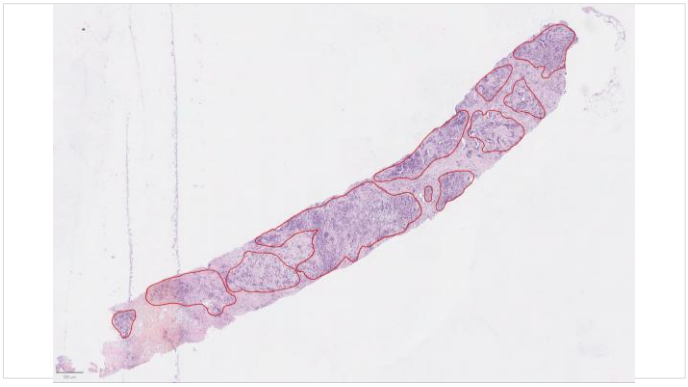
Multiplex8+
RESULTS

PATIENT		SAMPLE		ORDERING PHYSICIAN
Name:		Specimen ID:	MDX-PT-664	Name:
ID:		Date of Collection:		Address:
Date of Report:		Source:	Breast	Contact:
Initial or revised:	Original	Type:	Neoadjuvant	Information about revision:
		Quality:		Revision reason (if applicable:

TEST RESULT

Receptor	Gene	NGS Output (TPM)	NGS Positivity Threshold (TPM)	NGS Result	FISH Concordance
ER	*ESR1*	0.934	≥5.0	NEGATIVE	CONCORDANCE
PR	*PGR*	0.473	≥1.4	NEGATIVE	CONCORDANCE
HER2	*ERBB2*	30.291	≥154.7	LOW	CONCORDANCE
Ki-67	*MKI67*	65.997	≥18.9	POSITIVE	CONCORDANCE

LASER CAPTURE MICRODISSECTION



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

AUTHORISATION

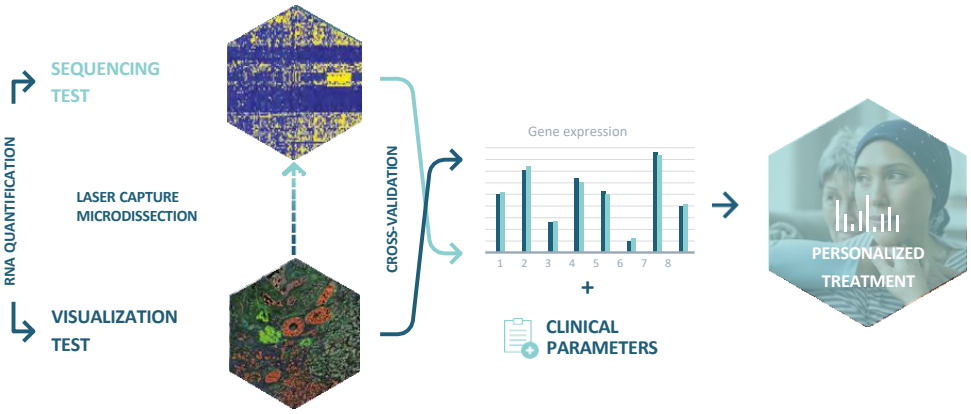
Reviewer	Releaser
Name:	Name:

Multiplex8+ - RESULTS EXPLANATION

Patient Name:	Date of collection:	Date of Report:

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 1 082 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.

INTERPRETATION GUIDE

In the following report, each gene/gene signature is given a percentile score, which ranks the expression level in the context of the patients included in our retrospective cohort. For the four main breast cancer biomarkers, estrogen receptor *(ESR1)*, progesterone receptor *(PGR)*, Her2 receptor *(ERBB2)*, and Ki67 *(MKI67)*, these percentile rankings are in the context of all 1 013 eligible patients. For all other genes/gene signatures, the percentile rankings are in the context of other patients belonging to the same **MOLECULAR SUBTYPE**. For example, for patients classified as Luminal A, the genes and gene signature will receive a percentile score compared to all Luminal A samples in our retrospective validation. The percentile scores do not necessarily imply a given level of sensitivity or resistance to a therapy.

