Supplementary Methods

Animals:

All animal protocols were in accordance with APLAC, the Stanford IACUC. Germ-free (GF) C57BL/6J (Jackson Labs stock number 000664) mice were singly housed and maintained in gnotobiotic isolators on a strict 12h light cycle. Conventionally housed *Fut2-/-* mice (B6.129X1-Fut2tm1Sdo/J; backcrossed 12 generations with C57BL/6J) were delivered by Caesarean section and maintained in gnotobiotic isolators (1). Eight week old GF mice were humanized by oral gavage of 200µl of human fecal sample prepared by mixing stored frozen human fecal sample obtained from a healthy anonymous donor (male, age 38, American diet) with filter-sterilized pre-reduced phosphate buffered saline. Mice were fed autoclaved polysaccharide rich standard (SD) diet (Purina LabDiet 5K67) or an irradiated custom diet containing 68% glucose w/v, 18% protein w/v and 7% fat w/v (Bio-Serv, http://bio-serv.com). Fresh fecal samples were collected while mice were on the polysaccharide-rich SD diet or the glucose-rich PD diet and stored at -80^{o}C till further processing. For quantitative RT-PCR, cecal contents were collected from humanized mice on PD diet at the time of sacrifice and stored at -80^{o}C.

For mono-colonization, seven week old GF Fut2+ and Fut2- mice were each inoculated with 10^{8} CFU of *Bacteroides thetaiotaomicron* strain VPI-5482 (ATCC 29148) from an overnight culture grown in tryptone-yeast extract-glucose (TYG) medium. Animals were kept on either the polysaccharide-rich SD diet (Fut2+ n=5, Fut2-, n=4) or the PD diet (Fut2+ n=4, Fut2-, n=4). Animals were sacrificed 10 days later and cecal contents including mucus were placed in a tube with 2-3 volumes of RNA Protect (Qiagen, www.qiagen.com). The solution was mixed by vortexing and then centrifuged (3,000 x g for 20 min at 23^{o}C). The resulting pellet was resuspended in 1 mL of TE buffer (10 mM Tris, 1mM EDTA, pH 8.0) containing 1 mg/mL of lysozyme (specific activity 50,000U/mg; Sigma, www.sigma-aldrich.com) and total RNA was isolated (RNeasy Midi kit from Qiagen; yield=50-200 g/cecum). Genomic DNA was removed by treatment with DNAfree (Ambion; www.ambion.com).

GeneChip analyses

Custom Affymetrix *B. thetaiotaomicron* GeneChips have been described in earlier publications (2) and were based on the finished genome of *B. thetaiotaomicron* VPI-5482 (3). Results were visualized using DNA- Chip analyzer v1.3 (dChip; www.biostat.harvard.edu/complab/dchip/). Comparisons were performed on specified GeneChip datasets to identify differentially expressed using the following criteria: ‘upregulated’ defined as fold change>1.2 and a false discovery rate (FDR) of 7.5%. Among the upregulated genes, only genes with a q value less than 5% were considered significant. We also included in the up-regulated gene list those genes that were a part of a PUL (defined as containing at least one SusC/D homolog) with at least two members of the locus with q value less than 5%. Additional members of such PUL were included as being significant with q value less than 7%. All GeneChip data have been deposited in the Gene Expression Omnibus (GEO) database (www.ncbi.nlm.nih.gov/projects/geo).

To profile the *B. thetaiotaomicron* transcriptome *in vivo*, cDNA targets were prepared from 5-10 g aliquots of each RNA sample using protocols described in the *E. coli* Antisense Genome Array manual (Affymetrix). RNA was reverse-transcribed using Superscript-II RT (Invitrogen). The RNA template was destroyed by incubation with 0.25 N NaOH for 30 min at 65°C. The cDNA product was isolated (QiaQuick Spin columns; Qiagen), fragmented (DNase-I; www1.amershambiosciences.com), and biotinylated (Enzo-BioArray Terminal Labeling Kit). Standard Affymetrix protocols were used for hybridization of the cDNA targets to each *B. thetaiotaomicron* GeneChip. GeneChip data of the bacterial response to the studied diets and host genotypes were normalized using R program by RMA-MS (4), and the statistical significance of observed differences in *B. thetaiotaomicron* gene expression was determined using SAM (5).

Culture conditions for *Bacteroides thetaiotaomicron*: An inoculum from overnight growth of *B. thetaiotaomicron* VPI5482 in TYG medium was added to minimal medium (MM) with specific carbon source. MM contained 100mM KH_2PO_4 (pH 7.2), 15mM NaCl, 8.5mM $(NH_4)_2SO_4$, 4mM L- cysteine, 1.9μM hematin/200μM L-histidine (prepared together as a 1,000x solution), 100μM $MgCl_2$, 1.4μM $FeSO_4 \cdot 7H_2O$, 50μM $CaCl_2$, 1μg/mL vitamin K_3, and 5ng/mL vitamin B_{12}. All carbon sources were added to MM [final concentration 0.5% (w/v)]. Media were filter sterilized using a Millipore Express filter unit (0.22μm pore diameter). 2' fucosyl-lactose, 3'fucosyl- lactose, lacto-difucose were purchased from GlycoTech; lacto-N-tetraose, lacto-fucopentaose, lacto-N-difucohexaose were purchased from Accurate Chemical & Scientific Corp. Other monosaccharides and disaccharides were purchased from Sigma.

Genotyping: Mouse genomic DNA was prepared from ear tissue obtained by ear punch. PCR amplification using three primers F: 5'CCTGCCATGCTTTCTTTCCTG3' R: 5'ATTCCTTCTCTGACAGGGTTTGG3' (WT), 5'TGGGTAACGCCAGGGTTTTC3' yielded either a 191bp band (KO) or 154 bp band (WT) or both (HT).

Quantitative RT-PCR analysis Quantitative RT-PCR was performed using gene-specific primers with SYBR Green (ABgene) in a MX3000P thermocycler (Stratagene). For *in vitro* studies using *B. thetaiotaomicron* in minimal medium supplemented with glucose or pure glycan, experiments were performed in triplicate and the results reported are mean values ± SEM. Primer pairs used were (i) BT1273F 5'TGCGGAGACAATGGATATGA3', BT1273R 5'ACATCGCGTCCGTAAATACC 3' and (ii) BT4247F 5'CGGTACCCAAAAGAAGGTCA3' and BT4247R 5'AAGTACCGATACCGCGAATG3'. For analysis in humanized mice fed a PD diet, cecal contents were collected from 5 Fut2- mice and 4 Fut2+ mice and processed to prepare cDNA. Primer pairs used were (i) BT4244F 5'TATTCGGCAGTCGGAGATGT3' BT4244R 5' GAATCTCGAAAGTCGTGAAGG3' and (ii) BT4263F 5' GCTGGTATCGCTTTGACTGA3' BT4263R 5' GCGTTAACTGATGCCATGTG3'.

16S rRNA pyrosequencing and data analysis: After isolation of fecal DNA (MoBio fecal DNA kit), 626 bp amplicons (including a unique 12bp Golay barcode) spanning variable regions 3-5 (V3-V5) were generated from bacterial 16SrRNA genes using barcoded forward primer (338F, 906R). Samples were subjected to multiplex pyrosequencing with a Roche 454 instrument and Titanium chemistry. Post processing of pyrosequencing data was done using QIIME1.4.0.(6). As a first step, sequence data and metadata were combined to de-multiplex the barcoded reads and quality filtering was done using the default parameters in QIIME. Sequences were grouped into OTUs (Operational Taxonomic Units) at 97% sequence similarity using uclust. Taxonomy was assigned using RDP classifier against GreenGenes database, sequences were aligned and phylogenetic tree was built from reference sequences using FastTree. An OTU table showing counts of each OTU in each sample was produced. To control for the sequencing effort, OTU table was rarified at a single sequencing depth of 2000 sequences/fecal sample for samples obtained from time points D28 and D56. KEGG-level imputed metagenomic analysis was performed using PiCRUST (http://picrust.github.com). CAZY GH assignments(7) were made using an HMM (hidden Markov model) database(8) and a local database of 2770 fully sequenced genomes. Samples from the 4 weekly time points D29-D56 were run on a different 454 run and the OTU table generated was rarified at a sequencing depth of 500 sequences/sample.(9, 10)

Alpha diversity was determined using Shannon and Chao1 index and is represented as rarefaction curves. Beta diversity was determined using unweighted UniFrac (11) and the results presented as principal coordinate axis (PCoA) plots. The OTU's were summarized at different taxonomic levels from phylum to genus and differences in the relative abundance at different taxonomic levels were determined using ANOVA with a false discovery rate of 5%.

Non-targeted UPLC-MS metabolic profiling of urine and feces: Fecal samples were extracted using OASIS solid phase extraction cartridges. Samples were mixed 1:1 with acetonitrile and 5 µL of sample was used. Chromatographic separation was performed in ACQUITY Ultra performance Liquid Chromatography system. Mass spectrometry was performed on Exactive (Thermo Fisher) operated in positive electrospray mode. The instrument was mass calibrated with a solution containing dodecyl sulfate (m/z 265), sodium taurocholate (m/z 514) and Ultramark 1621 (m/z 1280, 1380, 1480, 1580, 1680, 1780). Data was collected in continuous mode. The web-based program MetaboAnalyst was used for statistical analysis (www.metaboanalyst.ca).

Sparse canonical correlation analysis: The following transformations were made in order to make the analysis more robust: Only OTU's that were present at the level of at least 2 reads in more than three samples were retained. A robust thresholding method was used setting to 50 all read numbers larger than 50. Similarly for metabolites, if a feature had a value of 0 in more than 4 samples it was excluded from the analysis. For those with less than 4 zeros, these 0 were retained, but all other values were given a log transformation. A standard log (X+1) transformation was done to account for values which may be zero. The transformed data were then subjected to a sparse canonical correlation analysis with a penalty of 0.15, providing a set of non-zero coefficients.

Accession Numbers: GeneChip datasets have been deposited in the Gene Expression Omnibus (GEO; http://www.ncbi.nlm.nih.gov/geo/) under accession numbers GSE45641. The 16S sequence data has been deposited in the European Molecular Biology Laboratory (EMBL)

Nucleotide Archive with accession number ERP003630, and can also be found in the QIIME Database under the study ID 1452. (http://www.microbio.me/qiime/).

Supplemental Figures

Fig. S1. Comparison of microbial communities from humanized WT (Fut2+/+) and HT (Fut2+/-) mice. (A). Intra-individual and inter-individual differences between gut microbial communities from humanized WT and HT mice on D28. Difference in alpha diversity using the Shannon index (B) and beta diversity using unweighted UniFrac distance metric (C) between WT and HT mice.

Fig. S2. Effect of gut mucus fucosylation on alpha diversity of a human microbiota transplanted into gnotobiotic mice fed a plant polysaccharide-rich standard diet. Rarefaction curves using Chao1 measure of alpha diversity in fecal samples obtained from humanized Fut2+ (n=18) and Fut2- (n=10) animals.

Fig. S3. Effect of diet on the metabolic profiles present in urine and feces recovered from Fut2+ and Fut2- mice. Volcano plot showing metabolites that are significantly higher (>2 fold change and $p<0.05$) in the urine (A, B) or feces (C, D) of humanized Fut2+ and Fut2- mice fed a polysaccharide-rich SD diet (A, C) or the glucose-rich PD (B, D) diet.

Fig. S4. PCoA and Procrustes analysis of V3-5 16S rRNA and fecal metabolites. Two circles connected by a line represent the two different data types from the same fecal sample. The overall goodness of fit (M^2) for the different data types is 0.346 ($p<0.05$)

Fig. S5. Sparse canonical correlation analyses of fecal OTU's and metabolites. Biplot showing the output from a principal component analysis (PCA) performed on the reduced set of combined metabolomic features (green arrows and labels) and OTU's (purple arrows and labels corresponding to the family or genera of these OTU's) within fecal samples from humanized mice that were chosen by the sparse Canonical Correlation Analysis. The two linear combinations of variables had a correlation of 0.987. The PCA biplot of the first principal plane presents 96% of the variance of this reduced set of variables.

Fig. S6. Effect of diet and genotype on host mucin glycan GH representation in imputed community metagenome and microbial community composition. (A) Enrichment of 8 GH families associated with mucin glycan degradation were determined to illustrate effect of diet (left) and genotype (right). 5 GHs (FDR < 0.05) are significantly enriched in humanized Fut2+ mice on PD diet as compared to SD diet while no GH's are significantly different in humanized Fut2- mice on PD diet as compared to SD diet. 6 GHs (FDR < 0.05) are enriched in humanized Fut2- mice on SD diet as compared to Fut2+ mice while no GH's are significantly different in Fut2- mice on PD diet as compared to Fut2+mice. Ranges represent percent change in GH copy numbers between communities; solid boxes denote FDR < 0.05. (B) Pairwise comparisons (dotted line) of the mean percent of mucin-associated GH copy numbers in panel A are plotted as a function of diet and mean mucin-associated GH percent increase. Greek letters correspond to panel A to indicate comparisons. (C) Significant ($p<0.05$; ANOVA, FDR<5%) genus level differences in gut microbial communities of humanized Fut2+ mice on the plant polysaccharide-rich SD diet (D28; n=18) compared to the PD diet (D56; n=9). These genera were not significantly different in humanized Fut2- mice on SD diet compared with PD diet. Data are shown as averages ± SEM.*$P<0.05$

References

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Fig. S1

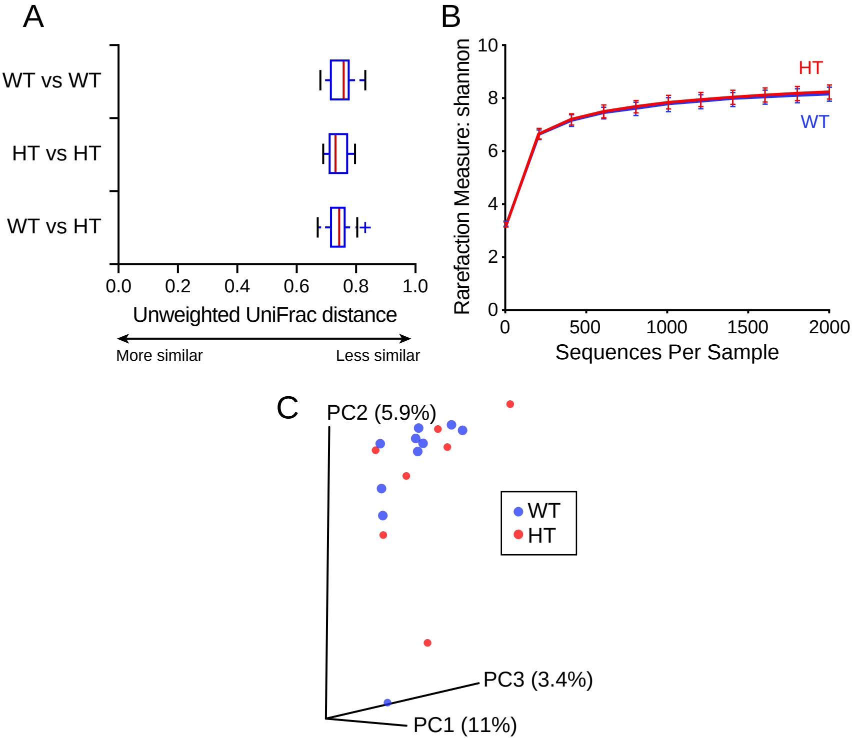
A
WT vs WT
HT vs HT
WT vs HT
0.0
0.2
0.4
0.6
0.8
1.0
Unweighted UniFrac distance
More similar
Less similar
B
Rarefaction Measure: shannon
10
8
6
4
2
0
0
500
1000
1500
2000
Sequences Per Sample
HT
WT
C
PC2 (5.9%)
PC3 (3.4%)
PC1 (11%)
● WT
● HT

