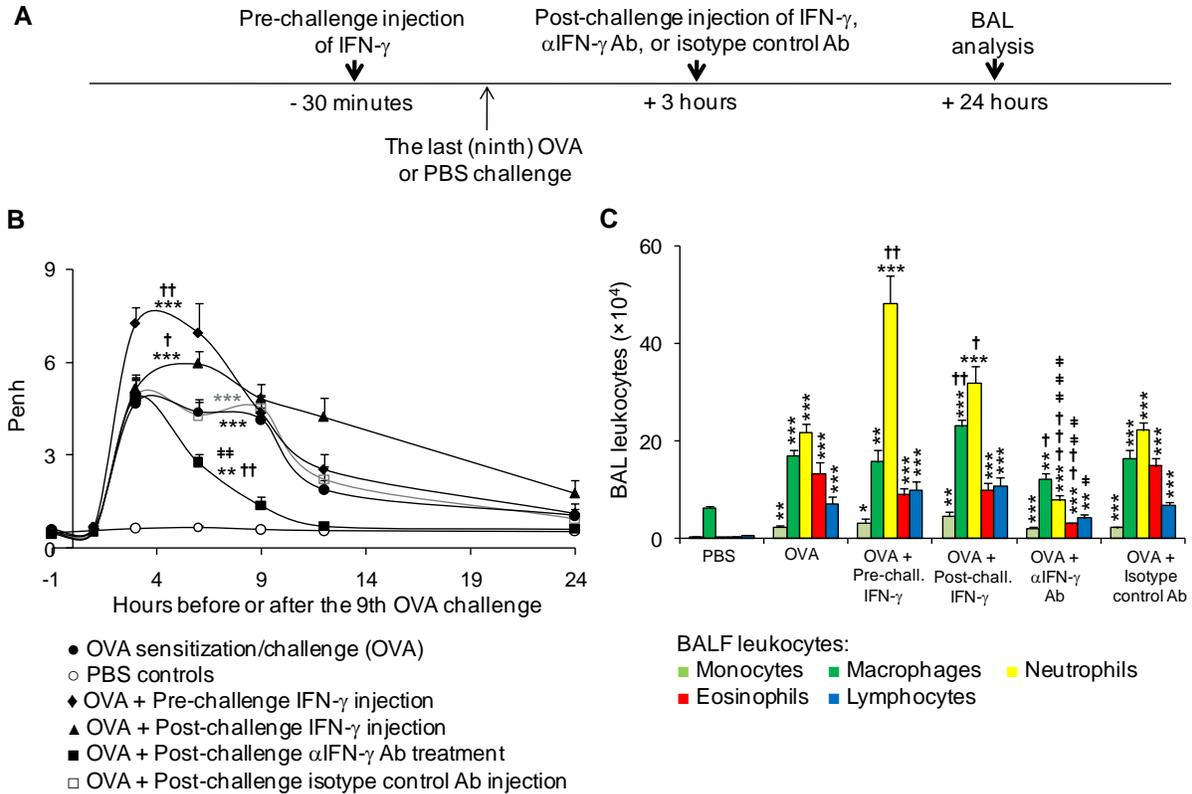
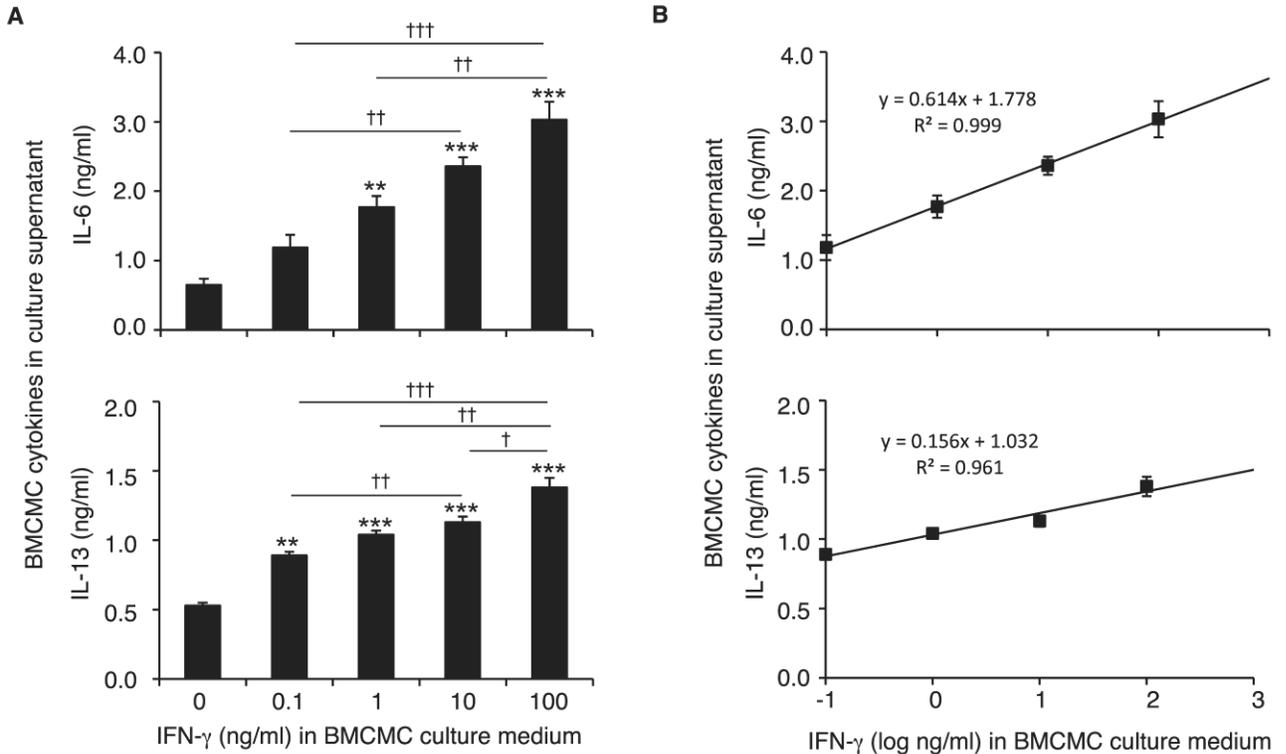


Supplemental Figures and Tables, and Supplemental Methods for Supplemental Figures 7-12 and Supplemental Tables 2 and 3.



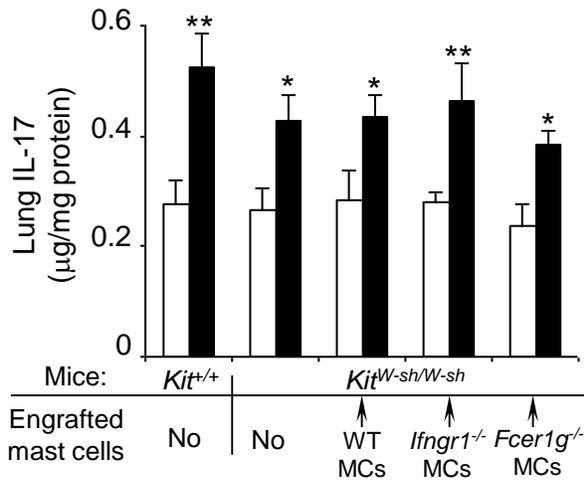
Supplemental Figure 1

Effects of treatment with IFN- γ or a neutralizing monoclonal antibody to (α IFN- γ Ab) on the development of antigen (OVA)-induced changes in Penh responses and numbers of leukocytes in the bronchoalveolar lavage (BAL) fluid of C57BL/6-*Kit*^{+/+} wild-type (WT) mice in our standard model of chronic allergic inflammation of the airways. (A) Treatment protocols: Different groups of WT C57BL/6/J mice received either an intra-peritoneal (*i.p.*) injection of IFN- γ (5 μ g per mouse) at 30 min before or 3 h after the last (ninth) OVA or PBS challenge or received an *i.p.* injection of α IFN- γ Ab or an isotype-matched control Ab (100 μ g per mouse) at 3 h after the last (ninth) OVA or PBS challenge; (B) Changes in Penh measured 1 h before and 1, 3, 6, 9, 12, and 24 h after the ninth OVA or PBS challenge in mice that were sensitized and challenged with OVA (OVA/OVA) or mock sensitized and challenged with PBS (PBS controls); (C) Numbers of leukocytes in BAL fluid recovered from the lungs 24 h after the ninth OVA or PBS challenge. * P < 0.05, ** P < 0.01, *** P < 0.001 versus PBS control group; † P < 0.05, †† P < 0.01, ††† P < 0.001 versus OVA/OVA group; for α IFN- γ Ab-treated group: ‡ P < 0.05, ‡‡ P < 0.01, ‡‡‡ P < 0.001 versus group treated with isotype control Ab. Data are presented as mean + s.e.m. (n = 5 per group). (B) ANOVA; (C) unpaired Student's *t*-test (2-tailed).



