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Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome

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Mouse strains

2 4



BE1 mice transferred to BE3 BE2 mice transferred to BE3 Order;Family 1.00 Anaeroplasmatales;Anaeroplasmataceae Bacteroidales:unclassified Bacteroidales:Odoribacteraceae Bacteroidales:Paraprevotellaceae Bacteroidales:Bacteroidaceae 0.75 Bacteroidales;Porphyromonadaceae Bacteroidales;Prevotellaceae Fraction Bacteroidales:Rikenellaceae Bacteroidales;S24-7 Burkholderiales; Alcaligenaceae 0.50 Clostridiales;unclassified Clostridiales;Clostridiaceae Clostridiales;Lachnospiraceae Clostridiales;Ruminococcaceae Deferribacterales;Deferribacteraceae 0.25 Erysipelotrichales;Erysipelotrichaceae Lactobacillales:Lactobacillaceae RF39:unclassified Verrucomicrobiales;Verrucomicrobiaceae YS2:unclassified 0.002 4 6 8 4 2 6 8 Time at BE3 (wks) Time at BE3 (wks)

Supplementary Fig. 1. Effect of the built environment on the structure of the gut microbiome. a, Hierarchical clustering of mouse fecal microbial composition of the top 300 most abundant OTUs. Built environments (BE) are indicated in blue (BE2; barrier facility) and red (BE1; SPF facility). **b**, Stability of the gut microbial structure 2, 4, 6 and 8 weeks after transfer from BE1 and BE2 to BE3. Samples were separated by BE at birth (BE1: left; BE2: right). Relative abundances of the 20 most common families (representing >95% of the total data) over time are shown.

b

Microbes



Supplementary Fig. 2. Polar dendrogram of OTU counts and metabolome profiles. Polar dendrograms using Bray-Curtis distance metric were generated for all mice based on normalized OTU counts (top) and metabolite abundance levels (bottom). Labels are colored by strain and include built environment at time of collection, the collection time-point at BE3 (2, 4, 6 or 8 weeks after arrival; microbiome only), the strain name (not including the original derivation location (Tau, Geni), but all from Unc) and sex.



Supplementary Fig. 3. Visual representation of OTU correlation network. **a**, Network edges (gray lines) connect significantly correlated OTUs (ovals; colored at the family level). Correlation (>0.5) based on Spearman rank (p<1E-10). **b**, The genomic intervals with significant linkage ($-\log_{10}$ (p-value)>6) to individual OTUs are shown within three individual correlation sub-networks.



Supplementary Fig. 4. Association of microbial abundance with host phenotypes. a, Random forest analysis to assess the association between microbial abundance at the family level and mouse peripheral blood B cell counts, body weight and rotarod performance. Significant associations are indicated in green (p<0.05). However, these associations were not significant after adjusting for multiple comparisons using Benjamini-Hochberg **b**, Random permutation analysis to assess significance of association between microbial abundance and host phenotypes. Upper whiskers extend to the highest value that is within 1.5 * inter-quartile range (IQR). The lower whiskers represent the lowest value within 1.5 * IQR.



Supplementary Fig. 5. Metabolite profiles are controlled by the local diet.

a, Hierarchical clustering of fecal metabolite levels in 24 CC strains maintained on two distinct diets (BE1 and 2; Labdiet Picolab 3500 and BE3; Labdiet Prolab 5053). **b**, Microbial abundance was measured in fecal samples of five CC strains (males and females were analyzed separately for each strain) maintained for one week on standard chow (Labdiet Picolab 5053; Diet 1), one week on autoclaved chow (Labdiet Prolab 3500; Diet 2) followed by one week on standard chow (p=0.273, R2 = 0.0079 between two diets, ADONIS).

