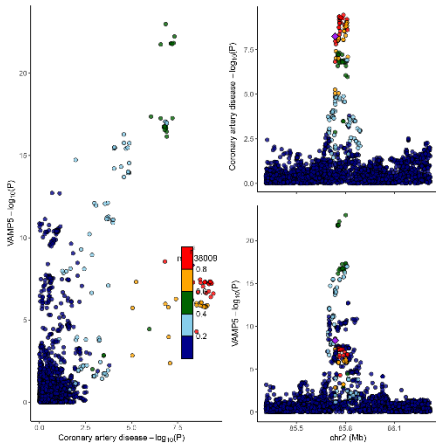
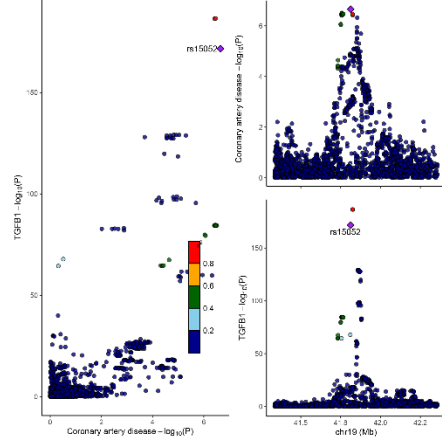
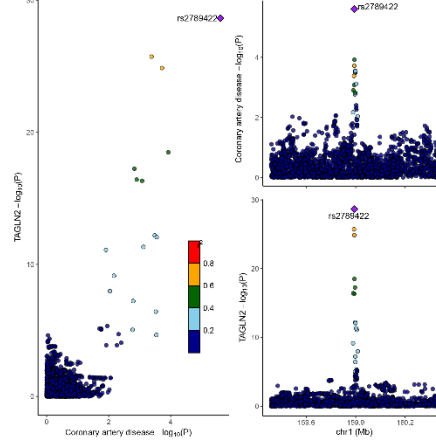
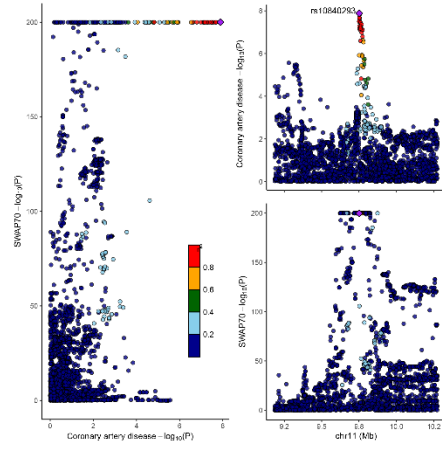
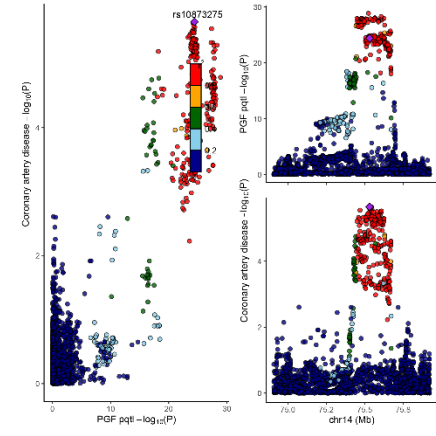
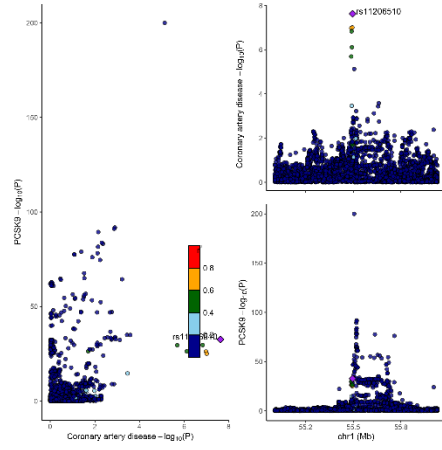
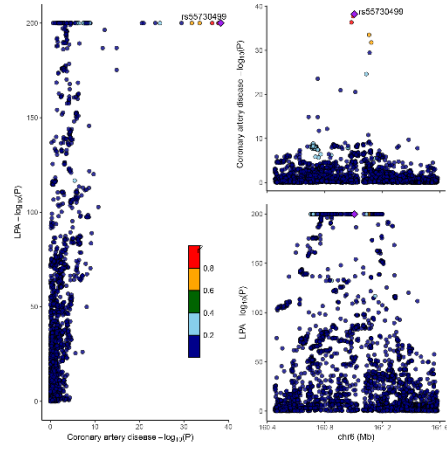




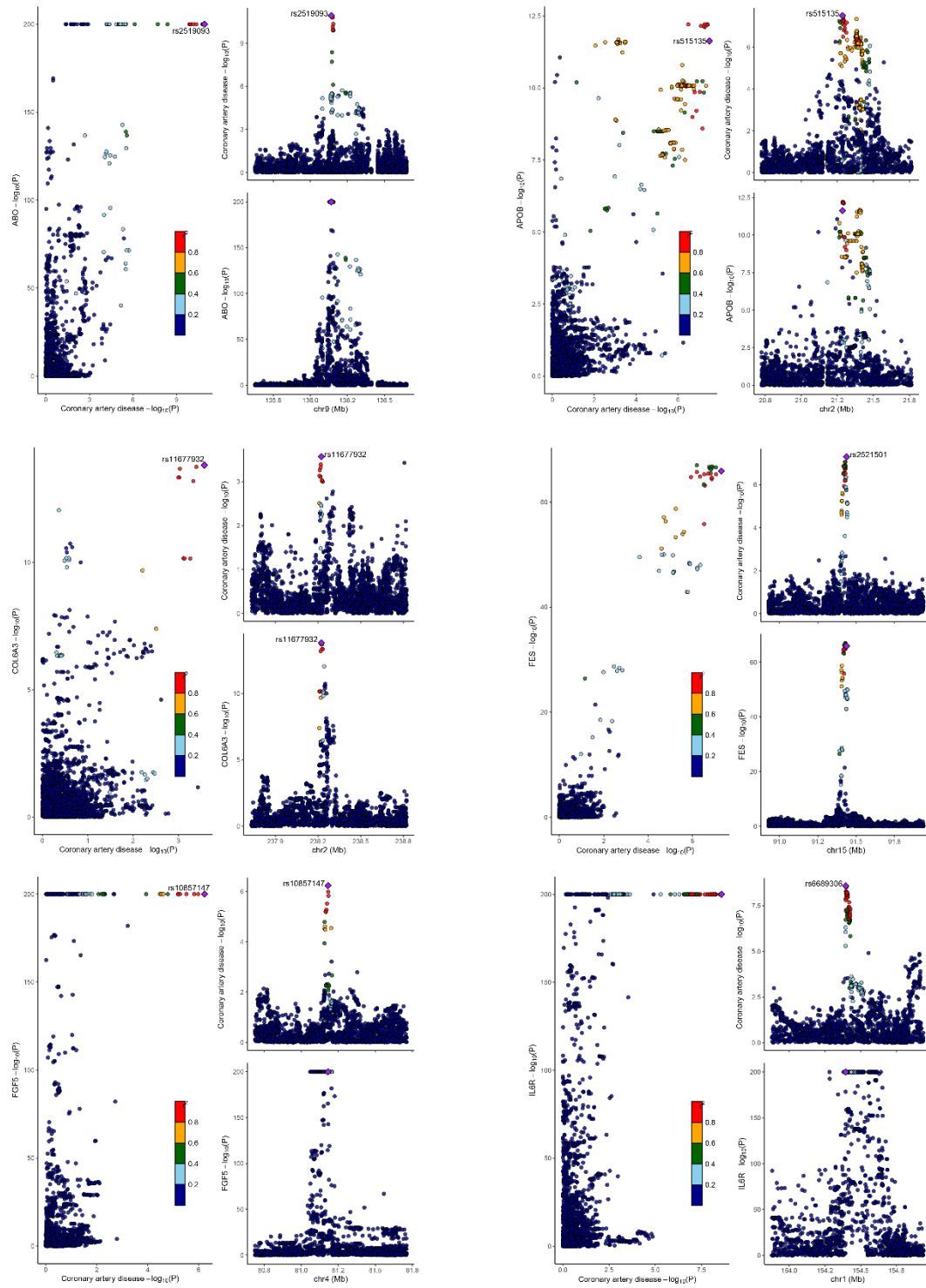


Fig S1 Regional association plot for colocalization analysis of causal protein with CHD risk. The lead SNP is shown as a purple diamond. SNPs within ± 500 kb of the protein quantitative trait locus were included; $p_{12}=1e-5$, prior probability a SNP is associated with both protein and CHD.

