
Tumorale Heterogenität – SATURN-3

Carsten Denkert

Philipps Universität Marburg

in Kooperation mit

2.- 3. März 2023

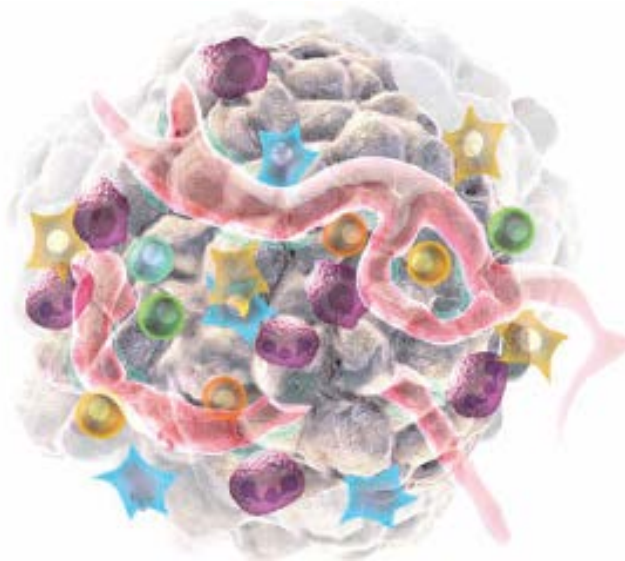
GBG Jahrestreffen



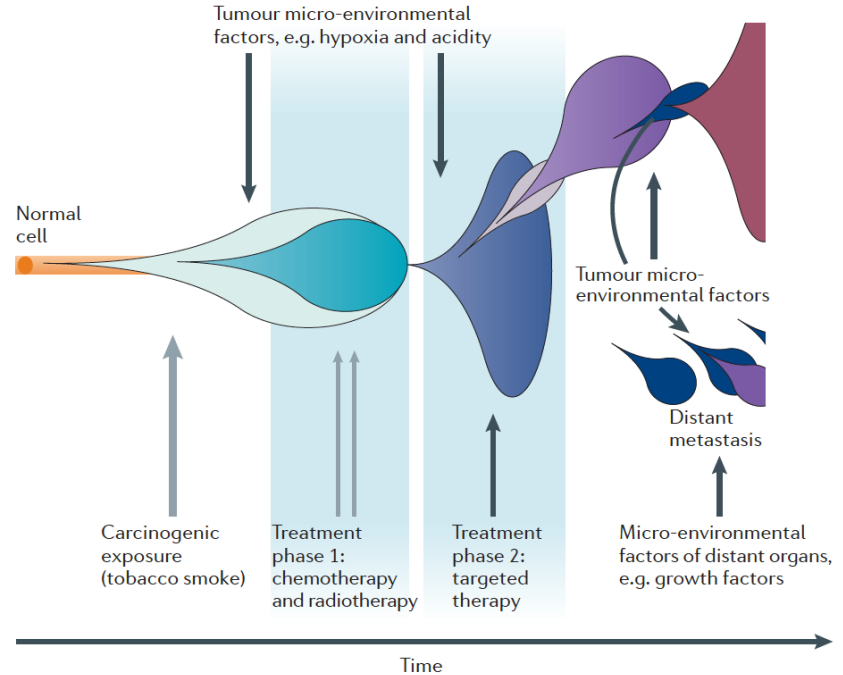
Conflict of Interest

- **Advisory board, honoraria: Teva, Novartis, Molecular Health, Pfizer, Roche, Amgen, MSD, Daiichi Sankyo, Astra Zeneca**
- **Licensing fees: VMscope digital pathology software**
- **Research funding: Myriad**

Heterogenität von Tumoren als Herausforderung für die Therapie



räumlich



zeitlich

Spatial and Temporal Intratumoral Heterogeneity in 3 hard-to-treat Cancers

Koordinatoren

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Gesamtbudget: 18 Mio Euro
Antragstellung seit 2020



