

Running Title: Fecal microbiota transplant and gut functions

Fecal microbiota transplant from highly feed efficient donors affects cecal physiology and microbiota in low- and high-feed efficient chickens

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Table S1 Total feed intake (TFI), total body weight gain (TBWG), and residual feed intake (RFI) values of low and high RFI broiler chickens receiving either a fecal microbiota transplant (FMT) or a control transplant (CT)¹

Item ^a	FMT		CT			P value		
	Low RFI	High RFI	Low RFI	High RFI	SEM	FMT	RFI	FMT×RFI
TFI (g)	2315	2631	2327	2568	57.3	0.665	<0.001	0.517
TBWG (g)	1641	1654	1656	1640	39.8	0.980	0.964	0.724
RFI (g)	-108	198	-117	155	25.2	0.310	<0.001	0.506

Data are presented as least-square means and pooled SEM. Low RFI FMT females, $n = 8$; low RFI FMT males, $n = 7$; high RFI FMT females, $n = 7$; high RFI FMT males, $n = 6$; low RFI CT females, $n = 7$; low RFI CT males, $n = 7$; high RFI CT females, $n = 7$; high RFI CT males, $n = 7$.

^aTFI, TBWG and RFI were calculated for the experimental period from 9 to 30 days post-hatch.

Sex affected TFI, TBWG ($P < 0.001$) and RFI ($P < 0.05$).

Table S2 Alpha-diversity of bacterial microbiota communities in ileal and cecal digesta of low and high residual feed intake (RFI) broiler chickens receiving either a fecal microbiota transplant (FMT) or a control transplant (CT)¹

Index	FMT		CT		SEM	P value		
	low RFI	high RFI	low RFI	high RFI		FMT	RFI	FMT×RFI
Jejunum								
Observed OTUs	102	90	83	106	14.11	0.913	0.685	0.214
Simpson	0.75	0.73	0.68	0.72	0.050	0.475	0.788	0.543
Shannon	2.26	2.14	1.85	2.10	0.201	0.266	0.759	0.358
Ceca								
Observed OTUs	314	312	336	338	31.76	0.458	0.997	0.944
Simpson	0.94	0.93	0.94	0.93	0.010	0.663	0.528	0.878
Shannon	3.77	3.76	3.87	3.79	0.090	0.420	0.615	0.699

¹Data are presented as least-square means and pooled SEM. Low RFI FMT females, *n* = 8; low RFI FMT males, *n* = 7; high RFI FMT females, *n* = 7; high-RFI FMT males, *n* = 6; low RFI CT females, *n* = 7; low-RFI CT males, *n* = 7; high-RFI CT females, *n* = 7; high-RFI CT males, *n* = 7.

Table S3 Relative abundance of bacterial phyla (% of all reads) present in jejunal and cecal digesta of low and high residual feed intake (RFI) broiler chickens receiving either a fecal microbiota transplant (FMT) or a control transplant (CT)¹

Phyla	FMT		CT		SEM	P value		
	low RFI	high RFI	low RFI	high RFI		FMT	RFI	FMT×RFI
Jejunum								
<i>Firmicutes</i>	59.1	51.3	70.7	59.6	8.030	0.222	0.245	0.838
<i>Proteobacteria</i>	32.6	39.0	24.7	34.6	8.200	0.457	0.328	0.833
<i>Cyanobacteria</i>	7.5	9.1	4.3	5.2	3.073	0.258	0.688	0.902
<i>Tenericutes</i>	0.20	0.01	0.04	0.04	0.063	0.290	0.137	0.135
<i>Actinobacteria</i>	0.31	0.48	0.11	0.48	0.169	0.542	0.118	0.540
Other	0.28	0.12	0.10	0.13	0.120	0.492	0.567	0.418
Ceca								
<i>Firmicutes</i>	92.4	93.5	95.1	92.3	2.510	0.764	0.730	0.441
<i>Proteobacteria</i>	6.6	5.2	3.3	6.9	2.500	0.769	0.665	0.318
<i>Tenericutes</i>	0.68	1.01	1.15	0.40	0.264	0.788	0.429	0.045
<i>Actinobacteria</i>	0.09	0.15	0.11	0.12	0.025	0.892	0.209	0.302
Other	0.21	0.17	0.27	0.23	0.034	0.096	0.225	0.980

¹Data are presented as least-square means and pooled SEM. Low RFI FMT females, n = 8; low RFI FMT males, n = 7; high RFI FMT females, n = 7; high-RFI FMT males, n = 6; low RFI CT females, n = 7; low-RFI CT males, n = 7; high-RFI CT females, n = 7; high-RFI CT males, n = 7.

