Electronic supplementary information

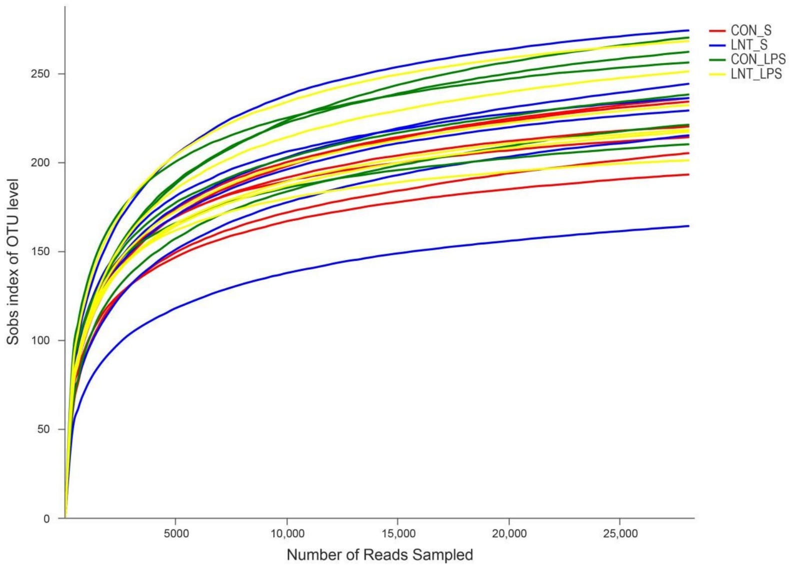

Fig. S1 Rarefaction curves. CON_S, piglets fed with the control diet and injected with saline; LNT_S, piglets fed with the lentinan diet and injected with saline; CON_LPS, piglets fed with the control diet and challenged with lipopolysaccharide; LNT_LPS, piglets fed with the lentinan diet and challenged with lipopolysaccharide.

Table S1 Primer sequences used for real-time PCR

Gene	Forward (5' - 3')	Reverse (5' - 3')
TLR4	TCAGTTCTCACCTTCCTCCTG	GTTCATTCCTCACCCAGTCTTC
LBP	GAACACAGCCGAATGGTCTAC	GGAAGGAGTTGGTGGTCAGT
CD14	CGTTTGTGGAGCCTGGAAG	TGCGGATGCGTGAAGTTG
MD2	TGCAATTCCTCTGATGCAAG	CCACCATATTCTCGGCAAAT
MyD88	GATGGTAGCGGTTGTCTCTGAT	GATGCTGGGGAACTCTTTCTTC
IRAK1	CAAGGCAGGTCAGGTTTCGT	TTCGTGGGGCGTGTAGTGT
TRAF6	CAAGAGAATACCCAGTCGCACA	ATCCGAGACAAAGGGGAAGAA
NOD1	CTGTCGTCAACACCGATCCA	CCAGTTGGTGACGCAGCTT
NOD2	GAGCGCATCCTCTTAACTTTCG	ACGCTCGTGATCCGTGAAC
RIP2	CAGTGTCCAGTAAATCGCAGTTG	CAGGCTTCCGTCATCTGGTT
NF-κB	AGTACCCTGAGGCTATAACTCGC	TCCGCAATGGAGGAGAAGTC
TNF-α	AAGACACCATGAGCACTGAGA	CGACCAGGAGGAAGGAGAAG
IL-1β	GCTAACTACGGTGACAACAATAATG	CTTCTCCACTGCCACGATGA
IL-6	AAGGTGATGCCACCTCAGAC	TCTGCCAGTACCTCCTTGCT
HSP70	GCCCTGAATCCGCAGAATA	TCCCCACGGTAGGAAACG
GAPDH	CGTCCCTGAGACACGATGGT	GCCTTGACTGTGCCGTGGAAT

CD14, cluster of differentiation 14; HSP70, heat shock protein 70; IL, interleukin; IRAK1, IL-1 receptor-associated kinase 1; LBP, lipolysaccharide binding protein; MD2, myeloid differential protein 2; MyD88, myeloid differentiation factor 88; NOD, nucleotide binding oligomerization domain protein; RIP2, receptor-interacting serine/threonine-protein kinase 2; TLR4, toll-like receptor 4; TNF-α, tumor necrosis factor-α; TRAF6, TNF receptor associated factor 6.

