|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Summary** | **Complete** | **Fragmented** | **Missing** |
| *Amphizoa insolens* DNA3784 | C:34.7%[S:34.5%,D:0.2%],F:31.2%,M:34.1%,n:2442 | 848 | 761 | 833 |
| *Bembidion* sp.nr. *transversale* DNA2544 | C:59.3%[S:57.5%,D:1.8%],F:27.2%,M:13.5%,n:2442 | 1,446 | 664 | 332 |
| *Bembidion lividulum* DNA4161 | C:29.8%[S:29.6%,D:0.2%],F:35.4%,M:34.8%,n:2442 | 726 | 865 | 851 |
| *Chlaenius sericeus* DNA4821 | C:78.7%[S:78.2%,D:0.5%],F:15.6%,M:5.7%,n:2442 | 1,923 | 380 | 139 |
| *Lionepha* *tuulukwa* DNA3782 | C:68.5%[S:68.3%,D:0.2%],F:20.1%,M:11.4%,n:2442 | 1,673 | 491 | 278 |
| *Omoglymmius hamatus* DNA3783 | C:7.3%[S:7.3%,D:0.0%],F:28.3%,M:64.4%,n:2442 | 178 | 690 | 1,574 |
| *Pterostichus melanarius* DNA3787 | C:30.7%[S:30.7%,D:0.0%],F:33.5%,M:35.8%,n:2442 | 750 | 817 | 875 |
| *Trachypachus gibbsii* DNA3786 | C:45.8%[S:45.2%,D:0.6%],F:31.5%,M:22.7%,n:2442 | 1,119 | 770 | 553 |

Table S6. Results of BUSCO analysis on eight genome assemblies using the 2442 gene Endopterygota odb9 reference set. Summary column shows results in BUSCO notation: C:complete [S:single-copy, D:duplicated], F:fragmented, M:missing, n:number of genes used. Genes classified as “complete” have lengths within two standard deviations of the BUSCO group mean length. “Complete” genes found only once are classified as “single-copy”, while those that are found multiple times are classified as “duplicated.” Partially recovered genes are classified as “fragmented,” and genes not recovered at all are classified as “missing.”