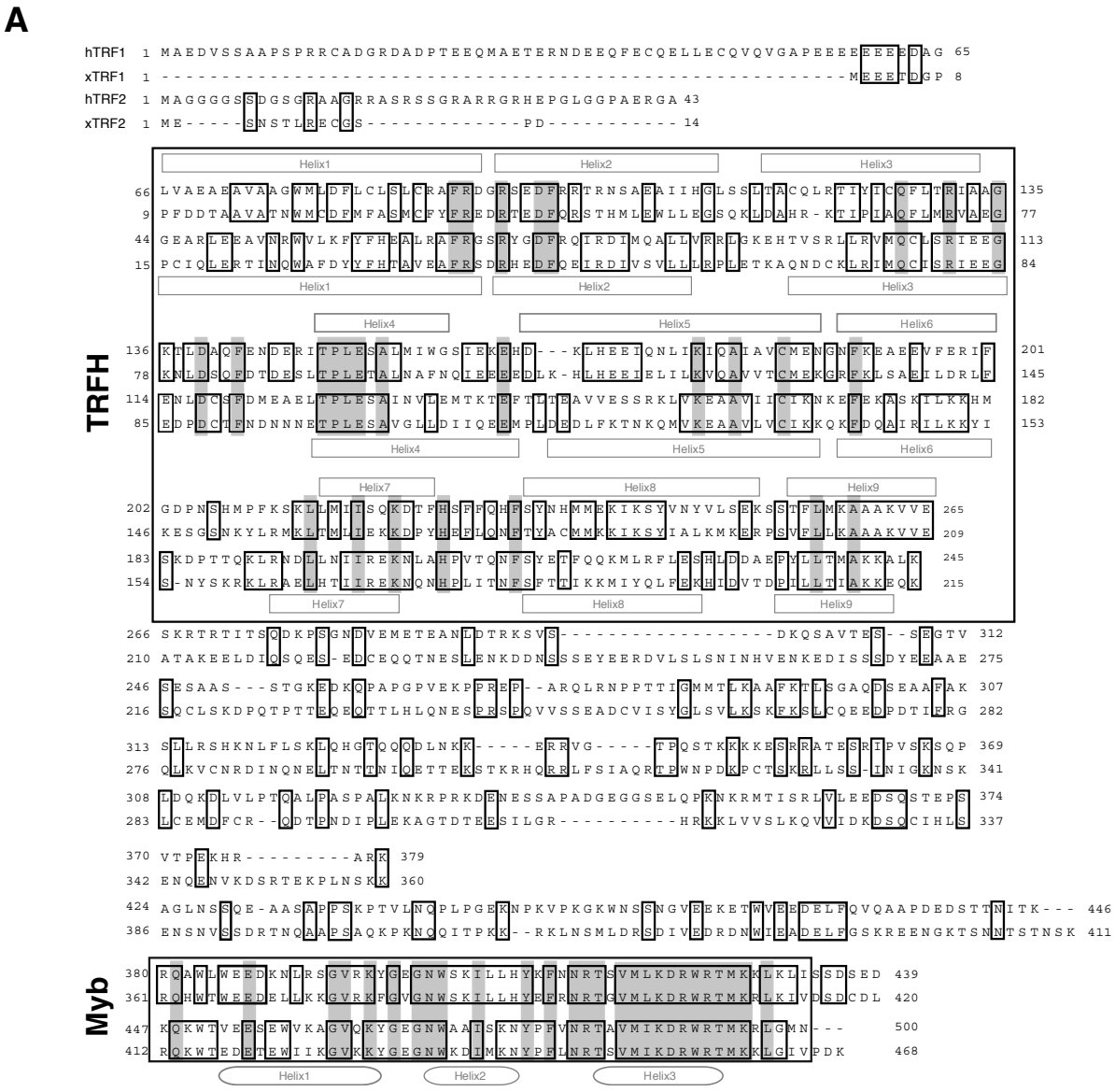

Nishiyama *et al*. Supplementary Figure 1

Supplementary Figure 1

Structures of xTRF1 and xTRF2

(A) Amino acid sequences of human and *Xenopus* TRF1s and TRF2s are aligned.

Amino acid residues conserved between human and *Xenopus* TRF1s or TRF2s are boxed, and residues conserved among the four proteins are hatched. The xTRF1 and xTRF2 sequences are available from GenBank/EMBL/DDBJ under accession numbers AF525882 and DQ118429. Positions of the α helices deduced from hTRF1 (Fairall et al., 2001) are indicated below or above the sequences.

(B) Schematic representation of the domain structures of human and *Xenopus* TRF proteins and the % identities at the TRFH, linker and Myb domains. We could not prepare antibodies that are sufficiently sensitive to detect endogenous xTRF1 in simple immunoblot experiments of the extracts. In contrast, endogenous xTRF2 was easily detected in immunoblot experiments using anti-xTRF2 antibodies. When endogenous xTRF1 was first immunoprecipitated from a large volume of extracts and the precipitates were immunoblotted with anti-xTRF1 antibodies, we were able to detect endogenous xTRF1 showing the expected mobility on SDS-PAGE (data not shown). We then deduced the relative abundance of endogenous xTRF1 and xTRF2 by calibrating the immunoprecipitated endogenous proteins with standard recombinant xTRF1 and xTRF2 proteins, and found that the amount of endogenous xTRF1 is several-fold less than that of endogenous xTRF2 (data not shown).

Reference

Fairall, L, Chapman, L, Moss, H, de Lange, T and Rhodes, D (2001) Structure of the TRFH dimerization domain of the human telomeric proteins TRF1 and TRF2. *Mol Cell* **8:** 351-361