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CPXV-GRI  ATGACGAAAGTTATCATCATCTTAGGATTCTTGATTATTAATACAAATTCATTGT--CTATGAAATGTGAACAAGGTGTCTCATATTATAATTCACAAGAAT 100
CMLV      ATGACGAAAGTTATCATCATCTTAGGATTCTTGATTATTAATACAAATTCATTGT--CTATGAAATGTGAACAAGGTGTCTCATATTATAATTCACAAGAAT 100
MPXV-Z96  ATGACGAAAGTTATCATCATCTTAGGATTCTTGATTATTAATACAAATTCGTTGTGTCTATGAATGTGAACAATGTGTCTCATATTATAATACACAAGAAT 102
ECTV      ATGACGAAAGTTATCATCATCTTAGGATTCTTGATTATTAATACAAATTCATTGT--CTATGAAATGTGAA-----CAAGAAT 76
CPXV-BR   ATGACGAAAGTTATCATCATCTTAGATTCTTGATTATTAATACAAATTCATTGT--CTATGAAATGTGAACAAGGTGTCTCATATTATAATTCACAAGAAT 100

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CPXV-GRI  TAAAGTGTTGTAAACTATGTAAGCTAGGAACATATTCAGATCATCGATGTGATAAATACAGCGATACCATTT-GTGGGCATTGTCCGAGTGACACATTCACG 201
CMLV      TAAAGTGTTGTAAACTATGTAAGCCAGGAACATATTCAGATCATCGATGTGATAAATACAGCGATACCATTT-GTGGACATTGTCCGAGTGATACATTCACG 201
MPXV-Z96  TAAAGTGTTGTAAACTATCTAAGCCAGGAACATATTCAGATCATCGATGTGATAAATACAGCGATACCATCT-GTGGACATTGTCCAAGTGACACATTCACG 203
ECTV      TAAAGTGTTGTAAACTATGTAAGCCAGGAACATATTCAGATCATCGATGTGATAAATACAGCGATACCATTT-GTGGGCATTGTCCGAGTGACGCATTCACG 177
CPXV-BR   TAAAGTGTTGTAAACTATGTAAGCCAGGAACATATTCAGATCATCGATGTGATAAATACAGCGATACCATTTTGTGGACATTGTCCGAGTGACACATTCACG 202

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CPXV-GRI  TCAATATATAATCGTTCTCCTTGGTGTTCATAGTTGTAGAGGTCCATGTGGTACTAATCGAGTAGAGGTCACACCTTGTACACCTACCACAAATAGAATCTGT 303
CMLV      TTAATA--TAAATCGTTCTCCTTGGTGTTCATAGTTGTAGAGGTTTCATGTGGTACTAATCGAGTAGAGGTCACACCTTGTACACCTACCACAAATAGAATCTGT 301
MPXV-Z96  TCAATATATAATCGTTCTCCTCGGTGTTCATAGTTGTAGAGGT-----CACACCTTGTACACCTACCACAAATAGAATCTGT 279
ECTV      TCAATATATAATCGTTCTCCTTGGTGTTCATAGTTGTAGAGGT-----CACATCTTGTACACCTACCACAAATAGAATCTGT 253
CPXV-BR   TCAATATATAATCGTTCTCCTTGGTGTTCATAGTTGTAGAGGT-----CACACCTTGTACACCTACCACAAATAGAATCTGT 278

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CPXV-GRI  CATT-GTGACTCGAATAGTTATTGTCTCCTTAAAGCTTCTGATGGTAACTGTGTTACATGTGCTCCTAAAACAAAATGTGGTTCGTGGGTATGGAAAGAAAGG 404
CMLV      CATTGTGACTTGAATAGTTATTGTCTCCTTAAAGCTTCTGATGGTAACTGTGTTACATGTGTTCCCTAAAACAAAATGTGGTTCGTGGGTATGGAAAGAAAGG 403
MPXV-Z96  CATT-GTGACTCGAATAGTTATCGTCTCCTTAAAGCTTCTGATGGTAACTGTGTTACATGTGCTCCTAAAACAAAATATGGTTCGTGTGTACGGAAAGAAAGG 380
ECTV      CATT-GTGTCTCGAATAGTTATTGTCTCCTTAAAGCTTCTGATGGTAACTGTGTTACATGTGCTCCTAAAACAAAATGTGGTTCGTGGATATGGAAAGAAAGG 354
CPXV-BR   CATT-GTGACTCGAATAGTTATTGTCTCCTTAAAGCTTCTGATGGTAACTGTGTTACATGTGCTCC----- 343

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CPXV-GRI  AGAAGATGAAATGGGTAATACCATTGTAAGAAATGTCGGAAGGGTACTTATTCAGATATTGTATCTGACTCTGATCAATGTAAACC AATGACAAGATAA 504
CMLV      AGAAGATGAAATGGGTAATACCATTGTAAGAAATGTCGGAAGGGTACTTATACAGATATTGTATCTGACTCTGATCAATGTAAACC AATGACAAGATAA 503
MPXV-Z96  AGAAAATGATATGG--AATACCATTGTAAGAAATGTCGGAAGGGTACTTATTCAGATATTGTATCTGACTCTGATCAATGTAAACC TATGACAAGATAA 478
ECTV      GGAAGATGAAATGGGTAACACCATTGTAAGAAATGTCGGAAGGTGTACGTATTCAGATATTGTATCTCACTCTGATCCATGTAAACC AAGGACGAGATAA 454
CPXV-BR   ----- 343

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Supplementary Figure S3. Multiple sequence alignment of CrmE orthologs.

Multiple sequence alignment of CrmE orthologs from CPXV-GRI, CMLV, MPXV, ECTV and CPXV-BR is shown. Dots represent the first nucleotide of each triplet for the intact CPXV-GRI CrmE gene. An asterisk denotes a second potential start codon. Insertions and deletions that lead to frame shifts (blue) and resulting stop codons (red) are highlighted.