**Table S1:** Base composition and strand bias of Panorpidae.

| Species | Whole genome | | AT | GC | PCGs | | tRNAs | | rRNAs | | A+T-rich region | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Size(bp) | AT(%) | skew | skew | Size(bp) | AT(%) | Size(bp) | AT(%) | Size(bp) | AT(%) | Size(bp) | AT(%) |
| *Cerapanorpa brevicornis* | 16337 | 77.4 | 0 | -0.158 | 11196 | 76.2 | 1464 | 76 | 2118 | 79 | 1521 | 84.8 |
| *Cerapanorpa byersi* | 16317 | 76.3 | 0.004 | -0.157 | 11193 | 74.9 | 1469 | 75.6 | 2113 | 78.8 | 1496 | 84.3 |
| *Cerapanorpa dubia* | 16322 | 76 | 0.002 | -0.153 | 11193 | 74.4 | 1470 | 75.3 | 2111 | 78.6 | 1502 | 85.3 |
| *Cerapanorpa nanwutaina* TTH | 16312 | 76 | 0.004 | -0.157 | 11196 | 74.5 | 1469 | 75.5 | 2112 | 78.5 | 1492 | 85.1 |
| *Cerapanorpa nanwutaina* ZQ | 16328 | 76.2 | 0.005 | -0.16 | 11193 | 74.6 | 1470 | 75.5 | 2114 | 78.7 | 1505 | 85.4 |
| *Dicerapanorpa magna* LP | 16449 | 76.9 | 0.004 | -0.152 | 11202 | 75.5 | 1465 | 75.3 | 2109 | 78.8 | 1642 | 84.9 |
| *Dicerapanorpa magna* MCS | 16452 | 76.8 | 0.006 | -0.152 | 11202 | 75.3 | 1465 | 75.5 | 2109 | 78.9 | 1645 | 85.1 |
| *Dicerapanorpa magna* TTH | 16455 | 76.9 | 0.005 | -0.155 | 11202 | 75.5 | 1474 | 75.7 | 2108 | 78.9 | 1641 | 84.8 |
| *Dicerapanorpa magna* WLD | 16452 | 76.9 | 0.004 | -0.152 | 11202 | 75.5 | 1466 | 75.6 | 2111 | 78.9 | 1642 | 84.8 |
| *Dicerapanorpa minshana* 1 | 16444 | 76.8 | 0.006 | -0.156 | 11202 | 75.4 | 1466 | 75.3 | 2107 | 78.7 | 1639 | 85 |
| *Dicerapanorpa minshana* 2 | 16449 | 76.7 | 0.005 | -0.156 | 11202 | 75.3 | 1467 | 75.1 | 2109 | 78.7 | 1641 | 85 |
| *Dicerapanorpa minshana* 3 | 16446 | 76.7 | 0.006 | -0.158 | 11202 | 75.3 | 1467 | 75.4 | 2108 | 78.7 | 1639 | 84.8 |
| *Furcatopanorpa longihypovalva* HSD | 17123 | 77.8 | 0.018 | -0.163 | 11205 | 75.6 | 1472 | 75.1 | 2112 | 79.4 | 2252 | 87.5 |
| *Furcatopanorpa longihypovalva* LP | 17088 | 77.7 | 0.019 | -0.165 | 11205 | 75.7 | 1471 | 75 | 2111 | 79.4 | 2219 | 87.6 |
| *Furcatopanorpa longihypovalva* MCS | 17080 | 77.6 | 0.018 | -0.164 | 11205 | 75.6 | 1471 | 75 | 2111 | 79.4 | 2211 | 87.3 |
| *Furcatopanorpa longihypovalva* TTH | 17051 | 77.7 | 0.017 | -0.169 | 11205 | 75.7 | 1471 | 75.2 | 2111 | 79.5 | 2182 | 87.5 |
| *Neopanorpa brisi* | 16339 | 76.3 | -0.009 | -0.183 | 11211 | 74.8 | 1459 | 76.3 | 2099 | 78.3 | 1561 | 84.6 |
| *Neopanorpa chelata* | 16337 | 76 | -0.006 | -0.182 | 11202 | 74.1 | 1458 | 76.4 | 2098 | 78.5 | 1562 | 85.1 |
| *Neopanorpa claripennis* 1 | 16358 | 76.4 | -0.001 | -0.165 | 11205 | 74.7 | 1458 | 75.7 | 2100 | 78.7 | 1578 | 85.9 |
| *Neopanorpa claripennis* 2 | 16359 | 76.4 | 0 | -0.167 | 11205 | 74.8 | 1458 | 75.5 | 2100 | 78.7 | 1579 | 85.6 |
| *Neopanorpa claripennis* 3 | 16369 | 76.4 | 0.001 | -0.169 | 11205 | 74.7 | 1467 | 75.9 | 2101 | 78.6 | 1579 | 85.8 |
| *Neopanorpa longiprocessa* 1 | 16337 | 77.2 | -0.013 | -0.152 | 11205 | 75.6 | 1458 | 76.4 | 2106 | 79.7 | 1552 | 86.3 |
