

**Table S1. Summary of the identified 17 *SICEP* genes**

Gene name	Locus ID	Chromosome localization	Genomic sequence (bp)	CDS sequence (bp)	Transcript sequence (bp)	Protein sequence (AA)	Molecular weight (DA)	PI	CEP Motif (15AA)
<i>SICEP1</i>	Solyc01g107570	ch01: 87387917-87388172 forward	255	255	255	85	9372.84	8.22	NVVVKNSGPSPGIGH
<i>SICEP2</i>	Solyc02g065040	ch02: 34178842-34179079 reverse	237	237	237	79	8700.95	6.82	PSPGHVDGHSPGIGH
<i>SICEP3</i>	Solyc02g087020	ch02:47583756-47583996 reverse	240	240	240	80	8639.74	8.81	LTEAKNSGPSPGEGH
<i>SICEP4</i>	Solyc02g090590	ch02:50187107-50187356 reverse	249	249	249	83	9090.54	9.6	VDAFSSPGHSPGIGH
<i>SICEP5</i>	Solyc02g090600	ch02:50192522-50193044 reverse	522	522	522	174	19058.76	9.86	NYAPKQTGNSPGIGH NYTPNQTGNSPGIGH SIDDIKAGHSPGIGH
<i>SICEP6</i>	Solyc02g090610	ch02:50203465-50203768 forward	303	303	303	101	10818.55	9.6	PPPGHPDGHSPGIGH
<i>SICEP7</i>	Solyc02g092890	ch02:51889669-51889942 forward	273	273	273	91	9800.43	8.71	YLGIKNSGPSPGEGH
<i>SICEP8</i>	Solyc03g044180	ch03:7705647-7705914 forward	267	267	267	89	9605.11	9.6	TLGDIKDGSPGVGH TLGGIKAGPSPGEGH
<i>SICEP9</i>	Solyc03g044530	ch03:8919360-8919723 reverse	363	363	363	121	13256.43	6.58	DFGPTGPGHSPGIGH
<i>SICEP10</i>	Solyc03g044560	ch03:9418566-9418884 reverse	318	318	318	106	12094.83	9.83	VSFDNLKDHSPGIGH
<i>SICEP11</i>	Solyc03g044580	ch03:9458192-9458528 forward	336	336	336	112	12331.02	9.05	GFSPYGRGHSPGIGH
<i>SICEP12</i>	Solyc07g062320	ch07:64931818-64932058 reverse	240	240	240	80	8063.94	9.16	VYGNLNI GPSPGEGH VYGNLNTGPSPGEGH
<i>SICEP13</i>	Solyc07g062330	ch07:64935912-64936116 reverse	204	204	204	68	7365.5	6.7	IYGNLNTGPSPGEGH
<i>SICEP14</i>	Solyc07g062340	ch07:64941677-64941929 reverse	252	252	252	84	8952.31	7.91	IYGNLNTKPSPGEGH
<i>SICEP15</i>	Solyc07g062350	ch07:64952870-64953239 reverse	369	369	369	123	12777.46	7.85	IYGNLNTGPSPGVGH VYGNLNTGPSPGEGH VYGNLNTGPSPGEGH

<i>SICEP16</i>	Solyc07g062360	ch07:64962982-64963669 reverse	687	687	687	229	23619.59	9.92	VYGNLKYDPSRGAGH VYHNLRSPSPGAGH VYGNLRSGPSPGAGH VYGNLRSPSPGAGH
<i>SICEP17</i>	Solyc07g062370	ch07:64980820-64981756 reverse	936	936	936	312	32878.64	9.65	VKSESHSSPSPGEGH