Fig. S2

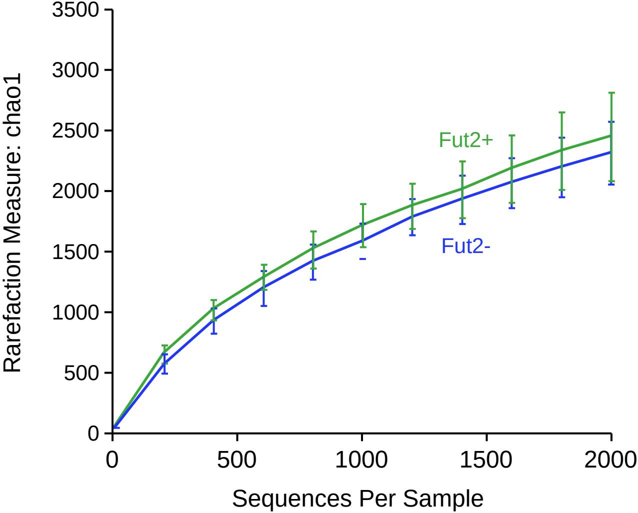
3500
3000
2500
2000
1500
1000
500
0
Rarefaction Measure: chao1
Fut2+
Fut2-
0
500
1000
1500
2000
Sequences Per Sample

Fig. S3

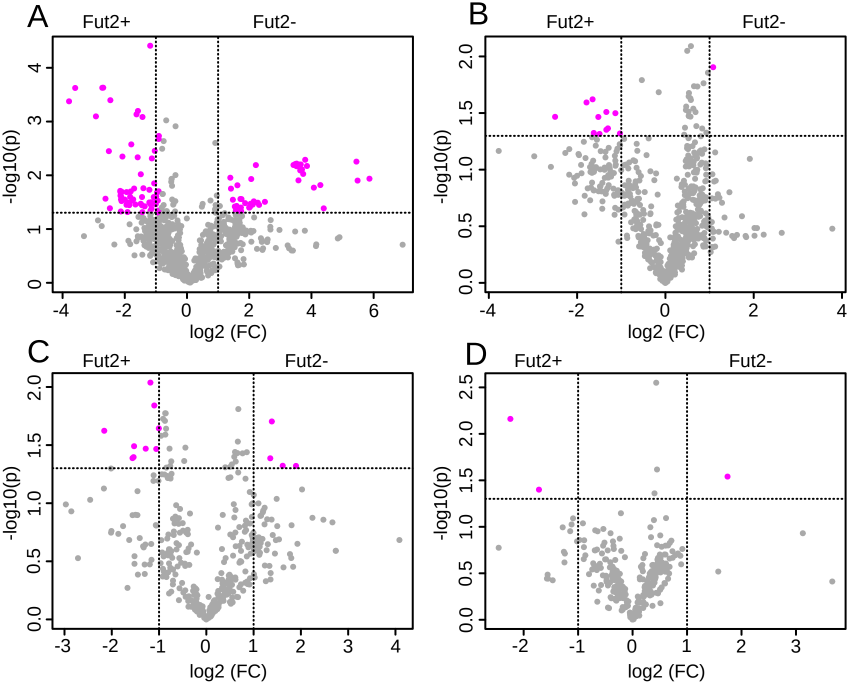
A
Fut2+
Fut2-
-log10(p)
0
1
2
3
4
-4
-2
0
2
4
6
log2 (FC)
B
Fut2+
Fut2-
-log10(p)
0.0
0.5
1.0
1.5
2.0
-4
-2
0
2
4
log2 (FC)
C
Fut2+
Fut2-
-log10(p)
0.0
0.5
1.0
1.5
2.0
-3
-2
-1
0
1
2
3
4
log2 (FC)
D
Fut2+
Fut2-
-log10(p)
0.0
0.5
1.0
1.5
2.0
2.5
-2
-1
0
1
2
3
log2 (FC)

Fig. S4

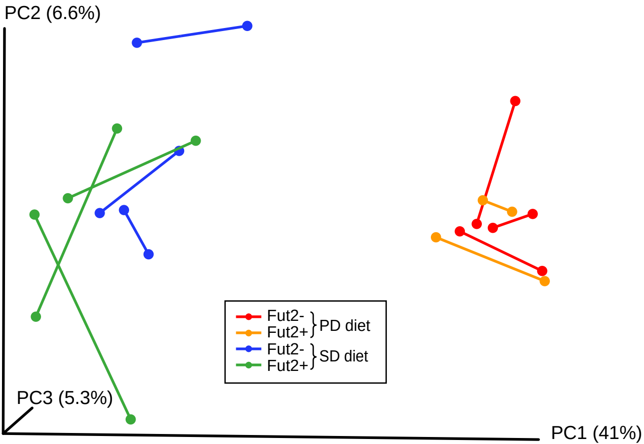

Fig. S5

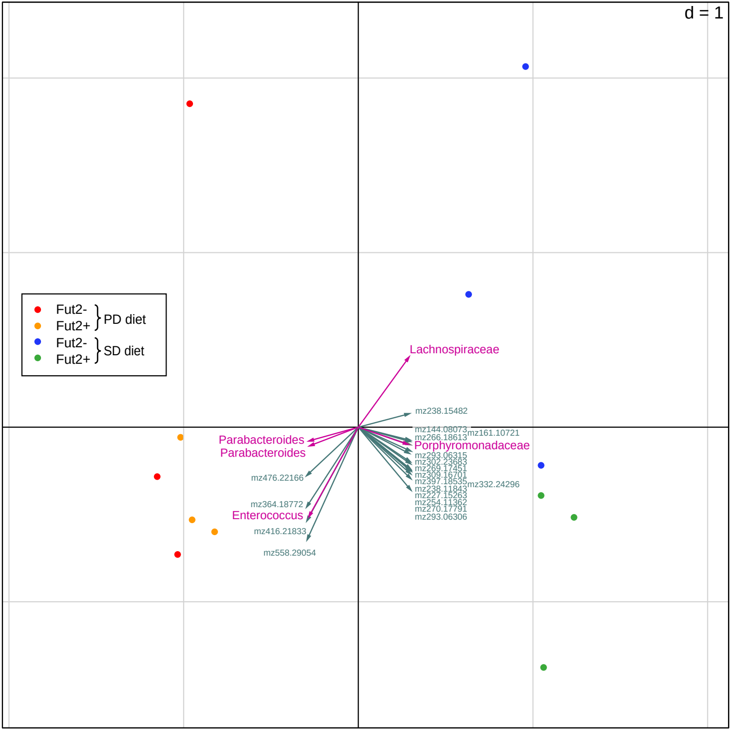
d = 1
● Fut2-
● Fut2+
PD diet
● Fut2-
● Fut2+
SD diet
Lachnospiraceae
mz238.15482
mz144.08073
mz161.10721
mz266.18613
Porphyromonadaceae
mz293.06315
mz302.23683
mz269.17451
mz309.16701
mz397.18535
mz332.24296
mz238.11843
mz227.15263
mz254.11362
mz270.17791
mz293.06306
Parabacteroides
Parabacteroides
mz476.22166
mz364.18772
Enterococcus
mz416.21833
mz558.29054

Fig. S6

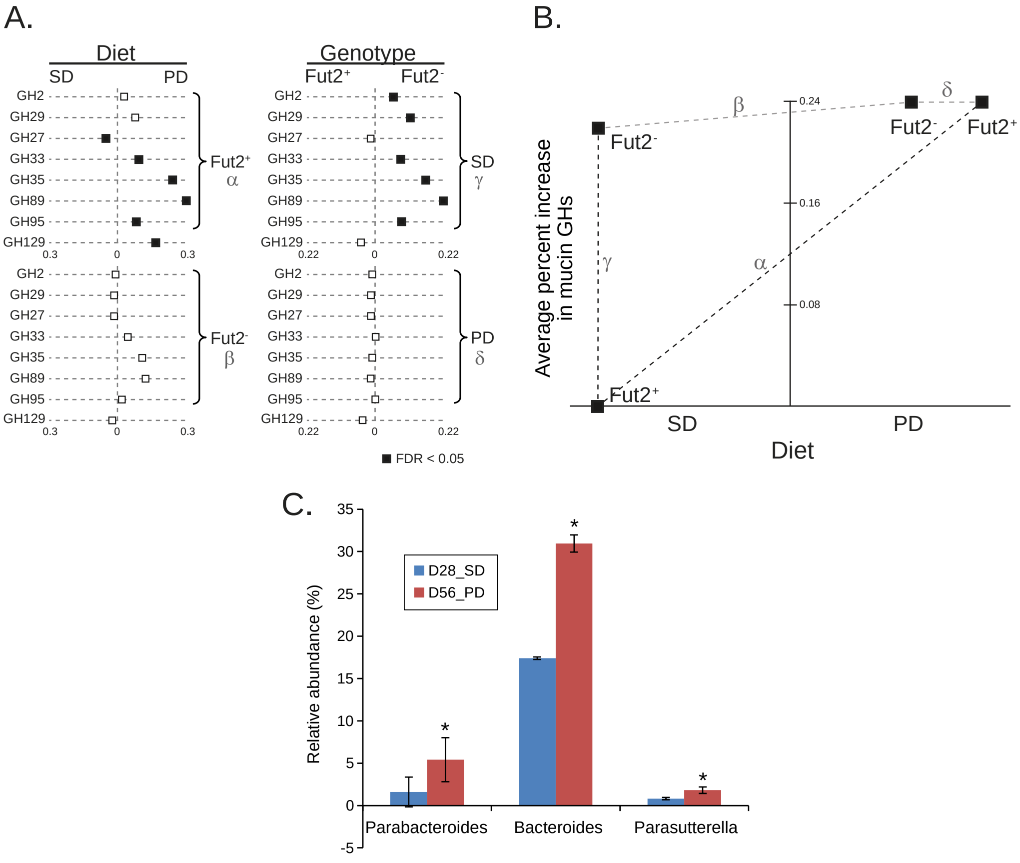
A.
Diet
SD
PD
GH2
GH29
GH27
GH33
GH35
GH89
GH95
GH129
0.3
0
0.3
Fut2⁺
α
Fut2⁻
β
Genotype
Fut2⁺
Fut2⁻
0.22
0
0.22
SD
γ
PD
δ
■ FDR < 0.05
B.
Average percent increase in mucin GHs
0.24
0.16
0.08
Fut2⁻
Fut2⁺
β
δ
γ
α
SD
PD
Diet
C.
Relative abundance (%)
35
30
25
20
15
10
5
0
-5
D28_SD
D56_PD
*
Parabacteroides
Bacteroides
Parasutterella

Table S1. Significant differences (p<0.05 ANOVA with FDR 5%) at different taxonomic levels between microbial communities from Fut2+ and Fut2- mice fed a standard diet.

	Probability	FDR_corrected	Fut2+_mean	Fut2-_mean	Consensus Lineage
Phylum					
	0.00152	0.00912187	0.009529412	0.0239	Bacteria; Proteobacteria
Class					
	0.002334	0.023344366	0.008558824	0.0225	Bacteria; Proteobacteria; Betaproteobacteria
Order					
	0.002078	0.022857569	0.008441176	0.02235	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales
Family					
	0.0003	0.005405692	0.002264706	0.00575	Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae
	0.001873	0.016860252	0.008176471	0.022	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae
	0.004849	0.02181938	0.174058824	0.2651	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae
	0.004564	0.027381968	0.105352941	0.0453	Bacteria; Firmicutes; Clostridia; Clostridiales; Other
Genus					
	1.96E-05	0.000665703	0.016029412	0.03055	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides
	0.000269	0.004577942	0.002205882	0.00575	Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium
	0.001873	0.021231428	0.008176471	0.022	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Parasutterella
	0.004849	0.032971508	0.174058824	0.2651	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
	0.004564	0.038791121	0.105352941	0.0453	Bacteria; Firmicutes; Clostridia; Clostridiales; Other; Other
OTU					
	4.83E-08	1.90E-05	0	0.00425	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae
	4.43E-05	0.008736197	0.000264706	0.0012	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
	0.000438	0.024669405	0.005735294	0.0139	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
	0.000191	0.025023369	0.001794118	0.00555	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides
	0.000573	0.025072956	0.000647059	0.00225	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales
	0.000649	0.025586788	0.000235294	0.0012	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides
	0.000527	0.025967852	8.82E-05	0.00065	Bacteria; Firmicutes
	0.00043	0.02821245	0.018705882	0.00405	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
	0.000309	0.030431163	0.001235294	0.00395	Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium
	0.000407	0.032105316	0.002029412	0.00515	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
	0.001097	0.036027909	0.001705882	0.0064	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Parasutterella
	0.001077	0.038562643	0.000794118	0.0023	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides
	0.001586	0.041665937	5.88E-05	0.0005	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
	0.001409	0.042705377	0.040323529	0.09035	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
	0.001557	0.043815828	8.82E-05	0.0005	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Parasutterella

	0.001823	0.044883368	0.000941176	0.0032	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides
	0.002165	0.047395583	0.000147059	0.00065	Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae; Eubacterium
	0.002478	0.048807318	0.000823529	0.0037	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae
	0.002109	0.048880602	0.000205882	0.00085	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Porphyromonadaceae; Parabacteroides
	0.002608	0.048926647	8.82E-05	0.00045	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Parasutterella
	0.002739	0.049047896	0.001941176	0.0004	Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Bacteroidaceae; Bacteroides

Table S2. Significantly different (p<0.05, t-test and >2-fold change) masses for urinary metabolites between humanized Fut2+ and Fut2- mice on standard diet.

Fut2+ > Fut2-				Fut2- > Fut2+		
m/z	**Fold change**	**p.value**		**m/z**	**Fold change**	**p.value**
435.1346	14.82206	0.000426		304.1265	2.4523	0.011232
452.1552	12.92908	0.00024		213.1118	2.488	0.017927
174.1122	8.145312	0.000812		145.1319	2.5966	0.028848
453.1602	7.068137	0.000239		76.03983	2.7112	0.038639
259.1043	6.92329	0.000237		192.7746	2.7731	0.045969
466.1308	6.582845	0.02759		194.0808	2.8131	0.038574
191.1389	6.105752	0.003602		195.0841	2.822	0.037612
360.1283	5.969793	0.041582		168.1125	2.8726	0.015532
175.1154	5.905628	0.000406		234.0348	2.8731	0.047054
471.0533	4.738438	0.019736		225.123	2.9064	0.045781
469.0564	4.72858	0.020539		233.04	2.9941	0.049013
447.0744	4.712535	0.024184		91.05376	3.0511	0.040921
410.1048	4.674863	0.047657		212.1107	3.0737	0.027905
331.0445	4.657662	0.028504		239.1385	3.0955	0.047108
449.0702	4.649649	0.025051		240.1413	3.1016	0.040376
470.06	4.64792	0.021516		263.1166	3.1275	0.047144
448.0784	4.60278	0.03056		211.1073	3.1449	0.028048
262.9998	4.598124	0.02043		209.6259	3.4104	0.033369
219.1685	4.512635	0.004535		388.158	3.7346	0.040371
222.4212	4.306076	0.028567		286.1038	3.7467	0.040291
171.1012	4.27899	0.02891		387.1546	3.8016	0.039279
227.0394	4.120992	0.035893		425.1107	3.8648	0.034212
261.9964	4.111166	0.020773		224.0783	3.9069	0.011878
228.0774	4.027386	0.048876		214.1182	4.0405	0.035541
178.0327	4.011714	0.035175		216.0627	4.1418	0.030927
226.0364	4.003203	0.034752		222.0435	4.3324	0.00654
225.0438	3.986446	0.034657		410.1401	4.523	0.032767
176.0374	3.968569	0.032778		409.1366	4.6577	0.035993
224.0406	3.90564	0.035068		404.1812	5.302	0.031565
224.0484	3.875518	0.036416		304.1273	10.023	0.006513
240.1419	3.800836	0.025479		141.0181	10.441	0.006248
277.0944	3.750938	0.020249		302.1227	10.723	0.006863
294.1444	3.703978	0.002693		207.0513	10.746	0.006141
177.0412	3.630818	0.029946		307.0783	11.196	0.012585
184.0965	3.55101	0.028463		303.1264	11.488	0.006376
239.1388	3.476326	0.017856		299.5889	11.643	0.00821
241.0683	3.375869	0.035388		206.0479	11.78	0.00637
298.1473	3.296631	0.000745		211.0033	12.102	0.007884

335.1023	3.212748	0.004688		228.0321	12.437	0.009551
308.1607	3.194684	0.000643		223.0744	13.009	0.005211
246.0261	3.00102	0.034268		249.0754	13.534	0.006797
279.0827	2.997422	0.009688		316.1385	15.773	0.017183
322.1854	2.917238	0.036558		323.0522	18.238	0.015398
284.1962	2.915622	0.025691		500.1525	19.667	0.041713
190.1799	2.894188	0.049183		428.1154	40.738	0.005635
297.144	2.88542	0.000833		591.1687	41.814	0.012699
263.9921	2.828454	0.017621		592.1722	54.459	0.01171
180.0486	2.748385	0.038304				
236.1489	2.477087	0.032499				
367.1858	2.474451	0.018857				
211.169	2.468222	0.032442				
299.1596	2.431197	3.93E-05				
178.0529	2.412487	0.045893				
290.1957	2.402749	0.035263				
297.144	2.387604	0.032113				
255.1587	2.357879	0.042363				
290.1495	2.342579	0.004914				
298.1485	2.24482	0.025704				
366.159	2.22326	0.014317				
272.1425	2.195775	0.003558				
291.1645	2.147766	0.035009				
311.1301	2.144634	0.032025				
290.1221	2.124631	0.025069				
225.0539	2.088511	0.021105				
156.0652	2.056936	0.049838				
297.1439	2.052672	0.030004				
295.1513	2.026178	0.045821				
208.1805	2.01487	0.020068				
266.1494	2.011668	0.002138				
271.1395	2.00449	0.001877				

Table S3. Significantly different (p<0.05, t-test and >2-fold change) masses for urinary metabolites between humanized Fut2+ and Fut2- mice on PD diet.

