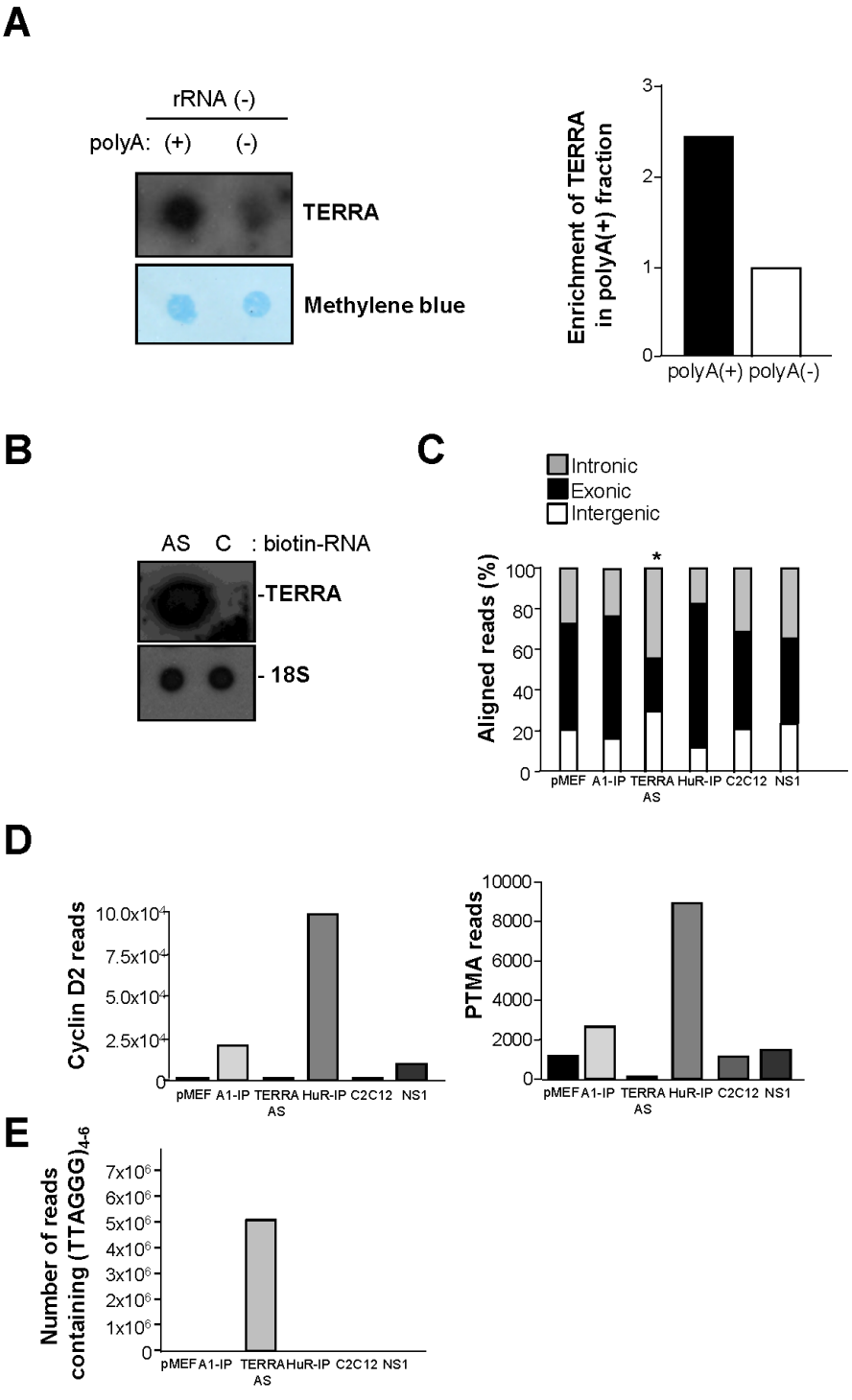
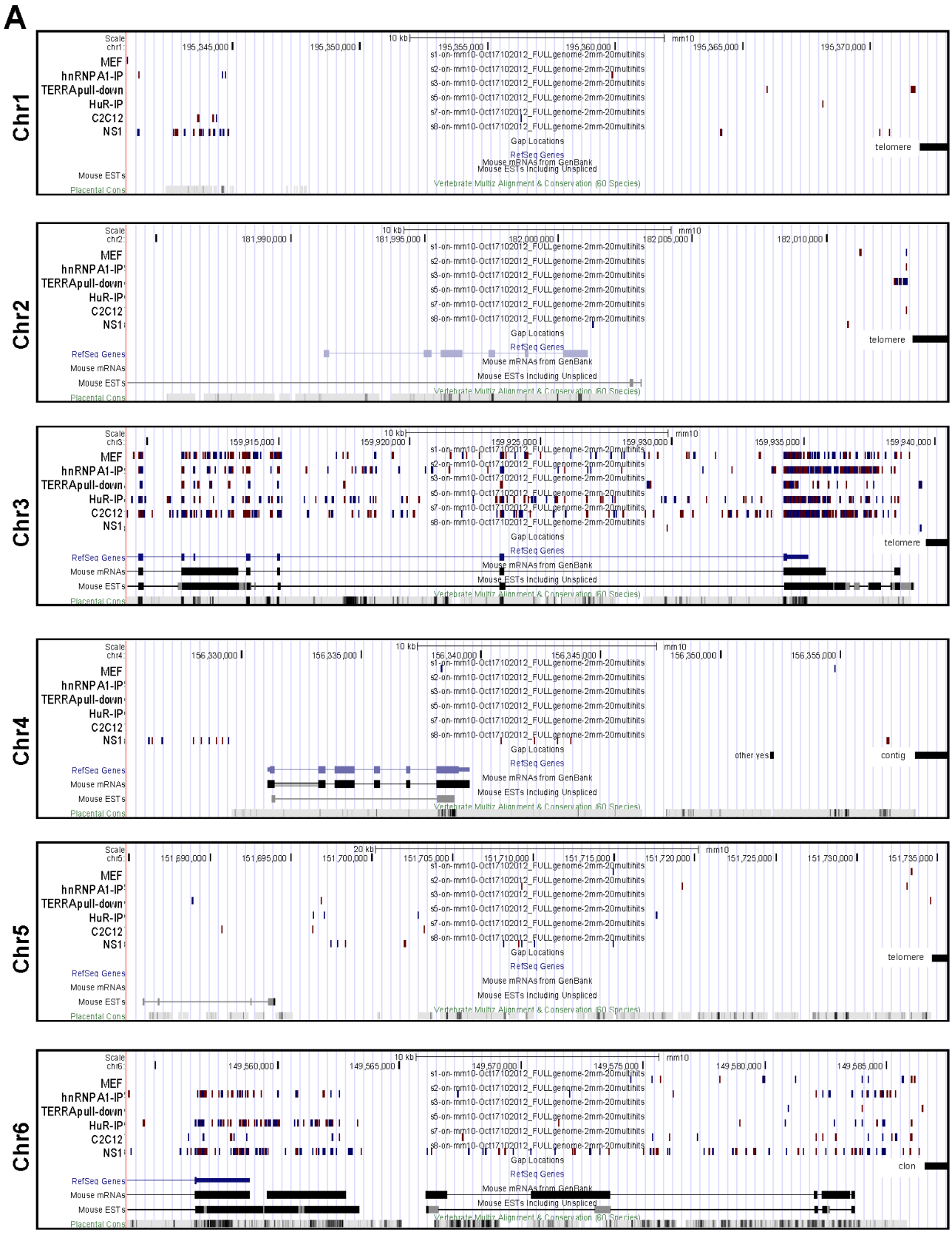
Supplementary Figures

