

Criteria for variant assessment.

We performed whole exome sequencing (WES) of the patient's tumor and matched germline DNA. The variants were called using MuTect2 with coverage >100x and >10% variant allele frequency (VAF) in tumors and <1% in the matched normal DNA. Resulting filtered variants were annotated using ANNOVAR RefSeq hg19. Synonymous and non-coding variants were excluded. To assess for the presence of additional oncogenic drivers including gene fusions that may have been missed by WES, we analyzed the tumors using the MSK-Solid Fusion Assay, an RNA-based targeted sequencing panel that utilizes the Archer Anchored Multiplex PCR (AMPTM) technology and next generation sequencing to detect gene fusions in hematologic and solid tumor samples (Zheng et al. 2014). The Archer custom heme and solid tumor panels were designed to target 200 and 62 specific genes, respectively, known to be recurrently involved in gene rearrangements.