Table S1. Oligonucleotides used for PCR-detection of the novel viruses.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Pool** | **Virus** | **Oligonucleotide name** | **Oligonucleotide sequence** | **Product length** | **Temperature** |
| 1 | Xanka Hybomitra Negev-like virus | NegevL-p1\_F | GATGCGTTAAAAGAAGCGAA | 310 | 50 |
| Negev\_p1\_P | (FAM)-ACCGACAAGCCAGTGATACCTGACA-(BHQ-1) |
| NegevL-p1\_R | TTGGACAAAACACGGAATTG |
| Razdolnyj Hybomitra Phasma-like virus | Orto\_p1\_F | TGTTGTTGCTAATGTTCCAC | 308 | 50 |
| Orto\_p1\_R | ATTCTGATGATTCCTGGGTG |
| 2 | Kamenushka Hybomitra Narna-like virus | Narn\_p2\_F | CGTTAATCATTTGGCGTTGA | 399 | 50 |
| Narn\_p2\_P | (FAM)-GCGCACTGAGGACAGTGGCC-(BHQ-1) |
| Narn\_p2\_R | CCATTTTTGAGGGTTGACAG |
| Volxa Hybomitra Toti-like virus | Toti\_p2\_F | AACTCGACGATGAATGTGAA | 358 | 50 |
| Toti\_p2\_P | (FAM)-GCAGCTTGGTATCTGATGGCGCT-(BHQ-1) |
| Toti\_p2\_R | GAGAAGTGACTCGTAAGGAC |
| Komarovka Hybomitra Solemo-like virus | Sole\_p2\_F | CGTGCATTCCCGCTATTTGT | 362 | 55 |
| Sole\_p2\_P | (FAM)-GCTCCCACTGTGCCTTGAC-(BHQ-1) |
| Sole\_p2\_R | AGTGATGCCAGCCCATGTTT |
| Barsukovka Hybomitra Ifla-like virus | Ifla\_p2\_F | TTTGTATTGATCCAGGTGCT | 363 | 52 |
| Ifla\_p2\_P | (FAM)-ACTTTGAGACCACCCCGCCA-(BHQ-1) |
| Ifla\_p2\_R | TTTCTGCTATGCCTAAAGGT |
| 3 | Big rock Hybomitra Ifla-like virus | C30\_p3\_F | TTCTTGCTGCACTAGTATTGA | 252 | 50 |
|  | TGGGTCTGTGTTGGACAATAACACCCA |
| C30\_p3\_R | GAATTGACTGATGATGCTTCT |
| 6 | Medvezhye Haematopota Flavi-like virus | LFla\_p6\_F | CCGAAAGTCAAGAAGAATGC | 286 | 50 |
| LFla\_p6\_R | CTGGATGGTATATGCGTTGA |
| Melisia Haematopota Negev-like virus | NegevL\_p6\_F | CGTATGTTTGTCATTCGCAA | 261 | 50 |
| NegevL\_p6\_P | (FAM)-CCATAGGCAGGGCAGTCACA-(BHQ-1) |
| NegevL\_p6\_R | CAGACCAAAAGGACTCATCA |
| Medvezhye Haematopota Xinmo-like virus | Anphe\_p6\_F | TTGTTATTATCCCAGGTGCC | 367 | 50 |
| Anphe\_p6\_R | CGTCCTCTTGGATCTGTTAG |
| Medvezhye pound Haematopota Permuto-like virus | Permu\_p6\_F | CCCAACGCATATCCTCATTA | 283 | 50 |
| Permu\_p6\_P | (FAM)-TGCCACGGGATGTTTCAACC-(BHQ-1) |
| Permu\_p6\_R | GAGCGGACAAATATACCCAT |
| Polka Haematopota Nora-like virus | C191\_p6\_F | TTTTGGAGGATTTGTGAATGC | 254 | 50 |
| C191\_p6\_P | (FAM)-GATCCTCACAGCCCGGCGTG-(BHQ-1) |
| C191\_p6\_R | CCTGAATCTTTCTGGCCTTAT |
| Polka Haematopota Xinmo-like virus | C223\_p6\_F | TACCAAGTAGGCAACATACC | 270 | 50 |
| C223\_p6\_R | TGTTTCAGACATGAACTGGT |
| 7 | Medvezhye Chrysops Negev-like virus | NegevL\_p7\_F | CATTGACCACATCTTGCATC | 400 | 52 |
| NegevL\_p7\_P | (FAM)-GGCATGTGAAGTGGTAATGGAATC-(BHQ-1) |
| NegevL\_p7\_R | ACTAAGGAGGGTCTAGTGTC |
| Big Soux River virus (strain Medveje) | BSR\_p7\_F | TTTAATATGCAACCACGGGA | 274 | 50 |
| BSR\_p7\_P | (FAM)-TGCGCACTCGTCCCGAATGA-(BHQ-1) |
| BSR\_p7\_R | TGGTAGAACAGGATTGTGTG |
| Medvezhye Chrysops Solemo-like virus | Sol1\_p7\_F | TCTTTCTTCAAGATCGGCAA | 326 | 50 |
| Sol1\_p7\_P | (FAM)-TCTGGGCGGCAGCAACTATG-(BHQ-1) |
| Sol1\_p7\_R | GGAGAGTCAGCATTGGTTTA |
| Melisia Chrysops Solemo-like virus | Sol2\_p7\_F | ATGATCAAACCGTGTTGAGA | 358 | 50 |
| Sol2\_p7\_P | (FAM)-AACCATTTGCCACAAGATCTGTAA-(BHQ-1) |
| Sol2\_p7\_R | CAGTGATCAGAGCCTTAGAC |
| Polka Chrysops Solemo-like virus | Sol3\_p7\_F | AAAGTAAAACCAGGCGTTTG | 268 | 50 |
| Sol3\_p7\_P | (FAM)-AACTCGAACGATTGATGCGGT-(BHQ-1) |
| Sol3\_p7\_R | AACTCGATGTATTCTGGCTC |
| Medvezhye Chrysops Narna-like virus | Nar1\_p7\_F | TTTTCTTCGACATATGGGCA | 255 | 50 |
| Nar1\_p7\_R | GCTTTGATATCAGATGCTGC |
| Medvezhye Chrysops Narna-like virus 2 | Nar2\_p7\_F | ACAGTGCGAAGTTGTTATCT | 327 | 50 |
| Nar2\_p7\_P | (FAM)-CAAATGGCTCGGCTTGGTAGATCG-(BHQ-1) |
| Nar2\_p7\_R | AGATCGGATAGCTTCGTCTA |
| Medvezhye Chrysops Solinvi-like virus | Soli\_p7\_F | ACATTGCCTTTTCCATTGTG | 335 | 50 |
| Soli\_p7\_R | AAAAGTTAGGCGTGACAGAT |
| Medvezhye Chrysops Rhabdo-like virus | Rha\_p7\_F | AGAGGCTCTCACTGACAATA | 292 | 50 |
| Rha\_p7\_P | (FAM)-TGGCTGACGGATCTGAGATCCCT-(BHQ-1) |
| Rha\_p7\_R | CCCTCCTAAATGTCCTTTCC |
| 8 | Medvezhye Chrysops Ifla-like virus | Ifla\_p8\_F | CATAAGAAGCATAACGACGC | 350 | 50 |
| Ifla\_p8\_P | (FAM)-ACGATCTCCCGATTTCATCCATTCTGA-(BHQ-1) |
| Ifla\_p8\_R | TGTGATGTGTCCTTACTTCG |
| Medvezhye Chrysops Toti-like virus | Toti\_p8\_F | TGGTAACATCCAGTTCACAG | 387 | 50 |
| Toti\_p8\_P | (FAM)-TGCCGCTATGGGGGAGGCAT-(BHQ-1) |
| Toti\_p8\_R | TTTTCCGCCGTTATAGGTAG |
| Istie Chrysops Solemo-like virus | Sole\_p8\_F | ATTCCAATTCCGAGTCAACA | 268 | 50 |
| Sole\_p8\_P | (FAM)-AGTTGGGTAATTTCGGGGTCTTGGA-(BHQ-1) |
| Sole\_p8\_R | CGACCCTCCAAAAGTAAAGA |
| Medvezhye Chrysops Xinmo-like virus | Rha\_p8\_F | GTTCAAGCTTAGGGGTTACA | 255 | 50 |
| Rha\_p8\_P | (FAM)-TCACGCACATGGTACAGATGCAA-(BHQ-1) |
| Rha p8\_R | TATGTGATGCCAGTACGTTT |
| Medvezhye Chrysops Phasma-like virus | Orto\_p8\_F | GCATGCACTCATAGATGTTG | 260 | 50 |
| Orto\_p8\_R | GTGACTGGATTATCAACGGA |
| 9 | Medvezhye Tabanus Phasma-like virus | Orto\_p9\_F | ACTACAAGTTTAGGTGCCAG | 370 | 50 |
| Orto\_p9\_R | ATGATGTGTTAACTGCTGGT |
| Medvezhye Tabanus Chu-like virus | Rha\_p9\_F | TCACTTAAAGTTGCGGATGA | 334 | 50 |
| Rha\_p9\_R | TTACAACTTATGGACACGCA |
| Medvezhye Tabanus Toti-like virus | Toti\_p9\_F | AGTCTTAGCCTATACAGCCA | 353 | 50 |
| Toti\_p9\_P | (FAM)-TCCTCCATGCCCGGCTTGAGT-(BHQ-1) |
| Toti\_p9\_R | TGATTAGGCCACATGTGAAA |

