



**Supplementary Figure 3** Hierarchical clustering analysis of human and mouse HCC without *Acox1*<sup>-/-</sup> and ciprofibrate-induced HCC models and comparison of predicted outcome. **(a)** Dendrogram of cluster analysis. Orthologous genes with an expression ratio that has at least 2-fold difference relative to reference in at least 10% of tissues in one of both data sets were selected for hierarchical analysis (1,950 genes). Please note that memberships of each tissue in cluster analysis are not changed even after removing *Acox1*<sup>-/-</sup> and ciprofibrate-induced HCC models from mouse HCC data set before standardization. Red and blue color bars represent human and mouse HCC tissues respectively. Identities of each HCC tissues were shown in right end of each row. **(b)** Columns represent each tissue as indicated in **(a)** and rows represent outcomes of various prediction methods as indicated at the end of rows. Each cell represents memberships of tissues when a particular human sample-trained prediction method was applied in human and mouse sets (as indicated in Table 1). The crimson and green color in cells represent subclass A and B respectively.