Table S4 Relative abundance of most abundant bacterial genera (>0.1% of all reads) present in jejunal and cecal digesta of low and high residual feed intake (RFI) broiler chickens receiving either a fecal microbiota transplant (FMT) or a control transplant (CT)¹

Genus	FMT		CT		SEM	P value		FMT×RFI
	low RFI	high RFI	low RFI	high RFI		FMT	RFI	
Jejunum								
<i>o_Clostridiales;f__;g__</i>	2.38	1.68	0.86	1.75	0.730	0.324	0.895	0.281
<i>f_Enterobacteriaceae;g__</i>	28.92	34.74	23.62	31.90	8.528	0.635	0.413	0.886
<i>g_Lactobacillus</i>	38.58	31.79	55.42	38.37	9.614	0.229	0.221	0.596
<i>f_Ruminococcaceae;g__</i>	3.02	0.85	0.68	0.94	0.701	0.116	0.178	0.088
<i>g_Turicibacter</i>	3.79	8.49	4.51	15.09	4.076	0.374	0.067	0.474
<i>o_Streptophyta;f__;g__</i>	7.46	9.08	4.32	5.18	3.073	0.258	0.688	0.902
<i>f_Peptostreptococcaceae;g__</i>	—	7.14	3.94	7.41	0.31	3.780	0.658	0.179
<i>g_Anaerotruncus</i>	—	0.20	0.075	0.034	0.12	0.082	0.482	0.844
<i>g_Ruminococcus</i>	—	0.17	0.038	0.098	0.095	0.062	0.902	0.283
<i>f_Lachnospiraceae;g__</i>	—	0.32	0.092	0.13	0.15	0.088	0.449	0.260
<i>g_[Ruminococcus]</i>	—	0.52	0.066	0.040	0.10	0.166	0.190	0.245
<i>g_Oscillospira</i>	—	0.26	0.084	0.078	0.051	0.076	0.168	0.191
<i>g_Bacillus</i>	—	0.22	0.39	0.14	0.10	0.191	0.339	0.721
<i>g_Enterococcus</i>	—	1.42	1.41	0.42	1.62	0.633	0.534	0.352
<i>o_RF39;f__;g__</i>	—	0.21	0.015	0.042	0.043	0.062	0.290	0.137
<i>g_Coprococcus</i>	—	0.054	0.076	0.014	0.026	0.035	0.197	0.630
<i>g_Blautia</i>	—	0.080	0.058	0.021	0.031	0.024	0.086	0.806
<i>o_Rickettsiales;f__;g__</i>	—	0.92	0.75	0.55	0.50	0.322	0.345	0.743
<i>o_Clostridiales;f__;g__</i>	—	0.23	0.79	0.72	0.21	0.386	0.911	0.952
<i>g_Acinetobacter</i>	—	1.18	0.65	0.015	0.38	0.600	0.239	0.892
<i>g_Sphingomonas</i>	—	0.18	0.58	0.041	0.24	0.173	0.175	0.090
<i>f_0319-6G20;g__</i>	—	0.16	0.53	0.042	0.35	0.199	0.455	0.092
<i>f_Christensenellaceae;g__</i>	—	0.012	0.014	0	0.003	0.008	0.163	0.764
<i>g_Phenylbacterium</i>	—	0.17	0.48	0.036	0.15	0.118	0.053	0.075
<i>g_Dorea</i>	—	0.020	0.10	0.013	0.017	0.037	0.209	0.239
<i>g_Lactococcus</i>	—	0.049	0.81	0.010	0.056	0.274	0.153	0.146
<i>f_Clostridiaceae;g__</i>	—	0.068	0.050	0.022	0.060	0.041	0.655	0.814
<i>g_Clostridium</i>	—	0.43	0.20	0.065	0.068	0.211	0.256	0.596
<i>f_Lachnospiraceae;f__;g__</i>	—	0.020	0.001	0.010	0.030	0.011	0.400	0.965
<i>g_Proteus</i>	—	0.13	0.080	0.002	0.007	0.061	0.107	0.716
Ceca								
<i>o_Clostridiales;f__;g__</i>	57.30	56.40	62.10	57.32	3.919	0.469	0.473	0.623
<i>f_Enterobacteriaceae;g__</i>	3.33	5.12	3.08	6.92	1.897	0.685	0.144	0.591
<i>g_Lactobacillus</i>	0.68	0.35	1.23	0.90	0.254	0.036	0.195	0.995
<i>f_Ruminococcaceae;g__</i>	17.63	16.60	14.03	16.41	1.853	0.312	0.718	0.363
<i>g_Turicibacter</i>	0.70	0.95	0.69	0.84	0.320	0.863	0.540	0.879
<i>f_Peptostreptococcaceae;g__</i>	—	0.02	0.02	0.01	0.02	0.006	0.320	0.550
<i>g_Anaerotruncus</i>	—	2.67	4.19	4.04	4.13	1.508	0.668	0.597
<i>g_Ruminococcus</i>	—	3.11	3.70	2.57	2.94	0.380	0.093	0.215
<i>f_Lachnospiraceae;g__</i>	—	2.39	2.55	1.87	2.18	0.317	0.167	0.449