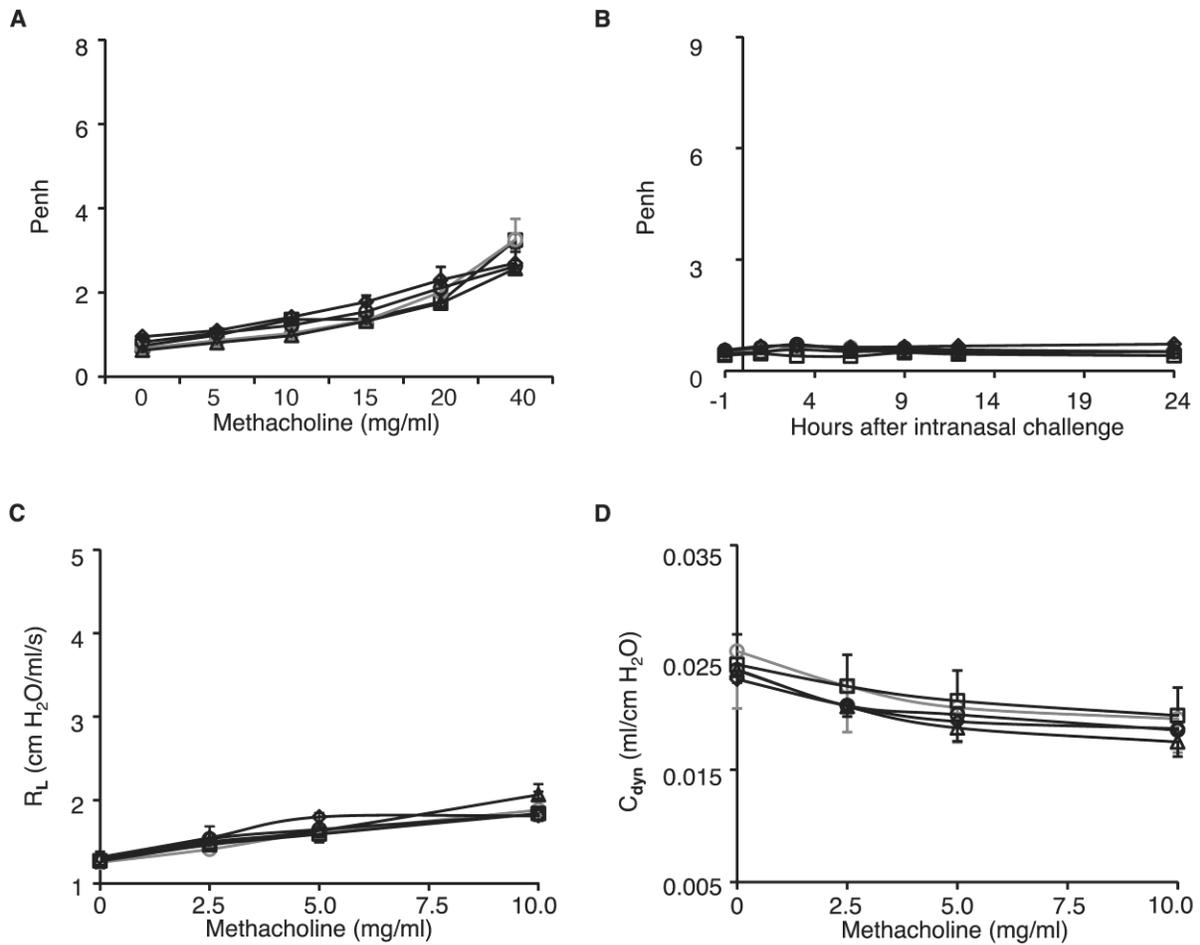
Supplemental Figure 2

Influence of IFN- γ on the production of cytokines by mast cells *in vitro*. (A) The culture supernatants of anti-DNP IgE-sensitized BMCMCs from wild type C57BL/6 mice were collected 24 h after addition of DNP (10 ng/ml) or DNP (10 ng/ml) plus various concentrations of IFN- γ . Data were calculated from results pooled from three independent experiments, each of which gave similar results. ** $P < 0.01$, *** $P < 0.001$ vs. values from the corresponding BMCMCs stimulated with 10 ng/ml DNP alone (no added IFN- γ). † $P < 0.05$, †† $P < 0.01$, ††† $P < 0.001$ vs. group indicated. $n = 3$ per group. (B) The dose response curves representing the correlation between the concentration of IL-6 (top) or IL-13 (bottom) in the BMCMC culture supernatants and the concentration of IFN- γ added to the culture medium.



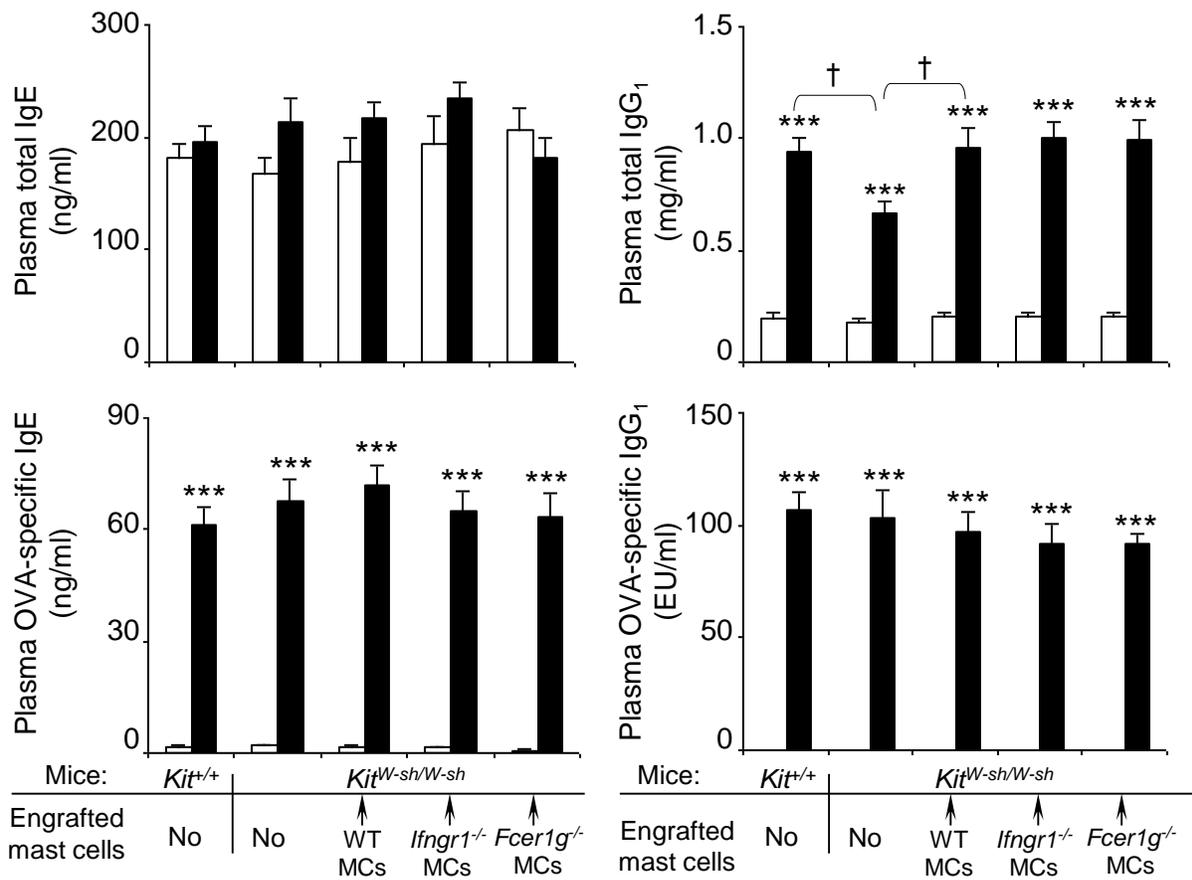
Supplemental Figure 3

IL-17 level in the lung tissues. Tissues were sampled 24 h after the ninth OVA or PBS challenge. Open bars, PBS-treated groups; solid bars, OVA-sensitized and challenged groups. * $P < 0.05$, ** $P < 0.01$ versus values for corresponding PBS-treated control group (unpaired Student's t -test, 2-tailed). Data are presented as mean + s.e.m. ($n = 6-10$ per group).



