

Table S1. Nucleotide composition and skewness levels calculated for sequenced majority strand of the six mitogenomes of *Monopterus albus*

| Region(s)/Genes | Size(bp) | Nucleotides Composition | | | | | | AT-Skew | GC-Skew |
|------------------------------|----------|-------------------------|------|------|------|------|------|---------|---------|
| | | A | T | G | C | A+T | G+C | | |
| MZ597543, selecting breed | | | | | | | | | |
| Whole mitogenome | 16621 | 28.9 | 27.1 | 14.5 | 29.5 | 56 | 44 | 0.032 | -0.341 |
| PCGs | 10899 | 26.5 | 28.4 | 13.5 | 31.6 | 54.9 | 45.1 | -0.034 | -0.403 |
| 1st condon positions | 3633 | 28.5 | 21.4 | 22.2 | 27.9 | 49.9 | 50.1 | 0.141 | -0.113 |
| 2nd condon positions | 3633 | 28.1 | 40.3 | 18.9 | 12.7 | 59.2 | 40.8 | -0.362 | -0.379 |
| 3rd condon positions | 3633 | 32.2 | 23.5 | 5.5 | 38.9 | 55.7 | 44.4 | 0.157 | -0.753 |
| tRNAs | 983 | 32 | 27.1 | 18.1 | 22.8 | 59.1 | 40.9 | 0.084 | -0.114 |
| rRNAs | 2621 | 34.4 | 22.6 | 18.6 | 24.4 | 57 | 43 | 0.206 | -0.136 |
| KP779622.1, Guizhou province | | | | | | | | | |
| Whole mitogenome | 16622 | 28.8 | 27.2 | 14.5 | 29.5 | 56 | 44 | 0.029 | -0.342 |
| PCGs | 10902 | 26.5 | 28.5 | 13.4 | 31.6 | 55 | 45 | -0.038 | -0.405 |
| 1st condon positions | 3634 | 28.5 | 21.6 | 22 | 27.9 | 50.1 | 49.9 | 0.137 | -0.12 |
| 2nd condon positions | 3634 | 19.1 | 40.1 | 12.6 | 28.2 | 59.2 | 40.8 | -0.355 | -0.382 |
| 3rd condon positions | 3634 | 31.8 | 23.9 | 5.6 | 38.7 | 55.7 | 44.3 | 0.142 | -0.748 |
| tRNAs | 985 | 32.3 | 27 | 18 | 22.7 | 59.3 | 40.7 | 0.089 | -0.117 |
| rRNAs | 2625 | 34.4 | 22.6 | 18.5 | 24.5 | 57 | 43 | 0.206 | -0.138 |
| KP779623.1, Guangxi province | | | | | | | | | |
| Whole mitogenome | 16622 | 28.9 | 27.1 | 14.5 | 29.4 | 56 | 43.9 | 0.032 | -0.339 |
| PCGs | 10902 | 26.6 | 28.4 | 13.5 | 31.4 | 55 | 44.9 | -0.033 | -0.398 |
| 1st condon positions | 3634 | 28.7 | 21.5 | 22.2 | 27.6 | 50.2 | 49.8 | 0.145 | -0.107 |
| 2nd condon positions | 3634 | 19 | 40.3 | 12.7 | 28 | 59.3 | 40.7 | -0.36 | -0.376 |
| 3rd condon positions | 3634 | 32.1 | 23.4 | 5.7 | 38.7 | 55.5 | 44.4 | 0.156 | -0.743 |
| tRNAs | 983 | 32.1 | 27.1 | 18 | 22.8 | 59.2 | 40.8 | 0.086 | -0.117 |
| rRNAs | 2622 | 34.3 | 22.6 | 18.3 | 24.8 | 56.9 | 43.1 | 0.206 | -0.15 |
| KP779624.1, Hunan province | | | | | | | | | |
| Full genome | 16622 | 28.8 | 27.2 | 14.5 | 29.5 | 56 | 44 | 0.028 | -0.342 |
| PCGs | 10902 | 26.4 | 28.6 | 13.5 | 31.6 | 55 | 45.1 | -0.04 | -0.402 |
| 1st codon position | 3634 | 28.2 | 22 | 21.9 | 27.9 | 50.2 | 49.8 | 0.124 | -0.121 |

| | | | | | | | | | |
|--------------------------------|-------|------|------|------|------|------|------|--------|--------|
| 2nd codon position | 3634 | 19.1 | 40 | 12.6 | 28.4 | 59.1 | 41 | -0.354 | -0.386 |
| 3rd codon position | 3634 | 31.9 | 23.8 | 6 | 38.4 | 55.7 | 44.4 | 0.146 | -0.731 |
| tRNAs | 983 | 32 | 27.2 | 18 | 22.8 | 59.2 | 40.8 | 0.082 | -0.117 |
| rRNAs | 2622 | 34.5 | 22.6 | 18.3 | 24.6 | 57.1 | 42.9 | 0.209 | -0.146 |
| KP779625.1, Guangdong province | | | | | | | | | |
| Full genome | 16622 | 28.9 | 27.2 | 14.6 | 29.4 | 56.1 | 44 | 0.03 | -0.337 |
| PCGs | 10902 | 26.5 | 28.5 | 13.6 | 31.4 | 55 | 45 | -0.037 | -0.396 |
| 1st codon position | 3634 | 28.6 | 21.5 | 22.1 | 27.8 | 50.1 | 49.9 | 0.143 | -0.116 |
| 2nd codon position | 3634 | 18.9 | 40.2 | 12.9 | 28 | 59.1 | 40.9 | -0.361 | -0.368 |
| 3rd codon position | 3634 | 32 | 23.8 | 5.8 | 38.4 | 55.8 | 44.2 | 0.146 | -0.74 |
| tRNAs | 983 | 32.3 | 26.9 | 18 | 22.8 | 59.2 | 40.8 | 0.093 | -0.117 |
| rRNAs | 2622 | 34.4 | 22.6 | 18.5 | 24.6 | 57 | 43.1 | 0.207 | -0.141 |
| NC_003192.1, unknown | | | | | | | | | |
| Full genome | 16622 | 28.9 | 27.2 | 14.5 | 29.5 | 56.1 | 44 | 0.031 | -0.341 |
| PCGs | 10899 | 26.5 | 28.5 | 13.4 | 31.6 | 55 | 45 | -0.036 | -0.403 |
| 1st codon position | 3633 | 28.5 | 21.5 | 22.2 | 27.8 | 50 | 50 | 0.139 | -0.111 |
| 2nd codon position | 3633 | 18.9 | 40.3 | 12.7 | 28.1 | 59.2 | 40.8 | -0.362 | -0.378 |
| 3rd codon position | 3633 | 32.1 | 23.6 | 5.4 | 38.8 | 55.7 | 44.2 | 0.153 | -0.755 |
| tRNAs | 983 | 32.1 | 27.1 | 18 | 22.8 | 59.2 | 40.8 | 0.086 | -0.117 |
| rRNAs | 2622 | 34.4 | 22.5 | 18.5 | 24.5 | 56.9 | 43 | 0.209 | -0.14 |