|  |  |  |  |
| --- | --- | --- | --- |
|  | **Regier Read Mapping Coverages** | | |
|  | **Untrimmed** | **IQR Trim** | **Difference** |
| *Amphizoa insolens* DNA3784 | 7.85 | 7.38 | -0.47 |
| *Bembidion* sp. nr. *transversale* DNA2544 | 92.72 | 82.00 | -10.71 |
| *Bembidion lividulum* DNA4161 | 8.72 | 8.20 | -0.52 |
| *Chlaenius sericeus* DNA4821 | 30.54 | 27.47 | -3.07 |
| *Lionepha* *tuulukwa* DNA3782 | 9.59 | 9.59 | 0.00 |
| *Omoglymmius hamatus* DNA3783 | 10.40 | 5.02 | -5.38 |
| *Pterostichus melanarius* DNA3787 | 6.33 | 5.68 | -0.65 |
| *Trachypachus gibbsii* DNA3786 | 22.54 | 21.18 | -1.36 |

Table S11. Regier read mapping mean coverages before and after removing outliers using the 3\*IQR rule. The columns “Untrimmed” and “IQR Trim” indicate the mean coverage of each sample before and after, respectively, removing outlier. The column “Difference” is the difference in coverage between “IQR Trim” and “Untrimmed.”