

(A)

(169 bp, 96% similarity)

Pa atp6-atp8  
 Pa rns4-trnC  
 Pa trnH-nad5  
 Pa trnK-nad4-trnf  
 Pa trnS1-trnS2-nad1-trnI-trnG-nad3-trnW  
 Pa trnQ-nad2-trnV-trnP  
 Pa trnM-trnL1-rnl-trnV  
 Pa trnR-nad4L-cox3-trnA  
 Pa trnF-cob-trnI  
 Pa cox1-trnL2  
 Pa trnD-trnY-cox2-nad6

TGGAA GCAGGAGGCTCTGGAA GATGACCAA TTTATTTAGCCCTAGGCCA TCGCCTAGGAAA TGTATTA TAA GTTACCCATGGTAA GTTGTAA CTAATAGAGGGTTTTCCAA CCCTAGTAGGCC- TACTCCGCTAGGCTAAT 149  
 TGGAA GCAGGAGGCTCTGGAA GATGACCAA TTTATTTAGCCCTAGGCCA TCGCCTAGGAAA TGTATTA TAA GTTACCCATGGTAA GTTGTAA CTAATAGAGGGTTTTCCA ..... 117  
 TGGAA GCAGGAGGCTCTGGAA GATGACCAA TTTATTTAGCCCTAGGCCA TCGCCTAGGAAA TGTATTA TAA GTTACCCATGGTAA GTTGTAA CTAATAGAGGGTTTTCCA ..... 139  
 TGGAA GCAGGAGGCTCTGGAA GATGACCAA TTTATTTAGCCCTAGGCCA TCGCCTAGGAAA TGTATTA TAA GTTACCCATGGTAA GTTGTAA CTAATAGAGGGTTTTCCAAA CCC- ..... 122  
 TGGAA GCAGGAGGCTCTGGAA GATGACCAA TTTATTTAGCCCTAGGCCA TCGCCTAGGAAA TGTATTA TAA GTTACCCATGGTAA GTTGTAA CTAATAGAGGGTTTTCCAAA CCCCTAGTAGGCCATAGCTATAAA GTTAA G 150  
 TGGAA GCAGGAGGCTCTGGAA GATGACCAA TTTATTTAGCCCTAGGCCA TCGCCTAGGAAA TGTATTA TAA GTTACCCATGGTAA GTTGTAA CTAATAGAGGGTTTTCCAAA CCCCTCC- ..... 125  
 TGGAA GCAGGAGGCTCTGGAA GATGACCAA TTTATTTAGCCCTAGGCCA TCGCCTAGGAAA TGTATTA TAA GTTACCCATGGTAA GTTGTAA CTAATAGAGGGTTTTCCAAA CCCCTCC- ..... 126  
 TGGAA GCAGGAGGCTCTGGAA GATGACCAA TTTATTTAGCCCTAGGCCA TCGCCTAGGAAA TGTATTA TAA GTTACCCATGGTAA GTTGTAA CTAATAGAGGGTTTTCCAAA CCCCTCC- ..... 127  
 TGGAA GCAGGAGGCTCTGGAA GATGACCAA TTTATTTAGCCCTAGGCCA TCGCCTAGGAAA TGTATTA TAA GTTACCCATGGTAA GTTGTAA CTAATAGAGGGTTTTCCAA- ..... 118  
 TGGAA GCAGGAGGCTCTGGAA GATGACCAA TTTATTTAGCCCTAGGCCA TCGCCTAGGAAA TGTATTA TAA GTTACCCATGGTAA GTTGTAA CTAATAGAGGGTTTTCCAA- ..... 101  
 TGGAA GCAGGAGGCTCTGGAA GATGACCAA TTTATTTAGCCCTAGGCCA TCGCCTAGGAAA TGTATTA TAA GTTACCCATGGTAA GTTGTAA CTAATAGAGGGTTTTCCAGCTGGTAAA CCCATCTACTAA CCCT- TTAA G 149

→57F

Pa atp6-atp8  
 Pa rns4-trnC  
 Pa trnH-nad5  
 Pa trnK-nad4-trnf  
 Pa trnS1-trnS2-nad1-trnI-trnG-nad3-trnW  
 Pa trnQ-nad2-trnV-trnP  
 Pa trnM-trnL1-rnl-trnV  
 Pa trnR-nad4L-cox3-trnA  
 Pa trnF-cob-trnI  
 Pa cox1-trnL2  
 Pa trnD-trnY-cox2-nad6

AGGCT- ..... 154  
 ..... 117  
 ..... 139  
 ..... 122  
 CCTAGCCTCTAATTTAC 169  
 ..... 125  
 ..... 126  
 ..... 127  
 ..... 118  
 ..... 101  
 TTGCCCGCTAGCCT- ..... 164

(B)

(453 bp, 92% similarity)

