



Fig. S3. Box plots for microRNAs (miRNAs) selected by principal component analysis. Expression patterns for the 24 miRNAs used to discriminate between hepatobiliary tumor and non-tumor samples. Vertical left axis shows miRNA expression levels. Adjusted *P*-values are indicated in Table S2. hsa, homo sapiens (human); Be, benign hepatobiliary tumor; CC, cholangiocarcinoma; YCC, cholangiocarcinoma of young individuals (younger than 50 years old); HCC, hepatocellular carcinoma; T, tumor; NT, non-tumor.