Supporting Information

Nanopore counter for highly sensitive evaluation of DNA methylation and application for in vitro diagnostics

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Oligonucleotides

Table S1. Oligonucleotides used in this study.

Name	Sequence (5′→3′)
PUC57-SEPT9	PUC57- GATATCCGGCTAGCTCTGCACTGCAGGAGCGCGG GCGCGGCGCCCCAGCCAGCGCGCAGGGCCCGGG CCCCGCCGGGGGCGCTTCCTCGCCGCTGCCCTCC GCGCGACCCGCTGCCCACCAGCCATCATGTCGGA

	CCC<mark>CGCG</mark>GTCAAC<mark>GCGC</mark>AGCTGGATGGGATCATTTCGGACTTCGAAGGTGGGTGCTGGGCTGGCTGCTGCGGCCGCGGACGTGCTGGAGAGGACCCTGCGGGTGGGCCTGGCGCGGGACGGGGGTGCGCTGAGGGGAGACGGGAGTGCGCTGAGGGGAGACGGGACCC
317bp-Forward primer	ATGCATCTAGATATCCGGC
317bp-Reverse primer	ATATCGGGTCCCGTCTCC
406bp-Forward primer	GGAGAAAATACCGCATCAGGC
406bp-Reverse primer	CCCAGCACCCACCTTCG
806bp-Forward primer	CCTCTTCGCTATTACGCCAG
806bp-Forward primer	ATTACCGCCTTTGAGTGAGC

Note: Highlighted red sequence: The recognition sites of HhaI and BstUI endonucleases
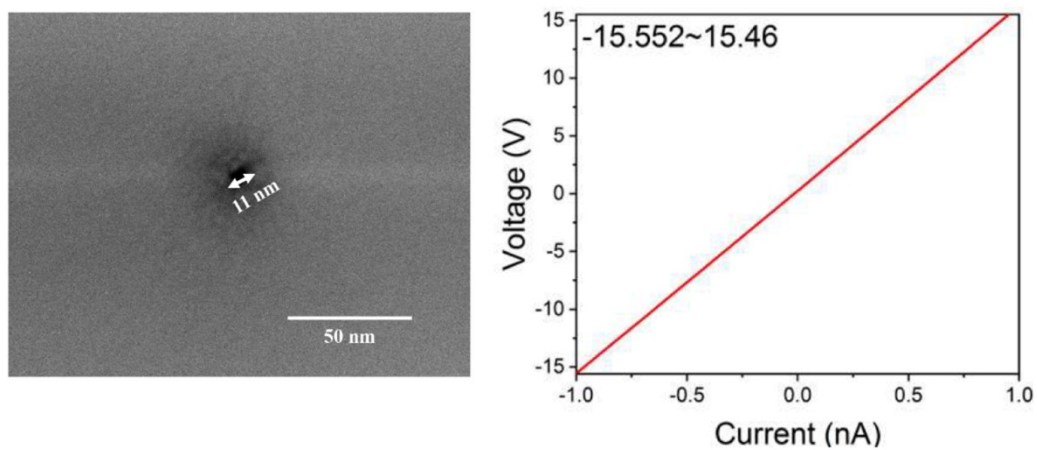
Supplementary figures

Fig. S1 (a) Top view of SEM image of a typical glass nanopore. (b) I-V curve of a typical glass nanopore in the test buffer (4 M LiCl).
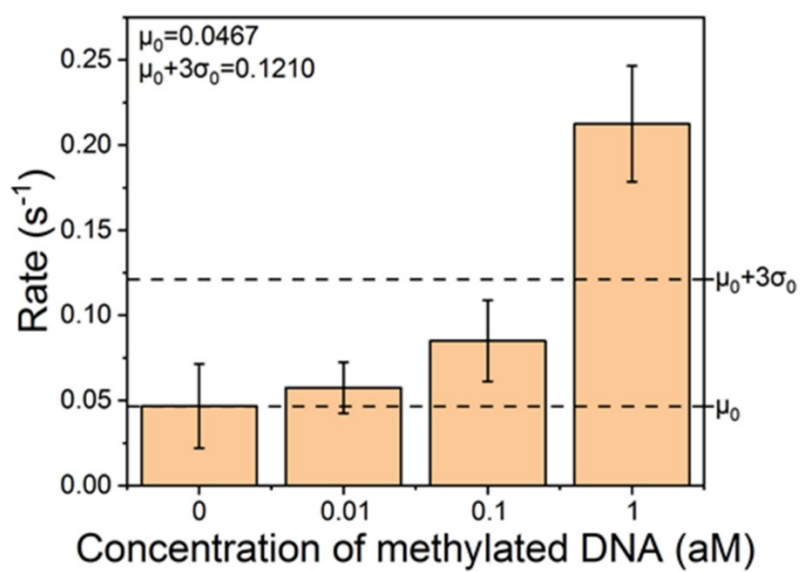

Fig. S2 The noise level of the sensor with zero input and the calculation of the LOD of the sensor.
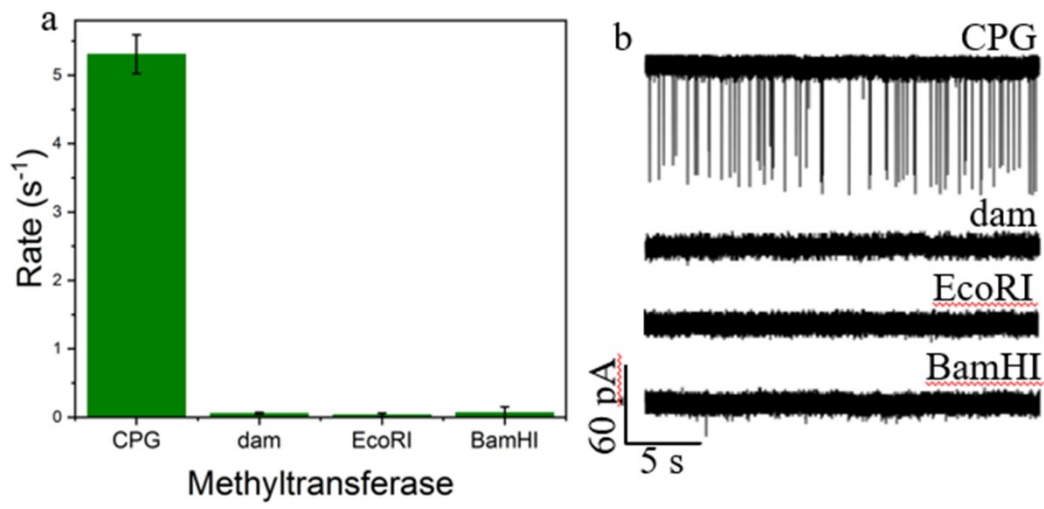
Fig. S3 Performance of the sensor to other type of methylation. Only CpG methylation can generate the translocation signal, showing good selectivity.