

Tr14 vs. saline control at 12h

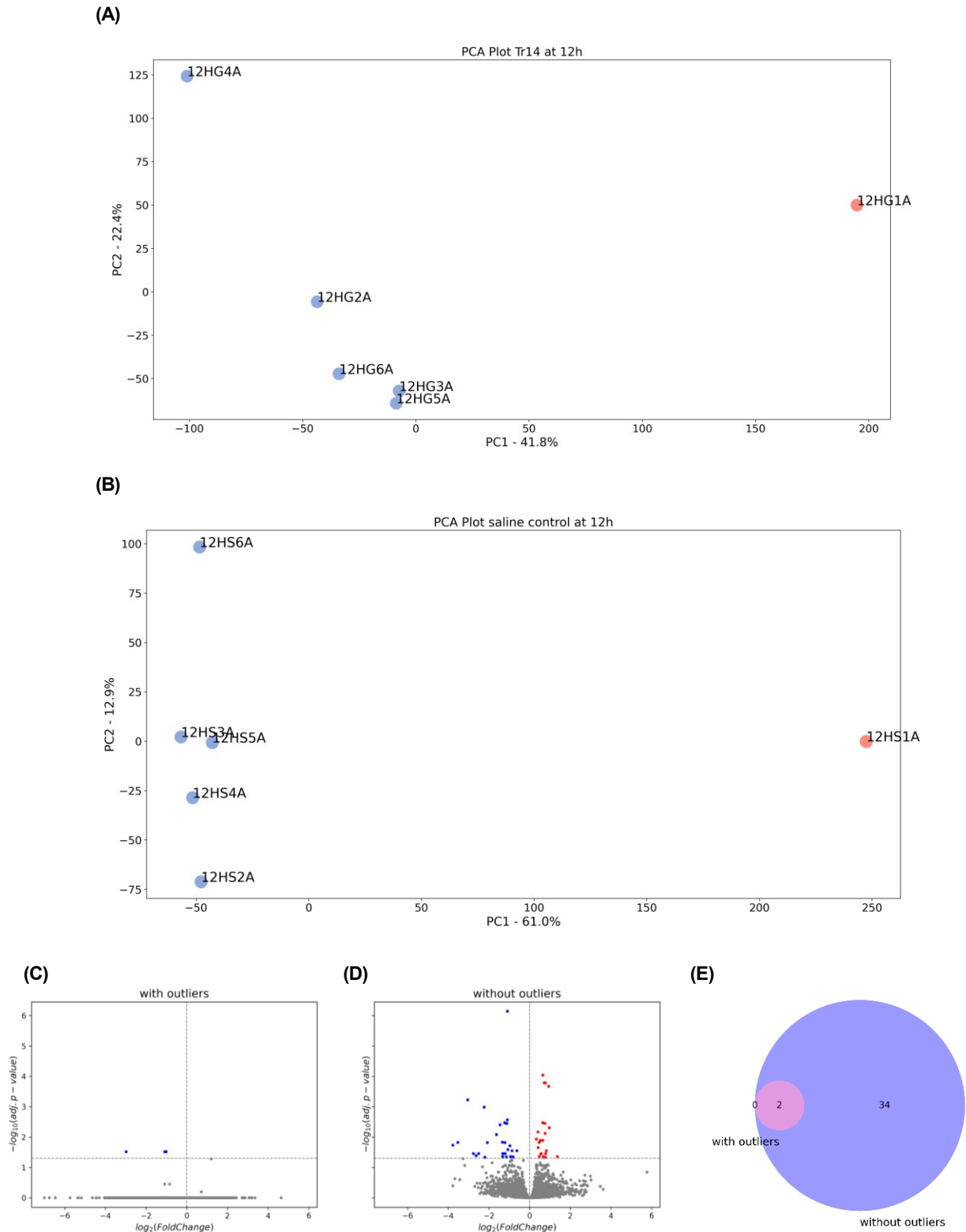


Figure S1: PCA analysis of RNA-seq samples for Tr14 treatment (A) and saline control (B) at 12h. Outliers (orange) were removed afterward. (C and D) Volcano plots showing the impact of outlier removal on the DeSeq2 differential analysis for Tr14 vs. control. (E) Venn diagram comparing the number of significant genes (adj. p -value < 0.05) before and after the removal of outliers.

