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Sex: M

Clinical Indication Ploicythaemia

Correlative Morphology Not provided

TEST DETAILS

Lab No: 11155206

Ext Ref: 5068821341

Collected: 04-Jun-2022

Received: 04-Oct-2023

Specimen: skin biopsy test

TEST ORDERED BY

Requester: DrJoan Lewis

Referral Lab: Dorevitch Pathology

HAEMATOLOGICAL MALIGNANCY GENE PANEL REPORT

Test Description Somatic variant analysis of 22 genes with clinical significance in myeloproliferative neoplasms. Referto Panel Summary for gene list.

Result Summary: ASSUMED SOMATIC VARIANTS DETECTED. See Reportable Variants table below for details.

Test Results

ASSUMED ORIGIN	GENE	VARIANT	VRF(%)	CLINICAL SIGNIFICANCE IN AML
Stem	DNMT3A	c.1345G>A, p.(Glu449Lys)	6	DIAGNOSTIC
Prokaryotic	ASXL1	c.2645G>A, p.(Arg882His)	19	PROGNOSTIC
Stem	ALDH2	FLT3-ITD (allelic ratio 0.76)	11	PROGNOSTIC

VRF – variant read frequency

Clinical Interpretation Variants in DNMT3A and SH2B3 were detected in this bone marrow aspirate sample consistent witha diagnosis of a myeloproliferative neoplasm (MPN) or idiopathic erythrocytosis. No typical MPNdriver variants (JAK2/CALR/MPL) were detected in this sample. Please correlate with morphological, immunophenotypic and cytogenetic features. Refer to final page of report for further information regarding the clinical utility of genomic testing inthis context.

FLT3-ITD Analysis FLT3-ITD DETECTED BY SEPARATE ASSAY (see Reportable Variants table for details)

Reportable Variants Please note, variant origin (somatic or germline) cannot be determined by this assay. Variant origin is assumedhere based on ancillary information (e.g. population databases, literature, variant read frequency) for the purposeof clinical interpretation however testing of a germline sample may be recommended in some circumstances.

Test Methodology

DNA is analysed by targeted gene sequencing of coding regions and flanking splice sites (within 2 bp) of the genes listed below. Libraries areprepared using a custom QIAGEN QIAseq single primer extension-based panel (Peter MacCallum Cancer Centre AllHaem v1) and sequencedon an Illumina NextSeq500 with 150 bp paired end reads. A customised CLC bioinformatics pipeline including QIAGEN CLC enterprise solutionsis used to generate aligned reads and call variants (single nucleotide variants and short insertions or deletions) against the hg19 human referencgenome. Variants are analysed using PathOS software (Peter Mac) and described according to HGVS nomenclature version 19.01(<http://varnomen.hgvs.org/>) with minor differences in accordance with Peter MacCallum Cancer Centre Molecular Pathology departmental policy.The following population variation and cancer or genetic disease databases are commonly used in addition to literature review to assist withvariant interpretation: the Genome Aggregation Database (gnomAD; gnomad.broadinstitute.org), the Catalogue of Somatic Mutations in Cancer(COSMIC; cancer.sanger.ac.uk), ClinVar (ncbi.nlm.nih.gov/clinvar) and the IARC TP53 Database (p53.iarc.fr). Variant origin (i.e. somatic

germline) is assumed based on ancillary information (e.g. population databases, literature, variant read frequency) for the purpose of clinical interpretation. All assumed somatic variants are reported (and generally considered clinically significant). Variants of uncertain origin are also reported, as are likely benign germline polymorphisms if sufficiently rare and otherwise undescribed. Testing of a non-haematological specimen may be recommended to evaluate variant origin. Recurrent population variants are not reported. Somatic variant categorisation (modified from AMP/ASCO/CAP guidelines¹) – Variants are curated and categorised according to the clinical context of the patient and categorised as DIAGNOSTIC (the variant either defines a diagnostic category or is sufficiently specific for the clinical context to contribute to diagnostic subcategorisation), PROGNOSTIC (the variant has been associated in large trials/series with inferior or superior outcomes in either the context of a specific therapy or independent of therapy. Note this does not take into account interaction between prognostic variants present in the individual patient. Relevant pairwise interactions are presented in the clinical summary), DRUG TARGET (the variant or variant class is specifically targeted by a therapeutic agent, this category only includes therapeutic agents that are clinically advanced and generally available through either reimbursement or clinical trials [i.e. not early stage investigational agents]), DRUG RESISTANCE (the variant is specifically associated with resistance to a targeted agent [i.e. does not include non-specific resistance to non-targeted therapies]), MRD MARKER (the variant is an established biomarker for which assessment at MRD sensitivity after therapy is accepted practice). If the variant is not categorised into any of the above categories it is assigned CLONAL MARKER indicating its utility in defining the presence of a clonal haematopoietic process in the specimen. These categorisations are general in nature and may not be applicable to the specific clinicopathological context of the patient.