Fut2+ > Fut2-				**Fut2- > Fut2+**		
m/z	**Fold Change**	**p.value**		**m/z**	**Fold Change**	**p.value**
368.1926756	0.31866	0.023852		305.1845096	2.1161	0.012416
397.2261072	0.28967	0.025419				
216.0089013	0.39541	0.030865				
234.13331	0.4557	0.031621				
394.1710136	0.17688	0.034053				
261.1805802	0.34868	0.034149				
254.1383583	0.4055	0.043056				
274.12824	0.39552	0.044298				
396.218109	0.32458	0.047254				
347.1334156	0.48975	0.047778				
275.1962316	0.35546	0.048227				

Table S4. Significantly different (p<0.05, t-test and >2-fold change) masses for fecal metabolites between humanized Fut2+ and Fut2- mice on standard diet.

Fut2+ > Fut2-				**Fut2- > Fut2+**		
m/z	**Fold change**	**p.value**		**m/z**	**Fold change**	**p.value**
578.2800263	4.467676362	0.023807		306.0807789	2.5526	0.041072
427.0880047	2.952116668	0.040949		174.0385192	2.6114	0.019797
484.1216389	2.904696895	0.04015		445.2409566	3.0638	0.047615
615.2798424	2.884338044	0.032329		291.1802804	3.7223	0.047764
241.071466	2.432616522	0.033951				
266.1384405	2.270920858	0.009167				
293.0630604	2.145186202	0.014425				
393.2076553	2.083767452	0.034145				
232.0968862	2.006621852	0.022698				

Table S5. Significantly different (p<0.05, t-test and >2-fold change) masses for fecal metabolites between humanized Fut2+ and Fut2- mice on PD diet.

Fut2+ > Fut2-				Fut2- > Fut2+		
m/z	Fold change	p.value		m/z	Fold change	p value
146.1651207	4.737315837	0.006904		72.08143573	3.348	0.028815
393.2364179	3.292289458	0.039828				

Table S6. Discriminatory metabolites based on random Random Forests Classifier between humanized Fut2+ and Fut2- mice on standard diet.

m/z	Mean_decrease_in_accuracy
169.0426	0.008
347.2159	0.005333333
290.1962	0.005333333
94.0450	0.004
284.2210	0.004
331.2068	0.004
244.1543	0.003333333
146.1651	0.002666667
72.0814	0.002
110.0096	0.002
128.0191	0.002
276.1318	0.002
267.1240	0.002
310.2253	0.002
142.0346	0.001333333
86.0606	0.001333333
376.1843	0.001333333
403.1574	0.001333333
229.1434	0.001333333
347.2112	0.001333333
370.2584	0.001333333
266.1387	0.001333333
323.1706	0.001333333
494.2102	-0.001
143.9968	-0.001333333
268.1038	-0.001333333
319.1628	-0.001333333
385.1511	-0.001333333
303.1708	-0.001333333
248.1354	-0.001333333
430.2033	-0.001333333
319.1661	-0.001333333
281.1922	-0.001333333
230.1188	-0.001333333
526.3237	-0.001333333
220.1544	-0.001333333
149.0721	-0.001333333
123.0807	-0.001333333
318.2013	-0.001333333
592.3222	-0.001333333
173.1547	-0.001333333
282.1550	-0.002
140.0023	-0.002

171.9916	-0.002
354.2022	-0.002
231.1591	-0.002
346.1851	-0.002
252.1883	-0.002
164.1363	-0.002
235.1543	-0.002
492.2360	-0.002
511.3129	-0.002
285.9691	-0.002
591.3183	-0.002
308.2059	-0.002666667
270.1099	-0.004

Table S7. Imputed genes from the microbial communities of mice on SD and PD diets at KEGG level 2.

KEGG Level 2	SD Diet Mean	PD Diet Mean
Membrane Transport	0.1242783	0.12789727
Carbohydrate Metabolism	0.121309812	0.121732725
Amino Acid Metabolism	0.099278825	0.099563917
Replication and Repair	0.083813074	0.083452106
Energy Metabolism	0.059459054	0.05864909
Translation	0.052489032	0.051638819
Poorly Characterized	0.04491741	0.044531658
Metabolism of Cofactors and Vitamins	0.043188937	0.04248141
Cellular Processes and Signaling	0.040690914	0.041076994
Nucleotide Metabolism	0.039395157	0.039605513
Lipid Metabolism	0.029995135	0.029376473
Transcription	0.028870699	0.02831977
Metabolism	0.028431355	0.027739471
Genetic Information Processing	0.023188168	0.024287642
Xenobiotics Biodegradation and Metabolism	0.022772551	0.02256834
Folding, Sorting and Degradation	0.022686923	0.022974972
Glycan Biosynthesis and Metabolism	0.020887635	0.023043367
Enzyme Families	0.020168914	0.020094077
Metabolism of Terpenoids and Polyketides	0.015579637	0.016283269
Metabolism of Other Amino Acids	0.014995878	0.014709748
Signal Transduction	0.014909194	0.014280703
Cell Motility	0.014254934	0.011179372
Biosynthesis of Other Secondary Metabolites	0.010667105	0.009785173
Cell Growth and Death	0.005004842	0.004901653
Infectious Diseases	0.003194528	0.003360811
Transport and Catabolism	0.003137331	0.003210015
Endocrine System	0.002888757	0.003034939
Signaling Molecules and Interaction	0.001764128	0.00202971
Environmental Adaptation	0.001618472	0.001541726
Nervous System	0.001117435	0.001139647
Cancers	0.001028475	0.001100939
Immune System	0.000996724	0.000957413
Metabolic Diseases	0.000984337	0.00101531
Neurodegenerative Diseases	0.000961013	0.000898636
Immune System Diseases	0.000508963	0.000650139
Excretory System	0.00028169	0.000320532
Digestive System	0.000279197	0.000564316
Circulatory System	3.25E-06	1.13E-06
Cardiovascular Diseases	2.21E-06	1.20E-06

Table S8. Imputed Glycoside Hydrolases compared across different diets. FDR < 0.05 highlighted green, GH abundances that are significantly increased in those communities on PD diet are highlighted orange.

GHs	Probability	FDR corrected	SD Diet mean	PD Diet mean
GH70	3.86E-09	4.25E-07	4.34E-05	0.000166394
GH61	9.68E-09	5.32E-07	6.10E-06	1.87E-05
GH68	2.65E-08	9.71E-07	3.24E-05	8.66E-05
GH126	1.32E-07	3.63E-06	7.96E-05	0.000213617
GH65	5.32E-07	1.17E-05	0.003074357	0.003849159
GH119	1.26E-06	2.31E-05	2.28E-06	6.79E-06
GH52	1.26E-06	1.98E-05	6.84E-06	2.04E-05
GH81	1.26E-06	1.73E-05	9.12E-06	2.72E-05
GH75	3.34E-06	4.08E-05	2.35E-05	0.000168224
GH24	5.79E-06	6.37E-05	0.00648103	0.005071203
GH57	6.97E-06	6.97E-05	0.006270352	0.004319449
GH45	8.75E-06	8.02E-05	3.80E-06	8.01E-06
GH128	8.75E-06	7.40E-05	3.80E-06	8.01E-06
GH15	1.79E-05	0.000140529	0.003189267	0.002437687
GH130	7.60E-05	0.000557461	0.015484423	0.01646965
GH23	8.32E-05	0.000571975	0.029029056	0.024342383
GH12	9.69E-05	0.000626804	5.86E-06	9.70E-06
GH35	0.000148478	0.000907368	0.00900328	0.010845236
GH38	0.000319979	0.001852511	0.005859508	0.006410674
GH1	0.000491097	0.002701034	0.005900936	0.008792705
GH37	0.00063278	0.003314564	9.88E-05	0.00020396
GH129	0.000685447	0.003427236	0.000918884	0.001106938
GH27	0.000722037	0.003453221	0.00783621	0.007471216
GH18	0.000809088	0.00370832	0.014775368	0.016426728
GH3	0.001067092	0.004695203	0.050897713	0.047754202
GH89	0.001353949	0.005728247	0.00484954	0.006085551
GH6	0.001563752	0.006370842	3.11E-05	2.21E-05
GH10	0.002572504	0.010106264	0.003194689	0.002744838
GH31	0.002911476	0.01104353	0.020374231	0.021977991
GH115	0.003119667	0.011438777	0.005446182	0.006375392
GH105	0.003203178	0.011366115	0.013393378	0.015677665
GH43	0.003267118	0.011230719	0.069428753	0.076209979
GH50	0.003626892	0.012089639	0.001561891	0.001931894
GH66	0.004155904	0.013445571	0.001084269	0.00132377
GH93	0.004350216	0.013672109	0.001042178	0.00128392
GH22	0.004393135	0.013423469	0.000515825	0.000637101
GH67	0.004531437	0.013471841	0.001604223	0.001950441
GH88	0.004608598	0.013340678	0.008961107	0.01007045

GH17	0.004965056	0.014004005	9.90E-06	1.30E-05
GH121	0.00507168	0.01394712	0.000517325	0.000636329
GH46	0.00507168	0.013606947	0.000517325	0.000636329
GH55	0.005081721	0.013309269	0.00051788	0.00063685
GH114	0.00570396	0.014591525	0.002170806	0.001574016
GH107	0.006994798	0.017486996	0.00051353	0.000628344
GH91	0.007034278	0.017194903	0.001028594	0.00125791
GH117	0.007095264	0.016966935	0.002061708	0.0025194
GH85	0.008338161	0.019514845	0.00027707	0.000214964
GH87	0.010482366	0.024022088	7.04E-05	9.35E-05
GH28	0.014193902	0.031863862	0.021634645	0.024310143
GH19	0.014620929	0.032166043	4.75E-05	3.81E-05
GH108	0.016040138	0.034596377	5.24E-05	3.94E-05
GH33	0.017781411	0.037614524	0.015059355	0.015942557
GH123	0.023578513	0.048936537	0.005811688	0.005121626
GH64	0.026239893	0.053451634	5.11E-06	4.13E-06
GH109	0.027425301	0.054850602	0.05944138	0.054224782
GH101	0.029550689	0.058045996	0.000183881	0.000266518
GH74	0.030625145	0.059101156	0.007052303	0.005766464
GH5	0.03895966	0.07388901	0.015226891	0.016501192
GH76	0.041017989	0.076474217	0.016436192	0.017759745
GH71	0.042896435	0.078643464	3.58E-06	2.91E-06
GH95	0.045021859	0.081186958	0.016087949	0.016888462
GH51	0.047533633	0.084333864	0.016226465	0.015615091
GH80	0.049356759	0.086178467	3.60E-06	2.94E-06
GH84	0.058016448	0.09971577	0.003589147	0.003684283
GH99	0.072092292	0.12200234	0.006971145	0.00779533
GH63	0.076890459	0.128150764	0.00370048	0.004022534
GH104	0.077431081	0.127125655	0.000994614	0.000796285
GH77	0.083498063	0.135070395	0.015714645	0.013777774
GH32	0.101575519	0.161931986	0.013900722	0.015008614
GH112	0.116109192	0.182457301	0.002043294	0.001694291
GH13	0.119092675	0.184509779	0.074142367	0.066831381
GH54	0.150157599	0.229407443	2.07E-06	1.71E-06
GH79	0.150157599	0.226264875	4.14E-06	3.43E-06
GH4	0.152107775	0.226106152	0.011457239	0.010893577
GH127	0.173053911	0.253812402	0.01880408	0.018129316
GH73	0.188328662	0.272580958	0.016366981	0.015505748
GH116	0.253119602	0.361599431	0.002509893	0.002645595
GH39	0.318856847	0.449669913	0.001587378	0.001364777
GH92	0.366877748	0.510842434	0.052602211	0.050493713

GH62	0.383332028	0.527081539	0.000115861	9.69E-05
GH9	0.386264553	0.524556801	0.004441201	0.003975864
GH125	0.407866173	0.547137549	0.00686574	0.006637221
GH25	0.420659572	0.557500638	0.011930978	0.012851487
GH59	0.454201712	0.594787956	0.000262108	0.000290962
GH124	0.477575915	0.61803942	0.000577514	0.00050804
GH98	0.531532956	0.679867735	0.000182266	0.00020155
GH36	0.53953822	0.682174761	0.017009062	0.017595748
GH102	0.551259289	0.689074111	0.000367586	0.00034254
GH103	0.567726264	0.701684146	0.000481637	0.000531191
GH53	0.597770805	0.730608761	0.004168998	0.004372658
GH30	0.637502114	0.770606951	0.010108498	0.009930241
GH2	0.659017533	0.787955746	0.087124331	0.086506038
GH94	0.660397322	0.781115113	0.005407808	0.005081827
GH82	0.676690577	0.791871952	0.000179985	0.000192792
GH97	0.697330912	0.807435793	0.021756947	0.02216002
GH8	0.719571396	0.824508891	0.001197834	0.001140695
GH78	0.739590113	0.838710438	0.027739431	0.027590628
GH16	0.760444563	0.853560224	0.009878202	0.009755509
GH106	0.77558737	0.861763744	0.008822731	0.008693305
GH14	0.806282343	0.886910578	6.14E-05	5.86E-05
GH42	0.810464502	0.882684111	0.00623121	0.006338398
GH113	0.860080054	0.927537313	0.001567838	0.001606101
GH26	0.915863921	0.9781071	0.006802706	0.006834917
GH110	0.928500807	0.982068161	0.005355196	0.00533355
GH29	0.929923155	0.97420521	0.023642805	0.023720986
GH11	0.930242819	0.965346321	0.001672867	0.001661096
GH20	0.971044208	0.998269746	0.038423243	0.038366944
GH44	0.978087461	0.996200192	0.000236775	0.000237828
GH48	0.978087461	0.987060741	0.000236775	0.000237828
GH120	0.99712162	0.99712162	0.001279283	0.001279597

Table S9. Imputed Glycoside Hydrolases compared across different diets in Fut2+ mice. FDR < 0.05 highlighted green, mucin glycan-degrading related GHs highlighted orange.

