

**Supplementary Table 1** Effects of dietary oil sources on raw reads, sequences and OTUs of intra-uterine growth retarded weanling pigs

	NBW		IUGR		BW	Diet	BW×Diet
	SO	FO	SO	FO			
Raw reads	69140±3065	65388±4498	64066±2722	66597±4657	0.618	0.875	0.419
High quality sequences	64227±2524	60419±4193	59996±2752	62762±4143	0.789	0.882	0.354
OTUs	581±18	596±24	601±12	566±37	0.846	0.708	0.317

Mean values with their standard error, n = 8 in each group

NBW, normal birth weight; IUGR, intrauterine growth retarded; SO, soybean oil; FO, flaxseed oil.

**Supplementary Table 2** The relative abundances of nine phyla (% , > 1% in at least one sample) and Firmicutes/Bacteroidetes ratio

	NBW		IUGR		BW	Diet	BW×Diet
	SO	FO	SO	FO			
<i>Firmicutes</i>	73.84±4.83	73.50±3.27	76.79±1.66	80.22±2.05	0.115	0.605	0.667
<i>Bacteroidetes</i>	17.94±3.38	20.19±2.27	16.84±1.49	14.49±2.06	0.233	0.907	0.189
<i>Proteobacteria</i>	1.56±0.40	2.56±1.30	0.67±0.19	0.76±0.22	0.037	0.927	0.800
<i>Euryarchaeota</i>	2.14±1.26	1.24±0.29	1.47±0.40	0.54±0.14	0.751	0.941	0.900
<i>Actinobacteria</i>	0.54±0.30	1.21±0.48	0.20±0.04	2.23±0.93	0.943	0.017	0.239
<i>Spirochaetes</i>	0.77±0.31	0.55±0.19	1.97±0.64	0.73±0.49	0.393	0.040	0.151
<i>Tenericutes</i>	0.30±0.08	0.35±0.05	0.52±0.26	0.36±0.11	0.791	0.905	0.417
<i>Melainabacteria</i>	0.05±0.01	0.10±0.02	0.05±0.01	0.09±0.02	0.549	0.017	0.155
<i>Unidentified Bacteria</i>	0.13±0.03	0.08±0.03	0.90±0.63	0.11±0.05	0.238	0.210	0.268
<i>Others</i>	0.31±0.13	0.20±0.13	0.49±0.20	0.46±0.29	0.365	0.159	0.913
<i>Firmicutes/ Bacteroidetes</i>	5.42±1.17	4.13±0.65	4.92±0.62	5.29±0.61	0.685	0.577	0.321

Mean values with their standard error, n = 8 in each group

NBW, normal birth weight; IUGR, intrauterine growth retarded; SO, soybean oil; FO, flaxseed oil.

Mean values within a row with different superscript letters were significantly different ( $P < 0.05$ )

**Supplementary Table 3** The relative abundances of 23 genera (% , > 1% in at least one sample) in the colonic digesta of weanling pigs

	NBW		IUGR		BW	Diet	BW×Diet
	SO	FO	SO	FO			
<i>Lactobacillus</i>	25.15±5.63	13.24±2.70	20.97±4.61	25.27±6.38	0.607	0.341	0.301
<i>Campylobacter</i>	0.06±0.02	0.06±0.03	0.86±0.60	0.09±0.05	0.336	0.598	0.361
<i>Agathobacter</i>	4.96±1.81	3.52±0.82	2.88±0.57	5.06±1.89	0.662	0.702	0.325
<i>Streptococcus</i>	2.49±1.59	3.90±1.74	2.21±1.32	2.87±1.19	0.785	0.361	0.921
<i>Terrisporobacter</i>	1.32±0.48	4.07±1.64	1.93±1.28	0.98±0.39	0.147	0.585	0.421
<i>Methanobrevibacter</i>	2.11±1.24	1.16±0.27	1.44±0.41	0.52±0.14	0.752	0.975	0.936
<i>Selenomonas</i>	2.08±1.13	2.42±1.09	0.84±0.38	1.42±0.55	0.374	0.210	0.714
<i>Megasphaera</i>	1.37±0.46	1.78±1.05	1.50±0.93	0.77±0.20	0.659	0.819	0.987
<i>Roseburia</i>	2.24±0.66	2.81±0.88	2.14±0.68	1.89±0.47	0.326	0.590	0.582
<i>Faecalibacterium</i>	1.90±0.48	2.56±0.64	2.28±0.47	3.70±0.86	0.303	0.147	0.777
<i>Sarcina</i>	0.18±0.09	0.48±0.34	1.22±0.88	0.03±0.02	0.723	0.803	0.908
<i>Blautia</i>	2.34±0.68ab	2.90±0.58ab	1.72±0.36b	3.46±0.41a	0.924	0.008	0.254
<i>Bifidobacterium</i>	0.39±0.30ab	1.01±0.47ab	0.05±0.02b	1.92±0.94a	0.744	0.047	0.469
<i>Alloprevotella</i>	1.35±0.56	1.02±0.36	0.99±0.35	0.51±0.15	0.293	0.239	0.638
<i>Anaerovibrio</i>	1.13±0.54	0.78±0.19	1.16±0.17	0.67±0.22	0.718	0.173	0.177
<i>Dialister</i>	0.20±0.17	0.24±0.11	0.07±0.05	0.88±0.44	0.519	0.293	0.988
<i>Butyricoccus</i>	1.20±0.22	0.85±0.18	1.32±0.28	1.28±0.31	0.262	0.483	0.518
<i>Succinivibrio</i>	0.48±0.34	0.17±0.06	0.02±0.01	0.27±0.13	0.481	0.245	0.740
<i>Subdoligranulum</i>	1.36±0.28	1.23±0.27	1.19±0.25	1.66±0.21	0.702	0.426	0.179
<i>Parabacteroides</i>	0.39±0.16	0.43±0.13	0.61±0.25	0.16±0.05	0.429	0.114	0.017
<i>Oscillospira</i>	0.16±0.03	0.42±0.16	0.31±0.09	0.27±0.07	0.733	0.374	0.093
<i>Desulfovibrio</i>	0.36±0.07	0.28±0.08	0.32±0.08	0.33±0.16	0.361	0.312	0.859
<i>Phascolarctobacterium</i>	0.33±0.06b	0.54±0.09ab	0.64±0.06a	0.61±0.12a	0.022	0.324	0.102
<i>Others</i>	33.13±4.40	40.07±3.62	42.73±3.30	34.03±5.06	0.845	0.734	0.056

