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Supporting Information

Molecularly Resolved, Label-free Nucleic Acid Sensing at Solid-liquid Interface using Non-ionic DNA Analogues

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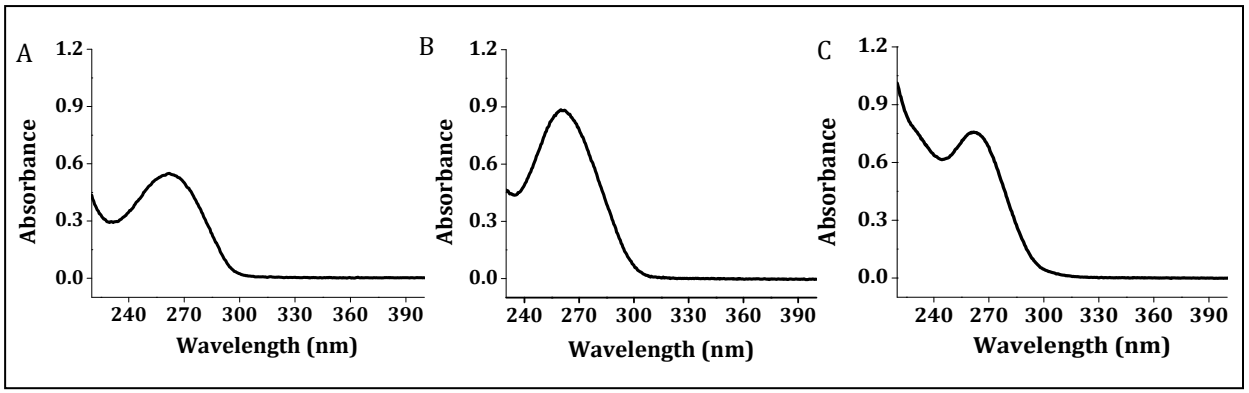

Figure S1: UV absorption (concentration calculated from the UV data) of fully modified (A) ssDNA (4.5 μM), (B) ssPNA (7.5 μM) and (C) ssMO (6.2 μM) at 260 nm.

