DISCLAIMER
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POLICY

CHRONIC MYELOGENOUS LEUKEMIA

**BCR-ABL1** qualitative testing for the presence of the fusion gene may be considered medically necessary for the diagnosis of chronic myeloid leukemia (see Policy Guidelines section).

**BCR-ABL1** testing for messenger RNA transcript levels by quantitative real-time reverse transcription–polymerase chain reaction at baseline before initiation of treatment and at appropriate intervals (see Policy Guidelines section) may be considered medically necessary for monitoring of chronic myeloid leukemia treatment response and remission.

Evaluation of ABL kinase domain (KD) single nucleotide variants to assess patients for tyrosine kinase inhibitor resistance may be considered medically necessary when there is an inadequate initial response to treatment or any sign of loss of response (see Policy Guidelines section); and/or when there is a progression of the disease to the accelerated or blast phase.

Evaluation of ABL KD single nucleotide variants is considered investigational for monitoring in advance of signs of treatment failure or disease progression.

ACUTE LYMPHOBLASTIC LEUKEMIA

**BCR-ABL1** testing for messenger RNA transcript levels by quantitative real-time reverse transcription–polymerase chain reaction at baseline before initiation of treatment and at appropriate intervals during therapy (see Policy Guidelines section) may be considered medically necessary for monitoring of Philadelphia chromosome–positive acute lymphoblastic leukemia treatment response and remission.

Evaluation of ABL KD single nucleotide variants to assess patients for tyrosine kinase inhibitor resistance may be considered medically necessary when there is an inadequate initial response to treatment or any sign of loss of response.

Evaluation of ABL KD single nucleotide variants is considered investigational for monitoring in advance of signs of treatment failure or disease progression.
POLICY GUIDELINES

DIAGNOSIS OF CHRONIC MYELOGENOUS LEUKEMIA AND ACUTE LYMPHOBLASTIC LEUKEMIA
Qualitative molecular confirmation of the cytogenetic diagnosis (ie, detection of the Philadelphia chromosome) is necessary for accurate diagnosis of chronic myelogenous leukemia (CML). Identification of the Philadelphia chromosome is not necessary to diagnose acute lymphoblastic leukemia (ALL); however, molecular phenotyping is usually performed at the initial assessment (see Determining Baseline RNA Transcript Levels and Subsequent Monitoring subsection).

Distinction between molecular variants (ie, p190 vs p210) is necessary for accurate results in subsequent monitoring assays.

DETERMINING BASELINE RNA TRANSCRIPT LEVELS AND SUBSEQUENT MONITORING
Determination of BCR-ABL1 messenger RNA transcript levels should be done by quantitative real-time reverse transcription–polymerase chain reaction–based assays, and reported results should be standardized according to the International Scale.

For CML, testing is appropriate at baseline before the start of imatinib treatment, and testing is appropriate every 3 months when the patient is responding to treatment. After a complete cytogenetic response is achieved, testing is recommended every 3 months for 2 years, then every 3 to 6 months thereafter during treatment.

Without a complete cytogenetic response, continued monitoring at 3-month intervals during treatment is recommended. It has been assumed that the same time points for monitoring imatinib are appropriate for dasatinib and nilotinib and will likely also be applied to bosutinib and ponatinib (see Rationale section).

More frequent monitoring is indicated for patients diagnosed with CML who are in complete molecular remission and are not undergoing treatment with a tyrosine kinase inhibitor (TKI).

For ALL, the optimal timing remains unclear and depends on the chemotherapy regimen used.

TKI RESISTANCE
For CML, inadequate initial response to TKIs is defined as failure to achieve a complete hematologic response at 3 months, only minor cytogenetic response at 6 months, or major (rather than complete) cytogenetic response at 12 months.

Unlike in CML, ALL resistance to TKIs is less well studied. In patients with ALL receiving a TKI, a rise in the BCR-ABL mRNA level while in hematologic complete response or clinical relapse warrants variant analysis.

Loss of response to TKIs is defined as hematologic relapse, cytogenetic relapse, or 1-log increase in BCR-ABL1 transcript ratio and therefore loss of major molecular response.

Kinase domain single nucleotide variant testing is usually offered as a single test to identify T315I variant or as a panel (that includes T315I) of the most common and clinically important variants.

GENETICS NOMENCLATURE UPDATE
The Human Genome Variation Society nomenclature is used to report information on variants found in DNA and serves as an international standard in DNA diagnostics. It is being implemented for genetic testing medical evidence review updates starting in 2017 (see Table PG1). The Society’s nomenclature is recommended by the Human Variome Project, the HUman Genome Organization, and by the Human Genome Variation Society itself.
The American College of Medical Genetics and Genomics and the Association for Molecular Pathology standards and guidelines for interpretation of sequence variants represent expert opinion from both organizations, in addition to the College of American Pathologists. These recommendations primarily apply to genetic tests used in clinical laboratories, including genotyping, single genes, panels, exomes, and genomes. Table PG2 shows the recommended standard terminology—“pathogenic,” “likely pathogenic,” “uncertain significance,” “likely benign,” and “benign”—to describe variants identified that cause Mendelian disorders.

Table PG1. Nomenclature to Report on Variants Found in DNA

<table>
<thead>
<tr>
<th>Previous Definition</th>
<th>Updated Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mutation</td>
<td>Disease-associated variant</td>
</tr>
<tr>
<td>Variant</td>
<td>Change in the DNA sequence</td>
</tr>
<tr>
<td>Familial variant</td>
<td>Disease-associated variant identified in a proband for use in subsequent targeted genetic testing in first-degree relatives</td>
</tr>
</tbody>
</table>

Table PG2. ACMG-AMP Standards and Guidelines for Variant Classification

<table>
<thead>
<tr>
<th>Variant Classification</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pathogenic</td>
<td>Disease-causing change in the DNA sequence</td>
</tr>
<tr>
<td>Likely pathogenic</td>
<td>Likely disease-causing change in the DNA sequence</td>
</tr>
<tr>
<td>Variant of uncertain significance</td>
<td>Change in DNA sequence with uncertain effects on disease</td>
</tr>
<tr>
<td>Likely benign</td>
<td>Likely benign change in the DNA sequence</td>
</tr>
<tr>
<td>Benign</td>
<td>Benign change in the DNA sequence</td>
</tr>
</tbody>
</table>

ACMG: American College of Medical Genetics and Genomics; AMP: Association for Molecular Pathology.

CODING
A new code was effective April 1, 2018:
0040U BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis, major breakpoint, quantitative.
See the Codes table for details.

