



Molecular genetic diagnostics in breast cancer patients: Insights from a real life cohort

Dr. Martin Schulze, Center for Human Genetics, Tübingen, Germany



Conflict of interest



- Full-time employee at the Center for Human Genetics in Tübingen, Germany
- Nothing to declare



Patient cohort from Germany and other countries

- The Center for Human Genetics in Tübingen (~200 staff) offers a broad range of molecular genetic diagnostics with a focus on cancer and rare diseases (CLIA certified)
- We offer **germline testing** and **somatic tumour diagnostics**
- Our patients are counselled directly in Tübingen and we receive additional samples from German hospitals and private clinics
- Samples from international patients are also part of the cohort provided by our partner:
Center for Genomics and Transcriptomics



Germline & somatic diagnostic testing

- Germline diagnostic testing for 3719 cancer patients since 2016
 - Including 1024 breast cancer patients (~27%)
- Somatic diagnostic testing for 7426 cancer patients since 2018
 - Including 948 breast cancer patients (~13%)
- All germline cases received either panel (>120 genes) or exome sequencing (WES)
- All somatic diagnostics are based on tumour:normal comparison (>700 gene panel or WES)

- Diagnostic yield is defined as an ACMG/ACGS class 4/5 variant is detected (likely pathogenic (LP) / pathogenic (P))
- *BRCA1+2*: 6.45% yield
- Core genes (sum total): 11.23% yield
- Another 5.83 % cases had LP/P variants in other genes!
- Remark: Our center is not specialized in HBOC patient care; hence our cohort is not enriched in familial HBOC cases!

