SUPPORTING INFORMATION

2 **METHODS**

1

3 Generation of mEar2-deficient mice

All mice were housed in a specific pathogen-free animal facility with a regular 12-h light/dark cycle at an appropriate temperature and humidity. All experimental procedures used in this study were approved by the Animal Care and Use Committee of the Kansai Medical University (No:22-048). Female C57BL/6J mice (6-8 weeks old) were purchased from Shimizu Experimental Materials (Kyoto, Japan).

The mEar2-targeting vector was designed to replace exon 2 with a Cre-Enhanced Green 9 10 Fluorescent Protein (Cre-EGFP) and PGK promoter-driven neomycin resistance cassette (Fig. S1A). The 4.3 kb long and 2.1 kb short arm genomic DNA fragments were obtained from the 11 C57BL/6 mouse Bac genomic clone (ID: RP23-262F9 and RP23-344C13, Roswell Park 12 13 Cancer Institute, USA). To produce the long arm fragment and Cre-EGFP, the 1.4 kb 3' side of the long arm fragment and Cre-EGFP fragment amplified from the pCAG-Cre:GFP 14 plasmid (Addgene, #13776) were inserted in pBlueScriptII SK+ (Invitrogene, USA). The 5' 15 side of the long arm fragment was amplified via PCR, digested using PspOMI and XmaI, and 16 inserted in pBS-NEO-DTA by Unitech Co. (Kashiwa, Japan). The short-arm fragment was 17 amplified using PCR, digested with XmaI and PspOMI, and inserted into the pBS-loxP-FRT-18 19 Neo-FRT vector (Unitech, Japan). The targeting vector was constructed by subcloning the 5' 20 long arm and Cre-EGFP digested using XmaI and MluI and the short arm fragment digested using MluI and SacII into the pBS-DTA vector with the 5' side of the long arm fragment 21 22 digested using Xma and SacII. The sequences of the targeted vectors were confirmed via DNA sequencing. The targeting vector was linearized via SacII digestion and electroporated 23 into C57BL/6-derived embryonic stem cells. Southern blotting and PCR were performed to 24 25 verify homologous recombination in G418-gancyclovir-resistant clones. To generate chimeric mice, targeted embryonic stem clones were injected into ICR blastocysts. Heterozygous F1 26 27 offspring (derived from ES clone #53 and 65) were produced by mating chimeric males with C57BL/6 females. Heterozygous offspring were crossed to generate homozygous embryos. 28 29 mEAR2 deficient mice are available from RIKEN BioResource Research Center. Genotyping via PCR using DNA samples from tail biopsies was performed to classify mice into wild type 30 $(mEAR2^{+/+})$, heterozygous $(mEAR2^{+/-})$, and homozygous $(mEAR2^{-/-})$ animals. For the list of 31

32 all primers, see the supplementary table S1.

33 AAI model

AAI was induced in mEAR2^{-/-} and mEAR2^{+/+} mice as our previous report.¹ Briefly, mice 34 were sensitized through 2 intraperitoneal (i.p.) injections of 10 µg unpurified Der f 1. 35 (Dermatophagoides farinae) (Institute of Tokyo Environmental Allergy, Japan), referred to 36 37 HDM antigen, mixed with 2 mg of aluminum hydroxide (Thermo Fisher Scientific, USA) at days 0 and 14. Then, mice were intranasally (i.n) challenged with 20 µL PBS or 5 µg HDM in 38 20 µL PBS from day 21 to day 25. AHR was evaluated by measuring the airway resistance 39 upon nebulization of increasing methacholine concentrations using invasive plethysmography 40 41 (FinePointe RC; Buxco Research Systems, Winchester, UK) 48 hours after the last challenge. Lung inflammation was assessed using histology and bronchoalveolar lavage fluid (BALF) 42 43 analysis. The mRNA and/or protein levels of cytokines, mEAR2 in the lung tissue and/or 44 BALF, and the total immunoglobulin E (IgE) in the serum were measured by qPCR and

45 ELISA on days 0, 14, 20, and 27.

46 Lung sample preparation

47 The left and right lung lobes were collected for histological analysis and RNA extraction,

- 48 respectively. The left lung was fixed with 4% paraformaldehyde for 24 h and then freeze-
- 49 dried in super cry embedding medium (Leica Microsystems, Land Hessen, Germany) in
- 50 isopentane (Nacalai Tesque, Kyoto, Japan) cooled in liquid nitrogen. Freshly frozen samples

- 51 were sectioned following the Kawamoto method ³ and stained with hematoxylin and eosin for
- 52 morphological analysis.