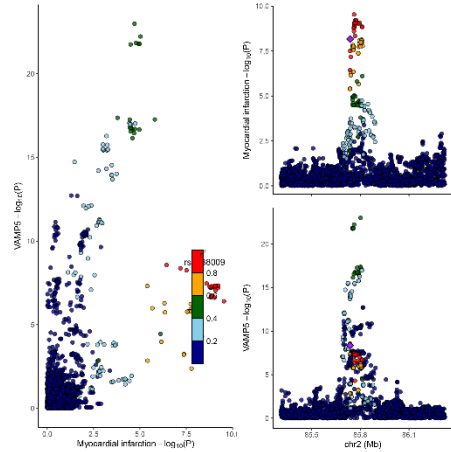
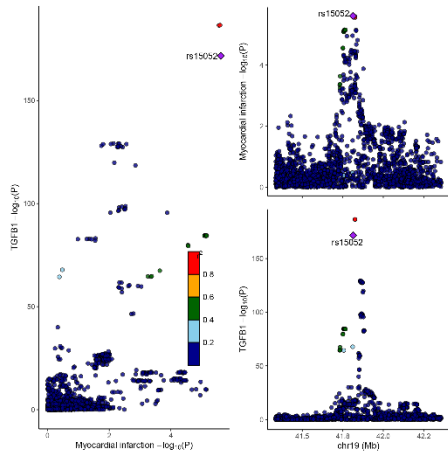
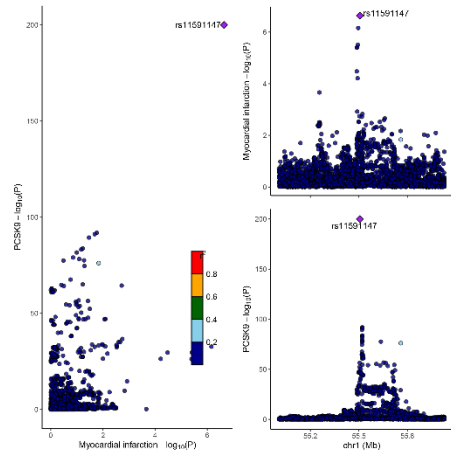
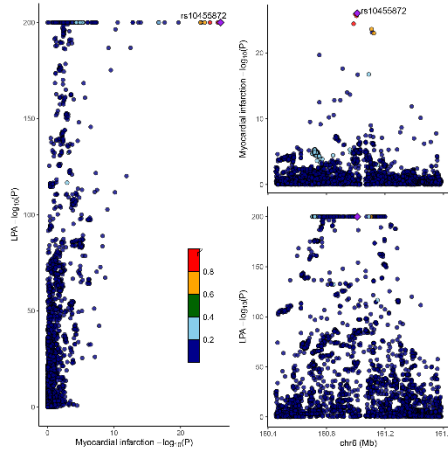
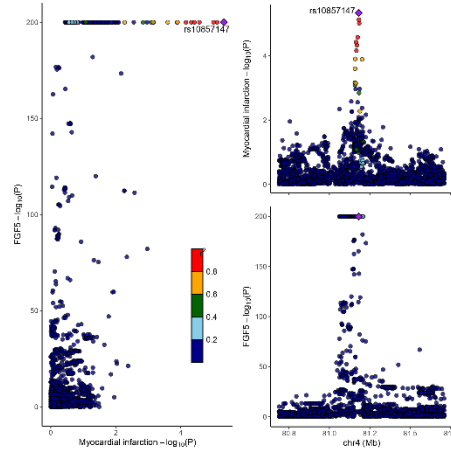
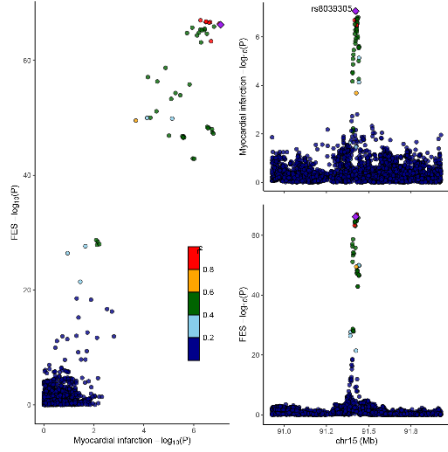
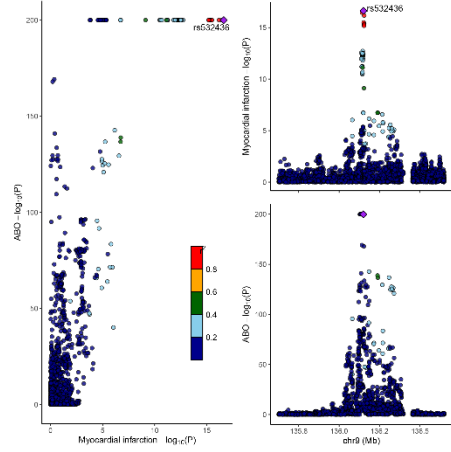


Fig S2 Regional association plot for colocalization analysis of causal protein with MI risk. The lead SNP is shown as a purple diamond. SNPs within ± 500 kb of the protein quantitative trait locus were included; $p_{12}=1e-5$, prior probability a SNP is associated with both protein and MI.

