

Supplementary Tables and Figures

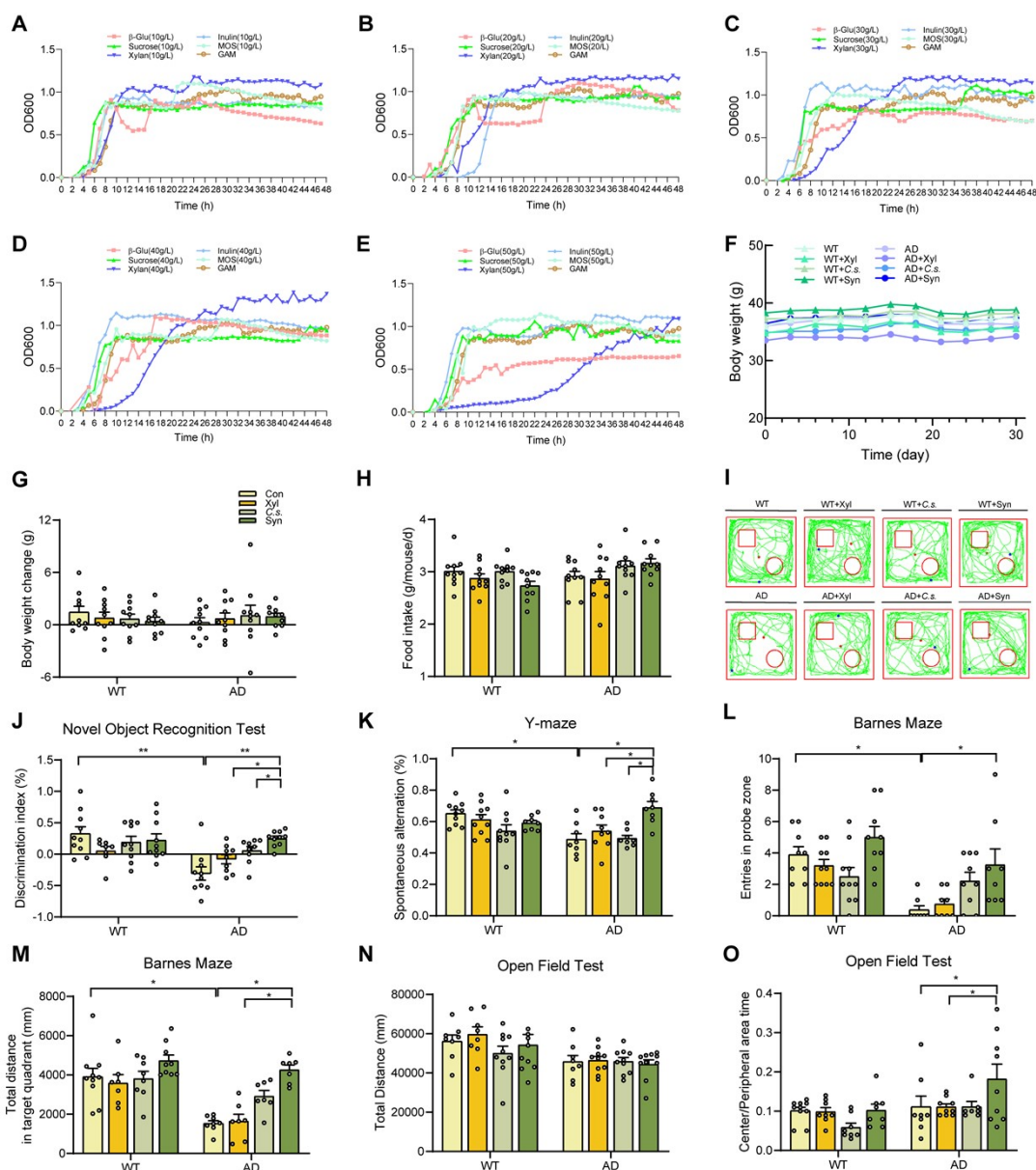


Fig.S1 Effect of different carbon sources on the growth curve of *C. sporogenes*

(A-E) Growth curves of *C. sporogenes* containing different concentrations of carbon source, 10 g/L (A), 20 g/L (B), 30 g/L (C), 40 g/L (D), and 50 g/L (E) (n = 3). **(F)** Body weight change trend across all 8 groups. (The groups included WT+Xyl, WT+C.s. and WT+Syn groups). **(G)** Body weight change across all 8

