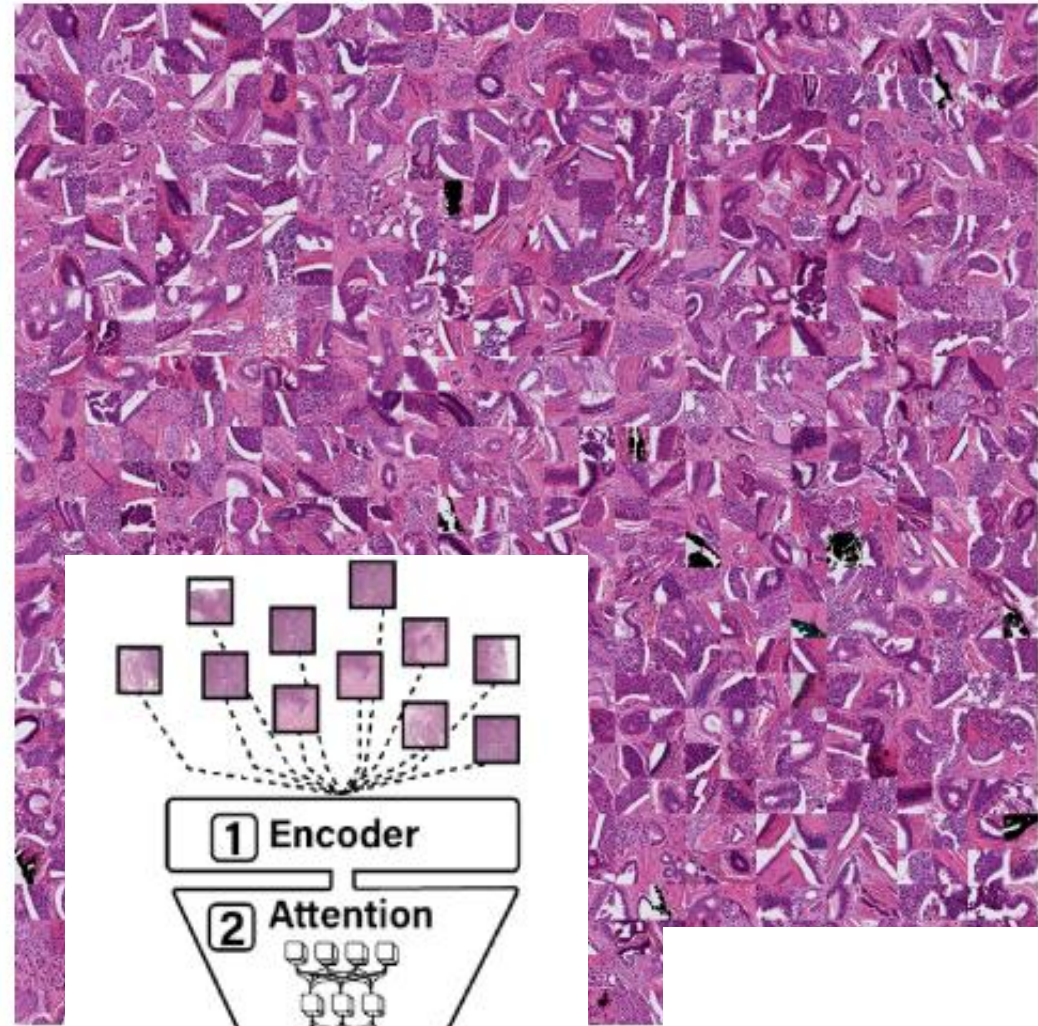


Pr Anne Vincent-Salomon  
Department of Pathology  
Institut CURIE Paris and PSL University, France

# Digitalization of Pathology Department and the Use of Artificial Intelligence in Practice



ENSEMBLE, PRENONS  
LE CANCER DE VITESSE

# My disclosures in relation with this presentation

---

- Ibex Medical Analytics: grant for research, honoraria, stock options, travel supports
- Astra-Zeneca: grants for research, travel supports, honoraria
- Daiichi-Sankyo: honoraria for lectures
- MSD and MSD Avenir: grant research
- Owkin: grant for research
- Prima: grant for research
- Myriad: honoraria

# Outlines of my talk

---

1- Introduction

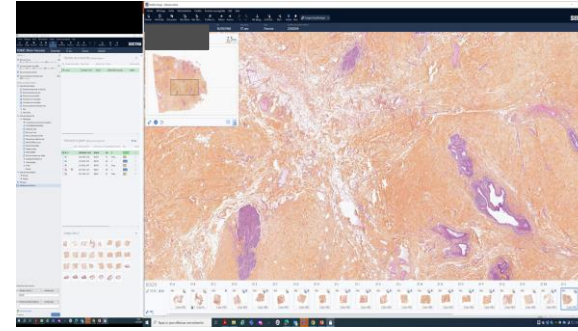
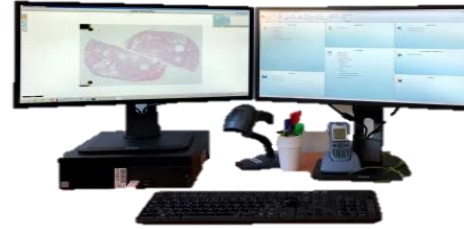
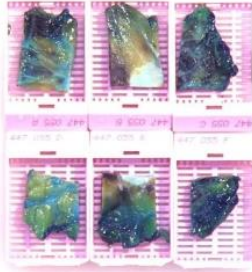
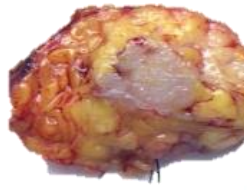
2- Diagnosis of breast cancer using AI

3- Prediction of Homologous Recombination Deficiency (HRD) in breast cancers using AI

4- Digital transition of Institut Curie's pathology department

5- Perspectives

# DIGITAL PATHOLOGY



Surgical specimen



Health Data Warehouse  
- Whole slide images  
- Clinical and pathological datas

- Transformation of a **glass** slide into a **digital** slide (Whole slide images, WSI):  
generated by digital scanners  
→ **An additional step** in the pathology technical workflow
  - Scanners
  - Image management system + Laboratory Management System
  - WSI Storage capacities

# What can computer vision scientists do for pathologists ?

---

## AI Diagnostic tools to help pathologists in time consuming tasks

- Diagnosis of lymph node metastases
- Diagnosis of breast cancer
- Mitotic count
- Quantification of markers assessed by immunohistochemistry

## Development of predictive and prognostic surrogate markers from digitalized H&E slides

- Molecular classes status (without IHC)
- Genomic status of *BRCA1 or 2*
- To predict response to neoadjuvant therapy
- To define prognosis

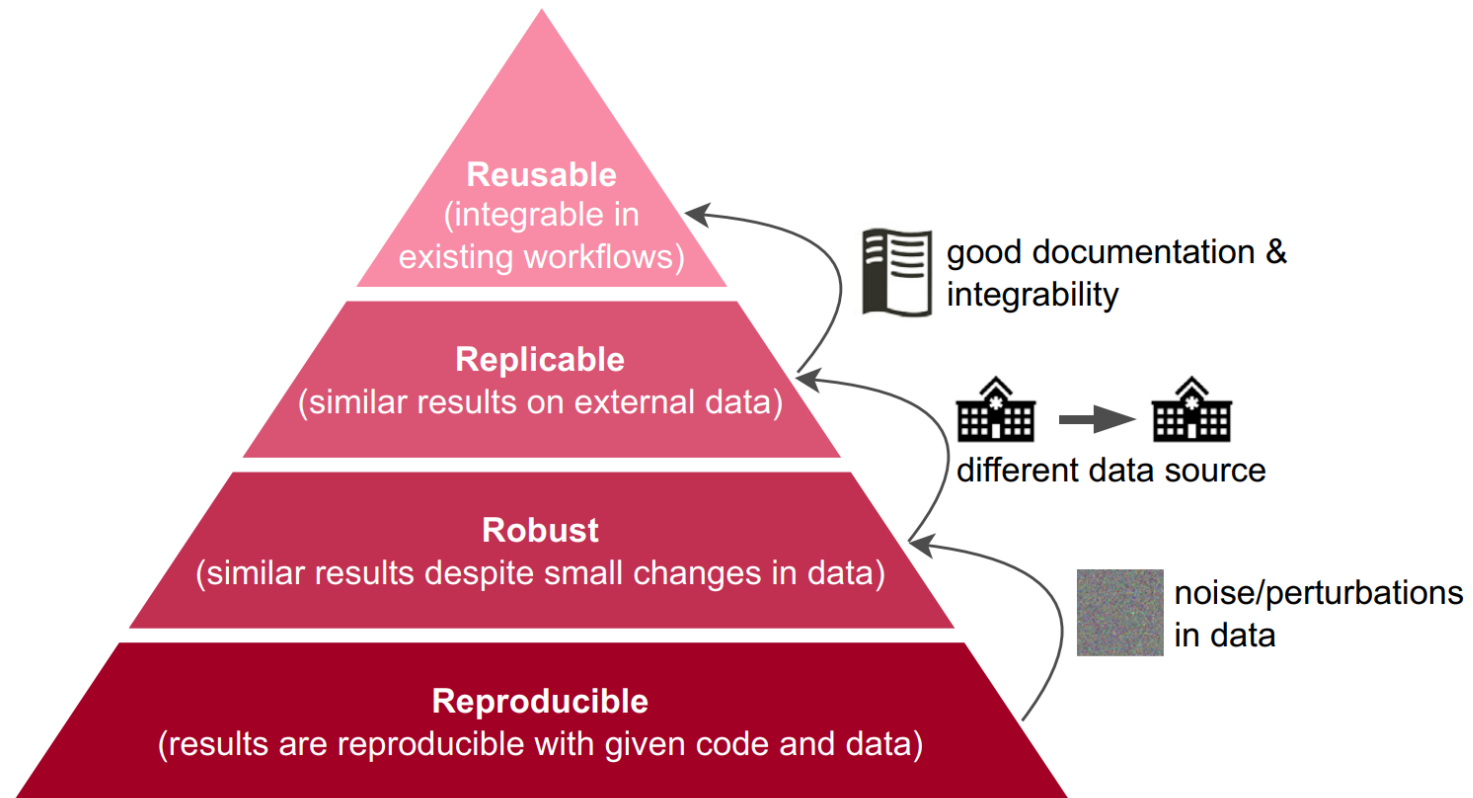
Etc....

- Improve pathologists workflow and reduce turn around time
- Increase accuracy, reduce inter-observer variability
- “**Second reads**” before final sign out to ensure clinically significant lesions have not been missed (QA)



# AI TOOLS IN PATHOLOGY:

Developed by pathologists with computational vision scientists +++



**Figure 2.**

Reproducibility, robustness, replicability, and reusability in the context of deep learning algorithms for computational pathology.

# Outlines of my talk

---

1- Introduction

2- Diagnosis of breast cancer using AI

3- Prediction of Homologous Recombination Deficiency (HRD) in breast cancers using AI

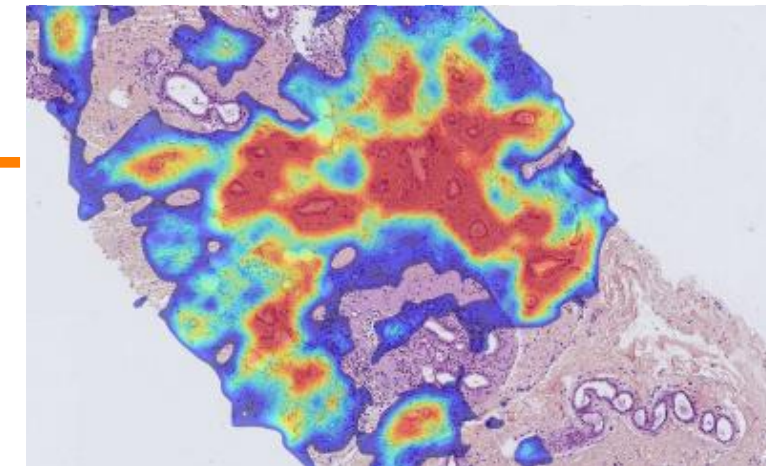
4- Digital transition of a pathology department

5- Perspectives

# Validation and real-world clinical application of an artificial intelligence algorithm for breast cancer detection in biopsies

Judith Sandbank<sup>1,2</sup>, Guillaume Bataillon<sup>3,7</sup>, Alona Nudelman<sup>1</sup>, Ira Krasnitsky<sup>2</sup>, Rachel Mikulinsky<sup>2</sup>, Lilach Bien<sup>2</sup>, Lucie Thibault<sup>3</sup>, Anat Albrecht Shach<sup>4</sup>, Geraldine Sebag<sup>2</sup>, Douglas P. Clark<sup>2</sup>, Daphna Laifenfeld<sup>2,8</sup>, Stuart J. Schnitt<sup>5,6</sup>, Chaim Linhart<sup>2</sup>, Manuela Vecsler<sup>2</sup> and Anne Vincent-Salomon<sup>3</sup>

NPJ Breast cancer 2022



## Internal training Set (n=2167 cases)

Set	Analysis	Number of cases	AUC* [95% CI]	Specificity [95% CI]	Sensitivity [95% CI]	PPV NPV
Internal test set (MHS)	Invasive vs. non-invasive	1090 (173 invasive, 917 non-invasive)	0.998 [0.996;1.000]	98.27% [95.03%;99.41%]	99.02% [98.15%;99.48%]	95.0%, 99.7%
	DCIS vs. benign/other	908 <sup>a</sup> (27 DCIS, 881 benign)	0.999 [0.997;1.000]	98.64% [97.56%;99.30%]	100% [84.50%;100%]	69.3%, 100%
	IDC vs. ILC	169 <sup>b</sup> (156 IDC, 13 ILC)	0.932 [0.862;1.000]	NA <sup>c</sup>	NA <sup>c</sup>	NA <sup>c</sup>

\* AUC – area under the ROC\*\* curve

\*\*The Receiver Operator Characteristic (ROC) curve plots the True Positive Rate against False Positive Rate at various threshold values and shows the performance of a classification model at all classification thresholds.



