170 genes
15 cancer types
6 variant classes
One test

powered by:

AUGUSTA UNIVERSITY
MEDICAL COLLEGE
OF GEORGIA

IBM Watson for Genomics

AugustaOncoTarget.com
simultaneously looks for six different variant classes in both the DNA and RNA of 170 genes in a patient biopsy. Within 20 minutes, Watson identifies gene variants, categorizes them according to similar pathways of action and identifies drugs that target the abnormalities.

**Gene Panel**

- **BLADDER**: MSH6, PMS2, TSC1, RET
- **BRAIN**: BRAF, CDKN2A, EGFR, FGFR1, IDH1, IDH2, NF1, PDGFRα, PTEN, TP53, 1p/19q deletion
- **BREAST**: AKT1, AR, BRCA1, BRCA2, ERBB2, FGFR1, FGFR2, PIK3CA, PTEN
- **COLORECTAL**: AKT1, BRAF, HRAS, KRAS, MET, MLH1, MSH2, MSH6, NRAS, PIK3CA, PMS2, PTEN, SMAD4, TP53
- **GASTRIC**: BRAF, KIT, KRAS, MET, MLH1, PDGFRα, TP53
- **HEPATOBILIARY**: BRAF, EGFR, FGFR gene fusions, HER2, IDH1, IDH2, KRAS, MAP2K1, MAP2K2
- **HRD (Homologous Recombination Deficiency)**: ATM, BARD1, BRCA1, BRCA2, BRIP1, CHEK2, MRE11A, NBN, PALB2, RAD51C, RAD51D
- **LEUKEMIA**: AKT1, ALK, BAP1, BCL2, BCL6, BRAF, BRCA1, BRCA2, BRIP1, BTK, CCND1, CCND2, CCNE1, CD79A, CD79B, CDH1, CDK12, CDK4, CDK6, CDKN2A, CEBPA, CHEK1, CHEK2, EGFR, EP300, EZH2, IDH1, IDH2, JAK1, JAK3
- **LUNG**: AKT1, ALK, BRAF, DDR2, EGFR, ERBB2, FGFR1, FGFR3, KRAS, MAP2K1, MET, NRAS, PIK3CA, PTEN, RET, TP53
- **OVARIAN/ UTERINE**: BRAF, BRCA1, BRCA2, KRAS, PDGFRα, FOXL2, TP53
- **PANCREATIC**: ATM, KRAS, MTOR, NF1
- **PROSTATE**: AR, ERG, TMPRSS2
- **SKIN**: BRAF, CTNNB1, GNA11, GNAQ, KIT, MAP2K1, NF1, NRAS, PDGFRα, PI3KCA, PTEN, TP53
- **SOFT-TISSUE/ RHABDOMYOSARCOMA**: ALK, EWSR1, KIT, NTRK1, PAX3, PAX7
- **THYROID**: BRAF, EGFR, HRAS, KRAS, NRAS, NTRK3, PPARG

Variant detection from both DNA and RNA targets
**Major Features**

- Covers all major classes of variants (SNPs, InDels, CNVs, Fusions and Splice Site Variants) simultaneously tests DNA & RNA
- 170-genes included based on NCCN and ESMO guidelines, the latest literature and pharma clinical trials
- Calculates Tumor Mutation Burden (TMB) for prediction of response to immunotherapies
- Includes MSI testing by DNA fragment analysis
- Targets genes involved in homologous recombination deficiency (HRD) for prediction of response to PARPi
- Concise personalized summary by multidisciplinary tumor boards
- High analytical sensitivity and specificity. Can detect targets with MAF ≥ 5% in samples with ≥ 7 copies of amplifiable targets in tissue with ≥ 30% tumor content.
- Extensively validated following AMP and CAP guidelines
- Testing in a CLIA certified laboratory

### Capabilities Overview

<table>
<thead>
<tr>
<th>Analysis of DNA</th>
<th>Yes</th>
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<tbody>
<tr>
<td>Analysis of RNA</td>
<td>Yes</td>
</tr>
<tr>
<td>Genes covered</td>
<td>170</td>
</tr>
<tr>
<td>Variant classes covered</td>
<td>SNPs, InDels, CNVs, Fusions, Splice Variants</td>
</tr>
<tr>
<td>Analytics</td>
<td>Illumina BaseSpace + IBM Watson for Genomics + in-house informatics pipeline</td>
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<tr>
<td>Reporting format</td>
<td>Automated report + Personalized reports by domain experts + counseling if requested</td>
</tr>
<tr>
<td>Tumor mutation burden (TMB)</td>
<td>Yes</td>
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<tr>
<td>Starting material</td>
<td>FFPE / Fresh tissue / Bone marrow / FNA</td>
</tr>
<tr>
<td>Library preparation &amp; Sequencing platform</td>
<td>Illumina target enrichment &amp; Illumina sequencing by synthesis chemistry</td>
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When to refer

All patients undergoing treatment for solid tumors can benefit from the Augusta OncoTarget Panel. The results can assist oncologists in selecting targeted therapies as an adjunct to standard chemotherapies. The test can be especially useful in cases where conventional therapies have not yielded favorable results.

Sample requirements

- **FFPE Block** (made with 10% buffered formalin) and an adjacent slide section if available along with pathology reports. A minimum of 30% tumor content is recommended in sections with area $\geq 5\text{mm}^2$. Our pathologist will examine the sections/slides and the molecular lab will ascertain extracted DNA/RNA quality and quantity prior to initiation of sequencing.

- Fresh frozen tissue, bone marrow and FNA (Fine Needle Aspiration) samples are also accepted. Please contact the laboratory for storage and transport conditions for sample types other than FFPE blocks.

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**8 Step Process**

1. Receipt of FFPE sample
2. Evaluation of section by Pathologist
3. DNA & RNA extraction, quality and quantity estimation
4. Next generation sequencing
5. Alignment and Variant Calling
6. Cloud and IBM analytics
7. Interpretation and personalized reporting
8. Tumor Board Discussion