Table S2 Effects of lentinan (LNT) on growth performance of weaning piglets before lipopolysaccharide challenge

Item	Basal diet	LNT diet	SEM	*P* value
Initial body weight, kg	7.9	7.9	0.3	0.849
Final body weight, kg	14.6	14.8	0.6	0.854
Average daily gain, g	335	346	24	0.738
Average daily feed intake, g	592	639	39	0.418
Feed/gain	1.77	1.85	0.09	0.469

Values are mean and pooled SEM, n = 12 (1 pig/pen).

Table S3 Effects of lentinan (LNT) on bacterial communities diversity in cecal digesta of weaned pigs after 4 h lipopolysaccharide (LPS) challenge

Item	Saline		LPS		SEM	*P* value		
	CON	LNT	CON	LNT		Diet	LPS	Interaction
shannon	3.67	3.62	3.61	3.75	0.14	0.730	0.797	0.509
simpson	0.0574	0.0640	0.0842	0.0515	0.0142	0.372	0.623	0.184
ace	237	249	265	246	12	0.760	0.285	0.215
chao	240	259	268	246	13	0.896	0.574	0.139

Values are mean and pooled SEM, n = 6 (1 pig/pen).

Table S4 Effects of lentinan (LNT) on bacterial composition in cecal digesta of weaned pigs after 4 h lipopolysaccharide (LPS) challenge

Item	Saline		LPS		SEM	*P* value		
	CON	LNT	CON	LNT		Diet	LPS	Interaction
Phylum								
Actinobacteria	0.95	1.10	1.33	1.28	0.44	0.912	0.527	0.823
Bacteroidetes	49.05	57.82	34.02	52.23	4.58	0.008	0.036	0.316
Firmicutes	45.02	36.02	57.88	43.44	4.24	0.012	0.027	0.528
Proteobacteria	2.02	1.50	3.23	1.49	0.83	0.186	0.477	0.470
Tenericutes	2.92	3.49	3.49	1.49	0.91	0.442	0.441	0.174
Genus								
Actinobacillus	0.91	0.36	1.06	0.22	0.30	0.034	0.996	0.637
Alloprevotella	4.41	7.11	6.80	5.15	2.13	0.809	0.922	0.319
Anaerofilum	0.50	0.36	0.29	0.41	0.25	0.975	0.765	0.622
Anaerotruncus	0.66	0.38	0.55	0.58	0.16	0.437	0.785	0.362
Bacteroides	5.57	2.43	1.45	3.21	2.08	0.742	0.432	0.252
Blautia	2.76	3.17	4.18	2.30	1.03	0.482	0.792	0.278
Catenibacterium	0.20	0.18	0.56	0.50	0.20	0.839	0.104	0.925
Catenisphaera	0.33	0.21	0.85	0.29	0.26	0.213	0.272	0.405
Clostridium_sensu_stricto_6	0.30	0.30	0.30	0.33	0.15	0.926	0.916	0.907
Collinsella	0.69	1.04	0.53	0.68	0.41	0.542	0.539	0.812
Coprococcus_1	0.41	0.56	0.60	0.59	0.23	0.753	0.638	0.716
Coprococcus_3	1.54	0.83	1.67	0.78	0.30	0.015	0.908	0.762
Escherichia-Shigella	0.68	1.00	2.18	0.85	0.59	0.400	0.266	0.177
Faecalibacterium	1.82	2.83	0.81	1.65	0.45	0.050	0.024	0.854
Holdemanella	0.40	0.19	0.43	0.26	0.16	0.258	0.765	0.923
Intestinibacter	0.92	0.72	1.23	1.48	0.25	0.914	0.042	0.371
Lachnospiraceae_NK4A136_group	1.11	1.80	2.58	1.24	0.70	0.646	0.520	0.164
Lachnospiraceae_UCG-007	0.15	0.61	0	0.16	0.16	0.064	0.073	0.349
Lactobacillus	1.17	0.65	0.01	0.11	0.44	0.639	0.067	0.491
Megamonas	0.37	0.18	0.22	0.29	0.10	0.546	0.869	0.212
Oscillospira	0.69	0.43	1.96	0.74	0.35	0.048	0.038	0.188
Parabacteroides	8.43	6.53	7.87	7.91	1.96	0.640	0.836	0.627
Phascolarctobacterium	8.98	4.62	19.67	9.91	3.15	0.036	0.019	0.402
Prevotella_1	4.82^{ab}	3.06^{a}	0.69^{ab}	5.62^{b}	1.53	0.312	0.613	0.041
Prevotella_2	5.17	4.18	0.55	1.89	2.09	0.935	0.113	0.584
Prevotella_7	1.24	1.49	0.27	2.16	1.12	0.351	0.898	0.470
Prevotella_9	4.68	7.66	0.73	5.99	1.91	0.043	0.157	0.558
Prevotellaceae_NK3B31_group	5.57	12.50	9.52	9.03	3.72	0.397	0.949	0.330
Prevotellaceae_UCG-001	0.34	0.62	0.46	0.50	0.25	0.527	0.992	0.648
Prevotellaceae_UCG-003	3.03	1.31	0.89	1.46	0.69	0.419	0.167	0.114
Rikenellaceae_RC9_gut_group	0.62	0.71	0.32	1.01	0.32	0.241	0.994	0.354
Roseburia	0.31	0.36	0.23	0.20	0.13	0.961	0.353	0.750