4 0 0		D				
1.00•		Hypoxanthine				
		Xanthine				
		L-Homoserine				
		D-Xylose				
		L-Phenylalanine				
		D-Galaciose				
		5-Hydroxyindoleacetate				
		Thymine				
		5-Aminopentanoate				
		Uraçil				
		4-Guanidinobutanoate				
		L-Isoleucine				
0.75∎		Orthophosphate				
		Cholic acid				
		L-Lysine				
		L-Serine				
		Glycerol				
		L-Tryptophan				
Se		3-Hydroxyphenylacetate				
lit		Dehvdroalanine				
0		Benzoate				
at		(R,R)-Butane-2,3-diol				
et		Linoleate				
E		Octadecanoic acid				
₩ 0.50		Maltose				
č						
<u>0</u>		(S)-Lactate				
T I		Hexade <u>c</u> anoic acid				
bd		D-Fructose				
2		Nicotinate Dedecanois asid				
<u> </u>		Sucrose				
		L-Alanine				
		3-Methyl-2-oxobutanoic acid				
		L-Proline				
		myo-Inositol				
0.25•		Cholesterol				
		alpha.alpha-Trehalose				
		Tetradecanoic acid				
		(9Z)-Octadecenoic acid				
		I-Cysteine				
		Cellobiose				
		L-Methionine				
		Fumarate				
		L-Glutamine				
		Succinate D Mannasa				
0.00 •		L-Threonine				
	Dietary Non-dietary	Phenyllactate				
	metabolites metabolites	-	ДII	Diet 1	Diet 2	
	(n=37) (n=21)		samples	samples	samplas	
	(Samples	samples	samples	
		a				
		Correla	tion Level			P - 4
	Consistent				In both c	liets
	Contrasting				📕 In Diet 1	only
	-	-0.3	0.0 0.3		In neithe	er diet

Supplementary Fig. 6. Shifts in community metabolic capacity explain observed variation in non-dietary metabolites. a, Proportions of dietary and non-dietary metabolites whose measured variation is consistent (positively correlated) or contrasting (negatively correlated) with community metabolic potential (as predicted by metabolic modeling). b, Correspondence between variation in community metabolic potential and variation in measured metabolite concentration across all samples and across sample subsets from each diet and facility. The far right bar indicates whether each metabolite was detected in the chow from either facility.



Supplementary Fig. 7. Potential taxonomic contributors to metabolic modeling-based metabolite predictions. The three bars on the left indicate whether each metabolite's variation was consistent or contrasting with the predicted community metabolic potential across all samples and across sample subsets from each facility (BE1 and BE2: Diet 2; BE3: Diet 1) and diet. The right grid shows the number of OTUs in each taxonomic category identified as potential contributors to community metabolism, based on consistent variation patterns and metabolic capacity.



Supplementary Fig. 8. Potential taxonomic contributors to metabolite abundance for mice housed at BE3. Potential taxonomic contributors to metabolite variation for mice maintained on Labdiet Prolab 5053 (BE3). Individual OTUs shown (circles; colored at the family level) are those whose metabolic capacity and variation across samples are consistent with the entire community metabolic potential and with measured variation in the linked metabolites (squares). Green, orange and pink clouds behind OTU sub-networks indicate Clostridiales, Bacteroidales or Lactobacillales enrichment. Edge color indicates whether a given OTU potentially impacts a certain metabolite variation via synthesis (blue edges), degradation (green edges), or both (purple edges).



Supplementary Fig. 9. Relative contribution of built environment (BE) and genetics to microbial abundance. The percent deviance (% Dev) of microbial abundance across CC strains explained by BE and genetic factors are shown. Genetic factors contribute more than built environment (BE) to the total microbiome variation. Inset shows an example of the effect of a SNP on chromosome 5 on Lactobacillus abundance, where BE has no effect. Upper whiskers extend to the highest value that is within 1.5 * inter-quartile range (IQR). The lower whiskers represent the lowest value within 1.5 * IQR. Supplementary Fig. 10. Summary plots from permutation of 16S data to obtain FDR estimates for QTL analyses. We performed 1,000 permutations of strain identifiers and then computed the Mann-Whitney U at each SNP for (A) data combined at the family level, (B) 15 OTUs in the lower and (C) upper quintiles of sum of p-values across all SNPs and (D) the 15 OTUs with the lowest overall sum of p-values.





