Table S1: Ingredient list of the inpatient omnivore menus, Related to **Figure 1**.

Menu A	**MenuB**
Breakfast: Scrambled Eggs English Muffin Butter Jelly	Breakfast: Plain yogurt Jam Peanut Butter Apple slices
Lunch: Ham Sandwich on wheat bread with lettuce and mayonnaise Broccoli and cheese soup Apple slices Pretzels	Lunch: Turkey and American cheese Sandwich on Wheat Salad greens with red cabbage, carrots, and Italian Dressing Potato Chips Fresh Grapes
Snack: American cheese Saltines Graham crackers	Snack: Graham crackers Peanut butter Orange slices Milk (skim)
Dinner: Roasted Chicken Breast Mashed Potatoes Cooked Carrots Salad greens with red cabbage, carrots, and Italian Dressing White Dinner Roll with Butter Pound Cake with Strawberries	Dinner: Spaghetti with Meatballs (beef) and Marinara Sauce Salad greens with red cabbage, carrots, and Ranch Dressing Shortbread cookies
Snack: Rice cake Peanut butter Milk (2%)	Snack: Vanilla milkshake

Table S3: PubMed PMID annotations for primary source literature describing the involvement of metabolites identified in **Figure 7B** in a bacterial metabolic pathway.

Metabolite Name	HMDB ID	References		
histamine	HMDB00870	PMID 16960050	PMID 15935495	
diaminopimelate	HMDB01370	PMID 10881998	PMID 10508663	
4-acetamidobutanoate	HMDB03681	PMID 29808030		
quinolinate	HMDB00232	PMID 14700627	PMID 23471408	
agmatine	HMDB01432	PMID 7791519	PMID 17099215	
xanthurenate	HMDB00881	PMID 6029734		
N6-acetyllysine	HMDB00206	PMID 26687465		
N6-acetyl-L-lysine	HMDB00206	PMID 26687465		
hydrocinnamate (phenylpropionate)	HMDB00764	PMID 29168502		
pyridoxamine	HMDB01431	PMID 16350099	PMID 27890703	
N-acetylglutamine	HMDB06029	PMID 30008290		
urocanic acid	HMDB00301	PMID 16742726	PMID 10443033	
indole	HMDB00738	PMID 14569285	PMID 20070374	
D-alany-D-alanine	HMDB03459	PMID 26526529	PMID 2386365	
acetytyrosine	HMDB00866			
pipecolic acid	HMDB00716	PMID 16418868		
N-acetylhistamine	HMDB13253	PMID 4225158		
2-hydroxy-3-methylpentanoate	HMDB00317	PMID 9873747		
phenyllactate	HMDB00779	PMID 20660314		
indoleacetate	HMDB00197	PMID 22447903	PMID 27102537	PMID 29168502
indolelactate	HMDB00671	PMID 6791576	PMID 20925672	PMID 29168502
indole-3-propionate	HMDB02302	PMID 29168502		
methylimidazole acetic acid	HMDB02820	PMID 2228870	PMID 13804909	
gentisate	HMDB00152	PMID 23418504	PMID 26394696	
ornithine	HMDB00214	PMID 3534538	PMID 16887608	
homovanillate	HMDB00118	PMID 8586270		
leucylglycine	HMDB28929	PMID 19734283		
formylmethionine	HMDB01015	PMID 26866044		
3-hydroxyanthranilic acid	HMDB01476	PMID 14700627		
tryptamine	HMDB00303	PMID 22447903		
imidazoleacetic acid	HMDB02024	PMID 4925814	PMID 11330718	
cadaverine	HMDB02322	PMID 21684749		
citrulline	HMDB00904	PMID 15939575		
imidazole propionate	HMDB02271	PMID 30401435	PMID 22933560	
2-aminoadipate	HMDB00510	PMID 16232683		

Table S4: Characteristics of participants, Related to **STAR Methods**.

	Vegan diet (n=10)	Omnivore diet (n=10)	EEN diet (n=10)	P value
Age (median years, range)	24.3 (20.5 – 32.2)	27.0 (22.3 – 60.8)	32.2 (20.3 – 59.5)	0.12
Male sex	6	8	6	0.69
White race	9	9	9	>0.99
Hispanic ethnicity	0	1	1*	0.75
BMI	21.3 (19.7 – 25.1)	23.4 (20.5 – 28.2)	28.2 (20.3 – 35.4)	0.003

[*]Self-reported ethnicity information was not provided.

