Supporting Information Legends

Figure S1. MBP-tagged hTTP TZF fragment binds to ARE in a zinc-dependent manner in FA analysis. MBP alone does not bind to ARE. (a)(c) ARE_{13} probes. (b)(d) ARE_{19} probes.

Figure S2. TZF motif of hTTP binds to ARE_{19} (a) better than MutG (b) in RNA electrophoretic mobility shift assays (EMSA). RNA-protein complexes are indicated by asterisk. (c) Binding curves were plotted by fitting the fraction of RNA bound (total bound RNA in all bands divided by the sum of bound and unbound RNA) as a function of protein concentration with the Hill equation.

Figure S3. Comparison of TZF motifs of TTP (P26651), TIS11B (P17431), TIS11D (P47974), Cth1 (P47976), Cth2 (P47977), MEX-5 (Q9XUB2), MEX-6 (Q09436), POS-1 (BAA33854), AtC3H14 (At1g68100), AtC3H15 (At1g68200), and 11 members of AtTZF family. Sequence alignment is carried out using Clustal Omega program (http://www.ebi.ac.uk/Tools/msa/clustalo/index.html). Cysteine (C) and histidine (H) residues are highlighted in yellow background. Human TZFs (TTP, TIS11B, and TIS11D), yeast TZFs (Cth1 and Cth2), Arabidopsis TZFs (AtC3H14 and AtC3H15) are characterized by $Cx_8Cx_5Cx_3H$-$_{X18}$-$C_{X8}C_{X5}C_{X3}H$. Nematode TZFs (MEX-5, MEX-6, and POS-1) contain $C_{X8\text{-}9}C_{X5}C_{X3}H$-$_{X23}$ -$C_{X8\text{-}10}C_{X5}C_{X3}H$ motifs. Arabidopsis TZFs (AtTZF1 to AtTZF11) contain a $C_{X7\text{-}8}C_{X5}C_{X3}H$-$_{X16}$-$C_{X5}C_{X4}C_{X3}H$ motif. Conserved amino acids with aromatic side chains (Tyr170, Phe176, Tyr208, and Phe214) in TIS11d are underlined. Basic amino acid residues are denoted by purple letters (not including histidine), while acidic residues are in blue letters.

Figure S4. RNA EMSA results of different TZF domains binding to ^{32}P-labeled ARE_{19} probe. **(**a) TZF domain of hTTP. (b) TZF domain of AtC3H15. (c) TZF domain of AtTZF1.

Figure S5. Plant-specific RR-TZF domain from *Arabidopsis thaliana* and rice (*Oryza sativa*). Sequence alignment is conducted using Clustal Omega program (http://www.ebi.ac.uk/Tools/msa/clustalo/index.html). A conserved $C_{X5}H_{X4}C_{X3}H$ motif is indicated by green background, and two other conserved motifs (SHDWTEC and ARRRDPR(R/K)) are boxed. Basic amino acid residues are denoted by purple letters (not including Histidine), while acidic residues are in blue letters. Small hydrophobic amino acids are highlighted in red, whereas the rest of the amino acids are in green color.

Figure S6. Determine the effects of AtTZF1 and hTTP on mRNA stability and accumulation using a maize protoplast transient expression system. High efficiency protoplast transformation shown by the expression of various constructs in maize protoplasts.

Figure S7. mCherry (a) and PP2A (b) expression levels in samples with Actinomycin D treatments in time course mRNA half-life assays.

Table S1. Primers used for molecular cloning.

Table S2. Primers for quantitative RT-PCR analyses.

Methods S1. Data analysis for EMSA results.