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(54) **Titre : COMPOSITIONS ET METHODES POUR MODIFIER DES ACIDES BILIAIRES AFIN DE REGULER LE METABOLISME DES LIPIDES ET DES STEROIDES**
(54) **Title: COMPOSITIONS AND METHODS FOR MODIFYING BILE ACIDS TO REGULATE LIPID AND STEROID METABOLISM**

(57) **Abrégé/Abstract:**
Provided herein are methods and compositions related to treating or preventing metabolic disorder.

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Abstract:

Provided herein are methods and compositions related to treating or preventing metabolic disorder.

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

CROSS-REFERENCE TO RELATED APPLICATION

- 5 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

- 10 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
- 15 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
- 20 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
- 25 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, hypercholesterolemia, 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
- 30 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 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 (tauricholic 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.

5 **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
10 BSH-expression *B. thetaiotaomicron*. C. Relative combined plasma triglycerides (TG) of mice monocolonized with BSH-expression *B. thetaiotaomicron*. D. Relative cholesterol esters (CE) of mice monocolonized with BSH-expression *B. thetaiotaomicron*. All values normalized to sex-matched littermates, *= p<0.05 two-tailed t-test. BSH3 corresponds to
15 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
20 monocolonized with individual *T. sanguinis* isolates.

Figure 6 shows levels of circulating serum bile acids and cholesterol in mice monocolonized 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*
25 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
30 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 $\pm$ 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 phylogenetic 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. thetaiotaomicron*. 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**, phosphatidylglycines (PG), or **i**, phosphatidylserines (PS) of mice monocolonized with *bsh*-expressing *B. thetaiotaomicron*. **j**, Relative white adipose tissue weight of mice monocolonized with *bsh*-expressing *B. thetaiotaomicron*. All values
 5 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**,
 10 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
 15 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
 20 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 7 α -HSDH gene. **a**, Table depicting amino acid similarity and sequence coverage between closest
 25 predicted 7 α -HSDH homolog in noted isolate genome and 7 α -HSDH gene from *Clostridium absolum*. **b**, Chromatograms of cholic acid (CA) or cholic acid with 2 hydrogens removed (CA-2H) from *E. coli* cultures expressing the MOL361 HSDH homolog (7 α -HSDH) or non-bile modifying gene sequence in the same plasmid (cell
 30 homolog (7 α -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 $\pm$ 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*. OD₆₀₀ readings of noted *B. thetaiotaomicron* strains in BHI-S medium. Each point represents mean $\pm$ 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 $\pm$ SEM. Statistical comparison done with Welch's ANOVA with Dunnett'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**, tauroolithocholic 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, # = $p \leq 0.1$ (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**,
 5 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
 10 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, *= $p < 0.05$.

15 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,
 20 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
 25 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-
 30 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.

5 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).

10 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
15 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
20 prevention of a metabolic disorder in a subject (e.g., a subject with a lipid metabolic disorder, such as hyperlipidemia, hypercholesterolemia, 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,
25 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
30 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
5 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
10 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
15 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- α
hydroxysteroid dehydrogenase). Additionally, strains of *Escherichia coli* and *Bacteroides*
20 *thetaiotaomicron* were developed to express *Turicibacter sanguinis* bile-modifying genes
(e.g., genes encoding bile salt hydrolase or - α 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*
25 *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*
30 *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
5 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
10 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
15 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.,
20 *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%,
25 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	<i>Turicibacter sanguinis</i> MOL361	ATGTGTACAGGACTTAGCTTAGTTACAAAAGATAATAAGCATTTATTTGGACGAAAATTTAGA TGTAACCCGTACATATGGACAAGCTGTTCAATATGTTCCAAGAAAATTTATGATTGGTTCAATAT TGTGAGTGATGAACATATACGTCAAAGTATGCTTGTATTGGGATGGGAAATTGTTGTGGATC GTCTTCCCCTTCTTTTGTATGCAGTTAATGAAAAGGATTAGCAGGTGCCGGTTAAATTTTA CGCATTTTGTCTAAGTTTAACGAAAAGCTGTTGATGGAAAAACGAAATATTTCAAGGTTCAACT TTCTTATACTGGGCATTAAAGTAATTTCTCAAATTTAGATGAATTTAAAGAGCCTTAAAAACA GTTAATTATTACGAAATATTCAGTTAAAGAAGGCTTCTGTTGCAGGACTTCACCTGGATGTT TACAGATTTAAGTGGAATAAGTATTGTCAATTGAGTACATGGAAAGATGGAAATGCACGTATACG ACAAATCCAGTAGGAGCCTTAACAAATGATCCAACTTTCCCTTGGCATTTAACAAATCTATGC CAATATGTAAACATTAGATACAAAAACTCCAGCACCAAAACAATTTGGAGAAATATGTTGCTAA ACCAATTTGGTCATGGGCTTAATATGTGTGGAATCCCAGGAGATGCTTCTCCAGCTGCACGAT TTGTTCGAACAGTCTATTTCCGTGATACAGTTGTCTGAGCAGATGATGAAGTCAAGTGGTGT CAGCATTCCTTCCAAGTGCTAACAGGTGTTACCGTCAATAAAAGGAAGCGAAAATTGATCCAAAT GGAGATATGAATTACACCGTCTATAAATCTTGTATGTGCCAAGAATCAGGAACATACTACTA CACAGATTATAAAACCGTCGTATTAGTGCCGTTTIGCTTATCAAAAGCCGACCTAGATGGAA AAGAAATCATCAGCTTTTGAATATCAAGGTAAACAAGATATTTTATTCTCCAAAACCTAA

BSH Group II	<i>Turicibacter sanguinis</i> H121	ATGTGTACAGGGTTAAGTTTAACTACTAAAGAATGGA AAAACACTTCTTTGGT AGAAATTTAGATGTTCCCGCTTCATACGGACAATCTGTTCATATCATTCCAA GAAATTTCAATTGGCTAAATGTGCTAAATGGTGAAACATTAGCTTCTAAAT ATGCGTGTATTGGAAATGGGAAATCGTTGTAGATAATCATCCACTTCTTTTGA TGCAGTCAATGAAAAAGGATTAGCTGGTGTGGATTAAACCTTTACGCACCTT TGCTAAATTTAATGAAAAATGCCATCGATGGAAAAATAAATAATCTCCGCATC TGACTTTGTATACTGGGCACCTTAGTAACCTTTGCGGATTTAAATGAGTTACGT CAAGCGTTAGAAAAATTTAGTACTGACTAATAATCCATTGAGCATGAGCCTT CCAGTTGCAGGCTTTCACCTGGATGTTCACTGATTTAICTGGGCGTAGTATCG TGATTGAAAAATATGGCCGACGGTATGCATATTCATGAAAAATCCAGTTGGTG TTTTAACGAATGACCCAACTTTTGTATTGGCACTTA ACTAATTTAAGACAGTA TGTTACCCCTTGAAAAAGCAACACCCGGCTCCAAAAACAATGGGAGATTIAC GCTTCATCCATATGGTTCATGGTTTAGGAAATGTGTGGAATTCAGGAGATGC TTCACCTGCTGCACGATTGTTAGAACGGTCTTCTTTAGAGATTCAATCGTT GAAGCGAATGATGAATCAGTGGCGTTACTGCTTTCCTCAACGTGTTAACA GGGTAAACAGTTATTAAGGGTCTGAAGTTGATCCCGATGGCTCAATGAAT TATACCGTGTATAAATCAGCGATGTGTCAAGAAAGTGGAACTTACTATTAT ACCGATTATTACAATCGACGTATCAATGCCGTTAAATTATCAAAATGCTAAT TTAGACTCAAAAAGAAATTACAAGTTTCCCTTATCAAGGAGAGCAAGATATC TTGTTCCAAAAACTAA
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BSH Group III	<i>Turicibacter sanguinis</i> 1E2	ATGTGCACAGGATTATGCTTATCTACAAAGGATGGAAAAACATCTTTTGGGACGAAACCTTGATGTTCTCTCTTATAAACCAGGCCGTTCAAATGTTCCTCAAGGAATTTAAGTGGCTAACGTTGCGACCCAAAGAAACAATCACCTCTAAATACGCTTGCAATAGCCATGGGAATCGTCAATTGACAATCACCTCTCTCTTTGACGGGTAAATGAAAAAGGATTAGCTGGTGAGGATTAAATTTACACACTTCGAAAAATTCCTTCAACTGCIGTAAAAAGATAAAATCTCTTATCAGCTTCTGATTCGTCATTTGGGTGCTGAGTACGTTTTCATCTTTAAGCGAGTTAAAAAGACCTTACCCTCTGTTATCTTAACAAGTATTCCTTCAAAACCGGATTTACCAGTTGCGGGATTACATTGGATTTTACAGATAAAACAGGTGAAAGTATTGTATTGAATATATGGAAGACGGAATGCATATCCACGATAATCCAGTCGGTGTCTAACAAACGACCCAACTTCGACTGGCAATTAACTTAAGCCCAATATGTAAACCTTTCTGTAAACTCCACAACAGAAAGAAATGGGGAATCTACTCGTTAAACCATTTGGTCAATGGACTTGGCATGTGCGGAATTCCAGGAGACGGTTCTCCCGCTGCAAGATTGTCCGCACCGTCTTTTCCGIGATGCCGTTGTTGGAGCCGACGATGAAATAAGTGGGGTTACAGCCTTCTTTAATGTTCTATCAAGATTACGGTGATGAAGGATCTGAAATTGACCCCGATGGATCCATGAACCTTACCGTTTATAAATCAGCCATGTGTCAAGAACTCTCAAACTTATTACTACACAGATTACTATAACCGTCGAATCAACGCGGTAAATTAACACCTGATACAATGAATGCTGACCACATTACAACGTTCCCTTACCTAGGAAAAACAAGATATTGTATATCAAAATTAA
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BSH Group IV	<i>Turicibacter sanguinis</i> MOL361	ATGTGTACAGCATTTATCATTAACAGCAAAAGATGGTTCACATTTATTTCGGT AGAAATATGGATATTGAATATTCAATTTAATCAATCAATTTATTATTAACACCAC GTCGTTTGTATTATAAAAATCGTGCAACAGGTGAAATGAATCAAAACAAAGT ATGCGATTATTGGAATGGGAACCATTTATTGATGAACATCCATGTTATGCAG AGCTTTTAAATGAAAAGGATTAGCGGCAGCAGGATTAAACTTCCCTAACT ACGCACACTGGGATGAAAAAGCAATCGAAGGAAAAACAAATATCCCTCCT TATGATTTAGTTTTATGGGTCACCTTCAAATTTTGAAACAGTTAAAGAAAGTA AAAGAAAGCTTTAAAGATGTTGTTTTAGTTGATGTTCCAGTCAATGAACAA ACTCCAAATTGCTCCTTTACACTGGAATGATTTGTGATAAAACAGGTGAAAGT ATCGTTGTAGAAAAAACAGTAAATGGTTTAAAGTGTATGGATAATAAAGTA GGAGTTTAAACGAATGCGCCCACTTTTGATTGGCATTTAACAAACTTAACT CAATACATGGGATTAAACGTCGACACACCAAAAGATATAACACTCGGAGA ACAAGAAATTACATCCATTAGGGCAAGGGCTTGGTGCTTTCTCATTAACAGG AGATTATTCATCACCATCACGATTGTAAAGCTGCTTTCTTACGTAATAAT ATCGATTATGCAAATGTAAATTACTCTGGAATCAGTGAATTTCTTCCACATCT TAAACGGAGTIGCAAATGGTTCGAGGATCAGTCGTTACTCCTCAACATTAA ATGACATTACGTTATATACATCTTGTATGGATCAAGAACGTGGAATTATTT ATTACAATACTTATACAAATCATACGATTTCATCTATTAAATATGCATAATGA AGATTTAGACGCAAAAGAAATTAAATCATTTAAATTTAATGATGAATTTC TGTAATTTTACAAATTTAA
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BSH Group V	<i>Turicibacter sanguinis</i> MOL361	ATGTGTACAGCTATTACATTAAAGACACAAAGATGGATTGCAATGCATTAGGG AGAAATTAGATATTGTGGCTTATTAGATGTTGCTGTTATTTGATCCGA GGTCATATGCATTTACTCATACTATCATGAGTCTAAAAAGAAAAATAAT ACGGATGGTTGGAAATGTCTACGACGTTTGAAATAATCATGTCTTATTAGTTG ACGGATGAATGAAAAGGGATTAGCTTGGCGTGTATTAGAGTTACCTAAAT ATGCTTCATGGAGTAAAGCATTTGGATAAAGATAAAATAAATATGGCTCCTT ATGATTTTGTTTATTGGATTTTAGCAAATTTTCAATCTCTTGAGGAAGTAAA AGACGGATTAAATAATGTAAATCTAGTTAATGATCGCTTGAAAGGGAAG AGGTATCAGTAGATGTTCAATTGGATTGTAACTGATCGTACAGGACAGTCTA TTGTAATAGAAAAACGAAGGGGAATTTTCGAATTTATAATAATAAGGTGG GAGTTTAACTAATGCTCCACATTCGATTGGCATCTCATAAATTTAAATCG GTATATGAATATACAAAGTGACGAAATCCGCATAAGGTGAAAGTGGGACATC AGGAGTTAAGTTTIGACTCAGAAAGGTTTGGGGGAATCGGACTACAGGAG ATGTTTCATCTTCATCTCGTTTGTAAAGCAGCTTTTCTAAGAAATCATAT TAGAGTAGAAAAAGGAGAAAGATGCTTTAATAACAAGTACTTTTCATATTT AAGTAAATGTGGCTGTTATCAAAAGGAACTGCTGTTACTTGCCACCAACAATA TTTGAAAAACGCAGTGTACTAGTTGTATGTGTTTAGAGACAGCGCTTTATTA CTATAACACTTATAATAATAATCAAAATAATGCTATTTCATTTATTGACGAG AATTTAGATGCCTCTGAAAGTTAAAGTGTTCCTTATCAAGATAAACTGGTA GTACAGAAACAAATTAA
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BSH Group VI	<i>Turicibacter sanguinis</i> H121	GTGTGTACAGCCAATTACATTAAACAAGCGAAAAATCATCATCTTGTGTGGA CGGAATTTTGATATTCACCCCAATGAATGATTTATCAGTTGCTTTAGTTCCAC GAGAAATTTGAATATGTAAATCGTGTGACGAATGAAGAAATGAAACGAAA TATGCAGTTTTAGGAATGGGATTATTTTATGAAAATCATATTTCTTTTGTG ATGGAGTAAATGAAAAGGATTATCTTGTCTGATGTTACAAATTATCTAAGT TTTCTACTTGGAGTCATAAATCAGGAAGGATAAGGTCAATATAGCCCCAT ATGATGTAGCTTTTGGGTTTATCTAATTTTCAACGATTCTGAATTAAT GGAAGTCTTAAACAGTTAAATATTGTGGCTCTTCTGTGATCATCAACGGC ATTATCGACAGAAATTCAATTGGCTTGTAGTGATACGAGTGGTCAATCGAT CGTCATTGAGCGAACAAGAGATAAGTTAACAGTTTATAATAATAAGGTAG GCGTTTTAGCAAAATCTCTCAACCTTTGATTGGCATTTAAATAACTTAGATTG TTATATTAAATGTCAAATCAGAGCAGCCAGAGGAAACTAAATGGGGACAAC AAATGTTATCGCCTTATTCTAATGGCTTTGGTACGATTGGACTTCCTGGCGA TTTTTCTCTCCGTACGATTGTAAAGGCTGCTTTTACGAAATCATGTG AACGTTGGGGAAGGTGATGAATCAGCAATTAGTGAATGCTTTCATATACTA GATAACTTTGTGTACCACTGGGGTGGTTGAGACTCCAAAAGAAAAGA GTGTCATTTGACTAAGTATAGTGCATGTCTTTTGTAGAGACTCAATTATAT TATTATAAGACCCAGCAGTAATCAGCAAAATCAAGTCATTGATTAAACAAA GAAAAATTTAGATGCTAAAGGATTAAACTATTTCCTTATCCCAACAAGATT ACAGTCCATGATCAGAAATTAG
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BSH Group VII	<i>Turicibacter sanguinis</i> 1E2	ATGTGTACAGCAATCTCAATCAAGCATCAAAACAGACCACGCATTTTATAGCA AGAAACTTTGATTATGATTCGACCAGTCAATTAAAGTTAGCTAAATATCCA AGAAATTATAGCTCCCGCTTGAACCAACGCTCAACACCTTTAAAAACCCGA TATTCGATCATTTGGCATGATGCTATGGCATGAAGGAACCCATGTCCTAGTA GATGGCATGAATGAAAAGGGGCTATCAGGTGCCATTTTAAATTTACCTGAC GCCTGCGTGTGGAATAAAGCCCTCATTTCCGATGGCATCAATCTCTTACCTA CCGATGTCCTCTTCTATTGTTATCGCAGTTTCTTCTGTCAACCGAATTAA GCGGCCATTCACTCAACTCAATATTGTGGCCCCCGAGGATCATCCCTTTGCT AAACCCTCAATTCACTGGATGTTTTCGGATAAAACCTGGTGAGTCAATC GTCGTCGAACAAACGGAATCAGGCCTATGTATTATGATAACCCATATTGGG GTTCTAACTAATGGGCCAACCTTCGATCAACAATTAAATCAACATTTCCCCCT ATCTCAAAAGATAGCCAAACGGCTCCTCCCTCCAGGAGATGATTCCTCTC CCTCACGCTTTATCCGGCGGGGTATTAAACACCATCTTCAAATGGACTC AACAGCCGCTATCGACGGTAACCTCATTTGCTTTACATCTAGGAAATGTCG CCTCCTCTCCCTGGGATTTTAAAGCAACACAGGAGAAGAGTTTGAGACGC GTTATACAGCTTGTATGGACCTTAAACACTTGGCTATTACCTGAAATGGT ATCATCATCTAAAGACTCAAAATCATTTGACTTAAACAAAGAGCAGGATGAA AGCAAGACGCTGACTTTTTTTTGAGTAA
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BSH Group VIII	<i>Turicibacter sanguinis</i> MOL361	GTGAAGGAAGGAACCATCCCCCTTACAACCTATCTTTGCCGTTACTTACTCT TAAAGTATGTGTGCTACCGTCGAAGAAGTCATTTCAAAATTAGAAAAATGATG TTACACTTATCGCAAAGCCTGTCTTCGGGGATATCCGTAATACTCACTGGAT GTTTAGTGACCGTACAGGAGAAACCATCATCATTTGAACCTGATGTAGATAA ACTGAAGATTCAACCGACATTCAATGGCGCTCTTAACAAATAGTCCAAATTA CGATTGGCATCGTACCAATTATTAAATTACTGCAATATACGAAGTCTCGA TTATTCAAGCGTTACACTGAATGACGATACGATTGAAGCCTGTTTCTCAGG GAGCGGAGCAGCTGGACTGCCAGGAGATTTTAGCTCGCCATCTCGATTAC ACGTTTAGCCTTCCTCAAAAATTACGCCCTGCAAAAGGAAAAAATGAAACCGA AGCTGTTACCTATATGTTCCAAACATTTAAAAACGTTCAATTTCCAATGGG GATCGTTGAAGTTGGCGAAGATAAAACCATACGGAGCATGATAGTGCGG TCGTTTATTGTGATTACACGATTTACACTGCCGTTATGTGCTCTGAAATCTCTT CGCTATTACTGGGTAAGCTACCAAAACATGCGTATTCAATGTGTGGATATG AACCCATTAAATTGAGAAAAACAAAGCTGTTCATTCGAATTAAATCCTATA AATGACATCAAAATATCTTAATTAA
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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%,
 5 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.

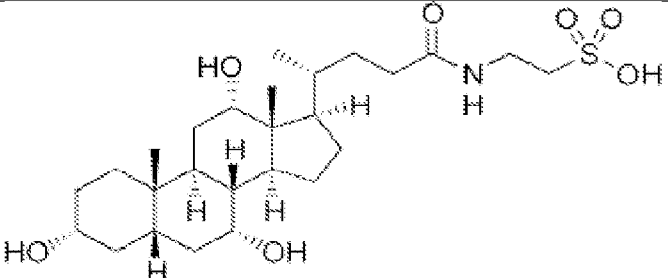
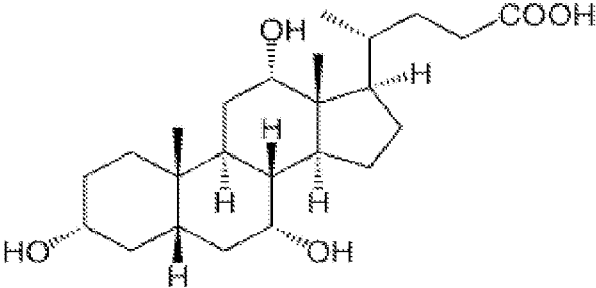
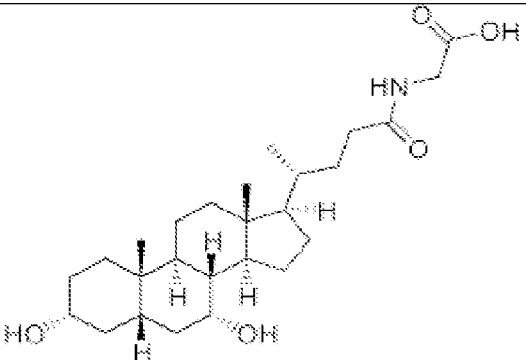
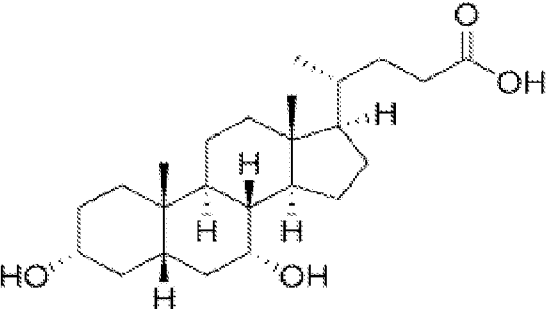
Exemplary 7-alpha hydroxysteroid dehydrogenase nucleic acid sequence:

10 >MOL361_HSDH (locus tag: HLK68_RS02750)
 ATGCGAAAATTAGAGAATGCAATAGCTCTTGTCACGTCTTCAACAAGAGGTATT
 GGGTTAGCGTGTGCTAAAAAATTAGCGAGTGAGGGTGCCATTGTTTATATGGG
 AGTTCGTCGTTTAGAGGTCCTCAAGAAATTTGTGATGAAGTGGCTAAAGAGG
 GTTTGAAAATGAAGCCTGTCTTTTTTGACGCCTACAACATTGATTCTTATGAAA
 15 CGATGGTAGAAGAAGTGATTAGGGAACAAGGTAAGATTGATATTTTAGTTAAT
 AATTTTGGAACTGGAAGACCGGAAGTAGATTTAGATTTAGTTAGTGGAGATGA
 GAAAGCTTTTTTTGATATTTTAGAAGCGAATATCGGATCAGTTTATCGTATCTCT
 AAAGTGGTGATTCTCATATGATTAAACAAGGAAAAGGAAGCATTGTTAATATT
 TCATCGATTGGTGGAAACGGTCCCAGATATTTCTCGTATTGGTTATGGTGTTTCAA
 20 AAGCAGGCGTTAACAATATAACTCAACAAATCGCTATGCAGTATGCGCGCTAT
 AATATAAGATGTAATGCGGTATTACCAGGTTTAACAGCAACCGATGCAGCTCTT
 GATAATATGCCAGAACAATTTATTAAGTCTTTCTTATCGCATGTTTCTTTAAATC
 GCATGGGAACACCTGAAGACATGGCGAATGCGGTTCTATTTTTCGCTAGCGATG
 ATTCTTCTTATGTAACGGGGGATATTATGGAGGTATCAGGTGGTTATCATTTAG
 25 GAACACCACAATATGCTGATTTTGTGTTGGTCGTAAAGTAGTTGAGGAAAAG

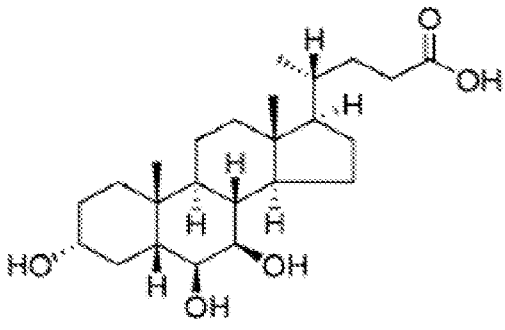
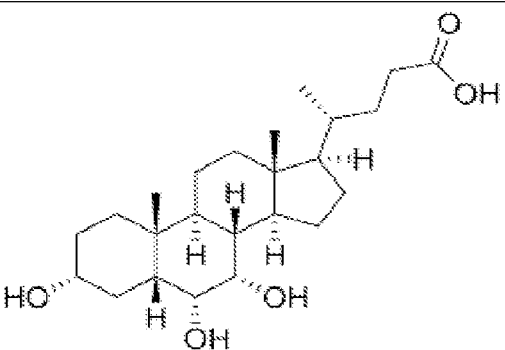
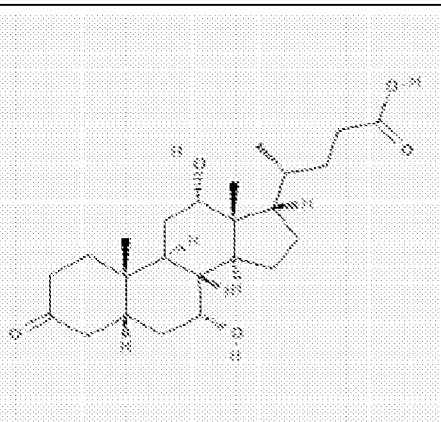
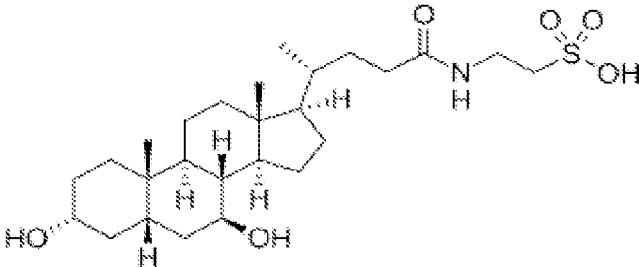
In some embodiments, the 7-alpha hydroxysteroid dehydrogenase is at least 40%, at least 41%, at least 42%, at least 43%, at least 44%, at least 45%, at least 46%, at least 47%, at least 48%, at least 49%, at least 50%, at least 51%, at least 52%, at least 53%, at least
 30 54%, at least 55%, at least 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 absolum* 7-alpha hydroxysteroid dehydrogenase.

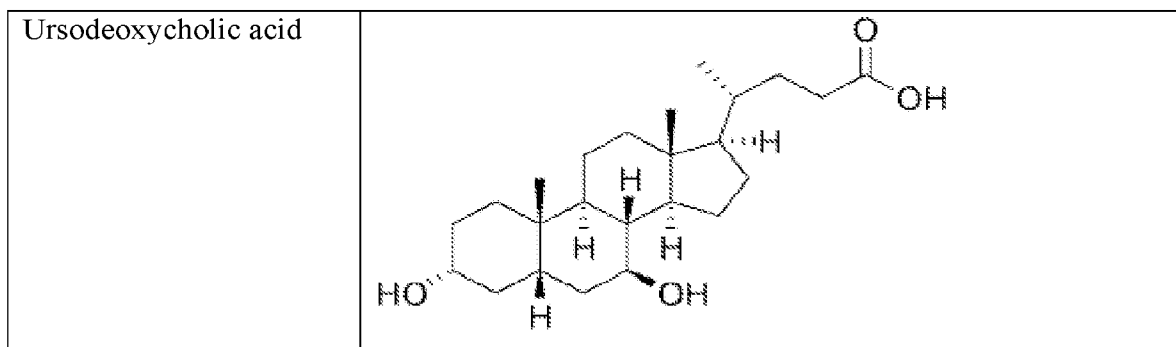
In certain embodiments, the bile salt or bile acid is any one of the bile salts or bile
 35 acids listed in Table 3. In some embodiments, administration of the composition increases a bile acid in the subject.

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)	The chemical structure of Deoxycholic acid (DCA) is a steroid with a hydroxyl group at C-3, a ketone at C-12, and a carboxylic acid side chain at C-14. The side chain is a 7-oxoheptanoic acid derivative. Stereochemistry is indicated with wedges and dashes.
Glycocholic acid	The chemical structure of Glycocholic acid is a steroid with hydroxyl groups at C-3 and C-12, and a glycoconjugate side chain at C-14. The side chain is a 7-oxoheptanoic acid derivative with a glycine moiety. Stereochemistry is indicated with wedges and dashes.
7-keto deoxycholic acid	The chemical structure of 7-keto deoxycholic acid is a steroid with a hydroxyl group at C-3, a ketone at C-7, and a carboxylic acid side chain at C-14. The side chain is a 7-oxoheptanoic acid derivative. Stereochemistry is indicated with wedges and dashes.
Taurochenodeoxycholate	The chemical structure of Taurochenodeoxycholate is a steroid with hydroxyl groups at C-3 and C-12, and a taurochenodeoxycholate side chain at C-14. The side chain is a 7-oxoheptanoic acid derivative with a taurochenodeoxycholate moiety. Stereochemistry is indicated with wedges and dashes. A sodium ion (Na+) is shown as a counterion.
Tauro-beta-muricholic acid	The chemical structure of Tauro-beta-muricholic acid is a steroid with hydroxyl groups at C-3, C-7, and C-12, and a tauro-beta-muricholic acid side chain at C-14. The side chain is a 7-oxoheptanoic acid derivative with a tauro-beta-muricholic acid moiety. Stereochemistry is indicated with wedges and dashes. A sodium ion (Na+) is shown as a counterion.

Beta-muricholic acid	 Chemical structure of Beta-muricholic acid, a pentacyclic triterpene carboxylic acid. It features a steroid-like core with a carboxylic acid group at C-28 and hydroxyl groups at C-3, C-14, and C-15.
Hyocholic acid	 Chemical structure of Hyocholic acid, a pentacyclic triterpene carboxylic acid. It features a steroid-like core with a carboxylic acid group at C-28 and hydroxyl groups at C-3 and C-14.
3-dehydrocholic acid	 Chemical structure of 3-dehydrocholic acid, a pentacyclic triterpene carboxylic acid. It features a steroid-like core with a carboxylic acid group at C-28 and a ketone group at C-3.
Tauroursodeoxycholic	 Chemical structure of Tauroursodeoxycholic acid, a pentacyclic triterpene sulfonic acid. It features a steroid-like core with a sulfonic acid group at C-28 and hydroxyl groups at C-3 and C-14.