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Clinical diagnostic

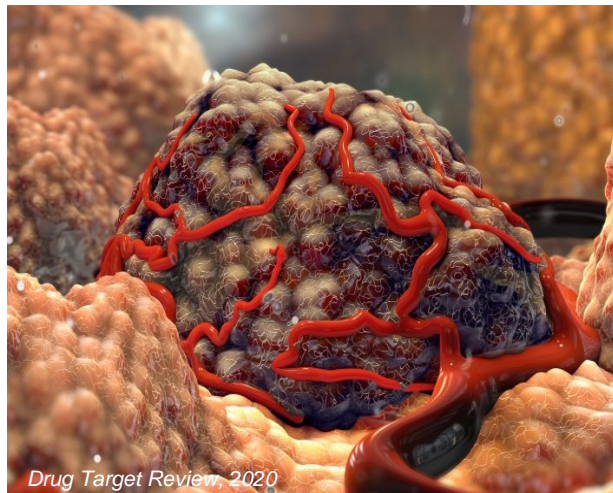
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Georg-Speyer-Haus, Frankfurt
Barbara Grüber
University Hospital Essen
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Andreas Trumpp
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Hard - To - Treat SATURN³ Cancers



Challenge

Therapy Resistance and **Metastasis** remain the major problems in cancer treatment.

Major clinical need:

Breast Cancer (Luminal B, Triple Negative)

Colorectal cancer (CRC, non-MSI)

Pancreatic cancer (PDAC)

Resistance to: radiotherapy, chemotherapy, targeted concepts (if available) and immune-checkpoint blockade

Problem: Intra-tumour heterogeneity (ITH):

→ Interplay of cellular, genetic and epigenetic processes that change dynamically during disease progression, metastasis, and therapy pressure.

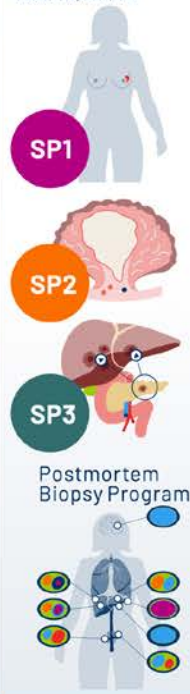






SERIAL MULTI-REGION SAMPLING

Therapies: CTx, RTx, ICI, PARPi, CDK4/6i, VEGFRI; EGFRi



BIOMATERIAL



SC-OMICS & BIOINFORMATICS

SP4

Transcriptome
ScRNA-seq, snRNA-seq



Chromatin activity
ScRNA-seq, snRNA-seq



Genome
targeted scDNA-seq



Cell surface markers
CITE-seq



T cell receptor
TCR-seq



Spatial „omics“
transcriptome & histology



Liquid biopsy
cell-free DNA/RNA, CTC



SP5



Cell subtypes



Gene regulation



Tumor subclones



Environment & immune repertoire



Cell-cell interactions



Clonal evolution

MECHANISMS

SP6



Cell type plasticity



Reprogramming of microenvironment



Immune escape



Metastasis

TRANSLATION

SP7



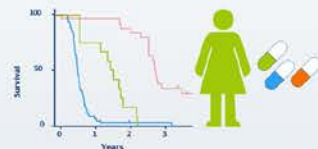
NOVEL ITH BIOMARKERS

- Validation in multiple trial cohorts
- Cross entity evaluation
- Response and ITH monitoring
- Biomarkers



NOVEL THERAPEUTIC STRATEGIES

- Novel treatment schemes
- Targeting of ITH
- Clinical trial protocols for each entity



SP8

SAMPLE & DATA MANAGEMENT



Heterogenität von Tumoren – klinische und translationale Studien

▪ intertumorale Heterogenität

- verschiedene Tumor-Subtypen
- Tumoren verhalten sich unterschiedlich

Klinische Strategie

- Subtypen-spezifische klinische Studien
- ausreichend große klinische Studienkohorten

▪ zeitliche intratumorale Heterogenität

- Tumoren verändern sich unter der Therapie

- Vergleich von Tumorproben im Verlauf
- liquid biopsies

▪ räumliche intratumorale Heterogenität Tumoren bestehen aus verschiedenen Zelltypen

- Immunzellen; Bindegewebszellen; Tumorzellen

- Analyse von verschiedenen Zelltypen
- Analyse von verschiedenen Regionen im Tumor

