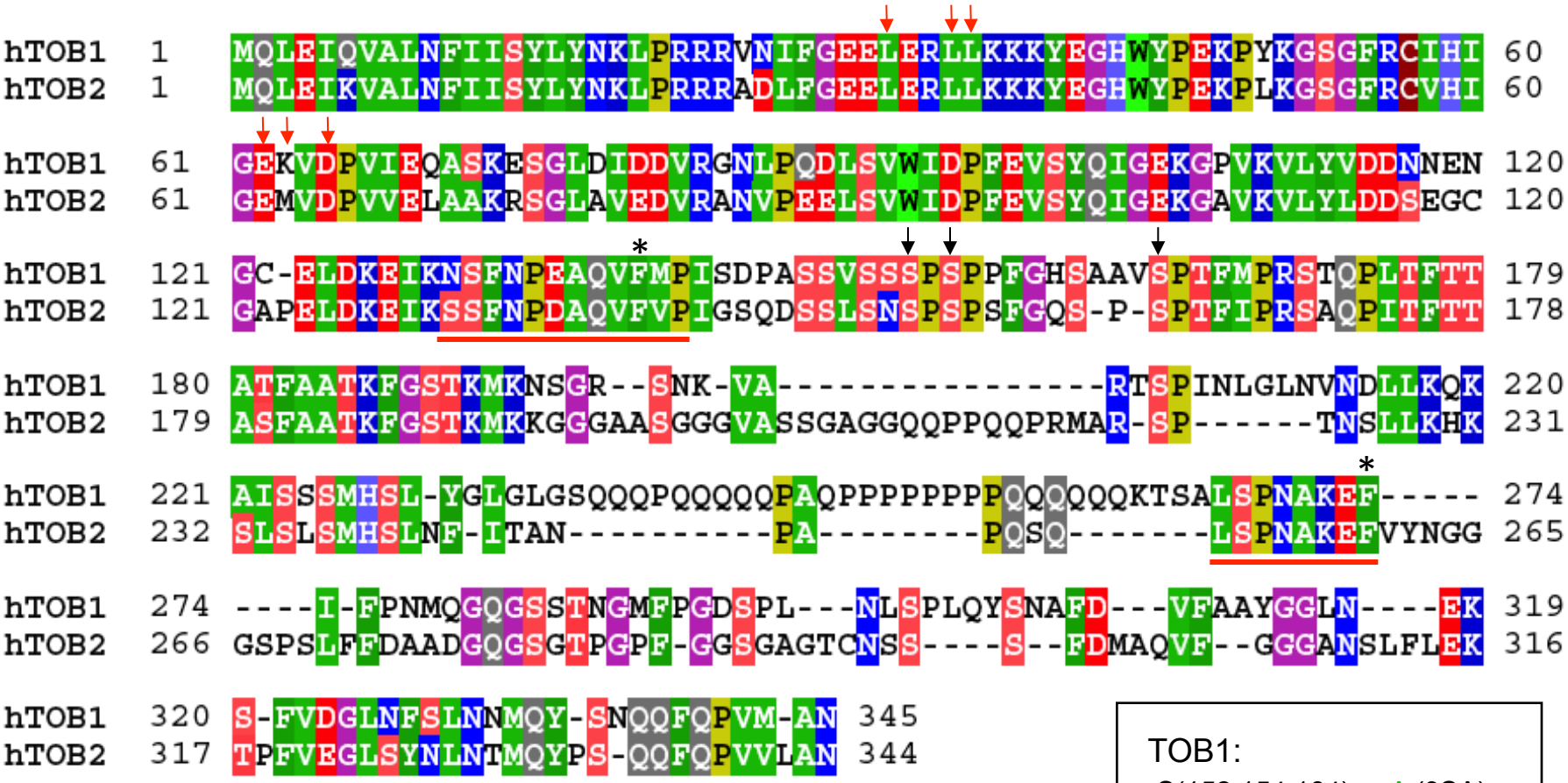
SUPPLEMENTARY FIGURE LEGENDS

Supplementary figure 1. Protein sequence alignment of human TOB1 and TOB2 proteins. Different symbols denote the specific mutations introduced into wild-type proteins. Red line underlines PAM2 motifs.

Supplementary figure 2. Secondary structure prediction of TOB1 wild-type vs. TM mutant. The analysis indicates no apparent change in the predicted secondary structures between wild-type and TM mutant.

Supplementary figure 3. The ability of TOBs to promote deadenylation and decay is not affected by the phosphorylation status of three conserved serines during G0 to G1 transition. (**A**) Northern blot analyses of deadenylation and decay of reporter transcript (BBB+12bs mRNA) in cells expressing MS2, MS2-TOB1, MS2-TOB2, or the 3SA and 3SE mutants of the MS2-TOBs. Cell transfection and poly(A)$^-$ mRNA (A-) preparation were as described in the Fig. 1 legend. Cells were cultured in medium with 0.5% serum for 24 hours prior to serum stimulation. Following serum stimulation, samples were taken at the indicated times after tetracycline addition. (**B**) Western blot analysis of protein levels for MS2-TOBs and their mutant derivatives, with GAPDH served as loading control. mRNA half-life (t1/2) determination is described under Materials and Methods section.



