Supplementary Table 1: Mass spectrometry peptide sequence

SOS1

MQAQQLPYEF	FSEENAPKWR	GLLVPALKKV	QGQVHPTLES	NDDALQYVEE	LILQLLNMLC	QAQPRSASDV	
EERVQKSFPH	PIDK WAIADA	OSAIEK RKRR	NPLSLPVEKI	HPLLKEVLGY	KIDHQVSVYI	VAVLEYISAD	
ILKLVGNYVR	NIRHYEITKQ	DIKVAMCADK	VLMDMFHQDV	EDINILSLTD	EEPSTSGEQT	YYDLVKAFMA	
EIRQYIRELN	LIIK <u>VFREPF</u>	VSNSKLFSAN	DVENIFSRIV	DIHELSVK LL	GHIEDTVEMT	DEGSPHPLVG	
SCFEDLAEEL	AFDPYESYAR	DILRPGFHDR	FLSQLSKPGA	ALYLQSIGEG	FK EAVQYVLP	R LLLAPVYHC	
SOSE_HPI:IPI00020134	1.2 Protein Referen	ce and Reputation	LANVOSGMEKI	CSKSLAKRRL	SESACRFYSQ	QMKGKQLAIK	
KMNEIQK NID	GWEGKDIGQC	CNEFIMEGTL	TRVGAKHERH	IFLFDGLMIC	CKSNHGQPRL	PGASNAEYR L	
KEKFFMR KVQ	INDKDDTNEY	KHAFEIILKD	ENSVIFSAKS	AEEKNNWMAA	LISLQYRSTL	ERMLDVTMLO	
EEKEEOMRLP	SADVYRFAEP	DSEENIIFEE	NMOPK AGIPI	IKAGTVIKLI	ER LTYHMYAD	PNFVRTFLTT	
YRSFCKPQEL	LSLIIER fei	PEPEPTEADR	IAIENGDOPL	SAELKRFRKE	YIQPVQLR VL	NVCRHWVEHH	
FYDFERDAYL	LQRMEEFIGT	VR GKAMKK <u>WV</u>	ESITKIIQRK	KIARDNGPGH	NITFQSSPPT	VEWHISRPGH	
IETFDLLTLH	PIEIAR <mark>OLTL</mark>	LESDLYRAVO	PSELVGSVWT	KEDKEINSPN	LLKMIRHTTN	LTLWFEKCIV	
ETENLEERVA	VVSRIIEILQ	VFQELNNFNG	VLEVVSAMNS	SPVYR LDHTF	EQIPSROKKI	LEEAHELSED	
<u>HYK</u> KYLAKLR	SINPPCVPFF	GIYLTNILK <u>T</u>	EEGNPEVLKR	HGKELINFSK	RRKVAEITGE	IQQYQNQPYC	
LRVESDIKR <mark>F</mark>	FENLNPMGNS	MEKEFTDYLF	NKSLEIEPRN	PKPLPRFPKK	YSYPLKSPGV	RPSNPRPGTM	
RHPTPLOOEP	RKISYSRIPE	SETESTASAP	NSPR TPLTPP	PASGASSTTD	VCSVFDSDHS	SPFHSSNDTV	
FIQVTLPHGP	RSASVSSISL	TKGTDEVPVP	PPVPPR RRPE	SAPAESSPSK	IMSKHLDSPP	AIPPROPTSK	
AYSPRYSISD	RTSISDPPES	PPLLPPREPV	RTPDVFSSSP	LHLOPPPLGK	KSDHGNAFFP	NSPSPFTPPP	
PQTPSPHGTR	RHLPSPPLTO	EVDLHSIAGP	PVPPR OSTSO	HIPKLPPKTY	KREHTHPSMH	RDGPPLLENA	HSS

