

“Molekylære subtyper af brystkræft”

DBC G´ s 40 års jubilæumsmøde, 18-19. Januar 2018
Hotel Marselis, Århus

- Maria Rossing, MD, PhD
- Enheden for Genomisk Medicin, GM4113, Rigshospitalet

Genomisk Medicin, Rigshospitalet

What is Genomic Medicine??

“an emerging medical discipline that involves using genomic information about an individual as part of their clinical care (e.g., for diagnostic or therapeutic decision-making) and the health outcomes and policy implications of that clinical use”

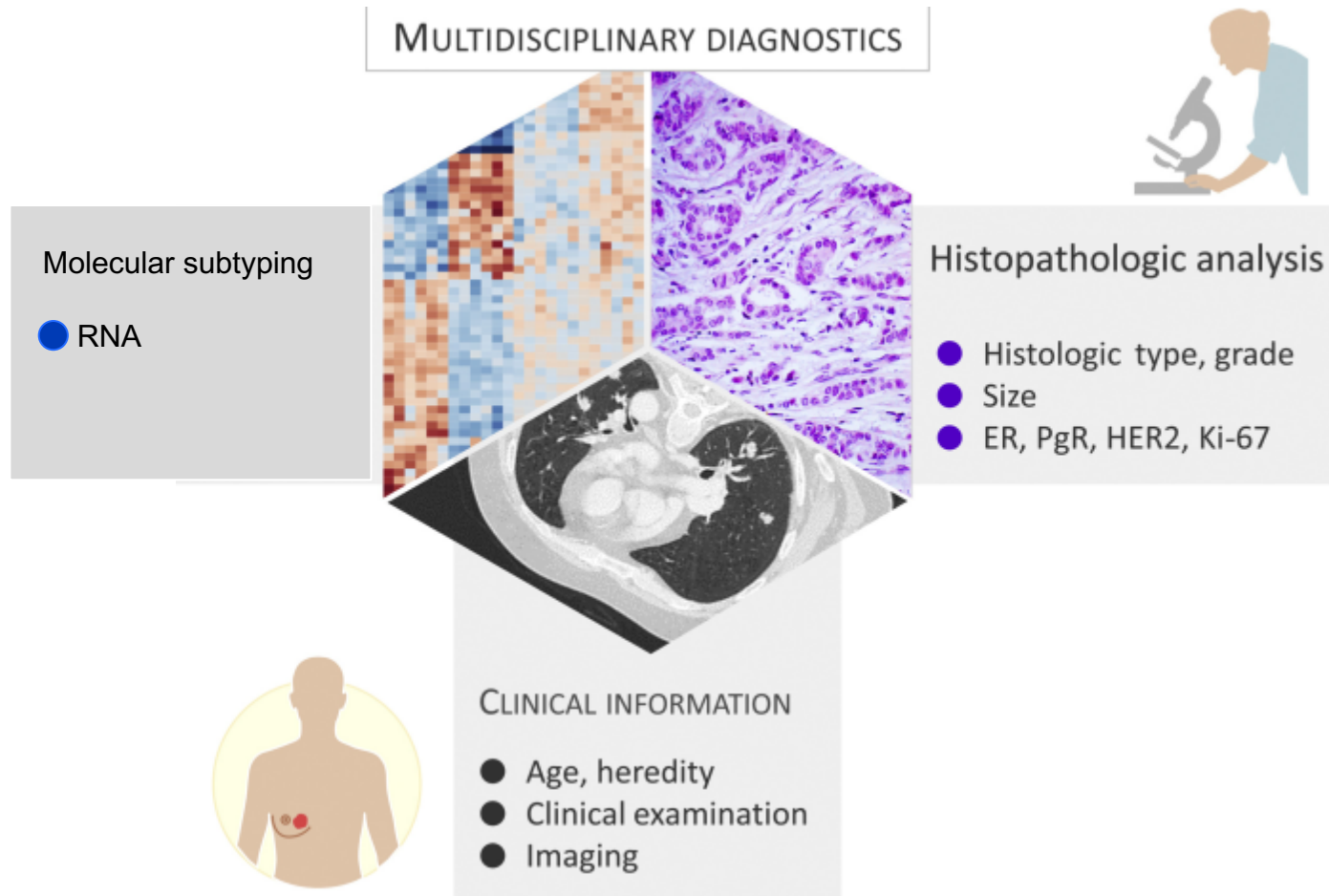


National Human
Genome Research
Institute



- sikre effektiv og præcis diagnostik og facilitere behandlingsbeslutninger
- skal være på forkant med molekylærgenetiske analyser
- sikre at de kliniske afdelinger har adgang til high-throughput teknologier

Brystkræftdiagnostik er blevet multidisciplinær



letters to nature

.....

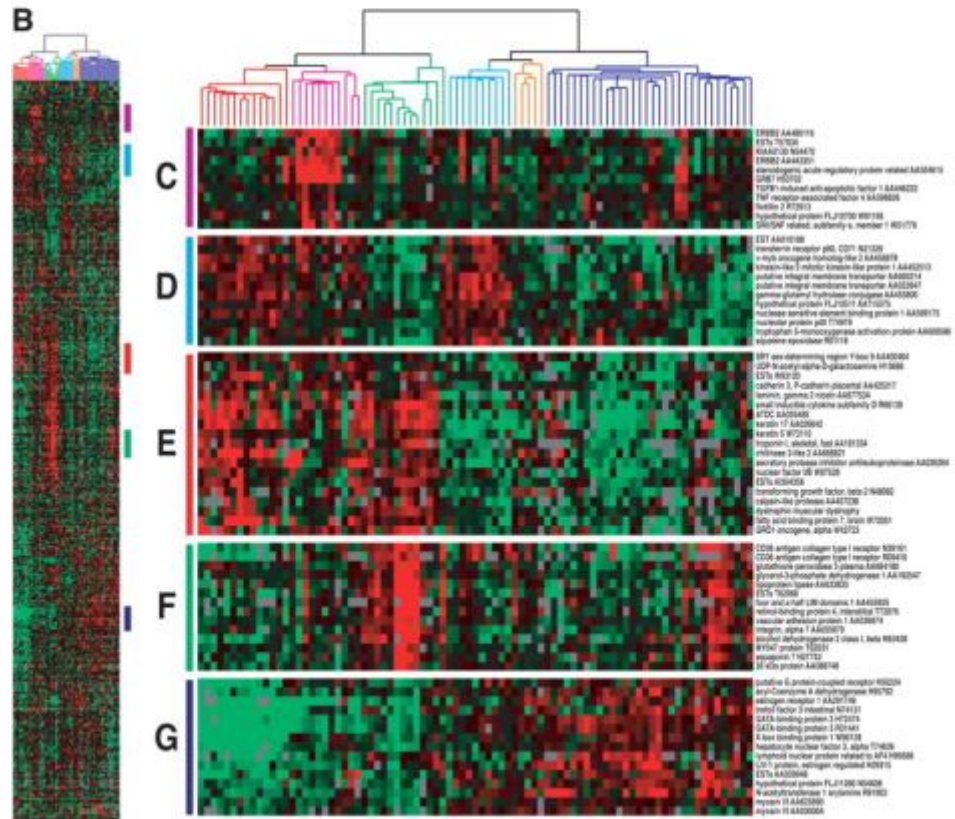
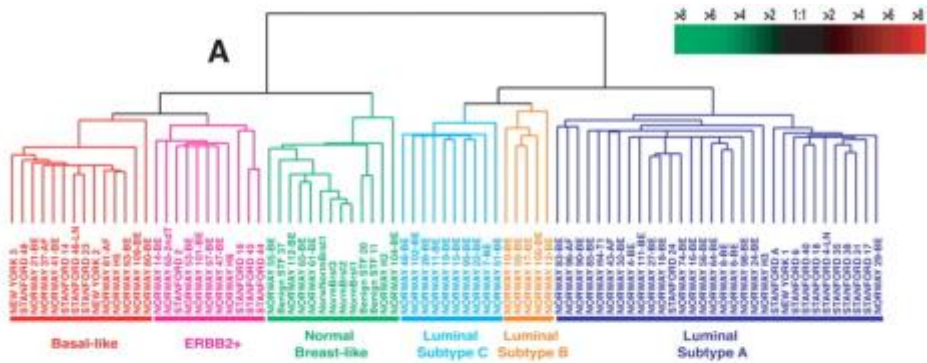
Molecular portraits of human breast tumours

**Charles M. Perou^{*†}, Therese Sørlie^{†‡}, Michael B. Eisen^{*},
Matt van de Rijn[§], Stefanie S. Jeffrey^{||}, Christian A. Rees^{*},
Jonathan R. Pollack[¶], Douglas T. Ross[¶], Hilde Johnsen[‡],
Lars A. Akslen[#], Øystein Fluge[☆], Alexander Pergamenschikov^{*},
Cheryl Williams^{*}, Shirley X. Zhu[§], Per E. Lønning^{**},
Anne-Lise Børresen-Dale[‡], Patrick O. Brown^{¶††} & David Botstein^{*}**

