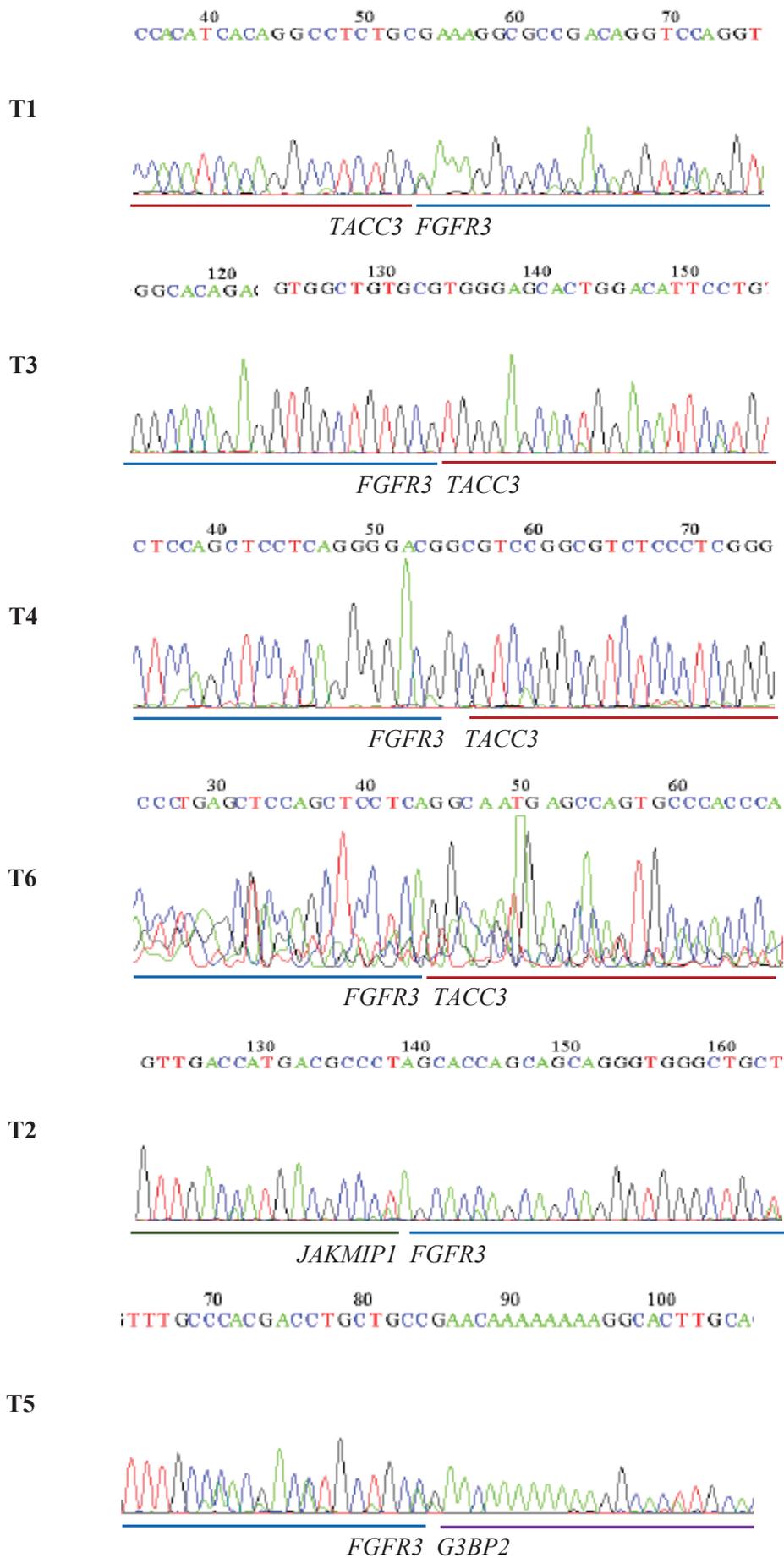
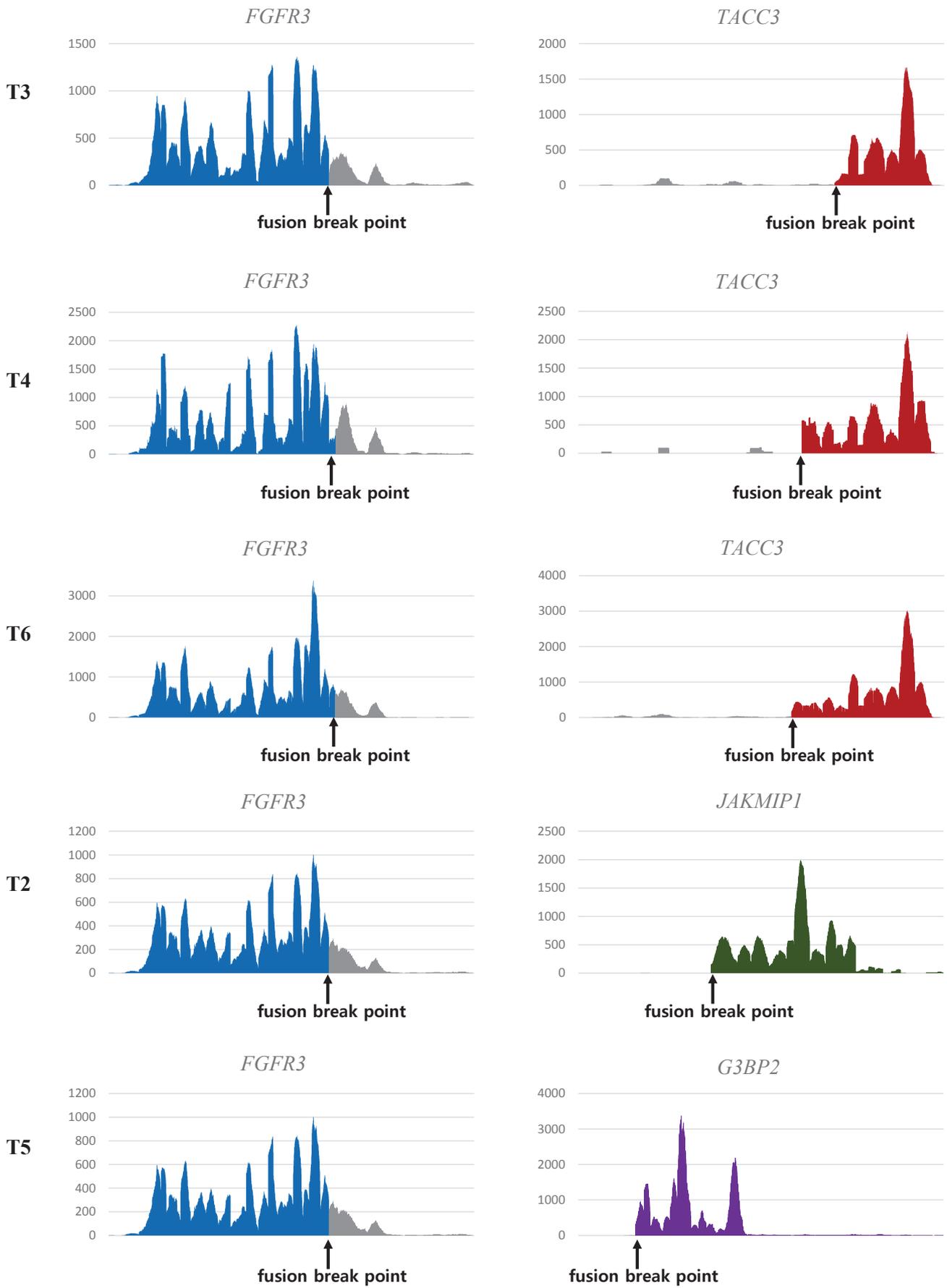


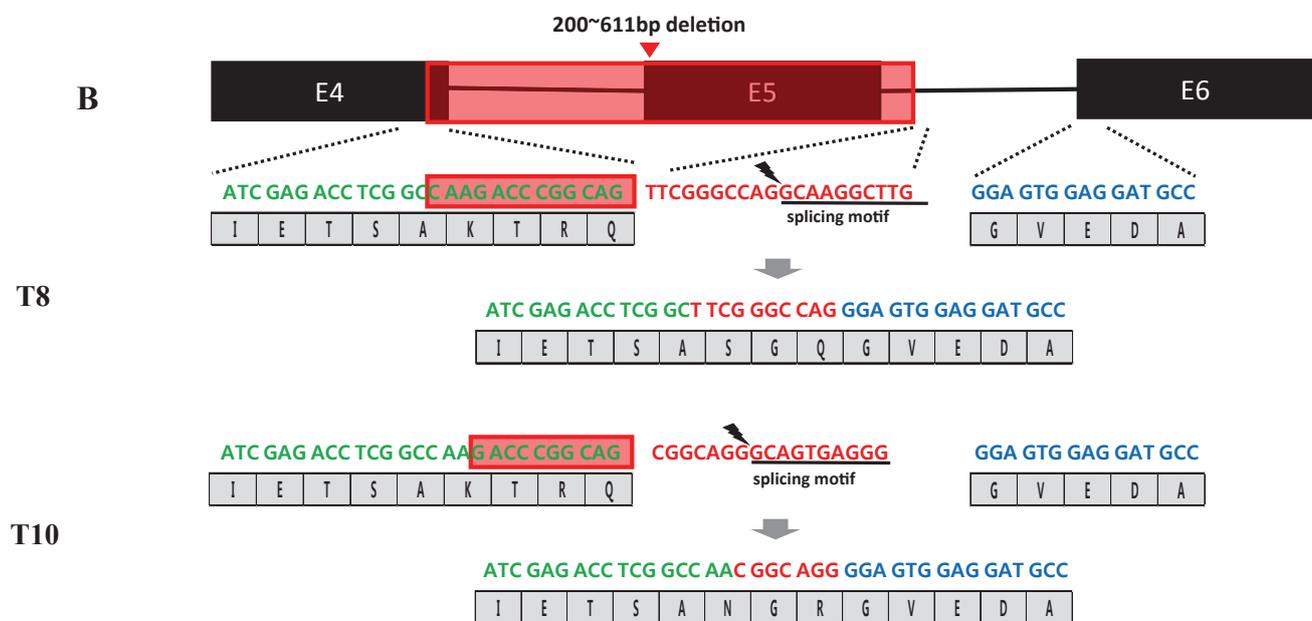
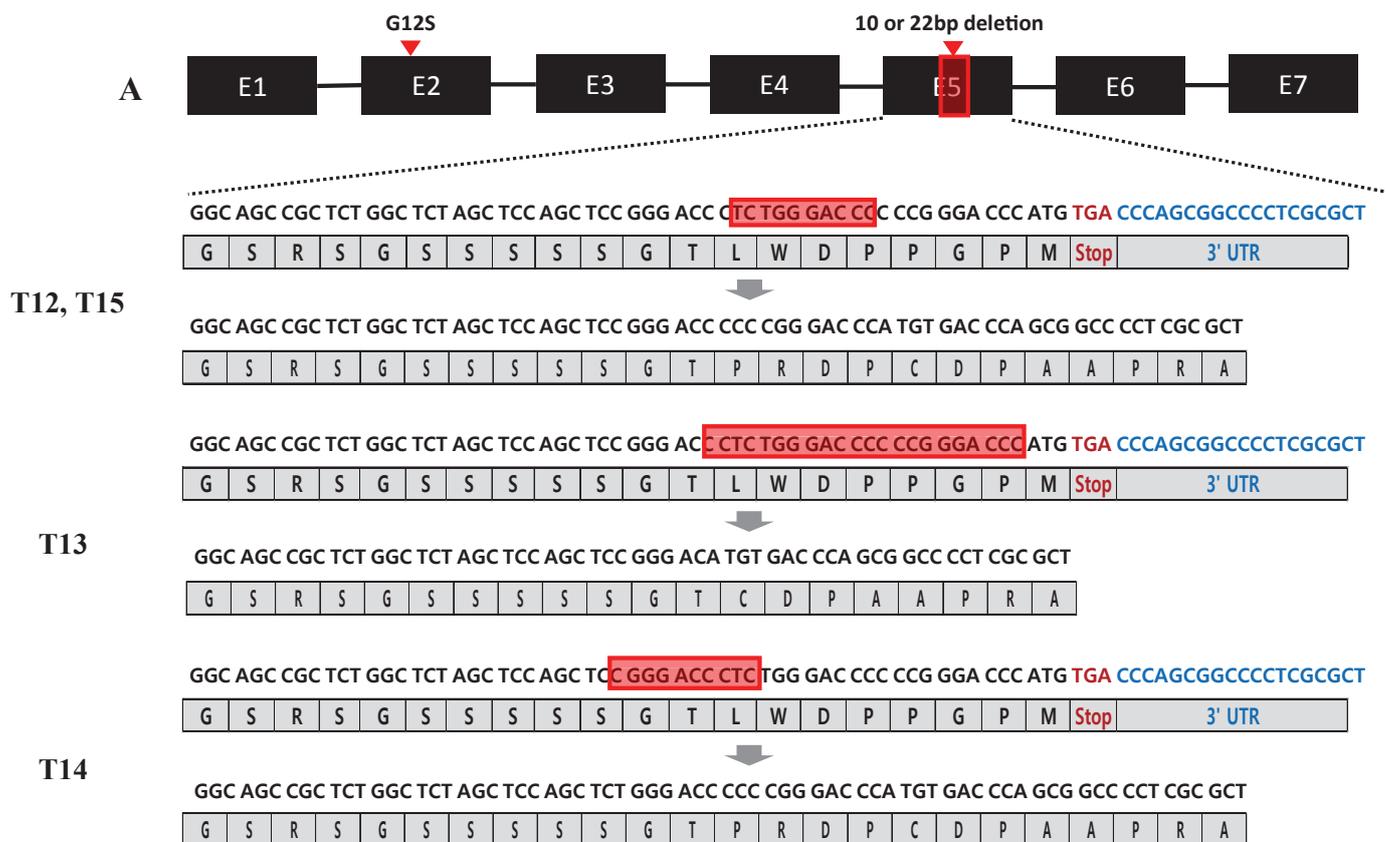
