Honeybee Iflaviruses Pack Specific tRNA Fragments from Host Cells in Their Virions

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Table SI 1: The list of screened nucleosides in analysed digested RNA from virions.

| Name                              | Short name | Fragment structure | Exact fragment mass (Da) | Detected exact mass [X+H]^+ | Retention time (LC) |
|-----------------------------------|------------|--------------------|--------------------------|-----------------------------|----------------------|
| Adenosine                         | A          | ![Image](image)    | 135.054                  | 136.062                     | 8.2 min              |
| 2′-O-methyladenosine              | Am         | ![Image](image)    | 135.054                  | 136.062                     | 13.3 min             |
| 1-methyladenosine                 | m1A        | ![Image](image)    | 149.070                  | 150.078                     | 4.3 min              |
| N6-methyladenosine                | m6A        | ![Image](image)    | 149.070                  | 150.078                     | 13.6 min             |
| N6-threonylcarbamoyladenosine     | t6A        | ![Image](image)    | 279.121                  | 280.128                     | 20.3 min             |
| Guanosine                         | G          | ![Image](image)    | 151.049                  | 152.057                     | 9.1 min              |
| 2′-O-methylguanosine              | Gm         | ![Image](image)    | 151.049                  | 152.057                     | 13.8 min             |
| 1-methylguanosine                 | m1G        | ![Image](image)    | 165.065                  | 166.072                     | 13.6 min             |
| N2-methylguanosine                | m2G        | ![Image](image)    | 165.065                  | 166.072                     | 13.8 min             |
| Compound                    | Structure | m/z  | Relative Abundance | Retention Time |
|-----------------------------|-----------|------|--------------------|----------------|
| 7-methylguanosine           | ![Structure](image) | 166.072 | 166.072           | 5.9 min        |
| Cytidine                    | ![Structure](image) | 111.043 | 112.051           | 2.9 min        |
| 2'-O-methylcytidine         | ![Structure](image) | 111.043 | 112.051           | 6.7 min        |
| 3-methylcytidine            | m^3^C     | 125.059 | 126.067           | 3.9 min        |
| 5-methylcytidine            | m^5^C     | 125.059 | 126.067           | 4.4 min        |
| Uridine                     | U         | 112.027 | 113.035           | 5.0 min        |
| 2'-O-methyluridine          | Um        | 112.027 | 113.035           | 13.5 min       |
| 5-methyluridine             | m^5^U     | 126.043 | 127.051           | 11.4 min       |

Table SI 2: Codon usage of SBV.

