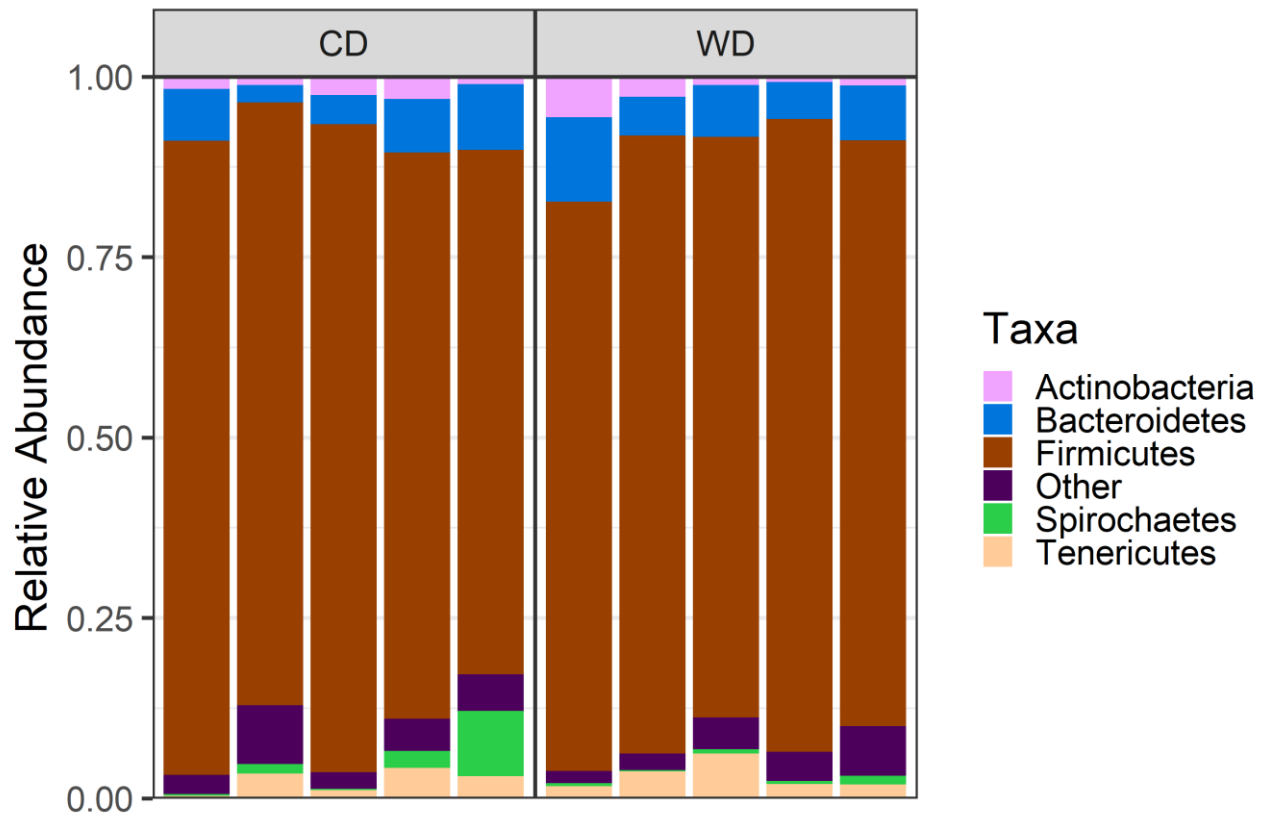


*Supplementary Material*

**Western diet-induced maternal microbial dysbiosis is associated with steatosis and altered expression of microRNAs in baboon fetal liver and placenta**

Kameron Y. Sugino<sup>1,†</sup>, Ashok Mandala<sup>1,†</sup>, Rachel C. Janssen<sup>1</sup>, Sunam Gurung<sup>2</sup>, MaJoi Trammell<sup>3</sup>, Michael W. Day<sup>3</sup>, Richard S. Brush<sup>4</sup>, James F. Papin<sup>5</sup>, David W. Dyer<sup>3</sup>, Martin-Paul Agbaga<sup>4,6</sup>, Jacob E. Friedman<sup>1,7</sup>, Marisol Castillo-Castrejon<sup>7,8</sup>, Karen R. Jonscher<sup>1,9,\*</sup> and Dean A. Myers<sup>2</sup>



**Supplementary Figure S1.** Microbial abundances of the top five most abundant phyla for each feces sample. The 15 lower abundant phyla are displayed as “Other”.

