

Supplementary Figure S2 DNA methylation profiles of 19 samples of normal liver tissue (NLT) from patients with morbid obesity and 36 samples of NLT from patients with liver metastases of primary colorectal cancer without hepatitis virus infection, chronic hepatitis, liver cirrhosis or hepatocellular carcinoma. Principal component analysis (A) and unsupervised hierarchical clustering (maximum distance, complete linkage method) (B) using all 444,907 probes did not reveal any heterogeneity of DNA methylation profiles among the 55 NLT samples: 19 with morbid obesity (gray) were not discriminated from 36 with liver metastases of primary colorectal cancer (black).