

```

10          20          30          40          50          60
=====+=====+=====+=====+=====+=====+
MpCPT7.25  -----
MpCPT7.48  MLVATTTLQLAHGEVAKVLETHSMYKRDPWRRWVRTLTFTFIQLTVQANSAQRSQIVAWLNRL
AtCPT3     -----
AtCPT4     -----
AtCPT5     -----
MpCPT7.26  -----
MpCPT7.42  -----
MpCPT7.37  -----
MpCPT7.16  -----
AtCPT7     -----
AtCPT9     -----
AtCPT1     -----
AtCPT2     -----
AtCPT8     -----
AtCPT6     -----

```

```

          70          80          90          100          110          120
=====+=====+=====+=====+=====+=====+
MpCPT7.25  -----
MpCPT7.48  HANIRLFEFETNVFVLATIAYGLAQSHQALGAFPTGEKDAlVSSVMSMADKLSADDRRKP
AtCPT3     -----
AtCPT4     -----
AtCPT5     -----
MpCPT7.26  -----
MpCPT7.42  -----
MpCPT7.37  -----
MpCPT7.16  -----
AtCPT7     -----
AtCPT9     -----
AtCPT1     -----
AtCPT2     -----
AtCPT8     -----
AtCPT6     -----

```

```

          130          140          150          160          170          180
=====+=====+=====+=====+=====+=====+
MpCPT7.25  -----MAVYGSLC
MpCPT7.48  VPTTFSAVEKFLAPQLSSVHLRSILASMSALLDLAQKPRFSTALRRPWSWAKFLLLRTLA
AtCPT3     -----
AtCPT4     -----
AtCPT5     -----
MpCPT7.26  -----
MpCPT7.42  -----MESVVARCV
MpCPT7.37  -----MESVVDRCV
MpCPT7.16  -----MGAAKVIHGSGVQNFVTCKSPDM
AtCPT7     -----MLSLRVPTP
AtCPT9     -----MLSLFS---
AtCPT1     -----MLSLLSSDS
AtCPT2     -----MLSLLS---
AtCPT8     -----MLSMLWFLl
AtCPT6     -----MLSILS---

```

```

          190      200      210      220      230      240
=====+=====+=====+=====+=====+=====+
MpCPT7.25  RAMSLRVLAPEAPGD-RGLVNLNLRPFQPLWYHLHYVACPRILTVDGFFGVLFRCDP SLR
MpCPT7.48  RDISLRVLSPTTAGEPPGALLSLARIFQPFWYHFHYSACPRVLTLAGLFETLVGCDPSLN
AtCPT3     -----MAELPGQIRHIGGRMSQLL
AtCPT4     -----MNTTREEVGEFTQIF
AtCPT5     -----MNTLEEVDSTHIF
MpCPT7.26  -----
MpCPT7.42  NLKSVQ-----LSTIYKTHCEAAAPMELSMSRSTIPGASIS
MpCPT7.37  RLRSIQ-----LSTIYKTHCEAAAPMELSMSRSTFPGASIS
MpCPT7.16  QSDCFRPTSCSGSTSAPGFSGRGSSCRWLLRERVAGGSSNRIFDLNGRRAEEEFWVAI LP
AtCPT7     TSFDFR-----R-YQAGDLERRWRLSRDSFL
AtCPT9     VVFTFL-----ALFLIPGLFISRRLNVPLSL
AtCPT1     SLLSLL-----FLFLIPCLFITSYIGFPVFL
AtCPT2     TLVALP-----FLFLIPCLFITSYICFPVFL
AtCPT8     SLLSLL-----LLPCLR-----PCFP
AtCPT6     SLLSLL-----FLFIISCFFITSHFWFPLSL

