

Effects of E-Cigarette flavoring chemicals on Human Macrophages and Bronchial Epithelial Cells

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Supplementary analysis - Modeling of predictors of toxicity profiles. Detailed Methods and Results.

Background

Due to the vast number of e-cigarette flavoring chemicals available on the market, we used machine learning to develop a method to illustrate an approach to extrapolate toxicological data from the chemicals we tested in order to predict their relative toxicity based on shared physicochemical characteristics. Clustering is a machine learning technique that involves the grouping of data points based on shared properties (Kriegel et al., 2011; Färber et al., 2010). We analyzed our accrued toxicity data in order to develop a protocol to potentially predict the general toxicity of untested chemicals based on their physicochemical properties. Chemicals were grouped based on their combined assay results. Physicochemical properties (solubility, density, molecular weight, listed Safety Data Sheet hazards, functional groups, and canonical SMILES) were then used to attempt to predict the group classification of the chemicals to uncover any driving properties behind the groups that were determined from assay results (i.e., properties that were potentially causing the toxicity effects seen in the assays). The simplified molecular-input line-entry system (SMILES) is a way of describing the structure of a molecule as a single line of text. (e.g., vanillin: COC1=C[C=CC(=C1)C=O]O).

Methods

Clustering

Average viability, lactate dehydrogenase (LDH), intracellular reactive oxygen species (ROS), and cytokine concentration (IL-1 β , IL-6, IL-8, and TNF- α) were calculated for each chemical and stratified by cell type and time point. Groupings of the 30 chemicals plus the propylene glycol, vegetable glycerin (PG/VG) vehicle control (phosphate buffer solution [PBS] control and positive control excluded) were determined based on treatment averages from all seven assays using Hierarchical Clustering (Euclidean distance as metric). Human bronchial epithelial cells (BEAS-2B) cell type dendrograms were cut to form four groups of chemicals with similar assay patterns, and THP-1 (activated and naïve) dendrograms were cut to form three groups of chemicals. The number of groups for each cell type was determined by cutting the dendrogram at the largest height that still resulted in distinct groupings of chemicals based on toxicity. Grouping in this manner allowed the separation of different “classes” of toxicity (e.g., high potency versus medium or low potency) within the chemicals without creating overly specific groupings for investigation of any commonalities amongst the physicochemical properties. All clustering analyses were performed at the highest dose group for each cell type-chemical treatment combination.

Modeling

Replicates (50, 100, and 150) for each chemical–assay–time point–cell type combination were randomly generated from a Normal distribution with mean and standard deviation equal to the corresponding sample mean and sample standard deviation. For example, the sample mean and sample standard deviation results from each assay from vehicle control treatment of BEAS-2B at the 4-hour time point were used as the mean and standard deviation parameters of the

Normal distribution to randomly generate 50, 100, and 150 data points per assay. This was repeated for each cell type–time point–chemical treatment combination for all assays. Physicochemical properties including molecular weight (g/mol), density (g/mL), solubility in H₂O (mM), Safety Data Sheet (SDS) hazard classifications, functional group list, and canonical SMILES were repeated uniformly across replicates within each chemical. Data generation was performed from the sample statistics due the moderately-high dimensionality of the dataset once stratified by cell type and timepoint, which could result in biased or overstated modeling results due to the small size of the training dataset once split for testing versus training. Three replication sizes (50, 100, and 150) were used to test the sensitivity of modeling results based on replication number.

Each set of replicated data was randomly split 80/20 for training/testing, respectively. The physicochemical property data were used in a classification Random Forest (number of trees = 500, seed set to 1234) to classify materials into groups corresponding to the groupings that were determined from the stratified Hierarchical Clustering of the assay averages. Variable importance was assessed by Mean Decrease in Accuracy and Mean Decrease in Gini Index. Results displayed are for sets from 150 replications since results were consistent across replication number.

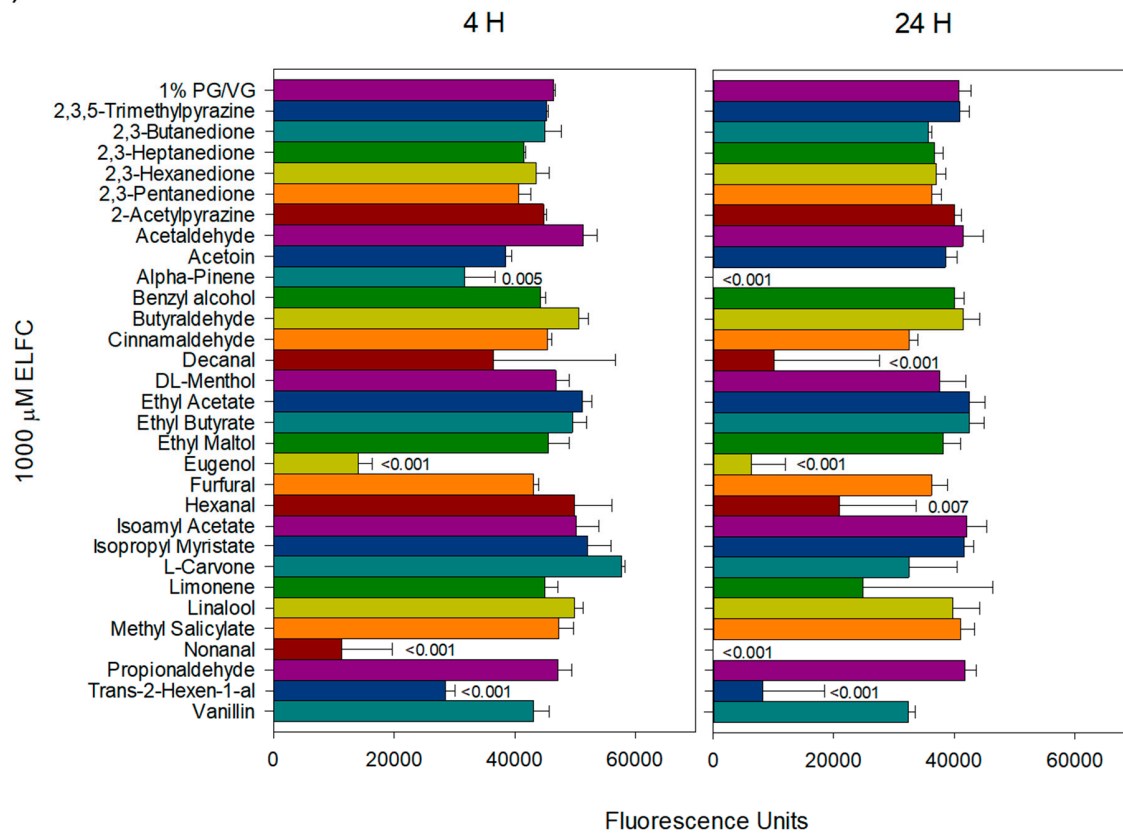
All clustering and modeling analyses were conducted in R version 3.6.0 using randomForest package for modeling [34,35].

Results

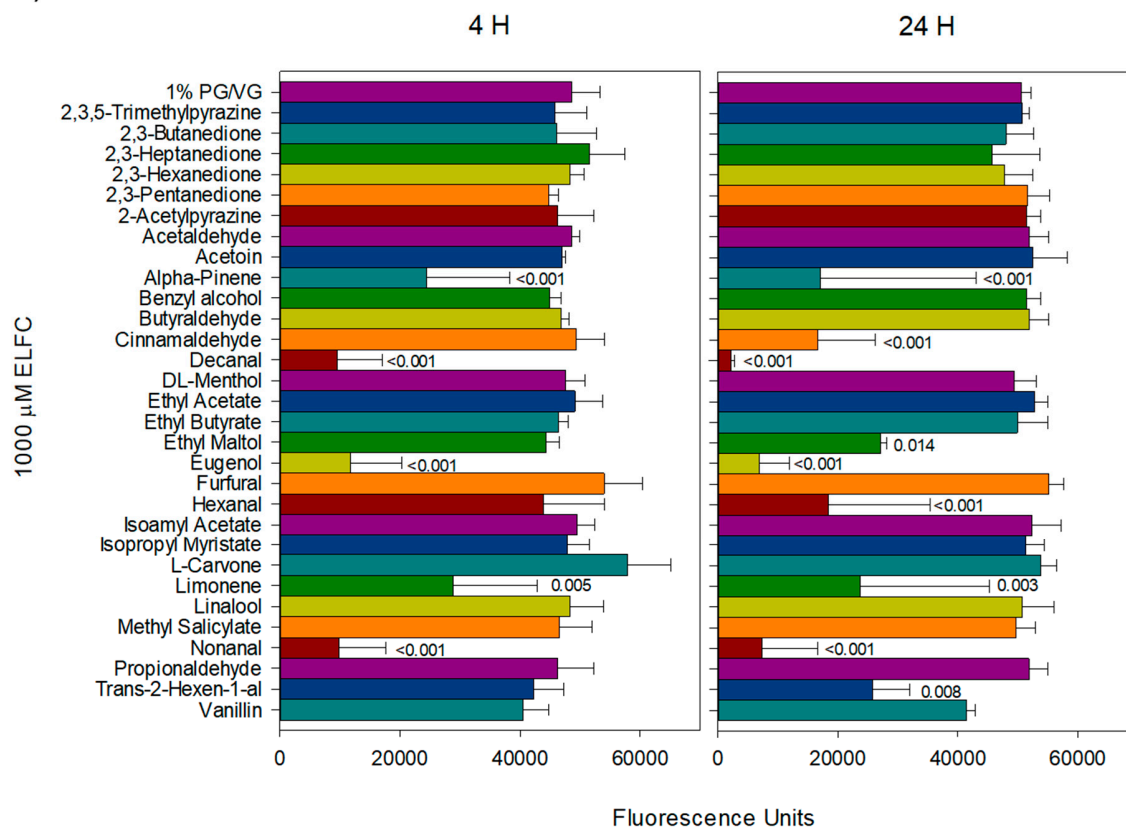
Across all cell types and time points, decanal, eugenol, and nonanal consistently were placed in the most potent groupings (Figures S9-S11). Additionally, Alpha-pinene [(-)- α -Pinene] and Limonene [(R)-(+)-Limonene] were commonly grouped in the high/moderate toxicity grouping (ref fig/table of clustering results). Random forest results showed that canonical SMILES and functional groups were the most important physicochemical properties in accurately (100% accuracy in all cell types and time points) predicting a compound's toxicity grouping, which was determined via clustering based on average assay results. Canonical SMILES and functional groups were also the top two variables of importance when Mean Decrease in Gini Index was evaluated. Other physicochemical properties, such as solubility, density, molecular weight, and SDS hazard were consistently less important and did not display a uniform trend for prediction of toxicity grouping across cell types and time points. Common functional groups amongst the chemicals within the most potent groupings include benzenes and aldehydes, as well as isoprenes and methyl groups.

After grouping flavoring chemicals by their toxicity and analyzing by solubility, molecular weight, density, functional groups, and canonical SMILES, our model suggests that the most effective method to accurately predict the toxicity of a flavoring chemical is by assessing the canonical SMILE signature for effects on BEAS-2B cells and functional group for THP-1 cells. The flavoring chemicals which appear to affect cells the most fall into the categories of aldehydes with large carbon chains attached, compounds containing benzene rings, and chemicals classified as monoterpenes, which contain two isoprene groups.

