:0	1.1206539	1.160306	1.5992636	1.0012825	0.8573877	1.0500579	1.081961 4	1.055829 3	1.323657 6	0.856428 7
TG 54:5-FA18:1	49.132863	73.376607	60.634013	109.03741	43.513611	55.024643	28.95437 4	24.46984 3	32.51414 7	81.86564 6
TG 54:5-FA18:2	77.775072	101.36628	94.857614	178.18765	66.78242	81.167564	45.87436 5	37.97075 4	49.96139 3	123.0072 3
TG 54:5-FA18:3	4.7903383	9.4811678	5.8616903	6.8152574	4.2275198	6.2045859	3.072396 1	2.780589 5	4.001846 7	8.106771 5
TG 54:5-FA20:2	0.4932892	0.6330879	0.463059	0.5155041	0.3840774	0.5244033	0.293014 7	0.282756	0.312300 9	0.658346 5
TG 54:5-FA20:3	4.2450382	4.3658788	4.579077	3.1576291	2.7961194	4.4109897	2.508805 3	2.871105 1	2.735740 7	4.654342 2
TG 54:5-FA20:4	4.0348867	5.8203564	9.8803267	3.446961	3.3989538	5.3652634	2.478217 6	3.218961 4	3.380567 2	7.115248 4
TG 54:5-FA20:5	0.1753756	0.3326637	0.4234766	0.1558244	0.197898	0.1836064	0.322893 9	0.260700 4	0.314517 3	0.155377 2
TG 54:5-FA22:1	0.3550676	0.4624936	0.3995844	0.7186361	0.2712683	0.3484835	0.212632 8	0.181263 4	0.229057 8	0.569816

TG 54:5-FA22:4	0.122759	0.1046573	0.218345	0.0976408	0.0913823	0.1020538	0.062713 4	0.085827 2	0.122898 6	0.211522 2
TG 54:5-FA22:5	0.5651498	0.6287319	0.6560205	0.3255742	0.3451252	0.4452573	0.541778 4	0.433544 3	0.542689	0.505767 7
TG 54:6-FA16:0	5.2026666	5.3839028	6.1156022	3.7548901	3.4209423	6.1139759	4.828652 1	5.299926 2	5.564777	5.845551 6
TG 54:6-FA16:1	0.594619	0.9590042	0.6756281	0.4298076	0.4675005	0.9052873	0.308625 2	0.376426 3	0.512438 3	0.921449 1
TG 54:6-FA18:1	8.4592688	11.712008	8.9133954	9.8605864	6.7394686	11.283297	6.760039	5.647511 4	7.822563	11.47230 8
TG 54:6-FA18:2	54.476976	41.047431	73.444397	133.64708	39.103051	49.179985	40.81759 2	31.18833 5	34.75977 4	82.16821 5
TG 54:6-FA18:3	7.8233194	10.339774	7.7460116	9.9148366	6.4001349	10.18123	6.244433 3	4.951537 2	6.219012 2	9.906354 7
TG 54:6-FA20:3	0.596303	0.6746448	0.6292875	0.5174927	0.4428117	0.7236201	0.304516 4	0.364617 5	0.342855 9	0.784474 1
TG 54:6-FA20:4	7.9455403	6.1266282	14.437307	6.9382839	5.7510325	9.3418635	6.880008 5	8.129953 4	7.292884 5	9.326041 2
TG 54:6-FA20:5	6.5955865	7.6712711	5.4380815	4.1905094	3.7216168	8.4258418	6.038508 8	6.579541 7	8.593711 9	7.881658 4
TG 54:6-FA22:5	0.565235	0.7080745	0.7601431	0.289024	0.4196427	0.6964413	0.395268 5	0.499906 1	0.675507 2	0.889593 9
TG 54:6-FA22:6	2.8100895	4.6887907	3.2530068	2.1759469	3.0404141	3.4864916	4.831634 7	4.102250 2	4.402764 3	4.657640 8
TG 54:7-FA16:1	0.6645832	1.2003398	0.7444573	0.4169	0.5229523	1.1054491	0.542254 7	0.712641 5	0.961465 9	1.357447 5
TG 54:7-FA18:1	0.9791063	1.38759	0.8017178	0.6990874	0.7588038	1.372599	0.827688 1	0.626045 3	1.068931 2	1.447248 7
TG 54:7-FA18:2	10.476725	7.2147484	8.6980643	9.3955076	6.5168746	12.064637	11.57268 9	8.547485 7	9.984787 1	8.282820 7
TG 54:7-FA18:3	5.091929	3.7184071	4.4231061	5.1993361	3.6072713	6.1725275	5.587842 8	3.553433	4.268153 4	4.380753 1

