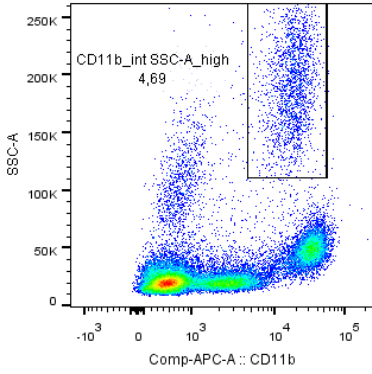


A Gated on SSC^{hi} CD11b^{int} SiglecF⁺



B

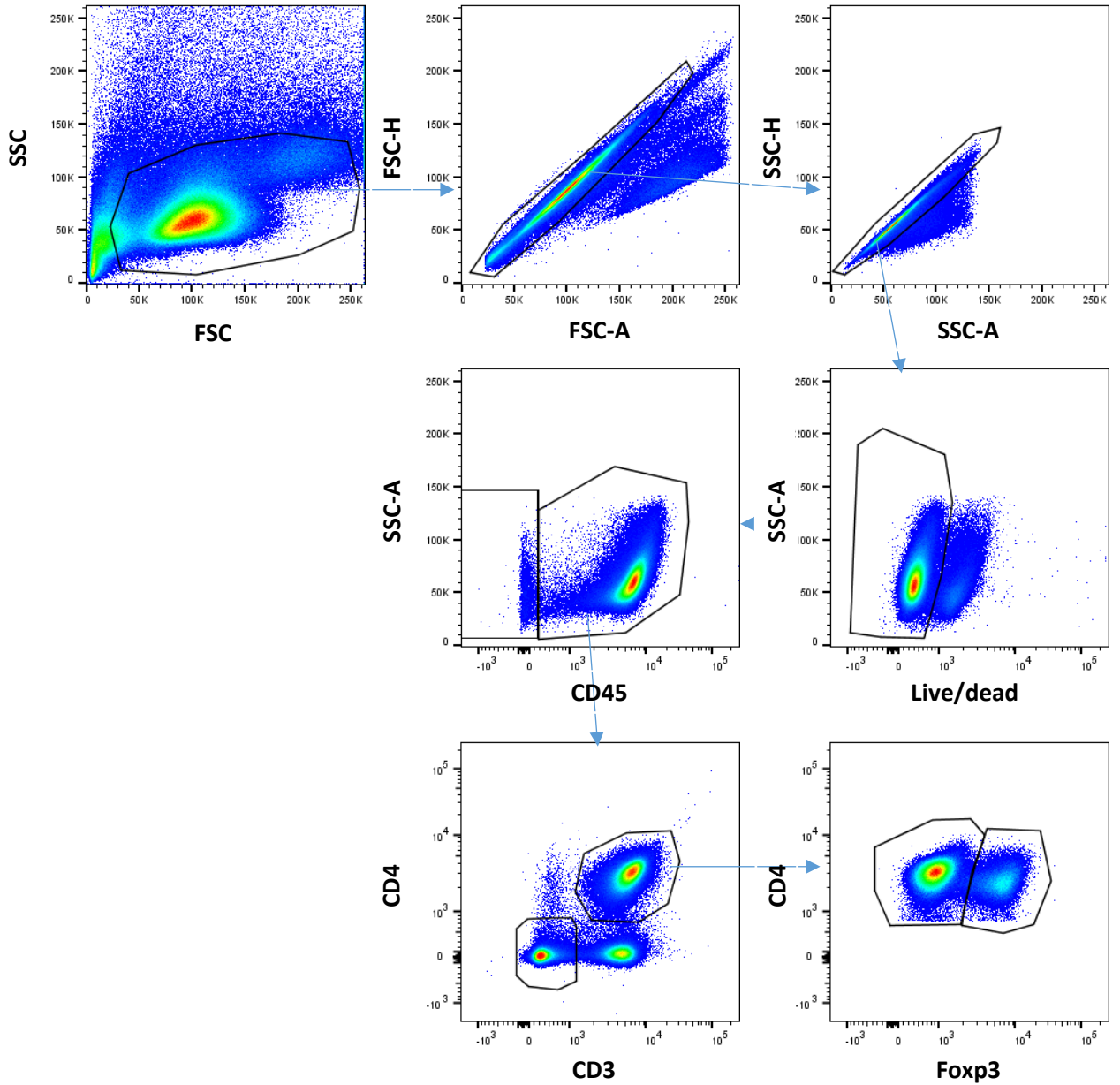


Fig. S1. Gating strategy employed for flow cytometric analysis of eosinophils in mouse whole lung (A) and for regulatory T cells (T regs) in mouse cervical lymph nodes (B).