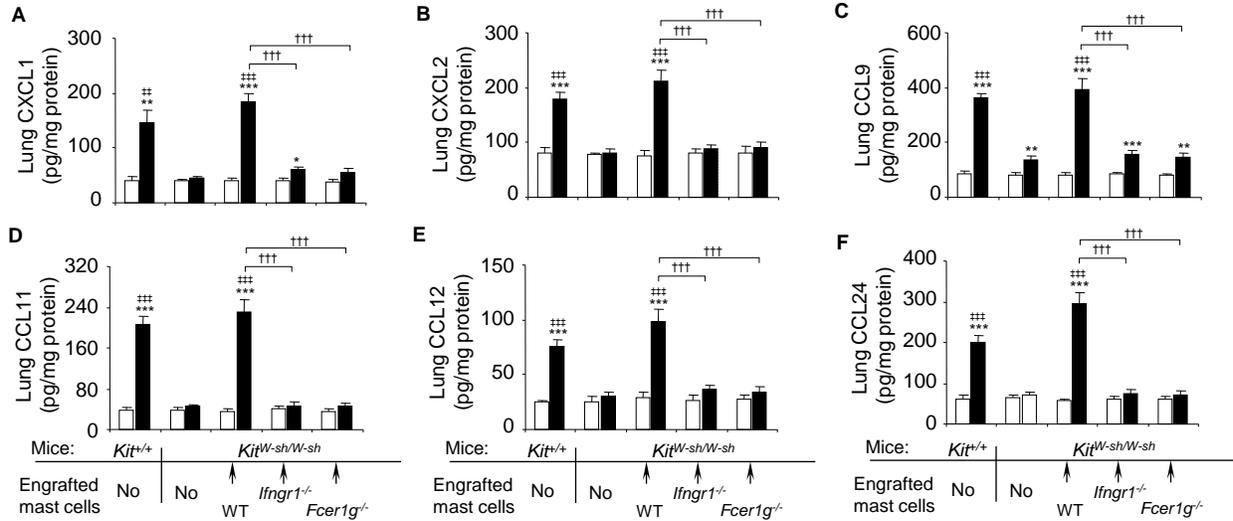
Supplemental Figure 4

Airway responses following intranasal challenge with PBS in mice mock sensitized with PBS. **(A)** Penh responses to aerosolized methacholine measured 24 h after the eighth PSB challenge. **(B)** PBS challenge-induced changes in Penh measured 1 h before and 1, 3, 6, 9, 12, and 24 hours after the ninth OVA or PBS challenge. **(C-D)** Changes in R_L and C_{dyn} to aerosolized methacholine administered 24 h after the ninth PBS challenge. Data are from PBS-treated WT C57BL/6 (empty grey circles), mast cell-deficient C57BL/6-*Kit*^{W-sh/W-sh} (empty black squares), WT C57BL/6 BMCMCs → C57BL/6-*Kit*^{W-sh/W-sh} (empty black circles), *Ifngr1*^{-/-} BMCMCs → C57BL/6-*Kit*^{W-sh/W-sh} (empty black diamonds), or *Fcer1g*^{-/-} BMCMCs → C57BL/6-*Kit*^{W-sh/W-sh} (empty black triangles) mice, $n = 6$ to 12 per group (**A** and **B**); $n = 4$ to 6 per group (**C** and **D**). The values for the PBS-treated WT C57BL/6 mice and mast cell-deficient C57BL/6-*Kit*^{W-sh/W-sh} mice are also shown in Figure 4, for comparison to the values for OVA-sensitized and OVA-challenged groups.



Supplemental Figure 5

Plasma levels of total IgE/IgG₁ and antigen-specific IgE/IgG₁. Plasma concentrations of total or OVA-specific IgE and IgG₁ antibodies in C57BL/6-*Kit*^{+/+} wild-type mice, mast cell-deficient C57BL/6-*Kit*^{W-sh/W-sh} mice, or C57BL/6-*Kit*^{W-sh/W-sh} mice engrafted with BMCMCs derived from C57BL/6 wild-type mice (WT MCs), C57BL/6-*Ifngr1*^{-/-} mice (*Ifngr1*^{-/-} MCs) or C57BL/6-*Fcer1g*^{-/-} mice (*Fcer1g*^{-/-} MCs) that were OVA-sensitized and challenged (solid bars) or treated with PBS (open bars). Blood was sampled 24 h after the 9th OVA or PBS challenge. ****P* < 0.001 versus values for corresponding PBS-treated control group; †*P* < 0.05 versus the group indicated (unpaired Student's *t*-test). Data are presented as mean + s.e.m. (*n* = 6-10 per group).



Supplemental Figure 6

Chemokine levels in the lung. The protein levels of a panel of chemokines CXCL1 (A), CXCL2 (B), CCL9 (C), CCL11 (D), CCL12 (E), and CCL24 (F) measured in the lungs 24 h after the ninth OVA or PBS challenge. Data are from WT C57BL/6 (*Kit*^{+/+}) mice, mast cell-deficient C57BL/6-*Kit*^{W-sh/W-sh} (*Kit*^{W-sh/W-sh}) mice, WT BMCMCs→C57BL/6-*Kit*^{W-sh/W-sh} mice, *Ifngr1*^{-/-} BMCMCs→C57BL/6-*Kit*^{W-sh/W-sh} mice, or *Fcgr1g*^{-/-} BMCMCs→C57BL/6-*Kit*^{W-sh/W-sh} mice treated with OVA (black bars), and the corresponding PBS-treated control mice (white bars). **P* < 0.05, ***P* < 0.01, ****P* < 0.001 versus the corresponding PBS controls; ##*P* < 0.01, ###*P* < 0.001 versus OVA-sensitized and challenged *Kit*^{W-sh/W-sh} mice; ††† *P* < 0.001 versus group indicated (unpaired Student's *t*-test, 2-tailed). Data are presented as mean + s.e.m. (*n* = 6-10 per group).

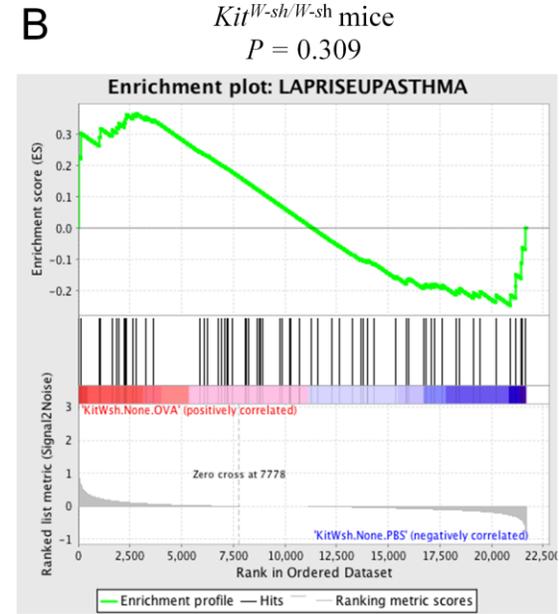
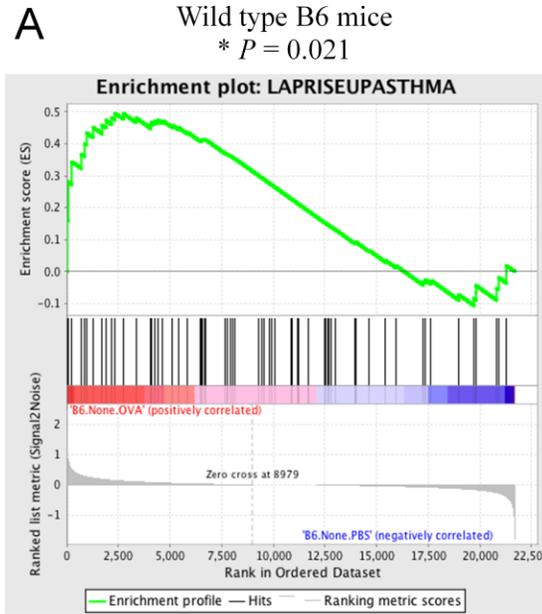
Supplemental Methods for Gene Set Enrichment Analysis (data shown in Supplemental Figures 7-12 Supplemental Methods for Gene Set Enrichment Analysis (data shown in Supplemental Figures 7-12 and Supplemental Tables 2 and 3)

Mouse gene expression arrays were processed using GCRMA implemented in Bioconductor for R (1, 2) to provide probe intensities. The data were entered into the public repository, the Gene Expression Omnibus, with an accession number of GSE27066. To identify a set of genes upregulated in human asthma, we obtained a previously published publicly-available gene expression dataset (3) measuring gene expression in bronchial biopsies from four patients with asthma and four subjects without asthma. The intensity levels were quantile normalized and differential expression of probes was detected using Significance Analysis of Microarrays (4). The probes were matched to genes using AILUN (5), and a set of 96 genes were found to have significant up-regulation of expression in the human asthma samples (*P* value < 0.01). We considered these 96 genes as a “gene set” or “signature” reflecting genes up-regulated in human asthma. Employing the commonly used non-parametric, rank based tool, Gene Set Enrichment Analysis (GSEA version 2) (6), we looked for enrichment in differential expression in the mouse samples of these genes up-regulated in human asthma. Of the 96 genes in our asthma “gene set”, GSEA identified 67 homologues measured on our microarrays. GSEA calculates an enrichment score (very similar to a Kolmogorov-Smirnov statistic), giving weight to highly differentially expressed genes (highly ranked relative to other genes) in the gene set of interest. The significance of this enrichment is calculated using a permutation test over all samples to obtain a *P* value.