# Galen Breast AI Validation study: Invasive Carcinoma Detection

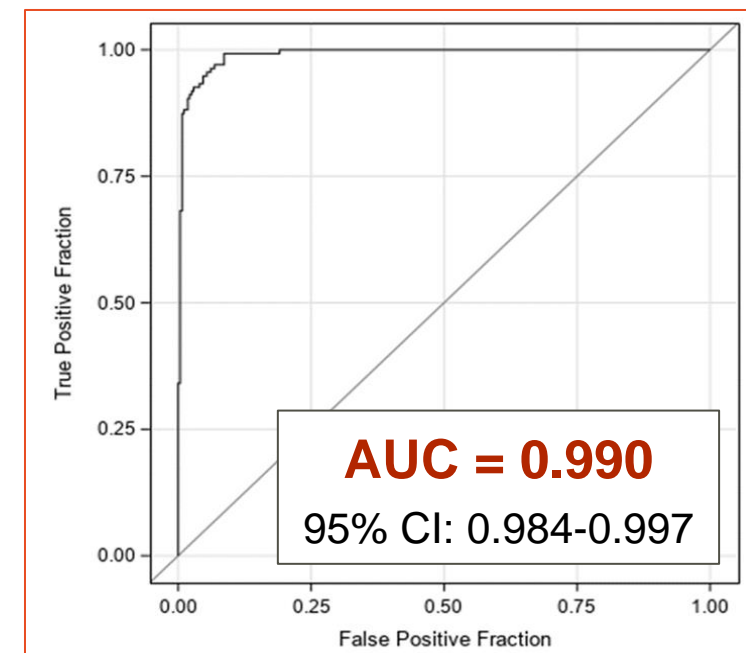
N=436 cases\* (156 invasive\*\*; 135 DCIS/ADH; 145 benign)

Performance		95% Confidence Limits	
Sensitivity	95.51%	91.03%	97.81%
Specificity	93.57%	90.07%	95.90%
PPV	89.22%	83.61%	93.07%
NPV	97.40%	94.73%	98.73%

PPV – positive predictive value  
NPV- negative predictive value

**\*\* 34 rare invasive carcinomas types: fusiform metaplastic, tubular, apocrine, mucinous, micropapillary, acinic cells carcinomas**

## ROC CURVE



AUC – area under the ROC curve; Galen Breast invasive probability score versus the ground truth diagnosis after discrepancy review

\* Performance on consecutive biopsies is expected to be higher

# Galen Breast detection of Invasive lobular carcinoma

N= 153 cases (98 IDC; 55 ILC)

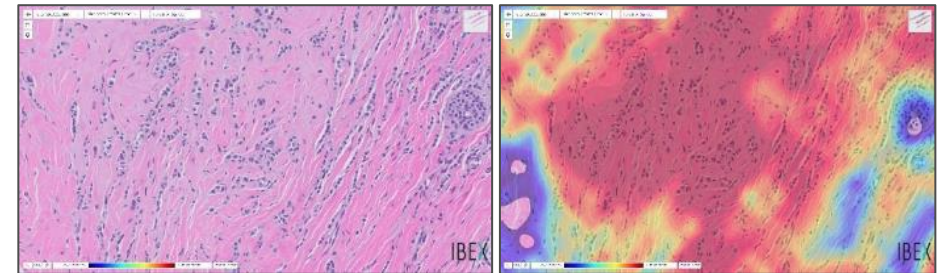
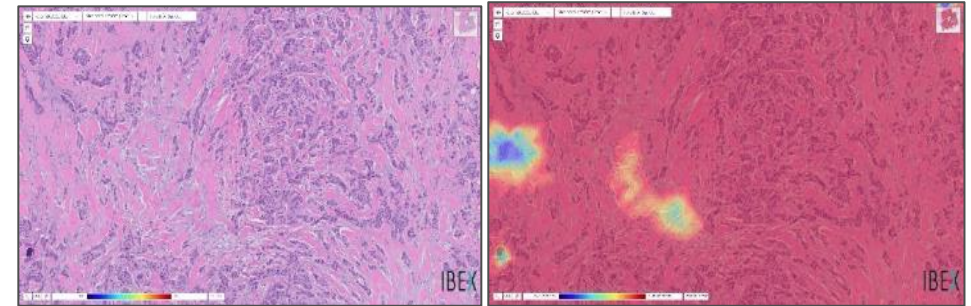
Heatmaps display:  
low probability in blue  
high probability in red

Performance

95% Confidence Interval

AUC	0.973	0.996	0.948
Sensitivity	92.9%	97.1%	85.8%
Specificity	92.7%	97.1%	82.7%
PPV	95.8%	98.3%	89.6%
NPV	87.9%	95.0%	76.7%

IC-NST



Invasive Lobular carcinoma

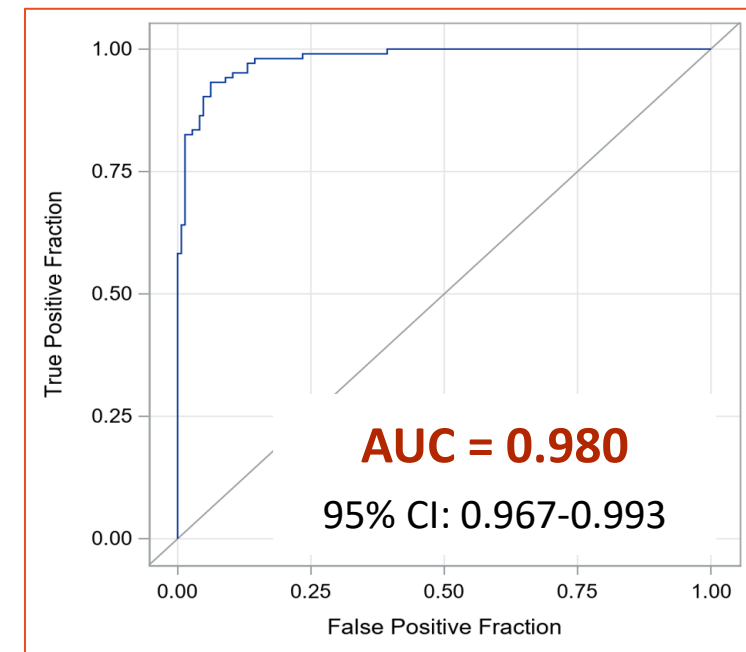
# Galen Breast AI Validation study: In Situ Ductal Carcinoma Detection

N= 248 cases (103 DCIS; 145 benign/other)

Performance		95% Confidence Limits	
Sensitivity	93.79%	88.63%	96.70%
Specificity	93.20%	86.63%	96.67%
PPV	91.4%	84.51%	95.43%
NPV	95.1%	90.24%	97.61%

Performance for DCIS and ADH detection versus benign is  
AUC=0.949, Sensitivity=87.41%, Specificity=86.9%

ROC CURVE



AUC – area under the ROC curve; Galen Breast in-situ probability score versus the ground truth diagnosis after discrepancy review

\*\*cohort enriched with low grade DCIS ; Performance on consecutive biopsies is expected to be higher

# Galen Breast identification of DCIS nuclear grade

(Intermediate and High) grade DCIS versus (ADH and Low) Grade DCIS

N= 134 cases (88 IG/HG DCIS; 46 LG DCIS/ADH)

	Performance	95% Confidence Interval	
AUC	0.921	0.965	0.878
Sensitivity	84.1%	90.3%	75.1%
Specificity	84.8%	92.4%	71.8%
PPV	91.4%	95.8%	83.2%
NPV	73.6%	83.6%	60.4%

**Note:** These studies do not represent a typical case distribution in a lab, since low grade and ADH were **enriched** in order to allow sufficient statistical power for various analyses;  
Performance on consecutive biopsies is expected to be higher



# TILs Detection in invasive carcinomas (cut-off: > 30% TILs for heatmap)

In pure invasive carcinomas

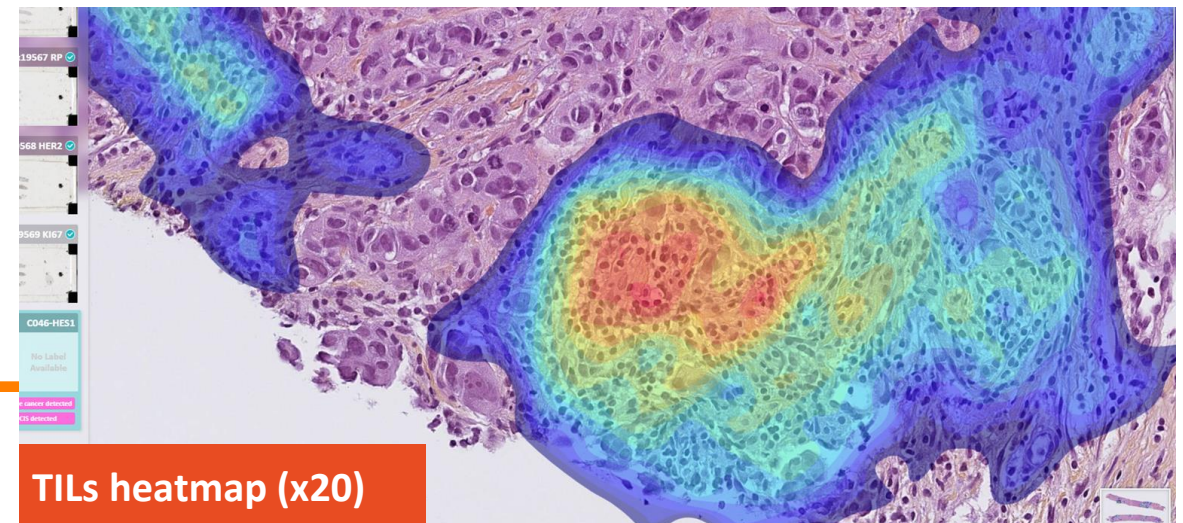
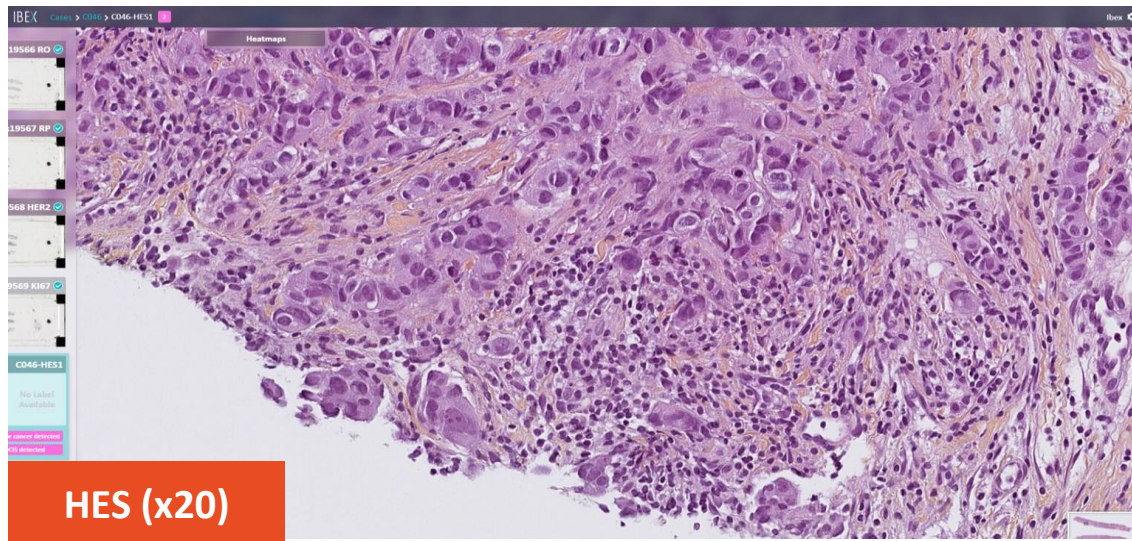
N= 47 cases (19 TILs positive; 28 TILs negative)

Performance		95% Confidence Interval	
AUC	0.953	0.892	1.0
Sensitivity	94.7%	73.5%	99.9%
Specificity	85.7%	67.9%	94.9%

in Invasive carcinomas associated with DCIS

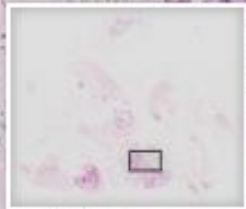
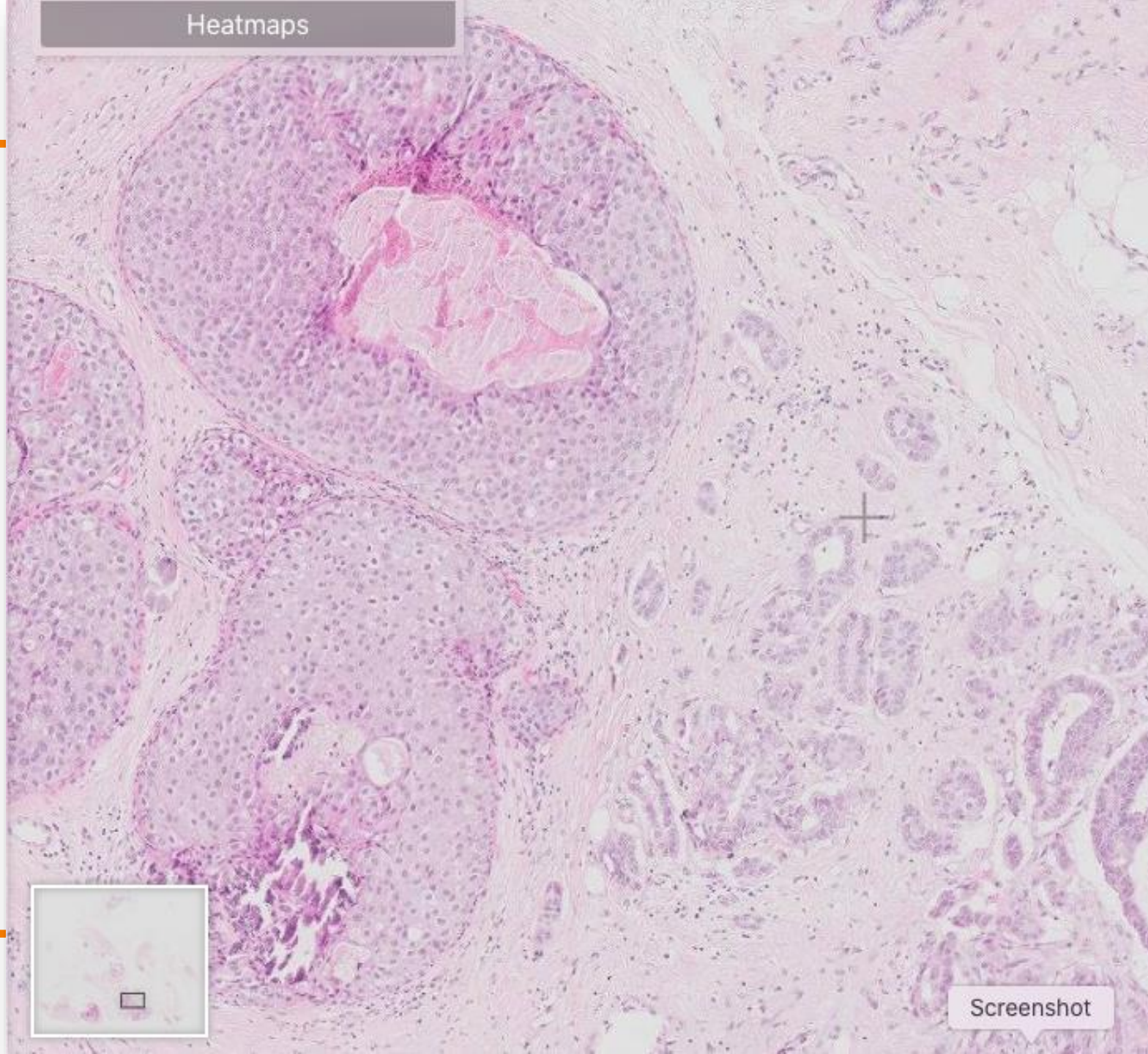
N= 109 cases (32 TILs positive; 77 TILs negative)

Performance		95% Confidence Interval	
AUC	0.965	0.934	0.996
Sensitivity	93.8%	78.8%	99.3%
Specificity	85.7%	76.3%	92.0%





