Supplementary Figure S2

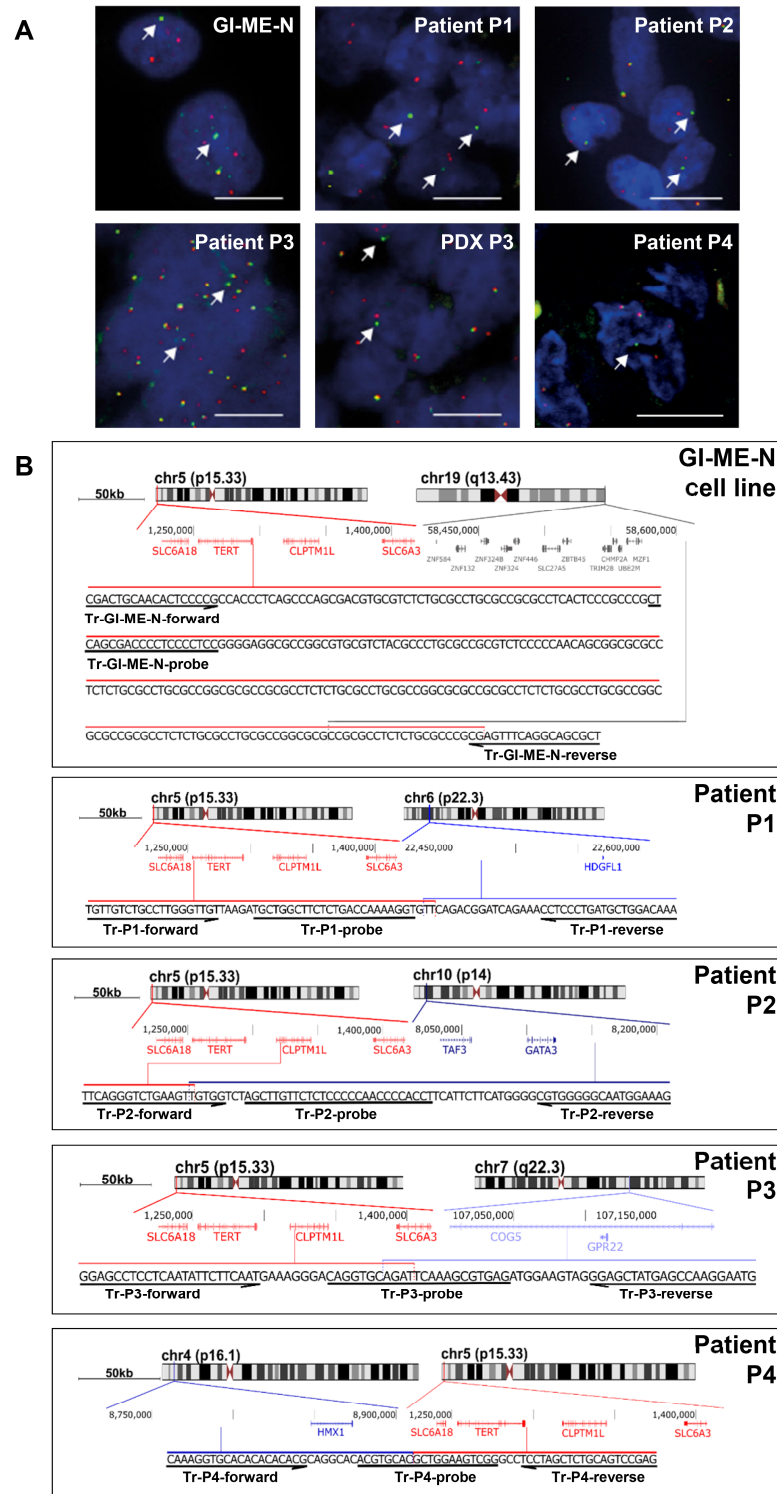**Fig. S2. Characterization of the *TERT* locus in neuroblastoma tissue samples and preclinical disease models. A**, *TERT* break-apart FISH results shown for GI-ME-N cells, the diagnostic tumor samples from the indicated patients and a patient-derived xenograft maintained in mice that was established from residual primary tumor tissue collected from patient P3 at diagnosis. A yellow signal indicates that the *TERT* gene (green) and the *CLPTM1L* gene (red) remain in their correct localization next to each other, while a green signal indicates a *TERT* rearrangement, since it is no longer attached to the red-labeled *CLPTM1L* gene. Scale bar=10 μM. **B**, Genome sequences at the *TERT* rearrangement breakpoints (targeted sequencing) are shown with the primer and probe binding sites established for ddPCR-based *TERT* breakpoint detection in GI-ME-N cells and patient tumor tissue samples. The sequence of the *TERT* locus is indicated in red, the rearrangement partner is indicated in grey (GI-ME-N) or blue (tumors).