| Codon | Count | %     | aa     |
|-------|-------|-------|--------|
| GAT   | 128   | 4.477089892 | Asp    |
| AAT   | 99    | 3.462749213  | Asn    |
| GAA   | 99    | 3.462749213  | Glu    |
| TTT   | 97    | 3.392794683  | Phe    |
| TAT   | 94    | 3.287862889  | Tyr    |
| ACT   | 84    | 2.938090241  | Thr    |
| TTG   | 81    | 2.833158447  | Leu    |
| ATG   | 80    | 2.798181182  | Met    |
| Codon | Frequency | Amino Acid |
|-------|-----------|------------|
| ATA   | 79        | Ile        |
| ATT   | 77        | Ile        |
| GCT   | 77        | Ala        |
| GTA   | 75        | Val        |
| AAG   | 73        | Lys        |
| GTG   | 72        | Val        |
| TTA   | 72        | Leu        |
| GTT   | 70        | Val        |
| AAA   | 69        | Lys        |
| CAA   | 69        | Gln        |
| GAG   | 68        | Glu        |
| AGT   | 66        | Ser        |
| GGA   | 65        | Gly        |
| GGT   | 59        | Gly        |
| TCT   | 56        | Ser        |
| ACA   | 54        | Thr        |
| GCA   | 49        | Ala        |
| GGG   | 49        | Gly        |
| CCT   | 48        | Pro        |
| TCA   | 44        | Ser        |
| AGA   | 43        | Arg        |
| CCA   | 43        | Pro        |
| CAT   | 42        | His        |
| GCG   | 41        | Ala        |
| TGG   | 41        | Trp        |
| ACG   | 40        | Thr        |
| CAG   | 40        | Gln        |
| TGT   | 33        | Cys        |
| AAC   | 32        | Asn        |
| CGA   | 32        | Arg        |
| AGG   | 30        | Arg        |
| CCG   | 29        | Pro        |
| TAC   | 29        | Tyr        |
| CGT   | 28        | Arg        |
| CCC   | 26        | Pro        |
| ACC   | 25        | Thr        |
| CTT   | 24        | Leu        |
| TCG   | 23        | Ser        |
| GAC   | 20        | Asp        |
| TCC   | 20        | Ser        |
| CAC   | 19        | His        |
| GCC   | 19        | Ala        |
| ATC   | 18        | Ile        |
| TTC   | 18        | Phe        |
| CTG   | 17        | Leu        |
| codon | count | %            | aa  |
|-------|-------|--------------|-----|
| GAT   | 123   | 4.250172771  | Asp |
| AAT   | 114   | 3.93918452   | Asn |
| GAA   | 108   | 3.731859019  | Glu |
| ATT   | 102   | 3.524533518  | Ile |
| TAT   | 101   | 3.489979267  | Tyr |
| TTA   | 100   | 3.45425017   | Leu |
| GCT   | 86    | 2.971665515  | Ala |
| TTT   | 83    | 2.868002764  | Phe |
| AAA   | 82    | 2.833448514  | Lys |
| GGT   | 81    | 2.798894264  | Gly |
| ATG   | 80    | 2.764340014  | Met |
| CAA   | 79    | 2.729785764  | Gln |
| AAG   | 77    | 2.660677263  | Lys |
| GTT   | 77    | 2.660677263  | Val |
| TTG   | 74    | 2.557014513  | Leu |
| ACT   | 71    | 2.453351762  | Thr |
| CCT   | 67    | 2.315134762  | Pro |
| CAT   | 62    | 2.142363511  | His |
| GAG   | 62    | 2.142363511  | Glu |
| CGT   | 57    | 1.96959226   | Arg |
| TGG   | 57    | 1.96959226   | Trp |
| GTG   | 55    | 1.90048376   | Val |
| GGA   | 53    | 1.831375259  | Gly |
| TCT   | 52    | 1.796821009  | Ser |
| TGT   | 51    | 1.762266759  | Cys |
| CCA   | 50    | 1.727712509  | Pro |

Table SI 3: Codon usage of DWV.
Table SI 4: List of host tRNAs present in virions.

| tRNA in SBV | tRNA in DWV | Bee - codon usage |
|-------------|-------------|-------------------|
| 1. Lys CTT  | Gly GCC-1   | Glu GAA           |
| 2. Gly GCC-1| Asp GTC     | Lys AAA           |
|   | SBV – co-packed tRNA | C position | % of reads without conversion to U in this position |
|---|---------------------|------------|---------------------------------------------------|
| 3. | Lys TTT             | Lys TTT    | Asn AAT                                           |
| 4. | Asp GTC             | Glu CTC    | Asp GAT                                           |
| 5. | Ala TGC             | His GTG    | Gln CAA                                           |
| 6. | Glu CTC             | Glu TTC    | Leu TTA                                           |
| 7. | Glu TTC             | Met-1 CAT  | Glu GAG                                           |
| 8. | Val AAC             | Ala TGC    | Ile ATT                                           |

*Table SI 5: List of co-packed host tRNAs confirmed by bisulfite sequencing for SBV.*

|   | DWV – co-packed tRNA | C position | % of reads without conversion to U in this position |
|---|---------------------|------------|---------------------------------------------------|
| 9. | Ala AGC             | 49         | 100                                               |
| 10.| Ala TGC             | 49         | 97                                                |
| 11.| Asp GTC             | 48         | 33                                                |
| 12.| Glu CTC             | 49         | 95                                                |
| 13.| Glu TTC             | 49         | 98                                                |
| 14.| Gly TCC             | 49         | 100                                               |
| 15.| 50                  | 100       |
| 16.| His GTG             | 48         | 75                                                |
| 17.| 49                  | 77        |
| 18.| Val CAC             | 49         | 100                                               |