**Supplementary Figure S1. Results of Sanger Sequencing at the *FGFR3* Fusion Breakpoint.** The fusion breakpoint found in NGS was confirmed by bidirectional PCR and Sanger sequencing using tumor DNA.



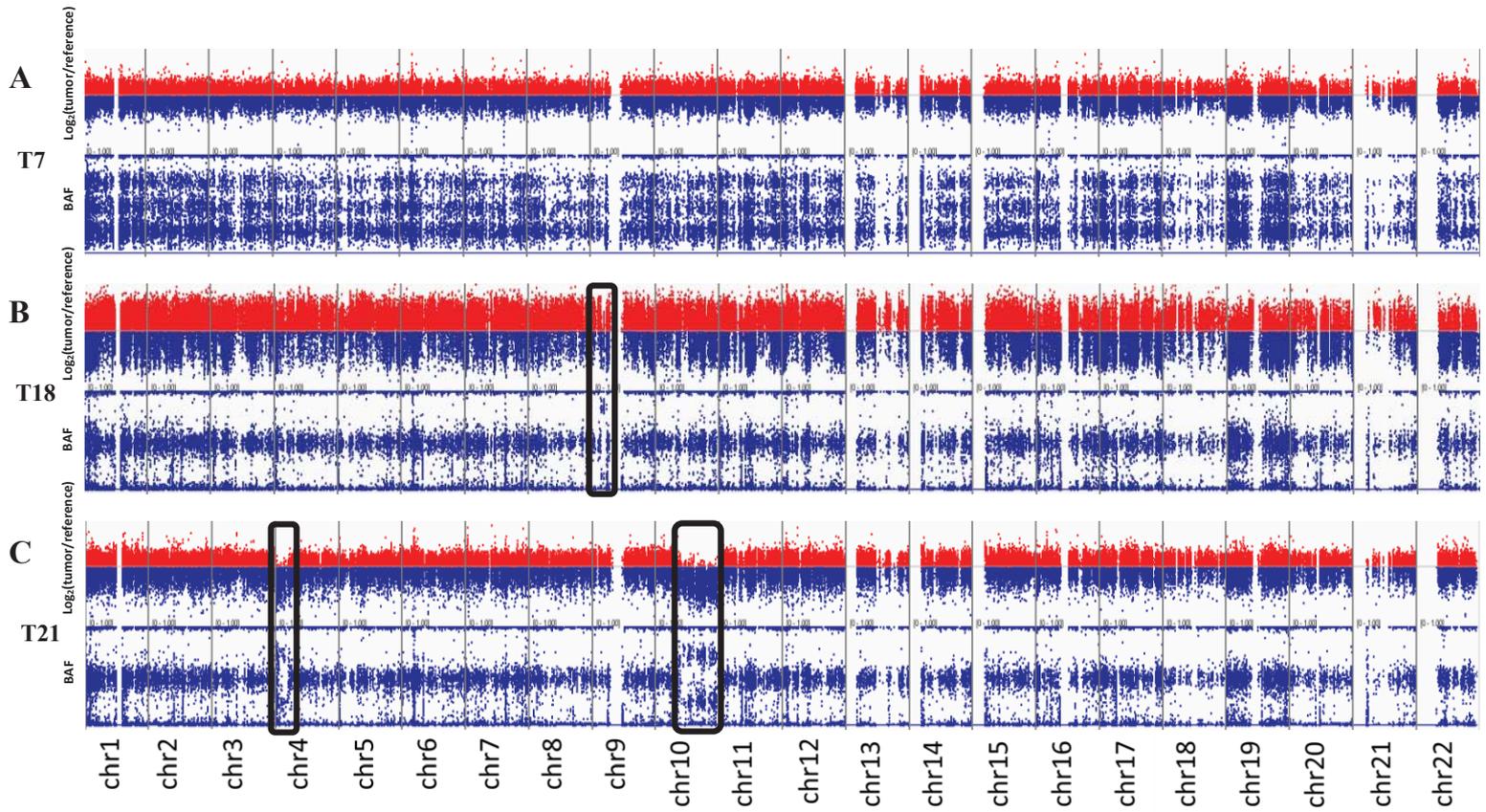
**Supplementary Figure S2. Gene Expression Before and