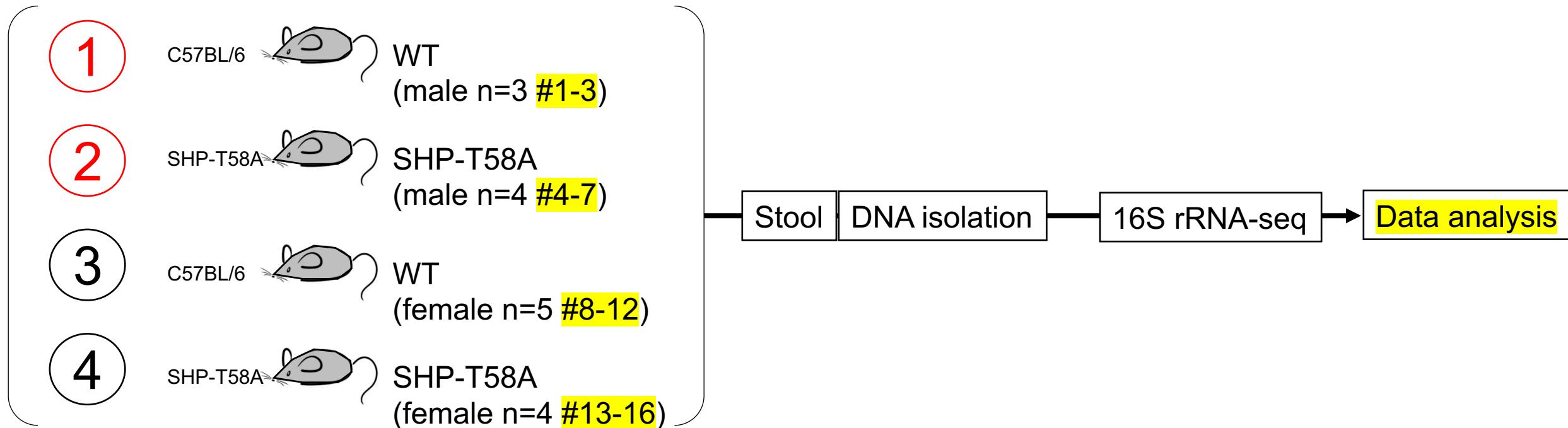


Procedure



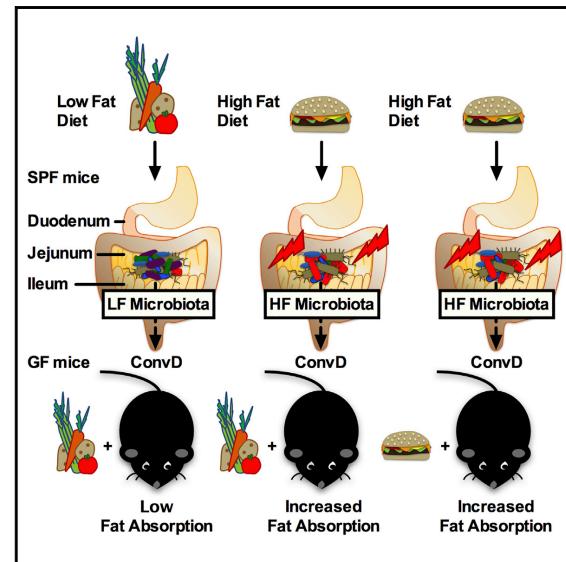
* The most important compare group is (1) and (2).