*Table SI 6: List of co-packed host tRNAs confirmed by bisulfite sequencing for DWV.*
| Residue | C position | % of reads without conversion to U in this position |
|---------|------------|--------------------------------------------------|
| Glu CTC | 90         | 5.5                                              |
| Glu TTC | 1080       | 5.0                                              |
| Gly GCC | 1142       | 7.5                                              |
| Gly TCC | 4557       | 6.7                                              |
| His GTG | 4676       | 5.9                                              |
| Lys TTT | 4684       | 5.3                                              |

Table SI 7: Detected positions of m<sup>5</sup>C in SBV genomic RNA.
| Position | m$^2$C Position | DWV after bisulfite sequencing |
|----------|-----------------|--------------------------------|
| 1663     | 5.6             | 4801                           |
| 1685     | 5.1             | 4813                           |
| 1949     | 5.1             | 5008                           |
| 1956     | 7.6             | 5744                           |
| 1973     | 5.8             | 6114                           |
| 2031     | 5.1             | 6461                           |
| 2154     | 5.2             | 6648                           |
| 2316     | 7.1             | 6741                           |
| 2633     | 9.1             | 6843                           |
| 2700     | 10.4            | 7233                           |
| 2768     | 5.2             | 7240                           |
| 2783     | 6.3             | 7437                           |
| 3285     | 6.1             | 7439                           |
| 3729     | 5.7             | 7469                           |
| 3993     | 6.0             | 7513                           |
| 4077     | 6.3             | 7811                           |
| 4207     | 8.7             | 8142                           |
| 4209     | 9.1             | 8378                           |
| 4278     | 6.2             | 8491                           |
| 4509     | 5.8             | 8671                           |
| 4554     | 5.9             | 8772                           |

Table SI 8: Detected positions of m$^2$C in DWV genomic RNA.

DWV – after bisulfite sequencing
| C position | % of reads without conversion to U in this position |
|------------|--------------------------------------------------|
| 321        | 6.5                                              |
| 1073       | 16.7                                             |
| 1096       | 7.4                                              |
| 1113       | 5.9                                              |
| 1170       | 5.1                                              |
| 4512       | 7.4                                              |
| 5874       | 6.7                                              |
| 7055       | 9.1                                              |
| 7541       | 5.5                                              |
| 9009       | 5.1                                              |

Table S1 9: Presence of typical eucaryotic tRNA adenosine modifications in analysed RNA from virions.

|           | Genome length (nt) | t^6A/100A | mS^t^6A/100A | i^6A/100A |
|-----------|-------------------|-----------|--------------|-----------|
| SBV       | 8832              | 0.02 ± 0.01 | 0.01 ± 0.004 | 0.01 ± 0.004 |
| DWV       | 10071             | 0.16 ± 0.01 | 0.06 ± 0.004 | 0.03 ± 0.04 |
| RV2       | 7120              | 0.00       | 0.00         | 0.00       |
| E18       | 7410              | 0.00       | 0.00         | 0.00       |
Figure SI 1: Cryo-electron micrographs of purified SBV (a) and DWV (b) virions after DNase and RNase treatment and before RNA isolation. Smaller particles in the background are pentamers of capsid protein protomers originating from disrupted capsids. Scale bar 100 nm.
Figure SI 2: The results of Tape station analysis of purified RNA from viral particles (a) and from Honeybees (b).
Standards

Figure SI 3: Extracted Ion Chromatograms for adenosine a guanosine standards.
Standards

Figure SI 4: Extracted Ion Chromatograms for cytidine and uridine standards.
Figure SI 5: Extracted Ion Chromatograms for detected nucleosides in Sacbrood virus.
Figure SI 6: Extracted Ion Chromatograms for detected nucleosides in Deformed wing virus.
Figure SI 7: Extracted Ion Chromatograms for detected nucleosides in human rhinovirus type 2.
Figure SI 8: Extracted Ion Chromatograms for detected nucleosides in human Echovirus 18.