Glycoside Hydrolase	Probability	FDR Corrected	SD diet mean	PD diet mean
GH70	9.76E-07	0.000107306	4.77E-05	0.000145118
GH61	3.69E-06	0.000202802	6.62E-06	1.64E-05
GH15	6.91E-06	0.000253474	0.003301082	0.002411039
GH130	1.60E-05	0.00035252	0.015150275	0.016543869
GH68	1.59E-05	0.00043675	3.43E-05	7.61E-05
GH35	4.79E-05	0.000877805	0.00834214	0.010888576
GH23	6.04E-05	0.000949712	0.03034079	0.024088108
GH75	7.42E-05	0.001020358	1.89E-05	0.00016281
GH81	0.00012185	0.001218501	1.00E-05	2.24E-05
GH52	0.00012185	0.001340351	7.53E-06	1.68E-05
GH119	0.00012185	0.001489279	2.51E-06	5.60E-06
GH89	0.000252649	0.002137798	0.004349078	0.006145541
GH65	0.000241203	0.002211024	0.003153163	0.003865055
GH115	0.000373597	0.002739712	0.005124841	0.006411111
GH38	0.00036008	0.0028292	0.005802169	0.00645118
GH43	0.000428958	0.002949086	0.066702923	0.076540102
GH126	0.000480087	0.003106445	9.91E-05	0.000196369
GH27	0.000562672	0.003257574	0.007939384	0.007473503
GH105	0.000537483	0.003284617	0.012442691	0.015750792
GH121	0.000929231	0.003650552	0.000461185	0.000641314
GH67	0.000853936	0.003757318	0.001452838	0.001963656
GH46	0.000929231	0.003785757	0.000461185	0.000641314
GH93	0.000835342	0.00382865	0.000929771	0.001292535
GH66	0.001012332	0.00383988	0.000971619	0.001328709
GH55	0.000920326	0.003893686	0.000461618	0.000641816
GH117	0.001150536	0.003954969	0.001836299	0.00254403
GH85	0.000827472	0.003957474	0.000308174	0.000204817
GH91	0.001136289	0.004031993	0.000915791	0.001270289
GH88	0.000811801	0.004059003	0.00848858	0.01013201
GH107	0.001126026	0.004128762	0.000457097	0.000634566
GH50	0.000762063	0.004191344	0.001394273	0.001943076
GH22	0.000805869	0.004221218	0.000459609	0.000642203
GH10	0.001502836	0.005009452	0.003498153	0.002711299
GH45	0.001801744	0.005662623	4.09E-06	6.76E-06
GH128	0.001801744	0.005829171	4.09E-06	6.76E-06
GH18	0.002002083	0.006117474	0.014656723	0.016510054
GH6	0.002569922	0.00764031	3.17E-05	2.06E-05
GH3	0.002942702	0.008518348	0.052159536	0.047789403

GH28	0.003039154	0.008571973	0.02009679	0.024507281
GH114	0.003239215	0.008907841	0.002476207	0.001539622
GH37	0.003592252	0.00963775	9.34E-05	0.000199861
GH95	0.005846077	0.015311153	0.015653293	0.016928944
GH33	0.006016566	0.015391216	0.014529821	0.015949732
GH19	0.007509884	0.018774709	4.91E-05	3.62E-05
GH57	0.008877302	0.021700072	0.006074314	0.004347144
GH24	0.00978291	0.023393916	0.006312376	0.005069234
GH74	0.01165108	0.027268486	0.008093605	0.005563735
GH76	0.013237452	0.030335828	0.015357068	0.017889408
GH99	0.01461156	0.032801461	0.006307646	0.007852947
GH12	0.022817509	0.048267808	6.10E-06	8.40E-06
GH129	0.023350691	0.048463697	0.000955275	0.001126951
GH63	0.024048634	0.048987959	0.003392272	0.004065447
GH4	0.022787849	0.049150263	0.011890587	0.010927319
GH73	0.0227214	0.049987079	0.017031662	0.015306078
GH64	0.02563707	0.051274141	5.18E-06	3.96E-06
GH77	0.031350522	0.061581383	0.017433674	0.013560886
GH13	0.034113091	0.065832281	0.081872403	0.065854419
GH51	0.040152658	0.076151593	0.016545848	0.015589951
GH71	0.055350117	0.103195134	3.59E-06	2.80E-06
GH80	0.057335657	0.105115372	3.61E-06	2.81E-06
GH103	0.058986175	0.106368513	0.000348159	0.000497387
GH112	0.066233532	0.11564585	0.002383416	0.001651961
GH9	0.065633289	0.116446159	0.005558923	0.003859172
GH62	0.083231843	0.140853889	0.000150555	9.19E-05
GH116	0.082064053	0.141047591	0.002312412	0.002669697
GH108	0.085523517	0.142539195	5.11E-05	3.96E-05
GH124	0.089613364	0.147126418	0.000770902	0.00048995
GH109	0.115883786	0.187459066	0.059001434	0.054150899
GH39	0.118675333	0.18919256	0.00192534	0.001330915
GH14	0.148315365	0.233067002	7.90E-05	5.44E-05
GH97	0.157794595	0.2444705	0.02007869	0.022485967
GH8	0.164198177	0.250858326	0.001489908	0.001096228
GH48	0.187128626	0.278164173	0.000326763	0.000230959
GH44	0.187128626	0.281974641	0.000326763	0.000230959
GH94	0.197899586	0.290252726	0.006592783	0.004946336
GH1	0.209455326	0.303159025	0.006978173	0.008514196
GH104	0.220788065	0.311367784	0.000967459	0.000797671
GH87	0.21797101	0.311387158	7.10E-05	8.19E-05
GH54	0.228374041	0.314014307	2.01E-06	1.65E-06

GH79	0.228374041	0.317989172	4.03E-06	3.30E-06
GH29	0.240762714	0.326961711	0.022259068	0.023898827
GH11	0.258954546	0.347378049	0.001910305	0.001636856
GH82	0.278049179	0.368498912	0.00025274	0.000187794
GH26	0.296180457	0.387855361	0.007335961	0.006782533
GH20	0.300873351	0.389365513	0.035978343	0.038784531
GH110	0.321219378	0.397012715	0.004996283	0.005411129
GH98	0.318314432	0.39789304	0.000255252	0.000195431
GH31	0.311472477	0.398395028	0.020958638	0.021923237
GH59	0.315407084	0.398790566	0.000348321	0.000275659
GH17	0.327637029	0.400445257	1.04E-05	1.16E-05
GH2	0.36566997	0.442018645	0.084937304	0.086937382
GH84	0.371202535	0.443829117	0.003621304	0.003679407
GH106	0.385939428	0.456487495	0.008137487	0.008756009
GH113	0.40674661	0.470969759	0.001891995	0.001587791
GH78	0.41135444	0.471343629	0.027079539	0.027682319
GH123	0.404732341	0.473622952	0.005610902	0.005233045
GH120	0.443013797	0.50238678	0.001390841	0.001272455
GH42	0.459621391	0.515901561	0.006850836	0.006269676
GH16	0.467720745	0.519689717	0.009295831	0.009799699
GH30	0.502679007	0.552946908	0.009551626	0.009993698
GH25	0.508999773	0.554356189	0.013802413	0.012496974
GH53	0.566812063	0.611267911	0.004677558	0.004303171
GH36	0.61570424	0.657548217	0.01825721	0.01745752
GH92	0.641525109	0.678536173	0.049048534	0.05098848
GH125	0.668922142	0.700775577	0.006454063	0.006666643
GH102	0.692428582	0.718557963	0.000312796	0.000332399
GH101	0.765495372	0.786957859	0.000236667	0.000252563
GH32	0.847111528	0.862798778	0.014656949	0.01487443
GH127	0.878644182	0.886705138	0.018096995	0.018225737
GH5	0.975133646	0.975133646	0.016353537	0.016389033

Table S10. Imputed Glycoside Hydrolases compared across different diets in Fut2- mice. FDR < 0.05 highlighted green, mucin glycan-degrading related GHs highlighted orange.

Glycoside Hydrolase	Probability	FDR Corrected	SD diet mean	PD diet mean
GH75	5.74E-06	0.000157719	2.98E-05	0.000177968
GH70	5.57E-06	0.000204058	4.74E-05	0.000204692
GH61	5.23E-06	0.000287905	6.32E-06	2.29E-05
GH126	1.37E-05	0.000301581	6.61E-05	0.000244662
GH68	3.53E-06	0.000388132	3.25E-05	0.000105597
GH128	0.000132959	0.001329587	3.83E-06	1.03E-05
GH12	7.58E-05	0.001390366	5.53E-06	1.20E-05
GH45	0.000132959	0.001462546	3.83E-06	1.03E-05
GH81	0.000129321	0.00158059	9.97E-06	3.58E-05
GH119	0.000129321	0.001778164	2.49E-06	8.94E-06
GH52	0.000129321	0.002032187	7.48E-06	2.68E-05
GH37	0.00044348	0.004065236	9.59E-05	0.000211339
GH17	0.000523977	0.004433647	9.16E-06	1.56E-05
GH65	0.002346629	0.018437801	0.003106584	0.003820546
GH87	0.002971422	0.021790425	6.80E-05	0.000114243
GH101	0.007826502	0.0538072	0.000137195	0.000291636
GH1	0.00832438	0.053863634	0.00555209	0.009294022
GH129	0.015179214	0.092761866	0.000911157	0.001070915
GH24	0.024233077	0.140296759	0.006257187	0.005074748
GH57	0.025520568	0.140363123	0.005983108	0.004269598
GH59	0.031808232	0.16661455	0.000203126	0.000318506
GH98	0.033436762	0.16718381	0.000135618	0.000212563
GH5	0.035096601	0.167853308	0.014621261	0.016703077
GH82	0.050722946	0.232480171	0.000133125	0.00020179
GH15	0.070494342	0.310175105	0.003027042	0.002485654
GH31	0.10003289	0.407541405	0.020454233	0.022076547
GH38	0.105749897	0.415446022	0.005934892	0.006337765
GH3	0.098653811	0.417381506	0.050405703	0.047690841
GH44	0.120095191	0.426144226	0.000174219	0.000250192
GH48	0.120095191	0.440349034	0.000174219	0.000250192
GH27	0.11624533	0.440930563	0.007725352	0.007467099
GH18	0.132588382	0.455772562	0.015104325	0.016276741
GH84	0.152715103	0.466629482	0.003588538	0.003693061
GH123	0.145664888	0.471268754	0.005777051	0.004921073
GH35	0.150844365	0.47408229	0.009586748	0.010767224
GH23	0.145068772	0.483562573	0.027723873	0.024800077
GH25	0.187042867	0.541439877	0.011001167	0.013489609
GH78	0.182995765	0.544041464	0.028286593	0.027425584

GH127	0.196327497	0.553744222	0.019039661	0.017955758
GH108	0.242832653	0.65150224	4.67E-05	3.89E-05
GH130	0.254965658	0.652237729	0.015892492	0.016336056
GH14	0.239438479	0.658455817	4.61E-05	6.63E-05
GH32	0.253832973	0.664800642	0.013886346	0.015250146
GH43	0.393294873	0.665575939	0.072132463	0.075615757
GH46	0.3812773	0.66572227	0.000563136	0.000627355
GH124	0.390981779	0.671999932	0.00042078	0.000540602
GH89	0.269013544	0.672533859	0.005254418	0.00597757
GH26	0.405068414	0.675114023	0.006520293	0.006929209
GH121	0.3812773	0.676459726	0.000563136	0.000627355
GH55	0.380510519	0.686166509	0.00056355	0.000627911
GH92	0.28081061	0.686425935	0.053866479	0.049603133
GH105	0.306206885	0.687403211	0.014139637	0.015546037
GH125	0.438011016	0.688303025	0.006955556	0.006584262
GH107	0.434011745	0.691902781	0.000559329	0.000617144
GH104	0.377675554	0.692405182	0.000973744	0.000793789
GH2	0.290216194	0.693995247	0.088241907	0.08572962
GH33	0.360239387	0.695198817	0.015338155	0.015929642
GH9	0.467993736	0.695666364	0.003629706	0.004185911
GH93	0.354739248	0.696809237	0.001133047	0.001268415
GH109	0.374817017	0.698811388	0.058261303	0.05435777
GH10	0.476854783	0.699387015	0.002945804	0.002805208
GH114	0.349898717	0.699797434	0.001962448	0.001635926
GH22	0.369072228	0.699964571	0.000561849	0.000627917
GH51	0.30593334	0.701097237	0.016183303	0.015660341
GH91	0.433743089	0.701643233	0.001119991	0.001235626
GH53	0.466415246	0.702817495	0.00402353	0.004497736
GH62	0.508486709	0.708019468	8.47E-05	0.000105744
GH115	0.348149152	0.709192716	0.005786285	0.006311097
GH97	0.535226337	0.709336109	0.022645848	0.021573315
GH106	0.523074021	0.710347436	0.009088521	0.008580438
GH117	0.433669264	0.711994314	0.002243925	0.002475065
GH110	0.466370017	0.712509748	0.005497614	0.005193909
GH11	0.531192176	0.71257487	0.001562609	0.001704729
GH28	0.51855143	0.713008216	0.022749236	0.023955293
GH8	0.506167297	0.713825675	0.001046081	0.001220736
GH6	0.305247572	0.71440921	2.85E-05	2.48E-05
GH50	0.331628749	0.715277694	0.001699608	0.001911766
GH66	0.326119857	0.717463686	0.00117436	0.00131488
GH30	0.463219751	0.717664402	0.010287291	0.009816017

GH20	0.50303339	0.718619129	0.039391929	0.037615286
GH88	0.347767317	0.721781224	0.009318412	0.009959643
GH36	0.501923494	0.726468216	0.016749424	0.017844558
GH67	0.344764617	0.729309767	0.00172656	0.001926655
GH29	0.571090679	0.747856842	0.024272159	0.023400872
GH113	0.622206293	0.786697612	0.001453481	0.001639059
GH16	0.619683636	0.792618604	0.010022405	0.009675966
GH112	0.645460083	0.797759653	0.001946763	0.001770485
GH102	0.617302464	0.798862012	0.000397622	0.000360793
GH42	0.640424449	0.800530561	0.006100568	0.006462098
GH95	0.675389339	0.825475858	0.016513718	0.016815593
GH99	0.72020978	0.851861031	0.007403918	0.00769162
GH76	0.705526923	0.852834743	0.017122016	0.017526352
GH94	0.714388178	0.854159778	0.004872742	0.005325711
GH77	0.75600399	0.88468552	0.014743235	0.014168174
GH54	0.789276644	0.904379487	1.73E-06	1.83E-06
GH4	0.798782355	0.90583566	0.011026181	0.010832839
GH74	0.807433505	0.906302914	0.00635203	0.006131377
GH79	0.789276644	0.913899272	3.45E-06	3.65E-06
GH80	0.830209339	0.922454821	3.06E-06	3.16E-06
GH64	0.921780156	0.930236854	4.37E-06	4.44E-06
GH39	0.918283593	0.935288845	0.001465497	0.001425728
GH85	0.916648103	0.942348517	0.000236803	0.000233229
GH71	0.909167325	0.943475526	3.04E-06	3.10E-06
GH13	0.894128389	0.945712719	0.069624603	0.068589914
GH73	0.904761314	0.947845186	0.015720134	0.015865153
GH63	0.890832599	0.951374621	0.003905313	0.003945292
GH120	0.86920035	0.956120385	0.001267169	0.001292453
GH116	0.889802701	0.959591148	0.002628411	0.002602212
GH103	0.887232155	0.966292446	0.000570045	0.000592038
GH19	0.972990545	0.972990545	4.12E-05	4.14E-05

Table S11. Imputed Glycoside Hydrolases compared across genotypes in mice on SD diet. FDR < 0.05 highlighted green, mucin glycan-degrading related GHs highlighted orange.

