

```
          10          20          30          40          50          60
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV  GTTTAACAGTCTCCAAATACTGCTTGATATGAAGGAAGATCTTCAGTTATGCTGCATTTTC
>NcROP40     -----
>NcROP40-long -----
Consensus NcLiv -----
Consensus NcSp7 -----
Consensus NcSp1H -----
Aa.sequence  -----
```

```
          70          80          90         100         110         120
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV  AATTGGCGGGCGGTAGAGCCCAGGGGGAGCCTGCCTCATTTTAGGCCGGATGGCCGCGGTC
>NcROP40     -----
>NcROP40-long -----
Consensus NcLiv -----
Consensus NcSp7 -----
Consensus NcSp1H -----
Aa.sequence  -----
```

```
         130         140         150         160         170         180
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV  AGACATTCTGTGCTAGTGCACCTCTTCCGTATCTTGACTCCGCCAATACTCCCCAGCCC
>NcROP40     -----
>NcROP40-long -----
Consensus NcLiv -----
Consensus NcSp7 -----
Consensus NcSp1H -----
Aa.sequence  -----
```

```
         190         200         210         220         230         240
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV  GCCACCTTGGAAAACCTCCCCACCGATCTACAGACTGACACCAGCCACAGCAAAAGCACGT
>NcROP40     -----
>NcROP40-long -----
Consensus NcLiv -----
Consensus NcSp7 -----
Consensus NcSp1H -----
Aa.sequence  -----
```

```
         250         260         270         280         290         300
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV  GCCTCTTTTTTAAGAACGCATGGCTGACTGCTAGCGCTGTTCAATCCGTTGACGTCGCGC
>NcROP40     -----
>NcROP40-long -----
Consensus NcLiv -----
Consensus NcSp7 -----GC-----
Consensus NcSp1H -----
Aa.sequence  -----
```

```
         310         320         330         340         350         360
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV  AAGGTTGGGCTCTGGACAGATTCCGCCGCGCAGAATTGGCGCTAGTCTAGATCACAGACA
>NcROP40     -----
>NcROP40-long -----
Consensus NcLiv -----AATTGGCGCTAGTCTAGATCACAGACA-----
Consensus NcSp7  AAGGTTGGGCTCTGGACAGATTCCGCCGCGCAGAATTGGCGCTAGTCTAGATCACAGACA
Consensus NcSp1H -----
Aa.sequence  -----
```

370 380 390 400 410 420
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV CGATCGTTTTGAGCCGGTGTGGTTCCGAAAGTTCTTGAGTACAGGGTCTGGCTCCTACCCG
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv CGATCGTTTTGAGCCGGTGTGGTTCCGAAAGTTCTTGAGTACAGGGTCTGGCTCCTACCCG
Consensus NcSp7 CGATCGTTTTGAGCCGGTGTGGTTCCGAAAGTTCTTGAGTACAGGGTCTGGCTCCTACCCG
Consensus NcSp1H -----
Aa. sequence -----

430 440 450 460 470 480
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV TACTTTGGTGCATAAATCTGTCCGGATGTATTATTCTTCTTTTGTGAAGTTTTGTTTCATA
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv TACTTTGGTGCATAAATCTGTCCGGATGTATTATTCTTCTTTTGTGAAGTTTTGTTTCATA
Consensus NcSp7 TACTTTGGTGCATAAATCTGTCCGGATGTATTATTCTTCTTTTGTGAAGTTTTGTTTCATA
Consensus NcSp1H -----TATTCTTCTTTTGTGAAGTTTTGTTTCATA
Aa. sequence -----

490 500 510 520 530 540
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV GTGTTAAGCTTGTAAGCAGCTGACGTCAACTGATTATGTCTTGCGAGATCCCGCCTAGAC
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv GTGTTAAGCTTGTAAGCAGCTGACGTCAACTGATTATGTCTTGCGAGATCCCGCCTAGAC
Consensus NcSp7 GTGTTAAGCTTGTAAGCAGCTGACGTCAACTGATTATGTCTTGCGAGATCCCGCCTAGAC
Consensus NcSp1H GTGTTAAGCTTGTAAGCAGCTGACGTCAACTGATTATGTCTTGCGAGATCCCGCCTAGAC
Aa. sequence -----

550 560 570 580 590 600
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV AGACACAAACCAACCGAACGTCTGGGATTCCAGTGTGTAGCCGAATAGATTTAGCAAAAT
>NcROP40 -----
>NcROP40-long -----AT
Consensus NcLiv AGACACAAACCAACCGAACGTCTGGGATTCCAGTGTGTAGCCGAATAGATTTAGCAAAAT
Consensus NcSp7 AGACACAAACCAACCGAACGTCTGGGATTCCAGTGTGTAGCCGAATAGATTTAGCAAAAT
Consensus NcSp1H AGACACAAACCAACCGAACGTCTGGGATTCCAGTGTGTAGCCGAATAGATTTAGCAAAAT
Aa. sequence -----Me

610 620 630 640 650 660
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV GAGACACTCCTTGTGCTTTTTCGATATTTGCACTCGAATGCTTGGTGCTGCTTCTGACTTT
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv GAGACACTCCTTGTGCTTTTTCGATATTTGCACTCGAATGCTTGGTGCTGCTTCTGACTTT
Consensus NcSp7 GAGACACTCCTTGTGCTTTTTCGATATTTGCACTCGAATGCTTGGTGCTGCTTCTGACTTT
Consensus NcSp1H GAGACACTCCTTGTGCTTTTTCGATATTTGCACTCGAATGCTTGGTGCTGCTTCTGACTTT
Aa. sequence tArgHisSerLeuCysPheSerIlePheAlaLeuGluCysLeuValLeuLeuLeuThrPh

