

## Supplementary Data

### Sequence-Dependent DNA Deformability Studied using Molecular Dynamics Simulations

Fujii Satoshi, Hidetoshi Kono, Shigeori Takenaka, Nobuhiro Go and Akinori Sarai

#### **1. A MD result with a coupling time of 1.0 ps for the heat bath yields a similar conformational ensemble to those obtained by MD simulations with a smaller coupling time.**

We used a smaller coupling time for the heat bath to obtain a canonical ensemble because it has shown that a MD simulation with a larger coupling time in the weak coupling thermostat proposed by Berendsen et al. [J. Chem. Phys. 81, 3684 (1984)] produces an ensemble closer to the microcanonical ensemble [Morishita, T. J. Chem. Phys., 113, 2976 (2000)].

A molecular dynamics simulation with a coupling time of 1.0 ps for the heat bath (other conditions were the same as those described in Methods section) were carried out on a 12-mer dsDNA which has AATT sequence at the center (5'-CGCGAATTCGCG-3'). The base-pair step parameters were calculated based on the ensemble of the last 9ns of a 10ns-long MD simulation (see Table S1 below).

**Table S1. Averaged base-pair step parameters over the last 9 ns (9000 conformations sampled at every 1 ps) of a 10ns-long-molecular dynamics simulation for a tetrameric sequence of AATT.**

steps	N	Twist	s.d.	Tilt	s.d.	Roll	s.d.	Shift	s.d.	Slide	s.d.	Rise	s.d.
AATT	9000	32.2	3.1	-0.1	3.6	-0.2	4.0	0.03	0.52	-1.04	0.38	3.35	0.26

These values are very close to those obtained by the MD simulation with a coupling time of 1.0 fs for the heat bath (See Table S2, AATT row). The deformability  $S$  was calculated to be  $2.0 \text{ deg}^3 \text{ \AA}^3$ . This value was also close to a value of 2.7 derived from the ensemble of a 10-ns MD simulation with a coupling time of 1.0 fs for the heat bath. These results show that the MD simulations with the small coupling constant produce reasonably good ensembles of conformations at least in the space of 6 base-pair step parameters.

## 2. The table of tetrameric step parameters

**Table S2. Averaged base-pair step parameters over the last 9 ns (9000 conformations sampled at every 1 ps) of 10ns-long-molecular dynamics simulations for 136 tetrameric sequences.**

