Supplemental Data

Structural basis of human PRDM9 allele C specific recognition of its cognate DNA sequence

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Supplemental Figure S1-S5

Supplemental Table S1

Figure S1
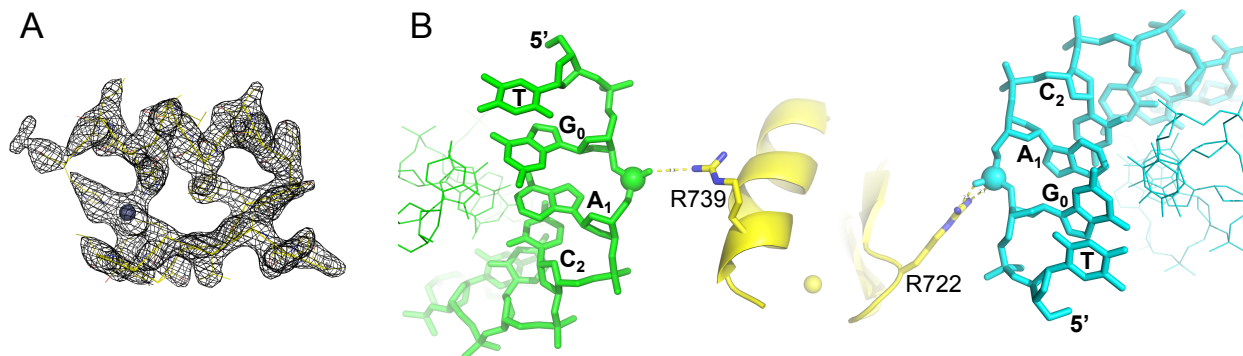
Supplemental Figure S1. Mol C in the space group $P2_1$

(A) The omit electron density (grey mesh), contoured at 3.0σ above the mean, is shown for Mol C, which contains only one ordered ZF, as no electron density was observed for the rest of the fingers.

(B) Although no internal symmetry existed for each ZF module, two arginine residues (R722 and R739) of Mol C (colored in yellow) interact respectively with the DNA phosphate group between G_0 and A_1 of two DNA molecules.

Figure S2
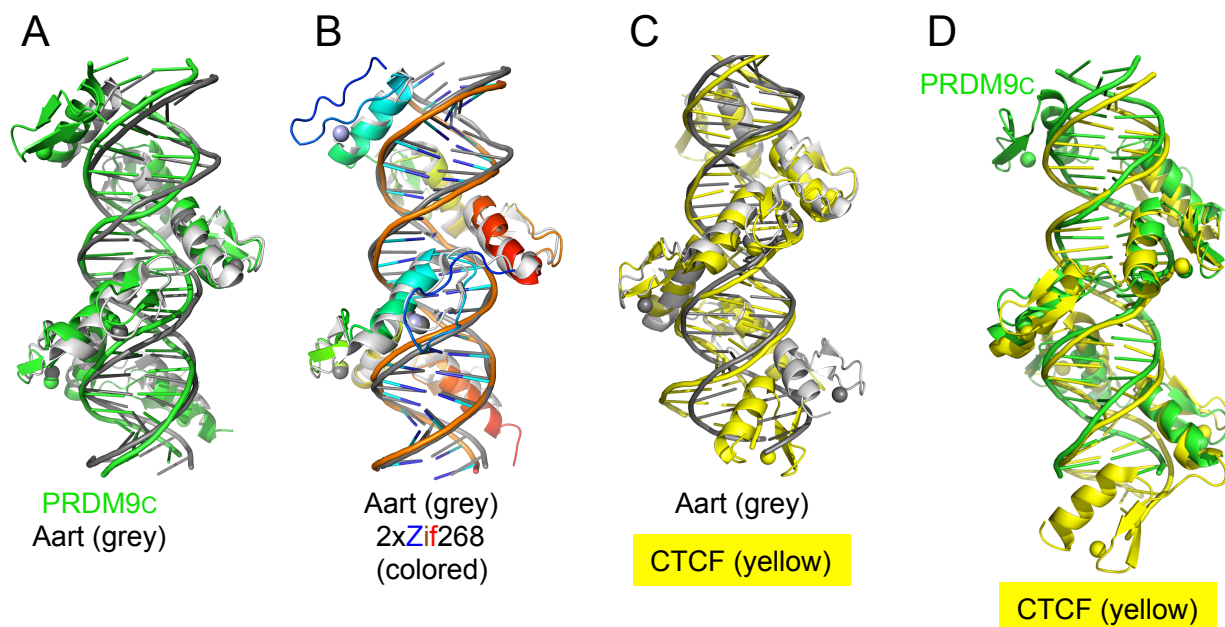
Supplemental Figure S2. Structural comparison among six-fingers structures

(**A**) Superimposition of PRDM9c (green) and six-finger designed Aart (grey; PDB 2I13).