10/3/13 9:44 AM

SOS2

MQQAPQPYEF	FSEENSPKWR	GLLVSALRKV	QEQVHPTLSA	NEESLYYIEE	LIFQLLNKLC	MAQPRTVQDV	EERVQKTFPH
PIDKWAIADA	QSAIEKRKRR	NPLLLPVDKI	HPSLKEVLGY	KVDYHVSLYI	VAVLEYISAD	ILK lagnyvf	NIRHYEISQO
DIK VSMCADK	VLMDMFDQDD	IGLVSLCEDE	PSSSGELNYY	DLVRTEIAEE	RQYLRELNMI	IKVFR EAFLS	DR KLFKPSDI
EKIFSNISDI	HELTVKLLGL	IEDTVEMTDE	SSPHPLAGSC	FEDLAEEQAF	DPYETLSQDI	LSPEFHEHFN	KLMARPAVAL
HFQSIADGFK	EAVRYVLPRL	MLVPVYHCWH	YFELLKQLKA	CSEEQEDREC	LNQAITALMN	LQGSMDRIYK	QYSPRRRPGD
PVCPFYSHQL	RSKHLAIKKM	NEIQKNIDGW	EGKDIGQCCN	EFIMEGPLTR	IGAKHERHIF	LFDGLMISCK	PNHGQTR LPG
YSSAEYR LKE	KFVMRKIQIC	DKEDTCEHK <u>H</u>	AFELVSKDEN	SIIFAAKSAE	EKNNWMAALI	SLHYRSTLDR	MLDSVLLKEE
NEQPLRLPSP	EVYRFVVK <u>DS</u>	EENIVFEDNL	OSR SGIPIIK	GGTVVKLIER	LTYHMYADPN	FVRTFLTTYR	SFCKPQELLS
LLIER feipe	PEPTDADK LA	IEK <u>GEQPISA</u>	DLK RFRK <u>EYV</u>	OPVOLR ILNV	FRHWVEHHFY	DFERDLELLE	RLESFISSVR
GKAMKKWVES	IAKIIRRKKQ	AQANGVSHNI	TFESPPPPIE	WHISKPGQFE	TFDLMTLHPI	EIARQLTLLE	SDLYRKVQPS
ELVGSVWTKE	DKEINSPNLL	KMIRHTTNLT	LWFEKCIVEA	ENFEERVAVL	SRIIEILQVF	QDLNNFNGVL	EIVSAVNSVS
VYRLDHTFEA	LQERKR <u>KILD</u>	EAVELSQDHF	KYLVKLKSI	NPPCVPFFGI	YLTNILK <u>TEE</u>	GNNDFLKKKG	KDLINFSKRR
KVAEITGEIQ	QYQNQPYCLR	IEPDMRR <mark>FFE</mark>	NLNPMGSASE	K EFTDYLFNK	SLEIEPRNCK	QPPRFPRKST	FSLKSPGIRP
NTGR <u>HGSTSG</u>	TLR GHPTPLE	REPCKISFSR	IAETELESTV	SAPTSPNTPS	TPPVSASSDL	SVFLDVDLNS	SCGSNSIFAP
VLLPHSKSFF	SSCGSLHK LS	EEPLIPPPLP	PR KKFDHDAS	NSKGNMK <u>SDD</u>	DPPAIPPR QP	PPPKVKPR <u>VP</u>	VPTGAFDGPL
HSPPPPPR D	PLPDTPPPVP	LRPPEHFINC	PFNLQPPPLG	HLHRDSDWLR	DISTCPNSPS	TPPSTPSPRV	PRRCYVLSSS
QNNLAHPPAP	PVPPRQNSSP	HLPKLPPKTY	KRELSHPPLY	RLPLLENAET	PO		

Grb2

httr MEAIAKYDFK ATADDELSFK RGDILKVLNE ECDQNWYKAE LNGKDGFIPK NYIEMKPHPW FFGKIPRAKA EEMLSKQRHD GAFLIRESES APGDFSLSVK
FGNDVQHFKV LRDGAGKYFL WVVKFNSLNE LVDYHRSTSV SRNQQIFLRD IEQMPQQPTY VQALFDFDPQ EDGELGFRRG DFIHVMDNSD PNWWKGACHG
QTGMFPRNYV TPVNRNV

