

**Table S1.** Sequences of TERC genes used to BLAST-Search TERC-ITS loci. The sequence corresponding to the telomeric repeat template is in bold.

Species	Assembly	TERC sequence from genomic assembly used to BLAST-search TERC-ITSs	Coordinates	TERC NCBI accession number (when available)	Species used to identify the TERC sequences with BLAST
<i>Homo sapiens</i>	GRCh38.p13 (28/02/2019)	1 GGGTTGCGGA GGGTGGGCCT GGGAGGGGTG GTGGCCATTT TTTGT <b>CTAAC</b> <b>CCTAA</b> CTGAG AAGGGCGTAG 71 GCGCCGTGCT TTTGCTCCCC GCGCGCTGTT TTTCTCGCTG ACTTTCAGCG GCGGAAAAAG CCTCGGCCTG 141 CCGCCTTCCA CCGTTCATTC TAGAGCAAAC AAAAAATGTC AGCTGCTGGC CCGTTCGCCC CTCCCGGGGA 211 CCTGCGGCGG GTCGCCTGCC CAGCCCCCGA ACCCCGCCTG GAGGCCGCGG TCGGCCCGGG GCTTCTCCGG 281 AGGCACCCAC TGCCACCGCG AAGAGTTGGG CTCTGTCAAG CCGGGGTCTC TCGGGGGCGA GGGCGAGGTT 351 CAGGCCTTTC AGGCCGCGAG AAGAGGAACG GAGCGAGTCC CCGCGCGCGG CGCGATTCCC TGAGCTGTGG 421 GACGTGCACC CAGGACTCGG CTCACACATG C	chr3:169764610-169765060	NR_001566	<i>Homo sapiens</i> (NR_001566)
<i>Pan troglodytes</i>	Clint_PTRv2 (19/01/2018)	1 GGGTTGCGGA GGGTGGGCCT GGGAGGGGTG GTGGCCATTT TTTGT <b>CTAAC</b> <b>CCTAA</b> CTGAG AAGGGCGTAG 71 GCGCCGTGCT TTTGCTCCCC GCGCGCTGTT TTTCTCGCTG ACTTTCAGCG GCGGAAAAAG CCTCGGCCTG 141 CCGCCTTCCA CCGTTCATTC TGGAGCAAAC AAAAAATGTC AGCTGCTGGC CCGTTCGCCC CTCCCGGGGA 211 CCTGCGGCGG GTCGCCTGCC CAGCCCCCGA ACCCCGCCTG GAGGCCGCGG TCGGCCCGGG GCTTCTCCGG 281 AGGCACCCAC TGCCGCGCGG AAGAGTTGGG CTCTGTCAAG CCGGGGTCTC TCGGGGGCGA GGGCGAGGTT 351 CAGGCCTTTC AGGCCGCGAG AAGAGGAACG GAGCGAGTCC CCGCGCGCGG CGCGATTCCC TGAGCTGTGG 421 GACGTGCACC CAGGACTCGG CTCACACATG	chr3:167800495-167800944	No	<i>Homo sapiens</i> (NR_001566)
<i>Gorilla gorilla gorilla</i>	Kamilah_GGO_v0 (28/08/2019)	1 GGGTTGCGGA GGGTGGGCCT GGGAGGGGTG GTGGCCATTT TTTGT <b>CTAAC</b> <b>CCTAA</b> CTGAG AAGGGCGTAG 71 GCGCCGTGCT TTTGCTCCCC GCGCGCTGTT TTTCTCGCTG ACTTTCAGCG GCGGAAAAAG CCTCGGCCTG 141 CCGCCTTCCA CCGTTCATTC TGGAGCAAAC AAAAAATGTC AGCTGCTGGC CCGTTCGCCC CTCCCGGGGA 211 CCTGCGGCGG GTCGCCTGCC CAGCCCCCGA ACCCCGCCTG GAGGCCGCGG TCGGCCCGGG GCTTCTCCGG 281 AGGCACCCAC TGCCGCGCGG AAGAGTTGGG CTCTGTCAAG CCGGGGTCTC TCGGGGGCGA GGGCGAGGTT 351 CAGGCCTTTC AGGCCGCGAG AAGAGGAACG GAGCGAGTCC CCGCGCGCGG CGCGCTTCCC TGAGCTGTGG 421 GACGTGCACC CAGGACTCGG CTCACACATG C	chr3:166181647-166182097	No	<i>Homo sapiens</i> (NR_001566)
<i>Pongo pygmaeus abelii</i>	Susie_PABv2 (19/01/2018)	1 GGGTTGCGGA GGGTGGGCCT GGGAGGGGTG GTGGCCATTT TTTGT <b>CTAAC</b> <b>CCTAA</b> CTGAG AAGGGCGGTC 71 GCGCCGTGCT TTTGCTCCCC GCGCGCTGTT TTTTTCGCTG ACTTTCAGCG GCGGAAAAAG CCTCGGCCTG 141 CCGCCTTCCA CCGTTCATTC TGGAGCAAAC AAAAAATGTC AGCTGCTGGC CCGTTCGCCC CTCCCGGGGA 211 CCTGCGGCGG GTCGCCTGCC CAGCCCCCGA ACCCCGCCTG GAGGCCGCGG TCGGCCCGGG GCTTCTCCGG 281 AGGCACCCAC TGCCGCGCGG AAGAGTTGGG CTCTGTCAAG CCGGGGTCTC TCGGGGGCGA GGGCGAGGTT 351 CAGGCCTTTC AGGCCGCGAG AAGAGGAACG GAGCGAGTTC CCGCGCGCGG CGCGCTTCCC TGAGCTGTGG 421 GACGTGCACC CAGGACTCGG CTCACACT GC	chr3:167351202-167351648	No	<i>Homo sapiens</i> (NR_001566)
<i>Macaca mulatta</i>	Mmul_10 (13/02/2019)	1 GGGTTGCGGA GGGTGGGCCT GGGAGAGGTG GCGGCCATTT TTTGT <b>CTAAC</b> <b>CCTAA</b> CTGAG AAGGGCGTAG 71 GCGCCGCGCT TTTGCTCCCC GCGCGCTGTT TTTCTCGCTG ACTTTCAGCG GCGGAAAAAG CCTCGGCCTA 141 CCGCCTTCCA CCGTTCATTC TGGAGCAAAC AAAAAATGTC AGCTGCTGGC CCGTTCGCCC CTCCCGGGGA 211 CCTGCGGCGG GTCGCCTGCC CAGCCCCCGA ACCCCGCCTG GAGGCCGCGG TCGGCCCGGG GCTTCTCCGG 281 AGGCGCCCAT GTTCGCCGCG AAGAGTTGGG CTCTGTCAAG CCGGGGTCTC TCGGGGGTGA GGGCGAGGTA 351 CAGGCCTTTC AGGCCGCGAG AAGAGGAACG GAGCGGAGTC CCCGCGCGG GCGCGCTTCC CTGAGCTGTG 421 GGACGTGCAC CCAGGACTCG GCTCACACAT GCAG	chr2:74696847-74697300	NR_033816	<i>Macaca mulatta</i> (NR_033816)
<i>Callithrix jacchus</i>	Callithrix_jacchus_c j1700_1.1 (22/05/2020)	1 GGGTTGCGGA GGGTGGGCCT GGGAGGGGTG TGGCCATTTT TTTT <b>CTAACC</b> <b>CTAA</b> CTGAGA CGGGCGTAGG 71 CGCCGTGCTT TTGCTCCCCG CCGCTGTGTT TTCTCGCTGA CTTTCAGCGT TCGGAAAAAG CTCGGCCTAC 141 CGCCTTCCAC CGTTCATTCT GGAGCAAACA AAAAAATGTC GCGCTGGCG AGTTCGCCCC TCCCGGGGAC 211 CTGCGGCGGG TAGCTGCCT AGCCCCCGAA CCCCGCCTGG AGGCCGCGGT CGGCCCGGGG CTTTCTCCGA 281 GGGCCCCATT GCCGCCGCGA AGAGTTGGGC TCTGTCAAGC GCGGGTGTCT GGGGGGCGAG GGTGAGGCTC 351 AGGCCTTTCA GGCCGCAGGA AGAGGAACGG AGCGAGTTCC CACGCACGGC GCGCTTCCCT GAGCTGTGGG 421 ACGTGCACCC AGAACTCGGC TCACACATGC AGT	chr17:10422651-10423104	NR_033817	<i>Callithrix jacchus</i> (NR_033817)