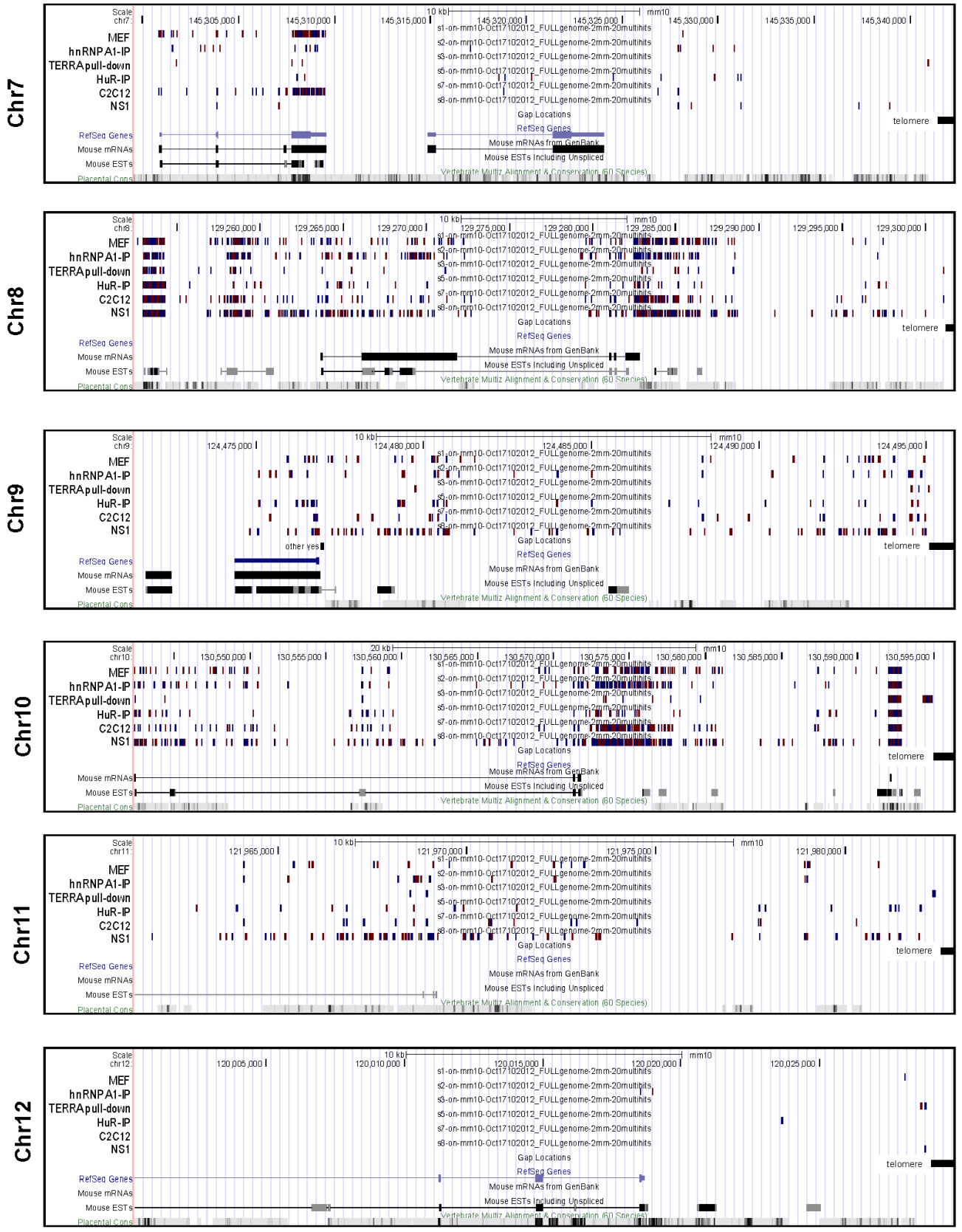


Lopez de Silanes_Suppl. Fig.1

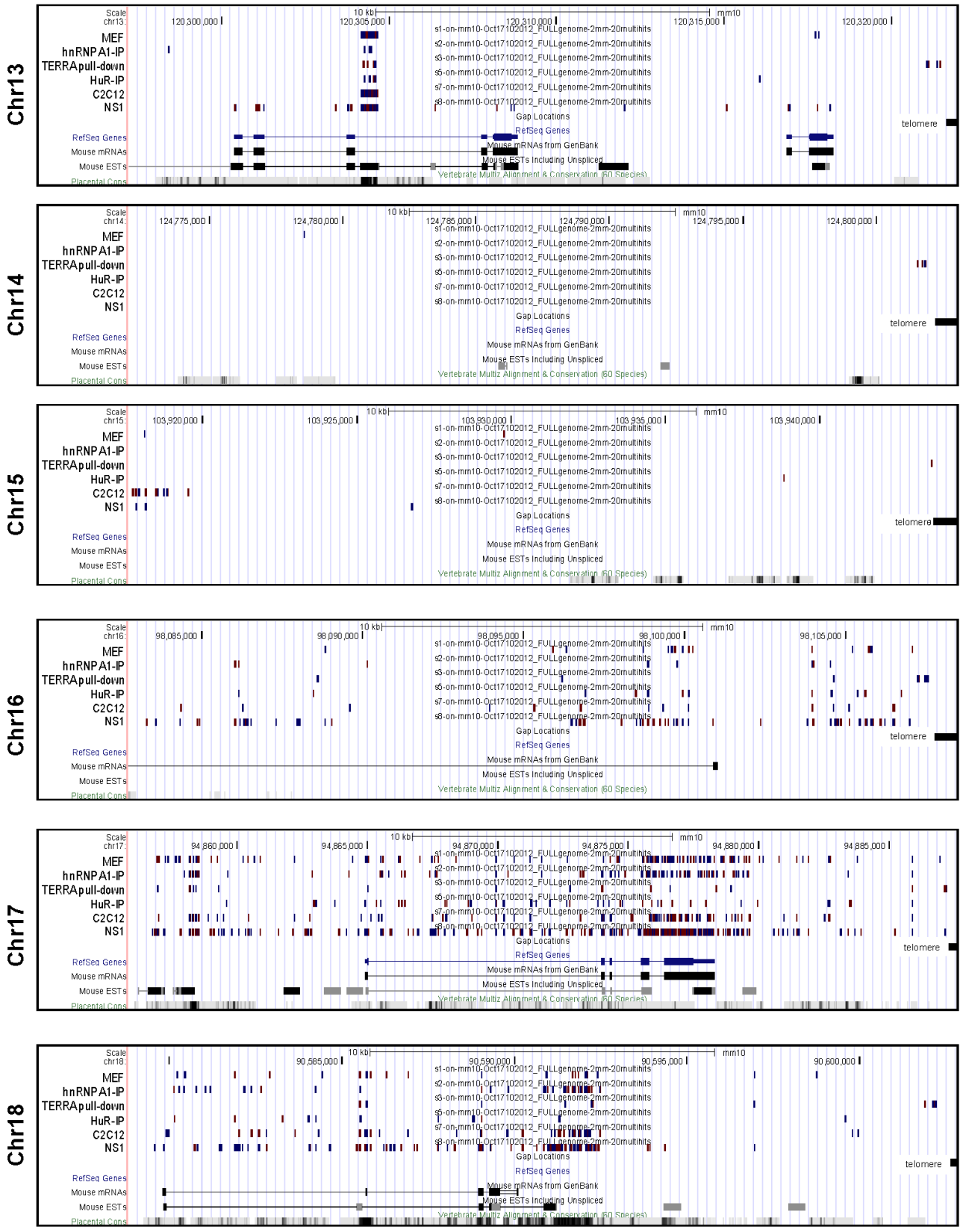
Supplementary Figure 1. Quality check of reads and alignments upon RNA-seq. (A) Total RNA was first depleted for rRNAs and then polyA (+) and polyA(-) fractions obtained. TERRA detection in these fractions was carried out by RNA dot blot using a ^{32}P-dCTP labelled TERRA probe; Methylene blue was used as a loading control. **(B)** Biotin pull-down was carried out using nuclear protein lysates from pMEFs and an oligo complementary to the TERRA telomeric track (AS) as a bait, whereupon RNA was isolated and used for TERRA detection by RNA dot-blot. A biotinylated RNA corresponding to a random sequence of the same length as the biotinlylated TERRA antisense oligo (N_{48}) was used as control (C). **(C)** Percentage of aligned RNA-seq reads in intragenic (intronic+exonic) and intergenic regions within the different samples. * $(TTAGGG)_{3-6}$ constitute 60% of the total number of reads in the the biotin pull-down sample (TERRA AS) and were not counted in this analysis **(D)** Number of reads aligned under the cyclin D2 and PTMA mRNAs within the different samples. **(E)** Total number of reads containing four-to-six TTAGGG repeats within the different samples.



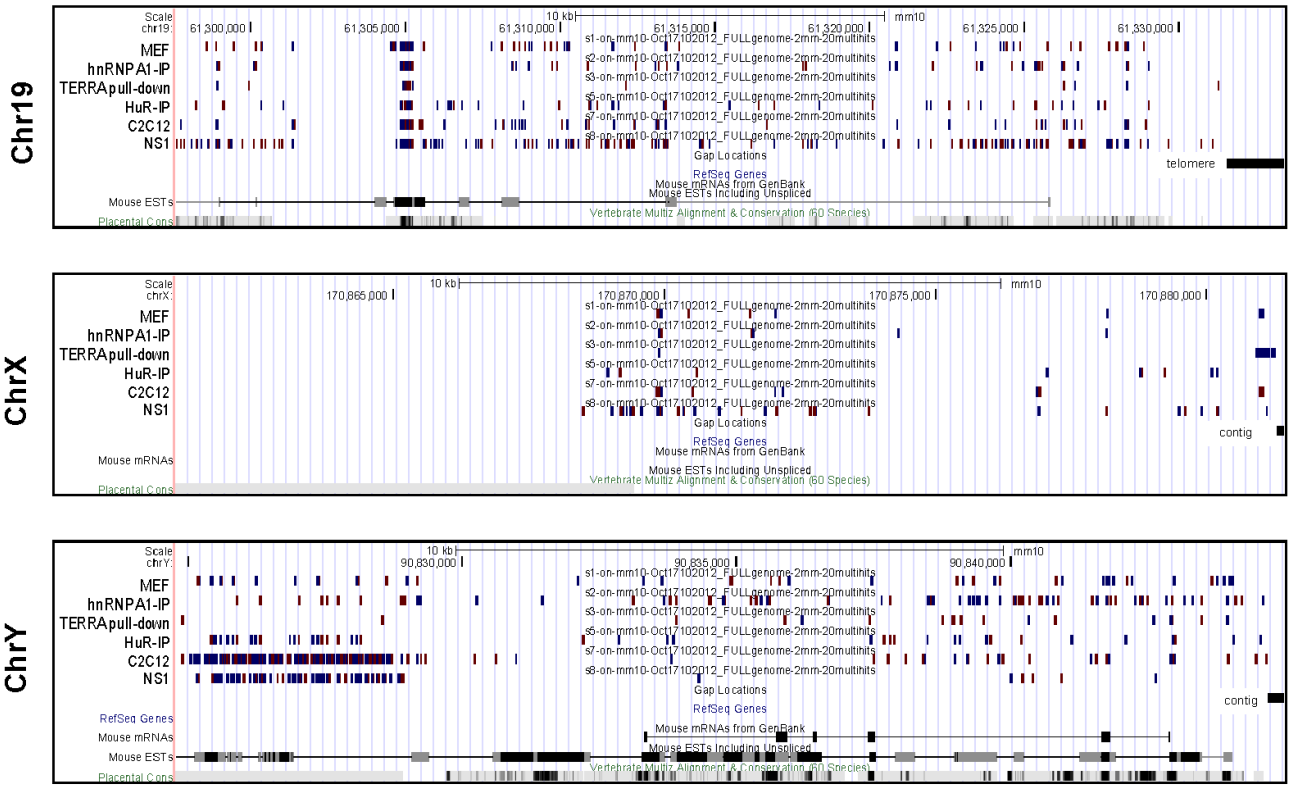
Lopez de Silanes_Suppl. Fig. 2



Lopez de Silanes_Suppl. Fig. 2 (cont)



Lopez de Silanes_Suppl. Fig. 2 (cont)



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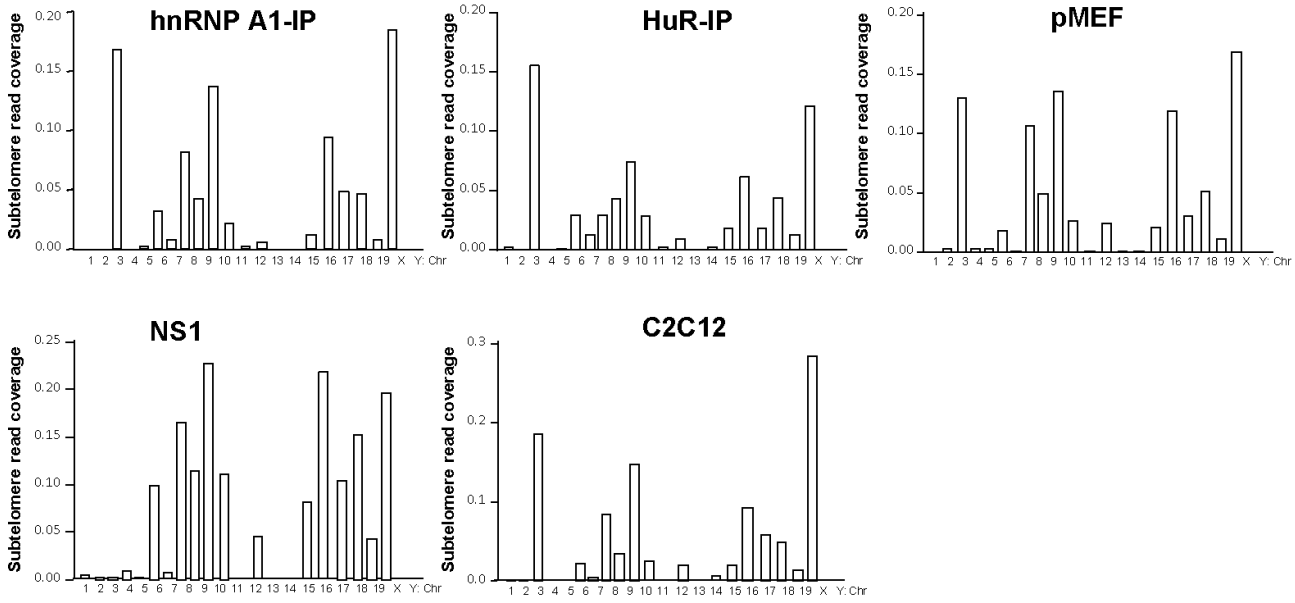
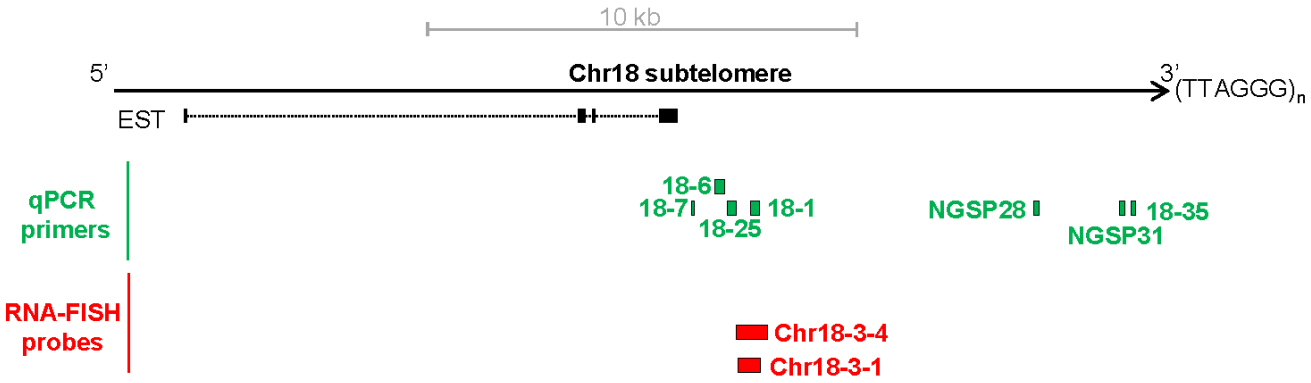
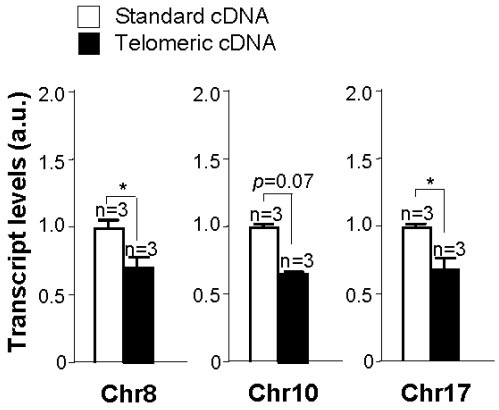


Lopez de Silanes_Suppl. Fig. 2 (cont)

