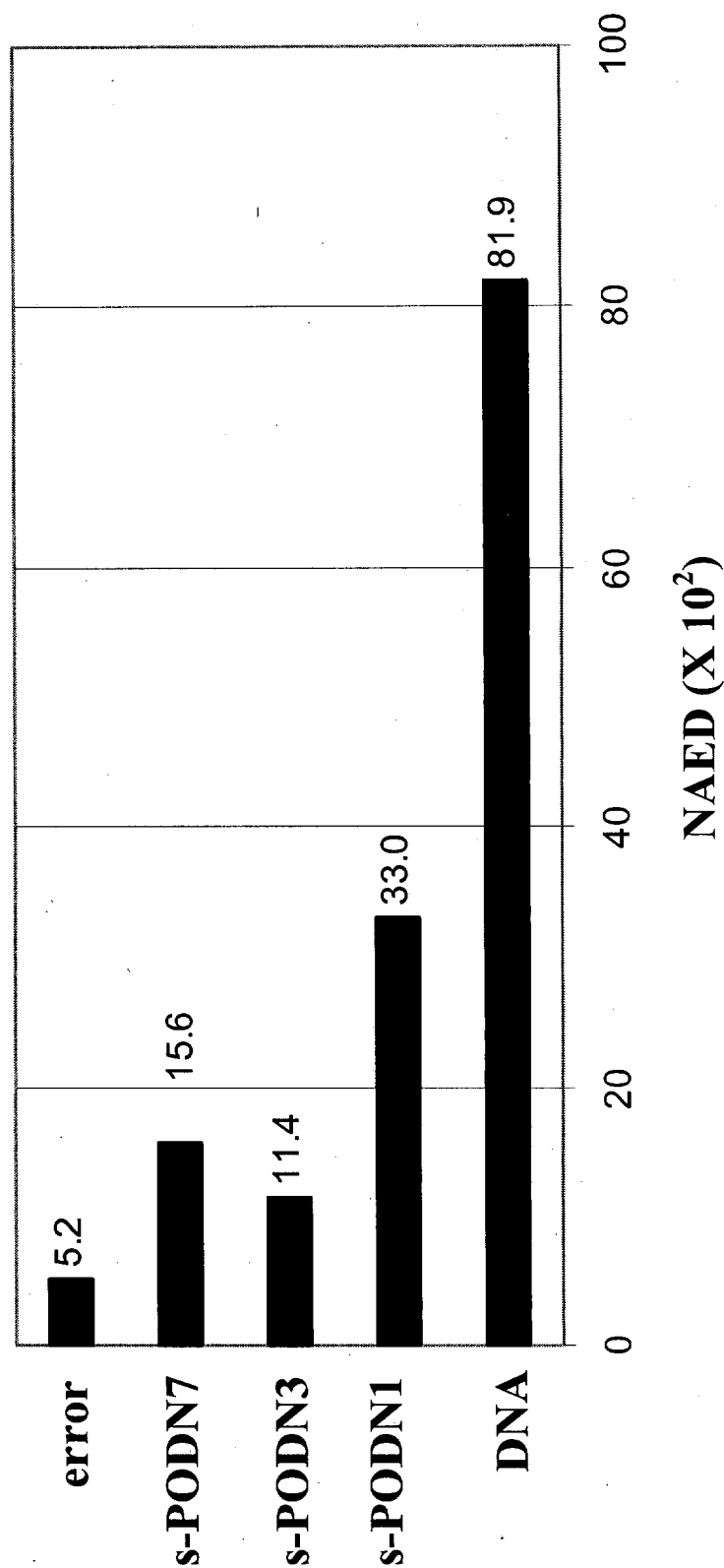