Percent p−values ≤ threshold







0.4 p-value

0.6

0.0

0.2

















-log10(p-value)

6

8

I,

2

0.25 -

0.00 -

0







Percent p−values ≤ threshold







Percent p−values ≤ threshold









p-value









0.4 p-value

0.6

0.2

0.0











Percent p−values ≤ threshold







Percent p−values ≤ threshold











0.4 p-value

0.6

0.2

0

0.0






















0.4 p-value





Percent p−values ≤ threshold







Percent p−values ≤ threshold







Percent p−values ≤ threshold









Percent p−values ≤ threshold







2







Percent p−values ≤ threshold













Percent p−values ≤ threshold







Percent p−values ≤ threshold







Percent p−values ≤ threshold







Percent p−values ≤ threshold







Percent p−values ≤ threshold







Percent p−values ≤ threshold







Percent p−values ≤ threshold









0.4 p-value 0.6

0.2

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Percent p−values ≤ threshold









-log10(p-value)

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Percent p−values ≤ threshold













Supplementary Table 1. Meta data of samples used in 16S and metabolite analysis.

16S Amplicons Lab and BE Female Male Total Week 0 BE1 - SPF BE2 - Barrier LBNL Week 2 Week 4 Week 6 Week 8 Week 10, generation 2 Grand Total

Metabolies							
Row Labels	Female	Male	Total				
UNC	27	28	55				
Week 0	27	28	55				
BE1 - SPF	15	15	30				
BE2 - Barrier	12	13	25				
LBNL	26	33	59				
Week 8	26	23	49				
Week 10		10	10				
Grand Total	53	61	114				

BE and Strain	Female	Male	Total	В
BE1 - SPF	76	79	155	В
CC008	5	5	10	
CC011	5	6	11	
CC013	4	6	10	
CC016	4	5	9	
CC021	5	4	9	
CC026	4	4	8	
CC028	5	4	9	
CC030	5	5	10	
CC032	5	5	10	
CC033	5	5	10	
CC036	5	6	11	
CC038	5	6	11	
CC050	5	5	10	
CC052	5	5	10	
CC057	4	3	7	
CC061	5	5	10	
BE2 - Barrier	66	72	138	В
CC001	4	3	7	
CC002	5	5	10	
CC004	5	5	10	
CC010	5	5	10	
CC019	5	6	11	
CC037	5	6	11	
CC039	5	5	10	
CC040	5	5	10	
CC041	5	6	11	
CC042	4	6	10	
CC051	4	6	10	
CC055	5	4	9	
CC059	4	5	9	
CC065	5	5	10	
Grand Total	142	151	293	G

BE and Strain	Female Ma	le Tota	al
BE1 - SPF	30	32	62
CC008	2	2	4
CC011	2	3	5
CC013	2	2	4
CC016	1	2	3
CC021	2	1	3
CC026	2	1	3
CC028	2	2	4
CC030	2	2	4
CC032	2	3	5
CC033	2	2	4
CC036	2	3	5
CC038	2	3	5
CC050	2	2	4
CC052	2	2	4
CC057	1		1
CC061	2	2	4
BE2 - Barrier	23	29	52
CC001	1	2	3
CC002	2	2	4
CC004	2	2	4
CC010	2	2	4
CC019	1	2	3
CC037	2	3	5
CC039	2	2	4
CC040	1	1	2
CC041	1	2	3
CC042	1	3	4
CC051	2	3	5
CC055	2	1	3
CC059	2	2	4
CC065	2	2	4
Grand Total	53	61	114

Supplementary Table 2. Normalized amplicon abundance. See separate excel sheet.

Supplementary Table 3. Differentially abundant fecal operational taxonomic units (OTUs) between animal facility built environments (BE1 vs BE2). See separate excel sheet.

Supplementary Table 4. P-values for each genetic locus obtained using Mann-Whitney U test for all OTUs. See separate excel sheet.

Supplementary Table 5. Joint QTL intervals and candidate genes. See separate excel sheet.

