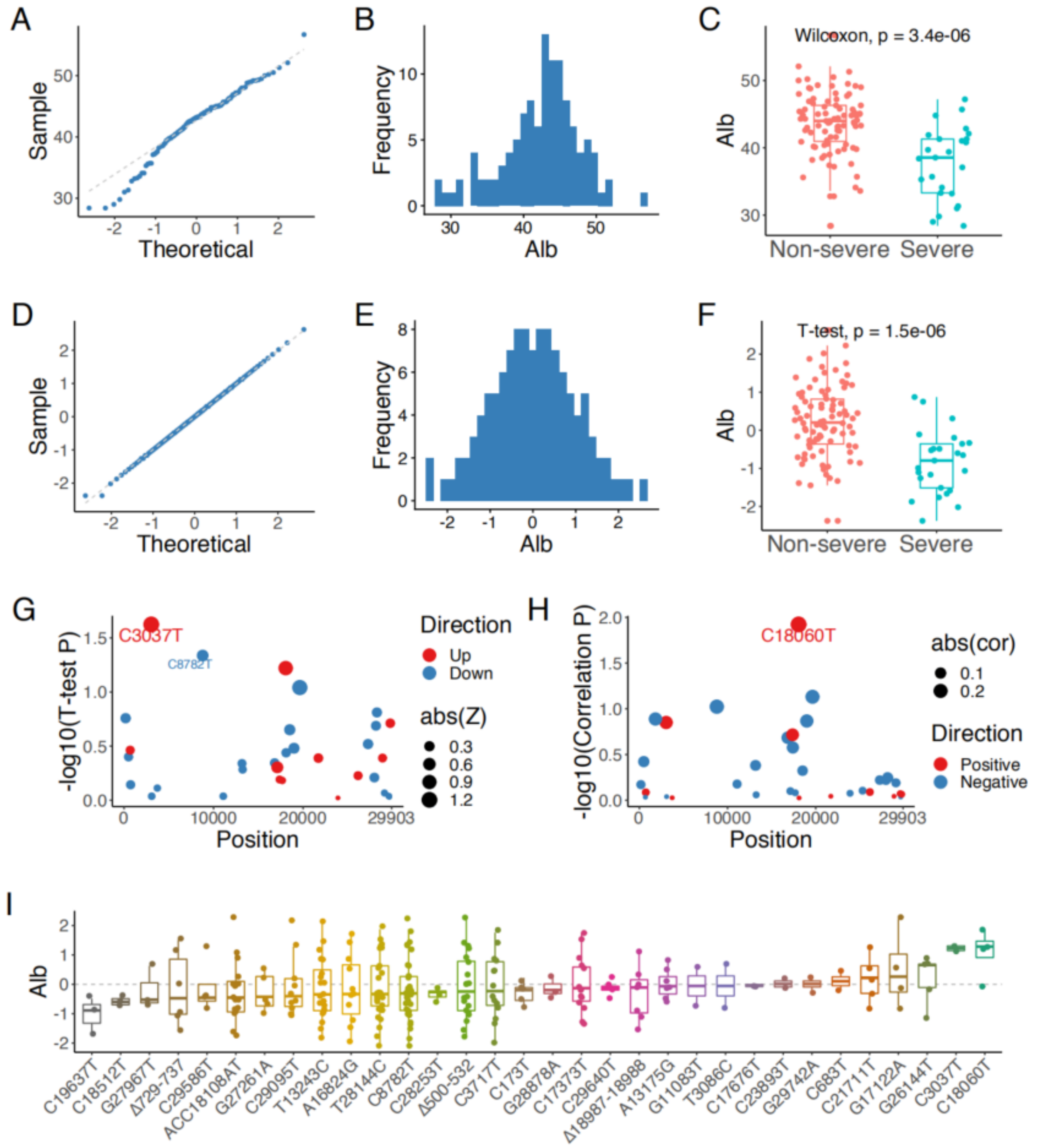
Data S1. Normalization and association of SARS-CoV-2 genetic variants with 117 clinical phenotypes (related to Figure 3)

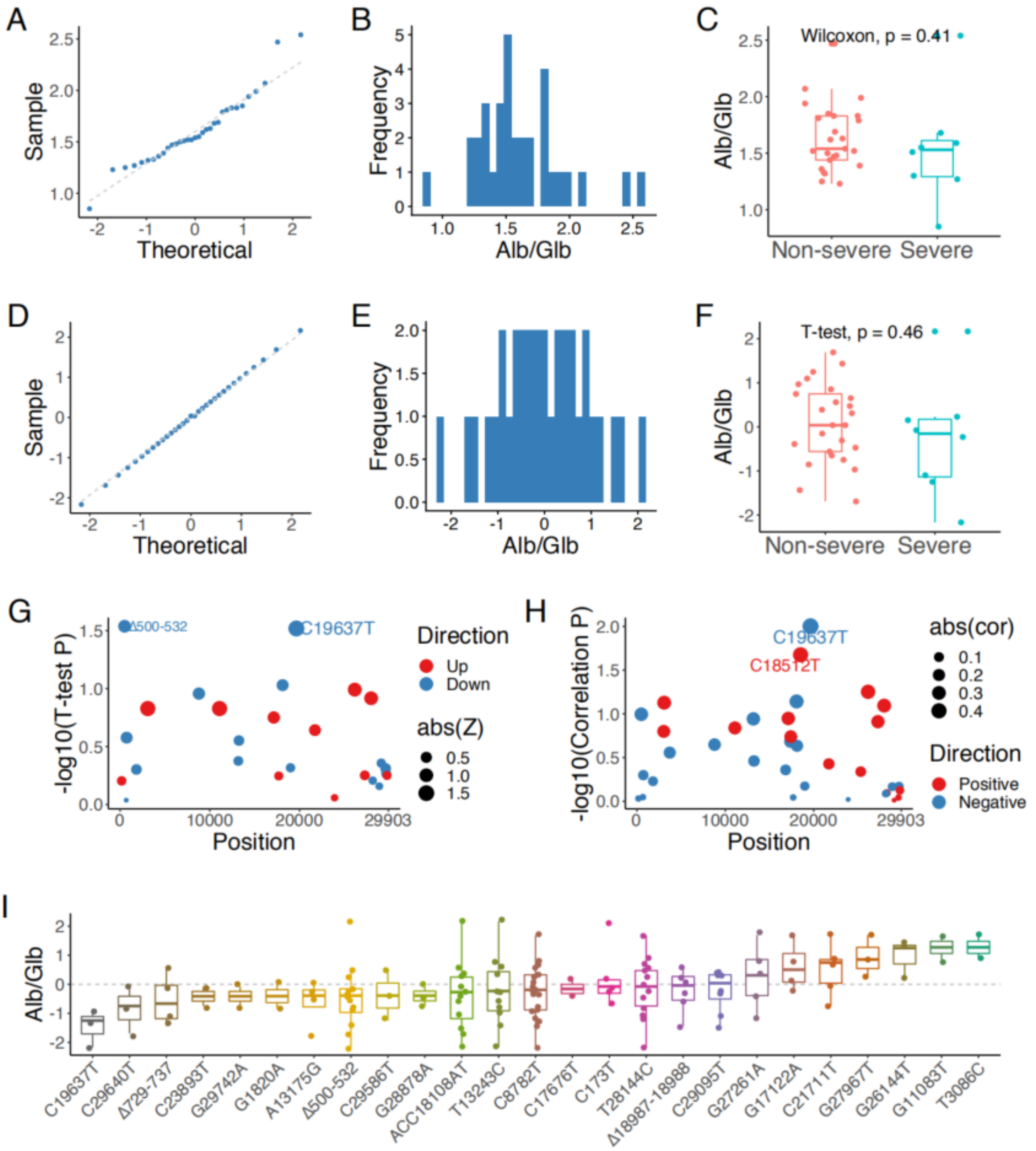
Contents

1. Alb (albumin)



For Alb (albumin, g/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Alb in the non-severe and severe COVID-19 patients before (**C**, p = 3.4×10^{-6}, Wilcoxon test) and after normalization (F, p = 1.5×10^{-6}, T-test). (**G**) Variants C3037T and C8782T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C18060T has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of Alb, cases with C18060T and C3037T tend to have the highest Z score, whereas G1820A and C19637T have the lowest.

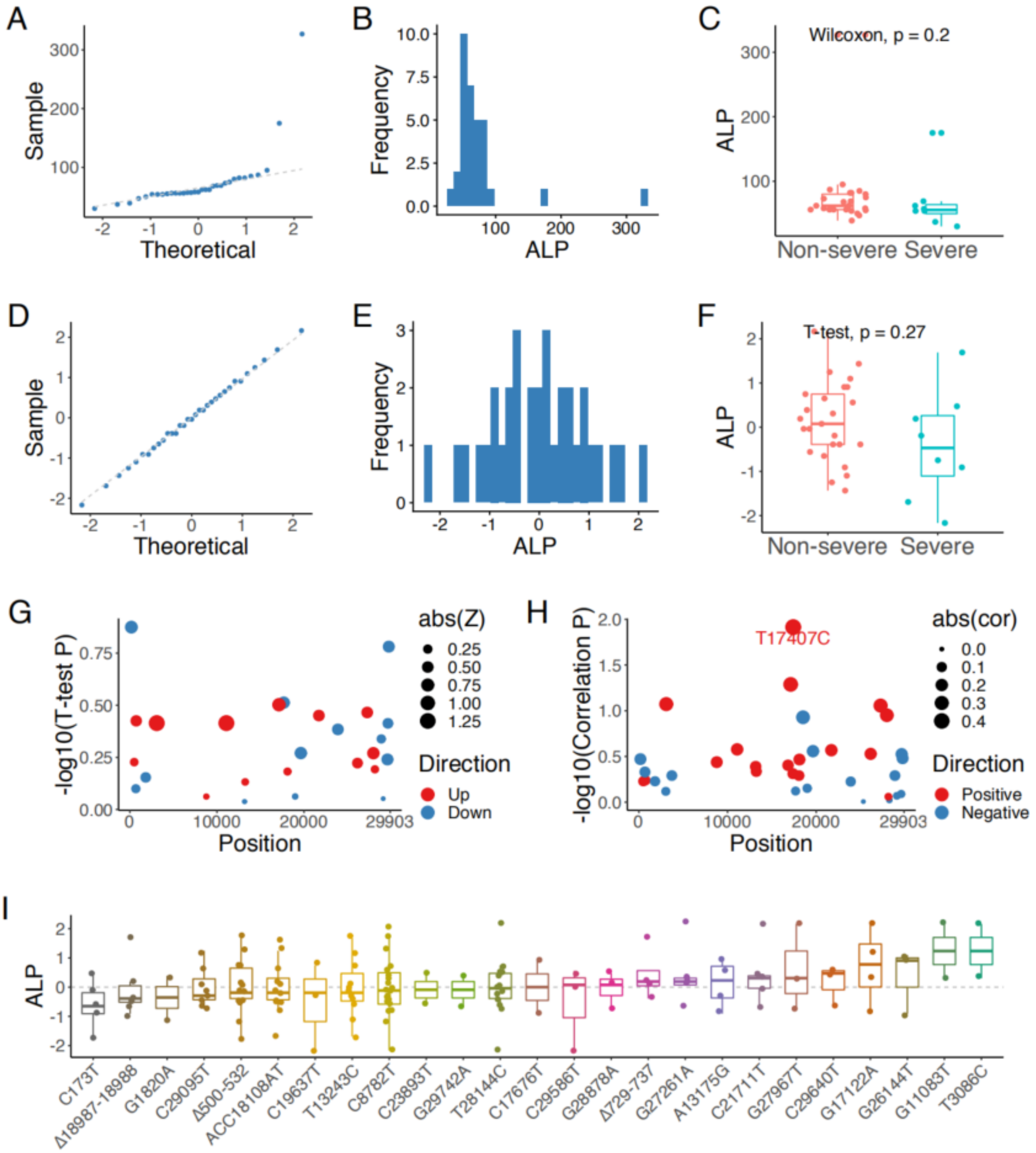
2. Alb/Glb (albumin/globulin)



For Alb/Glb (Albumin/globulin ratio), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Alb/Glb in the non-severe and severe COVID-19 patients before (**C**, p = 0.41, Wilcoxon test) and after normalization (**F**, p = 0.46, T-test). (**G**) Variants Δ500-532 and C19637T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C19637T and C18512T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of Alb/Glb, cases with T3086C and G11083T tend to have the highest Z score, while cases with C19637T and

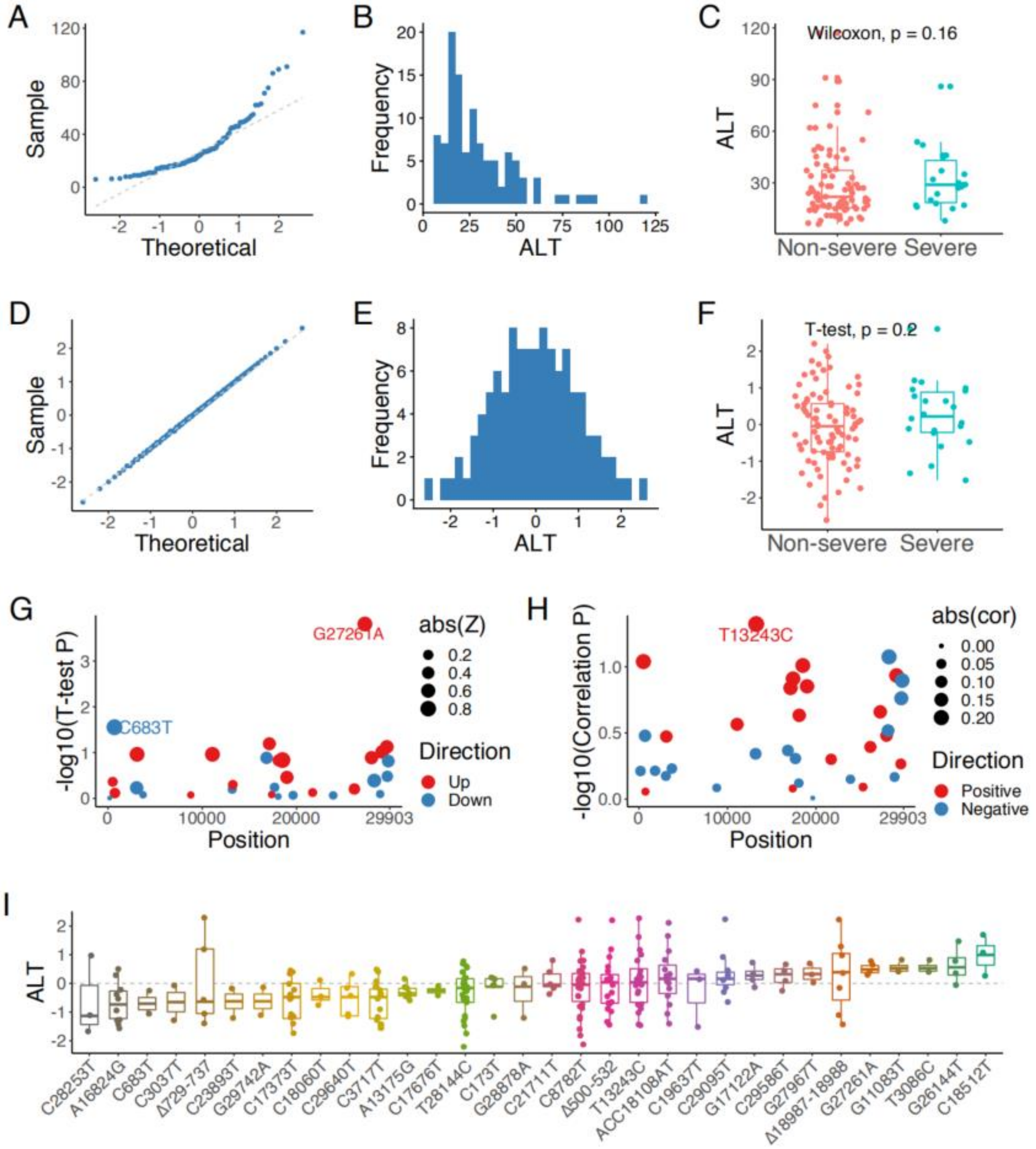
C29640T have the lowest.

3. ALP (alkaline phosphatase)



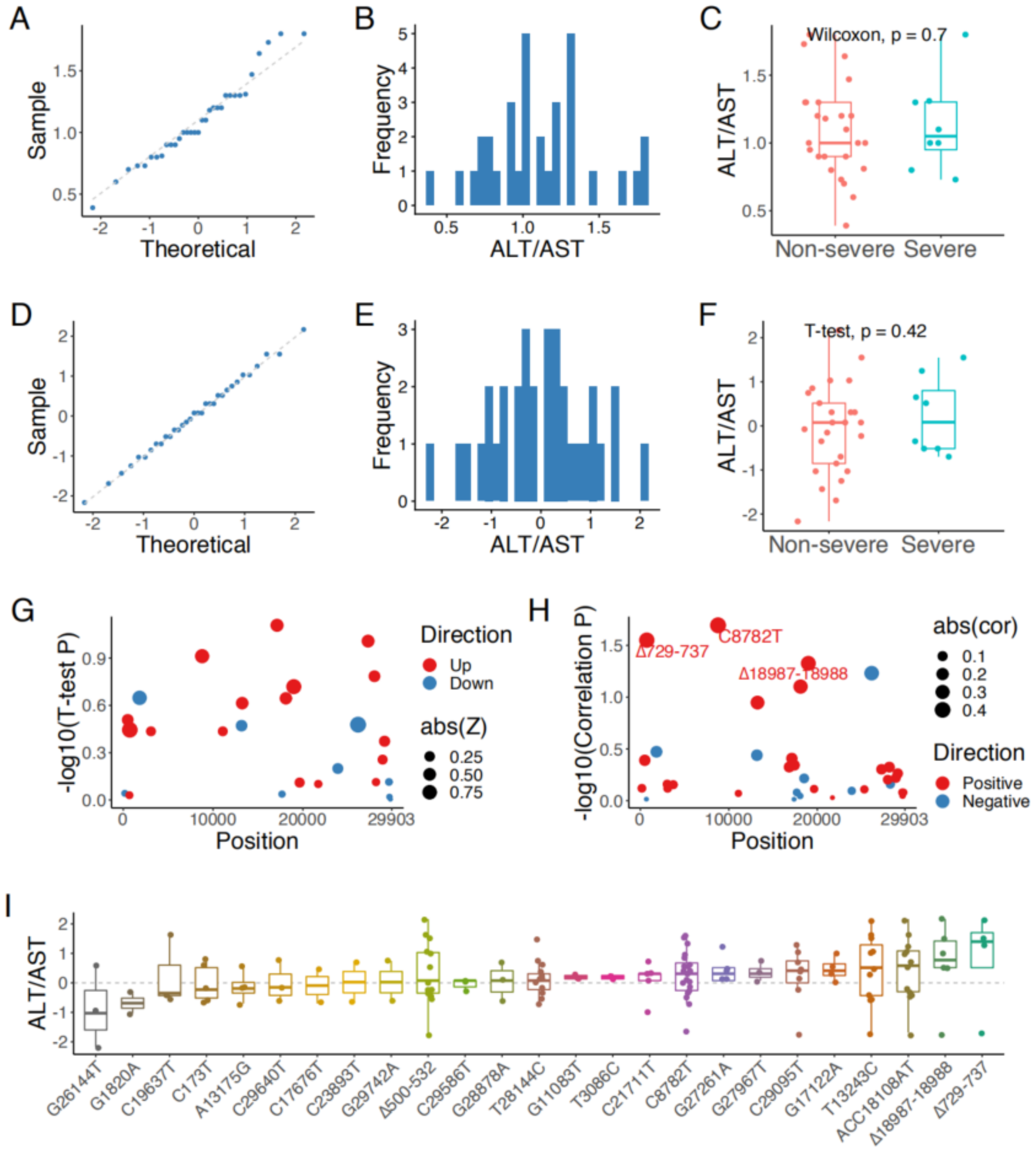
For ALP (alkaline phosphatase, U/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared ALP in the non-severe and severe COVID-19 patients before (**C**, p = 0.2, Wilcoxon test) and after normalization (**F**, p = 0.27, T-test). (**G**) No variant passes P value cut-off of 0.05 in T test. (**H**) Variant T17407C has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of ALP, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C173T tends to have the lowest.

4. ALT (alanine aminotransferase)



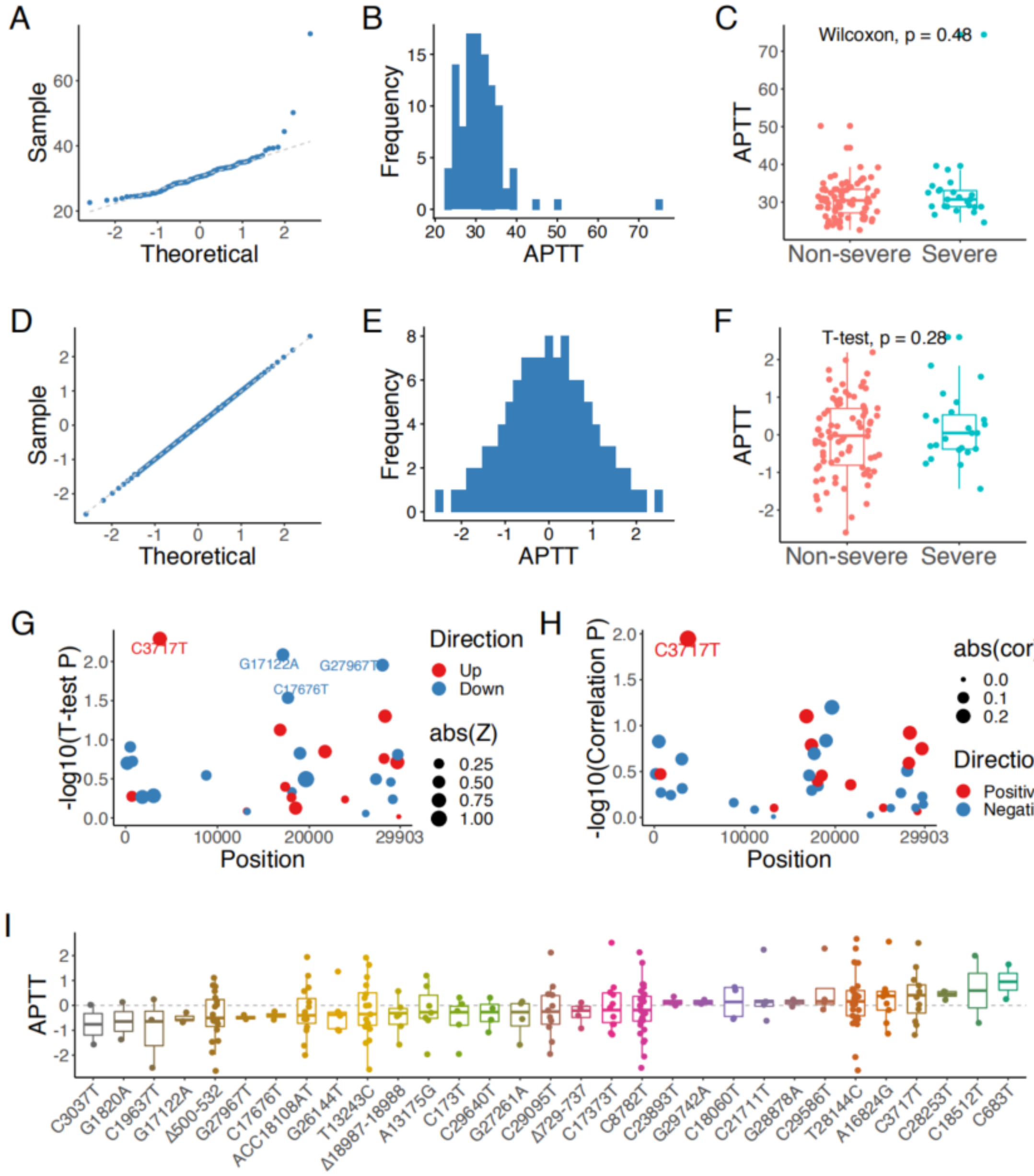
For ALT (alanine aminotransferase, U/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared ALT in the non-severe and severe COVID-19 patients before (**C**, p = 0.16, Wilcoxon test) and after normalization (**F**, p = 0.2, T-test). (**G**) Variants G27261A and C683T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant T13243C has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of ALT, cases with C18512T and G26144T tend to have the highest Z score, whereas cases with C28253T and A16824G have the lowest.

5. ALT/AST (alanine transaminase / aspartate transaminase ratio)



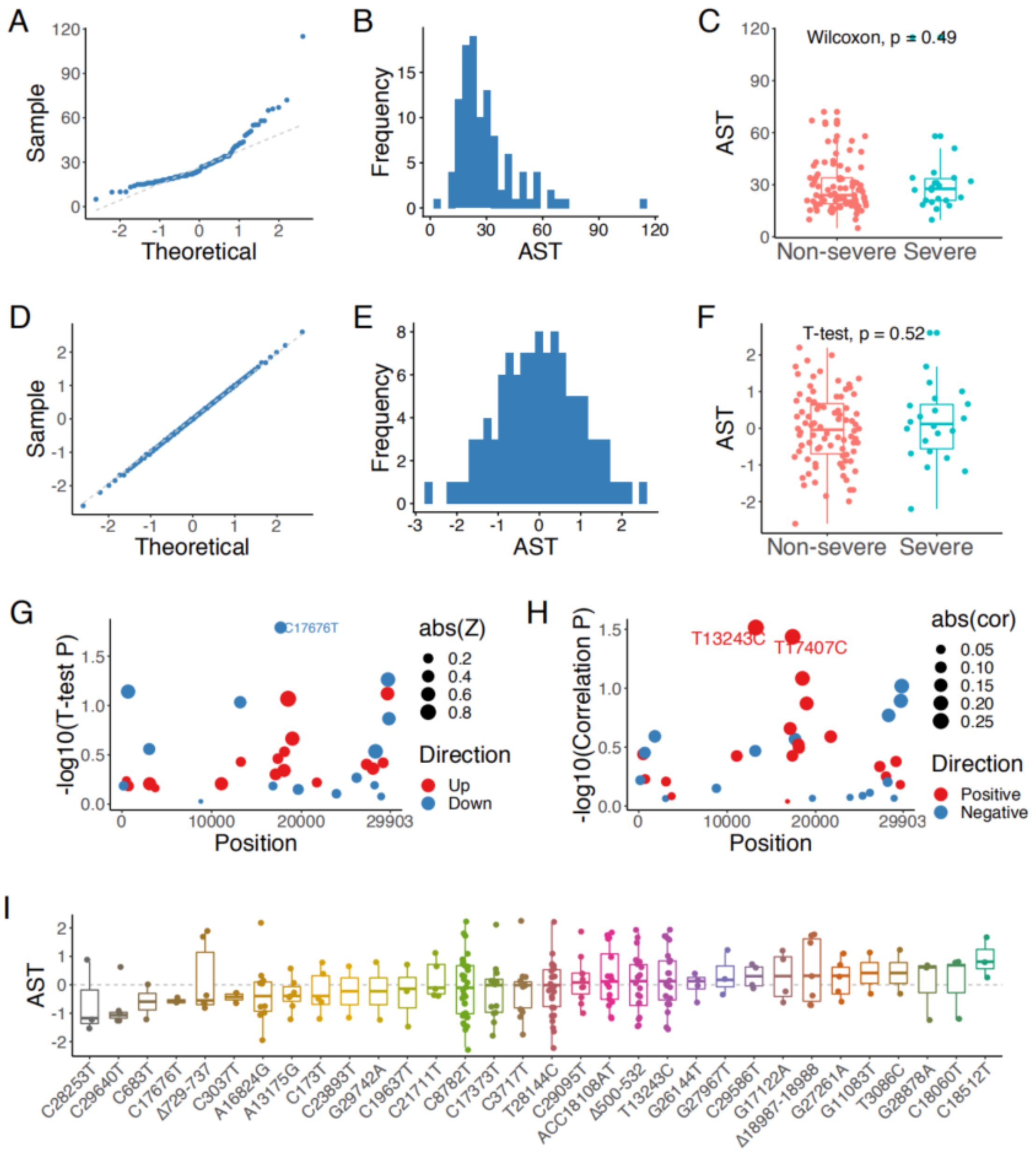
For ALT/AST (alanine transaminase / aspartate transaminase ratio), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared ALT/AST in the non-severe and severe COVID-19 patients before (**C**, p = 0.7, Wilcoxon test) and after normalization (**F**, p = 0.42, T-test). We further performed association analyses between the 35 genetic variants and ALT/AST using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. (**H**) Variants C8782T, Δ729-737 and Δ18987-18988 have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of ALT/AST, cases with Δ729-737 and Δ18987-18988 tend to have the highest Z score, whereas cases with G26144T and G1820A have the lowest.

6. APTT (thromboplastin time)



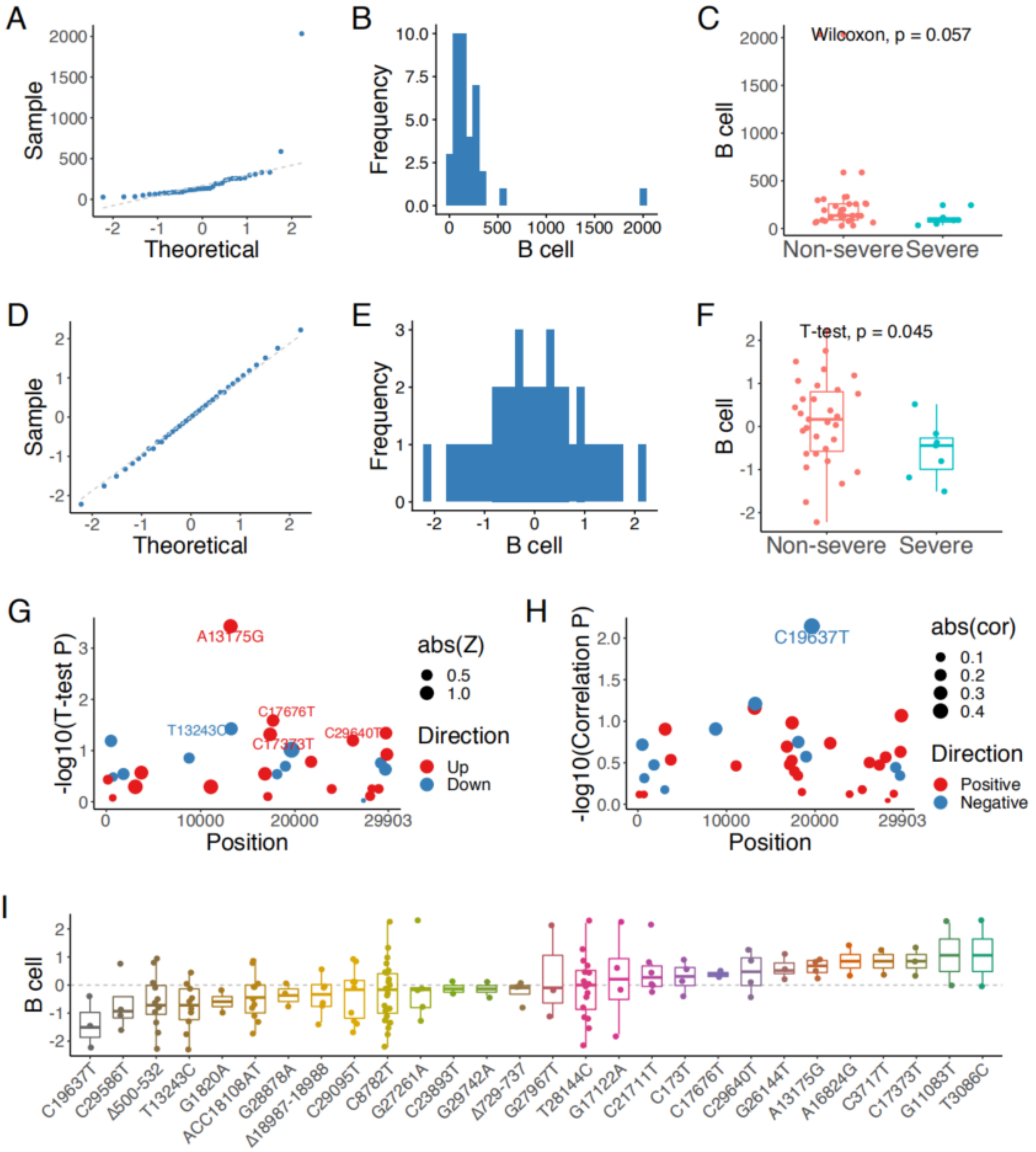
For APTT (thromboplastin time, sec), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared APTT in the non-severe and severe COVID-19 patients before (**C**, p = 0.48, Wilcoxon test) and after normalization (**F**, p = 0.28, T-test). We further performed association analyses between the 35 genetic variants and APTT using T-test and Pearson correlation. (**G**) Variants C3717T, G17122A, G27967T and C17676T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C3717T has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of APTT, cases with C683T and C18512T tend to have the highest Z score, whereas cases with C3037T and G1820A have the lowest.

7. AST (aspartate aminotransferase)



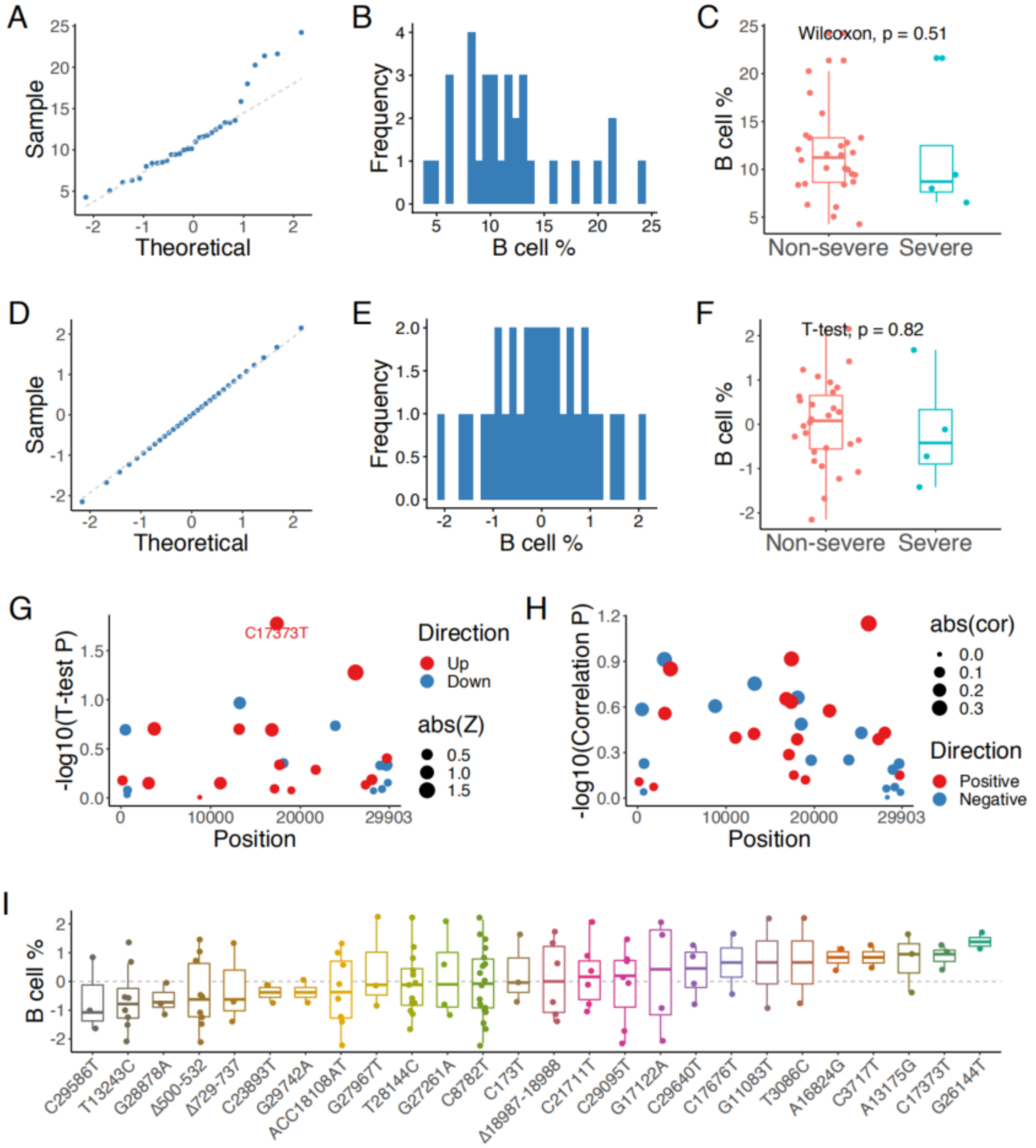
For AST (aspartate aminotransferase, U/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared AST in the non-severe and severe COVID-19 patients before (**C**, p = 0.49, Wilcoxon test) and after normalization (F, p = 0.52, T-test). (**G**) Variant C17676T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T13243C and T17407C have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of AST, cases with C18512T have the highest Z score, whereas cases with C29640T and C28253T have the lowest.

8. B cell count



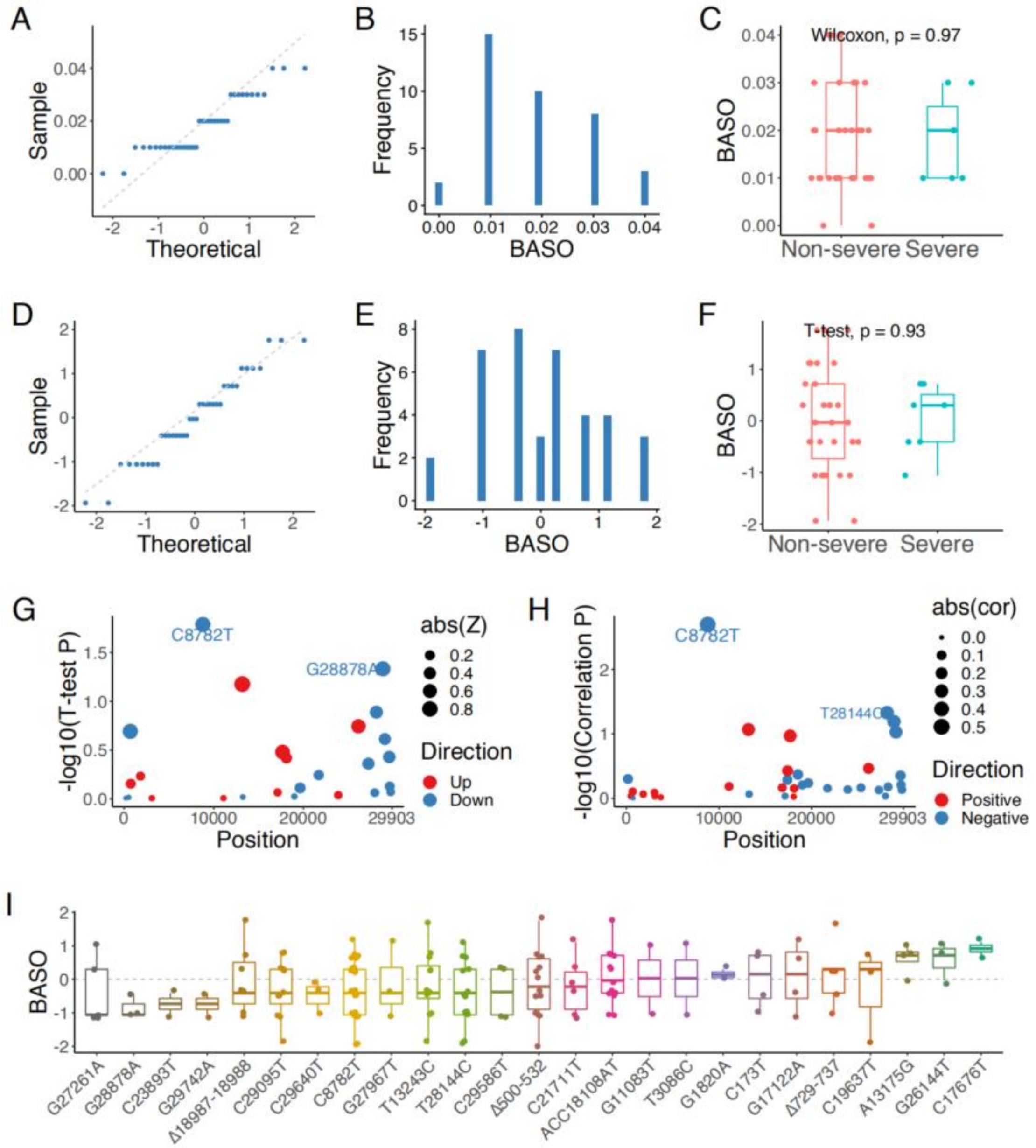
For B cell count (×10^9/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared B cell counts in the non-severe and severe COVID-19 patients before (**C**, p = 0.057, Wilcoxon test) and after normalization (**F**, p = 0.045, T-test). We further performed association analyses between the 35 genetic variants and B cell using T-test and Pearson correlation. (**G**) Variants A13175G, C17676T, C17373T, T13243O and C29640T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C19637T has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of B cell, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C19637T and C29586T have the lowest.

9. B cell percentage



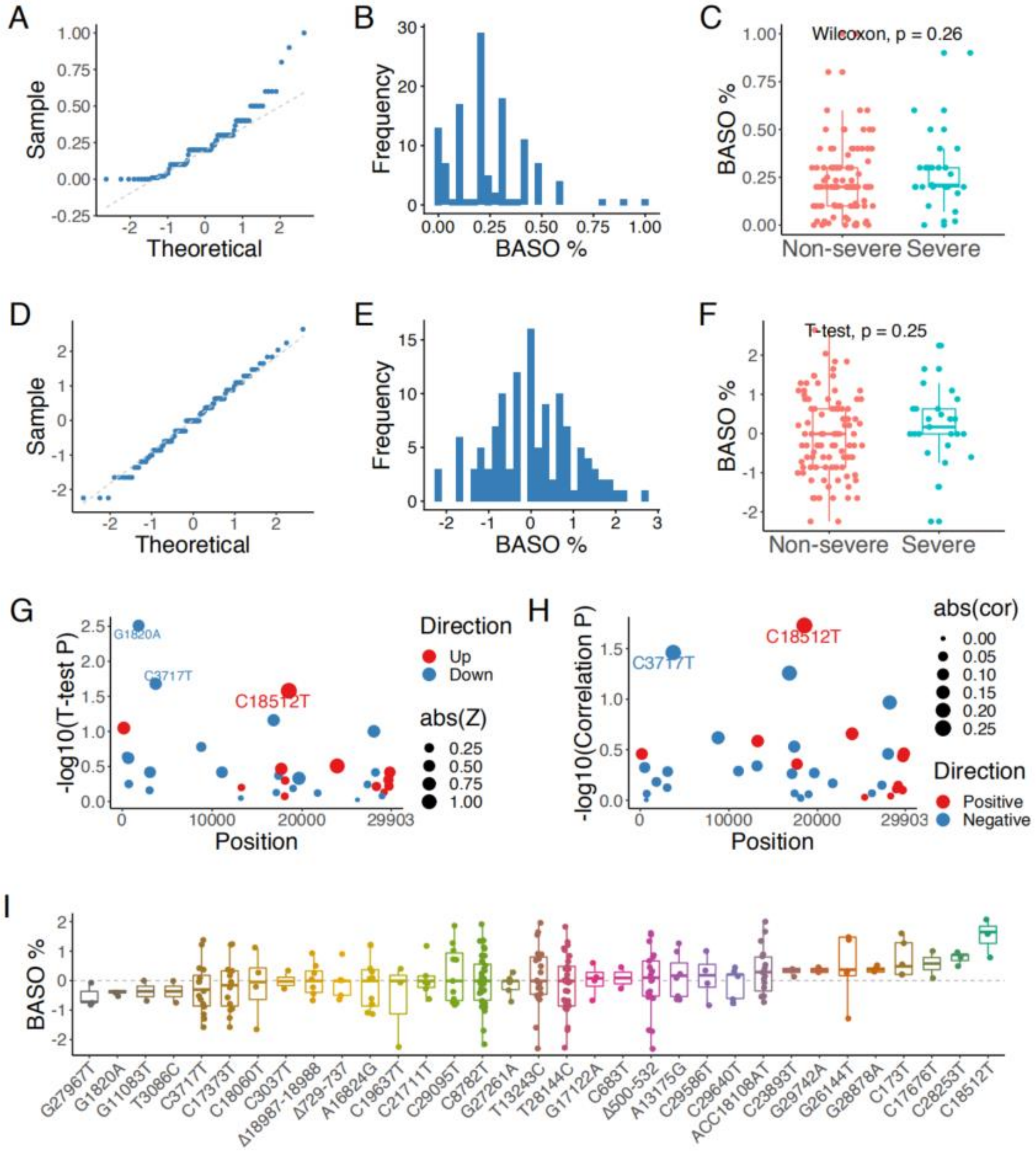
For B cell % (B cell percentage, %), quantile-quantile (QQ) plot and distribution plot before (A and B) and after normalization (D and E) were shown. We compared B cell % in the non-severe and severe COVID-19 patients before (C, p = 0.51, Wilcoxon test) and after normalization (F, p = 0.82, T-test). Variant C17373T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (H) No variant in Pearson correlation was has P value below 0.05. After sorting Z score values of B cell %, cases with G26144T and C17373T tend to have the highest Z score, whereas cases with C29586T and T13243C have the lowest.

10. BASO (Basophil count)



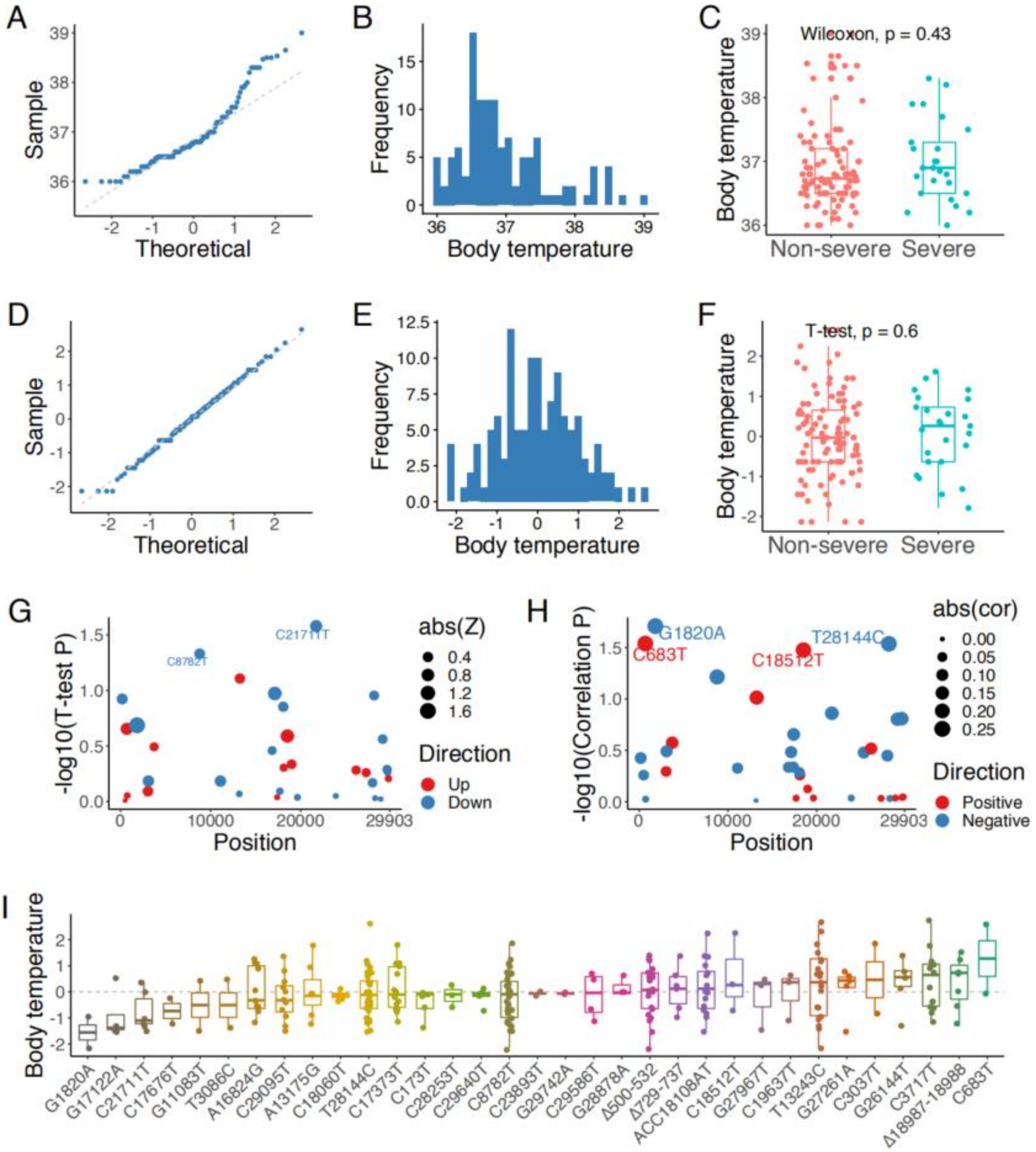
For BASO (Basophil count, ×10^9/L), quantile-quantile (QQ) plot and distribution plot before (A and B) and after normalization (D and E) were shown. We compared BASO in the non-severe and severe COVID-19 patients before (C, p = 0.97, Wilcoxon test) and after normalization (F, p = 0.93, T-test). We further performed association analyses between the 35 genetic variants and BASO using T-test and Pearson correlation. (G) Variants C8782T and G28878A pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (H) Variants C8782T and T28144C have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (I) After sorting Z score values of BASO, cases with C17676T and G26144T tend to have the highest Z score, whereas cases with G27261A and G28878A have the lowest.

11. BASO % (Basophil percentage)



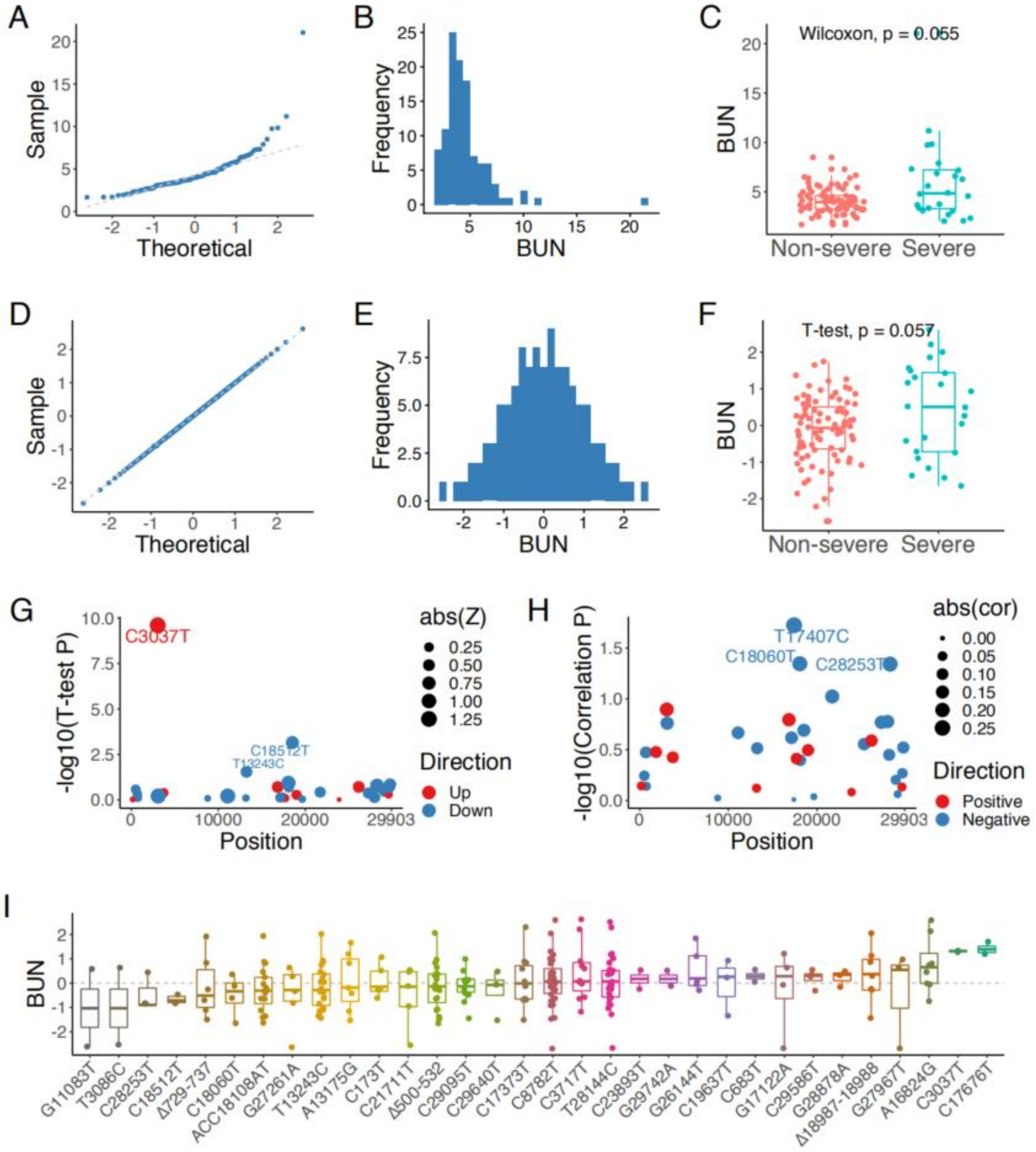
For BASO % (basophil percentage, %), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared BASO % in the non-severe and severe COVID-19 patients before (**C**, p = 0.26, Wilcoxon test) and after normalization (**F**, p = 0.25, T-test). We further performed association analyses between the 35 genetic variants and BASO% using T-test and Pearson correlation. (**G**) Variants G1820A, C3717T and C18512T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C18512T and C3717T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of BASO %, cases with C18512T and C28253T tend to have the highest Z score, whereas cases with G27967T and G1820A have the lowest.

12. Body temperature



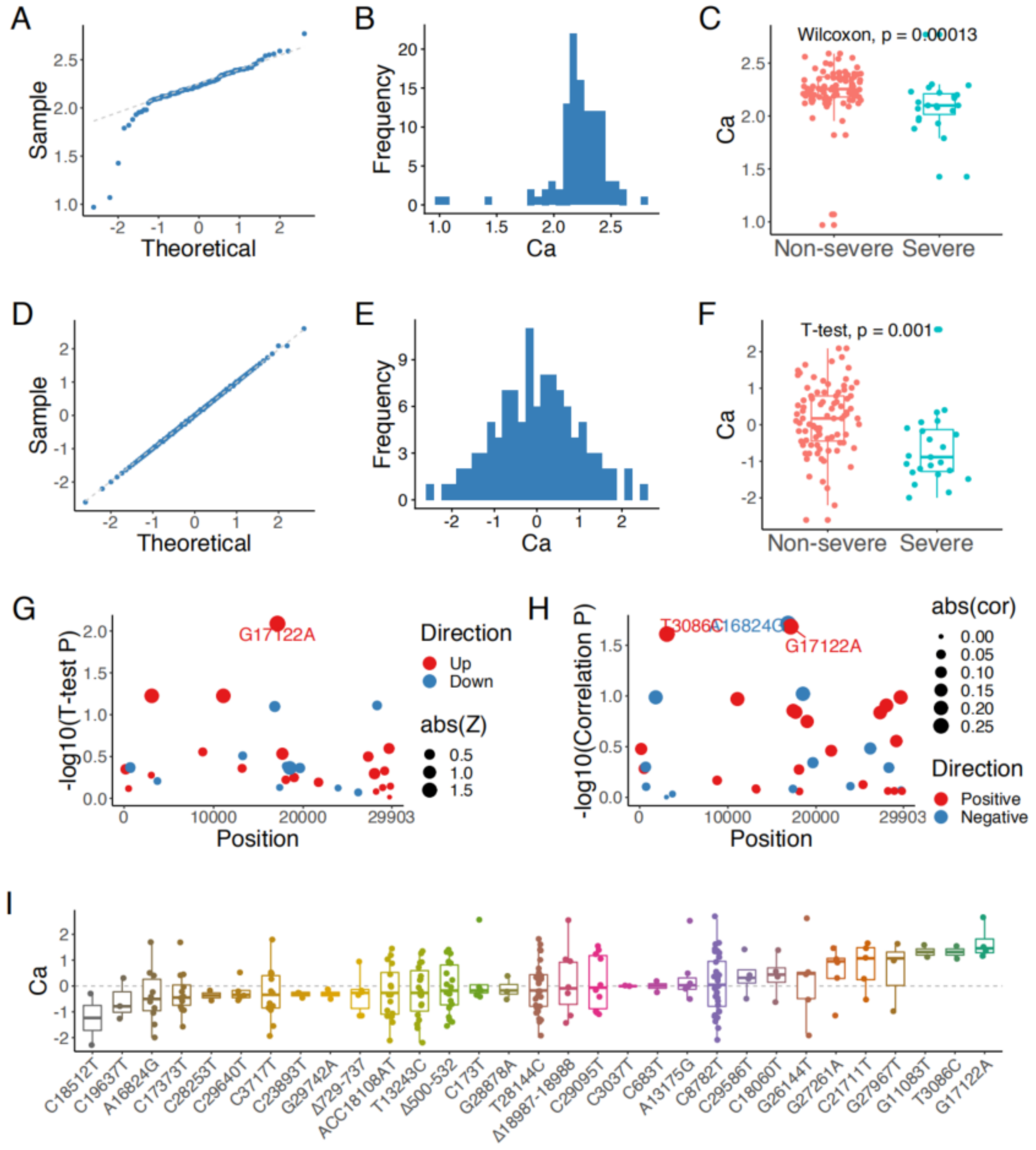
For Body temperature (°C), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (D and E) were shown. We compared Body temperature in the non-severe and severe COVID-19 patients before (**C**, p = 0.43, Wilcoxon test) and after normalization (**F**, p = 0.6, T-test). (**G**) Variants C21711T and C8782T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (H) Variants G1820A, C683T, C18512T and T28144C have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (I) After sorting Z score values of Body temperature, cases with C683T and Δ18987-18988 tend to have the highest Z score, whereas cases with G1820A and T17122A have the lowest.

13. BUN (blood urea nitrogen)



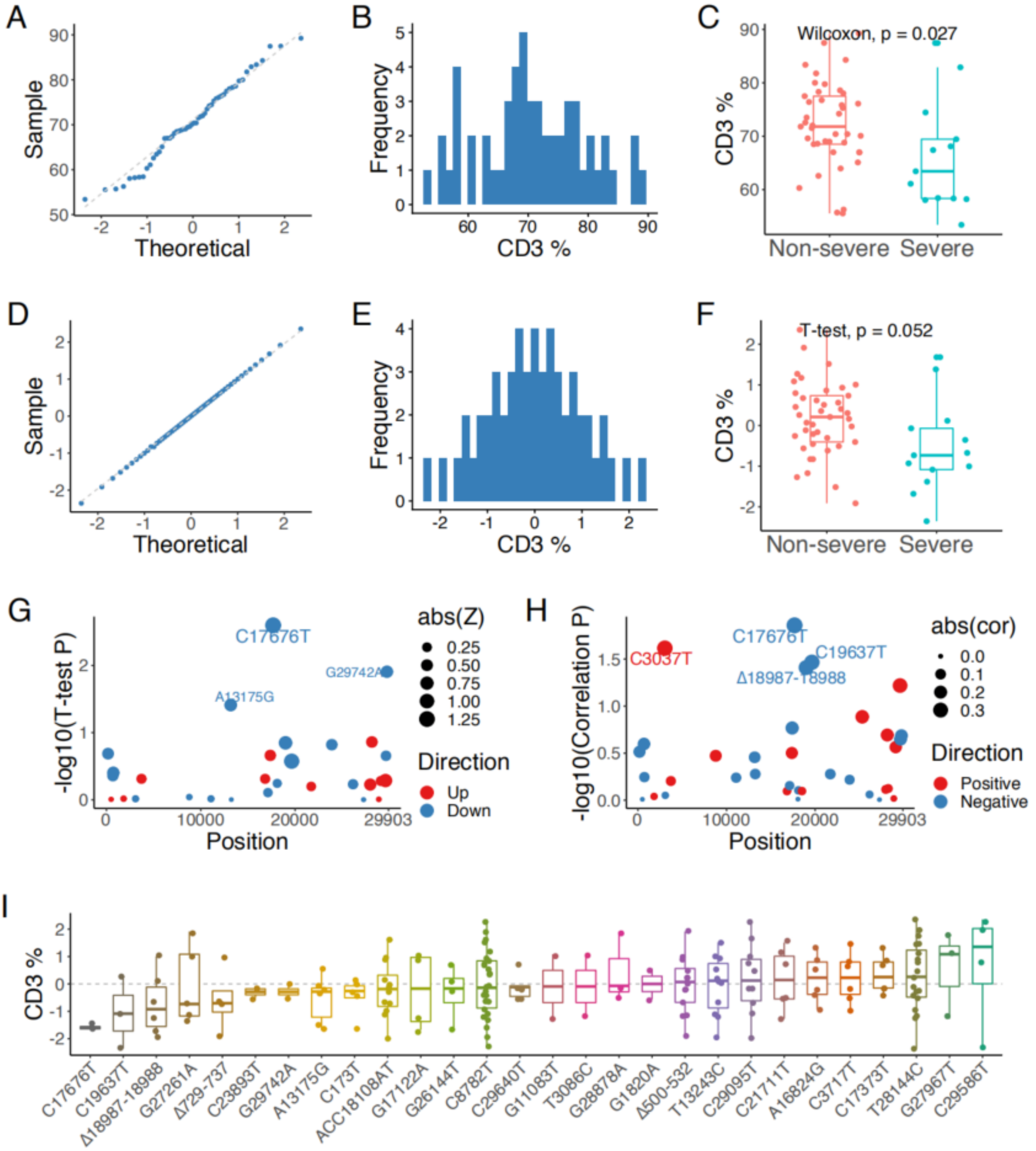
For BUN (blood urea nitrogen, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared BUN in the non-severe and severe COVID-19 patients before (**C**, p = 0.055, Wilcoxon test) and after normalization (**F**, p = 0.057, T-test). We further performed association analyses between the 35 genetic variants and BUN using T-test and Pearson correlation. (**G**) Variants C3037T, C18512T and T13243C pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T17407C, C18060T and C28253T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of BUN, cases with C17676T and C3037T tend to have the highest Z score.

