

Supplementary Materials

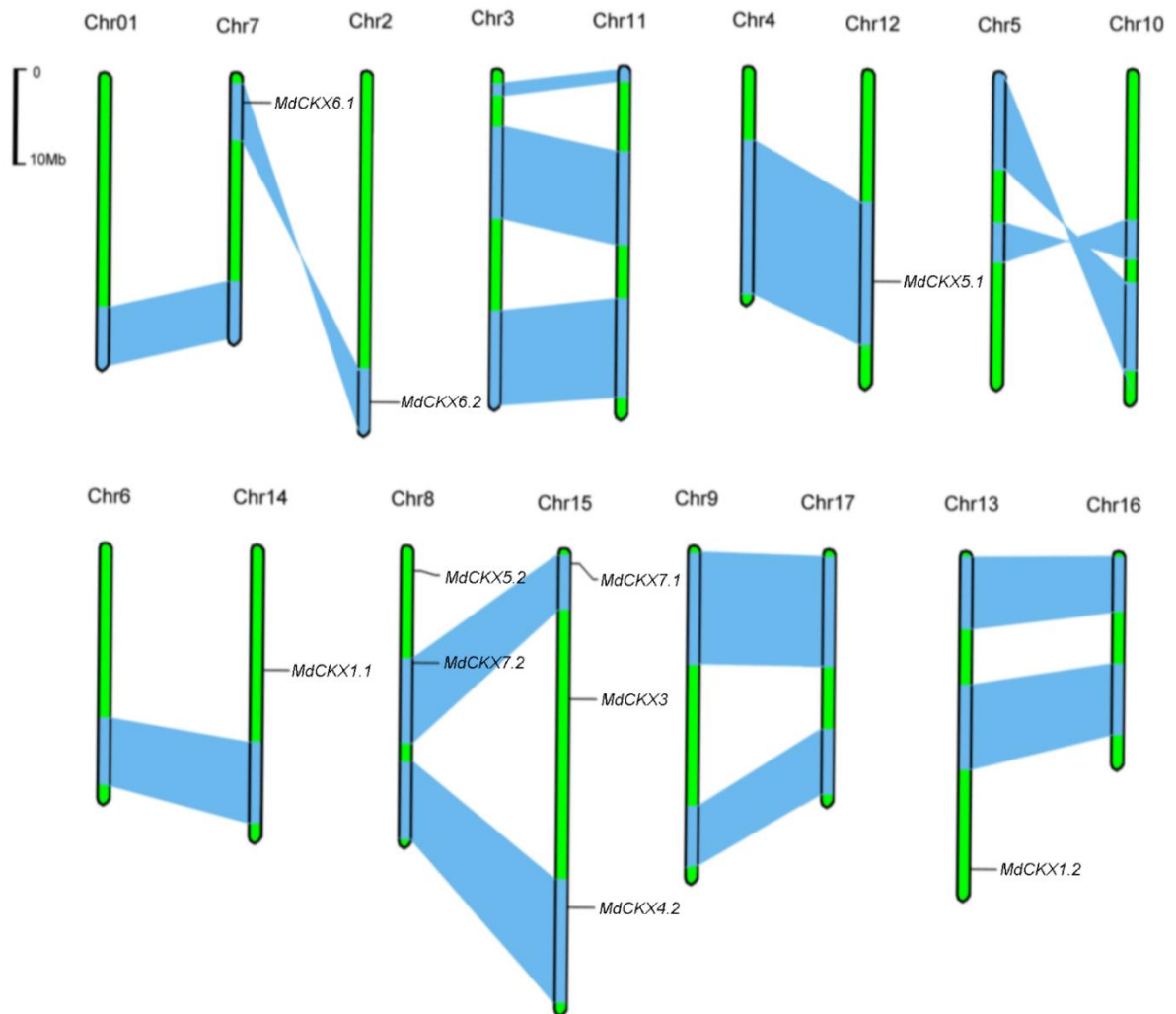


Figure S1. Genomic distribution of *MdCKX* family genes. Each chromosome is indicated by the number (Chr01-Chr17). The scale bar represents a 10.0 Mb chromosomal distance. Segmented duplicate homologous blocks are indicated with a blue shadow.