steps	N	Twist	s.d.	Tilt	s.d.	Roll	s.d.	Shift	s.d.	Slide	s.d.	Rise	s.d.
AAAA	9000	35.1	5.2	-1.7	4.2	2.7	5.0	-0.21	0.58	-0.60	0.59	3.48	0.32
AAAC	9000	34.6	5.5	-1.9	4.2	1.0	5.1	-0.06	0.54	-0.72	0.61	3.39	0.32
AAAG	8999	34.3	4.5	-2.1	4.1	0.8	5.0	0.05	0.50	-0.72	0.52	3.34	0.30
AAAT	8998	35.8	4.8	-2.3	4.0	2.1	4.8	-0.23	0.51	-0.68	0.56	3.46	0.31
CAAA	8998	33.9	6.2	-2.0	4.1	1.6	5.5	-0.30	0.67	-0.36	0.65	3.33	0.30
CAAC	9000	35.1	6.9	-2.7	4.0	0.2	5.4	-0.30	0.67	-0.32	0.61	3.32	0.29
CAAG	9000	35.2	5.3	-2.7	3.9	1.2	5.3	-0.26	0.63	-0.32	0.61	3.32	0.28
CAAT	8997	35.2	5.2	-3.0	4.1	1.0	5.1	-0.38	0.60	-0.51	0.59	3.35	0.30
GAAA	8999	28.4	7.4	-1.7	4.4	4.2	6.1	-0.06	0.61	-0.41	0.78	3.20	0.32
GAAC	9000	32.5	6.2	-3.0	4.4	1.2	5.3	-0.16	0.61	-0.52	0.65	3.30	0.32
GAAG	9000	32.5	5.6	-2.2	4.0	0.7	5.3	0.10	0.55	-0.64	0.55	3.26	0.30
GAAT	9000	33.9	4.6	-2.3	4.1	1.0	4.7	-0.17	0.50	-0.72	0.54	3.35	0.30
TAAA	8999	36.2	5.1	-1.7	4.1	2.8	5.7	-0.54	0.66	-0.12	0.58	3.38	0.30
TAAC	9000	35.5	4.3	-2.6	4.1	2.3	5.3	-0.83	0.80	0.08	0.76	3.32	0.30
TAAG	8998	33.1	5.7	-2.7	4.2	1.8	5.4	-0.18	0.73	-0.45	0.65	3.28	0.30
TAAT	8999	37.6	5.2	-2.9	4.1	1.1	5.3	-0.61	0.63	-0.26	0.57	3.40	0.29
AAGA	9000	31.3	5.9	-1.6	4.3	5.0	5.1	-0.05	0.73	-0.88	0.66	3.48	0.35
AAGC	9000	33.0	5.0	-2.6	4.4	4.2	5.2	-0.26	0.67	-1.05	0.57	3.54	0.31
AAGG	8999	32.6	5.3	-2.0	4.5	3.1	5.1	-0.02	0.69	-1.07	0.59	3.51	0.32
AAGT	9000	33.9	4.9	-2.9	4.4	4.6	4.9	-0.28	0.62	-1.10	0.53	3.57	0.32
CAGA	9000	31.6	7.2	-2.6	4.3	3.4	5.2	-0.25	0.92	-0.54	0.66	3.38	0.33
CAGC	9000	35.3	5.4	-3.2	4.1	2.4	5.6	-0.54	0.74	-0.41	0.60	3.44	0.31
CAGG	8999	31.1	6.4	-2.7	4.2	2.1	5.2	-0.02	0.75	-0.86	0.71	3.41	0.33
CAGT	8998	35.2	5.7	-4.8	4.3	3.7	5.5	-0.57	0.80	-0.55	0.68	3.48	0.32
GAGA	9000	27.8	6.3	-0.9	4.2	4.0	5.3	0.10	0.64	-1.00	0.67	3.38	0.35
GAGC	8999	29.3	5.9	-1.7	4.3	2.6	5.0	-0.01	0.66	-1.05	0.62	3.38	0.34

