Supplemental Information:
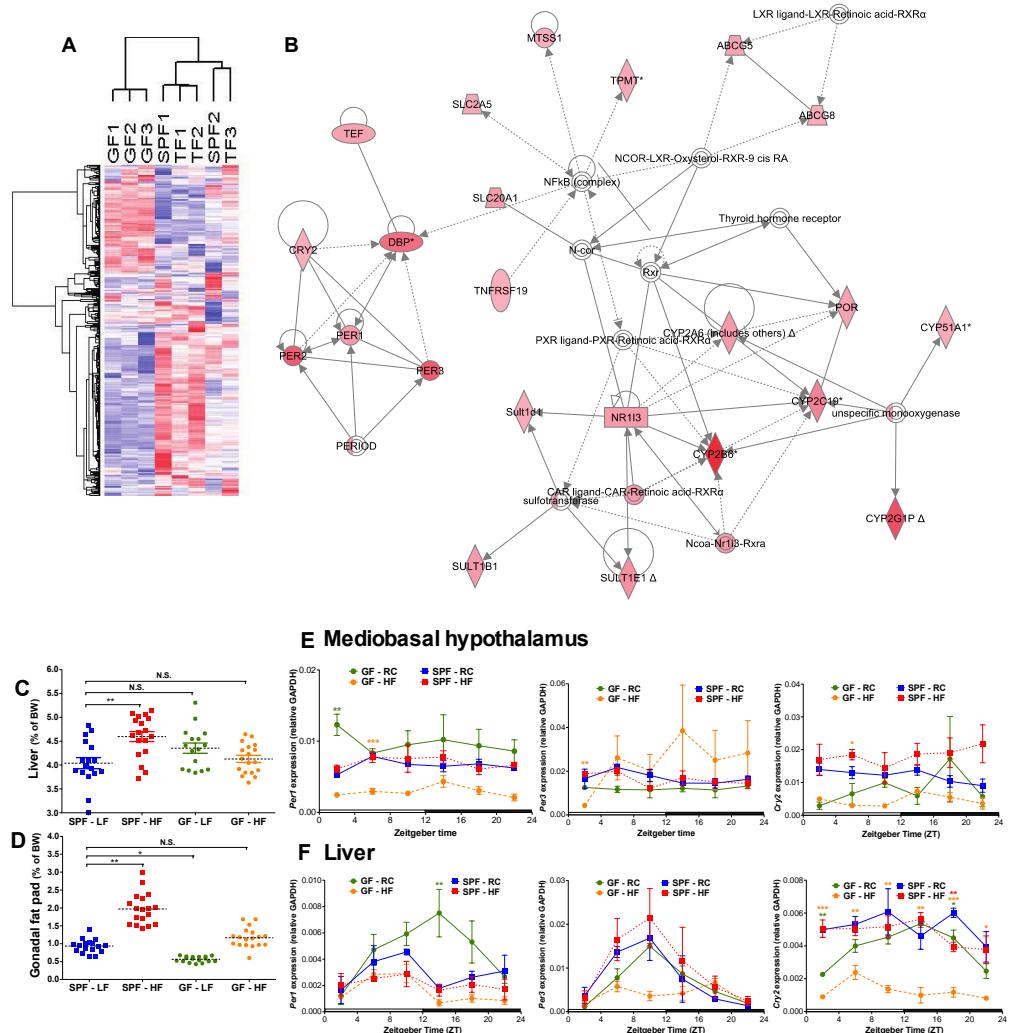
Figure S1. Germ-free mice liver gene transcriptomes cluster separately from colonized mice resulting in altered expression of metabolic gene network pathways, related to Figure 1. Livers from age- and gender-matched germ-free (GF), conventionalized (TF, fecal transplant), and specific pathogen-free (SPF) C57Bl/6 mice were harvested and microarray analysis using Affymetrix Mouse Genome 430 2.0 array was performed (*n* = 2 or 3 per group). Unsupervised heat map (**A**) representing the most variable genes across all samples. Network analysis (**B**) with differentially expressed genes upregulated in liver of GF mice compared to TF mice. Differentially expressed genes were identified by SAM (Significant Analysis of Microarray) software with criteria of fold change > 1.3 and false discover rate <5%. The GF up-regulated genes were submitted to IPA (Ingenuity Pathway Analysis) software, which makes use of its Ingenuity Pathways Knowledge Base (IPKB) with large amounts of individually modeled relationships between gene objects to dynamically generate significant biological networks. The submitted genes that are mapped to the corresponding gene objects in the IPKB are called "focus genes." The focus genes were used to generate biological networks. Gonadal fat pad (**C**) and liver weight (**D**) expressed as percent of body weight (BW) in GF and SPF mice and expressed as mean ± s.e.m. N.S., not significant, *p<0.05, **p<0.01 compared to RC. Diurnal patterns of relative circadian gene expression (*Per1, Per3,* and *Cry2)* in mediobasal hypothalamus (**E**) and liver (**F**) from GF and SPF mice fed RC or HF for five weeks. Data represents mean ± s.e.m. *p<0.05, **p<0.01, ***p<0.001 via one-way ANOVA followed by Dunnett's post-test relative to SPF-RC control. Star color represents treatment exhibiting significant differences from SPF-RC (See Table S2 for CircWave rhythmicity analyses).
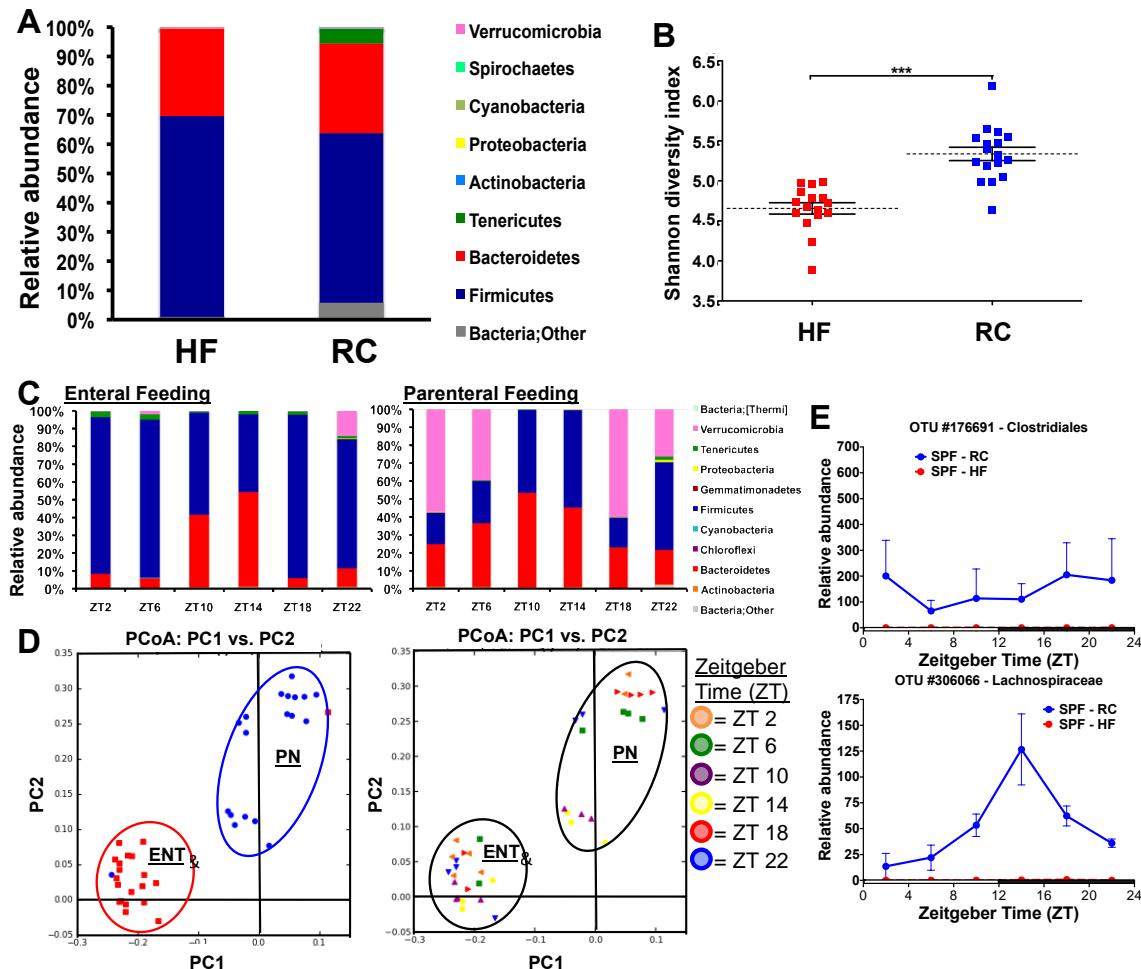
Figure S2. **Gut microbiota structural profile is altered by high fat diet yet gut microbes from parenterally-fed (PN) mice still demonstrate diurnal variation despite altered community structure, related to Figure 2. (A-B)** Cecal samples from SPF C57Bl/6 male mice fed HF or RC diet over 5 weeks were collected over 24 hours (*n*=2 to 3 mice/ZT time point and subjected to 16S amplicon sequencing via Miseq (**A)**, Distribution of bacterial phyla between HF and RC-fed mice. Shannon diversity indices (**B**) are shown for individual mice and represented as means ± s.e.m. ***p<0.001 determined via unpaired t-test. Additionally, cecal samples were collected