

Supplemental On-line Materials

Assembling a model human microbiota in gnotobiotic mice

B. caccae ATCC 43185 (GenBank genome accession number NZ_AAVM000000000), *B. ovatus* ATCC 8483 (NZ_AAXF000000000), *B. thetaiotaomicron* VPI-5482 (NC_004663), *B. hydrogenotrophica* DSM 10507 (NZ_ACBZ000000000), *M. formatexigens* DSM 14469 (NZ_ACCL000000000), *C. symbiosum* ATCC 14940, *C. aerofaciens* ATCC 25986 (NZ_AAVN000000000), *E. coli* str. K-12 substr. MG1655 (NC_000913), and *E. rectale* ATCC 33656 (NC_012781) were obtained from public strain repositories (ATCC or DSMZ). A draft genome assembly for *C. symbiosum* ATCC 25986 is available at the Washington University Genome Center public web site (http://genome.wustl.edu/pub/organism/Microbes/Human_Gut_Microbiome/Clostridium_symbiosum/assembly/Clostridium_symbiosum-1.0/output/). We isolated *D. piger* GOR1 from a healthy human by plating serial dilutions of freshly voided feces under strictly anaerobic conditions (80% H₂/20% CO₂ at 15 psi) onto plates containing medium with the following components (quantities expressed per liter): K₂HPO₄ (0.3g); KHPO₄ (0.3g); (NH₄)SO₄ (0.3g); NaCl (0.6g); MgSO₄·7H₂O (0.13g); CaCl₂·2H₂O (0.008g), yeast extract (0.5g); NH₄Cl (1.0g); NaHCO₃ (5.0g); dithiothreitol (0.5g); sodium formate (3.0g); Noble agar (10g); 5 ml of a 0.2% (w/v) solution of Fe(NH₄)₂(SO₄)₂·6H₂O, 1 ml of a 0.2% (w/v) solution of resazurin; cysteine (1g), 10 ml of trace mineral solution (ATCC), and 10 ml of a vitamin solution (ATCC). The genome sequence of *D. piger* was determined by 454 FLX and FLX Titanium pyrosequencing. For both *C. symbiosum* and *D. piger*, genes were identified using Glimmer3.0 (17), tRNAScan 1.23 (18), and RNAmmer 1.2 (19). All 10 genomes were annotated using PFAM v23; 20) and String COG version 7.1 (21). Annotations for all 40,669 predicted protein-coding genes in the 10 genomes can be found at http://gordonlab.wustl.edu/modeling_microbiota/.

Each community member was grown anaerobically in 5 ml of TYG_s medium (12) in Balch tubes. Inoculation times were staggered so that all organisms reached stationary phase within a 24 h window. Just prior to gavage, equal volumes (1 ml) of each culture were pooled and mixed regardless of the final stationary phase density reached by each mono-culture (OD₆₀₀ values ranged from 0.4 to >2.0). Each germ-free mouse was subsequently gavaged with 300 µl of the pooled cultures.

Refined diet composition, experimental design, and data processing

We initially designed a set of eleven diets (**Fig. S1B,C** and **Table S1**), each differing in their concentrations of casein (protein), corn oil (fat), cornstarch (polysaccharide), and sucrose (simple sugar). Nine of the diets consisted of all possible combinations of high, medium, and low casein and corn oil, with a fixed amount of cornstarch and the remainder as sucrose (**Fig. S1B**; diets A-I). Using sucrose as the 'remainder' for these initial nine diets generated a negative correlation between sucrose concentration and casein/fat concentration. Therefore, two diets, one with high starch and low sucrose and the other with low starch and high sucrose, were designed to lessen this negative correlation (see diets J and K in **Fig. S1C**).

Initially, all mice were co-housed and given the diet labeled 'E' in **Fig. S1D** (5% fat, 20% protein, 62% carbohydrate). Mice were then individually caged in the gnotobiotic isolator, and every two weeks each animal received another randomly selected diet (second, third and fourth diet periods in **Fig. S1D**). Mouse 13 received only control diet E to determine if there was any 'drift' in steady state over the 8-week period.

We estimated the steady state mean absolute abundance of each community member for each of the 36 mouse/diet combinations for the second, third, and fourth diet periods shown in **Fig. S1D**. To do so, DNA was isolated from fecal samples taken from each mouse on days 1, 2, 4, 7, and 14 of a diet and analyzed by COmmunity PROfiling by sequencing (COPRO-Seq). This generally applicable method relies on the massive

number of short reads generated by the Illumina GA-II instrument during shotgun sequencing of total community DNA (22). Briefly, “informative” tags are identified that map uniquely to a single location in one species’ genome. These tags are then summed to generate raw “counts” of each species’ abundance. To account for non-unique matches, species-specific counts are normalized by the “Informative Genome Fraction” of each genome (defined as the fraction of all possible k-mers a genome can produce that are unique). Up to 16 barcoded fecal DNA samples were pooled in each sequencing lane: we generated a minimum of 50,000 reads per sample so that all organisms comprising $\geq 0.02\%$ of the community could be detected (for a mouse colonized at 10^{12} cfu/ml cecal contents or feces, this represents $\sim 10^8$ cfu/ml; at this sequencing depth, all species were detected in all samples). We used total DNA yield per fecal pellet as a proxy for community biomass and multiplied the relative abundance of each species by the mean total DNA yield per fecal pellet for a particular diet to estimate the absolute abundance of each species in units of nanograms per fecal pellet. The absolute abundance N_{impd} of each species i in mouse m on diet period p on day d was calculated $N_{impd} = F_{impd}T_j$ where F_{impd} is the Informative Genome Fraction adjusted fraction of species i in mouse m on diet period p on day d as measured by COPRO-Seq and T_j is the mean total DNA yield per fecal pellet for all samples taken from mice on diet j . Fecal pellets were used because they reflect overall microbiota composition in the gut (6,10) and they provided us with the only means to sample each mouse over time. Mice were weighed during each diet period (Table S10). Although there was a trend towards increased weight gain as levels of casein and corn oil were increased (Table S11), there were no significant correlations between any of the diet perturbations and weight gain.

Model description and performance evaluation

Population growth can be modeled as exponential growth with a carrying capacity:

$$\text{Equation 1 } \frac{dN}{dt} = rN \left(1 - \frac{N}{K}\right)$$

where r is the growth rate, N is the population size, and K is the carrying capacity.

Extending the above equation to include multiple species (i) and multiple diets (j), the model becomes:

$$\text{Equation 2 } \frac{dN_i}{dt} = r_{ij}N_i \left(1 - \frac{N_i}{K_{ij}}\right)$$

where K_{ij} is the carrying capacity of species i on diet j (i.e. the steady-state level). We were interested in predicting the steady-state abundance of each species in the synthetic community as a function of the ingredients in the host diet. Thus, we can ignore the time-specific abundance of each community member $N_i(t)$ on each diet and the growth rate r , assuming it is sufficiently large to allow each community member to reach their carrying capacity for each diet within the period that a given mouse was consuming the diet.

To predict the steady-state levels (K_{ij}) for each community member i given each diet j , we measured the abundance of each community member for each mouse and diet combination (**Fig. S1D,E**). The absolute abundance K_{impd} for each community member (i) in a specific mouse (m) for a specific diet period (p) for a given day (d) was calculated as described above. These abundances were averaged across all available time points for each mouse after the microbiota had reached steady-state (d_s) for a specific diet period (i.e., the cells in the diet/mouse matrices in **Fig. S1D,E**; see below for estimation of steady-state). On average, 2.7 samples were available per mouse per diet period to give the steady-state abundance of each species (i) in the fecal microbiota for a given mouse (m) and diet period (p) combination in **Fig. S1D,E**.

$$\text{Equation 3 } y_{imp} = \text{mean}(K_{impd}) \text{ where } d \geq d_s$$

These y_{imp} values served as the data for the linear model described in the main text.

Scoring model performance

All of the models used in this study were linear. Therefore, we could score each model by using R^2 , which for linear models represent the proportion of variance in the system that is explained by the model. We used the R^2 for each species in the community separately to calculate a weighted mean R^2 , where the weights represent the fraction of total fecal DNA content represented by each species (i.e., the R^2 for abundant taxa are given more weight than those of less abundant taxa). By using this weighted scoring schema, our final R^2 metric represents the amount of the total variation in species DNA content that can be explained by the model. An alternative method is to weight each species' R^2 equally, which produces similar albeit slightly worse results (**Table S2**).

Estimating steady-state

Since our model assumes the microbiota is at steady-state, we want to only include values of species abundance from time points after the microbiota reaches steady-state for a given diet period (i.e. we need to define d_s in Equation 3). To determine the time required by the microbiota to reach steady-state after a diet switch, we fed nine 22-week-old C57Bl/6J mice a low protein/low fat diet for 7d, followed by a switch to the high protein/high fat diet for 13 d (**Fig. S1B** diets A and I respectively). All mice were sampled approximately once every 24 h with twice-daily sampling around the time of the diet switch. To estimate whether the community had stabilized at a given time point, we measured (i) the total microbial community biomass using DNA yield (ng/fecal pellet) as a marker, and (ii) the relative abundance of each species using the Informative Genome Fraction estimated from Illumina DNA sequencing. We found that the biomass of the gut microbiota was stable at the end of the first diet, highly variable during the initial time points after the diet transition, and then stable again by the fourth day after the diet switch (although even by 24h after the switch, the mean

yield largely reflects final steady-state abundance on the new diet). Similar results were found for the relative abundance data, although the relative abundance of each species appeared to stabilize faster than biomass (**Fig. S5A** compared with **Fig. S5B**). Given the results for both the biomass and relative abundance metrics, we set the number of days required by the microbiota to reach steady-state to four (i.e. $d_s=4$).

Comparing more complex models

Although the linear model performed well (see main text and **Table S2**), more complex linear and nonlinear models could perhaps yield even better predictive ability. We therefore repeated the cross validation procedure for the casein, corn oil, sucrose, starch diet combinations (see main text) using models that allowed for interactions between variables, quadratic terms, and interactions with quadratic terms:

Linear $y_i = \beta_0 + \beta_A X_A + \beta_B X_B,$

Interaction $y_i = \beta_0 + \beta_A X_A + \beta_B X_B + \beta_{AB} X_A X_B,$

Quadratic $y_i = \beta_0 + \beta_A X_A + \beta_B X_B + \beta_{AA} X_A X_A + \beta_{BB} X_B X_B,$

Pure Quadratic $y_i = \beta_0 + \beta_A X_A + \beta_B X_B + \beta_{AA} X_A X_A + \beta_{BB} X_B X_B + \beta_{AB} X_A X_B,$

We used Akaike information criterion (AIC) as the scoring metric to allow for comparisons between these models with varying numbers of parameters and found the linear model performed best overall (**Table S2**). Given the slightly asymptotic behavior of the microbiota at extremely low and high casein concentrations (**Fig. 1**), we also attempted to fit a nonlinear logistic function to the data to account for these saturation points. However, we found that the lack of data at and beyond the asymptote made the nonlinear regression difficult to reliably fit. While it is interesting to question whether the microbiota will reach and maintain an asymptotic behavior with sampling at extreme concentrations of these ingredients, moving beyond the current maximum and

minimum casein values would be unrealistic in terms of modern human eating habits and would be unhealthy for the animals.

Transcriptional responses of the microbiota to host diet perturbations

To deplete total microbial community RNA of 16S, 23S, 5S rRNA and tRNA species prior to synthesis of cDNA with random hexanucleotide primers, each fecal RNA preparation was subjected to column-based size-selection and hybridization to custom biotinylated oligonucleotides directed at conserved regions of bacterial rRNA genes present in human gut communities, followed by streptavidin-bead based capture of the hybridized RNA sequences (10). RNA-Seq data were normalized as described previously (10). After normalization, we filtered the list to remove all transcripts whose total number of counts (\log_2) summed across all 36 RNA-Seq expression profiles was < 64 (2^6). This threshold was chosen to be as inclusive as possible while still requiring a sufficient number of reads so that a dynamic range of roughly 5-fold could be detected across the 17 sampled diets. For example, if a transcript linearly increases 5-fold in response to diets with a 20-fold range in their casein concentration, with the lowest concentration yielding a number of reads that was just below level of detection for both replicates and the highest casein concentration yielding 5 reads for that transcript per replicate, we would require 55 reads. After normalization and filtering, we were left with a list of 26,643 genes across the 10 species ($64 \pm 20\%$ of the annotated genes in each species were detected as 'expressed'). For each of these genes, we calculated the correlation and the p-value of the correlation between (i) each of the four perturbed refined diet ingredients and (ii) the \log_2 (gene expression) in reads per million per kilobase (RPKM) (14) (**Table S12**). Multiple hypotheses correction was performed using the Storey procedure (23).