670 680 690 700 710 720
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV TCAGTGGTTCGATCACTTTGAACGGGCCACCGCTACGGCACTCCGATCGAAGACGTACCA
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv TCAGTGGTTCGATCACTTTGAACGGGCCACCGCTACGGCACTCCGATCGAAGACGTACCA
Consensus NcSp7 TCAGTGGTTCGATCACTTTGAACGGGCCACCGCTACGGCACTCCGATCGAAGACGTACCA
Consensus NcSp1H TCAGTGGTTCGATCACTTTGAACGGGCCACCGCTACGGCACTCCGATCGAAGACGTACCA
Aa. sequence eGlnTrpPheAspHisPheGluArgAlaThrAlaThrAlaLeuArgSerLysThrTyrGl

```

              730          740          750          760          770          780
>NCLIV_chrV      ....|....|....|....|....|....|....|....|....|....|....|....|
>NcROP40         GGCATTGGGATTTCGCCGAAGGTTCTGACAGCGAGACACAGCACGAGGAGGCAGCGAGCGG
-----
>NcROP40-long    GGCATTGGGATTTCGCCGAAGGTTCTGACAGCGAGACACAGCACGAGGAGGCAGCGAGCGG
Consensus NcLiv  GGCATTGGGATTTCGCCGAAGGTTCTGACAGCGAGACACAGCACGAGGAGGCAGCGAGCGG
Consensus NcSp7  GGCATTGGGATTTCGCCGAAGGTTCTGACAGCGAGACACAGCACGAGGAGGCAGCGAGCGG
Consensus NcSp1H GGCATTGGGATTTCGCCGAAGGTTCTGACAGCGAGACACAGCACGAGGAGGCAGCGAGCGG
Aa.sequence      nAlaLeuGlyPheAlaGluGlySerAspSerGluThrGlnHisGluGluAlaAlaSerGl

              790          800          810          820          830          840
>NCLIV_chrV      ....|....|....|....|....|....|....|....|....|....|....|....|
>NcROP40         CGACACACCATTGGTAGGGGGGGCAGACCACGGAAGAGAAGTCCGCTTTCTCGCCTTGG
-----
>NcROP40-long    CGACACACCATTGGTAGGGGGGGCAGACCACGGAAGAGAAGTCCGCTTTCTCGCCTTGG
Consensus NcLiv  CGACACACCATTGGTAGGGGGGGCAGACCACGGAAGAGAAGTCCGCTTTCTCGCCTTGG
Consensus NcSp7  CGACACACCATTGGTAGGGGGGGCAGACCACGGAAGAGAAGTCCGCTTTCTCGCCTTGG
Consensus NcSp1H CGACACACCATTGGTAGGGGGGGCAGACCACGGAAGAGAAGTCCGCTTTCTCGCCTTGG
Aa.sequence      yAspThrProLeuValGlyGlyAlaArgProArgLysArgSerProLeuSerArgLeuGl

              850          860          870          880          890          900
>NCLIV_chrV      ....|....|....|....|....|....|....|....|....|....|....|....|
>NcROP40         CTCTTTCTTTTCGCAGACGCGGAGGCAGACGAGGAAATGTGGAAGGAGACTCTCAAGGCGC
-----
>NcROP40-long    CTCTTTCTTTTCGCAGACGCGGAGGCAGACGAGGAAATGTGGAAGGAGACTCTCAAGGCGC
Consensus NcLiv  CTCTTTCTTTTCGCAGACGCGGAGGCAGACGAGGAAATGTGGAAGGAGACTCTCAAGGCGC
Consensus NcSp7  CTCTTTCTTTTCGCAGACGCGGAGGCAGACGAGGAAATGTGGAAGGAGACTCTCAAGGCGC
Consensus NcSp1H CTCTTTCTTTTCGCAGACGCGGAGGCAGACGAGGAAATGTGGAAGGAGACTCTCAAGGCGC
Aa.sequence      ySerPhePheArgArgArgGlyGlyArgArgGlyAsnValGluGlyAspSerGlnGlyAl

              910          920          930          940          950          960
>NCLIV_chrV      ....|....|....|....|....|....|....|....|....|....|....|....|
>NcROP40         CAGTGAAGAAGGAGAACAGCTGTTAGGTCACCCACAGCCACACACACACACGGGGGGGCGCT
-----
>NcROP40-long    CAGTGAAGAAGGAGAACAGCTGTTAGGTCACCCACAGCCACACACACACACGGGGGGGCGCT
Consensus NcLiv  CAGTGAAGAAGGAGAACAGCTGTTAGGTCACCCACAGCCACACACACACACGGGGGGGCGCT
Consensus NcSp7  CAGTGAAGAAGGAGAACAGCTGTTAGGTCACCCACAGCCACACACACACACGGGGGGGCGCT
Consensus NcSp1H CAGTGAAGAAGGAGAACAGCTGTTAGGTCACCCACAGCCACACACACACACGGGGGGGCGCT
Aa.sequence      aSerGluGluGlyGluGlnLeuLeuGlyHisProSerHisThrHisThrArgGlyGlyLe

              970          980          990          1000         1010         1020
>NCLIV_chrV      ....|....|....|....|....|....|....|....|....|....|....|....|
>NcROP40         GCGGTTTCGGGCGCAAAAAACAGAATACACCCACGAGGCAATGGTGAAATCCCTGCACAA
-----
>NcROP40-long    GCGGTTTCGGGCGCAAAAAACAGAATACACCCACGAGGCAATGGTGAAATCCCTGCACAA
Consensus NcLiv  GCGGTTTCGGGCGCAAAAAACAGAATACACCCACGAGGCAATGGTGAAATCCCTGCACAA
Consensus NcSp7  GCGGTTTCGGGCGCAAAAAACAGAATACACCCACGAGGCAATGGTGAAATCCCTGCACAA
Consensus NcSp1H GCGGTTTCGGGCGCAAAAAACAGAATACACCCACGAGGCAATGGTGAAATCCCTGCACAA
Aa.sequence      uArgPheGlyArgLysLysGlnAsnThrProHisGluAlaMetValLysSerLeuHisLy

              1030         1040         1050         1060         1070         1080
>NCLIV_chrV      ....|....|....|....|....|....|....|....|....|....|....|....|
>NcROP40         GTTCTTGAGCAAGAACGTAGTGGAGGCAATGTCCCTAGAAGATTTTGTAGCAGAACTCGG
-----
>NcROP40-long    GTTCTTGAGCAAGAACGTAGTGGAGGCAATGTCCCTAGAAGATTTTGTAGCAGAACTCGG
Consensus NcLiv  GTTCTTGAGCAAGAACGTAGTGGAGGCAATGTCCCTAGAAGATTTTGTAGCAGAACTCGG
Consensus NcSp7  GTTCTTGAGCAAGAACGTAGTGGAGGCAATGTCCCTAGAAGATTTTGTAGCAGAACTCGG
Consensus NcSp1H GTTCTTGAGCAAGAACGTAGTGGAGGCAATGTCCCTAGAAGATTTTGTAGCAGAACTCGG
Aa.sequence      sPheLeuSerLysAsnValValGluAlaMetSerLeuGluAspPheValAlaGluLeuGl

