

Overview

Useful For

Aiding in the distinction between the myeloproliferative neoplasm polycythemia vera (PV) and other secondary erythrocytosis

Reflex Tests

Test ID	Reporting Name	Available Separately	Always Performed
JAKXR	JAK2 Exon 12-15 Sequencing, Reflex	No, (Bill Only)	No

Testing Algorithm

Both DNA and RNA are extracted. The algorithm starts with a highly sensitive DNA-based *JAK2* V617F test by allele specific PCR. If the *JAK2* V617F result is negative or very low positive (0.06%-0.6%), *JAK2* exon 12-15 Sanger sequencing test will be performed on the stored RNA sample. If a *JAK2* V617F mutation (>0.6%) is detected, the algorithm stops and no further testing will be performed.

The Sanger sequencing covers *JAK2* exons 12 through the first 90% of exon 15, which spans the region containing essentially all mutations reported in myeloproliferative neoplasms. The following algorithms are available in Special Instructions.

[-Erythrocytosis Evaluation Testing Algorithm](#)

[-Myeloproliferative Neoplasm: A Diagnostic Approach to Bone Marrow Evaluation](#)

[-Myeloproliferative Neoplasm: A Diagnostic Approach to Peripheral Blood Evaluation](#)

Special Instructions

- [Myeloproliferative Neoplasm: A Diagnostic Approach to Peripheral Blood Evaluation](#)
- [Myeloproliferative Neoplasm: A Diagnostic Approach to Bone Marrow Evaluation](#)
- [Erythrocytosis Evaluation Testing Algorithm](#)

Method Name

Allele-Specific Polymerase Chain Reaction (AS-PCR) and Sanger Sequencing

NY State Available

Yes

Specimen

Specimen Type

Varies

Shipping Instructions

Specimen must arrive within 5 days (120 hours) of collection.

Necessary Information

The following information is required:

1. **Pertinent clinical history**
2. **Clinical or morphologic suspicion**
3. **Date of collection**
4. **Specimen source**

Specimen Required

Submit only 1 of the following specimens:

Specimen Type: Blood

Container/Tube: EDTA (lavender top) or ACD-B (yellow top)

Specimen Volume: 10 mL

Collection Instructions:

1. Invert several times to mix blood.
2. Send specimen in original tube.
3. Label specimen as blood.

Specimen Type: Bone marrow aspirate

Container/Tube: EDTA (lavender top) or ACD-B (yellow top)

Specimen Volume: 4 mL

Collection Instructions:

1. Invert several times to mix blood.
2. Send specimen in original tube.
3. Label specimen as bone marrow.

Forms

If not ordering electronically, complete, print, and send a [Hematopathology/Cytogenetics Test Request \(T726\)](#) with the specimen.

Specimen Minimum Volume

Blood: 4 mL

Bone Marrow: 2 mL

Reject Due To

Gross hemolysis	Reject
Paraffin-embedded bone marrow aspirate clot or biopsy blocks Slides Paraffin shavings Heparin Moderately to severely clotted	Reject

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Refrigerated (preferred)	5 days	
	Ambient	5 days	

Clinical and Interpretive

Clinical Information

The Janus kinase 2 (*JAK2*) gene codes for a tyrosine kinase (*JAK2*) that is associated with the cytoplasmic portion of a variety of transmembrane cytokine and growth factor receptors important for signal transduction in hematopoietic cells. Signaling via *JAK2* activation causes phosphorylation of downstream signal transducers and activators of transcription (STAT) proteins (eg, STAT5) ultimately leading to cell growth and differentiation. The *JAK2* V617F is located in exon 14 and present in 50% to 60% of primary myelofibrosis and essential thrombocythemia, and 95% to 98% of polycythemia vera (PV). In the rest of the polycythemia vera cases, over 50 different mutations have been reported within exons 12 through 15 of *JAK2* and essentially all of the non-V617F *JAK2* mutations have been identified in polycythemia vera. These mutations include point mutations and small insertions or deletions. Several of the exon 12 mutations have been shown to have biologic effects similar to those caused by the V617F mutation such that it is currently assumed other nonpolymorphic mutations have similar clinical effects. However, some mutations may not be well characterized and requires further clinical and research evaluation.

Reference Values

An interpretive report will be provided.

Interpretation

The results will be reported as 1 of the 3 following states:

- Positive for *JAK2* V617F mutation
- Positive for *JAK2* mutation (other than V617F)
- Negative for *JAK2* mutations

If the result is positive, a description of the mutation at the nucleotide level and the altered protein sequence are reported.

A positive mutation status is highly suggestive of a myeloid neoplasm and may support a diagnosis of polycythemia vera in the appropriate clinical setting. Correlation with clinicopathologic findings and other laboratory results is necessary in all cases.

