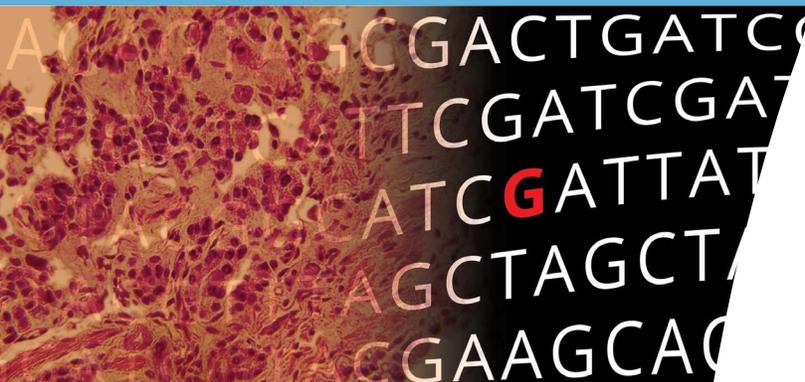




CANCER TESTING

at Washington University



Genomic profiling to enable personalized patient care

Next-generation sequencing (NGS) for efficient, cost-effective and robust somatic variant analysis

Concise, expert interpretations by board-certified clinical genomicists, reported back to the ordering physician

Expert consultation available to physicians in result interpretation and in other technical and clinical considerations

Testing covered by most insurance; preauthorization performed by GPS



Improved tests for maximum information

Advantages of our improved tests

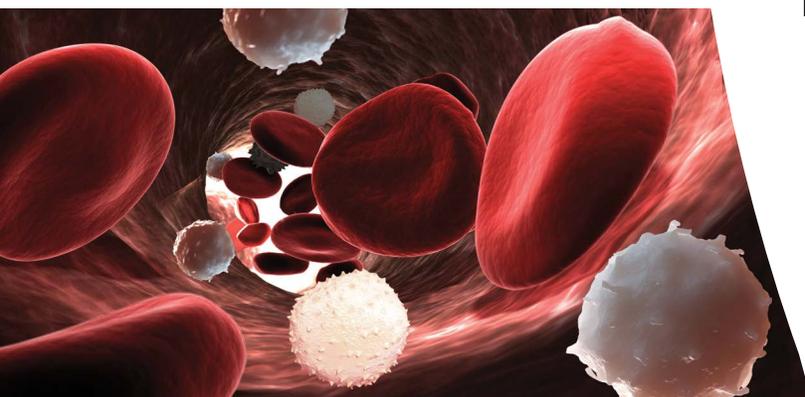
Additional predictive targets for improved and more immediate clinical utility of tests

Wide range of variant types detected, including point mutations, insertions and deletions and multiple structural rearrangements

Improved reports with easy-to-understand result summaries and interpretations

Improved sensitivity, enabling detection of variants at low allelic fraction

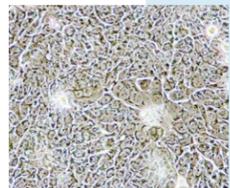
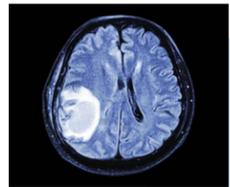
Lower DNA input requirement for successful results from limited tissue samples





Targeted hybridization capture-based NGS for comprehensive tumor profiling

Genomics and Pathology Services (GPS) offers clinically validated next-generation sequencing (NGS) tests for **solid tumors** and **hematopoietic disorders**. Results provide physicians with useful information for cancer diagnosis, prognosis (disease stratification) and treatment selection. For information on specialized **disease-specific gene sets**, please contact us at (314) 747-7337.



► Solid Tumor Gene Set

Test includes total exonic coverage for **somatic variants arising in 65 genes** and six selected translocations that are clinically actionable in a wide range of adenocarcinomas, squamous cell carcinomas, gliomas, sarcomas and melanomas.

Indications for testing include cancer cases in early stage disease where a mutational profile from multiple genes informs diagnosis or disease stratification, prognosis, or treatment options. For late stage cancers, the test is designed to evaluate options for alternative treatments, including targeted therapies.

Genes tested include *AKT1, AKT2, AKT3, ALK*, ATM, BAP1, BRAF, BRCA1, BRCA2, BRIP1, CDH1, CDKN2A, CREBBP, CSF1R, CTNNA1, DDR2, EGFR, ERBB2, ERBB3, ERBB4, ESR1, FANCA, FGFR1, FGFR2*, FGFR3*, FGFR4, FLT1, FLT3, FLT4, GNAS, HRAS, IDH1, IDH2, JAK1, JAK2, KDR, KIT, KRAS, MAP2K1, MAP2K2, MET, MLH1, MTOR, MYC, NF1, NOTCH1, NOTCH2, NRAS, NTRK1*, PALB2, PDGFRA, PDGFRB, PIK3CA, PTEN, RAD54B, RB1, RET*, RIT1, ROS1*, SMAD4, STK11, TP53, TSC1, TSC2* and *VHL*.

