

## Supporting Information

### Ellagic acid ameliorates alcohol-induced cognitive and social dysfunction through the gut microbiota-mediated CCL21-CCR7 axis

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**Table S1 Key resources in the current study**

<b>Reagent or resource</b>	<b>Source</b>	<b>Identifier</b>
<b>Antibodies</b>		
IBA-1	Abcam	Cat# ab178847; RRID:AB_2832244
CCL21	Thermo Fisher	Cat# 500-P114BT; RRID:AB_2929279
Goat anti-Mouse IgG (H+L) Cross-Adsorbed Secondary Antibody, HRP	Thermo Fisher Scientific	Cat# a16078; RRID:AB_2534752
<b>Chemicals</b>		
Ellagic acid	Nanjing DASF Biotechnology	CAS NO 476-66-4
Metronidazole	Dalian Meilun biological Technology Co	CAS NO 443-48-1
Ampicillin	Dalian Meilun biological Technology Co	CAS NO 7177-48-2

Vancomycin hydrochloride	Dalian Meilun biological Technology Co	CAS NO 1404-93-9
Neomycin Sulfate	Dalian Meilun biological Technology Co	CAS NO 1405-10-3
Hematoxylin	Poly-scientific	S212
Eosin	StatLab	SL98-1
TB Green™ Premix Ex Taq™ II	TaKaRa	RR820Q
Sterile ethanol liquid diet	TROPHIC Animal Feed High-tech Co.	AIN-93M
<b>Software and Algorithms</b>		
ImageJ v2.3.0	National Institutes of Health	RRID:SCR_003070
Super Maze	XR-Xmaze	<a href="http://www.softmaze.com/">http://www.softmaze.com/</a>
R (v4.2.1)	R Team	<a href="https://www.r-project.org/">https://www.r-project.org/</a>

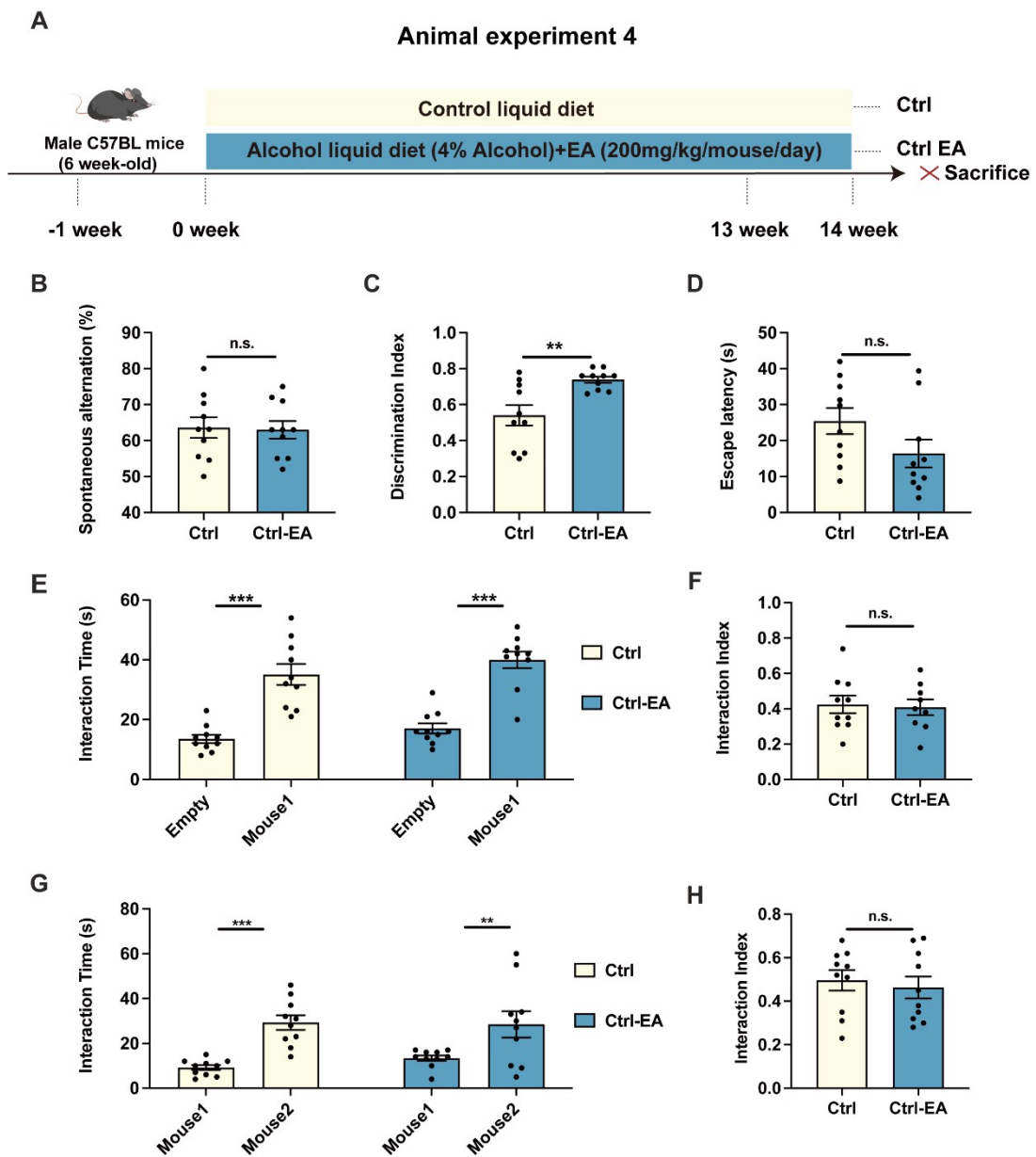
**Table S2 Primer sequences for qRT-PCR**