BENEFIT APPLICATION
Some Plans may have contract or benefit exclusions for genetic testing.

BACKGROUND

MYELOGENOUS LEUKEMIA AND LYMPHOBLASTIC LEUKEMIA

Chronic Myelogenous Leukemia
Chronic myelogenous leukemia (CML) is a clonal disorder of myeloid hematopoietic cells, accounting for 15% of adult leukemias. The disease occurs in chronic, accelerated, and blast phases, but is most often diagnosed in the chronic phase. If left untreated, chronic phase disease will progress within 3 to 5 years to the accelerated phase, characterized by any of several specific criteria such as 10% to 19% blasts in blood or bone marrow, basophils comprising 20% or more of the white blood cell count, or very high or very low platelet counts. From the accelerated phase, the disease progresses into the final phase of blast crisis, in which the disease behaves like an acute leukemia, with rapid progression and short survival. Blast crisis is diagnosed by the presence of either more than 20% myeloblasts or lymphoblasts.
in the blood or bone marrow, large clusters of blasts in the bone marrow on biopsy, or development of a solid focus of leukemia outside the bone marrow.

Extensive clinical data have led to the development of congruent recommendations and guidelines developed both in North America and in Europe on the use of various types of molecular tests relevant to the diagnosis and management of CML. These tests are useful in the accelerated and blast phases of this malignancy.

**Acute Lymphoblastic Leukemia**

Acute lymphoblastic leukemia (ALL) is characterized by the proliferation of immature lymphoid cells in the bone marrow, peripheral blood, and other organs. ALL is the most common childhood tumor, and represents 75% to 80% of acute leukemias in children. ALL represents only 20% of all leukemias in the adult population. The median age at diagnosis is 14 years; 60% of patients are diagnosed at before 20 years of age. Current survival rates for patients with ALL have improved dramatically over the past, primarily in children, largely due to a better understanding of the molecular genetics of the disease, incorporation of risk-adapted therapy, and new targeted agents. Current treatment regimens have a cure rate among children of about 80%. Long-term prognosis among adults is poor, with cure rates of 30% to 40%. Prognosis variation is explained, in part, by different subtypes among age groups, including the *BCR-ABL* fusion gene, which has a poor prognosis and is much less common in childhood ALL.

**Disease Genetics**

Philadelphia (Ph) chromosome–positive leukemias are characterized by the expression of the oncogenic fusion protein product Bcr-Abl1, resulting from a reciprocal translocation between chromosomes 9 and 22. This abnormal fusion product characterizes CML. In ALL, with increasing age, the frequency of genetic alterations associated with favorable outcomes declines and alterations associated with poor outcomes, such as *BCR-ABL1*, are more common. In ALL, the Ph chromosome is found in 3% of children and 25% to 30% of adults. Depending on the exact location of the fusion, the molecular weight of the protein can range from 185 to 210 kDa. Two clinically important variants are p190 and p210; p190 is associated with ALL, while p210 is most often seen in CML. The product of *BCR-ABL1* is also a functional tyrosine kinase; the kinase domain (KD) of the Bcr-Abl protein is the same as the KD of the normal Abl protein. However, the abnormal Bcr-Abl protein is resistant to normal regulation. Instead, the enzyme is constitutively activated and drives unchecked cellular signal transduction resulting in excess cellular proliferation.

**Diagnosis**

Although CML is diagnosed primarily by clinical and cytogenetic methods, qualitative molecular testing is needed to confirm the presence of the *BCR-ABL1* fusion gene, particularly if the Ph chromosome was not found, and to identify the type of fusion gene, because this information is necessary for subsequent quantitative testing of fusion gene messenger RNA transcripts. If the fusion gene is not confirmed, then the diagnosis of CML is called into question.

Determining the qualitative presence of the *BCR-ABL1* fusion gene is not necessary to establish a diagnosis of ALL.

**Standardization of BCR-ABL1 Quantitative Transcript Testing**

A substantial effort has been made to standardize the *BCR-ABL1* qRT-PCR testing and reporting across academic and private laboratories. In 2006, the National Institute of Health Consensus Group proposed an IS for *BCR-ABL1* measurement. The IS defines 100% as the median pretreatment baseline level of *BCR-ABL1* RNA in early chronic phase CML; as determined in the pivotal IRIS trial, major molecular
response is defined as a 3-log reduction relative to the standardized baseline, or 0.1% BCR-ABL1 on the IS. In the assay, BCR-ABL1 transcripts are quantified relative to 1 of 3 recommended reference genes (eg, ABL) to control for the quality and quantity of RNA and to normalize for potential differences between tests.

**Treatment and Response and Minimal Residual Disease**

Before initiation of therapy for CML or ALL, quantification of the BCR-ABL transcript is necessary to establish baseline levels for subsequent quantitative monitoring of response during treatment.

Quantitative determination of BCR-ABL1 transcript levels during treatment allows for a very sensitive determination of the degree of patient response to treatment. Evaluation of trial samples has consistently shown the degree of molecular response correlates with risk of progression. Also, the degree of molecular response at early time points predicts improved rates of progression-free and event-free survival. Conversely, rising BCR-ABL1 transcript levels predict treatment failure and the need to consider a change in management. Quantitative polymerase chain reaction–based methods and international standards for reporting have been recommended and adopted for treatment monitoring.

Imatinib (Gleevec; Novartis), a tyrosine kinase inhibitor (TKI), was originally developed specifically to target and inactivate the Abl tyrosine kinase portion of the Bcr-Abl1 fusion protein to treat patients with CML. In patients with chronic phase CML, early imatinib study data indicated a high response rate to imatinib compared with standard therapy, and long-term follow-up has shown that continuous treatment of chronic phase CML results in “durable responses in [a] large proportion of the patients with a decreasing rate of relapse.” As a result, imatinib became the primary therapy for most patients with newly diagnosed chronic phase CML.

With the established poor prognosis of Ph-positive ALL, standard ALL chemotherapy alone has long been recognized as a suboptimal therapeutic option, with 60% to 80% of patients achieving a complete response, significantly lower than that achieved in Ph-negative ALL. The inclusion of TKIs to frontline induction chemotherapy has improved complete response rates, exceeding 90%.