GeparNuevo neoadjuvant trial – longitudinal gene expression

Durvalumab cohort

88

Placebo (=CTX) cohort

86

A: core biopsy before Tx

77

B: core biopsy after window

37

C: core biopsy after Nab-P

11

D: residual tumor

5

A: core biopsy before Tx

71

B: core biopsy after window

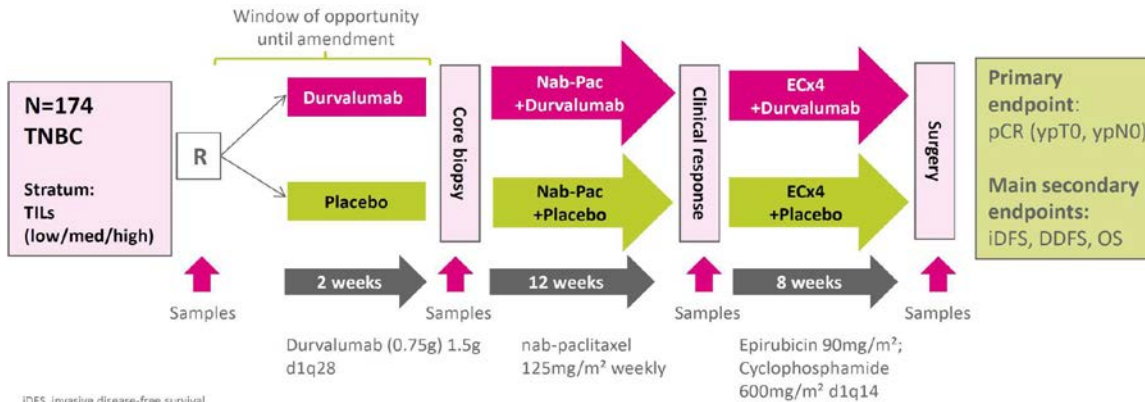
35

C: core biopsy after Nab-P

16

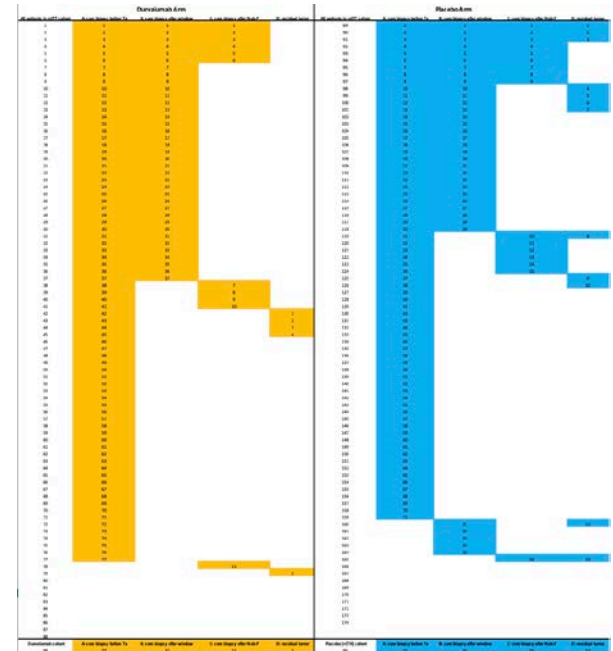
D: residual tumor

12



iDFS, invasive disease-free survival
DDFS, distance disease-free survival
OS, overall survival

45% two paired samples
10% three longitudinal samples
0.6% four longitudinal samples



GeparNuevo neoadjuvant trial

Durvalumab cohort	A: core biopsy before Tx	B: core biopsy after window	C: core biopsy after Nab-P	D: residual tumor
88	77	37	11	5
Placebo (=CTX) cohort	A: core biopsy before Tx	B: core biopsy after window	C: core biopsy after Nab-P	D: residual tumor
86	71	35	16	12



HTG oncology biomarker panel (2449 genes)
– linked to 24 pathways

FFPE samples analyzed in Marburg:

GBG GeparNuevo: 264 samples
GBG Penelope: 1700 samples
GBG GeparDouze: 470 samples
Pancreatic cancer: 200 samples