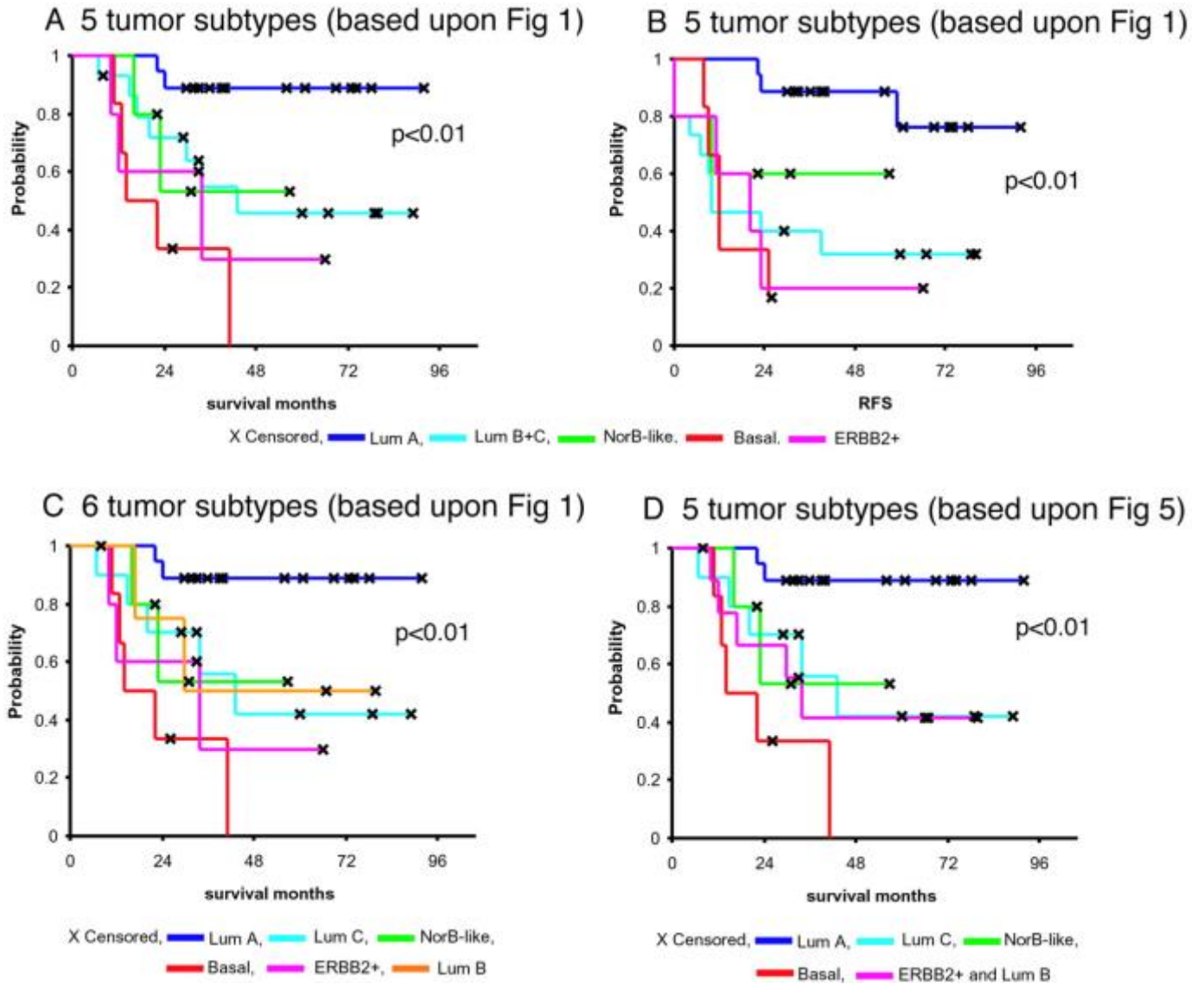
NATURE | VOL 406 | 17 AUGUST 2000 | www.nature.com

Gene expression patterns of breast carcinomas distinguish tumor subclasses with clinical implications

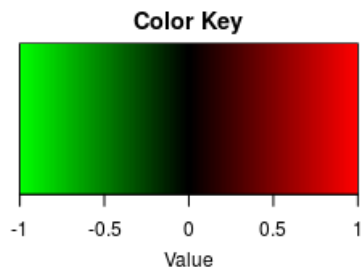
Therese Sørlie^{a,b,c}, Charles M. Perou^{a,d}, Robert Tibshirani^e, Turid Aas^f, Stephanie Geisler^g, Hilde Johnsen^b, Trevor Hastie^e,
Michael B. Eisen^h, Matt van de Rijnⁱ, Stefanie S. Jeffrey^j, Thor Thorsen^k, Hanne Quist^l, John C. Matese^c,
Patrick O. Brown^m, David Botstein^c, Per Eystein Lønning^g, and Anne-Lise Børresen-Dale^{b,n}



Therese Sørlie et al. PNAS 2001;98:10869-10874

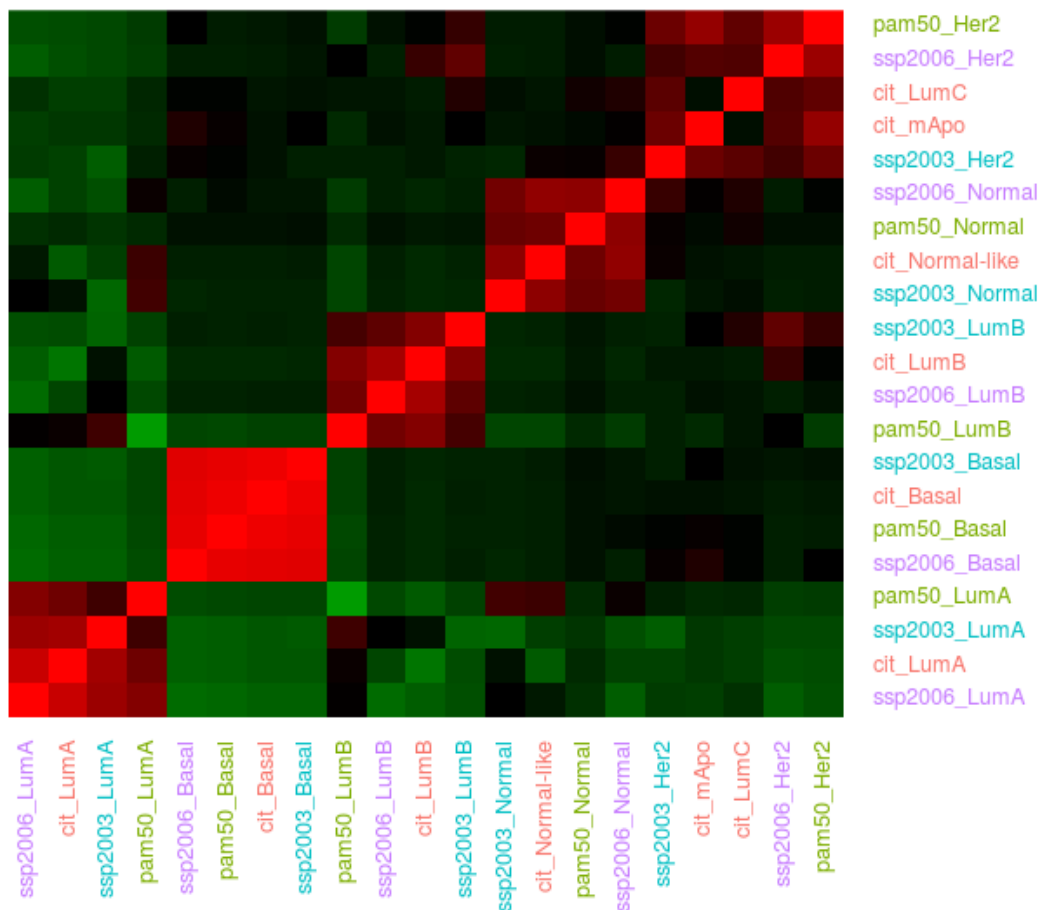


Korrelation af subtyper; forskellige signaturer



Hierarchical cluster analysis, unsupervised

- PAM50, 50
- SSP2006 (Hu, BMC)
- SSP2003 (Sørлие, PNAS)
- CIT (Guedj, Oncogene)