from age-matched male SPF C57Bl/6 male mice fed via enteral feeding (ENT) or via intravenous infusion with parenteral nutrition (PN) for 72 hours and harvested every four hours over a 24-hour period (*n*=2 to 5 mice/Zeitgeber (ZT) time point). Cecal DNA subjected to 16S rRNA amplicon sequencing via Illumina Miseq (**C**)**,** Average relative abundance of bacterial phyla between ENT and PN at each ZT time point. Multi Response Permutation Procedure (MRPP) analysis showed that both ENT and PN showed significant clustering by ZT time (ENT delta value = 0.0004; PN delta value = 0.0002) (**D**), Principal Coordinate Analysis (PCoA) plot of the weighted UniFrac distances colored by dietary treatment and by ZT time point (PC, principle coordinate). Analysis of similarity (ANOSIM) of both weighted and unweighted β-diversity showed significant differences (p=0.001) in community structure induced by dietary delivery strategy. Multivariate analysis showed that ZT time point was a significant factor for both ENT (ADONIS R^2 = 0.2824, p=0.001) and PN (ADONIS R^2 = 0.3164, p=0.001). Fecal OTUs (**E**) from RC-fed animals that also exhibit significant rhythmicity (as determined by empirical JTK_CYLCE) in cecal contents (see Figure 2F for cecal data). Data represents mean ± s.e.m. Fecal eJTK_CYCLE empirical p-values: OTU #176691 = 0.057; OTU #306066 = 0.073.
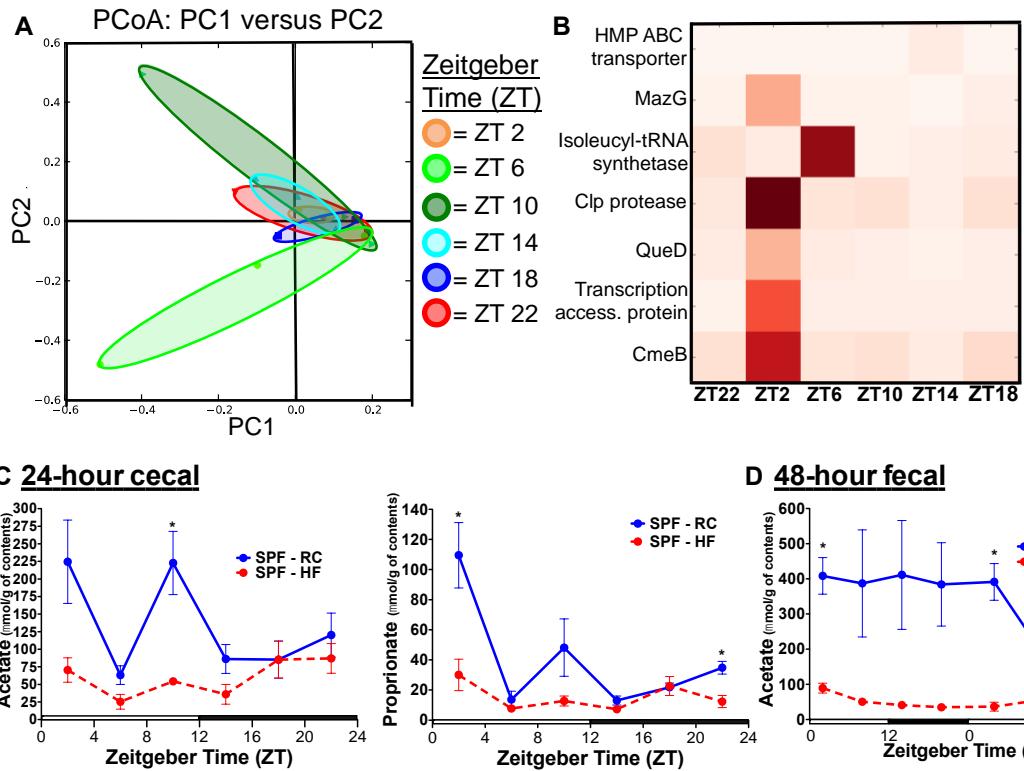
Figure S3. Metagenomic analysis of cecal contents from RC-fed mice reveals no significant change in annotated genes across Zeitgeber time, yet diurnal oscillations in SCFA production are detectable, related to Figure 3. Cecal samples from age-matched male SPF C57Bl/6 male mice fed RC diet for 5 weeks and subjected to shotgun metagenomic sequencing. Abundance tables of SEED annotations were normalized to equivalent sampling depth across samples and the Principal Coordinate Analysis (PCoA) plot (**A**) was generated using QIIME. The PCoA plot is colored by ZT time point (PC = principle coordinate). Heatmap of individual microbial genes (**B**) exhibiting significant diurnal patterns across ZT from metagenomic analysis. Diurnal acetate and proprionate concentration measured by GC-MS-MS from cecal contents (**C**) collected over 24 hours or fecal pellets (**D**) collected over 48 hours from mice fed RC and HF for 5 weeks at time of harvest (cecal) or by repeated sampling every 6 hours over 48 hours (fecal) from individual mice (expressed as µmol/g of content) (*n*=2 to 3 mice/Zeitgeber (ZT) time point). Data represent mean ± s.e.m. *p<0.05 determined via unpaired t-test at each time point. See Table S6 for CircWave rhythmicity analyses of SCFAs.

