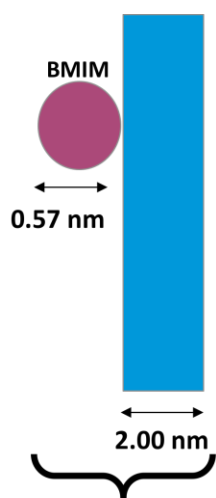


Supporting information

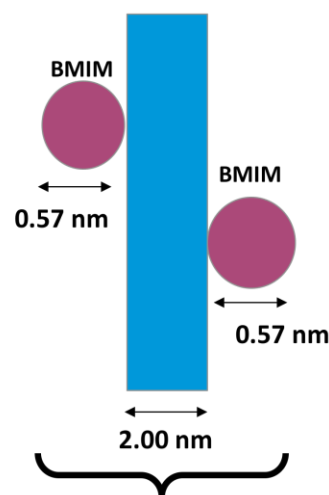
Ionic Liquid Prolongs DNA Translocation through Graphene Nanopore

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Total = $0.57 + 2.00 = 2.57$ nm (diameter of the pore) Hence, radius of 1.30 nm. (close to 1.285 nm)



Total = $0.57 + 2.00 + 0.57 = 3.14$ nm (diameter of the pore) Hence, radius of 1.55 nm. (close to 1.57 nm)

Figure S1. Schematic diagram showing choice of pore radius based on DNA and BMIM ion size.

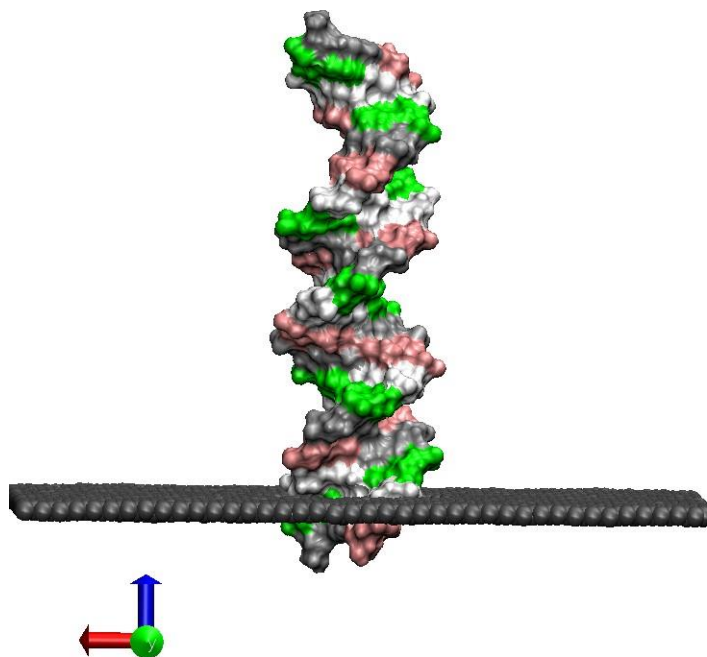
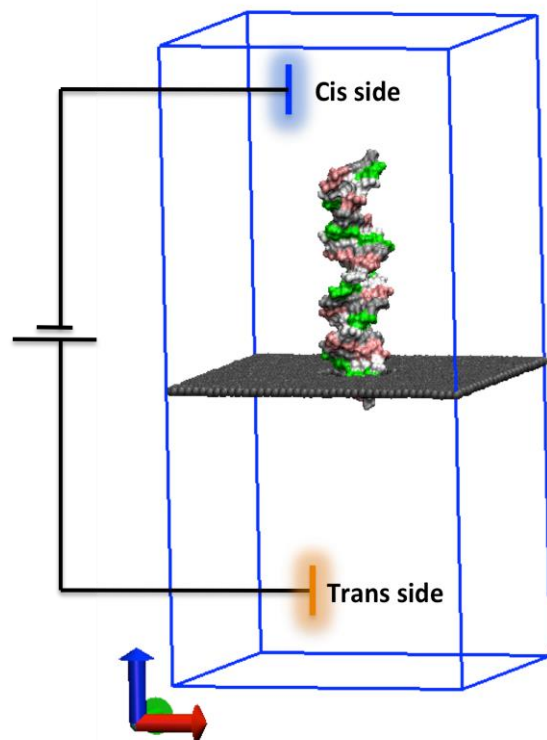


Figure S2. Snapshots showing initial configuration. Bottom panel is a zoomed view of the top panel.

