**Table S3. *Nasonia vitripennis* genome mapping results of TTATTGGG neighboring sub-telomeric region assembly.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Assembled subtelomeric contig** | **Scaffold alignment  coordinates\*** | **% sequence identity** | **BLAT E-value** | **Chr mapping results** |
| k141\_435 | SCAFFOLD16: 1-102 | 100% | 2.87E-46 | chr1\_start |
| k141\_288 | SCAFFOLD116: 738598-738720 | 95.12% | 4.38E-48 | chr2\_start |
| k141\_435 | SCAFFOLD309: 3-403 | 86.63% | 3.36E-115 | chr2\_end |
| k141\_273 | SCAFFOLD18: 3693741-3693482 | 88.46% | 1.28E-84 | chr3\_start |
| k141\_435 | SCAFFOLD28: 1899952-1899551 | 96.77% | 0 | chr3\_end |
| k141\_321 | SCAFFOLD4: 5241320-5241887 | 100% | 0 | chr4\_start |
| k141\_395 | SCAFFOLD9: 4815-4930 | 100% | 2.74E-54 | chr4\_end |
| k141\_435 | SCAFFOLD2: 1-307 | 96.10% | 3.25E-140 | chr5\_end |

\* Physical location from *Nasonia vitripennis* reference assembly v2.1 (GCA\_000002325.2).