Table SI 10: NGS library sequences.

| Sequence Type                        | Sequence                                |
|--------------------------------------|-----------------------------------------|
| 3'-adapter                           | 5’p-CNNNNNNAGATCGGAAGAGCACACGTCTG-(C3)  |
| RT primer                            | 5’CAGACGTGTGCTCTTCCGAT                  |
| cDNA-anchor-sense oligonucleotide     | 5’p-CAGATCGGAAGAGCGTCGTGT-(C3)          |
| cDNA anchor-antisense oligonucleotide| 5’ACACGACGCTCTTCCGATCTGGG               |
## Table SI 11: NGS primers.

| m1^A mapping | Forward primer | Reverse primer |
|--------------|----------------|----------------|
| SBV_m^8A_SS III | CACGCTACGTACACGAGCTCTCTCCGATCT | ACTAGCAGTACAGACGCTCTCTCCGATCT |
| SBV_m^1A_SS III | CAGTAGACGTAACACGAGCTCTCTCCGATCT | CGATCGTATACAGACGCTCTCTCCGATCT |
| SBV_m^8A_TGIRT | ACGCCGATATACACGAGCTCTCTCCGATCT | AGTACGCTATACAGACGCTCTCTCCGATCT |
| SBV_m^1A_TGIRT | ACTGTACGTACACGAGCTCTCTCCGATCT | ATAGAGTACTACAGACGCTCTCTCCGATCT |

## Bisulfite seq.

| Forward primer | Reverse primer |
|----------------|----------------|
| SBV+ | ACGAGTGCGTAACACGAGCTCTCTCCGATCT |
| SBV- | TGATACGTCTACACGAGCTCTCTCCGATCT |
| DWV + | ATCAGACAGACACGAGCTCTCTCCGATCT |
| DWV- | TACTGAGCTTACACGAGCTCTCTCCGATCT |

## Table SI 12: Probes and templates used for Northern blot

| Name | Sequence (starting at 5'end) |
|------|------------------------------|
| LysTTT 3'end | TGGCCCGAACAGGGACTCG |
| LysTTT 5'end | GACTGAGCTATCCGGGCG |
| LysTTT central | CCGTCAATAAGCTCCTGCTGAC |
| LysCTT 3'end | TGGCCCAACGTGGGGCTC |
| LysCTT 5'end | GACTGAGCTACCCGGGCA |
| AspGTC 3'end | TCTCCCGACGGGAATCG |
| AspGTC 5'end | CACTATACATAGGGAAA |
| GlyGCC-1 3'end | TCGATCGGGCGGAATCGA |
| GlyGCC-1 5'end | CCACGAAACCACGATG |
| GluCCTC 3'end | TCCGGTACCGGAATCGA |
| GluCCTC 5'end | CCACTGAGCATTACCGA |
| LysTTT ladder 21nt sense | CAGTAATACGACTCATATAGGCGATCCCTGCTCCGAG |
| LysTTT ladder 21nt antisense | TGCCCGGAAACAGGGACTCG |
| LysTTT ladder 38nt sense | CAGTAATACGACTCATATAGGCGATCCCTGCTCCGAG |
| LysTTT ladder 38nt antisense | TGCCCGGAAACAGGGACTCG |
| LysTTT ladder 75nt sense | CAGTAATACGACTCATATAGGCGATCCCTGCTCCGAG |
| LysTTT ladder 75nt antisense | TGCCCGGAAACAGGGACTCG |
Figure SI 9: Bioinformatic data for Lys CTT confirmed m1A in position 59.
Figure S1 10: Bioinformatic data for Gly GCC confirmed m^1A in position 56.
Lys.TTT

Overall statistics

|              | 114444-m1ASBY-sh | 114444-m6ASBY-sh | 114444-m1ASBYT-sh | 114444-m6ASBYT-sh |
|--------------|------------------|------------------|-------------------|------------------|
| Total reads  | 2452             | 2223             | 129               | 139              |
| Coverage     | 1035 (60%)       | 1039 (43%)       | 85 (40%)          | 57 (40%)         |
| Average errors | 17 (0.68%)      | 16 (0.60%)       | 1 (0.02%)         | 1 (0.02%)        |
| Total errors  | 1.77%            | 1.57%            | 0.2%              | 0.2%             |
| Total "A" errors | 1.40%          | 1.22%            | 8.15%             | 7.10%            |

Figure SI 11.1: Bioinformatic data for Lys TTT.
Figure SI 12: Bioinformatic data for Asp GTC.
Table SI 12: Bioinformatical data – presence of $m^1A$ in SBV genomic RNA.