53 *Eosinophil differentiation from bone marrow and functional assays*

Eosinophils were differentiated from the bone marrow (BM) of $mEAR2^{-/-}$ and $mEAR2^{+/+}$

- 55 mice as previously described.² BM cells were cultured at 5×10^{6} /mL in medium containing
- 56 RPMI 1640 (Invitrogen, USA) with 20% FBS (Gibco, USA), 100 IU/mL penicillin, 10 μg/mL
- 57 streptomycin (Gibco, USA), 2 mM glutamine (Invitrogen), 25 mM HEPES, 1x non-essential
- amino acids, 1 mM sodium pyruvate (Gibco, USA), 50 μ M β -mercaptoethanol (Sigma, Germany), 100 ng/mL stem cell factor (SCF; PeproTech, USA), and 100 ng/mL FLT3-ligand
- 60 (FLT3-L; PeproTech, USA) from day 0 to day 4. On day 4, the medium containing 10 ng/mL
- 61 recombinant interleukin-5 (rmIL-5; R&D Systems, USA) was replaced with a medium
- 62 without SCF and FLT3-L. On day 8, the cells were seeded into new dishes, and half of the
- 63 medium was replaced with fresh medium containing rmIL-5 every other day. Morphological
- and functional analyses of BM-derived eosinophils (BMDE) from mEAR2^{-/-} and mEAR2^{+/+}
- 65 mice were performed via microscopic counting following diff-quick staining, chemotaxis 66 assay, and cytokine profiling using qPCR on day 14.

67 *Chemotaxis assay*

- For the chemotaxis assay, an eosinophil suspension $(0.5 \times 10^6 \text{ cells/mL})$ was applied to the upper chamber of a 24-well-type Chemotaxis cell chamber (5 µm pore, polycarbonate
- membrane) in RPMI-1640 medium. Chemoattractant solution (10 μ g eotaxin-1, PeproTech,
- USA) was injected into the lower chamber, and the plate was incubated at 37 °C for 3 h. After gentle washing, both the upper and lower cells were incubated with APC-SiglecF (BD
- Bioscience, USA) and analyzed using the FACS Calibur flow cytometer acquire the events
- vithin 30 s. At the end of the assays, we calculated the chemotactic index by dividing the
- number of eosinophils that migrated over the membrane towards the chemoattractant by the
- 76 number of eosinophils remaining at baseline.⁴

77 Co-culture of sensitized splenocytes and BMDE

- Co-culture experiments with splenocytes and BMDE from mEAR2^{+/+} or mEAR2^{-/-} mice were performed as previous described with modification.⁵ Briefly, spleens were collected from mEAR2^{+/+} and mEAR2^{-/-} 8-weeks-old mice after sensitization using 10 μ g HDM with 2 mg aluminum hydroxide i.p. at day 0 and 7. Splenocytes were resuspended in RPMI with 10% FBS, followed by removal of red blood cells treated with lysis buffer (BD Bioscience, USA). 3 × 10⁶ splenocytes /mL and 3 × 10⁶ BMDE cells/mL were individually cultured or cocultured in the RPMI medium with or without 40 μ g/mL HDM and incubated for 96 h at
- 85 37 °C with 5% CO₂. Then, the cells and supernatant were harvested, and type 2 cytokines (IL-
- 4, -5, and -13) analysis was performed using qPCR and ELISA.

87 Statistical analysis

Bata are presented as the means \pm standard error of the mean (SEM). Statistical significance was determined using the Student's t-test or Mann–Whitney U test. The threshold of significance for all tests was considered p < 0.05 for all tests.