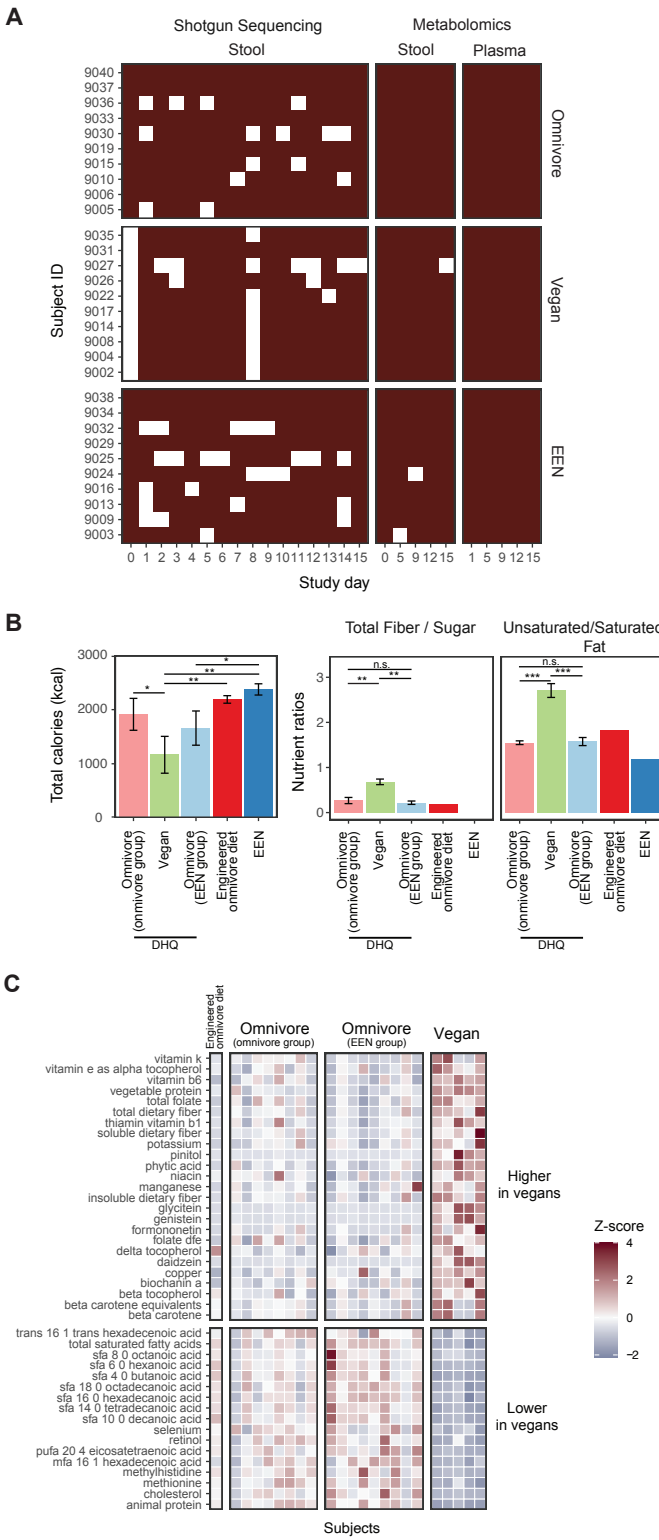

Figure S1. Dietary composition and samples collected in the FARMM study, Related to **Figure 1**. A) Samples collected and processed for each subject. The tiles are filled if data are available for that subject. Stool was collected each day when available. Plasma was collected only 5 days out of the 15 day course. B) Total caloric intake, total fiber to simple sugar ratio, and the unsaturated to saturated fat ratios of the participants usual diets as well as the study diets (linear model, *p<0.05, **p<0.01, ***p<0.001). C) All the nutrients that are significantly higher or lower in the vegan diets compared to all the baseline omnivore diets (linear models, *q<0.05,**q<0.01, ***q<0.001). The engineered omnivore diet is also shown as reference. EEN diet is not shown since the constituents are proprietary information. The values represent Z-scores for each nutrient.