TG 54:7-FA20:4	0.923502	0.8510052	1.3937621	0.7015802	0.7073967	1.2670384	0.655115 3	0.782706 2	0.853340 1	1.052309 1
TG 54:7-FA20:5	15.689321	9.2390035	8.3679805	9.8157946	7.1338787	16.819412	19.40398 7	17.71030 8	19.38117 8	10.84366 3
TG 54:7-FA22:5	0.3898452	0.3301954	0.4741761	0.2906896	0.1977486	0.3930694	0.302681 2	0.334285 7	0.490624 8	0.470554 7
TG 54:7-FA22:6	2.9412202	5.7026083	2.7139558	1.6971106	2.1736408	4.3144537	2.455009 9	3.422561 7	4.460109 4	7.107918 2
TG 54:8-FA18:2	1.2026018	0.9001796	0.9253274	1.0245284	0.6833828	1.4824816	1.231751 3	1.107607 1	1.401003 6	1.159619 5
TG 54:8-FA18:3	0.9125025	0.5089961	0.6210165	0.566435	0.5242764	1.1799095	0.983091 3	0.751341 9	0.952023 4	0.571023 3
TG 54:8-FA20:4	0.1389829	0.0987761	0.1412895	0.0989314	0.0888604	0.10703	0.111348 6	0.103981 1	0.133649 4	0.115236 6
TG 54:8-FA20:5	1.6835158	1.2966606	1.0383133	1.1385534	0.9893126	2.1251267	1.570601 8	1.646366 6	2.292179 4	1.740589 1
TG 54:8-FA22:6	1.6958192	2.1056517	1.7119025	1.3317854	0.9952366	2.073546	1.736159 7	2.297429 8	2.568632 3	3.513857 3
TG 55:1-FA16:0	11.985884	11.351112	7.5431999	9.164662	6.4381221	13.386236	16.00351 2	17.00383 3	17.42803 6	14.04020 6
TG 55:1-FA18:1	1.772846	3.3761952	1.692457	1.549361	1.3846252	2.5576971	1.789980 9	1.516122 6	2.358550 7	2.580526
TG 55:2-FA18:1	1.5625577	1.8427527	2.1669996	1.6636767	1.6298574	1.3157373	1.080188 6	0.756931	1.613082 1	1.444738 5
TG 55:2-FA18:2	2.7573084	3.010312	2.1419693	2.1964132	1.9760088	3.2526393	3.358144 1	2.710104 7	3.431113 2	2.748411 6
TG 55:3-FA18:1	3.0319306	4.0181895	3.2160746	4.9341415	3.5960141	2.0292507	1.424287 1	1.098289 9	2.374404 5	4.848866 9
TG 55:3-FA18:2	2.6047316	2.4241758	3.6018097	2.8238709	2.5936621	1.9437678	2.012887 6	1.331078 3	2.603438 7	1.981024 7
TG 55:4-FA18:1	6.3730674	4.4091635	4.9976414	12.670491	7.0343263	3.7176087	2.062297 9	1.611890 4	2.977770 5	9.311966 8

TG 55:4-FA18:2	4.3925807	2.9511537	4.5417128	7.2534452	4.4540404	2.583523	2.285700 2	1.981894 9	3.049498 7	4.663916 6
TG 55:5-FA18:1	6.0635994	2.0682981	4.4689334	13.587629	6.0151006	2.9789839	2.456159 4	1.654555 8	2.600320 3	6.865425 1
TG 55:5-FA18:2	8.4093259	2.5806949	6.7291793	19.229803	7.5113793	3.6852198	3.335689 9	2.098497 9	3.473271 7	8.756333 5
TG 55:5-FA20:4	0.2698623	0.2187761	0.4756662	0.2876703	0.2548771	0.2610854	0.192814 4	0.228789 3	0.236064 6	0.363904 1
TG 55:7-FA15:0	0.1950142	0.2589216	0.1469709	0.1801653	0.0914799	0.1578619	0.160088 2	0.159395	0.242649 8	0.210554 9
TG 55:7-FA22:6	0.8651161	1.5146913	0.8094771	0.6554949	0.5633901	0.7749584	0.744113 8	0.779839 8	1.159532 5	1.313793 2
TG 56:1-FA16:0	1.6053275	0.4040616	1.4224951	1.4284581	0.9871831	0.8317609	1.431322 3	1.274758 8	1.524845 4	1.243129
TG 56:1-FA18:1	0.7798805	0.8511859	1.1755655	0.8583834	0.5754086	0.6080868	0.567731 8	0.394318 4	0.827681	0.726428 8
TG 56:10-FA18:2	2.0985675	1.7868047	2.7954954	2.4434142	2.1756658	1.525474	1.495372	1.057319 6	1.987516 4	1.420934 9
TG 56:2-FA16:0	1.2375164	0.5515216	2.6198029	1.1760987	0.8150949	0.4167057	0.702079 1	0.439532 1	1.078398 6	0.571892 1
TG 56:2-FA18:0	0.9688168	0.8033405	1.3378648	1.1016261	1.0918091	0.5418894	0.712282 1	0.472932 4	0.933247 2	0.623717 3
TG 56:2-FA20:0	4.0569991	3.5399992	4.3033478	6.8505747	3.6487857	2.9409767	2.047882 3	1.910835 8	2.469449 1	4.182561 9
TG 56:2-FA20:1	2.0404791	1.2625549	2.6400593	1.4686756	1.8962891	0.8780679	1.098572 2	0.554591 4	1.478343 5	0.801051 7
TG 56:3-FA16:0	0.8685676	0.3522645	2.1764449	0.9117486	0.5291865	0.3215187	0.540697 5	0.418984 1	0.866577 4	0.440997 7
TG 56:3-FA18:0	1.8526984	1.3220453	2.3065065	1.8593845	2.0211286	1.0014426	1.134341 3	0.837839 8	1.471340 8	1.064997 7

