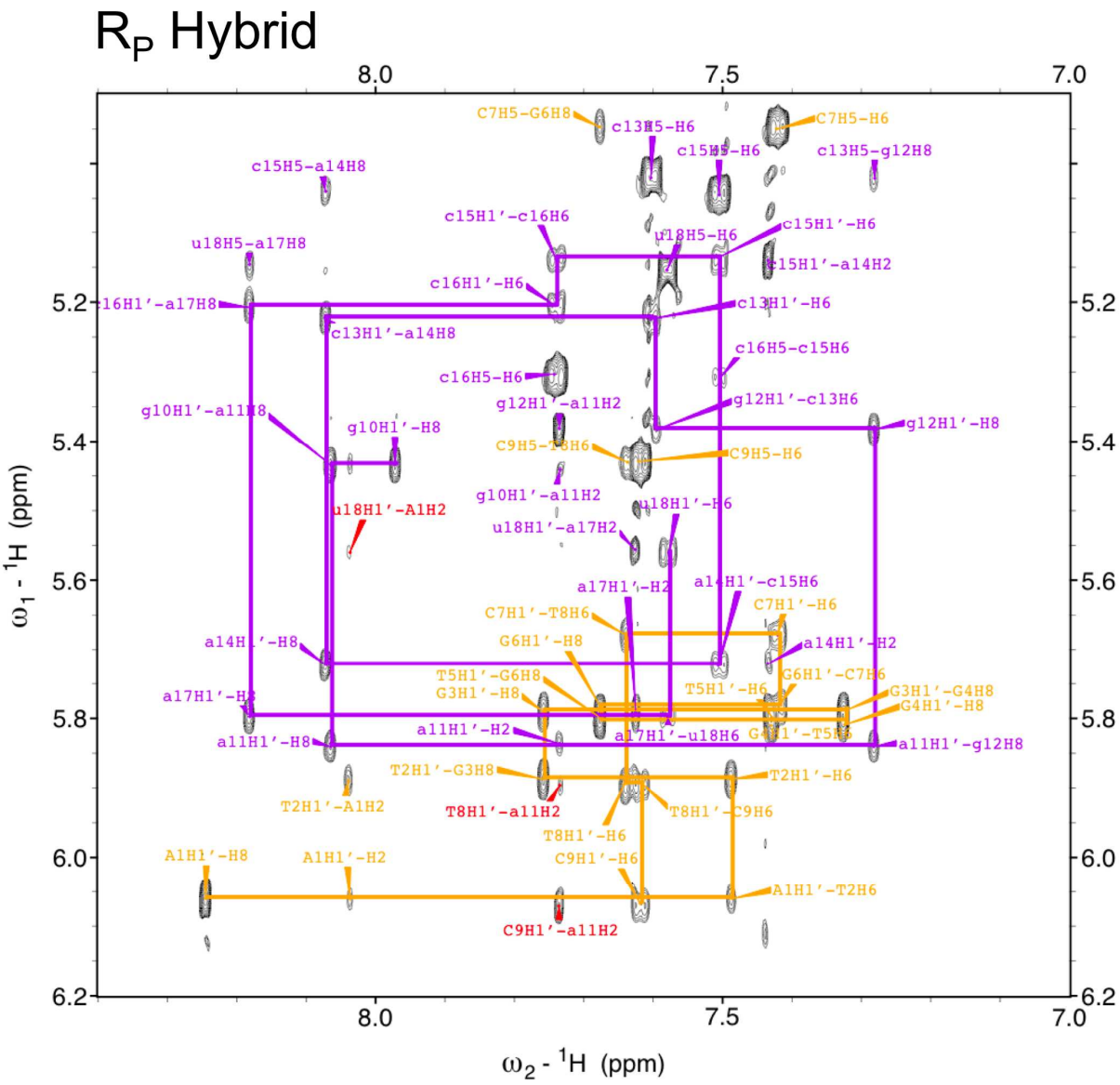
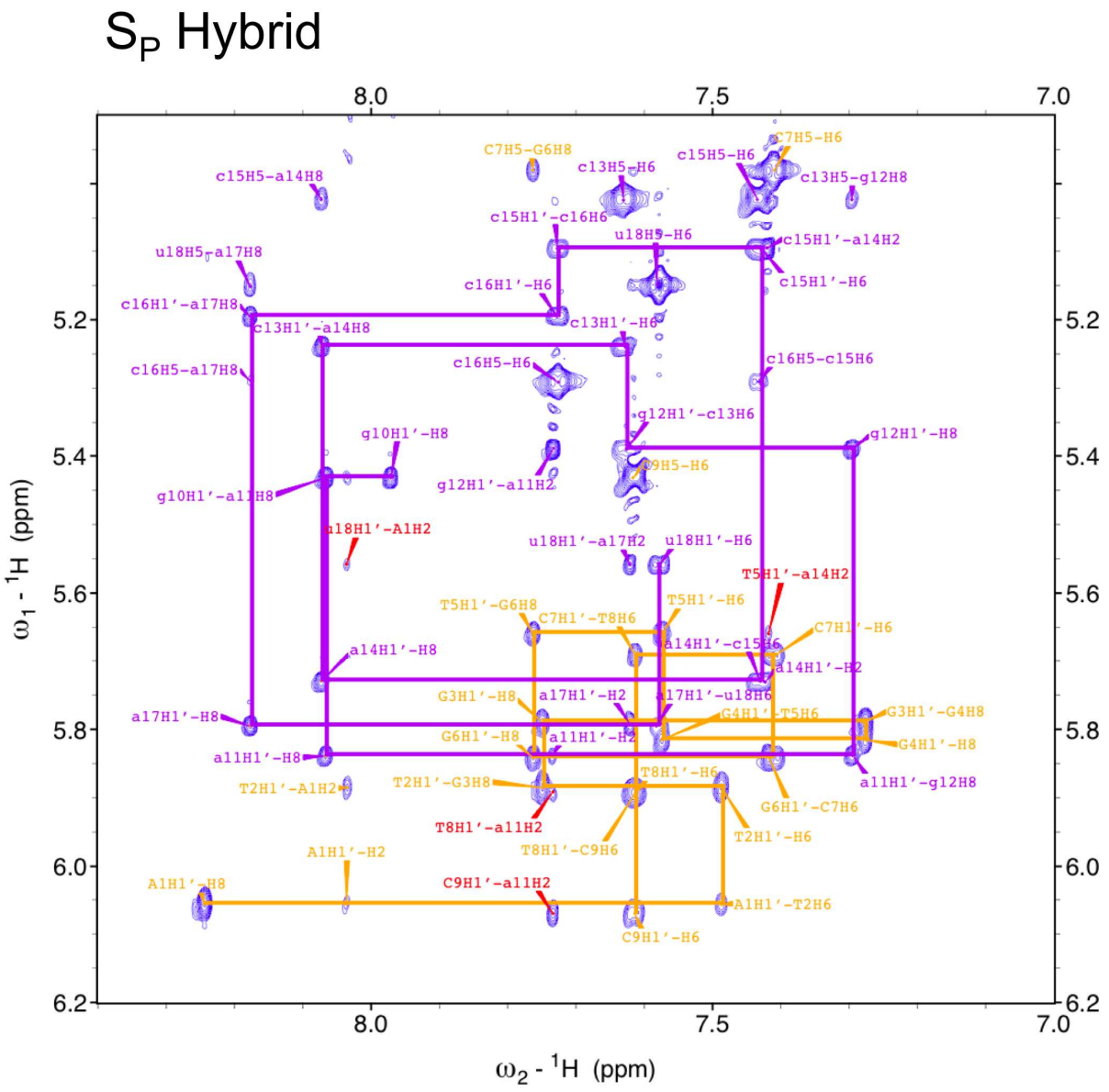
Supporting Information