Tr14 vs. saline control at 72h

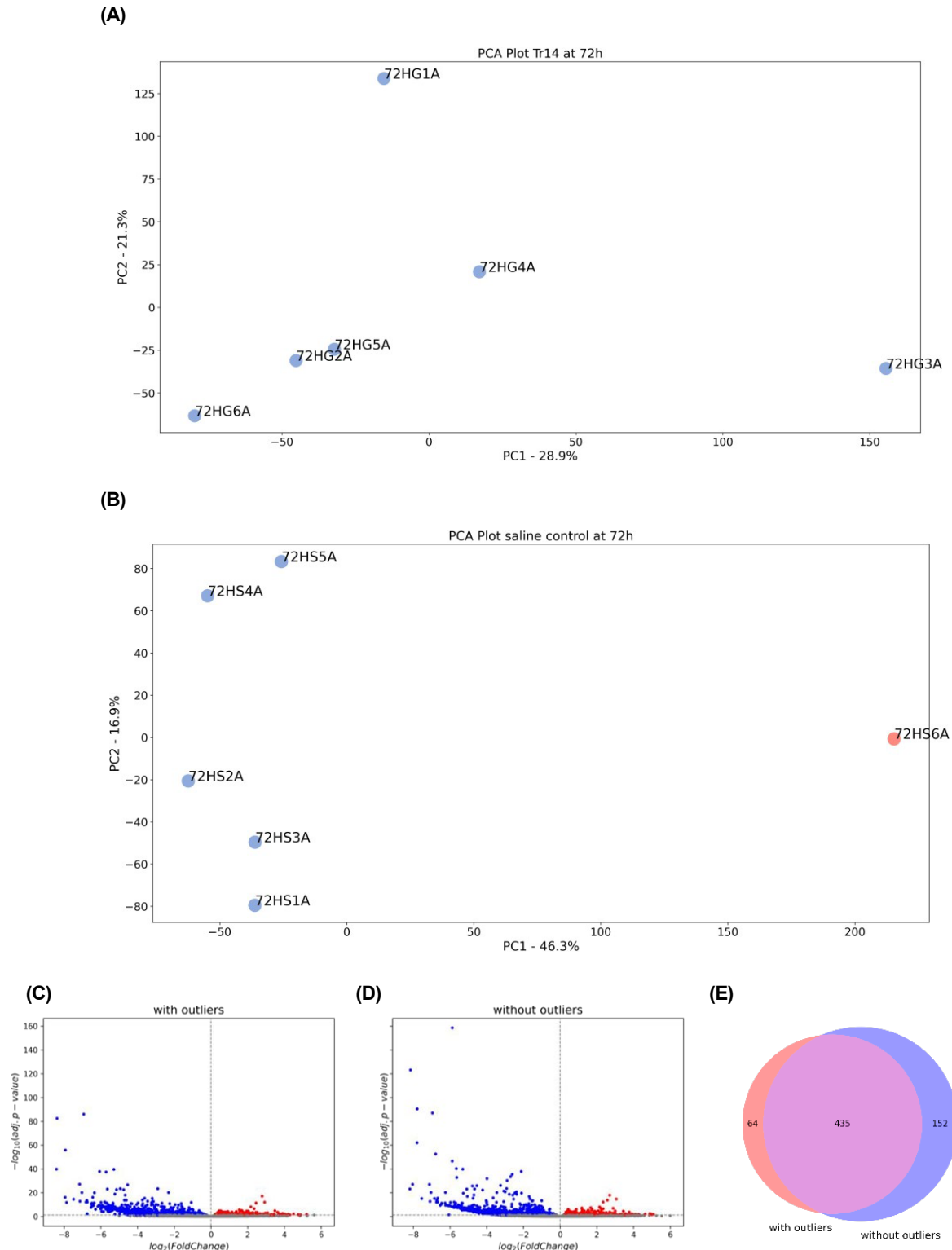


Figure S2: PCA analysis of RNA-seq samples for Tr14 treatment (A) and saline control (B) at 72h. Outliers (orange) were removed afterward. (C and D) Volcano plots showing the impact of outlier removal on the DeSeq2 differential analysis for Tr14 vs. control. (E) Venn diagram comparing the number of significant genes (adj. p -value < 0.05) before and after the removal of outliers.