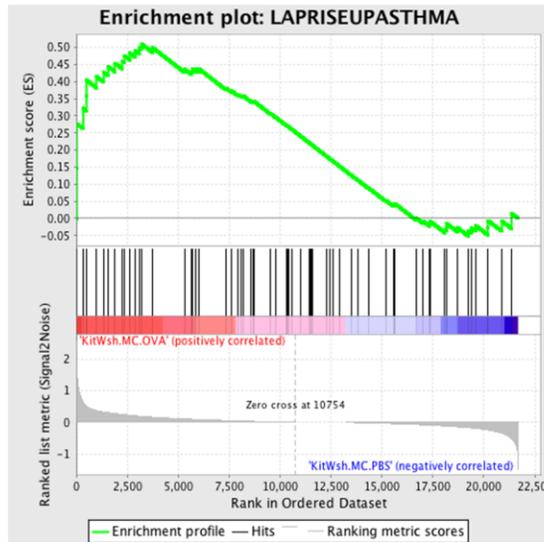
Supplemental References

1. Gentleman, R.C., Carey, V.J., Bates, D.M., Bolstad, B., Dettling, M., Dudoit, S., Ellis, B., Gautier, L., Ge, Y., Gentry, J., et al. 2004. Bioconductor: open software development for computational biology and bioinformatics. *Genome Biology* 5:R80.
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4. Tusher, V.G., Tibshirani, R., and Chu, G. 2001. Significance analysis of microarrays applied to the ionizing radiation response. *Proc Natl Acad Sci U S A* 98:5116-5121.
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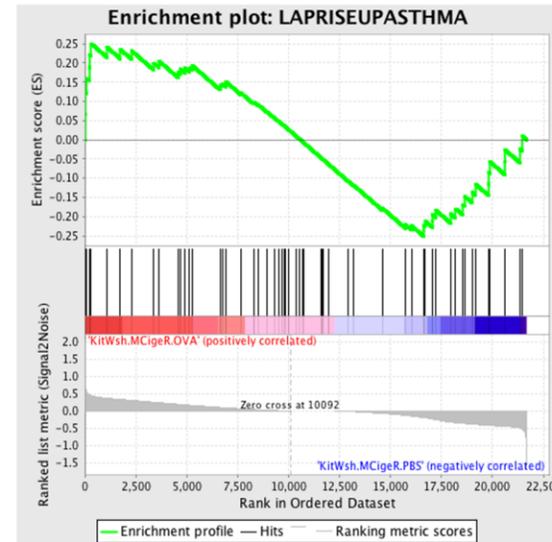
Supplemental Figure 7



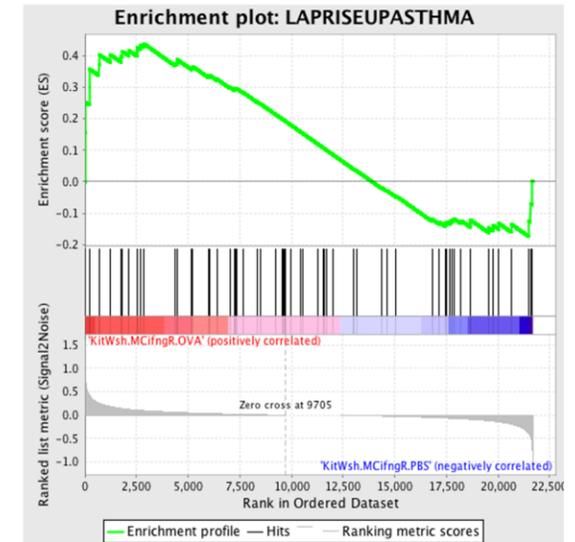
C WT BMCMCs \rightarrow $Kit^{W-sh/W-sh}$ mice
* $P = 0.020$



D $Fcer1g^{-/-}$ BMCMCs \rightarrow $Kit^{W-sh/W-sh}$ mice
 $P > 0.73$



E $Ifngr1^{-/-}$ BMCMCs \rightarrow $Kit^{W-sh/W-sh}$ mice
 $P = 0.089$

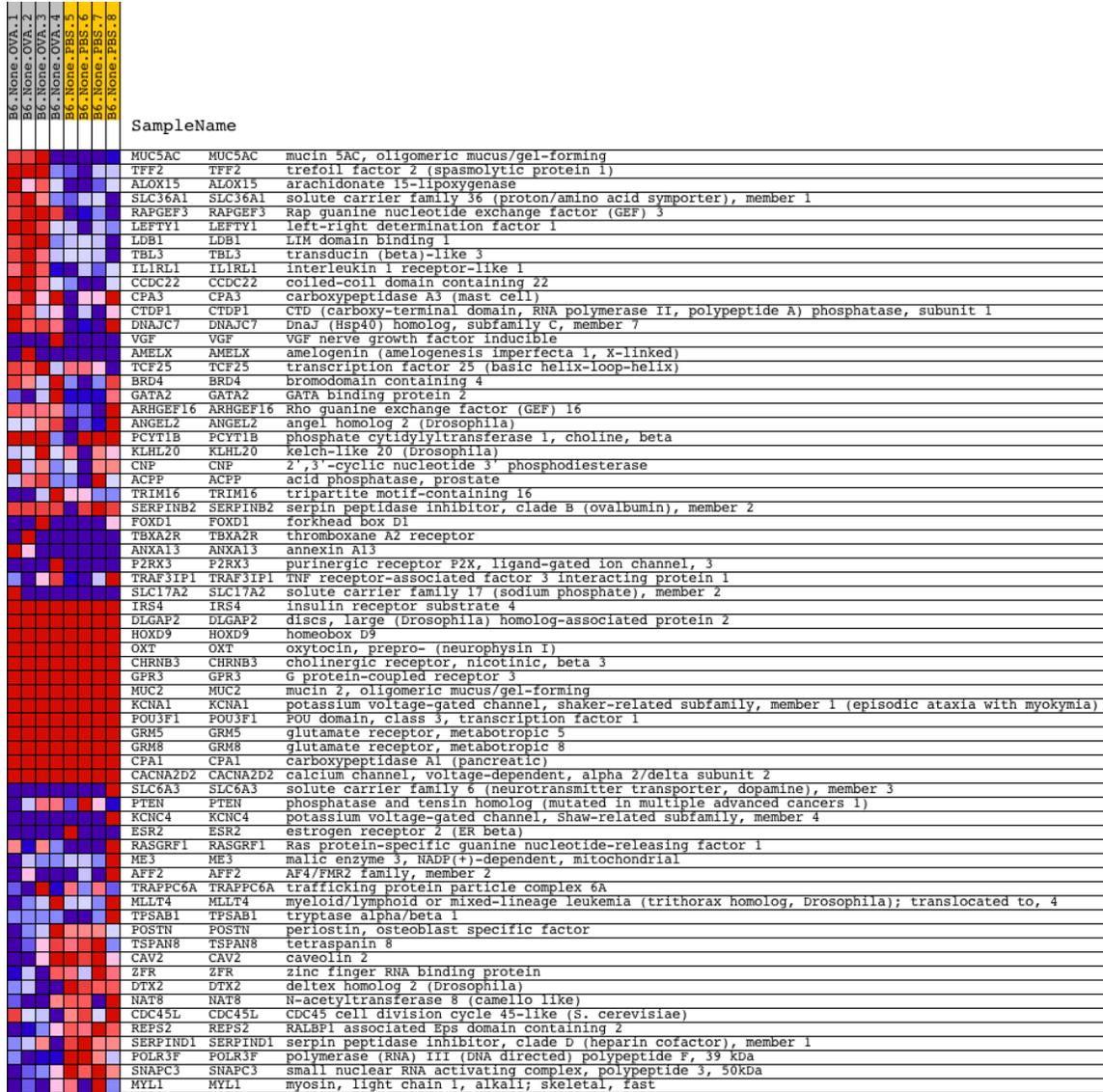


Supplemental Figure 7

Gene Set Enrichment Analysis comparing genes upregulated in bronchial biopsy specimens of human patients with asthma and genes upregulated in OVA-sensitized and OVA-challenged mice in our standard model of chronic allergic inflammation of the airways. Whole lung samples of OVA-sensitized and OVA-challenged mice were contrasted with samples from the corresponding control mice treated with PBS, based on results of gene expression analysis using Affymetrix Mouse Genome 430 2.0 arrays. These mouse expression profiles were examined against a set of genes found to be upregulated in human asthma (suppl. ref. 3 [Laprise, C., Sladek, R., Ponton, A., Bernier, M.C., Hudson, T.J., and Laviolette, M. Functional classes of bronchial mucosa genes that are differentially expressed in asthma. *BMC Genomics*. 2004;5(1):21]). Only the wild type B6-*Kit*^{+/+} mice (**A**) and the WT BMCMCs→*Kit*^{W-sh/W-sh} mice (**C**) were found to be significantly ($P < 0.05$) enriched for increased expression of genes upregulated in human asthma. By contrast, mast cell-deficient *Kit*^{W-sh/W-sh} mice (**B**) and *Kit*^{W-sh/W-sh} mice that had been engrafted with BMCMCs lacking either FcεR1γ (**D**) or IFN-γR1 (**E**) were not significantly enriched for increased expression of genes upregulated in human asthma.

