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Are all invasive lobular cancers the same?

Expert: **Prof Frederique Penault-Llorca**, Jean Perrin Center, Clermont-Ferrand, France

Discussant: **Dr Simona Volovat**, Grigore T. Popa University of Medicine, Iasi, Romania

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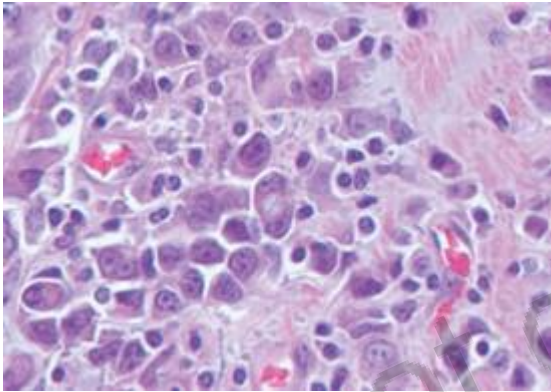
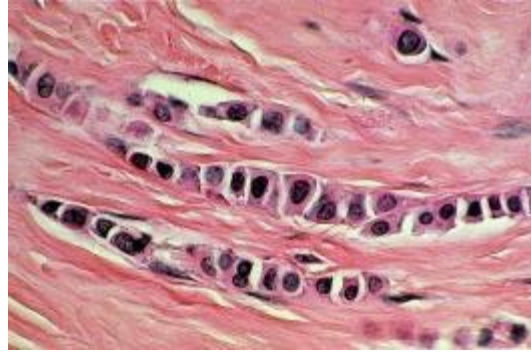
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Are all invasive lobular cancers the same?



Frédérique Penault-Llorca MD, PhD

COI: Pr Frédérique Penault-Llorca

Personal:

- AbbVie, AstraZeneca, Bayer, BMS, Daiichi Sankyo, Genomic Health, Gilead, GSK, Lilly, MERCK lifa, MSD, Myriad, Nanostring, Novartis, Pfizer, Pierre-Fabre, Roche, Seagen, Tesaro

Institutional:

- Abbvie, Agendia, AstraZeneca, Bayer, BMS, Genomic Health, MSD, Myriad, Nanostring, Roche

Congress Invitation:

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Objectives

- To understand the specificities of invasive lobular carcinoma
- To understand the heterogeneity of invasive lobular carcinoma in terms of
 - Morphology
 - Biology
 - Therapeutic opportunities

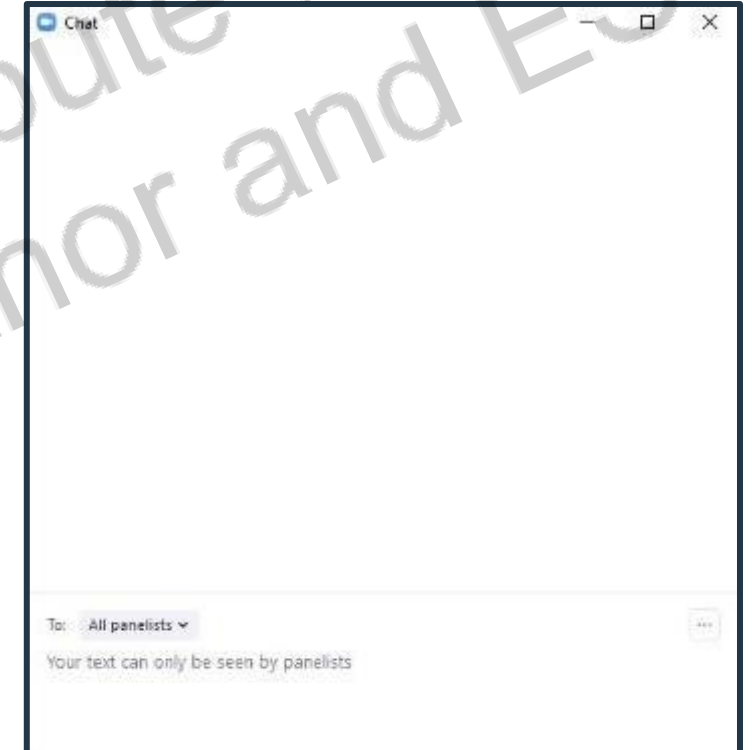
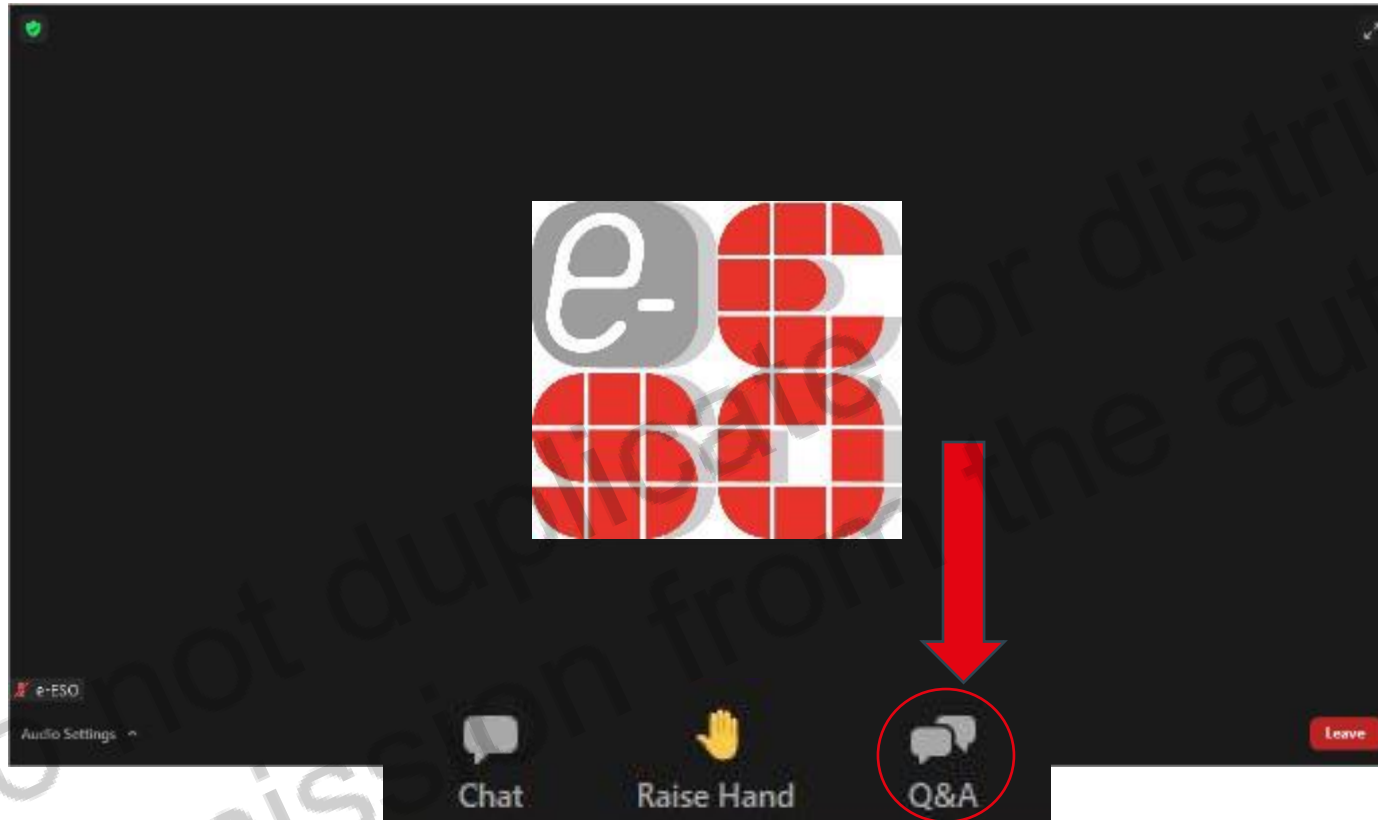


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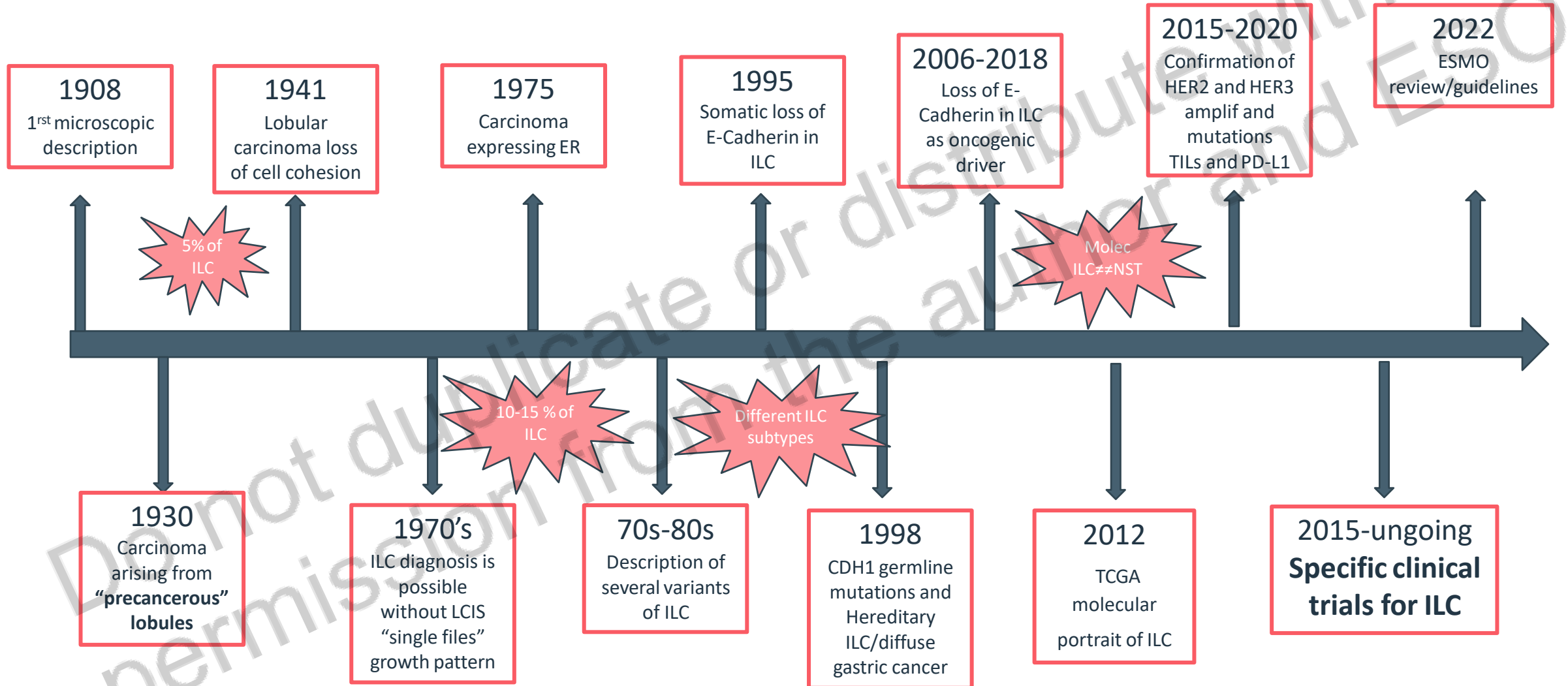


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Lobular carcinoma: the most frequent special histopathological type of breast cancer

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Evolving landscape of ILC



Clinicopathological features

- ILC is the **most common special type** of BC [WHO classification of tumors of the breast (5th edition) 2019]
- **10–15%** of all BC cases, less common in Asian populations (2–6%)
- **Different clinical presentation** from BC of no special type (NST BC): associated with
 - higher patient age, higher pT stage, higher nodal stage, lower histological grade, and over-represented in bilateral and primary metastatic BC
 - Lower rates of pathological complete response to neoadjuvant chemotherapy,
 - Higher rate of positive resection margins
 - a **distinct pattern of metastatic dissemination**: metastasis to the digestive tract, ovaries, bones, leptomeningeal, orbital soft tissue, and skin less CNS, lung metastasis
 - Higher rate of multiple metastases compared to other BCs

