

Table 1 Suppl. Primer sequences used for quantitative reverse transcription PCR analysis.

Forward primer	Sequence	Reverse primer	Sequence
<i>β-actin-F</i>	CCGACCGTATGAGCAAGGAAA	<i>β-actin-R</i>	TTCCTGTGGACAATGGATGGA
<i>CsCBL1F</i>	ATCGGCAGCAAGCTTTGTTC	<i>CsCBL1R</i>	TGGACAGTGGTGATCAAAGC
<i>CsCBL5F</i>	TGGAAGGAATTTGCGGGAAG	<i>CsCBL5R</i>	TTCAGTGTGCAGCACAAAGC
<i>CsCBL7F</i>	GCAAATGCTGATTGCGCTTC	<i>CsCBL7R</i>	TTGCCATCCTGGTTCACATC
<i>CsCBL8F</i>	AAGATGTGTTTGCCAGCTG	<i>CsCBL8R</i>	TTGATTGTACCGGCCACAC
<i>CsCIPK1F</i>	ACACCCAACCCCAAGAAAAC	<i>CsCIPK1R</i>	TTTTTCTGGCGTTGCAGGTG
<i>CsCIPK2F</i>	ATTTTGGGCTGAGTGC GTT	<i>CsCIPK2R</i>	AACTTCGGGCGCAACATAAG
<i>CsCIPK3F</i>	TGTGAATAGCGCCA ACTTGC	<i>CsCIPK3R</i>	TGCAGGAGATGACGTTAGGTTT
<i>CsCIPK4F</i>	TGCAGCAACAACAGGATCAG	<i>CsCIPK4R</i>	TGCTGCTGTTCTTGTGCTTC
<i>CsCIPK9F</i>	AAACGGAGGCGTTTGAAGG	<i>CsCIPK9R</i>	TTCTTCGCCAATTGTTCCG
<i>CsCIPK13F</i>	TATCTGGTCTTGTGGCGTGATC	<i>CsCIPK13R</i>	TGCGCACATCAGCTGAAAAC

Table 2 Suppl. Details of synteny analysis of *Citrus sinensis* calcineurin B-like proteins (*CsCBLs*) and calcineurin B-like protein interacting protein kinases (*CsCDPKs*) between *Arabidopsis thaliana* and *Citrus sinensis*.

	Location	Syntenic relationships
<i>CsCBL4</i>	chr4	Cs4g18590.3 == <i>AtCBL10</i> , AT4G33000 NC_003075.7 rna-NM_119454.2
<i>CsCBL5</i>	chr5	Cs5g02080.1 == <i>AtCBL8</i> , AT1G64480 NC_003070.9 rna-NM_001334162.1
<i>CsCBL7</i>	chr5	Cs5g07690.1 == <i>AtCBL1</i> , AT4G17615 NC_003075.7 rna-NM_117870.4
	chr5	Cs5g07690.1 == <i>AtCBL9</i> , AT5G47100 NC_003076.8 rna-NM_001344708.1
<i>CsCIPK3</i>	chr2	Cs2g08190.5 == <i>AtCIPK23</i> , AT1G30270 NC_003070.9 rna-NM_102766.6
<i>CsCIPK4</i>	chr2	Cs2g09340.1 == <i>AtCIPK15</i> , AT5G01810 NC_003076.8 rna-NM_120259.4
<i>CsCIPK5</i>	chr2	Cs2g09400.1 == <i>AtCIPK11</i> , AT2G30360 NC_003071.7 rna-NM_128589.2
	chr2	Cs2g09400.1 == <i>AtCIPK14</i> , AT5G01820, NC_003076.8 rna-NM_120260.3
<i>CsCIPK6</i>	chr2	Cs2g28990.1 == <i>AtCIPK3</i> , AT2G26980 NC_003071.7 rna-NM_179763.4
<i>CsCIPK7</i>	Chr3	Cs3g16840.1 == <i>AtCIPK8</i> , AT4G24400 NC_003075.7 rna-NM_118573.4
<i>CsCIPK8</i>	Chr4	Cs4g01450.1 == <i>AtCIPK6</i> , AT4G30960 NC_003075.7 rna-NM_119244.3
<i>CsCIPK10</i>	Chr6	Cs6g09730.1 == <i>AtCIPK15</i> , AT5G01810 NC_003076.8 rna-NM_120259.4
<i>CsCIPK11</i>	Chr6	Cs6g09770.1 == <i>AtCIPK22</i> , AT2G38490 NC_003071.7 rna-NM_129406.4
	Chr6	Cs6g09770.1 == <i>AtCIPK14</i> , AT5G01820 NC_003076.8 rna-NM_120260.3
<i>CsCIPK12</i>	Chr7	Cs7g06310.1 == <i>AtCIPK16</i> , AT2G25090 NC_003071.7 rna-NM_128066.4
	Chr7	Cs7g06310.1 == <i>AtCIPK5</i> , AT5G10930 NC_003076.8 rna-NM_121131.3
	Chr7	Cs7g06310.1 == <i>AtCIPK25</i> , AT5G25110 NC_003076.8 rna-NM_122420.2
<i>CsCIPK14</i>	Chr9	Cs9g01260.2 == <i>AtCIPK17</i> , AT1G48260 NC_003070.9 rna-NM_001333316.1
	Chr9	Cs9g01260.2 == <i>AtCIPK1</i> , AT3G17510 NC_003074.8 rna-NM_112631.3
<i>CsCIPK15</i>	Chr9	Cs9g08000.1 == <i>AtCIPK7</i> , AT3G23000 NC_003074.8 rna-NM_113200.3
	Chr9	Cs9g08000.1 == <i>AtCIPK4</i> , AT4G14580 NC_003075.7 rna-NM_117538.2

