

Fig. S1

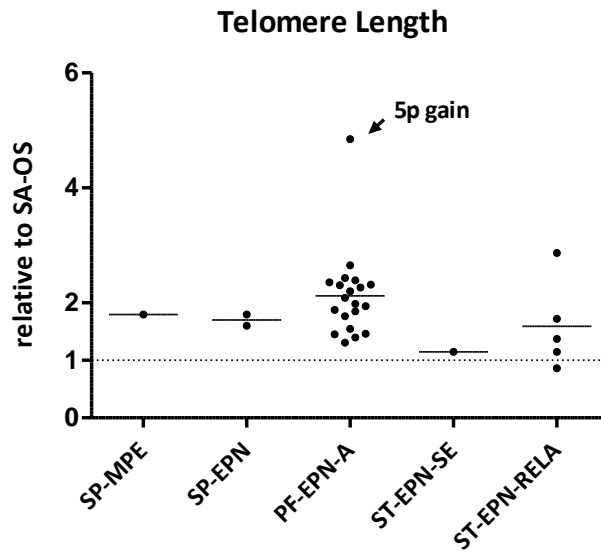


Fig. S1 Telomere length in ependymoma subgroups. Telomere length of ependymoma samples relative to SA-OS cells. Mean is depicted as solid line. The dotted line at 1 defines the reference.

Fig. S2

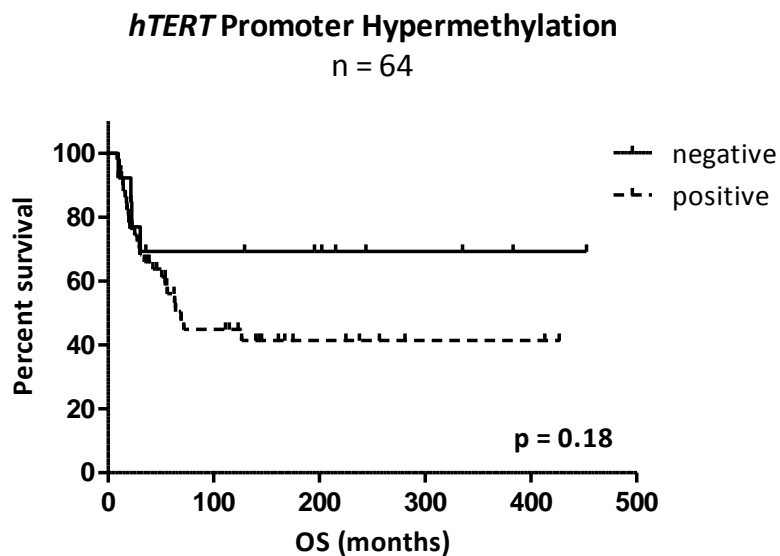


Fig. S2 *hTERT* promoter hypermethylation. Overall survival calculated for promoter hypermethylation status in the cohort diagnosed between 1965 and 2015 (n = 64). OS, overall survival