**Supplemental Table S1.** qPCR primer sequences for mRNA expression.

<b>Gene</b>	<b>Forward Primer</b>	<b>Reverse Primer</b>
<i>ACACA</i>	AGCCCTCAACAAAGTCCTCG	AGTGGGTCACCCCATTGTTG
<i>ACTA2</i>	GGCAAGTGATCACCATCGGA	GTGGTTTCATGGATGCCTGC
<i>ACTB</i>	GGGAAATCGTGCGTGACATT	AGGTAGTTTCGTGGATGCCA
<i>CCR2</i>	TTGACGTGAAGCAAATCGGG	CCAGCATGTTGCCACAAAA
<i>COL1A1</i>	AAGGACAAGAGGCACGTCTG	CAGGAAGGTCAGCTGGATGG
<i>COL3A1</i>	GGTCCAAAGGGTGACAAGGG	GGCCAGGAGGACCAATAGGA
<i>FAP</i>	AGTTTCAGCGACTACGCCAA	TCTTGATCAGTGCGTCCGTC
<i>FASN</i>	GAGCACAACAGGGTGCTAGA	TTGATGATCAGGTCCACGGC
<i>HMOX1</i>	AGCAACAAAGCGCAAGACTC	GATCCATCGGAGAAGCGGAG
<i>ICAM1</i>	CAGTTCGTGCTGAAAGCCAC	ATCGGGGTCCATACAGGACA
<i>IL10</i>	CTGAGAACCACGACCCAGAC	GAAGAAATCGATGACAGCGCC
<i>IL12B</i>	GCAGCTGGTCATCTCTTGGT	CACCATTCTCCAGGGGCAT
<i>IL1B</i>	GCTCTCCACCTCCAGGGACAGG	TGAGGCCCAAGGCCACAGGT
<i>IL1B</i> *	TGAAAGCTCTCCACCTCCAG	TTGGGCAGACTCGAATTCCA
<i>IL6</i>	CAGTTCCTGCAGAAAAAGGCAA	GAGATGCGTCGTCATGTCCT
<i>IL6</i> *	ATGCAATAACCACCCCTGAA	CTGCAGCCACTGGTTCTGT
<i>IL8</i> *	CCTTTCACCCCAAATTTATC	TTCTGTATTGACGCAGTGTGG
<i>MCPI (CCL2)</i>	TTCTGTGCCTGCTGCTCATAG	GGGGGCATTGATTGCATCTGG
<i>NCF4</i>	ATACCTGCCCTCAACGCCTA	CGGGGACACACTCTTGACTT
<i>NFE2L2 (NRF2)</i>	TCTGCCAACTACTCCCAGGT	AACGTAGCCGAAGAAACCTCA
<i>NOS2</i>	AAGACCAGGCTGTCGTTGAG	GGATTCTGCAGCTGAGTGGT
<i>PDGFA</i>	AAGCAGCCAACCAGATGTGA	AGACCCGCACACTGGCAATAA
<i>RPS9</i>	TTGAAGCTGATCGGCGAGTAT	TTCATCAAGCGTCAGCAGTT
<i>SREBF1 (SREBP1)</i>	GGATTGCACGTTCTGAAGACAT	AGAGAGGAGCTCAGTGTGGT
<i>TGFB1</i>	GAGCCCTGGACACCAACTAC	GAGGTCCTTGCGGAAGTCAA
<i>TLR4</i>	GCTTCCTCCGTTTTCCAGAACTGC	TGGAGAGGTGGCTTAGGCTCTGA
<i>TNF</i>	TCGAACCCCAAGTGACAAGCCT	GCCATTGGCCAGGAGGGCAT
<i>TNF</i> *	TTCAGCTGGAGAAGGGTGAT	CCAAAGTAGACCTGCCCAGA
<i>TNFSF12</i>	CAGGACCCATCGGAACTGAA	CCGTGTTTTCCGGCCTTTAG
<i>TREM2</i>	ATCTACAACCCACGATGCG	CAGAGATCTCCAGCATCCCG
<i>VCAM1</i>	TTTTTGTC AATGTTGCCCC	CAGGCTGTAGCTCCCCATTAG
<i>VEGFA</i>	CCCACTGAGGAGTCCAACAT	CTCCTATGTGCTGGCCTTGG

\* Denotes qPCR primer set used in placental tissue.

**Supplemental Table S2.** Differential expression levels of inflammatory genes in fetal liver.

Gene	Fold change	P value	Comment
<i>TNF</i>			Undetectable amplification
<i>CCL2</i>	1.090	0.707	
<i>TLR4</i>	0.888	0.630	
<i>NOS2</i>			Undetectable amplification
<i>IL10</i>	1.391	0.486	
<i>TGFBI</i>	1.228	0.451	
<i>PDGFA</i>	1.240	0.364	
<i>IL12B</i>	1.156	0.733	

**Supplementary Table S3.** Tests of the *Firmicutes/Bacteroidetes* ratio with diet group and maternal parameters.

Variable	Value	P value
Diet group*	15	0.6905
Body weight	0.43030	0.2145
SSF	0.24316	0.4984
CRP	-0.33333	0.3807
Triglycerides	-0.11667	0.7650
Fasting glucose	0.53333	0.1392
Fasting insulin	-0.35758	0.3104
HDL	-0.40606	0.2443
LDL/VLDL	-0.24268	0.5292
Days gestation	0.16035	0.6803
Maternal weight at delivery	0.53333	0.1392
Placental weight	0.22893	0.5855

Variables analyzed by Spearman's correlation and rho value shown (excluding diet group).

\*Association analyzed by Wilcoxon rank sum test.

CRP, C-reactive protein; SSF, sum of skin folds.