DNA Methylation biomarkers of therapeutic response to demethylating agent decitabine in NSCLC

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DNA methylation plays an import role in both tumorigenesis and therapy resistance. Demethylating agent regimens have shown efficacy in hematological malignancies, and are actively studied for other cancer types. High variability and heterogeneity were observed in drug response to demethylating agent from different patients. In this study, we proposed a novel approach to predict the drug response to decitabine with DNA methylation status identified from formalin-fixed and paraffin-embedded tissues (FFPE). In the model training stage, xxx public methylation-decitabine response dataset were collected and a random forest model with xx features was successfully trained with sensitivity= xx, specificity=xx of and AUC= xx. In the model test stage, we collected 60 patients (30 responders and 30 non-responders) and applied target DNA methylation sequencing to generate methylation profile for xx, xxx, xxx, xxx, xxx, xx. We observed the prediction accuracy as high as 85% with sensitivity = xx, specificity = xx and AUC=xxx. In conclusion, we proposed a novel prediction model based on DNA methylation profiles to decitabine response in non-small cell lung cancer patient therapy.

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