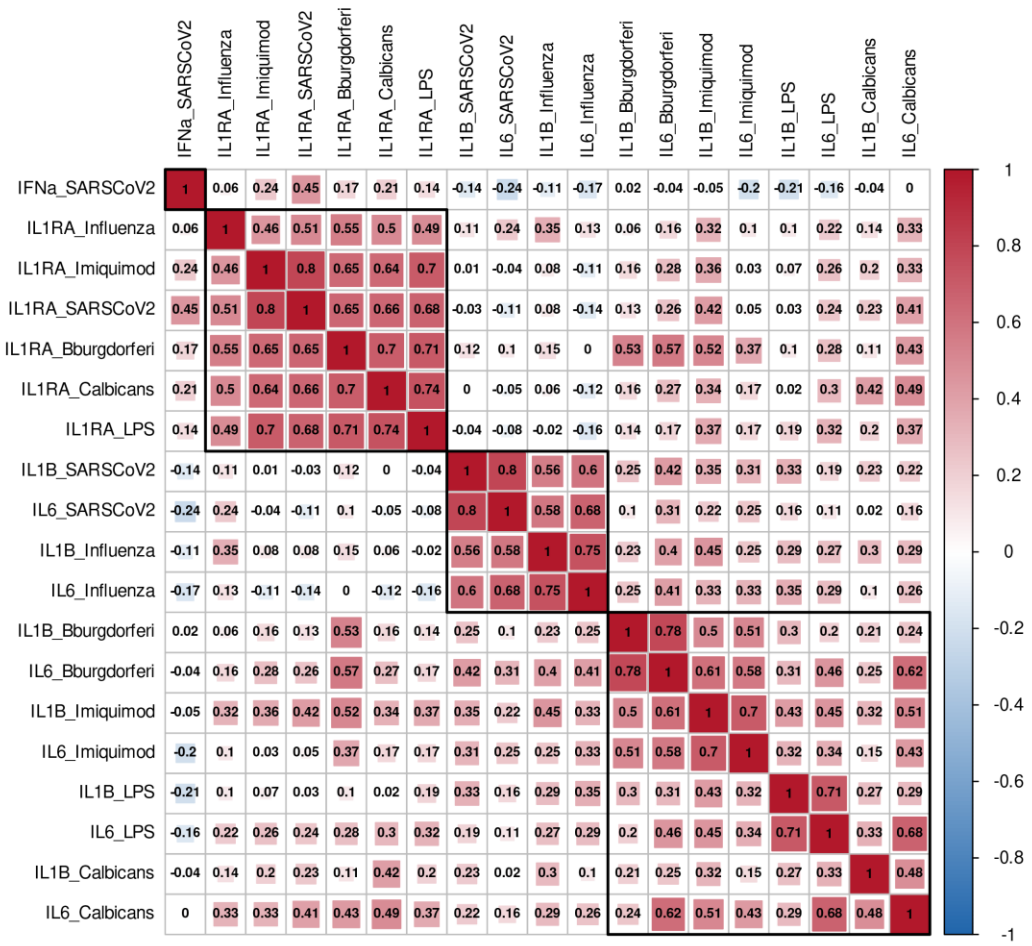

Figure S1: Correlation heatmap of cytokine following SARS-CoV-2 stimulation
Heatmap visualizing pairwise spearman correlation coefficient (r) across all cytokine-stimulation pairs. Each cell represent a pair, where the color represents the correlation direction and the text depict the correlation coefficient. Correlation are filtered using $P < 0.05$.