Heatmaps

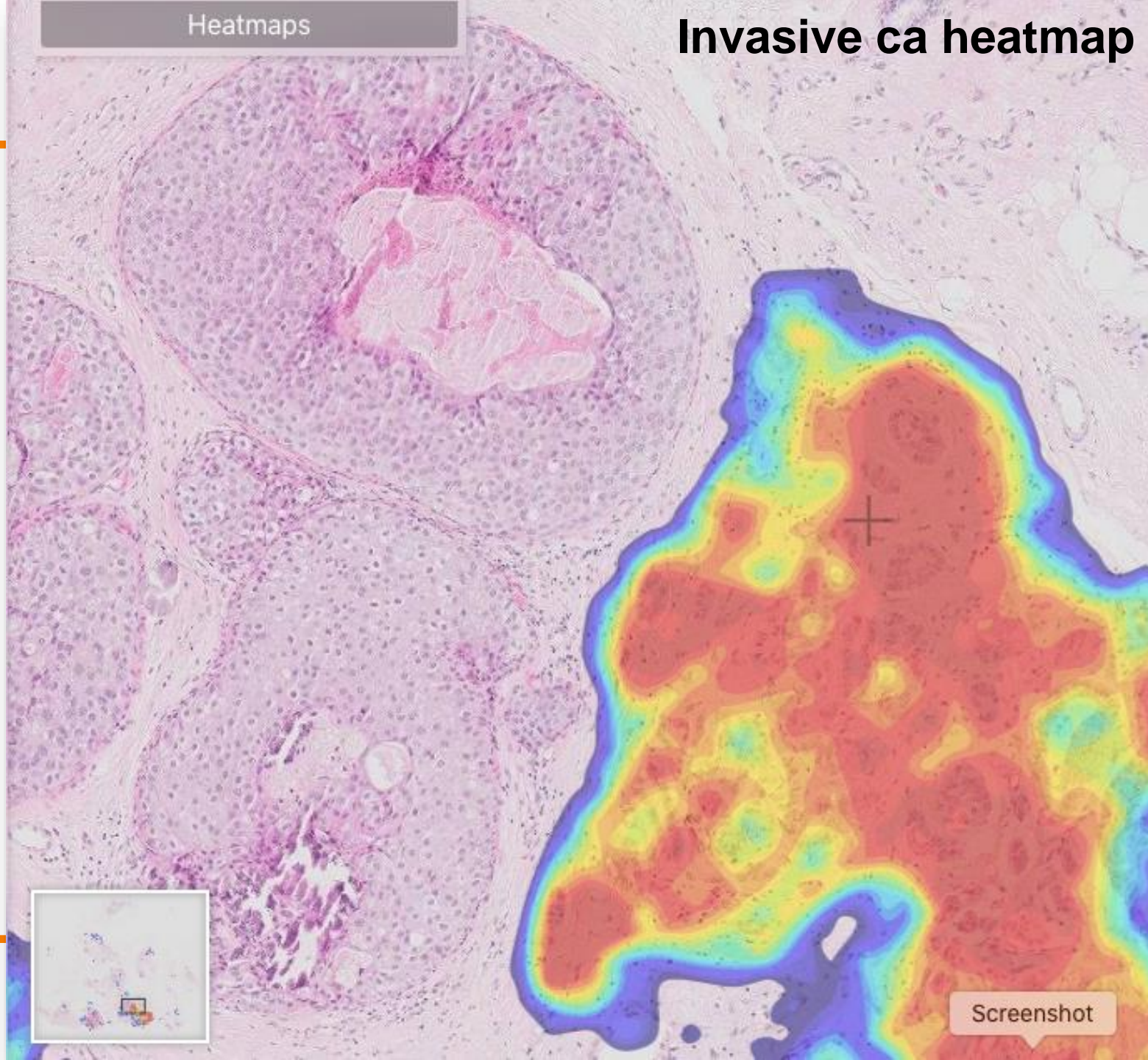


Screenshot



Heatmaps

# Invasive ca heatmap

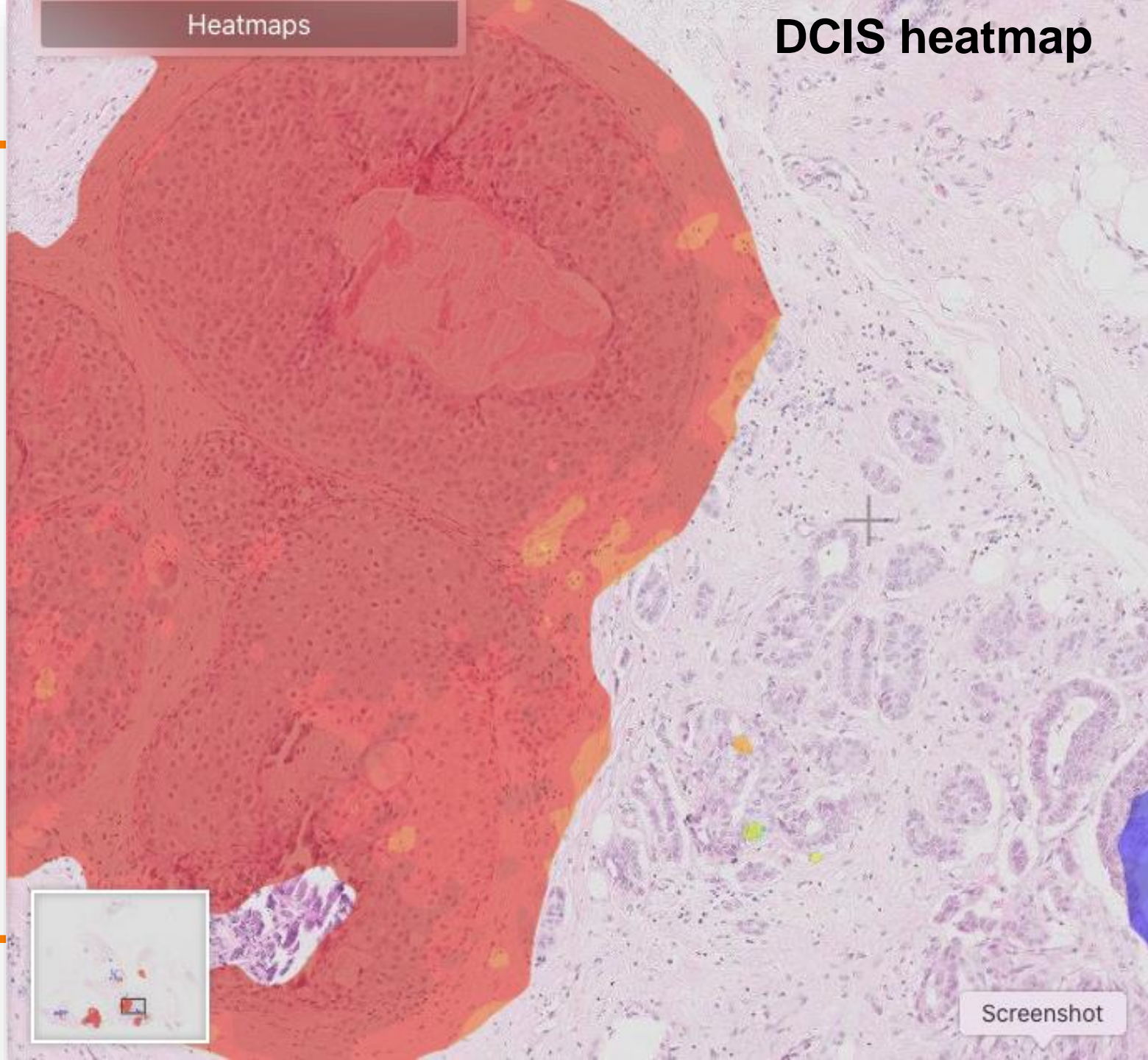


Screenshot



Heatmaps

# DCIS heatmap



Screenshot

# GALEN BREAST ALGORITHM: PERFORMANCES IN 5 INDEPENDENT STUDIES FROM DIFFERENT LABS AROUND THE WORLD (different scanners, different stainings...)

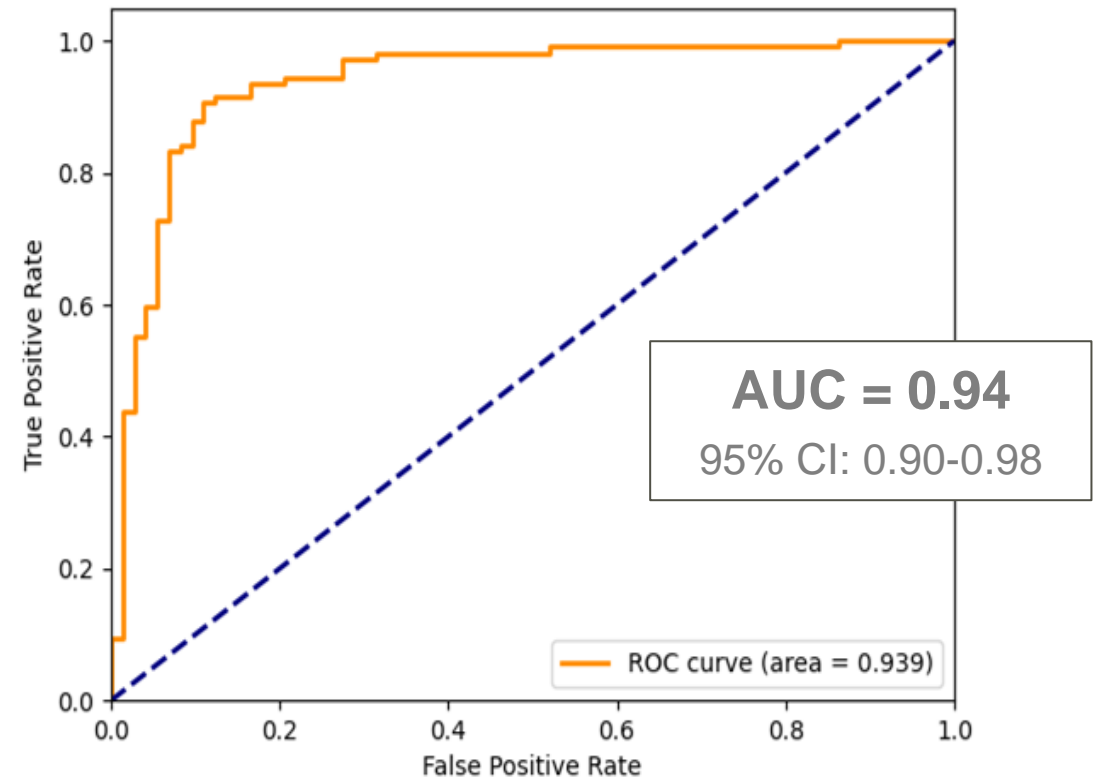
	Number of Cases	Specimen Type	Invasive Ca AUC	DCIS AUC
Sandbank, 2022 <i>Test Set</i>	<b>1998</b>	<b>CNB</b>	<b>0.998</b>	<b>0.999</b>
Sandbank, 2022 <i>Validation set</i>	<b>684</b>	<b>CNB</b>	<b>0.990</b>	<b>0.980</b>
Assaad, 2023*	<b>475</b>	<b>CNB</b>	<b>0.98</b>	<b>0.99</b>
Shaker, 2024*	<b>108</b>	<b>CNB</b>	<b>0.976</b>	<b>0.975</b>
Lami, 2024	<b>100</b>	<b>CNB</b>	<b>0.997</b>	<b>0.975</b>
Broeckx, 2023*	<b>248</b>	<b>Excisions</b>	<b>0.986</b>	<b>0.994</b>

\*meeting abstracts  
Lamy et al, Pathology 2024

# GALEN BREAST PERFORMANCE IN ANOTHER VALIDATION SET TO IDENTIFY IDC VERSUS ILC

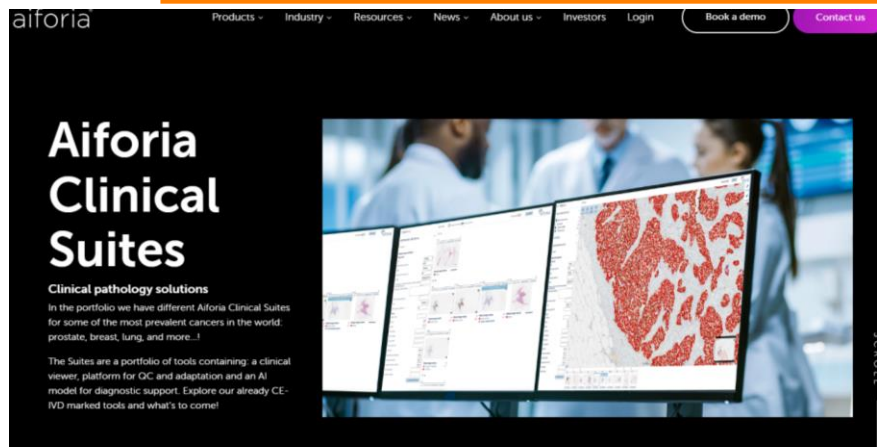
**N= 180 cases (107 IDC; 73 ILC)**

Performance	
<b>Sensitivity</b>	<b>90.7%</b>
<b>Specificity</b>	<b>89%</b>
<b>PPV</b>	<b>92%</b>
<b>NPV</b>	<b>87%</b>
<b>AUC (95% CI)</b>	<b>0.94 (0.90, 0.98)</b>





# AI to quantify biomarkers: many AI tools available on the market



**aiforia** Products Industry Resources News About us Investors Login Book a demo Contact us

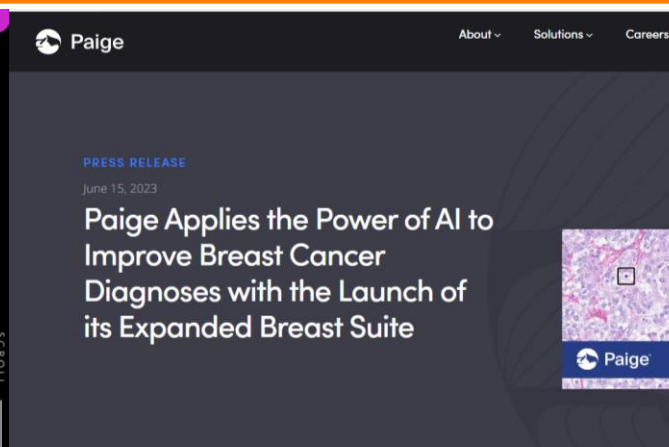
## Aiforia Clinical Suites

**Clinical pathology solutions**

In the portfolio we have different Aiforia Clinical Suites for some of the most prevalent cancers in the world: prostate, breast, lung, and more...!

The Suites are a portfolio of tools containing: a clinical viewer, platform for QC and adaptation and an AI model for diagnostic support. Explore our already CE-IVD marked tools and what's to come!