(**B**) Superimposition of Aart (grey) and two copies of the three-finger Zif268 (colored in rainbow) (PDB 1P47).

(**C**) Superimposition of Aart (grey) and six-fingered CTCF ZF2-7 (yellow) (PDB 5T0U). Note, the last finger deviates between the two structures (RMSD=2.0 Å for 113 pairs of Cα atoms).

(**D**) Superimposition of PRDM9c (green) and six-fingered fragment of human CTCF ZF2-7 (PDB 5T0U). Note only five fingers are aligned between the two structures (RMSD=2.5 Å for 125 pairs of Cα atoms). The first ZF of PRDM9c and the last ZF of CTCF were excluded in the alignment.

Figure S3
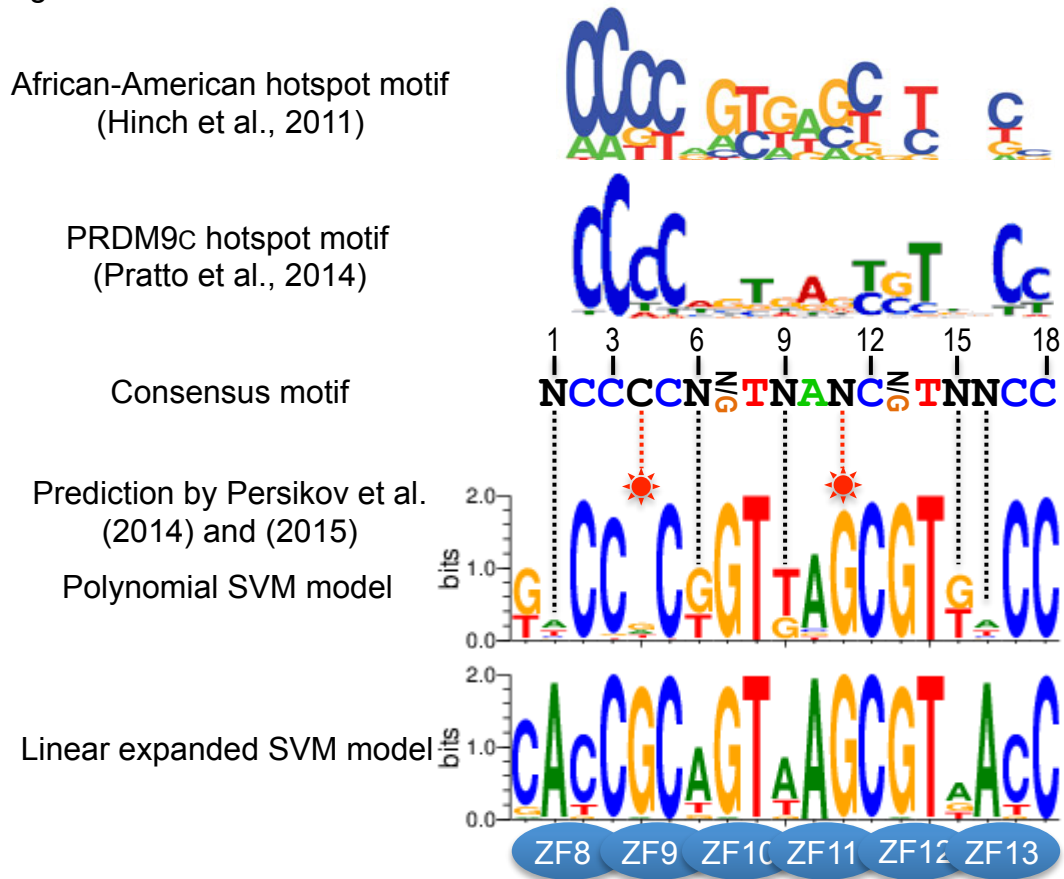
Supplemental Figure S3. Comparison of experimentally determined consensus sequence motifs (1,2) (top two lines) and predictions made by SVM (support vector machines)-based algorithms (3) (Bottom two lines).
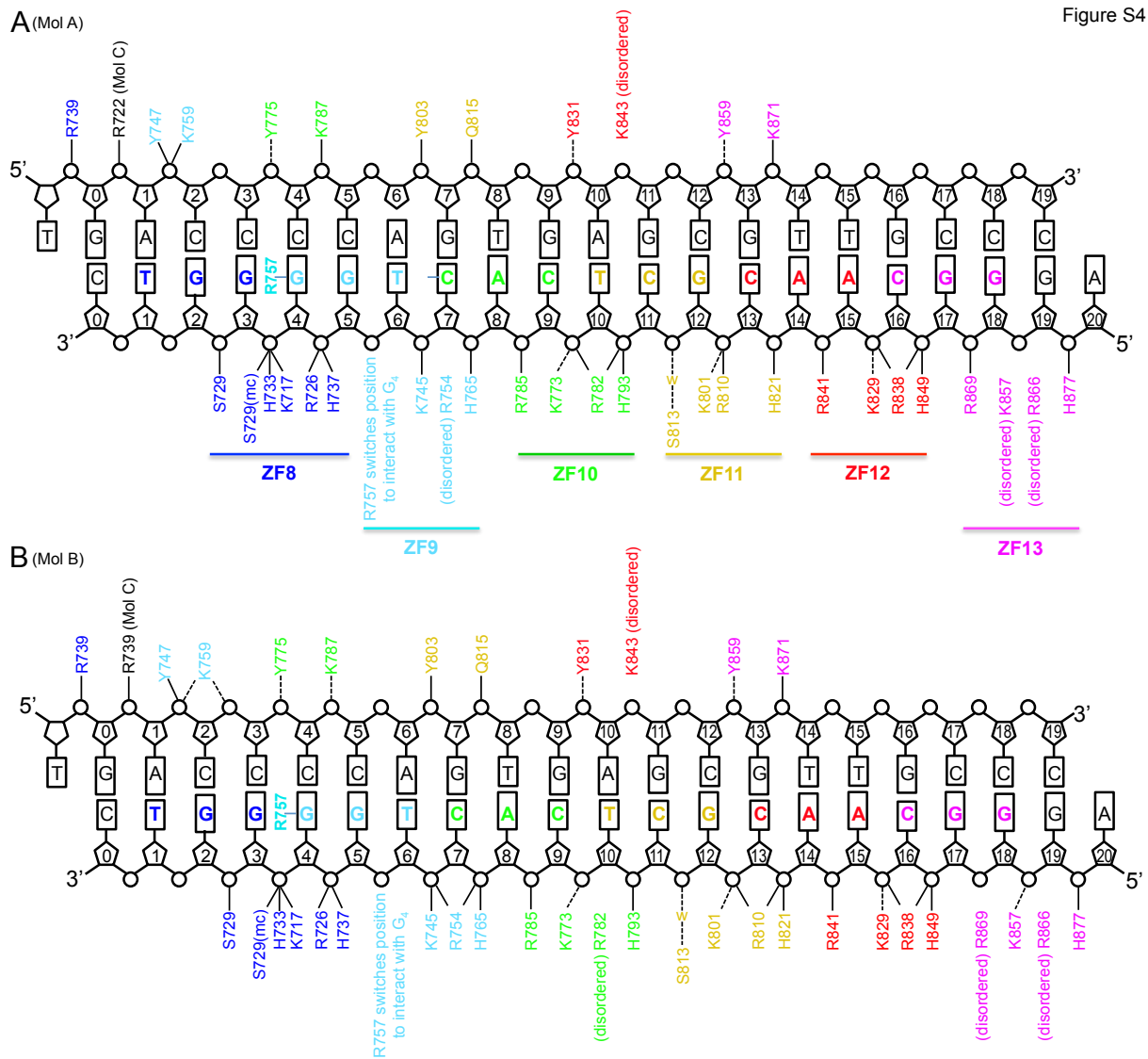
Figure S4