Supplementary Table 6. Linkage analysis of microbial families. See separate excel sheet.

Supplementary Table 7. Candidate genes in genetic loci associated with specific microbial families. See separate excel sheet. Supplementary Table 8. Human genome-wide association studies of microbiome associated diseases.

PubMed ID GWAS study 22412388 Crohn's disease 21102463 Crohn's disease 17684544 Crohn's disease 18587394 Crohn's disease 23266558 Crohn's disease 23128233 Crohn's disease 17435756 Crohn's disease 17447842 Crohn's disease 17554261 Crohn's disease 17804789 Crohn's disease 20570966 Crohn's disease 22293688 Crohn's disease 22936669 Crohn's disease 23850713 Crohn's disease 23665963 Crohn's disease 21298027 Crohn's disease and celiac disease 22482804 Crohn's disease and psoriasis 18723019 Crohn's disease and sarcoidosis (combined) 25557950 Crohn's disease-related phenotypes 21699788 Ulcerative colitis or Crohn's disease 23936387 Celiac disease 24999842 Celiac disease 20190752 Celiac disease 17558408 Celiac disease 18311140 Celiac disease 21383967 Celiac disease or Rheumatoid arthritis 20848476 Ulcerative colitis 19915572 Ulcerative colitis 20228799 Ulcerative colitis 19122664 Ulcerative colitis 21297633 Ulcerative colitis 23511034 Ulcerative colitis 18836448 Ulcerative colitis 19915573 Ulcerative colitis 20228798 Ulcerative colitis 24837172 Ulcerative colitis 25082827 Ulcerative colitis 25248455 Irritable bowel syndrome
24797007 Irritable bowel syndrome 24487271 Erythema nodosum in inflammatory bowel disease 17068223 Inflammatory bowel disease 18758464 Inflammatory bowel disease 19915574 Inflammatory bowel disease (early onset) 19268274 Body mass (lean) 23108985 Body mass (lean) 21037115 Body mass in chronic obstructive pulmonary disease 19079260 Body mass index 20935630 Body mass index 20966902 Body mass index 19079261 Body mass index 23563607 Body mass index 22344221 Body mass index 17434869 Body mass index 17903300 Body mass index 18454148 Body mass index 19851299 Body mass index 20397748 Body mass index 21253498 Body mass index 21701565 Body mass index 21701570 Body mass index 22333899 Body mass index 22344219 Body mass index 22446040 Body mass index 22982992 Body mass index 23583978 Body mass index 23669352 Body mass index 24064335 Body mass index 24348519 Body mass index 24827717 Body mass index 24861553 Body mass index 25133637 Body mass index 25378290 Body mass index (change over time) 24281739 Body mass index (education interaction) 23192594 Body mass index (interaction) 22417934 Body mass index and cholesterol (psychopharmacological treatment) 19584900 Body mass index and fat mass 23517042 Body mass index in asthmatics 23300278 Type 2 diabetes 22158537 Type 2 diabetes 22961080 Type 2 diabetes

23945395 Type 2 diabetes 24509480 Type 2 diabetes 20581827 Type 2 diabetes 21874001 Type 2 diabetes 25483131 Type 2 diabetes 22456796 Type 2 diabetes 25102180 Type 2 diabetes 17293876 Type 2 diabetes 17460697 Type 2 diabetes 17463248 Type 2 diabetes 17463249 Type 2 diabetes 17668382 Type 2 diabetes 17846124 Type 2 diabetes 17846125 Type 2 diabetes 17846126 Type 2 diabetes 18372903 Type 2 diabetes 18711366 Type 2 diabetes 18711367 Type 2 diabetes 19056611 Type 2 diabetes 19401414 Type 2 diabetes 20174558 Type 2 diabetes 20418489 Type 2 diabetes 20818381 Type 2 diabetes 20862305 Type 2 diabetes 21490949 Type 2 diabetes 21573907 Type 2 diabetes 21647700 Type 2 diabetes 21799836 Type 2 diabetes 22101970 Type 2 diabetes 22238593 Type 2 diabetes 22693455 Type 2 diabetes 23209189 Type 2 diabetes 23532257 Type 2 diabetes 23937595 Type 2 diabetes 24101674 Type 2 diabetes 24390345 Type 2 diabetes 23386860 Type 2 diabetes (dietary heme iron intake interaction) 24465431 Type 2 diabetes (young onset) and obesity 17848626 Type 2 diabetes and 6 quantitative traits 22179738 Type 2 diabetes and gout 19734900 Type 2 diabetes and other traits 21150874 Type 2 diabetes nephropathy

