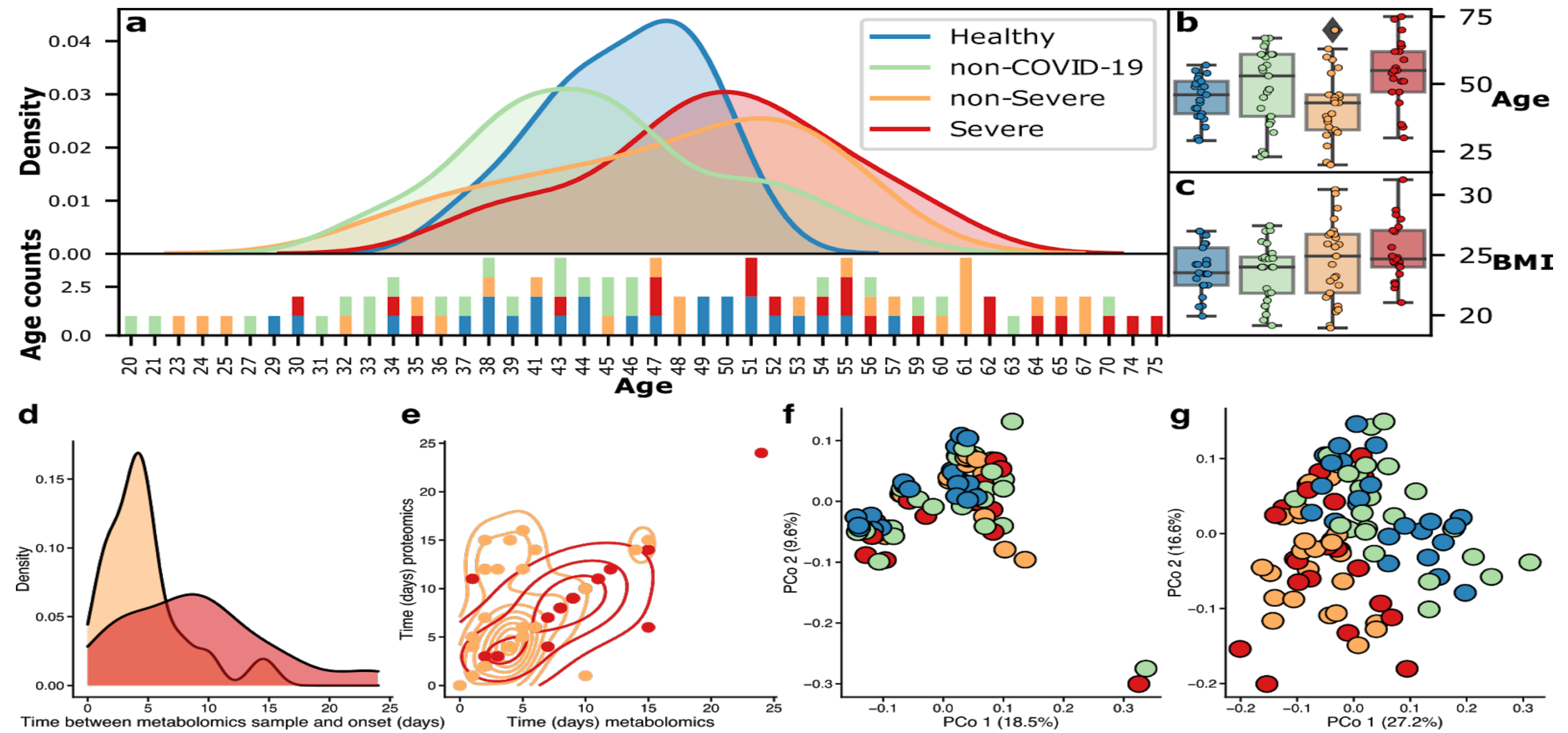# Investigating functional epidemiology of proteins and metabolites as biomarkers