<i>g_[Ruminococcus]</i>	2.42	2.79	1.30	1.79	0.460	0.025	0.352	0.904
<i>g_Oscillospira</i>	2.06	2.16	1.88	2.04	0.199	0.458	0.524	0.874
<i>g_Bacillus</i>	0.34	0.61	2.68	0.81	0.927	0.176	0.392	0.254
<i>g_Enterococcus</i>	0.075	0.076	0.087	0.079	0.034	0.834	0.913	0.908
<i>o_RF39;f__;g__</i>	0.68	1.01	1.15	0.40	0.264	0.788	0.429	0.045
<i>g_Coprococcus</i>	0.89	0.76	0.74	0.82	0.107	0.708	0.835	0.345
<i>g_Blautia</i>	0.75	0.92	0.67	0.79	0.141	0.478	0.308	0.856
<i>o_Clostridiales;f__;g__</i>	0.15	0.10	0.09	0.10	0.027	0.341	0.500	0.327
<i>g_Sphingomonas</i>	1.00	0.001	0.002	0.003	0.500	0.322	0.322	0.321
<i>f_0319-6G20;g__</i>	0.67	0.001	0.001	0	0.333	0.322	0.322	0.323
<i>f_Christensenellaceae;g__</i>	0.37	0.44	0.42	0.44	0.106	0.825	0.693	0.781
<i>g_Phenylobacterium</i>	0.62	0.001	0.001	0.001	0.310	0.322	0.322	0.322
<i>g_Dorea</i>	0.27	0.24	0.16	0.18	0.042	0.047	0.912	0.528
<i>g_Clostridium</i>	0.027	0.032	0.027	0.038	0.006	0.585	0.165	0.674
<i>f_Lachnospiraceae;f__;g__</i>	0.18	0.27	0.15	0.21	0.035	0.190	0.032	0.520
<i>g_Proteus</i>	0.12	0.037	0.25	0.016	0.129	0.661	0.230	0.549
<i>f_Dehalobacteriaceae;g__</i>	0.13	0.13	0.10	0.10	0.028	0.313	0.941	0.990
<i>f_Bacillaceae;g__</i>	0.016	0.022	0.098	0.035	0.023	0.050	0.229	0.146
<i>g_Slackia</i>	0.041	0.084	0.051	0.061	0.020	0.743	0.184	0.405
<i>f_Erysipelotrichaceae;g__</i>	0.044	0.061	0.041	0.033	0.010	0.114	0.664	0.220
<i>g_Coprobacillus</i>	0.033	0.074	0.031	0.027	0.018	0.162	0.305	0.203
<i>f_Coriobacteriaceae;g__</i>	0.025	0.037	0.040	0.032	0.007	0.473	0.770	0.139
<i>f_Ruminococcaceae;g__</i>	0.030	0.027	0.048	0.049	0.008	0.012	0.889	0.833
<i>g_Eggerthella</i>	0.022	0.024	0.019	0.024	0.005	0.755	0.506	0.819
<i>f_[Mogibacteriaceae];g__</i>	0.012	0.009	0.010	0.017	0.004	0.490	0.541	0.224

¹Data are presented as least-square means and pooled SEM. Low RFI FMT females, *n* = 8; low RFI FMT males, *n* = 7; high RFI FMT females, *n* = 7; high-RFI FMT males, *n* = 6; low RFI CT females, *n* = 7; low-RFI CT males, *n* = 7; high-RFI CT females, *n* = 7; high-RFI CT males, *n* = 7.