Sample Percentile
Low (1-33)
Medium (<33-66)
High (<66-100)

Percentile groups and ranges

Subtype	# of patients
Luminal A	432
Luminal B	313
HER2	87
Basal-like	181
All patients	1 013

Number of patients in each molecular subtype and total retrospective cohort that are used to determine percentile rankings

Multiplex8+ - RESULTS INTERPRETATION SUMMARY

Patient Name:	Date of collection:	Date of Report:

RESULTS SUMMARY

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

RECEPTOR STATUS

Sample	ESR1	PGR	ERBB2	MKI67
A	–	–	– low	+

MOLECULAR SUBTYPE

Intrinsic subtype	TNBC subtype
Basal-like	Mesenchymal (M)

THERAPY	KEY FINDINGS	PREDICTED CLINICAL BENEFIT*
Anthracycline/taxane chemotherapy	Molecular subtype, prognostic risk, gene expression, gene expression signature	Higher possibility of benefit
Pembrolizumab	Molecular subtype, prognostic risk, gene expression signature	Higher possibility of benefit
Gemcitabine and Capecitabine	Gene expression	Higher possibility of benefit
5-fluorouracil (5-FU)	Gene expression	Higher possibility of benefit
Sacituzumab govitecan (Trodelvy)	Gene expression	Higher possibility of benefit
Trastuzumab deruxtecan (Enhertu)	Gene expression	Higher possibility of benefit
Bevacizumab (Avastin)	Molecular subtype, gene expression, gene expression signature	Higher possibility of benefit
Methotrexate	Gene expression	Higher possibility of benefit
PI3K inhibitor (alpelisib/Piqray)	Gene expression signature	Higher possibility of benefit (off-label, clinical trials)
ADCs in clinical trials	Gene expression	Higher possibility of benefit (off-label, clinical trials)
PARP inhibitor (Veliparib), carboplatin	Gene expression signature	Lower possibility of benefit

*Predicted Clinical Benefit is based on inferences from various data sources. The relationship of Multiplex8+ results to actual Clinical benefit has not been validated.

Multiplex8+ - RESULTS INTERPRETATION

Patient Name:	Date of collection:	Date of Report:

MOLECULAR SUBTYPE

Intrinsic subtype	TNBC subtype [2-4]
Basal-like	Mesenchymal (M)

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].

RECEPTOR STATUS

Sample	ESR1	PGR	ERBB2	MKI67
A	–	–	– low	+

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

INTERPRETATION

- The results from the Multiplex8+ are concordant with the immunohistochemistry findings.

INTERPRETATION

- The biology of the Basal-like tumor type is consistent with the immunohistochemical and clinical designation.
- The basal-like subtype is similar to TNBC because it often lacks expression of hormone and HER2 receptors. Although patients with basal-like breast cancer respond better to chemotherapy, they are more susceptible to early relapse and have poorer prognosis.
- The Mesenchymal TNBC subtype is characterized by elevated expression of genes involved in epithelial-mesenchymal transition and growth factor pathways, cellular proliferation, an immunosuppressed tumor microenvironment, association with metaplastic histological subtype, poor responses to chemotherapy, and reduced survival[2–4]. M may respond well to treatments targeting the PI3K/mTOR pathways.

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	
Prognosis	HR+_ Prognostic	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.	N/A	
	TNBC_ Prognostic_ MDX	MultiplexDX (MDX) 60-gene signature for recurrence-free survival risk prediction for TNBC patients. The signature was derived from the MDX-BRCA retrospective cohort[1], comprising 159 TNBC patients and validated on 508 TNBC patients from two large international cohorts spanning Asia, Europe, and the USA.	Low risk	

Multiplex8+ - GENE SIGNATURES

Patient Name:	Date of collection:	Date of Report:

Treatment type/ Pathway	Gene signature	Description	Sample A 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].	Low (7)	
	PGR		Low (14)	
	ESR1_PGR average	The average gene expression of ESR1 and PGR. Higher levels of hormone receptors are predictive markers for endocrine therapies.	Low (7)	
	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].	High (82)	
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 (12)	
	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].	Medium (43)	
	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].	High (73)	
	pSTAT3-GS	A signature that predicts phosphorylation of STAT3 and was found to be predictive of trastuzumab resistance in the FinHer study [12].	High (96)	
	Her2 amplicon_ MDX	Proprietary MDX 43-gene signature used to assess Her2 status.	High (67)	
	Module7_ ERBB2	Her2-signaling signature predictive of response to multiple anti-Her2 treatments in the I-SPY2 trial [13].	Medium (39)	
	T-DM1_pred	The trastuzumab emtansine (T-DM1) predictive signature is a Research Use Only classifier that combines 19 genes/gene signature involved in the mechanism of action of T-DM1 and was shown to predict response in the T-DM1 arm of the I-SPY2 trial (https://www.nature.com/articles/s41467-024-55583-2).	Low (12)	
Proliferation	AURKA	Aurora Kinase A (AURKA) is a protein coding gene involved in cell proliferation and is an independent prognostic marker in breast cancer.	High (69)	
	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].	High (88)	
	Module11_ proliferation	Proliferation index used in I-SPY2 trial broadly predictive of pathological complete response in hormone receptor positive patients [4].	High (79)	
	Proliferation_ MDX	Proprietary MDX 7-gene signature used to assess cellular proliferation and cross-validate MKI67 expression levels.	High (92)	
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.	Medium (40)	
	CDK6		Medium (57)	
	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].	High (70)	
	CCND3		Low (28)	
	CDKN2D		High (78)	
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].	High (96)	