Molekylære subtyper; div. platforme

The NEW ENGLAND JOURNAL of MEDICINE

ESTABLISHED IN 1812

AUGUST 25, 2016

VOL. 375 NO. 8

70-Gene Signature as an Aid to Treatment Decisions in Early-Stage Breast Cancer



mammaprint

oncotype DX[®]
Breast Cancer Assay

Uncover the Unexpected™

Signature	Quality of gene expression	Gene expression	Residual gene score	Top 100 Residual gene score
ER, PR, p53, Ki67, Her2, Cyclin D1, Topoisomerase II α , CDK2, CDK4, CDK6, CDK8, CDK9, CDK10, CDK11, CDK12, CDK13, CDK14, CDK15, CDK16, CDK17, CDK18, CDK19, CDK20, CDK21, CDK22, CDK23, CDK24, CDK25, CDK26, CDK27, CDK28, CDK29, CDK30, CDK31, CDK32, CDK33, CDK34, CDK35, CDK36, CDK37, CDK38, CDK39, CDK40, CDK41, CDK42, CDK43, CDK44, CDK45, CDK46, CDK47, CDK48, CDK49, CDK50, CDK51, CDK52, CDK53, CDK54, CDK55, CDK56, CDK57, CDK58, CDK59, CDK60, CDK61, CDK62, CDK63, CDK64, CDK65, CDK66, CDK67, CDK68, CDK69, CDK70	--	--	--	--
Nodes	ER+, No patients treated			

prosigna™ Breast cancer gene signature assay

Subtypeklassifikationsmodel på RH - 2014

Oncogene (2012) 31, 1196-1206

© 2012 Macmillan Publishers Limited. All rights reserved 0950-9232/12

www.nature.com/fonc

ONCOGENOMICS

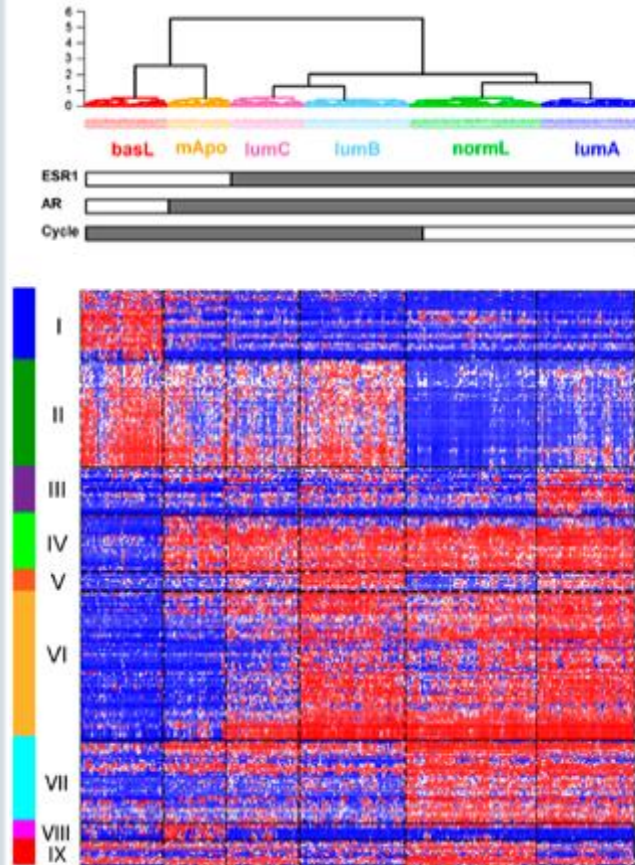
A refined molecular taxonomy of breast

M Guedj^{1,15}, L Marisa^{1,15}, A de Reynies^{1,15}, B Orset
F Lerebours⁶, P Finetti⁷, M Longy⁵, P Bertheau⁸, I
JP Feugeas^{10,11,12}, I Bièche⁶, J Lehmann-Che^{10,11,12},
H de Thé^{10,11,12,15} and C Theillet^{2,13,14,15}

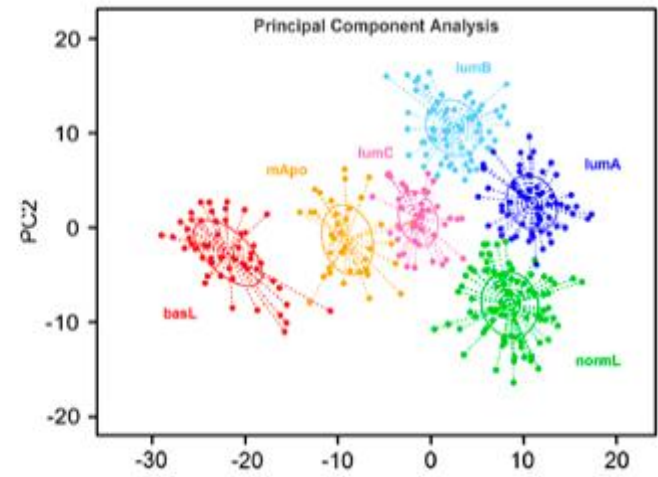
¹Ligue Nationale Contre le Cancer, Cartes d'Identité des Tumeurs pour
Cancérologie de Montpellier, Montpellier, France; ²CRLC Val d'Aurelle
Pathology, CRLC Val d'Aurelle Paul Lamarque, Montpellier, France
Université Victor Segalen Bordeaux-2, Bordeaux, France; ⁶Oncogenet
René Huguenin, St Cloud, France; ⁷Department of Molecular Oncology
Institut Paoli Calmette, Marseille, France; ⁸Hopital St Louis APHP,
Paris, France; ⁹Fédération Nationale des Centres de Lutte Contre le Cancer
Saint-Louis APHP, Paris, France; ¹⁰INSERM/CNRS UMR 944/7212, Paris
Paris-7 Denis Diderot, Paris, France; ¹¹INSERM U896, CRLC Val d'Aurelle-Paul Lamarque, Montpellier, France and ¹⁴Université
Montpellier 1, Montpellier, France

- 256 gener
- 6 subklasser
- Genomisk data (incl.CNV)
- Korrelerer med kliniske karakteristika og prognose
- Robust (>3000 pt.)
- Affymetrix platform (open)
- "In house"