Table S2. Oligonucleotides used for internal control Poliovirus RT-qPCR.

|  |  |
| --- | --- |
| Oligonucleotide | Sequence |
| PVR1 | 5’-CGAACGTGATCCTGAGTGTT-3’ |
| PVP1 | (ROX)-TTGATTCATGAATTTCCTTCATTGGCA-(BHQ-2) |
| PVL1 | 5’- GGCAGACGAGAAATACCCAT- 3’ |

Table S3. Characteristics of viruses with complete and partial coding sequences.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Pool** | **Virus** | **Presence in the pool (%)** | **Comparison protein** | **Closest relative** | **Q cover** | **Identity** |
| 1 | Xanka Hybomitra Negev-like virus | 0.01 | ORF1 (RdRp) | [URQ09136.1] Halyomorpha halys negev-like virus 1 | 61% | 42.2% |
| 2 | Kamenushka Hybomitra Narna-like virus | <0.01% | RdRp | [QVG74774.1] Riboviria sp. | 89% | 52.5% |
| Volxa Hybomitra Toti-like virus | 0.01 | RdRp | [UPT53761.1] Bactrocera zonata toti-like virus | 99% | 41.1% |
| Komarovka Hybomitra Solemo-like virus | <0.01% | RdRp | [UJG28005.1] Ulaatai Melophagus solemo-like virus | 75% | 63.6% |
| CP | [APG75767.1] Hubei sobemo-like virus 48 | 93% | 52.7% |
| 6 | Medvezhye Haematopota Flavi-like virus | 0.29 | Polyprotein | [QTJ63573.1] Orthopteran flavi-related virus | 15% | 41.7% |
| Melisia Haematopota Negev-like virus | 0.23 | ORF1 (RdRp) | [URQ09136.1] Halyomorpha halys negev-like virus 1 | 61% | 39.2% |
| Medvezhye Haematopota Xinmo-like virus | 0.18 | RpRp | [YP\_009337182.1] Hubei diptera virus 11 | 98% | 35.9% |
| Medvezhye pound Haematopota Permuto-like virus | 0.03 | Polyprotein | [WKV34304.1] Riboviria sp. | 61% | 35.8% |
| 7 | Medvezhye Chrysops Negev-like virus | 1.08 | ORF1 (RdRp) | [UPT53679.1] Zeugodacus tau negev-like virus | 73% | 44.3% |
| Big Soux River virus (strain Medvezhye) | 0.48 | ORF1 | [ATI98938.1] Big Sioux River virus | 99% | 99.9% |
| Medvezhye Chrysops Solemo-like virus | 0.13 | RdRp | [YP\_009330098.1] Hubei sobemo-like virus 13 | 73% | 51.1% |
| CP | [YP\_009342449.1] Wuhan house centipede virus 5 | 99% | 37.7% |
| Melisia Chrysops Solemo-like virus | 0.28 | RdRp | [UCS96389.1] Riboviria sp. | 81% | 55.7% |
| CP | [APG75767.1] Hubei sobemo-like virus 48 | 86% | 52.6% |
| Polka Chrysops Solemo-like virus | 0.05 | RdRp | [QIJ70118.1] Jeffords solemo-like virus | 95% | 39.5% |
| CP | [QHA33885.1] Atrato Sobemo-like virus 3 | 86% | 35.4% |
| Medvezhye Chrysops Narna-like virus | 0.61 | RdRp | [UHR49680.1] Sanya cydistomyia duplonotatay narnavirus 1 | 91% | 51.2% |
| Medvezhye Chrysops Narna-like virus 2 | 0.23 | RdRp | [UHR49680.1] Sanya cydistomyia duplonotatay narnavirus 1 | 92% | 51.4% |
| 8 | Medvezhye Chrysops Ifla-like virus | 0.02 | Polyprotein | [UQJ82152.1] Exitianus exitiosus virus 2 | 95% | 34.5% |
| Medvezhye Chrysops Toti-like virus | 0.03 | RdRp | [YP\_009333170.1] Hubei toti-like virus 19 | 98% | 60% |
| Istie Chrysops Solemo-like virus | 0.01 | RdRp | [QXV86400.1] Solemoviridae sp. | 68% | 46.6% |
| CP | [APG75767.1] Hubei sobemo-like virus 48 | 98% | 42.2% |
| Medvezhye Chrysops Xinmo-like virus | 0.01 | L | [YP\_009337182.1]Hubei diptera virus 11 | 98% | 39.2% |