A.) BEAS-2B



B.) Naïve THP-1



C.) Activated THP-1

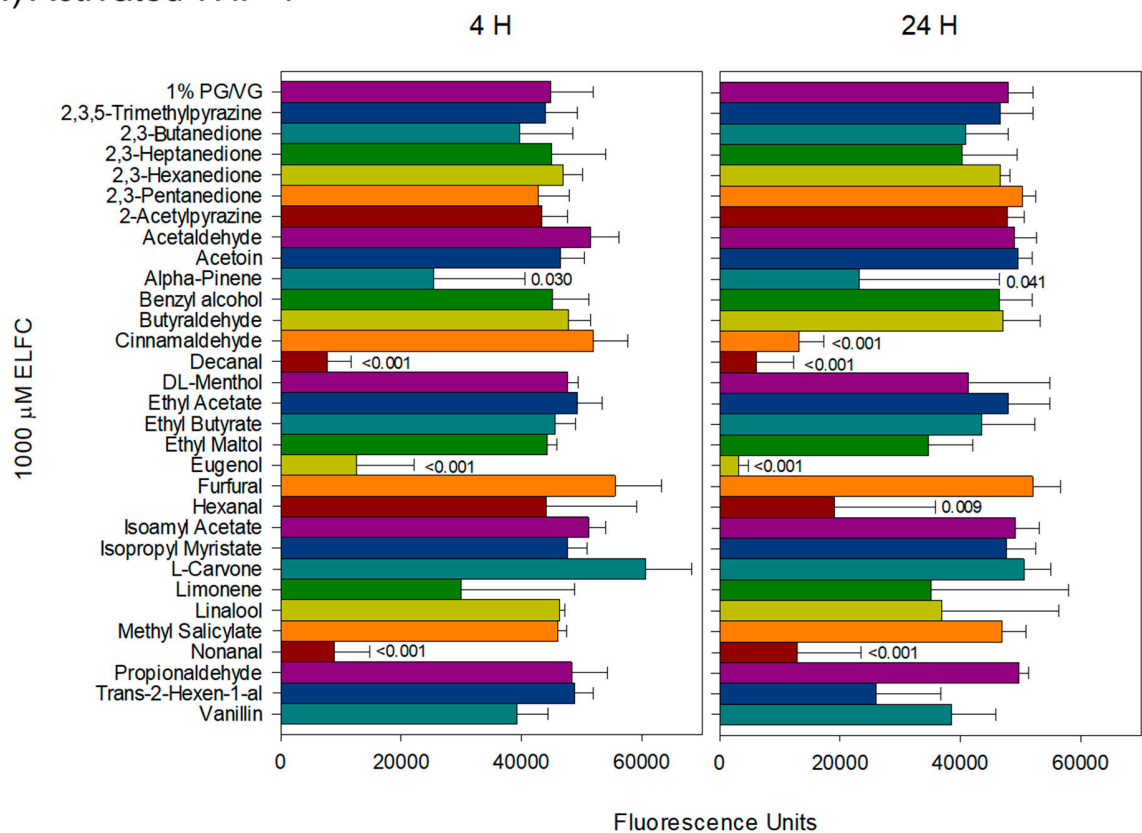
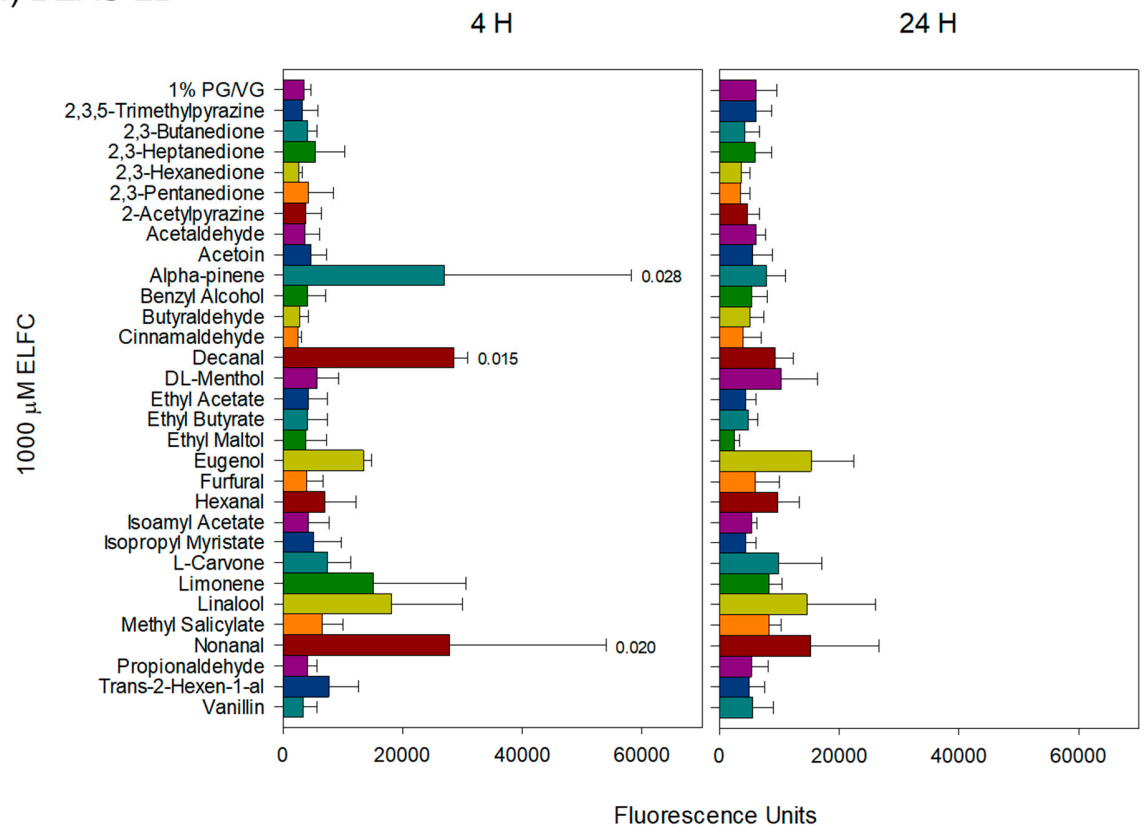
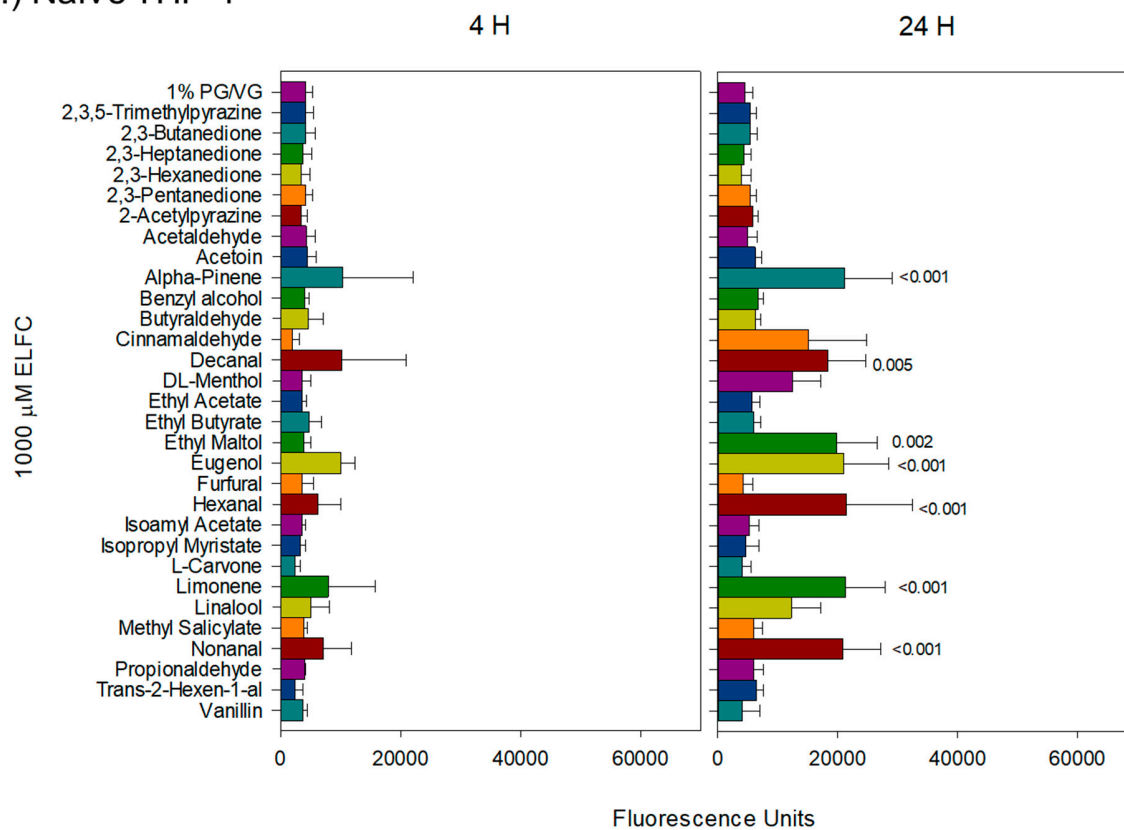


Figure S1. Cell Viability

A.) BEAS-2B



B.) Naïve THP-1



C.) Activated THP-1

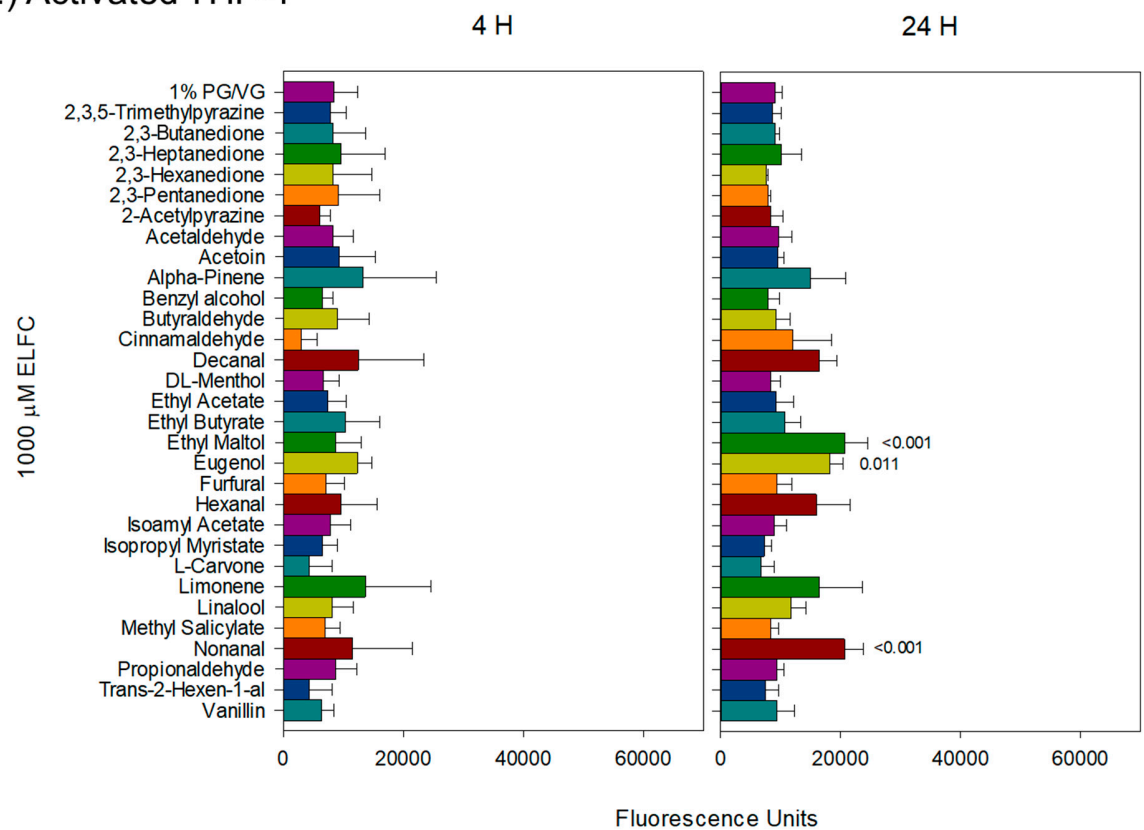
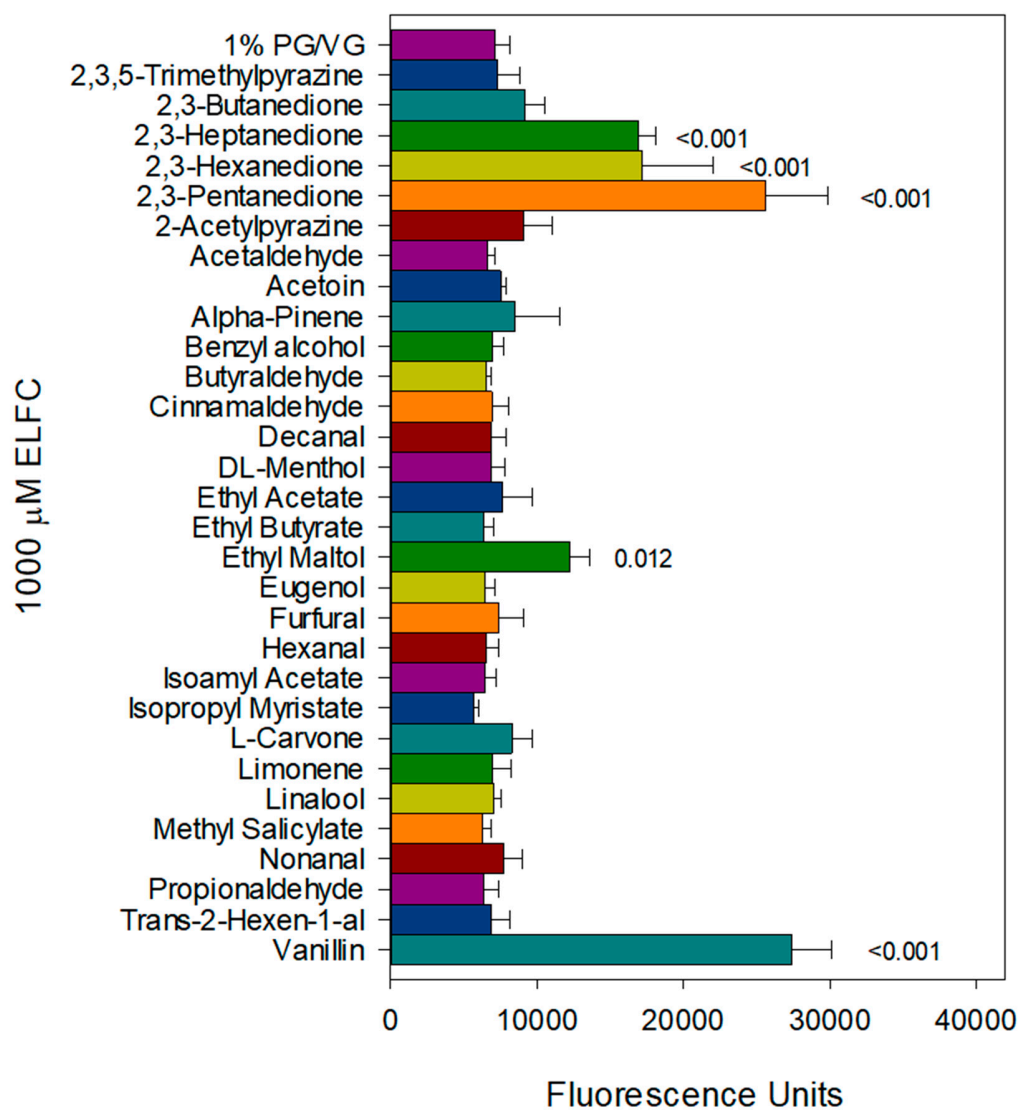


