

A

RnM10	TTATTCTTTTCTCTT	TAGA--AACCTGAA-----	AAAT-----	GGGGGTATAGCTCAGTGGTAGAGCATTGACTG----	CAGA--AACCTGAA-----	GAATAATGGCTTTGG	rA255326946
MmM10	TTGTACTTTTCTCTT	-----	-----	-----	TAGA--AACCTGAA-----	GAATAATGGTTTGG	NT_039692
Cys	-----	-----	-----	GGGGGTATAGCTCAGGGGTAGAGCATTGACTG----	CAGA--	TCAAGAGGTCCCTGG	
RnM11	GCCTTTCCTGTCGTT	TGG--ATATAGCTTG----	AACC-----	GCCGTGATTGTATAGTGGTTAGTACTCTGCGTTG----	TGG--ATATAGCTTG----	GACC-GAGAACTG	rL47735968
MmM11	GCCTTTCCTGTCA-T	-----	-----	-----	TGG--ATACGGCTTG----	GACCAGAGAACTG	NT_081106
His	-----	-----	-----	GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTG----	TGG--	CCGCAGCAACCTCGG	
RnM12	AAAAAAATGTTTATT	TAA---ATAAGACAGAGAA--GGT-----	GCCTCGTTAGCGCAGTAGGTAGCGCGTCAGTCTCA--	TAA---ATAAGACAGAGAA--	ACTCTGTATATTCCCT	rJ18073956	
MmM12	AAAAAAA-GTT-ATT	-----	-----	TAA---ATAAGACAAAGAA--	ACTCTGTACATTCCA	NT_039515	
Met	-----	-----	GCCTCGTTAGCGCAGTAGGTAGCGCGTCAGTCTCA--	TAA-----	TCTGAAGGTCGTGAG		
RnM13	GTTAGCGGAACCTCTT	TAA---GAGCATTTCTGCA--GGGT-----	GCCTCGTTAGCGCAGTAGGTAGTGCCTCAGTCTCA--	TAA---GAGCATTTCTGCA--	TGTTTTGTTTCAGATC	rB105403210	
MmM13	GTTAGGGGAATCAT	-----	-----	TCA---TAGCATTTAGAA--	TCTCTGGTTTCAGATC	NT_039228	
Met	-----	-----	GCCTCGTTAGCGCAGTAGGTAGCGCGTCAGTCTCA--	TAA-----	TCTGAAGGTCGTGAG		
RnM14	GTCTTAGAACCCCTTT	AAGA--AGTCTCATCTC--AACAGCC-----	GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTG----	AAGA--AGTCTCATCTC--	TTCAGAGGCAGAAGT	rG99226341	
MmM14	GTC-TGGAACATTTT	-----	-----	AAGA--AGGCTCATCTC--	CTCAAAGACAGAAGT	NT_078782	
Phe	-----	-----	GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTG----	AAGA-----	TCTAAAGGTCCCTGG		
RnM15	TCATGACTTTACT-G	CTAGA-TAAATCACAAAGT-CACTT-----	GTAGTCGTGGCCGAGTGGTTAAGGCAATGGA-----	CTAGA-TAAATCACAAA--	GTGTATGTTAGAGTC	rR7983332	
MmM15	CCATGACTTGACTGG	-----	-----	-TAGA-TAAATCACAAA--	GTGTAGGTAGCA-TC	NT_039678	
Ser	-----	-----	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGA-----	CTAGA-----	AATCCATTGGGGTTT		
RnM16	TTAAAGAGGAAATTT	AC---AAATAAGTGTGGAA-----	GTTTCCGTAGTGTAGTGGTTATCACATTGCCTC----	ACA---AATAAGTGTGGAA--	GCTAAAAGCATGGTC	rF62938057	
MmM16	TTAAACAGGAAATTT	-----	-----	ACA---AATAAGTCCGAAA--	GCTAAAAGCATGACC	NT_039551	
Val	-----	-----	GTTTCCGTAGTGTAGTGGTtATCACGTTGCCTA----	ACA-----	CGCGAAAGGtCCCCG		