Pa cox1-trnL2  
 Pa trnH-nad5  
 Pa trnK-nad4-trnf  
 Pa trnR-nad4L-cox3-trnA  
 Pa atp6-atp8  
 Pa trnF-cob-trnI  
 Pa rns4-trnC  
 Pa trnD-trnY-cox2-nad6  
 Pa trnM-trnL1-rnl-trnV  
 Pa trnQ-nad2-trnV-trnP  
 Pa trnS1-trnS2-nad1-trnI-trnG-nad3-trnW

..... TTGCCAATGGCTCCGCACATGATGCTTACTAGTAACTAA GTAA GCCATGGTA 54  
 ..... CACTGAGTATATTTTAA TACAATGGCAATGGCTCCGCACATGATGCTTACTAGTAACTAA GTAA GCCATGGTA 79  
 ..... -AGGCTGGTACCCGGGGCAATCTCTCTCTATTGAGAGAGAAA TCCCATGGATTCTCCGGGAGC- CAATTGCCAATGGCTCCGCACATGATGCTTACTAGTAACTAA GTAA GCCATGGTA 126  
 GGCCTCTGGGAGCTTAGGTGAAA GGGTGGTGGTGGGCAATCTCTCTCTATTGAGAGAGAAA TCCCATGGATTCTCCGGGAGC- CAATTGCCAATGGCTCCGCACATGATGCTTACTAGTAACTAA GTAA GCCATGGTA 150  
 ..... -CTGGCCTTAGGTGAAA GGGTGGTGGTGGGCAATCTCTCTCTATTGAGAGAGAAA TCCCATGGATTCTCCGGGAGC- CAATTGCCAATGGCTCCGCACATGATGCTTACTAGTAACTAA GTAA GCCATGGTA 141  
 ..... -GAA GGGTGGTGGTGGGCAATCTCTCTCTATTGAGAGAGAAA TCCCATGGATTCTCCGGGAGC- CAATTGCCAATGGCTCCGCACATGATGCTTACTAGTAACTAA GTAA GCCATGGTA 129  
 ..... -ATCTCTAAA CTCTCTCAA GAGAGAGAAA TCCCATGGATTCTCCGGGAGC- CAATTGCCAATGGCTCCGCACATGATGCTTACTAGTAACTAA GTAA GCCATGGTA 111  
 ..... 0  
 ..... 0  
 ..... 0  
 ..... 0

Pa cox1-trnL2  
 Pa trnH-nad5  
 Pa trnK-nad4-trnf  
 Pa trnR-nad4L-cox3-trnA  
 Pa atp6-atp8  
 Pa trnF-cob-trnI  
 Pa rns4-trnC  
 Pa trnD-trnY-cox2-nad6  
 Pa trnM-trnL1-rnl-trnV  
 Pa trnQ-nad2-trnV-trnP  
 Pa trnS1-trnS2-nad1-trnI-trnG-nad3-trnW

AGAGTTTTAA CAAA TACACCGTATTTGTAGTCCCGATGACCCCCCTTCTATGCTTCTCTATTAAA TGAATA- TTTGGGGTCATAATCGGG- AAA TTACTCCATTGAGTGGTAAA TTTATCCCCATAGCTCAGGATAAGGG 202  
 AGAGTTTTAA CAAA TACACCGTATTTGTAGTCCCGATGACCCCCCTTCTATGCTTCTCTATTAAA CTGAGATAATTTGGGGTCATAATCGGG- AAA TTACTCCATTGAGTGGTAAA TTTATCCCCATAGCTCAGGATAAGGG 228  
 AGAGTTTTAA CAAA TACACCGTATTTGTAGTCCCGATGACCCCCCTTCTATGCTTCTCTATTAAA CTGAGATAATTTGGGGTCATAATCGGG- AAA TTACTCCATTGAGTGGTAAA TTTATCCCCATAGCTCAGGATAAGGG 275  
 AGAGTTTTAA CAAA TACACCGTATTTGTAGTCCCGATGACCCCCCTTCTATGCTTCTCTATTAAA CTGAGATAATTTGGGGTCATAATCGGG- AAA TTACTCCATTGAGTGGTAAA TTTATCCCCATAGCTCAGGATAAGGG 299  
 AGAGTTTTAA CAAA TACACCGTATTTGTAGTCCCGATGACCCCCCTTCTATGCTTCTCTATTAAA CTGAGATAATTTGGGGTCATAATCGGG- AAA TTACTCCATTGAGTGGTAAA TTTATCCCCATAGCTCAGGATAAGGG 290  
 AGAGTTTTAA CAAA TACACCGTATTTGTAGTCCCGATGACCCCCCTTCTATGCTTCTCTATTAAA CTGAGATAATTTGGGGTCATAATCGGG- AAA TTACTCCATTGAGTGGTAAA TTTATCCCCATAGCTCAGGATAAGGG 278  
 AGAGTTTTAA CAAA TACACCGTATTTGTAGTCCCGATGACCCCCCTTCTATGCTTCTCTATTAAA CTGAGATAATTTGGGGTCATAATCGGG- AAA TTACTCCATTGAGTGGTAAA TTTATCCCCATAGCTCAGGATAAGGG 260  
 ..... 0  
 ..... 0  
 ..... 0  
 ..... 135  
 ..... 0