Kim_PrimerSorted_Demultiplexed			
	1MB10	V3_F357_N_V4_R805-MB10_AATGCAGTGT_R1.fastq	39,806
	MB10	V3_F357_N_V4_R805-MB10_AATGCAGTGT_R2.fastq	39,806
	MB11	V3_F357_N_V4_R805-MB11_ATATGGTGGA_R1.fastq	35,610
	MB11	V3_F357_N_V4_R805-MB11_ATATGGTGGA_R2.fastq	35,610
	MB12	V3_F357_N_V4_R805-MB12_ACTCAGTTAC_R1.fastq	35,104
	MB12	V3_F357_N_V4_R805-MB12_ACTCAGTTAC_R2.fastq	35,104
	MB13	V3_F357_N_V4_R805-MB13_AAGTGCATG_R1.fastq	39,080
	MB13	V3_F357_N_V4_R805-MB13_AAGTGCATG_R2.fastq	39,080
	MB14	V3_F357_N_V4_R805-MB14_CCACAGAGTG_R1.fastq	38,300
	MB14	V3_F357_N_V4_R805-MB14_CCACAGAGTG_R2.fastq	38,300
	MB15	V3_F357_N_V4_R805-MB15_AGTGGTGATC_R1.fastq	32,469
	MB15	V3_F357_N_V4_R805-MB15_AGTGGTGATC_R2.fastq	32,469
	MB16	V3_F357_N_V4_R805-MB16_ACTTCTTAGC_R1.fastq	42,803
	MB16	V3_F357_N_V4_R805-MB16_ACTTCTTAGC_R2.fastq	42,803
	MB1	V3_F357_N_V4_R805-MB1_CACGAAGAGC_R1.fastq	36,087
	MB1	V3_F357_N_V4_R805-MB1_CACGAAGAGC_R2.fastq	36,087
	MB2	V3_F357_N_V4_R805-MB2_CATACCTGAT_R1.fastq	40,380
	MB2	V3_F357_N_V4_R805-MB2_CATACCTGAT_R2.fastq	40,380
	MB3	V3_F357_N_V4_R805-MB3_GACGTGCTTC_R1.fastq	36,480
	MB3	V3_F357_N_V4_R805-MB3_GACGTGCTTC_R2.fastq	36,480
	MB4	V3_F357_N_V4_R805-MB4_ATTGTGGAGT_R1.fastq	31,171
	MB4	V3_F357_N_V4_R805-MB4_ATTGTGGAGT_R2.fastq	31,171
	MB5	V3_F357_N_V4_R805-MB5_TCTGGTCTCA_R1.fastq	10,224
	MB5	V3_F357_N_V4_R805-MB5_TCTGGTCTCA_R2.fastq	10,224
	MB6	V3_F357_N_V4_R805-MB6_AGGTAAGAGG_R1.fastq	41,429
	MB6	V3_F357_N_V4_R805-MB6_AGGTAAGAGG_R2.fastq	41,429
	MB7	V3_F357_N_V4_R805-MB7_TCCTGACAGA_R1.fastq	41,214
	MB7	V3_F357_N_V4_R805-MB7_TCCTGACAGA_R2.fastq	41,214
	MB8	V3_F357_N_V4_R805-MB8_GCACTGTTGC_R1.fastq	3,186
	MB8	V3_F357_N_V4_R805-MB8_GCACTGTTGC_R2.fastq	3,186
	MB9	V3_F357_N_V4_R805-MB9_ACCATGAGTC_R1.fastq	57,970
	MB9	V3_F357_N_V4_R805-MB9_ACCATGAGTC_R2.fastq	57,970
	Total Reads:		
			1,122,626

Cell Host & Microbe

Small Intestine Microbiota Regulate Host Digestive and Absorptive Adaptive Responses to Dietary Lipids

Graphical Abstract



Authors

Kristina Martinez-Guryn,
Nathaniel Hubert, Katya Frazier, ...,
Catherine A. Reardon, Vanessa Leone,
Eugene B. Chang

