

SUPPLEMENTAL DATA

Table S1. The composition of experiment diet.

	SCD group	CGA group
Diet ingredients (%)		
Corn	72.14	72.14
Soybean meal	15.24	15.24
Soybean phospholipid	6.65	6.65
L-lysine 98%	0.40	0.40
L-methionine	0.06	0.06
L-threonine	0.15	0.15
Soybean oil	2.80	2.80
Salt	0.30	0.30
CaHPO ₄	0.33	0.33
Limestone	0.93	0.93
Premix *	1.00	1.00
Total	100	100
Nutrient levels (%)		
Digestible energy (MJ/kg)	13.77	13.77
Crude protein	15.29	15.29
Crude fat	2.64	2.64
Crude fibre	3.48	3.48
Crude ash	2.05	2.05
Salt	0.30	0.30
Calcium	0.55	0.55
Total phosphorus	0.56	0.56
Available phosphorus	0.39	0.39
Lysine	0.99	0.99
Methionine	0.31	0.31
Methionine+cystatin	0.57	0.57
Threonine	0.70	0.70
Chlorogenic acid	0	0.05

Note: *Providing the following per kilogram chow: Fe 100.0 mg; Zn 80.0 mg; Cu 30.0 mg; Se 0.30 mg; I 0.55 mg; Mn 20.0 mg; VA 5400 IU; VD₃ 300 IU; VK₃ 2.20 mg; VE 40.0 mg; VB₁ 2.10 mg; VB₂ 8.0 mg; VB₆ 3.50 mg; VB₁₂ 0.04 mg; nicotinic acid 47.50 mg; pantothenic acid 21.0 mg; folic acid 1.25 mg; biotin 0.20 mg; chow carrier with zeolite powder.

Table S2. Statistics of all samples.

Sample	Total tags	Effective tags	Effective (%)	OTUs
Ctrl 1	63340	59958	94.66	1626
Ctrl 2	59012	56803	96.26	1393
Ctrl 3	61211	59067	96.50	1188
Ctrl 4	65884	64137	97.35	1122
Ctrl 5	59256	57807	97.55	1088
Ctrl 6	56691	52480	92.57	1090
CGA 1	70662	68211	96.53	1137
CGA 2	75092	72615	96.70	1562
CGA 3	41097	38857	94.55	1375
CGA 4	58879	56951	96.73	1463
CGA 5	63548	61249	96.38	1392
CGA 6	49079	46744	95.24	1405

Table S3. Representational bacterial phyla in CGA group compared to Ctrl group. Some bacterial phyla relatively high abundance or significant changes between groups were selected in the table. Student's T-test was used to determine the significance of the difference.

Bacteria genera	Avg. Ctrl (%)	Avg. CGA (%)	Fold change (Avg. CGA/ Avg. Ctrl)	p-value
<i>Acidobacteria</i>	0.0103	0.0326	3.17	0.0462
<i>Actinobacteria</i>	0.6781	1.6248	2.40	0.1649
<i>Bacteroidetes</i>	44.1066	44.1555	1.00	0.9579
<i>Chloroflexi</i>	0.0056	0.0253	4.54	0.0540
<i>Cyanobacteria</i>	0.8373	0.4628	0.55	0.2553
<i>Elusimicrobia</i>	0.0021	0.0090	4.21	0.0659
<i>Firmicutes</i>	42.7285	41.9774	0.98	0.9023
<i>Proteobacteria</i>	5.4113	6.3644	1.18	0.7032
<i>Spirochaetes</i>	1.7817	1.9246	1.08	0.8893
<i>Synergistetes</i>	0.0064	0.0176	2.73	0.0523
<i>Tenericutes</i>	3.2662	2.4050	0.74	0.2546

Table S4. Genus level abundance of bacterial taxa in chyme samples that were determined by pyrosequencing of 16S rDNA tags. A total of 287 genera of intestinal microbes were detected, the following is the number of microbial genera in each group at different relative abundance level.

group	total	relative abundance $>10^{-5}$	relative abundance $>10^{-4}$	relative abundance $>10^{-3}$	relative abundance $>10^{-2}$
Ctrl group	230	180	99	43	8
CGA group	270	230	123	46	8

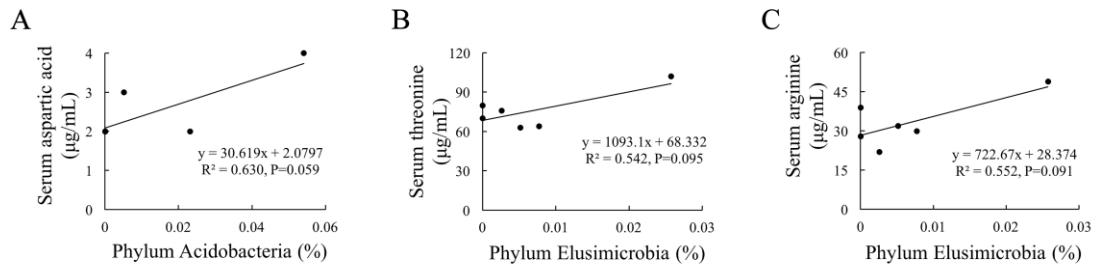


Figure S1. Correlation analysis of the relative abundance of microbial communities and amino acids absorption. A) Correlation between relative abundance of phylum Acidobacteria and serum aspartic acid level. B) Correlation between relative abundance of phylum Elusimicrobia and serum threonine level. C) Correlation between relative abundance of phylum Elusimicrobia and serum arginine level.

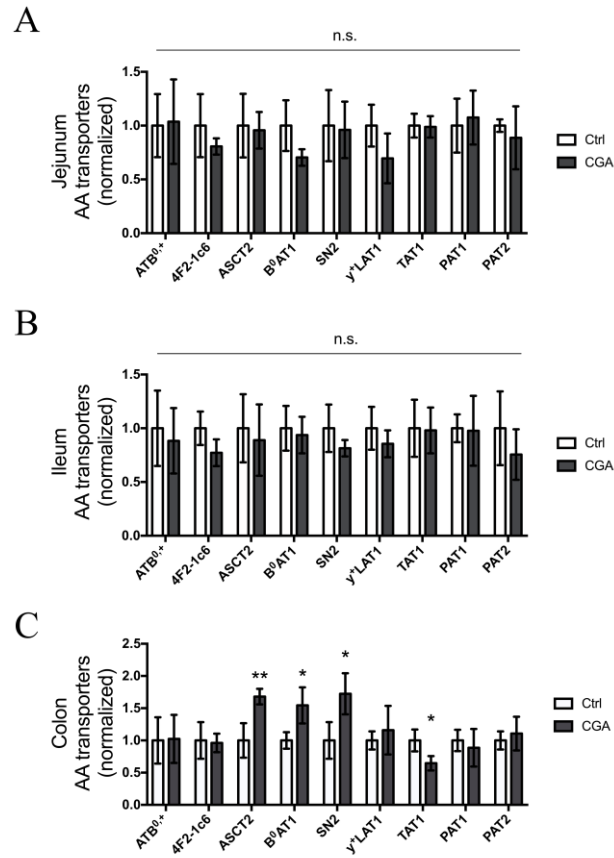


Figure S2. Changes of amino acid transporters after CGA supplemented. A) mRNA expression of amino acid transporters in jejunum. B) mRNA expression of amino acid transporters in ileum. C) mRNA expression of amino acid transporters in colon.