Supplemental Tables:

Table S1. Dietary composition, Related to Figure 1, Figure 2, and Figure 3

Study Diets	[a]Regular Chow (RC)	[b]18% Saturated milk fat (HF)
Fat (% kcal)	**18**	**37.4**
Saturated	2.6	24.3
-C16:0 Palmitic	2.0	9.7
-C18:0 Stearic	0.6	4.67
-C14:0 Myristic	0	4.4
-Other	0	5.5
Monounsaturated	3.5	11.9
-C18.1 Oleic	3.5	10.5
-Other	0	1.4
Polyunsaturated	9.9	1.3
-C18.2 Linoleic	0	1.1
-C18.3 Linolenic	0.9	0.2
Protein (% kcal)	**24**	**16**
Carbohydrate (% kcal)	**58**	**47**
Starch	58	11.8
Sucrose	0	23.2
Maltodextrin	0	11.8
Fiber (g/kg)	**147**	**45**

[a]Regular chow (RC), 2018S Harlan Teklad Global 18% Protein Rodent Diet. Ingredients in order of inclusion: Ground wheat, ground corn, wheat middlings, dehulled soybean meal, corn gluten meal, soybean oil, calcium carbonate, dicalcium phosphate, brewers dried yeast, iodized salt, L- lysine, DL-methionine, choline chloride, kaolin, magnesium oxide, vitamin E acetate, menadione sodium bisulfite complex (source of vitamin K activity), manganous oxide, ferrous sulfate, zinc oxide, niacin, calcium pantothenate, copper sulfate, pyridoxine hydrochloride, riboflavin, thiamin mononitrate, vitamin A acetate, calcium iodate, vitamin B12 supplement, folic acid, biotin, vitamin D3 supplement, cobalt carbonate.

[b]18% Saturated milk fat (HF), Harlan-Teklad TD.97222 customized diet. Ingredients include (g/kg): Casein (195), DL-Methionine (3), Sucrose (254.924), Corn starch (130), Maltodextrin (140), Anhydrous milkfat (180), cholesterol (2.04), cellulose (45), mineral mix, AIN-76 (35), calcium carbonate (4), vitamin mix Teklad (10), choline bitartrate (1), Ethoxyquin, antioxidant (0.036).