TG 56:3-FA18:1	6.3389076	7.7025637	8.1873739	10.19397	5.7809596	3.2058063	2.556332 5	1.762607 7	4.522042 2	6.596568 5
TG 56:3-FA18:2	2.8977192	1.7819532	4.4499044	3.6983712	2.4375531	1.3397813	1.884386 7	1.367933 1	2.810087 2	1.617700 9
TG 56:3-FA20:0	6.9828324	3.7430023	7.032396	15.053239	5.1763197	4.1551708	3.585296 2	2.982341 9	3.572077 3	6.370544 9
TG 56:3-FA20:1	4.2666704	5.594468	5.6705014	5.1765392	4.0611273	2.4562741	2.033105 6	1.393576 8	3.201593	3.760707 9
TG 56:3-FA20:2	0.189712	0.2476521	0.2879046	0.1539378	0.1763879	0.1449998	0.104086 4	0.101213 7	0.175407 2	0.198652 6
TG 56:4-FA16:0	0.4597227	0.3026011	0.9480736	0.43515	0.3280954	0.2688797	0.211931 6	0.252737 5	0.327596 8	0.346038 8
TG 56:4-FA18:0	0.4822086	0.5732347	0.632315	0.5177534	0.4376078	0.3916621	0.442904 7	0.442365 7	0.475664 5	0.575331 3
TG 56:4-FA18:1	9.9798616	11.023924	12.356659	13.926203	8.2441948	5.1741089	3.984571 8	2.724446 4	5.809342 8	8.323954 8
TG 56:4-FA18:2	9.3698736	6.5342645	12.401547	15.010556	6.8044602	4.3490774	4.456414 5	3.121339 4	6.109029 7	6.504260 3
TG 56:4-FA20:1	9.2085936	7.7089376	12.146546	12.200068	7.022541	4.5844626	3.784428 3	2.667994 3	5.365482 1	6.460827 8
TG 56:4-FA20:2	0.6399904	2.6814872	0.8346819	0.5373963	0.5998813	0.692102	0.349946 1	0.287432 6	0.499208 6	1.301304 4
TG 56:4-FA20:3	0.3566796	0.4674991	0.3869436	0.2993454	0.3163095	0.3194446	0.260072 5	0.221264 2	0.221673 4	0.453794 1
TG 56:4-FA20:4	0.1306434	0.2156942	0.2684216	0.0713189	0.1109671	0.1413474	0.198906 3	0.186358 4	0.109676 7	0.123315 2
TG 56:4-FA22:4	0.042223	0.023489	0.0535058	0.0735336	0.0666587	0.03835117	0.055235 2	0.047311 6	0.074958 7	0.030345 7
TG 56:5-FA16:0	0.6862304	0.6504839	1.5056035	0.566482	0.4183962	0.5502818	0.462404 1	0.403659 1	0.526062 6	0.890051 6
TG 56:5-FA18:0	0.7925047	0.9227338	0.8766011	0.7003672	0.5950562	0.9214197	0.716528 3	0.620823 8	0.755698 3	1.014976 3

