

St CDPK4	1	ATGGGCAACaCATGCCGTGGATCTA	TGGAGGCAAAA	CTTTTCAGGGT	TACaCTCAGCCT	aAGATAGTT	70	
St CDPK5	1	ATGGGCAACgCATGCCGTGGATCTT	CGGAGGCAAAA	CTTTTCAGGGC	TACCCTCAGCCT	aAGAT----	66	
St CDPK4	71	CCTGCTCCACCAATCA	TAAcCCCTTCTCCGGCAATTC	TTATTCCTTCTTGACAAAT	TTTTCTCCCA	CCCAg	140	
St CDPK5	66	-----CATTCA	GAAATCC-----AATTC	CAATCCAAAC	---ATAAT	CCGATCCCCAA	113	
St CDPK4	141	TAAcGCTCAaCAGAA	TAGCAATCACA	GAAGGAGCATTCTT	TGTCTCTTGTTAGT	CCCCAGAAAAGCTAGC	210	
St CDPK5	144	-----ACCA	AAAAAGCAACA	-----CCCT	CGGTCA	-----	144	
St CDPK4	211	ATGAATCGTTcCGGG	AGTAACTAGGCTTATTAT	GTAAAGGGTCATATGACCCC	GAATATTCCGCATCTTT		280	
St CDPK5	145	ATGAATCGTAcAAGC	ACTAACcCAGTCTATTAC	GTCCCGGTCATAAGACCCC	TAAcATTCCGCATCTAT		214	
St CDPK4	281	ATACTTcGGGA	AGAAATAGGACA	AGGGCAGTTGGCAC	ACTTATTTATGCACA	GAGAAATCTACCGG	350	
St CDPK5	215	ACACCCcCGGCC	CAAACTAGGACA	AGGGTCAGTTGGCAC	ACTTATTTATGCACC	GAAATGTCTCCGG	284	
St CDPK4	351	TGCTcGAGTATGCCT	TAAATCAATCTCA	AGAGGAAAGTGA	TCTCAGGAGGATGT	CAAGATGTAGa	420	
St CDPK5	285	TATCGAcTACGCCT	TAAATCTATTGC	CAAGAGAAA	CTCATCTCAAGGAGGATGT	GAAGATGTcAGG	354	
St CDPK4	421	AGGAAATTCAGATA	AATGCATCATTTGTCTGGT	CATAGGAAATATGTTACT	TATAAAGGGCCTTATGAGG		490	
St CDPK5	355	AGGAAATTCAGATA	AATGCACCATTTGTCTGGT	CACAAAA	CATCGTTTCATCA	AGGGTcCTTATGAGG	424	
St CDPK4	491	ATCCTTTATATGTT	CATATTGTcATGGAGATA	TGTA	GTGGCGGTGA	GTTGTTGATCGGATCAT	CAACG	560
St CDPK5	425	ATCGTTTGTATGTT	CATATTGTcATGGAA	CTTTCTGGTGGCGGTGA	ATTGTTGACCG	CATCATCAAA	494	
St CDPK4	561	AGGACAT	TACACTGAGAGAA	AGGCACTGAA	TTGACTAAAA	TATTGTTGGGTTGTG	GAGGCCGTGCAT	630
St CDPK5	495	AGGACAT	TACACTGAGAGAA	AGGCTGCCGA	TTGACTAAAA	TATTGTTGGGTTGTG	GAGGCCATGCCAT	564
St CDPK4	631	TCTCTTGGT	GTTATGCATAGAGATCTCAA	ACCTGAGAATTTCTTGTGGT	TAAaAGGATA	AATGATTTCT	700	
St CDPK5	565	TCACTTGGAG	TATGCATAGAGATCTCAA	ACCTGAGAATTTCTTGTGGT	TAAcAAGGAT	CATGATTTCT	634	
St CDPK4	701	CTC	CAAGCCATTGATTTGGACTCTCT	CTTTTCTCTCAAGCCAGG	CAAAATATTCACAGAT	GTCTGTTGG	770	
St CDPK5	635	CTC	CAAGCCATTGATTTGGACTCTCA	CTATTCTTCAAGCCAGG	CAAAATATTCACAGAT	GTCTGTTGG	704	
St CDPK4	771	TAGTCCATAT	TATGTTGGCTCCTGAGGTGC	TTTTGAAGCATTATGGTCC	TGAAGCTGATGTCTGGACAGCA		840	
St CDPK5	705	GAGTCCATAcTACG	TGCTCCTGAGGTGC	TTTTGAAGCATTATGGTCC	TGAAGCAGATGTCTGGACAGCA		774	
St CDPK4	841	GGAGTCATAC	CTACATACTGCTAAGTGG	GTGCCACCATT	TGGGCTGAAACACAGCAGGGA	AATATTTG	910	
St CDPK5	775	GGCTCATACTCTA	TATCTGCTAAGTGG	GTGCCACCATT	TGGGCTGAAACACAGCAGGGA	AATATTTG	844	
St CDPK4	911	ACG	CAGTCTGAAAGGGCACATTG	ATTTTACTCAGATCCTTGGCC	ATTGATATCTGAGAGTGC	AAAAGA	980	
St CDPK5	845	ATG	CAGTCTGAAAGGGCACATTG	ATTTTACTCAGATCCTTGGCC	TTTATTATCTGAGAGTGC	AAAAGA	914	
St CDPK4	981	TCT	TATCCGGAAGATGTTCTGCATGC	AGCCCTCGAGCGGTTAACTGCTCAT	GAAAGTATTCTGT	CATCCT	1050	