Supplemental Figure S4. **Schematics of PRDM9C-DNA backbone phosphate interactions**

Solid lines indicate conventional H-bonds; dashed lines indicate inter-atomic distance >3.5 Å;

mc=main chain atom. Note two arginine residues of Mol C are involved in the interaction with

the phosphate group between G0 and A1 (see Fig. S1B).

S-5
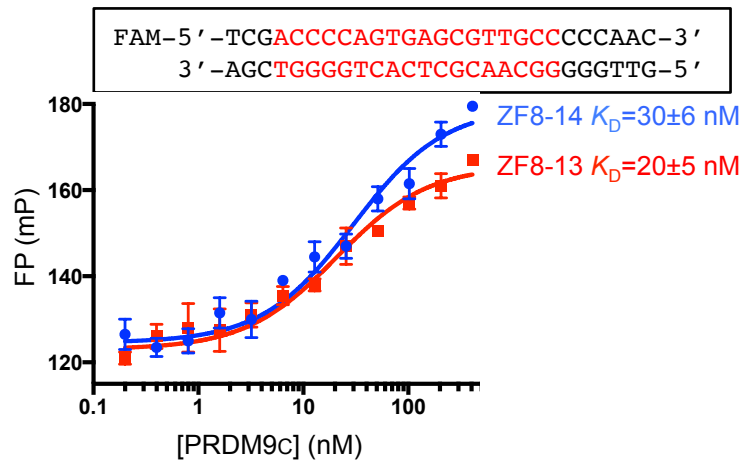
Figure S5

Supplemental Figure S5. DNA-binding data

DNA binding affinities of PRDM9c ZF8-13 and ZF8-14 against the FAM-labeled oligo, under the conditions of 350 mM NaCl and the probe DNA concentration of 5 nM. Fluorescence polarization (Y-axis) was used to measure the dissociation constants (K_D), as described (4,5). DNA-binding data represent the mean ± SEM of two independent determinations performed in duplicate.

