LAPS and the ALPPS was 85.7% (6/7) and 78.6% (11/14). The incidence of major complications was 36.4% (4/11) of the ALPPS group and 50.0% (3/6) of the LAPS group after the 2 stages operation. One patient died of the ALPPS group. Additionally, the median increase in FLR, median operative time and blood loss during the two stages of the LAPS were similar to those subjected to ALPPS.

Conclusions LAPS has a potential advantage in eliminating major complications of PHLF associated with classic ALPPS. LAPS may achieve the same effect of promoting significant growth of the FLR in patients with HBV-related HCC, albeit at the cost of longer interval time.

IDDF2020-ABS-0069 PREDICTION OF MICROVASCULAR INVASION BEFORE SURGERY IN PATIENTS WITH HEPATOCELLULAR CARCINOMA: A NOMOGRAM MODEL BASED ON INFLAMMATORY MARKERS

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Background Microvascular invasion (MVI) remains a risk factor for tumor recurrence and metastasis in hepatocellular carcinoma (HCC). No effective and well-recognized method can detect MVI before surgery. Inflammatory markers reflect the immune environment and have been proven to be related to prognosis as well as the presence of MVI in HCC. We aimed to establish an MVI predictive model based on inflammatory markers.

Methods Data of 1058 cases of HCC patients treated in the First Affiliated Hospital of Sun Yat-sen University from November 2003 to December 2015 were collected. In a ratio of 7 : 3, patients were divided into the training group (740 cases) and the validating group (318 cases). Inflammatory factors related to MVI diagnosis in HCC patients were selected by LASSO regression analysis, and were then integrated into an 'Inflammatory Score'. A prognostic Nomogram model was established by combining the Inflammatory Score and the independent factors determined by multivariate logistic regression analysis. The consistency index (C-index) and the area under the curve (AUC) were used to evaluate the predictive efficacy of the model.

Results A total of 1058 HCC patients were included in this retrospective study, 430 of whom (40.6%) were diagnosed with MVI. Sixteen inflammatory factors, including neutrophil, neutrophil to lymphocyte ratio, platelet to lymphocyte ratio, etc., were selected by LASSO regression analysis to establish an Inflammatory Score. Multivariate logistic regression analysis showed that Inflammatory Score (OR = 2.186, 97.5% CI: 1.656–2.950), age (OR = 0.987, 97.5% CI: 0.973–1.000), alpha fetoprotein (OR = 1.923, 97.5% CI: 1.380–2.690), tumor size (OR = 2.308, 97.5% CI: 1.656–3.220) were independent factors in the diagnosis of MVI in HCC patients. These four factors were then used to establish a Nomogram for MVI prediction. The C-index of the Nomogram prediction model was 0.72. The AUC for the training and validating group were 0.720 and 0.721, respectively.

Conclusions The Nomogram prediction model drawn in this study has a high prognostic value, which is capable of improving the diagnosis efficiency of MVI in HCC patients.

IDDF2020-ABS-0078 IMMUNOSCORE CLASSIFICATION FROM HEPATOCELLULAR CARCINOMA HISTOPATHOLOGY IMAGES USING DEEP LEARNING: A PRELIMINARY STUDY

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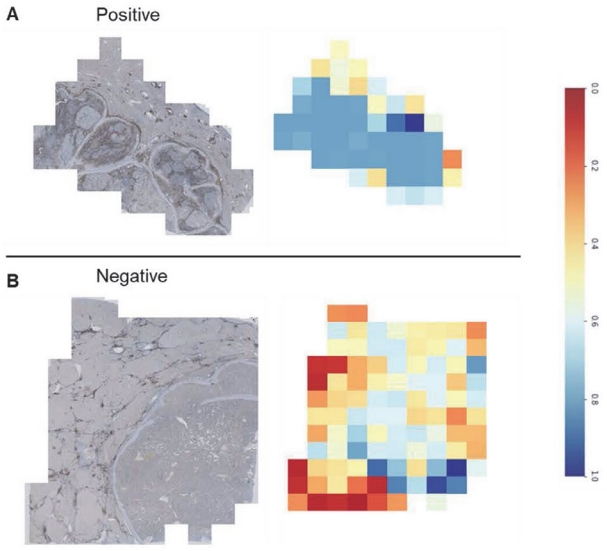
Background Immunotherapy is a recent advance for the treatment of hepatocellular carcinoma (HCC). Immunoscore assessment plays a critical role in precision immunotherapy and can predict prognosis in patients with HCC. This study aims to develop a deep-learning model to automated analyze histopathology images for classification of immunoscore (CD3 or CD8, 0–2 vs. 3–4) in HCC.

Methods We trained a patch-based deep convolutional neural network (Resnet-18) on whole-slide images to automatically classify immunoscore into 0–2 or 3–4. The data were randomly split into a training and testing dataset. The performance was first estimated on the training dataset with nine-folded cross-validation and then further validated on the testing dataset. Cross-entropy was used as a model-optimized loss function and the accuracy as well as the area under the receiver operating characteristic curve (AUC) were calculated for the identification values. Heatmaps were also generated by our model to visualize the regions the most associated with the classification.

Results We included 28 images from a study cohort of 28 HCC patients for training (18 images) and testing (10 images) the model. After iterative training, an optimized architecture



Abstract IDDF2020-ABS-0078 Figure 1 Heatmaps of patch-based tissue slides generated by the model in the testing dataset