

### Supplemental Fig. 1. Heat-induced telomere shortening in *ten1-3* and *ctc1-3* mutants.

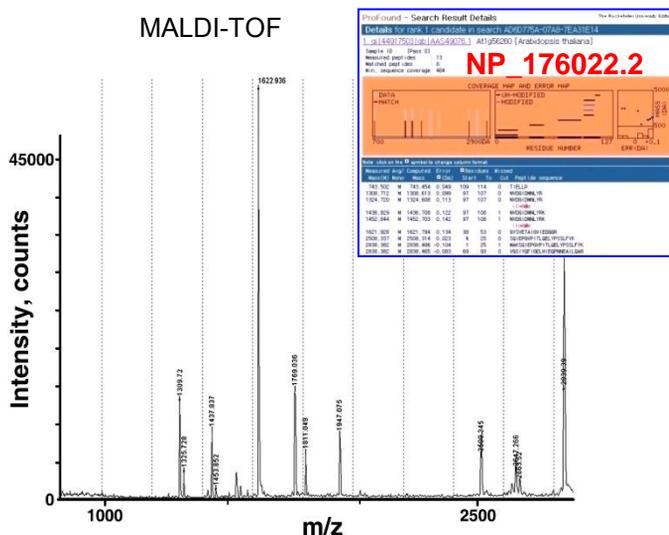
(A-D) PETRA was used to evaluate telomere length following heat shock. 1L and 2R represent individual subtelomeric primers. Blots were hybridized  $^{32}\text{P}$  labeled (TTTAGGG) $_5$ . (D) PETRA of a time course experiment where DNA was isolated 1 hr or 3 h after heat shock. (E) Telomerase activity in two week-old seedlings measured by Q-TRAP. Data were normalized to WT; each data point represents three biological replicates. *p* values are indicated.

A

**MAKSQIEPGVPITLQELYPSSLFYKEGVSRLRVTAMLRGYSVETAIGVIED 50**  
**GGRSLKINTQNIIRDVSFRVGSIIYQFIGELHIEQPNNAILQARTGRNVDG 100**  
**IDMNLRYRKTIELLRQFLKEEDNSNMVE 127**

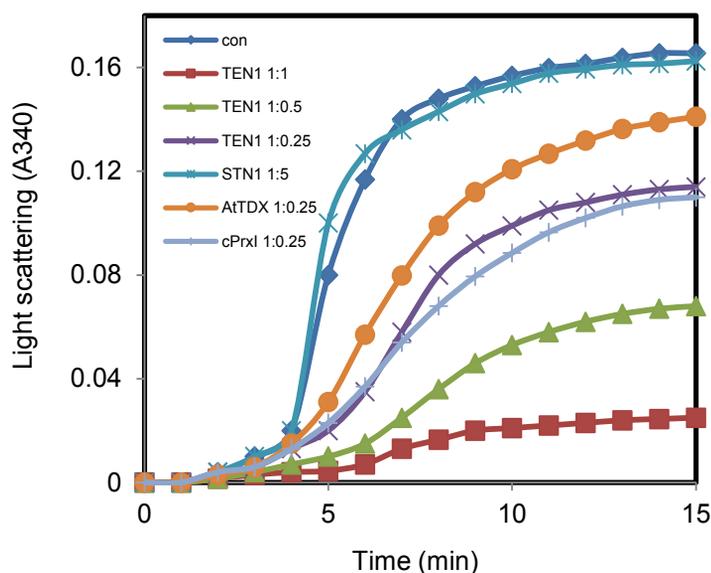
AtTEN1

B



**Supplemental Fig. 2. Characterization of AtTEN1 protein.**

(A) FoldIndex prediction for AtTEN1. Red indicates a predicted disordered segment in the C-terminus. (B) Mass spectrometry results for purified AtTEN1. Purified protein was subjected to sMALDI-TOF analysis, which identified the protein as AtTEN1.



### Supplemental Fig. 3. Chaperone activity of *A. thaliana* TEN1 protein.

Chaperone activity was measured by using 1.5  $\mu$ M citrate synthase (CS) as a substrate. Thermal-aggregation of the substrate was examined in the presence or absence of AtTEN1 at molar ratios of CS to TEN1 of 1:0.25, 1:0.5 and 1:1 at 43°C. Also shown are data for *A. thaliana* thioredoxin-like chaperone (AtTDX), yeast peroxiredoxin (cPRxI) and a negative control reaction with only CS substrate (con).



Name	Accession No.	Relative expression level after treatment									
		38°C				4°C			Oxidative		
		0.25h	3h	3h + 1h recovery	3h + 3h recovery	0.5h	3h	12h	0.5h	3h	12h
TEN1	AT1G56260	1.306	2.276	1.506	1.188	1.544	1.303	1.030	1.434	1.462	1.060
STN1	AT1G07130	0.710	0.596	0.853	0.953	0.577	1.075	0.652	0.768	0.908	0.959
CTC1	AT4G09680	1.068	1.312	1.387	0.934	0.984	0.966	1.288	0.976	0.995	0.981
TERT	AT5G16850	0.991	1.131	0.946	0.992	1.003	0.962	1.135	0.871	0.968	0.890
Ku70	AT1G16970	0.645	0.415	1.319	0.835	0.655	0.564	0.541	0.581	0.540	0.573
Ku80	AT1G48050	1.099	0.399	1.133	0.903	0.961	0.793	0.665	0.976	1.007	0.925
POT1a	AT2G05210	1.687	1.658	1.357	1.337	1.465	1.156	0.859	1.184	1.499	1.424

**Supplemental Table 1. Transcriptome data for *A. thaliana* telomere-related transcripts in response to abiotic stressors.** Data as reported by Killian et al. 2007 were obtained from the AtGenExpress Visualization Tool using the Affymetrix ATH1 microarray. The untreated basal levels of the mRNAs are set to 1.