Highly expressed transcripts for each species

We examined the highest 10% expressed genes in each community member (http://gordonlab.wustl.edu/modeling_microbiota/), as major metabolic activities of gut microbes have consistently been identified among the abundant genes (10,24,25). Among the most highly expressed genes in *B. thetaiotaomicron*, were those encoding components of glycolysis / gluconeogenesis pathways (e.g. BT1658-1660, BT1672, 1691), the pentose phosphate pathway (e.g. BT3946-3950), plus members of polysaccharide utilization loci (PULs), including one PUL predicted to act on O-glycan containing mucins (BT0317-0319; S12), and another PUL involved in the degradation of fructans (BT1757-1763 and BT1765; 26). In addition to several peptidases (BT2522, BT2706, BT3926, BT4583), genes predicted to be involved in the metabolism of glutamate (glutamate dehydrogenase (BT1973); glutamate decarboxylase (BT2570)), glutamine (glutaminase (BT2571)), serine (L-serine dehydrate (BT4678)), aspartate (aspartate ammonia lyase (BT2755)), asparagine (L-asparaginase (BT2757)), and branched-chain amino acids (branched-chain alpha-keto acid dehydrogenase (BT0311-12)) were highly expressed. Similar results were observed in *B. caccae* and *B. ovatus*. Although the ability of colonic Bacteroides to access protein has not been extensively explored, there is evidence that members of this genus have extracellular proteolytic activity (27), and can incorporate amino acids into cellular components other than proteins (28). This feature, combined with their ability to use complex polysaccharides not accessible to other members in the community (including host glycans), may explain why they benefit from increased levels of dietary protein (casein).

Among the most highly expressed genes in *C. symbiosum* were components of the hydroxyglutarate pathway for degradation of glutamate (Csym2026-2031), the most abundant amino acid in casein (25.3% w/w), and a sodium/ glutamate transporter (Csym3971). This pathway yields crotonyl-CoA, which is metabolized to butyrate, acetate, H₂ and ATP. Genes encoding components of the pathway for butyrate production (Csym1328-1334) were also among the highest expressed.

Another Firmicute that grows on amino acids is the acetogenic bacterium *B. hydrogenotrophica*. Genes predicted to encode key enzymes of the acetyl-CoA pathway involved in the reductive assimilation of CO₂ were among the most highly expressed in this species (e.g., carbon monoxide dehydrogenase (Rumhyd0314-0320)), as were genes involved in fermentation of aliphatic (Rumhyd0546-0555) and aromatic amino acids (Rumhyd1109-1113), and the metabolism of ribose (Rumhyd2245-2256).

E. coli also benefited from higher levels of protein; among its most highly expressed genes were components of a cytochrome d terminal oxidase involved in the consumption of oxygen (b0733-0734), genes involved in the utilization of simple sugars (e.g., b2092-2097 (galactitol), b2416-2417 (glucose), b2801-2803 (fucose)) and several genes involved in the metabolism of tryptophan (b3708-b3709), aspartate (b1439) asparagine (b2957), and threonine (b3114-3117).

C. aerofaciens expressed high levels of transcripts encoding proteins predicted to be involved in the catabolism of arginine (COLAER0352-356, COLAER1230), plus components of several phosphotransferase systems (a predicted sucrose-specific PTS (COLAER0919-0921), a predicted mannose/fructose/N-acetylgalactosamine-specific PTS (COLAER1259-1260) and a predicted mannitol/fructose PTS (COLAER0058-0061)).

Levels of *E. rectale* and *M. formatexigens* decreased as protein increased. Inspection of their most highly expressed genes suggested that they focus on catabolism of carbohydrates. For example, among the most highly expressed genes in *M. formatexigens* were components of several ABC transporters with predicted specificities for monosaccharides/oligosaccharides (e.g., BRYFOR5076-BRYFOR5080, BRYFOR06841-06843), and genes encoding key enzymes of the acetyl-CoA pathway (e.g., BRYFOR06355-06360). There was no clear evidence of genes involved in catabolism of amino acids being highly expressed.

D. piger also decreased as casein levels increased. *D. piger* is fairly restricted in its metabolism: it can use a few substrates (e.g., lactate, H₂, succinate) to reduce different

forms of sulfur to H₂S and generate energy, and it can oxidize lactate and pyruvate incompletely to acetate (29). Among its most highly expressed genes were components of the sulfate reducing pathway (DpigGOR12316-18, DpigGOR110789-10794), a C4-dicarboxylate transport system (DpigGOR12113-2115), subunits of a Ni-Fe hydrogenase, and several genes predicted to be involved in lactate metabolism (DpigGOR11071-1075). Three predicted transporters of amino acids were highly expressed, but there was no evidence of further metabolism of these amino acids, which likely indicates that they are used for protein biosynthesis.

Simulation of negatively correlated species with constant behavioral responses

Using Equation 2 above, we want to create a simulated 2-member community where one member (species1 = N_1) is casein limited (C) and the second member (species2 = N_2) is negatively influenced in proportion to the abundance of species1 (α_{12}) (e.g., species1 could consume a limiting resource of species2, produce an inhibitory compound, or act through apparent competition). We assume that both species have the same growth constant ($r_1 = r_2$) on all diets and that species1 is able to convert a proportion (s) of the casein into increases in population size ($K_1 = sC$; note that 1.3, 2/3, 0, 2/3, and 15 were used for constants r , s , α_{21} , α_{12} , and K_2 respectively, but this choice of values is arbitrary and similar results can be obtained over a wide-range of stable values):

$$\text{Equation 4 } \frac{dN_1}{dt} = r_1 N_1 \left(1 - \frac{N_1 + \alpha_{21} N_2}{K_1} \right)$$

$$\text{Equation 5 } \frac{dN_2}{dt} = r_2 N_2 \left(1 - \frac{N_2 + \alpha_{12} N_1}{K_2} \right)$$

Simulating the above equations, where every ten days we change the amount of casein (C) from 2, 5, 10, 20, and 40% respectively, yields the result shown in **Fig. S4** where

species1 increases with increased casein while species2 decreases, during which time both maintain the same behaviors.

This type of behavior at the transcriptional level of a microbial community resembles similar phenomena observed in macro-ecology. For example, if two species of naturally co-occurring grasshoppers, one that eats almost exclusively grasses (*Ageneotettix deorum*) and the other that eats both grasses and forbs (*Melanoplus sanguinipes*), are co-housed to compete in environments with different dietary contexts, the final population size of each grasshopper species is dependent not only on the ability of *A. deorum* to compete for grass (i.e. its essential resource), but also *M. sanguinipes*' ability to utilize both grass and forbs. Thus, if the amount of grass available to the grasshoppers is held constant while the amount of forbs is increased, the population of *A. deorum* decreases even though it maintains the constant behavioral response of exclusively eating grass (30).

Design, administration, and modeling of complex diets

The following commercially available eight pureed human baby foods were used as the source ingredients to construct a set of 48 meals: peaches (Gerber 3rd foods®; Gerber Products Company); apple sauce (Gerber 3rd foods); peas (Gerber 2nd foods®), sweet potatoes (Gerber 3rd foods); chicken (Gerber 2nd foods); beef (Gerber 2nd foods), oats (Gerber Single Grain with VitaBlocks®); and rice (Gerber Single Grain with VitaBlocks). Oats and rice were purchased dry and mixed with dH₂O in a 1:5 ratio prior to use (e.g., a meal with 6g of oats contained 1g dried oats and 5g dH₂O). Each meal consisted of four ingredients randomly selected from the set of eight total pureed human foods, with different concentrations of the four ingredients used in different diet periods. Meals were autoclaved and each mouse was fed a sequence of 5 different diets, with each diet provided for 1 week. The order of presentation of the 48 diets to the 8 gnotobiotic mice is described in **Table S8**. The table shows how we interposed, between each 1 week period of administration of a given pureed baby food meal, a 1 week period

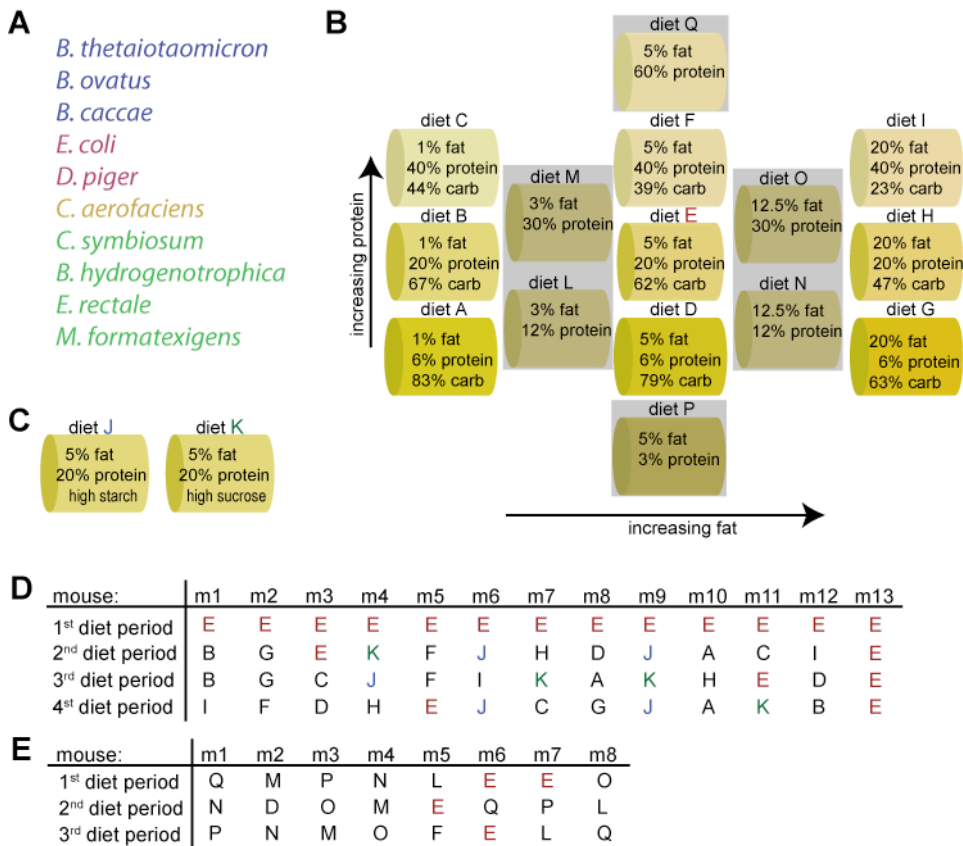
of consumption of one of the 17 diets composed of refined ingredients to ensure mice obtained adequate amounts of vitamins and minerals.

We measured absolute abundance of each bacterial community member on days 1, 5, 6, and 7 of each human baby food diet. As before, the abundance values (y_{imp}) were calculated from the mean of all samples within a given diet period. However, we excluded day 1 in case the microbiota had not yet reached steady state by 24h. To cover more of the potential “meal” space, the schema for the complex diets used less replication than was used for the refined diets, so there were fewer fecal pellets available to estimate the DNA yield data used to calculate absolute abundance of each species. Therefore, to estimate DNA yields for each diet, we used a nearest neighbor smoothing procedure where the DNA yield for each sample was calculated as a weighted average of the ten nearest samples with weights corresponding to the Euclidean distance from the true sample to the Nth-nearest sample (e.g., the nearest samples would be exact replicates and have a weight of 1.0).

The modeling performance was estimated with a species abundance weighted R^2 as described above using the following equation:

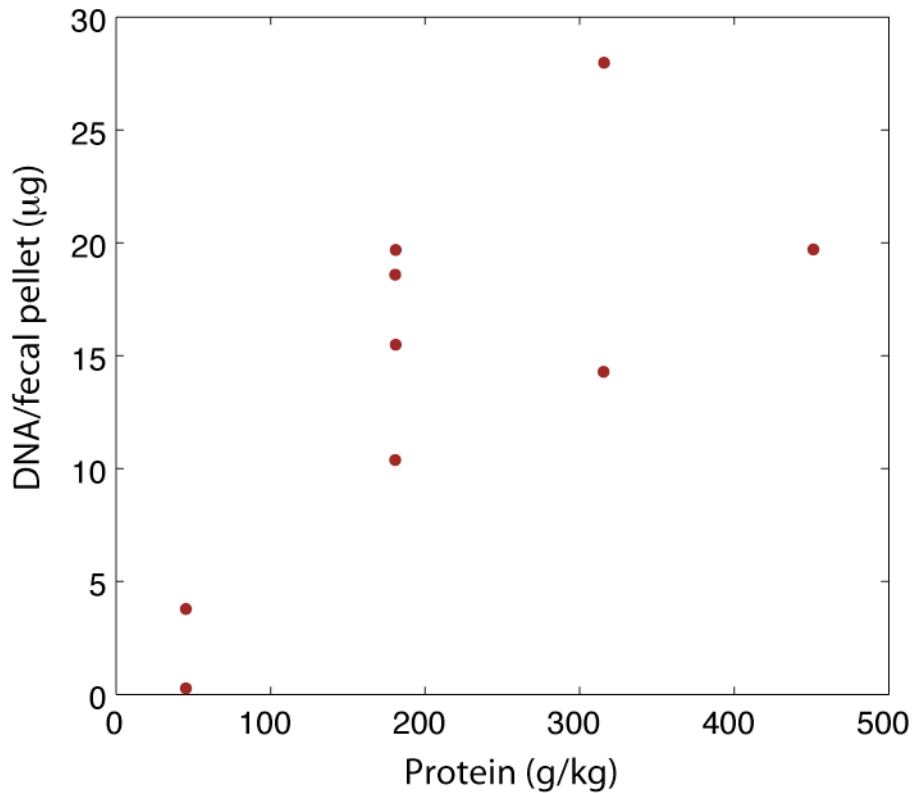
$$y_i = \beta_0 + \beta_{apple}X_{apple} + \beta_{peach}X_{peach} + \beta_{pea}X_{pea} + \beta_{sweetpotato}X_{sweetpotato} + \beta_{chicken}X_{chicken} + \beta_{beef}X_{beef} + \beta_{oats}X_{oats} + \beta_{rice}X_{rice}$$

where the variables correspond to the concentration of each pureed ingredient in each meal. The final performance metric was the mean of ten replicates of 10-fold cross-validation on the 48 samples. The performance when training on the larger set (n~43) and testing on the smaller set (n~5) was similar to training and testing using the larger set only (weighted $R^2=0.62$ and $R^2=0.66$ respectively).