Pa cox1-trnL2  
 Pa trnH-nad5  
 Pa trnK-nad4-trnf  
 Pa trnR-nad4L-cox3-trnA  
 Pa atp6-atp8  
 Pa trnF-cob-trnI  
 Pa rns4-trnC  
 Pa trnD-trnY-cox2-nad6  
 Pa trnM-trnL1-rnl-trnV  
 Pa trnQ-nad2-trnV-trnP  
 Pa trnS1-trnS2-nad1-trnI-trnG-nad3-trnW

GTTTACCTGGGAGTTTTAGCACGAGAA TGGTTTTACCAAGTAGATAA- TTTATTTAA TTCCTTTTTGGGAA TAA TTCCTATGCTCATATAGA- GTATCTACTATTTTATAGATTTTAA GATTTGACTCCCCACGGGCCA 350  
 GTTACCTGGGAGTTTTAGCACGAGAA TGGTTTTACCAAGTAGATAA- TTTATTTAA TTCCTTTTTGGGAA TAA TTCCTATGCTCATATAGA- GTATCTACTATTTTATAGATTTTAA GATTTGACTCCCCACGGGCCA 376  
 GTTACCTGGGAGTTTTAGCACGAGAA TGGTTTTACCAAGTAGATAA- TTTATTTAA TTCCTTTTTGGGAA TAA TTCCTATGCTCATATAGA- GTATCTACTATTTTATAGATTTTAA GATTTGACTCCCCACGGGCCA 423  
 GTTACCTGGGAGTTTTAGCACGAGAA TGGTTTTACCAAGTAGATAA- TTTATTTAA TTCCTTTTTGGGAA TAA TTCCTATGCTCATATAGA- GTATCTACTATTTTATAGATTTTAA GATTTGACTCCCCACGGGCCA 446  
 GTTACCTGGGAGTTTTAGCACGAGAA TGGTTTTACCAAGTAGATAA- TTTATTTAA TTCCTTTTTGGGAA TAA TTCCTATGCTCATATAGA- GTATCTACTATTTTATAGATTTTAA GATTTGACTCCCCACGGGCCA 438  
 GTTACCTGGGAGTTTTAGCACGAGAA TGGTTTTACCAAGTAGATAA- TTTATTTAA TTCCTTTTTGGGAA TAA TTCCTATGCTCATATAGA- GTATCTACTATTTTATAGATTTTAA GATTTGACTCCCCACGGGCCA 426  
 GTTACCTGGGAGTTTTAGCACGAGAA TGGTTTTACCAAGTAGATAA- TTTATTTAA TTCCTTTTTGGGAA TAA TTCCTATGCTCATATAGA- GTATCTACTATTTTATAGATTTTAA GATTTGACTCCCCACGGGCCA 408  
 ..... -TAGATAA TCTATTTAAGCTCTTTTTAGGAGCTTATCCCATGCTCATATAGA- GTATCTACTATTTTATAGATTTTAA GATTTGACTCCCCACGGGCCA 108  
 ..... -ATATTTTATAGATTTTAA GATTTGACTCCCCACGGGCCA 46  
 GTTACCTGGGAGTTTTAGCACGAGAA TGGTTTTACCAAGTAGATAA- TTTATTTAA TTCCTTTTTGGGAA TAA TTCCTATGCTCATATAGA- GTATCTACTATTTTATAGATTTTAA GATTTGACTCCCCACGGGCCA 283  
 ..... -GAGTATATATATATATGTATATATATACGTA TTTTATAGATTTTAA GATTTGACTCCCCACGGGCCA 79

57R ←

Pa cox1-trnL2  
 Pa trnH-nad5  
 Pa trnK-nad4-trnf  
 Pa trnR-nad4L-cox3-trnA  
 Pa atp6-atp8  
 Pa trnF-cob-trnI  
 Pa rns4-trnC  
 Pa trnD-trnY-cox2-nad6  
 Pa trnM-trnL1-rnl-trnV  
 Pa trnQ-nad2-trnV-trnP  
 Pa trnS1-trnS2-nad1-trnI-trnG-nad3-trnW

\*\*\*  
 GGT 353  
 GGT 379  
 GGT 426  
 GGT 449  
 GGT 441  
 GGT 429  
 GGT 411  
 GGT 111  
 GGT 49  
 GGT 286  
 GGT 81

**Additional file 3** - Alignment of nucleotide sequences of parts of the non-coding regions upstream (A) and downstream (B) of the coding regions of the 11 mitochondrial minichromosomes of *Polyplax asiatica*, the louse of the greater bandicoot rat, *Bandicota indica*. 57F and 57R are the primers used to amplify the coding regions of all mitochondrial minichromosomes of *Polyplax asiatica*.