Table S2. Mediobasal hypothalamus (MBH) and liver CircWave cosinor statistical output, related to Figure 1

	Housing	Diet	Gene target	F-statistic (1 sinewave)	P-value	R^2	F-statistic (sinewave + 1 harmonic)	P-value	R^2
MBH	SPF	RC	*bmal1*	0.40	0.677	0.054	2.13	0.139	0.416
	SPF	HF	*bmal1*	2.65	0.103	0.261	1.19	0.363	0.269
	GF	RC	*bmal1*	2.75	0.098	0.282	1.99	0.161	0.398
	GF	HF	*bmal1*	3.97	0.041	0.346	1.94	0.164	0.374
	SPF	RC	*clock*	2.01	0.171	0.223	1.64	0.229	0.353
	SPF	HF	*clock*	1.29	0.305	0.147	0.62	0.655	0.161
	GF	RC	*clock*	1.10	0.361	0.136	0.65	0.641	0.177
	GF	HF	*clock*	1.65	0.229	0.180	2.89	0.065	0.470
	SPF	RC	*per1*	0.91	0.424	0.116	2.20	0.130	0.423
	SPF	HF	*per1*	1.32	0.298	0.150	0.58	0.680	0.152
	GF	RC	*per1*	0.00	0.997	0.000	0.31	0.866	0.094
	GF	HF	*per1*	2.95	0.083	0.282	2.75	0.074	0.458
	SPF	RC	*per2*	1.55	0.249	0.181	1.42	0.284	0.322
	SPF	HF	*per2*	0.89	0.430	0.106	0.10	0.446	0.235
	GF	RC	*per2*	1.07	0.370	0.133	1.15	0.382	0.278
	GF	HF	*per2*	1.12	0.352	0.130	0.80	0.546	0.198
	SPF	RC	*per3*	3.73	0.050	0.348	2.08	0.146	0.410
	SPF	HF	*per3*	1.25	0.316	0.143	2.58	0.087	0.443
	GF	RC	*per3*	0.12	0.890	0.017	0.09	0.983	0.030
	GF	HF	*per3*	5.61	0.015	0.428	3.13	0.052	0.490
	SPF	RC	*cry1*	1.20	0.331	0.146	1.97	0.163	0.397
	SPF	HF	*cry1*	0.32	0.733	0.041	0.15	0.960	0.044
	GF	RC	*cry1*	0.88	0.437	0.112	0.44	0.775	0.129
	GF	HF	*cry1*	9.35	0.002	0.555	5.38	0.009	0.623
	SPF	RC	*cry2*	1.61	0.238	0.187	1.94	0.169	0.393
	SPF	HF	*cry2*	0.53	0.597	0.066	0.25	0.907	0.070
	GF	RC	*cry2*	0.57	0.576	0.076	0.69	0.614	0.187
	GF	HF	*cry2*	2.29	0.135	0.234	4.31	0.020	0.570
Liver	SPF	RC	*bmal1*	61.55	0.000	0.897	46.38	0.000	0.939
	SPF	HF	*bmal1*	25.92	0.000	0.776	14.97	0.000	0.822
	GF	RC	*bmal1*	72.53	0.000	0.912	46.87	0.000	0.940
	GF	HF	*bmal1*	2.46	0.119	0.247	1.27	0.336	0.281
	SPF	RC	*clock*	23.77	0.000	0.773	10.81	0.001	0.783
	SPF	HF	*clock*	19.85	0.000	0.723	9.71	0.001	0.749
	GF	RC	*clock*	20.34	0.000	0.744	11.41	0.000	0.792
	GF	HF	*clock*	3.88	0.044	0.341	2.62	0.084	0.446
	SPF	RC	*per1*	1.09	0.365	0.134	2.45	0.103	0.449
	SPF	HF	*per1*	0.81	0.464	0.097	0.51	0.728	0.136
	GF	RC	*per1*	7.81	0.005	0.527	3.55	0.039	0.542
	GF	HF	*per1*	9.14	0.003	0.549	9.44	0.001	0.744
	SPF	RC	*per2*	4.50	0.031	0.391	2.90	0.068	0.491
	SPF	HF	*per2*	4.36	0.032	0.368	2.75	0.074	0.459
	GF	RC	*per2*	19.61	0.000	0.737	9.75	0.001	0.765
	GF	HF	*per2*	2.86	0.091	0.290	3.38	0.045	0.529
	SPF	RC	*per3*	13.21	0.001	0.670	8.80	0.002	0.762
	SPF	HF	*per3*	6.99	0.007	0.483	3.58	0.035	0.524
	GF	RC	*per3*	25.17	0.000	0.782	20.57	0.000	0.873
	GF	HF	*per3*	1.35	0.290	0.153	5.18	0.010	0.614
	SPF	RC	*cry1*	45.53	0.000	0.867	20.76	0.000	0.874
	SPF	HF	*cry1*	38.46	0.000	0.846	25.59	0.000	0.895
	GF	RC	*cry1*	66.15	0.000	0.904	29.20	0.000	0.907
	GF	HF	*cry1*	2.75	0.096	0.2685	1.40	0.287	0.301
	SPF	RC	*cry2*	0.30	0.744	0.044	0.37	0.822	0.120
	SPF	HF	*cry2*	2.89	0.093	0.271	2.40	0.104	0.425
	GF	RC	*cry2*	19.45	0.000	0.735	12.17	0.000	0.802
	GF	HF	*cry2*	2.96	0.083	0.283	4.26	0.020	0.567

Blue p-value indicates p<0.1; Red p-value indicates p<0.05

Table S3. Empirical JTK_Cycle cecal and fecal OTU rhythmicity, Related to Figure 2