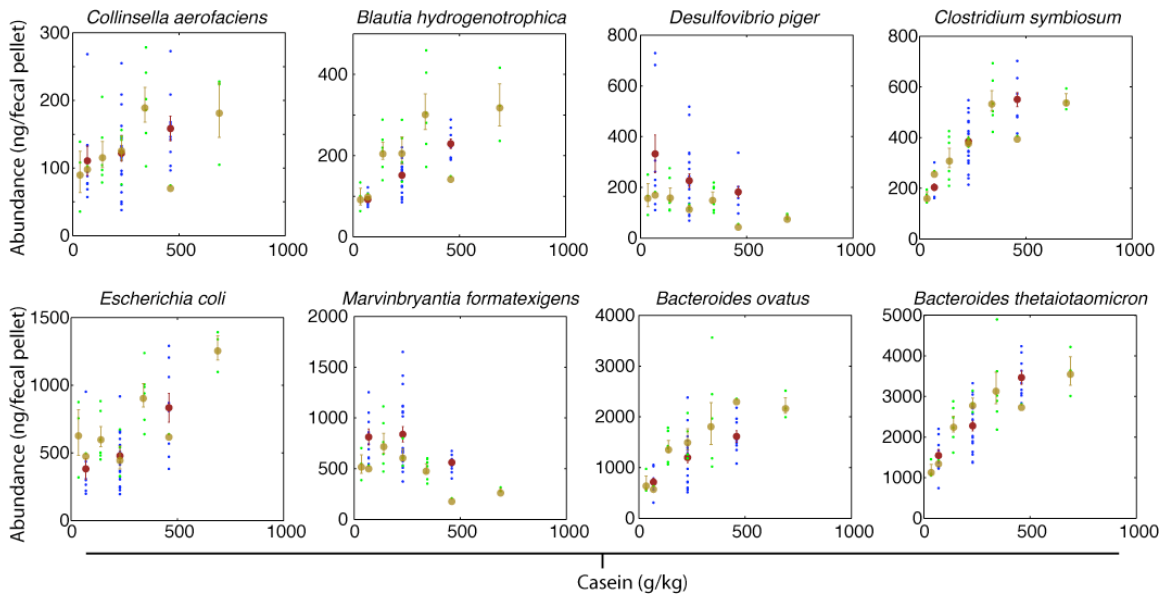


Supplemental Fig. 1 - Study design for refined diets. Two sets of gnotobiotic mice harboring a synthetic microbiota composed of ten sequenced human gut bacterial species were presented a total of 17 diets differing in their concentrations of casein (protein), corn oil (fat), sucrose (simple sugar), and cornstarch (polysaccharide). **(A)** The model community used for all experiments consisted of sequenced bacterial species from the four most abundant phyla in the adult human gut microbiota: Bacteroidetes (blue), Firmicutes (green), Actinobacteria (yellow), and Proteobacteria (red). **(B,C)** The first screen consisted of 11 refined diets: 9 of these diets (A-I in panel B) represent all possible combinations of high, medium, and low protein and fat; the two additional diets (J and K in panel C) contained high sucrose/low starch and high starch/low sucrose, respectively. **(D)** In the first experiment, 13 gnotobiotic mice harboring the 10-member community were each fed a randomly selected diet every two weeks for eight

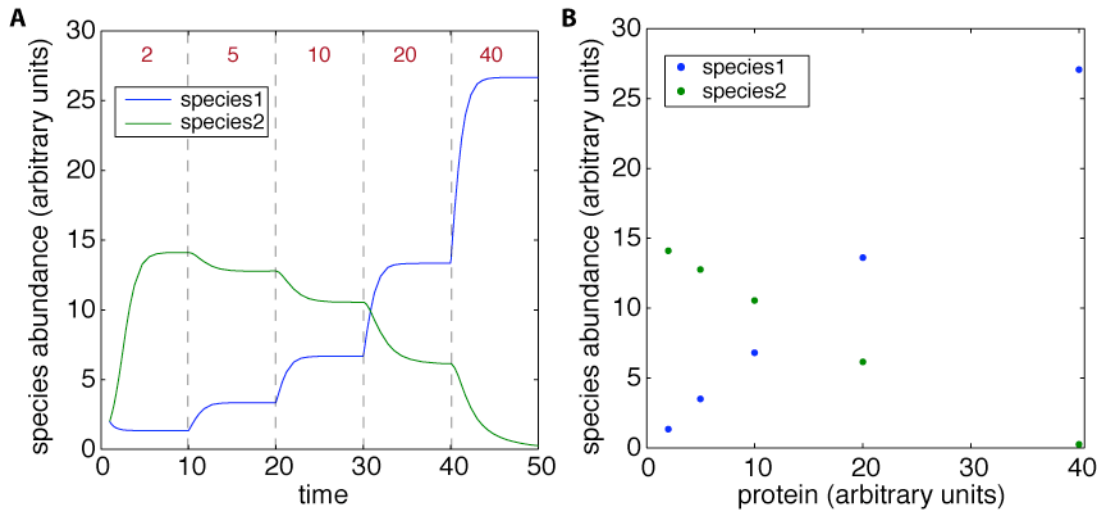
weeks (i.e., four total diets per mouse). **(E)** In a follow-up experiment, six additional diets were designed (shaded diets in panel **B**; diets L-Q) and 8 gnotobiotic mice harboring the 10-member community were each presented a randomly selected diet every two weeks for six weeks. Analyses of the shotgun sequencing data revealed that steady state levels of community members were achieved within 24 h of a diet change. Therefore, we averaged the values from all five time points sampled within a diet period to obtain the mean absolute abundance of each community member for each of the refined diet periods.



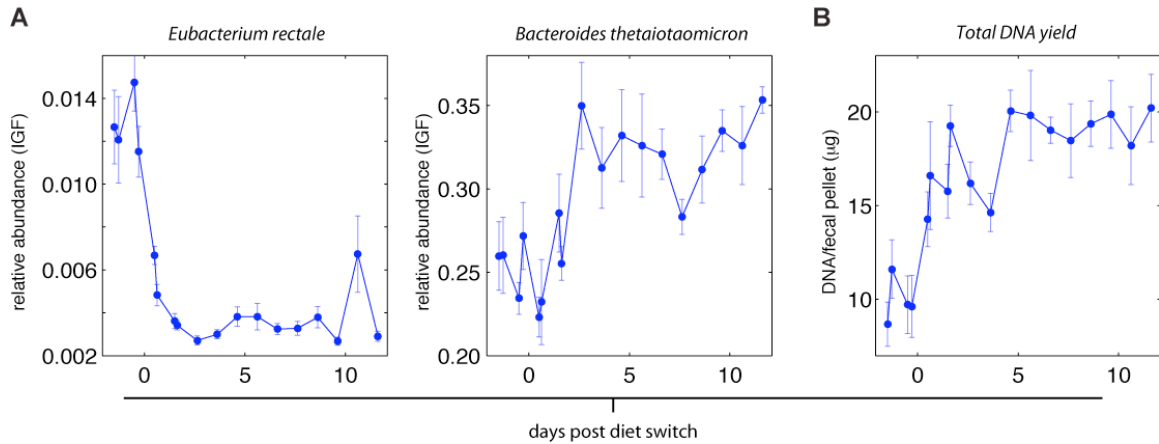
Supplemental Fig. 2 – Total community DNA yield as a function of protein concentration. Nine different 15-week-old gnotobiotic male C57Bl/6J mice harboring the 10-member community were each given a randomly selected diet containing varying amounts of three different refined protein sources (soy, egg white solids, and lactalbumin), and two different refined fat sources (olive oil and lard) (see **Table S4** for diet schema). Each mouse was sampled on days 5, 6, and 7 of the diet period. DNA was extracted from each fecal pellet and the three samples from each mouse were averaged to produce the final DNA yield per fecal pellet (see **Table S13** for results of DNA measurements).



Supplemental Fig. 3 - Changes in species abundance as a function of changes in the concentration of casein in the host diet. Changes are apparent for all species in the model microbiota (note that the responses of *E. rectale* and *B. caccae* are shown in **Fig. 1B** of the main text). Data obtained from the first and second set of mice are shown in blue and green, respectively, while mean values \pm S.E.M are shown in red and tan, respectively.



Supplemental Fig. 4 - Simulation of competition for limiting resources. (A) Using equations 4 and 5 for species1 and species2, both species were initialized to a population size of 2 and a diet switch was initiated every ten days, increasing casein abundance at each switch (red numbers indicate % casein for each diet period). (B) The steady-state values of the simulation in panel A mirror the findings in our mouse datasets where the increase in a bacterial species (species1) that is casein limited leads to a decrease in species2 with increasing dietary casein.



Supplemental Fig. 5 - Estimation of steady state. Nine adult male gnotobiotic mice harboring the ten-member model human gut community were fed a low-fat, low-protein diet (diet A in **Fig. S1B**) for 7-days and then switched to a high-fat, high-protein (diet I in **Fig. S1B**) at time-point zero for 13 days. The relative abundance of each of the taxa was subsequently defined using shotgun sequencing of fecal DNA to determine their Informative Genome Fraction (IGF). **(A)** The relative abundance of each bacterium changes rapidly within hours of a diet switch, reaching steady state levels by the third day (shown are the two species with the greatest increase and decrease respectively in relative abundance). Mean values \pm SEM are plotted at each time point. **(B)** Changes in total fecal DNA yield also increased rapidly in the first 24 h after the diet switch, reaching steady state levels on the fourth day.

