



**Supplemental Figure 2:** Genome-wide B allele frequency (BAF) (ring 1) and predicted subclonal clusters (ring 2) as determined by the TITAN software program for A) Plexiform neurofibroma, B) Pre-Treatment, C) Post-Treatment D) Recurrent tumor samples. Plexiform neurofibroma (A) had very few regions of allelic imbalance and contained one predominant clonal cluster (black). Pre (B), Post-Treatment (C) and Recurrent (D) tumor samples contained large chromosomal regions of allelic imbalance and additional subclonal clusters, corresponding to the genomic aberrations (red, blue).