TG 56:5-FA18:1	2.9431145	7.6634489	3.3889469	2.5358745	2.3918964	3.1312465	1.377918 5	1.279815 9	1.725649	4.805194 6
TG 56:5-FA18:2	12.037402	7.9948286	15.035152	17.453492	8.1216459	5.2720888	5.535987 1	3.482078 7	6.167439 8	7.897662 3
TG 56:5-FA20:1	6.8958683	3.9813884	9.8790765	9.0861901	4.8461084	3.0344686	3.587290 1	2.289946 5	3.998269 3	3.814094 4
TG 56:5-FA20:2	1.2861763	3.2472608	1.2456492	1.0710782	1.0425892	1.2860054	0.627595 6	0.512875 9	0.763281 4	1.916028 3
TG 56:5-FA20:3	0.9172697	3.5474895	0.9192529	0.7886125	0.7332004	1.4098092	0.498989 6	0.534491 5	0.507391 1	1.842367 6
TG 56:5-FA20:4	1.4332458	1.7146645	1.7350408	1.1110639	1.2088776	1.7321703	1.047610 1	1.084511 3	1.221097 4	1.808348 8
TG 56:5-FA22:4	0.7308692	0.9226774	1.8036466	0.5436839	0.6437692	0.7581861	0.385956 6	0.472939 3	0.573858 6	1.205075 6
TG 56:5-FA22:5	0.2015121	0.2667668	0.2854471	0.0933575	0.1725375	0.1739907	0.122589 4	0.249327 5	0.365138 7	0.226818 5
TG 56:6-FA16:0	3.4613036	4.4042039	4.2832694	2.2375756	1.6784443	3.4172603	2.432479 5	3.031733 7	3.615643	4.086548 8
TG 56:6-FA18:0	0.8885323	1.0923573	0.9890578	0.7516937	0.6452656	1.0867573	0.885004 6	0.988046 3	0.871797 8	1.011281 7
TG 56:6-FA18:1	3.7766052	8.0391856	3.7948818	2.6728948	2.4714614	5.0526011	2.318052 5	2.566643 4	3.110785 1	5.900193
TG 56:6-FA18:2	3.7423415	5.1306671	3.9140648	3.5971202	2.6931907	3.9981367	2.455980 8	2.232019 3	2.530612 3	3.971509 5
TG 56:6-FA18:3	0.8931425	0.6106358	0.9608954	0.7450631	0.5917072	0.5013023	0.615779 6	0.378274	0.644739 1	0.551563
TG 56:6-FA20:2	1.0267291	1.4180455	0.8557055	0.825594	0.7729226	0.9621205	0.587252 9	0.550134 7	0.634644 6	1.014994 2
TG 56:6-FA20:3	1.4916871	4.1681356	1.3094256	1.2509107	1.376673	2.3331937	0.836684 3	0.859436 4	0.902644 4	2.636861 6
TG 56:6-FA20:4	2.9365472	5.2750639	4.2368224	2.7261381	2.4095983	3.9899925	2.415110 2	2.494497 1	2.132188 1	4.723527 2

TG 56:6-FA20:5	0.7372065	0.7571044	0.6769615	0.5581847	0.5033641	0.6488954	0.683003 6	0.583155 9	0.827677 4	0.553947
TG 56:6-FA22:4	1.5758439	0.9830193	2.621979	1.3207136	0.9928337	1.3041008	1.059857 7	1.233263 3	1.290612 9	1.613533 8
TG 56:6-FA22:5	4.392556	7.0899398	5.2886666	2.4241936	2.2516055	4.6920814	3.053634	3.395095 7	4.717342 7	6.145525 1
TG 56:6-FA22:6	0.7467765	1.3375705	0.8842041	0.6456339	0.5448526	0.8383656	0.990017 9	1.224341 2	1.347386 4	0.770439 2
TG 56:7-FA16:0	8.4372408	13.666753	6.726199	5.336389	4.3435003	9.9295654	7.560401 7	8.826085 5	10.63073 1	13.42350 2
TG 56:7-FA16:1	0.2459189	0.5703723	0.3226427	0.1593889	0.1617147	0.3123023	0.164459 9	0.148013 5	0.241127 1	0.497131 9
TG 56:7-FA18:0	0.3703799	0.5282138	0.421635	0.2842657	0.3424564	0.4189773	0.551807 4	0.429329 5	0.636183 8	0.408634 2
TG 56:7-FA18:1	5.3292084	12.568113	4.9873512	4.0777142	3.4849841	7.4095063	4.541812 2	5.575014 9	6.739719 7	11.34141 6
TG 56:7-FA18:2	6.1604503	5.9731691	4.5076686	4.4439819	3.388059	6.645437	5.386705	5.271990 3	5.868015 9	5.781692 7
TG 56:7-FA18:3	0.5557767	0.4476897	0.3594393	0.3499501	0.2723238	0.4839814	0.382925 1	0.333861 8	0.422575 6	0.393143 3
TG 56:7-FA20:3	1.3978676	1.6424278	0.8556819	1.1227105	0.8723537	1.599319	0.876838 6	0.818157 2	0.713755 8	1.505613 4
TG 56:7-FA20:4	3.0032954	4.880848	4.3022199	3.1473891	2.6305747	4.3693575	2.261673 1	2.476908 1	2.296704 7	5.308726 6
TG 56:7-FA20:5	2.3926594	6.5482441	2.6159518	1.8851647	1.7595492	3.6857045	2.191881 9	2.381799 8	3.073786 9	3.893207 1
TG 56:7-FA22:4	0.2237968	0.2561369	0.3116775	0.2288011	0.2137181	0.2535707	0.192057 9	0.173913 2	0.199927 7	0.297759 2
TG 56:7-FA22:5	8.7398492	7.9146475	8.0152869	5.4549508	4.0041084	8.7185772	8.339858 2	9.135769 4	10.21137 2	7.899116 9
TG 56:7-FA22:6	29.775174	61.786093	25.318778	21.264002	18.539068	37.592969	27.46251 5	33.99641 4	40.88210 4	61.85195 2