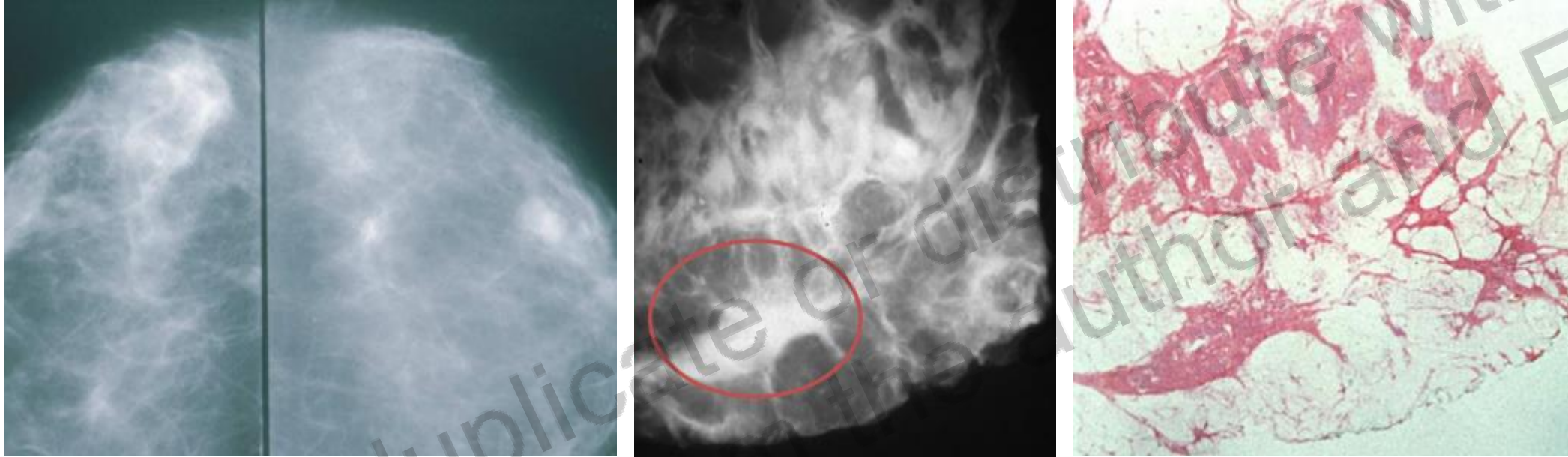
Clinicopathological features

- **Different biology/NST BC:** different mutational characteristics including **E-Cadherin mutations**, different DNA copy numbers, different gene expression profiles, and tumor microenvironment
- **Different subtypes of ILC** with different morphology, prognosis, molecular alterations possibly impacting therapy

Clinical features

Histopathology

Clinical presentation



- ILCs are generally palpable, a **high false-negative mammography rate** is possible
- More often **larger tumour, multifocal and bilateral** and with nodal involvement
- **More frequent late relapses**, frequently occurring >10 years after diagnosis



Risk factors

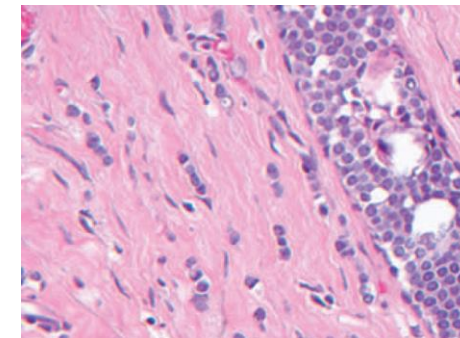
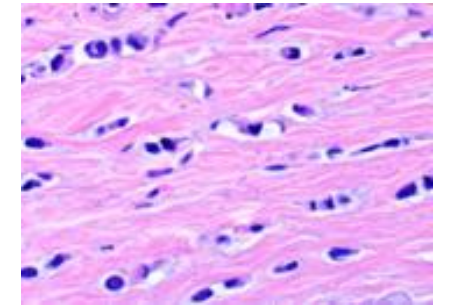
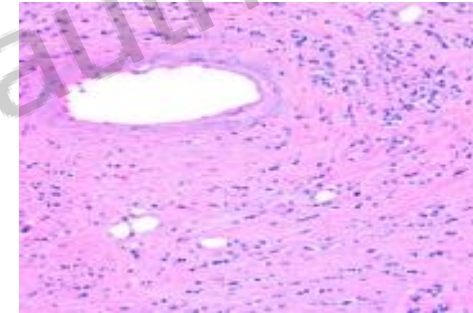
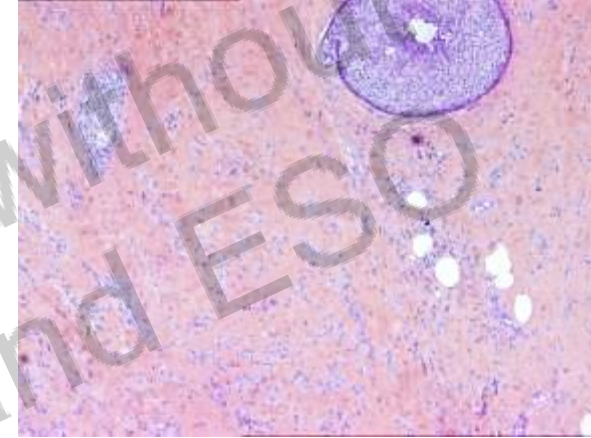
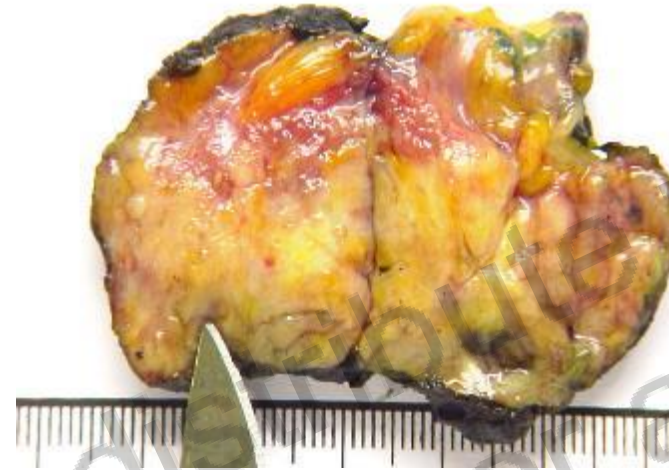
- **Estrogen related:** Early menarche, use of progesterone-based HRT, late age at first live birth and alcohol consumption are more strongly associated with the risk of developing ILC as compared to NST.
- **Obesity** in postmenopausal women does not seem to affect the risk of developing ILC over NST
- **High risk germline mutations: BRCA2 and CDH1** (the gene coding for E-cadherin)
- Moderate risk germline mutations: ATM, CHEK2 and PALB2
- No clinically relevant risk germline BRCA1 mutations
- **Classically absent in males** (exceptional cases in BRCA2 and CDH1 mutation carriers)

<https://doi.org/10.1016/j.annonc.2022.05.006> ; DOI: 10.3389/fonc.2022.891426

Classical ILC

Classical ILC (70%)

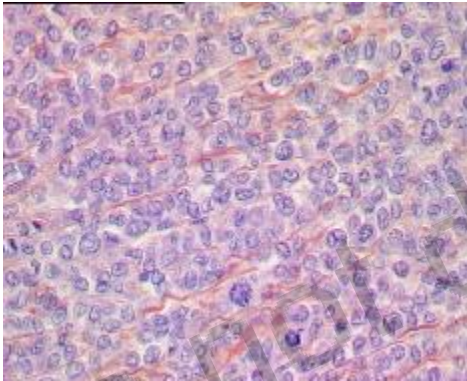
- **Single cell infiltration** and a characteristic targetoid pattern of growth with minimal associated stromal response.
- This pattern of subtle invasion is such that **the size of the tumour often exceeds the imaging findings** and **obtaining clear surgical margins may be challenging**.



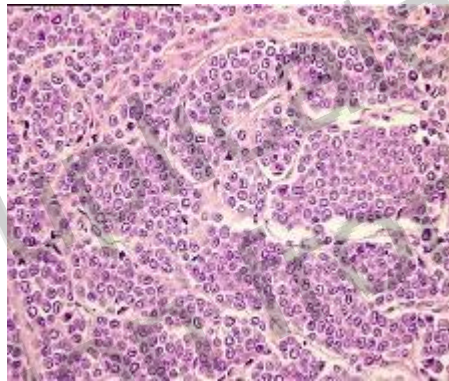
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ILC variants

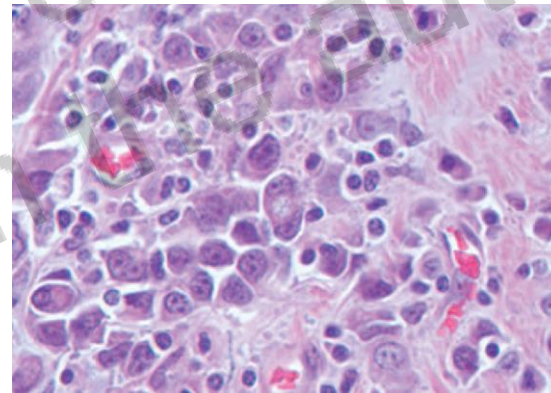
- ILC variants account for up to 70% (~30-40%) of ILC cases
- Common variants: The **WHO** classification of tumors of the breast (5th edition) mentions **four different ILC variants** (solid, alveolar, pleomorphic, tubulolobular)



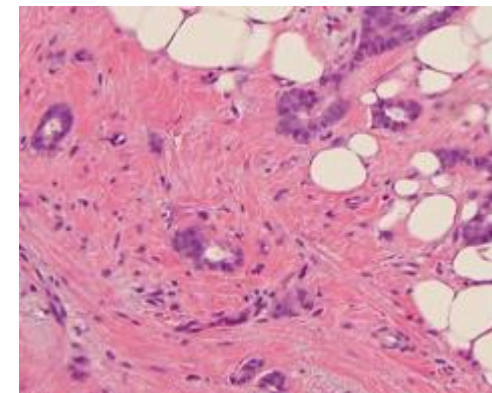
Solid



Alveolar

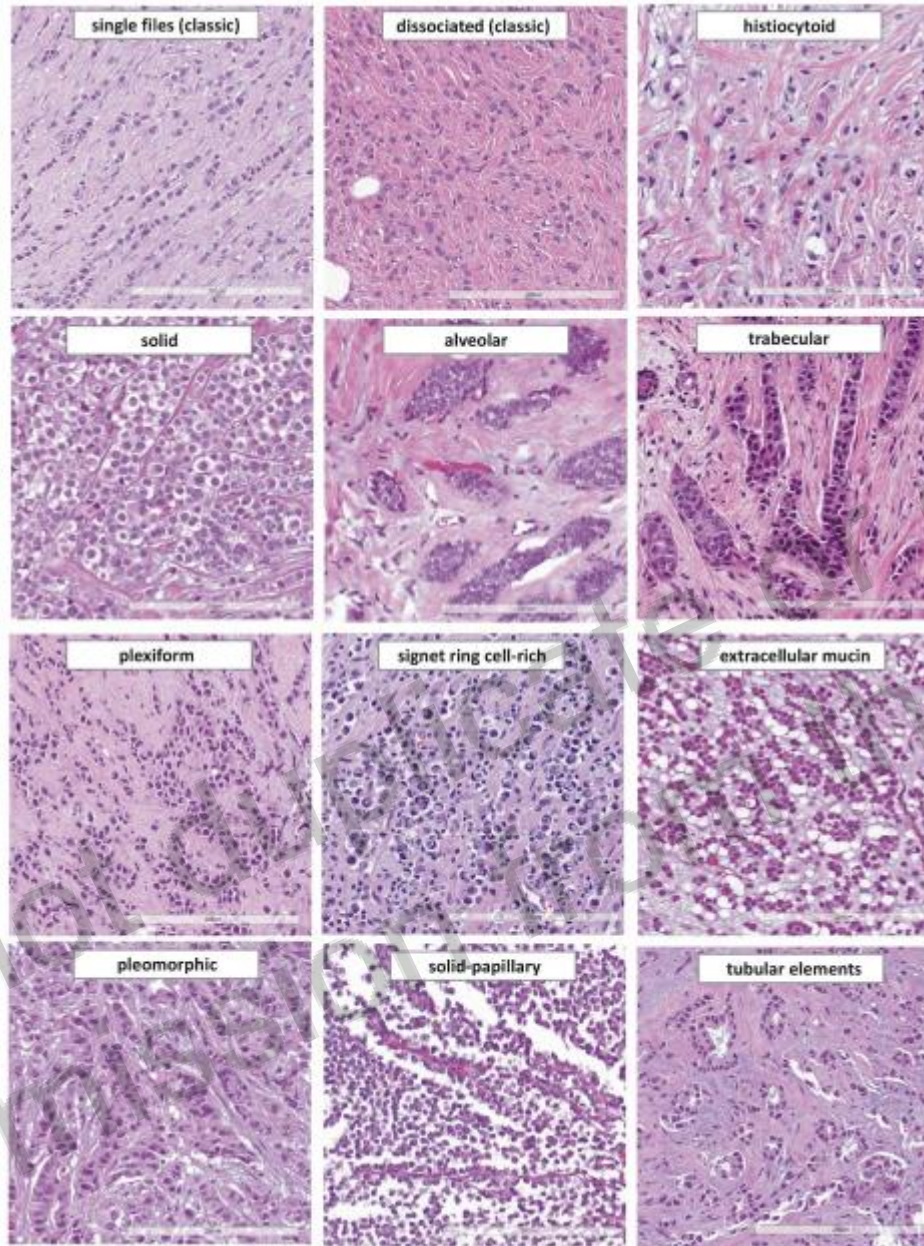


Pleiomorphic



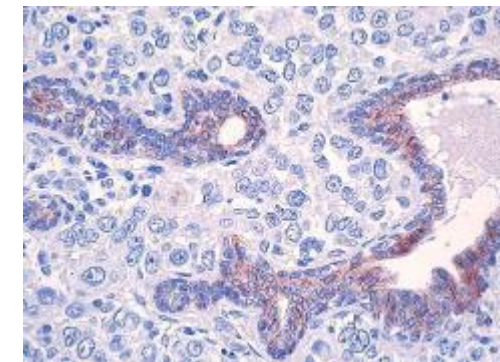
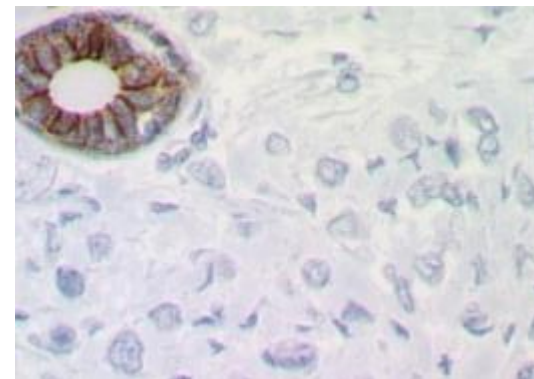
Tubulolobular

