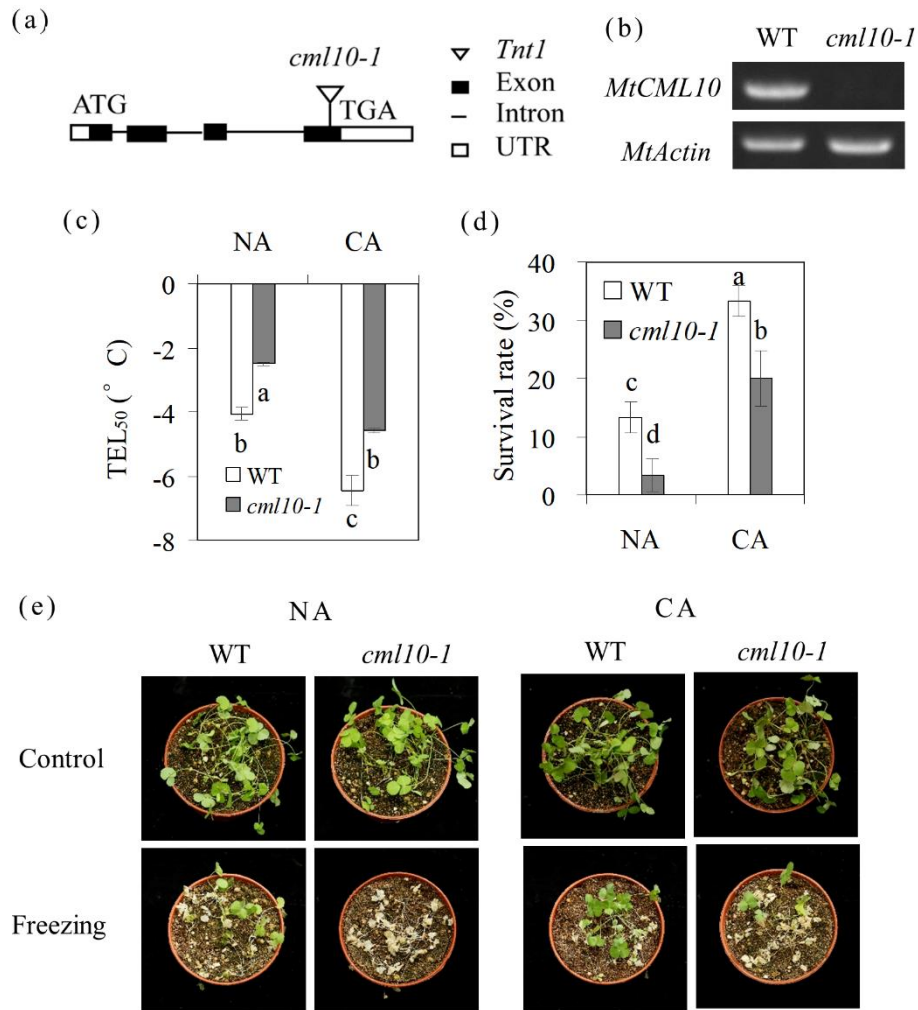
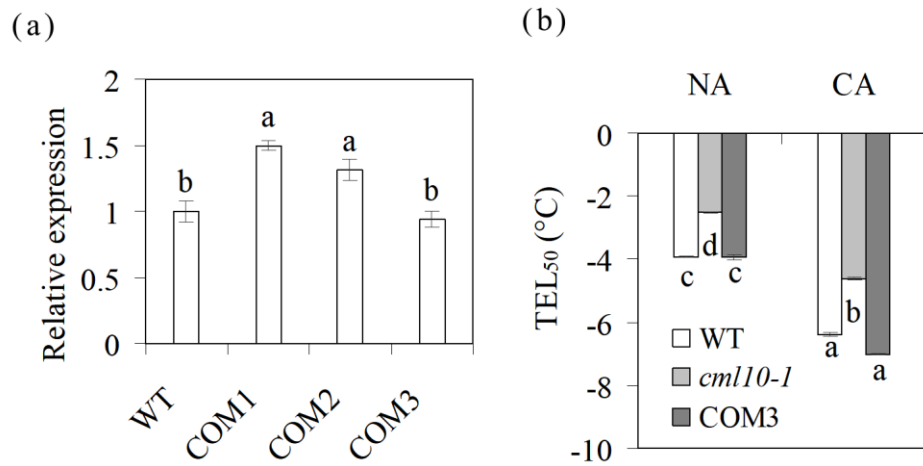


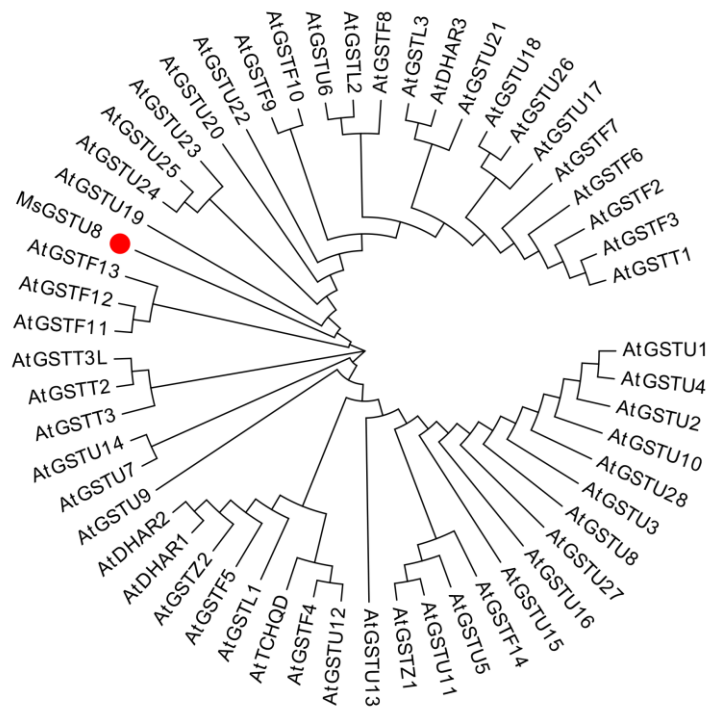
Supplemental Figure S1 Phylogenetic tree of MsCML10 and fifty AtCMLs. The phylogenetic tree was generated by neighbor joining method using MEGA-X software and the sequences were downloaded from phytozome (<https://phytozome-next.jgi.doe.gov/>).