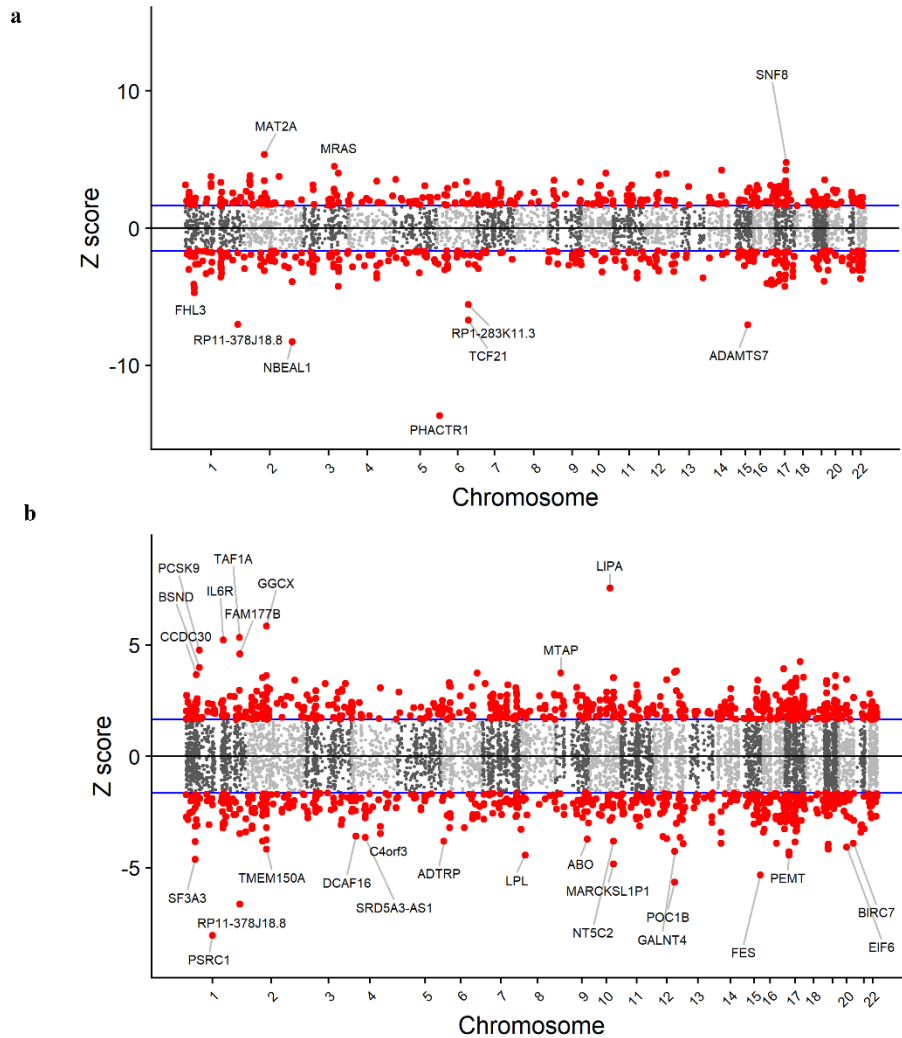


Fig S3 TWAS result of Plasma Proteins Linked to CHD and MI. (a) Results of TWAS analysis of CHD-related plasma proteins. (b) Results of TWAS analysis of MI-related plasma proteins. The horizontal axis indicates the different chromosome regions. The vertical axis is the linear sum of the Z score weights of the independent SNPs. A Z value greater than one means that there is a strong positive correlation between gene expression and disease risk.