Table 3 Suppl. Fragments per kilobase of exon model per million mapped reads measured in each treatment.

Gene name	gene_id	W_Non1	W_Non2	W_Non3	W_AMF	W_AMF	W_AMF	D_Non1	D_Non2	D_Non3	D_AMF	D_AMF	D_AMF
				1	2	3					1	2	3
CsCBL1	Cs1g18400.1	123.279	147.488	149.735	17.1715	25.3243	15.8012	140.744	119.147	130.585	15.6449	11.7953	14.4456
		89	07	34	28	66	39	54	92	97	51	04	84
CsCBL2	Cs2g01320.1	9.77020	11.1381	11.6095	8.98011	8.75728	7.96434	9.14805	9.93580	10.9704	8.37920	10.1891	8.35893
		7	35	89	13	1	59	48	5	89	33	17	78
CsCBL3	Cs4g08230.1	68.6645	75.1892	74.7243	65.9552	74.8744	57.1303	80.3181	63.9072	69.6254	63.9301	56.0605	56.3072
		11	88	96	6	92	96	02	69	01		18	58
CsCBL4	Cs4g18590.3	13.2144	14.6935	13.9043	24.4152	24.9146	17.1412	12.4038	10.3652	10.9201	19.9385	16.7720	15.4299
		62	59	62	72	28	19	05	45	96	28	57	51
CsCBL5	Cs5g02080.1	38.4233	46.9138	35.0579	49.9289	64.8788	59.7339	48.1296	34.6590	31.8555	50.9016	53.9077	40.9004
		93	49	56	61	3	04	33	23	35	38	49	77
CsCBL6	Cs5g02090.1	0	0	0.07740	0.51212	0.16326	0.07974	0	0	0	0.06505	0.06793	0.12184
				47	04	53	05				63	4	46
CsCBL7	Cs5g07690.1	38.4984	38.9111	39.279	51.8052	45.1472	51.6382	54.0898	40.7177	40.8362	46.7681	42.4154	49.757
		39	95		47	66	75	17	79	8	38	11	
CsCBL8	orange1.1t02	106.114	136.199	74.4151	67.8863	83.7327	59.5223	59.7656	59.3869	65.4217	54.4640	45.1138	60.2942
	723.1	73	64	11	83	73	7	02	06	78	35	55	4
CsCIPK1	Cs2g04710.1	321.440	341.855	359.974	134.885	123.349	125.540	318.658	349.434	413.738	125.811	128.517	153.906
		42	12	12	63	95	59	23	2	03	48	63	6
CsCIPK2	Cs2g04720.1	0.20034	0.38688	0.27414	0.58300	0.50595	0.74134	0.23384	0.21560	0.38559	0.40321	0.93233	0.78216
		44	49	51	18	89	7	61	63	38	86	49	34
CsCIPK3	Cs2g08190.5	200.546	228.245	207.961	88.8532	109.872	105.454	224.734	215.186	195.595	103.826	118.304	110.609
		68	98	99	77	35	14	34	29	14	73	68	36
CsCIPK4	Cs2g09340.1	23.7995	23.4386	28.7745	26.0165	33.9596	26.9507	26.4848	28.4381	25.6919	28.9184	30.0702	29.6175