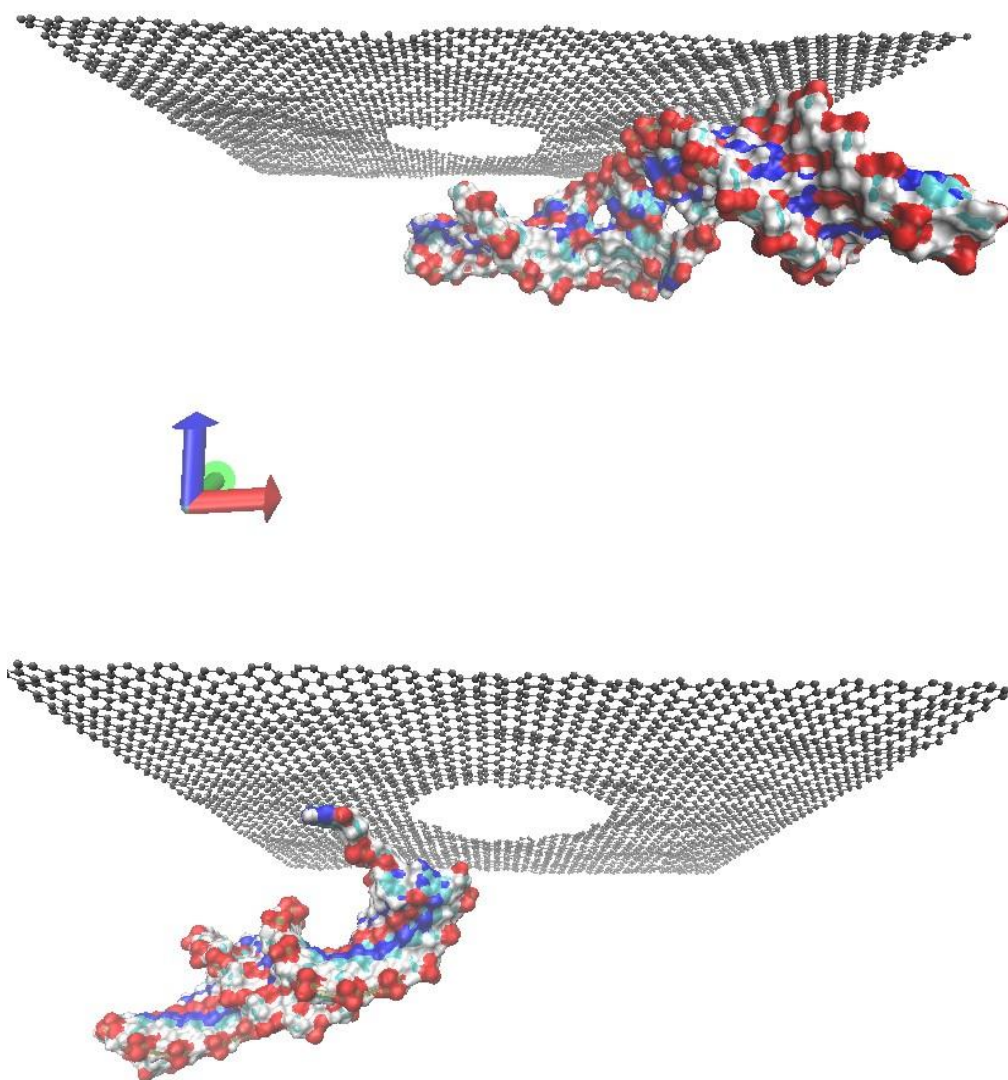


Figure S3. Configuration showing dG₂₀ stuck to graphene surface for nanopore of 2.6 nm diameter and voltage of 0.05 V/nm.

