

Supplementary Fig. 1. Secondary structure inferred with tRNA-Scan [33] from *trnW₁* and *trnW₂* gene sequences of the southern elephant seal louse, *Lepidophthirus macrorhini*.

AT-rich (56 bp; 80.3%)

| | |
|--------------------|---|
| <i>Q-nad1-T-W</i> | ATAGCACTRAGATAGGAAATTTAACATAAAGGTTAAAATTTTTACAAATTA |
| <i>nad2</i> | ATAGCACTAAGATAGGAAATTTAACATAAAGGTTAAAATTTTTACAAATTA |
| <i>I-cox1-L1</i> | ACATCA--GGGTTAAGAATACTAGCACGAAATTGGATTTTTTTACAAATTA |
| <i>M-cox2</i> | ATAGCACTGAGATAGGAAATTTAACATAAAGGTTAAAATTTTTACAAATTA |
| <i>H-nad5-W</i> | ATAGCACTRAGATAGGAAATTTAACATAAAGGTTAAAATTTTTACAAATTA |
| <i>P-cox3-A</i> | ATAGCACTGAGATAGGAAATTTAACATAAAGGTTAAAATTTTTACAAATTA |
| <i>E-cob</i> | ATAGCACTRAGATAGGAAATTTAACATAAAGGTTAAAATTTTTACAAATTA |
| <i>atp8-atp6-N</i> | ATAGCACTRAGATAGGAAATTTAACATAAAGGTTAAAATTTTTACAAATTA |
| <i>K-nad4</i> | ATAGCACTAAGATAGGAAATTTAACATAAAGGTTAAAATTTTTACAAATTA |
| <i>Y-F</i> | TAGCACTAAGATAGGAAATTTAACATAAAGGTTAAAATTTTTACAAATTA |
| <i>rrnS-D</i> | ATAGCACTAAGATAGGAAATTTAACATAAAGGTTAAAATTTTTACAAATTA |
| <i>L2-rrnL-V</i> | ATAGCACTAAGATAGGAAATTTAACATAAAGGTTAAAATTTTTACAAATTA |

GC-rich (63 bp; 60.7%)

| | |
|--------------------|--|
| <i>Q-nad1-T-W</i> | CCTCCCCAAATAGG-GCATTITTTATGCTTTTATTTGGGGGGGGTAAGGGGGGGGCCCCCATAACCC |
| <i>nad2</i> | CCTCTCCAAATTGGAGCATTITTAATGCTTTAATTTGGGGGGGGTAAGGGGGGGGCCCCCATAACCC |
| <i>I-cox1-L1</i> | CTCTCCCCAAATAGG-GCATTITTTATGCTTTTATTTGGGGGGGGTAAGGGGGGGGCCCCCATAACCC |
| <i>M-cox2</i> | CCTCCCCAAATAGG-GCATTITTTATGCTTTTATTTGGGGGGGGTAAGGGGGGGGCCCCCATAACCC |
| <i>H-nad5-W</i> | CCTCTCCAAATTGGAGCATTITTAATGCTTTAATTTGGGGGGGGTAAGGGGGGGGCCCCCATAACCC |
| <i>P-cox3-A</i> | CCTCCCCAAATAGG-GCATTITTTATGCTTTTATTTGGGGGGGGTAAGGGGGGGGCCCCCATAACCC |
| <i>E-cob</i> | CTCTCCCCAAATAGG-GCATTITTTATGCTTTTATTTGGGGGGGGTAAGGGGGGGGCCCCCATAACCC |
| <i>atp8-atp6-N</i> | TCCTCTCCAAATTGGAGCATTITTAATGCTTTAATTTGGGGGGGGTAAGGGGGGGGCCCCCATAACCC |
| <i>K-nad4</i> | CCTCTCCAAATTGGAGCATTITTAATGCTTTAATTTGGGGGGGGTAAGGGGGGGGCCCCCATAACCC |
| <i>Y-F</i> | CTCTCTCCAAATTGGAGCATTITTTATGCTTTAATTTGGGGGGGGTAAGGGGGGGGCCCCCATAACCC |
| <i>rrnS-D</i> | CTCTCTCCAAATTGGAGCATTITTAATGCTTTAATTTGGGGGGGGTAAGGGGGGGGCCCCCATAACCC |
| <i>L2-rrnL-V</i> | CTCTCCCCAAATAGG-GCATTITTTATGCTTTTATTTGGGGGGGGTAAGGGGGGGGCCCCCATAACCC |

Supplementary Fig. 2. Conserved non-coding AT-rich motifs and GC-rich motifs among the mitochondrial minichromosomes of the southern elephant seal louse, *Lepidophthirus macrorhini*.

AT-rich (85 bp; 71.8%)

E-cob
Q-nad1-T
P-cox3
cox2
K-nad4
nad2
H-nad5
G-nad3-W
I-cox1
rrnS-S2-R-C

TATAGAGTTTATAGTAGGTTCCCTATAGAAATTCCTAGTAGGAAGGTGCAATTTTGCAAAAATCACACACATTTWATACACTTTTTT
TATAGAGTTTATAGTAGGTTCCCTATAGAAATTCCTAGTAGGAAGGTGCAATTTTGCAAAAATCACACACATTTAATACACTTTTTT
TATAGAGTTTATAGTAGGTTCCCTATAGAAATTCCTAGTAGGAAGATGCAATTTTACAAAAATAACATACATTTTATACACTTTTTT
TATAGAGTTTATAGTAGGTTCCCTATAGAAATTCCTAGTAGGAAGGTGCAATTTTGCAAAAATCACACACATTTTATACACTTTTTT
TATAGAGTTTATAGTAGGTTCCCTATAGAAATTCCTAGTAGGAAGGTGCAATTTTGCAAAAATCACACACATTTAATACACTTTTTT
TATAGAGTTTATAGTAGGTTCCCTATAGAAATTCCTAGTAGGAAGGTGCAATTTTGCAAAAATCACACACATTTTATACACTTTTTT
TATAGACTTTTATAGTAGGTTCCGTATAGAAATTCCTAGTAGGAAGATGCAATTTTACAAAAATAACATACATTTTATACACTTTTTT
TATAGAGTTTATAGTAGGTTCCCTATAGAAATTCCTAGTAGGAAGGTGCAATTTTGCAAAAATCACACACATTTAATACACTTTTTT
TATAGAGTTTATAGTAGGTTCCCTATAGAAATTCCTAGTAGGAAGGTGCAATTTTGCAAAAATCACACACATTTAATACACTTTTTT

