

Supplementary Table 1. Genomic coordinates and detection probes for *P.falciparum* structural RNAs.

Supplementary Table 2. Features and genomic location of ribosomal RNAs (rRNAs) and transfer RNAs (tRNAs) in *P.falciparum*.

Supplementary Figure 1.

(a.) Schematic representation of the location of individual probes for detection and mapping of *P.falciparum* telomerase RNA. The template region of the RNA is shown as an open box on the large and small transcripts (grey). Individual probes (underlined) and their locations are shown with respect to nucleotide positions on chromosome 9. These probes were used for both northern and RNase Protection Assays (RPA). (b.) RNase protection assay with cRNA Probe 4-14 (chr9:763,162-763,441) used to map the 3' end of telomerase RNA transcript. Lane 1, probe alone (digested with RNase); lane 2, probe alone (no RNase) and lane 3, RNA with probe (digested with RNase). (c.) Probe-16-17 (chr9:761,052-761,328) was used to map the 5' end of telomerase RNA. Lane 1, RNA with probe (digested with RNase); lane 2, probe alone (digested with RNase) and lane 3, probe alone (no RNase). RNase undigested probe is shown as input. Protected fragments shown as 'P' on the blots.

Supplementary Figure 2.

Sequence Alignment of *P.falciparum* U1 snRNA. ss: Splice site. SM corresponds to putative Sm Protein binding motif. Pf: *P. falciparum*, Pr: *P. reichenowi*, Pv: *P. vivax*, Pk: *P. knowlesi*, Pg: *P. gallinaceum*, Pc: *P. chabaudi*, Pb: *P. berghei*, Py: *P. yoelii yoelii*, Hu and Mu are human and mouse sequences respectively (same abbreviations used in all snRNA alignments).

Supplementary Figure 3.

Sequence Alignment of *P.falciparum* U2 snRNA. BP: Branchpoint sequence. Helix 2a terminal loop sequence and its conserved complementarity marked in 'x'. SM corresponds to putative Sm Protein binding motif. U2-U6 helices and branchpoint (BP) sequences are shown as [::].

Supplementary Figure 4.

Sequence Alignment of *P.falciparum* U4 snRNA. Non-canonical pairing in terminal loop of U4 helix I is shown by 'x'. SM corresponds to putative Sm Protein binding motif.

Supplementary Figure 5.

Sequence Alignment of *P.falciparum* U5 snRNA

Supplementary Figure 6.

Sequence Alignment of *P.falciparum* U6 snRNA. U4-U6 and U2-U6 pairings are shown at the bottom of alignments.

Supplementary Figure 7.

(a.) Primer extension reaction on 6% denaturing polyacrylamide-urea gel : Lane M-100 is a 100 bp ladder marker , Lane 1 - RNase MRP, Lane 2 - RNase P, Lane 3 - U3 snoRNA, Lane 4 - SRP-RNA and Lane M - 10 is a 10bp ladder marker. (b.) U3 RNA alignment shown in dot-bracket structure. Pf: *P. falciparum*, Pv: *P. vivax*, Pr: *P. reichenowi*, Pk: *P. knowlesi*, Pg: *P.*