14. Ca^{2+} (serum calcium)



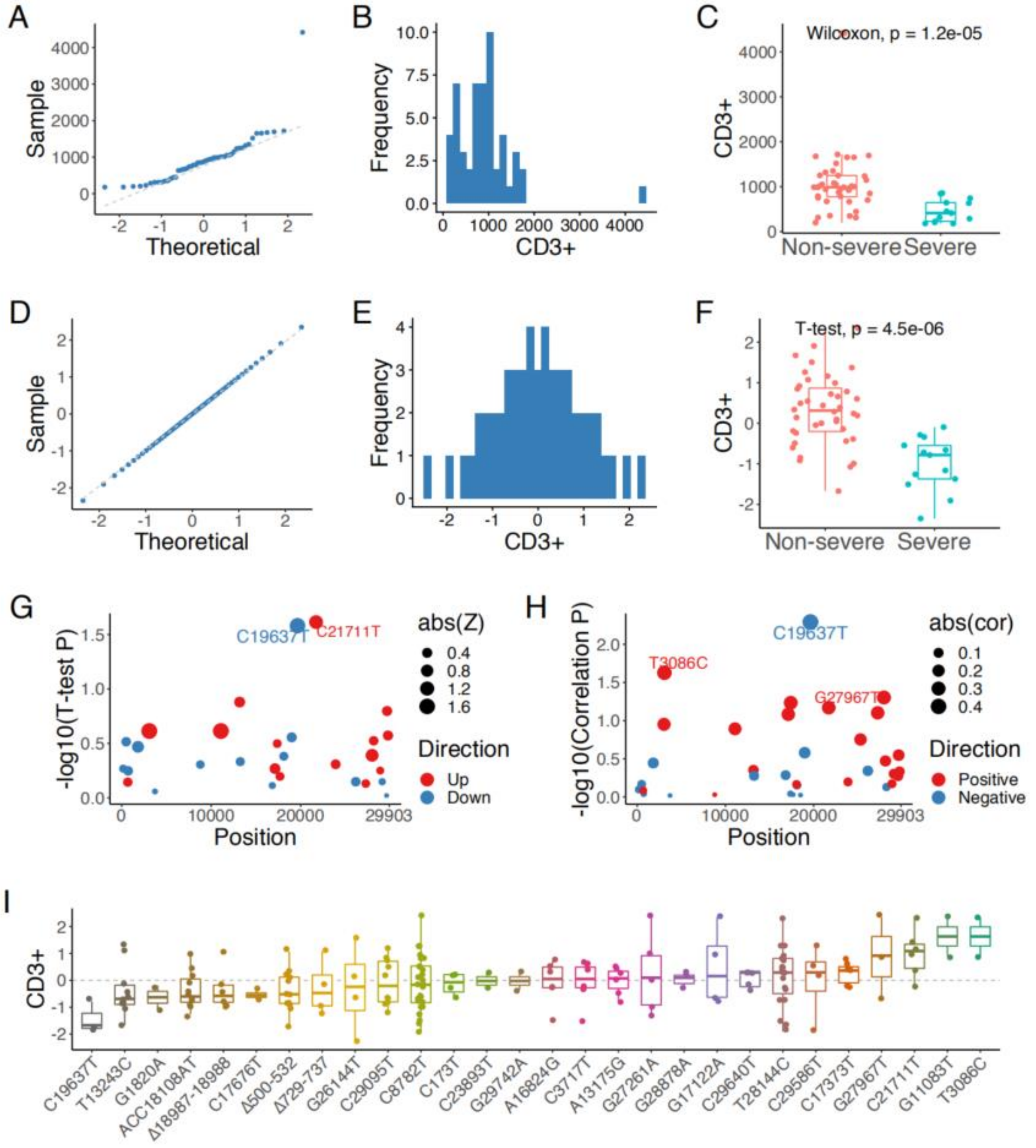
For Ca^{2+} (serum calcium, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Ca^{2+} in the non-severe and severe COVID-19 patients before (**C**, $p = 1.3\times10^{-4}$, Wilcoxon test) and after normalization (**F**, $p = 1.0\times10^{-3}$, T-test). (**G**) Variant G17122A passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants A16824G, T3086C and G17122A have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of Ca^{2+}, cases with G17122A, T3086C and G11083T have the highest Z score, whereas cases with C18512T has the lowest.

15. CD3 % (CD3 percentage)



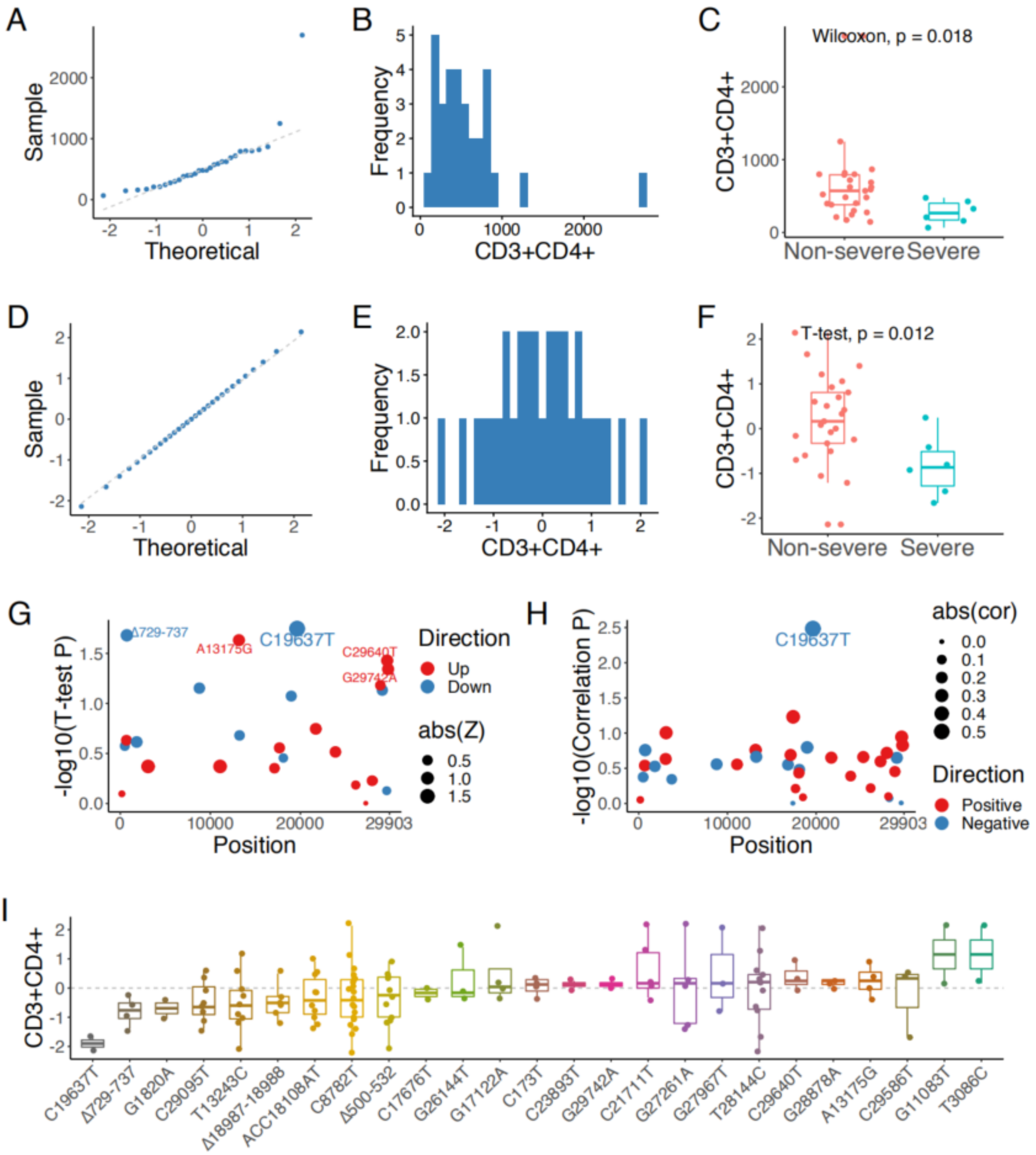
For CD3 % (CD3 percentage, %), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CD3 % in the non-severe and severe COVID-19 patients before (**C**, p = 0.027, Wilcoxon test) and after normalization (**F**, p = 0.052, T-test). We further performed association analyses between the 35 genetic variants and CD3 % using T-test and Pearson correlation. (**G**) Variants C17676T, G29742A and A13175G pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C17676T, C3037T, C19637T and Δ 18987-18988 have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of CD3 %, cases with C29586T tends to have the highest Z score, whereas cases with C17676T has the lowest.

16. CD3$^+$ (CD3$^+$ T cell count)



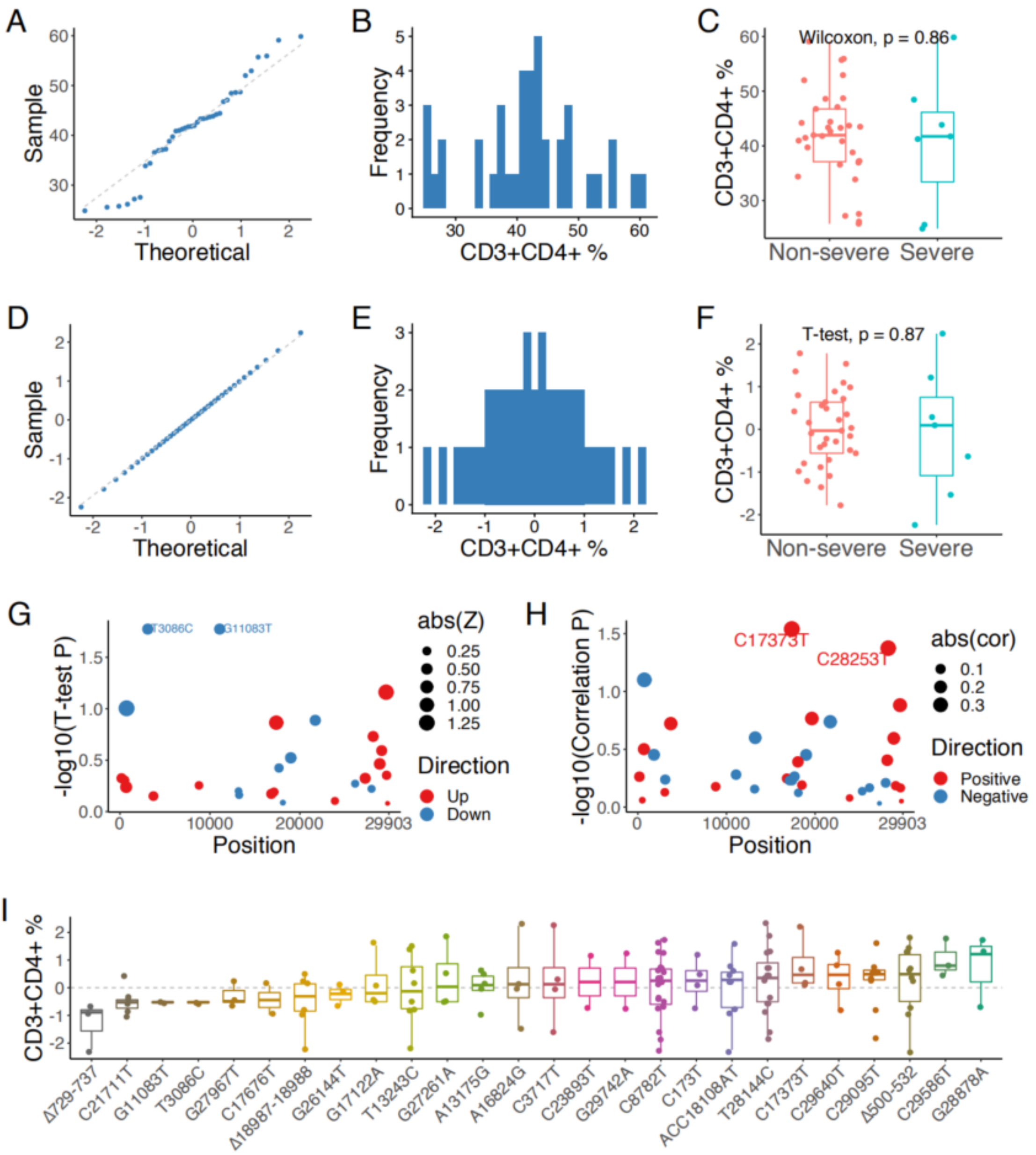
For CD3$^+$ (CD3$^+$ T cell count, cell/μl), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CD3$^+$ in the non-severe and severe COVID-19 patients before (**C**, $p = 1.2\times10^{-5}$, Wilcoxon test) and after normalization (**F**, $p = 4.5\times10^{-6}$, T-test). We further performed association analyses between the 35 genetic variants and CD3$^+$ using T-test and Pearson correlation. (**G**) Variants C19637T and C21711T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C19637T, T3086C and G27967T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of CD3$^+$, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C19637T has the lowest.

17. CD3$^+$ CD4$^+$ (CD3$^+$ CD4$^+$ count)



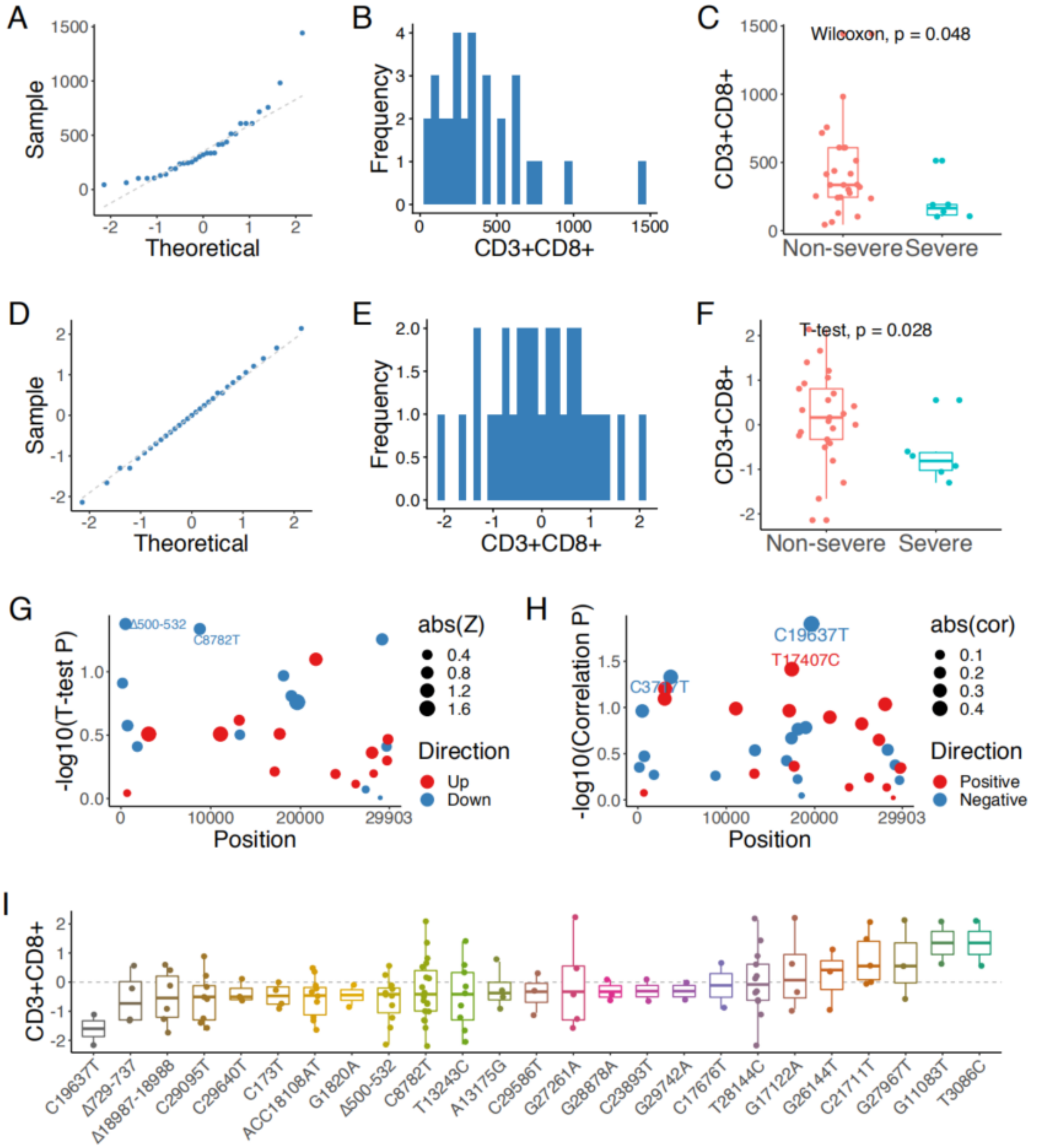
For CD3$^+$ CD4$^+$ (CD3$^+$ CD4$^+$ count, ×10^9/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CD3$^+$ CD4$^+$ in the non-severe and severe COVID-19 patients before (**C**, p = 0.018, Wilcoxon test) and after normalization (**F**, p = 0.012, T-test). We further performed association analyses between the 35 genetic variants and CD3$^+$ CD4$^+$ using T-test and Pearson correlation. (**G**) Variants Δ729-737, A13175G and C19637T et al pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C19637T has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of CD3$^+$ CD4$^+$, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C19637T and Δ729-737 have the lowest.

18. CD3$^+$ CD4$^+$ % (CD3$^+$ CD4$^+$ percentage)



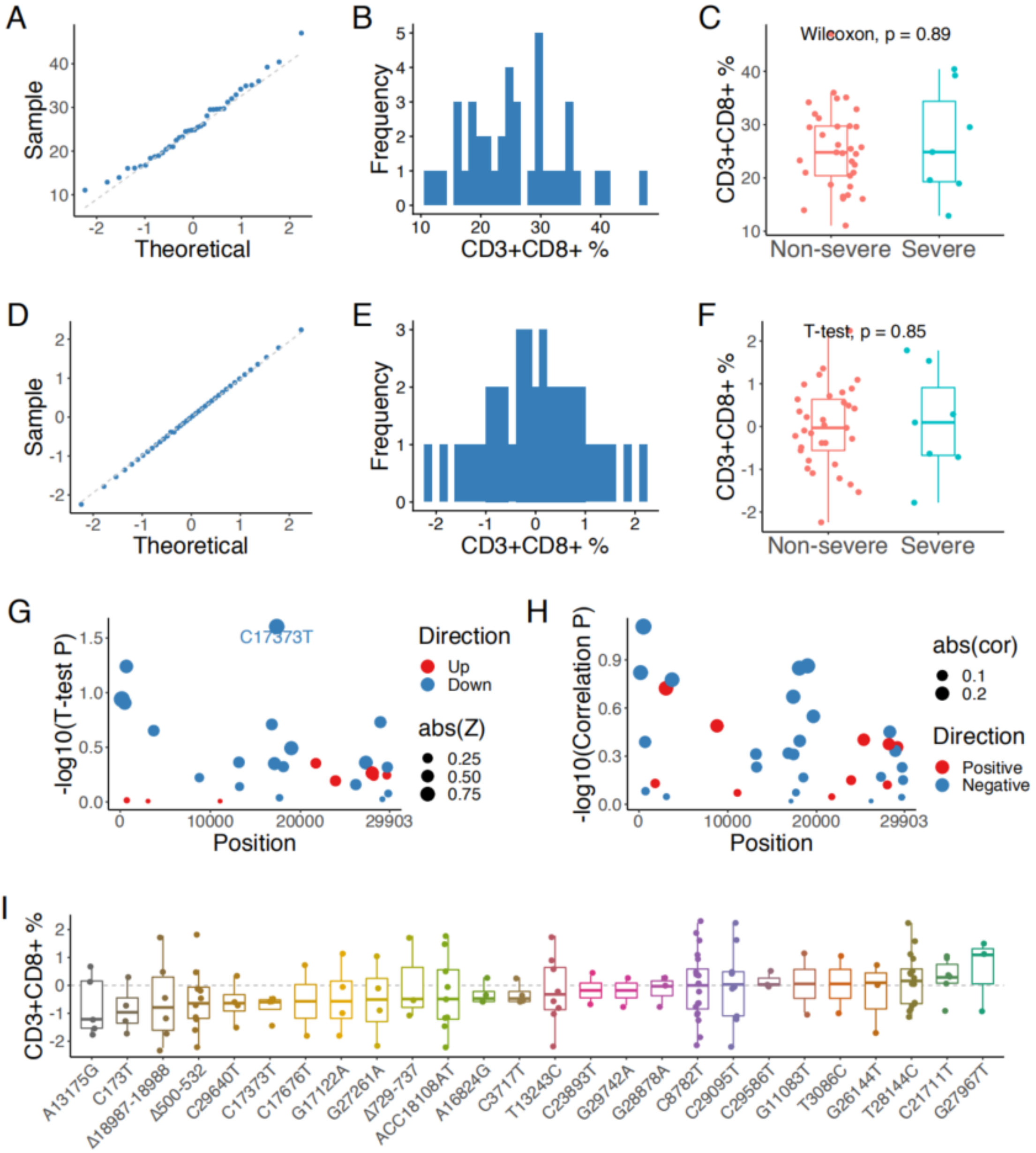
For CD3$^+$ CD4$^+$ % (CD3$^+$ CD4$^+$ percentage), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CD3$^+$ CD4$^+$ % in the non-severe and severe COVID-19 patients before (**C**, p = 0.86, Wilcoxon test) and after normalization (**F**, p = 0.87, T-test). (**G**) Variants T3086C and G11083T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C17373T and C28253T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of CD3$^+$ CD4$^+$ %, cases with G28878A and C29586T tend to have the highest Z score, whereas cases with Δ729-737 and C21711T have the lowest.

19. CD3$^+$ CD8$^+$ (CD3$^+$ CD8$^+$ count)



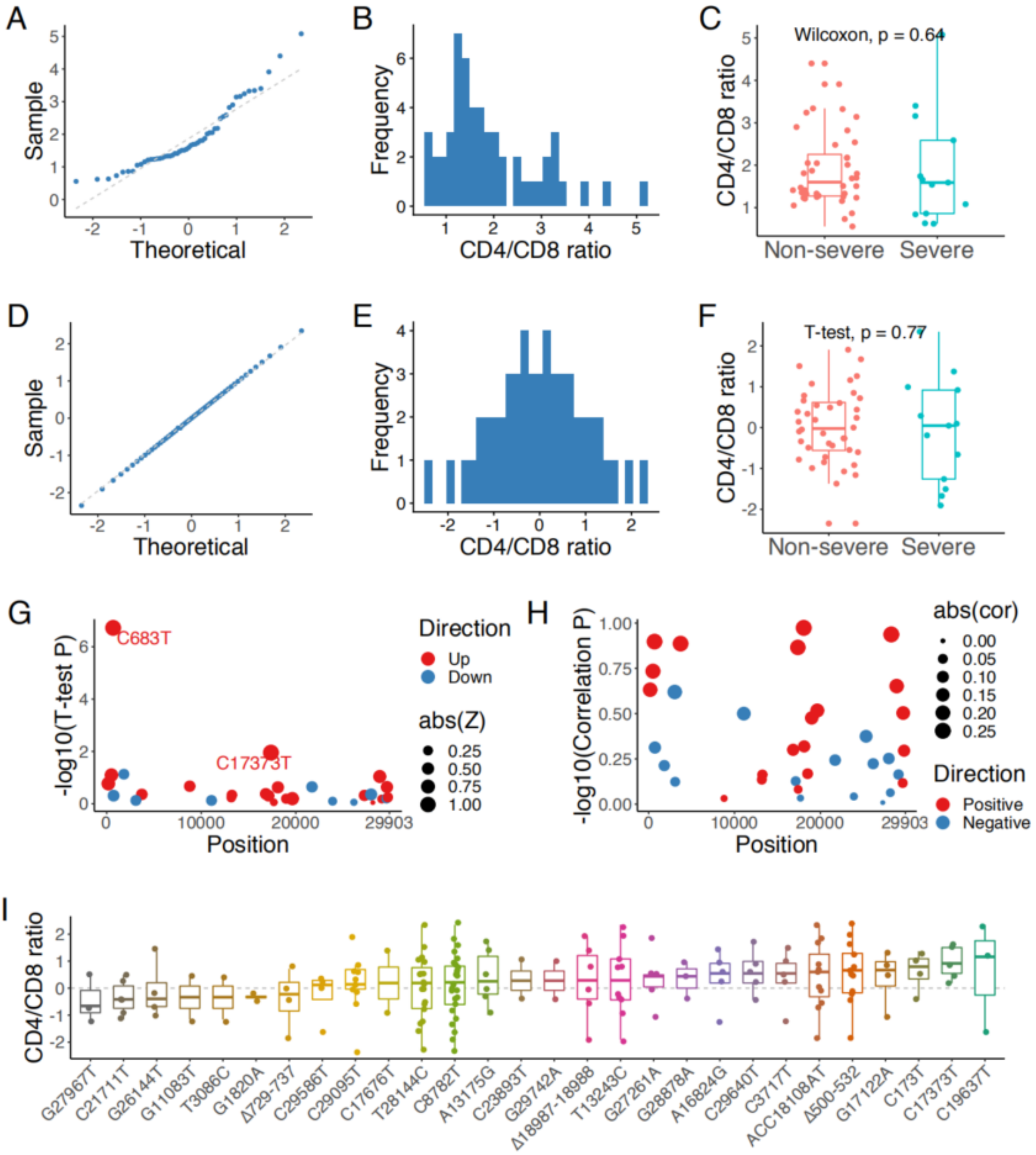
For CD3$^+$ CD8$^+$ (CD3$^+$ CD8$^+$ count, ×10^9/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CD3$^+$ CD8$^+$ in the non-severe and severe COVID-19 patients before (**C**, p = 0.048, Wilcoxon test) and after normalization (**F**, p = 0.028, T-test). We further performed association analyses between the 35 genetic variants and CD3$^+$ CD8$^+$ using T-test and Pearson correlation. (**G**) Variants Δ500-532 and C8782T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C19637T, T17407C and C3717T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of CD3$^+$ CD8$^+$, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C19637T and Δ729-737 to have the lowest.

20. CD3$^+$ CD8$^+$ % (CD3$^+$ CD8$^+$ percentage)



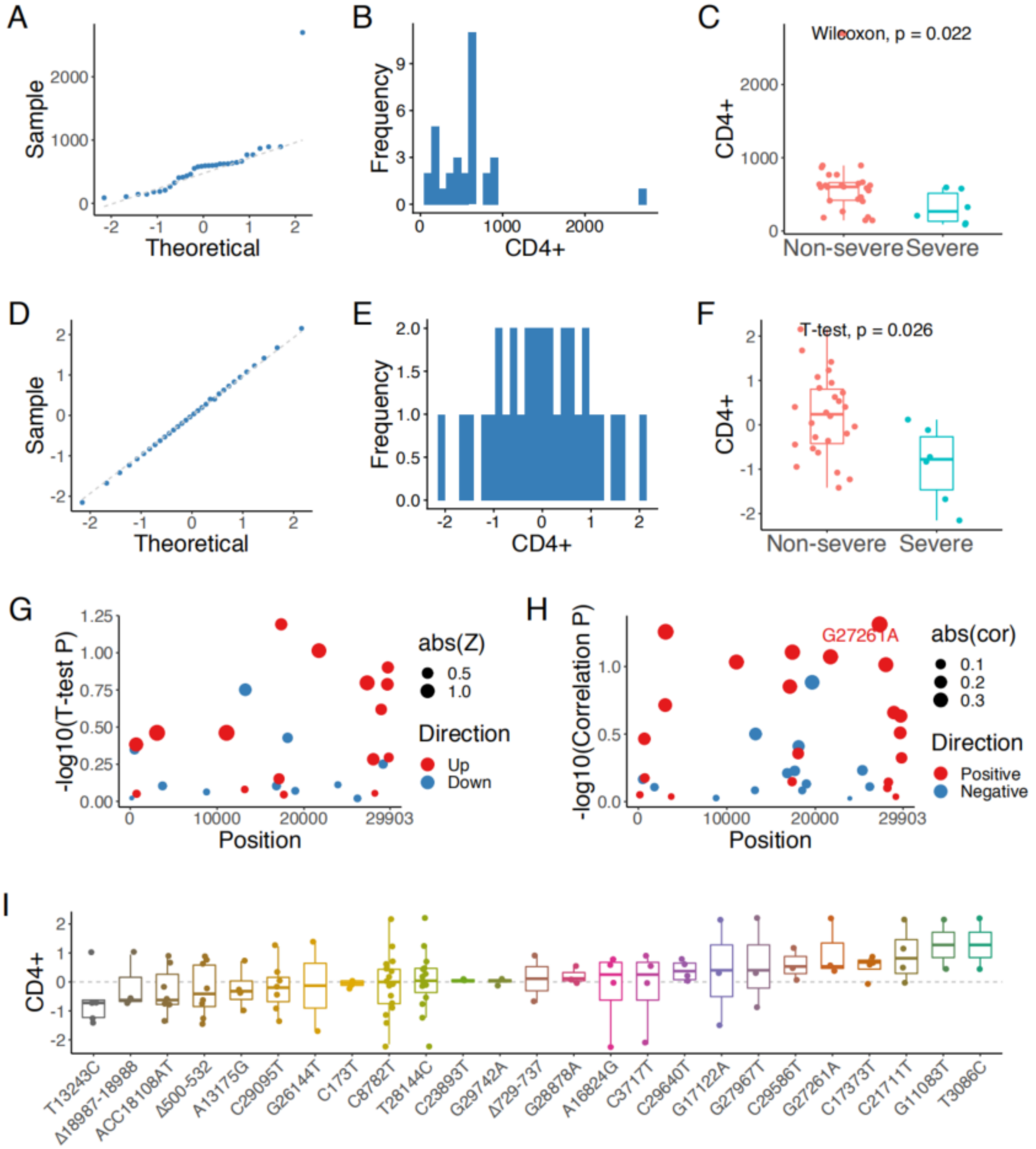
For CD3$^+$ CD8$^+$ % (CD3$^+$ CD8$^+$ percentage), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CD3$^+$ CD8$^+$ % in the non-severe and severe COVID-19 patients before (**C**, p = 0.89, Wilcoxon test) and after normalization (**F**, p = 0.85, T-test). We further performed association analyses between the 35 genetic variants and CD3$^+$ CD8$^+$ % using T-test and Pearson correlation. (**G**) Variant C17373T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) No variant in Pearson correlation was has P value below 0.05. After sorting Z score values of CD3$^+$ CD8$^+$ %, cases with G27967T and C21711T tend to have the highest Z score, whereas cases with A13175G and C173T have the lowest.

21. CD4/CD8 ratio (%)



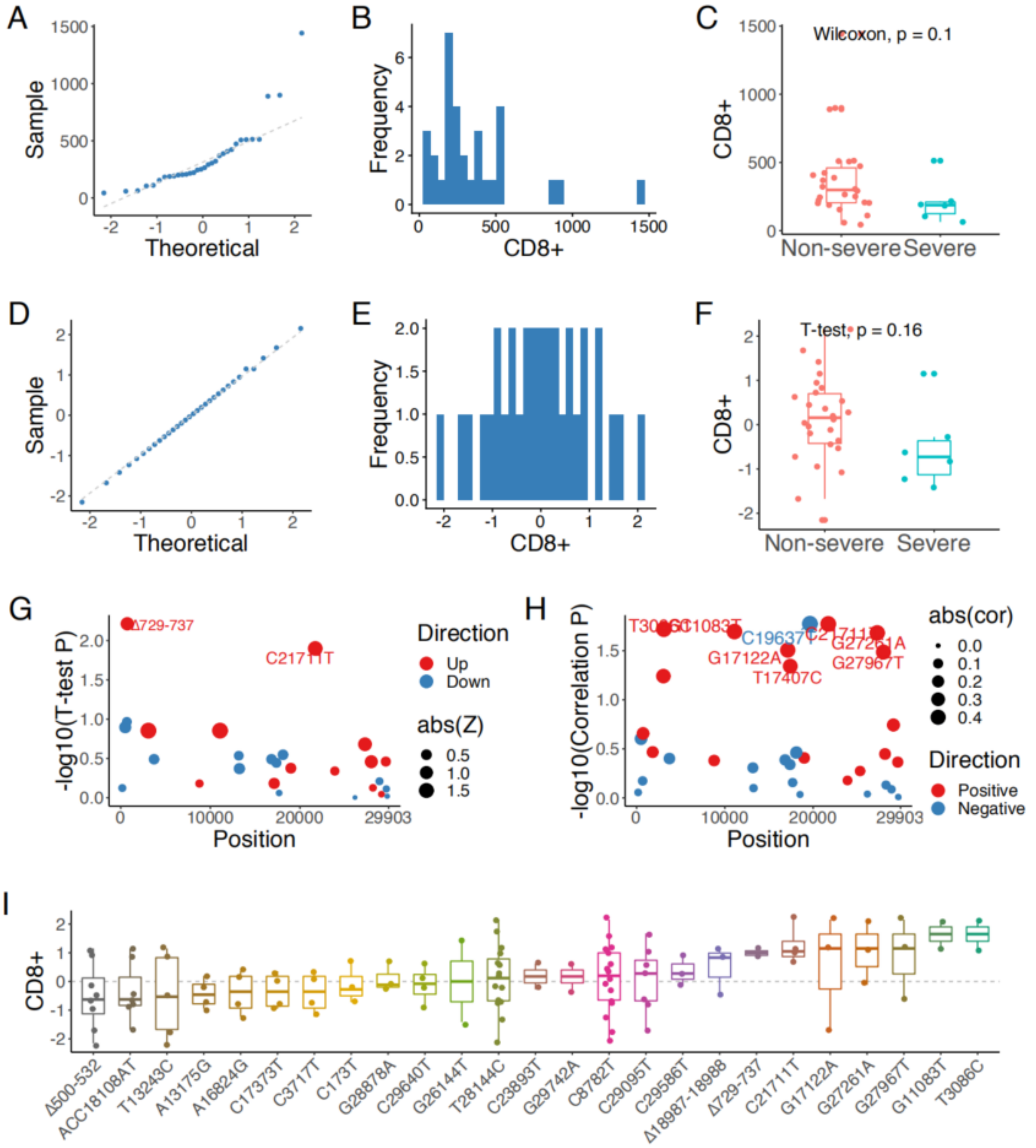
For CD4/CD8 ratio (%), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CD4/CD8 ratio in the non-severe and severe COVID-19 patients before (**C**, p = 0.64, Wilcoxon test) and after normalization (**F**, p = 0.77, T-test). We further performed association analyses between the 35 genetic variants and CD4/CD8 ratio using T-test and Pearson correlation. (**G**) Variants C683T and C17373T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) No variant has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of CD4/CD8 ratio, cases with C19637T and C17373T tend to have the highest Z score, whereas cases with G27967T and C21711T have the lowest.

22. CD4$^+$ (CD4 absolute count)



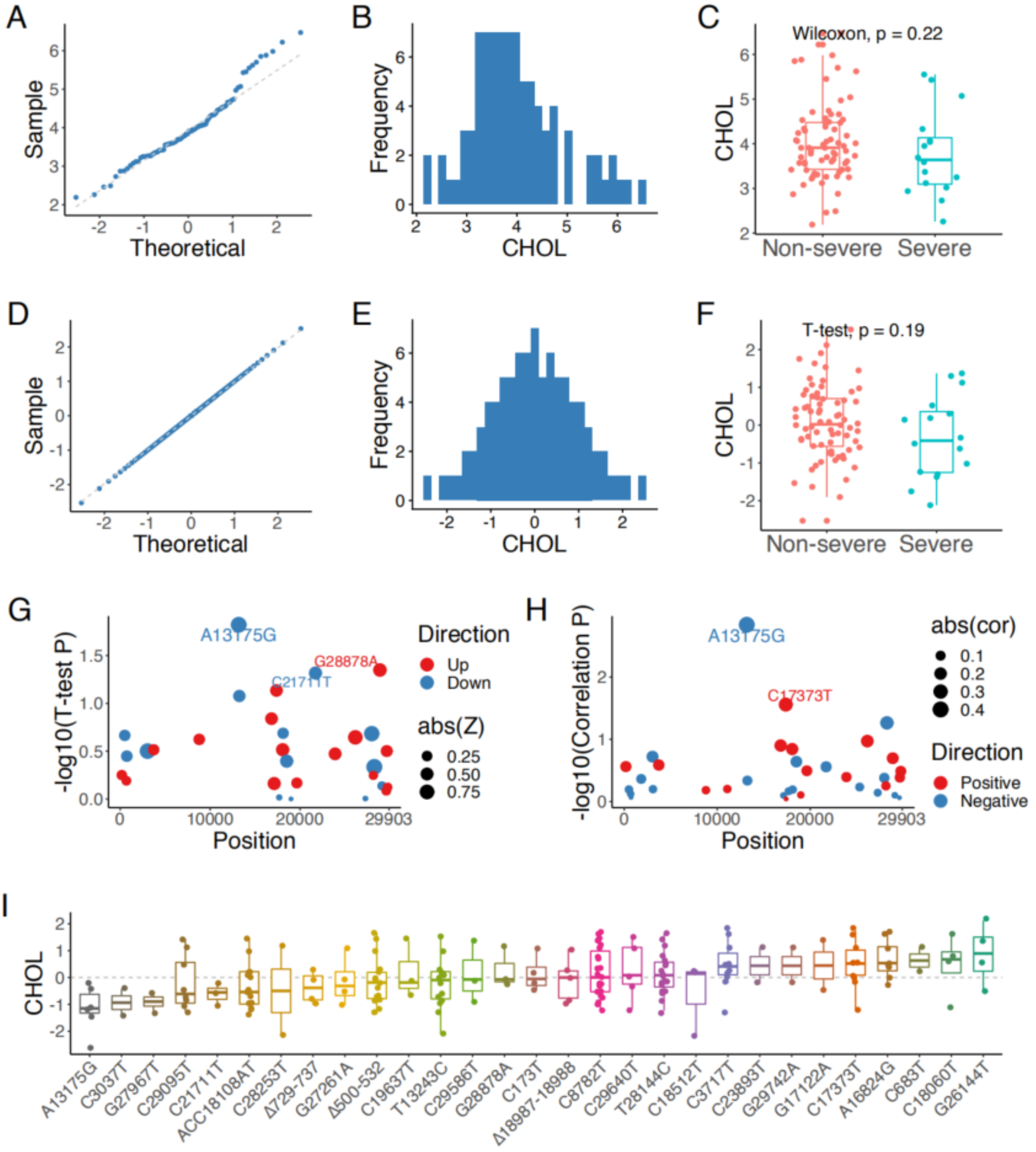
For CD4$^+$ (CD4 absolute count, cell/μl), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CD4$^+$ in the non-severe and severe COVID-19 patients before (**C**, p = 0.022, Wilcoxon test) and after normalization (**F**, p = 0.026, T-test). We further performed association analyses between the 35 genetic variants and CD4$^+$ using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant G27261A in Pearson correlation was with P value below 0.05. After sorting Z score values of CD4$^+$, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with T13243C and Δ18987-18988 have the lowest.

23. CD8$^+$ (CD8 absolute count)



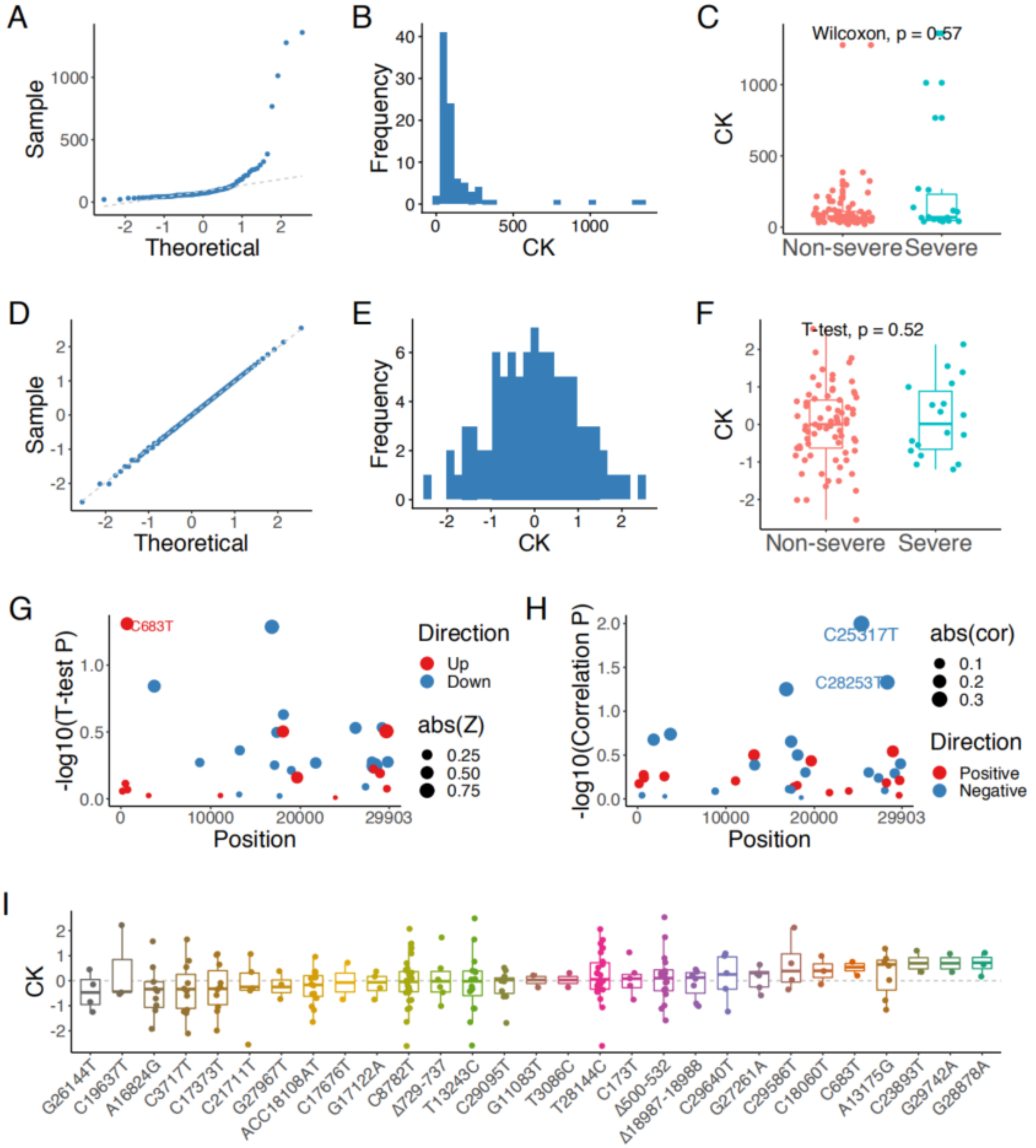
For CD8$^+$ (CD8 absolute count, cell/µl), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CD8$^+$ in the non-severe and severe COVID-19 patients before (**C**, p = 0.1, Wilcoxon test) and after normalization (**F**, p = 0.16, T-test). We further performed association analyses between the 35 genetic variants and CD8$^+$ using T-test and Pearson correlation. (**G**) Variants Δ729-737 and C21711T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C19637T, G11083T and T3086C et al have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of CD8$^+$, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with Δ500-532 and ACC18108AT have the lowest.

24. CHOL (cholesterol)



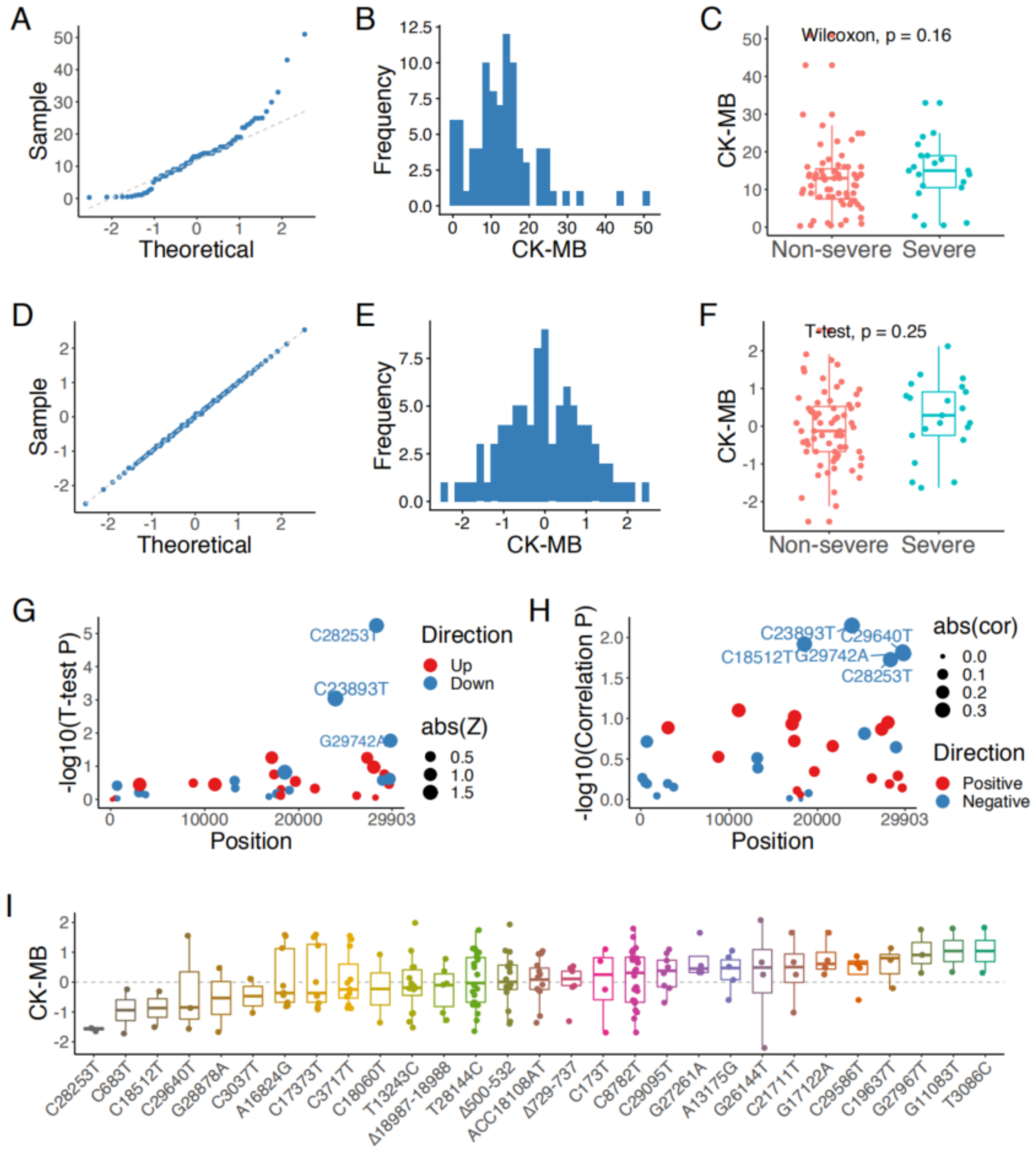
For CHOL (cholesterol, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CHOL in the non-severe and severe COVID-19 patients before (**C**, p = 0.22, Wilcoxon test) and after normalization (**F**, p = 0.19, T-test). We further performed association analyses between the 35 genetic variants and CHOL using T-test and Pearson correlation. (**G**) Variants A13175G, G28878A and C21711T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants A13175G and C17373T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of CHOL, cases with G26144T and C18060T tend to have the highest Z score, whereas cases with A13175G and C3037T have the lowest.

25. CK (creatine kinase)



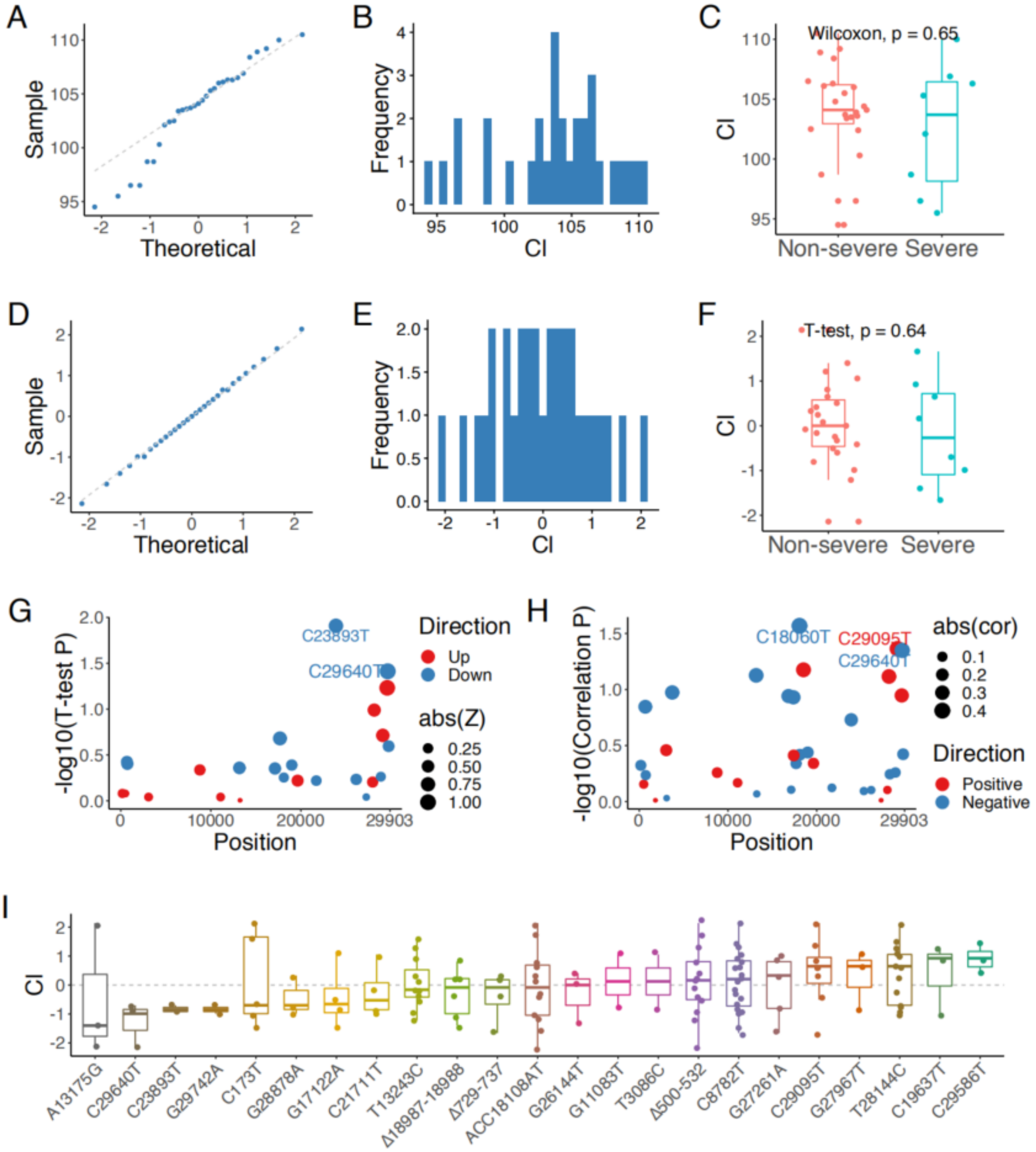
For CK (creatine kinase, U/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CK in the non-severe and severe COVID-19 patients before (**C**, p = 0.57, Wilcoxon test) and after normalization (**F**, p = 0.52, T-test). We further performed association analyses between the 35 genetic variants and CK using T-test and Pearson correlation. (**G**) Variant C683T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C25317T and C28253T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of CK, cases with G28878A and G29742A tend to have the highest Z score, whereas cases with G26144T and C19637T have the lowest.

26. CK-MB (creatine kinase-MB)



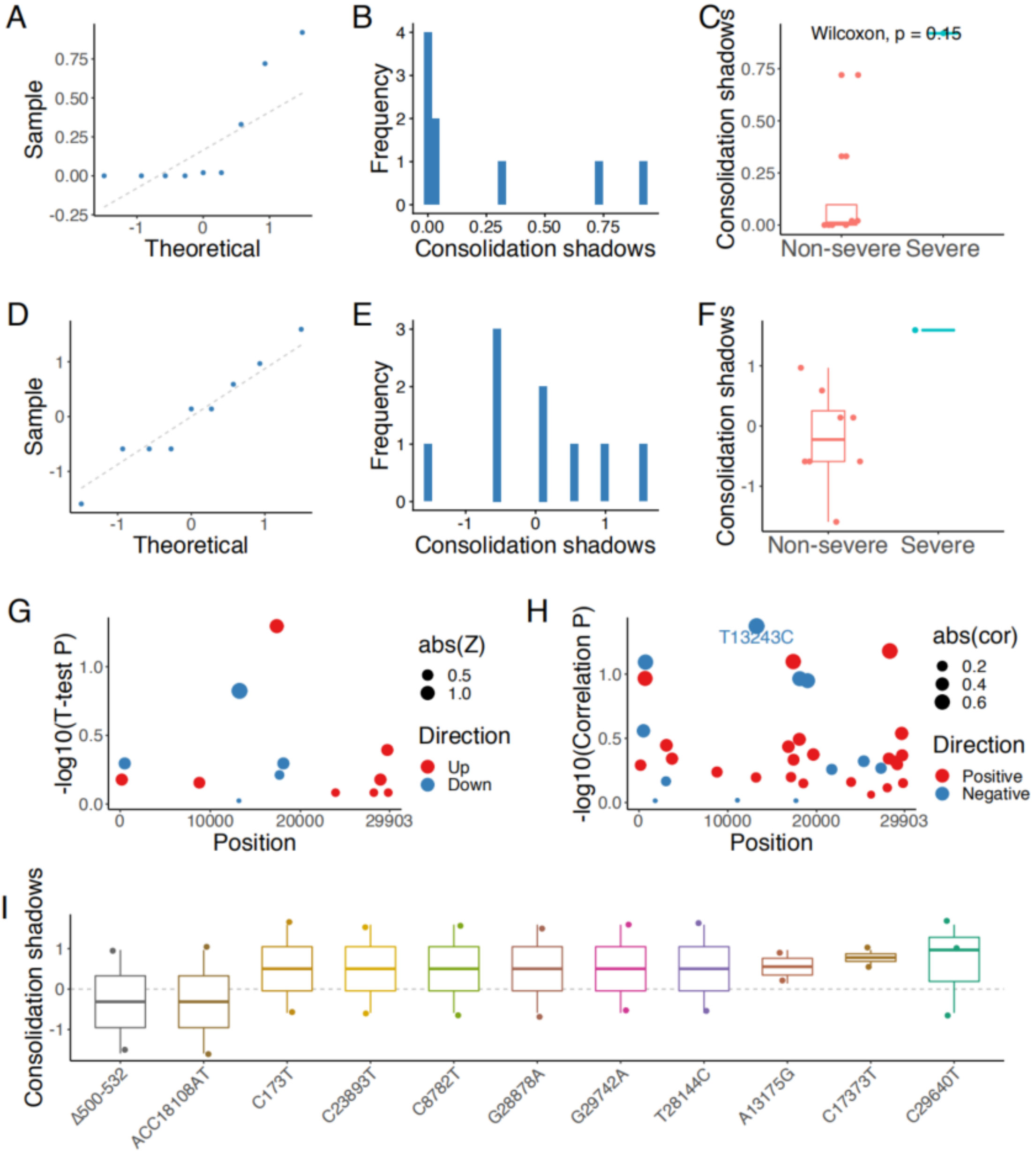
For CK-MB (creatine kinase-MB, U/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CK-MB in the non-severe and severe COVID-19 patients before (**C**, p = 0.16, Wilcoxon test) and after normalization (**F**, p = 0.25, T-test). We further performed association analyses between the 35 genetic variants and CK-MB using T-test and Pearson correlation. (**G**) Variants C28253T, C23893T and G29742A pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C23893T, C18512T and C29640T et al have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of CK-MB, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C28253T and C683T have the lowest.

27. Cl (chloride)



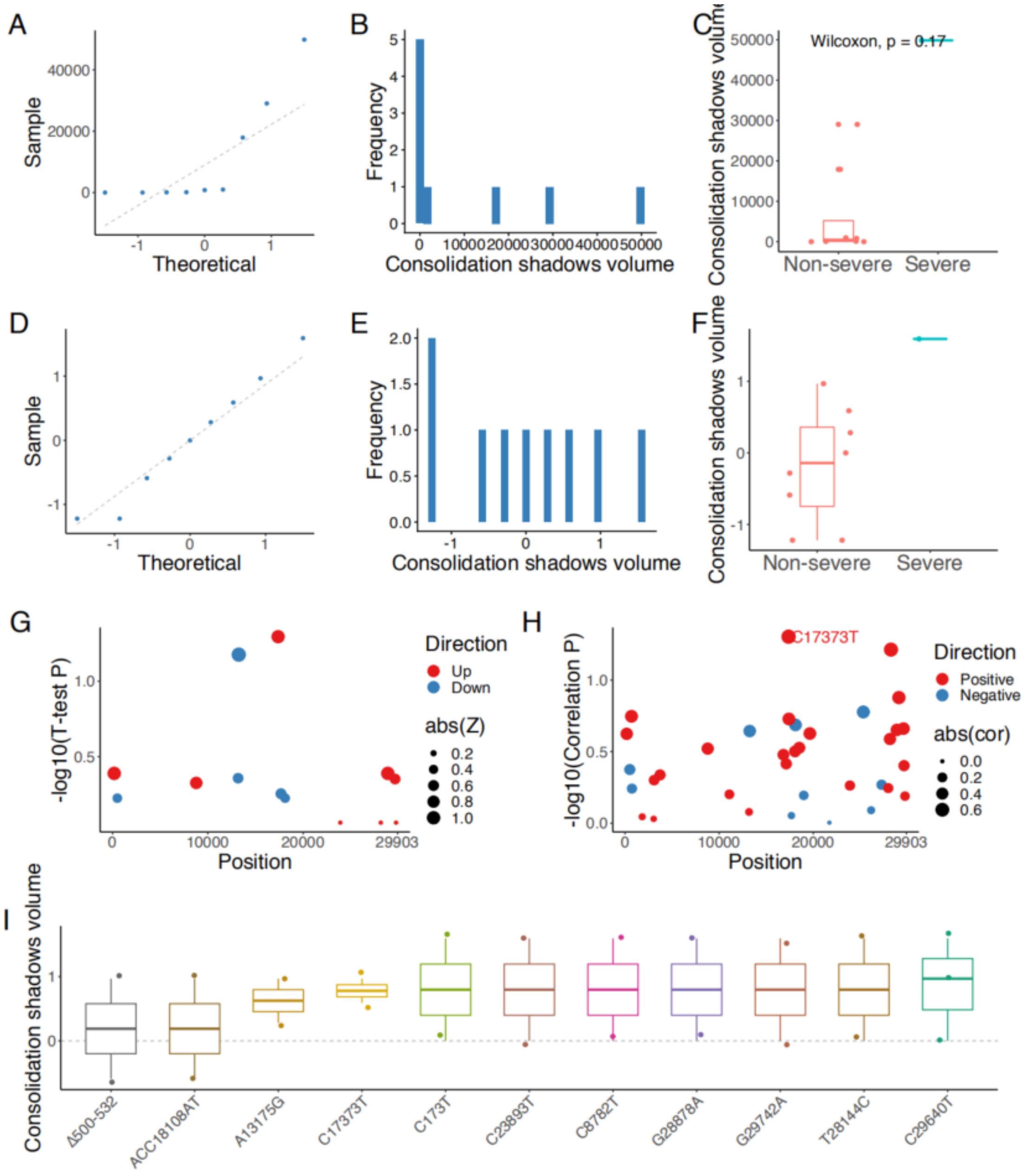
For Cl (chloride, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Cl in the non-severe and severe COVID-19 patients before (**C**, p = 0.65, Wilcoxon test) and after normalization (**F**, p = 0.64, T-test). (**G**) Variants C23893T and C29640T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C18060T, C29095T and C29640T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of Cl, cases with C29586T and C19637T tend to have the highest Z score, whereas cases with A13175G and C29640T have the lowest.