GC-rich (81 bp; 61.7%)

E-cob
Q-nad1-T
P-cox3
cox2
K-nad4
nad2
H-nad5
G-nad3-W
I-cox1
rrnS-S2-R-C

CCCCAGGAGGTGGACGTCTGTCCCTCCTGGGGGGGGTAGGGGGGGGTCGAATAAATACTCCCCGATATACTCCCCAGAG
CCCCAAGAGGTTGACGTAAGTCCCTCTTGGGGGGGGTAGGGGGGGGTCGAATAAATACTCCCCGATATACTCCCCAGAG
CCCCAAGAGGTTGACGTAAGTCCCTCTTGGGGGGGGTAGGGGGGGGTCGAATAAATACTCCCCGATATACTCCCCAGAG
CCCCAGGAGGTGGACGTCTGTCCCTCCTGGGGGGGGTAGGGGGGGGTCGAATAAATACTCCCCGATATACTCCCCAGAG
CCCCAAGAGGTTGACGTAAGTCCCTCTTGGGGGGGGTAGGGGGGGGTCGAATAAATACTCCCCGATATACTCCCCAGAG
CCCCAAGAGGTTGACGTAAGTCCCTCTTGGGGGGGGTAGGGGGGGGTCGAATAAATACTCCCCGATATACTCCCCAGAG
CCCCAAGAGGTTGACGTAAGTCCCTCTTGGGGGGGGTAGGGGGGGGTCGAATAAATACTCCCCGATATACTCCCCAGAG
CCCCAAGAGGTTGACGTAAGTCCCTCTTGGGGGGGGTAGGGGGGGGTCGAATAAATACTCCCCGATATACTCCCCAGAG
CCCCAGGAGGTGGACGTCTGTCCCTCCTGGGGGGGGTAGGGGGGGGTCGAATAAATACTCCCCGATATACTCCCCAGAG
CCCCAGGAGGTGGACGTCTGTCCCTCCTGGGGGGGGTAGGGGGGGGTCGAATAAATACTCCCCGATATACTCCCCAGAG

Supplementary Fig. 3. Conserved non-coding AT-rich motifs and GC-rich motifs among the mitochondrial minichromosomes of the northern fur seal louse, *Proechinophthirus fluctus*.

AT-rich (60 bp; 60%)

| | |
|-------------------|--|
| <i>atp8-atp6</i> | AGGGGGGAAAAATCCCCCGAAACCAAGGGTTTTTTTGGGTTTTTAAACTC |
| <i>H-nad5</i> | AGGGGGGAAAAATCCCCCGAAACCAAGGGTTTTTTTGGGTTTTTAAACTC |
| <i>Q-nad1-T</i> | AGGGGGGAAAAACAGCCCGAAACCGGAGTTTTTTTGGTTTTTAAACTC |
| <i>K-nad4</i> | AGGGGGGAAAAATCCCCCGAAACCAAGGGTTTTTTTGGGTTTTTAAACTC |
| <i>Y-cox2-N</i> | AGGGGGGAAAAATCCCCCGAAACCAAGGGTTTTTTTGGGTTTTTAAACTC |
| <i>I-cox1-A</i> | AGGGGGGAAAAATCCCCCGAAACCAAGGGTTTTTTTGGGTTTTTAAACTC |
| <i>nad2</i> | AGGGGGGAAAAATCCCCCGAAACCAAGGGTTTTTTTGGGTTTTTAAACTC |
| <i>E-cob</i> | AGGGGGGAAAAATCCCCCGAAACCAAGGGTTTTTTTGGGTTTTTAAACTC |
| <i>S2-R-nad4L</i> | AGGGGGGAAAAATCCCCCGAAACCAAGGGTTTTTTTGGGTTTTTAAACTC |
| <i>P-cox3</i> | AGGGGGGAAAAATCCCCCGAAACCAAGGGTTTTTTTGGGTTTTTAAACTC |
| <i>G-nad3-W</i> | AGGGGGGAAAAATCCCCCGAAACCAAGGGTTTTTTTGGGTTTTTAAACTC |
| <i>L2-rrnL</i> | AGGGGGGAAAAATCCCCCGAAACCAAGGGTTTTTTTGGGTTTTTAAACTC |
| <i>rrnS-L1</i> | AGGGGGGAAAAATCCCCCGAAACCAAGGGTTTTTTTGGGTTTTTAAACTC |

AT-rich (46 bp; 67.4%)

| | |
|-------------------|---|
| <i>atp8-atp6</i> | CCTCAAGAGGT-GACCTTGTTGCCCT--CTTGGGGGGGG--AAGGGGGGGGG-AGA |
| <i>H-nad5</i> | CCTCAAGAGGT-GAC-GCATGTTGCCCT--CTTGGGGGGGG--AAGGGGGGGGG-AGA |
| <i>Q-nad1-T</i> | CCCCAAGAGGTTGACCTTGTTGCCCT--CTTGGGGGGGG--TAGGGGGGGGGCAG- |
| <i>K-nad4</i> | CTCCAAG-GGA-C AATTTCTGTTGTTTCCCTTGGGGGGGGGTAAAGGGGGGGGG-TGT |
| <i>Y-cox2-N</i> | CCTCAAGAGGT-GA-C TTTTGTGCCCT--CTTGGGGGGGG--AAGGGGGGGGGCAG- |
| <i>I-cox1-A</i> | CCCCAAGAGGTTGACCTTGTTGCCCT--CTTGGGGGGGGGAGGGGGGGGGTAAAT |
| <i>nad2</i> | CCCCAAGAGGTTGACCTTGTTGCCCT--CTTGGGGGGGG--TAGGGGGGGGGCAG- |
| <i>E-cob</i> | CCCCAAGAGGTTGA-C TTTTGTGCCCT--CTTGGGGGGGG--AAGGGGGGGGGCATT |
| <i>S2-R-nad4L</i> | CCCCAAGAGGTTGACCTTGTTGCCCT--CTTGGGGGGGG--AAGGGGGGGGGCAGT |
| <i>P-cox3</i> | CCTCAAGAGGT-GA-C TTTTGTGCCCT--CTTGGGGGGGG--AAGGGGGGGGG-- |
| <i>G-nad3-W</i> | CTCCAAG-GGAAC AATTTCTGTTGTTTCCCTTGGGGGGGGGTAAAGGGGGGGGG-TGT |
| <i>L2-rrnL</i> | CCCCAAGAGGTTGA-C TTTTGTGCCCT--CTTGGGGGGGG--AAGGGGGGGGG-AGA |
| <i>rrnS-L1</i> | CCCCAAGAGGTTGACCTTGTTGCCCT--CTTGGGGGGGG--AAGGGGGGGGGCAGT |