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Supplementary Table S1. Primers List

Gene	Forward	Reverse
P1-P2	ACTGAGGCAAGGTGGGAATAGT	GCATTTCATTCCTAGTTCCCATTAG
P3-P4	AGCAAGAGAGCTCACGTACACC	TGCACGTTCACCGGCATCAAC
P5-P6	TGAAGTTCATCTGCACCACCGG	TTCTGACTCAGGAGAGGCGAC
Southern	AGCTGACCCTGAAGTTCATCTG	TATAGACGTTGTGGCTGTTGTAGTT
probe	AGEIGACCEIGAAGIICATEIG	
ActB	TCGAGTCGCGTCCACC	GGGAGCATCGTCGCCC
IL-4	ACACCACAGAGAGTGAGCTCG	TGCAGCTCCATGAGAACACTAG
IL-5	AGGATGCTTCTGCACTTGAG	AGCTGTGTCAAGGTCTCTTTC
IL-13	AAAACTGCAGCAAGACCGTG	CCAGAGCCCACTGCTTCAAT
IFNγ	ACTCAAGTGGCATAGATGTGG	AAGACTTCAAAGAGTCTGAGGTAG
TNFα	TGTCTACTCCCAGGTTCTCTTC	GCAGAGAGGAGGTTGACTTTC
T-bet	CCCACAAGCCATTACAGGATGT	TGCCTTCTGCCTTTCCACAC
IL-17A	TACAGTGAAGGCAGCAGCGATC	ACATTCTGGAGGAAGTCCTTGG
IL-22	ATCGTCAACCGCACCTTTAT	GACTCCTCGGAACAGTTTCTC
IL-25	ACAGGGACTTGAATCGGGTC	TGGTAAAGTGGGACGGAGTTG
TGF-β	ACCATCCATGACATGAACCGG	AGCAGTTCTTCTCTGTGGAGC
IL-6	CCACGGCCTTCCCTACTTCA	CCACGATTTCCCAGAGAACATG
mEAR1	GGTCAAACCCCTTCCCAGAA	CATTGGGTATAATTTGTTGC
mEAR2 –	CAGGACAACCAGCCCTA	CTGTCTGCTTTGTGGCT
Exon1		
mEAR2 –	TGCTTGAGTCTCGACTTTGT	TTGGGTATAAGGTGTTCTCC
Exon2		
mEAR3	CTGCTGCTAAGACTTGTCC	CAGCATTTCAACATTACATCGG
mEAR4	CGATGTGATGCTGTAATGAGG	TCTTGTCGGCATAGTGAGG
mEAR5	GTCTGAAGCTGCTTGAATCC	CGTCTTTGCAAGTCTTGGG
mEAR6	CCAATGCAGATACCAAACAAAGG	GCAGTAGCAGATGATCGAAGG
mEAR8	AACAGGTTTAGAAGAACATGTAAGG	GTATAATTTGTTGCCCGACTGG
mEAR9	GCCATCCAGTATATCAATAATAATGCC	TGTTCTTCTAGACCTGTTAATACGC
mEAR10	ATGGGTCCAAAGCTGCTTGAG	TACGCTGCATTTCAACATTAC
mEAR11	CTCCGGCCAGTCATTATTCC	CGATGAATGAAGGTACAAAGTGC
mEAR12	AACAGGTTTAGAAGAACATGTAAGG	CTTCTCCGACTGGTGATGC
mEAR14	TGTTGGGACTTGTCCTAATGC	CTGTTAACAACCCTCATTACAGC

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(A) Locus of restriction enzyme recognition sites and probe for Southern blot analysis. (B) 112 Southern blot to identify correctly targeted embryonic stem cell clones. Southern probe 113 detected targeted band following digestion with BgIII or HindIII. (C) Gene maps of the 114 targeting construct and mEAR2 locus before and after homologous recombination with primer 115 sets used for genotyping (D) Genotyping results of mEAR2-deficient mice indicated as wild-116 type (mEAR2^{+/+}), heterogeneous (mEAR2^{+/-}), and homogenous (mEAR2^{-/-}). (E) RT-PCR of 117 mEARs in the lung tissues from wild-type (mEAR2^{+/+}), heterogeneous (mEAR2^{+/-}), and 118 homogenous (mEAR2^{-/-}) mice. 119





121 Fig. S2. mEAR2 contributes to the development of Allergic Airway Inflammation

122 (A) HDM-induced allergic airway inflammation model (AAI). (B) qPCR of Th1, Th2, Th17 123 cytokines, TGF- β , and IL-6 in the lung tissues. (C-E) qPCR of IL-4, -5, and -13 in the lung 124 tissues on days 0, 14, 20, and 27. (F) qPCR of mEAR2 in the lung tissues upon HDM-induced 125 AAI. (G) qPCR of IL-4, -5, and -13 for culture experiments. Data are expressed as means ± 126 SEM (n = 3 - 4 for each group). * Significantly different from mEAR2^{+/+}/HDM group (p 127 <0.05). ND: not detected. BMDE: bone marrow-derived eosinophils.