Figure S2. LDH

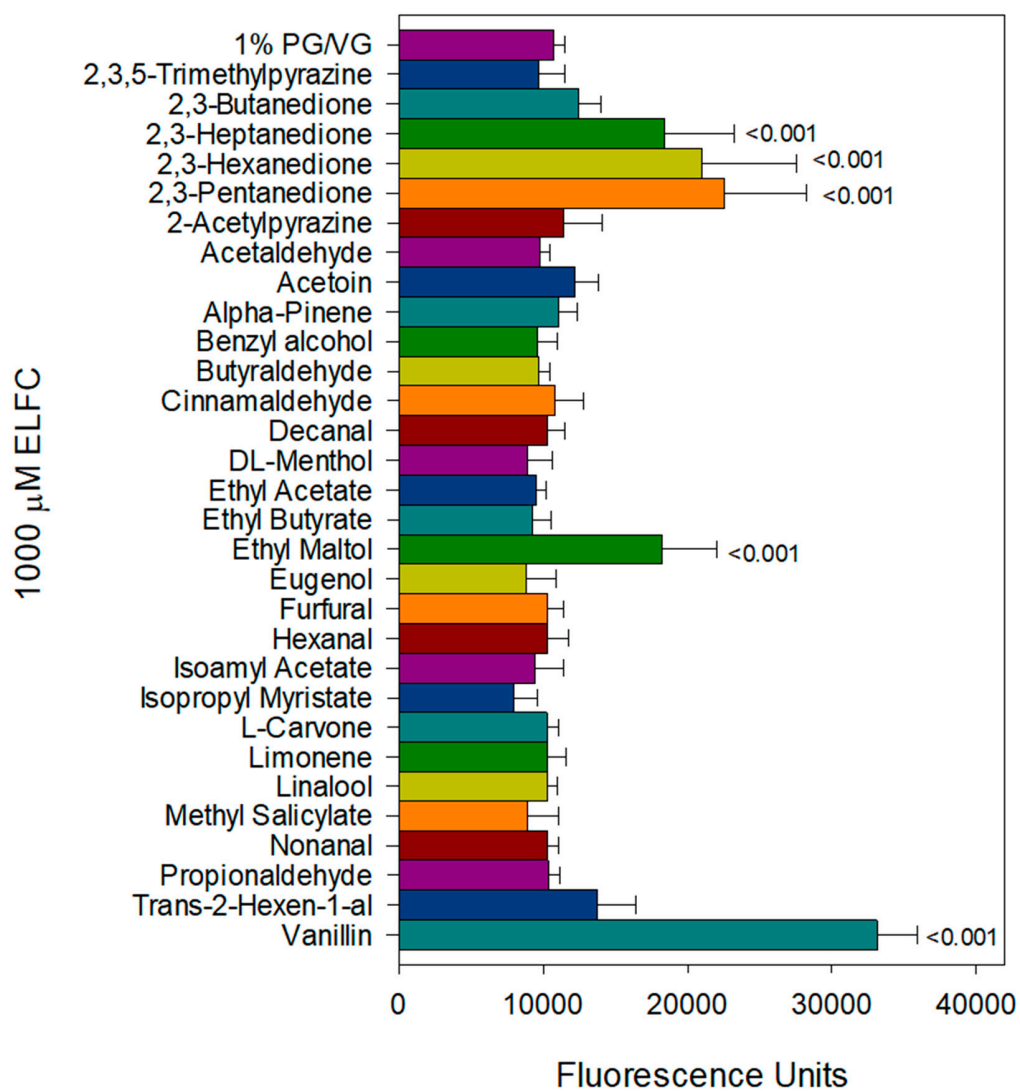
A.) BEAS-2B

6 H



B.) Naïve THP-1

6 H



C.) Activated THP-1

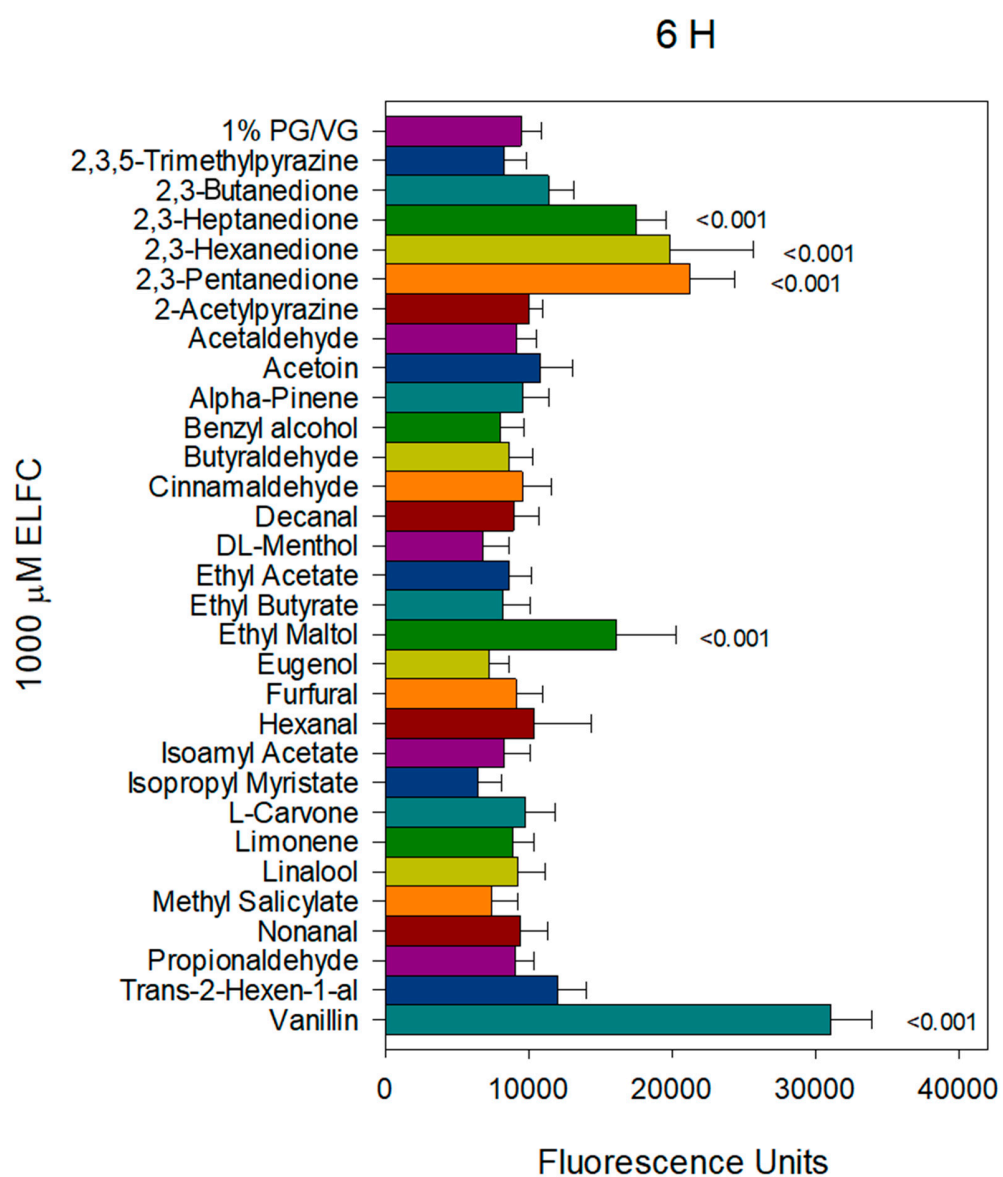
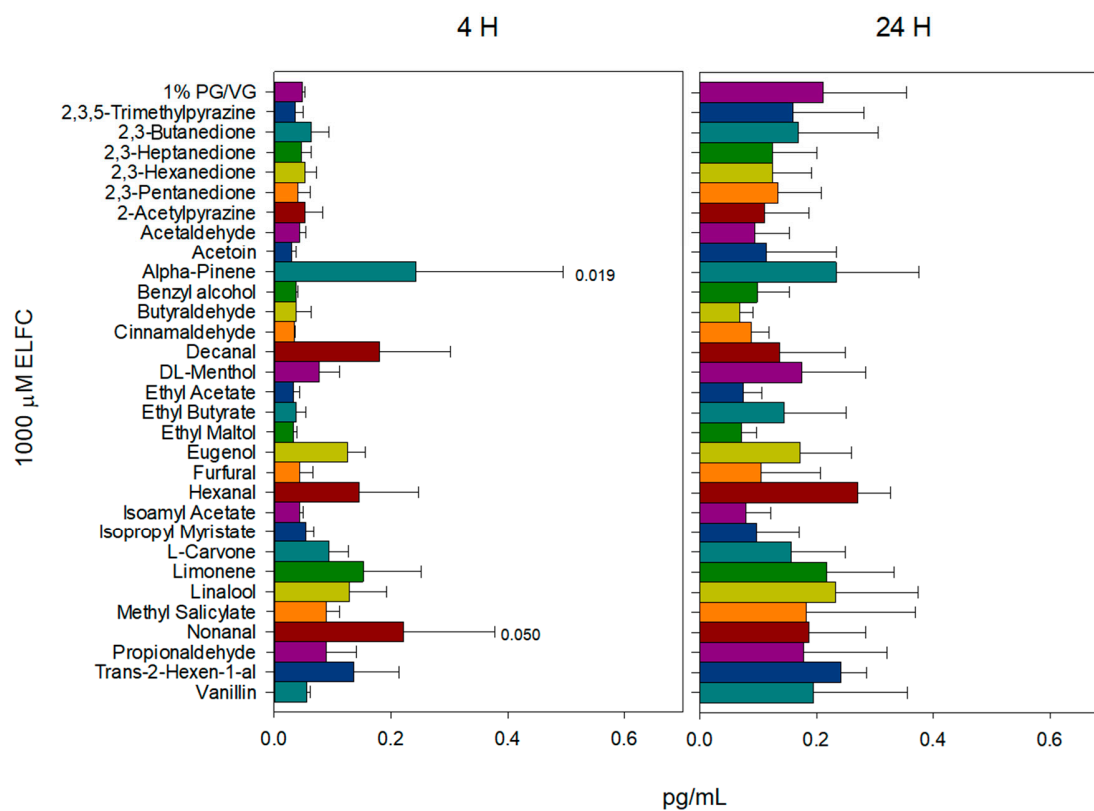
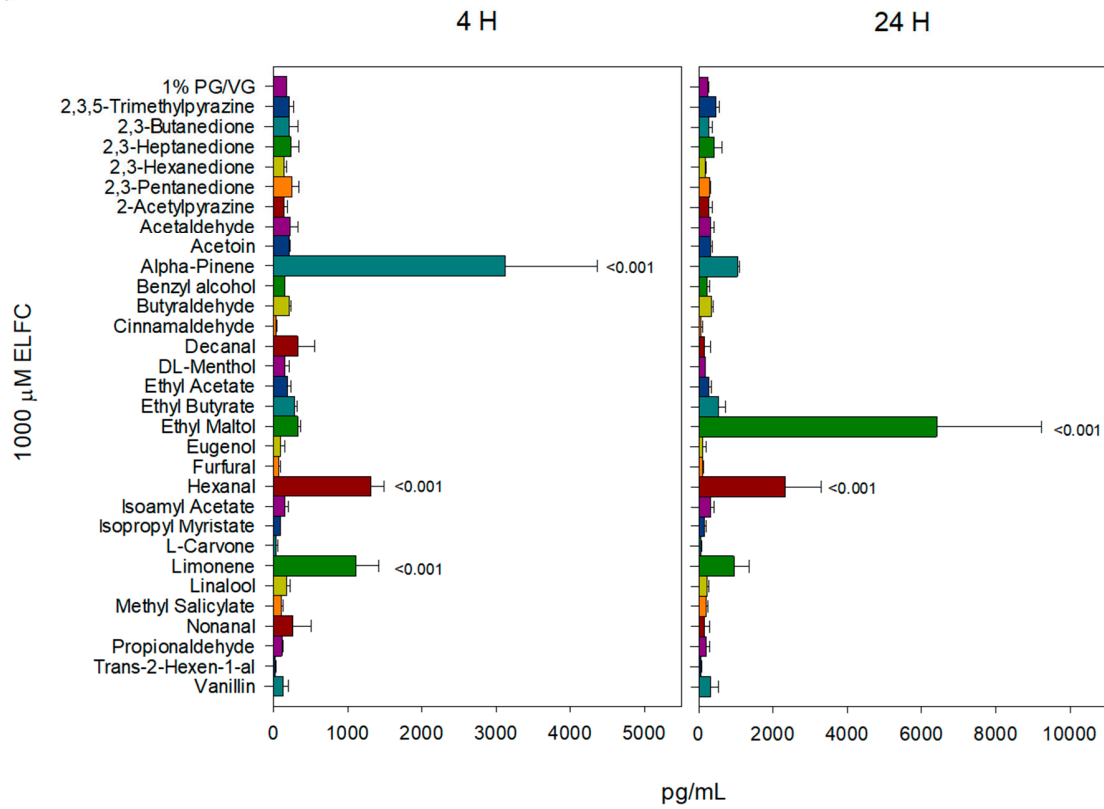