<i>Saimiri boliviensis</i>	saiBol1 (17/11/2011)	1 GGGTTGCGGA GGGTGGGCTT GGGAGGGGTG GCGGCCATTT TTTCT <b>CTAAC</b> <b>CCTAA</b> CTGAG ACGGGCGTAG 71 GCGCCGTGCTT TTTGCTCCCC GCGCGTGTGT TTTCTCGCTG ACTTTTCAGCG TTCGGAAAAG CCTCGGCCTA 141 CCGCCTTCTA CCGTTTCATC TGGAGCAAAC AAAAAATGTC AGCCGCTGGC CTGTTTCGCC CTCCCGGGGA 211 CCTGCGGCGG GTAGCCTGCC CAGTCCCCGA ACCCGCGCTG GAGGCGCGG TCGGCCCGGG GCTTCTCCGG 281 AGGCGCCCAT TGCCGCCGCG AAGAGTTCGG CTCTGTCAAG CGCGGGTGTG TCGGGGGCGA GGGTGAGGCT 351 CAGGCCTTTC AGGCCGACAG AAGAGGAACG GAGCGAGTTC CCGCGCGCGG CGCGCTTCCC TGAGCTGTGG 421 GACGTGCACC CAGAAGTCGG CTCACACATG CAGT	Scaffold00013:8978910-8979363	No	<i>Callithrix jacchus</i> (NR_033817)
<i>Microcebus murinus</i>	Mmur_3.0 (06/02/2017)	1 GGGTTGCGGA GGGTGGGCCC GGGAGGGGTG TCGGCCATTA GTGC <b>CTAAC</b> <b>CTAA</b> CTGAGA AGGGCGTAGG 71 GCGCGTGCTT TTTGCTTCCC GCGCGTGTGT TTTCTCGCTG CTTTCAGCGG GCGGAAAAGC CTTGGCCTAC 141 TGCCGTCCAC AGTCTAGTTT GGAGCAAACA AAAAATGTCA GCGCTGGCCG GTTCACCCCT CCCGGGACCT 211 GCGGTGGCTC GCGCGCCCTG CCGGAGCCCT TGCCATAAGG CCGCGGTGCA CTTGGGGCTT CTCCGAGGT 281 GCCCAATGTC GCGCGAAGA GTTGGGCTCT GTCAGCCGCG GGTCTTTCGG GTGCCAAGGG CGAGGCTCAG 351 GCCTGTGTCG CGCAGGAAAG TAACGGAGCG GGTCCCTTCA CGCGGTGCGC TTCCCTGAGC AGTGGGACTT 421 GCGCCCGGGA CTCAGCTCCT ACATACATC	chr1:63529673-63530121	No	<i>Callithrix jacchus</i> (NR_033817)
<i>Mus musculus</i> *	GRCm39/mm39 (07/2020)	1 AC <b>CTAACCT</b> GATTTTCATT AGCTGTGGGT TCTGGTCTTT TGTTCCTCGC CCGCTGTTTT TCTCGCTGAC 71 TTCCAGCGGG CCAGGAAAGT CCAGACCTGC AGCGGGCCAC CGCGCGTTCC CGAGCCTCAA AAACAAACGT 141 CAGCGCAGGA GCTCCAGGTT CCGCGGAGCG TCCGCGGCGC CGGGCCGCC AGTCCCGTAC CCGCTACAG 211 GCGCGGCGCG GCCTGGGGTC TTAGACTCC GCTGCCGCGC CGAAGAGCTC GCCTCTGTCA GCGCGGGGC 281 GCGGGGGCT GGGGCCAGGC CGGGCAGCG CCGCAGGAC AGGAATGGAA CTGGTCCCCG TGTTCGGTGT 351 CTTACCTGAG CTGTGGGAAG TGCACCCGGA ACTCGGTTCT CACAACC	chr3:96321753-96322149	NR_001579.1	<i>Mus musculus</i> (NR_001579)
<i>Rattus norvegicus</i> *	mRatBN7.2 (10/11/2020)	1 GT <b>CTAACCT</b> ATTGTTATAG CTGTGGGTTC TGTTCCTTTT TTCTCCGCC GCTGTTTTTC TCGTGACTT 71 TCAGCGGGCC TGGAAAGTTC AGACCTGCAG CCGGTCACCG CGCATTTCTG AACCTCAAAA AATGTCAGCG 141 TAGGAGCTCT GGTGCCAGAG CTCGCGGCGC CTGGGCCGCC CAGCCCGGTA CCCGCTGGA GGCCGCGGAC 211 GGCCTGGGGT CTTAGAATC CGCTGCCGCC GTGAAGAGCT AGTCTCTGTT AGCTACGGGG CACCGGGCGC 281 TGGGTCAGG CCGGAGAGC GCCGAAGGA CAGTAACGGA ACTGGTCCCT GAGTTCGGTG GCTTTCCTGA 351 GATGTGGGAA GTGCACCTGG AACTCAGTTC CTACAACC	chr2:112815654-112816041	NR_001567.1	<i>Rattus norvegicus</i> (NR_001567)
<i>Cricetulus griseus</i>	CriGri_1.0 (23/08/2011)	1 GT <b>CTAACCT</b> GAATTCTGAG AGCTGTGGGT ACTGTGCTTT CGTCTCCGCC CGTGTTTTTT CTCGCTGACT 71 TCCAGCGGGC GGGAAAGTCC AGACCTGCAG CCGGCCATCG CGCGTTTTCC ACCACAAAAA AATGTCAGCG 141 CTGGGCTCAT GTGCCTGGAG CCTTGCGGCC GGCCGCCAG CCCCACACC GCCTGAGGCC GCGTCCGCC 211 TGGAGTCTTC GGGCTCCGCT GCCGCCGCGA AGAGCTAGAC TCTGTCAGCC GCGGGGCGTC AGGGGCTGGG 281 GCGAGCCCCG GCAGCGCCGC AAGCAGAGAA ACGGAGCTGG TCCCGTGAAC GGTGACTTCC CTGAGTTGTG 351 GGAAATGCAC CAGGAACTCG GTTCCACAAA CC	scaffold2001:731353-731734	No	<i>Mus musculus</i> (NR_001579)
<i>Oryctolagus cuniculus</i>	OryCun2.0 (20/10/2009)	1 GGGCTGAGGA GGGTGGGCTC GGGAGGGGCC CGGTCAATTC TCAT <b>CTAAC</b> <b>CTAA</b> CTGAGC AGGGCGTAGG 71 CGCCCGCGCT TTTGTTCCCC GCGCGTGTGT TTTCTCGCTG ACTTTTCAGCG CGTGGGAAAA GCCTTGCCCT 141 ACCGCCGTCC ACCGTTTCATT TCGCAGTAAA CAAAAATGT CAGCCGCTGG CCGGTTTCGCC CTTCCCGGGG 211 ACCTGCGGGT GCTCGCCCGC CCGGCCCGCC TGCCCCGCCT GAGGCGCGG TCGGCCCGGG GCTTCTCCGG 281 AGGTGCCCAA TGCCGCCGCG AAGAGTTAGG CTCTGTCAAG CGCGGGTCCC TCGGGGGCCA AGGGCAGGCG 351 GCAGGCCGTC TGCCCGCAGG GAGAGGAACG GAGCGGGTCC CCCAGCGTGG TGCGCTTCCC TGAGCTGTGG 421 GACTTGACCC CGGGACTCGG CTCAAACACG C	chr14:64663221-64663671	AF221918.1	<i>Oryctolagus cuniculus</i> (AF221918)
<i>Equus caballus</i> **	equCab3.0 (05/01/2018)	1 GGGTGGGGGA GAGTGGGTCT GGGCGGGGCG GCGGTCACGT TTTGT <b>CTAAC</b> <b>CCTAA</b> CTGAG CTGGCGGAG 71 GCGCCGCGCT TTTGCTCCCC GCGCGTGTGT TTTCTCGCTG ACTTTTCAGCG GCGGAAAAAG CCTCGGTCTA 141 CCGCCACTTA CCATCCAGTC TGGAGTAAAC AAAAAATGTC AGCCGCTGGC TCGCTCGCCC CTCCCGGGAC 211 CCTGCGACGG CTCGCCCGCC CAGCCCCCTG GCCCCGCTG GAGGCGCGG TCGGCCCGGG GCTTCTCCGG 281 AGGCGCCCAA TGCCCGCGCG AAGAGTTGGG CTCTGTCAAG CGCGGGTCCC TCGGGGGCCA GGGACGAGGC 351 TCTGGCCGCA GGGAGAGGAA CGGAGCGGGT CCCCAGCGCG GGTGCGCTTC CTGAGCTGTG GGGACGTGCA 421 CCGGGGACTC GGCTCAAACA CGT	chr19:12584771-12585213	AF221925.1	<i>Equus caballus</i> (AF221925)