```

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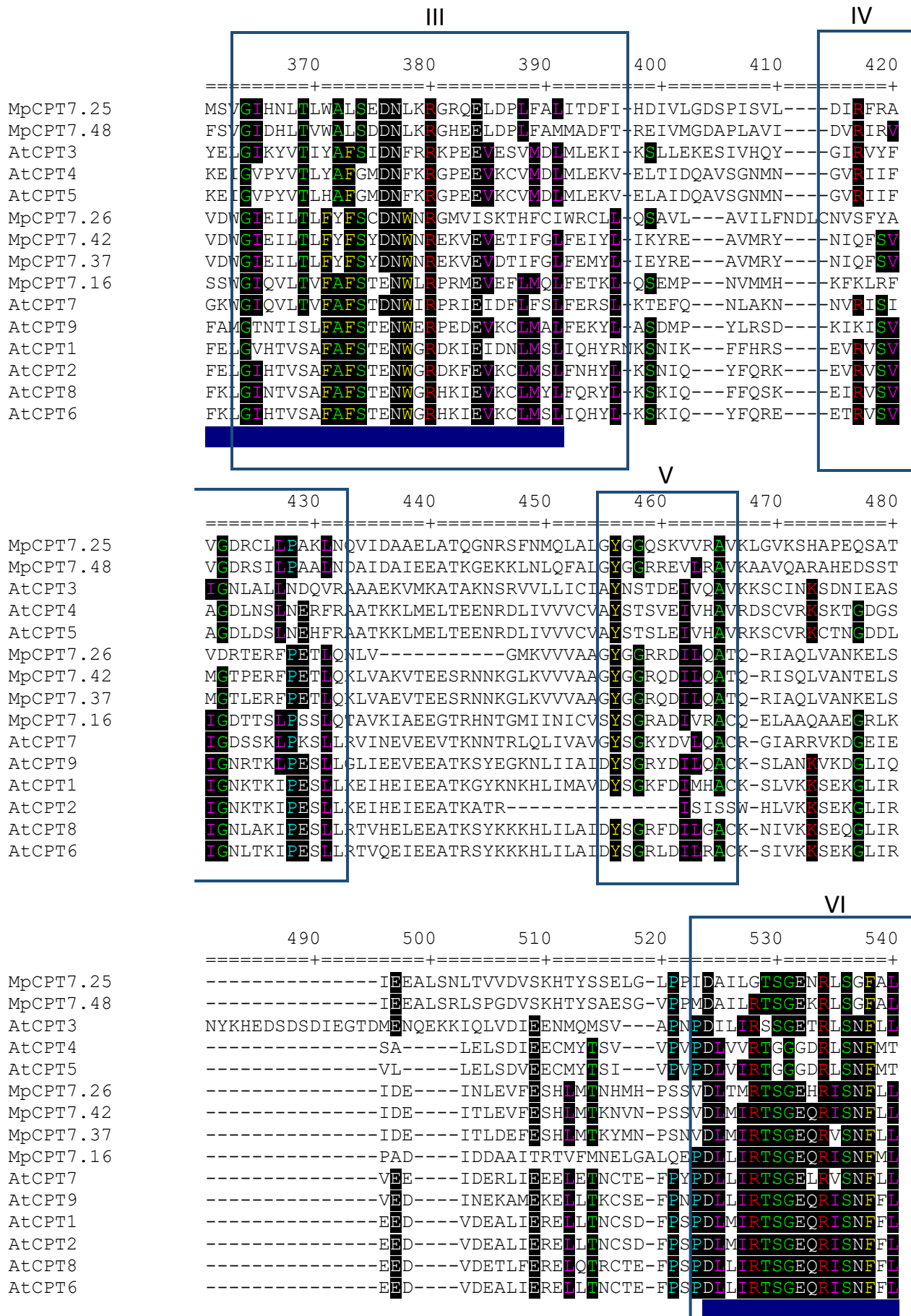
          250      260      270      280      290      300
=====+=====+=====+=====+=====+=====+
MpCPT7.25  ATEDEVYREIFGAQSSGLSGRRGCGGGGATARLPQVPSVGSTPAPPPRFAASSLVG SVRE
MpCPT7.48  TVVDDVHREIFGAPPVG-----KFAPSEAHLPQLPNGVAGAAPADLTNQSFIAAVRE
AtCPT3     EQIYGFSR-RSLFRVISMGP
AtCPT4     NALMSLMR-KFIFKVLRVGP
AtCPT5     NALMSLMR-KFLFRVLCVGP
MpCPT7.26  -----
MpCPT7.42  SHRARELR-VLSRRTLGRKPFPGAPVNGCVGMLHETAGTASADSCAD-----LSQTKR
MpCPT7.37  SHLARELR-ISRRTLGRNPFPGALVNGCGGTLHGIAATASADSCAD-----MSQQKS
MpCPT7.16  KRRANFRK-ARRVLGLGDQPHSSLNFGSRVESPNTSIGGRLQPQVSSSPVDPKSRGESAP
AtCPT7     SFSPKFEE-NRGFRF-GVKSSKSDVSFTAEEEEET-----
AtCPT9     TNILRFIK-IIASKY--DDEEERNEKRGTMG EKQ-----
AtCPT1     LKLIGLIK-IKAAR--DNEKR--DEGTYVVRED-----
AtCPT2     TKLLGLIK-FKAARDDDDNEKR--DEATCVVREE-----
AtCPT8     AK--GSLK-----NKKKIDKGTYYVVGEE-----
AtCPT6     PKILGFIK-ITSSRD-DYDNEQR-DEGTYVVGVE-----

```