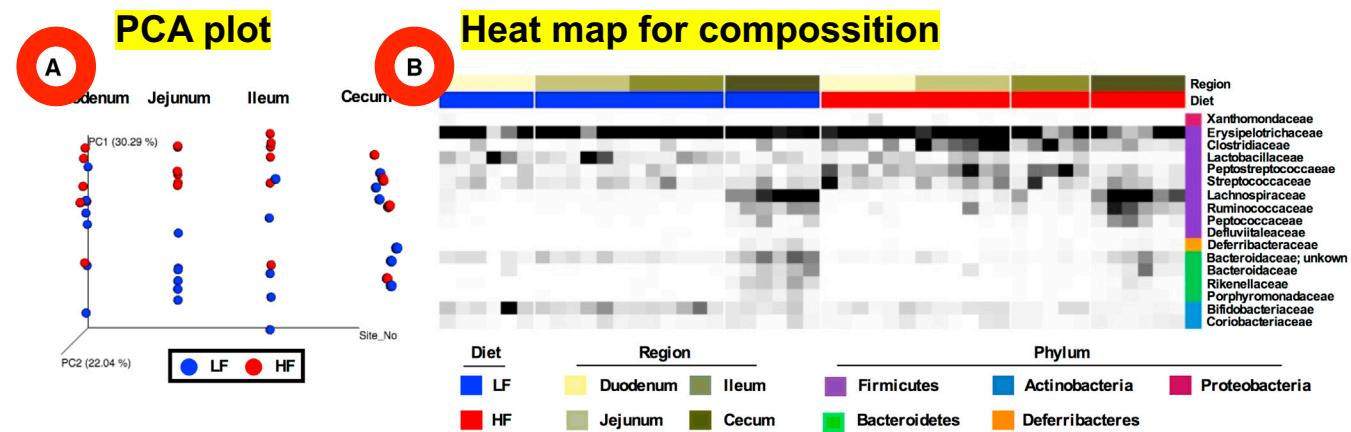
Correspondence

echang@medicine.bsd.uchicago.edu

In Brief

Martinez-Guryn et al. demonstrate that small intestinal microbiota are critical transducers of dietary signals that allow the host to adapt to variations in lipid digestion and absorption. High-fat diet-induced jejunal microbiota directly promote mucosal lipid absorption and are potentially a factor contributing to conditions of over- and undernutrition.

Microbiome population and composition

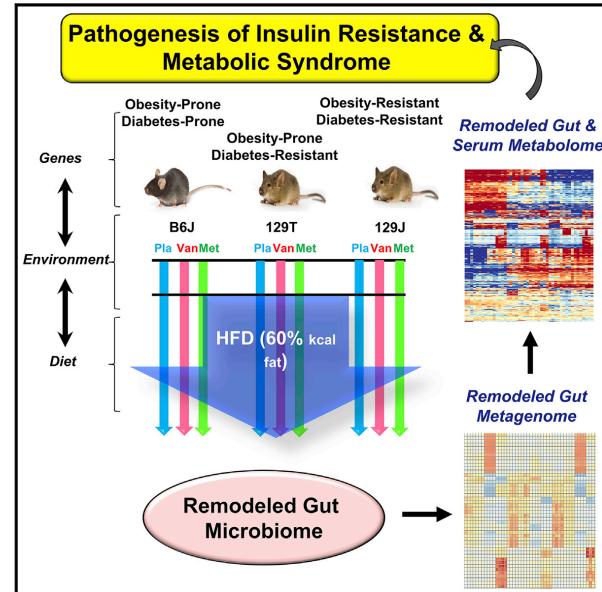


Highlights

- Small bowel microbiota regulate host dietary fat digestion and absorption
- Gut microbes and their mediators drive lipid absorption through multiple mechanisms
- Specific bacterial strains influence processes underlying intestinal lipid absorption
- High-fat diet-induced jejunal microbiota directly increase gut lipid absorption

Diet, Genetics, and the Gut Microbiome Drive Dynamic Changes in Plasma Metabolites

