

Supplementary Data

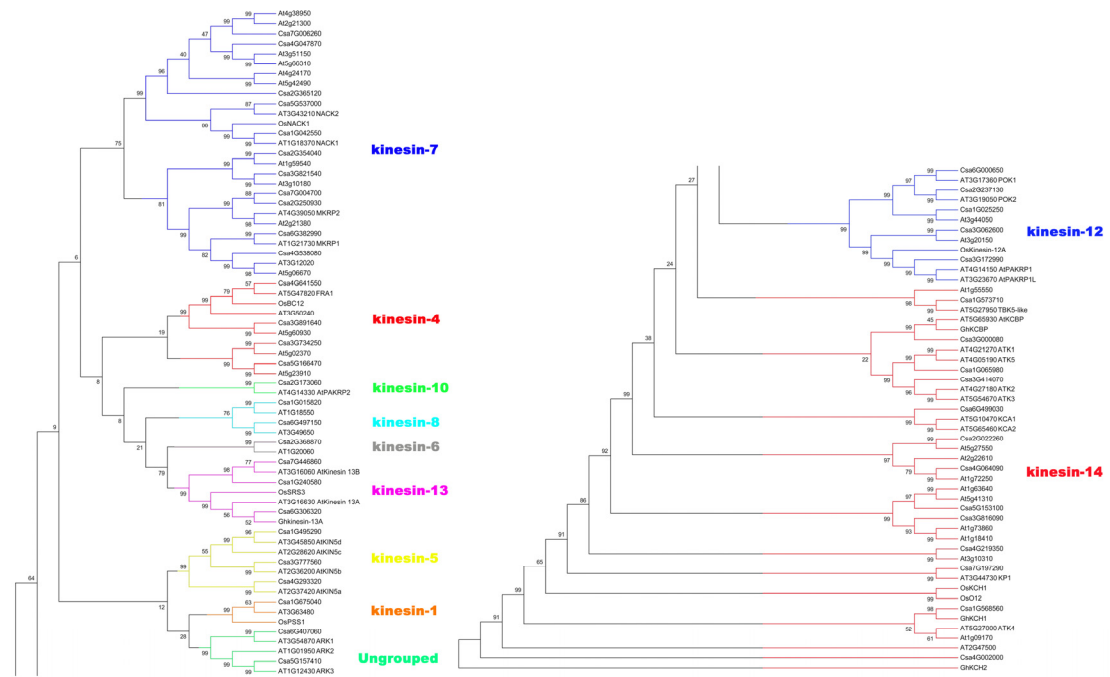


Fig. S1 Phylogenetic analysis of predicted cucumber kinesins and other representatives of kinesins in plant indicated that all predicted kinesins distribute in 14 families and one plant-specific ungrouped family.

