

Supplementary Materials: Comprehensive genome-wide analysis and expression pattern profiling of the *SIHVA22* gene family unravels their likely involvement in the abiotic stress adaptation of tomato

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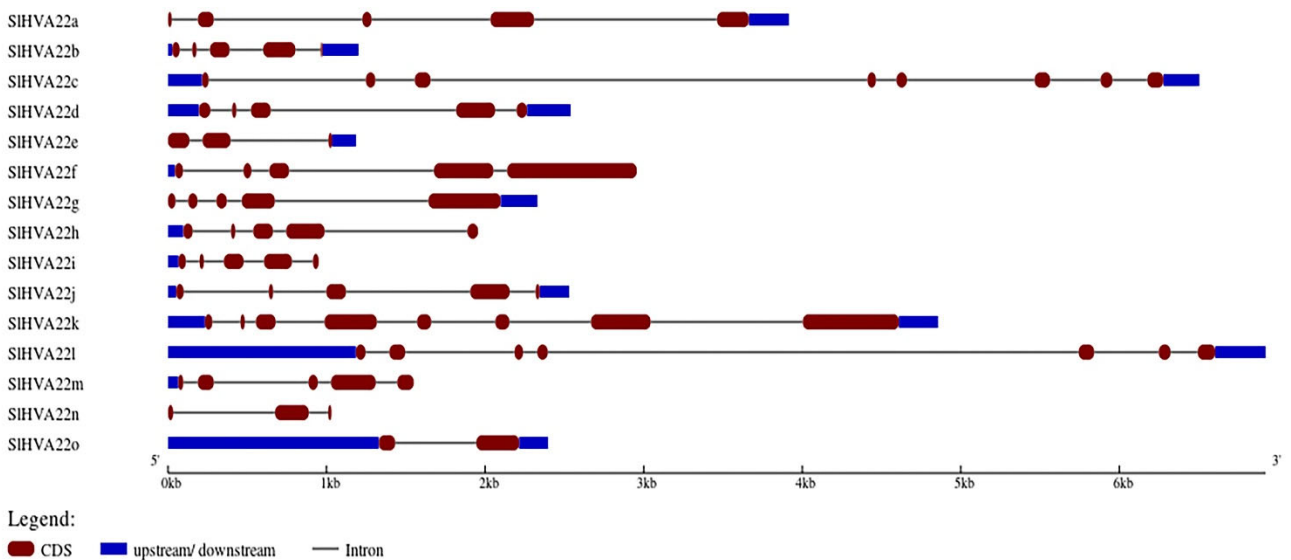


Figure S1. Schematic depiction of the exon-intron structure of *SIHVA22* genes. Dark red boxes represent exons, black lines indicate introns, and blue boxes denote untranslated regions.

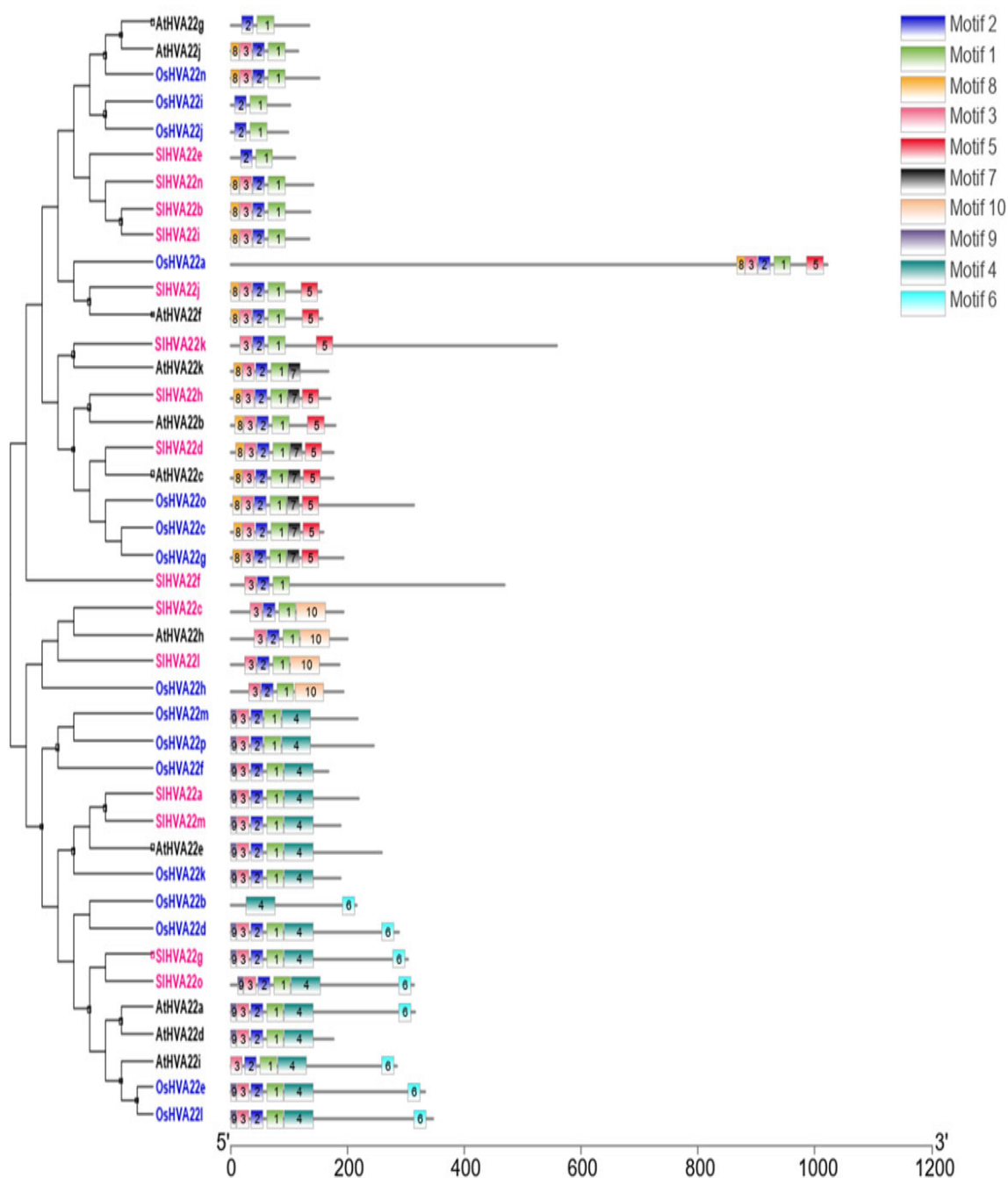


Figure S2. Conserved motif analysis of HVA22 proteins from tomato, *Arabidopsis* and rice. Motif 1 and motif 2 are located in the TB2/DP1/HVA22 domain. Different colored boxes signify different motifs, with the motif names in the center.

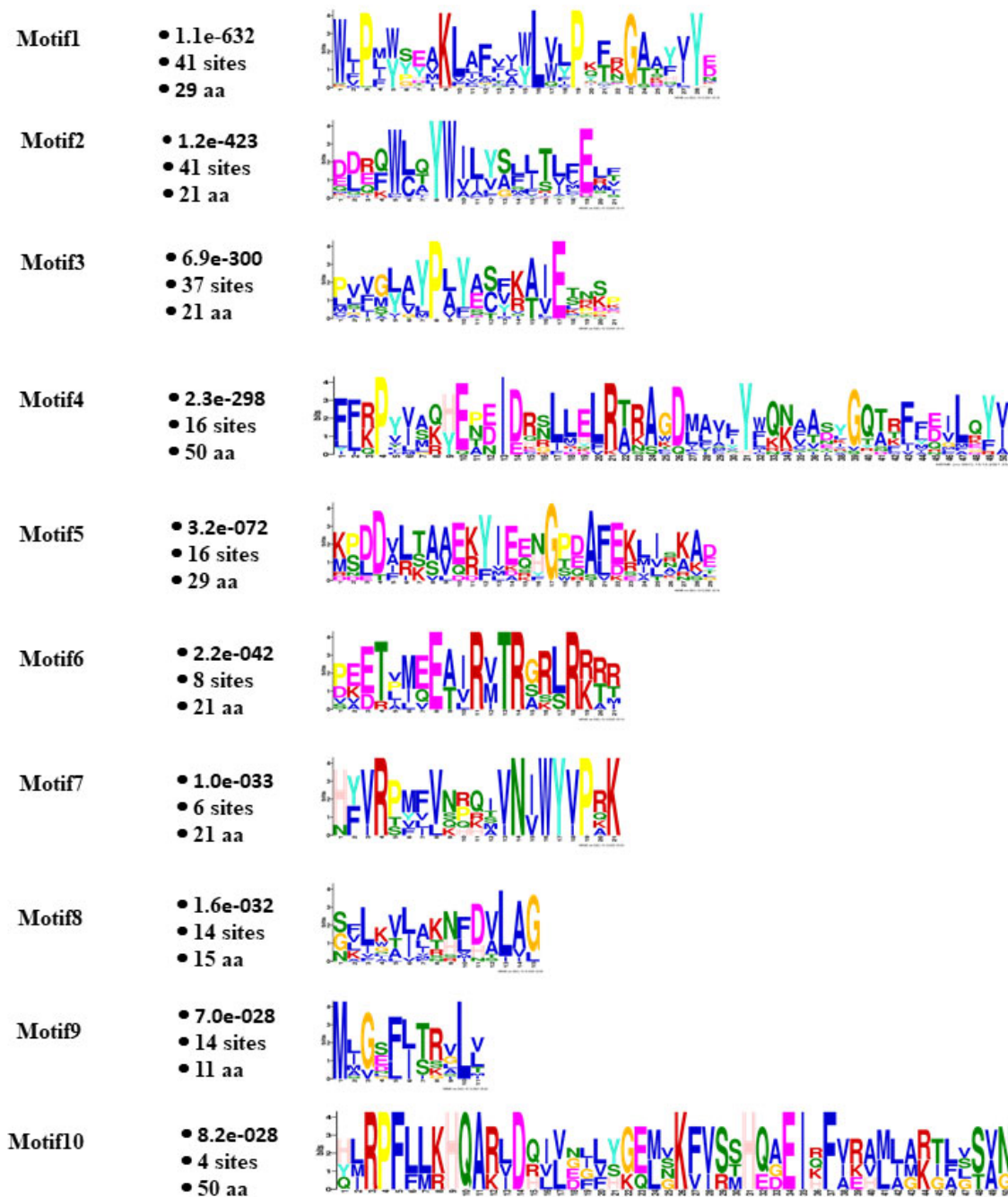


Figure S3. Overview of conserved motifs of HVA22 proteins from tomato, *Arabidopsis* and rice.

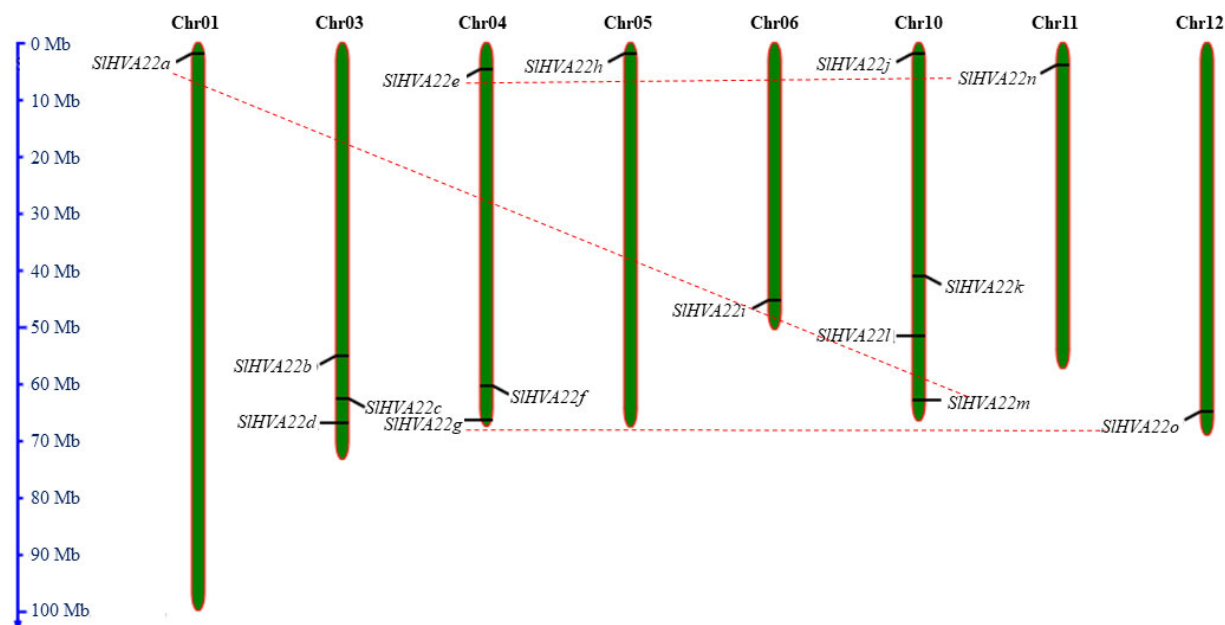


Figure S4. Chromosome locations of *SIHVA22* genes. The chromosome numbers are labelled at the top of chromosomes and the length of chromosomes can be estimated by the scale bar on the left shown in megabases (Mb). The duplicated gene pairs are linked by the red dotted lines.

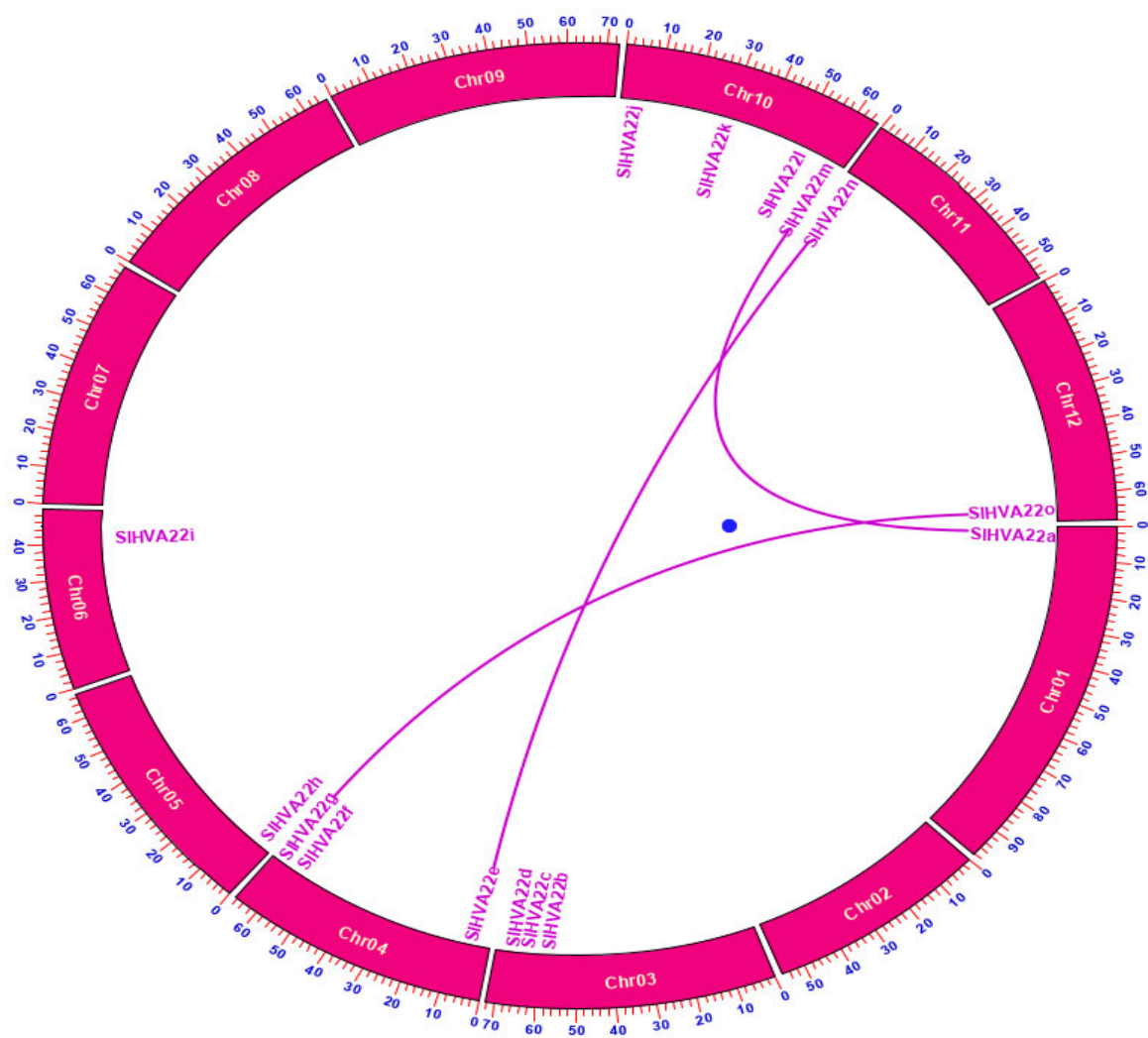


Figure S5. Gene duplication analysis of *HVA22* genes in tomato. Chromosome numbers and gene positions are indicated and the length of each chromosome is displayed on a megabase scale (Mb). The segmentally duplicated gene pairs are interconnected by pink red lines.

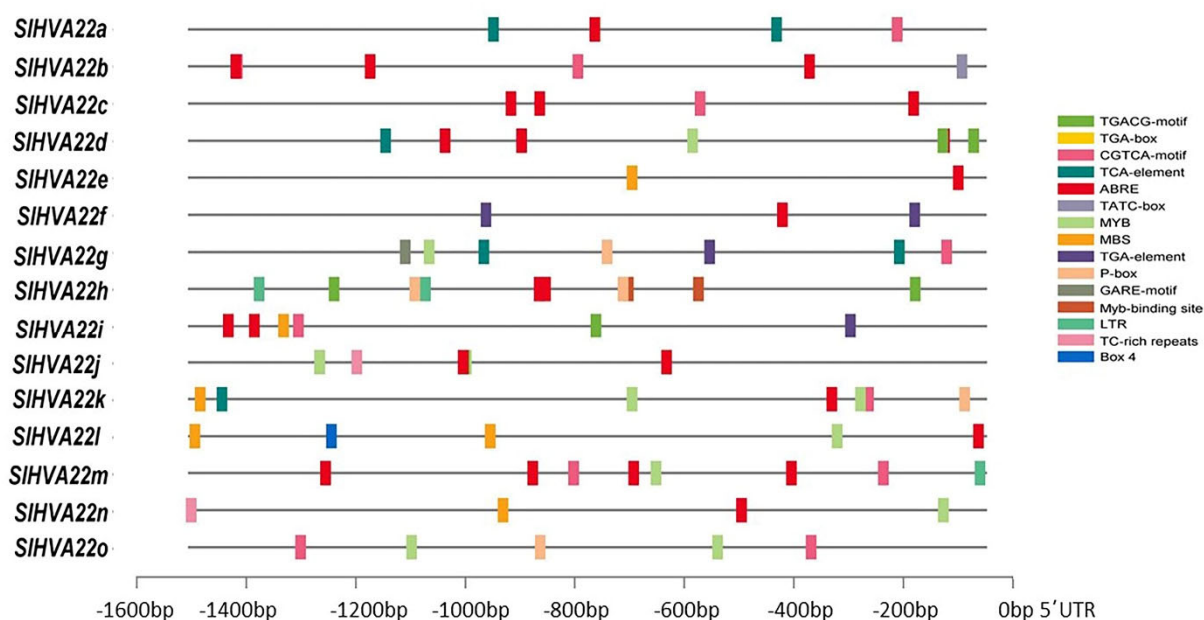


Figure S6. Predicted *cis*-acting elements in the promoters of *SIHVA22* genes. The identified elements are: drought-responsive MYB-binding site (MBS) and MYB elements, defense and stress-responsive elements (TC-rich repeats), jasmonic acid-responsive elements (CGTCA-motif), TCA-elements (related to the SA response), auxin responsive elements (TGA-element and TGA-box), ABA-responsive elements (ABRE), low-temperature-responsive elements (LTR), and P-box, GARE- and TATC-elements associated with GA response. The scale denotes the positions of cis-regulatory elements in regard to the translation start site (taken as +1 bp).

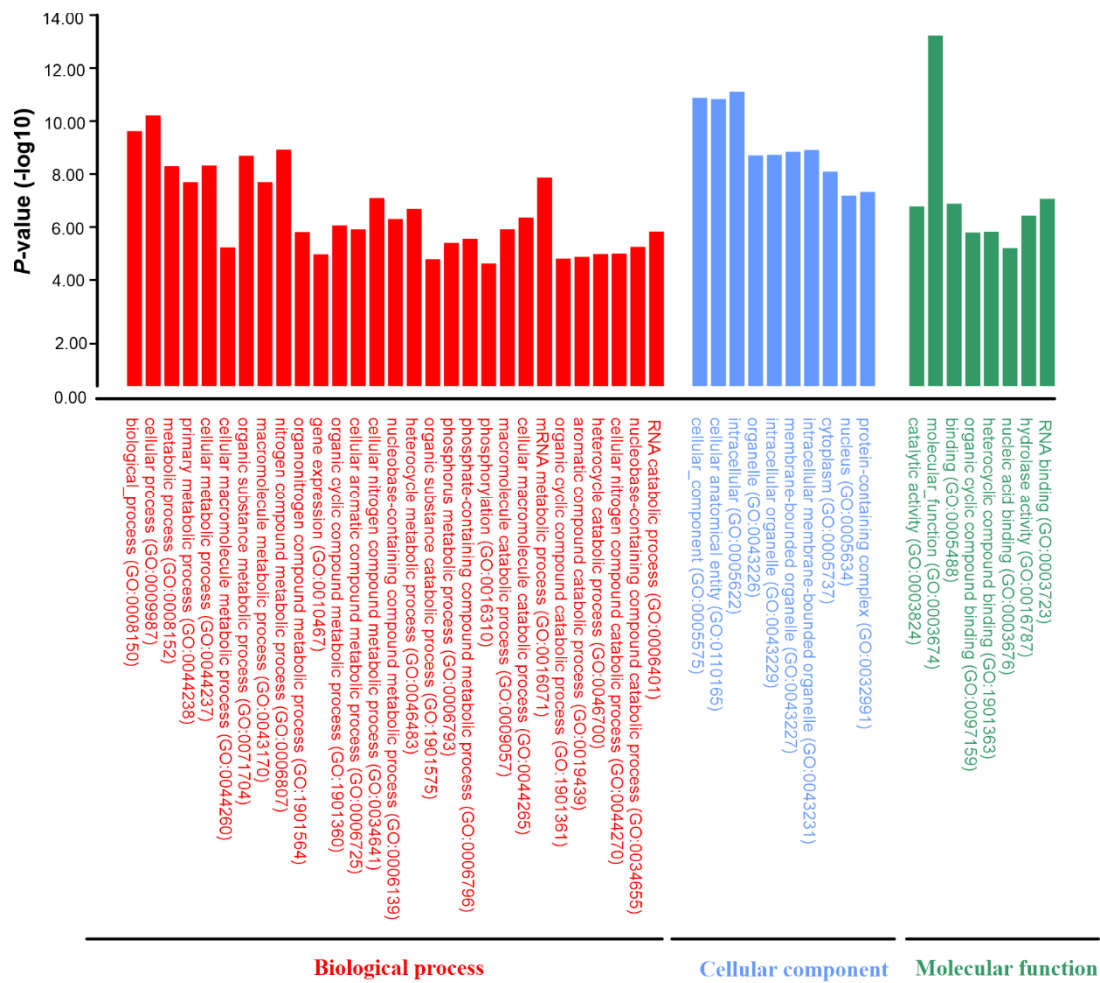


Figure S7. The enriched GO terms for co-expressed genes of four *SIHVA22* genes.