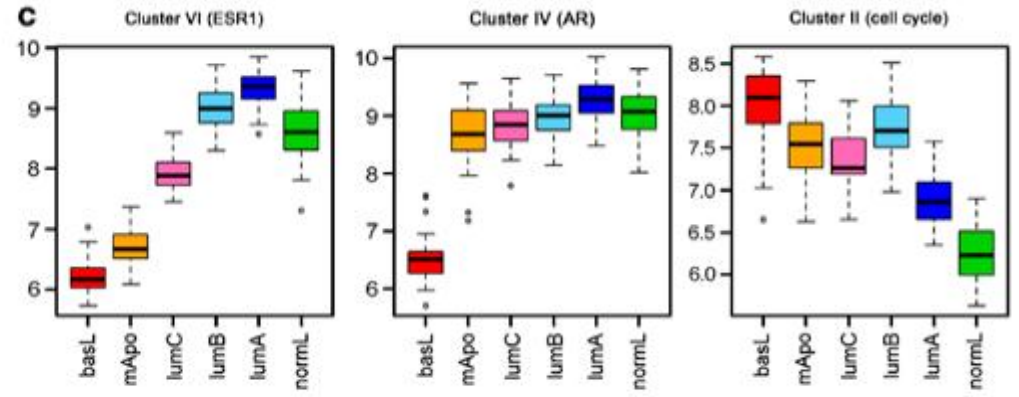
a



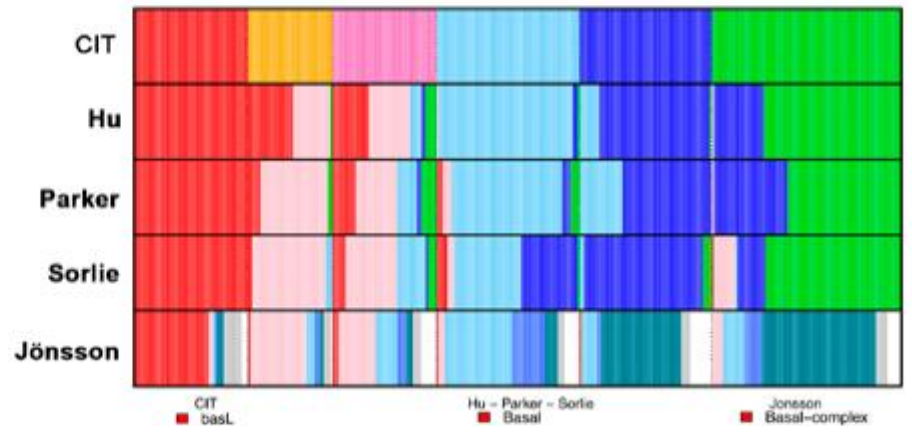
b

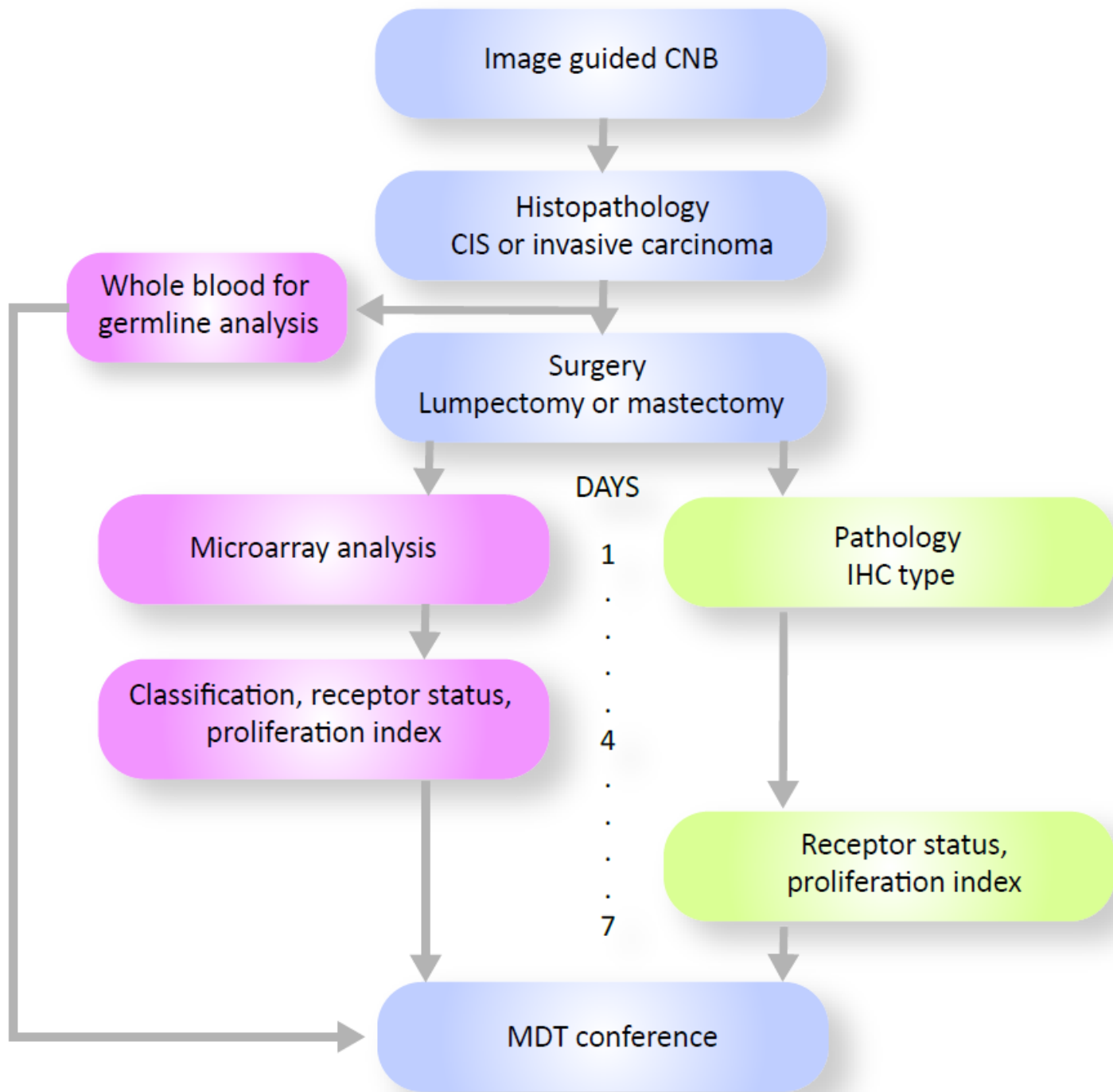


c



d





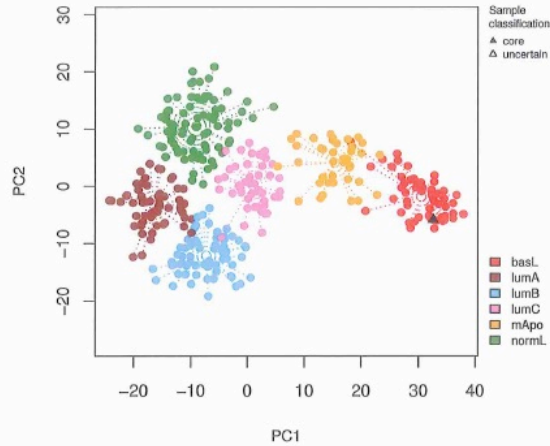


Figure 1: PCA on CIT data used to classify dataset & sample (black).

	Classification	Confidence	Mixed
CIT	basL	CORE	-
PAM50	Basal	HIGH	-

CIT: Possible confidences are: CORE, MIXED, and OUTLIER. If the confidence is MIXED, *Classification* lists the second of the two overlapping clusters under *Mixed*. In the case of an OUTLIER, the nearest cluster is listed under *Classification*.

PAM50: *Confidence* relates to the correlation coefficient (r) between the sample and the nearest cluster of PAM50 classification. Possible confidences are: HIGH ($r \geq 0.75$), LOW ($0.75 > r \geq 0.25$), and OUTLIER ($r < 0.25$).

Expression profiles

Her2	ERBB2	negative
Estrogen receptor	ESR1	negative
Progesterone receptor	PCR	negative

Proliferation Index(PI) score (tumor PI >5.5): 8.34

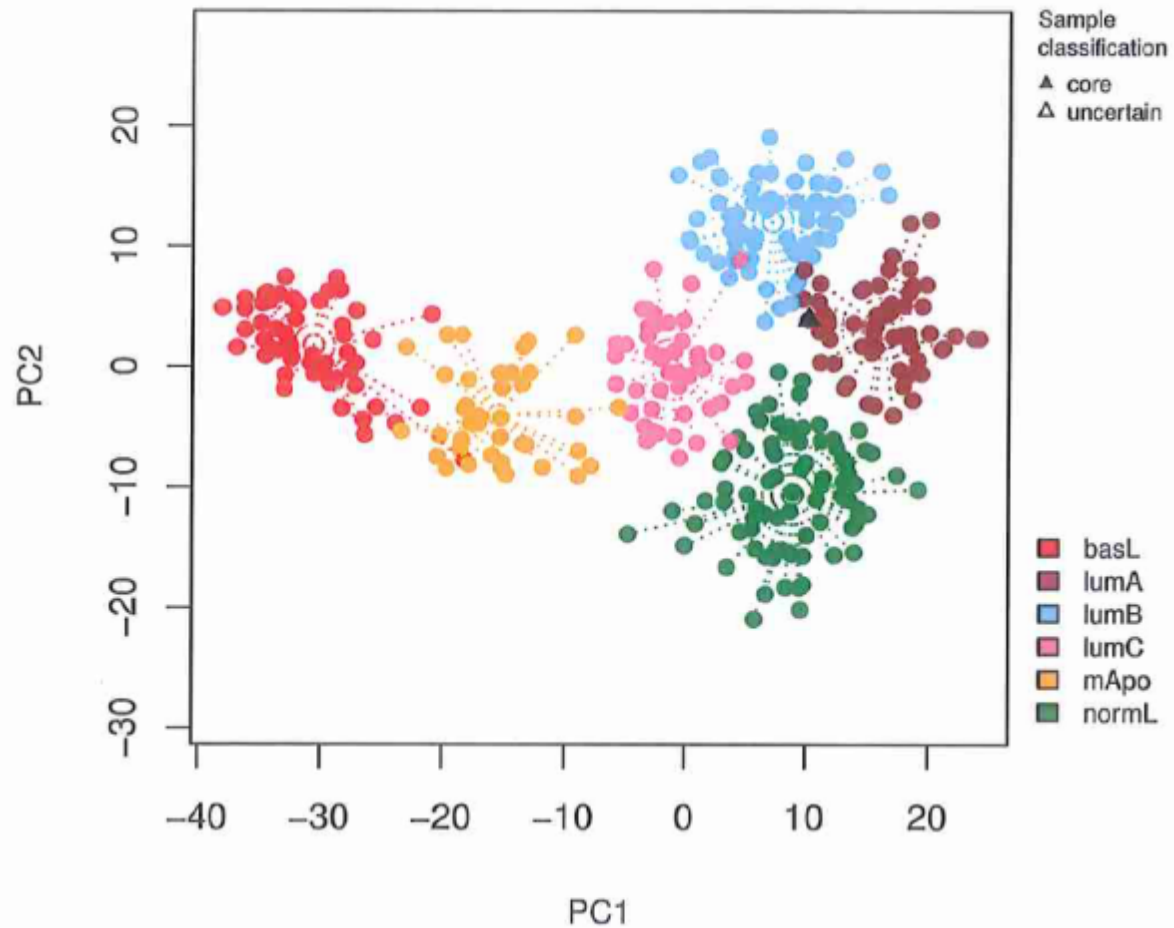


Figure 1: PCA on CIT data used to classify dataset & sample (black).

	Classification	Confidence	Mixed
CIT	lumA	CORE	--
PAM50	LumA	LOW	--

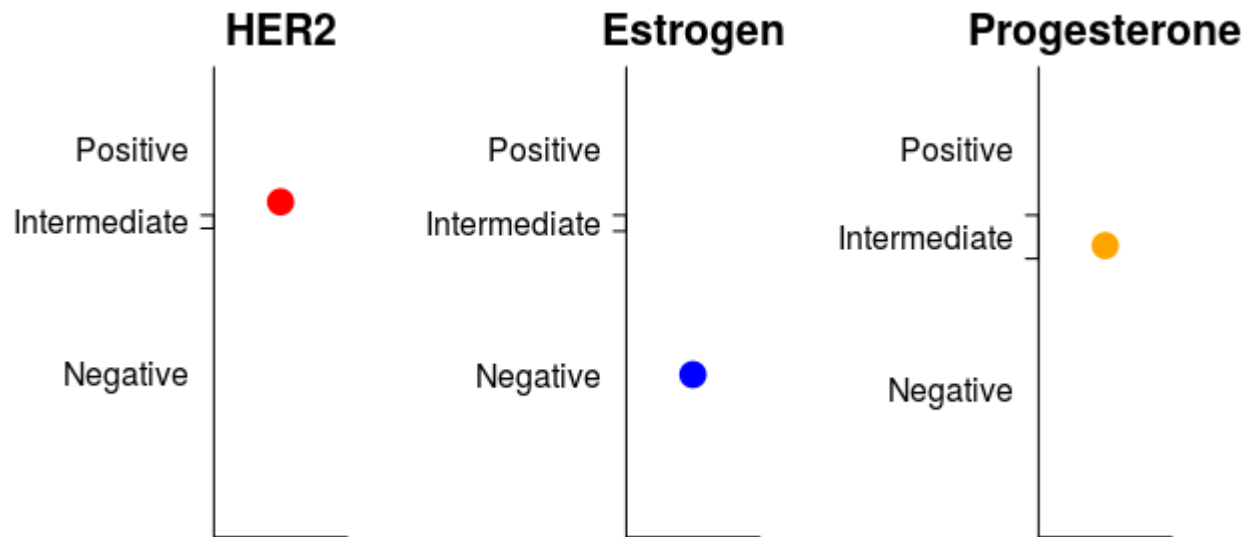
Receptorstatus og proliferation

Expression profiles

Her2	ERBB2	negative
Estrogen receptor	ESR1	positive
Progesterone receptor	PGR	intermediate