Table S4. Characteristics of genome fragments detected in the study.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Pool | Contig type and assigned name | Contig name | Closest relative | Protein | Q cover | Identity |
| 1 | **Orthophasma-like**  Razdolnyj Hybomitra Phasma-like virus | NODE\_8\_length\_1310\_ | [QXV86665.1] Tibet bird virus 1 | nucleocapsid | 89% | 42.8% |
| NODE\_19\_length\_530\_ | [QID77675.1] Pink bollworm virus 2 | RdRp | 100% | 69.3% |
| NODE\_21\_length\_478\_ | [YP\_009666959.1] Seattle Prectang virus | RdRp | 100% | 46% |
| NODE\_22\_length\_468\_ | [UHK03218] Hangzhou zicrona caerulea phasmavirus 1 | RdRp | 99% | 53.3% |
| 2 | **Iflaviridae-like**  Barsukovka Hybomitra Ifla-like virus | NODE\_11\_length\_1234\_ | [WEU50803.1] Chrysopa pallens | Polyprotein | 93% | 35.7% |
| NODE\_20\_length\_639\_ | [CAF1136435.1] Ceratitis capitata iflavirus 3 | Polyprotein | 96% | 48.4% |
| NODE\_21\_length\_616\_ | [UJG27957.1] Khandagaity Melophagus ifla-like virus | Polyprotein | 100% | 36.9% |
| NODE\_24\_length\_577\_ | [WEU50803.1] Chrysopa pallens | Polyprotein | 100% | 31.8% |
| NODE\_27\_length\_467\_ | [QZZ63343.1] Leuven wasp-associated virus 3 | Polyprotein | 99% | 46.1% |
| NODE\_28\_length\_466\_ | [UUG74229.1]XiangYun picorna-like virus 4 | Polyprotein | 79% | 57.6% |
| NODE\_37\_length\_408\_ | [UQJ82152.1] Exitianus exitiosus virus 2 | Polyprotein | 100% | 63% |
| 3 | **Iflaviridae-like**  Big rock Hybomitra Ifla-like virus | NODE\_30\_length\_381\_ | [CAF1136435] Ceratitis capitata iflavirus 3 | Polyprotein | 98% | 39.6% |
| 6 | **Nora virus-like**  Polka Haematopota Nora-like virus | NODE\_191\_length\_616\_ | [ASM93992]Caledonia beadlet anemone Nora virus-like virus 1 | ORF2 | 96% | 42.9% |
| **Xinoviridae-like**  Polka Haematopota Xinmo-like virus | NODE\_223\_length\_580\_ | Hubei diptera virus 11 | RdRp | 97% | 53.6% |
| 7 | **Solinviviridae-like**  Medvezhye Chrysops Solinvi-like virus | NODE\_115\_length\_1354\_ | [UHK03205.1] Hangzhou Solinvi-like virus 2 | Polyprotein | 99% | 38% |
| NODE\_146\_length\_1248\_ | [UHK03205.1] Hangzhou Solinvi-like virus 2 | Polyprotein | 99% | 72% |
| NODE\_267\_length\_903\_ | [UHK03205.1] Hangzhou Solinvi-like virus 2 | Polyprotein | 99% | 68.6% |
| NODE\_312\_length\_849\_ | [UHK03205.1] Hangzhou Solinvi-like virus 2 | Polyprotein | 100% | 75.5% |
| NODE\_382\_length\_787\_ | [UHK03205.1] Hangzhou Solinvi-like virus 2 | Polyprotein | 99% | 74.2% |
| NODE\_574\_length\_664\_ | [UHK03205.1] Hangzhou Solinvi-like virus 2 | Polyprotein | 100% | 75.1% |
| NODE\_617\_length\_640\_ | [UHK03205.1] Hangzhou Solinvi-like virus 2 | Polyprotein | 100% | 46.5% |
| 7 | **Rhabdo-like**  Medvezhye Chrysops Rhabdo-like virus | NODE\_9\_length\_4303\_ | [AJG39162.1] Wuhan Fly Virus 3 | L | 99% | 36.8% |
| 7 | **Rhabdo-like**  Melisia Chrysops Rhabdo-like virus | NODE\_120\_length\_1338\_ | [YP\_009336837.1] Hubei lepidoptera virus 2 | L | 95% | 46.6% |
| NODE\_12\_NODE\_108\_ | [UZC34538.1] jopcycgri virus 1 | L | 99% | 50% |
| 8 | **Orthophasma-like**  Medvezhye Chrysops Phasma-like virus | NODE\_16\_length\_3720 | [QXV86663.1]Tibet bird virus 1 | RdRp | 99% | 52% |
| NODE\_43\_length\_2382\_ | [YP\_010086190.1] Anopheles triannulatus orthophasmavirus | Glycoprotein | 90% | 29.4% |
| NODE\_163\_length\_1495\_ | [QXV86665.1]Tibet bird virus 1 | N | 69% | 39.1% |
| NODE\_299\_length\_1184\_ | [QXV86663.1]Tibet bird virus 1 | RdRp | 99% | 31.5% |
| 8 | Solinviviridae-like | NODE\_2118\_length\_528\_ | [UHK03205.1]Hangzhou Solinvi-like virus 2 | Polyprotein | 67% | 82.4% |
| NODE\_3267\_length\_436\_ | [UHK03205.1]Hangzhou Solinvi-like virus 2 | Polyprotein | 99% | 70.8% |
| NODE\_4305\_length\_385\_ | [UHK03205.1]Hangzhou Solinvi-like virus 2 | Polyprotein | 99% | 50.8% |
| 9 | **Orthophasma-like**  Medvezhye Tabanus Phasma-like virus | NODE\_10\_length\_1088\_ | [QXV86665.1] Tibet bird virus 1 | N | 97% | 38.9% |
| NODE\_47\_length\_434\_ | [YP\_009666982] Ganda bee virus | Glycoprotein | 98% | 37.9% |
| 9 | **Toti-like**  Medvezhye Tabanus Toti-like virus | NODE\_20\_length\_755\_ | [YP\_009333170.1]Hubei toti-like virus 19 | VP2 | 99% | 67% |
| NODE\_24\_length\_700\_ | [YP\_009333170.1]Hubei toti-like virus 19 | VP2 | 96% | 79.2% |
| NODE\_64\_length\_393\_ | [YP\_009333170.1]Hubei toti-like virus 19 | VP2 | 100% | 67.7% |
| NODE\_69\_length\_384\_ | [YP\_009333169.1]Hubei toti-like virus 19 | VP1 | 100% | 72.4% |
| 9 | **Chu-like**  Medvezhye Tabanus Chu-like virus | NODE\_19\_length\_798\_ | [YP\_010798609.1] megalopteran chu-related virus 119 | Glycoprotein | 39% | 52.8% |
| NODE\_22\_length\_739\_ | [YP\_010798611.1] megalopteran chu-related virus 119 | RdRp | 97% | 34.8% |
| NODE\_25\_length\_693\_ | [APG78769.1] Hubei chuvirus-like virus 4 | RdRp | 99% | 48.3% |
| NODE\_35\_length\_520\_ | [YP\_010798611.1] megalopteran chu-related virus 119 | RdRp | 100% | 32.4% |
| NODE\_36\_length\_509\_ | [YP\_010798611.1] megalopteran chu-related virus 119 | RdRp | 98% | 54.5% |

Table S5. Similarity estimation within tabanid negev-like viruses using discontiguous megablast on the full genome.

|  |  |  |
| --- | --- | --- |
|  | Xanka Hybomitra Negev-like virus | Medvezhye Chrysops Negev-like virus |
| Xanka Hybomitra Negev-like virus | - | 68.9% (51% Q cover) |
| Melisia Haematopota Negev-like virus | 70.1% (57% Q cover) | 71.2% (68% Q cover) |

Table S6. Similarity estimation within tabanid xinmo-like sequences using L protein amino acid sequence.

|  |  |  |
| --- | --- | --- |
|  | Medvezhye Haematopota Xinmo-like virus | NODE\_223\_length\_580\_ |
| Medvezhye Haematopota Xinmo-like virus | - | 57.2% (97% cover) |
| Medvezhye Chrysops Xinmo-like virus | 60.1% (98% cover) | 52.9% (98% cover) |

Table S7. Similarity estimation within tabanid ifla-like sequences using polyprotein amino acid sequence.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Pool | Contig Name | Query cover to the GenBank Entry | Identity to the GenBank Entry | Query cover to Medvezhye Chrysops Ifla-like virus | Identity to the Medvezhye Chrysops Ifla-like virus |
| 2 | NODE\_11\_length\_1234\_ | 93% | 35.7% | 93% | 50.0% |
| NODE\_20\_length\_639\_ | 96% | 48.4% | 99% | 59.3% |
| NODE\_21\_length\_616\_ | 100% | 36.9% | 99% | 43.4% |
| NODE\_24\_length\_577\_ | 100% | 31.8% | 100% | 35.0% |
| NODE\_27\_length\_467\_ | 99% | 46.1% | 99% | 54.5% |
| NODE\_28\_length\_466\_ | 79% | 57.6% | 79% | 59.6% |
| NODE\_37\_length\_408\_ | 100% | 63% | 100% | 72.5% |
| 3 | NODE\_30\_length\_381\_ | 98% | 39.6% | 98% | 79.9% |

Table S8. Similarity estimation within tabanid solinvi-like sequences using polyprotein amino acid sequence.

