SUPPLEMENTARY FIGURE LEGENDS

Supplementary Figure 1. hTERT and SRSF3 splice variant enrichment after cycloheximide treatment. Jurkat, UM-UC-3 and BT-459 cells were treated with 100 μg/ml cycloheximide or DMSO as vehicle control for 5 h before total RNA was harvested and analyzed by RT-qPCR.

Supplementary Figure 2. Total SRSF3 and hTERT splice variant mRNA abundance in ribosome-containing fractions. Copy numbers were obtained for each transcript relative to a standard of known DNA concentrations by RT-qPCR.

Supplementary Figure 3. Unaltered microscopy image shown in Figure 3.

Supplementary Figure 4. SRSF11 and hnRNPH2 binding sites in pSpliceExpress-hTERT.

Supplementary Figure 5. A, In cell line GM847, hTR co-immunoprecipitated with FLAG-WT-hTERT, FLAG-D868A-hTERT and FLAG-β-deletion using hTR-specific primers as shown in D below. hTR was co-immunoprecipitated with FLAG-WT-hTERT, FLAG-D868A-hTERT and FLAG-β-deletion at 4, 5, and 14 fold % input amounts over vector, respectively. Thus, because the β-deletion protein is immunoprecipitated at lower levels, hTR co- immunoprecipitated with FLAG-D868A and FLAG-β-deletion with high efficiency. B, RTA of the immunoprecipitates shown in A. C, Western blot of the input hTERT constructs expressed in cell line GM847. * indicates a non-specific band; positions of the TERT isoforms are indicated. D, hTR-specific primer pairs used for quantitative RT-PCR in Figure 5A (annealing to the 5' region of hTR) and in Supplementary Figure 5A (annealing to the 3' region of hTR

Supplementary Figure 6. UM-UC-3 lysates from experiment in 5C were analyzed by Western blotting with antibodies specific for hTERT N-terminus (1) or GAPDH.

Asterisk indicates non-specific band.

Supplementary Figure 7. hTR RNA expression levels in breast cancer cell lines. hTR were expressed as transcript numbers normalized to GAPDH transcript numbers x 10^4. Bars represent means of 2-4 biological replicates done in triplicate reactions with SD in ascending order according to telomerase activity in each cell line.

Supplementary Figure 8. Modal telomere length stayed relatively constant after 20 continues passages in randomly selected breast cell lines.

Supplementary Figure 9. Telomerase activity and relative expression of hTERT α+β+ and β-deletion mRNAs in breast cancer cell line subtypes. A, Relative expression of α+β+ hTERT is significantly higher in basal vs. luminal subtypes (ANOVA, Tukey post test). B, β-deletion is significantly lower in basal vs. luminal subtypes (ANOVA, Tukey post test). C, log(RTA) is significantly higher in basal compared to luminal subtypes ANOVA, Bonferroni post test). Asterisks indicate $P < 0.05$.

Supplementary Table 1. Breast cell lines used in this study.

Supplementary Table 2. Summary of results for 45 breast cancer cell lines and 5 non-malignant cell lines.

Supplementary Table 3. Correlation of hTERT α/β splice variants, telomerase activity, telomere length and hTR in 50 breast cancer cell lines. Pearson correlation coefficients are shown with corresponding p-values in parentheses.

Supplementary Table 4. Primers used in this study

REFERENCES

1. Cohen SB, Graham ME, Lovrecz GO, Bache N, Robinson PJ, Reddel RR. Protein composition of catalytically active human telomerase from immortal cells. Science. 2007;315:1850-3.