Graphical Abstract



Authors

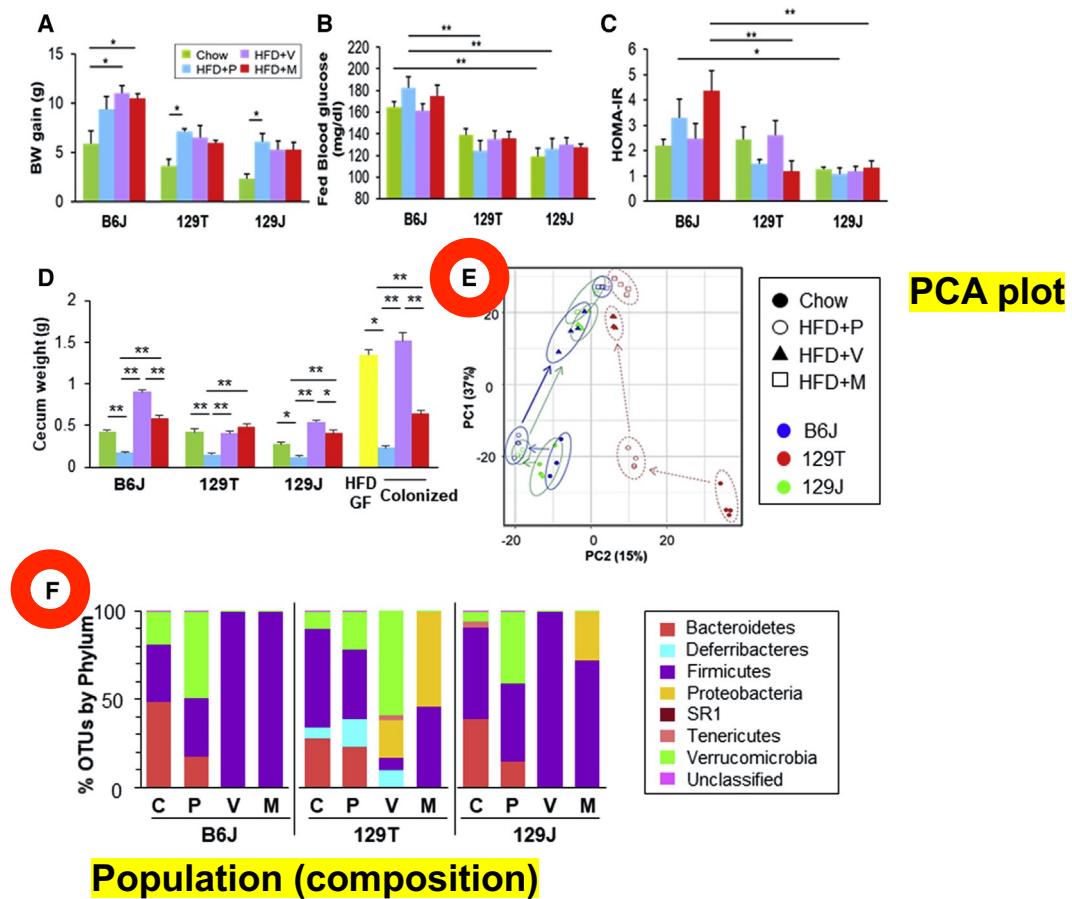
Shiho Fujisaka, Julian Avila-Pacheco, Marion Soto, ..., Lynn Bry, Clary B. Clish, C. Ronald Kahn

Correspondence

c.ronald.kahn@joslin.harvard.edu

In Brief

Fujisaka et al. show that mice with differing propensities to obesity and diabetes have differing metabolomic responses to diet and antibiotic treatment. Several serum metabolites correlate with changes in the gut microbiota or with insulin resistance across strains. Thus, diet, genetics, and the gut microbiota interact to create distinct plasma metabolomic responses.

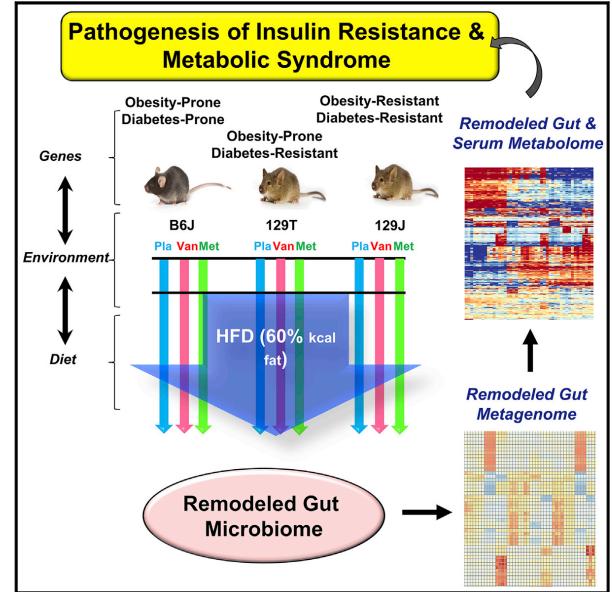


Highlights

- Risk of diabetes and obesity in mice is associated with differences in gut bacteria
- Effects of diet, host genetics, and the microbiome are reflected in the metabolome
- 18 plasma metabolites correlate with insulin resistance across strains and diets
- More than 1,000 unidentified MS peaks are also regulated by diet, genes, and the gut microbiota

Diet, Genetics, and the Gut Microbiome Drive Dynamic Changes in Plasma Metabolites