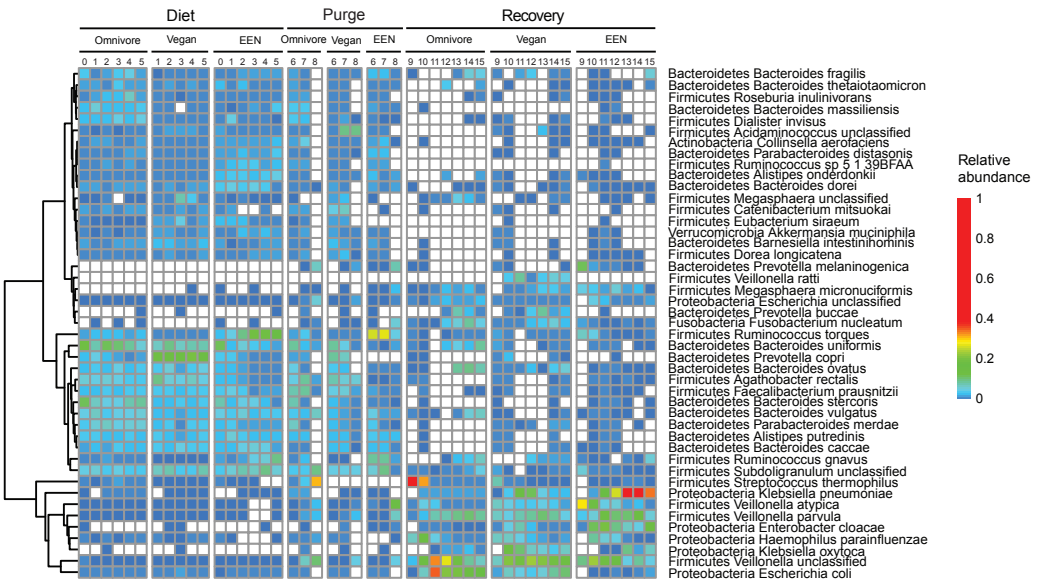

Figure S2. Relative abundance of the bacterial species that have a mean relative abundance of greater than 0.5% across all samples, Related to **Figure 2**. The relative abundances were then averaged for each diet and study day. The values represent the mean abundance of subjects for the annotated diet and study day.

