

Supporting Information

Probing Low Abundant DNA Methylation by CRISPR-Cas12a-assisted Cascade Exponential Amplification

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Table S1. Details of the sequences used in the article

Title	Sequence (5'-3')
Methylated	GAGGGTGGGG ^m CGGAC ^m CG ^m CGTG ^m CGCT ^m CGG ^m CGG ^m CTG
Unmethylated	GAGGGTGGGGCGGACCGCGTGCGCTCGGCGGCTG
Padlock	CACGCGGTCCGCCCCACCCTCCCTCAGCAAAAAACAGAAATTACCCTATAGTG AGTCGTATATTAATAACATCCAAAATTACCTCAGCCAGCCGCCGAGCG
sgRNA	UAAUUUCUACUAAGUGUAGAUUUAUAGUGAGUCGUAUAAU
Reporter probe	FAM-TTTTAAAATTATA-BHQ

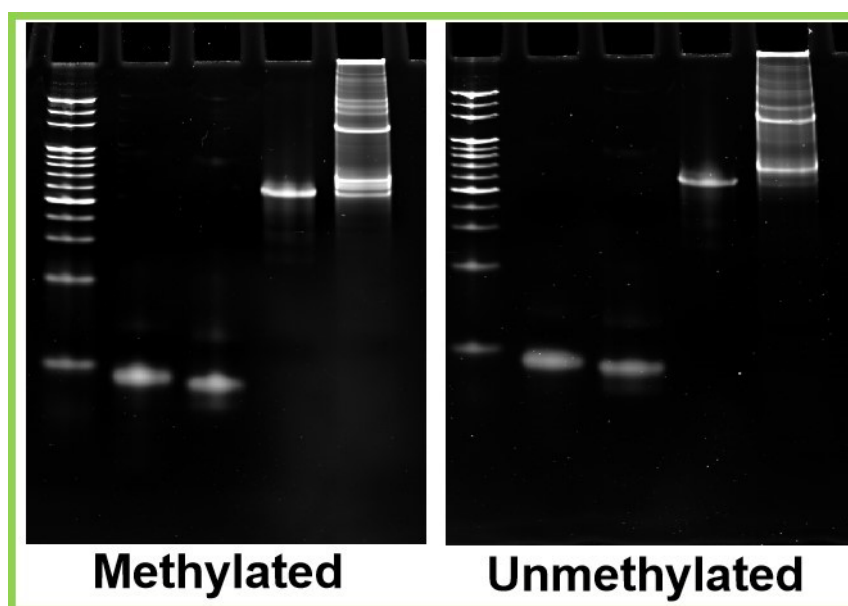


Figure S1. PAGE analysis result of the RCA process with methylated (left) and Unmethylated DNA sequence (right) before bisulfite treatment.

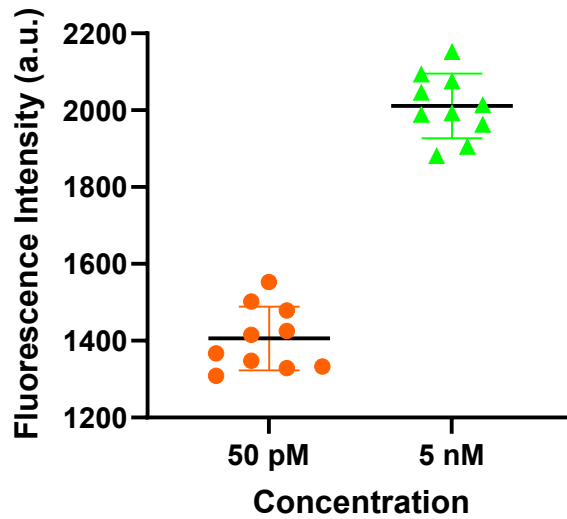


Figure S2. Repeatability of the CAM approach among 10 replicated experiments using samples with 5 nM and 50 pM of methylated DNA. Error bars represent standard derivation, $n = 10$ technical duplicates.

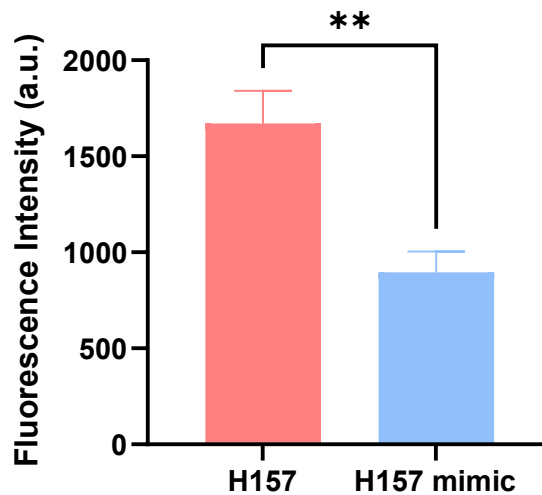


Figure S3. The peak of the fluorescence intensity with the amount of genomic DNA extracted from human lung cancer cells H157 and H157 mimic. Error bars represent standard derivation, $n = 3$ technical duplicates. $**p < 0.01$