

**Table S1.** Primer used for cloning and RT-qPCR analysis.

Primer Name	Sequence	Analysis
<i>CiAct2</i> for	5'-CCAAATCCAGCTCATCAGTCG-3'	RT-qPCR
<i>CiAct2</i> rev	5'-TCTTTCGGCTCCGATGGRGAT-3'	RT-qPCR
<i>CiTub2</i> for	5'-GCACGGCATTGATGTGACC-3'	RT-qPCR
<i>CiTub2</i> rev	5'-GAACAACCTCCCGCCACT-3'	RT-qPCR
<i>AtXTH29-3'</i> clonefor	5'-TGGTATCGTCGTCGCTTTCT-3'	Cloning
<i>AtXTH29-3'</i> clonerev	5'- GTCCAGTATCTCTAAACCGG-3'	Cloning
<i>CiXTH29RT</i> for	5'-TGATAAAGTTGCCAGGAGCG-3'	RT-qPCR
<i>CiXTH29RT</i> rev	5'-AGGCTTTCCTTCTAGGTTCC-3'	RT-qPCR
<i>CsLEA4</i> for	5'-CGGCTTGGGTATGCTAATGT-3'	RT-qPCR
<i>CsLEA4</i> rev	5'- CGTCAAGGCAAGAAAAATTG -3'	RT-qPCR

Descriptions	Graphic Summary	Alignments	Taxonomy					
Sequences producing significant alignments								
Download Select columns Show 100								
select all 11 sequences selected								
GeneBank Graphics Distance tree of results MSA Viewer								
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per Ident	Pos. Len	Accession
Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase 29 (XTH29) mRNA	Arabidopsis thal.	1258	1258	100%	0.0	89.71%	1383	NM_118617.3
Arabidopsis thaliana clone G103022 putative xyloglucan endo-transglucosylase (AtXTH29) mRNA contig	Arabidopsis thal.	1258	1258	100%	0.0	89.71%	1105	AY133103.1
Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase 29 (XTH29) mRNA	Arabidopsis thal.	1218	1218	98%	0.0	89.70%	1382	NM_001345113.3
PREDICTED Arabidopsis thaliana subunit beta (putative) xyloglucan endotransglucosylase/hydrolase (putative)	Arabidopsis thal.	1075	1075	100%	0.0	84.91%	1457	XM_002080792.2
PREDICTED Arabidopsis thaliana subunit beta (putative) xyloglucan endotransglucosylase/hydrolase (putative)	Arabidopsis thal.	1042	1042	96%	0.0	84.85%	1093	XM_001010874.1
PREDICTED Carosella rubella (putative) xyloglucan endotransglucosylase/hydrolase protein 29 (LOC170)	Carosella rubella	928	928	100%	0.0	80.68%	1242	XM_006289214.2
PREDICTED Carosella sativa (putative) xyloglucan endotransglucosylase/hydrolase protein 29 (LOC304)	Carosella sativa	926	926	100%	0.0	81.03%	1200	XM_015406371.2
PREDICTED Carosella sativa (putative) xyloglucan endotransglucosylase/hydrolase protein 29 (LOC304)	Carosella sativa	915	915	100%	0.0	80.74%	1234	XM_015405129.1
PREDICTED Carosella sativa (putative) xyloglucan endotransglucosylase/hydrolase protein 29 (LOC304)	Carosella sativa	911	911	99%	0.0	80.71%	1263	XM_015404548.1
PREDICTED Carosella rubella (putative) xyloglucan endotransglucosylase/hydrolase protein 29 (LOC170)	Carosella rubella	894	894	96%	0.0	80.75%	961	XM_023739312.1
PREDICTED Carosella sativa (putative) xyloglucan endotransglucosylase/hydrolase protein 29 (LOC304)	Carosella sativa	881	881	96%	0.0	80.60%	960	XM_018232729.1
Arabidopsis thaliana genome assembly chromosome 4	Arabidopsis thal.	833	1221	96%	0.0	89.99%	18725877	LR02545.3
Arabidopsis thaliana genome assembly chromosome 4	Arabidopsis thal.	833	1209	96%	0.0	89.59%	18104425	LR009773.1
Arabidopsis thaliana genome assembly chromosome 4	Arabidopsis thal.	833	1209	96%	0.0	89.58%	18579300	LR009708.1
Arabidopsis thaliana genome assembly chromosome 4	Arabidopsis thal.	833	1209	96%	0.0	89.56%	18619438	LR215055.1
Arabidopsis thaliana genome assembly chromosome 4	Arabidopsis thal.	833	1221	96%	0.0	89.50%	22582341	CG258885.3
Arabidopsis thaliana sylex001 0021 chromosome 4 sequence	Arabidopsis thal.	833	1209	96%	0.0	89.59%	70003804	CP5880747.1
Arabidopsis thaliana sylex001 0412 chromosome 4 sequence	Arabidopsis thal.	833	1209	96%	0.0	89.56%	20418078	CP5880737.1
Arabidopsis thaliana sylex001 0470 chromosome 4 sequence	Arabidopsis thal.	833	1209	96%	0.0	89.56%	30379551	CP5880731.1

