GenPath®
ONCOLOGY

Final Report

PHYSICIAN
SAMPLE, PHYSICIAN
ONCOLOGY HOSPITAL

PATIENT
SAMPLE, PATIENT
DOB: **Age:** **Sex:**
Ethnicity:
Patient ID:
Address:

SAMPLE
Specimen ID: XXXXXXXXX
Date of Report:
Date Collected:
Date Received:
Source: Bone marrow
Clinical Information:
Provided ICD-10 codes:

ONKOSIGHT ADVANCED PAN HEME FUSION NGS PANEL

INTERPRETATION

POSITIVE: P2RY8 -> CRLF2 gene fusion is DETECTED.

No pathogenic gene fusions detected involving ABL1, ABL2, ALK, BCL11B, BCL2, BCL6, BCR, BIRC3, CBFB, CCND1, CCND3, CDK6, CHD1, CHIC2, CIITA, CREBBP, CSF1R, DEK, DUSP22, EBF1, EIF4A1, EPOR, ERG, ETV6, FGFR1, GLIS2, IKZF1, IKZF2, IKZF3, JAK2, KAT6A, KLF2, KMT2A, MALT1, MECOM, MKL1, MLF1, MLLT10, MLLT4, MYC, MYH11, NF1, NFKB2, NOTCH1, NTRK3, NUP214, NUP98, PAG1, PAX5, PBX1, PDCD1L G2, PDGFRA, PDGFRB, PICALM, PML, PRDM16, PTK2B, RARA, RBM15, ROS1, RUNX1, RUNX1T1, SEMA6A, SETD2, STIL, TAL1, TCF3, TFG, TP63, TYK2 or ZCCHC7.

P2RY8-CRLF2 may identify a subset of BCP-ALL and AML patients with specific features and adverse outcomes that could be improved by risk-directed treatment (PMID: 36814093, https://ash.confex.com/ash/2015/webprogramscheduler/Paper78936.html)

RESULTS

Tumor Type: Precursor B-lymphoblastic leukemia (B-ALL).

5'GENE FUSION TRANSCRIPT	3'GENE FUSION TRANSCRIPT
P2RY8;exon:1;XM_006724443.3	**CRLF2;exon:1;NM_022148.3**

METHOD

RNA is isolated from peripheral blood, bone marrow aspirate or FFPE slides. Tissue sections are reviewed by a pathologist; specimens with minimal tumor cells may be rejected. RNA is isolated from the selected area of the sample. Anchored multiplex PCR for targeted next-generation sequencing is performed. The sequenced sample is a reverse transcription PCR-amplified fragment library in which each sample is uniquely identified by ligation of a short oligonucleotide barcode. The panel targets multiple rearrangements and the resultant sequence identifies the exons of the fusion transcript arising from that target and the partner gene. Each sample is monitored for quality to ensure reliable fusion detection. IKZF1 is targeted for exon skipping but not for gene fusion. Variants are identified by an automated process that takes into account statistical confidence of base calling and alignment and mapping quality [Archer Analysis vs 6.2.7]. The software requires a single read spanning two separate genes of at least 23bp each to be considered a valid fusion candidate and each read that spans the same breakpoint is grouped together. A final consensus sequence is constructed and used to annotate the two (or more) fusion partners by comparing to the human genome with BLAST and annotations from the RefSeq database cross-referenced with the manufacturers database of known fusions published in the literature [Archer Quiver Database]. The assay can detect RNA fusions in samples containing 5% or more cells with the chromosomal translocation.

Wojciech Swat, PhD, FACMG
Pathologist
This report was electronically signed.

BioReference Health, LLC
481 Edward H. Ross Drive
Elmwood Park, NJ 07407
(800) 627-1479

Tamera Paczos, M.D.
Laboratory Director

Created: 06/14/2023 1:16 PM