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
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
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 (Å)
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