Images courtesy F Penault-LLorca



But more ILC variants have been described in the literature

- Some variants are named for their **growth pattern**, such as solid ILC.
- Other variants are named for **cytologic features**, such as pleomorphic ILC.
- Some variants are associated
 - With **distinct molecular alterations** (therapeutic targets)
 - With **different clinical outcome**
- **Common feature:** loss or low expression of E-Cadherin

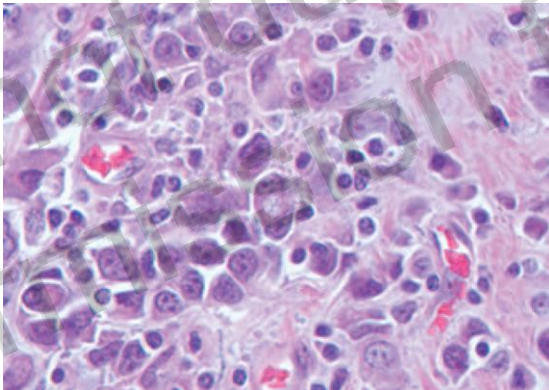


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Some featured subtypes

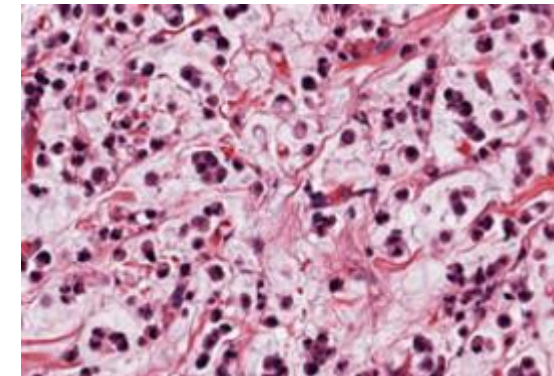
Pleiomorphic ILC (5%)

- **De-differentiated variant**
- **high nuclear grade and SBR3**
- E-cadherin-negative
- **RS frequently >25, N+**
- **11–42% TP53m, HER2 amplification, and mutations**
- Survival similar to ILC if corrected for HER2



ILC with Extracellular Mucin

- 80% classic ILC and 20% signet ring cells floating in pools of extracellular mucin (MUC2).
- Both tumor components → E-cadherin-negative
- **N+ ~Over 50% of the cases**
- **12–40%, HER2 amplification**
- **high nuclear grade** is also frequently reported
- TP53 and PIK3CA mutations associated with relapses

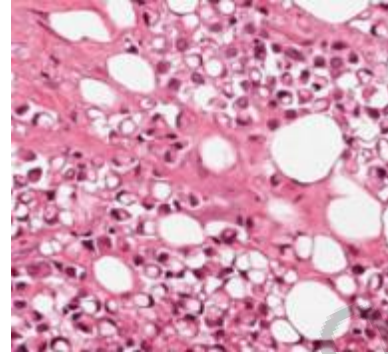


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Some featured subtypes

Histiocytoid ILC

- Rare
- Frequently **TN, AR+, apocrine like** HER2amp
- Metastasis to the eyelid

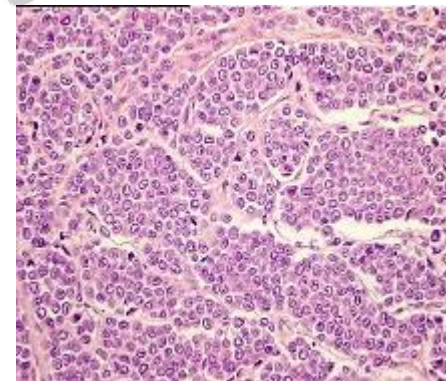
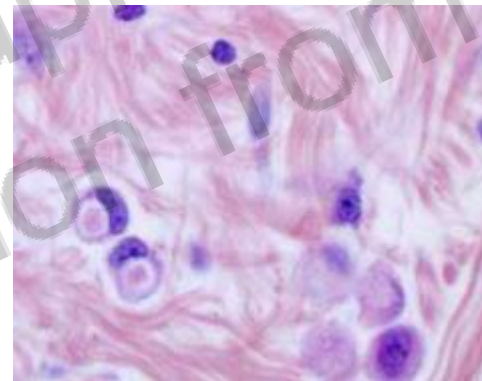


Solid ILC and solid papillary ILC

- Rare poorer prognosis
- Differential diagnosis with lymphoma
- Mutation of ARID1A, TP53 CN gain of ESR1

Signet Ring Cell-Rich ILC

- >50 high power field
- Close to classical ILC

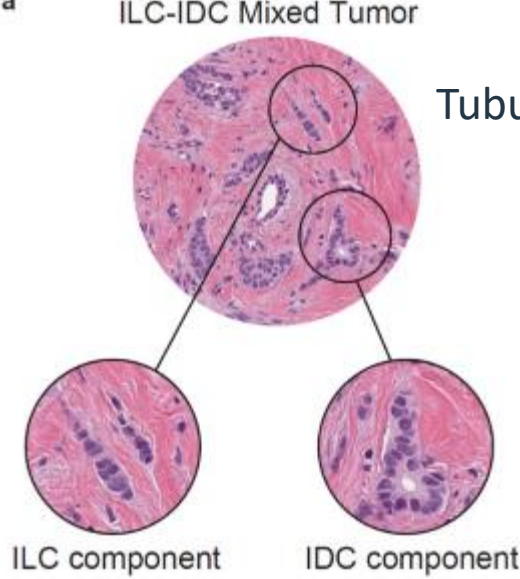


Alveolar ILC

- CN gain on chromosome 11q13.3 (CCND1) and 11q14 (PAK1)

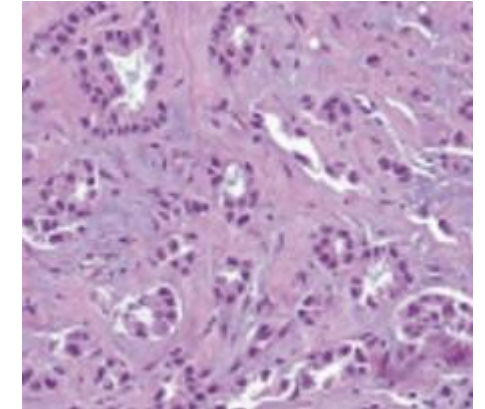
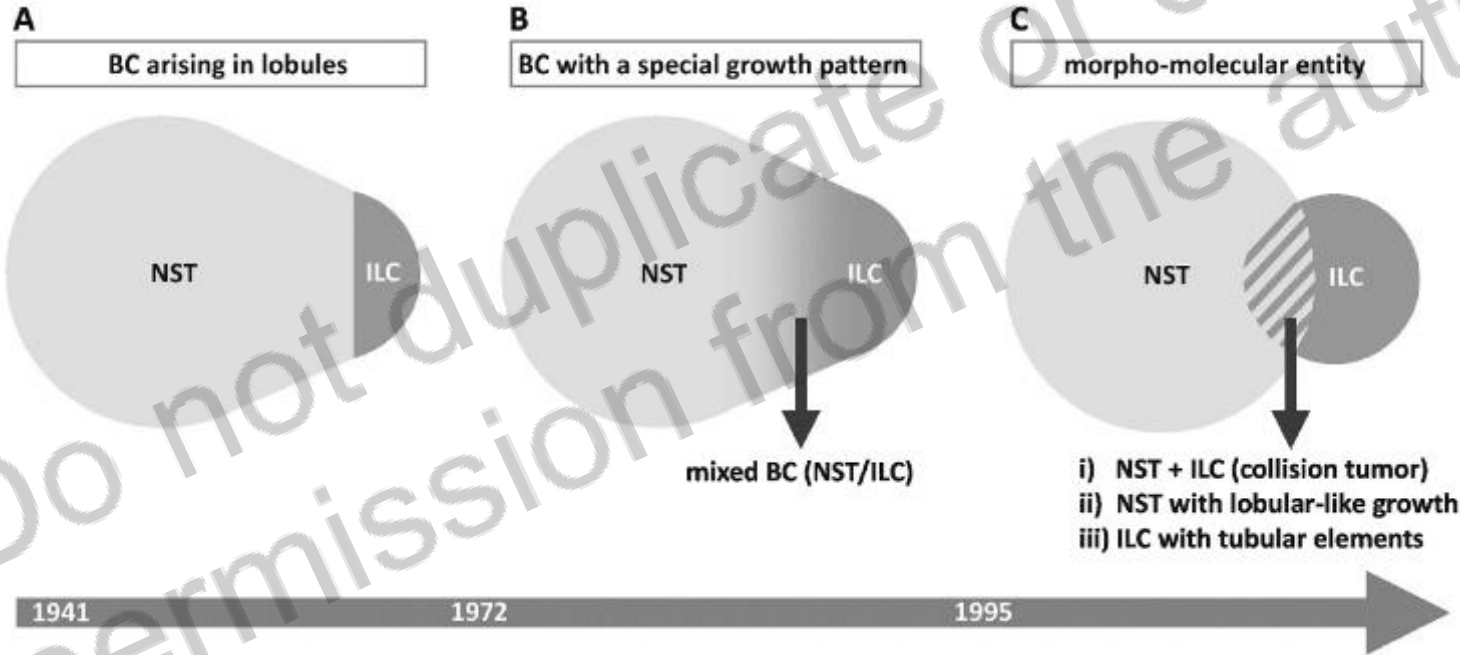
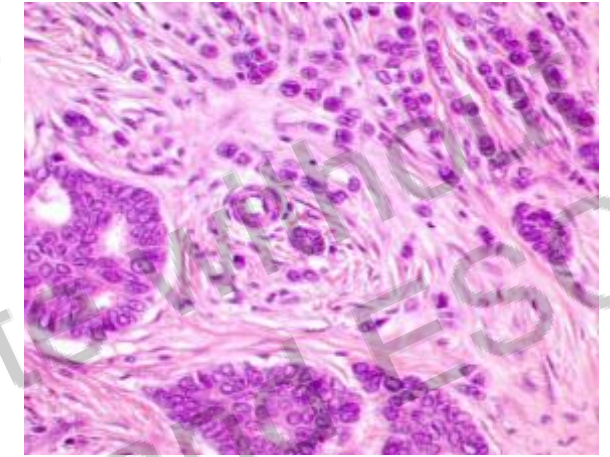
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Some featured subtypes



Tubulo lobular (collision tumor?)

E-Cad neg in ILC, +
in Tubular/NST



ILC with tubular elements
(both components are E-Cad neg)

