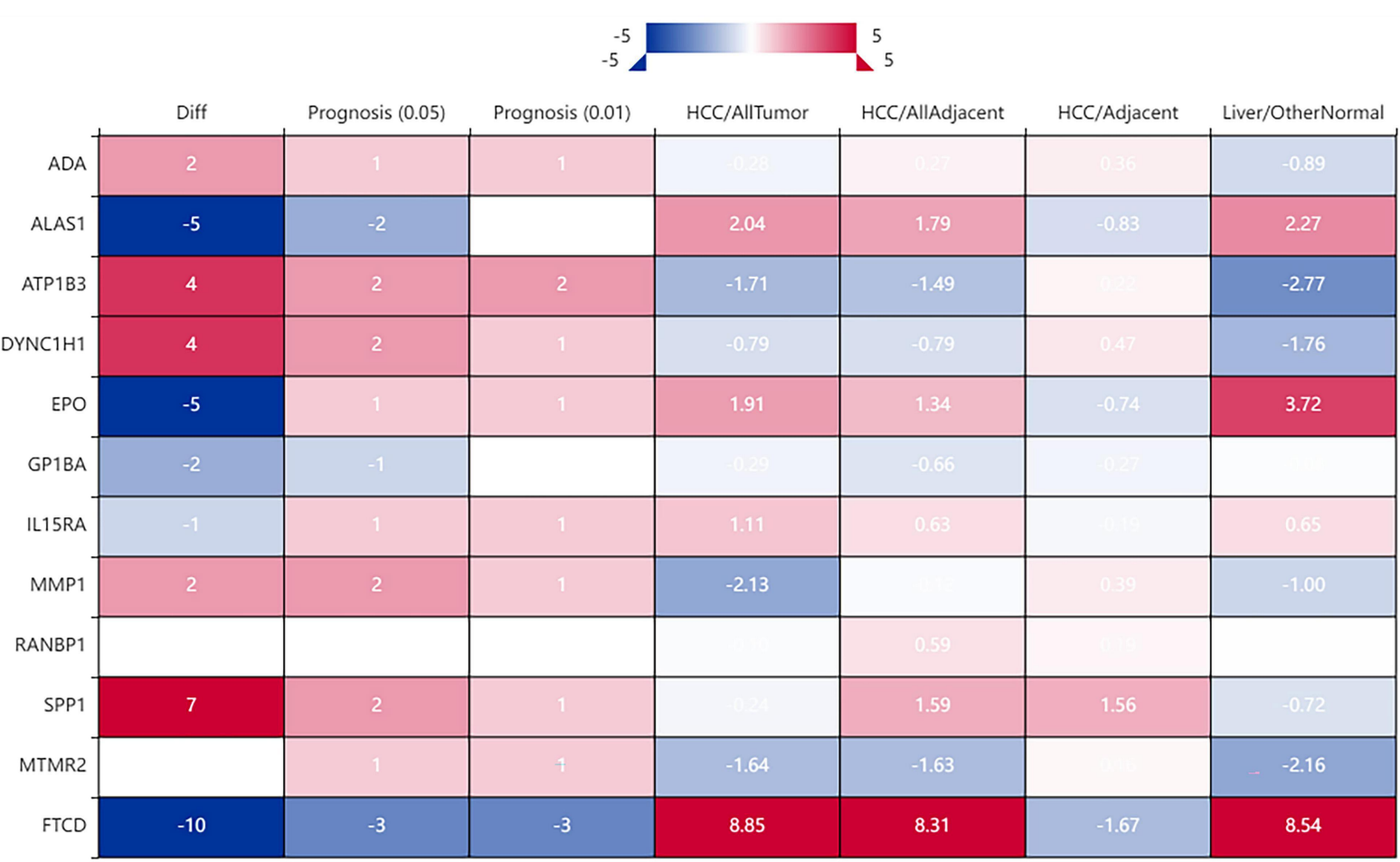


**Additional file 7: Fig. S7** The expression of 12 characteristic genes of the risk signature in HCC from HCCDB database. Diff: the number of differentially expressed datasets; Red/Blue for consensus up-regulated/down-regulated. Prognosis: the number of significant datasets by survival analysis; Red/Blue for UNFavorable/Favorable. HCC/AllTumor: Red/Blue for positive/negative fold change in log2 scale by comparing HCC with all tumors (TCGA data). HCC/AllAdjacent: Red/Blue for positive/negative fold change in log2 scale by comparing HCC with all adjacent samples (TCGA data). HCC/Adjacent: Red/Blue for positive/negative fold change in log2 scale by comparing HCC with adjacent samples (HCCDB data). LiverOtherNormal: Red/Blue for positive/negative fold change in log2 scale by comparing liver with normal tissues (GTEx&TCGA data).