A)

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

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GenPept

Graphics

Distance tree of results

Multiple alignment

MSA Viewer

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per Ident	Pos. Len	Accession
<input checked="" type="checkbox"/>	unnamed protein product (Arabidopsis thaliana)	Arabidopsis thal.	479	479	100%	3e-170	88.13%	279	CAI5335397.1
<input checked="" type="checkbox"/>	unnamed protein product (Arabidopsis thaliana)	Arabidopsis thal.	481	481	100%	1e-169	89.13%	343	CAA0365775.1
<input checked="" type="checkbox"/>	xyloglucan endotransglucosylase/hydrolase 29 (Arabidopsis thaliana)	Arabidopsis thal.	480	480	100%	3e-168	88.13%	357	NP_183838.1
<input checked="" type="checkbox"/>	Ghosech xyloglucanase family 16 (Arabidopsis suessii)	Arabidopsis sue.	480	480	100%	4e-168	88.13%	357	KAG7625217.1
<input checked="" type="checkbox"/>	xyloglucan endotransglucosylase C-terminal (Arabidopsis suessii)	Arabidopsis sue.	471	471	100%	2e-165	88.52%	357	KAG7540886.1
<input checked="" type="checkbox"/>	xyloglucan endotransglucosylase/hydrolase 29 (Arabidopsis thaliana)	Arabidopsis thal.	468	468	99%	3e-160	94.92%	283	NP_001229723.1
<input checked="" type="checkbox"/>	Ghosech xyloglucanase family 16 (Arabidopsis suessii)	Arabidopsis sue.	467	467	99%	4e-165	94.92%	283	KAG7625218.1
<input checked="" type="checkbox"/>	Ghosech xyloglucanase family 16 (Arabidopsis suessii)	Arabidopsis sue.	465	465	98%	9e-160	89.10%	255	KAG7625219.1
<input checked="" type="checkbox"/>	xyloglucan endotransglucosylase C-terminal (Arabidopsis suessii)	Arabidopsis sue.	456	456	96%	4e-161	88.41%	255	KAG7540887.1
<input checked="" type="checkbox"/>	PREDICTED <i>Carosella rubella</i> xyloglucan endotransglucosylase/hydrolase protein 29 (Carosella rubella)	Carosella rubella	445	445	100%	4e-155	82.21%	381	XP_010488431.1
<input checked="" type="checkbox"/>	xyloglucan endotransglucosylase C-terminal (Arabidopsis thaliana x Arabidopsis suessii)	Arabidopsis thal.	481	481	100%	1e-154	88.70%	1800	KAG7616246.1
<input checked="" type="checkbox"/>	PREDICTED <i>Carosella rubella</i> xyloglucan endotransglucosylase/hydrolase protein 29 (Carosella rubella)	Carosella rubella	443	443	100%	3e-154	91.34%	381	XP_010488473.1
<input checked="" type="checkbox"/>	PREDICTED <i>Carosella rubella</i> xyloglucan endotransglucosylase/hydrolase protein 29 (Carosella rubella)	Carosella rubella	441	441	98%	1e-153	91.74%	360	XP_010488762.1
<input checked="" type="checkbox"/>	unnamed protein product (Arabidopsis thaliana)	Arabidopsis thal.	439	439	100%	5e-153	86.66%	338	CAI8276102.1
<input checked="" type="checkbox"/>	<i>Carosella rubella</i> xyloglucan endotransglucosylase/hydrolase protein 29 (Carosella rubella)	Carosella rubella	438	438	100%	2e-152	91.81%	381	XP_005285078.1
<input checked="" type="checkbox"/>	<i>Carosella rubella</i> xyloglucan endotransglucosylase/hydrolase protein 29 (Carosella rubella)	Carosella rubella	438	438	100%	2e-152	90.65%	357	XP_005285078.1
<input checked="" type="checkbox"/>	unnamed protein product (Microthloexia reticulata)	Microthloexia ret.	438	438	100%	2e-152	88.51%	364	CAA2528827.1
<input checked="" type="checkbox"/>	xyloglucan endotransglucosylase/hydrolase protein 29 (Carosella rubella)	Carosella rubella	432	432	100%	3e-151	88.70%	284	KAG7544458.1