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

In some embodiments, administration of the composition decreases white adipose
5 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
10 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 <i>T. saunginis</i>
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%,
5 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
10 AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCAA
GTCGAGC
GAACCACTTCGGTGGTGAGCGGCGAACGGGTGAGTAACACGTAGGTTATCTGC
CCATCAG
ACGGGGACAACGATTGGAAACGATCGCTAATACCGGATAGGACGAAAGTTTAA
15 AGGTGCT
TCGGCACCCTGATGGATGAGCCTGCGGCGCATTAGCTAGTTGGTAGGGTAAA
GGCCTAC
CAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACTG
AGACACG
20 GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGCGAAAG
CCTGACC
GAGCAACGCCGCGTGAATGATGAAGGCCTTCGGGTTGTAAAATTCTGTTATAA
GGGAAGA
ATGGCTCTAGTAGGAAATGGCTAGAGTGTGACGGTACCTTATGAGAAAGCCAC
25 GGCTAAC

TACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCGAGCGTTATCCGGAATTATT
GGGCGT
AAAGAGCGCGCAGGTGGTTGATTAAGTCTGATGTGAAAGCCCACGGCTTAACC
GTGGAGG
5 GTCATTGGAAACTGGTCAACTTGAGTGCAGAAGAGGGAAGTGGAATTCCATGT
GTAGCGG
TGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCTTCCTGGTC
TGTAAC
GACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGT
10 CCACGCC
GTAAACGATGAGTGCTAAGTGTTGGGGGTCGAACCTCAGTGCTGAAGTTAACG
CATTAAG
CACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGG
GACCCGC
15 ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAG
GTCTTGA
CATACCAGTGACCGTCCTAGAGATAGGATTTTCCCTTCGGGGACAATGGATACA
GGTGGT
GCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTAAAGTCCCGCAACGAG
20 CGCAAC
CCCTGTCGTTAGTTGCCAGCATTAGTTGGGGACTCTAACGAGACTGCCAGTGA
CAAAC
GGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCTTATGACCTGGGCTAC
ACACGTG
25 CTACAATGGTTGGTACAAAGAGAAGCGAAGCGGTGACGTGGAGCAAACCTCAT
AAAGCCA
ATCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGTTGGAATCGCTAG
TAATCG
CGAATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC
30 ACACCA
CGAGAGTTTACAACACCCGAAGTCAGTGGCCTAACCGCAAGGAGGGAGCTGCC
TAAGGTG
GGGTAGATGATTGGGGTGAAGTCGTAACAAGGTATCCCTACCGGAAGGTGGGG
ATGGATC
35 ACCTCCTT

>1E2
AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCAA
GTCGAGC
40 GAACCACTTCGGTGGGAAGCGGCGAACGGGTGAGTAACACGTAGGTGATCTGC
CCATCAG
ACGGGGACAACGATTGGAAACGATCGCTAATACCGGATAGGACGAAAGTTTAA
AGATGCT
CCTGGCATCACTGATGGATGAGCCTGCGGCGCATTAGCTAGTTGGTGGGGTAA
45 AGGCCTA
CCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGAACGGCCACACTGGGACT
GAGACAC
GGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGCGAAA
GCCTGAC
50 CGAGCAACGCCGCGTGAATGAAGAAGGCCTTCGGGTGTAAAATTCTGTTATA

AGGGAAG
AAAGGTGATAGGAGGAAATGACTATCAATTGACGGTACCTTATGAGAAAGCCA
CGGCTAA
CTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTA
5 TTGGGCG
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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, hypercholesterolemia, acid lipase disease, Barth syndrome, Fabry
10 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.

15 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
20 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)
25 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
30 (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
 5 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, cefmetam, cefmenoxime, cefmetazole, cefminox, cefodizime, cefonicid, cefoperazone, ceforanide, cefotaxime, cefotetan, cefotiam, cefoxitin, cefpimizole, cefpiramide, cefpirome,
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 15 doxycyclin, epicillin, erythromycin A, ethambutol, fenbenicillin, flomoxef, florfenicol, floxacillin, flumequine, fortimicin A, fortimicin B, forfomycin, foraltadone, fusidic acid, gentamycin, glyconiazide, guamecycline, hetacillin, idarubicin, imipenem, isepamicin, josamycin, kanamycin, leucomycins such as leucomycin A1, lincomycin, lomefloxacin, loracarbef, lymecycline, meropenam, metampicillin, methacycline, methicillin, mezlocillin,
 20 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, pipacillin, piperacillin, pirlimycin,
 25 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, tilmicin, tobramycin,
 30 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.

5 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*
10 *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
15 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, buccally, sublingually, parenterally, and rectally, as by powders, ointments, drops, liquids, gels,
20 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
25 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,
30 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
5 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
10 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
15 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
20 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-
25 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
30 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
5 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
10 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)
15 magnesium stearate, 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
20 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
25 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, Enterococcus, Lactococcus and Staphylococcus, Peptostreptococcus. In certain embodiments, the composition is substantially free of bacteria that increase the risk of metabolic disorder. Such bacteria
30 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.

5 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
10 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
15 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
20 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
25 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
30 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,
5 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
10 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
20 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
25 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 (tauricholic acid,
30 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

- 5 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 absolum* 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	7 α - 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
 5 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
 10 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
 15 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. thetaiotaomicron*. C. Relative combined plasma triglycerides (TG) of
 20 mice monocolonized with BSH-expression *B. thetaiotaomicron*. D. Relative cholesterol esters (CE) of mice monocolonized with BSH-expression *B. thetaiotaomicron*. 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
 25 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 monocolonized 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 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 physiology⁸⁻¹⁰.

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 fat²⁷. 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 mice³⁸. 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.

5

Table 5

Isolate	Derived from	Source	Reference	Notes
MOL361	human	DMSZ	Bosshard, 2002	<i>Turicibacter sanguinis</i> 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	
<i>Bacteroides thetaiotaomicron</i> VPI-5482	human	Justin Sonnenburg/ Fatima Enam	Xu, 2003	background strain
<i>B. thetaiotaomicron</i> pWW3837	N/A	rederived for this work	Whitaker, 2017	referred to as "WT" in this work
<i>Bt</i> -BSH-IV:MOL361	N/A	this work	N/A	WT <i>B. thetaiotaomicron</i> with BSH-IV from MOL361 in place of GFP
<i>Bt</i> -BSH-I:MOL361	N/A	this work	N/A	WT <i>B. thetaiotaomicron</i> with BSH-I from MOL361 in place of GFP

<i>Bt</i> -BSH-II:H121	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-II from H121 in place of GFP
<i>Bt</i> -BSH-III:1E2	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-III from 1E2 in place of GFP
<i>Escherichia coli</i> C41-pLys	N/A	Lucigen	N/A	expression strain
<i>Escherichia coli</i> 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 lipids³⁸. 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 chosen 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 report³⁸, 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 dicarboxylate 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
5 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
10 between changes in specific lipid species and mass of adipose tissue.

Table 6

		Fold Change				
		Welch's Two-Sample t-Test (bold indicates p<0.1)				
Sub Pathway	Biochemical Name	$\frac{MOL36}{1}$ GF	$\frac{1E2}{-}$ GF	$\frac{H121}{GF}$	$\frac{T12}{9}$ GF	$\frac{CON}{V}$ 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)-decanoate (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-arachidonoylglycerol (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-linolenoyl-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-docosaheptaenoyl-GPC (18:0/22:6)	1.04	0.88	0.94	1.11	1.15
Phosphatidylethanolamine (PE)	1-stearoyl-2-docosaheptaenoyl-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-HHTe	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-palmitoleyl-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'-Methylenbis(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-furanpropionate (CMPF)		0.80	0.86	0.92	0.98	1.21
Fatty Acid Metabolism (Acyl Carnitine, Monounsaturated)	3-decenylcarnitine		1.11	1.05	1.60	1.39	0.72
Secondary Bile Acid Metabolism	3-dehydrocholate		6.49	8.20	12.43	10.8_8	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-hydroxybutyrylglutamate**	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-hydroxyoctanoylglutamate	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-hydroxyseubate		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-acetyl catechol 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-dihydrouacil	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	83.2 5	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)	acetyl carnitine (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)	adipoyl carnitine (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-ketoglutarate*	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)	arachidonoyl carnitine (C20:4)	1.33	1.22	1.74	1.44	0.77
Fatty Acid Metabolism (Acyl Choline)	arachidonoyl choline	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	53.0 3	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	betonidine	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	1.00	1.00	1.26
Benzoate Metabolism	catechol sulfate	1.16	0.83	1.19	0.74	1.19	0.74	167.54
Ceramides	ceramide (d16:1/24:1, d18:1/22:1)*	1.19	1.04	0.93	1.58	1.58	1.44	1.44
Ceramides	ceramide (d18:1/20:0, d16:1/22:0, d20:1/18:0)*	1.03	0.64	0.81	0.87	0.81	0.87	1.34
Ceramides	ceramide (d18:2/24:1, d18:1/24:2)*	1.12	1.08	0.94	1.13	0.94	1.13	1.15
Primary Bile Acid Metabolism	chenodeoxycholate	2.99	5.14	6.81	6.61	6.81	6.61	0.52
Inositol Metabolism	chiro-inositol	1.63	2.10	2.08	1.81	2.08	1.81	1.09
Primary Bile Acid Metabolism	cholate	16.37	27.6 2	35.33	28.3 7	35.33	28.3 7	1.70
Sterol	cholesterol	0.88	0.89	0.92	0.96	0.92	0.96	0.99
Sterol	cholesterol sulfate	0.97	1.13	1.08	1.10	1.08	1.10	0.43
Phospholipid Metabolism	choline	0.91	0.87	0.90	1.09	0.90	1.09	1.08
Phospholipid Metabolism	choline phosphate	0.99	0.77	0.87	0.88	0.87	0.88	0.79
Food Component/Plant	cinnamate	0.91	0.95	0.89	1.35	0.89	1.35	9.54
Food Component/Plant	cinnamoylglycine	1.03	0.73	0.68	7.87	0.68	7.87	75.87
Fatty Acid, Branched	cis-3,4-methyleneheptanoate	1.21	1.23	3.26	1.67	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	1.81	1.17	1.13
Medium Chain Fatty Acid	cis-4-decenoate (10:1n6)*	0.89	1.01	1.78	1.22	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	1.81	1.34	1.15
TCA Cycle	citrate	0.99	1.34	1.21	1.38	1.21	1.38	1.07
Fatty Acid, Branched	citronellic acid	0.82	0.88	0.76	1.13	0.76	1.13	0.76
Urea cycle; Arginine and Proline Metabolism	citruiline	0.96	1.27	1.10	1.17	1.10	1.17	0.79
Corticosteroids	corticosterone	1.26	2.29	1.80	1.33	1.80	1.33	1.21
Creatine Metabolism	creatine	1.02	1.25	1.16	1.23	1.16	1.23	1.10
Creatine Metabolism	creatinine	0.96	1.10	1.03	1.17	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	cysteinyglycine 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)	1.21	1.08	1.68	1.42	0.84
Fatty Acid Metabolism (Acyl Carnitine, Polyunsaturated)	1.36	1.06	1.46	1.64	1.06
Tetrahydrobiopterin Metabolism	0.99	0.82	0.97	0.76	1.27
Food Component/Plant	0.68	15.8 0	0.30	0.63	1.31
Food Component/Plant	0.38	0.26	0.26	0.78	0.62
Food Component/Plant	0.16	0.10	0.08	0.55	0.29
Pyrimidine Metabolism, Orotate containing	1.29	0.95	0.78	0.83	1.26
Glycolysis, Gluconeogenesis, and Pyruvate Metabolism	1.45	1.56	2.08	1.73	0.90
Chemical	0.84	0.79	0.80	0.65	4.06
Urea cycle; Arginine and Proline Metabolism	0.98	0.98	0.98	1.05	0.67
Glycine, Serine and Threonine Metabolism	0.94	0.94	0.94	0.88	0.81
Fatty Acid, Dicarboxylate	0.77	1.14	1.06	1.23	0.77
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	0.80	1.86	1.01	1.67	0.58
Fatty Acid, Dicarboxylate	0.74	0.91	1.20	1.49	0.84
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	0.83	1.10	0.92	0.98	0.51
Fatty Acid Metabolism (Acyl Choline)	0.96	0.81	0.75	0.68	1.18
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	0.77	1.33	0.95	1.19	0.69
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	0.79	0.86	0.84	1.03	0.31
Fatty Acid Metabolism (Acyl Carnitine, Polyunsaturated)	1.32	0.89	1.94	1.55	1.08
Long Chain Polyunsaturated Fatty Acid (n3 and n6)	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-glutamyl-alanine		0.95	0.96	1.37	2.42	1.53
Gamma-glutamyl Amino Acid	gamma-glutamyl-citrulline*		0.76	0.93	1.08	0.77	1.12
Gamma-glutamyl Amino Acid	gamma-glutamyl-glutamate		1.01	1.05	0.87	0.97	2.89
Gamma-glutamyl Amino Acid	gamma-glutamyl-glutamine		0.99	1.05	0.96	1.11	2.16
Gamma-glutamyl Amino Acid	gamma-glutamyl-glycine		0.90	0.91	0.86	0.96	2.07
Gamma-glutamyl Amino Acid	gamma-glutamyl-histidine		0.94	0.98	1.00	0.81	1.85
Gamma-glutamyl Amino Acid	gamma-glutamyl-isoleucine*		0.80	0.96	0.89	0.96	1.57
Gamma-glutamyl Amino Acid	gamma-glutamyl-leucine		0.80	0.91	0.93	0.92	1.87
Gamma-glutamyl Amino Acid	gamma-glutamyl-methionine		0.84	0.86	0.94	0.76	2.57
Gamma-glutamyl Amino Acid	gamma-glutamyl-phenylalanine		0.83	1.07	1.06	1.02	1.62
Gamma-glutamyl Amino Acid	gamma-glutamyl-serine		1.01	0.96	1.05	0.90	1.73
Gamma-glutamyl Amino Acid	gamma-glutamyl-threonine		0.97	1.12	1.09	1.06	1.88
Gamma-glutamyl Amino Acid	gamma-glutamyl-tryptophan		0.91	1.04	1.14	0.91	2.07
Gamma-glutamyl Amino Acid	gamma-glutamyl-tyrosine		0.85	0.94	0.96	0.88	1.82
Gamma-glutamyl Amino Acid	gamma-glutamyl-valine		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	glutarylcarmitine (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	hexadecenenedioate (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	hypotaaurine	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	indoleacetyl glycine	1.25	3.10	1.13	0.85	1.05
Tryptophan Metabolism	indoleacrylate	0.91	1.14	1.07	40.9 ₃	55.13
Tryptophan Metabolism	indolelactate	0.73	0.93	1.08	0.87	1.00
Tryptophan Metabolism	indolepropionate	1.22	1.11	1.37	29.5 ₇	171.90
Tryptophan Metabolism	indolepropionyl glycine	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)	isocaprolylcarnitine	2.88	1.38	1.59	0.77	4.62
Fatty Acid Metabolism (Acyl Glycine)	isocaproyl glycine	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 (15:0)	0.81	0.78	1.08	1.14	3.58
Leucine, Isoleucine and Valine Metabolism	isovaleryl carnitine (C5)	0.81	1.00	0.92	0.74	2.08
Leucine, Isoleucine and Valine Metabolism	isovaleryl glycine	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)	lignoceroyl carnitine (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)	linolenoyl carnitine (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)	linoleoyl carnitine (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-l-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 (NAAAG)		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-isoptreanine		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-acetyl-citrulline		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-acetyl/methionine	0.81	0.85	0.91	0.84	1.63
Methionine, Cysteine, SAM and Taurine Metabolism	N-acetyl/methionine sulfoxide	0.92	1.14	1.12	0.97	1.38
Aminosugar Metabolism	N-acetyl/neuraminic acid	1.16	1.19	1.15	0.97	1.08
Phenylalanine Metabolism	N-acetyl/phenylalanine	0.75	0.91	0.98	0.90	0.61
Urea cycle; Arginine and Proline Metabolism	N-acetyl/proline	0.87	0.86	0.97	1.01	1.02
Polyamine Metabolism	N-acetyl/putrescine	1.28	1.16	1.24	1.22	1.24
Food Component/Plant	N-acetyl/pyrrolidine	0.84	1.12	1.08	0.98	1.16
Glycine, Serine and Threonine Metabolism	N-acetyl/serine	0.96	0.82	0.92	0.89	1.85
Methionine, Cysteine, SAM and Taurine Metabolism	N-acetyl/taurine	0.93	1.05	1.18	1.02	2.57
Glycine, Serine and Threonine Metabolism	N-acetyl/threonine	0.81	0.74	0.92	0.85	1.22
Tryptophan Metabolism	N-acetyl/tryptophan	0.64	0.82	0.86	0.91	0.79
Tyrosine Metabolism	N-acetyl/tyrosine	0.78	0.83	0.99	0.84	0.49
Leucine, Isoleucine and Valine Metabolism	N-acetyl/valine	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-formyl/methionine	0.78	0.81	0.67	0.99	1.18
Tyrosine Metabolism	N-formyl/phenylalanine	0.88	1.04	1.20	1.53	1.22
Aminosugar Metabolism	N-glycyl/neuraminic acid	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-methyl/pipecolate	0.92	0.97	0.99	0.83	1.16
Urea cycle; Arginine and Proline Metabolism	N-methyl/proline	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-phytyosphingosine (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	115.9 ₁	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	phenylacetyl glycine		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	spingomyelin (d18:2/16:0, d18:1/16:1)*	1.00	1.01	0.91	1.12	0.99
Sphingomyelins	spingomyelin (d18:2/18:1)*	1.13	1.04	1.11	1.01	0.84
Sphingomyelins	spingomyelin (d18:2/21:0, d16:2/23:0)*	1.06	0.87	0.93	1.21	0.81
Sphingomyelins	spingomyelin (d18:2/23:0, d18:1/23:1, d17:1/24:1)*	0.85	0.80	0.88	0.82	0.74
Sphingomyelins	spingomyelin (d18:2/23:1)*	0.97	0.97	0.99	0.98	0.77
Sphingomyelins	spingomyelin (d18:2/24:1, d18:1/24:2)*	1.01	1.04	0.99	1.01	0.91
Sphingomyelins	spingomyelin (d18:2/24:2)*	1.05	1.16	1.04	1.18	0.93
Sphingosines	spingosine	1.27	1.12	1.12	1.21	1.19
Sphingosines	spingosine 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)	tetradecadienedioate (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	thiopropine	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	tiglylcarmitine (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	14.6 0	45.21 4	82.9	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 signaling⁴⁰. 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/TGR5⁴¹. 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 study profiled 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 (β MCA) (**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 (G β MCA) (**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 size³⁸. 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

5

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 species²¹: 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 acids⁴², increasing their polarity and modulating their affinity for host bile acid receptors⁴³. The study searched the *Turicibacter* genomes for homologs of the characterized 7 α -hydroxysteroid dehydrogenase (7 α -HSDH²¹) 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 reaction⁴⁴. Because *in vitro* experiments showed only isolates from the MOL361 group performed bile dehydrogenation, the study cloned the putative 7 α -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 7 α -HSDH homolog (**Fig. 16d**), but this homolog did not act on DCA (**Fig. 16e**), supporting its annotation as a 7 α -HSDH.

Conjugation increases bile acid solubility and emulsification ability⁴⁵, 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.

20 *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 vector⁴⁸ 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 7 α -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 significant *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 7 α 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.

5 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

10

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 7 α -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 luminal 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 7 α -HSDH homologs the study tested, will further explain how these bacteria wield 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 disease⁶⁹ and depression⁷⁰, and selective serotonin reuptake inhibitors (SSRIs) have been found to negatively affect *Turicibacter* growth and colonization⁷¹, potentially because they inhibit activity of its unique serotonin transporter³⁸. 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

20 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 200 μ L gavage containing $\sim 10^6$ colony-forming units (CFU) of *Turicibacter* or $\sim 10^8$ 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).

5 *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 YCFA⁷⁴ (pH 7.4, per liter: 100mM MOPS, 10g casitone, 2.5g yeast extract, 2g glucose, 2g maltose monohydrate, 2g cellobiose, 44mg MgSO₄, 68mg CaCl₂, 0.9g NaCl, 10mg hemin, 0.45g K₂HPO₄, 0.45g KH₂PO₄, 4g NaHCO₃, 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 OD₆₀₀=0.41-0.51). Subcultures were all then diluted to OD₆₀₀=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. OD₆₀₀ 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
5 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
10 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% CO₂/5% H₂/90% N₂ atmosphere.

Genomic DNA was extracted in a 96-well format from the consolidated
15 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.

20 *qPCR screening of novel Turicibacter isolates*

Genomic DNA from 538 isolates was screened for *Turicibacter* 16S and the *Turicibacter* TuriSERT³⁸ 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
25 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

30 *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 pWW3837⁴⁸ 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 described⁴⁸. *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'o⁷⁵ was used to profile and visualize the different *Turicibacter* strain DNA sequences to locate putative bile salt hydrolase and 7 α -HSDH homologs in contig groups, generate variability profiles, and measure gene coverage and detection statistics. Average nucleotide identity (ANI) was calculated using OrthoANIm⁷⁶ (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). 7 α -HSDH sequence comparisons were performed using tblastn⁷⁷ 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 K₂EDTA 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 extraction⁷⁹. 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 parameters⁸⁰, 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 Fiji⁷⁸ Adiposoft⁷⁹ plug-in (version 1.1.16).

qRT-PCR measurement of liver transcripts

5 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
10 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-
15 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 $\Delta\Delta C_t$ method with auto-thresholded C_t values with *ppia* as the house-
20 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 = $0.05 < 0.2$.
25 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.

- 5 **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.

10

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	TCCAAATTATCAACAAATGCTGTATAAAT	Turicibacter discovery/qPCR	this study
TuriSERT-MOL361_F	GGGTTTGCAGATGCGGG	Turicibacter discovery/qPCR	this study
TuriSERT-MOL361_R	AATTATCAACCAACCGCTGTATAAAT	Turicibacter discovery/qPCR	this study
TuriSERT-1E2_F	GGGTTTGTGATGCCGC	Turicibacter discovery/qPCR	this study
TuriSERT-1E2_R	CCCAAATTATCAACTACTGTGTATAAAT	Turicibacter discovery/qPCR	this study
pET21_F	CTCGAGCACCACCACCAC	linearize pET21 <i>E. coli</i> expression vector	this study
pET21_R	GAATACCTCCTTAAGTTGTCTAGAAGG	linearize pET21 <i>E. coli</i> expression vector	this study
BSHIMOL361_F	aacaacttaaggaggtattcATGTGTACAGGACTTAGC	insert into pET21	this study
BSHIMOL361_R	tgggtgggtgggtcgcagGTTTTGGAAATAAAATATCTTGT TTACCTTG	insert into pET21	this study
BSHIIH121_F	aacaacttaaggaggtattcATGTGTACAGGGTTAAGTTTAA C	insert into pET21	this study
BSHIIH121_R	tgggtgggtgggtcgcagGTTTTGGAAACAAGATATCTTGC TCTCC	insert into pET21	this study
BSHIII1E2_F	aacaacttaaggaggtattcATGTGCACAGGATTATGC	insert into pET21	this study
BSHIII1E2_R	tgggtgggtgggtcgcagATTTTGATAACAAATATCTTGT TTCCTAGG	insert into pET21	this study
BSHIVMOL361_F	aacaacttaaggaggtattcATGTGTACAGCATTATCATTAAC	insert into pET21	this study
BSHIVMOL361_R	tgggtgggtgggtcgcagATTTGTAAATTACAGCAAAT TCATCATTA	insert into pET21	this study

BSHVMOL361_F	aacaactaaaggaggtattcATGTGTACAGCTATTACATTAAAG	insert into pET21	this study
BSHVMOL361_R	tgggtgggtgggtgctcgagATTTTGTGTTCTGTACTACCAGTTTATCT	insert into pET21	this study
BSHVIH121_F	aacaactaaaggaggtattcATGTGTACAGCCATTACATTAAAAAC	insert into pET21	this study
BSHVIH121_R	tgggtgggtgggtgctcgagATTCTGTATCATGGACTGTTAATCTTGT	insert into pET21	this study
BSHVIII1E2_F	aacaactaaaggaggtattcATGTGTACAGCAATCTCAATC	insert into pET21	this study
BSHVIII1E2_R	tgggtgggtgggtgctcgagCTCAAAAAGTCAGCGTCTTG	insert into pET21	this study
BSHVIIIMOL361_F	aacaactaaaggaggtattcATGAAGGAAGGAACCATC	insert into pET21	this study
BSHVIIIMOL361_R	tgggtgggtgggtgctcgagATTAAGATATTGATGTCATTTATAGGATTTAATTCG	insert into pET21	this study
7A_HSDS_F	aacaactaaaggaggtattcATGCGAAAATTAGAGAATGCAATAGC	insert into pET21	this study
7A_HSDS_R	tgggtgggtgggtgctcgagCTTTTCCTCAACTACTTTACGACC	insert into pET21	this study
pWW3837_fwd	GGATCTGATTACAAGGAC	linearize pWW3837 <i>B. thetaiotaomicron</i> overexpression vector	this study
pWW3837_rev	TATTTTAAATTTTGTGAATCCATAGATC	linearize pWW3837 <i>B. thetaiotaomicron</i> overexpression vector	this study
pWW_BSHIVMO_L361_F	tggattcaaaaaatttaaaataATGTGTACAGCATTATCATTAAC	insert into pWW3837	this study
pWW_BSHIVMO_L361_R	tcgiccttgtaatcagatccATTTTGTAAATTACAGCAAAATTC	insert into pWW3837	this study
pWW_BSHIMOL361_F	tggattcaaaaaatttaaaataATGTGTACAGGACTTAGC	insert into pWW3837	this study

pWW_BSHIMOL 361_R	tcgicccttgtaatcagatccGTTTTTGGAAATAAAATATCTTGT TAC	insert into pWW3837	this study
pWW_BSHIII1E2 F	tggattcaaaaaaatttaataATGTGCACAGGATTATGC	insert into pWW3837	this study
pWW_BSHIII1E2 R	tcgicccttgtaatcagatccATTTTGATAACAATAATCTTGT TC	insert into pWW3837	this study
pWW_BSHIII121 F	tggattcaaaaaaatttaataATGTGTACAGGGTTAAGTTTA AC	insert into pWW3837	this study
pWW_BSHIII121 R	tcgicccttgtaatcagatccGTTTTTGGAAACAAGATATCTTG	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	GTCCGGGATATTCAAGGATGCA	Cyp7a1 transcript measurement	Sayin, 2013

Table 8

Isolate	Derived from	Source	Reference	Notes
MOL361	human	DMSZ	Bosshard, 2002	<i>Turicibacter sanguinis</i> 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	
<i>Bacteroides thetaiotaomicron</i> VPI-5482	human	Justin Sonnenburg/Fatima Enam	Xu, 2003	background strain
<i>B. thetaiotaomicron</i> pWW3837	N/A	rederived for this work	Whitaker, 2017	referred to as "WT" in this work
<i>Bt</i> -BSH-IV:MOL361	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-IV from MOL361 in place of GFP
<i>Bt</i> -BSH-I:MOL361	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-I from MOL361 in place of GFP
<i>Bt</i> -BSH-II:H121	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-II from H121 in place of GFP
<i>Bt</i> -BSH-III:1E2	N/A	this work	N/A	WT B. thetaiotaomicron with BSH-III from 1E2 in place of GFP

<i>Escherichia coli</i> C41-pLys	N/A	Lucigen	N/A	expression strain
<i>Escherichia coli</i> 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									
4.89		2.31	1.93		1.19			0.90	
1.12		1.06	32.93		83.25			2.94	
1.08		1.18	1.11		1.09			1.02	
1.23		0.99	2.08		1.43			0.77	
1.15		1.23	1.74		1.74			0.98	
1.05		1.23	1.18		1.05			1.24	
0.68		0.48	1.20		1.27			1.12	
2.73		0.56	0.66		0.86			0.63	
1.01		0.11	1.29		2.68			1.10	
0.99		0.99	0.67		3.14			0.63	
1.07		0.75	1.51		1.12			0.64	
0.81		1.24	1.00		0.92			0.74	
0.98		0.96	0.88		1.12			0.44	
0.75		0.85	1.17		1.07			1.02	
0.99		1.00	0.69		0.68			0.57	
0.80		0.87	1.05		1.00			1.04	
0.41		0.34	1.78		2.25			0.78	
0.33		0.30	0.64		0.54			0.43	
0.85		1.01	0.34		0.63			0.29	
0.97		1.30	1.23		0.93			0.79	
0.85		0.74	0.98		1.02			1.18	
1.03		1.04	0.78		0.78			0.98	
0.61		1.15	1.15		1.11			1.21	
0.80		0.87	0.98		0.79			1.27	
0.89		0.82	0.87		0.95			0.97	
0.71		1.04	0.87		0.76			0.75	
			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)										
<u>MOL361</u>		<u>1E2</u>		<u>H121</u>		<u>T129</u>		<u>CONV</u>		
<u>GF</u>		<u>GF</u>		<u>GF</u>		<u>GF</u>		<u>GF</u>		
p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-value	q-value	p-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

[illegible]

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:W T-F3	Bt:WT- M18	Bt:WT- F19	Bt:BSHIV/MO L361-M4	Bt:BSHIV/MO L361-M5	Bt:BSHIV/MO L361-M6	Bt:BSHIV/MO L361-F7
CE 12:0	2.8205 287	2.6197 959	2.6684 662	1.55510 72	0.70867 25	3.7873036	2.3219351	1.5967224	3.7409552
CE 14:0	6.4658 433	6.1418 65	4.7465 62	5.10770 41	3.16882 51	7.0848343	5.9334441	4.6227474	6.7166259
CE 14:1	4.6458 692	3.9346 624	3.9778 745	2.99610 49	1.17774 62	5.5002478	3.4343202	2.7790632	5.9470227
CE 15:0	7.7324 218	8.0865 727	5.9072 193	6.28981 84	4.35137 3	8.9020616	7.8689673	5.5831207	8.2884003

