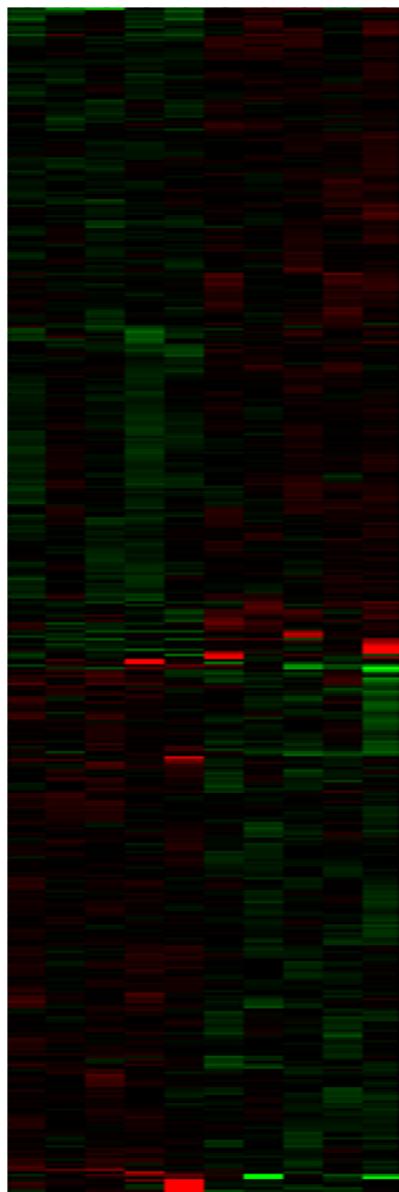


**Supplementary Table S1 – Primer and probe sequences for quantitative RT-PCR**

Gene	Sequence (5' -> 3')	Tm (°C)
<i>Ccl2</i> (NM_011333.3)	F: GCTGGAGCATCCACGTGTT R: TGGTGAATGAGTAGCAGCAGGT P: CTCAGCCAGATGCAGTTAACGCC	60
<i>Cxcl1</i> (NM_008176.3)	F: ACCGAAGTCATAGCCACACTC R: CTCCGTTACTTGGGGACACC	60
<i>Gapdh</i> (NM_008084.2)	F: <i>TGTGCAGTGCCAGCCTCGTC</i> R: GGATGCATTGCTGACAATCT	60
<i>Tnf</i> (NM_013693.2)	F: GAACTTGGGTGATCGGT R: GTGAGGGTCTGGGCCATAGA P: CAAAGGGATGAGAAGTCCCAAATGGCC	60

**Supplementary Figure S1 – Profile of gene expression in the lung exposed to aerosol released from ultrasonic humidifier with tap water, high-silica water, or ultrapure water**

**Experiment #** 3 2 1 4 5 3 2 1 4 5  
**Water** Ultrapure T S T S S



**Upregulated genes**

Enriched in mitosis, meiosis and related categories

**Differentially expressed genes**

Enriched in major histocompatibility complex (MHC) molecules, endocytosis, antigen processing, and cell adhesion molecules.

Among 15984 mRNAs with quantitative fluorescence signal (raw data  $\geq 100$ ), the data for genes with small variations among the ultrapure water groups are sorted into hierarchical clustering. “S” and “T” indicate high-silica water and tap water, respectively. The details of each experiment number were shown in Table 1.

**Supplementary Table S2 – Differentially expressed genes with relevant enriched GO and pathways**

Genes colored orange and blue were upregulated and downregulated by particles generated by the humidifier with tap water or high-silica water.