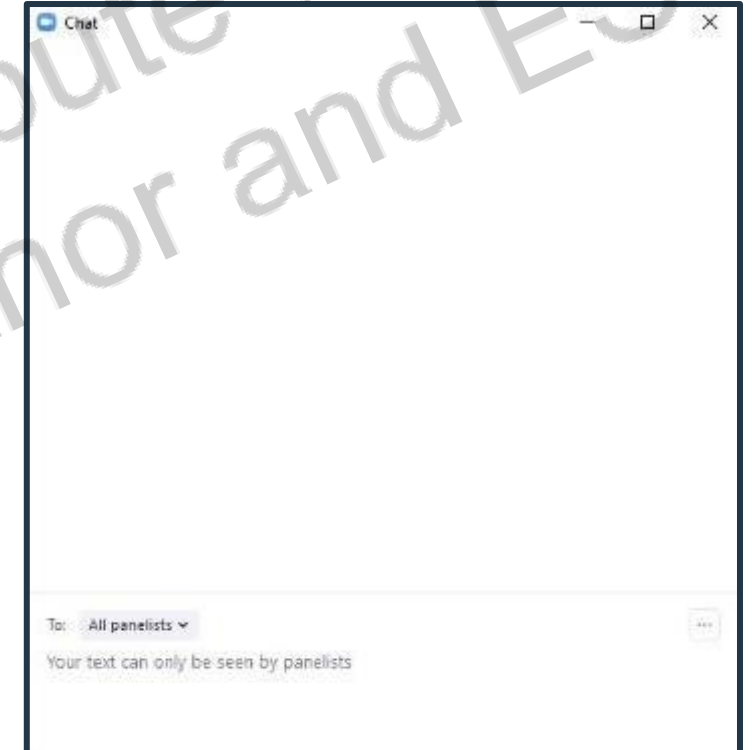
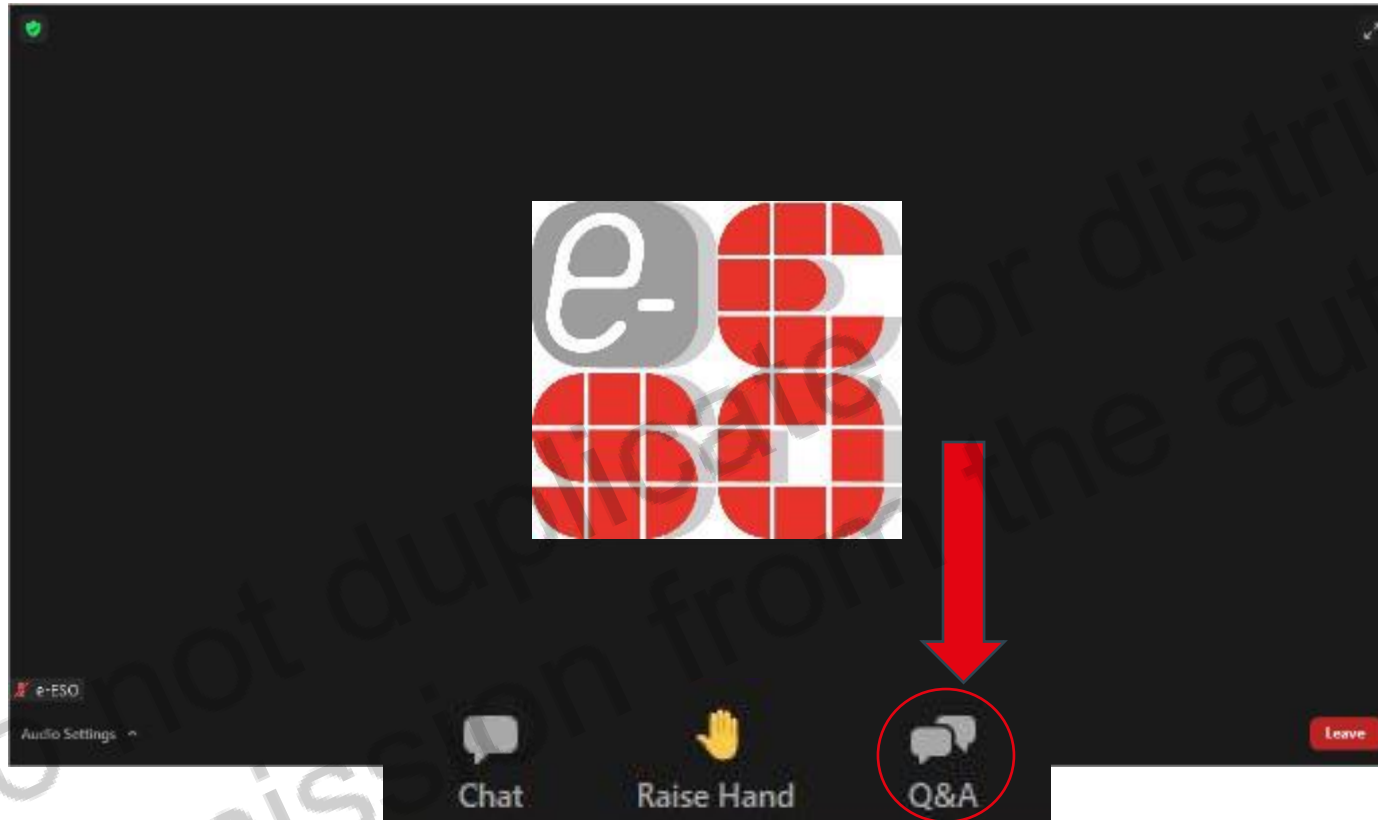


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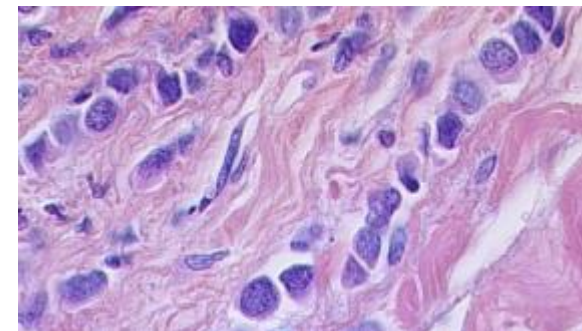
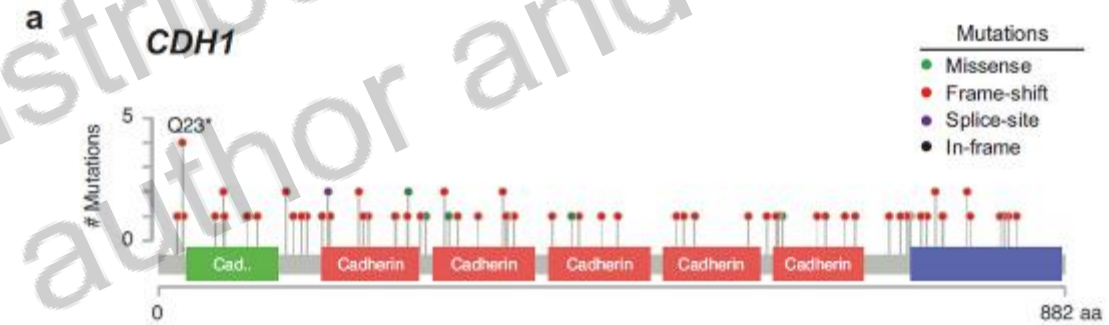
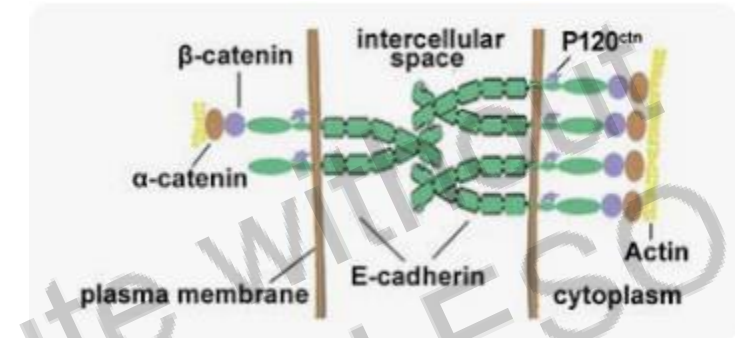


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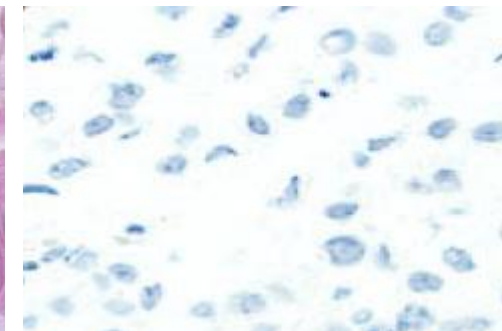
What is shared?

E cadherin down regulation

- **Loss or aberrant expression of the cell-to-cell adhesion molecule E-cadherin supports the diagnosis of ILC.**
- Observed in the majority of ILC (>85% of the cases)
- Predominantly caused by **somatic mutations** and LOH, in *CDH1* gene mapping in 16q22.1 accompanied by allelic loss of the remaining allele
- In rare cases: **promoter methylation** of *CDH1*
- Mutational loss of E-cadherin causes **cytosolic translocation** of p120-catenin (p120), multifaceted protein that plays crucial roles in the pathobiology of ILC.
- When the E-cadherin stain is difficult to interpret → use of IHC for **beta-catenin** loss of membranous staining and cytoplasmic accumulation of **p120** = lobular phenotype



Classical ILC



E-Cadherin

Molecular signatures → need for specific signatures

Test	Ref.	Cohort	Results	Study conclusion
GGI/MapQuantDx™	[89]	166 ILC	Test outperformed grade	Prognostic value in ILC
MammaPrint	[90]	217 ILC	Independent value of MammaPrint, specifically in lymph node-negative ILC	
	[91]	487 ILC (255 CILC)	10.2% CILC and 22.8% of ILC variants were high risk	Prognostic value in ILC
OncotypeDx	[55]	353 ILC	20% low-, 72% intermediate-, and 8% high-risk score	ILC more likely low/int score but 5-year DMFS equivalent to non-ILC
	[92]	30 ILC	All ILC low or int risk	Questions utility in ILC; more data required
	[93]	97 ILC	1% of ILC (non-pleomorphic) record high-risk RS	Questions utility in ILC; more data required
	[94]	102 ILC	Different RS distribution in ILC v IBC-NST	More data required
	[95]	59 ILC	50% ILC in low risk	More data required
	[96]	9037 ILC SEER data	38.1% ILC intermediate risk; 2.4% high risk	More data required
	[97]	7316 ILC SEER data	72% ILC in intermediate-risk group; 8% high risk	Adjuvant Ctx did not confer survival benefit to int or high risk; note LN+ cases included
	[98]	49,819 ILC Genomic Health clinical lab 2004–2017	63.9% ILC in low risk, 33.6 in intermediate, 2.5% in high risk	Classic ILCs have lower average RS (16.3) compared to IDC (18.4) and ILC variants (18.2), and lower rate of tumours with high scores (2.5% vs. 10.7% vs. 8.4%, respectively)
Prosigna	[99]	341 ILC Danish Breast Cancer Group	ILC had poorer 10-year DR rates than ROR matched IDC	Prognostic value in ILC
EndoPredict/EPclin	[100]	470 ILC TransATAC and ABCSG 6/8	63.4% were low EPclin risk group (a 10-year DR risk of 4.8%) compared to 172 (36.6%) women in the high-risk group (110-year DR risk of 26.6%)	Significant prognostic value; Ctx in low-risk group not indicated

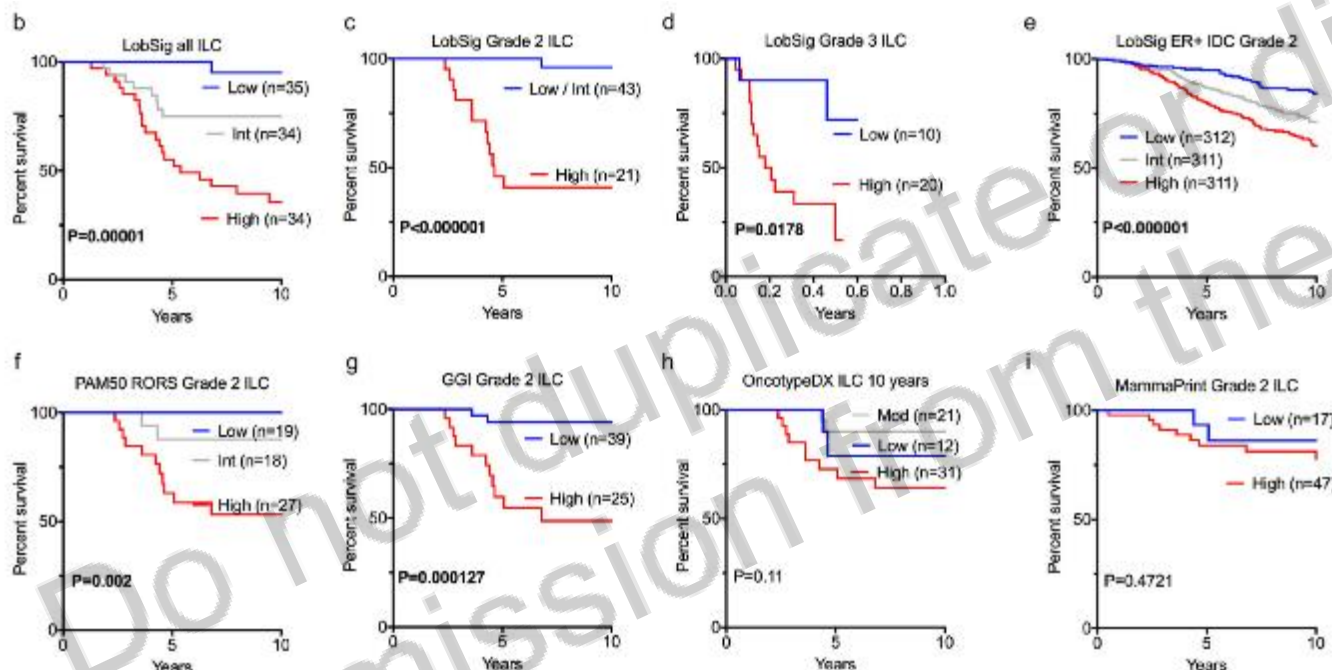
GGI, MammaPrint OK

OncotypeDx utility or ILC ?

Prosigna Endopredict OK

LobSig is a multigene predictor of outcome in invasive lobular carcinoma

Amy E. McCart Reed¹, Samir Lal^{1,5}, Jamie R. Kutasovic¹, Leesa Wockner², Alan Robertson³, Xavier M. de Luca¹, Priyakshi Kalita-de Croft¹, Andrew J. Dalley¹, Craig P. Coorey¹, Luyu Kuo¹, Kaltin Ferguson¹, Colleen Niland¹, Gregory Miller^{1,4}, Julie Johnson¹, Lynne E. Reid¹, Renique Males¹, Jodi M. Saunus¹, Georgia Chenevix-Trench², Lachlan Coin³, Sunil R. Lakhani^{1,4} and Peter T. Simpson¹

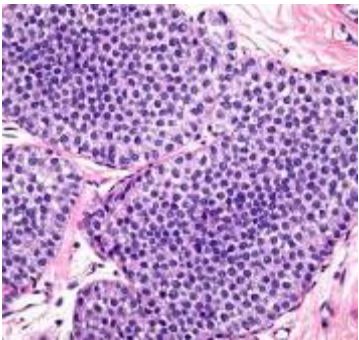


- **LobSig high tumors** were enriched for mutations in **ERBB3** (P = 0.00007), **ERBB2** (P = 0.0002), **BIRC6** (P = 0.005), **AKT1** mutations (P=0.02), **ROS1** (P < 0.01); amplifications of **PRMT2** (P= 7.329e-08), **S100B** (P= 7.33e-08) and **DIP2A** (P = 7.99e-07; 21q22.3); and for deletions of **CTCF** (16q22.1; P= 8.41e-11), **C17ORF39** (17p11.2; P= 4.597e-09) and **ARID1A** (1p36.11; P = 8.045e-06).
- **The LobSig low tumors** showed a relatively quiet genome.