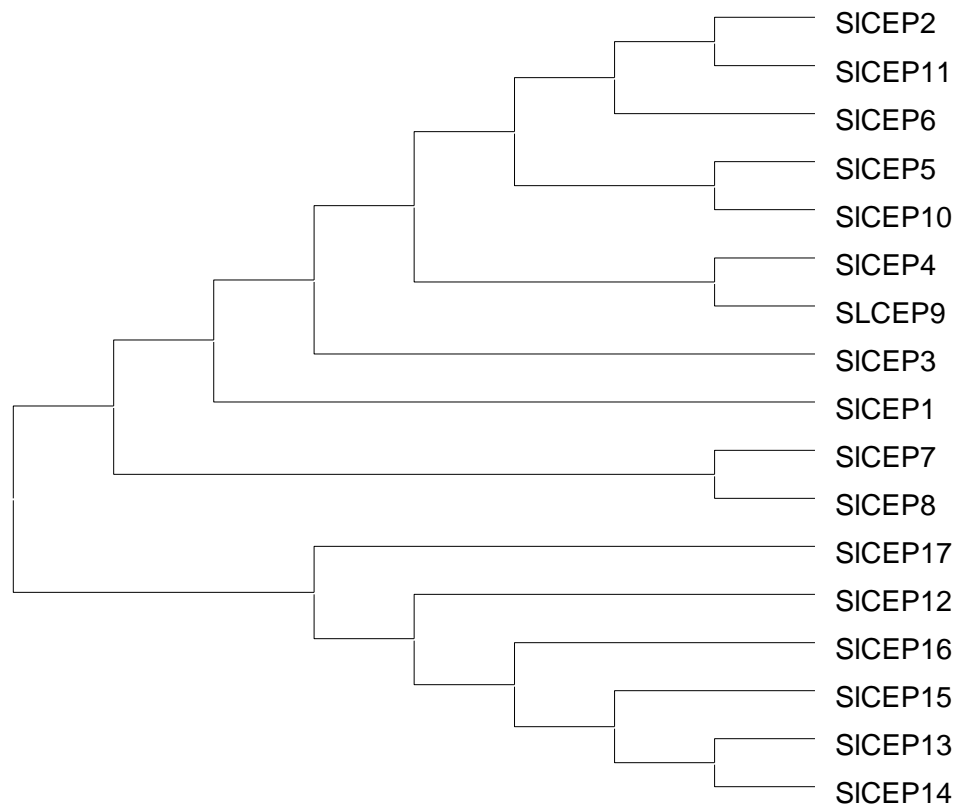
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**Table S2. Predication of N-terminal signal peptide of SICEP proteins**

