PathGroup
Physician Centered. Patient Focused.

# SmartGenomics™ Breast Profile

**Oncology Services**

Clinical to Genomic

## Advanced Standard of Care

**PathGroup SmartGenomics: Breast** is designed for ***use at diagnosis, relapse or refractory disease*** in suspected or proven metastatic breast cancer to uncover therapeutic options and aid in treatment planning to improve patient outcomes

- Clinically actionable genomic information for 44 gene mutations, immunohistochemistry (IHC), cytogenetic abnormalities (FISH), and whole genome copy number changes (CMA)
- Clinical indications, prognostic data and potential therapies presented in a comprehensive report
- Full results in 7 to 10 days

## Tailored Genomic Breast Profile

| Next Generation Sequencing (NGS) | |
|---|---|
| AKT1 | Seen in invasive breast cancer and predictive of responsiveness to PI3K inhibition in vitro and on outcome after adjuvant tamoxifen |
| APC | Altered in up to 70% of sporadic breast cancers, known to mediate chemotherapeutic resistance |
| AR | Mutation implicated in resistance to antiandrogen therapy |
| BRAF | Predictive of response to the mTOR inhibitor everolimus in conjunction with analysis of KRAS, PIK3CA and PTEN |
| BRCA1/2 | Somatic mutations predictive of response to PARP inhibitors |
| CCND1 | Mutation implicated in predisposition to ductal carcinoma in situ of the breast |
| CDH1 | Identified in both lobular and ductal carcinomas |
| CDK4/6 | Targetable mutation through CD4/6 inhibition |
| CHEK2 | Acts as a tumor-suppressor gene in breast cancer |
| CTNNB1 | Implicated in activation of the Wnt signaling pathway in invasive breast cancer |
| EGFR | Potentially targetable, documented in TNBC |
| ERBB2/4 | Response to HER2-targeted therapy reported |
| ESR1 | Mutation recently implicated in endocrine resistance |
| FGFR1/2/3 | Activated signaling recently reported as driver, potentially targetable |
| FLT3 | Can be downregulated through CDK6 inhibition |
| GATA3 | Mutations define a unique subtype of luminal-like breast cancer with improved survival |
| HRAS | Ras pathway activation in breast cancer functions as a tumor and metastasis suppressor |
| JAK3 | Deregulation by activating mutations shown to confer invasive growth advantage |
| KDR | Thought to correlate with increased lymph node metastasis |
| KIT | Potential target in TNBC |
| KMT2D | Commonly mutated in HER2+, contribute to breast cancer initiation and progression |
| KRAS | Breast tumors with KRAS codon 12 mutations seem to present a worse prognosis |
| MET | De-regulation plays critical role in resistance to target-agents, such as anti-HER2 strategies |

*(profile components listing continued on back)*

| | |
|---|---|
| MLH1 | Thought to contribute to breast cancer initiation |
| NPM1 | Potential driver in TNBC |
| NRAS | May play a role in breast cancer metastasis |
| PDGFRA | Potential target in TNBC |
| PIK3CA | May predict resistance to trastuzumab, potentially targetable |
| PTCH1 | Potentially targetable through hedgehog pathway inhibition |
| PTEN | Mutation associated with high risk of recurrence and axillary lymph node metastasis |
| PTPN11 | Thought to play a role in intrinsic and acquired resistance to targeted cancer drugs |
| RB1 | Associated with resistance to anthracyclines/mitomycin in primary breast cancer |
| SETD2 | Mutations make cancer cells vulnerable to drug inhibiting the protein WEE1 |
| SMAD4 | Contributes to the formation of osteolytic bone metastases and invasive ductal carcinoma |
| SMO | Potentially targetable through hedgehog pathway inhibition |
| SRC | Targetable, important in the growth of breast cancer independent of hormonal receptor or HER2 status |
| TP53 | Associated with more aggressive disease and worse overall survival |
| TSC1/2 | Potential prediction of response to mTOR inhibition |
| **Immunohistochemistry (IHC)** | |
| ER | Response to hormonal therapy |
| PR | Response to hormonal therapy |
| HER2 | Predicitve of possible response to traztuzumab |
| **Fluorescence In Situ Hybridization (FISH)** | |
| HER2(ERBB2) | Predictive of possible response to traztuzumab |
| **Cytogenomic Microarray (CMA)** | |
| | Genome wide copy number changes for therapeutic and prognosic guidance |