B)

**Figure S1.** Comparison of *CiXTH29* nucleotide (A) and amino acid (B) sequence with all the other sequences present in BLAST database.

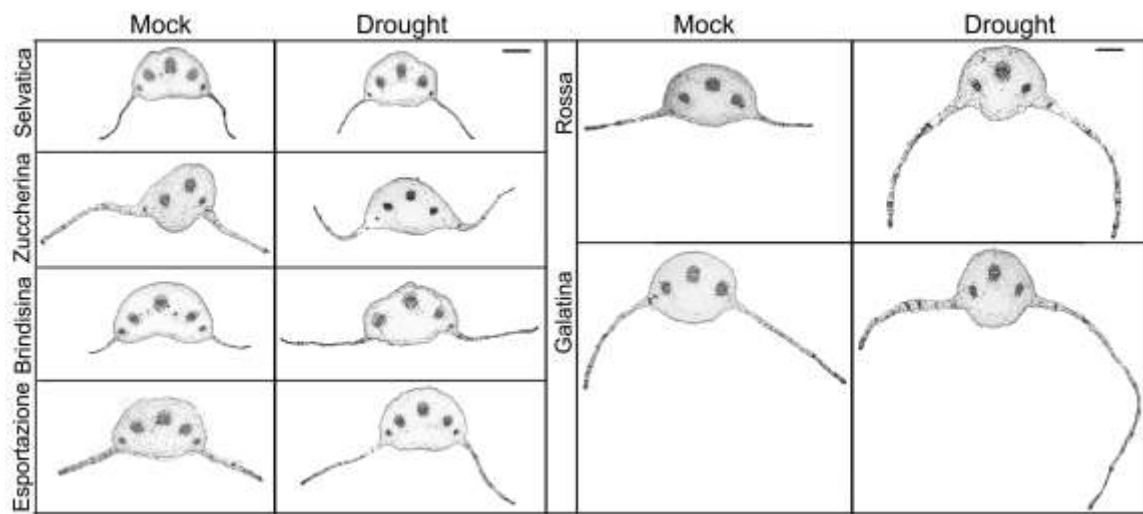
Descriptions									
Sequences producing significant alignments									
Download Select columns Show 100									
Select all 0 sequences selected									
GenBank Genomes Database RefSeq NCBI									
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident.	Acc. Len	Accession	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	35272351	<a href="#">L10102542.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	35401407	<a href="#">L10099745.2</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	35044433	<a href="#">L10099779.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	29179729	<a href="#">L10099783.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	29653075	<a href="#">L10099758.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	35243396	<a href="#">L10099750.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	35045930	<a href="#">L10210352.1</a>	
<input type="checkbox"/> Arabidopsis thaliana Late embryogenesis abundant protein, group 1 protein (AtLEA-1), mRNA	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	858	<a href="#">NM_102991.4</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	33709400	<a href="#">X0291810.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	33225756	<a href="#">X0291805.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	33394868	<a href="#">X0291800.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	32900767	<a href="#">X0291791.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	33352777	<a href="#">X0291784.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	33064871	<a href="#">X0291788.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	33630734	<a href="#">X0291790.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	34277122	<a href="#">X0291785.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	33155062	<a href="#">X0291730.1</a>	
<input type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 1	<a href="#">Arabidopsis thal</a>	113	113	92%	3e-21	95.46%	33341246	<a href="#">X0291741.1</a>	