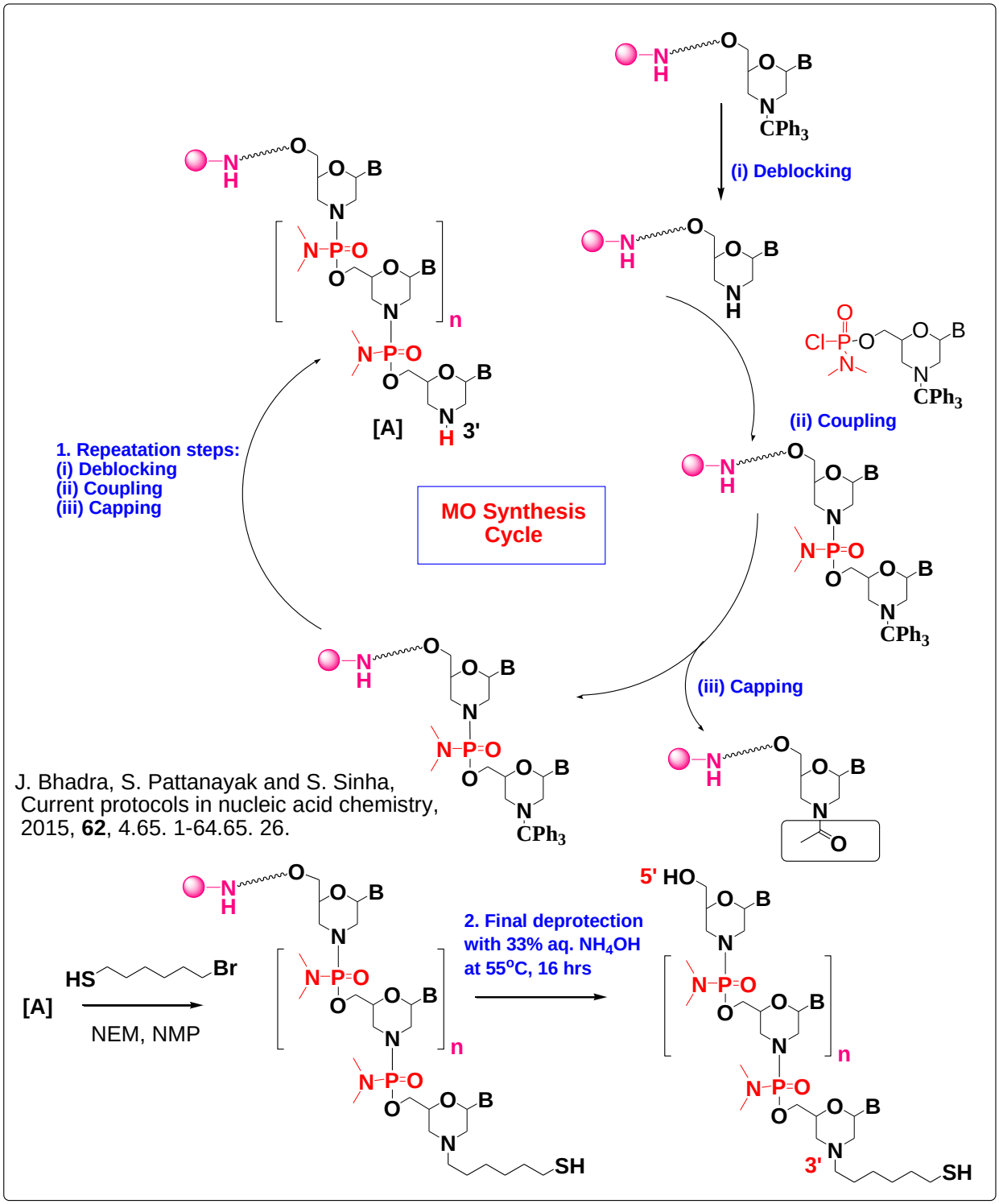

Figure S2: The MO synthesis cycle.

