**Supplementary Materials**

**Supplemental Table S1. GO and KEGG enrichment analysis of DEGs between HIGA-E and HIGA-NE.**

*(A.) GO enrichment results.*

| *GO term* | *Category* | *-log10(p-value)* |
|---|---|---|
| *Nucleosome assembly* | *Biological process* | *5.374* |
| *Chromatin assembly* | *Biological process* | *5.229* |
| *Nucleosome organization* | *Biological process* | *5.159* |
| *Chromatin assembly or disassembly* | *Biological process* | *5.132* |
| *DNA packaging* | *Biological process* | *4.871* |
| *Protein–DNA complex assembly* | *Biological process* | *4.708* |
| *Chromatin remodeling* | *Biological process* | *4.402* |
| *Protein–DNA complex subunit organization* | *Biological process* | *4.387* |
| *DNA conformation change* | *Biological process* | *4.031* |
| *Negative regulation of myeloid cell differentiation* | *Biological process* | *3.3* |
| *DNA replication-dependent nucleosome assembly* | *Biological process* | *3.258* |
| *Regulation of myeloid cell differentiation* | *Biological process* | *3.258* |
| *Chromatin organization* | *Biological process* | *2.703* |
| *Immune system process* | *Biological process* | *2.665* |
| *Regulation of hemopoiesis* | *Biological process* | *2.231* |

| | | |
|---|---|---|
| *Nucleosome* | *Cellular component* | *10.171* |
| *DNA packaging complex* | *Cellular component* | *10.171* |
| *Protein–DNA complex* | *Cellular component* | *9.755* |
| *Chromatin* | *Cellular component* | *5.792* |
| *Chromosome* | *Cellular component* | *3.536* |
| *Protein heterodimerization activity* | *Molecular function* | *5.847* |
| *Protein dimerization activity* | *Molecular function* | *3.52* |
| *DNA binding* | *Molecular function* | *3.034* |
| *RNA polymerase II core promoter sequence-specific DNA binding* | *Molecular function* | *2.226* |

*(B.) KEGG pathway enrichment results.*

| *Pathway* | *Category* | *Gene count* | *Adjusted p-value* |
|---|---|---|---|
| *Systemic lupus erythematosus* | *KEGG* | *8* | *7.32e-11* |
| *Neutrophil extracellular trap formation* | *KEGG* | *8* | *5.46e-10* |
| *Alcoholism* | *KEGG* | *8* | *5.46e-10* |
| *Viral carcinogenesis* | *KEGG* | *4* | *7.13e-04* |

*Note: Downregulated pathways were predominant in HIGA-E compared with HIGA-NE.*

**Supplemental Table S2. Composition and particle size distribution of ISO 12103-1, A1 ultrafine test dust (Arizona test dust).**

