

NextGen GeneCORE Sarcoma Fusion panel

Your Test Results

Case Number:
Patient Name:
DOB/Sex:
Patient Location:
Hospital Name:
Physician Name:
Date & Time of Accessioning:
Date & Time of Reporting:

Test Code

G5066

Test Name

NextGen GeneCore Sarcoma Fusion panel

TAT

6 weeks

Specimen Information

Add on case no 102240007688

Clinical Indication

Feature are suggestive of Clear cell carcinoma

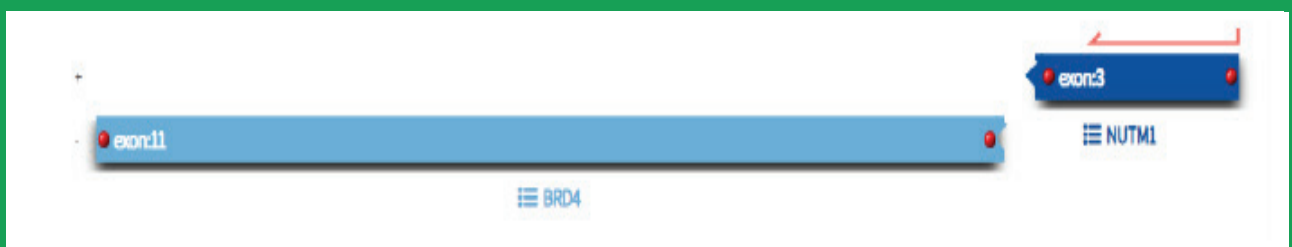
Methodology

Next Generation Sequencing

Results

Positive
(Fusion of clinical significance was detected)

Variant Category	Genes	Break Points	%Reads
Fusion	BRD4→NUTM1	chr19:15364963, chr15:34640170	75.34





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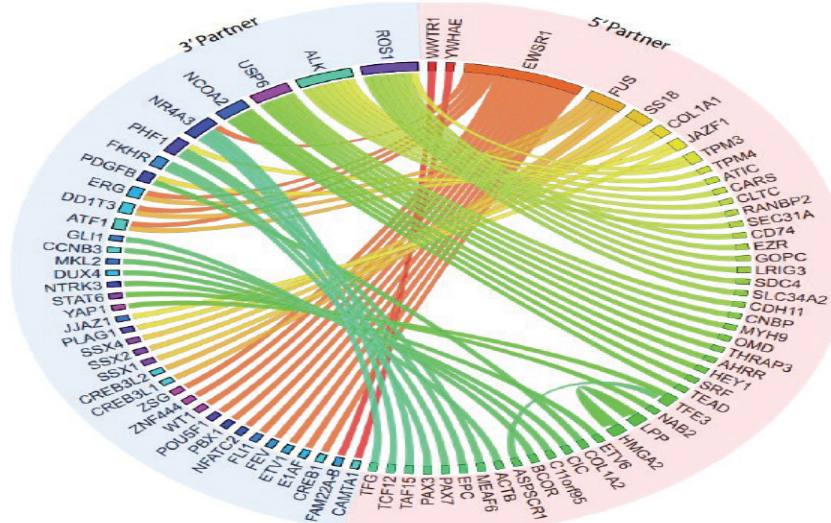
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- Genomic translocations represent an important aspect in sarcoma biology
- Translocations have been reported in 20-30% of soft tissue cancers, with more than 30 distinct gene fusions recurring in specific sarcoma subtypes
- Traditional methods of detecting translocations, such as FISH, lack the high-resolution molecular characterization crucial for understanding the identity of these fusion partners
- Amplicon-based enrichment methods (such as RT-PCR or traditional targeted sequencing) enable fusion identification, but require that fusion partners and breakpoints be known in advance
- This Sarcoma Panel is a targeted sequencing assay that simultaneously detects and identifies fusions of 56 genes associated with soft tissue cancers
- Using proprietary enrichment, fusions of all genes in this panel can be identified in a single sequencing assay, even without prior knowledge of fusion partners or breakpoints

Assay Targets

ALK, BCOR, BRAF, CAMTA1, CCNB3, CIC, CSF1, EGFR, EPC1, ERG, ESR1, EWSR1, FGFR1, FGFR2, FGFR3, FOS, FOSB, FOXO1, FUS, GLI1, HMGA2, JAZF1, MDM2, MEAF6, MET, MGEA5, MKL2, MYOD1, NCOA1, NCOA2, NR4A3, NTRK1, NTRK2, NTRK3, NUTM1, PAX3, PDGFB, PHF1, PLAG1, PRKCA, PRKCB, PRKCD, RAF1, RET, ROS1, SS18, STAT6, TAF15, TCF12, TFE3, TFG, USP6, VCP, VGLL2, YAP1, YWHAE





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- RNA was extracted from FFPE Tissue Block
- The libraries were prepared and sequenced on next generation sequencing platform
- The raw read sequences obtained from NGS are processed to remove adapters and filter poor quality reads.
- Clinically relevant fusions were identified and annotated using published variants in literature and a set of diseasesdatabases.

Disclaimer

- This test is limited to Sarcoma related fusion identification analysis only, It should be noted that this test does not sequenceall bases in a human genome and this report is limited only to variants with evidence for causing or contributing to disease/clinical details provided to CORE Diagnostics Pvt. Ltd.
- By providing drug and clinical trial information for the reported diagnosis, CORE Diagnostics Pvt. Ltd. is not guaranteeing thatany drug or clinical trial is necessarily appropriate for this patient. Healthcare providers should evaluate and interpret theinformation provided in this report, along with all other available clinical information about this patient, to determine the best treatment decisions in their own independent medical judgment. Patient management decisions should not be basedon a single test, including this one, nor solely on the information contained in this report.
- The drugs listed on the report are not ranked in any specific order as to predicted efficacy or appropriateness for this pa-tient. CORE Diagnostics Pvt. Ltd. makes no guarantee or promise as to the effectiveness or suitability (or lack thereof) of anydrug listed on this report. For more detailed information, healthcare providers should refer to the package insert for each FDA-approved drug listed in this report, and go to clinicaltrials.gov for information regarding drugs in clinical trial.

References

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- Schwarz, J.M., et al., MutationTaster2: mutation prediction for the deep-sequencing age. Nat Methods, 2014. 11(4): p.361-2.

Conditions Of Reporting

01. The tests are carried out in the lab with the presumption that the specimen belongs to the patient named or identified in the bill/test request form
02. The test results relate specifically to the sample received in the lab and are presumed to have been generated and transported per specific instructions given by the physicians/laboratory
03. The reported results are for information and are subject to confirmation and interpretation by the referring doctor
04. Some tests are referred to other laboratories to provide a wider test menu to the customer
05. Core Diagnostics Pvt. Ltd. shall in no event be liable for accidental damage, loss, or destruction of specimen, which is not attributable to any direct and mala fide act or omission of Core Diagnostics Pvt. Ltd. or its employees. Liability of Core Diagnostics Pvt. Ltd. for deficiency of services, or other errors and omissions shall be limited to fee paid by the patient for the relevant laboratory services