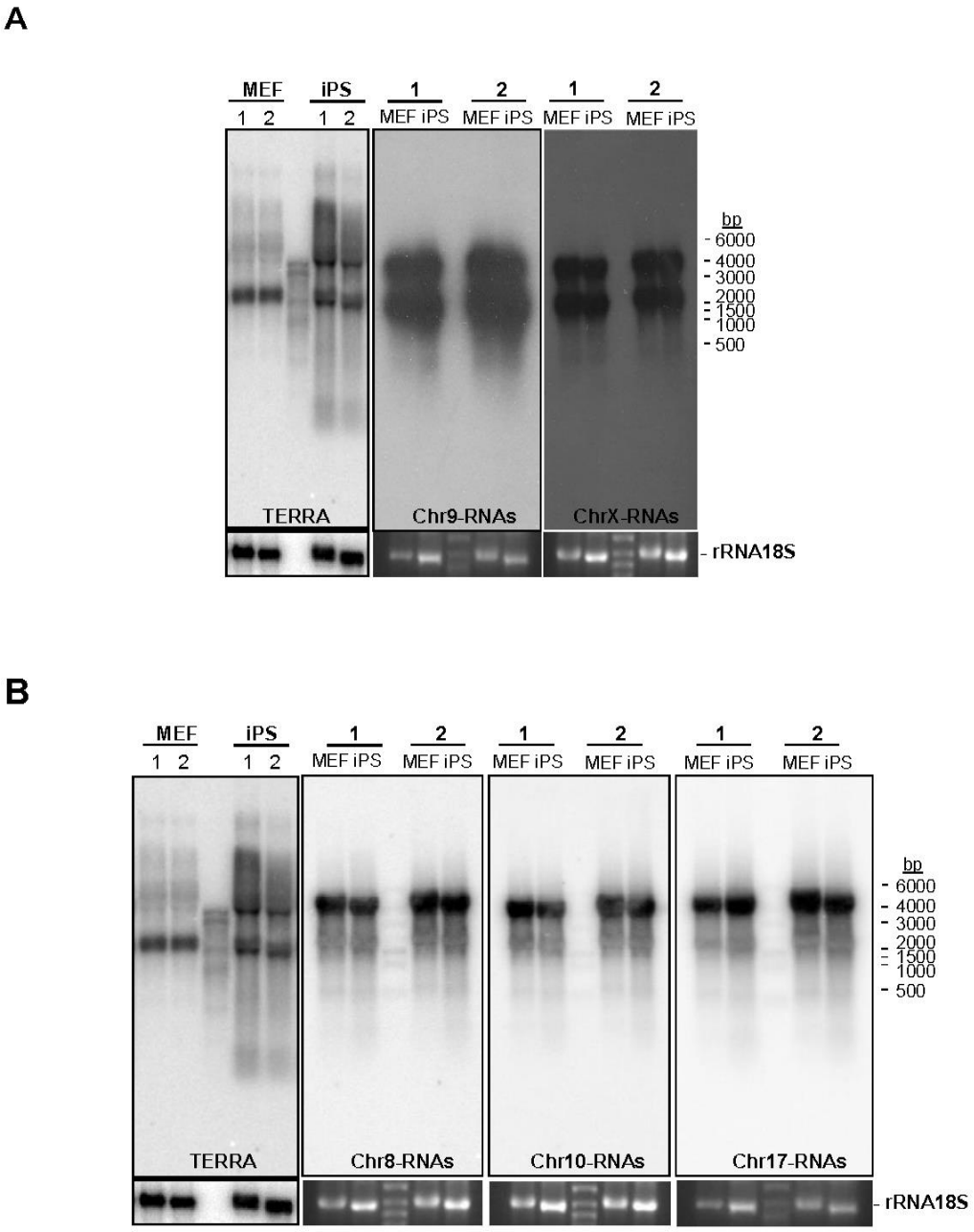
Supplementary Figure 2. RNA-seq read alignments and read density at the subtelomeres of all chromosomes. (A) UCSC snapshot showing (from top to bottom) the genomic scale, the RNA-seq read alignments for all the samples (S1-S8) within a 20-kb region just adjacent to the telomere of all chromosomes, annotated Ref Seqs, mRNAs and ESTs and mammal conservation. 'Telomere', 'clone' and 'contig' UCSC annotation can be seen as a solid bar on the right side of the snapshot. **(B)** Graphs show the read density corresponding to the samples that are not shown in Figure 1A in a 30-kb region adjacent to the telomere of each chromosome. Note that chromosome 4 and Y are not sequenced until the telomere.



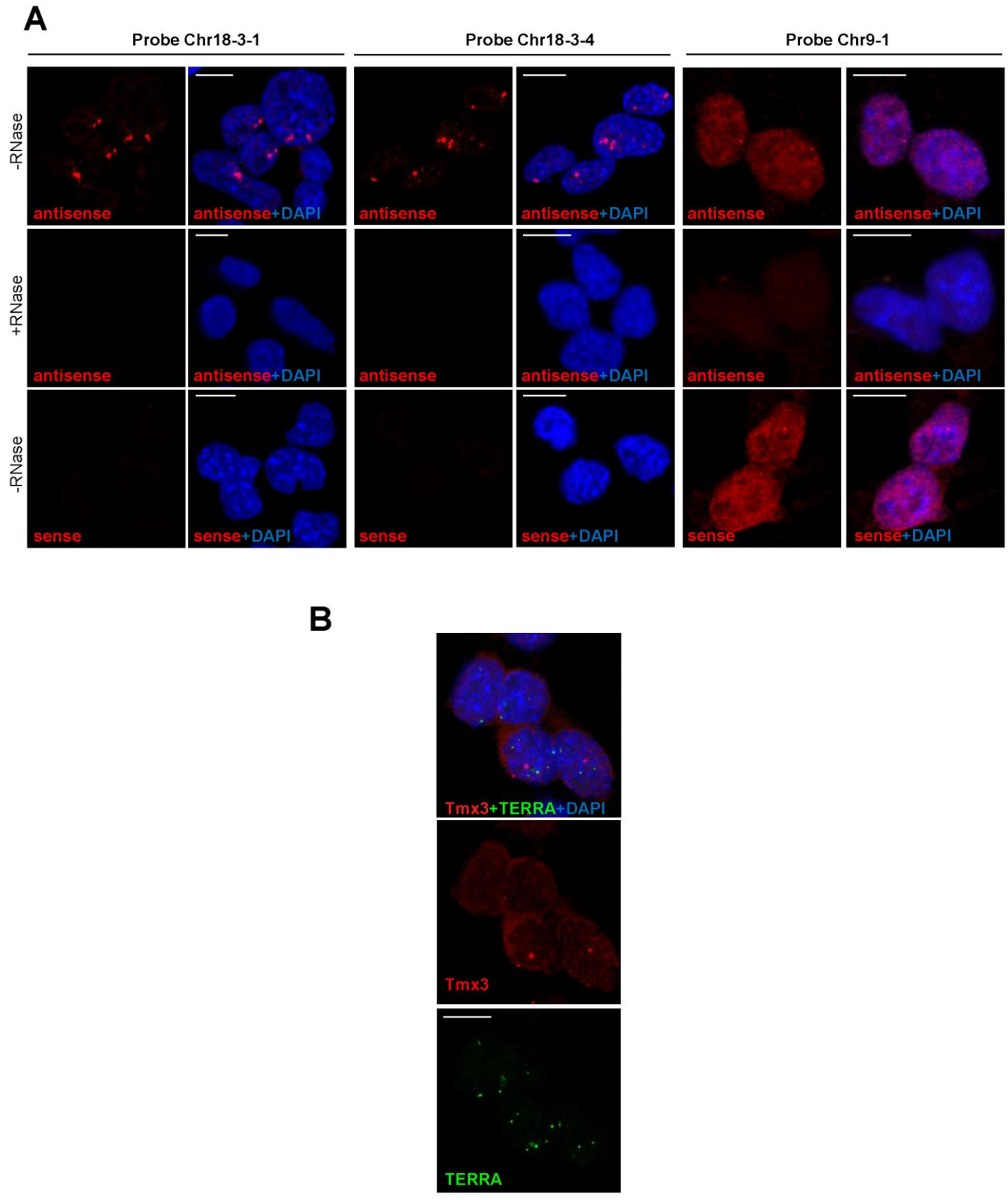
Supplementary Figure 3. Genomic position of primers and RNA-FISH probes at the subtelomere of chromosome 18. Diagram showing, from top to bottom, genomic scale, annotated EST and the position of qRT-PCR primers and RNA-FISH probes.



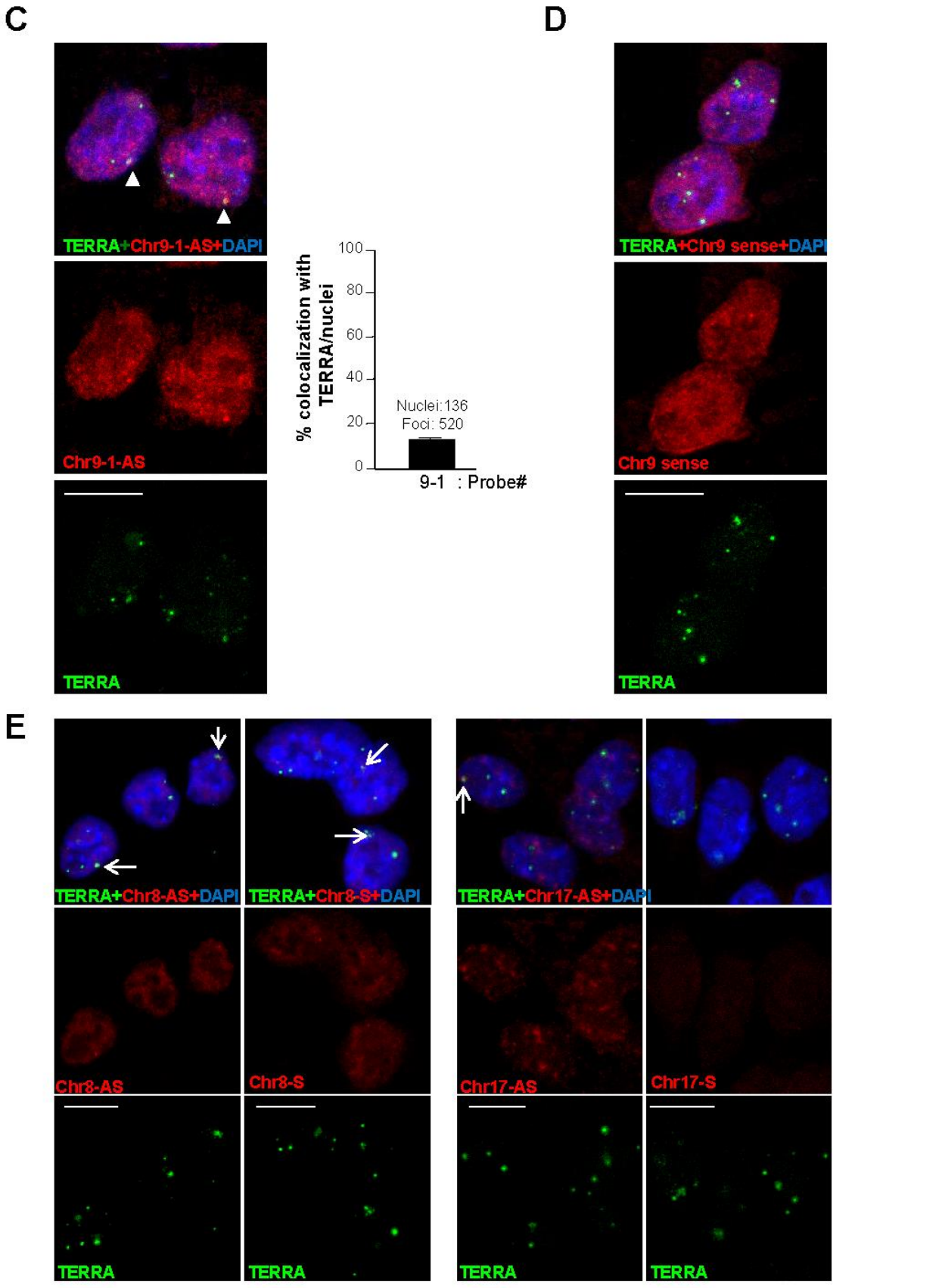
Supplementary Figure 4. Chromosome 8, 10 and 17 are not enriched in the telomeric cDNA. Reverse-transcribed RNA prepared with either an oligo complementary to the telomeric repeat (4xCCCTAA) ('telomeric cDNA') or with random hexamers ('standard cDNA) was used for qPCR detection of chromosome 8, 10 and 17 transcripts. Data provided are the mean values ±s.e.m from three different iPS clones. Statistical analysis carried out with The Student's *t*-test (*$p < 0.05$ and **$p < 0.001$).



Supplementary Figure 5. Transcripts arising from chromosome 9 and X render a size-restricted TERRA-like smear. (A) Northern blotting using ^{32}P-dCTP labelled probes targeting either TERRA or transcripts arising from the subtelomere of chromosome 9 and X or (**B)** from 8, 10 and 17 in two different clones of iPS and their parental pMEFs; rRNA 18S from ethidium bromide gel was included as a loading control. Note that the sample order in the TERRA Northern blot is different from the other ones but the samples loaded are the same for all Northern blots.