Core genes

BRCA2

BRCA1

CHEK2

ATM

PALB2

BRIP1

BARD1

RAD51C

RAD51D

TP53

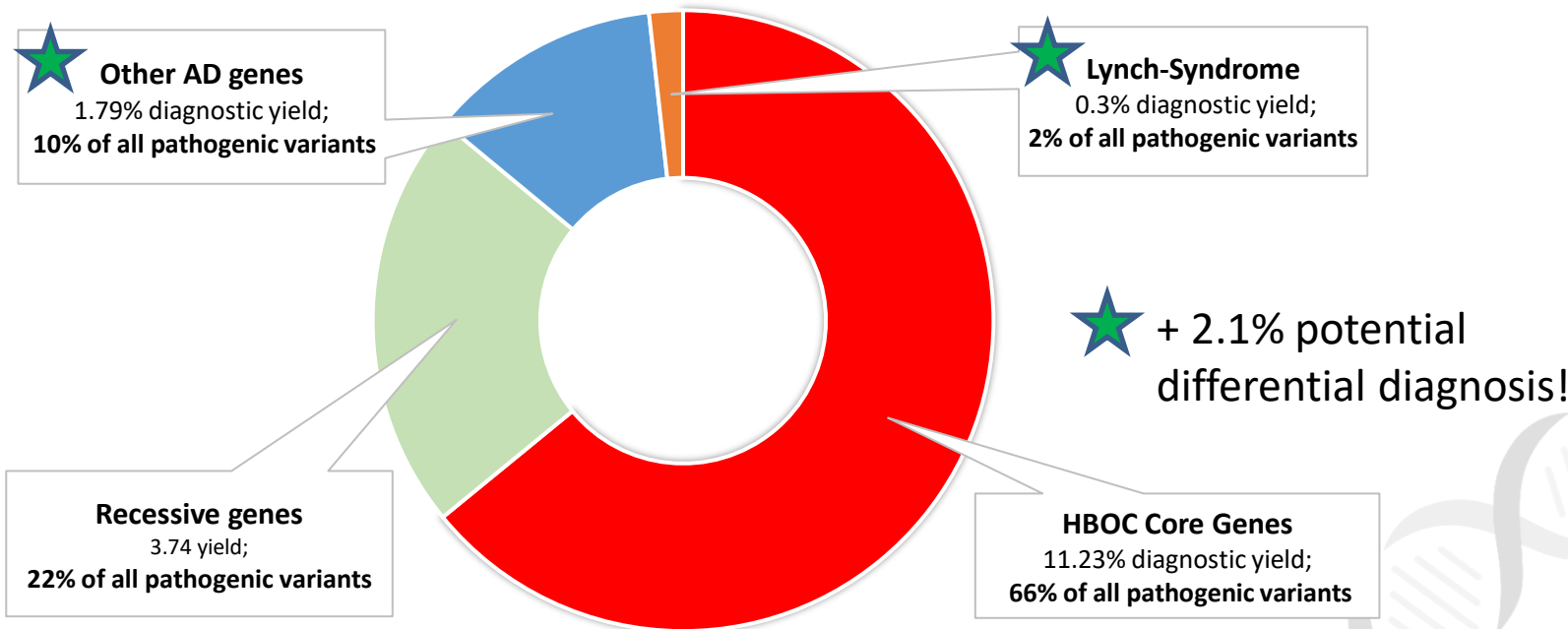
CDH1

NF1

PTEN

STK11

Distribution of pathogenic variants among gene groups

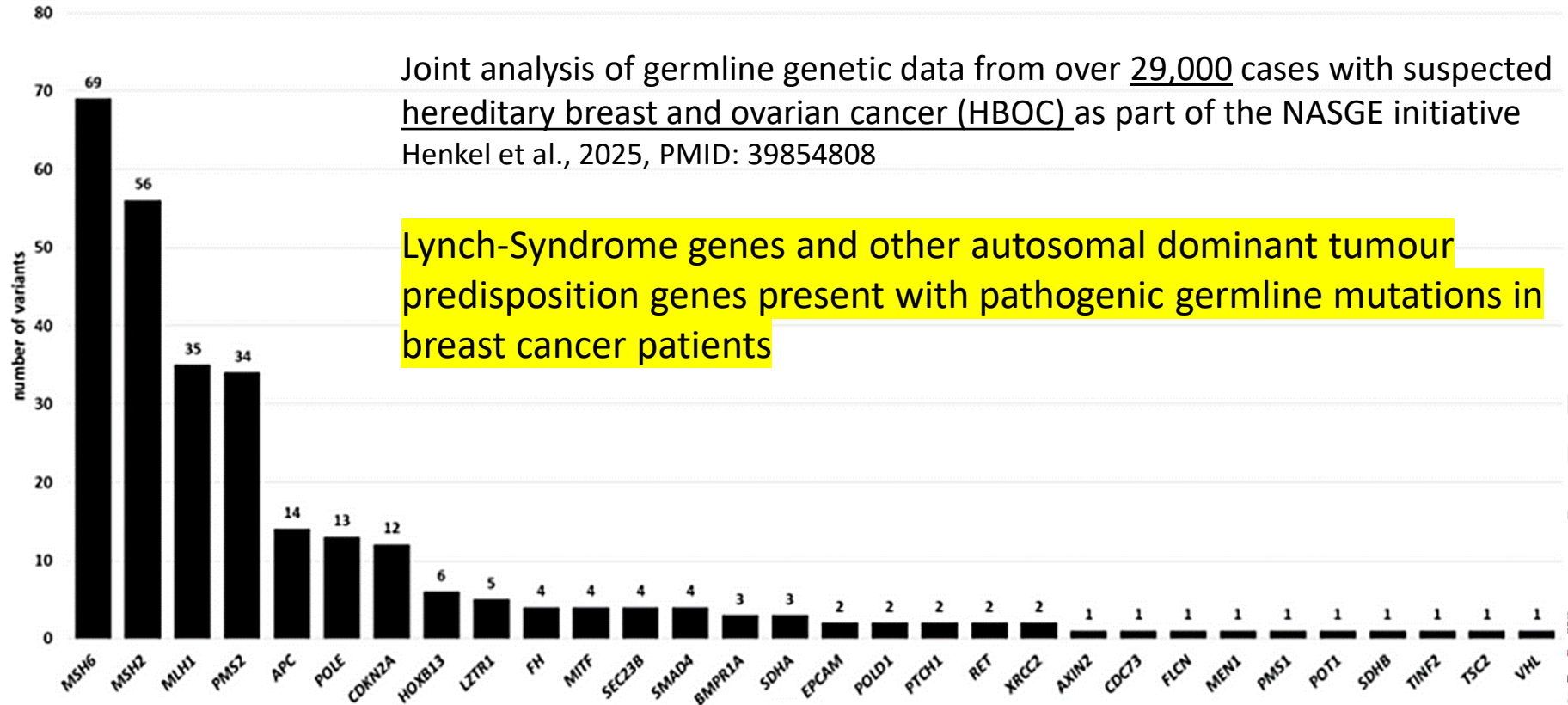


Heterozygous carriers at risk?