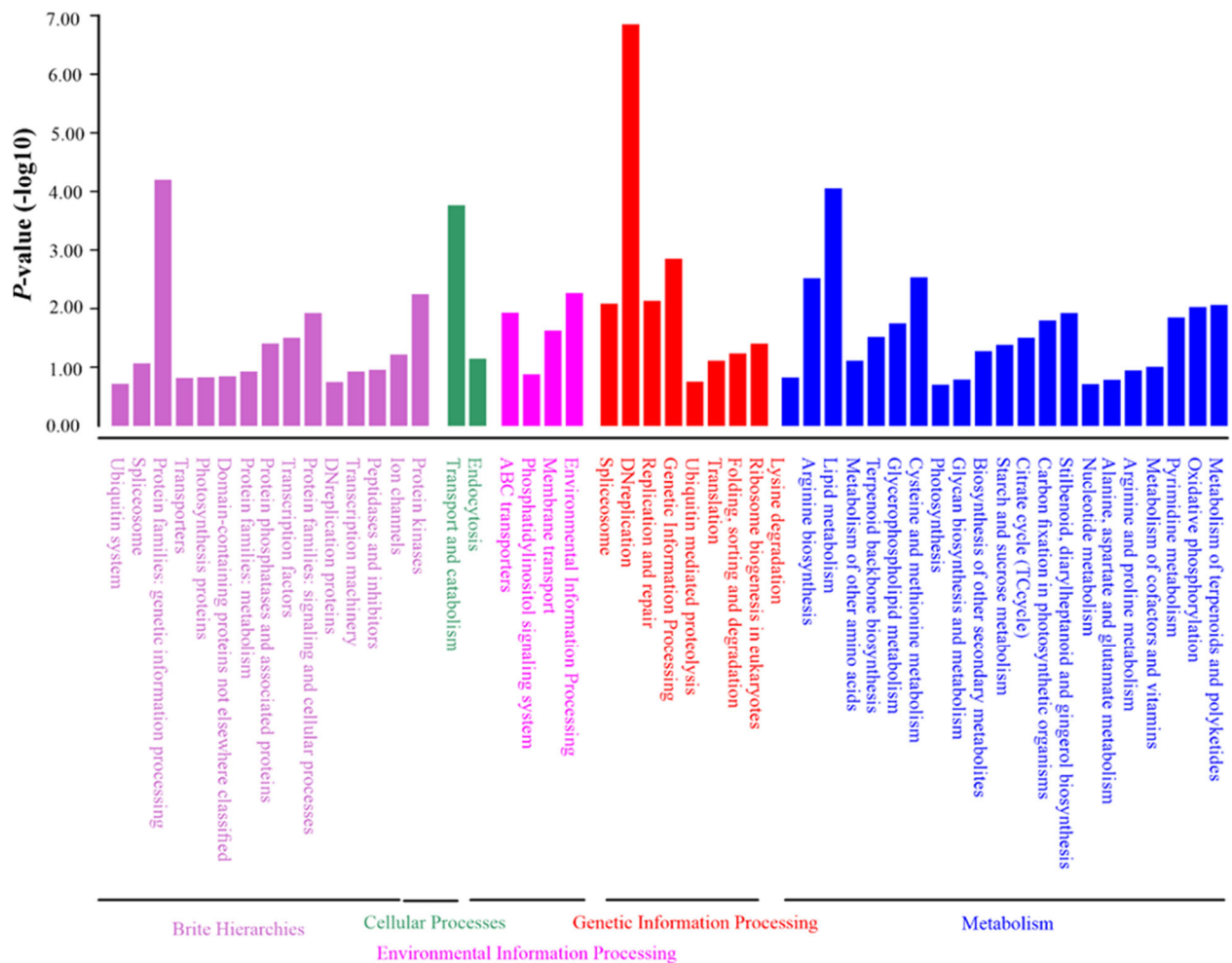


Figure S8. The biological pathways determined by KEGG analysis. The co-expressed genes of four *SIHVA22* genes having p-value less than 0.01 were subjected to KEGG analysis (see Figure 6).

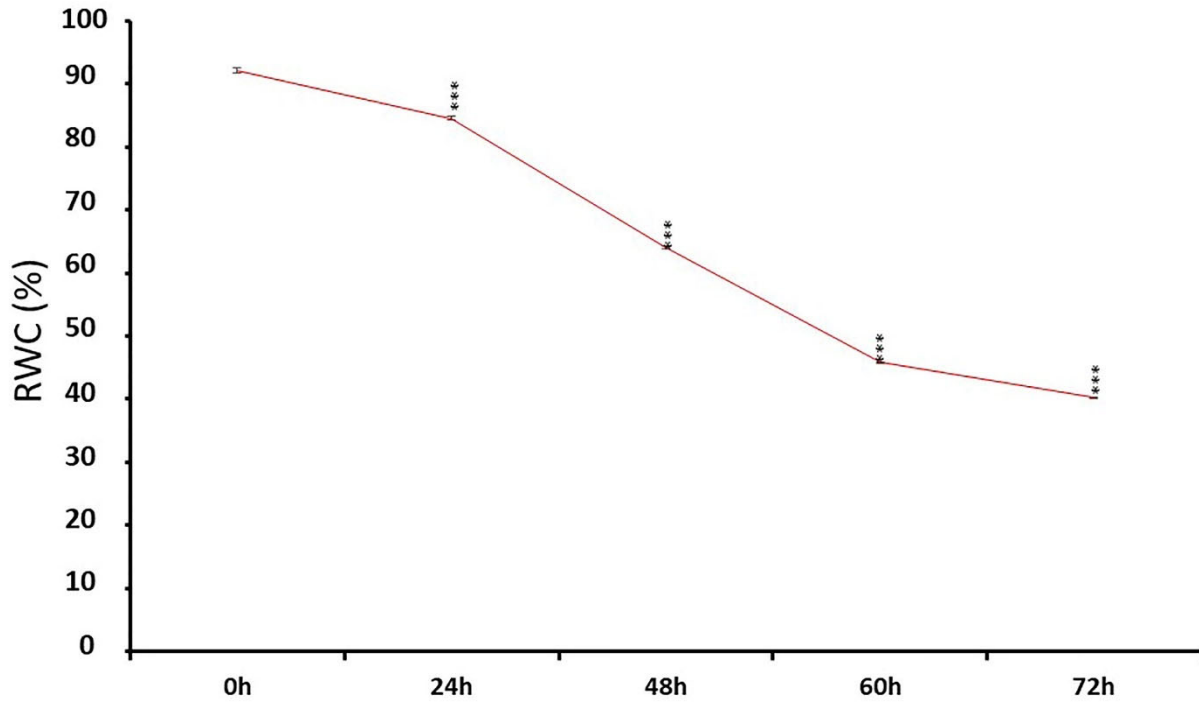


Figure S9. Measurement of relative water content (RWC) of leaf sampled at 0, 24, 48, 60 and 72h after the start of drought treatment. Error bars indicate standard deviations of the means of three independent biological replicates. The asterisk marks (* for p-value < 0.05, ** for p-value < 0.01, and *** for p-value < 0.001) analyzed using Student's *t*-tests denotes the significant differences between the samples (0h) and drought-treated samples.

Table S1. In silico analysis of the *HVA22* genes and corresponding proteins in tomato genome

Gene Name	Locus name	ORF (bp)	Chromosome No.	Protein					Subcellular Localization	No. of Introns
				Length (aa)	TB2/DP1/HVA2 2 domain Start-End (aa)	MW (kDa)	PI	GRAVY		
<i>SIHVA22a</i>	Solyc01g007780	663	1	220	19-97	25.80	9.35	-0.510	Nucleus	4
<i>SIHVA22b</i>	Solyc03g097420	411	3	136	24-98	15.84	9.37	0.210	Extracellular	4
<i>SIHVA22c</i>	Solyc03g110920	585	3	194	42-118	21.79	6.37	0.111	Endoplasmic reticulum	7
<i>SIHVA22d</i>	Solyc03g116350	531	3	176	32-107	20.50	6.41	0.005	Extracellular	4
<i>SIHVA22e</i>	Solyc04g014420	333	4	110	5-77	13.04	5.34	-0.034	Cytoplasm	2
<i>SIHVA22f</i>	Solyc04g076610	1410	4	469	32-108	53.34	9.03	-0.147	Nucleus	4
<i>SIHVA22g</i>	Solyc04g081340	915	4	304	19-96	33.64	8.95	-0.389	Chloroplast	4
<i>SIHVA22h</i>	Solyc05g007300	516	5	171	28-104	20.24	7.67	-0.101	Endoplasmic reticulum	4
<i>SIHVA22i</i>	Solyc06g072680	408	6	135	24-98	15.66	8.80	0.210	Chloroplast	4
<i>SIHVA22j</i>	Solyc10g007820	471	10	156	24-98	18.03	9.26	0.026	Chloroplast	4
<i>SIHVA22k</i>	Solyc10g047670	1680	10	559	24-100	63.67	8.73	-0.449	Nucleus	7
<i>SIHVA22l</i>	Solyc10g051300	564	10	187	32-108	21.86	7.02	-0.092	Endoplasmic reticulum	6
<i>SIHVA22m</i>	Solyc10g082040	570	10	189	19-97	22.23	8.84	-0.215	Extracellular	4
<i>SIHVA22n</i>	Solyc11g010930	429	11	142	24-98	16.85	8.58	0.065	Cytoplasm	2
<i>SIHVA22o</i>	Solyc12g089290	372	12	314	31-108	35.11	9.38	-0.399	Chloroplast	1

Table S2. Sequence homology across SlHVA22 proteins

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
SlHVA22a (A)	100%														
SlHVA22b (B)	17.64%	100%													
SlHVA22c (C)	15.97%	21.32%	100%												
SlHVA22d (D)	13.63%	37.50%	18.18%	100%											
SlHVA22e (E)	16.36%	70.90%	22.72%	39.09%	100%										
SlHVA22f (F)	10.90%	27.20%	14.94%	27.84%	25.45%	100%									
SlHVA22g (G)	44.09%	21.32%	15.97%	17.61%	19.09%	12.50%	100%								
SlHVA22h (H)	16.37%	33.82%	22.80%	67.25%	37.27%	26.90%	21.05%	100%							
SlHVA22i (I)	17.77%	73.33%	22.22%	37.77%	69.09%	28.14%	19.25%	34.81%	100%						
SlHVA22j (J)	11.53%	44.11%	17.94%	44.87%	40.90%	27.56%	16.66%	44.23%	44.44%	100%					
SlHVA22k (K)	14.09%	33.08%	18.55%	37.50%	34.54%	11.72%	12.82%	39.18%	31.11%	32.05%	100%				
SlHVA22l (L)	16.04%	22.05%	60.96%	18.75%	23.63%	17.64%	18.71%	23.39%	22.96%	21.15%	21.39%	100%			
SlHVA22m (M)	63.49%	19.11%	19.57%	16.47%	17.27%	13.22%	49.20%	17.54%	18.51%	14.10%	15.87%	19.78%	100%		
SlHVA22n (N)	16.19%	71.32%	21.12%	36.61%	67.27%	23.23%	18.30%	31.69%	64.44%	39.43%	28.16%	21.12%	17.60%	100%	
SlHVA22o (O)	43.18%	22.05%	17.01%	17.61%	20%	14.01%	65.46%	19.88%	22.96%	15.38%	11.14%	19.25%	46.03%	21.12%	100%

Table S3. List of *cis*-acting elements in the upstream regions of *SIHVA22* genes

Gene	Cis element	Consensus sequence	Location	Strand	organism	Function
<i>SIHVA22a</i>	3-AF3 binding site	CACTATCTAAC	10	-	<i>Pisum sativum</i>	part of a conserved DNA module array (CMA3)
	GATA-motif	AAGATAAGATT	129	+	<i>Arabidopsis thaliana</i>	part of a light responsive element
	TGACG-motif	TGACG	157	+	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
	TGA-box	TGACGTAA	157	+	<i>Glycine max</i>	part of an auxin-responsive element
	CGTCA-motif	CGTCA	157	-	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
	CAAT-box	CAAAT	354	+	<i>Pisum sativum</i>	common cis-acting element in promoter and enhancer regions
	TCA-element	CCATCTTTTT	384	-	<i>Nicotiana tabacum</i>	cis-acting element involved in salicylic acid responsiveness
	TCT-motif	TCTTAC	406	-	<i>Arabidopsis thaliana</i>	part of a light responsive element
	ABRE	ACGTG	726	-	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
	G-Box	CACGTT	726	+	<i>Pisum</i>	cis-acting regulatory element involved in light

					<i>sativum</i>	responsiveness
	GT1-motif	GGTTAAT	890	+	<i>Avena sativa</i>	light responsive element
	Unnamed__1	GAATTTAATTAA	892	-	<i>Glycine max</i>	60K protein binding site
	Box 4	ATTAAT	895	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	TCA-element	CCATCTTTTT	917	+	<i>Nicotiana tabacum</i>	cis-acting element involved in salicylic acid responsiveness
	AT-rich element	ATAGAAATCAA	1253	-	<i>Glycine max</i>	binding site of AT-rich DNA binding protein (ATBP-1)
<i>SIHVA22b</i>	TATC-box	TATCCCA	35	+	<i>Oryza sativa</i>	cis-acting element involved in gibberellin-responsiveness
	GCN4_motif	TGAGTCA	236	-	<i>Oryza sativa</i>	cis-regulatory element involved in endosperm expression
	Box 4	ATTAAT	257	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	ABRE	CACGTG	322	+	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
	G-box	CACGTG	322	+	<i>Arabidopsis thaliana</i>	cis-acting regulatory element involved in light responsiveness
	Box 4	ATTAAT	374	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	ARE	AAACCA	383	+	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
	O2-site	GATGA(C/T)(A/G)TG(A/G)	433	-	<i>Zea mays</i>	cis-acting regulatory element involved in zein

					metabolism regulation
Box 4	ATTAAT	488	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
CGTCA-motif	CGTCA	758	+	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
CAT-box	GCCACT	939	-	<i>Arabidopsis thaliana</i>	cis-acting regulatory element related to meristem expression
ARE	AAACCA	1068	+	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
Box 4	ATTAAT	1139	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
ABRE	CACGTG	1149	-	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
G-box	CACGTG	1149	-	<i>Arabidopsis thaliana</i>	cis-acting regulatory element involved in light responsiveness
GT1-motif	GGTTAA	1179	-	<i>Arabidopsis thaliana</i>	light responsive element
MRE	AACCTAA	1181	+	<i>Petroselinum crispum</i>	MYB binding site involved in light responsiveness
3-AF3 binding site	CACTATCTAAC	1341	-	<i>Pisum sativum</i>	part of a conserved DNA module array (CMA3)
CGTCA-motif	CGTCA	1399	+	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
O2-site	GTTGACGTGA	1401	-	<i>Zea mays</i>	cis-acting regulatory element involved in zein metabolism regulation

SIHVA22c	ABRE	ACGTG	1402	-	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
	G-box	CACGTC	1402	+	<i>Zea mays</i>	cis-acting regulatory element involved in light responsiveness
	HD-Zip 1	CAAT(A/T)ATTG	1453	-	<i>Arabidopsis thaliana</i>	element involved in differentiation of the palisade mesophyll cells
	TGACG-motif	TGACG	528	-	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
	O2-site	GATGATGTGG	36	+	<i>Zea mays</i>	cis-acting regulatory element involved in zein metabolism regulation
	G-box	tgACACGTGGCA	125	+	<i>Lycopersicon esculentum</i>	cis-acting regulatory element involved in light responsiveness
	ABRE	GACACGTGGC	126	+	<i>Triticum aestivum</i>	cis-acting element involved in the abscisic acid responsiveness
	Unnamed__1	GAATTTAATTAA	165	+	<i>Glycine max</i>	60K protein binding site
	CGTCA-motif	CGTCA	528	+	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
	Box 4	ATTAAT	752	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	Box 4	ATTAAT	814	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	G-box	ACACGTG(G/t)CACC	827	-	<i>Lycopersicon esculentum</i>	cis-acting regulatory element involved in light responsiveness
	ABRE	GCAACGTGTC	830	+	<i>Hordeum</i>	cis-acting element involved in the abscisic acid

					<i>vulgare</i>	responsiveness
	G-box	CACGTG	832	-	<i>Arabidopsis thaliana</i>	cis-acting regulatory element involved in light responsiveness
	ABRE	ACGTG	884	-	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
	GA-motif	ATAGATAA	925	+	<i>Arabidopsis thaliana</i>	part of a light responsive element
	Box 4	ATTAAT	939	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	TCT-motif	TCTTAC	962	-	<i>Arabidopsis thaliana</i>	part of a light responsive element
	Box 4	ATTAAT	1028	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	Box 4	ATTAAT	1191	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	O2-site	GATGA(C/T)(A/G)TG(A/G)	1319	-	<i>Zea mays</i>	cis-acting regulatory element involved in zein metabolism regulation
	Box 4	ATTAAT	1377	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	Box 4	ATTAAT	1487	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
<i>SIHVA22d</i>	TGACG-motif	TGACG	13	-	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
	G-box	TACGTG	67	+	<i>Arabidopsis thaliana</i>	cis-acting regulatory element involved in light responsiveness

ABRE	ACGTG	68	+	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
TGACG-motif	TGACG	71	+	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
ACE	CTAACGTATT	336	+	<i>Petroselinum crispum</i>	cis-acting element involved in light responsiveness
Gap-box	CAAATGAA(A/G)A	419	-	<i>Arabidopsis thaliana</i>	part of a light responsive element
MYB	CAACCA	542	-	<i>Arabidopsis thaliana</i>	involved in drought-inducibility
AT1-motif	AATTATTTTTTATT	806	-	<i>Solanum tuberosum</i>	part of a light responsive module
G-box	TACGTG	864	-	<i>Arabidopsis thaliana</i>	cis-acting regulatory element involved in light responsiveness
ABRE	ACGTG	864	-	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
Box 4	ATTAAT	877	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
chs-CMA1a	TTACTTAA	980	+	<i>Daucus carota</i>	part of a light responsive element
G-Box	CACGTT	1007	-	<i>Pisum sativum</i>	cis-acting regulatory element involved in light responsiveness
ABRE	ACGTG	1008	+	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
GATA-motif	AAGGATAAGG	1019	+	<i>Solanum</i>	part of a light responsive element

					<i>tuberosum</i>	
	ARE	AAACCA	1096	-	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
	TCA-element	CCATCTTTTT	1120	+	<i>Nicotiana tabacum</i>	cis-acting element involved in salicylic acid responsiveness
	Box III	atCATTTTCACt	1190	-	<i>Pisum sativum</i>	protein binding site
	GA-motif	ATAGATAA	1314	+	<i>Arabidopsis thaliana</i>	part of a light responsive element
	ATCT-motif	AATCTAATCC	1355	+	<i>Pisum sativum</i>	part of a conserved DNA module involved in light responsiveness
	Box 4	ATTAAT	1436	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
<i>SIHVA22e</i>	Box 4	ATTAAT	7	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	G-box	TACGTG	42	-	<i>Arabidopsis thaliana</i>	cis-acting regulatory element involved in light responsiveness
	ABRE	ACGTG	42	-	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
	O2-site	GATGACATGG	118	+	<i>Zea mays</i>	cis-acting regulatory element involved in zein metabolism regulation
	circadian	CAAAGATATC	187	-	<i>Lycopersicon esculentum</i>	cis-acting regulatory element involved in circadian control
	I-box	cCATATCCAAT	199	+	<i>Flaveria trinervia</i>	part of a light responsive element

	Box 4	ATTAAT	254	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	GT1-motif	GGTTAA	460	-	<i>Arabidopsis thaliana</i>	light responsive element
	GT1-motif	GGTTAAT	635	+	<i>Avena sativa</i>	light responsive element
	MBS	CAACTG	656	-	<i>Arabidopsis thaliana</i>	MYB binding site involved in drought-inducibility
	LAMP-element	CTTTATCA	750	+	<i>Pisum sativum</i>	part of a light responsive element
	AE-box	AGAAACTT	806	-	<i>Arabidopsis thaliana</i>	part of a module for light response
	O2-site	GATGATGTGG	1007	+	<i>Zea mays</i>	cis-acting regulatory element involved in zein metabolism regulation
	Box 4	ATTAAT	1053	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	Box II	TGGTAATAA	1244	+	<i>Solanum tuberosum</i>	part of a light responsive element
<i>SIHVA22f</i>	TGA-element	AACGAC	124	-	<i>Brassica oleracea</i>	auxin-responsive element
	AE-box	AGAAACAA	151	-	<i>Arabidopsis thaliana</i>	part of a module for light response
	G-box	CACGTC	372	-	<i>Zea mays</i>	cis-acting regulatory element involved in light responsiveness
	ABRE	ACGTG	373	+	<i>Arabidopsis</i>	cis-acting element involved in the abscisic acid

					<i>thaliana</i>	responsiveness
	G-box	CACGAC	403	+	<i>Zea mays</i>	cis-acting regulatory element involved in light responsiveness
	TGA-element	AACGAC	931	+	<i>Brassica oleracea</i>	auxin-responsive element
	Box 4	ATTAAT	945	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	GT1-motif	GGTTAA	962	-	<i>Arabidopsis thaliana</i>	light responsive element
	HD-Zip 1	CAAT(A/T)ATTG	1102	-	<i>Arabidopsis thaliana</i>	element involved in differentiation of the palisade mesophyll cells
	Box 4	ATTAAT	1181	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	ARE	AAACCA	1246	+	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
	ARE	AAACCA	1401	+	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
	RY-element	CATGCATG	1418	-	<i>Helianthus annuus</i>	cis-acting regulatory element involved in seed-specific regulation
	ARE	AAACCA	1461	-	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
<i>SIHVA22g</i>	CGTCA-motif	CGTCA	64	-	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
	A-box	CCGTCC	149	+	<i>Petroselinum crispum</i>	cis-acting regulatory element

TCA-element	CCATCTTTTT	153	+	<i>Nicotiana tabacum</i>	cis-acting element involved in salicylic acid responsiveness
AT1-motif	AATTATTTTTTATT	172	-	<i>Solanum tuberosum</i>	part of a light responsive module
ARE	AAACCA	492	-	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
TGA-element	AACGAC	510	+	<i>Brassica oleracea</i>	auxin-responsive element
GC-motif	CCCCCG	527	+	<i>Zea mays</i>	enhancer-like element involved in anoxic specific inducibility
GT1-motif	GTGTGTGAA	542	-	<i>Solanum tuberosum</i>	light responsive element
CCAAT-box	CAACGG	569	+	<i>Hordeum vulgare</i>	MYBHv1 binding site
MSA-like	(T/C)C(T/C)AACGG(T/C)(T/C)A	641	+	<i>Catharanthus roseus</i>	cis-acting element involved in cell cycle regulation
P-box	CCTTTTG	703	-	<i>Oryza sativa</i>	gibberellin-responsive element
LAMP-element	CTTTATCA	916	-	<i>Pisum sativum</i>	part of a light responsive element
TCA-element	CCATCTTTTT	935	-	<i>Nicotiana tabacum</i>	cis-acting element involved in salicylic acid responsiveness
GARE-motif	TCTGTTG	1083	-	<i>Brassica oleracea</i>	gibberellin-responsive element
MYB	CAACCA	1038	-	<i>Arabidopsis</i>	involved in drought-inducibility

