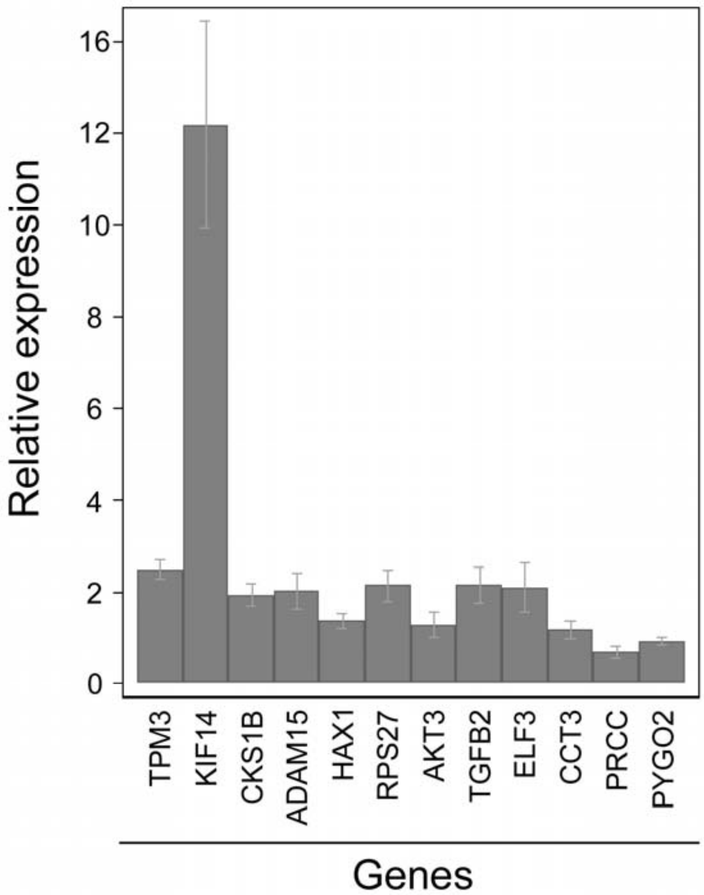

**Supplementary Figure 1**. Expression levels of 12 candidate genes located in the RARs on 1q. Mean RNA expression levels (tumor/normal ratio) of 12 candidate genes were calculated by real-time qRT-PCR in 20 HCCs. cDNA from a non-neoplastic part of liver, which showed no septal fibrosis or liver cirrhosis, was used as normal control. Human *GAPDH* gene was used as an internal control for qRT-PCR. Error bars represent mean ± standard error of mean.