

Supplementary

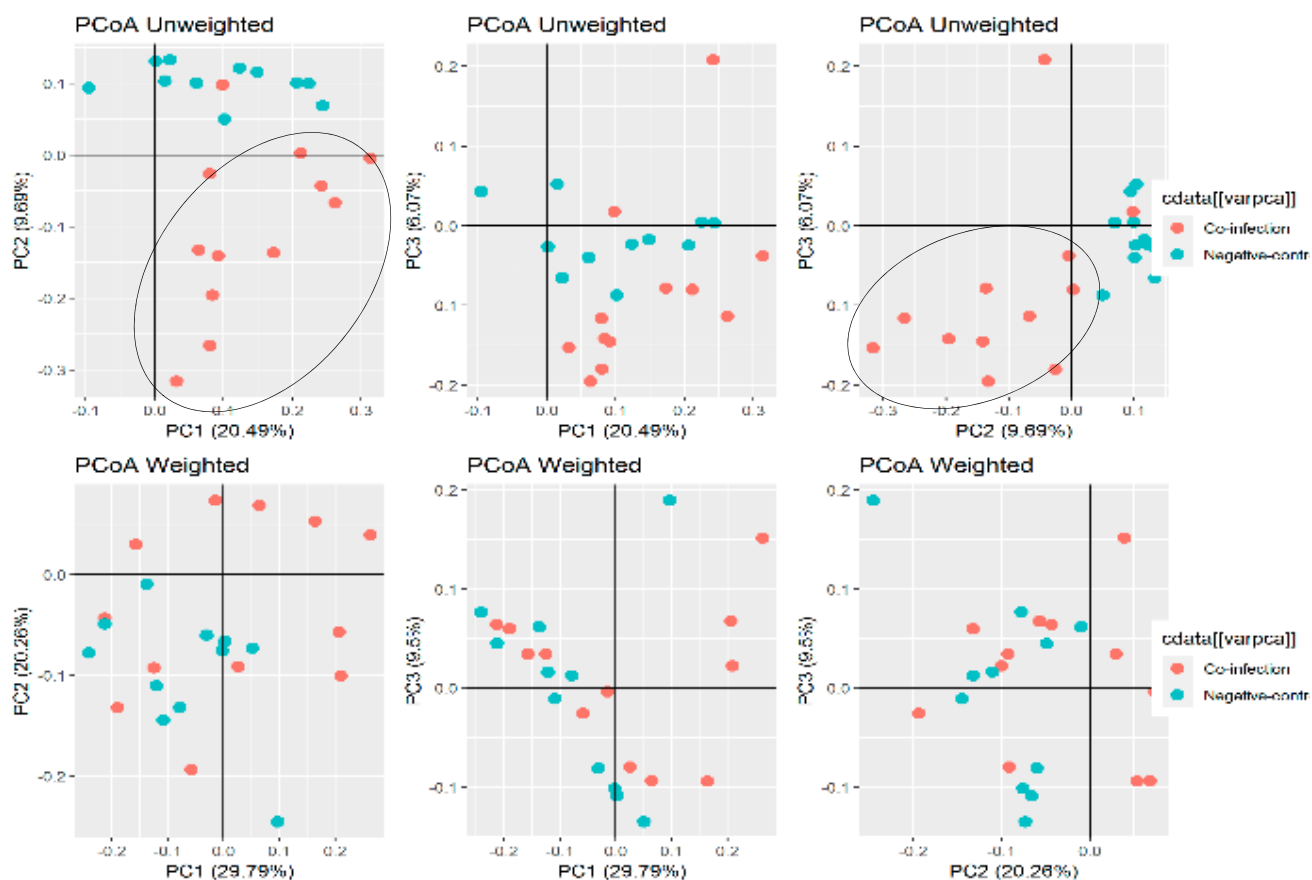


Figure S1: Principal coordinate analysis. The colors correspond to the groups made by Unifrac associated to fecal microbial communities. The beta diversity distance matrix was calculated to generate the diversity plot of swine microbiota samples at 21 days post infection comparing the coinfection and negative groups. It is possible to observe in the circles the formation of a close cluster in the coinfection group.



Figure S2: Principal coordinate analysis. The colors correspond to the groups made by Unifrac associated to fecal microbial communities. The beta diversity distance matrix was calculated to generate the diversity plot of swine microbiota samples at 5 and 21 days post infection comparing the groups.