SCROLL

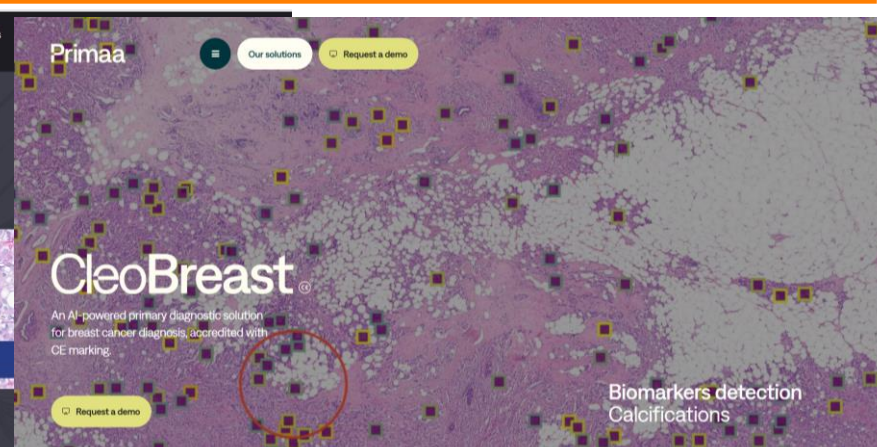


**Paige** About Solutions Careers

**PRESS RELEASE**  
June 15, 2023

## Paige Applies the Power of AI to Improve Breast Cancer Diagnoses with the Launch of its Expanded Breast Suite

Paige



**Primaai** Our solutions Request a demo

## CleoBreast

An AI-powered primary diagnostic solution for breast cancer diagnosis, accredited with CE marking.

Request a demo

Biomarkers detection  
Calcifications



**DiaDeep**

## DiaDeep develops clinical tools to identify the most effective anti-cancer treatment for the best matching patients

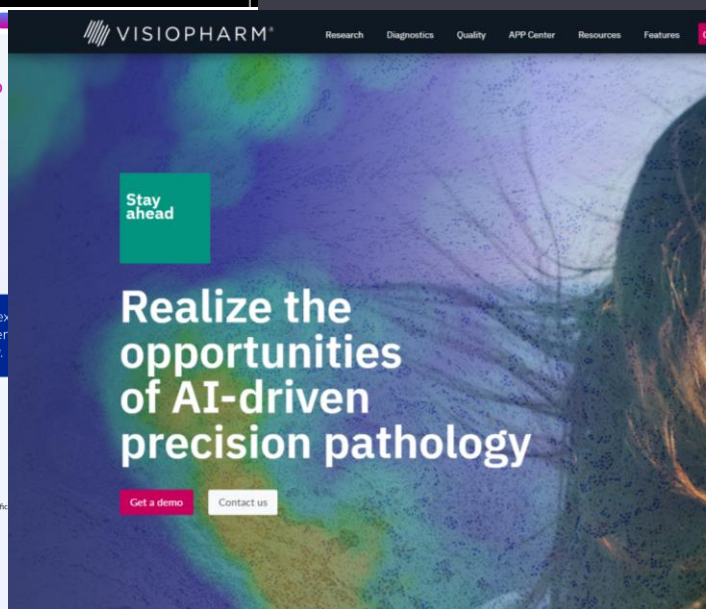
Our technology is designed to generate the most accurate molecular data from histology slides within minutes, which will lead to better diagnosis and treatment of disease.

See more

Patients with cancer might undergo inefficient, ex treatments with significant side effects & other patier chance for an effective targeted therapy.

Identifying the best line of treatment for precision oncology starts with

- Predictive biomarkers
- Treatment identification
- Outcomes prediction

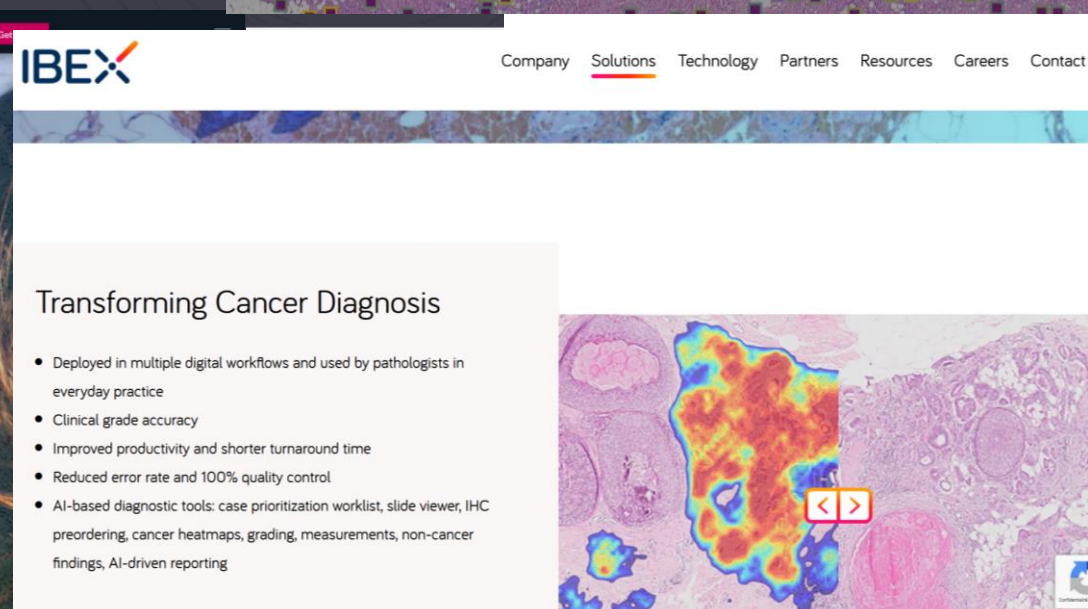


**VISIOPHARM** Research Diagnostics Quality APP Center Resources Features Get

Stay ahead

## Realize the opportunities of AI-driven precision pathology

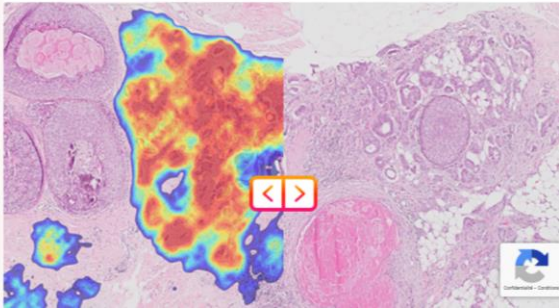
Get a demo Contact us



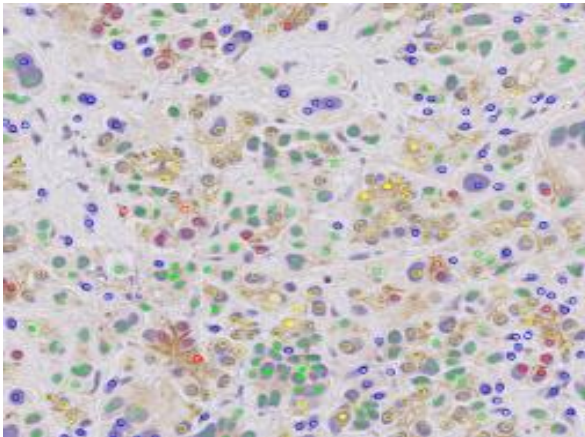
**IBEX** Company Solutions Technology Partners Resources Careers Contact

## Transforming Cancer Diagnosis

- Deployed in multiple digital workflows and used by pathologists in everyday practice
- Clinical grade accuracy
- Improved productivity and shorter turnaround time
- Reduced error rate and 100% quality control
- AI-based diagnostic tools: case prioritization worklist, slide viewer, IHC preordering, cancer heatmaps, grading, measurements, non-cancer findings, AI-driven reporting



## Automatic identification of infiltrating cells + Classification and scoring according to ASCO/CAP guidelines



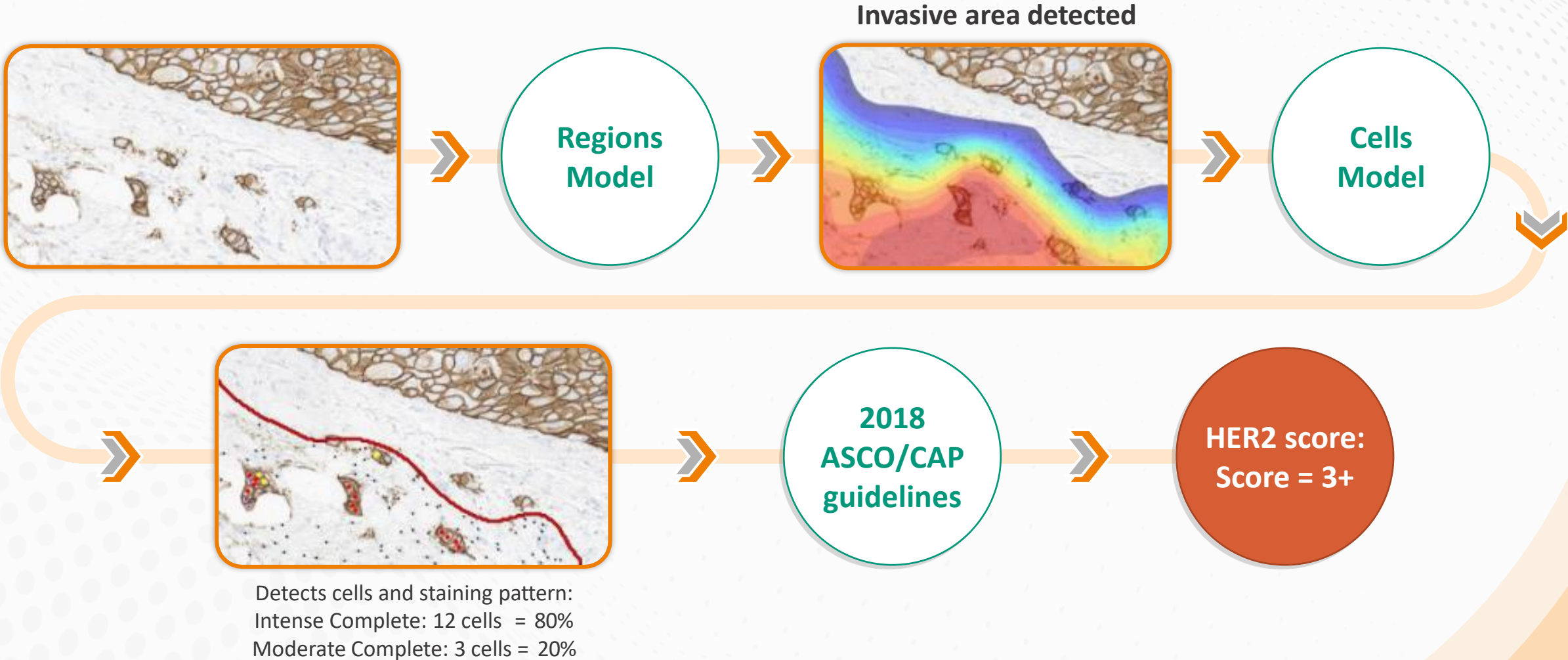
HER2 evaluation at a cell level

- Not invasive
-  Not stained
-  Faint incomplete
-  Moderate incomplete
-  Intense incomplete
-  Faint complete
-  Moderate complete
-  Intense complete

- **Fully automated pipeline.**
- **The pathologist does not select the area of interest**
- **"Transfer Learning Reading" technology uses H&E algorithms to train IHC reading algorithms.**
- **Combining infiltrative versus *in situ* diagnostic analysis and quantification of stainings**



# AI Solution for Evaluation of HER2 Immunostain: IBEX Breast HER2



# Outlines of my talk

---

1- Introduction

2- Diagnosis of breast cancer using AI

3- Prediction of Homologous Recombination Deficiency (HRD) in breast cancers using AI

4- Digital transition of a pathology department

5- Perspectives

## Germline (and somatic) *BRCA1* & 2:

---

- **An approved biomarker for**
  - **TNBC and ER+ HER2- metastatic breast cancers**
  - **High-risk early breast cancers**
- **In the NCCN and ESMO guidelines**



# Detection of *BRCA1* or *2* mutation by a systematic sequencing approach

---

- Is feasible for Triple Negative Breast Cancers:
  - That represent 15 to 18% of all breast cancers
  - Knowing that the identification of a *BRCA1* mutation is found in only 15% of TNBC
- May be difficult to extend to all luminal Breast Cancers because of:
  - The volume & logistics
  - The costs



We aimed at developing an AI algorithm that would predict HRD directly from whole slide images and that could become a **screening tool for triage of tumors more likely to be mutated**

# Collaboration between 3 teams from the Institut CURIE hospital and research center

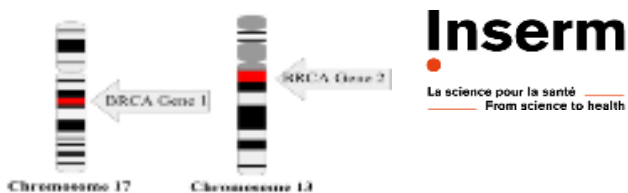
## Pathologists



**BATAILLON Guillaume**  
**VINCENT-SALOMON Anne**  
Department of pathology



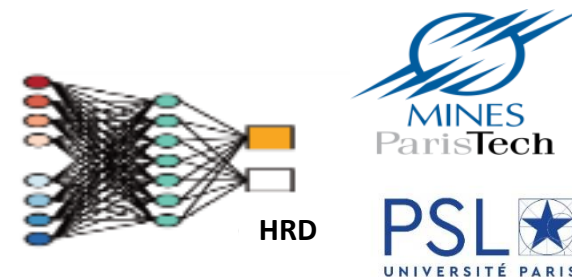
## Geneticists



**STERN Marc-Henri** **STOPPA LYONNET Dominique**  
INSERM U830 Department of genetics



## Computational scientists



**WALTER Thomas**  
**LAZARD Tristan (PhD)**  
INSERM U900



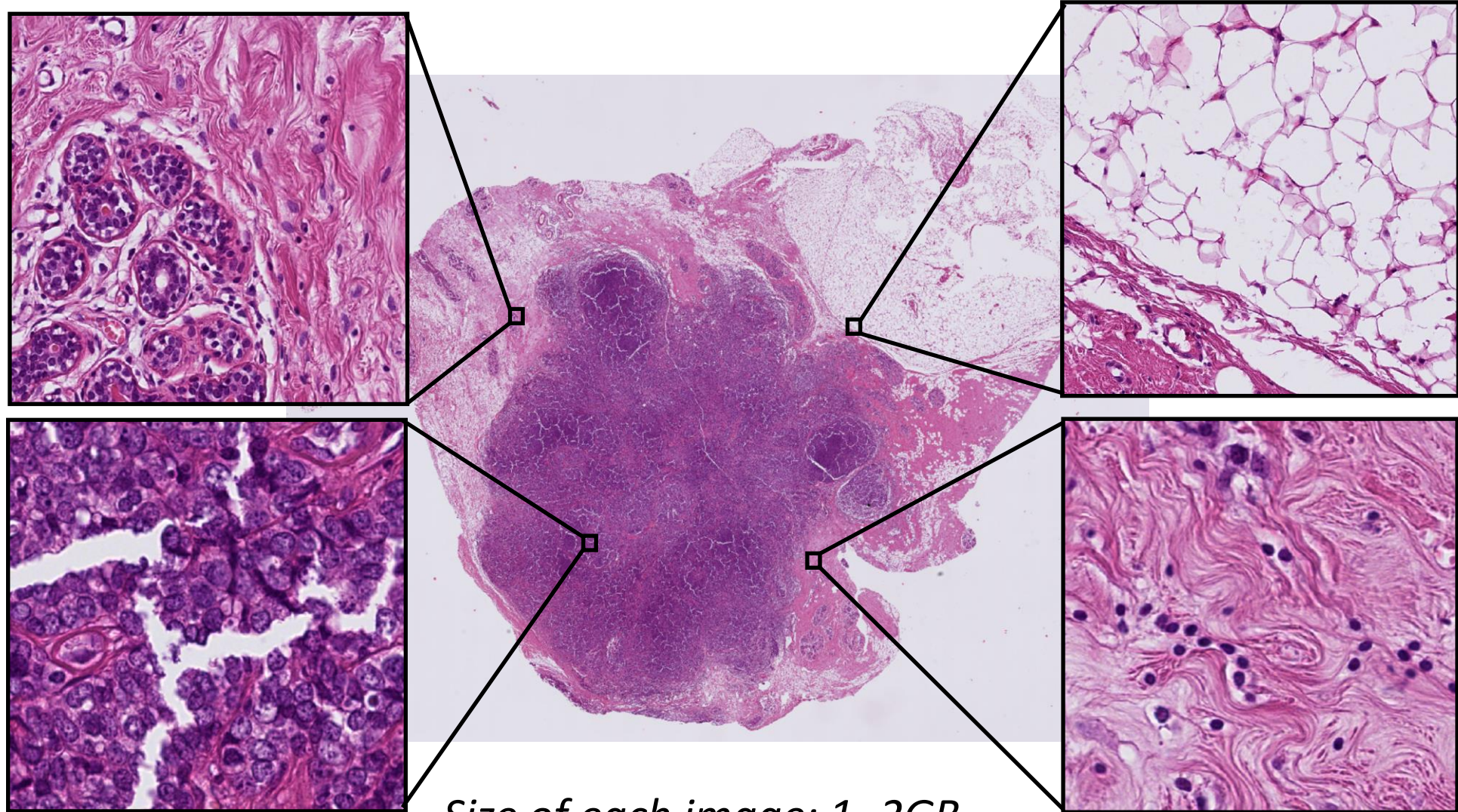
# Two datasets for HRD prediction

---

- **The Curie dataset: 715 of luminal and TNBC breast cancers patients HE slides** (surgical specimens, no neoadjuvant treatment)
- **Known Homologous Recombination status (ground truth):**
  - **309** Homologous recombination proficient (**HRP**) tumors
    - assessed with the Large State Transition (LST) method
  - **406** Homologous recombination deficient (**HRD**) tumors
    - Germline *BRCA1* & *2*
    - Sporadic *BRCA1* & *2* (49 cases)
- **the TCGA dataset:**
  - **800 cases (slides and genomic analyses by SNP6.0)**
  - **Homologous Recombination status determined by the LST method**

