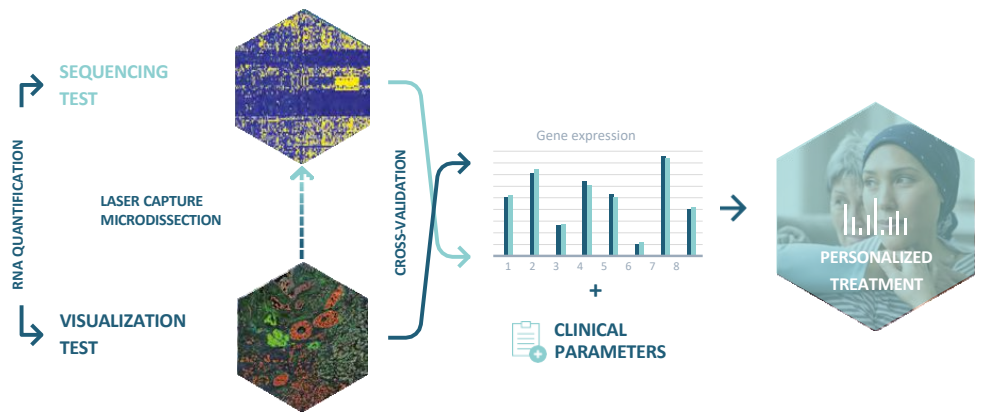


| PATIENT | | SAMPLE | | ORDERING PHYSICIAN | |
|--------------|--|---------------------|-----------|--------------------|--|
| Name: | | Specimen ID: | MDX-PT-23 | Name: | |
| ID: | | Date of collection: | | Address: | |
| Report date: | | Type: | | Contact: | |

TEST DESCRIPTION

The **Multiplex8+** breast cancer test assesses RNA-based biomarkers by conducting a **VISUALIZATION TEST** that uses RNA fluorescent in situ hybridization (RNA-FISH) to visualize a panel of biomarkers. Based on the expression of these biomarkers and the tissue histology, laser capture microdissection is used to dissect out regions of interest. With these tumor-enriched samples, a **SEQUENCING TEST** that utilizes total RNA next generation sequencing to survey gene expression in a spatially resolved manner, is further carried out. Analytical validation of **Multiplex8+** was conducted on a large retrospective cohort of 1 080 breast tumors.



THE TEST PROVIDES INFORMATION ABOUT:

- 1. RECEPTOR STATUS:** for RNA expression of the estrogen receptor, progesterone receptor, Her2 receptor, and Ki67 measured and cross-validated by the two tests.
- 2. MOLECULAR SUBTYPE:** based on RNA gene expression tumor biology.
- 3. GENE SIGNATURES:** personalized for patients' tumor biology and clinical status.

A SUMMARY IS PROVIDED BELOW AND ADDITIONAL DETAILS ARE PROVIDED IN THE FOLLOWING PAGES

RESULTS SUMMARY

RECEPTOR STATUS

| Sample | ESR1 | PGR | ERBB2 | MKI67 |
|--------|------|-----|----------|-------|
| A | + | + | - low | - |
| B | | | | |

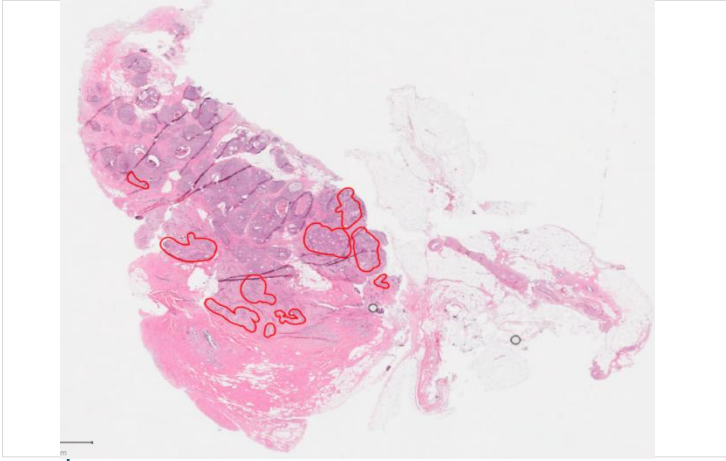
MOLECULAR SUBTYPE

| Intrinsic subtype | TNBC subtype |
|-------------------|--------------|
| Luminal A | - |
| | |