Antibody	Catalog	Dilution	Time
MCEMP1	N/A	1:1000 in 5 % milk in TBST	18 h, 4°C
Phospho-KIT	Cell Signaling, 3391S	1:1000 in 5% BSA in TBST	18 h, 4°C
KIT	Cell Signaling, 3074S	1:2000 in 5% BSA in TBST	18 h, 4°C
SOS1	Cell Signaling, 12409S	1:1000 in 5% BSA in TBST	18 h, 4°C
Grb2	Santa Cruz, C-23	1:1000 in 5% BSA in TBST	18 h, 4°C
4G10	EMD Millipore, 05-321	1:1000 in 5% BSA in TBST	18 h, 4°C
4G10-HRP	EMD Millipore, 16-105	1:1000 in 5% BSA in TBST	18 h, 4°C
P-Tyr-1000	Cell Signaling, 8952S	1:1000 in 5% BSA in TBST	18 h, 4°C
Phospho-lκBα	Cell Signaling, 9241S	1:1000 in 5% BSA in TBST	18 h, 4°C
ΙκΒα	Cell Signaling, 4814S	1:1000 in 5% BSA in TBST	18 h, 4°C
Phospho-MEK1/2	Cell Signaling, 9154S	1:1000 in 5% BSA in TBST	18 h, 4°C
MEK1/2	Cell Signaling, 9122S	1:1000 in 5% BSA in TBST	18 h, 4°C
Phospho-p38	Cell Signaling, 9211S	1:1000 in 5% BSA in TBST	18 h, 4°C
p38	Cell Signaling, 9212S	1:1000 in 5% BSA in TBST	18 h, 4°C
Phospho-JNK	Cell Signaling, 9251S	1:1000 in 5% BSA in TBST	18 h, 4°C
JNK	Cell Signaling, 4668S	1:1000 in 5% BSA in TBST	18 h, 4°C
Phospho-ERK	Cell Signaling, 4370S	1:1000 in 5% BSA in TBST	18 h, 4°C
ERK	Cell Signaling, 4695S or 9101S	1:1000 in 5% BSA in TBST	18 h, 4°C
GST	Santa Cruz, B-14	1:1000 in 5 % milk in TBST	18 h, 4°C
Actin	Santa Cruz, C4	1:1000 in 5 % milk in TBST	18 h, 4°C
Tubulin	Santa Cruz, B7	1:1000 in 5 % milk in TBST	18 h, 4°C
rabbit-Flag	Sigma, F7425	1:1000 in 5 % milk in TBST	18 h, 4°C
mouse-Flag	Sigma, F1804	1:1000 in 5 % milk in TBST	18 h, 4°C
rabbit-HA	Covance, PRB-101P	1:1000 in 5 % milk in TBST	18 h, 4°C
mouse-HA	BioLegend, 16B12	1:1000 in 5 % milk in TBST	18 h, 4°C
mouse Flag-HRP	abcam ab49763, M2	1:4000 in 5 % milk in TBST	1 h, 23°C
mouse HA-HRP	BioLegend 901519, 16B12	1:4000 in 5 % milk in TBST	1 h, 23°C

Supplementary Table 2: List of antibodies used for immunoblotting

mouse V5-HRP	Thermo R961-25	1:5000 in 5 % milk in TBST	1 h, 23°C
mouse IgG-HRP	Cell Signaling, 7076	1:1000 in 5 % milk in TBST	1 h, 23°C
rabbit IgG-HRP	Cell Signaling, 7074	1:1000 in 5 % milk in TBST	1 h, 23°C

Gene	Sense primer (5'-3')	Antisense primer (5'-3')
Mouse Gapdh	GGTCCTCAGTGTAGCCCAAG	AATGTGTCCGTCGTGGATCT
Mouse II4	AGATGGATGTGCCAAACGTCC	AATATGCGAAGCACCTTGGAA
Mouse II5	TCACCGAGCTCTGTTGACAA	CCACACTTCTCTTTTTGGCG
Mouse II6	TATAATCAGGAAATTTGCCTA	GTTAGGAGAGCATTGGAAAT
Mouse II10	GCCAAGCCTTATCGGAAATG	AAATCACTCTTCACCTGCTCC
Mouse II13	TGCGGTTACAGAGGCCATGCA	TGAGGAGCTGAGCAACATCAC
Mouse Tnf	CTTCTGTCTACTGAACTTCGGG	TGATCTGAGTGTGAGGGTCTG
Mouse Ifng	GCTTTGCAGCTCTTCCTCAT	GTCACCATCCTTTTGCCAGT
Mouse Cc/2	CATCCACGTGTTGGCTCA	GATCATCTTGCTGGTGAATGAGT
Mouse Ccl4	GCTCCAAGCCAGCTGTGGTA	CGCTGGAGCTGCTCAGTTC
Mouse Ccl11	CAGATGCACCCTGAAAGCCATA	TGCTTTGTGGCATCCTGGAC
Mouse Ccr5	CGTTCCCCCTACAAGAGACT	ACCCACAAAACCAAAGATGA
Mouse Cxcl10	TGCTGGGTCTGAGTGGGACT	CCCTATGGCCCTCATTCTCAC

