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Supplemental information

miR-204 silencing reduces mitochondrial autophagy and ROS production in a murine AD model via the TRPML1-activated STAT3 pathway

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Table S1 Primer sequences of RT-qPCR

Target	Sequence
TRPML1	F: 5’-GGAGTTTGTCAATGGCTGGT-3’
	R: 5’-GAATGACACCGACCCAGACT-3’
miR-204	F: 5’-GGTTCCCTTTGTCATCC-3’
	R: 5’-TGCGTGTCGTGGAGTC-3’
U6	F: 5’-GCTTCGGCAGCACATATACTAAAAT-3’
	R: 5’-CGCTTCACGAATTTGCGTGTCAT-3’
GAPDH	F: 5’-GCTTCGGCAGCACATATACTAAAAT-3’
	R: 5’-AGATGATGACCCTTTTGGCTC-3’

RT-qPCR: reverse transcription quantitative polymerase chain reaction; TRPML1: transient receptor potential mucolipin-1; miR: microRNA; GAPDH: glyceraldehyde-3-phosphate dehydrogenase; F: forward; R: reverse.

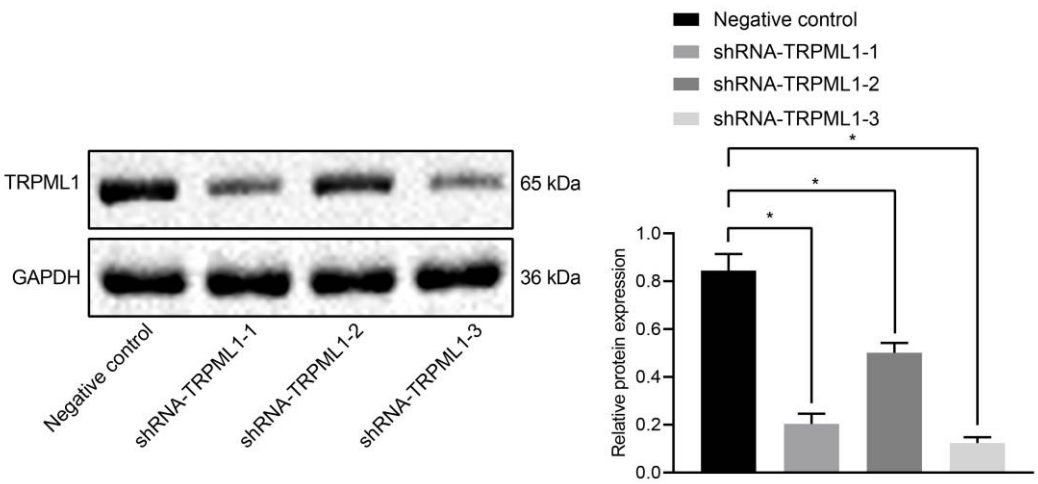

Fig. S1 The off-target efficacy of shRNAs against TRPML1 (sh-TRPML1-1, sh-TRPML1-2, sh-TRPML1-3)

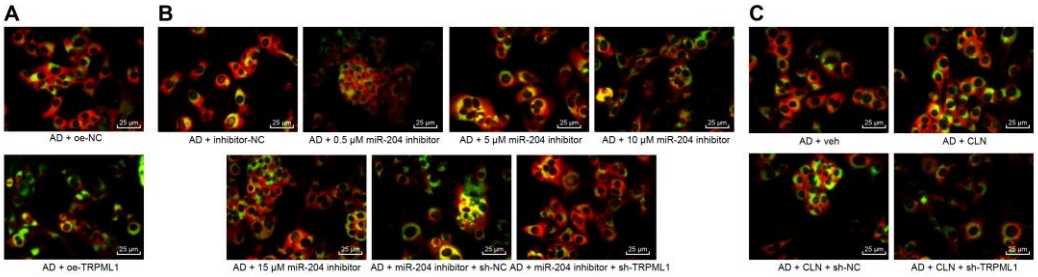

Fig. S2 Co-localization of mitochondria and lysosomes after different treatment detected by Mitotracker (green) and Lysotracker (red) staining. A: co-localization of mitochondria and lysosomes after TRPML1 overexpression treatment. B: co-localization of mitochondria and lysosomes after miR-204 inhibitor (0.5 μM, 5 μM, 10 μM, and 15 μM) and sh-TRPML1 treatment. C: co-localization of mitochondria and lysosomes after CLN and sh-TRPML1 treatment. The yellow color indicates the merging of Mitotracker and Lysotracker.

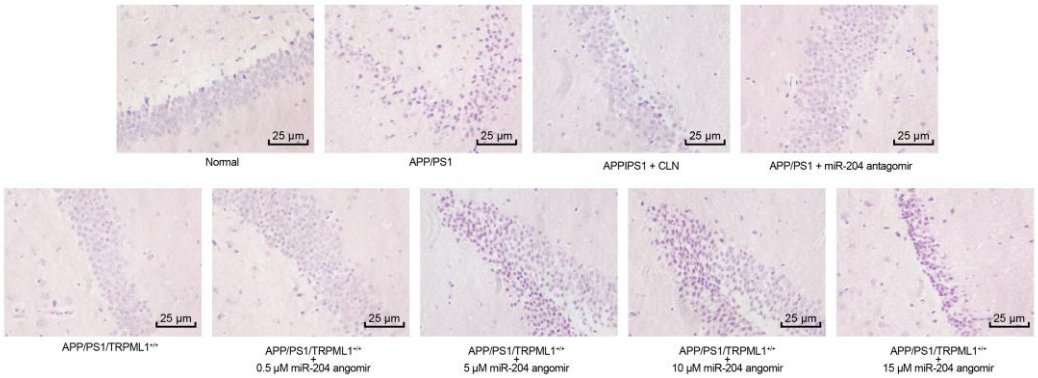

Fig. S3 HE staining was used to detect the pathological changes of hippocampus in mice.