RELEVANT TREATMENT

| THERAPY | KEY FINDINGS | CLINICAL BENEFIT |
|---------------------------|---|----------------------|
| Adjuvant chemotherapy | Prognostic signature, gene expression, gene expression signature, molecular subtype | No predicted benefit |
| Endocrine therapy | Gene expression, gene expression signature, molecular subtype | Predicted benefit |
| Veliparib and Carboplatin | Gene expression, gene expression signatures | Predicted benefit |

LASER CAPTURE MICRODISSECTION



Based on histological assessment and RNA-FISH biomarker expression, one sample (**Sample A**) was laser capture microdissected for further analysis.

RECEPTOR STATUS

| Sample | ESR1 | PGR | ERBB2 | MKI67 |
|--------|------|-----|----------|-------|
| A | + | + | - low | - |
| B | | | | |

Receptor status was determined using both the **VISUALIZATION TEST** and **SEQUENCING TEST**: the table shows results after cross-validation.

INTERPRETATION

- The results from both RNA-FISH and RNA-SEQ are concordant with the IHC findings.

MOLECULAR SUBTYPE

| Intrinsic subtype | TNBC subtype ²⁻⁴ |
|-------------------|-----------------------------|
| Luminal A | - |
| | |

Based on the **SEQUENCING TEST**, we used a consensus subtyping approach consisting of our proprietary 293 gene molecular subtyping signature, a research-based PAM50 test and the AIMS method to classify the intrinsic molecular subtype ¹. TNBC subtype, if applicable, was classified according to Lehmann ²⁻⁴.

INTERPRETATION

- The biology of the Luminal A tumor type is consistent with the immunohistochemical and clinical designation.
- Luminal A tumors are characterized by expression of ER and/or PR and either negative or low expression of Her2 and the proliferation marker KI67. Luminal A tumors are low grade, have favorable prognosis, and respond well to endocrine therapies such as tamoxifen or aromatase inhibitors.

GENE SIGNATURE

- Based on the assigned molecular subtype, and TNBC subtype (if applicable), we evaluated several individual genes and gene signatures that demonstrate prognostic and predictive potential in early and advanced/metastatic settings.

| Treatment type/ Pathway | Gene signature | Description | Sample A Percentile | Sample B Percentile |
|-------------------------|--------------------------------|---|---------------------|---------------------|
| Prognosis | Consensus prognostic signature | The prognostic signature is derived from a consensus of three research-based prognostic signatures, including the 21-gene signature GENE21 ⁵ , the 70-gene GENE70 signature ⁶ , and the 50-gene risk of relapse based on subtype alone (ROR-S) signature ⁷ . The prognostic signatures are intended for early-stage breast cancer patients with ER+/Her2- IHC, lymph node-negative, or 1-3 positive lymph nodes. The score is reported as high, intermediate, or low. Patients with high signature scores are at a greater risk of relapse and may benefit from adjuvant chemotherapy, while patients with low scores have lower risk of relapse and may not benefit from adjuvant chemotherapy. | Low | |