28. Consolidation shadow percentage



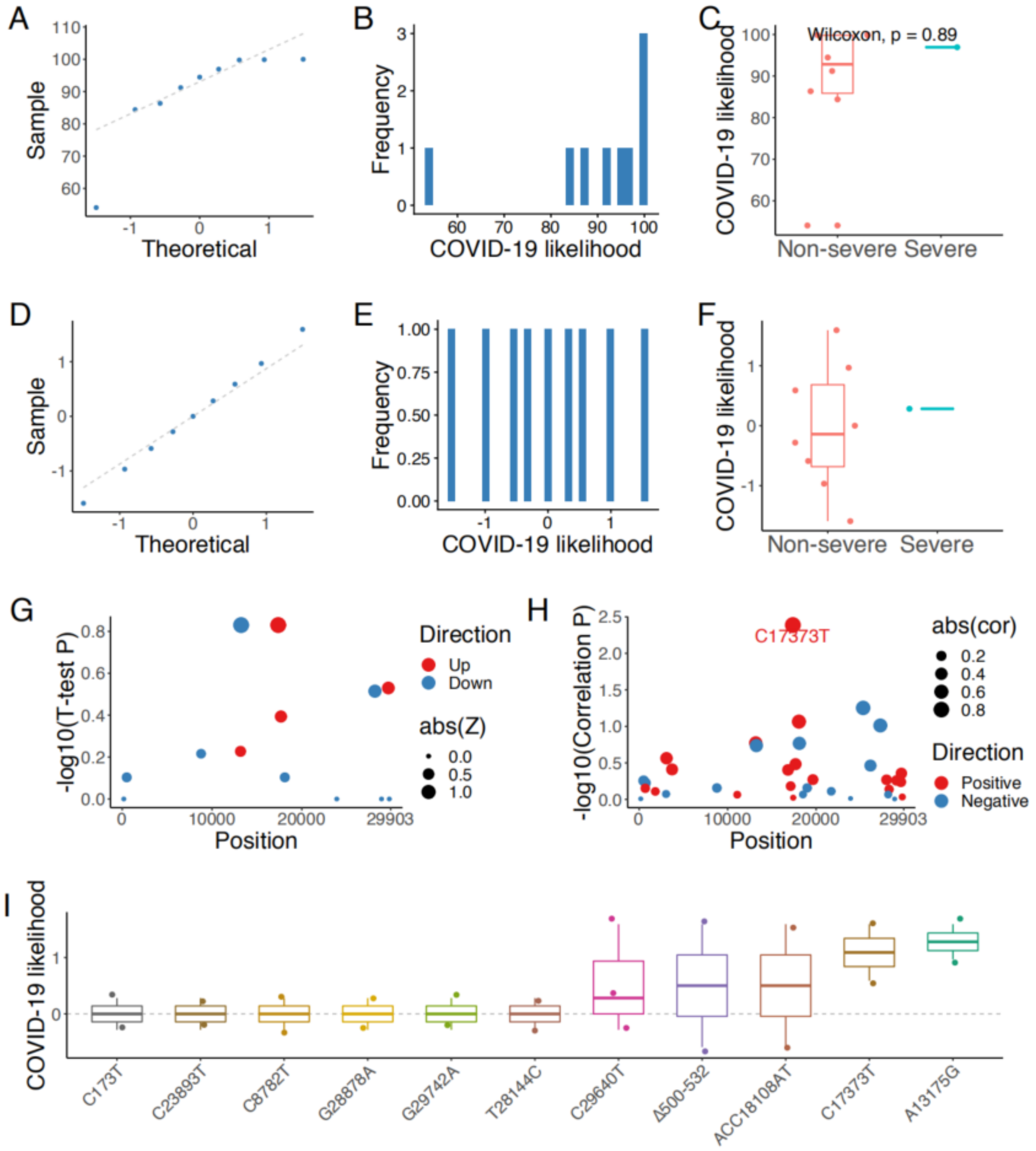
For Consolidation shadows percentage (%), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Consolidation shadows in the non-severe and severe COVID-19 patients before (**C**, p = 0.15, Wilcoxon test) and after normalization (**F**). (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant T13243C in Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of Consolidation shadows, cases with C29640T and C17373T tend to have the highest Z score, whereas cases with Δ500-532 and ACC18108AT have the lowest.

29. Consolidation shadows volume



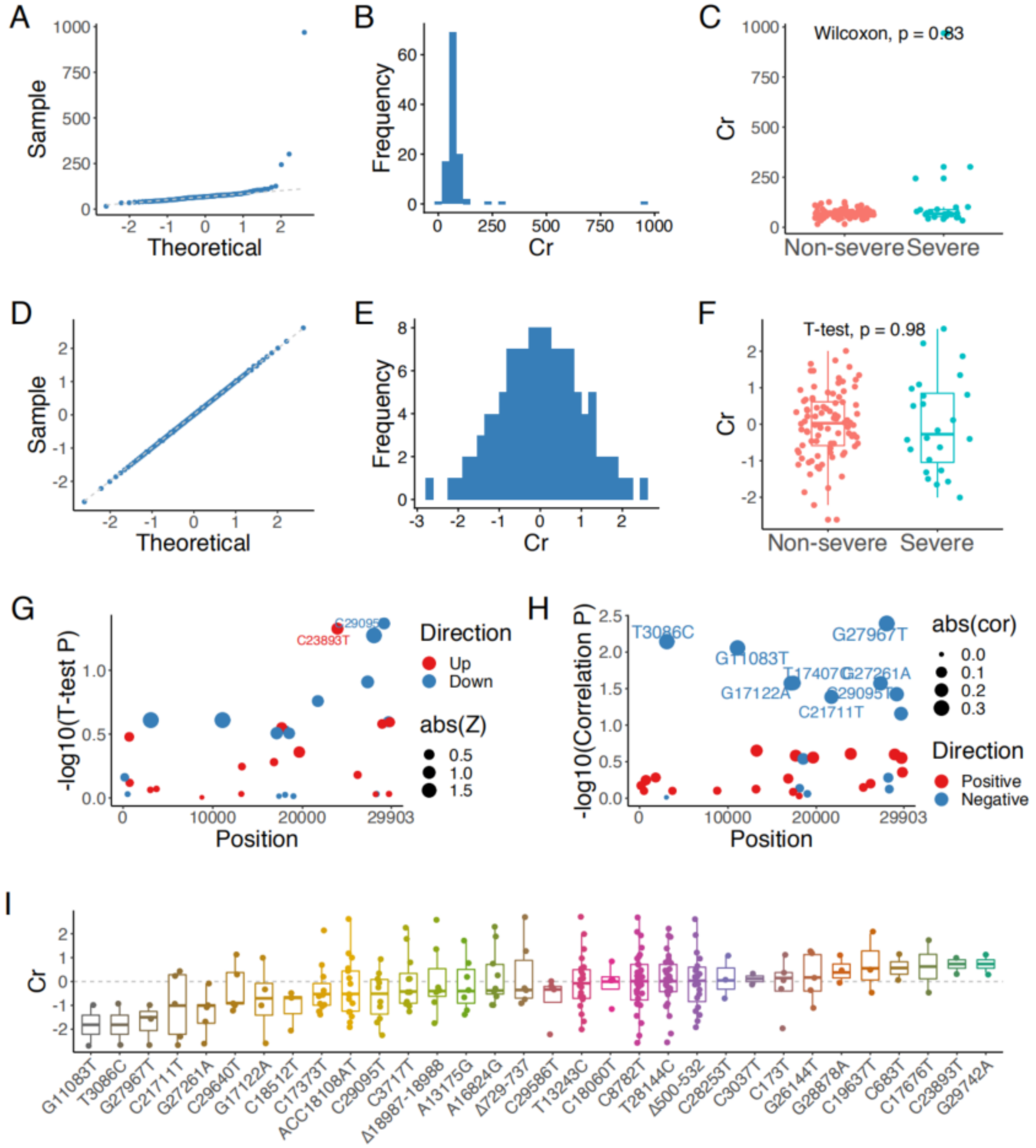
For Consolidation shadows volume (mm^3), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Consolidation shadows volume in the non-severe and severe COVID-19 patients before (**C**, p = 0.17, Wilcoxon test) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and Consolidation shadows volume using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C17373T in Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of Consolidation shadows volume, cases with C29640T and T28144C tend to have the highest Z score, whereas cases with Δ500-532 and ACC18108AT have the lowest.

30. COVID-19 likelihood



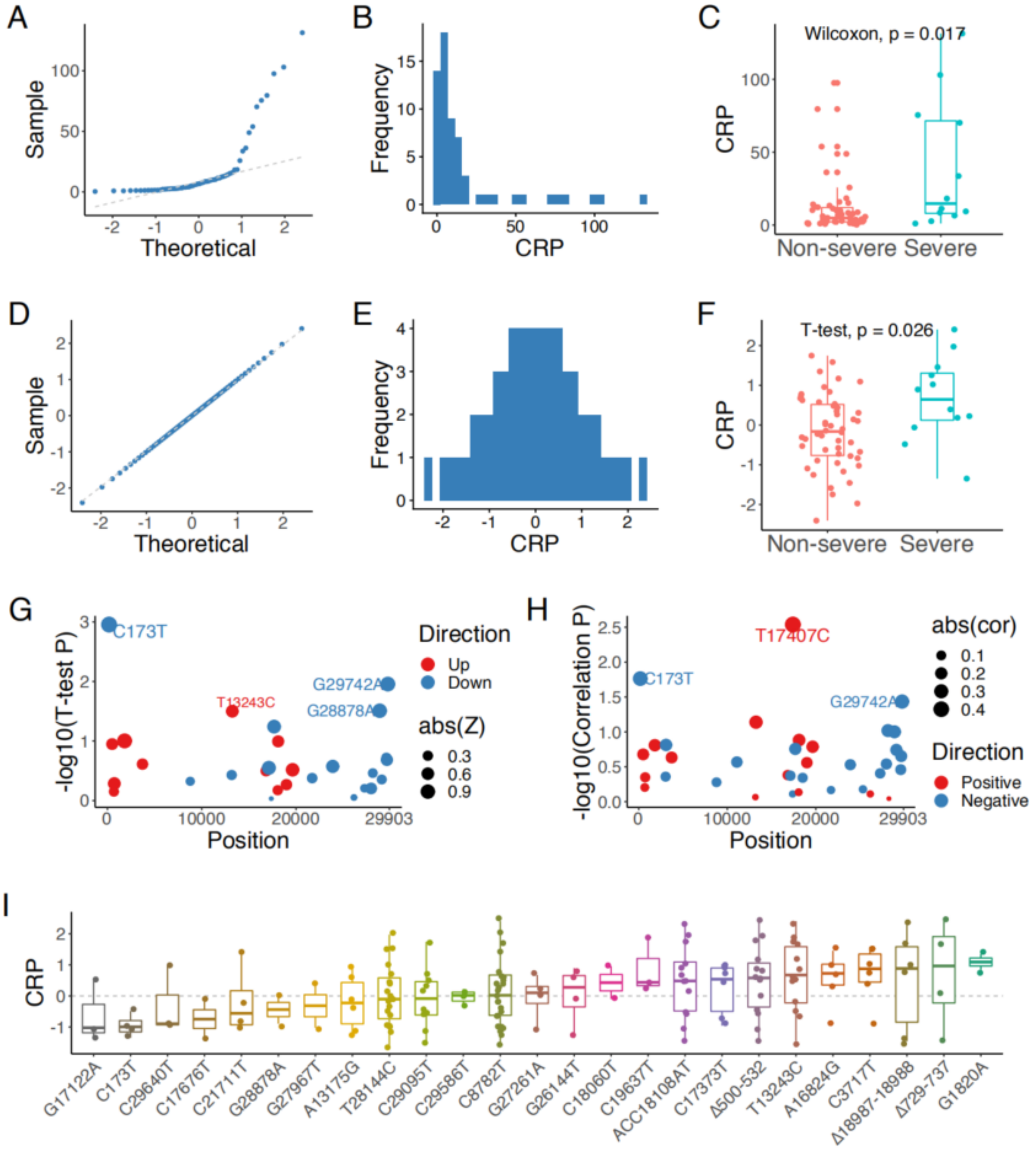
For COVID-19 likelihood (diagnostic accuracy of COVID-19), %, quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared COVID-19 likelihood in the non-severe and severe COVID-19 patients before (**C**, p = 0.89, Wilcoxon test) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and COVID-19 likelihood using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C17373T in Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of COVID-19 likelihood, cases with A13175G and C17373T tend to have the highest Z score, whereas cases with C173T and C23893T have the lowest.

31. Cr (creatinine)



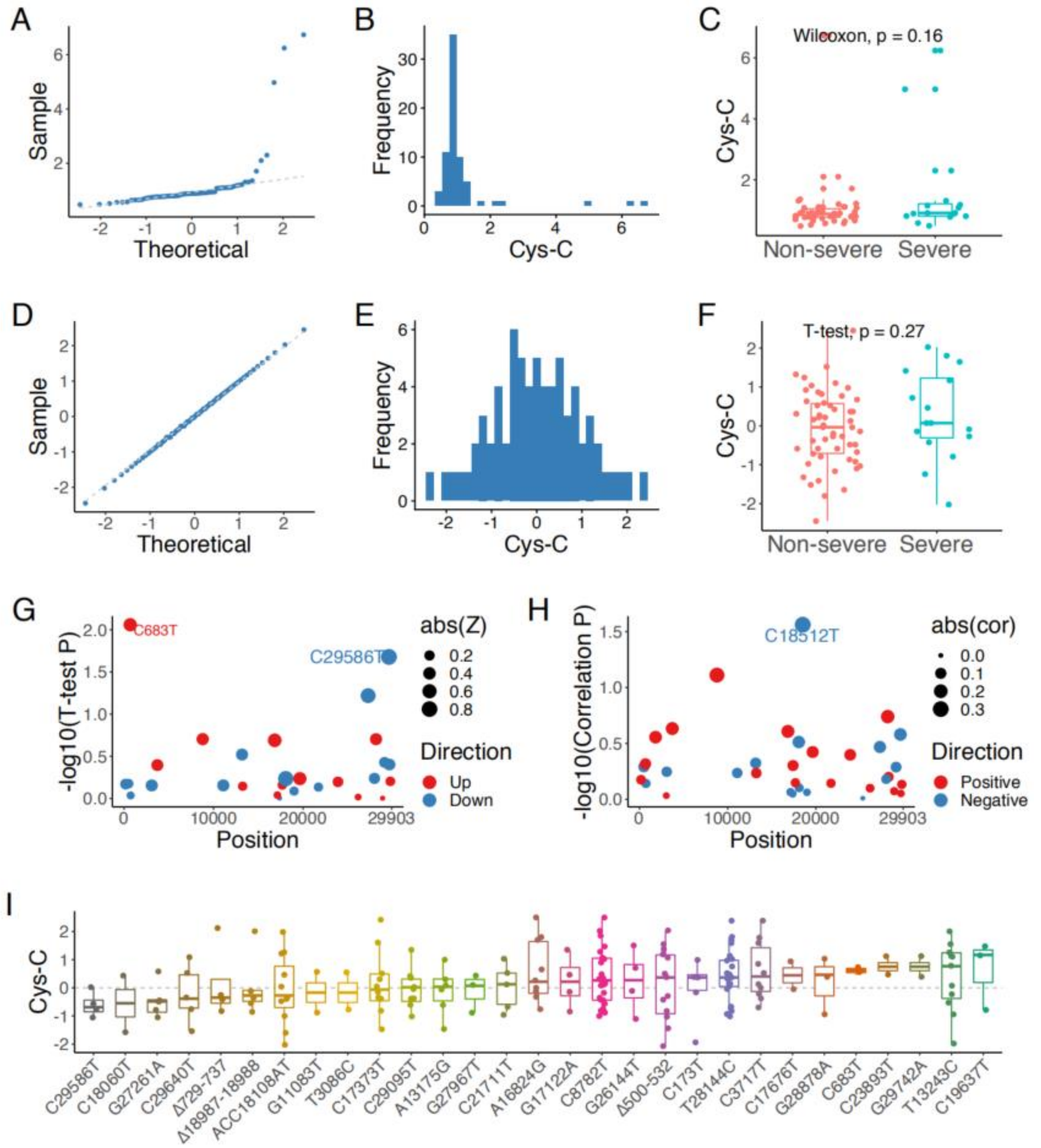
For Cr (creatinine, μmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Cr in the non-severe and severe COVID-19 patients before (**C**, p = 0.83, Wilcoxon test) and after normalization (**F**, p = 0.98, T-test). We further performed association analyses between the 35 genetic variants and Cr using T-test and Pearson correlation. (**G**) Variants C29095T and C23893T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T3086C, G11083T and G27967T et al have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of Cr, cases with G29742A and C23893T tend to have the highest Z score, whereas cases with G11083T and T3086C have the lowest.

32. CRP (C-reactive protein)



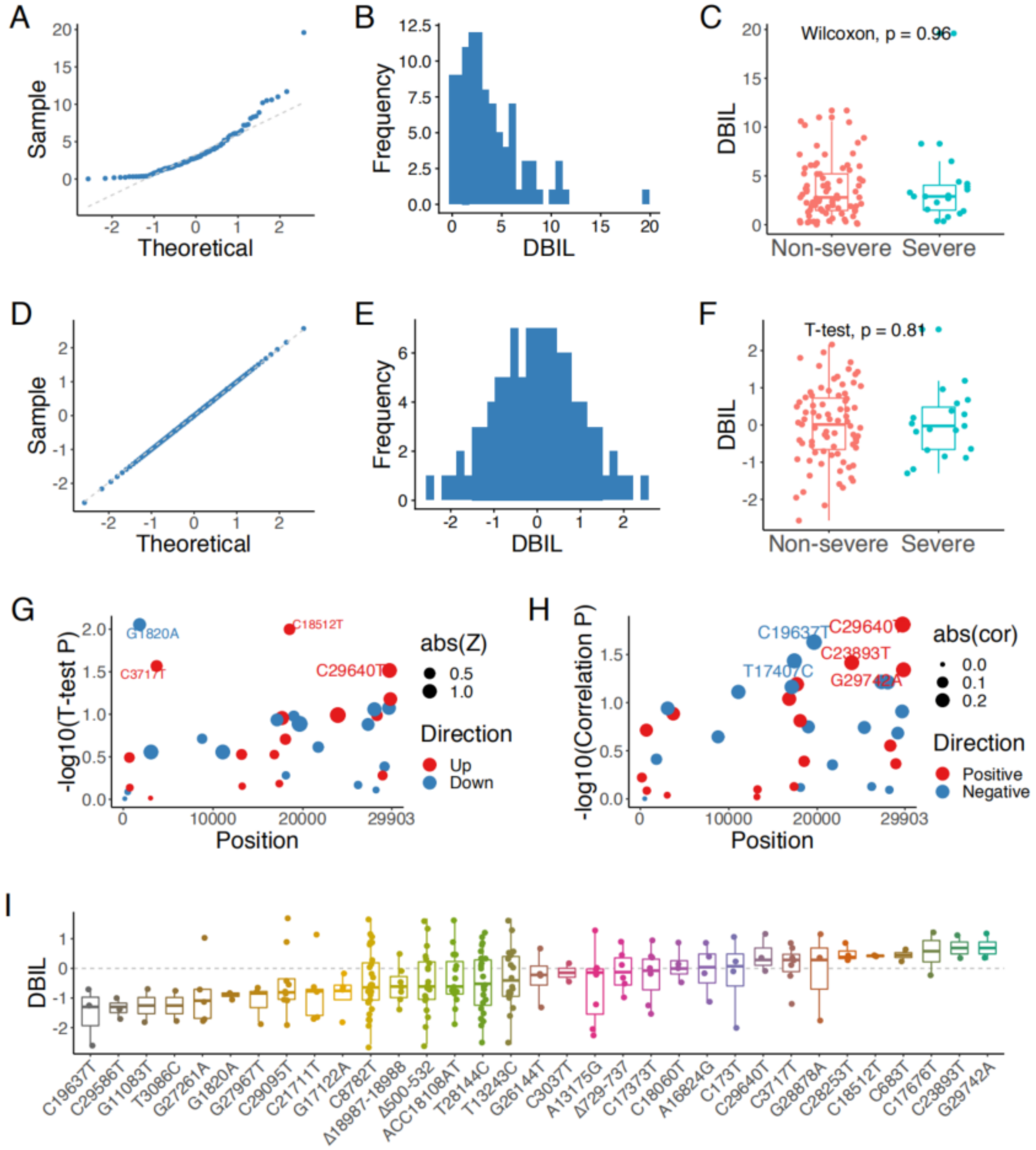
For CRP (C-reactive protein), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared CRP in the non-severe and severe COVID-19 patients before (**C**, p = 0.017, Wilcoxon test) and after normalization (**F**, p = 0.026, T-test). We further performed association analyses between the 35 genetic variants and CRP using T-test and Pearson correlation. (**G**) Variants C173T, G29742A, G28878A and T13243C pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T17407C, C173T and G29742A have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of CRP, cases with G1820A and Δ729-737 tend to have the highest Z score, whereas cases with G17122A and C173T have the lowest.

33. Cys-C (Cystatin C)



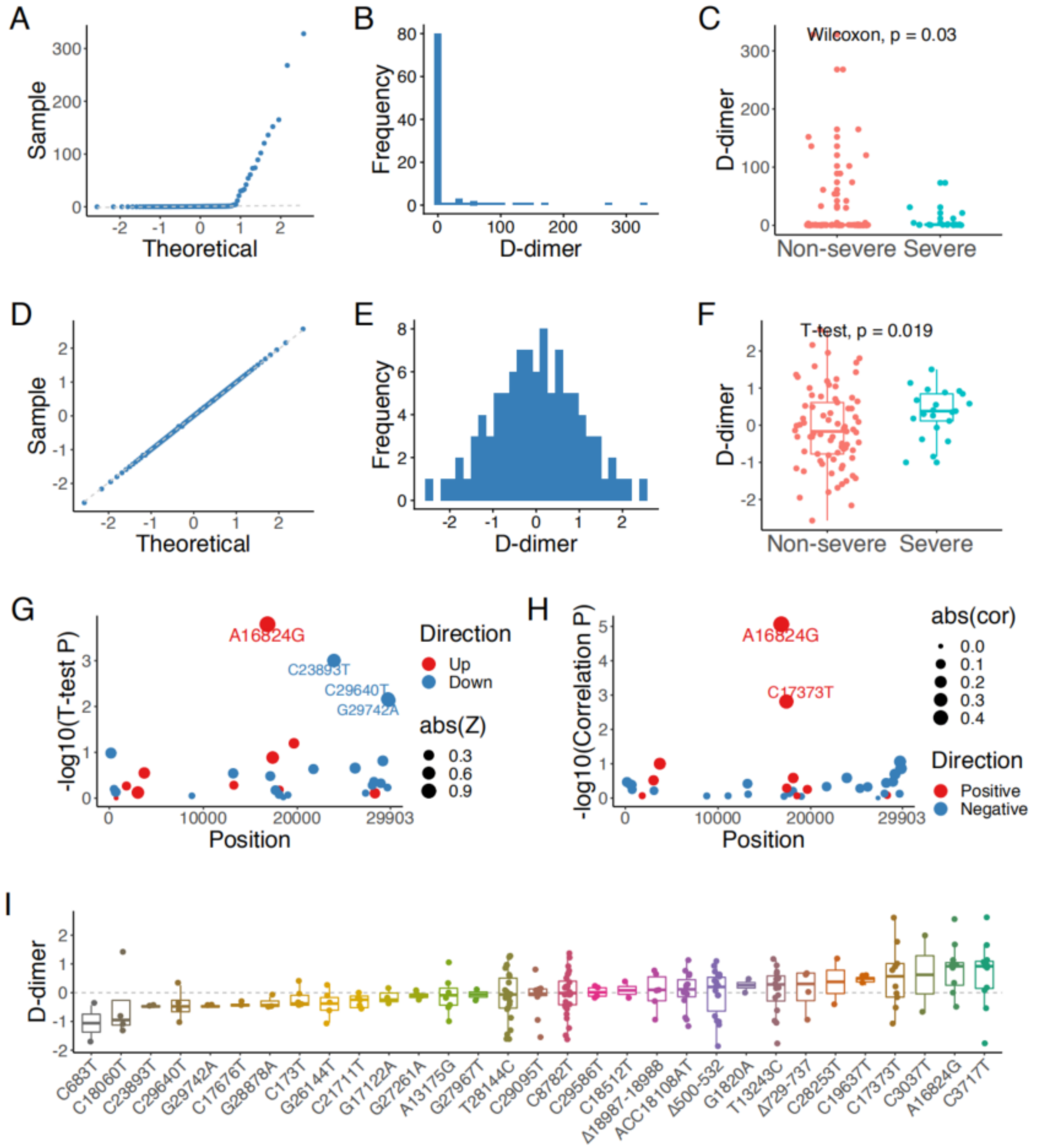
For Cys-C (Cystatin C, mg/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Cys-C in the non-severe and severe COVID-19 patients before (**C**, p = 0.16, Wilcoxon test) and after normalization (**F**, p = 0.27, T-test). We further performed association analyses between the 35 genetic variants and Cys-C using T-test and Pearson correlation. (**G**) Variants C683T and C29586T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C18512T has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of Cys-C, cases with C19637T and T13243C tend to have the highest Z score, whereas cases with C29586T and C18060T have the lowest.

34. DBIL (direct bilirubin)



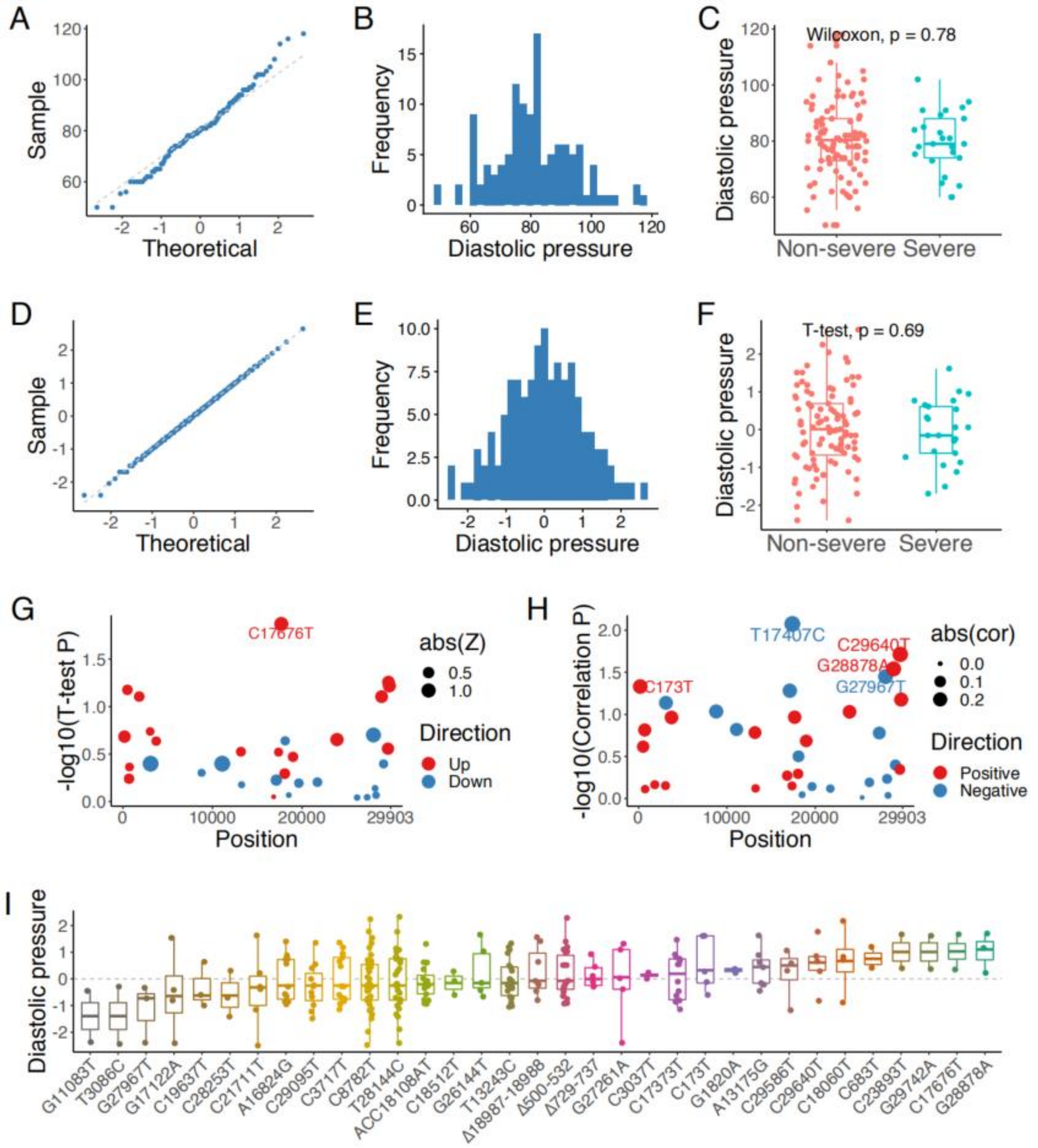
For DBIL (direct bilirubin, µmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared DBIL in the non-severe and severe COVID-19 patients before (**C**, p = 0.96, Wilcoxon test) and after normalization (**F**, p = 0.81, T-test). We further performed association analyses between the 35 genetic variants and DBIL using T-test and Pearson correlation. (**G**) Variants G1820A, C3717T, C18512T and C29640T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C19637T, C29640T and C23893T et al have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of DBIL, cases with G29742A and C23893T tend to have the highest Z score, whereas cases with C19637T and C29586T have the lowest.

35. D-dimer



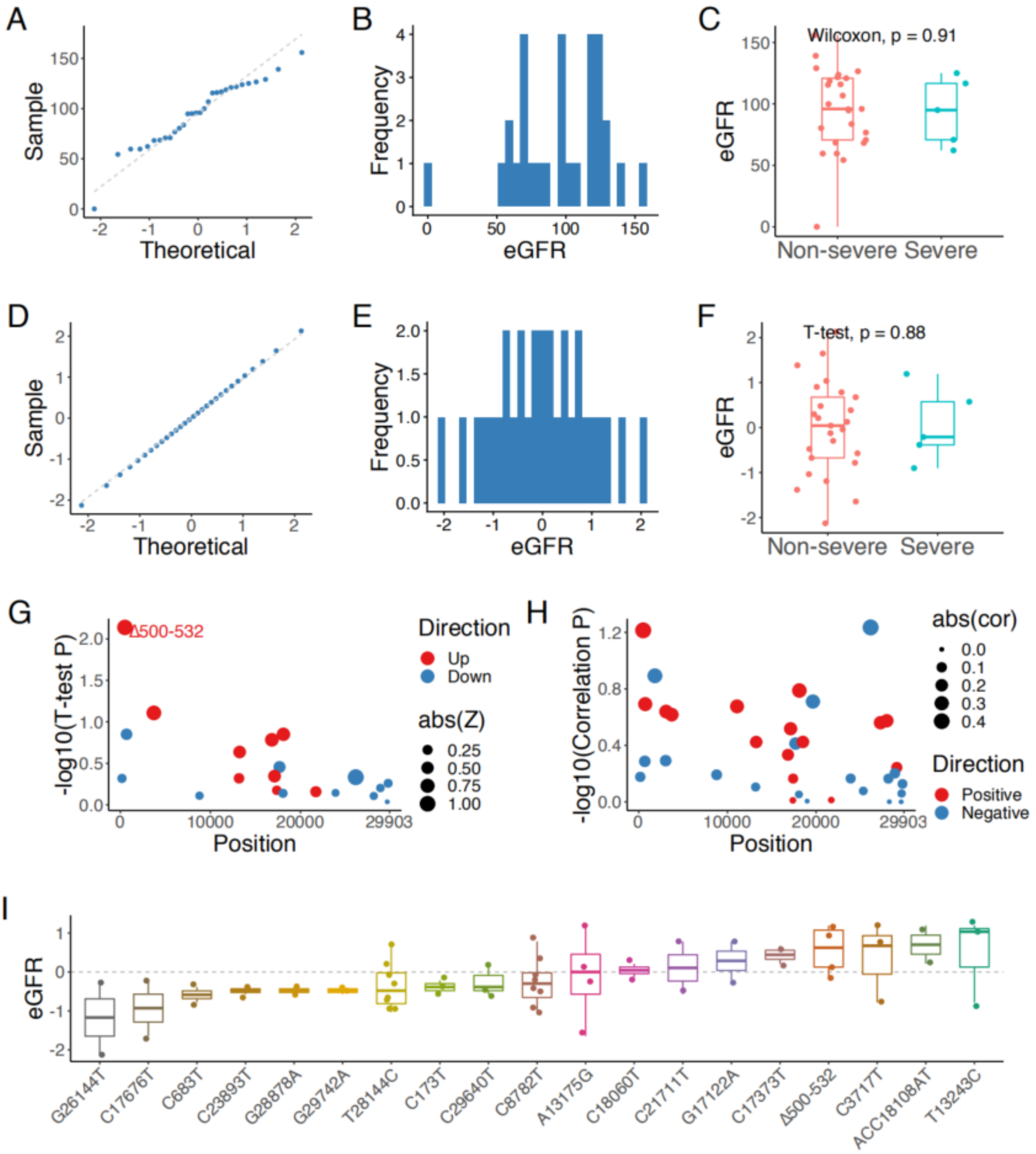
For D-dimer (ng/mL), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared D-dimer in the non-severe and severe COVID-19 patients before (**C**, p = 0.03, Wilcoxon test) and after normalization (**F**, p = 0.019, T-test). We further performed association analyses between the 35 genetic variants and D-dimer using T-test and Pearson correlation. (**G**) Variants A16824G, C23893T, C29640T and G29742A pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants A16824G and C17373T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of D-dimer, cases with C3717T and A16824G tend to have the highest Z score, whereas cases with C683T and C18060T have the lowest.

36. Diastolic pressure



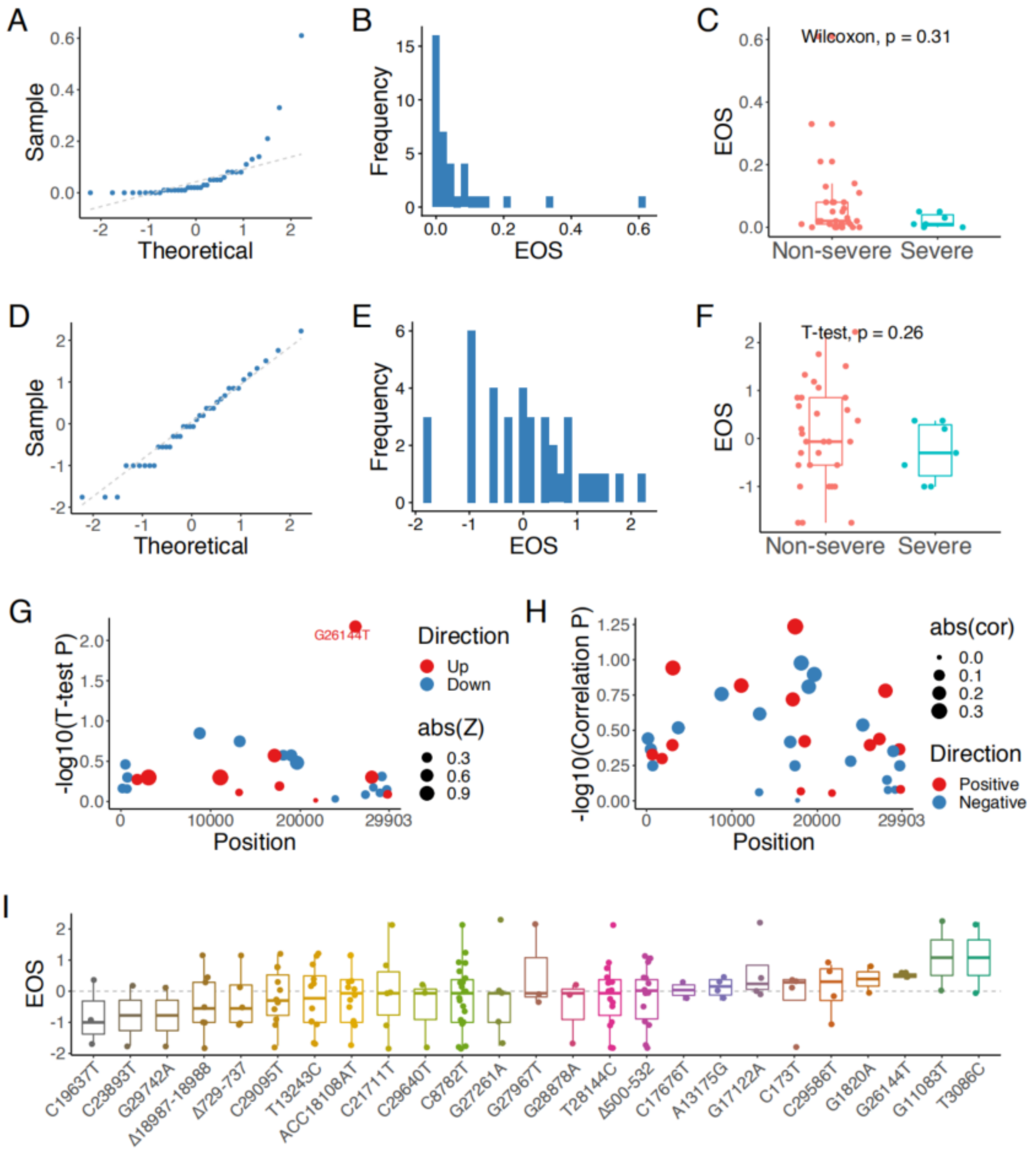
For Diastolic pressure (mmHg), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Diastolic pressure in the non-severe and severe COVID-19 patients before (**C**, p = 0.78, Wilcoxon test) and after normalization (**F**, p = 0.69, T-test). We further performed association analyses between the 35 genetic variants and Diastolic pressure using T-test and Pearson correlation. (**G**) Variant C17676T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T17407C, C29640T and G28878A et al have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of Diastolic pressure, cases with G28878A and C17676T tend to have the highest Z score, whereas cases with G11083T and T3086C have the lowest.

37. eGFR (estimated glomerular filtration rate)



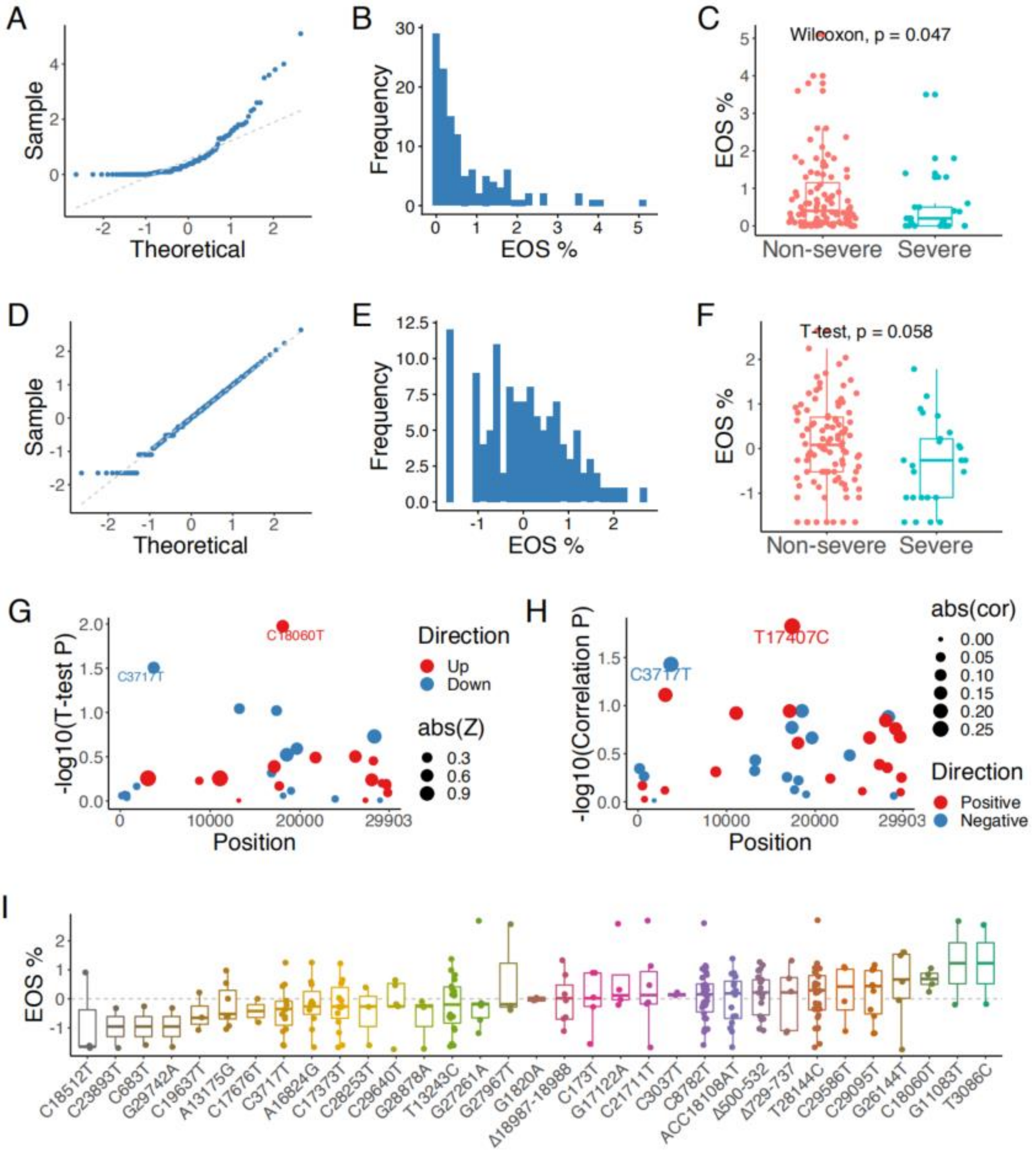
For eGFR (estimated glomerular filtration rate, %), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared eGFR in the non-severe and severe COVID-19 patients before (**C**, p = 0.91, Wilcoxon test) and after normalization (**F**, p = 0.88, T-test). We further performed association analyses between the 35 genetic variants and eGFR using T-test and Pearson correlation. (**G**) Variant △500-532 passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) No variant in Pearson correlation was has P value below 0.05. After sorting Z score values of eGFR, cases with T13243C and ACC18108AT tend to have the highest Z score, whereas cases with G26144T and C17676T have the lowest.

38. EOS (eosinophil count)



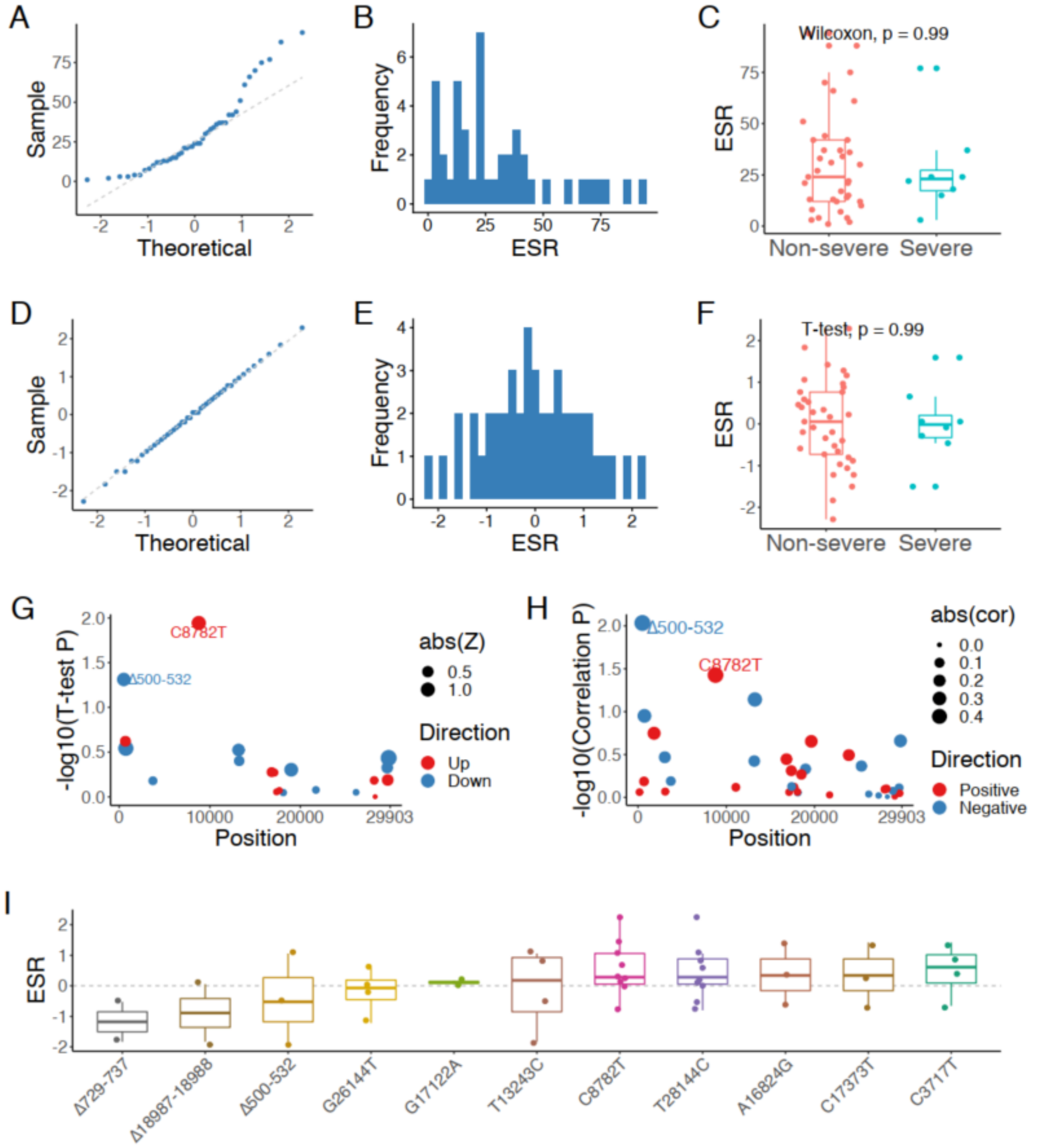
For EOS (eosinophil count, ×10^9/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared EOS in the non-severe and severe COVID-19 patients before (**C**, p = 0.31, Wilcoxon test) and after normalization (**F**, p = 0.26, T-test). We further performed association analyses between the 35 genetic variants and EOS using T-test and Pearson correlation. (**G**) Variant G26144T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) No variant in Pearson correlation was has P value below 0.05. After sorting Z score values of EOS, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C19637T and C23893T have the lowest.

39. EOS % (eosinophil percentage)



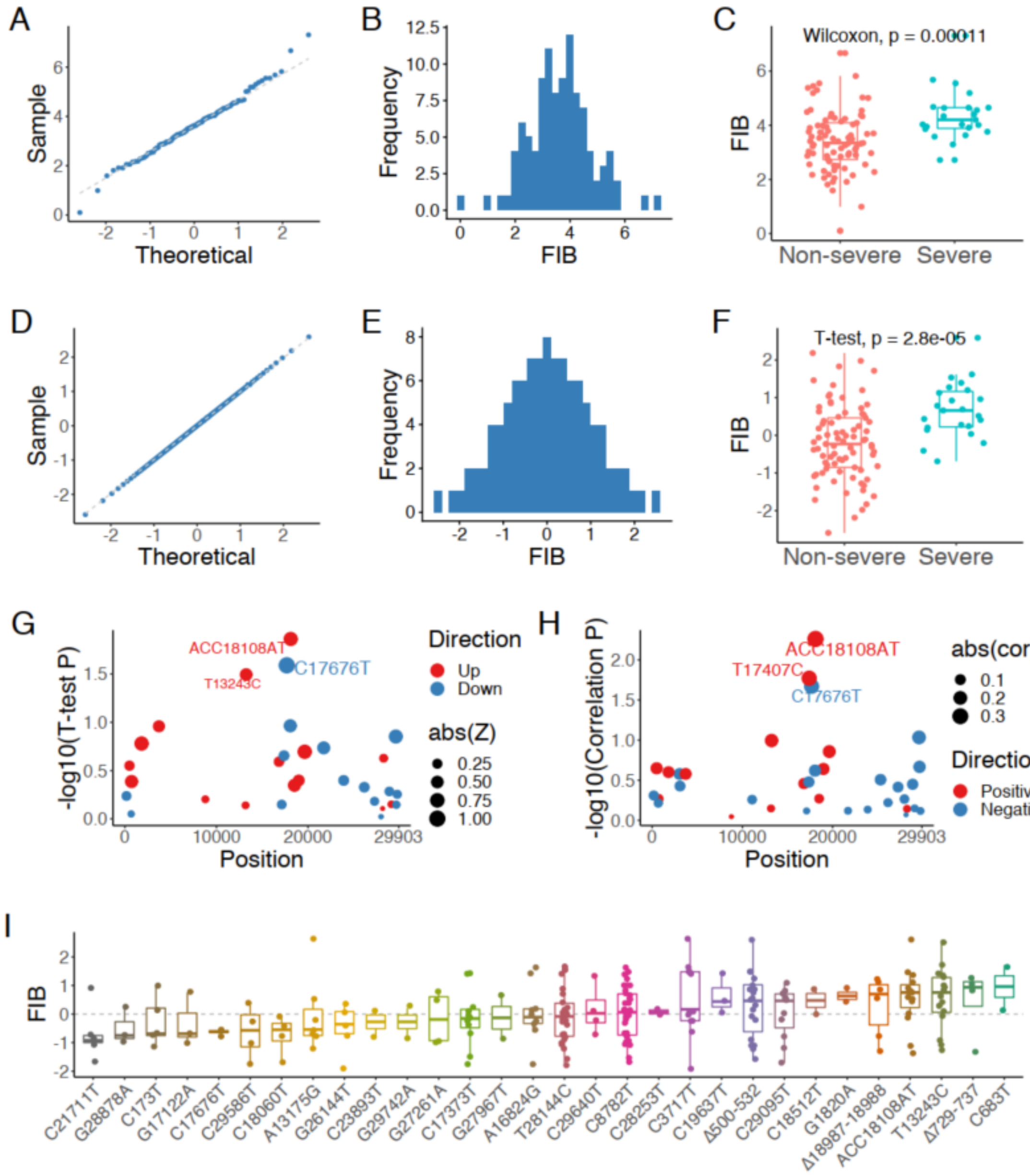
For EOS % (eosinophil percentage), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared EOS % in the non-severe and severe COVID-19 patients before (**C**, p = 0.047, Wilcoxon test) and after normalization (**F**, p = 0.058, T-test). We further performed association analyses between the 35 genetic variants and EOS % using T-test and Pearson correlation. (**G**) Variants C18060T and C3717T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C3717T and T17407C have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of EOS %, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C18512T and C23893T have the lowest.

40. ESR (erythrocyte sedimentation rate)



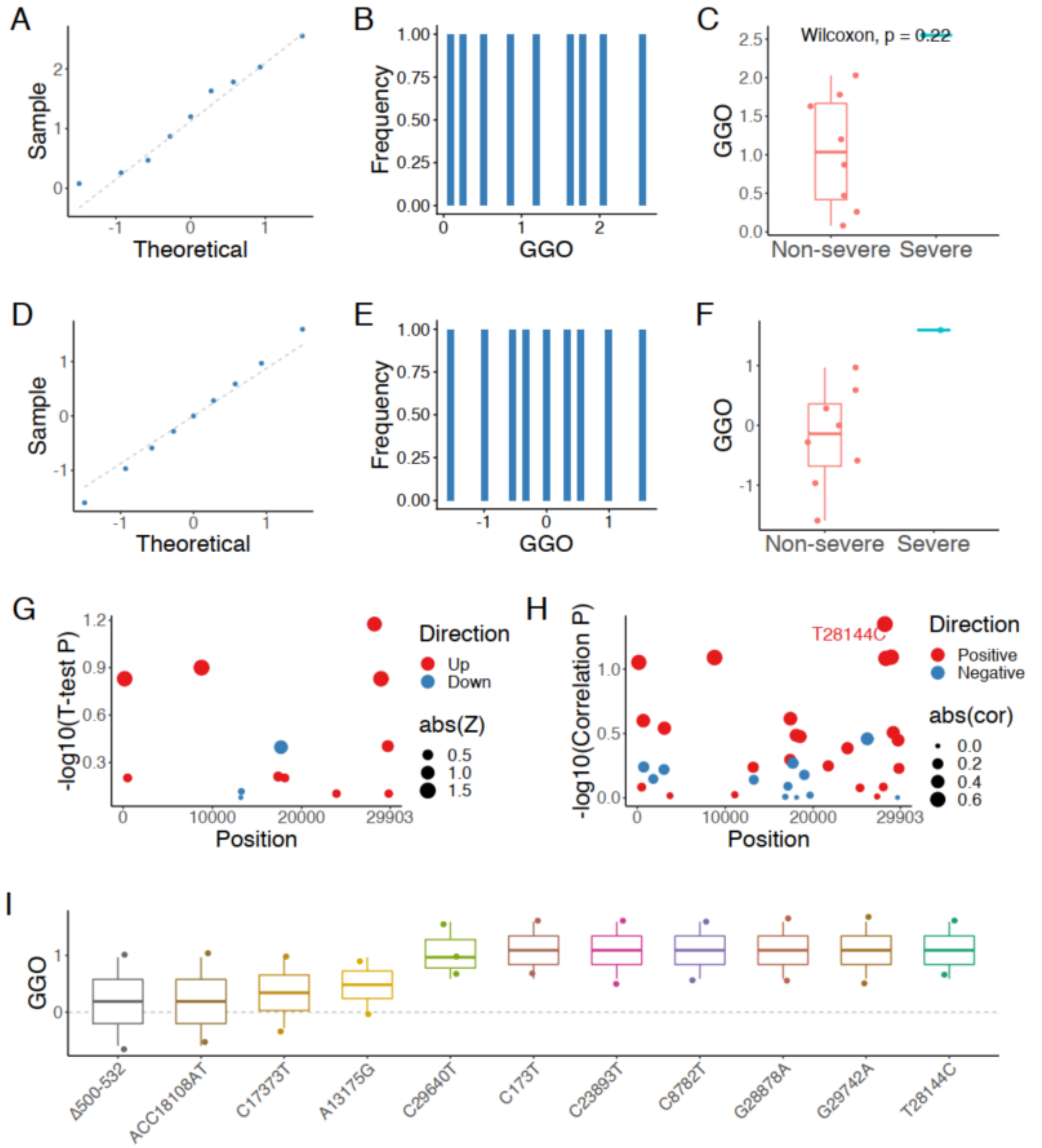
For ESR (erythrocyte sedimentation rate, mm/h), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared ESR in the non-severe and severe COVID-19 patients before (**C**, p = 0.99, Wilcoxon test) and after normalization (**F**, p = 0.99, T-test). We further performed association analyses between the 35 genetic variants and ESR using T-test and Pearson correlation. (**G**) Variants C8782T and Δ500-532 in the T test (**G**) and Pearson correlation were with P value below 0.05 (**H**). After sorting Z score values of ESR, cases with C3717T and C17373T tend to have the highest Z score, whereas cases with Δ729-737 and Δ18987-18988 have the lowest.

41. FIB (fibrinogen)



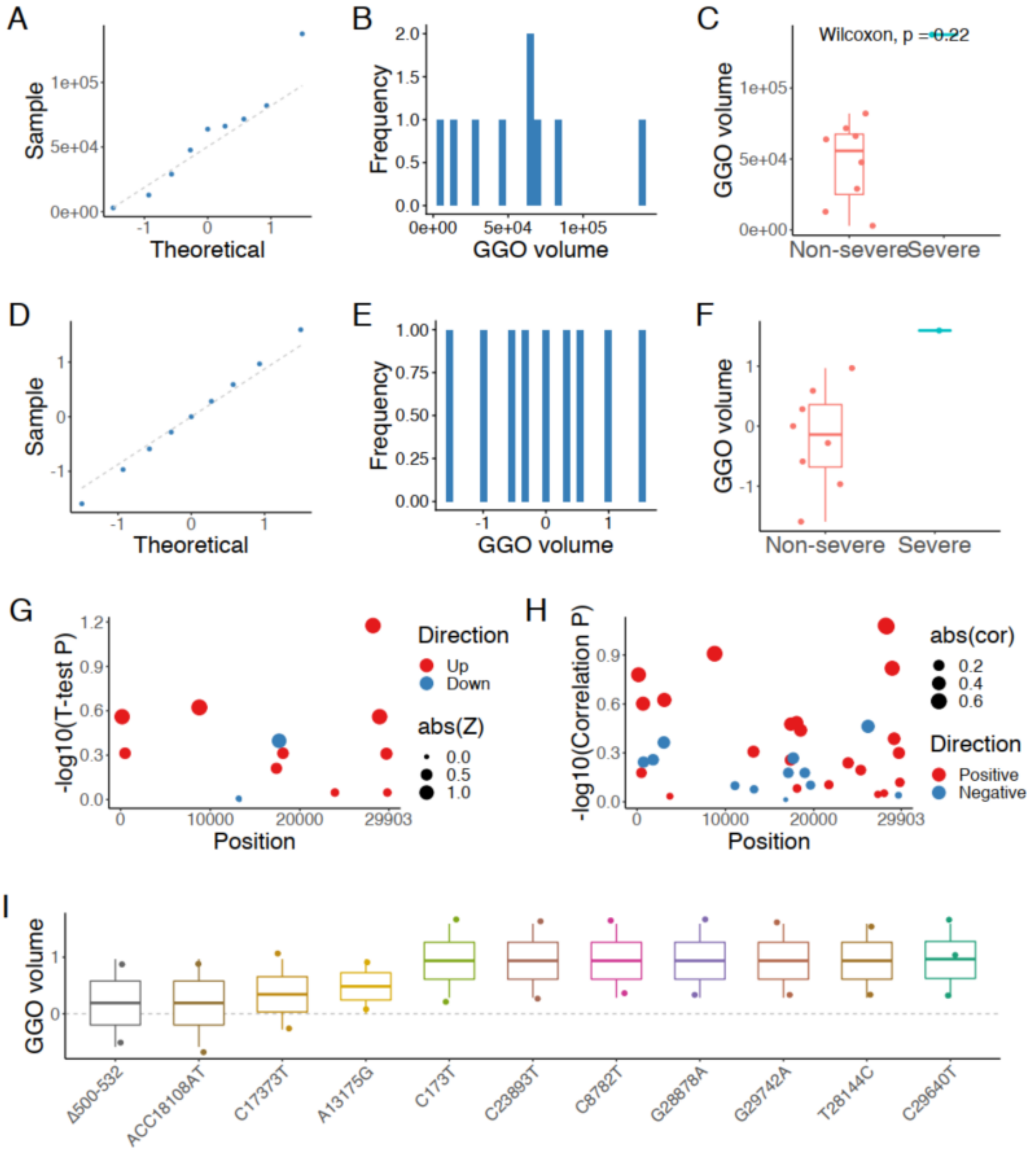
For FIB (fibrinogen, g/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared FIB in the non-severe and severe COVID-19 patients before (**C**, p = 1.1×10^{-4}, Wilcoxon test) and after normalization (**F**, p = 2.8×10^{-5}, T-test). We further performed association analyses between the 35 genetic variants and FIB using T-test and Pearson correlation. (**G**) Variants ACC18108AT, T13243C and C17676T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants ACC18108AT, T17407C and C17676T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of FIB, cases with C683T and Δ729-737 tend to have the highest Z score, whereas cases with C21711T and G28878A have the lowest.

42. GGO (ground-glass opacities)



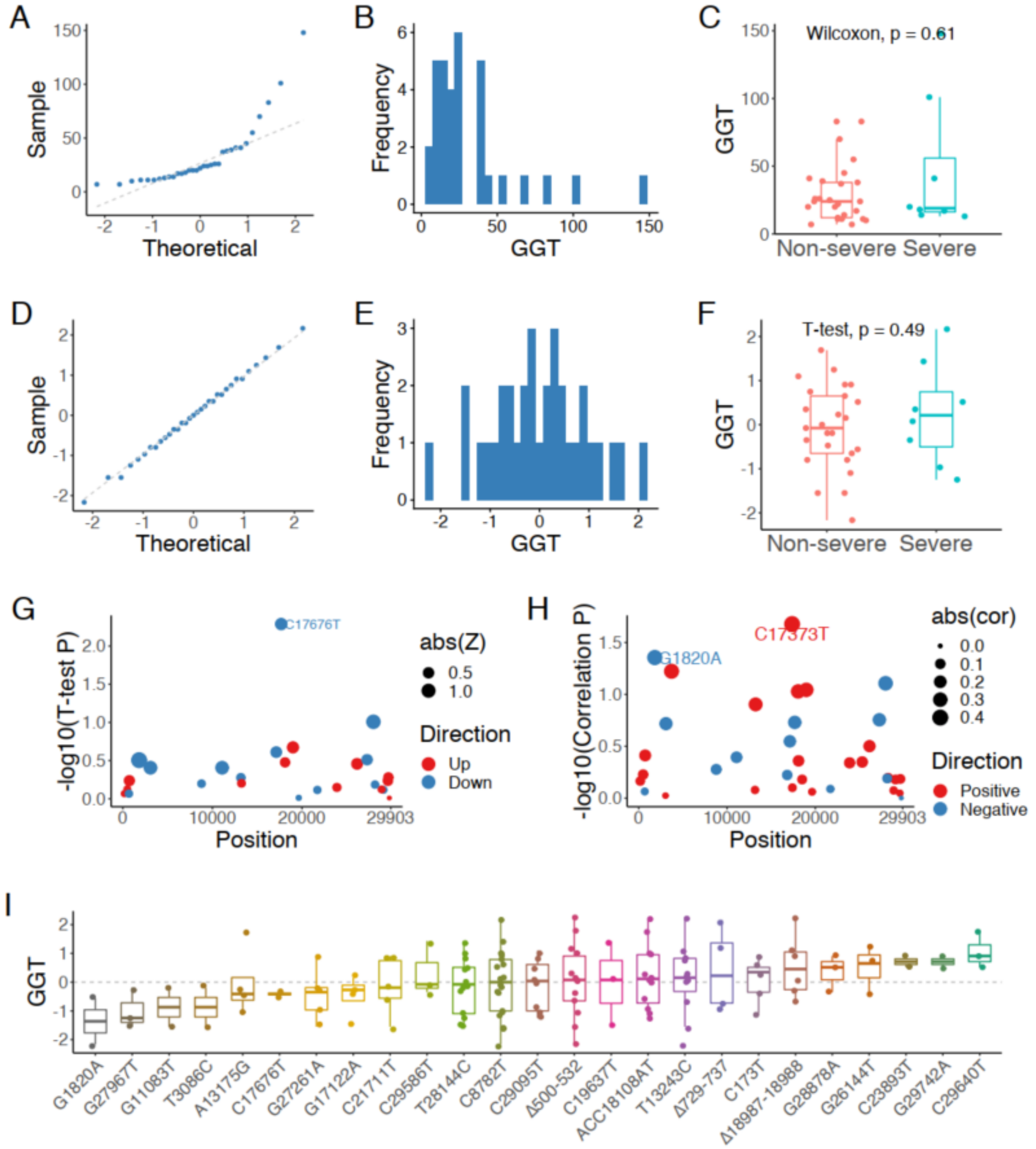
For GGO (ground-glass opacities, %), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared GGO in the non-severe and severe COVID-19 patients before (**C**, p = 0.22, Wilcoxon test) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and GGO using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant T28144C in Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of GGO, cases with T28144C and G29742A tend to have the highest Z score, whereas cases with Δ500-532 and ACC18108AT have the lowest.