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Supplemental Table 1. Composition of refined diets: seventeen perturbations to casein, sucrose, corn starch, and corn oil concentrations

Diet ID:	First set of diets											Second set of diets					
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
Harlan Teklad Diet Number:	TD.09049	TD.09050	TD.09051	TD.09052	TD.09053	TD.09054	TD.09055	TD.09056	TD.09057	TD.09058	TD.09059	TD.09620	TD.09621	TD.09622	TD.09623	TD.09624	TD.09625
	g/kg	g/kg	g/kg	g/kg	g/kg	g/kg	g/kg	g/kg	g/kg	g/kg	g/kg	g/kg	g/kg	g/kg	g/kg	g/kg	g/kg
Casein	69	230	460	69	230	460	69	230	460	230	230	138	345	138	345	35	690
L-Cystine	0.9	3	6	0.9	3	6	0.9	3	6	3	3	1.8	4.5	1.8	4.5	45	9
Sucrose	675.88	514.13	283.08	633.46	471.66	240.66	473.98	312.38	81.38	171.66	571.66	585.425	377.525	484.52	276.42	667.61	108.11
Corn Starch	100	100	100	100	100	100	100	100	100	400	0	100	100	100	100	100	0
Maltodextrin, Lo-Dex 10	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50
Cellulose (Fiber)	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50	50
Corn Oil	10	10	10	50	50	50	200	200	200	50	50	30	30	125	125	50	50
79055 Mineral mix, Ca-P Deficient	12.73	12.73	12.73	13.4	13.4	13.4	16.08	16.08	16.08	13.4	13.4	13.06	13.06	14.74	14.74	13.4	13.4
Calcium Carbonate	2.6	6.25	11.3	2.6	6.4	11.3	3	6.5	11.6	6.4	6.4	4.2	8.8	4.5	9	1.9	12.25
Calcium Phosphate	12.5	7.5	0.5	13.4	8.3	1.4	16.4	11.4	4.3	8.3	8.3	10.7	4.3	12.5	6.4	14.4	0
40077 Vitamin mix	14.25	14.25	14.25	15	15	15	18	18	18	15	15	14.625	14.625	16.5	16.5	15	15
Choline Bitartrate	2.1	2.1	2.1	2.2	2.2	2.2	2.6	2.6	2.6	2.2	2.2	2.15	2.15	2.4	2.4	2.2	2.2
Ethoxyquin (Liquid)	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
Protein (% by weight)	6.1	20.3	40.6	6.1	20.3	40.6	6.1	20.3	40.6	20.3	20.3	12.2	30.5	12.2	30.5	3.1	60.9
Protein (% of kcal)	6.7	22.7	46.5	6.3	21.5	44.1	5.3	18.0	36.8	22.2	21.3	13.1	33.5	11.7	29.7	3.2	67.1
Carbohydrate (% by weight)	82.7	66.6	43.5	78.6	62.4	39.3	62.9	46.8	23.7	59.4	63.4	73.7	52.9	63.8	43	82	17
Carbohydrate (% of kcal)	90.7	74.3	49.7	81.8	66.0	42.6	55.1	41.5	21.4	64.9	66.4	79.4	58.1	61.1	41.9	85.1	18.7
Fat (% by weight)	1.1	1.2	1.5	5.1	5.2	5.5	20.1	20.2	20.5	5.2	5.2	3.1	3.4	12.6	12.9	5	5.7
Fat (% of kcal)	2.6	3.1	3.8	11.9	12.5	13.3	39.6	40.4	41.7	12.9	12.3	7.5	8.4	27.2	28.3	11.7	14.1
kcal/g diet	3.6	3.6	3.5	3.8	3.8	3.7	4.6	4.5	4.4	3.7	3.8	3.7	3.6	4.2	4.1	3.9	3.6

Calcium carbonate and calcium phosphate were used to maintain calcium and phosphorus levels at 0.5% and 0.35%, respectively, across all diets with the exception of the diet with the highest level of protein (TD.09621) where the phosphorus present in casein brings its level to 0.48%. Vitamin and mineral mixes were adjusted based on the caloric density of each diet.

Custom diets designed for this study are now commercial available from Harlan Teklad using the Harlan Teklad Diet Number above.

Supplemental Table 2. Model performance measurements for individual species in experiments involving variations in dietary casein, corn oil, corn starch and sucrose concentrations

A. R² performance measurements for linear model				
	cross validation	prediction on new diets		
<i>Eubacterium rectale</i> ATCC 33656	0.25	0.68		
<i>Collinsella aerofaciens</i> ATCC 25986	0.08	0.42		
<i>Blautia hydrogenotrophica</i> DSM 10507	0.70	0.63		
<i>Desulfovibrio piger</i> GOR1	0.08	0.13		
<i>Clostridium symbiosum</i> ATCC 14940	0.70	0.70		
<i>Escherichia coli</i> str. K-12 substr. MG1655	0.22	0.61		
<i>Marvinbryantia formatexigens</i> DSM 14469	0.08	0.43		
<i>Bacteroides ovatus</i> ATCC 8483	0.69	0.54		
<i>Bacteroides thetaiotaomicron</i> VPI-5482	0.69	0.50		
<i>Bacteroides caccae</i> ATCC 43185	0.78	0.80		
mean	0.43	0.54		
weighted mean (weighted by species abundance)	0.61	0.61		

B. Cross validation comparison of AIC scores across different models				
	linear	interaction	quadratic	pure quadratic
<i>Eubacterium rectale</i> ATCC 33656	121.3	132.9	140.9	129.5
<i>Collinsella aerofaciens</i> ATCC 25986	161.5	174.9	182.9	170.7
<i>Blautia hydrogenotrophica</i> DSM 10507	137.0	150.8	158.8	146.3
<i>Desulfovibrio piger</i> GOR1	193.3	205.9	213.9	201.8
<i>Clostridium symbiosum</i> ATCC 14940	169.7	181.2	189.7	177.2
<i>Escherichia coli</i> str. K-12 substr. MG1655	200.0	213.3	221.3	209.4
<i>Marvinbryantia formatexigens</i> DSM 14469	199.4	210.6	218.6	206.7
<i>Bacteroides ovatus</i> ATCC 8483	204.9	216.5	224.5	212.4
<i>Bacteroides thetaiotaomicron</i> VPI-5482	211.6	222.0	229.7	218.2
<i>Bacteroides caccae</i> ATCC 43185	206.8	220.8	228.8	216.3

Supplemental Table 3. Stepwise regression selection of diet ingredients significantly associated with changes in species abundance.

	Casein	Sucrose	Corn Starch	Corn Oil
<i>Eubacterium rectale</i> ATCC 33656	1.10E-07	0.43	0.35	1.00
<i>Collinsella aerofaciens</i> ATCC 25986	3.13E-03	0.21	0.49	0.26
<i>Blautia hydrogenotrophica</i> DSM 10507	1.51E-08	0.24	0.65	0.18
<i>Desulfovibrio piger</i> GOR1	1.13E-02	0.31	0.90	0.12
<i>Clostridium symbiosum</i> ATCC 14940	2.63E-15	0.64	2.44E-03	0.65
<i>Escherichia coli</i> str. K-12 substr. MG1655	1.57E-07	9.38E-03	0.55	0.56
<i>Marvinbryantia formatexigens</i> DSM 14469	1.31E-03	0.65	0.97	0.48
<i>Bacteroides ovatus</i> ATCC 8483	1.36E-07	0.32	0.06	0.36
<i>Bacteroides thetaiotaomicron</i> VPI-5482	3.29E-12	0.43	0.74	0.38
<i>Bacteroides caccae</i> ATCC 43185	4.48E-19	0.47	0.52	0.76

Significant p-values from regression are shown in boldface

Supplemental Table 5. Correlation of species abundance with mouse diet casein concentration

	correlation with casein	p-value
<i>Eubacterium rectale</i> ATCC 33656	-0.61	1.1E-07
<i>Collinsella aerofaciens</i> ATCC 25986	0.37	3.1E-03
<i>Blautia hydrogenotrophica</i> DSM 10507	0.64	1.5E-08
<i>Desulfovibrio piger</i> GOR1	-0.32	1.1E-02
<i>Clostridium symbiosum</i> ATCC 14940	0.77	1.3E-13
<i>Escherichia coli</i> str. K-12 substr. MG1655	0.61	8.5E-08
<i>Marvinbryantia formatexigens</i> DSM 14469	-0.40	1.3E-03
<i>Bacteroides ovatus</i> ATCC 8483	0.61	1.4E-07
<i>Bacteroides thetaiotaomicron</i> VPI-5482	0.74	3.3E-12
<i>Bacteroides caccae</i> ATCC 43185	0.86	4.5E-19

Supplemental Table 6. Responses of 8-member and 9-member subset communities to low and high casein

A. Increase in total community DNA from low casein to high casein

Community	mean total DNA yield (ng/fecal pellet)		percent increase
	diet G (low casein)	diet I (high casein)	
8-member	8568	13800	61%
9-member	12448	16875	36%
10-member	7692	11718	52%

8-member and 9-member community samples were from 13 to 14-week old NMRI mice
 10-member community samples were from 10 to 16-week old C57Bl/6J mice

B. Species-level responses to changes in casein concentration

Species	8-member	9-member	10-member
<i>Bacteroides caccae</i> ATCC 43185	p	p	p
<i>Clostridium symbiosum</i> ATCC 14940	p	p	p
<i>Bacteroides thetaiotaomicron</i> VPI-5482	p	p	p
<i>Blautia hydrogenotrophica</i> DSM 10507	-	-	p
<i>Escherichia coli</i> str. K-12 substr. MG1655	p	p	p
<i>Eubacterium rectale</i> ATCC 33656	n	n	n
<i>Bacteroides ovatus</i> ATCC 8483	p	p	p
<i>Marvinbryantia formatexigens</i> DSM 14469	n	n	n
<i>Collinsella aerofaciens</i> ATCC 25986	n	p	p
<i>Desulfovibrio piger</i> GOR1	-	n	n

species are sorted by the p-value of the correlation between casein and species abundance for the 10-member community (Table S5)

n = negatively correlated with casein concentration

p = positively correlated with casein concentration

- = not present in community

Table S7. RNA-Seq sampling statistics

A. Reads per sample and sample time					
Sample Name (on GEO)	Diet/Mouse Group	Diet Period	Sample Day	Mouse	number of CDS reads
D3_10_m10	Initial (Figure S1D)	3 rd	10	m10	3939788
D3_10_m11	Initial (Figure S1D)	3 rd	10	m11	683369
D3_10_m12	Initial (Figure S1D)	3 rd	10	m12	2963483
D3_10_m13	Initial (Figure S1D)	3 rd	10	m13	1929913
D3_10_m1	Initial (Figure S1D)	3 rd	10	m1	3239713
D3_10_m2	Initial (Figure S1D)	3 rd	10	m2	3002474
D3_10_m3	Initial (Figure S1D)	3 rd	10	m3	2972819
D3_10_m4	Initial (Figure S1D)	3 rd	10	m4	2315742
D3_10_m5	Initial (Figure S1D)	3 rd	10	m5	6853955
D3_10_m6	Initial (Figure S1D)	3 rd	10	m6	2948119
D3_10_m7	Initial (Figure S1D)	3 rd	10	m7	2156624
D3_10_m8	Initial (Figure S1D)	3 rd	10	m8	5235157
D3_10_m9	Initial (Figure S1D)	3 rd	10	m9	4920923
D4_10_m10	Initial (Figure S1D)	4 th	10	m10	3507538
D4_10_m11	Initial (Figure S1D)	4 th	10	m11	2616729
D4_10_m12	Initial (Figure S1D)	4 th	10	m12	2376241
D4_10_m13	Initial (Figure S1D)	4 th	10	m13	2246908
D4_10_m1	Initial (Figure S1D)	4 th	10	m1	2123506
D4_10_m2	Initial (Figure S1D)	4 th	10	m2	3099173
D4_10_m3	Initial (Figure S1D)	4 th	10	m3	1504222
D4_10_m4	Initial (Figure S1D)	4 th	10	m4	1748333
D4_10_m5	Initial (Figure S1D)	4 th	10	m5	4486170
D4_10_m6	Initial (Figure S1D)	4 th	10	m6	1797683
D4_10_m7	Initial (Figure S1D)	4 th	10	m7	1582584
D4_10_m8	Initial (Figure S1D)	4 th	10	m8	3851143
D4_10_m9	Initial (Figure S1D)	4 th	10	m9	6288279
E1_14_m1	Follow-up (Figure S1E)	1 st	14	m1	1600692
E1_14_m2	Follow-up (Figure S1E)	1 st	14	m2	3413945
E1_14_m3	Follow-up (Figure S1E)	1 st	14	m3	2829664
E1_14_m4	Follow-up (Figure S1E)	1 st	14	m4	2921925
E1_14_m8	Follow-up (Figure S1E)	1 st	14	m8	2221047
E2_14_m1	Follow-up (Figure S1E)	2 nd	14	m1	3676356
E2_14_m3	Follow-up (Figure S1E)	2 nd	14	m3	3897906
E2_14_m4	Follow-up (Figure S1E)	2 nd	14	m4	4443428
E2_14_m6	Follow-up (Figure S1E)	2 nd	14	m6	5105594
E2_14_m8	Follow-up (Figure S1E)	2 nd	14	m8	3736835

B. Number of expressed genes/species with ≥ 64 sequencing reads			
Species	Genes Observed	Total Genes in Genome	% Observed Genes
<i>Eubacterium rectale</i> ATCC 33656	453	3621	13%
<i>Collinsella aerofaciens</i> ATCC 25986	1779	2367	75%
<i>Blautia hydrogenotrophica</i> DSM 10507	2612	3869	68%
<i>Desulfovibrio piger</i> GOR1	1660	2487	67%
<i>Clostridium symbiosum</i> ATCC 14940	3141	5128	61%
<i>Escherichia coli</i> str. K-12 substr. MG1655	2969	4132	72%
<i>Marvinbryantia formatexigens</i> DSM 14469	3173	4896	65%
<i>Bacteroides ovatus</i> ATCC 8483	3785	5536	68%
<i>Bacteroides thetaiotaomicron</i> VPI-5482	3696	4778	77%
<i>Bacteroides caccae</i> ATCC 43185	3375	3855	88%