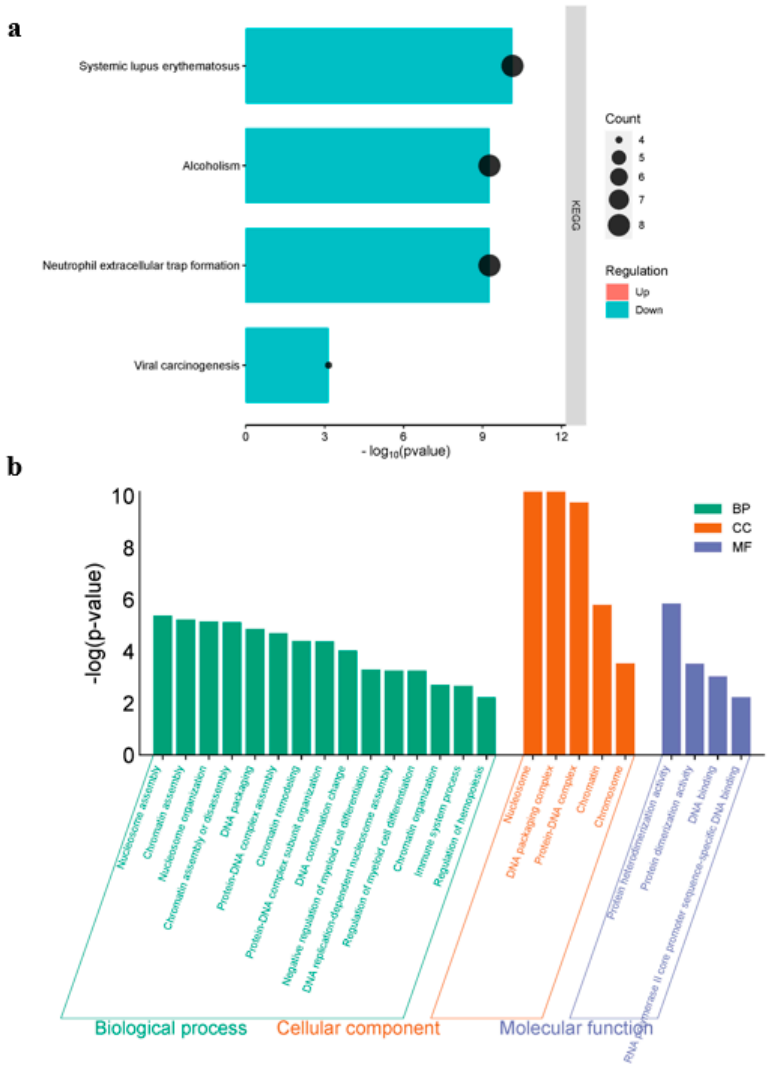
| Component | Weight % (approx.) |
|---|---|
| Silicon dioxide (Quartz) | 69–77% |

| | |
|---|---|
| Aluminum oxides | 8–14% |
| Iron oxides | 4–7% |
| Potassium oxides | 2–5% |
| Calcium oxides | 2.5–5.5% |
