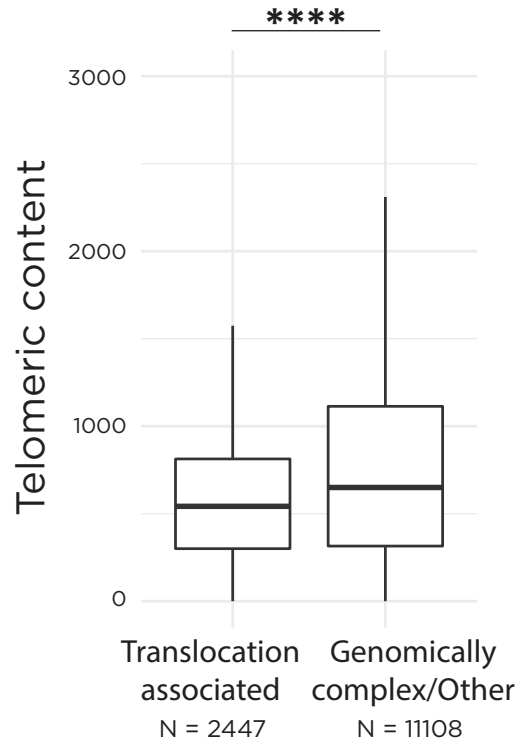
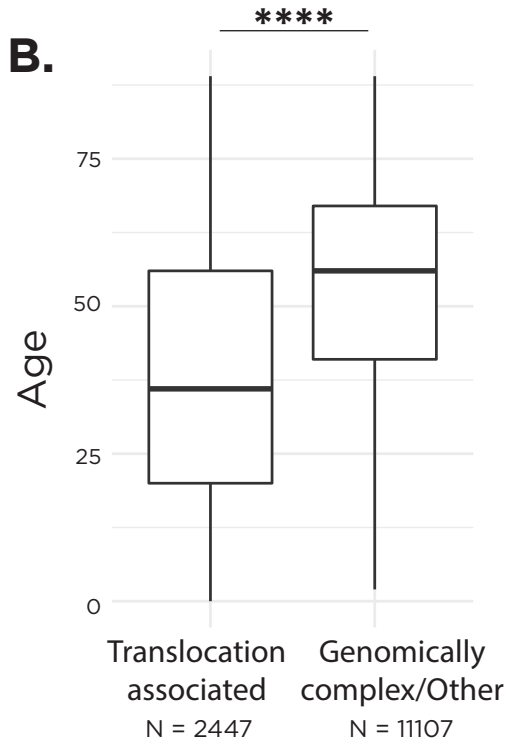
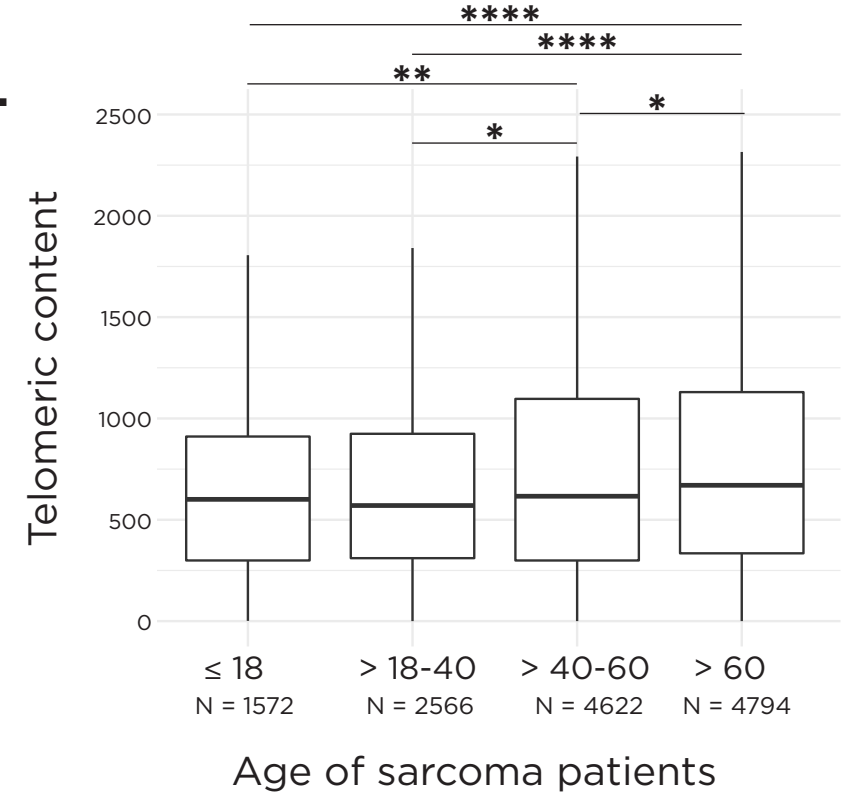


