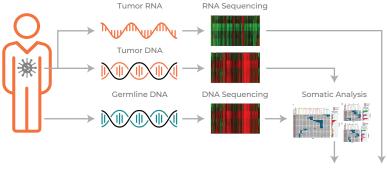


by EXACT SCIENCES



Complete The Genomic Picture By Including DNA+RNA To Obtain The Most Actionable Insights For Therapy Selection

The OncoExTra[™] test is an **ultra-comprehensive genomic profiling assay** that incorporates tumor whole-exome (DNA) and whole-transcriptome^{*} (RNA) sequencing with paired tumor-normal analysis to identify alterations biomarkers in individuals diagnosed with advanced cancers. Findings are mapped to a knowledgebase of FDA-approved targeted treatment options as well as relevant clinical trial options.



Clinical Curation and Identification of Targeted Treatment Options (FDA-approved and experimental)

WES (DNA) - Allows for comprehensive analysis of all protein-coding genes in a sample.

WTS (RNA) - Allows the identification of transcript variants and fusion genes that may be undetectable through conventional CGP tests which only employ DNA analysis.



Comprehensive Without Compromise

- The OncoExTra test interrogates ~20,000 genes.³
- IO signatures including tumor mutational burden (TMB) and microsatellite instability (MSI).
- 15 optional immunohistochemistry (IHC) stains[†] including PD-L1 (SP142, 22C3, SP263) and MMR (Mismatch Repair) proteins.
- Patient-matched tumor-normal sample to rule out benign variants.³



All About Actionability

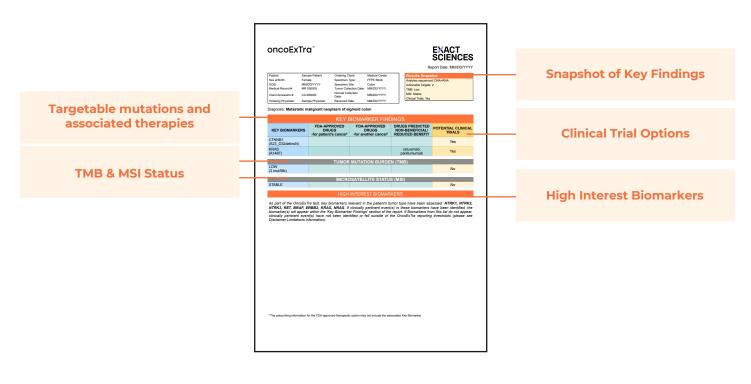
- Reports clinically actionable mutations, copy number alterations, transcript variants/fusions through DNA and RNA analyses.
- FDA-approved therapies and clinical trial options based on the patient's results are also reported.
- In a clinical utilization study, at least one clinically actionable variant was identified in 83.9% of reports (1267/1509).³

According to one estimate, 20% of cancer morbidity occurs in tumors driven by translocations and gene fusions. Many of these alterations are actionable and may be missed by panel-based tests and WES alone.^{1,2}

Case study: Previously Undetected RAS mutation in Colon Cancer

- A 48-year-old female was diagnosed with cancer of the sigmoid colon. Patient underwent a subsequent resection of the primary tumor and a biopsy of the adrenal gland at the same time confirmed metastatic disease.
- Subsequently she had laparoscopic adrenalectomy and began chemotherapy.
- Upon disease progression, NGS testing was ordered on the original metastatic sample.
- Patient was identified as KRAS wild-type (WT) and treated with an anti-EGFR monoclonal antibody to which the patient did not respond. Upon further disease progression the OncoExTra™ test (WES/WTS) was performed on a repeat biopsy.
- A rare activating KRAS (A146T) mutation on exon 4 was identified which predicts anti-EGFR monoclonal antibody resistance.

This case study is for educational purposes only and is not clinical, diagnostic, or treatment advice for any particular patient. Results and outcomes may vary. Providers should use their clinical judgment and experience when deciding how to diagnose or treat patients. Exact Sciences does not recommend or endorse any particular course of treatment or medical choice.



To Learn More: OncoExTra.com To Order: OncoExTra.com/order



References: 1. Drenner, Basu GD, Goodman LJ, et al. The value of comprehensive genomic sequencing to maximize the identification of clinically actionable alterations in advanced cancer patients: a case series. Oncotarget. 2021; 12/1856-1847. 2. Nikanjam M, Okamura P, Barkauskas DA, Kurzrock R. Targeting fusions for improved outcomes in oncology treatment. Cancer. 2020; 1261315-1321. 3. White T, Szelinger S, LoBello J, et al. Analytic validation and clinical utilization of the comprehensive genomic profiling test, Oncotarget 2021; 276-739 Disclaimer: The OncoEXTra test is not a FDA cleared or approved IVD device or companion diagnostic for the referenced biomarkers and FDA approved therapies

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OncoExTra has been validated according to the guidelines set forth by the New York State Department of Health Oncounternand beel waraake accounting to the global index exit of may then even from a date deparatherer to internate Whole exome (DNA) events have been validated to include point mutations, indek, and copy number alterations, as well as MSI analysis and TMB calculation. Whole transcriptome (RNA) has been validated to report on select fusion genes and special transcripts.

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