|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Read Mapping** | | |  | **CovEST Basic** | | |  | **CovEST Repeat** | | |  | **GenomeScope** | | |
|  | **Mean** | **SD** | **% Error** |  | **Mean** | **SD** | **% Error** |  | **Mean** | **SD** | **% Error** |  | **Mean** | **SD** | **% Error** |
| *Arabidopsis thaliana* | 178.2 | 30.2 | (13.5%) |  | 124.3 | 9.1 | 20.8% |  | 163.9 | 49.2 | (4.4%) |  | 123.3 | 3.5 | 21.5% |
| *Caenorhabditis elegans* | 108.7 | 6.8 | (8.7%) |  | 89.5 | 11.7 | 10.5% |  | 107.3 | 2.0 | (7.3%) |  | 99.4 | 1.8 | 0.6% |
| *Drosophila melanogaster* | 158.3 | 41.2 | 9.5% |  | 135.8 | 3.3 | 22.4% |  | 191.3 | 23.6 | (9.3%) |  | 143.6 | 8.9 | 17.9% |
| Average Absolute % Error |  |  | 10.6% |  |  |  | 17.9% |  |  |  | 7.0% |  |  |  | 13.3% |

Table S15. Summary of model organism genome size results using sequence-based methods. For all three species, n=4. Percent error values are underestimates unless indicated with parentheses. Mean and SD given in Mb. CovEST Basic, CovEST Repeat, and GenomeScope analyses were conducted using a k value of 21.