CE 16:0	94.824 119	110.61 56	66.643 962	92.8838 35	102.397 89	102.64703	117.33327	91.306014	104.91616
CE 16:1	39.880 856	36.488 747	37.473 816	34.9003 3	40.8660 78	48.55576	36.965479	35.164076	59.936962
CE 17:0	5.4668 457	6.7739 6	4.7752 674	4.14493 22	5.74866 99	6.0347891	5.1248054	4.8563874	8.8076864
CE 18:0	6.3159 394	10.467 799	6.5826 592	5.95662 61	10.5325 25	7.9967056	7.6187395	8.9330937	9.8273594
CE 18:1	111.49 877	117.22 932	93.758 816	106.767 81	161.710 18	133.15325	124.77739	113.8683	174.19722
CE 18:2	1269.2 477	1336.7 69	630.02 152	1305.41 59	845.008 91	1211.9108	1551.6136	1238.8906	1009.6038
CE 18:3	32.711 933	27.695 203	22.682 603	24.0397 16	14.9962 7	33.995486	28.873226	22.52118	35.130521
CE 18:4	2.8879 007	2.5508 695	2.4524 69	1.69790 54	0.78619 28	3.3322451	2.0003131	1.6622857	3.5794448
CE 20:0	182.01 825	206.57 895	141.48 872	142.848 37	74.5683 54	280.55408	246.67964	170.17931	214.63787
CE 20:1	64.637 982	45.724 015	48.898 568	24.2662 67	7.84494 79	99.456283	35.5104	22.627029	76.698798
CE 20:2	3.0316 554	2.7334 719	2.4809 102	1.62859 87	1.16654 34	4.4698197	2.5348995	1.6221844	3.5719475
CE 20:3	30.379 84	29.895 242	18.384 904	26.9154 97	21.6434 08	33.240605	36.125895	26.328802	28.329695
CE 20:4	651.39 374	675.67 728	451.34 758	639.292 92	566.068 75	621.61545	727.91604	609.21378	643.76897
CE 20:5	138.16 244	138.97 544	89.619 751	136.969 98	65.9866 75	137.7666	131.93953	128.62414	187.31013
CE 22:0	4.0863 535	4.5512 026	3.2621 362	3.65051 6	1.87723 93	6.3029716	5.1685927	3.7459906	5.2218917
CE 22:1	3.4158 462	4.1205 707	2.7336 285	2.51593 11	1.75722 23	5.8519202	4.1874624	3.4442345	4.8870524

CE 22:2	33.929 538	36.256 921	27.897 029	25.6029 58	18.4934 93	44.610371	40.249936	28.660134	43.033129
CE 22:4	4.0442 349	4.5442 532	4.5200 824	3.09091 89	1.67037 63	6.1336069	3.9351662	2.9722126	6.7771842
CE 22:5	7.9402 796	7.9242 285	5.4879 236	10.0434 53	3.63773 31	10.895008	8.142855	6.667991	9.0509172
CE 22:6	191.60 182	202.29 939	109.88 072	212.128 26	119.578 23	214.21908	249.06159	221.67861	200.00841
CE 24:0	65.758 526	88.389 117	58.183 396	61.3843 61	52.4919 47	87.666522	101.2581	72.096024	88.924235
CE 24:1	15.800 786	16.026 549	12.423 203	12.5089 93	5.82380 23	19.861932	16.142133	13.267948	23.308043
Cer d18:0/24:1	0.2097 789								
Cer d18:1/14:0									
Cer d18:1/16:0	0.2015 476	0.1917 517	0.1776 299	0.11978 56	0.18424 49		0.1398755	0.1102742	0.1898528
Cer d18:1/18:0									
Cer d18:1/20:0									
Cer d18:1/22:0	0.6920 071	0.7539 929	0.3587 54	0.77135 94	0.21847 41	0.4934352	0.9425068	0.7410147	0.3199908
Cer d18:1/24:0	1.1543 339	1.2065 794	0.8508 07	1.17657 79	0.59770 65	0.9571946	1.194078	1.0892943	0.8309422
Cer d18:1/24:1	0.4964 801	0.4353 349	0.7819 596	0.46774 49	0.67115 91	0.4986169	0.5404877	0.4433059	0.9395859
DG 12:0 18:1									0.3027643
DG 12:0 18:2		0.6651 082							

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DG 18:1 20:4							0.43733 1						
DG 18:1 22:6							1.30121 75			0.9143947		0.7912277	
DG 18:2 20:4							0.60117 54						
DG 18:2 22:6							4.55189 66			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	7.6508 198	4.1567 734	8.2689 331	5.10858 77	3.33805 86	9.3832301	7.2763555	6.0817505	10.114626
FA 20:1	6.6773 09	4.2147 559	6.1757 319	4.92048 43	3.14166 36	6.2157708	6.0971532	5.4506142	6.203513
FA 20:2	1.9556 585	1.5324 989	2.0890 886	1.88132 94	1.49416 89	2.2402655	2.2237762	1.912577	2.1586639
FA 20:3	2.3588 725	2.1457 153	2.4215 541	2.40110 64	2.03614 05	2.4758157	2.5757548	2.2433928	2.5411972
FA 20:4	5.4373 061	4.2648 726	5.1055 686	6.11676 05	5.59723 58	4.4885234	6.1759078	5.2897709	5.3080196
FA 20:5	2.5039 149	1.8907 828	2.3896 583	3.61402 89	1.86084 91	2.37195	3.1090194	2.6273052	2.6906945
FA 22:0	3.3066 335	3.0522 546	3.7980 334	3.13992 32	3.11134 03	3.5722035	3.7896794	3.8039068	4.1189881
FA 22:1	3.4596 428	3.2855 745	4.9224 876	3.85675 65	3.08828 55	4.4863584	4.5281177	5.121508	4.5193462
FA 22:2	2.0614 965	1.3560 67	2.0523 042	1.52323 41	1.28439 9	1.7711761	1.6673192	1.6389668	1.8223979
FA 22:4	1.4336 785	1.4403 398	1.5714 955	1.36198 41	1.26012 64	1.5491645	1.5374407	1.2704374	1.6345007
FA 22:5	7.4855 619	3.7617 243	6.0325 457	6.03963 57	4.70230 34	4.9595861	5.4321507	3.99973	4.820024
FA 22:6	7.4607 314	5.6343 261	6.4215 594	10.2538 5	7.23296 3	8.0006422	9.8147395	7.991949	6.6864033
FA 24:0	2.3304 737	2.4191 614	2.8331 303	2.16845 47	1.95259 79	2.4602981	2.242451	2.2197227	2.5833424
FA 24:1	2.9466 557	3.4732 579	3.9699 698	2.97002 43	2.48504 25	3.5519963	3.281878	3.4335373	3.4138354
HexCER d18:1/16:0	0.1545 452	0.1698 333	0.2656 102	0.15070 09	0.21004 13		0.2174336	0.2246891	0.3402799
HexCER d18:1/18:0			0.1072 293						

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LPC 20:3	5.1385 759	3.9881 821	3.7485 552	5.11363 6	5.50049 93	5.8982847	5.2630298	3.9399311	4.2257873
LPC 20:4	11.033 09	8.4130 512	9.7060 455	12.8561 52	14.0713 44	9.0718493	12.048316	10.636414	11.881264
LPC 20:5	0.5423 802	0.5136 143	0.7691 267	1.27191 64	0.53426 6	0.5104891	0.6059468	0.7952598	0.9635305
LPC 22:5				0.58328 07					
LPC 22:6	2.0886 178	1.6363 887	1.0574 953	2.65571 29	1.97067 44	1.583261	2.2732971	2.5065484	1.7118868
LPE 16:0	4.6524 31	4.9927 175	6.6616 515	4.78671 55	4.19987 27	4.9320033	5.1685804	4.8439743	5.4025164
LPE 18:0	1.5216 276	1.9123 469	2.0088 568	2.08163 76	1.67962 16	1.7326299	2.2097112	1.8207728	2.0085508
LPE 18:1	0.8676 029	0.9684 716	1.1917 729	0.97036 06	0.91522 06	1.071815	0.8754013	0.8200818	1.3734043
LPE 18:2	2.2288 526	1.5618 217	1.8576 233	2.28177 46	1.18704 92	1.7280446	2.5053641	1.8663292	2.5472963
LPE 20:4	0.3769 819				0.41037 75				
LacCER d18:1/16:0									
LacCER d18:1/18:1									
LacCER d18:1/22:0				0.21057 64	0.18845 32				
PA 34:1	0.3623 669	0.3614 799	0.3400 997	0.31037 98		0.41597	0.2350231	0.2030481	0.2546081
PA 34:2	1.1125 444	1.1475 055	1.4342 789	1.26770 31	0.48057 3	1.4632951	1.0787222	1.0872302	1.1572885
PA 34:3				0					

PA 34:4	2.1722 584	2.2957 797	2.3042 85	2.35354 6	2.34589 93	2.2302908	2.1824796	2.2253009	2.3108795
PA 34:5	0.5879 593	0.5911 502	0.5300 71	0.51195 79	0.58517 14	0.7286388	0.5623052	0.4593841	0.6883496
PA 36:1	0.1399 251	0.1033 33	0.1803 42	0.15705 04		0.2375611	0.1119514	0.1530752	0.137257
PA 36:2	0.7181 603	0.8546 272	0.7649 533	0.86478 34	0.34045 28	0.8092042	0.7135106	0.7199199	0.8171991
PA 36:3	0.2750 549	0.3330 728	0.3369 643		0.15950 41	0.3155845	0.1959801		0.2897679
PA 36:4	0.1699 153		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		0.2413 801	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	0.5312 391		0.3901 075	0.43216 36		0.6136904		0.3990097	0.5658538
PC 12:0_18:0									
PC 12:0_18:3	0.9516 506	0.9515 332	1.3564 576	0.71364 13		1.4204447	0.7939776	0.6976693	1.1425444
PC 14:0_18:1	0.9826 846	0.8275 452	0.6261 948	1.03673 3	1.00260 43	1.1598772	1.0163837	0.7421172	0.7698949
PC 14:0_18:2	1.5941 643	1.4554 149	1.5548 906	2.01402 36	1.10524 36	1.8644396	1.8186553	1.5738887	1.5625056

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PC 16:0_22:1	0.4661 571								0.4811686				
PC 16:0_22:2	0.5365 972												
PC 16:0_22:4	2.1515 552	1.9825 612											
PC 16:0_22:5	18.856 182	14.883 168	13.368 53	26.0740 11	6.11454 66				26.096301	15.516014	14.769679		16.7086
PC 16:0_22:6	261.55 015	243.20 883	199.09 218	245.911 59	114.303 03				341.39018	293.78849	295.33079		280.01678
PC 16:1_17:0				0.84799 9									
PC 16:1_18:0		0.4287 625	0.6602 891		0.32556 53					0.3742509			0.5864761
PC 16:1_18:1	4.7338 655	3.2700 366	4.0289 137	4.55570 39	4.24813 29				5.163692	3.7844677	3.4015024		4.5517931
PC 16:1_18:2	9.7178 348	7.2881 76	8.6191 036	12.3067 19	5.80600 33				11.049385	11.117694	8.0805665		9.968546
PC 16:1_20:0			0.3829 046										0.4077208
PC 17:0_18:1	1.1949 968	0.9936 145	0.7784 824	1.31113 42	0.67585 88				0.9719682	1.2057371	0.9717043		1.2166262
PC 17:0_18:2	6.5548 207	5.8891 959	4.3938 884	5.94589 17	3.64343 6				5.3814728	6.5466363	5.3323982		4.6167551
PC 17:0_20:3	1.1478 307	1.2387 562	1.8389 309	1.26528 36	1.05889 94								
PC 17:0_20:4	7.3487 346	5.8982 442	5.6766 055	5.68447 08	4.31950 64				1.8622108		1.6838527		1.5903021
PC 17:0_22:6				7.73493 88					6.1059494	5.6725041	5.0926687		6.2811532
PC 18:0_18:0	1.0165 327	0.9348 12	0.8645 78	0.94535 7	0.89684 41				7.3941676	4.9454498			6.2410566
									0.7552522	0.7453348	0.8010022		0.7201723

PC 18:0_18:1	21.409 108	19.282 087	18.947 198	23.3757 87	14.5933 85	21.284393	20.859985	18.264372	18.603444
PC 18:0_18:2	316.10 263	289.52 771	249.29 724	321.001 08	210.266 52	249.23208	325.60727	282.99265	259.35498
PC 18:0_18:3	0.9656 271	0.9971 363	1.0104 403	0.98684 8	0.74320 77	0.8496963	0.9000294		1.0960125
PC 18:0_20:0	5.5726 356	5.3516 609	5.3626 152	5.42566 27	2.88639 49	5.4951477	5.7611424	4.8107611	5.8982747
PC 18:0_20:1	1.1205 816	0.7241 698	1.1351 01	0.72200 03		1.0527433	0.4859271	0.6747496	0.8406792
PC 18:0_20:2	1.4943 641	1.2228 866	1.0019 389	1.23441 91	0.93650 66	1.9716078	1.4342582	1.2016526	1.4273453
PC 18:0_20:3	23.348 929	22.279 982	21.405 096	23.9821 7	19.5311 75	23.335819	24.89359	23.793304	22.215929
PC 18:0_20:4	99.446 27	82.690 822	125.14 022	125.912 29	87.5682 91	77.669151	100.70658	95.962686	114.3578
PC 18:0_20:5	10.210 375	12.921 765	13.123 048	17.2573 22	7.34553 88	11.340938	10.114149	12.615384	22.421087
PC 18:0_22:4									
PC 18:0_22:5	3.7815 329	4.1919 711	4.9857 778	8.88461 53	2.46966 12	5.6029272	4.3147222	3.5984808	5.0716102
PC 18:0_22:6	64.546 072	63.386 773	55.412 251	76.3869 49	40.6563 11	71.295631	72.643411	79.013509	63.536882
PC 18:1_18:1	5.9198 401	5.3350 813	4.2002 282	5.64736 19	4.65868 15	6.091454	5.0068441	3.8849068	5.5629563
PC 18:1_18:2	70.823 563	60.863 87	46.617 588	60.2214 91	47.9215 41	61.238711	62.581128	45.59193	57.787173
PC 18:1_18:3									
PC 18:1_20:0	2.1610 547	1.8750 072	1.5194 017	2.01204 36	1.29684 41	2.6378534	1.9286398	1.6780902	2.2270545

PC 18:1_20:1		0.4718 633	0.4332 295				0.7337087			
PC 18:1_20:2			0.5384 662	0.37613 19	0.30697 66		0.8245082			0.4562686
PC 18:1_20:3	4.4822 126	4.2987 855	3.8056 748	3.95220 85	4.81783 36		6.4704668	4.1484012	3.6547625	6.2330707
PC 18:1_20:4	17.009 433	14.391 104	21.609 525	18.5936 84	17.7411 96		22.745374	15.719424	15.139215	24.583303
PC 18:1_20:5			3.5063 687	3.33481 26	1.82512 9		3.5122328		2.6963802	5.8428591
PC 18:1_22:5										
PC 18:1_22:6	16.596 759	18.282 796	15.188 555	18.4572 46	12.3871 77		24.759821	16.417923	18.772914	26.836021
PC 18:2_18:2	13.904 155	11.477 931	6.1220 212	15.9835 29	7.25867 99		11.714548	12.660191	9.952324	8.4140665
PC 18:2_18:3	1.0345 669			1.91309 52						
PC 18:2_20:0	10.610 847	9.7997 463	5.2704 961	10.6954 68	4.74107 39		9.0988478	11.196696	8.2020042	6.2650265
PC 18:2_20:1	2.1477 282	1.9306 927	1.1216 934	2.04227 42	0.97154 57		1.4104702	2.1906743	1.3961018	1.0852024
PC 18:2_20:2	1.0604 397	0.8069 84	0.4492 2	0.83031 67	0.50055 76		0.9773994		0.7913684	0.7127922
PC 18:2_20:3	2.1369 208	1.8111 33	1.2668 275	1.97866 85	1.18349 23		2.6199001	2.0755734	1.6922532	2.1042944
PC 18:2_20:4	6.2442 814	4.7554 584	4.5617 017	9.49983 49	4.03694 91		6.1711988	6.9933756	5.7628693	5.0029924
PC 18:2_20:5		1.7966 727								
PC 18:2_22:6				5.23012 77					4.6286618	

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PE 18:1_20:4	3.3713 824					4.52495 56						
PE 18:1_22:0	1.7109 477					1.00340 41				4.850343		4.540962
PE 18:2_18:2	0.2482 566											
PE O- 16:0/18:1												
PE O- 16:0/18:2	0.7526 089											
PE O- 16:0/20:4												
PE O- 18:0/16:0	0.7979 952											1.5469198
PE O- 18:0/18:1	1.0921 612					0.70847				1.7676861		
PE O- 18:0/18:2	3.4293 909					4.96866 99						
PE O- 18:0/20:4	3.1922 201					4.09328 39						
PE P- 16:0/16:0	0.3613 248											
PE P- 16:0/18:1	0.4907 919											
PE P- 16:0/18:2	0.9410 121					1.54596 61						
PE P- 16:0/20:4	2.4403 893					2.68429 13						
PE P- 18:0/16:0	0.8475 06					0.67046 68						1.8016999
PE P- 18:0/18:1	0.7186 229									1.6609995		

PE P- 18:0/18:2	2.0318 167							2.46340 18					
PE P- 18:0/20:4	3.6852 475							4.98165 37					
PE P- 18:1/18:1	0.2215 604												
PE P- 18:1/18:2	0.3486 617												
PE P- 18:1/20:4	0.6580 275												
PG 16:0 18:1	0.1693 643	0.2076 305				0.14854 38	0.12575 9	0.1584124	0.1436004	0.1103193		0.1063306	
PG 16:0 18:2	0.1667 104	0.2485 909	0.1008 355			0.22224 6	0.15915 37		0.136307	0.1145947		0.1339546	
PG 16:1 18:1	0.1669 876	0.1154 631	0.1525 019			0.15841 27	0.09131 23	0.1876074	0.127165				
PG 16:1 18:2	0.8902 2	0.6049 412	0.4659 629			0.67965 58	0.37684 01	0.552141	0.6018899	0.4583627		0.4270092	
PG 17:0 20:0	0.6620 726	0.6560 983	0.5360 821			0.50014 87	0.61181 73	0.5162376	0.6540045	0.5901231		0.5908622	
PG 17:0 22:1													
PG 18:0 18:0	0.1412 476												
PG 18:0 18:1		0.2361 327	0.1329 718			0.19846 17		0.1440503	0.1263403	0.1448448		0.1783942	
PG 18:0 18:2	0.4766 788	1.0065 034	0.7426 733			1.20347 21	0.46917 67	0.5468217	0.9249107	0.7326062		0.7064147	
PG 18:0 20:0	0.3574 497	0.5695 422	0.4418 251			0.75917 24	0.36097 37	0.3635171	0.6173787	0.8075624		0.3965746	
PG 18:0 20:4	0.6585 933	1.9340 681	0.9280 979			1.89327 69	0.84814 6	1.3606769	1.2296107	1.1475034		0.8619081	

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PI 14:0_18:2		0.5266 699	0.4218 556	0.64009 44	0.35947 88	0.3387243	0.3915612	0.5107716	
PI 15:0_18:1			0.1938 417						
PI 15:0_20:1		0.2791 117							
PI 15:0_20:2	0.5740 008	0.5286 127	0.2876 439	0.47029 41		0.4454927	0.5750447	0.3525391	0.319505
PI 15:0_22:0	0.9820 666	0.9041 702	0.6961 68	1.01529 11	0.89683 55	0.8241674	0.9291576	0.9915339	0.8212537
PI 15:0_22:1	0.3761 289	0.2795 974	0.3317 28			0.4128059	0.3352466		
PI 15:0_22:2	0.8263 05	0.5316 56	0.4874 384			0.696532			
PI 15:0_22:4	0.9821 08	0.9060 597	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	0.1444 704	0.1570 128			0.12053 82				
PI 16:0_18:0		0.2409 552							
PI 16:0_18:1	2.1493 831	1.8736 974	1.2283 189	1.77465 2	1.09219 82	1.3733989	1.7975194	1.2234567	1.0995522
PI 16:0_18:2	10.479 836	8.4896 564	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	3.1130 446	2.6431 88	2.2393 512	2.45091 49	1.29519 27	3.9908452	4.6399219	2.7629671	2.2355459
PI 16:0_20:4	11.878 469	8.9718 084	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										
PI 17:0_20:3											0.3503346		
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	1.5031 693	1.1322 582	1.1923 019	1.62841 72		1.050388	1.8063181	1.884107	2.2659987
PI 18:0_22:4									
PI 18:0_22:5	1.3738 957			1.44431 3		1.8532739	1.1957084	0.8709617	1.2361753
PI 18:0_22:6	1.6814 039	1.2623 365	1.2317 289	2.43287 63	0.71697 48	1.6104206	2.6667573	1.6048492	2.3750762
PI 18:1_18:1	0.5491 862	0.4843 313	0.2500 876	0.52014 05	0.29415 15	0.3880064	0.6036555	0.4267206	0.3183867
PI 18:1_18:2	2.1644 557	1.7254 539	0.9383 775	2.67390 68	1.28183 94	2.1455805	2.5172453	1.7032011	1.5549687
PI 18:1_20:0									
PI 18:1_20:3	0.5448 613			0.38491 9		0.8656771	0.6811497	0.4512296	
PI 18:1_20:4	3.5896 363	2.5445 041	2.0676 146	3.95274 36	1.93464 34	4.4410561	4.370778	3.7303713	6.1309085
PI 18:2_18:2	0.2171 772			0.26990 76		0.1925706	0.3400813		
PI 18:2_20:0									
PI 20:0_20:4	1.1764 133			0.97684 78			0.8542495	0.9136481	
PS 16:0_18:2								0.9707876	
PS 16:0_22:6									
PS 16:1_18:1				1.99247 02					
PS 16:1_18:2	1.5124 787	4.8231 702	2.7012 247	4.19712 21	1.01423 15	4.0212022	2.911965	3.8071667	
PS 17:0_20:0	1.3133 503	0.9197 031	0.7848 314	1.32571 64	1.19832 63	1.1586325	1.2849639	1.338248	1.1721793
PS 17:0_20:3	0.9616 992	1.6396 155	2.5181 126	2.10311 1	1.01719 48	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	1.7598 494						4.11274 09					
PS 20:0_22:6							4.04592 9					
SM d18:1/14:0	0.9993 765	1.0398 783	1.1385 214	0.93287 12	0.65929 49	1.0906381	1.0205519	0.8668596			1.3147461	
SM d18:1/16:0	34.869 876	38.191 305	29.739 705	34.4974 89	31.1433 08	28.386125	38.519616	34.478444			39.957699	
SM d18:1/18:0	3.7939 545	4.0176 7	4.1169 515	3.52912 81	4.03805 13	3.2350868	3.3389482	2.7969878			5.2054917	
SM d18:1/18:1	1.8001 195	1.8276 435	1.7695 944	1.51447 83	1.62204 62	1.5588204	1.4544809	1.1748554			2.0878258	
SM d18:1/20:0	37.650 12	34.622 669	28.980 684	35.7014 5	25.9105 34	36.282235	44.835776	36.61861			32.114441	
SM d18:1/20:1	1.8660 219	1.9115 481	2.0143 407	2.04640 32	1.18260 62	2.1776245	1.9143468	1.7028057			1.8904184	
SM d18:1/22:0	44.227 358	45.098 631	30.438 054	48.9116 33	29.5873 71	36.580506	52.779384	45.550604			34.741739	
SM d18:1/22:1	14.008 544	14.273 929	9.1861 414	15.0771 61	8.81514 13	13.802555	14.825387	12.220575			10.217126	
SM d18:1/24:0	13.475 545	13.549 401	10.226 827	15.1862 01	7.98322 95	15.069362	16.356129	13.810742			11.636069	
SM d18:1/24:1	23.760 403	24.693 226	35.476 848	26.7065 06	32.4920 31	33.130793	30.726971	24.512321			41.862909	
SM d18:1/26:0	2.0671 055	2.0088 18	2.7703 769	1.72489 93	1.22747 37	2.9296086	2.0599659	1.6178563			2.8122598	
SM d18:1/26:1	3.4291 923	2.9535 914	3.9041 673	2.92772 54	2.06877 25	3.7602491	3.373527	2.7283356			3.9898355	
TG 36:0- FA12:0				0.06543 59								
TG 38:0- FA12:0		0.0525 861										

[illegible]

TG 44:2- FA18:1	0.1002 235	0.1426 105	0.1151 046	0.09833 22	0.11900 82	0.1139609			
TG 44:2- FA18:2	0.3113 861	0.2196 385	0.1821 682	0.23788 34	0.08529 46	0.1492738	0.0753891	0.072418	0.1546914
TG 44:3- FA18:2	0.1762 771	0.1339 955	0.1349 222	0.17131 02	0.10018 02	0.1123487		0.0628604	0.1211179
TG 45:0- FA16:0	0.1764 751	0.1891 155	0.1723 448	0.10517 83	0.09466 64	0.0945794		0.0393235	0.1008726
TG 45:1- FA16:0	0.3422 002	0.3405 265	0.3519 845	0.30220 69	0.14700 92	0.2214947			0.2685366
TG 45:1- FA18:1	0.1427 185	0.1747 835	0.1244 083	0.10547 94	0.08671 14	0.1103588			0.1001569
TG 46:0- FA12:0		0.0188 204							
TG 46:0- FA14:0	0.1441 458	0.3416 178	0.1174 405	0.09597 42	0.25057 49	0.0785441			0.079324
TG 46:0- FA16:0	0.3583 508	0.6770 417	0.2391 886	0.21614 33	0.56900 48	0.2046641	0.1022079	0.1386451	0.2064385
TG 46:1- FA12:0	0.1812 865	0.3353 912	0.2269 384	0.18623 89	0.20892 72	0.134479	0.0808734	0.0938203	0.1479049
TG 46:1- FA14:0	0.1042 023	0.2251 789	0.0979 177	0.07416 35	0.41636 79				
TG 46:1- FA14:1	0.0671 574	0.1084 214	0.0918 377						
TG 46:1- FA16:0	0.4593 47	0.4077 429	0.3216 662	0.32902 26	0.47339 26	0.1807162	0.0955533	0.1465118	0.1784064
TG 46:1- FA16:1	0.0760 867	0.1620 882			0.22883 06			0.0553183	0.0738789
TG 46:1- FA18:0	0.0757 591	0.0631 355							
TG 46:1- FA18:1	0.1268 022	0.1267 111	0.0987 503	0.08997 12	0.13557 13				0.066477

TG 46:2- FA12:0	0.4043 214	0.4626 78	0.3722 513	0.54431 01	0.26916 7	0.297199	0.186059	0.310203	0.2659397
TG 46:2- FA14:0	0.0915 075	0.1860 228	0.0557 306	0.09243 57	0.23925 94				
TG 46:2- FA14:1					0.08614 06				
TG 46:2- FA16:0	0.2975 112	0.3449 468	0.3267 521	0.28743 64	0.28044 74	0.2192219	0.1130917	0.1939097	0.2220612
TG 46:2- FA16:1		0.0717 48			0.17366 09				
TG 46:2- FA18:1	0.2158 867	0.2517 339	0.1674 785	0.14604 54	0.21092 5	0.1456551		0.0737394	0.1603307
TG 46:2- FA18:2	0.1714 222	0.2040 687	0.1297 138	0.18082 82	0.19879	0.0906908	0.0943251	0.1199915	0.0954149
TG 46:3- FA12:0	0.0765 029	0.1170 348	0.1022 393	0.11075 76		0.0776156	0.0724944		0.0586901
TG 46:3- FA14:1									
TG 46:3- FA16:0	0.4229 518	0.3914 254	0.3373 896	0.38586 5	0.21521 34	0.2567284	0.1021225	0.1811726	0.2435641
TG 46:3- FA16:1					0.07429 99	0.0663381			
TG 46:3- FA18:1	0.2720 723	0.2370 481	0.2018 71	0.15448 79	0.17314 38	0.144012	0.0634237	0.0618317	0.1519463
TG 46:3- FA18:2	0.3226 704	0.2466 315	0.2307 267	0.29450 07	0.15005 83	0.1672243	0.0862868	0.124388	0.2131068
TG 46:3- FA18:3				0.05895 16					
TG 46:4- FA18:2	0.2654 947	0.2664 548	0.1456 473	0.25234 43	0.14599 39	0.1507081	0.0910469	0.0936337	0.1437477
TG 47:0- FA14:0		0.0551 229							

TG 47:0- FA15:0	0.2895 62	0.7072 061	0.1731 099	0.12386 03	0.30698 52	0.1393496	0.1274257	0.1246439	0.2063207
TG 47:0- FA16:0	0.7308 895	1.6623 77	0.3646 042	0.40374 51	0.72944 04	0.3785637	0.2800475	0.2555864	0.3750349
TG 47:0- FA17:0	0.0689 932								
TG 47:1- FA14:0		0.0911 324							
TG 47:1- FA15:0	0.1256 706	0.2386 102	0.0810 789		0.12473 02	0.0662982			0.0706723
TG 47:1- FA16:0	0.3633 394	0.5626 882	0.2624 998	0.29667 51	0.25909 86	0.1936208	0.1063523	0.1304063	0.1712996
TG 47:1- FA16:1	0.1383 728	0.2269 611	0.1015 693	0.08354 77	0.13929 8			0.0600491	0.0790713
TG 47:1- FA17:0		0.0565 174							
TG 47:1- FA18:1	0.1261 135	0.1575 263	0.0908 777	0.08062 31	0.09947 35	0.0705052	0.0553943		0.1076564
TG 47:2- FA14:0	0.0746 359	0.1340 601			0.07367 06				
TG 47:2- FA15:0	0.0820 559	0.1648 785			0.08731 34				
TG 47:2- FA16:1		0.0708 823	0.0655 11		0.07230 64				
TG 47:2- FA18:1	0.1857 605	0.1494 693	0.1241 262	0.09922 44	0.13479	0.1144508		0.0523303	0.1053969
TG 47:2- FA18:2	0.2106 392	0.2912 339	0.1846 377	0.19519 55		0.1080924	0.0845058	0.0947603	0.1375082
TG 48:0- FA14:0	0.0552 307	0.2054 076	0.0674 788	0.04747 66	0.05587 11	0.0420689	0.0541532	0.0483308	0.0507646
TG 48:0- FA16:0	3.9485 906	8.2115 884	2.4008 179	2.10537 26	7.67179 47	2.272737	0.8635929	1.1643249	2.1744401