TG 56:8-FA16:0	12.609236	11.993414	7.8116981	9.7363588	6.5313522	13.836611	16.907793	17.81581	18.526628	15.235317
TG 56:8-FA16:1	0.7824397	2.1787695	0.7378088	0.6298401	0.5348103	1.2545158	0.565041 9	0.748705	1.153700 3	1.998766 7
TG 56:8-FA18:1	1.8627595	3.6926794	1.7367745	1.4901331	1.4550792	2.7252813	1.970002 1	1.637404 9	2.374875 6	2.877253 8
TG 56:8-FA18:2	10.629407	11.071816	7.3308471	8.4981206	5.622619	12.117656	14.06281 6	14.43633 8	14.49133 8	13.21168
TG 56:8-FA18:3	0.6229203	0.4971111	0.4707572	0.4801542	0.3862951	0.5993351	0.594416	0.572925 7	0.642639 5	0.560614 6
TG 56:8-FA20:4	2.1759817	2.1589263	2.7164772	2.6648445	1.5492202	2.6190226	2.176561 9	2.05117	1.766200 2	3.348651 2
TG 56:8-FA20:5	4.6735972	7.7382871	3.491882	3.8154731	2.8156342	6.4865852	5.071843 5	4.565968 6	5.325413 4	5.953318 1
TG 56:8-FA22:5	1.7551594	1.4907639	1.2270485	1.2694301	0.9494264	1.7240079	1.662211 1	1.809387 2	1.937610 1	1.997642 9
TG 56:8-FA22:6	63.853732	65.395593	39.277455	49.162551	32.61186	72.203484	86.24589 3	92.82115 4	92.96291 6	81.34338 8
TG 56:9-FA18:3	0.5305573	0.5219917	0.4082774	0.3584168	0.3301804	0.75433	0.749167 7	0.610723 3	0.780760 9	0.496023 9
TG 56:9-FA20:4	0.5032954	0.4609231	0.5746126	0.4494741	0.3226074	0.601354	0.548390 7	0.489803 1	0.567315 5	0.457327
TG 56:9-FA20:5	4.1437991	3.4082135	2.7151285	3.5725437	2.2052415	4.5787302	5.534850 8	4.278124 3	4.817500 6	3.180181 4
TG 56:9-FA22:6	6.5491319	8.3111554	3.7400223	4.7039784	3.7364909	8.4070867	6.334961 9	7.096022 9	8.798070 4	10.23532 9
TG 57:10-FA22:6	0.5110137	0.5777839	0.4875674	0.5406665	0.327727	0.5320371	0.439350 1	0.459654 7	0.433532	0.562010 3
TG 57:2-FA18:1	2.9251516	8.2252034	2.0409277	2.4302746	2.0894928	4.2865151	2.925546 9	2.972343 9	3.395299 7	5.659001 9

