Supplementary Materials S2. Next-generation sequencing from SGLV nucleic acid positive ticks

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| ID | Total reads | fragment | Mapped reads count | Consensus length | Comsensus length(％)\* | Average coverage |
| YB129 | 77233010 | L | 9101 | 11924 | 99.36% | 101.54 |
| M | 7899 | 4313 | 99.49% | 188.22 |
| S | 4965 | 1862 | 98.99% | 358.59 |
| YB131 | 91070778 | L | 7021 | 11642 | 97.01% | 76.38 |
| M | 6186 | 4316 | 99.56% | 145.91 |
| S | 4936 | 1869 | 99.36% | 360.05 |
| YB132 | 38259238 | L | 19772 | 11822 | 98.51% | 222.72 |
| M | 12167 | 4312 | 99.47% | 275.5 |
| S | 9344 | 1823 | 96.92% | 659.13 |
| YB133 | 91968760 | L | 24484 | 11925 | 99.37% | 272.82 |
| M | 27112 | 4313 | 99.49% | 644.49 |
| S | 16009 | 1869 | 99.36% | 1158.94 |
| YB140 | 105749804 | L | 44046 | 11925 | 99.37% | 488.98 |
| M | 35064 | 4321 | 99.68% | 851.32 |
| S | 13958 | 1864 | 99.10% | 1005.14 |
| YB143 | 80576328 | L | 15214 | 11882 | 99.01% | 170.28 |
| M | 10779 | 4317 | 99.58% | 334.18 |
| S | 8463 | 1867 | 99.26% | 617.9 |
| YB149 | 86351240 | L | 19921 | 11925 | 99.37% | 220.97 |
| M | 15451 | 4313 | 99.49% | 372.35 |
| S | 9221 | 1874 | 99.63% | 662.74 |
| YB150 | 77793090 | L | 10851 | 11650 | 97.08% | 117.96 |
| M | 7006 | 4316 | 99.56% | 169.31 |
| S | 6733 | 1869 | 99.36% | 487.49 |
| YB153 | 74357612 | L | 6355 | 11930 | 99.41% | 70.41 |
| M | 2785 | 4313 | 99.49% | 66.21 |
| S | 2077 | 1865 | 99.15% | 144.05 |
| YB161 | 66216664 | L | 2037 | 11906 | 99.21% | 22.63 |
| M | 2085 | 4313 | 99.49% | 50.4 |
| S | 1440 | 1858 | 98.78% | 103.52 |
| YB162 | 80071308 | L | 6380 | 11931 | 99.42% | 70.89 |
| M | 4299 | 4313 | 99.49% | 104.96 |
| S | 3531 | 1878 | 99.84% | 247.8 |
| YB263 | 40155138 | L | 839 | 11696 | 97.46% | 9.24 |
| M | 243 | 4114 | 94.90% | 5.3 |
| S | 1060 | 1871 | 99.47% | 75.58 |
| YB273 | 40608924 | L | 2760 | 11881 | 99.00% | 31 |
| M | 2966 | 4317 | 99.58% | 67.03 |
| S | 3553 | 1871 | 99.47% | 259.8 |
| YB278 | 38824520 | L | 586 | 11074 | 92.28% | 6.3 |
| M | 505 | 4321 | 99.68% | 10.93 |
| S | 353 | 1827 | 97.13% | 25.28 |
| YB299 | 35390140 | L | 1568 | 11868 | 98.89% | 16.54 |
| M | 688 | 4310 | 99.42% | 14.58 |
| S | 1224 | 1862 | 98.99% | 86.16 |
| YB389 | 37083898 | L | 854 | 11835 | 98.62% | 9.2 |
| M | 424 | 3712 | 85.63% | 9.28 |
| S | 251 | 1868 | 99.31% | 17.35 |
| YB402 | 38457029 | L | 162 | 8685 | 72.37% | 1.82 |
| M | 143 | 3055 | 70.47% | 3.08 |
| S | 121 | 1834 | 97.50% | 8.19 |
| YB407 | 41970572 | L | 205 | 8682 | 72.34% | 2.32 |
| M | 186 | 3922 | 90.47% | 5.25 |
| S | 373 | 1868 | 99.31% | 20.30 |
| YB431 | 32552752 | L | 668 | 11511 | 95.92% | 7.11 |
| M | 112 | 4019 | 92.71% | 2.58 |
| S | 270 | 1845 | 98.09% | 18.84 |

Note: \* The percentage of the length of the obtained SGLV consensus sequence relative to the full genome of reference strain (SGLV strain HLJ1202, GI: NC079000-2).