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### Introduction

Colorectal cancer (CRC) is the third most common type of cancer in the United States. Although chemotherapy, radiation, and targeted therapies can improve survival rates, recent studies have shown that gene immunotherapies to improve outcomes for patients with advanced CRC.

Targeted therapies that use monoclonal antibodies (mAbs) to EGFR have been shown to benefit some CRC patients. In addition, KRAS has been the only predictive biomarker for anti-EGFR therapy in metastatic CRC. 40%–60% of patients with wild-type KRAS do not respond to anti-EGFR therapy. To accurately predict response to treatments and improve clinical outcomes, additional prediction and treatment methods are imperative.

### Methods and Results

**55 FFTE samples** were selected from a cohort of 488 patients with matching FF and FFPE samples. Six FF samples were selected from all FFPE samples. The total number of gene fusion events was detected among the 55 FFPE samples.

### Results

**Figure 1. Colorectal cancer sample cohort selection strategy.** The cohort was selected by filtering out colorectal cancer patients with an estimated Tumor-Infiltrating Lymphocytes (TILs) greater than 50% (TILs<50%).

**Figure 2. Multi-platform samplings.** Samples derived from the same 55 FFTE tissues were assayed across multiple platforms. The method is designed to compare RAS signature scores with DNA analysis (i.e. mutation status). A box plot shows the distribution of RAS signature scores across different platforms.

**Figure 3. Forecast for the analysis.** Six samples were selected from all 18 samples. Six samples were used to detect potential association between RAS gene signature and the level of chromosomal rearrangements.

**Figure 4. Consistent RAS signature scores between different platforms.** (A) RAS scores calculated from multiple platforms are significantly correlated. All samples have q > 0.05.

**Figure 5. RAS signature scores versus mutation status.** Samples with lower RAS scores have significantly fewer gene fusion events detected than samples with higher RAS scores.

**Figure 6. The number of mutation versus RAS status.** Distributions of all 18 genes have significantly higher number of non synonymous mutations than KRAS wild type samples.

**Figure 7. RAS signature scores and the number of gene fusion events.** (A) Distribution of gene fusion events of all samples. Only high and medium confidence gene fusion events based on results from JAXT were considered. Samples with higher number of gene fusion events have significantly higher RAS signature scores (p < 0.01).

**Figure 8. Scatter plot of enriched GO cluster representations.** Multidimensional scaling is applied to the list of significantly enriched GO scores in fusion genes found in the CRC samples.

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### References