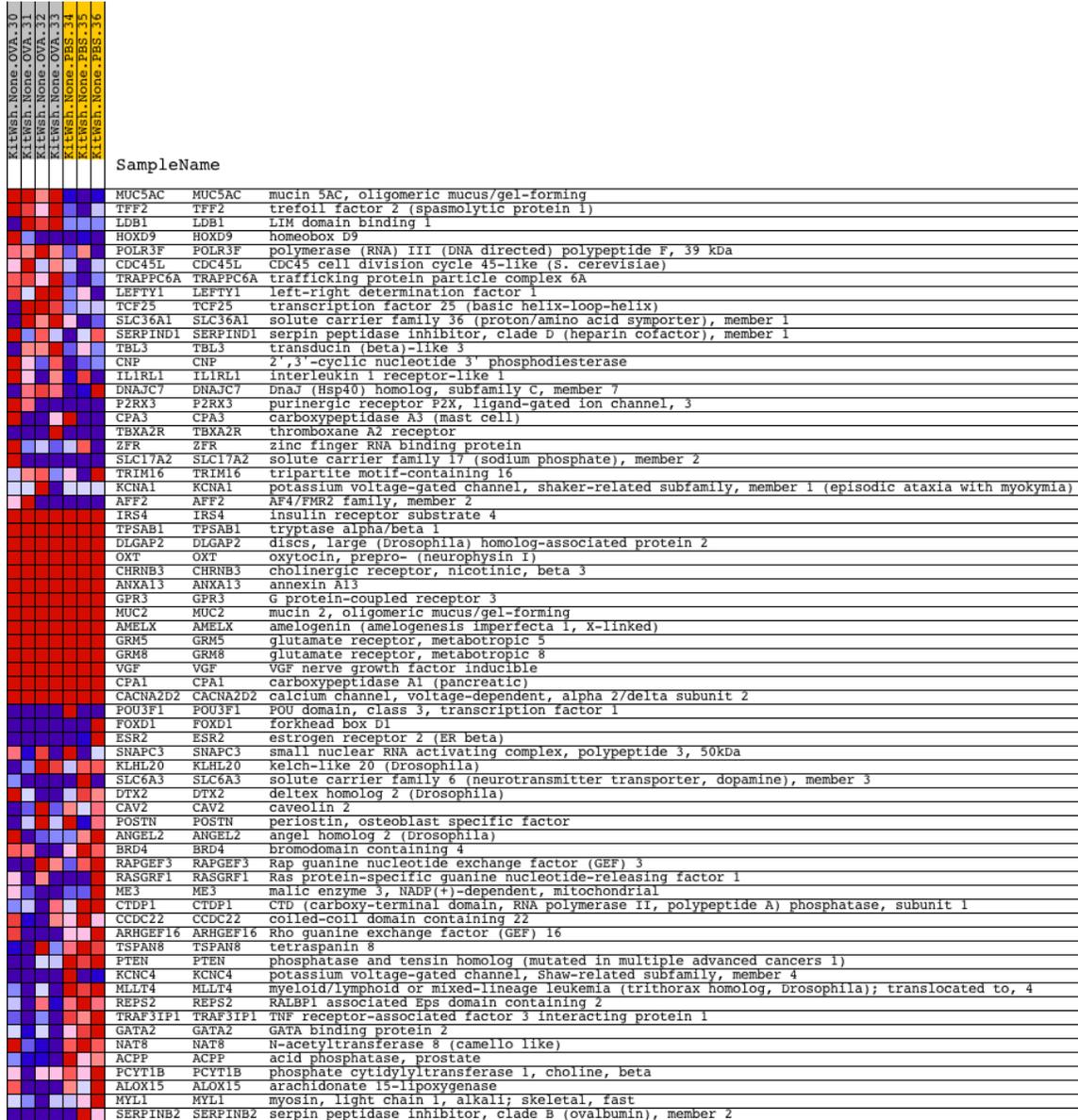
Supplemental Figure 8

Heatmap of expression levels for the 67 mouse homologues of the genes up-regulated in human asthma for the wild type mice as reported by GSEA. The gray columns represent samples taken from WT C57BL/6 mice challenged with OVA (B6.None.OVA.1-4) and the yellow columns represent control samples from WT C57BL/6 mice challenged with PBS (B6.None.PBS.5-8).



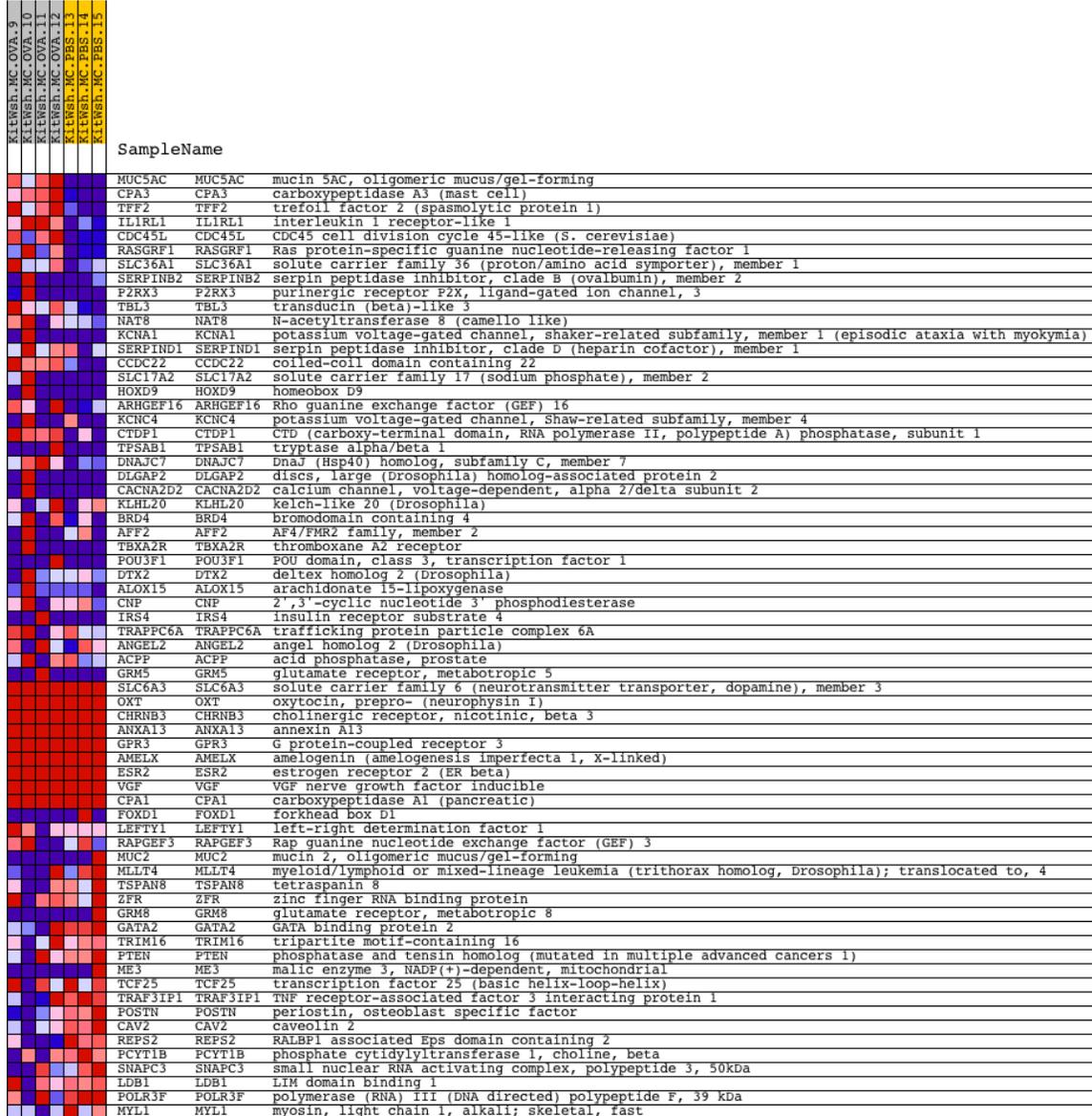
Supplemental Figure 9

Heatmap of expression levels for the 67 mouse homologues of the genes up-regulated in human asthma for mast cell-deficient C57BL/6-*Kit*^{W-sh/W-sh} mice as reported by GSEA. The gray columns represent samples taken from C57BL/6-*Kit*^{W-sh/W-sh} mice challenged with OVA (KitWsh.None.OVA.30-33) and the yellow columns represent control C57BL/6-*Kit*^{W-sh/W-sh} mice challenged with PBS (KitWsh.None.PBS.34-36).