```

1090 1100 1110 1120 1130 1140
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV TGTCGACCATCGTGCAATTCAACCTCCATTCTTTTCGCAAGGGCGAGGGCGCGTTCGAGAGC
>NcROP40 TGTCGACCATCGTGCAATTCAACCTCCATTCTTTTCGCAAGGGCGAGGGCGCGTTCGAGAGC
>NcROP40-long TGTCGACCATCGTGCAATTCAACCTCCATTCTTTTCGCAAGGGCGAGGGCGCGTTCGAGAGC
Consensus NcLiv TGTCGACCATCGTGCAATTCAACCTCCATTCTTTTCGCAAGGGCGAGGGCGCGTTCGAGAGC
Consensus NcSp7 TGTCGACCATCGTGCAATTCAACCTCCATTCTTTTCGCAAGGGCGAGGGCGCGTTCGAGAGC
Consensus NcSp1H TGTCGACCATCGTGCAATTCAACCTCCATTCTTTTCGCAAGGGCGAGGGCGCGTTCGAGAGC
Aa.sequence yValAspHisArgAlaIleGlnProProPhePheArgLysGlyGluGlyAlaSerArgAl

1150 1160 1170 1180 1190 1200
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV TGTCGGGTATTTTCGCGGAGCAGCAAAAAGCCAGAAGTATCTGAAGAGACGCGGAAAACCTTT
>NcROP40 TGTCGGGTATTTTCGCGGAGCAGCAAAAAGCCAGAAGTATCTGAAGAGACGCGGAAAACCTTT
>NcROP40-long TGTCGGGTATTTTCGCGGAGCAGCAAAAAGCCAGAAGTATCTGAAGAGACGCGGAAAACCTTT
Consensus NcLiv TGTCGGGTATTTTCGCGGAGCAGCAAAAAGCCAGAAGTATCTGAAGAGACGCGGAAAACCTTT
Consensus NcSp7 TGTCGGGTATTTTCGCGGAGCAGCAAAAAGCCAGAAGTATCTGAAGAGACGCGGAAAACCTTT
Consensus NcSp1H TGTCGGGTATTTTCGCGGAGCAGCAAAAAGCCAGAAGTATCTGAAGAGACGCGGAAAACCTTT
Aa.sequence aValGlyTyrPheAlaGluGlnGlnLysProGluValSerGluGluThrArgLysThrLe

1210 1220 1230 1240 1250 1260
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV GGAAGCGGTTGAACAGTTCTGCCTGCCGGACAGCCACTGTCTTTTCACACTACATACGA
>NcROP40 GGAAGCGGTTGAACAGTTCTGCCTGCCGGACAGCCACTGTCTTTTCACACTACATACGA
>NcROP40-long GGAAGCGGTTGAACAGTTCTGCCTGCCGGACAGCCACTGTCTTTTCACACTACATACGA
Consensus NcLiv GGAAGCGGTTGAACAGTTCTGCCTGCCGGACAGCCACTGTCTTTTCACACTACATACGA
Consensus NcSp7 GGAAGCGGTTGAACAGTTCTGCCTGCCGGACAGCCACTGTCTTTTCACACTACATACGA
Consensus NcSp1H GGAAGCGGTTGAACAGTTCTGCCTGCCGGACAGCCACTGTCTTTTCACACTACATACGA
Aa.sequence uGluAlaValGluProValLeuProAlaGlyGlnProLeuSerPheHisThrThrTyrAs