Treatment response is evaluated initially by hematologic response (normalization of peripheral blood counts), then by cytogenetic response (percentage of cells with Ph-positive metaphase chromosomes in a bone marrow aspirate). Complete cytogenetic response (0% Ph-positive metaphases) is expected by 6 to 12 months after initial treatment with the TKI imatinib. It is well established that most “good responders” who are considered to be in morphologic remission but relapse may still have considerable levels of leukemia cells, referred to as minimal residual disease (MRD). Among children with ALL who achieve a complete response by morphologic evaluation after induction therapy, 25% to 50% may still have detectable MRD based on sensitive assays. Current methods used for MRD detection include flow cytometry (sensitivity of MRD detection, 0.01%), or polymerase chain reaction–based analyses (Ig and T-cell receptor gene rearrangements or analysis of BCR-ABL transcripts), which are the most sensitive methods of monitoring treatment response (sensitivity, 0.001%). Most ALL patients can be tested with Ig and T-cell receptor gene arrangement analysis, whereas only Ph-positive patients can be tested with polymerase chain reaction analysis of BCR-ABL transcripts.

**Treatment Resistance**

Imatinib treatment usually does not completely eradicate malignant cells. Not uncommonly, malignant clones resistant to imatinib may be acquired or selected during treatment (secondary resistance), resulting in disease relapse. Also, a small fraction of chronic phase malignancies that express the fusion gene do not respond to treatment, indicating intrinsic or primary resistance. The molecular basis for resistance is explained in the following section. When the initial response to treatment is inadequate or
there is a loss of response, resistance variant analysis is recommended to support a diagnosis of resistance (based on hematologic or cytogenetic relapse) and to guide the choice of alternative doses or treatments.\textsuperscript{7,10}

Structural studies of the Abl-imatinib complex have resulted in the design of second-generation Abl inhibitors, including dasatinib (Sprycel; Bristol-Myers Squibb) and nilotinib (Tasigna; Novartis), which were initially approved by the U.S. Food and Drug Administration for treatment of patients resistant or intolerant to prior imatinib therapy. Trials of both agents in newly diagnosed chronic phase patients have shown that both are superior to imatinib for all outcomes measured after 1 year of treatment, including complete cytogenetic response (primary outcome), time to remission, and rates of progression to accelerated phase or blast crisis.\textsuperscript{11,12} Although initial follow-up was short, early and sustained complete cytogenetic response was considered a validated marker for survival in CML. The Food and Drug Administration (FDA) has approved third-generation TKIs, ponatinib and bosutinib. Ponatinib is indicated for the treatment of patients with T315I-positive CML or Ph-positive ALL, or for whom no other TKI is indicated. Bosutinib is indicated for Ph-positive CML with resistance or intolerance to prior therapy.

For patients with increasing levels of \textit{BCR-ABL1} transcripts, there is no strong evidence to recommend specific treatment; possibilities include continuation of therapy with dasatinib or nilotinib at the same dose, or imatinib dose escalation from 400 to 800 mg daily, as tolerated, or therapy change to an alternative second-generation TKI.\textsuperscript{7}

**Molecular Resistance**

Molecular resistance is most often explained as genomic instability associated with the creation of the abnormal \textit{BCR-ABL1} gene, usually resulting in point mutations within the \textit{ABL1} gene KD that affects protein kinase-TKI binding. \textit{BCR-ABL1} single nucleotide variants (SNVs) account for 30\% to 50\% of secondary resistance.\textsuperscript{10} (Note that new \textit{BCR-ABL} SNVs also occur in 80\% to 90\% of cases of ALL in relapse after TKI treatment and in CML blast transformation.)\textsuperscript{13} The degree of resistance depends on the position of the variant within the KD (ie, active site) of the protein. Some variants are associated with moderate resistance and are responsive to higher doses of TKIs, while other variants may not be clinically significant. Two variants, designated T315I and E255K (nomenclature indicates the amino acid change and position within the protein), are consistently associated with resistance.

The presence of \textit{ABL} SNVs is associated with treatment failure. A large number of variants have been detected, but extensive analysis of trial data with low-sensitivity variant detection methods has identified a small number of variants consistently associated with treatment failure with specific TKIs; guidelines recommend testing for information on these specific variants to aid in subsequent treatment decisions. The recommended method is sequencing with or without denaturing high-performance liquid chromatography screening to reduce the number of samples to be sequenced. Targeted methods that detect the variants of interest for management decisions are also acceptable if designed for low sensitivity. High-sensitivity assays are not recommended.

Unlike imatinib, fewer variants are associated with resistance to dasatinib or nilotinib.\textsuperscript{14,15} For example, Guilhot et al (2007)\textsuperscript{16} and Cortes et al (2007)\textsuperscript{17} studied the use of dasatinib in imatinib-resistant CML patients in the accelerated phase and in blast crisis, respectively, and found that dasatinib response rates did not vary by the presence or absence of baseline tumor cell \textit{BCR-ABL1} variants. However, neither dasatinib nor nilotinib is effective against resistant clones with the T315I variant.\textsuperscript{13,16} Other treatment strategies are in development for patients with drug resistance.
Other acquired cytogenetic abnormalities such as BCR-ABL gene amplification and protein overexpression have also been reported.\textsuperscript{18} Resistance unrelated to kinase activity may result from additional oncogenic activation or loss of tumor suppressor function, and may be accompanied by additional karyotypic changes.\textsuperscript{10} Resistance in ALL to TKIs is less well studied. In patients with ALL receiving a TKI, a rise in the BCR-ABL level while in hematologic complete response or clinical relapse warrants variant analysis.

**REGULATORY STATUS**
On July 2016, QuantideX\textsuperscript{®} qPCR BCR-ABL IS Kit (Asuragen) was approved by FDA through the de novo 510(k) pathway (DEN160003). This test may be used in patients with diagnosed t(9;22) positive CML, during treatment with TKIs, to measure BCR-ABL mRNA transcript levels. It is not intended to diagnose CML. FDA classification code: OYX.

On December 2017, the MRDx\textsuperscript{®} BCR-ABL Test (MolecularMD) was approved by FDA through the 510(k) pathway (K173492). The test may be used in patients diagnosed with t(9;22) positive CML, during treatment with TKIs, to measure BCR-ABL mRNA transcript levels. It is also intended for use “in the serial monitoring for BCR-ABL mRNA transcript levels as an aid in identifying CML patients in the chronic phase being treated with nilotinib who may be candidates for treatment discontinuation and for monitoring of treatment-free remission.” FDA classification code: OYX.

Additionally, clinical laboratories may develop and validate tests in-house and market them as a laboratory service; laboratory-developed tests must meet the general regulatory standards of the Clinical Laboratory Improvement Amendments. The BCR-ABL1 fusion gene qualitative and quantitative genotyping tests and ABL SNV tests are available under the auspices of the Clinical Laboratory Improvement Amendments. Laboratories that offer laboratory-developed tests must be licensed by the Clinical Laboratory Improvement Amendments for high-complexity testing. To date, FDA has chosen not to require any regulatory review of this test.