Glycoside Hydrolase	Probability	FDR Corrected	Fut2+ mean	Fut2- mean
GH44	0.001825461	0.022311186	0.00029331	0.000135013
GH59	0.002763145	0.023380454	0.000316085	0.000164951
GH101	0.002368595	0.023685953	0.000231331	9.85E-05
GH28	0.007355226	0.023796321	0.020380482	0.023892139
GH62	0.002606739	0.023895111	0.000147037	5.97E-05
GH74	0.007316021	0.024386737	0.0077776	0.005746769
GH76	0.00729255	0.025068141	0.01564758	0.017855694
GH48	0.001825461	0.025100084	0.00029331	0.000135013
GH14	0.002303117	0.025334284	7.72E-05	3.29E-05
GH63	0.00715597	0.025392152	0.003478726	0.004099637
GH99	0.007035394	0.025796446	0.006441777	0.007924007
GH93	0.006482868	0.026411685	0.000945555	0.001216099
GH73	0.007022767	0.026638081	0.017080007	0.015083535
GH50	0.006370049	0.026950206	0.001416912	0.001822852
GH9	0.001722835	0.027073114	0.005217454	0.003043946
GH89	0.006898432	0.027100982	0.004425106	0.005613521
GH33	0.00929724	0.027640442	0.014672754	0.015755237
GH105	0.009134228	0.02791014	0.012563257	0.014887595
GH55	0.006346478	0.027924501	0.000469342	0.000605248
GH67	0.010530625	0.028252897	0.001473669	0.001839221
GH95	0.009039253	0.028409081	0.015654946	0.016867354
GH88	0.010431756	0.028687329	0.008557839	0.009686991
GH13	0.009960952	0.028834336	0.079623688	0.06427599
GH117	0.006305802	0.028901592	0.001866999	0.002412182
GH23	0.011037473	0.028907668	0.030284908	0.026768522
GH35	0.003687762	0.028975272	0.008424463	0.010045152
GH78	0.010426983	0.029409439	0.0272799	0.028566586
GH130	0.001640964	0.030084342	0.015156539	0.016074613
GH121	0.006302087	0.030140417	0.000468768	0.000604728
GH26	0.013173932	0.03019026	0.007154594	0.006169308
GH1	0.01308762	0.0306306	0.006665285	0.004525108
GH115	0.012563287	0.030710257	0.005121989	0.006029729
GH2	0.012032874	0.030781769	0.085539908	0.089976293
GH77	0.012907158	0.030864943	0.016954957	0.013482084
GH19	0.013811561	0.031005544	5.15E-05	4.04E-05
GH29	0.014977039	0.03108442	0.02268453	0.025367702
GH116	0.014741103	0.031183103	0.002376967	0.002749159
GH103	0.014499858	0.031274203	0.00038806	0.000650076

GH8	0.012552344	0.03138086	0.001386974	0.000857381
GH46	0.006302087	0.031510436	0.000468768	0.000604728
GH4	0.001435568	0.031582491	0.011947805	0.01057422
GH114	0.01442697	0.031739335	0.002397872	0.001762087
GH91	0.006250475	0.032740583	0.000931049	0.001204176
GH97	0.016491451	0.033593697	0.020624319	0.023795676
GH107	0.006208728	0.034148004	0.00046469	0.000601441
GH5	0.017234512	0.034469025	0.01592437	0.013971427
GH82	0.005072379	0.034872609	0.000221007	0.000106146
GH22	0.00620003	0.035894908	0.000467122	0.000603492
GH17	0.018409343	0.036161209	1.07E-05	8.48E-06
GH98	0.005016219	0.036785609	0.000223439	0.000108156
GH66	0.006156939	0.037625736	0.000988342	0.001256937
GH43	0.005829819	0.03772236	0.066773098	0.074208931
GH106	0.019805985	0.038222075	0.008351396	0.009671133
GH126	0.001402201	0.038560529	9.66E-05	4.91E-05
GH25	0.022731966	0.043112349	0.013132876	0.009767562
GH64	0.023262641	0.043371026	5.52E-06	4.37E-06
GH124	0.001223119	0.044847686	0.000727125	0.000308213
GH85	0.000421381	0.046351939	0.000311054	0.0002159
GH11	0.025718583	0.047150736	0.001819753	0.001408472
GH10	0.000892373	0.049080499	0.003411708	0.002804055
GH112	0.028945109	0.052196097	0.002269774	0.00163563
GH94	0.032430405	0.057537816	0.006159717	0.004054371
GH12	0.035714514	0.062358674	6.30E-06	5.08E-06
GH15	0.040075632	0.068879992	0.003325714	0.002943662
GH71	0.041749821	0.070653543	3.87E-06	3.07E-06
GH45	0.04333715	0.071150545	4.08E-06	3.30E-06
GH80	0.044569067	0.07209702	3.89E-06	3.09E-06
GH128	0.04333715	0.072228584	4.08E-06	3.30E-06
GH20	0.046063013	0.073433788	0.036956979	0.041062517
GH127	0.048357104	0.075989735	0.018346203	0.019628257
GH113	0.050759357	0.078641257	0.001771441	0.001201352
GH39	0.052084825	0.079574039	0.001796276	0.001211363
GH3	0.057666335	0.086894477	0.051700982	0.049451828
GH30	0.062180976	0.091198764	0.009770775	0.010716399
GH61	0.062173768	0.092420467	6.53E-06	5.31E-06
GH92	0.065204437	0.094374842	0.05053606	0.056321283
GH27	0.0690073	0.097317986	0.007883458	0.007751162
GH16	0.068755033	0.098221476	0.009527749	0.010509017
GH68	0.070728431	0.098482625	3.46E-05	2.85E-05

GH110	0.07197884	0.098970904	0.005150528	0.005723597
GH6	0.074734609	0.101491444	3.33E-05	2.73E-05
GH102	0.093133503	0.123429943	0.000337048	0.000422556
GH125	0.092287594	0.123800431	0.00663865	0.007274502
GH36	0.113895259	0.147393865	0.017719597	0.015730099
GH53	0.113108622	0.148118433	0.004456743	0.003651059
GH52	0.125625044	0.155266909	7.29E-06	6.03E-06
GH70	0.1276124	0.155970712	4.62E-05	3.82E-05
GH119	0.125625044	0.157031305	2.43E-06	2.01E-06
GH81	0.125625044	0.158836263	9.73E-06	8.04E-06
GH84	0.12443402	0.159159793	0.003614979	0.003542649
GH42	0.14110644	0.170568224	0.006554033	0.005650129
GH54	0.156789113	0.185449488	2.22E-06	1.80E-06
GH129	0.159879538	0.187093076	0.000936122	0.000887854
GH79	0.156789113	0.187465243	4.44E-06	3.59E-06
GH87	0.172839912	0.200130425	7.31E-05	6.54E-05
GH51	0.239652585	0.27460192	0.016387868	0.015935939
GH120	0.245159148	0.278015529	0.001329911	0.001188154
GH108	0.251932262	0.28278111	5.51E-05	4.76E-05
GH32	0.275789529	0.30643281	0.014253058	0.013266518
GH65	0.29075515	0.319830664	0.003119714	0.002992713
GH75	0.314479407	0.342502325	2.04E-05	2.91E-05
GH18	0.388091213	0.41852974	0.014595257	0.015099568
GH109	0.477480982	0.509931146	0.060161386	0.058145371
GH31	0.575584506	0.608791304	0.02051965	0.020112478
GH104	0.720343242	0.754645301	0.001010175	0.000966604
GH57	0.801797968	0.824278285	0.006319628	0.006181654
GH38	0.794560072	0.824543471	0.005851495	0.005873931
GH37	0.862749265	0.878726103	9.94E-05	9.76E-05
GH24	0.924907568	0.924907568	0.006494217	0.006457293
GH123	0.917988371	0.926410282	0.005797871	0.00583656

Table S12. Imputed Glycoside Hydrolases compared across genotypes in mice on PD diet. FDR < 0.05 highlighted green, mucin glycan-degrading related GHs highlighted orange.

Glycoside Hydrolase	Probability	FDR Corrected	Fut2+ mean	Fut2- mean
GH84	0.907088351	0.968735132	0.003679407	0.003693061
GH37	0.895366682	0.975151832	0.000199861	0.000211339
GH66	0.904937526	0.975913019	0.001328709	0.00131488
GH3	0.93204341	0.97642643	0.047789403	0.047690841
GH95	0.861138911	0.97654928	0.016928944	0.016815593
GH4	0.894270255	0.98369728	0.010927319	0.010832839
GH108	0.931365859	0.985098505	3.96E-05	3.89E-05
GH50	0.859727334	0.985104237	0.001943076	0.001911766
GH104	0.986796363	0.986796363	0.000797671	0.000793789
GH65	0.890633338	0.989592598	0.003865055	0.003820546
GH27	0.981362094	0.990365416	0.007473503	0.007467099
GH51	0.883206006	0.99135368	0.015589951	0.015660341
GH93	0.838659685	0.991963069	0.001292535	0.001268415
GH105	0.859401351	0.995096302	0.015750792	0.015546037
GH109	0.959196078	0.995392156	0.054150899	0.05435777
GH24	0.981206418	0.999376907	0.005069234	0.005074748
GH75	0.855338046	1.0009275	0.00016281	0.000177968
GH113	0.837914538	1.001854339	0.001587791	0.001639059
GH33	0.975080411	1.002419114	0.015949732	0.015929642
GH67	0.833445098	1.007461107	0.001963656	0.001926655
GH35	0.831564485	1.016356593	0.010888576	0.010767224
GH115	0.830730563	1.02674564	0.006411111	0.006311097
GH120	0.82140317	1.026753962	0.001272455	0.001292453
GH55	0.815731291	1.031384391	0.000641816	0.000627911
GH121	0.815268482	1.042785268	0.000641314	0.000627355
GH46	0.815268482	1.05505333	0.000641314	0.000627355
GH99	0.813237932	1.064954435	0.007852947	0.00769162
GH22	0.81092951	1.074725857	0.000642203	0.000627917
GH57	0.804645107	1.079401972	0.004347144	0.004269598
GH16	0.799459607	1.085685887	0.009799699	0.009675966
GH88	0.785111623	1.093193399	0.01013201	0.009959643
GH106	0.798229036	1.097564925	0.008756009	0.008580438
GH15	0.783165231	1.104463787	0.002411039	0.002485654
GH38	0.77950929	1.1135847	0.00645118	0.006337765
GH125	0.777155689	1.124830602	0.006666643	0.006584262
GH117	0.775559552	1.137487342	0.00254403	0.002475065
GH91	0.774477923	1.151250966	0.001270289	0.001235626
GH107	0.773403793	1.165402976	0.000634566	0.000617144

GH43	0.770747292	1.177530585	0.076540102	0.075615757
GH36	0.766200711	1.187071525	0.01745752	0.017844558
GH89	0.763317094	1.199498291	0.006145541	0.00597757
GH29	0.712228247	1.20530934	0.023898827	0.023400872
GH78	0.762639886	1.215802717	0.027682319	0.027425584
GH18	0.75463218	1.220728527	0.016510054	0.016276741
GH31	0.744320113	1.222018096	0.021923237	0.022076547
GH28	0.712153035	1.224013029	0.024507281	0.023955293
GH114	0.740822761	1.234704601	0.001539622	0.001635926
GH102	0.697900225	1.238210076	0.000332399	0.000360793
GH53	0.710358203	1.240307974	0.004303171	0.004497736
GH129	0.697372789	1.257557489	0.001126951	0.001070915
GH42	0.696601278	1.277102344	0.006269676	0.006462098
GH39	0.693717257	1.293371157	0.001330915	0.001425728
GH30	0.692463882	1.313293569	0.009993698	0.009816017
GH26	0.692216378	1.335856167	0.006782533	0.006929209
GH77	0.686127299	1.347750053	0.013560886	0.014168174
GH79	0.677274921	1.354549843	3.30E-06	3.65E-06
GH54	0.677274921	1.379634099	1.65E-06	1.83E-06
GH94	0.666526876	1.383357668	0.004946336	0.005325711
GH127	0.656468315	1.388682975	0.018225737	0.017955758
GH116	0.650915646	1.403935706	0.002669697	0.002602212
GH32	0.650367396	1.430808271	0.01487443	0.015250146
GH112	0.64489805	1.447730315	0.001651961	0.001770485
GH13	0.637475741	1.460881905	0.065854419	0.068589914
GH76	0.612075429	1.463658635	0.017889408	0.017526352
GH73	0.632903464	1.481263427	0.015306078	0.015865153
GH23	0.607676057	1.485430361	0.024088108	0.024800077
GH92	0.604710348	1.51177587	0.05098848	0.049603133
GH71	0.602692146	1.541770607	2.80E-06	3.10E-06
GH5	0.543184699	1.57237676	0.016389033	0.016703077
GH63	0.572734849	1.575020835	0.004065447	0.003945292
GH82	0.601460094	1.575252626	0.000187794	0.00020179
GH1	0.592412526	1.589399459	0.008514196	0.009294022
GH11	0.566971611	1.599150698	0.001636856	0.001704729
GH20	0.539598071	1.604210481	0.038784531	0.037615286
GH2	0.53741307	1.642095492	0.086937382	0.08572962
GH80	0.535510053	1.683031596	2.81E-06	3.16E-06
GH9	0.532172875	1.721735771	0.003859172	0.004185911
GH123	0.52175488	1.739182934	0.005233045	0.004921073
GH98	0.519888019	1.787115065	0.000195431	0.000212563

GH97	0.51713533	1.834996333	0.022485967	0.021573315
GH64	0.516592007	1.894170692	3.96E-06	4.44E-06
GH48	0.514764748	1.952555942	0.000230959	0.000250192
GH44	0.514764748	2.022290082	0.000230959	0.000250192
GH25	0.501253291	2.042143037	0.012496974	0.013489609
GH70	0.227152401	2.082230342	0.000145118	0.000204692
GH101	0.500539565	2.117667389	0.000252563	0.000291636
GH8	0.443469642	2.120941767	0.001096228	0.001220736
GH126	0.38841601	2.136288054	0.000196369	0.000244662
GH103	0.469412907	2.151475823	0.000497387	0.000592038
GH110	0.489863429	2.155399086	0.005411129	0.005193909
GH10	0.432020755	2.160103773	0.002711299	0.002805208
GH124	0.418654144	2.192950277	0.00048995	0.000540602
GH59	0.219462771	2.194627705	0.000275659	0.000318506
GH19	0.383511942	2.220332293	3.62E-05	4.14E-05
GH14	0.265100933	2.243161739	5.44E-05	6.63E-05
GH87	0.16834734	2.314775921	8.19E-05	0.000114243
GH62	0.382379993	2.336766625	9.19E-05	0.000105744
GH74	0.363354037	2.351114355	0.005563735	0.006131377
GH61	0.215813739	2.373951128	1.64E-05	2.29E-05
GH81	0.152960259	2.403661213	2.24E-05	3.58E-05
GH85	0.353222358	2.428403712	0.000204817	0.000233229
GH68	0.200695725	2.452947745	7.61E-05	0.000105597
GH130	0.337163148	2.472529749	0.016543869	0.016336056
GH6	0.321463237	2.525782578	2.06E-05	2.48E-05
GH52	0.152960259	2.804271416	1.68E-05	2.68E-05
GH119	0.152960259	3.365125699	5.60E-06	8.94E-06
GH128	0.137276751	3.775110662	6.76E-06	1.03E-05
GH45	0.137276751	5.033480883	6.76E-06	1.03E-05
GH12	0.127873096	7.033020278	8.40E-06	1.20E-05
GH17	0.107724968	11.84974646	1.16E-05	1.56E-05

Table S13. Genes significantly differentially regulated (>1.2 fold change and q<5%) in *B. thetaiotaomicron* mono-associated Fut2- versus Fut2+ mice fed a PD diet.