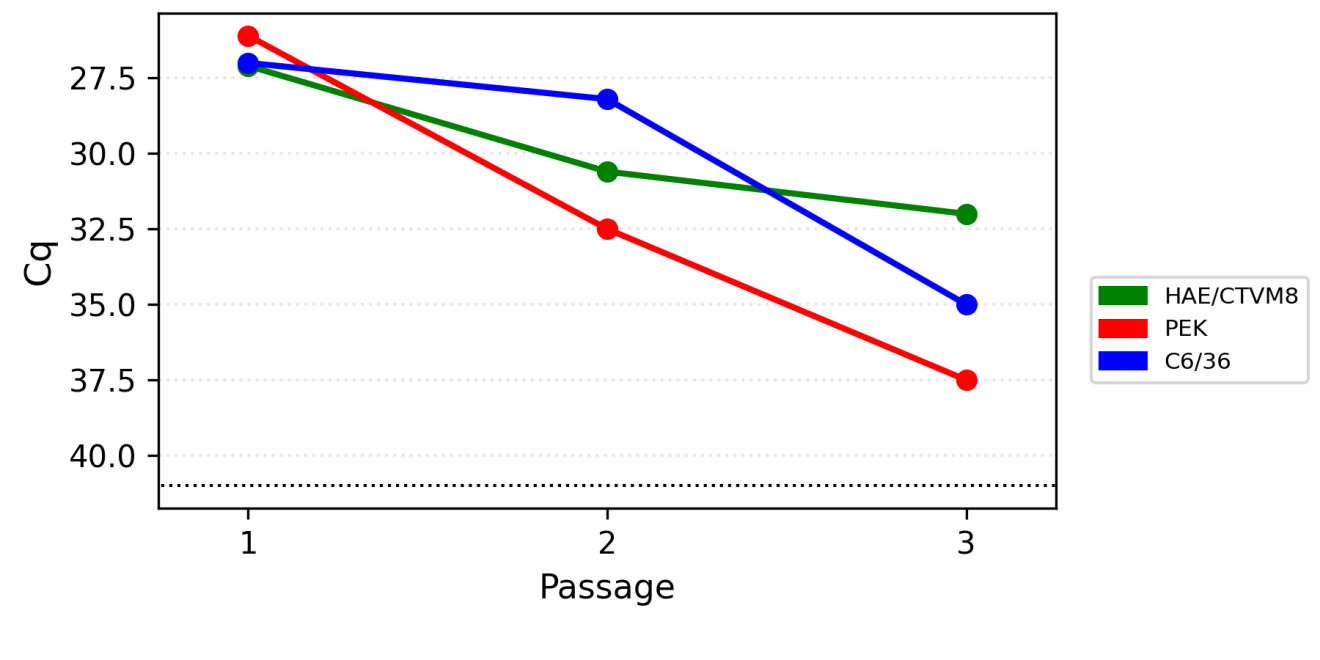
|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Pool 8 contig name | Pool 8 abundance | Pool 7 relative | Q cover | Identity |
| NODE\_2118\_length\_528\_ | 10 reads | NODE\_146\_length\_1248\_ | 35% | 99.5% |
| NODE\_3267\_length\_436\_ | 3 reads | NODE\_312\_length\_849\_ | 93% | 99.0% |
| NODE\_4305\_length\_385\_ | 5 reads | NODE\_146\_length\_1248\_ | 99% | 96.9% |

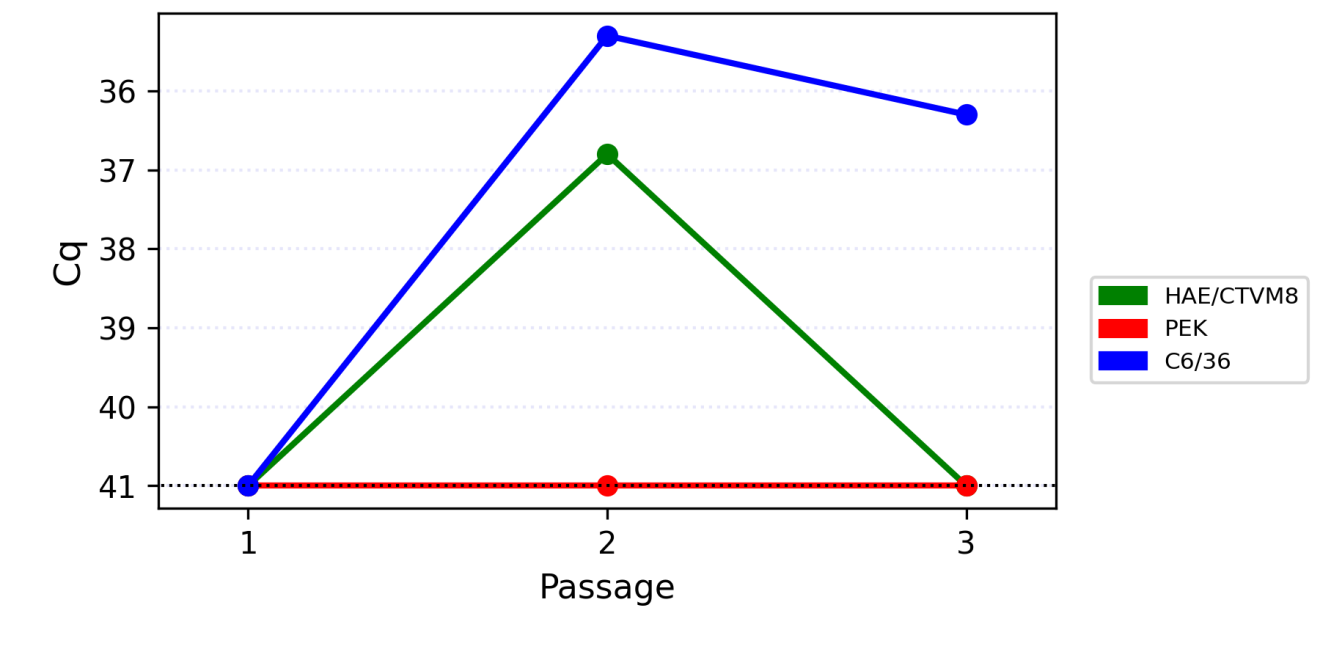
Table S9. Similarity estimation of pool 1 orthophasma-like contig with orthophasma-like sequences from pools 8 and 9 using amino acid sequences.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Pool 1 contig name | Pool 8 relative | Q cover | Identity | Pool 9 relative | Q cover | Identity |
| NODE\_8\_length\_1310\_ | NODE\_163\_length\_1495\_ | 85% | 46.3% | NODE\_10\_length\_1088\_ | 89% | 62.6% |
| NODE\_19\_length\_530\_ | NODE\_16\_length\_3720\_ | 100% | 77.3% | no | - | - |
| NODE\_21\_length\_478\_ | NODE\_16\_length\_3720\_ | 100% | 56.2% | no | - | - |
| NODE\_22\_length\_468\_ | NODE\_16\_length\_3720\_ | 99% | 58.4% | no | - | - |

Table S10. Similarity estimation of pool 9 orthophasma-like contig with orthophasma-like sequences from pools 8 and 1 using amino acid sequences.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Pool 9 contig name | Pool 8 relative | Q cover | Identity | Pool 1 relative | Q cover | Identity |
| NODE\_10\_length\_1088\_ | NODE\_163\_length\_1495\_ | 86 | 45.9% | NODE\_8\_length\_1310\_ | 93% | 62.6% |
| NODE\_47\_length\_434\_ | NODE\_43\_length\_2382\_ | 98 | 42.0% | no | - | - |

Figure S1. Dynamic of the real-time quantification cycle (Cq) during passages of the Xanka Hybomitra negev-like virus. Black dotted line represents qPCR detection limit (41 cycles).

  
  
Figure S2. Dynamic of the real-time quantification cycle (Cq) during passages of the Volxa Hybomitra toti-like virus. Black dotted line represents qPCR detection limit (41 cycles).