**RATIONALE**
This evidence review was created in February 2013 and has been updated regularly with searches of the MEDLINE database. The most recent literature update was performed through August 22, 2018.

Evidence reviews assess whether a medical test is clinically useful. A useful test provides information to make a clinical management decision that improves the net health outcome. That is, the balance of benefits and harms is better when the test is used to manage the condition than when another test or no test is used to manage the condition.

The first step in assessing a medical test is to formulate the clinical context and purpose of the test. The test must be technically reliable, clinically valid, and clinically useful for that purpose. Evidence reviews assess the evidence on whether a test is clinically valid and clinically useful. Technical reliability is outside the scope of these reviews, and credible information on technical reliability is available from other sources.

Laboratory tests for to detect the BCR-ABL1 fusion gene are used to identify chronic myelogenous leukemia (CML) and Philadelphia (Ph) chromosome—positive acute lymphoblastic leukemia (ALL) and have different clinical uses. Briefly, they are as follows:

1. **Diagnosis:** patients who do not have the BCR-ABL fusion gene by definition do not have CML. In contrast, identification of the BCR-ABL1 fusion gene is necessary, although not sufficient, for diagnosis. Relevant test technologies are cytogenetics (karyotyping; recommended) or
fluorescence in situ hybridization (acceptable in the absence of sufficient sample for karyotyping).

2. Monitoring BCR-ABL1 RNA transcripts for residual disease during treatment or disease remission; relevant, standardized test technology is quantitative reverse transcription–polymerase chain reaction (RT-PCR). Note that a baseline measurement after confirmation of a CML diagnosis and before treatment begins is strongly recommended.

3. Identification and monitoring of variants for drug resistance at response failure or disease progression; various test technologies are in use (not standardized) including RT-PCR and Sanger sequencing.

**DIAGNOSIS AND PRETREATMENT WORKUP OF CHRONIC MYELOGENOUS LEUKEMIA**

**Clinical Context and Test Purpose**
The purpose of BCR-ABL1 fusion gene qualitative testing in individuals with suspected CML is to inform a diagnosis and establish baseline for monitoring treatment.

The question addressed in this evidence review is: Does use of qualitative testing for BCR-ABL1 improve the net health outcome in individuals with suspected CML?

The following PICOTS were used to select literature to inform this review.

**Patients**
The relevant population of interest is individuals with suspected CML.

**Interventions**
The test being considered is BCR-ABL1 fusion gene qualitative testing.

**Comparators**
The following practices are currently being used to diagnose CML: clinical and cytogenetic methods.

**Outcomes**
The general outcome of interest is test validity.

**Timing**
Follow-up over years is of interest to monitor outcomes.

**Setting**
Patients with suspected CML are actively managed by a hematologist and oncologist in an outpatient setting.

**Study Selection Criteria**
For the evaluation of clinical validity of the BCR-ABL1 fusion gene qualitative testing, studies that met the following eligibility criteria were considered:

- Reported on the accuracy of the marketed version of the technology (including any algorithms used to calculate scores)
- Included a suitable reference standard (describe the reference standard)
- Patient/sample clinical characteristics were described
- Patient/sample selection criteria were described.
Clinical Studies
While the diagnosis of CML is based on the presence of characteristic cellular abnormalities in bone marrow, the presence of the Ph chromosome and/or confirmation of the BCR-ABL1 fusion gene is essential. The initial evaluation of chronic phase CML should include bone marrow cytogenetics, not only to detect the Ph chromosome, but also to detect other possible chromosomal abnormalities. If bone marrow is not available, fluorescence in situ hybridization analysis with dual probes for BCR and ABL genes or qualitative RT-PCR can provide qualitative confirmation of the fusion gene and its type.

Section Summary: Diagnosis and Pretreatment Workup of Chronic Myelogenous Leukemia
The evidence on diagnosis and pretreatment workup in patients with CML includes validation studies. The sensitivity of testing BCR-ABL transcript levels with RT-PCR is high compared with conventional cytogenetics. Baseline measurement of BCR-ABL transcript levels is recommended as part of the initial evaluation, confirming the fusion gene, ensuring that it is detectable (rare variants requiring nonstandard probes may occur), and providing a baseline for monitoring response to treatment.

MONITORING TREATMENT RESPONSE AND CML REMISSION

Clinical Context and Test Purpose
The purpose of BCR-ABL1 quantitative testing at appropriate intervals in patients diagnosed with CML is to monitor treatment response and remission.

The question addressed in this evidence review is: Does use of quantitative testing of BCR-ABL1 improve the net health outcome in individuals with CML?

The following PICOTS were used to select literature to inform this review.

Patients
The relevant population of interest is individuals diagnosed with CML.

Interventions
The test being considered is BCR-ABL1 quantitative testing at appropriate intervals.

Quantitative RT-PCR (qRT-PCR) measurement of BCR-ABL1 RNA transcript levels is the method of choice for assessing response to treatment because of the high sensitivity of the method and strong correlation with outcomes. Compared with conventional cytogenetics, qRT-PCR is more than 3 logs more sensitive and can detect 1 CML cell in the background of 100,000 or more normal cells. Quantitative RT-PCR testing can be conducted on peripheral blood, eliminating the need for bone marrow sampling. The goal of treatment is complete molecular response (CMR), which has variable definitions based on the assay. However, only a small minority of patients achieve CMR on imatinib. More often, patients achieve a major molecular response (MMR), which may be defined as a BCR-ABL1 transcription level of 0.01% or less on the International Scale or a 3-log or more reduction in BCR-ABL1 mRNA from the standardized baseline.

Comparators
The following practice is currently being used to diagnose CML: cytogenetics.

Outcomes
The general outcomes of interest are disease-specific survival, test validity, and change in disease status.

Timing
Follow-up over years is of interest to monitor outcomes.
Setting
Patients diagnosed with CML are actively managed by a hematologist and oncologist in an outpatient setting.

Study Selection Criteria
For the evaluation of clinical validity of the BCR-ABL1 qualitative testing, studies that met the following eligibility criteria were considered:

- Reported on the accuracy of the marketed version of the technology (including any algorithms used to calculate scores)
- Included a suitable reference standard (describe the reference standard)
- Patient/sample clinical characteristics were described
- Patient/sample selection criteria were described.

