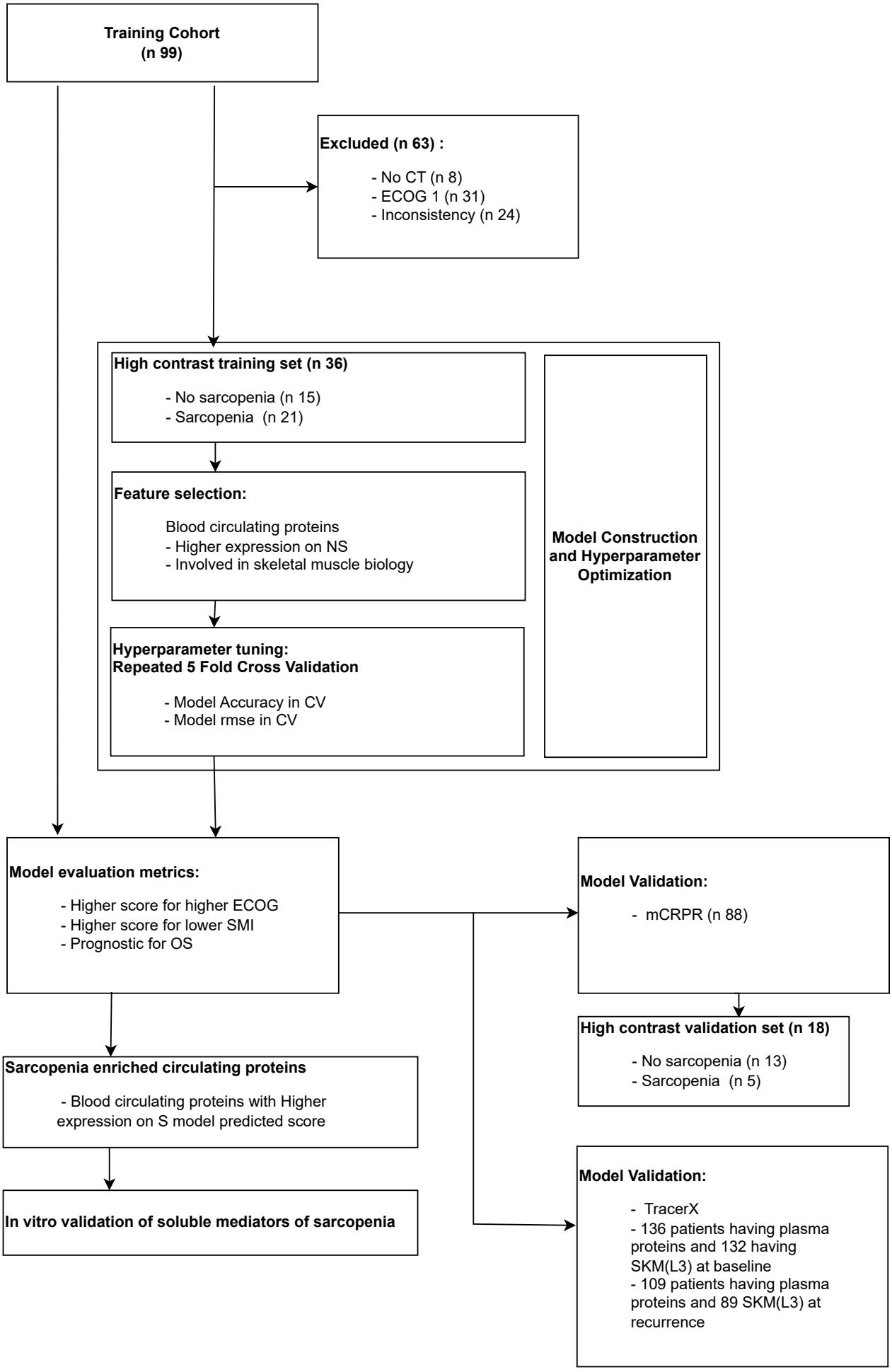
