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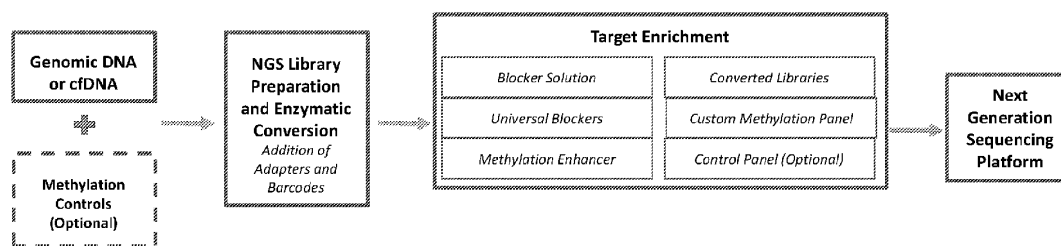


FIG. 34

(57) Abstract: Provided herein are compositions and methods for identifying post-transcriptional nucleic acid modifications. Further provided herein are synthetic blocking libraries. Further provided herein are methods for designing synthetic blocking libraries, and application towards methylome analysis.