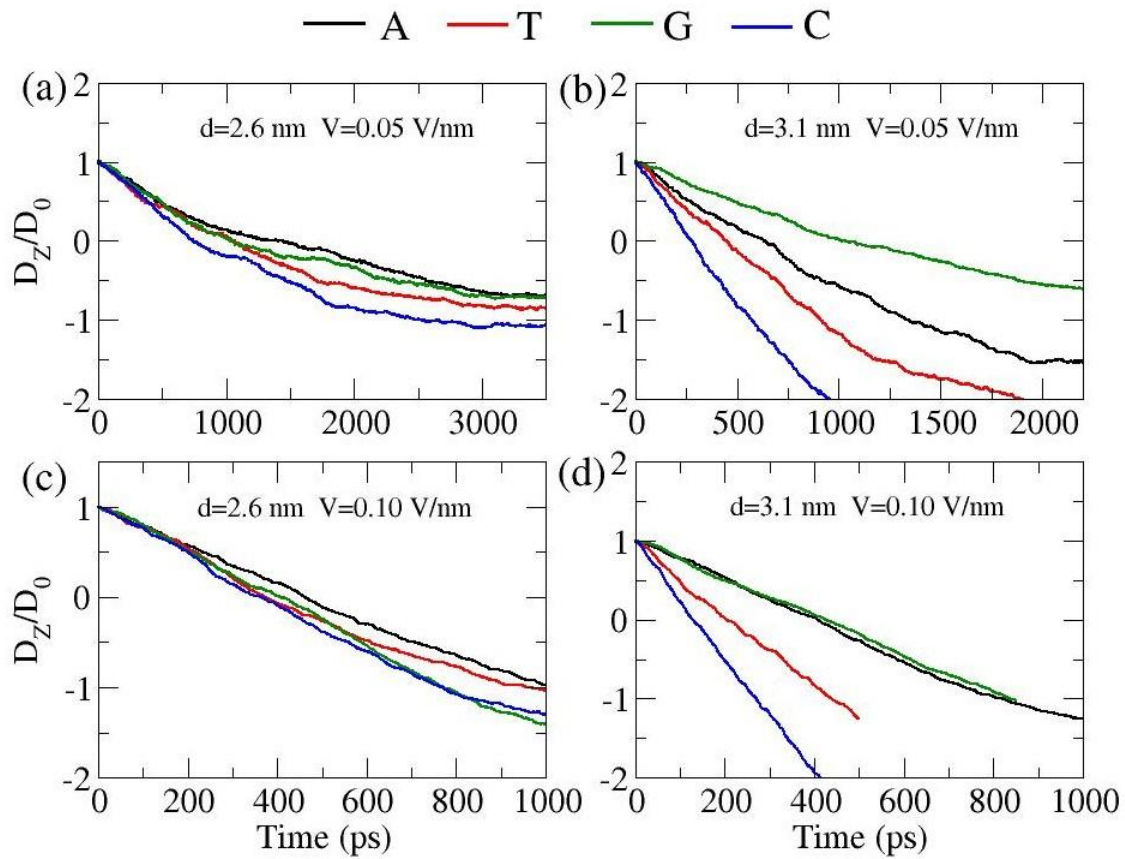


Figure S4. The Z-component of DNA movement (D_z) is normalized by its value at $t=0$ ($D_z(t=0)$). We have plotted normalized movement (D_z/D_0) in all cases. The normalized DNA COM movements for polynucleotide systems (a) Diameter (d) = 2.6 nm, $V=0.05$ V/nm; (b) $d=3.1$ nm, $V=0.05$ V/nm; (c) $d=2.6$ nm, $V=0.10$ V/nm; (d) $d=3.1$ nm, $V=0.10$ V/nm. Color indicators: A- black, T- red, G- green, C- blue.