GENE SIGNATURE

| Treatment type/ Pathway | Gene signature | Description | Sample A Percentile | Sample B Percentile |
|-------------------------|------------------------|--|---------------------|---------------------|
| Luminal signatures | ESR1 | The ESR1 and PGR genes encode for the estrogen (ER) and progesterone (PR) hormone receptors, respectively, which are involved in growth, metabolism, and reproductive functions. High ER/PR is predictive of endocrine therapies and low or negative ER/PR is associated with poor prognosis ⁸ . | Medium (37%) | |
| | PGR | | High (80%) | |
| | ESR1_PGR average | The average gene expression of ESR1 and PGR. Higher levels of hormone receptors are predictive markers for endocrine therapies. | Medium (47%) | |
| | E2F4_score | This gene signature assesses activity of the E2F4 transcription factor and its targets. A high E2F4 signature is associated with endocrine resistance to aromatase inhibitors and may predict sensitivity to CDK4/6 inhibitors ⁹ . | Low (6%) | |
| Her2 | ERBB2 | The ERBB2 gene is translated into Her2, a receptor tyrosine kinase involved in cell growth/proliferation and is both a prognostic marker and predictive of response to Her2 targeted therapies ⁸ . | Low (30%) | |
| | MUC4 | Mucin 4 (MUC4) is a glycoprotein that is implicated in resistance to trastuzumab through interactions with the Her2 receptor. High MUC4 is associated with reduced sensitivity to trastuzumab ¹⁰ . | Low (24%) | |
| | NRG1 | NRG1 codes for neuregulin 1, a ligand of the Her3 receptor. In the phase II NeoSphere trial, high NRG1 gene expression was associated with reduced response to neoadjuvant trastuzumab, but not combination trastuzumab-pertuzumab ¹¹ . | Medium (36%) | |
| | pSTAT3-GS | A signature that predicts phosphorylation of STAT3 and was found to be predictive of trastuzumab resistance in the FinHer study ¹² . | Medium (59%) | |
| | Her2 amplicon_MDX | Proprietary MDX 43-gene signature used to assess Her2 status. | Low (16%) | |
| | Module7_ERBB2 | Her2-signaling signature predictive of response to multiple anti-Her2 treatments in the I-SPY2 trial ¹³ . | Low (14%) | |
| Proliferation | AURKA | Aurora Kinase A (AURKA) is a protein coding gene involved in cell proliferation and is an independent prognostic marker in breast cancer. | Low (7%) | |
| | MKI67 | MKI67 codes for the marker of proliferation Ki67 protein, a marker of poor prognosis in ER+/Her2- tumors, but not Her2+ or TNBC tumors. Ki67 levels are also predictive of sensitivity to neoadjuvant endocrine and chemotherapies ⁸ . | Low (6%) | |
| | Module11_proliferation | Proliferation index used in I-SPY2 trial broadly predictive of pathological complete response in hormone receptor positive patients ⁴ . | Low (7%) | |
| | Proliferation_MDX | Proprietary MDX 7-gene signature used to assess cellular proliferation and cross-validate MKI67 expression levels. | Low (7%) | |
| CDK4/6 inhibitors | CDK4 | Cyclin-dependent kinases 4 and 6 (CDK4 and CDK6) are important proteins that regulate cell cycle progression from G1 to S phases. They are the main targets of CDK4/6 inhibitors such as palbociclib (Ibrance), ribociclib (Kisqali), and abemaciclib (Verzenio); however, it is unclear whether their expression level predicts CDK4/6 inhibitor sensitivity. | Low (21%) | |
| | CDK6 | | Low (21%) | |
| | CCNE1 | Elevated expression of the G1/S cell cycle regulators, CCNE1, CCND3, and CDKN2D, was associated with resistance to palbociclib (Ibrance) in the single-arm phase II neoadjuvant trial (NeoPalAna) ¹⁴ . | Low (9%) | |
| | CCND3 | | Low (3%) | |
| | CDKN2D | | Low (31%) | |
| PIK3CA mutations | PIK3CA-GS | A gene signature that is predictive of mutations in the PIK3CA gene and consequently the PI3K inhibitor alpelisib (Piqray). A high PIK3CA-GS score is also associated with activation of the PI3K/AKT pathway and loss of mTORC1 signaling, which may be relevant for response to mTOR inhibitors (e.g., everolimus) ¹⁵ . | Medium (47%) | |