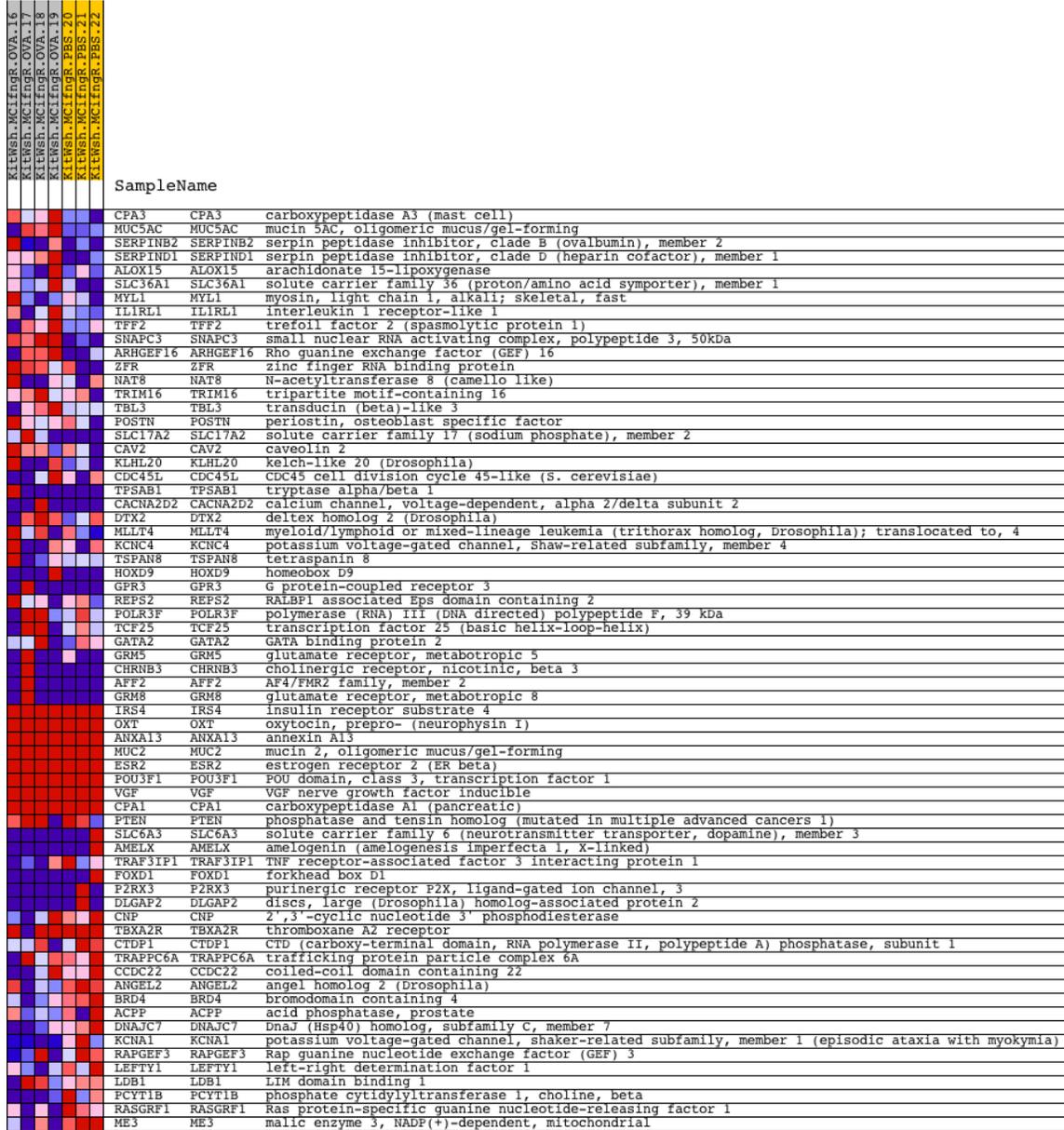
Supplemental Figure 10

Heatmap of expression levels for the 67 mouse homologues of the genes up-regulated in human asthma for mast cell-deficient C57BL/6-*Kit*^{W-sh/W-sh} mice engrafted with bone marrow-derived cultured mast cells (BMCMCs) from C57BL/6 wild type mice. The gray columns represent samples taken from C57BL/6 BMCMC engrafted C57BL/6-*Kit*^{W-sh/W-sh} mice challenged with OVA (KitWsh.MC.OVA.9-12), and the yellow columns represent control WT C57BL/6 BMCMC engrafted C57BL/6-*Kit*^{W-sh/W-sh} mice challenged with PBS (KitWsh.MC.PBS.13-15).



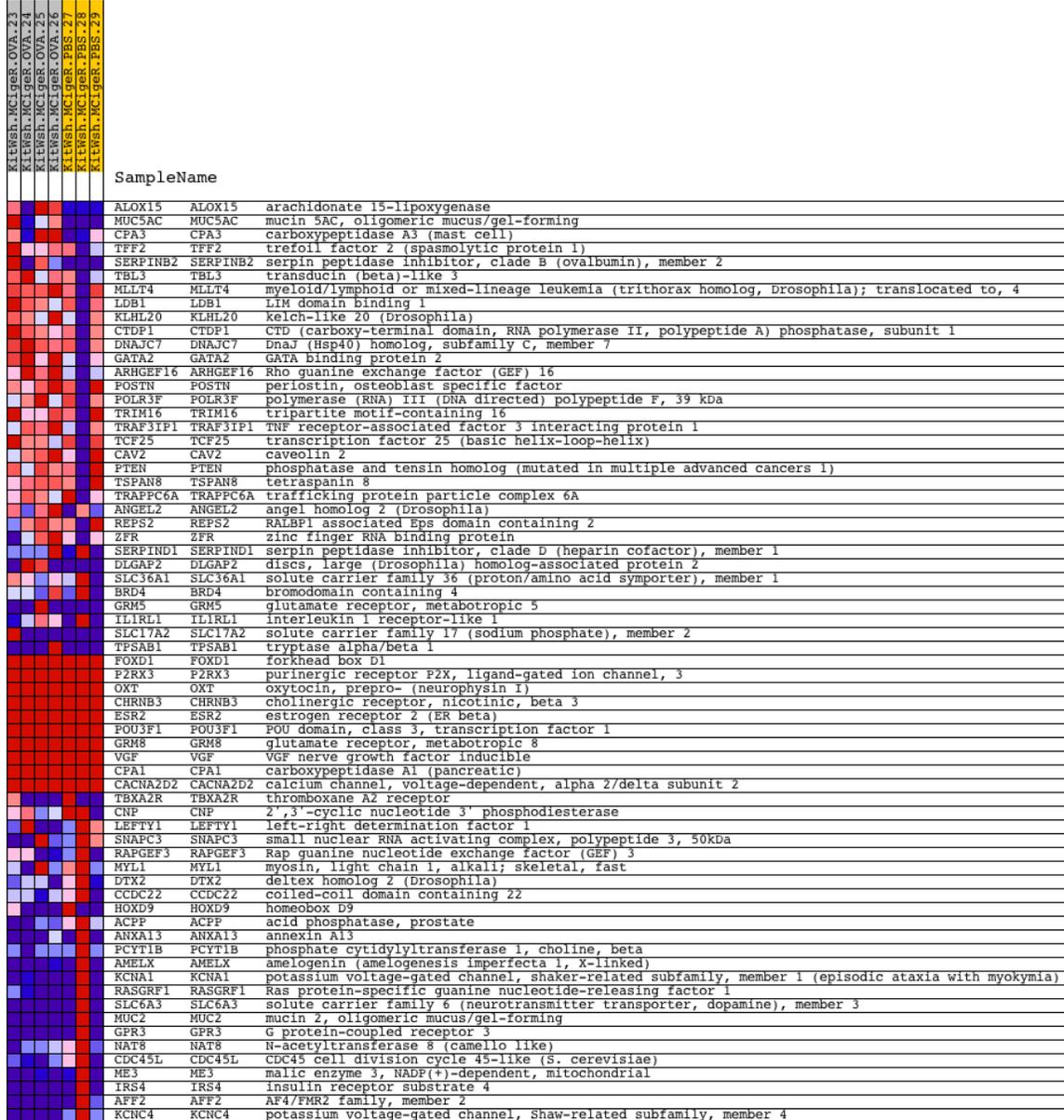
Supplemental Figure 11

Heatmap of expression levels for the 67 mouse homologues of the genes up-regulated in human asthma for mast cell-deficient C57BL/6-*Kit*^{W-sh/W-sh} mice engrafted with bone marrow-derived cultured mast cells (BMCMCs) from C57BL/6 mice deficient in the interferon gamma receptor (*Ifngr1*^{-/-}). The gray columns represent samples taken from *Ifngr1*^{-/-} BMCMC engrafted C57BL/6-*Kit*^{W-sh/W-sh} mice challenged with OVA (KitWsh.MCifngR.OVA.16-19) and the yellow columns represent control *Ifngr1*^{-/-} BMCMC engrafted C57BL/6-*Kit*^{W-sh/W-sh} mice challenged with PBS (KitWsh.MCifngR.PBS.20-22).