- HTG oncology biomarker panel (2449 genes) – linked to 24 pathways

GeparNuevo trial – alterations induced by durvalumab alone

Durvalumab cohort

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37

A: core biopsy before Tx

71

B: core biopsy after window

35

window duration: 2 weeks

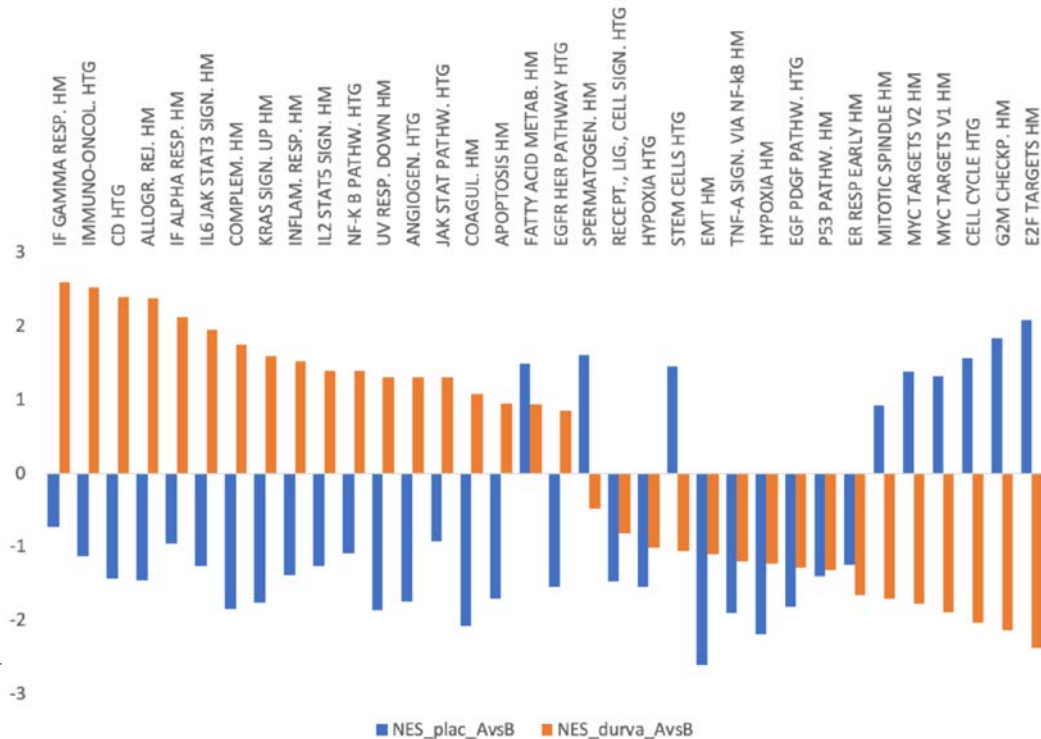
= one dose of durvalumab (no CTX)

compared to placebo (just the biopsy)

IF GAMMA RESP. HM
IMMUNO-ONCOL. HTG
CD HTG
ALLOGR. REJ. HM
IF ALPHA RESP. HM
IL6 JAK STAT3 SIGN. HM
COMPLEM. HM
KRAS SIGN. UP HM
INFLAM. RESP. HM



NES (GSEA)