Table S5 Differences in the concentration of total short-chain fatty acids (SCFA) and molar proportions (%) of the individual SCFA in crop, jejunal, ileal and cecal digesta of low and high residual feed intake (RFI) broiler chickens receiving either a fecal microbiota transplant (FMT) or a control transplant (CT)¹

Item	FMT		Control		SEM	FMT	P value	
	Low RFI	High RFI	Low RFI	High RFI			RFI	FMT × RFI
Crop								
Total SCFA (μmol/g)	43.1	44.7	60.2	59.6	7.91	0.052	0.955	0.885
Molar proportion (%)								
Acetate	89.1	87.2	90.3	89.4	1.163	0.152	0.249	0.658
Propionate	1.73	2.39	0.99	0.67	0.416	0.006	0.686	0.250
Isobutyrate	6.89	6.81	7.06	8.64	1.003	0.329	0.458	0.412
Butyrate	1.08	1.48	0.93	0.88	0.198	0.068	0.383	0.259
Isovalerate	0.20	0.33	0.04	0.01	0.081	0.005	0.544	0.353
Valerate	0.33	0.64	0.19	0.10	0.133	0.017	0.427	0.136
Caproate	0.72	1.18	0.55	0.30	0.157	0.002	0.486	0.029
Jejunum								
Total SCFA (μmol/g)	47.9 ^b	61.7 ^a	55.0 ^{ab}	54.7 ^{ab}	3.24	0.994	0.041	0.036
Molar proportion (%)								
Acetate	89.74	89.14	88.26	88.06	0.844	0.144	0.635	0.812
Propionate	0.55	0.48	0.53	0.40	0.099	0.635	0.350	0.746
Isobutyrate	8.48	9.31	10.34	10.65	0.791	0.055	0.472	0.737
Butyrate	0.31	0.33	0.27	0.22	0.076	0.335	0.854	0.693
Isovalerate	0.47	0.42	0.37	0.40	0.142	0.682	0.957	0.804
Valerate	0.03	0.02	0.02	0.01	0.021	0.535	0.602	0.865
Caproate	0.43	0.28	0.21	0.26	0.100	0.259	0.655	0.343
Ileum								
Total SCFA (μmol/g)	41.2	44.9	38.5	38.8	3.06	0.158	0.514	0.586
Molar proportion (%)								
Acetate	91.62	91.38	91.83	91.24	0.471	0.942	0.382	0.715
Propionate	0.79	0.81	0.78	0.85	0.122	0.880	0.700	0.862
Isobutyrate	6.94	7.05	6.73	7.23	0.358	0.958	0.396	0.592
Butyrate	0.07	0.06	0.13	0.07	0.053	0.557	0.459	0.604
Isovalerate	0.55	0.55	0.35	0.50	0.122	0.325	0.559	0.567
Valerate
Caproate	0.03	0.14	0.17	0.12	0.079	0.481	0.708	0.292
Ceca								
Total SCFA (μmol/g)	147.0	155.9	126.6	139.1	13.71	0.186	0.460	0.896
Molar proportion (%)								
Acetate	80.57	82.12	81.88	81.58	1.795	0.830	0.740	0.609
Propionate	5.15	6.02	4.65	4.34	0.515	0.044	0.607	0.266
Isobutyrate	0.75	0.54	0.93	1.00	0.173	0.081	0.710	0.430
Butyrate	11.40	9.50	10.27	10.16	1.724	0.891	0.579	0.607
Isovalerate	0.70	0.52	0.80	1.07	0.192	0.106	0.816	0.263

Valerate	1.06	0.90	1.10	1.20	0.148	0.263	0.839	0.381
Caproate	0.37	0.39	0.38	0.66	0.110	0.231	0.190	0.262

¹Data are presented as least-square means and pooled SEM. Low RFI FMT females, $n = 8$; low RFI FMT males, $n = 7$; high RFI FMT females, $n = 7$; high-RFI FMT males, $n = 6$; low RFI CT females, $n = 7$; low-RFI CT males, $n = 7$; high-RFI CT females, $n = 7$; high-RFI CT males, $n = 7$. ND, not detected.