```

          310      320      330      340      350      360
=====+=====+=====+=====+=====+=====+
MpCPT7.25  HLMCAYLRSLAASGGMAPRHLGVIMDGNRRISRQNRIGSLVDDGHRQGGGRK-ILEVLTWS
MpCPT7.48  HLKAYLRTRLAGPGQLPRHLGVIMDGNRRFSRQHGIGSVLEGHRIGARR-ILQFMTWS
AtCPT3     -----IPCHIAFIMDGNRRYAKKCGILD-GSGHKAGFSA-IMSMLQYC
AtCPT4     -----IPTNISFIMDGNRRFAKRNLEGLDAGHRAGFIS-VKYILQYC
AtCPT5     -----IPTNISFIMDGNRRFAKHNLIGLDAGHRAGFIS-VKYILQYC
MpCPT7.26  -----MPKHVAIILDGNRRYSKARGLRG-GEGFEVLLKKSLKEAVRVS
MpCPT7.42  RIELPPELNP-----EMPKHVALILDGNRRYSKARGVRG-SEGFEVGLKKSLKDAVRVS
MpCPT7.37  RIEFPPELNP-----EMPKHVALILDGNRRYSKARGVRG-SECFVGLKKSLKEAVRVS
MpCPT7.16  KIVLPSELRP-----ELMPKHVAIIMDGNRSFWAQCRGMHA-GFGHAAGAEALRRVAKIA
AtCPT7     ---LPEELHA-----ELMPKHVAIIMDGNRFWAKNRGLIQP-WDGHRAGVEALKEIVELC
AtCPT9     -----KRGR-----NIMPKHVAVILDGNRRWAEKRGIGT-SEGHEAGARRIMENAKDC
AtCPT1     -----GLQR-----ELMPKHVAIILDGNRRWAKRAGITT-SQGHEAGAKRLIDIAELC
AtCPT2     -----ELQR-----ELMPKHVSFILDGNRRWAKRDGLTT-AQGHEAGTKRIIIEIAEVC
AtCPT8     --ETPKELQR-----ELMPKHVAVIMDGNRRWAKQTGLLT-SQGYEAGAKRLLEFADLC
AtCPT6     -----ELQR-----ELMPKHVAVIMDGNRRWAKRAGLLT-SQGHEAGAKRLIEFSELC

```



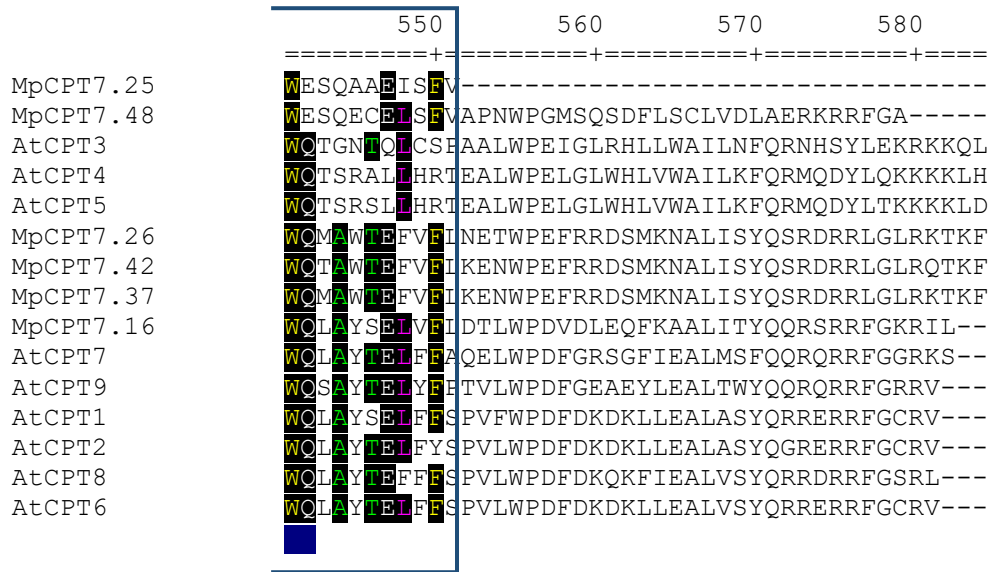


Figure S1. Multiple alignment of amino acid sequences of *cis*-prenyltransferases of *A. thaliana* and *M. polymorpha*. Black color and boxes indicate the most conserved regions of amino acid sequences. I to VI are conserved regions.

Alignment of Sequence_1: [Mpol_Tak1_ATG] with Sequence_2: [Mpol_Ko#1_ATG]

Similarity : 267/268 (99,63 %)

```
Seq_1 1  M E S V V D R C V R L R S I Q L S T I Y 60
          ATGGAATCTGTGGTGGACAGATGTGTGAGGCTCAGATCCATTCAACTGTCCACGATTAC