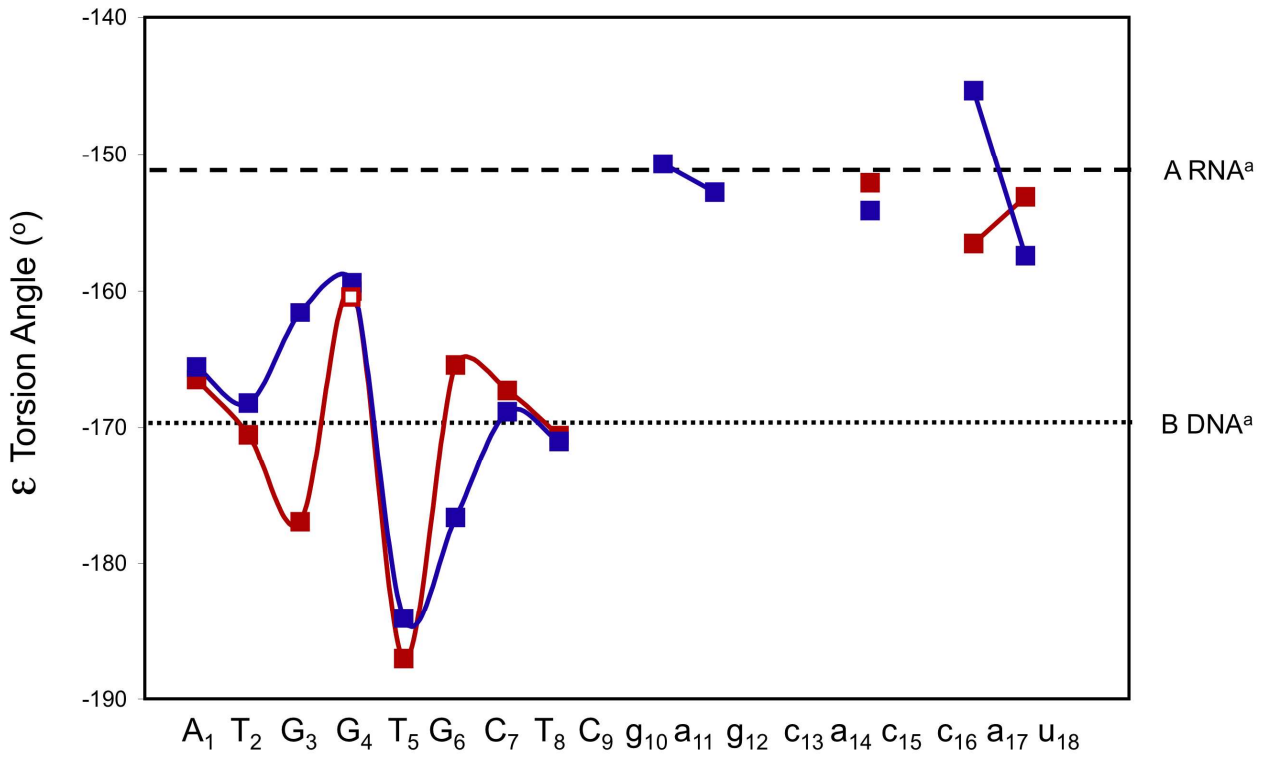


S1 A

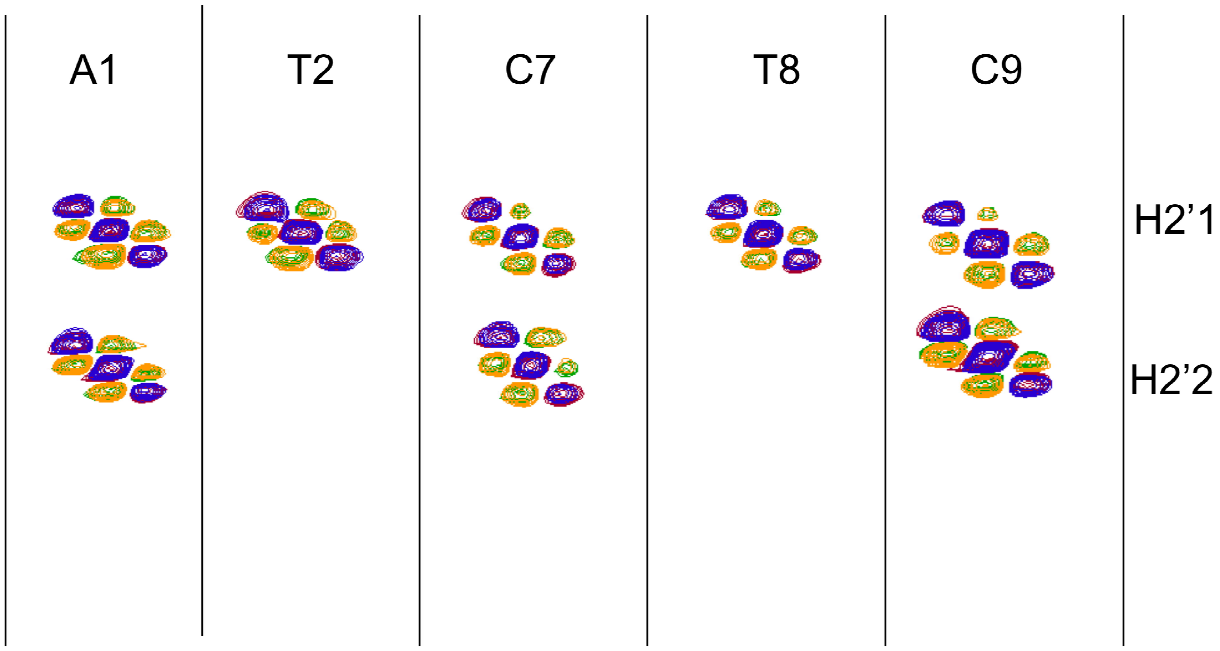


S1 B

S1: 150 ms NOESY base (H6/H8) to sugar (H1') pathway for R_P hybrid (A) and S_P hybrid (B). DNA pathways and cross peaks shown in orange. RNA pathways and cross peaks shown in purple. Inter-strand cross peaks labeled in red. Sample conditions: ~1.0 mM duplex 10 mM sodium phosphate, 100 mM NaCl, 0.1 mM EDTA, pH* 6.6, 298 K, ^{1}H referenced to DSS.



S2: ■ ε torsion angles for R_P hybrid, ■ ε torsion angles for S_P hybrid. □ Data not available, value measured from final NMR structure. [a] Values from Blackburn, Nucleic Acids in Chemistry and Biology 3rd edition.



S3: {^{31}P} Low flip angle COSY. DNA H1'–H2'1 and H1'–H2'2 cross peaks at the ends of each duplex are shown. R_P hybrid cross peaks shown in red and green, S_P hybrid cross peaks in yellow and blue. Aligning each set of cross peaks reveals that $^{3}J_{H1'\text{-}H2'1}$, $^{3}J_{H1'\text{-}H2'2}$, and $\sum J_{H1'}$ are identical.

R_P Hybrid

	H1'	H2/H5/CH_3	H2'1	H2'2	H3'	H4'	H6/H8	^{13}C1'	^{13}C6 / ^{13}C8	^{31}P	NH[a]	^{11}B	BH_3
A1	6.259	8.039	2.727	2.843	4.874	4.277	8.246	87.8	142.4	-	-	-	-