1270 1280 1290 1300 1310 1320
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV CAGAAAAGGCTCTTACTTCAAAAAGAGGCAGCTTGTTTTACCGAGATTTCTTCGAGTTCTT
>NcROP40 CAGAAAAGGCTCTTACTTCAAAAAGAGGCAGCTTGTTTTACCGAGATTTCTTCGAGTTCTT
>NcROP40-long CAGAAAAGGCTCTTACTTCAAAAAGAGGCAGCTTGTTTTACCGAGATTTCTTCGAGTTCTT
Consensus NcLiv CAGAAAAGGCTCTTACTTCAAAAAGAGGCAGCTTGTTTTACCGAGATTTCTTCGAGTTCTT
Consensus NcSp7 CAGAAAAGGCTCTTACTTCAAAAAGAGGCAGCTTGTTTTACCGAGATTTCTTCGAGTTCTT
Consensus NcSp1H CAGAAAAGGCTCTTACTTCAAAAAGAGGCAGCTTGTTTTACCGAGATTTCTTCGAGTTCTT
Aa.sequence pArgLysGlySerTyrPheLysArgGlySerLeuPheHisArgAspPhePheGluPhePh

1330 1340 1350 1360 1370 1380
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV CATTGATGGGCAACCTTTTGATCTGAGGATACTCCCACTACCGAGCGGTGAAGAGGGGGA
>NcROP40 CATTGATGGGCAACCTTTTGATCTGAGGATACTCCCACTACCGAGCGGTGAAGAGGGGGA
>NcROP40-long CATTGATGGGCAACCTTTTGATCTGAGGATACTCCCACTACCGAGCGGTGAAGAGGGGGA
Consensus NcLiv CATTGATGGGCAACCTTTTGATCTGAGGATACTCCCACTACCGAGCGGTGAAGAGGGGGA
Consensus NcSp7 CATTGATGGGCAACCTTTTGATCTGAGGATACTCCCACTACCGAGCGGTGAAGAGGGGGA
Consensus NcSp1H CATTGATGGGCAACCTTTTGATCTGAGGATACTCCCACTACCGAGCGGTGAAGAGGGGGA
Aa.sequence eIleAspGlyGlnProPheAspLeuArgIleLeuProLeuProSerGlyGluGluGlyGl

1390 1400 1410 1420 1430 1440
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV AGCTACGCTGGAACGATACAAAAGGAGCTGGAAAATGAGCGGAGTGTTCGACTTCAATT
>NcROP40 AGCTACGCTGGAACGATACAAAAGGAGCTGGAAAATGAGCGGAGTGTTCGACTTCAATT
>NcROP40-long AGCTACGCTGGAACGATACAAAAGGAGCTGGAAAATGAGCGGAGTGTTCGACTTCAATT
Consensus NcLiv AGCTACGCTGGAACGATACAAAAGGAGCTGGAAAATGAGCGGAGTGTTCGACTTCAATT
Consensus NcSp7 AGCTACGCTGGAACGATACAAAAGGAGCTGGAAAATGAGCGGAGTGTTCGACTTCAATT
Consensus NcSp1H AGCTACGCTGGAACGATACAAAAGGAGCTGGAAAATGAGCGGAGTGTTCGACTTCAATT
Aa.sequence uAlaThrLeuGluArgTyrLysLysGluLeuGluAsnGluArgSerValArgLeuGlnPh

1450 1460 1470 1480 1490 1500
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV TGATGTGGGTTCTGCTCAACGTGTCGTGGAGGCCTTTCACACTGTACATTCCATTTCAAGT
>NcROP40 TGATGTGGGTTCTGCTCAACGTGTCGTGGAGGCCTTTCACACTGTACATTCCATTTCAAGT
>NcROP40-long TGATGTGGGTTCTGCTCAACGTGTCGTGGAGGCCTTTCACACTGTACATTCCATTTCAAGT
Consensus NcLiv TGATGTGGGTTCTGCTCAACGTGTCGTGGAGGCCTTTCACACTGTACATTCCATTTCAAGT
Consensus NcSp7 TGATGTGGGTTCTGCTCAACGTGTCGTGGAGGCCTTTCACACTGTACATTCCATTTCAAGT
Consensus NcSp1H TGATGTGGGTTCTGCTCAACGTGTCGTGGAGGCCTTTCACACTGTACATTCCATTTCAAGT
Aa.sequence eAspValGlySerAlaGlnArgValValGluAlaPheHisCysHisIleProPheGlnVa

1510 1520 1530 1540 1550 1560
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV GCTGCAGTTTACAAGCGACAGAAAGGTCGTCTCACTTGGGTTAGACCTCAAGATGCCCAA
>NcROP40 GCTGCAGTTTACAAGCGACAGAAAGGTCGTCTCACTTGGGTTAGACCTCAAGATGCCCAA
>NcROP40-long GCTGCAGTTTACAAGCGACAGAAAGGTCGTCTCACTTGGGTTAGACCTCAAGATGCCCAA
Consensus NcLiv GCTGCAGTTTACAAGCGACAGAAAGGTCGTCTCACTTGGGTTAGACCTCAAGATGCCCAA
Consensus NcSp7 GCTGCAGTTTACAAGCGACAGAAAGGTCGTCTCACTTGGGTTAGACCTCAAGATGCCCAA
Consensus NcSp1H GCTGCAGTTTACAAGCGACAGAAAGGTCGTCTCACTTGGGTTAGACCTCAAGATGCCCAA
Aa.sequence lLeuGlnPheThrSerAspArgLysValValSerLeuGlyLeuAspLeuLysMetProAs