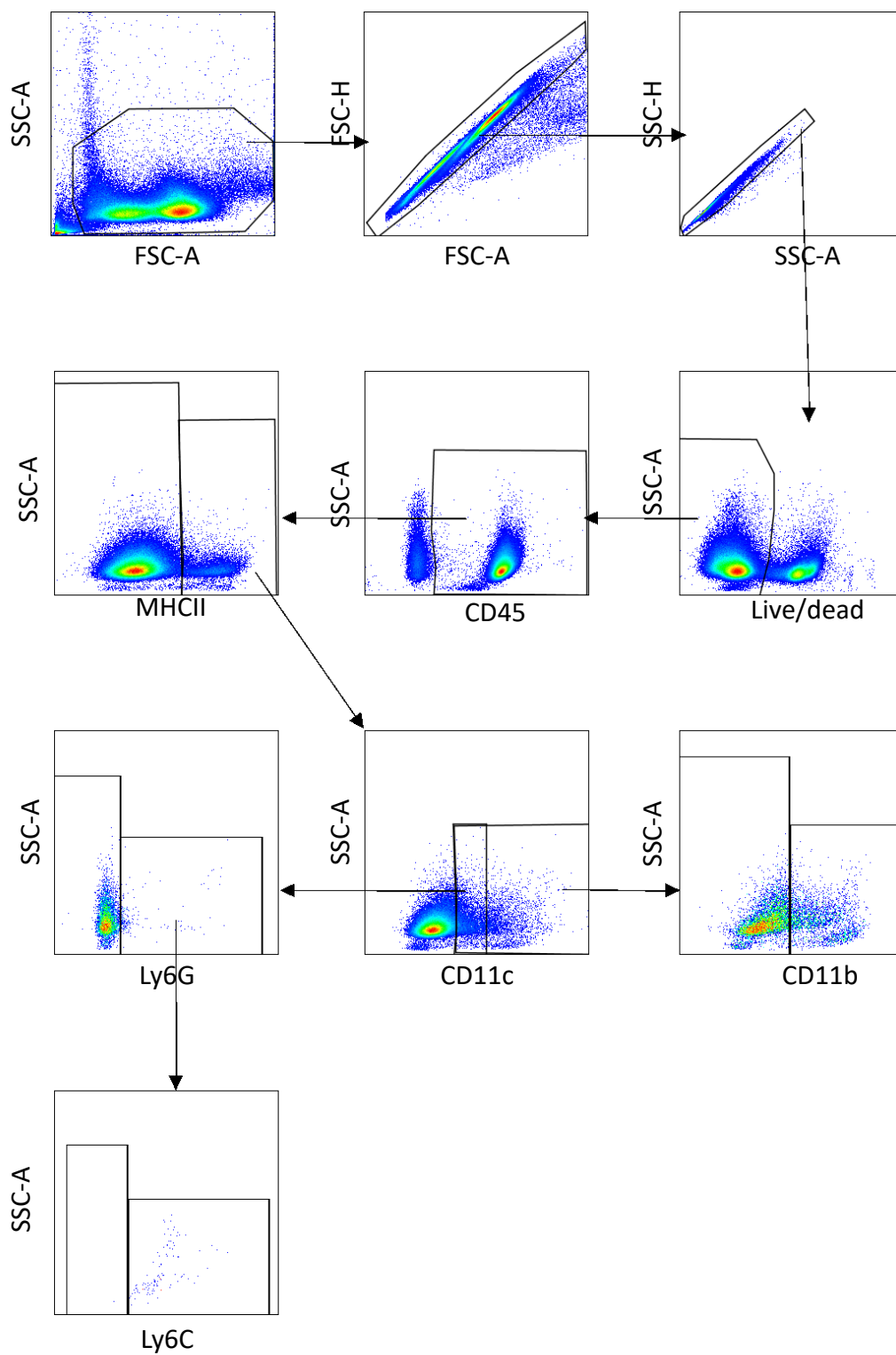
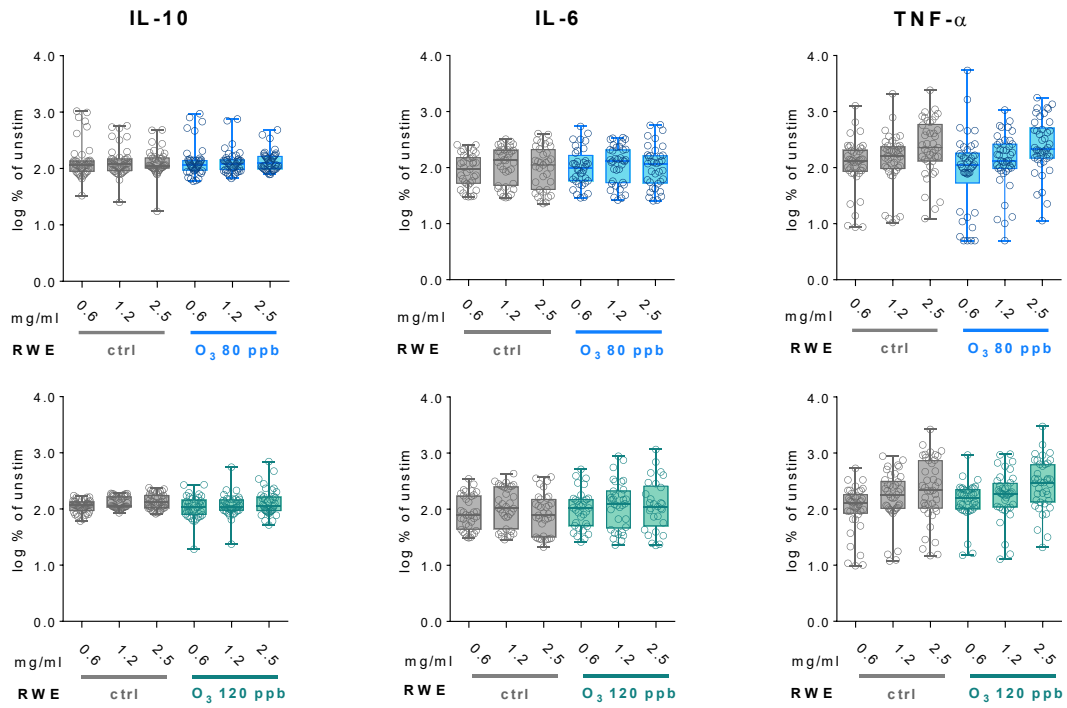