<i>Bos taurus</i>	ARS-UCD1.2 (11/04/2018)	1 GGGTTGCGGA GGGTGGGCC CGGGTTGGTG GCAGCCATTT CTCAT <b>CTAAC CCTAA</b> TTGAG ACAGGCGTAG 71 GCGCTGTGCT TTTGGTTACC GCGCGCTGTT TTTCTCGCTG ACTTTCAGCG GGCGGAAAAAG CCTCGGCCTA 141 CCGCCATCCA CCATCCAGTC TGCAACAAAC AAAAAATGTC AGCCGCTGGC TCGCTCACCT CTCCCGGGAA 211 CCTGCGGTGG TCCGCCCCGC CAGCCCCAGT GCCCCGCCTG AGGCCGCGGT CGGCCCGGTG CTTCTCCGGA 281 GGTGTCCATT GCCGCCGTGA AGAGTTGGGC TCTGTCAGCC GCGGGTCGCT CGGTGGGCCG AGGCATGGCT 351 GTAACCGCAG GGAAAGGAAC GGAGTGGGGT CCCCGCGCGC GGTGCGCTTC CCTGAGCTGT GGGACTTGCA 421 CCCGGGACTC GGCTCAGACA TCC	chr1:97612791-97613232	NR_001576.1	<i>Bos taurus</i> (NR_001576)
<i>Sus scrofa</i>	Sscrofa11.1 (07/02/2017)	1 GGGTTGCGGA GGGTGGGCC AGGAGCGGTG GCGGCCATTT TTAAAGT <b>CTA ACCCTAA</b> CTG AAGGAGCGT 71 AGGCGCTGCG CTTTGTCTTC ACGCGCGCTG TTTTTCGCTG TGACTTTCAG CGGGCGGAAA AGCCTCGGCC 141 TACCGCCATC CACCATCCAG TCTGAAACAA ACAAAAAATG TCAGCCTCTG GCTCGCTCAC TGCTCCCGGG 211 AACCTGCGGT GGTCGCCCC CCCAGCCCC GCGCCCCGCC TGAGGCCGCG GTCGGCCCGG GGCTTCTCCG 281 GAGGCGCCCA TTGCCGCCGC GAAGAGTTGG GCTCTGTCTG CCGCGGGTCC CTCGGGGGCC AAGGCGAGGC 351 TCTGACCGCA GGGAAAGGAA CGGAGTTGGT CCCCGCGCGC TGTGCGCTTC CTAAGCTGT GGGCTGTGCA 421 CCTGGGACTC GGCTCAGACA CTT	chr13:108426066-108426508	AF221920.1	<i>Sus scrofa</i> (AF221920)
<i>Felis catus</i>	Felis_catus_9.0 (20/11/2017)	1 GGGTTGTGGA GGGTGGGCTT GGGAGGGGAA GCGGTCAGTT TTTGT <b>CTAAC CCTAA</b> CTGAG AAGGCGCTAG 71 GCGCCGCGCT TTTGTTTCCC GCACGCTGTT TTTTTCGCTG ACTTTCAGCG GGCGGAAAAAG CCTCGGCCTA 141 CCGCCGTCCA CCGTACAGTT TGAGGCAAAAC AAAAAATGTC AGCTGCTGAC TTGCTCGCCC CTCCCAGGAC 211 CCTGCGGTGG CTCGCCTCCT TAGCCCCGC TCCTCCGCTA GAGGCCGCGG TCGGCCCGGG GCTTCTCCGG 281 AGGCACCCAT TGCCGTCGCG AAGAGTTGGG CTCTGTCTG CCGGGTCCC TTGGGGGGCG CGAGGCGGAG 351 GCTCTGACCG CAGGGAGAGA AACGGGAGCA GGTCCCCGCG CGCGGTGCGC TTCCCTGAGC TGTGGGACTT 421 GCACCCGGGA CTGGGCTCAG ACACAT	chrC2:98452545-98452964	AF221939.1	<i>Felis catus</i> (AF22193)
<i>Canis lupus familiaris</i>	ROS_Cfam_1.0 (03/09/2020)	1 GGAGGGTGGG CCCGGGAGAG GCGCGGCCG GCCTCCGT <b>CT AACCCTAA</b> CT GAGCAGGGCG TGGGCGCCGC 71 GCTTTTGTTC CCCGCGCGCT GTTTTCTCTG CTGACTTTCA GCGGGCGGAA AAGCCTCGGC CTACCGCCGT 141 CCACCGTCCG GGTCTGCAGC CAACAACAAA AAATGTCTAG CGCTGGCTCG CTCGCCCTC CCGGGAGCCT 211 GCGGCCGCTC GCCCGCTCGG CCCCCGCGT CCGCCCGGA GGCCGCGGCC GGCCCGGGC TTCTCCGGAG 281 GCGCCCACTG CCGTCGCGAA GAGTTGGGCT CTGTGAGCCG CGGGCCGCTT GGGGGCCGCA GGGCGGGGCT 351 CGGGCCGCGG GGAGAGCAAC GGAGCGGGT CCCGCGCGCG GTGCGTCTCC CTGAGCTGTG GGACTCGCAC 421 CCGGGACCGG GCTCGCACAC	chr34:34447071-34447510	No	<i>Felis catus</i> (AF221939)
<i>Loxodonta africana</i>	LoxAfr3.0 (15/07/2009)	1 TGCGGTGGGT TGAGGAGGAT ACGCCCGGGA GGGCGGTGGT CTGTTCTGTT <b>CTAACCCTAA</b> CTGATAAGGG 71 CGTAGGCGCC GTGCTTTTGT TCCCCGCGCG TTGTTTTTCT CGTGACTTT CAGCGGGCGG GAAAAGCCTC 141 GGTCTACCGC CGTCTACCGA TAGCCTGGAG CAAACAAAAA AATGTACGCC GCCGGCCGCT CGCCCTCCC 211 GGGAACCTGC AGTGGCTCGC CCGCCAGCC CCGCTCCCCG CCTGGAGGCC GCGGTGCGCC TGGGGCTTCT 281 CCGGAGGTTT CCGTGCCTGC CGCGAAGAGT TGGGCTCTGT CAGCCGCGGG TCCCCGGGA ACCAAGGGCG 351 AGGCTGGGGC CTCCTGAACG CAGGAGAGA AACGGAGCGG TTCCCCGCGT GCGTGCCTTT CCCTGAGTTG 421 TGGGATGTGC GCTCGGGGCT CAGCTCCGAC AGGT	Scaffold_42:10605978-10606432	No	<i>Elephas maximus</i> (AF221932)
<i>Tapirus indicus</i>	TapInd_v1_BIUU (15/01/2019)	1 GGGTGGTGGG GAGTGGGTCC GGGAGGGCTG GCGGTCATGC TTTGT <b>CTAAC CCTAA</b> CTGAG CCGGGCGTAG 71 GCGCCGCGCT TTTGCTCCCC GCGCGCTGTT TTTCTCGCTG ACTTTCAGCG GGCGGAAAAAG CCTCGGCCTA 141 CCGCCACTTA CCATCCAGTC TGGAACAAAC AAAAAATGTC AGCCGCTGGC TCGCTCGCTC TTCCCGGGAT 211 CCTGCGGTGG CTCGCCCCGC CGGCCCCGCG GCCCCGCTG GAGGCCGCGG TCGGCCCGGG GCTTCTTCGG 281 AGGCACCCAA TGCCGCCGCG AAGAGTTGGG CTCTGTCTAG CCGGGGTGCC TCGGGGGCCA AGGGCGAGGC 351 TCTGGCCGCA GGGAGAGGAA CGGAGCGGGT CCCCGCGCGC GGTGCGCTTC CCTGAGCTGT GGGACGTGCA 421 CCCGGGACTC GGCTCAAACA CGT	Scaffold15412:32659-33101	No	<i>Equus caballus</i> (AF221925)