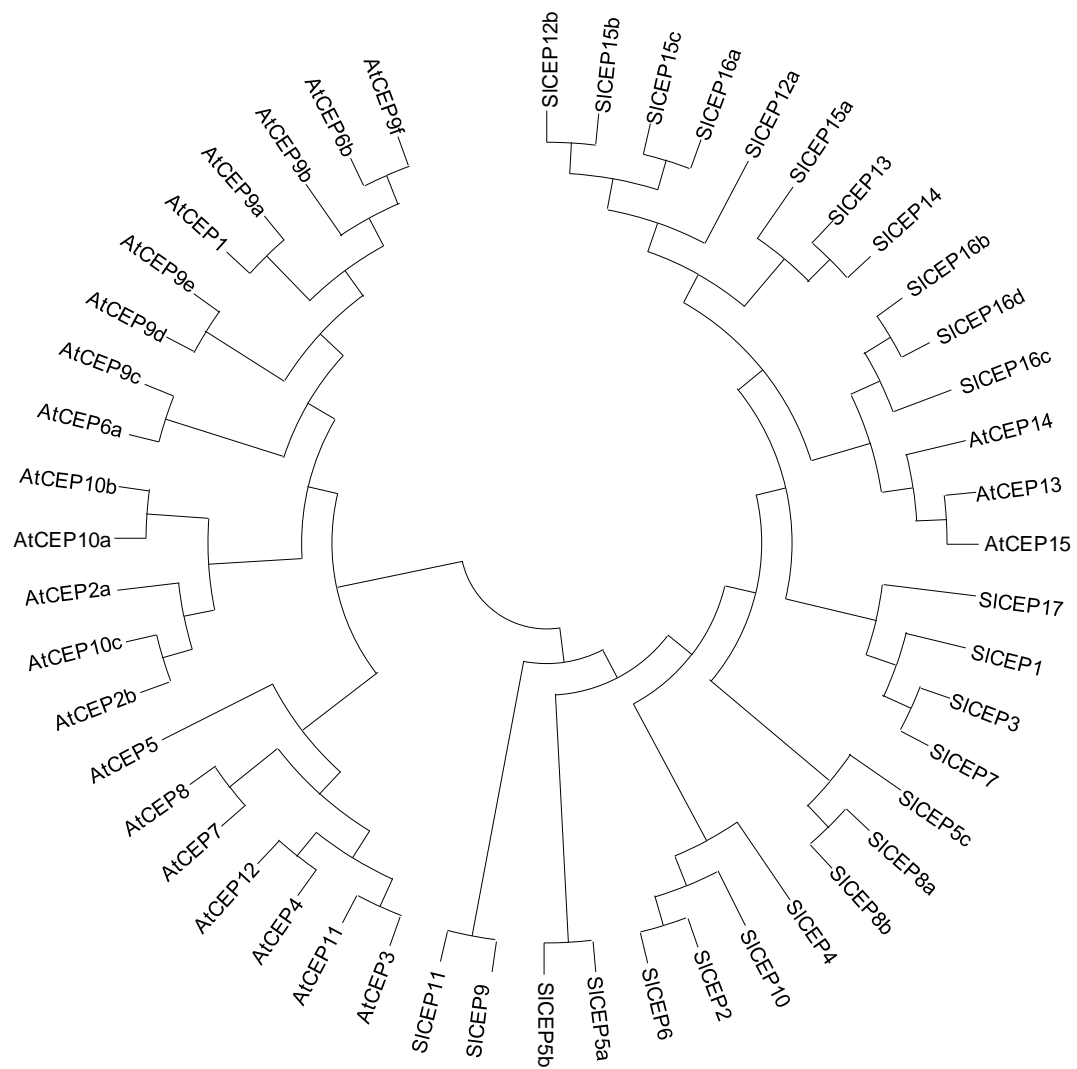
Protein	Position in sequence	Sequence	Probability	Predictated by
SICEP1	29-30	ATE <b>AR</b> PFI	0.6155	SignalP 5.0
SICEP2	24-25	IVE <b>SI</b> EGR	0.5206	SignalP 5.0
SICEP3	24-25	CIQ <b>CR</b> PIT	0.8301	SignalP 5.0
SICEP4	23-24	FSQ <b>GR</b> NLA	0.5008	SignalP 5.0
SICEP5	52-53	FAE <b>GR</b> QLK		Signal-CF
SICEP6	27-28	SIE <b>GR</b> HLLK	0.3919	SignalP 5.0
SICEP7	28-29	ASE <b>AR</b> PLD	0.4857	SignalP 5.0
SICEP8	24-25	ASE <b>AR</b> PLN	0.7908	SignalP 5.0
SICEP9	31-32	CVE <b>A</b> IRHL		Signal-CF
SICEP10	27-28	FTE <b>GR</b> QLN	0.5818	SignalP 5.0
SICEP11	26-27	TIQ <b>SI</b> EGR	0.3915	SignalP 5.0
SICEP12				
SICEP13	23-24	CFE <b>AR</b> TQL	0.5082	SignalP 5.0
SICEP14	23-24	CFE <b>AR</b> TQL	0.5064	SignalP 5.0
SICEP15	23-24	CFE <b>AR</b> TQL	0.4620	SignalP 5.0
SICEP16	23-24	CFE <b>AK</b> TQS	0.4772	SignalP 5.0
SICEP17	21-22	SFE <b>AR</b> KQF	0.7030	SignalP 5.0