Supplementary Fig. 4. Conserved non-coding AT-rich motifs and GC-rich motifs among the mitochondrial minichromosomes of the Weddell seal louse, *Antarctophthirus carlinii*.

AT-rich (65 bp; 68.7%)

atp8-atp6
H-nad5
Q-nad1-T
K-nad4
Y-cox2-N
I-cox1-A
nad2
E-cob
S2-R-nad4L
P-cox3
G-nad3-W
L2-rrnL
rrnS-L1

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TTTTTCCTATAAGTGGTTTTTTGTCATAAAGTAATCCA-TTAAGAGTGGCCAAATTTGACAAAAAA
TTTTTCCTATAAGTGGTTTTTTGTCAGATAAAGTAATCCA-TTAAGAGTGGTCGAATTTGACAAAAAA
TTTTTACTATAGCACATTTCTTGTCATAATATGG-ATCCACTTAAGAGTGGTCAAATCGACAAAAAAT
TTTTTCCTATAACACATTTCTTCTCAGATATGG-ATCCACTTAAGAGTGGTAGTTTTCCTCATTTTTTT
TTTTTACTATAGCACATTTTTTTGTCAGATATGGAATCCA-TTAAGAGAGGCCATTTTGACAAAAATA
TTTTTACTATAGCACATTTCTTGTCATAATATGG-ATCCACTTAAGAGTGGTCAAATCGACAAAAAAT
TTTTTCCTATAAGCGGTTTTTTGTCAGATATGGAATCCA-TTAAGAGAGGCCATTTTGACAAAAATA
TTTTTACTATAGCACATTTTTTTGTCAGATATGGAATCCA-TTAAGAGAGGCCATTTTGACAAAAATA
TTTTTCCTATAAGTGGTTTTTTGTCAGATAAAGTAATCCA-TTAAGAGTGGTCGAATTTGACAAAAAA
TTTTTCCTATAAGTGGTTTTTTGTCATAAAGTAATCCA-TTAAGAGTGGCCAAATTTGACAAAAAA
TTTTTACTATAGCACATTTTTTTGTCAGATATGGAATCCA-TTAAGAGAGGCCATTTTGACAAAAATA
TTTTTCCTATAAGTGGTTTTTTGTCATAAAGTAATCCA-TTAAGAGTGGCCAAATTTGACAAAAAA
TTTTTCCTATAAGTGGTTTTTTGTCAGATAAAGTAATCCA-TTAAGAGTGGTCGAATTTGACAAAAAA
TTTTTCCTATAAGTGGTTTTTTGTCAGATAAAGTAATCCA-TTAAGAGTGGTCGAATTTGACAAAAAA

```

GC-rich (37 bp; 64.9%)

atp8-atp6
H-nad5
Q-nad1-T
K-nad4
Y-cox2-N
I-cox1-A
nad2
E-cob
S2-R-nad4L
P-cox3
G-nad3-W
L2-rrnL
rrnS-L1