Clinical Studies
Results from the IRIS trial, reported by Druker et al (2006), showed that patients who had a CMR or MMR had a negligible risk of disease progression at 1 year, and a significantly lower risk of disease progression at 5 years than patients who had neither.22 At 8-year follow-up, none of the patients who achieved an MMR at 1 year progressed to the accelerated phase of disease or to a blast crisis. Similar near absence of progression in patients who achieved an MMR has been reported in registration studies of nilotinib and dasatinib.11,12,21

Several studies have used these tests to guide discontinuation of select tyrosine kinase inhibitors (TKIs) in CML patients who have achieved an appropriate molecular response, and to monitor treatment-free remission.23-31 The largest of these studies, the EURO-SKI trial, reported by Saussele et al (2018), evaluated discontinuation of TKIs in 755 patients with CML who had been treated with TKIs for more than 3 years and had achieved a molecular response graded as MR4 (BCR-ABL1 transcription level of 0.01% or less on the International Scale IS) for at least 1 year.32 Molecular response was assessed monthly for the first 6 months, every 6 weeks for the remainder of the year, and then every 3 months for at least 3 years. The trigger to resume treatment with TKIs was loss of MMR. Treatment-free remission rate was 50% at 2 years (95% CI 46-54); loss of MMR despite restarting TKIs was seen in 2 patients. Similar findings were reported by Ross et al (2019) in recent updates of the ENESTfreedom Study, a large single-arm phase 2 study, which evaluated discontinuation of first-line treatment with nilotinib in the 190 CML patients who had been treated with nilotinib for more than 2 years and achieved sustained deep molecular response.33 Molecular response was assessed monthly for the next 48 weeks, every 6 weeks for 48 weeks, and then every 3 months for the time remaining. The trigger to resume treatment with TKIs was loss of MMR. Treatment-free remission rate was 49% at 96 weeks (95% CI, 42% to 56%); loss of MMR despite restarting TKIs was seen in 1 patient. Adverse events including musculoskeletal pain were noted in both the EURO-SKI and ENESTfreedom Study; no progression to CML accelerated phase or blast crisis was noted.

The degree of molecular response has also been reported to correlate with risk of progression in patients treated with imatinib.34 Timing of the molecular response is also important; the degree of molecular response at early time points predicts the likelihood of achieving CMR or MMR and predicts improved rates of progression-free and event-free survival.35-38 While early and strong molecular response predicts durable long-term remission rates and progression-free survival, studies have not been conclusive that molecular response is predictive of overall survival.39-41

Based on imatinib follow-up data, it is recommended that, for patients with a complete cytogenetic response, molecular response to treatment be measured every 3 months for 2 years, then every 3 to 6
months thereafter.\textsuperscript{7,42} Without complete cytogenetic response, continued monitoring at 3-month intervals is recommended. It has been assumed that the same time points for monitoring imatinib are appropriate for dasatinib and nilotinib,\textsuperscript{7} and would likely also be applied to bosutinib and ponatinib.

Rising $BCR-ABL1$ transcript levels are associated with increased risk of variants and treatment failure.\textsuperscript{43-48} However, what constitutes a clinically significant rise to warrant variant testing is not known. Factors affecting the clinically significant change include the variability of the specific assay used by the laboratory and the level of molecular response achieved by the patient. Thresholds used include 2- to 10-fold increases, and increases of 0.5 to 1 log, respectively.\textsuperscript{44,49} Because of potential variability in results and lack of agreement across studies for an acceptable threshold, rising transcript levels alone are not viewed as sufficient to trigger variant testing or changes in treatment.\textsuperscript{50}

Section Summary: Monitoring Treatment Response and CML Remission
Quantitative RT-PCR measurement of $BCR-ABL1$ RNA transcript levels is the method of choice for monitoring CML during treatment and in disease remission because of the high sensitivity, strong correlation with outcomes, and ability to sample in peripheral blood.

IDENTIFICATION OF $ABL$ KINASE DOMAIN SINGLE NUCLEOTIDE VARIANTS TO ASSESS TKI RESISTANCE IN CML

Clinical Context and Test Purpose
The purpose of the evaluation for $ABL$ kinase domain (KD) single nucleotide variants (SNVs) in patients diagnosed with CML and inadequate initial response, loss of response, and/or disease progression is to assess for TKI resistance.

The question addressed in this evidence review is: Does evaluation for $ABL$ KD SNVs improve the net health outcome in individuals with CML and inadequate initial response, loss of response, and/or disease progression?

The following PICOTS were used to select literature to inform this review.

Patients
The relevant population of interest is individuals diagnosed with CML and inadequate initial response, loss of response, and/or disease progression.

Interventions
The test being considered is testing for $ABL$ KD SNVs to assess for TKI resistance.

Screening for $BCR-ABL1$ KD SNVs in chronic phase CML is recommended for patients with (1) inadequate initial response to TKI treatment, (2) evidence of loss of response, or (3) progression to accelerated or blast phase CML.\textsuperscript{7} Testing for KD SNVs, in the setting of potential treatment failure, may help to select from among other TKI treatments or allogeneic cell transplantation.

Comparators
The following practice is currently being used to assess TKI resistance among patients with inadequate initial response, loss of response, and/or disease progression: standard workup without genetic testing.

Outcomes
The general outcomes of interest are disease-specific survival, test validity, and medication use.

Timing
Follow-up over years is of interest to monitor outcomes.
**Setting**

Patients with CML are actively managed by a hematologist and oncologist in an outpatient setting.

**Study Selection Criteria**

For the evaluation of clinical validity of the ABL KD SNV testing, studies that met the following eligibility criteria were considered:

- Reported on the accuracy of the marketed version of the technology (including any algorithms used to calculate scores)
- Included a suitable reference standard (describe the reference standard)
- Patient/sample clinical characteristics were described
- Patient/sample selection criteria were described.

**Clinical Studies**

The Agency for Healthcare Research and Quality published a systematic review, conducted by Terasawa et al (2010), who assessed BCR-ABL1 pharmacogenetic testing for TKIs in CML. 51 Reviewers concluded that the presence of any BCR-ABL1 variant did not predict differential response to TKI therapy, although the presence of the T315I variant uniformly predicts TKI failure. Reviewers were strongly criticized by respected pathology organizations for insufficient attention to several issues. Importantly, they grouped studies that used KD SNV screening methods with those that used targeted methods, and grouped studies that used variant detection technologies with very different sensitivities.