Genes upregulated in Fuc-			
Gene ID	**Annotation**	**Fold Change**	**q-value(%)**
BT0026	putative transposase	1.46	2.05
BT0027	putative transposase	1.37	2.22
BT0057	hypothetical protein	1.2	2.16
BT0059	conserved hypothetical protein	1.24	3.74
BT0061	putative tyrosine-protein kinase ptk	1.31	1.65
BT0072	putative ABC transporter, ATP-binding protein	1.26	2.22
BT0073	putative ABC transporter, ATP-binding protein	1.31	1.49
BT0074	Peptidase S24 and S26, C-terminal	1.4	0
BT0123	NADH-ubiquinone oxidoreductase subunit	1.34	2.22
BT0130	putative oxidoreductase	1.21	2.22
BT0163	putative outer membrane protein	1.35	2.22
BT0164	putative outer membrane protein, alpha-2-macroglobulin-like	1.38	2.05
BT0260	acyltransferase family protein	1.34	2.16
BT0284	putative peptidoglycan binding protein (LPXTG motif)	1.45	3.53
BT0297	putative outer membrane lipoprotein silC precursor	1.4	1.65
BT0298	cation efflux system protein (outer membrane protein)	1.3	3.53
BT0299	cation efflux system (AcrB/AcrD/AcrF family)	1.27	2.22
BT0300	cation efflux system (AcrB/AcrD/AcrF family)	1.3	0
BT0301	ATP-binding transport protein natA (Na+ ABC transporter)	1.39	3.28
BT0317	SusC homolog	1.29	3.28
BT0318	SusD homolog	1.36	3.53
BT0319	conserved hypothetical protein	1.33	2.22
BT0346	ribose 5-phosphate isomerase B	1.25	3.28
BT0433	putative xylose repressor	1.23	2.22

BT0434	Pyridine nucleotide-disulphide o	1.47	1.49
BT0435	Twin-arginine translocation pathway signal	1.56	2.22
BT0436	arabinose-proton symporter	1.58	2.22
BT0437	N-acylglucosamine 2-epimerase	1.83	4.24
BT0439	SusC homolog	1.83	2.22
BT0440	SusD homolog	1.73	4.16
BT0441	putative chitobiase	1.66	4.69
BT0442	glycerophosphoryl diester phosphodiesterase	1.62	5.69
BT0444	hypothetical protein	1.51	2.22
BT0454	arabinose-proton symporter (Arabinose transporter)	1.54	2.63
BT0542	tRNA/rRNA methyltransferase, SpoU	1.23	3.28
BT0558	mannose-1-phosphate guanylyltransferase	1.22	4.71
BT0562	putative ABC transporter ATP-binding protein	1.22	2.22
BT0623	putative UDP-glucose 4-epimerase	1.22	4.71
BT0659	conserved hypothetical protein	1.51	2.22
BT0669	putative cation efflux system protein	1.64	0
BT0671	outer membrane protein TolC, putative	1.46	2.22
BT0672	drug efflux protein	1.34	2.22
BT0673	NADP(H) oxidoreductase	1.34	1.49
BT0693	putative ABC transport system, membrane protein...	1.23	4.24
BT0726	conserved hypothetical protein	1.36	2.05
BT0764	hypothetical protein	1.31	1.49
BT0765	putative protease	1.4	0
BT0780	acetyltransferase	1.31	2.22
BT0781	conserved hypothetical protein	1.32	2.22
BT0785	glutamine synthetase I	1.22	3.53
BT0881	conserved hypothetical protein	1.42	2.63
BT1078	putative transcriptional regulator	1.26	4.24

BT1088	conserved hypothetical protein	1.25	4.16
BT1099	putative arginase	1.23	2.22
BT1100	alpha-glucan phosphorylase , GT_35	1.34	4.24
BT1102	6-phosphofructokinase	1.3	4.16
BT1105	phosphoglycerate mutase 1	1.22	3.28
BT1108	Multiple antibiotic resistance (MarC)-related proteins	1.34	2.22
BT1109	ferritin A	1.31	2.22
BT1170	hypothetical protein	1.51	0
BT1200	conserved hypothetical protein	1.4	3.28
BT1247	Peptidase M14, carboxypeptidase	1.3	2.05
BT1329	putative thiol peroxidase	1.22	4.71
BT1337	putative aminopeptidase C , CPS 4	1.37	3.74
BT1366	conserved hypothetical protein	1.27	3.28
BT1383	oxidoreductase, aldo/keto reductase	1.2	2.22
BT1411	methylated-DNA--protein-cysteine methyltransferase	1.28	2.22
BT1425	conserved hypothetical protein	1.23	3.53
BT1501	major outer membrane protein OmpA	1.6	3.28
BT1502	conserved hypothetical protein	1.63	2.22
BT1507	conserved hypothetical protein	2.25	2.22
BT1512	conserved hypothetical protein, putative surface protein	1.27	4.24
BT1554	alanine dehydrogenase	1.53	2.05
BT1556	conserved hypothetical protein	1.37	4.16
BT1557	conserved hypothetical protein	1.53	1.65
BT1558	conserved hypothetical protein	1.49	0
BT1559	RNA polymerase ECF-type sigma factor	1.36	1.65
BT1590	hypothetical protein	1.52	1.65
BT1591	conserved hypothetical protein	1.56	0
BT1624	putative secreted sulfatase	1.21	3.74

BT1627	beta-hexosaminidase precursor , GH_20	1.28	2.22
BT1661	two-component system sensor histidine kinase	1.22	2.22
BT1720	phosphoenolpyruvate phosphomutase precursor , CPS 6	1.33	4.71
BT1777	glycoside hydrolase family 95	1.21	1.65
BT1784	conserved hypothetical protein	1.39	2.22
BT1800	putative two-component system sensor histidine kinase	1.34	2.16
BT1801	two-component system sensor histidine kinase	1.22	4.71
BT1802	two-component system sensor histidine kinase	1.28	3.28
BT1810	GAF domain-containing protein, involved in signal transduction	1.43	0
BT1838	putative alanyl dipeptidyl peptidase	1.39	4.16
BT1839	conserved hypothetical protein	1.24	2.22
BT1924	putative metal-dependent hydrolase	1.3	1.65
BT1932	putative transposase	1.25	2.63
BT1980	transposase	1.3	2.22
BT1988	conserved hypothetical protein	1.28	1.65
BT1994	conserved hypothetical protein	1.62	2.63
BT1995	hypothetical protein	1.6	3.53
BT2030	conserved hypothetical protein	1.22	3.53
BT2087	conserved hypothetical protein	1.34	4.16
BT2097	Six-hairpin glycosidase	1.39	0
BT2117	outer membrane protein, putative	1.63	2.22
BT2118	transporter, AcrB/D/F family	1.6	4.16
BT2119	transmembrane protein precursor, possibly involved in transport	1.66	2.22
BT2170	conserved hypothetical protein	1.55	2.22
BT2235	Ribbon-helix-helix	1.25	4.71
BT2240	TPR-domain containing protein	1.22	1.65
BT2297	putative reverse transcriptase	1.24	4.71
BT2374	conserved hypothetical protein	1.24	2.22

BT2385	conserved hypothetical protein	1.26	4.16
BT2386	AsnC family transcriptional regulator	1.23	4.71
BT2392	NHL repeat-containing protein	2.86	3.53
BT2393	SusC homolog	3.09	3.28
BT2394	SusD homolog	3.77	2.22
BT2395	hypothetical protein	3.66	2.22
BT2485	major outer membrane protein OmpA	1.21	4.69
BT2486	Collagen triple helix repeat	1.61	1.65
BT2522	Xaa-Pro aminopeptidase	1.22	4.71
BT2550	beta-glucanase precursor , GH_13	1.23	3.28
BT2559	SusD homolog	1.28	4.71
BT2628	two-component system sensor histidine kinase/response regulator, hybrid (one-component system)	1.34	2.16
BT2629	putative alpha-1,2-mannosidase , GH_92	1.51	0
BT2630	conserved hypothetical protein with endonuclease/exonuclease/phosphatase family domain	1.22	2.22
BT2691	methenyltetrahydrofolate cyclohydrolase	1.47	4.24
BT2694	putative urocanate hydratase	1.4	3.53
BT2695	conserved hypothetical protein	1.28	2.63
BT2750	putative protein-tyrosine-phosphatase	1.29	3.74
BT2771	putative serine/threonine-protein kinase pknB	1.27	2.63
BT2784	hypothetical protein	1.65	2.22
BT2927	putative cell wall-associated protein precursor	1.28	3.74
BT2975	putative nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase	1.28	1.65
BT3004	SWIM Zn-finger domain protein	1.21	2.22
BT3057	N-acetylgalactosamine-6-sulfatase precursor	1.41	3.53
BT3059	Quinonprotein alcohol dehydrogenase	2.89	0
BT3060	EGF-like region	1.93	2.05
BT3061	putative transmembrane protein	2.3	0

BT3086	alpha-glucosidase II , GH_31	3.2	0
BT3087	cycloisomaltooligosaccharide glucanotransferase , GH_66	2.24	0
BT3088	conserved hypothetical protein	2.56	0
BT3089	SusD homolog	2.03	0
BT3090	SusC homolog	2.62	0
BT3114	beta-galactosidase , GH_2	1.2	3.74
BT3115	putative proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehydraogenase	1.77	3.28
BT3125	hypothetical protein	1.41	2.22
BT3169	alpha-xylosidase , GH_31	1.67	4.24
BT3170	Intradiol ring-cleavage dioxygen	1.26	4.24
BT3196	transcriptional regulator	1.23	4.24
BT3206	hypothetical protein	1.28	2.22
BT3232	gluconate 5-dehydrogenase	1.24	4.71
BT3233	Galactose mutarotase-like	1.35	2.22
BT3234	conserved hypothetical protein	1.48	0
BT3235	conserved hypothetical protein	3.23	4.69
BT3236	conserved hypothetical protein	3.28	4.71
BT3237	Peptidase M, neutral zinc metallopeptidases, zinc-binding site	3.1	4.69
BT3238	SusD homolog	3.13	5.69
BT3239	SusC homolog	2.82	4.71
BT3294	putative alpha-glucosidase , GH_97	1.24	2.22
BT3411	pyrophosphate-energized vacuolar membrane proton pump	1.46	3.74
BT3432	conserved hypothetical protein	1.21	3.28
BT3467	putatuve glycosylhydrolase , GH_43	1.26	1.49
BT3508	conserved hypothetical protein	1.29	4.69
BT3509	Calreticulin/calnexin	1.29	2.22
BT3510	hypothetical protein	1.21	4.24
BT3527	alpha-1,2-mannosidase , GH_92	1.24	3.74

BT3528	Uncharacterised conserved protein UCP28846	1.25	3.74
BT3529	aldose 1-epimerase precursor	1.26	3.74
BT3572	hypothetical protein	1.32	2.16
BT3673	TonB	1.61	3.28
BT3721	conserved hypothetical protein	1.3	0
BT3784	putative alpha-1,2-mannosidase , GH_92	1.35	2.22
BT3786	two-component system sensor histidine kinase/response regulator, hybrid (one-component system)	1.22	2.05
BT3854	SusC homolog	1.32	2.63
BT3855	SusD homolog	1.29	4.24
BT3857	Flavodoxin	1.24	2.22
BT3874	conserved hypothetical protein	1.73	0
BT3886	conserved hypothetical protein	1.38	0
BT3896	TonB	1.47	0
BT3897	putative thiol:disulfide interchange protein DsbE	1.23	3.74
BT3993	RNA polymerase ECF-type sigma factor	1.29	0
BT3994	putative alpha-1,2-mannosidase , GH_92	1.32	3.74
BT4034	hypothetical protein	1.25	4.24
BT4035	Helix-turn-helix type 3	1.3	4.16
BT4038	SusD homolog	1.43	1.65
BT4039	SusC homolog	1.38	2.16
BT4040	putative galactose oxidase precursor	1.39	2.22
BT4137	two-component system sensor histidine kinase/response regulator, hybrid (one-component system)	1.21	2.22
BT4199	putative transcriptional regulator	1.28	4.69
BT4200	putative transcriptional regulator	1.33	4.24
BT4201	putative transcriptional regulator	1.23	3.74
BT4202	hypothetical protein	1.51	3.74
BT4221	conserved hypothetical protein	1.27	1.65

BT4241	beta-galactosidase , GH_2	1.44	3.28
BT4242	putative transporter	1.37	3.74
BT4243	Hexosaminidase, GH_109	1.49	2.05
BT4244	Coagulation factor 5/8 type, C-terminal	2.44	0
BT4245	Coagulation factor 5/8 type, C-terminal	2.08	1.49
BT4246	SusD homolog	1.98	2.22
BT4247	SusC homolog	1.8	1.65
BT4248	putative anti-sigma factor	2.13	4.24
BT4249	conserved hypothetical protein	1.85	1.49
BT4287	hypothetical protein	1.58	3.53
BT4304	glycoside transferase family 4	1.24	2.22
BT4305	putative alpha-amylase , GH_57	1.21	4.16
BT4311	glucose/galactose transporter	1.35	4.24
BT4337	beta-hexosaminidase precursor , GH_20	1.38	2.22
BT4343	putative DNA helicase	1.27	2.22
BT4359	alpha-N-acetylglucosaminidase precursor , GH_89	1.31	2.22
BT4384	conserved hypothetical protein	1.61	0
BT4408	conserved hypothetical protein	1.54	0
BT4474	Gonadotropin, beta chain	1.26	4.16
BT4484	MgtC/SapB transporter	1.26	3.28
BT4575	Peptidase M, neutral zinc metallopeptidases, zinc-binding site	1.3	2.22
BT4576	hypothetical protein	1.41	4.24
BT4652	Oligosaccharide lyase	1.22	4.71
BT4656	N-acetylglucosamine-6-sulfatase precursor	1.27	3.74
BT4718	putative aquaporin	1.45	0
Genes upregulated in Fuc+			
Gene ID	**Annotation**	**Fold Change**	**q-value(%)**

BT0122	3-oxoacyl-[acyl-carrier-protein] synthase III	0.66	2.24
BT0153	conserved hypothetical protein	0.7	3.74
BT0158	Na(+)/H(+) antiporter	0.69	2.58
BT0159	Rubrerythrin	0.66	3.53
BT0178	conserved hypothetical protein	0.71	2.24
BT0179	SsrA-binding protein	0.64	2.24
BT0180	5-methyltetrahydrofolate-homocysteine methyltransferase	0.63	2.24
BT0181	putative NADH dehydrogenase/NAD(P)H nitroreductase	0.68	2.63
BT0189	conserved hypothetical protein, putative anti-sigma factor	0.75	2.58
BT0206	SusC homolog	0.37	2.58
BT0207	SusD homolog	0.39	2.58
BT0208	hypothetical protein	0.35	2.58
BT0209	hypothetical protein	0.42	3.74
BT0210	leucine-rich repeat protein, function unknown	0.37	5.69
BT0211	Leucine-rich repeat	0.45	6.57
BT0236	Beta tubulin	0.78	2.58
BT0246	putative integral membrane protein, with calcineurin-like phosphoesterase domain	0.76	2.22
BT0247	conserved hypothetical protein	0.73	2.22
BT0248	RNA polymerase ECF-type sigma factor	0.75	2.24
BT0307	phosphofructokinase	0.81	2.58
BT0308	glycoside hydrolase family 25	0.57	4.69
BT0376	putative transcriptional regulator , CPS 1	0.7	3.53
BT0377	conserved hypothetical protein , CPS 1	0.72	3.74
BT0377	conserved hypothetical protein , CPS 1	0.73	4.24
BT0379	UDP-glucose 6-dehydrogenase , CPS 1	0.78	4.71
BT0381	capsular polysaccharide biosynthesis protein capD , CPS 1	0.71	4.69
BT0382	capsular polysaccharide biosynthesis protein Cps4K , CPS 1	0.79	4.24
BT0412	putative Na+/sulfate symporter	0.81	4.24

