

Supplementary Materials: Fumonisin-Exposure Impairs Age-Related Ecological Succession of Bacterial Species in Weaned Pig Gut Microbiota

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Table S1. Pairwise ADONIS tests between treatments for each day of sampling. * *p*-adjusted values < 0.05 and † *p*-adjusted-values < 0.10, “false discovery rate” test.

R2	Control D0	Control D8	Control D15	Control D22	Control D29					
Control D0										
Control D8	NS									
Control D15	0.235 *	NS				R2 Adonis	<0.25	0.25-0.30	0.30-0.50	>0.50
Control D22	0.269 *	0.169 †	NS			High R2-ADONIS indicates well separated groups				
Control D29	0.216 *	0.167 †	NS	NS						
FB1 D0	0.243 *					FB1 D0	FB1 D8	FB1 D15	FB1 D22	FB1 D29
FB1 D8		0.229 *				NS				
FB1 D15			0.356 *			NS	NS			
FB1 D22				0.506 *		0.180 *	0.234 *	NS		
FB1 D29					0.297 *	0.216 *	0.163 †	NS	0.159 †	

Table S2. Phylum relative abundance (%) in fecal microbiota from Control and FB1 exposed piglets.

Phylum	Treatment ¹			<i>p</i> -value			<i>p</i> -adjusted ²	
	Control	FB1	SEM	Group	Date	Group x Date	Group	Date
Actinobacteria	1.12	0.25	0.154	0.012	0.060	0.124	0.059	0.075
Bacteroidetes	15.10	13.30	0.713	0.462	0.125	0.327	0.462	0.125
Firmicutes	80.48	83.17	0.887	0.125	0.054	0.352	0.157	0.075
Proteobacteria	2.29	1.18	0.188	0.047	0.010	0.172	0.079	0.025
Spirochaetae	1.01	2.03	0.254	0.031	0.009	0.108	0.078	0.025

¹FB1 pigs were fed with a diet supplemented with 12ppm/kg FB1 for 29 days; Control pigs received the same diet without any supplementation. Fecal sampling took place weekly.

²Values obtained with “false discovery rate” test.

Table S3. Percentage (%) of main bacterial families in fecal microbiota from Control vs FB1-exposed pigs.

Family	Treatment				<i>p</i> value		<i>p</i> adjusted	
	Control	FB1	SEM	Group	Date	Group x Date	Group	Date
Firmicutes								