Supplemental Table 8. Composition of and experimental design for complex diets composed of pureed baby foods

	mouse1	mouse2	mouse3	mouse4	mouse5	mouse6	mouse7	mouse8	g/ kg	
week1	apple sauce	peas	sweet potatoes	peaches	oatmeal	sweet potatoes	rice	beef	666.7	BABY FOOD MEAL 1
	peaches	peaches	chicken	peas	rice	apple sauce	apple sauce	peaches	222.2	
	chicken	chicken	beef	oatmeal	beef	beef	sweet potatoes	sweet potatoes	55.6	
	sweet potatoes	oatmeal	peas	rice	sweet potatoes	peaches	beef	rice	55.6	
week2	TD.09052	TD.09623	TD.09621	TD.09622	TD.09620	TD.09624	TD.09625	TD.09054		Refined Diet
week3	apple sauce	peas	sweet potatoes	peaches	oatmeal	sweet potatoes	rice	beef	666.7	BABY FOOD MEAL 2
	peaches	peaches	chicken	peas	rice	apple sauce	apple sauce	peaches	222.2	
	chicken	chicken	beef	oatmeal	beef	beef	sweet potatoes	sweet potatoes	55.6	
	sweet potatoes	oatmeal	peas	rice	sweet potatoes	peaches	beef	rice	55.6	
week4	TD.09620	TD.09623	TD.09621	TD.09622	TD.09625	TD.09624	TD.09052	TD.09054		Refined Diet
week5	sweet potatoes	chicken	beef	apple sauce	apple sauce	apple sauce	peas	peaches	666.7	BABY FOOD MEAL 3
	oatmeal	peaches	rice	oatmeal	peaches	beef	apple sauce	oatmeal	222.2	
	peaches	beef	peas	chicken	chicken	chicken	sweet potatoes	sweet potatoes	55.6	
	peas	rice	chicken	beef	rice	peaches	peaches	chicken	55.6	
week6	TD.09049	TD.09053	TD.09050	TD.09056	TD.09058	TD.09053	TD.09051	TD.09059		Refined Diet
week7	peas	chicken	peaches	peaches	peas	chicken	sweet potatoes	peas	666.7	BABY FOOD MEAL 4
	rice	sweet potatoes	peas	peas	chicken	peaches	rice	rice	222.2	
	apple sauce	rice	rice	apple sauce	oatmeal	rice	peaches	sweet potatoes	55.6	
	beef	oatmeal	beef	chicken	sweet potatoes	oatmeal	beef	peaches	55.6	
week8	TD.09053	TD.09051	TD.09059	TD.09053	TD.09050	TD.09049	TD.09058	TD.09056		Refined Diet
week9	oatmeal	oatmeal	sweet potatoes	peaches	sweet potatoes	peas	peaches	chicken	421.1	BABY FOOD MEAL 5
	rice	apple sauce	rice	oatmeal	oatmeal	chicken	beef	beef	421.1	
	chicken	beef	chicken	sweet potatoes	chicken	rice	oatmeal	peas	105.3	
	apple sauce	rice	peas	beef	rice	peaches	rice	apple sauce	52.6	
week10	TD.09053	TD.09053	TD.09053	TD.09055	TD.09057	TD.09055	TD.09057	TD.09053		Refined Diet
week11	peas	apple sauce	peaches	sweet potatoes	sweet potatoes	beef	apple sauce	apple sauce	250	BABY FOOD MEAL 6
	oatmeal	rice	oatmeal	beef	apple sauce	peas	oatmeal	rice	250	
	beef	oatmeal	rice	peaches	peaches	chicken	rice	peaches	250	
	chicken	beef	sweet potatoes	rice	beef	oatmeal	beef	chicken	250	

Custom Harlan Teklad Diet Numbers are provided for the weeks mice were on refined diets; details are Table S1.

Supplemental Table 9. Stepwise regression selection of complex diet ingredients significantly associated with changes in species abundance.

	Apple	Beef	Chicken	Oat	Pea	Peach	Rice	Sweet Potato
<i>Desulfovibrio piger</i> GOR1	0.37	0.18	1.26E-04	6.08E-03	0.81	0.10	2.27E-06	0.17
<i>Collinsella aerofaciens</i> ATCC 25986	0.06	4.49E-05	5.55E-07	0.26	0.10	0.91	0.08	0.19
<i>Blautia hydrogenotrophica</i> DSM 10507	0.14	1.73E-03	5.62E-06	0.99	0.14	0.21	0.50	0.57
<i>Clostridium symbiosum</i>	1.14E-03	7.29E-04	2.30E-04	0.25	0.16	4.96E-04	0.35	0.84
<i>Escherichia coli</i> str. K-12 substr. MG1655	4.30E-04	1.42E-03	8.63E-05	0.85	0.28	0.38	7.74E-05	0.70
<i>Bryantella formatexigens</i> DSM 14469	0.48	0.07	0.87	0.38	0.98	0.10	0.96	0.18
<i>Eubacterium rectale</i> ATCC 33656	3.77E-05	0.27	0.07	6.27E-06	0.13	2.76E-03	0.68	0.58
<i>Bacteroides caccae</i> ATCC 43185	0.28	7.56E-06	2.00E-05	0.37	0.57	0.76	2.46E-03	3.72E-02
<i>Bacteroides thetaiotaomicron</i> VPI-5482	2.31E-05	0.78	0.12	3.51E-03	1.94E-02	6.52E-04	0.31	0.43
<i>Bacteroides ovatus</i> ATCC 8483	0.20	0.46	1.00	1.43E-08	0.92	0.11	0.16	0.34

Table S10. Mean Weight Gain (g/diet period)

mouse	m1	m2	m3	m4	m5	m6	m7	m8	m9	m10	m11	m12	m13
2 nd diet period	0.891	1.400	1.909	2.291	1.527	-1.909	-1.655	-1.145	2.927	0.636	0.255	2.291	0.636
3 rd diet period	0.800	0.000	0.600	1.200	0.300	0.600	0.100	1.400	-0.100	1.900	1.200	-0.700	1.000
4 th diet period	1.400	2.800	0.700	2.300	1.100	2.400	1.300	2.700	3.300	0.300	1.100	1.900	2.700

Table S11. Weight gain as a function casein and corn oil concentration

A. Weight gain per diet period as a function of Casein concentration

% Casein	Mean Weight Gain (g/diet period)	SEM
7%	0.589	0.386
23%	1.233	0.295
46%	1.233	0.294

B. Weight gain per diet period as a function of Corn oil concentration

% Corn Oil	Mean Weight Gain (g/diet period)	SEM
1%	0.900	0.180
5%	1.110	0.301
20%	1.211	0.463

BACCAC03166	3.92E-02	-0.35	RUMHYD00057	2.00E-02	-0.39
BACCAC03167	3.52E-02	-0.35	RUMHYD00079	3.31E-02	-0.36
BACCAC03174	3.65E-02	-0.35	RUMHYD00184	4.71E-02	-0.33
BACCAC03184	4.65E-02	-0.33	RUMHYD00278	1.33E-02	-0.41
BACCAC03200	2.57E-02	-0.37	RUMHYD00303	3.17E-02	-0.36
BACCAC03241	2.27E-03	-0.49	RUMHYD00327	3.67E-02	-0.35
BACCAC03279	1.51E-02	-0.40	RUMHYD00411	4.09E-02	-0.34
BACCAC03290	4.35E-02	0.34	RUMHYD00412	4.43E-02	-0.34
BACCAC03330	4.13E-02	-0.34	RUMHYD00419	2.41E-03	-0.49
BACCAC03341	2.97E-02	-0.36	RUMHYD00456	4.91E-02	-0.33
BACCAC03384	3.25E-02	-0.36	RUMHYD00475	3.45E-02	-0.35
BACCAC03403	4.59E-02	-0.33	RUMHYD00501	3.77E-02	-0.35
BACCAC03412	4.39E-02	-0.34	RUMHYD00585	3.40E-02	-0.35
BACCAC03436	1.63E-02	-0.40	RUMHYD00621	2.73E-03	-0.48
BACCAC03446	2.15E-02	-0.38	RUMHYD00714	5.47E-03	0.45
BACCAC03448	2.01E-02	-0.39	RUMHYD00721	4.16E-02	-0.34
BACCAC03450	9.68E-03	-0.43	RUMHYD00739	4.25E-02	-0.34
BACCAC03453	4.20E-02	-0.34	RUMHYD00764	3.92E-02	-0.35
BACCAC03455	5.86E-03	-0.45	RUMHYD00781	3.08E-02	0.36
BACCAC03484	2.22E-02	-0.38	RUMHYD00791	4.72E-02	-0.33
BACCAC03502	7.12E-03	-0.44	RUMHYD00875	1.43E-02	-0.40
BACCAC03509	1.80E-02	-0.39	RUMHYD00900	1.74E-02	-0.39
BACCAC03546	1.52E-02	-0.40	RUMHYD01024	1.26E-03	-0.52
BACCAC03548	4.32E-02	-0.34	RUMHYD01047	2.21E-03	-0.49
BACCAC03561	6.44E-04	-0.54	RUMHYD01091	3.72E-02	-0.35
BACCAC03569	3.07E-02	-0.36	RUMHYD01275	4.95E-02	-0.33
BACCAC03571	1.43E-02	-0.40	RUMHYD01291	4.86E-02	0.33
BACCAC03576	3.39E-03	-0.48	RUMHYD01396	2.97E-02	-0.36
BACCAC03585	1.35E-02	-0.41	RUMHYD01409	7.12E-03	-0.44
BACCAC03630	4.90E-02	-0.33	RUMHYD01603	2.38E-02	-0.38
BACCAC03649	4.88E-02	-0.33	RUMHYD01626	4.92E-02	0.33
BACCAC03667	3.75E-02	-0.35	RUMHYD01631	4.14E-02	-0.34
BACCAC03683	3.61E-02	-0.35	RUMHYD01651	3.36E-02	-0.35
BACCAC03718	3.47E-04	-0.56	RUMHYD01654	3.05E-02	-0.36
BACCAC03719	7.75E-04	-0.53	RUMHYD01673	2.61E-02	-0.37
BACCAC03836	4.38E-02	-0.34	RUMHYD01712	8.23E-03	-0.43
BACCAC03838	1.44E-02	-0.40	RUMHYD01891	3.60E-02	0.35
BACCAC03890	1.50E-02	-0.40	RUMHYD01893	4.12E-02	0.34
BACCAC03904	3.64E-02	-0.35	RUMHYD02053	3.12E-02	-0.36
COLAER00051	4.78E-02	0.33	RUMHYD02056	2.76E-02	-0.37
COLAER00093	9.92E-03	0.43	RUMHYD02105	3.82E-02	-0.35
COLAER00454	4.77E-02	-0.33	RUMHYD02244	3.07E-02	-0.36
COLAER00889	8.86E-04	0.53	RUMHYD02245	7.39E-03	0.44
COLAER00897	4.94E-02	0.33	RUMHYD02247	2.52E-03	0.49
COLAER01064	5.40E-03	0.45	RUMHYD02248	8.84E-03	0.43
COLAER01108	2.72E-02	0.37	RUMHYD02249	8.49E-03	0.43
COLAER01634	3.84E-02	0.35	RUMHYD02250	9.89E-04	0.53
COLAER01647	4.86E-02	0.33	RUMHYD02251	3.72E-02	0.35
COLAER01686	4.12E-02	0.34	RUMHYD02252	2.59E-02	0.37
COLAER01755	4.22E-02	0.34	RUMHYD02253	3.53E-03	0.47
COLAER01776	2.05E-02	0.38	RUMHYD02254	2.35E-02	0.38
COLAER01950	4.15E-02	0.42	RUMHYD02256	1.07E-02	0.42
COLAER02318	4.35E-02	0.34	RUMHYD02339	4.42E-02	0.34
COLAER02388	2.93E-02	-0.36	RUMHYD02402	2.75E-02	-0.37
BACOVA00068	3.00E-02	-0.36	RUMHYD02471	3.19E-02	0.36
BACOVA00250	4.28E-02	0.34	RUMHYD02718	1.76E-02	-0.39
BACOVA00280	1.69E-02	-0.40	RUMHYD02805	3.52E-02	0.35
BACOVA00301	4.00E-02	-0.34	RUMHYD02880	2.44E-02	-0.37
BACOVA00382	4.67E-02	0.33	RUMHYD02890	4.08E-02	-0.34
BACOVA00406	3.50E-02	-0.35	RUMHYD03006	3.11E-02	0.36
BACOVA00559	8.09E-03	-0.43	RUMHYD03078	2.85E-02	-0.37
BACOVA00726	4.86E-02	-0.33	RUMHYD03084	4.63E-02	-0.33
BACOVA00800	3.92E-02	-0.33	RUMHYD03218	4.48E-02	-0.34
BACOVA00836	3.77E-02	0.35	RUMHYD03264	5.64E-03	-0.45
BACOVA00867	6.33E-03	-0.45	RUMHYD03300	1.89E-03	-0.50
BACOVA00925	3.01E-02	0.36	RUMHYD03463	3.59E-02	-0.35
BACOVA00932	3.23E-02	-0.36	RUMHYD03511	2.30E-02	0.38
BACOVA00972	2.58E-02	0.37	RUMHYD03554	1.88E-02	-0.39
BACOVA01042	6.66E-03	0.44	RUMHYD03588	4.82E-02	-0.33
BACOVA01189	3.66E-02	-0.35	RUMHYD03602	4.10E-02	0.34
BACOVA01192	1.64E-02	-0.40	RUMHYD03626	4.94E-02	-0.33
BACOVA01405	4.20E-02	-0.34	RUMHYD03645	4.75E-02	-0.33
BACOVA01639	1.68E-03	0.50	RUMHYD03646	1.01E-02	-0.42
BACOVA02033	1.13E-02	0.41	RUMHYD03686	3.69E-02	-0.35
BACOVA02107	4.35E-02	-0.34	RUMHYD03700	1.71E-02	-0.39
BACOVA02120	2.82E-02	-0.37	RUMHYD03701	2.09E-02	-0.38
BACOVA02250	1.85E-02	-0.39	RUMHYD03742	4.28E-02	0.34
BACOVA02331	4.97E-02	0.33	RUMHYD03836	3.11E-02	-0.36
BACOVA02349	2.25E-02	-0.38	BRYFOR05030	8.94E-03	-0.43
BACOVA02379	3.84E-02	0.35	BRYFOR05031	4.12E-02	-0.34
BACOVA02396	3.61E-02	0.35	BRYFOR05052	3.87E-02	-0.35
BACOVA02606	1.41E-02	0.41	BRYFOR05055	1.40E-02	-0.41
BACOVA02654	1.82E-02	-0.39	BRYFOR05081	1.45E-02	0.40
BACOVA02736	3.07E-03	-0.48	BRYFOR05091	4.41E-02	-0.34
BACOVA02796	3.90E-02	-0.35	BRYFOR05092	6.94E-03	-0.44
BACOVA02902	3.67E-02	-0.35	BRYFOR05107	2.78E-02	0.37
BACOVA02956	1.61E-02	0.40	BRYFOR05111	4.34E-03	-0.46
BACOVA03131	4.89E-02	-0.33	BRYFOR05141	5.49E-03	-0.45
BACOVA03161	2.81E-02	-0.37	BRYFOR05161	3.77E-02	-0.35
BACOVA03236	8.63E-03	-0.43	BRYFOR05162	3.38E-02	-0.35
BACOVA03519	2.38E-02	-0.38	BRYFOR05175	3.23E-02	-0.36
BACOVA03520	2.43E-02	-0.37	BRYFOR05177	4.66E-02	-0.33
BACOVA03637	1.83E-02	0.39	BRYFOR05186	1.42E-02	-0.41
BACOVA03777	2.25E-02	0.38	BRYFOR05202	2.74E-02	-0.37
BACOVA03846	3.92E-02	-0.35	BRYFOR05217	3.15E-02	-0.36
BACOVA04004	2.93E-02	-0.36	BRYFOR05218	1.10E-02	-0.42
BACOVA04024	3.01E-02	0.36	BRYFOR05286	2.32E-02	-0.38
BACOVA04043	2.66E-02	-0.37	BRYFOR05288	4.78E-02	-0.33
BACOVA04271	3.05E-02	0.36	BRYFOR05374	3.13E-02	-0.36
BACOVA04289	3.67E-02	-0.35	BRYFOR05398	1.71E-02	-0.40
BACOVA04338	4.97E-02	-0.33	BRYFOR05400	2.04E-02	-0.39
BACOVA04390	4.78E-02	-0.33	BRYFOR05441	3.07E-03	-0.48
BACOVA04628	1.33E-02	0.41	BRYFOR05442	1.61E-02	-0.40
BACOVA04878	1.62E-02	-0.40	BRYFOR05486	2.83E-02	-0.37
BACOVA05181	8.00E-03	-0.44	BRYFOR05511	1.22E-02	-0.41
BACOVA05242	3.69E-02	-0.35	BRYFOR05548	3.80E-02	0.35
BACOVA05310	1.79E-02	0.39	BRYFOR05582	1.37E-02	-0.41
BACOVA05382	3.87E-02	0.35	BRYFOR05605	4.95E-02	-0.33
BACOVA05535	4.00E-03	0.47	BRYFOR05614	2.61E-02	-0.37
RUMHYD00057	8.40E-03	0.43	BRYFOR05628	1.83E-02	-0.39
RUMHYD00066	1.08E-02	0.42	BRYFOR05632	6.48E-03	-0.45
RUMHYD00276	1.97E-02	0.39	BRYFOR05728	7.98E-03	-0.44
RUMHYD00327	3.39E-02	0.35	BRYFOR05749	6.32E-03	-0.45
RUMHYD00412	3.77E-02	0.35	BRYFOR05763	2.46E-02	-0.37
RUMHYD00419	7.39E-03	0.44	BRYFOR05790	4.65E-02	-0.33
RUMHYD00462	9.54E-03	-0.43	BRYFOR05792	3.79E-02	-0.35
RUMHYD00498	1.82E-02	0.39	BRYFOR05797	2.74E-02	-0.37
RUMHYD00563	3.54E-02	0.35	BRYFOR05800	1.35E-02	-0.41