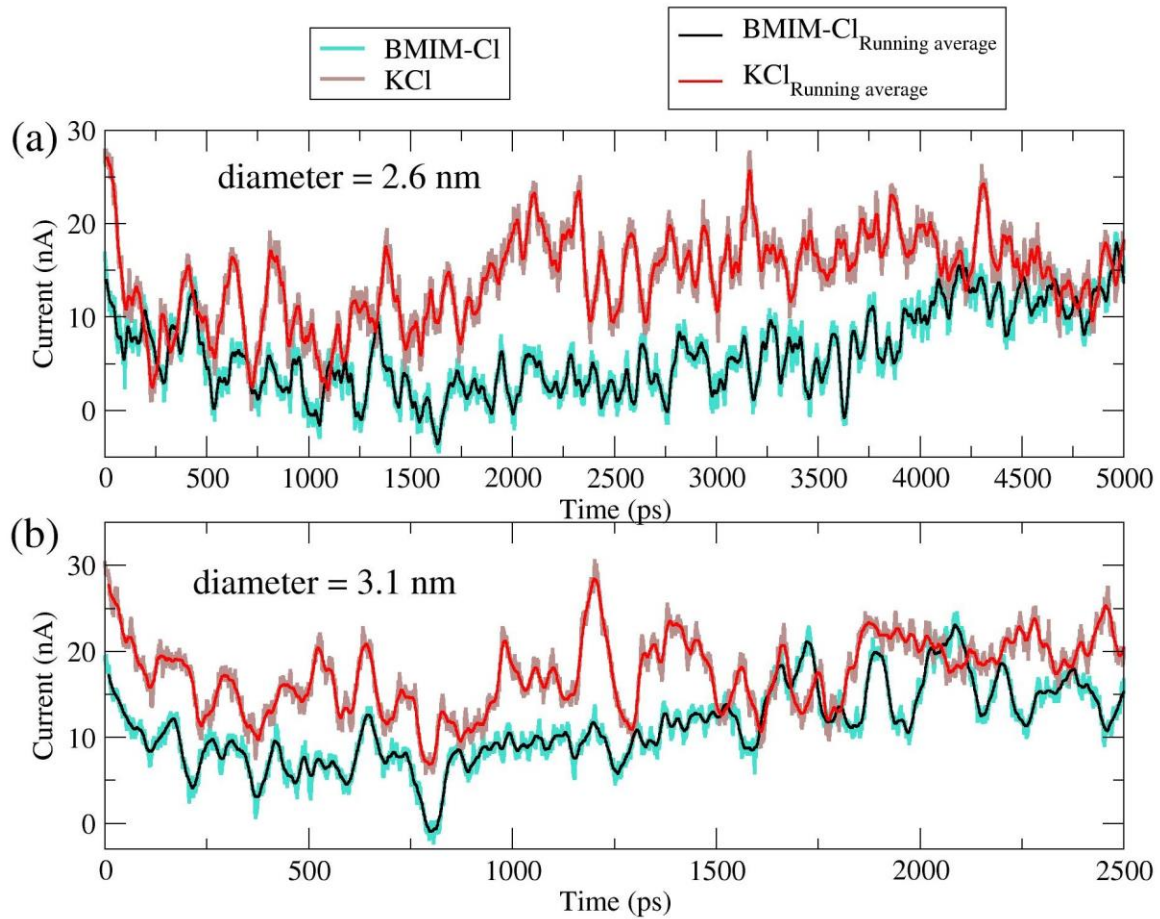


Figure S5. The current values for DNA translocation in case of (a) smaller nanopore ($d = 2.6$ nm) and (b) larger nanopore ($d = 3.1$ nm) using lag value of 50 ps in the presence of KCl (brown line) and BMIM-Cl (turquoise line). The running average are plotted for KCl (Red line) and BMIM-Cl simulations (Black line) to visually observe number of blockade events.