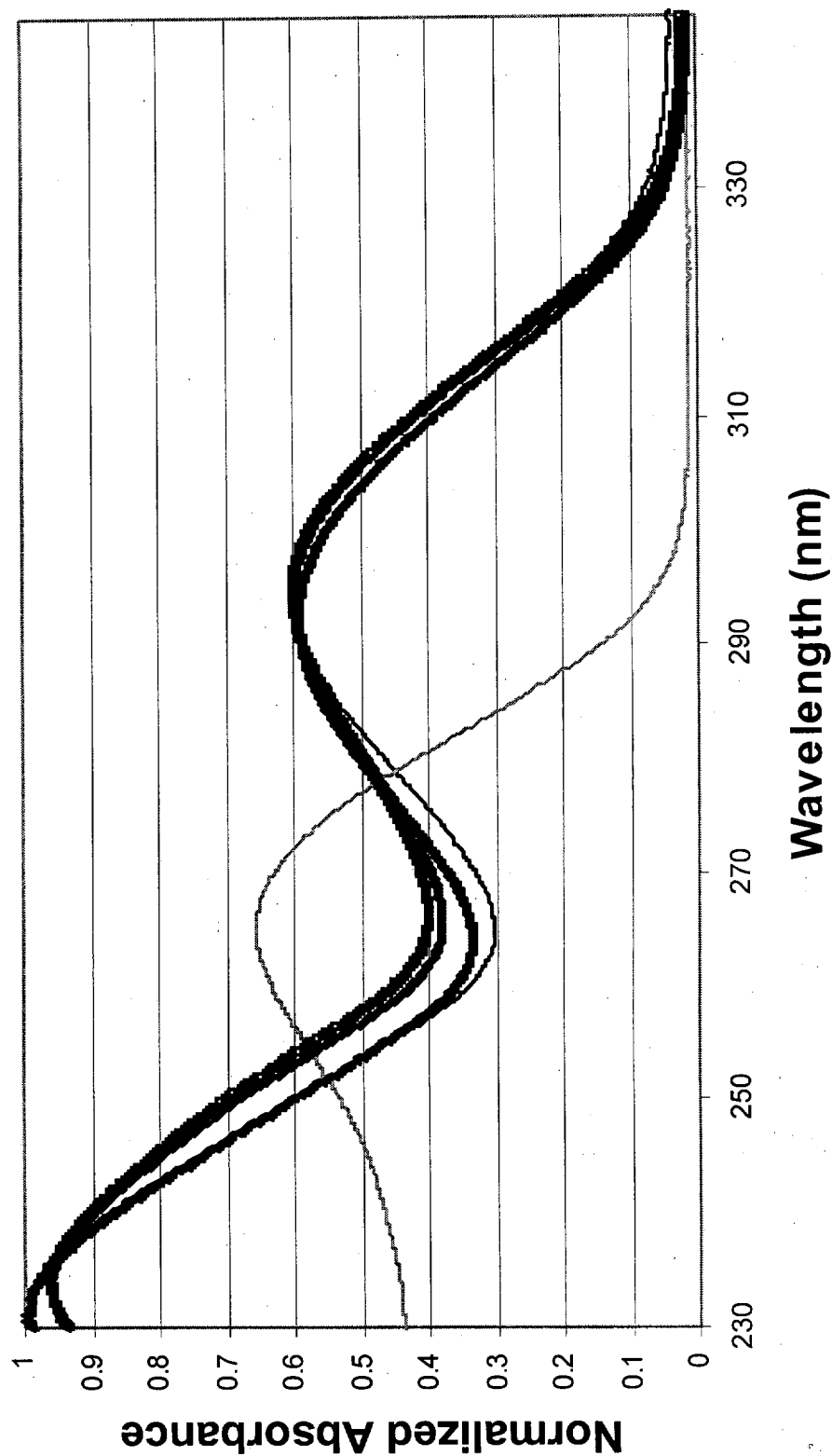