| Sodium oxides | 1–4% |
| Magnesium oxides | 1–2% |
| Titanium dioxide | 0–1% |

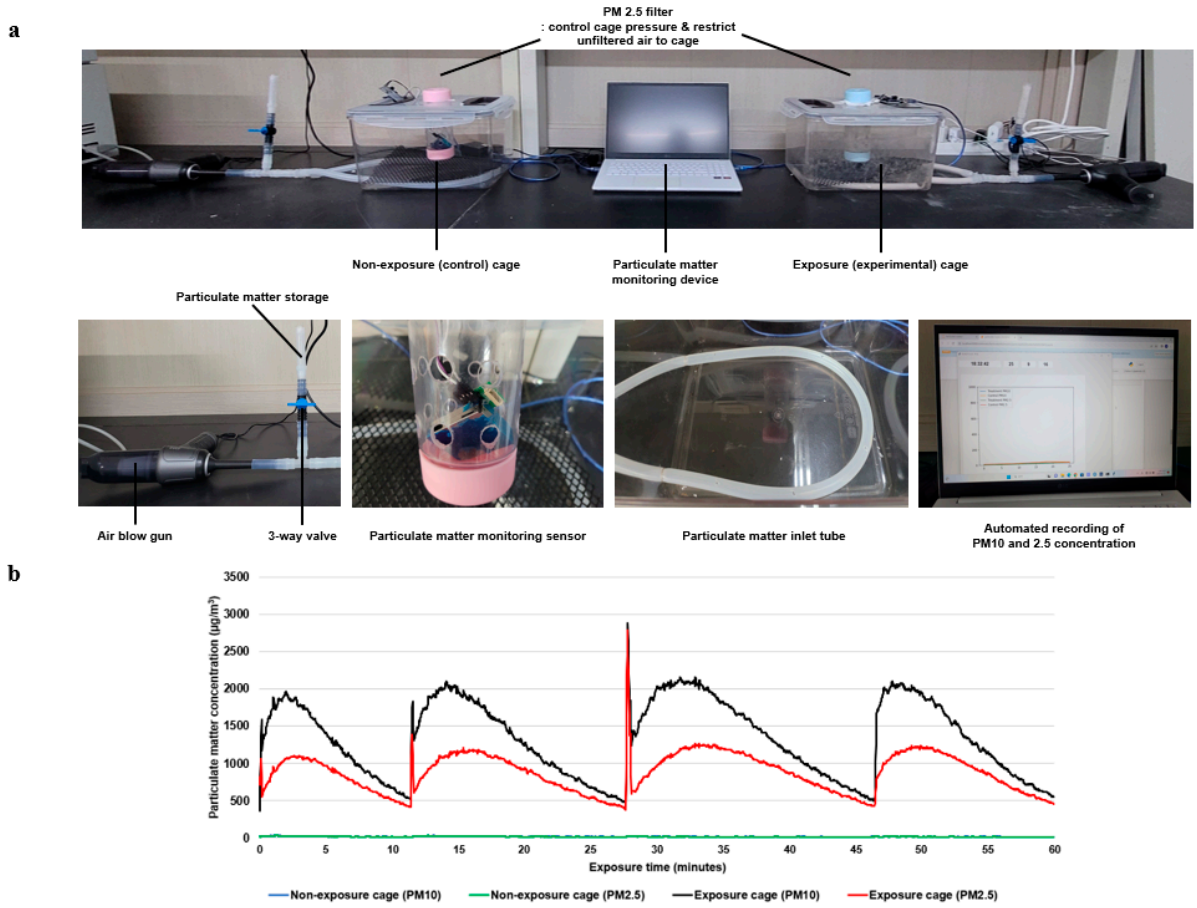
**Supplemental Table S3. Particle size distribution of ISO 12103-1, A1 ultrafine test dust (Arizona test dust).**