Diet	Taxonomy	OTU ID	Phase	Asymmetry	Mean	Std Dev	Max	Min	Max Amp	FC	IQR FC	Tau	P-value	empP	BH1
RC - fecal	p_Firmicutes; c_Clostridia; o_Clostridiales	175307	8	4	7.67	5.49	25	1	24	25	2.25	0.46	0.0006	0.02	0.77
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_Oscillospira	174770	2	12	422.08	400.06	1463	28	1435	52.25	4.90	0.46	0.0007	0.02	0.77
	p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_S24-7	190673	14	12	78.38	31.01	180	34	146	5.29	1.5	0.44	0.0010	0.03	0.77
	p_Firmicutes; c_Clostridia; o_Clostridiales	199215	2	20	269.46	217.94	964	34	930	28.35	3.31	0.42	0.0018	0.04	0.77
	p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_S24-7	177414	8	20	557.63	208.16	1130	157	973	7.20	1.67	0.42	0.0018	0.04	0.77
	p_Firmicutes; c_Clostridia; o_Clostridiales	196709	2	12	899.25	696.31	3002	122	2880	24.61	3.08	0.41	0.0021	0.05	0.77
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_Oscillospira	321484	8	4	29.25	21.22	75	0	75	-10000	3.14	0.41	0.0025	0.05	0.77
	p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_S24-7	182361	14	12	266.54	181.92	822	72	750	11.42	2.32	0.38	0.0041	0.07	0.81
	p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_S24-7	186028	8	20	647.54	259.47	1268	250	1018	5.10	1.43	0.38	0.0048	0.08	0.81
	p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_S24-7	197623	14	20	365.79	192.98	799	129	670	6.19	2.71	0.37	0.0056	0.09	0.81
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; g_[Ruminococcus]; s_gnavus	4390754	2	4	8.63	7.42	30	2	28	15	2.75	0.37	0.0065	0.10	0.81
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae	173939	2	20	284.79	539.08	2579	4	2575	644.75	7.15	0.36	0.0065	0.10	0.81
HF - fecal	p_Firmicutes; c_Clostridia; o_Clostridiales	273504	2	20	1	0.71	2	0	2	-10000	2	0.46	0.0007	0.02	1.00
	p_Firmicutes; c_Clostridia; o_Clostridiales	177574	20	20	0.71	0.98	3	0	3	-10000	NA	0.44	0.0010	0.02	1.00
	p_Firmicutes; c_Clostridia; o_Clostridiales	175901	20	4	0.67	0.94	4	0	4	-10000	NA	0.39	0.0035	0.06	1.00
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Clostridiaceae	268733	8	20	47.88	58.421	216	1	215	216	19.8	0.37	0.0056	0.09	1.00
	p_Firmicutes; c_Bacilli; o_Lactobacillales; f_Streptococcaceae; g_Lactococcus	1100972	8	20	3934	2297.83	11353	720	10633	15.77	2.31	0.37	0.0056	0.09	1.00
RC - cecum	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_Ruminococcus	261365	18	6	1.65	1.61	4	0	4	-10000	NA	0.66	6.38E-05	0.004	0.18
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_Oscillospira	178959	16	6	17.94	28.18	125	0	125	-10000	4.05	0.64	9.74E-05	0.005	0.18
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae	2374993	16	6	50.41	31.94	115	0	115	-10000	2.14	0.60	0.0002	0.01	0.18
	p_Firmicutes; c_Clostridia; o_Clostridiales	267411	8	22	7.12	8.57	30	0	30	-10000	5.63	0.60	0.0002	0.01	0.18
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae	4440624	10	2	29.88	116.78	497	0	497	-10000	NA	0.59	0.0003	0.02	0.18
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae	258550	18	20	4.35	4.41	18	0	18	-10000	6	0.59	0.0003	0.02	0.18
	p_Firmicutes; c_Bacilli; o_Lactobacillales; f_Lactobacillaceae; g_Lactobacillus	259993	2	8	3.18	2.79	7	0	7	-10000	24	0.58	0.0005	0.02	0.21
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae	306066	16	4	60.59	38.10	150	0	150	-10000	2.66	0.54	0.0009	0.03	0.32
	p_Firmicutes; c_Clostridia; o_Clostridiales	191811	10	20	0.24	0.55	2	0	2	-10000	0	0.51	0.0017	0.06	0.41
	p_Firmicutes; c_Clostridia; o_Clostridiales	176691	12	22	204.65	215.47	743	0	743	-10000	11.81	0.52	0.0017	0.06	0.41
	p_Firmicutes; c_Clostridia; o_Clostridiales	189585	14	2	4.18	7.56	32	0	32	-10000	2.75	0.50	0.0023	0.07	0.41
	p_Firmicutes; c_Clostridia; o_Clostridiales	185177	12	14	0.24	0.64	2	0	2	-10000	0	0.48	0.0030	0.09	0.41
	p_Firmicutes; c_Clostridia; o_Clostridiales	262527	16	6	13.29	33.63	147	0	147	-10000	5.17	0.48	0.0030	0.09	0.41
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae	134065	8	22	40	147.11	628	0	628	-10000	NA	0.49	0.0030	0.09	0.41
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Clostridiaceae	261590	6	20	2	2.11	8	0	8	-10000	2	0.49	0.0030	0.09	0.41
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_Ruminococcus	267042	16	12	46.29	25.42	117	0	117	-10000	1.67	0.48	0.0030	0.09	0.41
HF - cecum	p_Firmicutes; c_Clostridia; o_Clostridiales	4418586	12	2	0.38	0.70	2	0	2	-10000	NA	0.60	0.0004	0.02	0.85
	p_Firmicutes; c_Clostridia; o_Clostridiales	259820	12	14	2	2.09	7	0	7	-10000	NA	0.58	0.0006	0.02	0.85
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae	263272	12	20	76.31	34.08	120	21	99	5.71	2.28	0.55	0.0012	0.04	0.85
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_Oscillospira	167034	12	22	85.13	33.38	140	30	110	4.67	2.04	0.54	0.0017	0.05	0.85
	p_Firmicutes; c_Clostridia; o_Clostridiales	174320	14	2	0.63	0.86	2	0	2	-10000	NA	0.52	0.0023	0.09	0.85
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae	265793	12	18	145.69	59.25	263	14	249	18.79	1.71	0.51	0.0023	0.09	0.85
	p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae	180535	20	22	80.88	35.76	148	26	122	5.69	2	0.51	0.0023	0.09	0.85