Supporting Material Figure 1: The Normalized Absolute Ellipticity Differences (NAEDs) at 20 °C between the single strand PODN and other unpropynylated/propynylated single strands. For example, the bar with a value of 81.9 and labeled DNA quantifies the differences between the CD spectra of 5'-dCCCCUUU-3' and 5'-dC¹⁸C¹⁹U¹⁹C¹⁹C¹⁹U¹⁹U¹⁹-3'.



Supporting Material Figure 2: The absorbance spectra of single strands (~0.01 mM) at 90 °C: 5'-dCCCUCUUU-3' (grey), 5'-dC^pC^pU^pC^pU^pU^p-3' (black), 5'-dC^pC^pU^pC^pC^pU^pU^p-3' (Δ), 5'-dC^pC^pUC^pC^pU^pU^p-3' (□), and 5'-dC^pC^pU^pC^pC^pU^pU^p-3' (◇).



Supporting Table 1: Thermodynamic Parameters of DNA:RNA and PODN:RNA Hybrid Duplexes Containing Various 5' and 3' Dangling Ends ^a									
	reference symbol	1/T _m Plots					Curve-Fit Parameters		
		-ΔG ₃₇ (kcal/mol)	-ΔH ^o (kcal/mol)	-ΔS ^o (kcal/mol)	T _m (°C) ^b	-ΔG ₃₇ (kcal/mol)	-ΔH ^o (kcal/mol)	-ΔS ^o (kcal/mol)	T _m (°C) ^b
d(5'CCUCCUU3')									
r(5'AAGGAGG3')	7-mer	-7.6 ± 0.1	-53.3 ± 2.0	-147.3 ± 6.4	43.3	-7.7 ± 0.2	-60.0 ± 4.8	-168.7 ± 15.5	43.1
r(5'AAGGAGGA3')	8-mer	-8.9 ± 0.1	-61.2 ± 1.8	-168.6 ± 5.7	49.3	-9.1 ± 0.2	-68.4 ± 3.9	-191.2 ± 11.8	49.3
r(5'AAAGGAGGA3')	9-mer	-9.4 ± 0.2	-62.0 ± 2.4	-169.7 ± 7.1	52.0	-9.6 ± 0.3	-68.7 ± 2.9	-190.5 ± 8.3	51.8
d(5'C ^p C ^p U ^p C ^p C ^p U ^p U ^p 3')									
r(5'AAGGAGG3')	7-mer	-15.3 ± 0.4	-80.9 ± 4.0	-211.6 ± 11.3	74.5	-14.6 ± 0.1	-74.6 ± 1.9	-193.5 ± 5.7	74.7
r(5'AAGGAGGA3')	8-mer	-16.2 ± 0.6	-79.0 ± 5.2	-200.4 ± 14.7	80.2	-16.0 ± 0.5	-77.6 ± 4.1	-198.5 ± 11.6	80.1
r(5'AAAGGAGGA3')	9-mer	-18.2 ± 0.3	-89.0 ± 3.1	-228.5 ± 10.8	83.6	-17.9 ± 0.3	-86.4 ± 5.3	-220.8 ± 8.3	84.1
r(5'AAGGAGG3')									
d(5'CCCUCUUU3')	DNA-5'C	-8.3 ± 0.1	-56.1 ± 3.0	-154.2 ± 9.6	46.9	-8.4 ± 0.2	-60.4 ± 4.9	-167.5 ± 15.3	47.1
d(5'CCUCCUU3')	DNA-3'C	-7.8 ± 0.1	-51.4 ± 2.1	-140.7 ± 6.8	44.8	-7.8 ± 0.1	-53.8 ± 4.3	-148.3 ± 13.8	44.5
d(5'C ^p C ^p C ^p U ^p C ^p C ^p U ^p U ^p 3')	PODN-5'C ^p	-15.6 ± 0.4	-79.6 ± 3.4	-206.2 ± 9.9	76.9	-16.0 ± 1.0	-82.4 ± 9.3	-214.2 ± 26.6	75.0
d(5'C ^p C ^p U ^p C ^p C ^p U ^p U ^p 3')	PODN-3'C ^p	-16.0 ± 0.4	-88.0 ± 3.6	-232.3 ± 10.5	74.4	-14.3 ± 0.5	-71.6 ± 4.4	-184.5 ± 12.9	77.0

^aMeasured in 1.0 M NaCl, 0.05 mM Na₂EDTA, 20 mM sodium cacodylate, pH 7. Values in parentheses indicate that the ΔH^o values determined from T_m⁻¹ vs ln(C_T/4) plots and from curve fitting differ by more than 15%, thus indicating non-two-state melting. Errors are based on the standard deviations of the thermodynamic parameters and were calculated as described in (12). Significant figures are given beyond error estimates to allow accurate calculation of T_m and other parameters. ^bT_m for a total strand concentration of 1 × 10⁻⁴ M.

Supporting Table 2: Thermodynamic Parameters of the DNA s-DNAs, PODN, and s-PODNs when Bound to, 5'-UAAAGGAGGAG-3'.^a