Tr14 vs. saline control at 96h

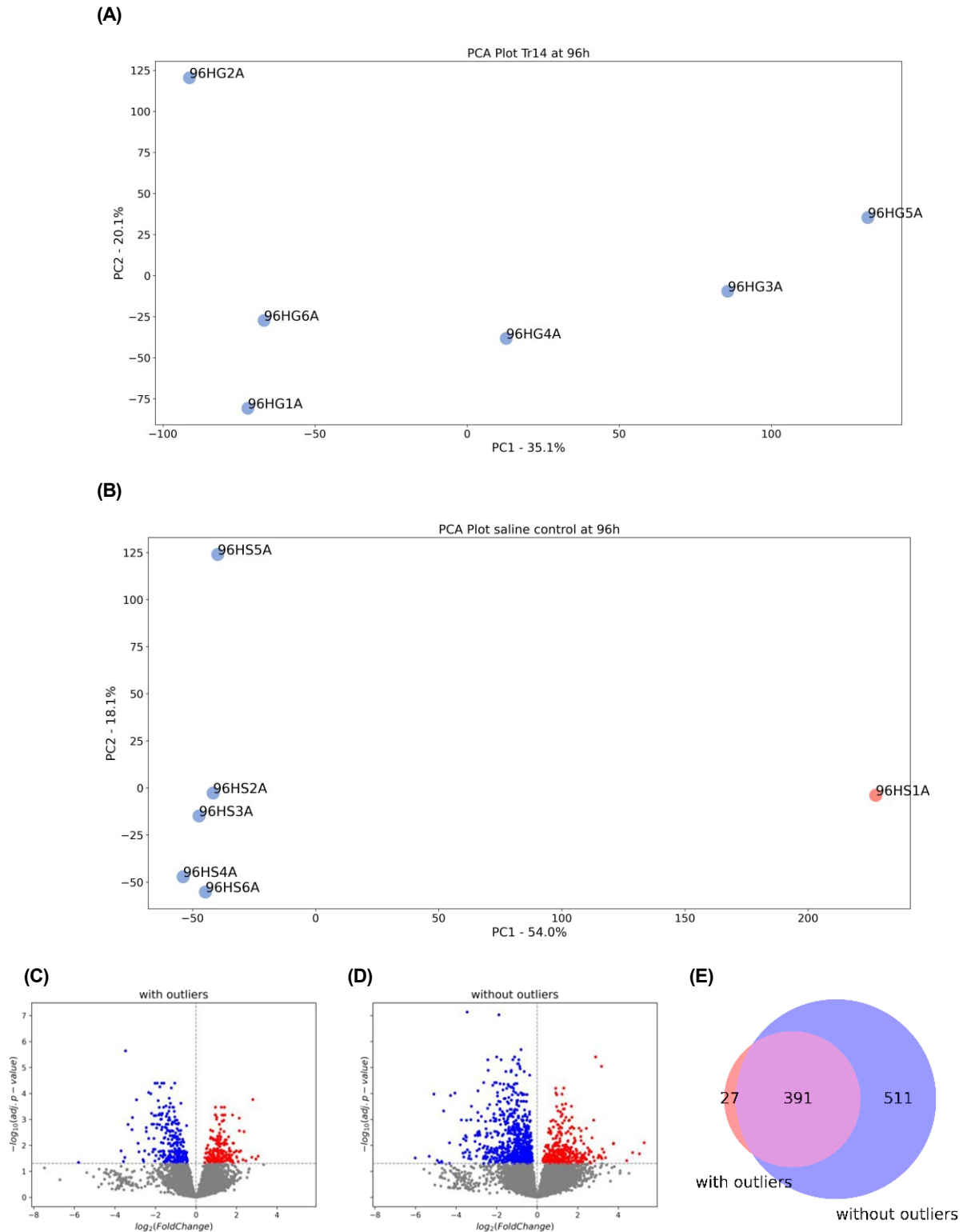


Figure S3: PCA analysis of RNA-seq samples for Tr14 treatment (A) and saline control (B) at 96h. Outliers (orange) were removed afterward. (C and D) Volcano plots showing the impact of outlier removal on the DeSeq2 differential analysis for Tr14 vs. control. (E) Venn diagram comparing the number of significant genes (adj. p -value < 0.05) before and after the removal of outliers.

