

**Table S1** Effects of dietary BS and XOS supplementation on mean count of clean sequences and OTUs of weaned piglets

Ileum			Colon		
Sample Name	Effective sequences	OTUs	Sample Name	Effective sequences	OTUs
IBD1	31701	335	CBD1	38218	782
IBD2	37638	271	CBD2	38047	1229
IBD3	34771	300	CBD3	34257	1032
IBD4	35871	598	CBD4	27067	1011
IBD5	36151	241	CBD5	38300	1336
IBD6	32264	384	CBD6	27436	822
IBD7	29337	379	CBD7	29425	971
IBD8	34976	491	CBD8	32641	1101
IBS1	32718	282	CBS1	27687	647
IBS2	30725	395	CBS2	34589	1100
IBS3	29749	481	CBS3	31761	1072
IBS4	32021	450	CBS4	27699	1078
IBS5	31148	517	CBS5	31901	1161
IBS6	38376	448	CBS6	30570	1009
IBS7	34462	401	CBS7	27530	1024
IBS8	33757	407	CBS8	27647	1098
IXOS1	32965	446	CXOS1	27931	1065
IXOS2	35070	607	CXOS2	35561	788
IXOS3	33601	354	CXOS3	41429	1223
IXOS4	28874	514	CXOS4	28071	1144
IXOS5	35628	567	CXOS5	29310	1081
IXOS6	29182	227	CXOS6	29275	886
IXOS7	32183	518	CXOS7	29010	1013
IXOS8	32108	388	CXOS8	35689	1045

IBSXOS1	31469	423	CBSXOS1	31951	994
IBSXOS2	29816	458	CBSXOS2	27042	950
IBSXOS3	33395	546	CBSXOS3	32387	1371
IBSXOS4	28099	276	CBSXOS4	31700	884
IBSXOS5	31260	461	CBSXOS5	36858	1073
IBSXOS6	29402	325	CBSXOS6	33288	1191
IBSXOS7	27465	262	CBSXOS7	29891	958
IBSXOS8	27795	241	CBSXOS8	27974	1107

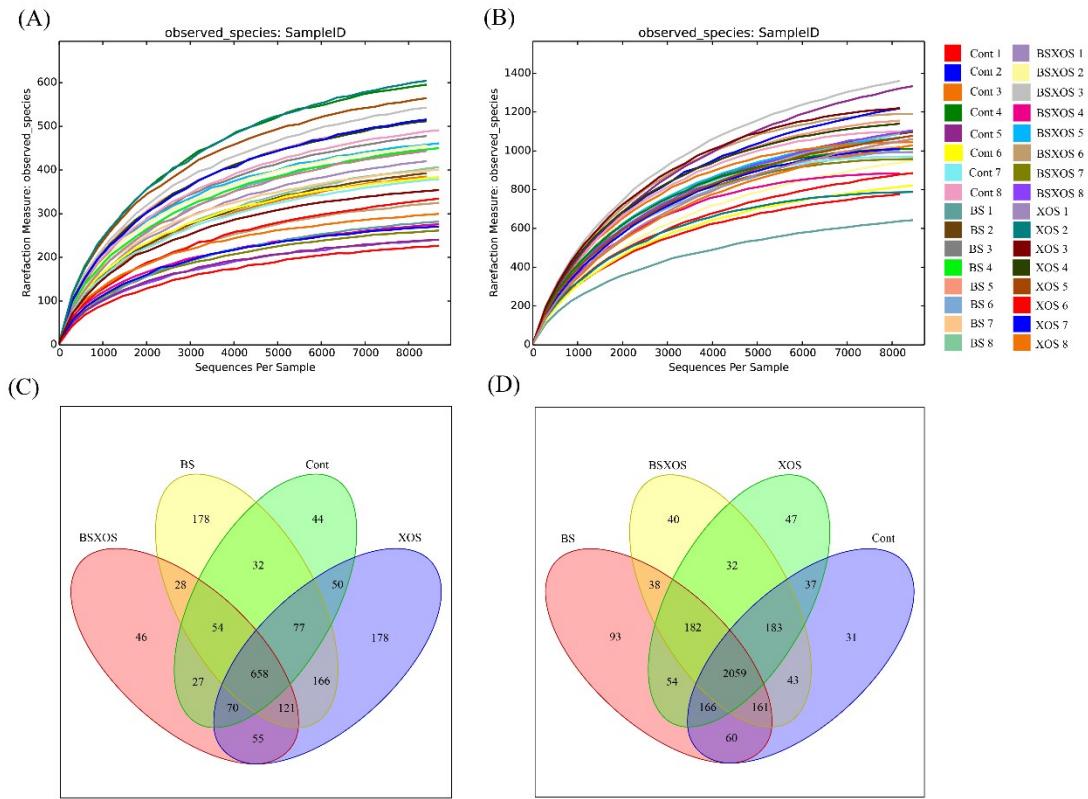
Data are expressed as means with pooled SEM ( $n = 8$ ).

