**Fig S9** BTRC is clinically relevant.

(A) BTRC copy aberrations stratify glioma patient survival outcome. Patient stratification based on BTRC copy gains (>2.2 copies) and losses (<1.8 copies) demonstrated an association with the prognostic survival of patients (Fig S10A; log rank test P=2.5E-07). (B) Left panel, BTRC functional gene modules stratify patients into two molecular subgroups (Low BTRC subgroup and High BTRC subgroup). Hierarchical clustering of 544 mRNA transcripts distinctly segregated into 2 patient subgroups in (i) REMBRANDT and (ii) Gravendeel. Log-rank test p-value for REMBRANDT and Gravendeel: 2.15E-14 & <E-30, respectively. Samples and genes are represented in columns and rows respectively. The patient group in green box above had relatively high BTRC expression and associated with better survival (53 months and 3.2 years in REMBRANDT and Gravendeel, respectively; right panel); whilst the patient group in the red box above was associated with low BTRC expression and had poor survival (16.9 months and 0.69 years in REMBRANDT and Gravendeel, respectively; right panel). BTRC functional transcriptome is a significant predictor of patient survival (log rank P< E-10). (C) BTRC copy changes inversely correlate with PI3K-AKT and PLK4 mRNA expression in glioma patients. Box-and-Whisker plots denote the BTRC copy changes significantly correlated with mRNA expression of (i) BTRC, (ii) AKT2, (iii) PI3KCD and (iv) PLK4.