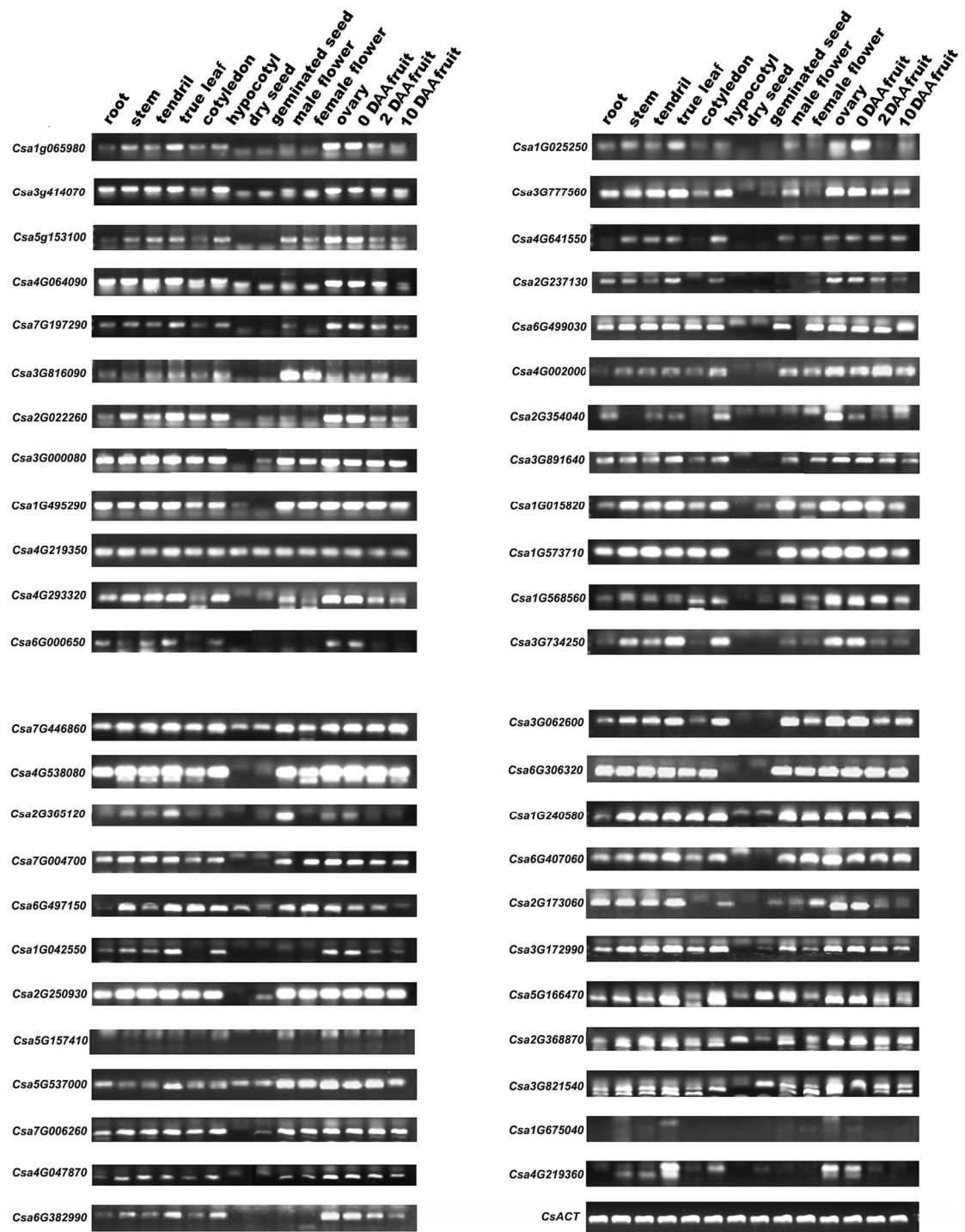


Fig. S2 Expression of forty-seven cucumber kinesin genes during vegetative (root, stem, tendril, true leaf, cotyledon and hypocotyl) and reproductive development (dry seed, geminated seed, male flower, female flower, ovary, 0 DAA fruit, 2 DAA fruit and 10 DAA fruit) by using RT-PCR.