Proliferation Index(PI) score (tumor PI >5.5): 6.29

Ny "feature" på svar

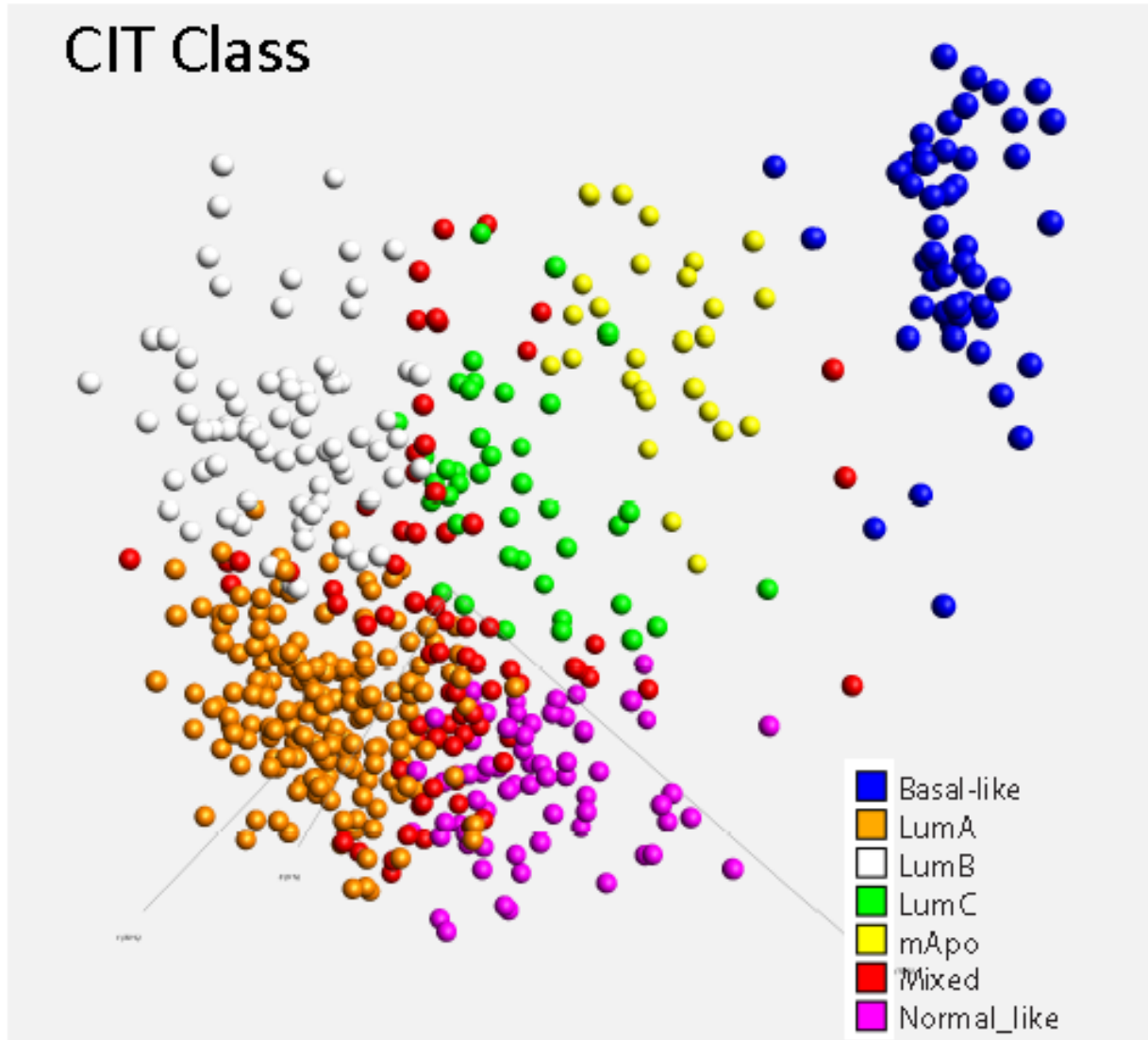


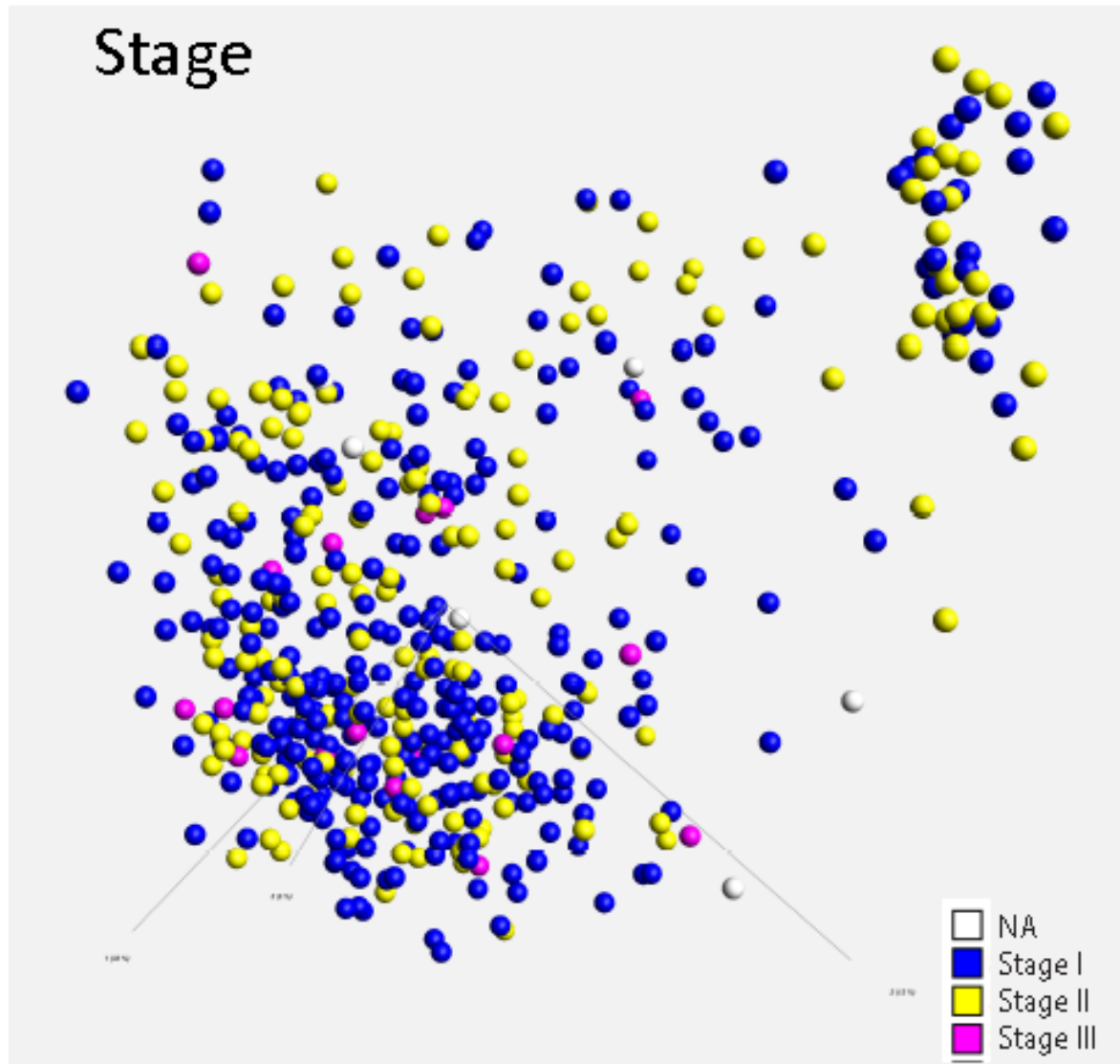
Status efter 1 år med molytlære subtyper

- Opstart nov. 2014
- Succesrate
- Fordeling
- Receptor (mRNA vs IHC)
- Ki67 vs Prol. Index (PI)
- Genetisk disponering