Figure S3. Intracellular ROS

A.) BEAS-2B



B.) Naïve THP-1



C.) Activated THP-1

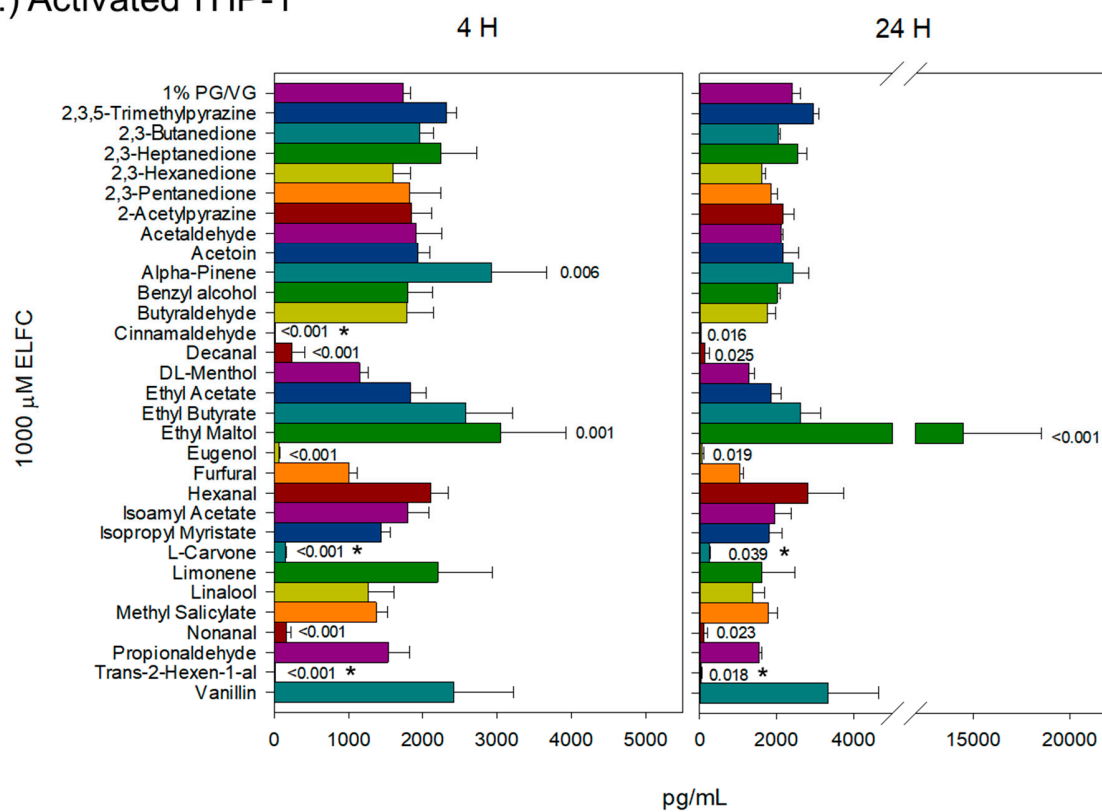
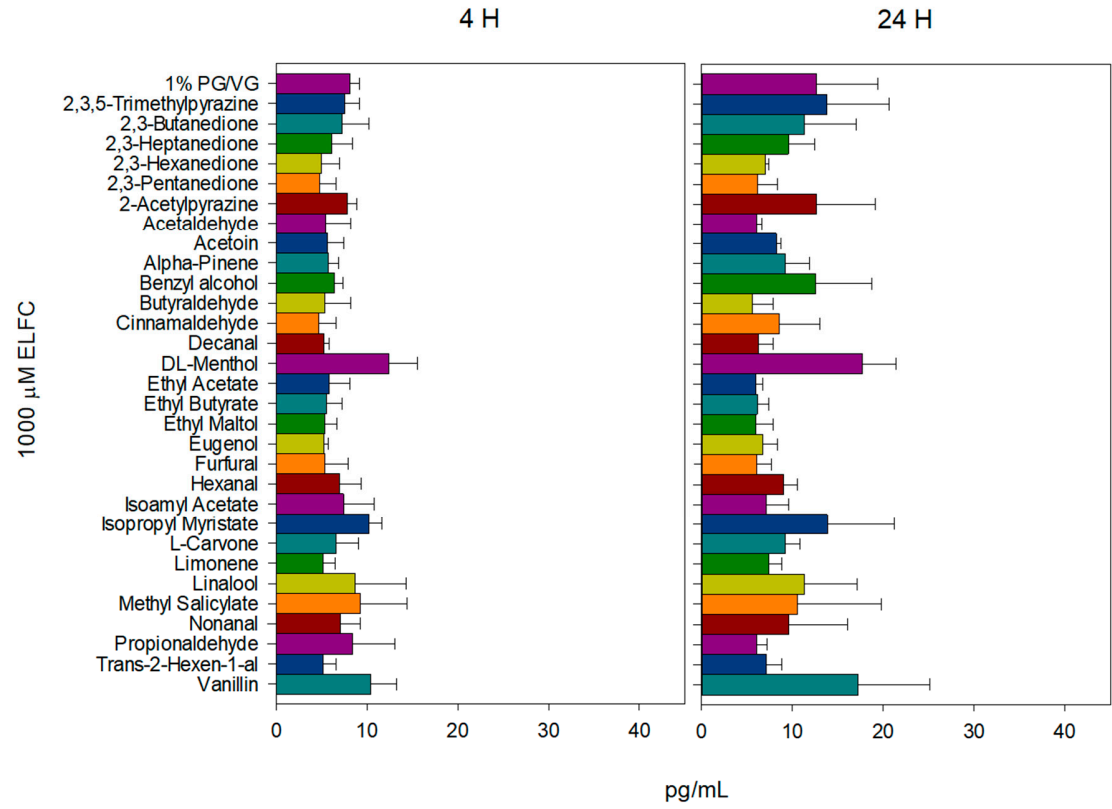
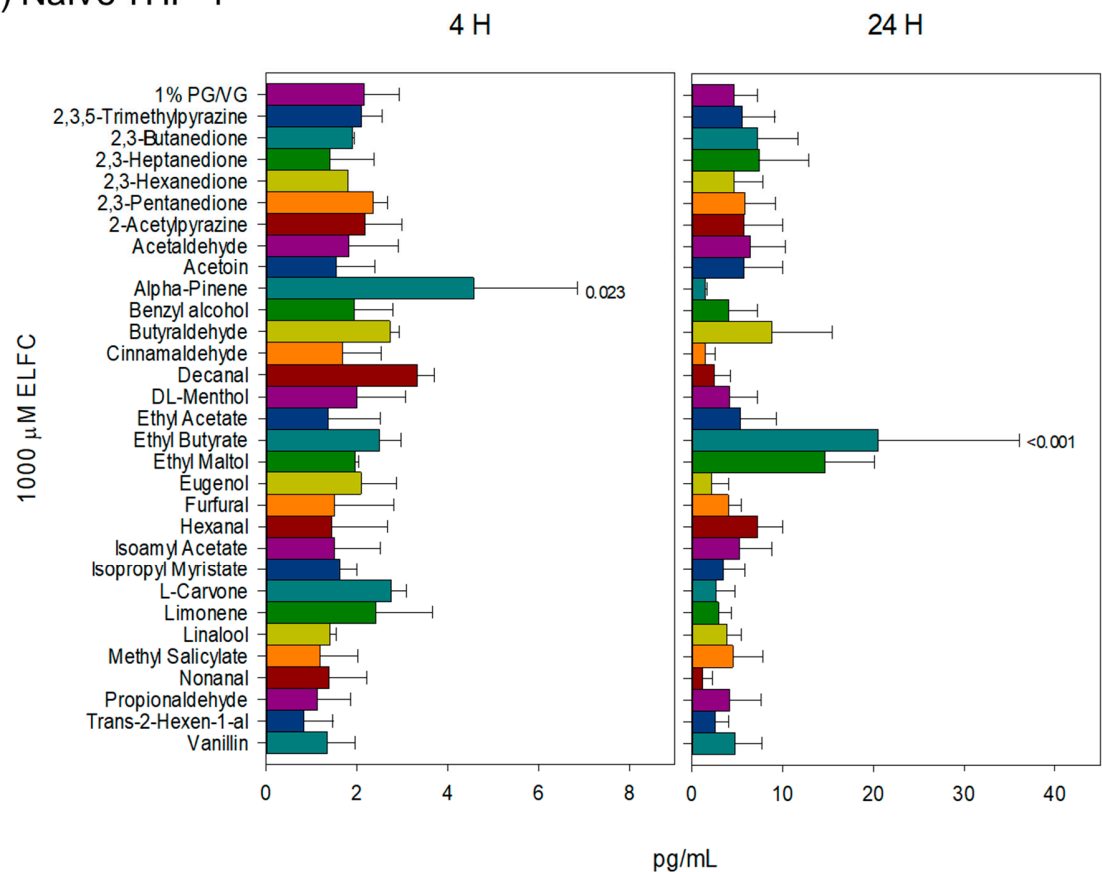