↓ : amino acids mutated to abolish CAF1 interaction

↓ : serines mutated to alter phosphorylation state

* : F to A change to abolish PABP interaction

—— : PAM2 motifs

TOB1:

S(152,154,164) -> A (3SA)
S(152,154,164) -> E (3SE)
L(32,35,36) -> G (3LG)
E62,K63,D65 -> A (TM)

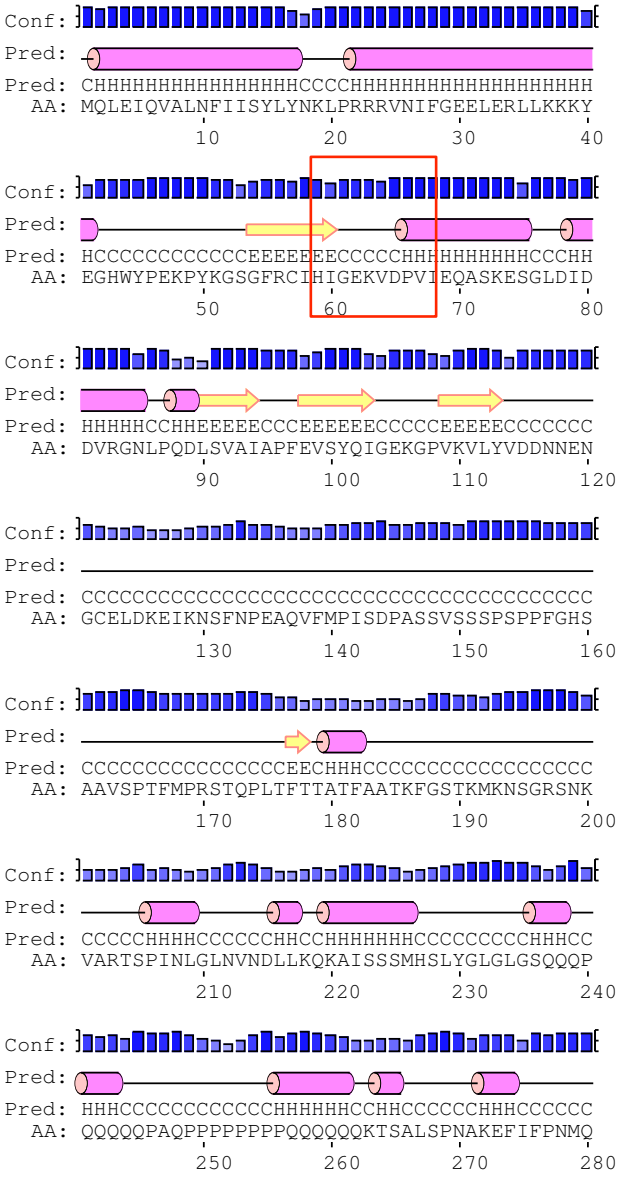
TOB2:

S(153,155,163) -> A (3SA)
S(153,155,163) -> E (3SE)
L(32,35,36) -> G (3LG)
E62,M63,D65 -> A (TM)