GAGG	9000	27.7	6.0	-1.5	4.2	3.1	5.3	0.26	0.69	-1.09	0.65	3.42	0.37
GAGT	9000	32.5	4.7	-2.3	4.4	3.2	5.2	-0.29	0.60	-1.17	0.54	3.50	0.32
TAGA	9000	30.8	7.4	-1.6	4.5	3.5	5.4	-0.28	0.91	-0.69	0.69	3.37	0.35
TAGC	9000	34.3	5.3	-3.1	4.2	2.5	5.5	-0.51	0.80	-0.58	0.63	3.38	0.32
TAGG	9000	29.2	7.5	-1.9	4.6	3.2	5.8	-0.23	0.79	-0.95	0.68	3.35	0.35
TAGT	8999	33.9	5.8	-3.2	4.5	3.7	5.4	-0.52	0.80	-0.80	0.67	3.44	0.32
AGAA	8999	35.3	6.9	1.0	4.6	2.9	5.6	-0.30	0.66	-0.48	0.77	3.47	0.32
AGAC	9000	35.0	5.6	0.3	4.5	2.3	5.5	-0.12	0.67	-0.68	0.70	3.41	0.31
AGAG	8999	36.1	5.8	0.2	4.6	2.1	6.2	0.02	0.60	-1.06	0.68	3.48	0.34
AGAT	9000	37.6	4.7	2.6	4.4	2.2	5.2	-0.26	0.51	-1.04	0.55	3.59	0.33
CGAA	8999	36.9	6.8	-0.1	4.4	3.1	5.7	-0.53	0.74	-0.02	0.68	3.42	0.30
CGAC	9000	37.8	4.6	-3.2	4.5	1.6	5.0	-1.02	0.57	0.36	0.48	3.33	0.28
CGAG	9000	38.0	5.1	-2.2	4.7	2.2	5.2	-0.74	0.70	0.24	0.62	3.39	0.29
CGAT	9000	38.8	5.5	-2.4	4.5	2.7	5.0	-0.86	0.57	0.20	0.55	3.46	0.31
GGAA	9000	35.9	6.3	-1.1	4.7	3.5	5.4	-0.57	0.71	-0.19	0.74	3.33	0.32
GGAC	9000	36.4	5.9	-1.2	4.5	1.6	5.5	-0.41	0.69	-0.33	0.69	3.31	0.30
GGAG	8999	35.0	5.1	-1.4	4.5	1.4	5.3	-0.20	0.68	-0.64	0.71	3.33	0.30
GGAT	8999	36.7	5.3	-1.0	4.6	1.8	5.4	-0.32	0.65	-0.58	0.69	3.42	0.31
TGAA	9000	36.9	6.3	-0.5	4.5	2.5	5.3	-0.60	0.70	-0.12	0.70	3.40	0.31
TGAC	8999	38.9	4.6	-1.6	4.5	1.7	5.1	-0.77	0.59	0.14	0.53	3.36	0.28
TGAG	9000	37.0	5.7	-2.3	4.6	1.6	5.7	-0.59	0.74	-0.10	0.70	3.33	0.29
TGAT	9000	36.4	6.7	-1.4	4.6	2.9	5.9	-0.37	0.78	-0.32	0.74	3.35	0.30
AGGA	9000	31.5	4.8	2.4	4.3	6.3	4.9	0.09	0.59	-1.45	0.64	3.69	0.34
AGGC	9000	32.9	5.2	1.2	4.4	4.8	5.1	-0.05	0.61	-1.26	0.72	3.63	0.33
AGGG	9000	32.3	4.8	1.3	4.4	4.5	5.2	0.09	0.61	-1.34	0.71	3.60	0.32
AGGT	9000	33.1	4.8	1.4	4.3	5.9	4.8	-0.07	0.56	-1.53	0.60	3.72	0.31
CGGA	9000	32.5	8.6	0.6	4.4	5.1	5.5	-0.26	0.83	-0.28	0.75	3.49	0.33
CGGC	9000	36.4	5.0	-1.9	4.2	3.8	5.6	-0.69	0.64	-0.12	0.64	3.45	0.30
CGGG	9000	31.9	5.6	1.5	4.4	4.9	5.1	0.12	0.77	-1.03	0.82	3.56	0.32
CGGT	9000	37.4	5.2	-0.8	4.3	4.7	5.4	-0.58	0.68	-0.45	0.75	3.62	0.30
GGGA	8999	30.8	6.6	1.3	4.4	5.9	5.1	-0.01	0.64	-1.24	0.71	3.57	0.37
GGGC	9000	31.3	5.7	0.1	4.5	5.0	5.0	-0.13	0.70	-1.24	0.74	3.52	0.34

