

FREQUENTLY ASKED QUESTIONS

BCR/ABL1 TESTING

Q Do I need a bone marrow sample for the molecular BCR-ABL testing?

A If the purpose of BCR-ABL1 testing is to “rule out” CML (i.e. low clinical suspicion of neoplasm), a peripheral blood specimen will likely be sufficient. However, at diagnosis in a patient strongly suspected of CML (or another myeloid neoplasm), a bone marrow is typically obtained and can be used for initial BCR-ABL1 testing. Initial testing (whether peripheral blood or bone marrow) should include a screening RT-PCR assay to identify the specific BCR-ABL1 transcript type, and a quantitative initial value determination for that transcript (e.g. p210). The BCRFX assay achieves both requirements. Following a diagnosis of CML, BCR-ABL1 p210 quantitative mRNA levels can be followed using peripheral blood samples, because the blood levels are highly correlated with bone marrow burden. It is recommended that a 12 month (on therapy) bone marrow be performed to confirm complete cytogenetic response and to exclude non-BCR-ABL1 clonal genetic abnormalities that can arise in a small number of CML patients.

Q “Why can’t you do one test to detect p190 and p210 at the same time? I see other labs doing this...”

A Mayo Clinic’s quantitative BCR-ABL1 tests are highly optimized to achieve high analytical sensitivity, which is lost when trying to multiplex more than one target; in addition, International Scale (IS) reporting of p210 transcript levels in CML is based on dedicated single target (p210) assays.

Q What if I need FISH testing to track a very rare (non-p210 or p190) BCR-ABL1 transcript type not identified on the screening diagnostic RT-PCR panel; can I obtain real time PCR monitoring in this situation?

A FISH testing is available on a case by case basis, please contact the Mayo Laboratory Inquiry team and discuss your needs with a consultant in the Cytogenetics Laboratory. For very rare alternative BCR-ABL1 fusion transcripts identified by our screening RT-PCR assay at the time of diagnosis (e.g. p230, ABL1 a3 exon junctions, etc.), dedicated quantitative assays are not yet available. However, follow-up testing can be done using the BADX qualitative screening assay. Although the latter assay does not provide a quantitative measurement of a rare BCR-ABL1 transcript, it is sensitive to ~0.1% and can be used to assess relative disease burden in such cases.

Q I’ve always ordered FISH testing for patients both at diagnosis and for monitoring, how will I know which test to order for my patients.

A We offer a number of applicable test algorithm for patients to assist with appropriate test ordering. The algorithms are Clickable and by clicking on a test ID it will guide you to the information on the test you are interested in. You can always also choose to contact our Molecular Hematopathology lab directors, or designates for more information.

Q Is the quantitative BCR-ABL1 value at diagnosis clinically significant?

A The initial quantitative value established the diagnostic level of disease burden that is then used as the starting measurement to follow patients subsequently receiving therapy (e.g. tyrosine kinase inhibitors). The actual value itself is not highly significant on its own. Furthermore, diagnostic levels of BCR-ABL1 in CML or Ph+ ALL span a range of relatively high quantitative values based on initial disease burden and patient-specific factors, so the initial value is not prognostically significant as a single parameter.

Q Is the reflex test useful for rare BCR-ABL1 transcript forms, such as the e19/a2 p230 type?

A No. This reflex test does screen for the common (p210, p190) and rare BCR-ABL1 variants, but is intended to provide quantitative results for only the p210 or p190 BCR-ABL1 transcript types at the time of diagnosis, in order to know which fusion should be followed in subsequent minimal residual disease assessment. In the situation of a rare BCR-ABL1 variant fusion, the specific p210 (BCRAB) and p190 (BA190) tests would not be able to identify the alternate transcript (false negative) and cannot be used for minimal disease monitoring after therapy is initiated. However, in the event of a rare transcript being detected, the patient can still be monitored using the qualitative BADX diagnostic assay; although a numerical value cannot be provided, the sensitivity of the BADX test is ~0.1% and can provide a relative assessment of disease burden.