

Supplementary table 1. Primers used in this study.

Gene	Nucleotide sequence (5'-3')
<i>IFN-γ</i> -F	TTCAGCTTGCCTGACTTTG
<i>IFN-γ</i> -R	GGTCCACCATTAGGTACATCTG
<i>IL-4</i> -F	CCCGAGTGTCAAGTGGCTTA
<i>IL-4</i> -R	TGATGATGCCGAAATAGCAG
<i>IL-10</i> -F	GGGCTATTGTCCTGACTGC
<i>IL-10</i> -R	GGGCTCCCTAGTTCTCTTCC
<i>IL-17</i> -F	ATCCTCGTCCCCTGTCAGTGC
<i>IL-17</i> -R	ACATGCTGAGGGAAGTTCTTGTGTC
<i>IL-1β</i> -F	CAGCCATGGCCATAGTACCT
<i>IL-1β</i> -R	CCACGATGACAGACACCATC
<i>TNF-α</i> -F	ACAGGCCAGCTCCCTCTTAT
<i>TNF-α</i> -R	CCTCGCCCTCCTGAATAAAT
<i>IL-5</i> -F	GACTGGTGGCAGAGACCTTGAC
<i>IL-5</i> -R	CTTCAATGCATAGTTGGTATTGT
<i>IL-13</i> -F	CTGACCACCAAGCATGCAGTACT
<i>IL-13</i> -R	GCTGCAGTCGGAGATGTTGA
<i>pIgR</i> -F	AGCCAACCTCACCAACTTCC
<i>pIgR</i> -R	CTGCTAATGCCAGACCAC
<i>J-chain</i> -F	GTGTGCCGGATTACTTCCA

<i>J-chain-R</i>	AGTGGTGAGGTGGGATCAGA
β - <i>actin</i> -F	CTGCGGCATCCACGAAACT
β - <i>actin</i> -R	AGGGCCGTGATCTCCTTCTG

704

Supplementary table 2. Organ indices of piglets in stage 1 and 2.

	CON1	GABA1	<i>P</i> value (1)	CON2	GABA2	<i>P</i> value (2)
Heart	0.492±0.004	0.511±0.014	0.239	0.576±0.055	0.613±0.04	0.599
Liver	2.037±0.054	2.0±0.1	0.749	2.433±0.176	2.574±0.146	0.553
Spleen	0.159±0.015	0.155±0.017	0.870	0.198±0.019	0.23±0.024	0.309
Kidney	0.548±0.009	0.579±0.027	0.323	0.571±0.024	0.588±0.029	0.655
Lung	1.176±0.037	1.153±0.069	0.776	1.669±0.253	1.845±0.261	0.639

705

706

Supplementary table 3. Gut microbial alpha diversity indices of piglets in stage 1 and 2.

	CON1	GABA1	<i>P</i> value (1)	CON2	GABA2	<i>P</i> value (2)
Ace	562.68±41.39	519.47±22.77	0.382	606.04±9.31	627.72±22.43	0.393
Chao1	559.06±44.77	518.77±22.68	0.441	697.94±9.26	1015.20±316.82	0.34
Observed Species	519.67±35.85	483.50±27.65	0.443	565.00±11.57	562.17±24.96	0.92
Shannon	5.947±0.296	5.713±0.235	0.55	6.620±0.140	6.222±0.389	0.358
Simpson	0.941±0.016	0.946±0.010	0.834	0.974±0.003	0.939±0.027	0.214

707

708 **Supplementary figure legends**

709 **Figure S1 Dietary GABA did not affect the growth performance of piglets.**

710 Growth performance of piglets in (A) stage 1 and (B) stage 2. Data are presented as
711 mean \pm SEM, analyzed by unpaired t-test with Welch's correction or Mann–Whitney
712 *U* test.

713

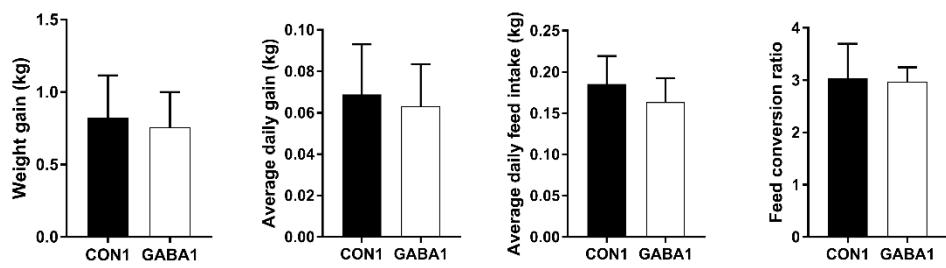
714 **Figure S2 Dietary had little effect on the composition of gut microbiota.** (A) to (E)

715 the relative abundances of main strains in the phylum, class, order, family, and genus
716 level in normal piglets; (F) PCoA analysis of gut microbiota in normal piglets; (G) to
717 (H) the relative abundances of main strains in the phylum, class, order, family, and
718 genus level in ETEC infected piglets; (F) PCoA analysis of gut microbiota in ETEC
719 infected piglets.