					<i>thaliana</i>	
	ATC-motif	AGCTATCCA	1151	-	<i>Arabidopsis thaliana</i>	part of a conserved DNA module involved in light responsiveness
	ATC-motif	AGTAATCT	1166	+	<i>Spinacia oleracea</i>	part of a conserved DNA module involved in light responsiveness
	ARE	AAACCA	1183	-	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
	ARE	AAACCA	1272	-	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
	ARE	AAACCA	1450	-	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
<i>SIHVA22h</i>	TGACG-motif	TGACG	123	+	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
	3-AF1 binding site	TAAGAGAGGAA	200	+	<i>Solanum tuberosum</i>	light responsive element
	ATCT-motif	AATCTAATCC	285	-	<i>Pisum sativum</i>	part of a conserved DNA module involved in light responsiveness
	ACE	CTAACGTATT	313	-	<i>Petroselinum crispum</i>	cis-acting element involved in light responsiveness
	Box 4	ATTAAT	378	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	Myb-binding site	CAACAG	531	-	<i>Nicotiana tabacum</i>	involved in drought-inducibility
	Myb-binding site	CAACAG	663	-	<i>Nicotiana tabacum</i>	involved in drought-inducibility

MRE	AACCTAA	638	-	<i>Petroselinum crispum</i>	MYB binding site involved in light responsiveness
P-box	CCTTTTG	673	-	<i>Oryza sativa</i>	gibberellin-responsive element
G-Box	CACGTT	818	-	<i>Pisum sativum</i>	cis-acting regulatory element involved in light responsiveness
ABRE	ACGTG	819	+	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
G-box	CACGTC	830	-	<i>Zea mays</i>	cis-acting regulatory element involved in light responsiveness
ABRE	ACGTG	831	+	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
GT1-motif	GGTTAA	842	+	<i>Arabidopsis thaliana</i>	light responsive element
4cl-CMA2b	TCTCACCAACCACA	860	+	<i>Solanum tuberosum</i>	light responsive element
Box 4	ATTAAT	984	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
LTR	CCGAAA	1045	+	<i>Hordeum vulgare</i>	cis-acting element involved in low-temperature responsiveness
P-box	CCTTTTG	1065	-	<i>Oryza sativa</i>	gibberellin-responsive element
AE-box	AGAAACTT	1155	-	<i>Arabidopsis thaliana</i>	part of a module for light response
TGACG-motif	TGACG	1217	+	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness

<i>SIHVA22i</i>	3-AF3 binding site	CACTATCTAAC	1245	+	<i>Pisum sativum</i>	part of a conserved DNA module array (CMA3)
	LTR	CCGAAA	1358	-	<i>Hordeum vulgare</i>	cis-acting element involved in low-temperature responsiveness
	AE-box	AGAAACTT	4	+	<i>Arabidopsis thaliana</i>	part of a module for light response
	MRE	AACCTAA	78	-	<i>Petroselinum crispum</i>	MYB binding site involved in light responsiveness
	Box 4	ATTAAT	142	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	TGA-element	AACGAC	245	-	<i>Brassica oleracea</i>	auxin-responsive element
	3-AF1 binding site	TAAGAGAGGAA	284	-	<i>Solanum tuberosum</i>	light responsive element
	TGACG-motif	TGACG	724	-	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
	AT-rich element	ATAGAAATCAA	793	+	<i>Glycine max</i>	binding site of AT-rich DNA binding protein (ATBP-1)
	O2-site	GATGATGTGG	1055	-	<i>Zea mays</i>	cis-acting regulatory element involved in zein metabolism regulation
	CGTCA-motif	CGTCA	1284	+	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
	MBS	CAACTG	1312	+	<i>Arabidopsis thaliana</i>	MYB binding site involved in drought-inducibility
	ABRE	ACGTG	1367	-	<i>Arabidopsis</i>	cis-acting element involved in the abscisic acid

					<i>thaliana</i>	responsiveness
	G-box	CACGTC	1367	+	<i>Zea mays</i>	cis-acting regulatory element involved in light responsiveness
	G-Box	CACGTG	1415	-	<i>Pisum sativum</i>	cis-acting regulatory element involved in light responsiveness
	ABRE	ACGTG	1416	+	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
<i>SIHVA22j</i>	TCT-motif	TCTTAC	17	-	<i>Arabidopsis thaliana</i>	part of a light responsive element
	AE-box	AGAAACTT	26	+	<i>Arabidopsis thaliana</i>	part of a module for light response
	GT1-motif	GTGTGTGAA	103	+	<i>Solanum tuberosum</i>	light responsive element
	AE-box	AGAAACAA	217	+	<i>Arabidopsis thaliana</i>	part of a module for light response
	ARE	AAACCA	271	-	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
	TCT-motif	TCTTAC	343	+	<i>Arabidopsis thaliana</i>	part of a light responsive element
	TCT-motif	TCTTAC	515	+	<i>Arabidopsis thaliana</i>	part of a light responsive element
	ATCT-motif	AATCTAATCC	575	+	<i>Pisum sativum</i>	part of a conserved DNA module involved in light responsiveness
	G-Box	CACGTG	590	+	<i>Pisum</i>	cis-acting regulatory element involved in light

				<i>sativum</i>	responsiveness
ABRE	ACGTG	591	+	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
TCT-motif	TCTTAC	711	-	<i>Arabidopsis thaliana</i>	part of a light responsive element
GT1-motif	GGTTAAT	761	-	<i>Avena sativa</i>	light responsive element
GT1-motif	GGTTAA	762	-	<i>Arabidopsis thaliana</i>	light responsive element
MYB	CAACCA	968	-	<i>Arabidopsis thaliana</i>	involved in drought-inducibility
O2-site	GTTGACGTGA	970	+	<i>Zea mays</i>	cis-acting regulatory element involved in zein metabolism regulation
TGACG-motif	TGACG	972	+	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
G-box	CACGTC	973	-	<i>Zea mays</i>	cis-acting regulatory element involved in light responsiveness
ABRE	ACGTG	974	+	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
RY-element	CATGCATG	1035	-	<i>Helianthus annuus</i>	cis-acting regulatory element involved in seed-specific regulation
TC-rich repeats	GTTTTCTTAC	1174	-	<i>Nicotiana tabacum</i>	cis-acting element involved in defense and stress responsiveness
TCT-motif	TCTTAC	1174	-	<i>Arabidopsis thaliana</i>	part of a light responsive element

SIHVA22k	MYB	CAACCA	1244	-	<i>Arabidopsis thaliana</i>	involved in drought-inducibility
	GARE-motif	TCTGTTG	1244	-	<i>Brassica oleracea</i>	gibberellin-responsive element
	Box 4	ATTAAT	1424	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	P-box	CCTTTTG	30	-	<i>Oryza sativa</i>	gibberellin-responsive element
	CGTCA-motif	CGTCA	211	+	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
	MYB	CAACCA	226	+	<i>Arabidopsis thaliana</i>	involved in drought-inducibility
	O2-site	GATGATGTGG	229	-	<i>Zea mays</i>	cis-acting regulatory element involved in zein metabolism regulation
	ABRE	ACGTG	280	-	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
	G-box	TACGTG	280	-	<i>Arabidopsis thaliana</i>	cis-acting regulatory element involved in light responsiveness
	MYB	CAACCA	656	-	<i>Arabidopsis thaliana</i>	involved in drought-inducibility
	GA-motif	ATAGATAA	1027	+	<i>Arabidopsis thaliana</i>	part of a light responsive element
	ARE	AAACCA	1171	+	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
	Box 4	ATTAAT	1195	-	<i>Petroselinum</i>	part of a conserved DNA module involved in light

					<i>crispum</i>	responsiveness
	GCN4_motif	TGAGTCA	1209	-	<i>Oryza sativa</i>	cis-regulatory element involved in endosperm expression
	Box 4	ATTAAT	1379	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	TCA-element	TCAGAAGAGG	1428	-	<i>Brassica oleracea</i>	cis-acting element involved in salicylic acid responsiveness
	MBS	CAACTG	1469	-	<i>Arabidopsis thaliana</i>	MYB binding site involved in drought-inducibility
<i>SIHVA22l</i>	G-Box	CACGTT	3	-	<i>Pisum sativum</i>	cis-acting regulatory element involved in light responsiveness
	ABRE	ACGTG	4	+	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
	GATA-motif	GATAGGG	134	-	<i>Pisum sativum</i>	part of a light responsive element
	MYB	CAACCA	270	-	<i>Arabidopsis thaliana</i>	involved in drought-inducibility
	GATA-motif	AAGATAAGATT	295	+	<i>Arabidopsis thaliana</i>	part of a light responsive element
	TCT-motif	TCTTAC	485	+	<i>Arabidopsis thaliana</i>	part of a light responsive element
	MBS	CAACTG	923	+	<i>Arabidopsis thaliana</i>	MYB binding site involved in drought-inducibility
	Gap-box	CAAATGAA(A/G)A	1129	+	<i>Arabidopsis thaliana</i>	part of a light responsive element

SIHVA22m	Box 4	ATTAAT	1222	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	GT1-motif	GGTTAA	1270	-	<i>Arabidopsis thaliana</i>	light responsive element
	GT1-motif	GGTTAA	1344	+	<i>Arabidopsis thaliana</i>	light responsive element
	MBS	CAACTG	1479	-	<i>Arabidopsis thaliana</i>	MYB binding site involved in drought-inducibility
	LTR	CCGAAA	1	-	<i>Hordeum vulgare</i>	cis-acting element involved in low-temperature responsiveness
	Box 4	ATTAAT	30	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	ARE	AAACCA	39	-	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
	Box 4	ATTAAT	58	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	Box 4	ATTAAT	70	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	Box 4	ATTAAT	97	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	CGTCA-motif	CGTCA	183	-	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
	AE-box	AGAAACAA	228	+	<i>Arabidopsis thaliana</i>	part of a module for light response

TCT-motif	TCTTAC	296	+	<i>Arabidopsis thaliana</i>	part of a light responsive element
G-Box	CACGTT	355	-	<i>Pisum sativum</i>	cis-acting regulatory element involved in light responsiveness
ABRE	ACGTG	356	+	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
GT1-motif	GGTTAA	375	+	<i>Arabidopsis thaliana</i>	light responsive element
Box 4	ATTAAT	449	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
ARE	AAACCA	485	+	<i>Zea mays</i>	cis-acting regulatory element essential for the anaerobic induction
Box 4	ATTAAT	492	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
MYB	CAACCA	611	-	<i>Arabidopsis thaliana</i>	involved in drought-inducibility
G-box	CACGTC	653	+	<i>Zea mays</i>	cis-acting regulatory element involved in light responsiveness
ABRE	ACGTG	653	-	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
TGACG-motif	TGACG	766	+	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
CGTCA-motif	CGTCA	766	-	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
GATA-motif	AAGATAAGATT	822	-	<i>Arabidopsis</i>	part of a light responsive element

				<i>thaliana</i>	
G-box	TACGTG	842	+	<i>Arabidopsis thaliana</i>	cis-acting regulatory element involved in light responsiveness
ABRE	ACGTG	843	+	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
AT-rich sequence	TAAAATACT	853	+	<i>Pisum sativum</i>	element for maximal elicitor-mediated activation (2copies)
CCAAT-box	CAACGG	935	-	<i>Hordeum vulgare</i>	MYBHv1 binding site
Box 4	ATTAAT	976	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
Box 4	ATTAAT	1042	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
Box 4	ATTAAT	1132	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
Box 4	ATTAAT	1158	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
TCT-motif	TCTTAC	1219	-	<i>Arabidopsis thaliana</i>	part of a light responsive element
ABRE	ACGTG	1233	-	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
G-Box	CACGTT	1233	+	<i>Pisum sativum</i>	cis-acting regulatory element involved in light responsiveness
Box 4	ATTAAT	1385	-	<i>Petroselinum</i>	part of a conserved DNA module involved in light

SIHVA22n					<i>crispum</i>	responsiveness
	GT1-motif	GGTTAA	2	+	<i>Arabidopsis thaliana</i>	light responsive element
	Box 4	ATTAAT	8	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	MYB	CAACCA	70	-	<i>Arabidopsis thaliana</i>	involved in drought-inducibility
	O2-site	GTTGACGTGA	184	-	<i>Zea mays</i>	cis-acting regulatory element involved in zein metabolism regulation
	LS7	CAGATTTATTTT	296	-	<i>Zea mays</i>	part of a light responsive element
	Box 4	ATTAAT	324	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	ABRE	GACACGTGGC	450	+	<i>Triticum aestivum</i>	cis-acting element involved in the abscisic acid responsiveness
	G-Box	CACGTG	452	+	<i>Pisum sativum</i>	cis-acting regulatory element involved in light responsiveness
	Box 4	ATTAAT	528	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	TCT-motif	TCTTAC	580	+	<i>Arabidopsis thaliana</i>	part of a light responsive element
	MBS	CAACTG	899	-	<i>Arabidopsis thaliana</i>	MYB binding site involved in drought-inducibility
	Box 4	ATTAAT	1000	-	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness

SIHVA22o	TC-rich repeats	GTTTTCTTAC	1486	+	<i>Nicotiana tabacum</i>	cis-acting element involved in defense and stress responsiveness
	TCT-motif	TCTTAC	1490	+	<i>Arabidopsis thaliana</i>	part of a light responsive element
	ACA-motif	AATCACAACCATA	9	-	<i>Arabidopsis thaliana</i>	part of gapA in (gapA-CMA1) involved with light responsiveness
	Box 4	ATTAAT	80	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	Box 4	ATTAAT	112	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	Box 4	ATTAAT	177	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	CGTCA-motif	CGTCA	319	-	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness
	Box 4	ATTAAT	412	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	Box 4	ATTAAT	421	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
	ACE	CTAACGTATT	427	-	<i>Petroselinum crispum</i>	cis-acting element involved in light responsiveness
	MYB	CAACCA	495	-	<i>Arabidopsis thaliana</i>	involved in drought-inducibility
	LAMP-element	CCTTATCCA	604	-	<i>Spinacia oleracea</i>	part of a light responsive element

Box 4	ATTAAT	707	+	<i>Petroselinum crispum</i>	part of a conserved DNA module involved in light responsiveness
Sp1	GGGCGG	818	+	<i>Oryza sativa</i>	light responsive element
P-box	CCTTTTG	829	+	<i>Oryza sativa</i>	gibberellin-responsive element
GATA-motif	GATAGGG	843	-	<i>Pisum sativum</i>	part of a light responsive element
GT1-motif	GGTTAA	1066	-	<i>Arabidopsis thaliana</i>	light responsive element
MYB	CAACCA	1071	-	<i>Arabidopsis thaliana</i>	involved in drought-inducibility
MBSI	TTTTTACGGTTA	1091	+	<i>Petunia hybrida</i>	MYB binding site involved in flavonoid biosynthetic genes regulation
CGTCA-motif	CGTCA	1280	+	<i>Hordeum vulgare</i>	cis-acting regulatory element involved in the MeJA-responsiveness

Table S4. miRNA target sites predicted in tomato *HVA22* genes

MIRN	Targ	Expe	U	MIRN	MIR	Targ	Targ	MIRNA_aligned_f	align	Target_aligned_fr	Inhi
A_Acc.	et_Ac	ctatio	P	A_star	NA_e	et_st	et_en	ragment	ment	agment	bitio
	c.	n	E\$	t	nd	art	d				n
sly- MIR94 74-5p	<i>SlHV</i> <i>A22a</i>	5	-1	1	22	1045	1066	UGUAGAAGUCA UGAAUAAAAUG	: :::: : ::::: : : :::	CCUUUUUCUUA UGGUUUUAACA	Clea vage

Sly-MIR53 03a	<i>SIHV</i> <i>A22b</i>	5	-1	1	21	586	606	UUUUUGAAGAG UUCGAGCAAC	∴∴∴ ∴∴∴∴∴ ∴	UGUGUUUACAC UCUUCACAAA	Clea vage
sly-MIR53 03	<i>SIHV</i> <i>A22b</i>	5	-1	1	21	586	606	UUUUUGAAGAG UUCGAGCAAC	∴∴∴ ∴∴∴∴∴ ∴	UGUGUUUACAC UCUUCACAAA	Clea vage
Sly-MIR94 79	<i>SIHV</i> <i>A22c</i>	5	-1	1	22	825	846	GAGAAUGGUAG AGGGUCGGACC	∴ ∴∴∴∴∴ ∴	GUACCGUCUCU CUAUUGUACUU	Clea vage
sly-MIR94 75-5p	<i>SIHV</i> <i>A22c</i>	4	-1	1	21	314	334	AACGAUCUCUA CAUUGUAGGC	∴ ∴∴∴∴∴ ∴	UGCUGUUCUGU AGGGAUUGUU	Clea vage
sly-MIR94 79-3p	<i>SIHV</i> <i>A22c</i>	5	-1	1	22	825	846	GAGAAUGGUAG AGGGUCGGACC	∴ ∴∴∴∴∴ ∴	GUACCGUCUCU CUAUUGUACUU	Clea vage
Sly-MIR39 5a	<i>SIHV</i> <i>A22d</i>	5	-1	1	21	904	924	CUGAAGUGUUU GGGGGAACUC	∴∴∴∴∴ ∴∴∴	CUUUUCUCCUA GAUACUUUGU	Clea vage
Sly-MIR39 6a	<i>SIHV</i> <i>A22d</i>	5	-1	1	21	737	757	UUCCACAGCUU UCUUGAACUG	: ∴∴∴∴∴ ∴ ∴ ∴	CUGUUUAGGAA GGCAGAGGAG	Clea vage
sly-MIR16 6c-5p	<i>SIHV</i> <i>A22d</i>	4.5	-1	1	21	576	596	GGGAUGUUGUC UGGCUCGACA	∴∴∴∴∴ ∴∴	UAGUAAGCCAG AUGACAUCCU	Clea vage

sly-MIR39 6a-5p	<i>SIHV</i> <i>A22d</i>	5	-1	1	21	737	757	UUCCACAGCUU UCUUGAACUG	: :..... : :	CUGUUUAGGAA GGCAGAGGAG	Clea vage
sly-MIR16 6c-5p	<i>SIHV</i> <i>A22f</i>	4	-1	1	21	877	897	GGGAUGUUGUC UGGCUCGACA	: :..... :.....	GUUUGAACCCAG AUAAAAUCUC	Clea vage
sly-MIR19 17	<i>SIHV</i> <i>A22g</i>	5	-1	1	21	1302	1322	AUUAUAUAAAGA GUGCUAAAGU	: :..... :.....	CAAUUACCAUU CAUUAUUAUU	Clea vage
Sly-MIR48 2a	<i>SIHV</i> <i>A22j</i>	5	-1	1	22	47	68	UUUCCAAUUCC ACCCAUUCCUA	: :..... :.....	UUCCAAUGGGU GCUAUUGGAAC	Tran slatio n
Sly-MIR60 24	<i>SIHV</i> <i>A22j</i>	5	-1	1	21	58	78	UUUAGCAAGAG UUGUUUUACC	: :..... :.....	GCUAUUGGAAC UAUUGCUAAA	Clea vage
Sly-MIR10 535	<i>SIHV</i> <i>A22k</i>	4	-1	1	24	301	323	UUGGCAUAAGU UUGUGAAAGCC GG	: :..... :.....	ACCUAUUUGAC AAACUUAU- CCAA	Clea vage
Sly-MIR15 9b	<i>SIHV</i> <i>A22k</i>	4	-1	1	20	101	120	AUUUACUCUUC UAGGAUCCU	: :..... :	UUGAACUGAGA AGAGUAAAU	Clea vage
Sly-MIR60 23	<i>SIHV</i> <i>A22k</i>	4.5	-1	1	22	576	597	UUACUACGGUC AGGAAUCUUAU	: :..... :.....	GAAACAUUUCU GUCUGUGGUAG	Tran slatio n

sly- MIR94 75-5p	<i>SIHV</i> <i>A22l</i>	5	-1	1	21	271	291	AACGAUCUCUA CAUUGUAGGC	∴ ∴∴∴∴∴ ∴	UGCUGUUCUGU GGGGGUUGUU	Clea vage
Sly- MIR39 5a	<i>SIHV</i> <i>A22m</i>	5	-1	1	21	464	484	CUGAAGUGUUU GGGGGAACUC	∴∴∴ ∴∴∴∴ ∴	AAGUUCUUGCA AAUGCUUGAG	Clea vage
sly- MIR53 02a	<i>SIHV</i> <i>A22n</i>	4.5	-1	1	21	481	501	AAACGAGGUUU GUUACUUUGG	∴ ∴∴∴∴∴ ∴	GAAGAUUAACA AGUUUUGUUG	Clea vage
Sly- MIR60 24	<i>SIHV</i> <i>A22o</i>	5	-1	1	21	707	727	UUUAGCAAGAG UUGUUUUACC	∴∴∴∴∴ ∴∴∴ ∴	CAAAAAACGAC UCCAGCUGAA	Clea vage
sly- MIR94 70-5p	<i>SIHV</i> <i>A22o</i>	4.5	-1	1	21	211	231	UGAAAUCCAUG AGCCUAAACU	∴ ∴ ∴∴∴∴∴ ∴	GCUUUUGUUUC AUGGGUCCA	Clea vage

Table S5. Target sites for post-translational modifications of tomato HVA22 proteins

Protein	Phosphorylation sites	N-glycosylation sites
SIHVA22a	S9, S30, <u>S55</u> , T86, T92, S99, S143, S145, S149, S153, S162, S165, S169, S173, S175, S176, S177, S178, S179, S186, S189, S190, S199, S202, S209, S212, S214, S215	N126
SIHVA22b	T9, S28, T35, S36, T54, Y105, S107, S108, Y109, S114, S116, T121, T130	
SIHVA22c	S12, S22, S36, T46, T52, S70, S72, Y83, Y111, T112, S161, T177, <u>T187</u> , S188, S190, <u>S194</u>	N10
SIHVA22d	S17, Y34, S36, T42, S44, T62, S79, Y104, T107, S128, T135, Y140, T146, S165, Y174	
SIHVA22e	S7, S13, T14, S15, T33, T69, Y72, T74, Y85, S90, T100, Y109	
SIHVA22f	S5, S16, S26, Y34, S36, S42, S46, S47, Y48, <u>T67</u> , S76, S86, S110, T119, S124, S130, S135, S139, <u>T150</u> , S154, T160, S166, S173, Y175, Y186, S201, S202, T208, S229, S258, <u>S265</u> , S278, S284, T305, S321, <u>T349</u> , <u>S380</u> , S401, S421, T425, Y431, S433, S438, S464,	
SIHVA22g	S4, Y21, T51, T86, Y88, S108, S129, S144, S146, T152, T154, S158, S159, T165, S167, S172, S173, S175, S189, S190, S192, S193, S194, S200, S206, S207, T223, T224, S226, S228, S231, T232, S236, T239, S243, S245, S247, S255, T256, S257, S271, S282, S295, T298, S301	
SIHVA22h	S3, S24, Y30, T31, S32, T38, S40, T49, S55, T58, <u>S63</u> , S65, S75, S123, T130, Y135, T157, <u>T164</u> , Y169	
SIHVA22i	T30, S18, T35, S36, T54, Y105, S114, S121, S126, T129, S130, <u>T134</u>	
SIHVA22j	T6, S27, S28, S34, S36, T45, <u>S51</u> , T54, S123, S129, Y133	
SIHVA22k	S7, S28, T34, <u>S54</u> , S108, S110, S115, Y117, S128, S146, <u>S154</u> , <u>S165</u> , Y176, Y179, S180, S181, T191, T193, S194, T201, T205, S210, <u>T218</u> , S236, T249, T278, <u>T289</u> , T290, S297, S306, Y308, T317, S320, S323, S349, S361, T373, T374, T378, T381, S397, T413, T415, S416, T427, T440, T442, S448, S471, T472, T485, T493, S510, S540, T543, Y550	N113, N163, N203, N321
SIHVA22l	S12, S26, T36, S62, Y73, T103, S132, S168, <u>T180</u> , S181, S83	
SIHVA22m	S55, S62, S87, T92, <u>T103</u> , S108, Y141, S144, S146, T150, S155, T161, T162, S166, S167, Y176, S185	N126
SIHVA22n	S28, T34, <u>S35</u> , S51, T54, S108, S109, S110, S111, S112, S119, S1124, T133, Y142	
SIHVA22o	S16, Y33, T63, T98, Y100, S104, <u>T115</u> , Y142, T145, S156, S158, T159, T163, S169, S170, T176, T178, S184, T189, T193, S201, T202, S204, S205, S206, S219, T226, S230, S232, S233, S234, T240, T249, S252, S253, S255, S266, S268, S272, T279, T292, S305, T308	N284

Putative casein kinase (CKI and CKII) phosphorylation sites are underline and colored in red.