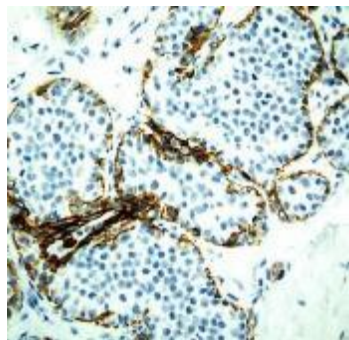
What differs?

Carcinogenesis: 3 subtypes of LCIS with ≠ molecular alterations

WHO 2019



Classical-CLCIS E-Cadherin loss

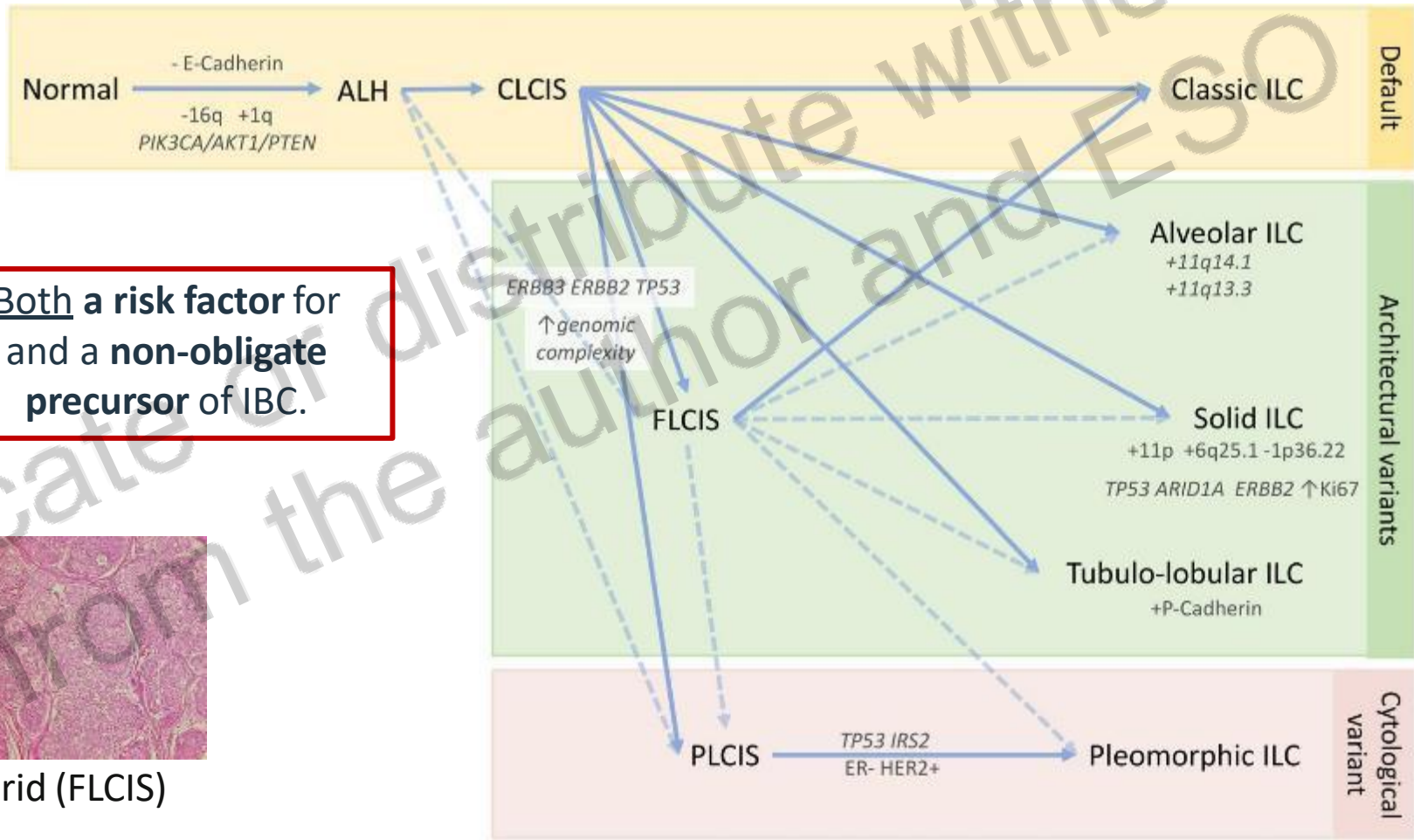


Pleomorphic (PLCIS), E-Cadherin loss



Florid (FLCIS)

Both a risk factor for and a non-obligate precursor of IBC.



PLCIS may be RE, PR- and HER2+

PCLIS and FLCIS on biopsy → surgical verification



Histopathological differences between classical ILC and variants

Classical ILC

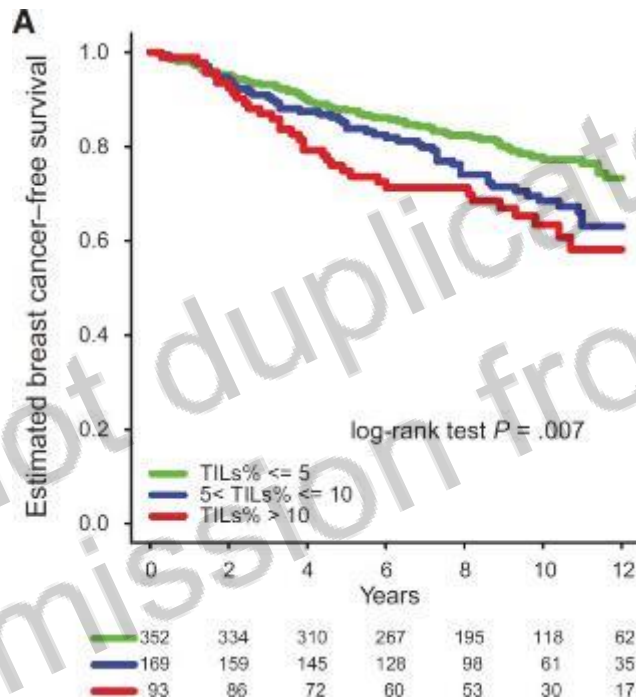
- ER+, PR+, HER2 non amplified – lumA
- Grade 2 tumors
- HER2 amplifications ~0%
- HER2 mutations ~6%
- Absent or low TILS

Rare types - Pleiomorphic

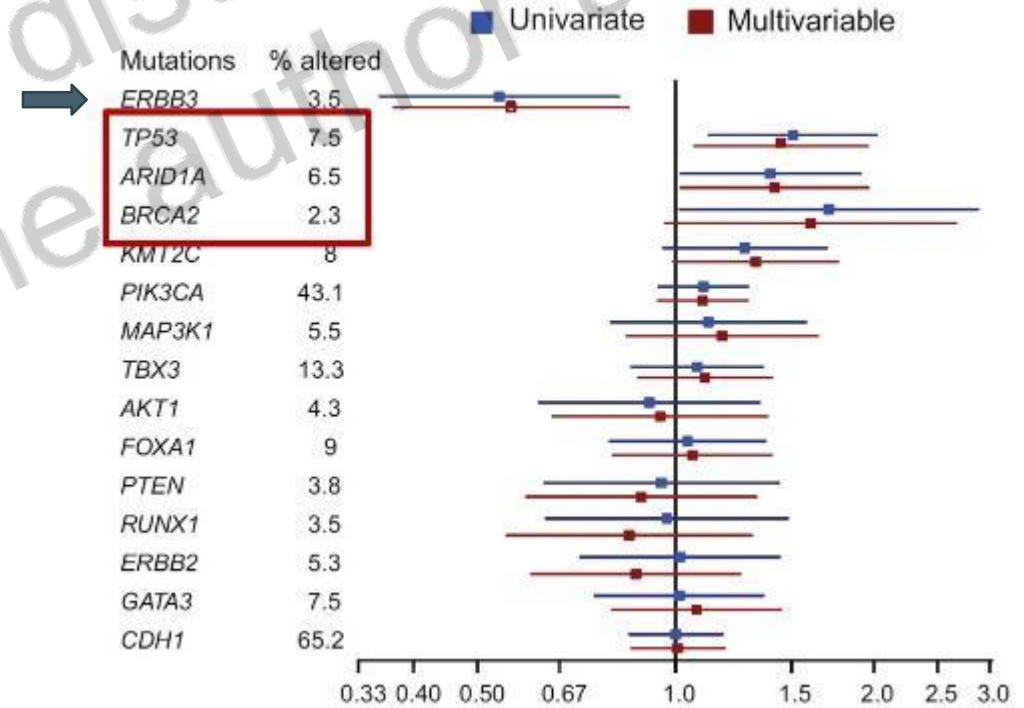
- 2-9% of TN-ILC (express AR, *HER2* & *HER3* mutations and *ESRRAm*)
- Grade 3 tumors in pleiomorphic or other non classical (~12%)
- HER2 amplifications up to 25% (incl Apocrine variant)
- HER2 mutations ~15%
- TILs high (>15%) younger age poor Prognostic

TILs in ILC

TILs in ILC= poor prognosis



Fold change in TILS and mutation status



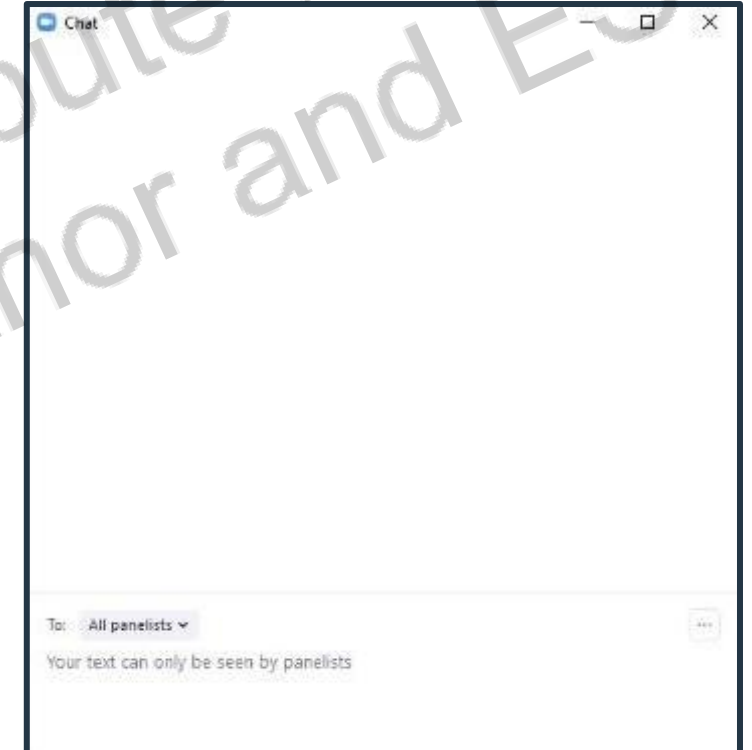
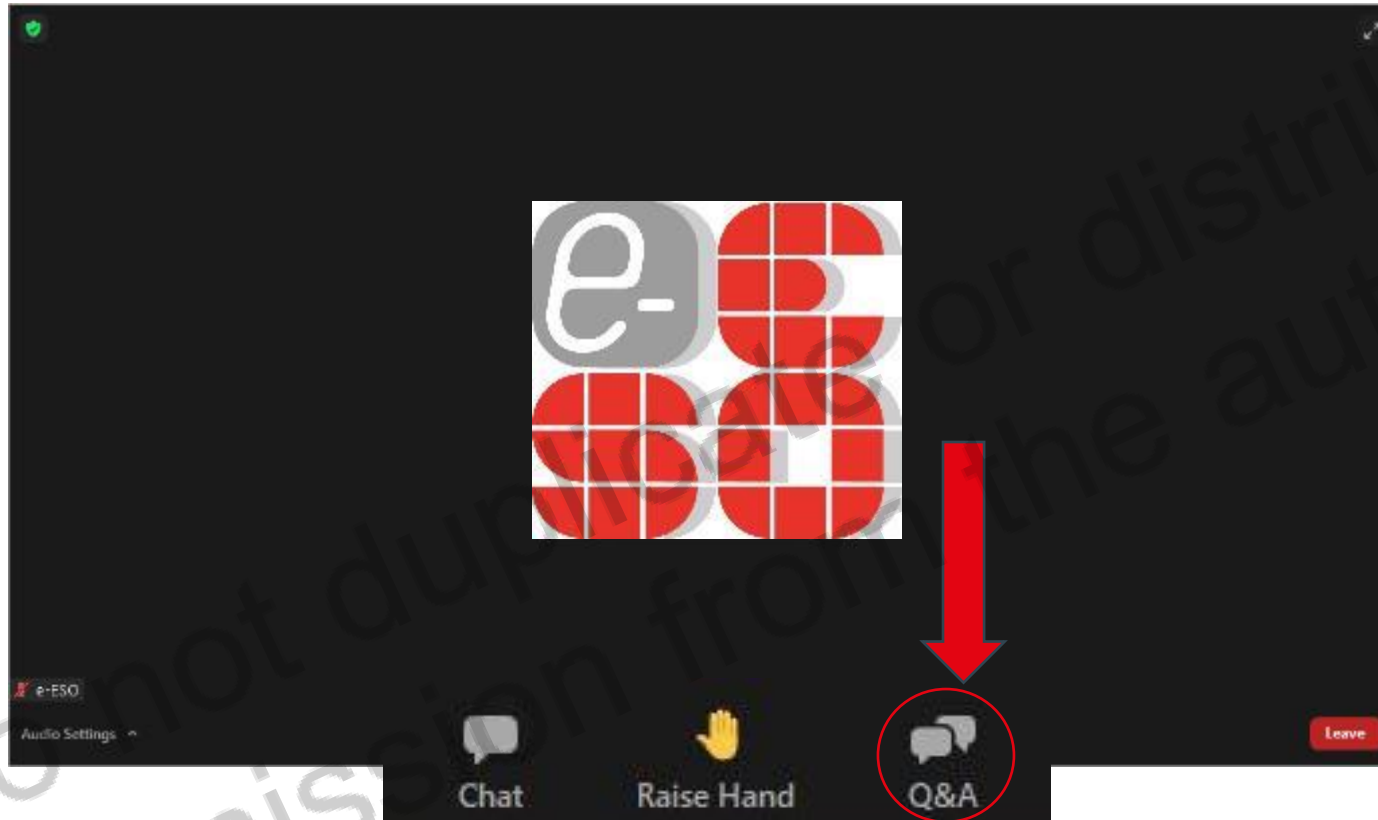