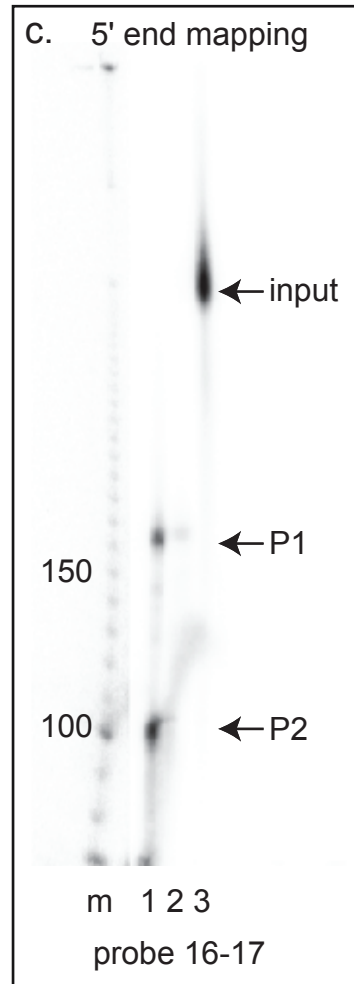
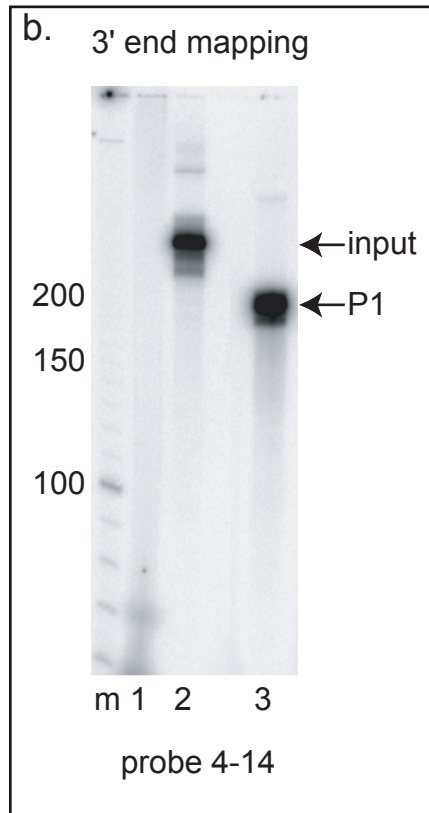
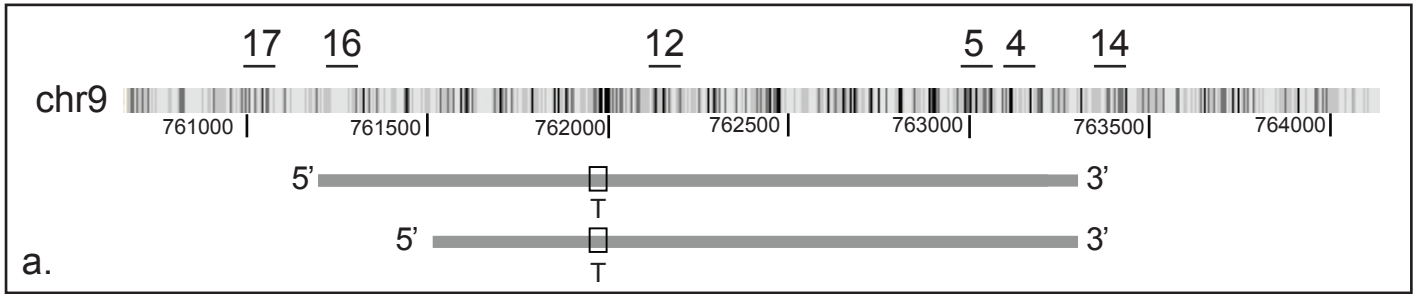
gallinaceum, Pc: *P. chabaudi* and Pb: *P. berghei*. U3 structural elements are shown on the top of alignments and helices are shown at the bottom of the alignment.

Supplementary Figure 8.