<b>Gene</b>	<b>Forward Primer</b>	<b>Reverse Primer</b>
<b><i>Tnfa</i></b>	CTCATGCACCACCATCAAGG	ACCTGACCACTCTCCCTTTG

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<b><i>Ii6</i></b>	CCTCTGGTCTTCTGGAGTAC	ACTCCTTCTGTGACTCCAGC
	C	
<b><i>Ii10</i></b>	ATAACTGCACCCACTTCCCA	GGGCATCACTTCTACCAGGT
<b><i>Iba1</i></b>	TGACGGACCCCAAAGATGA	TCTCCACAGCCACAATGAGT
<b><i>Ccl21a</i></b>	ATCCCGGCAATCCTGTTCTC	CCCTTGGAGCCCTTTCCTTT
<b><i>Ccl21b</i></b>	CTGGTGGTAACGAGGCTCA	AATGGTGTCCCAGTTGCCTC
<b><i>Ccl21c</i></b>	GTGGTAACGAGGCTCAC	CCAGCCTAAGATCCTGCCTT
<b><i>Ccl21d</i></b>	CATCCCGGCAATCCTGTTCT	TTCTCTTGCAGCCCTTGGAG
<b><i>Tnfrsf17</i></b>	CAGCTTGACGGATCGGCT	CCCCTTGGGTTTGCTCTTGA
<b><i>Total</i></b>	ACTCCTACGGGAGGCAGCA	GGACTACHVGGGTWTCTAA
<b><i>bacteria</i></b>	G	T
		AGAGAGCTTGATGGCTTGG
<b><i>Bace2</i></b>	AGTAACTTCGCTGTGGCAGG	C
	AGAGCGGGAATGGTGAAGA	AGTTGATCTGTCTCCGCTTG
<b><i>Fos</i></b>	C	G
<b><i>Npas4</i></b>		
<b><i>Rab3a</i></b>	TTTGCAGGACGTCAGCTAGG	CTGTGGCGGAAGCCATCTTA

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**Fig. S1. Effects of UA on cognitive and social functions in non-alcohol diet mice.**

**(A)** Timeline of animal experiment 4 depicting the non-alcohol diet with EA treatment.

**(B)** For the Y-maze, spontaneous alternations were recorded. E

**(C)** For the Barnes maze, escape latency was recorded.

**(D)** The discrimination index between the novel and familiar objects was calculated for the novel object recognition test.