^{a,b}Different superscripts within a row indicate significant difference ($P \leq 0.05$).

Table S6 Differences in visceral organ size of low and high residual feed intake (RFI) broiler chickens receiving either a fecal microbiota transplant (FMT) or a control transplant (CT)¹

Item	FMT		CT		SEM	P value		FMT × RFI
	low RFI	high RFI	low RFI	high RFI		FMT	RFI	
Body weight (BW) at sampling (kg)	2.38	2.38	2.43	2.44	0.070	0.432	0.968	0.974
Length (cm/kg BW)								
Duodenum	12.6	12.3	11.5	11.5	0.40	0.024	0.630	0.693
Jejunum	42.3	41.6	41.5	39.3	1.44	0.282	0.307	0.629
Ileum	13.3	12.9	12.6	13.1	0.55	0.622	1.000	0.402
Ceca (average of the two)	6.4	6.6	6.3	5.8	0.23	0.061	0.485	0.168
Colon	3.1	3.2	3.2	3.1	0.14	0.952	0.746	0.346
Total gut	84.2	83.1	81.4	78.6	2.20	0.100	0.376	0.695
Weight (g/kg BW)								
Crop	3.1	3.2	3.2	3.0	0.30	0.864	0.812	0.737
Proventriculus	4.1	4.1	4.1	4.4	0.19	0.565	0.412	0.450
Gizzard	12.5	14.6	13.4	13.0	0.63	0.571	0.203	0.054
Duodenum	5.0	4.9	4.8	4.8	0.22	0.527	0.740	0.809
Jejunum	16.1	17.0	15.8	16.2	0.54	0.300	0.216	0.693
Ileum	2.5	2.8	2.7	2.7	0.14	0.769	0.357	0.243
Ceca (average of the two)	1.1	1.0	1.1	1.0	0.04	0.618	0.027	0.864
Colon	1.3	1.3	1.3	1.3	0.07	0.844	0.648	0.711
Total gut	45.8	48.9	46.4	46.4	1.02	0.348	0.143	0.134
Pancreas	1.9	1.9	1.7	1.8	0.06	0.188	0.663	0.527
Liver	21.2	21.1	21.5	20.8	0.70	0.974	0.503	0.648
Heart	5.5	5.7	5.1	5.5	0.23	0.205	0.157	0.819

¹Data are presented as least-square means and pooled SEM. Low RFI FMT females, n = 8; low RFI FMT males, n = 7; high RFI FMT females, n = 7; high-RFI FMT males, n = 6; low RFI CT females, n = 7; low-RFI CT males, n = 7; high-RFI CT females, n = 7; high-RFI CT males, n = 7.

Table S7 Differences in intestinal histo-morphology of low and high residual feed intake (RFI) broiler chickens receiving either a fecal microbiota transplant (FMT) or a control transplant (CT)¹