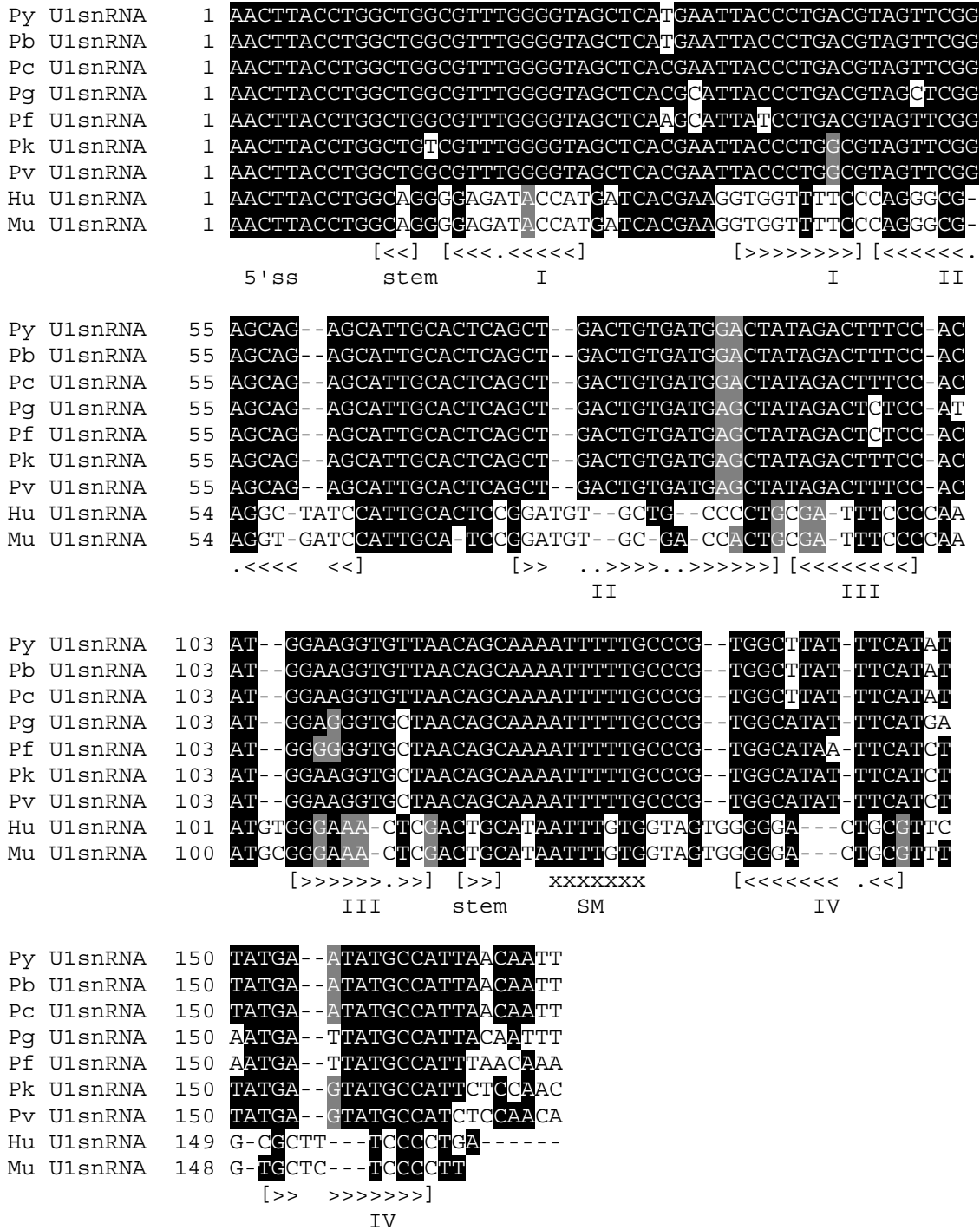
Sequence alignment of the upstream SNPE element for all U RNAs from various species of malaria parasite. Pf: *P. falciparum*, Pr: *P. reichenowi*, Pv: *P. vivax*, Pk: *P. knowlesi*, Pg: *P. gallinaceum*, Pc: *P. chabaudi*, Pb: *P. berghei*, Py: *P. yoelii yoelii*

Supplementary Figure 9. (a.) *P.falciparum* SRP-RNA detected on the Northern blot (b.).