Tr14 vs. saline control at 120h

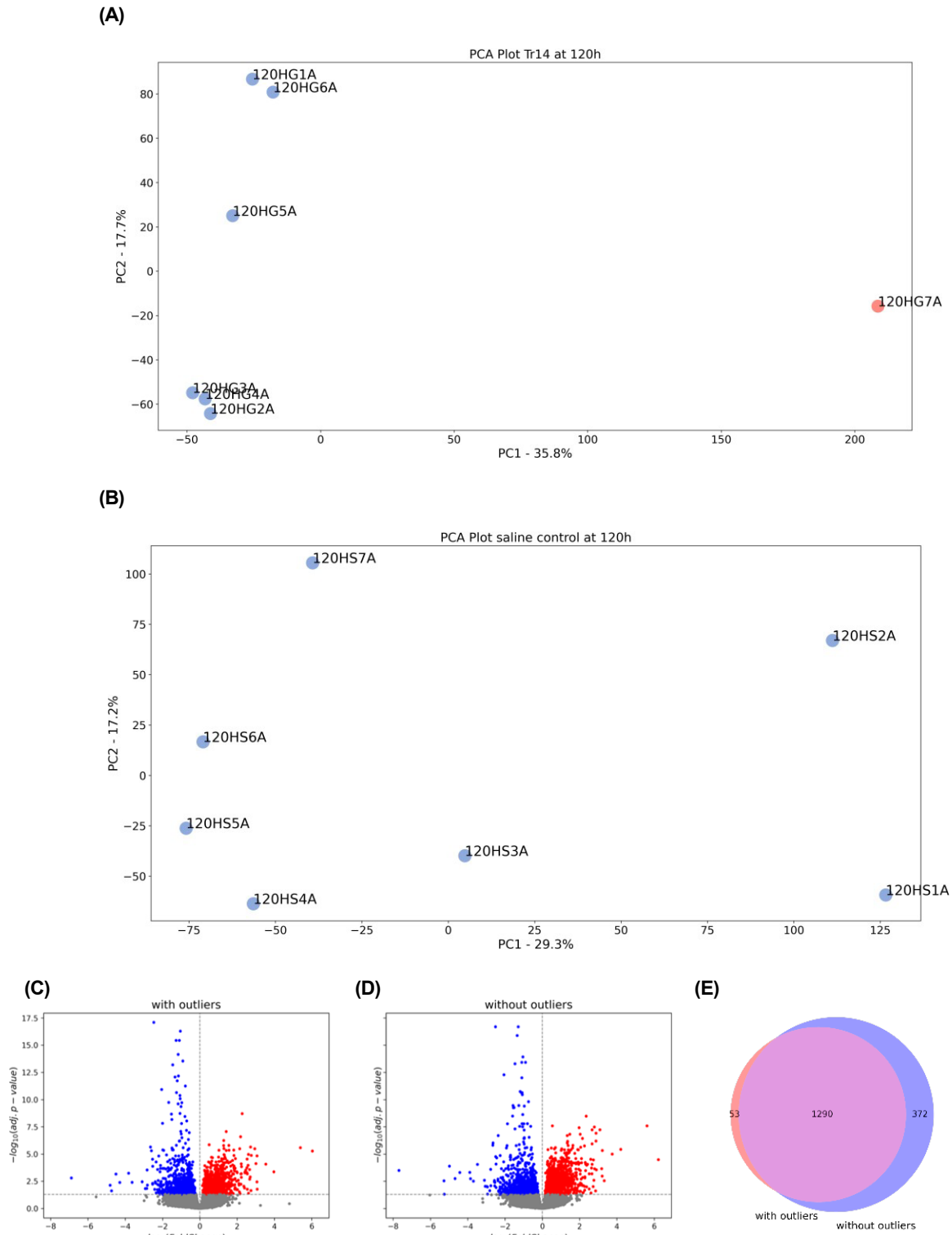


Figure S4: PCA analysis of RNA-seq samples for Tr14 treatment (A) and saline control (B) at 120h. Outliers (orange) were removed afterward. (C and D) Volcano plots showing the impact of outlier removal on the DeSeq2 differential analysis