## Highly specific SNP detection using 2-D graphene electronics and

## **DNA strand displacement**

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## **Supplementary Materials:**



Figure S1. The structure of DS probe with specific sequences. The aqua color strand is complementary target strand, and strand with single mismatch has T instead of G in the middle of the sequence. The red strand with the black toehold is normal side (N) and the counterpart is weak side (W), which contains 4 inosine (I), indicated with green letter. The left set is strand sequence used in FET experiment and the right set is the strand sequence used in real time fluorescence measurement experiment. The quencher (black balloon) and Texas red fluorophore (red balloon) are shown.



Figure S2. Fluorescence measurements with different toehold lengths. A) 10 nt of toehold is used. Similar level of strand displacement was observed for both the perfect match strand and the single mismatch target. B) 5 nt of toehold does not induce the strand displacement with the perfect match target strand. C) Using 7 nt of toehold, single mismatch was well discriminated. X-axis is time (seconds) and Y axis is relative intensity of fluorescence. The concentration of DS probe was 20 nM and the concentrations of the target strands are shown in the plots.



Figure S3. Modification of DS probe as DNA tweezers and gel electrophoresis analysis. A) Left: Hinge part is added to bound DS probe when it is displaced. Right: The partial triple strand is stably constructed. The displacement reaction is not affected by the hinge as there is 10 nt of loop part. B) Gel electrophoresis plot of single mismatch discrimination. The left lane shows strand displacement of DNA tweezers by perfect match T and the right lane shows the strand displacement by single mismatch T. The red arrow indicates DNA bands. C) Specific sequences and structure of DNA tweezers. The hinge part is in pink color.



Figure S4. Histogram of the height of DS probe on graphene substrate in fluid. DS probe height is mostly in the range of 2 nm to 6 nm with the average height  $3.6 \pm 1.4$  nm (n = 254).



Figure S5. AFM images of A) graphene surface and B) PASE coated graphene surface in air. Both image sizes are 1  $\mu$ m x 1  $\mu$ m and z range is 20 nm C) Left: High resolution AFM image of DS probe on graphene substrate in air. Right: The 3-D image of the DS probe on the surface. Image size is 100 nm x 100 nm and z range is 3 nm.



Figure S6. Example of I-V curve shift before and after DS probe functionalization. The curve consistently shifted down and left after the functionalization.



Figure S7. I-V curve comparison with different buffer solution as liquid gate. A. 12.5 mM of MgCl<sub>2</sub> buffer solution B.  $1 \times PBS$  which contains 137 mM of NaCl and other ions. MgCl<sub>2</sub> buffer showed clearer shifts of the curve in negative X-axis.



Figure S8. The detailed graphs of Dirac point shifts. Experimental conditions are same as for the data shown in Figure 4.



Figure S9. Data from same tests shown in Figure 4 with different source voltage. It shows the same trend of Dirac point shifts (left side) and resistance change (downside).



Figure S10. Another set of I-V curve with different dimensions (2 mm  $\times$  7 mm) of graphene channel. The top graph shows the strand displacement with the perfect match T and the bottom panel shows the strand displacement with the single mismatch T.



Figure S11. I-V curve shifts with a single stranded probe. Only normal side (N) of DS probe was used as probe strand instead of DS probe. The single mismatch T was used for this test. I-V curve shifts down and left as much as for perfect match T induced with DS probe.

Table S1. Sequences used in the experiments

W	TGA AAG IGT TTT AAT AAT AGA ATT TTA AAA IAC TIG TAI A
Ν	CCT TAT TTC TAC CAG TCT TTT AAA ATT CTA TTA TTA AAA CCC TTT CA
W for gel test	TGA AAG IGT TTT AAT AAT AGA ATT TTA AAA IAC TIG TAI ATT TTT TTT TTC TCT ATC AAT CTC TAA CAC CC
N for gel test	GGG TGT TAG AGA TTG ATA GAG CGG CCT TAT TTC TAC CAG TCT TTT AAA ATT CTA TTA TTA AAA CCC TTT CA
Perfect match T	TGA AAG GGT TTT AAT AAT AGA ATT TTA AAA GAC TGG TAG AAA TAA GG
Single mismatch T	TGA AAG GGT TTT AAT AAT ATA ATT TTA AAA GAC TGG TAG A AA TAA GG