

## Supporting Information

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**Table S1.** Primers used for qRT-PCR

Gene	Primer Sequence (5' to 3')	GeneBank No.	TM (°C)
<i>GAPDH</i>	F: TCGGAGTGAACGGATTTG R: CCTGGAAGATGGTGATGG	NM_001206359.1	60
<i>LDH</i>	F: AGTCGTCTCAATCTGGTGCA R: CACACGGTGCTTGGGTAATC	NM_001113287.1	62
<i>PGK1</i>	F: CGCCACTGAATTGCCAAGAT R: CATGACGACCCTCTTTCCT	NM_001099932.2	58
<i>MyHC I</i>	F: CGTGGACTACAACATCATAGGC R: CTTTGCCCTTCTCAACAGGT	NM_213855	64
<i>MyHC IIa</i>	F: GGAGATCGACGACCTTGCTA R: CTCCTTGGATTTCAGCTCGC	NM_214136	58
<i>MyHC IIx</i>	F: GAAACCGTCAAGGGTCTACG R: CGCTTCCTCAGCTTGTCTCT	NM_001104951	64
<i>MyHC IIb</i>	F: GTTCTGAAGAGGGTGGTAC R: AGATGCGGATGCCCTCCA	NM_001123141	63
<i>SOD1</i>	F: AGACCTGGGCAATGTGACTG R: GTGCGGCCAATGATGGAATG	NM_001190422	62
<i>GPXI</i>	F: GTGAATGGCGCAAATGCTCA R: ATTGCGACACACTGGAGACC	NM_214201	60
<i>GST</i>	F: CCAACCCAGAAGACTGCTCA R: CATTCAGGTGGGCTCTTCGT	AB000884	60
<i>Keap1</i>	F: ACGACGTGGAGACAGAAACGT R: GCTTCGCCGATGCTTCA	NM_001114671	62
<i>NRF2</i>	F: GCCCCTGGAAGCGTTAAAC R: GGACTGTATCCCCAGAAGGTTGT	XM_003133500	60
<i>CAT</i>	F: CAGATGAAGCATTGGAAGGAGC R: TTGTCTCCTATCGGATTCCCAG	NM_214301	60
<i>18sRNA</i>	F: GAGCGAAAGCATTTGCCAAG R: GGCATCGTTTATGGTCGGAAC	NM_001244062	60

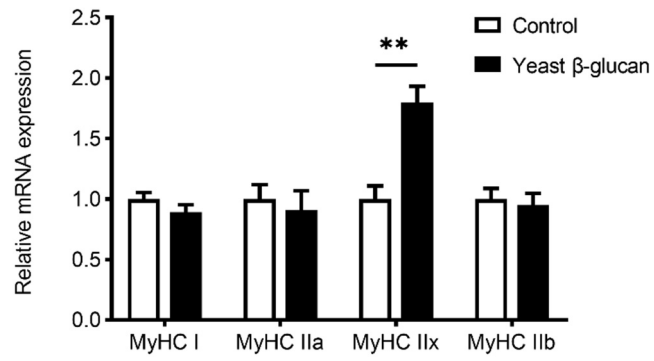
**Table S2.** Effects of dietary yeast  $\beta$ -glucan supplementation on texture profile analysis of the Longissimus Thoracis muscle in finishing pigs (n = 8)

Items	Yeast $\beta$ -glucan levels (mg/kg)					SEM	P value		
	0	50	100	200	400		ANOVA	Linear	Quadratic
Hardness, N	39.34	32.42	38.61	35.08	35.45	2.34	0.24	0.54	0.61
Adhesiveness, mJ	0.07	0.08	0.09	0.08	0.07	0.01	0.57	0.75	0.19
Cohesiveness, Ratio	0.45	0.44	0.48	0.48	0.46	0.01	0.02	0.28	0.03
Springiness, mm	2.99	3.04	3.09	3.07	2.99	0.08	0.82	0.82	0.27
Gumminess, N	19.02 <sup>ab</sup>	15.59 <sup>b</sup>	22.70 <sup>a</sup>	18.65 <sup>ab</sup>	18.09 <sup>ab</sup>	1.49	0.03	0.85	0.33
Chewiness, mJ	50.89	48.82	63.05	55.32	54.74	4.47	0.23	0.58	0.23