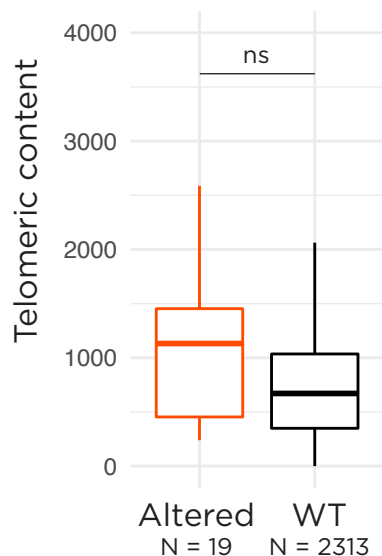
A.**B.****C.**

Supplementary Figure 1

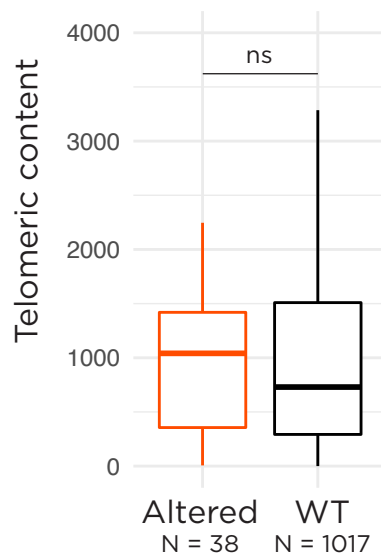
Boxplot displaying the distribution of telomeric content values (A) and age (B) of samples within translocation-associated diseases vs genomically complex/other sarcoma diseases. C. Boxplot showing the telomeric content of samples by age group. * denotes $p < 0.05$, ** denotes $p < 0.01$, and **** denotes $p < 0.0001$.

DAXX

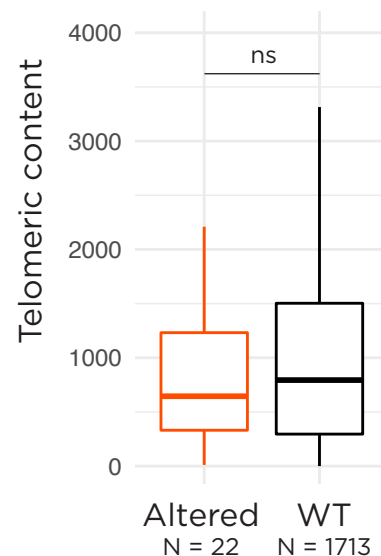
Soft tissue sarcoma (nos)