Supplementary Table 3: List of qRT-PCR primers

Antibody	Catalog	Dilution	Time
Phospho-JNK	Cell Signaling, 9255S	1:200 in 0.1% BSA in PBST	18 h, 4°C
Phospho-MITF	Millipore Sigma, SAB4503940	1:500 in 0.1% BSA in PBST	18 h, 4°C
Alexa Fluor-488 Goat-anti-Rabbit IgG	Invitrogen, A11008	1:500 in 0.1% BSA in PBST	1 h, 23°C
Alexa Fluor-568 Goat-anti-Rabbit IgG	Invitrogen, A11011	1:500 in 0.1% BSA in PBST	1 h, 23°C
Hoechst 33342	Invitrogen, H3570	1:5000	N/A

Supplementary Table 4: List of antibodies used for immunofluorescence

Antibody	Catalog	Dilution
CD45-APC-Cy7	clone 30-F11; BD, 557659	1:100
KIT(CD117)-PE	clone 2B8; BD, 553355	1:200
FcɛRI-Alexa488	clone MAR-1, Biolegend, 134330	1:200
Mouse Lineage Cocktail-APC	BD, 558074	10 μl / 5x10 ⁵ cells
Ly-6G-APC	clone 1A8; Biolegend, 127614	1:200
Ly-6C-BV650	clone HK1.4; Biolegend, 128049	1:200
CD11b-Alexa488	clone M1/70; BD, 557672	1:200
CD11c-BV421	clone HL3; BD, 562782	1:200
Siglec-F-PE	clone E50-2440; BD, 552126	1:200
LIVE/DEAD Fixable Blue	Thermo Fisher, L34962	1 µl / million cells
CD16/CD32	BD, 553142	1 μg (2 μl) / million cells

Supplementary Table 5: List of antibodies used for flow cytometry







Supplementary Figure 1 MCEMP1 interacts with Grb2-SOS signal complex and induces ITAM-dependent signal transduction.

a, ITAM motif sequence alignment of MCEMP1 from human and mouse. The conserved YENI residue is shown in red font. b, Schematics of TKX1 expression system and identification of SOS1/2 as the phosphorylated MCEMP1 interacting proteins. E. coli TKX1 strain contains elk tyrosine kinase which has broad specificity and efficiently phosphorylates mammalian proteins. TKX1 strain was transformed with GST-tagged plasmids encoding human MCEMP1 cytoplasmic domain (MCEMP1-C) either wild-type (GST-WT) or tyrosine to phenylalanine mutant (GST-YF). Purified GST-tagged MCEMP1 proteins were incubated with HMC-1 cell lysates. MCEMP1 protein complexes were enriched by GST-pulldown and visualized on silver stained-SDS-PAGE. Mass spectrometry identified SOS1/2 from 150 kDa size band in GST-WT lane. c, Identification of Grb2 as the phosphorylated MCEMP1 interacting protein. MCEMP1 proteins were purified from C57 cells expressing vector control (VEC) or wild-type MCEMP1 (WT) by immunoprecipitation (IP) with anti-Flag antibody. MCEMP1 protein complexes were visualized on silver stained-SDS-PAGE. Mass spectrometry identified Grb2 from 25 kDa size band of WT MCEMP1. d. GST-pulldown assay of MCEMP1 interaction with Grb2-SOS1/2 signal complex in an ITAM dependent manner. GST-pulldown elutes and whole cell lysates (WCL) were analyzed by immunoblotting (IB) with the indicated antibodies, e, Effect of SOS SH3 domain inhibitor on MCEMP1 interaction with SOS in 293T cells. f, MCEMP1 tyrosine phosphorylation and its interaction with Grb2 and SOS1 in HMC-1 cells. HMC-1 cells expressing VEC, WT MCEMP1, or YF mutant MCEMP1 were treated with αFlag for the indicated time and cell lysates were IP with anti-Flag antibody. Immunoprecipitates and WCL were analyzed by IB with the indicated antibodies. **g**, Gene expressions of *II6*, *Tnf*, *ccl4*, and *ccl11* in C57, DC2.4, or J774.1 cells after αFlag treatment. Data are representative of at least two independent experiments in **b-f**. Data are presented by mean ± s.e.m. and p-values were determined by two-way ANOVA with Sidak's multiple comparison in g (n=3). ns, not significant.

