Supplementary Figure S1

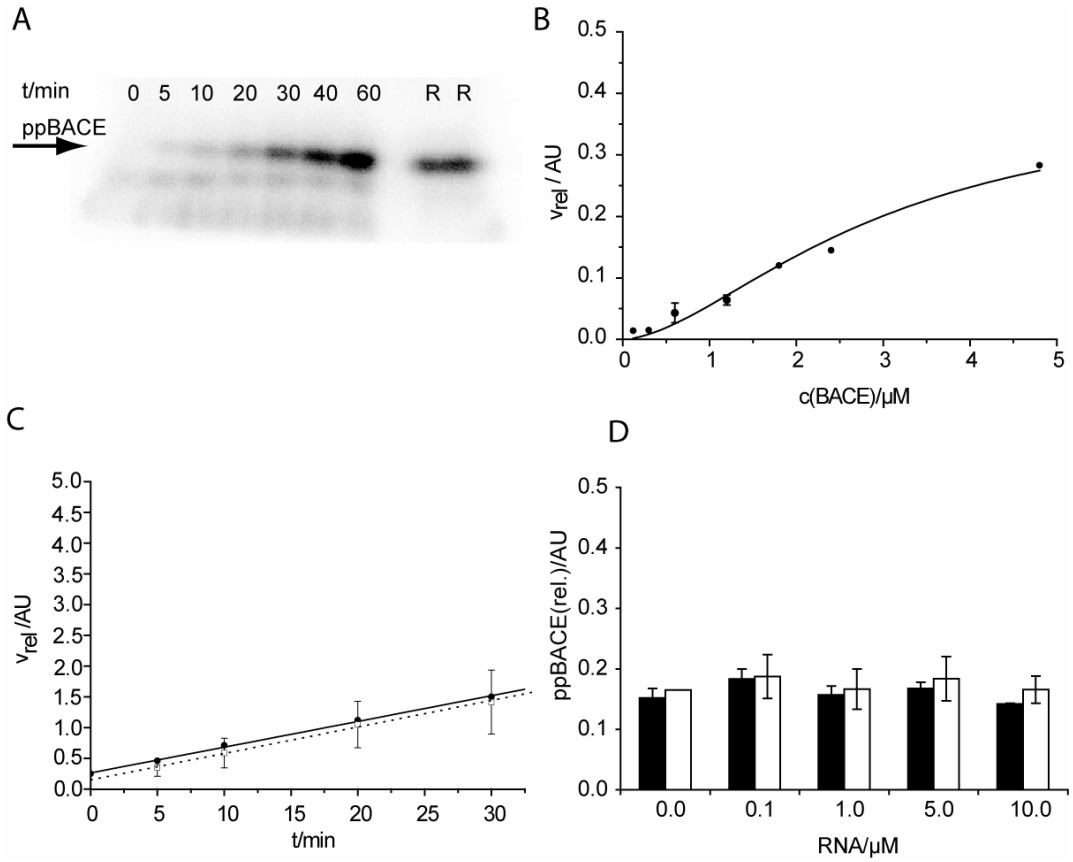

Figure S1. *In vitro* phosphorylation experiments of BACE1-CT with Casein kinase I (CK-1) and γ-[32P]-ATP. A, SDS-PAGE analysis of BACE1-CT after phosphorylation with γ-[32P]-ATP by CK-1 at indicated time points and for a reference sample. *B*, Determination of kinetic parameters of Casein kinase I (CK-1) for BACE-CT from initial velocity measurements. A KM value of 2.9±1.2 µM and a Vmax of 0.39±0.12 AU (Arbitrary Units) were determined. *C*, Time course of *in vitro* phosphorylation of BACE1-CT without RNA (black dots and line) and in the presence of 5 µM S10 aptamer (white rectangles and dotted line) show that the initial velocities of BACE1-CT phosphorylation by CK-1 are not affected. Conditions: 10 µM ATP, PBS pH 7.4, 5 mM MgCl2, 5 mM DTT, 300 U CK1. *D*, Product formation of BACE1-CT phosphorylation is not altered by concentrations of up to 10 µM S10 aptamer (black bars) or non-binding control RNA (white bars). Conditions: 10 µM ATP, PBS pH 7.4, 5 mM MgCl2, 5 mM DTT, 10 U CK1.

