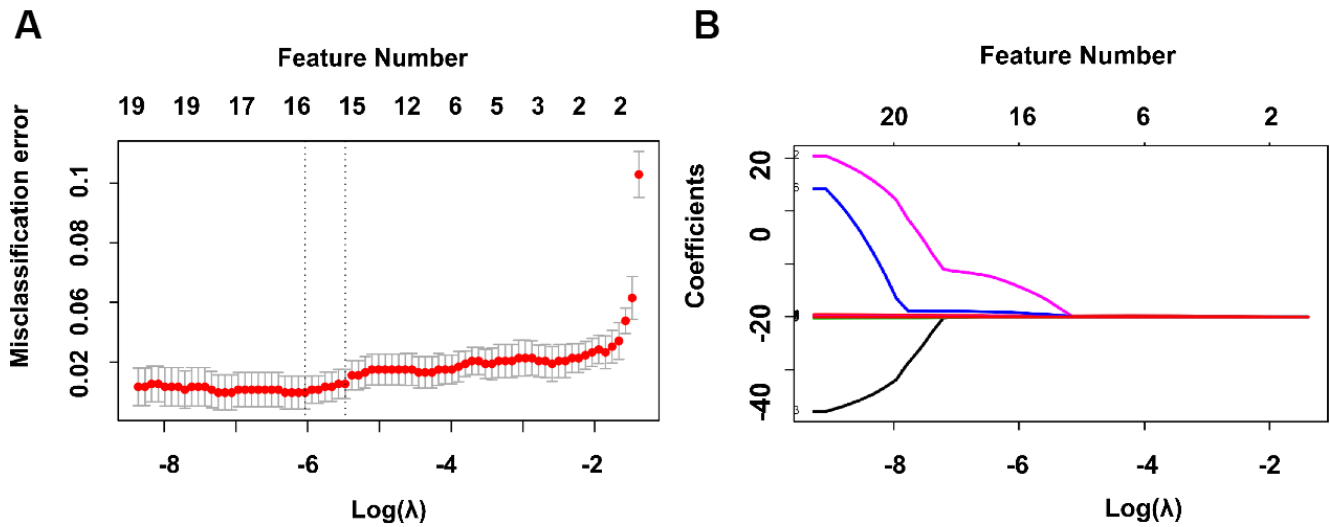
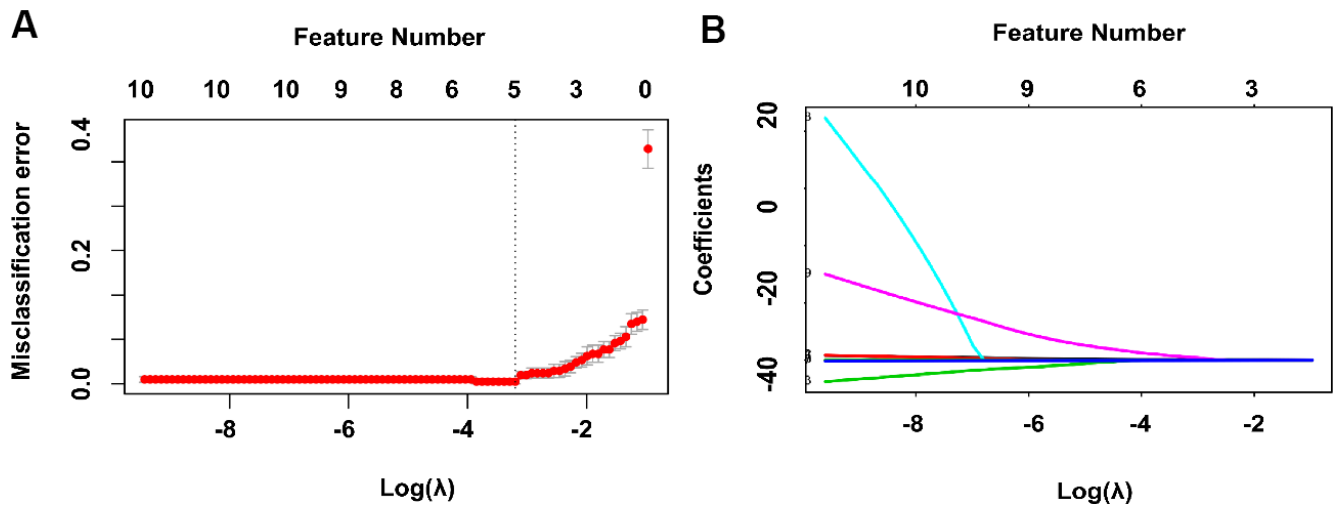


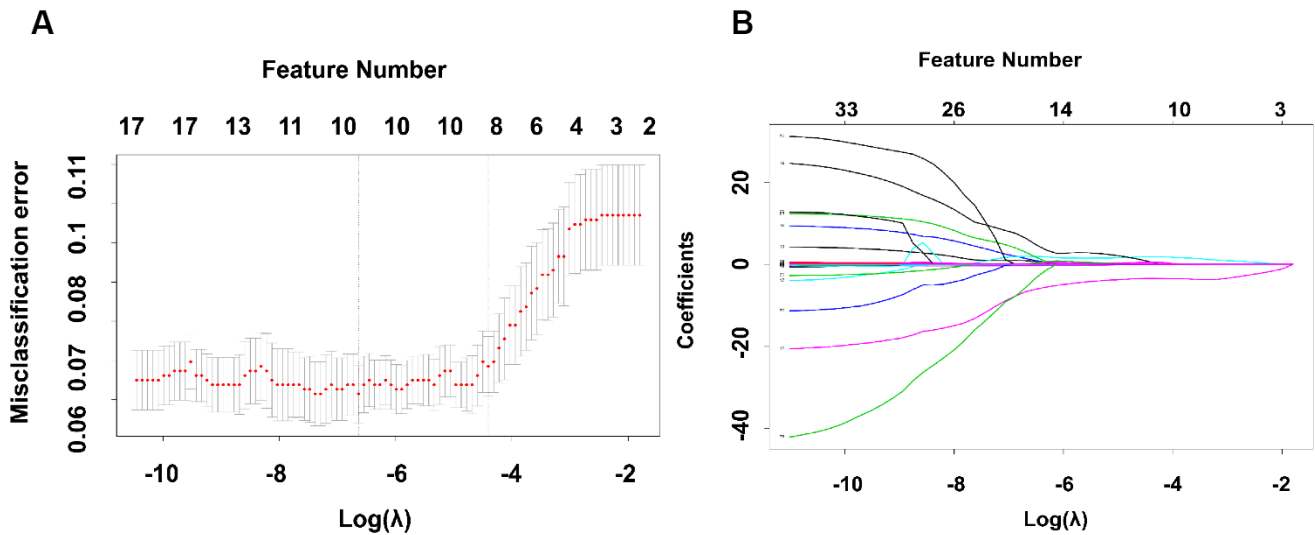
SUPPLEMENTARY FIGURES



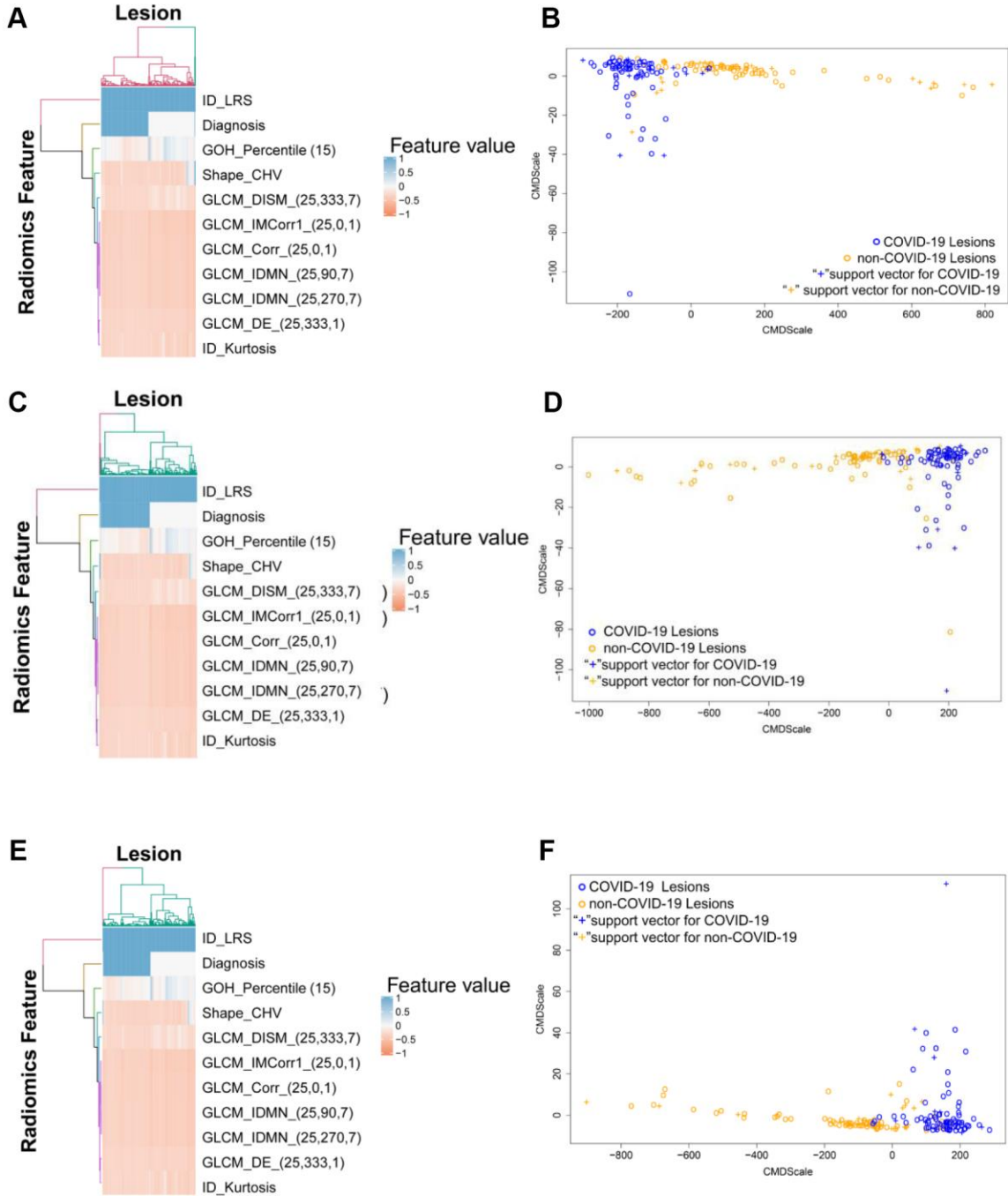
Supplementary Figure 1. The LASSO process to select the radiomic features for the construction of the patient-based risk score using radiomic features only. (A) The radiomic features selection procedure using LASSO regression method. To determine the best features combination for building the risk score, the control parameter λ value in the LASSO model was selected via 4-fold cross-validation with minimum criteria. The x-axis is the value of $\log(\lambda)$ and the y-axis is the binomial deviance in the 4-fold cross validation method 100 times. The upper x-axis is the number of non-zero-coefficient features with a given λ . The red curve indicated the average binomial deviance value with the vertical bars showing the upper and lower boundaries. The left vertical dotted line defined the λ with the least binomial deviance. The right vertical dotted line indicates the largest value of λ such that the binomial deviance is within one standard error of the minimum binomial deviance. (B) The LASSO coefficient profiles of the radiomic features. The figure shows the feature coefficient change with the tuning of λ value. The dotted line was plotted at the λ value determined in (A) resulting 16 non-zero-coefficient radiomic features.

