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(54) Title: METHODS AND SYSTEMS FOR METHYLATION SEQUENCING

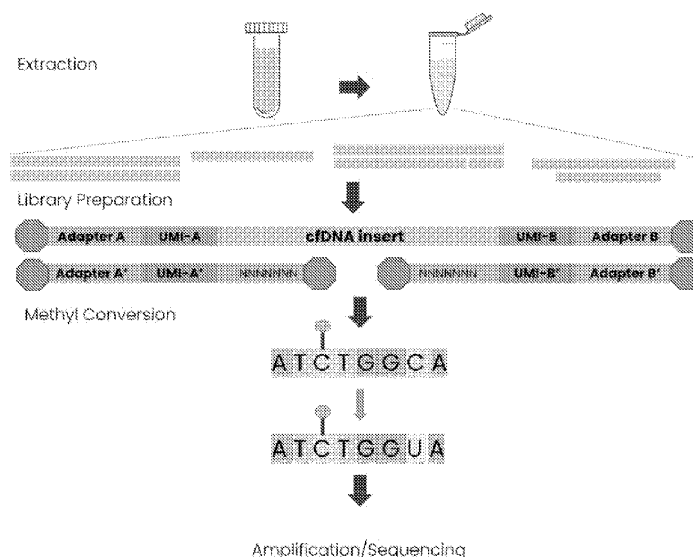


FIG. 2

(57) Abstract: Methods and systems provided herein address limitations of nucleic acid methylation sequencing and uses thereof for detection of disease by improving the quality, sensitivity, and accuracy. Methods provided herein further include minimally-destructive methylation conversion methods and nucleic acid library preparation techniques that improve methylation sequencing by minimizing signal loss and biases. Further provided herein are greater accuracy and more complete methylation state information, which permits higher quality feature generation for use in machine learning models and classifier generation.

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