<i>Sarcophilus harrisii</i>	mSarHar1.11 (07/11/2019)	1 GTGCGGACGG GCTGCGTGGG CCGGTGCGTC CGTCTTGCCA CAT <b>CTAACC</b> TAAATTCGCG CTGGTTGAAG 71 TGGCTTCTCC TGGGCGATCG CTCGCTGTTT TTGTGGCTGG CTTTCAGCGG GCTGGAGGAG CCGGGAGCGG 141 AGGCGGAGGA CCGAGCCAAA AACGTGAGCC GAGGCCGGGC GGCCCCGCTC GTGGCCCGTC CGCACTGTCC 211 GGGCCAGGCC CCGGCCGAA CCCCTGGAG ACGCCTCCCG CAAGGTCTGC GCTGCGCCGC GGAGCCCCGG 281 CTGCCCACGT AGAGGCGGCG GCCGTCTCGG GGCCCCCGAG TCGGGGGCGC CCACTGCGGC GCCTAAGAGC 351 TCGTCTCTGT CAGCCTCGGG TGCACTGCGG CCGCGGTCG AGCCCTAAGG CCGGGCGTGG GGCGGGGGCC 421 GCAGGGAGAG TAACCGTGAG CCGGCGCCCA GCCTTCAGGG CGTCCCTCG AGCTATGGGA GCTGCCCCCG 491 GGCACGGCTC AGACACCC	chr3:27711683-27712190	No	<i>Dasyurus hallucatus</i> (AF221919)
<i>Macropus eugenii</i>	Meug_1.1 (06/11/2009)	1 CGGGCGGTGC GGCTGCAGCG GCGGGTCCCC TGGTCTTGCC CTT <b>CTAACC</b> CTAAATGCGC TCTGGGTGAA 71 GTGGCTCCTC CCGGGGGGTG CCCGCTGTTT TGGTGGCTGG CTTTCTGCGG GCAGGAGGAG CCGGGAGCGG 141 AGCGGAGACA GGAGGAAAAA ACGTCAGCCG AGGCTGGGCG GCGCCGACG TGGCCCGTCC GCCCGTCCA 211 GGTCCACCCC GGCCGAACC CCGGAGGAC GTCCCCGCG GGGCTGTGC TCGCCACGG AGCCCCGGCC 281 GCCCAGGAGC AGAGGCGGCG GCCGTCTCGG GGCCCTGCG TCGGGGGCA CCACTGAGG CCGCCAAGAG 351 CTGGGCTCTG TCAGCCTTGG GGTGCGCGTG GGGCGGTGGG CGAGCCCCAA GGCCGGGCGG GGGCGGAGG 421 CCTCAGGAG AGTAAGCGTG AGCGGCGCCC GCACTGCAGG GCACTCCCTC GAGCCATGGG AGCTGCCCC 491 GGGCTCGGCT CAGACACCC	Scaffold_317:57-565	No	<i>Dasyurus hallucatus</i> (AF221919)
<i>Hirundo rustica</i>	bHirRus1.pri.v2 (02/03/2021)	1 TGTGCCGGGG TGGGAGGCC CTGCGGCCGA <b>TTAACCCCTAA</b> TGGAGGCTGC CTCCCTCACA CCCGCCGCT 71 GTTTTACTCG CTGACTTTCA GCGGGCAAAG GGAGCGGCCC AGGGAAAGGG GGGGATGGAG GGGGGGAAAA 141 AAAGTTCAGG CCTCAAAAAA AGCCAGCGAG GGGGATCCAC ACCCGGCCCC ACCCTGGGGT CCCTGTCCCT 211 CCTCCGCGAC CAGGGGTGGT CCGCCCTCG CCCCTCGTGG AGCGCGCGGT CGCAGGCCCG AGCGCCACTA 281 CCGCCGCGAA GAGTTCGTCT CTGTGAGCCT CGGCGGCGGC CGGATCGGA GGGCCGGCCC GCCCACCCAG 351 GGCAGCCGGG GGACCCAGC AGAACAAAAC GGGGACGGCG CCGCGGGGCG CTGAGCACCC GTGGCTCCCA 421 AAGACGTGGA GTGCGCGGTC GCGCCGCCCC CGACACCC	chr10:21958559-21959016	No	<i>Anodorhynchus hyacinthinus</i> (AF221924)
<i>Gallus gallus</i>	GRCg6a (27/03/2018)	1 ACGCGTGGCG GGTGGAAGGC TCCGCTGTGC <b>CTAACCCCTAA</b> TCGGGGGAAT TGATGGTGCT GTCGCCGCGC 71 TCCCTCCGCC CGCCCGCTGT TTTACTCGCT GACTTTCAGC GGGCGAGAGG AGCCGCCCCG GGGGGGAGGC 141 GGGCGGCGGG AGGGGGCCGG GCGCCGCGG CGGTGGGGGT CCGGGGGGGG AGAGAAAGGG CCGAAAGGGG 211 CTCCGCGGCC AAAAAACGT CAGCGAGGGG TCCGCTCGCC CCGATCCGCC CTGGGGTCCC CGCTCGCGTG 281 GCCGCGGTGC GCCGGCACCC GCCATTGCCG CCGCGAAGAG TTCGCCTCTG TCAGCCTCGG CGGCGCGCGG 351 GAGGTGCGGC GCGCGGCCCC GCGCCCCAG CAGAGCAAAC GGGAGCGGCG CCCCCGGGT AACCCCGCG 421 CTCCCTGCG CCGTGGGGCG CCGGACGGC GTCGCTCCCA CACGC	chr9:20115803-20116267	NR_001594.1	<i>Gallus gallus</i> (NR_001594)
<i>Xenopus laevis</i>	Xenopus_laevis_v2 (09/08/2016)	1 AATCAGCGTT TAAAGCTCAA TGTGGACGGA GGTCTCTGTT TCG <b>CTAACC</b> TAATACACTG GCTTCAGGGC 71 GATGGCTCTT CGCGGCGGTG CTTGTTGTTT TACTTGCTGA CTTTCAGCGG GCACGGAGAG CAAGCGTAGA 141 CGACGACTAA AAAACGTGAG CTGGGAGACT CCTCCGTTG CACAGCCGA CCTGCTCCAT TGCCCAAGAG 211 CCCC GGTTT TCTCTGTGGA ATGTATCAGG CGTCCCCGG TCTGTCTGTC TGGGGCCGCG GTCGGCATCA 281 TCTGCTGTCG CGAAGAGTTC GTCTCTGTTA GCCCTTGGGG GCCCTGGTGC GGAGTGGAGA GTCCGGGTCT 351 GGGGGGTGCG GAGAACAAAA GGGGGCGCGC TGGTGCTCAG GCTCAGTCAT GCTTCCCTT AGTTGTGGGA 421 TATGCGTGTT CAGCCAGTCC CCGACATGT	chr9_10S:63011121-63011569	AF221908	<i>Xenopus laevis</i> (AF221908)
<i>Takifugu rubripes</i>	FTakRub1.2 (05/06/2019)	1 ACGGAGTGTC TCT <b>CTAACC</b> CTAAATTATC TCGGCTCCCT GTACTCGGCG TTTGCTGTTT TTGTCTGGCT 71 TTCAGGAAAC TACAGGGAGT CTTGGACGTC TCGGTTACAG GATCAAAAAA GCCAAGAAAA TCACTCCGTC 141 GCGTTCAGGT CCCCCCAGG AACACCGAGA GCCCTGTTGT GGTCACTCCG GCTGCCGCAA AGAGTTGGTC 211 TCTGCTGCTC CGGTGCTTGG GCGGGATCAC CAAGGACTGA ACAGAGAAAC AGTGAGCGTG GTGACTCTAC 281 CGGTCTCTCC AATGTCCCGG TTAGGATACC CAAGCTCAAA CACTC	chr5:12035678-12036002	EF569638.1	<i>Takifugu rubripes</i> (EF569638)