a *Mcemp1*^{+/+} ATGCATGCATCAGCCTCCCAGGATAAGAACCGGAGGA *Mcemp1*^{-/-} ATGCATGCATCAGCCTCCCAGGA------GGA 11bp deletion





2.5% agarose











Mcemp1^{+/+}

□ Mcemp1^{-/-}

h







Supplementary Figure 2 Generation of *Mcemp1-/-* mice.

a, Genomic DNA sequence of the first coding region of *Mcemp1* from *Mcemp1^{+/+}* or *Mcemp1^{-/-}* littermate mice. 11 base pairs out-of-frame deletion was shown in *Mcemp1^{-/-}* mice. **b**, Genotyping of *Mcemp1^{+/+}* and *Mcemp1^{-/-}* mice by T7 endonuclease I assay. bp, base pair. **c**, Loss of MCEMP1 protein expression in *Mcemp1^{-/-}* mice. Immunohistochemistry staining for MCEMP1 expression in the lungs. Scale bar, 100 µm. **d**, Total cell numbers of *Mcemp1^{+/+}* or *Mcemp1^{-/-}* bone marrow-derived macrophages (BMDM) cultured with macrophage colony-stimulating factor (MCSF) for 7 days (n=4 per group). **e**,**f**, Percentages of KIT/FccRI double-positive PC (e) or BM (f) from *Mcemp1^{-/-}* BM cultured with either SCF (g) or IL-3 (h) for the indicated days (n=4 per group). **i**, Representative flow cytometry plots illustrating the gating strategy to identify KIT and FccRI double positive cells (KIT+FccRI+) and KIT single positive cells (KIT+FccRI-). Heatmaps of top DEGs of KIT+FccRI+ PCMC versus KIT+FccRI- cells and lung mast cells (MC) versus other lung cells. Images are representative of two independent experiments in **b** and **c**. Data are presented as violin plots with lines at median and quartiles in **d-h**. *P*-values were determined by two-tailed unpaired *t*-test in **d** and by two-way ANOVA with Sidak's multiple comparison in **e-h**. ns, not significant.



MCEMP1 WT

MCEMP1 YF

Supplementary Figure 3 MCEMP1 enhances KIT autophosphorylation.

a, Co-immunoprecipitation assay for human and mouse MCEMP1 and KIT interaction in 293T cells. **b**, Co-immunoprecipitation assay of human MCEMP1 and mouse KIT in 293T cells. **c**, Co-immunoprecipitation assay of MCEMP1 and KIT in C57 cells expressing vector (VEC), wild-type MCEMP1 (WT), or YF mutant (YF). Cell lysates were immunoprecipitated with anti-Flag antibody or IgG control. **d**, Co-immunoprecipitation assay for MCEMP1 interaction with KIT truncation construct (JM-KD1) in 293T cells. **e**, Immunoblot analysis of KIT phosphorylation upon α Flag stimulation in C57 cells. **f**, MCEMP1 oligomers captured by disuccinimidyl suberate (DSS) or bis(sulfosuccinimidyl) suberate (BS³) non-cleavable crosslinkers. C57 cells expressing MCEMP1 WT or YF mutant were stimulated with control, α Flag, or SCF and then subjected to 2.5 mM DSS or BS³ crosslinking for 30 min. Crosslinked cells were used for immunoblotting with anti-Flag antibody. Data are representative of at least two independent experiments in **a-f**.