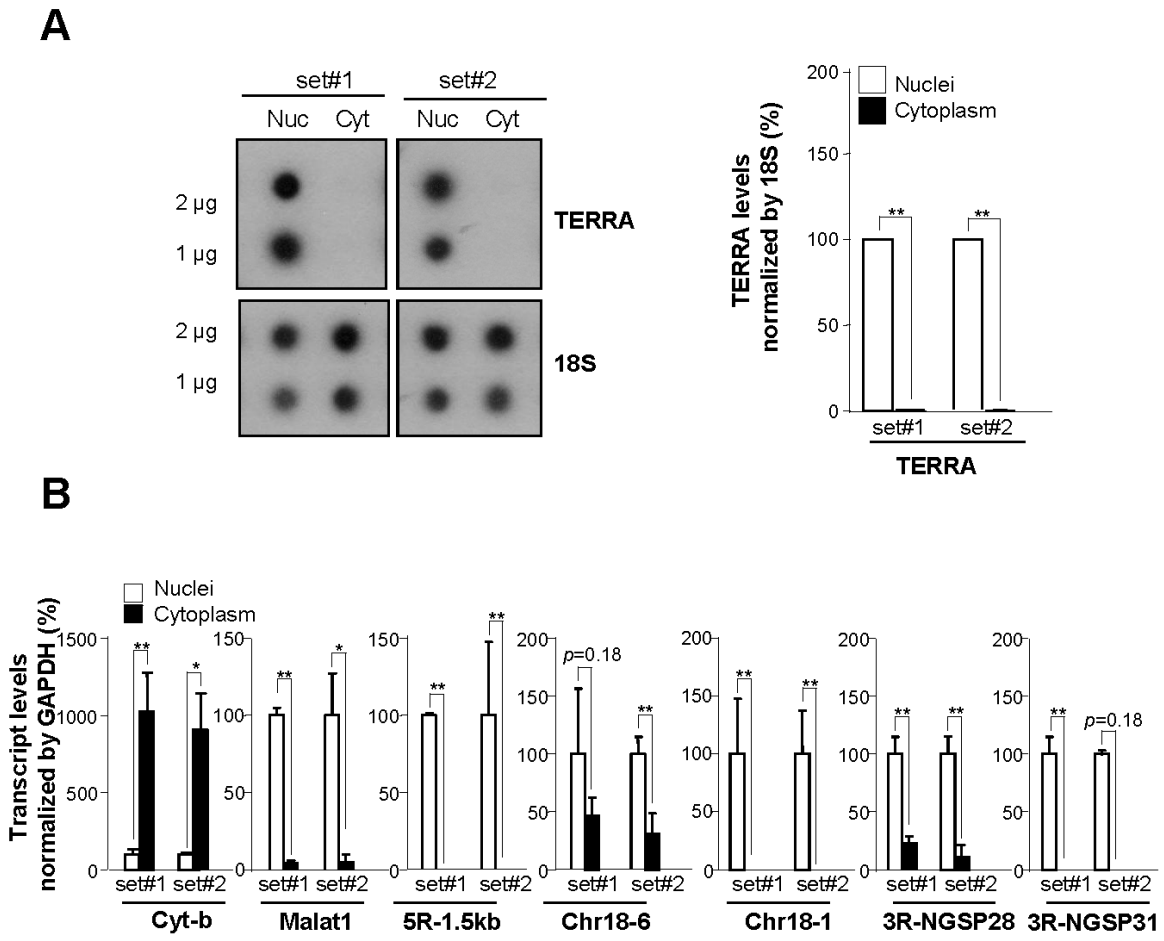


Lopez de Silanes_Suppl. Fig. 6

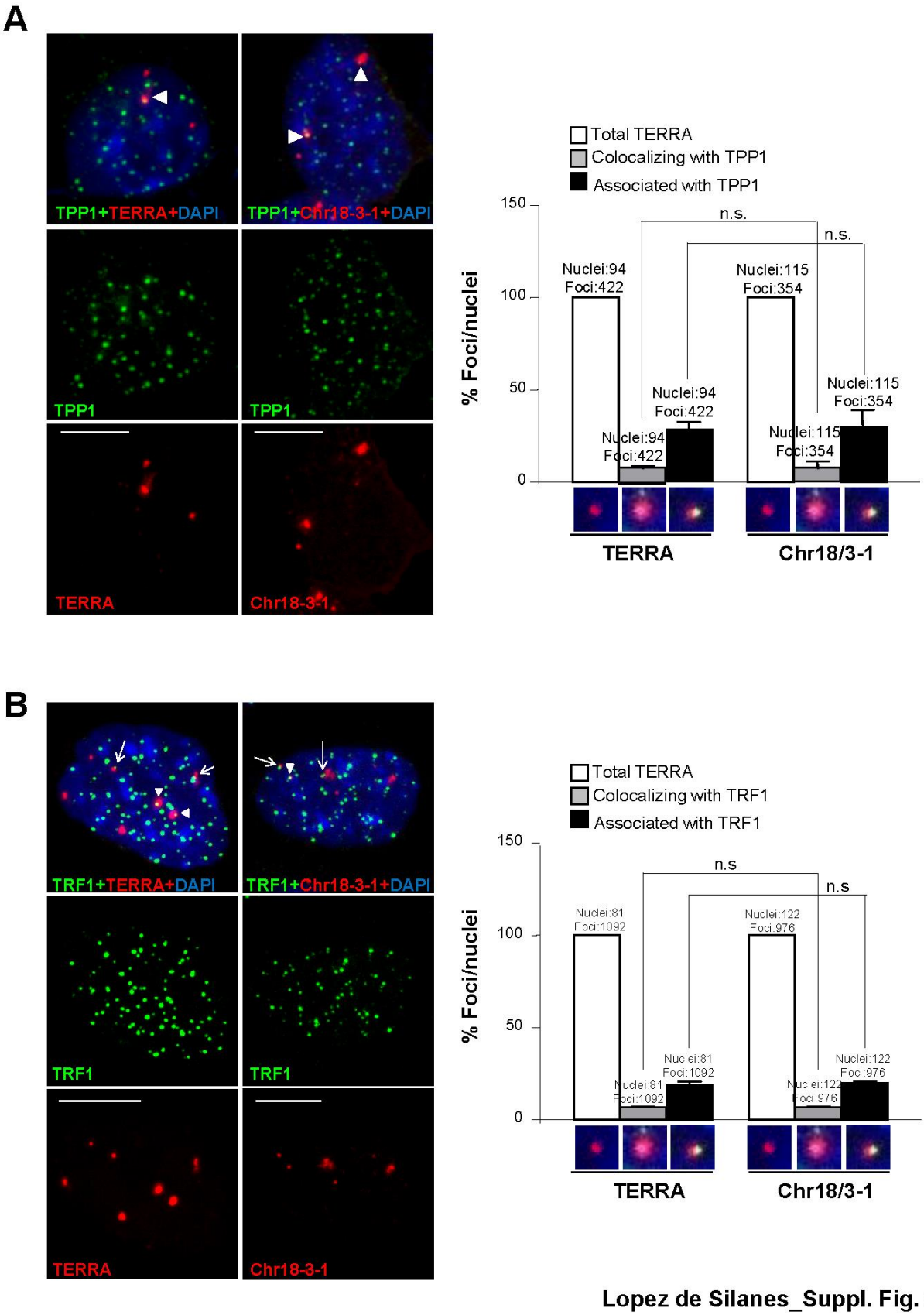


Lopez de Silanes_Suppl. Fig. 6 (cont)

Supplementary Figure 6. Specificity of RNA-FISH probes. Confocal microscopy images from RNA-FISH preparations using **A)** the *antisense* and *sense* strands of the RNA-FISH probes in the absence or presence of RNase. **B)** Confocal microscopy images of double RNA-FISH preparations using probes targeting either TERRA (green) or Tmx3 (red). Tmx3 is the first gene annotated in the chromosome 18 subtelomere. **C)** Same as in B) but using a probe targeting chromosome 9-RNAs (red) or TERRA's telomeric track (green). The graph shows the percentage of colocalization of chromosome 9-RNAs with TERRA spots (mean+s.d, n=number of nuclei). Total number of foci and nuclei analyzed are indicated **D)** Same as in C) but using a probe against the negative strand of chromosome 9-RNAs (sense probe). **E)** Same as in C) but targeting chromosome 8 or 17 (red). Scale bars: 10 μm

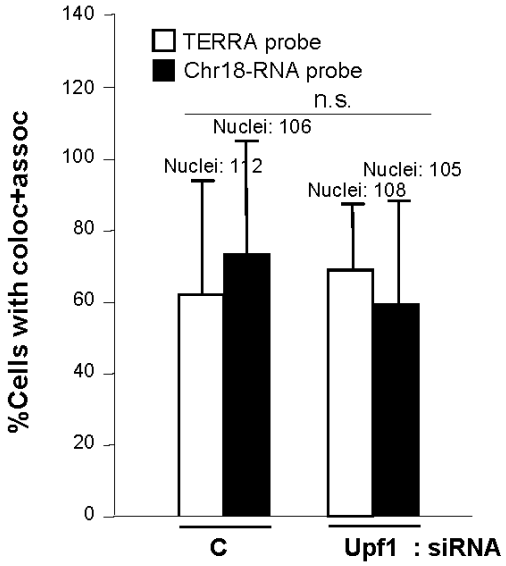


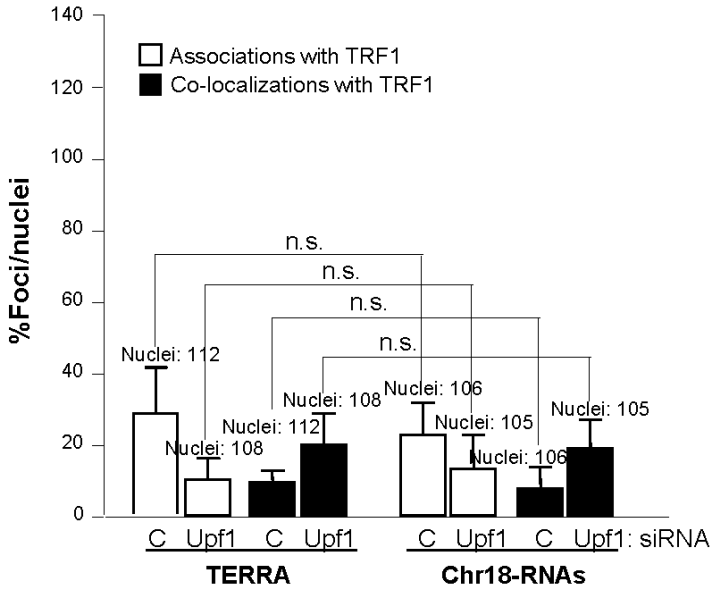
Supplementary Figure 7. Chromosome 18-RNAs are enriched in the nuclear compartment. RNA isolated from nuclear and cytoplasmic fractions from two independent set of pMEFs was used for **(A)** (*Left)* RNA dot-blot TERRA detection by RNA. Hybridization of 18S rRNA was included as a loading control. (*Right*) Quantification of TERRA signals normalized by 18S (mean+s.d, n=3 technical replicates in two independent set of pMEFs). **(B)** RT-qPCR detection of chromosome 18 transcripts in nuclear and cytoplasmic fractions (mean+s.d, n=3 technical replicates in two independent sets of pMEFs). Detection of *Malat1*, a known nuclear long-non coding RNA, and cytochrome b, a known cytoplasmic mRNA, serve to monitor the purity of the different fractions. Student's *t*-test was used for statistical analysis (*$p < 0.05$ and **$p < 0.001$).