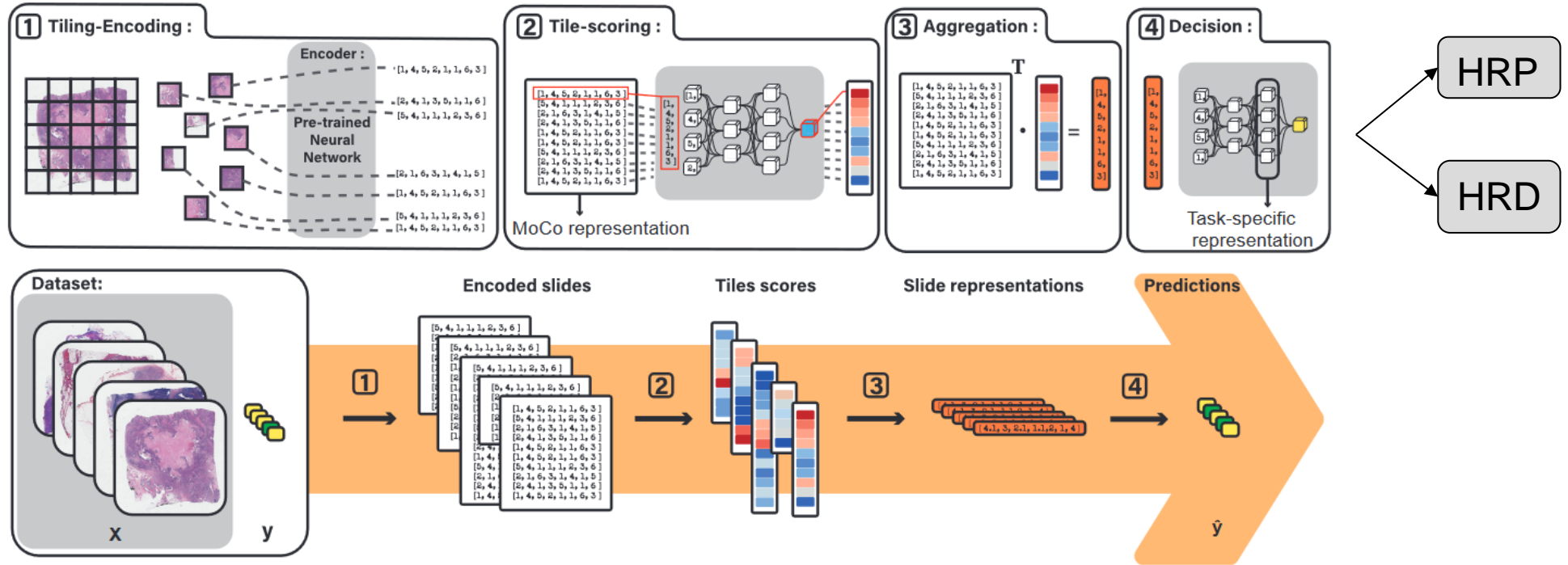


# Computational challenge: one slide = many images



*Size of each image: 1- 2GB  
~ 50.000 images (256x256)*

# Methods: End to End pipeline and Multiple Instance Learning



WSI divided into tile images (224 x 224 pixels)

Tiles are encoded into a vector using the self-supervised technique momentum contrast (MoCo)

The slide representation are classified by the decision module into HRP or HRD



# Performance of the algorithm on the TCGA dataset & the Curie dataset

## Prediction of HRD

	AUC		$B_{Acc}$	
	Mean	SD	Mean	SD
TCGA <sub>raw</sub>	0.71	0.10	0.59	0.08

→ Consistent with previous published analyses showing an AUC = 0.74\*

	AUC		$B_{Acc}$	
	Mean	SD	Mean	SD
Curie <sub>raw</sub>	0.88	0.03	0.81	0.02

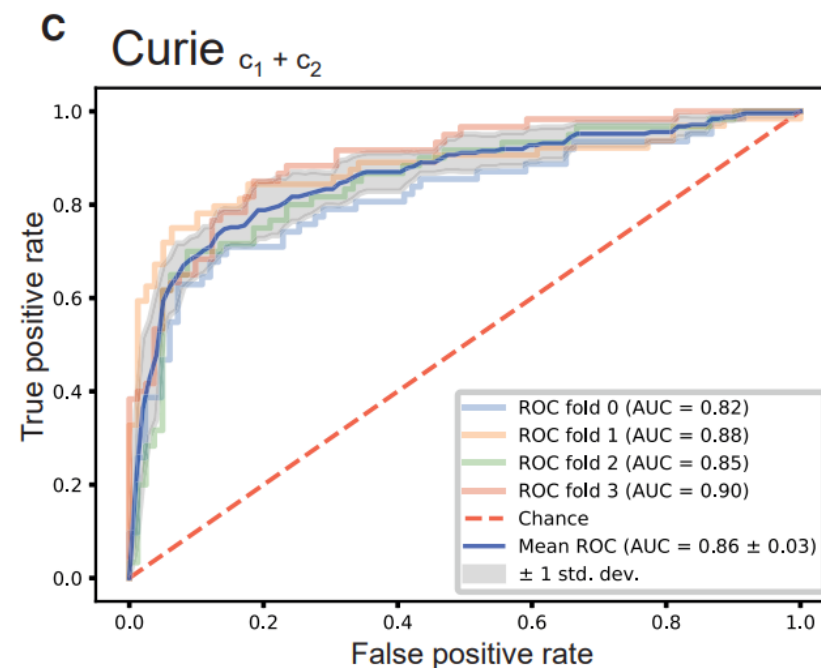
(\*Diao *et al* Nat Com 2021)

# Performance of the algorithm on the Curie series after technical biases correction

Tumor blocks from Curie data set were prepared over a period of 25 years (During this time, protocols for block preparation have changed)

**Table 1. Classification performances**

	AUC		$B_{Acc}$	
	Mean	SD	Mean	SD
Curie <sub>raw</sub>	0.88	0.03	0.81	0.02
Curie $c_1 + c_2$	0.86	0.03	0.78	0.04



The **Receiver Operator Characteristic (ROC)** curve plots the **TPR** against **FPR** at various threshold values and shows the performance of a classification model at all classification thresholds.

# Performance of the algorithm on the TCGA dataset after correction of the biological confounder “molecular class”

Prediction of HRD	AUC		$B_{Acc}$	
	Mean	SD	Mean	SD
TCGA <sub>raw</sub>	0.71	0.10	0.59	0.08
TCGA $c_3^*$	0.63	0.08	0.54	0.02

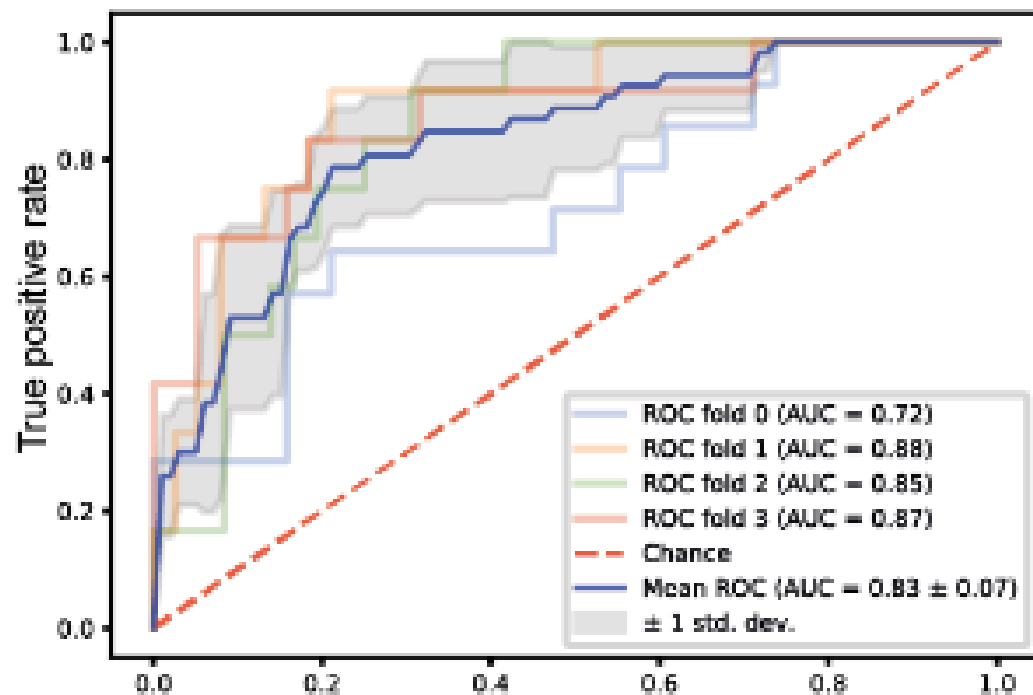
\* $c_3$ : bias of the molecular class

This result suggested that a NN trained on the entire BC cohort of TCGA for HRD prediction without stratification or bias correction might actually predict to a large extent the molecular subtype

Prediction of Molecular classes in the TCGA with our algorithm: AUC = 0.89

# Results for luminal breast cancer patients after correction of technical bias

251 Luminal WSI (188 HRD, 63 HRP)



**AUC = 0.83**

**Sensitivity: 88%**

**Specificity: 57%**

**Positive predictive value: 86%**

Ground Truth = genomic status  
Luminal (n= 251)

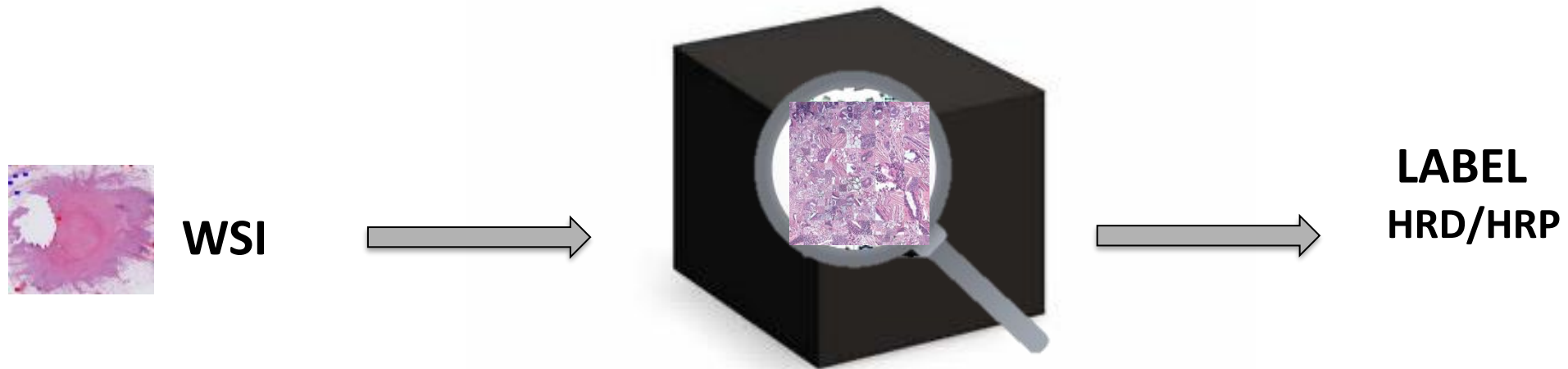
AI Prediction	HRD	HRP
HRD	166	27
HRP	22	36
<b>Total</b>	<b>188</b>	<b>63</b>



# Opening the black box for pathologists is important !

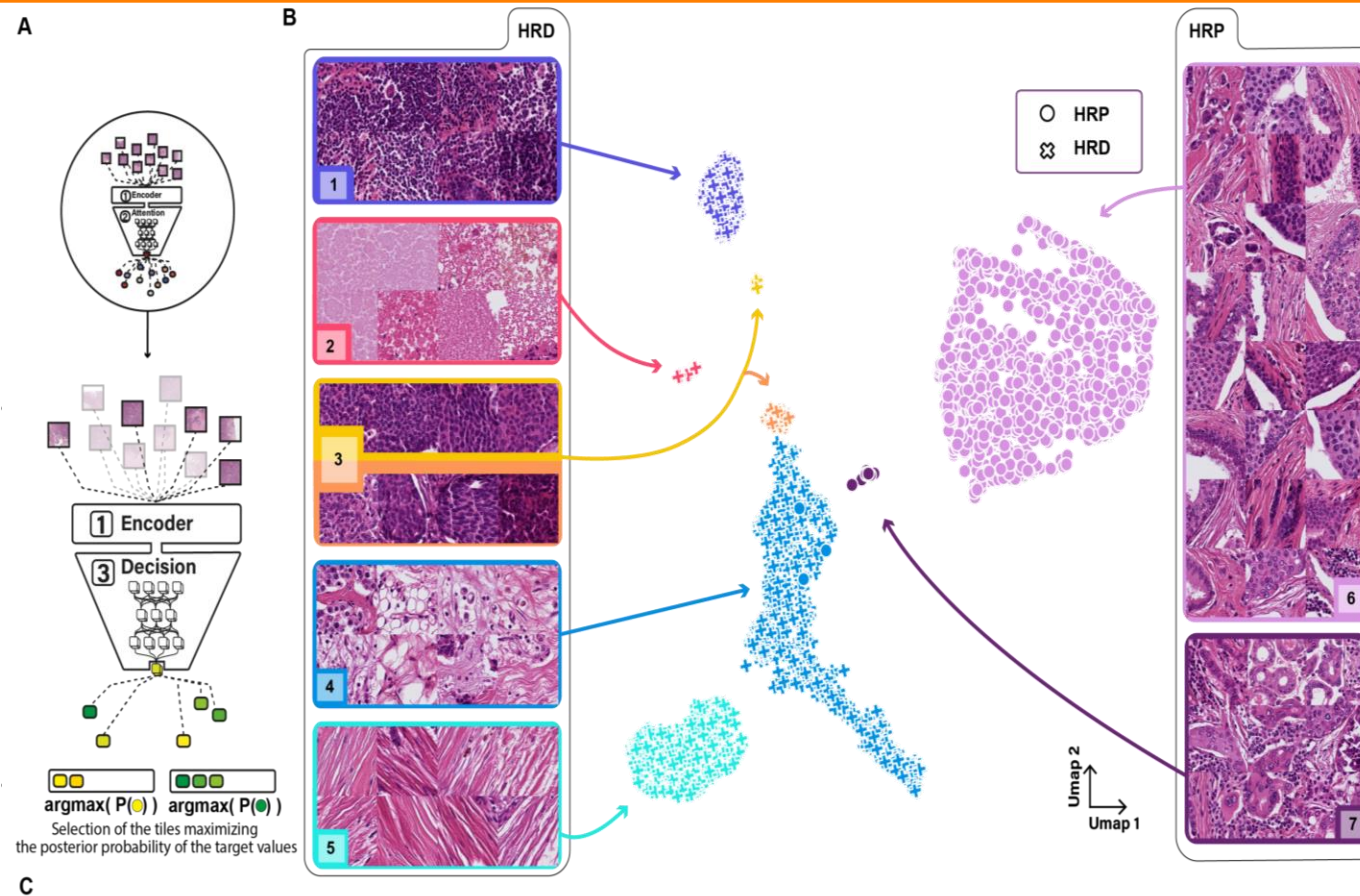
---

To visualize and understand the TILE features that weighted in the algorithm and that weighted the most to predict the label



- To pave the way for MACHINE TEACHING !