43. GGO volume (volume of ground-glass opacity)



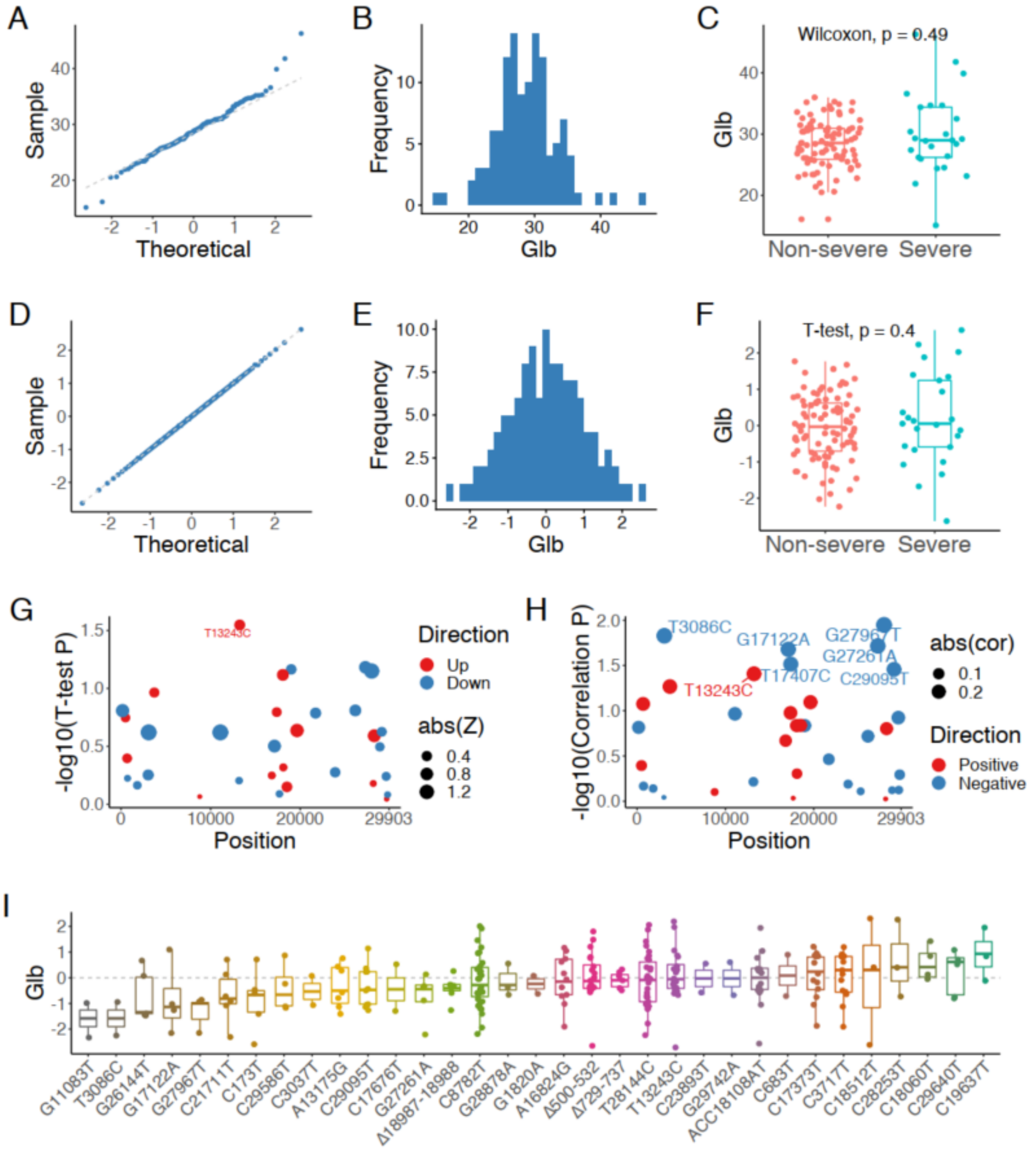
For GGO volume (volume of ground-glass opacity, mm^3), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared GGO volume in the non-severe and severe COVID-19 patients before (**C**, p = 0.22, Wilcoxon test) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and GGO volume using T-test and Pearson correlation. (**G**) No variant in the T test (**G**) and Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of GGO volume, cases with C29640T and T28144C tend to have the highest Z score, whereas cases with Δ500-532 and ACC18108AT have the lowest.

44. GGT (gamma-glutamyl transferase)



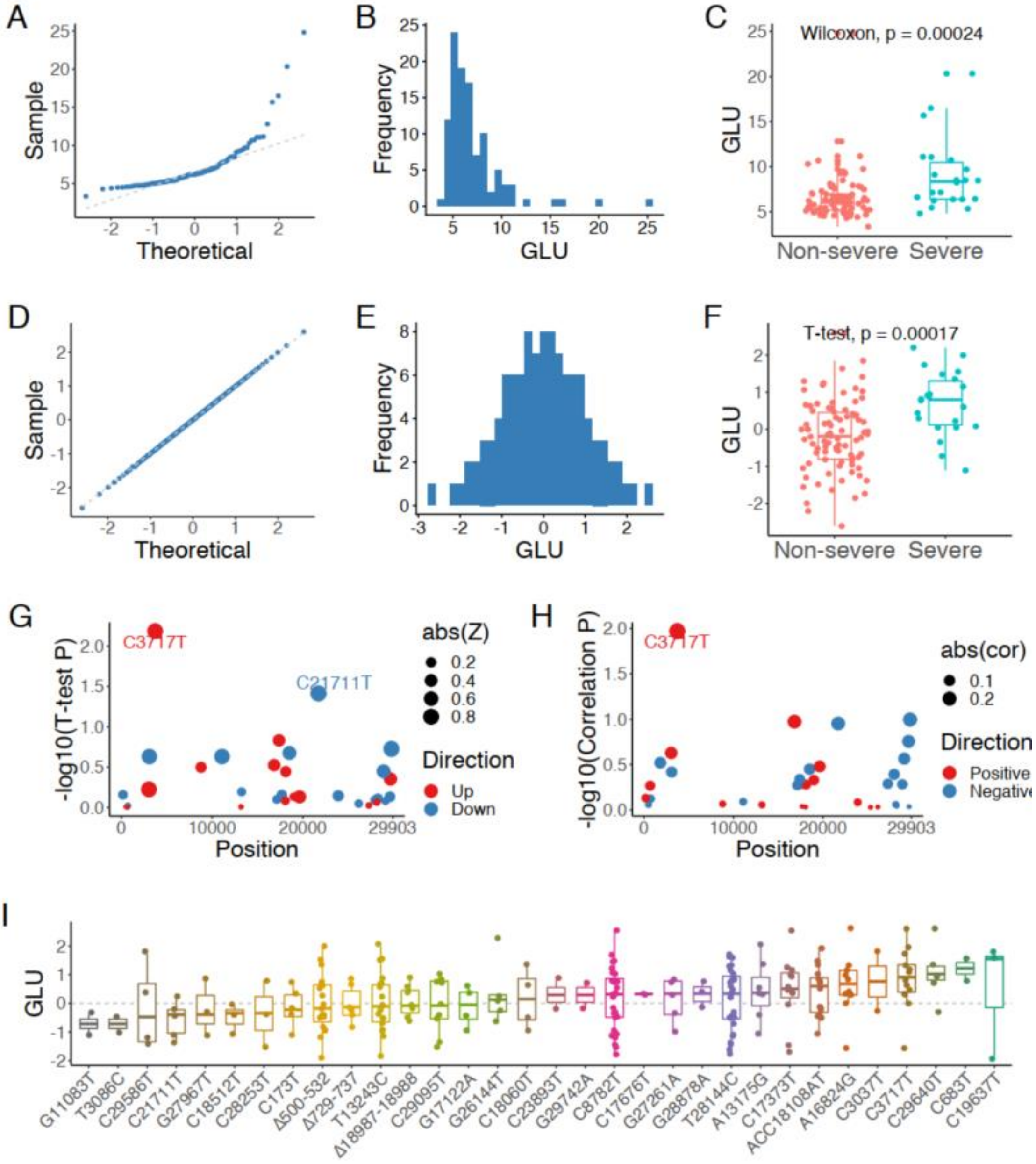
For GGT (gamma-glutamyl transferase, U/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared GGT in the non-severe and severe COVID-19 patients before (**C**, p = 0.61, Wilcoxon test) and after normalization (**F**, p = 0.49, T-test). We further performed association analyses between the 35 genetic variants and GGT using T-test and Pearson correlation. (**G**) Variant C17676T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants G1820A and C17373T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of GGT, cases with C29640T and C29742A tend to have the highest Z score, whereas cases with G1820A and G27967T have the lowest.

45. Glb (globin)



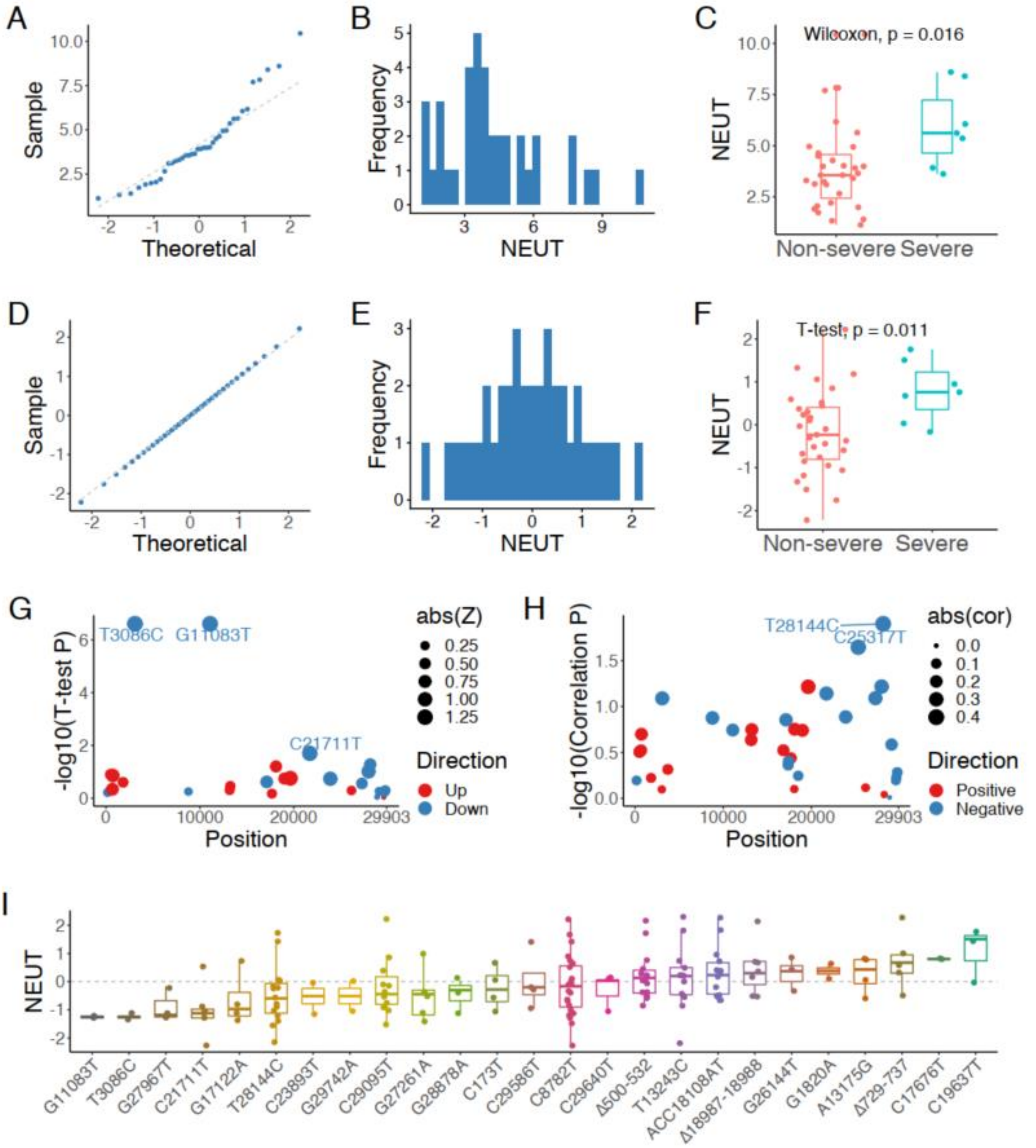
For Glb (globin, g/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Glb in the non-severe and severe COVID-19 patients before (**C**, p = 0.49, Wilcoxon test) and after normalization (**F**, p = 0.4, T-test). We further performed association analyses between the 35 genetic variants and Glb using T-test and Pearson correlation. (**G**) Variant T13243C pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T3086C, T13243C, G17122A, T17407C, G27967T, G27261A and C29095T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of Glb, cases with C19637T and C29640T tend to have the highest Z score, whereas cases with G11083T and T3086C have the lowest.

46. GLU (glucose)



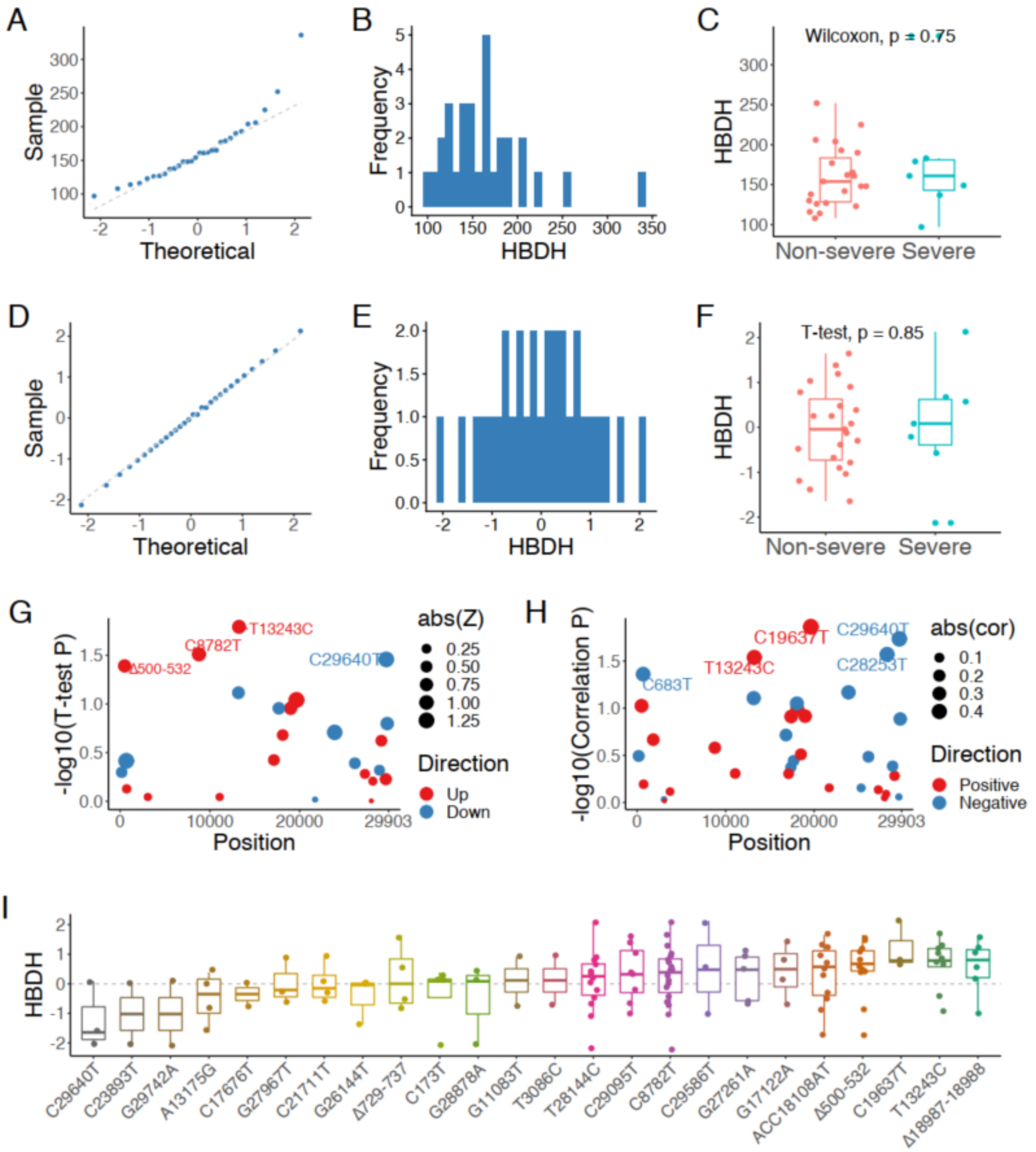
For GLU (glucose, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared GLU in the non-severe and severe COVID-19 patients before (**C**, p = 2.4×10^{-4}, Wilcoxon test) and after normalization (**F**, p = 1.7×10^{-4}, T-test). We further performed association analyses between the 35 genetic variants and GLU using T-test and Pearson correlation. (**G**) Variants C3717T and C21711T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C3717T has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of GLU, cases with C19637T and C683T tend to have the highest Z score, whereas cases with G11083T and T3086C have the lowest.

47. NEUT (neutrophil count)



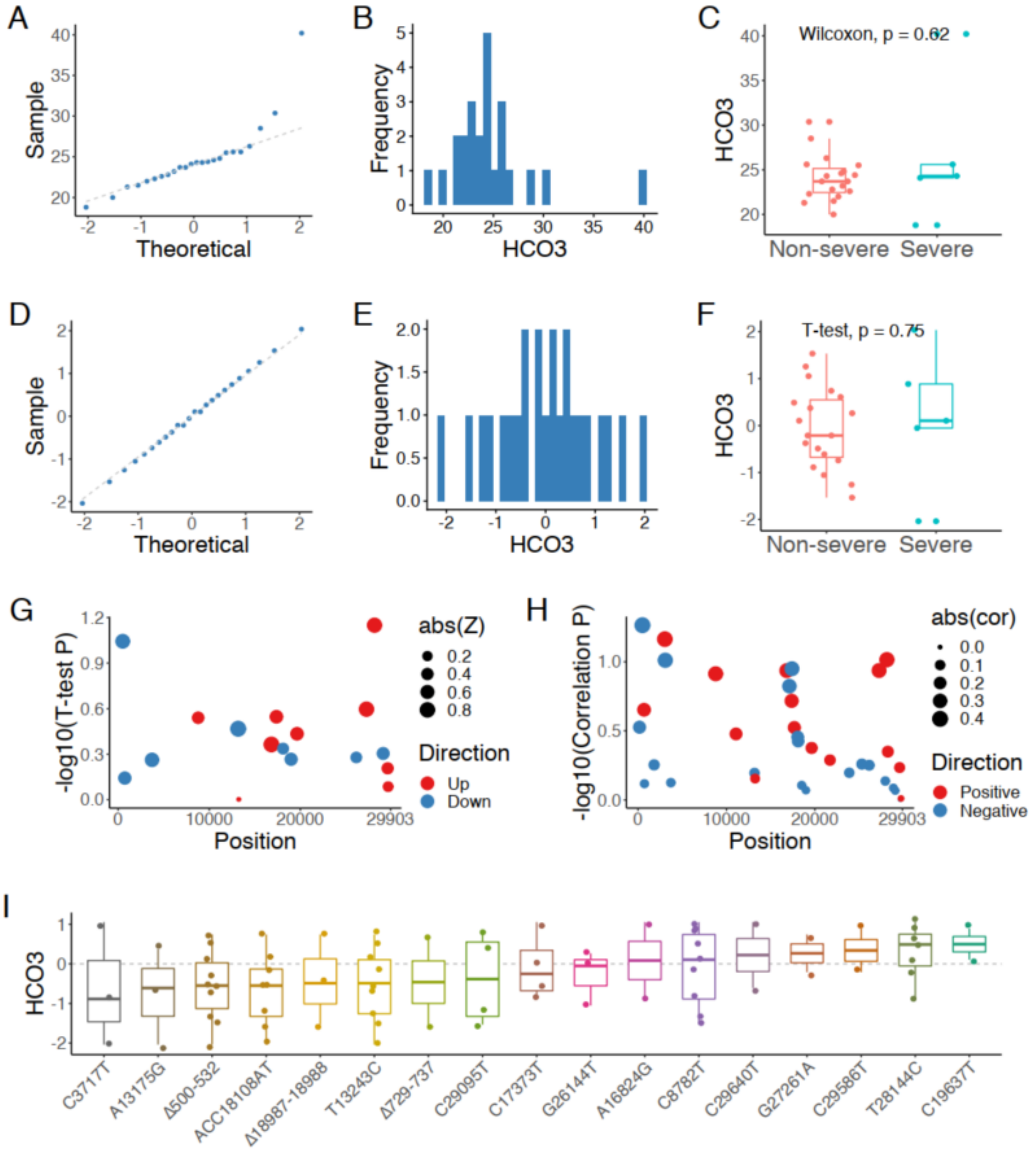
For NEUT (neutrophil count, ×10^9/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared GLU in the non-severe and severe COVID-19 patients before (**C**, $p = 1.6\times10^{-2}$, Wilcoxon test) and after normalization (**F**, $p = 1.1\times10^{-2}$, T-test). We further performed association analyses between the 35 genetic variants and NEUT using T-test and Pearson correlation. (**G**) Variants T3086C, G11083T and C21711T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T28144C and C25317T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of NEUT, cases with C19637T and C17676T tend to have the highest Z score, whereas cases with T3086C and G27967T have the lowest.

48. HBDH (α-Hydroxybutyrate dehydrogenase)



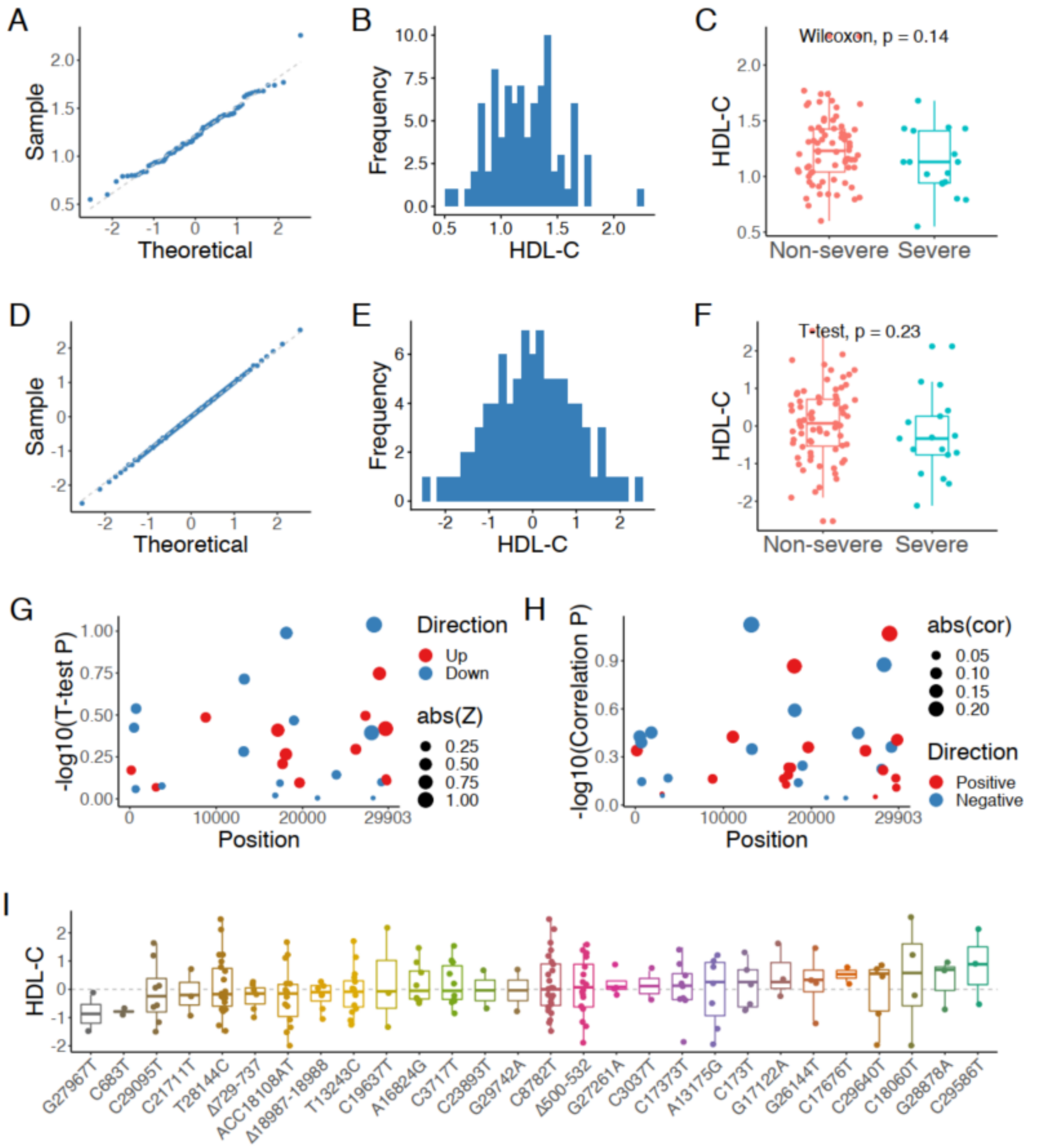
For HBDH (α-Hydroxybutyrate dehydrogenase, U/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared HBDH in the non-severe and severe COVID-19 patients before (**C**, p = 0.75, Wilcoxon test) and after normalization (**F**, p = 0.85, T-test). We further performed association analyses between the 35 genetic variants and HBDH using T-test and Pearson correlation. (**G**) Variants Δ500-532, C8782T, T13243C and C29640T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C683T, T13243C, C19637T, C29640T and C28253T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of HBDH, cases with Δ18987-18988 and T13243C tend to have the highest Z score, whereas cases with C29640T and C23893T have the lowest.

49. HCO3- (bicarbonate)



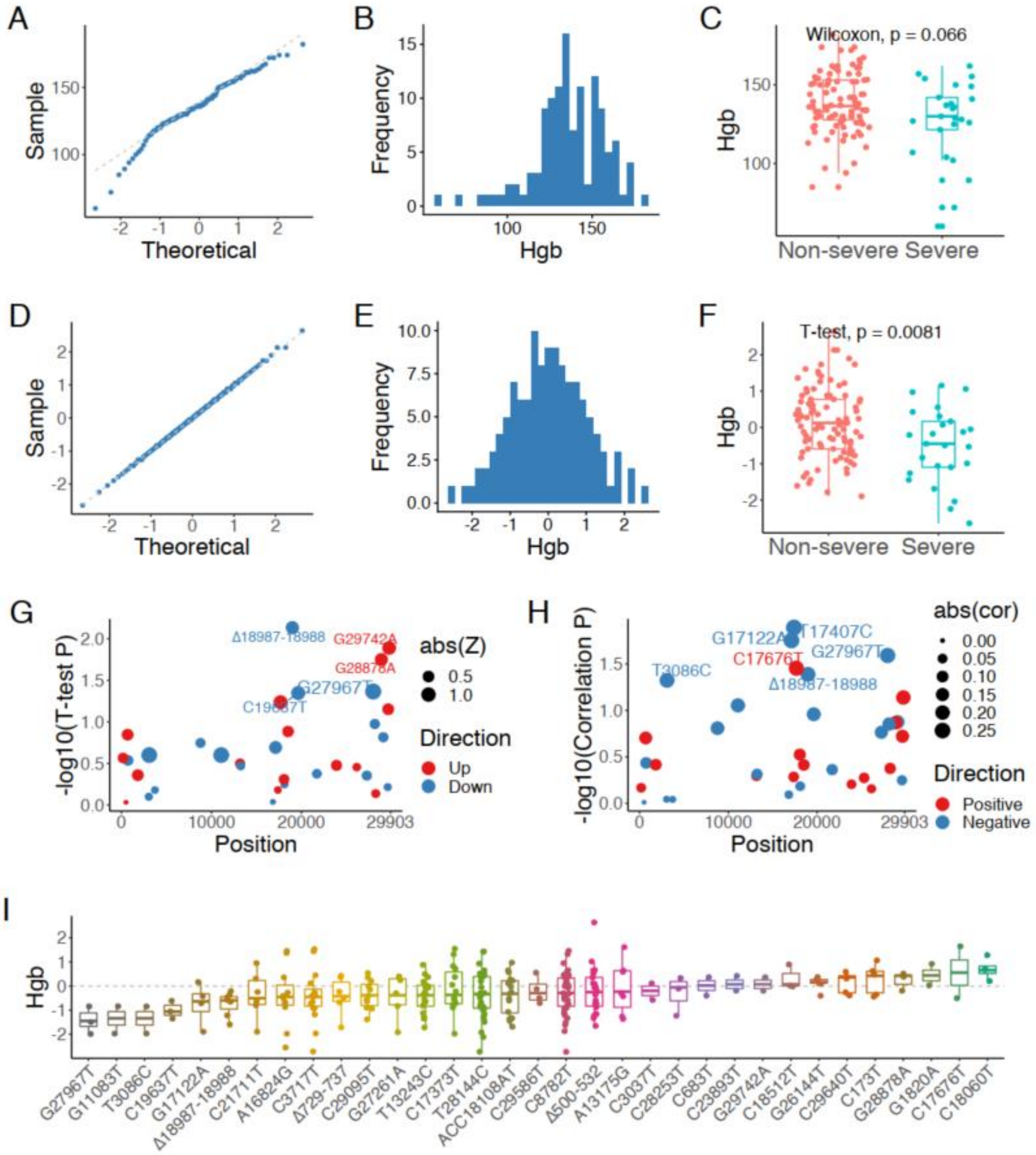
For HCO3 (bicarbonate, mEq/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared mEq/L in the non-severe and severe COVID-19 patients before (**C**, p = 0.62, Wilcoxon test) and after normalization (**F**, p = 0.75, T-test). We further performed association analyses between the 35 genetic variants and mEq/L using T-test and Pearson correlation. (**G**) No variant in the T test (**G**) and Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of HCO3, cases with C19637T and T28144C tend to have the highest Z score, whereas cases with C3717T and A13175G have the lowest.

50. HDL-C (high-density lipoprotein cholesterol)



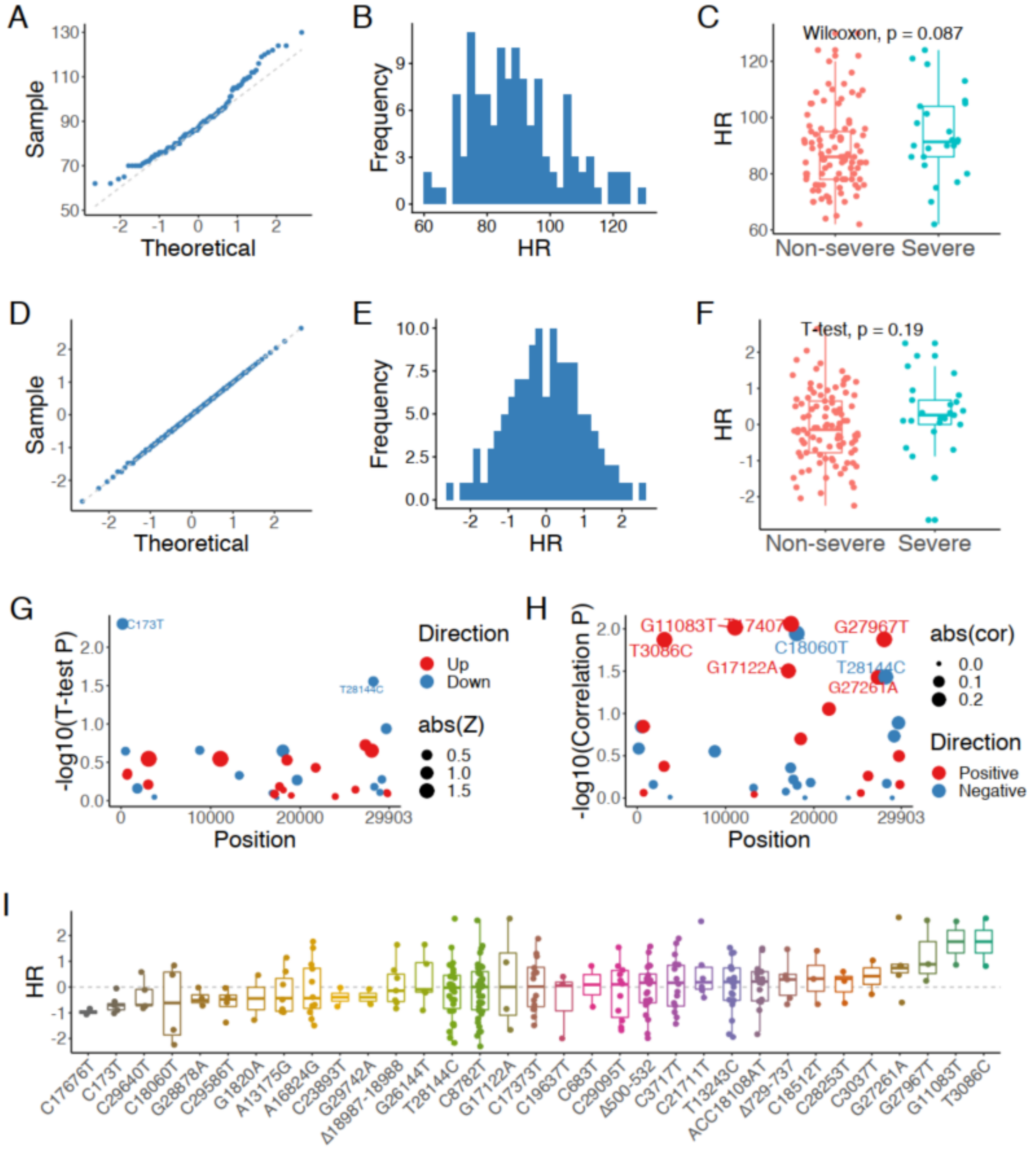
For HDL-C (high-density lipoprotein cholesterol, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared HDL-C in the non-severe and severe COVID-19 patients before (**C**, p = 0.14, Wilcoxon test) and after normalization (**F**, p = 0.23, T-test). We further performed association analyses between the 35 genetic variants and HDL-C using T-test and Pearson correlation. (**G**) No variant in the T test (**G**) and Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of HDL-C, cases with C29586T and G28878A tend to have the highest Z score, whereas cases with G27967T and C683T have the lowest.

51. Hgb (hemoglobin)



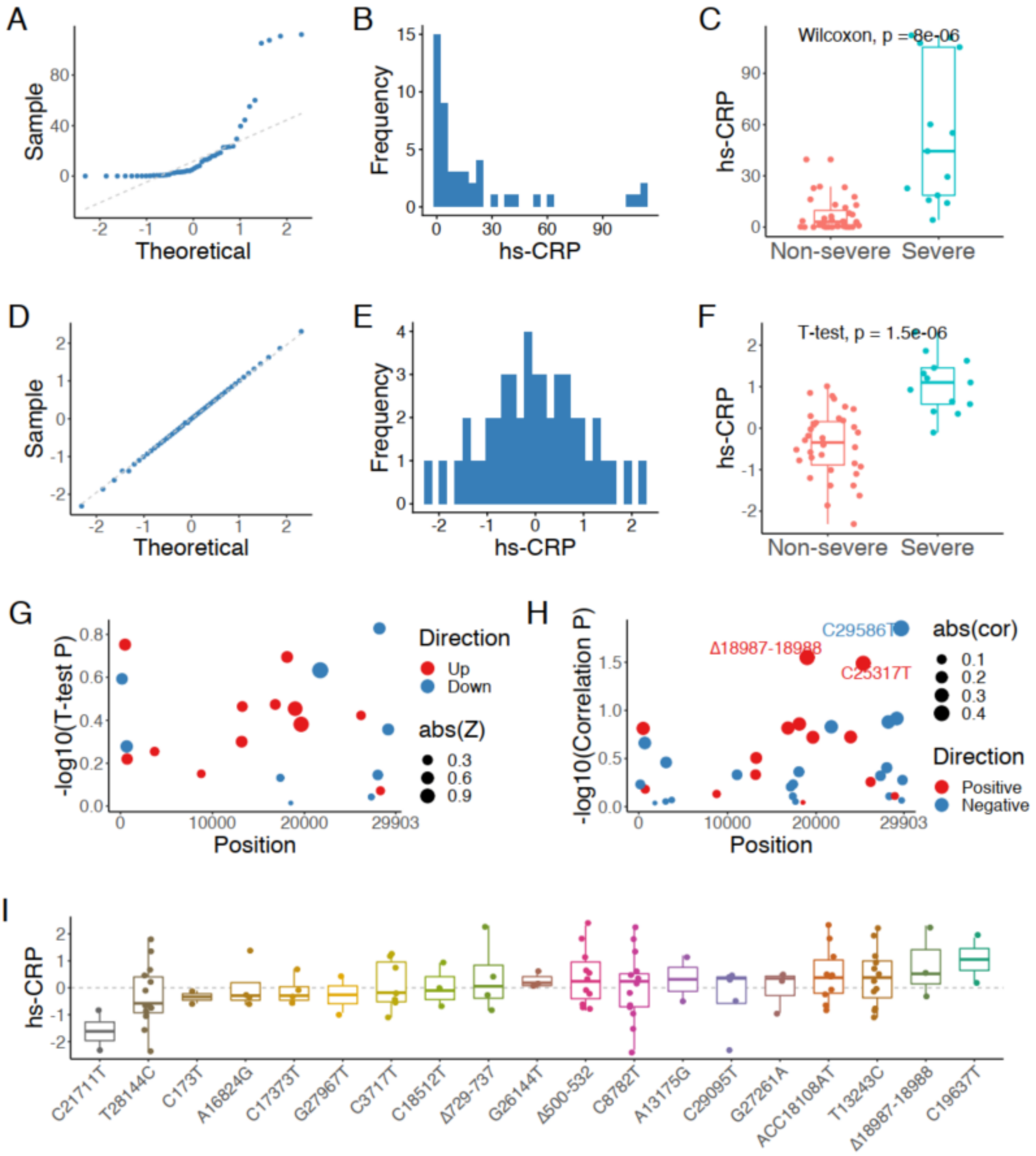
For Hgb (hemoglobin, g/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Hgb in the non-severe and severe COVID-19 patients before (C, $p = 6.6\times10^{-2}$, Wilcoxon test) and after normalization (**F**, $p = 8.1\times10^{-3}$, T-test). (**G**) Variants C19637T, G27967T, G28878A, G29742A and Δ18987-18988 pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T3086C, G17122A, C17676T, T17407C, G27967T and Δ18987-18988 have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of Hgb, cases with C18060T and C17676T tend to have the highest Z score, whereas cases with G27967T and G11083T have the lowest.

52. HR (heart rate)



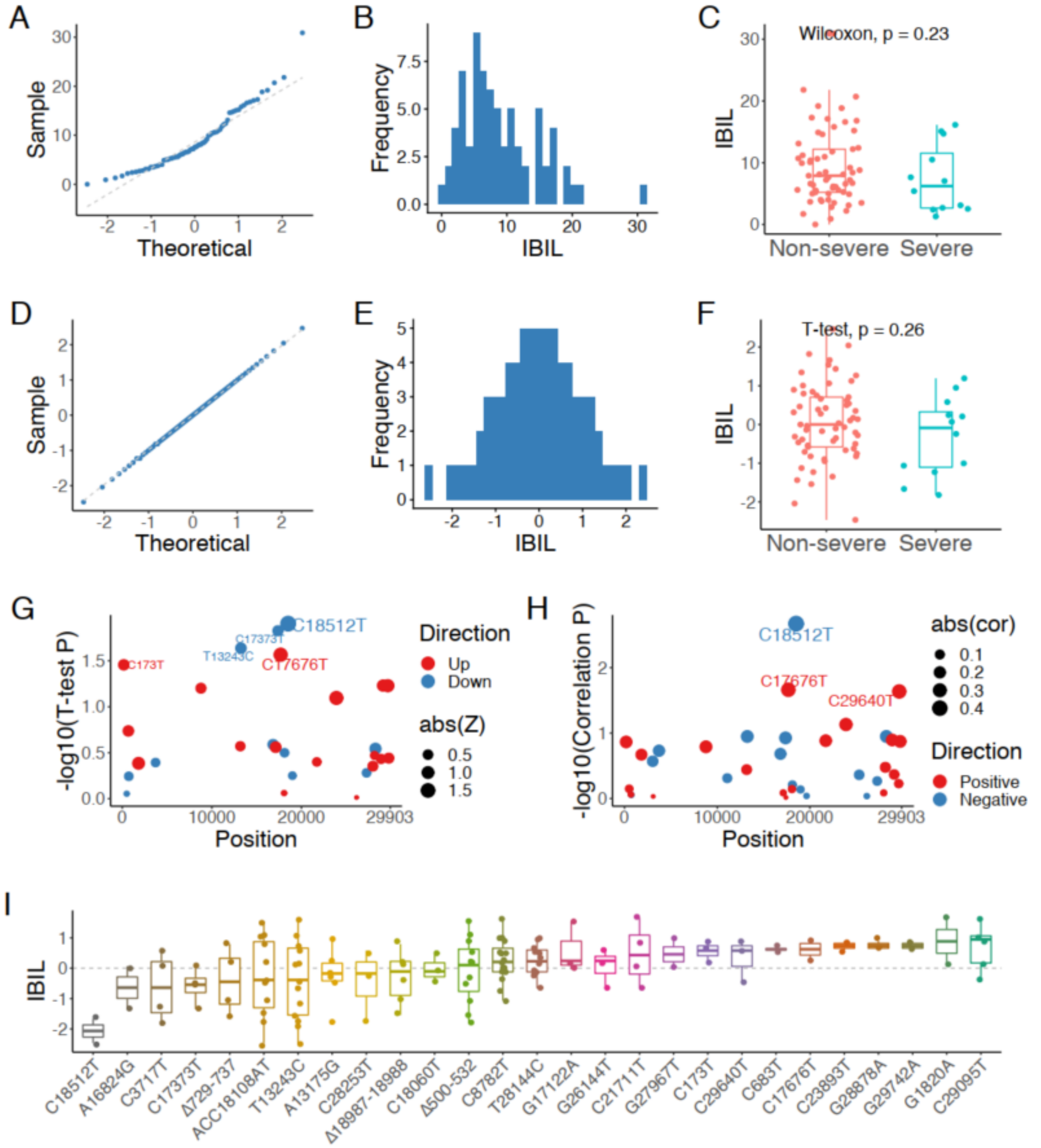
For HR (heart rate, times/min), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared HR in the non-severe and severe COVID-19 patients before (**C**, $p = 8.7\times10^{-2}$, Wilcoxon test) and after normalization (**F**, p = 0.19, T-test). (**G**) Variants C173T and T28144C pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T3086C, G11083T, T17407C, G17122A, C18060T, G27967T, T28144C and G27261A have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of HR, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C17676T and C173T have the lowest.

53. hs-CRp (hypersensitive C-reactive protein)



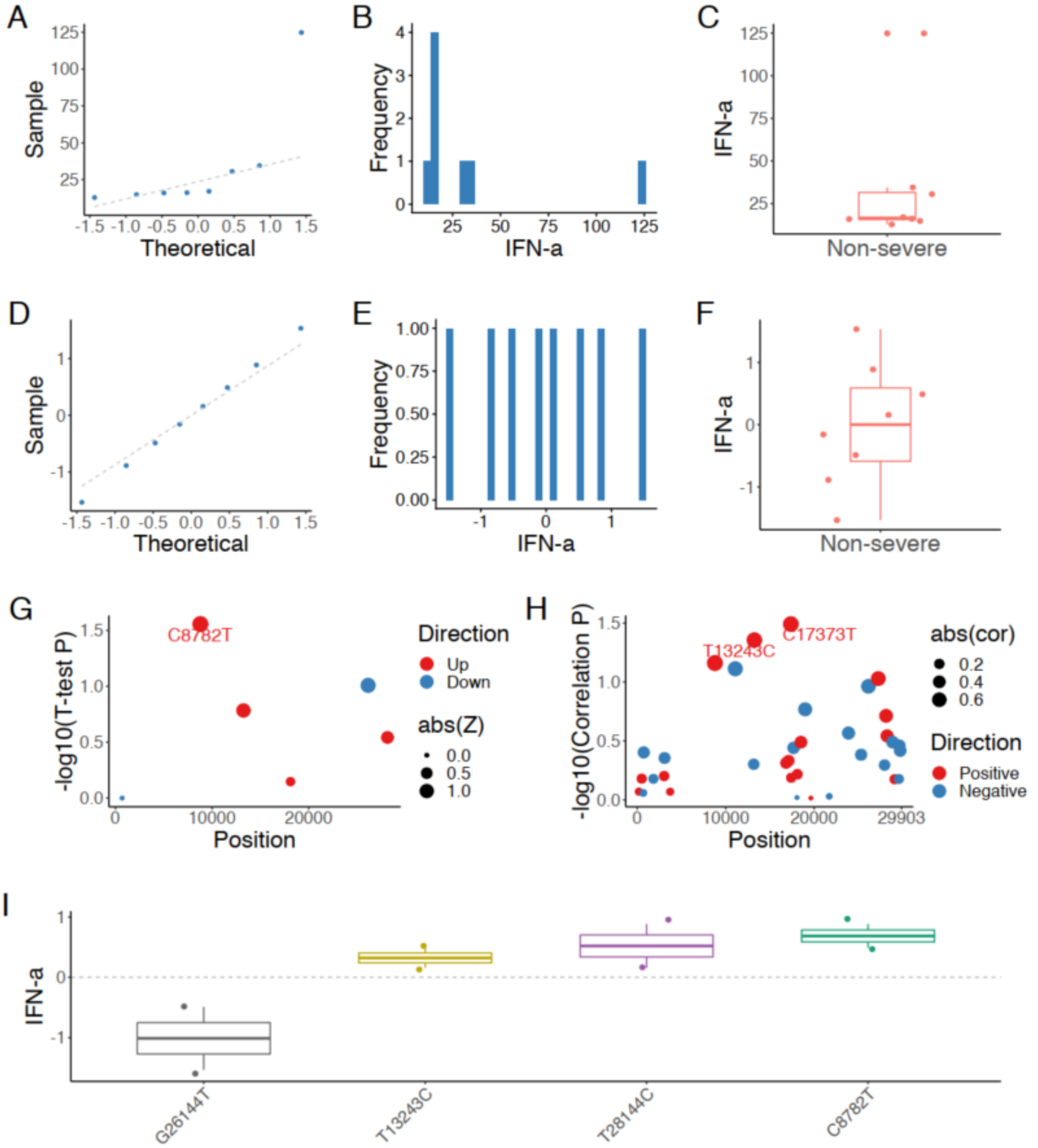
For hs-CRp (hypersensitive C-reactive protein, mg/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared hs-CRp in the non-severe and severe COVID-19 patients before (**C**, p = 8.0×10^{-6}, Wilcoxon test) and after normalization (**F**, p = 1.5×10^{-6}, T-test). We further performed association analyses between the 35 genetic variants and hs-CRp using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants Δ18987-18988, C29586T and C25317T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of hs-CRp, cases with C19637T and Δ18987-18988 tend to have the highest Z score, whereas cases with C21711T and T28144C have the lowest.

54. IBil (indirect bilirubin)



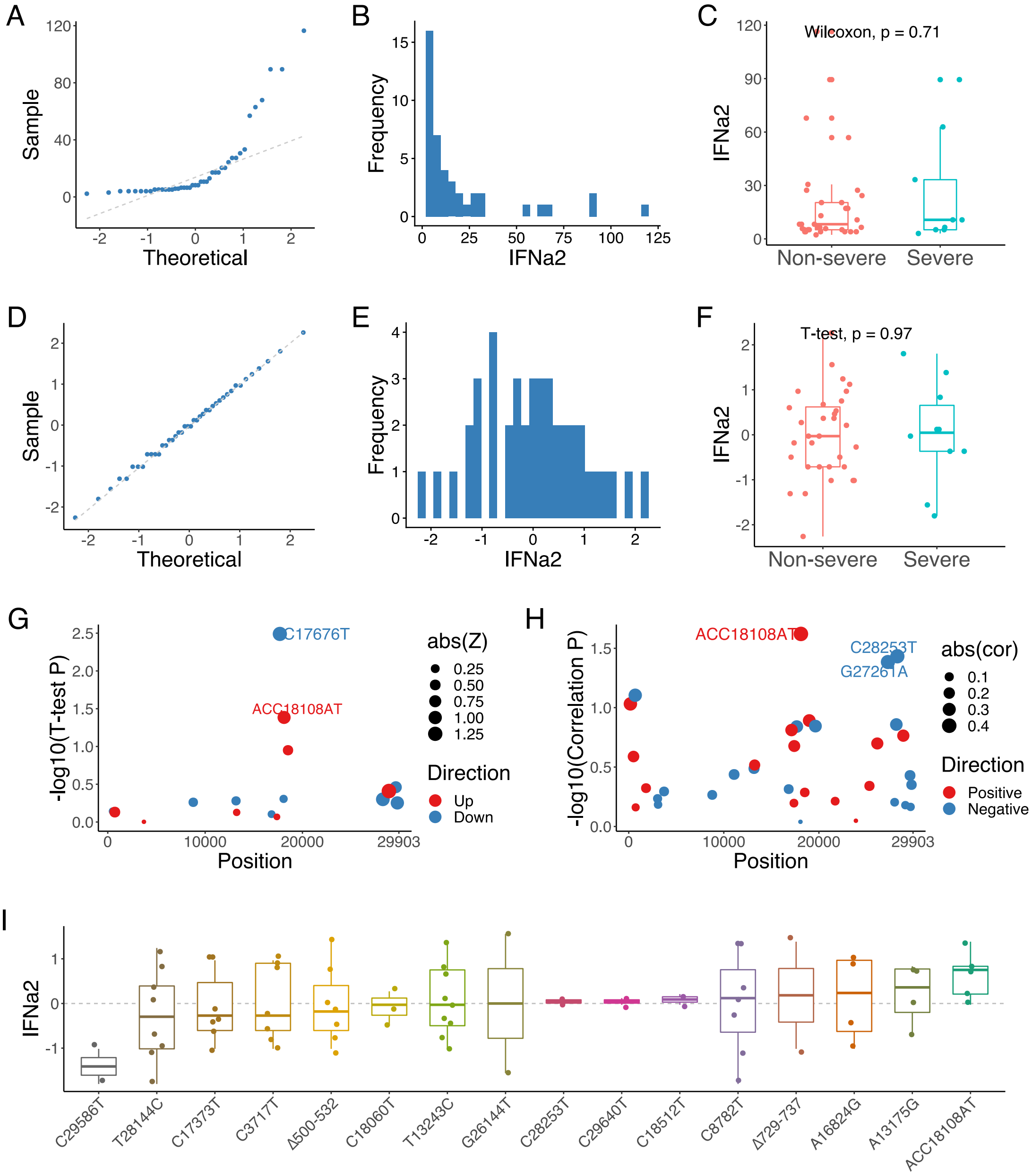
For IBil (indirect bilirubin, μmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IBIL in the non-severe and severe COVID-19 patients before (**C**, p = 0.23, Wilcoxon test) and after normalization (**F**, p = 0.26, T-test). We further performed association analyses between the 35 genetic variants and IBil using T-test and Pearson correlation. (**G**) Variants C173T, T13243C, C17373T, C17676T and C18512T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C17676T, C18512T and C29640T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IBil, cases with C29095T and G1820A tend to have the highest Z score, whereas cases with C18512T and A16824G have the lowest.

55. IFN-α (interferon alpha)



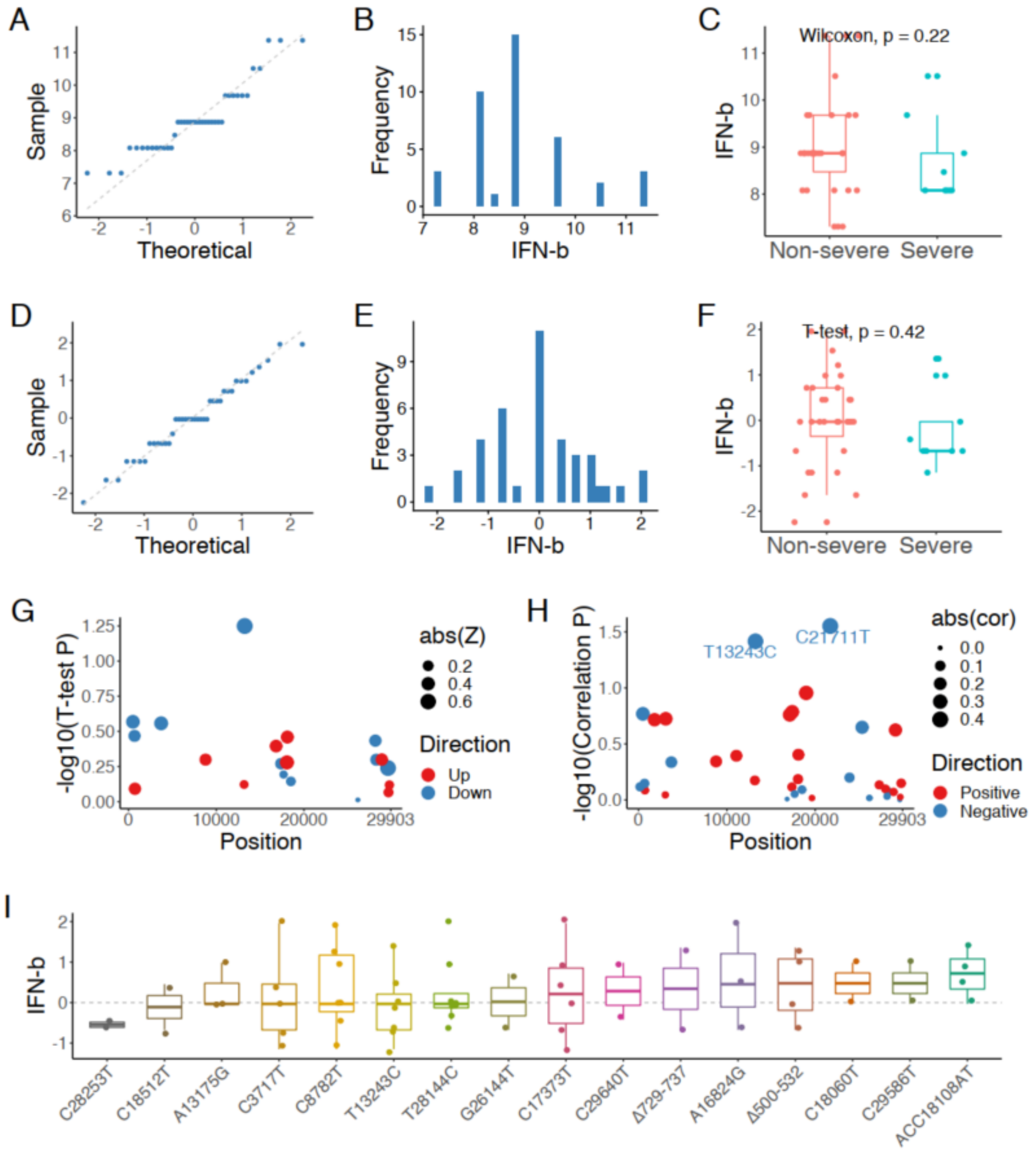
For IFN-α (interferon alpha, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IFN-α in the non-severe and severe COVID-19 patients before (**C**) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and IFN-α using T-test and Pearson correlation. (**G**) Variant C8782T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T13243C and C17373T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IFN-α, cases with C8782T and T28144C tend to have the highest Z score, whereas cases with G26144T and T13243C have the lowest.

56. IFNα2 (interferon alpha-2)



For IFNα2 (interferon alpha-2, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IFNa2 in the non-severe and severe COVID-19 patients before (**C**, p = 0.71, Wilcoxon test) and after normalization (**F**, p = 0.97, T-test). We further performed association analyses between the 35 genetic variants and IFNα2 using T-test and Pearson correlation. (**G**) Variants C17676T and ACC18108AT pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants ACC18108AT, C28253T and G27261A have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IFNα2, cases with ACC18108AT and A13175G tend to have the highest Z score, whereas cases with C29586T and T28144C have the lowest.

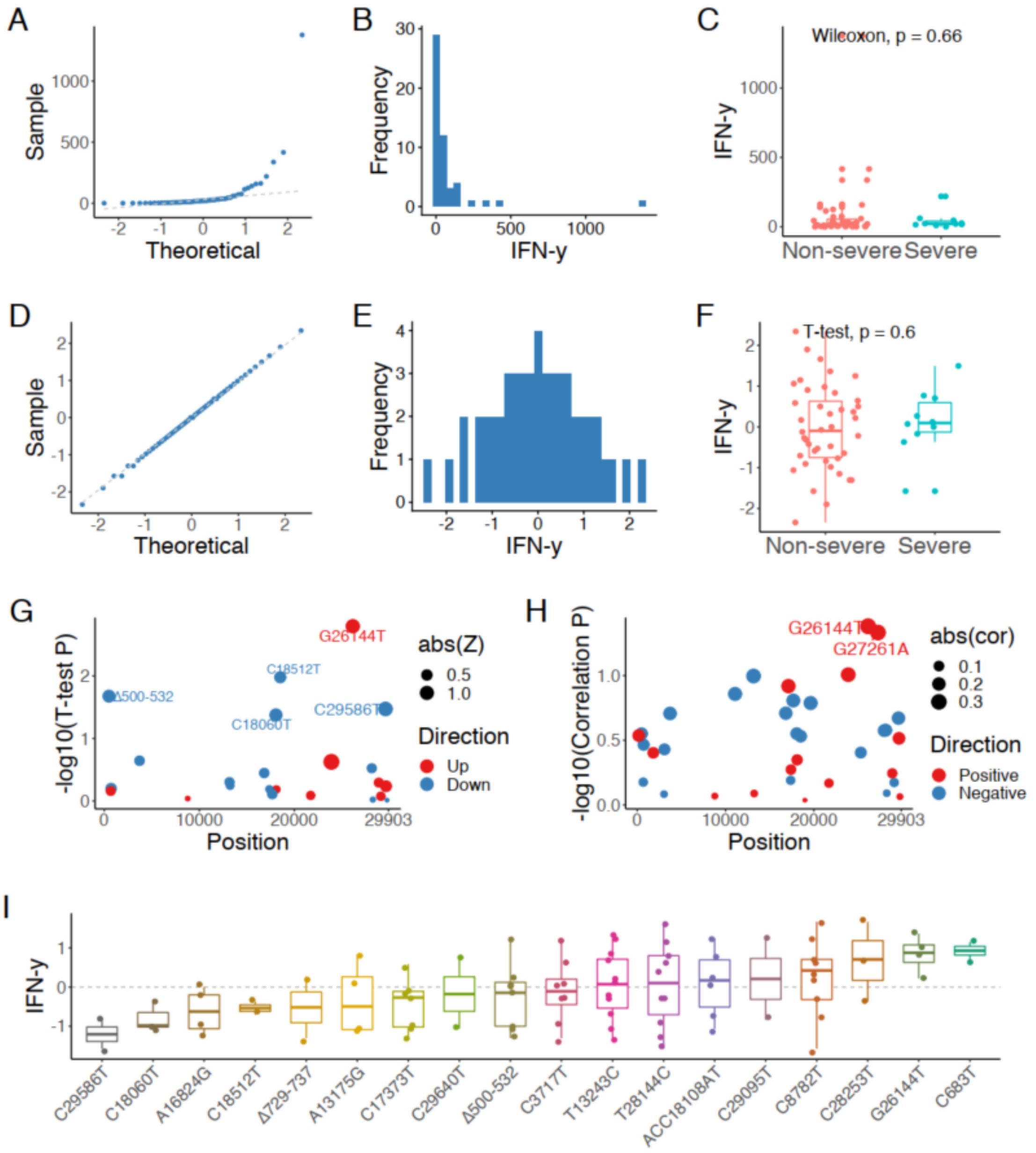
57. IFN-β (interferon beta)



For IFN-β (interferon beta, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IFN-β in the non-severe and severe COVID-19 patients before (**C**, p = 0.22, Wilcoxon test) and after normalization (**F**, p = 0.42, T-test). We further performed association analyses between the 35 genetic variants and IFN-β using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T13243C and C21711T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IFN-β, cases with ACC18108AT and C29586T tend to have the highest Z score, whereas cases with C28253T and

C18512T have the lowest.