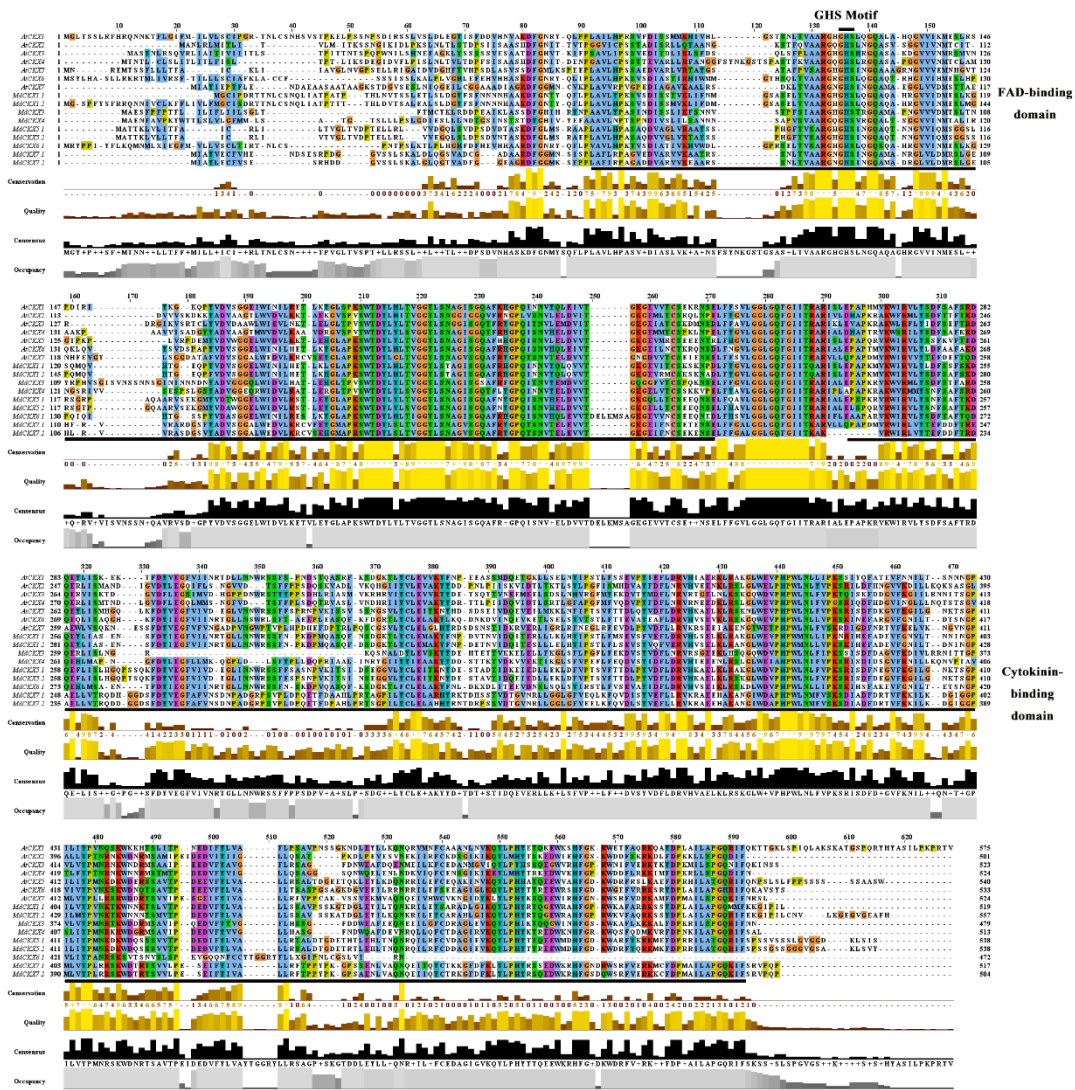


Figure S2. Amino acid alignment of MdCKXs and AtCKXs. FAD-binding domain, cytokinin-binding domain, and GHS motif are indicated by black lines.