Uterus leiomyosarcoma

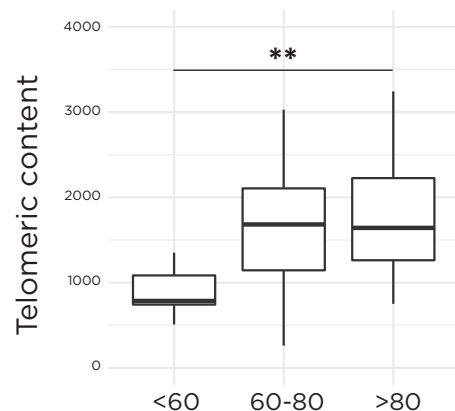


Leiomyosarcoma

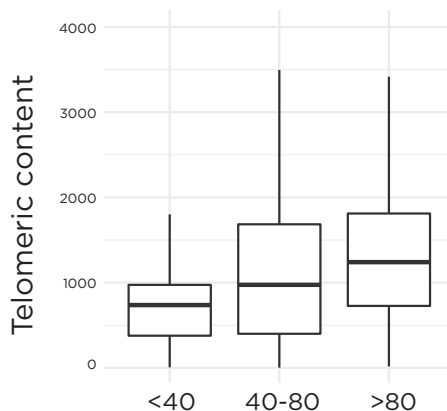


Supplementary Figure 2

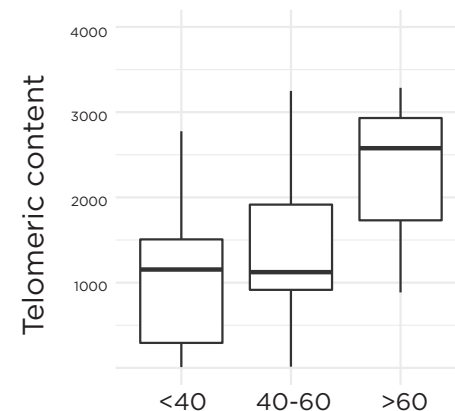
The impact of alterations in *DAXX* on the telomeric content values of samples within diseases harboring at least 20 altered samples, yet not identified in our screen. ns, not significant.

A.*RAD51B* altered
uterus leiomyosarcoma

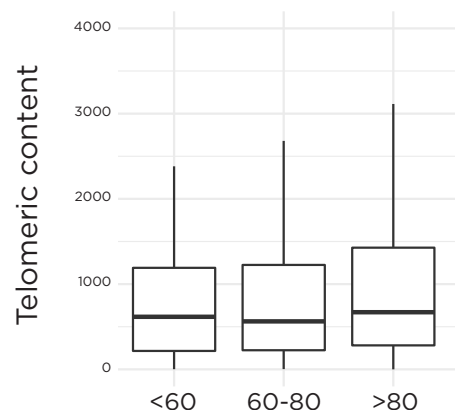
Computational tumor purity

B.*GID4* altered
soft tissue sarcoma (nos)

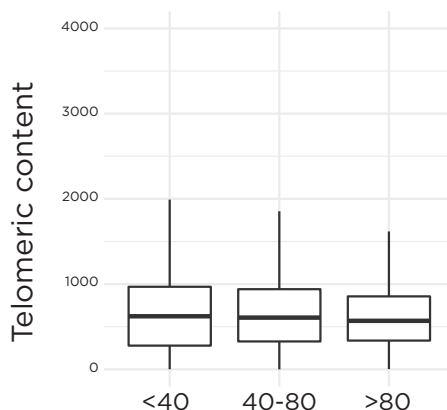
Computational tumor purity

C.*POT1* altered
angiosarcoma

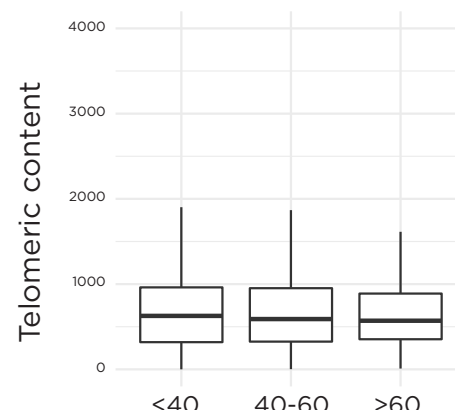
Computational tumor purity

D.WT
uterus leiomyosarcoma

Computational tumor purity

E.WT
soft tissue sarcoma (nos)

