

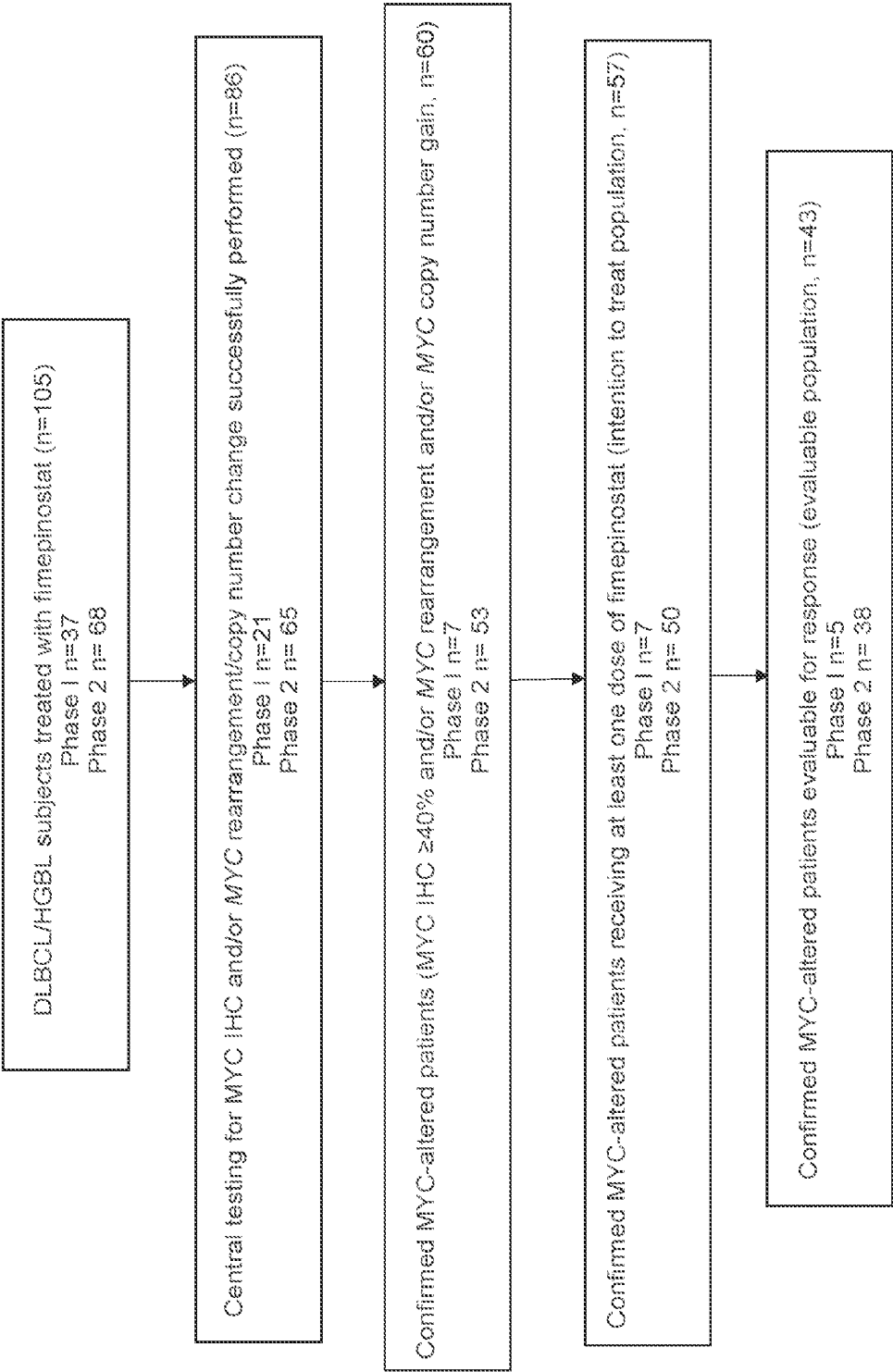


FIG. 1

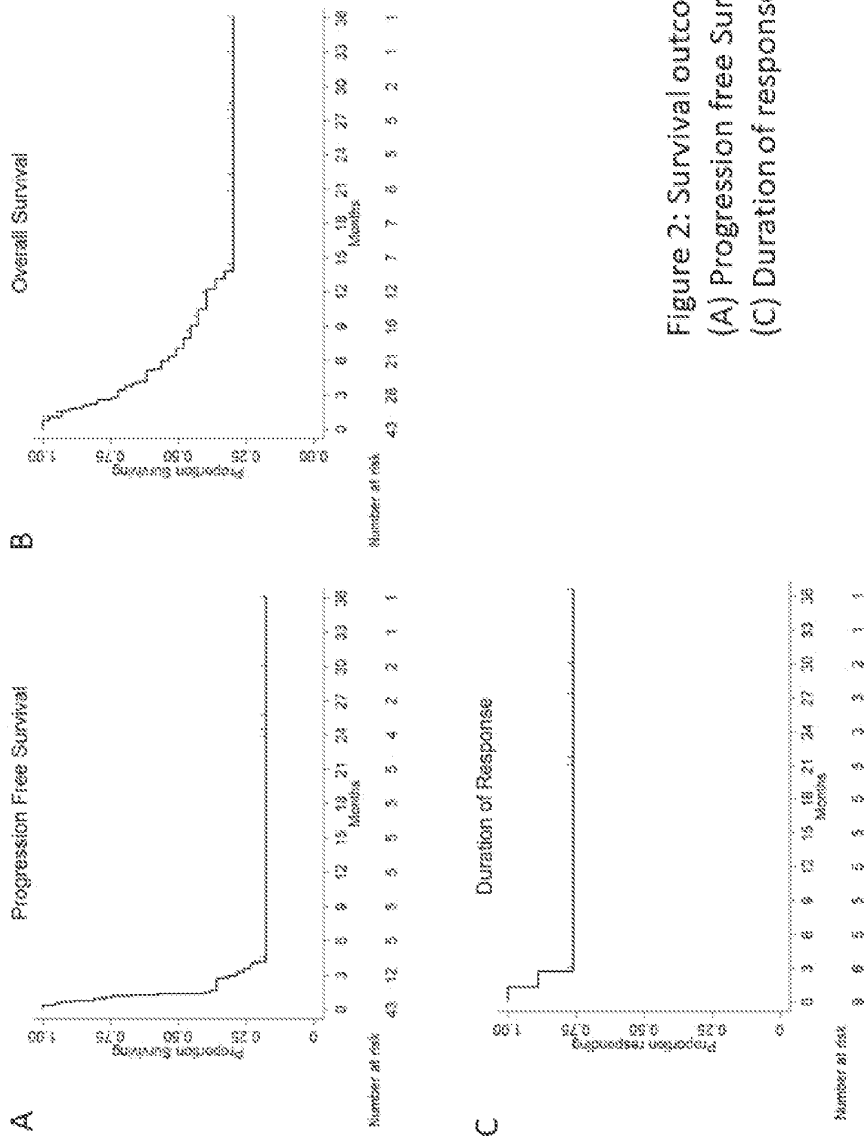


Figure 2: Survival outcomes of evaluable population
(A) Progression free Survival. (B) Overall survival.
(C) Duration of response in responding patients.

