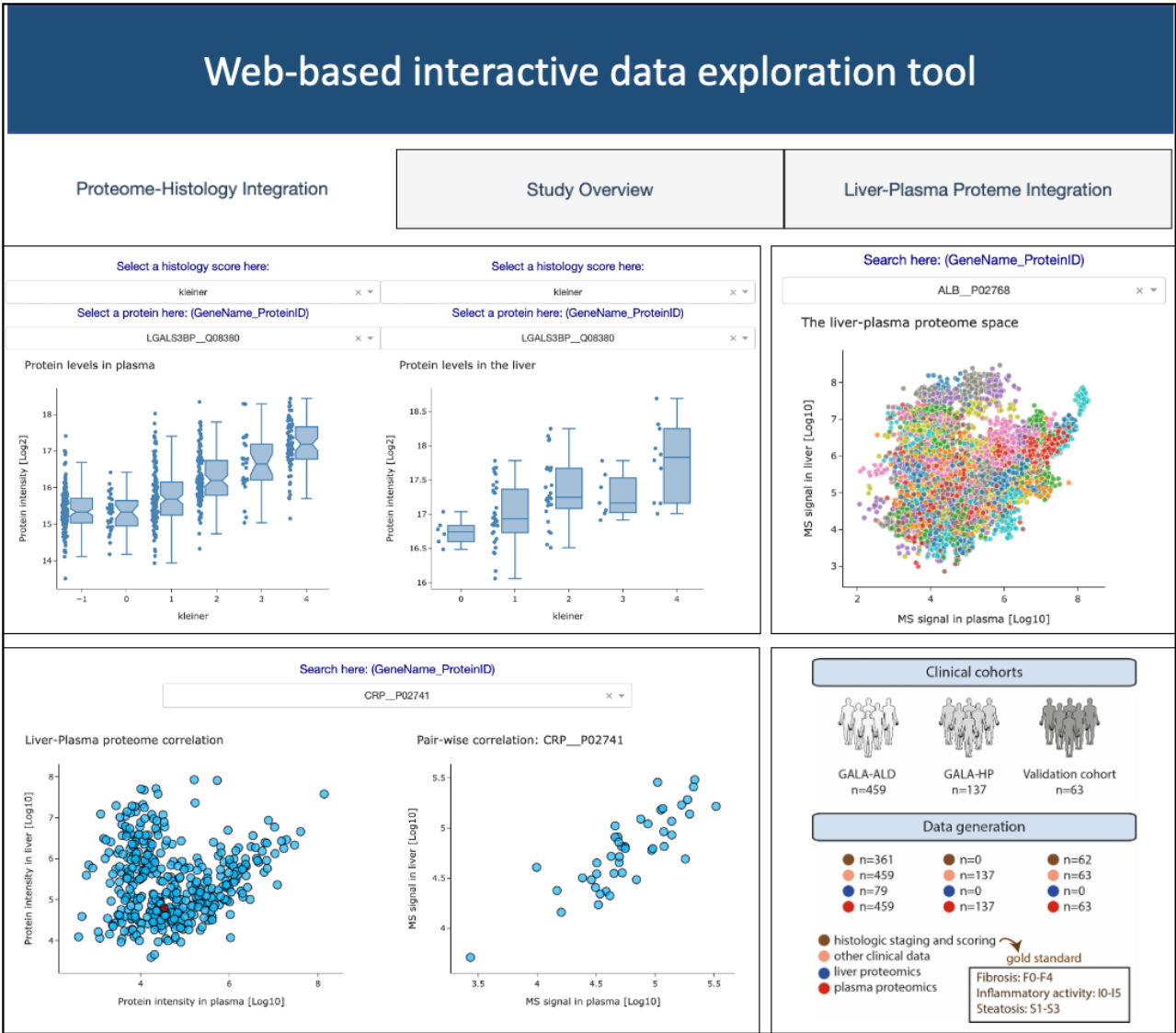

Supplementary information

**Noninvasive proteomic biomarkers for
alcohol-related liver disease**

In the format provided by the
authors and unedited

1 **Supplementary Figure 1**



2

3 **Supplementary Figure 1. An interactive, web-based data exploration tool built with the open-source Dash**