Table S4. Empirical JTK_Cycle Biolog™ substrate and sensitivity chemical rhythmicity, related to Figure 3

Diet	Substrate[a]	Waveform	Phase	Asymmetry	Mean	Std Dev	Max	Min	Max Amp	FC	IQR FC	Tau	P-value	empP	BH1
RC	GlcLPrln	cosine	20	4	0.56	0.25	0.84	0.05	0.78	16.42	1.50	0.68	4.78E-07	3.95E-05	0.002
	LAlanine	cosine	20	4	0.54	0.24	0.78	0.05	0.73	15.60	1.52	0.66	9.83E-07	7.80E-05	0.002
	FormcAcd	cosine	20	4	0.63	0.29	0.83	0.08	0.75	10.40	1.11	0.66	9.83E-07	7.80E-05	0.002
	aHydBtAc	cosine	20	4	0.65	0.23	0.82	0.08	0.73	9.66	1.15	0.65	1.39E-06	0.0001	0.002
	ActctcAc	cosine	14	12	0.74	0.25	0.91	0.11	0.80	8.50	1.07	0.64	1.95E-06	0.0001	0.002
	BrmScAcd	cosine	20	4	0.57	0.17	0.69	0.06	0.63	12.17	1.10	0.62	7.02E-06	0.0004	0.004
	AceticAc	cosine	14	12	0.78	0.19	0.90	0.09	0.81	10.06	1.06	0.62	7.02E-06	0.0004	0.004
	aKBtrcAc	cosine	20	4	0.68	0.15	0.78	0.09	0.70	8.92	1.11	0.60	1.28E-05	0.0006	0.006
	D-Rffns	cosine	20	4	0.70	0.22	0.84	0.08	0.76	10.61	1.11	0.60	1.28E-05	0.0006	0.006
	DAsprAcd	cosine	20	4	0.60	0.26	0.86	0.07	0.80	12.78	1.55	0.57	3.90E-05	0.0018	0.012
	Inosine	cosine	20	4	0.58	0.25	0.80	0.05	0.75	15.52	1.25	0.56	3.90E-05	0.0018	0.012
	LLctcAcd	cosine	20	4	0.60	0.22	0.78	0.05	0.73	14.35	1.37	0.56	5.09E-05	0.0023	0.014
	DMalcAcd	cosine	20	4	0.66	0.21	0.81	0.05	0.75	14.87	1.13	0.55	5.09E-05	0.0023	0.014
	QuincAcd	cosine	20	4	0.58	0.21	0.77	0.06	0.71	12.73	1.47	0.52	0.0002	0.0058	0.030
	PrpncAcd	cosine	14	12	0.74	0.25	0.96	0.08	0.87	11.40	1.08	0.52	0.0002	0.0058	0.029
	D-Mlbios	cosine	14	12	0.68	0.18	0.82	0.10	0.72	8.22	1.18	0.51	0.0002	0.0072	0.033
	D-Fucose	cosine	20	4	0.69	0.18	0.82	0.10	0.72	8.40	1.13	0.51	0.0002	0.0072	0.033
	Pectin	cosine	20	4	0.57	0.19	0.74	0.06	0.68	12.32	1.23	0.49	0.0004	0.011	0.047
	DSaccAcd	cosine	20	4	0.62	0.24	0.89	0.06	0.84	15.61	1.22	0.48	0.0004	0.013	0.048
	L-Rhmnse	cosine	20	4	0.69	0.15	0.80	0.10	0.70	8.15	1.10	0.48	0.0004	0.013	0.048
	gAmButAc	cosine	20	4	0.67	0.23	0.81	0.08	0.73	10.28	1.08	0.48	0.0005	0.013	0.048
	D-Turns	cosine	20	4	0.65	0.22	0.82	0.08	0.74	10.61	1.11	0.47	0.0007	0.016	0.056
	LAsprAcd	cosine	20	4	0.63	0.21	0.81	0.05	0.76	14.83	1.15	0.46	0.0008	0.019	0.061
	Stchys	cosine	20	4	0.64	0.21	0.83	0.08	0.75	10.47	1.29	0.46	0.0008	0.019	0.061
	Glucrnmd	cosine	20	4	0.65	0.15	0.79	0.22	0.57	3.56	1.14	0.46	0.0010	0.023	0.063
	L-Fucose	cosine	20	4	0.71	0.14	0.80	0.13	0.68	6.40	1.11	0.46	0.0010	0.023	0.063
	bHDLBAcd	cosine	20	4	0.72	0.17	0.83	0.08	0.75	10.43	1.08	0.46	0.0010	0.023	0.063
	a-D-Lcts	cosine	20	4	0.68	0.19	0.85	0.08	0.77	11.17	1.13	0.44	0.0015	0.033	0.080
	LHstdine	cosine	20	4	0.67	0.20	0.85	0.05	0.80	15.66	1.35	0.44	0.0015	0.033	0.080
	CitrcAcd	cosine	14	12	0.67	0.14	0.82	0.05	0.77	15.99	1.07	0.43	0.0018	0.039	0.092
HF	3MthlGlc	cosine	20	4	0.71	0.17	0.91	0.07	0.84	13.27	1.06	0.52	0.0002	0.007	0.32
	DGlctAcd	cosine	20	4	0.73	0.16	0.87	0.09	0.77	9.37	1.10	0.50	0.0003	0.011	0.32
	MthylPyr	cosine	20	4	0.62	0.11	0.79	0.23	0.56	3.38	1.15	0.49	0.0004	0.013	0.32
	QuincAcd	cosine	14	12	0.64	0.20	0.80	0.06	0.74	12.80	1.08	0.45	0.0016	0.035	0.43
	D-Mlbios	cosine	20	4	0.74	0.16	0.99	0.09	0.89	10.61	1.10	0.44	0.0020	0.042	0.43
	LArgnine	cosine	8	20	0.74	0.09	0.84	0.51	0.33	1.64	1.10	0.44	0.0020	0.042	0.43
	bHDLBAcd	cosine	20	4	0.72	0.21	0.88	0.08	0.80	10.85	1.06	0.43	0.0024	0.049	0.43
Diet	Chemical	Waveform	Phase	Asymmetry	Mean	Std Dev	Max	Min	Max Amp	FC	IQR FC	Tau	P-value	empP	BH1
RC	8%_NaCl	cosine	20	4	0.53	0.23	0.80	0.12	0.68	6.71	1.67	0.66	9.83E-07	7.80E-05	0.002
	SdmBtyrt	cosine	20	4	0.64	0.23	0.90	0.17	0.73	5.22	1.56	0.59	1.70E-05	0.0008	0.007
	RfmycnSV	cosine	20	4	0.49	0.20	0.93	0.14	0.79	6.85	1.57	0.58	2.26E-05	0.0011	0.009
	4%_NaCl	cosine	8	20	0.59	0.16	0.76	0.13	0.63	5.88	1.22	0.48	0.0004	0.013	0.049
	pH_5	cosine	20	4	0.26	0.10	0.55	0.04	0.51	12.71	1.71	0.46	0.0008	0.019	0.061
	Mincycln	cosine	20	1	0.17	0.01	0.20	0.15	0.048	1.31	1.13	0.46	0.0010	0.023	0.062
	SdmBromt	cosine	8	12	0.29	0.16	0.62	0.10	0.52	6.00	3.70	0.45	0.0010	0.023	0.063
	D-Serine	cosine	20	4	0.51	0.25	0.81	0.07	0.75	12.02	2.54	0.45	0.0012	0.028	0.073
	TtrzmBlu	cosine	20	12	0.27	0.08	0.60	0.20	0.40	2.99	1.18	0.44	0.0015	0.033	0.080
HF	SdmBromt	cosine	8	12	0.27	0.17	0.55	0.10	0.45	5.46	4.07	0.52	0.0002	0.0070	0.32
	LthmChlr	cosine	8	20	0.11	0.03	0.24	0.09	0.16	2.80	1.24	0.43	0.0024	0.049	0.431