Multiplex8+ - GENE SIGNATURES

Patient Name:	Date of collection:	Date of Report:

Treatment type/ Pathway	Gene signature	Description	Sample A Percentile	
Chemotherapy	TOP1	The gene encoding DNA topoisomerase I, an enzyme critical for DNA transcription, is a target for anticancer drugs.	**High (100)**	
	TOP2A	The gene encoding DNA topoisomerase IIa, an enzyme critical for DNA transcription, is a target for anticancer drugs.	**High (82)**	
	RAD51	The DNA repair protein RAD51 homolog 1 (RAD51) is involved in the repair of damaged DNA and is associated with resistance to chemotherapy.	**High (89)**	
	ERCC1	The DNA excision repair protein ERCC-1 (ERCC1) is involved in the repair of DNA damage and is associated with resistance to chemotherapy.	**High (85)**	
	TYMS	The Thymidylate Synthetase (TYMS) gene encodes a protein involved in DNA biosynthesis and is the target of the antimetabolite chemotherapy, 5-Fluorouracil [16].	**High (90)**	
	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].	**Medium (37)**	
	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].	**High (74)**	
	SLC19A1	SLC19A1 codes for the reduced folate carrier 1 (RFC1) protein, which transports methotrexate into the cell [18].	**Low (22)**	
	CDK12	The protein product of the Cyclin Dependent Kinase 12 (CDK12) gene regulates transcription, DNA repair pathways, and cell cycle [19].	**Medium (40)**	
	Chemotherapy_ MDX	MultiplexDX (MDX) 45-gene signature predicting pathological complete response (pCR) to neoadjuvant chemotherapy for TNBC patients, developed and validated on 938 TNBC patients from 20 diverse cohorts, including randomized Phase 2 and 3 trials.	**pCR positive**	
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.	**Medium (35)**	
	CD274	CD274 codes for the immune checkpoint marker PD-L1. PD-L1 is the target of atezolizumab (Tecentriq), an immunotherapy approved for the first-line treatment of metastatic TNBC.	**High (89)**	
	CTLA4	Cytotoxic T lymphocyte-associated antigen 4 (CTLA4) is an immune checkpoint marker.	**Low (23)**	
	Immunotherapy _MDX	MultiplexDX (MDX) 5-gene signature predicting pathological complete response (pCR) to neoadjuvant immunotherapy for TNBC patients, developed and validated on 60 TNBC patients from the I-SPY2 pembrolizumab and durvalumab arms.	**pCR positive**	
DNA damage and repair	VCpred_TN	DNA damage repair / immune signature predictive of response to veliparib (PARP inhibitor) and carboplatin (I-SPY2 trial) [13].	**Medium (50)**	
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).	**High (67)**	
	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].	**High (80)**	

Multiplex8+ - GENE SIGNATURES

Patient Name:	Date of collection:	Date of Report:

Treatment type/ Pathway	Gene signature	Description	Sample A Percentile	
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 (12)**	
	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 HR+/HER2– or TNBC [24] and also the drug datopotamab deruxtecan (Datroway), an ADC being investigated in clinical trials for metastatic HR+/HER2- breast cancer[25].	**High (73)**	
	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.	**Low (17)**	
	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 (12)**	
	FOLR1	FOLR1 encodes the protein Folate Receptor Alpha, which is an antibody-drug conjugate target under investigation in several phase 1 and 2 clinical trials for breast cancer.	**Medium (39)**	
	F3	F3 codes for tissue factor, coagulation factor III a target of several antibody-drug conjugates in phase 1 and 2 clinical trials.	**Medium (42)**	
	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 (75)**	
	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 (29)**	
	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 phase 1 and 2 clinical trial for advanced solid cancers, including breast cancer.	**High (68)**	