Christensenellaceae	1.49	2.55	0.361	0.121	0.001	0.003	0.218	0.006
Clostridiaceae	5.09	3.60	0.694	0.371	0.177	0.000	0.471	0.208
Erysipelotrichaceae	0.07	0.05	0.014	0.019	0.005	0.001	0.051	0.017
Eubacteriaceae	0.11	0.00	0.016	0.002	0.096	0.405	0.009	0.137
Family XIII Clostridiales	0.71	0.92	0.074	0.387	0.008	0.028	0.471	0.024
Lachnospiraceae	22.23	15.33	0.771	0.001	0.000	0.685	0.006	0.001
Lactobacillaceae	20.25	40.20	2.468	0.010	0.051	0.101	0.031	0.084
Peptococcaceae	0.14	0.37	0.031	0.000	0.002	0.005	0.001	0.008
Peptostreptococcaceae	5.08	3.57	0.596	0.419	0.004	0.001	0.471	0.016
Ruminococcaceae	17.09	15.97	0.565	0.395	0.868	0.066	0.471	0.902
Streptococcaceae	0.11	0.07	0.048	0.657	0.053	0.344	0.657	0.084
Veillonellaceae	7.94	0.50	0.920	0.001	0.016	0.029	0.005	0.036
Bacteroidetes								
Bacteroidaceae	0.10	0.13	0.034	0.068	0.109	0.605	0.131	0.148
Bacteroidales RF16 group	0.02	0.19	0.024	0.000	0.975	0.011	0.000	0.975
Bacteroidales S24-7 group	1.06	1.23	0.097	0.414	0.000	0.653	0.471	0.001
p-2534-18B5 gut group	0.15	0.11	0.064	0.138	0.013	0.326	0.233	0.032
Porphyromonadaceae	0.81	0.32	0.132	0.166	0.039	0.023	0.263	0.076
Prevotellaceae	11.11	10.07	0.623	0.623	0.046	0.923	0.657	0.083
Rikenellaceae	1.81	1.24	0.121	0.024	0.121	0.000	0.054	0.156
Proteobacteria								
Campylobacteraceae	0.08	0.12	0.022	0.397	0.264	0.103	0.471	0.296
Desulfovibrionaceae	0.37	0.35	0.040	0.639	0.001	0.012	0.657	0.007
Rickettsiales Incertae Sedis	0.00	0.11	0.016	0.000	0.001	0.001	0.000	0.005
Sphingomonadaceae	0.26	0.22	0.018	0.325	0.156	0.593	0.471	0.191
Succinivibrionaceae	1.42	0.13	0.177	0.001	0.018	0.434	0.006	0.038
Syntrophaceae	0.06	0.04	0.009	0.021	0.320	0.084	0.051	0.346
Actinobacteria								
Coriobacteriaceae	1.08	0.22	0.153	0.010	0.056	0.160	0.031	0.084
Spirochaetaceae								
Spirochaetaceae	1.01	2.03	0.254	0.031	0.009	0.108	0.064	0.024

