

Historical RNA expression profiles from the extinct Tasmanian tiger

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Supplemental Files

Supplemental File 1: miRTrace quality control report using RNA trimmed sequences from skeletal muscle and skin tissues.

Supplemental File 2: miRTrace quality control report using untrimmed RNA sequences from skeletal muscle and skin tissues.

Supplemental File 3: Metatranscriptomic classification of trimmed RNA reads >30 nt from skeletal muscle tissue according to the KrakenUniq pipeline (>1000 *k*-mers; >200 species-specific reads).

Supplemental File 4: Metatranscriptomic classification of untrimmed RNA reads >30 nt from skeletal muscle tissue according to the KrakenUniq pipeline (>1000 *k*-mers; >200 species-specific reads).

Supplemental File 5: Metatranscriptomic classification of trimmed RNA reads >30 nt from skin tissue according to the KrakenUniq pipeline (>1000 *k*-mers; >200 species-specific reads).

Supplemental File 6: Metatranscriptomic classification of untrimmed RNA reads >30 nt from skin tissue according to the KrakenUniq pipeline (>1000 *k*-mers; >200 species-specific reads).

Supplemental File 7: FASTA file of pre-miRNA hairpin sequences from the entire list of annotated microRNAs in the thylacine genome (N = 325).

Supplemental File 8: Pre-miRNA hairpin structure and supporting RNA reads of two selected putative novel thylacine-specific microRNA candidates according to the miRDeep2 algorithm. Msc: skeletal muscle. Skn: skin. The miRNA identified as scaffold_2_6678 corresponds to Tcy-*Novel-18*, while scaffold_7_26772 corresponds to Tcy-*Novel-16-P11*.

***Supplemental Files 1-6** can be found in html format in the Extended Data online.

Supplemental File 7

>Tcy-Let-7-P1c scaffold_3:238189863-238189929(+)
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>Tcy-Mir-7379 scaffold_7:75972357-75972413(-)
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>Tcy-Mir-7382 scaffold_7:80355694-80355752(+)
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Mature

Star

gaucacggggauguuaguucgugaaagauagugagcuucugauguuuaauaauaccaccaggagcucguugucuucuaaauuaauagacgaaaagucccgua			
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