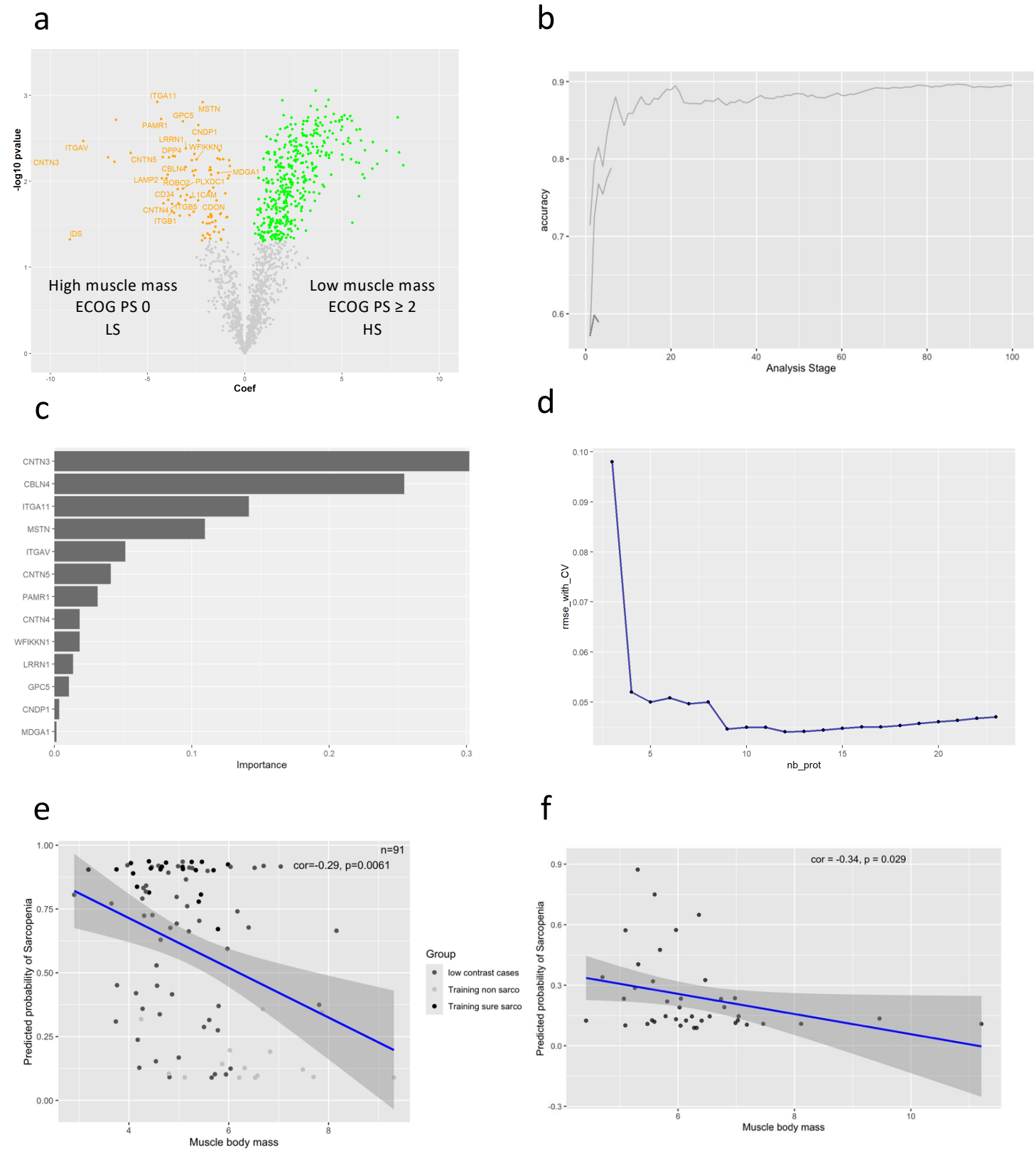
Supplementary figure 1. study scheme