<i>Scyliorhinus torazame</i>	Storazame_v1.0 (02/08/2018)	1 GGGGCGGTGT CGTTTTTTAC <b>TAACCCTAAT</b> TTGGTGTAAG TGGTTGGGCC TCCCTCACGC TGCGGGAAAC 71 CTCGCTGTTT TCTTGGCTAA CTTTCAGCGA GAAGGTGAGG AGGGTTGGCG GCAAAAAGGT TGGGCAGCAA 141 CGGCGAGCGA ACAAAAAAAG TTAGAGCCGA GGCGCCGTTT TTTCCTCCCC CGCGGCCTGG TCTGAGGGTA 211 ACAAGGCCCT GCGGGAGAGG CGCACAAACA ATGGGGGCCG CGGTCCGGCT AACGGTAGAG GAGGCTGGCC 281 CTCATCGCTT TCCAGGCCCA GCCACTCCGG GCCGCGGTCA GCCCCGGCTT CCCCCTCGGG GGGGGGCCTA 351 ATGCTGCCGC GAAGAGTTCG GCTCTGTCAG CCCGGCCGGG CCAGGGTGA GGCCTGCACA GAGGACACA 421 GGACCGGGG GCGGGGATA GCAACTTCCC GCAGGGGACA TTAATATCA GTACCAGTG GCTTCCATGT 491 GGCTGCATCT CCCGAAGCAA TGGGAGCTGC AAGGCTGCCC TGGTCATACA	scf_scyto00003180:22255-22794	No	<i>Rhizoprionodon porosus</i> (AF221915)
<i>Petromyzon marinus</i>	kPetMar1.pri (24/02/2020)	1 CTCCTCCGTTG GCGCGGAGC TCTTGCTCGT <b>TCTAACCCTA</b> ATTGTTTCCT TTGGCCTCTC TCAATTGTTT 71 GCTGAGTTTT GGCCGAGGTC CAGCAAAACG AGAGAGGCGT TCCACGGGCG TTGGTTTAAA ACTTGACAAA 141 CCTCGGCTCC CACCAATCGG GGAGTTAGGC CTCGCAATC GTGTTACCCC CCCCCGCCAA CCTCGTCGGC 211 TCGCTTCCCA CGACCTCGCC TGGCCCCGGC GGTCCCGGCC TTCGTGCCCT CGCCCGCGGG AGGAGTTCGC 281 CTCGCGCGCC TCGCGAGCCG AGCCGTGGGG GGCCACGAT GCGAGAGTAA CGAGAGGGTT CGGGTCTCCG 351 CTGGGCTTCC CCCTGATTGG TGGGGATTGC ACTTCTGGCC GCCTCTTACA TGT	chr27:7475598-7476001	BK012865.1	<i>Petromyzon marinus</i> (BK012865)
<i>Lethenteron camtschaticum</i>	LetJap1.0 (13/09/2013)	1 CACTCCCCGT TGGCCTCCGA GCTTCTTGCT CGTT <b>CTAACC</b> <b>CTAA</b> TTGTTT CATTTGGCCT CTTCTCAATA 71 TTTGCTGAGT TTTGGCCGAG GTCCAGCAAA AACGAGAGAG GCGTTCCACG GACGTTGGTT TTAAACTTG 141 ACAAACTCG GCTCCACCA TTCGGGAGT AAGGCCTCCG CAATCGGGTG CGAGTTTCCC CCCCCAACC 211 TCATCCACG GCCTCGCCTG GCGCCGGCGT GCGCGGCTT CGTGCCCTCG CCGCCGGGAG GAGTTCGTCT 281 CCGCCGCCAC GCGAGCCCTG GGGGGGGGGG CCCCCACGAT GCGAGAGTAA CGAGAGGGTT CGGGTCTACG 351 ATGGGCTTCC CCCTTGATTG GTGGGGATTG CACCTCTGGC GCCTCTTAC ATTT	contig065527:144-547	BK012866.1	<i>Lethenteron camtschaticum</i> (BK012866)
<i>Eptatretus burgeri</i>	Eburgeri_3.2 (24/10/2017)	1 CACTCCCCGT TGGCCTCCGA GCTTCTTGCT CGTT <b>CTAACC</b> <b>CTAA</b> TTGTTT CATTTGGCCT CTTCTCAATA 71 TTTGCTGAGT TTTGGCCGAG GTCCAGCAAA AACGAGAGAG GCGTTCCACG GACGTTGGTT TTAAACTTG 141 ACAAACTCG GCTCCACCA TTCGGGAGT AAGGCCTCCG CAATCGGGTG CGAGTTTCCC CCCCCAACC 211 TCATCCACG GCCTCGCCTG GCGCCGGCGT GCGCGGCTT CGTGCCCTCG CCGCCGGGAG GAGTTCGTCT 281 CCGCCGCCAC GCGAGCCCTG GGGGGGGGGG CCCCCACGAT GCGAGAGTAA CGAGAGGGTT CGGGTCTACG 351 ATGGGCTTCC CCCTTGATTG GTGGGGATTG CACCTCTGGC GCCTCTTAC ATTT	chr27:7475598-7476001	BK012871.1	<i>Eptatretus burgeri</i> (BK012871)

**Table S2.** Vertebrate TERC-ITS loci used in this study.

\*Loci previously identified [34,35].

		TERC-like sequence							
Locus number	Species	Insertion site	Position within TERC RNA sequence	Length (bp) (Number of mismatches)	TERC region	ITS length (bp) (Number of mismatches)	Locus organization	Insertion site modification	TERC used as reference for secondary structure analysis
1	<i>Homo sapiens</i>	chr6:33092493-33092517	8-32	25 (3)	Pseudoknot domain, template	6 (0)	B	Insertion + Deletion	<i>Homo sapiens</i>
	<i>Pan troglodytes</i>	chr6:32607352-32607376	8-32	25 (5)	Pseudoknot domain, template	6 (0)			
	<i>Gorilla gorilla gorilla</i>	chr6:33158042-33158066	8-32	25 (5)	Pseudoknot domain, template	6 (0)			
	<i>Pongo pygmaeus abelii</i>	chr6:33417464-33417488	8-32	25 (3)	Pseudoknot domain, template	6 (1)			
	<i>Macaca mulatta</i>	chr4:136413412-136413436	8-32	25 (3)	Pseudoknot domain, template	6 (0)			
	<i>Callithrix jacchus</i>	chr4:38087779-38087802	8-31	24 (3)	Pseudoknot domain, template	6 (0)			
	<i>Saimiri boliviensis</i>	scaffold00008:30970797-30970821	8-32	25 (4)	Pseudoknot domain, template	6 (0)			
2	<i>Homo sapiens</i>	chr18:73830841-73830884	15-45	31 (10)	Pseudoknot domain, template	14 (0)	B	Not Informative	
	<i>Pan troglodytes</i>	chr18:68063103-68063146	15-45	31 (10)	Pseudoknot domain, template	14 (0)			
	<i>Gorilla gorilla gorilla</i>	chr18:67137871-67137914	15-45	31 (10)	Pseudoknot domain, template	14 (1)			
	<i>Pongo pygmaeus abelii</i>	chr18:69355462-69355505	15-45	31 (11)	Pseudoknot domain, template	14 (1)			
	<i>Macaca mulatta</i>	chr18:6421937-6421980	15-45	31 (10)	Pseudoknot domain, template	14 (0)			
	<i>Callithrix jacchus</i>	chr13:112407855-112407879	15-45	31 (15)	Pseudoknot domain, template	14 (3)			
3	<i>Microcebus murinus</i>	chr3:9808477-9808511	120-154	35 (2)	Pseudoknot domain, J2a/3	43 (1)	A	Insertion + Deletion	
4	<i>Microcebus murinus</i>	chr4:11270478-11270504	142-168	27 (0)	Pseudoknot domain, J2a/3	43 (0)	A	Insertion + Deletion	
5	<i>Microcebus murinus</i>	chr6:96205947-96205978	124-154	31 (2)	Pseudoknot domain, J2a/3	25 (0)	A	Not Informative	
6	<i>Microcebus murinus</i>	chr14:66686502-66686535	127-161	35 (4)	Pseudoknot domain, J2a/3	32 (1)	A	Insertion + Deletion	

7	<i>Microcebus murinus</i>	chr32:2429016-2429039	129-156	28 (2)	Pseudoknot domain, J2a/3	38 (6)	A	Insertion + Deletion	<i>Mus musculus musculus</i>
8	<i>Mus musculus</i> *	chr1:46771696-46771729	341-374	31 (5)	ScaRNA Domain	57 (0)	A	Deletion	
9	<i>Mus musculus</i> *	chr1:69071165-69071214	346-395	50 (2)	ScaRNA Domain	139 (16)	A	Insertion	
10	<i>Mus musculus</i> *	chr4:119841389-119841433	351-392	42 (1)	ScaRNA Domain	53 (3)	A	Deletion	
11	<i>Mus musculus</i> *	chr5:25644087-25644123	357-393	37 (3)	ScaRNA Domain	21 (2)	A	No modification	
12	<i>Mus musculus</i> *	chr6:67988979-67989022	351-394	44 (1)	ScaRNA Domain	93 (0)	A	Not Informative	
13	<i>Mus musculus</i> *	chr8:23257793-23257830	351-388	38 (3)	ScaRNA Domain	213 (32)	A	Not Informative	
	<i>Rattus norvegicus</i> *	chr16:69254731-69254768	351-388	38 (4)	ScaRNA Domain	58 (8)			
14	<i>Mus musculus</i> *	chr9:47869714-47869777	314-373	60 (1)	ScaRNA Domain	68 (1)	A	No modification	
15	<i>Mus musculus</i> *	chr10:20335691-20335788	289-388	98 (10)	ScaRNA Domain	108 (4)	A	No modification	
16	<i>Mus musculus</i> *	chr10:58382382-58382499	271-388	118 (11)	ScaRNA Domain	27 (1)	A	Deletion	
17	<i>Mus musculus</i> *	chr11:86905013-86905050	343-381	38 (4)	ScaRNA Domain	55 (6)	A	Not Informative	
18	<i>Mus musculus</i>	chr12:7976282-7976348	316-384	68 (12)	ScaRNA Domain	77 (3)	A	Not Informative	
	<i>Rattus norvegicus</i>	chr6:30794373-30794428	319-375	56 (8)	ScaRNA Domain	259 (42)			
19	<i>Mus musculus</i> *	chr12:111293353-111293433	308-388	81 (5)	ScaRNA Domain	13 (0)	A	Deletion	
20	<i>Mus musculus</i> *	chr13:3641558-3641615	331-384	54 (7)	ScaRNA Domain	22 (2)	A	Not Informative	
	<i>Rattus norvegicus</i> *	chr17:66620909-66620960	331-384	53 (9)	ScaRNA Domain	22 (2)			
21	<i>Mus musculus</i>	chr17:77320142-77320174	360-392	33 (2)	ScaRNA Domain	58 (4)	A	Insertion + Deletion	
22	<i>Mus musculus</i> *	chrX:65734790-65734861	322-395	74 (3)	ScaRNA Domain	23 (1)	A	Deletion	
23	<i>Mus musculus</i> *	chrX:99124249-99124300	328-377	52 (9)	ScaRNA Domain	25 (1)	A	Not Informative	
	<i>Rattus norvegicus</i> *	chrX:65181452-65181501	328-377	52 (9)	ScaRNA Domain	43 (4)			

