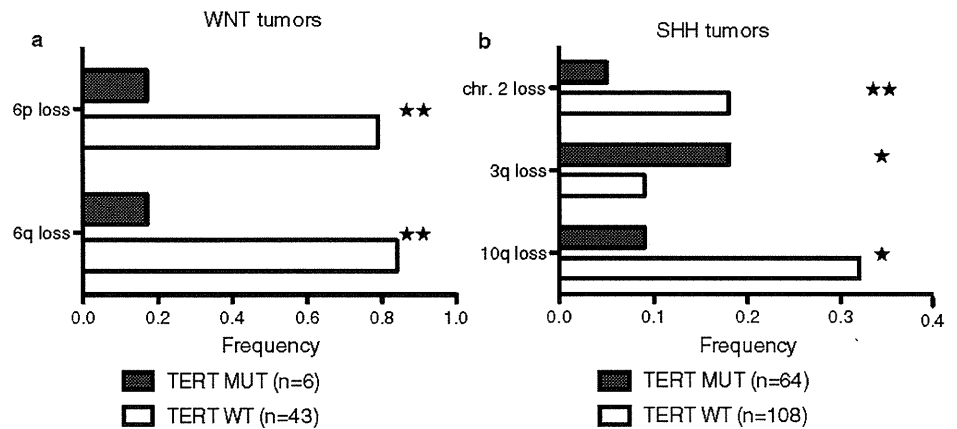


Fig. 3 *TERT* promoter mutations delineate prognostic subsets within non-infant SHH and Group 4 medulloblastomas. Kaplan–Meier estimate displaying overall survival (OS) in non-infant medulloblastomas (>3 years of age at diagnosis) according to *TERT* mutational status

across subgroups (a), in SHH tumors (b), in SHH tumors (*TP53* mutated/wild-type) (c), and Group 4 (d). Survival differences were calculated using continuous log-rank tests

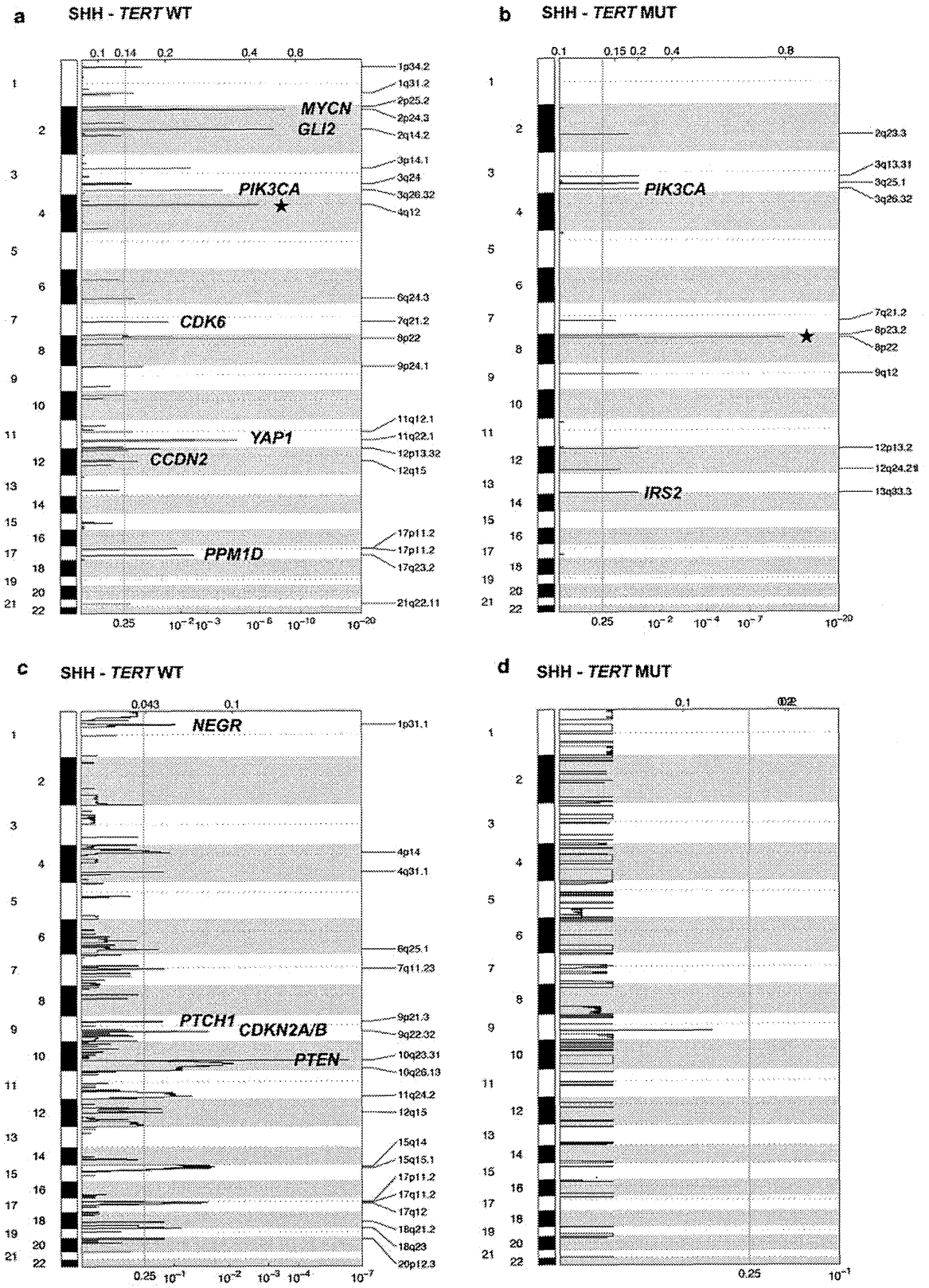
Fig. 4 WNT and SHH medulloblastoma harbor distinct broad genomic imbalances depending on the mutational status of *TERT*. Bar graphs indicating the frequency of broad cytogenetic alterations in WNT (a), and SHH (b) tumors. ★★ $p < 0.01$; ★ $p < 0.05$; MUT mutation, WT wild-type