Table S6. Secondary structural components identified in SIHVA22 proteins

No.	Protein name	α - Helix	β - Strand	Coil
1	SIHVA22a	4	-	5
2	SIHVA22b	4	-	5
3	SIHVA22c	4	-	5
4	SIHVA22d	4	-	5
5	SIHVA22e	5	-	6
6	SIHVA22f	13	9	22
7	SIHVA22g	6	-	7
8	SIHVA22h	5	-	6
9	SIHVA22i	4	-	5
10	SIHVA22j	5	-	6
11	SIHVA22k	22	4	27
12	SIHVA22l	4	-	5
13	SIHVA22m	4	-	5
14	SIHVA22n	4	-	5
15	SIHVA22o	5	2	6

Table S7. Secondary structure validation for SIHVA22 proteins through I-TASSER

No.	Locus name	Type	TM-Score	RMSD
1	Solyc01g007780	SIHVA22a	0.37±0.12	12.8±4.2
2	Solyc03g097420	SIHVA22b	0.35±0.12	12.1±4.4
3	Solyc03g110920	SIHVA22c	0.33±0.11	13.4±4.1
4	Solyc03g116350	SIHVA22d	0.48±0.15	9.3±4.6
5	Solyc04g014420	SIHVA22e	0.37±0.13	10.8±4.6
6	Solyc04g076610	SIHVA22f	0.61±0.14	9.0±4.6
7	Solyc04g081340	SIHVA22g	0.28±0.09	16.5±3.0

8	Solyc05g007300	SIHVA22h	0.52±0.15	8.6±4.5	TM-score, Template modeling score; RMSD: root-mean- square deviation between residues
9	Solyc06g072680	SIHVA22i	0.40±0.14	10.5±4.6	
10	Solyc10g007820	SIHVA22j	0.42±0.14	10.6±4.6	
11	Solyc10g047670	SIHVA22k	0.48±0.15	12.3±4.4	
12	Solyc10g051300	SIHVA22l	0.34±0.11	13.2±4.1	
13	Solyc10g082040	SIHVA22m	0.25±0.07	16.0±3.2	
14	Solyc11g010930	SIHVA22n	0.44±0.14	9.8±4.6	
15	Solyc12g089290	SIHVA22o	0.31±0.10	15.5±3.3	

structurally aligned by TM-align.

Table S8. Parameters for 3D structure modeling of SIHVA22 proteins

No.	Type	C-Score	No. of Decoys	Cluster Density
1	SIHVA22a	-3.07	922	0.0519
2	SIHVA22b	-3.30	1598	0.0450
3	SIHVA22c	-3.44	1322	0.0413
4	SIHVA22d	-1.92	4470	0.1999
5	SIHVA22e	-3.00	2119	0.0628
6	SIHVA22f	-0.82	600	0.2500
7	SIHVA22g	-4.11	922	0.0173
8	SIHVA22h	-1.63	4406	0.2545
9	SIHVA22i	-2.69	1307	0.0889
10	SIHVA22j	-2.56	1710	0.1036
11	SIHVA22k	-1.95	600	0.0948
12	SIHVA22l	-3.41	1274	0.0411

13	SIHVA22m	-4.41	705	0.0138
14	SIHVA22n	-2.32	1430	0.1254
8	SIHVA22o	-3.74	1157	0.0268

C-Score, confident score.

Table S9. Gene Ontology (GO) annotation for SIHVA22 proteins

Name	Molecular Process	Biological Process	Cellular component
SIHVA22a	protein-transporting ATPase activity, protein binding, cation transmembrane transporter activity	transport	integral component of membrane, plasma membrane
SIHVA22b	protein-transporting ATPase activity, xenobiotic transmembrane transporter activity, antiporter activity, protein binding	establishment of localization, cellular process	cell periphery, intrinsic component of membrane
SIHVA22c	transmembrane transporter activity	cellular process, organic substance transport	integral component of membrane, plasma membrane
SIHVA22d	cytoskeletal protein binding, dystroglycan binding, cell adhesion molecule binding, inorganic cation transmembrane transporter activity	wound healing, cell migration, cell- cell adhesion, exocytosis	intercalated disc, obsolete cell- substrate adherens junction
SIHVA22e	signaling receptor binding, ATP binding,	obsolete multi-organism process, response to stimulus	cytoplasm

	transferase activity			
SIHVA22f	P-type potassium transmembrane transporter activity, sodium ion transmembrane transporter activity, purine ribonucleoside triphosphate binding, ion binding	response to chemical, transition metal ion transport	integral component of membrane	
SIHVA22g	ion binding			
SIHVA22h	cell adhesion molecule binding, cytoskeletal protein binding, dystroglycan binding	cell-cell junction assembly, adherens junction organization	obsolete contractile fiber part, adherens junction	
SIHVA22i	transition metal ion binding, monooxygenase activity	small molecule metabolic process		
SIHVA22j	transferase activity, metal ion binding	isoprenoid biosynthetic process		
SIHVA22k	ion binding, ion transmembrane transporter activity	response to chemical, transition metal ion transport	plasma membrane, integral component of membrane	
SIHVA22l	protein specific domain binding,	aerobic respiration, electron transport	obsolete cytoplasmic	

	electron activity	transfer	chain		part, intracellular membrane-bounded organelle
SIHVA22l	metal ion binding		metabolic process		Intracellular anatomical structure, membrane
SIHVA22n	guanyl ribonucleotide binding, purine ribonucleoside triphosphate binding		tricarboxylic acid cycle, proton transmembrane transport, G protein-coupled receptor signaling pathway		intrinsic component of membrane
SIHVA22o	signaling binding	receptor	anatomical structure involved in morphogenesis	formation	plasma membrane

Table S10. Annotated pathways of co-expressed genes with *SIHVA22* genes

Term	MainClasses	GeneHitsInSelectedSet	AllGenesInSelectedSet	P-value	GeneListInSelectedSets
Metabolism of terpenoids and polyketides	Metabolism	2	130	0.0085951	[Solyc11g007020, Solyc06g062330]
Oxidative phosphorylation	Metabolism	5	130	0.0094008	[Solyc12g005060, Solyc06g067920, Solyc10g051350, Solyc11g011470, Solyc01g087120]

Pyrimidine metabolism	Metaboli sm	2	130	0.014 1336	[Solyc05g010150, Solyc10g005880]
Metabolism of cofactors and vitamins	Metaboli sm	3	130	0.098 1085	[Solyc12g042460, Solyc07g043590, Solyc12g096590]
Arginine and proline metabolism	Metaboli sm	1	130	0.113 3896	[Solyc07g043590]
Alanine, aspartate and glutamate metabolism	Metaboli sm	2	130	0.163 5698	[Solyc10g080320, Solyc10g078550]
Nucleotide metabolism	Metaboli sm	4	130	0.193 2533	[Solyc10g080320, Solyc08g079020, Solyc05g010150, Solyc10g005880]
Carbohydrate metabolism	Metaboli sm	6	130	0.261 2796	[Solyc06g071920, Solyc07g007790, Solyc12g049590, Solyc03g097410, Solyc11g008720, Solyc09g090140]
Glyoxylate and dicarboxylate metabolism	Metaboli sm	1	130	0.585 3759	[Solyc09g090140]
Nitrogen metabolism	Metaboli sm	2	130	0.631 6198	[Solyc10g078550, Solyc06g074990]
Phenylalanine metabolism	Metaboli sm	1	130	0.631 6198	[Solyc08g068680]
Energy metabolism	Metaboli sm	12	130	0.717 8608	[Solyc06g071920, Solyc12g005060, Solyc06g067920, Solyc02g011990, Solyc10g051350, Solyc08g067320, Solyc11g011470, Solyc10g078550, Solyc01g087120, Solyc06g074990, Solyc09g064580, Solyc09g090140]
Purine metabolism	Metaboli sm	3	130	0.781 4045	[Solyc10g080320, Solyc08g079020, Solyc05g010150]
Pantothenate and Cobiosynthesis	Metaboli sm	1	130	0.989 8759	[Solyc07g043590]
Stilbenoid, diarylheptanoid and gingerol biosynthesis	Metaboli sm	1	130	0.011 852	[Solyc12g088170]

Carbon fixation in photosynthetic organisms	Metabolism	2	130	0.015 8787	[Solyc06g071920, Solyc09g090140]
Citrate cycle (TCcycle)	Metabolism	1	130	0.031 2843	[Solyc09g090140]
Starch and sucrose metabolism	Metabolism	2	130	0.041 388	[Solyc07g007790, Solyc11g008720]
Biosynthesis of other secondary metabolites	Metabolism	3	130	0.053 2613	[Solyc12g088170, Solyc12g042460, Solyc11g008720]
Glycan biosynthesis and metabolism	Metabolism	1	130	0.161 8181	[Solyc08g076570]
Photosynthesis	Metabolism	3	130	0.198 2193	[Solyc12g005060, Solyc02g011990, Solyc09g064580]
Glycerolipid metabolism	Metabolism	1	130	0.357 6286	[Solyc09g014350]
Selenocompound metabolism	Metabolism	1	130	0.719 5953	[Solyc10g081510]
Cysteine and methionine metabolism	Metabolism	2	130	2.92E -03	[Solyc10g081510, Solyc09g090140]
Glycerophospholipid metabolism	Metabolism	2	130	0.017 7595	[Solyc09g014350, Solyc07g055980]
Terpenoid backbone biosynthesis	Metabolism	1	130	0.030 3528	[Solyc11g007020]
Metabolism of other amino acids	Metabolism	4	130	0.077 0684	[Solyc09g065900, Solyc10g081510, Solyc07g043590, Solyc11g008720]
Inositol phosphate metabolism	Metabolism	2	130	0.271 6742	[Solyc12g049590, Solyc03g097410]
Pyruvate metabolism	Metabolism	1	130	0.274 5623	[Solyc09g090140]

Glycolysis / Gluconeogenesis	Metaboli sm	1	130	0.396 317	[Solyc06g071920] [Solyc11g007020, Solyc12g005060, Solyc10g080320, Solyc01g079390, Solyc10g081510, Solyc05g010150, Solyc10g005880, Solyc12g096990, Solyc07g055980, Solyc12g096590, Solyc06g062330, Solyc09g065900, Solyc12g042460, Solyc06g067920, Solyc08g067320, Solyc07g007790, Solyc12g049590, Solyc07g043590, Solyc02g011990, Solyc09g014350, Solyc08g079020, Solyc10g078550, Solyc06g074990, Solyc03g097410, Solyc08g076570, Solyc11g008720, Solyc09g090140, Solyc12g088170, Solyc06g071920, Solyc10g051350, Solyc11g011470, Solyc08g068680, Solyc01g087120, Solyc09g064580]
Metabolism	Metaboli sm	34	130	0.465 0306	
beta-Alanine metabolism	Metaboli sm	1	130	0.512 635	[Solyc07g043590]
Riboflavin metabolism	Metaboli sm	1	130	0.586 2166	[Solyc12g096590]
Ubiquinone and other terpenoid- quinone biosynthesis	Metaboli sm	1	130	0.615 5432	[Solyc12g042460]
Zeatin biosynthesis	Metaboli sm	1	130	0.625 7011	[Solyc06g062330]
Cyanoamino acid metabolism	Metaboli sm	1	130	0.802 6207	[Solyc11g008720]
Flavonoid biosynthesis	Metaboli sm	1	130	0.810 2446	[Solyc12g088170]
Lipid metabolism	Metaboli sm	2	130	8.85E -05	[Solyc09g014350, Solyc07g055980]

Arginine biosynthesis	Metaboli sm	1	130	0.003 0303	[Solyc10g078550]
Lysine degradation	Metaboli sm	2	130	0.149 4335	[Solyc01g079390, Solyc12g096990]
Photosynthesis - antennproteins	Metaboli sm	1	130	0.215 7282	[Solyc08g067320]
Amino acid metabolism	Metaboli sm	8	130	0.294 0862	[Solyc10g080320, Solyc01g079390, Solyc10g081510, Solyc12g096990, Solyc10g078550, Solyc08g068680, Solyc07g043590, Solyc09g090140]
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	Metaboli sm	1	130	0.527 6394	[Solyc08g076570]
Glutathione metabolism	Metaboli sm	1	130	0.670 6342	[Solyc09g065900]
Phenylpropanoid biosynthesis	Metaboli sm	3	130	0.271 8919	[Solyc12g088170, Solyc12g042460, Solyc11g008720]
Ribosome biogenesis in eukaryotes	Genetic Informati on Processin g	1	130	0.039 5269	[Solyc07g063270]
Folding, sorting and degradation	Genetic Informati on Processin g	14	130	0.058 0914	[Solyc02g082460, Solyc10g012240, Solyc06g005990, Solyc06g082600, Solyc05g056110, Solyc10g077030, Solyc02g078210, Solyc08g008130, Solyc09g082320, Solyc11g045130, Solyc07g016200, Solyc06g084210, Solyc11g019920, Solyc10g084050]
Translation	Genetic Informati on Processin g	11	130	0.077 1657	[Solyc09g009120, Solyc09g030390, Solyc09g075290, Solyc12g096540, Solyc12g008570, Solyc12g035650, Solyc09g092090, Solyc07g006010, Solyc12g014600, Solyc07g063270, Solyc10g018610]

Ubiquitin mediated proteolysis	Genetic Information Processing	4	130	0.175 7509	[Solyc08g008130, Solyc10g012240, Solyc06g082600, Solyc02g078210]
Protein processing in endoplasmic reticulum	Genetic Information Processing	4	130	0.285 3175	[Solyc06g082600, Solyc06g084210, Solyc11g019920, Solyc10g084050]
RNdegradation	Genetic Information Processing	4	130	0.356 2572	[Solyc02g082460, Solyc11g045130, Solyc06g005990, Solyc05g056110]
mRNsurveillance pathway	Genetic Information Processing	3	130	0.410 4152	[Solyc09g009120, Solyc09g030390, Solyc12g014600]
Ribosome	Genetic Information Processing	4	130	0.502 6504	[Solyc09g075290, Solyc12g096540, Solyc09g092090, Solyc10g018610]
Base excision repair	Genetic Information Processing	1	130	0.533 5866	[Solyc06g076660]

Nucleotide excision repair	Genetic Information Processing	2	130	0.672 89	[Solyc06g076660, Solyc02g067670]
Basal transcription factors	Genetic Information Processing	1	130	0.966 3864	[Solyc10g079370] [Solyc02g082460, Solyc06g076660, Solyc12g008570, Solyc12g035650, Solyc09g092090, Solyc06g082600, Solyc05g056110, Solyc10g077030, Solyc10g079370, Solyc09g082320, Solyc11g045130, Solyc11g044340, Solyc07g008880, Solyc10g018610, Solyc11g019920, Solyc01g067830, Solyc10g012240, Solyc06g005990, Solyc02g078210, Solyc09g009120, Solyc09g030390, Solyc08g008130, Solyc09g009300, Solyc09g075290, Solyc12g096540, Solyc07g016200, Solyc06g084210, Solyc07g006010, Solyc03g033600, Solyc12g014600, Solyc07g063270, Solyc02g067670, Solyc10g084050]
Genetic Information Processing	Genetic Information Processing	33	130	0.001 4094	
Replication and repair	Genetic Information Processing	2	130	0.007 3591	[Solyc06g076660, Solyc02g067670]
Mismatch repair	Genetic Information Processing	1	130	0.356 3425	[Solyc06g076660]

Aminoacyl-tRNA biosynthesis	Genetic Information Processing	1	130	0.468 2645	[Solyc12g008570]
Transcription	Genetic Information Processing	6	130	0.952 1377	[Solyc01g067830, Solyc09g009300, Solyc11g044340, Solyc07g008880, Solyc03g033600, Solyc10g079370]
DN replication	Genetic Information Processing	1	130	1.41E -07	[Solyc06g076660]
Nucleocytoplasmic transport	Genetic Information Processing	3	130	0.757 9823	[Solyc09g030390, Solyc12g035650, Solyc07g006010]
Spliceosome	Genetic Information Processing	5	130	0.008 2091	[Solyc01g067830, Solyc09g009300, Solyc11g044340, Solyc07g008880, Solyc03g033600]
Proteasome	Genetic Information Processing	3	130	0.362 5192	[Solyc09g082320, Solyc07g016200, Solyc10g077030]

Environmental Information Processing	Environmental Information Processing	8	130	0.0054095	[Solyc09g008240, Solyc02g090390, Solyc12g099830, Solyc07g064820, Solyc08g081610, Solyc12g049590, Solyc03g097410, Solyc02g071350]
Membrane transport	Environmental Information Processing	2	130	0.0237072	[Solyc09g008240, Solyc02g071350]
Phosphatidylinositol signaling system	Environmental Information Processing	2	130	0.1318688	[Solyc12g049590, Solyc03g097410]
Plant hormone signal transduction	Environmental Information Processing	2	130	0.6157035	[Solyc02g090390, Solyc12g099830]
MAPK signaling pathway - plant	Environmental Information Processing	3	130	0.344657	[Solyc02g090390, Solyc07g064820, Solyc08g081610]
ABC transporters	Environmental	2	130	1.17E-02	[Solyc09g008240, Solyc02g071350]

	Information Processing				
	Environmental Information Processing				
Signal transduction		6	130	0.390 2295	[Soly02g090390, Soly02g099830, Soly07g064820, Soly08g081610, Soly02g049590, Soly03g097410]
Cellular Processes	Cellular Processes	3	130	0.212 3418	[Soly02g099080, Soly03g031650, Soly02g049590]
Endocytosis	Cellular Processes	1	130	0.071 6251	[Soly02g099080]
Phagosome	Cellular Processes	1	130	0.570 4954	[Soly02g049590]
Transport and catabolism	Cellular Processes	3	130	1.72E -04	[Soly02g099080, Soly03g031650, Soly02g049590]
Autophagy - other	Cellular Processes	1	130	0.371 0518	[Soly03g031650]
Plant-pathogen interaction	Organismal Systems	2	130	0.990 845	[Soly08g081610, Soly07g047960]
Organismal Systems	Organismal Systems	2	130	0.810 2446	[Soly08g081610, Soly07g047960]
Environmental adaptation	Organismal Systems	2	130	0.445 2339	[Soly08g081610, Soly07g047960]

Protein kinases	Brite Hierarchies	4	130	0.005 674	[Solyc02g090390, Solyc12g099830, Solyc07g064820, Solyc06g073630]
Ion channels	Brite Hierarchies	2	130	0.060 5392	[Solyc07g052390, Solyc07g007690]
Peptidases and inhibitors	Brite Hierarchies	5	130	0.110 3079	[Solyc10g024320, Solyc09g082320, Solyc07g016200, Solyc10g077030, Solyc02g079000]
Transcription machinery	Brite Hierarchies	5	130	0.117 5514	[Solyc09g009120, Solyc02g094360, Solyc06g083260, Solyc11g012740, Solyc10g079370]
DNreplication proteins	Brite Hierarchies	4	130	0.178 0005	[Solyc06g076660, Solyc10g049360, Solyc03g033600, Solyc07g066660]
Messenger RNbiogenesis	Brite Hierarchies	14	130	0.217 4993	[Solyc02g082460, Solyc05g032850, Solyc12g035650, Solyc04g077060, Solyc06g005990, Solyc01g090480, Solyc05g056110, Solyc12g040510, Solyc09g009120, Solyc09g030390, Solyc11g045130, Solyc07g006010, Solyc12g014600, Solyc10g084050]
GTP-binding proteins	Brite Hierarchies	1	130	0.269 3477	[Solyc12g099080]
Glycosyltransferases	Brite Hierarchies	1	130	0.359 8012	[Solyc01g073750]
Cytoskeleton proteins	Brite Hierarchies	2	130	0.504 0355	[Solyc08g008130, Solyc12g098630]

Lipid biosynthesis proteins	Brite Hierarchies	1	130	0.636 7832	[Solyc09g014350]
Ribosome	Brite Hierarchies	4	130	0.725 7998	[Solyc09g075290, Solyc12g096540, Solyc09g092090, Solyc10g018610]
Amino acid related enzymes	Brite Hierarchies	1	130	0.744 7201	[Solyc12g008570]
Translation factors	Brite Hierarchies	2	130	0.927 6829	[Solyc07g008610, Solyc11g045120]
Protein families: signaling and cellular processes	Brite Hierarchies	22	130	0.011 852	[Solyc12g099080, Solyc12g005270, Solyc07g052390, Solyc10g079200, Solyc08g079020, Solyc10g078550, Solyc06g074990, Solyc02g071350, Solyc12g040510, Solyc09g008240, Solyc08g081190, Solyc06g071920, Solyc08g008130, Solyc02g070530, Solyc12g098630, Solyc05g009690, Solyc07g007690, Solyc04g081150, Solyc09g008490, Solyc10g054930, Solyc11g019920, Solyc10g084050]
Transcription factors	Brite Hierarchies	5	130	0.031 2843	[Solyc09g009100, Solyc08g081610, Solyc10g054330, Solyc07g047960, Solyc01g073910]
Protein phosphatases and associated proteins	Brite Hierarchies	4	130	0.039 4022	[Solyc04g074190, Solyc04g081900, Solyc07g007690, Solyc04g056340]
Protein families: metabolism	Brite Hierarchies	20	130	0.117 494	[Solyc04g074190, Solyc12g008570, Solyc12g005060, Solyc02g011990, Solyc06g073630, Solyc04g081900, Solyc09g014350, Solyc10g077030, Solyc02g079000, Solyc04g056340, Solyc02g090390, Solyc01g073750,

					Solyc10g024320, Solyc09g082320, Solyc12g099830, Solyc07g064820, Solyc07g016200, Solyc08g067320, Solyc07g007690, Solyc09g064580]
Domain-containing proteins not elsewhere classified	Brite Hierarchies	1	130	0.141 7706	[Solyc09g008490]
Photosynthesis proteins	Brite Hierarchies	4	130	0.148 5029	[Solyc12g005060, Solyc02g011990, Solyc08g067320, Solyc09g064580]
Transporters	Brite Hierarchies	8	130	0.151 2258	[Solyc09g008240, Solyc08g081190, Solyc02g070530, Solyc10g079200, Solyc05g009690, Solyc06g074990, Solyc10g054930, Solyc02g071350]
Chromosome and associated proteins	Brite Hierarchies	9	130	0.198 7293	[Solyc11g066160, Solyc05g021530, Solyc12g005270, Solyc01g079390, Solyc07g006010, Solyc10g049360, Solyc12g096990, Solyc04g081150, Solyc07g066660]
Exosome	Brite Hierarchies	11	130	0.287 4254	[Solyc09g008240, Solyc12g099080, Solyc06g071920, Solyc12g005270, Solyc08g079020, Solyc10g078550, Solyc04g081150, Solyc02g071350, Solyc12g040510, Solyc11g019920, Solyc10g084050]
					[Solyc06g076660, Solyc07g008610, Solyc08g081610, Solyc02g094360, Solyc12g014470, Solyc12g098630, Solyc11g045130, Solyc10g054930, Solyc11g019920, Solyc05g032850, Solyc04g074190, Solyc05g054100, Solyc04g077060, Solyc06g005990, Solyc02g011990, Solyc06g074990, Solyc02g079000, Solyc12g009610, Solyc12g040510, Solyc09g030390, Solyc06g071920, Solyc02g090390, Solyc10g024320, Solyc09g009300, Solyc07g064820, Solyc05g021530, Solyc02g067670, Solyc10g084050, Solyc04g008510, Solyc08g023590, Solyc06g082600, Solyc07g052390, Solyc12g096990, Solyc10g077030, Solyc07g008880, Solyc12g049590, Solyc04g081150, Solyc07g007810, Solyc01g067830,
Brite Hierarchies	Brite Hierarchies	105	130	0.586 2166	