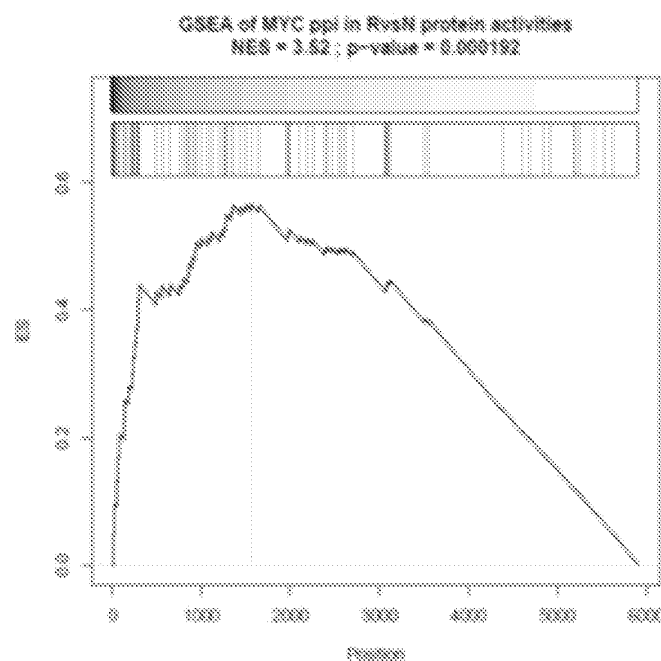


Figure 3: GSEA of 67 B cell context-specific MYC-interacting proteins (red vertical lines) in the list of proteins sorted from the most to the least differentially active between fimepinostat responder and non-responder patients.

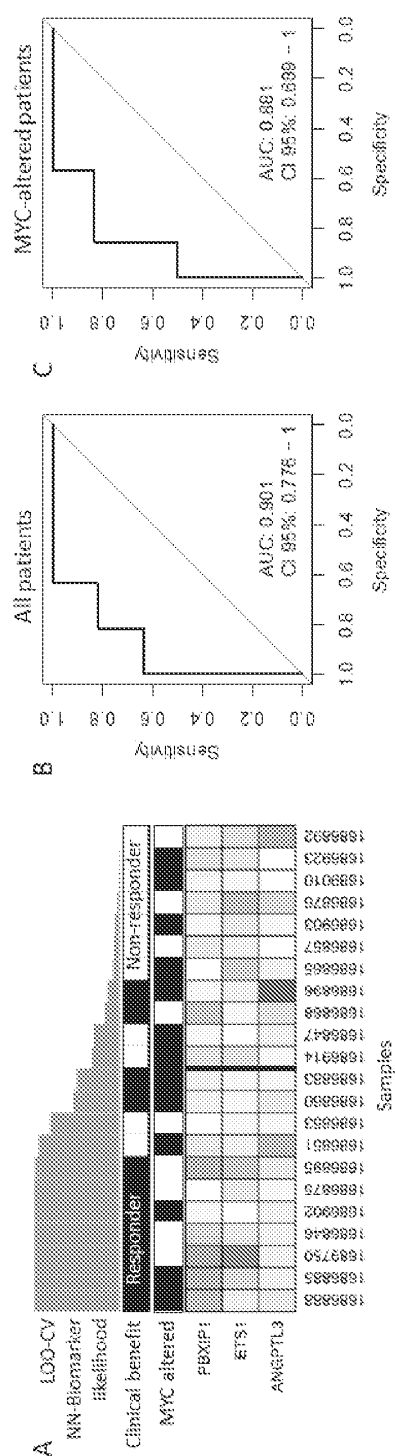


Figure 4: LOO-CV analysis for fimepinostat response biomarkers. (A) Heatmap showing the VIPER-inferred activity for the three fimepinostat response MR proteins used by the biomarkers (rows) for all samples. The clinical samples included in the analysis (columns) were rank-sorted based on the predicted likelihood of response by the NN-biomarker (heatmap above the heatmap), estimated using LOO-CV. Patients that responded to fimepinostat (CR and PR) and patients that did not respond for fimepinostat (PD) are shown in black and white, respectively (Clinical benefit row). Patients with MYC altered disease are indicated in black in the MYC altered row. (B and C) ROC analysis for the LOO-CV performed on all samples ($n = 22$) (B) and only on the MYC altered samples ($n = 13$) (C). Area under the ROC (AUC) and its 95% confidence interval (CI) is shown inside each plot.