Multiplex8+ - INTERPRETATION*

INTERPRETATION*

- The patient is classified as low risk according to the TNBC_Prognostic_MDX signature. In our preliminary analysis of 177 patients included in a retrospective study of patients with TNBC receiving neoadjuvant treatment, low-risk patients had better outcomes than high-risk patients, as assessed by the probability of 2-year recurrence-free survival (RFS). Low-risk patients also had higher pCR rates following both neoadjuvant chemotherapy and chemoimmunotherapy.
- The patient is classified as Chemotherapy_MDX pCR-positive. In our preliminary analysis of 177 patients included in a retrospective study of patients with TNBC receiving neoadjuvant treatment, patients with a positive Chemotherapy_MDX signature had higher pCR rates following neoadjuvant chemotherapy compared with patients with a negative Chemotherapy_MDX signature. However, the high expression of the chemotherapy resistance markers RAD51 and ERCC1 should be noted.
- The patient is classified as Immunotherapy_MDX pCR-positive. In our preliminary analysis of 177 patients included in a retrospective study of patients with TNBC receiving neoadjuvant treatment, patients with a positive Immunotherapy_MDX signature had higher pCR rates following neoadjuvant chemoimmunotherapy (i.e., the KEYNOTE-522 regimen) compared with patients with a negative Immunotherapy_MDX signature.

**Supporting literature can be found in the relevant gene description above. This report and its citation coverage are currently being revised.*

Multiplex8+ - INTERPRETATION*

Patient Name:	Date of collection:	Date of Report:

INTERPRETATION*

- Expression levels of nucleoside transporters, such as SLC29A1, are associated with sensitivity to gemcitabine and capecitabine, with both intermediate and high expression levels predicting sensitivity. In addition, high TYMS expression may predict a response to 5-fluorouracil (5-FU) and chemotherapeutic agents metabolized to 5-FU, such as capecitabine.
- The sample shows high TACSTD2 expression. TACSTD2 encodes Trop-2, which is the target of sacituzumab govitecan (Trodelvy), an ADC approved for the treatment of metastatic TNBC. In biomarker analyses from the phase III pivotal ASCENT study, patients with high/intermediate Trop-2 expression benefited from sacituzumab govitecan. The cytotoxic component of this ADC, SN-38, targets TOP1, which is highly expressed in the sample. The expression of both the ADC target and the target of its cytotoxic component suggests that sacituzumab govitecan may be effective in the advanced/metastatic setting.
- As the sample is classified as ERBB2-low, the patient may benefit from treatment with the antibody–drug conjugate (ADC) trastuzumab deruxtecan (Enhertu), which is approved for patients with metastatic breast cancer with low HER2 expression. The cytotoxic component of this ADC, deruxtecan, targets TOP1, which is highly expressed in the sample. The expression of both the target antigen and the target of the cytotoxic component suggests that trastuzumab deruxtecan may be effective in patients with advanced or metastatic disease.
- Classification of the tumor as the mesenchymal (M) TNBC subtype, together with high expression of angiogenesis markers (VEGFA and Hypoxia/Angiogenesis/Inflammatory_MDX), suggests that bevacizumab (Avastin) may be a relevant treatment option in the metastatic setting.
- Intermediate CDK12 expression is associated with increased sensitivity to methotrexate-based chemotherapy regimens.
- A high PIK3CA-GS score may indicate the presence of PIK3CA mutations. In the METABRIC cohort, PIK3CA mutations were detected in 16.1% of patients with the basal-like subtype. ER+/HER2− patients with certain PIK3CA mutations may be eligible for treatment with the PI3K inhibitor alpelisib in combination with fulvestrant. The mesenchymal TNBC subtype is also hypothesized to respond to PI3K inhibitors. As alpelisib is not approved for patients with basal-like/TNBC disease, its use would be considered off-label; therefore, participation in clinical trials should be considered.
- The sample shows high expression of several targets of antibody–drug conjugates (ADCs), including SLC39A6 and VTCN1. These targets are currently being investigated in clinical trials for TNBC.
- Intermediate expression of the VCpred_TN gene signature suggests that the patient is unlikely to benefit from PARP inhibitors (veliparib) and carboplatin.

**Supporting literature can be found in the relevant gene description above. This report and its citation coverage are currently being revised.*

AUTHORISATION

Reviewer	Releaser
Name:	Name:

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