Ruminiclostridium_9	0.44	0.80	0.75	0.68	0.18	0.428	0.584	0.238
Ruminococcaceae_NK4A214_group	0.33	0.23	0.48	0.31	0.17	0.440	0.505	0.836
Ruminococcaceae_UCG-005	0.38	0.46	0.57	0.30	0.17	0.580	0.908	0.299
Ruminococcaceae_UCG-008	0.45	0.31	0.53	0.39	0.19	0.474	0.658	0.991
Ruminococcaceae_UCG-014	2.21	2.39	2.52	2.45	0.75	0.947	0.808	0.870
Ruminococcus_1	0.27	0.28	0.38	0.20	0.20	0.687	0.940	0.659
Solobacterium	0.44	0.30	1.12	0.12	0.29	0.059	0.388	0.150
Streptococcus	2.55	3.26	1.60	6.00	2.39	0.298	0.712	0.450
Subdoligranulum	2.45	2.34	2.20	1.53	0.80	0.636	0.518	0.731
Sutterella	0.52^{b}	0.09^{a}	0.12^{a}	0.36^{ab}	0.13	0.447	0.597	0.014
[Eubacterium]_coprostanoligenes_group	1.80	4.79	2.37	0.87	1.70	0.664	0.336	0.201
[Eubacterium]_eligens_group	0.28	0.59	0.36	0.64	0.22	0.192	0.754	0.950
[Ruminococcus]_torques_group	0.51	0.26	0.29	0.21	0.17	0.345	0.441	0.653
norank_f__Bacteroidales_S24-7_group	6.50	2.28	4.31	4.44	1.48	0.184	0.992	0.158
norank_f__Ruminococcaceae	0.41	0.54	0.32	0.87	0.15	0.037	0.456	0.174
norank_o__Mollicutes_RF9	3.18	2.97	3.51	1.37	0.98	0.247	0.526	0.337
unclassified_f__Lachnospiraceae	1.96	2.63	2.64	4.98	1.10	0.183	0.182	0.454
unclassified_f__Ruminococcaceae	1.64	1.62	1.33	1.41	0.38	0.929	0.505	0.892

Values are mean and pooled SEM, n = 6 (1 pig/pen). Labeled means in a row without a common letter differ, $P < 0.05$.