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Supplemental Material to:

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Gut microbial diversity is reduced and is associated with colonic inflammation in a piglet model of short bowel syndrome

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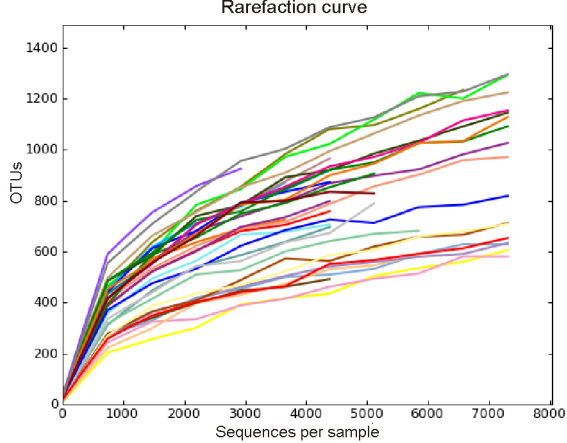
Supplementary table 1: List of primer sequences and Universal ProbeLibrary probe combinations used in this study.

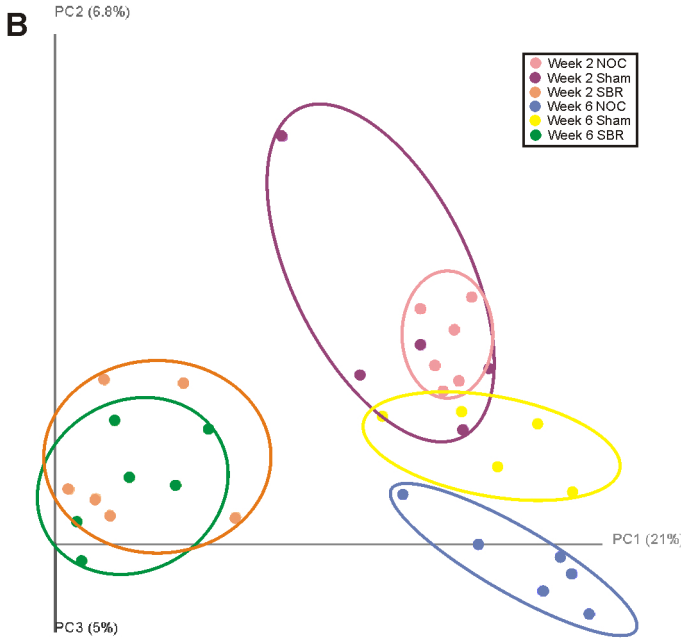
Primer	**Sequence 5' to 3'**	**UPL Probe**
RPL32 Forward	aactggccatcagggtcac	#64
RPL32 Reverse	cacaactggaactcctgtctattc	
IL1B Forward	ccaattcagggaccctacc	#19
IL1B Reverse	catggctgcttcagaaacct	
IL8 Forward	ttcttctttatccccaaactgg	#41
IL8 Reverse	ccacatgtcctcaaggtagga	
IL18 Forward	actttactttgtagctgaaaacgatg	#85
IL18 Reverse	tttaggttcaagcttgccaaa	
TNF Forward	ttgtcgctacatcgctgaac	#32
TNF Reverse	ccagtagggcggttacagac	

Figure S1. Rarefaction curve and principle component analysis of samples sequenced by high-throughput DNA sequencing. **(A)** Rarefaction curves for each group at 97% similarity indicated that the total bacterial diversity present was well represented. Number of operational taxonomic units (OTUs) identified as a function of the number of sequence tags sampled. **(B)** Principle component analysis revealed that the small bowel resection (SBR) groups at week 2 and week 6 clustered together, and were distinct from the non-operation control (NOC) and sham groups.

A


Rarefaction curve
OTUs
Sequences per sample
0
200
400
600
800
1000
1200
1400
0
1000
2000
3000
4000
5000
6000
7000
8000

B


PC2 (6.8%)
PC1 (21%)
PC3 (5%)
Week 2 NOC
Week 2 Sham
Week 2 SBR
Week 6 NOC
Week 6 Sham
Week 6 SBR