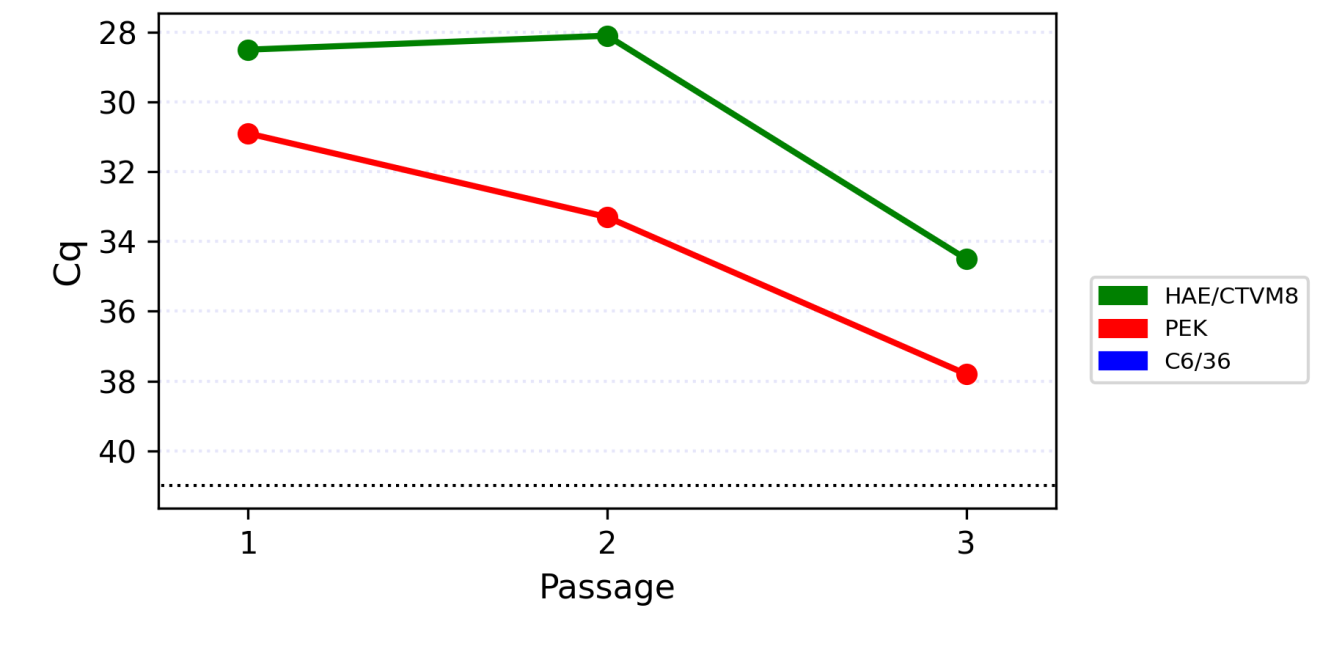
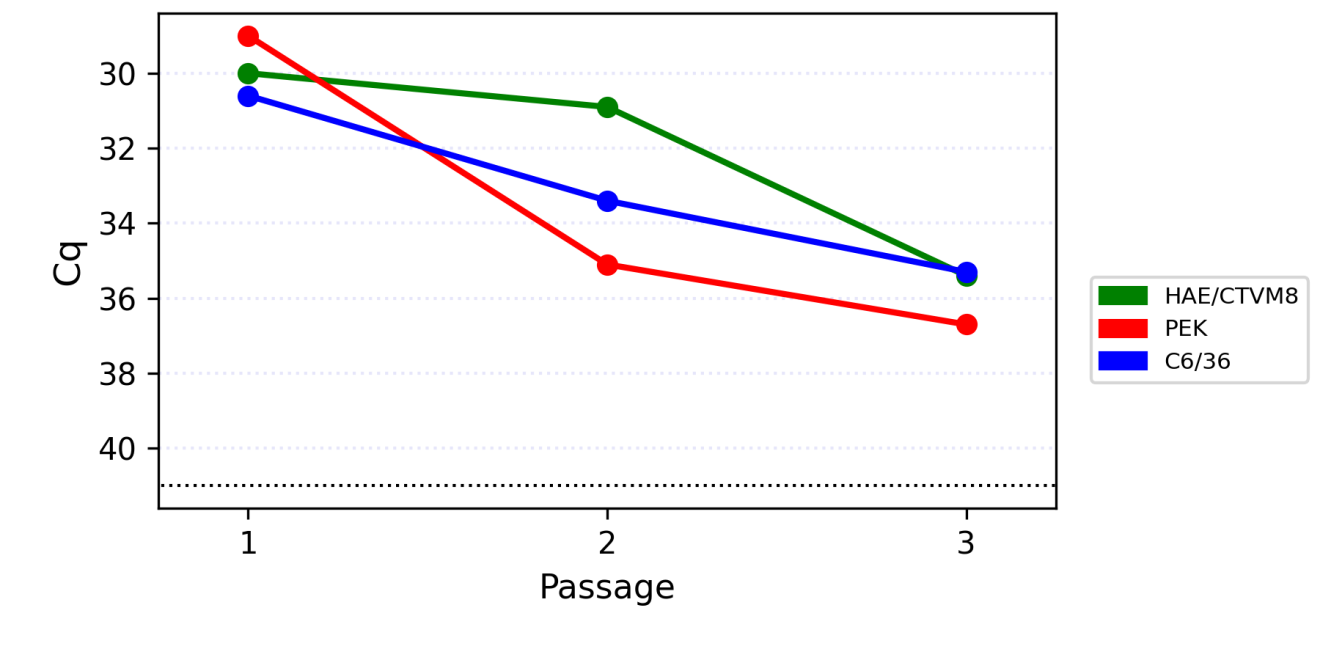


Figure S3. Dynamic of the real-time quantification cycle (Cq) during passages of the Kamenushka Hybomitra narna-like virus. Black dotted line represents qPCR detection limit (41 cycles).

Figure S4. Dynamic of the real-time quantification cycle (Cq) during passages of the Medvezhye pound Haematopota permuto-like virus. Black dotted line represents qPCR detection limit (41 cycles).

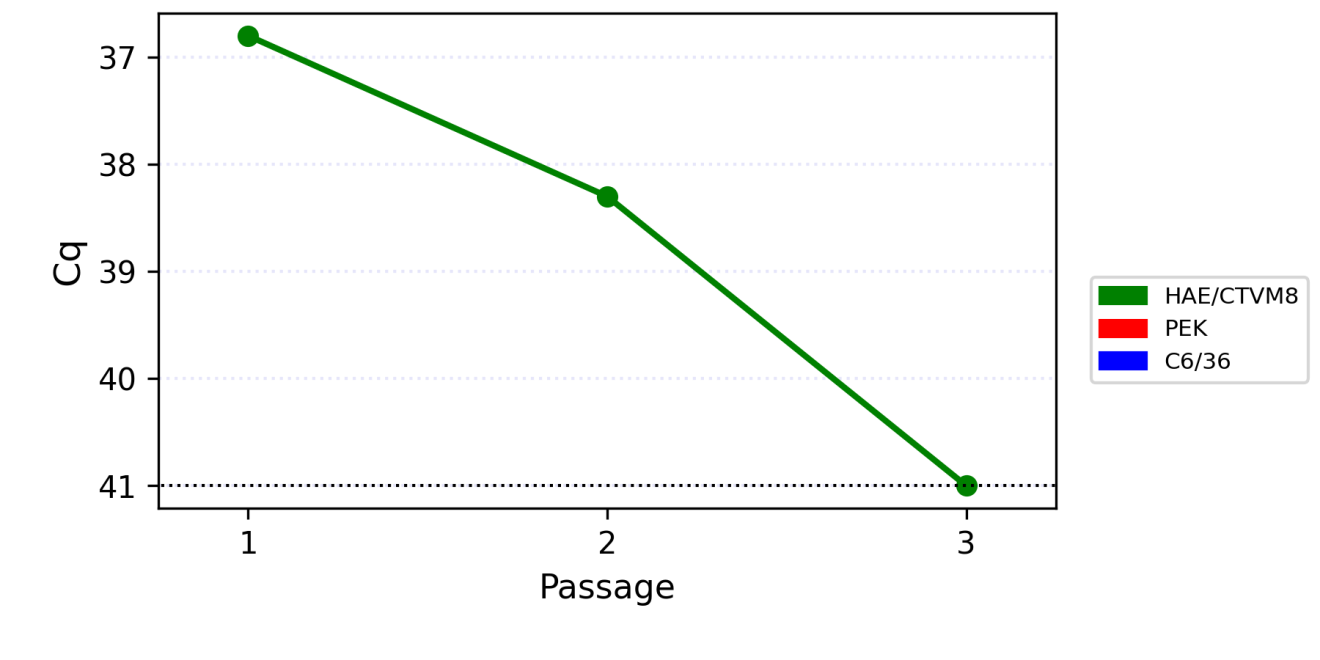


Figure S5. Dynamic of the real-time quantification cycle (Cq) during passages of the Polka Haematopota nora-like virus. Black dotted line represents qPCR detection limit (41 cycles).

Figure S6. Dynamic of the real-time quantification cycle (Cq) during passages of the Big Soux River virus (strain Medvezhye). Black dotted line represents qPCR detection limit (41 cycles).

