



Supplemental Figure 8. Discrimination of MN risk using reduced set of proteomics features. Shown are the receiver operating (ROC) curves including the 95% confidence interval (lighter shading) for a MN risk model incorporating basic clinical features alongside CH and proteomics. The clinical model incorporates age, sex, ancestry, smoking status, blood counts, and sample age. Shown in red is a model incorporating all 115 proteins associated with MN risk. We compared this to models including a smaller number of proteomics features, specifically the top 10 (green) or blue (25) proteins calculated by frequency of inclusion across multiple iterations of the LASSO model.