GGGG	9000	29.7	5.0	0.8	4.3	5.0	5.1	0.10	0.57	-1.43	0.57	3.44	0.34
GGGT	8999	32.3	4.6	0.9	4.4	5.0	5.0	-0.07	0.59	-1.48	0.62	3.64	0.32
TGGA	9000	35.1	6.6	-0.9	4.6	5.6	5.6	-0.62	0.79	-0.43	0.75	3.43	0.31
TGGC	9000	33.8	6.1	0.4	4.6	4.8	5.1	-0.37	0.79	-0.80	0.85	3.55	0.33
TGGG	8999	31.3	5.4	1.1	4.6	4.6	5.2	0.15	0.66	-1.23	0.78	3.54	0.34
TGGT	9000	34.2	5.8	0.1	4.9	6.0	5.5	-0.27	0.81	-0.89	0.93	3.59	0.32
AACA	9000	32.5	4.5	-0.8	4.0	1.9	4.8	0.10	0.66	-0.99	0.51	3.39	0.29
AACC	8999	28.0	3.9	1.5	3.9	-0.4	4.5	0.90	0.51	-0.82	0.40	3.28	0.27
AACG	8999	33.2	5.0	-0.4	4.2	0.5	5.7	0.30	0.74	-0.74	0.51	3.42	0.30
AACT	9000	34.9	4.2	-1.8	3.8	-1.1	5.3	0.11	0.63	-0.88	0.58	3.49	0.28
CACA	9000	32.3	5.1	-1.2	4.0	1.3	5.5	0.23	0.75	-0.69	0.51	3.32	0.29
CACC	9000	32.9	4.8	-0.4	3.8	-0.3	5.0	0.30	0.63	-0.93	0.56	3.32	0.29
CACG	9000	31.1	5.4	-0.3	4.2	0.6	5.6	0.29	0.80	-0.56	0.48	3.29	0.30
CACT	9000	33.8	4.9	-2.2	3.8	-0.1	5.4	0.04	0.73	-0.83	0.58	3.41	0.29
GACA	9000	31.1	5.6	0.2	4.2	0.3	5.2	0.41	0.77	-0.66	0.57	3.31	0.30
GACC	8999	32.8	4.1	-0.3	3.8	0.9	4.6	0.36	0.61	-1.00	0.47	3.36	0.28
GACG	9000	30.2	5.4	0.0	4.2	1.4	5.1	0.25	0.72	-0.68	0.50	3.30	0.31
GACT	9000	33.4	4.0	-2.2	3.9	1.4	4.8	0.04	0.69	-0.94	0.50	3.45	0.29
TACA	9000	32.3	4.3	-2.2	4.0	0.9	5.0	0.21	0.62	-1.05	0.54	3.37	0.31
TACC	9000	32.3	5.1	0.3	4.0	0.5	4.9	0.41	0.60	-0.95	0.56	3.33	0.31
TACG	9000	31.5	5.6	-0.2	4.2	0.2	5.7	0.09	0.79	-0.61	0.50	3.32	0.32
TACT	9000	33.9	4.2	-1.3	4.0	0.0	5.2	0.04	0.72	-1.01	0.57	3.41	0.29
AATA	9000	33.8	3.4	-1.2	3.8	0.0	4.2	0.27	0.50	-1.22	0.44	3.32	0.27
AATC	9000	31.4	3.5	0.7	3.7	-1.0	4.3	0.11	0.55	-1.05	0.44	3.30	0.27
AATG	8999	32.3	3.6	0.7	3.7	-1.1	4.5	0.11	0.61	-0.95	0.43	3.33	0.27
AATT	9000	32.3	3.3	0.2	3.7	-0.5	4.3	-0.04	0.55	-1.02	0.40	3.37	0.27
CATG	9000	29.6	4.6	-0.1	3.9	0.9	5.0	-0.03	0.70	-0.82	0.43	3.25	0.29
GATC	9000	30.4	4.1	0.5	3.8	-0.5	4.6	0.00	0.58	-0.94	0.44	3.25	0.28
GATG	9000	28.1	4.6	0.0	4.0	1.9	4.8	-0.17	0.65	-0.78	0.44	3.17	0.29
TATA	8999	30.5	4.2	0.5	4.0	0.8	4.8	-0.03	0.68	-1.02	0.48	3.24	0.28
TATC	8969	30.4	4.1	0.1	3.9	-0.4	4.7	-0.04	0.66	-0.92	0.45	3.23	0.28
TATG	8999	29.9	4.4	0.8	3.9	0.8	5.1	-0.09	0.73	-0.82	0.42	3.23	0.28