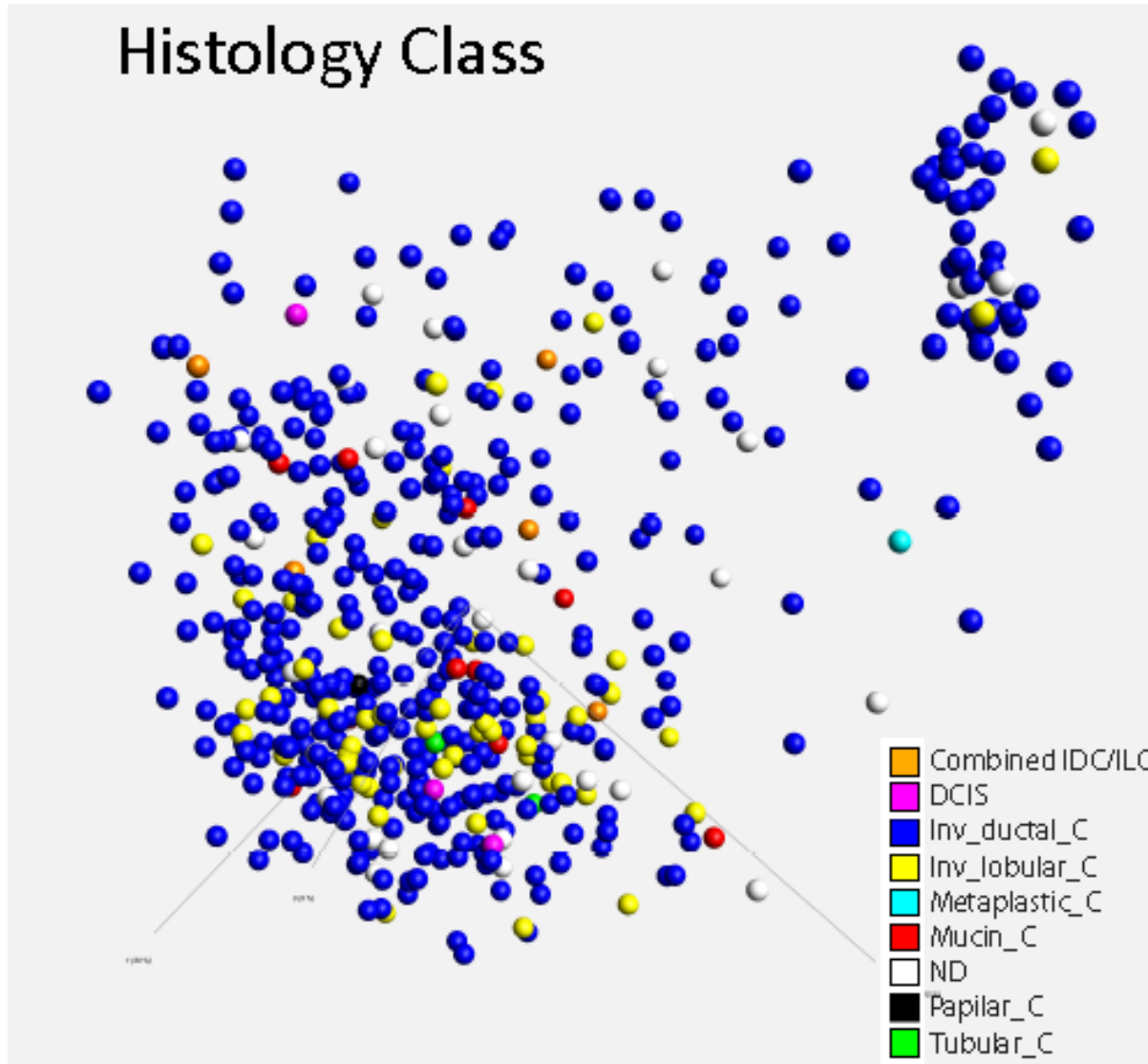
- Stadiet I-III: 524 vævsprøver
- 4 prøver udgik (1 QC af RNA og 3 normalvæv)
- I alt 520 til subtype (3-10 dage)

CIT Class





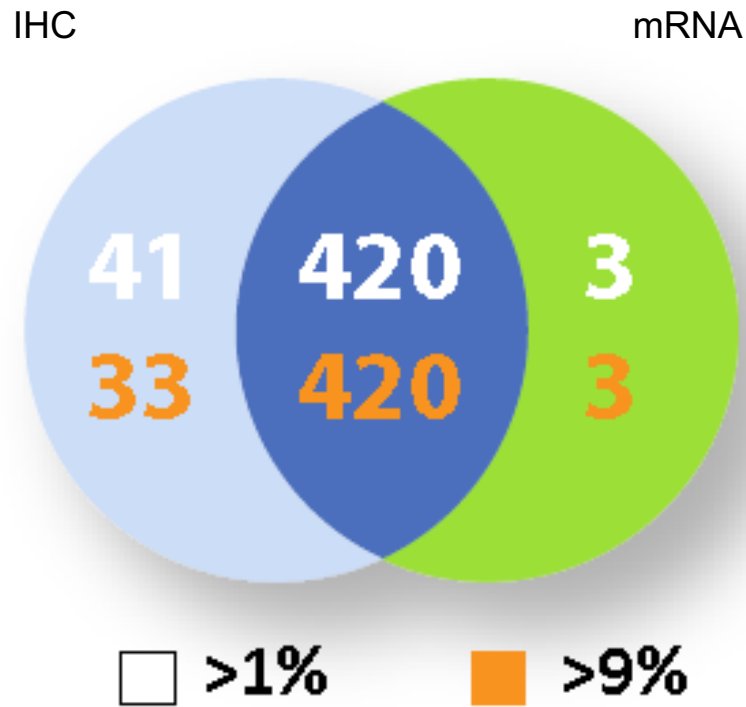
Histology Class



Subtype fordeling

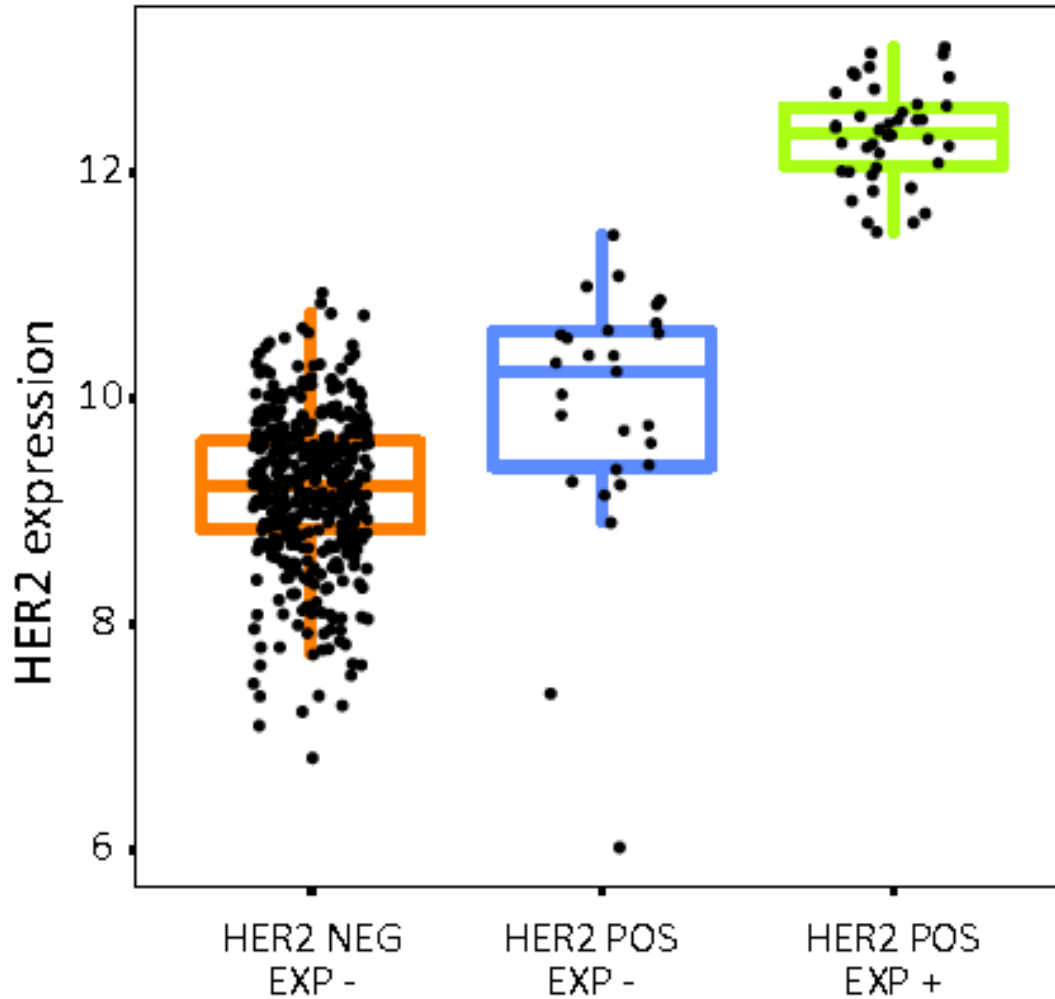
Subclass	BasL	mApo	LumC	LumB	LumA	NormL	Mixed
All (n=520)	50	28	40	76	182	68	76
	(9.6%)	(5.4%)	(7.7%)	(14.6%)	(35.0%)	(13.1%)	(14.6%)

Receptorstatus_ER



91% overensstemmelse (420/461)