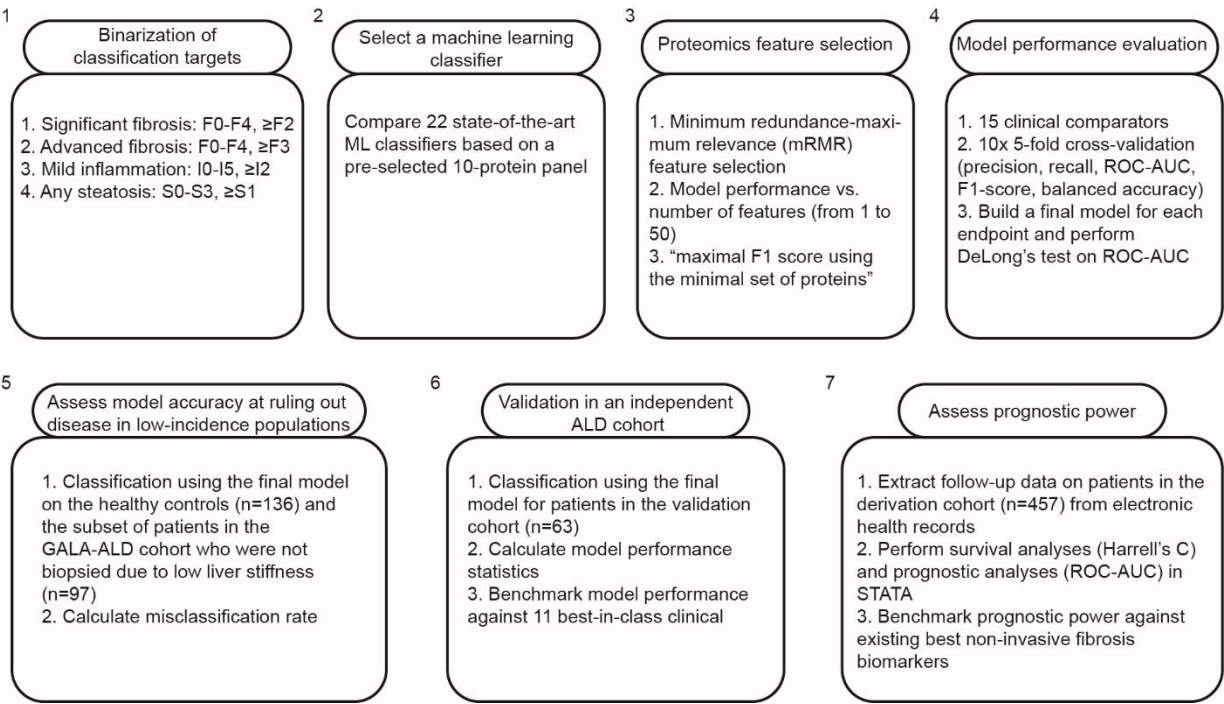
4 **framework.** This tool enables dynamic data visualization and query for results, including protein abundance

5 as a function of disease severity (liver histology scores), projection of plasma proteome to the liver space,

6 and pairwise correlation between liver and plasma samples.

