

Pt-SCL6 A

1 AGAAAGAGAAAACAGAGAGAAAACCCACCGAAAAGAACCTGCATCGAAACTCATCTTCAGAATCAGAAGAGGAAAGCTTATTGTAGCAAAGA
91 GTGTGTGTGTTCCGAGTCTTGAGGTACTGAGCTAGCAAAGAGGGCGATAGAGCCCGCCAAAGAAAGCTTGAGTTGTAGCTTTGTGCTTGT
181 TGTTCTGATCAAATTTGATTTTTGATTTTTGATTTCTGCTGGTTTGTATCTTCTTTGTATCGTACAAACTCATTAGTATTAGTCTCTTT
271 CTTTTGTAGCTTTCTAAACCTGTGAACTGGAGAGTCTGGGATTTGGGATTGTGGTAACACTGTTGTTGAGTTATTAGATGAGGG
M R
361 CCATGCCCTAGCCTTTGAGGATTTCAAGGGAAGGGGGCTTTAGATTTCTCTTCTTCTTCTCAGATTGCGGCAATTCATCATCAGC
A M P L A F E D F Q G K G A L D F S S S S S D S R Q F H H Q
451 AGCACAAGGAAGAAACAGACTGGCTACTCAGCAACAGCAACAGGGGAAAACAAGAAAGCAAATTTGCTATGTGGGCAAGTCCACCCTG
Q H K E E Q D W L L S N S N R G N K K A N C C Y V G S A T T
541 AGCCACATCAGTGTCTGATAACAGAAGAAGTCCAAGCCCTCCCAGTCTTCAACTGTCTTCTCTCTGGGCGGTGGTGGCTCT
E P T S V L D N R R S P S P P T S S S T L S S S L G G G G S
631 CCGCCACCGACACAACCGGCGTGGCGGACCAATGCCTTAGCAACCCCATCAGTAGATACCAACTGAAAAATGTGGAGGCT
S A T D T T G V A A T N A S S N P P S V D I T N T E K C G G
721 TGGGAATGGAAGACTGGGAGAGTGTGTGTCTGGTTCACCTAATCAAGAGCAGTCCATTTAAGGCTCATTATGGGTGATACCGATACC
L G M E D W E S V L S G S P N Q E Q S I L R L I M G D T D D
811 CATCTCTGGATTAACAAGATCTTGCATCAAGATACGGAATCAATGCAGGTTTGGTGTGGATCAGGCTAGTCTGGCTTTGAGA
P S L G L N K I L H Q D T E F N A G F G V V D Q A S L G F E
901 CACCTTTACTTCGGTCAGCAGCAATATTGACCTGATTTGTGGCAACAGTCAAGGCTTGGTCTGGTTCAAACCAAAATCACATT
T P F T S V S S N I D P D F V G N S A R L G S G S N Q N H I
991 TTTCAACAGCAGCAGCTACAATCTTACCTCCTCAAGCGTTTTTCAACCGCAACCAGTTGAAGCTTTGGATGAGAAGCCGAGATAT
F S T A A A T N L S P P P S V F Q P Q P V E A L D E K P Q I
1081 TCAGCCCTCAGCTGATAATGAATCAGAATCAAGCTCAGTATGCTCAAAATCCAGCTTATTCTTGCCCTTTCATATGCTCAAATGCAAG
F S P Q L I M N Q N Q A Q Y A Q N P A L F L P L S Y A Q M Q
1171 TGCATCAACTTTACCACGACCGCCCGCCGAAACGCTTAATCTTGGGCCAATCAAAGGTCCTTTCAGATTGCGGGCAGC
V H Q L L P P A P P P P K R L N L G P N Q K V P F S D S G Q
1261 AAGAGCTATTCTTCGACGACAGCCGCTTCAAAATGCTTCAACAACAAAGGAAAACATGGGCGTGACAACACAGCAACGAAGCAGAAGT
Q E L F L R R Q P L Q M L Q Q Q R E T M G V T T T A T K Q K