17653210 Type 2 diabetes nephropathy 19252134 Type 2 diabetes nephropathy 20037589 Metabolite levels 22916037 Metabolite levels 19043545 Metabolite levels 21931564 Metabolite levels 23281178 Metabolite levels 23378610 Metabolite levels 23934736 Metabolite levels (X-11787) 23319000 Metabolite levels (5-HIAA) Supplementary Table 9. Original intensity of metabolomics data of the detected metabolites from BE1/2 and BE3 mouse chow.

	BE3: LBNL Mouse chow			BE1/2: UNC- Mouse chow		
Metabolite	LBNL_1	LBNL_2	LBNL_3	UNC_A_1	UNC_A_2	UNC_A_3
1-methyl nicotinamide	2126109.5	834369.5	1206885.1	0.0	0.0	0.0
1-methylhydantoin	557566.8	728804.0	622438.9	140175.5	215532.9	316187.9
1-monopalmitin*	6632659.2	5650860.6	6267318.9	1533967.6	1441923.1	1549965.0
2-hydroxyglutaric acid	721951.6	643801.1	802270.0	0.0	0.0	0.0
3,4,5-trihydroxypentanoic acid	990480.9	842008.2	875281.4	121804.7	54112.6	98269.7
3-hydroxycholanic acid*	578125.2	556759.5	504158.5	467551.1	343444.8	267991.7
3-hydroxypyridine	516086.2	435066.1	488055.0	227212.2	231071.2	270617.5
4-guanidinobutyric acid	7322057.7	6068321.7	7592480.8	927115.7	985874.1	1357749.4
4-hydroxy-3-methoxybenzoic acid	452887.0	267793.6	432670.3	129645.6	112442.4	155757.0
aconitic acid	2097816.3	1489856.2	1120709.0	0.0	0.0	0.0
adenine	2522028.5	1756542.5	2298341.7	541575.7	579599.9	627925.6
adenosine	2458398.5	2007179.9	2292650.6	354308.2	367611.4	591184.9
allo-inositol	59855256.6	54103244.7	61595271.1	12621894.7	12288625.9	16417182.1
alpha tocophereol	127322.8	168792.0	192749.4	236637.2	238097.9	290908.8
alphatocoperol acetate*	609262.9	693354.0	1015326.8	472158.8	611265.7	779841.0
arabitol	784016.0	724202.7	822824.6	105693.1	102436.5	199011.9
arachidic acid	1597032.5	1423306.0	1762426.1	732253.1	665101.4	771094.7
behenic acid	1781203.2	1643339.5	2019126.6	490666.1	466727.8	566992.8
beta-alanine	955078.4	911969.5	1052738.3	376457.0	354349.4	409319.7
beta-sitosterol	142237.9	204863.6	225973.7	157630.1	162840.4	197755.5
campesterol	312126.3	409828.2	469957.8	361740.8	368188.7	459213.8
carbonate ion	6435064.7	8299850.2	7650514.5	5228611.7	7854240.5	7813798.4
cellobiose	110993267.0	96891621.0	106829413.3	0.0	0.0	0.0
cholesterol	1415142.1	1712389.6	1868015.8	1967546.7	1947785.9	2353065.3
citric acid	11686397.3	10713775.6	11517466.8	3014890.2	2880607.9	3991187.2
creatinine	2097023.6	3193038.3	1585909.4	400884.1	831720.2	1272215.7
cycloleucine	1136260.5	1778877.6	2004906.1	83997.5	0.0	200809.6
D-glucose	86842391.3	82790234.8	87342842.8	2481503.1	2851729.4	3517230.2
D-malic acid	5450160.2	4615308.4	5424313.4	1099127.6	1111796.4	1536904.5
D-mannitol	15983014.7	13058259.0	16479481.7	1522379.8	1542630.0	2114454.7
D-mannose	11155785.9	9746726.4	12093532.9	630966.5	919106.8	1158483.3
docosahexaenoic acid	1588950.5	1659463.5	2041589.4	1314377.3	1284288.8	1682744.3
D-sorbitol	49681360.1	38199145.3	50729511.2	1124642.6	1299996.1	1713214.5
D-threitol	1434317.5	1140781.4	1443399.4	127706.1	134579.0	169018.3
D-xylulose	1366056.1	1235124.2	1474876.3	101865.7	119560.6	287094.0
ethanolamine*	2095056.6	1793502.7	2230758.6	211726.1	240074.1	478144.0
fructose	62130471.8	55563046.3	59938062.4	6249818.3	7001392.2	8826772.2