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Focus on molecular targets

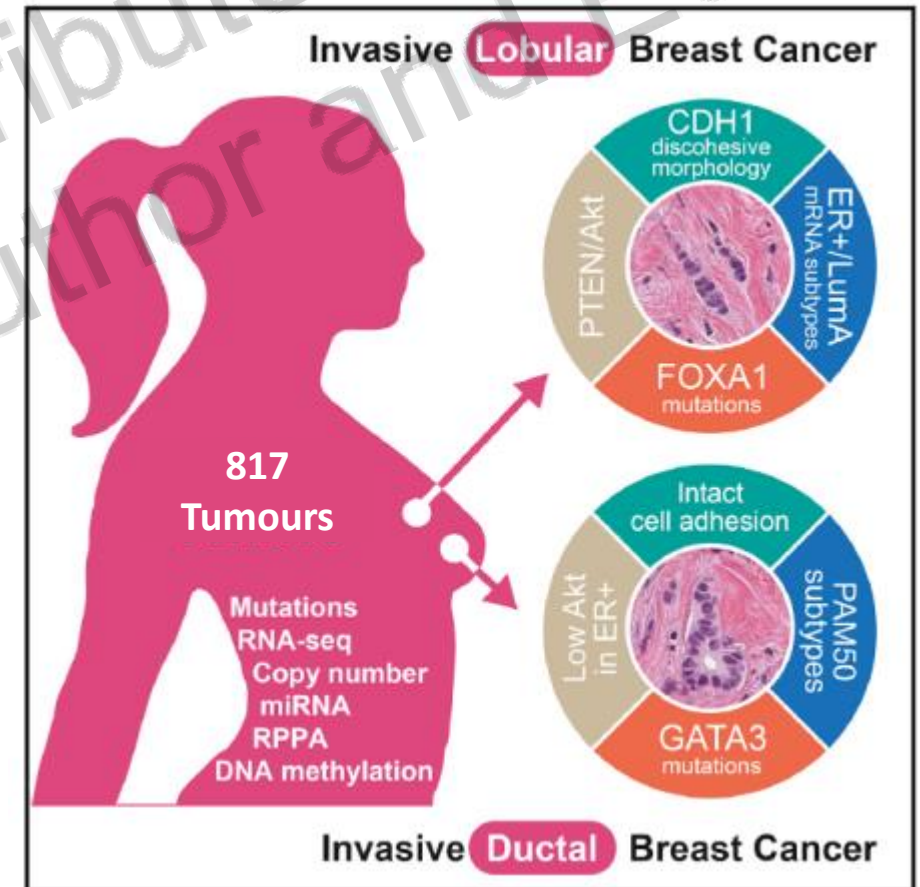
Specific/frequent molecular alterations

Lobular carcinomas (10-15%) and their precursors (lobular neoplasia):
CDH1 mutation (located on 16q), → the pathognomonic **loss of E-Cadherin** expression (adhesion protein): aspect of non cohesive cells
→ **PI3K alterations >50%** (with Akt/mTOR in 45%)
→ **AKT1, FOXA1, HER2, HER3, PTEN and TBX3** mutations in ILC>IDC
→ HER2 and AKT1 mutations associated with increased risk of early relapse
→ Histologic subtype–specific associations: **ESR1 gains in solid subtype, HER2 mutations in mixed non classic**, and TP53 mutations in both.

Comprehensive molecular portraits of invasive lobular BC

Giovanni Ciriello,^{1,2,23} Michael L. Gatz,^{3,4,23} Andrew H. Beck,⁵ Matthew D. Wilkerson,⁶ Suhni K. Rhee,⁷ Alessandro Pastore,² Hailei Zhang,⁸ Michael McLellan,⁹ Christina Yau,¹⁰ Cyriac Kandoth,¹¹ Reanne Bowlby,¹² Hui Shen,¹³ Sikander Hayat,² Robert Fieldhouse,² Susan C. Lester,⁵ Gary M.K. Tse,¹⁴ Rachel E. Factor,¹⁵ Laura C. Collins,⁵ Kimberly H. Allison,¹⁶ Yunn-Yi Chen,¹⁸ Kristin Jensen,^{16,17} Nicole B. Johnson,⁵ Steffi Oesterreich,¹⁹ Gordon B. Mills,²⁰ Andrew D. Cherniack,⁸ Gordon Robertson,¹² Christopher Benz,¹⁰ Chris Sander,² Peter W. Laird,¹³ Katherine A. Hoadley,³ Tari A. King,²¹ TCGA Research Network,²² and Charles M. Perou^{3,*}

- Invasive lobular carcinoma (ILC) is a **clinically** and **molecularly** distinct disease
- ILCs show **CDH1** and **PTEN** loss, AKT activation, and mutations in *TBX3* and *FOXA1*
- Proliferation and **immune-related** gene expression signatures define **3 ILC subtypes**
- Genetic features classify mixed tumours into lobular-like and ductal-like subgroups



ESCAT alterations in primary and metastatic ILC

Table 1. Actionability of the genomic alterations in primary and metastatic ILC as per ESCAT^{53,206}

	Readiness of use in clinical practice	ESCAT alterations in breast cancer	% Primary ILC (% primary NST)	% Metastatic ILC (% metastatic NST)
Tier I	Targets ready for implementation in routine clinical decisions	<i>ERBB2/HER2</i> amplification Germline <i>BRCA1</i> mutations Germline <i>BRCA2</i> mutations <i>NTRK1-3</i> fusions <i>PIK3CA</i> mutations MSI High TMB (>10 mutations/Mb)	7.4 (20.6) ²⁵ 0.3 (2.3) ^{25,55} 2.2 (2.4) ²⁵ 0 (0) 43-48 (33.5) ³¹ NA 4.7 (NA) ⁵⁴	6.8 (11.4) ⁵⁵ 0.6 (0) ³³ 38-47.2 (33.1) ^{42,55} NA 16 (5) ⁵⁸
Tier II	Investigational targets likely to define patients who benefit from a targeted drug, but additional data needed	<i>AKT1</i> mutations <i>ERBB2/HER2</i> mutations <i>ESR1</i> mutations <i>PTEN</i> loss	1.6-4 (3.1) ^{31,33} 3.9-5 (1.4) ^{31,33} 0-0.8 (0.8) ^{31,33} 13.4 (11.2) ³³	7.5-10 (6.4) ^{42,55} 14.3-15 (4.6) ^{42,55} 15.5-18 (15.3) ^{42,55} 14.3-15 (8.4) ⁴²
Tier III	Clinical benefit previously demonstrated in other tumour type or for similar molecular targets	Somatic <i>BRCA1</i> mutations Somatic <i>BRCA2</i> mutations <i>MDM2</i> amplifications <i>NF1</i> mutations <i>ERBB3/HER3</i> mutations	0 (2.9) ^{31,33} 0.8-2 (2.5) ^{31,33} 2-2.4 (4.7) ^{31,33} 1-3.9 (2.9) ^{31,33} 0.8-4 (2.3) ³¹	1.2 (1.9) ⁵⁵ 6.2 (3.5) ⁵⁵ 2-6.2 (4.2) ^{42,55} 7-7.5 (5.8) ^{42,55} 0-2.5 (1.9) ^{42,55}

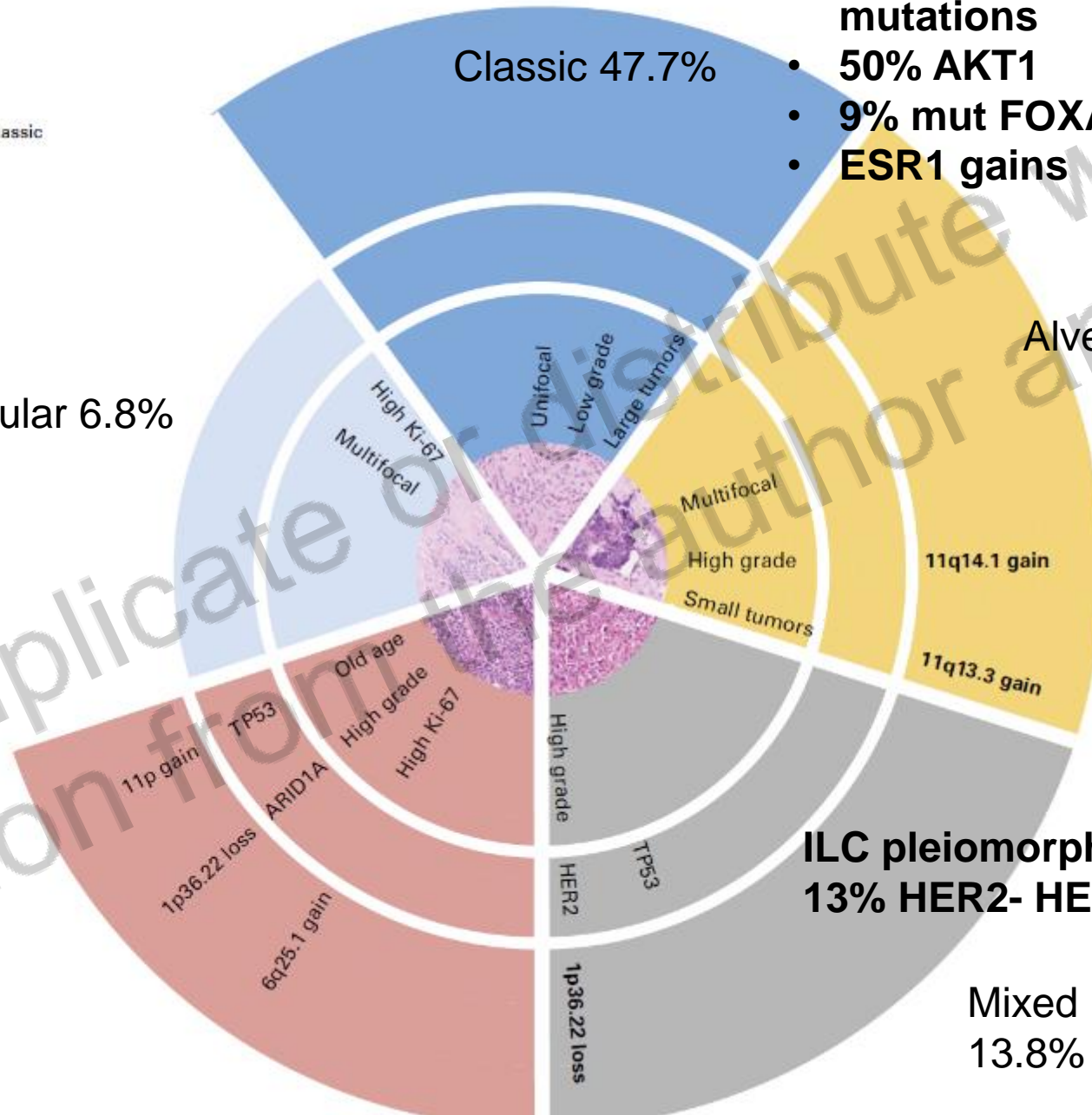
ESCAT alterations in primary and metastatic ILC