After the *FGFR3* Fusion Breakpoint.** Y-axis is read count per base pair.



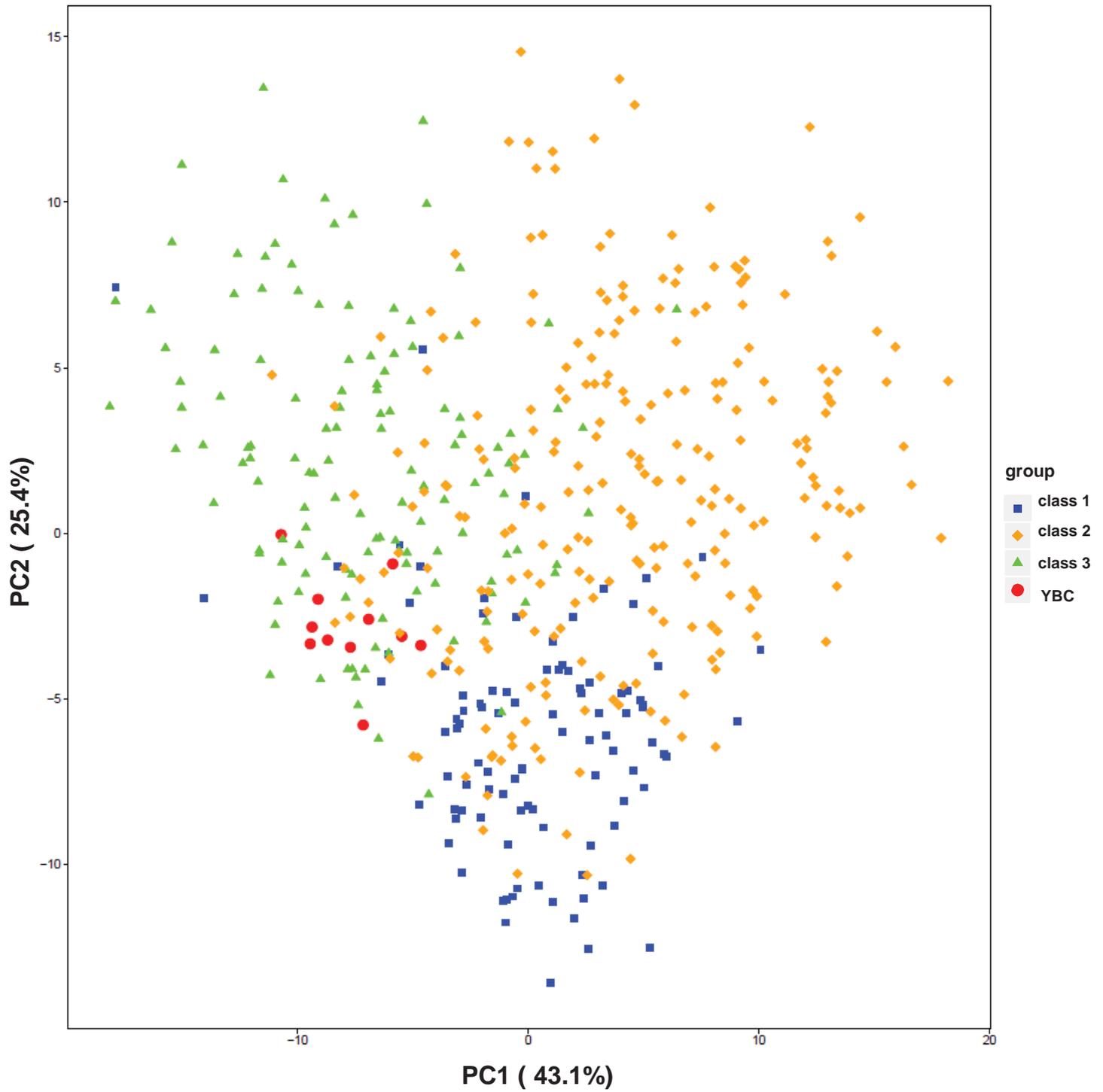
Supplementary Figure S3. Detailed Nucleotide