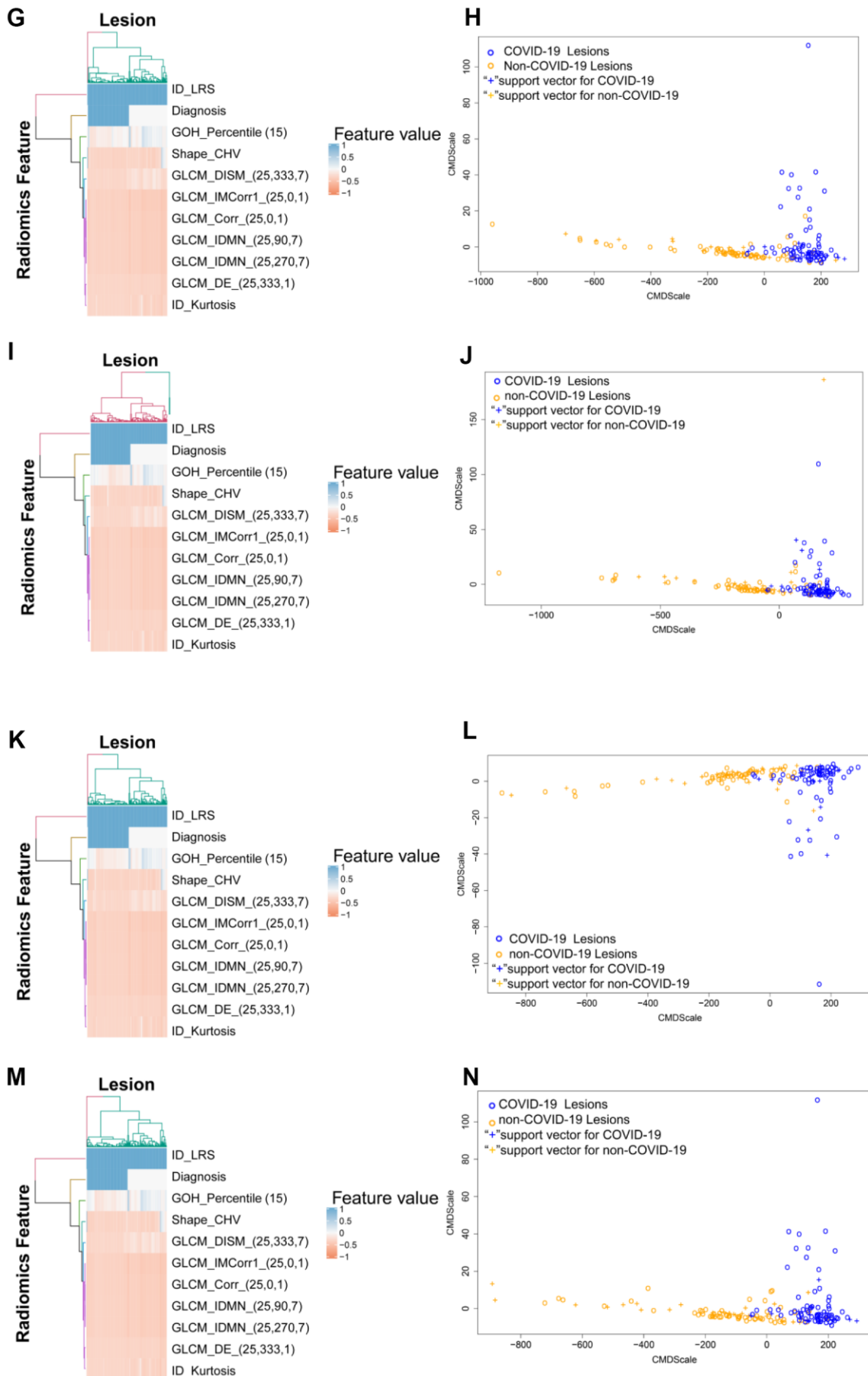


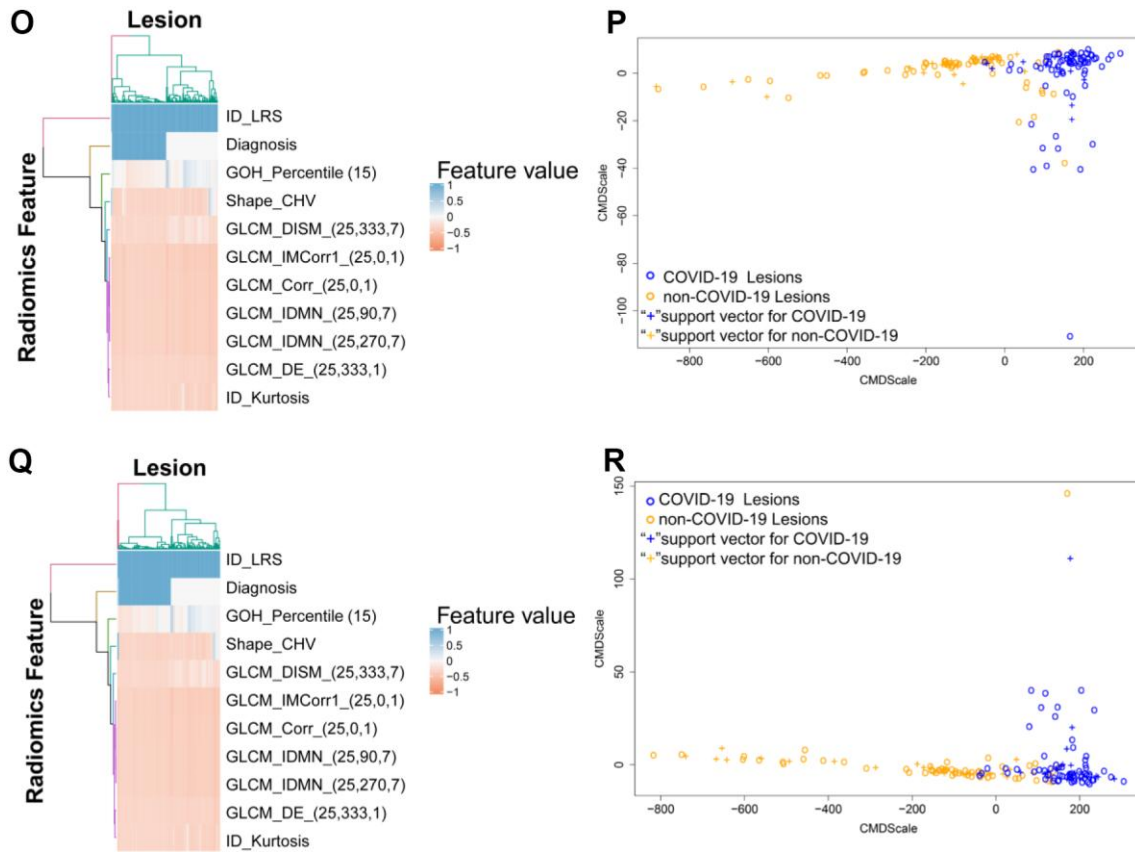
Supplementary Figure 2. The LASSO process to select the radiomics features and clinical variables for the construction of the patient-based risk score combining radiomic features and clinical variables. (A) The radiomic features and clinical variables selection procedure using LASSO regression method. To determine the best features combination for building the risk score, the control parameter λ value in the LASSO model was selected via 4-fold cross-validation with minimum criteria. The x-axis is the value of $\log(\lambda)$ and the y-axis is the binomial deviance in the 4-fold cross validation method 100 times. The upper x-axis is the number of non-zero-coefficient features with a given λ . The red curve indicated the average binomial deviance value with the vertical bars showing the upper and lower boundaries. The left vertical dotted line defined the λ with the least binomial deviance. The right vertical dotted line indicates the largest value of λ such that the binomial deviance is within one standard error of the minimum binomial deviance. (B) The LASSO coefficient profiles of the 17 radiomic features and clinical variables. The figure shows the feature coefficient change with the tuning of λ value. The dotted line was plotted at the λ value determined in (A) resulting 5 non-zero-coefficient radiomic features and clinical variables.