TG 48:0- FA18:0	0.0862 898	0.1758 155	0.0455 301		0.10912 94	0.0657765		0.052545	
TG 48:1- FA12:0		0.0997 29	0.0634 193	0.04249 67	0.05920 04	0.0559639		0.0389622	0.053434
TG 48:1- FA14:0	0.7162 274	1.6485 116	0.6205 012	0.60060 9	2.47340 04	0.4256515	0.177728	0.3652272	0.4404299
TG 48:1- FA14:1		0.0414 524	0.0311 841		0.04097 87	0.0320124			0.0314268
TG 48:1- FA16:0	1.9452 686	4.0433 162	1.7451 253	1.50283 61	6.20620 51	1.1208809	0.4403927	1.1175672	1.260267
TG 48:1- FA16:1	0.7190 5	1.3725 688	0.6386 837	0.43773 49	1.82700 01	0.4261376	0.1582044	0.3430394	0.5396712
TG 48:1- FA18:0		0.1079 671	0.0651 113	0.04151 49	0.05796 7				
TG 48:1- FA18:1	0.8307 162	1.5543 967	0.6223 605	0.64751 22	2.48737 15	0.3643414	0.2000306	0.3570876	0.4422836
TG 48:2- FA12:0	0.1732 923	0.3627 9	0.2456 43	0.33169 36	0.22279 08	0.1714558	0.1901899	0.1739268	0.1632616
TG 48:2- FA14:0	1.5957 487	3.0673 988	1.2734 297	1.98518 66	4.24138 78	0.9064424	0.5070281	0.9250909	0.8359406
TG 48:2- FA14:1	0.3602 779	0.4806 583	0.4179 452	0.40749 77	0.43858 37	0.3556391	0.1144468	0.1520788	0.3353055
TG 48:2- FA16:0	1.8527 95	3.2039 314	1.4770 517	2.05949 49	4.86516 35	0.9501145	0.4974965	1.0969339	0.8813328
TG 48:2- FA16:1	0.5552 692	1.0425 732	0.6406 021	0.49722 23	3.69585 12	0.2143962	0.0848409	0.2487348	0.3954042
TG 48:2- FA18:0					0.04692 38				
TG 48:2- FA18:1	0.3845 697	0.5588 091	0.3943 248	0.38329 79	1.51242 08	0.2249108	0.0822211	0.1691922	0.2462326
TG 48:2- FA18:2	1.4962 061	2.4539 02	0.9516 671	1.61998 18	2.88683 5	0.6219341	0.4568661	0.8041091	0.5925804

TG 48:3- FA12:0	0.2349 571	0.2557 866	0.2463 052	0.36669 06	0.26286 66	0.156383	0.1654355	0.1583307	0.189753
TG 48:3- FA14:0	0.3589 712	0.6660 057	0.3195 223	0.55599 95	1.53615 32	0.1770942	0.0909576	0.1447732	0.178992
TG 48:3- FA14:1	0.7436 727	0.8604 336	0.7688 73	1.00705 61	0.62504 56	0.595707	0.3221858	0.4442867	0.5307333
TG 48:3- FA16:0	0.5028 334	0.6069 152	0.4300 581	0.62279 49	0.71225 61	0.2510869	0.1496551	0.2571958	0.2877473
TG 48:3- FA16:1	0.3901 132	0.7441 17	0.3247 397	0.45495 09	1.71673 65	0.1355435	0.0971634	0.1766788	0.1859249
TG 48:3- FA18:1	0.2685 913	0.2393 855	0.2571 535	0.30088 49	0.33714 38	0.1389921	0.1078954	0.1418549	0.1995268
TG 48:3- FA18:2	0.5645 921	0.7872 708	0.5083 136	0.78554 89	1.44024 71	0.2892041	0.2102336	0.3654474	0.3457185
TG 48:3- FA18:3	0.1390 47	0.2153 217	0.0962 672	0.15963 2	0.25305 07	0.071502	0.0596925		0.0914637
TG 48:4- FA12:0	0.1743 581	0.2056 021	0.1646 782	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	0.1154 936	0.1105 89	0.1139 127	0.13318 24	0.09694 59	0.0780187			0.1010879
TG 48:4- FA16:0	0.2565 076	0.2756 937	0.2180 025	0.31240 32	0.19651 2	0.1404336	0.1058887	0.1428206	0.1845644
TG 48:4- FA16:1	0.0855 025	0.0981 283	0.0731 903	0.08403 83	0.16769 02				
TG 48:4- FA18:1	0.1799 82	0.1551 928	0.1491 224	0.17114 48	0.14323 63	0.0966586	0.0547356		0.1076921
TG 48:4- FA18:2	0.3744 723	0.2923 325	0.2994 386	0.66234 28	0.27885 2	0.1893407	0.1589458	0.2235882	0.2129653
TG 48:4- FA18:3			0.0791 365	0.08497 45	0.13389 23				

TG 48:5- FA18:2	0.2452 278	0.2102 118	0.1207 278	0.25806 63	0.14013 65	0.1188669	0.0671623	0.0744692	0.1152688
TG 48:5- FA18:3				0.07068 06					
TG 49:0- FA15:0	0.1823 326	0.3637 087	0.0612 99	0.07014 39	0.15029 33	0.1001131	0.0826393	0.0440121	0.1190868
TG 49:0- FA16:0	0.8264 445	2.1964 449	0.5057 289	0.73359 47	1.22178 91	0.4807038	0.3715407	0.3350866	0.5306922
TG 49:0- FA17:0	0.2810 993	0.7796 322	0.2190 268	0.20988 07	0.44218 93	0.2275348	0.1591298	0.1280073	0.2790563
TG 49:0- FA18:0	0.1996 5	0.5100 091	0.1562 04	0.17062 35	0.19623 23	0.1607143	0.1354145	0.1230254	0.1679639
TG 49:1- FA14:0	0.1089 882	0.1256 527	0.0680 693	0.06551 94	0.09335 03	0.0597432			
TG 49:1- FA15:0	0.9895 36	1.8586 152	0.4895 318	0.55629 93	1.10855 65	0.4088797	0.300707	0.3444821	0.5197119
TG 49:1- FA16:0	1.3687 916	2.7013 63	0.6487 933	0.77146 47	1.84979 34	0.5934146	0.44824	0.5215411	0.6761129
TG 49:1- FA16:1	0.1723 497	0.3174 026	0.1176 754	0.11243 68	0.16721 65		0.0987966	0.0965095	0.1029511
TG 49:1- FA17:0	0.1266 779	0.2328 488	0.1123 35	0.08649 08	0.18003 49				
TG 49:1- FA18:1	1.2502 59	2.3768 939	0.4224 691	0.56802 81	1.33180 16	0.3729231	0.4003544	0.447332	0.5145094
TG 49:2- FA14:0	0.1357 355	0.2569 424	0.1380 895	0.13312 1	0.23334 85	0.1064209		0.0723419	0.0799252
TG 49:2- FA15:0	2.1015 253	3.9108 146	0.8945 485	1.35914 02	2.41032 55	0.6391225	0.5890924	0.8002866	0.9705412
TG 49:2- FA16:0	2.1492 294	4.1342 668	0.7775 787	1.42225 34	2.62415 71	0.7821387	0.677355	0.7913746	0.9627218
TG 49:2- FA16:1	0.2330 277	0.4121 97	0.1555 394	0.17346 92	0.58379 31	0.0862098		0.0999663	0.1111738

TG 49:2- FA17:0	0.1255 553	0.1344 032		0.09108 28	0.12728 1					
TG 49:2- FA18:1	0.3717 967	0.5486 727	0.2378 246	0.27959 34	0.56784 98	0.1427549	0.0929981	0.124992	0.1989166	
TG 49:2- FA18:2	2.5505 657	4.3767 15	0.6168 179	1.53785 02	2.59933 22	0.6898973	0.776944	0.8223751	0.8898396	
TG 49:3- FA15:0	0.3816 416	0.6303 444	0.1570 056	0.30109 58	0.53017 84		0.0880526	0.1562116	0.1897655	
TG 49:3- FA16:0	0.4596 661	0.5814 927	0.2427 742	0.36264 58	0.29822 54	0.2100325	0.1513887	0.1718328	0.1700299	
TG 49:3- FA16:1	0.3120 98	0.5310 651	0.1753 786	0.28945 13	0.47848 6	0.1056665	0.0895974	0.1470993	0.1411855	
TG 49:3- FA18:2	0.6038 418	0.8178 718	0.2015 184	0.46578 36	0.67597 75	0.1606131	0.1746377	0.2095839	0.244418	
TG 49:3- FA18:3	0.1831 88	0.3246 273	0.0652 334	0.13133	0.15242 63			0.0685139	0.0543329	
TG 50:0- FA14:0		0.1157 022			0.06480 73					
TG 50:0- FA16:0	1.7385 367	4.2037 095	1.2334 604	1.02318 2	2.92726 43	1.3540954	0.4953029	0.5971833	1.2372507	
TG 50:0- FA18:0	0.8952 633	2.3917 683	0.7721 041	0.61221 21	1.74083 96	0.7612028	0.2798814	0.3849983	0.6119434	
TG 50:1- FA14:0	0.2132 421	0.4620 856	0.1428 993	0.10697 84	0.24843 55	0.1223472	0.0550094	0.0945309	0.111029	
TG 50:1- FA16:0	20.206 055	32.806 106	12.624 205	13.7386 92	47.5591 94	9.4640128	4.854393	9.5963082	10.790049	
TG 50:1- FA16:1	0.1661 512	0.5638 205	0.2682 506	0.17930 12	0.27825 05	0.1085254	0.0657543	0.1407601	0.1647485	
TG 50:1- FA18:0	0.4426 579	1.0055 325	0.3352 642	0.21860 19	0.72664 69	0.228732	0.135257	0.1710866	0.2008469	
TG 50:1- FA18:1	10.475 148	17.141 351	6.1954 016	6.96129 8	23.7888 46	4.6625948	2.6620547	4.8351493	5.8782542	

TG 50:1- FA20:1	0.2131 727	0.3757 233	0.0804 013	0.11185 41	0.11754 38	0.0852865				
TG 50:2- FA14:0	1.2172 966	2.7123 375	0.8400 772	1.22360 28	6.42479	0.5991186	0.2398934	0.4930645	0.5797633	
TG 50:2- FA14:1	0.1303 884	0.1494 73	0.1008 407	0.10998	0.04339 73				0.0999695	
TG 50:2- FA16:0	51.014 507	76.707 291	28.266 371	45.8020 92	107.171 85	22.235409	13.746652	28.447751	26.279952	
TG 50:2- FA16:1	5.9961 049	9.5039 403	5.1336 41	5.03856 75	26.7816 73	2.8437069	0.992189	3.1233334	4.0710917	
TG 50:2- FA18:0	0.3049 174	0.7307 76	0.1772 087	0.20658 86	0.61808 77	0.1710956	0.0942212	0.1448557	0.1496846	
TG 50:2- FA18:1	7.0665 506	12.389 412	6.0243 903	6.17203 82	35.4151 19	3.2052179	1.1576572	3.6213712	4.6669085	
TG 50:2- FA18:2	23.711 83	35.450 136	10.307 431	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	3.6236 82	5.7764 403	2.3403 926	5.25748 5	11.5484 97	1.2332112	0.7154104	1.5647695	1.6117622	
TG 50:3- FA14:1	0.2126 432	0.2465 451	0.1660 75	0.21869 82	0.25869 33	0.162391	0.0771609	0.0748739	0.1302865	
TG 50:3- FA16:0	14.719 169	18.612 614	10.081 868	17.6750 96	35.8533 47	5.4036603	3.0962856	8.8005992	8.4620613	
TG 50:3- FA16:1	12.734 35	16.450 715	9.2212 885	14.9502 69	36.8725 61	4.7890362	2.676799	7.1959101	7.7457749	
TG 50:3- FA18:0		0.1131 776	0.0778 99	0.07357 1	0.11814 43					
TG 50:3- FA18:1	4.2126 352	6.6074 8	2.9201 248	5.89378 59	14.9479 95	1.4942199	0.8464165	1.8974084	2.1132737	
TG 50:3- FA18:2	13.845 912	18.027 907	9.2725 58	17.1976 72	36.6916 74	4.726714	2.8172297	7.6350893	7.5313793	

TG 50:3- FA18:3	1.3018 442	1.9548 396	0.5221 239	1.33547 26	2.00317 87	0.4490515	0.320034	0.6493627	0.5351026
TG 50:3- FA20:3	0.0699 712	0.1108 695		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	0.3549 089	0.4667 227	0.2133 222	0.84916 28	0.70204 79	0.0921028	0.0824123	0.1486907	0.1718694
TG 50:5- FA20:4					0.07201 92				
TG 50:5- FA20:5	0.0762 016	0.1162 824		0.13098 08	0.12058 07				
TG 51:0- FA16:0	1.0147 801	2.0203 258	0.6167 036	0.82326 08	1.15321 56	0.5438967	0.5148612	0.4024885	0.4786144
TG 51:0- FA17:0	0.1364 161	0.3671 694	0.0874 393	0.07096 61	0.14583 47	0.0911394	0.0623271	0.0555239	0.1452181
TG 51:0- FA18:0	0.2197 797	0.5421 866	0.1618 422	0.19378 52	0.28946 2	0.1668634	0.1463227	0.1140164	0.2000654
TG 51:1- FA15:0	0.4281 813	1.0258 313	0.1893 054	0.20596 13	0.27353 81	0.1736771	0.1622362	0.1605917	0.2157684
TG 51:1- FA16:0	1.8936 352	3.7927 685	1.0097 799	1.22898 3	2.43056 17	0.9312853	0.5728276	0.7071291	1.0107052
TG 51:1- FA17:0	1.1370 13	2.2571 399	0.6843 432	0.73806 32	1.54419 7	0.6193492	0.2917443	0.4475011	0.6123094
TG 51:1- FA18:0	0.3552 161	0.8276 26	0.1869 367	0.22577 25	0.29008 04	0.1732907	0.178494	0.1457966	0.2001548
TG 51:1- FA18:1	1.3835 332	2.8066 154	0.5820 797	0.90037 31	1.70154 96	0.5403002	0.5322165	0.4021909	0.5359637
TG 51:2- FA15:0	1.2621 304	2.2112 927	0.4706 515	0.87581 01	2.17422 3	0.3931735	0.3431045	0.4752969	0.5493983
TG 51:2- FA16:0	4.8165 395	7.4225 009	2.8506 277	3.39848 52	6.72759 64	2.2361548	1.2539938	1.9430639	2.878816
TG 51:2- FA16:1	0.3058 574	0.5537 085	0.2843 025	0.20286 71	0.60155 35	0.1746657	0.0805017	0.1515742	0.2370841
TG 51:2- FA17:0	2.3531 48	4.3125 352	1.1705 69	2.08320 28	3.24444 68	1.098569	0.7219494	1.0092894	1.2391149
TG 51:2- FA18:1	3.0857 243	4.9010 568	1.3589 471	2.20859 53	6.52625 32	1.0361716	0.8522748	1.0976505	1.5048024

TG 51:2- FA18:2	3.1321 982	5.1468 995	0.8307 908	2.15952 7	3.51812 62	0.9368534	1.0398585	1.0405638	1.0774503
TG 51:3- FA15:0	3.1564 492	4.3443 25	0.9305 341	2.89554 95	4.22597 18	0.7711559	0.6658132	1.0814273	1.1893901
TG 51:3- FA16:1	0.7591 537	1.0249 801	0.5824 078	0.54117 4	1.23946 67	0.3074452	0.143291	0.2157391	0.5180954
TG 51:3- FA17:0	0.4060 29	0.6722 363	0.2061 497	0.37948 89	0.61151 43	0.1469259		0.1305047	0.234505
TG 51:3- FA18:2	4.8184 627	6.5154 981	1.6327 827	4.27200 53	6.65258 82	1.2256326	1.1127957	1.6562258	1.8284447
TG 51:3- FA18:3	0.1863 85	0.3792 968	0.0751 343	0.12291 86	0.18146 75	0.0538236	0.0820977	0.0586404	0.105916
TG 51:4- FA15:0	3.1605 252	3.6937 731	0.6929 097	3.80736 03	2.83706 31	0.55594	0.7233956	1.0663561	1.0541799
TG 51:4- FA16:1	0.3209 095	0.3738 898	0.1981 45	0.34024 67	0.55439 98	0.1168737	0.0533625	0.1198153	0.1769904
TG 51:4- FA18:2	5.7316 934	6.7045 284	1.3817 138	6.49891 42	5.24845 8	1.1092437	1.4094339	1.9270331	1.9091655
TG 51:4- FA18:3	0.4129 971	0.5638 143	0.1324 107	0.46481 69	0.49589 72	0.1033318	0.1054104	0.1202322	0.1449943
TG 51:4- FA20:4	0.1231 599	0.2965 333		0.11460 94	0.24534 56				0.0800788
TG 51:5- FA18:2	0.5757 298	0.6025 553	0.1605 176	0.69899 72	0.41330 37	0.1294699	0.1590393	0.1889852	0.1800415
TG 51:5- FA18:3	0.4005 831	0.5187 775		0.59695 38	0.40652 82	0.0797761	0.0789669	0.1424043	0.113302
TG 52:0- FA16:0	0.7667 196	1.8660 358	0.4970 621	0.60895 55	1.00932 48	0.4829108	0.2772335	0.3613799	0.4128438
TG 52:0- FA18:0	0.5552 973	1.2997 236	0.5615 337	0.36839 41	1.05647 46	0.5374302	0.198423	0.2986512	0.5714714
TG 52:0- FA20:0	1.5642 292	2.7501 728	1.0154 325	1.10549 36	1.89849 71	0.8362214	0.4311252	0.682129	0.974878

TG 52:1- FA16:0	6.6736 361	12.911 136	3.2718 375	3.78529 97	9.09336 97	2.7545041	1.4604231	2.2041307	2.7537787
TG 52:1- FA16:1	0.1549 066	0.2577 941	0.0831 889	0.11352 59	0.11485 25	0.0671226	0.0361242	0.0607646	0.0864084
TG 52:1- FA18:0	3.9345 866	8.1756 393	2.1515 479	2.56246 53	7.73015 99	1.9965096	1.2917519	1.7120894	1.7012358
TG 52:1- FA18:1	3.3887 41	6.7729 238	1.8663 996	2.29370 59	7.86222 35	1.6569039	1.2384972	1.6358227	1.6538934
TG 52:1- FA20:0	0.7973 263	1.3744 222	0.7153 314	0.78884 38	1.45334 46	0.3864153	0.1690192	0.4418918	0.5898947
TG 52:1- FA20:1	2.3136 221	4.1605 576	0.8004 408	1.08605 12	1.73060 41	0.7130532	0.3428215	0.4859449	0.6624744
TG 52:2- FA14:0	0.2313 1	0.4331 976	0.1362 914	0.17521 87	0.21152 23	0.1176631		0.0838903	0.1394508
TG 52:2- FA16:0	51.347 742	72.601 579	32.698 586	41.5319 11	156.488 54	25.763981	11.036686	24.918562	33.087643
TG 52:2- FA16:1	1.0480 1	1.7831 668	0.6319 507	0.60703 08	1.66043 39	0.3954152	0.1861579	0.379815	0.4524465
TG 52:2- FA18:0	8.8777 699	18.150 17	4.3728 922	7.17899 71	15.4215 54	4.291041	3.3170591	4.3863876	4.1429678
TG 52:2- FA18:1	78.840 597	105.45 099	52.709 204	62.8623 29	253.787 58	39.265478	14.277924	35.306177	52.050357
TG 52:2- FA18:2	7.2875 589	15.504 35	3.3030 745	6.09936 38	12.1086 16	3.2718052	2.9500625	3.6872417	3.3148391
TG 52:2- FA20:0	0.4149 579	0.5146 112	0.2873 244	0.53737 85	0.49400 52	0.1783756	0.1241431	0.1943127	0.1878847
TG 52:2- FA20:1	0.9761 73	1.4958 016	0.5223 72	0.46802 25	0.77626 03	0.3593247	0.1385536	0.2575165	0.3360672
TG 52:2- FA20:2	0.2128 131	0.3757 847	0.1302 183	0.17249 58	0.37339 05	0.1431585	0.0767898	0.1343119	0.1099008
TG 52:3- FA14:0	0.3539 47	0.6282 222	0.1853 75	0.25736 95	0.36667 79	0.1301628	0.0685963	0.0787219	0.1533257

TG 52:3- FA16:0	181.04 128	180.14 552	95.709 051	196.776 08	323.618 73	65.853039	42.294144	89.2412	99.862297
TG 52:3- FA16:1	4.8456 081	7.4150 673	3.4103 961	4.34925 24	23.2214 32	2.0021662	0.9314868	1.706596	3.3652718
TG 52:3- FA18:0	1.3141 802	2.4687 484	0.8346 093	1.29723 85	3.12475 35	0.6062168	0.4008462	0.6970274	0.8490305
TG 52:3- FA18:1	169.58 836	174.78 669	90.370 866	182.094 29	322.532 08	61.303354	38.844853	83.368946	93.812569
TG 52:3- FA18:2	155.66 159	157.90 813	78.432 066	164.180 36	269.587 9	55.053324	34.817633	74.977729	83.461188
TG 52:3- FA18:3	0.4461 283	0.7340 743	0.1916 44	0.33219 44	0.59190 66	0.1554355	0.1240236	0.1951167	0.2011448
TG 52:3- FA20:0	0.4609 591	0.3994 232	0.2261 416	0.50263 27	0.59236 41	0.1598806	0.0953997	0.2047656	0.268778
TG 52:3- FA20:1	0.5327 219	0.8965 884	0.2864 92	0.50705 02	0.49562 81	0.150281	0.0951005	0.1677819	0.1960536
TG 52:3- FA20:2	0.3439 007	0.4708 301	0.1606 374	0.27916 88	0.78431 06	0.112975	0.0709968	0.142475	0.1254268
TG 52:3- FA20:3	0.2892 428	0.5333 645	0.1260 413	0.21644 18	0.80985 28	0.1204244	0.1152723	0.1449751	0.167794
TG 52:3- FA22:1	0.0987 505	0.0727 133		0.10833 24	0.20586 98			0.0714696	0.0734819
TG 52:4- FA14:0	0.1573 287	0.2790 948	0.1010 939	0.18644 21	0.44822 68	0.063036	0.0705714	0.0766724	
TG 52:4- FA16:0	185.92 391	142.83 765	69.920 523	257.264 82	187.137 92	47.397475	48.273845	89.631471	77.960762
TG 52:4- FA16:1	14.264 977	16.070 153	7.6150 828	17.0926 76	40.8834 83	3.7306677	2.2217436	4.7611071	7.7469231
TG 52:4- FA18:0	0.2580 136	0.3936 901	0.1255 007	0.23447 24	0.31484 92	0.1457625	0.1098372	0.1285969	0.1111383
TG 52:4- FA18:1	24.106 637	24.206 976	11.852 289	30.8175 6	52.1794 65	6.3919623	4.5055092	9.564145	11.551861

TG 52:4- FA18:2	295.97 564	231.66 394	111.68 86	403.784 64	307.823 81	74.914788	76.726134	141.66353	121.63261
TG 52:4- FA18:3	16.038 892	15.533 379	6.9577 627	21.1285 13	24.3448 23	4.1830855	3.7935009	7.4287721	6.9313628
TG 52:4- FA20:0	1.1737 376	0.9894 146	0.4644 823	1.72583 33	1.18453 4	0.3530299	0.3749383	0.5964959	0.5841467
TG 52:4- FA20:2	0.2617 765	0.3338 533	0.1373 847	0.31169 47	0.39488 18	0.1044135	0.08033	0.1096558	0.1149723
TG 52:4- FA20:3	0.4842 615	0.6366 11	0.2183 272	0.53356 79	1.35070 33	0.1437358	0.1212525	0.2360233	0.1755522
TG 52:4- FA20:4	0.9703 097	1.8800 09	0.4297 368	0.84313 04	3.26120 35	0.3705178	0.3952276	0.6016983	0.4521094
TG 52:4- FA22:1	0.2526 431	0.1988 609	0.1116 071	0.33381 02	0.31806 93	0.0672598	0.0865242	0.1211843	0.1334744
TG 52:4- FA22:4	0.1501 178	0.0961 093		0.12890 64	0.14058 98				
TG 52:5- FA14:0	0.1423 183	0.2945 493	0.0771 618	0.17428 16	0.46578 55		0.0671772	0.0727901	0.067626
TG 52:5- FA16:0	17.281 363	14.385 162	6.9020 845	32.4789 84	19.0356 5	3.7027739	4.2187874	8.335151	6.3216119
TG 52:5- FA16:1	12.812 018	10.794 593	5.1566 616	20.1657 98	19.4070 56	2.4168817	2.2503708	4.1506541	5.4321902
TG 52:5- FA18:1	2.3129 102	2.1837 065	1.0204 57	3.63142 17	4.07954 54	0.4955626	0.4642747	0.8350168	1.0427918
TG 52:5- FA18:2	30.945 092	25.564 074	11.890 553	50.9019 01	39.7461 81	6.0951991	5.9580736	11.94356	12.246739
TG 52:5- FA18:3	21.349 343	16.945 245	8.0589 736	35.9750 41	23.0096 27	3.8960544	4.8429374	9.4114437	7.7788574
TG 52:5- FA20:3	0.1645 813	0.2836 253	0.0713 106	0.22256 41	0.45902 22	0.0698689		0.0777417	
TG 52:5- FA20:4	0.4674 603	0.9588 979	0.2895 049	0.50870 24	1.89190 94	0.1752022	0.1622974	0.3057629	0.2017303

TG 52:5- FA20:5	0.8289 374	1.3730 434	0.4418 99	1.30839 37	1.26975 54	0.4099726	0.4315259	0.6623686	0.5309
TG 52:5- FA22:5	0.4219 201	0.3734 419	0.1978 693	0.78884 78	0.56483 89	0.1358156	0.1337204	0.1797918	0.149192
TG 52:6- FA14:0	0.1963 823	0.4007 413	0.1853 534	0.36972 24	0.63438 68	0.1660321	0.1638423	0.1345684	0.1553651
TG 52:6- FA16:0	1.3458 147	1.2868 228	0.6678 608	3.26336 47	1.67203 62	0.2917484	0.4675045	0.8310068	0.6163659
TG 52:6- FA16:1	1.6973 041	1.4726 429	0.7086 077	3.28279 1	2.84446 45	0.3288712	0.3489234	0.6109406	0.6089058
TG 52:6- FA18:1	0.3379 649	0.3225 115	0.1379 403	0.54676 5	0.51886 1	0.1229481	0.1122953	0.1499241	0.156928
TG 52:6- FA18:2	3.1684 179	2.3620 931	1.1252 429	6.33171 11	3.44048 67	0.4725528	0.7327391	1.1397945	1.1487604
TG 52:6- FA18:3	2.4109 433	2.1079 644	0.9890 983	4.83046 62	3.46789 01	0.3911332	0.3610599	0.8531638	0.9525923
TG 52:6- FA20:4	0.2458 125	0.4905 146	0.1156 385	0.38284 44	0.78813 37	0.0812222	0.1182392	0.1494284	0.1218505
TG 52:6- FA20:5	0.5578 53	0.9158 62	0.4702 864	1.22614 68	1.44156 24	0.2647841	0.2227082	0.4679251	0.3611298
TG 52:6- FA22:6	0.4731 978	1.1556 833	0.3175 255	0.75717 61	1.48319 7	0.2979659	0.2412914	0.3627604	0.2225201
TG 52:7- FA16:0	0.8033 576	1.7231 856	0.5617 685	0.65556 97	0.92423 78	0.454794	0.4134891	0.2986108	0.3810906
TG 52:7- FA18:1	0.0416 918	0.1035 322	0.0676 006	0.12788 02	0.09131 56	0.0334788	0.0316713	0.0651681	0.0663145
TG 52:7- FA20:5	0.3435 659	0.4885 623	0.2344 919	1.23948 79	0.68350 77	0.1511984	0.1622765	0.2704014	0.1804205
TG 52:7- FA22:6	0.2296 282	0.4543 63	0.1574 212	0.32663 34	0.69994 48	0.193198	0.0970626	0.1466356	0.1056926
TG 52:8- FA16:1	0.1197 606	0.1800 51	0.0892 686	0.11180 95	0.11578 84				0.0701193

TG 52:8- FA18:2	0.0616 52	0.0964 738	0.0451 666	0.18017 17	0.08151 8	0.0401817	0.0851179	0.0444989	0.0894594
TG 53:0- FA16:0	4.2476 129	5.1425 623	2.1415 798	11.3514 71	5.94991 75	1.827885	2.3442901	3.3086784	2.3822572
TG 53:1- FA16:0	1.5009 644	2.9096 95	0.8206 321	1.42529 11	1.52664 34	0.6893881	0.7095471	0.487203	0.646575
TG 53:1- FA17:0	0.3703 054	0.8000 83	0.1756 088	0.24850 67	0.31872 49	0.1705199	0.1276866	0.1615272	0.204384
TG 53:1- FA18:0	0.5438 557	1.1340 122	0.2694 021	0.38447 99	0.50010 03	0.2783192	0.2921021	0.2387557	0.3247772
TG 53:1- FA18:1	0.9672 801	1.9274 277	0.4139 237	0.74687 37	0.96869 57	0.3124664	0.4938602	0.2628047	0.3173841
TG 53:2- FA16:0	3.8677 874	5.0276 666	2.8066 304	2.44690 59	4.33408 31	2.4028008	0.8405893	1.1701859	2.6587353
TG 53:2- FA17:0	1.0904 251	2.1222 605	0.6374 168	0.81789 88	2.28986 47	0.4702452	0.3789151	0.3956845	0.6570506
TG 53:2- FA18:1	4.6769 15	6.5228 307	3.0495 456	3.15637 86	6.53634 22	2.3230368	1.1633427	1.5735761	2.7798894
TG 53:2- FA18:2	2.0278 12	3.3584 349	0.6606 684	1.85932 76	2.22698 92	0.7000443	0.8472252	0.6284516	0.7055888
TG 53:3- FA16:0	11.580 927	9.7332 919	8.1261 43	7.75223 58	7.41834 39	5.608197	1.8544451	3.0499146	7.9576612
TG 53:3- FA17:0	2.9251 069	4.4721 229	1.3177 721	2.66032 13	4.83435 03	1.0032557	0.7077917	1.2678076	1.4621251
TG 53:3- FA18:2	6.6950 003	8.1320 557	3.0699 424	5.06019 34	6.79591 32	2.3382821	1.6476802	2.0911642	3.0441914
TG 53:4- FA16:0	14.015 095	8.7773 144	7.8768 571	10.7065 18	4.80613 91	4.8518635	2.1171963	3.20041	7.5043792
TG 53:4- FA17:0	2.8977 778	3.7951 498	0.9096 981	3.21961 28	3.22535 47	0.7900637	0.9104404	1.2134321	1.2229359
TG 53:4- FA18:2	14.918 321	13.766 074	6.8692 17	13.5397 77	10.6370 15	4.977886	3.1627442	4.2776544	7.134322