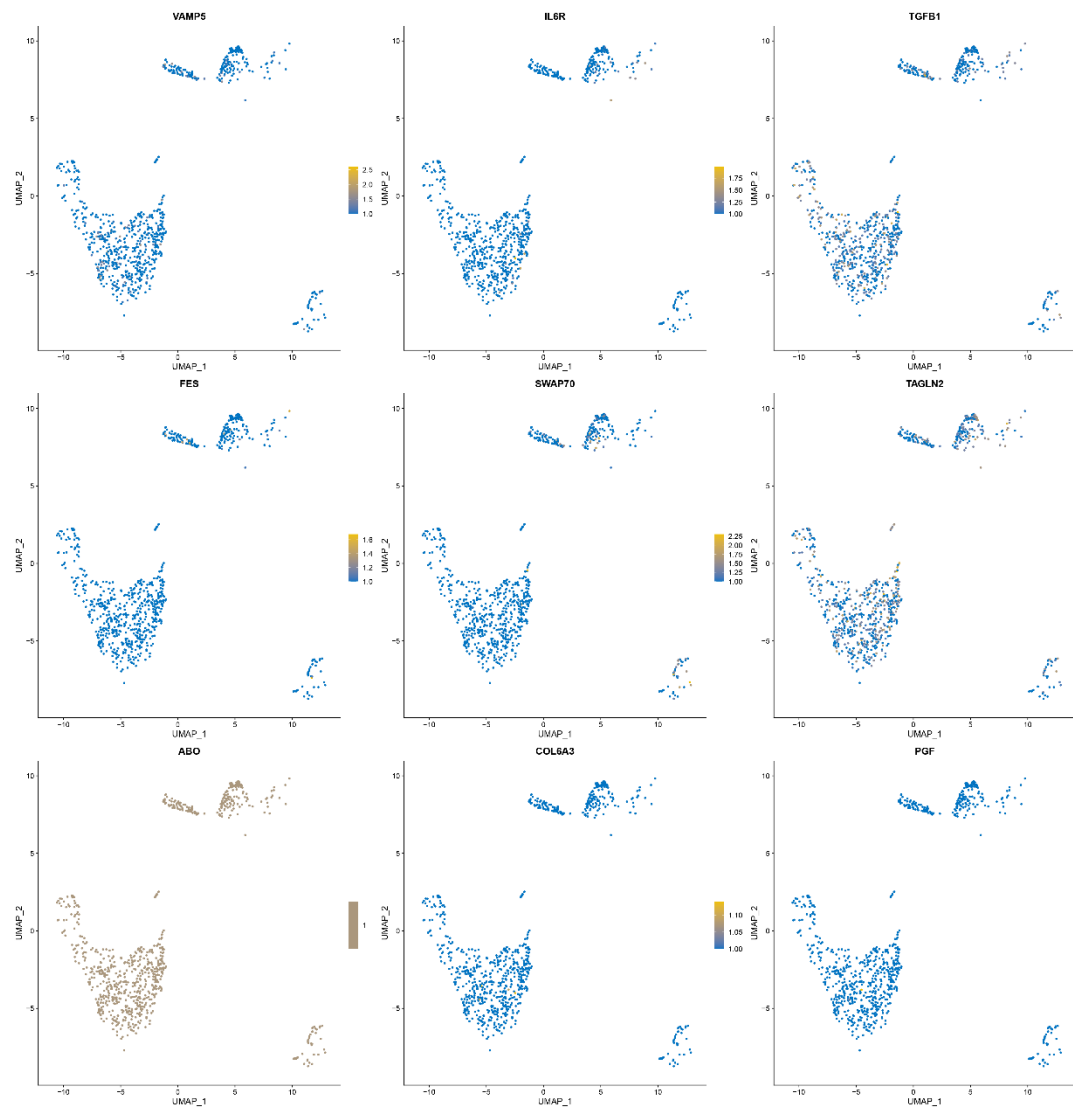


Fig S4 Expression of genes encoding CHD causal proteins at the single-cell level. The closer the color to yellow, the stronger the expression.