groups. **(H)** Food intake across all 8 groups (n = 8-10). **(I)** (D) Mouse trajectory of the new object recognition test across all 8 groups (n = 8-10). **(J)** The discrimination index of the new object recognition test across all 8 groups. (n = 8-10). **(K)** The spontaneous alternation of the Y-maze test across all 8 groups (n = 8-10). **(L)** Quantitative assessment of the number of times each mouse poked its head into each hole of the Barnes maze across all 8 groups (n = 8-10). **(M)** The total distance in target quadrant of the Barnes maze across all 8 groups (n = 8-10). **(N) (H)** The total distance traveled by mice in the open field test across all 8 groups (n = 8-10). **(O)** Center/peripheral area time in the open field test across all 8 groups (n = 8-10). Data are mean \pm SEM. *p < 0.05, **p < 0.01. Significant differences among means were determined by two-way ANOVA with Tukey's multiple comparisons test.

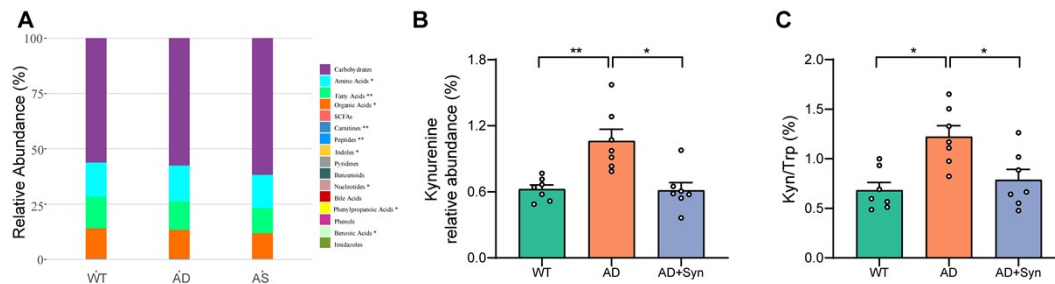


Fig.S2 Effects of synbiotic on plasma metabolites in 5xFAD mice

(A) Relative abundance of different types of metabolites in serum. **(B)** Relative abundance of kynurenine in serum (n = 7). **(C)** Relative abundance of kyn/trp in serum (n = 7). Data are mean \pm SEM. *p < 0.05, **p < 0.01. Significant differences among means were determined by one-way ANOVA with Tukey's multiple comparisons test.