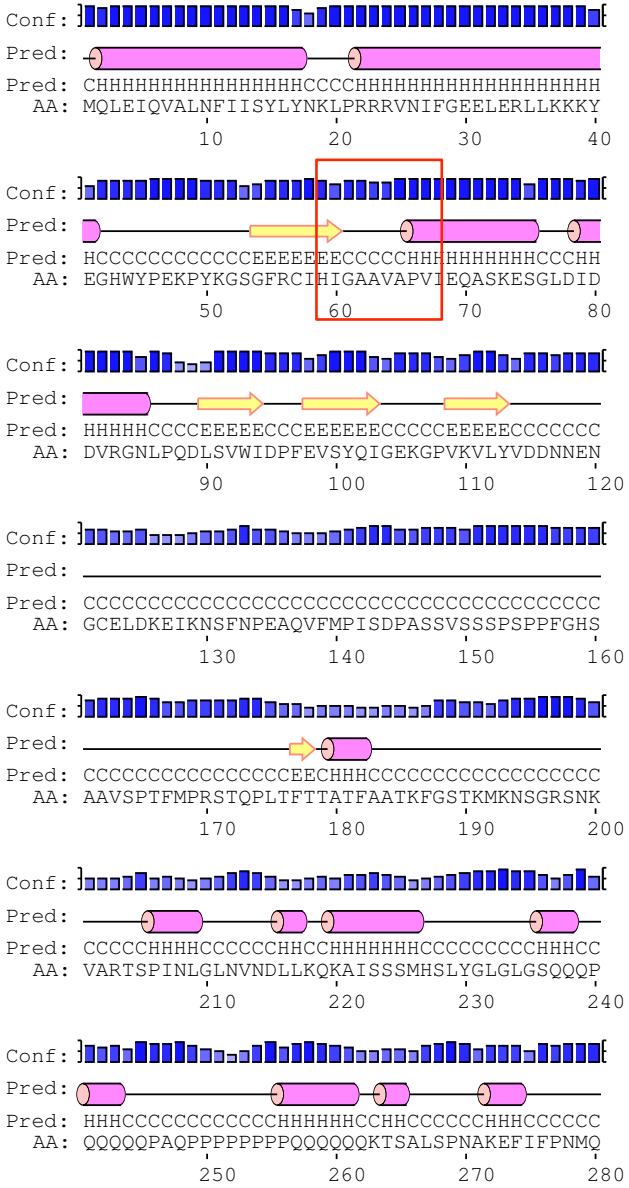
Shyu Supplementary Figure 1

Secondary structure prediction of TOB1 wild-type vs. TM mutant

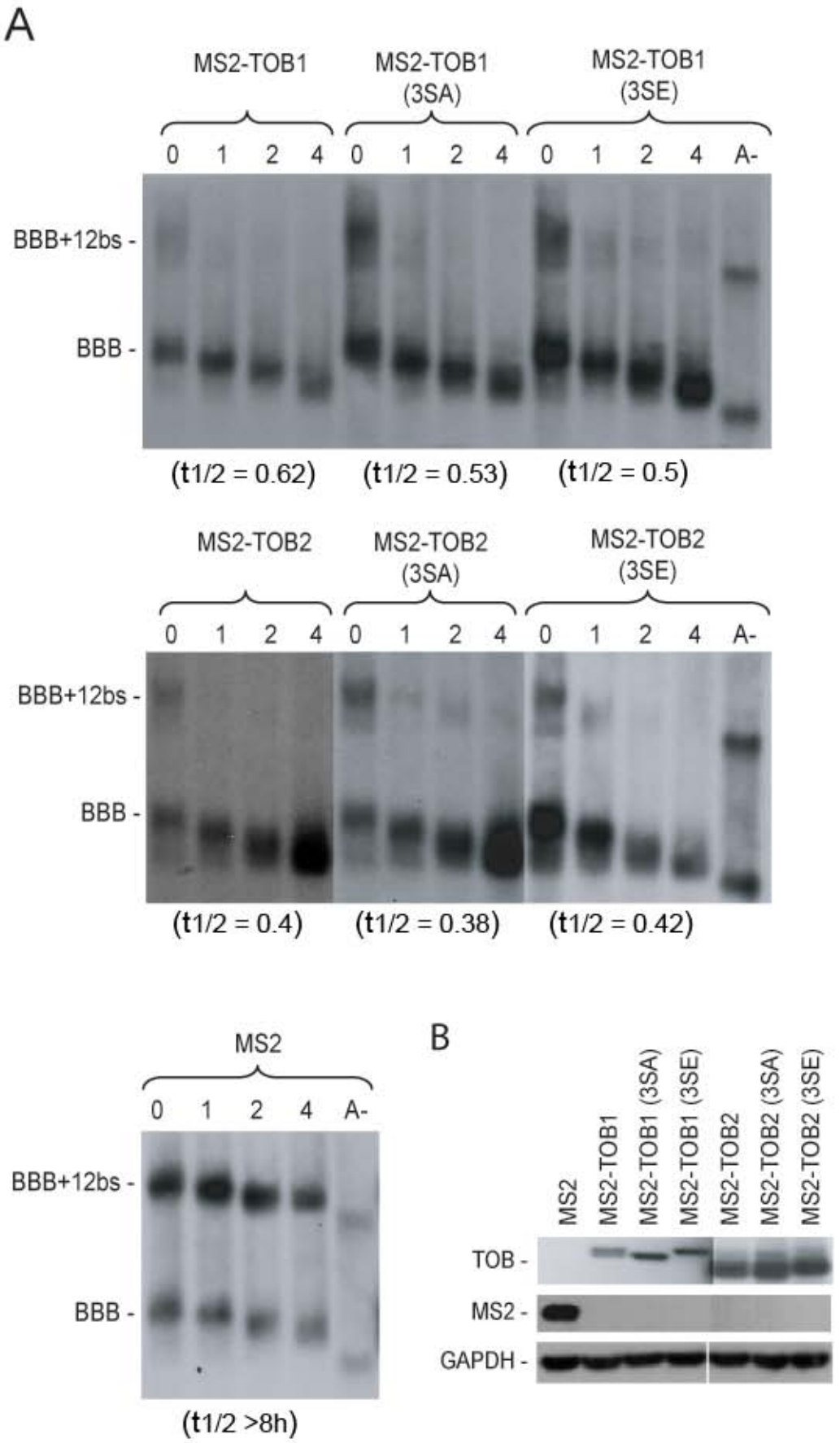
WILD TYPE



TM MUTATIONS (E62,K63,D65 -> A)



Shyu Supplementary Figure 2



Shyu Supplementary Figure 3