

Table S1. Summary of analyzed sequence information.

Sample type	Vaginal Delivered Neonates		C-section Delivered Neonates		Total
	Meconium	Stool	Meconium	Stool	
Number of samples	13	10	46	40	109
Number of sequences	130,990	106,891	473,580	365,274	1,076,735
Average sequences \pm SD	10,076 \pm 3,642	10,689 \pm 4,057	10,295 \pm 4,128	9,132 \pm 4,146	9,878 \pm 4,115
Number of sequences yielding OTUs	99,157	83,027	467,875	269,314	827,044
Average sequences yielding OTUs \pm SD	7,627 \pm 3,426	8,303 \pm 3,388	8,164 \pm 3,420	6,733 \pm 3,931	7,588 \pm 3,676
Number of OTUs	2,215	1,224	3,871	2,926	5,939
Average OTUs \pm SD	373 \pm 169	205 \pm 94	346 \pm 133	218 \pm 148	289 \pm 156

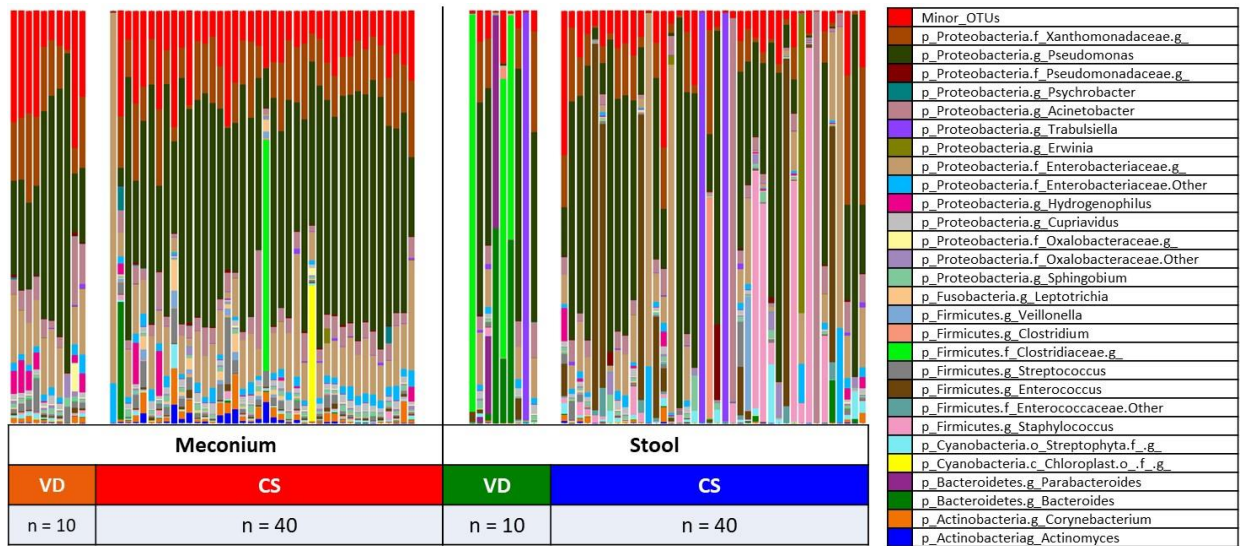
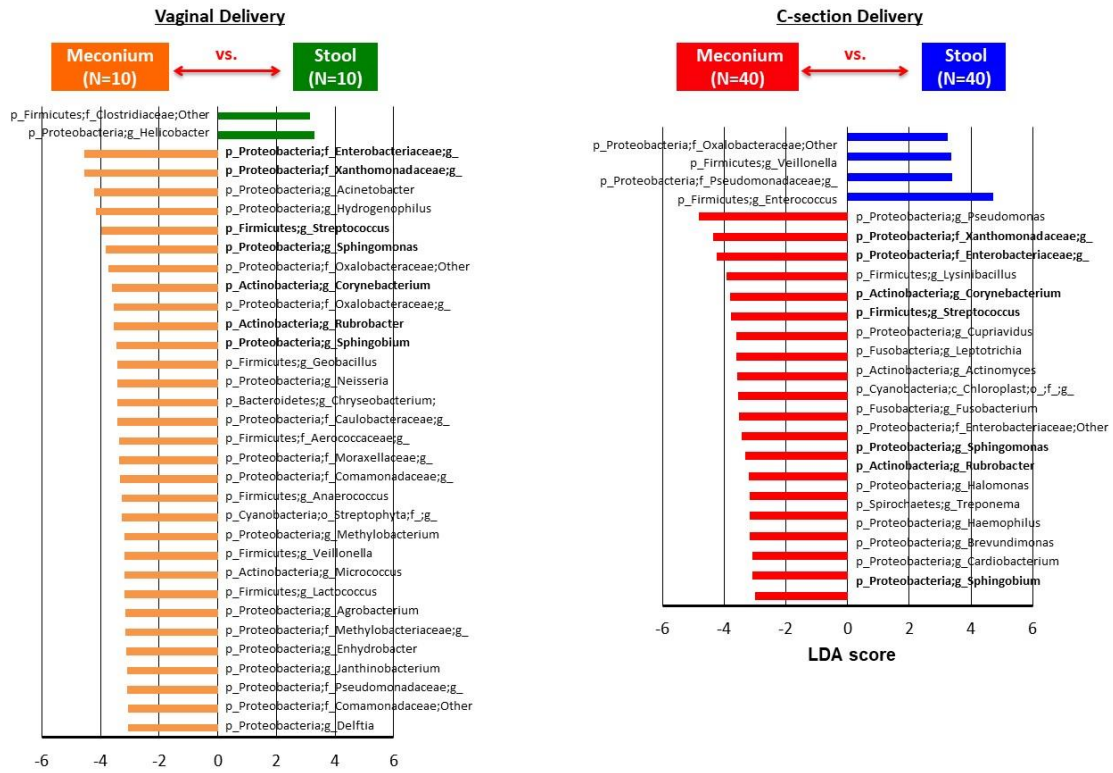


Figure S1. Differences in relative abundance of bacterial taxonomy in meconium or transitional stools according to mode of delivery. Bacterial taxonomic plots are shown at the lowest identifiable level, indicated by the letter preceding the underscore; f, family; g, genus. Each taxonomy (>1% of average relative abundance in any groups) is indicated by a different color at the genus level.

(A)**(B)**

KO Functional Categories	Vaginal Delivery			C-section			
	Meconium (n=10)	Stool (n=10)		Meconium (n=40)	Stool (n=40)		
Level 2	Level 3	P value	LDA	P value	P value	LDA	P value
Amino Acid Metabolism	Valine, Leucine and isoleucine degradation	0.04125	3.03	-	-	-	-
Xenobiotics Biodegradation and Metabolism		0.02334	3.47	-	-	-	-
Carbohydrate Metabolism	Amino sugar and nucleotide sugar metabolism		3.10	0.03429	-	-	-
Enzyme Families	Peptidases		3.07	0.04125	-	-	-
Carbohydrate Metabolism	Fructose and mannose metabolism		3.04	0.02837	-	-	-

Figure S2. Bacterial taxa **(A)** and Predictive functional profiling **(B)** comparisons between the meconium and transitional stool according to mode of delivery. **(A)** Histogram of overrepresented taxa in each group (LDA > 3.0). Bacterial taxa detected in both of delivery mode indicates using bold. **(B)** Overrepresented metabolic routes in predicted metagenomes were detected using LDA Effect Size (>3.0-fold) test.