Figure S4. IL-1 β

A.) BEAS-2B



B.) Naïve THP-1



C.) Activated THP-1

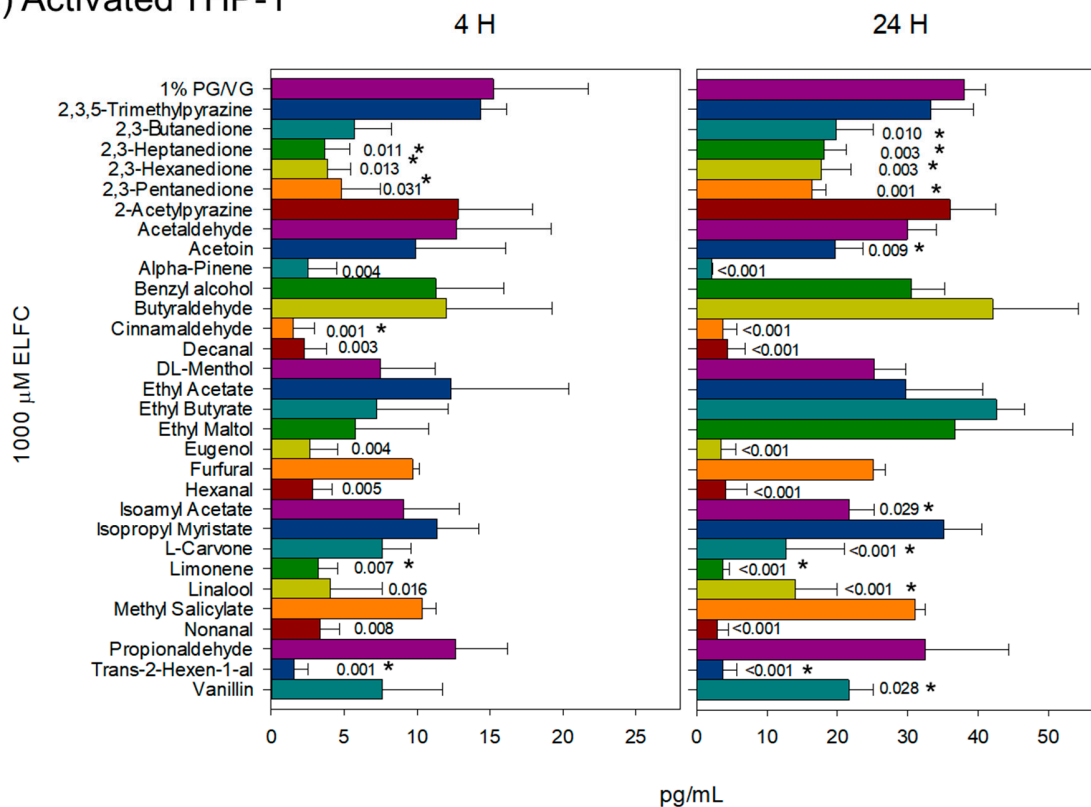
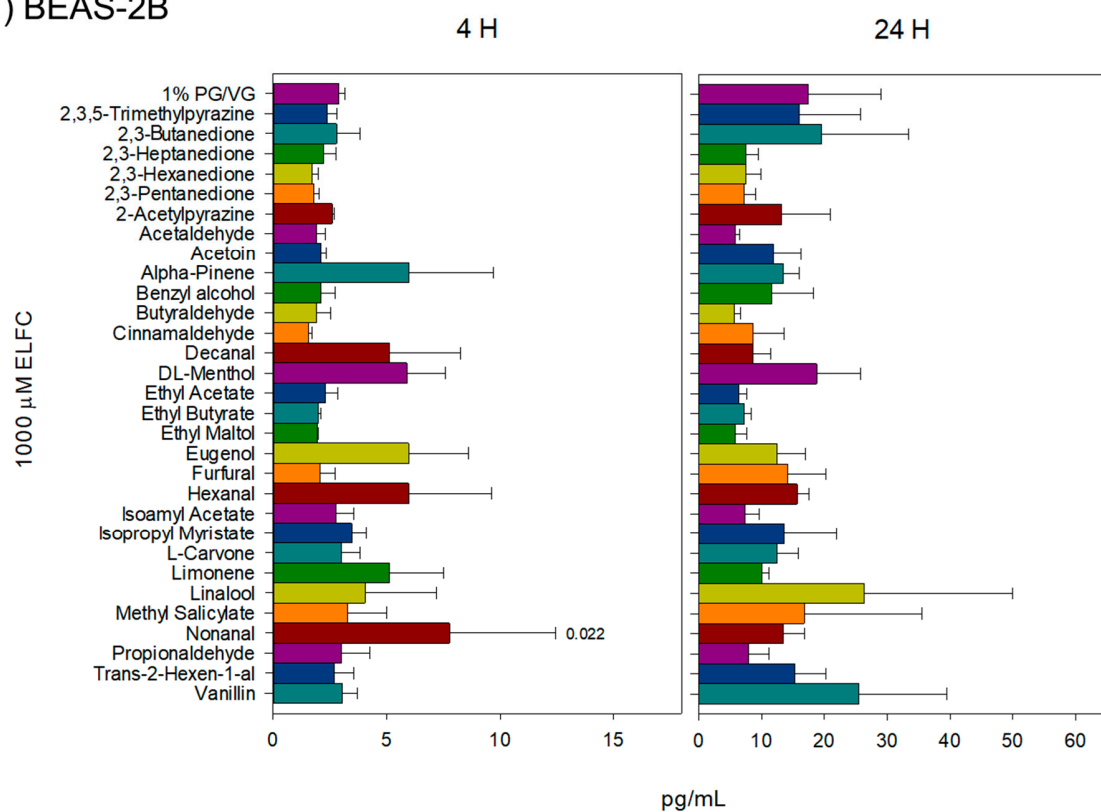
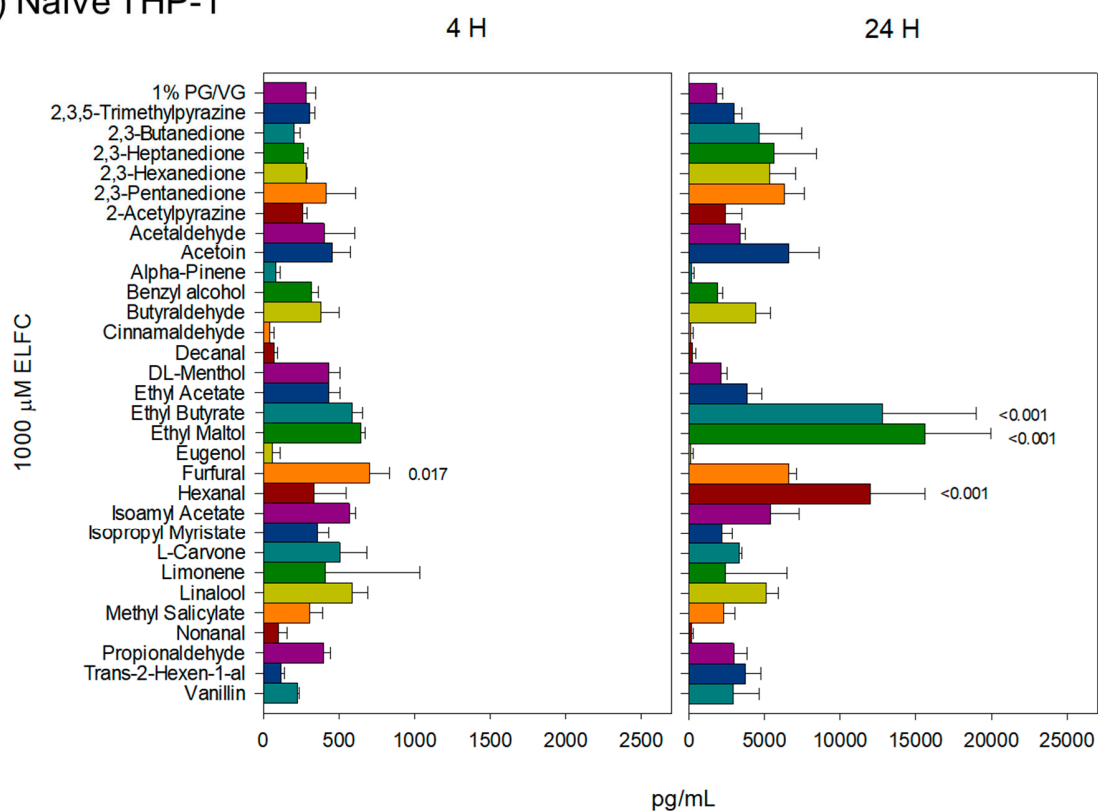