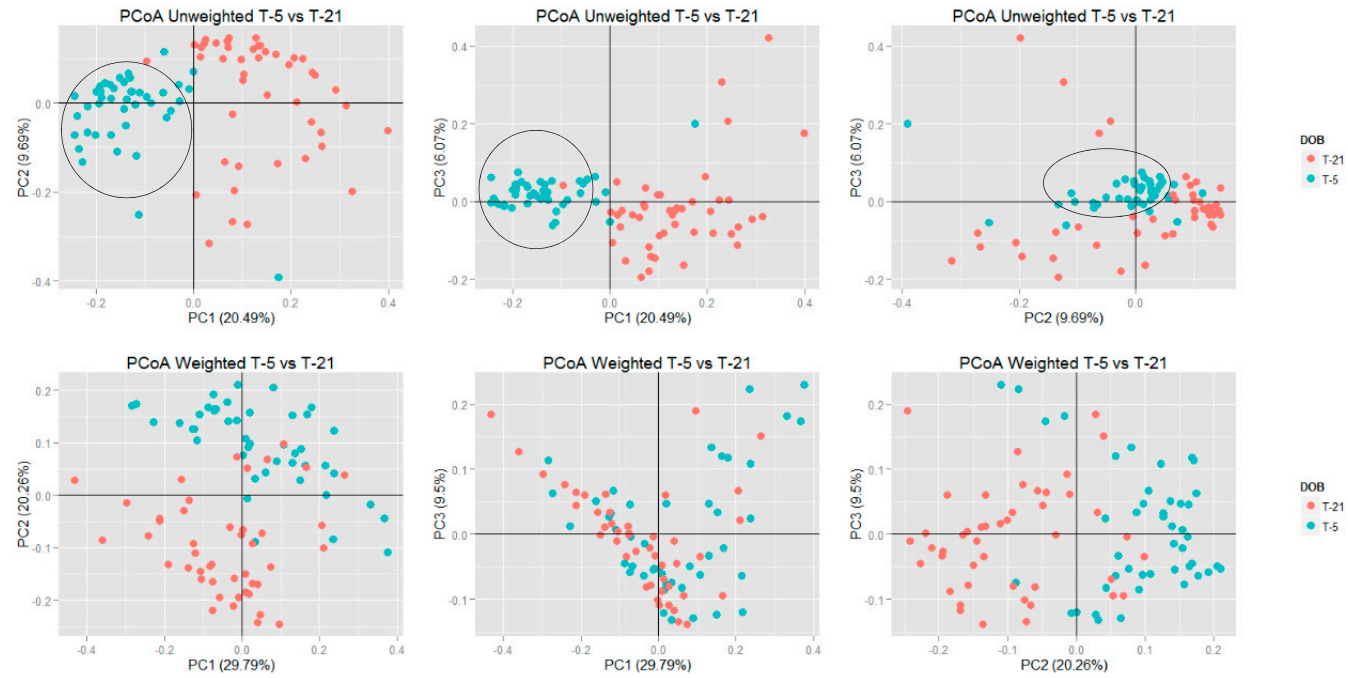


Figure S3: Principal coordinate analysis. The colors correspond to the groups made by Unifrac associated to fecal microbial communities. The beta diversity distance matrix was calculated to generate the diversity plot of swine microbiota samples at- 5 and 21 days post infection comparing the groups. It is possible to observe in the circles the formation of a close cluster in the coinfection group.

Table S1: Table of qPCR results comparing the fecal shedding, the letters “a,b” indicate statistical difference $P \leq 0.05$.

<i>Lawsonia intracellularis</i> PCR	DPI	CO	BRA	LAW	NEG
	-5	0a	0a	0a	0a
	3	9,82x10 ⁶ a	0a	3,52x10 ⁵ a	0a
	6	1,80x10 ⁵ a	0b	1,06x10 ⁶ a	0a
	10	1,03x10 ⁶ a	0b	7,42x10 ⁵ a	0b
	12	1,16x10 ⁶ a	0b	1,24x10 ⁶ a	0b
	15	7,62x10 ⁶ a	0b	6,66x10 ⁶ a	0b
	18	3,45x10 ⁶ a	0b	3,35x10 ⁶ a	0b
	21	2,81x10 ⁸ a	0b	1,96x10 ⁷ a	0b