Substrates[b]

				Sensitivity chemicals	
D-Raffinose	D-Melibiose	D-Salicin	L-Fucose	1% NaCl	Tetrazolium Violet
alpha-D-Glucose	D-Fructose	3-Methyl Glucose	D-Fructose-6-PO$_4$	Niaproof 4	1% Sodium Lactate
D-Sorbitol	D-Arabitol	Glycerol	L-Histidine	Troleandomycin	Tetrazolium Blue
Gelatin	L-Alanine	L-Aspartic Acid	Mucic Acid	Lincomycin	Potassium Tellurite
N-Acetyl-D-Galactosamine	L-Galactonic Acid Lactone	D-Gluconic Acid	D-Malic Acid	Vancomycin	Sodium Bromate
p-HydroxyPhenylatic Acid	D-Lactic Acid Methyl Ester	alpha-Keto-Butyric Acid	Propionic Acid	Nalidixic Acid	Tween-40
Tween 40	Alpha-HydroxyButyric Acid	Gentiobiose	D-Turanose	Aztreonam	
N-Acetyl-B-D-Mannosamine	D-Rehalose	N-Acetyl-D-Glucosamine	Pectin	pH 6	
alpha-D-Lactose	Beta-Methyl-D-Glucoside	D-Fucose	L-Rhamnose	4% NaCl	
D-Mannose	D-Galactose	D-Glucose-6-PO$_4$	D-Aspartic Acid	Fusidic Acid	
D-Mannitol	Myo-Inositol	L-Arginine	L-Pyroglutamic Acid	Rifamycin SV	
Glycyl-L-Proline	N-Acetyl Neuraminic Acid	Glucuronamide	Quinic Acid	Guanidine HCl	
D-Galacturonic Acid	D-Gluconic Acid	alpha-Keto-Glutaric Acid	L-Malic Acid	Minocycline	
Methyl Pyruvate	L-Lactic Acid	Acetoacetic Acid	Acetic Acid	Lithium Chloride	
Gamma-Amino-Butryric Acid	Beta-Hydroxy-D, L-Butyric Acid	Sucrose	Stachyose	Sodium Butyrate	
D-Maltose	D-Cellobiose	Dextrin	L-Glutamic Acid	pH 5	
Inosine	D-Serine	L-Serine		8% NaCl	
D-Saccharic Acid	Bromo-Succinic Acid	Formic Acid		D-serine	

[a]Grey shading indicates unique substrates/chemicals exhibiting significant rhythmicity within dietary treatment in fecal pellets collected via repeat sampling from individual mice over 48 hours (*n* = 3/treatment). Yellow shading indicates substrates/chemicals that exhibiting significant rhythmicity in both dietary treatments.