Fig. S2. Gating strategy employed for flow cytometric analysis of dendritic cells in mouse whole lung and cervical lymph nodes.

A **Non-atopic donors**



B **Atopic donors**

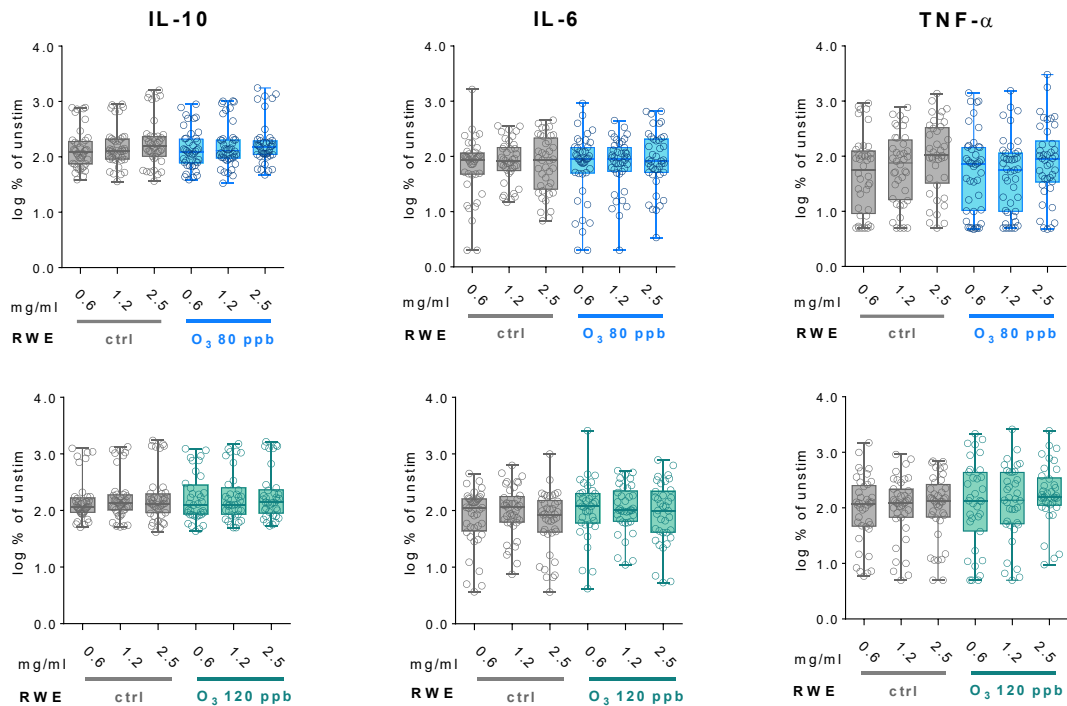
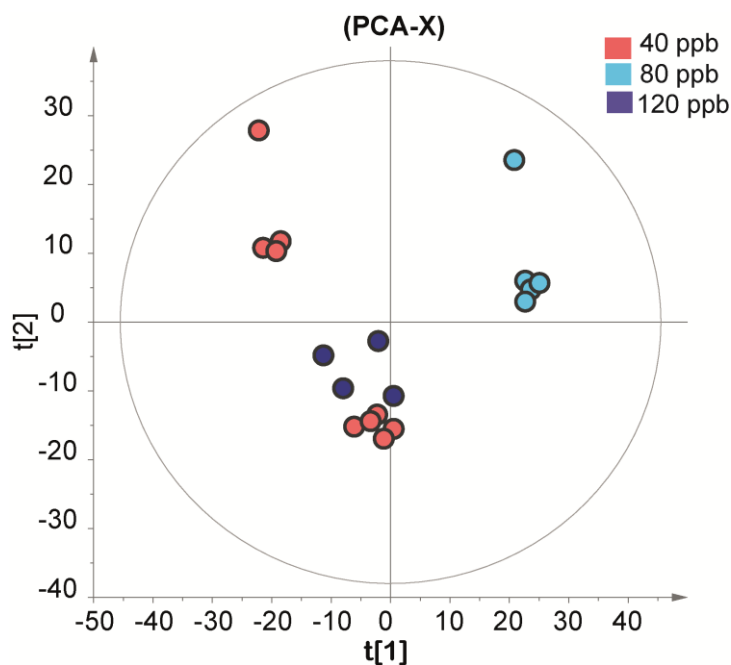