1351 TGGTAAACGATGAATTGGCAATCAGCAGTTCAGCAGGCAATAACTGACCAATTTCAAGGCTCAGAGCTGATCGAAACAGGTAATC
L V N D E L A N Q Q L Q Q A I T D Q I F K A S E L I E T G N
1441 CTGTACACGCGCAAGAGATATTGGCGGCTCAATCACCAGCTCACCAGTGGTAAGCTTTTCAGAGGGCTGCTTTTTATTCAAGG
P V H A Q E I L A R L N H Q L S P I G K P F Q R A A F Y F K
1531 AGGCCTACAGTACTTCCACATGAATATGAATAATAGTAGCTGGCTTTGCCCGTTATAGTATCATTTCAAGATTAGTCTTACA
E A L Q L L L H M N M N N S S L A L P G Y S I I F K I S A Y
1621 AATCTTCTGAAATCTACCGATTCTCAATTTGCTAATTTCACTTGTAAACCAAGCACTTCTGAAGCCTTGAAGGGTGAATAGAA
K S F S E I S P I L Q F A N F T C N Q A L L E A F E G C N R
1711 TCCACATTATAGATTTCGATATTGGATATGGTGGGCGAGTGGCTTCTTATGCAGGAGCTTGTTTGAGAAGTGAAGGCTCCTCCTCGC
I H I I D F D I G Y G G Q W A S L M Q E L V L R S E G P P S
1801 TTAATACTACTGCATTTGCTTCTCCGTCACACATGATGAGCTCGAGCTCAGCTTCACTCGAGAAAATTTGAAGCACTTTGCAAGTGA
L K I T A F A S P S T H D E L E L S F T R E N L K H F A S E
1891 TCAATATGCCGTTTGGAGCTTGAATTTAAGCCTTGAAGCTTAAATTTGCTTCTTTGGCGCTTCTTTTCCGGGATTAGAAAAGTGAAG
I N M P F E L E I L S L E A L N S A S L A L P F R G L E S E
1981 CAACTGCTGTAATCTCCCAATGGCACCTTCTGTAATACCCAGCAACCTTTCTTCCGTCGCTTTGCTTTGTAAGCAACTTAAACCA
A T A V N L P I G T F C N Y P A T F P S V L C F V K Q L K P
2071 AGATTGTTGTTCTTTGGATAGAGGCTGTGATCGAACAGATGTTCCATTTCCACCATACGATTGATGCACTCAGTCACTATCATGCC
K I V V S L D R G C D R T D V P F P H H T I H A L Q S Y S C
2161 TACTGAAATCGCTGGATGCTGTAATGTAATTTGGATGCCTTGCAAAAGATTGAGAGGTTTTGGTTATCCTTGATGAAAAAATTG
L L E S L D A V N V N L D A L Q K I E R F L V Y P C I E K I
2251 TATTAGGACGCCACCGTTCTCTGAGAGATTGCCTCCTTGAAGAGTCTGTTTATGCAATCTGGGTTGCTCCATTGACATTTAGTAACT
V L G R H R S P E R L P P W K S L F M Q S G F A P L T F S N
2341 TCACTGAGTCCAGGCTGACTGTTTGGTGAACGGACTCCAGTTAAGGGTTTCCATGTTGAGAAGAGACAGTCCCTCGCTGTTTTCTGCT
F T E S Q A D C L V Q R T P V K G F H V E K R Q S S L V F C
2431 GGCAGCGGAAAGAGCTTATCTTGGCCACTGCTTGGAGGTGCTAAGGAGTAGCAGCGGATATTGGTTGCAAAGGTGCCTAACACAGCTT
W Q R K E L I L A T A W R C*
2521 TGGTTTATGATTATTTGACTTTTCTGTTTGTGTTCTTATGCTAATGTCTATGAGCTTTGGGTTTATTGTCCAATCAACAACAAA
2611 ACATTTTCGTAGCTGTTATGATGCTGTTACTAAAAAATAAAAAAAAAAAAAAAAAA