¹FB1 pigs were fed with a diet supplemented with 12ppm/kg FB1 for 29 days; Control pigs were fed the same diet without any supplementation. Fecal sampling took place weekly.

²Values obtained with “false discovery rate” test.

Table S4. Percentage (%) of main genera in fecal microbiota from Control vs FB1-exposed pigs. Genus are sorted according to their *p*-adjusted value of group effect.

Genus	Treatment				<i>p</i> -value		<i>p</i> -adjusted	
	Control	FB1	SEM	Group	Date	Group x Date	Group	Date
[Bacteroides] pectinophilus group	0.16	0.00	0.036	0.000	0.406	0.341	0.000	0.465
Candidatus Hepatintcola	0.00	0.10	0.014	0.000	0.001	0.000	0.000	0.008
<i>Oscillibacter</i>	0.06	0.18	0.014	0.000	0.292	0.023	0.000	0.361
<i>Oscillospira</i>	0.02	0.12	0.010	0.000	0.966	0.257	0.000	0.966
Lachnospiraceae NK4B4 group	0.14	0.02	0.017	0.000	0.473	0.026	0.001	0.526
<i>Peptococcus</i>	0.13	0.34	0.029	0.000	0.003	0.008	0.002	0.020
<i>Mitsuokella</i>	6.41	0.27	0.809	0.000	0.041	0.042	0.003	0.100
[Eubacterium] eligens group	0.16	0.03	0.017	0.001	0.035	0.397	0.007	0.094
<i>Collinsella</i>	0.16	0.03	0.014	0.001	0.084	0.126	0.007	0.155
Ruminococcaceae UCG-005	0.96	2.51	0.179	0.001	0.038	0.551	0.008	0.097
<i>Succinivibrio</i>	1.42	0.13	0.177	0.001	0.018	0.434	0.008	0.058
<i>Roseburia</i>	4.00	1.47	0.324	0.001	0.000	0.099	0.010	0.002
<i>Pseudoramibacter</i>	0.11	0.00	0.016	0.002	0.096	0.405	0.015	0.165
<i>Ruminococcus</i>	2.58	1.49	0.170	0.003	0.125	0.000	0.018	0.193
<i>Olsenella</i>	0.82	0.04	0.147	0.004	0.036	0.053	0.023	0.094
<i>Syntrophococcus</i>	0.20	0.01	0.029	0.005	0.242	0.466	0.025	0.320
<i>Butyricoccus</i>	0.16	0.04	0.014	0.007	0.809	0.151	0.031	0.830
<i>Lachnospira</i>	0.27	0.15	0.036	0.008	0.397	0.093	0.034	0.461
<i>Lactobacillus</i>	20.25	40.20	2.468	0.010	0.051	0.101	0.043	0.108
<i>Dorea</i>	0.57	0.27	0.042	0.011	0.094	0.392	0.044	0.165
[Eubacterium] nodatum group	0.17	0.05	0.029	0.017	0.016	0.973	0.061	0.056
[Eubacterium] ruminantium group	0.15	0.06	0.024	0.017	0.069	0.446	0.061	0.130
<i>Desulfomonile</i>	0.06	0.04	0.009	0.021	0.320	0.084	0.069	0.383
<i>Faecalibacterium</i>	4.55	1.54	0.421	0.020	0.050	0.917	0.069	0.108
Lachnospiraceae UCG-001	0.10	0.04	0.010	0.023	0.584	0.036	0.072	0.641
[Eubacterium] rectale group	1.02	0.46	0.101	0.033	0.001	0.132	0.090	0.010
[Eubacterium] xylanophilum group	0.52	0.20	0.055	0.031	0.278	0.003	0.090	0.354
<i>Dialister</i>	1.29	0.06	0.175	0.032	0.018	0.060	0.090	0.058
<i>Treponema</i>	1.01	2.03	0.254	0.031	0.009	0.108	0.090	0.036
Lachnospiraceae NK3A20 group	1.01	0.03	0.367	0.036	0.064	0.597	0.094	0.123
<i>Oribacterium</i>	0.30	0.17	0.023	0.041	0.243	0.294	0.101	0.320
Ruminococcaceae UCG-008	1.97	2.66	0.217	0.040	0.047	0.000	0.101	0.108
Prevotellaceae NK3B31 group	1.96	2.91	0.282	0.043	0.217	0.014	0.102	0.312
Ruminococcaceae UCG-009	0.04	0.07	0.006	0.045	0.434	0.151	0.105	0.490
[Ruminococcus] gauvreauii group	1.06	0.73	0.101	0.051	0.004	0.001	0.111	0.020
Rikenellaceae RC9 gut group	1.59	1.19	0.110	0.049	0.093	0.000	0.111	0.165