**Table S2** Effects of dietary BS and XOS supplementation on metabolic pathway in the ileum and colon of weaned piglets

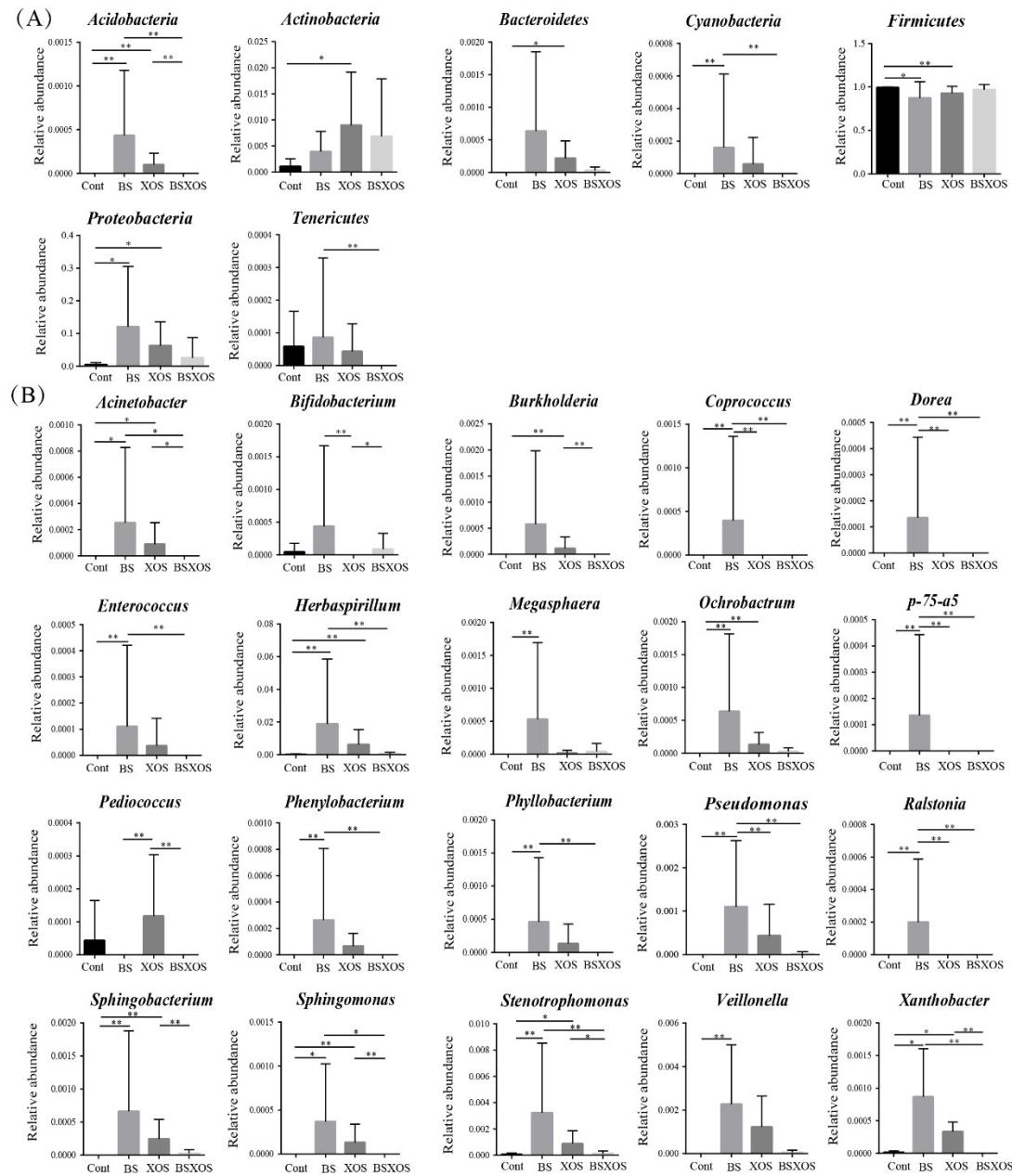
Items	-XOS		+XOS		SEM	P-values		
	-BS	+BS	-BS	+BS		BS	XOS	BS×XOS
<b>Ileum</b>								
AAM	0.078	0.078	0.078	0.073	0.002	0.52	0.62	0.53
BOSM	0.007	0.007	0.006	0.006	<0.001	0.86	0.48	0.83
CM	0.118	0.113	0.111	0.116	0.001	0.91	0.32	0.03
EM	0.047	0.049	0.049	0.048	<0.001	0.62	0.24	0.04
EF	0.022	0.022	0.022	0.022	<0.001	0.61	0.51	0.93
GBM	0.021	0.020	0.020	0.020	<0.001	0.93	0.42	0.44
LM	0.027	0.029	0.029	0.027	<0.001	0.10	0.94	0.04
MCV	0.030	0.032	0.033	0.030	<0.001	0.41	0.59	0.03
MOAA	0.015	0.016	0.016	0.015	<0.001	0.69	0.78	0.02
MTP	0.017	0.017	0.018	0.017	<0.001	0.80	0.52	0.07
NM	0.050	0.047	0.049	0.049	0.001	0.36	0.67	0.14
XBM	0.020	0.022	0.022	0.020	0.001	0.61	0.76	0.09
<b>Colon</b>								
AAM	0.096	0.095	0.096	0.096	<0.001	0.64	0.29	0.56
BOSM	0.010	0.010	0.010	0.009	<0.001	0.35	0.31	0.32
CM	0.102	0.104	0.104	0.104	<0.001	0.62	0.21	0.18
EM	0.057	0.055	0.057	0.057	<0.001	0.12	0.13	0.08
EF	0.022	0.022	0.022	0.022	<0.001	0.77	0.30	0.50
GBM	0.018	0.018	0.019	0.019	<0.001	0.93	0.40	0.91
LM	0.028	0.028	0.028	0.028	<0.001	0.63	0.75	0.64
MCV	0.043	0.042	0.043	0.043	<0.001	0.38	0.86	0.20
MOAA	0.014	0.014	0.015	0.014	<0.001	0.65	0.40	0.37
MTP	0.015	0.015	0.015	0.016	<0.001	0.88	0.04	0.34