Graphical Abstract



Authors

Shiho Fujisaka, Julian Avila-Pacheco, Marion Soto, ..., Lynn Bry, Clary B. Clish, C. Ronald Kahn

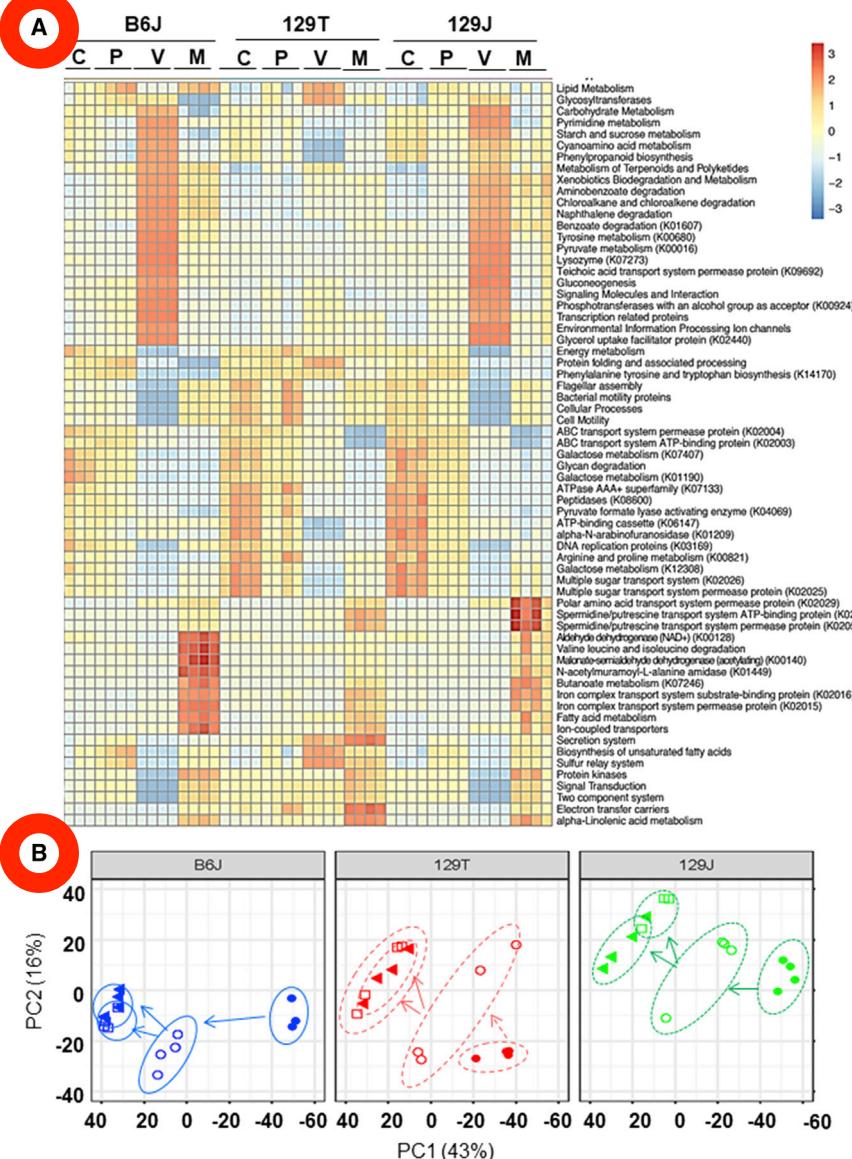
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Predicted Metabolic Pathway



Predicted Metabolic Pathway → PCA plot ?

Figure 2. Modifications of the Gut Microbiota Affect Predicted Functional Metabolic Pathways

(A) Heatmap of metabolic pathways of each group obtained from PICRUSt analysis of 16S rRNA sequencing data. C, chow placebo; P, HFD+placebo; V, HFD+vancomycin; M, HFD+metronidazole.