Genus	Treatment				p-value		p-adjusted	
	Control	FB1	SEM	Group	Date	Group x Date	Group	Date
Family XIII AD3011 group	0.31	0.65	0.060	0.053	0.000	0.019	0.113	0.005
<i>Anaerostipes</i>	0.50	0.79	0.141	0.055	0.236	0.166	0.114	0.320
<i>Blautia</i>	6.03	4.58	0.307	0.062	0.000	0.200	0.126	0.007
[Eubacterium] coprostanoligenes group	1.74	0.90	0.166	0.066	0.164	0.028	0.127	0.244
dgA-11 gut group	0.16	0.02	0.024	0.065	0.005	0.024	0.127	0.025
<i>Bacteroides</i>	0.10	0.13	0.034	0.068	0.109	0.605	0.128	0.180
<i>Ruminiclostridium</i>	0.42	0.55	0.031	0.083	0.232	0.085	0.152	0.320
<i>Coprococcus</i>	1.71	2.27	0.215	0.088	0.035	0.342	0.155	0.094
<i>Sarcina</i>	3.61	1.13	0.478	0.088	0.042	0.001	0.155	0.100
Family XIII UCG-001	0.08	0.06	0.006	0.097	0.014	0.011	0.167	0.052
Prevotellaceae UCG-003	0.19	0.08	0.024	0.117	0.004	0.001	0.196	0.021
Christensenellaceae R-7 group	1.49	2.55	0.361	0.121	0.001	0.003	0.199	0.008
<i>Anaerotruncus</i>	0.28	0.29	0.033	0.134	0.241	0.597	0.214	0.320
<i>Fusicatenibacter</i>	0.49	0.36	0.041	0.136	0.187	0.606	0.214	0.274
<i>Odoribacter</i>	0.15	0.11	0.064	0.138	0.013	0.326	0.214	0.051
Ruminococcaceae UCG-010	0.23	0.33	0.031	0.153	0.001	0.211	0.233	0.008
Ruminococcaceae NK4A214 group	0.49	0.71	0.066	0.211	0.003	0.004	0.315	0.020
Ruminococcaceae UCG-014	0.95	1.16	0.102	0.218	0.734	0.730	0.318	0.763
<i>Parabacteroides</i>	0.50	0.21	0.101	0.235	0.124	0.021	0.337	0.193
Subdoligranulum	1.02	1.57	0.160	0.265	0.049	0.872	0.373	0.108
[Eubacterium] hallii group	0.53	0.35	0.043	0.286	0.056	0.312	0.377	0.114
<i>Anaerovibrio</i>	0.07	0.13	0.015	0.281	0.632	0.445	0.377	0.675
<i>Porphyromonas</i>	0.22	0.09	0.064	0.273	0.311	0.776	0.377	0.378
<i>Prevotella</i>	8.30	6.52	0.612	0.286	0.060	0.685	0.377	0.119
<i>Terrisporobacter</i>	4.36	2.51	0.595	0.292	0.004	0.000	0.378	0.021
Lachnospiraceae ND3007 group	0.29	0.40	0.039	0.301	0.291	0.036	0.383	0.361
<i>Intestinibacter</i>	0.63	0.70	0.047	0.318	0.361	0.130	0.396	0.425
Ruminococcaceae UCG-013	0.09	0.11	0.012	0.321	0.015	0.056	0.396	0.052
<i>Sphingomonas</i>	0.26	0.22	0.018	0.325	0.156	0.593	0.396	0.237
<i>Campylobacter</i>	0.08	0.12	0.022	0.397	0.264	0.103	0.476	0.341
<i>Acetitomaculum</i>	0.10	0.10	0.024	0.549	0.685	0.341	0.647	0.721
<i>Romboustia</i>	0.08	0.33	0.093	0.557	0.020	0.167	0.647	0.060
<i>Mogibacterium</i>	0.14	0.15	0.012	0.610	0.052	0.019	0.698	0.108
<i>Desulfovibrio</i>	0.37	0.35	0.040	0.639	0.001	0.012	0.721	0.010
<i>Alloprevotella</i>	0.53	0.50	0.042	0.712	0.621	0.002	0.792	0.672
Lachnospiraceae NK4A136 group	1.16	1.14	0.116	0.743	0.008	0.085	0.815	0.033
<i>Lachnoclostridium</i>	0.53	0.58	0.128	0.800	0.020	0.386	0.832	0.060
Lachnospiraceae FCS020 group	0.13	0.14	0.010	0.796	0.922	0.331	0.832	0.933