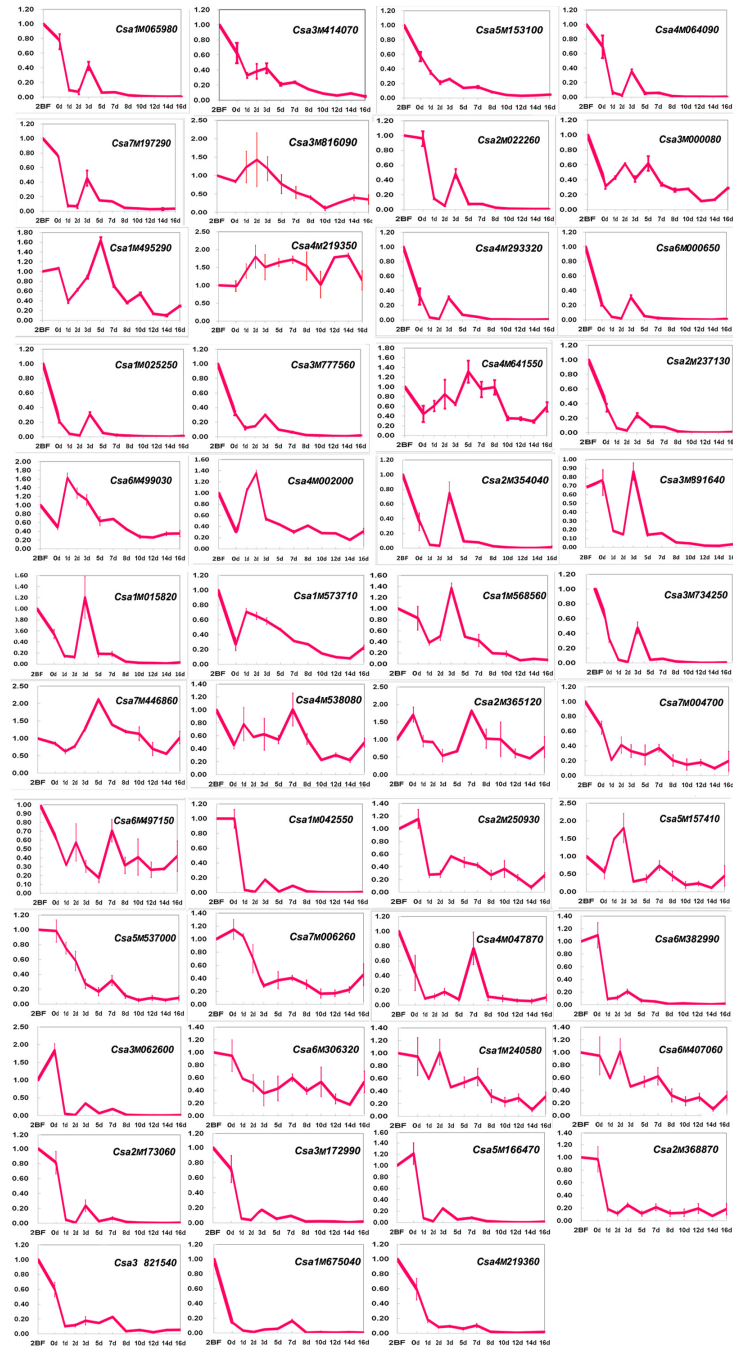


Fig. S3 Expression profiles of kinesin family genes during early fruit development in cucumber. Quantitative RT-PCR results of the expression of 47 kinesin genes during early 9930 fruit development. These data represent the fold changes in expression relative to the expression at -2 DAA. The error bars represent the standard error of the means (n=3).