Figure S5. IL-6

A.) BEAS-2B



B.) Naïve THP-1



C.) Activated THP-1

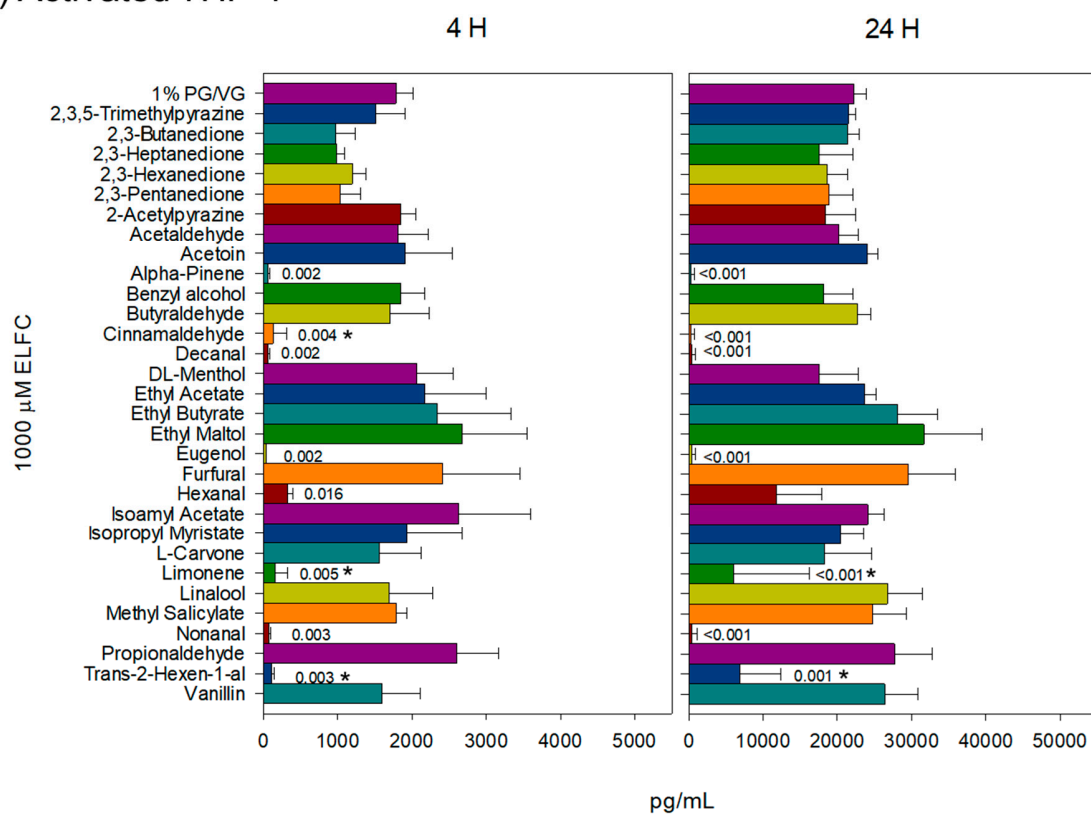
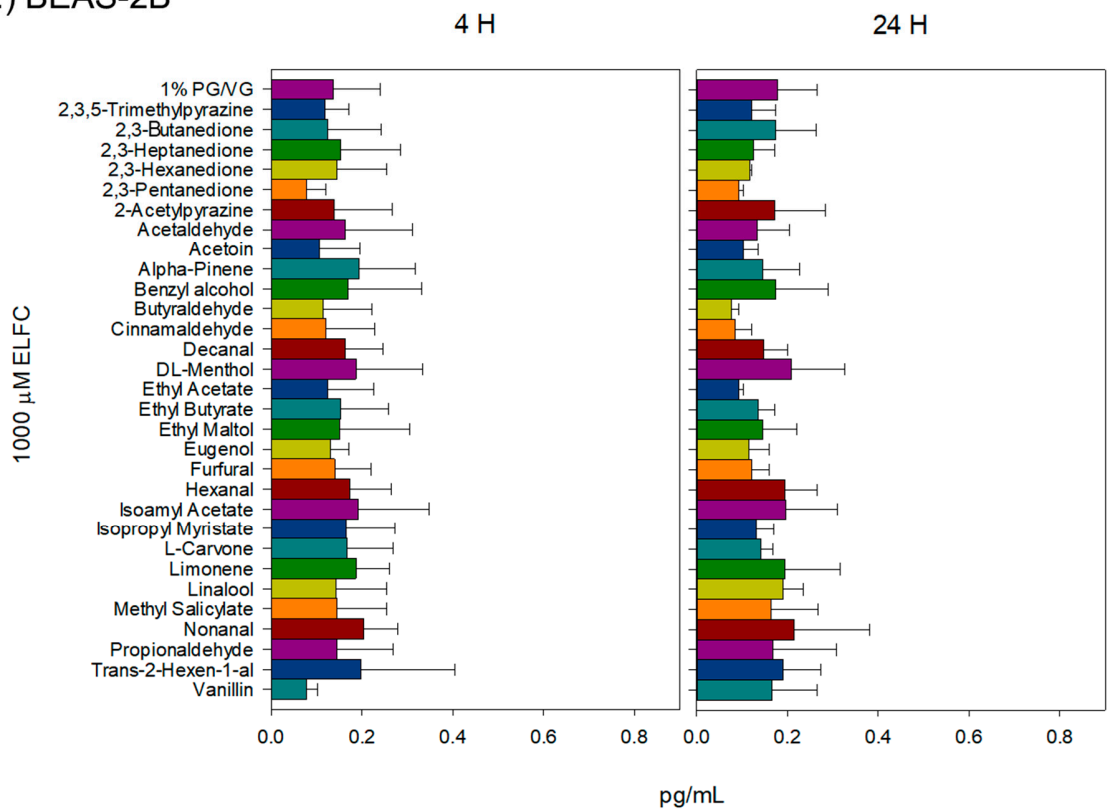
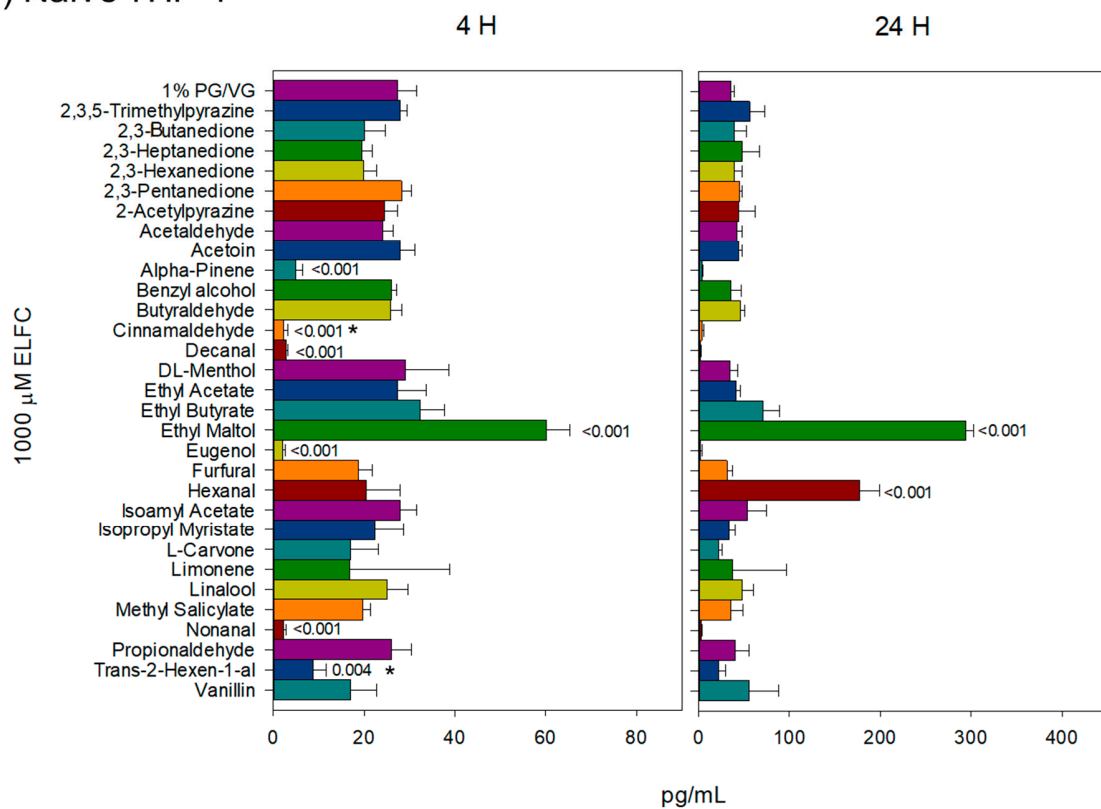


Figure S6. IL-8

A.) BEAS-2B



B.) Naïve THP-1



C.) Activated THP-1

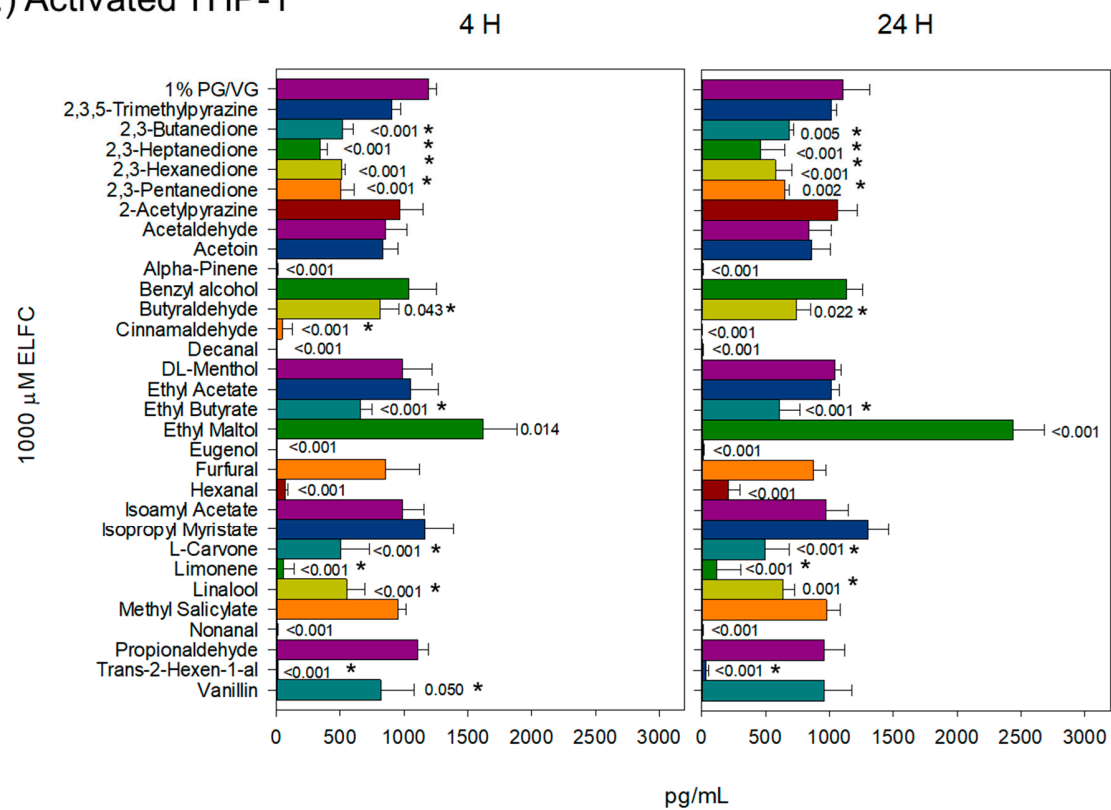
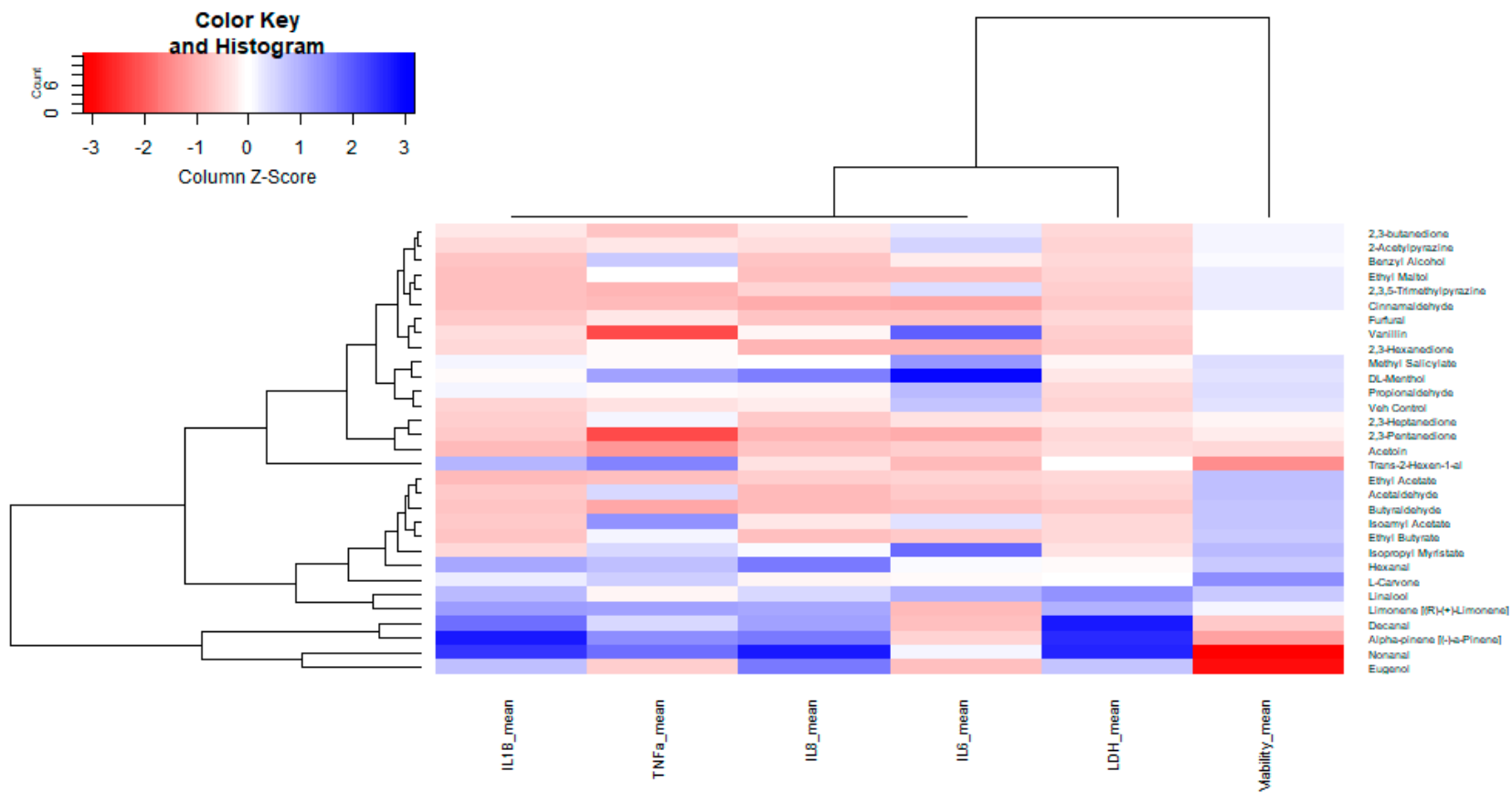