| *Neopanorpa longiprocessa* 2 | 16328 | 77.2 | -0.013 | -0.152 | 11205 | 75.6 | 1458 | 76.4 | 2098 | 79.7 | 1551 | 86.3 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Neopanorpa lui* | 16367 | 76.6 | 0 | -0.173 | 11205 | 74.9 | 1459 | 75.9 | 2102 | 78.7 | 1584 | 86 |
| *Neopanorpa nielseni* | 16222 | 77.8 | -0.017 | -0.167 | 11205 | 76.6 | 1461 | 76.2 | 2107 | 79.4 | 1434 | 86.2 |
| *Neopanorpa quadristigma* | 16272 | 78.2 | -0.01 | -0.157 | 11199 | 76.9 | 1462 | 76.5 | 2103 | 79.6 | 1489 | 87.4 |
| *Neopanorpa triangulata* | 16307 | 77.3 | -0.008 | -0.162 | 11196 | 75.6 | 1460 | 76.5 | 2100 | 79.3 | 1523 | 87.4 |
| *Panorpa chengi* | 16426 | 77.9 | 0.001 | -0.128 | 11202 | 76.4 | 1467 | 76.2 | 2114 | 79.6 | 1605 | 86.5 |
| *Panorpa curva* | 16375 | 77.2 | 0.007 | -0.147 | 11205 | 75.8 | 1482 | 76 | 2111 | 79 | 1548 | 85.2 |
| *Panorpa dispergens* | 16383 | 77.5 | 0.01 | -0.171 | 11202 | 76 | 1472 | 76 | 2115 | 78.9 | 1552 | 86.9 |
| *Panorpa fulvastra* 1 | 16279 | 77.5 | 0.002 | -0.136 | 11205 | 76.2 | 1468 | 76 | 2110 | 79.7 | 1460 | 85.7 |
| *Panorpa fulvastra* 2 | 16278 | 77.7 | 0.001 | -0.137 | 11202 | 76.4 | 1468 | 76 | 2110 | 79.8 | 1460 | 85.7 |
| *Panorpa fulvastra* 3 | 16277 | 77.6 | 0.001 | -0.135 | 11205 | 76.2 | 1468 | 76 | 2109 | 79.8 | 1460 | 85.8 |
| *Panorpa fulvastra* HDT | 16345 | 77.4 | 0.005 | -0.142 | 11193 | 75.8 | 1471 | 76.1 | 2107 | 79.7 | 1529 | 86.6 |
| *Panorpa* sp1 | 16304 | 77.9 | 0.004 | -0.145 | 11205 | 76.7 | 1467 | 76 | 2112 | 79.6 | 1491 | 86.8 |
| *Panorpa* sp2 | 16289 | 77.6 | 0.002 | -0.138 | 11205 | 76.2 | 1467 | 76.2 | 2114 | 79.7 | 1469 | 86.2 |
| *Panorpa* sp3 | 16328 | 78 | 0.002 | -0.144 | 11205 | 76.7 | 1466 | 76 | 2112 | 79.8 | 1516 | 86.8 |
| *Sinopanorpa digitiformis* 1 | 16394 | 76.8 | -0.005 | -0.157 | 11208 | 75.2 | 1484 | 76.4 | 2108 | 79 | 1511 | 84.7 |
| *Sinopanorpa digitiformis* 2 | 16399 | 76.8 | -0.005 | -0.158 | 11208 | 75.2 | 1484 | 76.4 | 2108 | 79 | 1510 | 84.6 |
| *Sinopanorpa nangongshana* 1 | 16378 | 76.8 | -0.005 | -0.159 | 11208 | 75.2 | 1479 | 76.4 | 2108 | 79.1 | 1512 | 84.6 |
| *Sinopanorpa nangongshana* 2 | 16479 | 76.8 | -0.005 | -0.159 | 11208 | 75.2 | 1479 | 76.4 | 2108 | 79 | 1637 | 84.7 |
| *Sinopanorpa nangongshana* 3 | 16358 | 76.6 | -0.005 | -0.159 | 11208 | 75.2 | 1479 | 76.4 | 2108 | 79.1 | 1512 | 84.6 |
| *Sinopanorpa tincta* | 16386 | 76.9 | -0.004 | -0.163 | 11208 | 75.5 | 1478 | 76.2 | 2110 | 78.8 | 1513 | 84.5 |
| *Cerapanorpa obtusa KX091860* | 16318 | 76.1 | 0.005 | -0.158 | 11196 | 74.6 | 1479 | 75.6 | 2112 | 78.7 | 1495 | 84.1 |
| *Neopanorpa chelata KX091857* | 16342 | 76 | -0.008 | -0.182 | 11202 | 74.2 | 1464 | 76.6 | 2100 | 78.5 | 1565 | 85.1 |
| *Neopanorpa pulchra FJ169955* | 15531 | 76.4 | -0.014 | -0.168 | 11193 | 76.2 | 1460 | 76.3 | 2134 | 78.1 | 718 | 74 |
| *Neopanorpa pulchra JX569848* | 16314 | 77.5 | -0.016 | -0.173 | 11193 | 76.3 | 1458 | 76.1 | 2102 | 78.7 | 1531 | 85.9 |
| *Panorpa debilis MK870081* | 17018 | 76.9 | -0.003 | -0.158 | 11190 | 75.2 | 1467 | 75.6 | 2108 | 79 | 2203 | 84.7 |

**Table S2:** Best partitioning scheme and models based on different datasets for Bayesian inference (BI) analysis selected by PartitionFinder.