AGCA	9000	36.2	4.9	1.0	4.2	0.9	5.2	0.12	0.70	-0.77	0.62	3.45	0.27
AGCC	8999	36.9	4.9	1.2	4.0	0.3	5.0	0.04	0.54	-1.00	0.59	3.49	0.28
AGCG	9000	37.4	5.3	1.0	4.1	-0.7	5.5	0.21	0.65	-0.54	0.60	3.51	0.29
AGCT	9000	37.5	4.5	-0.2	4.0	0.2	4.6	-0.07	0.52	-1.04	0.55	3.57	0.26
CGCG	9000	32.3	8.1	-0.5	4.4	1.0	5.7	-0.08	0.78	-0.16	0.47	3.31	0.32
GGCC	9000	35.5	5.1	0.0	4.1	0.8	5.0	-0.04	0.54	-0.89	0.57	3.35	0.30
GGCG	9000	37.1	5.1	0.2	4.1	1.1	5.0	-0.34	0.52	-0.89	0.64	3.39	0.28
TGCA	9000	37.1	5.4	0.1	4.2	-1.2	5.7	0.02	0.78	-0.26	0.57	3.38	0.28
TGCC	9000	34.6	6.3	0.8	4.2	0.1	5.1	0.12	0.68	-0.65	0.53	3.35	0.30
TGCG	8999	35.9	6.2	-0.4	4.2	-0.4	5.9	-0.08	0.78	-0.28	0.60	3.40	0.30
ACAA	8999	21.6	9.0	1.8	4.7	11.3	5.6	-0.39	0.63	-0.41	0.65	3.21	0.41
ACAC	9000	30.7	7.2	0.5	5.0	9.4	6.6	-0.35	0.76	-0.58	0.62	3.44	0.37
ACAG	9000	29.5	7.4	0.5	4.9	10.3	6.0	-0.22	0.77	-0.65	0.62	3.40	0.41
ACAT	8999	34.7	5.9	-0.4	5.0	11.3	6.2	-0.43	0.68	-0.77	0.63	3.65	0.36
CCAA	9000	20.0	6.3	1.9	4.6	9.8	5.3	-0.36	0.60	-0.41	0.46	3.07	0.34
CCAC	9000	26.6	6.7	0.3	4.9	8.7	6.0	-0.40	0.83	-0.36	0.56	3.21	0.33
CCAG	9000	23.4	5.9	1.2	4.5	9.1	5.4	0.06	0.62	-0.33	0.52	3.06	0.31
CCAT	9000	29.9	6.0	0.6	5.0	10.4	5.8	-0.39	0.76	-0.60	0.58	3.35	0.37
GCAA	8999	22.8	7.6	1.7	4.6	9.8	5.7	-0.20	0.69	-0.42	0.54	3.21	0.36
GCAC	9000	24.6	7.4	0.3	4.8	9.0	6.0	-0.45	0.73	-0.39	0.52	3.20	0.34
GCAG	9000	26.9	7.9	-0.1	4.9	8.7	6.1	-0.29	0.81	-0.37	0.60	3.23	0.36
GCAT	9000	30.6	6.3	0.5	5.0	10.0	6.1	-0.26	0.80	-0.70	0.60	3.49	0.39
TCAA	9000	24.3	8.2	-0.2	5.1	9.9	6.3	-0.46	0.78	-0.24	0.59	3.23	0.38
TCAC	9000	26.3	7.7	-1.2	4.9	9.4	6.3	-0.27	0.80	-0.19	0.71	3.19	0.36
TCAG	9000	22.9	7.6	-0.2	4.9	9.4	5.7	-0.33	0.80	-0.24	0.56	3.11	0.34
TCAT	8999	23.0	7.3	-0.6	4.9	11.1	5.9	-0.24	0.71	-0.15	0.51	3.16	0.33
ACGA	9000	28.8	9.9	0.8	5.6	9.6	6.2	0.08	0.92	-0.32	0.66	3.37	0.44
ACGC	9000	32.3	8.7	-0.2	5.4	9.0	6.0	-0.13	0.82	-0.31	0.61	3.43	0.40
ACGG	9000	29.3	9.7	0.0	5.3	8.6	5.9	-0.01	0.79	-0.39	0.66	3.32	0.44
ACGT	8999	28.5	5.8	-2.5	5.2	7.4	6.2	-0.88	0.63	-1.18	0.64	3.74	0.40
CCGG	9000	29.5	8.8	0.7	5.3	7.1	6.1	0.26	0.83	-0.08	0.65	3.21	0.37
GCGC	8999	31.6	6.7	1.1	5.5	7.6	6.1	0.25	0.88	-0.44	0.76	3.46	0.42

GCGG	9000	22.8	7.4	-0.5	5.0	6.5	5.7	-0.02	0.81	-0.23	0.50	3.02	0.32
TCGA	8997	19.3	8.2	-0.1	4.9	9.0	5.5	0.01	0.71	-0.25	0.53	3.04	0.36
TCGC	8999	22.9	7.2	-0.1	4.7	9.1	5.2	0.00	0.67	-0.32	0.51	3.11	0.35
TCGG	9000	25.9	6.8	-1.7	4.9	9.2	5.8	-0.28	0.69	-0.25	0.48	3.13	0.32
ATAA	9000	29.4	8.2	1.4	5.0	11.0	6.8	-0.07	0.84	-0.51	0.70	3.41	0.38
ATAC	8998	32.3	5.9	-0.1	4.9	9.3	7.5	-0.07	0.86	-0.60	0.70	3.44	0.36
ATAG	8999	26.8	8.3	0.4	5.0	10.5	7.0	0.30	0.90	-0.35	0.81	3.27	0.35
ATAT	8998	34.2	5.4	0.6	4.9	11.0	6.2	0.01	0.68	-0.86	0.60	3.61	0.35
CTAG	9000	24.8	7.4	0.1	4.9	10.4	6.7	0.10	0.93	-0.43	0.60	3.13	0.33
GTAC	9000	28.5	7.0	0.0	5.1	8.0	6.7	-0.34	1.05	-0.30	0.66	3.21	0.34
GTAG	9000	26.6	7.3	0.2	4.9	9.1	6.9	0.22	0.96	-0.32	0.66	3.19	0.31
TTAA	8998	20.8	10.3	-0.5	5.2	10.0	6.5	-0.28	0.91	0.81	1.23	3.10	0.32
TTAA*	7003	23.9	8.6	-0.5	5.1	10.1	7.0	-0.40	0.96	0.29	0.82	3.14	0.31
TTAC	8959	31.0	7.2	-2.4	5.1	9.2	6.7	-0.06	1.00	-0.21	0.75	3.39	0.37
TTAG	8999	17.0	10.7	-1.5	5.4	11.3	5.9	0.08	0.74	1.15	1.75	3.15	0.39
TTAG*	4940	23.7	9.1	-1.0	5.1	11.8	6.4	0.16	0.85	-0.32	0.79	3.22	0.36