BT0413	putative adenylylsulfate kinase	0.72	3.31
BT0415	sulfate adenylyltransferase subunit 1/adenylylsulfate kinase	0.77	3.31
BT0416	possible sulfotransferase	0.8	2.58
BT0417	conserved hypothetical protein	0.78	3.53
BT0421	tetratricopeptide repeat (TPR) family protein	0.79	2.24
BT0423	translation initiation factor IF-3	0.78	2.24
BT0424	50S ribosomal protein L35	0.7	3.74
BT0425	50S ribosomal protein L20	0.72	3.31
BT0426	4Fe-4S ferredoxin, iron-sulfur binding	0.75	3.53
BT0427	xanthine phosphoribosyltransferase	0.62	3.74
BT0431	putative aminodeoxychorismate lyase	0.68	2.63
BT0432	putative endonuclease BB0411	0.8	4.71
BT0502	TonB-dependent outer membrane receptor	0.5	4.69
BT0503	conserved hypothetical protein	0.66	4.16
BT0504	TonB-dependent outer membrane receptor	0.65	3.74
BT0505	Transcription factor, MADS-box	0.69	4.24
BT0521	putative acetyl transferase	0.62	0
BT0522	putative capsule-related protein	0.53	2.02
BT0523	putative glycosyltransferase	0.69	3.53
BT0539	putative Na+/sulphate transporter	0.83	4.16
BT0556	carbamoyl phosphate synthetase III (glutamine-hydrolyzing)	0.79	3.31
BT0573	lipoprotein protein, putative	0.79	2.22
BT0578	excinuclease ABC subunit A	0.77	2.58
BT0579	putative transcription regulator	0.78	3.74
BT0589	putative inner membrane protein translocase com...	0.71	2.24
BT0590	CTP synthase (UTP-ammonia ligase)	0.73	0
BT0603	conserved hypothetical protein , CPS 3	0.73	4.71
BT0616	Positive regulator of sigma(E),	0.65	4.16

BT0617	Na+-transporting NADH:ubiquinone oxidoreductase, Electron transport complex protein rnfB	0.58	0
BT0618	Na+-transporting NADH:ubiquinone oxidoreductase, Electron transport complex protein rnfC	0.58	2.02
BT0619	Na+-transporting NADH:ubiquinone oxidoreductase, Electron transport complex protein rnfD	0.61	2.05
BT0620	Na+-transporting NADH:ubiquinone oxidoreductase, Electron transport complex protein rnfG	0.6	1.49
BT0621	Na+-transporting NADH:ubiquinone oxidoreductase, Electron transport complex protein rnfE	0.56	2.05
BT0622	Na+-transporting NADH:ubiquinone oxidoreductase, Electron transport complex protein rnfA	0.63	2.58
BT0626	phenylalanyl-tRNA synthetase beta chain	0.66	2.24
BT0627	conserved hypothetical protein, with a conserved domain of unknown function	0.69	2.05
BT0637	DNA recombination protein rmuC homolog	0.81	4.24
BT0674	carboxynorspermidine decarboxylase	0.72	2.29
BT0675	N-acetylglucosamine-6-phosphate deacetylase	0.65	2.58
BT0676	N-acetylglucosamine-6-phosphate deacetylase	0.65	3.74
BT0684	putative long-chain-fatty-acid--CoA ligase	0.62	4.24
BT0698	3-methyl-2-oxobutanoate hydroxymethyltransferase	0.53	2.58
BT0699	putative sugar transporter	0.63	4.16
BT0703	conserved hypothetical protein	0.7	2.05
BT0743	penicillin-binding protein 1A (PBP-1a) , GT_51	0.78	4.69
BT0744	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase	0.63	2.22
BT0745	3-deoxy-manno-octulosonate cytidylyltransferase	0.63	2.63
BT0746	putative zinc protease	0.61	2.22
BT0752	putative RNA polymerase ECF-type sigma factor	0.73	1.49
BT0767	putative para-aminobenzoate synthase component I	0.73	4.24
BT0768	putative para-aminobenzoate synthase component I	0.74	2.02
BT0806	isoleucyl-tRNA synthetase	0.74	3.53

BT0809	putative lipoprotein	0.73	2.63
BT0810	conserved hypothetical protein	0.76	2.22
BT0821	putative permease	0.76	2.02
BT0822	putative metallo-beta-lactamase superfamily hydrolase	0.69	2.24
BT0829	UDP-glucose 6-dehydrogenase	0.71	2.24
BT0834	putative permease	0.56	2.24
BT0835	tRNA-guanine transglycosylase	0.72	2.58
BT0836	ATP-dependent protease	0.77	4.69
BT0837	ATP-dependent protease	0.75	3.53
BT0870	8-amino-7-oxononanoate synthase	0.72	3.31
BT0873	putative sulfatase	0.61	2.58
BT0883	conserved hypothetical protein	0.75	3.74
BT0905	BatC, conserved hypothetical protein	0.72	2.63
BT0906	BatB, conserved hypothetical protein	0.72	3.53
BT0907	BatA (Bacteroides aerotolerance operon)	0.72	2.58
BT0908	putative conserved membrane exported protein	0.74	2.24
BT0920	putative O-sialoglycoprotein endopeptidase	0.78	2.58
BT0924	S-layer domain	0.72	4.69
BT0925	ABC transporter, ATP-binding protein	0.7	3.74
BT0929	prolyl-tRNA synthetase	0.77	4.24
BT0973	conserved hypothetical protein	0.57	4.69
BT0974	conserved hypothetical protein, putative integral membrane protein	0.48	3.74
BT0975	conserved hypothetical protein, putative integral membrane protein	0.56	4.16
BT0999	putative acetyltransferase	0.69	3.31
BT1008	xylanase	0.48	4.16
BT1054	ATP-dependent helicase	0.77	2.22
BT1055	pyruvate formate-lyase activating enzyme	0.72	2.29

BT1084	conserved hypothetical protein	0.81	3.53
BT1158	Na+-translocating NADH-quinone reductase subunit	0.79	3.31
BT1159	Na+-translocating NADH-quinone reductase subunit	0.79	3.53
BT1160	Na+-translocating NADH-quinone reductase subunit	0.8	3.53
BT1162	putative outer membrane protein	0.75	2.58
BT1165	putative transmembrane surface-related protein ...	0.83	2.58
BT1166	glycoside transferase family 2	0.77	4.24
BT1177	putative polysaccharide biosynthesis protein	0.75	2.24
BT1204	Carboxypeptidase regulatory region	0.74	2.29
BT1205	putative ATPase, AAA family	0.71	2.22
BT1206	conserved hypothetical protein	0.56	3.31
BT1207	glycerate dehydrogenase (NADH-dependent)	0.67	4.16
BT1208	Cellular Component: integral to membrane (GO:1621)	0.63	3.31
BT1229	putative antiporter	0.72	3.31
BT1270	putative Na+/H+ antiporter	0.83	3.31
BT1271	30S ribosomal protein S16	0.72	3.31
BT1273	L-fucose isomerase	0.63	3.53
BT1274	L-fuculose-1-phosphate aldolase	0.64	3.74
BT1275	L-fuculose kinase	0.64	2.58
BT1276	mutarotase	0.62	2.24
BT1277	L-fucose permease	0.62	2.58
BT1288	spermidine/putrescine ABC transporter	0.64	4.24
BT1289	putrescine transport system permease protein potI	0.6	4.69
BT1307	hypothetical protein	0.65	4.16
BT1326	TPR-domain containing protein	0.67	2.05
BT1327	putative alkaline phosphatase	0.73	3.31
BT1359	Tetratricopeptide repeat family protein	0.76	3.31
BT1360	tRNA/rRNA methyltransferase	0.72	2.24

BT1362	flavoprotein	0.76	2.22
BT1363	DNA Pol III Epsilon Chain	0.81	3.74
BT1367	hydrolase, metal-dependent	0.75	4.69
BT1376	putative ATP-binding protein involved in cell division	0.78	4.24
BT1445	putative biotin synthesis protein bioC	0.66	4.24
BT1446	dethiobiotin synthetase	0.69	3.31
BT1472	glycoside transferase family 2	0.73	2.58
BT1474	ribosomal protein S6 modification protein-related protein	0.67	3.31
BT1475	ABC transporter, permease protein	0.74	2.63
BT1478	putative histidinol-phosphatase	0.75	3.31
BT1479	ABC transporter ATP-binding protein	0.81	2.24
BT1521	putative membrane protein	0.74	3.53
BT1522	putative aureobasidin A resistance protein	0.57	2.24
BT1523	CDP-diacylglycerol-inositol 3-phosphatidyltransferase	0.57	2.29
BT1524	hypothetical protein	0.53	2.22
BT1525	phosphatidylglycerophosphatase A	0.58	2.22
BT1526	myo-inositol-1-phosphate synthase	0.79	2.02
BT1551	Peptidase M1A and M12B	0.51	2.58
BT1552	SusC homolog	0.53	3.74
BT1553	SusD homolog	0.43	3.74
BT1564	putative GTP-cyclohydrolase protein	0.65	4.24
BT1599	BexA, membrane protein	0.71	2.29
BT1600	BexA, membrane proein	0.7	2.02
BT1601	putative signal recognition protein	0.76	2.24
BT1608	capsule biosynthesis protein capA	0.81	4.24
BT1617	RNA polymerase ECF-type sigma factor	0.76	2.22
BT1618	putative anti-sigma factor	0.61	3.74
BT1619	SusC homolog	0.51	4.71

BT1620	SusD homolog	0.49	4.69
BT1621	beta-hexosaminidase precursor , GH_20	0.51	6.57
BT1622	N-acetylgalactosamine-6-sulfatase precursor	0.58	6.57
BT1662	putative molybdenum transport ATP-binding protein	0.79	2.02
BT1669	phenylalanyl-tRNA synthetase alpha chain	0.66	2.02
BT1670	putative transmembrane transport protein	0.62	2.58
BT1671	endonuclease III	0.73	2.29
BT1673	thiamine biosynthesis protein, putative	0.75	4.71
BT1696	oxaloacetate decarboxylase beta chain	0.8	3.31
BT1697	pyruvate carboxylase subunit B	0.79	4.24
BT1729	peptide chain release factor 3 (RF-3)	0.63	2.24
BT1730	putative dTDP-4-dehydrorhamnose reductase	0.63	3.74
BT1731	conserved hypothetical protein	0.76	2.63
BT1736	chromate transport protein	0.82	3.74
BT1805	electron transfer flavoprotein alpha-subunit	0.81	2.58
BT1851	TPR-repeat-containing protein	0.79	2.24
BT1855	putative methyl transferase	0.76	4.16
BT1882	putative thiamine-monophosphate kinase	0.8	2.63
BT1883	putative alpha-1,6-mannanase , GH_73	0.83	2.63
BT1934	Cyclin-like	0.76	3.31
BT1936	hypothetical protein	0.82	2.22
BT1949	conserved hypothetical protein	0.63	3.53
BT2001	membrane-associated zinc metalloprotease	0.77	4.24
BT2004	RimM protein, required for 16S rRNA processing	0.77	4.69
BT2013	putative phosphohydrolases	0.78	4.24
BT2014	1,4-dihydroxy-2-naphthoate octaprenyltransferase	0.81	3.74
BT2035	putative ABC transporter ATP-binding protein	0.74	3.74
BT2046	putative cardiolipin synthetase	0.74	4.69

BT2056	hydrolase, putative	0.81	2.22
BT2069	GCN5-related N-acetyltransferase	0.64	3.31
BT2092	putative membrane protein	0.69	4.69
BT2133	conserved hypothetical protein	0.65	2.24
BT2137	transposase	0.75	2.22
BT2140	putative sodium-dependent transporter	0.77	4.24
BT2142	Mammalian cell entry related	0.8	2.24
BT2151	glycoside transferase family 2	0.73	4.24
BT2152	putative acetyltransferase	0.73	3.53
BT2153	putative Fe-S oxidoreductases	0.72	4.16
BT2160	putative regulatory protein	0.69	4.69
BT2161	50S ribosomal protein L9	0.67	4.71
BT2163	30S ribosomal protein S6	0.8	4.24
BT2177	putative membrane protein	0.71	4.71
BT2233	conserved hypothetical protein	0.8	3.53
BT2248	putative integral membrane protein	0.72	4.69
BT2254	putative pectate lyase , PL_10	0.82	3.53
BT2271	haloacid dehalogenase-like hydrolase	0.79	4.69
BT2317	conserved hypothetical protein	0.83	3.74
BT2328	conserved hypothetical protein	0.7	4.69
BT2390	putative TonB-dependent transmembrane receptor	0.73	4.71
BT2391	two-component system sensor histidine kinase/response regulator, hybrid (one component system)	0.59	2.58
BT2397	similar to Thiamin pyrophosphokinase, catalytic domain	0.83	2.58
BT2409	putative TonB-dependent outer membrane protein	0.72	2.24
BT2410	putative acetyltransferase	0.78	2.24
BT2411	conserved hypothetical protein	0.6	4.16
BT2413	homoserine O-succinyltransferase	0.74	3.53
BT2415	aspartate aminotransferase	0.83	4.69

BT2416	GTP cyclohydrolase II	0.74	2.24
BT2458	putative pyridine nucleotide-disulphide oxidoreductase	0.77	4.71
BT2460	SusD homolog	0.75	4.71
BT2497	membrane fusion efflux protein	0.81	3.74
BT2541	putative calcium-transporting ATPase	0.78	4.69
BT2542	putative haloacid dehalogenase-like hydrolase	0.65	2.22
BT2543	riboflavin biosynthesis protein ribF, putative riboflavin kinase	0.68	2.05
BT2563	polyribonucleotide nucleotidyltransferase	0.65	2.24
BT2591	hypothetical protein	0.81	4.24
BT2681	alginate O-acetylation protein	0.8	4.24
BT2682	putative periplasmic protein	0.75	2.58
BT2688	outer membrane efflux protein	0.77	2.63
BT2689	putative TetR transcriptional regulator	0.78	3.53
BT2702	30S ribosomal protein S4	0.76	3.53
BT2703	30S ribosomal protein S11	0.79	4.24
BT2706	methionine aminopeptidase	0.71	4.69
BT2719	50S ribosomal protein L29	0.81	2.58
BT2721	30S ribosomal protein S3	0.8	2.63
BT2722	50S ribosomal protein L22	0.83	3.53
BT2727	50S ribosomal protein L3	0.83	2.58
BT2729	elongation factor G	0.77	2.63
BT2733	DNA-directed RNA polymerase beta chain	0.72	4.71
BT2736	ribosomal protein L10	0.79	4.71
BT2737	50S ribosomal protein L1	0.77	2.58
BT2738	50S ribosomal protein L11	0.78	2.29
BT2739	transcription anti-termination protein	0.78	2.63
BT2791	uracil phosphoribosyltransferase	0.77	2.24
BT2803	ribokinase	0.44	2.02