for Tr14 vs. control. (E) Venn diagram comparing the number of significant genes (adj. p -value < 0.05) before and after the removal of outliers.

Diclofenac vs. topical control at 96h

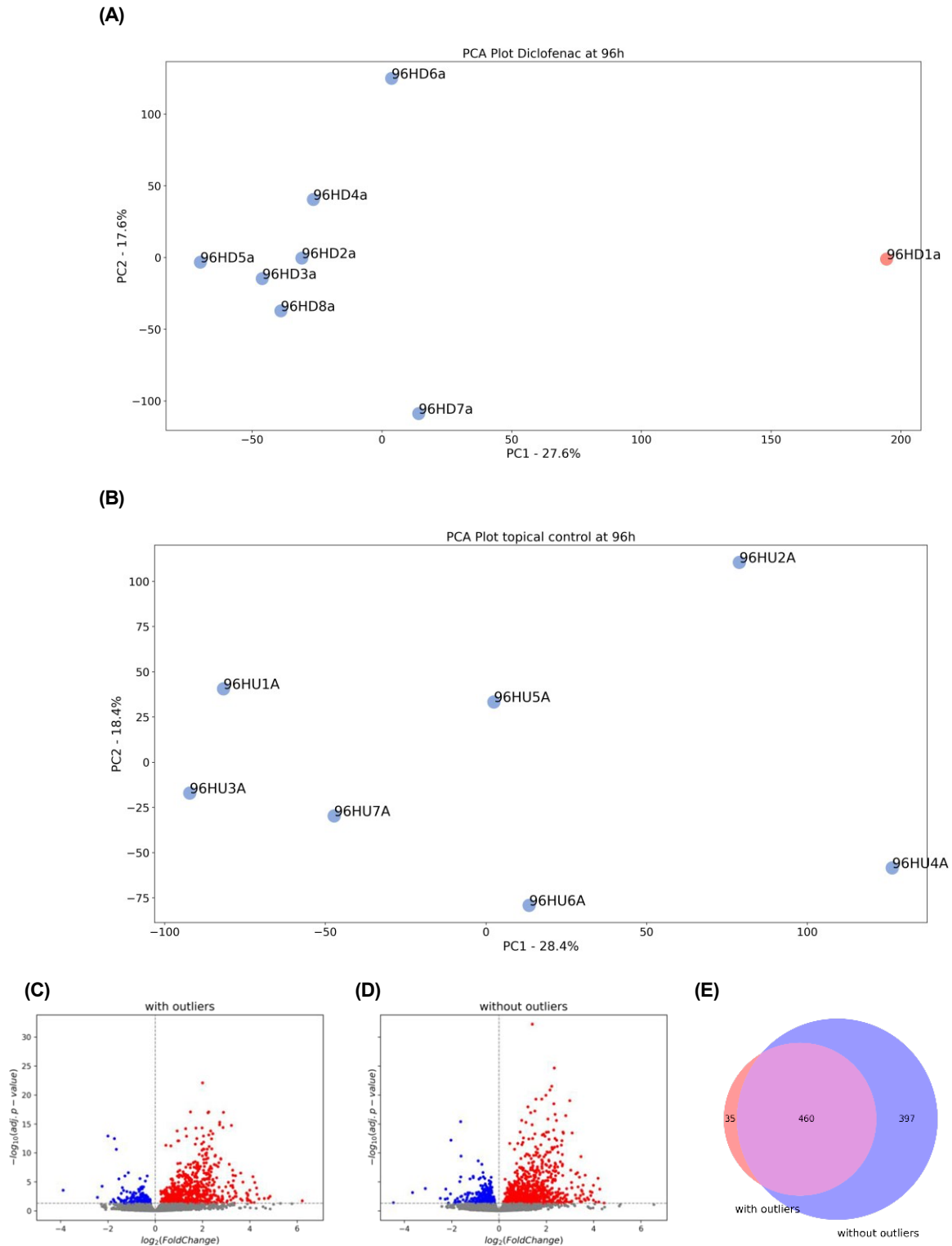
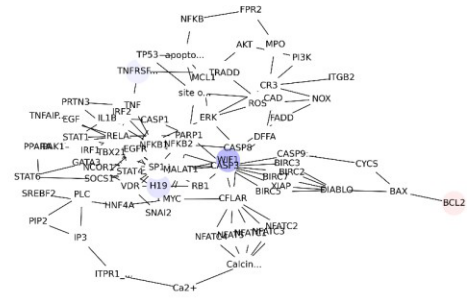
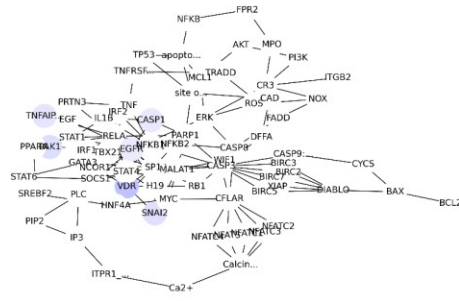