NM	0.039	0.039	0.039	0.040	<0.001	0.71	0.29	0.85
XBM	0.014	0.014	0.014	0.015	0.002	0.30	0.11	0.59

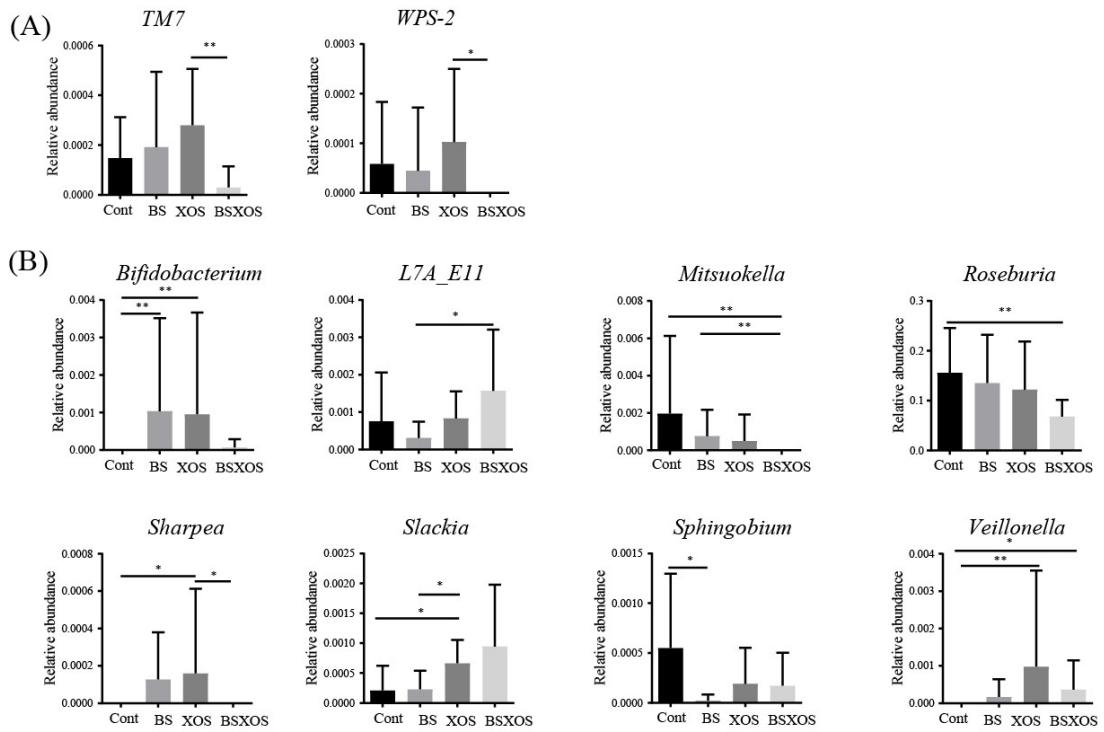
Data are expressed as means with pooled SEM ( $n = 8$ ). AAM, Amino Acid Metabolism; BOSM, Biosynthesis of Other Secondary Metabolites; CM, Carbohydrate Metabolism; EM1, Energy Metabolism; EF, Enzyme Families; GBM, Glycan Biosynthesis and Metabolism; LM, Lipid Metabolism; MCV, Metabolism of Cofactors and Vitamins; MOAA, Metabolism of Other Amino Acids; MTP, Metabolism of Terpenoids and Polyketides; NM, Nucleotide Metabolism; XBM, Xenobiotics Biodegradation and Metabolism; CM, Carbohydrate Metabolism; EM, Energy Metabolism; BS, *Bacillus subtilis*; XOS, xylo-oligosaccharides.



**Fig. S1.** The rarefaction curves were drawn in the ileum (A) and colon (B), respectively. Venn pictures showed the shared and unique OTUs in the ileum (C) and colon (D) of the four treatment groups, respectively.



**Fig. S2.** Taxonomic differences in piglets' intestinal microbiota at the phylum level (A) and the genera level (B) in ileum of weaned piglets ( $n = 8$ ). Values are expressed as means with their SD indicated by vertical bars. \*  $P < 0.05$ , \*\*  $P < 0.01$ . Discrepant bacteria at the phylum level were all listed and only the top 20 were listed on the genera level. Cont, piglets received a basal diet; BS, piglets received a basal diet with 500 g t<sup>-1</sup> BS; XOS, piglets received a basal diet with 250 g t<sup>-1</sup> XOS; and BS+XOS, piglets received a basal diet with 500 g t<sup>-1</sup> BS and 250 g t<sup>-1</sup> XOS.



**Fig. S3.** Taxonomic differences in piglets' intestinal microbiota at the phylum level (A) and the genera level (B) in colon of weaned piglets ( $n = 8$ ). Values are expressed as means with their SD indicated by vertical bars. \*  $P < 0.05$ , \*\*  $P < 0.01$ . Discrepant bacteria at phylum level and the genera level were all listed. Cont, piglets received a basal diet; BS, piglets received a basal diet with 500 g t<sup>-1</sup> BS; XOS, piglets received a basal diet with 250 g t<sup>-1</sup> XOS; and BS+XOS, piglets received a basal diet with 500 g t<sup>-1</sup> BS and 250 g t<sup>-1</sup> XOS.