and Amino Acid Changes in *HRAS* Deletion.



**Supplementary Figure S4. CNAs of Young-Onset Bladder Cancer (YBC).** Upper and lower panel represent  $\log_2$  (tumor/reference) ratio and B allele frequency of each tumor.

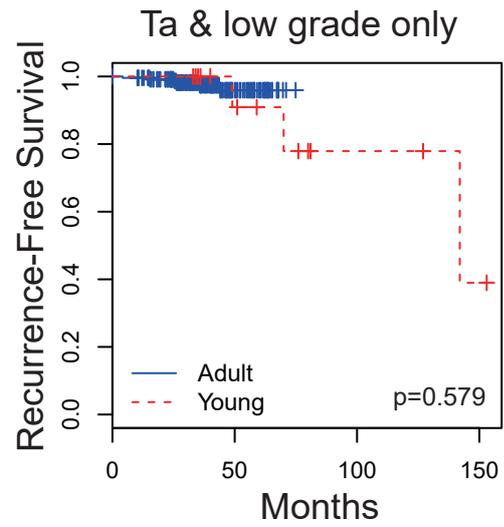
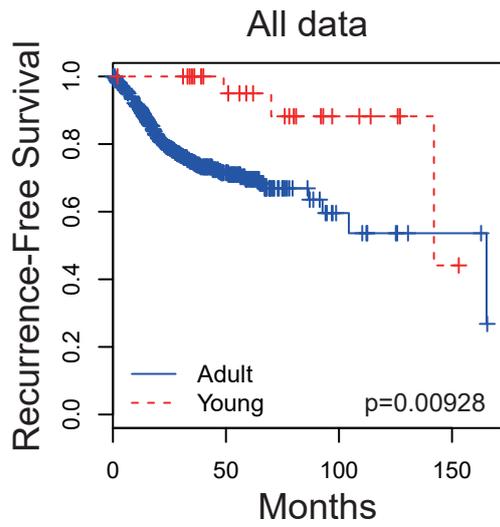