# Visualization of TILE features that weighted in the algorithm



Clusters corresponding to different tumors tissue pattern with a clear relation with HRD or HRP

**1** High density of Tumor Infiltrating Lymphocytes TILs

**2** Hemorrhagic suffusion associated to necrotic tissue

**3** Basal/hyperchromatic carcinomatous cells with nuclear atypia

**4** Adipose tissue with inflammatory changes associated with clear tumor cells

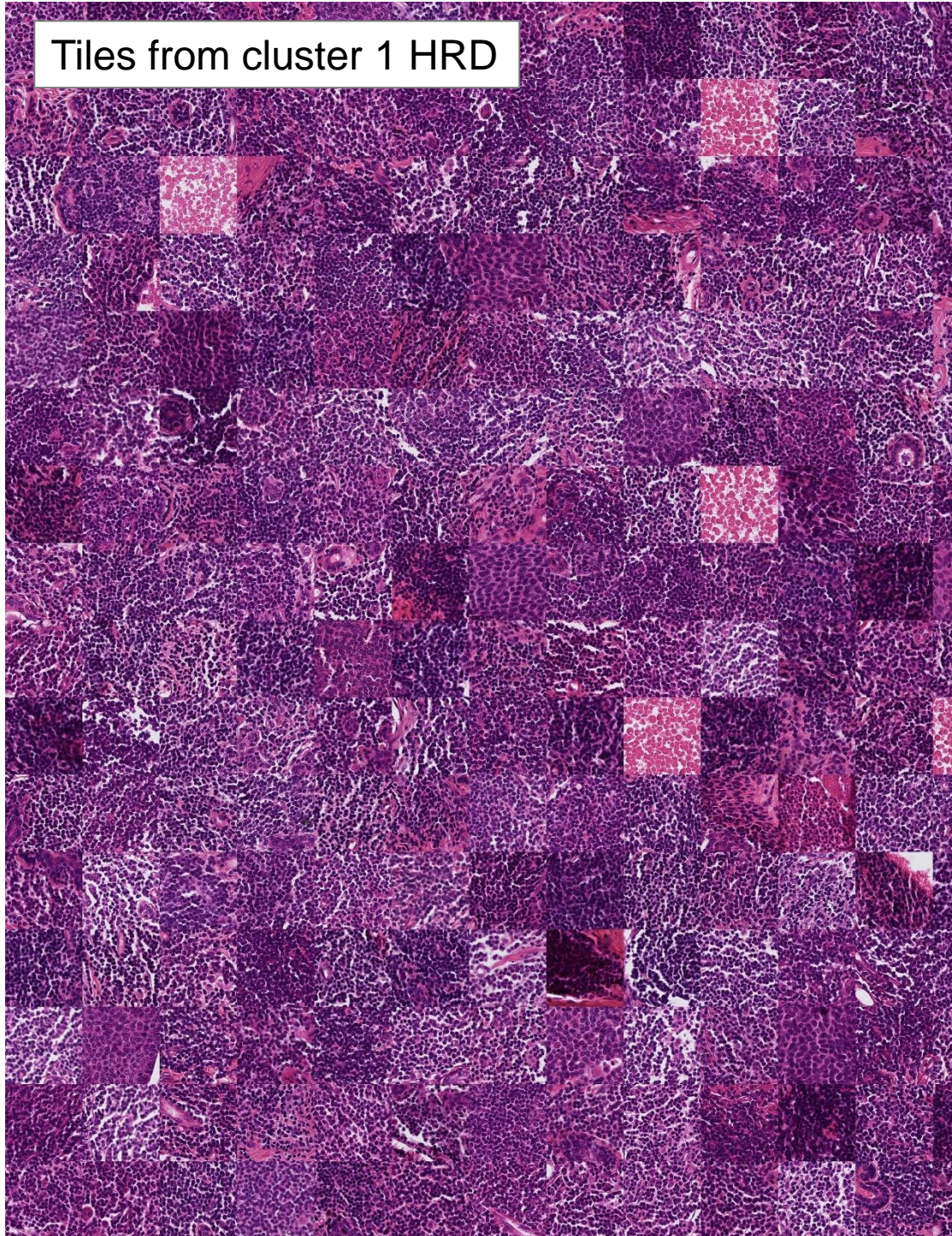
**5** Laminated fibrosis

**6** Low tumor cell density and clear spaces around cell nests

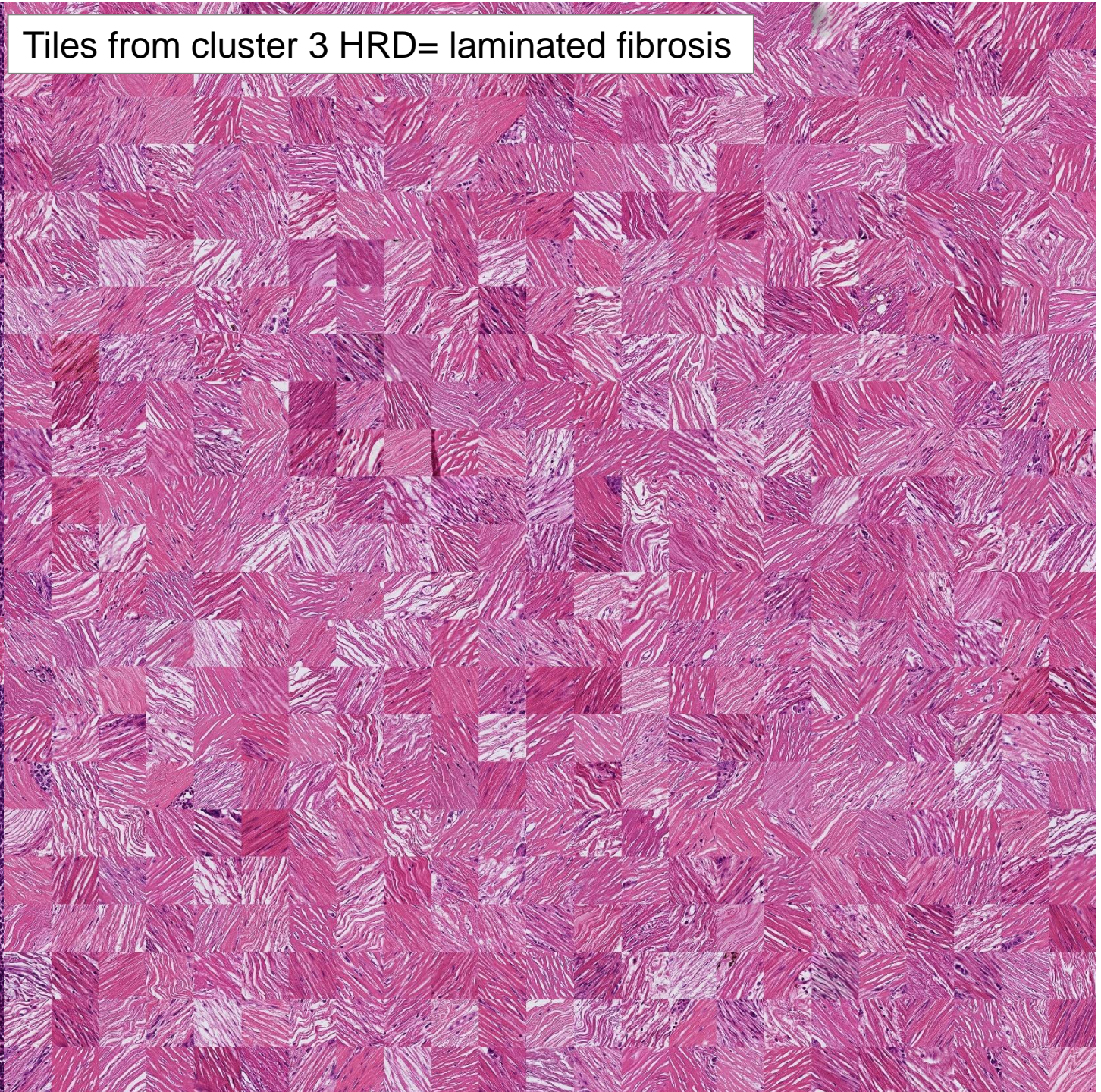
**7** Clear space surrounding apocrine cell nests



Tiles from cluster 1 HRD



Tiles from cluster 3 HRD= laminated fibrosis





**Deep learning identifies morphological patterns of homologous recombination deficiency in luminal breast cancers from whole slide images**

Graphical abstract

Authors

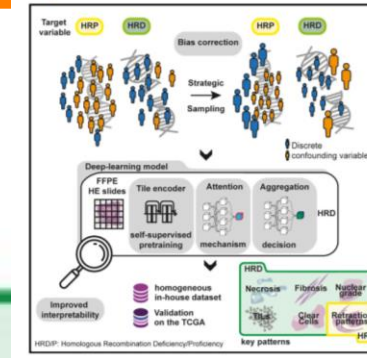
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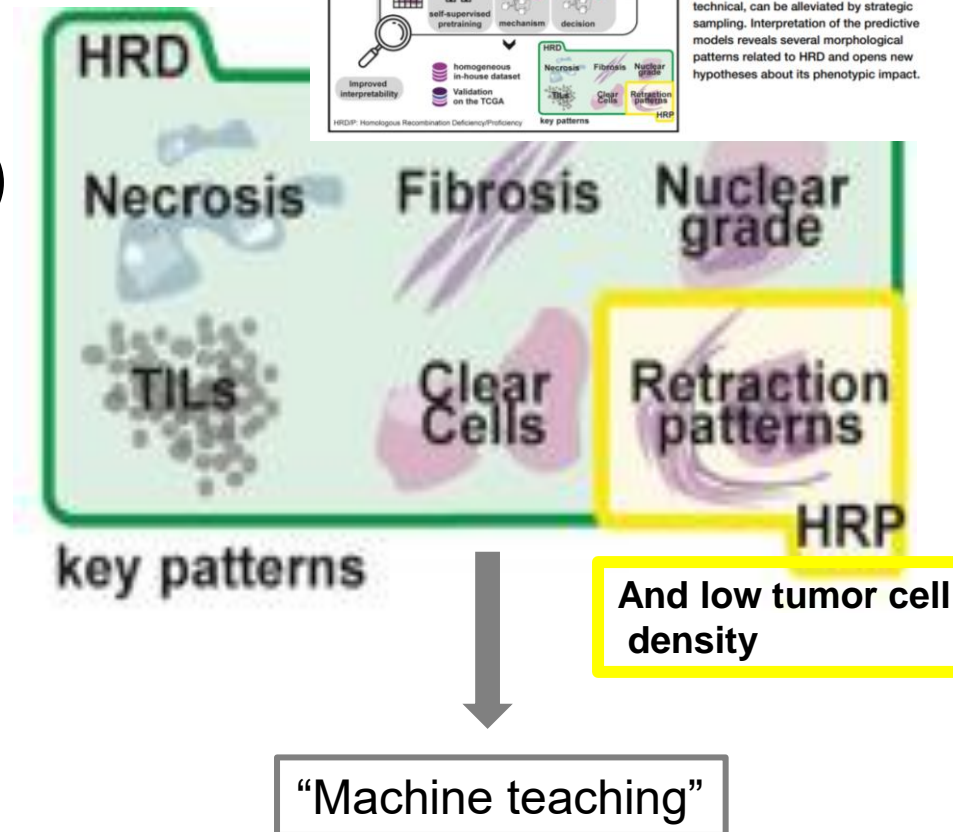
In brief

Deep-learning models predict homologous recombination deficiency (HRD) from H&E-stained pathology slides. Dataset biases, either biological or technical, can be alleviated by strategic sampling. Interpretation of the predictive models reveals several morphological patterns related to HRD and opens new hypotheses about its phenotypic impact.