A)

Download GenBank Graphics									
Arabidopsis thaliana Late embryogenesis abundant protein, group 1 protein (AtLEA4-1), mRNA									
Sequence ID: <a href="#">NM_102991.4</a> Length: 859 Number of Matches: 1									
Range 1: 159 to 223 GenBank Graphics									
Score	Expect	Identities	Gaps	Strand					
113 bits(125)	3e-21	64/65(98%)	0/65(0%)	Plus/Plus					
Query	6	GAGGAGGAAGAGATAGCGCACCAACGGAGGAAGGCGAAGGAAGCGAGAGCGAATATGGAT					65		
Sbjct	159	GAGGAGGAAGAGATAGCGCACCAACGGAGGAAGGCGAAGGAAGCGAGAGCGAATATGGAT					218		
Query	66	ATTCA					70		
Sbjct	219	ATGCA					223		

B)

**Figure S2.** Comparison of *CiLEA4* nucleotide sequence with all the other sequences present in BLAST database (A). Alignment of *CiLEA4* PCR product (query) with *AtLEA4* (Sbjct) (B).



**Figure S3.** Bright field images of leaf lamina thin transverse section of 6-week-old chicory varieties in mock and drought stress conditions.

Scale bar = 1 mm.

**Table S2.** Validation of reference genes in *C. intybus*. Ct values of the candidate reference genes *CiAct2* and *CiTub2* in 6-week-old chicory plants kept for further 10 days with (Mock) or without watering (Drought). Ct values of the three biological replicates for the six studied varieties. Means  $\pm$  SD of single independent experiments and Coefficient of Variation (CV) are reported.