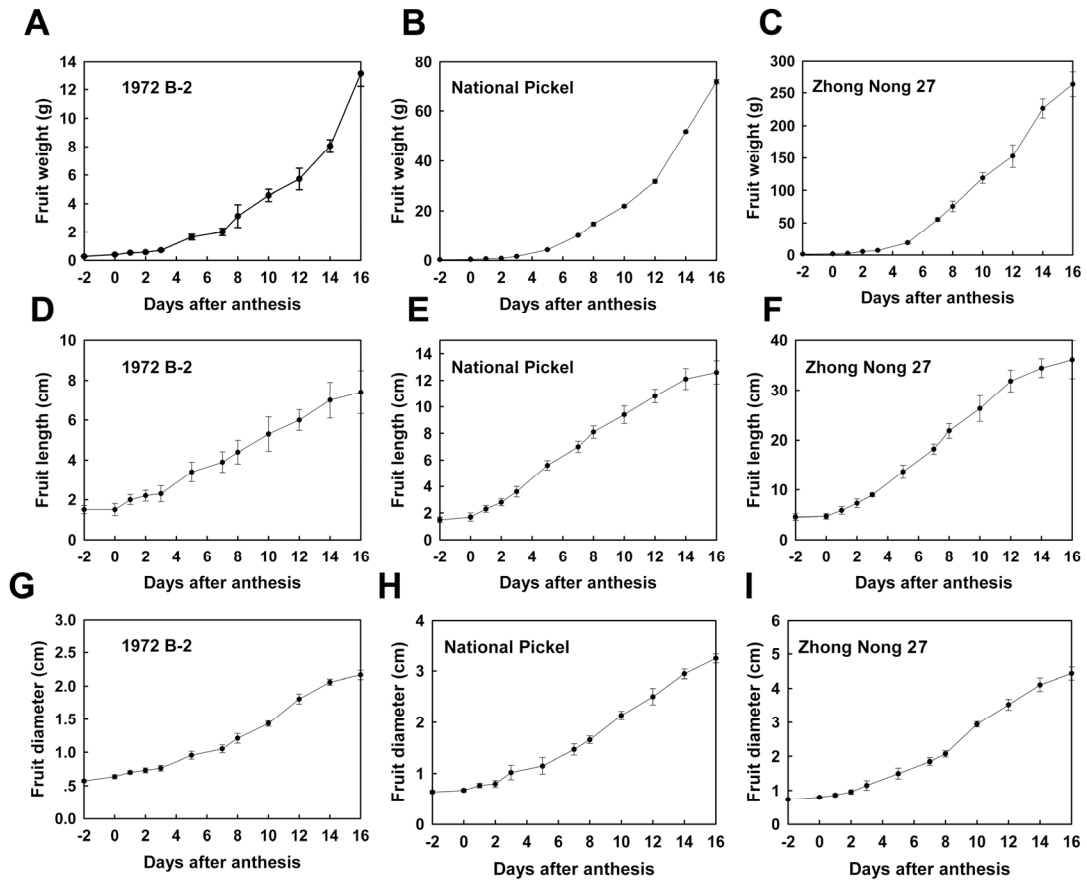


Fig. S4 Physiological changes in 1972 B-2, National Pickle and Zhong Nong 27 during early fruit development. Increase in weight of 1972 B-2 (A), National Pickle (B) and Zhong Nong 27 (C) fruit during early fruit development. Increase in length of 1972 B-2 (D), National Pickle (E) and Zhong Nong 27 (F) fruit during early fruit development. Increase in diameter of 1972 B-2 (G), National Pickle (H) and Zhong Nong 27 (I) fruit during early fruit development.

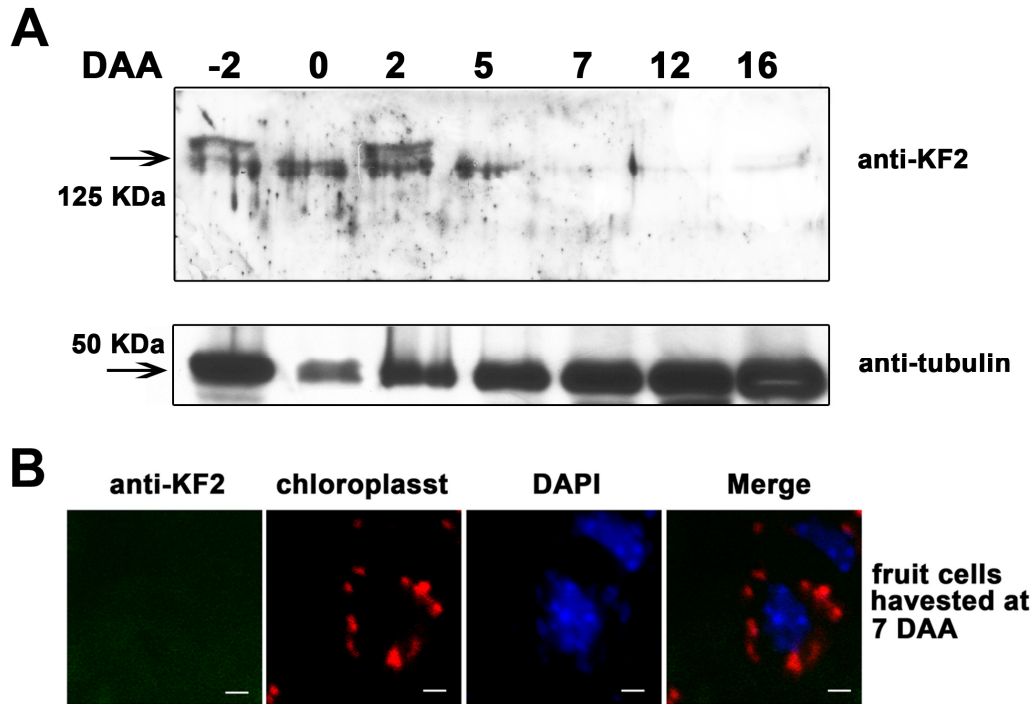


Fig. S5 Protein expression patterns of CsKF2 during cucumber early fruit development. (A) CsKF2 proteins exist predominantly in early stage (before 5 DAA) of cucumber fruit development. (B) It was failed to immunolable CsKF2 in fruit cells harvested at 7 DAA.

Table S1 Sequence-specific primers used for construction.

F represents forward; R represents reverse.