| SBV-CZ2 | 11bAS4-m1SBV-SBVCZ2.sam | 11bAS4-m6ASBV-SBVCZ2.sam | 11bAS4-m1ASBV-T-SBVCZ2.sam | 11bAS4-m6ASBV-T-SBVCZ2.sam | p-value |
|---------|-------------------------|--------------------------|----------------------------|---------------------------|--------|
| 71 (G)  | 0%                      | 0%                       | 0%                         | 0%                        | 0.08   |
| 115 (T) | 0%                      | 0%                       | 0%                         | 0%                        | 0.66   |
| 155 (A) | 11%                     | 11%                      | 16%                        | 0%                        | 0.31   |
| 177 (T) | 2%                      | 2%                       | 0%                         | 0%                        | 0.94   |
| 502 (T) | 2%                      | 0%                       | 0%                         | 0%                        | 0.83   |
| 848 (A) | 1%                      | 0%                       | 0%                         | 0%                        | 0.03   |
| 1242 (T)| 0%                      | 10%                      | 0%                         | 0%                        | 0.80   |
| 1534 (T)| 0%                      | 0%                       | 0%                         | 0%                        | 0.89   |
| 1561 (A)| 8%                      | 0%                       | 53%                        | 0%                        | 0.31   |
| 1652 (A)| 1%                      | 0%                       | 0%                         | 0%                        | 0.09   |
| 1892 (T)| 12%                     | 0%                       | 0%                         | 0%                        | 0.87   |
| 1986 (A)| 12%                     | 1%                       | 63%                        | 0%                        | 0.29   |
| 2567 (G)| 0%                      | 0%                       | 0%                         | 0%                        | 0.42   |
| 2812 (T) | 1%  | 8%  | 9%  | 3%  | 0.55 |
|----------|-----|-----|-----|-----|------|
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | 0.42 |
| I: 0%, D: 13% | I: 0%, D: 17% | I: 0%, D: 30% | I: 0%, D: 32% |
| (855)    | (528) | (10) | (25) |      |
| 2949 (T) | 1%  | 1%  | 2%  | 1%  | 0.07 |
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | ---- |
| I: 0%, D: 13% | I: 0%, D: 17% | I: 0%, D: 28% | I: 0%, D: 26% |
| (1529)   | (998) | (81) | (91) |      |
| 3333 (T) | 7%  | 12% | 0%  | 0%  | 0.29 |
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | 0.37 |
| I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 1% | I: 0%, D: 2% |
| (1499)   | (1146) | (101) | (128) |      |
| 3590 (A) | 6%  | 10% | 4%  | 12% | 0.03 |
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | 0.42 |
| I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% |
| (1673)   | (993) | (120) | (93) |      |
| 4142 (T) | 4%  | 10% | 0%  | 0%  | 0.08 |
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | ---- |
| I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% |
| (1599)   | (943) | (30) | (37) |      |
| 4216 (T) | 22% | 9%  | 22% | 5%  | 0.01 |
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | ---- |
| I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% |
| (1498)   | (942) | (21) | (40) |      |
| 4371 (T) | 13% | 4%  | 13% | 1%  | 0.03 |
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | 0.64 |
| I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% |
| (1472)   | (931) | (120) | (68) |      |
| 5363 (T) | 3%  | 20% | 2%  | 59% | 0.20 |
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | 0.37 |
| I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% |
| (1996)   | (1495) | (313) | (236) |      |
| 5571 (A) | 3%  | 1%  | 5%  | 0%  | 0.10 |
| 49% (T: 4%) | 48% (T: 4%) | 52% (T: 53%) | 52% (T: 53%) | 1.00 |
| I: 0%, D: 1% | I: 0%, D: 2% | I: 0%, D: 2% | I: 0%, D: 7% |
| (1952)   | (1456) | (157) | (229) |      |
| 5770 (T) | 3%  | 8%  | 0%  | 10% | 0.05 |
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | 0.92 |
| I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% |
| (2752)   | (1822) | (179) | (149) |      |