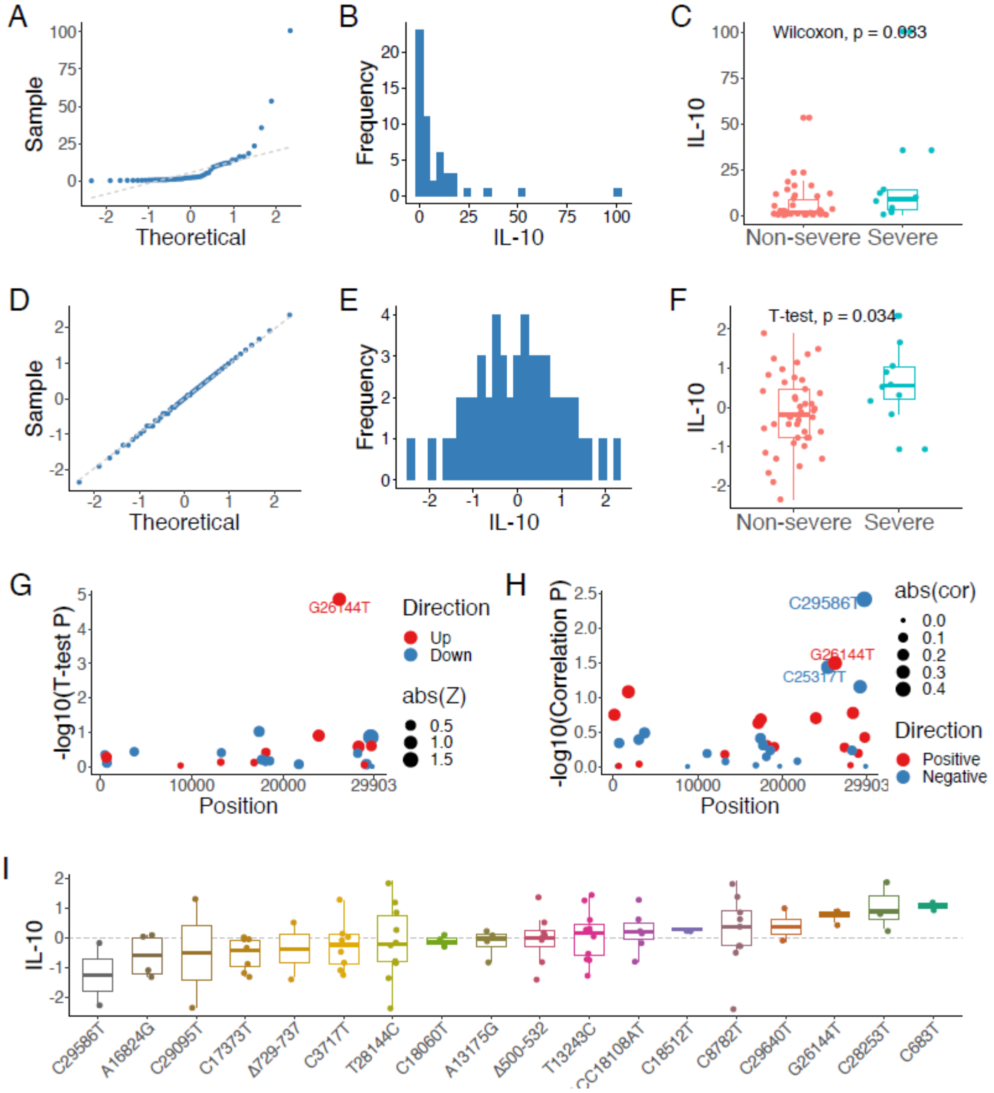
58. IFN-γ (interferon gamma)



For IFN-γ (interferon gamma, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IFN-γ in the non-severe and severe COVID-19 patients before (**C**, p = 0.66, Wilcoxon test) and after normalization (**F**, p = 0.6, T-test). We further performed association analyses between the 35 genetic variants and IFN-γ using T-test and Pearson correlation. (**G**) Variants Δ500-532, C18060T, C18512T, C29586T and G26144T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants G26144T and G27261A have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IFN-γ, cases with C683T and

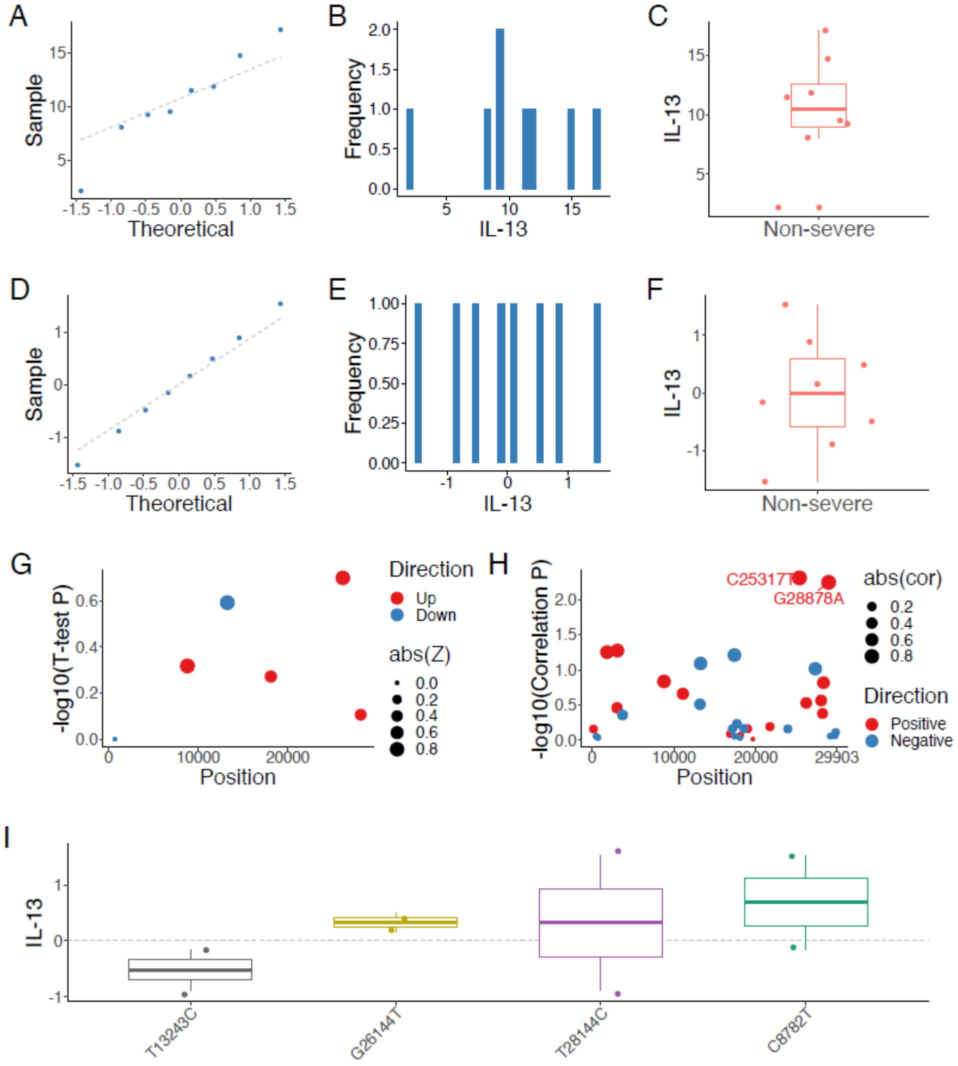
G26144T tend to have the highest Z score, whereas cases with C29586T and C18060T have the lowest.

59. IL-10 (interleukin 10)



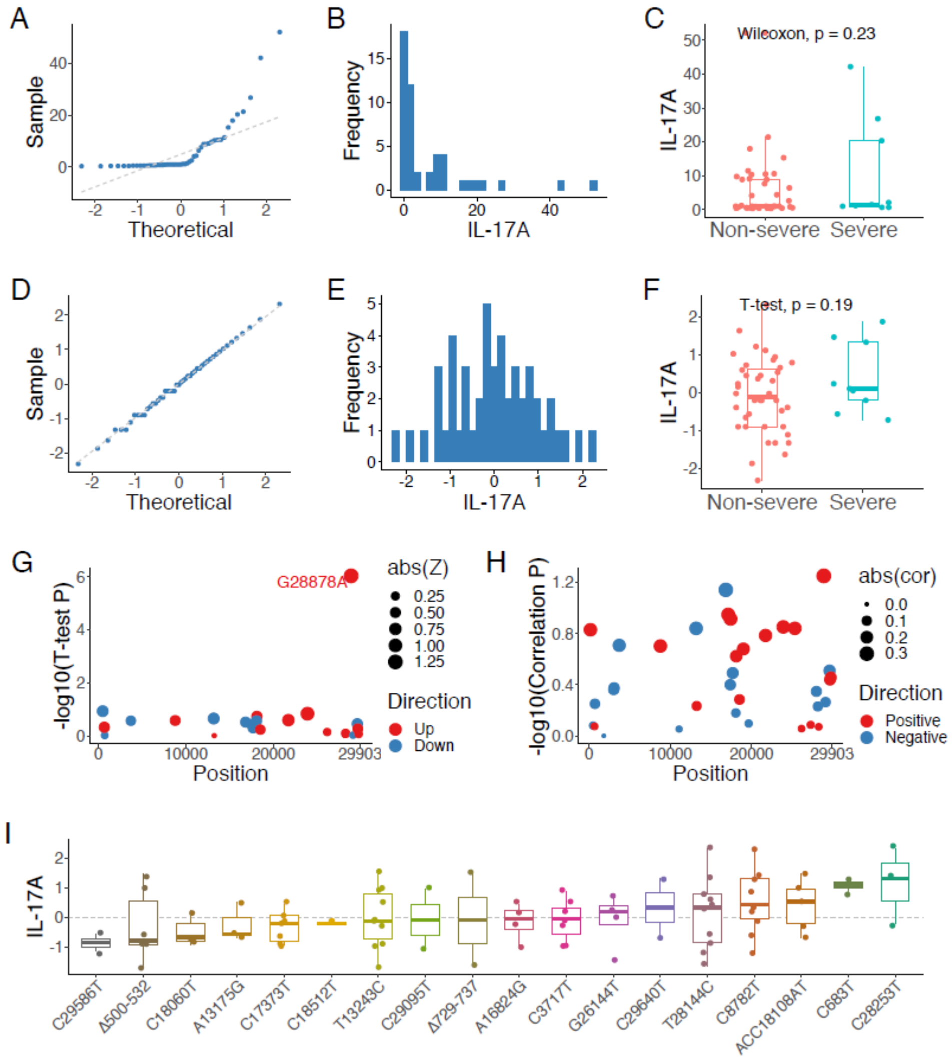
For IL-10 (interleukin 10, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-10 in the non-severe and severe COVID-19 patients before (**C**, p = 3.3×10^{-2}, Wilcoxon test) and after normalization (**F**, p = 3.4×10^{-2}, T-test). We further performed association analyses between the 35 genetic variants and IL-10 using T-test and Pearson correlation. (**G**) Variant G26T44T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C29586T, G26144T and C25317T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IL-10, cases with C28253T and C683T tend to have the highest Z score, whereas cases with C29586T and A16824G have the lowest.

60. IL-13 (interleukin 13)



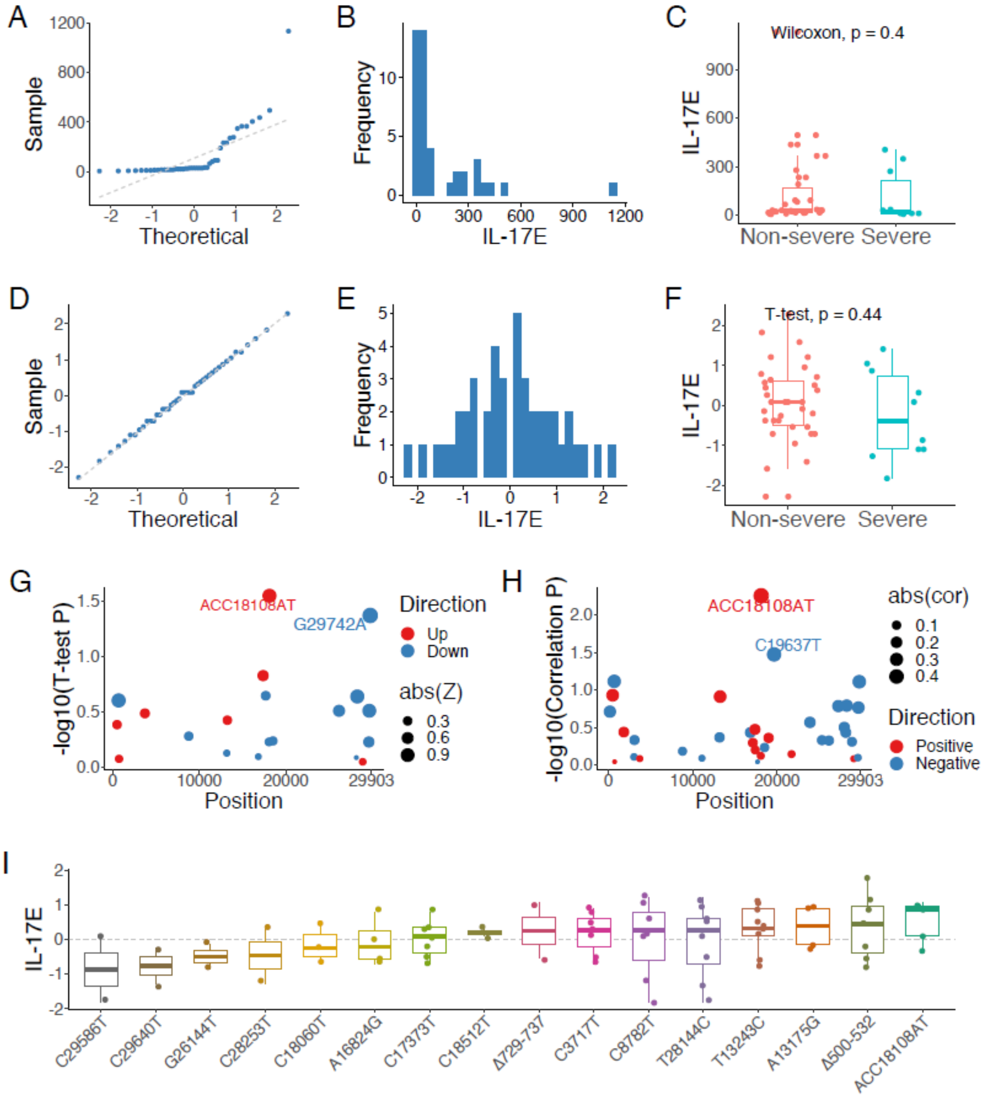
For IL-13 (interleukin 13, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-13 in the non-severe and severe COVID-19 patients before (**C**) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and IL-13 using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C25317T and G28878A have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IL-13, cases with C8782T and T28144C tend to have the highest Z score, whereas cases with T13243C have the lowest.

61. IL-17A (interleukin 17A)



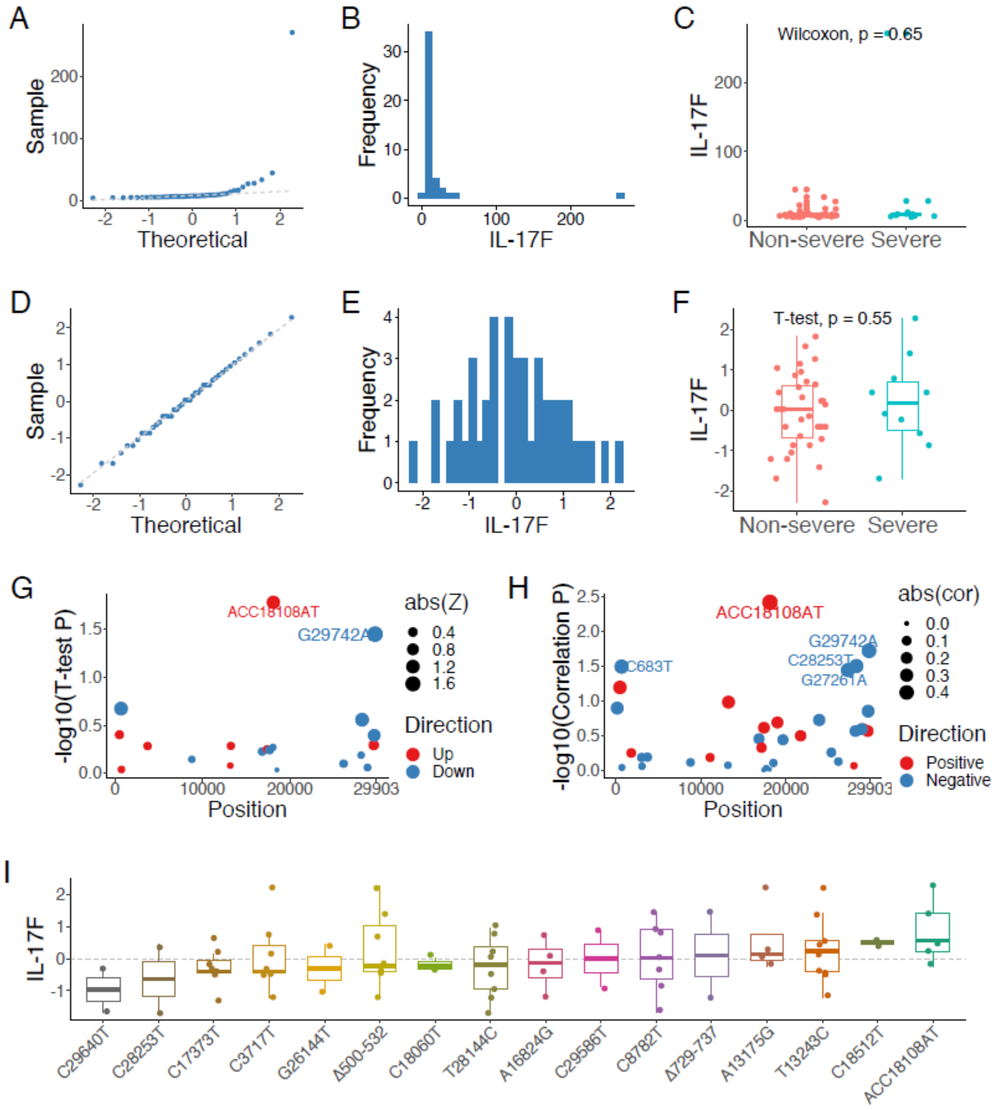
For IL-17A (interleukin 17A, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-17A in the non-severe and severe COVID-19 patients before (**C**, p = 0.23, Wilcoxon test) and after normalization (**F**, p = 0.19, T-test). We further performed association analyses between the 35 genetic variants and IL-17A using T-test and Pearson correlation. (**G**) Variant G28878A passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) No variant in Pearson correlation was has P value below 0.05. After sorting Z score values of IL-17A, cases with C28253T and C683T tend to have the highest Z score, whereas cases with C29586T and Δ500-532 have the lowest.

62. IL-17E (interleukin 17E)



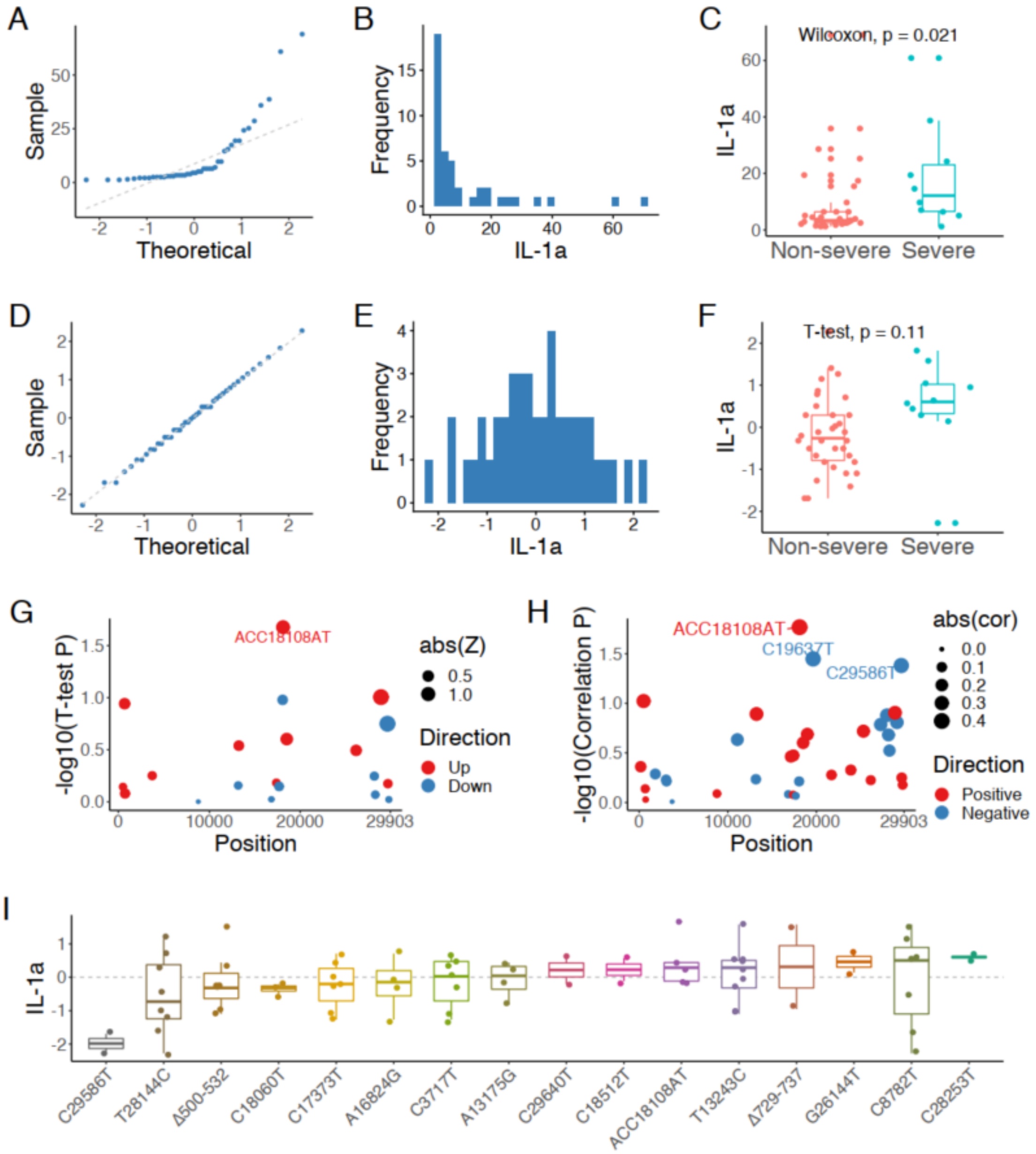
For IL-17E (interleukin 17E, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-17E in the non-severe and severe COVID-19 patients before (**C**, p = 0.4, Wilcoxon test) and after normalization (**F**, p = 0.44, T-test). We further performed association analyses between the 35 genetic variants and IL-17E using T-test and Pearson correlation. (**G**) Variants ACC18108AT and G29742A pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants ACC18108AT and C19637T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IL-17E, cases with ACC18108AT and △500-532 tend to have the highest Z score, whereas cases with C29586T and C29640T have the lowest.

63. IL-17F (interleukin 17F)



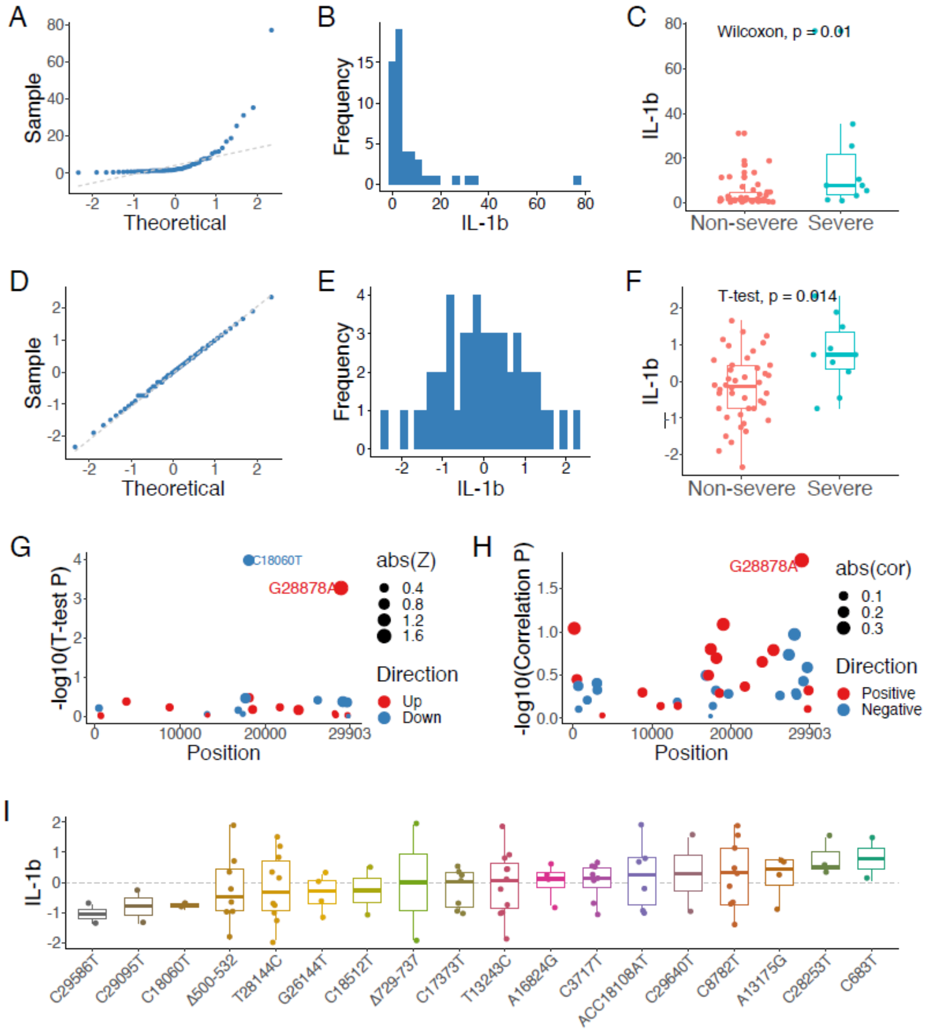
For IL-17F (interleukin 17F, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-17F in the non-severe and severe COVID-19 patients before (**C**, p = 0.65, Wilcoxon test) and after normalization (**F**, p = 0.55, T-test). We further performed association analyses between the 35 genetic variants and IL-17F using T-test and Pearson correlation. (**G**) Variants ACC18108AT and G29742A pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants ACC18108AT, G29742A, G28253T, G27261A and C683T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IL-17F, cases with ACC18108AT and C18512T tend to have the highest Z score, whereas cases with C29640T and C28253T have the lowest.

64. IL-1a (interleukin 1a)



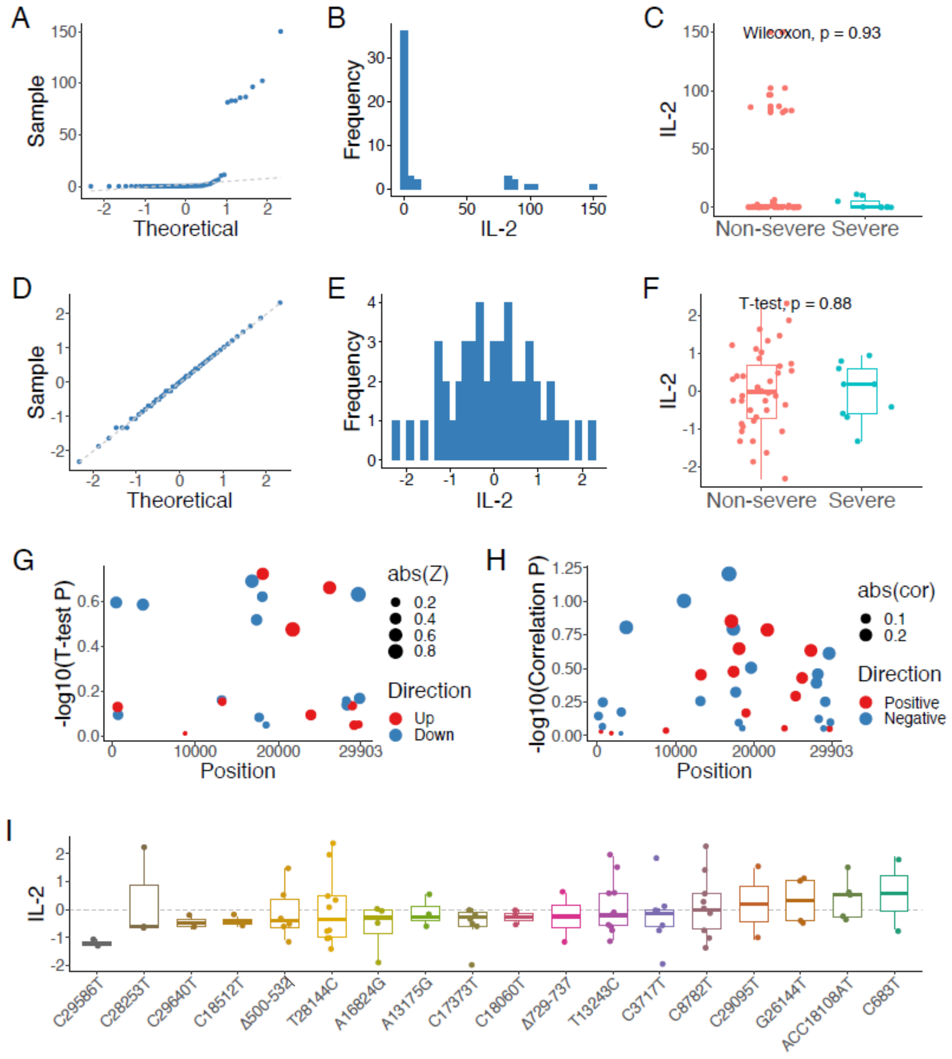
For IL-1a (interleukin 1a, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-1a in the non-severe and severe COVID-19 patients before (**C**, $p = 2.1 \times 10^{-2}$, Wilcoxon test) and after normalization (F, p = 0.11, T-test). We further performed association analyses between the 35 genetic variants and IL-1a using T-test and Pearson correlation. (**G**) Variant ACC18108AT passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants ACC18108AT, C19637T and C29586T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IL-1a, cases with C28253T and C8782T tend to have the highest Z score, whereas cases with C29586T and T28144C have the lowest.

65. IL-1b (interleukin 1b)



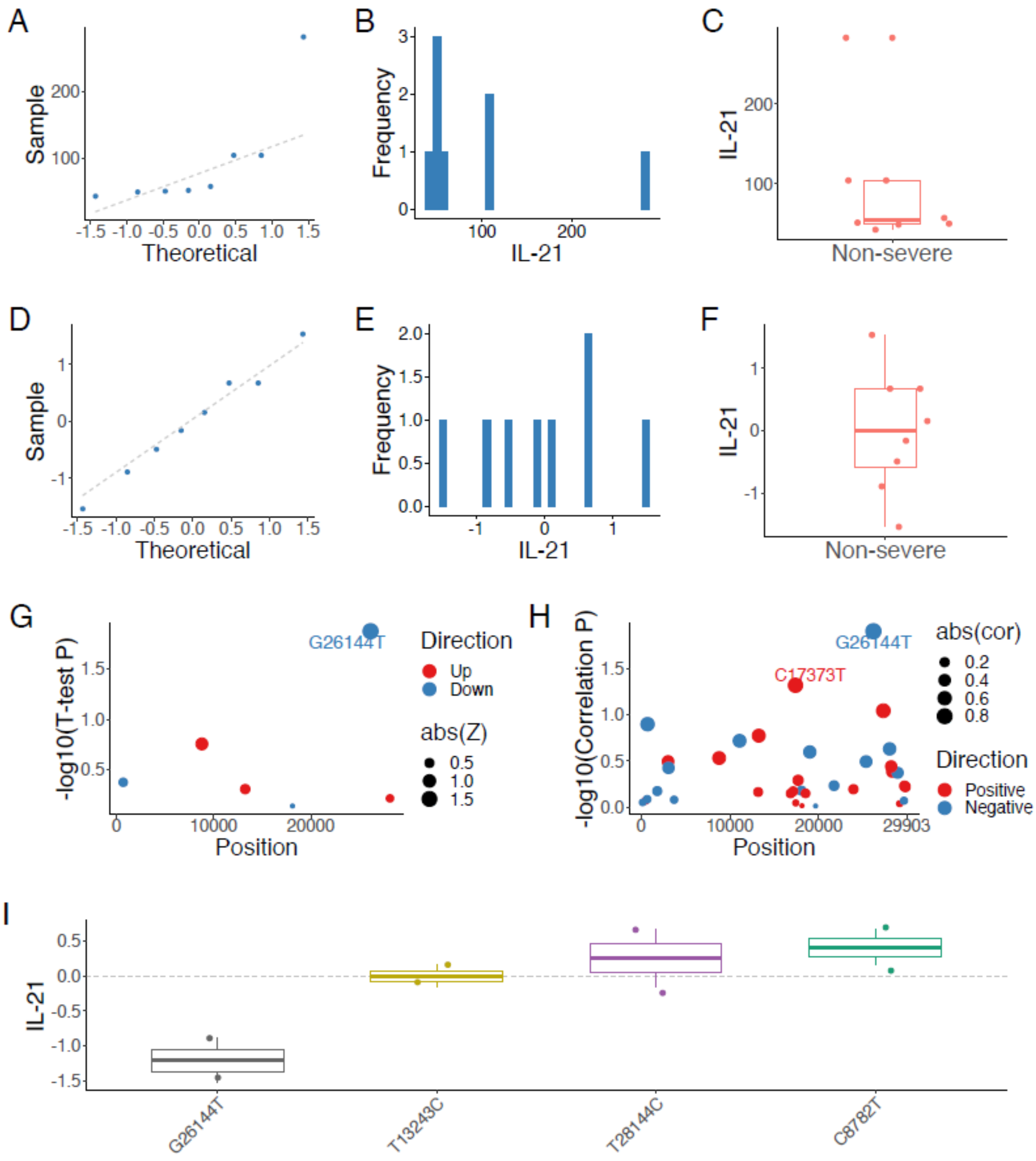
For IL-1b (interleukin 1b, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-1b in the non-severe and severe COVID-19 patients before (**C**, p = 0.01, Wilcoxon test) and after normalization (**F**, p = 1.4×10^{-2}, T-test). We further performed association analyses between the 35 genetic variants and IL-1b using T-test and Pearson correlation. (**G**) Variants G28878A and C18060T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant G28878A has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IL-1b, cases with C683T and C28253T tend to have the highest Z score, whereas cases with C29586T and C29095T have the lowest.

66. IL-2 (interleukin 2)



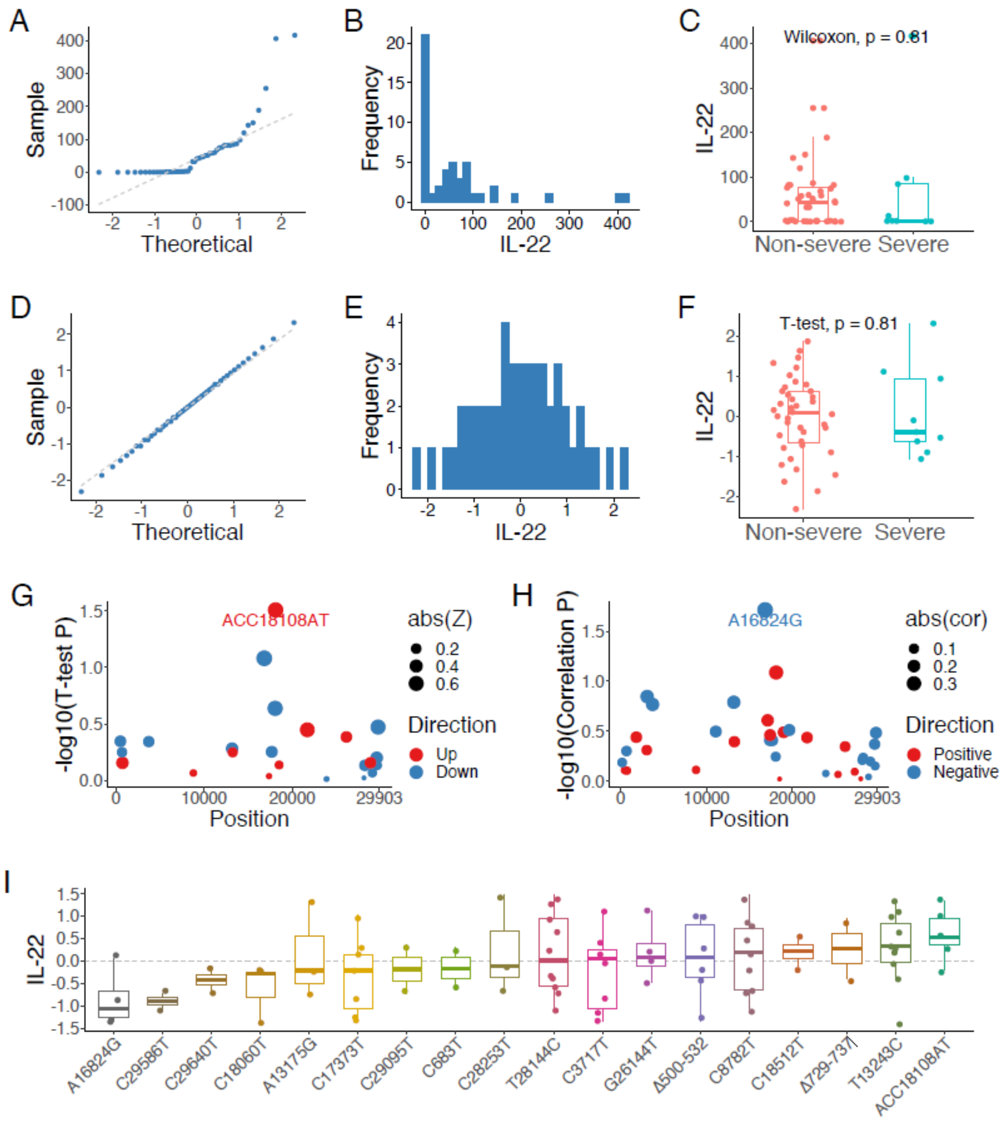
For IL-2 (interleukin 2, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-2 in the non-severe and severe COVID-19 patients before (**C**, p = 0.93, Wilcoxon test) and after normalization (**F**, p = 0.88, T-test). We further performed association analyses between the 35 genetic variants and IL-2 using T-test and Pearson correlation. (**G**) No variant in the T test (**G**) and Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of IL-2, cases with C683T and ACC18108AT tend to have the highest Z score, whereas cases with C29586T and C28253T have the lowest.

67. IL-21 (interleukin 21)



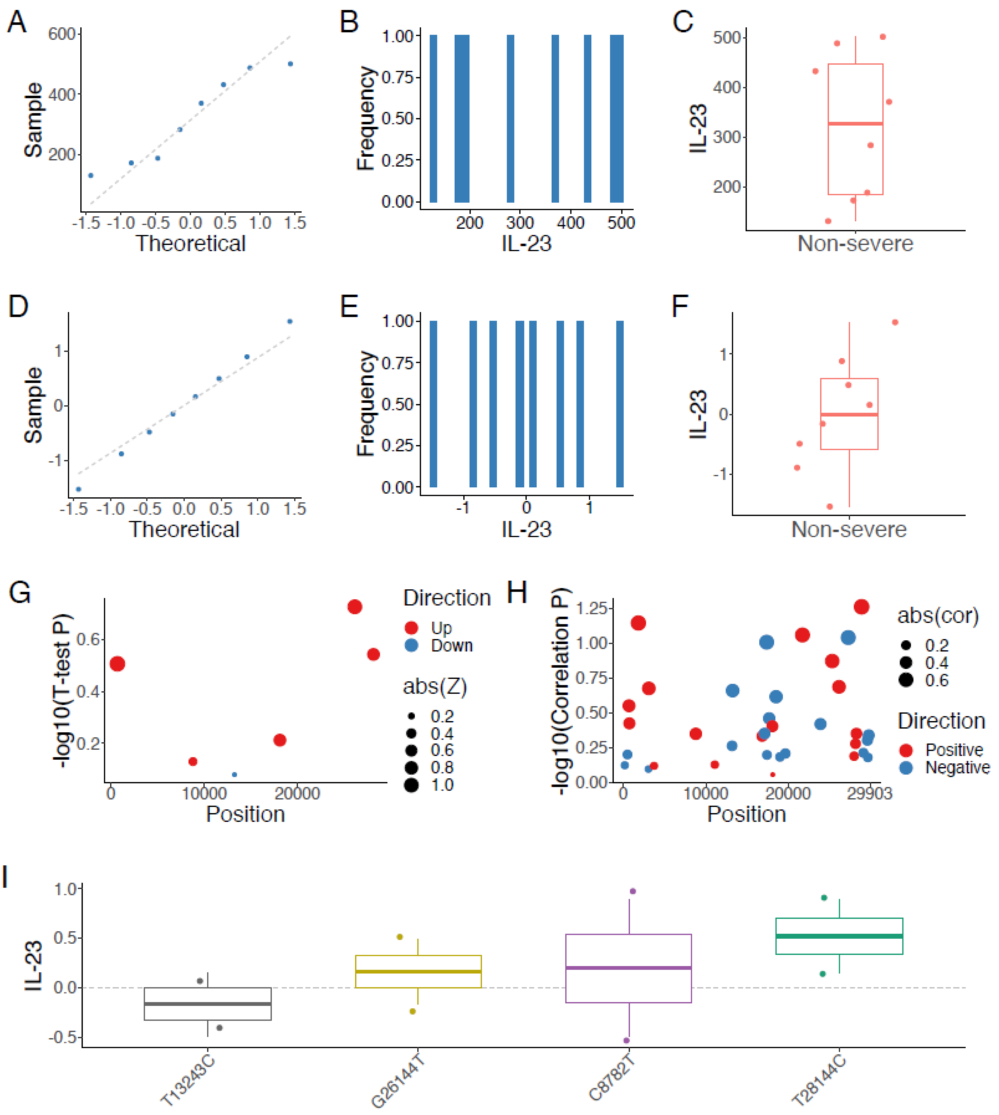
For IL-21 (interleukin 21, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-21 in the non-severe and severe COVID-19 patients before (**C**) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and IL-21 using T-test and Pearson correlation. (**G**) Variant G26144T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants G26144T and C17373T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IL-21, cases with C8782T and T28144C tend to have the highest Z score, whereas cases with G26144T have the lowest.

68. IL-22 (interleukin 22)



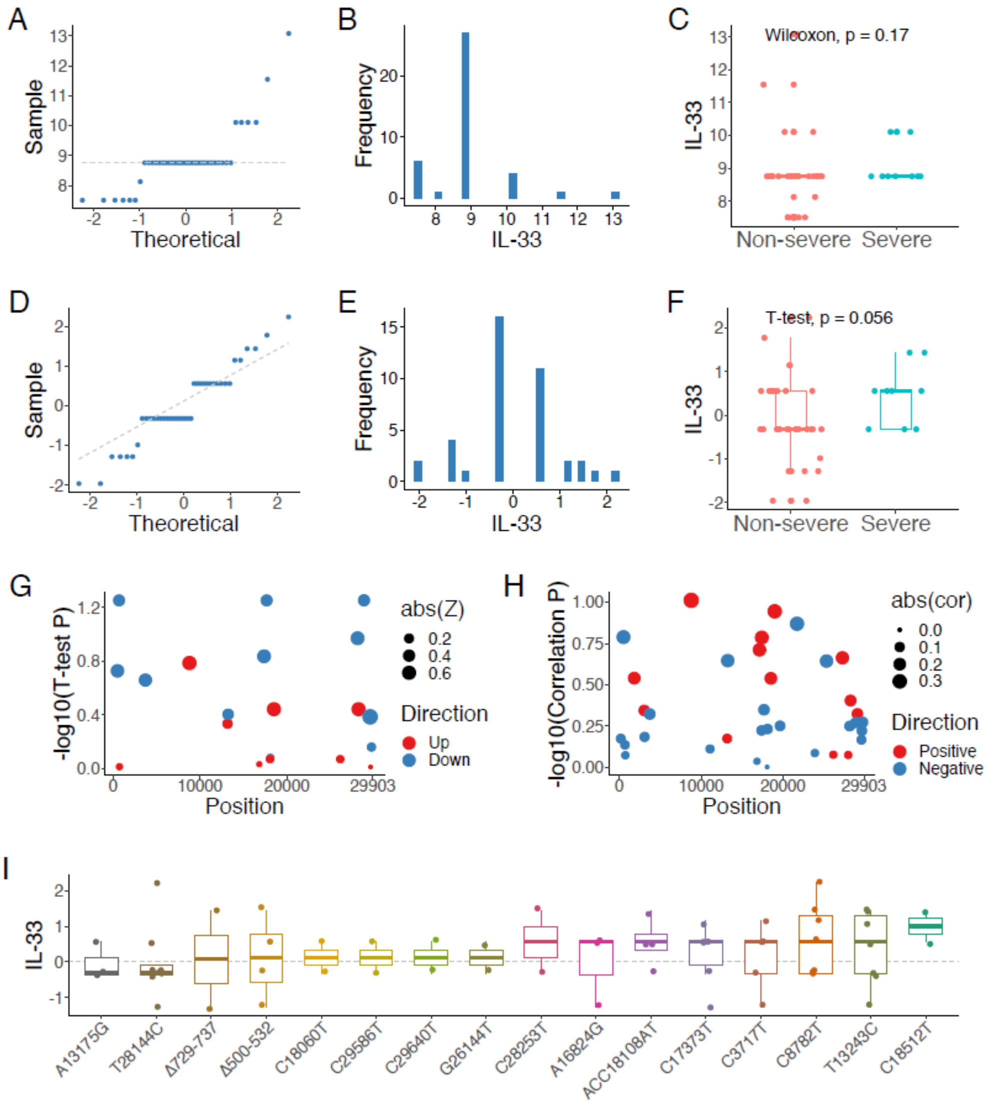
For IL-22 (interleukin 22, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-22 in the non-severe and severe COVID-19 patients before (**C**, p = 0.81, Wilcoxon test) and after normalization (**F**, p = 0.81, T-test). We further performed association analyses between the 35 genetic variants and IL-22 using T-test and Pearson correlation. (**G**) Variant ACC18108AT passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant A16824G has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IL-22, cases with ACC18108AT and T13243C tend to have the highest Z score, whereas cases with A16824G and C18060T have the lowest.

69. IL-23 (interleukin 3)



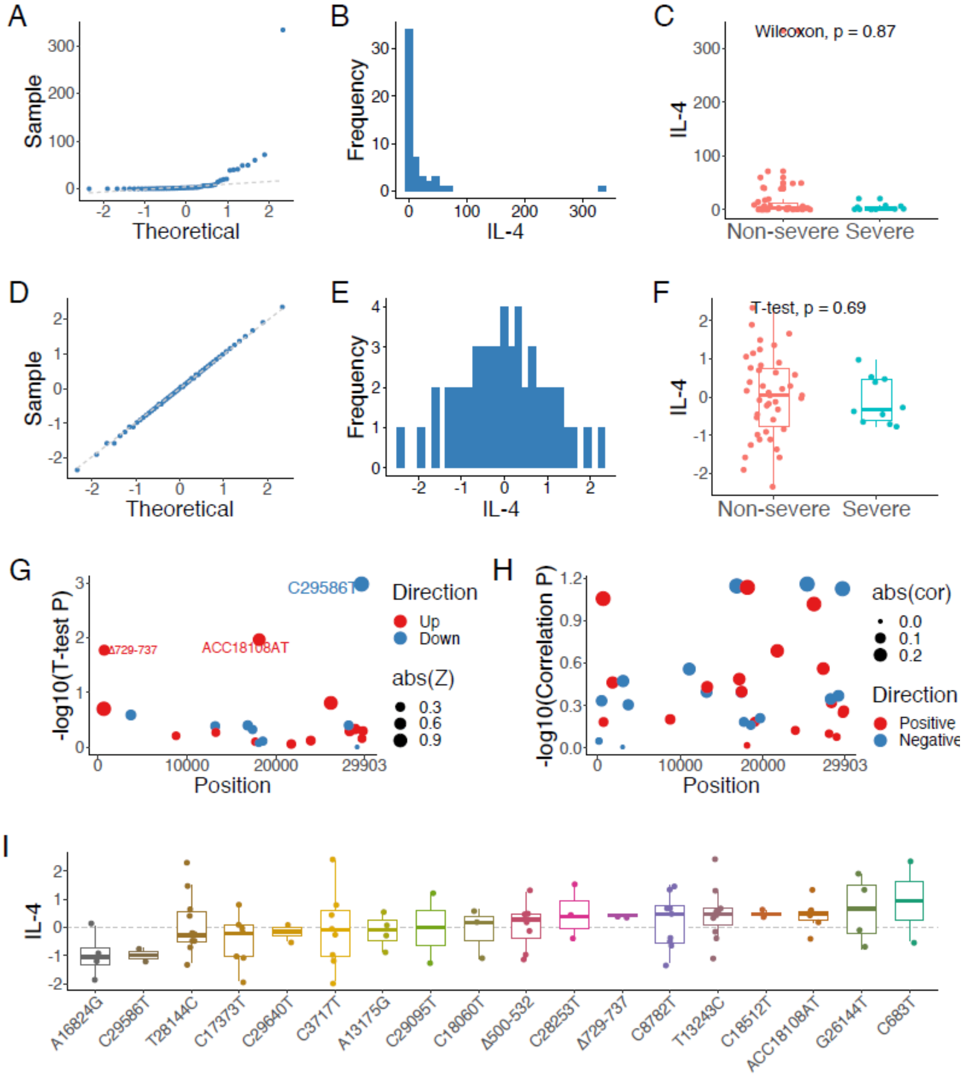
For IL-23 (interleukin 23, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-23 in the non-severe and severe COVID-19 patients before (**C**) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and IL-23 using T-test and Pearson correlation. (**G**) No variant in the T test (**G**) and Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of IL-23, cases with T28144C and C8782T tend to have the highest Z score, whereas cases with T13243C and G26144T have the lowest.

70. IL-33 (interleukin 33)



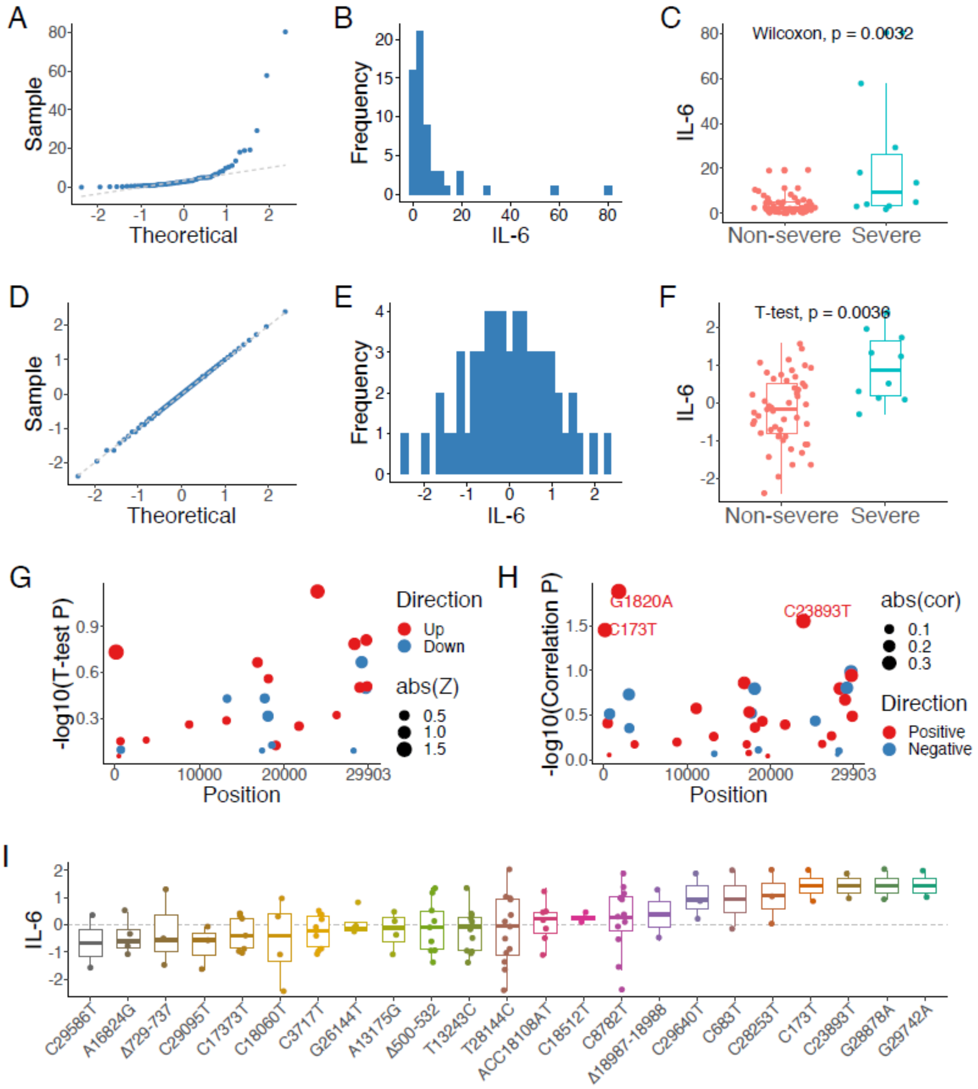
For IL-33 (interleukin 33, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-33 in the non-severe and severe COVID-19 patients before (**C**, p = 0.17, Wilcoxon test) and after normalization (**F**, $p = 5.6\times10^{-2}$, T-test). We further performed association analyses between the 35 genetic variants and IL-33 using T-test and Pearson correlation. (**G**) No variant in the T test (**G**) and Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of IL-33, cases with C18512T and T13243C tend to have the highest Z score, whereas cases with A13175G and T28144C have the lowest.

71. IL-4 (interleukin 4)



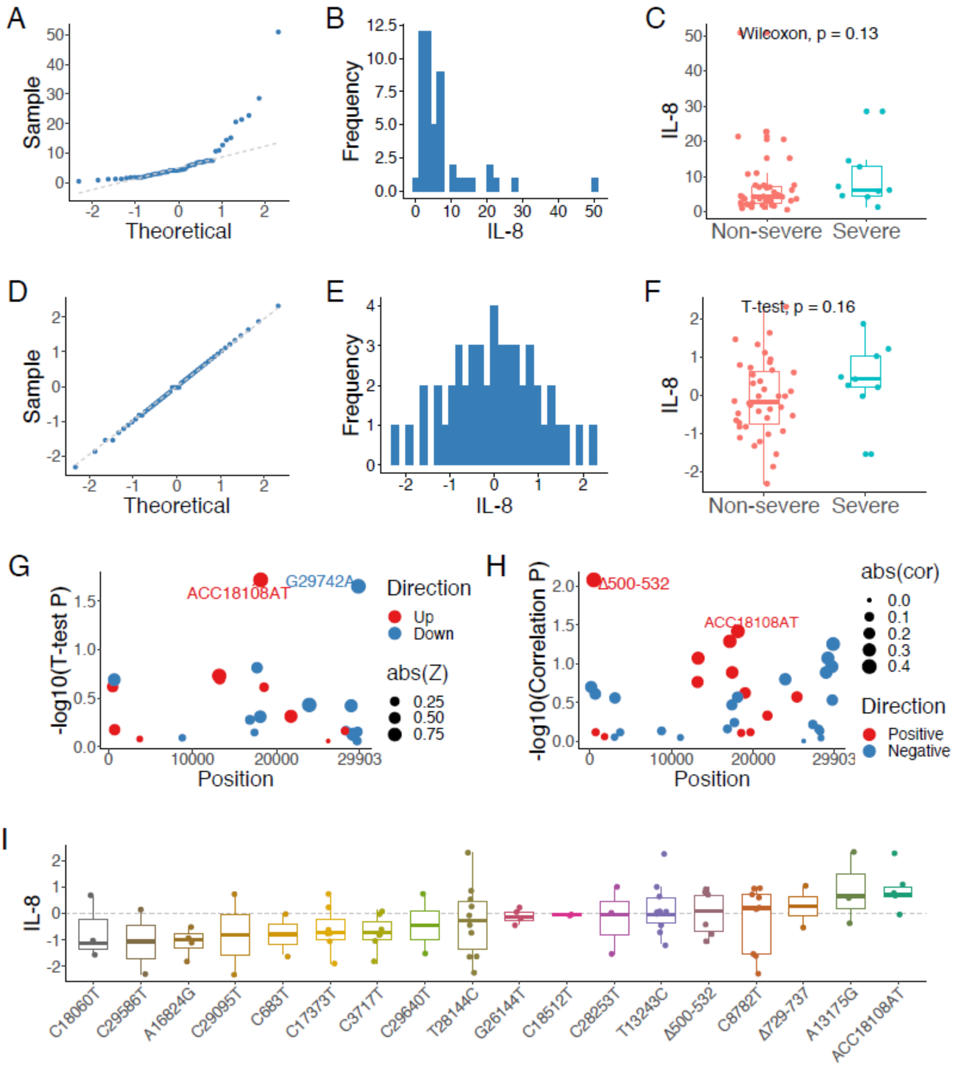
For IL-4 (interleukin 4, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-4 in the non-severe and severe COVID-19 patients before (**C**, p = 0.87, Wilcoxon test) and after normalization (**F**, p = 0.69, T-test). We further performed association analyses between the 35 genetic variants and IL-4 using T-test and Pearson correlation. (**G**) Variants C29586T, ACC18108AT and Δ729-737 pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) No variant has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IL-4, cases with C683T and G26144T tend to have the highest Z score, whereas cases with A16824G and C29586T have the lowest.

72. IL-6 (interleukin 6)



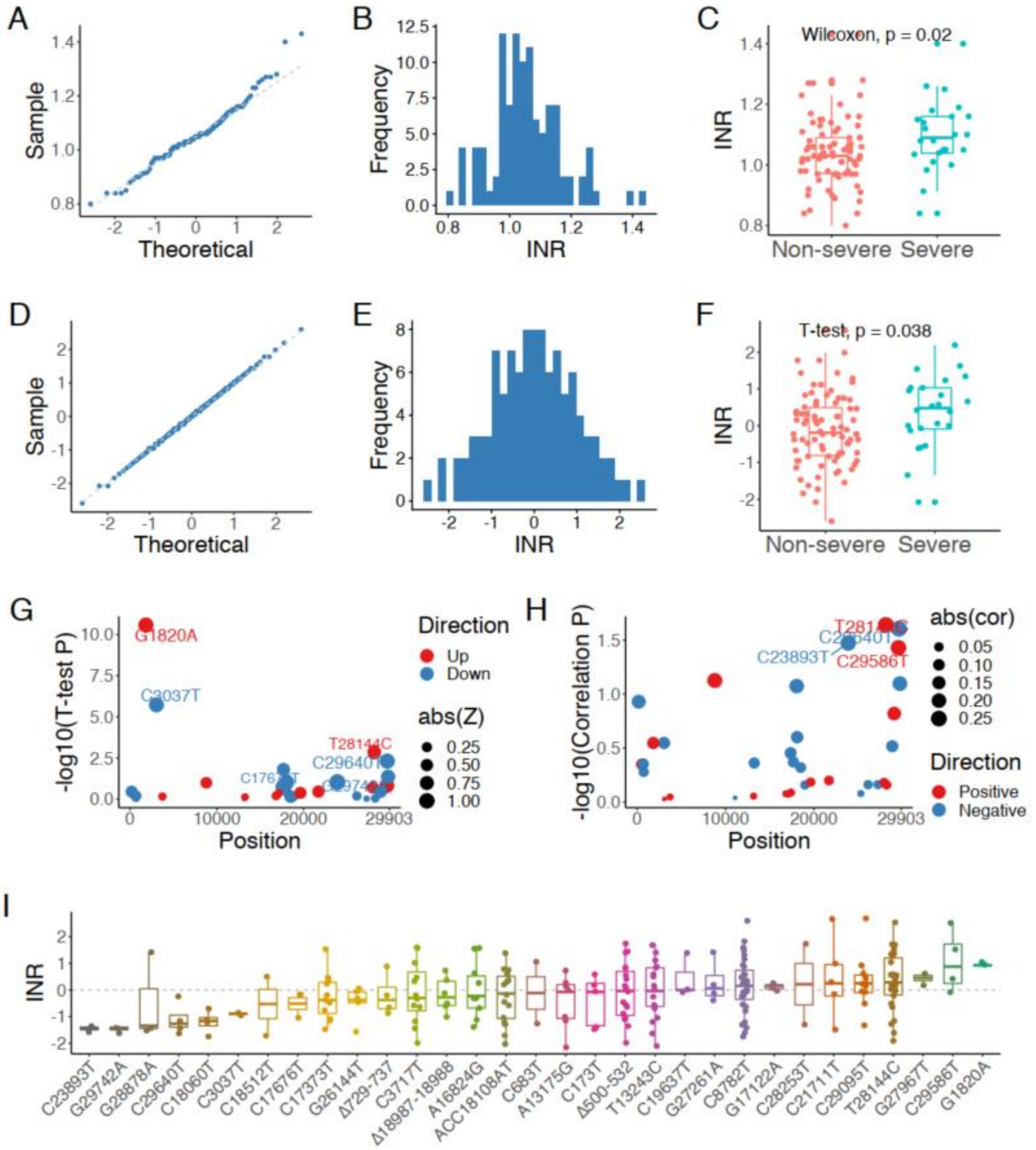
For IL-6 (interleukin 6, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-6 in the non-severe and severe COVID-19 patients before (**C**, p = 3.2×10^{-3}, Wilcoxon test) and after normalization (**F**, p = 3.6×10^{-3}, T-test). We further performed association analyses between the 35 genetic variants and IL-6 using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants G1820A, C23893T and C173T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IL-6, cases with G29742A and G28878A tend to have the highest Z score, whereas cases with C29586T and A16824G have the lowest.

