

Supporting Information for
**DNA Sequence-Dependent Ionic Currents in Ultra-Small Solid-State
Nanopores**

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Table S1: Data corresponding to Figure 4B. “M” refers to 5-methylcytosine.

| Sequence | I (pA) | |
|----------|----------|------------|
| ACA | 31.41 | ± 0.49 |
| AAA | 31.43 | ± 0.50 |
| ACG | 31.9 | ± 0.51 |
| AAG | 33.23 | ± 0.52 |
| AAC | 33.41 | ± 0.52 |
| CGA | 34.15 | ± 0.58 |
| AAT | 35.37 | ± 0.54 |
| GGC | 35.54 | ± 0.70 |
| AGA | 36.49 | ± 0.59 |
| ACC | 36.77 | ± 0.56 |
| CCA | 36.86 | ± 0.54 |
| GGA | 36.93 | ± 0.66 |
| CAG | 37.68 | ± 0.59 |
| GAA | 37.95 | ± 0.59 |
| GCA | 38.13 | ± 0.60 |
| ACT | 38.21 | ± 0.55 |
| AGC | 38.22 | ± 0.65 |
| TGA | 38.5 | ± 0.62 |
| CAA | 38.96 | ± 0.56 |
| CGG | 39.36 | ± 0.64 |
| ATA | 39.74 | ± 0.55 |
| GAC | 40.41 | ± 0.63 |
| GTA | 40.65 | ± 0.67 |
| GAG | 41.08 | ± 0.63 |
| CCG | 41.23 | ± 0.57 |
| CTA | 42.51 | ± 0.60 |
| GCG | 42.56 | ± 0.65 |
| CGC | 42.73 | ± 0.64 |
| GAT | 42.8 | ± 0.65 |
| GCC | 43.94 | ± 0.67 |
| CGT | 44.18 | ± 0.66 |
| CTG | 44.24 | ± 0.66 |
| TAA | 44.79 | ± 0.61 |
| CAC | 44.81 | ± 0.59 |
| CAT | 45.25 | ± 0.60 |
| ATG | 45.55 | ± 0.60 |
| TAG | 45.88 | ± 0.63 |
| TGC | 45.93 | ± 0.67 |
| ATC | 46.01 | ± 0.63 |
| GTC | 46.41 | ± 0.75 |
| GGT | 46.62 | ± 0.73 |
| AGT | 46.63 | ± 0.65 |
| TTA | 46.73 | ± 0.64 |
| AGG | 46.9 | ± 0.65 |
| GCT | 47.23 | ± 0.68 |
| GGG | 47.66 | ± 0.72 |
| TCA | 48.56 | ± 0.61 |
| TGG | 49.02 | ± 0.69 |
| TAC | 50.69 | ± 0.62 |
| TCG | 51.04 | ± 0.63 |
| TGT | 51.21 | ± 0.69 |
| CCC | 52.25 | ± 0.65 |
| ATT | 52.33 | ± 0.64 |
| TAT | 53.27 | ± 0.64 |
| CCT | 53.58 | ± 0.64 |

| | | |
|-------|-------|--------|
| GTG | 55.9 | ± 0.73 |
| TTG | 56.19 | ± 0.70 |
| CTC | 58.16 | ± 0.68 |
| TCC | 59.83 | ± 0.69 |
| GTT | 60.58 | ± 0.78 |
| CTT | 60.94 | ± 0.70 |
| TTC | 62.19 | ± 0.73 |
| TCT | 63.08 | ± 0.69 |
| TTT | 69.44 | ± 0.76 |
| <hr/> | | |
| AMA | 32.05 | ± 0.49 |
| AMG | 32.91 | ± 0.51 |
| AAM | 33.43 | ± 0.52 |
| MGA | 33.26 | ± 0.59 |
| GGM | 34.43 | ± 0.7 |
| AMM | 40.68 | ± 0.58 |
| MMA | 40.07 | ± 0.57 |
| MAG | 40.2 | ± 0.61 |
| GMA | 40.96 | ± 0.62 |
| AMT | 39.34 | ± 0.56 |
| AGM | 37.66 | ± 0.64 |
| MAA | 39.65 | ± 0.58 |
| MGG | 39.45 | ± 0.65 |
| GAM | 42.32 | ± 0.63 |
| MMG | 44.19 | ± 0.6 |
| MTA | 41.97 | ± 0.6 |
| GMG | 43.21 | ± 0.66 |
| MGM | 44.21 | ± 0.65 |
| GMM | 46.28 | ± 0.7 |
| MGT | 44.34 | ± 0.67 |
| MTG | 44.52 | ± 0.66 |
| MAM | 46.33 | ± 0.59 |
| MAT | 45.78 | ± 0.61 |
| TGM | 47.58 | ± 0.68 |
| ATM | 47.31 | ± 0.63 |
| GTM | 48.08 | ± 0.76 |
| GMT | 50.21 | ± 0.7 |
| TMA | 51.38 | ± 0.63 |
| TAM | 51.17 | ± 0.63 |
| TMG | 52.17 | ± 0.64 |
| MMM | 55.43 | ± 0.68 |
| MMT | 56.43 | ± 0.68 |
| MTM | 58.37 | ± 0.69 |
| TMM | 61.69 | ± 0.71 |
| MTT | 61.09 | ± 0.7 |
| TTM | 64.32 | ± 0.74 |
| TMT | 64.97 | ± 0.71 |

