

File S1. Nucleotide sequence used as a query for searches on arthropod genomes. (A) Nucleotide sequence used as a query for Blastn searches on arthropod genomes. Sequence coding catalytic core from the Rep domain highlighted in green, and region coding flanking amino acid sequences in grey. The flanking N-terminal region in grey includes the rest of the Rep domain and the C-terminal region includes part of the sequence coding intermediate amino acids between Rep and Hel domains. (B) Complete Rep/Hel amino acid sequence with colors corresponding to the same marked regions from the nucleotide sequence. Pif1 helicase domain marked in yellow.

A

TATTGTTTTGCCTTTAAATTTGCCTTTGAAATGGTTAATTATCAAATTTTTTAATTTCAAGGTGAAGAAACTACAAAGAAAGTTAGCTC
AATGAATTATTACGCATATCGTTTTGATGATTCGTCAAAATGCTGACAACATTTTGTGCGGTTTCGTCGATTGTTTCAGCAGTATTG
CGTTGACATGTATGTAAAAATAGAAACGGAACGTTTAAACATTCATTAGGTTGAACCAAGCCAAACTGCGTTCTGAGGAGTACATCCA
TTTACGTGATGCAGTTAATACTGAAGGAAATGCAGCTAATATTGGTTCGATTAACATTTCTGCCGGCGACATACATTGGTAGTCCACG
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AAAATGGATAGAAATTAATCAATTGCTGCTTCCCGGACAAACATCAAGTGATAGACACGACATCACAGCAGTATATTACAGGCAAAA
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CAAATATGTCACGAAAGGCAGTGA TATGGCGGTTTTTGGATTGCAATCCTCGAATACCAACGATGAAATTTACGCTATCAAGTTGG
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CGCTGAAGCCATTATCTGTGCA

B

MQNRRANNRGQQIDNLRRRTRYLSSADLNRAAFQYDCSNDYSLHPSVCIGQMDVVCEYCGALKFSGETPGLCCLNGKVKLPLLTPPP
EPLYSLLCGETQESRHLANTQKYNCFQMTSFGADIIIEERGFNPTFKIQGQIHHRIGSLLPFEDTQNKFLQIYFMGNMEEQLDRRL
EINAGMKRAILQDLQCLLHEHHLVRLFKSALERMPSDDYKVVIKADKRPSGTHEFTFNAPTVDVAIILVGEQLEKRDIVLRRD
GQLQQISETHRSYDTLQYPLMFQGEDGYFNIKMKNPLN GEETTKKVSSMNYAYRLMIRQNADNYLLRFRRLFQQYCVDMYVKIE
TERLTFIRLNQAKLRSEEYIHLRDAVNTEGNAANIGRLTILPATYIGSPRHMHEYAQDAMTYVRHYGRPDLFITFTCNPKWIEITQL
LLPGQTSDDRHDITARIFRQKIRSLMNFIVKQRFVGDTRCWMYSIEWQKRGLP HAHIL IWLVERIQPDQIDDI CAEIPDYEVDPDL
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SFKTHCNVEYCNVKS IKYICKYVTKGSDM AVFGLQSSNTNDEISRQVGRYVNCNEAIWRIFAFPIHERHPTVTHLAVHLENGQRV
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FYLRLLLVNVRGPTSFESLRTVNGVIFPTYRAACEELKLENDSHWDTTIAEAIICA SPSQIRTLFAIIISTCFPSNPCNLWHKYKD
NMSDILHQIRVSSRNHDIEMNEEIHNRALLIEDMCYLMCGNLLIRLGMPAPYREMNDAFNRELEREREYDHQELDLVVQTNVPLL
NYQQKKVYDTLMKAIDDENGLY FLDAPGGTGKTFMLSLVLATVVRARSNI AVAVASSGIAATLLEGCPMAKVLAVSKII IWDECTMA
HKRALEALNRTLKDLRNDSRCFGGAMILLSGDFRQILPVI PRSTAADEINACLKSSNLWRHVKKLQLTTNMRVALLNDTSAEDFSEQ
LLTIGNGQVPVDESSGLISFPNNFCNFVSSKDELINNVFPEIISNYKNEYWMSERAI LAANKNDVDDLNNIIQNKIIGTMHSFKSID
CVTNEDEATNYPIEFLNSLDVPGPLPHNLRLKVGSSVIMLRNINQPKLCNGTRLVVRKLMNNVIYATIMIGKFKGEQVLI PRI PMIP
TDMPEFEKRLQFP IRLAFAMTINKSQGQSLKVCGLNLEHSCFSHGQLYVACSRVGRPSALFV FAPDNKTKNVVYHKVLK