**KD SNVs and Treatment Outcomes**

Branford et al (2009) summarized the available evidence on KD SNVs detected after imatinib treatment failure, and subsequent treatment success or failure with dasatinib or nilotinib. 52 Studies referenced used direct Sanger sequencing, with or without denaturing high-performance liquid chromatography screening, to identify variants at low sensitivity. The authors surveyed variants detected in patients at imatinib failure at their own institution and compared results with a collation of variants derived from the literature. For both, the T315I variant was most common; although about 100 variants have been reported, the 7 most common (at residues T315, Y253, E255, M351, G250, F359, and H396) accounted for 60% to 66% of all variants in both surveys. Detection of the T315I variant at imatinib failure is associated with lack of subsequent response to high-dose imatinib or to dasatinib or nilotinib. For these patients, allogeneic cell transplantation was the only available treatment until the approval of new agents (eg, ponatinib). 53 Most common, however, does not necessarily correspond to clinically significant. Based on the available clinical studies, most imatinib-resistant variants remain sensitive to dasatinib and nilotinib. However, preexisting or emerging variants T315A, F317L, F317I, F317V, F317C, and V299L are associated with decreased clinical efficacy with dasatinib treatment following imatinib failure. Similarly, preexisting or emerging variants Y253H, E255K, E255V, and F359V, and F359C have been reported to have decreased clinical efficacy with nilotinib treatment following imatinib failure. In the Branford survey, 42% of patients tested had T315I or one of the dasatinib- or nilotinib-resistant variants. 52 As a result, guidelines recommend variant analysis only at treatment failure, and use of the T315I variant and the identified dasatinib- and nilotinib-resistant variants to select subsequent treatment. 54 Absent any of these actionable variants, various treatment options are available. Note that these data were obtained from studies of patients all initially treated with imatinib.

ABL KD SNV analysis is recommended if there is inadequate initial response (failure to achieve complete hematologic response at 3 months, only minor cytologic response at 6 months, or major [rather than complete] cytogenetic response at 12 months) or any sign of loss of response (defined as hematologic relapse, cytogenetic relapse, or 1-log increase in BCR-ABL1 transcript ratio and therefore loss of MMR).
Variant testing is also recommended for progression to accelerated or blast phase CML. Treatment recommendations based on variant(s) are shown in Table 1.

Because only a small number of variants have been recommended as clinically actionable, targeted assays may also be used to screen for the presence of actionable variants at treatment failure. Quantitative, targeted assays may also be used to monitor levels of already identified clinically significant variants after starting a new therapy because of initial treatment failure. Targeted assays use different technologies that can be very sensitive and pick up mutated cell clones at very low frequencies in the overall malignant population. Banked samples from completed trials have been studied with high-sensitivity assays to determine if monitoring treatment can detect low-level variants that predict treatment failure well in advance of clinical indications. Some results have been positive, but not all variants detected in advance predict treatment failure; more study is recommended before these assays are used for monitoring in advance of treatment failure.\(^{50,52}\) A direct correlation between low-sensitivity and high-sensitivity assays and a limited correlation with clinical outcomes support recommendations of sequencing, with or without denaturing high-performance liquid chromatography screening, for identification of variants.\(^{54}\) Although high-sensitivity assays identified more variants than did sequencing, the clinical impact of identifying additional variants is uncertain.

Variants other than point mutations can be detected in the \textit{BCR-ABL1} gene, including alternate splicing, insertions, deletions, and/or duplications. The clinical significance of such altered transcripts is unclear, and reporting such variants is not recommended.\(^{10,55}\)

\textbf{Section Summary: Identification of ABL KD SNVs to Assess TKI Resistance in CML}

Studies have evaluated pharmacogenetics testing for TKIs and have shown a correlation between certain types of variants and treatment response. Testing for SNVs, in the setting of potential treatment failure, may help to select from among other TKI treatments or allogeneic cell transplantation.

\textbf{MONITORING PH-POSITIVE ALL}

\textbf{Clinical Context and Test Purpose}

The purpose of \textit{BCR-ABL1} quantitative testing at baseline before and during treatment in patients with a diagnosis of Ph-positive ALL is to monitor treatment response and remission.

The question addressed in this evidence review is: Does quantitative testing of \textit{BCR-ABL1} improve the net health outcome in individuals with Ph-positive ALL?

The following PICOTS were used to select literature to inform this review.

\textbf{Patients}

The relevant population of interest is individuals with a diagnosis of Ph-positive ALL.

\textbf{Interventions}

The test being considered is \textit{BCR-ABL1} quantitative testing at baseline before and during treatment to monitor treatment response and remission.

\textbf{Comparators}

The following test is currently being used to monitor treatment response and remission in those diagnosed with Ph-positive ALL: cytogenetics.

\textbf{Outcomes}

The general outcomes of interest are disease-specific survival, test validity, and change in disease status.
Timing
Follow-up over years is of interest for to monitor outcomes.

Setting
Patients with Ph-positive ALL are actively managed by a hematologist or oncologist in an outpatient setting.

Study Selection Criteria
For the evaluation of clinical validity of the BCR-ABL1 quantitative testing, studies that met the following eligibility criteria were considered:
- Reported on the accuracy of the marketed version of the technology (including any algorithms used to calculate scores)
- Included a suitable reference standard (describe the reference standard)
- Patient/sample clinical characteristics were described
- Patient/sample selection criteria were described.

Diagnosis and Pretreatment Workup
The diagnosis of ALL is made by demonstrating 20% or greater bone marrow lymphoblasts; demonstration of the BCR-ABL fusion gene is not essential. However, identification of specific molecular subtypes is recommended at the time of diagnosis for optimal risk evaluation and treatment planning. The initial evaluation of ALL patients should include bone marrow sample for RT-PCR for BCR-ABL to establish the presence or absence of BCR-ABL, as well as baseline transcript quantification.

Monitoring for Residual Disease During Treatment and Disease Remission
Despite significantly higher complete response rates with TKIs in Ph-positive ALL, the response is typically short-lived, and relapses common. The principal aim of therapy after remission is to eradicate minimal residual disease (MRD), which is the prime cause of relapse.

Studies in children and adults with ALL have demonstrated a strong correlation between MRD and risk for relapse, as well as the prognostic significance of measuring MRD during and after initial induction therapy. A commonly used cutoff to define MRD positivity is 0.01%, with patients who attain an MRD less than 0.01% early during therapy having high odds of remaining in continuous complete response with contemporary postremission therapy.

A study of 3184 B-cell ALL children by Conter et al (2000) enrolled in the AIEOP-BFM ALL 2000 treatment protocol demonstrated that a risk classification algorithm based on MRD measurements using PCR on days 33 and 78 of treatment was superior to that of other risk stratification criteria based on white blood cell count, age, early response to prednisone, and genetic subtype. Patients with an MRD less than 0.01% on day 33 (42%) had a 5-year event-free survival of 92.3%.