73. IL-8 (interleukin 8)



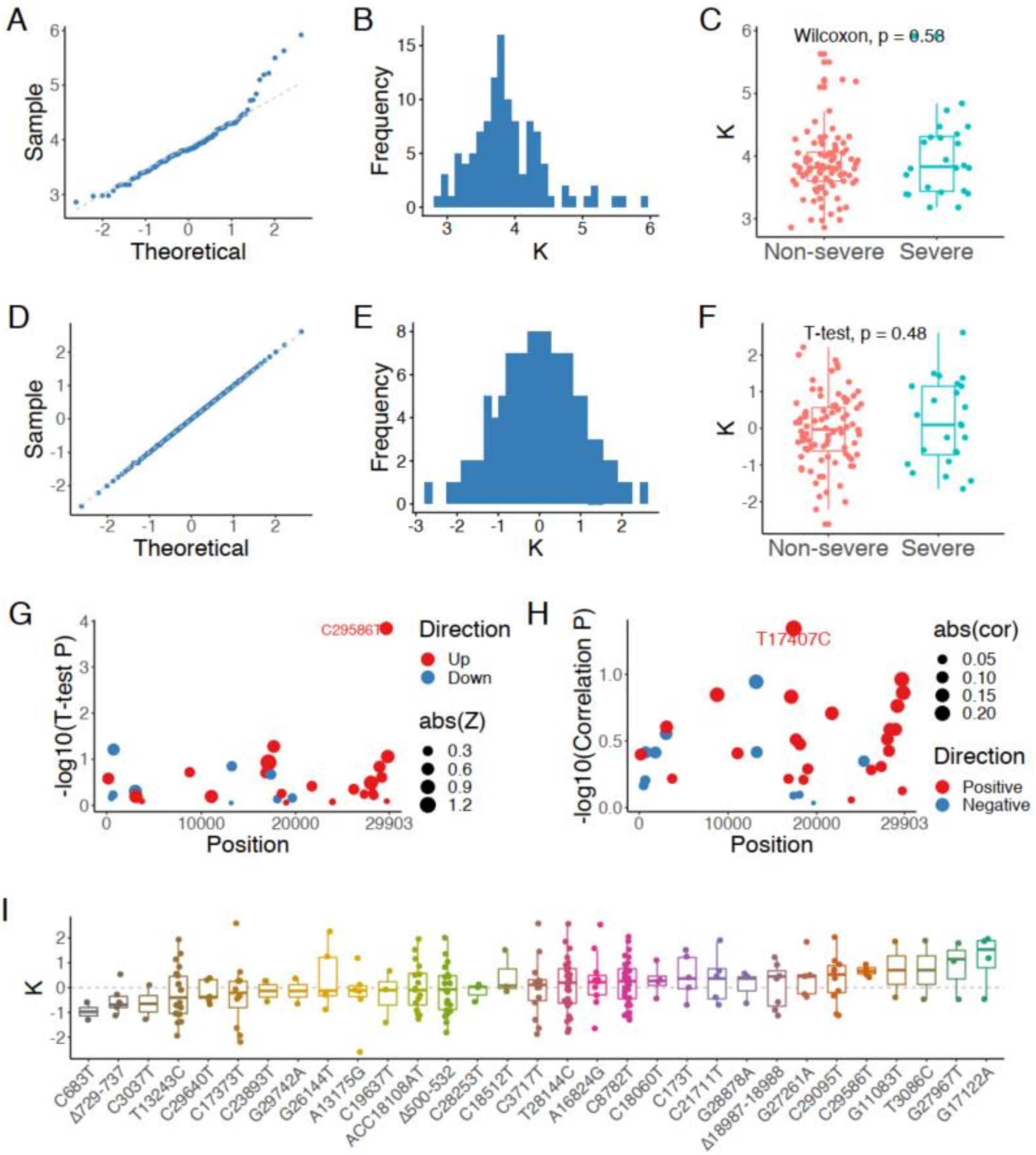
For IL-8 (interleukin 8, pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared IL-8 in the non-severe and severe COVID-19 patients before (**C**, p = 0.13, Wilcoxon test) and after normalization (**F**, p = 0.16, T-test). We further performed association analyses between the 35 genetic variants and IL-8 using T-test and Pearson correlation. (**G**) Variants ACC18108AT and G29742A pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants Δ500-532 and ACC18108AT have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of IL-8, cases with ACC18108AT and A13175G tend to have the highest Z score, whereas cases with C18060T and C29586T have the lowest.

74. INR (prothrombin time international normalized ratio)



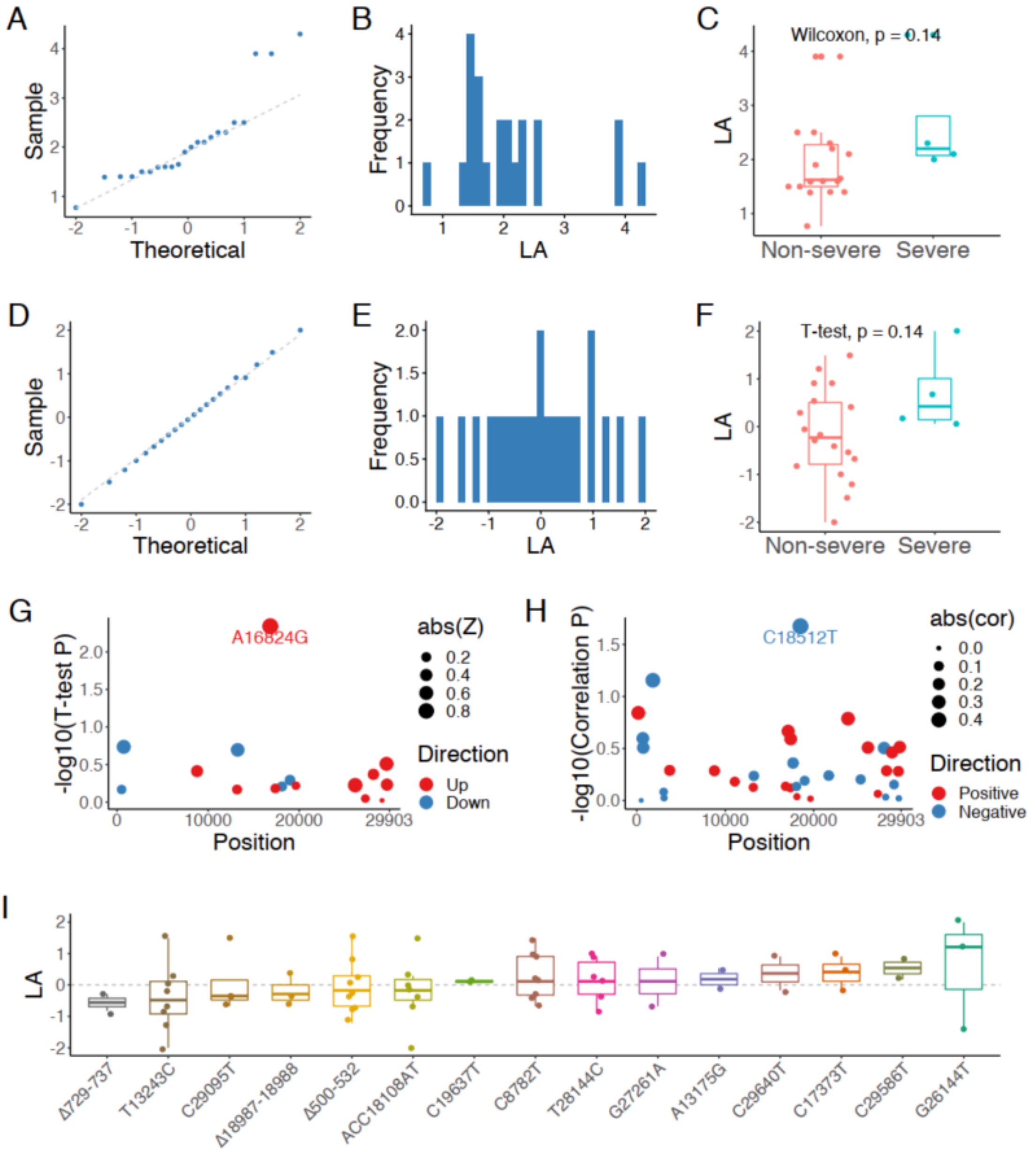
For INR (prothrombin time international normalized ratio), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared INR in the non-severe and severe COVID-19 patients before (**C**, p = 0.02, Wilcoxon test) and after normalization (F, p = 3.8×10^{-2}, T-test). (**G**) Variants C3037T, G1820A, C29640T, T28144C and G29743A pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C23893T and C29586T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of INR, cases with C29586T and G27967T tend to have the highest Z score, whereas cases with C23893T and G29742A have the lowest.

75. K$^+$ (serum potassium)



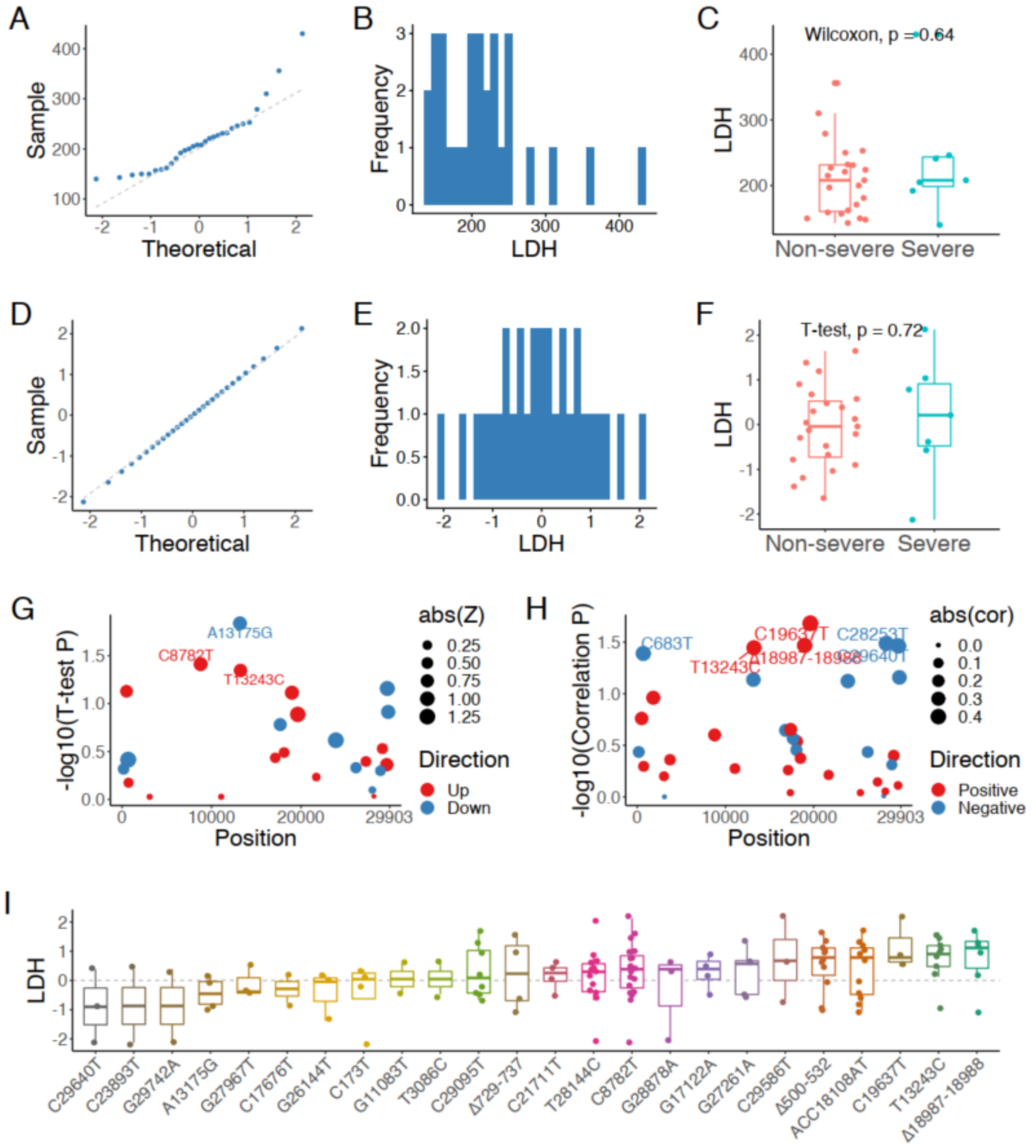
For K$^+$ (serum potassium, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared K in the non-severe and severe COVID-19 patients before (**C**, p = 0.53, Wilcoxon test) and after normalization (**F**, p = 0.48, T-test). We further performed association analyses between the 35 genetic variants and K using T-test and Pearson correlation. (**G**) Variant C29586T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant T17407C has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of K, cases with G17122A and G27967T tend to have the highest Z score, whereas cases with C683T and Δ729-737 have the lowest.

76. LA (lactic acid)



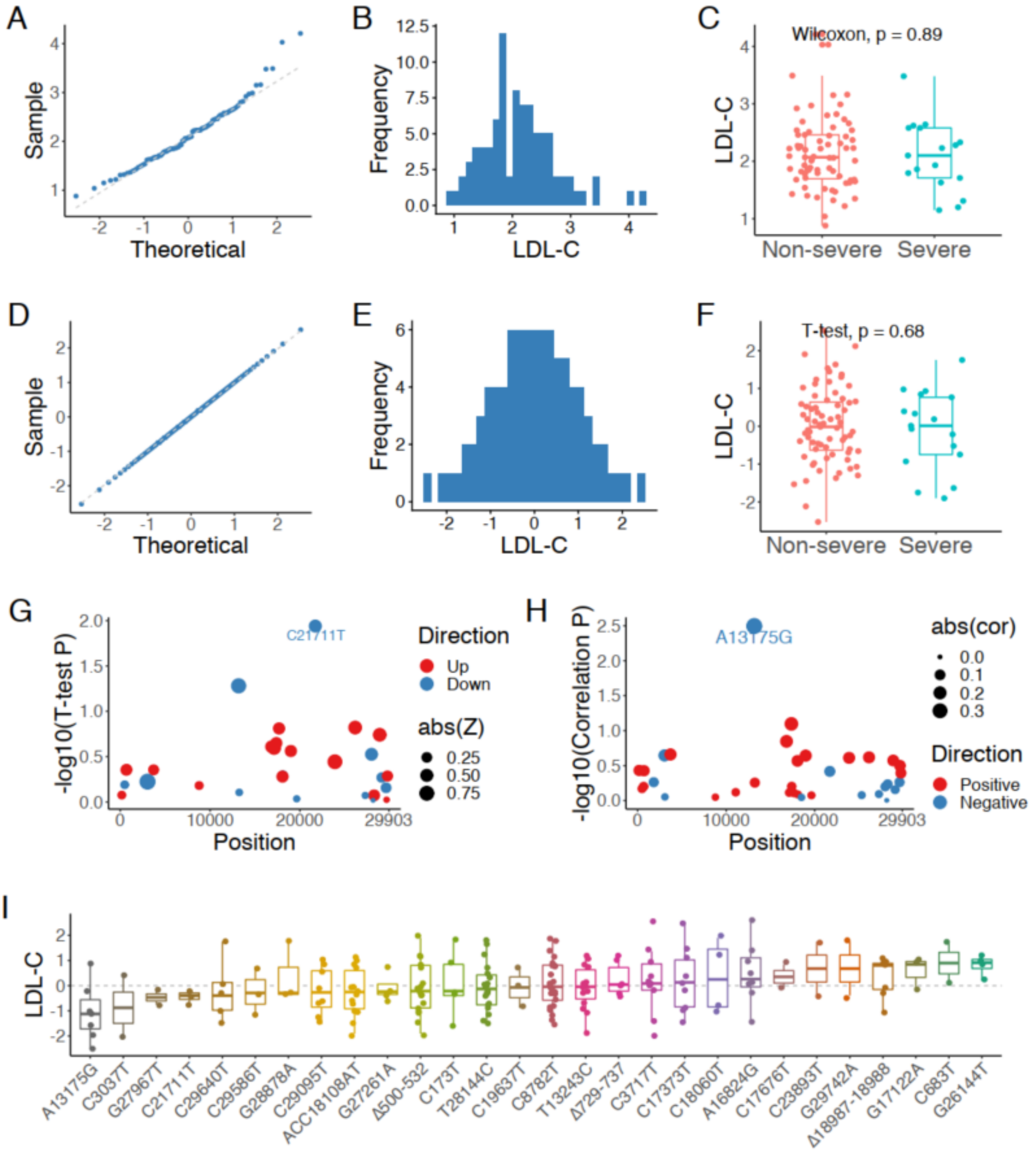
For LA (lactic acid, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared LA in the non-severe and severe COVID-19 patients before (**C**, p = 0.14, Wilcoxon test) and after normalization (**F**, p = 0.14, T-test). We further performed association analyses between the 35 genetic variants and LA using T-test and Pearson correlation. (**G**) Variant A16824G passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C18512T has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of LA, cases with G26144T and C29586T tend to have the highest Z score, whereas cases with Δ729-737 and T13243C have the lowest.

77. LDH (lactate dehydrogenase)



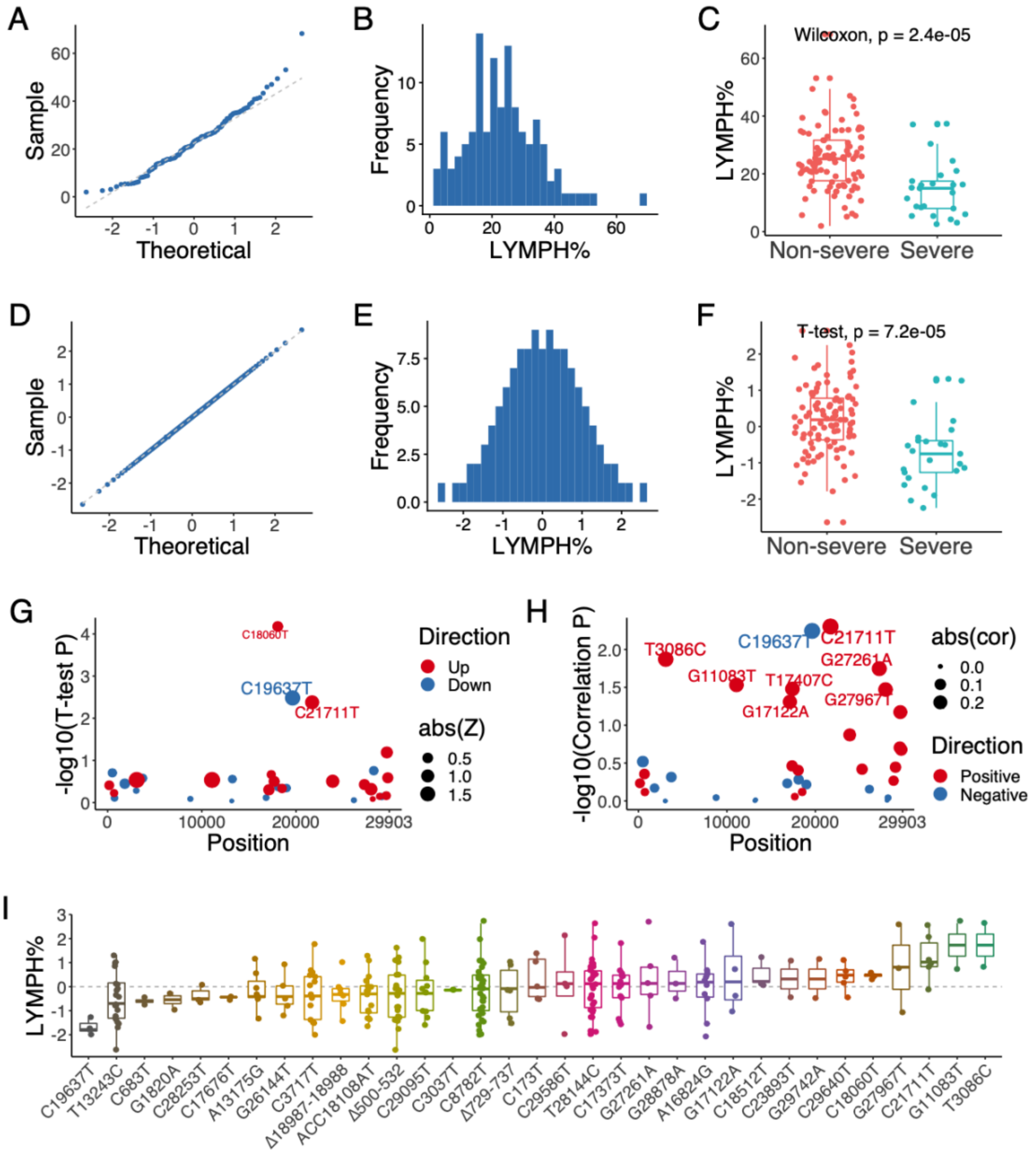
For LDH (lactate dehydrogenase, U/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared LDH in the non-severe and severe COVID-19 patients before (**C**, p = 0.64, Wilcoxon test) and after normalization (**F**, p = 0.72, T-test). We further performed association analyses between the 35 genetic variants and LDH using T-test and Pearson correlation. (**G**) Variants C8782T, T13243C and A13175G pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C683T, T13243C, Δ18987-18988, C19637T, C29640T and C28253T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of LDH, cases with Δ18987-18988 and T13243C tend to have the highest Z score, whereas cases with C29640T and C23893T have the lowest.

78. LDL-C (low-density lipoprotein cholesterol)



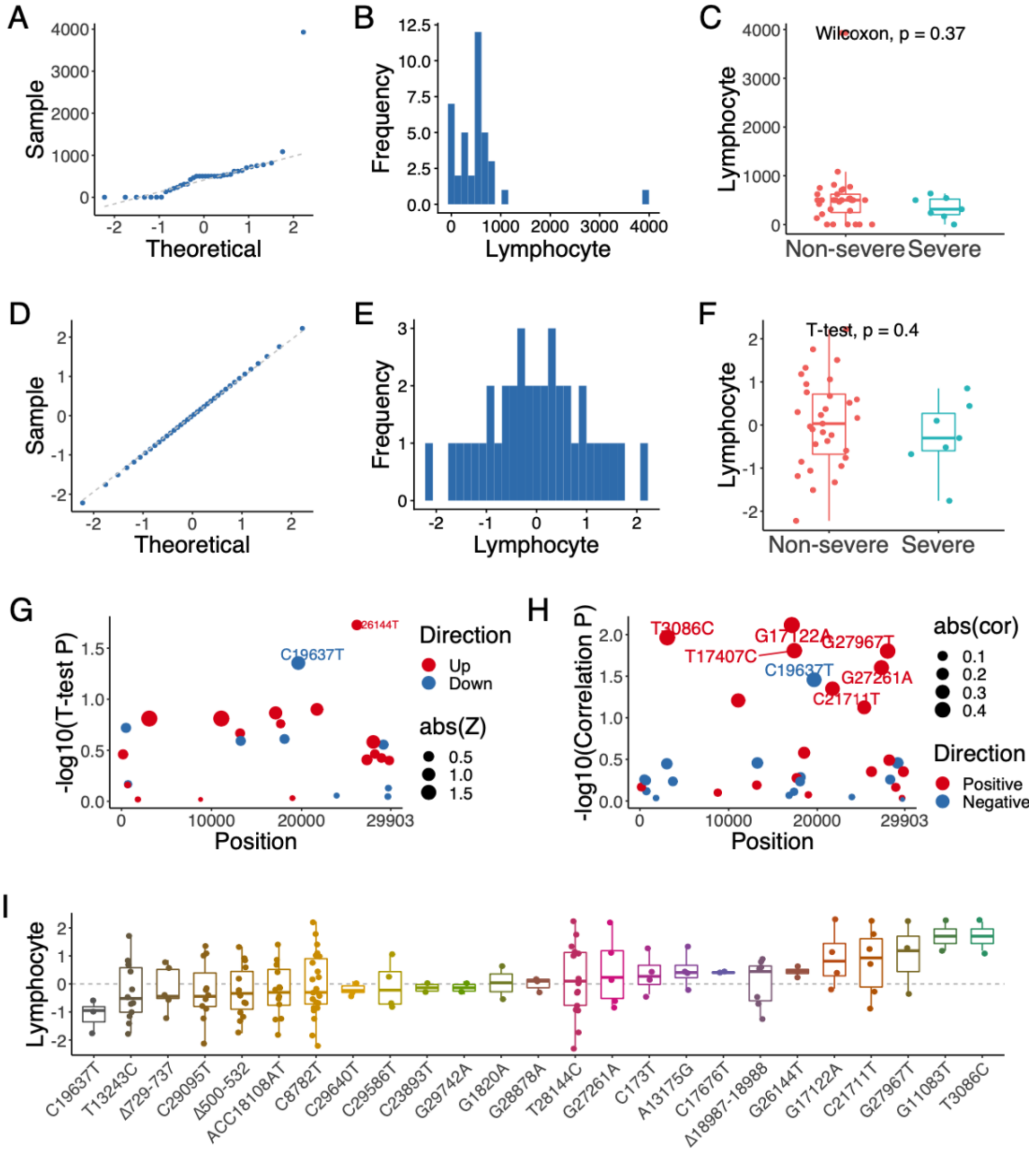
For LDL-C (low-density lipoprotein cholesterol, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared LDL-C in the non-severe and severe COVID-19 patients before (**C**, p = 0.89, Wilcoxon test) and after normalization (F, p = 0.68, T-test). (**G**) Variant C21711T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant A13175G has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of LDL-C, cases with G26144T and C683T tend to have the highest Z score, whereas cases with A13175G and C3037T have the lowest.

79. LYMPH % (lymphocyte percentage)



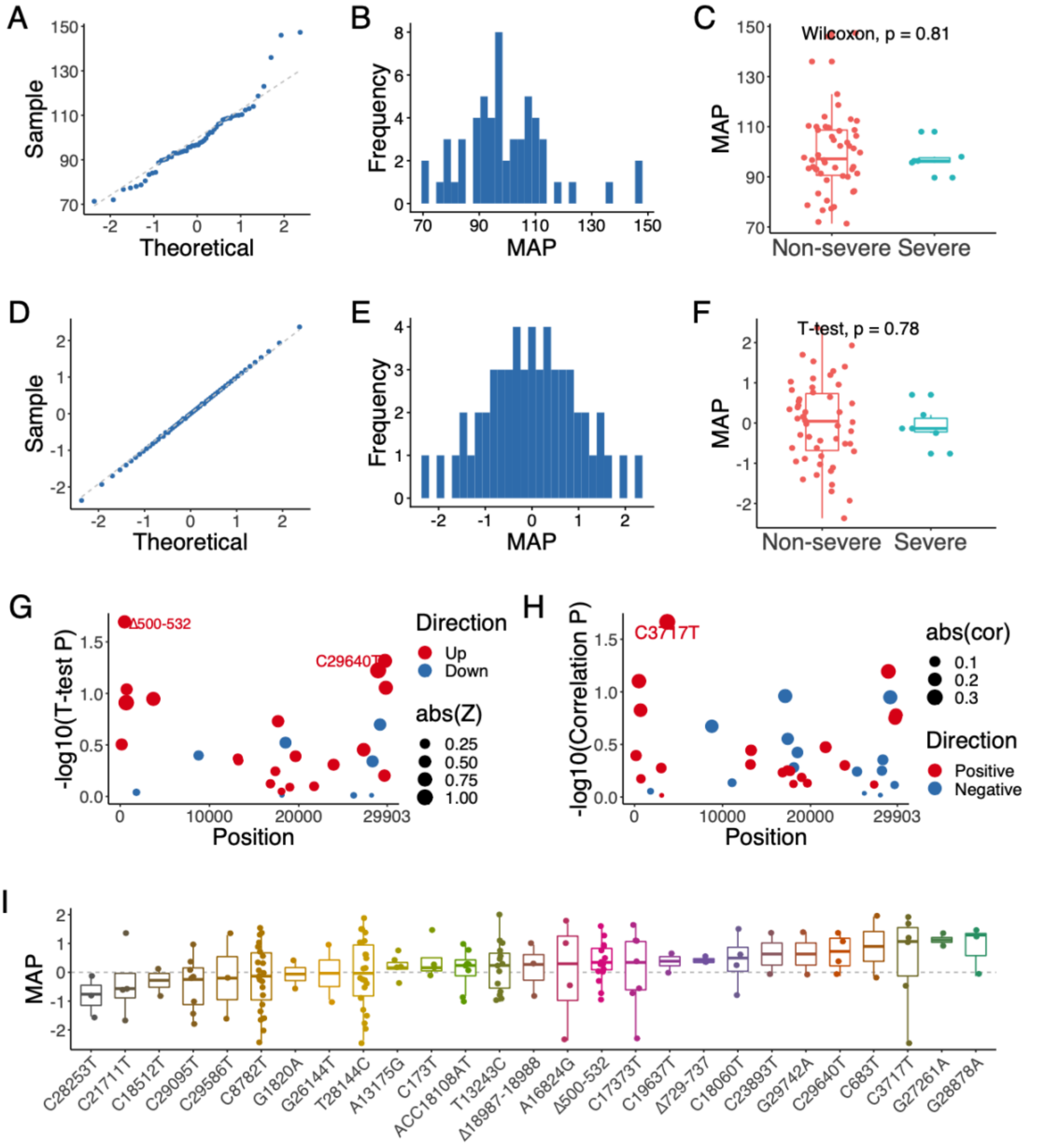
For LYMPH % (lymphocyte percentage), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared LYMPH % in the non-severe and severe COVID-19 patients before (**C**, $p = 2.4\times10^{-5}$, Wilcoxon test) and after normalization (**F**, $p = 7.2\times10^{-5}$, T-test). (**G**) Variants C19637T, C21711T and C18060T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T3086C, G11083T, C19637T, T17407C, G17122A, C21711T, G27261A and G27967T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of LYMPH %, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C19637T and T13243C have the lowest.

80. Lymphocyte (lymphocyte count)



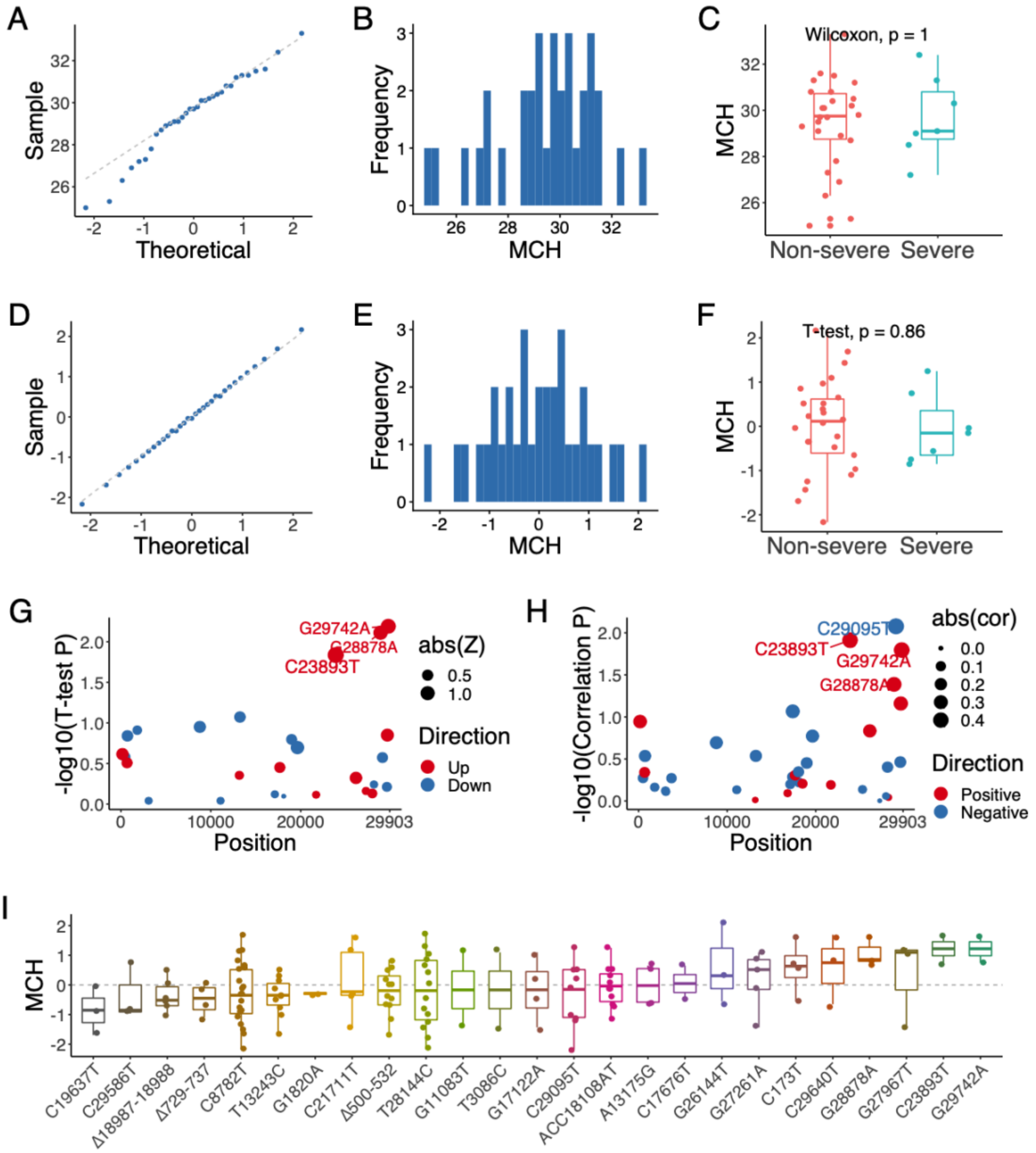
For lymphocyte (lymphocyte count, ×10^9/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared lymphocyte in the non-severe and severe COVID-19 patients before (**C**, p = 0.37, Wilcoxon test) and after normalization (F, p = 0.40, T-test). (**G**) Variants C19637T and G26144T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T3086C, G17122A, C19637T, T17407C, C21711T, G27967T and G27261A have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of lymphocyte, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C19637T and T13243C have the lowest.

81. MAP (mean arterial pressure)



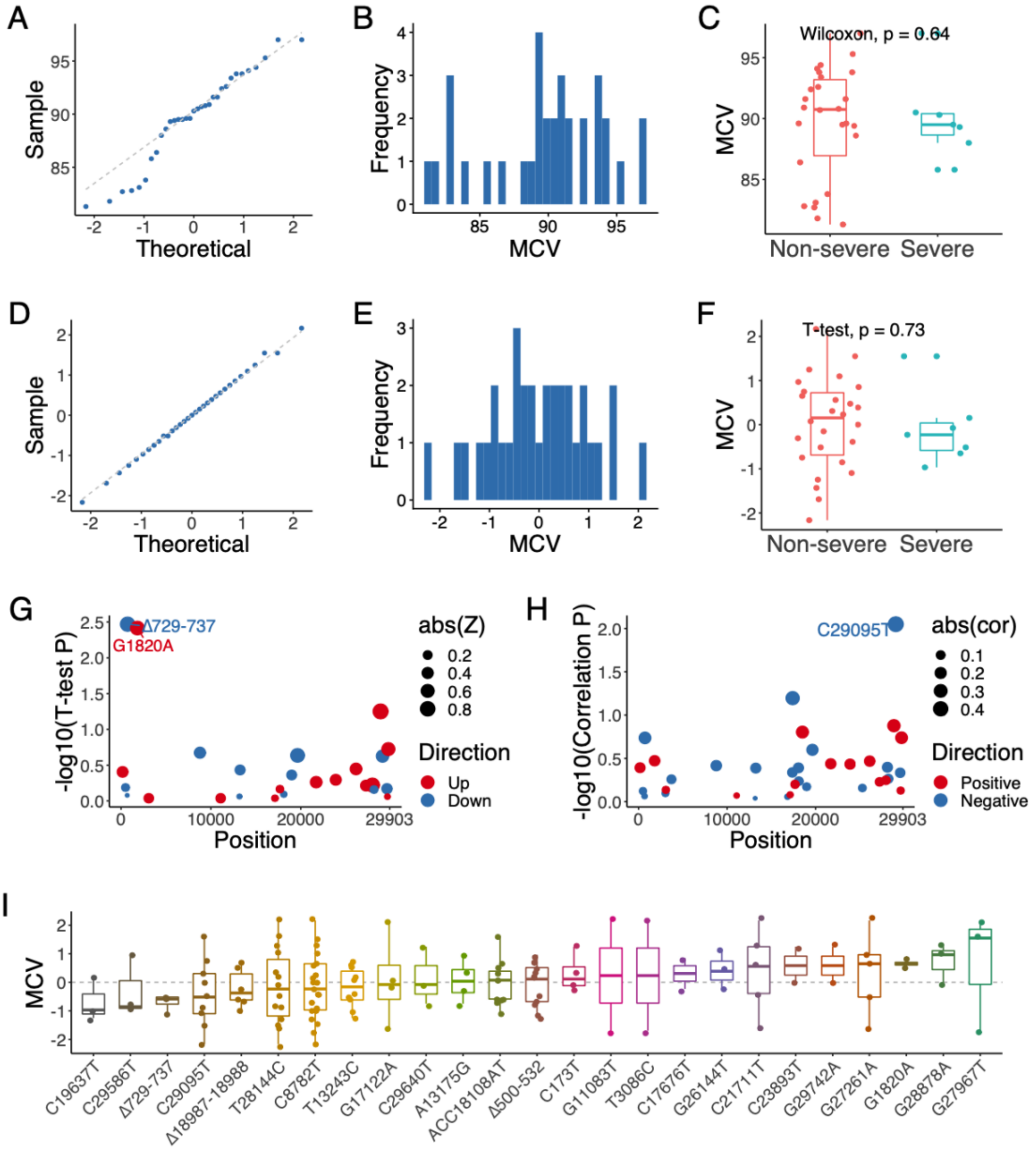
For MAP (mean arterial pressure, mmHg), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared MAP in the non-severe and severe COVID-19 patients before (**C**, p = 0.81, Wilcoxon test) and after normalization (**F**, p = 0.78, T-test). We further performed association analyses between the 35 genetic variants and MAP using T-test and Pearson correlation. (**G**) Variants Δ500-532 and C29640T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C3717T has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of MAP, cases with G28878A and G27261A tend to have the highest Z score, whereas cases with C28253T and C21711T have the lowest.

82. MCH (mean corpuscular hemoglobin)



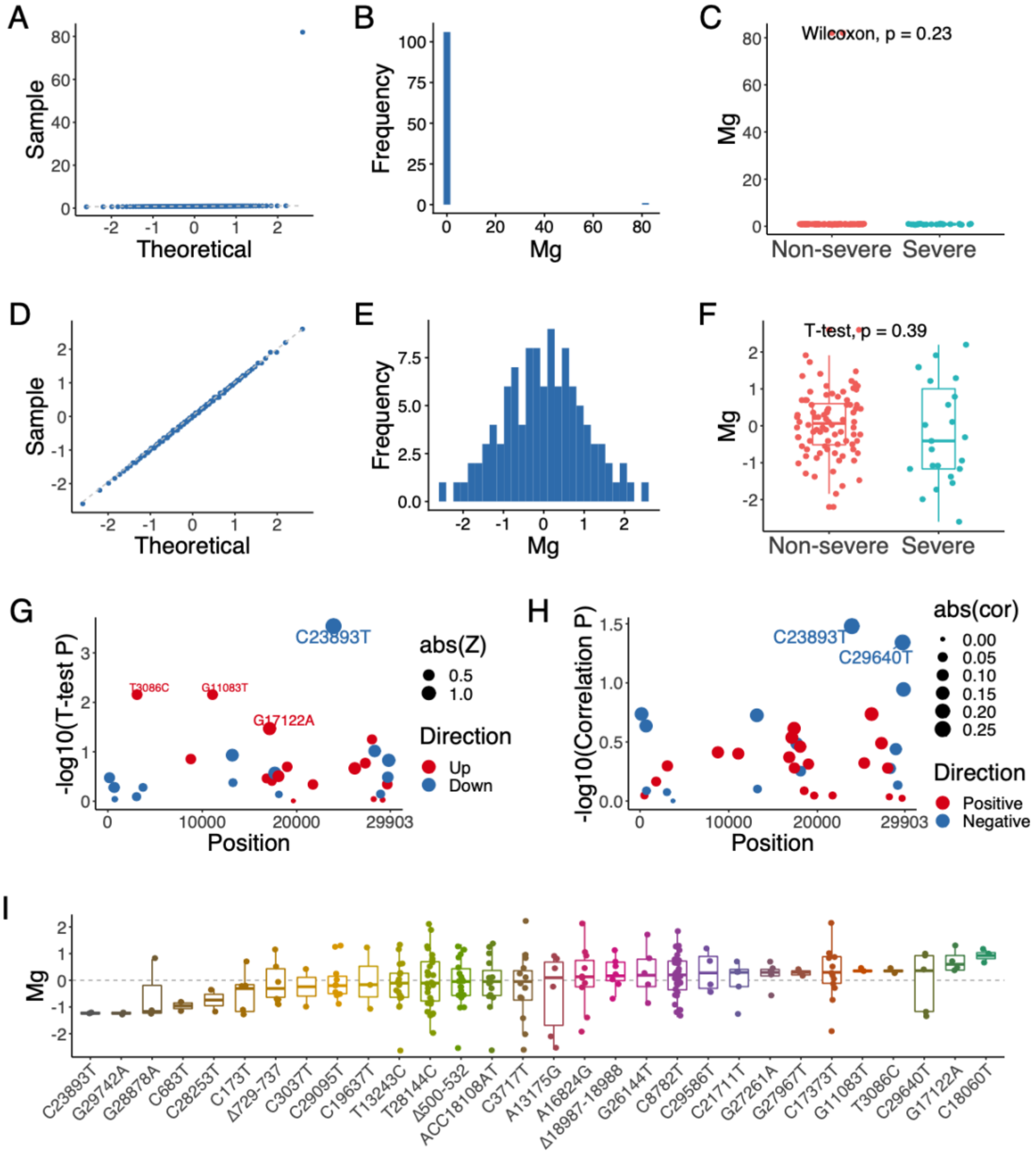
For MCH (mean corpuscular hemoglobin, pg/cell), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared MCH in the non-severe and severe COVID-19 patients before (**C**, p = 1.00, Wilcoxon test) and after normalization (F, p = 0.86, T-test). (**G**) Variants G29742A, C23893T and G28878A pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C23893T, C29095T, G29742A and G28878A have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of MCH, cases with G29742A and C23893T tend to have the highest Z score, whereas cases with C19637T and C29586T have the lowest.

83. MCV (mean corpuscular volume)



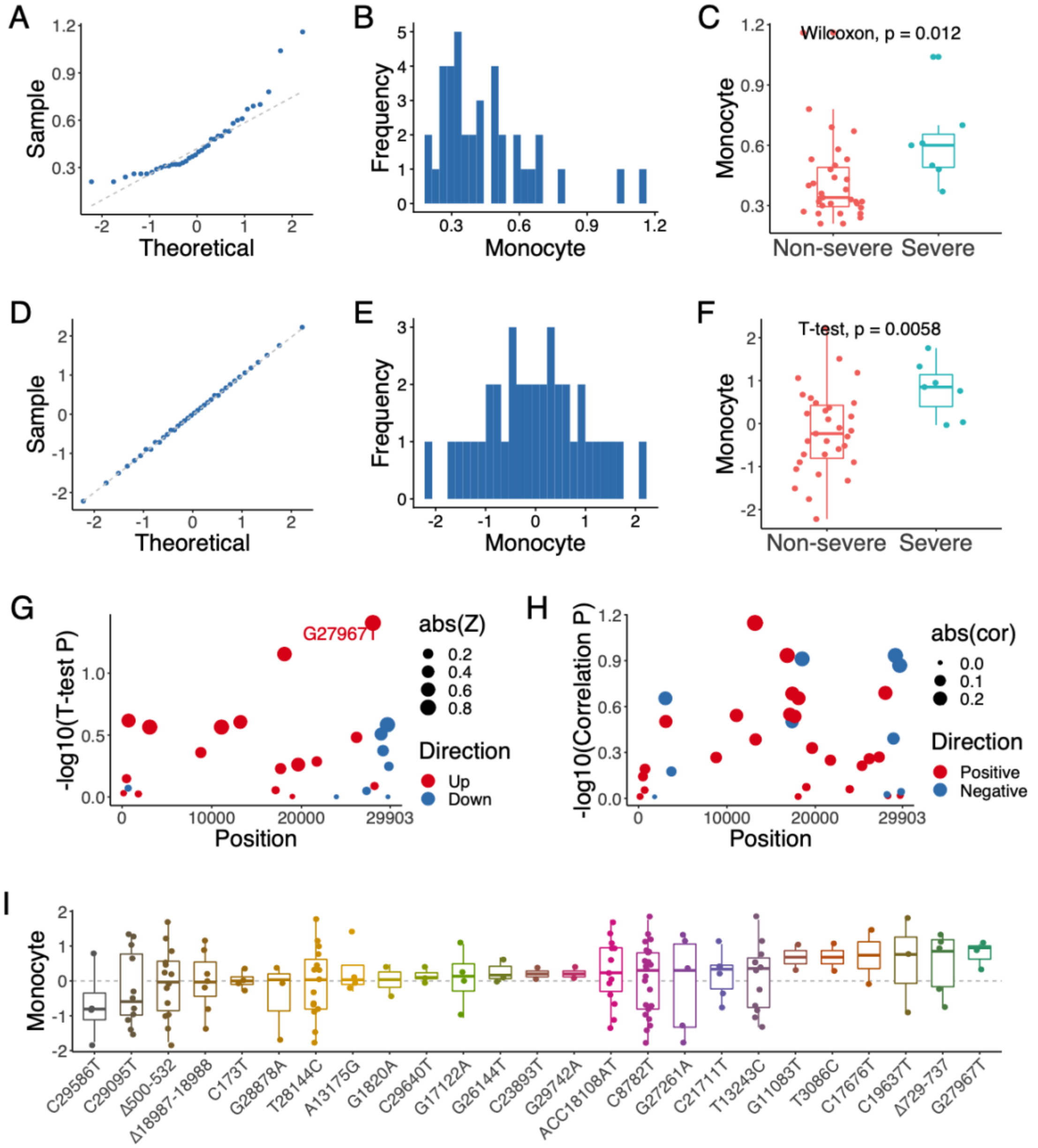
For MCV (mean corpuscular volume, fl), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared MCV in the non-severe and severe COVID-19 patients before (**C**, p = 0.64, Wilcoxon test) and after normalization (**F**, p = 0.73, T-test). We further performed association analyses between the 35 genetic variants and MCV using T-test and Pearson correlation. (**G**) Variants Δ729-737 and G1820A pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C29095T has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of MCV, cases with G27967T and G28878A tend to have the highest Z score, whereas cases with C19637T and C29586T have the lowest.

84. Mg^{2+} (serum magnesium)



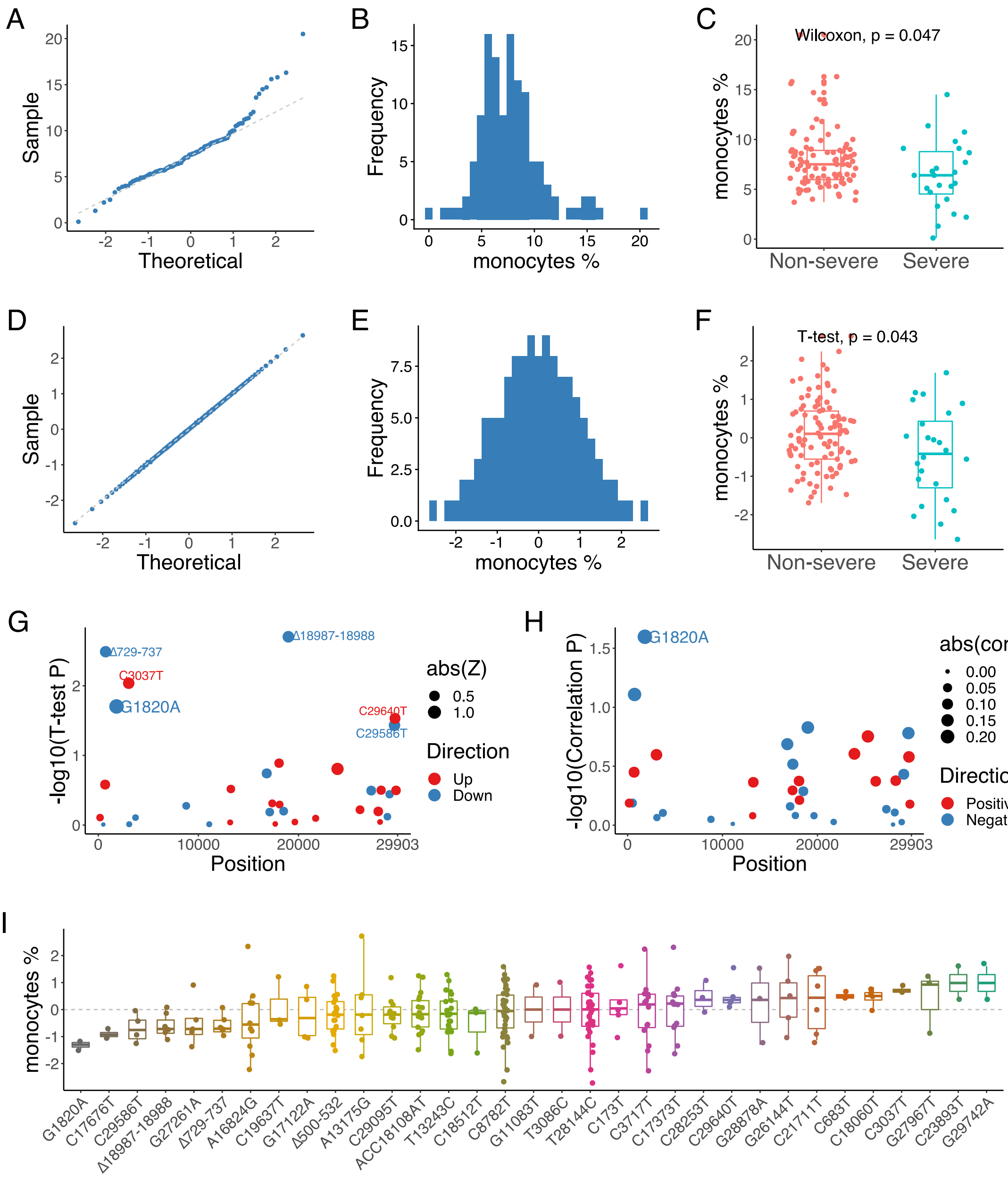
For Mg^{2+} (serum magnesium, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Mg in the non-severe and severe COVID-19 patients before (**C**, p = 0.23, Wilcoxon test) and after normalization (**F**, p = 0.39, T-test). We further performed association analyses between the 35 genetic variants and Mg using T-test and Pearson correlation. (**G**) Variants T3086C, G11083T, G17122A and C23893T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C23893T and C29640T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of Mg^{2+}, cases with C18060T and G17122A tend to have the highest Z score, whereas cases with C23893T and G29742A have the lowest.

85. Monocyte (monocyte count)



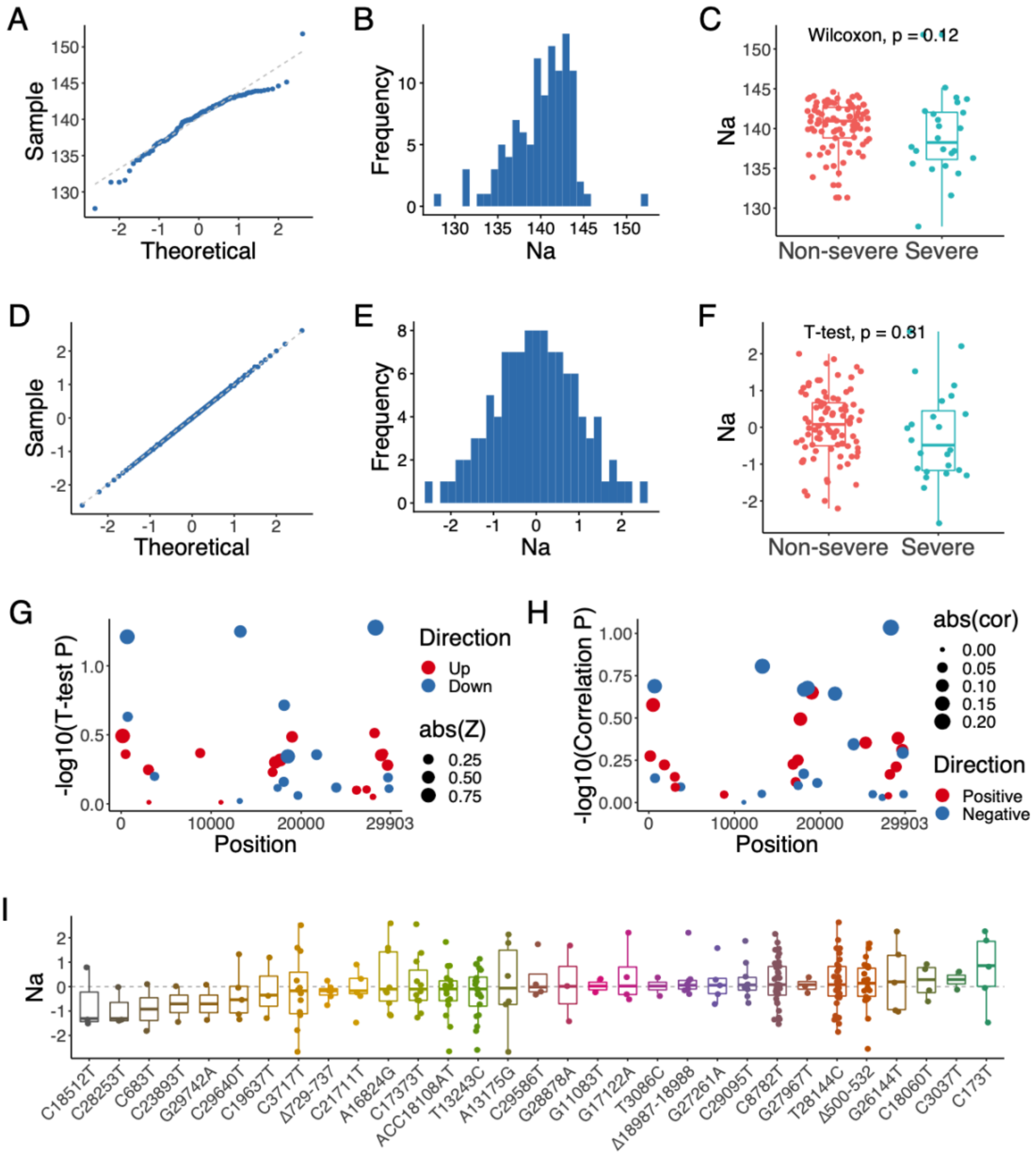
For monocyte (monocyte count, ×10^9/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared monocyte in the non-severe and severe COVID-19 patients before (**C**, $p = 1.2\times10^{-2}$, Wilcoxon test) and after normalization (**F**, $p = 5.8\times10^{-3}$, T-test). We further performed association analyses between the 35 genetic variants and monocyte using T-test and Pearson correlation. (**G**) Variant G27967T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) No variant in Pearson correlation was has P value below 0.05. After sorting Z score values of monocyte, cases with G27967T and Δ729-737 tend to have the highest Z score, whereas cases with C29586T and C29095T have the lowest.

86. Monocyte % (monocyte percentage)



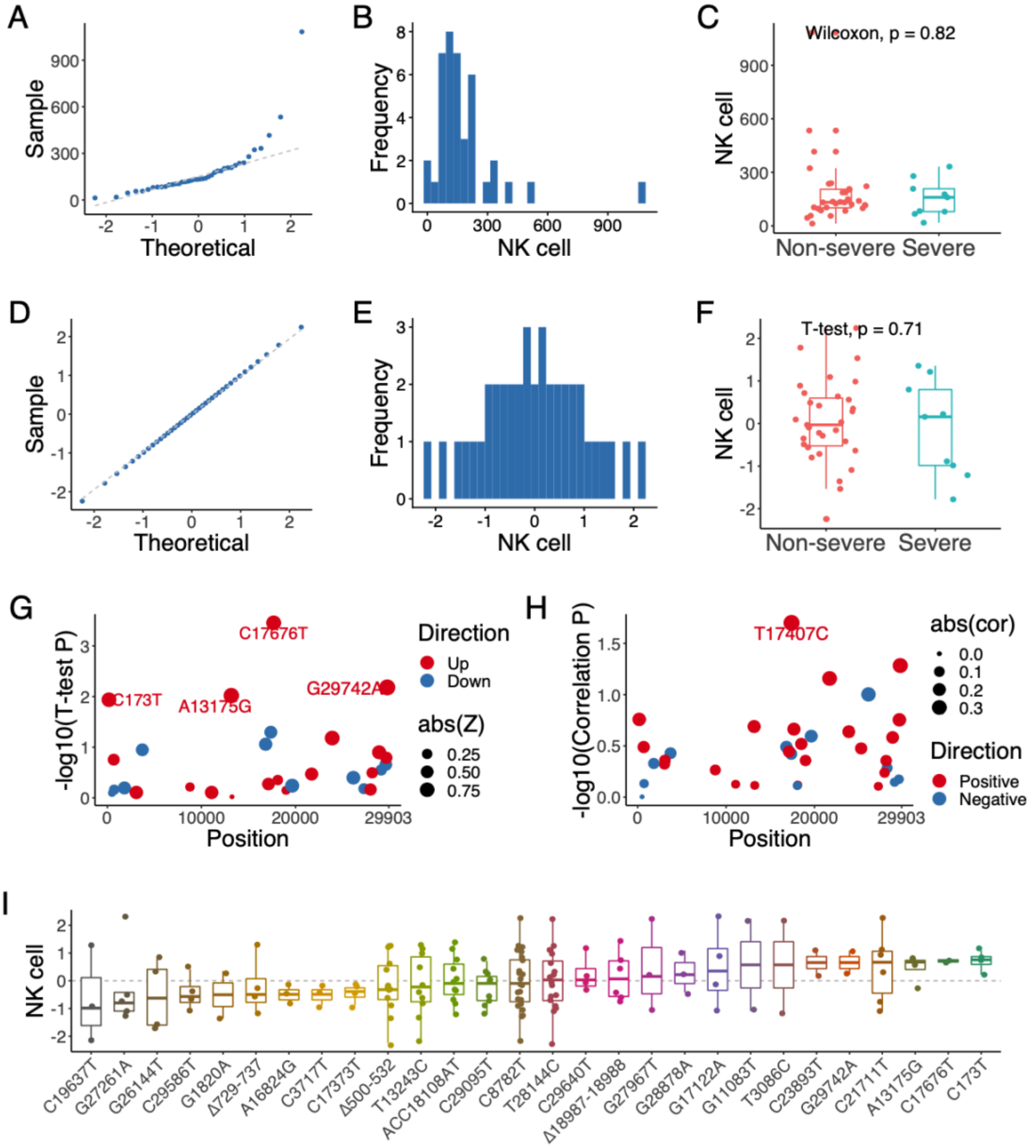
For Monocyte % (monocyte percentage), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Monocyte % in the non-severe and severe COVID-19 patients before (**C**, p = 0.047, Wilcoxon test) and after normalization (**F**, p = 0.043, T-test). (**G**) Variants Δ18987-18988, Δ729-737, C3037T, G1820A, C29640T and C29586T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants G1820A have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of Monocyte %, cases with G29742A and C23893T tend to have the highest Z score, whereas cases with G1820A and C17676T have the lowest.