Table S2: Data corresponding to Figure 4C.

| Sequence | I (pA) | |
|----------|----------|------------|
| GGC | 27.87 | ± 0.32 |
| AGA | 31.13 | ± 0.33 |
| GGA | 31.32 | ± 0.32 |
| AGC | 31.44 | ± 0.34 |
| GAG | 33.49 | ± 0.37 |
| GCG | 34.31 | ± 0.37 |
| CGA | 34.32 | ± 0.38 |
| GTC | 34.87 | ± 0.39 |
| GCC | 34.91 | ± 0.41 |
| ACG | 35.17 | ± 0.40 |
| AAA | 35.19 | ± 0.38 |
| GAA | 35.26 | ± 0.36 |
| GCA | 35.73 | ± 0.37 |
| AAG | 35.75 | ± 0.39 |
| TGA | 35.96 | ± 0.51 |
| GTA | 36.25 | ± 0.36 |
| GGT | 36.33 | ± 0.34 |
| GAC | 36.35 | ± 0.38 |
| CGG | 36.9 | ± 0.41 |
| CAG | 36.96 | ± 0.40 |
| AGT | 37.69 | ± 0.35 |
| GAT | 37.85 | ± 0.38 |
| ACA | 37.91 | ± 0.41 |
| CGC | 37.98 | ± 0.38 |
| CGT | 39.05 | ± 0.39 |
| ATA | 39.22 | ± 0.38 |
| AAC | 39.27 | ± 0.42 |
| CAA | 39.61 | ± 0.40 |
| TGC | 39.77 | ± 0.37 |
| ACC | 39.84 | ± 0.46 |
| AAT | 39.9 | ± 0.42 |
| GCT | 40.22 | ± 0.41 |
| AGG | 40.35 | ± 0.36 |
| TAA | 40.4 | ± 0.39 |
| GGG | 40.69 | ± 0.35 |
| ATC | 40.93 | ± 0.42 |
| ACT | 41.14 | ± 0.45 |
| TAG | 42.4 | ± 0.42 |
| TGG | 42.87 | ± 0.41 |
| CCG | 43.26 | ± 0.43 |
| CCA | 43.38 | ± 0.44 |
| CTG | 44.46 | ± 0.46 |
| CTA | 44.51 | ± 0.44 |
| TGT | 45.14 | ± 0.38 |
| ATG | 45.29 | ± 0.40 |
| GTG | 46.28 | ± 0.38 |
| CAT | 46.7 | ± 0.43 |
| CAC | 47.2 | ± 0.43 |
| TTA | 47.26 | ± 0.43 |
| TCG | 47.91 | ± 0.42 |
| TAC | 48.7 | ± 0.51 |
| GTT | 48.87 | ± 0.41 |
| TCA | 49.36 | ± 0.43 |
| ATT | 50.84 | ± 0.44 |
| TAT | 51.66 | ± 0.43 |
| TTG | 52.19 | ± 0.57 |

| | | |
|-------|-------|--------|
| CCC | 53.22 | ± 0.49 |
| CCT | 54.69 | ± 0.49 |
| TCC | 58.79 | ± 0.50 |
| CTC | 58.96 | ± 0.51 |
| TTC | 59.55 | ± 0.49 |
| CTT | 60.09 | ± 0.52 |
| TCT | 61.64 | ± 0.49 |
| TTT | 66.71 | ± 0.51 |
| <hr/> | | |
| GGM | 27.04 | ± 0.32 |
| AGM | 31.47 | ± 0.34 |
| GMG | 34.7 | ± 0.37 |
| MGA | 32.97 | ± 0.37 |
| GTM | 35.28 | ± 0.39 |
| GMM | 36.2 | ± 0.41 |
| AMG | 35.62 | ± 0.4 |
| GMA | 35.73 | ± 0.36 |
| GAM | 37.13 | ± 0.38 |
| MGG | 36.49 | ± 0.41 |
| MAG | 37.17 | ± 0.4 |
| AMA | 38.28 | ± 0.41 |
| MGM | 38.38 | ± 0.38 |
| MGT | 39.03 | ± 0.39 |
| AAM | 40.52 | ± 0.43 |
| MAA | 38.61 | ± 0.39 |
| TGM | 40.41 | ± 0.38 |
| AMM | 40.69 | ± 0.46 |
| GMT | 40.91 | ± 0.41 |
| ATM | 41.31 | ± 0.42 |
| AMT | 41.99 | ± 0.45 |
| MMG | 45.11 | ± 0.43 |
| MMA | 43.62 | ± 0.43 |
| MTG | 44.74 | ± 0.45 |
| MTA | 43.96 | ± 0.43 |
| MAT | 45.98 | ± 0.42 |
| MAM | 48.57 | ± 0.44 |
| TMG | 48.99 | ± 0.42 |
| TAM | 51.97 | ± 0.43 |
| TMA | 49.38 | ± 0.43 |
| MMM | 53.48 | ± 0.49 |
| MMT | 54.29 | ± 0.48 |
| TMM | 61.13 | ± 0.51 |
| MTM | 58.73 | ± 0.51 |
| TTM | 59.56 | ± 0.5 |
| MTT | 61.39 | ± 0.52 |
| TMT | 62.63 | ± 0.49 |