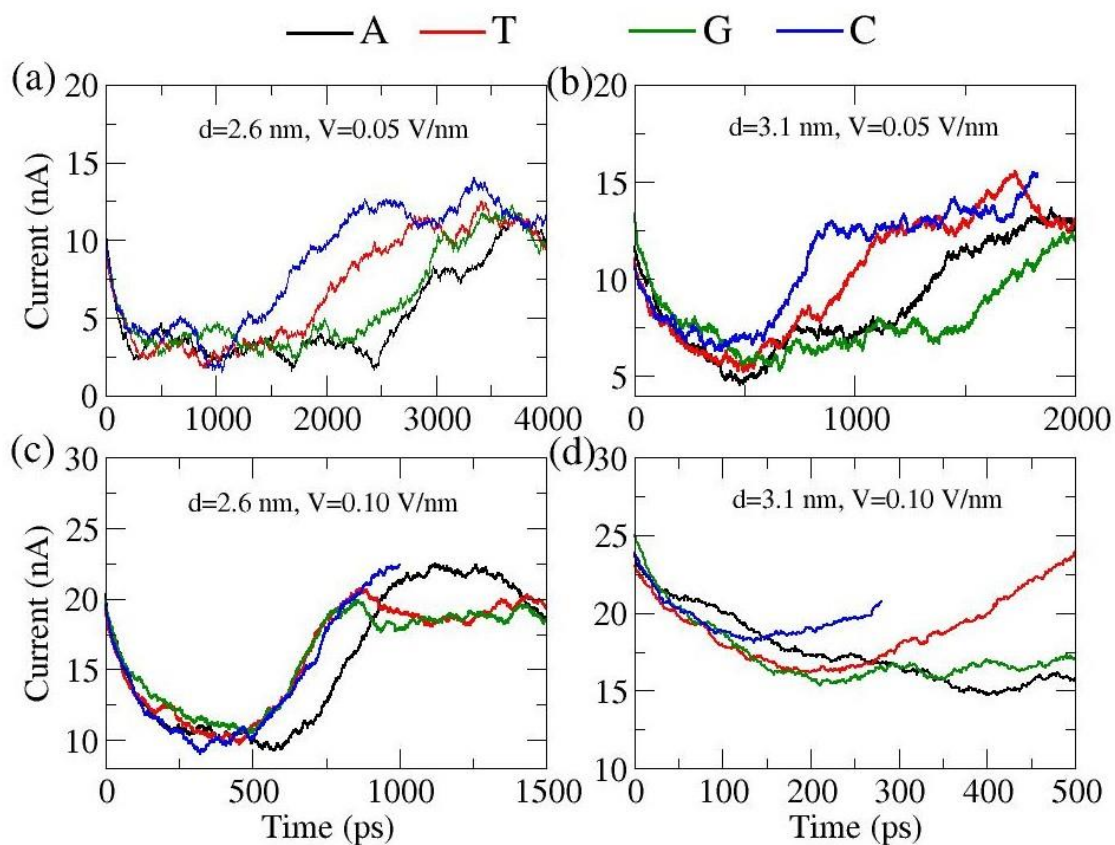


Figure S6. Ionic current of BMIM-Cl using lag of 250 ps for polynucleotide systems (a) Diameter (d) = 2.6 nm, $V=0.05$ V/nm; (b) $d=3.1$ nm, $V=0.05$ V/nm; (c) $d=2.6$ nm, $V=0.10$ V/nm; (d) $d=3.1$ nm, $V=0.10$ V/nm. Color indicators: A- black, T- red, G- green, C- blue.

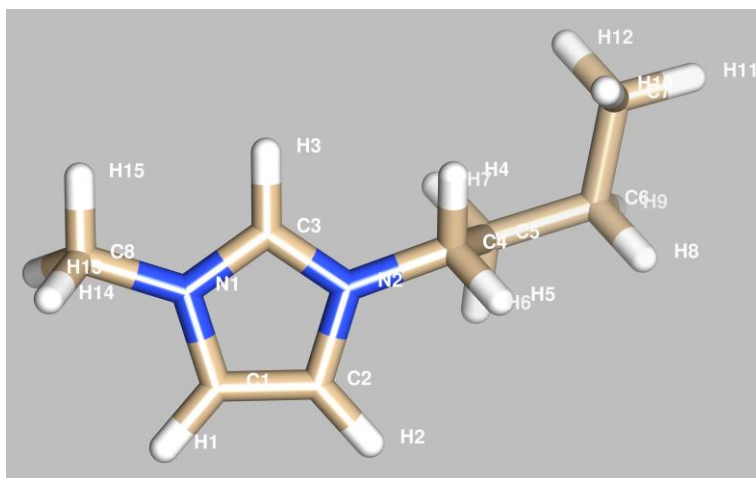


Figure S7. Structure of BMIM⁺ cation

Table S1. Table showing details of the systems and simulations performed in this study.