TG 53:4- FA18:3	0.6388 243	0.7468 301	0.2755 655	0.60911 59	0.60596 73	0.1858023	0.1842375	0.198834	0.2763517
TG 53:4- FA20:4	0.1272 693	0.3075 362		0.11117 62	0.31078 57	0.0720811		0.1023619	0.1187515
TG 53:5- FA20:4	0.1424 439	0.3356 04		0.13660 11	0.38034 94		0.0793691	0.1026881	0.1100391
TG 53:6- FA20:4	0.2003 996	0.3525 955	0.0681 078	0.27828 6	0.37694 33	0.0917831	0.0839878	0.0988559	0.0952365
TG 54:0- FA16:0	1.0569 358	1.5632 636	0.5856 054	1.70420 69	1.31549 56	0.4472048	0.3518319	0.5610114	0.5156977
TG 54:0- FA18:0	0.2040 24	0.5755 823	0.1462 488	0.14970 92	0.17866 09	0.1883626	0.1113161	0.1572485	0.1544483
TG 54:1- FA16:0	1.4279 457	3.0577 171	0.4893 788	0.96064 05	1.07139 97	0.5899687	0.3996565	0.4917901	0.4085917
TG 54:1- FA18:0	1.1947 155	2.4174 192	0.6927 467	0.59983 05	1.32238 64	0.7293486	0.3538761	0.4091904	0.6501827
TG 54:1- FA18:1	1.1157 1	2.1308 895	0.4470 423	0.72242 98	1.21883 66	0.4564969	0.4016515	0.4283797	0.414358
TG 54:1- FA20:0	8.5050 865	10.121 475	6.3978 143	7.12412 36	10.0875 58	4.2284494	1.9543683	3.7736812	5.8397347
TG 54:1- FA20:1	0.6691 468	1.4731 525	0.3438 378	0.39689 18	0.52976 47	0.2844958	0.195814	0.1940972	0.283856
TG 54:2- FA16:0	8.9526 236	11.771 103	5.1812 491	4.56085 36	5.78736 75	3.8451957	1.5200884	2.1897501	4.2476905
TG 54:2- FA18:0	3.2069 326	6.1000 954	1.7009 314	2.33091 77	7.90135 34	1.7052811	1.1611859	1.3806223	1.6555262
TG 54:2- FA18:1	10.091 905	13.593 951	5.4094 737	5.25472 66	13.0651 87	4.0934337	1.9170657	2.2060795	4.4030024
TG 54:2- FA18:2	2.0825 833	4.4412 165	0.5619 782	1.70814 27	1.83380 2	0.6957843	0.7368398	0.7157369	0.4633475
TG 54:2- FA20:0	13.894 576	14.092 234	7.4701 326	14.9704 68	10.4972 37	5.0828516	3.7198724	5.752682	7.3380866

TG 54:2- FA20:1	7.9622 434	10.546 174	3.9009 402	3.87629 14	6.21553 18	2.9347702	1.2237901	1.9495844	3.2305137
TG 54:2- FA20:2	0.1020 482	0.1422 435	0.0542 521	0.04969 07	0.10497 36	0.0491535	0.0470432	0.060971	0.0422958
TG 54:3- FA16:0	16.014 394	18.164 054	7.3646 433	9.97618 03	11.5154 39	5.8636621	2.8155022	3.7949985	6.4413979
TG 54:3- FA16:1	0.8785 092	1.3130 753	0.4638 668	0.48219 63	0.90174 89	0.3206534	0.1387181	0.259015	0.4233693
TG 54:3- FA18:0	11.736 116	18.745 361	4.8054 504	9.68185 2	21.7862 65	4.4475018	4.294082	4.099525	5.3136594
TG 54:3- FA18:1	28.354 089	37.656 194	14.751 021	22.4668 15	97.4738 11	12.149628	7.1306348	8.8347273	14.931585
TG 54:3- FA18:2	21.296 271	27.450 957	8.1920 195	14.2908 93	22.6813 14	7.0078536	5.1124369	5.5779731	7.907672
TG 54:3- FA18:3	0.1276 077	0.2167 008	0.0331 631	0.10865 09	0.05005 1	0.0380713	0.0387601	0.0510111	0.0742547
TG 54:3- FA20:1	15.063 265	18.275 388	5.8672 089	10.2521 27	10.3075 8	4.722779	2.6443797	3.4605367	5.2440971
TG 54:3- FA20:2	1.7010 212	2.5510 648	0.6932 38	1.21665 26	3.90900 36	0.8761056	0.377318	0.6594668	0.6102231
TG 54:3- FA20:3	0.1098 026	0.2180 13	0.0758 284	0.11185 28	0.25820 83	0.1002751	0.0675749	0.0517904	0.0793337
TG 54:4- FA16:0	5.0677 34	6.8801 603	2.0502 311	4.49601 71	10.0185 72	2.1214478	1.3467354	2.0334153	1.7303775
TG 54:4- FA16:1	1.3967 218	1.9647 968	0.6091 993	1.04094 67	1.54866 84	0.3522361	0.1980524	0.3229507	0.4952425
TG 54:4- FA18:0	14.611 005	21.996 436	4.2657 841	14.7940 77	21.8066 84	5.0536298	5.0809828	5.3803371	5.9356057
TG 54:4- FA18:1	60.789 947	58.575 622	26.589 805	59.2429 75	154.053 39	19.179928	12.354518	17.505698	28.617981
TG 54:4- FA18:2	49.524 948	60.415 03	18.239 93	48.7020 5	99.6053 13	16.201881	13.324545	16.076401	21.640582

TG 54:4- FA18:3	1.5515 854	2.3160 286	0.6248 832	1.51116 08	1.96456 66	0.554016	0.3993388	0.4842895	0.564307
TG 54:4- FA20:1	1.7223 785	2.3979 807	0.6522 999	1.35008 37	1.43020 19	0.4167508	0.2539765	0.4100528	0.5611465
TG 54:4- FA20:2	2.7935 661	3.8854 658	1.0480 813	3.03359 24	4.87573 97	1.2333806	0.7824843	1.2062879	0.8719666
TG 54:4- FA20:3	2.3682 542	3.7875 632	0.9465 084	1.82529 45	7.42144 88	0.9960642	0.5788144	0.8315327	0.7844698
TG 54:4- FA20:4	0.6648 643	1.4413 825	0.3442 315	0.62712 32	1.80909 36	0.304051	0.363295	0.4099971	0.4470534
TG 54:4- FA22:1	0.1391 211	0.1500 239	0.0980 523	0.15806 65	0.29869 07			0.0626116	0.0701874
TG 54:4- FA22:4	0.0839 699	0.1598 012		0.09597 67	0.21086 04	0.0595553		0.0567502	
TG 54:5- FA16:0	5.4849 618	7.2358 832	1.9172 768	5.67862 41	11.7126 65	1.881555	1.7428546	2.6757354	1.9395094
TG 54:5- FA16:1	0.5268 087	0.8066 427	0.2941 134	0.49886 14	1.80038 71	0.1909366	0.1275973	0.1620395	0.2330602
TG 54:5- FA18:0	1.3585 911	1.9107 719	0.4378 629	1.54893 53	1.80609 95	0.4298074	0.5093921	0.5418039	0.50865
TG 54:5- FA18:1	50.495 387	42.947 529	16.398 558	62.2902 34	82.0490 93	12.617612	11.53721	14.98279	19.211858
TG 54:5- FA18:2	80.086 869	65.378 237	24.367 219	94.8906 87	117.919 32	18.995343	18.463668	23.550998	27.864324
TG 54:5- FA18:3	5.3209 883	5.6346 057	2.0585 598	6.42445 74	10.4946 97	1.4148556	1.2242321	1.7489764	2.1359098
TG 54:5- FA20:2	0.4414 614	0.6089 485	0.1965 479	0.53066 45	1.04498 36	0.1626243	0.1271871	0.1525872	0.1439411
TG 54:5- FA20:3	4.8872 562	5.6034 911	1.6703 62	4.78054 56	9.44714 24	1.5783771	1.3714596	1.8364554	1.4916157
TG 54:5- FA20:4	5.5003 029	8.4962 377	2.2312 399	4.51929 68	15.1353 27	2.0042557	2.0442396	3.2588527	2.1185717

TG 54:5- FA20:5	0.2553 351	0.5361 597	0.1817 917	0.34471 66	0.36145 81	0.1068589	0.1816636	0.1700497	0.2108606
TG 54:5- FA22:1	0.3032 28	0.3117 231	0.1183 782	0.45575 91	0.50755 14	0.1288762	0.0745147	0.1087124	0.1477422
TG 54:5- FA22:4	0.1272 727	0.2235 992		0.08665 34	0.38751 51	0.0671353		0.0653657	
TG 54:5- FA22:5	0.4660 031	0.9325 174	0.1970 533	0.56374 16	0.99396 37	0.2950298	0.2029493	0.3710758	0.240676
TG 54:6- FA16:0	6.0335 258	8.9822 801	2.6365 311	8.53083 95	12.5604 96	2.5825391	2.9072743	4.2750503	2.844582
TG 54:6- FA16:1	0.5990 89	0.9293 616	0.2740 962	0.78827 46	1.93783 89	0.214861	0.1693474	0.2913428	0.2216829
TG 54:6- FA18:1	10.326 884	8.7227 667	3.7709 438	17.3790 91	15.1980 16	2.4781498	2.4147458	3.7222572	4.0015923
TG 54:6- FA18:2	61.815 759	51.262 882	14.954 941	92.0545 33	74.2406 11	12.625314	16.212122	19.255297	18.095346
TG 54:6- FA18:3	9.6676 737	7.5907 68	3.3041 114	16.4685 92	13.5465 61	2.1316227	2.0472388	3.3053318	3.4731654
TG 54:6- FA20:3	0.5998 054	0.7665 343	0.2762 541	0.73447 15	1.58572 57	0.1893737	0.1600041	0.2399598	0.1815231
TG 54:6- FA20:4	10.949 542	15.132 435	3.9644 147	12.5884 59	22.1482 27	3.3973996	5.2627358	7.774596	3.9128609
TG 54:6- FA20:5	5.9378 846	7.5554 47	3.5489 331	11.8262 96	10.3649 55	2.9214052	2.7336194	4.6699597	3.934164
TG 54:6- FA22:5	0.5148 296	0.9914 072	0.3051 514	0.74016 07	1.78298 21	0.3111672	0.1901904	0.4046401	0.2141926
TG 54:6- FA22:6	4.1298 577	8.0659 232	2.1072 532	5.19869 55	10.8375 31	2.6602073	2.2491477	3.4703786	2.3692195
TG 54:7- FA16:1	0.8123 07	1.2961 233	0.4478 898	1.22400 8	2.49559 9	0.3902063	0.3227032	0.507817	0.4461705
TG 54:7- FA18:1	1.2187 22	1.2654 578	0.4700 027	2.25536 95	2.07795 31	0.2601168	0.2732722	0.4515718	0.5387502

TG 54:7- FA18:2	13.580 665	9.9183 941	4.1356 057	32.6646 89	12.0981 32	2.5521404	3.8994476	5.7322653	4.5318738
TG 54:7- FA18:3	7.4319 229	4.8019 905	1.9999 82	16.1872 94	6.43709 05	1.102961	1.6560765	2.3634659	2.1995242
TG 54:7- FA20:4	1.2437 929	1.5154 882	0.5288 79	1.74556 87	2.48457 69	0.3321628	0.5169868	0.6340835	0.4284314
TG 54:7- FA20:5	14.678 852	14.33	7.0986 064	42.1077 27	15.6430 35	5.694712	8.3335617	11.540528	8.2479426
TG 54:7- FA22:5	0.2979 901	0.5651 939	0.2502 103	0.86933 12	0.75681 14.6355	0.1812628	0.168748	0.2236787	0.1451852
TG 54:7- FA22:6	3.3662 908	8.1844 578	1.9329 091	4.51088 46	93	1.9559613	1.1127317	2.1270857	1.4586173
TG 54:8- FA18:2	1.5621 241	1.6183 88	0.5938 083	4.12955 88	2.02551 9	0.4122099	0.474086	0.691645	0.5334023
TG 54:8- FA18:3	1.3265 494	0.9326 624	0.3806 759	3.72190 76	1.12625 48	0.2252398	0.2900356	0.5076647	0.4219699
TG 54:8- FA20:4	0.1603 936	0.1507 687		0.25316 71	0.21152 3		0.0848964	0.0868917	0.0689913
TG 54:8- FA20:5	1.5649 698	1.6704 649	0.8519 091	4.90862 82	1.96254 09	0.4978126	0.7103545	0.9864379	1.026847
TG 54:8- FA22:6	2.1421 981	4.9847 472	0.9508 513	4.80665 82	6.88080 02	1.0250043	0.808067	1.158411	0.7123751
TG 55:1- FA16:0	16.673 952	24.692 637	6.1206 674	26.3226 81	25.0466 64	7.8413438	8.2687812	9.897663	5.8282728
TG 55:1- FA18:1	2.0046 261	2.5714 038	0.8713 21	3.66089 67	3.95126 01	0.722358	1.0148536	0.9345371	1.0589913
TG 55:2- FA18:1	1.4513 383	2.0114 547	0.6122 664	1.06605 06	1.18493 39	0.4661685	0.5534987	0.4696796	0.4406161
TG 55:2- FA18:2	3.0314 747	3.6066 674	1.1346 3	7.83277 39	4.27069 4	1.0128494	1.9291381	1.8269053	1.4291506
TG 55:3- FA18:1	2.0585 485	2.8143 77	1.1647 276	1.33630 87	2.63374 19	0.987048	0.5904453	0.5790182	1.0890547

TG 55:3- FA18:2	2.5112 201	3.5595 945	0.7968 42	2.50992 95	2.01818 37	0.8022635	0.8599273	0.7517182	0.7587058
TG 55:4- FA18:1	3.7527 697	3.3832 971	2.3590 823	2.17353 24	3.63670 18	1.8041542	0.6854039	0.714954	2.2224567
TG 55:4- FA18:2	3.3466 396	4.1347 751	1.2629 397	2.59619 86	3.00981 83	1.121758	0.8933873	0.8423278	1.4628901
TG 55:5- FA18:1	4.0614 087	2.9353 514	1.9421 398	2.80673 44	2.49726 63	1.4028093	0.5887973	0.6420612	2.0839022
TG 55:5- FA18:2	4.9397 474	4.0363 189	2.2579 073	3.99207 69	3.28998 17	1.8671078	0.8447279	0.9038996	2.3567748
TG 55:5- FA20:4	0.3302 844	0.5749 31	0.1901 396	0.26518 92	0.58567 35	0.1189662	0.1322212	0.1392757	0.1591757
TG 55:7- FA15:0	0.2212 666	0.3976 608		0.34685 16	0.35998 02	0.1129848	0.0988586	0.1336245	
TG 55:7- FA22:6	1.1081 466	2.3657 445	0.4021 075	1.17929 53	2.55954 43	0.5102569	0.4393716	0.5066596	0.4626312
TG 56:1- FA16:0	1.4873 978	1.8928 984	0.7404 946	1.23505 37	0.89030 44	0.7946212	0.3936575	0.4270701	0.6429287
TG 56:1- FA18:1	0.6248 14	1.0397 617	0.2045 769	0.51545 51	0.75821 89	0.2576718	0.1892068	0.2059129	0.2302682
TG 56:10- FA18:2	1.9609 387	2.6477 014	0.6516 653	2.22232 59	1.74193 79	0.5544194	0.7490015	0.6138365	0.6935899
TG 56:2- FA16:0	1.2170 983	2.1679 236	0.2895 376	0.62429 08	0.62582 22	0.3457348	0.1941037	0.3596159	0.2359092
TG 56:2- FA18:0	0.8870 827	1.5418 278	0.3626 133	0.50202 11	0.57448 9	0.3405267	0.2340222	0.2490558	0.2767513
TG 56:2- FA20:0	2.5500 408	3.5914 546	1.3022 526	2.01652 46	3.34457 71	1.2001435	0.6545728	0.7506793	1.2848604
TG 56:2- FA20:1	2.6489 85	4.2210 498	0.5505 775	1.19967 65	1.16087 7	0.4969401	0.3514387	0.7798893	0.5338758
TG 56:3- FA16:0	0.9105 823	1.4461 297	0.2116 398	0.46448 6	0.52443 47	0.2693551	0.1623947	0.222974	0.202465

TG 56:3- FA18:0	1.9318 735	3.2811	0.5479 222	1.11800 07	1.17985 6	0.6370235	0.4687881	0.4471762	0.7172069
TG 56:3- FA18:1	4.6274 989	6.0861 956	1.6000 769	2.65736 95	4.42968 19	1.5079489	0.940014	1.0045348	1.4092503
TG 56:3- FA18:2	2.8018 919	4.8026 342	0.6145 379	1.92278 05	1.72741 61	0.7416043	0.5998386	0.6294855	0.6358615
TG 56:3- FA20:0	4.5001 211	5.2312 658	1.7088 34	4.38569 73	4.34434 22	1.3589295	1.0566043	1.1668834	1.7635889
TG 56:3- FA20:1	3.7385 964	5.6570 308	1.3166 761	2.24957 31	3.43866 52	1.1320697	0.7665379	0.835448	1.0458875
TG 56:3- FA20:2	0.2011 395	0.2684 299	0.1232 722	0.11909 46	0.22509 82	0.1007324		0.0757416	0.0814904
TG 56:4- FA16:0	0.4111 705	0.7109 103	0.1475 606	0.27350 38	0.45099 5	0.2113663	0.1236598	0.1321409	0.1152383
TG 56:4- FA18:0	0.5871 103	0.8438 946	0.2338 903	0.41614 66	1.07713 13	0.3109006	0.2125589	0.2517296	0.2422069
TG 56:4- FA18:1	7.7412 695	9.7747 716	2.1603 457	4.73689 3	8.70151 54	2.1178558	1.3726487	1.4207798	2.0212608
TG 56:4- FA18:2	7.8525 148	9.7788 444	1.7764 14	5.53330 34	6.19782 63	1.7606943	1.5216976	1.4217773	1.7117776
TG 56:4- FA20:1	7.4709 342	9.1312 534	1.9746 33	4.82333 46	6.75801 06	1.6391703	1.3305679	1.3724387	1.7641541
TG 56:4- FA20:2	0.5233 219	0.9745 61	0.2324 376	0.42658 46	1.77100 51	0.2876604	0.1987003	0.1937036	0.2263198
TG 56:4- FA20:3	0.3417 373	0.5540 104	0.1751 238	0.27526 04	0.69838 81	0.2068783	0.1161093	0.1389206	0.1448813
TG 56:4- FA20:4	0.2545 79	0.3559 325	0.0791 209	0.18242 53	0.33731 5	0.0584988	0.0696787	0.1244396	0.1026317
TG 56:4- FA22:4	0.0854 179	0.0907 876	0.0493 122	0.08443 49	0.09646 1	0.0348786		0.0400482	0.0293549
TG 56:5- FA16:0	0.7159 145	1.3184 153	0.2469 534	0.47390 02	1.98043 56	0.3662251	0.2166153	0.2601047	0.2204028

TG 56:5-FA18:0	0.8850 524	1.4439 586	0.4258 863	1.10803 92	1.88251 02	0.4342828	0.4192741	0.5873421	0.458429
TG 56:5-FA18:1	2.6310 314	3.6829 88	1.0529 09	2.53258 98	8.34801 8	1.0136317	0.8166999	0.8700802	0.8900812
TG 56:5-FA18:2	9.9259 854	12.258 039	2.1123 649	8.12520 94	9.68621 9	2.0995214	1.9581978	1.6748736	2.0862145
TG 56:5-FA20:1	6.2969 411	7.8934 648	1.2681 884	5.05577 46	5.13057 65	1.1025066	1.1656037	1.050095	1.2334813
TG 56:5-FA20:2	1.0147 257	1.3101 541	0.4005 251	1.09193 99	2.83118 47	0.4105291	0.2924457	0.3261276	0.3734059
TG 56:5-FA20:3	0.9847 249	1.3787 611	0.2999 353	0.93468 59	3.44588 98	0.4013768	0.2985394	0.2954675	0.3548246
TG 56:5-FA20:4	1.5766 593	2.5997 172	0.7336 081	1.67204 31	3.42153 3	0.6197983	0.7570365	1.0137477	0.7270278
TG 56:5-FA22:4	0.7154 601	1.5275 287	0.3168 577	0.59347 67	2.61998 19	0.3939148	0.2040218	0.3546272	0.2892052
TG 56:5-FA22:5	0.1729 507	0.5033 897	0.1263 558	0.18831 94	0.51401 97	0.1416765	0.0670676	0.1349828	0.1025994
TG 56:6-FA16:0	3.0376 066	5.2635 223	1.4508 586	4.29391 54	7.04515 38	2.1127163	1.2713407	2.1002805	1.3182833
TG 56:6-FA18:0	1.2032 618	1.6741 384	0.4518 471	1.50899 74	2.32385 5	0.4586946	0.5863147	0.7211207	0.5787229
TG 56:6-FA18:1	3.8587 114	5.1529 436	1.5634 172	4.84160 67	10.5304 97	1.7801753	1.2448844	1.9318219	1.4788141
TG 56:6-FA18:2	4.2610 113	5.0500 682	1.2477 612	4.75720 33	8.31954 26	1.2733473	1.3760635	1.5069401	1.2980081
TG 56:6-FA18:3	0.8806 479	1.0833 858	0.2854 349	0.87584 09	0.86457 4	0.2003903	0.2030821	0.2196675	0.272856
TG 56:6-FA20:2	0.9424 119	0.9800 017	0.2544 168	1.29253 52	1.77441 76	0.2958325	0.2671841	0.3089898	0.2288498
TG 56:6-FA20:3	1.8086 511	2.0310 587	0.5886 076	2.00389 86	5.46179 57	0.5496306	0.597933	0.4018371	0.5571395

TG 56:6- FA20:4	3.7740 665	5.1926 423	1.4647 051	4.72194 2	9.93814 32	1.2547935	1.8971065	2.0533189	1.6818709
TG 56:6- FA20:5	0.6789 722	1.0089 568	0.2969 792	0.76136 73	0.69955 49	0.2950887	0.2559368	0.3419274	0.3809835
TG 56:6- FA22:4	1.5850 258	2.6599 075	0.7115 769	1.51896 51	3.27244 33	0.7350663	0.604392	0.7748068	0.56615
TG 56:6- FA22:5	4.0254 463	6.6417 263	1.8592 347	5.43534 49	9.64778 08	2.8290148	1.4608326	2.4836942	1.7384518
TG 56:6- FA22:6	0.9734 636	2.5949 511	0.6436 185	1.04672 79	2.25211 13	0.751504	0.726655	0.8444883	0.5912649
TG 56:7- FA16:0	9.1512 296	16.267 969	3.9150 124	13.5240 38	21.5643 34	5.9515874	3.744312	5.9906689	4.0714884
TG 56:7- FA16:1	0.2327 158	0.4763 302	0.1272 221	0.32463 65	0.90563 4	0.1054186	0.0911294	0.1134666	0.0907182
TG 56:7- FA18:0	0.5086 872	0.7465 524	0.2060 841	0.72366 06	0.63203 84	0.1752225	0.2967104	0.2837779	0.2464262
TG 56:7- FA18:1	6.9363 519	11.785 773	3.0229 165	8.52434 38	18.8661 43	3.7722426	3.0024018	3.8786903	2.9844859
TG 56:7- FA18:2	6.4038 259	7.4156 788	2.1337 841	11.4547 6	10.8682 46	3.0951475	2.7829435	3.4420409	2.2313845
TG 56:7- FA18:3	0.5589 286	0.5848 945	0.2194 43	0.77084 99	0.88477 01	0.1894647	0.2355703	0.2203618	0.2262362
TG 56:7- FA20:3	1.6266 421	1.4388 493	0.5063 54	2.34177 53	3.20097 73	0.3885511	0.5172406	0.4531918	0.4219786
TG 56:7- FA20:4	4.0392 485	4.8270 857	1.5702 726	4.66833 17	10.3208 93	1.2728565	2.2024008	2.223826	1.7037889
TG 56:7- FA20:5	2.4270 05	3.2150 413	1.2578 101	4.60589 6	4.72336 67	1.1825602	1.4171166	1.5305505	1.719644
TG 56:7- FA22:4	0.2545 218	0.3589 297	0.1285 301	0.38419 44	0.61634 99	0.0966987	0.0932897	0.1157834	0.0759457
TG 56:7- FA22:5	8.4207 674	11.647 462	3.4905 71	15.8313 53	12.4190 49	5.2629013	3.4261964	6.0206173	3.4113526

TG 56:7- FA22:6	37.480 199	71.838 507	16.484 036	44.3961 31	104.547 31	23.699321	15.249527	22.207844	16.165728
TG 56:8- FA16:0	17.481 928	25.755 504	6.2479 496	28.2959 5	26.6539 48	8.6189046	8.501203	10.524562	6.2041971
TG 56:8- FA16:1	1.0104 419	1.8127 84	0.4082 954	1.61326 3	3.26869 12	0.4641719	0.2729016	0.4531839	0.4152545
TG 56:8- FA18:1	1.9921 016	2.7214 048	1.0372 561	4.13559 18	4.22016 93	0.8142325	1.075068	1.1093055	1.1591166
TG 56:8- FA18:2	14.965 107	20.456 987	5.3367 469	25.0663 04	23.4421 56	6.7880597	7.4691835	8.8421565	5.4891481
TG 56:8- FA18:3	0.6749 341	0.8419 695	0.3749 543	1.29124 42	0.98195 33	0.3422449	0.3253952	0.3853738	0.4598481
TG 56:8- FA20:4	3.2869 421	3.6549 752	1.0353 387	4.86290 07	6.84585 01	0.9195011	2.0882289	1.851915	1.15913
TG 56:8- FA20:5	4.8410 429	4.3609 643	2.2408 186	12.1862 21	6.78717 13	1.8137547	2.8601747	3.0162354	3.0602105
TG 56:8- FA22:5	1.7908 295	2.4965 627	0.7386 527	3.30483 2	2.94267 63	0.7515887	0.7695251	0.9132317	0.7367458
TG 56:8- FA22:6	87.438 101	133.21 554	32.156 357	144.022 02	141.880 85	43.66055	42.260405	52.23143	31.447729
TG 56:9- FA18:3	0.7498 126	0.8873 845	0.3052 722	1.75481 87	1.15752 31	0.2620616	0.4409529	0.4924434	0.3691867
TG 56:9- FA20:4	0.7186 468	0.7340 935	0.2692 57	1.38983 08	0.95839 47	0.1852792	0.4948824	0.4277223	0.2969902
TG 56:9- FA20:5	4.5520 409	3.4848 153	1.7973 331	14.4538 81	4.28913 88	1.3336767	3.1691505	2.912451	2.4825752
TG 56:9- FA22:6	8.1434 416	12.735 075	3.4025 847	15.6423 39	17.7868 9	3.1414011	3.0819116	3.7439769	3.0535839
TG 57:10- FA22:6	0.5412 725	0.6251 503	0.2947 949	0.74900 27	0.69238 86	0.2936681	0.4346307	0.4908074	0.3616793
TG 57:2- FA18:1	3.7211 37	5.2119 906	1.3624 439	6.05798 4	9.42640 82	1.7629437	1.7015253	1.6903471	1.5500499

TG 57:3- FA18:2	5.5987 165	6.2801 785	1.4527 449	11.5100 67	8.64111 9	1.8316734	3.103455	2.4948367	1.8371371
TG 58:10- FA18:2	6.0407 753	6.8646 482	1.6451 588	12.1981 96	9.03357 27	2.1901212	3.3529384	2.7756086	1.9817602
TG 58:10- FA20:4	0.7443 165	0.9841 477	0.3279 794	0.98924 17	1.59838 27	0.382375	1.2165959	0.9712472	0.5319373
TG 58:10- FA20:5	0.5474 57	0.5556 516	0.2999 17	1.24298 78	0.59628 03	0.271418	0.8662163	0.699298	0.422865
TG 58:10- FA22:5	0.7161 937	0.6897 743	0.2315 149	1.65302 66	0.75011 18	0.2526406	0.3163149	0.3223102	0.2215007
TG 58:10- FA22:6	16.464 956	18.660 486	4.5373 411	35.3699 89	28.6068 02	6.1555549	8.9849664	7.8462384	5.4737525
TG 58:2- FA18:1	0.4915 727	0.7846 022	0.2048 294	0.37935 16	0.42657 45	0.203343	0.1272409	0.1648197	0.1879674
TG 58:3- FA18:1	0.8698 818	1.2812 091	0.1740 012	0.46986 43	0.49476 39	0.2326443	0.1641794	0.271079	0.1765642
TG 58:5- FA18:1	0.2233 735	0.3326 88	0.1466 42	0.17773 12	0.39576 7	0.1246785	0.0999417	0.0819212	0.0939933
TG 58:6- FA16:0	0.2724 846	0.4475 274	0.1811 77	0.21719 49	0.30685 98	0.2176481	0.0778283	0.1127896	0.1340095
TG 58:6- FA18:0	0.1739 864	0.3068 491	0.0757 111	0.20736 15	0.38261 11	0.0870918	0.0857966	0.1096973	0.0767768
TG 58:6- FA18:1	0.3438 223	0.5448 021	0.1530 345	0.32913 34	1.16940 83	0.1776263	0.1238625	0.1277343	0.1211596
TG 58:6- FA20:4	0.3262 422	0.4873 101		0.34055 48	0.33435 86	0.1316785	0.1939291	0.1074326	0.0710855
TG 58:6- FA22:4	0.2136 403	0.3791 287	0.1049 51	0.20206 8	0.87922 51	0.1456562	0.1212736	0.0755035	0.0956114
TG 58:6- FA22:5	0.3578 078	0.5692 669	0.1874 64	0.44426 18	0.51577 28	0.2438624	0.1525418	0.140801	0.1789106
TG 58:7- FA16:0	0.8481 965	1.4958 569	0.3826 946	0.64597 87	1.43412 09	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		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:BSHIV MOL361- F16	Bt:BSHIV MOL361- F17	Bt:BSHIM OL361- M12	Bt:BSHIM OL361- M13	Bt:BSHI MOL361- F14	Bt:BSHI MOL361- F15	Bt:BSHI III E2- M8	Bt:BSHI II E2- M9	Bt:BSHI III E2- M10	Bt:BSHI III E2- F11
CE 12:0	3.6580931	0.7926343	1.7960596	2.57589	2.04201	1.040752	1.917684	2.196931	2.635470	2.178669
CE 14:0	6.3043649	4.3469295	5.194435	5.7531597	4.6540089	3.0124468	4.631894	4.631584	6.547751	5.606979
CE 14:1	5.4931365	1.428596	3.8780368	4.8809786	3.8167046	1.5069648	3.740955	3.314200	5.464810	4.191209
CE 15:0	8.4737029	4.2921358	6.5285139	7.1218766	5.6132151	3.1488501	5.170113	5.527765	7.853628	6.618575
CE 16:0	86.697314	93.028925	82.522357	72.835394	66.546174	57.003381	75.19167	77.98051	96.99198	93.95892
CE 16:1	37.124467	75.36668	35.297183	28.753677	32.103473	31.435352	28.82451	31.73774	43.02451	54.31576

