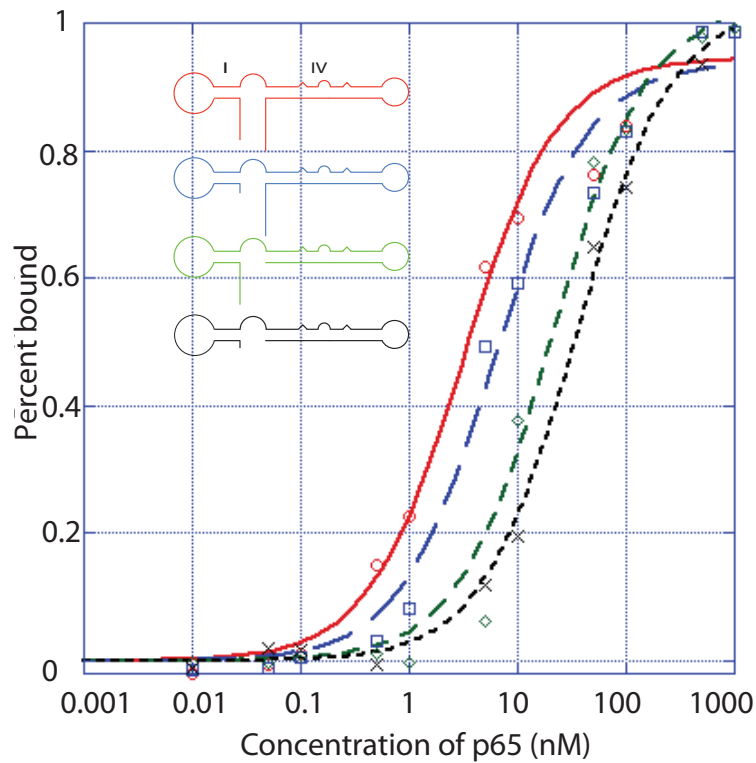
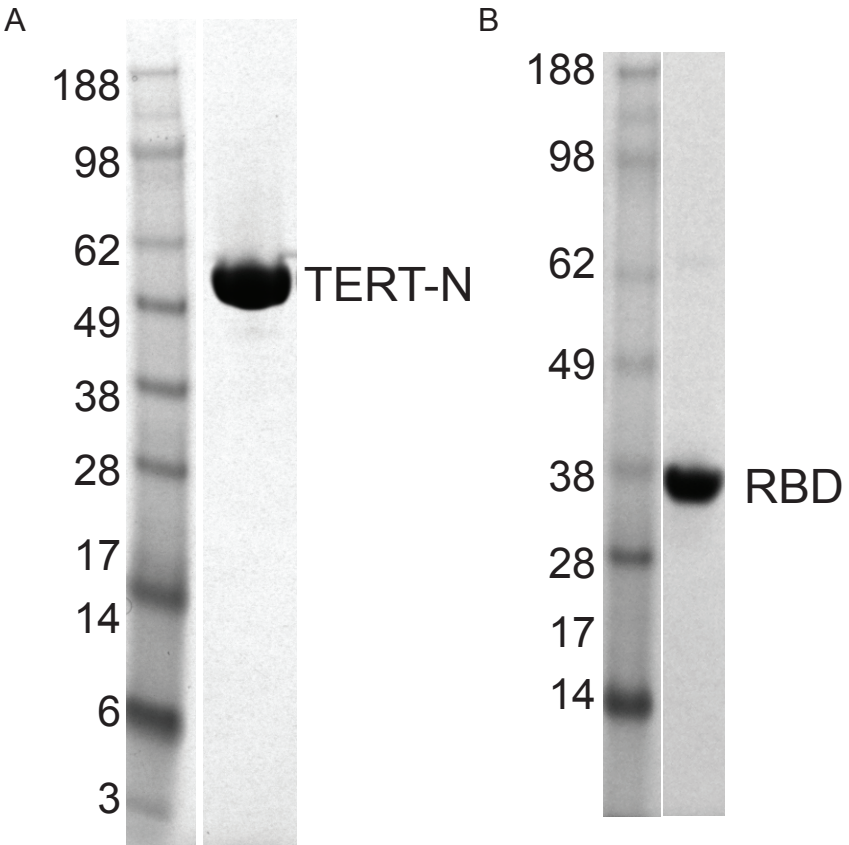


Supplementary figure 1. The affinity of p65 for cpRNA(31-25) is relatively tight but not highly specific. A. An electrophoretic mobility shift assay of < 0.5 nM cpRNA and the indicated concentrations of p65. B. The quantitation of panel A fit with a theoretical binding curve, K_d (apparent) = 38 nM. C. EMSA of p65 with various structured and unstructured RNAs. For each RNA, 0, 100 nM or 1000 nM p65 was added. The other RNAs tested were a 96-nucleotide hairpin (HP) containing the Ku arm of yeast TLC1 (gift of J. Pfungsten, U. of Colorado), a 74-nucleotide structured RNA from *E. coli* 23S rRNA (gift of D. McKay, U. of Colorado) and a synthesized oligoribonucleotide consisting of 10 uridines.



Supplementary Figure 2. The single-stranded regions of TER contribute modestly to p65 binding affinity. Analysis of electrophoretic mobility shift assays performed on constructs of TER containing stem I and IV as in O'Connor and Collins, 2006 (red). p65 has lower affinity for the RNA construct missing the 5' single-stranded region (blue), and even lower affinity for the construct missing the 3' single-stranded region (green). Elimination of both single-stranded regions of the RNA (black) results in approximately a 10-fold loss of binding affinity of p65. Kds range from 3.2 nM (red) to 35.3 nM (black).



Supplementary figure 3. SDS gels of (A) purified TERT-N (amino acids 1-516) and (B) TERT RBD (amino acids 216-516), both stained with Coomassie blue. These constructs were used in the nuclease protection assays.