Supplemental Methods

Quantitative Real Time RT PCR (qPCR): Lung tissue was either flash frozen or stored in RNAlater and subsequently used for reverse transcription PCR. One to five µg of purified RNA was used to synthesize complementary DNA, and real-time quantitative PCR was performed using SYBR Green I in an Applied Biosystem 7500 Fast Real Time PCR system. Relative gene expression of genes listed was evaluated based on the ddCT method[1]. Data were expressed as fold changes relative to *Xylt2+/+*. The list of primers is described in supplemental Table 1 below.

Supplemental Table 1

Target	Forward Primer	Reverse Primer	Accession number
F4/80 (Adgre1, Emr1)	TGCATCTAGCAATGGACAGC	GCCTTCTGGATCCATTTGAA	NM_010130
Il4	ATCATCGGCATTTTGAACGAGGTC	ACCTTGGAAGCCCTACAGACGA	NM_021283
Ccl2	GCTACAAGAGGATCACCAGCAG	GTCTGGACCCATTCCTTCTTGG	NM_011333.3
Ccl7	CAGAAGGATCACCAGTAGTCGG	ATAGCCTCCTCGACCCACTTCT	NM_013654.3
Ccl8	CCAGATAAGGCTCCAGTCACCT	GGCACTGGATATTGTTGATTCTCTC	NM_021443.3

LPS Challenge: LPS from E coli O111:B4 (Sigma#L630) was administered intranasally at a dose of 5 mg/Kg BW in a final volume of 50 µl/ mouse. Twenty four hours after LPS administration, mice were euthanized using isoflurane and tracheostomy was performed. Lungs were inflated with 750 ul of PBS twice to collect BALF. BALF was centrifuged and the pelleted cells were counted. Total BALF cells were counted using hemocytometer. To estimate the total number of red blood cells, hypotonic RBC lysis buffer was used to lyse red blood cells in the BALF and cells remaining in BALF were counted again. The cell count after RBC lysis was subtracted from cell count before RBC lysis.

1. Livak, K.J., Schmittgen, T.D.: Analysis of relative gene expression data using real-time quantitative PCR and the 2(-Delta Delta C(T)) Method. Methods **25**(4), 402-408 (2001).