Genus	Treatment				<i>p</i> -value		<i>p</i> -adjusted	
	Control	FB1	SEM	Group	Date	Group x Date	Group	Date
<i>Lactococcus</i>	0.10	0.04	0.047	0.771	0.119	0.104	0.832	0.193
<i>Marvinbryantia</i>	0.44	0.39	0.031	0.811	0.099	0.988	0.832	0.167
Ruminococcaceae UCG-002	1.25	1.14	0.119	0.795	0.001	0.019	0.832	0.008
<i>Barnesiella</i>	0.97	1.01	0.092	0.831	0.000	0.499	0.842	0.000
<i>Clostridium sensu stricto</i>	1.47	2.47	0.458	0.963	0.000	0.001	0.963	0.007

¹FB1 pigs were fed with a diet supplemented with 12ppm/kg FB1 for 29 days; Control pigs received the same diet without any supplementation. Fecal sampling took place weekly.

² Values obtained with “false discovery rate” test.

Table S5. Diet composition in percentage (%).

Ingredients	%
Wheat	47,500
Soya meal	24,300
Barley	22,900
Sunflower oil	1,400
Phytase	0,010
Lysine	0,465
DL-Methionine	0,165
L-Threonine	0,195
L-Tryptophan	0,045
Salt	0,235
CaHPO ₄	1,120
Calcium carbonate	1,000
Premix ¹	0,665

¹ Composition per kg of premix 2 000 000 UI of vitamin A, 400 000 of vitamin D3, 4 000 mg of vitamin E, 8 000 mg of vitamin C, 400 mg of vitamin B1, 1000 mg of vitamin B2, 2 170 mg of Pantothenic acid calcium salt, 4 000 mg of niacin, 6 mg of vitamin B12, 1000mg of vitamin B6, 400 mg of vitamine K3, 200 mg of folic acid, 40 mg of biotin, 12000 mg of choline chloride, 20 750 mg of Fe, 4 000 mg of Cu, 19 860 mg of Zn, 8 000 mg of Mn, 120 mg of I, 200 mg Co, 60 mg of Se.

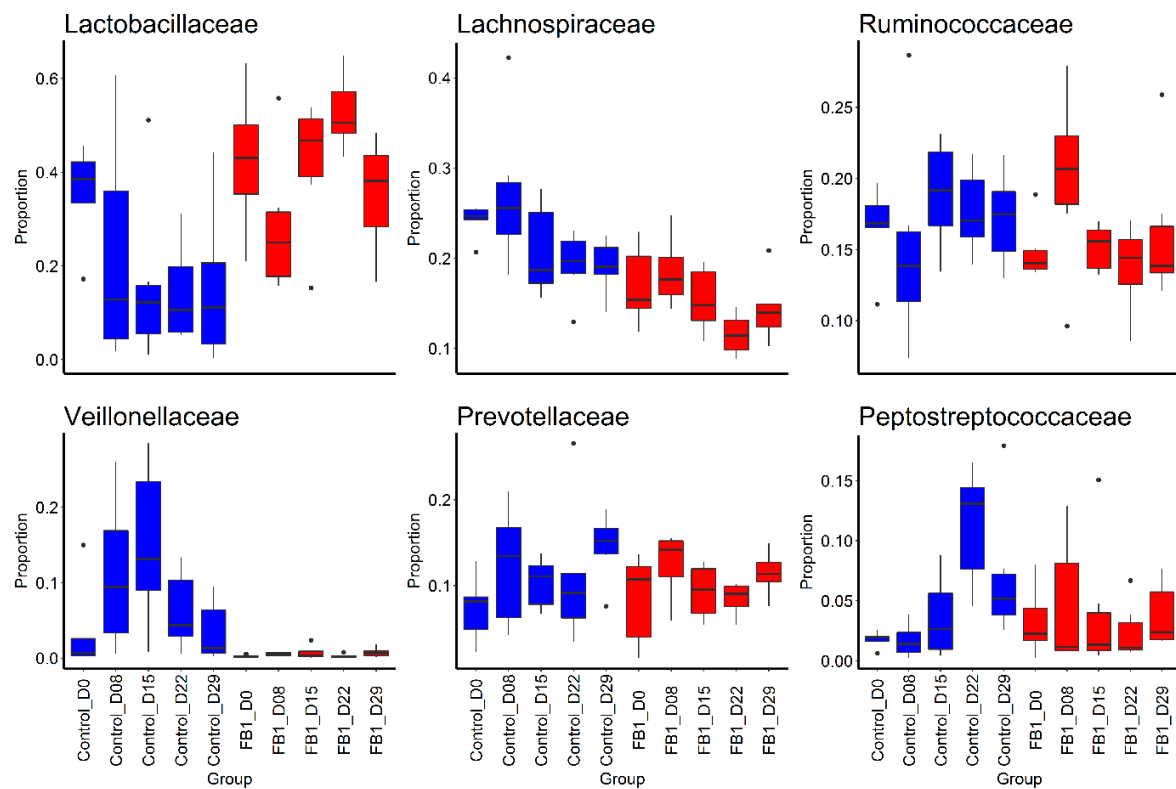


Figure S1. Relative abundance of main bacterial families in fecal microbiota from Control (blue) vs. FB1-exposed pigs (red).