Germline diagnostics

non-core genes_autosomal-dominant

■ (likely) pathogenic



Germline mutations – somatic diagnostics cases

- Patients present with breast cancer
 - All germline panel genes are always analysed in somatic diagnostics as part of the tumour-normal comparison workflow
 - Patients/referring physicians do not always request familial predisposition testing, though patients with hereditary breast cancer can be part of the cohort
- > Such patients are more likely have “sporadic”/non-hereditary breast cancer

Germline mutations in somatic diagnostics cases

Somatic cases - distribution of pathogenic germline variants among gene groups



Other AD genes
2.56% diagnostic yield;
13.18% of all pathogenic variants



Lynch-Syndrome
0.93% diagnostic yield;
5% of all pathogenic variants



+ 3.49 % potential differential diagnosis!

	Testing condition	
	Active tumor	Family history
Core Genes	9.67%	11.23%
Recessive genes	6.26%	3.74%
Other AD genes	2.56%	1.79%
Lynch-Syndrome	0.93%	0.3%

Recessive genes
6.26 yield;
32% of all pathogenic variants

HBOC core genes
9.67% diagnostic yield;
50% of all pathogenic variants

Somatic diagnostics - Biomarkers

- Somatic diagnostics covers the following additional Biomarkers
 - Homologous recombination deficiency (HRD) based on NGS data
 - Microsatellite instability (MSI) prediction and TMB calculation based on NGS data
 - Viral infection screening (HPV, EBV, CMV, MCV)
 - RNAseq-based **gene fusion analysis** (optional) + DNAseq-based breakpoint detection (default)

Somatic diagnostics - Biomarkers

- HRD was detected in 44% of analysis
- TMB high (>10) was determined for 4.33% of breast cancer cases
- MSI (unstable) was determined for 0.17% of breast cancer cases

-> Therapeutic options are detected outside the classic HBOC gene spectrum

- No cases presented with a viral infection of the tumor tissue



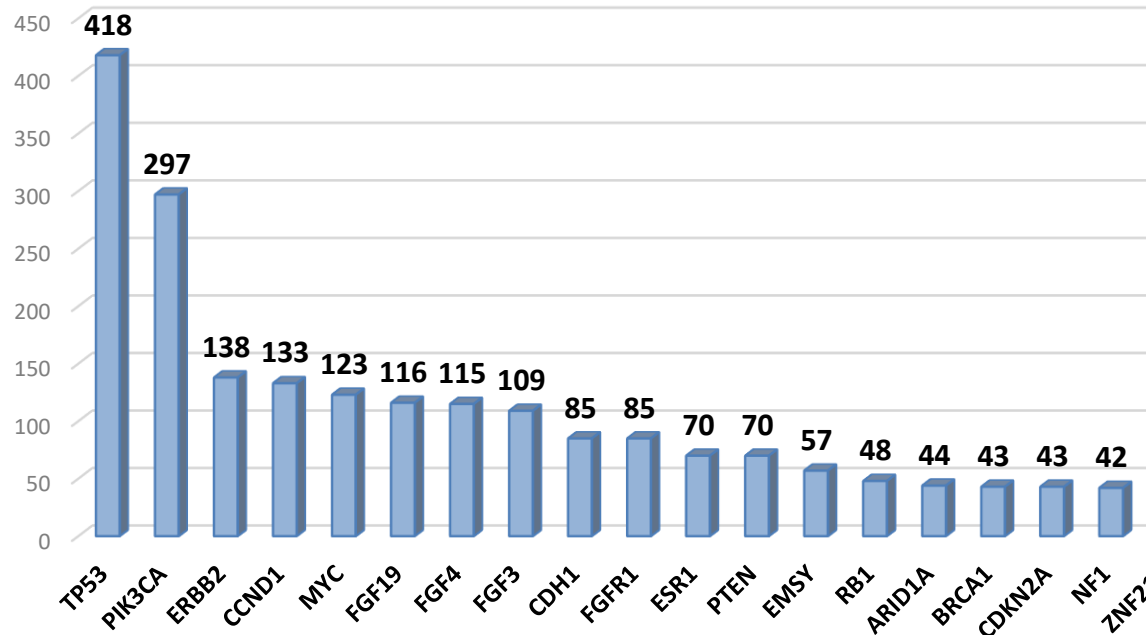
Somatic diagnostics – gene fusions in breast cancer?