T2	6.087	1.489	2.400	2.632	4.929	4.334	7.490	86.2	138.8	-0.513	13.766	-	-
G3	5.990	-	2.717	2.717	4.879	4.410	7.758	85.1	137.7	-0.292	12.334	-	-
G4	6.010	-	2.536	2.728	4.711	4.375	7.326	86.3	136.5	-0.111	13.078	-	-
T5	6.002	1.265	2.491	2.570	4.984	4.253	7.428	86.5	138.1	-0.749	13.708	-41.43	0.33
G6	5.984	-	2.634	2.634	4.720	4.349	7.677	85.8	137.3	94.00	12.458		
C7	5.878	5.147	2.320	2.579	4.601	4.260	7.420	87.8	141.8	-0.323	-	-	-
T8	6.095	1.503	2.314	2.615	4.844	4.228	7.639	86.7	139.4	-0.942	14.030	-	-
C9	6.270	5.630	2.175	2.258	4.530	4.045	7.620	86.7	143.9	-0.446	-	-	-
g10	5.633	-	4.825	-	4.626	4.342	7.973	91.8	138.8	-	12.488	-	-
a11	6.039	7.736	4.814	-	4.750	4.553	8.065	92.5	140.0	-0.119		-	-
g12	5.581	-	4.449	-	4.416	4.484	7.282	92.7	135.8	-0.23	13.294	-	-
c13	5.421	5.219	4.517	-	4.495	4.417	7.602	93.7	140.5	-0.71	-	-	-
a14	5.921	7.433	4.564	-	4.664	4.483	8.073	92.9	139.3	-0.377	-	-	-
c15	5.340	5.242	4.265	-	4.341	4.563	7.505	93.7	140.6	-0.613	-	-	-
c16	5.405	5.504	4.357	-	4.538	4.263	7.740	94.8	141.1	-0.677	-	-	-
a17	5.996	7.625	4.376	-	4.717	4.468	8.182	92.4	140.0	-0.503	-	-	-
u18	5.759	5.352	4.043	-	4.177	4.378	7.579	91.6	142.5	-0.438	13.425	-	-