87. Na^{+} (serum sodium)



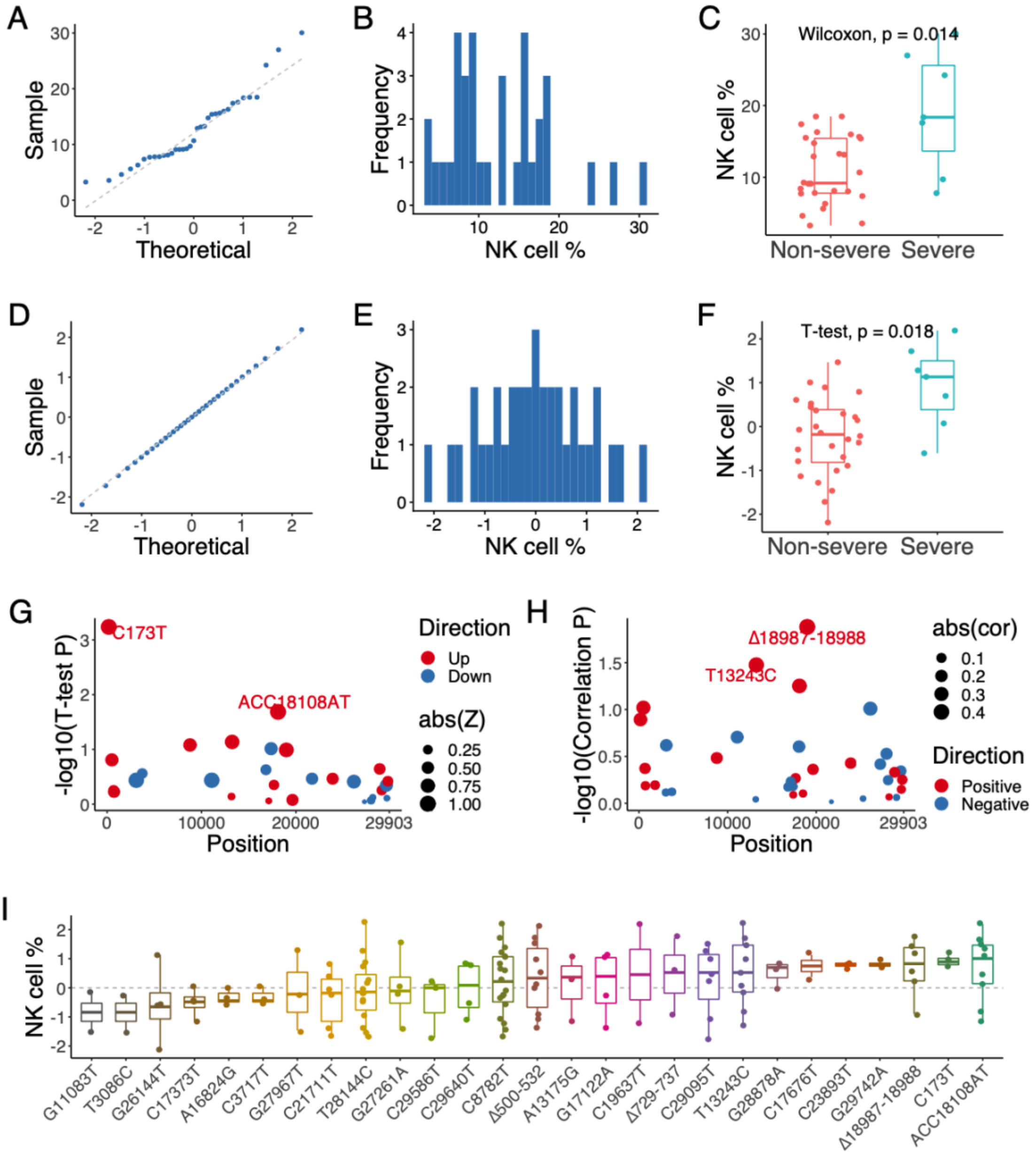
For Na^{+} (serum sodium, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared Na in the non-severe and severe COVID-19 patients before (**C**, p = 0.12, Wilcoxon test) and after normalization (**F**, p = 0.31, T-test). We further performed association analyses between the 35 genetic variants and Na using T-test and Pearson correlation. (**G**) No variant in the T test (**G**) and Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of Na, cases with C173T and C3037T tend to have the highest Z score, whereas cases with C18512T and C28253T have the lowest.

88. NK cell count



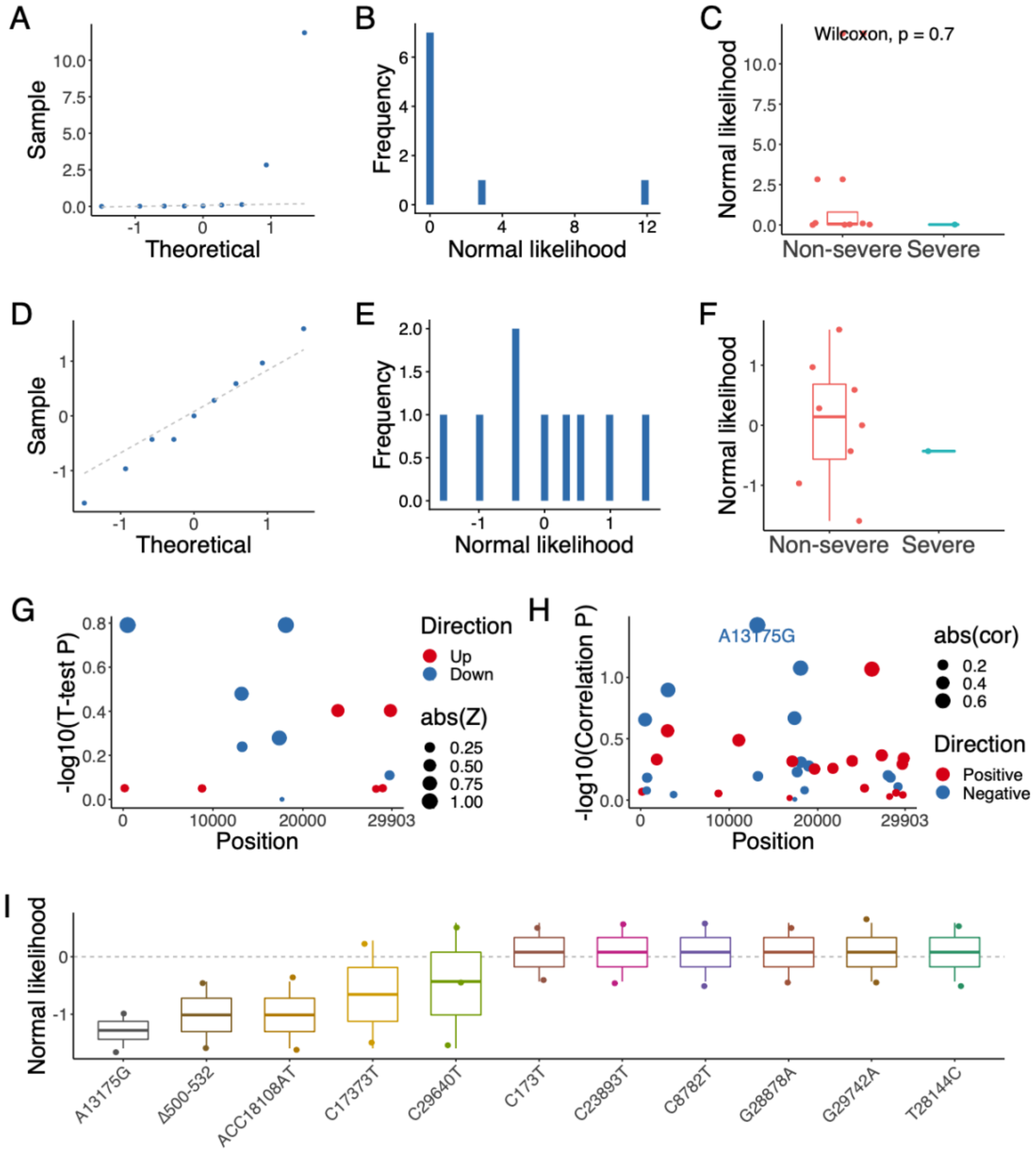
For NK cell count (cell/μl), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared NK cell in the non-severe and severe COVID-19 patients before (**C**, p = 0.82, Wilcoxon test) and after normalization (**F**, p = 0.71, T-test). We further performed association analyses between the 35 genetic variants and NK cell using T-test and Pearson correlation. (**G**) Variants C173T, A13175G, C17676T and G29742A pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant T17407C has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of NK cell, cases with C173T and C17676T tend to have the highest Z score, whereas cases with C19637T and G27261A have the lowest.

89. NK cell percentage



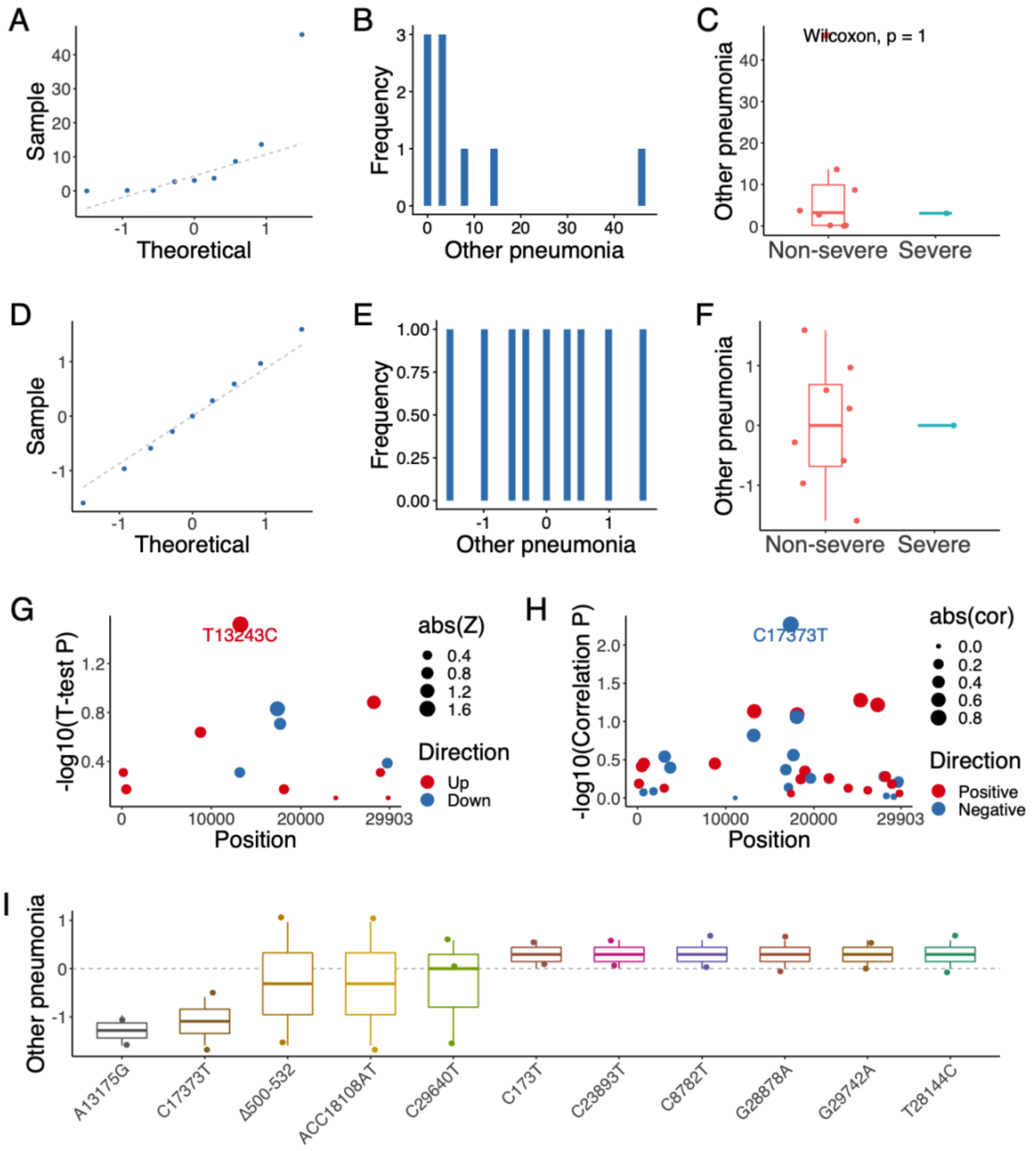
For NK cell % (NK cell percentage, %), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared NK cell % in the non-severe and severe COVID-19 patients before (**C**, p = 1.4×10^{-2}, Wilcoxon test) and after normalization (**F**, p = 1.8×10^{-2}, T-test). We further performed association analyses between the 35 genetic variants and NK cell % using T-test and Pearson correlation. (**G**) Variants C173T and ACC18108AT pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants Δ18987-18988 and T13243C have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of NK cell %, cases with C173T and ACC18108AT tend to have the highest Z score, whereas cases with G11083T and T3086C have the lowest.

90. Normal likelihood (diagnostic accuracy of normal)



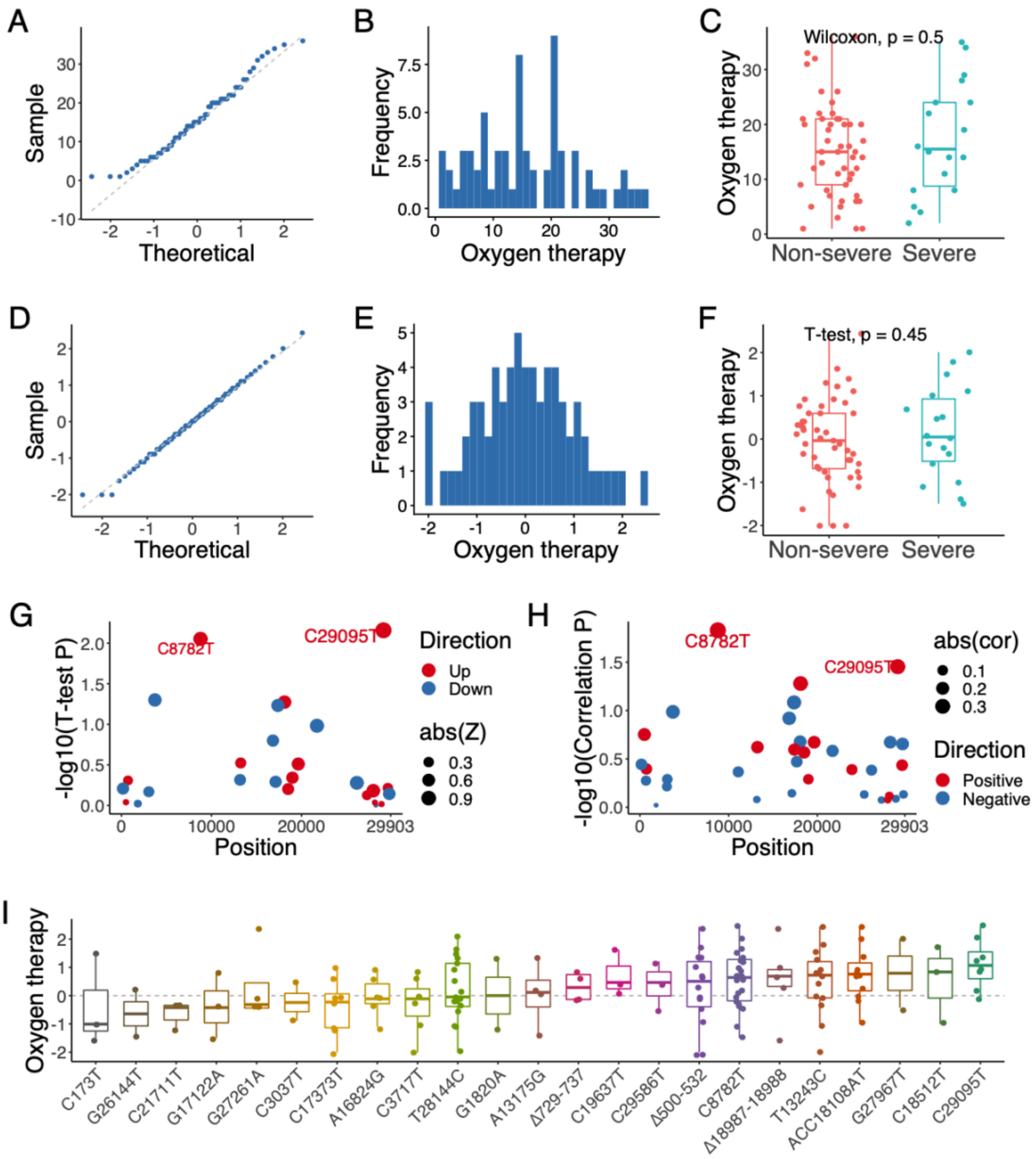
For normal likelihood (diagnostic accuracy of normal, %), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared normal likelihood in the non-severe and severe COVID-19 patients before (**C**, p = 0.7, Wilcoxon test) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and normal likelihood using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant A13175G in Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of normal likelihood, cases with T28144C and G29742A tend to have the highest Z score, whereas cases with A13175G and Δ500-532 have the lowest.

91. Other pneumonia



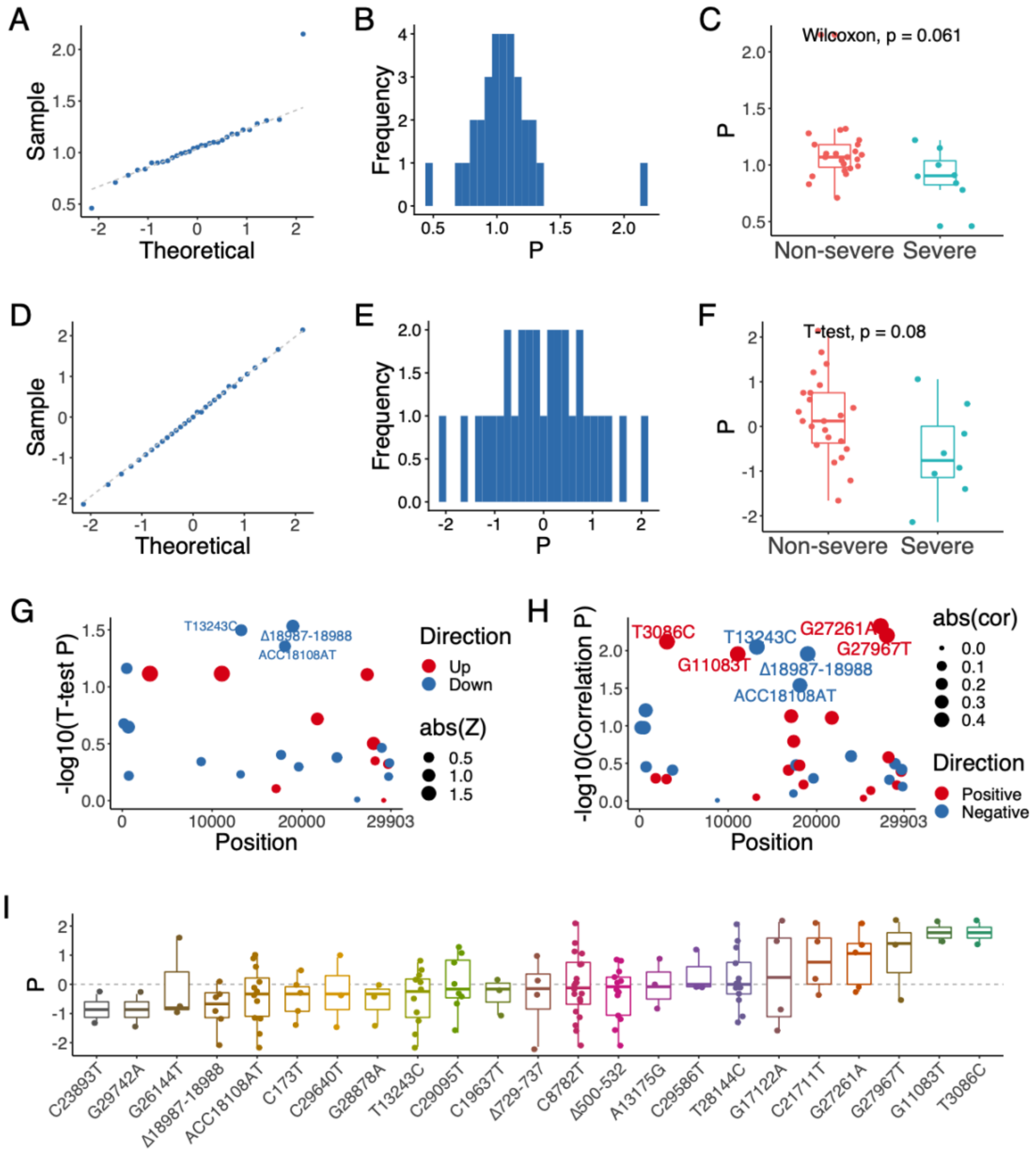
For other pneumonia (%), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared other pneumonia in the non-severe and severe COVID-19 patients before (**C**, p = 1, Wilcoxon test) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and other pneumonia using T-test and Pearson correlation. (**G**) Variant T13243C passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C17373T has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of other pneumonia, cases with T28144C and G29742A tend to have the highest Z score, whereas cases with A13175G and C17373T have the lowest.

92. Oxygen therapy



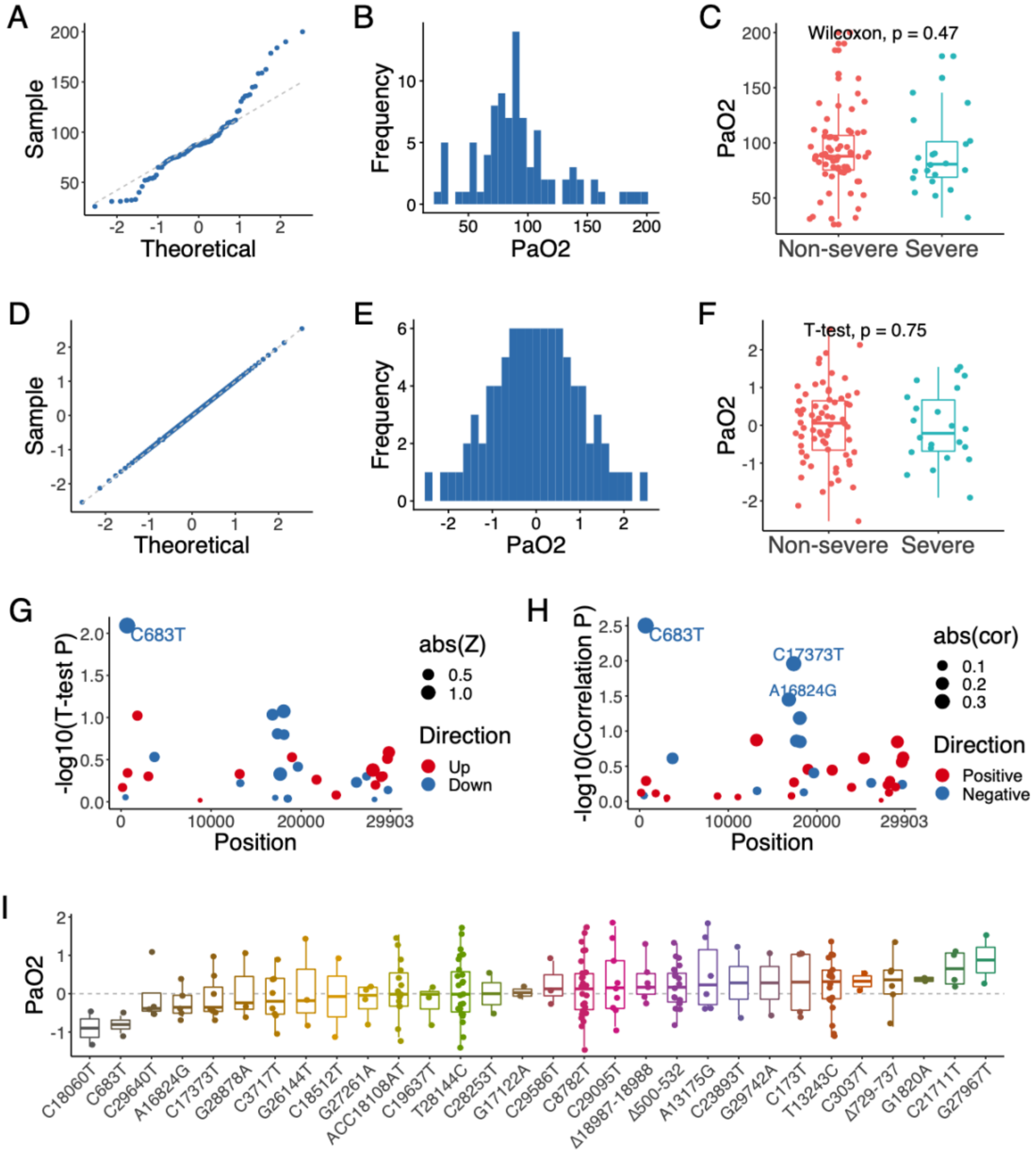
For oxygen therapy (day), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared oxygen therapy in the non-severe and severe COVID-19 patients before (**C**, p = 0.50, Wilcoxon test) and after normalization (**F**, p = 0.45, T-test). We further performed association analyses between the 35 genetic variants and oxygen therapy using T-test and Pearson correlation. (**G**) Variants C8782T and C29095T in the T test (**G**) and Pearson correlation were both with P value below 0.05 (**H**). After sorting Z score values of oxygen therapy, cases with C29095T and C18512T tend to have the highest Z score, whereas cases with C173T and G26144T have the lowest.

93. P (serum phosphorus)



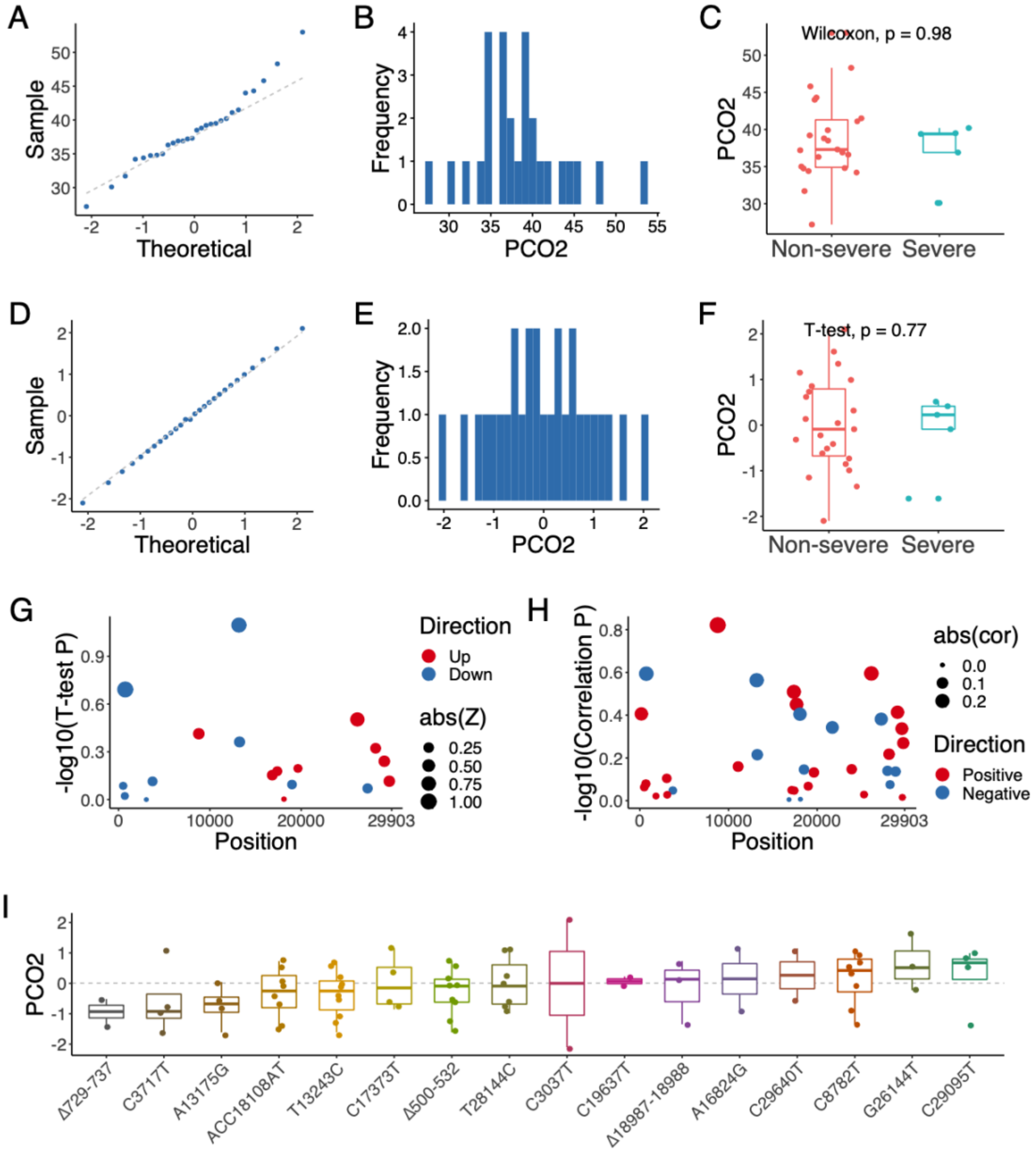
For P (serum phosphorus, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared P in the non-severe and severe COVID-19 patients before (**C**, p = 0.061, Wilcoxon test) and after normalization (**F**, p = 0.08, T-test). (**G**) Variants T13243C, Δ18987-18988 and ACC18108AT pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T3086C, G11083T, G27261A, G27967T, T13243C, ACC18108AT and Δ18987-18988 have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of P, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C23893T and G29742A have the lowest.

94. PaO_2 (partial pressure of oxygen)



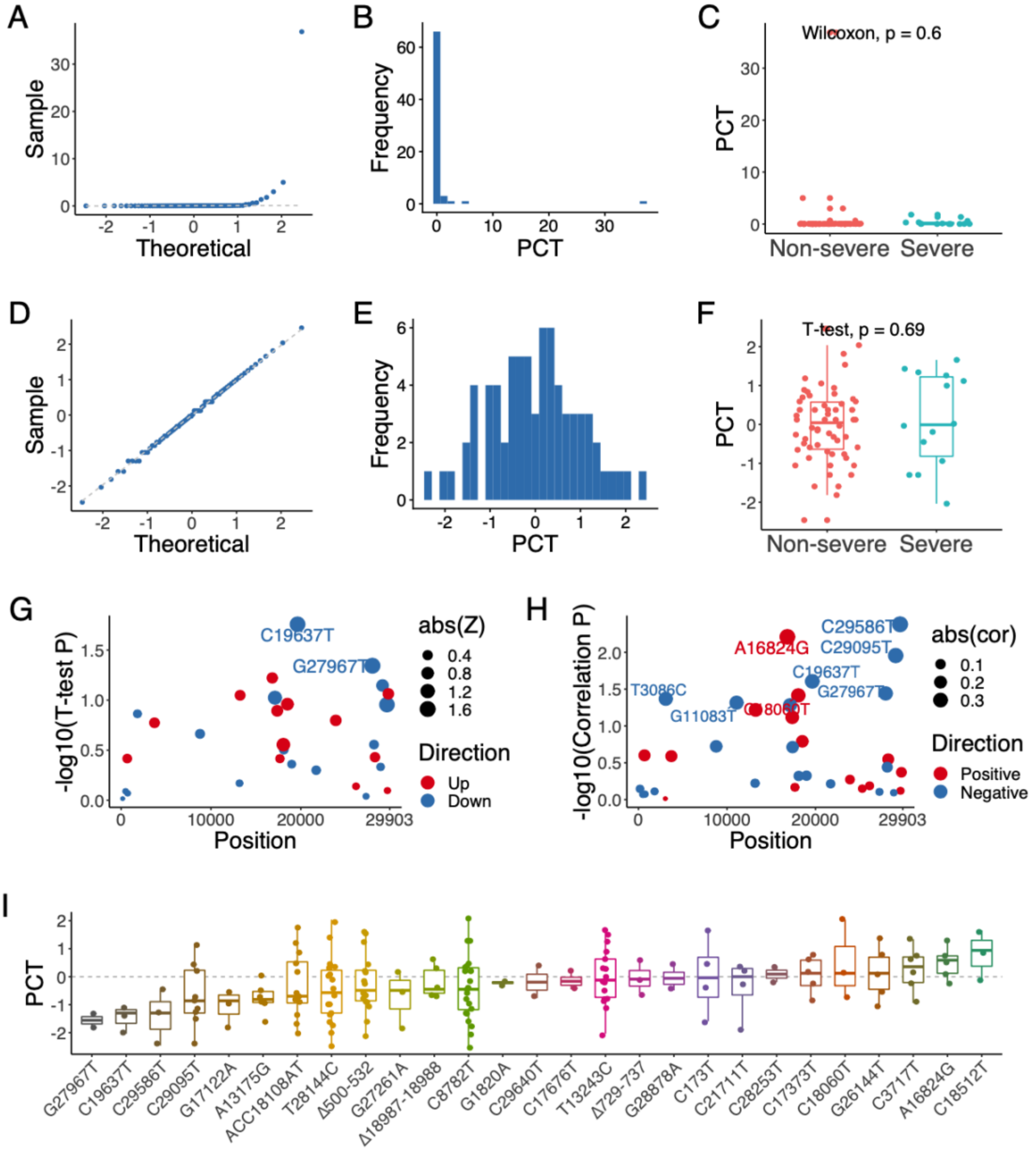
For PaO_2 (partial pressure of oxygen, mmHg), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared PaO_2 in the non-severe and severe COVID-19 patients before (**C**, p =0.47, Wilcoxon test) and after normalization (**F**, p =0.75, T-test). We further performed association analyses between the 35 genetic variants and PaO_2 using T-test and Pearson correlation. (**G**) Variant C683T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C683T, C17373T and A16824G have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of PaO_2, cases with C21711T and G27967T tend to have the highest Z score, whereas cases with C18060T and C683T have the lowest.

95. PCO_2 (partial pressure of carbon dioxide)



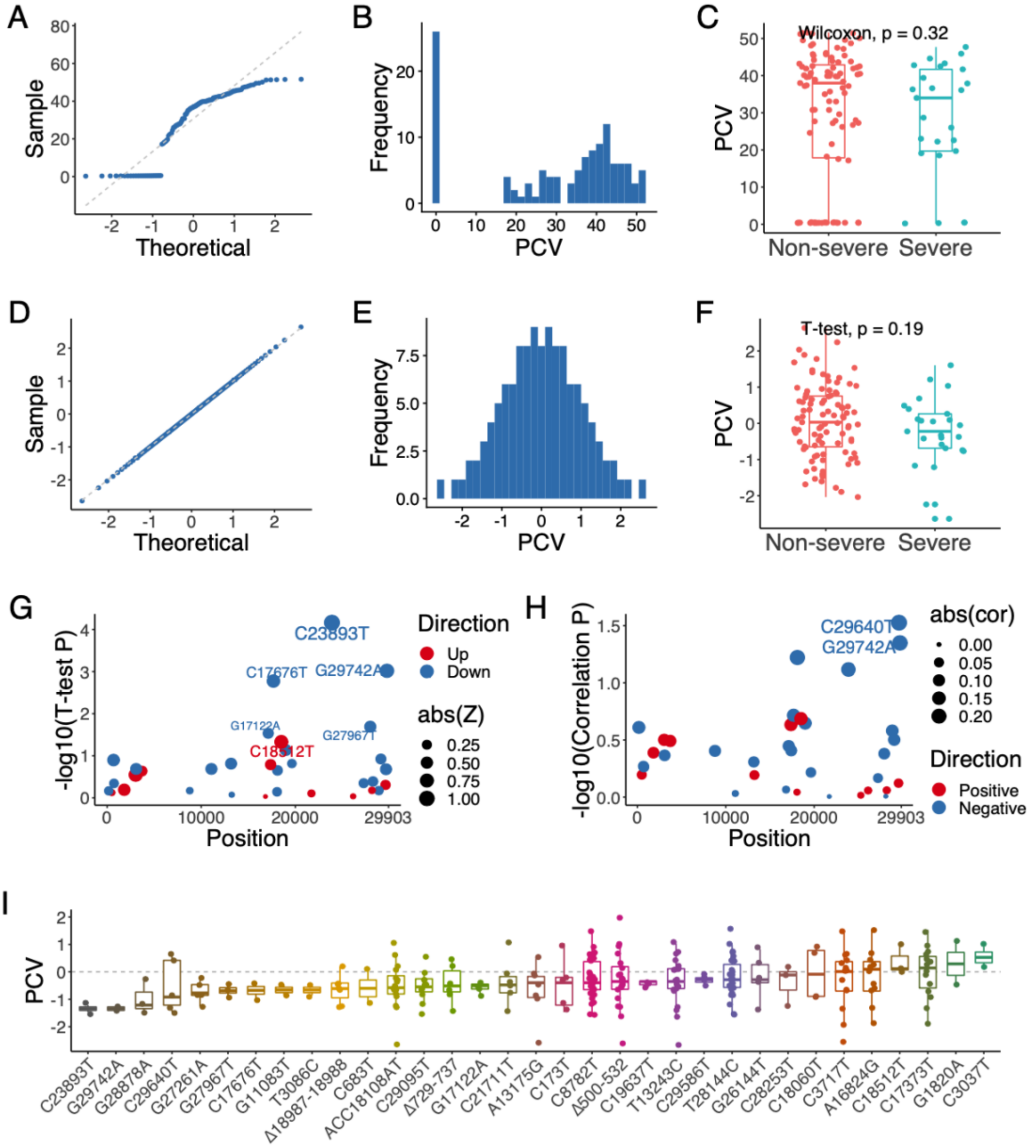
For PCO_2 (partial pressure of carbon dioxide, mmHg), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared PCO_2 in the non-severe and severe COVID-19 patients before (**C**, p =0.98, Wilcoxon test) and after normalization (**F**, p = 0.77, T-test). We further performed association analyses between the 35 genetic variants and PCO_2 using T-test and Pearson correlation. No variant passes P value cut-off of 0.05 in T test (**G**) or exceeds correlation P value cut-off of 0.05 (**H**). (**I**) After sorting Z score values of PCO_2, cases with C29095T and G26144T tend to have the highest Z score, whereas cases with Δ729-737 and C3717T have the lowest.

96. PCT (procalcitonin)



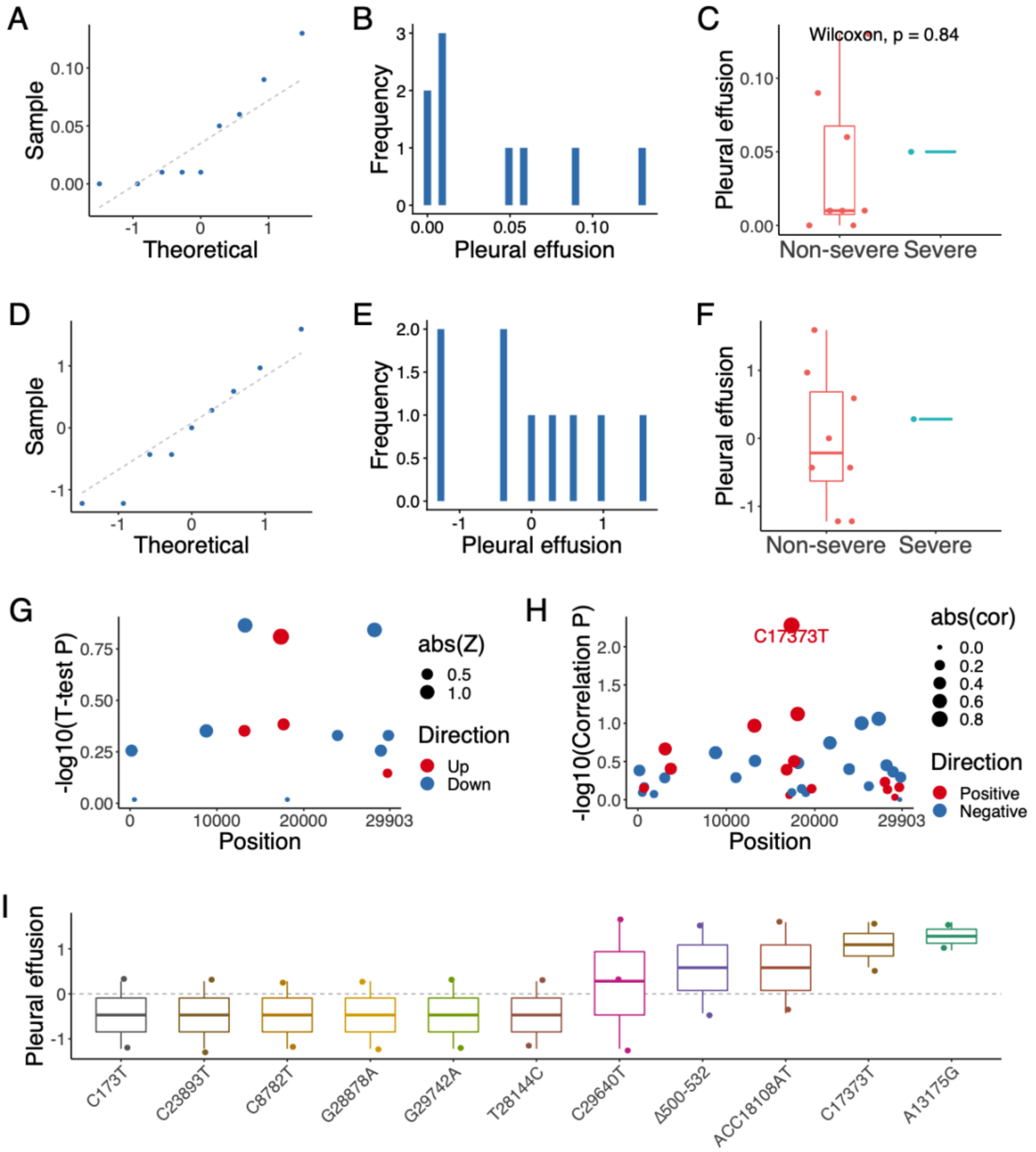
For PCT (procalcitonin, ng/mL), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared PCT in the non-severe and severe COVID-19 patients before (**C**, p = 0.60, Wilcoxon test) and after normalization (**F**, p = 0.69, T-test). We further performed association analyses between the 35 genetic variants and PCT using T-test and Pearson correlation. (**G**) Variants C19637T and G27967T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C18060T, T3086C, G11083T, A16824G, C29586T, C29095T, C19627T and G27967T in Pearson correlation were with PCT value below 0.05 (**H**). After sorting Z score values of PCT, cases with C18512T and A16824G tend to have the highest Z score, whereas cases with G27967T and C19637T have the lowest.

97. PCV (packed cell volume)



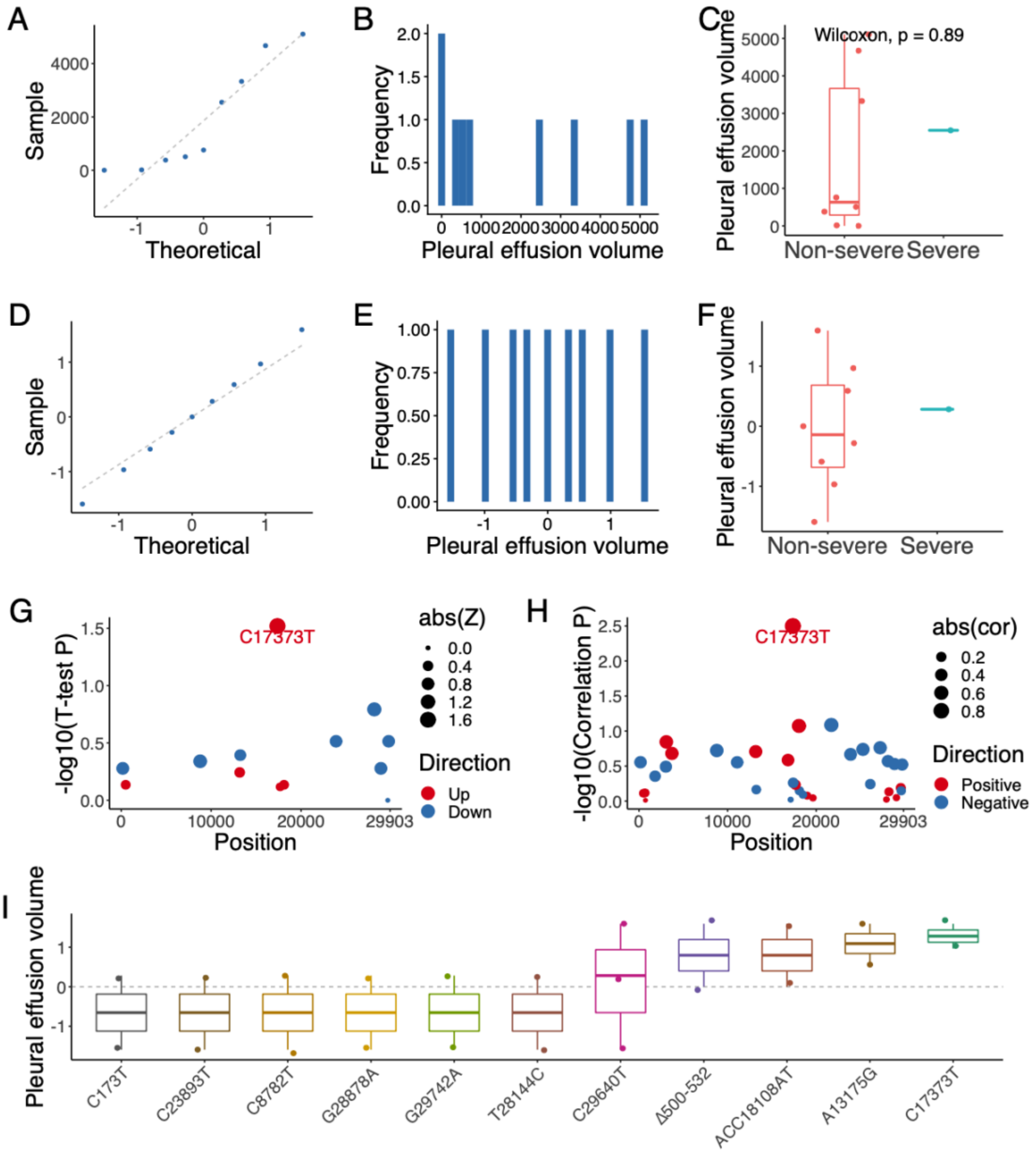
For PCV (packed cell volume, %), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared PCV in the non-severe and severe COVID-19 patients before (**C**, p = 0.32, Wilcoxon test) and after normalization (**F**, p = 0.19, T-test). We further performed association analyses between the 35 genetic variants and PCV using T-test and Pearson correlation. (**G**) Variants C23893T, C17676T, G29742A, G17122A, G27967T and C18512T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C29640T and G29742A in Pearson correlation were with PCV value below 0.05 (**H**). After sorting Z score values of PCV, cases with C3037T and G1820A tend to have the highest Z score, whereas cases with C23893T and G29742A have the lowest.

98. Pleural effusion (interstitium thickness)



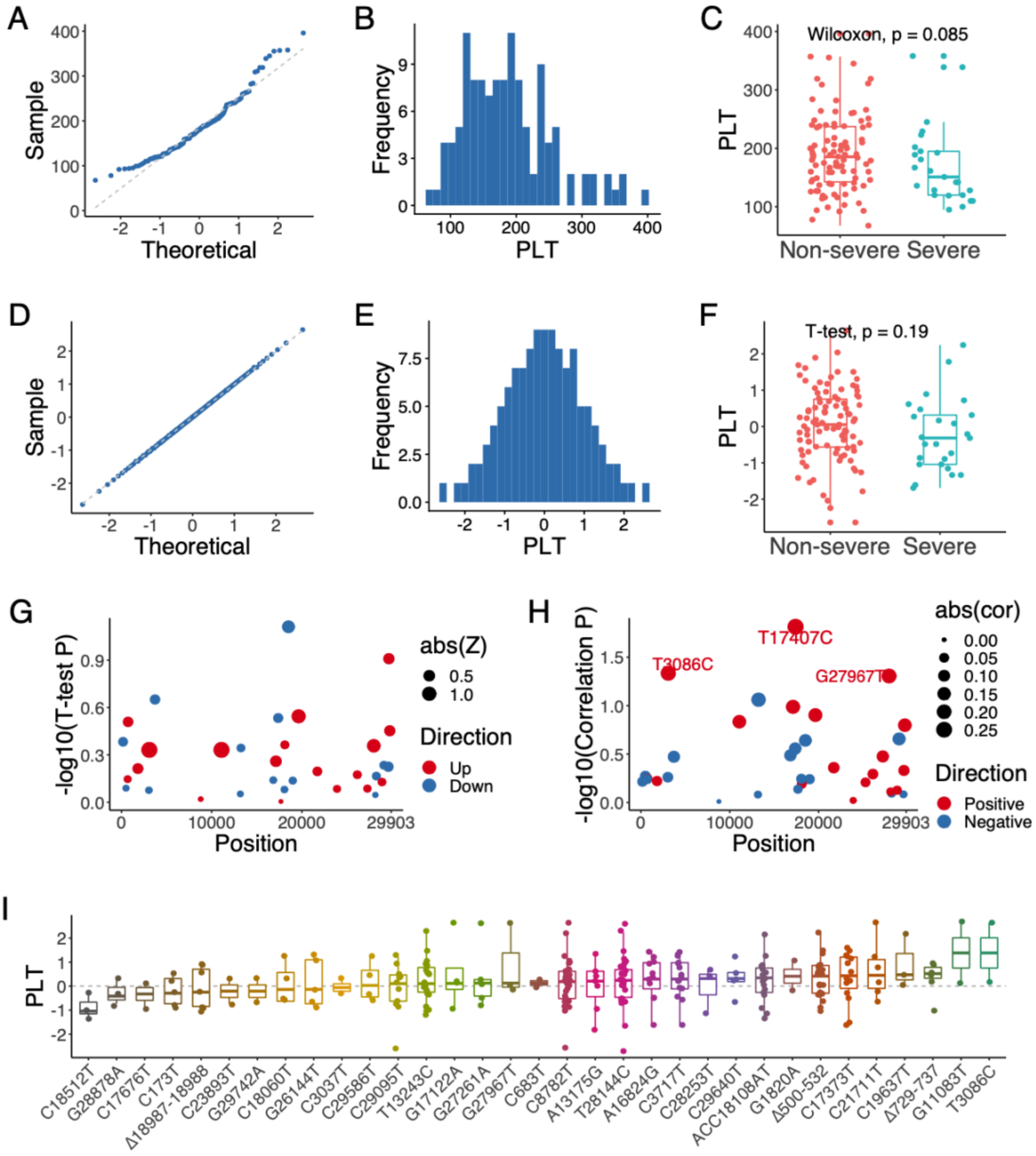
For pleural effusion (interstitium thickness, %), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared pleural effusion in the non-severe and severe COVID-19 patients before (**C**, p = 0.84, Wilcoxon test) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and pleural effusion using T-test and Pearson correlation. (**G**) No variant in the T test (**G**) variant C17373T in Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of pleural effusion, cases with A13175G and C17373T tend to have the highest Z score, whereas cases with C173T and C23893T have the lowest.

99. Pleural effusion volume (volume of interstitium thickness)



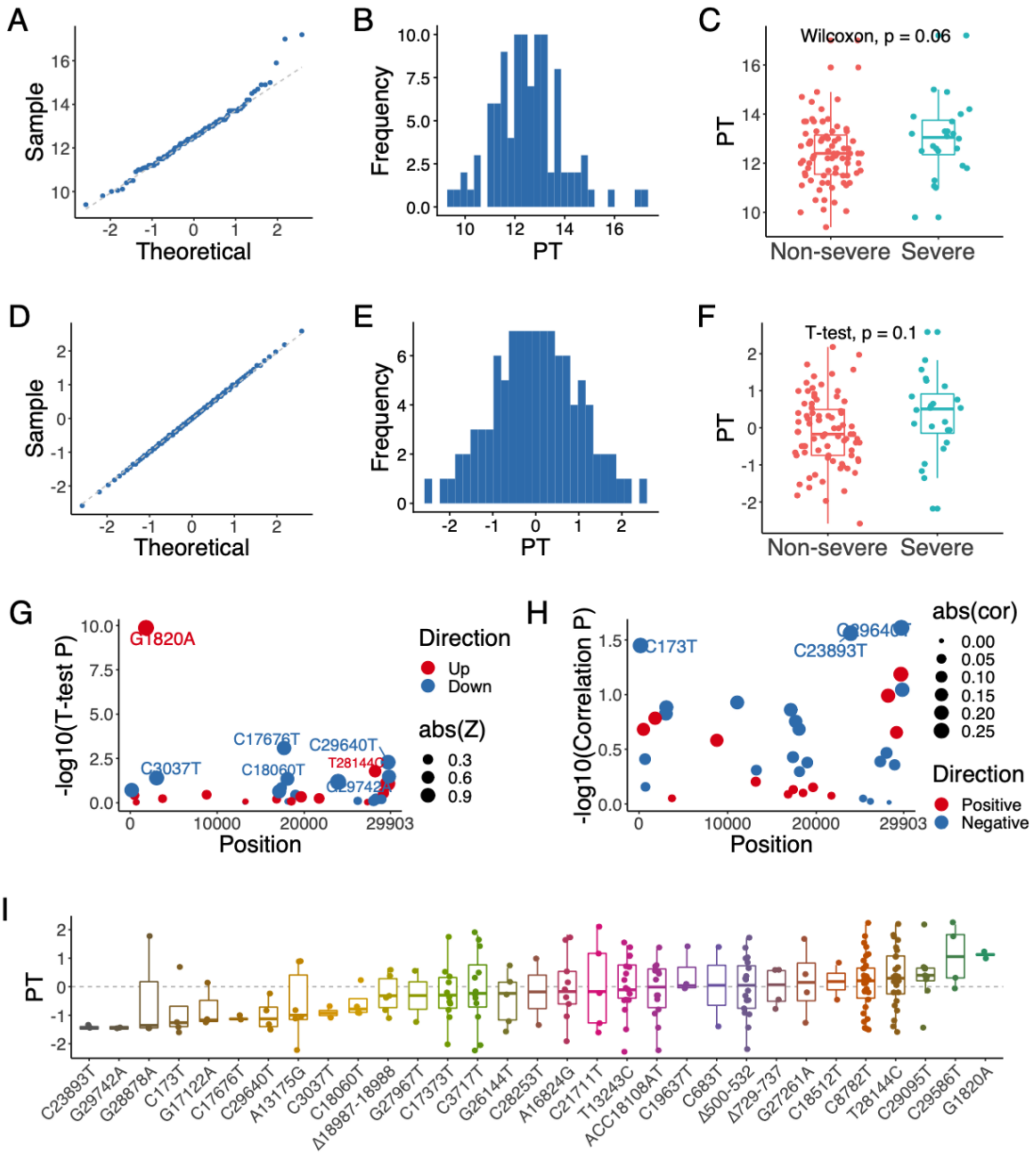
For pleural effusion volume (volume of interstitium thickness, mm^3), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared pleural effusion volume in the non-severe and severe COVID-19 patients before (**C**, p = 0.89, Wilcoxon test) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and pleural effusion volume using T-test and Pearson correlation. (**G**) Variant C17373T in the T test (**G**) and in Pearson correlation was both with P value below 0.05 (**H**). After sorting Z score values of pleural effusion volume, cases with C17373T and A13175G tend to have the highest Z score, whereas cases with C173T and C23893T have the lowest.

100. PLT (platelet count)



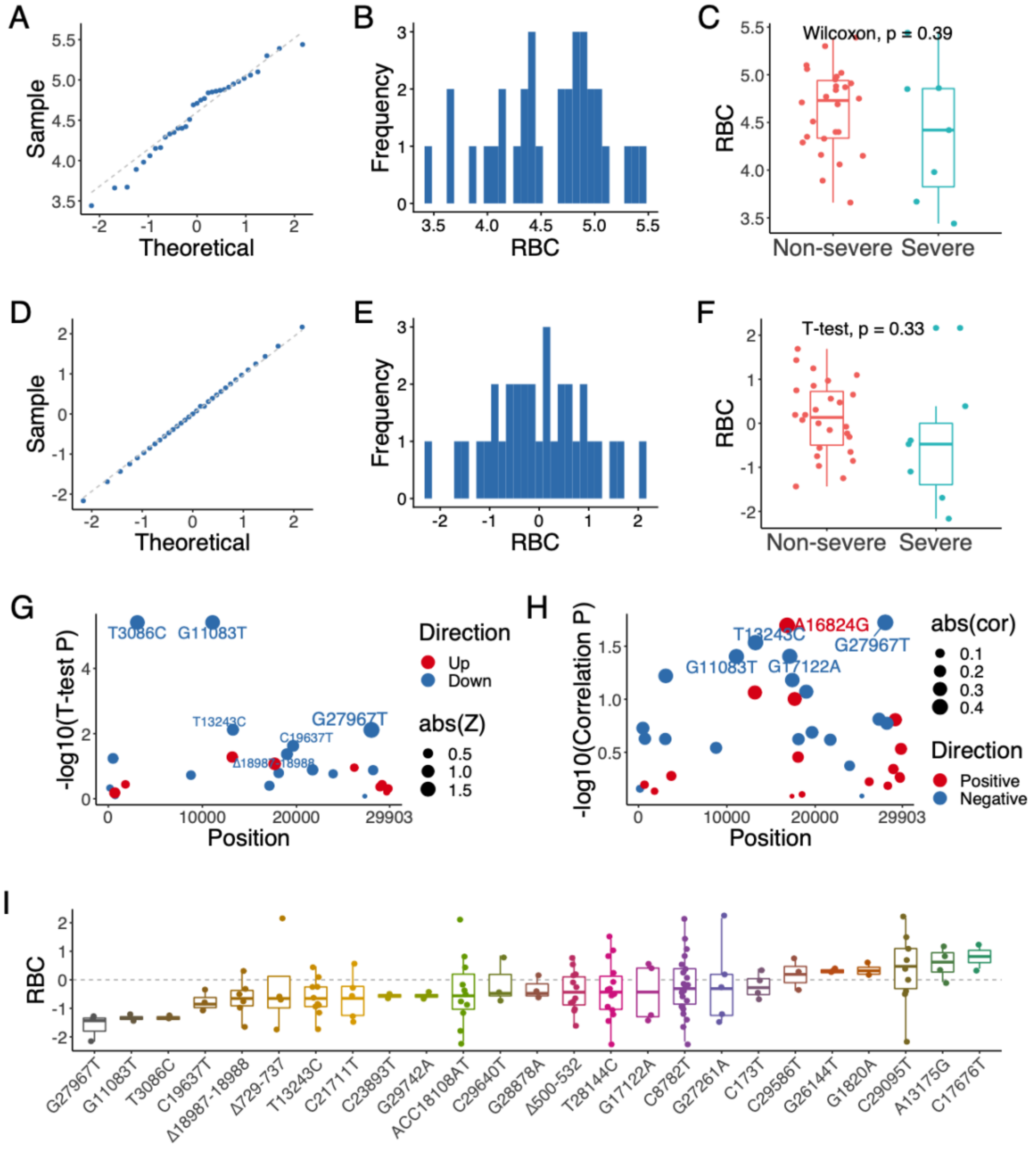
For PLT (platelet count, ×10^9/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared PLT in the non-severe and severe COVID-19 patients before (**C**, p = 0.085, Wilcoxon test) and after normalization (**F**, p = 0.190, T-test). We further performed association analyses between the 35 genetic variants and PLT using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants T3086C, T17407C and G27967T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of PLT, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C18512T and G28878A have the lowest.

101. PT (prothrombin time)



For PT (prothrombin time, sec), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared PT in the non-severe and severe COVID-19 patients before (**C**, p = 0.06, Wilcoxon test) and after normalization (**F**, p = 0.10, T-test). We further performed association analyses between the 35 genetic variants and PT using T-test and Pearson correlation. (**G**) Variants G1820A, C3037T, C17676T, C18060T, C29640T, T28144C and G29742A pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C173T, C23893T and C29640T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of PT, cases with G1820A and C29586T tend to have the highest Z score, whereas cases with C23893T and G29742A have the lowest.