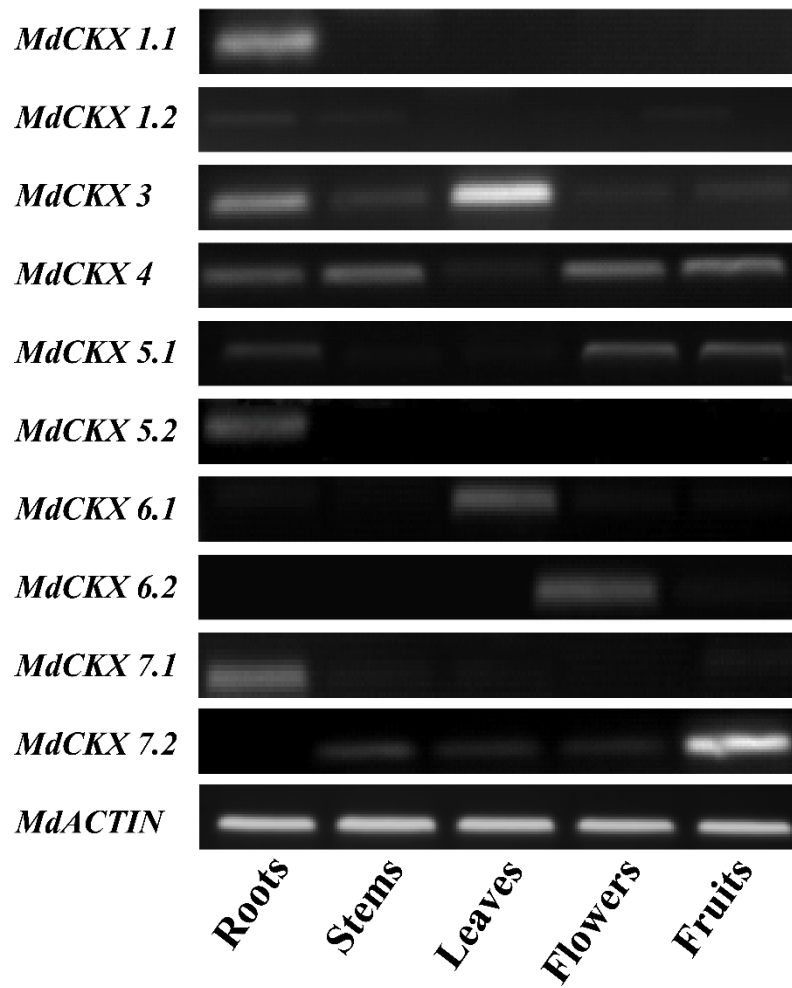


Figure S3. Organ-specific expression profiles of *MdCKX* genes in apple. Expression levels of *MdCKXs* genes were examined by semi-RT-PCR in apple roots, stems, leaves, flowers, and fruits. The *MdACTIN* was performed as an internal control.