References

1.	Hinch, A. G., Tandon, A., Patterson, N., Song, Y., Rohland, N., Palmer, C. D., Chen, G. K., Wang, K., Buxbaum, S. G., Akylbekova, E. L., Aldrich, M. C., Ambrosone, C. B., Amos, C., Bandera, E. V., Berndt, S. I., Bernstein, L., Blot, W. J., Bock, C. H., Boerwinkle, E., Cai, Q., Caporaso, N., Casey, G., Cupples, L. A., Deming, S. L., Diver, W. R., Divers, J., Fornage, M., Gillanders, E. M., Glessner, J., Harris, C. C., Hu, J. J., Ingles, S. A., Isaacs, W., John, E. M., Kao, W. H., Keating, B., Kittles, R. A., Kolonel, L. N., Larkin, E., Le Marchand, L., McNeill, L. H., Millikan, R. C., Murphy, A., Musani, S., Neslund-Dudas, C., Nyante, S., Papanicolaou, G. J., Press, M. F., Psaty, B. M., Reiner, A. P., Rich, S. S., Rodriguez-Gil, J. L., Rotter, J. I., Rybicki, B. A., Schwartz, A. G., Signorello, L. B., Spitz, M., Strom, S. S., Thun, M. J., Tucker, M. A., Wang, Z., Wiencke, J. K., Witte, J. S., Wrensch, M., Wu, X., Yamamura, Y., Zanetti, K. A., Zheng, W., Ziegler, R. G., Zhu, X., Redline, S., Hirschhorn, J. N., Henderson, B. E., Taylor, H. A., Jr., Price, A. L., Hakonarson, H., Chanock, S. J., Haiman, C. A., Wilson, J. G., Reich, D., and Myers, S. R. (2011) The landscape of recombination in African Americans. *Nature* **476**, 170-175
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4.	Patel, A., Hashimoto, H., Zhang, X., and Cheng, X. (2016) Characterization of How DNA Modifications Affect DNA Binding by C2H2 Zinc Finger Proteins. *Methods Enzymol* **573**, 387-401
5.	Patel, A., Horton, J. R., Wilson, G. G., Zhang, X., and Cheng, X. (2016) Structural basis for human PRDM9 action at recombination hot spots. *Genes Dev* **30**, 257-265

Supplemental Table S1. Local DNA base-pair parameters


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3DNA v2.0 (Date and time: Tue Jul 25 14:21:00 2017)
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Number of base-pairs: 40 for two DNA molecules (Mol A and Mol B)
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Detailed H-bond information: atom-name pair and length [O N]

Mol A:
   1 G-----C  [3] O6 - N4  3.01  N1 - N3  2.83  N2 - O2  2.54
   2 A-----T  [2] N6 - O4  3.03  N1 - N3  2.81
   3 C-----G  [3] O2 - N2  2.78  N3 - N1  2.91  N4 - O6  3.00
   4 C-----G  [3] O2 - N2  2.93  N3 - N1  2.99  N4 - O6  3.00
   5 C-----G  [3] O2 - N2  2.83  N3 - N1  2.87  N4 - O6  2.79
   6 C-----G  [3] O2 - N2  2.77  N3 - N1  2.87  N4 - O6  2.88
   7 A-----T  [2] N6 - O4  2.81  N1 - N3  2.75
   8 G-----C  [3] O6 - N4  3.01  N1 - N3  2.88  N2 - O2  2.80
   9 T-----A  [2] N3 - N1  2.78  O4 - N6  2.89
  10 G-----C  [3] O6 - N4  2.93  N1 - N3  2.75  N2 - O2  2.45
  11 A-----T  [2] N6 - O4  2.95  N1 - N3  2.81
  12 G-----C  [3] O6 - N4  2.75  N1 - N3  2.81  N2 - O2  2.74
  13 C-----G  [3] O2 - N2  2.76  N3 - N1  2.88  N4 - O6  2.92
  14 G-----C  [3] O6 - N4  3.05  N1 - N3  2.90  N2 - O2  2.62
  15 T-----A  [2] N3 - N1  2.66  O4 - N6  2.67
  16 T-----A  [2] N3 - N1  2.69  O4 - N6  2.83
  17 G-----C  [3] O6 - N4  2.47  N1 - N3  2.79  N2 - O2  2.96
  18 C-----G  [3] O2 - N2  2.63  N3 - N1  3.00  N4 - O6  3.22
  19 C-----G  [3] O2 - N2  2.57  N3 - N1  2.57  N4 - O6  2.55
  20 C-----G  [3] O2 - N2  2.47  N3 - N1  2.72  N4 - O6  2.88