(B) PCA of identified metabolites in the cecum for B6J, 129T, and 129J mice on either chow, HFD, HFD+vancomycin, or HFD+metronidazole at 11 weeks of age.

from HFD conventional mice but remained large in germ-free B6 mice colonized with gut bacteria of HFD-fed mice treated with vancomycin or metronidazole (Figure 1D). Principal-component analysis of 16S rRNA sequence data of cecal contents showed clear differences in community structure between the different experimental groups (Figure 1E), with both HFD and antibiotic treatment having a strong effect on the bacterial structure, with lesser but clear differences among strains. At the phylum level, the relative abundance of Firmicutes to Bacteroidetes was higher in both chow-fed 129 strains compared to B6J mice (Figure 1F). HFD feeding reduced Bacteroidetes in all strains of mice. Both antibiotics resulted in elimination of most of the bacteria, except for Firmicutes in B6J and 129J mice, whereas, in 129T mice, considerable Proteobacteria and Verrucomicrobia remained.

Microbial Modifications Affect Predicted Functional Pathways in the Microbiome

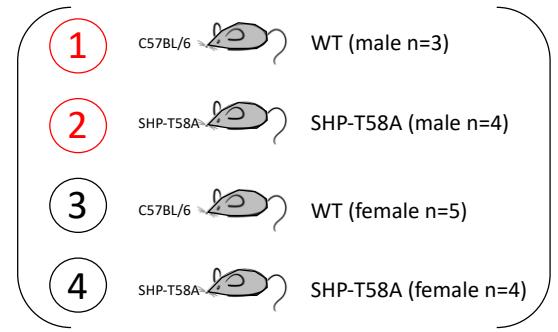
DATA analysis

1.PCA plot

2.Microbiome composition (heat map)

3.Predicted Functional Metabolic Pathways

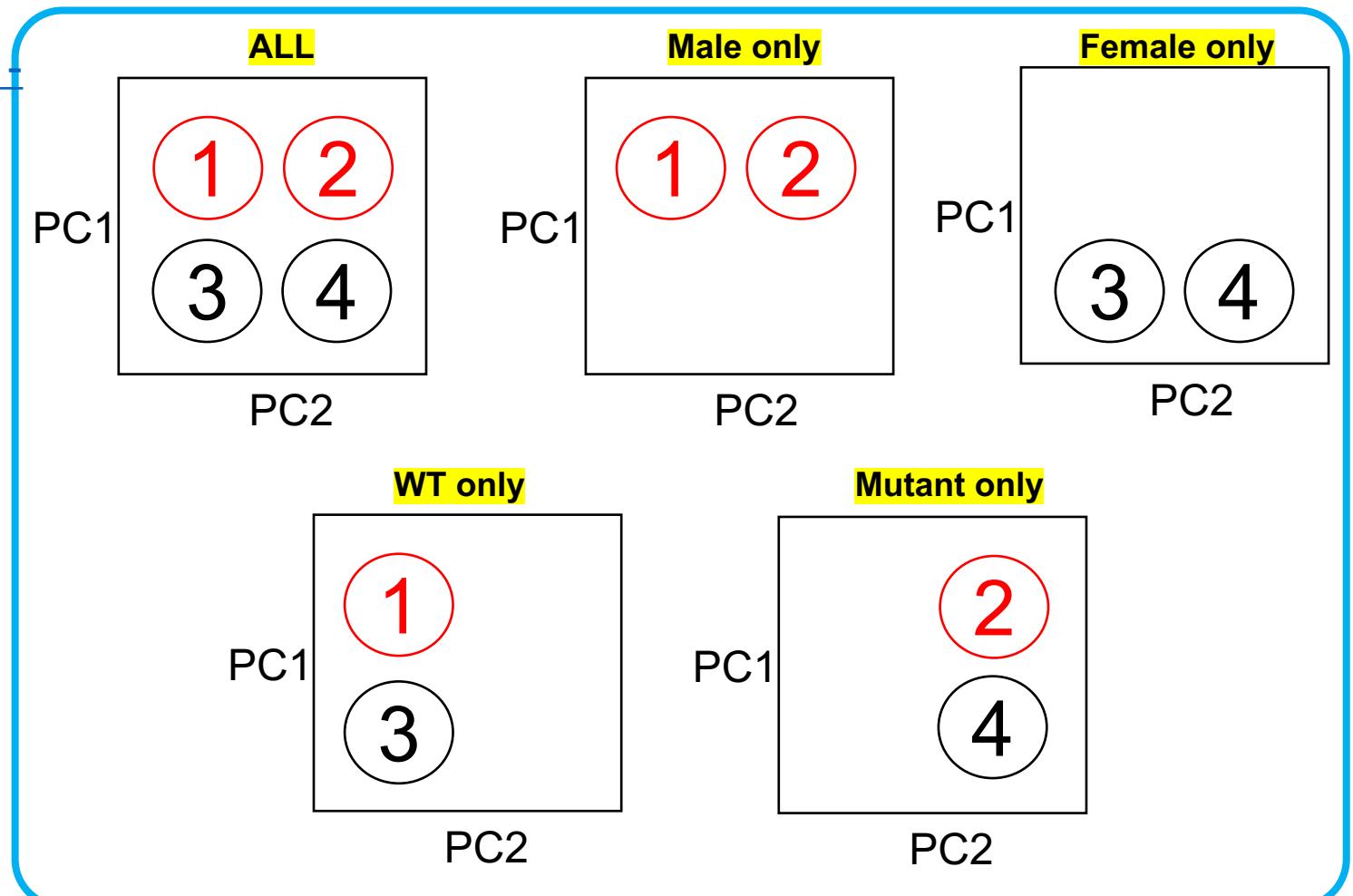
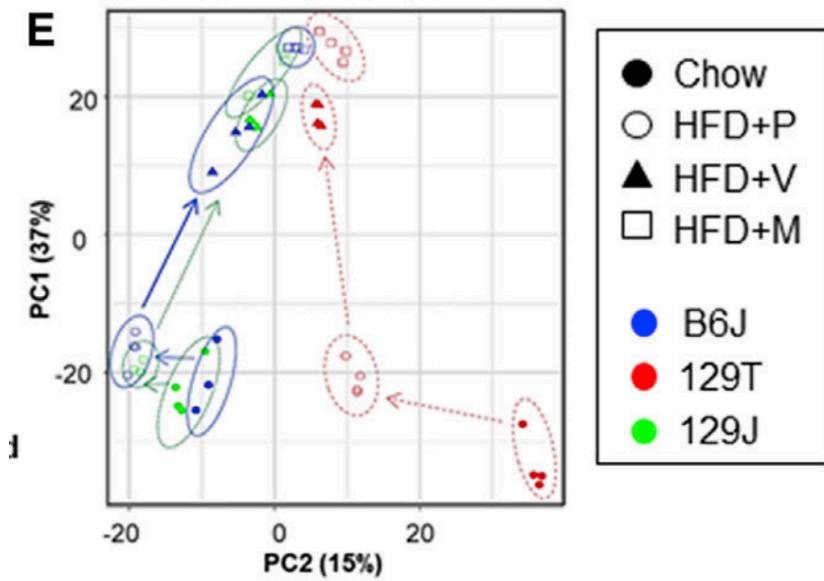
PCA Plot