Tier IV	Preclinical evidence of actionability	ARID1A mutations	5.5-6.3 (3.7) ³¹	8.7-15 (6.1) ^{42,55}
		ARID1B mutations	0.2-0.8 (2.1) ^{31,33}	2.5 (2.8) ⁵⁵
		Germline ATR mutations		NA
		Germline ATM mutations		1.03 (1.1) ²⁵
		Germline PALB2 mutations		0.37 (1.5) ²⁵
		CDH1 mutations	63-65 (2) ^{31,33}	69-75.8 (2.1) ^{42,55}
		Germline CDH1 mutations		0.54 (0.04) ²⁵
		IGF1R mutations	0-1.6 (0.8) ^{31,33}	0-13 (2.1) ^{42,55}
		INPP4B loss	0.8 (0.8) ³³	0.6 (0.3)
		MAP3K1 mutations	5.3-5.5 (8.2) ^{31,33}	7.5-17 (7) ^{42,55}
		MAP2K4 mutations	1.2-1.4 (4.9) ^{31,33}	2-4.3 (3.7) ^{42,55}
		MT4 mutations		NA
		MYC amplifications	4.7-6.3 (26.8) ^{31,33}	3.7-15 (11.6) ^{42,55}
		PIK3R1 mutations	0-1 (1.8) ³³	1.9 (2.7) ⁵⁵
		RUNX1 mutations/deletions	4-10.2 (2.5) ³³	5 (2.7) ⁵⁵
		CBFB mutations/deletions	3.2 (3.3) ³³	4.3 (3.5) ⁵⁵
		SF3B1 mutations	1.5-3.1 (2.5) ³³	3.1 (1.7) ⁵⁵
		TP53 mutations	7.3-7.9 (44) ^{31,33}	12-19.9 (42.9) ^{42,55}
Tier X	Lack of evidence of actionability	FGFR1 amplification	9.4-25 (13.9) ^{31,33}	14.3-15 (14.6) ^{42,55}
		CCND1 amplification	17.3-38 (16.2) ^{31,33}	19.9-24 (22.7) ^{42,55}
		ESR1 amplification	0.8-10 (3.5) ^{33,207}	1.0 (3.2) ⁵⁵
		FGFR4 mutations	0 (0.2) ³³	2.5 (1.0) ⁵⁵



- **ERBB2 & ERBB3 8.5% mutations**
- **50% AKT1**
- **9% mut FOXA1**
- **ESR1 gains**

ILC lumA: higher activation of AKT pathway (45%)



**ILC pleiomorphic 15% HER2 amplif
13% HER2- HER3 mutations**

Mixed non classic
13.8%

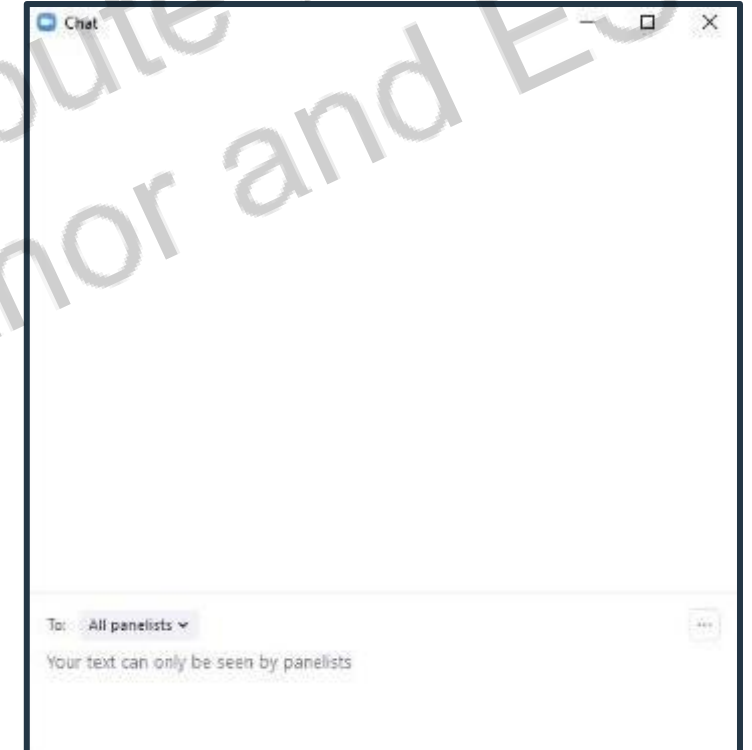
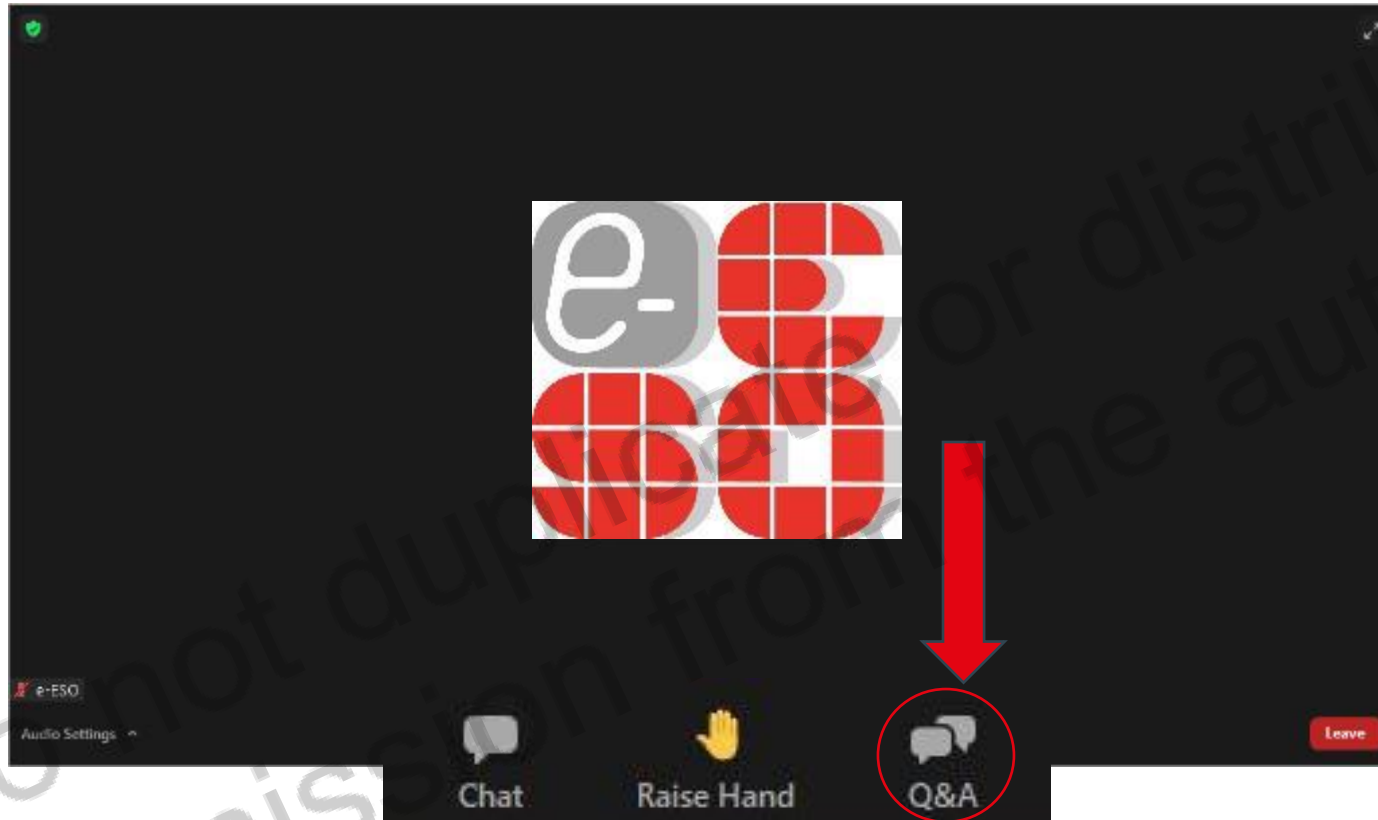


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In conclusion

Pathological characteristics

- Typically ER+/HER2- and grade 2
- ~50% 'classic' subtype
- Peculiar pattern of metastatic sites

Intrinsic subtypes

- Most are luminal A or B, with varying proportions between cohorts
- Very few basal-like or HER2-enriched

Alterations involved in ER signaling

- Higher rate of *FOXA1* and lower rate of *GATA3* mutations compared to IDC
- ~25% with *ESR1* gain
- Need to understand endocrine resistance

Multigene classifiers of recurrence

- Oncotype Dx™, MammaPrint®, Genomic Grade evaluated in ILC series
- Need for classifiers that can predict late recurrences

Lobular Breast Cancer

HER2 mutations

- Patients with *HER2* mutations have increased risk of early relapse
- Co-occurrence of *HER2* and *CDH1* mutations

Transcriptomic ILC subtypes

- TCGA and RATHER identified stable clusters
- Differences and clinical relevance to be further investigated

PI3K/Akt signaling pathway

- >50% with mutation in *AKT1/PIK3CA/PTEN*
- ~45% with altered Akt/mTOR signalling
- Patients with *AKT1* mutations have increased risk of early relapse

E-cadherin (CDH1) loss

- ~60% with *CDH1* mutations, >90% LOH
- No *CDH1* promoter hypomethylation
- *CDH1* can promote tumorigenesis in collaboration with other cancer gene

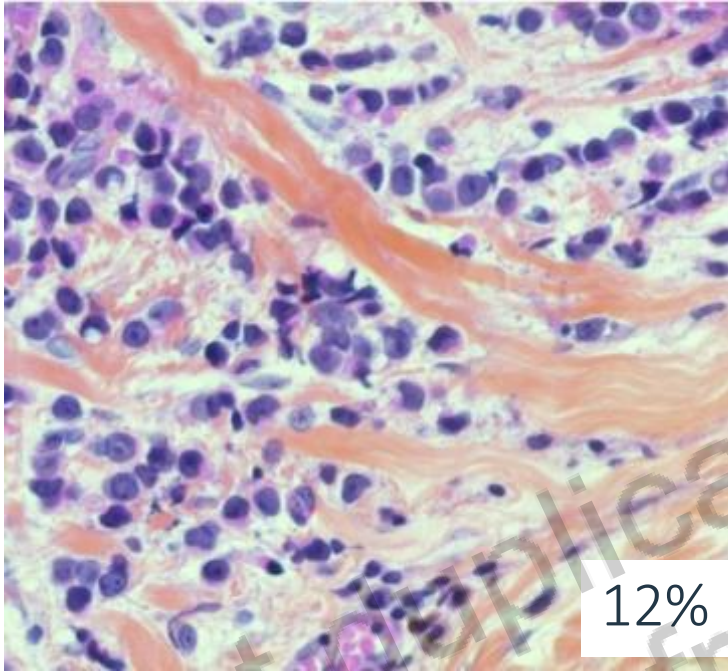
Molecular profiling at metastatic stage+++

LobSig

Ros inhibition

What is relevant for clinical practice?

Classical

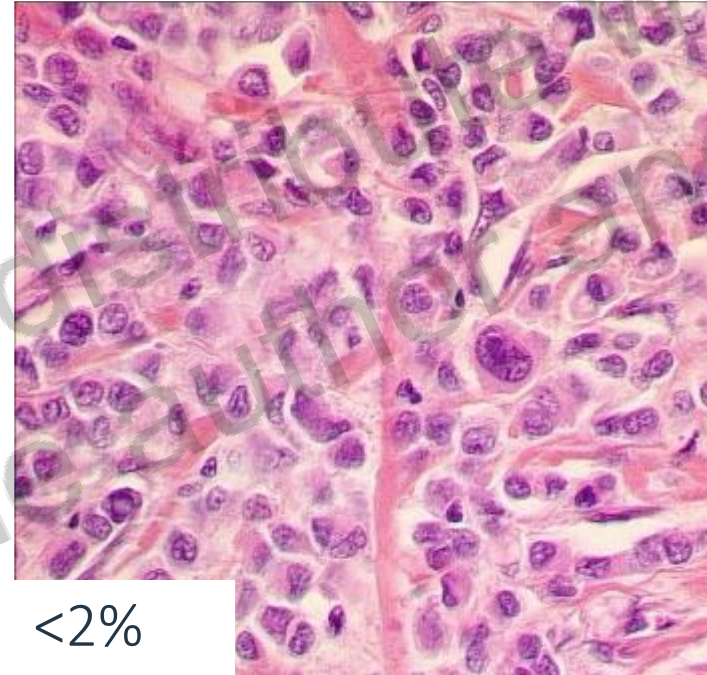


12%

HER2 amplification ~0%

- *CDH1* mutations ~85%
- *HER2*, *HER3* mutations ~8.5%
- *PIK3CA*, *AKT1*, *PTEN* mutations ~50%

Pleiomorphic and non classical high grade



<2%

HER2 amplification ~20-25%
POOR PROGNOSIS



Lobular carcinoma in summary

- E-cadherin Inactivation in 95% of cases
- ER+ > 90% of cases
- Low proliferation

Low chemosensitivity
ET, CDK4/6i sensitivity

- HER2 score 3+ < 5% of cases

- *HER2* Mutations :

- 6% classical ILC
- 15% ILC high grade

Targeted therapies such as anti HER2 TKIs?