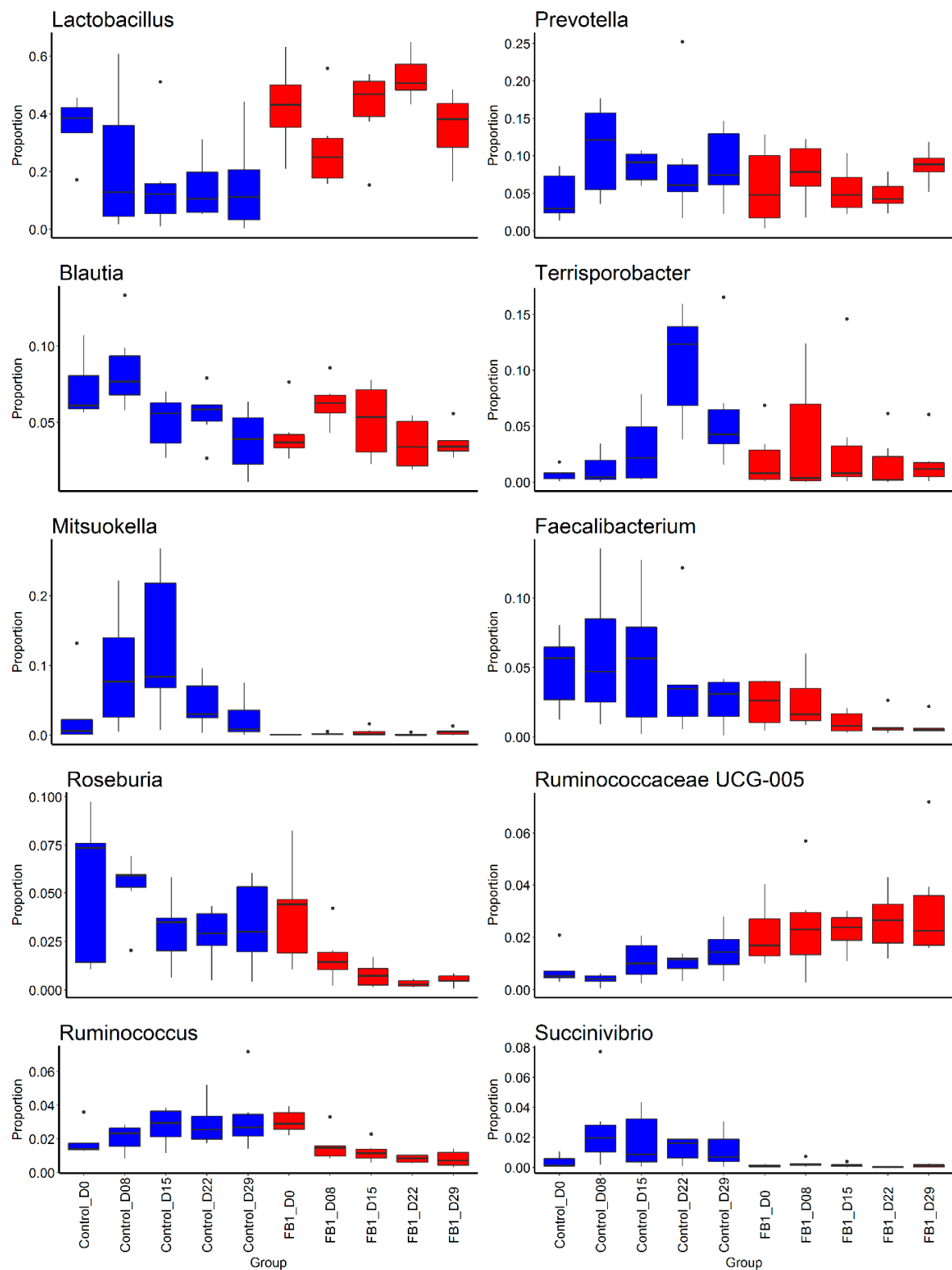


Figure S2. Relative abundance of main bacterial genera in fecal microbiota from Control (blue) vs. FB1-exposed pigs (red).