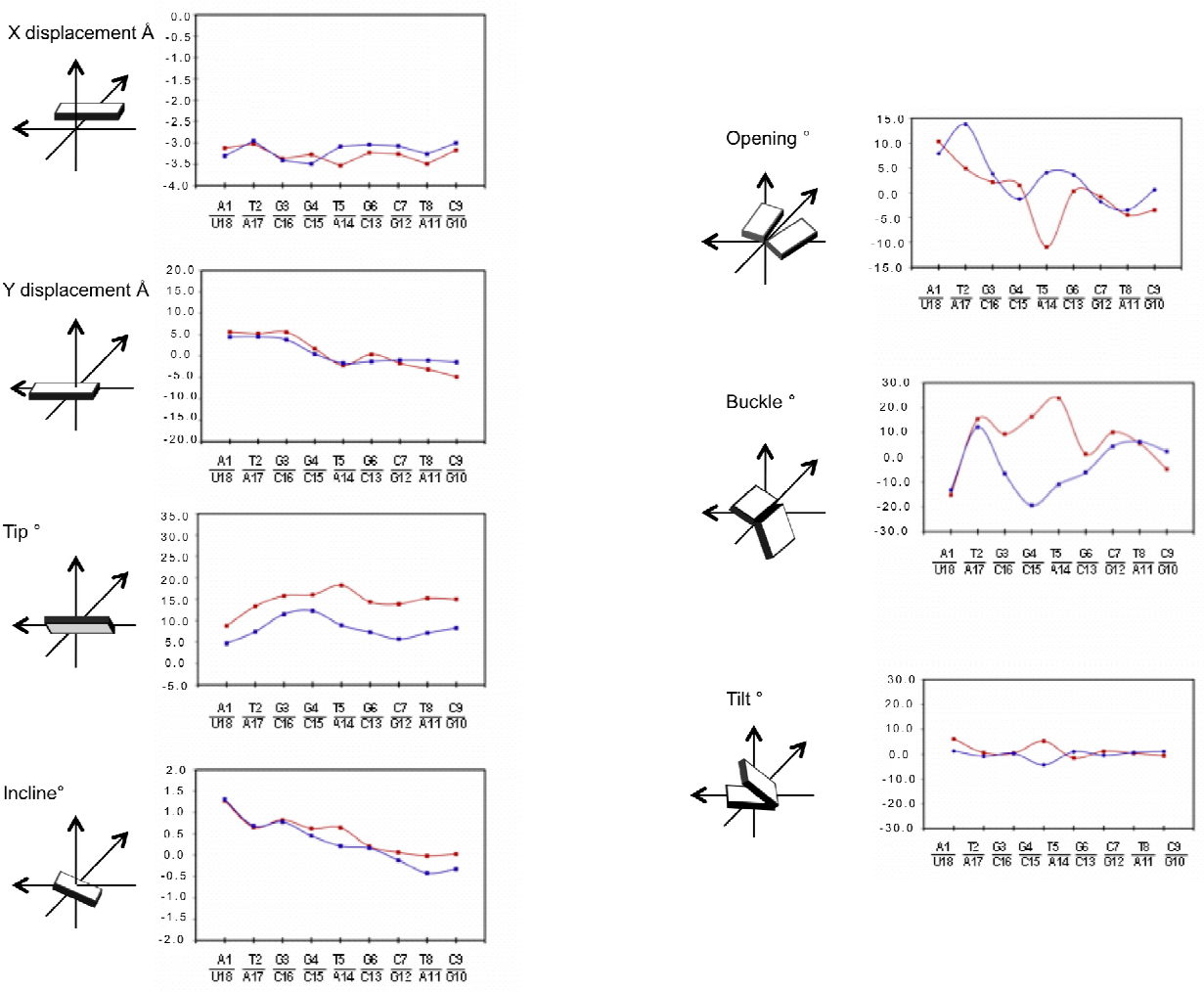
S_P Hybrid

	H1'	H2/H5/CH_3	H2'1	H2'2	H3'	H4'	H6/H8	^{13}C1'	^{13}C6 / ^{13}C8	^{31}P	NH[a]	^{11}B	BH_3
A1	6.256	8.036	2.720	2.842	4.874	4.279	8.244	87.8	142.4	-	-	-	-
T2	6.085	1.489	2.412	2.631	4.930	4.336	7.487	86.2	138.8	-0.520	13.733	-	-
G3	5.990	-	2.764	2.688	4.848	4.404	7.749	85.3	137.7	-0.244	12.294	-	-
G4	6.017	-	2.658	2.658	4.578	4.187	7.276	87.1	136.2	0.082	13.143	-	-
T5	5.860	1.241	2.505	2.539	4.812	4.178	7.574	87.3	137.6	-0.938	13.948	-42.11	0.42
G6	6.042	-	2.629	2.629	4.807	4.359	7.763	86.1	137.2	95.38	12.411		
C7	5.892	5.181	2.308	2.575	4.626	4.259	7.412	87.6	141.8	-0.429	-	-	-
T8	6.093	1.508	2.308	2.618	4.843	4.225	7.614	86.6	139.4	-0.925	14.024	-	-
C9	6.270	5.630	2.175	2.256	4.530	4.045	7.614	86.7	143.9	-0.463	-	-	-
g10	5.632	-	4.825	-	4.626	4.340	7.972	92.0	138.7	-	12.494	-	-
a11	6.039	7.733	4.809	-	4.750	4.558	8.067	92.6	139.9	-0.122	-	-	-
g12	5.590	-	4.431	-	4.483	4.428	7.295	92.6	135.8	-0.238	13.302	-	-
c13	5.439	5.222	4.524	-	4.515	4.415	7.630	93.7	140.6	-0.730	-	-	-
a14	5.931	7.421	4.601	-	4.658	4.494	8.073	92.9	139.3	-0.356	-	-	-
c15	5.296	5.223	4.256	-	4.318	4.378	7.431	93.9	140.5	-0.558	-	-	-
c16	5.395	5.490	4.344	-	4.543	4.292	7.727	94.0	141.1	-0.685	-	-	-
a17	5.995	7.620	4.377	-	4.717	4.469	8.177	92.4	140.0	-0.516	-	-	-
u18	5.759	5.350	4.040	-	4.174	4.374	7.579	91.7	142.5	-0.448	13.382	-	-