| 5929 (T) | 7%  | 2%  | 50% | 0%  | 0.32 |
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | ---- |
| I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 8% |
| (1972)   | (736) | (51) | (88) |      |
| 6282 (T) | 11% | 1%  | 0%  | 0%  | 0.03 |
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | 0.28 |
| I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% |
| (1952)   | (799) | (50) | (106) |      |
| 6345 (C) | 4%  | 11% | 0%  | 18% | 0.08 |
| 5% (T: 1%) | 8% (T: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0.84 |
| I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 8% |
| (2102)   | (1511) | (44) | (179) |      |
| 6388 (T) | 5%  | 9%  | 0%  | 0%  | 0.30 |
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | 0.32 |
| I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% |
| (1882)   | (1257) | (27) | (126) |      |
| 7348 (T) | 5%  | 12% | 9%  | 11% | 0.07 |
| 0% (0%)  | 0%  | 0%  | 0%  | 0%  | 0.25 |
| I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% | I: 0%, D: 0% |
| (1888)   | (888) | (91) | (115) |      |
| 7672 (T) 6% | 0% | 0% | 0% | 0% | 0.66 |
|-------------|----|----|----|----|------|
| 0% (A: 0%) | 0% (C: 0%) | 0% (G: 0%) | 0% (G: 0%) | 0% (A: 0%) | 0.42 |
| I: 0% (D: 3%) | I: 0% (D: 5%) | I: 0% (D: 8%) | I: 0% (D: 31%) | (1232) | (61) | (111) |
| 7670 (T) 12% | 5% | 11% | 0% | 0% | 0.7 |
| 0% (G: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0.42 |
| I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | (1200) | (74) | (69) |
| 8008 (T) 14% | 4% | 11% | 0% | 0% | 0.06 |
| 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 1%) | 0.42 |
| I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | (820) | (23) | (122) |
| 8206 (A) 4% | 0% | 0% | 0% | 0% | 0.49 |
| 45% (G: 44%) | 40% (D: 40%) | 100% (D: 100%) | 16% (G: 16%) | 0.28 |
| I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | (318) | (2) | (6) |
| 8210 (A) 1% | 0% | 0% | 0% | 0% | 0.76 |
| 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | -
| I: 1% (D: 0%) | I: 0% (D: 0%) | I: 50% (D: 0%) | I: 0% (D: 0%) | (267) | (2) | (5) |
| 8234 (T) 11% | 30% | 0% | 0% | 50% | 0.09 |
| 0% (A: 0%) | 0% (A: 0%) | 0% (G: 0%) | 0% (A: 0%) | 0% (A: 0%) | -
| I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | (1044) | (15) | (12) |
| 8752 (T) 0% | 0% | 0% | 0% | 0% | 0.86 |
| 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | -
| I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | (422) | (1) | (10) |
| 8767 (A) 2% | 0% | 0% | 0% | 0% | 0.75 |
| 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | -
| I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | (508) | (2) | (10) |
| 8779 (A) 1% | 2% | 0% | 0% | 12% | 0.34 |
| 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | -
| I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | I: 0% (D: 0%) | (521) | (2) | (7) |
| 8826 (A) 0% | 0% | 0% | 0% | 0% | 0.42 |
| 0% (C: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | 0% (A: 0%) | -
| I: 4% (D: 0%) | I: 2% (D: 0%) | I: 0% (D: 0%) | I: 50% (D: 0%) | (437) | (2) | (4) |

Overall statistics:

| libAS4-n1ASBV-SBVcZ2.sam libAS4-n6ASBV-SBVcZ2.sam libAS4-m1AS8VT-SBVcZ2.sam libAS4-m6AS8VT-SBVcZ2.sam libAS4-n8AS8VT-SBVcZ2.sam |
|---------------------------|---------------------------|---------------------------|---------------------------|---------------------------|
| Total reads               | 218071                    | 161841                    | 8379                      | 9844                      |
| Average coverage          | 1788 (n=720)              | 1229 (n=512)              | 69 (n=59)                 | 108 (n=132)               |
| Average errors            | 1 (o=13)                  | 1 (o=10)                  | 0 (o=1)                   | 0 (o=1)                   |
| Total errors              | 0.1%                      | 0.14%                     | 0.29%                     | 0.4%                      |
| Total "A" errors          | 0.83%                     | 0.84%                     | 0.1%                      | 0.13%                     |
Figure SI 13: Bioinformatic data – presence of m^1A in SBV genomic RNA.
