



**Supplementary Figure S4** DNA methylation profiles of 82 samples of adult control normal liver tissue from two data sets deposited in the GEO database (<https://www.ncbi.nlm.nih.gov/geo/>) (GSE61258 and GSE69852) (black circles), 113 samples of non-cancerous liver tissue showing non-alcoholic steatohepatitis (NASH-N) (red circles), and 37 samples of non-cancerous liver tissue showing chronic hepatitis or cirrhosis associated with hepatitis virus infection (viral-N) (blue circles). Principal component analysis using the 9,150 probes showed that the DNA methylation profiles of NASH-N samples differed distinctly from those of both control normal liver tissue samples from the public database and viral-N samples.