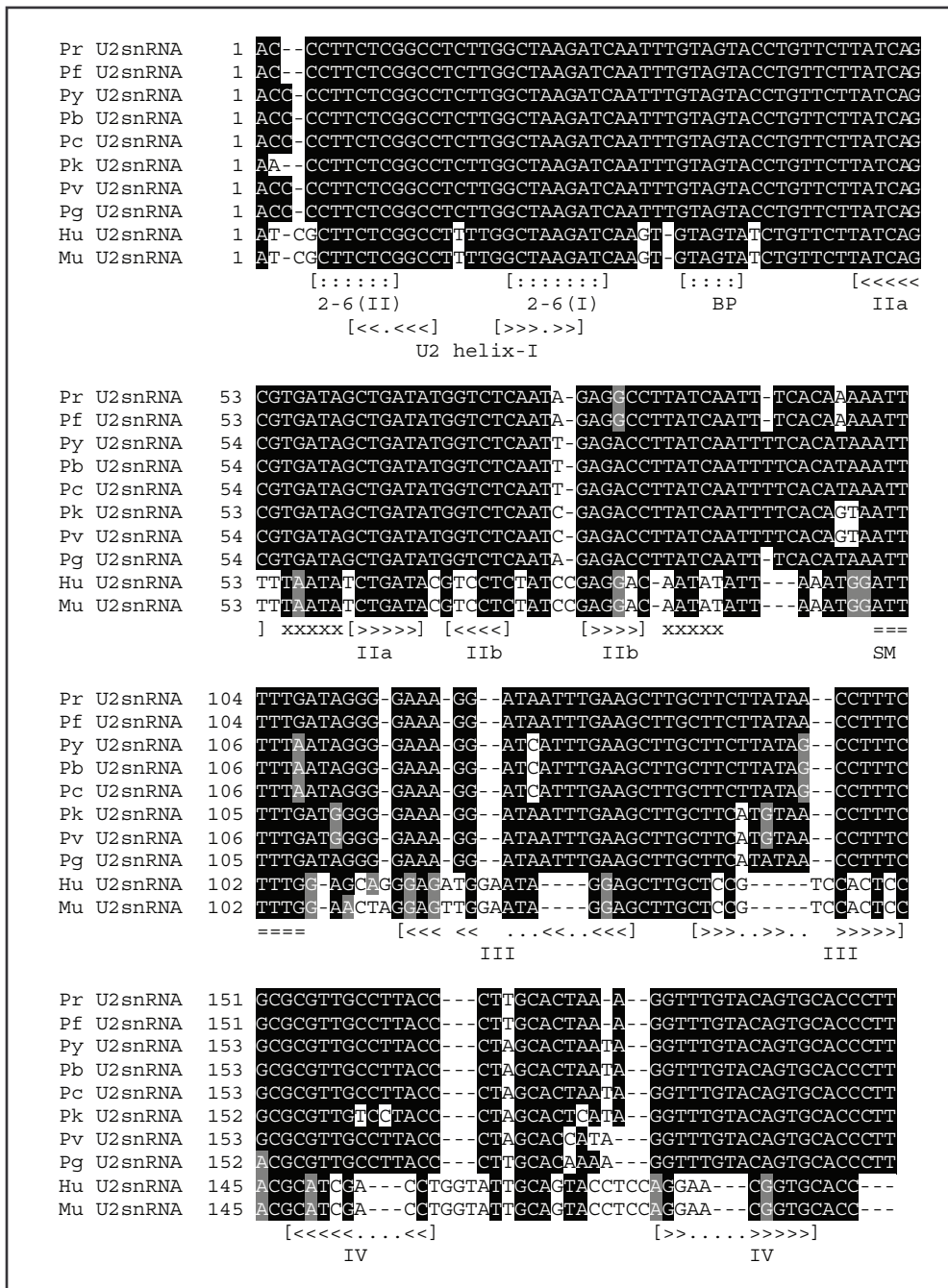
Multiple sequence alignment of SRP RNA. Helices denoted by 'H' with corresponding number from published structure model (see text) . Pf: *P. falciparum*, Pv: *P. vivax*, Pr: *P. reichenowi*, Pk: *P. knowlesi*, Pg: *P. gallinaceum*, Pc: *P. chabaudi*, Pb: *P. berghei*, and Py: *P. yoelii yoelii*.