Fig. S3

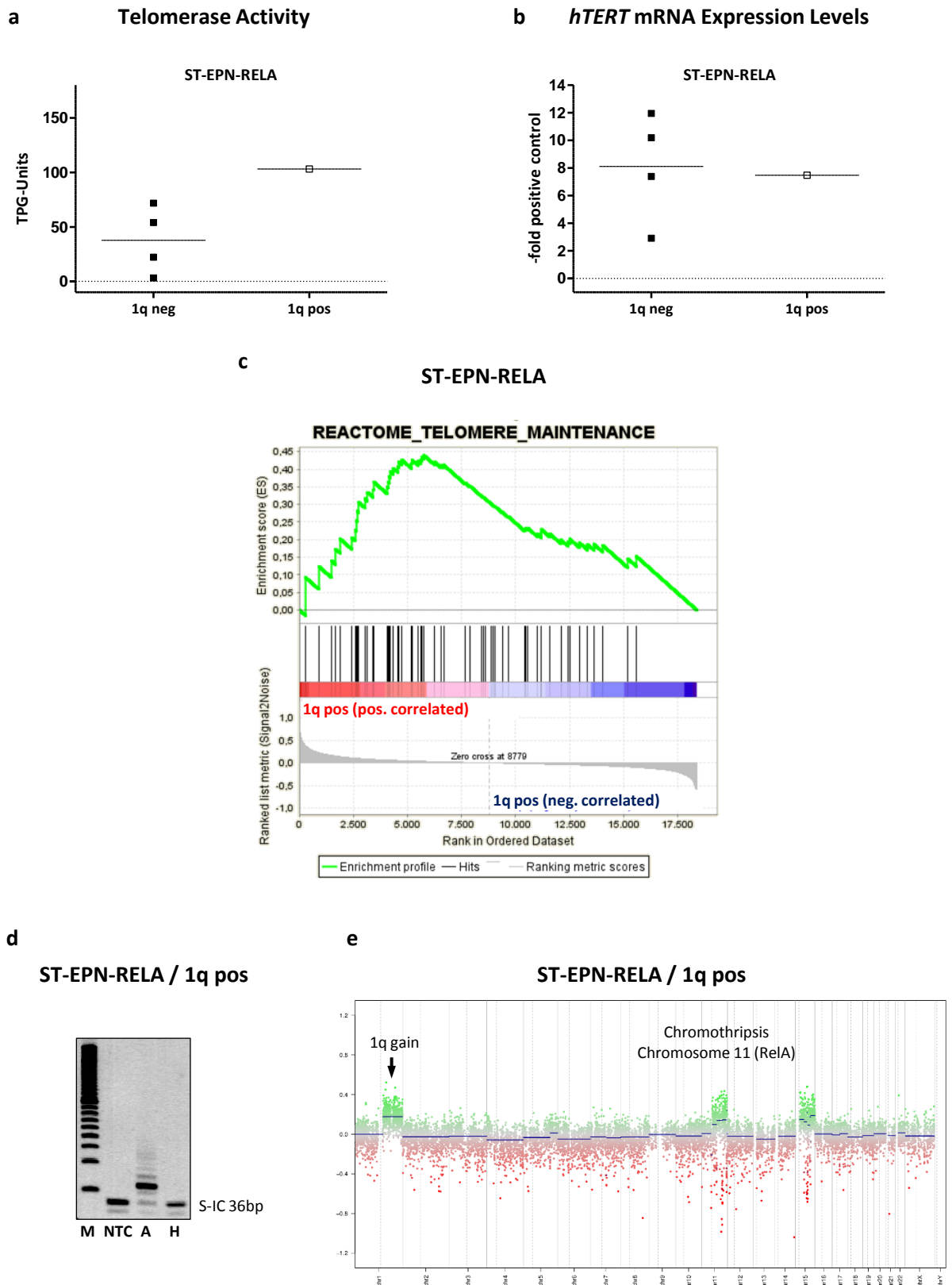


Fig. S3 Association of chromosome 1q gain and telomerase re-activation in ST-EPN-RELA. (a) Telomerase activity and (b) *hTERT* mRNA expression levels segregated according to chromosome 1q gain. (c) Gene set enrichment analysis (GSEA) for the term “Reactome Telomere Maintenance”. TRAP gels and copy-number profiles are shown for the single 1q gain positive ST-EPN-RELA tumor (d,e). pos, positive; neg, negative; TPG, total product generated; M, marker; NTC, no template control; A, active sample; H, heat inactivated sample

Fig. S4

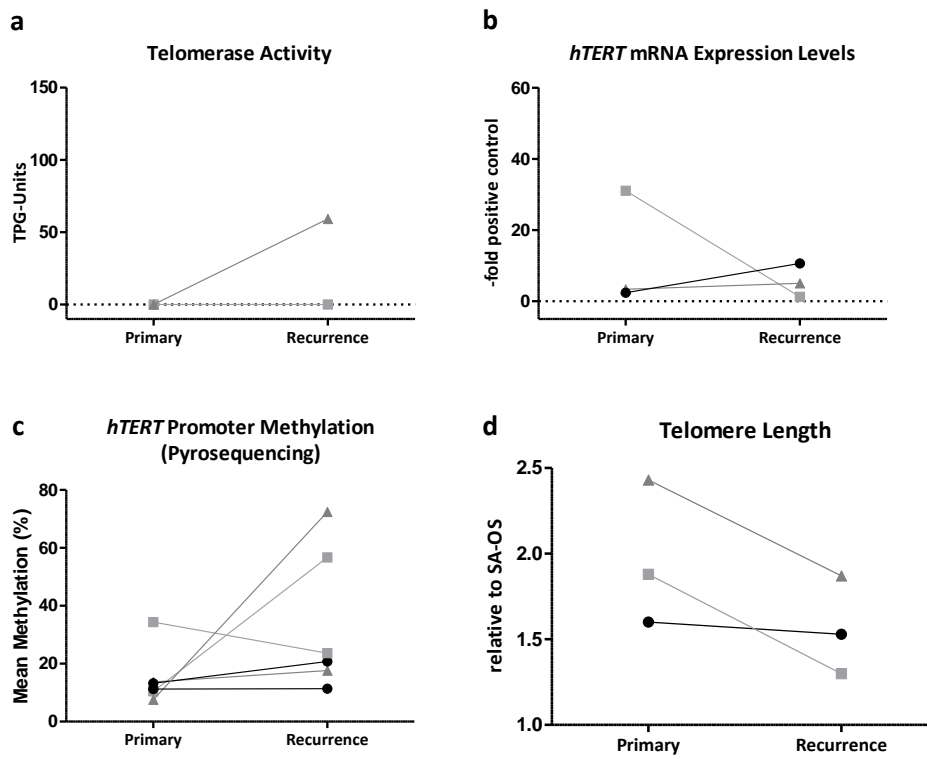


Fig. S4 Course of telomerase-associated markers upon disease recurrence. Graphs show (a) telomerase activity, (b) RNA-Expression, (c) hTERT promoter methylation and (d) telomere length in primary and recurrent patient samples. Lines connect corresponding primary and recurrent samples of individual patients. TPG, total product generated;