          |||
Seq_2 1  M E S V V D I C E A Q I H S T V H D L Q 58
          ATGGAATCTGTGGTGGACA--TCTGTGAGGCTCAGATCCATTCAACTGTCCACGATTAC
          |||
          K T H C E A A A P M E L S M S R S T F P
Seq_1 61  AAGACGCATTGTGAAGCTGCAGCACCGATGGAAC TAAGTATGAGTAGATCAACGTTTCCT 120
          |||
Seq_2 59  AAGACGCATTGTGAAGCTGCAGCACCGATGGAAC TAAGTATGAGTAGATCAACGTTTCCT 118
          D A L * S C S T D G T K Y E * I N V S W
          G A S I S S H L A R E L R I S R S R T L
Seq_1 121  GGCGGAGCATCAGCAGTCACCTAGCTCGTGAAC TCCGTATTTACGCTCCAGAACACTC 180
          |||
Seq_2 119  GGCGGAGCATCAGCAGTCACCTAGCTCGTGAAC TCCGTATTTACGCTCCAGAACACTC 178
          R E H Q Q S P S S * T P Y F T L Q N T R
          G R N P F P G A L V N G C G G T L H G I
Seq_1 181  GGCCGCAATCCGTTTCCTGGTGC ACTAGTGAATGGTTGCGGTGGTACGTTGCATGGGATA 240
          |||
Seq_2 179  GGCCGCAATCCGTTTCCTGGTGC ACTAGTGAATGGTTGCGGTGGTACGTTGCATGGGATA 238
          P Q S V S W C T S E W L R W Y V A W D S
          A A T A S A D S C A
Seq_1 241  GCCGCGACCGCATCAGCTGACAGTTGTGCA 268
          |||
Seq_2 239  GCCGCGACCGCATCAGCTGACAGTTGTGCA 268
          R D R I S * Q L C R
```

Figure S2. Sequence alignment of the target site of the MpCPT7.37 gene of mutant plant 1 and the native MpCPT7.37 gene site of wild-type plants. The translated amino acid sequence is indicated above the nucleotide sequence. Mutations are marked with a lattice sign, and possible stop codons are marked with an asterisk. ATG is the start codon (highlighted in red). The target genomic region is highlighted in blue.

Alignment of Sequence_1: [Mpol_Tak1_ATG] with Sequence_2: [Mpol_Ko#2_ATG]

Similarity : 237/252 (94,05 %)