Simulation ID	Sequence	Electrolyte	Voltage (V/nm)	Pore Diameter (nm)	Translocation time (ns)
1	dA ₂₀	BMIM-Cl	0.05	2.6	5.0
2	dC ₂₀	BMIM-Cl	0.05	2.6	5.0
3	dG ₂₀	BMIM-Cl	0.05	2.6	5.0
4	dT ₂₀	BMIM-Cl	0.05	2.6	5.0
5	dA ₂₀	BMIM-Cl	0.05	3.10	2.50
6	dC ₂₀	BMIM-Cl	0.05	3.10	2.50
7	dG ₂₀	BMIM-Cl	0.05	3.10	2.50
8	dT ₂₀	BMIM-Cl	0.05	3.10	2.50
9	dA ₂₀	BMIM-Cl	0.10	2.6	1.50
10	dC ₂₀	BMIM-Cl	0.10	2.6	1.50
11	dG ₂₀	BMIM-Cl	0.10	2.6	1.50
12	dT ₂₀	BMIM-Cl	0.10	2.6	1.50
13	dA ₂₀	BMIM-Cl	0.10	3.10	1.00
14	dC ₂₀	BMIM-Cl	0.10	3.10	1.00
15	dG ₂₀	BMIM-Cl	0.10	3.10	1.00
16	dT ₂₀	BMIM-Cl	0.10	3.10	1.00
17	d(ACGT) ₅	BMIM-Cl	0.05	2.6	3.50
18	d(ACGT) ₅	KCl	0.05	2.6	2.00
19	d(ACGT) ₅	BMIM-Cl	0.05	3.10	1.70
20	d(ACGT) ₅	KCl	0.05	3.10	1.10

Table S2. The translocation time of individual runs in each case of homo-polynucleotide sequence.

d=2.6 nm V=0.05 V/nm

Sequence	Run 1	Run 2	Run 3	average	SD
A	3090.0	2845.0	4580.0	3505.0	939.0
C	1888.0	2325.0	1737.0	1983.3	305.4
G	2810.0	3090.0	3190.0	3030.0	197.0
T	2980.0	2360.0	1950.0	2430.0	518.6

d=2.6 nm V=0.10 V/nm

Sequence	Run 1	Run 2	Run 3	average	SD
A	1040.0	1080.0	880.0	1000.0	105.8
C	980.0	840.0	790.0	870.0	98.5
G	890.0	920.0	990.0	933.3	51.3
T	770.0	890.0	910.0	856.7	75.7

d=3.1 nm V=0.05 V/nm

Sequence	Run 1	Run 2	Run 3	average	SD
A	1450.0	1990.0	1740.0	1726.7	270.2
C	1050.0	1695.0	900.0	1215.0	422.4
G	2253.0	2360.0	1961.0	2191.3	206.5
T	1263.0	1330.0	1020.0	1204.3	163.1

d=3.1 nm V=0.10 V/nm

Sequence	Run 1	Run 2	Run 3	average	SD
A	890.0	1026.0	844.0	920.0	94.6
C	374.0	488.0	506.0	456.0	71.6
G	842.0	840.0	840.0	840.7	1.2
T	626.0	540.0	685.0	617.0	72.9

Table S3. The blockade current of individual runs in each case of homo-polynucleotide sequence.

Blockade Current (nA) lag 250 ps

d=2.6 nm V=0.05 V/nm

Sequence	Run 1	Run 2	Run 3	average	SD
A	3.44	4.53	4.17	4.05	0.56
C	5.78	5.13	4.26	5.06	0.76
G	4.21	4.88	4.20	4.43	0.39
T	4.07	3.74	4.76	4.19	0.52

d=2.6 nm V=0.10 V/nm

Sequence	Run 1	Run 2	Run 3	average	SD
A	14.13	11.59	13.44	13.05	1.31
C	13.16	13.57	12.65	13.13	0.46
G	15.51	14.31	13.41	14.41	1.05
T	14.48	12.02	14.54	13.68	1.44

d=3.1 nm V=0.05 V/nm

Sequence	Run 1	Run 2	Run 3	average	SD
A	7.74	8.05	8.23	8.01	0.25
C	9.95	8.73	8.69	9.12	0.72
G	9.19	7.38	8.33	8.30	0.90
T	6.85	8.52	8.49	7.95	0.96

d=3.1 nm V=0.10 V/nm

Sequence	Run 1	Run 2	Run 3	average	SD
A	19.13	17.88	19.89	18.97	1.01
C	21.37	19.31	21.85	20.84	1.35
G	19.63	18.88	18.56	19.02	0.55
T	20.71	19.58	19.37	19.89	0.72