A negative mutation status makes a diagnosis of polycythemia vera highly unlikely, although it does not completely exclude this possibility, other myeloproliferative neoplasms or other neoplasms.

Cautions

A positive result is not specific for a particular diagnosis. Correlation with clinicopathologic findings and other laboratory results is necessary in all cases.

If this test is ordered in the setting of erythrocytosis and suspicion of polycythemia vera, interpretation requires correlation with a concurrent or recent prior bone marrow evaluation.

Clinical Reference

1. Baxter EJ, Scott LM, Campbell PJ, et al: Acquired mutation of the tyrosine kinase JAK2 in human myeloproliferative disorders. *Lancet* 2005 March 16;365(9464):1054-1061
2. James C, Ugo V, Le Couedic JP, et al: A unique clonal JAK2 mutation leading to constitutive signaling causes polycythaemia vera. *Nature* 2005 April 28;434(7037):1144-1148
3. Kralovics R, Passamonti F, Buser AS, et al: A gain-of-function mutation of JAK2 in myeloproliferative disorders. *N Engl J Med* 2005;352:1779-1790
4. Steensma DP, Dewald GW, Lasho TL, et al: The JAK2 V617F activating tyrosine kinase mutation is an infrequent event in both "atypical" myeloproliferative disorders and the myelodysplastic syndrome. *Blood* 2005;106:1207-1209
5. Ma W, Kantarjian H, Zhang X, et al: Mutation profile of JAK2 transcripts in patients with chronic myeloid neoplasias. *J Mol Diagn* 2009;11:49-53
6. Kilpivaara O, Levine RL: JAK2 and MPL mutations in myeloproliferative neoplasms: discovery and science. *Leukemia* 2008;22:1813-1817
7. Kravolics R: Genetic complexity of myeloproliferative neoplasms. *Leukemia* 2008;22:1841-1848

Performance

Method Description

Genomic DNA and RNA are extracted. Genomic DNA is extracted and 2 PCR reactions are used for each sample. In each reaction, a short fragment of genomic DNA, including the mutation site, is amplified using quantitative PCR in a real-time PCR instrument. In the first reaction, the 5' terminal base of the reverse primer matches the mutated sequence and the PCR conditions are such that it will only bind mutated DNA. In the second reaction, the 5' terminal base of the reverse primer matches the wild-type sequence and the PCR conditions are such that it will only bind the wild-type sequence. In both reactions, the PCR is monitored using TaqMan probe chemistry. The amount of mutated DNA and the amount of wild-type DNA is measured for each sample. In each run, the amount of mutated and wild-type DNA in a calibrator DNA sample is also measured. The calibrator is a mixture of DNA from a positive cell line (HEL) and a negative cell line (HL60) that is frozen in aliquots and expected to give an identical result in each run. Deviations in the calibrator result are assumed to be due to deviations in the run conditions and the sample results are corrected accordingly. Following each reaction, Relative Quantification Software is used to calculate the normalized mutated:wild-type ratio, which is expressed as a unitless ratio following correction with the calibrator data.

The formula for the normalized ratio is as follows:

Normalized ratio =	mutated/wild-type (sample)
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mutated/wild-type (calibrator)

The final result is reported as % *JAK2* V617F of total *JAK2* (ie, [mutated/mutated + wild-type] x 100%).(Unpublished Mayo method)

For the Sanger sequencing, total RNA is extracted from whole blood or bone marrow and cDNA synthesized from *JAK2* mRNA. A fragment spanning exons 12 through 15 is then amplified using standard PCR and the sequence is obtained using Sanger sequencing with analysis on an automated genetic analyzer.(Unpublished Mayo method)

PDF Report

No

Day(s) and Time(s) Test Performed

Monday through Friday

Analytic Time

7 days

Maximum Laboratory Time

10 days

Specimen Retention Time

DNA and RNA: 3 months

Performing Laboratory Location

Rochester

Fees and Codes

Fees

- Authorized users can sign in to [Test Prices](#) for detailed fee information.
- Clients without access to Test Prices can contact [Customer Service](#) 24 hours a day, seven days a week.
- Prospective clients should contact their Regional Manager. For assistance, contact [Customer Service](#).

Test Classification

This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the U.S. Food and Drug Administration.

CPT Code Information

81270-JAK2 V617

0027U (if appropriate)

LOINC® Information

Test ID	Test Order Name	Order LOINC Value
PVJAK	PV (JAK2 V617F, Exon 12-15) Reflex	In Process



Result ID	Test Result Name	Result LOINC Value
42395	PV Reflex Result	43399-5
MP037	Specimen Type	31208-2
42394	Final Diagnosis	50398-7