```

Seq_1  1  M E S V V D R C V R L R S I Q L S T I Y
      ATGGAATCTGTGGTGGACAGATGTGTGAGGCTCAGATCCATTCAACTGTCCACGATTTAC 60
      |||||||#####
Seq_2  1  ATGGAATCTGTGGTGGACAGAT-----CCATTCAACTGTCCACGATTTAC 45
      M E S V V D R S I Q L S T I Y

Seq_1  61  K T H C E A A A P M E L S M S R S T F P
      AAGACGCATTGTGAAGCTGCAGCACCGATGGAACCTAAGTATGAGTAGATCAACGTTTCCT 120
      |||||||
Seq_2  46  AAGACGCATTGTGAAGCTGCAGCACCGATGGAACCTAAGTATGAGTAGATCAACGTTTCCT 105
      K T H C E A A A P M E L S M S R S T F P

Seq_1  121 G A S I S S H L A R E L R I S R S R T L
      GGCGCGAGCATCAGCAGTCACCTAGCTCGTGAACCTCCGTATTTACGCTCCAGAACACTC 180
      |||||||
Seq_2  106 GGCGCGAGCATCAGCAGTCACCTAGCTCGTGAACCTCCGTATTTACGCTCCAGAACACTC 165
      G A S I S S H L A R E L R I S R S R T L

Seq_1  181 G R N P F P G A L V N G C G G T L H G I
      GGCCGCAATCCGTTTCCTGGTGCCTAGTGAATGGTTGCGGTGGTACGTTGCATGGGATA 240
      |||||||
Seq_2  166 GGCCGCAATCCGTTTCCTGGTGCCTAGTGAATGGTTGCGGTGGTACGTTGCATGGGATA 225
      G R N P F P G A L V N G C G G T L H G I

Seq_1  241 A A T A
      GCCGCGACCGCA 252
      |||||||
Seq_2  226 GCCGCGACCGCA 237
      A A T A
  
```

Figure S3. Sequence alignment of the target site of the MpCPT7.37 gene of mutant plant 2 and the native MpCPT7.37 gene site of wild-type plants. The translated amino acid sequence is indicated above the nucleotide sequence. Mutations are marked with a lattice sign; possible stop codons are marked with an asterisk. ATG is the start codon (highlighted in red). The target genomic region is highlighted in blue.

Alignment of Sequence_1: [Mpol_Tak1_ATG] with Sequence_2: [Mpol_Ko#5_ATG]

Similarity : 144/145 (99,31 %)

```

Seq_1  1      M E S V V D R C V R L R S I Q L S T I Y
          ATGGAATCTGTGGTGGACAGATGT-GTGAGGCTCAGATCCATTCAACTGTCCACGATTTA 59
          |||
Seq_2  1      M E S V V D R C C E A Q I H S T V H D L
          ATGGAATCTGTGGTGGACAGATGTTGTGAGGCTCAGATCCATTCAACTGTCCACGATTTA 60
          |||