Ranojoy Chatterjee, Abhigya Giri, Brendan Mann, Allen Ross, Keith A. Crandall, Ali Rahnavard
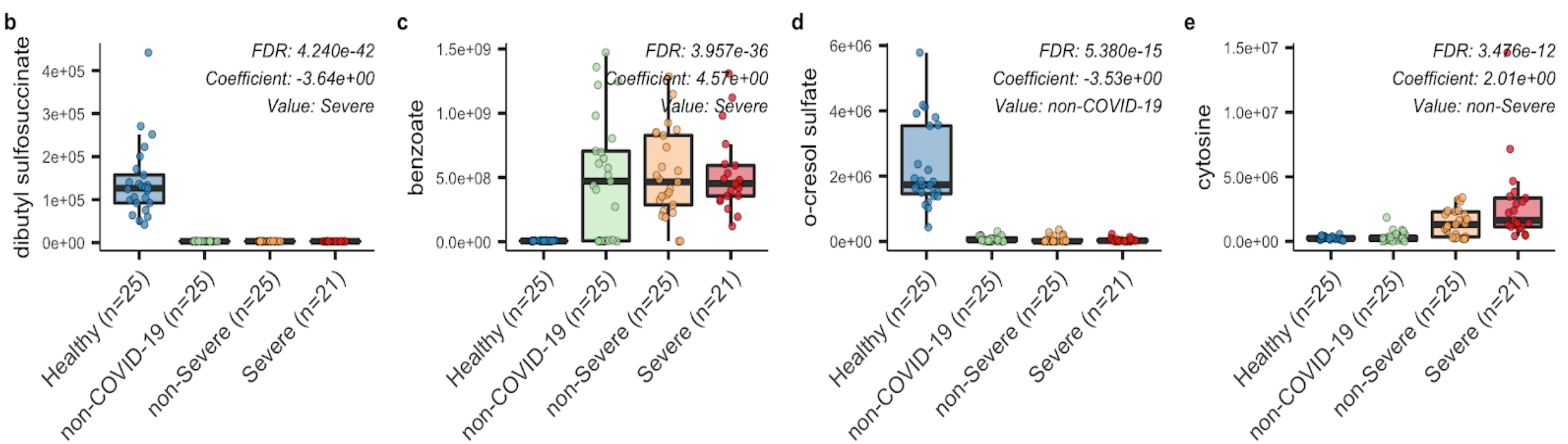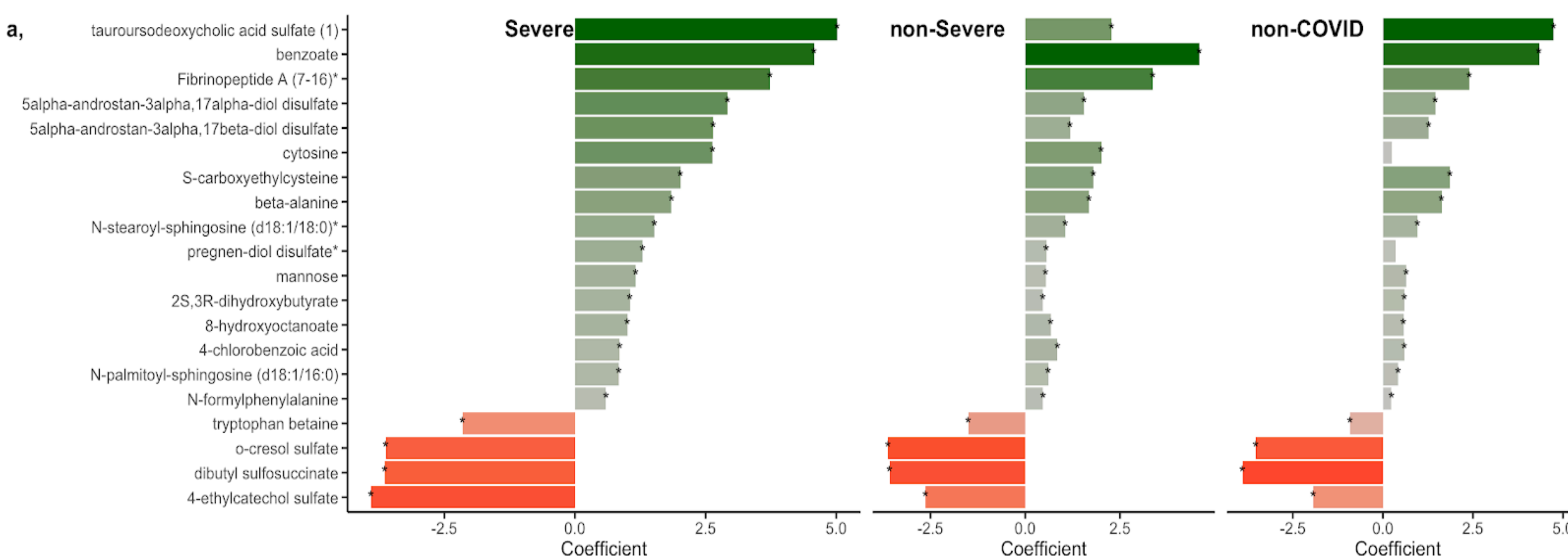
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Motivation:

➤ Investigate the changes in metabolites and proteomics for underlying health` status.

➤ Create a classification system using machine learning to predict health outcomes based on the omics data.

➤ Validate the results using statistical tools and approaches.

➤ Identify major pathways which are directly related to clinical info, thus aiding in better understanding of the underlying biological mechanism
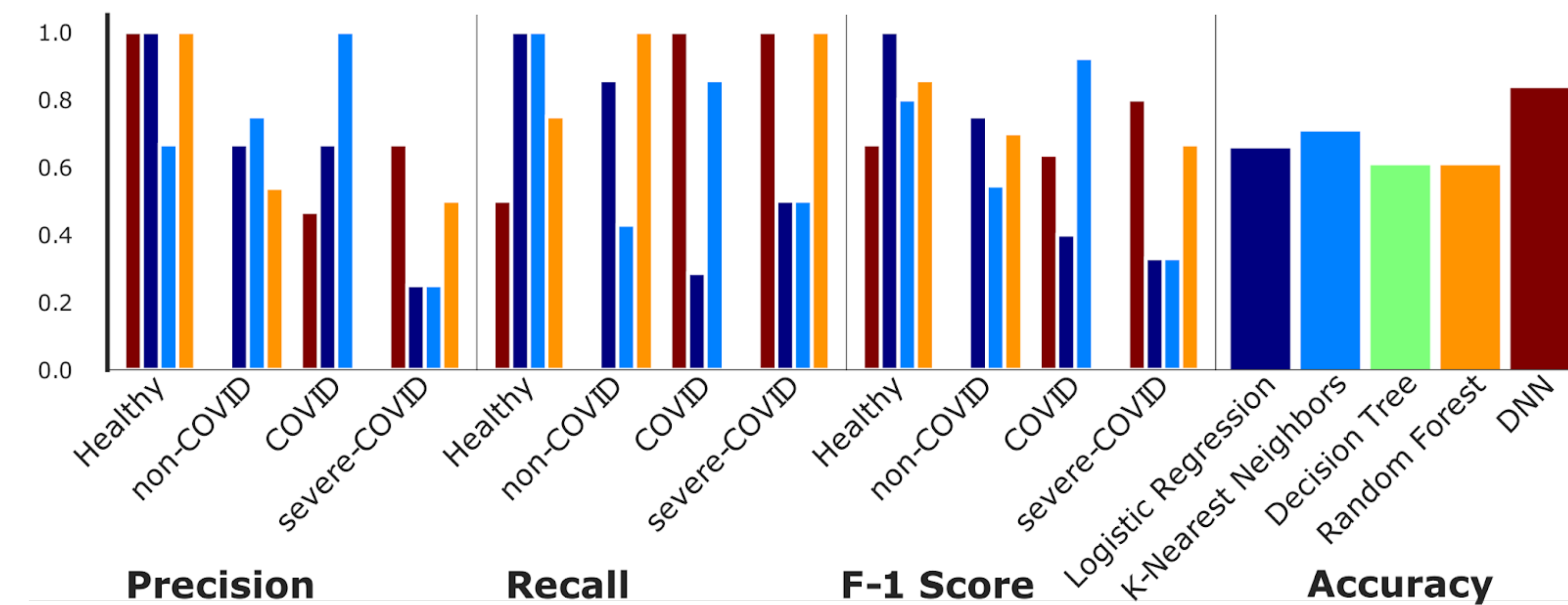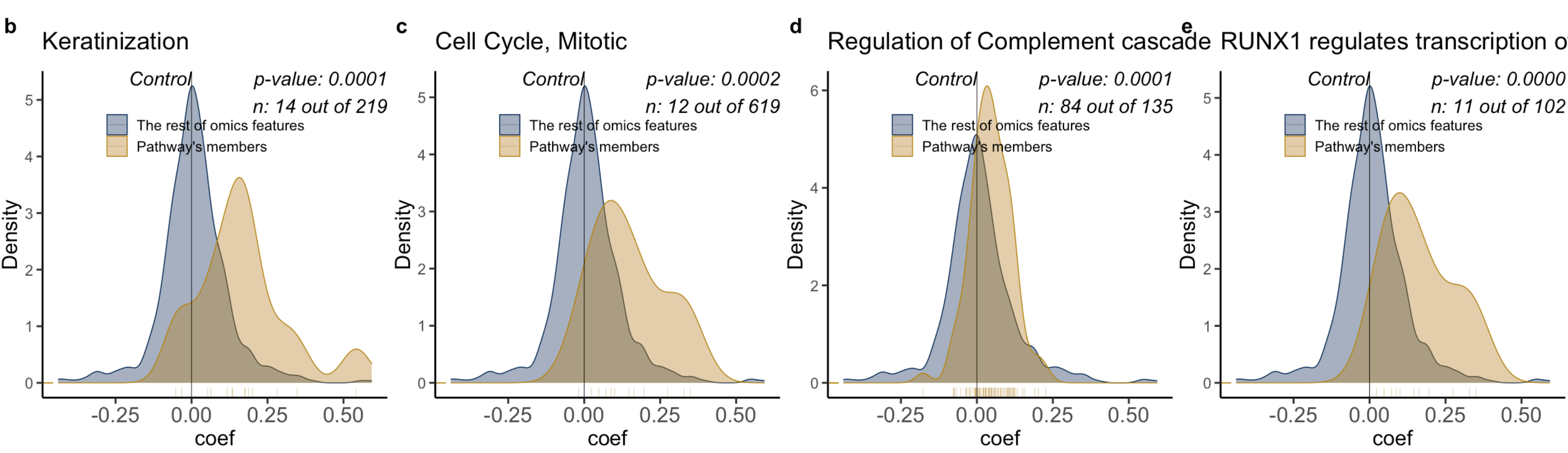
Metabolites of COVID-19:

Pathways of COVID-19:

b Keratinization — Control — p-value: 0.0001 — 14 out of 219
c Cell Cycle, Mitotic — Control — p-value: 0.0002 — 12 out of 619
d Regulation of Complement cascade — Control — p-value: 0.0001 — 84 out of 135
e RUNX1 regulates transcription o — Control — p-value: 0.0000 — 11 out of 102
The rest of omics features — Pathway's members

Deep learning for COVID-19 Predication:

Precision — Recall — F-1 Score — Accuracy

➤ Proteins and metabolites associated with health status and disease severity are indicative of lung, liver, and gut dysfunction and may represent potential biomarkers or therapeutic targets.

➤ Developed a DNN prediction model with an accuracy of 88%

https://www.rahnavard.org/