Mol B:
  21 G-----C  [3] O6 - N4  2.90  N1 - N3  2.87  N2 - O2  2.75
  22 A-----T  [2] N6 - O4  2.88  N1 - N3  2.77
  23 C-----G  [3] O2 - N2  2.70  N3 - N1  2.84  N4 - O6  2.91
  24 C-----G  [3] O2 - N2  2.73  N3 - N1  2.91  N4 - O6  3.05
  25 C-----G  [3] O2 - N2  2.65  N3 - N1  2.72  N4 - O6  2.71
  26 C-----G  [3] O2 - N2  2.59  N3 - N1  2.73  N4 - O6  2.80
  27 A-----T  [2] N6 - O4  2.55  N1 - N3  2.53
  28 G-----C  [3] O6 - N4  3.12  N1 - N3  2.95  N2 - O2  2.76
  29 T-----A  [2] N3 - N1  2.92  O4 - N6  3.00
  30 G-----C  [3] O6 - N4  2.73  N1 - N3  2.76  N2 - O2  2.69
  31 A-----T  [2] N6 - O4  2.74  N1 - N3  2.75
  32 G-----C  [3] O6 - N4  2.93  N1 - N3  2.89  N2 - O2  2.81
  33 C-----G  [3] O2 - N2  2.49  N3 - N1  2.78  N4 - O6  2.95
  34 G-----C  [3] O6 - N4  3.01  N1 - N3  2.96  N2 - O2  2.78
  35 T-----A  [2] N3 - N1  2.77  O4 - N6  2.98
  36 T-----A  [2] N3 - N1  2.68  O4 - N6  2.83
  37 G-----C  [3] O6 - N4  2.48  N1 - N3  2.71  N2 - O2  2.81
  38 C-----G  [3] O2 - N2  2.42  N3 - N1  2.74  N4 - O6  3.00
  39 C-----G  [3] O2 - N2  2.71  N3 - N1  2.70  N4 - O6  2.65
  40 C-----G  [3] O2 - N2  2.43  N3 - N1  3.00  N4 - O6  3.50
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Supplemental Table S1 – continues

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Local base-pair parameters

Mol A:
     bp        Shear     Stretch    Stagger     Buckle   Propeller   Opening
    1 G-C      -0.35      -0.16      -0.28      -5.73      -8.87       5.85
    2 A-T       0.29      -0.10       0.12       4.65     -13.03       1.22
    3 C-G       0.12      -0.09       0.12       0.03     -11.88       1.33
    4 C-G       0.31      -0.07       0.11      10.15     -15.03      -1.39
    5 C-G       0.13      -0.15       0.32     -14.37      -3.63      -2.42
    6 C-G       0.24      -0.17      -0.23       5.84       5.29      -0.12
    7 A-T       0.49      -0.19       0.21      14.26     -11.82      -2.42
    8 G-C      -0.54      -0.20       0.20       2.00     -16.94       2.18
    9 T-A      -0.24      -0.20      -0.32      -2.61     -13.24      -0.29
   10 G-C      -0.12      -0.22      -0.09      -3.57      -4.39       4.44
   11 A-T       0.35      -0.15       0.14       1.65     -11.12      -1.46
   12 G-C      -0.19      -0.25       0.09       2.01      -2.09      -1.60
   13 C-G       0.79      -0.28      -0.05      12.11      -5.02       0.54
   14 G-C      -0.35      -0.10      -0.20      -9.08      -4.74       3.30
   15 T-A      -0.39      -0.33      -0.21      -1.87     -10.68      -2.43
   16 T-A      -0.02      -0.28      -0.08      -4.34      -3.50       0.10
   17 G-C       0.52      -0.27      -0.19      -2.01      -5.01      -7.31
   18 C-G       0.41       0.02      -0.09       7.47      -3.59       6.14
   19 C-G       0.24      -0.48      -0.08      11.70     -13.46      -1.98
   20 C-G       0.22      -0.27      -0.14       3.43      -6.47       4.36

Mol B:
     bp        Shear     Stretch    Stagger     Buckle   Propeller   Opening
   21 G-C      -0.44      -0.21       0.07       2.45      -5.25       0.39
   22 A-T       0.31      -0.19       0.06       2.22     -13.53      -2.03
   23 C-G       0.36      -0.20       0.10      -3.50      -9.72       1.11
   24 C-G       0.33      -0.10       0.09      11.49     -15.74       1.98
   25 C-G       0.08      -0.28       0.09     -12.71      -0.80      -0.77
   26 C-G      -0.12      -0.25      -0.30       0.39       2.77       0.59
   27 A-T       0.00      -0.45       0.13      11.26      -8.51      -3.09
   28 G-C      -0.28      -0.04       0.18      -0.28      -9.00       3.36
   29 T-A      -0.04      -0.05      -0.24      -0.96      -9.28      -1.07
   30 G-C      -0.05      -0.24       0.02       0.49      -0.20      -0.54
   31 A-T       0.54      -0.24       0.22       3.66     -10.13      -5.70
   32 G-C      -0.16      -0.11      -0.20      -2.18      -8.54       0.93
   33 C-G       0.26      -0.19      -0.03      10.07      -1.64       4.16
   34 G-C      -0.30      -0.06      -0.43     -11.63      -6.32       1.31
   35 T-A       0.04      -0.21      -0.07      -1.68      -7.59       2.05
   36 T-A      -0.33      -0.29      -0.28      -2.21      -9.05       0.60
   37 G-C       0.61      -0.35      -0.27      -4.10      -5.32      -5.74
   38 C-G       0.25      -0.22      -0.02       4.30      -9.48       5.52
   39 C-G       0.40      -0.38      -0.38      12.90     -11.67      -1.22
   40 C-G       0.89      -0.01      -0.12      -0.92      -5.32      12.93
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       ave.      0.11      -0.20      -0.05       1.27      -7.59       0.57
       s.d.      0.35       0.11       0.19       7.05       5.01       3.65
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Supplemental Table S1 – continues