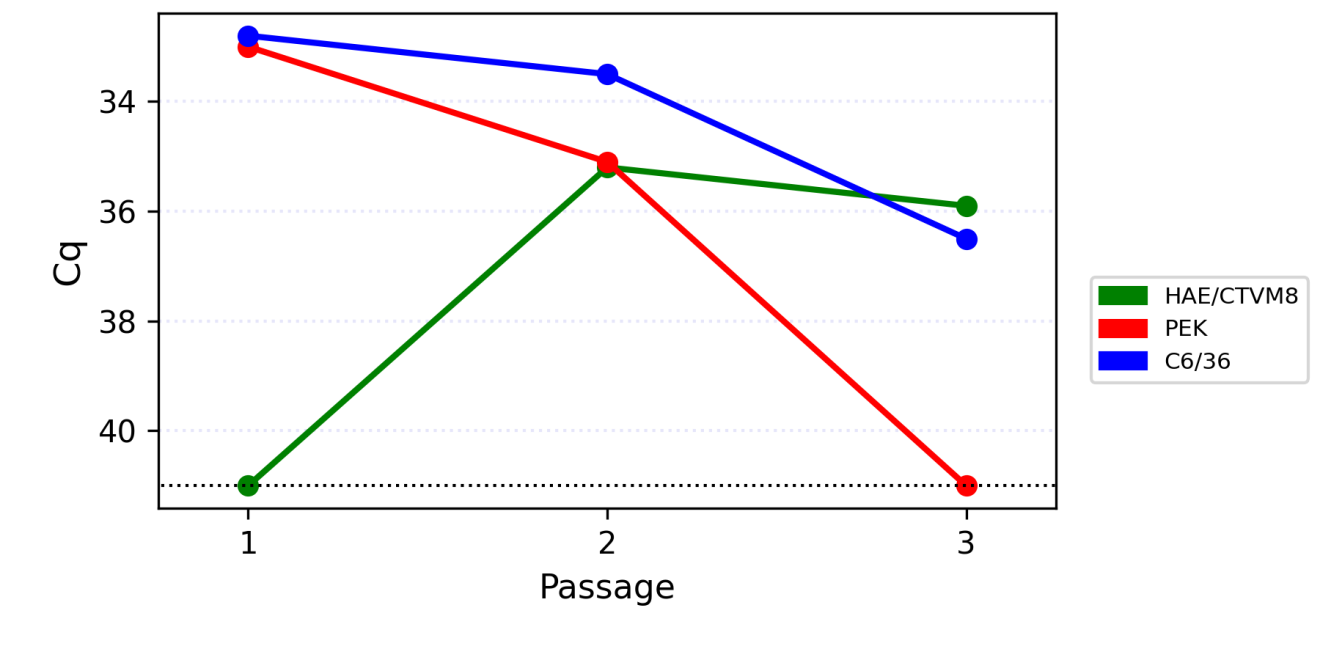


Figure S7. Dynamic of the real-time quantification cycle (Cq) during passages of the Melisia Chrysops solemo-like virus. Black dotted line represents qPCR detection limit (41 cycles).

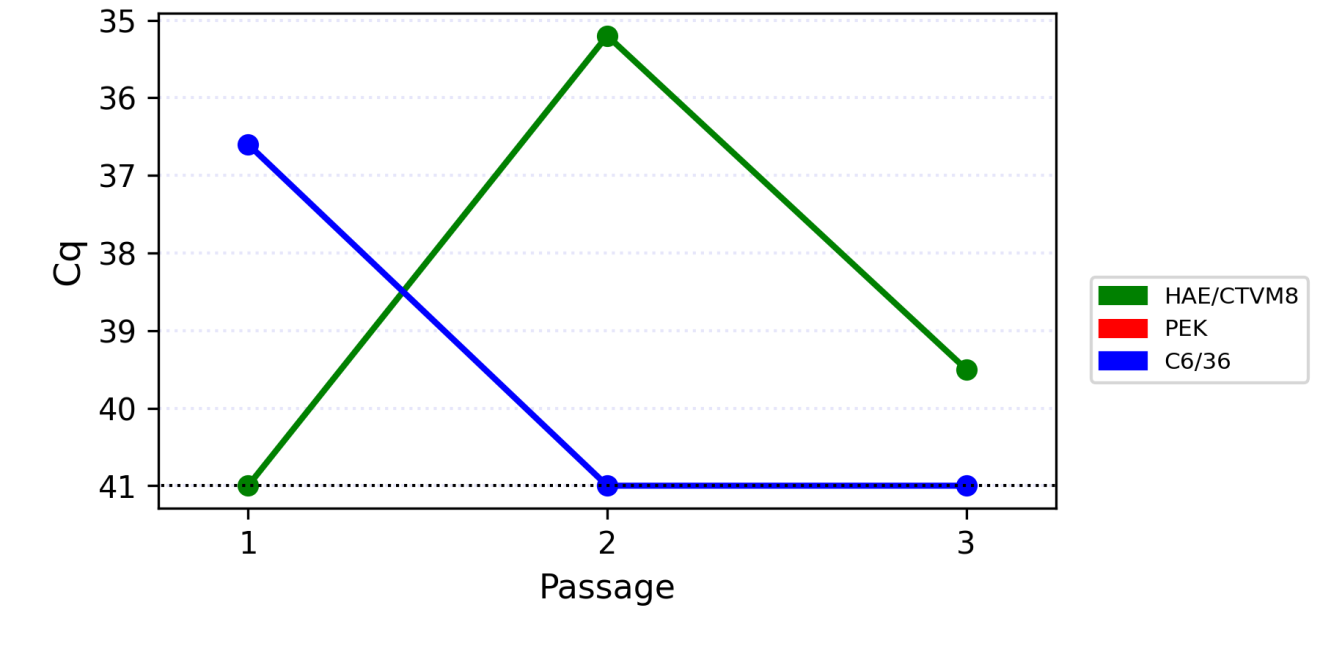


Figure S8. Dynamic of the real-time quantification cycle (Cq) during passages of the Polka Chrysops solemo-like virus. Black dotted line represents qPCR detection limit (41 cycles).