Fig. S3. Cytokine expression of monocyte-derived dendritic cells isolated from non-atopic donors (A) and atopic donors (B). IL-10, IL-6 and TNF α were measured in cell culture supernatants after 24 h stimulation with 0.6-2.5 mg/ml control- or O₃-RWE. n= 36-42 independent experiments using cells from 13 different donors (7 non-atopic; 6 atopic). One-way ANOVA (paired) or Mixed Model ANOVA (paired) with post-hoc pair-wise comparisons (ctrl. vs O₃. unstim, unstimulated).

A



B

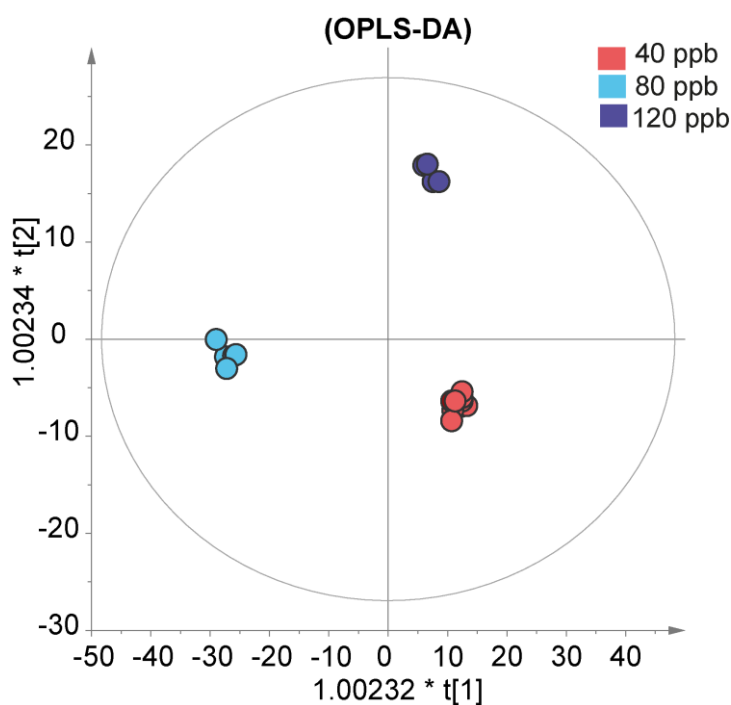


Figure S4. Principal Component Analysis (PCA-X) and Orthogonal Partial Least Squares–Discriminant Analysis (OPLS-DA) score plots showing sample clustering according to exposure level (40 ppb, 80 ppb, 120 ppb). The 40 ppb data represent the pool of all controls used for both 80 ppb and 120 ppb ozone fumigations. The unsupervised PCA model explained $R^2(X) = 44\%$ of the total variance. The supervised OPLS-DA model achieved $R^2(Y) = 0.9$ and $Q^2 = 0.8$, indicating strong model fit and predictive ability, with improved group separation compared to PCA.