Supplementary Figure 4 Altered gene expressions in *Mcemp1*-deficient PCMC and MCEMP1 expression in the lungs during OVA stimulation.

a, RNA-seq volcano plot of DEGs from *Mcemp1-/-* PCMC versus *Mcemp1+/+* PCMC. The volcano plot is presented as fold change in gene expression (\log_2 Fold change) against significance of change (- $\log_{10} P$ -value). The significantly upregulated genes are indicated in red and downregulated gene are indicated in blue. The cutoff of significant DEGs is a |Fold change| > 2 and *P*-value < 0.05. *p*-values in b-d were determined by Gene Specific Analysis (GSA) in Partek Flow software. **b**, IPA network association of DEGs from *Mcemp1-/-* PCMC versus *Mcemp1+/+* PCMC. Downregulated and upregulated genes are shown in green and red, respectively. **c**, Immunohistochemistry staining for MCEMP1 expression in the lung challenged with OVA. Scale bar, 100 µm. **d**, Immunofluorescent staining of MCEMP1 expression in the lung and gut of *Mcemp1+/+* and *Mcemp1-/-* mice challenged with OVA. Anti-MCEMP1 antibody (red) or DAPI (blue). Scale bar, 50 µm. Data are representative of two independent experiments in **c**,**d**.



Supplementary Figure 5 MCEMP1 exacerbates airway inflammation in OVA-induced chronic asthma model.

a, Representative flow cytometry plots illustrating the gating strategy to identify eosinophils (Eos), alveolar macrophages (AM), neutrophils (Neu), and Ly-6C-positive inflammatory monocytes (Mo). **b**, Percentages and absolute numbers of neutrophils in the lung were determined by flow cytometry (n=3 per group). **c**, Representative images of toluidine blue staining for mast cell counts in lung section. Eosin was used for counterstaining. Scale bar, 100 µm. **d**, Representative images of Masson's trichrome staining for collagen deposition. Collagen fibers were stained blue in the perivascular and parabronchial tissues. Scale bar, 100 µm. **e**, Percentages and absolute numbers of Ly-6C+ inflammatory monocytes and alveolar macrophages in the lungs were determined by flow cytometry (n=6 for saline group. n=3-4 for OVA group). Data are representative of two independent experiments in **c** and **d**. Data are presented as violin plots with lines at median and quartiles and *p*-values were determined by two-way ANOVA with Sidak's multiple comparison in **b** or by one-way ANOVA with Tukey's multiple comparison in **e**. ns, not significant.





a, Multiplex analysis of cytokines and growth factors in the BAL (n=3 for saline group, n=4 for OVA group). Data are presented as violin plots with lines at median and quartiles and *p*-values were determined by two-way ANOVA with Sidak's multiple comparison. ns, not significant. **b**, The total number of significant DEGs from RNA-seq. The cutoff of significant DEGs is a |Fold change| > 2 and *P*-value < 0.05. **c**,**d**, The volcano plots of DEGs from OVA-challenged versus saline-treated *Mcemp1*^{+/+} mice (c) or OVA-challenged versus saline-treated *Mcemp1*^{-/-} mice (d). The volcano plot is presented as fold change in gene expression (log₂ Fold change) against significance of change (-log₁₀ *P*-value). The significantly upregulated genes are denoted in red and downregulated gene are indicated in blue. *p*-values were determined by Gene Specific Analysis (GSA) in Partek Flow software

in **b-d**.



Supplementary Figure 7 The effect of MCEMP1 deficiency on lung resistance and lung ventilation.

a,**b**,**c** Lung function parameters, resistance of respiratory system (Rrs), newtonian resistance (Rn, central airway), and tissue damping (G, alveoli) in response to the indicated concentrations of methacholine were measured 1 day after the eighth intranasal challenge with OVA or saline (n=3 for saline group, n=4 for OVA group). **d**,**e**, Ventilation metrics; ventilation heterogeneity (VH) of small or large scale (n=3 per group). Data are presented as mean ± s.d. in **a**,**b**,**c** and as violin plots with lines at median and quartiles in **d**,**e**. *P*-values were determined by two-way ANOVA with Sidak's multiple comparison in **d**,**e**. ns, not significant.















Fig. 3b









SFig. 1f







MCEMP1 YF