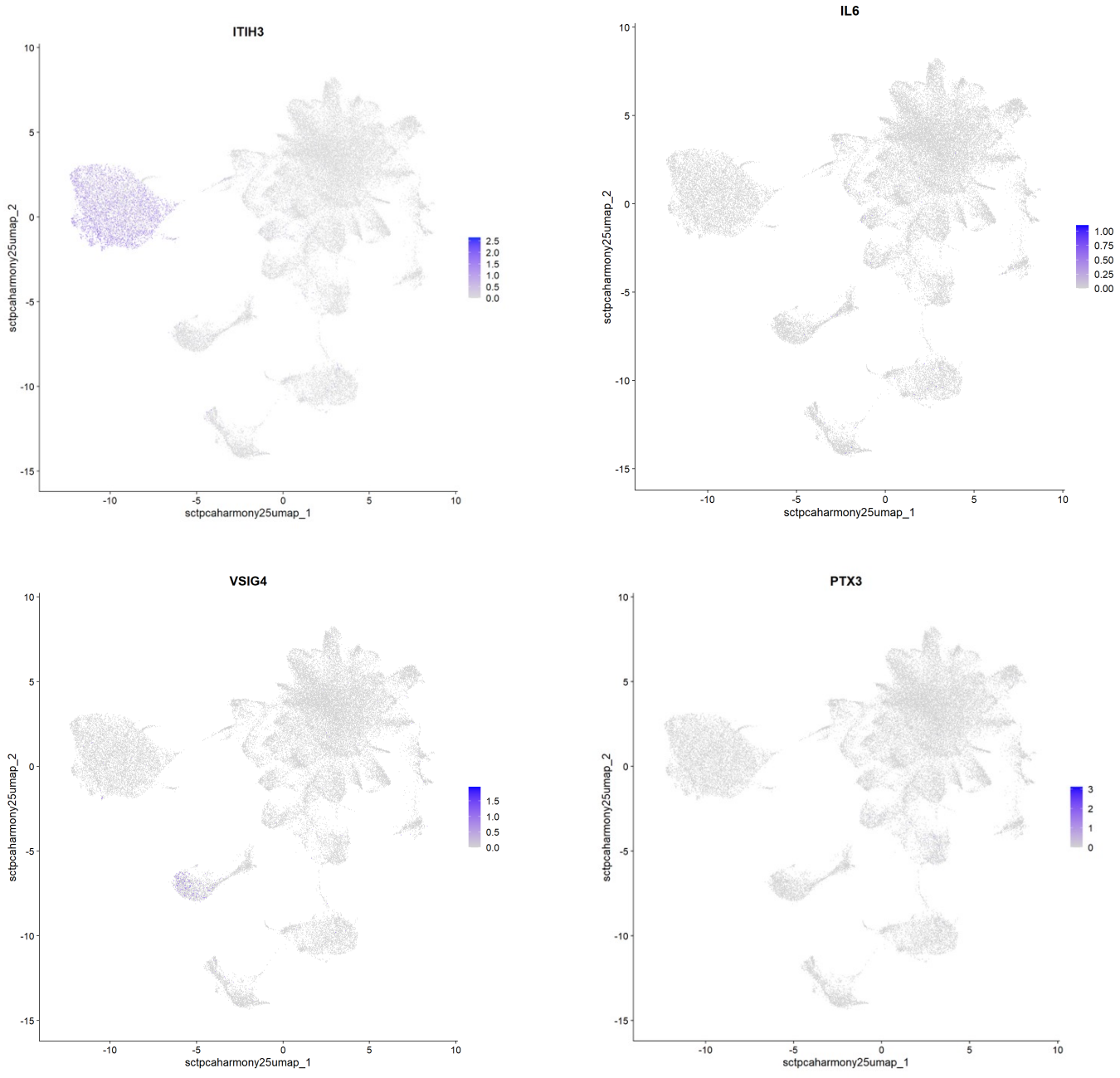


Supplementary Figure 2. Selection of plasma proteins for the sarcopenia proteomic signature

(A) Volcano plot showing differentially expressed plasma proteins between patients with high muscle mass and ECOG PS 0 (low probability of sarcopenia, LS) versus patients with low muscle mass and ECOG PS ≥ 2 (high probability of sarcopenia, HS) in the high-contrast training cohort. **(B)** Classification accuracy of the p23 proteomic model for sarcopenia prediction in the training cohort. **(C)** Variable importance of plasma proteins included in the p23 model, ranked according to their contribution to sarcopenia classification. (D) Plot showing root mean squared error (RMSE) for models with different number of proteins. Scatter plot showing the correlation between sarcopenia probability and 3D calculation of muscle body mass in MATCHR-immuno (E) and prostate (F) cohorts



Supplementary figure 3. Single-cell RNA sequencing analysis showing cell type–specific expression of ITIH3 in hepatic cells and no expression of IL6, VSIG3 and PTX3.



Supplementary figure 4. IL6 regulation of IGFBP1.

IL-6 regulates IGFBP1 expression in LHCN myoblasts and HepG2 cells but has not major direct impact on myoblast differentiation. Immunofluorescence (A, B) and western blot (C) analysis of LHCN myoblasts differentiated in DMEM containing 2% FBS with indicated concentrations of IL-6 (0–30 ng/ml) for 96 h. (D-F) HepG2 cells were treated with IL-6 (0–30 ng/ml) for 24 h or 48 h. (D) qPCR analysis of IGFBP1 mRNA expression in HepG2 cells. (E) Western blots analysis of IGFBP1 protein expression in HepG2 cell lysates at 24 h and 48 h. (F) Western blot analysis of secreted IGFBP1 in the culture supernatants of HepG2 cells at 24 h and 48 h. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001, compared with the control group (cells treated with 0 ng/mL IL-6).