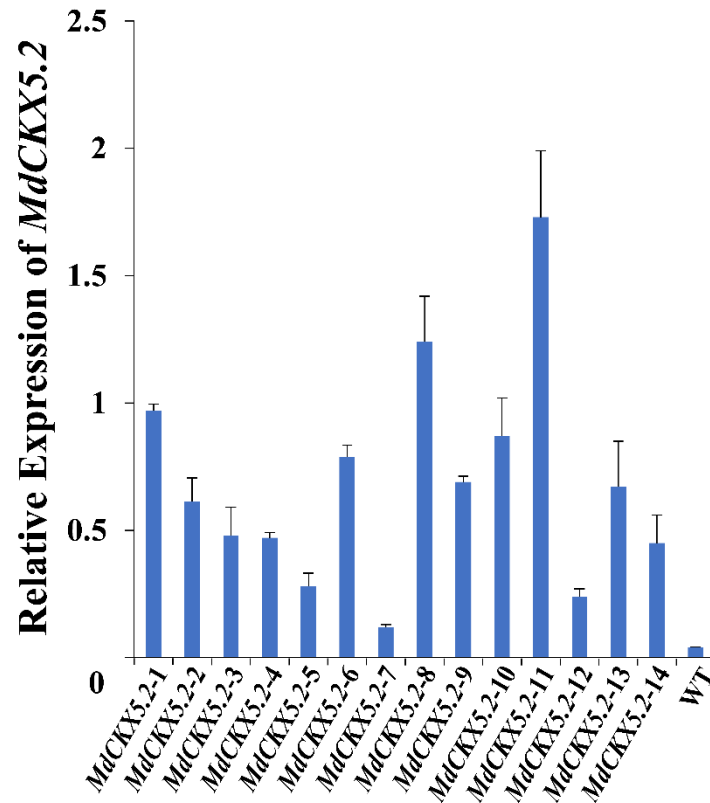


Figure S4. Relative expression levels of *MdCKX5.2* in the wild-type and transgenic *Arabidopsis*. Transgenic (*MdCKX5.2*-1 to -14) lines showing 3:1 segregation in T2 generation and wild-type (WT) lines were used to detect the *MdCKX5.2* expression levels by qRT-PCR. The *AtActin* gene was performed as an internal control. Error bars, \pm SD.

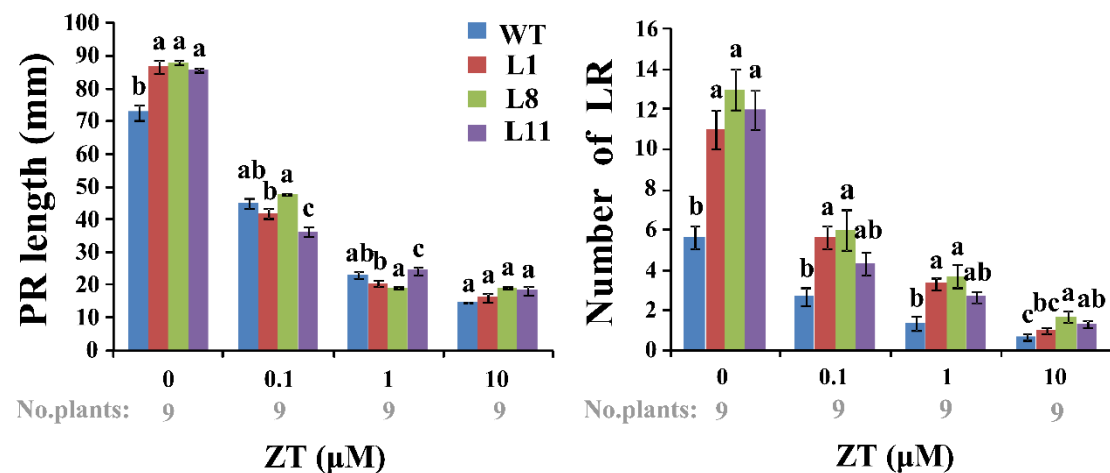


Figure S5. Primary root length and lateral roots number of transgenic and wild-type when *Arabidopsis* treated with ZT. Transgenic (L1, L8, and L11) lines and wild-type (WT) lines treatment with different concentration (0, 0.1, 1, and 10 μ M) ZT to detect primary root (PR) length and lateral root (LR) number. The gray numbers under the charts indicate the number of plants measured (No. plants). Error bars, \pm SD. The letters (a, b and c) indicate statistically significant differences ($p < 0.05$) between different groups by analysis of variance (ANOVA).