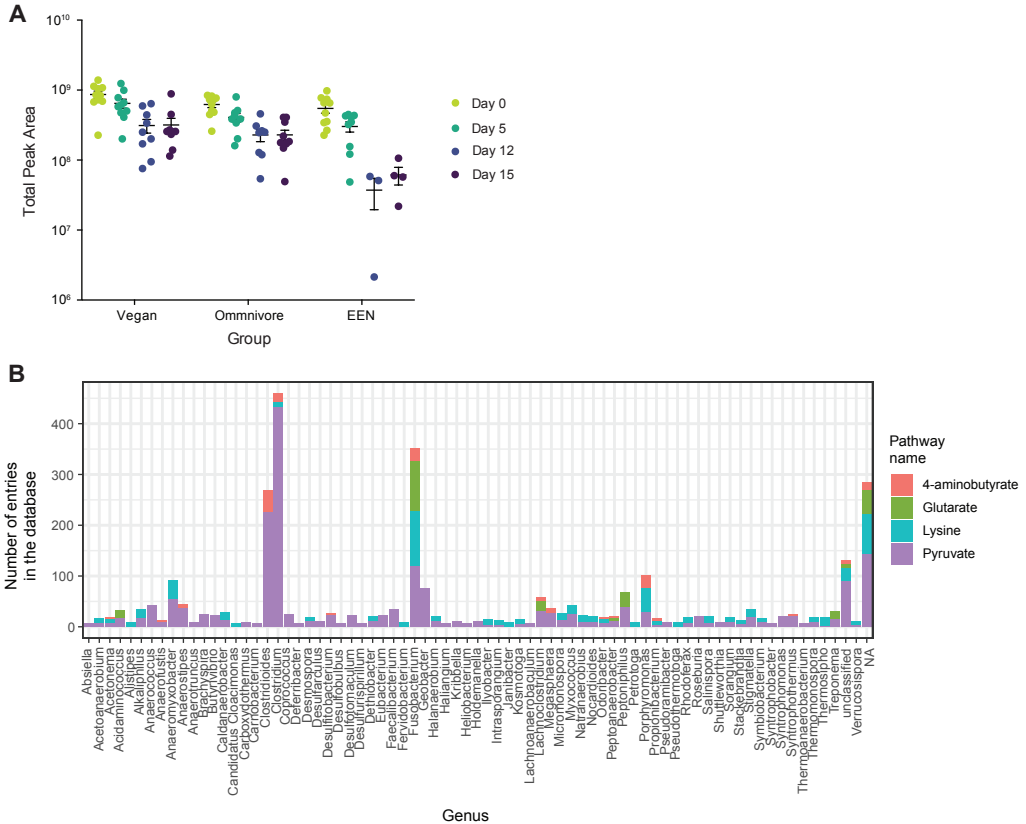

Figure S3. Stool butyrate levels and genera with genes related to various butyrate production pathways, Related to **Figure 4**. A) Stool butyrate levels (total peak area) on days 0, 5, 9, 12, and 15 of the study in the vegan, omnivore, and EEN groups. Data is presented as mean +/- SEM. Samples with butyrate levels below the limit of detection are not shown. On Day 9, butyrate levels were below the limit of detection in all but one sample and were excluded from this graph. B) The number of protein sequence entries in the IMG database and their corresponding organisms at the genus level for bacterial butyrate production. The counts are grouped by their pathway annotations for butyrate production pathways as described by Vital et al. (2014).

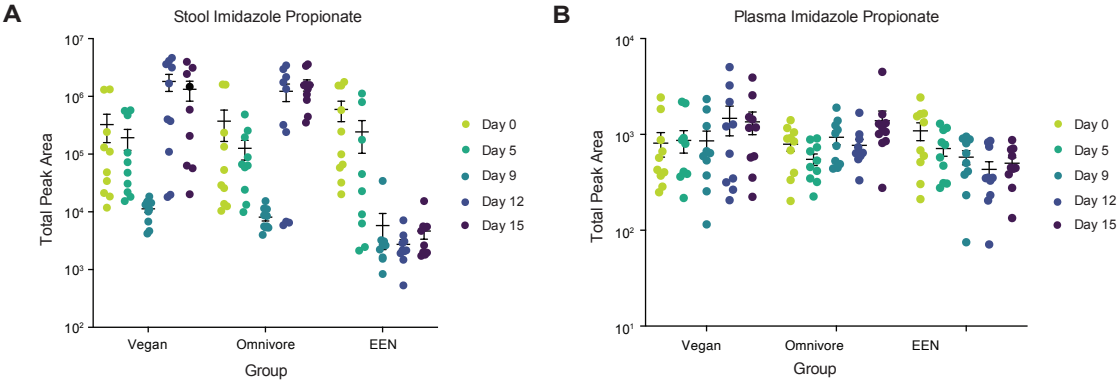

Figure S4. Imidazole propionate levels (total peak area) in stool and plasma in the vegan, omnivore, and EEN groups, Related to **Figure 7**. Data is presented as mean +/- SEM. Samples below the limit of detection are not shown. There are significant group (p=0.0043), time (p=0.0002), and group by time (p=0.0003) effects in stool; however, there is only a significant group by time (p=0.006) effect in plasma (mixed-effects modeling).