MRD is also a strong prognostic factor for children and adolescents with first-relapse ALL who achieve a second remission. Patients with an MRD of 0.01% or more are eligible for allogeneic hematopoietic cell transplantation, whereas achievement of MRD negativity may be an indication for chemotherapy.

Section Summary: Monitoring Ph-Positive ALL
Evidence on the diagnosis, pretreatment workup, and monitoring for residual disease during treatment and disease progression in patients with Ph-positive ALL includes a prospective cohort study and case series. These studies have shown a high sensitivity for BCR-ABL1 quantitative testing and a strong
correlation with outcomes, including the risk of disease progression. This may stratify patients to different treatment options.

IDENTIFICATION OF ABL KD SNVS ASSOCIATED WITH TKI RESISTANCE IN PH-POSITIVE ALL

Clinical Context and Test Purpose
The purpose of testing for ABL KD SNVs in patients with Ph-positive ALL and signs of treatment failure or disease progression is to assess for TKI resistance.

The question addressed in this evidence review is: Does testing of ABL KD SNVs improves the net health outcome in individuals with Ph-positive ALL?

The following PICOTS were used to select literature to inform this review.

Patients
The relevant population of interest is individuals with Ph-positive ALL and signs of treatment failure or disease progression.

Interventions
The testing being considered is an evaluation for ABL KD SNVs to assess for TKI resistance.

Comparators
The following practice is currently being used to monitor patients with Ph-positive ALL and signs of treatment failure or disease progression: standard workup without genetic testing.

Outcomes
The general outcomes of interest are test validity and medication use.

Timing
Follow-up over years is of interest to monitor outcomes.

Setting
Patients with Ph-positive ALL are actively managed by a hematologist or oncologist in an outpatient setting.

Study Selection Criteria
For the evaluation of clinical validity of the ABL KD SNV testing, studies that met the following eligibility criteria were considered:

- Reported on the accuracy of the marketed version of the technology (including any algorithms used to calculate scores)
- Included a suitable reference standard (describe the reference standard)
- Patient/sample clinical characteristics were described
- Patient/sample selection criteria were described.

Clinical Studies
Resistance to TKIs in ALL is less well studied. Detection of variants was used to evaluate sensitivity to second- or third-generation TKI in case series by Soverini et al (2016). Resistance does not necessarily arise from dominant tumor clone(s), but possibly in response to TKI-driven selective pressure and/or competition of other coexisting subclones. In patients with ALL receiving a TKI, a rise in the Bcr-Abl protein level while in hematologic complete response or clinical relapse warrants variant analysis.
Section Summary: Identification of ABL SNVs Associated With TKI Resistance in Ph-Positive ALL
Evidence on the identification of ABL SNVs associated with TKI resistance in patients with Ph-positive ALL includes case series. These studies have shown that specific imatinib-resistant variants are insensitive to one or both of the second-generation TKIs. These variants are used to guide medication selection.

SUMMARY OF EVIDENCE
For individuals who have suspected CML who receive BCR-ABL1 fusion gene qualitative testing to confirm the diagnosis and establish a baseline for monitoring treatment, the evidence includes validation studies. Relevant outcome is test validity. The sensitivity of testing with RT-PCR is high compared with conventional cytogenetics. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.

For individuals who have a diagnosis of CML who receive BCR-ABL1 fusion gene quantitative testing at appropriate intervals for monitoring treatment response and remission, the evidence includes a randomized trial and case series. Relevant outcomes are disease-specific survival, test validity, and change in disease status. Studies have shown a high sensitivity of this type of testing and a strong correlation with outcomes, including the risk of disease progression and survival, which may stratify patients to different options for disease management. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.

For individuals who have a diagnosis of CML with inadequate initial response, loss of response, and/or disease progression who receive an evaluation for ABL KD SNVs to assess for TKI resistance, the evidence includes a systematic review and case series. Relevant outcomes are disease-specific survival, test validity, and medication use. The systematic review and case series evaluated pharmacogenetics testing for TKIs and reported the presence of KD SNVs detected at imatinib failure. These studies have shown a correlation between certain types of variants, treatment response, and the selection of subsequent treatment options. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.

For individuals who have a diagnosis of Ph-positive ALL who receive BCR-ABL1 fusion gene quantitative testing at baseline before and during treatment to monitor treatment response and remission, the evidence includes a prospective cohort study and case series. Relevant outcomes are disease-specific survival, test validity, and change in disease status. As with CML, studies have shown a high sensitivity for this type of testing and a strong correlation with outcomes, including the risk of disease progression, which may stratify patients to different treatment options. Also, evidence of treatment resistance or disease recurrence directs a change in medication. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.

For individuals who have Ph-positive ALL and signs of treatment failure or disease progression who receive an evaluation for ABL1 KD SNVs to assess for TKI resistance, the evidence includes case series. Relevant outcomes are test validity and medication use. Studies have shown that specific imatinib-resistant variants are insensitive to one or both of the second-generation TKIs; these variants are used to guide medication selection. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.
SUPPLEMENTAL INFORMATION

PRACTICE GUIDELINES AND POSITION STATEMENTS

National Comprehensive Cancer Network

The National Comprehensive Cancer Network practice guidelines (v.1.2019) on chronic myelogenous leukemia outline recommended methods for diagnosis and treatment management of chronic myelogenous leukemia, including BCR-ABL1 tests for diagnosis, monitoring, and ABL kinase domain single nucleotide variants (see Table 1). Guidelines for discontinuation of tyrosine kinase inhibitor therapy are detailed; molecular monitoring is recommended every month for 1 year, every 6 weeks for the second year, and every 12 weeks afterward.

Table 1. Treatment Options Based on BCR-ABL1 Variant Profile

<table>
<thead>
<tr>
<th>Single Nucleotide Variants</th>
<th>Treatment Recommendation</th>
</tr>
</thead>
<tbody>
<tr>
<td>T315I</td>
<td>Ponatinib, omacetaxine, allogeneic HCT, or clinical trial</td>
</tr>
</tbody>
</table>

HCT: hematopoietic cell transplantation.

The National Comprehensive Cancer Network practice guidelines (v.1.2018) on acute lymphoblastic leukemia state that, if minimal residual disease is being evaluated, the initial measurement should be performed on completion of initial induction therapy; additional time points for minimal residual disease evaluation may be useful, depending on the specific treatment protocol or regimen used. Minimal residual disease is an essential component of patient evaluation during sequential therapy. Treatment options based on BCR-ABL Mutation Profile are shown in Table 2. The tyrosine kinase inhibitor treatment options for acute lymphoblastic leukemia are the same as for chronic myelogenous leukemia.