recurrent *TERT* promoter mutations makes a compelling argument that the increasing availability of whole-genome sequencing results may substantially add to a refined understanding of the mutational landscape of different biological and age-driven medulloblastoma subgroups, since earlier

next-generation sequencing studies focusing on the protein-coding regions had not encompassed gene-regulatory regions including promoter mutations.

In this study, we demonstrate that the mutational status of the *TERT* promoter can segregate individuals with SHH



◀**Fig. 5** Focal somatic copy number alterations are largely confined to *TERT* wild-type SHH medulloblastomas. GISTIC2 analysis indicating focal amplifications/deletions in 108 wild-type (a, c) and 64 mutant (b, d) SHH tumors, respectively. *Star* regions enriched for reported DNA copy number variations

and Group 4 medulloblastomas with distinct prognostic outcomes, while a prognostic impact of this mutation was not observed in glioblastomas [23]. Molecular mechanisms converging on *TERT* up-regulation were recently reported to be associated with dismal prognosis in pediatric brain cancers [4]. Our findings in Group 4 tumors with *TERT* mutations follow this pattern, while SHH tumors with *TERT* mutations comprise a prognostically favorable subgroup. Notably, survival curves of SHH tumors increasingly approximate with extended follow-up. We hypothesize that this pattern might be due to secondary malignancies and late relapses in older SHH tumors [36–38]. Since virtually all of the *TERT* promoter mutations encompass the mutational hotspots C228T and C250T, patient stratification can be carried out using a single PCR followed up with Sanger sequencing or with a single experiment using our newly designed Taqman-based genotyping assay. The latter assay is particularly suitable for routine clinical applications as it is highly sensitive and specific (5 ng DNA input is sufficient). Furthermore, our Taqman-based genotyping assay can be used on DNA derived from fresh-frozen and formalin-fixed paraffin-embedded tissue, since it only amplifies a short DNA fragment.

Both hotspot mutations C228T and C250T create an E-twenty-six (ETS) binding motif [10, 11] resulting in up-regulation of *TERT* expression at the mRNA level [2], which was not observed at the protein level in glioblastomas [43]. We now demonstrate that SHH tumors with *TERT* mutations are mostly mutually exclusive with those harboring 10q loss ($p = 0.017$). Notably, the relatively favorable prognosis of *TERT*-mutated SHH medulloblastomas may be explained by the relative lack of high-risk biomarkers [17, 18, 24, 44].

In summary, we describe the demographic, clinicopathological, and biological implications of *TERT* promoter mutations in a subgroup-specific fashion. This study underlines the dependence of adult WNT and SHH tumors to reacquire telomerase activity and suggests a potential prognostic utility of *TERT* mutational analysis in an era of individualized therapy.

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