RUMHYD00621	4.41E-03	0.46	BRYFOR05823	2.79E-03	-0.48
RUMHYD00663	1.44E-02	0.40	BRYFOR05875	4.10E-02	-0.34
RUMHYD00665	1.21E-02	0.41	BRYFOR05876	1.68E-02	-0.40
RUMHYD00675	2.69E-02	0.37	BRYFOR05903	3.21E-02	-0.36
RUMHYD00714	1.45E-02	-0.40	BRYFOR05996	2.58E-02	-0.37
RUMHYD00758	3.42E-02	0.35	BRYFOR05997	6.08E-03	-0.45
RUMHYD00762	1.29E-02	0.41	BRYFOR06002	1.27E-02	-0.41
RUMHYD00764	4.55E-02	0.34	BRYFOR06005	4.24E-02	-0.34
RUMHYD00775	2.92E-02	0.36	BRYFOR06014	1.41E-02	-0.41
RUMHYD00781	7.94E-03	-0.44	BRYFOR06021	2.97E-02	-0.36
RUMHYD00834	4.61E-02	-0.33	BRYFOR06048	4.79E-02	-0.33
RUMHYD00917	4.80E-02	-0.33	BRYFOR06073	4.49E-02	-0.34
RUMHYD00923	2.18E-02	-0.38	BRYFOR06078	7.82E-03	-0.44
RUMHYD01021	1.12E-02	0.42	BRYFOR06088	1.35E-02	-0.41
RUMHYD01023	4.13E-02	0.34	BRYFOR06102	1.49E-02	-0.40
RUMHYD01024	5.70E-04	0.55	BRYFOR06122	4.37E-02	0.34
RUMHYD01176	3.95E-02	0.34	BRYFOR06125	2.19E-02	-0.38
RUMHYD01186	4.57E-02	0.34	BRYFOR06126	4.13E-04	-0.56
RUMHYD01272	3.31E-02	0.36	BRYFOR06135	2.54E-03	-0.49
RUMHYD01288	4.32E-02	0.34	BRYFOR06183	7.44E-03	-0.44
RUMHYD01371	3.68E-02	0.35	BRYFOR06208	2.47E-02	-0.37
RUMHYD01409	6.53E-03	0.45	BRYFOR06215	2.16E-02	-0.38
RUMHYD01592	2.91E-02	-0.36	BRYFOR06219	3.12E-02	-0.36
RUMHYD01594	3.72E-02	-0.35	BRYFOR06231	3.34E-02	-0.36
RUMHYD01603	3.34E-02	0.36	BRYFOR06233	2.00E-02	-0.39
RUMHYD01722	3.79E-02	-0.35	BRYFOR06237	4.37E-02	-0.34
RUMHYD01731	3.50E-02	0.35	BRYFOR06239	1.43E-02	-0.41
RUMHYD01893	3.21E-02	-0.36	BRYFOR06241	2.88E-02	-0.36
RUMHYD01970	1.51E-02	0.40	BRYFOR06250	3.15E-02	-0.36
RUMHYD01986	2.53E-02	-0.37	BRYFOR06282	4.66E-02	-0.33
RUMHYD02003	1.40E-02	0.41	BRYFOR06287	3.20E-02	-0.36
RUMHYD02053	4.38E-02	0.34	BRYFOR06290	1.29E-02	-0.41
RUMHYD02073	2.33E-02	-0.38	BRYFOR06312	1.31E-02	-0.41
RUMHYD02093	2.84E-02	0.37	BRYFOR06317	3.39E-02	-0.35
RUMHYD02114	3.81E-02	0.35	BRYFOR06323	9.25E-04	-0.53
RUMHYD02239	4.31E-02	0.34	BRYFOR06330	3.53E-02	-0.35
RUMHYD02244	4.12E-02	0.34	BRYFOR06336	4.09E-02	-0.34
RUMHYD02245	4.89E-02	-0.33	BRYFOR06364	6.46E-03	-0.45
RUMHYD02247	1.80E-03	-0.50	BRYFOR06365	1.81E-03	-0.50
RUMHYD02248	9.66E-04	-0.53	BRYFOR06368	5.17E-04	-0.55
RUMHYD02249	4.45E-04	-0.56	BRYFOR06374	1.37E-02	-0.41
RUMHYD02250	4.11E-04	-0.56	BRYFOR06433	4.44E-02	-0.34
RUMHYD02252	6.05E-03	-0.45	BRYFOR06554	2.94E-02	-0.36
RUMHYD02253	1.17E-02	-0.42	BRYFOR06560	3.38E-02	-0.35
RUMHYD02254	1.77E-02	-0.39	BRYFOR06633	4.13E-02	-0.34
RUMHYD02255	4.59E-02	-0.33	BRYFOR06639	5.92E-03	-0.45
RUMHYD02256	4.44E-02	-0.34	BRYFOR06677	4.73E-02	-0.33
RUMHYD02473	4.31E-02	0.34	BRYFOR06691	1.03E-03	-0.52
RUMHYD02494	1.76E-02	0.39	BRYFOR06700	4.76E-02	-0.33
RUMHYD02753	4.00E-02	0.34	BRYFOR06718	2.74E-02	-0.37
RUMHYD02777	2.55E-02	-0.37	BRYFOR06793	4.76E-02	-0.33
RUMHYD02785	2.45E-02	-0.35	BRYFOR06855	4.90E-02	-0.33
RUMHYD02829	4.97E-02	-0.33	BRYFOR06856	4.14E-02	-0.34
RUMHYD02880	3.19E-02	0.36	BRYFOR06859	1.96E-02	-0.39
RUMHYD02890	4.76E-02	0.33	BRYFOR06893	4.42E-02	-0.34
RUMHYD03028	1.75E-02	0.39	BRYFOR06905	4.82E-02	-0.33
RUMHYD03033	4.36E-02	0.34	BRYFOR06933	2.51E-03	-0.49
RUMHYD03042	4.37E-02	0.34	BRYFOR06961	8.16E-03	-0.43
RUMHYD03106	3.81E-02	0.35	BRYFOR06976	1.93E-02	-0.39
RUMHYD03264	3.18E-02	0.36	BRYFOR06982	4.93E-02	-0.33
RUMHYD03300	3.54E-02	0.35	BRYFOR07066	7.31E-03	-0.44
RUMHYD03458	2.37E-02	-0.38	BRYFOR07108	2.80E-02	-0.37
RUMHYD03463	1.06E-02	0.38	BRYFOR07147	1.60E-02	-0.40
RUMHYD03511	2.48E-02	-0.37	BRYFOR07198	9.12E-03	-0.43
RUMHYD03626	3.76E-02	0.35	BRYFOR07260	2.25E-02	-0.38
RUMHYD03646	8.26E-03	0.43	BRYFOR07285	3.30E-02	-0.36
RUMHYD03700	2.32E-02	0.38	BRYFOR07301	4.86E-02	-0.33
RUMHYD03701	4.09E-02	0.34	BRYFOR07328	3.06E-02	-0.36
RUMHYD03735	3.18E-02	-0.36	BRYFOR07336	1.05E-02	-0.42
RUMHYD03755	4.78E-02	-0.33	BRYFOR07341	7.64E-03	-0.44
RUMHYD03774	4.44E-02	0.34	BRYFOR07351	4.43E-02	-0.34
RUMHYD03779	3.18E-02	-0.36	BRYFOR07375	8.08E-03	-0.43
RUMHYD03828	4.15E-02	0.34	BRYFOR07384	3.86E-02	-0.35
RUMHYD03862	1.76E-02	0.39	BRYFOR07405	1.56E-02	-0.40
BRYFOR05012	4.68E-03	0.46	BRYFOR07465	1.54E-02	-0.40
BRYFOR05030	4.28E-03	0.46	BRYFOR07490	2.88E-03	-0.48
BRYFOR05045	5.65E-03	0.45	BRYFOR07567	4.39E-02	-0.34
BRYFOR05052	4.61E-02	0.33	BRYFOR07609	1.61E-02	-0.40
BRYFOR05055	3.59E-03	0.47	BRYFOR07613	2.69E-02	-0.37
BRYFOR05067	3.77E-02	0.35	BRYFOR07642	4.43E-02	-0.34
BRYFOR05077	3.39E-02	-0.35	BRYFOR07644	5.04E-03	-0.46
BRYFOR05086	3.80E-02	0.35	BRYFOR07670	7.89E-03	-0.44
BRYFOR05089	1.27E-02	0.41	BRYFOR07723	2.42E-03	-0.49
BRYFOR05091	8.42E-03	0.43	BRYFOR07750	1.05E-02	0.42
BRYFOR05092	1.64E-03	0.51	BRYFOR07756	3.43E-02	-0.35
BRYFOR05166	1.84E-02	0.39	BRYFOR07763	2.18E-02	-0.38
BRYFOR05175	2.24E-02	0.38	BRYFOR07769	1.89E-02	-0.39
BRYFOR05177	3.64E-03	0.47	BRYFOR07770	4.02E-03	-0.47
BRYFOR05181	3.23E-02	0.36	BRYFOR07773	4.80E-03	-0.46
BRYFOR05186	1.60E-02	0.40	BRYFOR07829	4.21E-02	-0.34
BRYFOR05202	7.76E-03	0.44	BRYFOR07837	3.40E-02	0.35
BRYFOR05218	3.58E-02	0.35	BRYFOR07893	1.17E-02	-0.42
BRYFOR05234	3.43E-02	0.35	BRYFOR07953	3.00E-03	-0.48
BRYFOR05286	8.24E-03	0.43	BRYFOR07969	3.21E-02	-0.36
BRYFOR05303	3.94E-02	0.34	BRYFOR07981	2.34E-02	-0.38
BRYFOR05313	4.53E-02	0.34	BRYFOR08008	6.89E-04	-0.53
BRYFOR05338	2.16E-02	0.38	BRYFOR08040	1.58E-02	-0.40
BRYFOR05347	4.05E-02	0.34	BRYFOR08051	6.71E-03	-0.44
BRYFOR05349	4.82E-03	-0.46	BRYFOR08057	4.60E-02	-0.33
BRYFOR05361	1.27E-02	0.41	BRYFOR08058	4.05E-02	-0.34
BRYFOR05374	4.67E-02	0.33	BRYFOR08070	5.96E-04	-0.54
BRYFOR05381	6.22E-03	0.45	BRYFOR08145	4.93E-02	-0.33
BRYFOR05441	4.70E-04	0.55	BRYFOR08159	3.29E-02	-0.36
BRYFOR05442	4.02E-03	0.47	BRYFOR08161	3.35E-02	0.36
BRYFOR05480	3.18E-02	0.36	BRYFOR08173	2.27E-02	-0.38
BRYFOR05486	8.89E-03	0.43	BRYFOR08179	1.93E-02	-0.39
BRYFOR05511	2.18E-02	0.38	BRYFOR08180	1.98E-02	0.39
BRYFOR05544	1.61E-02	0.40	BRYFOR08219	4.44E-02	-0.34
BRYFOR05582	3.70E-02	0.35	BRYFOR08242	3.41E-02	-0.35
BRYFOR05605	1.13E-02	0.42	BRYFOR08269	1.58E-02	-0.40
BRYFOR05610	4.15E-02	0.34	BRYFOR08283	3.34E-02	-0.36
BRYFOR05614	4.29E-03	0.46	BRYFOR08343	1.66E-02	-0.40
BRYFOR05624	7.81E-03	0.44	BRYFOR08347	1.64E-02	-0.40
BRYFOR05627	4.26E-02	0.34	BRYFOR08369	4.82E-03	-0.46
BRYFOR05628	4.62E-02	0.33	BRYFOR08385	1.23E-02	-0.41
BRYFOR05629	1.92E-02	0.39	BRYFOR08390	1.42E-02	-0.41
BRYFOR05631	2.70E-02	0.37	BRYFOR08398	7.52E-03	-0.44
BRYFOR05632	4.14E-02	0.34	BRYFOR08400	1.73E-02	-0.39

