PCKMOKAE\_01272 MNKKHGFPLTLTALAIATAFPAYAAQAGAAALDAAQSQSLKEVTVRAA-KVGRRSKEATG 59

PCKMOKAE\_01566 MQQQHLFRFNILCLSLMTALPVYAENVQAGQAQ---EKQLDTIQVKAKKQKTRRDNEVTG 57

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PCKMOKAE\_01272 LGKIVKTSETLNKEQVLGIRDLTRYDPGVAVVEQGNGASGGYSIRGVDKNRVAVSVDGVA 119

PCKMOKAE\_01566 LGKLVKTADTLSKEQVLDIRDLTRYDPGIAVVEQGRGASSGYSIRGMDKNRVSLTVDGLA 117

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PCKMOKAE\_01272 QIQAFTVQGSLSGYGGRGGSGAINEIEYENISTVEIDKGAGSSDHGSGALGGAVAFRTKE 179

PCKMOKAE\_01566 QIQSYTAQAALGGTRTAGSSGAINEIEYENVKAVEISKGSNSVEQGSGALAGSVAFQTKT 177

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PCKMOKAE\_01272 AADLISDGKSRGIQAKTAYGSKNRQFMKSLGAGFSKDGWEGLLIRTERQGRETRPHGDIA 239

PCKMOKAE\_01566 ADDVIGEGRQWGIQSKTAYSGKNRGLTQSIALAGRIGGAEALLIRTGRHAGEIRAHEAAG 237

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PCKMOKAE\_01272 DGVEYGIDRLDAFRQTYDIKRKTTEPFFLVEGENTLKPVAKLAGYGIYLNRQLNRWVKER 299

PCKMOKAE\_01566 RGVQS-------FNRLAPVDDASTYAHFIVEEECK------NGGYEK-----------CK 273

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PCKMOKAE\_01272 IEQNQPLSAEEEAQVREAQARHENLSAQAYTGGGRILPDPMDYRSGSWLAKLGYRFG-GR 358

PCKMOKAE\_01566 ANPK---------KDVAGEDKRQTVSTRDYTGPNRFLADPLSYESRSWLFRPGFRFENKR 324

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PCKMOKAE\_01272 HYVGGVFEDTKQRYDIRDMTEKQYYGTDEAE------KFRDKSGVYDGDDFRDGLYFVPN 412

PCKMOKAE\_01566 HYIGGILERTQQTFDTRDMTVPAFLTKAVFDANSKQAGFLSGNGKYAGNHKYGGLFTSG- 383

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PCKMOKAE\_01272 IEEWKGDKNLVKGIGLKYSRTKFIDEHHRRRRMGLLYRYENEKYSDNWADKAVLSFDKQG 472

PCKMOKAE\_01566 --------ENNAPVGAEYGTGVFYDETHTKSRYGLEYVYTNAD-KDTWADYARLSYDRQG 434

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PCKMOKAE\_01272 VATDNNTLKLNCAVYPAVDKSCRASADKPYSYDSSDRFHYREQHNVLNASFEKSLKNKWT 532

PCKMOKAE\_01566 IGLDNHFQQTHCSA-DGSDKYCRPSADKPFSYYKSDRVIYGESHRLLQAAFKKSFDTAKI 493

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PCKMOKAE\_01272 KHHLTLGFGYDASKAISRPEQLSHNAARI--------------SESTG----FDEKNQ-- 572

PCKMOKAE\_01566 RHNLSVNLGYDRFGSNLRHQDYYYQSANRAYSLKTPPQNNGKKTSPNGSNTSPNGSNTSP 553

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PCKMOKAE\_01272 DKYRLGKPEVVEGSVCGYIETLRSRKCVPRKINGSNIHISLNDRFSIGKYFDFSLGGRYD 632

PCKMOKAE\_01566 YWVSIGRGNVVTRQICRSG-NNTYTDCTPRSINGKSYYAAVRDNVRLGRWADVGAGLRYD 612

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PCKMOKAE\_01272 RKNFTTSEELVRSGRYADRSWNSGIVFKPNRHFSVSYRASSGFRTPSFQELFGIDIYHDY 692

PCKMOKAE\_01566 YRSTHSDDGSVSTGTHRTLSWNAGIVLKPADWLDLTYRTSTGFRLPSFAEMYGWRSGDKI 672

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PCKMOKAE\_01272 PKGWQRPALKSEKAANREIGLQWKGDFGFLEISSFRNRYTDMIAVADQKTKLPDSAGRLT 752

PCKMOKAE\_01566 ----KAVKIDPEKSFNKEAGIVFKGDFGNLEASWFDNAYRDLIVRGYEAQ-I--KDGQEQ 725

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PCKMOKAE\_01272 EIDIRDYYNAQNMSLQGINILGKIDWNGVYGKLPEGLYTTLAYNRIKPKSVSNRPDL-SL 811

PCKMOKAE\_01566 TKGDPAYLNAQSARITGINILGKIDWNGVWDKLPEGWYSTFAYNRVRVRDIKKRADRTDI 785

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PCKMOKAE\_01272 RSYALDAVQPSRYVLGFGYDQPEGKWGANIMLTYSKGKNPDELAY----LAGDQ-KRYSA 866

PCKMOKAE\_01566 QSHLFDAIQPSRYVVGSGYDQPEGKWGVNGMLTYSKAKEITELLGSRALLNGNSRDTKAT 845

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PCKMOKAE\_01272 GRVTSSWKTADVSAYLNLKKRLTLRAAIYNIGNYRYVTWESLRQTAESTANRHGGDSNYG 926

PCKMOKAE\_01566 ARRTRPWYIVDVSGYYTVKKHFTLRAGVYNLLNHRYVTWENVRQTAAGAVNQHKNVGVYN 905

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PCKMOKAE\_01272 RYAAPGRNFSLALEMKF 943

PCKMOKAE\_01566 RYAAPGRNYTFSLEMKF 922

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**Supplementary Figure 4. Clustal alignment of sequences annotated as NGO1495 from Table 4.**