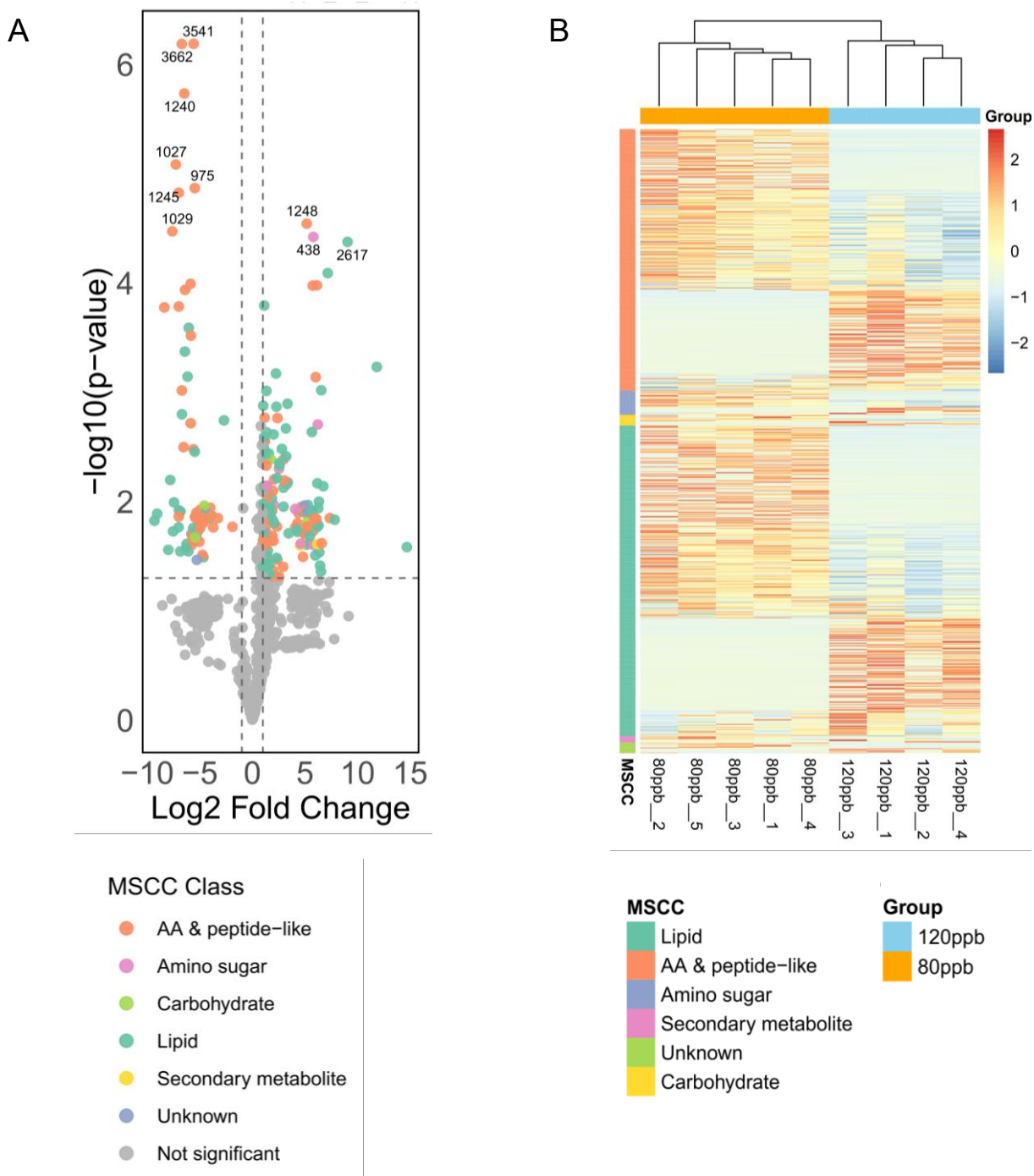


Figure S5. Volcano plot (A) and heatmap (B) of metabolites in response to ozone treatment at 80 ppb compared to 120 ppb. Rows represent individual metabolites, annotated by the multi-dimensional stoichiometric compound classification (MSCC) method. Columns represent biological replicates from control and ozone treatment groups. Metabolite intensities were normalized and scaled (z-score transformation, see methods); colors indicate the relative abundance of each metabolite in each sample, with -2 (in blue) and +2 (in red) indicating that the metabolite level is 2σ (sd) below and above the mean value of each metabolite, respectively. MSCC classes are color-coded as indicated in the legend.