Figure S5: PCA analysis of RNA-seq samples for diclofenac treatment (A) and placebo control (B) at 96h. Outliers (orange) were removed afterward. (C and D) Volcano plots showing the impact of outlier removal on the DeSeq2 differential analysis for diclofenac vs. control. (E) Venn diagram comparing the number of significant genes (adj. p -value < 0.05) before and after the removal of outliers.

Tr14

Diclofenac

96H



120H

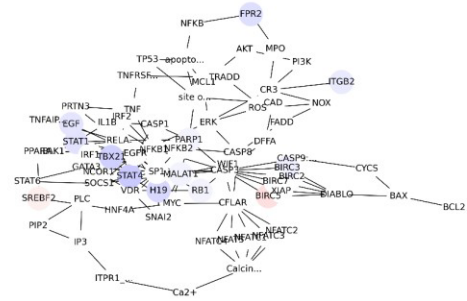
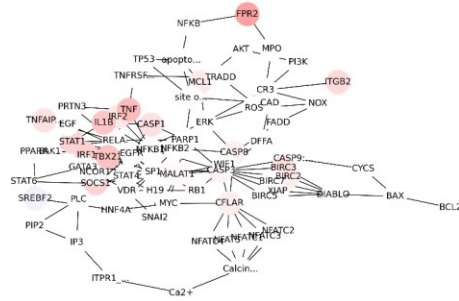


Figure S6: Core Regulatory Networks (CRNs) of the “apoptotic process” phenotype for Tr14 and Diclofenac treatment at 96 and 120 hours. Gene triplets in the molecular interaction map connected to the phenotype are ranked by $\log_2$ fold change values and network features. The highest ranked motifs were then selected and merged into the CRNs.

