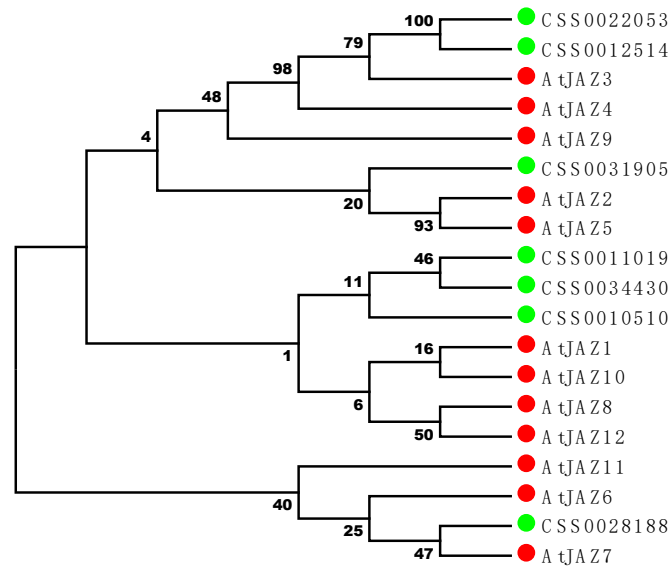


Supplementary Table S1. Primers for qRT-PCR analysis.

Gene	Primers for Real-time PCR	
	Forward Primer (5'–3')	Reverse Primer (5'–3')
<i>CsJAZ1</i>	TAAAACCGCCCAATGACGA	TTCCGAGGGCTGGAATAGGA
<i>CsJAZ2</i>	TCGTCGAGCTTCTCTCAGAC	CGTCACCGGAGTTCCATTTC
<i>CsJAZ3</i>	TTGCTTCTGTTGCAGGAACC	GGACCTGAACCTGAGTCTT
<i>CsJAZ4</i>	TGGCCAACCAACAAACCAA	CTCGTGGGAACGACTGAAAC
<i>CsJAZ7</i>	CGGATTACAACCACCACCAC	AAATCGTTAGCGGCTGTTCC
<i>CsJAZ8</i>	GCTAACTTTCGTGTGCGCTT	CCTCTGTCCGGATGTGTTCT
<i>CsJAZ10</i>	CCGCAGGGCATTAAAGTCTC	GTGAAGGGAAAGGTGAGGGA
<i>CsPPD</i>	TTCGTGAAGACAACCCTGCAGTT	GCACCGGGTAGGAGTGTG
<i>CsZML1</i>	CGTACCGACTGTTCCAACCA	TGGCCCTTCTTACGTTGCAT
<i>CsZML2</i>	CGGTGCTGGCAGCGT	GAAGCAGCCCTTTGTGGTTG
<i>CsZML3</i>	GCCGATCAGCTAACCTCTC	GAAGCAGCCCTTTGTGGTTG
<i>CsZML4</i>	ACGTGACTTCCGTGAATGCT	GGTATTTACGCCCTCCCAA
<i>CsZML5</i>	TGAAGACGGAGGAGGAGGAG	TGCAAAGAGTTCTCGGACCC
<i>CsZML6</i>	TGTGGGCAAACAAGGGAAC	TTTGGATCTGATGTGGCCGT
<i>CsZML7</i>	ACAAGCATGCCTACTGTCCC	AATTTCCATTCTCATTCTGGCTCA
<i>CsZML8</i>	TGAGCCAGAATGAGAATGGAAAT	ATCACTGCCAGTTCCAGCAA
<i>CsGAPDH</i>	TTTTTGGCCTTAGGAACCCAGAGG	GGGCAGCAGCCTTATCCTTATCAGT



Supplementary Figure S1. Phylogenetic tree of JAZ proteins from tea plant and *Arabidopsis*. The predicted full-length amino acid sequences of seven CsJAZ and 12 AtJAZ were used to construct a phylogenetic tree using MEGA5.1 by the neighbor-joining method.