Item	FMT		CT		SEM	P value		
	low RFI	high RFI	low RFI	high RFI		FMT	RFI	FMT×RFI
Jejunum								
Villus height (μm)	652.1	711.0	711.3	701.3	21.40	0.252	0.259	0.114
Villus width (μm)	47.7	47.9	48.0	48.4	1.11	0.746	0.803	0.969
Crypt depth (μm)	70.7	71.5	68.5	68.7	2.79	0.370	0.855	0.914
Villus surface	0.10	0.11	0.11	0.11	0.004	0.278	0.381	0.238
Villus height : crypt depth	9.9	10.5	10.9	10.7	0.38	0.118	0.619	0.283
Circular muscle (μm)	86.0	94.4	89.1	94.7	6.04	0.787	0.254	0.820
Longitudinal muscle (μm)	33.9	35.7	36.7	37.4	2.50	0.374	0.619	0.839
Goblet cells (counts /villus-crypt unit)	55.4	64.2	60.1	63.7	3.75	0.582	0.105	0.490
Lymphocytes (counts/villus-crypt unit)	12.9	15.3	13.9	14.1	1.25	0.953	0.294	0.403
Ileum								
Villus height (μm)	514.6	572.5	542.1	581.5	21.00	0.388	0.025	0.661
Villus width (μm)	51.7	53.1	51.8	52.2	1.38	0.770	0.504	0.723
Crypt depth (μm)	70.6	70.2	71.6	70.9	2.39	0.724	0.842	0.952
Villus surface	0.08	0.10	0.09	0.10	0.005	0.625	0.045	0.602
Villus height : crypt depth	7.4	8.3	7.7	8.3	0.39	0.693	0.081	0.722
Circular muscle (μm)	133.1	126.1	124.5	136.3	11.50	0.943	0.838	0.416
Longitudinal muscle (μm)	43.4	42.6	42.6	42.2	3.11	0.855	0.847	0.952
Goblet cells (counts /villus-crypt unit)	51.1	54.0	51.0	53.4	3.38	0.923	0.446	0.934
Lymphocytes (counts/villus-crypt unit)	13.6	15.6	13.5	13.8	1.56	0.559	0.476	0.589
Ceca								
Crypt depth (μm)	184.1	172.1	208.2	209.3	10.76	0.006	0.614	0.545
Circular muscle (μm)	200.8	206.1	232.3	218.2	11.38	0.062	0.697	0.398
Longitudinal muscle (μm)	50.2	57.9	55.8	52.3	3.38	0.997	0.539	0.107

Goblet cells (counts /villus-crypt unit)	3.5	3.5	4.7	4.6	0.60	0.068	0.958	0.943
Lymphocytes (counts/villus-crypt unit)	0.9	0.9	1.0	1.1	0.12	0.160	0.591	0.489

¹Data are presented as least-square means and pooled SEM. Low RFI FMT females, $n = 8$; low RFI FMT males, $n = 7$; high RFI FMT females, $n = 7$; high-RFI FMT males, $n = 6$; low RFI CT females, $n = 7$; low-RFI CT males, $n = 7$; high-RFI CT females, $n = 7$; high-RFI CT males, $n = 7$.

Table S8 Taxonomy of most influential bacterial operational taxonomic units (OTU) identified using sparse partial least squares-discriminant analysis and presented in the circos plots

Item	Taxonomy	Item	Taxonomy
Jejunum		Jejunum	
Component 1		Component 2	
OTU6	<i>Ruminococcaceae</i>	OTU9	<i>Lactobacillus</i>
OTU17	<i>Lactobacillus</i>	OTU10	<i>Lactobacillus</i>
OTU26	[<i>Ruminococcus</i>]	OTU34	<i>Lactobacillus</i>
OTU34	<i>Lactobacillus</i>	OTU37	<i>Lactobacillus</i>
OTU85	<i>Lactobacillus</i>	OTU68	<i>Enterococcus cecorum</i>
OTU134	<i>Lactobacillus</i>	OTU73	<i>Lactobacillus</i>
OTU139	<i>Lactobacillus</i>	OTU105	<i>Lactobacillus</i>
OTU556	<i>Sphingomonas</i>	OTU139	<i>Lactobacillus</i>
Ceca		Ceca	
Component 1		Component 2	
OTU19	<i>Anaerotruncus</i>	OTU11	<i>Clostridiales</i>
OTU29	<i>Clostridiales</i>	OTU2	<i>Clostridiales</i>
OTU44	<i>Clostridiales</i>	OTU69	<i>Ruminococcaceae</i>
OTU70	<i>Ruminococcus</i>	OTU131	<i>Ruminococcaceae</i>
OTU75	<i>Clostridiales</i>	OTU181	<i>Clostridiales</i>
OTU76	<i>Oscillospira</i>	OTU175	<i>Clostridiales</i>
OTU90	<i>Clostridiales</i>	OTU171	<i>Clostridiales</i>
OTU97	<i>Clostridiales</i>	OTU172	<i>Clostridiales</i>
OTU102	<i>Clostridiales</i>	OTU156	<i>Clostridiales</i>
OTU120	<i>Ruminococcus</i>	OTU166	<i>Clostridiales</i>
OTU126	<i>Oscillospira</i>	OTU182	<i>Clostridiales</i>
OTU146	<i>Clostridiales</i>	OTU176	<i>Clostridiales</i>
OTU150	<i>Clostridiales</i>	OTU48	RF39
OTU157	<i>Ruminococcaceae</i>	OTU187	<i>Clostridiales</i>
OTU162	<i>Ruminococcus</i>	OTU40	<i>Clostridiales</i>
OTU205	<i>Ruminococcus</i>	OTU224	<i>Clostridiales</i>
OTU212	<i>Clostridiales</i>	OTU67	<i>Clostridiales</i>
OTU221	<i>Ruminococcaceae</i>	OTU61	<i>Clostridiales</i>
OTU223	<i>Clostridiales</i>	OTU119	<i>Oscillospira</i>
OTU226	<i>Ruminococcus</i>	OTU59	<i>Clostridiales</i>