Figure S7. TNF- α

A)



B)

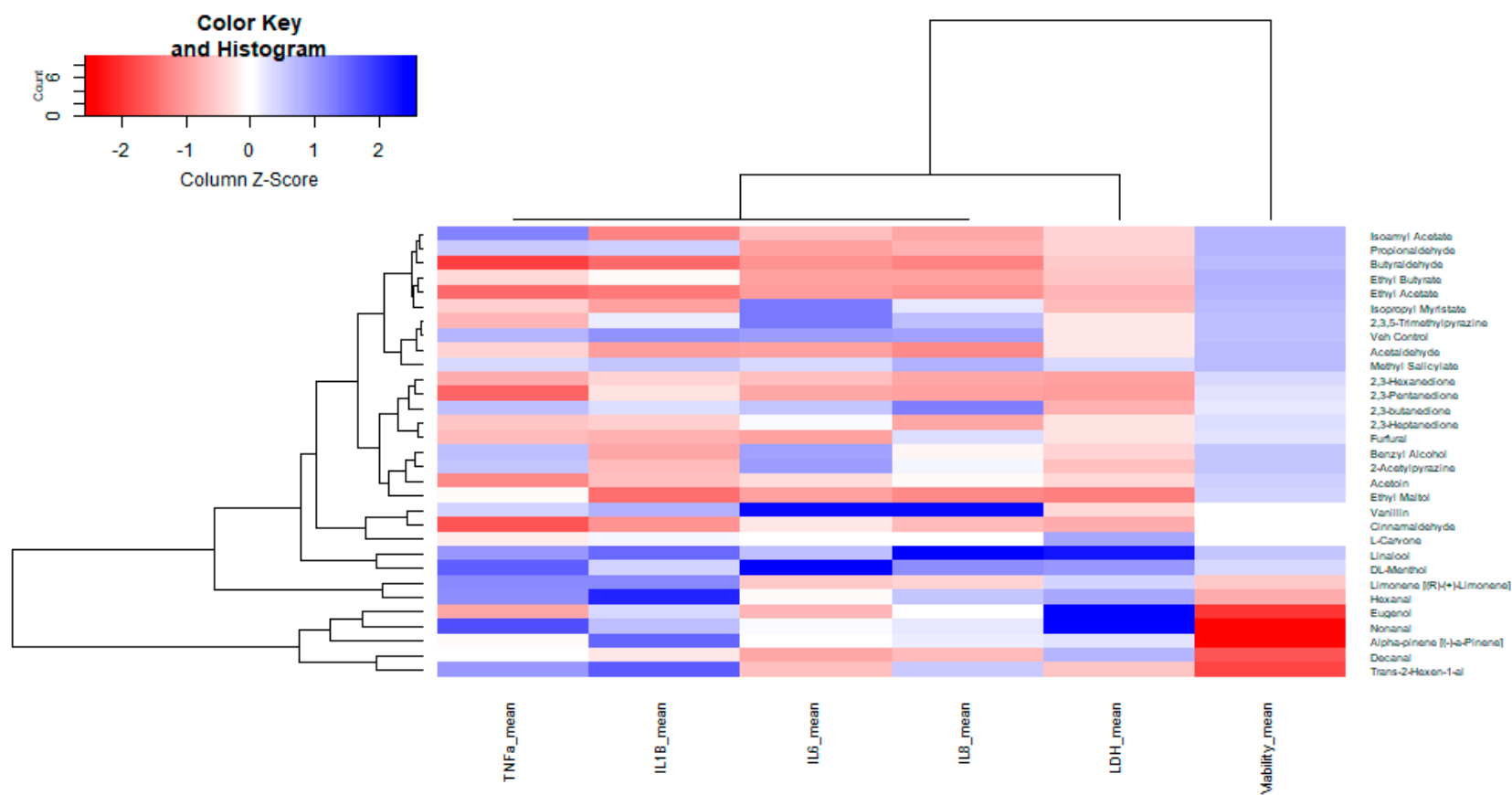
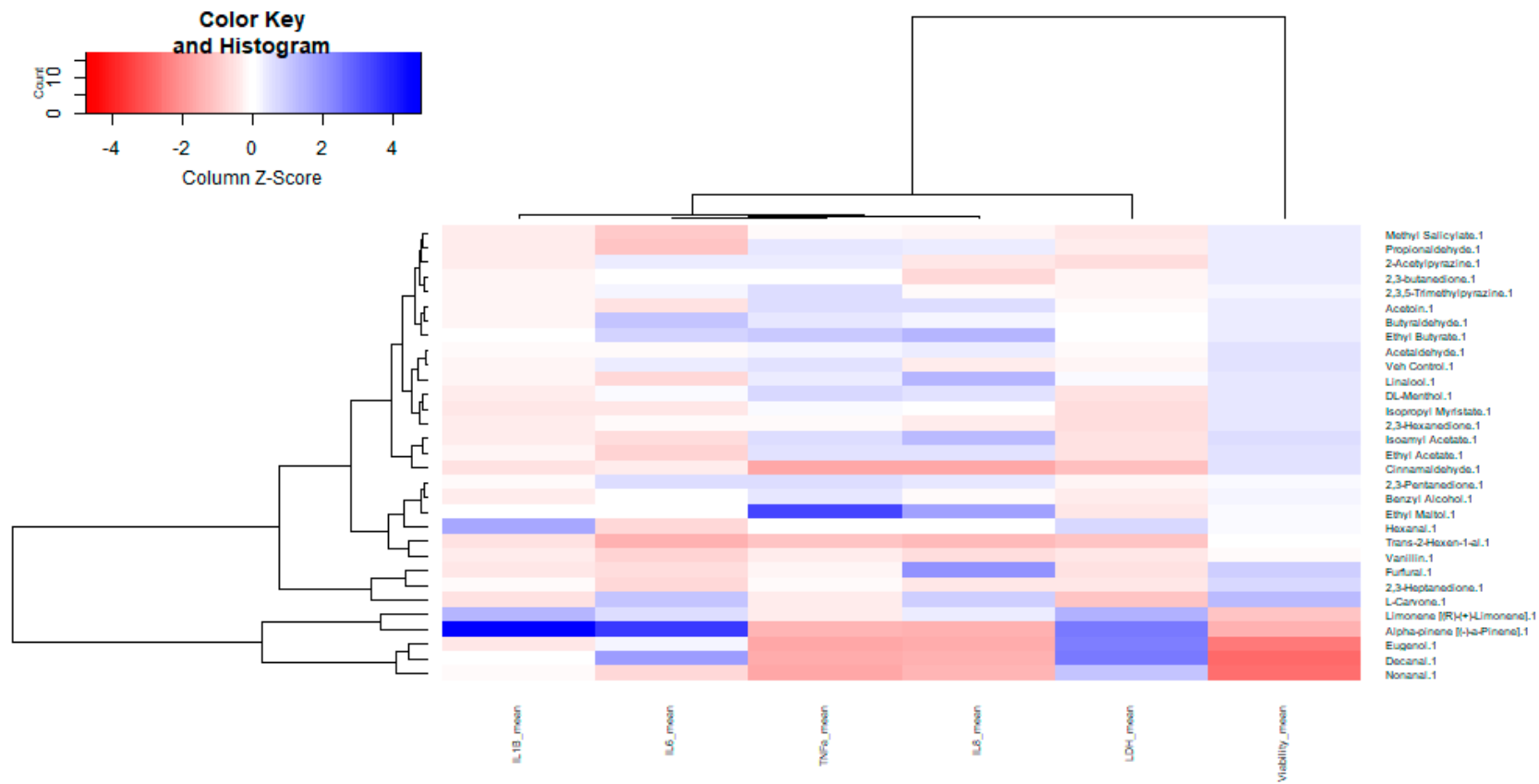


Figure S8. Heat map of clustering of toxicity tests in BEAS-2B. A) 4 hour B) 24 hour.

A)



B)