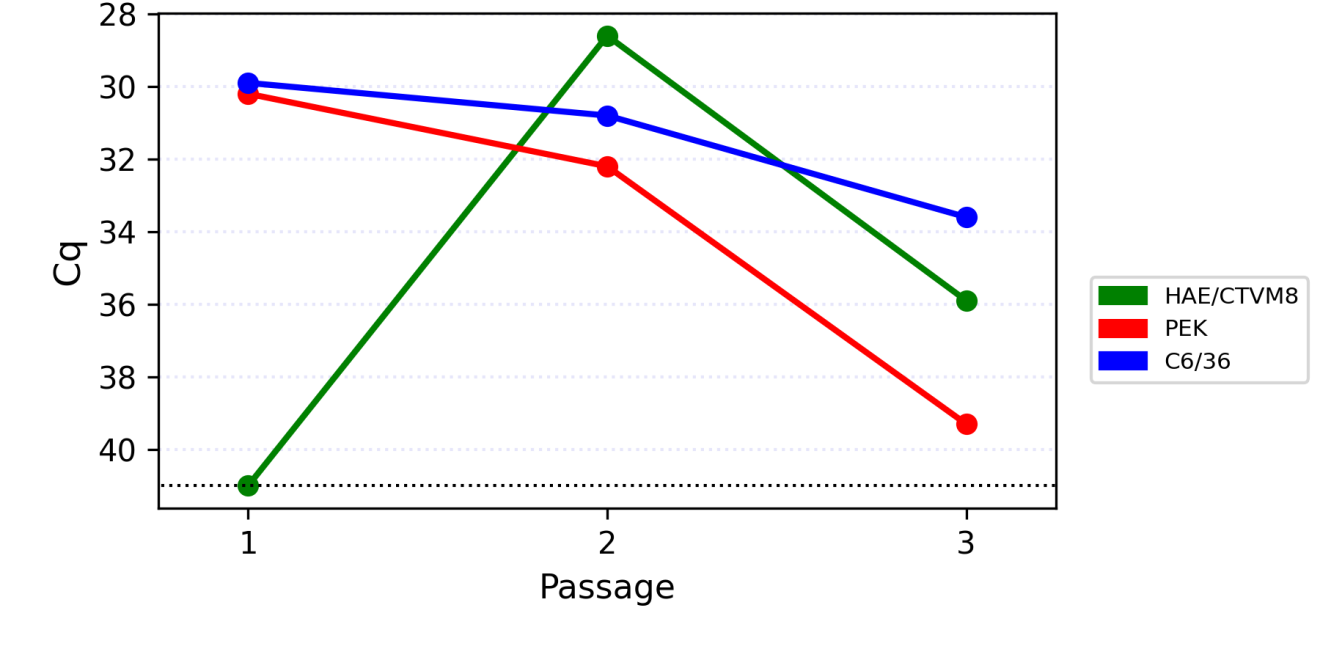
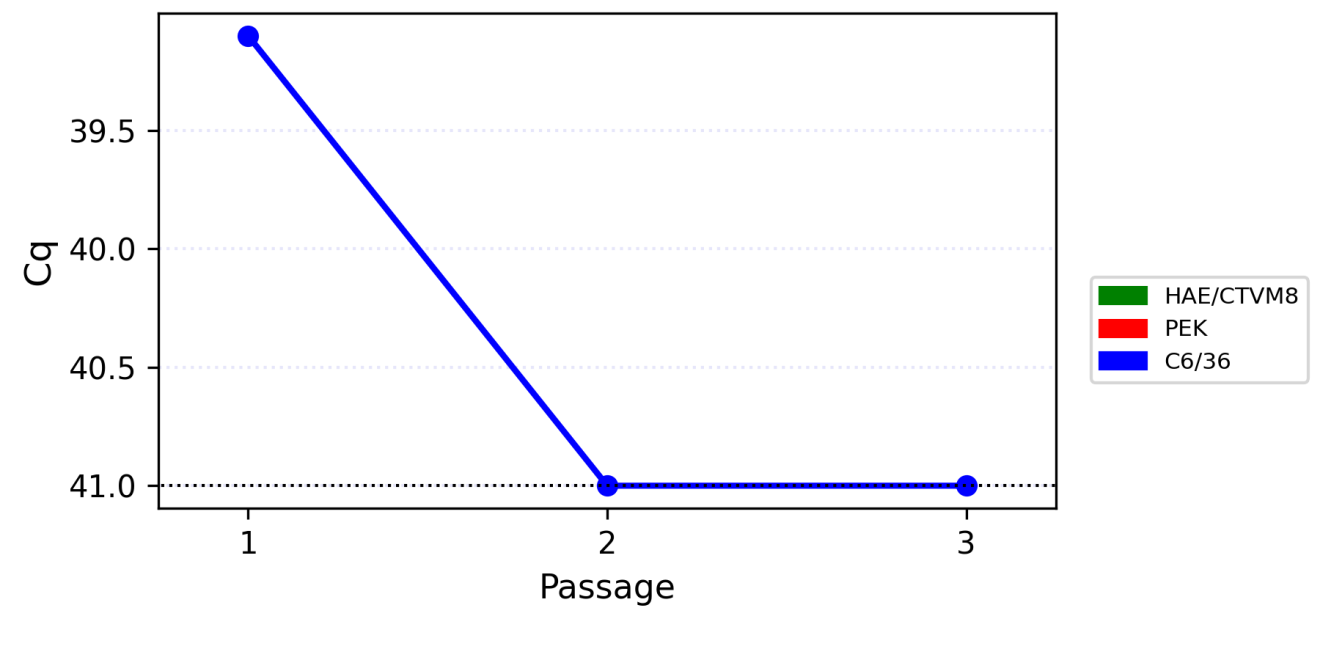
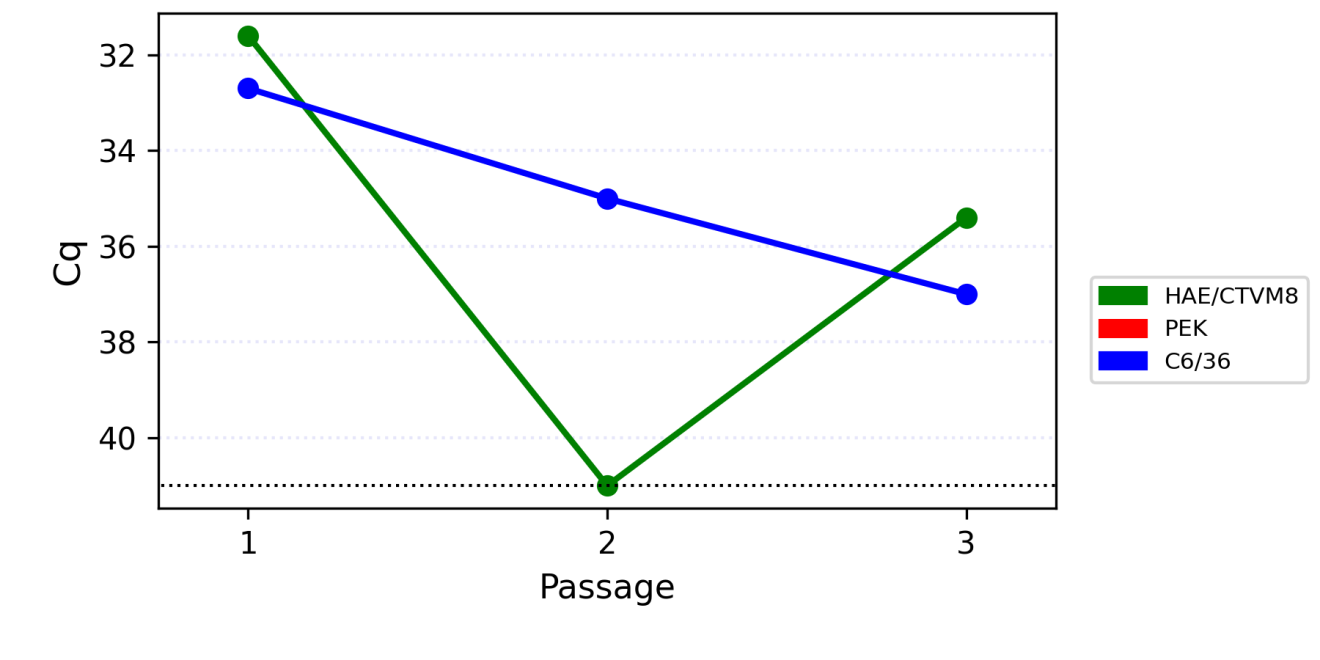
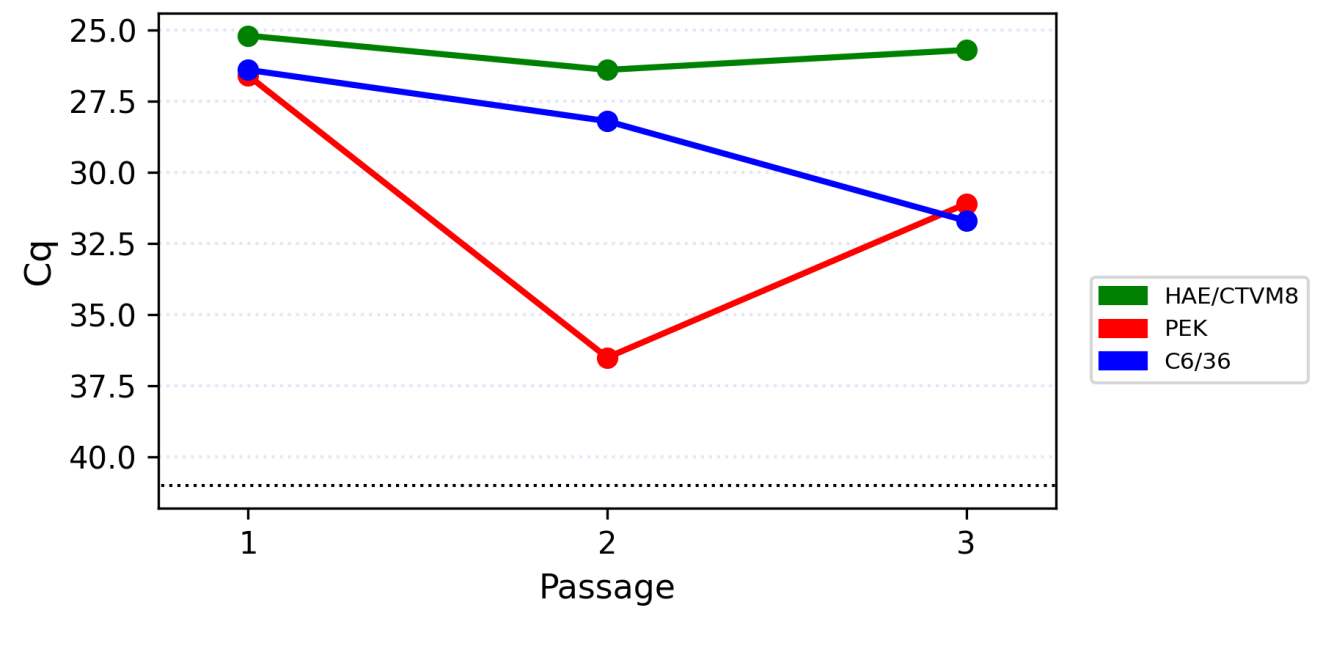