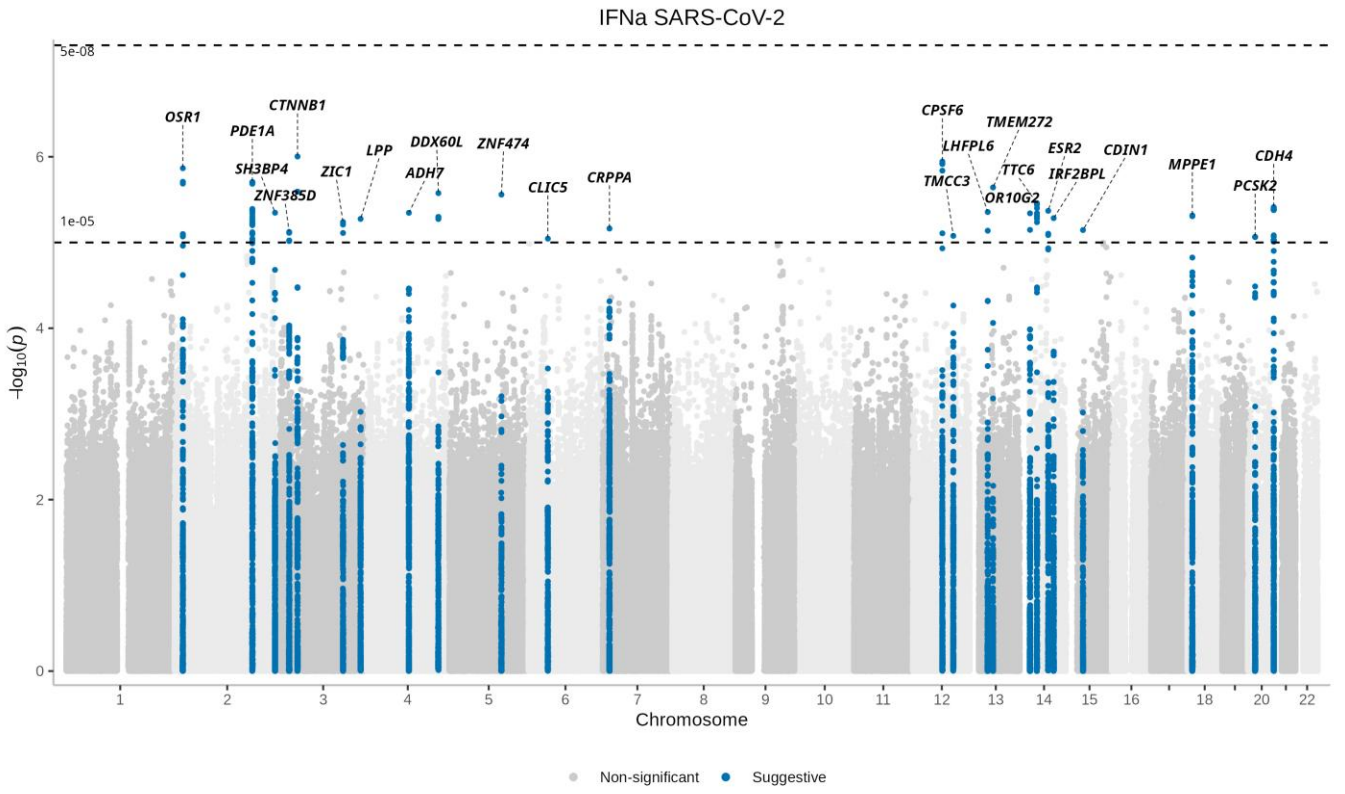

Figure S2: Manhattan plot of cQTL mapping using IFN-a following SARS-CoV-2 stimulation. Each point represents a genetic variants visualized by genomic position (x-axis) and the – log10(P) (y-axis). The black horizontal dashed line indicated genome-wide significant threshold (5e-8), while the blue dashed line represents the suggestive threshold (1e-5)

