Additional File 7:

rUN Blocked Primer

	Template Sequence A	C	G	T
A	11.4	2.5	12.2	0
C	6.4	10.4	0	9.0
G	13.8	0	4.6	3.0
T	0	11.1	11.9	2.9

rCN Blocked Primer

	Template Sequence A	C	G	T
A	5.6	1.8	10.2	0
C	8.8	9.6	0	8.6
G	9.8	0	3.2	0.3
T	0	2.1	0.2	0

rAN Blocked Primer

	Template Sequence A	C	G	T
A	3.1	1.0	6.1	0
C	9.3	10.2	0	8.3
G	13.2	0	2.5	5.9
T	0	5.0	7.1	4.0

rGN Blocked Primer

	Template Sequence A	C	G	T
A	6.2	3.0	11.4	0
C	9.5	7.3	0	4.7
G	13.1	0	6.0	3.2
T	0	4.5	11.5	0.3

Figure S5. Mismatch discrimination using rhPCR with the mismatch positioned at the "+1" position relative to the RNA base.

Sixteen synthetic oligonucleotide targets were employed where the base complementary to the single RNA residue in the blocked-cleavable primers was fixed (A, C, G, or T) and the base paired opposite position "+1" immediately 5′-to the RNA base in the primer was varied (A, C, G, or T). Likewise a set of 16 "rDDDDx" blocked-cleavable primers was employed where the RNA base was fixed (rA, rC, rG, or rU) and the base at the "+1" position was varied (A, C, G, or T). The target sequence and primers were otherwise the same as in Figure 2. Assay conditions and calculations of ΔCq values were the same as in Figure 7 in the manuscript. All reactions were run in triplicate.