Supplementary Figure 1



Supplementary Figure 2



Supplementary Figure 3

PgU1 TTTATGAAGTACAATTTTAGTATGTAAAAAATAACACAGTAAA
 PcU1 TCAATGAGGTACAATTCGGCGTTTAAAAATATACCCAATAAA
 PyU1 TCAATGAGGTACAATTTTCGGCGTTTAAAAATATACCCAATAAA
 PbU1 TCAATGAGGTACAATTCGGCGTTTAAAAATATACTCAATAAA
 PkU1 CCGATGAAGTACAATTTTCAGCAGGGAAAAAAGAACACAGTGAA
 PvU1 CCGATGAAGTACAATTTTCAGCATGGAAAAAATAACACAGTGAA
 PfU1 TAAAAAAGTACAGTTTCAGTATTGAAAAAGGAACACTATGAA
 PgU2 ATGAATAAGTACAACCTTTCATAGGGAAAAATATACATAATGAA
 PcU2 TCATATAGGTACACTTTTTGGTAGGGAGACAATTACATAGTGAA
 PbU2 TCACATAAGTACACTTTTTGGTAGGGAGATAAATACATAATGAA
 PyU2 TCATATAAGTACAATTTTGGTAGGGAGATAAATACATAATGAA
 PrU2 ATGTATAGGTACACTTTTTGGTAGGGAAATATATACATAGTGAA
 PfU2 ATGTATAAGTACACTTTTTGGTAGGGAAATATATACATAGTGAA
 PkU2 TCGAATAGGTACACTTTTTGGTAGGGAAAGATATACCTAGTGCG
 PvU2 CCGAATAGGTACACTTTTTGGTAGGGAAAGATATACCCAGTGGA
 PgU4 TTATATAGGTACACTTCCAATATTGAAAAAAGTACATAATTAA
 PcU4 TTAAATAAGTACATTTTTTCATATTGAAAAAATAACATAATTAAA
 PyU4 TTAAATAAGTACATTTTTTCATATTGAAAAAATAACATAATTAAA
 PbU4 TTAAATAAGTACACTTTTTTCATATTGAAAAAATAACATAATTCAA
 PrU4 GCTTATAAGTACAGTTTTTGGTAGGGAAAAACAACACAATAAAA
 PfU4 GCTTATAAGTACATTTTTTGGTAGGGAAAAACAACACAATAAAA
 PkU4 ACGCATAGGTACACTTTTTGGCATTGAAAAAATAACATACTTGG
 PvU4 TCGGATAGGTACACTTTTTGGCATTGAAAAAAGTACATACTGGG
 PgU5 TTCGAGTGGTATAAATTTGATATTTAAAAATATACATAATAAT
 PcU5 TATGAGTGGTACGATTTTTGATATTTAAAAATAACATAGTAAA
 PyU5 TATGAGTGGTACGATTTTTGATATTTAAAAATAACATAATAAAA
 PbU5 TATGAGTGGTACGATTTTTGATATTTAAAAACAATACATAATAAAA
 PfU5 TTGGAGAGGTACACTTTTTGGCATTGAAAAATATACATAGTAGA
 PkU5 TGTGAGAGGTACATTTTCAGTATTGAAAAACTTACATAGTGAC
 PvU5 TGCGAGAGGTACACTTTTCAGTATTGAAAAAATAACATAGTGAG
 PfU3 TTCGACAGGTACATTTTTTCGCGTTGAAAAAATAACACTATGGA
 PgU3 TTCAACTGGTACAATAATAGTGTTGAAAAATATACATAATCAA
 PcU3 ACTCAGTGGTACATTATTAGTATTGAAAAATTTACATAGTGGA
 PbU3 GCTCAGTGGTACATTATCGGTATTGAAATTTTTACATAATGAA