Lopez de Silanes_Suppl. Fig. 8

C





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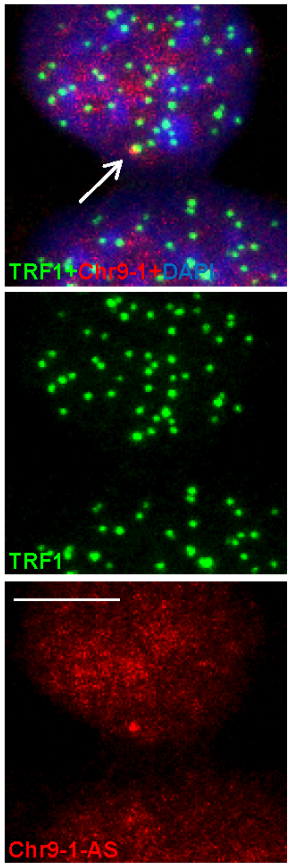
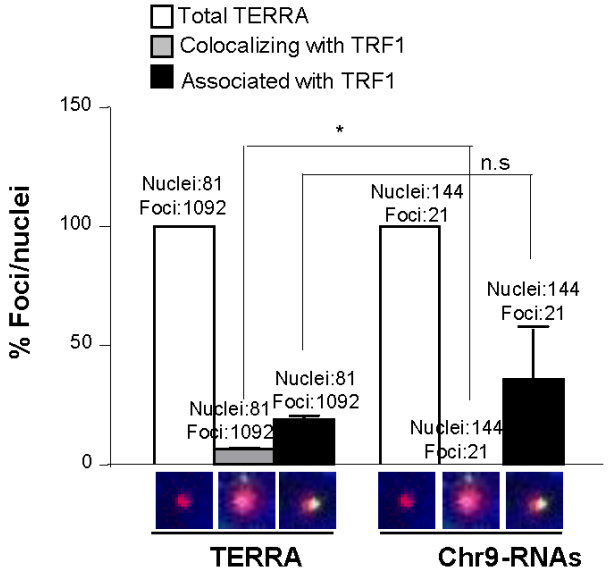
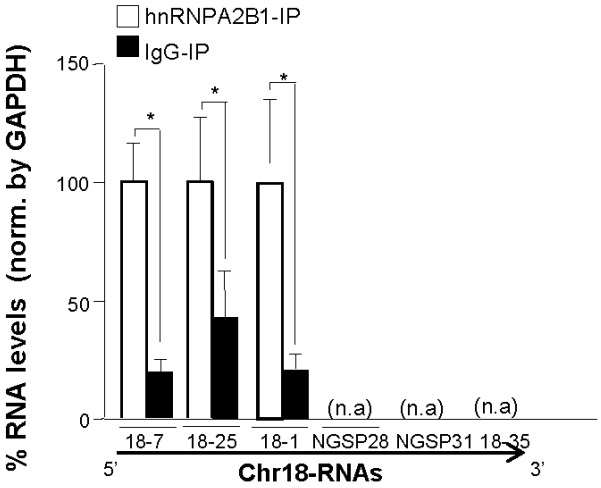




Lopez de Silanes_Suppl. Fig. 8 (cont)

Supplementary Figure 8. Chromosome 18- and 9-RNAs associate with telomeres as TERRA does. **(A)** Immunofluorescence followed by RNA-FISH to detect either TERRA or chromosome 18 transcripts foci (red) with either the telomere marker TPP1 protein or **(B)** TRF1 protein (green). Arrowheads and arrows indicate co-localization and association events, respectively. The percentages of either TPP1 or TRF1 foci co-localizing/associating with TERRA or Chromosome 18 RNAs per nuclei are represented (mean+s.e.m, n=number of nuclei; three different antibodies were used for telomere detection (TPP1, TRF1 and Rap1), see the results of Rap1 in **Fig. 2A**). **C)** Cells were transfected with either control siRNA or a siRNA against Upf1 and, two-days post-transfection, cells were processed for immunoflorescence to detect telomeres with a TRF1 antibody followed by RNA-FISH to detect either chromosome 18-RNAs or TERRA. (*Left*) The graph shows the percentage of cells with TRF1 colocalization/association with either Chromosome 18-RNAs or TERRA upon Upf1 downregulation (mean+s.e.m, n=number of nuclei). (*Right*) The percentages of TRF1 foci co-localizing/associating with TERRA or Chromosome 18-RNAs per nuclei upon Upf1 downregulation are also represented (mean+s.e.m, n=number of nuclei). **(D)** Same as in B) but using a probe against chromosome 9-RNAs (mean+s.e.m, n=number of nuclei). In all panels, the total number of foci and nuclei used for the analysis is indicated. Student's *t*-test was used for statistical analysis. Scale bars: 5 μm

A



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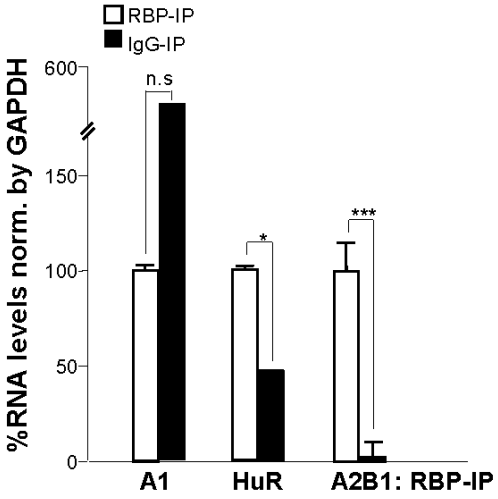

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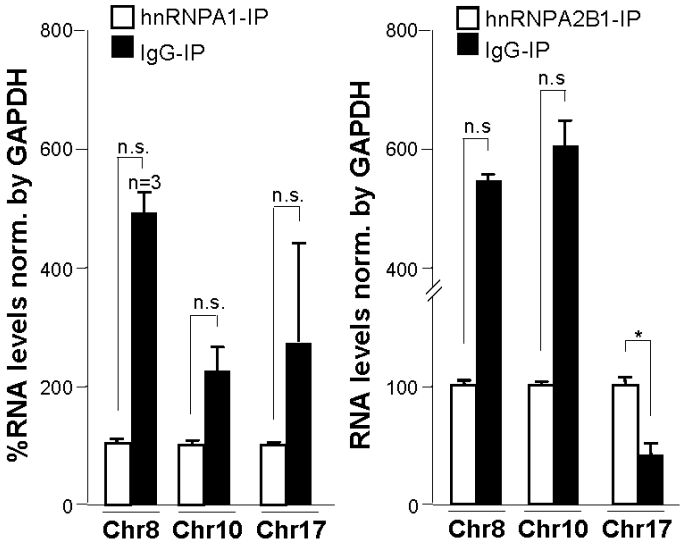
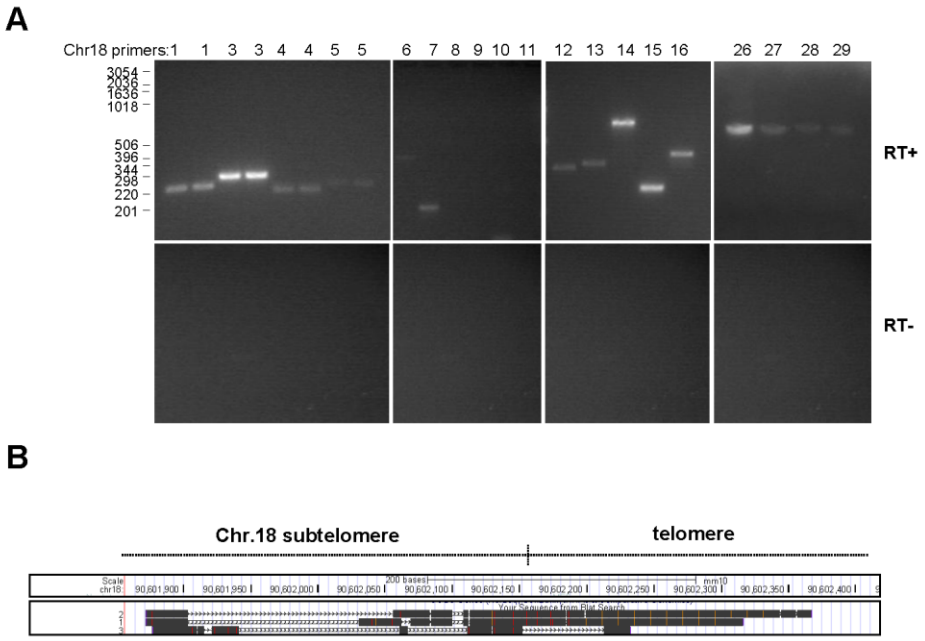
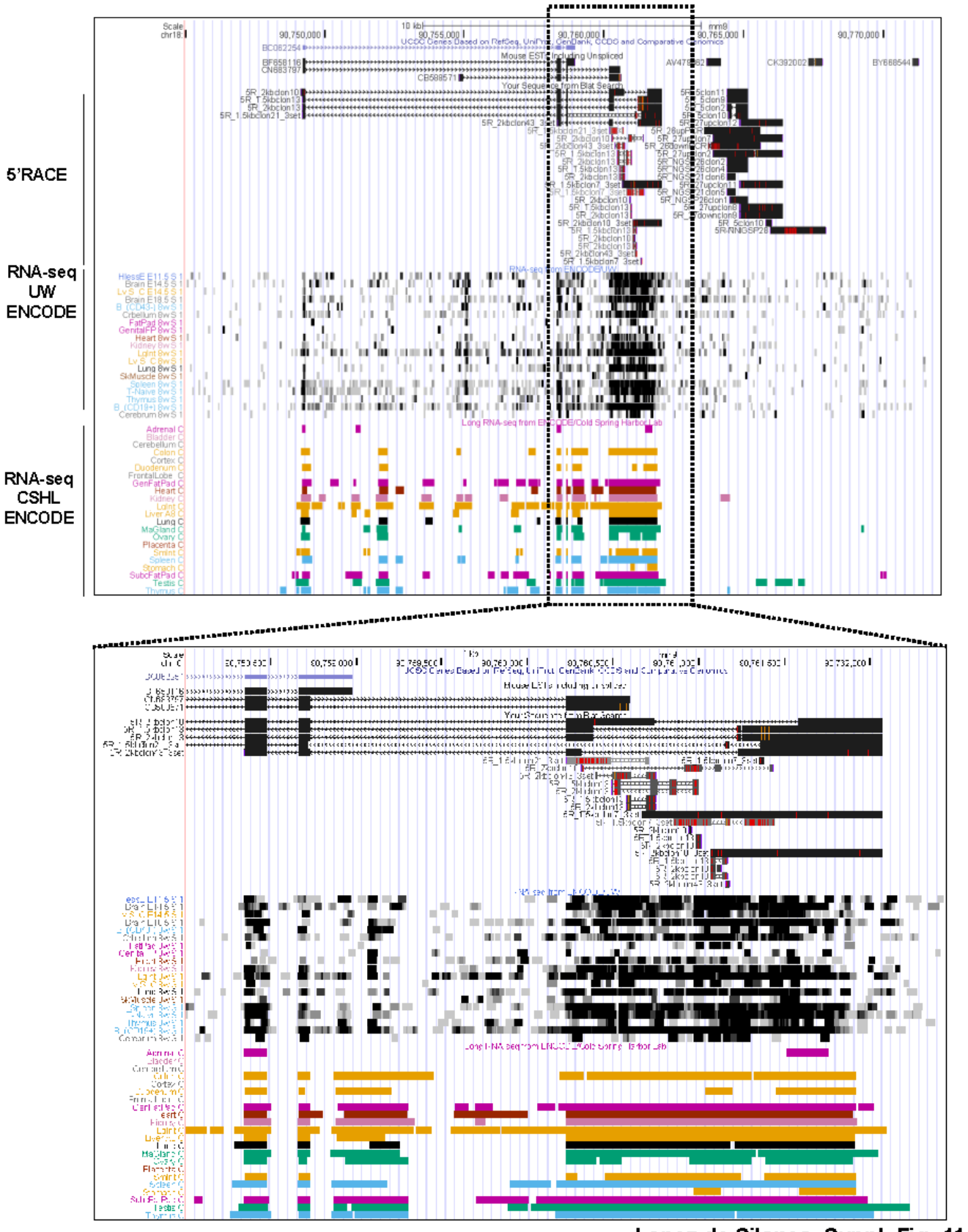


Lopez de Silanes_Suppl. Fig. 9

Supplementary Figure 9. Binding of TERRA RNA-binding proteins to chromosome 18, 9, 8, 10 and 17-RNAs. Immunoprecipitation (IP) assay of nuclear extracts prepared from iPS cells with antibodies recognizing the TERRA-bound RNA binding proteins under conditions that preserved mRNP complexes. RNAs isolated from IP material were subjected to qRT-PCR for **(A)** chromosome 18 **(B)** chromosome 9 and **C)** 8, 10 and 17 transcripts detection. The RNA-biding protein used is indicated in the different panels. GAPDH mRNA was used for normalization. Data was compared with respect an IgG-IP (mean values +s.e.m, in three different iPS clones). The Statistical analysis performed with the Student's *t*-test from three independent experiments (*$p < 0.05$, **$p < 0.001$ and ***$p < 0.0001$).