SICEP1	NV V V K N S G P S P G I G H
SICEP2	P S P G H V D G H S P G I G H
SICEP3	L T E A K N S G P S P G E G H
SICEP4	V D A F S S P G H S P G I G H
SICEP5a	N Y A P K Q T G N S P G I G H
SICEP5b	N Y T P N Q T G N S P G I G H
SICEP5c	S I D D I K A G H S P G I G H
SICEP6	P P P G H P D G H S P G I G H
SICEP7	Y L G I K N S G P S P G E G H
SICEP8a	T L G D I K D G P S P G V G H
SICEP8b	T L G G I K A G P S P G E G H
SICEP9	D F G P T G P G H S P G I G H
SICEP10	V S F D N L K D H S P G I G H
SICEP11	G F S P Y G R G H S P G I G H
SICEP12a	V Y G N L N I G P S P G E G H
SICEP12b	V Y G N L N T G P S P G E G H
SICEP13	I Y G N L N T G P S P G E G H
SICEP14	I Y G N L N T K P S P G E G H
SICEP15a	I Y G N L N T G P S P G V G H
SICEP15b	V Y G N L N T G P S P G E G H
SICEP15c	V Y G N L N T G P S P G E G H
SICEP16a	V Y G N L N T G P S P G E G H
SICEP16b	V Y H N L R S V P S P G A G H
SICEP16c	V Y G N L R S G P S P G A G H
SICEP16d	V Y G N L R S V P S P G A G H
SICEP17	V K S E S H S S P S P G E G H
AtCEP1	D F R P T N P G N S P G V G H
AtCEP2a	E F A P T N P E D S L G I G H
AtCEP2b	D F A P T N P G D S P G I R H
AtCEP3	T F R P T E P G H S P G I G H
AtCEP4	A F R P T H Q G P S Q G I G H
AtCEP5	D F R P T T P G H S P G I G H
AtCEP6a	D F G P T S P G N S P G I G H
AtCEP6b	D F E P T T P G H S P G V G H
AtCEP7	A F R P T N P G N S P G I G H
AtCEP8	E F R P T T P G N S P G I G H
AtCEP9a	D F V P T S P G N S P G V G H
AtCEP9b	D F A P T S P G H S P G V G H
AtCEP9c	D F A P T S P G N S P G I G H
AtCEP9d	D F A P T E E I R L Q K M N G
AtCEP9e	D F A P T T P G N S P G M G H
AtCEP9f	D F K P T T P G H S P G V G H
AtCEP10a	D F A P T N P G H N S G I G H
AtCEP10b	D F A P T N P G H S P G I G H
AtCEP10c	D F A P T N P G N S P G I R H
AtCEP11	A F R S T E P G H S P G V G H
AtCEP12	A F R P T G Q G P S Q G I G H
AtCEP13	I Y R R L E S V P S P G V G H
AtCEP14	V D R Y L R S V P S P G V G H
AtCEP15	I Y R R Q G D V P S P G I G H

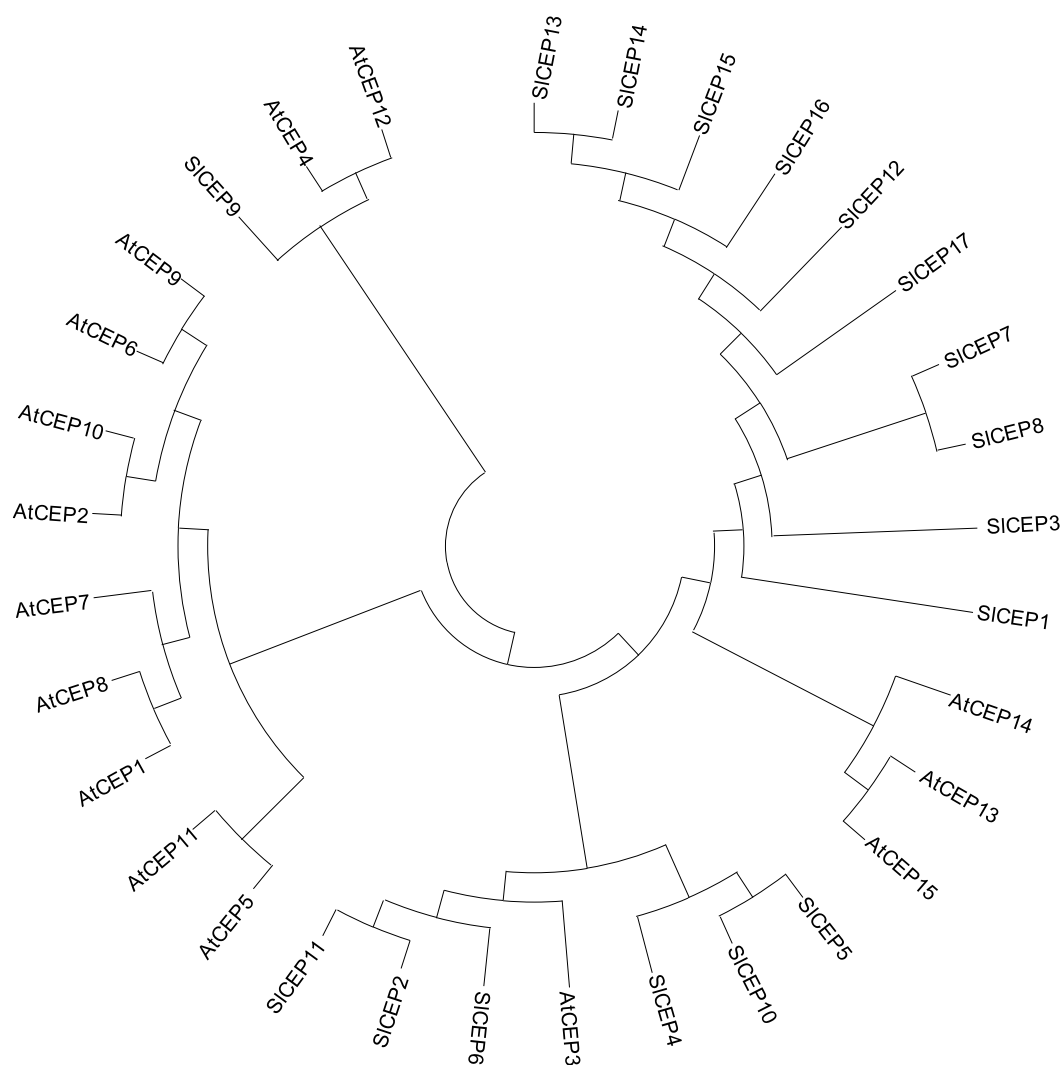
**Figure S1.** Alignment of CEP motifs in tomato and *Arabidopsis*.