					Solyc12g005270, Solyc10g079200, Solyc02g078210, Solyc09g009120, Solyc11g066160, Solyc08g008130, Solyc09g075290, Solyc11g045120, Solyc11g019930, Solyc06g084210, Solyc03g083020, Solyc07g066660, Solyc07g063270, Solyc11g012740, Solyc02g082460, Solyc12g099080, Solyc12g035650, Solyc10g054330, Solyc06g073630, Solyc10g076360, Solyc01g090480, Solyc11g068450, Solyc01g073750, Solyc01g073910, Solyc07g007690, Solyc05g026130, Solyc10g083600, Solyc04g056340, Solyc12g096540, Solyc09g009100, Solyc10g049360, Solyc12g014600, Solyc06g083260, Solyc09g008490, Solyc09g064580, Solyc12g008570, Solyc09g092090, Solyc12g005060, Solyc01g079390, Solyc03g031650, Solyc05g056110, Solyc02g071350, Solyc10g079370, Solyc09g008240, Solyc08g081190, Solyc09g082320, Solyc11g044340, Solyc08g067320, Solyc05g009690, Solyc10g018610, Solyc10g012240, Solyc04g081900, Solyc09g014350, Solyc08g079020, Solyc10g078550, Solyc08g062560, Solyc02g070530, Solyc12g099830, Solyc09g091830, Solyc12g044370, Solyc09g090740, Solyc01g090190, Solyc07g016200, Solyc07g047960, Solyc07g006010, Solyc03g033600]
Mitochondrial biogenesis	Brite Hierarchies	4	130	0.605 9362	[Solyc10g024320, Solyc12g008570, Solyc12g014470, Solyc03g031650]
Protein families: genetic information processing	Brite Hierarchies	79	130	6.34E -05	[Solyc02g082460, Solyc06g076660, Solyc12g099080, Solyc07g008610, Solyc12g035650, Solyc08g081610, Solyc10g054330, Solyc10g076360, Solyc01g090480, Solyc02g094360, Solyc11g068450, Solyc12g014470, Solyc11g045130, Solyc01g073910, Solyc11g019920, Solyc05g032850, Solyc05g026130, Solyc05g054100, Solyc04g077060, Solyc06g005990, Solyc10g083600, Solyc02g079000, Solyc12g009610, Solyc12g040510,

					Solyc09g030390, Solyc06g071920, Solyc10g024320, Solyc09g009300, Solyc12g096540, Solyc05g021530, Solyc09g009100, Solyc10g049360, Solyc12g014600, Solyc06g083260, Solyc02g067670, Solyc10g084050, Solyc04g008510, Solyc08g023590, Solyc12g008570, Solyc09g092090, Solyc06g082600, Solyc01g079390, Solyc03g031650, Solyc12g096990, Solyc05g056110, Solyc10g077030, Solyc10g079370, Solyc09g082320, Solyc11g044340, Solyc07g008880, Solyc05g009690, Solyc12g049590, Solyc04g081150, Solyc10g018610, Solyc07g007810, Solyc01g067830, Solyc10g012240, Solyc12g005270, Solyc02g078210, Solyc09g009120, Solyc11g066160, Solyc08g062560, Solyc08g008130, Solyc09g075290, Solyc09g091830, Solyc12g044370, Solyc09g090740, Solyc01g090190, Solyc07g016200, Solyc11g045120, Solyc11g019930, Solyc06g084210, Solyc07g047960, Solyc07g006010, Solyc03g033600, Solyc03g083020, Solyc07g066660, Solyc07g063270, Solyc11g012740]
CD molecules	Brite Hierarchies	2	130	0.339 3994	[Solyc09g008240, Solyc02g071350]
Transfer RNbiogenesis	Brite Hierarchies	3	130	0.395 1042	[Solyc12g008570, Solyc12g044370, Solyc03g083020]
Proteasome	Brite Hierarchies	3	130	0.512 635	[Solyc09g082320, Solyc07g016200, Solyc10g077030]
Membrane trafficking	Brite Hierarchies	14	130	0.597 7576	[Solyc12g099080, Solyc07g007810, Solyc05g026130, Solyc05g054100, Solyc03g031650, Solyc10g076360, Solyc12g009610, Solyc06g071920, Solyc11g068450,

					Solyc06g084210, Solyc05g009690, Solyc12g049590, Solyc11g019920, Solyc10g084050]
Spliceosome	Brite Hierarchies	7	130	0.085 5238	[Solyc09g030390, Solyc01g067830, Solyc09g009300, Solyc01g090190, Solyc11g044340, Solyc07g008880, Solyc03g033600]
Ribosome biogenesis	Brite Hierarchies	5	130	0.205 2012	[Solyc08g062560, Solyc09g090740, Solyc10g083600, Solyc07g063270, Solyc10g084050]
Ubiquitin system	Brite Hierarchies	7	130	0.191 198	[Solyc04g008510, Solyc08g008130, Solyc10g012240, Solyc06g082600, Solyc03g031650, Solyc11g019930, Solyc02g078210]
DNrepair and recombination proteins	Brite Hierarchies	3	130	0.246 1736	[Solyc06g076660, Solyc08g023590, Solyc02g067670]
Chaperones and folding catalysts	Brite Hierarchies	4	130	0.337 3161	[Solyc09g091830, Solyc12g014470, Solyc02g079000, Solyc11g019920]

Table S11. In silico subcellular localization of SIHVA22 proteins

SIHVA22a WoLFPSORT prediction nucl: 9, cyto: 2, extr: 1, cysk: 1, golg: 1

PSORT features and traditional PSORTII prediction

No.14 Nearest Neighbors

id	site	distance	identity	comments
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1	At2g39250.1	nucl	177.162	12.95%	[Arath]
2	WR29_ARATH	nucl	194.499	13.49%	[Uniprot] SWISS-PROT45:Nuclear.
3	At1g33030.1	cyto	196.351	14.20%	[Arath]
4	At1g22190.1	nucl	208.715	14.18%	[Arath]
5	ILLA_LEUGL	extr	217.269	11.36%	[Uniprot] SWISS-PROT45:Secreted.
6	At4g39780.1	nucl	223.392	12.13%	[Arath]
7	At5g65130.1	nucl	227.6	13.00%	[Arath]
8	At2g43130.1	golg	247.16	9.91%	[Arath]
9	At1g18450.1	nucl	249.344	14.29%	[Arath]
10	At1g64380.1	nucl	252.787	13.13%	[Arath]
11	RPB1_ARATH	nucl	256.002	4.84%	[Uniprot] SWISS-PROT45:Nuclear.
12	TTG1_ARATH	cyto	258.983	15.20%	[Uniprot] SWISS-PROT45:Cytoplasmic.
13	At3g60490.1	nucl	263.043	12.84%	[Arath]
14	At5g62500.1	cysk	264.822	11.60%	[Arath]

SIHVA22b WoLFPSORT prediction extr: 6, vacu: 3, nucl: 1, cyto: 1, mito: 1, plas: 1, golg: 1

PSORT features and traditional PSORTII prediction

14 Nearest Neighbors

No.id	site	distance	identity	comments
1	E13A_LYCES	extr	215.85 11.61%	[Uniprot] SWISS-PROT45:Extracellular.
2	At2g29960.1	cyto	251.258 12.44%	[Arath]
3	AFP4_RAPSA	extr	331.72 11.03%	[Uniprot] SWISS-PROT45:Secreted.
4	PHS1_PHALU	vacu	346.209 9.11%	[Uniprot] SWISS-PROT45:Cotyledonary membrane-bound vacuolar protein bodies.
5	GAS1_ARATH	extr	349.568 13.24%	[Uniprot] SWISS-PROT45:Secreted.
6	At1g21230.1	plas	357.998 6.41%	[Arath]
7	At5g17020.1	nucl	367.876 5.77%	[Arath]
8	VCLC_PEA	vacu	381.164 8.93%	[Uniprot] SWISS-PROT45:Cotyledonary membrane-bound vacuolar protein bodies.
9	AFP3_BRANA	extr	388.604 10.29%	[Uniprot] SWISS-PROT45:Secreted.
10	STSY_CATRO	vacu	394.169 11.08%	[Uniprot] SWISS-PROT45:Vacuolar.
11	ADT1_WHEAT	mito	402.523 9.97%	[Uniprot] SWISS-PROT45:Integral membrane protein. Mitochondrial inner membrane.
12	EXTN_TOBAC	extr	405.401 5.97%	[Uniprot] SWISS-PROT45:Extracellular matrix.
13	AFP1_BRANA	extr	405.71 12.50%	[Uniprot] SWISS-PROT45:Secreted.
14	At4g38240.1	golg	406.638 11.26%	[Arath]

SIHVA22c WoLFPSORT prediction E.R.: 4.5, E.R._plas: 4, nucl: 3, plas: 2.5, vacu: 2, chlo: 1, pero: 1

PSORT features and traditional PSORTII prediction

14 Nearest Neighbors

No.	id	site	distance	identity	comments
1	At2g23800.1	E.R.	240.68	13.56%	[Arath]
2	SPR1_IPOBA	vacu	269.291	12.61%	[Uniprot] SWISS-PROT45:Vacuolar.
3	At2g39970.1	pero	289.15	11.48%	[Arath]
4	At5g17020.1	nucl	323.826	6.42%	[Arath]
5	NCPR_PHAAU	E.R.	329.298	8.99%	[Uniprot] SWISS-PROT45:Endoplasmic reticulum. Anchored to the ER membrane by its N-terminal hydrophobic region.
6	At5g53470.1	plas	344.03	14.50%	[Arath]
7	At4g27780.1	E.R._plas	350.213	13.56%	[Arath]
8	At1g21270.1	plas	357.245	9.56%	[Arath]
9	SPRA_IPOBA	vacu	357.791	12.33%	[Uniprot] SWISS-PROT45:Vacuolar.
10	MAOC_FLATR	chlo	380.503	10.34%	[Uniprot] SWISS-PROT45:Chloroplast.
11	At2g18640.1	E.R.	381.884	13.17%	[Arath]
12	SC11_ARATH	nucl	383.116	8.61%	[Uniprot] SWISS-PROT45:Nuclear.
13	NTPA_PEA	nucl	387.156	10.11%	[Uniprot] SWISS-PROT45:Nuclear.

14 At4g24520.1 E.R. 389.521 8.95% [Arath]

SIHVA22d WoLFPSORT prediction extr: 4, vacu: 4, E.R.: 2, chlo: 1, cyto: 1, mito: 1, pero: 1

PSORT features and traditional PSORTII prediction

14 Nearest Neighbors

No.	id	site	distance	identity	comments
1	At2g29960.1	cyto	387.426	12.44%	[Arath]
2	MFPA_CUCSA	pero	402.102	9.24%	[Uniprot] SWISS-PROT45:Glyoxysomal. GO:0009514; C:glyoxysome; Evidence:NAS
3	At1g20330.1	E.R.	434.216	14.68%	[Arath]
4	At3g10570.1	mito	438.147	9.16%	[Arath]
5	CKX3_ARATH	extr	438.25	11.28%	[Uniprot] SWISS-PROT45:Extracellular.
6	At1g77590.1	chlo	459.169	8.25%	[Arath]
7	BG1_ARATH	E.R.	464.551	10.80%	[Uniprot] SWISS-PROT45:Endoplasmic reticulum.
8	ASPR_CUCPE	vacu	469.784	10.53%	[Uniprot] SWISS-PROT45:Vacuolar.
9	E13H_TOBAC	extr	471.476	13.57%	[Uniprot] SWISS-PROT45:Extracellular.
10	E13A_LYCES	extr	472.463	12.20%	[Uniprot] SWISS-PROT45:Extracellular.

11	VPEG_ARATH	vacu	474.38	9.80%	[Uniprot] SWISS-PROT45:Vacuolar.
12	AFP4_RAPSA	extr	478.689	13.64%	[Uniprot] SWISS-PROT45:Secreted.
13	At4g35350.1	vacu	480.851	13.24%	[Arath]
14	VPEB_ARATH	vacu	481.14	10.70%	[Uniprot] SWISS-PROT45:Vacuolar.

SIHVA22e WoLFPSORT prediction cyto_nucl: 6.33333, cyto: 5, nucl: 3.5, chlo: 3, cysk_nucl: 2.83333, mito: 2

PSORT features and traditional PSORTII prediction

14 Nearest Neighbors

No.	id	site	distance	identity	comments
1	UBIQ_ACECL	cyto_nucl	250.703	14.55%	[Uniprot] SWISS-PROT45:Nuclear and cytoplasmic.
2	UBIQ_ARATH	cyto_nucl	275.769	12.73%	[Uniprot] SWISS-PROT45:Nuclear and cytoplasmic.
3	UBIQ_CHLRE	cyto_nucl	275.769	13.64%	[Uniprot] SWISS-PROT45:Nuclear and cytoplasmic.
4	UBIQ_SOYBN	cyto_nucl	275.769	12.73%	[Uniprot] SWISS-PROT45:Nuclear and cytoplasmic.
5	At3g51260.1	cysk_nucl	291.017	16%	[Arath]
6	At1g04640.1	mito	294.507	10.64%	[Arath]
7	RPBX_BRANA	nucl	294.525	13.64%	[Uniprot] SWISS-PROT45:Nuclear.
8	GSHR_PEA	cyto	305.931	7.03%	[Uniprot] SWISS-PROT45:Cytoplasmic.

9	KADC_MAIZE	chlo	312.751	14.41%	[Uniprot] SWISS-PROT45:Chloroplast.
10	At4g34050.1	cyto	313.426	12.36%	[Arath]
11	At4g29430.1	mito	314.941	16.28%	[Arath]
12	At1g67990.1	cyto	316.814	15.02%	[Arath]
13	CRTI_SOYBN	chlo	319.005	6.49%	[Uniprot] SWISS-PROT45:Chloroplast; chromoplast.
14	RBMT_PEA	chlo	319.104	8.18%	[Uniprot] SWISS-PROT45:Chloroplast.

SIHVA22f WoLFPSORT prediction nucl: 12, extr: 2

PSORT features and traditional PSORTII prediction

14 Nearest Neighbors

No.	id	site	distance	identity	comments
1	At4g05420.1	nucl	418.573	11.49%	[Arath]
2	PGL2_JUNAS	extr	645.461	13.81%	[Uniprot] SWISS-PROT45:Secreted.
3	PGLR_ACTCH	extr	744.1	9.24%	[Uniprot] SWISS-PROT45:Secreted.
4	TBP2_ARATH	nucl	745.091	10.23%	[Uniprot] SWISS-PROT45:Nuclear.
5	TBP1_ARATH	nucl	760.569	10.23%	[Uniprot] SWISS-PROT45:Nuclear.
6	TBP2_MAIZE	nucl	777.428	10.23%	[Uniprot] SWISS-PROT45:Nuclear.
7	TBP_SOYBN	nucl	782.333	10.02%	[Uniprot] SWISS-PROT45:Nuclear.

8	TBP_TOBAC	nucl	792.556	10.45%	[Uniprot] SWISS-PROT45:Nuclear.
9	TBP1_MAIZE	nucl	801.295	10.02%	[Uniprot] SWISS-PROT45:Nuclear.
10	TBP1_WHEAT	nucl	802.263	11.73%	[Uniprot] SWISS-PROT45:Nuclear.
11	TBP_MESCR	nucl	802.758	9.59%	[Uniprot] SWISS-PROT45:Nuclear.
12	TBP_SOLTU	nucl	809.91	10.02%	[Uniprot] SWISS-PROT45:Nuclear.
13	TBP2_WHEAT	nucl	867.618	10.66%	[Uniprot] SWISS-PROT45:Nuclear.
14	TBP_ACECL	nucl	896.678	11.73%	[Uniprot] SWISS-PROT45:Nuclear.

SIHVA22g WoLFPSORT prediction chlo: 9, nucl: 4, cyto: 1

PSORT features and traditional PSORTII prediction

14 Nearest Neighbors

No.	id	site	distance	identity	comments
1	At1g06680.1	chlo	214.159	12.79%	[Arath] Subclass:thylakoid
2	RBS5_ACECL	chlo	234.773	12.17%	[Uniprot] SWISS-PROT45:Chloroplast.
3	At1g75080.1	nucl	255.792	11.01%	[Arath]
4	TRB2_ARATH	cyto	265.066	12.53%	[Uniprot] SWISS-PROT45:Cytoplasmic.
5	RBS2_CHLRE	chlo	268.684	11.18%	[Uniprot] SWISS-PROT45:Chloroplast.
6	FER2_SPIOL	chlo	271.163	8.88%	[Uniprot] SWISS-PROT45:Chloroplast.

7	RBS_LARLA	chlo	277.188	11.18%	[Uniprot] SWISS-PROT45:Chloroplast.
8	At3g14230.1	nucl	282.523	14.78%	[Arath]
9	RBS5_ACEME	chlo	283.165	11.18%	[Uniprot] SWISS-PROT45:Chloroplast.
10	At1g53910.1	nucl	284.295	13.69%	[Arath]
11	ALFC_CHLRE	chlo	285.83	12.57%	[Uniprot] SWISS-PROT45:Chloroplast.
12	RBS3_ACEME	chlo	286.93	12.50%	[Uniprot] SWISS-PROT45:Chloroplast.
13	At5g50080.1	nucl	287.647	13.82%	[Arath]
14	ALFC_ORYSA	chlo	288.087	14.32%	[Uniprot] SWISS-PROT45:Chloroplast.

SIHVA22h WoLFPSORT prediction E.R.: 3.5, cyto: 3, E.R._plas: 3, mito: 2, plas: 1.5, nucl: 1, extr: 1, vacu: 1, pero: 1

PSORT features and traditional PSORTII prediction

14 Nearest Neighbors

No.	id	site	distance	identity	comments		
1	ADT_CHLRE	mito	230.755	11.36%	[Uniprot] SWISS-PROT45:Integral	membrane	protein.
Mitochondrial inner membrane.							
2	At5g53470.1	plas	270.988	12.13%	[Arath]		
3	At4g27780.1	E.R._plas	327.684	12.99%	[Arath]		

4	MAOX_MESCR	cyto	355.97	9.23%	[Uniprot] SWISS-PROT45:Cytoplasmic.
5	At2g23800.1	E.R.	366.678	11.17%	[Arath]
6	MFPA_CUCSA	pero	384.506	9.10%	[Uniprot] SWISS-PROT45:Glyoxysomal. GO:0009514; C:glyoxysome; Evidence:NAS
7	At1g20330.1	E.R.	384.68	13.85%	[Arath]
8	F16Q_BRANA	cyto	391.039	13.27%	[Uniprot] SWISS-PROT45:Cytoplasmic.
9	E13A_LYCES	extr	391.103	13.99%	[Uniprot] SWISS-PROT45:Extracellular.
10	At3g30775.1	mito	393.43	10.37%	[Arath]
11	NCPR_CATRO	E.R.	395.882	8.96%	[Uniprot] SWISS-PROT45:Endoplasmic reticulum. Anchored to the ER membrane by its N-terminal hydrophobic region.
12	At5g17020.1	nucl	398.479	5.40%	[Arath]
13	F16Q_SPIOL	cyto	398.479	14.08%	[Uniprot] SWISS-PROT45:Cytoplasmic.
14	TIP2_TOBAC	vacu	406.185	12.40%	[Uniprot] SWISS-PROT45:Integral membrane protein; tonoplast membrane.

SIHVA22i WoLFPSORT prediction chlo: 11, cyto: 1.5, cyto_E.R.: 1.5, nucl_plas: 1

PSORT features and traditional PSORTII prediction

14 Nearest Neighbors

No.	id	site	distance	identity	comments
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1	CB2_PHYPA	chlo	225.936	12.27%	[Uniprot] SWISS-PROT45:Chloroplast thylakoid membrane.
2	CB23_POLMU	chlo	240.94	14.72%	[Uniprot] SWISS-PROT45:Chloroplast thylakoid membrane.
3	Atlg56330.1	cyto_E.R.	252.278	16.06%	[Arath]
4	PSY_CUCME	chlo	259.901	10.19%	[Uniprot] SWISS-PROT45:Chloroplast.
5	CRTI_ARATH Pubmed:9700076	chlo	261.119	9.72%	[Arath] [Uniprot] SWISS-PROT45:Chloroplast; chromoplast. Evidence:TAS
6	AAT5_ARATH Pubmed:7766905	chlo	267.813	10.82%	[Arath] [Uniprot] SWISS-PROT45:Chloroplast. Evidence:IDA
7	CB22_HORVU	chlo	269.008	14.02%	[Uniprot] SWISS-PROT45:Chloroplast thylakoid membrane.
8	CB28_PEA	chlo	269.629	13.81%	[Uniprot] SWISS-PROT45:Chloroplast thylakoid membrane.
9	PODK_FLATR	chlo	275.895	5.14%	[Uniprot] SWISS-PROT45:Chloroplast.
10	CB2A_SPIOL	chlo	276.431	11.61%	[Uniprot] SWISS-PROT45:Chloroplast thylakoid membrane.
11	At4g25100.1	chlo	277.09	12.26%	[Arath]
12	SODC_PANGI	cyto	279.73	9.21%	[Uniprot] SWISS-PROT45:Cytoplasmic.
13	PODK_FLABI	chlo	279.852	4.93%	[Uniprot] SWISS-PROT45:Chloroplast.
14	At5g65430.1	nucl_plas	287.866	14.11%	[Arath]

SIHVA22j WoLFPSORT prediction chlo: 8, extr: 2, vacu: 2, nucl: 1, plas: 1

PSORT features and traditional PSORTII prediction

14 Nearest Neighbors

No.	id	site	distance	identity	comments
1	KAP1_ARATH	chlo	355.038	14.13%	[Uniprot] SWISS-PROT45:Chloroplast.
2	CB11_LYCES	chlo	355.363	12.60%	[Uniprot] SWISS-PROT45:Chloroplast thylakoid membrane.
3	GAS3_ARATH	extr	363.373	13.46%	[Uniprot] SWISS-PROT45:Secreted.
4	CB21_GOSHI	chlo	368.78	16.98%	[Uniprot] SWISS-PROT45:Chloroplast thylakoid membrane.
5	AKT2_ARATH	plas	386.223	7.48%	[Uniprot] SWISS-PROT45:Integral membrane protein.
6	At4g08920.1	nucl	388.277	7.64%	[Arath]
7	CHMO_SPIOL	chlo	389.926	12.30%	[Uniprot] SWISS-PROT45:Chloroplast stroma.
8	ISPF_CATRO	chlo	391.167	12.71%	[Uniprot] SWISS-PROT45:Chloroplast.
9	CB24_LYCES	chlo	393.657	16.60%	[Uniprot] SWISS-PROT45:Chloroplast thylakoid membrane.
10	MYRO_BRANA	vacu	394.687	8.58%	[Uniprot] SWISS-PROT45:Vacuolar.
11	UCRB_TOBAC	chlo	399.487	13.16%	[Uniprot] SWISS-PROT45:Chloroplast thylakoid.
12	CKX4_ARATH	extr	403.08	9.73%	[Uniprot] SWISS-PROT45:Extracellular.
13	UCRA_TOBAC	chlo	404.234	12.72%	[Uniprot] SWISS-PROT45:Chloroplast thylakoid.
14	MYR3_SINAL	vacu	405.487	8.64%	[Uniprot] SWISS-PROT45:Vacuolar.