		98	28	48	72	36	8	51	56	9	62	17	28
CsCIPK5	Cs2g09400.1	205.466	203.537	122.375	164.690	203.727	333.015	177.801	124.506	123.067	166.356	177.919	221.890
		95	12	22	23	23	78	68	76	21	57	09	35
CsCIPK6	Cs2g28990.1	43.8070	45.3223	43.8201	27.3157	28.8500	25.3813	44.7008	39.6764	45.5250	22.5644	25.4674	23.5775
		58	13	33	51	23	12	92	22	96	29	49	98
CsCIPK7	Cs3g16840.1	8.44814	8.47698	10.3772	8.29065	9.10137	8.54987	8.67388	8.69059	10.4582	9.20794	9.29405	9.18034
		02	35	39	09	35	87	7	98	16	87	17	15
CsCIPK8	Cs4g01450.1	127.558	113.785	142.009	144.839	116.204	107.023	139.923	134.044	139.189	115.769	143.724	104.440
		63	04	49	2	86	69	16	15	51	69	21	79
CsCIPK9	Cs4g17990.1	53.0322	57.7017	59.6075	34.8073	39.3674	32.3446	48.1268	54.0582	56.2051	30.2573	32.8389	32.8403
		88	4	28	69	14	95	23	95	62	96	07	75
CsCIPK1	Cs6g09730.1	50.8560	45.3126	46.3155	67.9560	72.7761	66.8368	51.0317	53.6297	53.5085	59.2526	59.6221	63.6921
0		95	62	33	02	39	9	89	48	86	18	47	41
CsCIPK1	Cs6g09770.1	25.3071	24.9983	19.5738	25.4058	29.4787	47.9068	25.4099	15.1915	16.5283	30.5553	38.9316	47.4147
1		93	73	9	15	95	94	49	93	42	31	8	4
CsCIPK1	Cs7g06310.1	129.128	140.919	198.166	34.5527	48.2715	105.880	118.476	160.499	148.159	58.1360	78.3933	102.805
2		64	94	12	99	39	09	86	79	35	17	67	47
CsCIPK1	Cs7g30070.1	2.40499	1.57086	3.26672	8.63382	7.94301	7.16685	2.85532	1.83965	2.50623	6.33009	5.89334	7.30863
3		88	3	79	07	12	69	53	72	05	94	53	94
CsCIPK1	Cs9g01260.2	18.0445	15.2709	20.6452	29.5843	38.4113	32.6475	18.5702	20.5172	16.3264	21.8295	22.1300	20.7134
4		31	53	08	68	32	31	38	36	27	18	1	83
CsCIPK1	Cs9g08000.1	0	0	0	0	0	0	0	0	0	0	0	0
5													
CsCIPK1	orange1.1t00	4.02569	4.22906	5.17811	9.68420	11.0090	7.91644	6.70372	7.16284	7.77624	6.78271	9.52423	12.3132
6	555.2	64	58	99	71	56	4	71	63	82	94	66	17
CsCIPK1	orange1.1t02	1.25974	1.44646	4.25125	3.79796	2.45669	1.94979	1.02663	2.04578	2.11480	1.66416	1.91666	3.23141
7	758.1	62	7	77	13	47	8	15	07	2	15	2	43