TG 57:3-FA18:2	3.8714702	5.2758119	2.5995841	3.4569396	2.3986648	4.397532	5.213448 8	4.531767 2	4.467748 3	4.509099 2
TG 58:10-FA18:2	4.4221975	5.6416251	2.6529804	3.7763936	2.730768	4.8201172	5.597529 8	4.916739 9	4.853976 5	4.889231 9
TG 58:10-FA20:4	0.3602954	0.5947944	1.2955617	0.4794791	0.27571	0.6648903	0.485742 4	0.621440 9	0.672089	0.613402 5
TG 58:10-FA20:5	0.4589477	0.5085492	0.5842055	0.3804132	0.2307909	0.6864688	0.493403 9	0.538477 7	0.739106 5	0.410134 2
TG 58:10-FA22:5	0.6519632	0.5635677	0.3814518	0.683555	0.3717438	0.5826219	0.692604 3	0.530651	0.700810 8	0.597213
TG 58:10-FA22:6	11.012601	16.2022	5.70975	9.8273411	5.9107265	13.594511	15.93909 3	13.95346 1	13.22158 1	14.34390 6
TG 58:2-FA18:1	0.5655793	0.4087042	0.7088217	0.6494702	0.4428247	0.3774837	0.430571 3	0.285943 3	0.529882 7	0.658888 8
TG 58:3-FA18:1	0.9520621	0.6824714	1.5479557	1.2111454	0.698485	0.4473456	0.543578 3	0.345099 3	0.880733 4	0.508337 8
TG 58:5-FA18:1	0.3805348	0.3248975	0.3415479	0.2271275	0.2073949	0.1614809	0.161021 5	0.135055 4	0.180243 7	0.264713 5
TG 58:6-FA16:0	0.4071606	0.2420382	0.3581268	0.2729804	0.2389375	0.1984817	0.269854 6	0.233305 9	0.317959 8	0.314503 9
TG 58:6-FA18:0	0.1791477	0.2858965	0.1860051	0.1052963	0.1125213	0.1475264	0.117038 5	0.141536 4	0.205169 1	0.232242 9
TG 58:6-FA18:1	0.3726696	0.83848	0.5269109	0.3081526	0.2996956	0.4020197	0.244857 8	0.222440 9	0.289742 7	0.602324 4
TG 58:6-FA20:4	0.2927877	0.2218578	0.477532	0.3354714	0.1846971	0.1507009	0.232342 1	0.218291 5	0.268817	0.241556 7

TG 58:6-FA22:4	0.2727753	0.4974058	0.3550663	0.2120721	0.1635286	0.253629	0.173168 2	0.166290 6	0.182972		0.391585 1
TG 58:6-FA22:5	0.5336977	0.5273782	0.4034488	0.3419245	0.3287864	0.2864218	0.289067 9	0.289238 8	0.371945 5	0.392156 4	
TG 58:7-FA16:0	0.9316013	0.8096488	0.9028944	0.7159001	0.5317623	0.5723475	0.662554 2	0.631401	0.814515 8	0.952440 3	
TG 58:7-FA18:0	0.4920296	1.0502944	0.4935149	0.3798368	0.2978464	0.6502011	0.558453	0.571993 6	0.698736 8	0.603061 6	
TG 58:7-FA18:1	0.9285554	3.5404188	1.0927322	0.5467059	0.641561	1.313529	0.615405 4	0.745218 8	0.9385	1.947579 7	
TG 58:7-FA18:2	0.6114118	0.7149293	0.6139316	0.479611	0.4207244	0.5434133	0.430169 5	0.459995 2	0.565096 9	0.626713 9	
TG 58:7-FA20:4	0.3659079	0.3614029	0.5435331	0.3938844	0.2543175	0.2154777	0.246953	0.227272	0.295700 5	0.310574 8	
TG 58:7-FA22:4	0.4310534	0.6245193	0.514551	0.420332	0.3323576	0.4195333	0.28904	0.269800 5	0.320827 4	0.690942 6	
TG 58:7-FA22:5	0.9728607	3.2198796	0.9913563	0.6138967	0.6658026	1.3302385	0.715147 1	0.796486 9	1.038016	1.761552 2	
TG 58:7-FA22:6	2.4435418	3.1266005	1.6674724	1.876611	1.8109162	1.9428412	2.042200 4	1.927171 8	2.524204 1	2.751718 5	
TG 58:8-FA18:1	2.386662	11.574439	1.7922929	1.7035223	1.5438518	3.9614375	1.833869 9	1.938695 2	2.716182 9	6.488908 6	
TG 58:8-FA18:2	1.7110386	2.9330888	1.5741988	1.2333453	1.007014	1.9275435	1.763880 3	1.763028 6	1.878114 1	2.162289 1	
TG 58:8-FA20:3	0.1566683	0.2303862	0.1957884	0.1229247	0.0933209	0.177207	0.129121 1	0.113249 6	0.118048 4	0.172332 6	
TG 58:8-FA20:4	0.1964682	0.260833	0.4923346	0.2304887	0.1745199	0.2623375	0.186267 2	0.203341 4	0.244872 8	0.258092	
TG 58:8-FA22:5	1.8470517	4.4285245	1.5102366	1.302568	1.1322212	2.1241856	1.509959 9	1.553976 8	1.780785 1	2.680988 7	
TG 58:8-FA22:6	7.7558278	34.834972	6.1121957	6.3170695	5.8859621	12.047176	7.377725 4	9.020695 4	10.34054 9	20.48813 7	