Supplemental Figure 12

Heatmap of expression levels for the 67 mouse homologues of the genes up-regulated in human asthma for mast cell-deficient C57BL/6-*Kit*^{W-sh/W-sh} mice engrafted with bone marrow-derived cultured mast cells (BMCMCs) from C57BL/6 mice deficient in the signaling γ chain shared by Fc ϵ RI and Fc γ RIII (*Fcer1g*^{-/-}). The gray columns represent samples taken from *Fcer1g*^{-/-} BMCMC engrafted C57BL/6-*Kit*^{W-sh/W-sh} mice challenged with OVA (KitWsh.MCigeR.OVA.23-26) and the yellow columns represent control *Fcer1g*^{-/-} BMCMC engrafted C57BL/6-*Kit*^{W-sh/W-sh} mice challenged with PBS (KitWsh.MCigeR.OVA.PBS.27-29).



Supplemental Table 1. Dependence of features of this mouse model of chronic asthma on mast cells (MC) or on MC expression of IFN- γ R1 (MC IFN- γ R1) or Fc ϵ RI γ (MC Fc ϵ RI γ).

Increased in lungs of OVA-sensitized and challenged mice	Dependence ^A		
	MC	MC IFN- γ R1	MC Fc ϵ RI γ
IFN- γ & IL-17	No	0	0
IL-6 & IL-13	+++	+++	+++
IL-33	+++*	##	##
CXCL1	+++	##	+++
CXCL2	+++	+++	+++
CCL9	+++*	##	##
CCL11, CCL12 & CCL24	+++	+++	+++
Tissue mast cells	N/A	0	+++
Tissue neutrophils	+++	##	##
Tissue eosinophils	+++*	##	##
Leukocytes in BAL fluid ^B	+++	‡ or ##	‡ or ##
Airway response to antigen	+++	## or +++	## or +++
AHR to methacholine	+++	## or +++	## or +++
Collagen	+++	+++	+++
Airway goblet cells	+++	‡	‡
TIPM-1	+++	##	##
Integrin α 7	+++	+++	‡
MARCO	+++	+++	0
Arginase-1	+++	+++	+++
<i>Saa3</i> mRNA	+++	##	##

^A All listed features of the model except lung levels of IFN- γ and IL-17 were observed in OVA-sensitized and challenged *Kit*^{+/+} mice but were absent or only weakly expressed in OVA-sensitized and challenged genetically mast cell-deficient *Kit*^{W-sh/W-sh} mice. “MC dependence” is defined as the extent to which the expression of a specific feature in OVA sensitized and challenged *Kit*^{W-sh/W-sh} mice was restored to *Kit*^{+/+} levels in *Kit*^{W-sh/W-sh} mice which were engrafted with wild type *Kit*^{+/+} BMCMCs. “Mast cell IFN γ -R1 dependence” is defined as the extent to which expression of that feature in OVA-sensitized and challenged mice was stronger in wild type (WT) BMCMC-engrafted *Kit*^{W-sh/W-sh} (WT BMCMC \rightarrow *Kit*^{W-sh/W-sh}) mice versus *Ifngr1*^{-/-} BMCMC-engrafted (*Ifngr1*^{-/-} BMCMC \rightarrow *Kit*^{W-sh/W-sh}) mice; “Mast cell Fc ϵ RI γ

dependence” is defined as the extent to which expression of that feature in OVA-sensitized and challenged mice was stronger in WT BMCMC→*Kit*^{W-sh/W-sh} mice versus *Fcer1g*^{-/-} BMCMC-engrafted mice (*Fcer1g*^{-/-} BMCMC→*Kit*^{W-sh/W-sh}).

^B Results were different for different types of leukocytes.

No: Values in OVA-sensitized and challenged WT mice were significantly elevated ($P < 0.05$) versus corresponding values in PBS-treated mice, but not significant (N.S., $P > 0.05$) versus OVA-sensitized and challenged *Kit*^{W-sh/W-sh} mice.

+++ In OVA-sensitized and challenged mice, responses in WT BMCMC→*Kit*^{W-sh/W-sh} mice N.S. versus those in WT *Kit*^{+/+} mice and significantly higher than those in MC-deficient *Kit*^{W-sh/W-sh} mice.

In OVA-sensitized and challenged mice, significant responses (versus corresponding values in PBS-treated mice) in WT BMCMC→*Kit*^{W-sh/W-sh} mice and responses in *Ifngr1*^{-/-} or *Fcer1g*^{-/-} BMCMC→*Kit*^{W-sh/W-sh} mice N.S. versus those in the corresponding PBS-treated controls.

In OVA-sensitized and challenged mice, significant responses (versus corresponding values in PBS-treated mice) in WT BMCMC→*Kit*^{W-sh/W-sh} mice and responses in *Ifngr1*^{-/-} or *Fcer1g*^{-/-} BMCMC→*Kit*^{W-sh/W-sh} mice significantly higher than those in the corresponding PBS-treated mice but < 50% those in WT BMCMC→*Kit*^{W-sh/W-sh} mice.

In OVA-sensitized and challenged mice, significant responses (versus corresponding values in PBS-treated mice) in WT BMCMC→*Kit*^{W-sh/W-sh} mice and responses in *Ifngr1*^{-/-} or *Fcer1g*^{-/-} BMCMC→*Kit*^{W-sh/W-sh} mice significantly higher than those in the corresponding PBS-treated mice and significantly lower than but > 50% those in WT BMCMC→*Kit*^{W-sh/W-sh} mice.

0 In OVA-sensitized and challenged mice, significant responses (versus corresponding values in PBS-treated mice) in WT BMCMC→*Kit*^{W-sh/W-sh} mice but N.S. versus those in *Ifngr1*^{-/-} or *Fcer1g*^{-/-} BMCMC→*Kit*^{W-sh/W-sh} mice.

* Significant responses also seen in OVA sensitized and challenged mast cell-deficient *Kit*^{W-sh/W-sh} mice versus values in the corresponding PBS-treated *Kit*^{W-sh/W-sh} mice.

Supplemental Table 2

Genes up-regulated in human asthma. The 96 genes found to be up-regulated in human asthma in the data provided by Laprise, et al. (3), by Significance Analysis of Microarrays (SAM) at raw *P* value < 0.01.