Receptorstatus_HER2



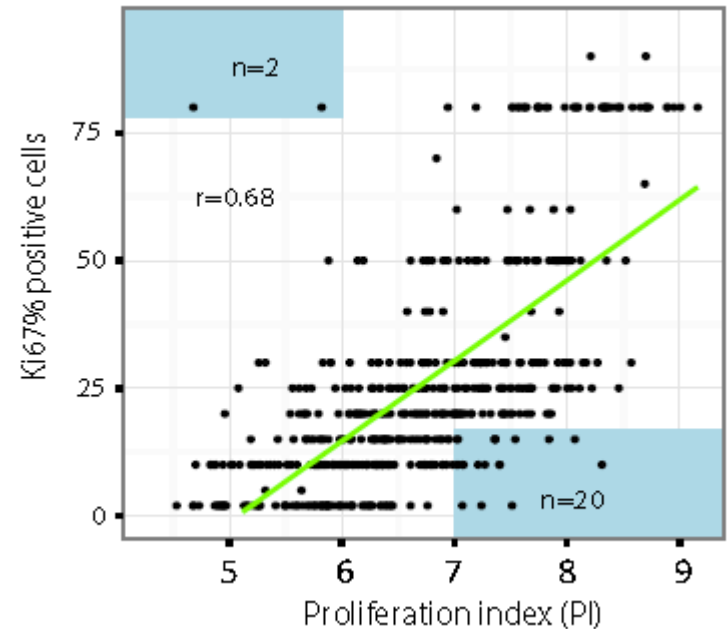
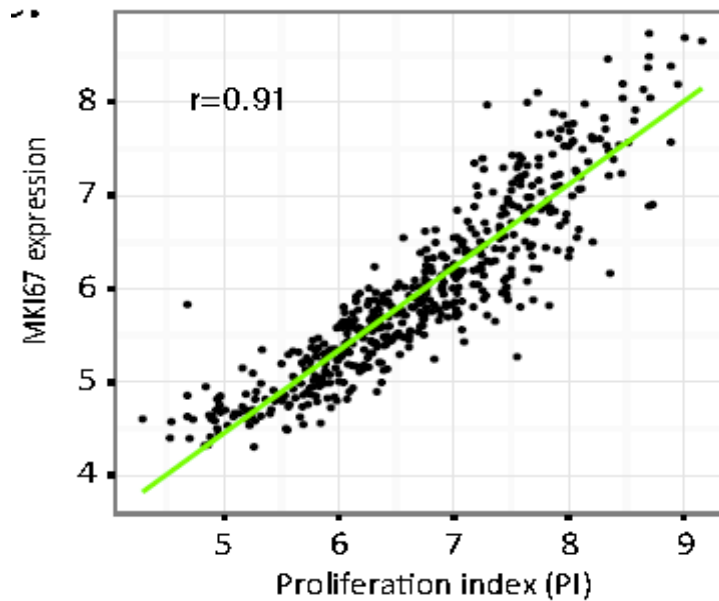
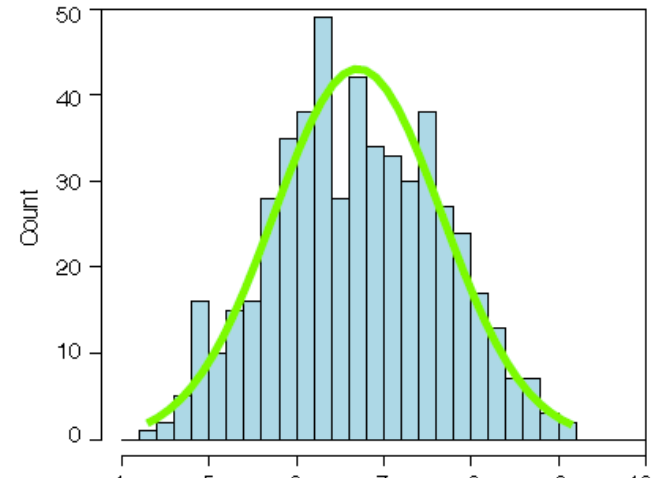
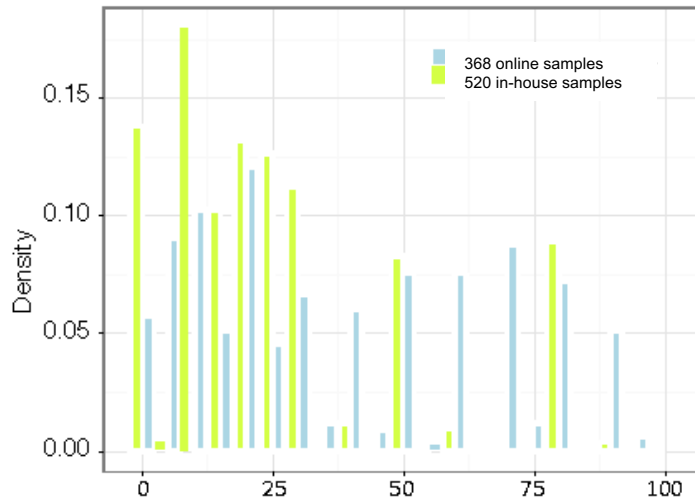
Receptorstatus_HER2

- HER2negativ (IHC (0-2) vs mRNA): ≈ 100% korrelation
- HER2+ status (IHC/FISH) vs mRNA: diskrepans 39% (27mRNA neg/69 HER2+)

- Reevaluering v/spec. mammapatolog
- Forklaring i 70% af prøverne med diskrepans
- Forskellige tumorer, intratumor heterogenitet, borderline, ændring til HER2 neg. ved 2. gennemgang

HER2-mRNA bestemmelse i kombination med subtypebestemmelse er et diagnostisk supplement til det eksisterende set-up.

Ki67_proliferative index



- >99% af tumorbiopsier kunne anvendes til molekylær subtypebestemmelse
- Diagnostisk rapport klar inden MDT

- >99% af tumorbiopsier kunne anvendes til molekylær subtypebestemmelse
- Diagnostisk rapport klar inden MDT
- 39 patienter var i Q2/intermediær (prognostic standard mortality rate index (PSMRI)) udviklet af DBCG
- 16 (41%) klassificeret som LumA (+antiendokrin behandling, - chemotherapy)

- >99% af tumorbiopsier kunne anvendes til molekylær subtypebestemmelse
- Diagnostisk rapport klar inden MDT
- 39 patienter var i Q2/intermediær (prognostic standard mortality rate index (PSMRI)) udviklet af DBCG
- 16 (41%) klassificeret som LumA (+antiendokrin behandling, - chemotherapy)
- Overvejende korrelation mRNA < IHC hormone receptor status
- IHC Ki67 proliferative index (PI) korrelerede ikke med mRNA PI index

- >99% af tumorbiopsier kunne anvendes til molekylær subtypebestemmelse
- Diagnostisk rapport klar inden MDT
- 39 patienter var i Q2/intermediær (prognostic standard mortality rate index (PSMRi)) udviklet af DBCG
- 16 (41%) klassificeret som LumA (+antiendokrin behandling, - chemotherapy)
- Overvejende korrelation mRNA > IHC hormone receptor status
- IHC Ki67 proliferative index (PI) korrelerede ikke med mRNA PI index
- 41 patienter med basal-like subtype blev *BRCA1/2* testet uanset familieanamnese
- 17% var bærere af en patogen *BRCA1/2* mutation

ACTA ONCOLOGICA, 2018
VOL. 57, NO. 1, 51–57
<https://doi.org/10.1080/0284186X.2017.1398837>