	reference symbol	1/Tm Plots			Curve-Fit Parameters				
		$-\Delta G_{37}^{\circ}$ (kcal/mol)	$-\Delta H^{\circ}$ (kcal/mol)	$-\Delta S^{\circ}$ (eu)	T_m (°C)	$-\Delta G_{37}^{\circ}$ (kcal/mol)	$-\Delta H^{\circ}$ (kcal/mol)	$-\Delta S^{\circ}$ (eu)	T_m (°C)
d(5'CCUCCUU3')	DNA	-9.6 ± 0.1	-62.80 ± 1.7	-171.4 ± 4.9	53.0	-9.85 ± 0.2	-69.0 ± 2.1	-190.7 ± 6.5	52.7
d(5'C ^p CUCCUU3')	s-DNA1	-9.6 ± 0.1	-65.62 ± 2.7	-180.66 ± 8.4	52.2	-9.79 ± 0.1	-70.5 ± 3.7	-195.7 ± 11.7	52.0
d(5'CC ^p UCCUU3')	s-DNA2	-10.0 ± 0.1	-61.0 ± 2.0	-164.4 ± 6.0	55.7	-10.5 ± 0.2	-70.0 ± 4.0	-191.8 ± 12.43	55.6
d(5'CCU ^p CCUU3')	s-DNA3	-10.1 ± 0.1	-64.0 ± 1.5	-173.7 ± 4.68	55.2	-10.2 ± 0.2	-66.6 ± 5.6	-182.0 ± 17.3	55.0
d(5'CCUC ^p CUU3')	s-DNA4	-10.6 ± 0.2	-68.2 ± 3.7	-185.7 ± 11.4	56.7	-10.7 ± 0.3	-70.1 ± 3.5	-191.4 ± 10.4	56.7
d(5'CCUCC ^p UU3')	s-DNA5	-10.2 ± 0.1	-61.6 ± 2.3	-165.7 ± 7.1	56.6	-10.7 ± 0.3	-70.4 ± 3.4	-192.5 ± 10.2	56.5
d(5'CCUCCUU ^p 3')	s-DNA6	-9.8 ± 0.1	-61.2 ± 1.8	-165.7 ± 5.5	54.6	-10.0 ± 0.23	-65.2 ± 4.8	-177.7 ± 14.7	54.7
d(5'CCUCCUU ^p 3')	s-DNA7	-9.6 ± 0.1	-62.0 ± 2.0	-169.6 ± 6.2	52.0	-9.7 ± 0.1	-69.1 ± 3.4	-191.5 ± 10.9	51.8
d(5'CCUCCUU3')	DNA 6-mer	-6.7 ± 0.1	-52.8 ± 1.9	-148.5 ± 6.3	38.1	-6.7 ± 0.1	-57.7 ± 4.8	-164.4 ± 15.3	38.2
d(5'C ^p U ^p C ^p C ^p U ^p 3')	PODN 6-mer	-13.8 ± 0.3	-75.8 ± 2.8	-199.9 ± 8.1	70.1	-13.3 ± 0.6	-70.5 ± 6.4	-184.4 ± 18.8	70.0
d(5'C ^p C ^p U ^p C ^p C ^p U ^p 3')	PODN	-18.4 ± 0.6	-89.3 ± 5.4	-228.7 ± 15.5	84.3	-18.2 ± 1.1	-88.3 ± 9.9	-226.1 ± 28.6	84.1
d(5'CC ^p U ^p C ^p C ^p U ^p 3')	s-PODN1	$-15.2 \pm .3$	-71.1 ± 2.9	-180.2 ± 8.4	79.9	-15.4 ± 0.4	-73.0 ± 3.0	-185.6 ± 8.3	79.9
d(5'C ^p CU ^p C ^p C ^p U ^p 3')	s-PODN2	-14.8 ± 0.2	-70.8 ± 2.0	-180.6 ± 4.9	78.2	-14.9 ± 0.4	-71.4 ± 4.1	-182.3 ± 10.3	78.2
d(5'C ^p C ^p UC ^p C ^p U ^p 3')	s-PODN3	-14.4 ± 0.2	-67.4 ± 3.9	-171.0 ± 11.0	77.8	-14.7 ± 0.5	-69.9 ± 4.5	-178.2 ± 12.9	77.8
d(5'C ^p C ^p U ^p CC ^p U ^p 3')	s-PODN4	-14.9 ± 0.2	-74.3 ± 1.8	-191.5 ± 5.1	76.5	-15.0 ± 0.5	-74.9 ± 5.1	-193.2 ± 14.7	76.4
d(5'C ^p C ^p U ^p C ^p CU ^p 3')	s-PODN5	-14.7 ± 0.2	-73.8 ± 1.4	-190.7 ± 4.2	75.3	-15.7 ± 0.4	-83.1 ± 3.6	-217.4 ± 10.3	75.4
d(5'C ^p C ^p U ^p C ^p C ^p UU ^p 3')	s-PODN6	-16.3 ± 0.3	-83.7 ± 2.4	-217.4 ± 6.9	78.0	$-15.4 \pm 0.1.1$	-76.2 ± 9.1	-195.9 ± 25.9	78.1
d(5'C ^p C ^p U ^p C ^p C ^p U ^p 3')	s-PODN7	-16.4 ± 0.3	-79.7 ± 3.0	-204.1 ± 5.2	80.9	-15.7 ± 0.8	-73.6 ± 5.8	-186.9 ± 16.3	80.9