St CDPK5	915	TCT	CATCCGGAAGATGTTATGCATGC	GACCCCTCAGAGCGGTTAACTGCTCAT	GAAAGTATTATGT	CATCCT	984	
St CDPK4	1051	TGGATTTG	CGAAAATGGTGTGGTCTCTG	ATAGAGCACTGGATCCTGCAGTACT	TTCTCGCCTAA	AAACAGT	1120	
St CDPK5	985	TGGATTTG	TGAAAATGGTGTGGTCTCTG	ATAGAGCACTTGATCCTGCAGTACT	TTCTCGCCTCA	AAACA	1054	
St CDPK4	1121	TCTCTGC	TATGAACAAGTTAAAAA	AGATGGCTTGGCGGGT	GATTGCTGAAAGCTTGTCT	GAAAGAACAGAT	1190	
St CDPK5	1055	TTCTCTGC	ATGAACAAGTTAAAAA	AGATGGCTTGGCGGGT	GATTGCTGAAAGCTTGTCT	GAAAGAACAGAT	1124	
Nb CDPK5	1	-----	-----	-----	GTGATCGCTGAAAGCTTGTCT	CGAGGAGGAGAT	32	
St CDPK4	1191	TGC	GGTCTGAGAGAGATGTTTAA	AGGCCATGGATACTGACAGT	AGTGGTGAATACATTT	CATGAACTA	1260	
St CDPK5	1125	TGC	CGGTCTTAAAGGAGATGTTTAA	AGGCCATGGATACTGATAAC	AGTGGTGAATACATTT	CATGAACTA	1194	
Nb CDPK5	33						102	
St CDPK4	1261	AAAGC	AGGCTTTGAGAAAA	TATGGCTCTACCTTAA	AGGATACGGAGATACGGGA	ACTTATGGATGCGGCTG	1330	
St CDPK5	1195	AAAGC	TGGTTGAGAAAA	TATGGCTCTACCTTAA	AGGATATAGAGATACGGGA	ACTTATGGATGCGGCTG	1264	
Nb CDPK5	103	AAAGC	TGGTTGAGAAAA	TATGGCTCTACCTTAA	AGGATATAGAGATACGGGA	ACTTATGGATGCGGCTG	172	
St CDPK4	1331	ATG	TGGACAATAGTGGAACTAT	TGACTATGGAGAATTCAT	TGCCGCAACTGTTCA	TCTAAATAAATGGAA	1400	
St CDPK5	1265	ATG	TGGACAATAGTGGAACTAT	TGACTATGGAGAATTCAT	TAGCAGCAACTATTCACCT	TAAACAATGGAA	1334	
Nb CDPK5	173	ATG	TGGACAATAGTGGAACTAT	TGACTATGGAGAATTCAT	TAGCAGCAACTATTCACCT	TAAACAATGGAA	242	
St CDPK4	1401	GCG	CGAGGAACATCTCATGGC	CGCATTTCAAATTTTTGACA	AGGATGGAAGTGGTTA	CATACCGGTTGAT	1470	
St CDPK5	1335	CCG	CGAGGAACATCTCATGGC	CAGCATTTCAGTATTTT	GACAAGGATGGAAGTGGTTA	TATTACTGTAGAT	1404	
Nb CDPK5	243	CCG	CGAAGAACATCTCATGGC	CAGCATTTCAGTATTTT	GACAAGGATGGAAGTGGTTA	TATTACTGTAGAT	312	
St CDPK4	1471	GAG	CTCCAAcAGCTTGTAT	AGAGCATAACATGACAGATGT	TACTTTGAGGATATTTATA	GAGAAAGTcG	1540	
St CDPK5	1405	GAG	CTCCAAcAGCTTGTAT	AGAGCATAACATGACAGATGT	TACTTTGAGGATATTTATA	GAGAAAGTcG	1474	
Nb CDPK5	313	GAG	CTCCAAcAGCTTGTAT	AGAGCATAACATGACAGATGT	TACTTTGAGGATATTTATA	GAGAAAGTcG	382	
St CDPK4	1541	ATC	AGGATAATGATGGACCA	AATGATATGGAGAATTTGTTGCT	TATGATGC	AAAAAGGAAATCCATGTA	1610	
St CDPK5	1475	ATC	AGGATAATGATGGACCA	AATGATATGGAGAATTTGTTGCT	TATGATGC	AAAAAGGAAATCCATGTA	1544	
Nb CDPK5	383	ATC	AGGATAATGATGGACCA	AATGATATGGAGAATTTGTTGCT	TATGATGC	AAAAAGGAAATCCATGTA	450	
St CDPK4	1611	AGG	cAGACGAACAATGCG	AAATAGTCTGAATTTc	AGCATGAGAGATGC	CCGGAGCTCACTAG	1674	
St CDPK5	1545	AGG	aAGACGAACgATGCG	AAATAGTCTGAATTTc	AGCATGAGAGATGC	CCGGAGCTCACTAG	1608	

Supplemental Figure 6. Alignment of the Nucleotide Sequences of St CDPK4, St CDPK5 and Nb CDPK5.

Conserved nucleotides are boxed in black. Partial sequence of Nb CDPK5 cDNA used for VIGS was shown. Multiple alignment of the nucleotide sequence was made using the CLISTAL W program (Thompson et al., 1994).