



Supplemental Figure 9. Discrimination of MN risk integrating Clonal Hematopoiesis Risk Score (CHRS) and proteomics. The CHRS model developed by Weeks et al. incorporates age, red blood cell indices, cytopenias, and CH mutation characteristics (single DNMT3A, high-risk mutations, multiple mutations, VAF). Discrimination of MN risk by CHRS without or with proteomics features (N = 115 MN risk protein) was performed using a cross validation approach. The analysis was conducted using all participants with proteomics data available (N = 46,237; left), only participants without CH or low risk CH (N = 45,923; middle), and only participants with medium or high risk CH (N = 314; right). The receiver operating (ROC) curves include the 95% confidence intervals (lighter shading).