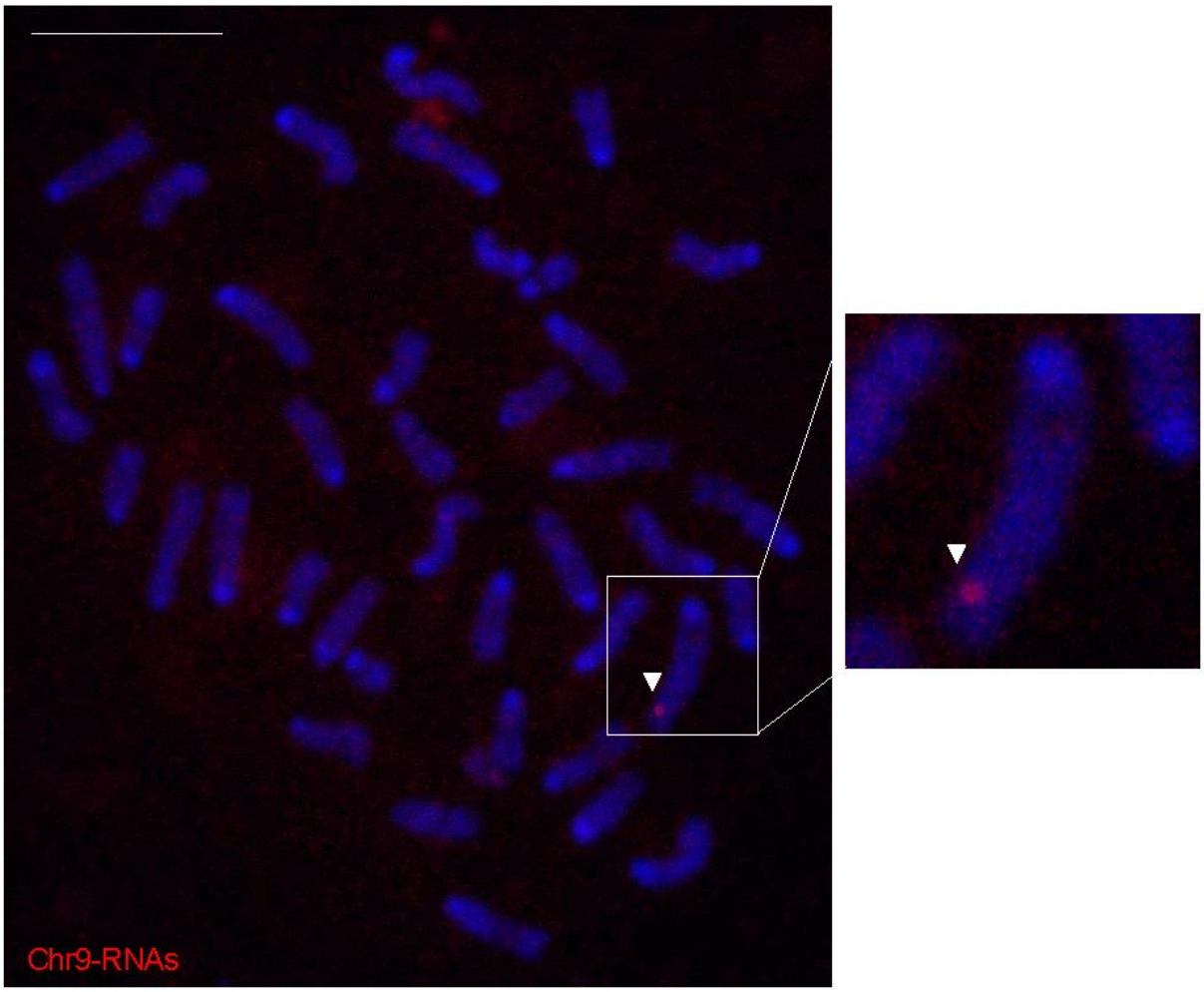


Supplementary Figure 10. Sequence alignment of 3'RACE TTAGGG-containing clones at the subtelomere of chromosome 18 (A) Upon DNase treatment**,** reverse-transcribed RNA from pMEFs was used for PCR detection of transcription arising from different genomic position at the subtelomere of chromosome 18. RT(-) reactions (RT performed in the absence of reverse transcriptase) is shown to exclude possible amplifications due to genomic DNA contamination. **B)** USCS snapshot showing, from top to bottom, start of the telomere (contiguous TTAGGG repeats), genomic scale, genomic position and aligned 3'RACE clones that contain TTAGGG repeats. Red lines indicate mismatches. **C)** The sequence of one of the clones obtained upon 3'RACE is shown. TTAGGG repeats are highlighted in red.



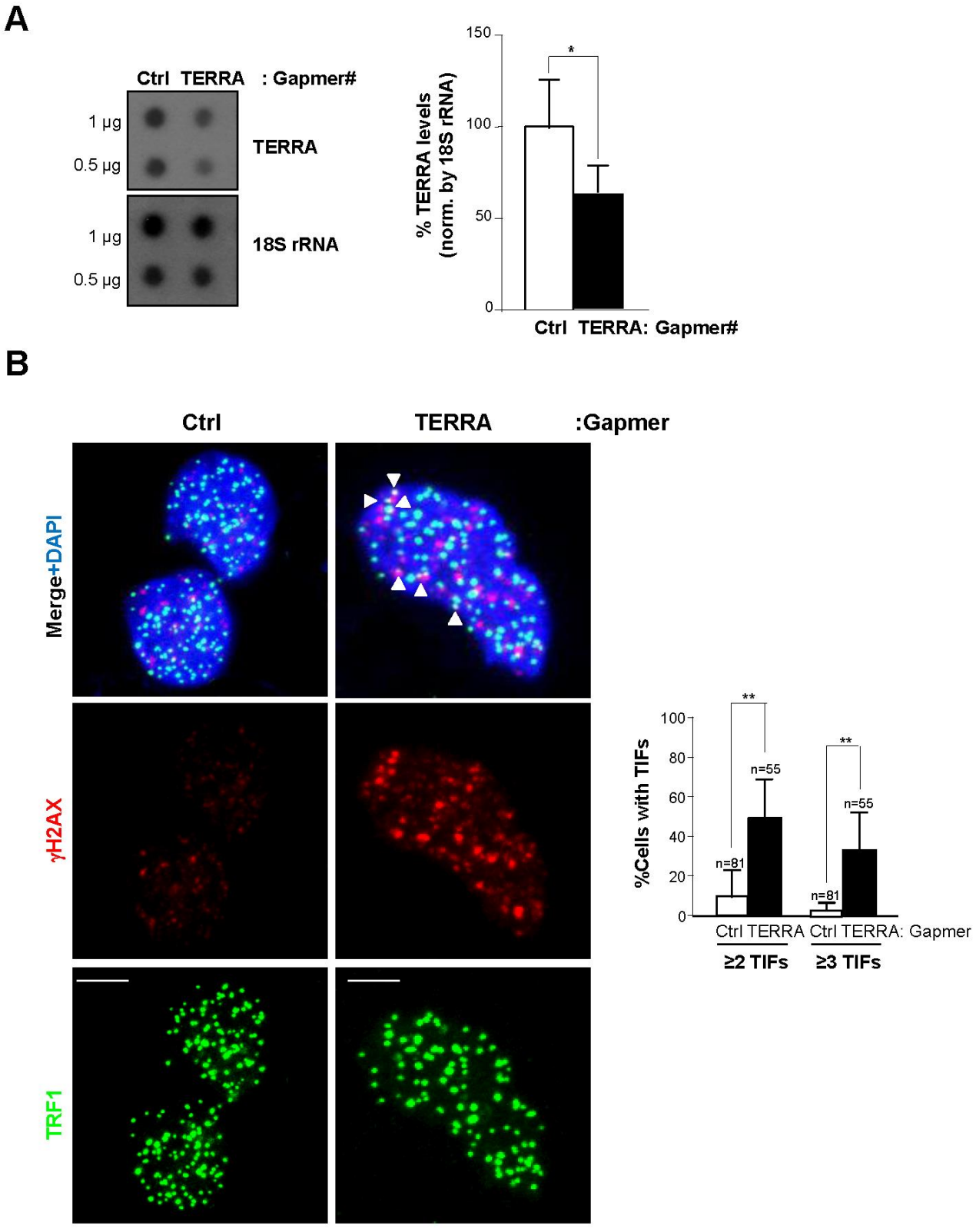
Lopez de Silanes_Suppl. Fig. 11

Supplementary Figure 11. Sequence of RACE clones overlap with external RNA-seq data at the subtelomere of chromosome 18. UCSC snapshot comparing the genomic position of the RACE products and the external RNA-seq data from UW and CSHL both from the ENCODE Project. Zoom region is shown for snapshot details.



Supplementary Figure 12. Chromosome 9-RNAs associate with chromosome-end in metaphase

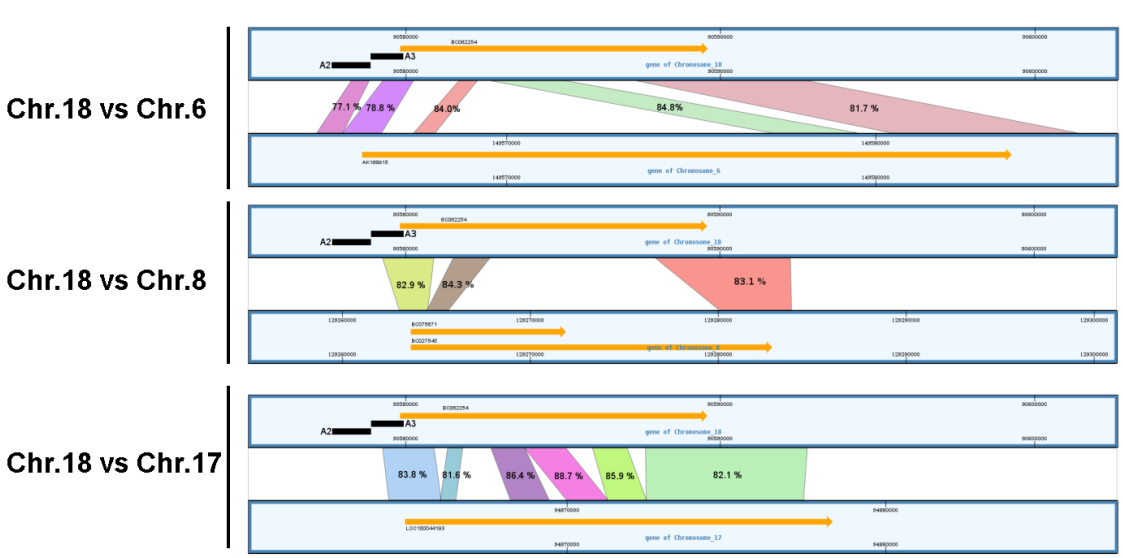
RNA-FISH on metaphases spreads using probes targeting chromosome 9-RNAs. Zoom of these associations is shown. Associations are labelled with arrowheads. Scale bars: 10 µm



Lopez de Silanes_Suppl. Fig. 13

Supplementary Figure 13. Downregulation of TERRA by targeting the telomeric track induce telomere damage. (A) Cells were transfected with control Gapmer (Ctrl) or with Gapmer against the telomere track (TERRA). TERRA levels were assessed 48-hrs post-transfection by RNA dot-blot using a ^{32}P-dCTP labeled probe; hybridization of 18S rRNA was included as loading control (Right) Quantification of the RNA dot-blot signals normalized by rRNA 18S (mean values +s.e.m.; three independent transfections). (**B)** Representative images of TRF1 (green) and γH2AX (red) fluorescence and of the merged images. Co-localization events (arrowheads) indicate telomere dysfunction-induced foci (TIF). (*Graph*) Percentage of cells with ≥2 or ≥3 TIFs/nuclei (mean values +s.d. ; three independent transfections). Student's *t*-test was used for statistical analysis (*$p < 0.05$ and **$p < 0.001$). Scale bars: 5 μm

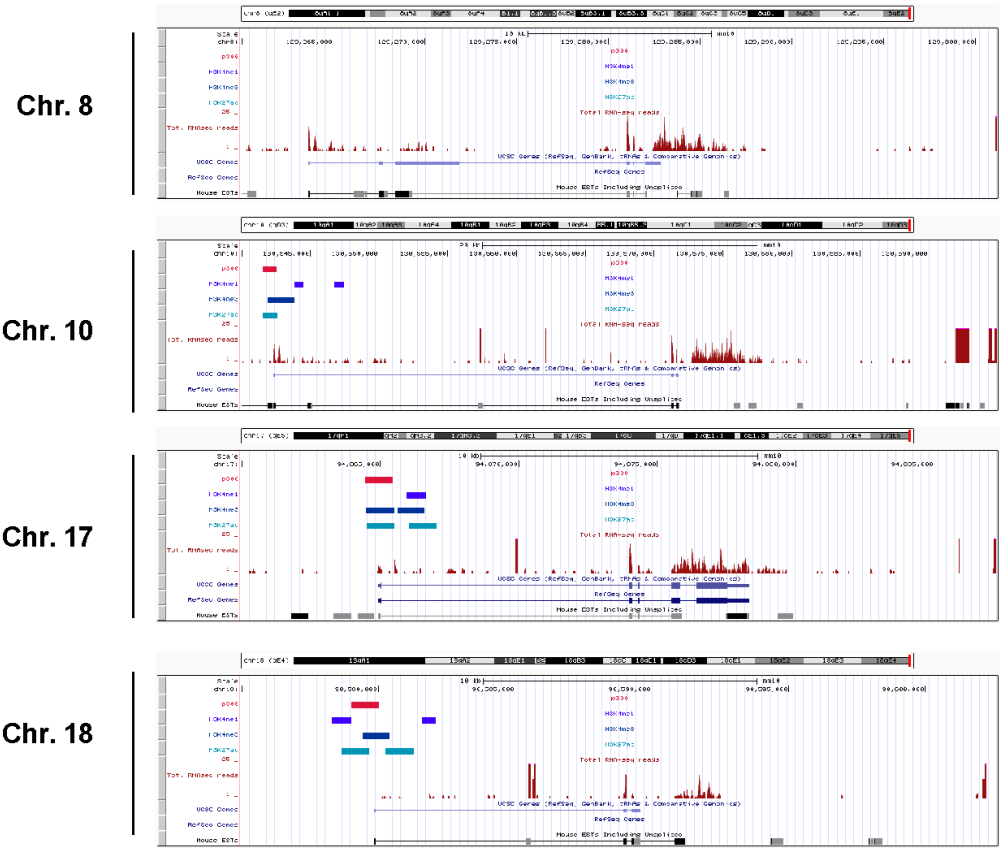
A



B

Chr.#	Start	End	Lenght (bp)	% identity	Distance to telomere
18	90578850	90579850	1000	100	22,790 bp
6	149564692	149566151	1459	47.2	20,396 bp
8	129262122	129263681	1559	47.6	37,533 bp
17	94863660	94864969	1310	48.4	22,303 bp