Figure S9. Dynamic of the real-time quantification cycle (Cq) during passages of the Medvezhye Chrysops narna-like virus 2. Black dotted line represents qPCR detection limit (41 cycles).

Figure S10. Dynamic of the real-time quantification cycle (Cq) during passages of the Medvezhye Chrysops rhabdo-like virus. Black dotted line represents qPCR detection limit (41 cycles).

Figure S11. Dynamic of the real-time quantification cycle (Cq) during passages of the Istie Chrysops solemo-like virus. Black dotted line represents qPCR detection limit (41 cycles).

Figure S12. Dynamic of the real-time quantification cycle (Cq) during passages of the Medvezhye Tabanus toti-like virus. Black dotted line represents qPCR detection limit (41 cycles).

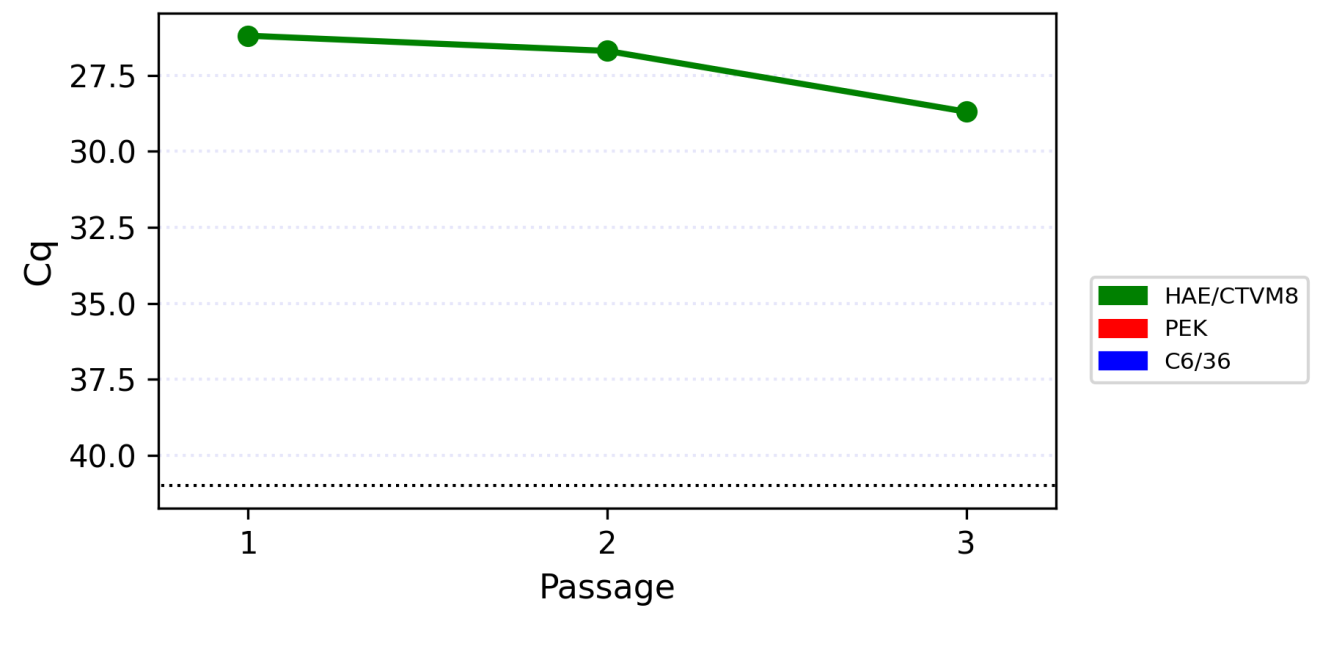


Figure S13. Dynamic of the real-time quantification cycle (Cq) during passages of the Komarovka hybomitra solemo-like virus. Black dotted line represents qPCR detection limit (41 cycles).

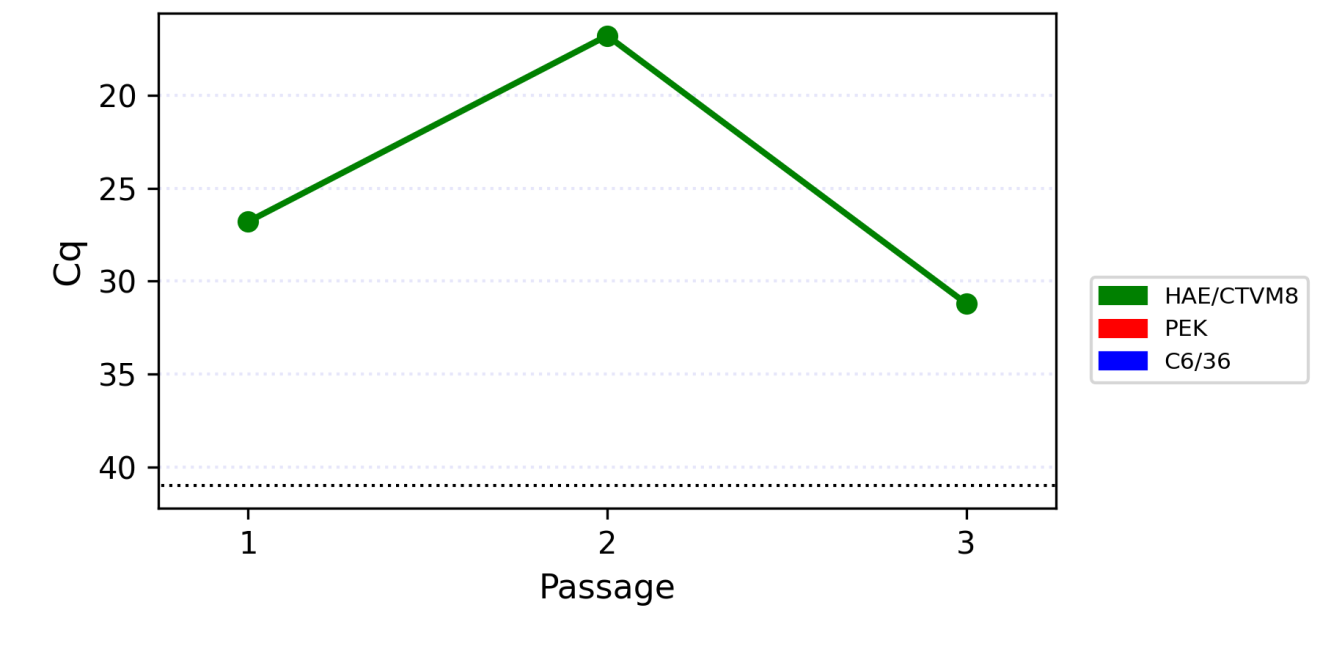


Figure S14. Dynamic of the real-time quantification cycle (Cq) during passages of the Barsukovka Hybomitra ifla-like virus. Black dotted line represents qPCR detection limit (41 cycles).