SIHVA22k WoLFPSORT prediction nucl: 13, pero: 1

PSORT features and traditional PSORTII prediction

14 Nearest Neighbors

No.	id	site	distance	identity	comments
1	At2g32950.1		nucl	288.734	13.78% [Arath]
2	TFB2_ARATH		nucl	327.372	14.13% [Uniprot] SWISS-PROT45:Nuclear.
3	TGAA_TOBAC		nucl	327.572	11.63% [Uniprot] SWISS-PROT45:Nuclear.
4	TF2B_ORYSA		nucl	351.031	13.06% [Uniprot] SWISS-PROT45:Nuclear.
5	TF2B_SOYBN		nucl	353.896	11.45% [Uniprot] SWISS-PROT45:Nuclear.
6	HSF8_LYCES		nucl	355.066	9.64% [Uniprot] SWISS-PROT45:Nuclear.
7	TT1_ARATH		nucl	358.463	15.21% [Uniprot] SWISS-PROT45:Nuclear.
8	PROL_ARATH		nucl	360.12	14.11% [Uniprot] SWISS-PROT45:Nuclear.
9	PRH_PETCR		nucl	370.796	11.67% [Uniprot] SWISS-PROT45:Nuclear.
10	HX1A_MAIZE		nucl	378.387	12.78% [Uniprot] SWISS-PROT45:Nuclear.
11	At2g35670.1		nucl	384.704	13.27% [Arath]
12	TGA7_ARATH		nucl	387.892	11.09% [Uniprot] SWISS-PROT45:Nuclear.
13	AG_LYCES		nucl	391.01	11.81% [Uniprot] SWISS-PROT45:Nuclear.
14	At1g79810.1		pero	394.711	13.77% [Arath]

SIHVA22I WoLFPSORT prediction E.R.: 6.5, E.R._plas: 5, cyto: 3, plas: 2.5, nucl: 1, mito: 1

PSORT features and traditional PSORTII prediction

14 Nearest Neighbors

No.	id	site	distance	identity	comments
1	At2g38960.1	E.R.	304.311	12.71%	[Arath] sequence changed in 2004
2	NCPR_PHAAU	E.R.	306.133	9.86%	[Uniprot] SWISS-PROT45:Endoplasmic reticulum. Anchored to the ER membrane by its N-terminal hydrophobic region.
3	At5g53470.1	plas	310.007	11.54%	[Arath]
4	At5g17020.1	nucl	323.072	6.14%	[Arath]
5	At4g24520.1	E.R.	324.888	7.66%	[Arath]
6	At4g27780.1	E.R._plas	339.809	12.99%	[Arath]
7	F16Q_BRANA	cyto	342.847	15.93%	[Uniprot] SWISS-PROT45:Cytoplasmic.
8	At5g61900.1	plas	352.559	9.69%	[Arath]
9	MAOX_MESCR	cyto	354.851	9.06%	[Uniprot] SWISS-PROT45:Cytoplasmic.
10	At1g20330.1	E.R.	359.631	10.53%	[Arath]
11	At3g30775.1	mito	368.086	11.60%	[Arath]
12	F16Q_ORYSA	cyto	378.832	15.34%	[Uniprot] SWISS-PROT45:Cytoplasmic.

13	FD3E_PHAAU	E.R.	386.398	15.79%	[Uniprot] SWISS-PROT45:Endoplasmic reticulum.
14	Atlg72280.1	E.R.	389.699	11.94%	[Arath]

The top two most similar predicted localization sites are highlighted in green.

Table S12. List of the HVA22 protein sequences used for phylogenetic analysis

Name	Accession	Sequence
CreHVA22a	Cre01.g027900	MIISAPICRVLMVVLGCAFPAYMTHKAVSSGNTQQLRHWCIYWLLMGFFMCVEWLADLSIF WLPLYEAKLLFVVALWHPRTHAAITLYDTYILPLLRLQHEATIDRHLSETRARLADAVTSQV NAAQGYVNNNAGAILQGLRTFSEQKPGAAPGSFSGQFTDLNHAKSQ
CreHVA22b	Cre03.g176930	MSVLEGVAHAVVQWVPLYFELKLVFVLWMTLPQTQGARMIEGILAPRLAAWERRLRGGS AGNGRGAAAAAKAGSERDEPAGAIAAAILQNDEDRGEGGSSKVKASLRNLFHRTHKSEG AEEAGGVRGSSGGGGGGGGGTAVGEGQEVGGVGGGGGVRLYSPLSAHLQQS
CreHVA22c	Cre03.g177500	MVLSFGLTYYYVCIFAELLFPTYASLKAIQSPGKLDQTQWLTYWVVYAFISTFESVGSIIQWIPL YYEIKLLFVLWMIAPQTQGARKIYEDHIMPLLKKYGDKIDPVFARAEQALESQYVNHLAKY VDKHGPAVLDAQALQAQKHGTVVAGMAQAAYQEQLKKAASGQPGAAAFSGAH
CreHVA22d	Cre17.g696850	MAEQVAELASGFLSFANQVAAPFLKAALATGTAAPVAVAAPTPVPVAASLGLKVLLEPQM GGVIFRAASNTVATIYPVYASAKAIESKDTADDVQWLTYWTLYGSMILAEHLADQALGKVP FYYHAKFAALLWLQLPQTRGAAYLYNRYYKPAMAQYGPHIDAVLSKGHNLLINLYAMYKV PIEAAVALGLQAWKSLLAAVKALSEDKKAVNKSDAVKPHAA
PpHVA22a	Pp3c1_21270	MMGSFITRAIIMVLGYIYPAYECYKIVERKRPDPEYLRFWCQYWVIIAVVTVVERFADALISW VPLYSEAKLAFIILWYPQTMGTTYVYNMLLRPLVAQHELEIDRNLNELRTRAGDVVLQWW QRGSVHAQARFSELLQFLAMQSNGSQQRSFPNQGVPPQGPAPAPAQGHGREYPPQNSPLYP QPAAGFPIDSSYPPEVRSHHETAPYPSSQGAQAGQELYPPIPPYSQPRRPYRSALSDGEGNF DIEVKHRVPFSSRMG
PpHVA22b	Pp3c2_21660	MAAAVSALGGELGLRLLLTPTASHVIVRTACTVVGIGFPIYSTHKAIENRNHSEQEELVYW AAYGCFSAEVFSDKLLSWCPFYHAKFVFLVWLQLPKNYGARHLYTSLLRPLLLKHHARL DRIVDGRNEMHKFVMNHQSEVQAVQRMKKFSVLVYQAAQDALQSARAIEGGSNPVGS RSSQESVTSPPSPSDSNYDETADDSGWIYTDHPRQSDQ
PpHVA22c	Pp3c3_14030	MGLLWPLSLRIYSLSGPAMMLIPLYASIMAIESADKEDDQQWLTYWVLYSLVSLMEMAAG PVLAWIPFYSTLKLIVASWLVLPPQFRGGIILYQKFVSPYLNATTGVSDQKLTEGQRKLLGSISSE TQALVSTYIKENRSDAFDRIMEIAVKDLNDNKVEEVMDKESSDPDSD

PpHVA22d	Pp3c4_23200	MGWLWALVLQGYAWSGPLMMLLYPLIASIMAIESPDMRDDRQWLTYWVLCSLALLLEIAL APVIVWIPFYSTIKLVIASWLVLQPFRGGTFLYENFVRPHFNDAAAAATNAQDPQQEWLERS VSPETQASVARFVEKHGSPGFELMRAALVHPKLSVDGMMKERGLVDENAS
PpHVA22e	Pp3c5_7630	MMGSFITRGVIMLLGYVYPAYECFKVVERNRPDLEHLRFWCQYWIIIASLTVFERVGDIFVSW VPMYNEAKLAFIILWYPKTLGTTYVYSSFLRPFVVKHESEIDHQLNELTTRAGDLAFFWWQ RGSAYIQAQVYQILAYVASQSNRTQQGTVVVRQVPPAARQASIFRPNAQIPRGPPRDPQPD QVHPPPVGRFPGHTPGGAGYPALNVEELHPPAALQAGTTLVPPVAGEAGPDLYPPPPGPNF TGSABRRRGRGAGTESAALLSENSDSYDVVEHSAENCPESRPESQLEKKSQQSHPSIGEEG VPLKVYNTRNRLRSGGSRSLSEWLPWLGSTPSGKDD
PpHVA22f	Pp3c6_23420	MVKTKVPGVFDCEEGLRYQLFKMMGSFITRGIIMLLGYVYPAYECFKVVEKNRPNLEHLRF WCQYWIIIAALTVFERLGEIMISWVPMYNEAKLAFIILWYPKTLGTSYVYFTFLRPFVVKHE SEIDRQLNELTTRAGDLAFFWWHRSSGYIQAQFYQLLAYVASQSNRTQQGTDSRQIPQPSRQ PPRPTSQIPHHDGPQGGPQVCPPPPSEGLPESAPGGAGYPPVNVEGPHPPPAAPLIGSGLYPP VAGQAGQGYPYPPPPGPHSTGSGVYRRRSGTGTGPANLLSEDSDSDSYDIVEHSAENRPE GRPEGRLESKPLQANPSTGVHDPVPLKVYNTRNRLRSSGSR
PpHVA22g	Pp3c10_4040	MAVGYYYPAYECYKIVERPMPDLEHLRFWCQYWMIIAVTVIERLADIVVSWVPMYSEAKL AFIILWYPKTMGTTYVYSTLLRPFVQYSEIDHNLNEVRTRAGDIALLLWWQKGSMYAQA RFYELLQFLASQSNKVQQNPSGAPSRTPAQGLSRGLPQGVPPQSYPPPGASGSETAPYPPQEA QAGQGQYPPPPSSSAGAHIRRSQSGRGVPVGDSDHGVVEKHSEKRTSYRLEDRTSGTSVGGQ NPPPRVQNTKTRPQTDSPWSISAWIPSLLGTTPSKKVD
PpHVA22h	Pp3c13_20961	MGWFWSLVLKSNALAGPIVMLLYPLYASVMAIESPFKEDDQQWLTYWVLYSFVSLLEMAA APVFAWIPLYSTIKLAVAAWLVLQPFRGGFIFYEKYVRPNFQNVGTGYSKALTESQRKFLATIS PETRSSVAKYIEAIGPESFENLIQKELEESRKKRAEEHQQGAVERNPHVE
PpHVA22i	Pp3c13_20970	MMLLYPLYASIMAIESHDKEDDQQWLTYWVLYSLVSLMEMAAGPVIAWIPFYSTFKLIASW LVLQPFRGGIILYEKFVSPYLNAATGVTDQKLTDGQRKWLGSISPEAQASVAAFIKENGSSAF DAFMKSATGDVKQDKIEETVEKKEGEAAGSSSDSD
PpHVA22j	Pp3c14_4540	MCIIFNSQKDLKRNLRPGWFTVVALDINCRKSRVEPLKMMGSFITRGIIMGLGYICPAYECYK VVDPRADLENLRFWCQYWMIIAVTVLERLGDIFISWMPMYCEAKLAFIILWYSKTMGT TCLYSKLLKPFVAKHESEIDHNLNELKTRAGEIALVWWQKWSIHVQARFHELLQFLARQSD RAQEGARGSSSRSHALNIPRGLTQGALLSHPPPPPPGITGSPAASYPSSQGSQAGQRIYPPPLS HSTGVHVQHQLRPLGIFDGEDSDHDVVEYHLGERAEHQSEERLERLVPASAGGQNLPPGV QNTRIRLQTDSPGNLSIWLPAWLGSTAPKKVDLQEGSRRYFGASYSFQLI
PpHVA22k	Pp3c16_15400	MMVSFITRGIIMLLGYVYPAYACFKVVERDRPDLEHLQFWCQYWIIIAALTVFERLGDVLVS WVPMYSEAKLAFIVYLWHPNTLGTKYVYSTFLRPIVARHEAEIDHHLHELTTRGGDLAYFW

		WQKCSNYAQSRIYELFSYVASQPNRTQQGSIARQSRRRPNFQGPPRGPPRPDYQGGPQVYPP APPAGYPGSTRAGYPPVNANTLEDSDSDYHVVEKIVESRPEGRPEGGMKSRSEQEVPPHVG NIRERVRADDSGGSRYLYGWLPGWFGTSSGKED
PpHVA22l	Pp3c26_3490	MGWFWTLVARSNVAGPIVMMLLYPLYASVMAIESPFKEDDQQWLTYWVLYSFSVLSLEMAA APVFAWIPLYSTIKLAIAAWLVLPPQFRGGVILYEFVKPHFYAALGGSADSSSLSSGQRKWLG SIKPETRTAIAKYVQVKGPEAFEKLVNSELVKSISQKPRVEENPHTE
PpHVA22m	Pp3c26_3510	MGWLSVAVLRGYALAGPVMMLLYPLYASIIAIESADKEDDQQWLTYWVLYSVVLSLEMAA GPVIAWIPFYSTTKLVIASWLVLPPQFRGGIILYEFVSPYLNAATGQTDQKLTHSQRKVLGSISP DAQASVAAYIKENGPFSFDELMRRETANMHDEKVAEEKKHHDGYSSSDPE
AmtrHVA22a	AMTR_s00010p00 257430	MGLGAFLKVVAQNIDVLGPIVTLVYPLYASVKAIESPSRVDDQQWLTYWVLYSMITLFEMT FYKAIAWFPFWSYAKLIAICWLVLPHYNGAAYVYEHYIRPCFVNPRQVNIWFFPGKKNALN NISDDARLAEKYLAENGPESEFEKLLRKAEMEIKPNRSSLSIFDENYRY
AmtrHVA22b	AMTR_s00016p00 231510	MLLYPLYASVRAIESPSKLDDEQWLAYWILYSFLTLMEMVAAPVLSWIPIWYQLKVAFAVWL VLPQFRGASFIYERFVREQLRKYDKAMGKGHRISPGKKNKFVDFVSPKAGEHEAY
AmtrHVA22c	AMTR_s00021p00 253210	MGVLGAIARNLDTVVGPMVMLIYPLYASIRAIIESPSALDDQQWLTYWVLYSLITLSELFSCWR ALAWFPLWPYMKLIFSLWLVLPIFNGAAYVYENVVKVHIPNLIKLNPDLTSSERRAIQMMTP EARGSVVERFIAKYGSDAFEKVKAEEKEAKKR
AmtrHVA22d	AMTR_s00030p00 233590	MFRVREDGITQQRIVLGAYPAYECFKCVEENKTDVDQLRFWCQYWIIVAMLTVFERAGDD FVSWLPMYGEAKVALFVYLWHSKTKGTTYVYQTFVRPYVSKHEGEFDRHLVEFRARAGGLF LMYWQCVARYGHARFFEILEYLSSQSSASNHPQNNKSEAQPSQAEREELKAAQVAIPHPPP PEKQSQGRKMTGFQKTKRV
AmtrHVA22e	AMTR_s00238p00 013230	LALGYTYPAYACFKTVEKNKPEIDQLCFWCQYWIIVAVLTVFERVGDTFVSWVPMYSEAKVA FLVYLWYPKTLGTSYVYETFLRPYVAKHETEIDRNLLELRARAGDIVVQFWQKTTSYGQTRIF EILQYVASQSSRPAPAQVSVDLGK
AmtrHVA22f	AMTR_s00280p00 015410	LALGYTYPAYACFKTVEKNKPEIDQLRFWCQYWIIVAMLTVFERVGDTFVSWVPMYSEAKV AFLVYLWYPKTLGTSYVYETFLRPYVAKHETEIDRNLLELRARAGDIVVQFWQKATSYGQTR IFEILQYVASQSSRPAPAQ
AmtrHVA22g	AMTR_s00059p00 092060	MALLGPQVAGEVGLRLLLCFPGSNIVVRTACCSVGIALPVYSTFKAIENKDQKEQEKWLLY WAVYGFSLSLVEAFADKILYWFPLYHYMHKFAFLVWLQLPTVEGAKQLYLKYLRFLLKYQRR DQILVVVSGEMRKFISAHQGEIQFMGAMVQKSVGAGFLVESHMLHLSALNYTRERSSRGL GRRNLNLRLLHHGNSRTWPRALRLQRSRAGGREESCGRELGLVLERRDRYRP
AtHVA22a	AT1G19950	MIGSFLTRGLVMVFGYAYPAYECYKAVEKNKPEMQQLRFWCQYWILVAALTIFERVGDALA SWVPLYCEAKLAFFIYLWFPKTRGTTYVYDSFFQPYVAKHENEIDRSLIELRTKAGDLAVIYC RKAVSYGQTRIVEILHFVALQSTPKPKPKKEKKQAAAPEEEEQKQPDLKATSQAASSNPQVRL

		QSKKPQLVTKEPISPKPLSSPRKQQQLQTETKEAKASVSQTKLTTLTPPGPPPPPPPPPSPTTA AKRNADPAQPSPTAEAEASQTVAAALPEPASEIQRASSKETIMEETLRITRGSRLRKARSAGAP R
AtHVA22b	AT1G69700	MPSNSGDDNVLQVLIKNFDVLALPLVTLVYPLYASVKAIETRSLPEDEQWLTYWVLYALISLF ELTFSKPLEWFPIWPYMKLFGICWLVLVPQFNGAEHYKHFIRPFYRDPQRATTKIWYVPHKK FNFFPKRDDDDILTAAEKYMEQHGTEAFERMIVKKDSYERGRSSRGINNHMIFDD
AtHVA22c	AT1G74520	MGSGAGNFLKVLRLNFDVLAGPVVSLVYPLYASVQAIETQSHADDKQWLTYWVLYSLTLI ELTFAKLIEWLPIWSYMKLILTCWLVIPYFSGAAYVYEHFVRPVFVNPRSINIWYVPPKMDIFR KPDDVLTA AEKYIAENGPD AFEKILSRADKSKRYNKHEYESYETMYGEGYQY
AtHVA22d	AT1G75700	MIGSFLTRGLLMVFGYAYPAYECFKTVELNKP EIQQLQFWCQYWIIVAALTIFERIGDALVSW LPMYSEAKLAFFIYLWFPKTKGTTYVYDSFFRPYIAKHENEIDRNLVKVKTRAKDMAMIY LQ KAINQGQTKFFEILQYITEQSTPKSKAEKKETTIPKLDDPILKVKENEVT K
AtHVA22e	AT2G36020	MLGDFIIRLLVLILGYTPAFECFKTVEKNKVDIEELRFWCQYWILLALISSFERVGDFFISWLP LYGEMKVVFVYLWYPKTKGTRHVYETLLKPYMAQHETEIDRKIMELRARAWDFFIFYFNN FAQAGQSTLIQGFQYVLAQSVRFSA AANQPPTERNVNMNAQSPVEMDNDPPSPRAPRPL NKSLSALRSLEKQTSRGRKWPPPTPPPTPGRDSAGTFNGDDGVNIPDTIPGSPLTDARAKLR RSNSRTQPAA
AtHVA22f	AT2G42820	MGFIIAIAKRFDALVGPGVMLLYPLYASFRAIESPTMLDDQQWLTYWIIYSLITIFELSVWRVL AWLPFWPYLKLLFCMWLVLP MFSGAAYIYSNFVRQYVKIGMNVGGGTNYTDEQRRVLQM MSLDARKSVQDYVDRFGWDSVEKAIAKAAEKETRKH
AtHVA22g	AT4G24960	MLLYPLYASVIAMESTTKVDDEQWLAYWIIYSFSLSTELILQSLIEWIPIWYTVKLVFVAWLVL P QFQGA AFIYNRVVREQFKKHGVL RSTH SKPTKPNILHSIFPHRSVPNSLTRDTRLTVTESEGW SRQKKPD
AtHVA22h	AT4G36720	MSGFASQIPSMALLGSGLTGEVGLRVLFSP LSSNIVLRTACCSIGIGLPVYSTFKAIESGDENEQ QKMLIYWAAYGSFSLVEVFTDKIISWFPLYHHVKFAFLVWLQLPTVEGSKQIYNNQIRPFLLR HQARVDQLVDGVYGEMVKVVRSHQGEIRFVRAMI AKILGSVNEDAPRLGEIANGSPVSET NSDSESDSNHED
AtHVA22i	AT5G42560	MVLGYAYPAYECYKTVEKNRPEIEQLRFWCQYWILVACLTVFERVGD AFVSWVPMYSEAKL AFFIYLWYPKTRGTTYVYESFFRPYLSQHENDIDHSLLELRTRAGDMAVIYWQRVASYGQTRI LEILQYVAAQSTPRPQPPQKRGGGRANQAPAKPKKAPVPQSEPEEVSLS SSSSSSSSENEGNEP TRKVSGPSRPRPTVTSVPAADPKNAGTTQIAQKSVASPIVNPPQSTTQVEPMQIEEVEGEAES GNENPNPEGPKETVMEETIRMTRGRLRKTRSEESR
AtHVA22j	AT5G50720	MTKLWTSLSALHSLAGPVVMLLYPLYASVIAIESPSKVDDEQWLAYWILYSFLT LSELILQSL L EWIPIWYTAKLVFVAWLVL P QFRGA AFIYNKVVREQFKKYGILKPKVEHQAE

AtHVA22k	AT5G62490	MSSGIGSLVKVIFKNFDVIAGPVISLVYPLYASVRAIESRSHGDDKQWLTYWALYSLIKLFELTF FRLLEWIPLYPYAKLALTSWLVLPGMNGAAYLYEHYVRSFLLSPHTVNVWYVPAKKDDDLG ATAGKFTPVNDSGAPQEKIVSSVDTSKYVGHSAFDDAYY
SIHVA22a	Solyc01g007780	MLGELITSSLVLVLGYAYPAFECYKTVENS RVEIEELRFWCQYWIIALLRIFESFGDVFM TWL PMYSEAKLALIIYLWYPKTKGTRYIYDTLLKPYVSRHEPDIDRGFLEFRTRAFDLAIYYWQNC TELGQAKFFQLLDFASPSRRDSHLISEQRNGTDHSRRSPPPSAPPSPSSSSSFGFFRRSKPSSDR RQPPPPSPRSDRRQPQSPRSYSSHSRY
SIHVA22b	Solyc03g097420	MSKLWALLTHLHALAGPVVMLLYPLYASVIAIESTSKLDDEQWLAYWILYSFLTLMEMLLQP ILQWIPWIWYEVKLGMAVLVLPQFRGA AFIYNKFVREKLIKKGSSYIQHKSQSPDGKTKNK IVDFITLKKGDH
SIHVA22c	Solyc03g110920	MAGMAMFASNLSSEMGLKLLSPLNTNVIVRTACCSVGIVLPVYSTFKAIETG NRNEQHKW LLYWAAYGSFSIVEAFTDKFLYWPLYHHVLAFLVWLQLPSAEGAKQLYTNHLRPFLMKH QARLDHILELFHGELGKFISTHQA EIQFAKVLLGKTLSSVGNILQQAQGRVVG TIEGPAEQ VETSESEDES
SIHVA22d	Solyc03g116350	MGGSGGGIVSLLKVIISNFDVLAGPVVSLVYPLYASIRAIETKSPVDDQQWLTYWILYSMITLF ELTFAKLIEWLPFWSYAKLIATCWLVIPYFNGAAYVYEHYIRTYIVQRKAVNIWYVPRKKDVF SKPDDILTAAEKYIKEHGTQAFEEMIHKADGERKTHTSNYVFYDDDYRY
SIHVA22e	Solyc04g014420	MLCRYASIVALESTSKLDDEQWLAYWILYSFLTLMVEMLFQPILNWIPIWYDVKLIGVAWLVLVLP QFRGATFIYETYVREKLIMNKYGDQGKSKKKS VHFMTPEKGEDEAYD
SIHVA22f	Solyc04g076610	MGLISFLLISAKILISCSFWIFCRPSVTLLCPLYASIRAIESDKESSYEKCLQYWVLFGLTTVLELT LAKPLTGFSFWHYAKGLASLLLVLVLPQFGVASYVYMN FVKPCLSPNPHIEYVTEKNKSMPME LSCADSSLLMSHPRRVLQKYTTFGESDTQLLTCTKSSSNIAMKCSNYVDAAPRHVEKYK KD NLQSLVIYEAESSPKCDRTICPKKVQMDWSCPLCLVSVSSEKCLKQHIKGRKHKLKEDEQRE HEMIMASKEAKLASKLEGNYLKD LLES LNQIKSLKFVELRGFNLPIRRPLRCCTWKKPKPG WTKLNTDGSIDRKRA GLGGLLRDYEGAAICACVSEVTCDDIFLVELLAIWRGLMLAVSIGIK MIWVESDSMGAVKAINKEQPHNQKAASCLQHIWKMLNKFQKYQVTHSWRETNRAADYL SKMEISGSDIVMWPREFHGPLCKIIAEDAQGS LYIRR
SIHVA22g	Solyc04g081340	MIGSFITRVLVMVFGYAYPAYECFKTVEMNKPDIQQLRFWCQYWILVAMLTVCERFGDAFIS WVPMYSEAKLAFVIYLWCPKTKGTTYVYDAFFKPVILRHEPEIDKS LLELRTRAGDMFFLYW QKAASYGQTRVFDILQYIASQSNPPPPTQTHRQSSRGRQPTASLNRRSSASATQVQAEEQAP RASSESSSEDEADS AEEAGSSKGPPPASTAAANAQKTTSPSKSLVSTVAASLNTQKASPSKSLA EITKPSTSVETR VVQIDSVPPTSATESVNPPAETALEEAVRVTRARSRKTRTSNNP
SIHVA22h	Solyc05g007300	MGSDNNVLAVIAKNIDVLALPLISLVYPLYTSIKAIETKS RADDRQWLTYWVLYSLITLFELSF SKLIEWFPIWSYAKLAAICWLVLVLPYFNGACYVYENFIRPFYRNPQVKI WYVPLKKDIFSKPDD