24	<i>Cricetulus griseus</i>	scaffold364:1907954-1908002	332-380	49 (5)	ScaRNA Domain	60 (9)	A	Insertion	
25	<i>Cricetulus griseus</i>	scaffold477:2816499-2816590	283-374	92 (14)	ScaRNA Domain	205 (30)	A	No modification	
26	<i>Cricetulus griseus</i>	scaffold628:177514-177557	336-378	43 (9)	ScaRNA Domain	36 (3)	A	Not Informative	
27	<i>Cricetulus griseus</i>	scaffold2535:334947-335044	283-380	98 (9)	ScaRNA Domain	113 (14)	A	Insertion + Deletion	
28	<i>Oryctolagus cuniculus</i>	chr20:24654676-24654712	245-281	37 (2)	CR4/CR5 domain	66 (1)	A	Insertion	<i>Equus caballus</i>
29	<i>Oryctolagus cuniculus</i>	chrUn0052:1868849-1868866	148-165	18 (0)	Pseudoknot domain, J2a/3	41 (1)	A	Insertion + Deletion	
30	<i>Bos taurus</i>	chr12:22246021-22246046	125-150	26 (0)	Pseudoknot domain, J2a/3	24 (1)	A	Insertion	
31	<i>Bos taurus</i>	chr20:7319073-7319096	124-147	24 (0)	Pseudoknot domain, J2a/3	23 (0)	A	Deletion	
32	<i>Sus scrofa</i>	chr7:70772067-70772095	139-167	29 (1)	Pseudoknot domain, J2a/3	40 (7)	A	Insertion + Deletion	
33	<i>Equus caballus*</i>	chr19:10034300-10034316	148-164	17 (0)	Pseudoknot domain, J2a/3	35 (0)	A	No modification	
34	<i>Tapirus indicus</i>	scaffold2309:127238-127269	128-160	33 (2)	Pseudoknot domain, J2a/3	26 (1)	A	Deletion	
35	<i>Loxodonta africana</i>	scaffold21:34372782-34372809	141-168	28 (0)	Pseudoknot domain, J2a/3	19 (1)	A	Insertion + Deletion	<i>Dasyurus hallucatus</i>
36	<i>Macropus eugenii</i>	scaffold107834:53871-53949	424-502	79 (15)	ScaRNA Domain	12 (1)	A	Insertion + Deletion	
37	<i>Hirundo rustica</i>	HRU5:20102963-20103004	106-146	42 (5)	Pseudoknot domain, J2a/3	10 (0)	A	Deletion	
38	<i>Xenopus laevis</i>	chr2L:82565752-82565772	54-64	11 (0)	Pseudoknot domain, template	28 (0)	C	Insertion + Deletion	
39	<i>Takifugu rubripes</i>	chr18:10170798-10170815	7-14	8 (0)	Pseudoknot domain, template	46 (1)	B	Not Informative	<i>Takifugu rubripes</i>
40	<i>Scyliorhinus torazame</i>	scf_scyto00000011:2181744-2181774	233-263	31 (4)	Region P4-P4.1	30 (1)	A	Not Informative	<i>Rhizoprionodon porosus</i>
41	<i>Scyliorhinus torazame</i>	scf_scyto00006538:68375-68401	4-19	16 (1)	Pseudoknot domain, template	27 (0)	B	Not Informative	

(a) HSA18:73830841 (locus #2)

3' - **CAAUCCC** - **AAUCUGUUUUUUACCGGUGGUG** -- **GGGAGGGUCCGGG** - 5'

HSA CTAAAAAGACCAAATGTAGG**AGGGTTAGGG**-**TTAGACAAA**ctATaGtgcCCACggCtgTCC**AGGCCCC**CGGGCTATCTCCTACCCCA  
PTR CTAAAAAGACCAAATGTAGG**AGGGTTAGGG**-**TTAGACAAA**ctATaGtgcCCACggCtgTCC**AGGCCCC**CGGGCTATCTCCTAtCCCA  
GGG CTAAAAAGACCAAATGTAGG**AcGGTTAGGG**-**TTAGACAAA**ctATaGtgcCCACtgCtgTCC**AGGCCCC**CGGGCTATCTCCTACCCCA  
PPA CTAAAAAGACCAAATGTAGG**AGGGTTAGGG**-**TcAGACAA**gctATaGtgcCCACtgCtgTCC**AGGCCCC**CGGaCTATCTCCTACCCCA  
MMU CTAAAAAGACCAAATGTAGG**AGGGTTAGGG**-**TTAGACAA**gctATaGcgcCCACtgCtgTCC**AGGCCCC**taGGCTATCTCCTACCCCA  
CJA CTAAAgAGACtgATGTAGG**AGGGTT**-**GGGaTT**-**GACtAG**ctGTGGtgcCCACggCtgTCC**AGGtCC**CaGGCTGcCTCCcAC-CCA

(b) MMR3:9808477 (locus #3)

5' - **GGCGGAAAAGCCUUGGCCUACUGCCGUCCACAGUC** - 3'

MMR AGCCCATCAGGTG----**GAAGA****GGCGGAAAAGCCTTGGCCTgCTGCGGTCCACtGTCCGG** (**TTAGGG**)<sub>6</sub> **TTAGG**TCATTAGACCG  
OGA AatCtATCgGGTgacat-----TaAcTAGttCa

(c) MMR4:11270478 (locus #4)

5' - **GCCGUCCACAGUCUAGUUUGGAGCAAA** - 3'

MMR TAAACCAGAAAGTCAG--- ---**TGGCCGTCCACAGTCTAGTTTGGAGCAAAA** (**GGGTTA**)<sub>7</sub> **ATGCA**CACAGTTCATGGGAG  
OGA TAAAgCtAGAAGTCAGctg.∫∫.tag-----CACAAATTCATGGGAG  
SBO TgAAgCCAGAAGTCAGttg.∫∫.tgg-----CACAGTTCATGGGAa  
CJA TgAAgCCAGAAGTCAGttg.∫∫.tgg-----CACAGTTCATGaGAa  
MMU TgAAgCCAGAAGTCAGttg.∫∫.tgg-----CACAGTTCATaGGAG  
PPA TgAAgCCAGAAGTCAGttg.∫∫.tgg-----CACAGTTCATaGGAG  
GGG TgAAgCCAGAAGTCAGttg.∫∫.tgg-----CACAGTTCATacGAG  
PTR TgAAgC-AGAAGTCAGttg.∫∫.tgg-----CACAGTTCATatGAG  
HSA agAAgC-AGAAGTCAGttg.∫∫.tgg-----CACAGTTCATacGAG  
|←16 bp→|

(d) MMR14:66686502 (locus #6)

5' - **AAGCCUUGGCCUACUGCCGUCCACAGUCUAGUUUGG** - 3'

MMR TCTTCAA-----**TTA**.∫∫.**TTGAAGCCTTGGCCTACTGCCaTcTACAGTcAGTcTG** (**GGTTAG**)<sub>4</sub> **AACCC**TTGCTCTGTA  
OGA TtTcgAAgccccct-----TTtgcCatac  
SBO aCTTtAAatccccct-----TTcCctTGTA  
CJA aCTTCAAAtttccccct-----TTcCctTGTA  
MMU cCTTtAAaaccct-----TTGCcaTGTA  
PPA ctTTCAAaaccct-----TTGCTaTGTA  
GGG TtTTCAAa-ccccct-----TTGCTaTGTA  
PTR ctTTCAAaaccct-----TTGCTaTGTA  
HSA ctTTCAAaaccct-----TTGCTaTGTA  
|←17bp→|

(e) MMR32:2429016 (locus #7)

5' - **GCCUUGG**.∫∫.**AGUCUAGUU** - 3'

MMR TTCC-----**CCA**.∫∫.**CATGCCTTGG**.∫∫.**AGTCCaGTTAGGGTTAcGGTTA** (**CCTAAC**)<sub>3</sub> **CCTAAGCA**.∫∫.**CCA**ATAC  
OGA TcCCcct.∫∫.act-----gTt-  
SBO TTCCcct.∫∫.acc-----ATAC  
CJA TTCCcctt.∫∫.acc-----ATAC  
MMU cTCCcct.∫∫.gcc-----ATAC  
PPA cTCCcct.∫∫.gcc-----ATAC  
GGG cTCCcct.∫∫.gcc-----ATAC  
PTR cTCCcct.∫∫.gcc-----ATAC  
HSA cTCCcct.∫∫.gcc-----ATAC  
|←58 bp→| |←18 bp→| |←11 bp→|

**Figure S1.** TERC-ITS loci in primates. For each locus, the top row shows the sequence of the telomerase RNA domain (light blue) homologous to the inserted TERC-like fragment. Species names are indicated on the left. The first species is the one in which the TERC-ITS was initially identified and the following species are listed according to the evolutionary distance from the first species. Telomeric repeats in TTAGGG and CCCTAA orientation are indicated in red and orange, respectively. The TERC-like sequences homologous to a region of the Telomerase RNA are indicated in light blue and the sequence complementary to a region of the Telomerase RNA in dark blue. Modifications of the insertion sites are shown: underlined nucleotides indicate deletions and green nucleotides indicate random sequence insertions. Nucleotides at the 3' end of the TERC-like sequence in frame with the inserted telomeric repeats are boxed.

