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Supporting data for "An expanded mammal mitogenome dataset from Southeast Asia"

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Abstract

Southeast (SE) Asia is one of the most biodiverse regions in the world and it holds approximately 20% of all mammal species. Despite this, the majority of SE Asia's genetic diversity is still poorly characterized. The growing interest in using environmental DNA (eDNA) to assess and monitor SE Asian species, in particular, threatened mammals - has created the urgent need to expand the available reference database of mitochondrial barcode and complete mitogenome sequences. We have partially addressed this need by generating 72 new mitogenome sequences reconstructed from DNA isolated from a range of historical and modern tissue samples.

Collection

 PROTOCOLS

1. [Extraction method A (FMS and CR)](#)

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2. [Extraction method B (FMS and CR)](#)

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3. [Extraction method C (FMS)](#)

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4. [Extraction Method D (PRP and RM)](#)

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5. **Extraction Method E (PRP)**

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6. **Extraction method F (CR)**

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7. **Illumina library construction for Extraction Method A, B, C (For FMS samples) and D, E (PRP and RM)**

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