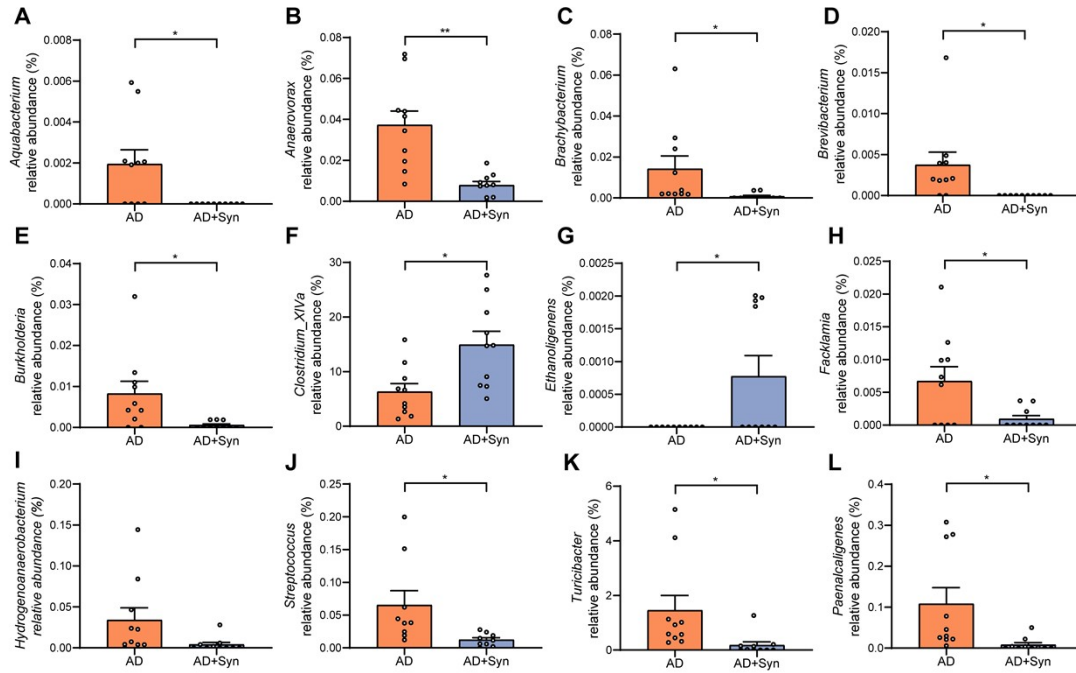


Fig.S3 Effects of synbiotic on gut microbiota in 5xFAD mice

(A-L) Relative abundance of *Aquabacterium*, *Anaerovorax*, *Brachybacterium*, *Brevibacterium*, *Burkholderia*, *Clostridium_XIVa*, *Ethanoligenens*, *Facklamia*, *Hydrogenoanaerobacterium*, *Streptococcus*, *Turicibacter*, and *Paenaltcaligenes* at the genus level (n = 9-10). Data are mean \pm SEM. *p < 0.05, **p < 0.01. Data are mean \pm SEM. *p < 0.05, **p < 0.01. Significant differences between means were determined by t-test.

Table S1 Compositions of AIN-93M diet

Classification	Content (g/kg)
Corn Starch	465.700
Maltodextrin	155.000
Casein	140.000
Sucrose	100.000
Cellulose	50.000
Soybean Oil	40.000
Mineral Mix, M1021	35.000
Vitamin Mix, V1010	10.000
L-Cystine	1.800
Choline chloride	2.500
Tert-Butylhydroquinone	0.036
Total (g)	1000.000

Table S2 Formulation of carbon source added to the culture medium

Concentration (g/L)	5	10	20	30	40
GAM (mL)	5	5	5	5	5
MOS (Xi'an Yuen sun Biological Technology Co., Ltd.) (g)	0.025	0.050	0.100	0.150	0.200
Xylan(X820567, Macklin Bio-Technology Co., Ltd, Shanghai, China) (g)	0.025	0.050	0.100	0.150	0.200
Inulin(S11143, Yuanye Bio-Technology Co., Ltd, Shanghai, China)	0.025	0.050	0.100	0.150	0.200
β -Glu (β -Glu is from highland barley)	0.025	0.050	0.100	0.150	0.200

Table S3 Primer sequences used for rRT-qPCR

Name	Forward Primers (5'-3')	Reverse Primers (5'-3')
<i>APP</i>	GCTGCCAGCTTGGCACTGC	GGCAACGGTAAGGAATCACGATGTGGGTG
<i>PSD-95</i>	TCTGTGCGAGAGGTAGCAGA	AAGCACTCCGTGAACTCCTG
<i>TNF-α</i>	CTCATGCACCACCATCAAGG	ACCTGACCACTCTCCCTTTG
<i>IBA-1</i>	TGATGAGGATCTGCCGTCCAAACT	TCTCCAGCATTGCTTCAAGGACA
<i>MUC2</i>	GAAGCCAGATCCCGAAACCA	CCAGCTTGTGGGTGAGGTAG
<i>ZO-1</i>	TGGGAACAGCACACAGTGAC	GCTGGCCCTCCTTTTAACAC
<i>Claudin-1</i>	AGCTGCCTGTTCCATGTACT	CTCCCATTTGTCTGCTGCTC
<i>COX-2</i>	TGAGCAACTATTCCAAACCAGC	GCACGTAGTCTTCGATCACTATC
<i>Mdr1b</i>	TACATCTTGGCGGACCTTAC	CGCTGGTTTCTTTTCTTTCTTC
<i>Cyp3a11</i>	TCTACCGATATGGGACTC	AAATGATGTGCTGGTGAT
<i>16S rDNA</i>	AGAGTTTGATCCTGGCTCAG	CTGCTGCCTCCCGTAGGAGT
<i>GAPDH</i>	TGGAGAAACCTGCCAAGTATGA	TGGAAGAATGGGAGTTGCTGT

Table S4 Formulation of carbon source added to the culture medium

Subject class	EC number	Known Activities
CE4	EC 3.2.1.37	β -xylosidase
GH1	EC 3.1.1.72	Acetyl xylan esterase
GH55	EC 3.2.1.58	exo- β -1, 3-glucanase
GH1	EC 3.2.1.25	β -mannosidase