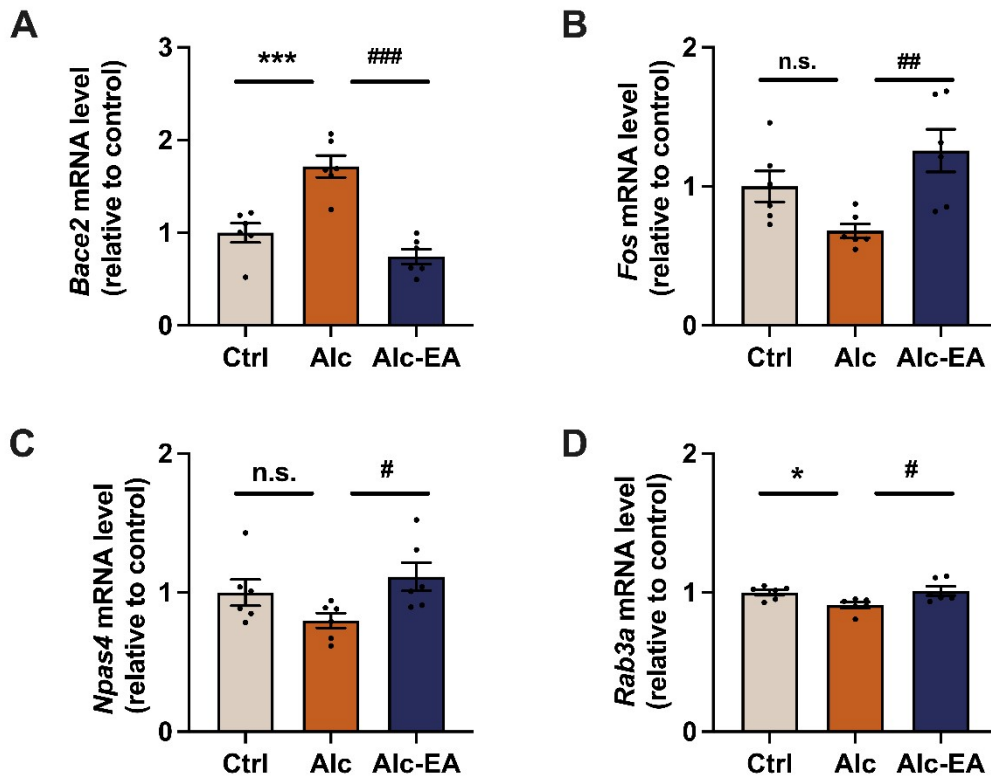
**(E)** In the sociability test, the interaction index was calculated.

**(F)** The sociability test recorded the time spent interacting with a mouse or an empty wire cage.

**(G)** In the social novelty test, the interaction index was calculated.

**(H)** In the social novelty test, the time spent interacting with a novel versus a familiar mouse was recorded.

Data presented as mean  $\pm$  SEM. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , compared with Alc group. Significant differences between mean values were determined by one-way ANOVA with Tukey's multiple comparisons test.



**Fig. S2. The mRNA expression levels of cognitive-related genes were analyzed based on RNA sequencing data from the hippocampus of mice.**

**(A)** The mRNA expression level of the *Bace2* gene in the hippocampus.

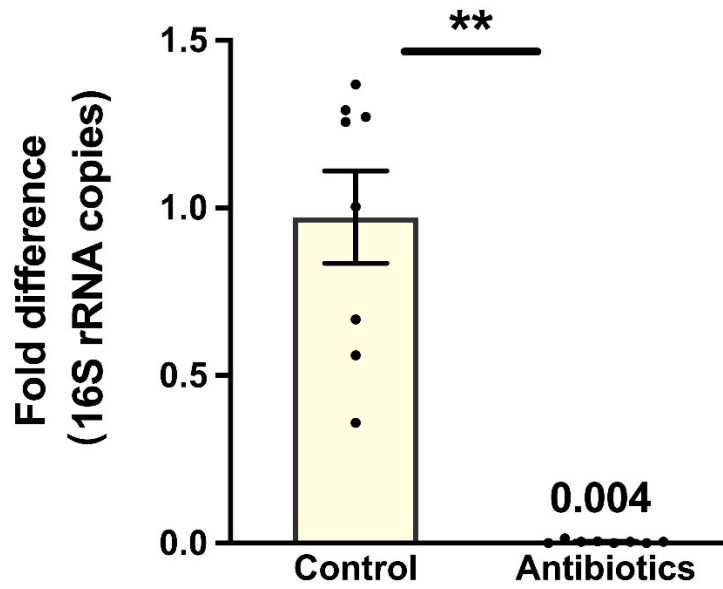
**(B)** The mRNA expression level of the *Fos* gene in the hippocampus.

**(C)** The mRNA expression level of the *Npas4* gene in the hippocampus.

**(D)** The mRNA expression level of the *Rab3a* gene in the hippocampus.

Data presented as mean  $\pm$  SEM. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , compared with Ctrl group, # $p < 0.05$ , ## $p < 0.01$ , ### $p < 0.001$ , compared with the Alc group.

Significant differences between mean values were determined by one-way ANOVA with Tukey's multiple comparisons test.



**Fig. S3. Removing gut microbiome effect diagram.**

Data were represented as mean  $\pm$  SEM ( $n \geq 8$ ); \*means compared to the “Control” group, \* $P < 0.05$ , \*\* $P < 0.01$