Example

PCA plot

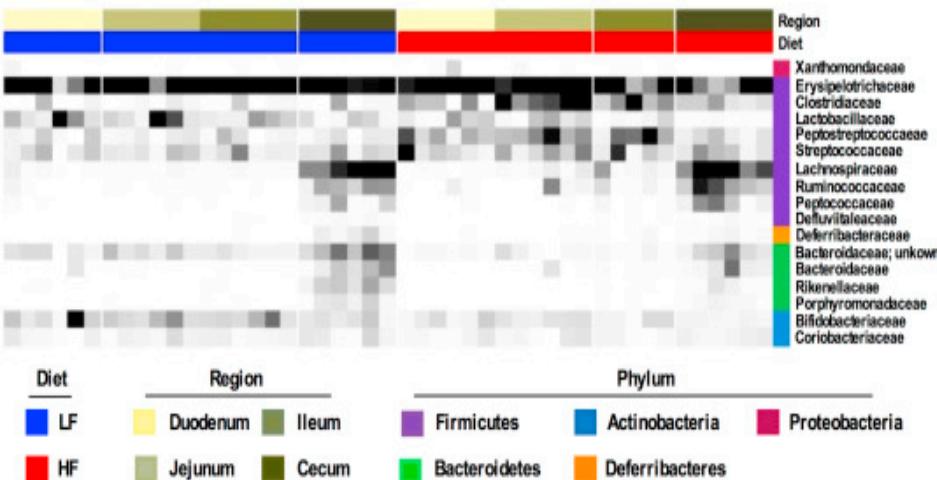
[https://www.cell.com/cell-reports/pdf/S2211-1247\(18\)30254-7.pdf](https://www.cell.com/cell-reports/pdf/S2211-1247(18)30254-7.pdf)