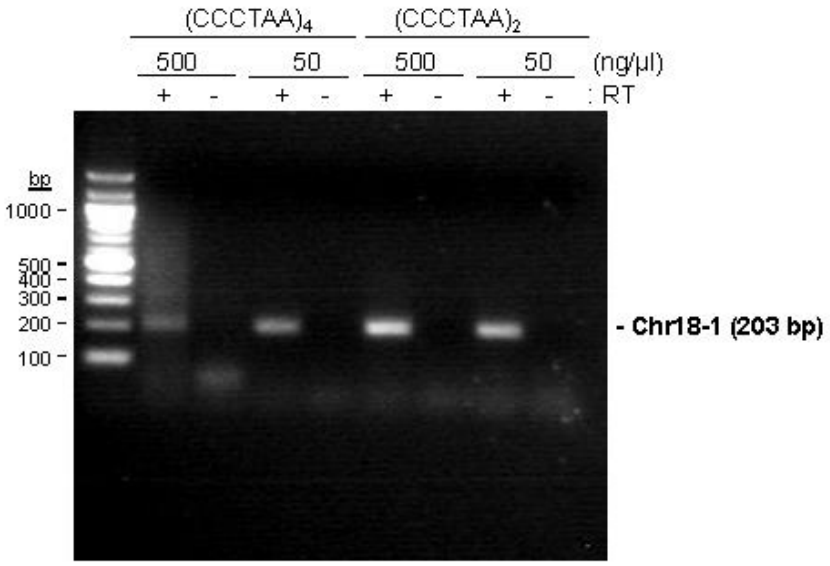
C



Lopez de Silanes_Suppl. Fig. 14

Supplementary Figure 14. Comparison of chromosome 18 subtelomere with the subtelomeres of all chromosomes. **(A)** Synteny blocks between chromosome 18 subtelomere with either chromosome 6, 8 or 17 subtelomeres is depicted. The percentage of synteny conservation is depicted in each block is shown. The chromosome 18 subtelomere region spans from the identified promoter region A2-A3 (black rectangules) to the telomere. In orange can be seen the annotated EST that overlaps with the RACE products. **(B)** Table showing the location, percentage of identity and distance to the telomere of A3 region from chromosome 18 and A3-like regions in chromosomes 6, 8 and 17. **(C)** UCSC snapshot showing, from top to bottom, chromosome ideogram indicating the position of the snapshot (red bar), ChIP data for p300 (red bar), H3K4me1 (violet bar), H3K3me3 (blue bar) and H3K27ac (light blue bar), aggregated RNA-seq reads, UCSC genes, Ref seq and annotated mouse ESTs.

Supplementary Notes



Supplementary Note 1: Raw image from Main Figure 2A. Reverse-transcribed RNA prepared with two different oligos complementary to the telomeric repeat $(CCCTAA)_4$ or $(CCCTAA)_2$ were used for PCR detection of chromosome 18 transcripts using primer Chr18-1. Two different concentrations of oligos were used. RT(-) reactions (performed in the absence of reverse transcriptase) are shown to exclude possible amplifications due to genomic DNA contamination. Markers and expected size for amplicon using primer hr18-1 is shown.

Supplementary Methods

Synteny analysis

The full mouse chromosome 18 was aligned with the rest of the mouse chromosomes in a pairwise manner with Lastz, an improved version of Blastz (Schwartz et al., 2003; Harris et al., 2007). From these aligments, syteny blocks were extracted and visualized with mGSV (Revanna et al., 2011) for the subtelomeric regions.

Identification of promoter A2 and A3-like regions in the subtelomeres of other chromosomes

Local alignments of the promoter A2 and A3 region from chromosome 18 was performed against the subtelomeres of chromosomes 6, 8 and 17 with the EMBOSS implementation of the Smith-Waterman algorithm (Smith et al., 1981; Rice et al., 2000).

Gapmer

Ctrl-Gapmer: GCGACGTAAACGGCCACAAG

Chromosome 18-Gapmer1**:** ATTTGGAGACTAGTG

TERRA-Gapmer: TAACCCTAACCCTAACCCTA

Northern blot probes

L-NB-chr18_1	GGGGGTTAGGGGTAAGGTTT
R-NB-chr18_1	AGGAATCACTGCTGGCATTT
L-NB-Chr8	CCATAAAGGCCTTCTCAAGC
R-NB-Chr8	CAGAGTTCATTACCTGCTCA
L-NB-Chr10/17	GGGAAATTGCTAAGCTGATGA
R-NB-Chr10	CAGATCCCATGTTCTGATGC

R-NB-Chr17	GTTCATTACCTGCGCATCAG
L-Chr9-NB1	GCATGCTCATTGAAGACC
R-Chr9-NB1	ACCAAGAGGGACTAGAGCTT
L-ChrX-NB1	GTGAAGGATTCAGCAAAGC
R-ChrX-NB1	GAACTGGAGTGAATGTGTCA

RNA-FISH

L-chr18_3_T7	ccaagcttctaatacgactcactatagggagaCGCTGAAGAGAAACCCTGTG
R-chr18_1_T7	ccaagcttctaatacgactcactatagggagaAGGAATCACTGCTGGCATTT
R-chr18_3_T7	ccaagcttctaatacgactcactatagggagaGGCATTTACTTTGACCAGGTG
R-chr18_4_T7	ccaagcttctaatacgactcactatagggagaCCCTCCAGTTTATTTACTTTGATACT
L_Chr8_T7	ccaagcttctaatacgactcactatagggagaCCATAAAGGCCTTCTCAAGC
R_Chr8_T7	ccaagcttctaatacgactcactatagggagaCAGAGTTCATTACCTGCTCA
L_Chr10/17_T7	ccaagcttctaatacgactcactatagggagaGGGAAATTGCTAAGCTGATGA
R_Chr10_T7	ccaagcttctaatacgactcactatagggagaCAGATCCCATGTTCTGATGC
R_Chr17_T7	ccaagcttctaatacgactcactatagggagaGTTCATTACCTGCGCATCAG
L-Chr9-FISHT7	ccaagcttctaatacgactcactatagggagaGCATGCTCATTGAAGACC
R-Chr9-FISHT7	ccaagcttctaatacgactcactatagggagaACCAAGAGGGACTAGAGCTT
L-ChrX-FISHT7	ccaagcttctaatacgactcactatagggagaGTGAAGGATTCAGCAAAGC
R-ChrX-FISHT7	ccaagcttctaatacgactcactatagggagaGAACTGGAGTGAATGTGTCA

Primers

RNA-seq validation and qPCR primers

L-chr18_1	GGGGGTTAGGGGTAAGGTTT
R-chr18_1	AGGAATCACTGCTGGCATTT
L-chr18_2	CCAAAGTACAGGTGACATGGTG

R-chr18_2	ACTGACACTGGCCTCACCTC
L-chr18_3	CGCTGAAGAGAAACCCTGTG
R-chr18_3	GGCATTTACTTTGACCAGGTG
L-chr18_4	CAGGTTAGGGTGAGCTTTAGTG
R-chr18_4	CCCTCCAGTTTATTTACTTTGATACT
L-chr18_5	TGAGAGGGATACTGGTCCTTG
R-chr18_5	CAGCTGCTTCCATTGCATTA
L-chr18_6	AAATCCTTTGCCTCTCATGG
R-chr18_6	GGCTTACGCATAGGATCTCAA
L-chr18_7	CATCATTGCAATCTTCGAGTG
R-chr18_7	TGGAGATTACAGTGTTGTGAATAGG
L-chr18_8	GGCATGAATTTGCCTCTGAA
R-chr18_8	CCGACTGCTCTTCTGAAGGT
L-chr18_9	GCCCAATTATTTGCAAGACC
R-chr18_9	CCCTCTCTCCCCTGTAAAAA
L-chr18_10	CTGTGTGACGTGCTCCCTGT
R-chr18_10	TGACCTCACAGGTGGCAGAA
L-chr18_11	CAGCTGAGACATGAAACATGG
R-chr18_11	GGCTTGGATTGAGTCCTTCA
L-chr18_12	AGCAAAACTGGCAGAAACTCA
R-chr18_12	CTTCACCTGGTGTTGGGATT
L-chr18_13	TAAGTGGGGAAAGCACCAGA
R-chr18_13	AAGCATCAGTAACAAGGAGACAA
L-chr18_14	TAAAACCTTTGCAGCCCATC
R-chr18_14	AAGCCCACTGCCATAGTGAT
L-chr18_15	CAACCTCGCATCTTTCATCA

R-chr18_15	AGCGGATCCTTTCAACACAC
L-chr18_16	GAAATGCTCCAAGAGATGGAA
R-chr18_16	CCTGCTTCACTTTTGTCCTTG
L-chr18_18	GAGGACTATTACCGCACACATT
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L-chr18_20	TCAGGGAAATAATCCCATTCA
R-chr18_20	GTTTTTGAAGCCGGGTCTCT
L-chr18_21	ACAGGTGGAGCCCTGAGATT
R-chr18_21	ATGGTGAGGGAGGATCTTTT
L-chr18_22	TTCTTTCCACCTTGATGATAATAGAC
R-chr18_22	GGCATTTACTTTGACCAGGTGT
L-chr18_23	CCCTCTGTATTCAACACTCAATG
R-chr18_23	TGAAGTTCAGAATGGTATGCAA
L-chr18_24	TCTCTCCAGCCCAGATGATT
R-chr18_24	TGGCAAAGTAAACCAGGACA
L-chr18_25	CTCCCAGGGCAGAAGAGTTT
R-chr18_25	TGCCCTTTGTCTTAGTCTGG
L-chr18_26	GGTCCTTGTATAGCTGCAACTCAG
R-chr18_26	TGCTTATCGTGTCTTGAAGTGG
L-chr18_27	TGAGTCCCAGACCAATGGA
R-chr18_27	CCATGAGAAGCAGTTACAGAGC
L-chr18_28	AACTCGTCTCGATGCTCTGG
R-chr18_28	TGGGTCAGGGTTTAGGAGAA
L-chr18_29	TCACCAGCAGTCTTTCAAGG

R-chr18_29	CTCAAACAGGAGACCCAAGC
L-chr18_30	CCAGCAGTCTTTCAAGGTTTTT
R-chr18_30	CCCTAACAACCCTAACCCTGA
L-chr18_31	TTAGCCGGGAAGTCTTTCAA
R-chr18_31	ACTACTGGTTAAGGTATGCACCA
L-chr18_32	TGGCCTGCCACAGATTTTA
R-chr18_32	TCCCTAACCCTAACAACCCTAAC
L-chr18_33	TGCTAAGGAGGAAAAGGCTAA
R-chr18_33	CCCTAACAACCCTAACCCTGA
L-chr18_34	TGGTGCATACCTTAACCAGTAGT
R-chr18_34	CTCACACTTCATACATATACTTTTTGG
L-chr18_35	CCTTAACCAGTAGTATTCTGAAGTCAC
R-chr18_35	GCCTTTTCCTCCTTAGCAGT
L-Chr1-1	ATACACCCGGTTTGGATG
R-Chr1-1	CTTGTGGCTCTTGGTATCTT
L-Chr1-2	ACAAGCTGACCTGTGAGTTC
R-Chr1-2	ATCTGGGACAAAGGCAAG
L-chr2_6	GAGTGCCTTACTATCTCCTAAGTTTT
R-chr2_6	TGGAGTTAATTTTGTGGAGGTTG
L-Chr2-13	CGAGTCTCAGAAAAGGGCAG
R-Chr2-13	TCACCAATTCTCCAACAGGG
L-Chr5-7	GAAGACTGAGGCAGAAGAGTT
R-Chr5-7	TGAGATCCCTTGCTACTTGC
L-Chr5-8	CTGAACCTTGTAGTTCCTCTG
R-Chr5-8	CTGTGAAAGGGTCATTCAAC
L-chr6_3	AGGTGTTCTGAGGCAAGCTC