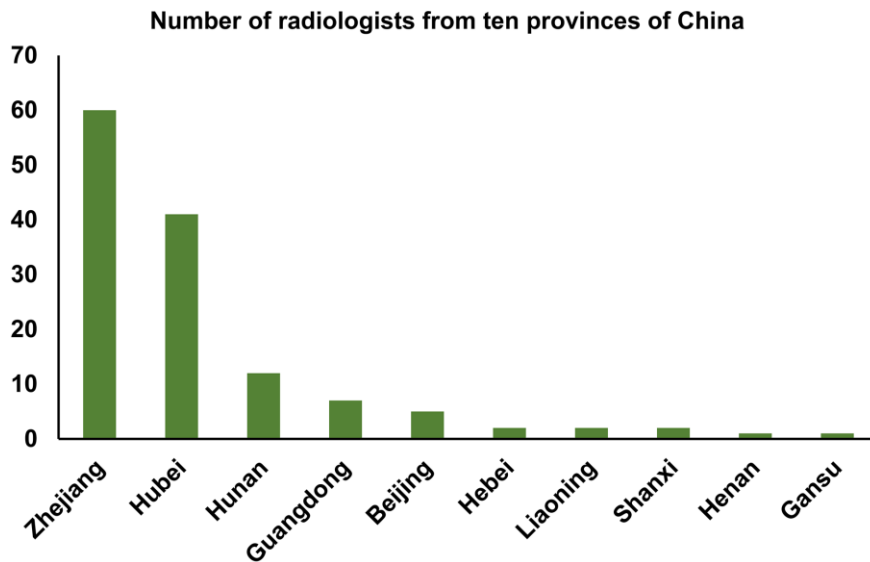
Supplementary Figure 3. The LASSO process to select the radiomic features for the construction of lesion-based risk score using radiomic features alone. (A) The radiomic features selection procedure using LASSO regression method. To determine the best features combination for building the risk score, the control parameter λ value in the LASSO model was selected via 4-fold cross-validation with minimum criteria. The x-axis is the value of $\log(\lambda)$ and the y-axis is the binomial deviance in the 4-fold cross validation method 100 times. The upper x-axis is the number of non-zero-coefficient features with a given λ . The red curve indicated the average binomial deviance value with the vertical bars showing the upper and lower boundaries. The left vertical dotted line defined the λ with the least binomial deviance. The right vertical dotted line indicates the largest value of λ such that the binomial deviance is within one standard error of the minimum binomial deviance. (B) The LASSO coefficient profiles of the radiomic features. The figure shows the feature coefficient change with the tuning of λ value. The dotted line was plotted at the λ value determined in (A) resulting the 10 non-zero-coefficient radiomic features.



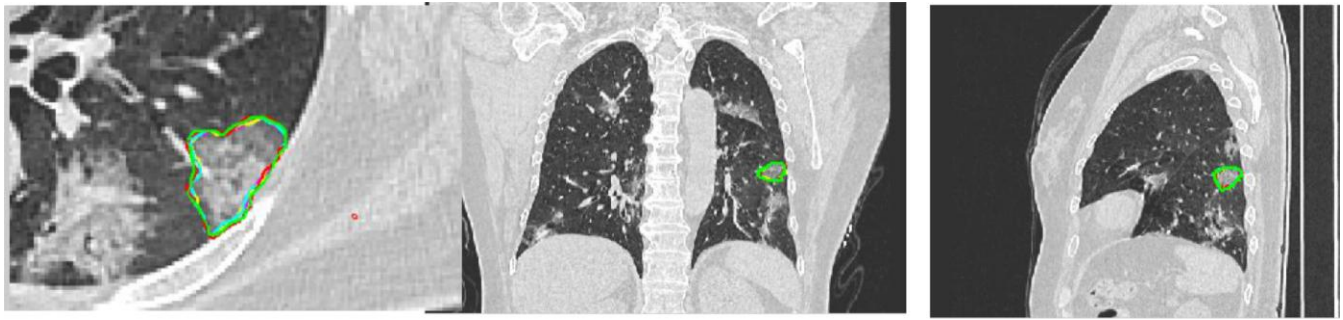




Supplementary Figure 4. The correlation of radiomics features and COVID-19 for each constituent SVM. (A, C, E, G, I, K, M, O, Q): The heat maps of correlation of radiomics features and COVID-19 for 9 individual constituent SVM. **(B, D, F, H, J, L, N, P, R):** The classical (metric) multidimensional scaling matrix to demonstrate the discriminative abilities of the individual constituent SVM to classify COVID-19 and non-COVID-19 using 9 constituent SVM individually. Abbreviations: SVM, support vector machine.



Supplementary Figure 5. The geographic distribution of 130 radiologists from 10 provinces in China including Hubei province, the epicenter of COVID-19 outbreak in China.



Supplementary Figure 6. Segmentations from 5 radiologists to delineate the volumes of interest in the same COVID-19 patient.