<i>ACPP</i>	<i>GRM8</i>	<i>PMS2L1</i>
<i>AFF2</i>	<i>HOXD9</i>	<i>POLR3F</i>
<i>ALOX15</i>	<i>IL1RL1</i>	<i>POSTN</i>
<i>AMELX</i>	<i>IRS4</i>	<i>POU3F1</i>
<i>ANGEL2</i>	<i>KCNA1</i>	<i>PRRC1</i>
<i>ANXA13</i>	<i>KCNB2</i>	<i>PSG4</i>
<i>ARHGEF16</i>	<i>KCNC4</i>	<i>PSG7</i>
<i>ATP10B</i>	<i>KIAA0408</i>	<i>PTEN</i>
<i>BRD4</i>	<i>KLHL20</i>	<i>RAPGEF3</i>
<i>C1ORF63</i>	<i>KLHL35</i>	<i>RASGRF1</i>
<i>CACNA2D2</i>	<i>KRT9</i>	<i>REPS2</i>
<i>CAV2</i>	<i>KRTAP26-1</i>	<i>SERPINB2</i>
<i>CCDC22</i>	<i>LDB1</i>	<i>SERPIND1</i>
<i>CD1C</i>	<i>LEFTY1</i>	<i>SLC17A2</i>
<i>CDC45L</i>	<i>LILRP2</i>	<i>SLC36A1</i>
<i>CHRN3</i>	<i>LOC100134197</i>	<i>SLC6A3</i>
<i>CNP</i>	<i>LOC81691</i>	<i>SNAPC3</i>
<i>CPA1</i>	<i>LPAR4</i>	<i>TBL3</i>
<i>CPA3</i>	<i>ME3</i>	<i>TBXA2R</i>
<i>CST1</i>	<i>MLLT4</i>	<i>TCF25</i>
<i>CST2</i>	<i>MUC2</i>	<i>TFF2</i>
<i>CST4</i>	<i>MUC3A</i>	<i>TPSAB1</i>
<i>CTDP1</i>	<i>MUC5AC</i>	<i>TPSB2</i>
<i>CYP2D6</i>	<i>MYL1</i>	<i>TPSD1</i>
<i>DLGAP2</i>	<i>NAT8</i>	<i>TRAF3IP1</i>
<i>DNAJC7</i>	<i>NOPI4</i>	<i>TRAPPC6A</i>
<i>DTX2</i>	<i>NOS2</i>	<i>TRIM16</i>
<i>ESR2</i>	<i>OXT</i>	<i>TRIM16L</i>
<i>FOXD1</i>	<i>P2RX3</i>	<i>TSPAN8</i>
<i>GATA2</i>	<i>PART1</i>	<i>VGF</i>
<i>GPR3</i>	<i>PCYT1B</i>	<i>ZFR</i>
<i>GRM5</i>	<i>PDX1</i>	<i>ZMIZ2</i>

Supplemental Table 3 Legend

Gene Set Enrichment Analysis for genes up-regulated in human asthma (fold change). The fold change (reported by GSEA as the rank metric) for the 67 mouse homologues of genes found to be up-regulated in human asthma. A positive number indicates increased expression of that gene in mice exposed to OVA, relative to mice in the same group (i.e., having the same genotype and mast cell engraftment status) challenged only with PBS, a zero indicates no change, and a negative number indicates decreased expression. “B6.None” mice are the C57BL/6 wild type control mice, not engrafted with *in vitro*-generated mouse bone marrow-derived cultured mast cells (BMCMCs). “KitWsh.None” are genetically mast cell-deficient C57BL/6-*Kit*^{W-sh/W-sh} mice without engrafted mast cells. “KitWsh.MC” are C57BL/6-*Kit*^{W-sh/W-sh} mice engrafted with wild type (WT) C57BL/6 BMCMCs. “KitWsh.MCifngR” are C57BL/6-*Kit*^{W-sh/W-sh} mice engrafted with BMCMCs derived from C57BL/6 mice deficient in the interferon gamma receptor (*Ifngr1*^{-/-}). “KitWsh.MCigeR” are mast cell-deficient C57BL/6-*Kit*^{W-sh/W-sh} mice engrafted with BMCMCs from C57BL/6 mice deficient in the signaling γ chain shared by the Fc ϵ RI and Fc γ RIII (*Fcer1g*^{-/-}).

Supplemental Table 3

Gene	B6.None	KitWsh.None	KitWsh.MC	KitWsh.MCifngR	KitWsh.MCigeR
<i>ACPP</i>	0.025	-0.304	0.002	-0.088	-0.233
<i>AFF2</i>	-0.016	0.001	0.041	0.000	-0.494
<i>ALOX15</i>	0.502	-0.391	0.016	0.258	0.910
<i>AMELX</i>	0.077	0.000	0.000	-0.005	-0.342
<i>ANGEL2</i>	0.045	-0.036	0.003	-0.069	0.042
<i>ANXA13</i>	0.008	0.000	0.000	0.000	-0.255
<i>ARHGEF16</i>	0.051	-0.083	0.107	0.109	0.186
<i>BRD4</i>	0.067	-0.052	0.043	-0.076	0.005
<i>CACNA2D2</i>	0.000	0.000	0.052	0.032	0.000
<i>CAV2</i>	-0.072	-0.031	-0.167	0.049	0.095
<i>CCDC22</i>	0.153	-0.079	0.196	-0.067	-0.201
<i>CDC45L</i>	-0.154	0.148	0.508	0.037	-0.420
<i>CHRNA3</i>	0.000	0.000	0.000	0.000	0.000
<i>CNP</i>	0.025	0.078	0.011	-0.055	-0.020
<i>CPA1</i>	0.000	0.000	0.000	0.000	0.000
<i>CPA3</i>	0.145	0.014	1.451	1.177	0.549
<i>CTDP1</i>	0.123	-0.076	0.097	-0.062	0.250
<i>DLGAP2</i>	0.000	0.000	0.058	-0.050	0.012
<i>DNAJC7</i>	0.101	0.020	0.089	-0.089	0.236
<i>DTX2</i>	-0.081	-0.029	0.031	0.024	-0.194
<i>ESR2</i>	-0.002	-0.008	0.000	0.000	0.000
<i>FOXD1</i>	0.009	-0.002	-0.003	-0.020	0.000
<i>GATA2</i>	0.061	-0.190	-0.077	0.001	0.191
<i>GPR3</i>	0.000	0.000	0.000	0.016	-0.417
<i>GRM5</i>	0.000	0.000	0.001	0.000	0.003
<i>GRM8</i>	0.000	0.000	-0.067	0.000	0.000
<i>HOXD9</i>	0.000	0.227	0.163	0.020	-0.233
<i>IL1RL1</i>	0.171	0.065	0.516	0.143	0.002
<i>IRS4</i>	0.000	0.000	0.004	0.000	-0.449
<i>KCNA1</i>	0.000	0.003	0.223	-0.120	-0.360
<i>KCNC4</i>	-0.002	-0.111	0.098	0.021	-0.535
<i>KLHL20</i>	0.026	-0.021	0.046	0.047	0.305
<i>LDB1</i>	0.225	0.239	-0.240	-0.191	0.332
<i>LEFTY1</i>	0.270	0.123	-0.007	-0.145	-0.073
<i>ME3</i>	-0.005	-0.063	-0.114	-0.561	-0.448
<i>MLLT4</i>	-0.016	-0.116	-0.040	0.021	0.367
<i>MUC2</i>	0.000	0.000	-0.032	0.000	-0.390
<i>MUC5AC</i>	1.143	1.826	1.685	0.728	0.794

<i>MYL1</i>	-0.382	-0.406	-0.503	0.184	-0.194
<i>NAT8</i>	-0.120	-0.263	0.243	0.103	-0.417
<i>OXT</i>	0.000	0.000	0.000	0.000	0.000
<i>P2RX3</i>	0.006	0.016	0.278	-0.025	0.000
<i>PCYT1B</i>	0.037	-0.308	-0.189	-0.370	-0.327
<i>POLR3F</i>	-0.259	0.167	-0.336	0.008	0.163
<i>POSTN</i>	-0.038	-0.031	-0.140	0.061	0.175
<i>POU3F1</i>	0.000	0.000	0.032	0.000	0.000
<i>PTEN</i>	-0.001	-0.094	-0.088	-0.004	0.089
<i>RAPGEF3</i>	0.277	-0.061	-0.016	-0.128	-0.150
<i>RASGRF1</i>	-0.003	-0.061	0.369	-0.447	-0.364
<i>REPS2</i>	-0.158	-0.138	-0.176	0.010	0.041
<i>SERPINB2</i>	0.022	-0.565	0.305	0.430	0.462
<i>SERPIND1</i>	-0.159	0.103	0.208	0.430	0.021
<i>SLC17A2</i>	0.004	0.005	0.189	0.061	0.001
<i>SLC36A1</i>	0.311	0.119	0.328	0.255	0.007
<i>SLC6A3</i>	-0.001	-0.027	0.000	-0.004	-0.383
<i>SNAPC3</i>	-0.269	-0.012	-0.239	0.123	-0.131
<i>TBL3</i>	0.183	0.098	0.252	0.063	0.444
<i>TBXA2R</i>	0.008	0.008	0.033	-0.060	-0.012
<i>TCF25</i>	0.072	0.121	-0.118	0.002	0.099
<i>TFF2</i>	0.838	0.635	0.658	0.140	0.473
<i>TPSAB1</i>	-0.025	0.000	0.093	0.036	0.001
<i>TRAF3IP1</i>	0.005	-0.150	-0.118	-0.018	0.100
<i>TRAPPC6A</i>	-0.016	0.142	0.004	-0.065	0.064
<i>TRIM16</i>	0.023	0.003	-0.087	0.098	0.157
<i>TSPAN8</i>	-0.047	-0.087	-0.041	0.021	0.089
<i>VGF</i>	0.078	0.000	0.000	0.000	0.000
<i>ZFR</i>	-0.074	0.006	-0.042	0.108	0.034