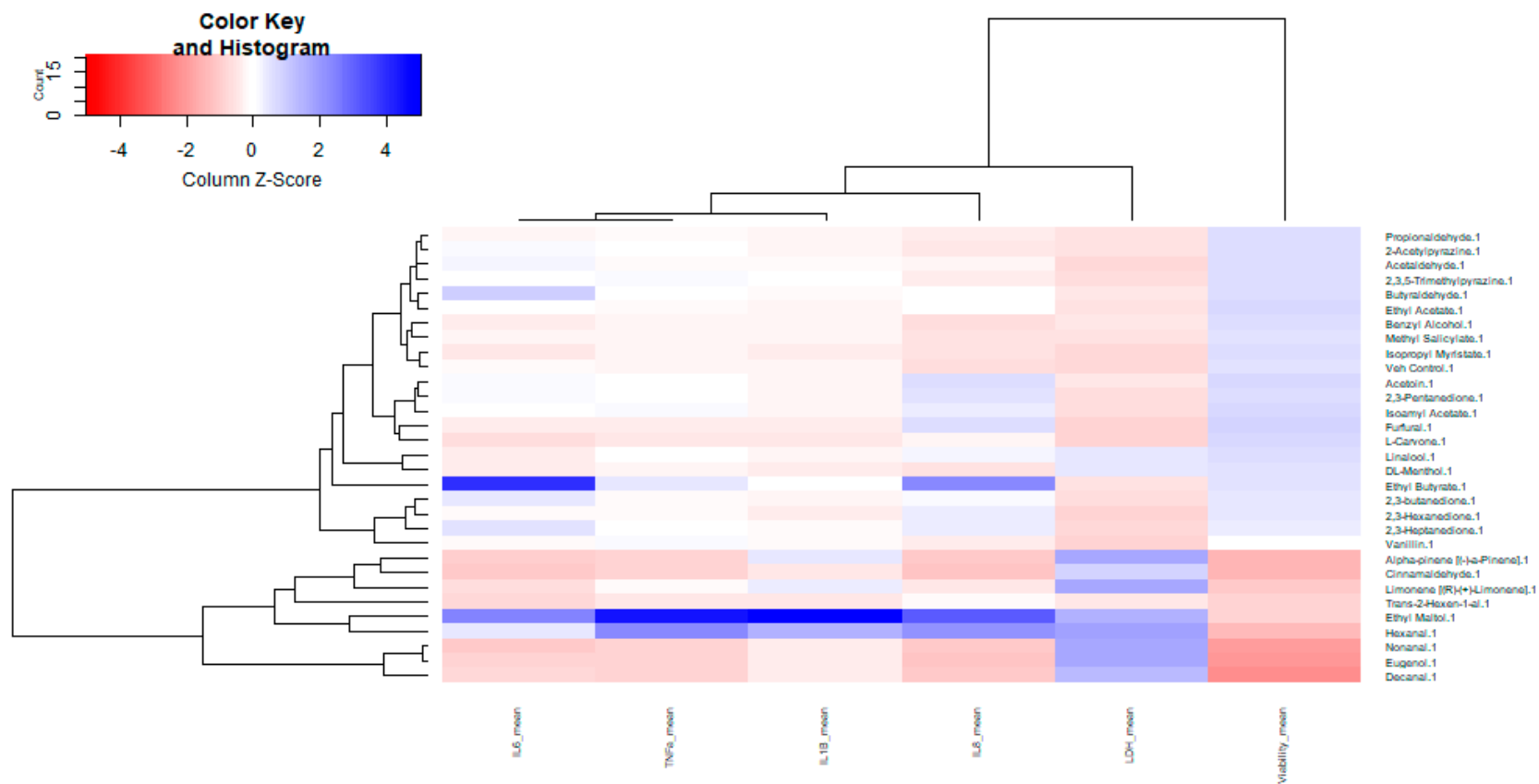
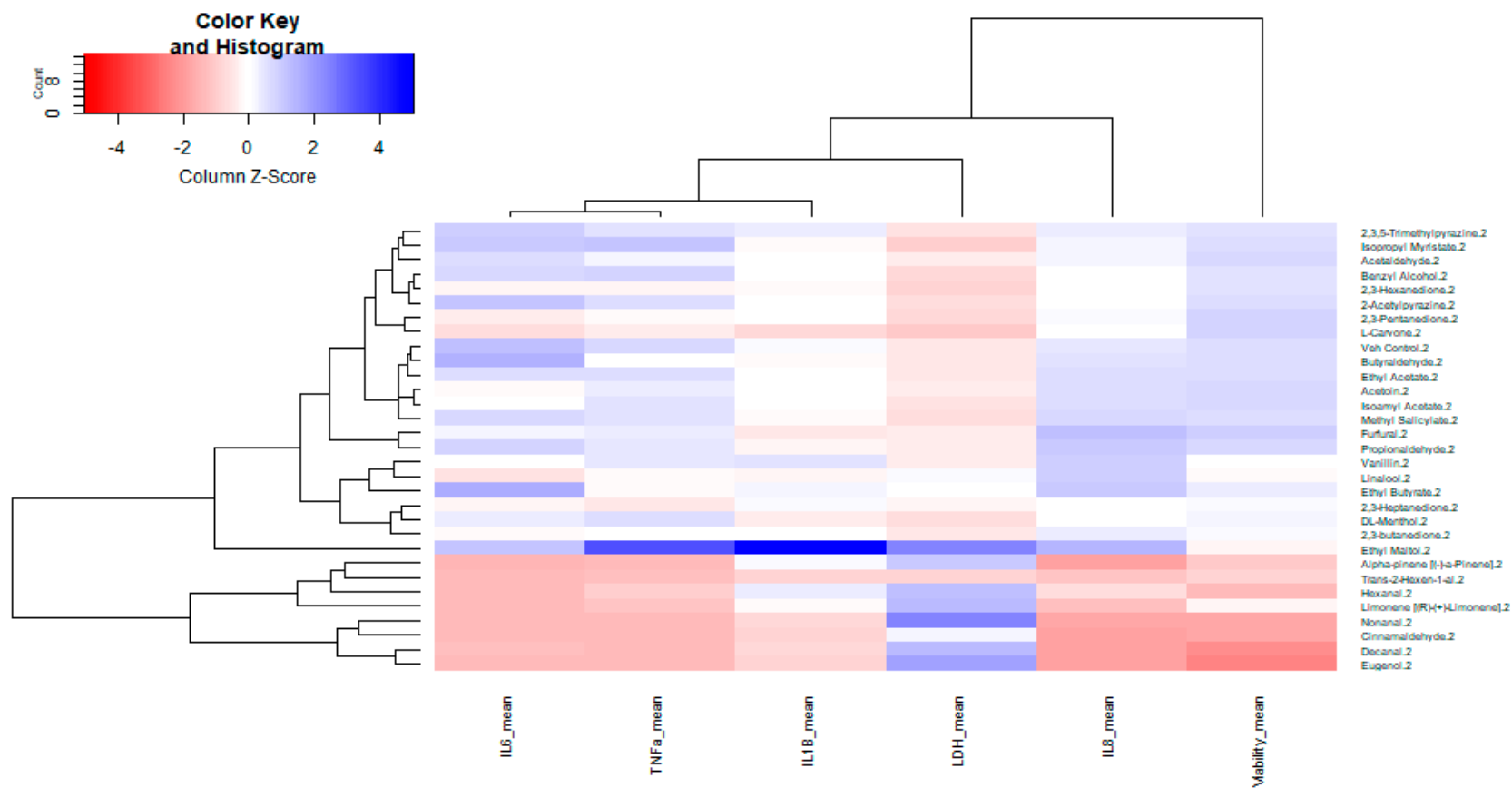


Figure S9. Heat map of clustering of toxicity tests in naïve THP-1. A) 4 hour B) 24 hour.

A)



B)

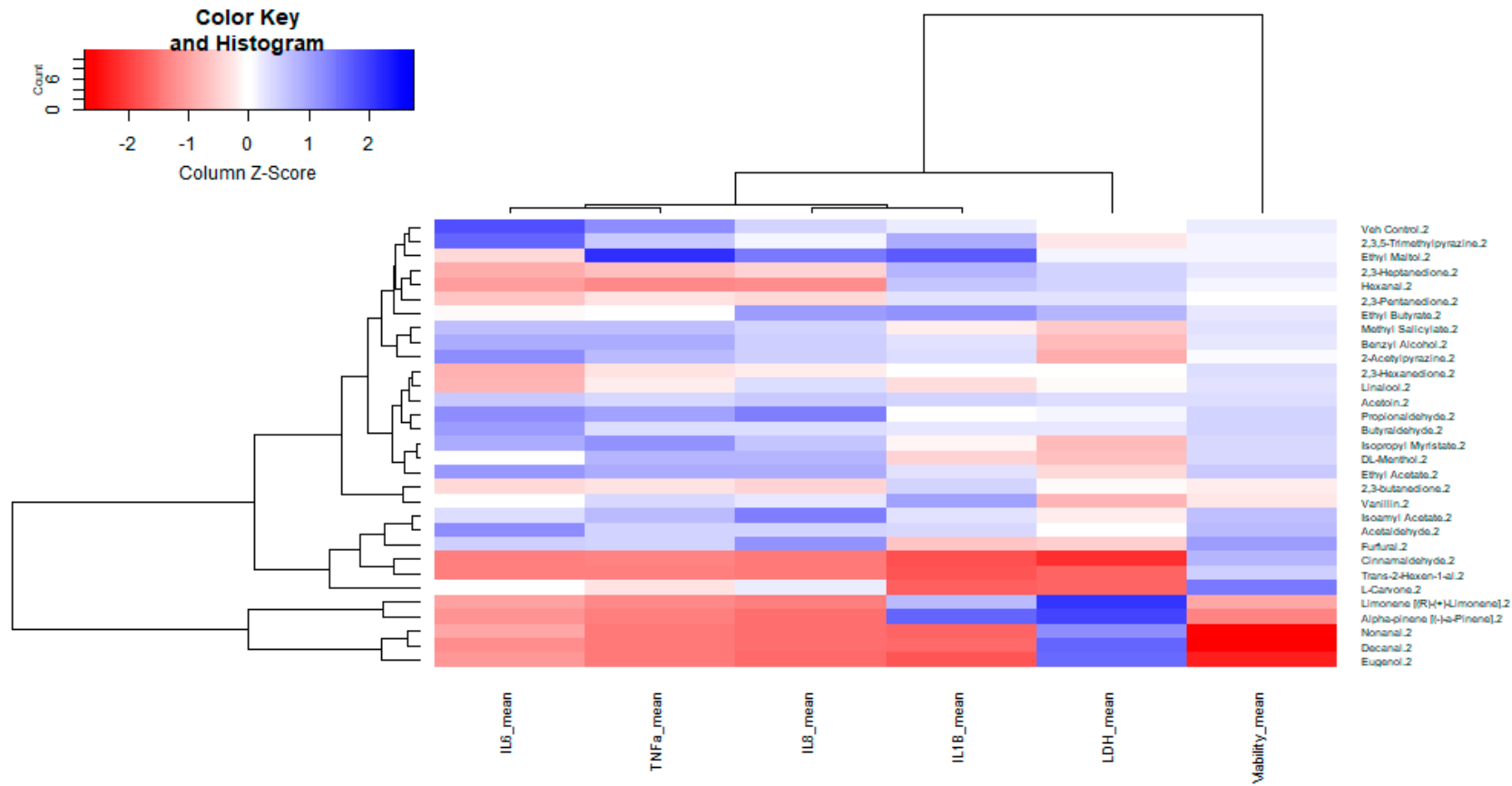


Figure S10. Heat map of clustering of toxicity tests in activated THP-1. A) 4 hour B) 24 hour.

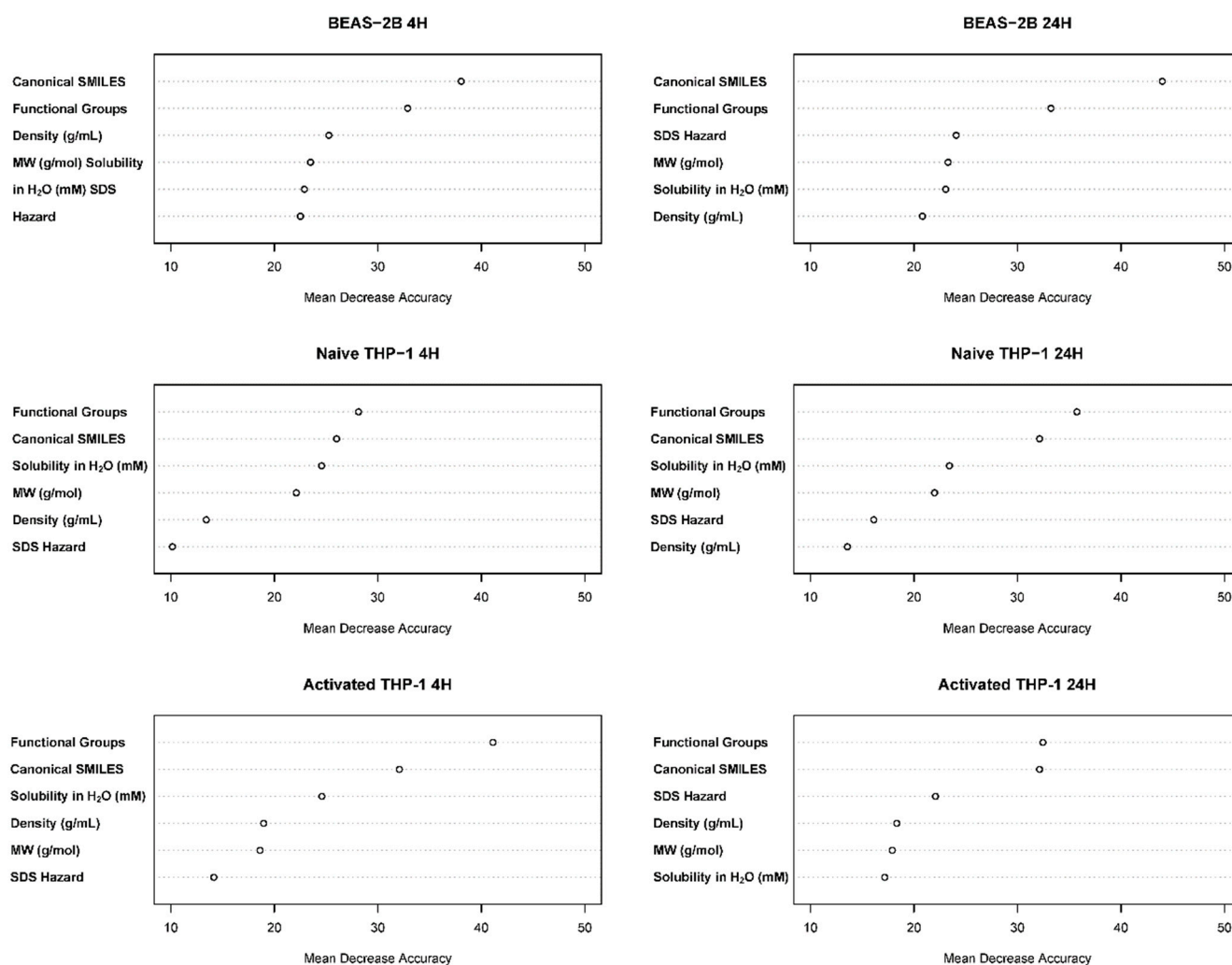


Figure S11. Important physicochemical properties in accurately predicting a compound's toxicity.

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