SNPE sequences aligned for Plasmodium U RNAs

Supplementary Figure 8

Chr	Coordinates		RNA gene	Strand	Oligonucleotides (5'→3')
	From	To			
chr1	218755	219062	RNAse MRP	-	AGATAACTAACTGTTTATCTCGGGGACTTTTCTA
chr1	394370	394644	RUF5	-	AGATATAGGATCAACAACAAAACAAAAATGTA
chr2	766389	767014	RNAse P	-	ATTCTTTAAATGCAGCATCTCAGACCTTCCTCC
chr2	767742	767583	RUF2	-	GCCACCGTATATACATTTGTTATATGAACAGATTTGAA
chr2	767976	768057	snoR01	-	CTTCTTAGAGGTTAATCAATCATTGGATTTAAAAATCAAATCATTTCG
chr3	365248	365391	U4 snRNA	+	GCTCTCTGCTTTTTTCAAGCATCGAG
chr3	398156	398238	snoR02	-	CATTGTGATGCATGAAAAAATATCTTCATGGTTATATACTTCAG
chr3	307897	308056	snoR03	+	ACGTAGTTCATTTATATAAACACATGGAACACAAATGG
chr4	564354	564506	RUF6-3	+	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr4	580183	580337	RUF6-9	+	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr4	595408	595562	RUF6-8	+	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr4	949391	949545	RUF6-6	+	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr4	961289	961443	RUF6-7	+	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr4	984358	984513	RUF6-11	+	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr5	465765	465944	snoR04	+	TAACGCAGTTTTTTTCTTCATCGCCTTAATAGC
chr7	563855	564009	RUF6-1	+	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr7	578528	578683	RUF6-2	+	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr7	593901	594056	RUF6-12	+	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr7	633326	633481	RUF6-13	+	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr8	240934	241120	RUF3	+	GTTTACTAATTCCTTAATAATATGGTTAATAGTAAGTG
chr8	428601	428756	RUF6-4	-	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr8	457150	457305	RUF6-10	-	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr8	1162304	1162401	snoR05	-	CTCTTCAATTTAAAAATAAAAAATCAGAGTGGATGGGATAGTCAC
chr8	240177	240261	snoR06*	+	AATTCACACACTTTTTATTCTGTTCTAACAAATGTGC
chr9	761201	763348	Telomerase RNA	+	CCTATATACAACCTCATGTTTCATG (Probe 12) GCATACACATAAATATTAGTCATATGTC (Probe 16)
chr11	378873	378786	snoR07	-	TTTTAGTCCGCCATCGCTCAA
chr11	388054	388123	snoR08	-	GGGCATAGTTATCATCAAATAAAATCAGAAGCAGAAGTCT
chr11	388680	388762	snoR09	-	AATTTATCTTCAAATAAATTTTCAGATGCCAAGCGTACG