[b]List of Biolog GEN III MicroPlate™ substrates and sensitivity chemicals

Table S5. **Microbial metabolite and gene abundance CircWave cosinor statistical output, related to Figure 3 and Figure 4**

	Housing	Diet	Measure	F-statistic (1 sinewave)	P-value	R^2	F-statistic (sinewave + 1 harmonic)	P-value	R^2
24h SCFA Cecal	SPF	RC	Acetate	0.97	0.397	0.088	1.67	0.201	0.270
	SPF	HF	Acetate	2.97	0.073	0.221	1.83	0.165	0.278
	SPF	RC	Butyrate	3.44	0.052	0.256	3.33	0.032	0.426
	SPF	HF	Butyrate	2.10	0.147	0.167	1.11	0.385	0.189
	SPF	RC	Proprionate	2.11	0.158	0.232	2.57	0.092	0.462
	SPF	HF	Proprionate	1.50	0.257	0.167	0.90	0.495	0.216
48h SCFA Fecal	SPF	RC	Acetate	0.60	0.557	0.054	0.30	0.874	0.059
	SPF	HF	Acetate	0.84	0.447	0.074	0.49	0.743	0.094
	SPF	RC	Butyrate	6.33	0.007	0.376	5.40	0.004	0.532
	SPF	HF	Butyrate	3.16	0.064	0.240	2.73	0.062	0.378
24h H_2S Cecal	SPF	RC	H_2S	9.03	0.003	0.546	4.40	0.018	0.575
	SPF	HF	H_2S	0.56	0.583	0.070	0.25	0.906	0.071
48h H_2S Fecal	SPF	RC	H_2S	0.78	0.472	0.076	0.66	0.627	0.135
	SPF	HF	H_2S	5.14	0.015	0.329	2.40	0.086	0.335
Microbial DNA	SPF	RC	Ros_Eub	1.33	0.298	0.160	1.23	0.353	0.291
	SPF	HF	Ros_Eub	0.49	0.624	0.065	0.85	0.519	0.222
	SPF	RC	16S	7.88	0.006	0.548	5.45	0.011	0.665
	SPF	HF	16S	1.77	0.206	0.202	1.18	0.371	0.283
	SPF	RC	dsrAB	2.50	0.115	0.250	1.68	0.213	0.341
	SPF	HF	dsrAB	1.94	0.181	0.217	2.94	0.066	0.495

	Treatment	Gene		F-statistic (1 sinewave)	P-value	R^2	F-statistic (sinewave + 1 harmonic)	P-value	R^2
Hepanoids	Acetate	bmal1		1.08	0.374	0.164	0.44	0.776	0.164
	Acetate	per2		2.36	0.140	0.300	0.10	0.473	0.300
	Butyrate	bmal1		6.51	0.014	0.542	2.66	0.102	0.542
	Butyrate	per2		4.74	0.033	0.463	1.94	0.188	0.463
	NaHS	bmal1		2.75	0.117	0.379	1.07	0.441	0.379
	NaHS	per2		0.39	0.686	0.080	0.15	0.956	0.080
	NoTrt	bmal1		3.50	0.067	0.389	1.43	0.299	0.390
	NoTrt	per2		0.66	0.534	0.108	0.27	0.889	0.108

Blue p-value indicates $p<0.1$; Red p-value indicates $p<0.05$

SUPPLEMENTAL EXPERIMENTAL PROCEDURES:

Host RNA extraction and analysis
Total RNA was extracted from MBH and liver as previously described (Wang et al., 2010). cDNA synthesis was performed using SuperScript II (Invitrogen) and random hexanucleotide primers. Forward and Reverse primers were added to iQSYBR Green PCR Supermix (Bio-rad) to amplify *clock*, *bmal1*, *per1-3*, and *cry1-2*. Real-time quantitative PCR was performed on a Lightcycler 480 System (Roche Applied Science). Gene expression levels were determined using the comparative C_T method normalizing target mRNA to GAPDH. Forward (F) and reverse (R) primer sequences are as follows: *clock*, *F*-ACCACAGCAACAGCAACAAC; *R*-GGCTGCTGAACTGAAGGAAG; *bmal1*, *F*-CCACCTCAGAGCCATTGATACA; *R*-GAGCAGGTTTAGTTCCACTTTGTCT; *per1*, *F*-TGAAGCAAGACCGGGAGA; *R*-CACACACGCCGTCACATC; *per2*, *F*-TGTGCGATGATGATTCGTGA; *R*-GGTGAAGGTACGTTTGGTTTGC; *per3*, *F*-AAAAGCACCACGGATACTGGC; *R*-GGGACCCTGTAGCTTGTC; *cry1*, *F*-CACTGGTTCCGAAAGGGACTC; *R*-CTGAAGCAAAAATCGCCACCT; *cry2*, *F*-CACTGGTTCCGCAAAGGACTA; *R*-CCACGGGTCGAGGATGTAGA.

Bacterial gene quantification
Rosburia butyryl-CoA: acetate CoA-transferase (*but*) gene copy number was determined from luminal cecal contents and fecal pellets as previously described (Vital et al., 2013; Louis et al., 2010). Genes were quantified by determining a standard curve for gene copy number by cloning primer sequences into pCR4-TOPO plasmids. Forward (F) and reverse (R) primer sequences are as follows: 16S rRNA, *F*-TCCTACGGGAGGCAGCAGT; *R*-GGACTACCAGGGTATCTAATCCTGTT; butyryl-CoA: acetate CoA-transferase G-_RosEub (*but*), *F*-TCAAATCMGGIGACTGGGTWGA; *R1*-TCGATACCGGACATATGCCAKGAG; *R2*-TCATAACCGCCCATATGCCATGAG.

Metagenomic library preparation and sequencing analysis
Metagenomic shotgun libraries were prepared using Illumina's NexteraXT Kit, sequenced on the Illumina MiSeq Platform, and data processed through the MG-RAST pipeline (http://metagenomics.anl.gov; Glass and Meyer, 2011). Processed hierarchical SEED annotations were downloaded using the matR package in R v2.15.2 (The R Development Core Team, 2008) and abundance tables were normalized to equivalent sampling depth, and analyzed using QIIME and R v2.15.2. Significant shifts in gene/pathway abundance between time points were assessed using ANOVA (Bonferroni correction for multiple tests; α = 0.05) (Caporaso et al., 2010). Heatmap plots were generated using the Matplotlib library (Hunter, 2007) in Python.

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