R-chr6_3	AAGACCCACCACACCAGTTC
L-Chr6-4	CTGCAATTGGGAAGAGCA
R-Chr6-4	CAGAGGGTTTCTCTCCAGTA
L-Chr7-1	GGGCTTTGTTATCTTGCTG
R-Chr7-1	AGAGTCATGTGGCTATCAGTC
L-Chr7-2	TAAGGACACAGGCCATACAC
R-Chr7-2	CCACTCAGCTCAGACATACA
L-Chr9-1	GCATGCTCATTGAAGACCAG
R-Chr9-1	ATTGGTCTCTGAGGTCTTGC
L-Chr9-2	TGCCTCTCAAGTGCTGTT
R-Chr9-2	GTAGGCATTGTGTCAGTCTCA
L-Chr11-7	TGTATTTGAAATTGATTATGAGAAGT
R-Chr11-7	TAAAGCCTTTGTACATCAATATG
L-Chr11-8	GGCTTTACCACATTGACTACA
R-Chr11-8	CTTTGCTTCTCCTGCTCAAC
L-Chr12-1	TTTGGCTACTGAGCAACTG
R-Chr12-1	CCAGAAACGTTCCATACTAAC
L-Chr12-2	CAAGCTTTGTTCCCTCAG
R-Chr12-2	AAAGCAATTTAAGATTTGTAGCA
L-Chr13-4	CAATGAAACTCCACCCACAG
R-Chr13-4	TCTGCCTCACCATCTGTGTA
L-Chr13-5	CCAAGACCCAGCTTCTGATTC
R-Chr13-5	TTTTGATGGTGTCTCTTGGGA
L-Chr14-1	GAGCTCAGATGCATCACTGT
R-Chr14-1	TTGATGAACAAAGGTCACTG
L-Chr14-2	TACCACCTACTAGCCTCCAGT

R-Chr14-2	GAGTATGACCTAACCCTGACTC
L-Chr15-1	CAGAATGGGTCAAGGATAGC
R-Chr15-1	CTCAAGTGCTGAAGGATGAC
L-Chr15-2	CTTCCCTTCCCTCTTCTGTA
R-Chr15-2	TGGGTTAGACCTTATCTGAGTT
L-Chr16-1	TGTAATTGGAGAGTACTATGATATGC
R-Chr16-1	ATTACACATACTGGAGAGAAATCTTAC
L-Chr16-2	CATGTGTAAGGTTTCTCTCCAGT
R-Chr16-2	CAATGTAGTAAATCCTTTGCTTCTC
L-Chr19-1	GTCTCCAACATCACATCTCTG
R-Chr19-1	GATGTGCATGTGAACTTTACTC
L-Chr19-2	CTTACATTCATAGGGTTTCTCTCTAGT
R-Chr19-2	GTGGTAAAGCCTTTGCATATCATAC
L-ChrX-1	GAGGTTCCTGTAAGTCTCCA
R-ChrX-1	CCTATGATGATGTGCATGTG
L-ChrX-2	GTTACAGAGAACTCGCATCTTC
R-ChrX-2	GGGCAATACCCTTTGTCC
L_Chr8-1	TCAATGCATCAGCAGCAG
R_Chr8-1	GGTAATGTTGCCTGATGAGC
L-Chr8-B	ATGAGCAGGTAATGAACTCTG
R_Chr8-B	GTGTGGGAGGATAGTCATGTA
L_Chr10-seg1	GTCTCAAGTGAAACAGACTGC
R_Chr10-seg1	GCAGTTCCAGAAAGATCACTG
L_Chr10-seg2	TCAGCAAATCATGGTTCAGAT
R_Chr17_1	TCTCAAGTGAAACAGACTGC
L-_Chr17EST	TGTCAAAGTTCCAGAAAACATGG

R-Chr17EST CTTTTGGGGATGACTGTGACAT

RACE

GSP1	CTGTGAAGGACAAAGGCTGT
NGSP	ACAGGGTTTCAGTGAATGGA
NUP	AAGCAGTGGTATCAACGCAGAGT
NUP_revisado	AGTGGTATCAACGCAGAGT
R-nested3kb-1	GAGAATGCAAAGGCTTTACCAC
3'NGSP	CTGGGGAAAGAGGAATGAAA
5RACE_GSP26	CACCAGTGCAGCGGTTTCAGCTTTA
5RACE_NGSP26	GCACTTCAGAGCCATCAGCTGCTTC
5RACE_NGSP21	CCCTCTCATAGCCTTTGGCAACCAC
5RACE_NGSP28	ACGGCTCTCTGAAGGTTTGCTGGAA
5RACE_GSP28	TTGCCATTGGTAAGCCACTGAGCTG
5RACE_NGSP29	AAGAAAGCAGGCTAAGCAGGCCACA
5RACE_GSP29	TTGATATGGGAAGGCCCAGACCACT
3RACE_NGSP3-1:	GGTTGGCTGGGGAAAGAGGAATGAA
3RACE_GSP3-1	CGCTGAAGAGAAACCCTGTGAATGTG
3RACE_NGSP26	GAATGGCAAGCCACTTCAAGACACG
3RACE_GSP26	AGCAGCTGATGGCTCTGAAGTGCTG
3RACE_GSP27	ACTGTGCAGGCCTTCTCACCAAACA
3RACE_NGSP27	AGTGTGGGGGCACCCTCAGAGACTA
3RACE_GSP28	GCAAACCTTCAGAGAGCCGTGGAGA
3RACE_NGSP28	TGCACATCAGCTCAGTGGCTTACCA
3RACE_GSP29	TGTGGCCTGCTTAGCCTGCTTTCTT
3RACE_NGSP29	TGGCTCTTAGCCGGGAAGTCTTTCA

3RACE_NNGSP29	GGTATGAGGAGTTCATGGTGACAAGC
5RACE_N_NGSP28	GCTCATCTTCAAAGGGGACTTCTTCC
5RACE_R_GSP29	GAAAGACTTCCCGGCTAAGAGCCAAG
L-GSP31sin29	TCCACAGTACAGAGGTGAGGCCAGTG
L-NGSP31sin29	GAGGCCAGTGTCAGTCTGTCCCTTCT
L-GSP30sin31	GGTTAGGGTCAAGGTCAGGGTTAGGG
L-NGSP30sin31	GGGTCAAGGTCAGGGTTAGGGTTGTT

Promoter cloning

L-PromoA1-KpnI	CGGGGTACCCCGTTTAGGCTCCCCTGCATTTA
R-PromoA1-HindIII	CCCAAGCTTGGGCCTGAGGCTAATTCTCCCACT
L-PromoA2-KpnI	CGGGGTACCCCGCCAATGCAATGTGGTCAGTC
R-PromoA2-HindIII	CCCAAGCTTGGGAAATTGCAGGTAGTTTTCACTGG
L-PromoA3-KpnI	CGGGGTACCCCGAAGGACTCAATCCAAGCCAAT
R-PromoA3-BglII	GAAGATCTTCTCACACAGGACCACTCAAGC
L-PromoB1-KpnI	CGGGGTACCCCGTTGTTTTCATTTTTGAAGACAGAG
R-PromoB1-HindIII	CCCAAGCTTGGGACAGAAAAGCATCAGTAACAAGGA
L-PromoB2-KpnI	CGGGGTACCCCGTGAGGTGAATAAATCAGGTTCA
R-PromoB2-HindIII	CCCAAGCTTGGGGCTCAGAGCTTTACCACACTG
L-PromoB3-KpnI	CGGGGTACCCCGGAAAAATCTCATAGAGAAAACAGATGC
R-PromoB3-BglII	GAAGATCTTCACGATGGGCTGCAAAGGT
L-PromoC1-KpnI	CGGGGTACCCCGACTCTCAGCTCCTCCAGCAC
R-PromoC1-BglII	GAAGATCTTCGCTGGCCTTGAACTCAGAAA
L-PromoC2-KpnI	CGGGGTACCCCGAGCCAGGGTGAAACAGAGAA
R-PromoC2-BglII	GAAGATCTTCATGGTGAGGGAGGATCTTTT
L-PromoD-KpnI	CGGGGTACCCCGTTAAAAGATCCTCCCTCACCA

R-PromoD-BglII	GAAGATCTTCTTGAAATCAACCCAAAATGC
L-PromoChIP-KpnI	CGGGGTACCCCGTGGGAGCAGCTTTCTAGTGG
R-PromoChIP-BglII	GAAGATCTTCGGAAAGCCTTGCTTGTTCAG

RT-qPCR

L-qPCR_5R1.5kb	TGCATTCATACGGTTCTCTCC
R-qPCR_5R1.5kb	GGCATGAAAGAATTCATACTAGAGA
L-qPCR-3R-NGSP31	GAGGAGTTCATGGTGACAAGC
R-qPCR-3R-NGSP31	AGGCCAAAGAAGGGACAGAC
L-qPCR-3RNGSP28	AAGGCAAGGGAAAAGGAGAC
R-qPCR-3RNGSP28	GGGGACACTCACTGAAGCTC
L-qPCR-Malat1	GTTACCAGCCCAAACCTCAA
R-qPCR-Malat1	CACTTGTGGGGAGACCTTGT
L-Cytb	ATTCCTTCATGTCGGACGAG
R-Cytb	ACTGAGAAGCCCCCTCAAAT
L-cyclinD2-qPCR	CCAGCAAAAGGAGAAGCTGT
R-cyclinD2-qPCR	TTCCAGTTGCAATCATCGAC
L-qPCR-Chr18	GCAAGCTCCGAAGTTGTGAT
R-qPCR-Chr18	CGCTTCTGTGAAGGATCCAG
L-qPCR-Chr8	TCCCACTGTCAATAACAGAC
R-qPCR-Chr8	CAAGCACAGGCTAGAAGTG
L-qPCR-Chr10	TCAGCAAATCATGGTTCAGAT
R-qPCR-Chr10	TGCATTGCATTTGACAACAG
L-qPCR_Chr17	TGTCAAAGTTCCAGAAAACATGG
R-qPCR_Chr17	CTTTTGGGGATGACTGTGACAT

qPCR primers for other chromosomes can be found in the RNA-seq validation section

Chromosome-18 TERRA promoter regions

>Region A2

CATGAGGTCCCTATTTGGCTATCCAATGCAATGTGGTCAGTCTTGAAATCTATACATACAACCAACA
GAAATGGGCTCAGCAAGTTTTATTCATATGTTTGAGCATACTTACTTGATTCTCAGCTAAGACCTTGT
AGTATAAGGTGAACATTCCAGAGACATTTCTGTCTATCATTTTTATAATTTACATATGTTTCTGTTGA
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AATCTCAGTTCTTTTGTCTTGGCATTTGTGATGGCTATTCTTTTTTTTTTTTTTTTTTTTTAAAGATT
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CTCTACTTAGCAAGTTCTTTTATTATTGGCATTAGACTCTACTTTAGAATTCTGGTATATACTGAAGA
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GCCAGTGTAATATTCTAATAAAGCCACATTATATGAAGTTGGTTCATCTAGAGAACCTTCACTAATA
CAGCTCTGTGTGAGAATGTGTGTTCACTTACCACTGAGGAAGATGTGCTGGGTAATAATAGTGCGCC
ACAGGGTTTGTCATCTGTTTCCTGTTTTTCTCCCAAGGTTCTCATACCTACCAGTGAAAACTACCTGC
AATTTACCTAAGTCCAGCAT

>Region A3

GAAGGACTCAATCCAAGCCAATTAGAGTATTTGACAGTTTACTGGGAGCAGCTTTCTAGTGGGTTCA
CTGATCACTTGAGACCAGAGAGAGAATGGGGGGGGGGGGGAGAAGCAAGCAGGAAGAGAAAAAT

GCAGGGGCGGGGGAGGGAGGGACAGGGAAAGTGGAGGAGGAAGGAGAGGGAGGGAGGAGAGAG

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GGCGCCTGAGAACCTCTTCACTGTGTCCTTTCAGCACACTCTAACCCTAAGGTAGGTGCTCATGTCA

CTCAAGACTCACTGGCCAATCAGAGCCTTCAGGAGAACCTTCCAATCAGAAGATGAGGCGGTTTCTT

CCGGGTGCCTTGCTGCAGGTTCCGCTTAATAGCTTATCAGGCTTGAGTGGTCCTGTGTGACGTGCTCC

CTGTCTGG

RACE sequences

Below are 25 representative RACE sequences. The remaining ones are also available upon request to the authors

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CATTGACTGCATTCATAGGGTTTCTCTCCAGTATGTGTTCTTTTATGTACTTGGAGATAACTATGAGN
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