```

GGGACAAATTTCTGTTGTTCCTTGGGGGGGGGTAAAGGGGGGGGG
GGTTGACCTTTGTGTCCCT--CTTGGGGGGGGGT--AGGGGGGGGG
GG-ACAATTTCTGTTGTTCCTTGGGGGGGGGTAAAGGGGGGGGG
GG-TGA-CGCATGTCCCT--CTTGGGGGGGGGT--AAGGGGGGGGG
GGTTGACCTTTGTGTCCCT--CTTGGGGGGGGGT--AGGGGGGGGG
GGTTGACCTTTGTGTCCCT--CTTGGGGGGGGGT--AGGGGGGGGG
GGTTGA-CTTTTGTCCCT--CTTGGGGGGGGGT--AAGGGGGGGGG
GGTTGA-CTTTTGTCCCT--CTTGGGGGGGGGT--AAGGGGGGGGG
GG-TGA-CTTTTGTCCCT--CTTGGGGGGGGGT--AAGGGGGGGGG
GGAACAAATTTCTGTTGTTCCTTGGGGGGGGGTAAAGGGGGGGGG
GGT-GA-CTTTTGTCCCT--CTTGGGGGGGGGT--AAGGGGGGGGG
GGTTGA-CTTTTGTCCCT--CTTGGGGGGGGGT--AAGGGGGGGGG
GGT-GA-CGCATGTCCCT--CTTGGGGGGGGGT--AAGGGGGGGGG

```

Supplementary Fig. 5. Conserved non-coding AT-rich motifs and GC-rich motifs among the mitochondrial minichromosomes of the crabeater seal louse, *Antarctophthirus lobodontis*.

GC-rich (26 bp; 69.2%)

| | |
|---------------|---|
| <i>nad2</i> | TTTACCCCCCTGGGTTTTGACCCAGGAGGG--AAAAAACCCC-CTA-CTAATT |
| <i>K-nad4</i> | TTTACCCCCCTGGGTTCTGACCCAGGAGGGA-AAAAACCCC-CTA-CTAATT |
| <i>rrnL-R</i> | TTACCCCCCCTGGGTTTTGACCCAGGAGGGAAAAAACCCC-CTA-CTAATT |
| <i>I-cox1</i> | TTTACCCCCCTGGGTTCTGACCCAGGAGGG--AAAAACCCC-CTA-CTAATT |
| <i>nad3-W</i> | TTTACCCCCCTGGGTTTTGACCCAG--GGGATATAAACCCCCTCTA-CTACTT |

Supplementary Fig. 6. Conserved non-coding GC-rich motifs among the mitochondrial minichromosomes of the Australian sea lion louse, *Antarctophthirus microchir*.

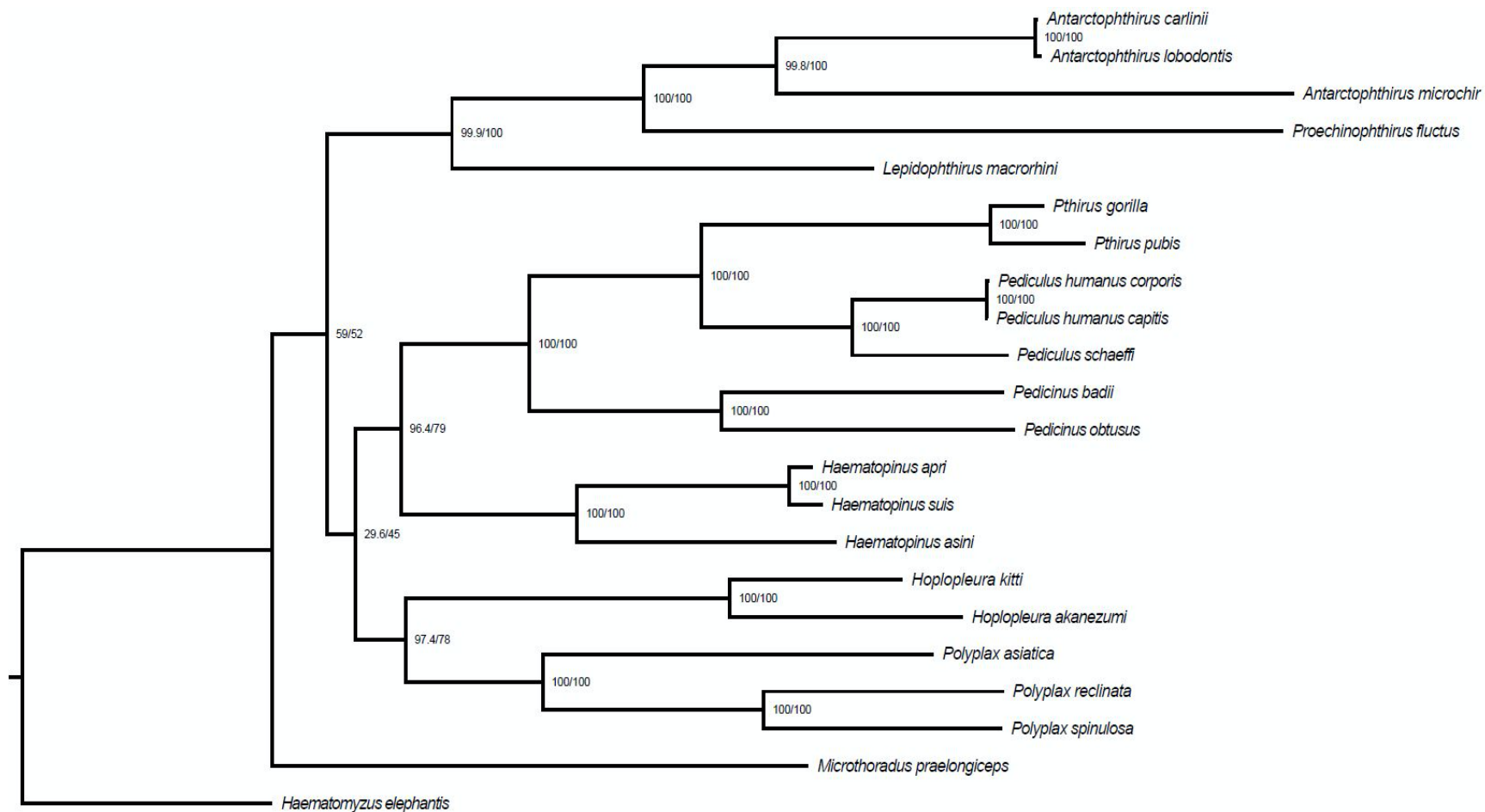
AT-rich (96 bp; 76.6% AT)

| | |
|------------------------|---|
| <i>F-T-D-H-R-nad4L</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>F-nad6-E-M</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>L1-12S</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>cob-S1</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>P-nad2-1</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>K-nad4</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>atp8-atp6</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>G-nad3-V-W-S2</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>Y-cox2</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>cox1</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>nad5</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>Lz-16S</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>nad1-Q</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |
| <i>cox3</i> | AAAACTTTAATTCATTTTTTGACCCTTGCACGTTAAACCTATGTAAACAGCATGGTTTTTTTTTAAATTTAGTTACTTATTTAAAAAAACATATG |

GC-rich (25 bp, 76% GC)

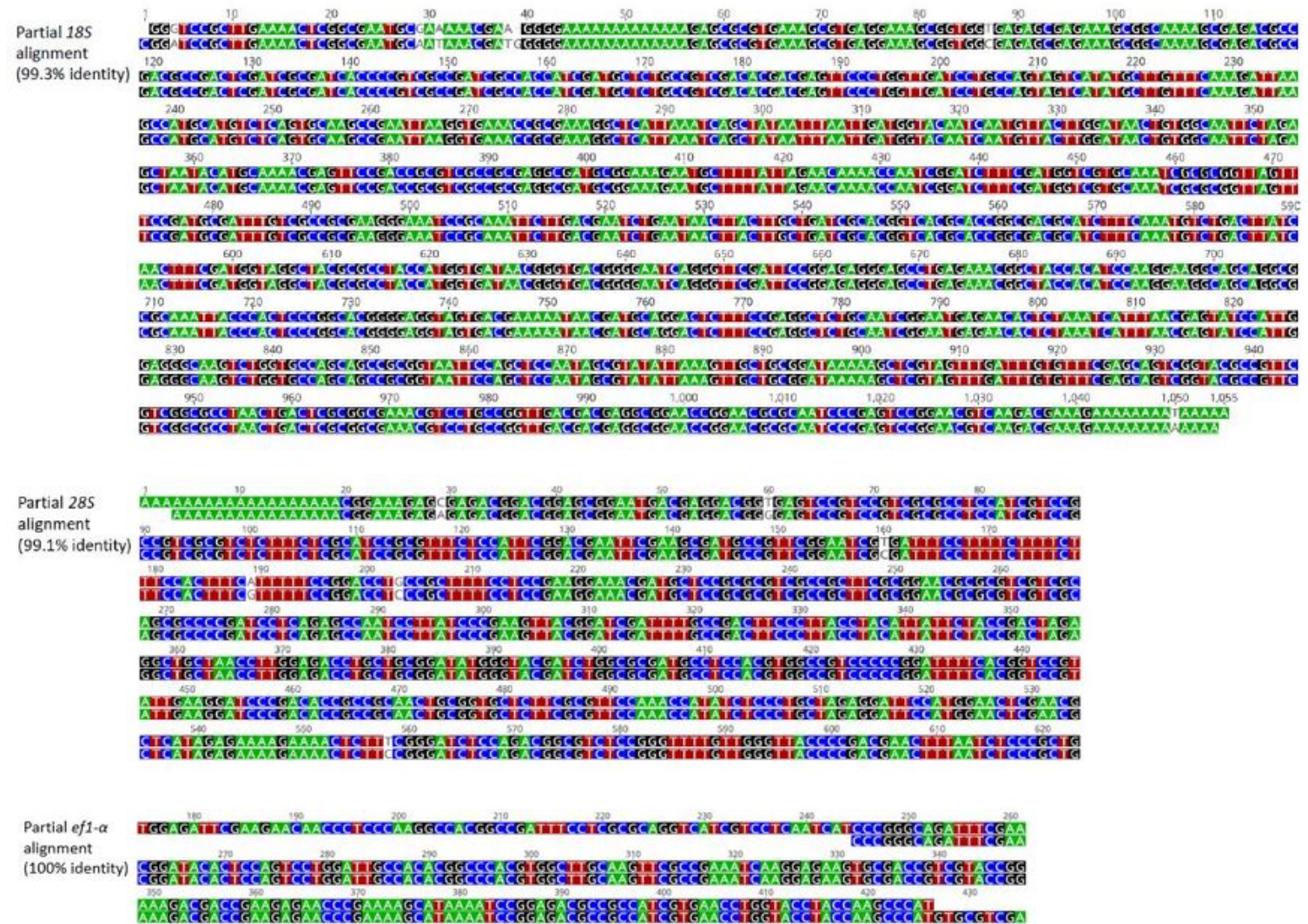
| | |
|------------------------|---|
| A | TATT-CC-CCTTTGGGGGGGGGAAGGGGGGGG |
| <i>F-T-D-H-R-nad4L</i> | TAATTTT-CCTTT-GGGGGGGGAAGGGGGGGGCCCCC |
| <i>F-nad6-E-M</i> | TATTTCC-CCTTT-GGGGGGGGAAGG-GGGGGGCCCCCTATCCC |
| <i>L1-12S</i> | TATTTCC-CCTTT-GGGGGGGGAAGGGGGGGGCCCCCTATCCC |
| <i>cob-S1</i> | TATTTTC-CCTTT-GGGGGGGGAAGG-GGGGGGCCCCCTATCCC |
| <i>P-nad2-1</i> | TAATTTT-CCTTT-GGGGGGGGAAGG-GGGGGGCCCCCTATCCC |
| <i>K-nad4</i> | TTTC-CCTTT-GGGGGGGGAAGG-GGGGGGCCCCCTATCCC |
| <i>atp8-atp6</i> | TATTTTC-CCTTT-GGGGGGGGAARGGGGGGGGGCCCC |
| <i>G-nad3-V-W-S2</i> | TATTTTC-CCTTT-GGGGGGGGAAGGGGGGGGCCCCC |
| <i>Y-cox2</i> | TATTTCC-CCTTT-GGGGGGGGAAGGGGGGGGCCCCCTATCCC |
| C | TAATTTTCTCCCTTTGGGGGGGG-AGGGGGGGGGGCCCCC |
| <i>cox1</i> | TTATTTT-CCTTT-GGGGGGGGAAGGGGGGGGSCCCC |
| <i>nad5</i> | TTTC-CCTTT-GGGGGGGGAAGG-GGGGGGCCCCCTATCCC |
| <i>Lz-16S</i> | TATTTCC-CCTTT-GGGGGGGGAAGGGGGGGGCCCCCTATCCC |
| <i>nad1-Q</i> | TTATTTT-CCTTT-GGGGGGGGAAGGGGGGGGGGCCCCCTATCCC |
| <i>cox3</i> | TAATTTT-CCTTT-GGGGGGGGAAGG-GGGGGGCCCCCTATCCC |