7

8 **Supplementary Figure 2**

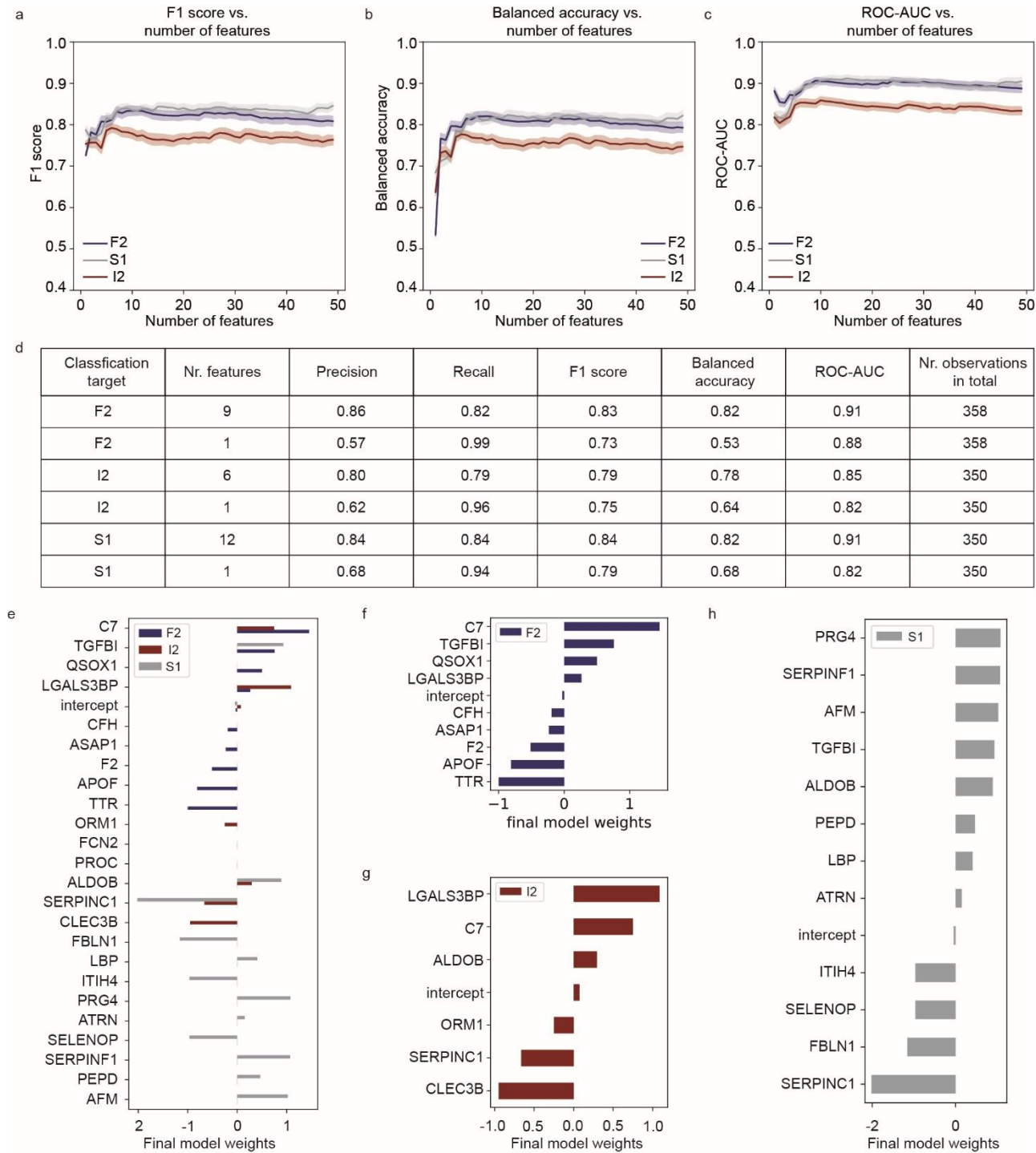


9

10 **Supplementary Figure 2. Overview of the machine learning pipeline.** This pipeline includes strategies for
11 the determination of classification targets, selection of the machine learning classifier, feature selection and
12 the evaluation of proteomics models' diagnostic and prognostic capabilities.

13

14 **Supplementary Figure 3**



15

16 **Supplementary Figure 3. Number of features in the marker panels and feature weights in logistic regression**
17 **models. a-c.** Value of F1 score (a), balanced accuracy (b) and ROC-AUC (c) for increasing number of features
18 from 1 to 50. Solid line stands for the mean from 5-fold ten times cross validation, with the upper and lower
19 border showing 95% confidence intervals. **d.** Comparison of classification performance between single-
20 protein (best performing) and panel-protein. **e.** Feature weights of all proteins forming marker panels for the
21 three prediction endpoints (F2, I2 and S1). **f-h.** Feature weights of proteins in the marker panel for predicting
22 significant fibrosis (f), mild inflammation (g), and any steatosis (h).