

Supplemental Table 1. Bacterial phyla correlated by Pearson's correlation to gestation stage and DF level.

	Stage		DF	
	Coefficient	<i>P</i> -value	Coefficient	<i>P</i> -value
Firmicutes	-0.691	<0.01	-0.017	0.890
Bacteroidetes	0.681	<0.01	0.031	0.795
Euryarchaeota	0.177	0.137	-0.141	0.236
Proteobacteria	0.450	<0.01	0.153	0.200
Spirochaetes	0.242	0.040	-0.264	0.025
Tenericutes	-0.576	<0.01	-0.090	0.454
Cyanobacteria	0.363	<0.01	-0.253	0.032
Actinobacteria	0.458	<0.01	0.157	0.187
Acidobacteria	0.328	<0.01	0.167	0.161
Planctomycetes	0.369	<0.01	-0.103	0.392
Verrucomicrobia	0.227	0.055	0.291	0.013
Fibrobacteres	0.448	<0.01	0.071	0.554
Saccharibacteria	-0.056	0.638	0.034	0.775
Chloroflexi	0.252	0.033	0.155	0.193
Synergistetes	0.417	<0.01	0.130	0.277
Firmicutes/Bacteroidetes	-0.698	<0.01	-0.003	0.983

DF, total dietary fiber, sum of soluble and insoluble fiber.

Supplemental Table 2. Bacterial genera correlated by Pearson's correlation to gestation stage and DF level.

Phyla	Genera	Stage		DF	
		Coefficient	P-value	Coefficient	P-value
Firmicutes	<i>Clostridium_sensu_stricto_1</i>	-0.536	<0.01	0.208	0.080
	<i>Streptococcus</i>	0.078	0.516	-0.263	0.026
	<i>Ruminococcaceae_NK4A214_group</i>	-0.493	<0.01	0.010	0.935
	<i>Ruminococcaceae_UCG-002</i>	-0.394	<0.01	-0.017	0.885
	<i>Ruminococcaceae_UCG-005</i>	-0.269	0.023	-0.073	0.542
	<i>Ruminococcaceae_UCG-010</i>	-0.531	<0.01	0.050	0.678
	<i>Ruminococcaceae_UCG-014</i>	-0.484	<0.01	-0.080	0.506
	<i>Turicibacter</i>	-0.559	<0.01	0.063	0.601
	<i>Terrisporobacter</i>	-0.494	<0.01	0.003	0.980
	<i>[Eubacterium]_coprostanoligenes_group</i>	-0.416	<0.01	-0.158	0.184
	<i>Romboutsia</i>	-0.531	<0.01	-0.036	0.763
	<i>Oscillospira</i>	0.346	<0.01	0.228	0.055
	<i>Ruminococcus_1</i>	0.326	<0.01	0.025	0.835
	<i>Sarcina</i>	0.322	<0.01	0.025	0.835
	<i>Anaerotruncus</i>	-0.242	0.041	-0.059	0.625
	<i>Blautia</i>	0.281	0.017	-0.096	0.425
	<i>Ruminiclostridium_6</i>	0.428	<0.01	0.214	0.071
	<i>[Anaerorhabdus]_furcosa_group</i>	-0.574	<0.01	0.039	0.745
	<i>Subdoligranulum</i>	0.395	<0.01	-0.177	0.136
	<i>Quinella</i>	0.412	<0.01	0.182	0.126
<i>Oscillibacter</i>	-0.429	<0.01	-0.034	0.778	
Bacteroidetes	<i>Prevotellaceae_NK3B31_group</i>	0.584	<0.01	-0.250	0.034
	<i>Prevotellaceae_UCG-001</i>	0.08	0.502	0.252	0.033
	<i>Prevotella_1</i>	0.488	<0.01	-0.303	0.010
	<i>Prevotella_9</i>	0.508	<0.01	-0.293	0.013
	<i>Prevotellaceae_UCG-003</i>	0.546	<0.01	-0.123	0.303
	<i>Parabacteroides</i>	0.489	<0.01	0.008	0.949
	<i>Alloprevotella</i>	0.654	<0.01	-0.012	0.919
Proteobacteria	<i>Desulfovibrio</i>	0.441	<0.01	0.097	0.417
	<i>Succinivibrio</i>	0.408	<0.01	-0.307	<0.01
	<i>Escherichia-Shigella</i>	0.411	<0.01	-0.001	0.995
Fibrobacteres	<i>Fibrobacter</i>	0.448	<0.01	0.066	0.584
Actinobacteria	<i>Bifidobacterium</i>	0.344	<0.01	-0.011	0.926

DF, total dietary fiber, sum of soluble and insoluble fiber.