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

CE 22:5	11.422316	7.5240562	8.3235345	6.7000833	6.145526	4.7610453	7.220776	6.900821	12.19584	8.153773
CE 22:6	194.24443	137.73733	159.81215	147.82835	98.604478	96.396379	162.3962	197.6468	232.0580	170.2550
CE 24:0	84.897984	36.092907	73.169007	69.870603	42.816916	49.410016	69.30800	90.26042	60.25439	62.77110
CE 24:1	19.021779	8.597845	12.596927	14.395107	9.8927974	9.1992214	13.54771	16.33936	17.47962	12.19381
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	0.117715	0.223032	0.232063
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	0.941416	0.943917	0.322307
Cer d18:1/24: 0	1.370194	0.7730831	1.0973682	1.1094032	0.7398598	0.8220561	0.767014	0.816998	1.229748	0.775851
Cer d18:1/24: 1	0.4898566	0.9129086	0.3556753	0.4892119	0.7715835	0.8537345	0.265146	0.360965	0.409509	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	0.486477	0.395402	0.470691	0.547604	7						
DG 16:0_16: 1																	
DG 16:0_18: 0							1.765074										
DG 16:0_18: 1	2.5817944	1.8087951	1.6630539	1.7503957	2.6014169	1.4336315	1.356389	1.610531	1.650687	3.057664	3						
DG 16:0_18: 2		2.763573		6.7373682	6.1725741	4.461057	7.462121	5.622636		4.382609	2						
DG 16:0_22: 6										0.419476	5						

DG 16:1_18: 1		0.3497686			0.3725159							
DG 16:1_18: 2		0.8462362		0.8885846	1.2487553	0.9681309	0.992130	0.628669				1.008602 1
DG 18:0_18: 1		0.1628333			0.2658465		0.198918					0.233913
DG 18:0_18: 2				1.021402	1.0614685	0.6156215		0.724487				0.604445 5
DG 18:1_18: 1	1.1659992	2.571286	0.67396	0.8076498	1.4789625	1.1393391	0.325585	0.588289	0.495302			2.204155 7
DG 18:1_18: 2		11.767728		12.888031	14.264311	10.309941	7.868521	6.625662				11.59995 8
DG 18:1_20: 1	0.7615155	0.3272946	0.3971991	0.461825	0.6434222		0.304779		0.372877			0.400346 3
DG 18:1_20: 2					0.3575817							
DG 18:1_20: 4												
DG 18:1_22: 6								1.647196				

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

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

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

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

PC 16:0_20: 5	25.280392	27.57052	23.478688	19.025419	19.856503	17.061245	33.06258	27.48516	41.35212	22.49174
PC 16:0_22: 1										
PC 16:0_22: 2								0.407212	0.346500	
PC 16:0_22: 4	1.9748346	2.1995301	1.9494395			1.184073	1.441792	1.986890	1.547835	2.653345
PC 16:0_22: 5	22.080952	14.49043	21.093556	16.154777	7.8923238	12.424314	11.86118	14.39411	18.86702	14.84085
PC 16:0_22: 6	299.1005	213.35375	213.45982	204.03926	122.5536	131.22938	212.4657	279.6372	290.3411	225.1088
PC 16:1_17: 0										
PC 16:1_18: 0	0.528965	0.8642824	0.4946834	0.6483476	0.5259313	0.4187057	0.360165		0.547364	0.616307
PC 16:1_18: 1	4.0820855	6.5929836	4.0611002	2.7940755	2.2093952	3.4389896	2.382943	3.084368	4.069300	5.249796
PC 16:1_18: 2	10.385903	8.1106863	9.8104437	10.227015	6.4156956	5.8865438	8.170820	9.143890	10.66947	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	13.27013	16.00753	10.56908
PC 18:2_18: 3			1.0152365	1.2659148			1.645928	1.153102		
PC 18:2_20: 0	13.560004	4.6144591	12.815477	15.621142	7.2747336	4.9900188	9.844936	12.72133	12.40464	6.756266
PC 18:2_20: 1	2.2026961	1.4672662	2.4188516	2.7374401	1.3479191	0.9831883	1.399436	1.720171	1.827944	1.184929
PC 18:2_20: 2		0.6730044		0.9414668	0.7053637	0.5120823	0.741574	0.893928	0.943206	0.649322
PC 18:2_20: 3	1.5370104	1.6650689	1.6854773	1.3340607	1.2182682	1.2756396	1.352194	1.878078	1.942360	1.147879
PC 18:2_20: 4	6.6944154	4.6085332	7.4458475	6.8119782	4.9196566	4.3635804	5.707795	7.335737	7.427928	4.651419
PC 18:2_20: 5									2.647928	
PC 18:2_22: 6									5.794243	
PC 20:0_20: 3								0.996701		

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 1	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									0.442294	0.635286		1.375775	8
PE 18:1_18: 2													
PE 18:1_20: 4													
PE 18:1_22: 0													
PE 18:2_18: 2													
PE O- 16:0/18:1										0.268291	9		
PE O- 16:0/18:2									1.112388	4	1.006937		
PE O- 16:0/20:4													
PE O- 18:0/16:0									0.786681	7	0.998596	1.504651	1.208453

PE O- 18:0/18:1		1.5966002	1.1639424	0.9519813	0.8295993	0.5877857	1.084603	1.171336	1.878433	1.253974
PE O- 18:0/18:2		4.9357352	5.3828136	6.2532496	3.7666863	2.9382706	4.495424	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	1.514180	1.310997		
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	1.664553	1.248785
PE P- 18:0/18:1				0.5606779		0.5503419	0.651209	0.785349	1.556765	
PE P- 18:0/18:2		3.6272203	2.4450253	2.9784499	2.3383754	2.1379844	2.470264	3.150325		
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	0.163501	0.195954
								7	8	8

PG 16:0_18: 2	0.2359194	0.1061032	0.2038487	0.2517634	0.1466308	0.0711554	0.111019 5	0.167097 5	0.209530 5	0.162839 4
PG 16:1_18: 1	0.1576093	0.1442568	0.1457008	0.1572669	0.1310393	0.1077339	0.107047 4	0.118773 9	0.173910 1	0.129381 4
PG 16:1_18: 2	0.5542768	0.3689965	0.6042037	1.1875482	0.4447837	0.3712546	0.605301 9	0.654552 9	0.704049 1	0.448855 9
PG 17:0_20: 0	0.467738	0.5670793	0.6132529	0.5347422	0.4900898	0.442292	0.436075 7	0.484912 9	0.647665 5	0.546041 5
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		0.119173 9	0.126896 5	0.225335 6	0.352785 4
PG 18:0_18: 2	0.9696397	0.7280405	0.6252484	0.5438926	0.3050322	0.2736724	0.576886 7	0.557455	1.046397 3	0.828816 3
PG 18:0_20: 0	0.4145912	0.6195734	0.3515381	0.3098329		0.2719803		0.460217 6	0.607558 9	0.394565 4
PG 18:0_20: 4	1.7485047	1.4473444	0.6714176		0.4459039	0.3674997	0.437276 2	0.875275 2	1.306328 3	1.850668 8

PG 18:0_22: 5		0.2208722											
PG 18:0_22: 6		0.9846528								0.734004 9	1.227555 2	1.076625 2	
PG 18:1_18: 1	0.0619913	0.0729047	0.0777824	0.089682		0.071527	0.0622067	0.048195 7	0.055722 2		0.082817 3	0.078448 2	
PG 18:1_18: 2	0.9168816	0.6554303	1.1012863	1.4213901		0.6340742	0.5626757	0.737283 7	0.806275 4		1.078865 6	0.893541 6	
PG 18:1_20: 0	0.1908533	0.1539914	0.1811683	0.1647266		0.1180515		0.117620 6	0.073153 4		0.228169 3	0.184880 3	
PG 18:1_20: 3				0.1786161			0.1310949		0.154806 9			0.186305 3	
PG 18:1_20: 4	1.4191404	0.9096994	1.5170754	1.7203575		0.9787871	1.1490735	1.142903 6	1.327495		1.5058	1.242864 5	
PG 18:1_22: 6												0.479228 1	
PG 18:2_18: 2	0.0922467	0.1022836	0.1111314	0.1537448		0.0882444	0.0667472	0.066924 7	0.076302 4		0.125129 8	0.119335 5	
PG 18:2_20: 0	1.7006949	1.222014	1.1984745	1.0055525		0.4190705	0.5096117	0.631791 0.631791	0.710008 2	1.797726 4	1.203907 9		

PG 18:2 20: 4												0.376364 9	0.460501 7	0.508590 5
PG 20:0 20: 3												0.107483 8	0.259894	
PG 20:0 20: 4												2.185279 1	4.074878 4	4.211412 8
PG 20:0 20: 5													0.492138 5	
PG 20:0 22: 6													0.810898 7	
PI 14:0 18: 1												0.931347 4	1.169101 1	1.136750 9
PI 14:0 18: 2													0.359783 6	
PI 15:0 18: 1														
PI 15:0 20: 1														
PI 15:0 20: 2													0.607099 8	

PI 15:0_22: 0	0.8757225	0.9009402	0.9355593	0.7818073	0.6272747	0.8423484	0.905253 3	0.746946 5	0.919704 5	0.819529
PI 15:0_22: 1	0.4444977			0.3958806	0.5060992		0.273059 2		0.496601 2	0.406067 6
PI 15:0_22: 2	0.7825777		0.6445555	0.8750171	0.6547906				1.004595 8	
PI 15:0_22: 4	1.0217005	0.8280067	1.0498038	0.635493	0.7637511	0.4939061	0.636977 5	1.047149 2	1.201185 6	0.716057 2
PI 15:0_22: 6										
PI 16:0_16: 0	0.1362584			0.2039762	0.1264624		0.125281 9		0.132138 6	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	1.268723 1	1.607715 7	1.829326 1	1.429813 4
PI 16:0_18: 2	8.6646599	3.9655445	9.5059483	10.977548	6.0424375	3.5245792	7.458859 7	8.834642 5	10.11538 8	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	0.429158 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	1.672323 1	1.977178 7	2.740522 7	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	2.622051 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									0.285530 1	0.376858 2		
PI 20:0_20: 4	0.9007487								0.863443 8	1.485000 9	1.217363 8	
PS 16:0_18: 2												
PS 16:0_22: 6												3.504417 3
PS 16:1_18: 1											1.831258 8	1.665252 2
PS 16:1_18: 2	3.8032818	2.7214689	2.3847824	2.261621	1.2009138				1.448805 8	1.824811 4	4.525443 6	2.468146 8
PS 17:0_20: 0	1.0023878	1.0558551	1.355176	1.1191074	1.1292857	0.9124057			1.230751 7	1.331897 1	1.050274 7	0.839159 3
PS 17:0_20: 3	3.0189494	1.5220105	1.0212647	1.7820961	1.0044666	0.8729661			1.505975 1	0.929964 5	2.086952 6	1.775640 4
PS 17:0_22: 1			1.3649461	1.2272117								
PS 18:0_18: 0	0.3933844	0.3433014	0.4019972	0.1766817					0.267360 9	0.230922	0.520858 4	0.378760 3

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

[illegible]

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

TG 42:0- FA16:0	0.1734713		0.1340947	0.1816362	0.1728721	0.0704887	0.110261 5	0.065563 8	0.109205 3	0.176816 1
TG 42:1- FA16:0	0.3532192	0.0663032	0.2111702	0.2865689	0.3470531	0.1262844	0.194184 3	0.129560 6	0.286550 6	0.356425
TG 42:1- FA16:1										
TG 42:1- FA18:1	0.1836688	0.0693574	0.1330502	0.1387798	0.1614376	0.0554884	0.088290 8	0.050802	0.103693 1	0.214473 8
TG 42:2- FA18:2	0.2563208	0.0524743	0.1220686	0.2384598	0.2252579	0.1070841	0.190823 3	0.120363 7	0.207204 6	0.204469 4
TG 44:0- FA12:0									0.074794 4	
TG 44:0- FA14:0									0.085335 2	
TG 44:0- FA16:0	0.1489813	0.0768734	0.1473583	0.1177972	0.1552815	0.076209	0.122703 4	0.082255 6	0.161490 1	0.128715 7
TG 44:1- FA14:0	0.0875478				0.0728069					
TG 44:1- FA16:0	0.5642972	0.1504893	0.2608048	0.491767	0.6178757	0.2045989	0.231835 1	0.195299 8	0.354205 7	0.616853 4
TG 44:1- FA18:1	0.3308591	0.0917967	0.2147673	0.2981831	0.3798459	0.1025641	0.139120 9	0.095636 2	0.172316 5	0.346919 7
TG 44:2- FA16:0	0.8563132	0.1243121	0.3525854	0.6555889	0.7058721	0.2790517	0.462474 4	0.299794 5	0.471496 5	0.624429 6
TG 44:2- FA16:1	0.1018693				0.1178661					0.078438 2
TG 44:2- FA18:1	0.2038794	0.0961852	0.1099243	0.1619264	0.2040979	0.0783651	0.094603 5	0.065155 2	0.145064	0.272937 3
TG 44:2- FA18:2	0.4265327		0.1924986	0.4194344	0.3621141	0.1250179	0.232061 9	0.138468 3	0.219558 5	0.284975 5

TG 44:3-FA18:2	0.2804639	0.0686336	0.1189619	0.2320123	0.2065347	0.1187343	0.146690	0.099009	0.157118	0.218331
TG 45:0-FA16:0	0.2336689		0.1745118	0.1495975	0.2460511	0.0860783	0.150679	0.121581	0.126139	0.193714
TG 45:1-FA16:0	0.636318	0.1221972	0.2972674	0.5330223	0.6123212	0.1952572	0.278353	0.189569	0.359426	0.501046
TG 45:1-FA18:1	0.2819835	0.0649913	0.1605244	0.2210928	0.31219	0.0871903	0.09411		0.144101	0.301872
TG 46:0-FA12:0									0.035114	0.019236
TG 46:0-FA14:0	0.1361691	0.1981686	0.3308466	0.1623113	0.1804284	0.1105493	0.210554	0.147007	0.354421	0.168364
TG 46:0-FA16:0	0.3464727	0.3951392	0.7858345	0.3160399	0.4559042	0.2642235	0.415312	0.318781	0.714623	0.421656
TG 46:1-FA12:0	0.3414086	0.1769308	0.2452723	0.2484961	0.2639001	0.1532531	0.193055	0.141442	0.256505	0.366791
TG 46:1-FA14:0	0.0968551	0.2151986	0.2267973	0.0891519	0.1238777	0.1444096	0.111668	0.079851	0.224349	0.239847
TG 46:1-FA14:1		0.03789		0.1006868	0.083904		0.066091		0.098008	0.088394
TG 46:1-FA16:0	0.5195409	0.2509648	0.3454351	0.4660782	0.6149436	0.2719879	0.345176	0.201661	0.494937	0.433765
TG 46:1-FA16:1		0.1552724	0.1944506		0.105703	0.0758109	0.091312	0.061319	0.221220	0.141927
TG 46:1-FA18:0	0.0844099		0.0603395	0.0914052	0.1040349	0.0472514			0.078888	0.068949
TG 46:1-FA18:1	0.1123859	0.1084171	0.1498065	0.1633013	0.1770966	0.0929974	0.100545	0.063425	0.160725	0.172346
TG 46:2-FA12:0	0.6508832	0.2048748	0.3289597	0.4485211	0.3736369	0.3111139	0.393997	0.384166	0.525571	0.428577
TG 46:2-FA14:0	0.0991126	0.0906001	0.2318025		0.0893532	0.0910819	0.076767	0.07732	0.182834	0.139926
							2		2	7

TG 46:2- FA14:1	0.076704																	0.070086	0.090395
TG 46:2- FA16:0	0.4430956	0.1705867	0.3111197	0.3887908	0.5246875	0.2480102	0.23886	0.247463	0.423305	0.419309								0.423305	0.419309
TG 46:2- FA16:1			0.0904431			0.0724963												0.085547	0.138791
TG 46:2- FA18:1	0.4160415	0.1678214	0.2450614	0.5044297	0.4036486	0.1552966	0.145094	0.114191	0.269591	0.515858								0.269591	0.515858
TG 46:2- FA18:2	0.2017807	0.091523	0.2465481	0.2567875	0.2034066	0.1464549	0.189594	0.146419	0.264963	0.179757								0.264963	0.179757
TG 46:3- FA12:0	0.1381745			0.1126086	0.0883903	0.0773066	0.084856	0.092208	0.108827									0.108827	
TG 46:3- FA14:1									0.061389									0.061389	
TG 46:3- FA16:0	0.6788316	0.1339208	0.3350392	0.4920131	0.5295577	0.2877378	0.412668	0.258687	0.418565	0.512758								0.418565	0.512758
TG 46:3- FA16:1				0.0638268														0.079307	0.104306
TG 46:3- FA18:1	0.3528204	0.16746	0.2820308	0.5718503	0.3835205	0.1651995	0.177786	0.138883	0.221484	0.436385								0.221484	0.436385
TG 46:3- FA18:2	0.468874	0.1087361	0.3010553	0.6367655	0.4091612	0.221904	0.300540	0.197662	0.262398	0.378469								0.262398	0.378469
TG 46:3- FA18:3	0.0875105			0.1000966	0.0541747				0.065110									0.065110	
TG 46:4- FA18:2	0.5155323	0.0903027	0.3184171	0.6893045	0.3709854	0.1850872	0.285298	0.150513	0.249390	0.350646								0.249390	0.350646
TG 47:0- FA14:0									0.076229									0.076229	
TG 47:0- FA15:0	0.2005785	0.1985321	0.2690262	0.2076032	0.2345931	0.1406018	0.179851	0.210491	0.260989	0.259859								0.260989	0.259859
TG 47:0- FA16:0	0.5426101	0.5741733	0.7551568	0.6541993	0.6351872	0.2968109	0.569174	0.488073	0.639214	0.592253								0.639214	0.592253

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			0.068035 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	0.558047	1.572062	2.018514
TG 48:1- FA14:1	0.0477201		0.047941	0.0713331	0.0700983			0.039320	0.055516	0.052870
TG 48:1- FA16:0	2.0405402	4.6370009	3.8916214	1.6118365	2.8622109	2.73839	1.919131	1.599626	3.192569	4.265484
TG 48:1- FA16:1	0.6952877	1.4461225	1.2221604	0.4657715	0.9930134	0.8423256	0.672043	0.544306	1.283588	1.280736
TG 48:1- FA18:0			0.0795692		0.1158598	0.0548862	0.052446		0.087737	0.070581
TG 48:1- FA18:1	0.7787915	1.7589387	1.8166574	0.8112683	1.2524199	1.0620822	0.750795	0.594407	1.418205	1.734407
TG 48:2- FA12:0	0.3970947	0.3376209	0.2437396	0.2523404	0.167279	0.1623675	0.165420	0.171432	0.334552	0.325747
TG 48:2- FA14:0	2.0010805	1.9062539	3.2025255	1.6771903	1.9059767	1.7990259	1.704798	1.396243	2.494911	2.865243
TG 48:2- FA14:1	0.6847022	0.3794672	0.3968431	0.4708732	0.5731153	0.3816639	0.351423	0.314414	0.513913	0.745333
TG 48:2- FA16:0	2.0433743	2.3304346	3.49249	1.6984654	2.3393499	2.3918109	1.661476	1.452569	2.718653	3.099865
TG 48:2- FA16:1	0.5968203	1.8302724	0.987529	0.2336536	0.8969549	1.2922653	0.365954	0.414774	0.975583	2.197230
TG 48:2- FA18:0			0.0635851		0.0720191		0.065012			0.062243
TG 48:2- FA18:1	0.5720919	0.8976441	0.5710451	0.4941951	0.6333573	0.5884974	0.242268	0.266068	0.591777	1.255900
TG 48:2- FA18:2	1.4801931	1.2392369	2.9619746	1.4915418	1.7387954	1.5701288	1.42477	1.239128	2.183921	1.834467
TG 48:3- FA12:0	0.3851228	0.2566412	0.2118588	0.2814318	0.2020692	0.2696239	0.200500	0.194861	0.289416	0.40815
TG 48:3- FA14:0	0.424881	0.4116128	0.5789764	0.29361	0.4324918	0.5527731	0.291723	0.292442	0.563703	0.874928
							6	7	2	2

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

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	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	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 5
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	1.3342193	1.6816282	1.6579544
TG 49:3-FA15:0	0.3240201	0.2677109	0.3684182	0.2473657	0.3138966	0.2928332	0.223192	0.2549106	0.3100836	0.3026984
TG 49:3-FA16:0	0.5316258	0.2596392	0.5021059	0.4158612	0.4175945	0.3184561	0.4339075	0.3058927	0.5179608	0.4280091
TG 49:3-FA16:1	0.2250679	0.3013429	0.2751478	0.1469854	0.2844688	0.2659902	0.1538777	0.2195063	0.2996897	0.3482659
TG 49:3-FA18:2	0.5781916	0.4183823	0.6062579	0.5341665	0.4792528	0.414847	0.4214309	0.3497939	0.6236318	0.5435552
TG 49:3-FA18:3	0.1164144	0.0928244	0.2440577	0.1254754	0.103698	0.0704969	0.1284138		0.150711	
TG 50:0-FA14:0			0.079764		0.0465159				0.0862267	0.0433651
TG 50:0-FA16:0	1.2972365	2.1006183	2.5195502	1.5092982	1.7411295	1.009738	1.7270204	1.3386907	2.5133704	1.8940153
TG 50:0-FA18:0	0.7447903	1.261576	1.4977706	0.7415518	1.0337665	0.7611723	1.0185777	0.806925	1.630502	1.1687823
TG 50:1-FA14:0	0.2280428	0.2565366	0.5431906	0.1961602	0.3369443	0.0929006	0.2679266	0.1786895	0.5314728	0.2663936
TG 50:1-FA16:0	19.816593	43.176568	34.193209	25.874947	24.238998	22.263958	13.953563	13.08588	21.236738	40.008273
TG 50:1-FA16:1	0.2037979	0.2816164	0.4777937	0.1795971	0.2574264	0.2461513	0.267766	0.2447563	0.4788656	0.2247379
TG 50:1-FA18:0	0.2760351	0.6167014	0.7007921	0.2868548	0.4281455	0.3638359	0.4392055	0.3598049	0.8311255	0.5578527
TG 50:1-FA18:1	10.039643	21.238661	18.44746	13.634336	13.30252	10.994402	7.4845042	6.39995	11.751632	19.412519
TG 50:1-FA20:1	0.1674062	0.1171634	0.3961039	0.1829244	0.225437	0.0716336	0.1910052	0.1035584	0.3293261	0.1114926
TG 50:2-FA14:0	1.203957	5.1946356	2.4170656	1.0327405	1.5328692	1.8196346	0.7455215	0.8118441	1.6781443	4.8427621

TG 50:2- FA14:1	0.1696579		0.1221657	0.1143741	0.1568221	0.0690482	0.100538 6	0.069143 7	0.133759 2	0.129027
TG 50:2- FA16:0	47.883399	59.126346	67.806945	53.292937	48.993033	49.597634	38.48015 1	36.99280 9	44.48445 9	77.76653 1
TG 50:2- FA16:1	6.8589073	20.754029	8.5147053	3.5180885	8.6447868	11.373878	3.296534 3	4.014876 6	6.503251 6	19.46754 8
TG 50:2- FA18:0	0.287905	0.331645	0.7693579	0.3300469	0.3525628	0.2116461	0.352045	0.310438 8	0.730449 7	0.391134 9
TG 50:2- FA18:1	8.2372625	28.448226	11.553806	4.8811066	10.428295	13.71995	3.895134 4	4.779739 8	8.707671 6	26.68779 9
TG 50:2- FA18:2	20.475887	18.193844	31.47809	26.819297	21.390551	18.316129	18.07997 1	15.77876 6	19.57016 8	27.89812 5
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 5	2.182527 4	3.641135 1	8.501660 5
TG 50:3- FA14:1	0.290925	0.3272196	0.1994229	0.3095209	0.2885874	0.1887497	0.155515 1	0.131403 2	0.261561 7	0.386045 7
TG 50:3- FA16:0	14.889003	16.524843	13.660646	8.0592916	15.239049	21.081459	10.27662 3		14.13045 7	21.66018 2
TG 50:3- FA16:1	13.494582	17.966866	11.986707	7.0451952	14.458107	19.945893	8.386018 7	9.623125 6	12.38929 7	23.37384 5
TG 50:3- FA18:0	0.1073664	0.0912536	0.1187388	0.0831952	0.1068622	0.071576	0.074352 2	0.073997 4	0.143089 3	
TG 50:3- FA18:1	4.685391	8.4202589	6.9450188	3.8519058	4.5877537	6.1545663	2.607058 7	2.803912 5	4.995441 7	10.62217 8
TG 50:3- FA18:2	14.532261	17.723644	15.083549	8.7231867	14.864219	20.114322	9.059648 5	10.39084 6	13.26143 4	23.48463 2
TG 50:3- FA18:3	0.8410076	0.89652	1.7351193	0.8310877	1.0103353	0.970943	1.241551 1	0.799892 3	1.362301 8	0.926549 2
TG 50:3- FA20:3	0.0748795	0.0572235					0.061813 9			

[illegible]

TG 50:5-FA20:5	0.0915241	0.0758645	0.0909715			0.07263	0.091083	0.106566	0.147866	0.080605
TG 51:0-FA16:0	0.7243584	1.2868787	1.0428648	0.8096233	1.2495329	0.8192845	1.088780	0.804997	1.444308	0.815167
TG 51:0-FA17:0	0.0531412	0.1412124	0.115521	0.1032015	0.119835	0.1276689	0.146528	0.078527	0.223956	0.122149
TG 51:0-FA18:0	0.1397367	0.3006806	0.2500178	0.1576755	0.1878507	0.1863272	0.277812	0.163683	0.352924	0.162541
TG 51:1-FA15:0	0.3027866	0.2957578	0.3129546	0.2076588	0.3297437	0.1606357	0.239733	0.190368	0.322831	0.243476
TG 51:1-FA16:0	2.0243127	2.2431716	3.0356763	2.2168965	2.5230582	1.3866922	1.503730	1.047996	2.150730	2.485473
TG 51:1-FA17:0	1.1714539	1.4942409	1.4586588	1.0152967	1.2556514	0.8880425	0.814946	0.696851	1.296666	1.601710
TG 51:1-FA18:0	0.2560935	0.3910887	0.4811509	0.2832377	0.2687661	0.2491109	0.322121	0.264455	0.416298	0.204846
TG 51:1-FA18:1	1.2698643	1.8172131	2.134536	1.4026611	1.4408459	0.9886625	1.005424	0.787959	1.614459	1.154178
TG 51:2-FA15:0	1.0309176	2.1259843	1.3980832	1.1494139	1.2165676	0.9792222	0.702998	0.781879	0.977749	1.773104
TG 51:2-FA16:0	5.3401864	5.6277642	6.2577672	5.6602063	6.0690508	3.9367435	2.785040	4.675240	6.720594	6.720594
TG 51:2-FA16:1	0.3431458	0.5281028	0.4264111	0.2623433	0.4516151	0.3133023	0.223047	0.191144	0.443621	0.655293
TG 51:2-FA17:0	2.4214159	2.1808581	2.5603341	2.0924809	2.1171157	1.6775066	1.872147	1.693194	2.358954	2.578834
TG 51:2-FA18:1	3.0245913	6.6679931	4.2422801	2.8367542	3.1934187	3.0261265	1.589792	1.599199	2.641821	5.268844
TG 51:2-FA18:2	2.5097916	2.8300374	4.4536591	2.8212391	2.5674984	1.8376409	1.813778	1.476327	2.661635	1.959462
TG 51:3-FA15:0	2.795581	2.9600152	2.6390398	2.8729273	2.5089022	2.2929344	1.519882	1.635845	1.814689	3.368652
							9	9	1	3