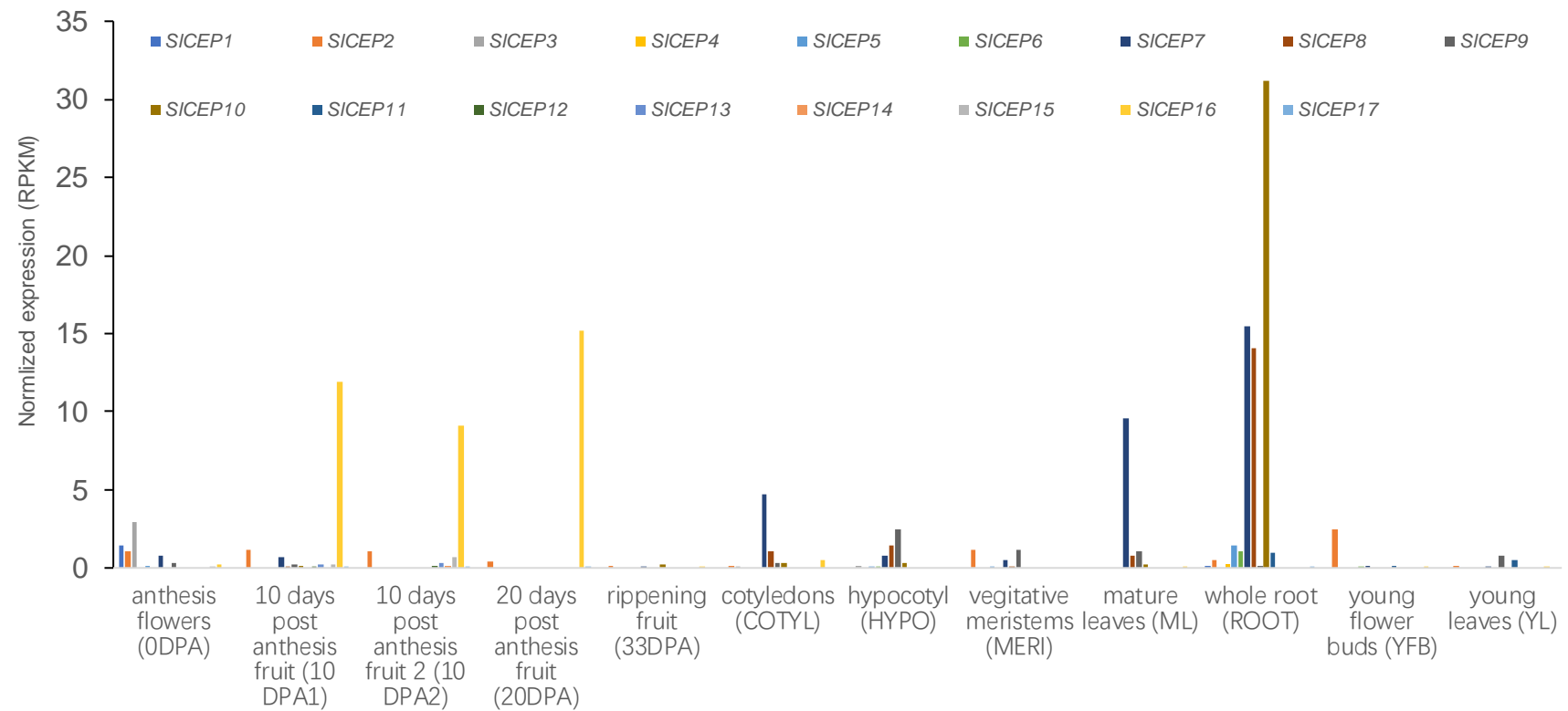
**Figure S2.** Phylogenetic tree of full-length SICEP proteins. The phylogenetic tree was build based on the full-length sequences of SICEP proteins with 1000 bootstrap replicates.