BRYFOR05695	1.93E-02	0.39	BRYFOR08449	8.65E-03	-0.43
BRYFOR05699	1.88E-02	0.39	BRYFOR08467	3.95E-02	-0.34
BRYFOR05728	9.61E-03	0.43	BRYFOR08475	1.30E-02	-0.41
BRYFOR05761	4.83E-02	0.33	BRYFOR08547	4.88E-03	-0.46
BRYFOR05763	4.58E-02	0.33	BRYFOR08637	3.67E-03	-0.47
BRYFOR05767	4.78E-02	0.33	BRYFOR08649	3.02E-02	-0.36
BRYFOR05772	9.53E-03	0.43	BRYFOR08666	5.92E-03	-0.45
BRYFOR05779	1.13E-02	0.42	BRYFOR08682	1.66E-02	-0.40
BRYFOR05787	4.03E-02	0.34	BRYFOR08683	1.79E-02	-0.39
BRYFOR05789	2.65E-02	0.37	BRYFOR08693	1.38E-03	-0.51
BRYFOR05790	1.18E-02	0.41	BRYFOR08711	1.22E-02	-0.41
BRYFOR05791	9.36E-03	0.43	BRYFOR08713	6.93E-03	-0.44
BRYFOR05792	2.50E-03	0.49	BRYFOR08718	4.38E-02	-0.34
BRYFOR05800	7.05E-03	0.44	BRYFOR08722	3.36E-02	-0.36
BRYFOR05823	3.60E-02	0.35	BRYFOR08742	2.94E-02	-0.36
BRYFOR05833	3.14E-02	0.36	BRYFOR08755	2.21E-02	0.38
BRYFOR05835	8.44E-03	0.43	BRYFOR08766	4.35E-02	-0.34
BRYFOR05839	3.73E-02	-0.35	BRYFOR08809	4.78E-02	-0.33
BRYFOR05847	6.56E-03	0.44	BRYFOR08820	2.65E-02	-0.37
BRYFOR05857	3.15E-02	0.36	BRYFOR08828	3.64E-02	-0.35
BRYFOR05870	4.08E-02	0.34	BRYFOR08829	3.74E-02	-0.35
BRYFOR05875	3.93E-02	0.35	BRYFOR08867	9.92E-03	-0.42
BRYFOR05903	2.13E-02	0.38	BRYFOR08871	2.48E-03	-0.49
BRYFOR05988	3.58E-02	0.35	BRYFOR08879	4.76E-02	-0.33
BRYFOR05996	6.02E-04	0.54	BRYFOR08889	2.97E-02	-0.36
BRYFOR05997	1.70E-03	0.50	BRYFOR08914	4.66E-03	-0.46
BRYFOR06001	1.51E-02	0.40	BRYFOR08921	1.33E-02	-0.41
BRYFOR06002	3.51E-02	0.35	BRYFOR08922	2.32E-02	-0.38
BRYFOR06005	1.05E-02	0.42	BRYFOR08951	4.25E-02	-0.34
BRYFOR06006	3.61E-02	0.35	BRYFOR08985	2.57E-02	-0.37
BRYFOR06021	7.59E-03	0.44	BRYFOR08999	3.56E-02	-0.35
BRYFOR06057	3.95E-02	0.34	BRYFOR09014	7.52E-04	-0.54
BRYFOR06073	1.05E-02	0.42	BRYFOR09017	1.07E-02	-0.42
BRYFOR06078	1.02E-02	0.42	BRYFOR09025	7.30E-03	-0.44
BRYFOR06088	1.69E-03	0.50	BRYFOR09067	8.22E-03	-0.43
BRYFOR06102	2.91E-04	0.57	BRYFOR09069	2.58E-02	-0.37
BRYFOR06117	2.63E-02	0.37	BRYFOR09080	3.14E-02	-0.36
BRYFOR06126	1.39E-03	0.51	BRYFOR09099	2.03E-03	-0.50
BRYFOR06135	4.33E-04	0.56	BRYFOR09101	1.14E-02	-0.42
BRYFOR06174	2.05E-02	0.38	BRYFOR09113	1.13E-02	-0.42
BRYFOR06179	4.72E-02	0.39	BRYFOR09121	1.49E-02	-0.40
BRYFOR06183	6.09E-03	0.45	BRYFOR09136	1.29E-02	-0.41
BRYFOR06200	4.35E-02	0.34	BRYFOR09138	3.23E-02	-0.36
BRYFOR06208	4.28E-03	0.46	BRYFOR09144	2.24E-02	-0.38
BRYFOR06219	1.57E-02	0.40	BRYFOR09177	4.68E-02	-0.33
BRYFOR06231	3.24E-02	0.36	BRYFOR09178	3.51E-02	-0.35
BRYFOR06233	6.59E-03	0.44	BRYFOR09187	6.49E-03	-0.45
BRYFOR06239	1.06E-02	0.42	BRYFOR09218	8.03E-03	-0.43
BRYFOR06241	2.89E-02	0.36	BRYFOR09225	4.07E-02	-0.34
BRYFOR06250	3.76E-02	0.35	BRYFOR09256	4.78E-02	-0.33
BRYFOR06259	4.05E-03	0.47	BRYFOR09272	1.66E-02	-0.40
BRYFOR06263	3.09E-02	0.34	BRYFOR09276	3.16E-03	-0.48
BRYFOR06270	2.96E-02	0.36	BRYFOR09310	8.87E-03	-0.43
BRYFOR06287	6.73E-04	0.54	BRYFOR09314	3.65E-02	-0.35
BRYFOR06290	8.73E-03	0.43	BRYFOR09315	3.68E-02	-0.35
BRYFOR06297	4.28E-02	0.34	BRYFOR09377	4.09E-02	-0.34
BRYFOR06311	5.95E-03	0.45	BRYFOR09412	9.50E-03	-0.43
BRYFOR06312	2.40E-02	0.38	BRYFOR09423	1.58E-02	-0.40
BRYFOR06317	8.76E-03	0.43	BRYFOR09428	2.82E-03	-0.48
BRYFOR06318	4.22E-02	0.34	BRYFOR09429	1.76E-02	-0.39
BRYFOR06323	1.28E-02	0.41	BRYFOR09430	4.61E-02	-0.33
BRYFOR06330	3.64E-02	0.35	BRYFOR09431	2.87E-03	-0.48
BRYFOR06333	4.72E-02	0.33	BRYFOR09456	4.79E-02	-0.33
BRYFOR06364	8.33E-03	0.43	BRYFOR09498	8.06E-03	-0.43
BRYFOR06365	4.81E-02	0.33	BRYFOR09533	4.58E-02	-0.33
BRYFOR06368	1.36E-02	0.41	BRYFOR09586	2.54E-02	-0.37
BRYFOR06374	1.52E-03	0.51	BRYFOR09600	4.70E-02	-0.33
BRYFOR06376	4.76E-02	0.33	BRYFOR09619	2.89E-02	-0.36
BRYFOR06377	4.04E-02	0.34	BRYFOR09656	2.01E-02	-0.39
BRYFOR06385	3.52E-02	0.35	BRYFOR09765	4.82E-02	-0.33
BRYFOR06429	2.80E-02	0.37	BRYFOR09768	1.37E-02	-0.41
BRYFOR06433	2.57E-02	0.37	BRYFOR09791	1.13E-02	-0.42
BRYFOR06492	1.77E-02	0.39	BRYFOR09812	1.40E-02	-0.41
BRYFOR06529	4.95E-02	0.33	BRYFOR09831	1.10E-03	-0.52
BRYFOR06554	8.97E-03	0.43	BRYFOR09843	3.84E-02	-0.35
BRYFOR06560	3.04E-02	0.36	BRYFOR09862	1.24E-02	-0.41
BRYFOR06563	2.28E-02	0.38	BRYFOR09878	4.53E-02	-0.34
BRYFOR06579	1.08E-02	0.42	BRYFOR09895	1.88E-02	-0.39
BRYFOR06601	2.05E-02	0.38	BRYFOR09910	4.52E-02	-0.34
BRYFOR06639	3.96E-02	0.34	BRYFOR09925	4.88E-02	-0.33
BRYFOR06659	1.03E-02	0.42			
BRYFOR06677	2.48E-02	0.37			
BRYFOR06687	1.93E-02	0.39			
BRYFOR06691	1.19E-02	0.41			
BRYFOR06700	4.05E-02	0.34			
BRYFOR06707	3.10E-03	0.48			
BRYFOR06738	3.07E-02	0.36			
BRYFOR06750	6.91E-03	0.44			
BRYFOR06793	3.27E-02	0.36			
BRYFOR06809	2.65E-02	0.37			
BRYFOR06816	4.82E-02	0.33			
BRYFOR06869	2.27E-02	-0.38			
BRYFOR06892	3.97E-03	0.47			
BRYFOR06893	2.18E-02	0.38			
BRYFOR06905	3.85E-02	0.35			
BRYFOR06933	1.17E-03	0.52			
BRYFOR06961	1.17E-03	0.52			
BRYFOR06976	4.51E-02	0.34			
BRYFOR06978	2.09E-02	0.38			
BRYFOR06982	1.70E-02	0.40			
BRYFOR06988	1.04E-02	0.42			
BRYFOR07011	4.77E-02	0.33			
BRYFOR07040	4.66E-02	0.33			
BRYFOR07066	7.34E-03	0.44			
BRYFOR07101	2.32E-02	0.38			
BRYFOR07102	4.78E-02	0.33			
BRYFOR07155	1.30E-02	0.41			
BRYFOR07161	3.13E-02	0.36			
BRYFOR07186	5.33E-03	0.45			
BRYFOR07187	4.68E-02	0.33			
BRYFOR07195	3.68E-02	0.35			
BRYFOR07198	2.03E-02	0.39			
BRYFOR07204	1.16E-02	0.42			
BRYFOR07211	7.69E-03	0.44			
BRYFOR07217	3.53E-02	0.35			
BRYFOR07228	9.19E-03	0.43			
BRYFOR07247	9.00E-03	0.43			
BRYFOR07248	1.65E-02	0.40			