<i>Brachyspira hyodysenteriae</i> PCR	DPI	CO	BRA	LAW	NEG
	-5	0 ^a	0 ^a	0 ^a	0 ^a
	3	0 ^a	0 ^a	0 ^a	0 ^a
	6	0 ^a	0 ^a	0 ^a	0 ^a
	10	3,82x10 ³ a	2,30x10 ³ ab	0 ^b	0 ^b
	12	2,50x10 ⁶ a	8,75x10 ³ a	0 ^b	0 ^b
	15	1,56x10 ⁷ a	5,02x10 ⁶ a	0 ^b	0 ^b
	18	1,14x10 ⁷ a	4,81x10 ⁶ a	0 ^b	0 ^b
	21	1,27x10 ⁷ a	1,82x10 ⁶ a	0 ^b	0 ^b

Table S2: Table evaluated fecal microbiome results and taxonomic groups with statistically significant differences separated by group $p \leq 0.05$.

Groups	Taxonomy	P value	Group with higher frequency
T21(Law_vs_Bra)	Family		
	Porphyromonadaceae	0.012886830493507	BRA
	Streptococcaceae	0.012886830493507	LAW
	Genus		
	<i>Parabacteroides</i>	0.012886830493507	BRA
T21(Co_vs_Bra)	<i>Streptococcus</i>	0.012886830493507	LAW
	Filo		
	Firmicutes	0.012879064669346	BRA
	Fusobacteria	0.0355240368313795	CO
	Class		
	Clostridia	0.0474483843880802	BRA
	Fusobacteriia	0.0355240368313795	CO
	Order		

T21(Co_vs_Law)	Clostridiales	0.0409535667814036	BRA
	Fusobacteriales	0.0355240368313795	CO
	Lactobacillales	0.0351950848989481	CO
	Family		
	[Paraprevotellaceae]	0.010705311873033	CO
	Clostridiaceae	0.00248543353268081	BRA
	Fusobacteriaceae	0.0355240368313795	CO
	Lactobacillaceae	0.0149386031285565	CO
	Genus		
	[Prevotella]	0.012879064669346	CO
	<i>Clostridium</i>	0.010705311873033	BRA
	<i>Fusobacterium</i>	0.0355240368313795	CO
	<i>Lactobacillus</i>	0.0149386031285565	CO
	<i>p-75-a5</i>	0.0474483843880802	CO
	Filo		
	Firmicutes	0.0256547699171202	LAW
	Fusobacteria	0.00631375918655783	CO
	Proteobacteria	0.0351950848989481	CO
	Class		
	Bacilli	0.00153997525783769	LAW
	Deltaproteobacteria	0.012879064669346	CO
	Epsilonproteobacteria	0.00591269060812482	CO
	Fusobacteriia	0.00631375918655783	CO
	Order		
	Campylobacterales	0.00591269060812482	CO
	Desulfovibrionales	0.010705311873033	CO
	Enterobacteriales	0.00830344690531291	CO
	Fusobacteriales	0.00631375918655783	CO
	Lactobacillales	0.000923824907537386	LAW
	Pasteurellales	0.0156848401759963	CO
	Family		
	[Odoribacteraceae]	0.00143598783526406	CO
	[Paraprevotellaceae]	0.000923824907537386	CO
	Bacteroidaceae	0.00187902637312587	CO
	Campylobacteraceae	0.00342874651022508	CO
	Desulfovibrionaceae	0.010705311873033	CO
	Enterobacteriaceae	0.00830344690531291	CO
	Fusobacteriaceae	0.00631375918655783	CO
	Lactobacillaceae	0.0127092847550734	LAW
	p-2534-18B5	0.0276173541564825	LAW
	Pasteurellaceae	0.0156848401759963	CO
	Porphyromonadaceae	0.00591269060812482	CO
	Streptococcaceae	0.0425377920562403	LAW