^aBases at which systematic substitutions and deletions occur are in bold. Errors are based on the standard deviations of the thermodynamic parameters and were calculated as described in (12). Significant figures are given beyond error estimates to allow accurate calculation of T_m .

Supporting Table 3: Thermodynamic Parameters of m-DNA Strands Bound to 5'-UAAAGGAGGAG-3'.^a

	1/T _m Plots					Curve-Fit Parameters			
	reference symbol	-ΔG ₃₇ ^o (kcal/mol)	-ΔH ^o (kcal/mol)	-ΔS ^o (eu)	T _m (°C)	-ΔG ₃₇ ^o (kcal/mol)	-ΔH ^o (kcal/mol)	-ΔS ^o (eu)	T _m (°C)
d(5'CCUCCU ^P U ^P 3')	m-DNA6,7	-10.4 ± 0.1	-64.6 ± 1.7	-174.6 ± 5.3	56.9	-10.8 ± 0.3	-70.9 ± 3.5	-193.8 ± 10.3	56.8
d(5'C ^P C ^P UCCUU3')	m-DNA1,2	-11.1 ± 0.2	-68.3 ± 3.1	-184.4 ± 9.4	59.3	-11.6 ± 0.4	-74.6 ± 6.1	-203.2 ± 12.3	59.4
d(5'CC ^P UCC ^P UU3')	m-DNA2,5	-11.4 ± 0.2	-67.3 ± 2.3	-180.4 ± 6.9	61.0	-11.2 ± 0.3	-65.06 ± 3.9	-173.6 ± 11.7	61.1
d(5'CCUC ^P C ^P UU3')	m-DNA4,5	-11.8 ± 0.3	-77.2 ± 4.7	-211.1 ± 14.2	59.6	-11.6 ± 0.3	-75.5 ± 3.5	-205.9 ± 10.4	59.5
d(5'C ^P C ^P UC ^P C ^P UU3')	m-DNA1,2,4,5	-12.6 ± 0.1	-71.6 ± 1.7	-190.2 ± 5.1	65.8	-13.5 ± 0.4	-82.7 ± 5.2	-223.2 ± 15.6	65.5
d(5'C ^P C ^P U ^P C ^P C ^P UU3')	m-DNA1,2,3,4,5	-13.4 ± 0.3	-70.1 ± 3.0	-183.0 ± 8.7	70.6	-13.7 ± 0.2	-74.7 ± 7.7	-196.7 ± 12.8	70.0

^aBases at which C5-1-propynyl substitutions occur are in bold. Errors are based on the standard deviations of the thermodynamic parameters and were calculated as described in (12). Significant figures are given beyond error estimates to allow accurate calculation of T_m.

Supporting Table 4: Modeling the Stability of Y^p-containing DNA:RNA Hybrid Duplexes. The RNA strand is 3'-GAGGAGGAAAU-5'