Table 2. Treatment Options Based on BCR-ABL1 Variant Profile

<table>
<thead>
<tr>
<th>Single Nucleotide Variants</th>
<th>Treatment Recommendation</th>
</tr>
</thead>
<tbody>
<tr>
<td>T315I</td>
<td>Ponatinib</td>
</tr>
</tbody>
</table>

U.S. PREVENTIVE SERVICES TASK FORCE RECOMMENDATIONS

Not applicable.

MEDICARE NATIONAL COVERAGE

There is no national coverage determination. In the absence of a national coverage determination, coverage decisions are left to the discretion of local Medicare carriers.

ONGOING AND UNPUBLISHED CLINICAL TRIALS

Some currently unpublished trials that might influence this review are listed in Table 3.
Table 3. Summary of Key Trials

<table>
<thead>
<tr>
<th>NCT No.</th>
<th>Trial Name</th>
<th>Planned Enrollment</th>
<th>Completion Date</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ongoing</td>
<td>Validation of Digital-PCR Analysis Through Programmed Imatinib Interruption in PCR Negative CML Patients (ISAV)</td>
<td>100</td>
<td>June 2019</td>
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<tr>
<td>NCT03263572</td>
<td>Phase II Study of the Combination of Blinatumomab and Ponatinib in Patients With Philadelphia Chromosome (Ph)-Positive and/or BCR-ABL Positive Acute Lymphoblastic Leukemia (ALL)</td>
<td>60</td>
<td>Nov 2024</td>
</tr>
</tbody>
</table>

NCT: national clinical trial.

a Denotes industry-sponsored or cosponsored trial.

REFERENCES


34. Press RD, Love Z, Tronnes AA, et al. BCR-ABL mRNA levels at and after the time of a complete cytogenetic response (CCR) predict the duration of CCR in imatinib mesylate-treated patients with CML. *Blood.* Jun 1 2006;107(11):4250-4256. PMID 16467199


44. Branford S, Rudzki Z, Parkinson I, et al. Real-time quantitative PCR analysis can be used as a primary screen to identify patients with CML treated with imatinib who have BCR-ABL kinase domain mutations. *Blood.* Nov 1 2004;104(9):2926-2932. PMID 15256429


53. Cortes JE, Kim DW, Pinilla-Ibarz J, et al. A Pivotal Phase 2 Trial of Ponatinib in Patients with Chronic Myeloid Leukemia (CML) and Philadelphia Chromosome-Positive Acute Lymphoblastic Leukemia (Ph+ALL) Resistant or Intolerant to Dasatinib or Nilotinib, or with the T315I BCR-ABL Mutation: 12-Month Follow-up of the PACE Trial. *American Society of Hematology 54th Annual Meeting, December 2012*. 2012:Abstract 163. PMID


BCR-ABL1 Testing in Chronic Myelogenous Leukemia and Acute Lymphoblastic Leukemia

CODES

<table>
<thead>
<tr>
<th>Codes</th>
<th>Number</th>
<th>Description</th>
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<tr>
<td>CPT</td>
<td>0040U</td>
<td>BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis, major breakpoint, quantitative</td>
</tr>
<tr>
<td></td>
<td>81206</td>
<td>BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; major breakpoint, qualitative or quantitative</td>
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<td>81207</td>
<td>BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; minor breakpoint, qualitative or quantitative</td>
</tr>
<tr>
<td></td>
<td>81208</td>
<td>BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; other breakpoint, qualitative or quantitative</td>
</tr>
<tr>
<td></td>
<td>81401</td>
<td>Molecular Pathology Procedure Level 2</td>
</tr>
<tr>
<td></td>
<td>81170</td>
<td>ABL1 (ABL proto-oncogene 1, non-receptor tyrosine kinase) (eg, acquired imatinib tyrosine kinase inhibitor resistance), gene analysis, variants in the kinase domain</td>
</tr>
<tr>
<td>ICD-10-CM</td>
<td>C91.00-C91.02</td>
<td>Acute lymphoblastic leukemia [ALL], code range</td>
</tr>
<tr>
<td></td>
<td>C92.10-C92.12</td>
<td>Chronic myeloid leukemia, BCR/ABL-positive code range</td>
</tr>
<tr>
<td></td>
<td>C92.20-C92.22</td>
<td>Atypical chronic myeloid leukemia, BCR/ABL-negative code range</td>
</tr>
<tr>
<td>ICD-10-PCS</td>
<td></td>
<td>Not applicable. ICD-10-PCS codes are only used for inpatient services. There are no ICD procedure codes for laboratory tests.</td>
</tr>
</tbody>
</table>

Type of service: Laboratory
Place of service: Outpatient

POLICY HISTORY

<table>
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<tr>
<th>Date</th>
<th>Action</th>
<th>Description</th>
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</thead>
<tbody>
<tr>
<td>03/13/14</td>
<td>Replace policy</td>
<td>Policy updated with literature review through January 21, 2014. References 3, 5-6, 46-47, and 56-57 added. Policy statements added for ALL, medically necessary prior to initiation of treatment, for disease monitoring and to evaluate for TKI resistance. Title also changed to add ALL.</td>
</tr>
<tr>
<td>07/10/14</td>
<td>Replace policy – correction only</td>
<td>Language added to the Policy Guidelines to clarify the timing of testing in patients who are responding to treatment or who have a complete cytogenetic response.</td>
</tr>
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<td>03/12/15</td>
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<td>Policy updated with literature review through February 2, 2015. No references added. Policy statements unchanged.</td>
</tr>
<tr>
<td>03/10/16</td>
<td>Replace policy</td>
<td>Policy updated with literature review through February 2, 2016; reference 31 added. Policy statements unchanged.</td>
</tr>
<tr>
<td>04/25/17</td>
<td>Replace policy</td>
<td>Blue Cross of Idaho annual review; no change to policy.</td>
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<tr>
<td>10/30/17</td>
<td>Replace policy</td>
<td>Blue Cross of Idaho adopted changes to policy as noted. Policy updated with literature review through August 23, 2017; reference 41 added; references 3 and 47 updated. Policy statements unchanged.</td>
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<tr>
<td>10/18/18</td>
<td>Replace policy</td>
<td>Blue Cross of Idaho adopted changes as noted, effective 10/18/2018.</td>
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</table>
Policy updated with literature review through August 22, 2018; references 23-33 added. Policy statements unchanged.