	Veillonellaceae	0.00594276612246729	LAW
	Genus		
	<i>[Eubacterium]</i>	0.00279865510717577	LAW
	<i>[Prevotella]</i>	0.00196463024569095	CO
	<i>Anaerovibrio</i>	0.0256783417053815	CO
	<i>Bacteroides</i>	0.00187902637312587	CO
	<i>Butyricimonas</i>	0.00197139594296633	CO
	<i>Campylobacter</i>	0.00342874651022508	CO
	<i>Catenibacterium</i>	0.027559127653885	CO
	<i>Desulfovibrio</i>	0.0256547699171202	CO
	<i>Dialister</i>	0.010705311873033	LAW
	<i>Fusobacterium</i>	0.00631375918655783	CO
	<i>Lactobacillus</i>	0.00175250848921009	LAW
	<i>Megasphaera</i>	0.00248543353268081	LAW
	<i>Odoribacter</i>	0.00142985438326551	LAW
	<i>Oscillospira</i>	0.0351950848989481	CO
	<i>p-75-a5</i>	0.00153997525783769	CO
	<i>Parabacteroides</i>	0.00704657239034717	CO
	<i>Shuttleworthia</i>	0.0238202172795873	LAW
	<i>Streptococcus</i>	0.0149386031285565	LAW
T21(co_vs_neg21)	Filo		
	Fusobacteria	0.00631375918655783	CO
	Class		
	Bacilli	0.0301176534687101	CO
	Deltaproteobacteria	0.0474483843880802	CO
	Fusobacteriia	0.00631375918655783	CO
	Opitutae	0.0133160403375067	NEG
	Order		
	Desulfovibrionales	0.00884804722804454	CO
	Enterobacteriales	0.00354574677030781	CO
	Fusobacteriales	0.00631375918655783	CO
	Lactobacillales	0.0256547699171202	NEG
	Pasteurellales	0.0156848401759963	CO
	Family		
	[Odoribacteraceae]	0.00362001666753251	CO
	[Paraprevotellaceae]	0.0072736188296829	CO
	Bacteroidaceae	0.00860879727082779	CO
	Christensenellaceae	0.0072736188296829	NEG
	Desulfovibrionaceae	0.00884804722804454	CO
	Enterobacteriaceae	0.00354574677030781	CO
	Fusobacteriaceae	0.00631375918655783	CO
	Lactobacillaceae	0.0175054975400099	NEG
	Pasteurellaceae	0.0156848401759963	CO

	Genus		
	<i>[Eubacterium]</i>	0.037417959614756	NEG
	<i>[Prevotella]</i>	7,77E-09	CO
	<i>Anaerovibrio</i>	0.0028415273840731	CO
	<i>Bacteroides</i>	0.00860879727082779	CO
	<i>Butyricimonas</i>	0.01045624760529	CO
	<i>Clostridium</i>	0.0474483843880802	CO
	<i>Desulfovibrio</i>	0.00594276612246729	CO
	<i>Fusobacterium</i>	0.00631375918655783	CO
	<i>Lactobacillus</i>	0.0127092847550734	NEG
	<i>Megasphaera</i>	0.0301176534687101	NEG
	<i>Odoribacter</i>	0.000422760407398187	NEG
	<i>p-75-a5</i>	0.00153997525783769	CO
	<i>Shuttleworthia</i>	0.0127092847550734	NEG
T21(law21_vs_neg21)	Class		
	<i>[Lentisphaeria]</i>	0.0453003901882632	NEG
	Bacilli	0.037417959614756	LAW
	Order		
	Campylobacterales	0.012837523673437	NEG
	GMD14H09	0.00463155837210344	LAW
	Lactobacillales	0.0473071819821046	NEG
	WCHB1-41	0.0298476426791938	NEG
	Family		
	Campylobacteraceae	0.00523650755848898	NEG
	p-2534-18B5	0.0359098003120898	NEG
	Porphyromonadaceae	0.0473071819821046	NEG
	RFP12	0.0354526082163918	NEG
	Streptococcaceae	0.0213986841852967	LAW
	Veillonellaceae	0.0192307692307692	LAW
	Genus		
	<i>Campylobacter</i>	0.0268002289808724	LAW
	<i>Catenibacterium</i>	0.037417959614756	NEG
	<i>Dialister</i>	0.00218478519730371	LAW
	<i>Megasphaera</i>	0.0156056085521693	LAW
	<i>Streptococcus</i>	0.012593249898966	LAW
	<i>Unassigned</i>	0.0225001812025638	NEG
T21(bra21_vs_neg21)	Genus		
	<i>Odoribacter</i>	0.00962198825643798	NEG