\*The conformations with slide > 2Å were excluded.



Table S3.  $S_{xy}$  (degree<sup>3</sup>Å<sup>3</sup>) of tetrameric steps (See Fig. 3)

Dimer	Tetrameric steps															
AA	AAAA	AAAC	AAAG	AAAT	CAAA	CAAC	CAAG	CAAT	GAAA	GAAC	GAAG	GAAT	TAAA	TAAC	TAAG	TAAT
11.2	7.7	7.1	4.8	4.8	10.0	9.3	6.7	6.5	19.1	11.4	7.4	4.9	9.1	9.7	11.4	7.2
AG	AAGA	AAGC	AAGG	AAGT	CAGA	CAGC	CAGG	CAGT	GAGA	GAGC	GAGG	GAGT	TAGA	TAGC	TAGG	TAGT
15.9	12.8	7.0	8.5	5.9	16.0	9.1	14.4	11.7	15.3	12.8	16.3	6.4	19.5	10.7	19.8	12.1
GA	AGAA	AGAC	AGAG	AGAT	CGAA	CGAC	CGAG	CGAT	GGAA	GGAC	GGAG	GGAT	TGAA	TGAC	TGAG	TGAT
15.7	16.9	12.4	13.8	6.5	14.7	5.5	9.9	7.6	16.5	12.2	11.5	11.0	12.0	6.5	13.3	16.1
GG	AGGA	AGGC	AGGG	AGGT	CGGA	CGGC	CGGG	CGGT	GGGA	GGGC	GGGG	GGGT	TGGA	TGGC	TGGG	TGGT
16.8	9.2	9.0	10.5	6.0	23.6	8.8	12.2	9.5	16.1	12.9	9.2	7.6	16.9	14.0	14.6	14.3
AC	AACA	AACC	AACG	AACT	CACA	CACC	CACG	CACT	GACA	GACC	GACG	GACT	TACA	TACC	TACG	TACT
9.4	6.5	3.0	9.4	5.7	9.1	6.5	9.5	8.0	11.5	4.5	9.3	5.7	6.8	7.9	10.6	7.4
AT	AATA	AATC	AATG	AATT			CATG			GATC	GATG		TATA	TATC	TATG	
5.5	2.8	3.1	3.5	2.7			6.3			4.4	5.7		6.3	5.1	6.3	
GC	AGCA	AGCC	AGCG	AGCT			CGCG			GGCC	GGCG		TGCA	TGCC	TGCG	
12.3	8.5	6.0	8.9	4.3			14.1			7.0	6.3		10.7	10.1	13.1	
CA	ACAA	ACAC	ACAG	ACAT	CCAA	CCAC	CCAG	CCAT	GCAA	GCAC	GCAG	GCAT	TCAA	TCAC	TCAG	TCAT
31.9	28.4	31.2	30.7	19.3	12.1	22.3	11.9	21.4	19.7	19.9	31.1	27.0	30.4	33.3	24.5	18.5
CG	ACGA	ACGC	ACGG	ACGT			CCGG			GCGC	GCGG		TCGA	TCGC	TCGG	
45.2	50.7	35.1	43.5	16.3			33.5			40.7	17.6		21.7	16.2	13.7	
TA	ATAA	ATAC	ATAG	ATAT			CTAG			GTAC	GTAG		TTAA	TTAC	TTAG	
57.3	47.5	33.4	54.0	17.9			34.2			38.0	34.5		55.5	47.4	56.4	