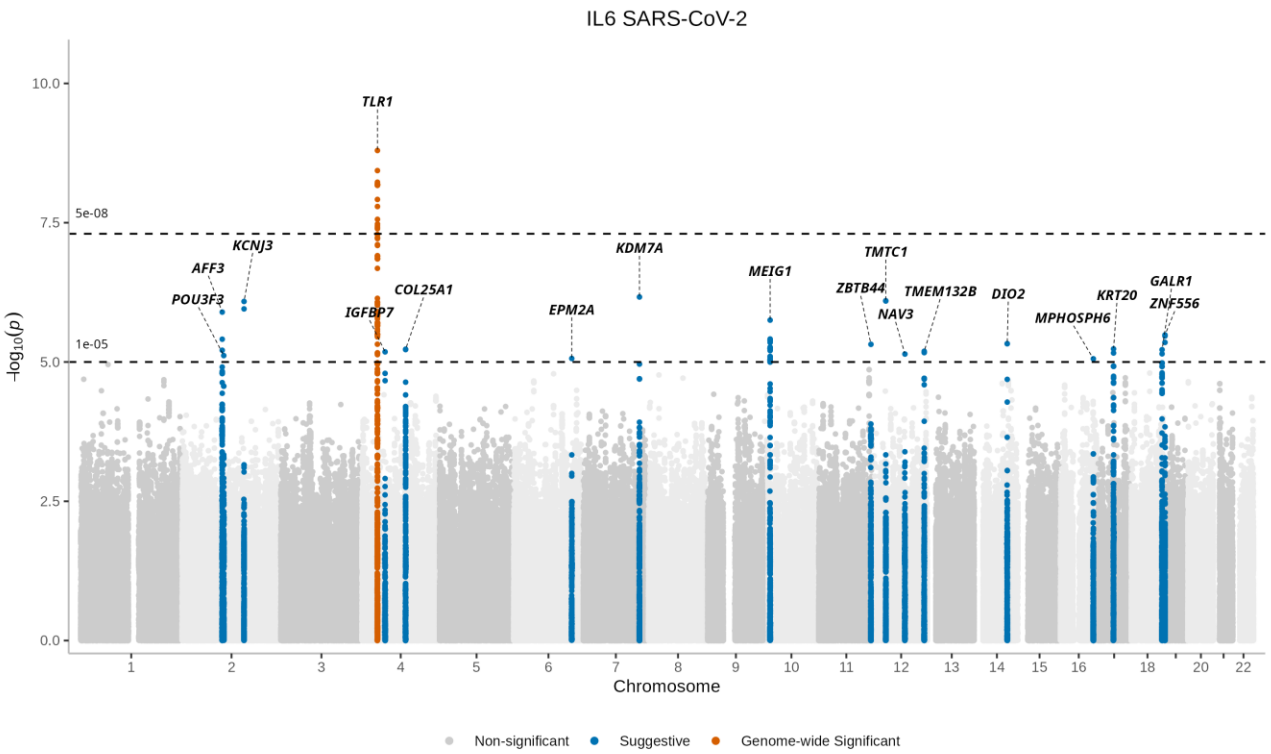

Figure S3: Manhattan plot of cQTL mapping using IL-6 following SARS-CoV-2 stimulation. Each point represents a genetic variants visualized by genomic position (x-axis) and the –log10(P) (y-axis). The black horizontal dashed line indicated genome-wide significant threshold (5e-8), while the blue dashed line represents the suggestive threshold (1e-5)