fumaric acid	1571650.9	1077810.8	1201089.9	340893.1	155174.6	542529.2
galactinol	4451909.5	6975948.7	7332221.5	860148.8	866737.7	1306845.8
galactonic acid	2423091.5	1847077.2	2324031.9	0.0	0.0	0.0
glucosyclycerol*	3461069.1	2912898.9	3603789.2	2370022.5	3940355.2	4982293.8
glyceric acid	1959202.0	1550837.3	2168663.1	462118.7	539667.2	649371.0
glycerol 3-phosphate	12221545.6	10970701.9	13672833.6	1466105.0	1573183.7	2208515.3
glycine	8066064.0	7328064.0	8720151.0	1477837.0	1506064.0	2231221.0
glycolic acid	840562.7	651374.1	743478.9	323100.5	434110.0	414457.7
heptadecanoic acid	867240.1	840130.9	894224.2	913488.7	1233376.4	1626433.0
hypoxanthine	1130596.2	1192099.3	1403418.4	367204.2	472047.9	692734.3
inosine	1590909.5	1770862.0	2170136.8	319284.1	342885.6	594708.1
L-(+) lactic acid	45583652.4	41941865.1	47482519.9	6165768.0	5412074.9	8080550.2
lactose	110218093.1	121070247.1	110924804.6	0.0	0.0	0.0
L-alanine	5864371.3	7630566.3	7211707.4	2404231.9	2920955.0	3516347.1
L-asparagine	4024455.1	4043611.8	4416636.9	295521.8	454659.2	689615.1
L-glutamic acid	4018705.3	3709658.5	4441862.6	356589.7	356094.7	499735.6
L-glutamine	81618.4	115028.2	127656.0	0.0	0.0	0.0
linoleic acid	85024430.8	91450024.7	100923726.6	44469675.8	41296369.8	48485161.7
L-isoleucine	2074075.6	3484561.7	4360543.6	202682.6	364768.2	455163.9
L-leucine	2692486.2	4636025.7	5467973.4	267550.4	419715.8	611460.4
L-lysine	2727212.7	2782655.1	3314048.5	873066.6	1146700.8	1199541.6
L-methionine	110507312.7	110799844.8	124877475.2	6854454.3	20501838.9	14059374.7
L-methionine sulfoxide	2182177.8	2136539.0	1848413.4	242345.3	448455.8	393968.3
L-ornithine	1151466.9	1173649.4	1356110.4	126318.8	115315.5	188437.9
L-phenylalanine	5024288.6	4795434.2	5332265.1	652338.1	713128.5	1016918.0
L-proline	4404501.5	7410057.6	9347580.7	181546.5	315387.9	466164.1
L-pyroglutamic acid	6686025.5	6232344.6	6556141.6	2609152.8	2836604.1	3646643.3
L-serine	5365866.7	5188074.7	6255800.7	626538.0	835526.6	1072518.5
L-threonic acid*	924453.3	774396.7	961600.6	132154.4	126427.3	168299.5
L-threonine	1618604.6	1567141.6	1845755.1	205436.1	237163.6	349895.4
L-tryptophan	11059540.1	10523443.8	12556155.8	1112436.5	1377941.5	2151207.9
L-tyrosine	3906266.5	3181860.1	4348948.2	709542.7	688845.7	1027830.2
L-valine	5185053.4	4806657.3	5699354.1	347642.9	491842.6	1020567.9
malonic acid	1228214.1	1008522.2	1266489.6	142272.0	165952.6	236273.2
maltose	9187141.3	8000796.5	9500608.0	485049.3	466348.6	698676.9
myo-inositol	14100822.0	11379143.4	14059320.4	1362049.5	1372830.2	1917219.8
myristic acid	5800400.2	4559156.1	6863875.2	3092800.0	2483012.7	2960274.6
N-acetyl-D-glucosamine	358848.1	301697.3	361071.8	0.0	0.0	0.0
nicotinic acid	856608.8	702007.1	2222556.3	226206.1	132075.3	187769.6
oleantile*	3722593.4	3610673.4	3299903.1	6166171.6	5614341.1	5237153.9
oleic acid	62408799.8	64816275.8	75596073.8	34958837.9	32498718.4	33410993.7