## Conclusions from this study

- Homologous recombination deficiency is predictable from H&E slides with high accuracy (0.83)
- **Biases** in computational pathology data can be alleviated by strategic sampling (the method of choice)
- We identified five HRD and two HRP-related morphological patterns  
→ A biological in vitro validation needed before using it





## Future steps:

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- Validation with external cohorts is on going
  - PhD Thesis of dr Raphaël BOURGADE (CHU de Nantes, France, Dr Loussouarn)
  - under the supervision of Prs Walter (INSERM 900 & Ecole des Mines-PSL University, and myself)
- It will be soon applied on HES from our patient Institut CURIE



# Outlines of my talk

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1- Introduction

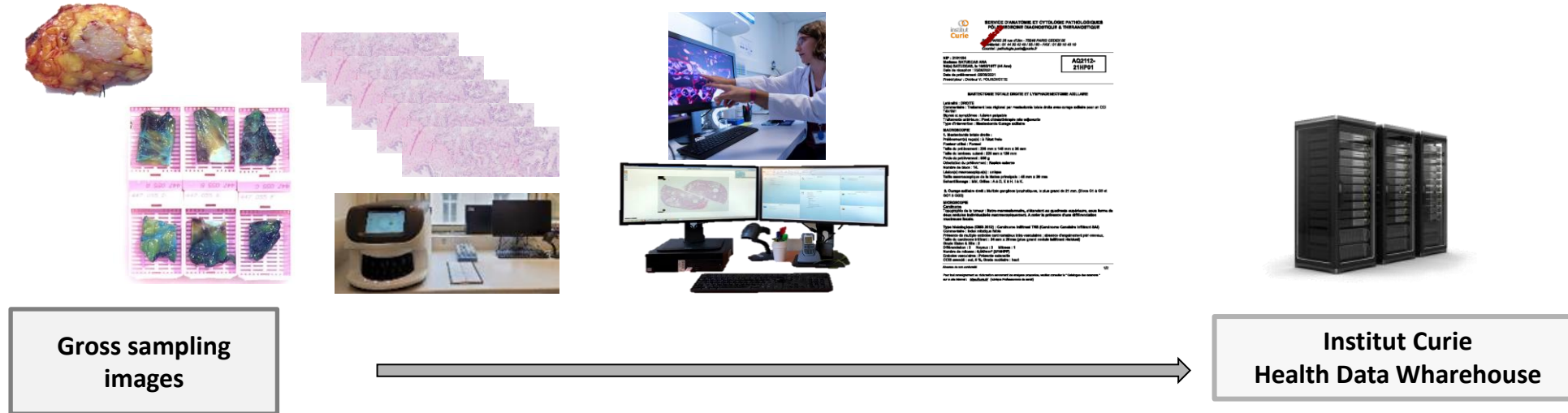
2- Diagnosis of breast cancer using AI

3- Prediction of Homologous Recombination Deficiency (HRD) in breast cancers using AI

**4- Digital transition of a pathology department**

5- Perspectives

# Transition to a digital lab at Institut Curie, France: from gross sampling to an Health Data Warehouse



- 1- It's a long process
- 2- This transition needs perseverance
- 3- The success of the digital transition: it's a team success
- 4- Integration of AI tools is an additional challenge

# Successful Digital Transformation of a pathology department

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- **Take the time to define the needs** adapted to our practice
  - **Associate the team, pathologists and technicians, to choose scanners and IMS**
  - **Human resources needed to set up the project (IT department and in pathology)**
  - **Distribution of the glass slides in parallel to the digitalized slides to let the time to pathologists to get used to digitalized slides (for 6 months)**
  - **Anticipate the Storage needs (costs +++)**
    - “Short-term” storage: 220 To (approx. 10 weeks workload)
    - “Long-term” storage: 25 To/year (approx. 1 slide/sample)
  - **IT Security issues & interoperability of the LIMS & IMS, solved thanks to the Data Protection Officer and the IT department**
  - **Financial and institutional support**
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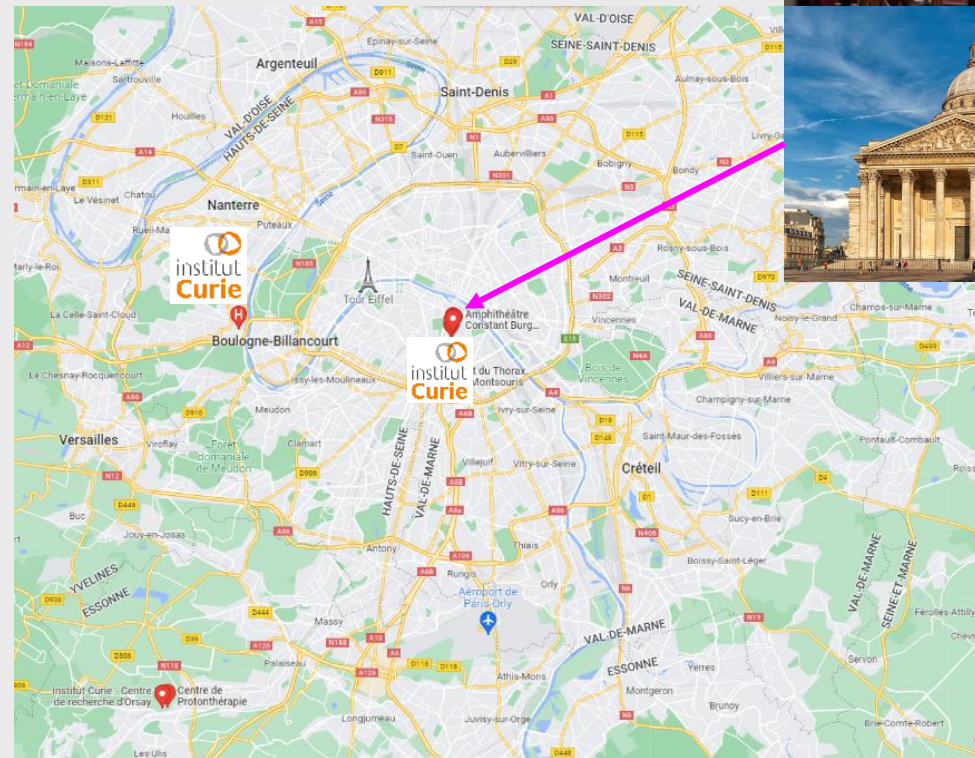




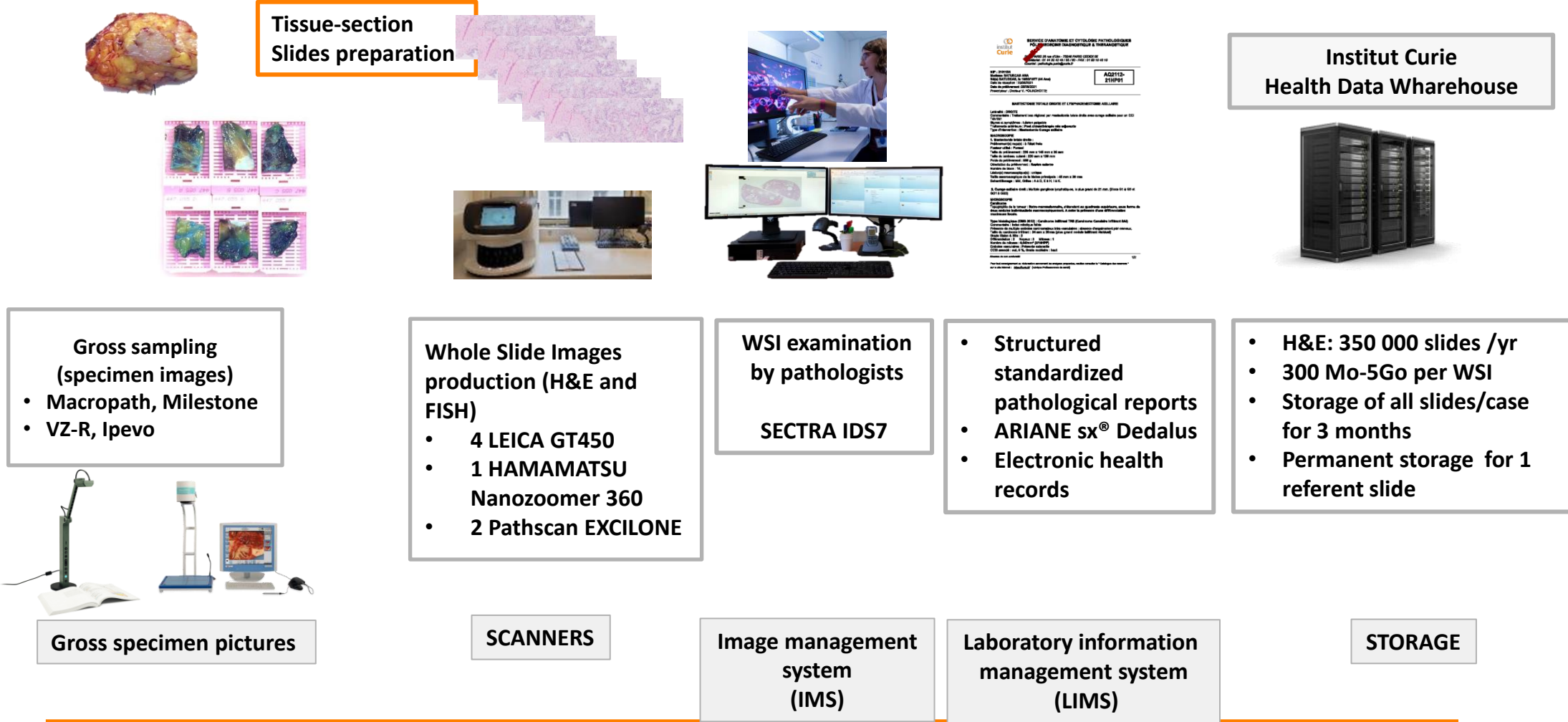
- **2 pathology units**
  - one in St CLOUD west part of Paris; and one in the Center of Paris
  - within one hour of public transportation

- **> 1600 slides per day**

- **The team = 20 pathologists**

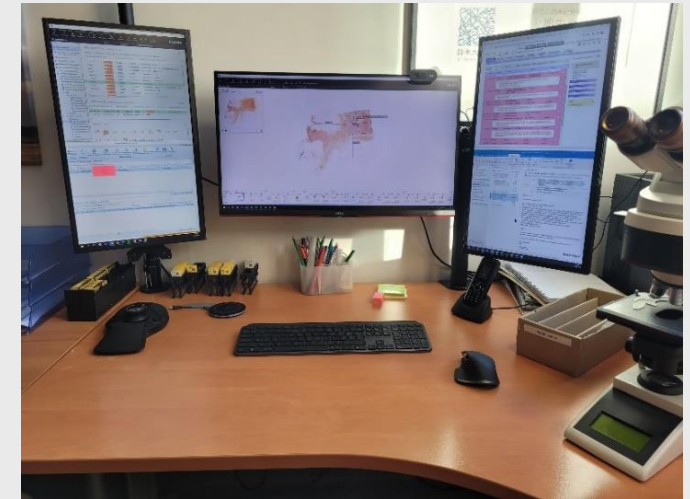


# Implementation of digital pathology for diagnosis at Institut Curie



- **Specifications provided by SECTRA (IMS editor)**

- Infrastructure
  - **Bandwidth**
  - **Latency**
- Workstation
  - **Processor**
  - **Graphics card**
  - **Monitors**
    - Resolution
    - Refresh rate



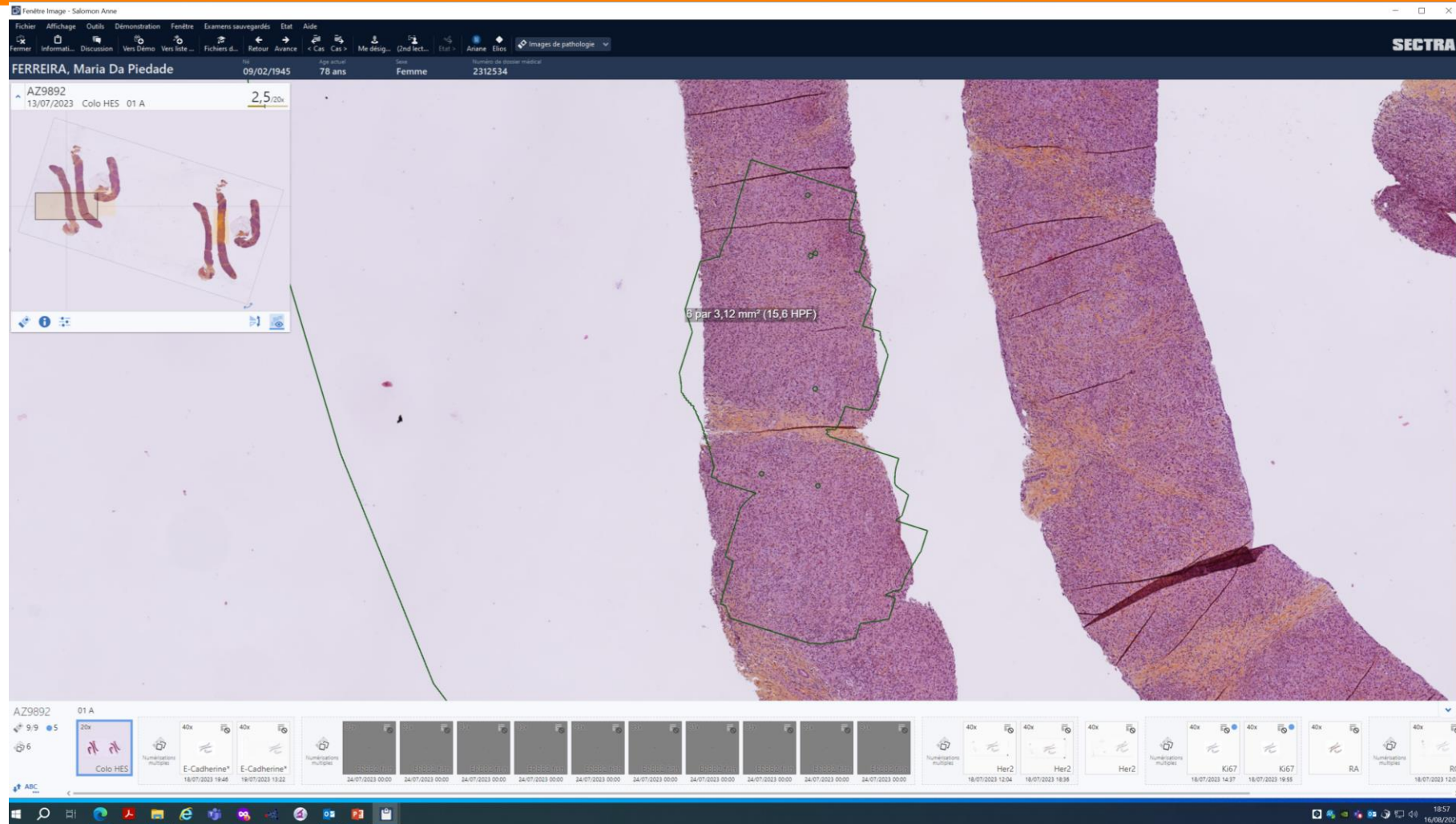
- **Choice by the pathologists**

- 3D mouse
- Screen choice (price, quality of the image and confort)





# Mitotic count: IDS7 by Sectra makes it easy to do !





# Evaluation of KI67 using the Sectra tool

The screenshot displays the Sectra software interface for image analysis. The main window shows a histological image of a tissue section with KI67 staining. A circular region of interest is highlighted, and the software's analysis tool is visible on the left side of the screen. The tool includes a selection area, a count of cells (13/40x), and a panel for adjusting the analysis parameters.

**Index KI67**

Sélectionner une zone

Nombre de cellules:

100 200 500 1000 2000

Choisissez le nombre de cellules à compter et placez le cercle sur le hotspot que vous souhaitez calculer.

**Corrigez le résultat**

Types de cellules visibles:

Tout  Positives  Négatives

Pour basculer entre l'affichage de toutes les cellules, des cellules positives seulement et des cellules négatives seulement pour une aide visuelle, appuyez sur Espace.

**Mode édition:**

Ajouter/basculer  Effacer

Ajouter nouveau type ou basculer entre types de cellules détectées en cliquant. Maintenir Ctr+1 enfoncé et cliquez ou tirez pour effacer des cellules.

