|  |  |  |  |
| --- | --- | --- | --- |
|  |  | **Regier** | **OrthoDB** |
|  | **Read Count** | **Coverage** | **Genome Size** | **Coverage** | **Genome Size** |
| *Amphizoa insolens* DNA3784 | 51,896,228 | 7.38 |  710.1  | 8.35 | 628.04 |
| *Bembidion* sp.nr. *transversale* DNA2544 | 701,179,000 | 82.00 |  1,291.1  | 93.36 | 1,134.10 |
| *Bembidion* sp.nr. *transversale* DNA5427 | 385,572,878 | 52.22 |  1,114.9  | 56.72 | 1,026.45 |
| *Bembidion* sp.nr. *transversale* DNA5428 | 218,017,252 | 36.66 |  897.9  | 40.55 | 811.80 |
| *Bembidion* sp.nr. *transversale* DNA5433 | 286,877,384 | 44.06 |  983.3  | 47.95 | 903.33 |
| *Bembidion lividulum* DNA4161 | 48,990,136 | 8.20 |  603.1  | 8.07 | 613.41 |
| *Chlaenius sericeus* DNA4821 | 74,877,844 | 27.47 |  411.5  | 28.93 | 390.84 |
| *Chlaenius sericeus* JMP068 | 92,333,434 | 35.74 |  390.1  | 40.73 | 342.32 |
| *Chlaenius sericeus* JMP069 | 72,013,564 | 27.92 |  389.5  | 31.7 | 343.02 |
| *Chlaenius sericeus* JMP070 | 53,119,248 | 22.63 |  354.5  | 22.82 | 351.43 |
| *Chlaenius sericeus* JMP071 | 69,184,928 | 27.27 |  383.1  | 29.11 | 358.92 |
| *Lionepha* *tuulukwa* DNA3782 | 73,040,060 | 9.59 |  769.1  | 11.23 | 657.13 |
| *Lionepha* *tuulukwa* DNA5435a | 110,544,262 | 32.22 |  518.1  | 34.16 | 488.68 |
| *Lionepha* *tuulukwa* DNA5436a | 115,669,748 | 33.46 |  522.1  | 36.19 | 482.67 |
| *Omoglymmius hamatus* DNA3783 | 75,837,778 | 5.02 |  1,525.7  | 5.91 | 1,295.26 |
| *Pterostichus melanarius* DNA3787 | 64,380,826 | 5.68 |  1,144.9  | 6.8 | 955.60 |
| *Pterostichus melanarius* JMP059 | 67,306,770 | 13.37 |  760.3  | 12.66 | 802.69 |
| *Pterostichus melanarius* JMP060 | 67,908,474 | 11.99 |  855.5  | 13.64 | 752.00 |
| *Pterostichus melanarius* JMP061 | 86,110,430 | 15.12 |  859.9  | 17.81 | 730.23 |
| *Pterostichus melanarius* JMP062 | 96,703,360 | 13.23 |  1,103.7  | 17.23 | 847.71 |
| *Trachypachus gibbsii* DNA3786 | 71,720,174 | 21.18 |  342.0  | 22.8 | 317.71 |

Table S9. Summary of read mapping genome size estimates for the Regier and OrthoDB gene sets using three different read filtering methods. Genome size is calculated by multiplying the read length by total number of reads, then dividing by coverage. Genome sizes are given in Mb.

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