



S1 Fig. Functional analysis of genes differentially expressed in HCC-associated HCV. Top-scored pathways (A), and diseases and bio functions (B) identified by IPA database (Ingenuity Pathway Analysis, <http://www.ingenuity.com/>) from the set of genes differentially expressed in HCV-associated HCC. Columns display the P-values calculated by Fisher's exact test (left axis). Dots indicate the percentage of downregulated genes (right axis). All categories show a striking majority (on average 90%) of downregulated genes.