Construct	Primer sequence (5' to 3')	Restriction site
KF1-N	F: GAATTCATGAATGGAATGGGGAGA; R: GTCGACTCAAGAGTTGCCCTCTCT	EcoR I Sal I
KF1-M	F: GGATCCATGGTTGCCAAGATCAAAG; R: CTCGAGTCAGACATTATTCCTTTTGAAAG	BamH I Xho I
KF2-C	F: GGTACCATGGTCTTGGACATGCTAG; R: CTCGAGTTAATAGTGCTGCTCTTGA	Kpn I Xho I
KF2-M	F: GGTACCATGGATCCACCCATCAAAG; R: CTCGAGTCAITCATTATGATTGGCTGA	Kpn I Xho I
KF3-M	F: GAATTCATGAAGGGTAGCATAAGAGTTT; R: GTCGACTCAGTTCACGAGCAG	EcoR I Sal I
KF3-C	F: GGTACCATGCAAATCGAGAATCCA; R: CTCGAGTTATTGTTTCTATTCCAGTTC	Kpn I Xho I
	For transient expression	
KF1	F: ACTAGTATGAATGGAATGGGGAGAC; B: GTCGACGTCAGATGAAGATATAAGTACA	Spe I Sal I
	For transient expression	
KF2	F: GTCGACATGAAGTCGAATCCAACAGG; B: GGTACCATAGTGCTGCTCTTGATATATAG	Sal I Kpn I

Table S2 Specific primers used for RT-PCR and quantitative RT-PCR.

F represents forward; R represents reverse.

Genes	Primers
<i>Csa1M065980</i>	F: TCTTCTCCAGCCATGCCTAG R: AATCTACAGGTCGCATGGTTG
<i>Csa3M414070</i>	F: CTATCTTCTTCAGCCATGTCTCG R: GTCGTGTATTGGTTAAACGCC
<i>Csa5M153100</i>	F: TCCAGAAAAACCAATCCACC R: CACCAATTGGAGAGCTTTTTTG
<i>Csa4M064090</i>	F: GACAAGGTCAAAGAAGCTGAAGC R: GACTACCTAACGGTCGACTTGC
<i>Csa7M197290</i>	F: GAACCACCACCAAGAATGACA R: GGTATTACCAAAAAATTCCCGC
<i>Csa3M816090</i>	F: GTTGAAAAGCCCAGATCTACA R: GCCATCTTCTACCAGACTTGAGTC
<i>Csa2M022260</i>	F: CAAGAAAAGGTTGAGATATCGAG R: GCGGTTTCTTCTCTGGAAT
<i>Csa3M000080</i>	F: CTCATGTATGCATCAAGAGTTG R: CTTTAGTATGTCGCTCGTTTTGG
<i>Csa1M495290</i>	F: GAATACACGGTTGATGAACCATC R: CCAGCTAAATGCTTTACATCTCC
<i>Csa4M219350</i>	F: GCTCTGAGAAGAAACAATATTACAGG R: TCTAGATTTTCTGCCCCTGT
<i>Csa4M293320</i>	F: GATTATCTGGTCGATCAGCATTG R: GAACTTTTCTTCTATCAAACCCC
<i>Csa6M000650</i>	F: GGGATACTGAAGACGAAAACA R: TTTGAGTTAGCCAACCTCATTG
<i>Csa1M025250</i>	F: GCTGAAAAGGCATGTAGATGAAT

	R: ATGGCATCGACCATCGTC
<i>Csa3M77560</i>	F: CAATATGGGGACTATGAGCCA R: GATGGTTTCTTTGCCATTACTC
<i>Csa4M641550</i>	F: TCGTGTAGGAGTTGAATGGTACC R: TGCCTGATCCATTCTGAAAGT
<i>Csa2M237130</i>	F: CGTTTTAAAGGCAGCTGGAG R: TCTTTGAACTTTCGGTGAAGG
<i>Csa6M499030</i>	F: TCGTCAGATAGTTGAGTTACTCCA R: CACCACACTTGATGATAAAAGGAG
<i>Csa4M002000</i>	F: GCCCAGAGTTAAGCAAGAACTTC R: TGTTTTCTATTCCAGTTCTGCG
<i>Csa2M354040</i>	F: TCTTCTCAGAGTGCCAAA R: GCTCCACGAAGTACGTCATAT
<i>Csa3M891640</i>	F: CACATTGGTAAAATCAAAGGCA R: AACGGGATGTTGACAACCTC
<i>Csa1M015820</i>	F: CAGAATAAGGTTGCAGAAGCA R: CAGGGATTGTGCCTGTAATGT
<i>Csa1M573710</i>	F: CTACAGGAGGACTGAAGAAGCA R: CACGTGGATGATGATCGCTA
<i>Csa1M568560</i>	F: CGGAGGCTCAAAGCAAG R: ACCATAGCTTTGTCGTCCA
<i>Csa3M734250</i>	F: TTGAATACAGCAAGCAGAGAGG R: CTCTTGACGCTTGCTGAATAAG
<i>Csa7M446860</i>	F: CTGTTGCAGGAAGAGGAAGATC R: ATAGATTGCTGCAGCCTTTTG
<i>Csa4M538080</i>	F: GATTAGCACAGGAGTTGATGAA R: CAACTTCTCTGATAAGGCTTTGAG
<i>Csa2M365120</i>	F: CAAACTTCAAGCTTGAAGGCTC R: TCTCGACCATAACATTCGTGC