GENE SIGNATURE

| Treatment type/ Pathway | Gene signature | Description | Sample A Percentile | Sample B Percentile |
|----------------------------|---|---|------------------------|------------------------|
| Chemotherapy | TOP1 | The gene encoding DNA topoisomerase I, an enzyme critical for DNA transcription, is a target for anticancer drugs. | Low (20%) | |
| | TOP2A | The gene encoding DNA topoisomerase IIa, an enzyme critical for DNA transcription, is a target for anticancer drugs. | Low (12%) | |
| | RAD51 | The DNA repair protein RAD51 homolog 1 (RAD51) is involved in the repair of damaged DNA and is associated with resistance to chemotherapy. | Low (21%) | |
| | ERCC1 | The DNA excision repair protein ERCC-1 (ERCC1) is involved in the repair of DNA damage and is associated with resistance to chemotherapy. | Low (9%) | |
| | TYMS | The Thymidylate Synthetase (TYMS) gene encodes a protein involved in DNA biosynthesis and is the target of the antimetabolite chemotherapy, 5-Fluorouracil ¹⁶ . | Low (12%) | |
| | SLC29A1 | SLC29A1 codes for the equilibrative nucleoside transporter 1 (ENT1) protein, which is a nucleoside transporter that is involved in transporting gemcitabine and capecitabine ¹⁷ . | Low (20%) | |
| | DHFR | Dihydrofolate reductase is an enzyme coded by the DHFR gene and is involved in folate metabolism and cell growth. It is the target of the antimetabolite chemotherapy, methotrexate ¹⁸ . | Low (14%) | |
| | SLC19A1 | SLC19A1 codes for the reduced folate carrier 1 (RFC1) protein, which transports methotrexate into the cell ¹⁸ . | Low (4%) | |
| | CDK12 | The protein product of the Cyclin Dependent Kinase 12 (CDK12) gene regulates transcription, DNA repair pathways, and cell cycle ¹⁹ . | Low (8%) | |
| | MAPs_Mitotic_kinases_neoadj_chemo118 | A 118-gene signature predicting response to neoadjuvant taxane chemotherapy ²⁰ . | Low (5%) | |
| | MAPs_Mitotic_kinases_neoadj_chemo17 | A 17-gene signature predicting response to neoadjuvant taxane chemotherapy ²⁰ . | Low (12%) | |
| | Early_Relapse_ER.Neg | Chemoresistance gene signature predicting early relapse in ER-negative (ER-) patients after taxane-anthracycline chemotherapy ²¹ . | Low (15%) | |
| | Residual_disease_ER.Neg | Chemoresistance gene signature predicting residual disease in ER-negative (ER-) patients after taxane-anthracycline chemotherapy ²¹ . | Low (7%) | |
| | Pathologic_response_ER.Neg | Chemosensitivity gene signature predicting pathological complete response in ER-negative (ER-) patients after taxane-anthracycline chemotherapy ²¹ . | Low (9%) | |
| | Early_Relapse_ER.Pos | Chemoresistance gene signature predicting early relapse in ER-positive (ER+) patients after taxane-anthracycline chemotherapy ²¹ . | Low (12%) | |
| | Residual_disease_ER.Pos | Chemoresistance gene signature predicting residual disease in ER-positive (ER+) patients after taxane-anthracycline chemotherapy ²¹ . | Low (12%) | |
| Pathologic_response_ER.Pos | Chemosensitivity gene signature predicting pathological complete response in ER-positive (ER+) patients after taxane-anthracycline chemotherapy ²¹ . | Low (16%) | | |

