

Template for Reporting Results of Biomarker Testing for Myeloproliferative Neoplasms

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For the Members of the Cancer Biomarker Reporting Committee, College of American Pathologists

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CAP MPN Biomarker Template Revision History

Version Code

The definition of the version code can be found at www.cap.org/cancerprotocols.

Version: MPN_Biomarkers 1.0.0.0

Summary of Changes

This is a new template.

MPN Biomarker Reporting Template

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Completion of the template is the responsibility of the laboratory performing the biomarker testing and/or providing the interpretation. When both testing and interpretation are performed elsewhere (eg, a reference laboratory), synoptic reporting of the results by the laboratory submitting the tissue for testing is also encouraged to ensure that all information is included in the patient's medical record and thus readily available to the treating clinical team.

MYELOPROLIFERATIVE NEOPLASMS (MPNs)

Select a single response unless otherwise indicated.

Note: Use of this template is optional.

+ SPECIMEN TYPE

- + ☐ Peripheral blood
- + ☐ Bone marrow
- + ☐ Isolated granulocytes from peripheral blood
- + ☐ Other (specify): _____

+ RESULTS

+ Cytogenetic Testing Results (karyotype)

- + ☐ No abnormalities detected
- + ☐ Abnormal karyotype detected (specify): _____

+ Fluorescence In Situ Hybridization (FISH) Testing

- + ☐ *BCR-ABL1*
 - + ☐ No *BCR-ABL1* fusion detected
 - + ☐ *BCR-ABL1* fusion detected (specify percent positive cells): _____%
- + ☐ *PDGFRA*
 - + ☐ No *PDGFRA* fusion detected
 - + ☐ *FIP1L1-PDGFR*A fusion detected (specify percent positive cells): _____%
 - + ☐ Other *PDGFRA* fusion detected (specify percent positive cells): _____%
- + ☐ *PDGFRB*
 - + ☐ No *PDGFRB* fusion detected
 - + ☐ *ETV6-PDGFRB* fusion detected (specify percent positive cells): _____%
 - + ☐ Other *PDGFRB* fusion detected (specify percent positive cells): _____%
- + ☐ *FGFR1*
 - + ☐ No *FGFR1* rearrangement detected
 - + ☐ *FGFR1* rearrangement detected (specify percent positive cells): _____%

+ BCR-ABL1 Transcript Reverse Transcription Polymerase Chain Reaction (RT-PCR) Testing+ ☐ No BCR-ABL1 fusions detected+ ☐ BCR-ABL1 fusions detected

If quantitative testing performed:

+ BCR-ABL1 normalized copy number (BCR-ABL1/reference gene): _____

+ Percent BCR-ABL1 on international scale (e13/14a2 (p210) fusions only): _____%

+ JAK2 p.V617F (c. 1849G>T) Mutation Testing+ ☐ No mutation detected+ ☐ Mutation detected

+ For JAK2 p.V617F, if test is quantitative, specify quantitative value: _____

Reported as:

+ ☐ Percent mutant allele burden+ ☐ Percent transcript levels+ ☐ Normalized copy number (V617F transcripts/reference gene)**+ Additional Mutation Testing**+ ☐ JAK2 exon 12+ ☐ No JAK2 exon 12 mutation detected+ ☐ JAK2 exon 12 mutation detected (specify mutation): _____+ ☐ MPL+ ☐ No MPL mutation detected+ ☐ MPL mutation detected (specify mutation): _____+ ☐ CALR (calreticulin)+ ☐ No CALR mutation detected+ ☐ CALR mutation detected (specify mutation): _____+ ☐ KIT+ ☐ No KIT mutation detected+ ☐ KIT mutation detected (specify mutation): _____+ ☐ Other (specify gene): _____+ ☐ No mutation detected+ ☐ Mutation detected (specify mutation): _____**+ METHODS****+ BCR-ABL1 Transcript RT-PCR Testing**

+ BCR-ABL1 RT-PCR assay sensitivity: _____

+ JAK2 p.V617F (c. 1849G>T) Mutation Testing

+ Assay sensitivity: _____

+ Assay method:

+ ☐ Allele-specific PCR+ ☐ Sanger sequencing+ ☐ Pyrosequencing+ ☐ Next-generation sequencing+ ☐ Other (specify): _____

