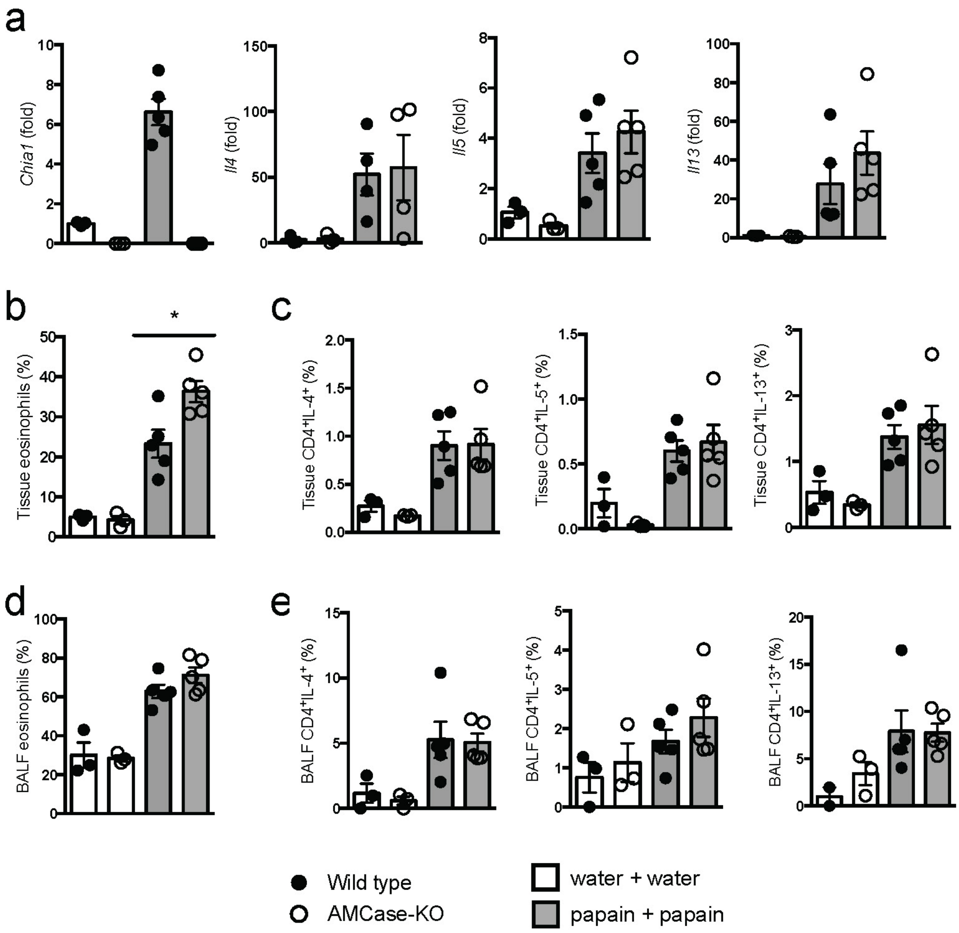
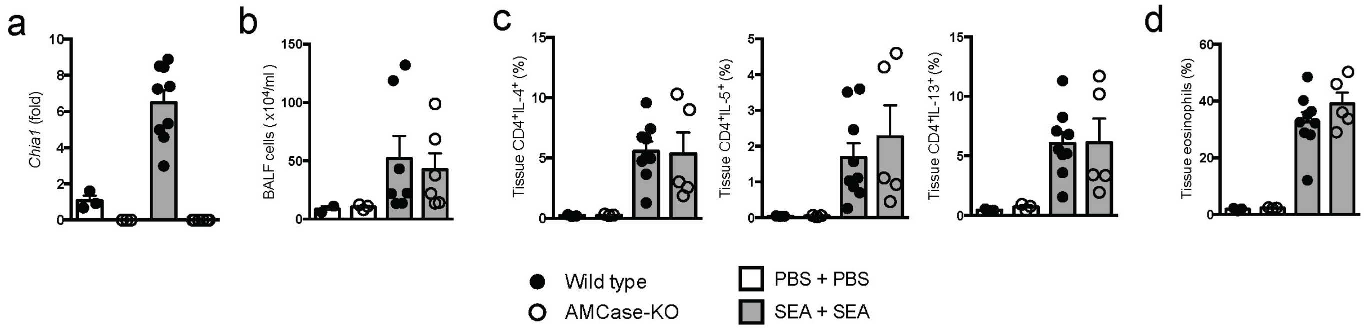


Supplementary Figure 1

Acute model of papain-induced type 2 allergic inflammation in the lung.