| Dataset | Partitioning scheme | Model | Dataset | Partitioning scheme | Model |
|---|---|---|---|---|---|
| PCG | P1: *cox1*_codon1, *atp6*_codon1 | GTR+G | PCG+R | P1: *cox3*_codon1, *atp6*_codon1, *cytb*_codon1 | GTR+G |
| | P2: *cox1*_codon2, *atp6*_codon2 | GTR+I | | P2: *atp6*_codon2, *cox1*_codon2 | GTR+I |
| | P3: *cox2*_codon3, *atp6*_codon3, *cox3*_codon3, *cytb*_codon3 | GTR+I+G | | P3: *cox2*_codon3, *atp6*_codon3, *cox3*_codon3, *cytb*_codon3 | GTR+I+G |
| | P4: *atp8*_codon1, *nad3*_codon1, *nad2*_codon1 | GTR+I+G | | P4: *atp8*_codon1, *nad3*_codon1, *nad2*_codon1 | GTR+I+G |
| | P5: *atp8*_codon2 | HKY+I | | P5: *atp8*_codon2 | HKY+I |
| | P6: atp8_codon3 | GTR+G | | P6: *atp8*_codon3 | GTR+G |
| | P7: *cox3*_codon1, *cox2*_codon*1*, *cox1*_codon1 | GTR+I+G | | P7: *cox2*_codon1, *cox1*_codon1 | GTR+I+G |
| | P8: *cox1*_codon3 | GTR+G | | P8: *cox1*_codon3 | GTR+G |
| | P9: *cytb*_codon2, *cox3*_codon2, *cox2*_codon2 | GTR+I+G | | P9: *cytb*_codon2, *cox3*_codon2, *cox2*_codon2 | GTR+I+G |
| | P10: *nad4*_codon1, *nad4L*_codon1, *nad1*_codon1 *nad5*_codon1 | GTR+I+G | | P10: *nad4*_codon1, *nad5*_codon1, *nad4L*_codon1, *nad1*_codon1 | GTR+I+G |
| | P11: *nad4L*_codon2, *nad5*_codon2, *nad1*_codon2 *nad4*_codon2 | GTR+I+G | | P11: *nad4L*_codon2, *nad5*_codon2, *nad1*_codon2, *nad4*_codon2 | GTR+I+G |
| | P12: *nad1*_codon3, *nad4L*_codon3, *nad4*_codon3 *nad5*_codon3 | GTR+G | | P12: *nad4L*_codon3, *nad1*_codon3, *nad5*_codon3, *nad4*_codon3 | GTR+G |
| | P13: *nad2*_codon2, *nad3*_codon2 | HKY+I+G | | P13: *nad2*_codon2, *nad3*_codon2 | HKY+I+G |
| | P14: *nad2*_codon3 | GTR+I+G | | P14: *nad2*_codon3 | GTR+I+G |
| | P15: *nad6*_codon3, *nad3*_codon3 | GTR+G | | P15: *nad3*_codon3, *nad6*_codon3 | GTR+G |
| | P16: *nad6*_codon1 | GTR+I+G | | P16: *nad6*_codon1 | GTR+I+G |
| | P17: *nad6*_codon2 | GTR+G | | P17: *nad6*_codon2 | GTR+G |
| | | | | P18: *rrnL* | GTR+I+G |
| | | | | P19: *rrnS* | GTR+I+G |
| PCG+RT | P1: *cytb*_codon1, *atp6*_codon1 | GTR+G | PCG12+R | P1: *atp6, cytb, cox3, cox2* | GTR+I+G |
| | P2: atp6_codon2, *cox1*_codon2 | GTR+I | | P2: *nad6, atp8* | GTR+I+G |
| | P3: *cox2*_codon3, *atp6*_codon3, *cox3*_codon3, *cytb*_codon3 | GTR+I+G | | P3: *cox1* | GTR+I+G |
| | P4: *trnH*, *nad2*_codon1, *trnT, atp8*_codon1 | GTR+I+G | | P4: *nad4, nad5, nad4L, nad1* | GTR+I+G |

| | | | |
|---|---|---|---|