	Sample	CiAct2					CV	Total Mean	SD	CV	CiTub-2					CV	Total Mean	SD	CV
		Ct value	Experiment 1 mean	SD	Experiment Total Mean	SD					Ct Value	Experiment mean	SD	Experiment Total Mean	SD				
Solonica	Shoot CTRL1	24.63	25.0869667	0.2709958	24.7053333	0.48735248	0.81889648	24.5725599	0.091901	0.026522	26.96	26.4233333	0.51731248	26.52	0.36285378	0.01443755	26.1570279	1.38475158	0.05299994
	Shoot CTRL2	25.96									27.82								
	Shoot CTRL3	23.37									26.09								
	Drought stress1	24.46	24.33	0.2689865							26.6168667	0.36521572							
	Drought stress2	24.09									26.35								
Zucchena	Drought stress3	24.49									26.83								
	Shoot CTRL1	24.70	25.0533333	0.2366071	24.975	0.48928337	0.81633858				25.807	26.089	0.40289858	27.1245	1.218661744	0.04585112			
	Shoot CTRL2	25.76									26.64								
	Shoot CTRL3	25.22									25.76								
	Drought stress1	24.53	24.8869667	0.583685							26.317	26.16	0.40260224						
Dondara	Drought stress2	24.59									26.569								
	Drought stress3	25.57									27.63								
	Shoot CTRL1	24.1	24.48	0.4687217	24.8869667	0.62944762	0.62525238				26.74	26.8689667	0.142118	27.086	0.01834367	0.002882517			
	Shoot CTRL2	24.36									26.94								
	Shoot CTRL3	23.81									27.01								
Ergasilime	Drought stress1	25.86	25.2833333	0.3437217							27.93	27.2753333	0.81019576						
	Drought stress2	24.76									26.238								
	Drought stress3	23.21									27.06								
	Shoot CTRL1	24.94	25.9869667	0.283784	24.8733333	0.77942714	0.85158968				25.718	24.881	0.73856278	26.035	1.43026195	0.05435622			
	Shoot CTRL2	23.68									24.36								
Rome	Shoot CTRL3	24.24									24.5								
	Drought stress1	25.59	25.36	0.153648							26.473	27.261	0.83617057						
	Drought stress2	28.4									27.86								
	Drought stress3	25.49									27.49								
	Shoot CTRL1	24.04	23.5133333	0.4742714	23.585	0.75968336	0.0369048				23.778	23.8609667	0.10677984	24.4263333	0.5852612	0.00396614			
Gaenna	Shoot CTRL2	23.12									24.869								
	Shoot CTRL3	23.30									24.1								
	Drought stress1	24.23	24.4766667	0.812318							25.21	24.85	0.51733088						
	Drought stress2	25.81									24.89								
	Drought stress3	25.17									24.25								
	Shoot CTRL1	24.54	23.89	0.35	24.185	0.3724255	0.81543281				24.37	24.2233333	0.18565146	25.7583333	1.68881131	0.06580036			
	Shoot CTRL2	23.89									24.17								
	Shoot CTRL3	23.64									24.43								
	Drought stress1	24.45	24.46	0.1571623							27.21	27.2833333	0.18876794						
	Drought stress2	24.34									27.13								
	Drought stress3	24.95									27.5								



**Figure S4.** 2.0% agarose gel showing *CiXTH29* amplicon sizes for the different variety. Lane L: 200bp DNA ladder, *CiXTH29* PCR amplimer (~ 100 bp) obtained from Selvatica (lane 1), Zuccherina di Trieste (lane 2), Brindisina (lane 3), Esportazione (lane 4), Rossa Italiana (lane 5) and Galatina (lane 6) variety cDNA.