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Local base-pair step parameters

Mol A:
    step     Shift     Slide     Rise     Tilt     Roll     Twist
 1 GA/TC     -1.18      1.71      3.02    -9.09    -1.88     44.34
 2 AC/GT      0.67     -0.79      3.35    -0.37    -0.93     32.40
 3 CC/GG      0.16      0.09      3.28     1.77    12.26     30.09
 4 CC/GG      0.25     -1.20      3.70     0.54     1.66     37.91
 5 CC/GG      1.23      0.42      2.93     7.03     7.47     32.29
 6 CA/TG     -0.97      0.60      3.23    -3.39    -2.29     33.75
 7 AG/CT      1.10     -1.16      3.68    -1.96     0.54     27.75
 8 GT/AC     -0.97     -0.81      3.38     4.00     4.18     35.83
 9 TG/CA      0.77      1.20      3.42    -1.15    10.26     31.29
10 GA/TC     -1.23      0.98      3.24    -4.80     2.28     38.29
11 AG/CT      0.63     -0.78      3.35     0.33    -1.09     28.62
12 GC/GC      0.31     -0.58      3.19     1.00     1.70     31.72
13 CG/CG      1.02     -1.49      4.05     1.62    -2.95     27.56
14 GT/AC     -0.39     -1.11      3.22     1.86     3.75     34.37
15 TT/AA     -0.24     -0.82      3.48    -1.60    -3.70     36.44
16 TG/CA     -0.37     -0.72      3.35     0.81     3.32     34.76
17 GC/GC      0.94     -0.55      3.06    -0.91     5.18     27.47
18 CC/GG     -1.13     -0.07      3.36    -2.13    -2.04     34.78
19 CC/GG      1.08      0.16      3.49     5.55     2.37     37.96

Mol B:
    step     Shift     Slide     Rise     Tilt     Roll     Twist
21 GA/TC     -1.05      1.28      3.43    -3.44     0.92     41.62
22 AC/GT      0.71     -0.73      3.38     0.07    -0.04     33.29
23 CC/GG      0.20     -0.02      3.03     0.94    12.86     28.46
24 CC/GG      0.22     -0.81      3.85     1.79    -1.03     38.92
25 CC/GG      1.02      0.40      2.99     5.91     6.83     30.85
26 CA/TG     -0.78      0.71      3.26    -3.22     2.31     31.66
27 AG/CT      0.69     -0.96      3.63    -3.32     0.02     33.94
28 GT/AC     -0.79     -0.69      3.33     3.93     3.81     32.99
29 TG/CA      0.41      1.11      3.35    -1.17     9.15     30.93
30 GA/TC     -1.20      0.78      3.29    -4.86     0.53     39.74
31 AG/CT      0.91     -0.60      3.57     4.62     0.23     29.23
32 GC/GC      0.32     -0.49      3.13    -3.10     1.94     27.65
33 CG/CG      0.89     -1.47      4.12     2.73    -3.94     30.22
34 GT/AC      0.09     -1.23      3.26    -0.33     2.45     35.97
35 TT/AA     -0.61     -0.82      3.42     2.56    -4.22     31.73
36 TG/CA      0.08     -0.28      3.54     1.53     5.60     37.70
37 GC/GC      0.67     -0.72      3.10    -1.07     3.04     25.36
38 CC/GG     -0.64     -0.38      3.27     1.27     0.44     33.58
39 CC/GG      1.07      0.14      3.71     3.87     1.55     42.06
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     ave.     0.10     -0.26      3.38     0.21     2.17     33.51
     s.d.     0.80      0.84      0.27     3.35     4.22      4.52
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Supplemental Table S1 – continues

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Local base-pair helical parameters