Supplementary Fig. 7. Conserved non-coding AT-rich motifs and GC-rich motifs among the mitochondrial minichromosomes of the gorilla louse, *Pthirus gorillae*.



0.01

Supplementary Fig. 8. Phylogenetic relationships among 21 species of sucking lice (Anoplura) inferred by maximum likelihood (ML) analysis of nucleotide sequences of five mitochondrial protein-coding genes. The elephant louse, *Haematomyzus elephantis*, was used as the outgroup. The ultrafast bootstrap support (%) / SH-aLRT support (%) were indicated near each node.



Supplementary Fig. 9. Alignment of partial 18S rRNA gene, 28S rRNA gene and *ef1-α* gene sequences between *Antarctophthirus carlinii* and *Antarctophthirus lobodontis*.

Supplementary Table 1. Mitochondrial minichromosomes of *Lepidophthirus macrorhini* - louse of southern elephant seal (*Mirounga leonine*)

| Minichromosome | Coding region size (bp) | Individual gene size (bp) | Assembled upstream non-coding region size (bp) | Assembled downstream non-coding region size (bp) | Number of Illumina sequence-reads | Mean coverage |
|--------------------|-------------------------|---------------------------|--|--|-----------------------------------|---------------|
| <i>atp8-atp6-N</i> | 937 | 189-675-70 | 300 | 300 | 27366 | 1900 |
| <i>E-cob</i> | 1152 | 63-1089 | 300 | 300 | 23907 | 1720 |
| <i>I-cox1-L1</i> | 1668 | 66-1536-65 | 300 | 300 | 37607 | 2232 |
| <i>M-cox2</i> | 820 | 67-699 | 300 | 300 | 21714 | 2023 |
| <i>P-cox3-A</i> | 921 | 67-786-66 | 300 | 300 | 29089 | 2553 |
| <i>Q-nad1-T-W1</i> | 1152 | 67-64-921-68 | 300 | 300 | 60472 | 3586 |
| <i>nad2</i> | 1114 | 1047 | 300 | 300 | 71155 | 5801 |
| <i>K-nad4</i> | 1395 | 69-1326 | 300 | 293 | 53047 | 3752 |
| <i>H-nad5-W2</i> | 1891 | 66-1539-70 | 300 | 170 | 22603 | 1434 |
| <i>L2-rrnL-V</i> | 1276 | 71-1139-66 | 300 | 273 | 75116 | 5679 |
| <i>rrnS-D</i> | 848 | 781-67 | 300 | 300 | 45830 | 4741 |

Supplementary Table 2. Sequence identities between *trnW*₁ and *trnW*₂ of the southern elephant seal louse, *Lepidophthirus macrorhini*, between *trnW* genes of *Lepidophthirus macrorhini* and other seal lice, and between *trnW* genes and other tRNA genes of *Lepidophthirus macrorhini*. Identities were generated with ClustalW in Geneious [29]: cost matrix IUB, gap open cost 15, gap extend cost 6.66.

| | <i>trnW</i> ₁ | <i>trnW</i> ₂ |
|--|--------------------------|--------------------------|
| <i>trnW</i> ₂ | 50% | |
| <i>trnW</i> (<i>Antarctophthirus carlinii</i>) | 68.7% | 55.1% |
| <i>trnW</i> (<i>Antarctophthirus lobodontis</i>) | 68.7% | 55.1% |
| <i>trnW</i> (<i>Antarctophthirus microchir</i>) | 69.1% | 42.6% |
| <i>trnW</i> (<i>Proechinophthirus fluctus</i>) | 55.4% | 48.5% |
| <i>trnA</i> | 44.8% | 44.8% |
| <i>trnD</i> | 50.7% | 50% |
| <i>trnE</i> | 48.4% | 50.9% |
| <i>trnH</i> | 50% | 48.5% |
| <i>trnI</i> | 47.8% | 47.8% |
| <i>trnK</i> | 50.7% | 53.6% |
| <i>trnL</i> ₁ | 46.9% | 52.2% |
| <i>trnL</i> ₂ | 49.2% | 43.7% |
| <i>trnM</i> | 51.5% | 42.6% |
| <i>trnN</i> | 50.7% | 53.5% |
| <i>trnP</i> | 48.5% | 38.8% |
| <i>trnQ</i> | 51.5% | 49.3% |
| <i>trnT</i> | 50% | 50% |
| <i>trnV</i> | 52.2% | 47.1% |

Supplementary Table 3. Mitochondrial minichromosomes of *Proechinophthirus fluctus* - louse of northern fur seal (*Callorhinus ursinus*)

| Minichromosome | Coding region size (bp) | Individual gene size (bp) | Assembled upstream non-coding region size (bp) | Assembled downstream non-coding region size (bp) | Number of Illumina sequence-reads | Mean coverage |