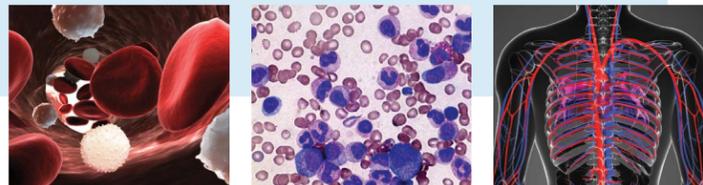


► Hematopoietic Disorders Gene Set

Test includes total exonic coverage for **somatic variants arising in 54 genes**, including translocations involving *MLL/KMT2A*, that are clinically actionable in myeloid, lymphoid and mixed lineage leukemias. It also includes genes that can help establish diagnosis and prognosis for pre-leukemic myelodysplastic and myeloproliferative syndromes.

Indications for testing include neoplastic hematopoietic disease where a mutational profile from multiple genes informs diagnosis or disease stratification, prognosis, or treatment options. For leukemias, the test is designed to evaluate options for therapies targeting signaling pathways and DNA methylation.

Genes tested include *ABL1, ASXL1, ATM, BCOR, BIRC3, BRAF, CALR, CBL, CEBPA, CSF1R, CSF3R, DNMT3A, EP300, ETV6, EZH2, FBXW7, FGFR4, FLT3, GATA1, GATA2, GATA3, IDH1, IDH2, IKZF1, IL7R, JAK2, JAK3, KDM6A, KIT, KRAS, KMT2A*, MPL, NF1, NOTCH1, NOTCH2, NPM1, NRAS, NSD1, PAX5, PDGFRA, PDGFRB, PTPN11, RUNX1, SETB1, SF3B1, SRSF2, STAG2, TERT, TET1, TET2, TP53, TSLP, U2AF1* and *ZRSR2*.



*Selected introns also sequenced for rearrangement detection

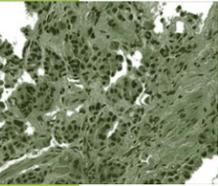
► Advantages of GPS testing

Efficient - Analysis of multiple genetic loci in a single test conserves valuable surgical specimens, and results in efficient cost and turnaround times

Comprehensive - Testing multiple genes and sequencing entire coding regions allow for the most comprehensive analysis and can identify recurrent and novel variants.

Sensitive - Hybridization capture-based NGS can detect mutations at low allele fraction, from small samples that yield only nanogram amounts of DNA.

Improved reports - Our clinical reports have been redesigned to include concise result summaries and interpretations. Variants with FDA approved therapies, prognostic information or other clinical courses of action are clearly highlighted.



► Ordering details

Complete requisition

- Fillable PDFs available on website
- Diagnoses and ICD9 codes required
- Ordering physician signature/date required
- Patient insurance information required

Fax or email requisition

- Fax: (314) 747-7336
- Email: gps@wustl.edu
- Include release form if specimens are from outside BJC HealthCare

GPS does the rest

- Tests are reimbursable and GPS performs insurance preauthorization
- For archival specimens, GPS coordinates sample acquisition

Specimen Types

- Excisional biopsies
- Core needle biopsies
- Cell blocks
- Leukemic blood
- Bone marrow aspirate



Acceptable materials for submission

- Tumor-containing FFPE blocks
- Unstained slides from tumor-containing FFPE block
- Blood/bone marrow in lavender-top EDTA tube

Acid decalcification, heparinized blood and incomplete requisition are not acceptable

i Please contact us at (314) 747-7337 if you have any questions.



CANCER TESTING at Washington University



Testing methodology

Tests are performed using targeted hybridization capture of tumor-derived genomic DNA coupled with next-generation sequencing (NGS). This approach enables deep, comprehensive coverage of all coding exons and key introns of ordered genes, and allows assessment of the molecular complexity of each DNA specimen, minimizing sampling bias even in cases of low DNA mass or quality.

Types of variation detected include single nucleotide variants (SNVs), small insertions and deletions (indels), selected larger indels, and structural rearrangements involving selected genes.

For solid tumors, this test is routinely performed using formalin fixed paraffin embedded (FFPE) tissues and is able to detect SNVs under 10% allelic fraction in the sequenced tissue.

Results and interpretation

DNA sequence data are analyzed by GPS' clinically validated bioinformatics pipeline to identify and annotate somatic variants associated with cancer.

Identified tumor mutations are interpreted by a board-certified clinical genomicist in the context of the patient's disease and other clinical findings, highlighting mutations associated with specific treatment options based on evidence from the medical literature.

Results are returned to the ordering physician in a concise clinical report.

Turnaround time

The turnaround time for testing and interpretation is three weeks from the time the specimen is received.

Ancillary testing

Other available services include expert pathologic evaluation by specialized pathologists including the use of immunohistochemistry, immunofluorescence and electron microscopy. A wide range of clinically

validated cytogenetic analyses are also available. Contact us for more information.

Selected references

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Sehn JK, Hagemann IS, et al. *Diagnostic Utility of Targeted Next-generation Sequencing in Problematic Cases*. Am J Surg Pathol. 2014 Apr;38(4):534-41.

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Sharma MK, et al. *Clinical genomicist workstation*. AMIA Summits Transl Sci Proc. 2013 Mar 18;2013:156-7.

Contact us to order a test or for more info

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