**Supplementary Figure S5. PCA Plots of YBC and the UROMOL Data.** PCA was calculated using the 117 genes from Fig. 3A.



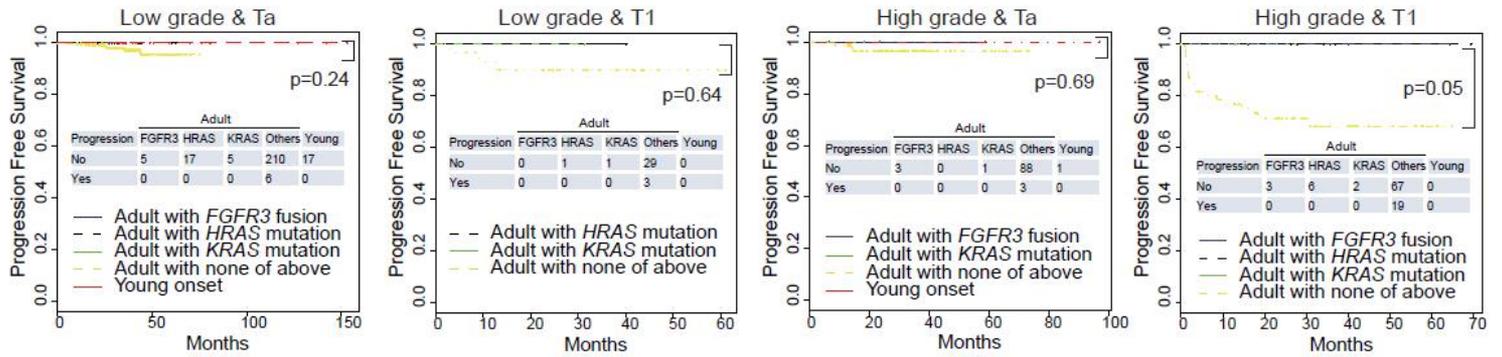
**Supplementary Figure S6. Overall Recurrence-Free Survival Rates of YBC and Adult Bladder Cancer (ABC).**

YBC showed better recurrence-free survival rates than ABC. When the survivals were compared after tumor stage and grade matching, there was no significant difference between YBC and ABC.