|-------------------------------------|-------------------------|---------------------------|--|--|-----------------------------------|---------------|
| <i>E-cob</i> | 1156 | 64-1092 | 200 | 200 | 23212 | 1495 |
| <i>I-cox1</i> | 1598 | 73-1503 | 200 | 200 | 26228 | 1314 |
| <i>cox2</i> | 765 | 765 | 200 | 264 | 24242 | 1997 |
| <i>P-cox3</i> | 849 | 67-783 | 200 | 200 | 22441 | 813 |
| <u><i>Q-nad1-T</i></u> | 1042 | 66-910-67 | 200 | 149 | 13414 | 915 |
| <i>nad2</i> | 1029 | 1029 | 200 | 200 | 34297 | 1370 |
| <i>G-nad3-W</i> | 481 | 67-345-65 | 200 | 200 | 4011 | 763 |
| <i>K-nad4</i> | 1379 | 70-1308 | 200 | 200 | 23312 | 1321 |
| <i>H-nad5</i> | 1739 | 60-1680 | 200 | 200 | 12873 | 631 |
| <i>rrnS-S₂-R-nad4L-C</i> | 1249 | 772-68-63-65 | 200 | 253 | 30866 | 1840 |

Supplementary Table 4. Mitochondrial minichromosomes of *Antarctophthirus carlinii* - louse of Weddell seal (*Leptonychotes weddelli*)

| Minichromosome | Coding region size (bp) | Individual gene size (bp) | Assembled upstream non-coding region size (bp) | Assembled downstream non-coding region size (bp) | Number of Illumina sequence-reads | Mean coverage |
|-------------------|-------------------------|---------------------------|--|--|-----------------------------------|---------------|
| <i>atp8-atp6</i> | 829 | 151-672 | 300 | 300 | 21419 | 1840 |
| <i>E-cob</i> | 1157 | 65-1092 | 300 | 297 | 11440 | 1063 |
| <i>I-cox1-A</i> | 1670 | 66-1539-64 | 300 | 300 | 18669 | 1283 |
| <i>Y-cox2-N</i> | 805 | 65-674-65 | 300 | 300 | 8032 | 919 |
| <i>P-cox3</i> | 848 | 62-786 | 300 | 241 | 13456 | 1488 |
| <i>Q-nad1-T</i> | 1040 | 68-903-68 | 300 | 300 | 12074 | 1173 |
| <i>nad2</i> | 1056 | 1056 | 300 | 300 | 11297 | 1083 |
| <i>G-nad3-W</i> | 529 | 69-345-72 | 300 | 300 | 17009 | 1864 |
| <i>K-nad4</i> | 1373 | 67-1305 | 300 | 300 | 13739 | 1095 |
| <i>H-nad5</i> | 1756 | 70-1681 | 300 | 300 | 16301 | 1077 |
| <i>S2-R-nad4L</i> | 420 | 70-69-279 | 300 | 300 | 8957 | 1098 |
| <i>L2-rrnL</i> | 1421 | 64-1357 | 300 | 300 | 28669 | 1779 |
| <i>rrnS-L1</i> | 908 | 839-69 | 300 | 300 | 19927 | 1858 |

Supplementary Table 5. Mitochondrial minichromosomes of *Antarctophthirus lobodontis* - louse of crabeater seal (*Lobodon carcinophagus*)

| Minichromosome | Coding region size (bp) | Individual gene size (bp) | Assembled upstream non-coding region size (bp) | Assembled downstream non-coding region size (bp) | Number of Illumina sequence-reads | Mean coverage |
|-----------------------------|-------------------------|---------------------------|--|--|-----------------------------------|---------------|
| <i>atp8-atp6</i> | 829 | 151-672 | 300 | 300 | 27025 | 2567 |
| <i>E-cob</i> | 1157 | 65-1092 | 300 | 300 | 39824 | 3188 |
| <i>I-cox1-A</i> | 1670 | 66-1539-64 | 300 | 300 | 56989 | 3572 |
| <i>Y-cox2-N</i> | 807 | 65-674-69 | 300 | 300 | 32791 | 3233 |
| <i>P-cox3</i> | 848 | 62-786 | 300 | 241 | 30577 | 2977 |
| <i>Q-nad1-T</i> | 1040 | 68-903-68 | 300 | 277 | 29362 | 2527 |
| <i>nad2</i> | 1056 | 1056 | 300 | 300 | 31499 | 2645 |
| <i>G-nad3-W</i> | 529 | 69-345-72 | 300 | 300 | 22343 | 2641 |
| <i>K-nad4</i> | 1373 | 67-1305 | 300 | 300 | 44979 | 3228 |
| <i>H-nad5</i> | 1756 | 70-1686 | 300 | 300 | 44907 | 2719 |
| <i>S₂-R-nad4</i> | 420 | 70-69-279 | 300 | 300 | 17670 | 2322 |
| <i>L₂-rrnL</i> | 1429 | 64-1365 | 300 | 266 | 51799 | 3296 |
| <i>rrnS-L₁</i> | 866 | 797-69 | 300 | 300 | 24709 | 2293 |