Mean values with their standard error, n = 8 in each group

NBW, normal birth weight; IUGR, intrauterine growth retarded; SO, soybean oil; FO, flaxseed oil.

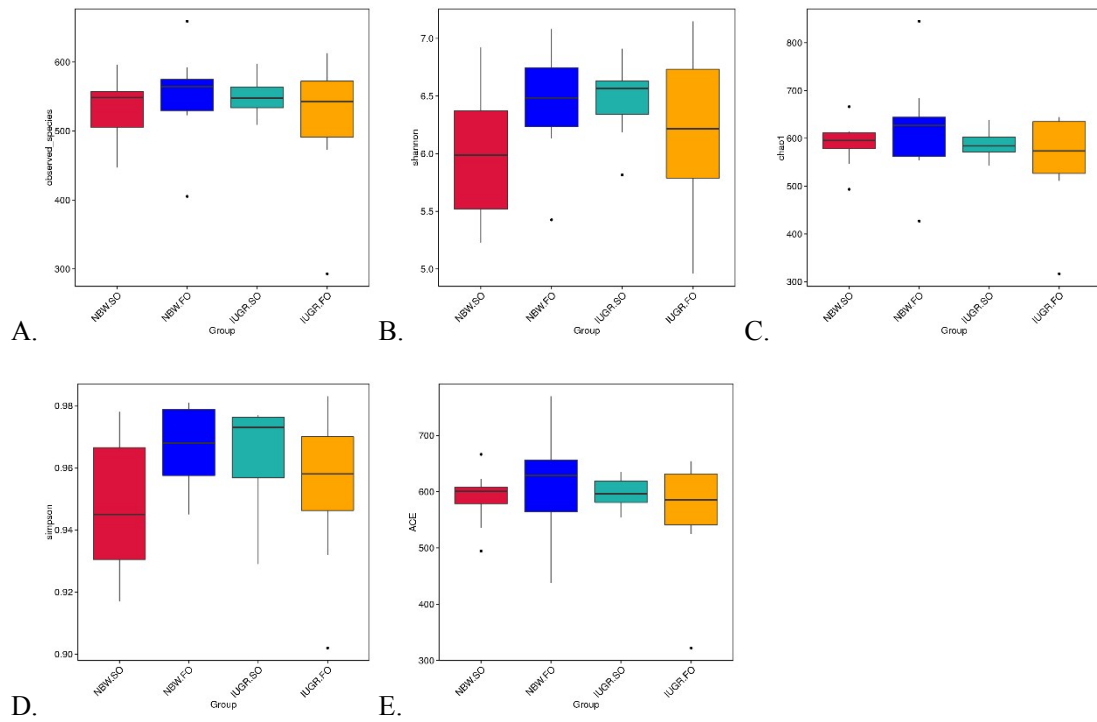
Mean values within a row with different superscript letters were significantly different ( $P < 0.05$ )

**Supplementary Table 4** Effects of different oil sources on concentrations of short chain fatty acids in colonic digesta of intra-uterine growth retarded weanling pigs

	NBW		IUGR		BW	Diet	BW×Diet
	SO	FO	SO	FO			
Acetate, mg/g	3.62±0.16	3.73±0.20	3.61±0.13	3.98±0.18	0.464	0.169	0.460
Propanoic acid, mg/g	2.47±0.26	2.33±0.14	2.15±0.14	2.56±0.15	0.797	0.460	0.139
Isobutyric acid, mg/g	0.15±0.02	0.19±0.03	0.18±0.02	0.20±0.02	0.245	0.190	0.554
Butyrate, mg/g	1.79±0.18	2.02±0.14	1.63±0.20	1.75±0.18	0.243	0.322	0.750
Isovaleric acid, mg/g	0.18±0.02	0.23±0.04	0.21±0.02	0.23±0.03	0.530	0.239	0.649
Valeric acid, mg/g	0.55±0.08	0.46±0.04	0.40±0.08	0.51±0.06	0.456	0.798	0.127

Mean values with their standard error, n = 8 in each group

NBW, normal birth weight; IUGR, intrauterine growth retarded; SO, soybean oil; FO flaxseed oil.



**Supplementary Figure 1** Differences on bacterial community diversity and richness among the four treatments. (A) Observed OTUs; (B) Shannon index; (C) Chao1 index; (D) Simpson index; (E) ACE. NBW, normal birth weight; IUGR, intrauterine growth retarded; SO, soybean oil; FO flaxseed oil.

