Figure S4

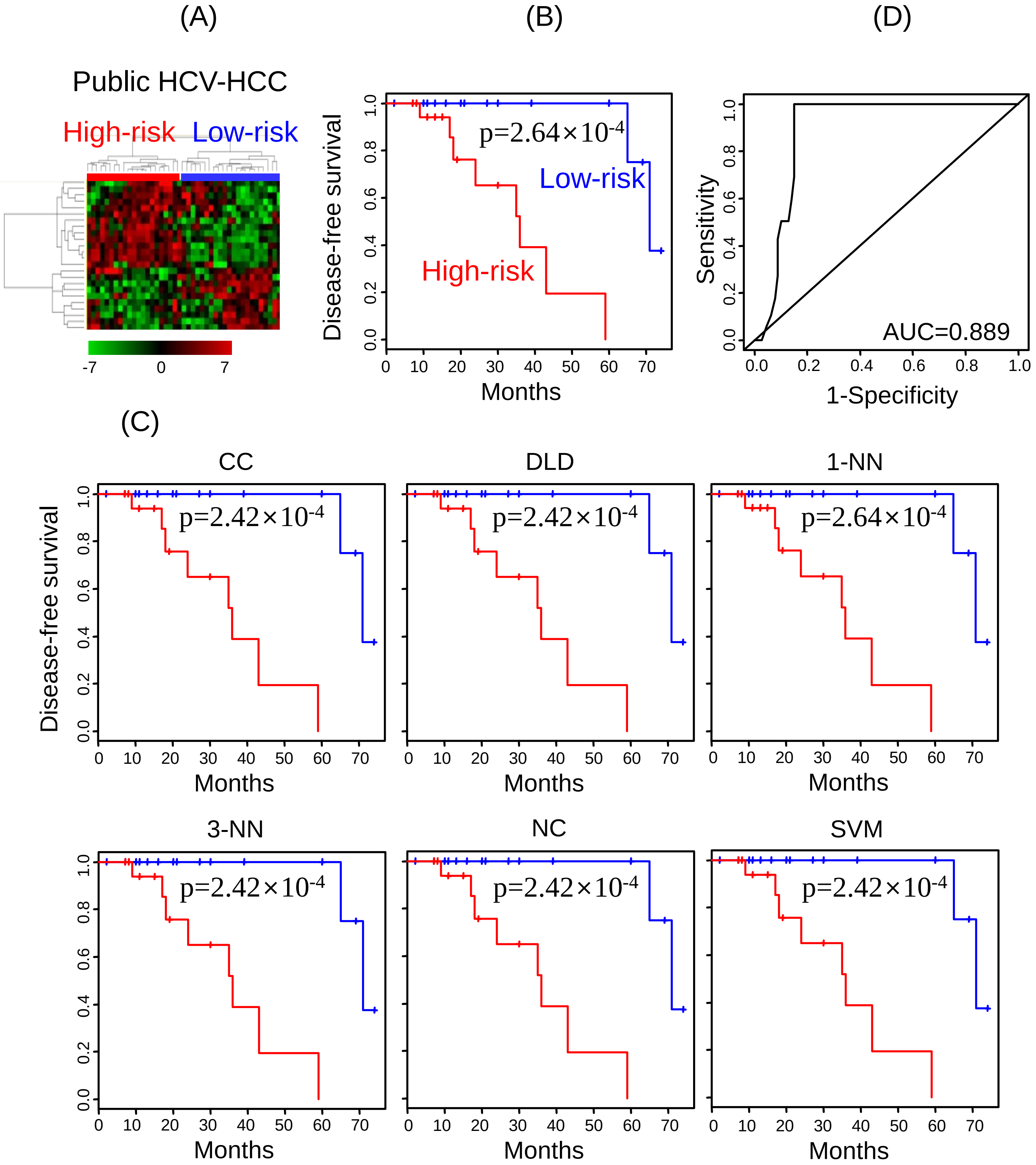

Figure S4. Cluster analysis of recurrence-related pathways. (A) Dendrogram of clustering pattern measured from the matrix of principal components of 32 recurrence-associated pathways (*p*-value<0.01) from public HCV-HCC. Samples were classified into two subgroups: low-risk and high-risk based on recurrence outcome. Columns represent individual samples, and rows pathways. Red and green colors reflect high and low levels of optimal principal component scores, respectively, as indicated by scale bars. **(B)** Kaplan-Meier plots for recurrence rates of the low- and high-risk subgroups. **(C)** Cross-validation of the low- and high-risk subgroups using six different algorithms: compound covariate (CC), diagonal linear discriminant (DLD), 1-nearest neighbor (1-NN), 3-nearest neighbor (3-NN), nearest centroid (NC) and support vector machine (SVM). **(D)** ROC curve computed with CC validation algorithm for subgroup classification.