Taylor & Francis
Taylor & Francis Group

ORIGINAL ARTICLE

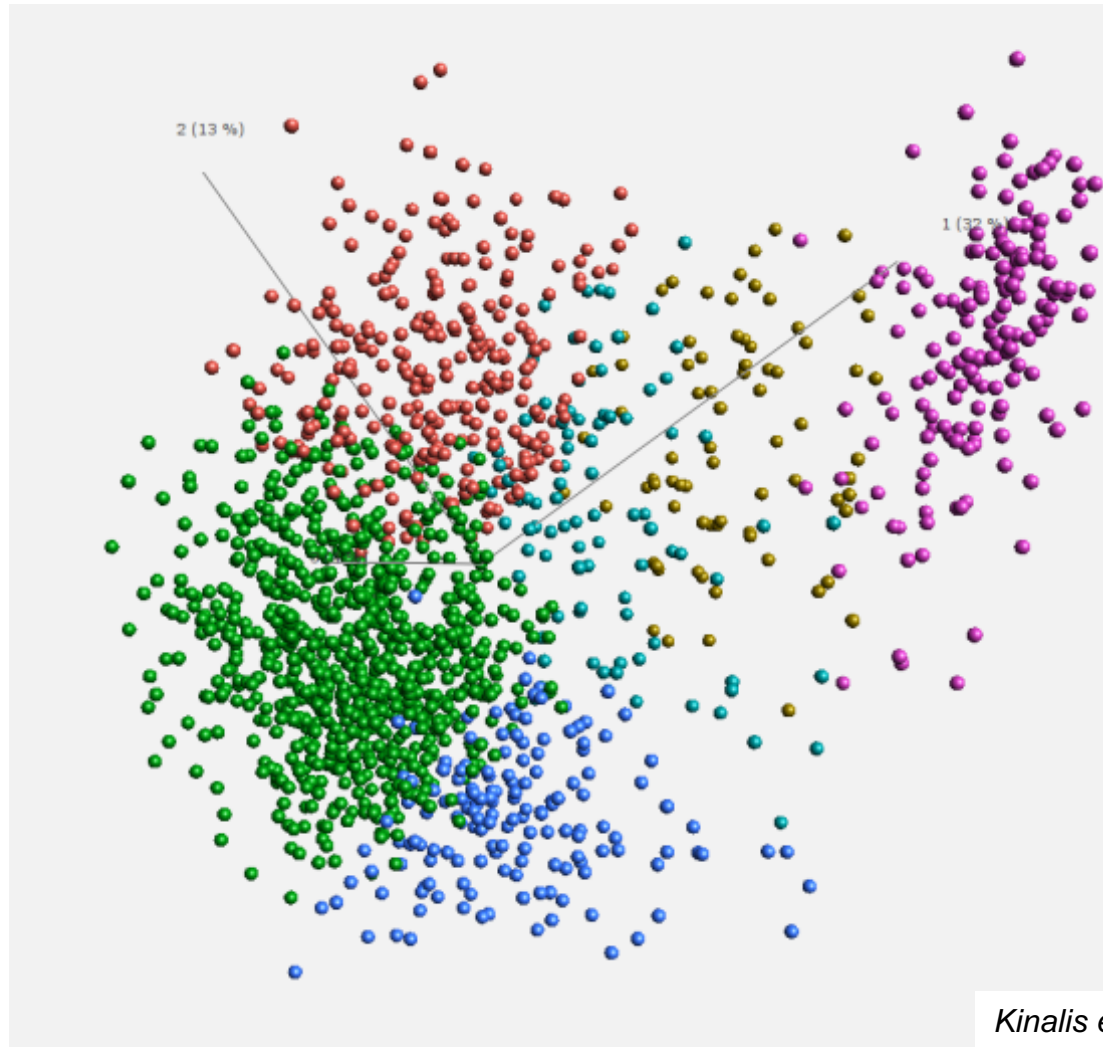


Characterization of basal-like subtype in a Danish consecutive primary breast cancer cohort

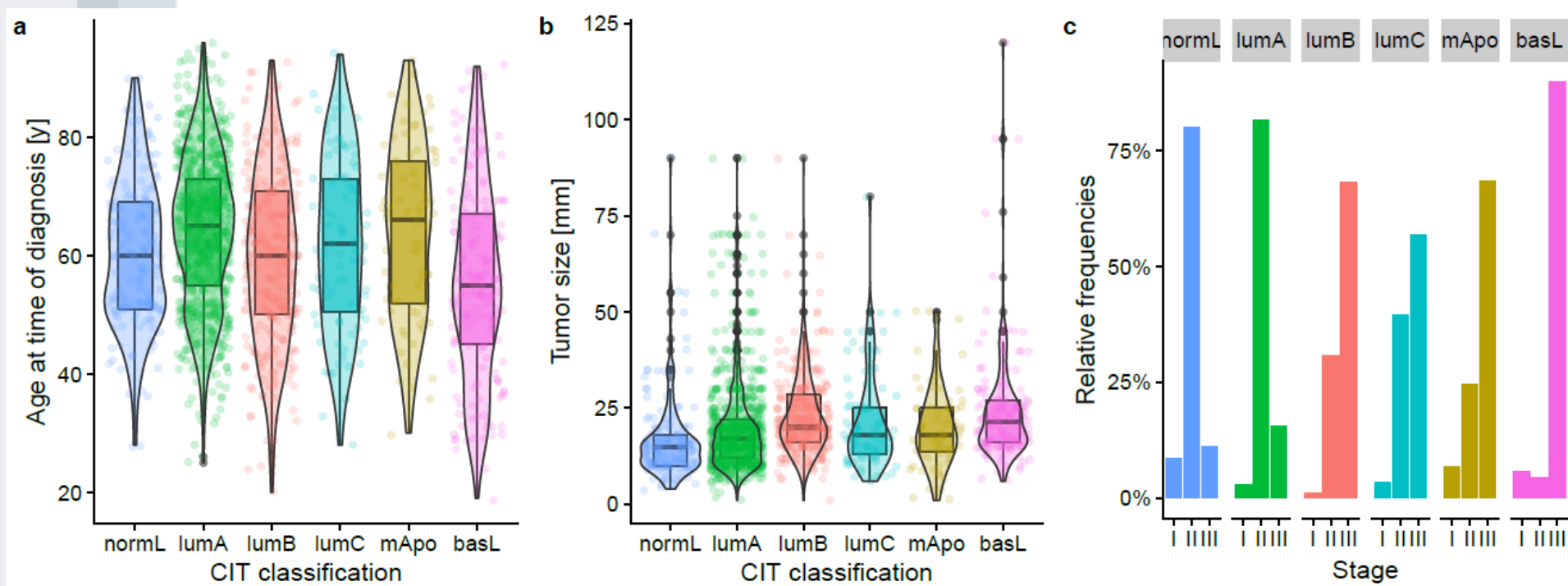
Savvas Kinalis^a, Finn Cilius Nielsen^a, Maj-Lis Talman^b, Bent Ejlersen^{c,d} and Maria Rossing^a

^aCenter for Genomic Medicine, Rigshospitalet, Copenhagen University Hospital, Copenhagen, Denmark; ^bDepartment of Pathology, Rigshospitalet, Copenhagen University Hospital, Copenhagen, Denmark; ^cDenmark Danish Breast Cancer Cooperative Group, Rigshospitalet, Copenhagen University Hospital, Copenhagen, Denmark; ^dDepartment of Clinical Oncology, Copenhagen University Hospital, Copenhagen, Denmark

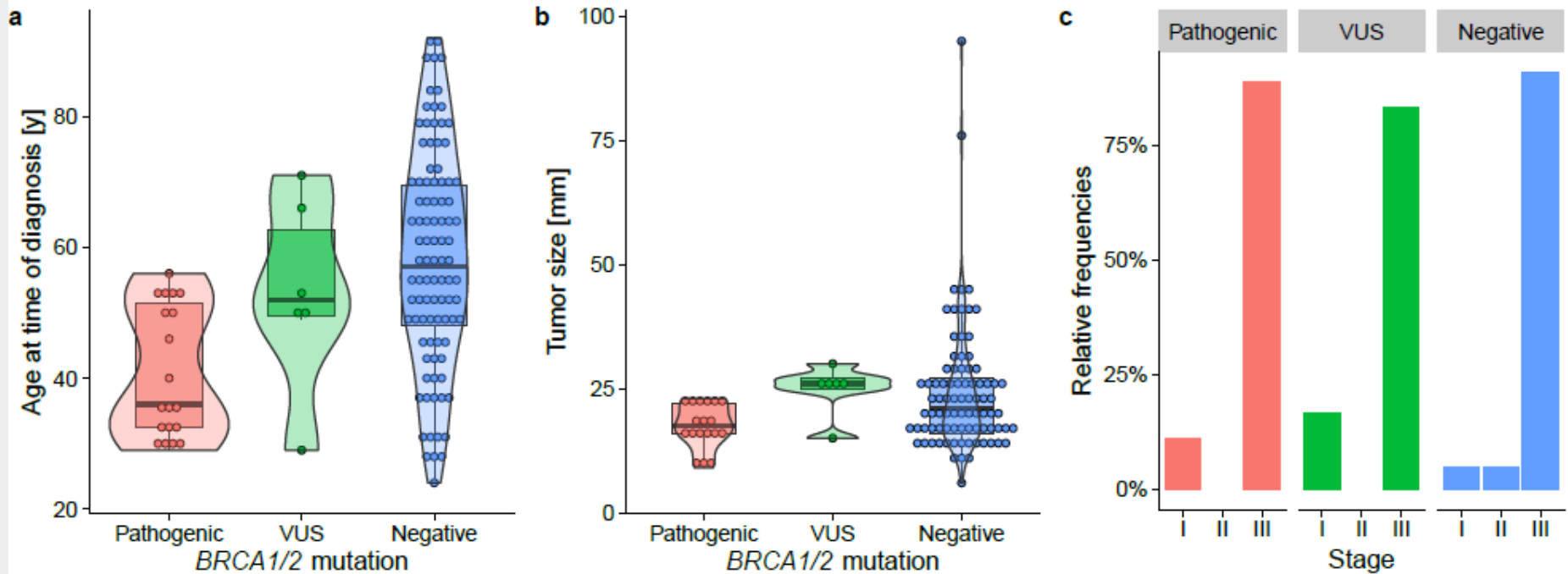
Basal-like subtype



Basal-like subtype (n=168)



Basal-like subtype; *BRCA1/2* screenet



Konklusion Basal-like patienter

- Laveste mediane alder
- Højeste mediane tumor størrelse
- Flertal diagnosticeret i stadie III
- 120 screenet (19 *BRCA1/2*-bærere)
- *BRCA1/2*-bærere var signifikant yngre

Tak til samarbejdspartnere

- Maj-Britt Jensen
- Ann Knoop
- Maj-Lis Talman
- Niels Kroman
- Finn Cilius Nielsen
- Bent Ejlersen