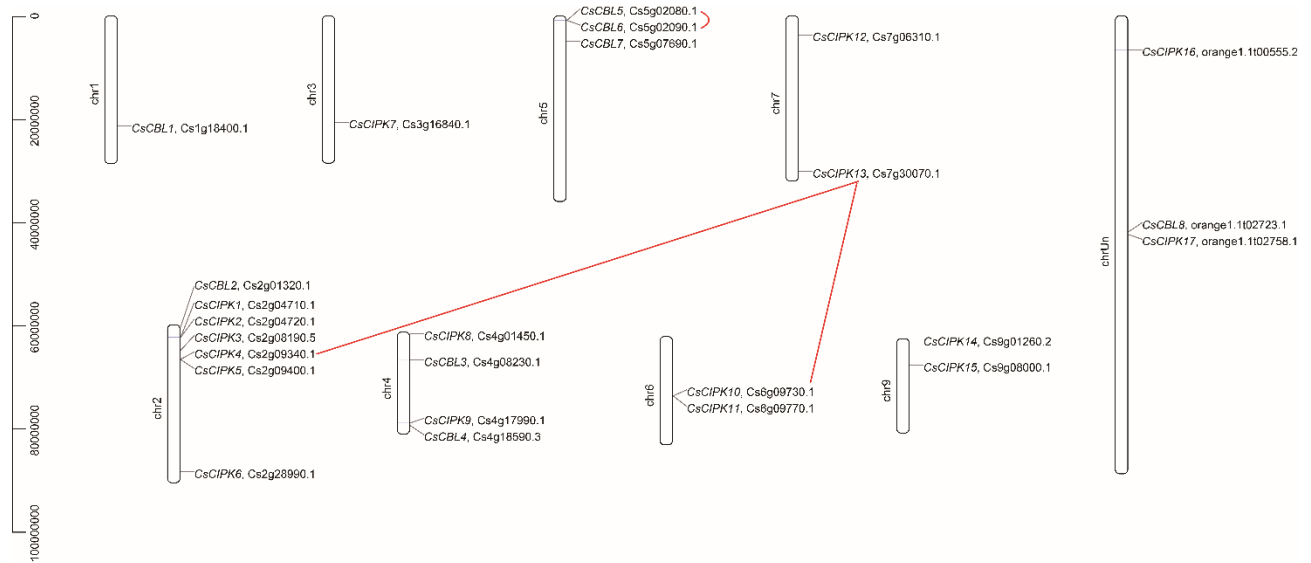


Fig. 1 Suppl. Chromosomal distribution of the *Citrus sinensis* calcineurin B-like proteins (CsCBLs) and calcineurin B-like protein interacting protein kinases (CsCIPKs). Chromosome numbers are provided at the top of each chromosome together with the approximate size. The CsCBLs and CsCIPKs were named based on their order on the chromosomes. Red lines indicate gene clusters with tandem duplications.

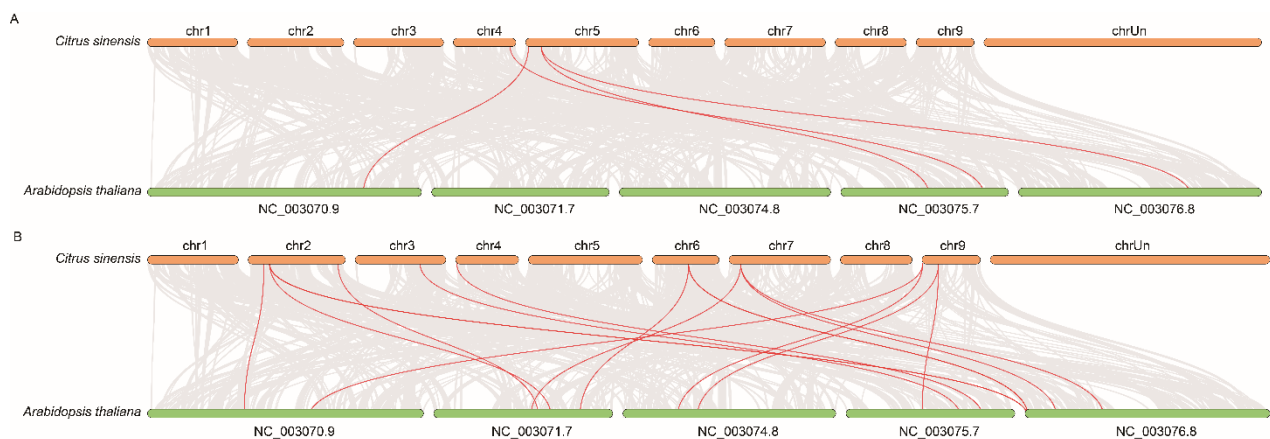


Fig. 2 Suppl. Synteny analysis of *Citrus sinensis* calcineurin B-like proteins (CsCBLs, A) and calcineurin B-like protein interacting protein kinases (CsCIPKs, B) between *Arabidopsis thaliana* and *Citrus sinensis*. Gray lines at the background indicate collinear blocks within *A. thaliana* and *C. sinensis* genomes, whereas red lines highlight the syntenic CBL and CIPK gene pairs, respectively.