Microbiome Composition (heat map)

Example

[https://www.cell.com/cell-host-microbe/fulltext/S1931-3128\(18\)30140-9](https://www.cell.com/cell-host-microbe/fulltext/S1931-3128(18)30140-9)



		MALE	FEMALE		
		C57BL/6	SHP-T58A	C57BL/6	SHP-T58A
1					
2					
3					
4					

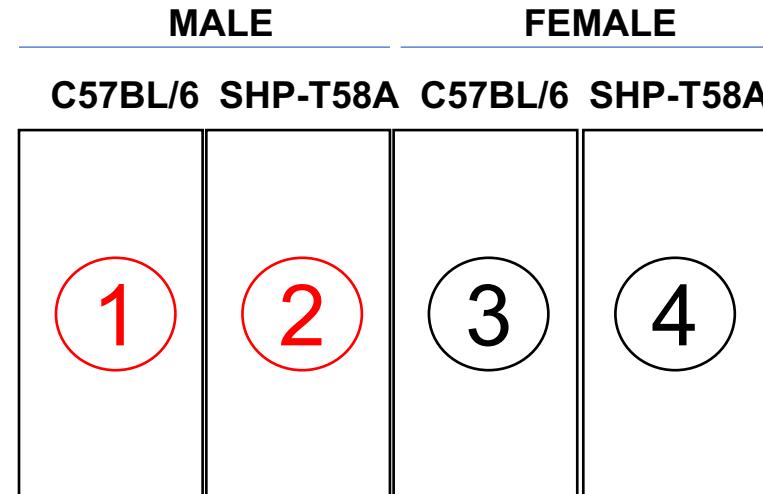
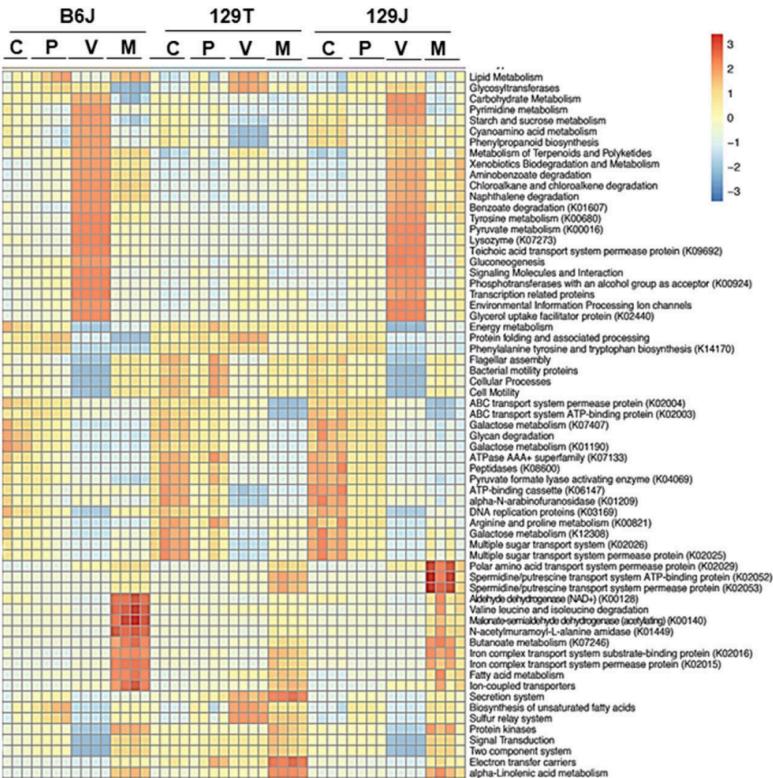
Bacteria 1
Bacteria 2
Bacteria 3
Bacteria 4
Bacteria 5
...



Predicted Functional Metabolic Pathways

Example

[https://www.cell.com/cell-reports/pdf/S2211-1247\(18\)30254-7.pdf](https://www.cell.com/cell-reports/pdf/S2211-1247(18)30254-7.pdf)



Bacteria 1
Bacteria 2
Bacteria 3
Bacteria 4
Bacteria 5
...