- 392 RNAseq-based fusion analyses were performed for breast cancer patients using an LDT panel (>200 genes)
- 3.6% of all analyses yielded a potentially druggable gene fusion
- Oncogenic effect is mostly via **activation of oncogenes**, but **inactivation of tumour suppressor genes** is also observed
- Fusions are mostly unique events
- Fusions of unknown significance (VUS) are frequently detected (29% of analysed cases)

Druggable fusions	
first gene	second gene
NDUFB9	ATRX
ESR1	ARMT1
ESR1	CCDC170
ESR1	MYO9A
ESR1	TBCE
NSD3	FGFR1
AGAP1	FGFR2
FGFR2	TMC3-AS1
PVT1	MYC
NF1	NF1
BCL9	NOTCH2
ANKRD30A	NRG1
ZNF652	NTRK3
CCDC127	TERT

Somatic diagnostics

**Top 30 genes with mutations in somatic diagnosis
of breast cancer patients affected**



Drug classes indicated - TOP 30 genes

PARP inhibitor

mTOR inhibitor

AKT inhibitor

FGFR inhibitor

MEK inhibitor

CDK4/6 inhibitor

PI3K inhibitor

Immune checkpoint inhibitor

HDAC inhibitor

HER2 inhibitor / Antibody-drug conjugate

Selective estrogen receptor degrader (SERD)

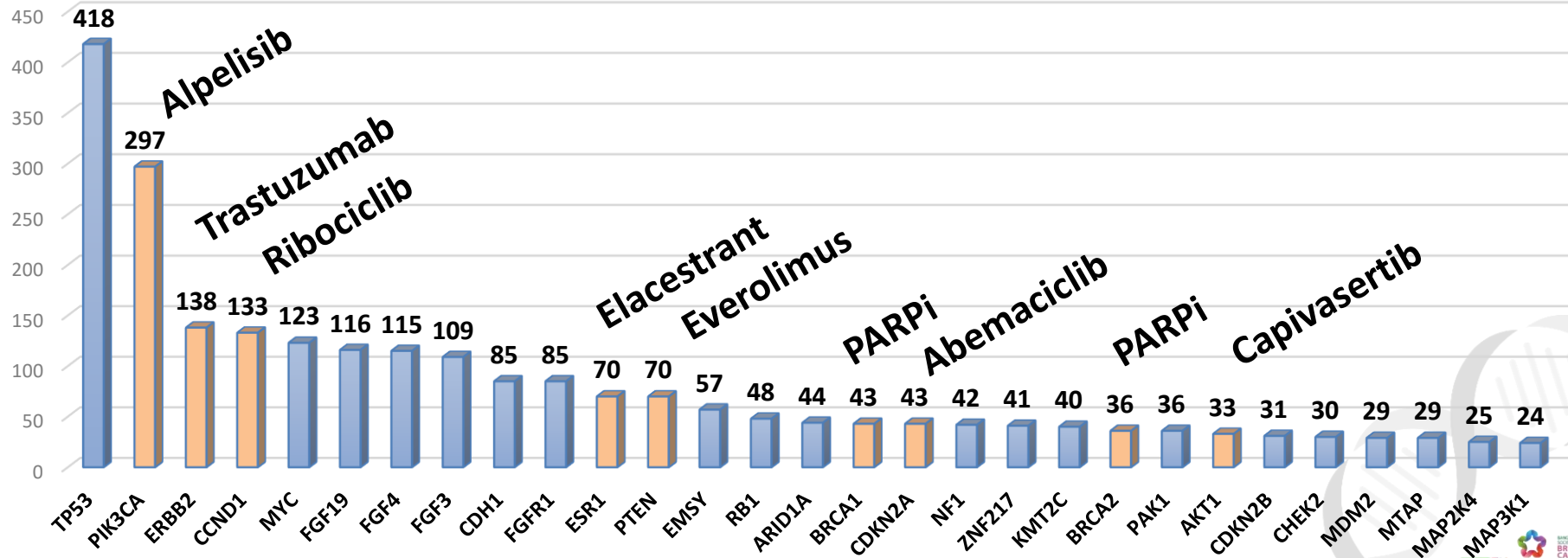
Endocrine therapy

EZH2 inhibitor

EGFR inhibitor

Somatic diagnostics

Top 30 genes with mutations identified via somatic diagnostics (SNV/CNV)
of breast cancer patients affected - **highlight**: FDA/EMA approved drugs available



Conclusions – genetic diagnostics in breast cancer

- Choose comprehensive panels in germline testing. It's not all in the core genes. For affected patients, always combine germline and somatic testing!
 - Always choose tumour:normal comparison to understand what really drives the cancer
 - This approach also allows a reliable calculation of biomarkers (e.g. TMB,...) based on NGS data
- For somatic diagnostics, fusion detection can lead to additional therapeutic options
- Selection of the best therapeutic option for a patient after somatic diagnostics does highly benefit from consulting a **molecular tumour board**

Thank you!

Zentrum für Humangenetik
Paul-Ehrlich-Str. 23
D-72076 Tübingen

info@humangenetik-tuebingen.de
www.humangenetik-tuebingen.de

