Supplemental Figure 10. Two-sample Mendelian randomization (MR) analyses of the causal effect of plasma protein levels on myeloid neoplasm (MN) risk in the UKBB (N=381,485). Regression lines for different MR methods are shown for (A) F7 and (B) IL17RA. Each black dot represents a single nucleotide variant (SNP) that is a protein quantitative trait loci (pQTL) for the corresponding protein on the x-axis and has associated error bars for each axis in gray. The slope of each fitted line represents the estimated MR effect and is colored by the specific MR method used. (C) Two-sample Mendelian randomization (MR) analyses of the causal impact of plasma protein levels on MN risk. Each dot represents the estimated MR effect for the corresponding protein with the corresponding 95% confidence interval.