Computational tumor purity

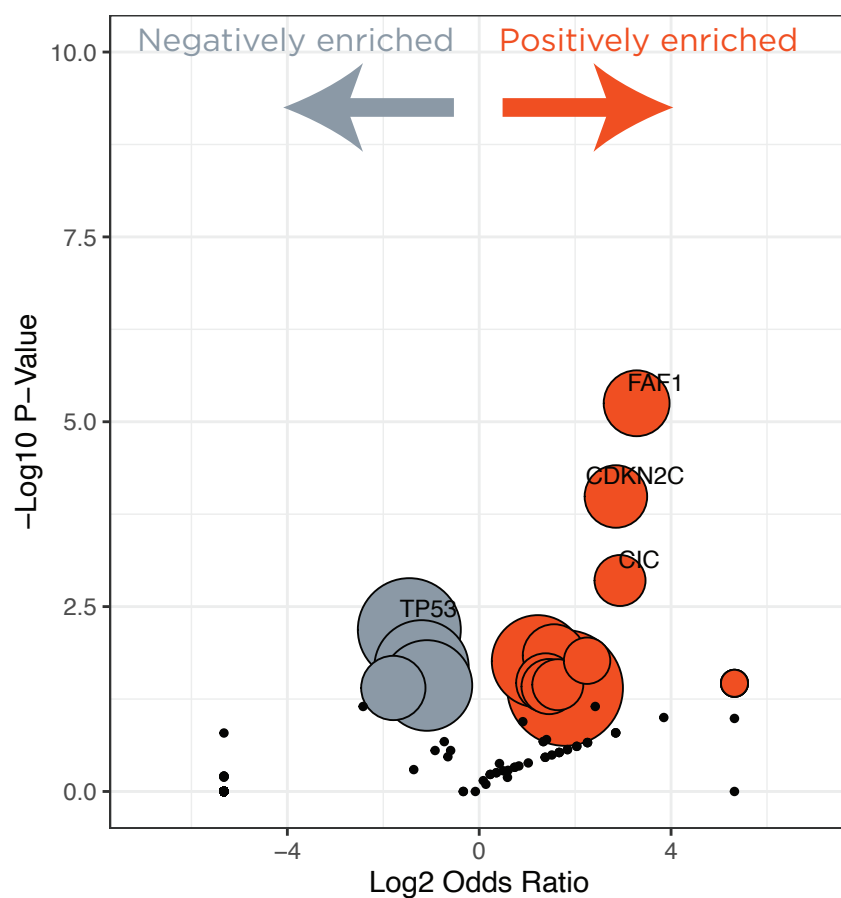
F.WT
angiosarcoma

Computational tumor purity

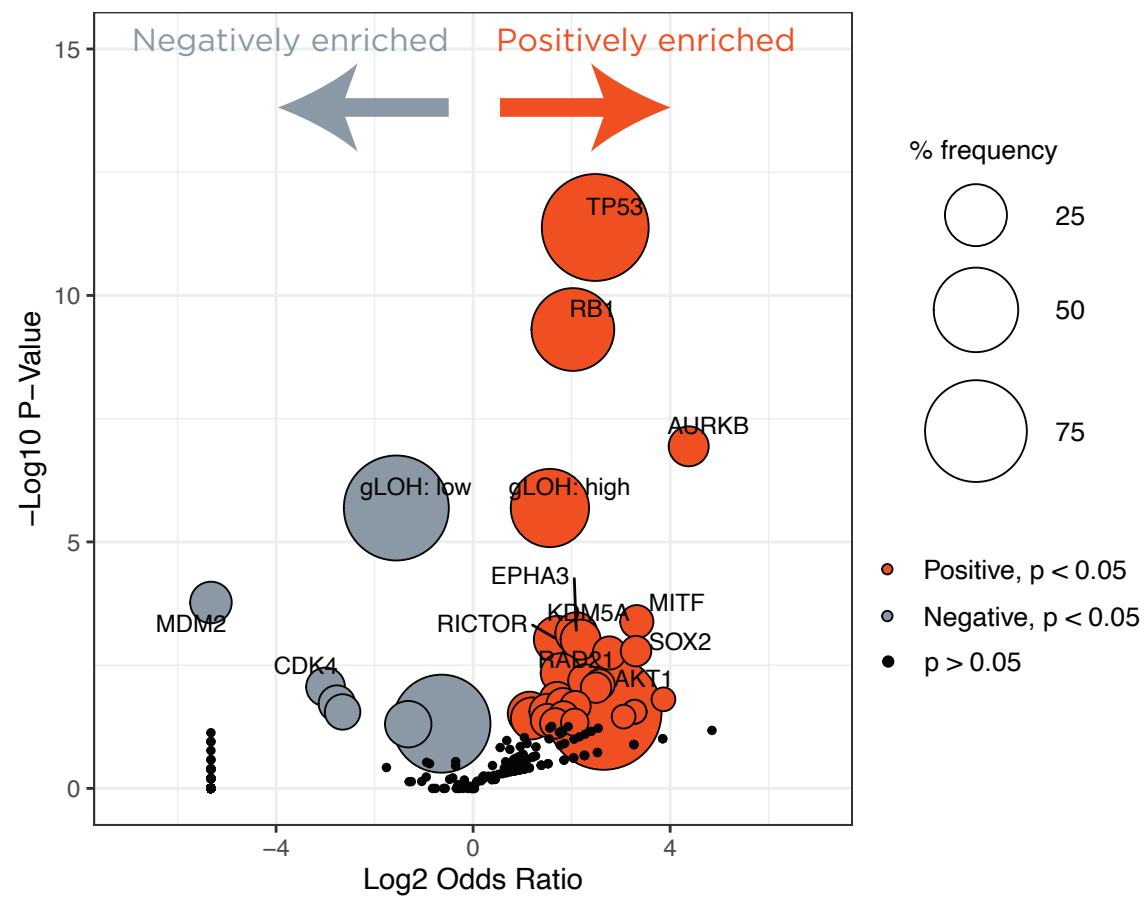
Supplementary Figure 3

Boxplots displaying the distribution of telomeric content values across samples within each computational tumor purity bin for *RAD51B* altered uterus leiomyosarcoma (A), *GID4* altered soft tissue sarcoma nos (B), and *POT1* altered angiosarcoma (C), as well as WT uterus leiomyosarcoma (D), soft tissue sarcoma nos (E), and angiosarcoma (F). WT indicates that samples lack known/likely alterations in any of the telomere-maintenance mechanism genes described in this work.

