Supplementary data

Table 1. Differentially phosphorylated upstream signal activators in BEAS-2B cell line and relevant downstream target genes analyzed using qRT-PCR.

Signaling pathway	Putative ligands	Upstream (DE) phosphorylated activators	Relevant target genes
TLR2 and TLR4	Lipoprotein and LPS	IKKα/β, NF-κB/AP-1	IL-6, IL-8 (CXCL8), NLRP3
TLR4	LPS	TBK1/IKKε, IRF3/7	IFN-β,-α
IFNAR	IFN-β,-α	pSTAT1/2	IFIT1
TNF-α and CXCR3 receptor	TNF-α	NF-κB, cJun/Fos, p38	TNF-α
NLRP3	Bacterial toxins, ATP, dsRNA, mtDNA, mtROS, K^+, LPS, silica, asbestos	IRAKs	IL-1β (mature 17 kDa form)
NLRP1	Muramyl dipeptide	NOD2	IL-1β (mature 17 kDa form)

Table 2. Differentially phosphorylated upstream signal transducers in THP-1 cell line and relevant downstream target genes analyzed using qRT-PCR.

Signaling pathway	Putative ligands	Upstream phosphorylated activators	Relevant target genes
TLR2, TLR4, TLR5	Lipoprotein, LPS, flagellin	IKKα/β, NF-κB/AP-1	IL-6, IL-8 (CXCL8),
TLR4, RIG-1, MDA5	LPS, short or long dsRNA	TBK1/IKKε, IRF3/7	IFN-β,-α
RIG-1, MDA5	short or long dsRNA	TBK1/IKKε, IRF3/7	Presence of RNA viruses in SBDE via virus specific or pan IAV primers
TLR9	Bacterial unmethylated CpG DNA	NF-κB/AP-1	16S rRNA amplification of SBDE DNA

Table 3. Primer sequences for qRT-PCR analysis.

Gene	Tm	Primer sequence	Amplicon size (bp)
IFN-β	55°C	CAATTTTCAGTGTCAGAAGCTCC (Fwd) AAAGTTCATCCTGTCCTTGAGG (Rev)	76
IFIT1	55°C	CCTTCCGCTATAGAATGGAGTG (Fwd) TGGATTCAGGGTTTTCAGGG (Rev)	141
IFN-α	55°C	TGAGGAAATACTTCCAAAGAATCAC (Fwd) TCTCATGATTTCTGCTCTGACAA (Rev)	92
IL-1β	55°C	AGCTGATGGCCCTAAACAGA (Fwd) CCTGAAGCCCTTGCTGTAGT (Rev)	112
IL-8	55°C	GGCTCTCTTGGCAGCCTTCCT (Fwd) TTTGGGGTGGAAAGGTTTGGA (Rev)	121
IL-6	55°C	TCCAAAGATGTAGCCGCCCCAC (Fwd) TTCTGCCAGTGCCTCTTTGCTG (Rev)	156
GAPDH	55°C	AGAACGGGAAGCTTGTCATC (Fwd) CATCGCCCCACTTGATTTTG (Rev)	79
TNF-α	55°C	GAGGCCAAGCCCTGGTATG (Fwd) CGGGCCGATTGATCTCAGC (Rev)	92