<i>Csa7M004700</i>	F: TAAAGGCACGGATGCAAGA R: CGGAACAAGCAAGTGAGCA
<i>Csa6M497150</i>	F: CTGGAATAGAGGAAGGAAGCC R: CCACCATGAAAAGAATGACTTGT
<i>Csa1M042550</i>	F: TCGCTCGTCAAGCATGAG R: GGATTCGTCCAGAGCTTGTTTA
<i>Csa2M250930</i>	F: CTCAAGGCAAAGATGCAGG R: CGGAACAAGCAAGAGAACAAG
<i>Csa5M157410</i>	F: TAGCACAGCATGAAGTGAACG R: CCGTAATCGTCTCATTTCAGC
<i>Csa5M537000</i>	F: CTGTTTATGCAAGTGCAAGGCT R: GGATCTGTCCATAGCTTGTTTAC
<i>Csa7M006260</i>	F: ACGGTCAGGTTCTGGAGGAT R: TTGAGACGTTGCAAGTTGC
<i>Csa4M047870</i>	F: CTGACACAAGCATTGAGTTTGA R: TTCCACACAAGATGAGCCAA
<i>Csa6M382990</i>	F: TCCCAAGTTATGCAGGCTG R: GGTAACCTTTCAGCTAAGTTTTGG
<i>Csa3M062600</i>	F: CATCAGTTGCAGAGGAGAGTTTTA B: TCGTCATGATACAGTGGTTCAAG
<i>Csa6M306320</i>	F: GGAGATAGTGCGAGAAGAAATGA B: CTTTTTCGGCTCAGTATCTCTTG
<i>Csa1M240580</i>	F: CGACATTGTTAGAGAGGAGATGAAC B: GTGCCACAAAACATTGTATTC
<i>Csa6M407060</i>	F: GCGCAAAATGAGGAAAATG B: ATGAGCCTGAACCTGAGCC
<i>Csa2M173060</i>	F: TCAGACCTGACGAACCAGAAT B: GTGCCCGGTAGCTTGTTCT
<i>Csa3M172990</i>	F: CTGCTCAGATGCGAGCAAT

	B: TGCTTTCATCATCATAAGCAGG
	F: CACAGCTAGCAAGGAAGAATTG
<i>Csa5M166470</i>	B: GCTCACCAGCTTCTTTTTTCAT
	F: ACCAAAAAGGAGACTTCTGCC
<i>Csa2M368870</i>	B: ATGCGAATGAGGGAGATGTT
	F: GATGCATGATGATGAGGTCA
<i>Csa3M821540</i>	B: TTCTCAAGTCCTTCGTGGC
	F: ATAGTATGGAGGGCCTGGT
<i>Csa1M675040</i>	B: GCTGGAAAATAATCATAACCAGTAGC
	F: CACACCATGAATGGTCCATCT
<i>Csa4M219360</i>	B: AGAAGGTCTCGGACTTGTTCATT
	F: TCCACGAGACTACCTACAATC
<i>Csa6a484600 (Cs.ACTIN)</i>	B: GTCATACGGTCAGCGAT

