|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **Genome Size** | **Repeat** | **Unique** | **Read Error**  **Rate** | **Fit Min** | **Fit Max** |
| *Amphizoa insolens* DNA3784 | - | - | - | 0% | 0% | 0% |
| *Bembidion* sp. nr. *transversale* DNA2544 | 1,113.67 | 888.97 | 224.70 | 0.18% | 90.29% | 97.26% |
| *Bembidion* sp. nr. *transversale* DNA5427 | 1,010.67 | 793.81 | 216.85 | 0.17% | 91.22% | 98.97% |
| *Bembidion* sp. nr. *transversale* DNA5428 | 945.51 | 744.29 | 201.21 | 0.18% | 91.16% | 99.06% |
| *Bembidion* sp. nr. *transversale* DNA5433 | 908.41 | 688.79 | 219.61 | 0.20% | 92.10% | 99.23% |
| *Bembidion lividulum* DNA4161 | - | - | - | 0% | 0% | 0% |
| *Chlaenius sericeus* DNA4821 | 414.46 | 185.88 | 228.58 | 0.16% | 96.68% | 99.73% |
| *Chlaenius sericeus* JMP068 | 374.46 | 155.32 | 219.14 | 0.19% | 96.57% | 99.64% |
| *Chlaenius sericeus* JMP069 | 374.67 | 158.34 | 216.33 | 0.21% | 96.60% | 99.48% |
| *Chlaenius sericeus* JMP070 | - | - | - | 0% | 0% | 0% |
| *Chlaenius sericeus* JMP071 | 377.09 | 162.36 | 214.72 | 0.21% | 96.57% | 99.58% |
| *Lionepha* *tuulukwa* DNA3782 | 545.72 | 367.11 | 178.61 | 0.06% | 95.81% | 99.49% |
| *Lionepha* *tuulukwa* DNA5435a | 483.39 | 303.42 | 179.97 | 0.17% | 94.90% | 99.32% |
| *Lionepha* *tuulukwa* DNA5436a | 493.63 | 312.77 | 180.86 | 0.20% | 94.77% | 99.35% |
| *Omoglymmius hamatus* DNA3783 | 74.03 | 67.29 | 6.74 | 2.43% | 73.44% | 91.11% |
| *Pterostichus melanarius* DNA3787 | 74.58 | 65.06 | 9.52 | 2.59% | 75.63% | 91.59% |
| *Pterostichus melanarius* JMP059 | - | - | - | 0% | 0% | 0% |
| *Pterostichus melanarius* JMP060 | - | - | - | 0% | 0% | 0% |
| *Pterostichus melanarius* JMP061 | - | - | - | 0% | 0% | 0% |
| *Pterostichus melanarius* JMP062 | - | - | - | 0% | 0% | 0% |
| *Trachypachus gibbsii* DNA3786 | 264.08 | 81.61 | 182.47 | 0.10% | 97.62% | 99.60% |

Table S8. GenomeScope results. Cells containing dashes indicate that GenomeScope failed to converge. Genome size estimates are given in Mb. Analyses were conducted using a k value of 21. See Vurture et al. 2017 for an explanation of the meaning of these values.