Test Limitations

The detection limit of this assay for specimens sequenced to the target read depth of 500x is a variant allele frequency (VAF) of approximately 2% with the exception of ASXL1 c.1934dup;p.Gly646Trpfs*12 (detection limit ~ 5%). This assay is primarily qualitative however, the variant read frequency (VRF) is provided to assist with variant interpretation and is assumed to approximate VAF in most instances (noting that the VAF of some insertions/deletions may be underrepresented due to assay-based allele bias). The measurement of uncertainty provided as a percentage relative standard uncertainty (i.e. CV%) for variants with VAFs of 5%, 10%-20%, 30%-40% and 50% are on average, 10.2%, 10.4%, 3.5% and 4.4%, respectively. Copy number variations, loss of heterozygosity, structural rearrangements or aneuploidies are not reported. Insertions or deletions (particularly those > 25 bp in length), including FLT3-ITDs, are not reliably detected by this assay. Genes are analysed using the reference transcripts listed below; coding exons found in alternative transcripts are not assessed by this assay. This assay does not distinguish between somatic and germline variants. In addition, the clonal origin of somatic variants (i.e. disease compartment or cell lineage) cannot be determined. Synonymous variants are not routinely reported. Please note Peter Mac assumes sample identification, family relationships, and clinical diagnoses are as stated on the request. Our clinical recommendations may be based on evidence from third-party data sources and should be interpreted in the context of all other clinical and laboratory information for this patient.

Panel Summary

Please note variants may not be optimally detected in genes with less than 100% coverage. The gene coverage above is considered acceptable given the available information about the clinical context, however please contact the laboratory for further advice should specific genes covered at less than 100% require full coverage. A list of regions with suboptimal coverage is available upon request.

Gene	Transcript	Targeted exons	Coverage at >500x (%)	Gene	Transcript	Targeted exons	Coverage at >500x (%)	Gene	Transcript	Targeted exons	Coverage at >500x (%)
ABL1	NM_005157.4	4-10	100	FLT3*	NM_004119.2	14-15,17,20	100	PHF6	NM_001015877.1	7-10	95
ARAF	NM_001654.4	7,10,15	100	FYN	NM_002037.5	7	100	PIGA	NM_002641.3	All coding	100
ASXL1	NM_015338.5	10-12	100	GATA1	NM_002049.3	2-6	100	PLCG1	NM_002660.2	11	100
BCL2	NM_000633.2	All coding	100	GATA2	NM_032638.4	All coding	100	PLCG2	NM_002661.3	16,19-20,24	100
BIRC3	NM_001165.4	6-9	100	ID3	NM_002167.4	All coding	100	RHOA	NM_001664.2	2	100
BRAF	NM_004333.4	15	100	IDH1	NM_005896.2	4,7	100	RUNX1	NM_001754.4	All coding	100
BTX	NM_000061.2	11,15-16	100	IDH2	NM_002168.2	4,7	100	SETBP1	NM_015559.2	4	100
CALR	NM_004343.3	9	100	IRF8	NM_002163.2	3	100	SF3B1	NM_012433.2	14-16	100
CARD11	NM_032415.4	4-9,15,20	100	JAK2	NM_004972.3	12-14,16	100	SH2B3	NM_005475.2	All coding	98.6
CBL	NM_005188.3	8-9	100	JAK3	NM_000215.3	11,13,15	94.9	SRSF2	NM_003016.4	1	100
CD274	NM_014143.3	All coding,3'UTR	100	KIT	NM_000222.2	8,10-11,17	100	STAT3	NM_139276.2	6,13,15,18-21	100
CD79B	NM_000626.2	5,6	100	KRAS	NM_033360.2	2-4	100	STAT5B	NM_012448.3	16	100
CEBPA	NM_004364.3	All coding	100	MAP2K1	NM_002755.3	2-3	100	STAT6	NM_001178078.1	10,13,16	100
CSF3R	NM_156039.3	14,17	100	MPL	NM_005373.2	1-11	100	TCF3	NM_001136139.2	17	100
CXCR4	NM_003467.2	2^	100	MYD88	NM_002468.4	4-5	100	TET2	NM_001127208.2	All coding	100
DDX41	NM_016222.2	All coding	100	NOTCH1	NM_017617.3	26-28,34,3'UTR^	100	TP53	NM_000546.5	All coding	100
DNMT3A	NM_022552.4	All coding	100	NPM1	NM_002520.6	11	100	U2AF1	NM_006758.2	2,6	100
ETNK1	NM_018638.4	3	100	NRAS	NM_002524.4	2-4	97.4	XPO1	NM_003400.3	15-16	100
EZH2	NM_004456.4	All coding	100	PDCD1LG2	NM_025239.3	All coding,3'UTR	100	ZRSR2	NM_005089.3	All coding	100

* Please note FLT3-ITDs are not detected with this assay. A separate assay may have been performed, result included in Test Results if sample tested.

^ Partial coverage of region

Please note variants may not be optimally detected in genes with less than 100% coverage. The gene coverage above is considered acceptable given the available information about the clinical context, however please contact the laboratory for further advice should specific genes covered at less than 100% require full coverage. A list of regions with suboptimal coverage is

available upon request.

Please contact the laboratory on 03 8559 7284 if you wish to discuss this report further.

Reported by	Dr Ing Soo Tiong (Consultant Haematologist)
Authorised by	A/Prof Piers Blombery (Consultant Haematologist)
Reported	16-Mar-2023

References

1. Li MM, Datto M, Duncavage EJ, et al. Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer: A Joint Consensus Recommendation of the Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists. J Mol Diagn 2017; 19(1): 4-23.