Descriptions							
Sequences producing significant alignments							
Download Select columns Show 100							
select all 32 sequences selected							
GenBank Graphics Distance tree of results MSA Viewer							
Description	Scientific Name	Max Score	Total Score	Query Cover	E Value	Per. Ident.	Acc. Num.
<input checked="" type="checkbox"/> Arabidopsis thaliana cytochrome oxidase subunit 2 (COX2), mRNA	<a href="#">Arabidopsis thal.</a>	182	182	100%	4e-44	100.00%	1363 NM_118517.3
<input checked="" type="checkbox"/> Arabidopsis thaliana cytochrome oxidase subunit 2 (COX2), mRNA	<a href="#">Arabidopsis thal.</a>	182	182	100%	4e-44	100.00%	1105 AY130703.5
<input checked="" type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 4	<a href="#">Arabidopsis thal.</a>	110	183	100%	2e-22	100.00%	18725877 LUT02543.1
<input checked="" type="checkbox"/> Arabidopsis thaliana cytochrome oxidase subunit 2 (COX2), mRNA	<a href="#">Arabidopsis thal.</a>	110	110	80%	2e-22	100.00%	1202 M130131311.1
<input checked="" type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 4	<a href="#">Arabidopsis thal.</a>	110	183	100%	2e-22	100.00%	21038885 CP110263.1
<input checked="" type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 4	<a href="#">Arabidopsis thal.</a>	110	183	100%	2e-22	100.00%	27502341 GAC00005.1
<input checked="" type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 4	<a href="#">Arabidopsis thal.</a>	110	183	100%	2e-22	100.00%	22104501 CP081128.2
<input checked="" type="checkbox"/> Arabidopsis thaliana cytochrome oxidase subunit 2 (COX2), mRNA	<a href="#">Arabidopsis thal.</a>	110	183	100%	2e-22	100.00%	21570073 CP080027.1
<input checked="" type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 4	<a href="#">Arabidopsis thal.</a>	110	183	100%	2e-22	100.00%	18580056 CP002097.1
<input checked="" type="checkbox"/> Arabidopsis thaliana DNA, chromosome 4, contig fragment No. 48	<a href="#">Arabidopsis thal.</a>	110	183	100%	2e-22	100.00%	188075 AL351548.2
<input checked="" type="checkbox"/> Arabidopsis thaliana DNA, chromosome 4, BAC clone F13C5 (BAC clone)	<a href="#">Arabidopsis thal.</a>	110	183	100%	2e-22	100.00%	111911 AL021711.2
<input checked="" type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 4	<a href="#">Arabidopsis thal.</a>	104	172	100%	9e-21	98.31%	18785480 LRR0748.2
<input checked="" type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 4	<a href="#">Arabidopsis thal.</a>	104	172	100%	9e-21	98.31%	19104405 LRR00773.1
<input checked="" type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 4	<a href="#">Arabidopsis thal.</a>	104	172	100%	9e-21	98.31%	18578309 LRR08788.1
<input checked="" type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 4	<a href="#">Arabidopsis thal.</a>	104	172	100%	9e-21	98.31%	18371560 LRR09783.1
<input checked="" type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 4	<a href="#">Arabidopsis thal.</a>	104	172	100%	9e-21	98.31%	18786787 LRR09738.1
<input checked="" type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 4	<a href="#">Arabidopsis thal.</a>	104	172	100%	9e-21	98.31%	18802281 LRR09753.1
<input checked="" type="checkbox"/> Arabidopsis thaliana genome assembly, chromosome 4	<a href="#">Arabidopsis thal.</a>	104	172	100%	9e-21	98.31%	18019438 LRR15055.1

**Figure S5.** Comparison of *CiXTH29* amplimer nucleotide sequence with *AtXTH29* nucleotide sequence.

		mRNA amount	
		<i>CiXTH29</i>	
		Mock	Drought
		$2^{-\Delta Cq} \pm SD$	$2^{-\Delta Cq} \pm SD$
	Selvatica	0,00340 $\pm$ 0,00040	0,0023 $\pm$ 0,00020
	Zuccherina	0,00270 $\pm$ 0,000040	0,0038 $\pm$ 0,00070
	Brindisina	0,00051 $\pm$ 0,00009	0,00426 $\pm$ 0,00037
	Esportazione	0,00098 $\pm$ 0,00060	0,00532 $\pm$ 0,00033
	Rossa	0,00111 $\pm$ 0,00021	0,005322 $\pm$ 0,00067
	Galatina	0,00147 $\pm$ 0,00038	0,00716 $\pm$ 0,00067

**Figure S6.** Amplification output values of *CiXTH29* mRNAs in mock condition and after drought stress. The values are expressed as  $2^{-\Delta Cq} \pm SD$  and are considered as proportional to the amount of mRNA target according to [56].

		mRNA amount	
		<i>CiLEA4</i>	
		Mock	Drought
		$2^{-\Delta Cq} \pm SD$	$2^{-\Delta Cq} \pm SD$
	Selvatica	0,00390 ± 0,00113	0,00450 ± 0,00063
	Zuccherina	0,00171 ± 0,00038	0,00137 ± 0,00029
	Brindisina	0,00083 ± 0,00030	0,00475 ± 0,00123
	Esportazione	0,00075 ± 0,00012	0,00337 ± 0,00027
	Rossa	0,00047 ± 0,00005	0,00199 ± 0,00014
	Galatina	0,00096 ± 0,00015	0,00228 ± 0,00017

**Figure S7.** Amplification output values of *CiLEA4* mRNAs in mock condition and after drought stress. The values are expressed as  $2^{-\Delta Cq} \pm SD$  and are considered as proportional to the amount of mRNA target according to [56].