Table S3. List of predicted kinesin genes in cucumber

Gene ID	predicted protein length (aa)	<i>Arabidopsis</i> homologue	Gene ID	predicted protein length (aa)	<i>Arabidopsis</i> homologue
<i>Csa1M065980</i>	798	ATK1	<i>Csa7M446860</i>	685	KINESIN-13B
<i>Csa3M414070</i>	752	ATK3	<i>Csa4M538080</i>	765	AT5G06670
<i>Csa5M153100</i>	1119	AT1G63640	<i>Csa2M365120</i>	956	AT2G21300
<i>Csa4M064090</i>	1118	AT1G72250	<i>Csa7M004700</i>	1068	MKRP2
<i>Csa7M197290</i>	1195	KP1	<i>Csa6M497150</i>	698	AT3G49650
<i>Csa3M816090</i>	1374	AT1G18410	<i>Csa1M042550</i>	960	HINKEL
<i>Csa2M022260</i>	794	AT5G27550	<i>Csa2M250930</i>	1083	MKRP2
<i>Csa3M000080</i>	1265	ZWI	<i>Csa5M157410</i>	914	ARK3
<i>Csa1M495290</i>	1051	AT3G45850	<i>Csa5M537000</i>	938	TETRASPORE
<i>Csa4M219350</i>	554	AT3G10310	<i>Csa7M006260</i>	1027	AT2G21300
<i>Csa4M293320</i>	1049	AT2G37420	<i>Csa4M047870</i>	993	AT3G51150

<i>Csa6M000650</i>	2224	POK1	<i>Csa6M382990</i>	1091	MKRP1
<i>Csa1M025250</i>	1393	AT3G44050	<i>Csa3M062600</i>	1139	AT3G20150
<i>Csa3M777560</i>	1009	AT2G36200	<i>Csa6M306320</i>	805	KINESIN-13A
<i>Csa4M641550</i>	1050	FRA1	<i>Csa1M240580</i>	715	AT3G16060
<i>Csa2M237130</i>	2916	POK2	<i>Csa6M407060</i>	1060	ARK1
<i>Csa6M499030</i>	1276	KCA1/KAC1	<i>Csa2M173060</i>	843	PAKRP2
<i>Csa4M002000</i>	1022	AT2G47500	<i>Csa3M172990</i>	1342	KINESIN-12B
<i>Csa2M354040</i>	842	ZCF125	<i>Csa5M166470</i>	712	AT5G23910
<i>Csa3M891640</i>	1274	AT5G60930	<i>Csa2M368870</i>	870	AT1G20060
<i>Csa1M015820</i>	759	AT1G18550	<i>Csa3M821540</i>	1251	AT3G10180
<i>Csa1M573710</i>	631	AT5G27950	<i>Csa1M675040</i>	171	AT3G63480
<i>Csa1M568560</i>	1094	ATK4	<i>Csa4M219360</i>	537	ATK4
<i>Csa3M734250</i>	622	AT5G02370			

47 kinesin genes were identified in cucumber genome by using the conserved motor domains of *Arabidopsis*, rice and mouse as queries to blast in cucumber genome database, and all these kinesins have corresponding homologues in *Arabidopsis*.

Table S4. Twelve cucumber kinesin genes showed the peak expressions in the rapid cell division phase (before 3 DAA) or cell expansion phase (after 5 DAA)

peak expressions are induced in rapid cell division phase (before 3 DAA)		peak expressions are induced in rapid cell expansion phase (after 5 DAA)	
Gene ID	<i>Arabidopsis</i> homologue	Gene ID	<i>Arabidopsis</i> homologue
<i>Csa3M816090</i>	AT1G18410	<i>Csa1M495290</i>	AT3G45850
<i>Csa6M499030</i>	KCA1/KAC1	<i>Csa7M446860</i>	KINESIN-13B
<i>Csa4M002000</i>	AT2G47500		
<i>Csa1M568560</i>	ATK4		
<i>Csa1M042550</i>	HINKEL		

<i>Csa2M250930</i>	MKRP2
<i>Csa5M157410</i>	ARK3
<i>Csa6M382990</i>	MKRP1
<i>Csa3M062600</i>	AT3G20150
<i>Csa5M166470</i>	AT5G23910

Table S5. A predicted chloroplast transit peptides (cTP) in N-terminus of CsKF2

Name	Length	Score	chloroplast transit peptides (cTP)	Score for the suggested cleavage site	cTP- length
CsKF2	1139 aa	0.569	Yes	-0.412	1 aa-38 aa

A chloroplast transit peptides (cTP) locating in CsKF2-N terminus (1 aa – 38 aa) was predicted by ChloroP 1.1 Server at <http://www.cbs.dtu.dk/services/ChloroP/>.