TG 58:9-FA18:1	2.9459309	8.5754168	1.9447587	2.3993738	2.1042849	4.2737825	3.159689 6	3.046972 4	3.626086 2	5.909583 4
TG 58:9-FA18:2	2.7295295	6.9428597	1.4298937	1.9884105	1.5960834	3.812873	2.987552 9	2.850046 6	3.155843 7	4.641603 1
TG 58:9-FA20:4	0.2882595	0.3583856	0.8170358	0.2368924	0.1536211	0.394354	0.246873 9	0.288465 8	0.303131 8	0.385236 4
TG 58:9-FA22:5	1.4641135	1.6897693	0.9048968	1.2096052	0.6884652	1.4583969	1.524616 1	1.325581 4	1.371508 2	1.459662 9
TG 58:9-FA22:6	14.145824	41.337822	7.9283992	11.781143	9.2052605	21.497229	14.71483 2	15.21978 2	16.28350 5	30.00194 4
TG 60:10-FA22:5	0.2012064	0.2397379	0.2211086	0.1585322	0.0877954	0.1869736	0.166304 3	0.209847 1	0.221094 9	0.163617 7
TG 60:10-FA22:6	0.9106939	1.8474356	0.7233486	0.8416592	0.4869296	1.0420907	0.895508 1	0.996363 5	0.963745 7	1.247215 3
TG 60:11-FA22:5	0.270961	0.2592851	0.3568713	0.2046883	0.1461545	0.2956254	0.253790 8	0.335368 1	0.481120 3	0.267621 3
TG 60:11-FA22:6	1.0093512	1.9912373	1.1997479	0.894561	0.5884267	1.5320034	1.223077 5	1.459361 3	1.618258 7	1.492114 2
TG 60:12-FA22:6	1.657596	2.8018163	1.7022288	1.5617667	0.7522003	2.7052629	3.090873 6	3.727230 1	4.324369 9	2.497459

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Incorporation by Reference

All publications and patent applications mentioned herein are hereby incorporated by reference in their entirety as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference. In case of conflict, the present application, including any definitions herein, will control.

Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

We Claim:

1. A method of preventing or treating a metabolic disorder in a subject, comprising administering to the subject a composition comprising a bacterial strain that expresses a bile salt-regulating gene or bile acid-regulating gene.

2. The method of claim 1, wherein the bacterial strain is *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*.

3. The method of claim 1 or 2, wherein the bacterial strain regulates the bile salt by glycine conjugation or taurine conjugation.

4. The method of any one of claims 1 to 3, wherein the bile salt-regulating gene encodes a bile salt hydrolase (BSH).

5. The method of claim 4, wherein the BSH is any one of the bile salt hydrolases listed in Table 1.

6. The method of any one of claims 1 to 5, wherein the bile acid-regulating gene encodes a 7-alpha hydroxysteroid dehydrogenase.

7. The method of claim 6, wherein the amino acid sequence of the 7-alpha hydroxysteroid dehydrogenase is at least 40% homologous to an amino acid sequence of a *Clostridium absonum* 7-alpha hydroxysteroid dehydrogenase.

8. The method of any one of claims 2 to 7, wherein the bile salt or bile acid is any one of the bile salts or bile acids listed in Table 3.

9. The method of any one of the preceding claims, wherein administration of the composition alters the subject's lipidome.

10. The method of any one of the preceding claims, wherein administration of the composition decreases white adipose tissue weight in the subject.

11. The method of any one of the preceding claims, wherein administration of the composition alters health-associated lipid biomarkers in the subject.

12. The method of claim 11, wherein administration of the composition decreases plasma triglycerides (TG) levels in the subject.

13. The method of claim 11, wherein administration of the composition decreases cholesterol levels and/or cholesterol ester (CE) levels in the subject.

14. The method of any one of the preceding claims, wherein administration of the composition decreases abdominal fat pad mass in the subject.

15. The method of any one of any one of the preceding claims, wherein administration of the composition increases a bile acid in the subject.

16. The method of claim 2 to 15, wherein the *T. sanguinis* bacterial strain is any one of the *T. sanguinis* bacterial strains listed in Table 4.