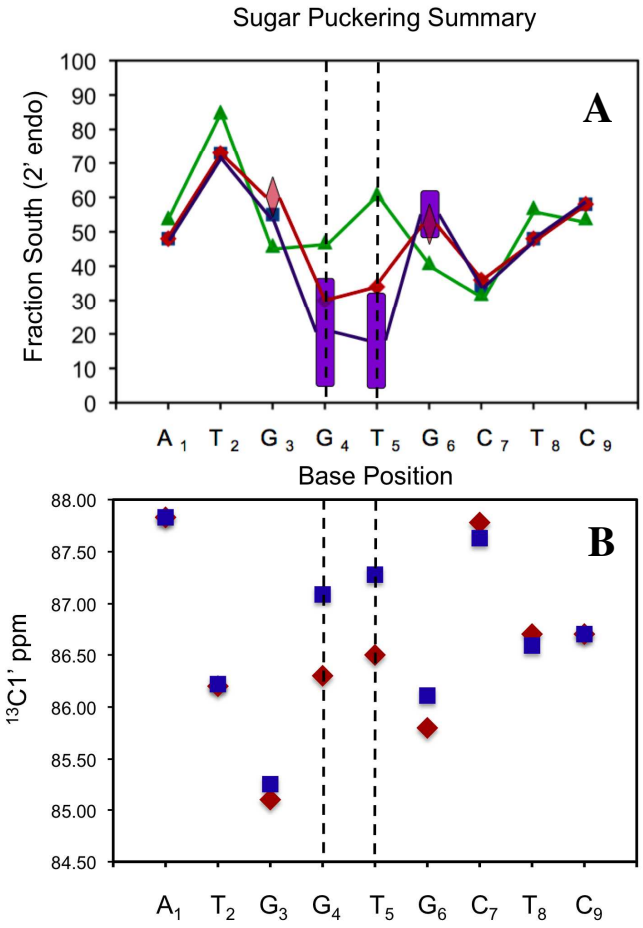
DNA / RNA hybrid control

	H1'	H2/H5/CH_3	H2'1	H2'2	H3'	H4'	H6/H8	NH	^{31}P
A1	6.250	8.032	2.723	2.840	4.868	4.273	8.242	-	
T2	6.086	1.478	2.404	2.634	4.927	4.336	7.490	nd	-0.53
G3	5.997		2.720	2.720	4.869	4.409	7.754	12.290	-0.29
G4	6.006		2.533	2.722	4.691	4.370	7.305	13.030	-0.10
T5	6.041	1.233	2.416	2.637	4.877	4.280	7.410	13.630	-0.81
G6	5.949		2.610	2.610	4.856	4.364	7.668	12.400	-0.37
C7	5.896	5.142	2.296	2.581	4.592	4.274	7.381	-	-0.21
T8	6.096	1.507	2.307	2.619	4.846	4.228	7.608	13.890	-0.91
C9	6.263	5.624	2.172	2.262	4.528	4.043	7.606	-	-0.46
g10	5.592		4.801		4.605		7.941	nd	
a11	6.018	7.713	4.798		4.742		8.046	-	-0.14
g12	5.585		4.444		4.434		7.303	13.200	-0.26
c13	5.417	5.224	4.506		4.508		7.628	-	-0.73
a14	5.918	7.476	4.589		4.665		8.082	-	-0.39
c15	5.337	5.252	4.262		4.338		7.507	-	-0.61
c16	5.398	5.502	4.361		4.536		7.735	-	-0.68
a17	5.993	7.618	4.376		4.716		8.174	-	-0.50
u18	5.754	5.344	4.038		4.173		7.571	nd	-0.45

S4: Chemical shifts for R_P hybrid S_P hybrid and Control hybrid. ^{1}H chemical shift assignments were determined for both duplexes from 2D NOESY pathways, with the assistance of 2D TOCSY and COSY experiments. Sugar H3' and H4' chemical shifts were used to assign the ^{31}P resonances via HPCOR experiments. Sample conditions are analogous to supporting information 1.



S5: Helical properties of the final NMR BH_3 modified DNA / RNA structures. R_P hybrid value in red, S_P hybrid values in blue. Structures are consistent with previously published DNA RNA hybrids. (19, 22)



C

R_P hybrid

Base	F_S	Chi	Base - H1'	Base - H3'	Base - H4'	Estimated F_S
T2	73	-108	6.00E+07	6.90E+07	ol	
T5	34	-136	ol	1.20E+08	3.00E+07	
G3		-143	4.80E+07	5.20E+07	2.00E+07	~ 58
G4	30	-153	6.00E+07	6.00E+07	2.10E+07	
G6		-150	6.00E+07	7.10E+07	3.10E+07	~ 60

D

S_P hybrid

Base	F_S	Chi	Base - H1'	Base - H3'	Base - H4'	Estimated F_S
T2	73	-124	1.20E+07	1.60E+07	5.50E+06	
T5		-159	1.30E+07	3.70E+07	6.00E+06	< 33
G3	55	-146	1.00E+07	1.40E+07	6.00E+06	
G4		-152	1.20E+07	2.20E+07	2.80E+07	< 38
G6		-146	9.10E+06	1.50E+07	6.30E+06	~ 55

S6: A) Summary of DNA sugar pucker (fraction south / 2' endo conformation) analysis. R_P hybrid DNA dominant sugar pucker (■) and S_P hybrid dominant DNA sugar pucker (■) derived from coupling constants using graphical method developed by (13) light color shaded rectangles and diamond ranges are estimated based on ^{13}C1' chemical shifts and NOESY intensities. Sugar pucker of an unmodified DNA RNA hybrid (▲) previously published (22)
B) ^{13}C1' chemical shifts for the R_P hybrid (■) and S_P hybrid (■).
C, D) Table of base (H8 / H6) to sugar (H1', H3', and H4') intensities. For the S_P hybrid G_6 H8-H1' and H3'-H1' cross peaks have similar intensities and chi's as G_3. For G_4, H8-H3' and H8-H4' are more intense compared to the corresponding G_3 and G_6 cross peaks establishing a more favored N type pucker. This is also supported by a higher C1' chemical shift observed for G_4. (Higher C1' ppm indicative of a more dominant N type sugar.) Comparing T_5 C1' to T_2 C1' and the R_P T_2 C1' and T_8 C1' suggests the highest N population for T_5 among all thymine sugars. Additionally this is supported by the increase in T_5 H6-H3' intensity compared to S_P T_2 and R_P T_2 (compare ratio of H6-H3'/H6-H1' when looking between hybrids, R_P T_2 ~ 1.2/1, S_P T_2 ~ 1.25/1, $S_P T_5$ ~ 1.8/1).

For the R_P hybrid G_3 and G_6 have a lower C1' compared to G_4 indicating a more great N type population. With muddled trends observed in the cross peak intensities (significant amount of overlap) similar C1' chemical shifts for S_P G_3 and G_6 suggest mixed populations with a possible slightly favored N conformation.