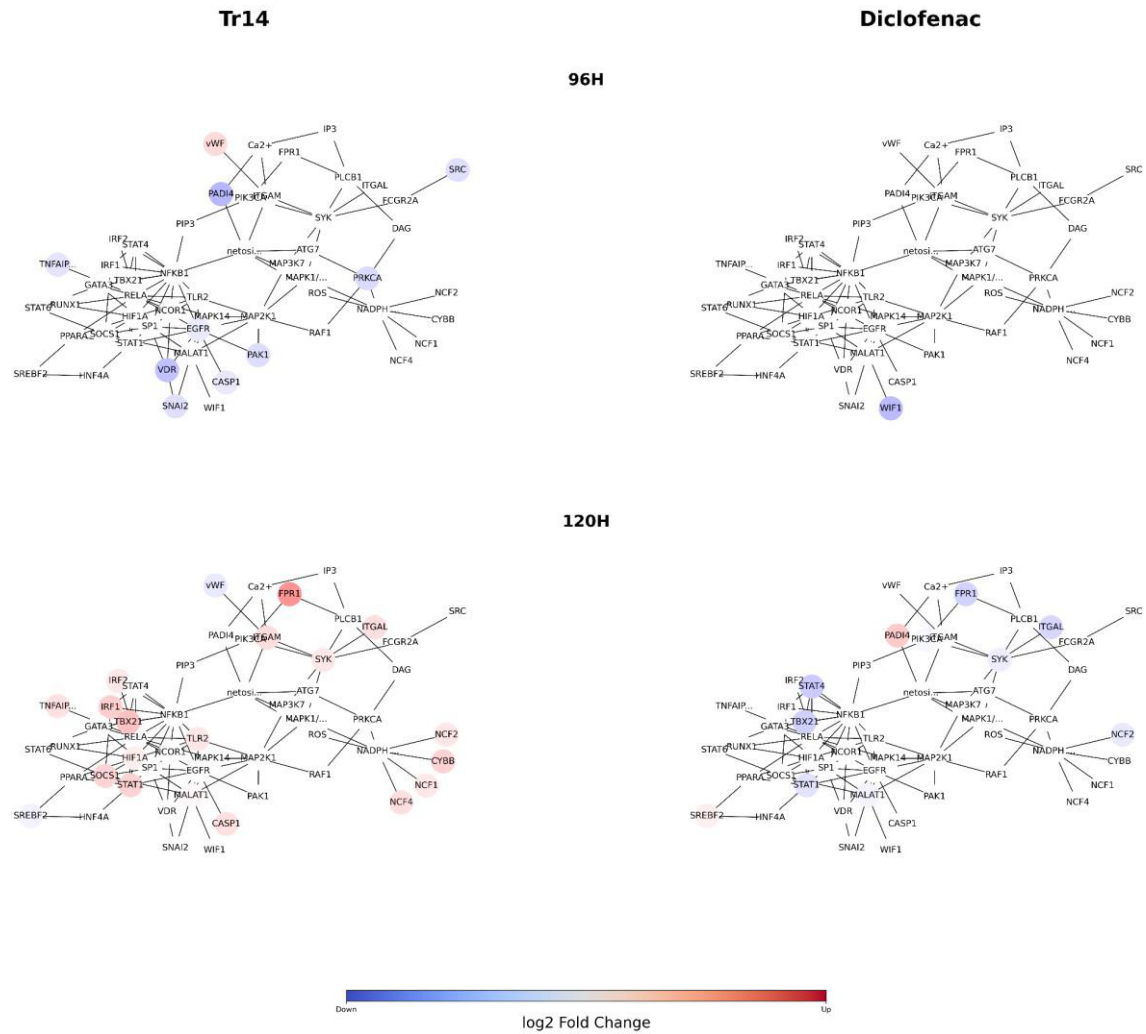
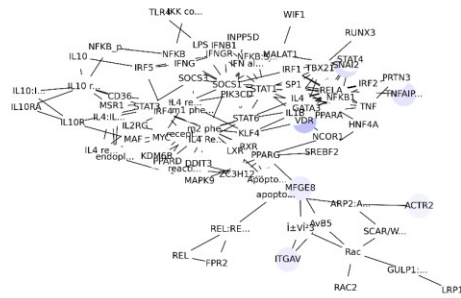


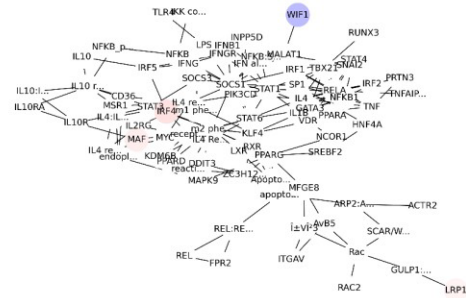
Figure S7: Core Regulatory Networks (CRNs) of the “NETosis” phenotype for Tr14 and Diclofenac treatment at 96 and 120 hours. Gene triplets in the molecular interaction map connected to the phenotype are ranked by $\log_2$ fold change values and network features. The highest ranked motifs were then selected and merged into the CRNs.

Tr14



Diclofenac

96H



120H