	ΔG° (Y ^p -containing duplex) (kcal/mol)	$\Delta \Delta G^\circ_i$ (kcal/mol)	Internal Y ^p bonus (x)	5' Dangling end bonus (y)	cooperative bonus (z)	Predicted $\Delta \Delta G^\circ_i$ (kcal/mol)	$\Delta \Delta G^{\circ b}$ (kcal/mol)
Antisense							
d(5C ^a CUCCUU3')	-9.6	0.00	0	0	0	0.17	0.170
d(5C ^a UCCUU3')	-10	-0.40	1	0	0	-0.85	-0.450
d(5CCU ^p CCUU3')	-10.1	-0.50	1	0	0	-0.85	-0.350
d(5CCU ^c CUU3')	-10.6	-1.00	1	0	0	-0.85	0.150
d(5CCUCC ^p UU3')	-10.2	-0.60	1	0	0	-0.85	-0.250
d(5CCUCCU ^p U3')	-9.8	-0.20	1	0	0	-0.85	-0.650
d(5CCUCCUU ^p 3')	-9.6	0.00	0	0	0	0.17	0.170
d(5C ^a U ^c C ^a C ^a U ^p 3')	-13.8	-7.10	4	1	1	-6.60	0.500
d(5CC ^p U ^c C ^a C ^a U ^p 3')	-15.2	-5.60	5	1	0	-5.98	-0.380
d(5C ^a C ^p U ^c C ^a U ^p 3')	-14.8	-5.20	4	1	0	-4.95	0.246
d(5C ^a C ^p U ^c C ^a U ^p 3')	-14.9	-5.30	4	1	0	-4.95	0.350
d(5C ^a C ^p U ^c C ^a U ^p 3')	-14.4	-4.80	4	1	0	-4.95	-0.150
d(5C ^a C ^p U ^c C ^a U ^p 3')	-14.7	-5.10	4	1	0	-4.95	0.150
d(5C ^a C ^p U ^c C ^a U ^p 3')	-16.3	-6.70	4	1	1	-6.60	0.100
d(5C ^a C ^p U ^c C ^a U ^p 3')	-16.4	-6.80	5	0	1	-6.60	0.200
d(5CCUCCU ^p U ^p 3')	-10.4	-0.80	1	0	0	-0.85	-0.050
d(5C ^a C ^p UCCUU3')	-11.1	-1.50	1	0	0	-0.85	0.650
d(5CC ^p UCC ^p UU3')	-11.4	-1.80	2	0	0	-1.88	-0.080
d(5CCUCC ^p C ^a UU3')	-11.8	-2.20	2	0	0	-1.88	0.320
d(5C ^a C ^p U ^c C ^a U ^p 3')	-12.6	-3.00	3	0	0	-2.90	0.100
d(5C ^a C ^p U ^c C ^a U ^p 3')	-13.4	-3.80	4	0	0	-3.92	-0.120
CCUCCUU	-9.6	0.00	0	0	0	0.17	0.170
Fitted Value (kcal/mol)			(-0.99)	(-1.17)	(-1.94)		

^aThe stability of each duplex predicted by the parameters determined by linear regression according to eq 2. $\Delta \Delta G^\circ_i$ is the free energy increment due to addition of propynyl groups. The fitted parameters are listed in the appropriate column at the bottom of the Table.

^b $\Delta \Delta \Delta G^\circ_i$ is the difference between the experimental $\Delta \Delta G^\circ_i$ and that predicted by the long-range cooperative model.

Supporting Table 5: Thermodynamic Parameters of DNA, PODN, and s-PODNs Bound to r(5'JAAAGGA/GAG3')^a

Antisense Strand	reference symbol	1/T _m Plots			Curve-Fit Parameters			
		-ΔG° ₃₇ (kcal/mol)	-ΔH° (kcal/mol)	-ΔS° (eu)	T _m (°C)	-ΔG° ₃₇ (kcal/mol)	-ΔH° (kcal/mol)	-ΔS° (eu)
d(5'C ^p C ^p U ^p C ^p C ^p U ^p U ^p 3')	PODN	-14.5 ± 0.7	-75.5 ± 6.2	-196.7 ± 8.0	73.8	-14.6 ± 0.5	-75.8 ± 4.1	-197.4 ± 11.7
d(5'CCUCCUU3')	DNA	(-7.9 ± 0.1)	(-62.7 ± 3.7)	(-176.6 ± 11.0)	44.3	(-7.9 ± 0.2)	(-51.5 ± 5.9)	(-140.7 ± 8.6)
d(5'C ^p C ^p U ^p CC ^p U ^p U ^p 3')	s-PODN4	-13.9 ± 0.4	-81.5 ± 3.7	-217.9 ± 10.9	67.9	-13.7 ± 0.6	-79.2 ± 6.4	-211.2 ± 18.6
d(5'C ^p C ^p U ^p C ^p CU ^p U ^p 3')	s-PODN5	-13.5 ± 0.3	-77.2 ± 3.2	-205.5 ± 9.5	67.8	-13.5 ± 0.6	-78.0 ± 6.3	-207.8 ± 18.6

^aPositions of C5-(1-propyne) deletions within the PODN strand are in bold. Values in parentheses indicate that the ΔH° values determined from T_m⁻¹ vs. ln(C_{7/4}) plots and from curve fitting differ by more than 15%, thus indicating non-two-state melting. Errors are based on the standard deviations of the thermodynamic parameters and were calculated as described in (12). Significant figures are given beyond error estimates to allow accurate calculation of T_m and other parameters.