Figure S9

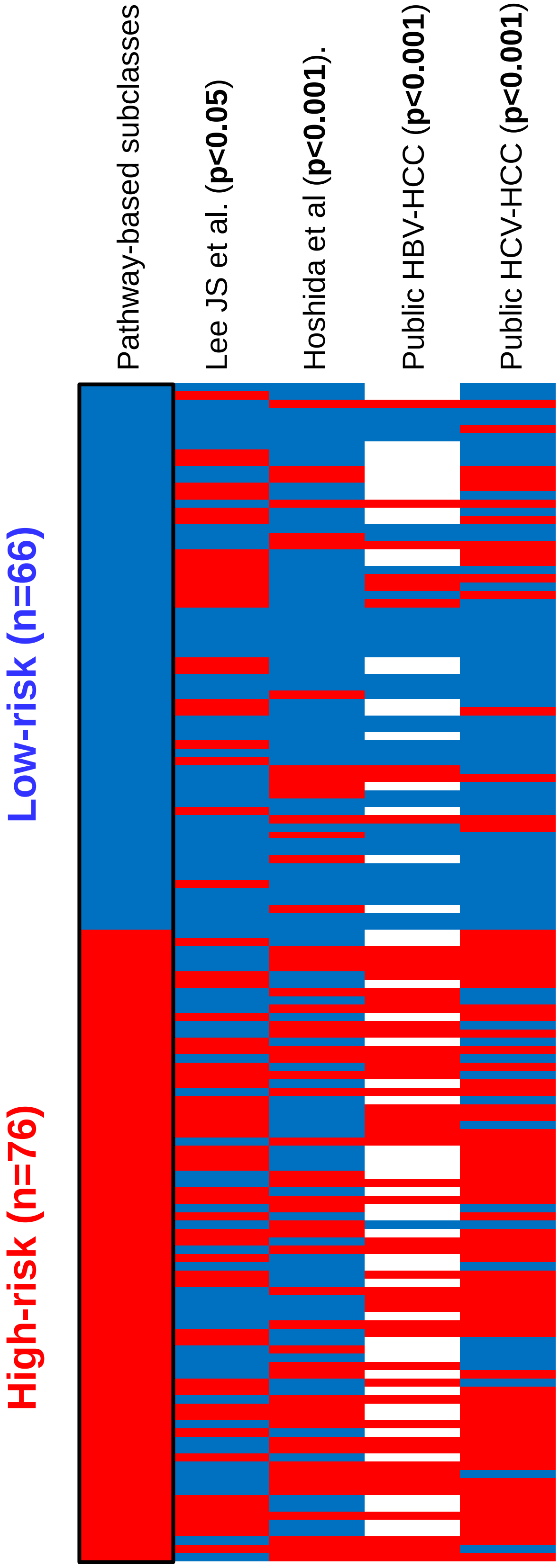

Figure S9. Comparison of patient classification. With previously reported prognosis-associated genes (Lee *et al*. [2], Hoshida *et al*. [8], public HBV-HCC [3] and public HCV-HCC [4] datasets), patient subclasses were determined using hierarchical clustering, and compared with subgroups obtained from our pathway-based method. Blue and red colors represent low- and high-risk subgroups, respectively, while white (public HBV-HCC) signifies the intermediate subgroup. Statistical significance was measured using Fisher's exact test in comparison with pathway-based low- and high-risk subclasses.