| Particle size | Fraction (%) |
|---|---|
| < 0.97 μm | 3–5% |
| < 1.38 μm | 7–10% |
| < 2.75 μm | 23–27% |
| < 5.50 μm | 65–69% |
| < 11.0 μm | 95.5–97.5% |
| < 22 μm | 100% |

Source: Product description of ISO 12103-1 Arizona test dust (DMT-Group, official specifications).

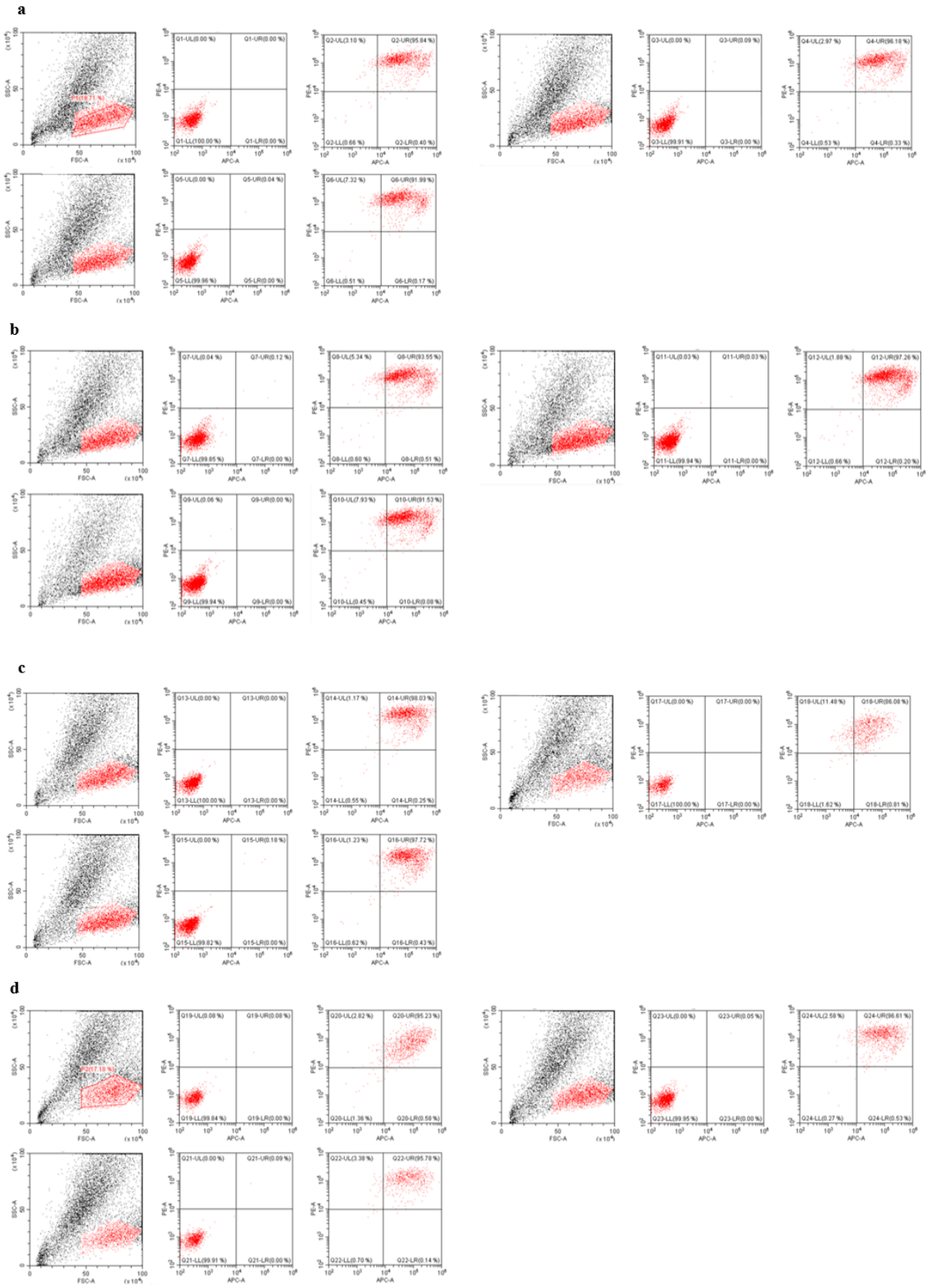



**Supplemental Figure S1. Functional enrichment analysis of DEGs in splenic CD19⁺ B cells from HIGA mice following PM exposure.** (**a.**) KEGG pathway enrichment analysis of downregulated genes in HIGA-E compared with HIGA-NE mice. Pathways such as systemic lupus erythematosus, neutrophil extracellular trap formation, and viral carcinogenesis were significantly enriched. (**b.**) GO enrichment analysis of DEGs in the same comparison. Downregulated genes were primarily associated with nucleosome assembly, chromatin organization, and DNA packaging, indicating altered genomic stability and epigenetic regulation.




**Supplemental Figure S2. PM exposure cage system and recording of particulate matter concentration.** (**a.**) The sealed PM exposure cage and automated PM measurement systems are shown. The central laptop is connected to the PM measurement sensors, enabling real-time automated recordings of the PM concentrations. (**b.**) During PM exposure, the measurements indicate that the PM exposure cage maintains $PM_{2.5}$ and $PM_{10}$ concentrations above a certain threshold. Additional PM is injected to sustain the target levels when the concentrations begin to decline. In contrast, the non-exposure cage maintains $PM_{2.5}$ and $PM_{10}$ concentrations close to zero, as observed in the data.

The Python and Arduino scripts used in this study are available on GitHub (https://github.com/MinhyeokLee/PMmonitor).



**Supplemental Figure S3. Verification results of CD19+ splenic B cell separation using FACS.** (**a.**) FACS validation results following CD19+ splenic B cell sorting from BALB/c-NE mice. (**b.**) FACS validation results following CD19+ splenic B cell sorting from BALB/c-E mice. (**c.**) FACS validation results following CD19+ splenic B cell sorting from HIGA-NE mice. (**d.**) FACS validation results following CD19+ splenic B

cell sorting from HIGA-E mice. The x-axis represents the CD19 marker, and the y-axis represents the CD20 marker. All samples demonstrated successful B cell separation with over 90% purity.