| Treatment type/ Pathway | Gene signature | Description | Sample A Percentile | Sample B Percentile |
|--|---|---|------------------------|------------------------|
| Immune system | PDCD1 | PDCD1 codes for the immune checkpoint marker PD-1. PD-1 is the target of pembrolizumab (Keytruda), an immunotherapy approved for the first-line treatment of metastatic TNBC. | Low (9%) | |
| | CD274 | CD274 codes for the immune checkpoint marker PD-L1. PD-L1 is the target of atezolizumab (Tecentriq), an immunotherapy approved for approved for the first-line treatment of metastatic TNBC. | Low (5%) | |
| | CTLA4 | Cytotoxic T lymphocyte-associated antigen 4 (CTLA4) is an immune checkpoint marker and the target of several immunotherapies such as durvalumab (Imfinzi). | Low (9%) | |
| | Module5_ TcellBcell | Immune signatures predictive of response to pembrolizumab in TNBC patients enrolled in (I-SPY2 trial) ¹⁴ . All signatures, with the exception of Mast_cells, were associated with increased probability of achieving pathological complete response. | Medium (59%) | |
| | Chemokine12 | | High (90%) | |
| | STAT1 | | Low (15%) | |
| | Dendritic_cells | | Low (22%) | |
| Mast_cells | Low (30%) | | | |
| DNA damage and repair | VCpred_TN | DNA damage repair / immune signature predictive of response to veliparib (PARP inhibitor) and carboplatin (I-SPY2 trial) ¹⁴ . | High (96%) | |
| Angiogenesis/ hypoxia | VEGFA | A gene coding for vascular endothelial growth factor, a protein involved in angiogenesis, vasodilation, and endothelial cell growth. VEGF is the target of the drug bevacizumab (Avastin). | Medium (38%) | |
| | Hypoxia / Angiogenesis / Inflammatory_ MDX | Proprietary MDX 7-gene signature used to assess hypoxia, angiogenesis, and inflammation. Signature includes genes known to be predictive of response to bevacizumab (Avastin) in the neoadjuvant GeparQuinto trial ²² . | Low (14%) | |
| ADC (antibody- drug conjugate) targets | ERBB2 | ERBB2 codes for the protein receptor Her2, which is a target for classical anti-Her2 treatments. Low and ultralow levels of Her2 can be eligible for treatment with the antibody-drug conjugate, trastuzumab deruxtecan (Enhertu) ²³ . | Low (30%) | |
| | TACSTD2 | TACSTD2 codes for Tumor-associated calcium signal transducer 2, also called Trop-2, which is the target of sacituzumab govitecan (Trodelvy), an antibody-drug conjugate approved for metastatic TNBC ²⁴ . | Medium (40%) | |
| | NECTIN4 | Nectin Cell Adhesion Molecule 4 (NECTIN4) is a cell adhesion molecule that is a target for antibody-drug conjugates in clinical trials for breast cancer. | Medium (37%) | |
| | ERBB3 | ERBB3 codes for a member of the epidermal growth factor receptor (EGFR) family of receptor tyrosine kinases. It is under investigation in clinical trials for the antibody-drug conjugate patritumab deruxtecan. | Low (9%) | |
| | FOLR1 | FOLR1 encodes the protein Folate Receptor Alpha, which is an antibody-drug conjugate target under investigation for the treatment of metastatic TNBC in several phase 1 and 2 clinical trials. | Medium (60%) | |
| | F3 | F3 codes for tissue factor, coagulation factor III a target of several antibody-drug conjugates in phase 1 clinical trials. | Medium (64%) | |
| | SLC39A6 | The SLC39A6 genes encodes for the zinc transporter LIV-1, which is highly expressed in luminal breast cancers and is under investigation in several phase 1 and 2 clinical trials. | High (88%) | |
| | TPBG | The trophoblast glycoprotein (TPBG) is overexpressed in many breast cancers and is the target of at least two antibody-drug conjugates undergoing phase 1 clinical trials. | Low (20%) | |

| Treatment type/ Pathway | Gene signature | Description | Sample A Percentile | Sample B Percentile |
|----------------------------|----------------|---|-------------------------|------------------------|
| | ROR2 | A gene that encodes the Receptor Tyrosine Kinase Like Orphan Receptor 2 protein, a target of the antibody-drug conjugate (Ozuriftamab Vedotin (BA3021/CAB-ROR2-ADC) that is under investigation in a phase clinical trial for advanced solid cancers, including TNBC. | Low (12%) | |
| | CD276 | This gene codes for an immune checkpoint marker called CD276 (also known as B7-H3). It is the target of the antibody-drug conjugate (Mirzotamab clezutoclax (ABBV-155) that is in a phase 1 and 2 clinical trial for advanced solid cancers, including breast cancer. | Low (6%) | |
| | VTCN1 | V-Set Domain Containing T Cell Activation Inhibitor 1 (VTCN1 also called B7-H4) is an immune checkpoint marker and the target of the antibody-drug conjugate, SGN-B7H4V, which is under investigation in a phase1 clinical trial for advanced solid cancers, including breast cancer. | High (75%) | |
| | CEACAM5 | A gene that encodes CEA Cell Adhesion Molecule 5 protein, a target of the antibody-drug conjugate Tusamitamab ravtansine (SAR408701) that is under investigation in a phase 2 clinical trial for advanced solid cancers, including breast cancer. | Medium (47%) | |