| P5: *atp8*_codon2, *trnG, trnW* | GTR+I | P5: *nad3, nad2* | HKY+I+G |
| P6: *atp8*_codon3 | GTR+G | P6: *rrnL* | GTR+I+G |
| P7: *cox1*_codon1 | GTR+I+G | P7: *rrnS* | GTR+I+G |
| P8: *cox1*_codon3 | GTR+G | | |
| P9: *cox2*_codon1, *cox3*_codon1 | GTR+I+G | | |
| P10: *cytb*_codon2, *cox3*_codon2, *cox2*_codon2 | GTR+I+G | | |
| P11: *nad4*_codon1, *nad5*_codon1, *trnL1, nad1*_codon1 | GTR+I+G | | |
| P12: *nad5*_codon2, *nad1*_codon2, *nad4*_codon2 | GTR+I+G | | |
| P13: *nad4L*_codon3, *nad1*_codon3, *nad5*_codon3, *nad4*_codon3 | GTR+G | | |
| P14: *nad3*_codon2, *nad2*_codon2 | HKY+I+G | | |
| P15: *nad2*_codon3 | GTR+I+G | | |
| P16: *nad3*_codon1, *trnI* | GTR+G | | |
| P17: *nad3*_codon3, *nad6*_codon3 | GTR+G | | |
| P18: *trnQ, trnV, nad4L*_codon1, *trnP, trnY* | GTR+I+G | | |
| P19: *nad4L*_codon2 | HKY+G | | |
| P20: *nad6*_codon1 | GTR+I+G | | |
| P21: *nad6*_codon2 | GTR+G | | |
| P22: *rrnL* | HKY+I+G | | |
| P23: *rrnS* | GTR+I+G | | |
| P24: *trnS1, trnL2, trnC, trnA, trnK* | HKY+I+G | | |
| P25: *trnD, trnE, trnM* | HKY+I+G | | |
| P26: *trnF, trnR, trnN, trnS2* | GTR+I+G | | |

**Table S3.** Best partitioning scheme and models based on different datasets for Maximum likelihood (ML) analysis selected by ModelFinder.

| Dataset | Partitioning scheme | Model | Dataset | Partitioning scheme | Model |
|---|---|---|---|---|---|
| PCG | P1: *cytb, atp6* | GTR+F+I+I+R4 | PCG+R | P1: *atp6, cox1, cox2, cox3, cytb, nad3* | GTR+F+I+G4 |
| | P2: *atp8* | GTR+F+I+G4 | | P2: *atp8, nad2, nad6* | K3Pu+F+I+G4 |
| | P3: *cox1, cox3* | GTR+F+I+I+R3 | | P3: *nad1, nad4L, nad4, nad5* | TIM+F+I+G4 |
| | P4: *cox2* | GTR+F+I+G4 | | P4: *rrnL, rrnS* | GTR+F+I+G4 |
| | P5: *nad1, nad4L* | TIM+F+I+I+R3 | PCG+RT | P1: *atp6, cox1, cox2, cox3, cytb* | GTR+F+I+G4 |
| | P6: *nad2* | GTR+F+I+G4 | | P2: *atp8, nad2, nad3, nad6, trnT* | TIM+F+I+G4 |
| | P7: *nad3* | GTR+F+I+G4 | | P3: *nad1, nad4L, nad4, nad5* | TIM+F+I+G4 |
| | P8: *nad4, nad5* | TIM+F+I+I+R4 | | P4: *rrnL, rrnS, trnF, trnN, trnR, trnS2, trnV* | GTR+F+I+G4 |
| | P9: *nad6* | GTR+F+I+G4 | | P5: *trnA, trnC, trnD, trnE, trnG, trnH, trnI, trnK, trnL1, trnL2, trnM, trnP, trnQ, trnS1, trnW, trnY* | TPM2u+F+I+G4 |
| PCG12+R | P1: *cytb, atp6, cox1, cox2, cox3* | TIM2+F+I+G4 | | | |
| | P2: *atp8, nad2, nad3, nad6* | TPM2u+F+I+G4 | | | |
| | P3: *nad1, nad4, nad5* | K3Pu+F+I+G4 | | | |
| | P4: *rrnL, rrnS* | GTR+F+I+G4 | | | |