**Figure S3.** Phylogenetic tree of AtCEP and SICEP proteins based on the CEP motifs. The phylogenetic tree was build based on the CEP motifs of SICEP and AtCEP proteins with 1000 bootstrap replicates.



**Figure S4.** Phylogenetic tree of full-length AtCEP and SlCEP proteins. The phylogenetic tree was build based on the full length of SlCEP and AtCEP proteins with 1000 bootstrap replicates.



**Figure S5.** Expression levels of *SICEPs* in tomato tissues. The expression data was extracted from a transcriptome analysis of various tissues in wild species *S. pimpinellifolium*, LA1589.



**Table S3 Primers used for qRT-PCR analysis**

<i>SICEP1F</i>	ATGGCTCGAGTTATCATTCA	<i>SICEP10F</i>	TATGCATTTACTTTCCTTCT
<i>SICEP1R</i>	AGGACCGGAGTTTTTCACCA	<i>SICEP10R</i>	TTCTTCATACCTTTGCTTTG
<i>SICEP2F</i>	TCCTTGCTATCTTTGTCCTT	<i>SICEP11F</i>	TTCAATCTATCGAGGGACGA
<i>SICEP2R</i>	CATTGTTTTGAACAGTGAAT	<i>SICEP11R</i>	CGTCAAATGTTCCCTTCTTT
<i>SICEP3F</i>	ATGAAAATGGGCACAACAAA	<i>SICEP12F</i>	ATGTTTATGGCAACTTGAAT
<i>SICEP3R</i>	AAGTTGATGAACTTTCATGC	<i>SICEP12R</i>	AAACATGACCCATTCTAGGA
<i>SICEP4F</i>	ATGGCTAAGTTTTATACCGT	<i>SICEP13F</i>	TATGTTAGTTTTTCGTTGCAC
<i>SICEP4R</i>	TTTATCTTCCTTTTCTTCGA	<i>SICEP13R</i>	TGTCCTTCACCAGGACTAGG
<i>SICEP5F</i>	GCTGAGGGAAGACAACCTGAA	<i>SICEP14F</i>	ACTATGTTAGTTTTTCGTTGC
<i>SICEP5R</i>	TCCGGTTTGCTTTGGTGCAT	<i>SICEP14R</i>	TCCTTCTCCAGGACTAGGTT
<i>SICEP6F</i>	AGGGAAGACATTTGAAGTTG	<i>SICEP15F</i>	TTGCACCATGTTTTGAAGCA
<i>SICEP6R</i>	TCTGAACCAGACTAGTTGGC	<i>SICEP15R</i>	GAGGTGGGCCAAAATGTCCG
<i>SICEP7F</i>	GTAAATGCAAGAGCTTCATG	<i>SICEP16F</i>	CTTGCTTCTTCGGCCCCATA
<i>SICEP7R</i>	TAAGGCCATTCTTGATAGCA	<i>SICEP16R</i>	ACCAGCTCCAATACTAAGGC
<i>SICEP8F</i>	ATGGTGAGATTTTCTTATTT	<i>SICEP17F</i>	AATTTAGCAAAGAAGGTAAC
<i>SICEP8R</i>	CTTAATATCACCCAATGTTA	<i>SICEP17R</i>	GACTCGAGACTGATTTCAAA
<i>SICEP9F</i>	ATGGTTATTGTAACAAACAC	<i>SlActinF</i>	CTCAGTCAGGAGAACAGGGT
<i>SICEP9R</i>	TGATACGAAATTTCCACAC	<i>SlActinR</i>	GCCTCCAGCCTTGTTGTAAA