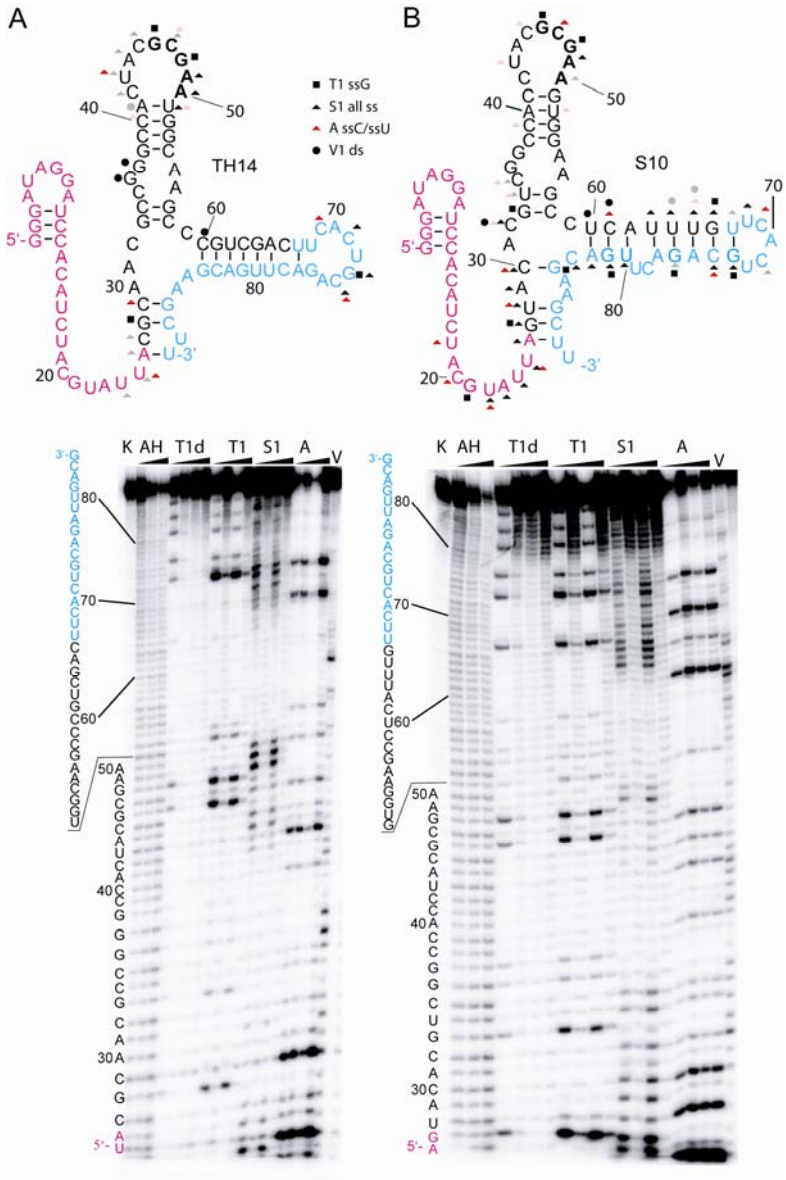

Figure S2. Structural probing of TH14 and S10. *A*, TH14 Secondary structure prediction of TH14 including data from enzymatic probing (upper panel) as well as cleavage pattern of 5'-[^{32}P]-labeled TH14 by alkaline hydrolysis (AH) and different nuclease digestions (denaturing T1, T1, S1, A and V nuclease) (lower panel). Black and red labels in the secondary structures indicate strong cuts, grey and pink labels symbolize weaker cuts. Red triangle: strong RNase A, pink triangle weak RNase A, black triangle: strong RNase S1, grey triangle: weak RNase S1, black circle: strong RNase V, grey circle: weak RNase V, black square: RNase T1. The 5'-primer binding site is shown in magenta, the 3'-primer binding site in cyan. *B*, Same for the aptamer S10.