(A)

```
  1  MIFYRNYINA DPFDDPFDDE GDEKDKKGKR KKKEKKEPKE PKIIIPKVPY IEIEEVEELE
 61  RIENEPNDSE NGDEDEDEAE IIYEKKIYYE EVVNFIDLYS FLYKNGIIFL WENLTMEVAN
121  KIIKLIICLD IYGDATETAS VLINCSKGSL LASRTLCNFM NEGSDINIET IGCGQVGGPG
181  IYALLGGRTR LAFPNCSFLL SRPNIKLDPR LPPSEYEVDA NIKLQICGSL QDIFTEKTGQ
241  PPEFIRDIGR RVRYMSAAEA REYGIIDEII RGFNFKKPED ETQEKSDKNG E
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(B)

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1
MON1_ClpP  ATGATTTTTTATCGAAATTACATAAACGCAGATCCTTTTGACGATCCTTTTGACGATGAA
Mon2_ClpP  ATGATTTTTGATCGAAATTACATAAACGCGGATCCTTTTGACGATCCTTCTGACGATGAA
61
MON1_ClpP  GGGGATGAAAAGGATAAAAAGGGTAAAAGGAAGAAGAAGGAGAAAAAAGAGCCTAAAGAG
Mon2_ClpP  GGGGATCTCGAAAAGGGAAGAAAAAGGAAGAAAAGGAGAAACCTAAAGAGCCTAAAGAG
121
MON1_ClpP  CCTAAAATAATTATCCCTAAAGTTCCTTATATAGAAATAGAAGAAGTTGAAGAGTTAGAA
Mon2_ClpP  CCTAAAATAATTATCCCTAAAGTTCCTTATATAGAAATAGAAGAAGTTGAAGAGTTCGAA
181
MON1_ClpP  AGAATTGAAAATGAACCTAATGACAGTGAAAATGGGGATGAGGA----------------
Mon2_ClpP  AGAATTGAAAATGAACCTAATGACAGTGAGTATGAGTATGAGGAAGAAATAGACGAAGTT
241
MON1_ClpP  ------------------------------------------------------------
Mon2_ClpP  GAAGAGTTCGAAAGAATTGAAAATGAACCTAATGACAGTGAGTATGAGTATGAGGAAGAA
301
MON1_ClpP  ------------------------------------------------------------
Mon2_ClpP  ATAGACGAAGTTGAAGAGTTCGAAAGAATTGAAAATGAACCTAATGACAGTGAGTATGAG
361
MON1_ClpP  ------------------------------------------------------------
Mon2_ClpP  TATGAGGAAGAAATAGACGAAGTTGAAGAGTTCGAAAGAATTGAAAATGAACCTAATGAC
421
MON1_ClpP  --TGAGGATGAGGCAGAAATAATTTATGAAAAAAAAATATATTATGAAGAAGTAGTAAAT
Mon2_ClpP  AGTGAGGCTGAGGAAGAAATAATTTAT-AAAAAAATATATATTATGAAGAAGTAGTAAAT
481
MON1_ClpP  TTTATTGATTTATATTCTTTTCTTTATAAGAACGGTATTATATTTCTATGGGAAAATCTC
Mon2_ClpP  TATATTGATTTAGATTCTTTTCTTTATAAGAAAGGTCTTATCTTTCTATGGGAAAATCTC
541
MON1_ClpP  ACTATGGAGGTCGCTAATAAAATTATAAAATTGATAATATGCCTTGATATTTATGGTGAT
Mon2_ClpP  ACTATGGAGGTCGCTAATAAAATTATACAATTGATAATATGCCTTGATATTTATGGTGAT
601
MON1_ClpP  GCGACGGAAACGGCAAGCGTTCTTATAAACTGCTCTAAAGGAAGCCTACTTGCTTCAAGG
Mon2_ClpP  GCGCCAGAAAAGGCAAGTGTTCTTATAAACTGCTCTAAGGGAAGCCTACTTGCTTCAAGG
661
MON1_ClpP  ACTCTTTGTAATTTCATGAATGAGGGGTCAGACATAAACATAGAGACAATAGGCTGCGGG
Mon2_ClpP  ACTCTTTGTAATTTCATGACTGAGGGGGCAGACATAAACATAGAGACAATAGGATGTGGA
721
MON1_ClpP  CAGGTTGGAGGACCGGGAATCTATGCCTTGCTTGGGGGAAGGACACGTTTAGCATTCCCT
Mon2_ClpP  CAGGTTGGAGGACCGGGAATCTATACCTTGCTTGGGGGAAGGACACGTTTTGCATTCCAT
781
MON1_ClpP  AACTGTTCGTTCCTGCTTTCTCGACCGAACATTAAATTGGATCCGCGTCTTCCACCCTCA
Mon2_ClpP  AACTGTAGGTTCCTGCTTTCCCGACCGAACATTAAATTTGATCCACGTCTTCCGCCCTCA
841
MON1_ClpP  GAATATGAAGTTGATGCAAACATAAAATTGCAGATATGTGGATCTCTACAAGATATTTTT
Mon2_ClpP  GAATATGAGGTTGATGCAAACATAAAATTGGAGATATGTAGGGGTCTAGAAGATATTTTT
901
MON1_ClpP  ACGGAAAAAACGGGGCAACCTCCTGAATTTATAAGAGATATAGGAAGAAGAGTGCGTTAT
Mon2_ClpP  ACGGAAAAAACGGGGCAACCTCCTGAATTTATAAGAGATATAGGAAGAGG---TTATTCT
961
MON1_ClpP  ATGTCCGCGGCAGAAGCCCGAGAGTACGGAATTATCGACGAGATCATACGTGGTTTTAAT
Mon2_ClpP  ATATCCGCGACAGAAGCCCGAGAGTACGGAATTATCGACTCGATCATACGTGGTTTTAAT
1021
MON1_ClpP  TTTAAAAAACCTGAGGATGAAACCCAGGAAAAATCAGACAAAAATGGGGAATAA
Mon2_ClpP  TTTAAAAAACCTGAGGATGAAACCCAGGAAAAAGAAGACAAAAATGGAGAATAA
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Figure S2. ClpP coding regions.

(A)   Predicted amino acid sequence of the ClpP protein from *M. hypopitys* MON1-VOLR. The ClpP protease domain (pfam00574) is shaded.

(B)   Alignment of the nucleotide sequences of ClpP coding regions from *M. hypopitys* MON1-VOLR (MON1-ClpP) and *M. hypopitys* MON2-KALR (MON2-ClpP) plastomes. 72-nt long sequence, tandemly duplicated in the MON2 (4 copies), is shaded and shown by an arrow. Note that there is a frameshift in the *clpP* reading frame in MON2 genome due to 1 bp deletion at bp 448, but it was not verified.