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

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

TG 52:3- FA18:0	1.2763495	1.7133461	2.0910342	0.9627955	1.3336419	1.4781271	1.141075	1.302994	1.893879	1.545605
TG 52:3- FA18:1	174.88873	258.65103	141.06041	148.60866	156.60496	209.1406	104.0543	107.8093	117.9426	271.0379
TG 52:3- FA18:2	156.7565	199.49521	125.7156	138.38149	137.71787	179.6046	94.96816	96.54881	104.4503	223.2091
TG 52:3- FA18:3	0.2698081	0.3688867	0.5193326	0.2492442	0.2585446	0.1682275	0.268599	0.345277	0.428300	0.300750
TG 52:3- FA20:0	0.44056	0.4847855	0.3386824	0.431655	0.4327753	0.4525288	0.281827	0.289368	0.370814	0.585154
TG 52:3- FA20:1	0.6060734	0.4079722	0.975902	0.4417718	0.5701668	0.3431968	0.430528	0.308500	0.693276	0.500019
TG 52:3- FA20:2	0.3682176	0.5671792	0.4811317	0.2352016	0.2938532	0.3083392	0.180536	0.217346	0.265003	0.548224
TG 52:3- FA20:3	0.21439	0.37042	0.3683485	0.2083149	0.2921846	0.2531652	0.188640	0.229572	0.225187	0.363921
TG 52:3- FA22:1	0.1153103	0.1205317	0.110085	0.1091036	0.0903327	0.1055136	0.073715			0.172996
TG 52:4- FA14:0	0.1425002	0.2015919	0.2707345	0.1431221	0.1373838	0.1279126		0.096987	0.170752	0.243929
TG 52:4- FA16:0	164.97308	96.126707	95.17048	141.50997	117.40282	166.11036	139.8034	118.9951	101.9318	141.8608
TG 52:4- FA16:1	14.661369	32.417835	12.281169	10.459327	15.478799	22.122878	6.783780	7.012593	10.56028	31.94233
TG 52:4- FA18:0	0.2172855	0.2005063	0.320214	0.1750467	0.2235736	0.2535724	0.210512	0.176492	0.317652	0.222374
TG 52:4- FA18:1	23.053441	39.407592	18.411478	16.323286	21.559979	31.430631	14.03696	13.09534	17.89991	39.73011
TG 52:4- FA18:2	265.26164	166.67548	163.00083	234.56763	190.23737	264.65094		187.9727	167.9457	237.5731
TG 52:4- FA18:3	14.133623	12.927781	10.202724	10.821798	11.121105	17.028967	11.19806	10.03585	10.78590	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	0.273985	0.353287
TG 52:6-FA16:0	1.0799661	0.589091	0.6736925	0.6524702	0.6633147	1.3420845	1.224938	1.147738	1.242744	0.727590
TG 52:6-FA16:1	1.3558552	1.3280897	0.9288204	0.7041337	1.038649	2.1429576	1.030369	0.934000	1.366348	1.525863
TG 52:6-FA18:1	0.3145821	0.4096499	0.4559209	0.2554782	0.2582942	0.3375333	0.255840	0.203706	0.439699	0.333534
TG 52:6-FA18:2	2.4168721	1.6298651	2.3847222	2.1994912	1.9078113	2.9148764	2.105162	1.736245	2.290379	2.158415
TG 52:6-FA18:3	1.9415205	1.3266991	1.1489733	1.106231	1.5050995	2.784962	1.570632	1.379041	1.797920	1.621755
TG 52:6-FA20:4	0.1980712	0.1605634	0.4644788	0.2265417	0.1764592	0.2266663	0.167548	0.191502	0.237038	0.325630
TG 52:6-FA20:5	0.7196177	0.7313897	0.6182325	0.3377007	0.5069501	0.8996269	0.552381	0.739812	1.092477	0.937766
TG 52:6-FA22:6	0.4139716	0.5634738	0.4706491	0.2721707	0.4408626	0.5048169	0.498528	0.506431	0.589060	0.683259
TG 52:7-FA16:0	0.6909957	0.9012393	0.8469388	0.596717	0.9396648	0.7146845	0.937023	0.663208	1.103282	0.731933
TG 52:7-FA18:1	0.109138	0.1530672	0.1404644	0.1002381	0.0717649	0.071793	0.067640	0.105848	0.122115	0.101923
TG 52:7-FA20:5	0.3549029	0.2599773	0.3229012	0.2963884	0.2534296	0.4804131	0.342398	0.453688	0.581821	0.422135
TG 52:7-FA22:6	0.2490547	0.1765621	0.1686797	0.1945049	0.1810212	0.240837	0.169050	0.247333	0.256001	0.388499
TG 52:8-FA16:1	0.1214252	0.1022354	0.1270967	0.0722262	0.1323832	0.1195702	0.122162	0.099171	0.189569	0.1052
TG 52:8-FA18:2	0.122768	0.1172708	0.1796123	0.1303247	0.0730547	0.1114209	0.141688	0.136825	0.153369	0.101192
TG 53:0-FA16:0	4.3931528	3.2693566	2.6320047	2.730951	2.2367062	4.8607764	5.505302	5.081736	5.743922	3.691995
							6	1	4	8

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

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

TG 54:3-FA16:0	20.669429	9.2656615	16.19026	16.944247	15.609173	8.2299069	10.17296 2	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 7
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	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	1.986968	2.077416	3.313361
TG 54:4-FA20:3	2.239067	4.451676	3.1750876	1.6091587	1.6670006	2.7074016	1.073546	1.163784	1.336287	3.798288
TG 54:4-FA20:4	0.4331668	0.6591145	0.7753412	0.3531731	0.3579099	0.5207677	0.441986	0.59629	0.520544	0.597830
TG 54:4-FA22:1	0.1461164	0.3831198	0.1993109	0.3063438	0.1606063	0.1766911	0.125522	0.102760	0.123142	0.331708
TG 54:4-FA22:4	0.074536	0.0813867	0.2345241		0.0956812	0.0829547	0.074414			0.131079
TG 54:5-FA16:0	4.7430051	4.793812	5.7889723	3.6233809	3.312278	5.0060141	3.226939	3.603620	3.400159	5.216221
TG 54:5-FA16:1	0.6520293	0.9812208	0.6770883	0.5668264	0.4798904	0.6651573	0.319391	0.281795	0.401029	1.016470
TG 54:5-FA18:0	1.1206539	1.160306	1.5992636	1.0012825	0.8573877	1.0500579	1.081961	1.055829	1.323657	0.856428
TG 54:5-FA18:1	49.132863	73.376607	60.634013	109.03741	43.513611	55.024643	28.95437	24.46984	32.51414	81.86564
TG 54:5-FA18:2	77.775072	101.36628	94.857614	178.18765	66.78242	81.167564	45.87436	37.97075	49.96139	123.0072
TG 54:5-FA18:3	4.7903383	9.4811678	5.8616903	6.8152574	4.2275198	6.2045859	3.072396	2.780589	4.001846	8.106771
TG 54:5-FA20:2	0.4932892	0.6330879	0.463059	0.5155041	0.3840774	0.5244033	0.293014	0.282756	0.312300	0.658346
TG 54:5-FA20:3	4.2450382	4.3658788	4.579077	3.1576291	2.7961194	4.4109897	2.508805	2.871105	2.735740	4.654342
TG 54:5-FA20:4	4.0348867	5.8203564	9.8803267	3.446961	3.3989538	5.3652634	2.478217	3.218961	3.380567	7.115248
TG 54:5-FA20:5	0.1753756	0.3326637	0.4234766	0.1558244	0.197898	0.1836064	0.322893	0.260700	0.314517	0.155377
TG 54:5-FA22:1	0.3550676	0.4624936	0.3995844	0.7186361	0.2712683	0.3484835	0.212632	0.181263	0.229057	0.569816

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

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

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

TG 56:3-FA18:1	6.3389076	7.7025637	8.1873739	10.19397	5.7809596	3.2058063	2.556332	1.762607	4.522042	6.596568
TG 56:3-FA18:2	2.8977192	1.7819532	4.4499044	3.6983712	2.4375531	1.3397813	1.884386	1.367933	2.810087	1.617700
TG 56:3-FA20:0	6.9828324	3.7430023	7.032396	15.053239	5.1763197	4.1551708	3.585296	2.982341	3.572077	6.370544
TG 56:3-FA20:1	4.2666704	5.594468	5.6705014	5.1765392	4.0611273	2.4562741	2.033105	1.393576	3.201593	3.760707
TG 56:3-FA20:2	0.189712	0.2476521	0.2879046	0.1539378	0.1763879	0.1449998	0.104086	0.101213	0.175407	0.198652
TG 56:4-FA16:0	0.4597227	0.3026011	0.9480736	0.43515	0.3280954	0.2688797	0.211931	0.252737	0.327596	0.346038
TG 56:4-FA18:0	0.4822086	0.5732347	0.632315	0.5177534	0.4376078	0.3916621	0.442904	0.442365	0.475664	0.575331
TG 56:4-FA18:1	9.9798616	11.023924	12.356659	13.926203	8.2441948	5.1741089	3.984571	2.724446	5.809342	8.323954
TG 56:4-FA18:2	9.3698736	6.5342645	12.401547	15.010556	6.8044602	4.3490774	4.456414	3.121339	6.109029	6.504260
TG 56:4-FA20:1	9.2085936	7.7089376	12.146546	12.200068	7.022541	4.5844626	3.784428	2.667994	5.365482	6.460827
TG 56:4-FA20:2	0.6399904	2.6814872	0.8346819	0.5373963	0.5998813	0.692102	0.349946	0.287432	0.499208	1.301304
TG 56:4-FA20:3	0.3566796	0.4674991	0.3869436	0.2993454	0.3163095	0.3194446	0.260072	0.221264	0.221673	0.453794
TG 56:4-FA20:4	0.1306434	0.2156942	0.2684216	0.0713189	0.1109671	0.1413474	0.198906	0.186358	0.109676	0.123315
TG 56:4-FA22:4	0.042223	0.023489	0.0535058	0.0735336	0.0666587	0.0383517	0.055235	0.047311	0.074958	0.030345
TG 56:5-FA16:0	0.6862304	0.6504839	1.5056035	0.566482	0.4183962	0.5502818	0.462404	0.403659	0.526062	0.890051
TG 56:5-FA18:0	0.7925047	0.9227338	0.8766011	0.7003672	0.5950562	0.9214197	0.716528	0.620823	0.755698	1.014976

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

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

TG 56:8-FA16:0	12.609236	11.993414	7.8116981	9.7363588	6.5313522	13.836611	16.90779	17.81581	18.52662	15.23531
TG 56:8-FA16:1	0.7824397	2.1787695	0.7378088	0.6298401	0.5348103	1.2545158	0.565041	0.748705	1.153700	1.998766
TG 56:8-FA18:1	1.8627595	3.6926794	1.7367745	1.4901331	1.4550792	2.7252813	1.970002	1.637404	2.374875	2.877253
TG 56:8-FA18:2	10.629407	11.071816	7.3308471	8.4981206	5.622619	12.117656	14.06281	14.43633	14.49133	13.21168
TG 56:8-FA18:3	0.6229203	0.4971111	0.4707572	0.4801542	0.3862951	0.5993351	0.594416	0.572925	0.642639	0.560614
TG 56:8-FA20:4	2.1759817	2.1589263	2.7164772	2.6648445	1.5492202	2.6190226	2.176561	2.05117	1.766200	3.348651
TG 56:8-FA20:5	4.6735972	7.7382871	3.491882	3.8154731	2.8156342	6.4865852	5.071843	4.565968	5.325413	5.953318
TG 56:8-FA22:5	1.7551594	1.4907639	1.2270485	1.2694301	0.9494264	1.7240079	1.662211	1.809387	1.937610	1.997642
TG 56:8-FA22:6	63.853732	65.395593	39.277455	49.162551	32.61186	72.203484	86.24589	92.82115	92.96291	81.34338
TG 56:9-FA18:3	0.5305573	0.5219917	0.4082774	0.3584168	0.3301804	0.75433	0.749167	0.610723	0.780760	0.496023
TG 56:9-FA20:4	0.5032954	0.4609231	0.5746126	0.4494741	0.3226074	0.601354	0.548390	0.489803	0.567315	0.457327
TG 56:9-FA20:5	4.1437991	3.4082135	2.7151285	3.5725437	2.2052415	4.5787302	5.534850	4.278124	4.817500	3.180181
TG 56:9-FA22:6	6.5491319	8.3111554	3.7400223	4.7039784	3.7364909	8.4070867	6.334961	7.096022	8.798070	10.23532
TG 57:10-FA22:6	0.5110137	0.5777839	0.4875674	0.5406665	0.327727	0.5320371	0.439350	0.459654	0.433532	0.562010
TG 57:2-FA18:1	2.9251516	8.2252034	2.0409277	2.4302746	2.0894928	4.2865151	2.925546	2.972343	3.395299	5.659001

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

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

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

Figure 1

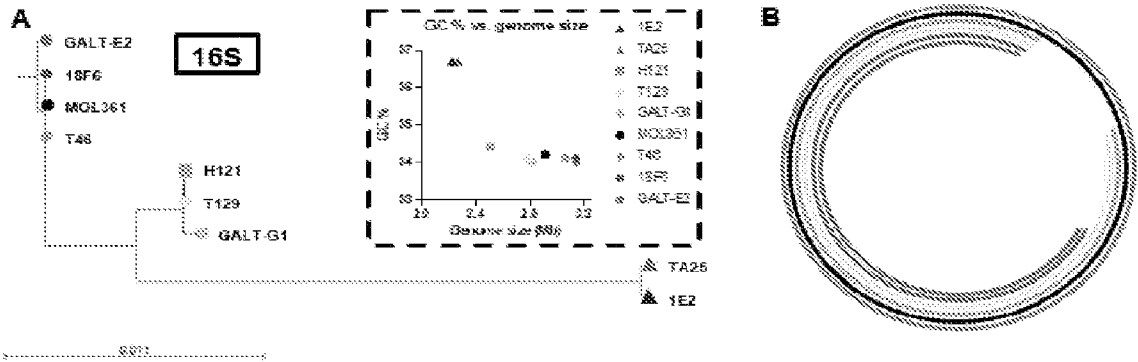


Figure 2

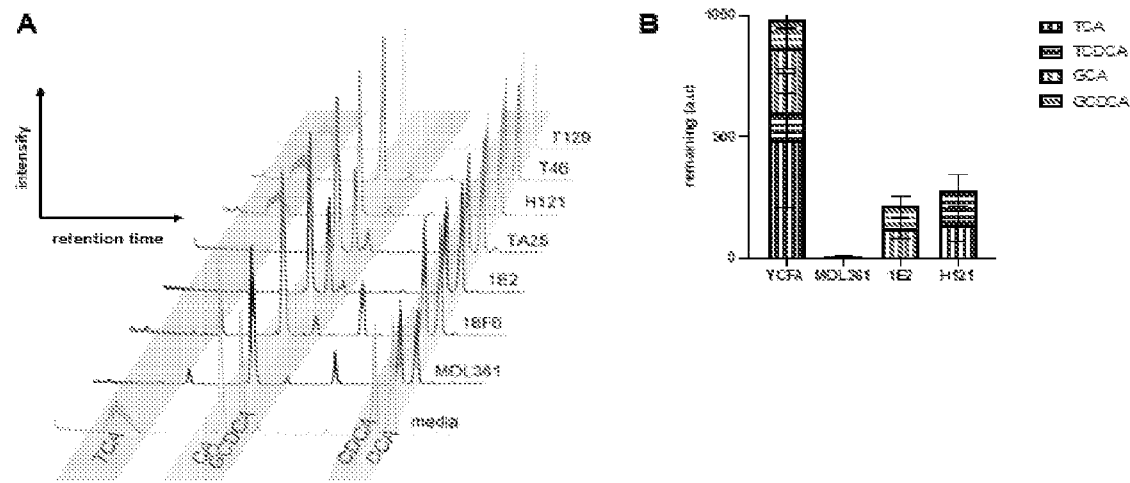


Figure 3

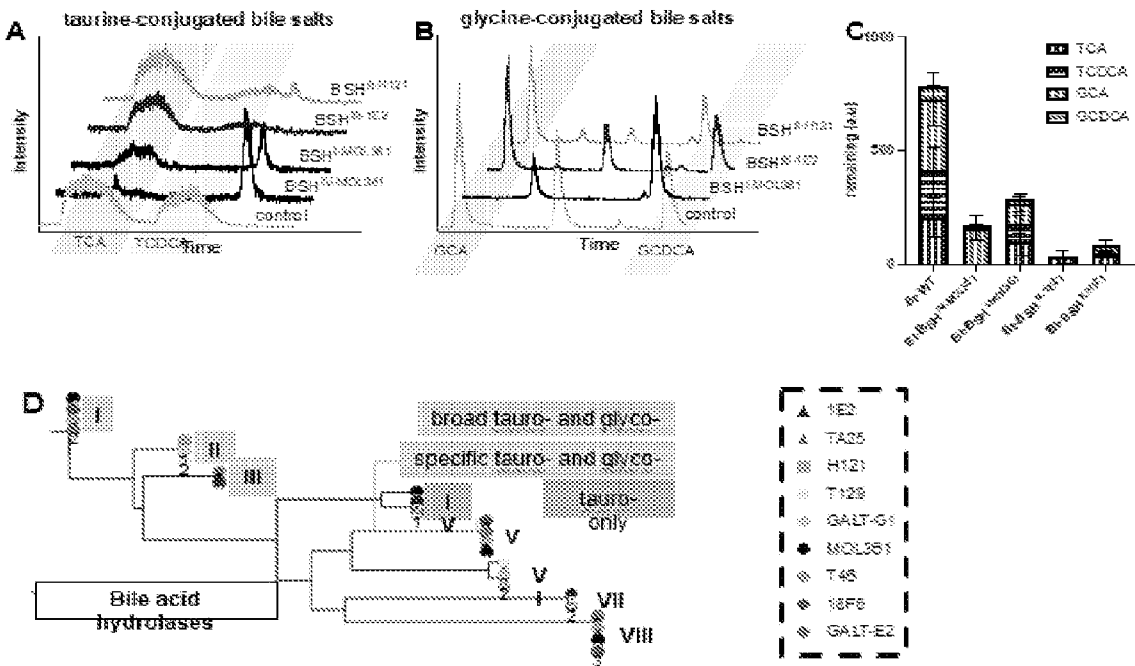


Figure 4

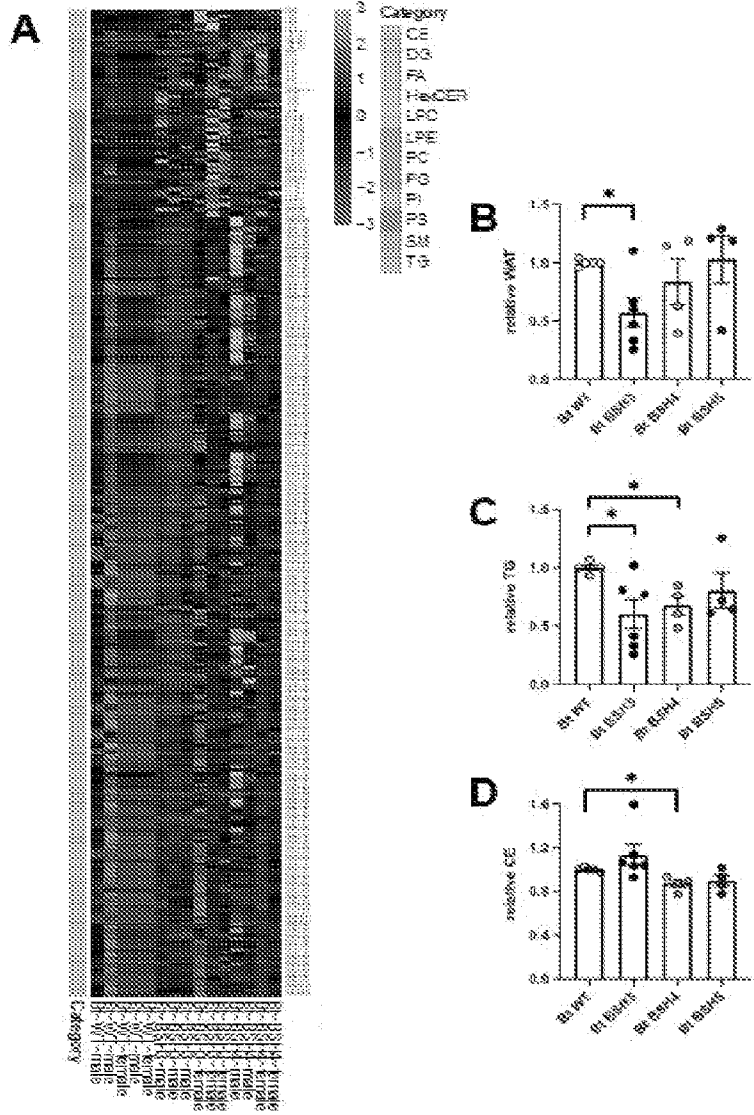


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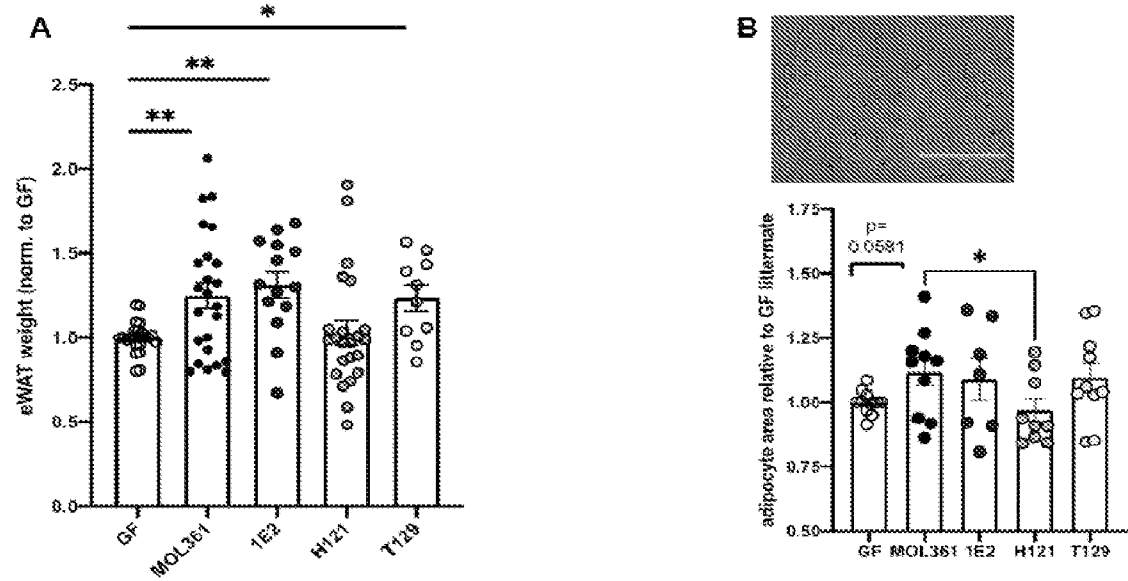


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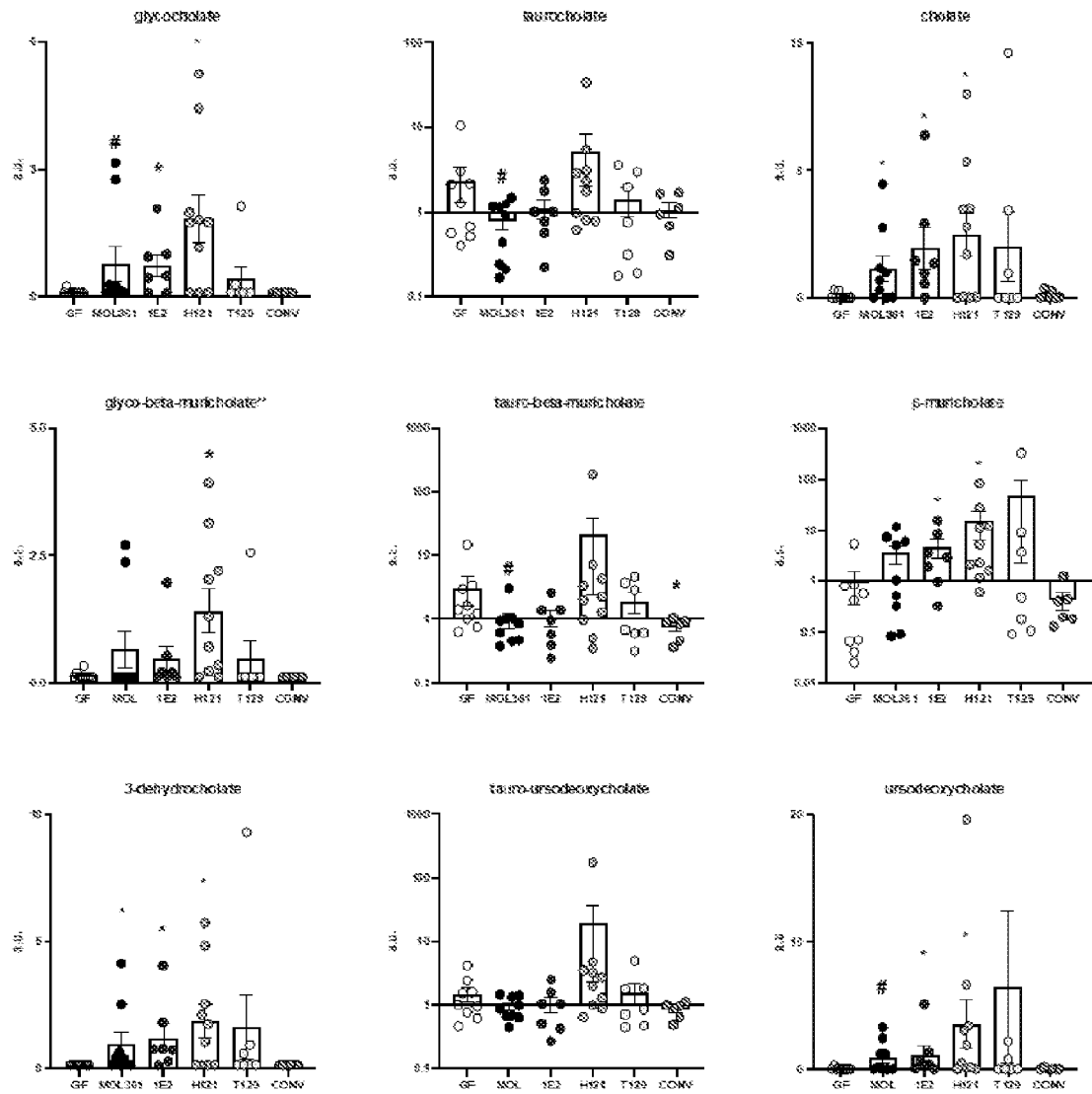


Figure 6 (cont.)

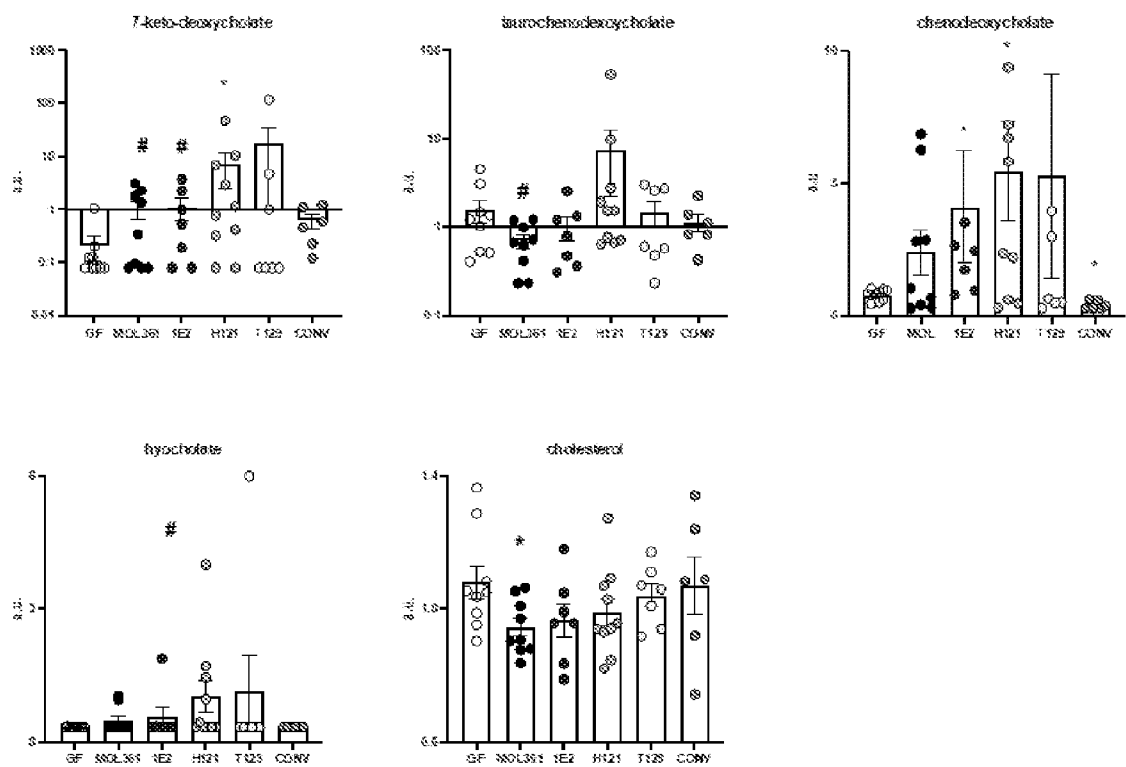


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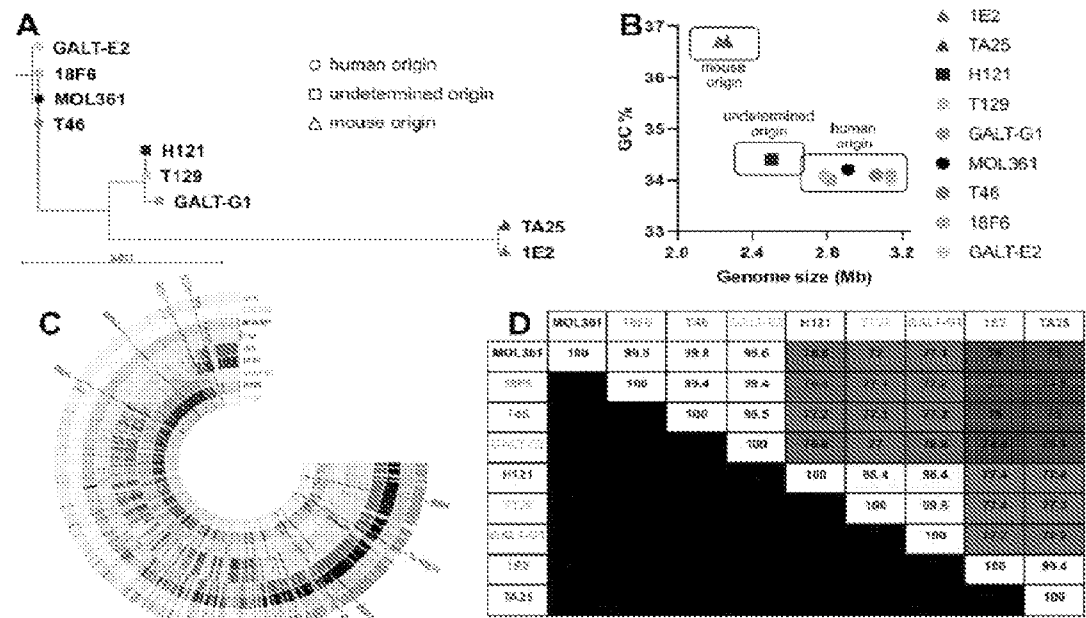


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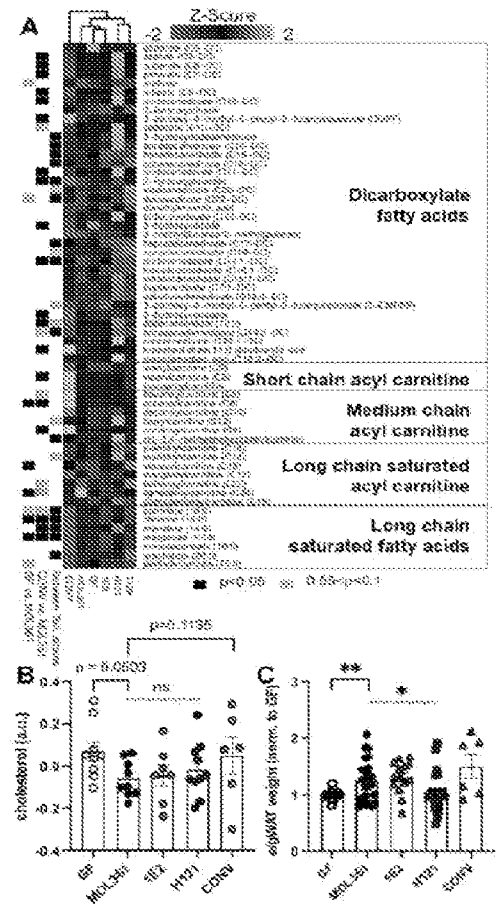