17. The method of any one of claims 1 to 16, wherein the composition is formulated for oral delivery.

18. The method of any one of claims 1 to 17, wherein the composition is a food product.

19. The method of claim 18, wherein the food product is a dairy product.

20. The method of claim 18, wherein the food product is yogurt.

21. The method of any one of claims 1 to 16, wherein the composition is formulated for rectal delivery.

22. The method of any one of claims 1 to 21, wherein the composition is self-administered.

23. A method of treating or preventing a metabolic disorder in a subject, comprising
(a) depleting the gut microbiota of the subject,

(b) administering a composition comprising a bacterial strain that expresses a bile salt-regulating gene or bile acid-regulating gene.

24. The method of claim 23, wherein the bacterial strain is *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron.*

25. The method of claim 24, wherein the *T. sanguinis* bacterial strain is any one of the *T. sanguinis* bacterial strains listed in Table 4.

26. The method of any one of claims 23 to 25, wherein the bacterial strain regulates the bile salt by glycine conjugation or taurine conjugation.

27. The method of any one of claims 23 to 26, wherein the bile salt-regulating gene encodes a bile salt hydrolase (BSH).

28. The method of claim 27, wherein the BSH is any one of the bile salt hydrolases listed in Table 1.

29. The method of any one of claims 23 to 28, wherein the bile acid-regulating gene encodes a 7-alpha hydroxysteroid dehydrogenase.

30. The method of claim 29, wherein the amino acid sequence of the 7-alpha hydroxysteroid dehydrogenase is at least 40% homologous to an amino acid sequence of a *Clostridium absonum* 7-alpha hydroxysteroid dehydrogenase.

31. The method of any one of claims 23 to 30, wherein the bile salt or bile acid is any one of the bile salts or bile acids listed in Table 3.

32. The method of any one of claims 23 to 31, wherein the composition is formulated for oral delivery.

33. The method of claim 32, wherein the composition is a food product.

34. The method of any one of claims 23 to 31, wherein the composition is formulated for rectal delivery.

35. The method of any one of claims 23 to 34, wherein the subject is given antibiotics to deplete the subject's gut microbiota.

36. The method of any one of claims 23 to 35, wherein the composition is self-administered.

37. The method of any one of the preceding claims, wherein the condition is a lipid metabolic disorder and/or a steroid metabolic disorder.

38. A bacterial strain comprising a bile salt-regulating gene or bile acid-regulating gene, wherein the bacterial strain expresses a bile salt-regulating gene or bile acid-regulating gene encoded by an exogenous nucleic acid.

39. A composition comprising the bacterial strain of claim 38.

40. A composition comprising a bacterial strain that expresses a bile salt-regulating gene or bile acid-regulating gene and a pharmaceutically acceptable carrier.

41. The composition of any one of claims 39 or 40, wherein the bacterial strain is *Turicibacter sanguinis, Escherichia coli,* or *Bacteroides thetaiotaomicron*.

42. The composition of claim 41, wherein the *T. sanguinis* bacterial strain is any one of the *T. sanguinis* bacterial strains listed in Table 4.

43. The composition of any one of claims 39 to 42, wherein the bacterial strain regulates the bile salt by glycine conjugation or taurine conjugation.

44. The composition of any one of claims 39 to 43, wherein the bile salt-regulating gene encodes a bile salt hydrolase (BSH).

45. The composition of claim 44, wherein the BSH is any one of the bile salt hydrolases listed in Table 1.

46. The composition of any one of claims 39 to 45, wherein the bile acid-regulating gene encodes a 7-alpha hydroxysteroid dehydrogenase.

47. The composition of claim 46, wherein the amino acid sequence of the 7-alpha hydroxysteroid dehydrogenase is at least 40% homologous to an amino acid sequence of a *Clostridium absonum* 7-alpha hydroxysteroid dehydrogenase.

48. The composition of any one of claims 39 to 47, wherein the bile salt or bile acid is any one of the bile salts or bile acids listed in Table 3.

49. The composition of any one of claims 39 to 48, wherein the composition is formulated for oral delivery.

50. The composition of claim 49, wherein the composition is a food product.

51. The composition of claim 50, wherein the food product is a dairy product.

52. The composition of claim 51, wherein the dairy product is yogurt.

53. The composition of any one of claims 39 to 48, wherein the composition is formulated for rectal delivery.

54. A method of making the composition of any one of claims 39 or 41-53, comprising transforming a bacterial strain with a gene expression construct encoding a bile salt-regulating gene or bile acid-regulating gene operably coupled to a promoter that promotes expression of the bile salt-regulating gene or bile acid-regulating gene in the bacterial strain

55. The method of claim 54, the method further comprising culturing the bacterial strain to allow expression of the bile salt-regulating gene or bile acid-regulating gene.