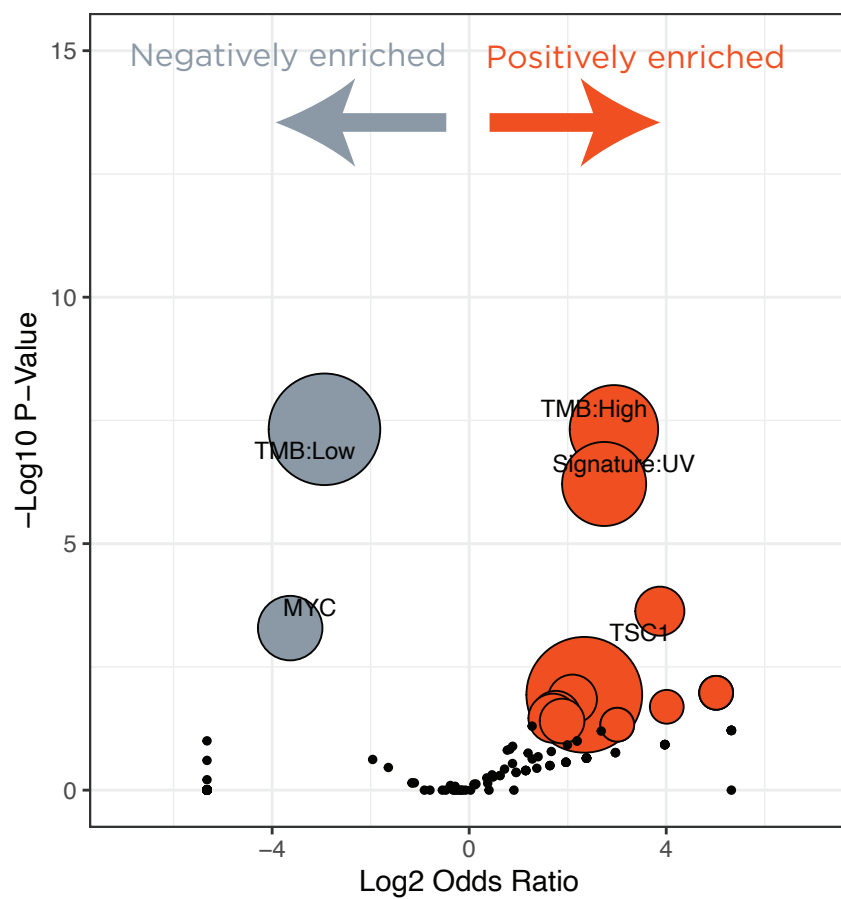
RAD51B altered
uterus leiomyosarcoma



GID4 altered
soft tissue sarcoma nos



POT1 altered
angiosarcoma

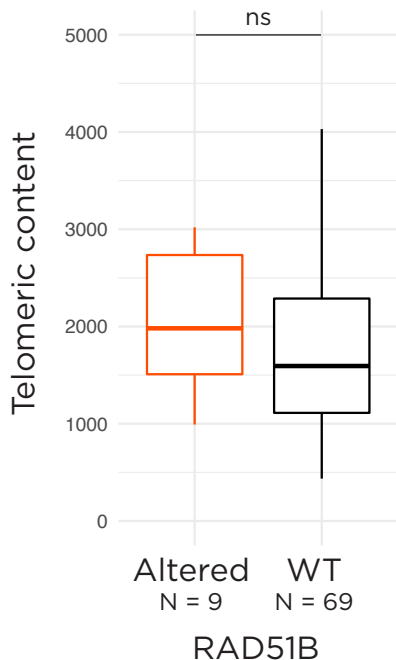


Supplementary Figure 4

Volcano plots showing the enrichment of genetic alterations and features across *RAD51B* altered uterus leiomyosarcoma, *GID4* altered soft tissue sarcoma nos, and *POT1* altered angiosarcoma. TMB, tumor mutational burden.

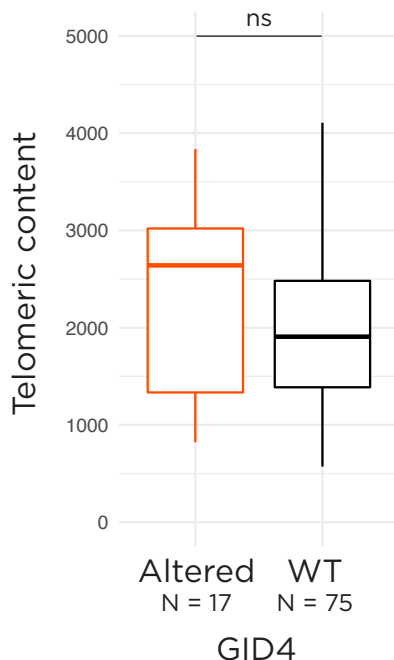
F1CDx cohort

Uterus leiomyosarcoma



F1CDx cohort

Soft tissue leiomyosarcoma

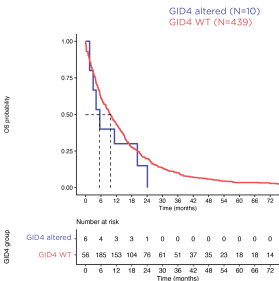


Supplementary Figure 5

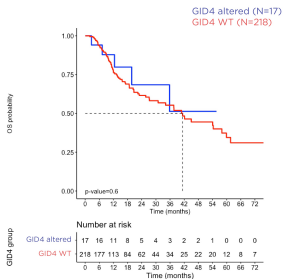
Boxplots displaying the telomeric content of samples profiled on the FoundationOne®CDx assay (F1CDx), specifically *RAD51B* altered vs *RAD51B* WT uterus leiomyosarcoma samples and *GID4* altered vs *GID4* WT soft tissue leiomyosarcoma samples. ns, not significant.

All sarcomas

CGDB cohort

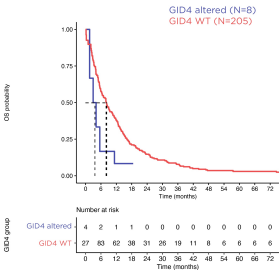


Australian cohort

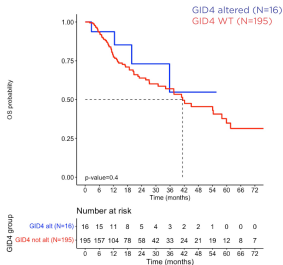


Soft tissue sarcomas

CGDB cohort



Australian cohort



Supplementary Figure 6

Kaplan-Meier survival curves for patients with GID4 WT vs altered sarcoma tumors in the CGDB cohort and the Australian cohort. Survival curves are also shown specifically for patients with soft tissue sarcomas.