Borano phosphate PARM-99 modification

A model borano phosphate linkage was built and stepwise minimized to the HF 6-31G* level of theory in Gaussian; the charge derivation calculations were then completed utilizing the R.E.D. automation script which uses Guassian (28) to calculate Molecular Electrostatic Potential (MEP) charges (HF 6-31G*) and AMBER RESP to convert these to restrained electrostatic potentials. The structure was reoriented in 3D space 14 times with MEP & RESP values calculated for each conformation; all values were then averaged (29a,b) Early test systems which included sugar rings on each side of the linkage indicated that that the charge distribution for the borano-phosphate linkage does not overly impact the charges outside of the phosphate group; as such the resulting RESP charges for the borano linkage were balanced to the overall parm99 nucleic acid phosphodiester group's charge. Within AMBER's ANTECHAMBER module, the BH3 atoms types were created using the calculated RESP charges and empirically determined B-P distances. ANTECHAMBER was used to calculate the B-H distances, angles, torsion angles, and force constants and generate the force-field modifications (26).

S7: Complete description of BH_3 parameters for structure derivation.

Rp borano modified DNA / RNA hybrid residual dipolar splittings for final structure

First atom			Last atom			Calc.	Exp.	Deviation	penalty	distance
C1'	DA5	1 -- H1'	DA5	1:		-1.891	-1.400	-0.491	0.241	1.090
C1'	DT	2 -- H1'	DT	2:		1.731	1.300	0.431	0.186	1.090
C1'	DG	4 -- H1'	DG	4:		-2.795	-2.900	0.105	0.011	1.090
C1'	DT	5 -- H1'	DT	5:		0.862	0.800	0.062	0.004	1.090
C1'	BGR	6 -- H1'	BGR	6:		5.468	5.500	-0.032	0.001	1.090
C1'	DC	7 -- H1'	DC	7:		4.512	4.200	0.312	0.097	1.090
C1'	DT	8 -- H1'	DT	8:		5.054	5.200	-0.146	0.021	1.090
C1'	DC3	9 -- H1'	DC3	9:		0.366	0.100	0.266	0.071	1.090
C1'	RG5	10 -- H1'	RG5	10:		-5.867	-6.300	0.433	0.188	1.090
C1'	RA	11 -- H1'	RA	11:		-11.324	-11.800	0.476	0.227	1.090
C1'	RG	12 -- H1'	RG	12:		-10.466	-10.400	-0.066	0.004	1.090
C1'	RC	13 -- H1'	RC	13:		-4.539	-4.500	-0.039	0.002	1.090
C1'	RA	14 -- H1'	RA	14:		1.123	1.500	-0.377	0.142	1.090
C1'	RC	15 -- H1'	RC	15:		4.270	4.100	0.170	0.029	1.090
C1'	RC	16 -- H1'	RC	16:		6.413	6.400	0.013	0.000	1.090
C1'	RA	17 -- H1'	RA	17:		4.084	4.200	-0.116	0.013	1.090
C1'	RU3	18 -- H1'	RU3	18:		1.484	1.000	0.484	0.234	1.090
C8	DA5	1 -- H8	DA5	1:		5.216	5.200	0.016	0.000	1.090
C6	DT	2 -- H6	DT	2:		2.054	2.400	-0.346	0.119	1.090
C8	DG	3 -- H8	DG	3:		2.676	1.800	0.876	0.767	1.090
C8	DG	4 -- H8	DG	4:		3.468	3.300	0.168	0.028	1.090
C6	DT	5 -- H6	DT	5:		9.551	9.900	-0.349	0.122	1.090
C8	BGR	6 -- H8	BGR	6:		10.362	9.800	0.562	0.316	1.090
C6	DC	7 -- H6	DC	7:		5.661	6.000	-0.339	0.115	1.090
C6	DT	8 -- H6	DT	8:		1.717	1.900	-0.183	0.033	1.090
C6	DC3	9 -- H6	DC3	9:		4.785	5.500	-0.715	0.511	1.090
C8	RG5	10 -- H8	RG5	10:		2.256	2.400	-0.144	0.021	1.090
C8	RA	11 -- H8	RA	11:		4.079	5.200	-1.121	1.257	1.090
C8	RG	12 -- H8	RG	12:		3.859	2.700	1.159	1.343	1.090
C6	RC	13 -- H6	RC	13:		9.374	9.500	-0.126	0.016	1.090
C8	RA	14 -- H8	RA	14:		6.670	6.500	0.170	0.029	1.090
C6	RC	15 -- H6	RC	15:		6.149	5.900	0.249	0.062	1.090
C6	RC	16 -- H6	RC	16:		4.328	3.800	0.528	0.279	1.090
C8	RA	17 -- H8	RA	17:		3.060	3.100	-0.040	0.002	1.090
C6	RU3	18 -- H6	RU3	18:		2.906	3.400	-0.494	0.244	1.090
C2	DA5	1 -- H2	DA5	1:		6.504	6.200	0.304	0.093	1.090
C2	RA	11 -- H2	RA	11:		1.681	1.400	0.281	0.079	1.090
C2	RA	14 -- H2	RA	14:		7.739	7.500	0.239	0.057	1.090
C2	RA	17 -- H2	RA	17:		4.102	3.800	0.302	0.091	1.090
C5	DC	7 -- H5	DC	7:		9.202	7.800	1.402	0.161	1.090
C5	RC	15 -- H5	RC	15:		9.298	10.700	-1.402	0.162	1.090
C5	RC	16 -- H5	RC	16:		9.519	10.800	-1.281	0.079	1.090