- ***PIK3CA* Mutations in 48% of the cases**

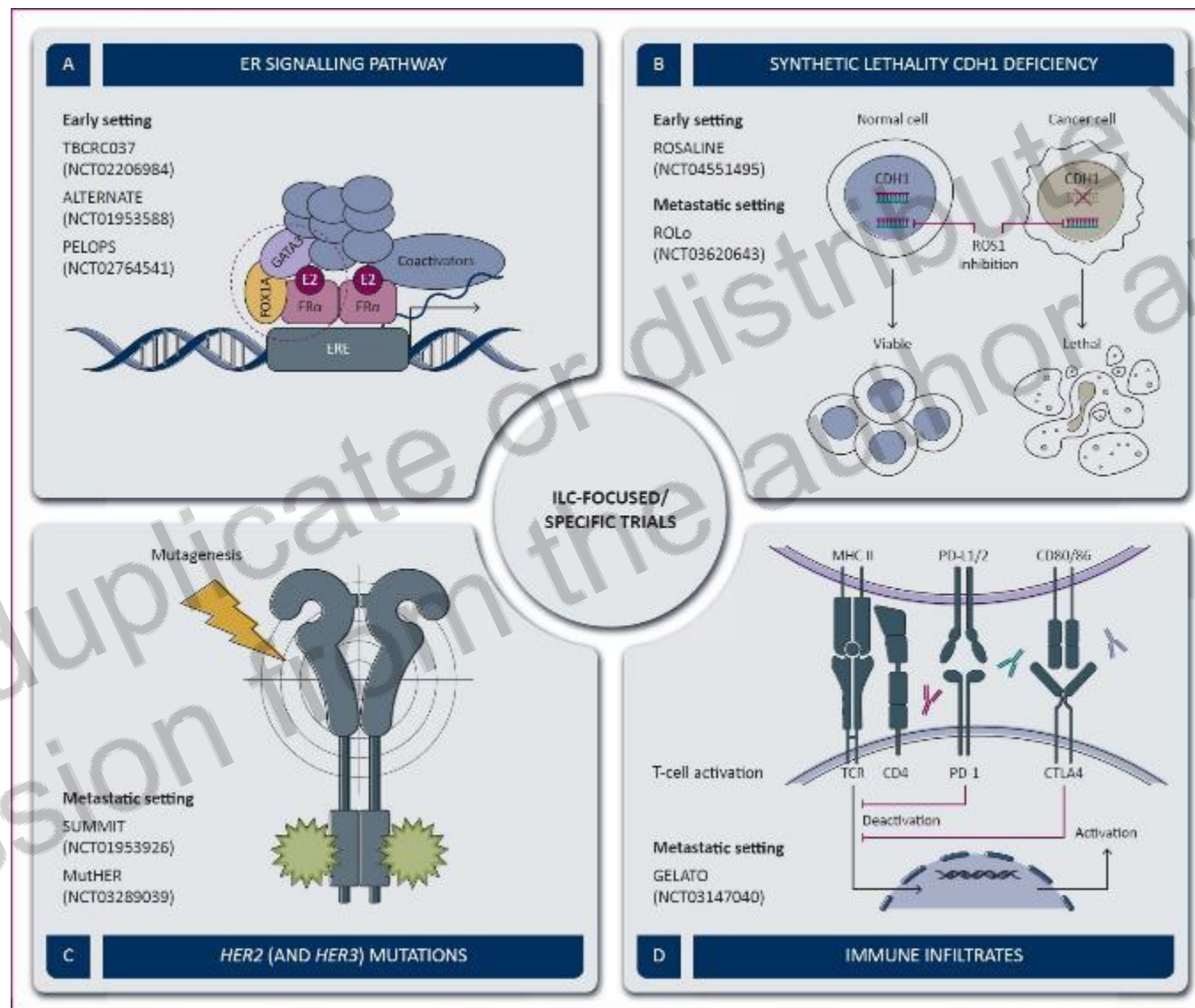
- Mutations *TP53*, *GATA3*, *FOXA1*, *RUNX1* ~ 5 -10% of the cases PTEN/AKT pathway activation mutually exclusive with *PIK3CA* mutations.

mTOR inhibitor
PIK3CA inhibitor

- **3 to 5 transcriptomic groups have been identified**

- « reactive-like » (good prognostic), « Immune-related » & « proliferative »
or « immune-related » & « hormone – related »

ILC-focused clinical trials



REVIEW

Current and future diagnostic and treatment strategies for patients with invasive lobular breast cancer

K. Van Baelen^{1,2}, T. Geukens^{1,3}, M. Maetens⁴, V. Tjan-Heijnen⁵, C. J. Lord⁶, S. Linn^{5,7,8}, F.-C. Bidard⁹, F. Richard¹⁰, W. W. Yang¹¹, R. E. Steele¹², S. J. Pettitt¹³, C. Van Ongeval¹⁴, M. De Schepper^{1,11}, E. Isnaldi¹⁵, I. Nevelsteen¹², A. Smeets¹², K. Punle¹⁶, L. Voorwerk^{1,14,17}, H. Wildiers¹⁸, G. Floris¹¹, A. Vincent-Salomon¹⁵, P. W. B. Derksen¹⁹, P. Neven²⁰, E. Senkus²¹, E. Sawyer²², M. Kok^{14,23} & C. Desmedt^{1,11}

Review

Lobular Breast Cancer: Histomorphology and Different Concepts of a Special Spectrum of Tumors

Matthias Christgen^{1,*}, Gábor Cserni^{2,3}, Giuseppe Floris⁴, Caterina Marchio^{5,6}, Lounes Djerroudi⁷, Hans Kreipe¹, Patrick W. B. Derksen⁸ and Anne Vincent-Salomon^{7,*}

McCart Reed et al. *Breast Cancer Research* (2021) 23:6
https://doi.org/10.1186/s13058-020-01384-6

Breast Cancer Research

REVIEW

Open Access

Invasive lobular carcinoma of the breast: the increasing importance of this special subtype

Amy E. McCart Reed^{1,2*}, Lauren Kalinowski^{1,3}, Peter T. Simpson^{1,2} and Sunil R. Lakhani^{1,4}



Review

Transcriptomic and genomic features of invasive lobular breast cancer

Christine Desmedt^{1,*}, Gabriele Zoppoli², Christos Sotiriou³, Roberto Salgado^{4,5}

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² Department of Animal Medicine (DAM), University of Ferrara, Ferrara, Italy; ³ Clinical Oncology, San Marino Hospital, San Marino, Italy

⁴ Department of Pathology (TOR), San Marino Hospital, San Marino, Italy

Comprehensive Review of Molecular Mechanisms and Clinical Features of Invasive Lobular Cancer

Nikhil Pramod^{1,*}, Akanksha Nigam^{1,*}, Mustafa Basree², Resham Mawalkar³, Saba Mehra⁴, Neelam Shinde⁵, Gary Tozbiakian⁶, Nicole Williams⁷, Sarmila Majumder⁸, Bhuvaneshwari Ramaswamy⁹

Review

Diagnostically Challenging Subtypes of Invasive Lobular Carcinomas: How to Avoid Potential Diagnostic Pitfalls

Nektarios Koufopoulos^{1,*}, Ioannis S. Pateras¹, Alina Roxana Gouloumis¹, Argyro Ioanna Teronimaki¹, Andriani Zacharitou¹, Aris Spathis¹, Danai Leventakou¹, Panagiota Economopoulou², Amanda Psyrris², Nikolaos Arkadopoulos³ and Ioannis G. Panayiotides¹

Thank you!



@PenaultLlorca

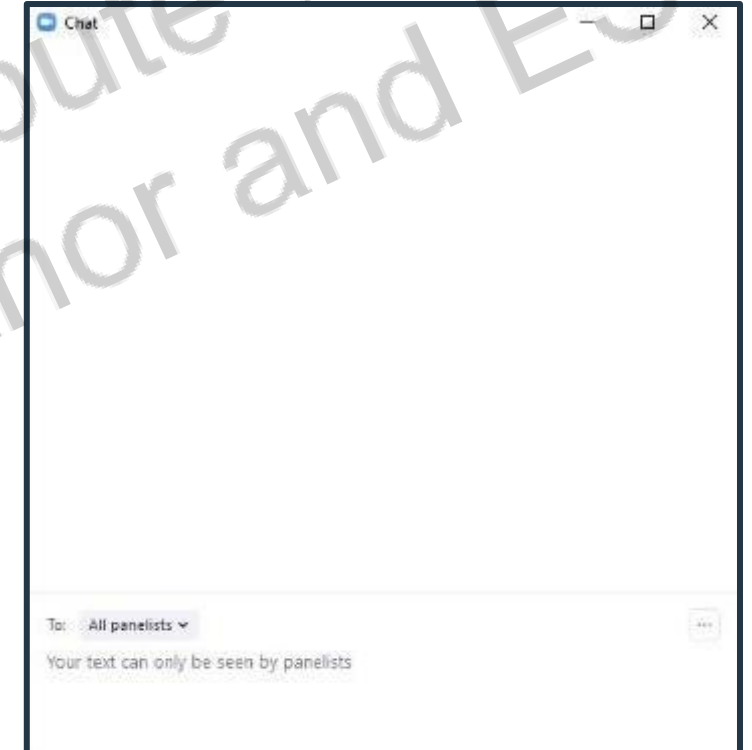
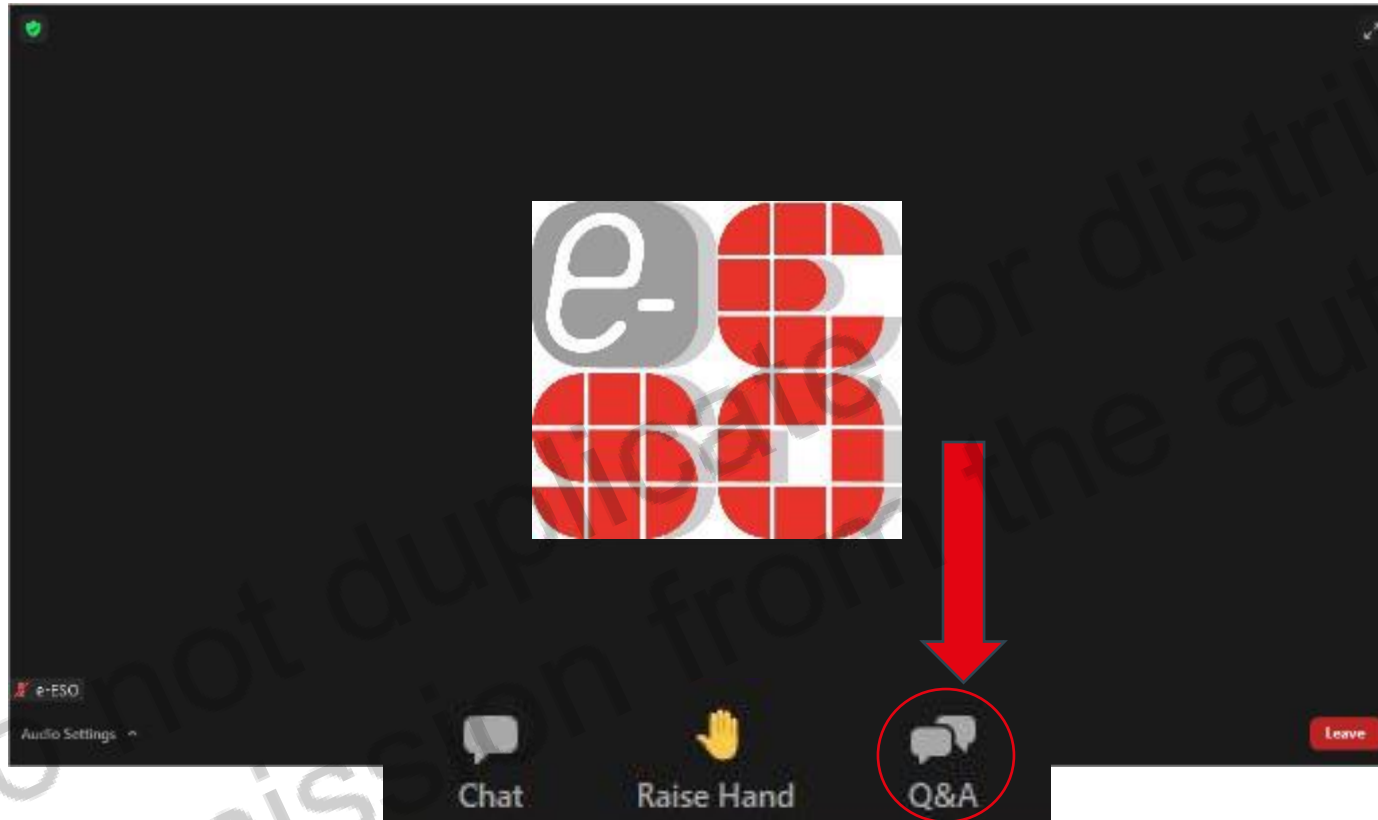


e-Session

Question & Answer Session

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The next e-ESO Session

will take place on 12th January 2022, at the same time

Primary axillary surgery: techniques and indications:

Expert: **Prof Andreas Karakatsanis**, Uppsala University; Uppsala University Hospital, Uppsala, Sweden

Discussant: **Dr Orit Kaidar-Person**, Head of Breast Radiation Unit, Sheba Tel Hashomer, Ramat Gan, Israel

Discussant: **Dr Corrado Tinterri**, Humanitas Cancer Center, Rozzano, Italy

Thank you!

for participating in this

e-session

For additional information, please visit

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