Seq_1  60      K T H C E A A A P M E L S M S R S T F P
          CAAGACGCATTGTGAAGCTGCAGCACCGATGGAACTAAGTATGAGTAGATCAACGTTTCC 119
          |||
Seq_2  61      Q D A L * S C S T D G T K Y E * I N V S
          CAAGACGCATTGTGAAGCTGCAGCACCGATGGAACTAAGTATGAGTAGATCAACGTTTCC 120
          |||

Seq_1  120     G A S I S S H L
          TGGCGCGAGCATCAGCAGTCACCTA 144
          |||
Seq_2  121     W R E H Q Q S P X
          TGGCGCGAGCATCAGCAGTCACCTA 145
          |||
```

Figure S4. Sequence alignment of the target site of the MpCPT7.37 gene of mutant plant 5 and the native MpCPT7.37 gene site of wild-type plants. The translated amino acid sequence is indicated above the nucleotide sequence. Mutations are marked with a lattice sign; possible stop codons are marked with an asterisk. ATG is the start codon (highlighted in red). The target genomic region is highlighted in blue.

Alignment of Sequence_1: [Mpol_Tak1_ATG] with Sequence_2: [Mpol_Ko#9_ATG]

Similarity : 271/272 (99,63 %)

```

Seq_1 1  M E S V V D R C V R L R S I Q L S T I Y 60
          ATGGAATCTGTGGTGGACAGATGTGTGAGGCTCAGATCCATTCAACTGTCCACGATTTAC
          |||
Seq_2 1  M E S V V D R L * G S D P F N C P R F T 59
          ATGGAATCTGTGGTGGACAGAT-TGTGAGGCTCAGATCCATTCAACTGTCCACGATTTAC
          |||
          K T H C E A A A P M E L S M S R S T F P
Seq_1 61  AAGACGCATTGTGAAGCTGCAGCACCGATGGAAC TAAGTATGAGTAGATCAACGTTTCCT 120
          |||
Seq_2 60  AAGACGCATTGTGAAGCTGCAGCACCGATGGAAC TAAAGTATGAGTAGATCAACGTTTCCT 119
          R R I V K L Q H R W N * V * V D Q R F L
          G A S I S S H L A R E L R I S R S R T L
Seq_1 121 GGCGCGAGCATCAGCAGTCACCTAGCTCGTGAAC TCCGTATTTACGCTCCAGAACACTC 180
          |||
Seq_2 120 GGCGCGAGCATCAGCAGTCACCTAGCTCGTGAAC TCCGTATTTACGCTCCAGAACACTC 179
          A R A S A V T * L V N S V F H A P E H S
          G R N P F P G A L V N G C G G T L H G I
Seq_1 181 GGCCGCAATCCGTTTCCTGGTGCAGTGAATGTTGCGGTGGTACGTTGCATGGGATA 240
          |||
Seq_2 180 GGCCGCAATCCGTTTCCTGGTGCAGTGAATGTTGCGGTGGTACGTTGCATGGGATA 239
          A A I R F L V H * * M V A V V R C M G *
          A A T A S A D S C A X
Seq_1 241 GCCGCGACCGCATCAGCTGACAGTTGTGCAGA 272
          |||
Seq_2 240 GCCGCGACCGCATCAGCTGACAGTTGTGCAGA 271
          P R P H Q L T V V Q X
```

Figure S5. Sequence alignment of the target site of the MpCPT7.37 gene of mutant plant 9 and the native MpCPT7.37 gene site of wild-type plants. The translated amino acid sequence is indicated above the nucleotide sequence. Mutations are marked with a lattice sign; possible stop codons are marked with an asterisk. ATG is the start codon (highlighted in red). The target genomic region is highlighted in blue.