B

MmM17	TACCTTCATCTTCTT	TGAA--ATACCTACAGAT--	GTGTA---GGTTCCATGGTCTAATGGTTAGCACTCTGGACTC-----	TGAA--ATACCTACAGAT--	TTTCATTATGCTTCT	mJ23697918
RnM17	TACCTCCATCTTCTT	-----	-----	TGAA--ATATCTTCAGCT--	TCTCATATGCTTCT	NW_047547
Gln	-----	-----	-----GGTTCCATGGTGTAATGGTtAGCACTCTGGACTC-----	TGAA--	TCCAGCGATCCGAGT	
MmM18	GCATTTTCTAGTGTA	TGAA--AACATCTGTA--	GTGCT---GGTTCCATGGTGTAATGGTTAGCACTCTGGACTC-----	TGAA--AACATCTGTA--	AATATATAATAATAA	mI7453409
RnM18	GCATTTTCTTGCTA	-----	-----	TAAA--AACATCTTTA--	AATATACAATAATTA	NW_047798
Gln	-----	-----	-----GGTTCCATGGTGTAATGGTtAGCACTCTGGACTC-----	TGAA--	TCCAGCGATCCGAGT	
MmM19	ATCCTAAATGATATC	CCAA--TAAACCACAGG--	GGTGCA--GTGTTGGTGGTATAGTGGTGAGCATAGCTGCCTT-----	CCAA--TAAACCACAGG--	AAACATTTTCATCTCT	mH38186775
RnM19	ATCCCAAATGATTTT	-----	-----	CCAA--TAAACCACAGG--	AAACACTTCTTCTCT	NW_047473
Gly	-----	-----	-----GC GTTGGTGGTATAGTGGTGAGCATAGCTGCCTT-----	CCAA--	GCAGTTGACCCGGGT	
MmM20	AAATTCCTCACTTAA	CCAA--ATACCTTCCTTGT--	GCT-----GC GTTGGTGGTAGAGTGGTGAGCATAGCTGCCTT-----	CCAA--ATACCTTCCTTGT--	CTCAAACCTTCTGTAA	mC48546050
RnM20	TTATCTGCACTTAA	-----	-----	CCAA--GTATTTTCTTGT--	CTCAAACCTTCTGCAA	NW_047625
Gly	-----	-----	-----GC GTTGGTGGTATAGTGGTGAGCATAGCTGCCTT-----	CCAA--	GCAGTTGACCCGGGT	
MmM21	GTGCTTGGGACCCAT	CTTTCAA-ATATGAGCCTGTG--	ACCT-----GTGTTAGTGGTATAGTGATGAGCATAGCTA-----	CTTTCAA-ATATGAGCCCATG--	GGGACCACAGGCTGC	mG83731046
RnM21	ATGCTTGGGACCTCG	-----	-----	CTTTC-AA-ATATGAACCTGTG--	GTGACCACAGGTTGC	NW_047562
Gly	-----	-----	-----GC GTTGGTGGTATAGTGGTGAGCATAGCTGC-----	CTT-CCAA-----	GCAGTTGACCCGGGT	
MmM22	TCTTTTATGTATCTT	TAAT--AATTTCTA-----	AAGGA---GCCTCGTTAGCGCAGTAGGTAGCGCTTCAGTCTCA-----	TAAT--AATTTCTA-----	GCTCACACAATGCCT	mS47548134
RnM22	CTTTTATGTATCTT	-----	-----	TAAT--AATTTCTA-----	GCCCATACAATGCCT	NW_047568
Met	-----	-----	-----GCCTCGTTAGCGCAGTAGGTAGCGCGTCAGTCTCA-----	TAAT--	CTGAAGGTCGTGAGT	
MmM23	AACATAATGGTCAT	TAA---CACTGTGTTTGC--	ACGGGT---GCCTCCTTAGCGCAATAGGCAGCGCGTCAGTCTCA-----	TAA---CACTGTGTTTGC--	CACTACACAACACTG	mE27687160
RnM23	AACAACAATGGTTGT	-----	-----	TAG---CACTGTGCTTGC--	CACCACAGAGCGCTG	NW_047430
Met	-----	-----	-----GCCTCGTTAGCGCAGTAGGTAGCGCGTCAGTCTCA-----	TAA---	TCTGAAGGTCGTGAG	
MmM24	TATTATTAACTCAC	AAG---ATACATACAAAGAC--	GT-----GCCTCCTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTG--	AAG---ATACATACAAAGAC--	TTATAAGTAGTTGGA	mC53607482
RnM24	TATTATTAAATACAC	-----	-----	AAG---AAACATACAAAGAT--	TTATAAGTAGTTGGG	NW_047625
Met	-----	-----	-----GCCTCGTTAGCGCAGTAGGTAGCGCGTCAGTCTCATAATCTG--	AAG---	GTCGTGAGTTCGATC	
MmM25	AGAGGAAAGCAGTCA	AGAAA--AGACCTGGAA-----	C TT-----GTAGTCGTGGCCGAGTGGTTAAGACGATGGACG-----	AGAAA--AGACCTGGAA-----	GTTTCAAGATATCGG	mB112776684
RnM25	AAAGGAAAACAGTCA	-----	-----	AGAAA--AGATCTAGAA-----	GTTTCAAGATATTGA	NW_047657
Ser	-----	-----	-----GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACT-----	AGAAA--	TCCATTGGGGTTTCC	

Supplementary Figure 2: tailless retropseudogenes presence/absence alignments.

Tailless retropseudogenes presence/absence alignments for (A) rat, and (B) mouse. In the alignments of orthologous loci for M10-M25 markers all repeats are boxed and priming sites are shaded. The non-orthologous, most closely related tRNA species is given in the last line of each of the alignments. Hyphens represent gaps in the sequences. Abbr.: *Mus musculus* (Mmu) and *Rattus norvegicus* (Rn). Accession numbers or internal reference numbers are shown in bold.