1570 1580 1590 1600 1610 1620
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV CATTGTTCTCATCTACCCGGGCACACGTGGGACGCTCGGCCAACTCTTTCCGTTGATACA
>NcROP40 CATTGTTCTCATCTACCCGGGCACACGTGGGACGCTCGGCCAACTCTTTCCGTTGATACA
>NcROP40-long CATTGTTCTCATCTACCCGGGCACACGTGGGACGCTCGGCCAACTCTTTCCGTTGATACA
Consensus NcLiv CATTGTTCTCATCTACCCGGGCACACGTGGGACGCTCGGCCAACTCTTTCCGTTGATACA
Consensus NcSp7 CATTGTTCTCATCTACCCGGGCACACGTGGGACGCTCGGCCAACTCTTTCCGTTGATACA
Consensus NcSp1H CATTGTTCTCATCTACCCGGGCACACGTGGGACGCTCGGCCAACTCTTTCCGTTGATACA
Aa.sequence nIleValLeuIleTyrProGlyThrArgGlyThrLeuGlyGlnLeuPheProLeuIleHi

1630 1640 1650 1660 1670 1680
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV TCAAGCAGCCCAGAATCAGAAAACCGCCCCCGCTGCTCTAGCTGCCCCGGCTGAGCGTGAC
>NcROP40 TCAAGCAGCCCAGAATCAGAAAACCGCCCCCGCTGCTCTAGCTGCCCCGGCTGAGCGTGAC
>NcROP40-long TCAAGCAGCCCAGAATCAGAAAACCGCCCCCGCTGCTCTAGCTGCCCCGGCTGAGCGTGAC
Consensus NcLiv TCAAGCAGCCCAGAATCAGAAAACCGCCCCCGCTGCTCTAGCTGCCCCGGCTGAGCGTGAC
Consensus NcSp7 TCAAGCAGCCCAGAATCAGAAAACCGCCCCCGCTGCTCTAGCTGCCCCGGCTGAGCGTGAC
Consensus NcSp1H TCAAGCAGCCCAGAATCAGAAAACCGCCCCCGCTGCTCTAGCTGCCCCGGCTGAGCGTGAC
Aa.sequence sGlnAlaAlaGlnAsnGlnLysThrAlaProAlaAlaLeuAlaAlaArgLeuSerValTh

1690 1700 1710 1720 1730 1740
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV GGTGCAGGCCATTAAGTTGGTTCGAGTACCAGTGGAAGAGGGATCTTGGTGAGTAACAT
>NcROP40 GGTGCAGGCCATTAAGTTGGTTCGAGTACCAGTGGAAGAGGGATCTTGGTGAGTAACAT
>NcROP40-long GGTGCAGGCCATTAAGTTGGTTCGAGTACCAGTGGAAGAGGGATCTTGGTGAGTAACAT
Consensus NcLiv GGTGCAGGCCATTAAGTTGGTTCGAGTACCAGTGGAAGAGGGATCTTGGTGAGTAACAT
Consensus NcSp7 GGTGCAGGCCATTAAGTTGGTTCGAGTACCAGTGGAAGAGGGATCTTGGTGAGTAACAT
Consensus NcSp1H GGTGCAGGCCATTAAGTTGGTTCGAGTACCAGTGGAAGAGGGATCTTGGTGAGTAACAT
Aa.sequence rValGlnAlaIleLysLeuValAlaValThrSerGlyArgGlyIleLeuValSerAsnIl

1750 1760 1770 1780 1790 1800
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV CTCGCCGAAAATTTCTTCCCCAGTAGAGATGGAATTCTTTATTTTGGTGGCTTCTCCTC
>NcROP40 CTCGCCGAAAATTTCTTCCCCAGTAGAGATGGAATTCTTTATTTTGGTGGCTTCTCCTC
>NcROP40-long CTCGCCGAAAATTTCTTCCCCAGTAGAGATGGAATTCTTTATTTTGGTGGCTTCTCCTC
Consensus NcLiv CTCGCCGAAAATTTCTTCCCCAGTAGAGATGGAATTCTTTATTTTGGTGGCTTCTCCTC
Consensus NcSp7 CTCGCCGAAAATTTCTTCCCCAGTAGAGATGGAATTCTTTATTTTGGTGGCTTCTCCTC
Consensus NcSp1H CTCGCCGAAAATTTCTTCCCCAGTAGAGATGGAATTCTTTATTTTGGTGGCTTCTCCTC
Aa.sequence eSerProGluAsnPhePheProSerArgAspGlyIleLeuTyrPheGlyGlyPheSerSe

1810 1820 1830 1840 1850 1860
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV AAAAGTAGCGGCAAACAAGCTGTACTACGAGACCGAGGGGGGCGCCCTGGTTCGAGGAGCC
>NcROP40 AAAAGTAGCGGCAAACAAGCTGTACTACGAGACCGAGGGGGGCGCCCTGGTTCGAGGAGCC
>NcROP40-long AAAAGTAGCGGCAAACAAGCTGTACTACGAGACCGAGGGGGGCGCCCTGGTTCGAGGAGCC
Consensus NcLiv AAAAGTAGCGGCAAACAAGCTGTACTACGAGACCGAGGGGGGCGCCCTGGTTCGAGGAGCC
Consensus NcSp7 AAAAGTAGCGGCAAACAAGCTGTACTACGAGACCGAGGGGGGCGCCCTGGTTCGAGGAGCC
Consensus NcSp1H AAAAGTAGCGGCAAACAAGCTGTACTACGAGACCGAGGGGGGCGCCCTGGTTCGAGGAGCC
Aa.sequence rLysValAlaAlaAsnLysLeuTyrTyrGluThrGluGlyGlyAlaLeuValGluGluPr