Total align constraint: 7.46

S8A

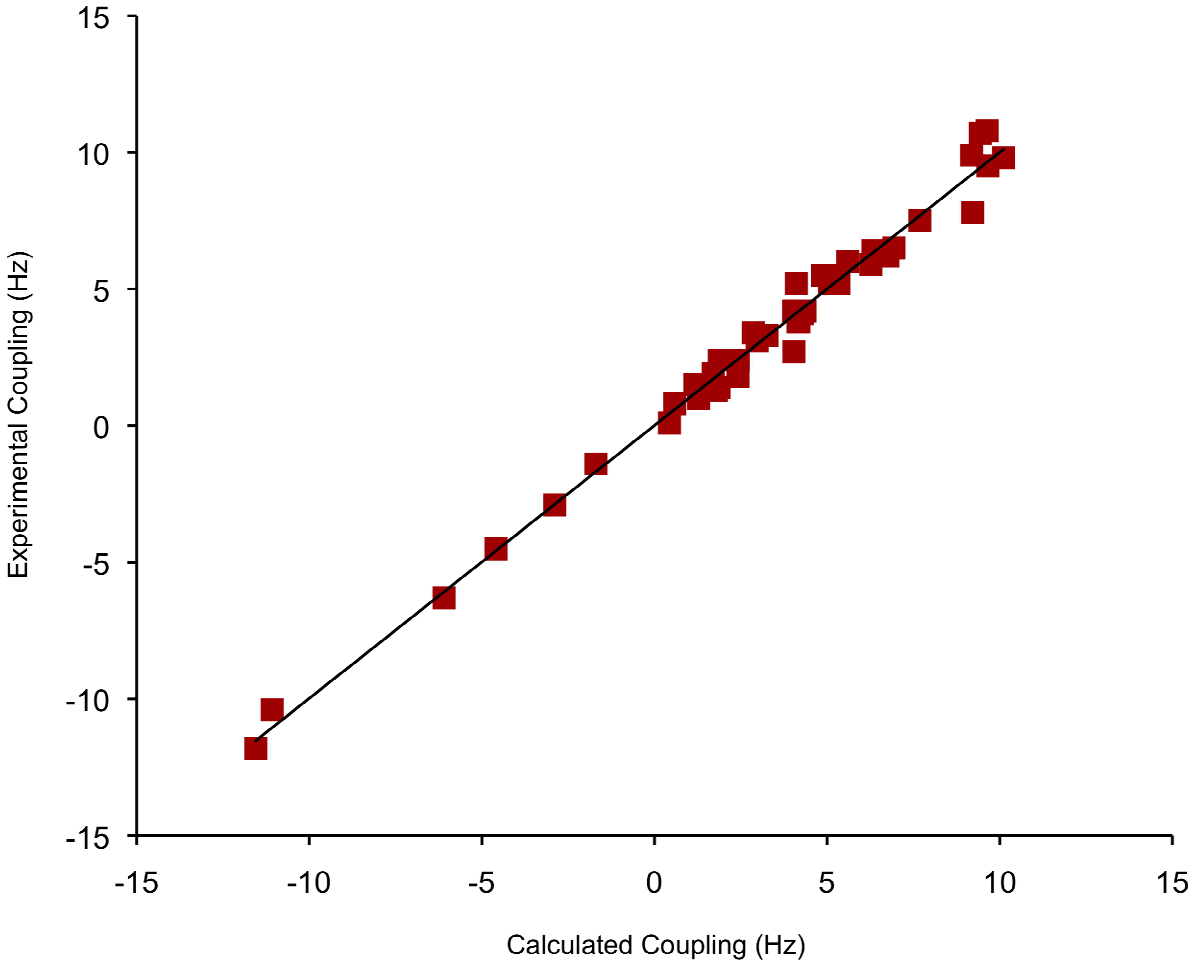
Sp borano modified DNA / RNA hybrid residual dipolar splittings for final structure

First atom			Last atom			Calc.	Exp.	Deviation	penalty	distance
C1'	DA5	1 -- H1'	DA5	1:		-0.308	-0.700	0.392	0.154	1.090
C1'	DT	2 -- H1'	DT	2:		7.435	7.400	0.035	0.001	1.090
C1'	DG	3 -- H1'	DG	3:		-0.788	-0.900	0.112	0.012	1.090
C1'	DG	4 -- H1'	DG	4:		-5.398	-5.500	0.102	0.010	1.090
C1'	DT	5 -- H1'	DT	5:		0.035	-0.100	0.135	0.018	1.090
C1'	BGS	6 -- H1'	BGS	6:		6.441	6.200	0.241	0.058	1.090
C1'	DC	7 -- H1'	DC	7:		6.709	6.400	0.309	0.095	1.090
C1'	DT	8 -- H1'	DT	8:		11.012	10.800	0.212	0.045	1.090
C1'	DC3	9 -- H1'	DC3	9:		4.602	4.700	-0.098	0.010	1.090
C1'	RG5	10 -- H1'	RG5	10:		-11.670	-11.900	0.230	0.053	1.090
C1'	RA	11 -- H1'	RA	11:		-16.108	-16.000	-0.108	0.012	1.090
C1'	RG	12 -- H1'	RG	12:		-15.797	-16.000	0.203	0.041	1.090
C1'	RC	13 -- H1'	RC	13:		-9.164	-9.100	-0.064	0.004	1.090
C1'	RA	14 -- H1'	RA	14:		-1.387	-1.200	-0.187	0.035	1.090
C1'	RC	15 -- H1'	RC	15:		3.513	3.500	0.013	0.000	1.090
C1'	RC	16 -- H1'	RC	16:		5.753	5.800	-0.047	0.002	1.090
C1'	RA	17 -- H1'	RA	17:		3.135	3.400	-0.265	0.070	1.090
C1'	RU3	18 -- H1'	RU3	18:		1.157	1.200	-0.043	0.002	1.090
C8	DA5	1 -- H8	DA5	1:		9.124	9.100	0.024	0.001	1.090
C6	DT	2 -- H6	DT	2:		2.717	2.600	0.117	0.014	1.090
C8	DG	3 -- H8	DG	3:		5.188	5.700	-0.512	0.262	1.090
C8	DG	4 -- H8	DG	4:		5.990	5.500	0.490	0.241	1.090
C6	DT	5 -- H6	DT	5:		14.252	15.400	-1.148	1.317	1.090
C8	BGS	6 -- H8	BGS	6:		15.920	15.600	0.320	0.102	1.090
C6	DC	7 -- H6	DC	7:		11.558	11.700	-0.142	0.020	1.090
C6	DT	8 -- H6	DT	8:		6.057	6.200	-0.143	0.020	1.090
C6	DC3	9 -- H6	DC3	9:		0.487	0.600	-0.113	0.013	1.090
C8	RG5	10 -- H8	RG5	10:		5.012	5.600	-0.588	0.345	1.090
C8	RA	11 -- H8	RA	11:		2.478	2.000	0.478	0.228	1.090
C8	RG	12 -- H8	RG	12:		9.806	9.800	0.006	0.000	1.090
C6	RC	13 -- H6	RC	13:		15.457	15.400	0.057	0.003	1.090
C8	RA	14 -- H8	RA	14:		14.693	14.200	0.493	0.243	1.090
C6	RC	15 -- H6	RC	15:		9.363	9.100	0.263	0.069	1.090
C6	RC	16 -- H6	RC	16:		6.160	6.700	-0.540	0.291	1.090
C8	RA	17 -- H8	RA	17:		4.243	4.100	0.143	0.021	1.090
C6	RU3	18 -- H6	RU3	18:		5.258	5.400	-0.142	0.020	1.090
C2	DA5	1 -- H2	DA5	1:		9.309	9.000	0.309	0.096	1.090
C2	RA	11 -- H2	RA	11:		3.370	3.400	-0.030	0.001	1.090
C2	RA	14 -- H2	RA	14:		15.311	15.900	-0.589	0.347	1.090
C2	RA	17 -- H2	RA	17:		6.138	6.000	0.138	0.019	1.090
C5	DC	7 -- H5	DC	7:		11.052	10.500	0.552	0.305	1.090
C5	DC3	9 -- H5	DC3	9:		9.959	10.000	-0.041	0.002	1.090
C5	RC	13 -- H5	RC	13:		0.520	0.100	0.420	0.176	1.090
C5	RC	15 -- H5	RC	15:		15.408	15.000	0.408	0.167	1.090
C5	RC	16 -- H5	RC	16:		15.019	15.600	-0.581	0.338	1.090