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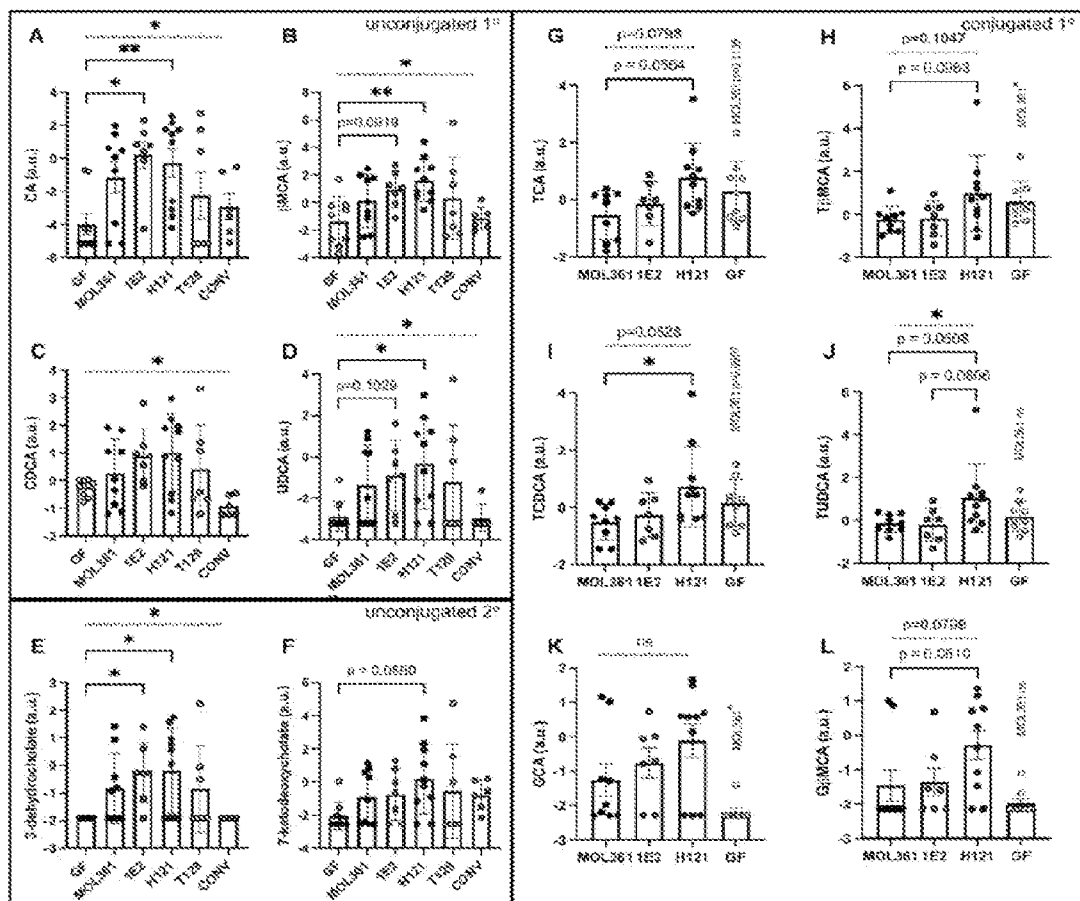


Figure 10

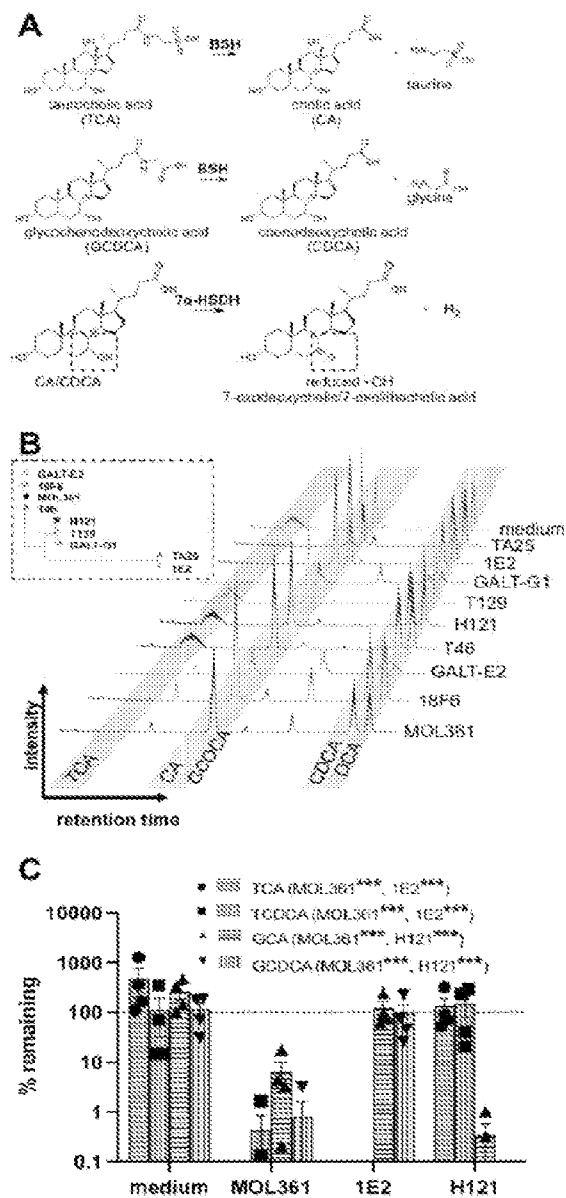


Figure 11

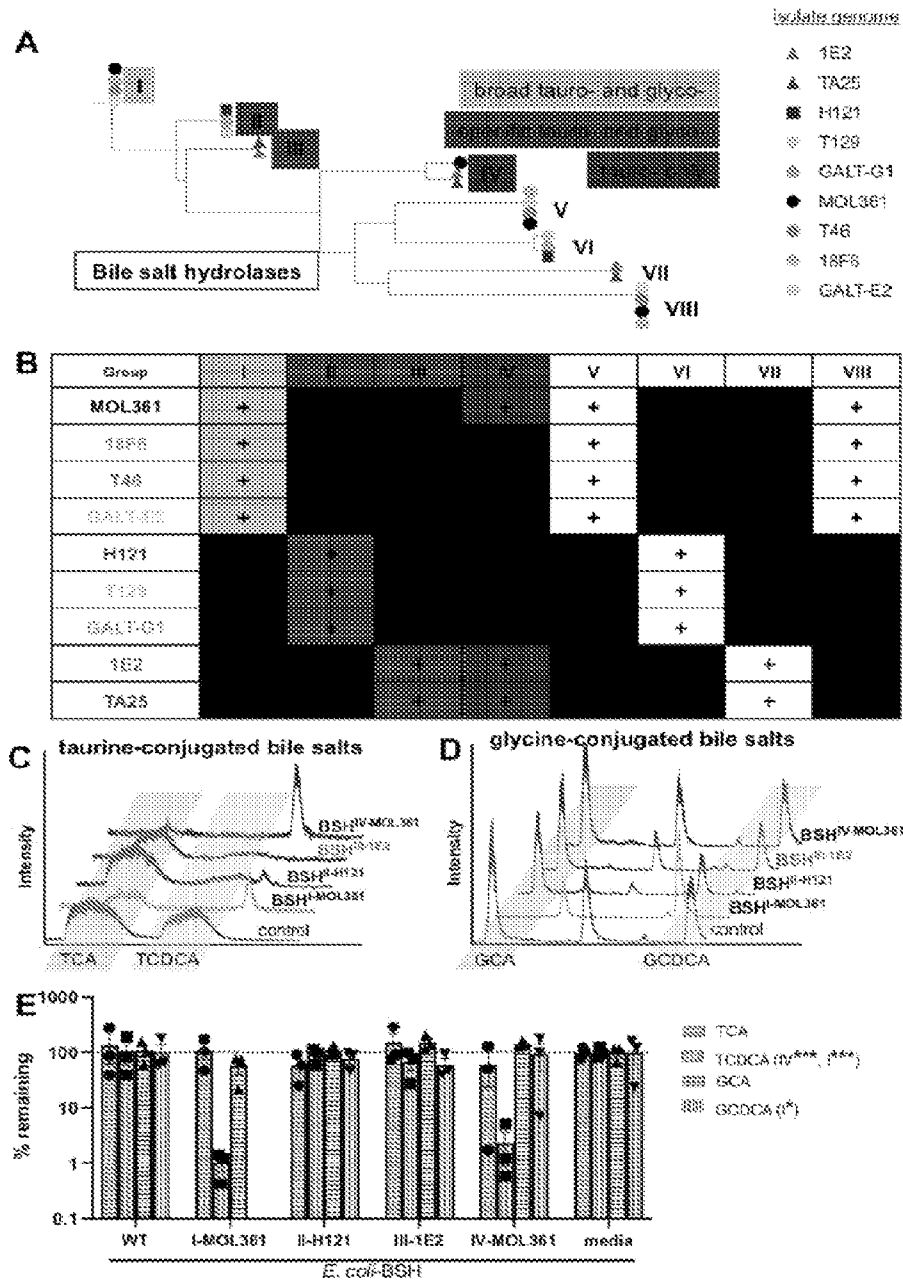


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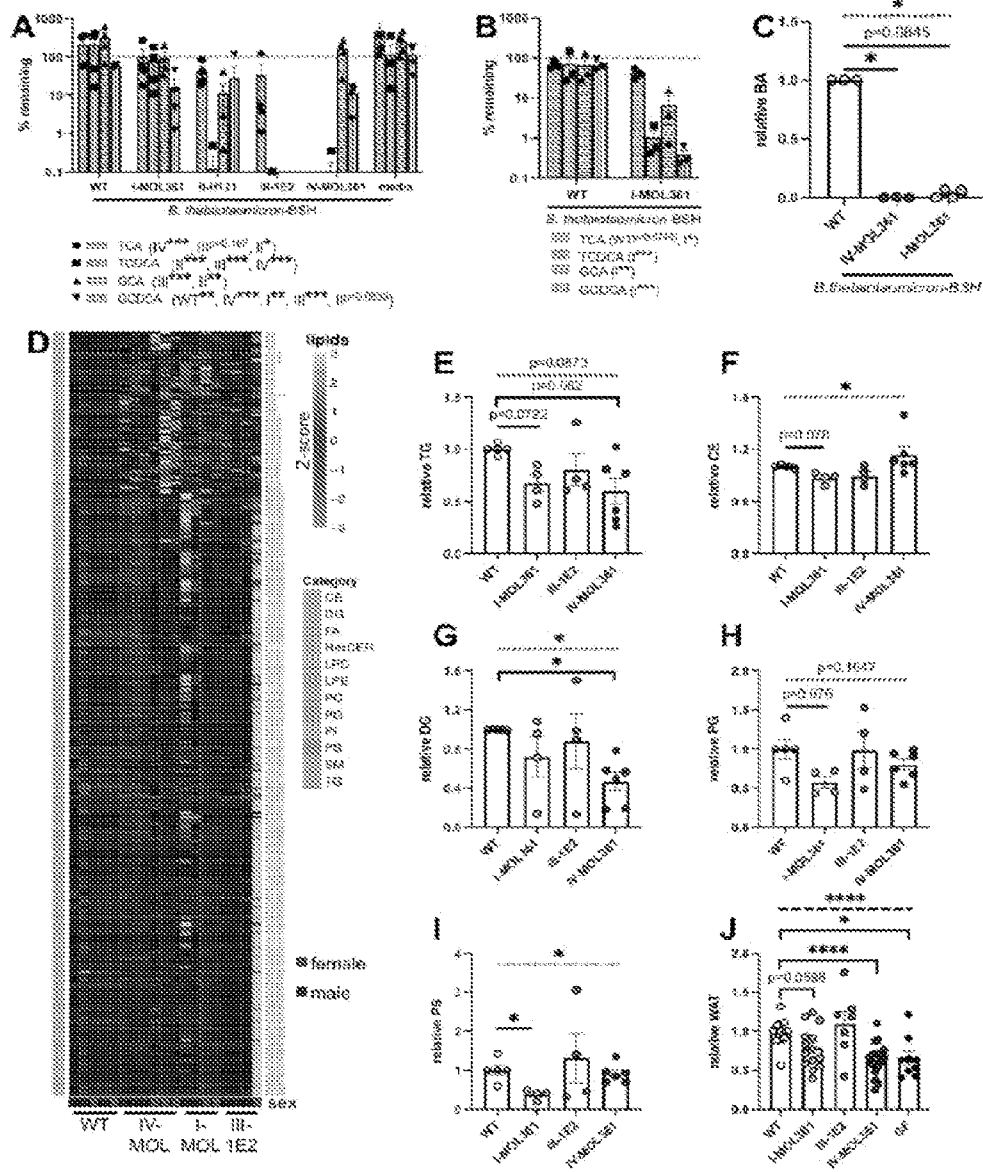


Figure 13

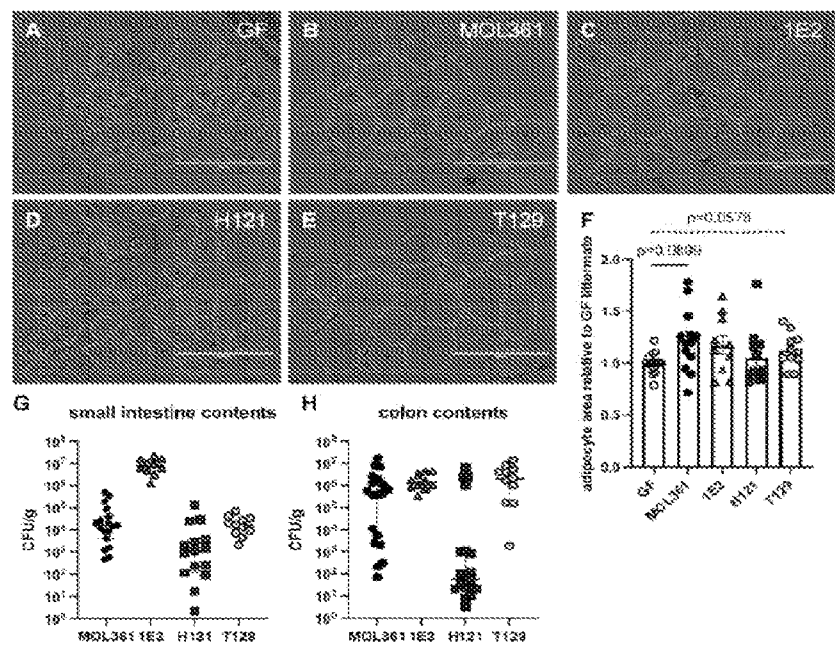


Figure 14

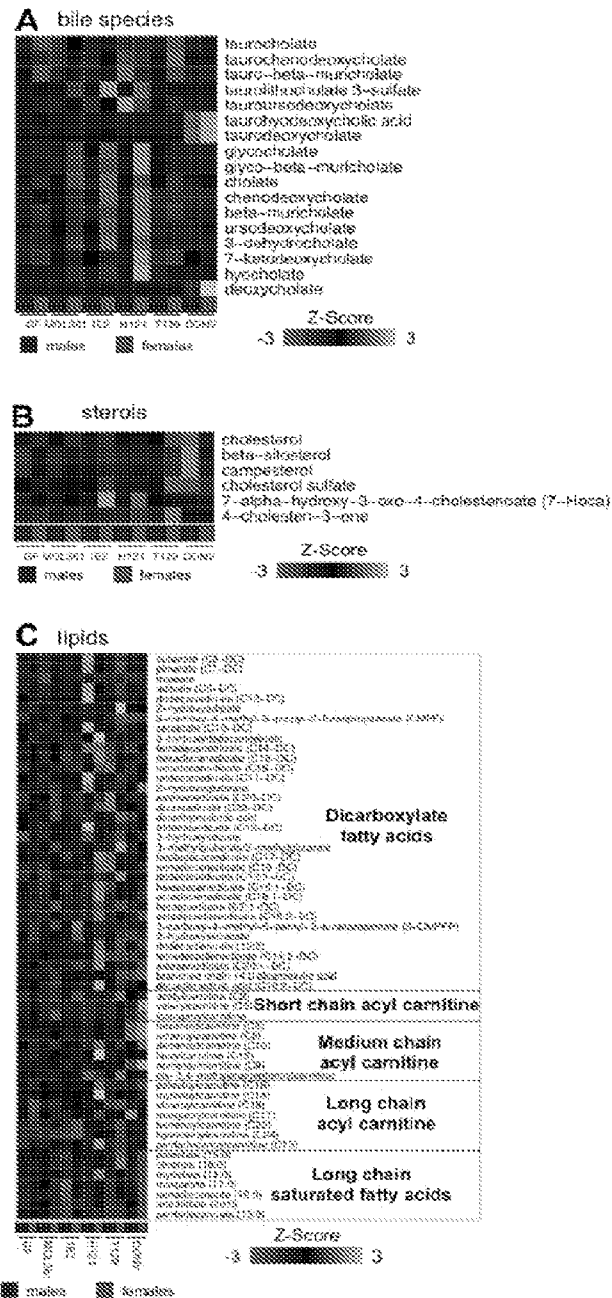


Figure 15

Turicibacter strain	Presence (+) or absence (-) of peak							Deconjugation ability
	TCA	Dehydrogenated CA	CA	GCDCA	Dehydrogenated CDCA	CDCA	DCA	
MOL361	-	+	+	-	+	+	+	Tauro- and glyco-deconjugation; dehydrogenation
18F6	-	+	+	-	+	+	+	
GALT-E2	-	+	+	-	+	+	+	
T46	+	-	+	-	-	+	+	Glyco-deconjugation
H121	+	-	+	-	-	+	+	
T129	+	-	+	-	-	+	+	
GALT-G1	-	-	+	-	+	+	+	Tauro- and glyco-deconjugation; some dehydrogenation
1E2	-	-	+	+	-	+	+	Tauro- deconjugation
TA25	-	-	+	+	-	+	+	

Red = outliers from genomic group

Figure 16

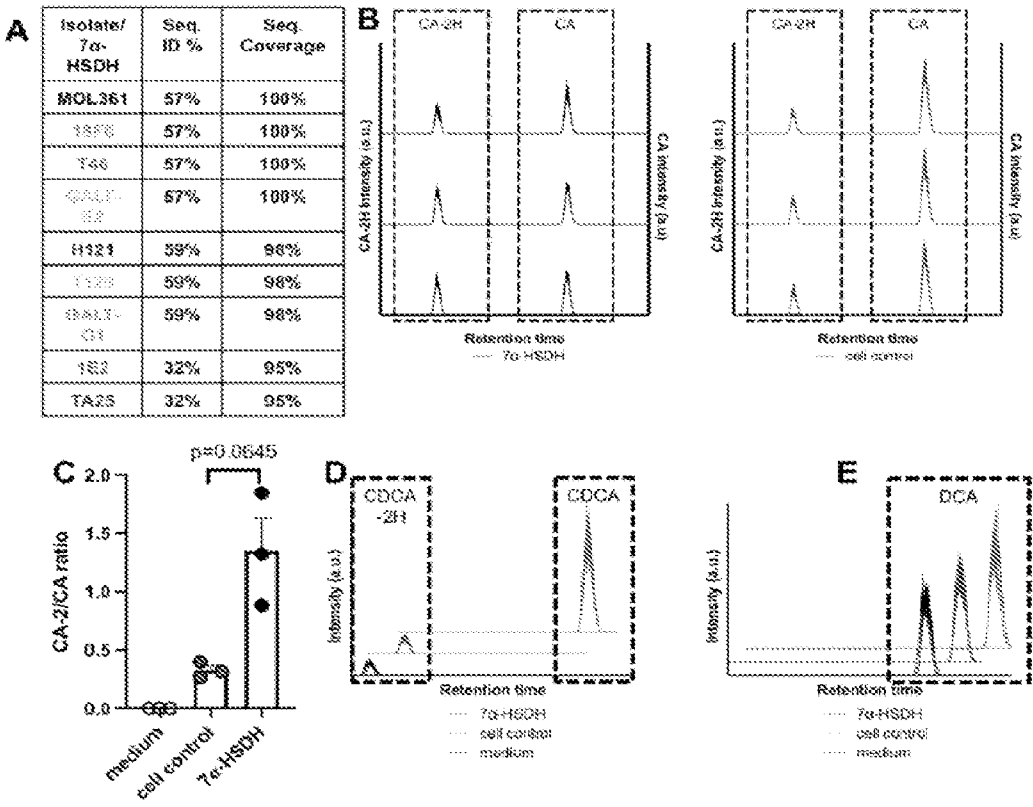


Figure 17

Bile salt hydrolase (<i>hsh</i>) gene	Presence (+) or absence (-) of peak				Deconjugation ability
	TCA	TCDCa	GCA	GCDCA	
I-MOL361	-	-	-	-	Tauro- and glyco- deconjugation
II-H121	+	-	+	-	-CDCA deconjugation
III-1E2	+	-	+	+	TCDCa deconjugation
IV-MOL361	-	-	+	+	Tauro- deconjugation

Figure 18

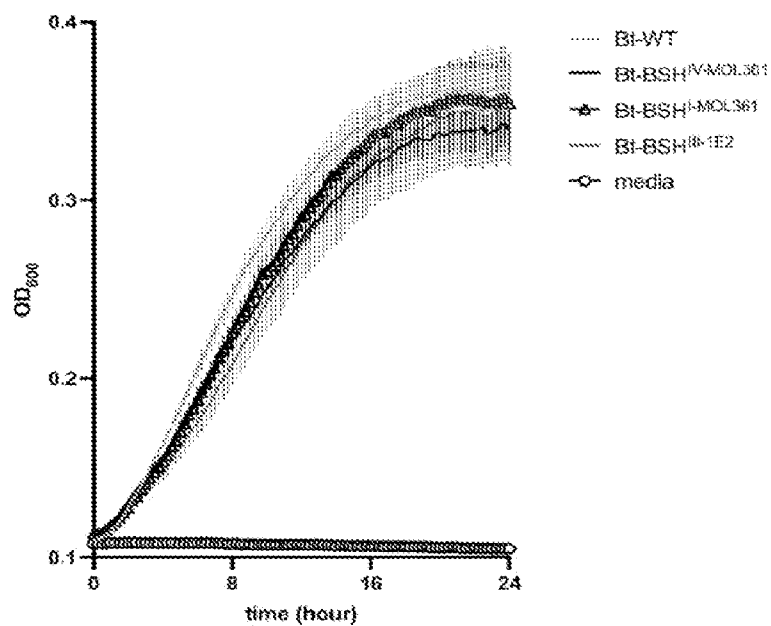


Figure 19

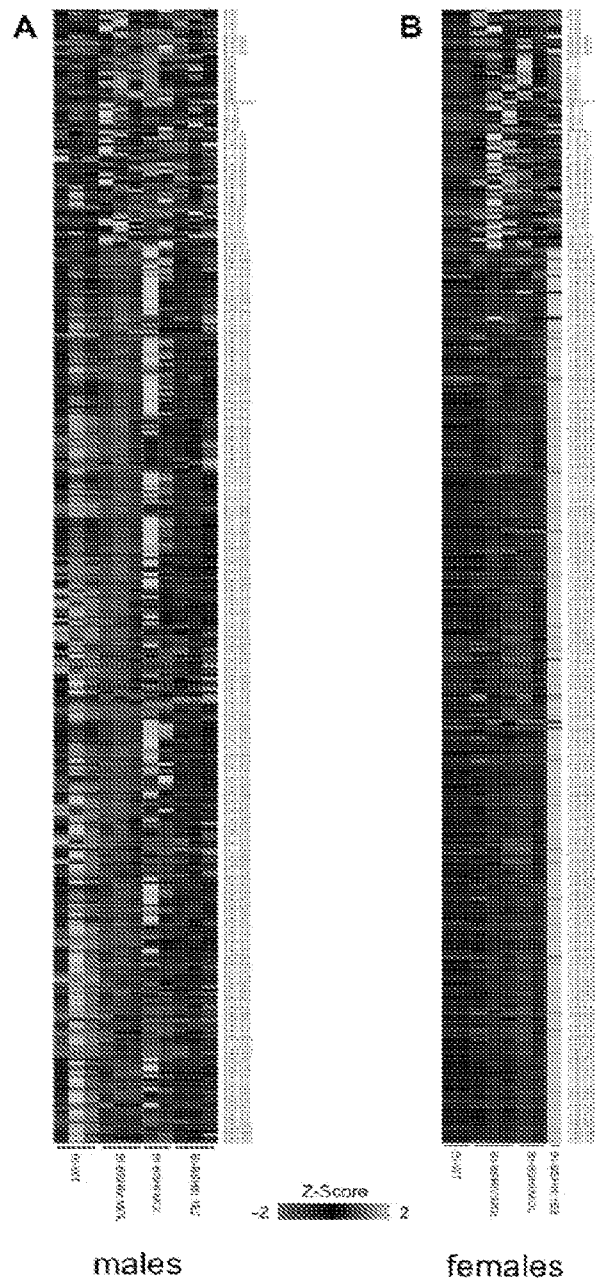


Figure 20

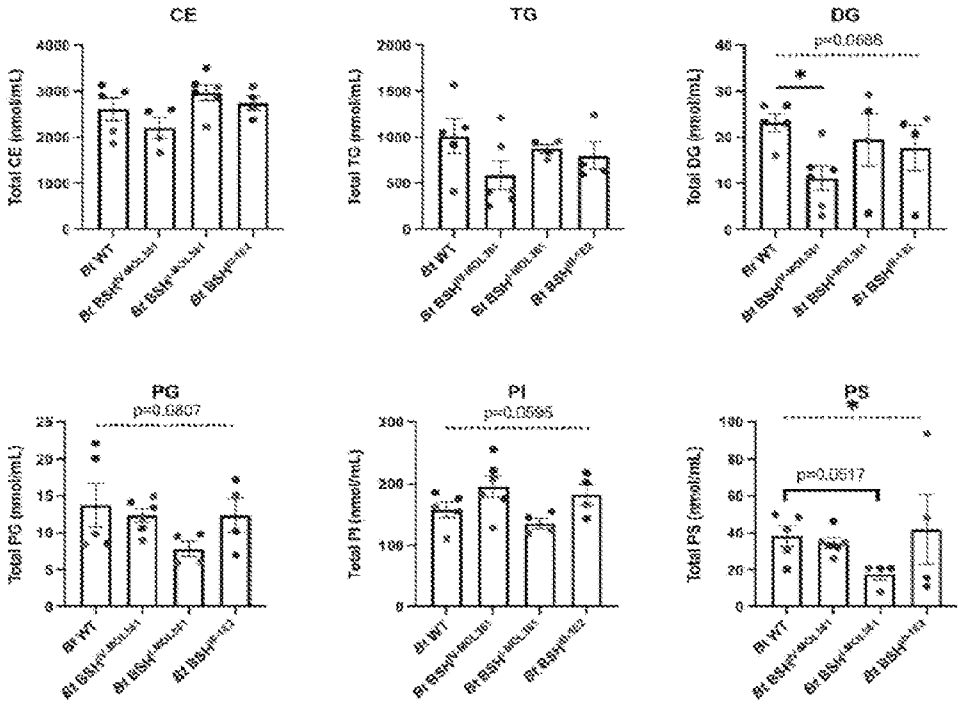


Figure 21

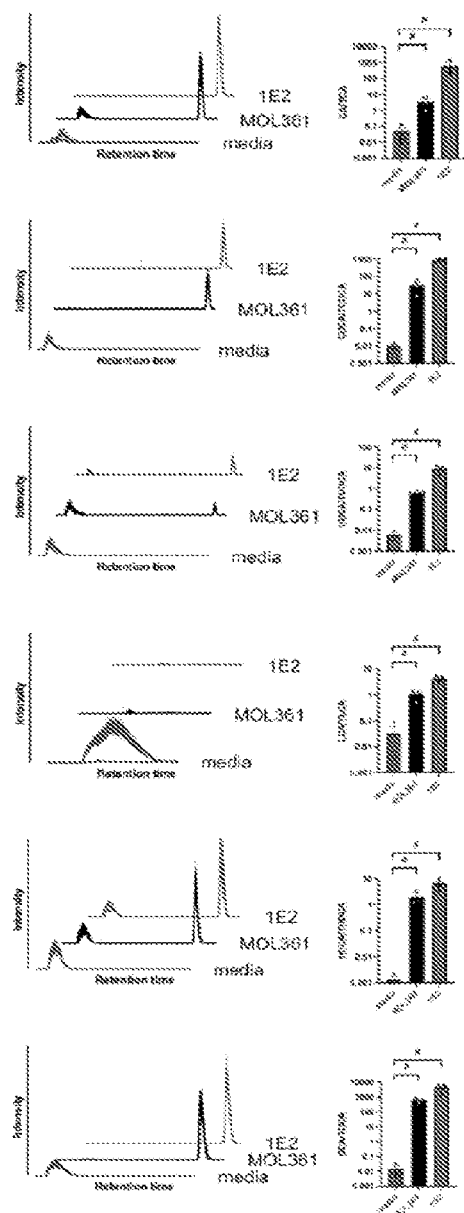
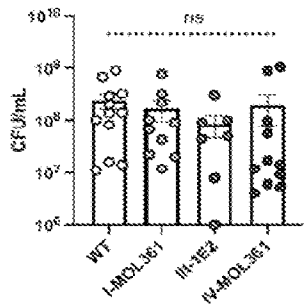
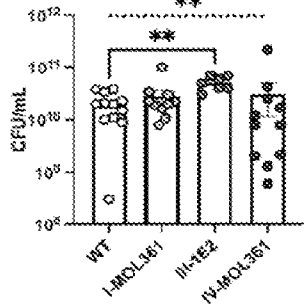


Figure 22

A small intestinal bacterial loads



B caecal bacterial loads



C colon bacterial loads

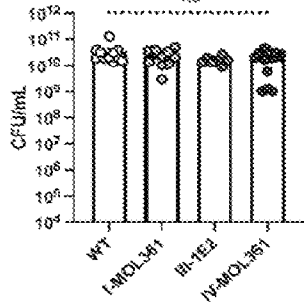


Figure 23