SIHVA22i	Solyc06g072680	VLTA AEKYIEEHGPQAFERLLAKADRDARTRRNNYMTFDDDDYRY MGKFLTLMTLHLAGPSVMLLYPLYASVVAIESTSKLDDEQWLAYWILYSFLTLMEMLLQP MLQWIPWIWYDLKLAMVAWLVLQPFRGA AFIYEK FVREKLINKYGARYFRDKSPPPVAVSPA KVS VKTSEDRTD
SIHVA22j	Solyc10g007820	MGAIGTIAKSLNALIGPGVMMLLYPLYSSMRAIESPSPLDDQQWLTYWVLYSFITLFELSCWKV LQWL PFWPFIKLVCCMWLVLP IFNGAAYIHENFIRKHV KVGSHVSSNYPQNQRKALQMMS LDARKSVEKYIEKYGPDAFDKVVRAAEREAKKH
SIHVA22k	Solyc10g047670	MDFLRFSLHFIDCLAWPVVALGYPICASIRAIETGSKYHMRKLVIIYWTIFSFSLFQHLFDKLI QWVPLWPYIKLITICWLVIPRFNGACYLVEVLVRPCLLVKWHDSISQFNSSCYVYLRLLCLCL SVNLRTVADWFNKP MEDRSLKNETFLSVVERYLEENGSDALEKLIANKYKDYSSKHHAEEI KPTDTSDEAGRITPNQTQCEGSGPVWEDITVMEHMAKHEAAEPKQVKS VKENPIIIIEQKMT GLQVKELVVPADAEEIKLPEVISPNRVQTEWTCALCQMTTTS EQNMKSHLNGRKHKHSKYE ALKICEQTPKSNGSLPVPTKSNQLNLEQVKHAAAAQPFHSTNEAAEPKEVKS VKEHPIQIE KKT TG VQTKDTAFPAEAKEIKLPEIDSVKNVKT EWTC AVCQVTTT SKGDLKCHLLGTRHRI KCEELKRTTKTERNPPSTSNMPELKQE QVKHALAAQYKNSTNKKLKENVQLGATTGQHQ RQTQVKNAGGATHNSKLWCSFC DIRCPDEIAMA AHLNGKKHLAKLQERMSLTGTWALN YANMQFYQGI
SIHVA22l	Solyc10g051300	MDPEVGLRLLFSPLASNIVVRTACCSVGVLVPVYSTFKAIEGRDENEQRKWLLYWAAYGSFS VVELFTDKFLYWFLYHYHMKFAFLVWLQLPTTDGARQMYMTHLRPFLKHQARLDQVVG F LYGQMSKFVSMHQA EIKFVRALLMRTFVSANQFASGFIHPERRHVSGAIEERRQQYDTS DSD DEE
SIHVA22m	Solyc10g082040	MLGNFITSVLILVLGYAYPAFECFKTIEKNKVEIHELRFWCQYWIIVGALRIFESFGDLFLSWLP MYGEAKLALFIYWLWYPKIKGTSHIYDTILKPFVAKYETDIDRSLMEFRAKAWDLAIYYWQNC TEIGQAKFLQMLEYIASQSKRGTIHPKSEKQDETTHRSSPTIDHKDFYGARAKLRRSNKGD
SIHVA22n	Solyc11g010930	MGHFWTLICYLHTLAGPVTMLLYPLYASVVAIETSDKLDDEQWLAYWIFYSFLTLMEMVLQ HVLEWIPWIWYDVKLIFVAWLVP HFRGA AFIYDKFVREKIIKRYRESSSSPQHINKSPKAKSK TKFVDFITPKKGEHEAY
SIHVA22o	Solyc12g089290	MQCNAGRFA GFKMIGSFLTRGLVMVFGYAYPAYECFKTVEMNKPDIQELRFWCQYWILIAL LTV CERVGD AFVSWVPMYSEAKLAFIYLWC PKTKGTTYVYDSFFRPVVLKHETEIDRNLLEL RTRAGDMA CLYWQNSASYVQTRFFDVLFQIASQSTPRPTQPQKQSSRGRQRTVTPPKCSA APATKVQTEKQAPPASTESSEKEADIKEKVKPSQPPPVATPASSASSNAQKTTPAEHAHQI TKASSLSKTEVMQVDQVSSSDNKS AKPLVD TVMEDNITAKPVD TVMVEAVRVTRARSRRTR PAPNP
StHVA22a	PGSC0003DMG40	MGGSGGGIVSLLKVIISNFDVLAGPVVSLVYPLYASIRAIETKSPVDDQQWLTYWILYSMITLF

	0000600	ELTFAKLIEWLPFWSYAKLIATCWLVIPYFNGAAYVVEHYIRTYIVQRKAVNIWYVPRKKDVF SKPDDILTAAEKYIKEHGTQAFEEMIHKADGERKTHTSNYVFYDDDDYRY
StHVA22b	PGSC0003DMG40 0003727	MIGSFITRVLVMVFGYAYPAYECFKTVEMNKPDIQQLRFWCQYWILVAMLTICERFGDAFIS WVPMYSEAKLAFVIYLWCPKTKGTTYVYDAFFKPVILRHEPEIDKNLLELRTRAGDMFFLY WQKAASYGQTRVFDILQYIASQSNPPPPTQSLHAYESIQLCCDATPQSPSLTVRADLKPQRQS SRGRQPTASLNNRRSSASATQVQAEEQAPRASSESSSEDEADSAAEEAGSSKGPPPASTAAANA QKTTTPSKSLVSTVAASLNTQKASPSRALAEIMKPSTSVETQVVQIDSVPSSTATSVNPPTETAL DEAVRVTRARSRKTRTSNNP
StHVA22c	PGSC0003DMG40 0004398	MFTNSFRYASIRAIQTDSKYHMRKLLTYWIIFSLFHHIFDKLIQWVPLWPYIKLITICWLVIPQF DGACYLYQKLIHPCLLVKLHDVITQFYGFYVYQRFVCLSVNLQIVADWLNKPMEDPSL KNVSFLTТАERYLEENGSDALLKLIANKCKDNNLNHHAAEEIKTTDTSVEAGTLIPNQTLCG ACPVWQNIKPMEHMAKYEAAQPKQVVIFNP
StHVA22d	PGSC0003DMG40 0009332	MGLISFLLISAKILLCCSFWIFCRPSVTLLCPLYASIRAIESDKESSYQKCLQYWVLFGLTTVLEL TLAKPLTGFSFWHYAKGLASLLLVLPQFGVASVYVMNFVKPCLSPNPLIEYVTEKNECMPME RSCADSSLSMPHPRRILQKYTTFGESDTQLLTCFKSPSNIVMECSDYVDAAPRHVKQDKKD NLQSFVIYEAESSPKCDRTIYPKKVQKNWSCPLCLSVSNEKCLKQHIGRKHKLKEDEERE HEMIMTSKEAKLASKLEGNLYKDLLESNLQIKSLKFVELRGFNLPIRRPLRCCTWKKPKPGW TKLNTDGSIDRKRAGLGGLLRDDEGVAICACVSEVTCGDIFLVELLAIWRGLMLAVSIGIKVI WVESDSMSAVKAINKEQPHNQKAASCLQHIWKILNKFQKYQVTHSWRETNRADYLSKM EISGSDIVMWPRDFHSPLCKIIAEDAQGSlyIRR
StHVA22e	PGSC0003DMG40 0010683	MDLVSVTIACINLLAWPMLALGYPLFVTIRAIEAGCVYDKRKVATYWLIFSLIYLFENIFAKFL EWWPLWSYLRLVFMVWLVIPQLNGAFYLYQNLVHPYLQFKLPNAIIQLCAEWLILKNHSV SINNETFLAVAESCLDENDSLIASKPECNEGQILGDDIQEMECTAKCNAVESNQIENISTSAI QVISKPVIPAVAILPDTSSTLAVFQTRWTCEICQVTVSSELTQSHLRGRKHHRAEAMLWCTFC NLRVSGEIDMIAHLKGKRHLAKLQETLTNSGAS
StHVA22f	PGSC0003DMG40 1015201	MQMGLKLLLSPLNTNVIVRTACCSVGIVLPVYSTFKAJETGNRNEQHKWLLYWAGDDAFQ NFTNFFCFANLEIAFFSTRY
StHVA22g	PGSC0003DMG40 0016187	MLLYPLYASVVAIETSDKLDDEQWLAYWIFYSFLTLMEMVLQHVLWIPWIYDVKLIFVAWL VFPQFRGAAFIYDKFVREKIIKRYRESSSSPQHNNKSPKAKSKTKFVDFITPKKGEHEAY
StHVA22h	PGSC0003DMG40 0016386	MLGELITSSLVLVLGYAYPAFECYKTIEKNRVEIEELRFWCQYWIIVALLRIFESIGDVFMWLP MYSEAKLALIYILWYPKTKGTGYIYDTLLKPYVSRHEPDIDRGFLEFRTRAFDLAIYYWQNCT ELGQAKFFQLLDFASPSRKDSQLSSEVLFSHTFSPYVFSSKQSLTEMQKKTVYNRTL
StHVA22i	PGSC0003DMG40 2023061	MGSDNNVLAVIAKNIDVLALPLISLVPLYTSIKAIETKSRAADDRQWLTYWVLYSLITLFELSF SKLIEWFPIWSYAKLGAICWLVLPHYFNGACYVYENFIRPFYRNPQVKIWWYVPLKKDIFSKPDD

StHVA22j	PGSC0003DMG40 0026482	VLTA AEKYIEEHGPQAFERLLAKQADRDARTRNNYMTFDDDYRY VFCRYASVVAIESTSKLDDEQWLAYWILYSFLTLMEMLLQPILQWIPIWYEVKLGMAVLVL PQFRGA AFIYNKFVREKLIK KYGSSYIHQKSHSPDGKTKNKIVDYITLKKVKL
StHVA22k	PGSC0003DMG40 0026483	MSKLWALLTHLHALAGPVVMLLYPLYASVVAIESTSKLDDEQWLAYWILYSFLTLMEMLLQP ILQCDCGMSFFEFLSDEINMPNSNDFRSDYLRTRYATLLLKYGLNKAETGYVSENDDPTRSKSD YTPPTKDDL VNVE
StHVA22l	PGSC0003DMG40 1026939	MFDILFCDDERYASVVAIESTSKLDDEQWLAYWILYSFLTLMEMLLQPMQWIPWIWYDLKLA LVAVLVLPQFRGA AFIYEK FVREKLITKYGARYFRDKSSPPKVS VKPSEDWTD
StHVA22m	PGSC0003DMG40 0029015	MDFLRFALPLIDCLAWPVVALGYPICASIRAIETGSKYHMRKLVYWTIFSFISLFQHLFDKFIQ WVPLWPHIKLITICWLVIPRFNGACYLYEVLVRPCLLVKWHDSISQLNSSCYVYLRLSCLCLS VNLQTVADWFNKP MEDQSLKNETFLSVVEGYLEENGSDALEKHIANKYKDYS LKHHAEEI KPTDTSDEAGRITPNQTQCEGGGPVWEDITVMEHMAKHEAAEPKQV KSLKENPIIEKKTK GLQVRELVPADAE EIKLPEVASSEKVQTEWTCALCEMTT TSEQNMKSHLNGRKH KAKYE GLKTCEQTSKSDGSLPVPTKSNQLNLEQVKHASAAQPQHSANKAVEPKQV KSVKEHP IQIE KKTTGVQIKDTAFPADAKEIKLPEINPLKNIQTEWTCAVCQVTTTSKHDLKCHLLGTRHRIK CEELKRTAKTERNPPSTSNIP ELKQKQVKHALAAQNKNSTNKKPKENVQLGATTRQHQRQ TQVKNAGGATHNSKLWCSFCDIRCPDEIAMA AHLNGKKHLAKLQERMSFTSGTSD*
StHVA22n	PGSC0003DMG40 0029421	MVFGYAYPAYECFKTVEMNKPDIQELRFWCQYWILVLLTV CERVGD AFVSWVPMYSEAK LAFIY LWCPKTGTTYVYDSFFRPVVLKHETEIDRN LLELRTRAGDMACLYWQNSASYVQT RFFDILQFIASQSTPRPTQPKQSSRGRQRTVTPPKRRSAAPATKVQTEKQ APPSSTESSEKE ADTKEKVKPSQPPP VATPASSASSVNAQKMTTAE AHAQITKASSLSKTQMMQIDQVPSSDN QSAKPLVD TVMEDSLTAKPVD TVMEEAVRVTRARSRRTRPAPNP
StHVA22o	PGSC0003DMG40 0030143	MGFLIFTLHIMEFLAWVPLWPYIKLITICWLVIPQFDGGCYLYQKLIHPCLLVKLHDAITQFYG FCYVYQRFLHVCLSVNLQIVADWLNKPMEDPSLKSESFLDTAERYLDENGSDALLKLIANK CKDNNLNHHAAEEIKTTDTSVEAGTLIPNQVLQLLFRAPCTV
StHVA22p	PGSC0003DMG40 0033909	MDPEVGLRLLFSPLASNIVVRTACCSVG VVLPVYSTFKAIEGRDENEQRKWLLYWAAYGSFS VVELFTDKFLHWFLYHYHMKFAFLVWLQLPTTDGARQMYMTHLRPFL LKHQARLDQVVG FLYGQMSKFVSVHQA EIKFVRALLMRTFVSANQFASGF IHPERRHVSGAIEGRRQQIDTSDS DDEE
CcHVA22a	Ciclev10029342m	MALSGEVGLRLLLCPIGSNIVVRTACCSVG TILPVYSTFKAIESKDENEKQKWLVYWAVYGSF SIAEMFADKILCWFLYHHVKFAFLVWLQLPSTNGAKYFYMSRLRPFLLRHQARLDQILESV NGEMSQFVSDHQVEFRFVRTLFMKTVALVNQTVKEIIHPVPTQANRAIEGPPESIPDSQSDN ED
CcHVA22b	Ciclev10033698m	MQNFACATLLHWLLLALNPYIKGSETNARPKKKVGLKSDFWGSSLRVPLNFV KLARKNH

		FEALGPVNSIAPNTQKSQTNKGRHLKQLMGARGSNNNNFLQVVVNNFDVLALPVVTLVY PLHASIKAIEARSASDDQQWLTYWVLYSMITLFELTFAKVLELITIWPYAKLIFSCWLVLQPQN GAAYVYRHFVRPFYMN PQSASSKIWYVPRKKNIFRQQDDILTAAEKYMQEHGTESFERLIA KTEREERSRKSNNYMIFDDDYRY
CcHVA22c	Ciclev10022553m	MGSGAGSFLKVLLKNFDVLAGPVVSLVYPLYASVRAIETKSPTDDRQWLTYWILYSMITLVEL TFAKVIEWIPIWSYAKLIFTCWLVIPQFSGAAYVYEHYLRPFFLNPQTINIWYVPRKKDVFSRP DDILTAAEKYMEENGTD AFEKLIHRADKSKRNYDHSTYEYDNVY
CcHVA22c*	Ciclev10022663m	MGVFFHLGHLLRYASVRAIETKSPTDDRQWLTYWILYSMITLVELTFAKVIEWIPIWSYAKLIF TCWLVIPQFSGAAYVYEHYLRPFFLNPQTINIWYVPRKKDVFSRPDDILTAAEKYMEENGTD AFEKLIHRADKSKRNYDHSTYEYDNVY
CcHVA22d	Ciclev10033011m	MSRFWNLIYGVHSLAGPVLMLLYPLYASVVAIESPSKVDDEQWLAYWILYSFLTITEMVLQP VLEWIPWYSVKLVLA AWLVLPQFRGA AFYIERFVRQQIRQYRGKDDHHQHQRKSSPTGT GKGKNKFVDFIMPCKGEHEAY
CcHVA22e	Ciclev10032960m	MGVLAVIAKRLDALIGPGVMLLYPLYASLRAIESPSTLDDQQWLTYWIIYSFITLFELSCYKVL AWLPFWAYMKLLFCMWLVLP MFHGAAYIYEKHIRRYVKIGGYVSPSSNYTADQRKVLQMM SLDARKSVSQYVEKHGWEAVERAIKAAEKETKKR
CcHVA22f	Ciclev10006951m	YISLETLERPSAPDYRQWMTYWIILSLVTTFEMLCWKT LGWFPVPNFIWAYLKLLIFVWLALP IFNGACFFYEKFIRVYYNNYVRRHLNNIIGV
OsHVA22a	LOC_Os01g52780	MRAVDASKCWPFGRGGGDGEPPPPLPPMEPPKRSRWWAHELAAERARQEARATGTEDAG GGVAGGGGSGKGA KRKGSRGRVRAERARKWRRSLQFGLLSKRKEKTSSRLLHYVLHKQLL SKHKGSTLRTQKEPSAQKSKHKGSTLRTQKELSAQKKFQNT HDCMSTHENNLNKQYIRGM DPSTGMGSNLVRKEAANSSVNKQNIKASEPTIYPLNPGCELVKNVAYPPKDDIFGDLPLLESS KVMFHSGVDELPTVIEDSFVTDQSGPEAISENVSLKLIPPSDMSVQTSSTLKD LVKKEGTPAK KSICILRNDVKKNLPSSAEFDGLNHNGINMVKTCLSDTQLKSTDVPALSSYSNKGLKSGSSN TAHTQQDCFSMNTNYCQEIRKPGTSIATSSVTVRTRTEAIESDRDMAVN SKKSTSISCALVPT ECHISSEGSVLSSAISQGSASAATSADGMSSYKSIPSQDSIPTSGLNGTFASNLFRESRKSVDTC TSLSKEDQCSWYSKLHPVCTPASIGSAFMKLPGLERIEISSCNIKTDENMSTNGRPANIVRCE KQQAVIGVPNIMQQGQRKTD FSDSQVQEKVLNGYLQQDVYHPCQPTVRLMGKTVSVCERS KEHRVPTMGKGWSDSTIVEDHPSSTSCHFPQKRLFPCQDSVTPSVHVKGSLDILQRIPSVTL P EARATIGNVQNRRLQPINTVSSSVRDCIWN SSGSQSVRQAEIKRATTINVNSRARHINLHOPP QEKYQKSTFSYDDPTSAPIYQSCQDLVAPVFEETKNRSLGWSLDDAIGPRILDFGSKVAGHGL EMSTNESNCVRASSGPVPVLETRSIPSSLSLA IYTLVQRLIEDIEKIQN KALHRSQQRIMGVL GALARHMDALVGPGIMLLYPLYASMRAIESPSTLDDQQWLTYWVLYSLITLFELSCWKVLQ WFPLWPYMKLLFCCWLVLPIFNGAAYIYETHVRRYFKIGQYVSPNYNERQRKALQMMSLD

OsHVA22b	LOC_Os02g02920	ARKSVERFIESHGPDALDKIIRAAEEEEAKRA MYSEAKLAFIVYLWYPKTQGTSYVYESFFKPYIGKHEAEIDRNLLELRTRAGDMAVHYFQKI ADYSHTRFYELQYIASQSEAQRSRPQAQQHQQRPPPPRTRQVNPAPPPVSPSPAPLPPQPP PPRNQAQADKAPIPVAPPGAAPPAQPPQPPQAGAEAVTTESTEATQAANPPATTASNPH QAPVIPDEETLIQEAIMTRSLRRRMGGA
OsHVA22c	LOC_Os02g51290	MGSGSGSFLKVVVKNLVDLAGPIVSLAYPLYASVRAIETKSAVDDQQWLTYWVLYSFITLFEL TFSPVLEWLPLWSYAKLFFNCWLVLVPYFNGAHVYEHFVRPMVNVQQIVNIWYIPRKDESD RPDDVISAAQRYIEQNGSRAFESLVNKNVLSTYGS
OsHVA22d	LOC_Os03g04030	MAGSFITGALMLILGYAYPAYDCYKTVELNKPEIEKLRFWCQYWILLAVLTVFDRVGDNFVS WLPAMYSEAKLAFVFLWYPKTLGTAYVYESFFKPWIAKYEADIDHNLLELRTRACDMAVLY FQKVSNYGQTRLYEILQYVASQSQTQTSRPQAREQQQRPPPAQTRQVNPAPQVPAPSVPL PPQPTQAPSAPPRNQTDTPVPVPPPGAESLAQPQAHAGPPQANASDGPQNTTEAMQIDP SGPSTSNARQSSIPDEDTLIQEAIMTRGRLRRRTAGSGPPPS
OsHVA22e	LOC_Os03g14610	MMGGFLSRVLLAFGYAYPAYECYKTVELNKPEIEQLIFWCQYWILVALMTVMERFGDFTIS WLPFYSEAKLMFFIYLWYPKTKGTTYIYGTFFRPYISQHENEIDRNLLELRARATDVVLYFQ KAATVGQNTFFDVLKYVASQSPSQRSSQPSQEPQQPKQQQAPVQQQPTQKQAPTVLRRS ASIAARQAAMAQQSQDAKTPSSPKIKRQASTKAAPVASTKLTGAAAPSTPKSDADAPKK NEAAPASLQVATPATKADVPASESPAPLPEAEADKMAIDEADDAVEGTEEGDPVPGETVE ERPMEETIRVTRSKLRRRTASEDPAGN
OsHVA22f	LOC_Os04g33880	MSVEFLTKALTALFGYAMPALCEFKAEIQRPGRTDHLRFWCQYWIILVILVIFDDIAGVLTSKI PMYSELRLAFLVYLWYPQTRGTDIVYDTFLRPLVMQYQPNIEERLRYLRANAGDILIFYLKNF TDRGYDLFLRGMEYIRSQTSRGSRTVCYQLLSVPYRKVF
OsHVA22g	LOC_Os06g12220	MGSGSFLKLLANNFDVLGAPLVSLAYPLYASVRAIETKSPVDDQQWLTYWVLYSFITLFELTF APVIEWLFPWSYAKLFFNCWLVLPCFHGAAYVYDHFVRPMPFVNRQIVNVWYVPRKENLSK PDDVLSAAERYIEQNGPEAFEKLISKSTRPSTSKRSTKQSILEEVESEHMAARAERESWGENPFY DKNYRC
OsHVA22h	LOC_Os07g38100	MALLAPAISGEVGLRLLAPLSSTVVIRTASCAIGVGLPVYSTFRAIEKKDQKEKERWLLYWA AYGSFSIAEIFADQILSSVPFYHVKFAILVWLQFPSNSGAKHVYRRYMRPFLLKHQAKIDRIL NILSKELNKFVSSHEDEIHFIHMAARGASTANYIINGPEQSEAVRAAIEGPNSTTTEEAGTP RNET
OsHVA22i	LOC_Os08g36440	MESPTKVDDEQWLAYWILYSFITLLEMVAEPVLYWIPVWYPVKVLFVAWLVLPPQFKGASFIY KKLVREQLRKYRARGGAAATVTAGEDHKVHIAKAEHDHGH
OsHVA22j	LOC_Os09g27730	MESTSKVDDEQWLVIWILYSLITLMEALHKVLYWIPLWYEAQVLFVAWLVLPPQFRGASFIY DKFVREQLKKNRVKLHEHHGHGHGHGADEHQSHVVRG

