|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Basic** | | **Repeat** | |
|  | **Genome Size** | **Coverage** | **Genome Size** | **Coverage** |
| *Amphizoa insolens* DNA3784 | 376.78 | 13.9 | 728.47 | 7.19 |
| *Bembidion* sp. nr. *transversale* DNA2544 | 932.04 | 113.49 | 2,140.04 | 49.43 |
| *Bembidion* sp. nr. *transversale* DNA5427 | 827.88 | 70.28 | 1,980.24 | 29.38 |
| *Bembidion* sp. nr. *transversale* DNA5428 | 813.44 | 40.44 | 1,924.27 | 17.1 |
| *Bembidion* sp. nr. *transversale* DNA5433 | 758.09 | 57.1 | 1,480.15 | 29.25 |
| *Bembidion lividulum* DNA4161 | 359.94 | 13.77 | 790.81 | 6.27 |
| *Chlaenius sericeus* DNA4821 | 386.92 | 29.14 | 608.44 | 18.53 |
| *Chlaenius sericeus* JMP068 | 410.91 | 33.89 | 751.89 | 18.52 |
| *Chlaenius sericeus* JMP069 | 395.86 | 27.46 | 704.51 | 15.43 |
| *Chlaenius sericeus* JMP070 | 409.81 | 19.57 | 796.39 | 10.07 |
| *Chlaenius sericeus* JMP071 | 412.78 | 25.3 | 624.53 | 16.72 |
| *Lionepha* *tuulukwa* DNA3782 | 442.32 | 16.66 | 659.97 | 11.17 |
| *Lionepha* *tuulukwa* DNA5435a | 340.38 | 49 | 423.66 | 39.37 |
| *Lionepha* *tuulukwa* DNA5436a | 346.52 | 50.39 | 578.96 | 30.16 |
| *Omoglymmius hamatus* DNA3783 | 627.13 | 12.2 | 1,188.94 | 6.44 |
| *Pterostichus melanarius* DNA3787 | 475.11 | 13.67 | 1,221.83 | 5.32 |
| *Pterostichus melanarius* JMP059 | 586.67 | 17.32 | 1,127.86 | 9.01 |
| *Pterostichus melanarius* JMP060 | 597.29 | 17.16 | 1,145.04 | 8.95 |
| *Pterostichus melanarius* JMP061 | 650.22 | 19.99 | 1,454.54 | 8.94 |
| *Pterostichus melanarius* JMP062 | 678.61 | 21.51 | 1,181.38 | 12.36 |
| *Trachypachus gibbsii* DNA3786 | 314.81 | 22.99 | 525.13 | 13.78 |

Table S10. CovEST genome size (in Mb) and coverage estimates for two models, Basic and Repeat, performed using a k value of 21.

a. Samples made with DNA extracted from different tissues of the same individual.