(a) Mus12:7976282 (locus #18)

5' - **AGGACAGGAAUG**. $\int\int$ .**GCACCCGGAACUC**-3'  
Mus AGTGCCTCCA**AGGACAGGG**-**TG**. $\int\int$ .**GCACCCaGAATCTT** (**TTAGGG**)<sub>12</sub> **TTAGG**-----ACAGGGTCATG  
RNO gGTGCCTCCA**AaacCgaGG**-**Ta**. $\int\int$ .**GCACCCaGAATCTCT** (**TTAGGG**)<sub>42</sub> **TTAGGGT**TAGATTTTGTCTATCCT-CATGGTCATG

(b) Mus17:77320142 (locus #21)

5' - **GCUGUGGGAA**. $\int\int$ .**UCGGUUCUCA**-3'  
Mus CTGGATTTCC**CTGTGGGAA**. $\int\int$ .**TCtGTTCTCAAGGAAAAAAAAA** (**TTAGGG**)<sub>9</sub> **TTAACCT**--- ---ATGTTCTCTAT  
RNO CTGGATTTtCT----- -----GGA. $\int\int$ .TTGATGTTtTCTAT  
|-----62 bp-----|

(c) CGR\_scaffold477:2816499 (locus #25)

5' - **GAGCCCCGGC**. $\int\int$ .**AAGUCGGUUC**-3'  
CGR CAGATATA. $\int\int$ .TTGTCA**GAGCCCTGGC**. $\int\int$ .**AAGTCGGTTCATAAAATTcA** (**GGGTTA**)<sub>33</sub> **GGGCCTGTAT**. $\int\int$ .ACGATGAT

(d) CGR\_scaffold628:177514 (locus #26)

5' - **CUUCCUGAGUUG**. $\int\int$ .**CUCGGUUCCAC**-3'  
CGR AACTCAG**CTTCTCTGAGcTG**. $\int\int$ .**CaCaGcTCaCACAGGa** (**GTTAGG**)<sub>5</sub> **GGGGGCTCAAACAACC**. $\int\int$ .TGAGGGAGCAGAAAGG

(e) CGR\_scaffold2535:334947 (locus #27)

5' - **GAGCCCCGG**. $\int\int$ .**UUCCCACAA**-3'  
CGR TTTCTGCC--- ---**CAG**. $\int\int$ .**GTGGAGCCCCaG**. $\int\int$ .**TTCCCAaA** (**TTAGGG**)<sub>18</sub> **TTAGGATA**. $\int\int$ .**ACAAGACAAATCA**  
MMM TTTCTGCC**Caca**. $\int\int$ .**tcc**--- --- ---AaACAAAtTaA  
RNO TTTCTGCC**Caca**. $\int\int$ .**cac**--- --- ---AaACAAAtTtA  
|-----60 bp-----|-----14 bp-----|-----19 bp-----|

(f) OCU20:24654676 (locus #28)

5' - **CCGCCUGAGGCCGCGGUCGGCCCCGGGGCUUCUCCGGA****GGU**-3'  
OCU ACGTGTCTATTGAT**GTGACCGCCTGAGGCCtCGGT**CGGCCCGGGGCT**TCTCtGGA****GGT** (**TAGGGT**)<sub>10</sub> **TGATTGTCTGCTGGCCT**  
LTI cCtTGCTCTATTGgT----- ---TctCTGCTGGCCT

(g) OCU\_Un0052:1868849 (locus #29)

5' - **UCCACCGUUCAUUUCGCA****GU**-3'  
OCU ATCCTTGATGCCACCT---- --**TCT**. $\int\int$ .**GTCTCCACCGTTCATTTGCA****GT** (**TAGGGT**)<sub>6</sub> **TAGAGACTATTAGAGTAAGA**  
LTI gaCaTgGAatCAACCTgtg. $\int\int$ .**tag**----- ---taACTgTTAGAGTAgGc  
|-----58 bp-----|-----38 bp-----|

(h) BTA12:22246021 (locus #30)

5' - **GAAAAGCCUCGGUCUACCGCCA****UCCA**-3'  
BTA TCAATCAATGGTAATAC**GAAAAGCCTCGGTCTACCGCCATCCA****AAAAA** (**GGGTTA**)<sub>4</sub> **TTT**. $\int\int$ .**TCTCAGGAGAGTTATTTCTG**  
OAR TCAATCAAcGGTAATgC----- ---CAGGAGAGTTATTTCTG  
SSC c-----GGTAgcAC----- ---CAGGAGgGTgATTcCTG  
TTR cCAAAaAATGGTAACAC----- ---CAGGAGgGTgATTCTG  
|-----13 bp-----|

(i) BTA20:7319073 (locus #31)

5' - **CGA****AAAGCCUCGGCCUACCGCCA****U**-3'  
BTA TGTCAGTA. $\int\int$ .GTG**GGA****AAAGCCTCGGCCTACCGCCAT****AAAAGAA** (**TTAGGG**)<sub>3</sub> **TTAGG**--- ---TCC. $\int\int$ .AACTGAAT  
OAR TGTCAGTA. $\int\int$ .GaG**GGA**----- ---gac. $\int\int$ .ggaTCC. $\int\int$ .AACTGAAT  
SSC TGcCA--- --- ---TGAAT  
TTR TGTCa--- --- ---TGAAT  
|-----62 bp-----|-----13 bp-----|-----141 bp-----|

(j) SSC7:70772067 (locus #32)

5' - **CCUACCGCCA****UCCACCAUCCAGUCU**-**GAA**-3'  
SSC TTGAAAGAAA-----**AGT**. $\int\int$ .**CAACCTACtGCCATCCACCATCCAGTCTGGAA** (**TTAGGG**)<sub>6</sub> **GTTAAC**AGTTAGACAA  
BTA TTGAAAGAAAtat. $\int\int$ .tgc----- ---AtTTtGgCAA  
OAR cTGAAAGAAAtat. $\int\int$ .tgc----- ---AtTTAGgCAA  
|-----53 bp-----|-----328 bp-----|

(k) TIN\_scaffold2309:127238 (locus #34)

5' - **AAGCCUCGGCCUACCGCCACUUACCAUCCAGUC** -3'  
**TIN** AAGGACCTGTTTGGGGT-----**AAGCCTCGGCC-ACCGCCACTTACCgTCCAGTCTA** (**GGGTTA**)<sub>4</sub> ACTAGCTCCATTTTCC  
**CSS** AAGGACCTGTctTGGGG-Tgcttta----- ACTAGCTCCATTTTcCC  
**ECA** AAGGACCTGTTTGGGGTacttta----- ACCAGCcCATTTTCC  
|←6 bp→|

(l) LAF\_scaffold21:34372782 (locus #35)

5' - **CCCUACGGCCGUCUACCGAUAGUCUGG** -3'  
**LAF** TTCAGCCCAGAGGTTG**GGCCTACGGCGTCTACCGATAGTCTGG** (**TAGGGT**)<sub>3</sub> **TTAC**----- ----CCCCACAGCACTAAGG  
**PCA** TTCAGCC-AGAGGTTG**GC**----- ----gcag.∫∫.ggtaCCCTACAGCACcAAGG  
|←14 bp→|

(m) MEU\_scaffold107834:53871 (locus #36)

5' - **CAGGGAGAGUAAGCG.∫∫.CCCCAGGCAUGGCUCA** -3'  
**MEU** ACTC-----**CTG.∫∫.CTACAGGGAGAGTAgcCa.∫∫.CCCCAGGCATGGCTCAATTA.∫∫.TTATTAGaGTTAGGG**AGTCT  
**SHA** ACTCacaaagata--- ----AaTtT  
|←9 bp→|←12 bp→| |←45 bp→|