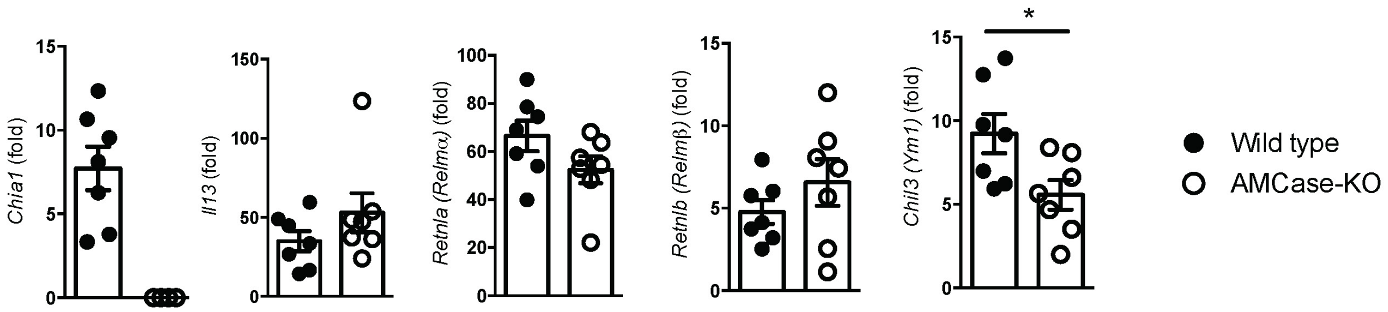
(**a**) Quantitative PCR analysis of gene expression in lung tissue from wild type mice or AMCase-KO mice sensitized and challenged intranasally with PBS (*n* = 3 mice per genotype) or papain (*n* =5 mice per genotype) expressed relative to water-treated wild type. (**b**) Quantification of eosinophils in lung tissue of mice in **a** (PBS: *n* = 3, papain: *n* = 5). (**c**) Intracellular cytokine analysis of lung tissue lymphocytes of mice in **a** (PBS: *n* = 3, HDM: *n* = 5). (**d**) Quantification of eosinophils in BALF of mice in **a** (PBS: *n* = 3, HDM: *n* = 5). (**e)** Intracellular cytokine analysis of BALF lymphocytes of mice in **a** (PBS: *n* = 3, HDM: *n* = 5). Error bars represent standard error of the mean, and each data point represents a value for an individual mouse.



Supplementary Figure 2

Acute model of SEA-induced type 2 allergic inflammation in the lung.

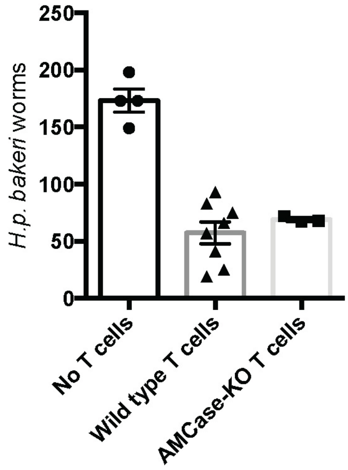
(**a**) Quantitative PCR analysis of gene expression in lung tissue from wild type mice or AMCase-KO mice sensitized and challenged intratracheally with PBS (*n* = 3 mice per genotype) or schistosoma egg antigen (SEA) (*n* = 9 mice per genotype) expressed relative to PBS-treated wild type. (**b**) Quantification of leukocytes in BALF of mice in **a** (PBS: *n* = 3, SEA: *n* = 6). (**c**) Intracellular cytokine analysis of lung tissue lymphocytes of mice in **a** (PBS: *n* = 3, WT/SEA: *n* = 9, KO/SEA: *n* = 5). (**d**) Quantification of eosinophils in lung tissue of mice in **a** (PBS: *n* = 3, WT/SEA: *n* = 9, KO/SEA: *n* = 5). Data are representative of three experiments with similar results. Error bars represent standard error of the mean, and each data point represents a value for an individual mouse.



Supplementary Figure 3

Gene expression in lung tissue during *N. brasiliensis* infection.

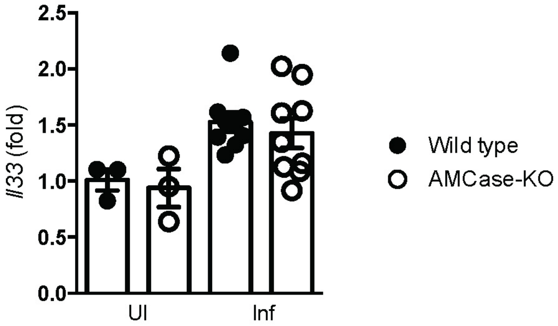
Quantitative PCR analysis of gene expression in lung tissue from wild type mice ($n = 7$) or AMCase-KO mice ($n = 7$) 8 days after primary infection with *N. brasiliensis.* Data shown relative to expression in lung tissue from naïve mice. *$P<0.05$ (Student's *t*-test). Data are representative of two experiments with similar results. Error bars represent standard error of the mean, and each data point represents a value for an individual mouse.



Supplementary Figure 4

Wild type and AMCase-deficient T cells are equally competent at clearing *H.p. bakeri* infection.

Quantification of *H.p. bakeri* worms recovered from intestines of TCRα KO mice that were recipients of $2x10^5$ T cells from previously infected wild type mice (triangles, *n* = 8), $2x10^5$ T cells from previously infected AMCase-KO mice (squares, *n* = 3), or no T cells (circles, *n* = 4).



Supplementary Figure 5

***Il33* expression in small intestine tissue 3.5 days after primary *H. p. bakeri* infection.**

Quantitative PCR analysis of *Il33* expression in proximal small intestine tissue from wild type mice or AMCase-KO mice 3.5 days post-infection (*n* = 9 per genotype) or from uninfected wild type or AMCase-KO (*n* = 3 per genotype). Error bars represent standard error of the mean, and each data point represents a value for an individual mouse.

Nature Immunology: doi:10.1038/ni.3417