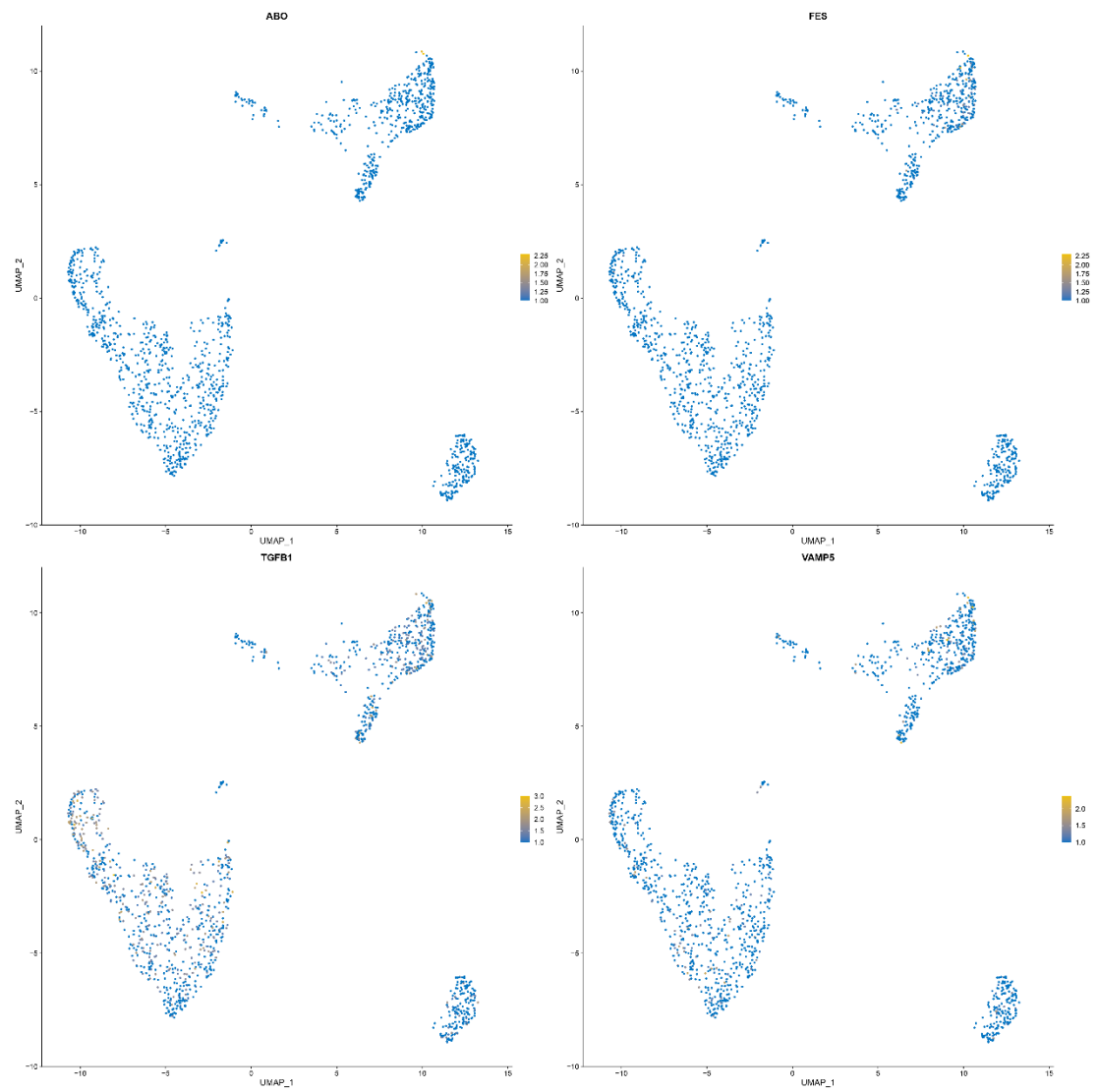


Fig S5 Expression of genes encoding MI causal proteins at the single-cell level. The closer the color to yellow, the stronger the expression.