OsHVA22k	LOC_Os09g36340	MAVLLITRLLTLVLGYAYPAYDCYKTLELNKPQIDQLRFWCQYWILLAFLLTLETITYFTVSWL PMYGEAKLALVLYLWYPKTRGAKHVYESYLQPVLARHEADIDRGLLQLRASAKDATASHL QAAVSLGRACFAEVAGRVSSQLQAARSSGGGGGRAGQADQLQKRQKINPEEEEEDEDATVS KTRR
OsHVA22l	LOC_Os10g09870	MMGDFLSRVLLLAFGYAYPAYECYKTVELNKPEIEKLIFWCQYWILVALLTVLERFGDFAISW LPLYSEAKLMFFIYLWCPRTKGTSYVYETFFRPYISQYENDIDCSILDLRVRAGDMLVVYWQK VAIIGQTTFFNILKYASAQSPAHSRSRSTQQSYPQKQQQAQPPQPKQSLPQQQQKQSLPQQ QQQQMPHEKPTTLRRAASAAARTAGIMQQSEDTKIAYSNPKTRRLLPKSAPTASTRSTVA ATKPVEDLKSSGMKLATEEAPSPSSNAAMPGSEPSAPPLPKSAEDDMSIDEVDIPIEDMDEPV ATPEETPMEEAIRVTRGRLRKRIAAVSTADGGAAN
OsHVA22m	LOC_Os11g05800	MLGELISKVLLVLFGYAMPAFECFKTLETRPDDAHMLRFWCQYWIIVSMVIACESFVSWMP MYGEIKLAFFVYLWYPKTKGSDVVYDSFIRPTVMQYEPNIEQRLEHLRANSGLIAFYIKNF ADKGTAFFMDFLRYVVSERPEAAANSEPQRSSWSSWNPFASRRQEPSPPPSAPPRERRFSGA DPDDEPPAIADVFRASLGGGAMNRRPHNNNNN
OsHVA22n	LOC_Os11g30500	MGKLWTLTHVHSLAGPTVMMLLYPLYASVQAMESPSKLDDEQWLAYWILYSFITLVEMLLES LIYWIPWYELKLLFIAWLALPNFRGAAFIYNRFVREQLRKHGLAGAGAGAAASVGKKDKS SPSSSPKDKEKTKSKFLSFVTPKDKHEAY
OsHVA22o	LOC_Os11g38920	MGSGSLLKVLAKNFDVLGVLALAYPLYASVKAIETKSPVDDQQWLTYWVMYSLITLFELT FASIIQWLPFWPSMKLIFICWLVLPHYFNGAAAFVYQNYVRPMFVKHQMVNWIWYVPQKKGLF GKSDDFLTALDKFIEENGPEALKKLTNKAGKSSKQSGKSWKDSKSSKESKDSKSSKESKEPKP SKDSKQLKPPKVSKEKPLKDSKEDKKAVKEDKKAASAKDSKEQKKALKDSKELKKALKDS KEQGSQKDSDELKPKSNKRVTFAEVEPEKELKASNSDWHPTSEYHSVYPEHNSWSSSFMIFE DENSYWN
OsHVA22p	LOC_Os12g06180	MLGELLSRILLLLFGYAMPAFECFKTVEARPNDAAHMLRFWCQYWIIVAMVIAFESLISWMP MYGEIKLAFFVYLWYPKTKGSDVVYDTFLRPVIMQYEPNIEQRLLHLRAKSGQLLSFYMKNF ADKGTAFFMDVLRVVSDDKPEGSNQEDSDAQPAACSVVGKKNHPAGNVGGQFLPDD PQQRNKKSGGWSPFATKRRPPSPRRPPQESLFESNPEAAAVAELKATINPRRRGAQNGK NYY
SbHVA22a	SORBI_3001G4357 00	MMGGFLSRVLLLAFGYAYPAYECYKTVELNKPEIEQLIFWCQYWILVALLTVLERFGDFTISW LPFYSEAKLMFFVYLWYPKTKGTTYVYGTFFKPYISQHENEIDRNLLLELRARATDMVVIYFQ KAASVGQNTFFDVLKYVAAQSPSQSRQRPQQESQQPQQQQPQVQVQVQLQQPQPQKQ AAPVMRRAASIAARQAAMAQQSQETKVPSPSPKIKRQTSKSGSVASTKPAAASTPKPAG SPKKGEVKPAADPVQTPATSANSPKSEPNAPPLPEAEGVDKMAIDEVSGDAAEGAEELDPA LEETPMEETIRVTRAKLRRRTATEDPAGN

SbHVA22b	SORBI_3002G221800	MGKTWALITHLHALAGPSLTLIYPLYASICAMESTTKVDDEQWLAYWIIYSFITLFEMAAENV LYWIPLWYEAKLLLVAWLVLPPQFRGASFIYDKFVREQLRKNGVRLHDHHGHGHGHAADH VPDVFQ
SbHVA22c	SORBI_3002G276500	MAVSFVTRLTLALGYAYPAYGCYKTLELNAPQMERLRFWCQYWILVAFLTAFESFADCALS WLPMYGEAKLAVVVYLWHPKTMGARHVYDDYLRPFLAAHEADIDRGLVELRARAADAT ASHLQAAVALGRACLSEVARRVSSQLQQAATSAGPAAQVR
SbHVA22d	SORBI_3003G283500	MGVLGTLARNLDALVGPGIMLLYPLYASMRAIESPSSLDDQQWLTYWVLYSLITLFELSCWK VLQWFPLWPYMKLLFCCWLVLPIFNGAAYIYEAHVRRYFKIGNYVSPYNERQRRVLQMMS LDARKSVERFIETHGPDALDKIIRAAEEEEAKRT
SbHVA22e	SORBI_3003G350600	MALLAPAISGEVGLRLLAPLSSNVVIRTASCAVGIGLPMYSTFRAIEKKDEKEKERLLLYWA AYGSFSIAEVFADKLLSSVPLYYHVKFAILVWLQFPSNSGSKHVYKRHLRPFFLKHQAKIDRF LNILSKELTKFVSSHEDEIRFIENMAIRGTTTANYIVNGLDQPEETQAANRIEGPNTTVTEETG VSGTET
SbHVA22f	SORBI_3004G018800	MIGSFITGILTLVLGYAYPAYDCYKTVELNRPEVEQLRFWCQYWILLAFITVLERVGENFVSW LPMYSEAKLAFIVYLWYPKTRGTAYVYESFFKPYIAKHETEIDRNLELRTRAGDMAVLYFQR VANYAQTRSIEILQYIASQSQTQSRPQAQQQQQRPPPPRTRQVNPAPPPVPAPSAPPMPPQ PAQAQVPPTPMPPPIPVAPPGAVPPAQPPPPPLAPEAAATNGPQDTEAMQVDPPrVSLSGA PPPLPPEETLIEEAIRLTRGRLRRRLVGGSGPPPN
SbHVA22g	SORBI_3004G237200	MGGSGSFLKVLVNNMDVLGPLVSLAYPLYASVRAIETKSAVDDQQWLTYWVLYSFITLFE LTFAPVLEWLFPWSYAKLFFNCWLVLPPQFNGAHVEHFVRPMIVNQQVVNIWYIPKKDE SGRPDDVISAAQRYIEQNGSKAFENLVNKFSSNPKRISILEEVEVERRARIQRESEAREVNPF NPEYQY
SbHVA22h	SORBI_3005G121200	MGKLWTILTHLHSLAGPTVMLLYPLYASVQAMESPSKLDDEQWLAYWILYSFITLMEMVLES LIYWIPIWYELKLLFIAWLALPNFRGAAFIYDKFVREQLRKHGLTTAAGSGSKKDDGKSSSP SSKDKDKPKSKFLAFVTPKKDHEAY
SbHVA22i	SORBI_3005G121300	MGKLWTILSHLHSLAGPTVTLLYPLYASVQAMESSKLDDEQWLAYWILYSFITLMEMLLQS LIYWIPVWYELKLLFMAWLVLPNFRGAAFIYNKFVREQVKKHISIQAAAGAGSTSNNNVTAN KDKKIVSTSPKEKSKGKLLSMVIPKKLKF
SbHVA22j	SORBI_3005G177900	MGSGSLLKVVANNFDVLGPLVALAYPLYASVKAIETKSPVDDQQWLTYWVLYSLITLFELT FASIIQWLPFWPSMKLIFICWLVLPPYFNGAAYVYQNYVRPAFIKNQMVNIWYVPQKKGLFG KSDDFLTALDKFVEENGTDALKKLANKAGKSFKQSGKSSKDSKESKSSKESKETKSSKDSKE

		LKQSKDAKQPKPSKDLKEPKSPKDPKSPKDSKEQKKAALRDPKKAVKDSKELKKALKDSK QQESLEDPKHEHTAKKAGKRVTFAEVEPEKELKASNSDWHPPSSDFHSAYPEQNSWASSFMIFE DENSYWNRGHPDC
SbHVA22k	SORBI_3006G0739 00	MSTELLTKFLTLLFGYAMPALCEFKAIEQRPGRADQLRFWCQYWIILVLLVMFDEIAGVLISKI PMYYELKLAFLVYLWYPKTRGTDIVYETFLQPLVMQYQPNIEARLQYLRANAGDILVFYLN FTERGYDLFLRVLDYVRSQASKGSRTTRFFSFRGERAERPSFADDDYATGGDRRDGGRHRRP RSGY
SbHVA22l	SORBI_3007G1536 00	MGKSWALVSHLHTIAGPSITLLYPLYASVCAMESPSKVDDEQWLSYWIISFITLLEMLAEPLL YWIPVWYPVKLLFVAWLVLPPQFKGASFIYEKLVREQLSKYRARYPRKGKGGGGAAAAADV DDDHKVHIAKAEHDHVQ
SbHVA22m	SORBI_3008G0423 00	MLGELLSKILLLLFGYAMPALCEFKTVETRPNDAMHLRFWCQYWIIVAMVIAVESVISWMP MYSEMKLAFVYLVWYPKTKGSDVVYDTFLRPVIMQYEPNIEQRLHLRAKSGQLISFYMKN FADKGTAFFMDVLRVYISEKPEGSNAELRNKKSGWSPFATKRRPPSPPEPLFDSNPDAALL AEALRGAIGAKPRRGSNDKHY
SbHVA22n	SORBI_3010G0919 00	MGSGSFLKVLANNFDVLGAPLISLAYPLYASVRAIETKNPVDDQQWLTYWVLYSFITLFELTF APIIEWLPFWSYAKLFFNCWLVLVPWFNGAAYVYDHFVRPTFVNQIVNIWYVPRNEKLGKS DDVLSAAERYIEQNGPEAFEKLISKSTKSSKSRTNKRSTLEAEAEENRAKAERESWDENPFYD KNYRY
ZmHVA22a	Zm00001eb009420	MAPPQSTPRKPACPRLPALPHRADSDGRSPQSLHPLAQLHLAASPTTRASMRAPMEGRP NPRTRSCSFTDTHRRVISFSSTGPGGEEATRRETPEETRKRLLELDALLEGLVEPKMRPPTPPP PPVLTYLRTAIRHRTEDEQSSVFCGFSQPMHLKAKGNIFPLRTSAFPSSHVKEKWAKN LYIASICYGRTVGIIRYASVHAHLGRTGSRRDDLESAYTLIFLIRGRLPWQGYQLVLPFNGAT YIYEAHVRRYFKIGSYVSPSYSEHHRRVLQMTSFNACRSVERFIDTHGPDALYRIIRAIQGFED EPPLWRRLASRPDVGLRGRASSLEEAGLAGPLESAGAVLDSQI
ZmHVA22b	Zm00001eb010740	MMGGFLSRVLLLAFGYAYPAYECYKTVELNKPQIEQLIFWCQYWILVALLTVLERFGDFTISW LPFYSEAKVLFFVYLWYPKTKGTTYVYGTFFKPYISQHENEIDRNLLELRARATDMVVLYFH KAASVGQNTFFDVLKYVAAQSPSRKSRLHPHQEPQQQQPQVQVELQQPQPQKQAAPVMR RGASIAARQAAMAQQSLETIPVPSSPKIKRQTSGRPGSVASTKPAAAASTPKPGGSPKKGEV KPAVDPVQTPATSADSPKSEPSAPPLSETEEVNDMAIDEVSGDAAEGAEELDPALLETMPMEE TIRVTRAKLRRRTATEDSAGN
ZmHVA22c	Zm00001eb037890	MGKSWSLISHLHTVAGPSITLLYPLYASVCAMESPSKADDEQWLSYWIISFVTLLEMLAEPL LHWVPVWYPAKVLFAAWLALPQFKGASFYVEKLVREQLRNYRARYPRKGAAAAAVGGD DDDHKVHIAKAEAEHDHVQ
ZmHVA22d	Zm00001eb073940	MFFVYLWYPKTKGTTYVYGTFFKPYISQHENEIDQNLELRARATDTQPPQQQQPQVQVQQ

ZmHVA22e	Zm00001eb083010	AQPQNQAAPVMRRASSIAARQAAMAQQSQETKPVQSSPKIKRQTSARSGSVASTKPPIAAS APKPGGSPKKGEVKPTADPVQTPTTGADSPKPEPSARSLPGVEGVDKMAIDEASGDAPEGA EELDPALEEETPIEEMIRVTRAKLRRRTTTEVPVGN LTAAKVQNSHAEGRAEWRLDLGKASYLNCLLHLSYIEQHESLENIFSSILETTAQAYGEDDN IQPSSGCTDAGQLCHHPVQELDTERASAETAARSGSTLFALFELLALPTFSKLVLPFNGAAYI YEAHVRHYFKIGNYVSPSYSEHHRRVLQMTSLDVCRSVERFIDTHGPDALDRIIRAEHVVTA LSVESYYRVFCIGLLVKHELRLREKNHVSQVSTCVVSPLQCVPSLWFSLLITTKTVGEALNKP VLGHLAMQKLSGTIQVVLEFFVEIQFDANGKISGAIRAYLVERSRVCQISDPERNYHCFCM LCSAPSETSMVA
ZmHVA22f	Zm00001eb092150	LGRTGYQLVLPIFNGAAYIYEAHVRRYFKIGSYVSPSYSEHHRRVLQMTSLNARRSVERFIDT HGPDALDRIIRAAEQEAKRT
ZmHVA22g	Zm00001eb100630	MGKTWALITHLHALAGPSLTLIYPLYASICAMESATRVDDDEQWLAYWIIYSFITLFEMAAEHV LYWIPLRYEAKLLLAAWLVLPHFGRGASFIYDRFVREQLRKNGVSLRGHHHGHAAHDVPHV FQAEHRHGVHS
ZmHVA22h	Zm00001eb112930	MGKLWTILTHLHSLAGPTVMLLYPLYASVRAMESPSKLDDEQWLAYWILYSFVTLMEMLLE SLIYWIPWIWYELKLLFIAWLVLPNFRGAAFIYDKFVREQLRKHGLTAAGSVKSSSPSSKDKDKP KNKFLAFVTPKKDHEAY
ZmHVA22i	Zm00001eb148430	MALLAPAISGEVGLRLLLAPLSSNIVMRTASCAVGIGLPVYSTFRAIEKKDEQEKERMLLYWA AYGSFSIAEVFADKLLSSVPLYHVKFAILVWLQFPSNSGSKHVYKRYLRPFLLKHQAKIDRFL NILSKELTKFVSSHEDIRFIENMAIRGATTANHIVNGLDQPEETQAVNTIEGPNTTVTEEAG VSGTET
ZmHVA22j	Zm00001eb208370	MIGSFITGMLTLVLGYAYPAYDCYKTVELNRPEVEQLRFWCQYWILLAFITVLERVGESFVSW LPMYSEAKLAFIVYLWYPKTRGTAYVYESFFKPYIAKHETEIDRNLLELRTRAGDMAVLYFQR VTNYAQTRSIEILQYIASQSPTQRQAHQQQQRPPPRTRQVNPAPPPIPAPSAPPMPPQPAQ AQVPPTPPRPLVPVPPGAVPPAPPPTAPEATATNGLQDTETMQVDPPRASLSGPPLPPEETL IEEAIRLTRGRLRRRLAGGSGPPQN
ZmHVA22k	Zm00001eb210700	MFFVYVLWYPKTKGTTYVYGTFFKPYISQHENEIDQNLELRARATDTQPPQQQQPQVQVQQ AQPQNQAAPVMRRASSIAARQAAMAQQSQETKPVQSSPKIKRQTSARSGSVASTKPPIAAS APKPGGSPKKGEVKPAADPVQTPTTGADSPKPEPSARSLPGVEGVDKMAIDEASGDAPEGA EELDPALEEETPIEEMIRVTRAKLRRRTTTEVPVGN
ZmHVA22l	Zm00001eb254850	MGGGSGSFLKVLVNNMDVLGAPLVSLAYPLYASVRAIETKSAVDDQQWLTYWVLYSFITLFE LTFAPVLEWLFPWSYAKLFFNCWLVLQPFGNGAAHVYEHFVRPMIVNQVQVNIWYIPKKDE SSRPDDVISAAQRYIEQNGSKAFENLVNKFSSNPRRSILEEVEVERRARIQLESEAREVNPFF NPEYQY

ZmHVA22m	Zm00001eb372500	MGSGSFLKVLAKNFDVLGAPLISLAYPLYASVRAIETKNPVDDQQWLTYWVLYSFVTLFELT FAPIIEWLPFWSYAKLFFNCWLVLVPWFNGAAYVYDHFVRPMPFVNRRIVNIWYVPRNEKLKG SDDVLSAAERYIEQNGPEAFEKLISKGITSLS
ZmHVA22n	Zm00001eb379710	MGSGSFLKVLAKNFDVLGAPVISHAYPLYASVRAIETKNPVDDQQWLTYWVLYSFVTLFELT LAPIIEWLPFWSYAKLFFNYWLVLVPWFNVASATTGHIPAAAARAPHHRPLGLTFPAHSAGA TAALLPRPDLLQPRFPIALGHRDSLRSRDARDVEGNLGARGGRL
ZmHVA22o	Zm00001eb398540	MMGGFLSRVLLLAFGYAYPAYECYKTVELNKPEIAQLIFWCQYWILVALLTVLERFGDFTISW LPFYSEAKLMFFVYLWYPKTKGTTYVYGTFFKPYISQHENEIDRNLLELRARATDTVVLYFQK AASAGQSTFFDVLKYVAAQSPSQSRQRLHQDSQQPPQQQQPQVQVQQAQPPQKQAAPV MRRASSIAARQAAMAQQSQETKPVSSSPKIKRQTSARSGSVASTKPPVAASALKPGGSPKKG EVKPAADPVQTPTTGADSPKPEPSAPSLPGAEGVDKMAIDEASGDAPEGAEEELDPALEEETP MEETIRVTRAKLRRRTATEDPAGN
ZmHVA22p	Zm00001eb422010	MSIELLTKFLTLLFGYAMPALCEFKAIEQRPGRADQLRFWCEYWIILVLLVMFDEIAGVLISKI PMYYELKLAFLVYLWYPKTRGTDIVYETFLQPLVMQYQPNIEARLQYLRANAGDILVFYLN FTERGYELFLRVLDYVRSQASRGSRTSFFSFRGERSERPSFTDDYVTGGDRRDGGRHRRPRS GY
ZmHVA22q	Zm00001eb438800	MMGGFLSRVLLLAFGYAYPAYECYKTVELNKPEIAQLIFWCQYWILVALLTVLERFGDFTISW LPFYSEAKLMFFVYLWYPKTKGTTYVYGTFFKPYISQHENEIDRNLLELRARATDTVVLYFQK AASAGQSTFF
ZmHVA22r	Zm00001eb441760	MIGSFITGMLTLVLGYAYPAYDCYKTVELNRPEVEQLRFWCQYWILLAFSLTVLERVGESEFVSW LPMYSEAKLAFIVYLWYPKTRGTAYVYESFFKPYIAKHETEIDRNLLELRTRAGDMAVLYFQR VTNYAQTRSIEILQYIASQSPTQRQAHQQQQRPPPPRTRQVNPAPPPIPAPSAPPMPPQPAQ AQVPPTPPRPLVPVPPGAVPPAPPPTAPEATATNGLQDTETMQVDPPRASLSGPPLPPEETL IEEAIRLTRGRLRRRLAGGSGPPQN

Table S13. List of primer sequences used for subcellular localization of selected *SIHVA22* genes

Gene Name	Primer sequence (5' to 3')
<i>SIHVA22a</i>	GCAGCCCGGGGATCCGAAAAGATGTTGGGAGAACTC CCATTCTAGAACTAGTGTATATGGACCGGTGAGAGG
<i>SIHVA22f</i>	GCAGCCCGGGGATCCATGGGTTTGATCAGCTTTCTTCTG A CCATTCTAGAACTAGTTCGTCTAATGTACAAGCTTCCT
<i>SIHVA22n</i>	GCAGCCCGGGGATCCATGGGTCATTTTTGGACTTTGATT T CCATTCTAGAACTAGTGTAAGCTTCATGCTCTCCCTTTTG

Table S14. The primer sequences used in qRT-PCR analysis

Gene Name	Forward Primer	Reverse Primer
<i>SIHVA22a</i>	GAAGAACTCAGATTTTGGTGCC	TGCCAATTTTGCTTCACTGTAC A
<i>SIHVA22b</i>	CATCTACATGCTCTAGCCGG	GGTTGAAGAAGCATCTCCATA AG
<i>SIHVA22c</i>	GTA CTACCAAGCAGAAATTCAG	TACTTGCTCTGCTGGCCCTT
<i>SIHVA22d</i>	CTGGAGGAGGTATAGTAAGCT	CATCCACAGGGGATTGCTC
<i>SIHVA22e</i>	GTGGAGATGCTATTTCAACCC	CTCTGGAGTCATGAAGTGAAC
<i>SIHVA22f</i>	TGCAGACCATCAGTGACATTG	AGTACGAGCAAGAGGGATGC
<i>SIHVA22g</i>	GCTTCGCAGTCAAATCCACC	GATTCAGAAGAAGCACGGGG
<i>SIHVA22h</i>	TCGTGCAGATGATCGACAATG	AACATGCTCCATTGAAGTAAG GT
<i>SIHVA22i</i>	ACTCACCTTCATACACTTGCC	GGAGCATCTCCATAAGAGTGA
<i>SIHVA22j</i>	GCAATTGAGAGCCCTTCACC	GATGAATGGCCAAAATGGTAG C
<i>SIHVA22k</i>	ATCACATGAGGAAGCTCGTCA	CATTAAACCGCGGTATCACCA
<i>SIHVA22l</i>	GGCAAATGTATATGACTCACCTT	TCCTCATCAGAAGTGCTCTCA
<i>SIHVA22m</i>	GCAAATGCTTGAGTATATAGCTTC	GTCCCCTTTGTTGGAACGTC

<i>SIHVA22n</i>	CATCATCATCATCACCACAACAT	AGTAAGCTTCATGCTCTCCCT
<i>SIHVA22o</i>	AAGCCTCACAACCACCTCCA	CTTAGACTCGAAGCTTTGGTG