Mol A:
    step      X-disp    Y-disp    h-Rise     Incl.       Tip   h-Twist
  1 GA/TC      2.39      0.76      3.12      -2.46     11.89     45.25
  2 AC/GT     -1.24     -1.27      3.37      -1.67      0.67     32.41
  3 CC/GG     -2.02      0.03      3.08      22.46     -3.25     32.49
  4 CC/GG     -2.08     -0.30      3.65       2.56     -0.83     37.95
  5 CC/GG     -0.42     -1.04      3.14      13.02    -12.25     33.84
  6 CA/TG      1.39      1.13      3.26      -3.92      5.81     33.99
  7 AG/CT     -2.56     -2.80      3.57       1.13      4.08     27.82
  8 GT/AC     -1.89      2.11      3.15       6.75     -6.45     36.28
  9 TG/CA      0.19     -1.58      3.59      18.41      2.07     32.91
 10 GA/TC      1.20      1.25      3.41       3.46      7.27     38.65
 11 AG/CT     -1.33     -1.21      3.39      -2.20     -0.66     28.64
 12 GC/GC     -1.36     -0.39      3.16       3.10     -1.83     31.78
 13 CG/CG     -2.20     -1.63      4.23      -6.16     -3.39     27.76
 14 GT/AC     -2.42      0.94      3.06       6.31     -3.13     34.62
 15 TT/AA     -0.76      0.14      3.55      -5.89      2.55     36.65
 16 TG/CA     -1.72      0.74      3.26       5.55     -1.36     34.93
 17 GC/GC     -2.26     -2.14      2.88      10.79      1.89     27.96
 18 CC/GG      0.21      1.55      3.42      -3.40      3.55     34.90
 19 CC/GG     -0.08     -0.88      3.61       3.61     -8.47     38.42

Mol B:
    step      X-disp    Y-disp    h-Rise     Incl.       Tip   h-Twist
 21 GA/TC      1.70      1.09      3.52       1.29      4.83     41.76
 22 AC/GT     -1.27     -1.23      3.38      -0.07     -0.12     33.29
 23 CC/GG     -2.32     -0.21      2.77      24.62     -1.80     31.19
 24 CC/GG     -1.06     -0.08      3.88      -1.54     -2.68     38.98
 25 CC/GG     -0.46     -0.83      3.14      12.51    -10.83     32.11
 26 CA/TG      0.87      0.82      3.37       4.21      5.87     31.90
 27 AG/CT     -1.64     -1.75      3.55       0.04      5.67     34.10
 28 GT/AC     -1.82      2.02      3.12       6.66     -6.86     33.43
 29 TG/CA      0.26     -0.96      3.51      16.70      2.14     32.24
 30 GA/TC      1.08      1.19      3.42       0.78      7.11     40.02
 31 AG/CT     -1.23     -0.69      3.66       0.46     -9.08     29.58
 32 GC/GC     -1.46     -1.36      3.04       4.04      6.44     27.88
 33 CG/CG     -1.78     -0.99      4.33      -7.49     -5.19     30.58
 34 GT/AC     -2.33     -0.20      3.18       3.97      0.54     36.06
 35 TT/AA     -0.69      1.59      3.44      -7.66     -4.65     32.10
 36 TG/CA     -1.19      0.08      3.46       8.61     -2.35     38.13
 37 GC/GC     -2.43     -1.79      2.96       6.88      2.43     25.56
 38 CC/GG     -0.73      1.31      3.24       0.76     -2.19     33.61
 39 CC/GG      0.01     -1.03      3.79       2.16     -5.38     42.26
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      ave.    -0.88     -0.20      3.39       3.90     -0.47     34.00
      s.d.     1.30      1.26      0.33       7.72      5.46      4.43
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Supplemental Table S1 – continues

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Structure classification: This is a right-handed nucleic acid structure
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Classification of each dinucleotide step in a right-handed nucleic acid
structure: A-like; B-like; TA-like; intermediate of A and B, or other cases
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Mol A:

step	Xp	Yp	Zp	XpH	YpH	ZpH	Form
1 GA/TC	−2.91	8.67	−1.47	−0.55	8.61	−1.83	B
2 AC/GT	−3.10	9.19	−0.00	−4.30	9.19	−0.26	B
3 CC/GG	−1.92	9.08	0.94	−3.86	8.10	4.21	
4 CC/GG	−2.54	8.94	1.16	−4.51	8.88	1.54	
5 CC/GG	−2.36	8.97	0.56	−2.61	8.64	2.45	
6 CA/TG	−2.94	8.91	−0.38	−1.49	8.87	−1.03	B
7 AG/CT	−3.33	8.97	0.38	−5.78	8.96	0.57	B
8 GT/AC	−3.67	8.95	−0.57	−5.35	8.96	0.36	B
9 TG/CA	−3.08	8.98	−1.03	−2.91	8.87	1.77	B
10 GA/TC	−2.95	8.82	−0.52	−1.73	8.84	−0.09	B
11 AG/CT	−3.04	9.17	0.09	−4.32	9.16	−0.25	B
12 GC/GC	−3.35	9.29	−0.11	−4.69	9.28	0.38	B
13 CG/CG	−3.30	8.81	0.89	−5.46	8.86	−0.03	
14 GT/AC	−2.56	8.72	1.53	−4.86	8.51	2.42	
15 TT/AA	−2.99	8.95	0.43	−3.72	8.95	−0.44	B
16 TG/CA	−3.00	9.04	0.23	−4.62	8.98	1.06	B
17 GC/GC	−2.66	9.21	0.57	−4.87	8.95	2.24	
18 CC/GG	−2.67	8.94	0.43	−2.42	8.95	−0.10	B
19 CC/GG	−3.06	8.86	−0.24	−3.17	8.86	0.33	B