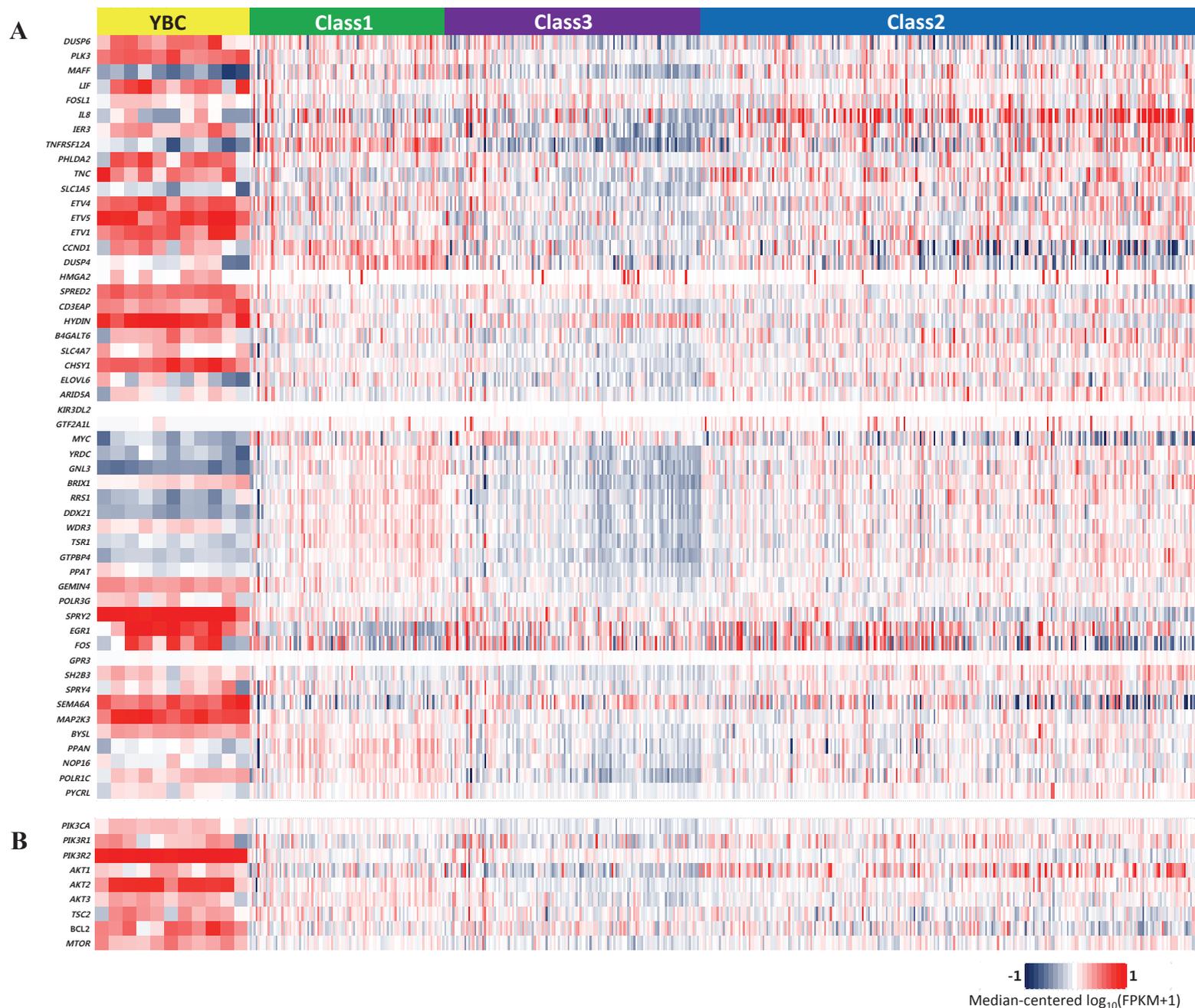
## Supplementary Figure S7. Progression-Free Survival Rates of YBC and ABC Subdivided by Grades and Stages.

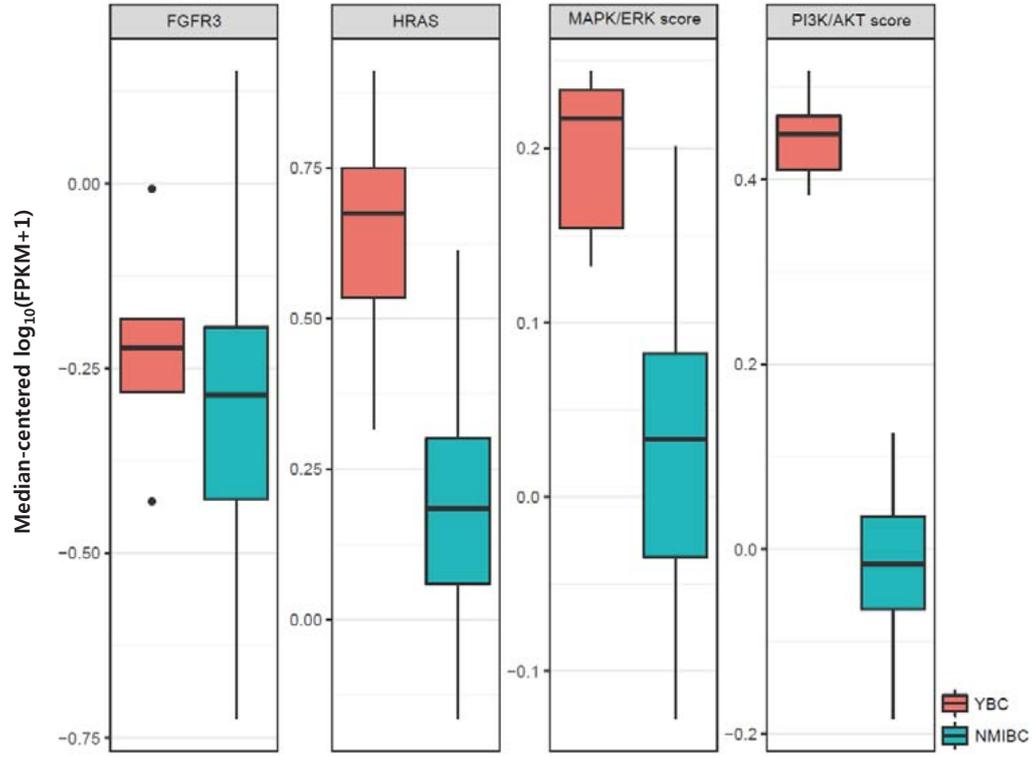
YBC and ABC with *FGFR3* fusion and *KRAS/HRAS* mutation showed better progression-free survival rates than ABC without these genetic alterations.



### Supplementary Figure S8. MAPK/ERK and PI3K/AKT Pathway Activity in YBC and the UROMOL data.

Expression profiles of 52 genes in the MAPK/ERK pathway (A) and 9 genes in the PI3K/AKT pathway (B) in the whole YBC and UROMOL samples are depicted as a heatmap. FGFR3 and HRAS gene expression level and MAPK/ERK and PI3K/AKT scores in samples with HRAS mutation (C) and FGFR3 fusion (D) are shown as box plots.



**C****D**