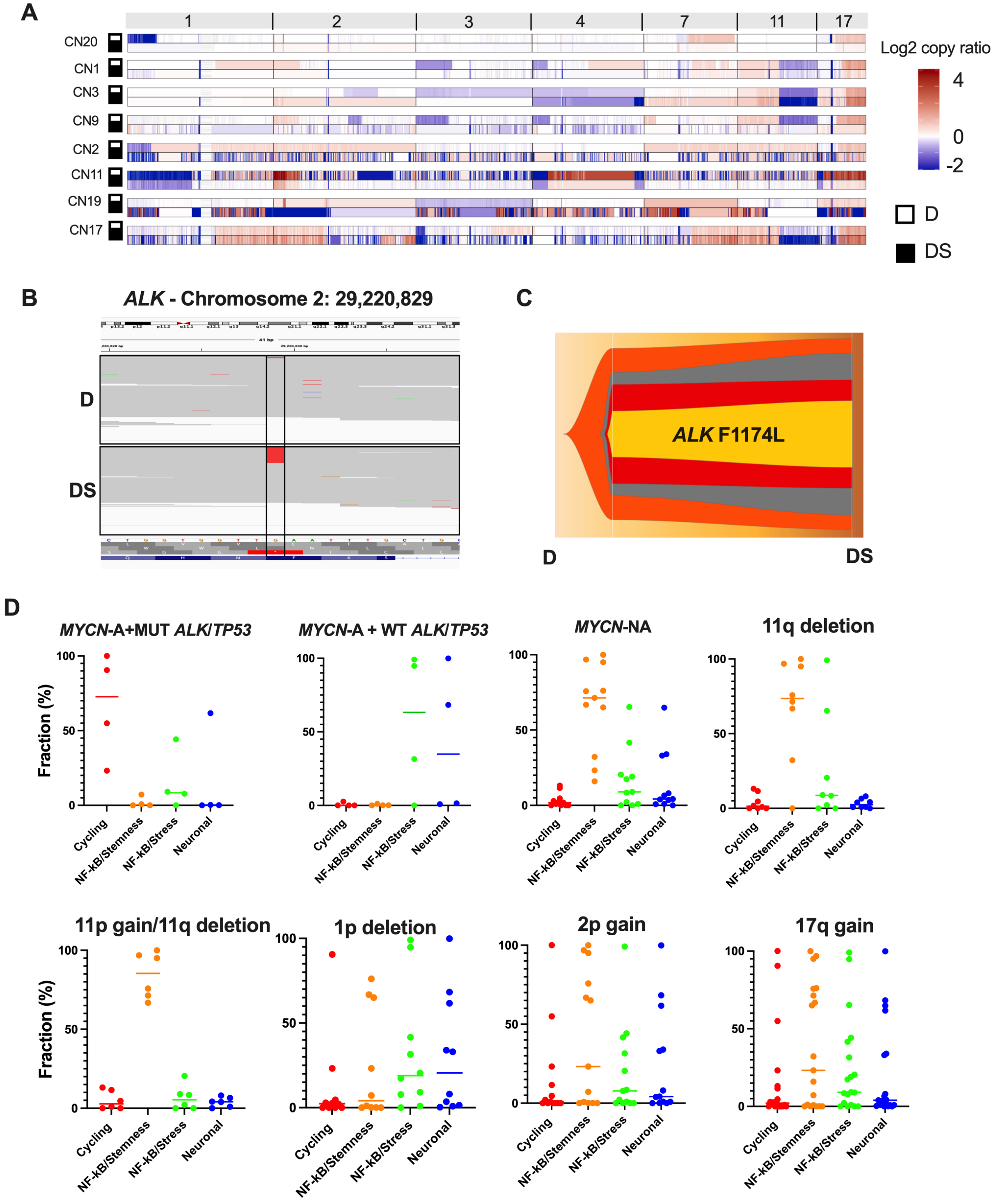
Supplementary Figure S3



Supplementary Figure S3. A. Heatmap of $\log_2$ copy ratio of chromosomes 1,2,3,4,7,11,17 for 8 pairs with low tumor purity at diagnosis (D) and definitive surgery (DS) resulting in indeterminate

CNV calling. Red – gain, blue -loss. **B.** Integrated Genome Viewer (IGV) screenshot for DNA at position 29,220,829 on chromosome 2, where the *ALK* gene is located, of a tumor obtained at diagnosis (D) and definitive surgery (DS) from patient CN14. Two reads (red) are aligned to T instead of G at diagnosis (VAF=1.5%) whereas multiple reads (red) aligned to T at definitive surgery (VAF=30%). **C.** Fishplot of the mutations percent from a tumor obtained from patient CN14 at diagnosis and definitive surgery showing clonal evolution of *ALK* subclone. **D**. Percent of persister subtypes in 19 surgical specimens for typical neuroblastoma genetic alterations at diagnosis (CHOP cohort), A- Amplified, NA- Non-Amplified, MUT – mutated, WT – wild type.