Supplementary Table 6. Mitochondrial minichromosomes of *Antarctophthirus microchir* – louse of Australian sea lion (*Neophoca cinerea*)

| Minichromosome | Coding region size (bp) | Individual gene size(bp) | Assembled upstream non-coding region size (bp) | Assembled downstream non-coding region size (bp) | Number of Illumina sequence-reads | Mean coverage |
|--------------------|-------------------------|--------------------------|--|--|-----------------------------------|---------------|
| <i>atp8-atp6-D</i> | 1083 | 180-645-67 | 250 | 250 | 79505 | 7055 |
| <i>cob</i> | 1215 | 1215 | 250 | 250 | 83187 | 7479 |
| <i>I-cox1</i> | 1607 | 65-1542 | 250 | 250 | 101204 | 6850 |
| <i>Y-cox2</i> | 792 | 69-723 | 250 | 250 | 47664 | 5050 |
| <i>P-cox3</i> | 908 | 68-840 | 250 | 250 | 56986 | 5541 |
| <i>nad1-T</i> | 991 | 82-909 | 250 | 250 | 76311 | 7167 |
| <i>nad2</i> | 996 | 996 | 250 | 250 | 63260 | 5917 |
| <i>nad3-W</i> | 384 | 312-68 | 250 | 250 | 30294 | 4601 |
| <i>K-nad4</i> | 1348 | 69-1278 | 250 | 250 | 71246 | 5459 |
| <i>nad5</i> | 1704 | 1704 | 250 | 250 | 85929 | 5561 |
| <i>rrnL-R</i> | 1443 | 1369-74 | 250 | 250 | 110797 | 9148 |
| <i>rrnS</i> | 731 | 731 | 250 | 250 | 74805 | 8256 |

Supplementary Table 7. Mitochondrial minichromosomes of *Pthirus gorilla* – louse of western gorilla (*Gorilla gorilla*)

| Minichromosome | Coding region size (bp) | Individual gene size (bp) | Assembled upstream non-coding region size (bp) | Assembled downstream non-coding region size (bp) | Number of Illumina sequence-reads | Mean coverage |
|---|-------------------------|---------------------------|--|--|-----------------------------------|---------------|
| <i>atp8-atp6</i> | 833 | 186-642 | 320 | 156 | 151286 | 17988 |
| <i>cob-S₁</i> | 1137 | 1071-64 | 320 | 316 | 165473 | 15005 |
| <i>cox1</i> | 1551 | 1551 | 320 | 159 | 169187 | 13484 |
| <i>Y-cox2</i> | 756 | 69-687 | 291 | 320 | 141626 | 16356 |
| <i>cox3</i> | 807 | 807 | 320 | 309 | 154255 | 17083 |
| <i>nad1-Q</i> | 970 | 897-59 | 320 | 320 | 163499 | 16013 |
| <i>P-nad2-I</i> | 1126 | 66-984-66 | 320 | 311 | 157520 | 14332 |
| <i>G-nad3-V-W-S₂</i> | 784 | 65-363-68-65-65 | 320 | 74 | 144350 | 18863 |
| <i>K-nad4</i> | 1338 | 68-1269 | 320 | 320 | 166965 | 13546 |
| <i>F-T-D-H-R-nad4L</i> | 859 | 65-66-70-68-65-276 | 320 | 320 | 137088 | 14455 |
| <i>nad5</i> | 1659 | 1659 | 320 | 320 | 183897 | 13054 |
| <i>F-nad6-E-M</i> | 749 | 65-489-64-67 | 320 | 199 | 135817 | 15392 |
| <i>L₁/L₂-rrnL</i> | 1288 | 68/68-1220 | 320 | 295 | 193756 | 16203 |
| <i>rrnS</i> | 819 | 67-752 | 257 | 320 | 135702 | 15075 |
| <i>A</i> | 65 | 65 | 320 | 44 | 8539 | 2478 |
| <i>C</i> | 64 | 64 | 320 | 34 | 427 | 129 |

Supplementary Table 8. Sequence identities between *Antarctophthirus carlinii* (louse of Weddell seal, *Leptonychotes weddelli*) and *Antarctophthirus lobodontis* (louse of crabeater seal, *Lobodon carcinophagus*)

| Gene | Identity | Gene | Identity |
|--------------|-----------------|------------------|-----------------|
| <i>atp8</i> | 100% | <i>trnG</i> | 100% |
| <i>atp6</i> | 98.1% | <i>trnH</i> | 100% |
| <i>cob</i> | 98.3% | <i>trnI</i> | 100% |
| <i>cox1</i> | 99.1% | <i>trnK</i> | 100% |
| <i>cox2</i> | 98.8% | <i>trn L1</i> | 100% |
| <i>cox3</i> | 98.5% | <i>trnL2</i> | 100% |
| <i>nad1</i> | 97.5% | <i>trnN</i> | 98.5% |
| <i>nad2</i> | 98.3% | <i>trnO</i> | 100% |
| <i>nad3</i> | 99.1% | <i>trnP</i> | 100% |
| <i>nad4</i> | 98.7% | <i>trnR</i> | 98.6% |