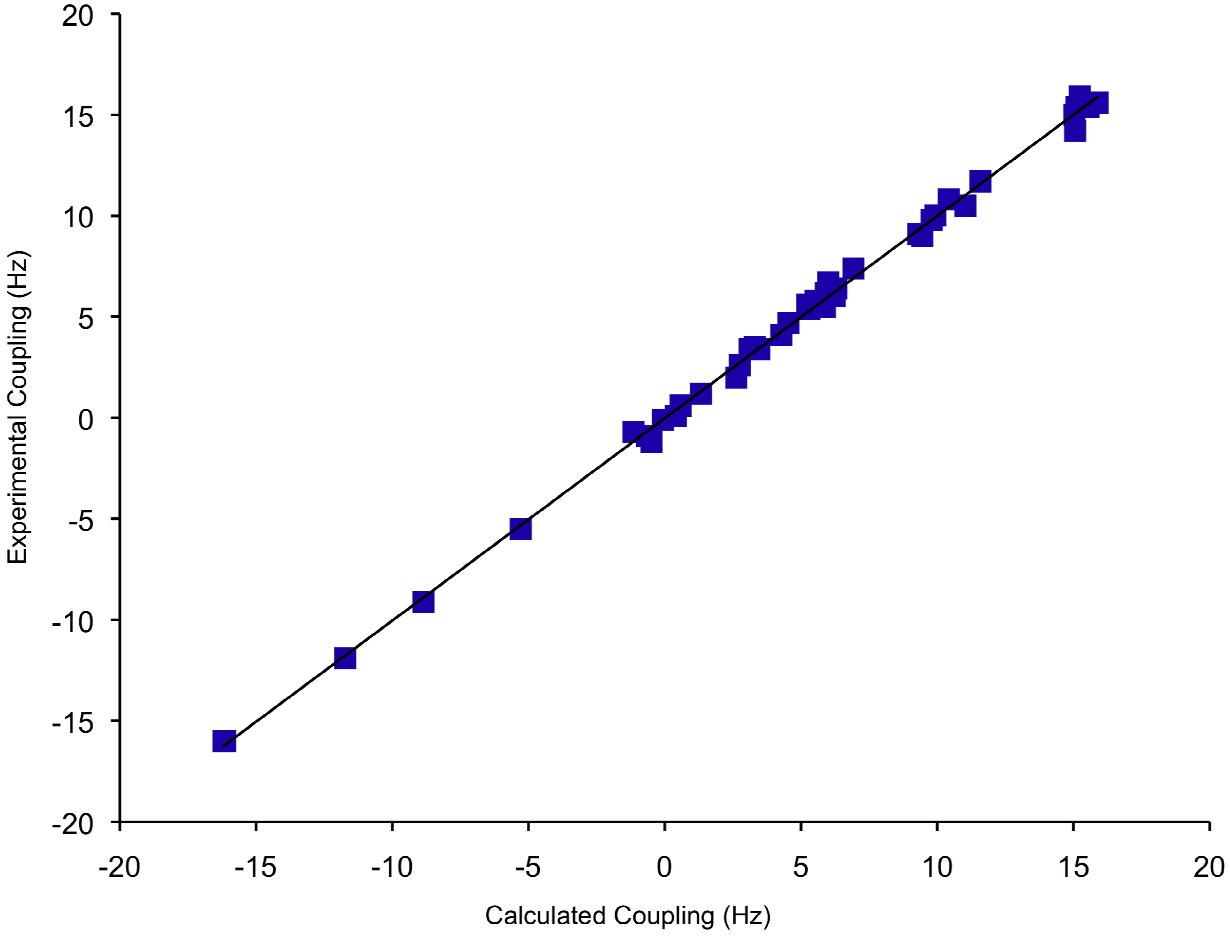
Total align constraint: 5.28

S8B

S8 A, B: Table of RDC parameters for both modified hybrids. Calculated values (Calc.) were derived from the final structures using Amber 9.0. Experimental values (Exp.) are derived from the difference between measured couplings in the presence and absences of pf1 bacterial phage. Penalties were calculated by Amber 9.0 using a dwt of 1.0.


15
10
5
0
-5
-10
-15
-15
-10
-5
0
5
10
15
Experimental Coupling (Hz)
Calculated Coupling (Hz)

S8 C



S8 D

S8 C,D: Plot of back calculated RDC values using REDCAT vs. experimentally measured values. R^2 values for R_P hybrid 0.987 (C), and S_P hybrid 0.998 (D).