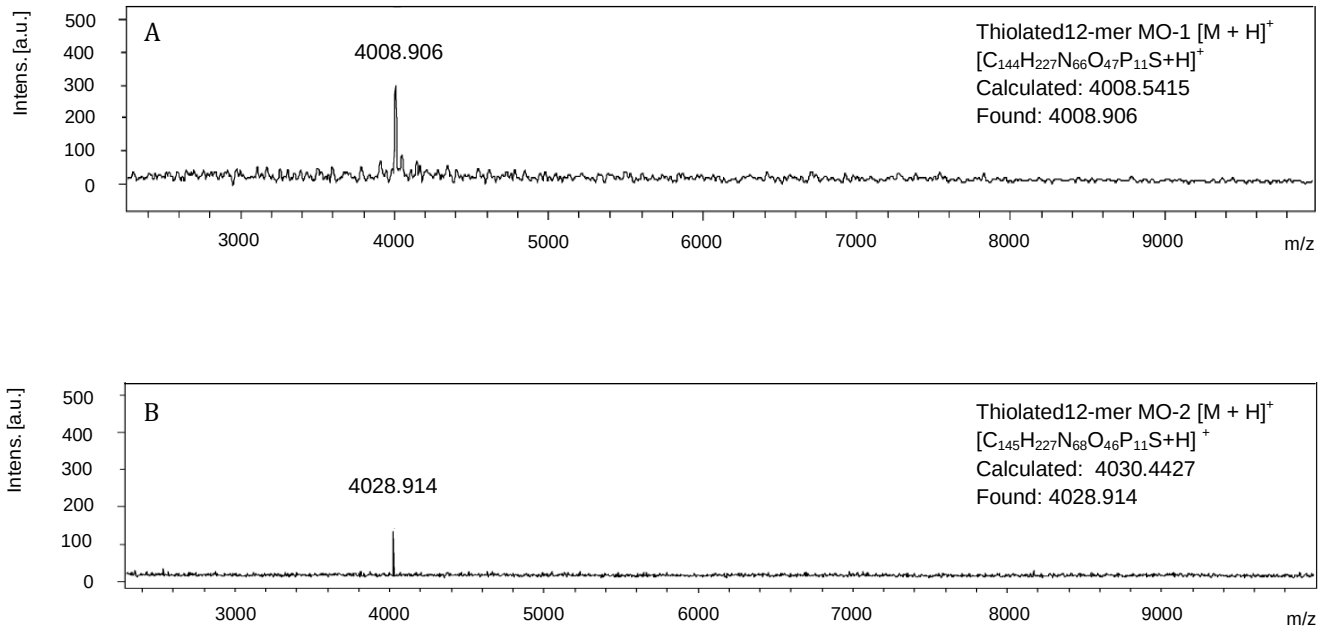

Figure S3: MALDI-TOF mass spectra of (A) MO-1 and (B) MO-2.

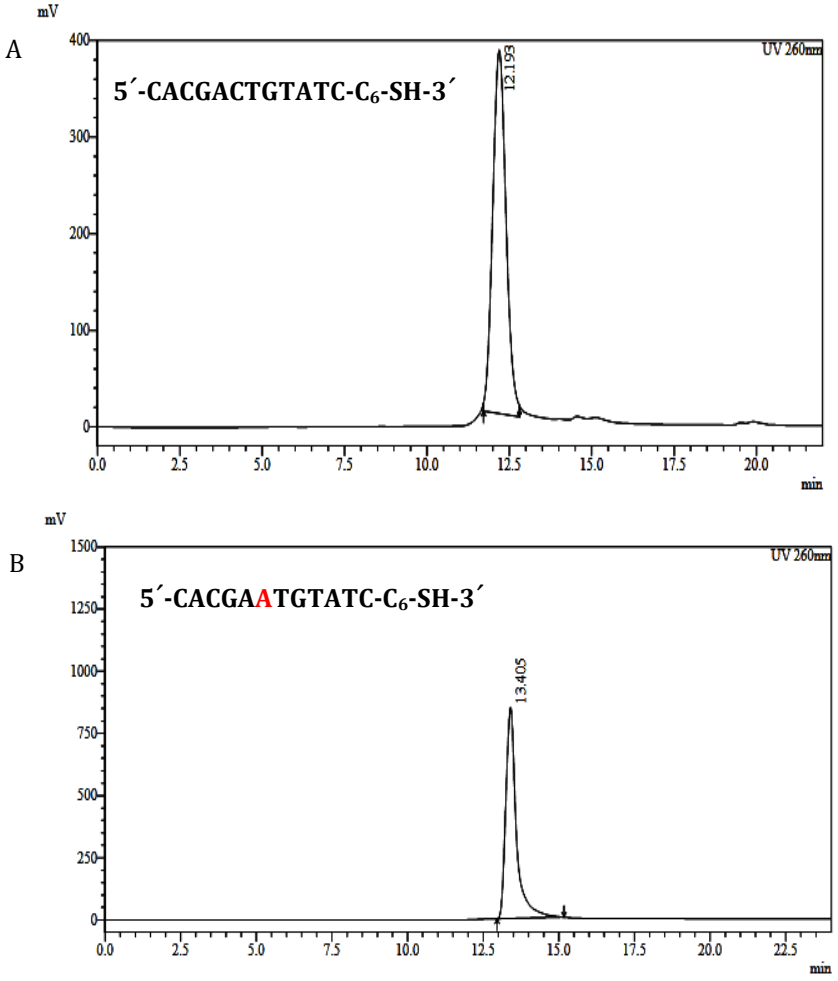

Figure S4: HPLC chromatogram of (A) MO-1 and (B) MO-2 in C-18 column, 5 µm, 4.6 mm I.D×250 mm, Gradient used 5-50 % CH_3CN in 0.1 M ammonium acetate (pH=7.1) for 25 min and then 50-5 % CH_3CN in 0.1 M ammonium acetate (pH=7.1) for 5 min, 1 ml/min flow rate.