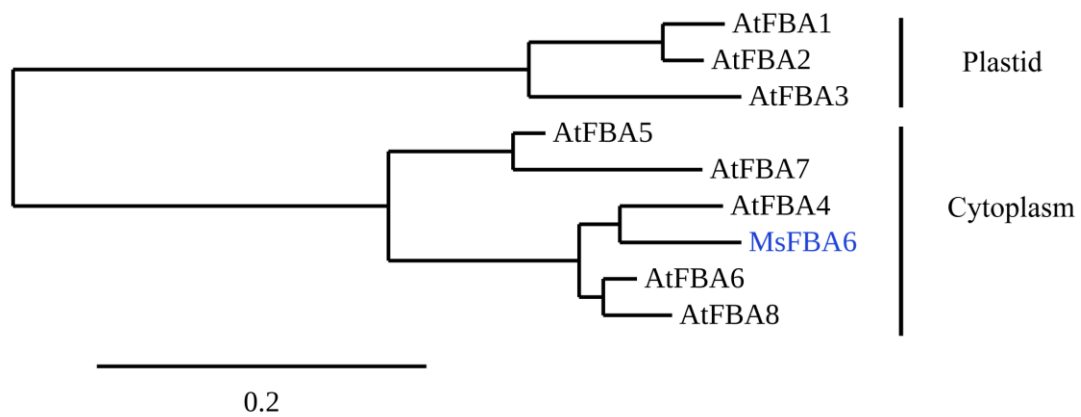
Supplemental Figure S3 Analysis of cold tolerance in *cml10-1* plants in comparison with the wild type (WT). A schematic diagram showing the insertion position of the *Tnt1* retrotransposon in *cml10-1* (a). Semi-quantitative RT-PCR was used to analyze *MtCML10* transcripts in the *cml10-1* line compared with WT plants (b). The temperature resulted in 50% electrolyte leakage (TEL_{50}) in WT and *cml10-1* (c) and survival rate of plants after freezing at -5°C (NA plants) or -7°C (CA plants) for 6 h (d). The freezing-treated plants were photographed after 2 d of recovery at room temperature (e). Means of three replicates and standard errors are presented; the same letter above the column indicates no significant difference at $P < 0.05$ using Duncan's test.



Supplemental Figure S4 Analysis of the complementary plants as compared with the *cml42* mutant and the wild type (WT). (a) Analysis of *cml10-1* transcript in complementing plants (COM) of *MsCML10* in *cml10-1* mutant and the wild type. (b) The temperature resulted in 50% electrolyte leakage (TEL_{50}) in non-acclimated (NA) and cold acclimated (CA) plants. Means of three replicates and standard errors are presented; the same letter above the column indicates no significant difference within each day at $P < 0.05$ using Duncan's test.



Supplemental Figure S5 Phylogenetic tree of MsGSTU8 and AtGSTs. The phylogenetic tree was generated by neighbor joining method using MEGA-X software and the sequences were downloaded from phytozome (<https://phytozome-next.jgi.doe.gov/>).



Supplemental Figure S6 Phylogenetic tree of MsFBA6 and AtFBAs. The phylogenetic tree was generated by neighbor joining method using MEGA-X software and the sequences were downloaded from phytozome (<https://phytozome-next.jgi.doe.gov/>). The bar represents the branch length equivalent to 0.2 amino acid changes per residue.

Supplemental Data

Supplemental Table S1 Primer sequences used for RT-qPCR and RT-PCR and the accession numbers of the analyzed genes.

	Gene name	Accession no.	Primer name	Sequence
RT-qPCR	<i>MsCML10</i>	OM049783	Y2230, forward	5'-CCCACTGAAGAAGAGCTACAAG-3'
			Y2231, reverse	5'-TTTCCTAGCCATCAAGTTCAAGA-3'
	<i>MtCML10</i>	MTR_1g076650	Y2232, forward	5'-CCCACTGAAGAAGAGCTACAAG-3'
			Y2233, reverse	5'-TTTCCTAGCCATCAAGTTCAAGA-3'
	<i>MtACTIN</i>	MTR_3g095530	Y4181, forward	5'-ATTCACGAGACCACCTAC-3'
			Y4182, reverse	5'-GAGCCACAACCTTAATCTTC-3'
RT-PCR	<i>MtCML10</i>	MTR_1g076650	Y4425, forward	5'-ATGGCACATGTCCTTAGT-3'
			Y4426, reverse	5'-TCATCGAATGGTCATCATC-3'
	<i>MtACTIN</i>	MTR_3g095530	Y4181, forward	5'-ATTCACGAGACCACCTAC-3'
			Y4182, reverse	5'-GAGCCACAACCTTAATCTTC-3'