1870 1880 1890 1900 1910 1920
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV GCCGAACGTGACTTCCAGGGGGGAGACGGTTCACCGCTGAAGACAACGCAGCAGACTTAGG
>NcROP40 GCCGAACGTGACTTCCAGGGGGGAGACGGTTCACCGCTGAAGACAACGCAGCAGACTTAGG
>NcROP40-long GCCGAACGTGACTTCCAGGGGGGAGACGGTTCACCGCTGAAGACAACGCAGCAGACTTAGG
Consensus NcLiv GCCGAACGTGACTTCCAGGGGGGAGACGGTTCACCGCTGAAGACAACGCAGCAGACTTAGG
Consensus NcSp7 GCCGAACGTGACTTCCAGGGGGGAGACGGTTCACCGCTGAAGACAACGCAGCAGACTTAGG
Consensus NcSp1H GCCGAACGTGACTTCCAGGGGGGAGACGGTTCACCGCTGAAGACAACGCAGCAGACTTAGG
Aa.sequence oProAsnValThrSerArgGlyArgArgPheThrAlaGluAspAsnAlaAlaAspLeuGl

1930 1940 1950 1960 1970 1980
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV ACGCACTCTCTTTGGCTTGTGGTGCGGCGGTTTCGCTTCCTGAGGATGAACCGAGTGGGCG
>NcROP40 ACGCACTCTCTTTGGCTTGTGGTGCGGCGGTTTCGCTTCCTGAGGATGAACCGAGTGGGCG
>NcROP40-long ACGCACTCTCTTTGGCTTGTGGTGCGGCGGTTTCGCTTCCTGAGGATGAACCGAGTGGGCG
Consensus NcLiv ACGCACTCTCTTTGGCTTGTGGTGCGGCGGTTTCGCTTCCTGAGGATGAACCGAGTGGGCG
Consensus NcSp7 ACGCACTCTCTTTGGCTTGTGGTGCGGCGGTTTCGCTTCCTGAGGATGAACCGAGTGGGCG
Consensus NcSp1H ACGCACTCTCTTTGGCTTGTGGTGCGGCGGTTTCGCTTCCTGAGGATGAACCGAGTGGGCG
Aa.sequence yArgThrLeuPheGlyLeuTrpCysGlyGlySerLeuProGluAspGluProSerGlyAr

1990 2000 2010 2020 2030 2040
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV GGCCGACGTGGATTTCTCCAATTGCGGGACAGACCTGCCGGATCCTGTCAAGAAGTTAAT
>NcROP40 GGCCGACGTGGATTTCTCCAATTGCGGGACAGACCTGCCGGATCCTGTCAAGAAGTTAAT
>NcROP40-long GGCCGACGTGGATTTCTCCAATTGCGGGACAGACCTGCCGGATCCTGTCAAGAAGTTAAT
Consensus NcLiv GGCCGACGTGGATTTCTCCAATTGCGGGACAGACCTGCCGGATCCTGTCAAGAAGTTAAT
Consensus NcSp7 GGCCGACGTGGATTTCTCCAATTGCGGGACAGACCTGCCGGATCCTGTCAAGAAGTTAAT
Consensus NcSp1H GGCCGACGTGGATTTCTCCAATTGCGGGACAGACCTGCCGGATCCTGTCAAGAAGTTAAT
Aa.sequence gAlaAspValAspPheSerAsnCysGlyThrAspLeuProAspProValLysLysLeuIl

2050 2060 2070 2080 2090 2100
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV TATGGGAGTGTCCGGCTCCCACGGACGCGCCCTCTCAGCGCCTCCCAGGTCTCGATAC
>NcROP40 TATGGGAGTGTCCGGCTCCCACGGACGCGCCCTCTCAGCGCCTCCCAGGTCTCGATAC
>NcROP40-long TATGGGAGTGTCCGGCTCCCACGGACGCGCCCTCTCAGCGCCTCCCAGGTCTCGATAC
Consensus NcLiv TATGGGAGTGTCCGGCTCCCACGGACGCGCCCTCTCAGCGCCTCCCAGGTCTCGATAC
Consensus NcSp7 TATGGGAGTGTCCGGCTCCCACGGACGCGCCCTCTCAGCGCCTCCCAGGTCTCGATAC
Consensus NcSp1H TATGGGAGTGTCCGGCTCCCACGGACGCGCCCTCTCAGCGCCTCCCAGGTCTCGATAC
Aa.sequence eMetGlyValSerGlySerHisGlyArgAlaProLeuSerAlaSerGlnValLeuAspTh

2110 2120 2130 2140 2150 2160
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV TCCAAACTATCAGGAGCTGCGCAGATTAGAAAAAGAAGTGTCTCAGAGTGTTCGCGGTGCG
>NcROP40 TCCAAACTATCAGGAGCTGCGCAGATTAGAAAAAGAAGTGTCTCAGAGTGTTCGCGGTGCG
>NcROP40-long TCCAAACTATCAGGAGCTGCGCAGATTAGAAAAAGAAGTGTCTCAGAGTGTTCGCGGTGCG
Consensus NcLiv TCCAAACTATCAGGAGCTGCGCAGATTAGAAAAAGAAGTGTCTCAGAGTGTTCGCGGTGCG
Consensus NcSp7 TCCAAACTATCAGGAGCTGCGCAGATTAGAAAAAGAAGTGTCTCAGAGTGTTCGCGGTGCG
Consensus NcSp1H TCCAAACTATCAGGAGCTGCGCAGATTAGAAAAAGAAGTGTCTCAGAGTGTTCGCGGTGCG
Aa.sequence rProAsnTyrGlnGluLeuArgArgLeuGluLysGluValSerGlnSerValAlaValAr