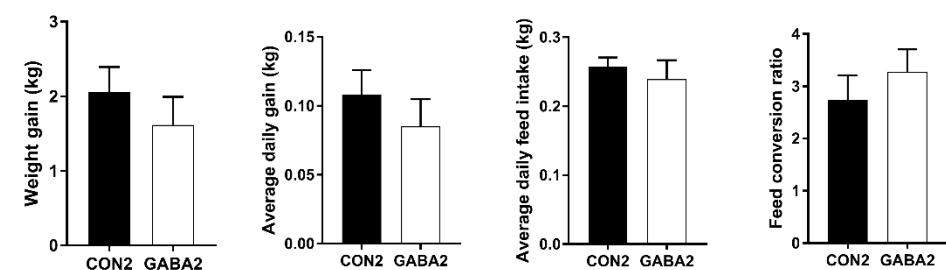
720

721 **Figure S1**

A



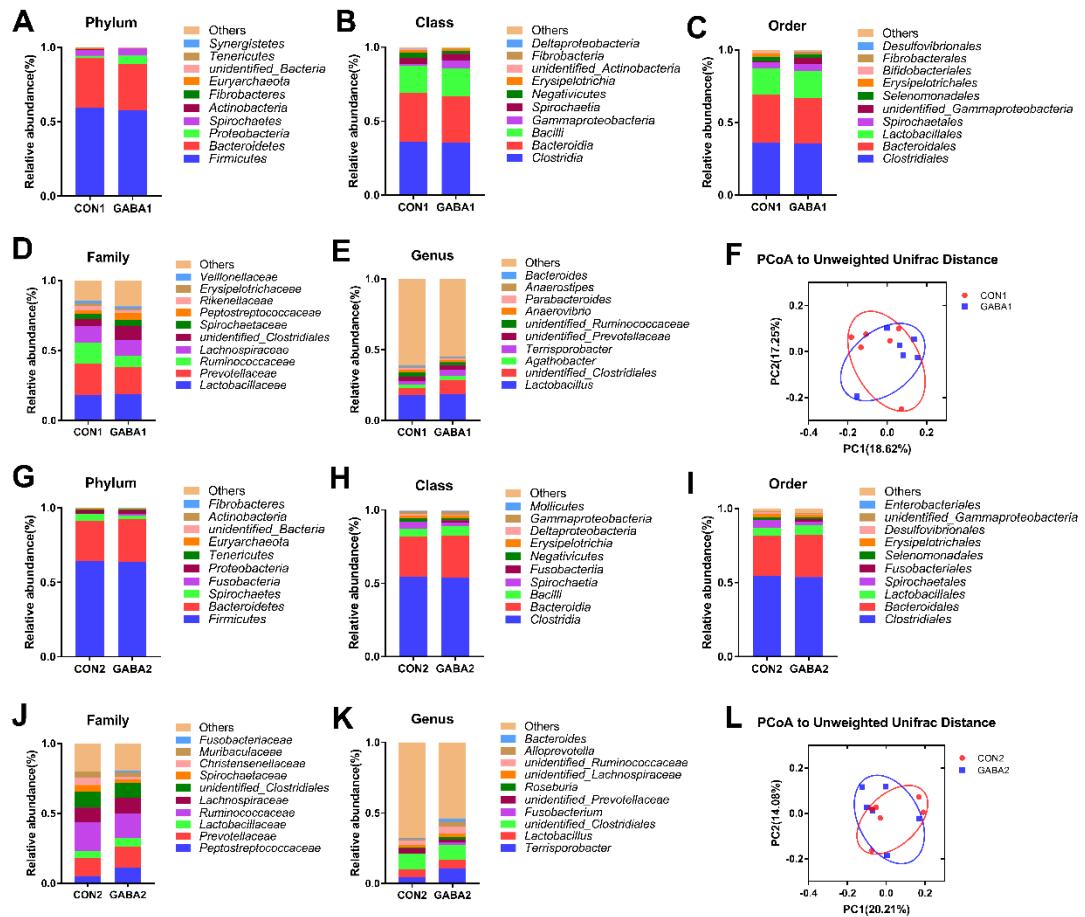
B



722

723

724 Figure S2



725