chr11	389376	389452	snoR10	-	TTAATCAGTTTGGGGCAGTACTATTGCTTCATTTT
chr11	390125	390328	snoR11	-	GTGCACAACTTGACTGCATAGGATGCTCACAATTTATAAC
chr11	392867	392951	snoR12	-	AATTTTCATCAAATAAATTTTTATCAGACATATGCTTGTG
chr11	1163501	1163601	snoR13	+	CAGACATCTAAGTGAAGGCTACAATAAAAAATTCATTGAGC
chr11	1458207	1458407	U2 snRNA	-	GTGAAATTGATAAGGCCTCTATTGA
chr12	479483	479609	snoR14	-	CCTTTGGCCCTAAATCAGGACAGC
chr12	576403	576572	U1 snRNA	-	ACCCCCATGTGGAGAGTCTATAGC
chr12	881975	882105	snoR15	-	TTTATCAGATTGAAAATACTCATTTTTTTTGACGCTC
chr12	1715814	1715968	RUF6-5	-	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr12	1731787	1731942	RUF6-14	-	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr12	1745271	1745409	RUF6-15	-	AAATTGTCGGCAAGCGGAGTCTGAACCAACGTTCTCACAAGG**
chr12	1857838	1858079	U3 snoRNA	+	GTTACGCGGACGCAAGCTCATTTA
chr13	243850	243969	snoR16	-	CGCTCAACTGAGTAATTGTTGAGTTTCAGTTATACTCAG
chr13	1213597	1213860	RUF1	+	TATTATGGGCGTTGAAAATACCGGGAATATGAAGAGA
chr13	1295141	1295220	snoR17	+	TTCAGAGATCTTGGTGAATAGCATAAAAAATCATCAAC
chr13	1324456	1324540	snoR18	+	ATCGGCTATTAATTTATCAACATGAAAATTTTTCAGTCCTATC
chr13	1479698	1479795	snoR19	-	CTACATTTAGTAGTATGAAATTTAAATGTGCGCCCATATATAATCA TC
chr13	1632636	1632740	U6 snRNA	-	TTACATTCCTTCTCGAACGTC
chr13	1637299	1637378	snoR20	+	GAACGTTCTACCATCTCCATTGATAATGTC
chr13	2049072	2049216	snoR21	+	TTTCAGTCAAATGCCTCAAATAATCATGATGAT
chr14	92791	92873	snoR22	-	AGAAGACGAACATATTTATAATATTCTCATGTCCCTACTTGC
chr14	782261	782563	SRP RNA	-	AGCCTGAGGCGGTTTCATGATTCATCA
chr14	972917	973000	snoR23	-	CTTCAAAGATGCAGAAGAACGAAAGTTAAATAATTTTTTTTATTCA TC
chr14	973287	973366	snoR24	-	CAGATACTATAATAATCATCAATAATTTTCAGACGTAATACCCAC
chr14	974146	974215	snoR25	-	CAGGACGCTTATAATTTCTCAAATTTTTCAAATCAGGTCTG
chr14	975372	975531	snoR26	-	AATGCTTAACTCGTTTTATCATTGCATAAACA
chr14	979604	979745	snoR27	+	TTGTATTATAAAATACGGCCCAACAAAAAATTTCTCAA
chr14	979907	979979	snoR28	+	CAACATAAATATTCGGACGGCACTTCCTTGAAG
chr14	981728	981813	snoR29	+	GCTCTTCAGACCCGAAAGGCTTTATATTATGAAAAGGTTG
chr14	982295	982369	snoR30	+	TCTGTATATTTTCAGTAACACAGACCAAGTTCTTCATATCATC
chr14	982450	982724	RUF4	+	TTGTATATACACATGAGGTGTATACATAATTTCTTTC
chr14	983011	983155	snoR31	+	CATTCTTTGAAAAATCTTGCCCGCTAGGGATTACAC
chr14	1888363	1888489	U5 snRNA	+	AACATACTTACTACACGGCAATCTT