Table S3: Data corresponding to Figure 4D.

| Sequence | I (pA) | |
|----------|----------|------------|
| GAA | 19.86 | ± 0.32 |
| GAC | 20.68 | ± 0.34 |
| GAG | 23.32 | ± 0.36 |
| GAT | 23.43 | ± 0.36 |
| GCA | 24.93 | ± 0.34 |
| AGA | 25.0 | ± 0.35 |
| GCC | 25.92 | ± 0.40 |
| AGC | 26.45 | ± 0.39 |
| AAG | 27.93 | ± 0.37 |
| GTA | 28.17 | ± 0.38 |
| GCG | 28.36 | ± 0.40 |
| GGA | 28.5 | ± 0.39 |
| TGA | 29.6 | ± 0.40 |
| CGA | 29.97 | ± 0.37 |
| AGT | 30.15 | ± 0.41 |
| ACG | 30.22 | ± 0.38 |
| GGC | 30.59 | ± 0.44 |
| GCT | 31.09 | ± 0.43 |
| AGG | 31.16 | ± 0.41 |
| ATG | 31.68 | ± 0.41 |
| ATA | 31.84 | ± 0.36 |
| AAA | 31.93 | ± 0.35 |
| ACC | 31.94 | ± 0.39 |
| ACA | 32.22 | ± 0.36 |
| AAT | 32.68 | ± 0.38 |
| AAC | 32.93 | ± 0.37 |
| GTC | 33.41 | ± 0.43 |
| GTG | 34.05 | ± 0.40 |
| ATC | 34.8 | ± 0.41 |
| ACT | 34.97 | ± 0.41 |
| CCA | 35.24 | ± 0.40 |
| CGC | 35.38 | ± 0.42 |
| TCG | 35.48 | ± 0.46 |
| TGC | 35.84 | ± 0.45 |
| CCG | 35.86 | ± 0.44 |
| CTG | 36.26 | ± 0.47 |
| CGG | 36.37 | ± 0.44 |
| TAA | 36.86 | ± 0.38 |
| ATT | 37.11 | ± 0.45 |
| TAG | 37.24 | ± 0.41 |
| TGG | 37.26 | ± 0.46 |
| CAG | 37.35 | ± 0.42 |
| TCA | 37.38 | ± 0.41 |
| CGT | 38.52 | ± 0.44 |
| TGT | 40.18 | ± 0.48 |
| TTG | 42.53 | ± 0.50 |
| TAT | 43.04 | ± 0.42 |
| GTT | 43.41 | ± 0.47 |
| CAA | 43.43 | ± 0.41 |
| TAC | 43.59 | ± 0.40 |
| CTA | 43.63 | ± 0.43 |
| GGT | 43.65 | ± 0.49 |
| CCC | 44.11 | ± 0.46 |
| TTA | 44.26 | ± 0.46 |
| TCC | 45.05 | ± 0.47 |
| GGG | 45.17 | ± 0.47 |

| | | |
|-----|-------|------------|
| CAT | 45.79 | ± 0.43 |
| CAC | 46.62 | ± 0.42 |
| CCT | 48.33 | ± 0.50 |
| TCT | 49.65 | ± 0.49 |
| CTC | 49.9 | ± 0.48 |
| CTT | 54.1 | ± 0.52 |
| TTC | 55.02 | ± 0.52 |
| TTT | 59.76 | ± 0.55 |

Table S4: Pairwise RMSD of DNA conformations featured in Figure 5. The RMSD was calculated using the coordinates of four nucleotides nearest the pore without alignment

| Conform. 1 | Conform. 2 | RMSD (\AA) |
|------------|------------|-----------------------|
| Y0 | Y1 | 3.487 |
| Y0 | Y2 | 6.095 |
| Y0 | Y3 | 1.180 |
| Y0 | X0 | 6.340 |
| Y1 | Y2 | 6.675 |
| Y1 | Y3 | 3.487 |
| Y1 | X0 | 5.973 |
| Y2 | Y3 | 6.101 |
| Y2 | X0 | 8.719 |
| Y3 | X0 | 6.68 |