

Supplementary Materials:

Table S1. Study of global differences in microbial composition among experimental groups using a permutational ANOVA (permanova). (A) Permanova results for beta diversity at phylum level. (B) Permanova results for beta diversity at genus level.

Comparisons	Df	SumsOfSqs	F.Model	R2	<i>p</i> -value	<i>p</i> -adjusted
(A) Phylum beta diversity permanova						
F- <i>Vangl2</i> ^{+/+} vs F- <i>Vangl2</i> ^{+/-Lp}	1	0.029	0.941	0.056	0.33	0.801
F- <i>Vangl2</i> ^{+/-Lp} vs C- <i>Vangl2</i> ^{+/-Lp}	1	0.138	3.875	0.195	0.067	0.268
C- <i>Vangl2</i> ^{+/-Lp} vs C- <i>Vangl2</i> ^{+/-Lp} -P	1	0.027	1.315	0.076	0.276	0.801
C- <i>Vangl2</i> ^{+/-Lp} -P-NS vs C- <i>Vangl2</i> ^{+/-Lp} -P-FA	1	0.044	3.756	0.190	0.053	0.265
C- <i>Vangl2</i> ^{+/-Lp} -P-NS vs C- <i>Vangl2</i> ^{+/-Lp} -P-CI	1	1	0.020	1.176	0.068	0.267
(B) Genus beta diversity permanova						
F- <i>Vangl2</i> ^{+/+} vs F- <i>Vangl2</i> ^{+/-Lp}	1	0.058	2.211	0.121	0.084	0.336
F- <i>Vangl2</i> ^{+/-Lp} vs C- <i>Vangl2</i> ^{+/-Lp}	1	0.153	5.815	0.267	0.001	0.005
C- <i>Vangl2</i> ^{+/-Lp} vs C- <i>Vangl2</i> ^{+/-Lp} -P	1	0.012	0.629	0.038	0.647	0.647
C- <i>Vangl2</i> ^{+/-Lp} -P-NS vs C- <i>Vangl2</i> ^{+/-Lp} -P-FA	1	0.026	1.661	0.094	0.152	0.336
C- <i>Vangl2</i> ^{+/-Lp} -P-NS vs C- <i>Vangl2</i> ^{+/-Lp} -P-CI	1	0.033	1.898	0.106	0.111	0.336

F, feces; C, cecum; P, pregnant; NS, non-supplemented; FA, supplemented with folic acid; CI, supplemented with D-*chiro*-inositol. *n* = 9 female mice per group.

Table S2. Significant differences at the genus level of microbiota from feces and cecum of non-pregnant *Vangl2^{+/Lp}* female mice ($n = 9$ per group).

Phylum	Genus	logFC	<i>p</i> -value	FDR
<i>p_Actinobacteria</i>	<i>g_Adlercreutzia</i>	-1.57	8.98×10^{-3}	3.46×10^{-2}
<i>p_Bacteroidetes</i>	<i>f_[Barnesiellaceae]_unclassified</i>	-0.85	1.41×10^{-3}	8.14×10^{-3}
<i>p_Deferribacteres</i>	<i>g_Mucispirillum</i>	2.71	6.88×10^{-4}	5.94×10^{-3}
<i>p_Firmicutes</i>	<i>c_Bacilli_unclassified</i>	-1.24	2.84×10^{-4}	3.28×10^{-3}
	<i>g_Staphylococcus</i>	-0.74	1.00×10^{-2}	3.69×10^{-2}
	<i>g_Enterococcus</i>	-3.05	2.74×10^{-4}	3.28×10^{-3}
	<i>g_Lactobacillus</i>	-1.79	2.45×10^{-3}	1.17×10^{-2}
	<i>g_Lactococcus</i>	-2.78	2.40×10^{-4}	3.28×10^{-3}
	<i>g_Streptococcus</i>	-1.52	1.32×10^{-3}	8.14×10^{-3}
	<i>g_Candidatus_Arthromitus</i>	-2.93	5.84×10^{-4}	5.91×10^{-3}
	<i>g_Dehalobacterium</i>	1.43	2.79×10^{-5}	1.13×10^{-3}
	<i>g_Anaerofustis</i>	2.55	1.35×10^{-4}	3.28×10^{-3}
	<i>f_Lachnospiraceae_unclassified</i>	0.62	7.86×10^{-3}	3.18×10^{-2}
	<i>g_Blautia</i>	-1.01	7.33×10^{-4}	5.94×10^{-3}
	<i>g_Marvinbryantia</i>	-0.98	1.38×10^{-2}	4.46×10^{-2}
	<i>g_Anaerotruncus</i>	2.38	9.23×10^{-4}	6.27×10^{-3}
	<i>f_Erysipelotrichaceae_unclassified</i>	-1.85	1.43×10^{-2}	4.46×10^{-2}
	<i>g_[Eubacterium]</i>	-1.37	5.66×10^{-3}	2.41×10^{-2}
	<i>g_Coprobacillus</i>	-2.71	2.15×10^{-4}	3.28×10^{-3}
<i>p_Proteobacteria</i>	<i>c_Betaproteobacteria_unclassified</i>	-0.97	1.36×10^{-2}	4.46×10^{-2}
	<i>g_Bilophila</i>	2.12	2.16×10^{-3}	1.10×10^{-2}
	<i>g_Desulfovibrio</i>	1.60	1.16×10^{-2}	4.10×10^{-2}
	<i>g_Helicobacter</i>	3.06	0	1.30×10^{-6}
	<i>g_Escherichia</i>	-1.37	9.29×10^{-4}	6.27×10^{-3}

The significant changes were determined using a Zero-inflated Gaussian mixture model using metagenomeSeq. logFC, log2 foldchange; FDR, False Discovery Rate adjusted *p*-value.