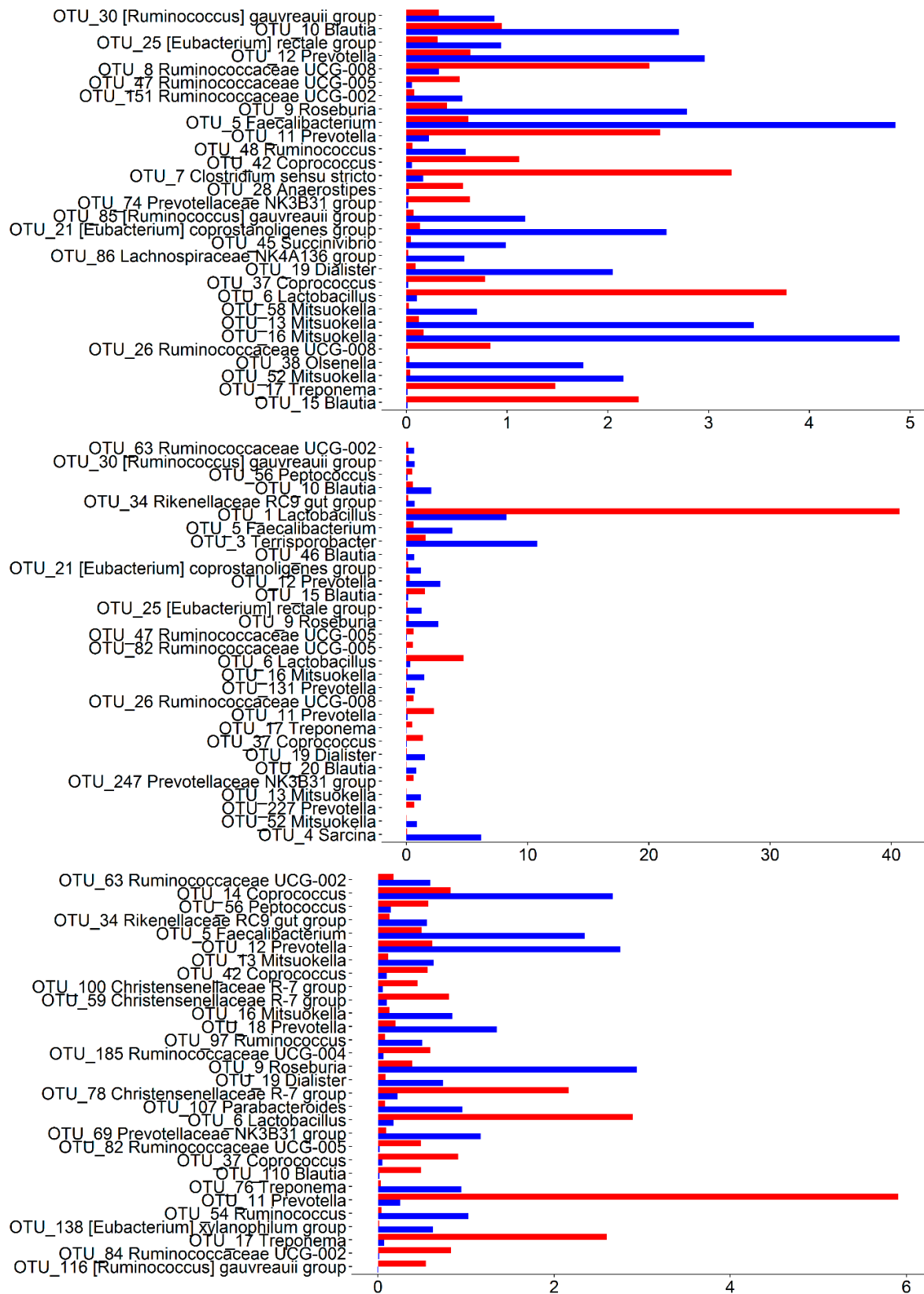


Figure S3. Relative abundance of 30 most abundant OTUs differentially abundant in fecal microbiota from Control (blue) vs. FB1-exposed pigs (red) at day 15 (top) day 22 (center) and day 29 (bottom) after FB1 exposure.