* Not detected; **RUF 6 genes have common probe

Suppl. Table 1

RNA gene	Type	Strand	Coordinates		
			From	To	
Ribosomal RNA (rRNA)	rRNA Operon on Chr-1	18S rRNA	+	474887	477036
		5.8S rRNA	+	477430	477591
		28S rRNA	+	478413	482527
	rRNA Operon on Chr-5	18S rRNA	+	1289593	1291685
		5.8S rRNA	+	1292044	1292203
		28S rRNA	+	1292402	1296192
	rRNA Operon on Chr-7	18S rRNA	+	1139139	1141225
		5.8S rRNA	+	1141590	1141749
		28S rRNA	+	1141948	1145735
	rRNA Operon on Chr8	28S rRNA	-	92940	98702
		5.8S rRNA	-	99972	100132
		5.8S rRNA	+	1281064	1281224
	rRNA Operon on Chr-11	18S rRNA	+	1922904	1925054
		5.8S rRNA	+	1925419	1925587
		28S rRNA	+	1925842	1930056
	rRNA Operon on Chr-13	18S rRNA	+	2796338	2798488
		5.8S rRNA	+	2798854	2799022
		28S rRNA	+	2799279	2803493
	5S Loci on Chr-14		+	779577	779697
			+	780206	780326
			+	781116	781236
	Transfer RNA (tRNA)	tRNA Gln on Chr-2 (CTG)	+	164268	164340
		tRNA Ile on Chr-3 (AAT)	-	528575	528649
		tRNA Val on Chr-3 (CAC)	+	527888	527961
		tRNA Asn on Chr-4 (GTT)	+	181287	181361
		tRNA Ile on Chr-4 (TAT)	-	476754	476827
		tRNA Ser on Chr-4 (AGA)	+	476114	476196
		tRNA Ala on Chr-4 (TGC)	+	524618	524690
		tRNA Glu on Chr-4 (CTC)	-	525050	525122
		tRNA Leu on Chr-5 (TAG)	+	451352	451432
tRNA Phe on Chr-5 (GAA)		-	603949	604023	
tRNA Leu on Chr-5 (TAA)		-	1151220	1151303	
tRNA Glu on Chr-5 (TTC)		+	1150227	1150300	
tRNA Arg on Chr-5 (TCG)		+	1208382	1208455	
tRNA Leu on Chr-6 (CAG)		-	861681	861762	
tRNA Ser on Chr-6 (TGA)		-	883560	883642	
tRNA Ala on Chr-6 (CGC)		+	861013	861085	
tRNA Ala on Chr-7 (AGC)		-	166914	166841	
tRNA Tyr on Chr-7 (GTA)		+	167417	167501	
tRNA Thr on Chr-7 (AGT)		+	381452	381525	
tRNA His on Chr-7 (GTG)		-	382106	382178	
tRNA Asn on Chr-7 (TTT)		-	384392	384465	
tRNA Asn on Chr-7 (CTT)		+	383245	383318	
tRNA Leu on Chr-7 (AAG)		+	727033	727113	
tRNA Asp on Chr-7 (GTC)		+	726172	726244	
tRNA Ser on Chr-7 (GCT)		-	728112	728194	
tRNA Val on Chr-7 (TAC)		+	1373436	1373509	
tRNA Thr on Chr-7 (TGT)		-	1374388	1374460	
tRNA Leu on Chr-11 (CAA)		-	142472	142556	
tRNA Gly on Chr-11 (TCC)		+	140970	141042	
tRNA Pro on Chr-12 (CGG)		+	666876	666948	
tRNA Val on Chr-12 (AAC)	+	2112862	2112935		
tRNA Gln on Chr-12 (TTG)	-	2113714	2113786		
tRNA Ser on Chr-13 (CGA)	-	1524305	1524387		
tRNA iMet on Chr-13 (CAT)	+	1575550	1575622		
tRNA Pro on Chr-13 (TGG)	-	1577120	1577192		
tRNA Arg on Chr-13 (TCT)	+	1631363	1631437		
tRNA Thr on Chr-13 (CGT)	-	2194238	2194311		
tRNA Cys on Chr-13 (GCA)	-	2779483	2779555		
tRNA Trp on Chr-13 (CCA)	-	2777413	2777485		
tRNA Arg on Chr-13 (ACG)	+	2776687	2776761		
tRNA Arg on Chr-13 (CCT)	+	2777955	2778029		
tRNA Gly on Chr-13 (GCC)	+	2780099	2780170		
tRNA Pro on Chr-14 (AGG)	+	778291	778363		
tRNA eMet on Chr-14 (CAT)	+	1545178	1545252		
tRNA Sec on Chr-14 (TCA)	-	1544100	1544190		

Suppl. Table 2