palatinose	10706016.7	10016736.8	13103133.8	0.0	0.0	0.0
palmitic acid	73592029.6	73332493.1	86356364.1	35673255.5	31253754.3	35746126.2
palmitoleic acid	574941.2	594742.7	714578.0	385355.6	335926.1	403013.5
pantothenic acid	415823.1	697680.4	503601.3	258901.1	244409.3	266708.9
phosphoric acid	65756631.4	56451983.9	68871679.2	16446307.0	16629347.8	22496900.7
propylene glycol	2584181.1	1856258.9	2125873.9	132246.0	151870.3	446334.1
pyruvic acid	2386638.1	1186755.1	1731189.4	558633.2	488166.7	789795.9
quinic acid	11088802.7	8942723.6	10973879.7	461418.7	514903.9	659114.1
raffinose	11427459.4	10816762.0	12093731.4	959229.0	1029130.8	1406925.7
ribitol	8785584.9	7868729.7	9208095.5	1388410.7	1426888.9	2014298.5
ribonic acid*	1475552.1	1377843.4	1488626.6	161046.6	187792.5	202912.1
salicylic acid	322414.6	297865.4	353517.3	118081.5	179914.8	153112.0
scyllo-inositol	337099.8	281756.9	370270.0	124142.6	131565.0	158742.0
shikimic acid	3427091.0	2686965.9	3316467.8	204529.4	168064.7	232916.4
stearic acid	20862731.4	19285698.6	22642105.2	10802078.1	9241130.2	9977450.8
stearonitrile*	270321.2	255271.4	273518.8	282507.3	235628.1	241512.2
succinic acid	4199743.3	3547581.9	4296277.7	797138.1	863474.1	1227261.2
sucrose	181013494.3	179109364.1	179658321.2	72184886.3	70116182.2	84515764.5
tagatose	10726625.1	8729155.6	9587581.3	487008.0	561048.5	707656.3
thymine	246185.0	230648.9	282921.7	136306.9	181674.4	219581.5
urea	2467256.9	2172084.3	2737484.3	133528.6	160053.8	307040.7
xylitol	1519739.9	1225709.9	1433826.7	347979.9	364995.0	468791.9

Supplementary Table 10. Metabolomics data including original intensity of the detected metabolites from murine feces and their z-scored transformed values in separate tabs. See separate excel sheet.

Supplementary Table 11. Metabolite profiles in fecal samples of four CC strains maintained on different diets. See separate excel sheet.

Supplementary Table 12. A list of all metabolites assayed and analyzed in terms of community metabolic potential for each subset of the data, detailing correlations between metabolomics data and community metabolic potential scores and potential taxonomic contributors.

See separate excel sheet.