**BRAF** somatic mutation testing – hematologic malignancies

The UNC Molecular Genetics Laboratory performs a targeted *BRAF* sequencing assay using next-generation sequencing to identify mutation that may aid in diagnosis and treatment of hematologic neoplasms.

**Rationale for testing:**
The presence of somatic gene mutations in *BRAF*, specifically in codon 600, may assist in distinguishing hairy cell leukemia from other B-cell neoplasms.

Nearly 100% of cases of hairy cell leukemia have a *BRAF* codon 600 (V600E) mutation in exon 15, while other splenic B-cell neoplasms are usually negative. The presence of a *BRAF* V600E mutation can aid in the diagnosis of hairy cell leukemia.

**Specimen Requirements for the Myeloid Mutation Panel:**
Bone marrow aspirate (1 mL, EDTA) or peripheral blood (3mL, EDTA) having at least q0% neoplastic cells, and refrigerated for up to 72 hours. Unacceptable sample types include: fresh, frozen, or paraffin embedded tissue. The assay is sensitive to variants above 5% allele frequency (10% clonal cells). This test is NOT appropriate for MRD monitoring. For patients undergoing repeat testing, previously detected variants will be reported to 3% VAF.

**Gene Regions Tested – *BRAF* exon 15**

**Limitations:**
Gene amplifications, translocations, and insertions or deletions over 90 bases in length are not reliably detected by this assay. Normal tissue is not tested to determine whether a gene variant is somatic (acquired) or germline (heritable). If the patient has evidence of a heritable cancer syndrome (e.g. different tumor types, early age of onset, family history), genetic counseling is recommended. To make a patient appointment, call the Cancer Genetics Clinic at (919) 843-8724.

**References:**

**Questions?**
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