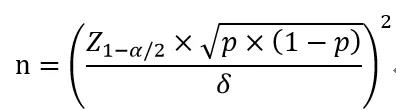
**Supplementary materials**

**Sample size calculation**

The study retrospectively enrolled patients with hepatocellular carcinoma pathologically confirmed by surgery and who underwent Gd-EOB-DTPA enhanced MRI within 1 month before surgery as the gold standard, aiming to evaluate the accuracy of the radiomics in predicting microvascular invasion of hepatocellular carcinoma. Sensitivity and specificity were both 0.80 in a previous study. The allowable error was 5%, a two-sided test was required, and α was 0.05, calculated as:

where Z1-α/2 is 1.96 by look-up table, *p*=0.80, δ=0.05, and n=246. The minimum sample size was estimated to be 246 cases. (See supplementary materials)

**Model application**

Radscore generated by radiomics features as a feature, together with other clinicoradiological features was used to establish the hybrid model. The hybrid model combined the features of all predicted values. Variance threshold method, correlation coefficient analysis, and the Lasso algorithm was used to screen features. We found that 18 features in the fusion sequence of AP and VP were the most important for predicting MVI. Those features were used to calculate the Radscore.

The Radscore regarded as a feature, together with AFP, APTT, tumor margin, capsule, intratumoral hemorrhage, arterial peritumoral enhancement, and peritumoral hypointensity on the hepatobiliary phase to establish a hybrid model that combined clinicoradiological factors and fusion radiomics signature of AP and VP. Before features screening, they were normalized using the Z-score, with all features having the same weight. In the risk factors screening of clinicoradiological model, classification index was examined using point-baserial analysis, continuous variables were evaluated through Pearson correlation analysis, and t-test was used to realize the correlation test. Finally, the Lasso algorithm was used to determine potential risk factors of MVI. Then these potential risk factors were used to establish the clinicoradiological model.

Generally, before the single-sequence radiomics feature screening, we performed correlation analysis and collinearity analysis to eliminate features with high collinearity. Subsequently, the remaining features were normalized and each feature was weighted equally for the final screening by Lasso. The final screened features and their lasso coefficients, the row matrix and the lasso intercept terms predicted values to obtain Radscore. Before fusion different sequences, such as fusion sequence of AP and VP, we spliced the features of AP and VP sequences by column, and obtained the features of fusion sequence and its Radscore according to the method of single-sequence feature screening. In conclusion, the corresponding Radscore and clinicoradiological factors were used to establish the hybrid model.