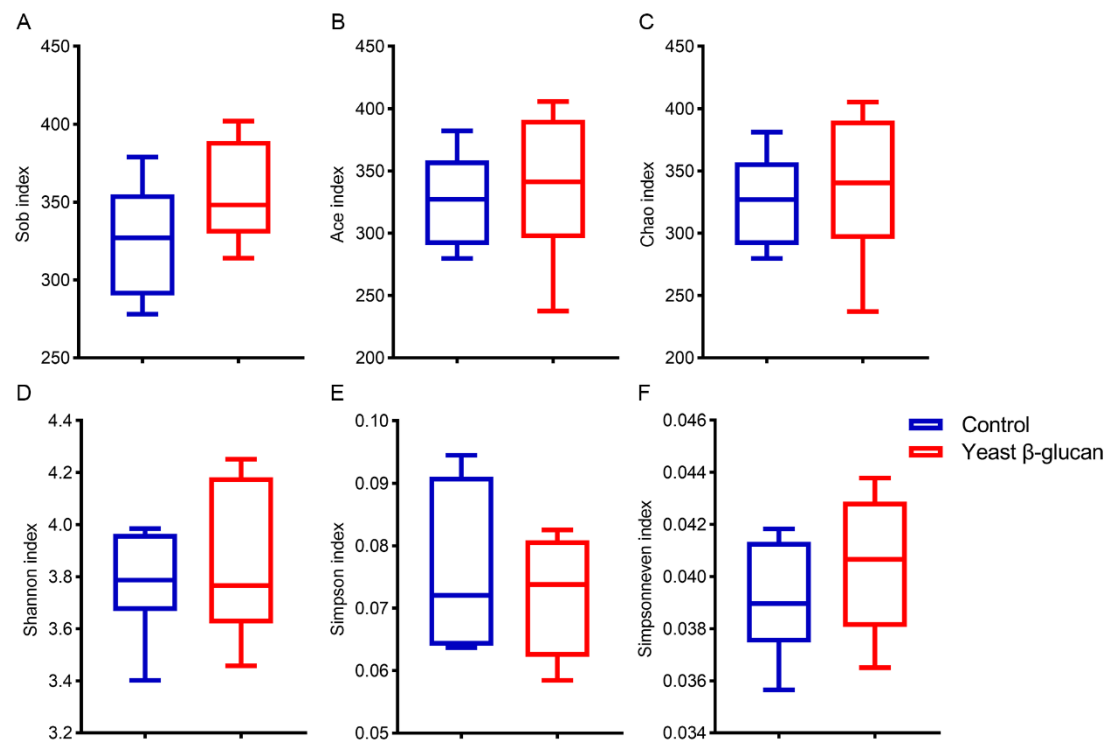
Note: Values with different superscripts means significant difference ( $p < 0.05$ ).

**Table S3.** Effects of dietary yeast  $\beta$ -glucan supplementation on fatty acid composition of the Longissimus Thoracis muscle in finishing pigs (% of Fresh Tissue, n = 8)

Items	Yeast $\beta$ -glucan levels (mg/kg)					SEM	P value		
	0	50	100	200	400		ANOVA	Linear	Quadratic
C14:0	1.20	1.38	1.37	1.39	1.40	0.08	0.36	0.19	0.24
C16:0	25.99	26.23	26.53	26.29	26.76	0.29	0.41	0.10	0.86
C16:1	3.23	3.25	3.02	3.22	3.41	0.12	0.26	0.16	0.20
C17:0	0.17	0.20	0.19	0.18	0.18	0.01	0.54	0.83	0.53
C18:0	14.19	14.48	14.97	14.96	14.46	0.30	0.28	0.70	0.04
C18:1n9c	41.97	41.56	42.00	41.26	41.10	0.52	0.64	0.20	0.87
C18:2n6c	8.43	8.79	8.00	8.47	8.47	0.55	0.90	0.99	0.80
C18:3n3	0.31	0.31	0.31	0.30	0.32	0.01	0.93	0.72	0.65
C20:0	0.27	0.30	0.28	0.28	0.30	0.01	0.41	0.37	0.85
C20:1	0.75	0.77	0.72	0.75	0.73	0.03	0.88	0.66	0.83
C21:0	0.35	0.38	0.36	0.37	0.37	0.02	0.75	0.52	0.84
C20:3n6	0.20	0.23	0.18	0.21	0.24	0.02	0.28	0.23	0.50
C20:4n6	1.39	1.61	1.25	1.55	1.70	0.17	0.39	0.21	0.67
C20:3n3	0.04	0.06	0.05	0.06	0.07	0.01	0.42	0.13	0.79
C24:0	0.04	0.05	0.04	0.05	0.05	< 0.01	0.32	0.08	0.90
SFA	42.74	42.87	44.27	43.84	44.09	0.53	0.16	0.08	0.21
MUFA	46.13	45.69	44.54	45.35	45.42	0.62	0.49	0.64	0.25
PUFA	10.58	11.26	10.88	10.81	11.03	0.83	0.98	0.88	0.96
n-3 PUFA	0.49	0.57	0.51	0.51	0.53	0.04	0.65	0.88	1.00
n-6 PUFA	10.01	10.63	9.44	10.23	10.40	0.72	0.81	0.75	0.75
Total fatty acids	82.41	88.72	89.60	73.47	71.87	10.47	0.65	0.23	0.95



**Figure S1.** Effects of dietary yeast  $\beta$ -glucan supplementation on mRNA expression of genes concerning myosin heavy-chain (MyHC) isoform of the *M. longissimus thoracic* in finishing pigs. Yeast  $\beta$ -glucan, dietary supplementation of 200 mg/kg yeast  $\beta$ -glucan. Data are expressed as the means  $\pm$  SEMs ( $n = 8$ ). \*\* $p < 0.01$ .



**Figure S2.** Boxplots of alpha diversity as measured by diversity index of the colon microbiome. Diversity index of (A) sob index, (B) Ace, (C) Chao, (D) Shannon, (E) Simpson and (F) Simpsonneven. Yeast  $\beta$ -glucan, dietary supplementation of 200 mg/kg yeast  $\beta$ -glucan. Alpha diversity indices were analyzed in Kruskal-Wallis to test for differences (n = 6).