6.8% (34 sur 500 sont positives)

AZ5590 01 A

6:7 4 40x 40x 40x 40x 40x 40x

Colo HES E-Cadherine\* Demande ERBB2 fish Her2 Ki67 RO RP

IDS7; Sectra

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5- Conclusions

## Conclusions (1)

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- Numerous algorithms are currently being developed by start-ups or academic research labs together with pathologists and to help pathologists:
  - For the diagnosis of breast cancer and axillary lymph node metastasis,
  - To increase reproducibility in biomarkers assessment,
- Economic models for the application of AI remains to be identified in many countries
- The generalization of digital transformation for pathology labs is needed for the use of AI, and is underway.
- Breast pathologists will use AI if it's **easy to use, time-saving, highly accurate and if it's facilitate their work !**

## Conclusions (2)

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- Computational pathology: a dynamic field that makes fast technological progresses
- Algorithms before their use into clinical practice have to solve **bias** issues, their availability on the market takes time.
- Common responsibility between computational scientists and pathologists to develop performant and robust tools to facilitate our work and to better diagnose our patients
- Long term collaboration between pathologists and computational scientists
- From academic research to clinical practice: who does fill the gap?  
→ Efficient tech transfer



# Foundation models: can determine the biomarkers status without any immunos

- Creation of large-scale deep neural network
- Trained on very large data sets (> 1 million slides)
- Algorithms named “self supervised” that do not necessitate pathologist annotations
- Diagnose frequent as well as rare cancers
- Can predict biomarkers

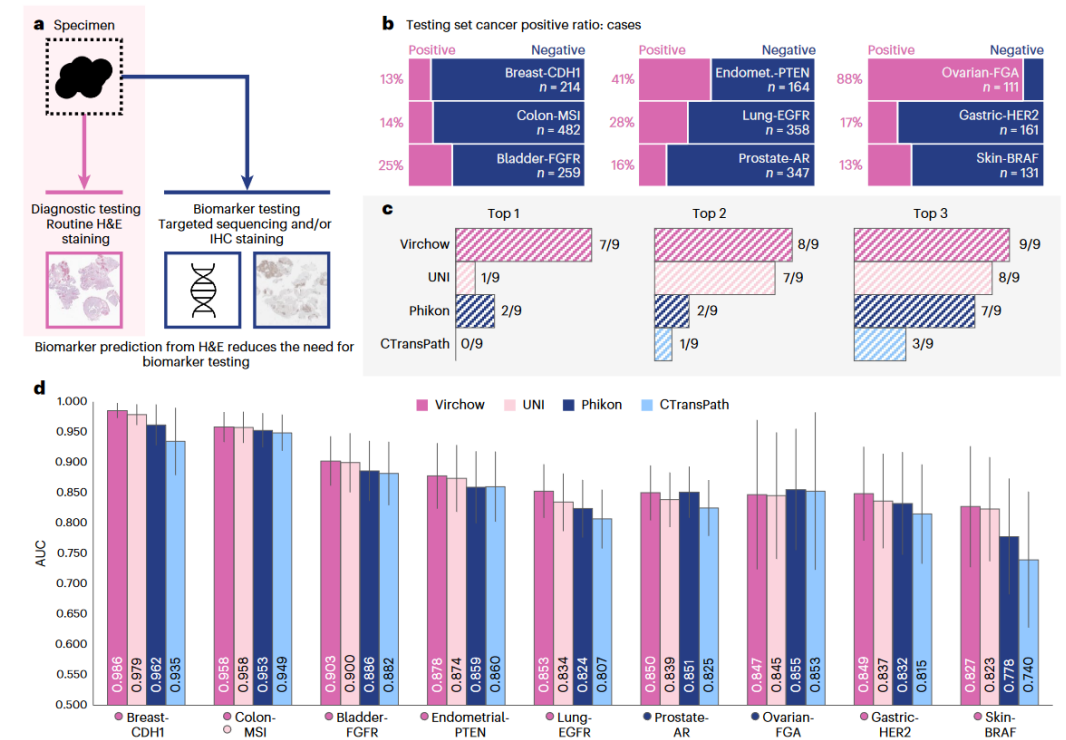
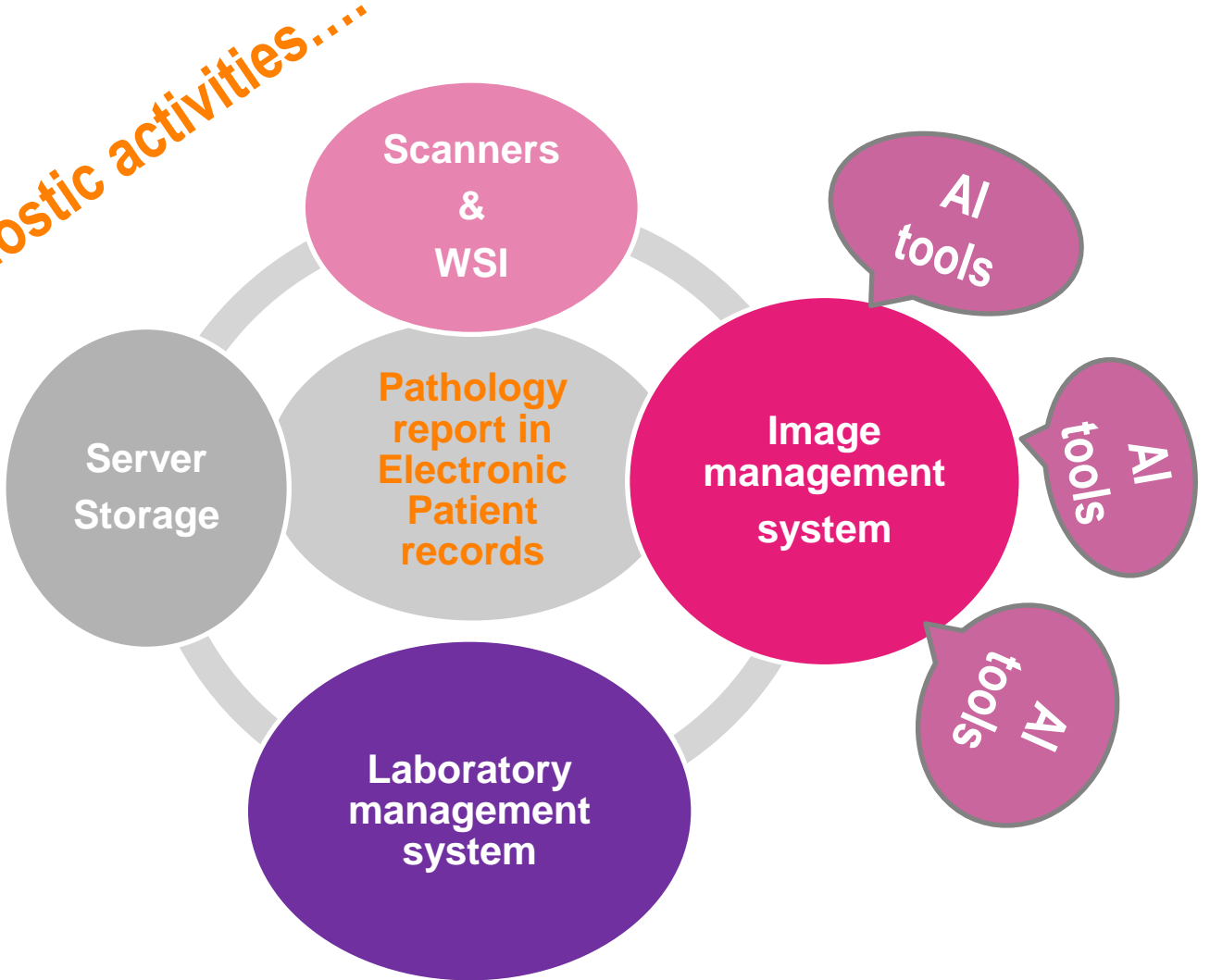


Fig. 4 | Biomarker prediction results. a, Virchow embeddings help predict the ranking across many biomarkers. d, Biomarker detection performance as

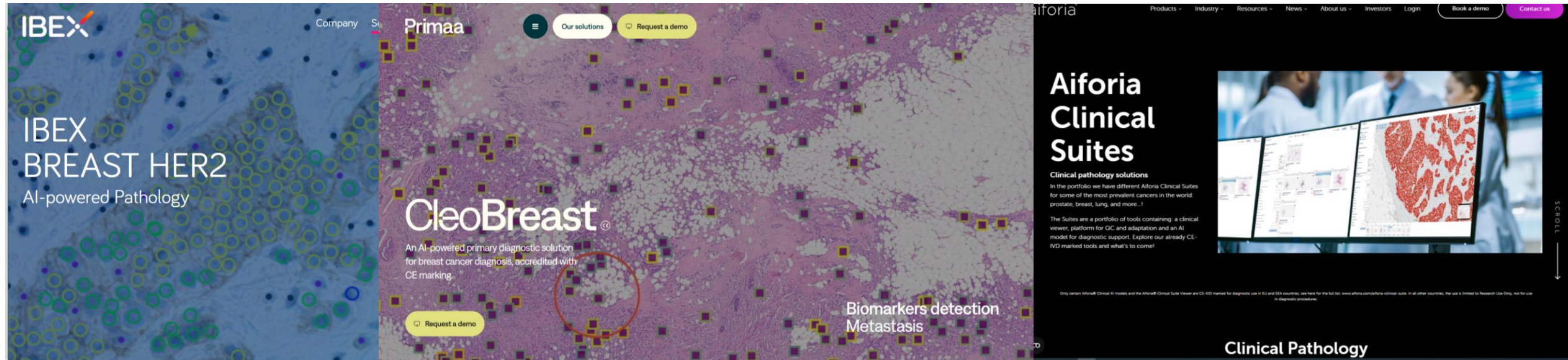
# AI IN BREAST PATHOLOGY TO ASSIST THE PATHOLOGISTS FOR DIAGNOSTIC ACTIVITIES

BREAST (core needle biopsies and surgical specimen)	lbex	Prima	Aiforia
	Galen Breast	Cleo Breast	Breast Cancer Clinical Suite
Invasive carcinoma	available	available	available
DCIS	available	available	available
architecture score	planned	unavailable	available
Nuclear grade	available	planned (Q1 2025)	available
Identification of mitosis and mitotic score	-	-	available
Identification of $\mu$ cal	-	available	available
Vascular invasion	-	available (CE label on going)	available
Axillary metastasis	planned	available	-
ER quantification	planned	planned (Q1 2025)	available
HER2 quantification	available	planned (Q1 2025)	available
KI67 quantification	-	planned (Q1 2025)	available
TILS quantification	available	planned (Q1 2025)	-

Today, one AI solution does not fit to all diagnostic activities.....



# At Institut Curie:



Ibex prostate and Breast  
go live next week !

In January 25

In June 25

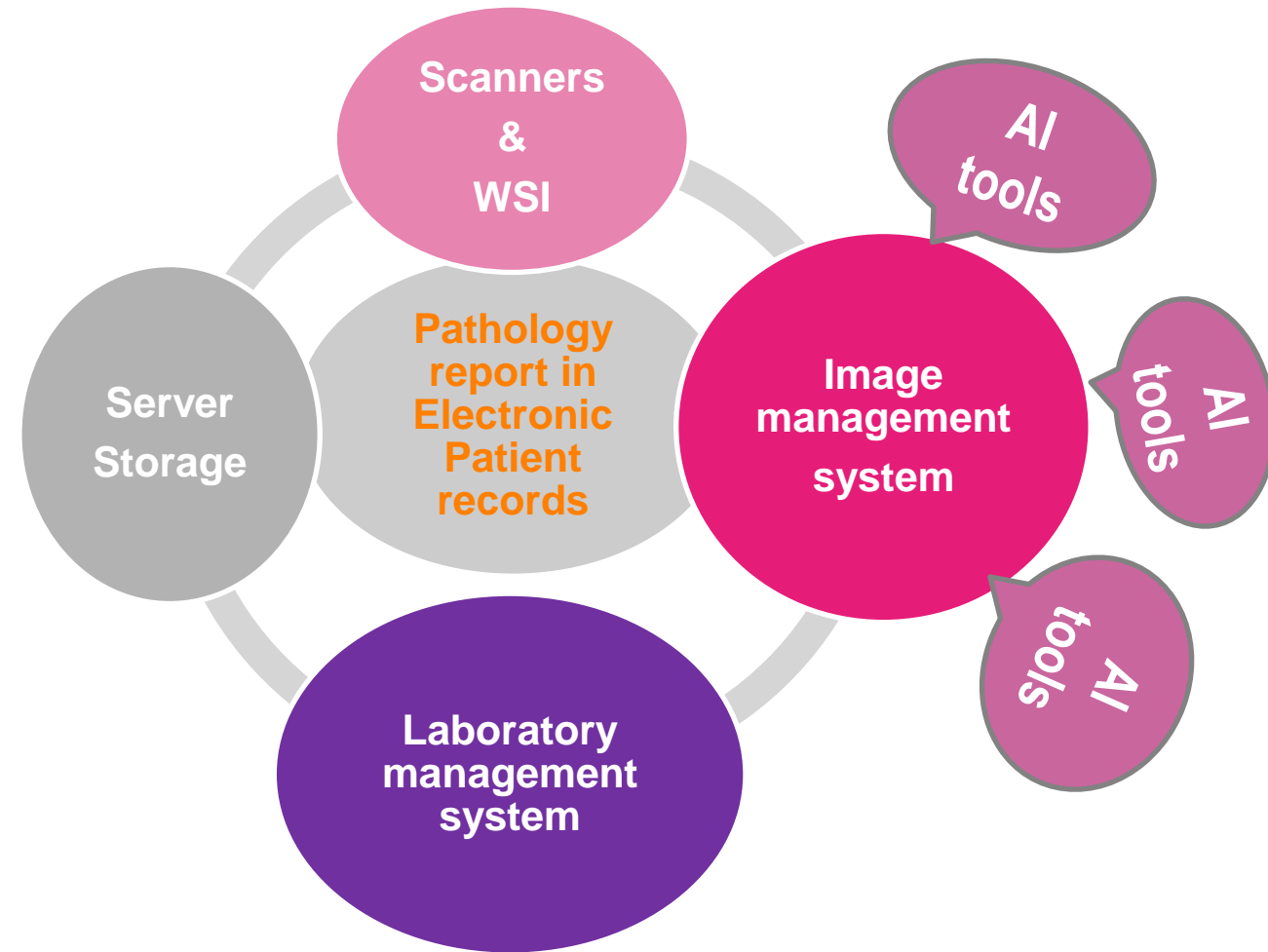
- We will welcome a master student in social sciences & economy who will help us during one year
- To evaluate the ergonomics of each tool, to list tasks performed by the solution
  - To summarize all steps needed to acquire and deploy an AI tool in a hospital
  - To identify the security issues and the IT requirements to implement the tools
  - To evaluate the cost and the benefit of using these AI tools



# CONCLUSIONS & TAKE HOME MESSAGES

## AI solutions in breast pathology

- **INTEROPERABILITY:**
  - Between informatics tools to set up digital pathology (Dicom format is becoming the standard)
- **SECURITY issues:** AI solutions accessible from clouds or on premise
- **ERGONOMY:** AI tools should be easy to use for pathologists
- **AI TOOLS ROBUSTNESS:** Involvement of pathologists; Control the bias; External validation
- **HUMAN GUARANTEE !**



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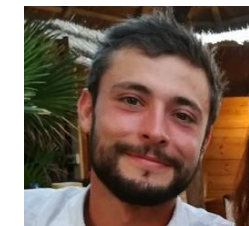
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**LAZARD Tristan (PhD)**  
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