Table S1. Primers used for the semiquantitative RT-PCR and quantitative RT-PCR analyses.

Gene name	Sense primer 5'-3'	Tm(°C)	Antisense-primer 5'-3'	Tm(°C)	R ²	Eff%
<i>MdCKX1.1</i>	TAATCATGGGGTGCATACCG	54.6	TTGCTCTCCAGTGTGAACCT	56.1	0.997	102.118
<i>MdCKX1.2</i>	TCCGCAGGCAGAATAACATT	54.1	TAGTGGGAGGAACTGGTATG	53.1	0.99	100.357
<i>MdCKX3</i>	TTACAGTGA CTCTCTACCTTTGC	54.0	CCCATTGTCCTTGTGAGTGAA	54.9	0.994	109.186
<i>MdCKX4</i>	GACAAGTCTACTCCTACCCT	52.5	CACCTCCAACATCAGCATAAG	53.3	0.992	91.415
<i>MdCKX5.1</i>	GAGGTCATCTTTCTTCTCCGCT	60.7	GGTCCCACTTGTCTTTGTTCAT-	55.1	0.996	103.145
<i>MdCKX5.2</i>	GGAGCACTTGACCAATCAGAACCG	56.6	CCACCACCAGAAGAACCCGATG	61.0	0.985	90.861
<i>MdCKX6.1</i>	CACCGTGGAGTTGTCATCAAT	55.1	ATAGGCTTTCATTCTGCTCCTCTG	55.8	0.997	101.732
<i>MdCKX6.2</i>	CTACTTAGTGGCATTCTCACCTCT	57.9	CCTTCCATTCTTCTGTGTAGCG	58.0	0.956	112.996
<i>MdCKX7.1</i>	GCGGGTGTAGAAGATGTGGC	59.2	TTCGCCTTTCCTGTAAACGA	56.4	0.995	101.106
<i>MdCKX7.2</i>	CAACACCGACCGCCCTCATCC	66.4	GAGTATCCCACTTGCTTCGCC	58.7	0.994	99.552
<i>MdACTIN</i>	ACACGGGGAGGTAGTGACAA	56.1	CCTCCAATGGATCCTCGTTA	59.8	0.997	107.186

Tm means melting temperature. R² means coincidence degree of standard curves. Eff% indicated the efficiency of primers.

Table S2. Genome-wide characteristics of MdCKXs.

Gene Name	Gene Identifier	Genomic Position	Best Homologs in Arabidopsis	Size (aa)	Mass (Da)	pI
<i>MdCKX1.1</i>	MDP0000223673	chr12:12131315..12133766	AT2G41510	519	58105.62	8.31
<i>MdCKX1.2</i>	MDP0000318353	chr13:32756755..32759813	AT2G41510	557	62468.60	6.98
<i>MdCKX3</i>	MDP0000271354	chr15:14868730..14874637	AT5G56970	479	53800.20	6.82
<i>MdCKX4</i>	MDP0000213431	chr15:37144019..37146164	AT4G29740	513	57307.66	6.55
<i>MdCKX5.1</i>	MDP0000250917	chr12:21638920..21644145	AT1G75450	538	59531.57	5.62
<i>MdCKX5.2</i>	MDP0000234983	chr8:1462054..1469715	AT1G75450	538	59585.45	5.52
<i>MdCKX6.1</i>	MDP0000256199	chr7:2018056..2019946	AT3G63440	472	52903.55	7.54
<i>MdCKX6.2</i>	MDP0000293966	chr2:34338879..34341015	AT3G63440	538	60646.22	6.61
<i>MdCKX7.1</i>	MDP0000238100	chr15:257331..261328	AT5G21482	517	57053.21	6.29
<i>MdCKX7.2</i>	MDP0000279125	chr8:9500230..9504286	AT5G21482	504	55943.35	6.16

The aa means amino acid. The pI means isoelectric point.