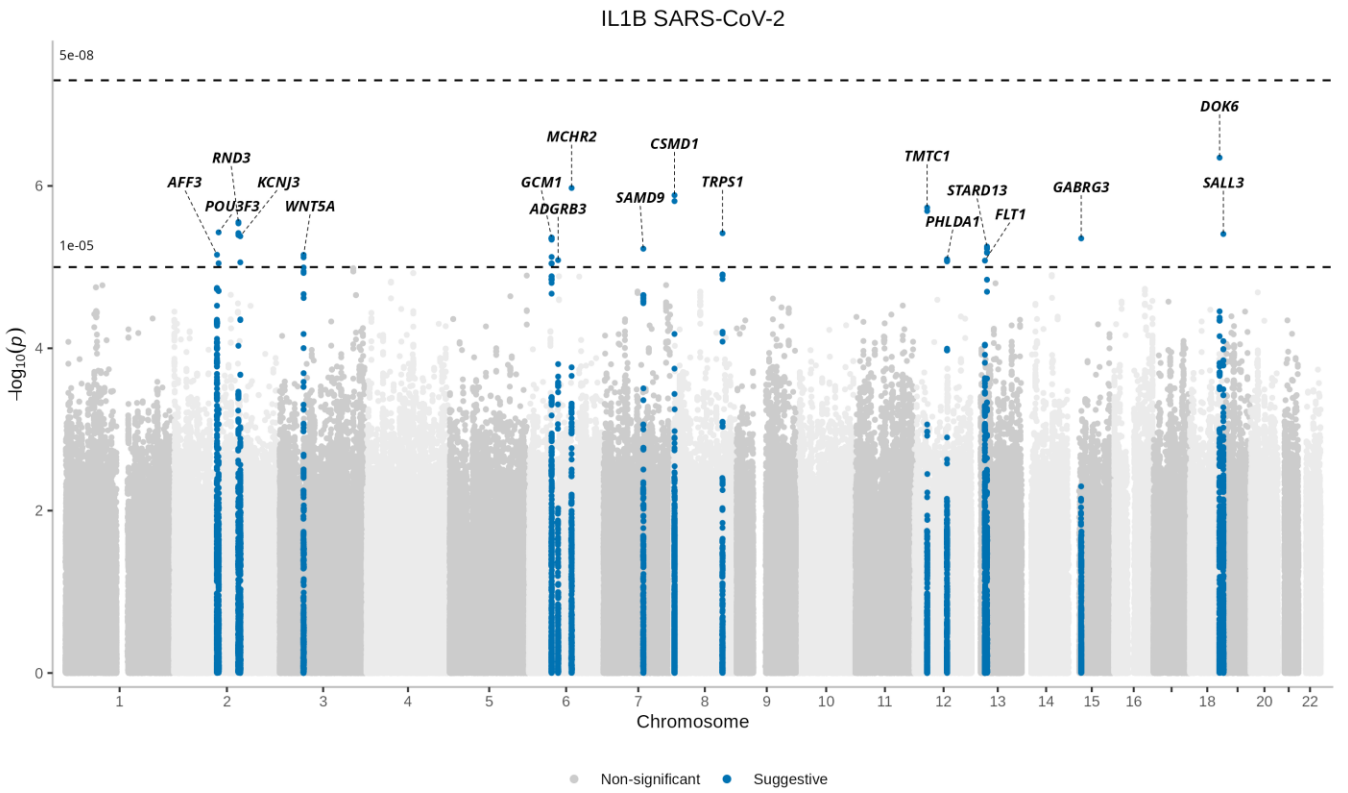

Figure S4: Manhattan plot of cQTL mapping using IL1B following SARS-CoV-2 stimulation. Each point represents a genetic variants visualized by genomic position (x-axis) and the – log10(P) (y-axis). The black horizontal dashed line indicated genome-wide significant threshold (5e-8), while the blue dashed line represents the suggestive threshold (1e-5)

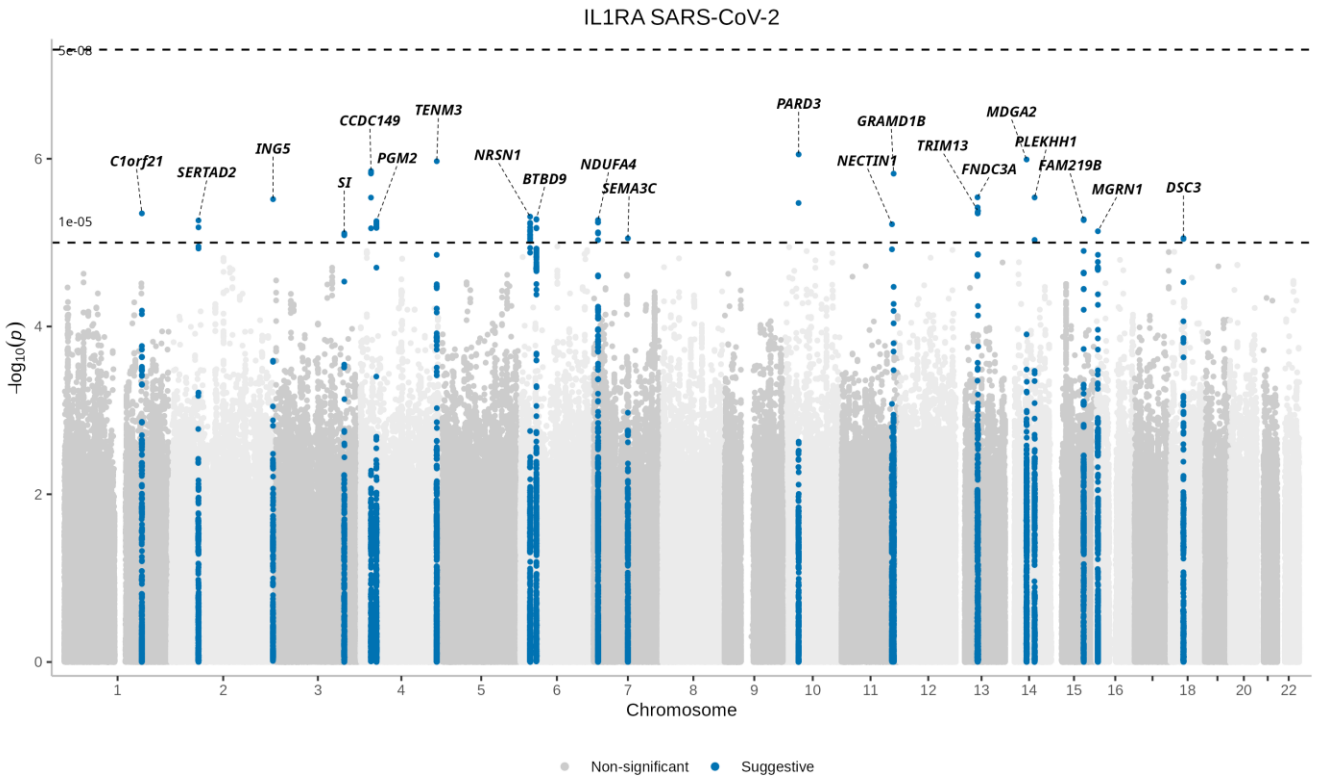

Figure S5: Manhattan plot of cQTL mapping using IL-1RA following SARS-CoV-2 stimulation. Each point represents a genetic variants visualized by genomic position (x-axis) and the – log10(P) (y-axis). The black horizontal dashed line indicated genome-wide significant threshold (5e-8), while the blue dashed line represents the suggestive threshold (1e-5)