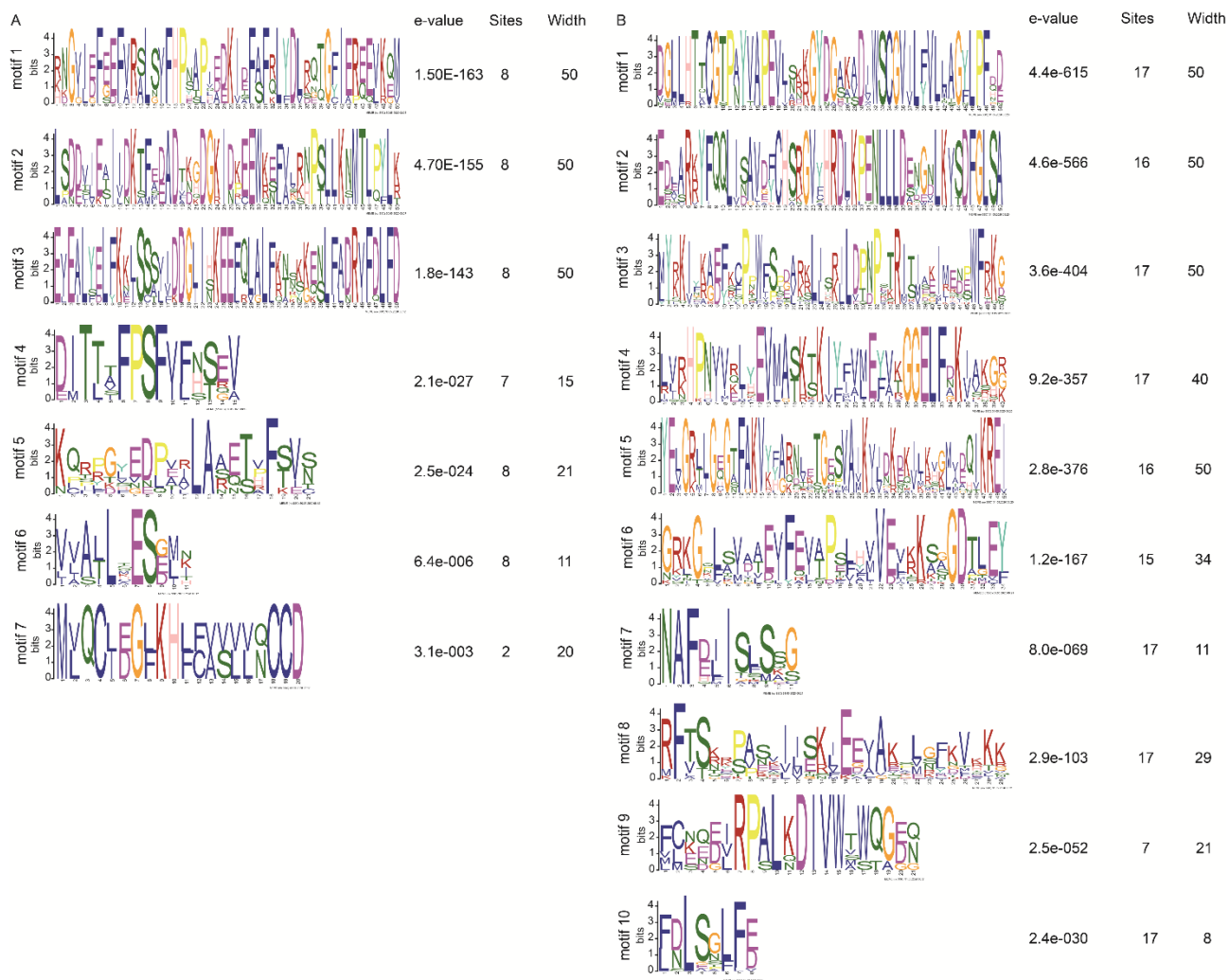


Fig. 3 Suppl. Analysis and distribution of conserved motifs in *Citrus sinensis* calcineurin B-like proteins (CsCBLs) and calcineurin B-like protein interacting protein kinases (CsCDPKs).