Pt-GRAS B

1 CAATATCTATCATAATATCTTGAATTTCCGCGGAACAAGGCAAGCGTTGCCATAAAATCATCTCCGATAGCAATAGGTTCTTTCAGA
91 GGTGTTGTTGAATTTATTAGCCAAAGTGAAGGAGAGCGGAATATGTTTATGATTTTTTGTGTTAACACTCATAAGCTCATAATGATCAA
M V Y D F L F N T H K L Y N D Q
181 AGGAGTAATCAAGCGATTGGCCTTCACTGGGCTTTCGATCGTTGATGCTATCCTACTTGCCATGATGTCGGATAACTCTGCTGCT
R S N Q A I G L Q L G L S I V D C Y P Y L P M M S D N S A A

271 TCTTCATGATTCTTCAGCCCAGAGATCAAAAAGAGGCTTAAGCGGACAATAAGTGTGGTGATGGTAGCCCAACCAGTACTCTTAGCCG
S S M I L Q P R D Q K R L K R T I S V G D G S P T S T L S R
361 AGTAGCAGCACTAGCAGCTTGAGTAATTTGCCAAGGCTTCAATTCAGGGACCATATTTGGACTTATACTCGAAGATACCTTGCTGCTGAA
S S S T S S L S N L P R L Q F R D H I W T Y T R R Y L A A E
451 GCTGTGAAGAAGCGCGCAGCTATGATCAAATCAGAAGATGGCTGCGACGGTGATCAACAAGATGGACCGCGGATGGGATGAGGCTC
A V E E A A A A M I K S E D G C D G D Q Q D G T A D G M R
541 GTTCAGCTCCTAATGCTTGCTGAAGCTGTCGCTTGTGCGGACAAGTCTCATGCCTCGGCTTTGTTATCCGAACCTCGTGCCAATGCT
V Q L L I A C A E A V A C R D K S H A S A L L S E L R A N A
631 TTGGTCTTTGGCTCTCTCTCCAGCGCGTCGCTTCTTGCTTTGTCCAAGGCTTGCTGACCGTCTTGCATCGGTCAGCCCTCTGGAGCG
L V F G S S F Q R V A S C F V Q G L A D R L A S V Q P L G A
721 GTAGGCTCCTTCGCGCCATCAATGAACATAATGGACATTGCTGGCTCGCGGAGAAGGAAGAAGCTTTTCGCCTTGCTATGAAATTTGC
V G S F A P S M N I M D I A G S R E K E E A F R L V Y E I C
811 CCACACATTCAGTTTGGTCACTTTGTGGCCAACTCATCCATATTGGAAGCCTTTGAGGGAGAGAGTTTAGTCCATGTTGTGGACTTAGGT
P H I Q F G H F V A N S S I L E A F E G E S L V H V V D L G
901 ATGACCCTAGGCTGCCACGCGGTGAGCAATGGCGCGGCTGATCGAAAGCCTCGCCAACCGCGTGGCCAACCGCCACGCGGCTTCGA
M T L G L P R G Q Q W R R L I E S L A N R A G Q P P R R L R
991 ATAAGTCCGTTGGCTTTGTGTTGAAAAATTCAAAGCATTGGTGTGAGCTTAAAGATTATGCGAAAACCTATGGCATCAATTTGGAG
I T A V G L C V E K F Q S I G D E L K D Y A K T Y G I N L E
1081 TTCTCTGGTGGAAAGCAACTTGAAAAATTCAGACTAAAGACATCAAAGTCTTGAACGAAGTGCCTGTTGTCAATAGCATACTT
F S V V E S N L E N L Q T K D I K V L E N E V L V V N S I L
1171 CAGCTGCATTGTGGTCAAAGAAAGCAGAGGAGCTCTAAATTCAGTGTGCAAATAATCCATGAGCTGTACCGAAAGTATTGGTGTCT
Q L H C V V K E S R G A L N S V L Q I I H E L S P K V L V L
1261 GTTGAGCAGGACTCAAGCCATAATGGCCATTTTTCTTGGGAGATTTCATGGAAGCGTTGCACTACTACTCAGCAATATTTGACTCCCTT
V E Q D S S H N G P F F L G R F M E A L H Y Y S A I F D S L
1351 GATGCCATGCTGCCAAGTATGACACAAAACGCGCAAAATAGAACAGTTTTACTTTGCAGAGGAGATAAAGAACATTGTGAGCTGTGAG
D A M L P K Y D T K R A K I E Q F Y F A E E I K N I V S C E
1441 GGGCTGCAAGGTGGAGAGGCACGAGAGGGTGGACCAATGGCGTCGAGGATGAGCCGTGCCGGTTCCAGGCGGCACCCATTAAGATG
G P A R V E R H E R V D Q W R R R M S R A G F Q A A P I K M
1531 ATAAATCAGGCACAGAAATGGCTCAAGAACAAGGTCTGTGAGGGTTACACGGTTGTTGAAGAGAAAGGTGCTTGGTTCTCGGCTGG
I N Q A Q K W L K N N K V C E G Y T V V E E K G C L V L G W
1621 AAATCCAAGCCTATATTGCTACTACTTGCTGGAATGCT**TAA**ACTACAGCTGCCTAATTCACAGTCTTCTACAAATAAAGTTTACC
K S K P I I A T T C W K C *
1711 AATAAAGTTAGAAGCAGCTATTTAATTATATAATGTCTTCCATTGCAATTACCGTGTGCAACTCCGGAGTCTGGAGTGATGAATGTT
1801 GTTTTATATTTCAGTGTGAGCAAGCTGTTTCAGGTGCTTGAACAGATGAAATAAAGATTTATGTATTGTTGGTTTTAAAAAAAAAAAAA
1891 AAAAAAAAAA

图 1 *Pt-SCL6* (A)和 *Pt-GRAS* (B) cDNA 全长与推导氨基酸序列

注: 黑体ATG为起始密码子, TAA为终止密码子; 方框为保守的GRAS结构域; 双下划线是miR171和miR1446的识别位点

Figure1 Nucleotide sequences of complete *Pt-SCL6* and *Pt-GRAS* cDNAs and their deduced amino acid sequences

Note: ATG (start codon) and TGA (stop codon) are shown in bold. Two boxes delineate the GRAS domains. The double-underlined sequences delineate the miR171 and miR1446 recognition sites