Supplemental online content for:

**Therapeutic Response of Metastatic Colorectal Cancer Harboring a KRAS Missense Mutation After Combination Chemotherapy With the EGFR Inhibitor Panitumumab**

*Emil Lou, MD, PhD; Donna D’Souza, MD; and Andrew C. Nelson, MD, PhD*


e**Figure 1:** Pileups of Next-Generation Sequencing Data From the Patient’s Primary Tumor
**eFigure 1.** Pileups of next-generation sequencing (NGS) data from the patient’s primary tumor. (A) Integrated Genome Viewer (IGV) image of NGS reads in exon 3 of *KRAS*, demonstrating detection of the c.175G>A (p.A59T) mutation (rs121913528; ClinVarID 12581). The total depth of coverage (DP) at this position was 5,914, with an alternate allele depth (AD) of 703, yielding a variant allele fraction (VAF) of 0.12. The estimated percent tumor nuclei in this sample (by morphologic review) was between 20% and 30%; thus, the detected VAF is consistent with a heterozygous somatic mutation present in the tumor cells. (B) IGV image of exon 2 of *KRAS*, showing no alterations detected with a minimum coverage of 3,221 in the amplicon. The allele frequency is set to a threshold of 0.02 in the coverage track of these images, demonstrating the absence of any other variant calls above background threshold.