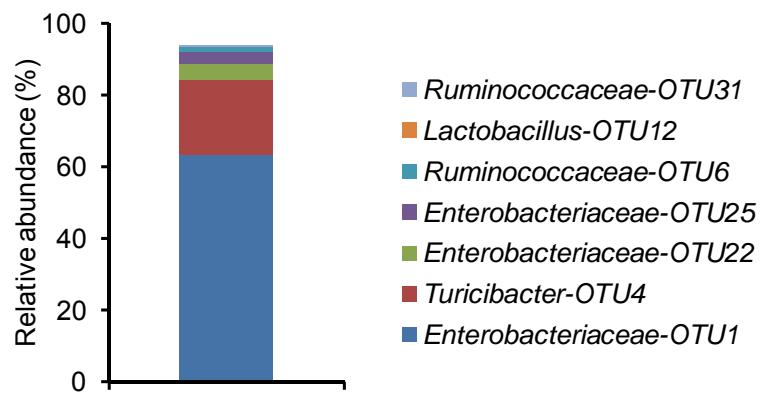


Figure S1 Taxonomic composition of fecal microbiota transplant (FMT). Mean values ($n = 8$; FMT inoculum of the three individual inoculation days of the two batches and pooled samples of the FMT inocula across the three inoculation days per batch). OTU, operational taxonomic unit. Only the most abundant OTUs are presented (relative abundance $>0.1\%$).

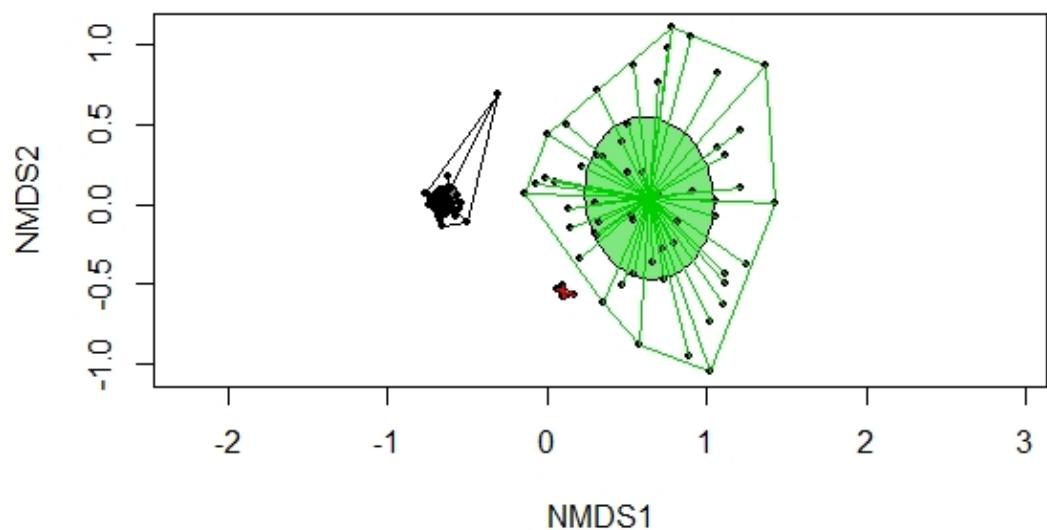


Figure S2 Nonmetric multidimensional scaling (NMDS) plot of pairwise Bray-Curtis dissimilarities between bacterial communities in jejunal (green) and cecal digesta (grey) and fecal microbiota transplant (red) ($> 0.01\%$ relative abundance).