2170 2180 2190 2200 2210 2220
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV TTCAGTGGTGGGGTGACGTCTTTTGAGTTTCTGGACCGTGGACTGGTATCTTAAGAGTGG
>NcROP40 TTCAGTGGTGGGGTGA-----
>NcROP40-long TTCAGTGGTGGGGTGA-----
Consensus NcLiv TTCAGTGGTGGGGTGACGTCTTTTGAGTTTCTGGACCGTGGACTGGTATCTTAAGAGTGG
Consensus NcSp7 TTCAGTGGTGGGGTGACGTCTTTTGAGTTTCTGGACCGTGGACTGGTATCTTAAGAGTGG
Consensus NcSp1H TTCAGTGGTGGGGTGACGTCTTTTGAGTTTCTGGACCGTGGACTGGTATCTTAAGAGTGG
Aa.sequence gSerValValGlyEnd-----

2230 2240 2250 2260 2270 2280
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV TTTTCCCGGATGGTCAGGAAGACTCTGAATGACCATTTAATGGGCCGTGTGGATGCGGGA
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv TTTTCCCGGATGGTCAGGAAGACTCTGAATGACCATTTAATGGGCCGTGTGGATGCGGGA
Consensus NcSp7 TTTTCCCGGATGGTCAGGAAGACTCTGAATGACCATTTAATGGGCCGTGTGGATGCGGGA
Consensus NcSp1H TTTTCCCGGATGGTCAGGAAGACTCTGAATGACCATTTAATGGGCCGTGTGGATGCGGGA
Aa.sequence -----

2290 2300 2310 2320 2330 2340
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV GTTGCTCTAAGGCGATTGCTTTTTGCTCTTTACCCCGATATCGCTGTGACTGCATAAGC
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv GTTGCTCTAAGGCGATTGCTTTTTGCTCTTTACCCCGATATCGCTGTGACTGCATAAGC
Consensus NcSp7 GTTGCTCTAAGGCGATTGCTTTTTGCTCTTTACCCCGATATCGCTGTGACTGCATAAGC
Consensus NcSp1H GTTGCTCTAAGGCGATTGCTTTTTGCTCTTTACCCCGATATCGCTGTGACTGCATAAGC
Aa.sequence -----

2350 2360 2370 2380 2390 2400
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV GCTGTCTGGGGTCTAATAAACAGAAGAGGACAACACAGCGGTTCCACAAGCTGCACACAG
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv GCTGTCTGGGGTCTAATAAACAGAAGAGGACAACACAGCGGTTCCACAAGCTGCACACAG
Consensus NcSp7 GCTGTCTGGGGTCTAATAAACAGAAGAGGACAACACAGCGGTTCCACAAGCTGCACACAG
Consensus NcSp1H GCTGTCTGGGGTCTAATAAACAGAAGAGGACAACACAGCGGTTCCACAAGCTGCACACAG
Aa.sequence -----

2410 2420 2430 2440 2450 2460
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV GCGCGTACCTCTTGCCTTTGTAGAACGAGTTGTGAATGCTGTCACCAATGAATGTGTTTT
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv GCGCGTACCTCTTGCCTTTGTAGAACGAGTTGTGAATGCTGTCACCAATGAATGTGTTTT
Consensus NcSp7 GCGCGTACCTCTTGCCTTTGTAGAACGAGTTGTGAATGCTGTCACCAATGAATGTGTTTT
Consensus NcSp1H GCGCGTACCTCTTGCCTTTGTAGAACGAGTTGTGAATGCTGTCACCAATGAATGTGTTTT
Aa.sequence -----

2470 2480 2490 2500 2510 2520
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV TGTGAAGTATACGTTTTGTCCGAACCGTTCCGTGGATCATGCCGCACCGGCGATTTTCAGT
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv TGTGAAGTATACGTTTTGTCCGAACCGTTCCGTGGATCATGCCGCACCGGCGATTTTCAGT
Consensus NcSp7 TGTGAAGTATACGTTTTGTCCGAACCGTTCCGTGGATCATGCCGCACCGGCGATTTTCAGT
Consensus NcSp1H TGTGAAGTATACGTTTTGTCCGAACCGTTCCGTGGATCATGCCGCACCGGCGATTTTCAGT
Aa.sequence -----

2530 2540 2550 2560 2570 2580
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV AGTCCAAGTGCGGATGGTTTTGCTGCCATCCATGCTCATGGTGGCCCTATTGCTCCCAAA
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv AGTCCAAGTGCGGATGGTTTTGCTGCCATCCATGCTCATGGTGGCCCTATTGCTCCCAAA
Consensus NcSp7 AGTCCAAGTGCGGATGGTTTTGCTGCCATCCATGCTCATGGTGGCCCTATTGCTCCCAAA
Consensus NcSp1H AGTCCAAGTGCGGATGGTTTTGCTGCCATCCATGCTCATGGTGGCCCTATTGCTCCCAAA
Aa. sequence -----