Mol B:

step	Xp	Yp	Zp	XpH	YpH	ZpH	Form
21 GA/TC	−2.75	8.78	−0.86	−1.12	8.80	−0.70	B
22 AC/GT	−2.99	9.16	0.02	−4.21	9.16	0.01	B
23 CC/GG	−2.02	9.11	0.91	−4.25	7.97	4.51	
24 CC/GG	−2.73	8.95	0.74	−3.71	8.96	0.51	
25 CC/GG	−2.81	8.82	0.01	−3.05	8.63	1.76	B
26 CA/TG	−3.09	8.93	−0.59	−2.17	8.95	0.01	B
27 AG/CT	−3.26	9.03	0.43	−4.78	9.03	0.46	B
28 GT/AC	−3.60	9.14	−0.54	−5.22	9.14	0.44	B
29 TG/CA	−2.97	8.95	−0.82	−2.73	8.82	1.71	B
30 GA/TC	−2.81	8.83	−0.45	−1.69	8.84	−0.42	B
31 AG/CT	−2.99	9.13	−0.09	−4.08	9.13	−0.06	B
32 GC/GC	−3.53	9.34	−0.35	−4.85	9.35	0.28	B
33 CG/CG	−3.37	8.76	0.74	−5.11	8.78	−0.37	
34 GT/AC	−2.48	8.50	1.80	−4.70	8.36	2.35	
35 TT/AA	−2.76	8.96	0.73	−3.40	8.98	−0.45	
36 TG/CA	−2.60	9.01	0.22	−3.69	8.89	1.49	B
37 GC/GC	−2.84	9.29	0.42	−5.22	9.17	1.50	B
38 CC/GG	−2.76	9.03	0.29	−3.49	9.02	0.42	B
39 CC/GG	−3.00	8.94	−0.01	−2.99	8.94	0.35	B

Supplemental Table S1 – continues

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Minor and major groove widths: direct P-P distances and refined P-P distances
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	Minor Groove		Major Groove	
	P-P	Refined	P-P	Refined
Mol A:				
1 GA/TC	---	---	---	---
2 AC/GT	---	---	---	---
3 CC/GG	13.8	---	15.2	---
4 CC/GG	14.6	14.6	19.2	19.0
5 CC/GG	14.4	14.4	17.6	17.5
6 CA/TG	12.7	12.7	18.7	18.6
7 AG/CT	11.1	10.9	19.4	19.4
8 GT/AC	12.2	12.0	18.6	18.4
9 TG/CA	14.0	14.0	16.9	16.3
10 GA/TC	14.1	13.9	19.9	19.7
11 AG/CT	13.4	13.3	19.2	19.1
12 GC/GC	13.3	13.2	18.5	18.4
13 CG/CG	12.0	11.9	22.4	22.3
14 GT/AC	10.6	10.5	21.7	21.7
15 TT/AA	12.1	11.9	19.1	19.1
16 TG/CA	13.6	13.4	18.4	18.3
17 GC/GC	13.6	---	18.9	---
18 CC/GG	---	---	---	---
19 CC/GG	---	---	---	---
20 CG/CG	---	---	---	---
Mol B:				
21 GA/TC	---	---	---	---
22 AC/GT	---	---	---	---
23 CC/GG	13.2	---	15.3	---
24 CC/GG	13.9	13.7	19.2	19.1
25 CC/GG	14.4	14.3	17.7	17.6
26 CA/TG	13.1	13.1	18.7	18.6
27 AG/CT	11.5	11.3	19.9	19.9
28 GT/AC	12.5	12.3	19.1	19.0
29 TG/CA	13.9	13.9	16.5	16.0
30 GA/TC	13.9	13.8	19.7	19.7
31 AG/CT	13.3	13.1	19.1	19.0
32 GC/GC	13.2	13.1	18.2	18.0
33 CG/CG	12.2	12.1	22.4	22.3
34 GT/AC	10.8	10.6	21.4	21.4
35 TT/AA	12.5	12.4	19.7	19.6
36 TG/CA	14.5	14.3	18.7	18.6
37 GC/GC	14.3	---	18.6	---
38 CC/GG	---	---	---	---
39 CC/GG	---	---	---	---