BT2804	ribokinase	0.53	4.69
BT2823	conserved hypothetical protein	0.75	4.71
BT2826	two-component system sensor histidine kinase/response regulator, hybrid (one component system)	0.61	4.69
BT2833	similar to endonuclease/exonuclease/phosphatase	0.69	2.02
BT2834	peptidyl-dipeptidase	0.75	3.74
BT2835	protein-export membrane protein SecD/SecF	0.82	3.74
BT2838	putative lipoprotein releasing system transmembrane permease	0.61	3.31
BT2937	putative glycosyltransferase	0.79	4.69
BT2938	glycoside transferase family 4	0.77	3.74
BT2976	FKBP-type peptidyl-prolyl cis-trans isomerase, outer membrane protein precursor	0.75	0
BT3070	Smf protein DNA processing chain A	0.68	4.24
BT3071	similar to thioesterase family protein	0.75	2.63
BT3074	Phosphoesterase, PA-phosphatase	0.76	4.69
BT3119	chloramphenicol acetyltransferase	0.67	3.74
BT3121	DNA mismatch repair protein mutS	0.74	2.58
BT3127	putative transmembrane protein	0.61	2.22
BT3128	putative xanthosine triphosphate pyrophosphatase	0.65	3.31
BT3209	similar to SAM dependent methyltransferase	0.76	2.22
BT3210	cell division protein FtsX	0.69	2.58
BT3211	conserved hypothetical protein	0.69	2.24
BT3212	putative bacitracin resistance protein	0.68	2.58
BT3213	tRNA pseudouridine synthase B	0.69	3.53
BT3214	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	0.77	4.16
BT3215	conserved hypothetical protein	0.72	4.69
BT3216	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine	0.68	2.05
BT3226	uroporphyrinogen-III synthase HemD, putative .	0.65	2.05
BT3227	putative ribonuclease P protein component	0.55	2.58

BT3228	conserved hypothetical protein	0.55	3.31
BT3247	Tetratricopeptide-like helical	0.79	4.71
BT3309	transcriptional regulator	0.7	4.71
BT3317	conserved hypothetical protein	0.59	2.02
BT3318	signal peptidase I	0.75	3.31
BT3325	conserved hypothetical protein	0.78	3.53
BT3352	haloacid dehalogenase-like hydrolase	0.83	4.24
BT3358	3-oxoacyl-[acyl-carrier-protein] synthase II	0.77	3.74
BT3366	glycoside transferase family 2	0.8	4.16
BT3367	glycoside transferase family 4	0.72	4.69
BT3368	glycoside transferase family 4	0.74	4.24
BT3372	glycoside transferase family 2	0.56	3.53
BT3374	putative carbamoyl-phosphate-synthetase	0.72	4.24
BT3375	aspartate aminotransferase	0.7	2.58
BT3376	nucleotide sugar transaminase	0.78	4.69
BT3379	glycoside transferase family 2	0.73	4.71
BT3380	putative membrane protein	0.78	2.63
BT3465	two-component system sensor histidine kinase/response regulator, hybrid (one-component system)	0.77	2.22
BT3473	hypothetical protein	0.72	4.24
BT3476	Cell surface receptor IPT/TIG	0.83	4.69
BT3478	integrase	0.6	2.58
BT3516	arabinan endo-1,5-alpha-L-arabinosidase A precursor , GH_43	0.8	2.24
BT3576	putative ribokinase	0.78	2.58
BT3577	putative protease	0.66	2.22
BT3578	conserved hypothetical protein	0.66	0
BT3598	beta-hexosaminidase precursor , GH_20	0.78	2.63
BT3606	sugar-proton symporter	0.78	4.71
BT3611	glycyl-tRNA synthetase	0.8	2.02

BT3612	putative FKBP-type peptidyl-prolyl cis-trans isomerase fkpA	0.76	3.74
BT3620	AmpG protein, beta-lactamase induction signal transducer	0.79	4.24
BT3688	putative acetyltransferase	0.68	3.74
BT3690	putative membrane protein	0.73	3.31
BT3691	conserved hypothetical protein, putative membrane protein	0.68	2.58
BT3692	phosphate acetyltransferase	0.68	4.16
BT3693	acetate kinase	0.75	4.24
BT3712	ribosomal large subunit pseudouridine synthase D	0.8	4.69
BT3715	conserved hypothetical protein	0.79	2.58
BT3725	putative outer membrane protein	0.78	3.74
BT3726	undecaprenyl pyrophosphate synthetase	0.79	4.69
BT3727	conserved hypothetical protein	0.75	3.74
BT3730	putative regulatory protein	0.75	2.05
BT3732	conserved hypothetical protein	0.7	2.22
BT3733	argininosuccinate lyase	0.72	2.58
BT3740	hypothetical protein	0.63	2.63
BT3742	conserved hypothetical protein	0.71	2.63
BT3743	conserved hypothetical protein	0.47	2.58
BT3814	rod shape-determining protein	0.58	2.58
BT3815	putative membrane protein	0.54	2.22
BT3816	penicillin-binding protein 2 (PBP-2)	0.66	3.31
BT3817	rod shape-determining protein rodA	0.6	2.58
BT3818	conserved hypothetical protein	0.67	0
BT3820	putative DNA polymerase III, delta subunit	0.78	3.31
BT3841	FKBP-type peptidyl-prolyl cis-transisomerase (trigger factor)	0.57	3.53
BT3842	ATP-dependent Clp protease proteolytic subunit 2	0.79	2.02
BT3843	ATP-dependent Clp protease ATP-binding subunit	0.79	0
BT3849	conserved hypothetical protein	0.79	2.58

BT3850	conserved hypothetical protein	0.8	2.58
BT3851	DNA mismatch repair protein mutL	0.82	4.16
BT3875	50S ribosomal protein L13	0.8	2.05
BT3876	30S ribosomal protein S9	0.78	3.53
BT3877	30S ribosomal protein S2 (BS1)	0.78	2.58
BT3878	elongation factor Ts (EF-Ts)	0.79	2.63
BT3883	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	0.81	2.24
BT3884	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	0.68	1.49
BT3924	ATP-dependent DNA helicase recG	0.73	2.24
BT3925	nucleoside diphosphate kinase	0.81	2.24
BT3926	putative peptidase	0.8	3.53
BT3928	conserved hypothetical protein	0.79	4.24
BT3938	ATP-dependent DNA helicase recQ	0.8	2.22
BT3944	putative chloride channel protein	0.76	4.24
BT3945	methionyl-tRNA formyltransferase	0.81	4.71
BT3967	putative two-component system sensor protein histidine kinase	0.76	4.69
BT3972	putative NTP pyrophosphohydrolase	0.64	2.29
BT3973	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	0.61	3.74
BT3979	putative methyltransferase	0.58	1.49
BT3980	conserved hypothetical protein	0.65	2.22
BT3982	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member	0.8	2.58
BT3995	alanyl-tRNA synthetase	0.65	2.24
BT4043	dimethyladenosine transferase	0.81	4.71
BT4044	putative dolichol-P-glucose synthetase	0.73	4.24
BT4080	putative cell surface protein	0.6	4.16
BT4081	SusC homolog	0.6	3.31
BT4082	SusD homolog	0.67	3.74
BT4083	hypothetical protein	0.55	3.74

BT4103	putative Sec-independent protein translocase	0.73	2.58
BT4104	DNA helicase	0.64	2.24
BT4112	putative Fibronectin	0.72	4.24
BT4114	SusC homolog	0.72	4.69
BT4187	exo-poly-alpha-D-galacturonosidase precursor , GH_28	0.82	4.69
BT4192	lipoic acid synthetase	0.77	0
BT4203	tRNA delta(2)-isopentenylpyrophosphate transferase	0.76	2.58
BT4207	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	0.82	2.58
BT4208	phosphohydrolase	0.53	2.24
BT4209	orotidine 5 -phosphate decarboxylase	0.63	2.29
BT4210	peptide chain release factor 1	0.72	3.31
BT4211	putative phosphoribosylformylglycinamidine cyclo-ligase	0.7	3.74
BT4218	phosphate starvation-inducible protein, PhoH	0.74	4.71
BT4238	putative permease	0.75	3.53
BT4257	putative histidinol-phosphatase	0.82	4.69
BT4308	pantoate--beta-alanine ligase	0.75	2.02
BT4315	HPr(Ser) phosphatase	0.69	2.58
BT4316	putative lipoprotein	0.75	2.29
BT4317	putative lipoprotein protein	0.75	2.24
BT4318	ATP-binding protein	0.78	2.24
BT4319	putative transmembrane protein	0.79	4.69
BT4320	putative zinc protease	0.78	3.74
BT4321	2-dehydro-3-deoxyphosphooctonate aldolase	0.78	3.53
BT4332	similar to 3'-5' exonuclease	0.81	2.22
BT4345	30S ribosomal protein S1	0.69	2.24
BT4353	valyl-tRNA synthetase	0.79	4.24
BT4363	putative alkaline phosphatase	0.77	2.22
BT4366	putative transcription regulator	0.78	4.69

BT4369	conserved hypothetical protein	0.71	2.24
BT4370	putative hemolysin	0.59	2.29
BT4371	peptidyl-prolyl cis-trans isomerase	0.79	2.58
BT4377	conserved hypothetical protein	0.59	0
BT4379	putative oxalate:formate antiporter	0.8	4.69
BT4387	adenylate kinase (ATP-AMP transphosphatase)	0.74	2.58
BT4388	GTP-binding protein	0.79	2.58
BT4389	conserved hypothetical protein	0.73	3.31
BT4390	B3/4	0.7	2.58
BT4391	putative metalloendopeptidase	0.78	4.24
BT4416	Cu2+ homeostasis protein CutC	0.73	2.24
BT4472	conserved hypothetical protein	0.73	3.31
BT4473	putative purine permease	0.78	3.31
BT4558	PP-loop	0.62	2.63
BT4559	conserved hypothetical protein	0.55	3.74
BT4560	thiamine biosynthesis lipoprotein apbE precursor	0.52	2.02
BT4561	conserved hypothetical protein, putative integral membrane protein	0.47	2.58
BT4562	conserved hypothetical protein	0.75	3.31
BT4563	conserved hypothetical protein	0.72	2.02
BT4564	glycoside transferase family 2	0.79	2.24
BT4565	putative transmembrane protein	0.77	3.31
BT4582	amidophosphoribosyltransferase precursor	0.66	4.16
BT4587	RNA-binding S4	0.68	2.58
BT4588	peptidyl-tRNA hydrolase	0.64	3.31
BT4593	YbbR-like	0.69	2.63
BT4594	putative dephospho-CoA kinase	0.58	2.58
BT4595	conserved hypothetical protein	0.74	4.69
BT4614	conserved hypothetical protein	0.81	4.71

BT4639	conserved hypothetical protein, putative membrane protein	0.83	3.74
BT4691	conserved hypothetical protein	0.78	4.69
BT4700	isochorismate synthase entC	0.81	3.53
BT4703	chloromuconate cycloisomerase	0.79	2.29
BT4704	O-succinylbenzoic acid--CoA ligase	0.67	2.58
BT4717	integral membrane protein, putative permease	0.74	4.24
BT4737	pyruvate formate-lyase activating enzyme	0.66	4.69

Table S14. Genes showing significantly different expression within PUL's in *B. thetaiotaomicron* mono-associated Fut2- versus Fut2+ mice fed PD diet. Relative expression for these genes in *B. thetaiotaomicron* mono-associated Fut2- and Fut2+ mice fed a standard diet are also shown.

		PD Diet		**SD Diet**	
Gene ID	**Gene Name**	**Fold Change**	**q-value(%)**	**Fold Change**	**q-value(%)**
BT0206	SusC homolog	0.37	2.58	0.93	32.83
BT0207	SusD homolog	0.39	2.58	0.69	6.48
BT0208	hypothetical protein	0.35	2.58	0.70	6.48
BT0209	hypothetical protein	0.42	3.74	0.75	10.61
BT0210	leucine-rich repeat protein, function unknown	0.37	5.69	0.81	25.68
BT0211	Leucine-rich repeat	0.45	6.57	0.78	17.54
BT0317	SusC homolog	1.29	3.28	1.14	12.21
BT0318	SusD homolog	1.36	3.53	1.19	10.61
BT0319	conserved hypothetical protein	1.33	2.22	1.22	3.46
BT0434	Pyridine nucleotide-disulphide o	1.47	1.49	1.29	9.07
BT0435	Twin-arginine translocation pathway signal	1.56	2.22	1.23	21.84
BT0436	arabinose-proton symporter	1.58	2.22	1.23	18.83
BT0437	N-acylglucosamine 2-epimerase	1.83	4.24	1.00	33.93
BT0439	SusC homolog	1.83	2.22	0.90	26.07
BT0440	SusD homolog	1.73	4.16	0.90	27.56
BT0441	putative chitobiase	1.66	4.69	1.02	33.93
BT0442	glycerophosphoryl diester phosphodiesterase	1.62	5.69	1.08	33.93
BT0444	hypothetical protein	1.51	2.22	1.06	33.93
BT1273	L-fucose isomerase	0.63	3.53	0.67	7.39
BT1274	L-fuculose-1-phosphate aldolase	0.64	3.74	0.80	5.56
BT1275	L-fuculose kinase	0.64	2.58	0.63	5.43
BT1276	mutarotase	0.62	2.24	0.56	3.34
BT1277	L-fucose permease	0.62	2.58	0.66	0.00
BT1551	Peptidase M1A and M12B	0.51	2.58	0.41	2.26

BT1552	SusC homolog	0.53	3.74	0.61	4.40
BT1553	SusD homolog	0.43	3.74	0.39	3.03
BT1617	RNA polymerase ECF-type sigma factor	0.76	2.22	0.61	4.40
BT1618	putative anti-sigma factor	0.61	3.74	1.24	27.56
BT1619	SusC homolog	0.51	4.71	0.94	32.83
BT1620	SusD homolog	0.49	4.69	0.94	30.57
BT1621	beta-hexosaminidase precursor , GH_20	0.51	6.57	0.96	32.83
BT1622	N-acetylgalactosamine-6-sulfatase precursor	0.58	6.57	1.07	32.14
BT2392	NHL repeat-containing protein	2.86	3.53	0.97	32.83
BT2393	SusC homolog	3.09	3.28	0.94	30.57
BT2394	SusD homolog	3.77	2.22	0.85	16.10
BT2395	hypothetical protein	3.66	2.22	0.76	12.21
BT3086	alpha-glucosidase II , GH_31	3.20	0.00	0.99	32.83
BT3087	cycloisomaltooligosaccharide glucanotransferase , GH_66	2.24	0.00	1.01	33.93
BT3088	conserved hypothetical protein	2.56	0.00	0.89	17.54
BT3089	SusD homolog	2.03	0.00	0.97	32.83
BT3090	SusC homolog	2.62	0.00	0.94	30.57
BT3235	conserved hypothetical protein	3.23	4.69	0.76	18.83
BT3236	conserved hypothetical protein	3.28	4.71	0.66	12.21
BT3237	Peptidase M, neutral zinc metallopeptidases, zinc-binding site	3.10	4.69	0.66	12.21
BT3238	SusD homolog	3.13	5.69	0.63	10.61
BT3239	SusC homolog	2.82	4.71	0.71	7.39
BT3854	SusC homolog	1.32	2.63	0.97	32.83
BT3855	SusD homolog	1.29	4.24	0.91	30.57
BT3857	Flavodoxin	1.24	2.22	0.90	26.07
BT4038	SusD homolog	1.43	1.65	0.86	25.68
BT4039	SusC homolog	1.38	2.16	0.84	25.68
BT4040	putative galactose oxidase precursor	1.39	2.22	0.82	17.54

BT4241	beta-galactosidase , GH_2	1.44	3.28	0.60	12.21
BT4242	putative transporter	1.37	3.74	0.66	14.85
BT4243	Hexosaminidase, GH_109	1.49	2.05	0.91	26.07
BT4244	Coagulation factor 5/8 type, C-terminal	2.44	0.00	0.79	28.86
BT4245	Coagulation factor 5/8 type, C-terminal	2.08	1.49	0.92	32.83
BT4246	SusD homolog	1.98	2.22	0.80	28.97
BT4247	SusC homolog	1.80	1.65	0.87	30.57
BT4248	putative anti-sigma factor	2.13	4.24	1.48	5.43