2590 2600 2610 2620 2630 2640
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV CGTTGAGACAACGAGTCTGTTTAGGGGATCGTACATCCGTTGACCTCTTCAAGACATGAA
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv CGTTGAGACAACGAGTCTGTTTAGGGGATCGTACATCCGTTGACCTCTTCAAGACATGAA
Consensus NcSp7 CGTTGAGACAACGAGTCTGTTTAGGGGATCGTACATCCGTTGACCTCTTCAAGACATGAA
Consensus NcSp1H CGTTGAGACAACGAGTCTGTTTAGGGGATCGTACATCCGTTGACCTCTTCAAGACATGAA
Aa. sequence -----

2650 2660 2670 2680 2690 2700
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV ATTGATGATAGGGAACAGCAGTATGTTGGTGACCGCACCTTTTCGGTGACGCGTTAGTGA
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv ATTGATGATAGGGAACAGCAGTATGTTGGTGACCGCACCTTTTCGGTGACGCGTTAGTGA
Consensus NcSp7 ATTGATGATAGGGAACAGCAGTATGTTGGTGACCGCACCTTTTCGGTGACGCGTTAGTGA
Consensus NcSp1H ATTGATGATAGGGAACAGCAGTATGTTGGTGACCGCACCTTTTCGGTGACGCGTTAGTGA
Aa. sequence -----

2710 2720 2730 2740 2750 2760
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV CCGTTTCTGGTTTGTCTGTCGCCGATACGGGGCGGTGACATAAGCAGTGACCAGAAGATAT
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv CCGTTTCTGGTTTGTCTGTCGCCGATACGGGGCGGTGACATAAGCAGTGACCAGAAGATAT
Consensus NcSp7 CCGTTTCTGGTTTGTCTGTCGCCGATACGGGGCGGTGACATAAGCAGTGACCAGAAGATAT
Consensus NcSp1H CCGTTTCTGGTTTGTCTGTCGCCGATACGGGGCGGTGACATAAGCAGTGACCAGAAGATAT
Aa. sequence -----

2770 2780 2790 2800 2810 2820
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV AAAATAGTGAGGAAATAAAGGTTGCTGGTAATGCAGCTTGATCAAGGACTAGGCAGCACA
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv AAAATAGTGAGGAAATAAAGGTTGCTGGTAATGCAGCTTGATCAAGGACTAGG-----
Consensus NcSp7 AAAATAGTGAGGAAATAAAGGTTGCTGGTAATGCAGCTTGATCAAGGACTAGGCAGCACA
Consensus NcSp1H AAAATAGTGAGGAAATAAAGGTTGCTGGTAATGCAGCTTGATCAAGGACTAGGCAGCACA
Aa. sequence -----

2830 2840 2850 2860 2870 2880
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV GAAGCGACATTTCCCGAATGTAACGATGCACGGTTCCGGAGCGAGATAGCTCGTAGCTTA
>NcROP40 -----
>NcROP40-long -----
Consensus NcLiv -----
Consensus NcSp7 GAAGCGACATTTCCCGAATGTAACGATGCACGGTTCCGGAGCGAGATAGCTCGTAGCTTA
Consensus NcSp1H GAAGCGACATTTCCCGAATGTAACGATGCACGGTTCCGGAGCGAGATAGCTCGTAGCTTA
Aa. sequence -----


```
                2890      2900      2910      2920      2930      2940
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV      CCCC GGTTCTTATGATGGTCCACTGATAAAATCGTGCCTTCGAAGAAGCATCTTTGATACA
>NcROP40         -----
>NcROP40-long    -----
Consensus NcLiv  -----
Consensus NcSp7  CCCC GGTTCTTATGATGGTCCACTGATAAAATCGTGCCTTCGAAGAAGCATCTTTGATACA
Consensus NcSp1H CCCC GGTTCTTATGATGGTCCACTGATAAAATCGTGCCTTCGAAGAAGCATCTTTGATACA
Aa.sequence      -----
```

```
                2950      2960      2970      2980      2990      3000
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV      CTGCAACCTGCTACACCAAAACTGCCATAACTGAATTGCTGAATGCAATTGTACCTGGAG
>NcROP40         -----
>NcROP40-long    -----
Consensus NcLiv  -----
Consensus NcSp7  CTGCAACCTGCTACACCAAAACTGCCATAACTGAATTGCTGAATGCAATTGTACCTGGA-
Consensus NcSp1H CTGCAACCTGCTACACCAAAACTGCCATAACTGAATTGCTGAATGCAATTGTACCTGGAG
Aa.sequence      -----
```

```
                3010      3020      3030      3040      3050      3060
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV      TCGCAACTGCTTCTCTCACGCGTACGAAGGATGCACTGGCAGGCTATCGTCTTAGCTACC
>NcROP40         -----
>NcROP40-long    -----
Consensus NcLiv  -----
Consensus NcSp7  -----
Consensus NcSp1H TCGCAACTGCTTCTCTCA-----
Aa.sequence      -----
```

```
                3070      3080      3090      3100      3110      3120
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
>NCLIV_chrV      TGCTTTTCGGTTGTCTCCATGAAGTGCTCTCAGGAAGCCACCGACGGAAGGACAGGAAGGT
>NcROP40         -----
>NcROP40-long    -----
Consensus NcLiv  -----
Consensus NcSp7  -----
Consensus NcSp1H -----
Aa.sequence      -----
```

```
                3130      3140      3150      3160      3170
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.
>NCLIV_chrV      AAAAAAGTGGTTGGTTCGATTTGTGCGAAGGGAAAGAGGAGCCGTTGTCAGCAGGCTGA
>NcROP40         -----
>NcROP40-long    -----
Consensus NcLiv  -----
Consensus NcSp7  -----
Consensus NcSp1H -----
Aa.sequence      -----
```