BRYFOR07255	3.09E-02	0.36
BRYFOR07260	1.03E-03	0.52
BRYFOR07261	1.47E-02	0.40
BRYFOR07285	1.16E-02	0.42
BRYFOR07301	2.60E-02	0.37
BRYFOR07336	1.78E-02	0.39
BRYFOR07337	3.16E-02	0.36
BRYFOR07341	3.36E-03	0.48
BRYFOR07344	4.92E-02	0.33
BRYFOR07345	2.81E-02	0.37
BRYFOR07350	1.84E-02	0.39
BRYFOR07373	1.23E-02	0.41
BRYFOR07375	2.27E-04	0.58
BRYFOR07379	2.29E-02	0.38
BRYFOR07382	1.94E-02	0.39
BRYFOR07384	3.52E-02	0.35
BRYFOR07405	1.71E-02	0.40
BRYFOR07406	2.41E-02	-0.38
BRYFOR07415	6.53E-03	0.45
BRYFOR07435	4.64E-02	0.33
BRYFOR07489	9.90E-03	0.42
BRYFOR07490	1.94E-03	0.50
BRYFOR07566	9.39E-03	0.43
BRYFOR07567	1.01E-02	0.42
BRYFOR07574	1.59E-02	0.40
BRYFOR07584	3.23E-03	0.48
BRYFOR07586	2.91E-02	0.36
BRYFOR07587	6.58E-03	0.44
BRYFOR07609	4.66E-03	0.46
BRYFOR07613	3.47E-03	0.47
BRYFOR07621	2.22E-02	0.38
BRYFOR07626	4.23E-02	0.34
BRYFOR07629	3.74E-02	0.35
BRYFOR07633	3.30E-02	0.36
BRYFOR07642	3.66E-02	0.35
BRYFOR07644	4.98E-05	0.62
BRYFOR07652	2.51E-02	0.37
BRYFOR07670	2.56E-04	0.57
BRYFOR07677	2.67E-02	0.37
BRYFOR07696	3.18E-02	0.36
BRYFOR07700	3.23E-02	0.36
BRYFOR07723	3.21E-03	0.48
BRYFOR07730	2.80E-02	0.37
BRYFOR07745	3.94E-02	0.34
BRYFOR07750	2.32E-02	-0.38
BRYFOR07756	1.24E-02	0.41
BRYFOR07763	2.03E-02	0.39
BRYFOR07770	3.69E-03	0.47
BRYFOR07773	2.37E-02	0.38
BRYFOR07797	1.92E-02	0.39
BRYFOR07809	3.36E-02	0.36
BRYFOR07841	2.10E-02	0.38
BRYFOR07860	3.63E-02	0.35
BRYFOR07866	4.51E-02	-0.34
BRYFOR07893	1.41E-02	0.41
BRYFOR07948	4.14E-02	0.34
BRYFOR07953	3.94E-03	0.47
BRYFOR07979	4.66E-02	0.33
BRYFOR07980	4.19E-02	0.34
BRYFOR07981	2.63E-02	0.37
BRYFOR08007	4.71E-02	0.33
BRYFOR08008	3.16E-03	0.48
BRYFOR08009	3.38E-02	0.35
BRYFOR08011	4.42E-02	0.34
BRYFOR08013	1.58E-02	0.40
BRYFOR08033	3.41E-02	0.35
BRYFOR08051	3.89E-03	0.47
BRYFOR08057	1.30E-02	0.41
BRYFOR08070	1.95E-03	0.50
BRYFOR08081	1.62E-02	0.40
BRYFOR08083	2.60E-02	0.37
BRYFOR08085	2.55E-02	0.37
BRYFOR08088	9.33E-03	0.43
BRYFOR08094	4.69E-03	0.46
BRYFOR08117	8.34E-03	0.43
BRYFOR08121	2.00E-02	0.39
BRYFOR08135	2.94E-02	0.36
BRYFOR08145	2.26E-03	0.49
BRYFOR08149	2.02E-02	0.39
BRYFOR08158	1.10E-02	0.42
BRYFOR08159	7.56E-03	0.44
BRYFOR08161	1.28E-02	-0.41
BRYFOR08172	2.66E-02	0.37
BRYFOR08173	1.94E-02	0.39
BRYFOR08179	3.78E-03	0.47
BRYFOR08190	2.17E-02	0.38
BRYFOR08194	1.63E-02	0.40
BRYFOR08219	4.20E-02	0.34
BRYFOR08227	2.25E-02	0.38
BRYFOR08242	2.16E-02	0.38
BRYFOR08246	4.11E-02	0.34
BRYFOR08269	1.21E-02	0.41
BRYFOR08270	3.69E-02	0.35
BRYFOR08283	3.04E-02	0.36
BRYFOR08292	3.74E-02	0.35
BRYFOR08318	4.64E-02	0.33
BRYFOR08327	4.60E-02	0.33
BRYFOR08343	6.31E-04	0.54
BRYFOR08346	1.38E-02	0.41
BRYFOR08368	9.34E-03	0.43
BRYFOR08369	1.91E-03	0.50
BRYFOR08376	1.90E-02	0.39
BRYFOR08385	4.84E-02	0.33
BRYFOR08390	2.78E-02	0.37
BRYFOR08397	3.91E-02	0.35
BRYFOR08398	9.26E-03	0.43
BRYFOR08400	1.21E-02	0.41
BRYFOR08425	9.91E-03	0.42
BRYFOR08438	8.92E-03	0.43
BRYFOR08440	8.07E-03	0.43
BRYFOR08475	4.16E-02	0.34
BRYFOR08534	5.08E-03	0.46
BRYFOR08547	4.04E-03	0.47
BRYFOR08588	2.82E-02	0.37
BRYFOR08589	1.71E-02	0.40
BRYFOR08617	2.63E-02	0.37
BRYFOR08637	1.58E-03	0.51
BRYFOR08645	4.62E-02	0.33

BRYFOR08666	8.06E-03	0.43
BRYFOR08682	2.50E-02	0.37
BRYFOR08683	2.41E-03	0.49
BRYFOR08693	2.42E-02	0.38
BRYFOR08713	2.80E-03	0.48
BRYFOR08722	3.79E-03	0.47
BRYFOR08737	1.83E-02	0.39
BRYFOR08742	7.02E-03	0.44
BRYFOR08766	1.01E-02	0.42
BRYFOR08799	2.05E-02	0.38
BRYFOR08801	3.54E-02	0.35
BRYFOR08818	9.43E-03	0.43
BRYFOR08828	4.85E-02	0.33
BRYFOR08829	4.02E-03	0.47
BRYFOR08835	2.01E-02	0.39
BRYFOR08839	4.51E-02	0.34
BRYFOR08854	1.38E-02	0.41
BRYFOR08863	2.80E-02	0.37
BRYFOR08867	1.86E-02	0.39
BRYFOR08871	4.95E-03	0.46
BRYFOR08879	4.14E-02	0.34
BRYFOR08889	2.21E-02	0.38
BRYFOR08891	4.76E-02	0.33
BRYFOR08908	1.96E-02	0.39
BRYFOR08914	2.43E-03	0.49
BRYFOR08921	1.43E-02	0.40
BRYFOR08922	1.48E-02	0.40
BRYFOR09004	6.05E-03	0.45
BRYFOR09014	1.54E-04	0.59
BRYFOR09017	1.55E-03	0.51
BRYFOR09025	4.26E-03	0.47
BRYFOR09033	4.98E-02	0.33
BRYFOR09046	3.50E-02	0.35
BRYFOR09067	7.95E-03	0.44
BRYFOR09069	9.67E-03	0.43
BRYFOR09080	2.67E-02	0.37
BRYFOR09090	3.52E-02	0.35
BRYFOR09099	5.90E-03	0.45
BRYFOR09101	1.69E-02	0.40
BRYFOR09106	2.36E-02	0.38
BRYFOR09120	7.12E-03	0.44
BRYFOR09121	1.10E-02	0.42
BRYFOR09123	1.55E-02	0.40
BRYFOR09135	1.69E-02	0.40
BRYFOR09136	2.37E-02	0.38
BRYFOR09138	4.24E-02	0.34
BRYFOR09144	1.61E-02	0.40
BRYFOR09145	4.76E-02	0.33
BRYFOR09155	1.43E-02	0.40
BRYFOR09177	1.94E-02	0.39
BRYFOR09181	1.68E-02	0.40
BRYFOR09187	4.46E-03	0.46
BRYFOR09218	3.75E-03	0.47
BRYFOR09239	1.88E-02	0.39
BRYFOR09255	4.42E-02	0.34
BRYFOR09256	4.09E-02	0.34
BRYFOR09260	5.14E-03	0.46
BRYFOR09268	4.03E-03	0.47
BRYFOR09272	1.34E-02	0.41
BRYFOR09276	4.23E-02	0.34
BRYFOR09296	6.22E-03	0.45
BRYFOR09310	5.65E-03	0.45
BRYFOR09324	4.45E-02	0.34
BRYFOR09327	2.26E-02	0.38
BRYFOR09330	1.20E-02	0.41
BRYFOR09359	1.62E-02	0.40
BRYFOR09412	3.23E-03	0.48
BRYFOR09428	2.24E-02	0.38
BRYFOR09429	1.21E-02	0.41
BRYFOR09431	2.29E-03	0.49
BRYFOR09436	3.76E-02	0.35
BRYFOR09445	1.98E-02	0.39
BRYFOR09456	1.26E-02	0.41
BRYFOR09461	1.18E-02	0.42
BRYFOR09498	8.42E-03	0.43
BRYFOR09514	4.67E-02	0.33
BRYFOR09551	4.22E-02	0.34
BRYFOR09553	2.85E-02	0.37
BRYFOR09570	6.95E-03	0.44
BRYFOR09597	3.46E-02	0.35
BRYFOR09598	2.57E-02	0.37
BRYFOR09600	3.59E-02	0.35
BRYFOR09601	2.28E-02	0.38
BRYFOR09619	2.62E-03	0.49
BRYFOR09658	2.06E-02	0.38
BRYFOR09685	2.50E-02	0.37
BRYFOR09751	2.55E-02	0.37
BRYFOR09765	1.02E-02	0.42
BRYFOR09768	1.53E-02	0.40
BRYFOR09773	3.31E-02	0.36
BRYFOR09786	3.50E-02	0.35
BRYFOR09812	9.82E-03	0.42
BRYFOR09823	3.03E-02	0.36
BRYFOR09828	8.02E-03	-0.43
BRYFOR09831	2.18E-03	0.49
BRYFOR09834	8.75E-03	0.43
BRYFOR09843	3.56E-02	0.35
BRYFOR09862	1.86E-02	0.39
BRYFOR09863	4.62E-02	0.33
BRYFOR09878	3.92E-02	0.35
BRYFOR09890	4.98E-02	-0.33
BRYFOR09895	2.64E-02	0.37
BRYFOR09910	9.15E-03	0.43
BRYFOR09924	1.87E-02	0.39
BRYFOR09925	4.82E-02	0.33

Supplemental Table 13. Fecal DNA yields from diverse protein diets

mouse	diet	nanograms (mean±SEM)
m1	TD.10321	19716 ± 5689
m2	TD.10309	15488 ± 7023
m3	TD.10314	3781 ± 2906
m4	TD.10316	27989 ± 5462
m5	TD.10311	10378 ± 1515
m6	TD.10319	14283 ± 3203
m7	TD.10310	18604 ± 1007
m8	TD.10307	259 ± 75
m9	TD.10308	19684 ± 9045