+ Other Mutation Testing (specify gene): _____

+ Assay sensitivity: _____

+ Assay method:

+ ___ Allele-specific PCR

+ ___ Sanger sequencing

+ ___ Pyrosequencing

+ ___ Next-generation sequencing

+ ___ Other (specify): _____

+ Exon(s)/codon(s) covered: _____

Explanatory Notes

Myeloproliferative neoplasms (MPNs) are clonal disorders characterized by the expansion of one or more myeloid lineages leading to increased bone marrow cellularity and elevated peripheral blood myeloid cell counts. The latter may manifest as granulocytosis, erythrocytosis, thrombocytosis, or a combination, depending on the disease subtype. The diagnosis and classification of MPNs require synthesis of the clinical, morphologic, immunophenotypic, and molecular genetic findings. Over the course of the last few years, the spectrum of genetic mutations identified in MPNs has expanded, and polymerase chain reaction (PCR) and/or sequence-based mutation testing is now routinely incorporated into the diagnostic workup. However, the diagnosis still relies heavily on the peripheral blood and bone marrow morphologic findings and the clinical features of the disease, particularly for those patients who do not have a disease-defining genetic abnormality.

In the 2008 World Health Organization (WHO) classification system, the category of MPNs includes chronic myelogenous leukemia (CML), chronic neutrophilic leukemia (CNL), polycythemia vera (PV), primary myelofibrosis (PMF), essential thrombocythemia (ET), chronic eosinophilic leukemia, NOS, mastocytosis, and myeloproliferative neoplasm, unclassifiable (MPN-U), and the clinical and pathologic findings may overlap with the category of myeloid and lymphoid neoplasms with eosinophilia and abnormalities of *PDGFRA*, *PDGFRB*, and *FGFR1*.¹ Classical cytogenetic karyotyping and fluorescence in situ hybridization (FISH) testing are often used in the evaluation of patients to test for the presence of t(9;22)(q34;q11.2);*BCR-ABL1*, particularly for those who present with neutrophilic leukocytosis, and for abnormalities of *PDGFRA*, *PDGFRB* and *FGFR1* for those patients who present with eosinophilia. Otherwise, patients with MPNs may have a variety of cytogenetic abnormalities. Various trisomies such as +8 and/or +9 are often identified. Given the degree of standardization and specialization that has occurred in *BCR-ABL1* testing, and the repeated nature of the analyses, the College of American Pathologists (CAP) has published a separate CML monitoring template for those patients known to have CML.

When the cytogenetic and/or FISH testing results are nonspecific or negative, it may be necessary to utilize additional molecular genetic tests. The *JAK2* p.V617F (c.1849G>T) somatic point mutation is present in almost all patients with PV and in a large proportion (40%-50%) of patients with ET or PMF. Both qualitative and quantitative testing methods are employed, although the utility of quantitation of the mutant *JAK2* allele burden remains somewhat controversial. A small percentage of patients with PV who lack evidence of a *JAK2* p.V617F mutation may have a mutation in exon 12 of *JAK2*, and these are often insertions or deletions.² Different testing methods are often utilized for *JAK2* p.V617F and *JAK2* exon 12 mutations, and it should be noted that different methods, for example Sanger sequencing and allele-specific PCR, may have markedly different sensitivities. Mutations in the *CALR* (calreticulin) gene were recently identified in the majority of patients with ET or PMF who lack *JAK2* mutations.^{3,4} Less commonly, mutations in the *MPL* gene are present in a subset of ET/PMF patients without *JAK2* or *CALR* mutations.³ *KIT* mutation testing is helpful for the diagnosis and subclassification of mastocytosis and is important for determining the likely response to tyrosine kinase inhibitor (TKI) therapy.⁵

Given the pace of recent findings, additional pathologically relevant mutations are likely to be identified and/or clinically validated in the near future. With this in mind, the template includes space for reporting other mutation testing, and future template updates will reflect additional molecular genetic findings that may be incorporated into the WHO classification system.

References

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3. Klampfl T, Gissinger H, Harutyunyan AS, et al. Somatic mutations of calreticulin in myeloproliferative neoplasms. *New Engl J Med*. 2013;369:2379-2390.
4. Nangalia J, Massie CE, Baxter EJ, et al. Somatic mutations of calreticulin in myeloproliferative neoplasms. *New Engl J Med*. 2013;369:2391-2405.
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