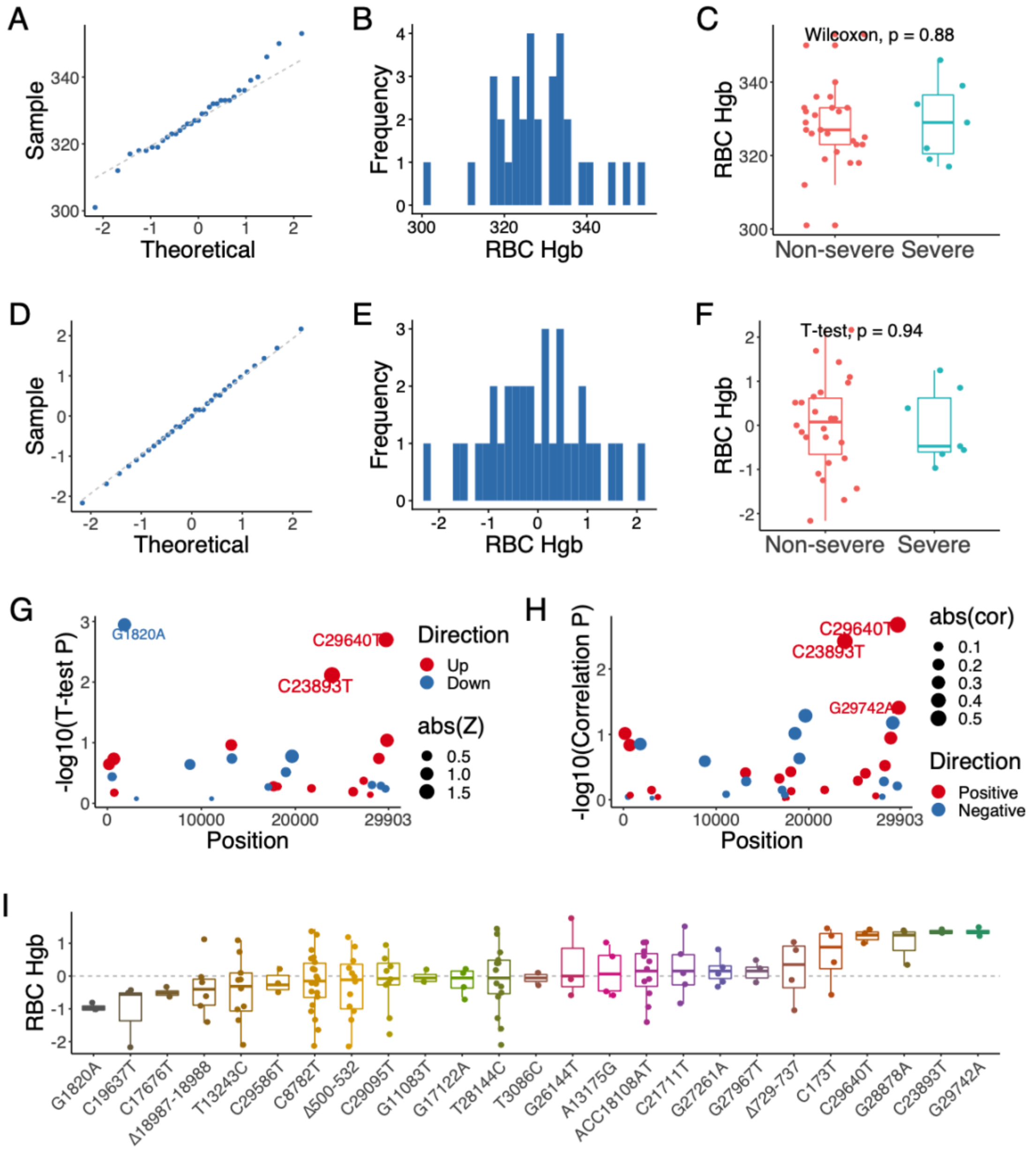
102. RBC (red blood cells count)



For RBC (red blood cells count, ×10^9/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared RBC in the non-severe and severe COVID-19 patients before (**C**, p = 0.39, Wilcoxon test) and after normalization (**F**, p = 0.33, T-test). We further performed association analyses between the 35 genetic variants and RBC using T-test and Pearson correlation. (**G**) Variants T3086C, G11083T, T13243C, G27967T, C19637T and Δ18987-18988 pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants A16824G, T13243C, G27967T, G11083T and G17122A have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of RBC, cases with C17676T and A13175G tend to have the highest Z score, whereas cases with

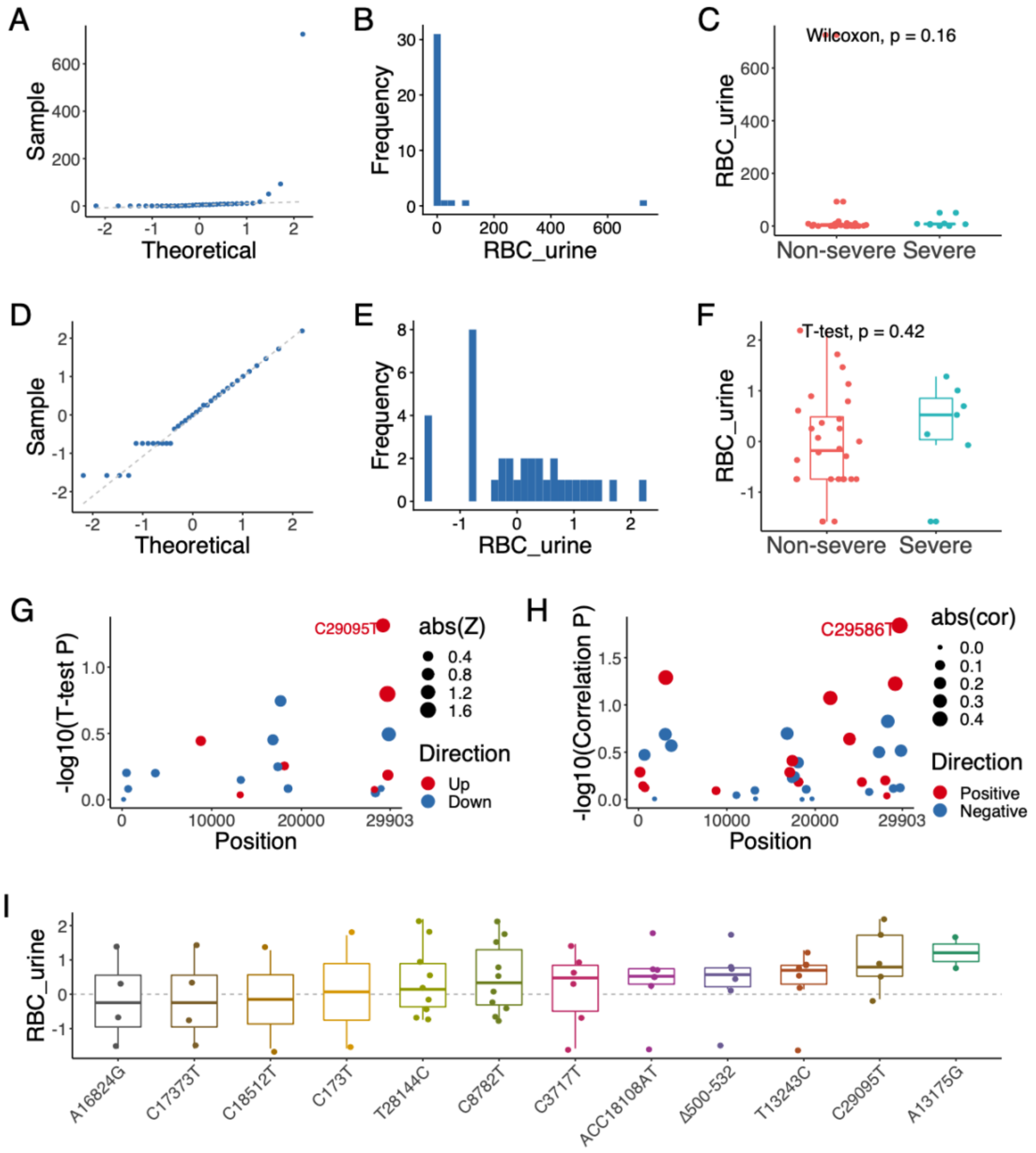
G27967T and G11083T have the lowest.

103. RBC Hgb (hemoglobin)



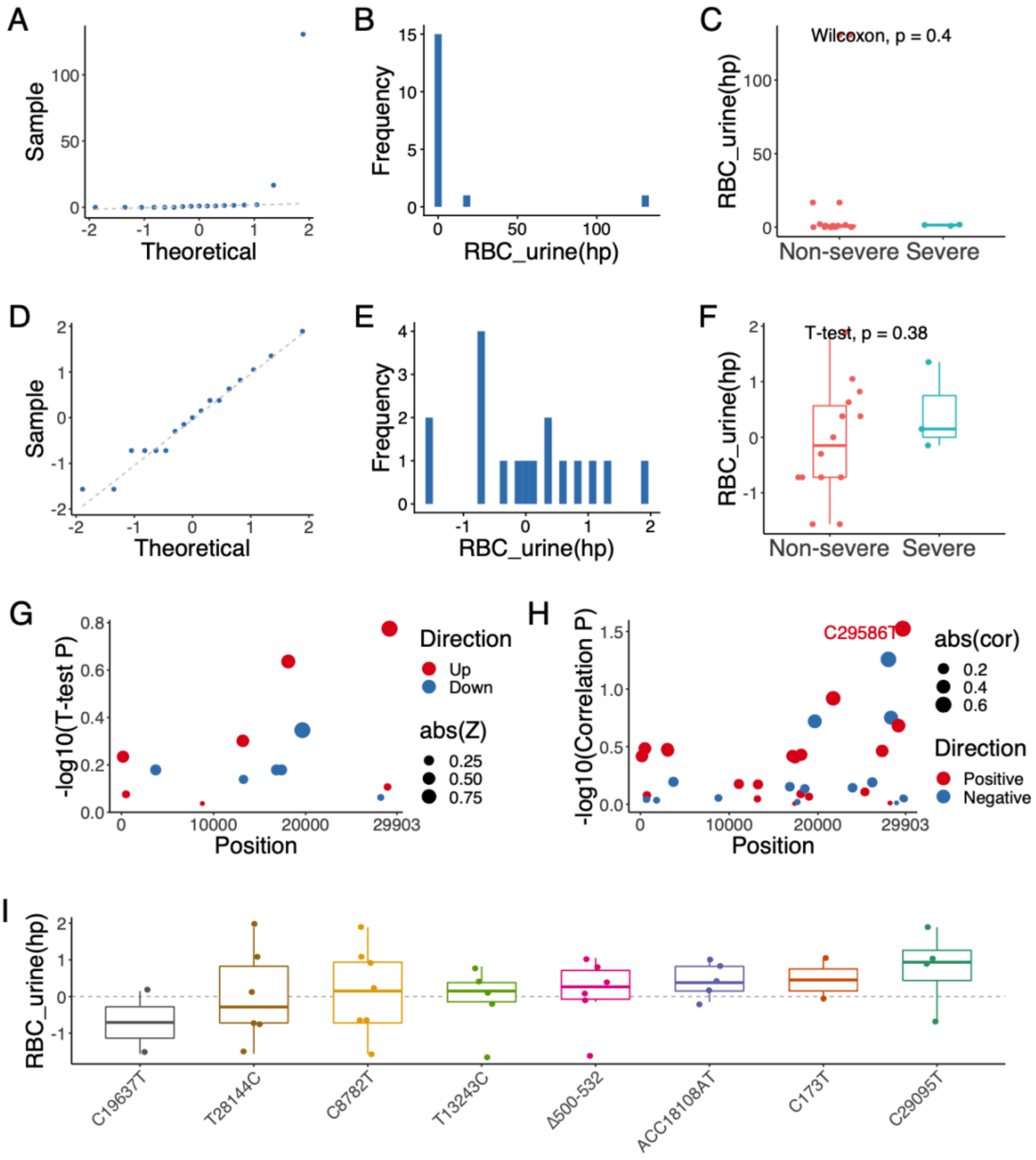
For RBC Hgb (hemoglobin, g/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared RBC Hgb in the non-severe and severe COVID-19 patients before (**C**, p = 0.88, Wilcoxon test) and after normalization (**F**, p = 0.94, T-test). We further performed association analyses between the 35 genetic variants and RBC Hgb using T-test and Pearson correlation. (**G**) Variants G1820A, C29640T and C23893T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C29640T, C23893T and G29742A have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of RBC Hgb, cases with G29742A and C23893T tend to have the highest Z score, whereas cases with G1820A and C19637T have the lowest.

104. RBC in urine



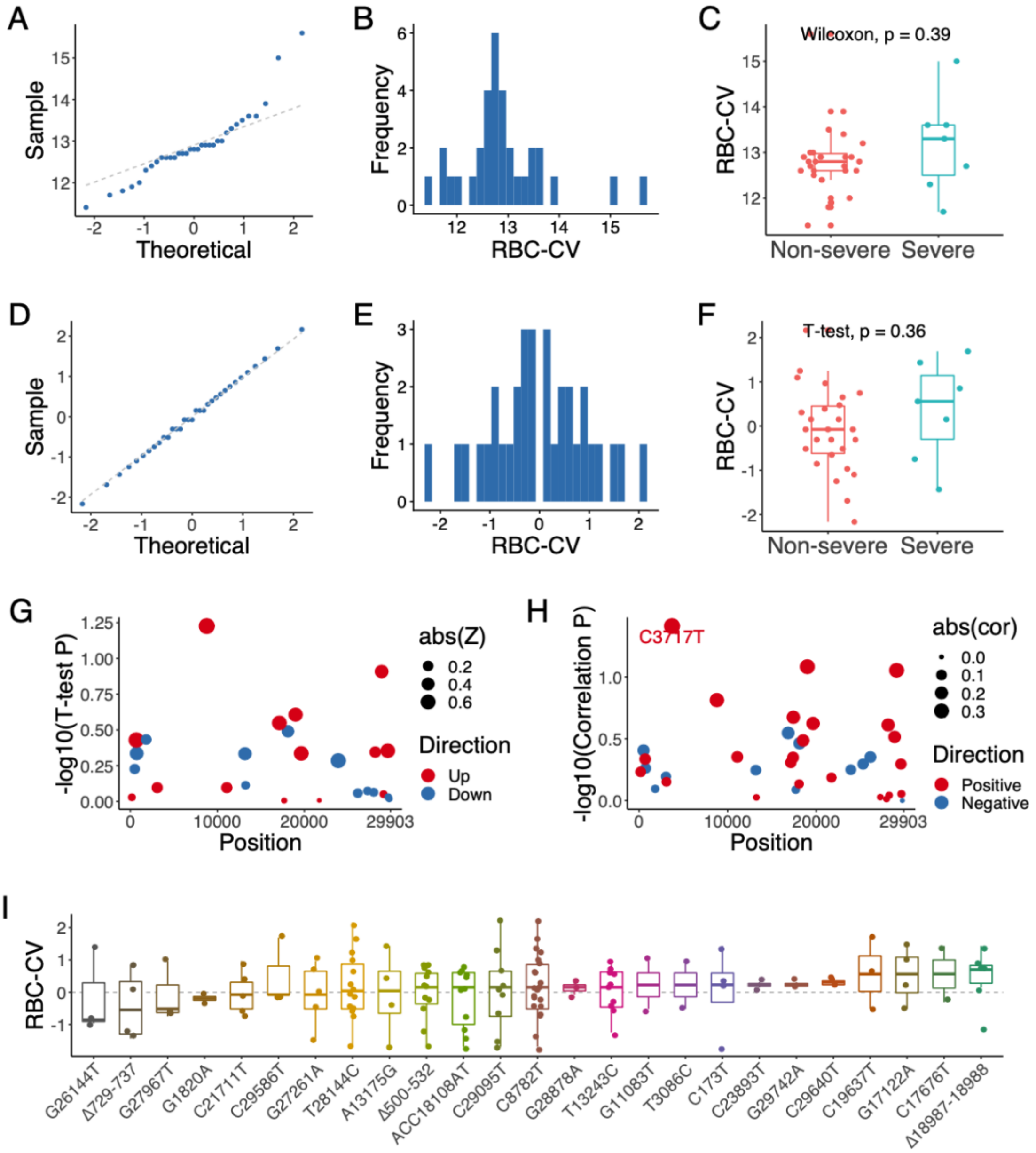
For RBC in urine (cell/μl), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared RBC urine in the non-severe and severe COVID-19 patients before (**C**, p = 0.16, Wilcoxon test) and after normalization (**F**, p = 0.42, T-test). (**G**) Variant C29095T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C29586T has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of RBC urine, cases with A13175G and C29095T tend to have the highest Z score, whereas cases with A16824G and C17373T have the lowest.

105. RBC/HPF (red blood cells per high power field)



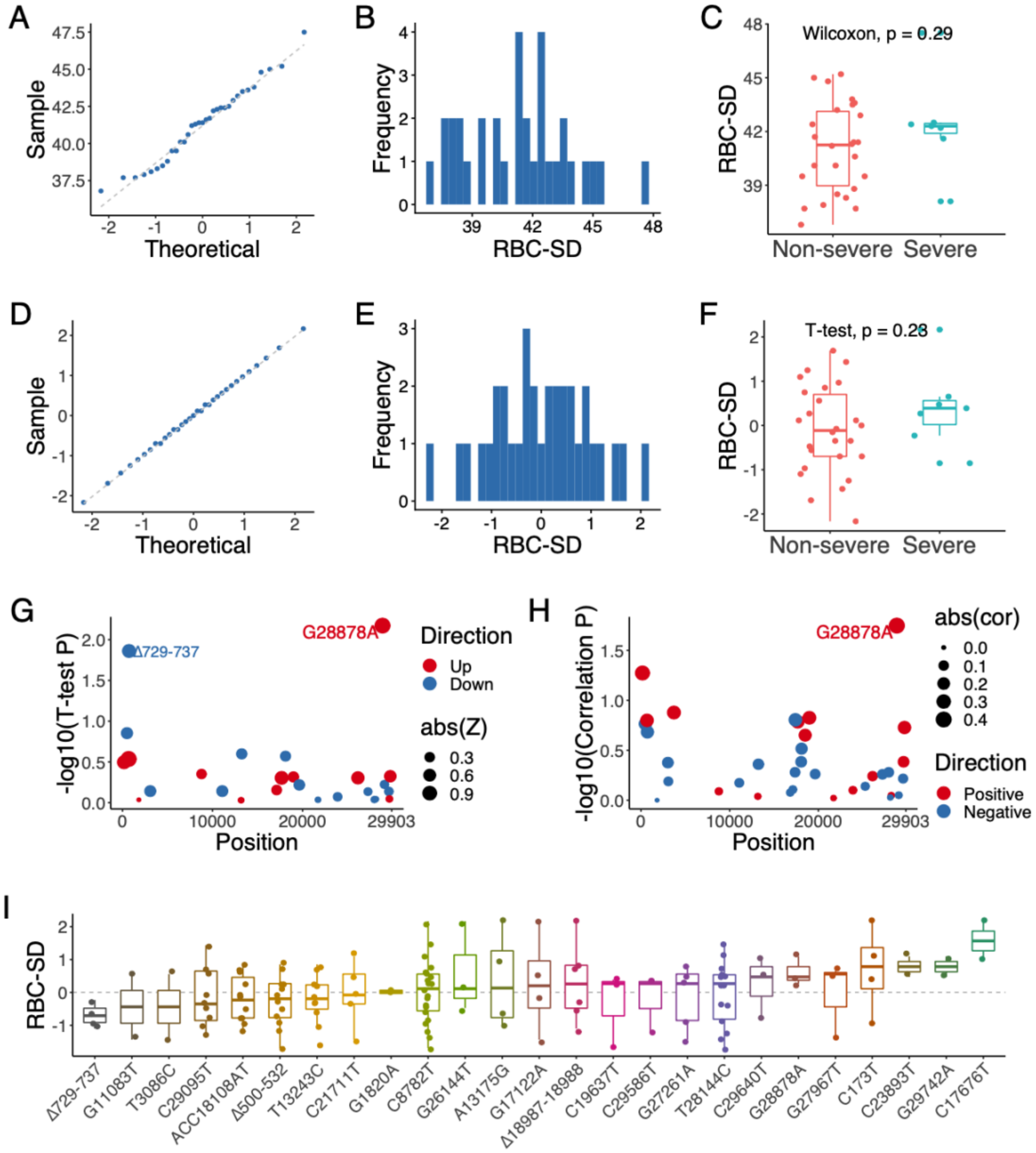
For RBC/HPF (red blood cells per high power field), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared RBC/HPF in the non-severe and severe COVID-19 patients before (**C**, p = 0.40, Wilcoxon test) and after normalization (F, p = 0.38, T-test). We further performed association analyses between the 35 genetic variants and RBC/HPF using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C29586T in Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of RBC/HPF, cases with C29095T and C173T tend to have the highest Z score, whereas cases with C19637T and T28144C have the lowest.

106. RDW-CV (red blood cell distribution width coefficient of variation)



For RDW-CV (red blood cell distribution width, %), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared RDW-CV in the non-severe and severe COVID-19 patients before (**C**, p = 0.39, Wilcoxon test) and after normalization (**F**, p = 0.36, T-test). We further performed association analyses between the 35 genetic variants and RDW-CV using T-test and Pearson correlation. (**G**) No variant passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C3717T in Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of RDW-CV, cases with C17676T and Δ18987-18988 tend to have the highest Z score, whereas cases with G26144T and Δ729-737 have the lowest.

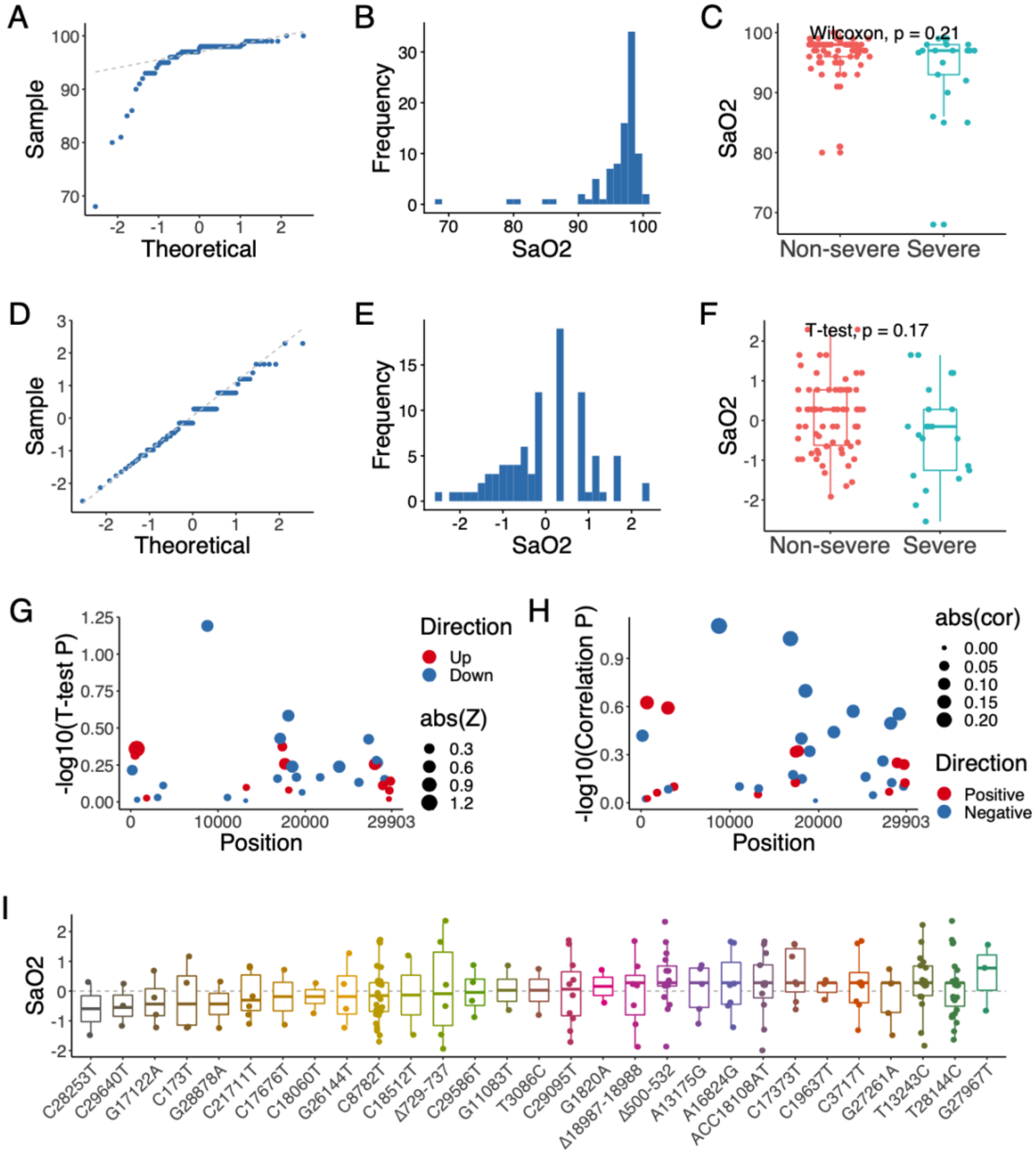
107. RDW-SD (red blood cell distribution standard deviation)



For RDW-SD (red blood cell distribution standard deviation, fl), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared RDW-SD in the non-severe and severe COVID-19 patients before (**C**, p = 0.29, Wilcoxon test) and after normalization (**F**, p = 0.23, T-test). We further performed association analyses between the 35 genetic variants and RDW-SD using T-test and Pearson correlation. (**G**) Variants G28878A and Δ729-737 pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant G28878A has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of RDW-SD, cases with C17676T and G29742A tend to have the highest

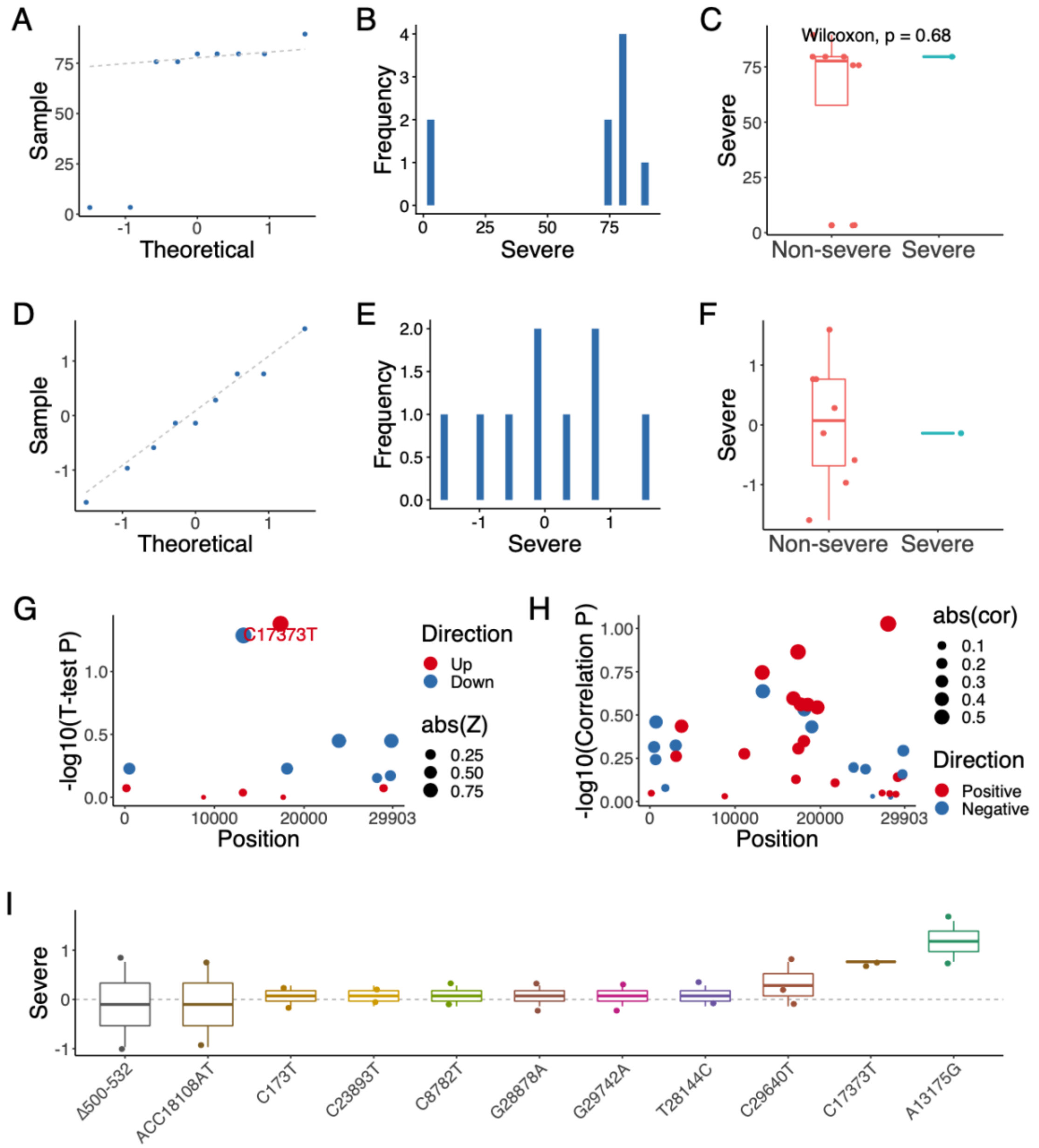
Z score, whereas cases with G11083T and Δ729-737 have the lowest.

108. SaO_2 (oxygen saturation)



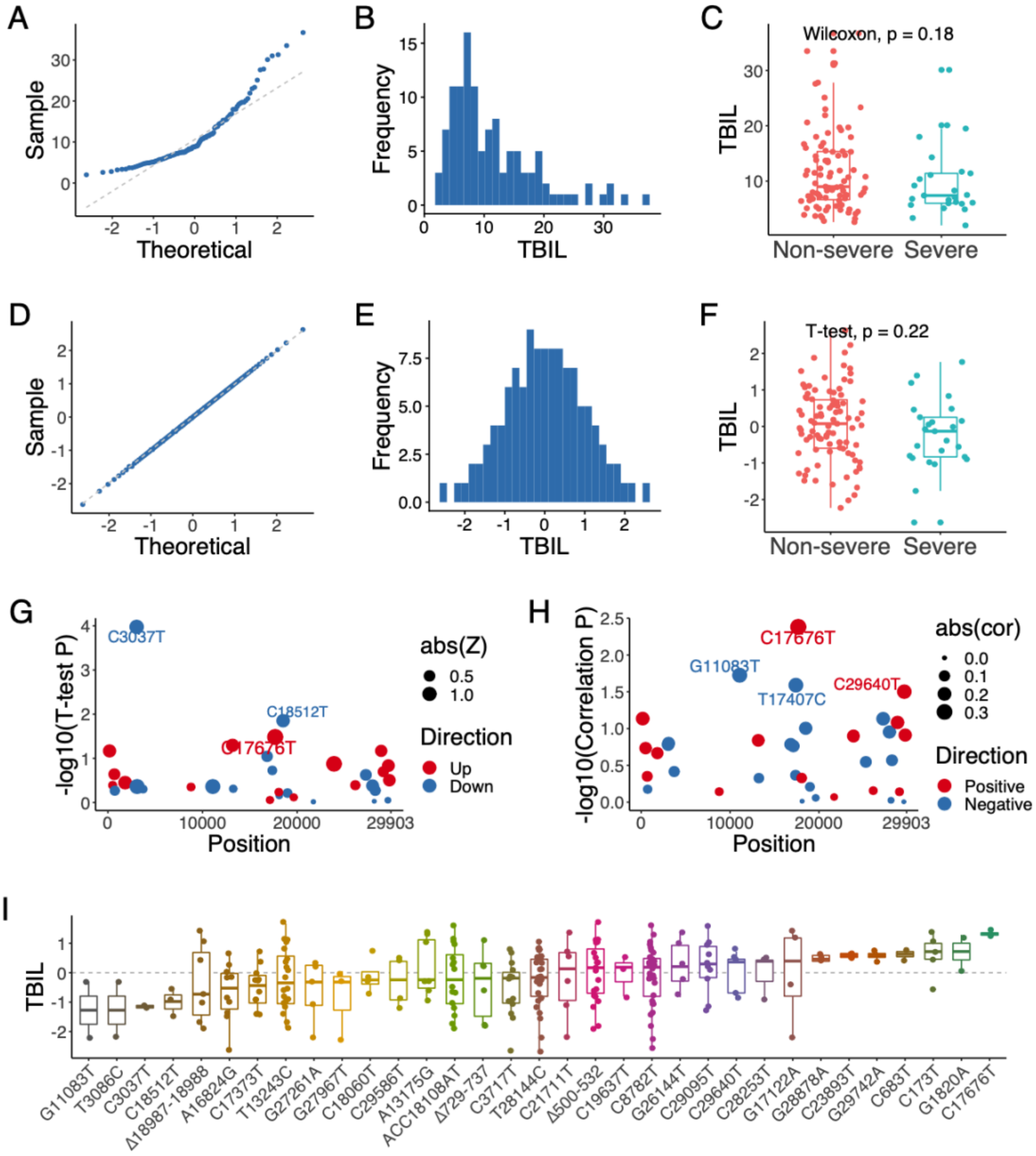
For SaO_2 (oxygen saturation, %), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared SaO_2 in the non-severe and severe COVID-19 patients before (**C**, p = 0.21, Wilcoxon test) and after normalization (**F**, p = 0.17, T-test). We further performed association analyses between the 35 genetic variants and SaO_2 using T-test and Pearson correlation. (**G**) No variant in the T test (**G**) and in Pearson correlation was with P value below 0.05 (**H**). After sorting Z score values of SaO_2, cases with T28144C and G27967T tend to have the highest Z score, whereas cases with C28253T and C29640T have the lowest.

109. Severe (severe probability)



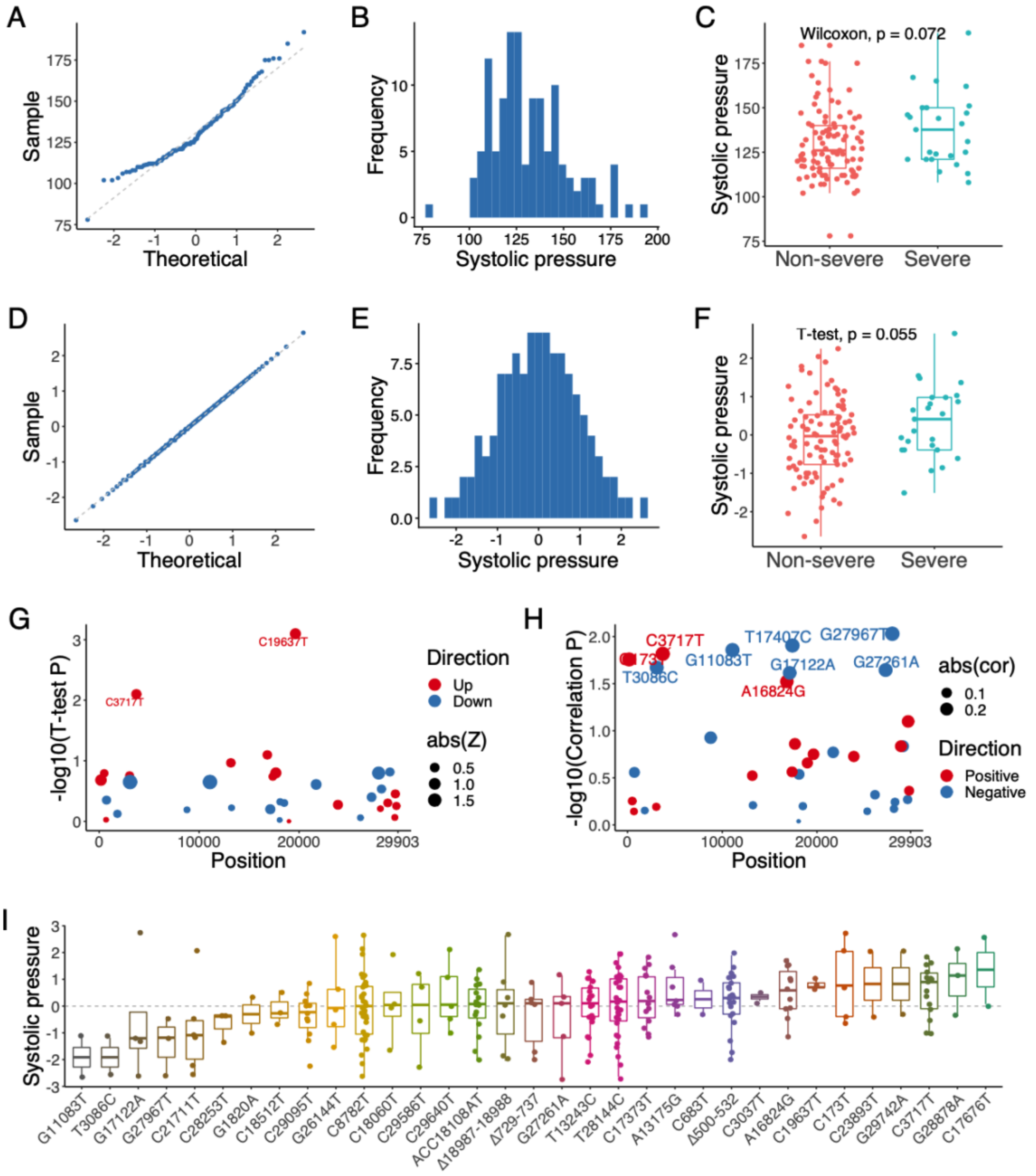
For severe (severe probability, %), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared severe in the non-severe and severe COVID-19 patients before (**C**, p = 0.68, Wilcoxon test) and after normalization (**F**). We further performed association analyses between the 35 genetic variants and severe using T-test and Pearson correlation. (**G**) Variant C17373T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) No variant in Pearson correlation was has P value below 0.05. After sorting Z score values of severe, cases with A13175G and C17373T tend to have the highest Z score, whereas cases with Δ500-532 and ACC18108AT have the lowest.

110. TBil (total bilirubin)



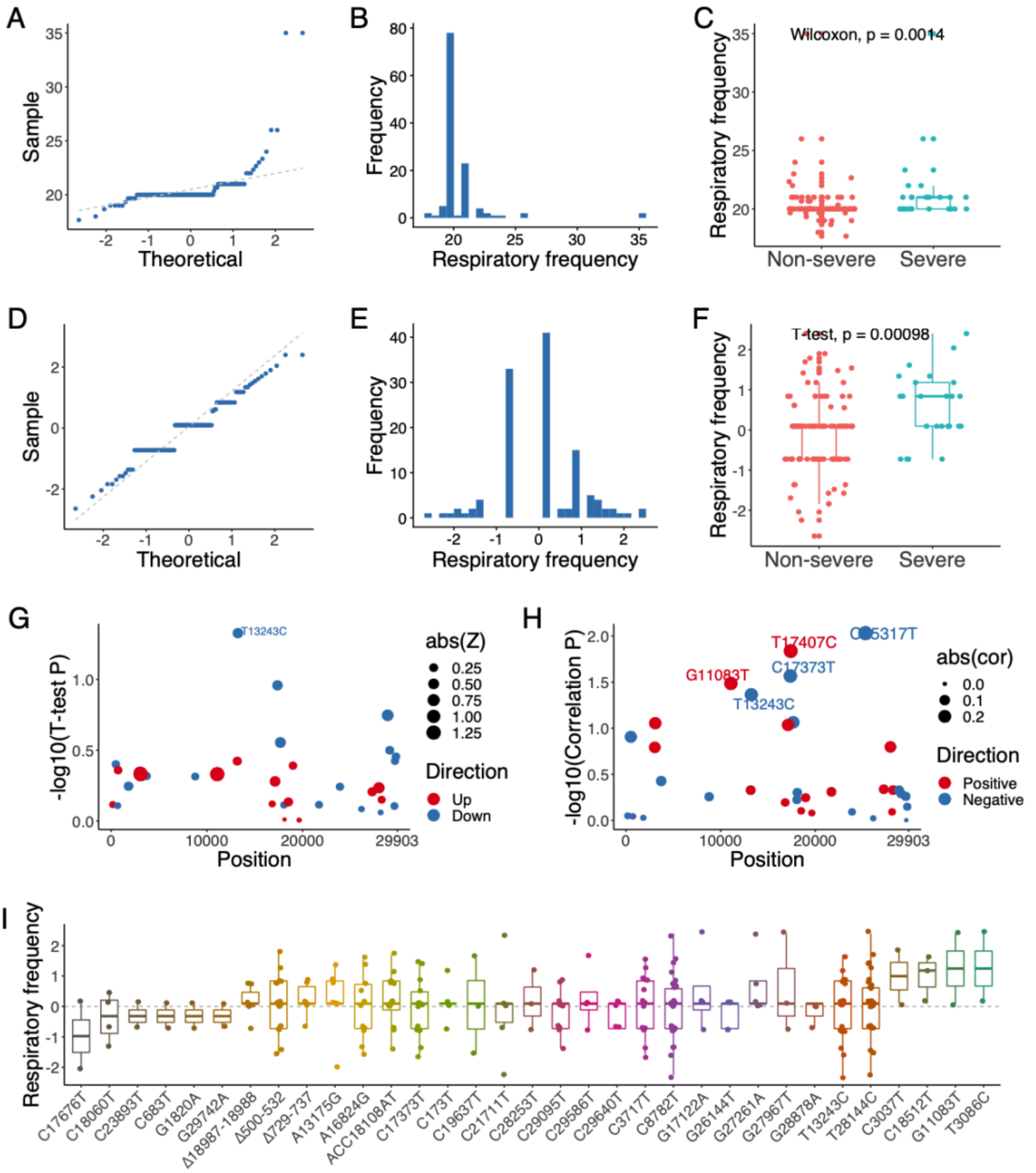
For TBil (total bilirubin, μmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared TBIL in the non-severe and severe COVID-19 patients before (**C**, p = 0.18, Wilcoxon test) and after normalization (**F**, p = 0.22, T-test). We further performed association analyses between the 35 genetic variants and TBil using T-test and Pearson correlation. (**G**) Variants C3037T, C17676T and C18512T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C17676T, T17407C, C29640T and G11083T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of TBil, cases with C17676T and G1820A tend to have the highest Z score, whereas cases with G11083T and T3086C have the lowest.

111. SP (systolic pressure)



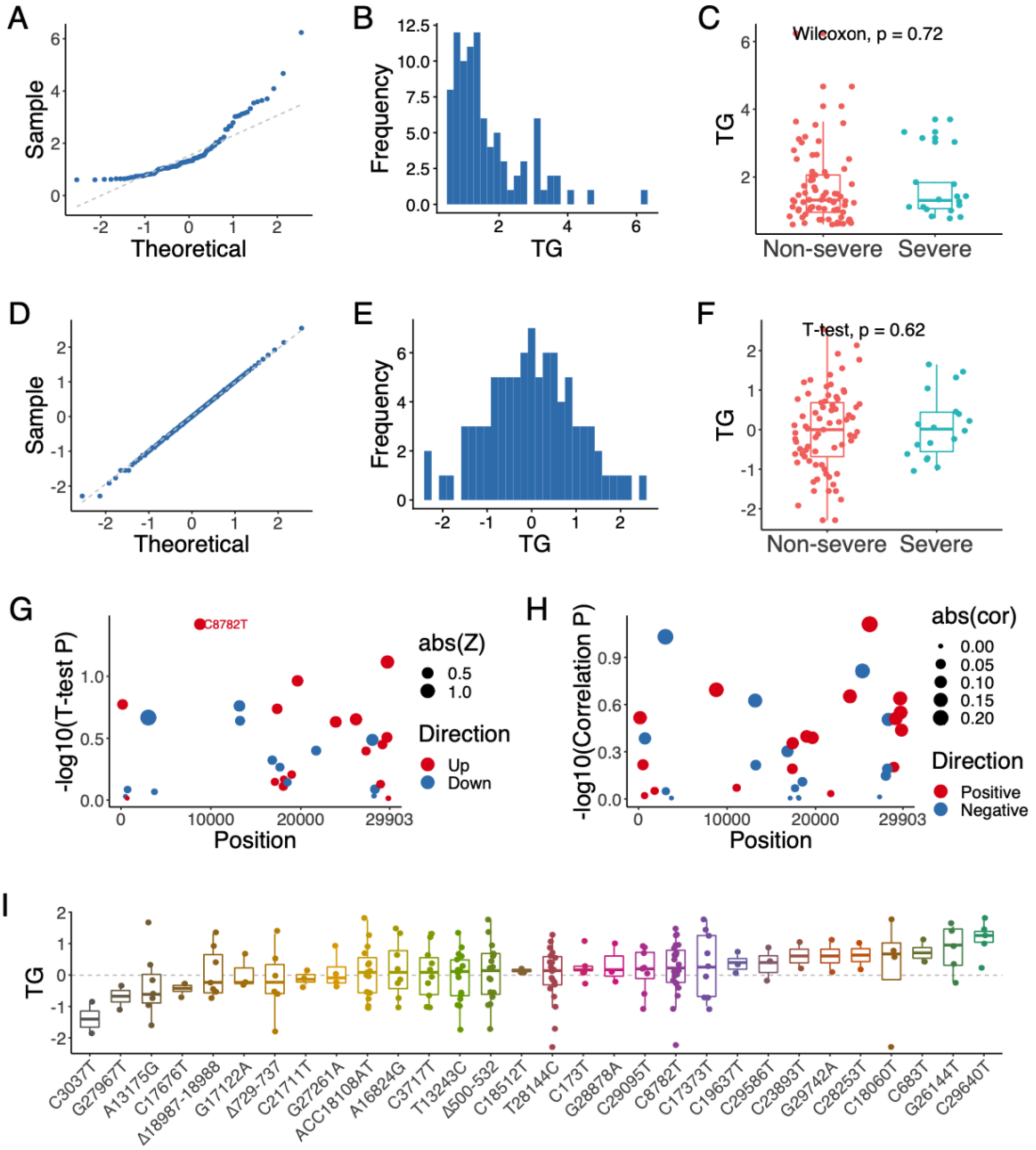
For SP (systolic pressure, mmHg), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared SP in the non-severe and severe COVID-19 patients before (**C**, $p = 7.2\times10^{-2}$, Wilcoxon test) and after normalization (**F**, $p = 5.5\times10^{-2}$, T-test). (**G**) Variants C3717T and C19637T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C3717T, T17407C, G27967T, G11083T, G17122A, G27261A, T3086C and C173T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of SP, cases with C17676T and G28878A tend to have the highest Z score, whereas cases with G11083T and T3086C have the lowest.

112. RF (respiratory frequency)



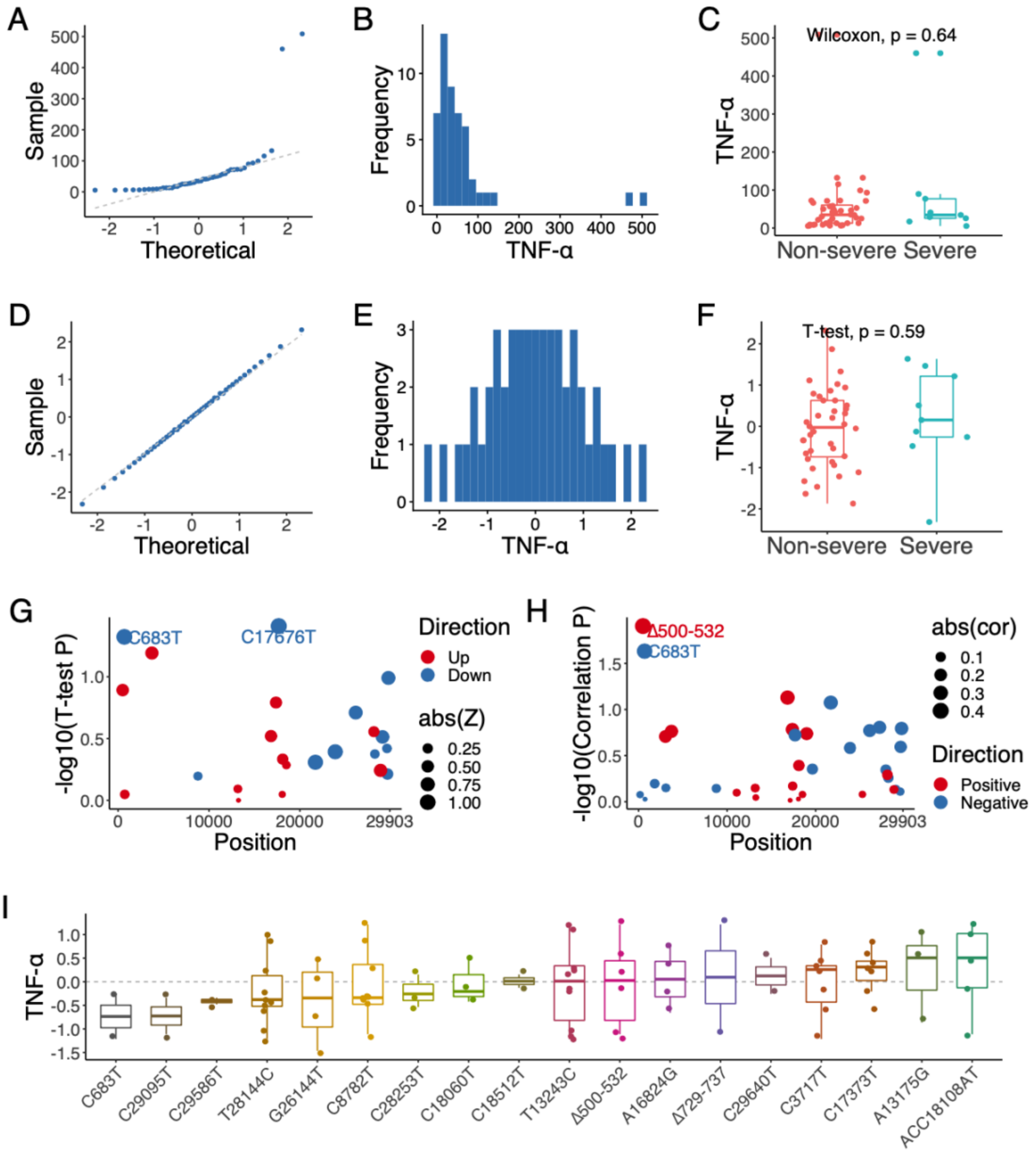
For RF (respiratory frequency, times/min), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared RF in the non-severe and severe COVID-19 patients before (**C**, p = 1.4×10^{-3}, Wilcoxon test) and after normalization (**F**, p = 9.8×10^{-4}, T-test). (**G**) Variant T13243C passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants C17373T, G11083T, T13243C and T17407C have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of RF, cases with T3086C and G11083T tend to have the highest Z score, whereas cases with C17676T and C18060T have the lowest.

113. TG (triglycerides)



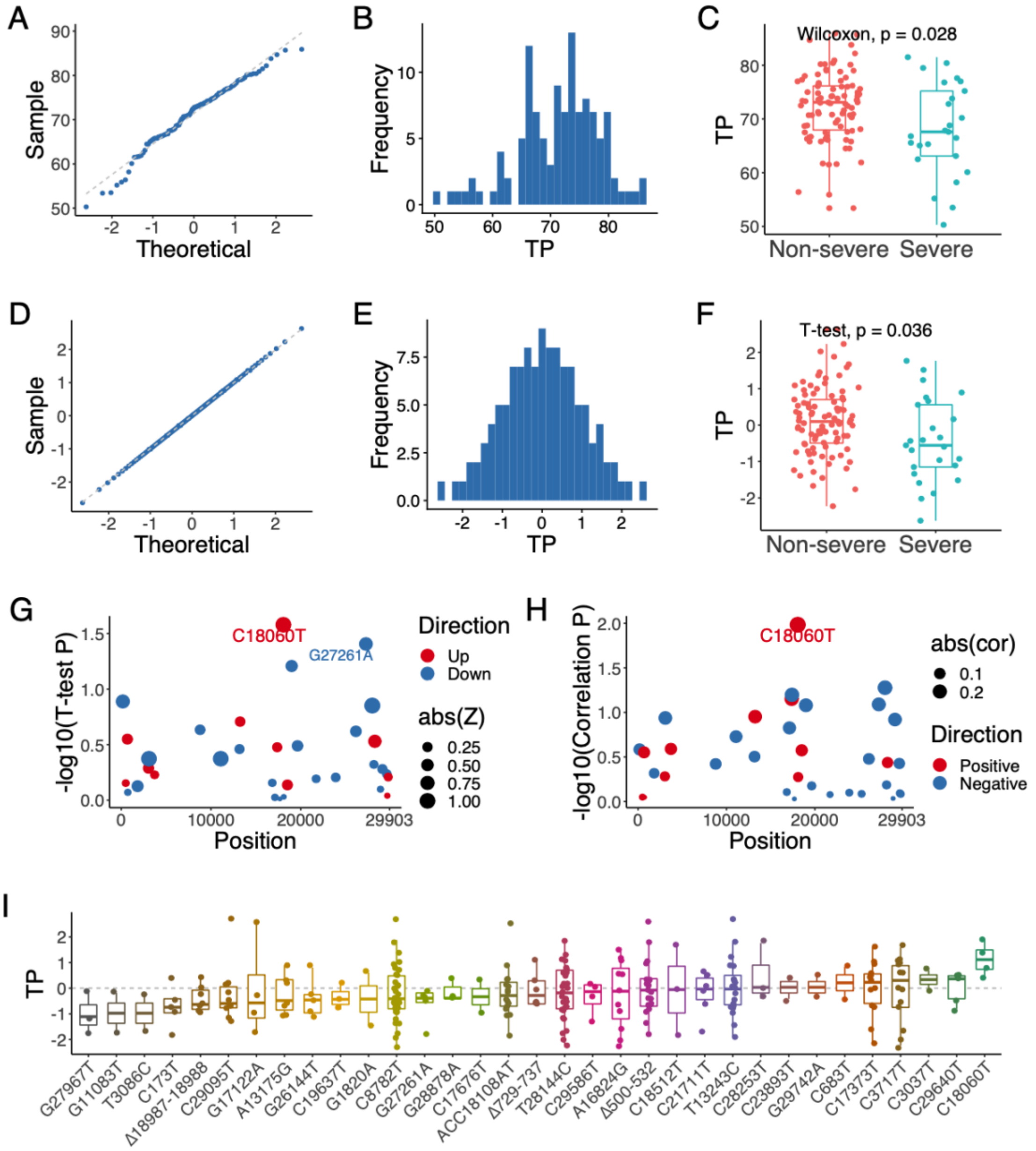
For TG (triglycerides, mmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared TG in the non-severe and severe COVID-19 patients before (**C**, p = 0.72, Wilcoxon test) and after normalization (**F**, p = 0.62, T-test). We further performed association analyses between the 35 genetic variants and TG using T-test and Pearson correlation. (**G**) Variant C8782T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) No variant in Pearson correlation was has P value below 0.05. After sorting Z score values of TG, cases with C29640T and G26144T tend to have the highest Z score, whereas cases with C3037T and G27967T have the lowest.

114. TNF-α (tumor necrosis factor alpha)



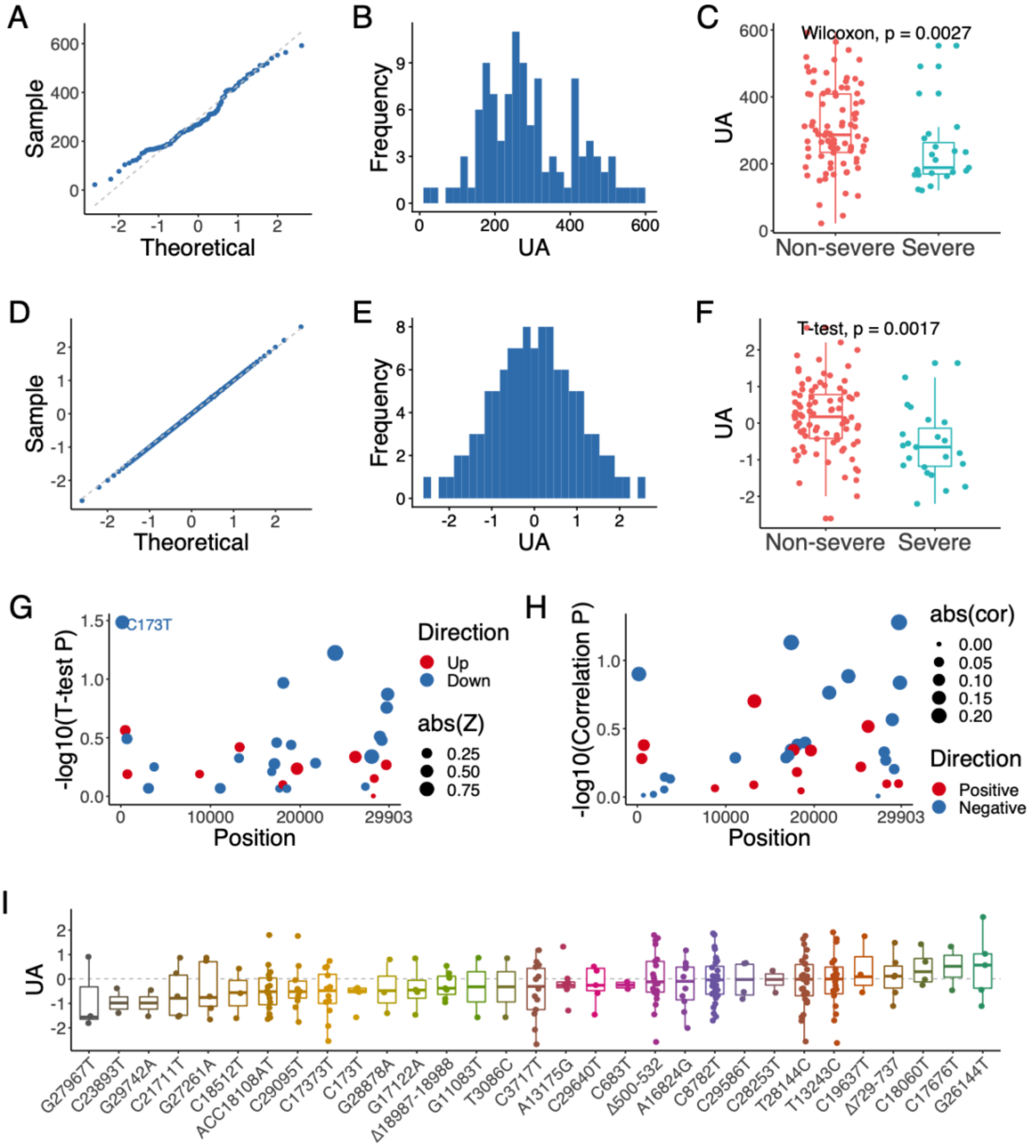
For TNF-α (tumor necrosis factor alpha pg/ml), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared TNF-α in the non-severe and severe COVID-19 patients before (**C**, p = 0.64, Wilcoxon test) and after normalization (**F**, p = 0.59, T-test). We further performed association analyses between the 35 genetic variants and TNF-α using T-test and Pearson correlation. (**G**) Variants C683T and C17676T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variants Δ500-532 and C683T have P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of TNF-α, cases with ACC18108AT and A13175G tend to have the highest Z score, whereas cases with C683T and C29095T have the lowest.

115. TP (total protein)



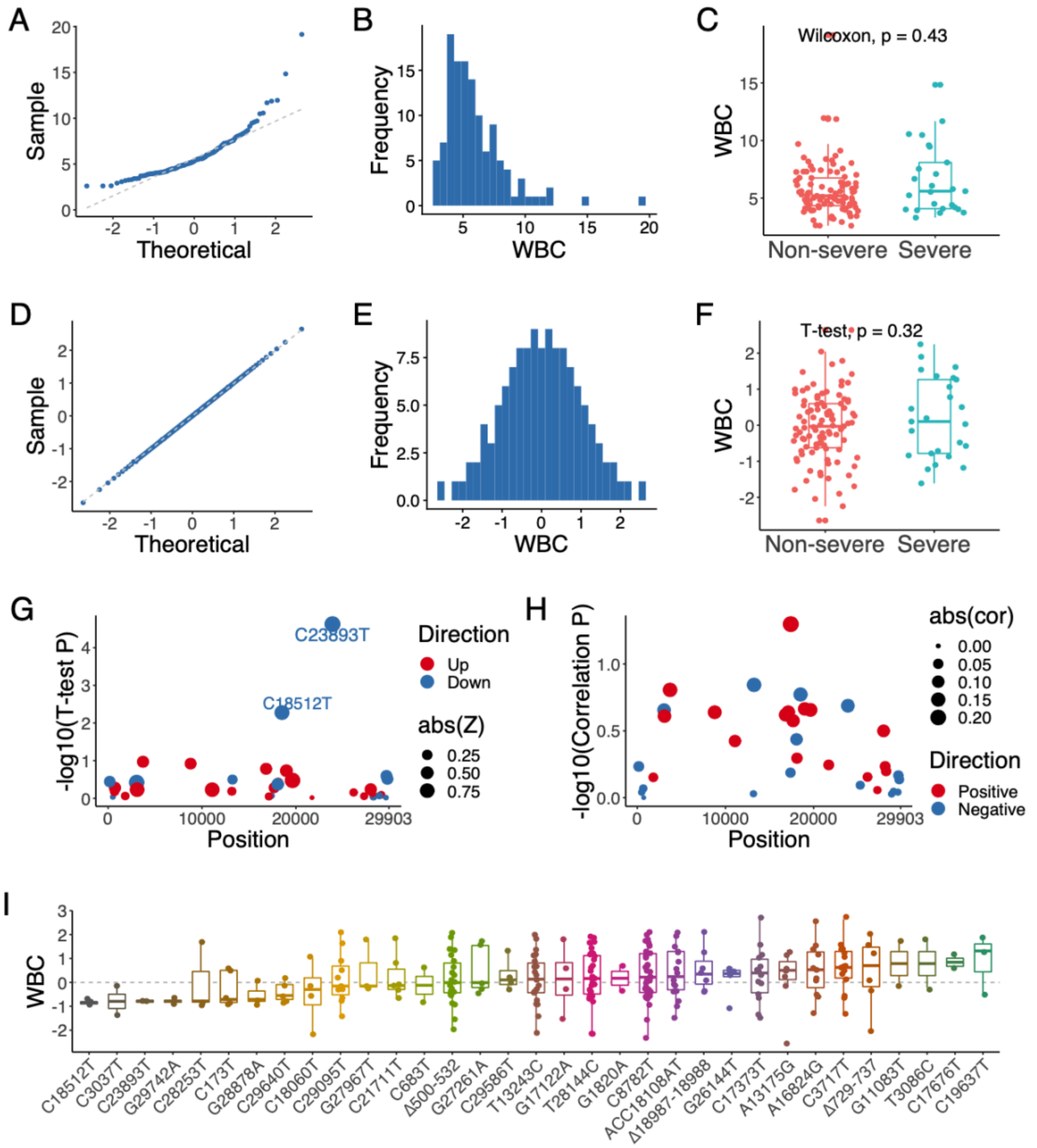
For TP (total protein, g/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared TP in the non-severe and severe COVID-19 patients before (**C**, p = 2.8×10^{-2}, Wilcoxon test) and after normalization (**F**, p = 3.6×10^{-2}, T-test). We further performed association analyses between the 35 genetic variants and TP using T-test and Pearson correlation. (**G**) Variants C18060T and G27261A pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) Variant C18060T has P value lower than 0.05 in Pearson correlation. Red and blue indicates positive and negative correlation, respectively. Size of the dots indicate absolute correlation coefficient. (**I**) After sorting Z score values of TP, cases with C18060T and C29640T tend to have the highest Z score, whereas cases with G27967T and G11083T have the lowest.

116. UA (uric acid)



For UA (uric acid, μmol/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared UA in the non-severe and severe COVID-19 patients before (**C**, p = 2.7×10^{-3}, Wilcoxon test) and after normalization (**F**, p = 1.7×10^{-3}, T-test). We further performed association analyses between the 35 genetic variants and UA using T-test and Pearson correlation. (**G**) Variant C173T passes P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) No variant in Pearson correlation was has P value below 0.05. After sorting Z score values of UA, cases with G26144T and C17676T tend to have the highest Z score, whereas cases with G27967T and T17407C have the lowest.

117. WBC (white blood cell count)



For WBC (white blood cell count, $\times 10^9$/L), quantile-quantile (QQ) plot and distribution plot before (**A** and **B**) and after normalization (**D** and **E**) were shown. We compared WBC in the non-severe and severe COVID-19 patients before (**C**, p = 0.43, Wilcoxon test) and after normalization (**F**, p = 0.32, T-test). We further performed association analyses between the 35 genetic variants and WBC using T-test and Pearson correlation. (**G**) Variants C18512T and C23893T pass P value cut-off of 0.05 in T test. Red indicates higher mean value in cases with the variants and blue indicates higher mean value in cases without the variant. The size of symbols indicates absolute Z score number. (**H**) No variant has P value lower than 0.05 in Pearson correlation. (**I**) After sorting Z score values of WBC, cases with C19637T and C17676T tend to have the highest Z score, whereas cases with C18512T and C3037T have the lowest.