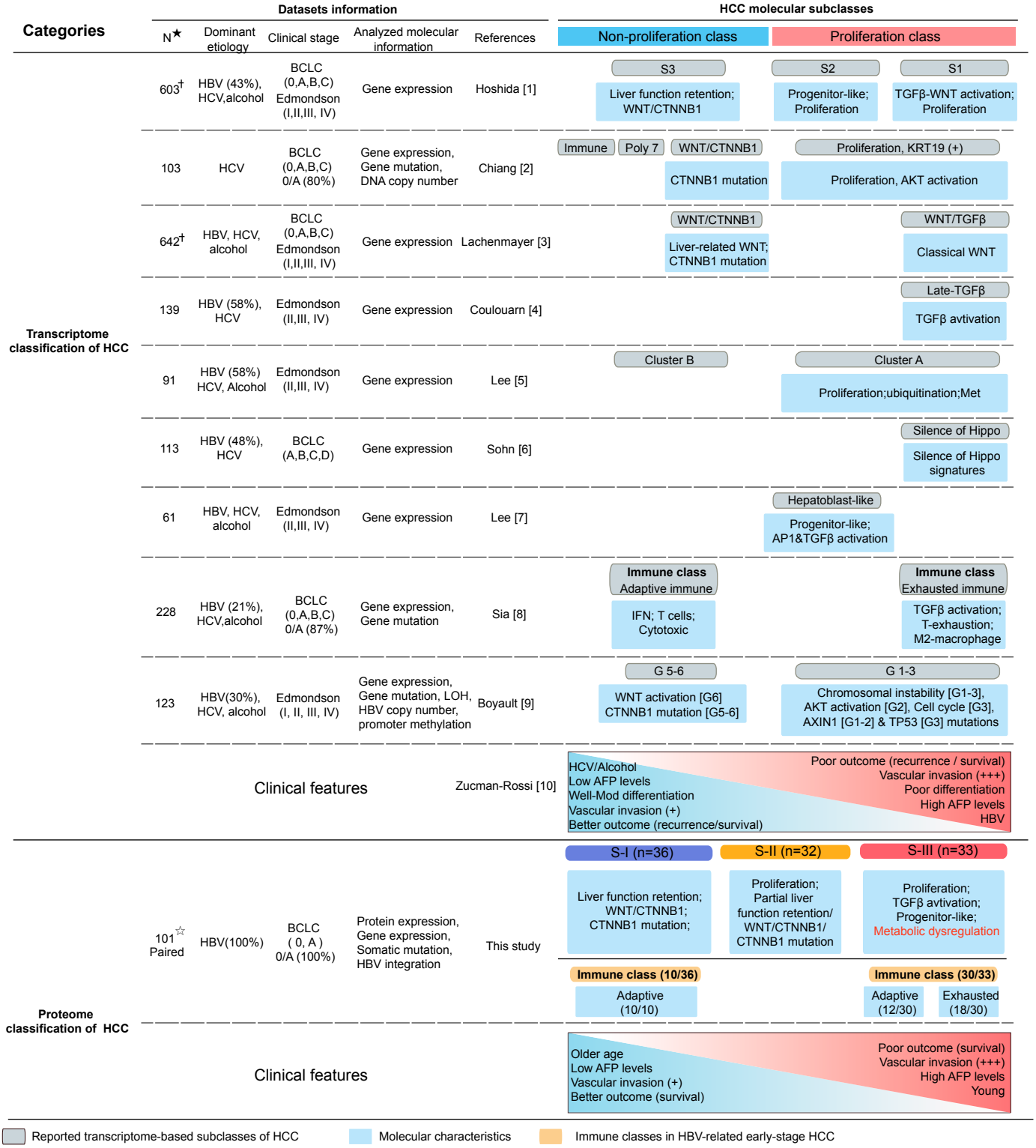

HBV: hepatitis B virus, **HCV**: hepatitis C virus, **Edmondson**: Edmondson and Steiner grading system, **BCLC**: Barcelona Clinic Liver Cancer staging system
★ Number of samples used to define classification, ☆ 199 samples (101 tumors and 98 paired non-tumor samples) used for proteome analysis. 101 tumor smaples used to define proteomic subtypes,199 samples used to identify signature proteins for each subtype.† Gene expression datasets collected from eight independent HCC corhorts.

Comparative analysis of proteome and transcriptome subclasses. Basic datasets information was displayed on the left panel. The right panel summarized the major HCC subclasses (grey box), and its relative molecular characteristics (blue box). The relationship between the molecular subclasses and the correlation with the clinical features were referenced to Zucman-Rossi et al.[10] and Hoshida et al.[11]. The novel characteristics captured by proteomics are indicated with red characters, while the features identified by both proteome and transcriptome are shown in black colour. Correspondence between proteomic and mRNA subclasses was evaluated by single sample GSEA analysis using the signature genes collected from literatures and defined by proteomics (Extended Data Fig.7a). Moreover, the clinical features were also employed to define the correlation between the subclasses.

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