

Additional file 2: Table S2: Statement on sample size and statistical measures.

Fig	Sample size	Definitions of statistical methods and measures
1a, b, c	n = 9, WT; n = 8, DcR3; n = 7, APP; n = 7, APP/DcR3.	one-way ANOVA
1d, e, f	n = 5, WT; n = 11, DcR3; n = 7, APP; n = 10, APP/DcR3.	one-way ANOVA
1 g, h	Mouse numbers: n = 40, WT; n = 8, DcR3; n = 37, APP; n = 6, APP/DcR3.	one-way ANOVA
2a, b	Slices for CA3: n = 8, WT; n = 7, DcR3; n = 10, APP; n = 10, APP/DcR3. Slices for CA1: n = 14, WT; n = 10, DcR3; n = 13, APP; n = 14, APP/DcR3. Slices for DG: n = 14, WT; n = 12, DcR3; n = 13, APP; n = 13, APP/DcR3. Each quantitative data from at least 3 mice per genotype.	one-way ANOVA
2 c, d	n = 5 mice per genotype.	one-way ANOVA
3b,c,e,f	Data were obtained from three independent experiments, and each treatment performed in quadruplicating.	one-way ANOVA
3d	Data were obtained from more than four independent experiments, and each treatment performed in quadruplicating.	one-way ANOVA
4 a, b	Mouse numbers: n = 6, APP; n = 4, APP/DcR3. Slice numbers: n = 34, APP; n = 24, APP/DcR3.	two-tailed unpaired Student's t test.
4 c, d	n = 6 mice per genotype.	two-tailed unpaired Student's t test.
5 a, b	Number of plaques analyzed: APP = 342, APP/DcR3 = 324. Each quantitative data from at least 3 mice per genotype.	two-tailed unpaired Student's t test.
5 c, d	Cell numbers: n=76, oA β ; n=74, oA β +DcR3.	two-tailed unpaired Student's t test.
6 a, b, c	Mouse numbers in TNF- α ELISA: n = 14, APP; n = 8, APP/DcR3; Mouse numbers in IL-1 β ELISA: n = 16, APP; n = 8, APP/DcR3; Mouse numbers in YM1 mRNA level: n = 15, APP; n = 7, APP/DcR3; Mouse numbers in YM1 ELISA: n = 9, APP; n = 6, APP/DcR3;	two-tailed unpaired Student's t test.
6 d	n = 3 per treatment	one-way ANOVA
7d	Data were obtained from three independent experiments, and each treatment performed in quadruplicating.	One-way ANOVA
S1 b	n = 6 mice per genotype.	One-way ANOVA

S1 c	Mouse numbers: n = 18, WT; n = 21, DcR3; n = 21, APP; n = 22, APP/DcR3.	One-way ANOVA
S2 b, c	Mouse numbers for CA3: n = 11, WT; n = 8, DcR3; n = 13, APP; n = 12, APP/DcR3; CA1: n = 12, WT; n = 8, DcR3; n = 13, APP; n = 12, APP/DcR3; and DG: n = 11, WT; n = 7, DcR3; n = 11, APP; n = 12, APP/DcR3.	One-way ANOVA
S3	Experiments were conducted for over 5 times with 3 regions for each treatment.	One-way ANOVA
S4	n = 4 per treatment	one-way ANOVA
S5	Slice numbers: n = 8 Each quantitative data from 4 mice per genotype.	two-tailed unpaired Student's t test.
S7	Sample numbers are presented in figures.	one-way ANOVA
S8 a, b	Slice numbers: n = 14, APP; n = 13, APP/DcR3. Each quantitative data from 4 mice per genotype.	two-tailed unpaired Student's t test.
S9 b	Data were obtained from two independent experiments, and each treatment performed in duplicating.	one-way ANOVA

Data are presented as the mean \pm s.e.m. from at least three independent experiments and were analyzed using Prism software (GraphPad) to determine the statistical significance of the difference. Differences between data sets were analyzed by Unpaired, two-tailed Student's *t*-tests or one-way ANOVA followed with the Bonferroni post hoc test. During multiple contrast analysis, the alpha was set as 0.05 (95% confidence intervals). A *p* value less than 0.05 was considered to be statistically significant.