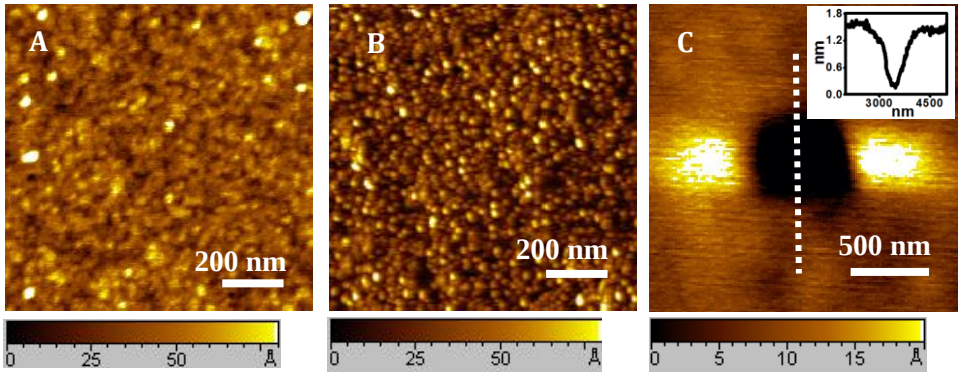

Figure S5: Topography image of (A) silicon [Z –range: 0-8 nm], (B) DNA film [Z –range: 0-8 nm], (C) scratched region. The inset figure corresponds to cross-section line profile over the scratched region [Z –range: 0-2 nm]. Z range scale bar has been shown in each case.

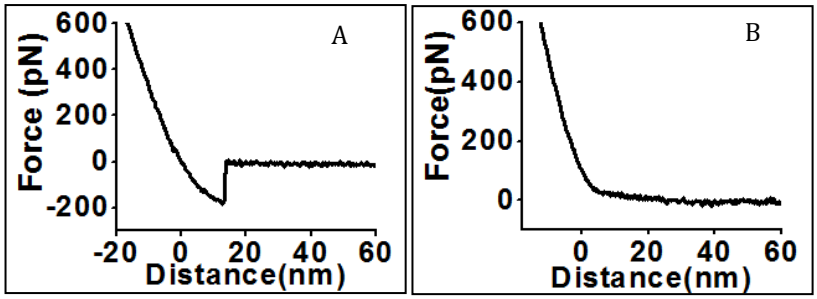

Figure S6: Representative force-distance curve for the case of (A) a typical unbinding peak from which the unbinding force values for fully matched or singly mismatched duplexes have been estimated, and the case of (B) fully non-complementary duplex, where no such unbinding is observed since no effective duplex was formed due to non-complementary sequence combination.

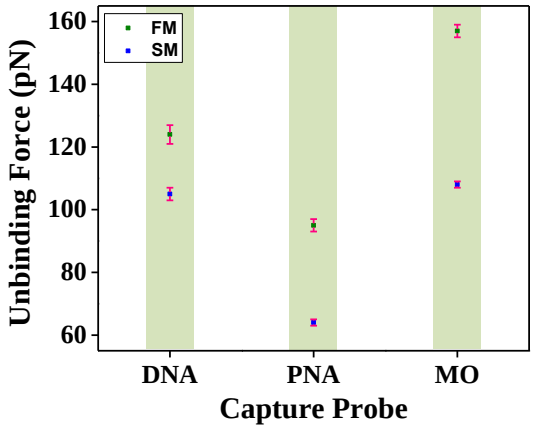

Figure S7: Unbinding force values obtained for the fully matched (FM) and singly mismatched (SM) duplex using different capture probes DNA (FM: DNA-1 – T-DNA-1; SM: DNA-2 – T-DNA-1), PNA (FM: PNA-1 – T-DNA-1; SM: PNA-2 – T-DNA-1) and MO (FM: MO-1 - T-DNA-2; SM: MO-2 – T-DNA-2) . The error bar signifies mean absolute deviation.