

Supplementary Figure 1. GSTA4 gene analysis in hepatocellular carcinoma (Oncomine database). Oncomine analysis of neoplastic vs. normal tissue showed that GSTA4 was significantly over-expressed inepatocellular carcinoma in different datasets (A: Chen [1]; B: Mas [2]; C: Roessler [3]; D: Roessler [3]). Box plots derived from gene expression data in Oncomine comparing expression of a specific GSTA4 gene in normal (left plot) and hepatocellular carcinoma tissue (right plot).

- [1] Chen X, Cheung ST, So S, Fan ST, Barry C, Higgins J, Lai KM, Ji J, Dudoit S, Ng IO, Van De Rijn M, Botstein D and Brown PO. Gene expression patterns in human liver cancers. Mol Biol Cell 2002; 13: 1929-1939.
- [2] Mas VR, Maluf DG, Archer KJ, Yanek K, Kong X, Kulik L, Freise CE, Olthoff KM, Ghobrial RM, McIver P and Fisher R. Genes involved in viral carcinogenesis and tumor initiation in hepatitis C virus-induced hepatocellular carcinoma. Mol Med 2009; 15: 85-94.
- [3] Roessler S, Jia HL, Budhu A, Forgues M, Ye QH, Lee JS, Thorgeirsson SS, Sun Z, Tang ZY, Qin LX and Wang XW. A unique metastasis gene signature enables prediction of tumor relapse in early-stage hepatocellular carcinoma patients. Cancer Res 2010; 70: 10202-10212.