INTERPRETATION AND RECOMMENDATIONS

- The low consensus prognostic signature and low clinical risk (T1b, pNO, G2, Stage IA) suggest this patient may not benefit from adjuvant chemotherapy and may have similar prognosis with endocrine therapy alone. The pivotal TAILORx and MINDACT trials demonstrated that individuals with low prognostic risk scores may be spared adjuvant chemotherapy.
- Foregoing chemotherapy is supported by low expression of proliferation genes and gene signatures as well as low expression of signatures for response to neoadjuvant/adjuvant taxane/anthracycline chemotherapy (e.g., MAPs_Mitotic_kinases_neoadj_chemo17).
- The classification of a luminal A subtype, moderate ESR1 expression, high PGR expression, and low E2F4 score suggests endocrine therapies like tamoxifen and aromatase inhibitors may be beneficial.
- The I-SPY2 trial proved that high VCpred_TN signature score (96th percentile), that reflects DNA repair deficiency and immune activation, predicts response to veliparib a carboplatin. This finding was further validated in the BrightNess trial.
- A high Chemokine12 signature and low Mast_cells signature was predictive of benefit to the immunotherapy pembrolizumab in the I-SPY2 trial.
- The Her2-low designation by both IHC and Multiplex8+ suggest potential benefit from the antibody drug-conjugate trastuzumab deruxtecan (Enhertu).
- The sample contains high expression of the antibody-drug conjugate targets SLC39A6 and VTCN1, which is under investigation in early clinical trials for breast cancer.

REFERENCES

1. Gendoo, D.M.A. et al. *Bioinformatics* 32(7): 1097–1099 (2016). 2. Lehmann, B. D. et al. *J Clin Invest* 121: 2750–2767 (2011). 3. Lehmann, B. D. et al. *PLoS One* 11: e0157368 (2016). 4. Bareche, Y. et al. *Ann Oncol* 29: 895–902 (2018). 5. Paik, S. et al. *N Engl J Med* 351(27): 2817–2826 (2004). 6. van't Veer, L.J. et al. *Nature* 415(6871): 530–536 (2002). 7. Parker, J.S. et al. *J Clin Oncol* 27(8): 1160–1167 (2009). 8. Cardoso, F. et al. *Ann Oncol* 30(8): 1194–1220 (2019). 9. Guerrero-Izquierdo, A.L. et al. *Clin Cancer Res* 24(11): 2517–2529 (2018). 10. Mercogliano, M.F. et al. *Clin Cancer Res* 23(3): 636–648 (2017). 11. Guardia, C. et al., *Clin Cancer Res* 27(18): 5096–5108 (2021). 12. Sonnenblick, A. et al. *BMC Med* 13:177 (2015). 13. Wolf, D. M. et al. *Cancer Cell* 40: 609–623.e6 (2022). 14. Ma, C.X. et al. *Clin Cancer Res* 23(15): 4055–4065 (2017). 15. Loi, S. et al. *PNAS* 107(22): 10208–10213 (2010). 16. Foekens, J.A. et al. *Cancer Res.* 61: 1421–1425 (2001). 17. Mackey, J.R. et al. *Clin Cancer Res.* 8(1): 110–116 (2002). 18. Yang, V. et al. *RSC Med Chem.* 11(6): 646–664 (2020). 19. Filippone, M.G. et al. *Nat Commun.* 13(1): 2642 (2022). 20. Rodrigues-Ferreira, S. et al. *Proc Natl Acad Sci USA* 116(47): 23691–23697 (2019). 21. Hatzis, C. et al. *JAMA* 305(18):1873–81 (2011). 22. Karn, T. et al. *Clin Cancer Res* 26: 1896–1904 (2020). 23. Modi, S. et al. *N Engl J Med* 387: 9–20 (2022). 24. Michaleas, S. et al. *ESMO Open* 7 (2022).