Epigenetic silencing of *HLF* aids precise medicine to human early non-small cell lung cancer in diagnosis and prognosis monitoring

*HLF* was found to be hyper-methylated in lung cancer in genome-wide small sample size studies. However, the performance, including sensitivity, specificity, of the prediction in large samples is not evaluated. Furthermore, the functions of *HLF* in lung cancer pathogenesis were unclear neither. In this study,