| <i>nad4L</i> | 98.9% | <i>trn S2</i> | 100% |
| <i>nad5</i> | 98.1% | <i>trnT</i> | 97.1% |
| <i>rrnL</i> | 98.9% | <i>trnW</i> | 100% |
| <i>rrnS</i> | 94.3% | <i>trnY</i> | 100% |
| <i>trnA</i> | 100% | Average identity | 99.03% |
| <i>trnE</i> | 100% | | |

Supplementary Table 9. Sequence identities between Weddell seal (*Leptonychotes weddelli*) and crabeater seal (*Lobodon carcinophagus*)

| Gene | Identity | Gene | Identity |
|--------------|-----------------|------------------|-----------------|
| <i>atp8</i> | 94.1% | <i>atp6</i> | 91.2% |
| <i>cob</i> | 92.5% | <i>cox1</i> | 93% |
| <i>cox2</i> | 93.7% | <i>cox3</i> | 92.2% |
| <i>nad1</i> | 94% | <i>nad2</i> | 92.4% |
| <i>nad3</i> | 90.8% | <i>nad4</i> | 91.5% |
| <i>nad4L</i> | 93.9% | <i>nad5</i> | 91.6% |
| <i>nad6</i> | 93.4% | <i>rrnS</i> | 96.1% |
| <i>rrnL</i> | 96.4% | <i>trnA</i> | 98.6% |
| <i>trnC</i> | 95.5% | <i>trnD</i> | 94% |
| <i>trnE</i> | 97.1% | <i>trnF</i> | 97.2% |
| <i>trnG</i> | 98.5% | <i>trnH</i> | 100% |
| <i>trnI</i> | 95.7% | <i>trnK</i> | 92.8% |
| <i>trnL1</i> | 97.2% | <i>trnL2</i> | 97.3% |
| <i>trnM</i> | 100% | <i>trnN</i> | 93.2% |
| <i>trnP</i> | 95.5% | <i>trnQ</i> | 91.8% |
| <i>trnR</i> | 95.7% | <i>trnS1</i> | 98.5% |
| <i>trnS2</i> | 96.6% | <i>trnT</i> | 92.9% |
| <i>trnV</i> | 94.1% | <i>trnW</i> | 97% |
| <i>trnY</i> | 98.5% | Average identity | 94.99% |

Supplementary Table 10. Species of parasitic lice included in the phylogenetic analyses in this study

| Species | Host | GenBank accession number | References |
|------------------------------------|---------------------------|---|------------------------|
| <i>Antarctophthirus microchir</i> | Sea lion | MW803082-93 | Present study |
| <i>Antarctophthirus carlinii</i> | Weddell seal | MW803073-81 | Present study |
| <i>Antarctophthirus lobodontis</i> | Crabeater seal | MW803064-72 | Present study |
| <i>Lepidophthirus macrorhini</i> | Elephant seals | MW803094-104 | Present study |
| <i>Proechinophthirus fluctus</i> | Fur seal | MW803105-114 | Present study |
| <i>Pthirus gorilla</i> | Gorilla | MW803115-131 | Present study |
| <i>Pedicinus obtusus</i> | Macaque | MT792495-506 | Fu & Dong et al., 2020 |
| <i>Pedicinus badii</i> | Colobus | MT721726-39 | Fu & Dong et al., 2020 |
| <i>Pediculus humanus corporis</i> | Human | FJ499473-90 | Shao et al., 2009 |
| <i>Pediculus humanus capitis</i> | Human | JX080388-407 | Shao et al., 2012 |
| <i>Pediculus schaeffi</i> | Chimpanzee | KC241882-97, KR706168-69 | Herd et al., 2015 |
| <i>Pthirus pubis</i> | Human | JQ976018, EU219987-95, HM241895-8, MT721740 | Shao et al., 2012; |
| <i>Polyplax asiatica</i> | Greater bandicoot rat | KF647751-61 | Dong et al., 2014b |
| <i>Polyplax reclinata</i> | Asian grey shrew | MW291451-61 | Dong et al., 2021 |
| <i>Polyplax spinulosa</i> | Asian house rat | KF647762-72 | Dong et al., 2014b |
| <i>Hoplopleura kitti</i> | Bower's white toothed rat | KJ648933-43 | Dong et al., 2014a |
| <i>Hoplopleura akanezumi</i> | Chevrier's field mouse | KJ648923-32 | Dong et al., 2014a |
| <i>Haematopinus apri</i> | Wild pig | KC814611-19 | Jiang et al., 2013 |
| <i>Haematopinus suis</i> | Domestic pig | KC814602-10 | Jiang et al., 2013 |
| <i>Haematopinus asini</i> | Horse | KF939318, KF939322, KF939324, KF939326, KJ434034-38 | Song et al., 2014 |
| <i>Microthoradus praelongiceps</i> | Guanacos | KX090378-KX090389 | Shao et al., 2017 |
| <i>Haematomyzus elephantis</i> | Elephant | KF933032- KF933041 | Shao et al., 2015 |