



Supplementary Figure 2 Hierarchical clustering analysis of survival genes (144 orthologous genes) in human and mouse HCC. A hierarchical clustering algorithm based on Pearson correlation coefficients was applied to group genes on the basis of similarity in the pattern over all tissues and tissues on the basis of similarity in the pattern over all genes. The data are presented in matrix format in which rows represent individual gene and columns represent each tissue. Each cell in the matrix represents the expression level of a gene feature in an individual tissue. The red and green color in cells reflect high and low expression levels respectively as indicated in the scale bar (log₂-transformed scale). In dendrogram of cluster tree, 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.