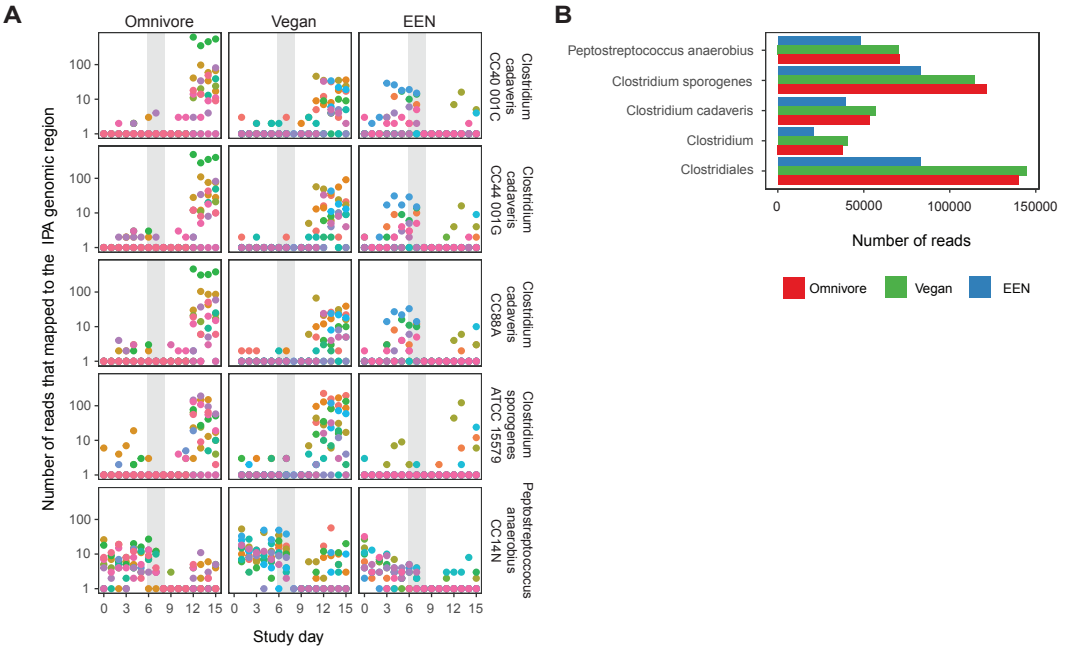

Figure S5. Relative abundance of 5 bacterial taxa previously described to produce IPA from tryptophan, Related to **Figure 7**. A) Reads were mapped to the genomic region responsible for IPA production for the five bacteria capable of reducing tryptophan to IPA. The number of reads that map to the region for each sample are represented in the figure. Each color is a different subject. B) The number of reads that map to the protein sequences of genes responsible for IPA production. If a sequence had multiple good hits to more than one protein sequence, the common ancestor of the originating organism was assigned.

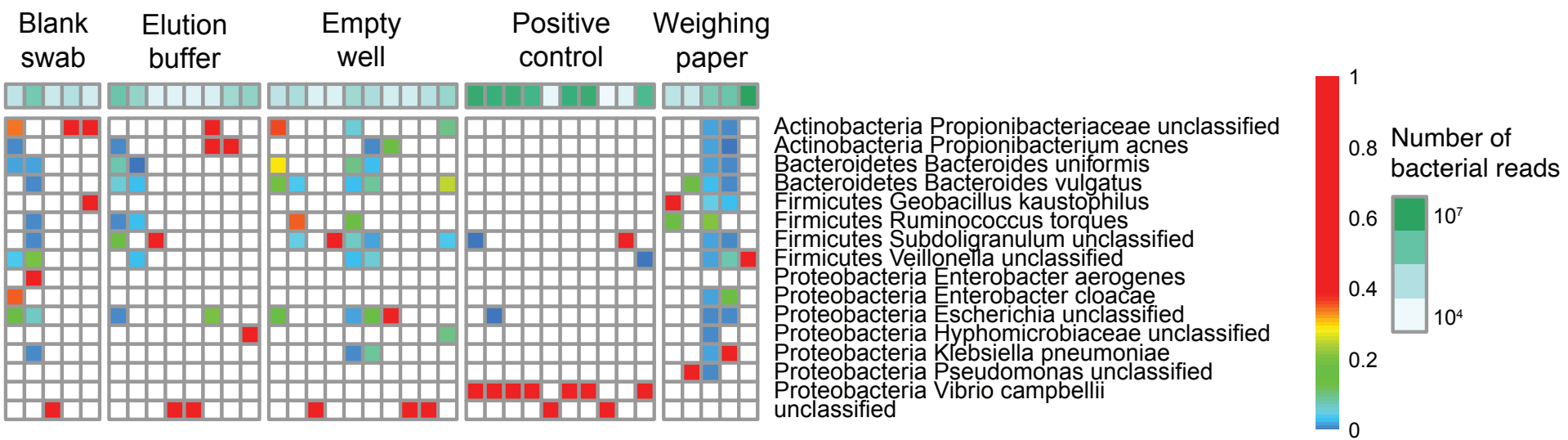

Figure S6. Common taxa in the negative and positive control samples, Related to **STAR Methods**. Positive controls consisted of DNA from Vibrio campbellii and Lambda phage. Elution buffer and wells without any sample DNA were used as negative controls to assess reagent contamination. Blank swabs and weighing paper were processed to assess environmental contamination.