In the past decades, large number of DNA methylation based cancer diagnostic biomarkers has been identified in NSCLC. The diagnostic or risk association for several of them has been quantitatively evaluated such as SHOX2 [[1](#_ENREF_1)], APC [[2](#_ENREF_2)], RASSF1A [[3](#_ENREF_3)], CDH13 [[4](#_ENREF_4)], MGMT [[5](#_ENREF_5)], RUNX3 [[6](#_ENREF_6)], RARbeta [[7](#_ENREF_7)], DAPK [[8](#_ENREF_8)], E-cadherin [[9](#_ENREF_9)] and P16 [[10](#_ENREF_10)]. However, the quantitative assessment of the diagnostic performance of the methylation status of FHIT in NSCLC were not investigated.

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