(n) HRU5:20102963 (locus #37)

5' - **GGCCAGGGAAAGG.∫∫.G-GAAAAAAGUU** -3'  
**HRU** GAAGACATAG**GGCCAGGGAAAGG.∫∫.GgGAA**----**AAGTTAAAAAATAGGGTTAGG**-----GTTATTTTCCCTGCTTCT  
**PDO** GAAGACATAG----- ----ctgcttctatgtGTTATTTTCCCTGCTTCT  
**CMO** GAAGACATAG----- ----ctgcttctatgtGTTATTTTCTcTGCTTCT

(o) XLA\_2L:82565752 (locus #38)

3' - **UUCGGUCACAUAAUCCCAAUC** -5'  
**XLA** TGAATCAGAAACACT**AAGCCAGTGTATTAGGGTTAGGGTTA** (**ACCCTA**)<sub>2</sub> **ATAC.∫∫.AAT**--- ---ATATAAAATATAAT  
**XTR** TGAATCAGAAACat**TAA**G----- ----ttc.∫∫.tcgAgATACAcctatAT  
|←45 bp→|←13 bp→|

(p) TRU18:10170798 (locus #39)

3' - **AAUCCCAAUCUUCUCUGU** -5'  
**TRU** GCTCAGCATCAACAACCTGGACTGATGTGATCTGA (**TTAGGG**)<sub>6</sub> **TTAGGGTTAGAAGAGACAGGAAGTGGACACAGACACGACTTT**

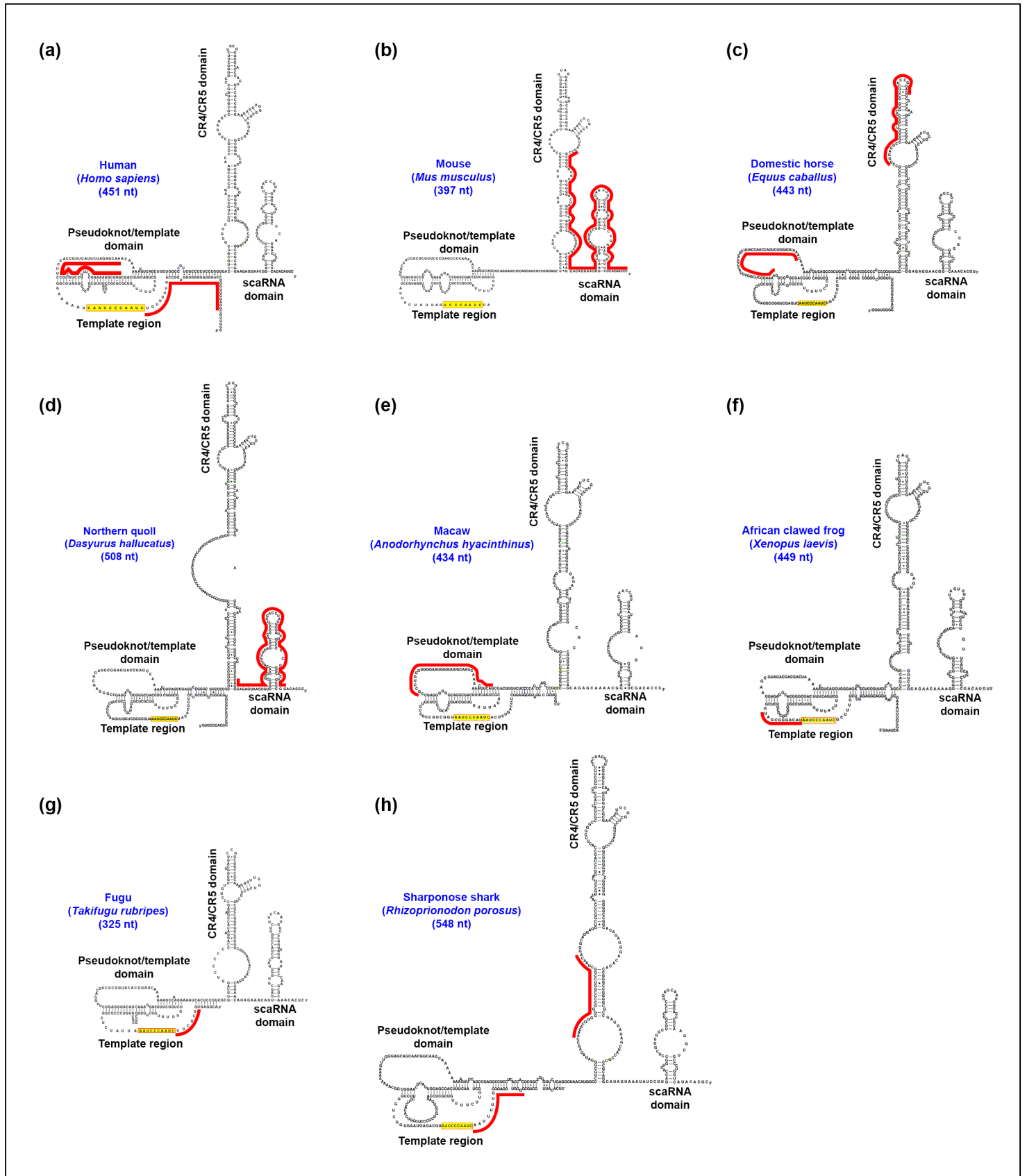
(q) STO\_scf\_scyto00000011:2181744 (locus #40)

5' - **CACAAGCAAUGGGGGCCCGGUCGGCUAAC** -3'  
**STO** ACCATTCTCCCGA**CACAAaCAATGGaGaCCCCtGTCCGGCTAACAGGAGGG** (**TTAGGG**)<sub>4</sub> **TTCTCCAGGAGAATCGGTGGACCGG**

(r) STO\_scf\_scyto00006538:68375 (locus #41)

3' - **AAUCCCAAUCAUUUUUU-GCUGUGGCG** -5'  
**STO** CCCCCCCCCCCCCC (**TAGGGT**)<sub>2</sub> **TAGGGTTAGGGTTAGTAAAAATCGACACCGCATCGGAAACTGGCCAGTGTCAAATTACATA**

**Figure S2.** TERC-ITS loci in non-primate vertebrates. For each locus, the top row shows the sequence of the telomerase RNA domain (light blue) homologous to the inserted TERC-like fragment. Species names are indicated on the left. The first species is the one in which the TERC-ITS was initially identified and the following species are listed according to the evolutionary distance from the first species. Telomeric repeats in TTAGGG and CCCTAA orientation are indicated in red and orange, respectively. The TERC-like sequences homologous to a region of the Telomerase RNA are indicated in light blue and the sequence complementary to a region of the Telomerase RNA in dark blue. Modifications of the insertion sites are shown: underlined nucleotides indicate deletions and green nucleotides indicate random sequence insertions. Short microhomologies between the TERC-like sequence and the 3' end of the break site are indicated with nucleotides with yellow background. Nucleotides at the 3' end of the TERC-like sequence in frame with the inserted telomeric repeats are boxed.



**Figure S3.** Regions of TERC-RNA homologous to TERC-ITS loci. The position of TERC-like sequences found at TERC-ITS loci as marked on the proposed secondary structures of the TERC RNA. Red lines cover the overall TERC regions retro-transcribed at relevant TERC-ITSs. The template region, which is retrotranscribed, by definition, at all loci, is not marked. **(a)** The seven primate TERC-ITSs are marked on the human TERC structure. The sequence immediately upstream of the telomeric repeat template is contained in two loci. The partially single stranded region J2a/3 in the pseudoknot is contained in five TERC-ITSs. **(b)** The TERC-like sequences from the 20 Rodentia loci are marked on the secondary structure of mouse TERC. All 20 TERC-like fragments from these species, in which the TERC RNA is lacking 43 nucleotides from the 5' end, derive from the scaRNA domain and the adjacent region, which are positioned at the 3' end of the TERC-RNA, far away from the pseudoknot. **(c)** The eight TERC-like sequences from non-primate and non-rodent mammals (rabbit, cow, pig, horse, tapir and elephant) are marked on the horse TERC RNA structure. Seven TERC-like fragments derive from the partially single stranded region J2a/3 within the pseudoknot. One TERC-like fragment (from rabbit locus 28) corresponds to a region of the CR4/CR5 domain. **(d-h)** TERC-like sequences from the loci found in a marsupial, a bird, a frog, a ray-finned fish and a shark are marked on the secondary structure of TERC from Northern quoll, macaw, African clawed frog, tiger pufferfish and sharpnose shark, respectively. Each sequence marked on these structures derives from one TERC-ITS.