MITOTIC SPINDLE HM
MYC TARGETS V2 HM
MYC TARGETS V1 HM
CELL CYCLE HTG
G2M CHECKP. HM
E2F TARGETS HM

GeparNuevo trial – durvalumab/CTX vs CTX alone

Durvalumab cohort

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Placebo (=CTX) cohort

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A: core biopsy before Tx

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A: core biopsy before Tx

71

12 weeks
Nab Paclitaxel

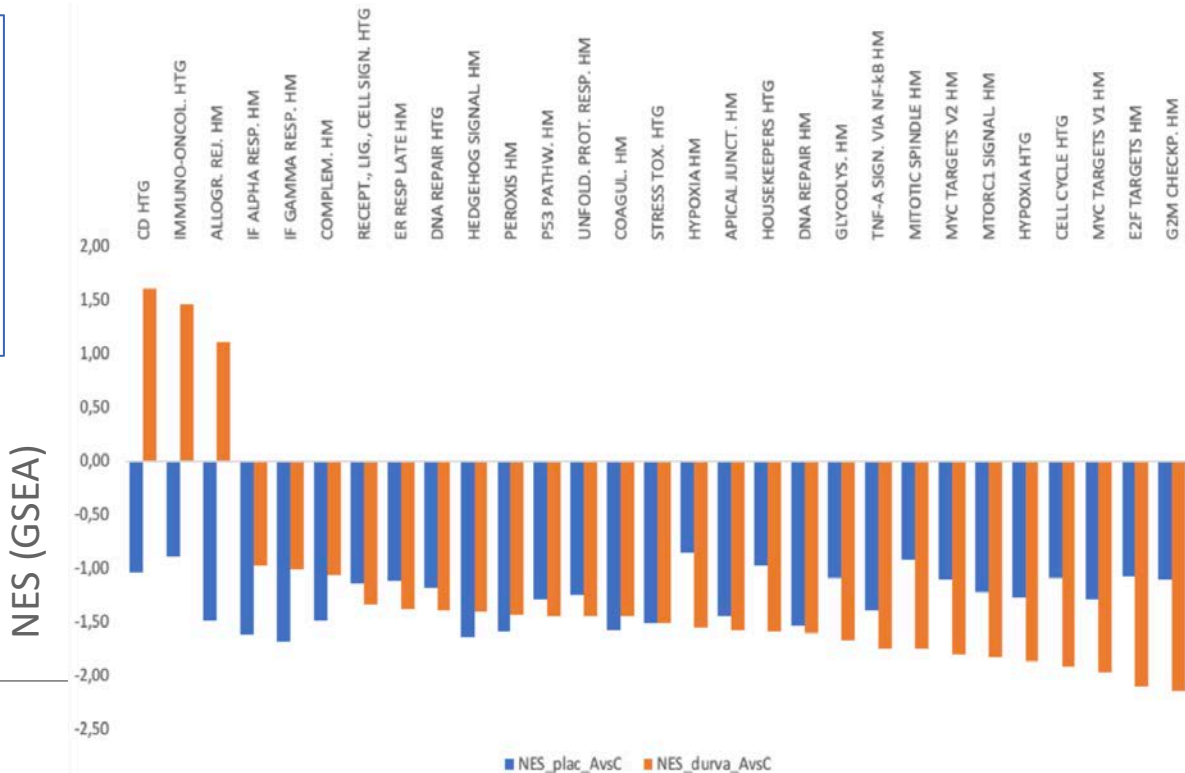
C: core biopsy after Nab-P

11

C: core biopsy after Nab-P

16

CD HTG
IMMUNO-ONCOL. HTG
ALLOGR. REJ. HM



GeparNuevo trial – durvalumab/CTX vs CTX alone

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A: core biopsy before Tx

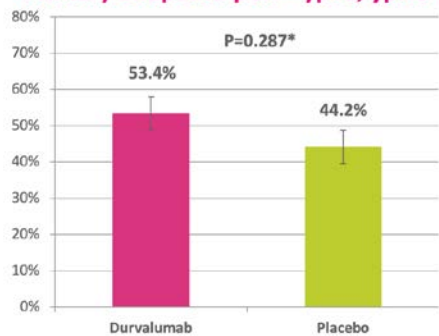
77

A: core biopsy before Tx

71

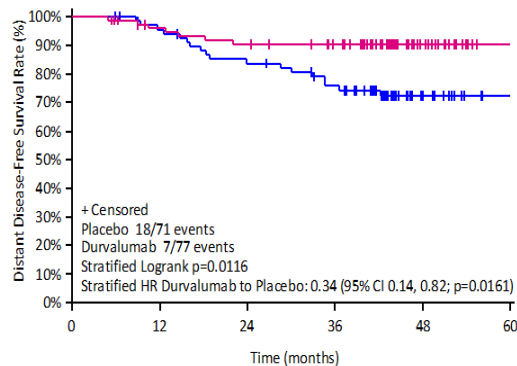
two different endpoints:
pCR and DDFS

Primary endpoint: pCR – ypT0, ypN0

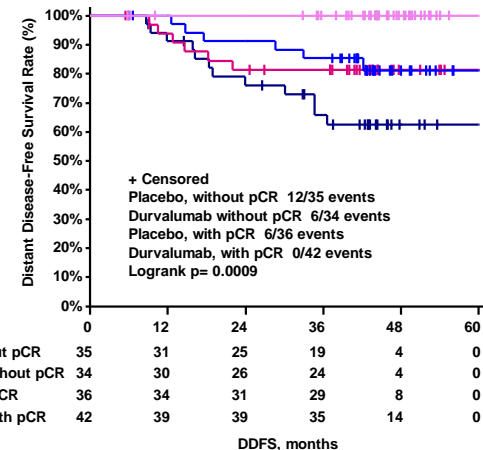


* Continuous corrected χ^2 test
** For stratification factor (TIL groups)

Loibl S, et al. Ann Oncol 2019



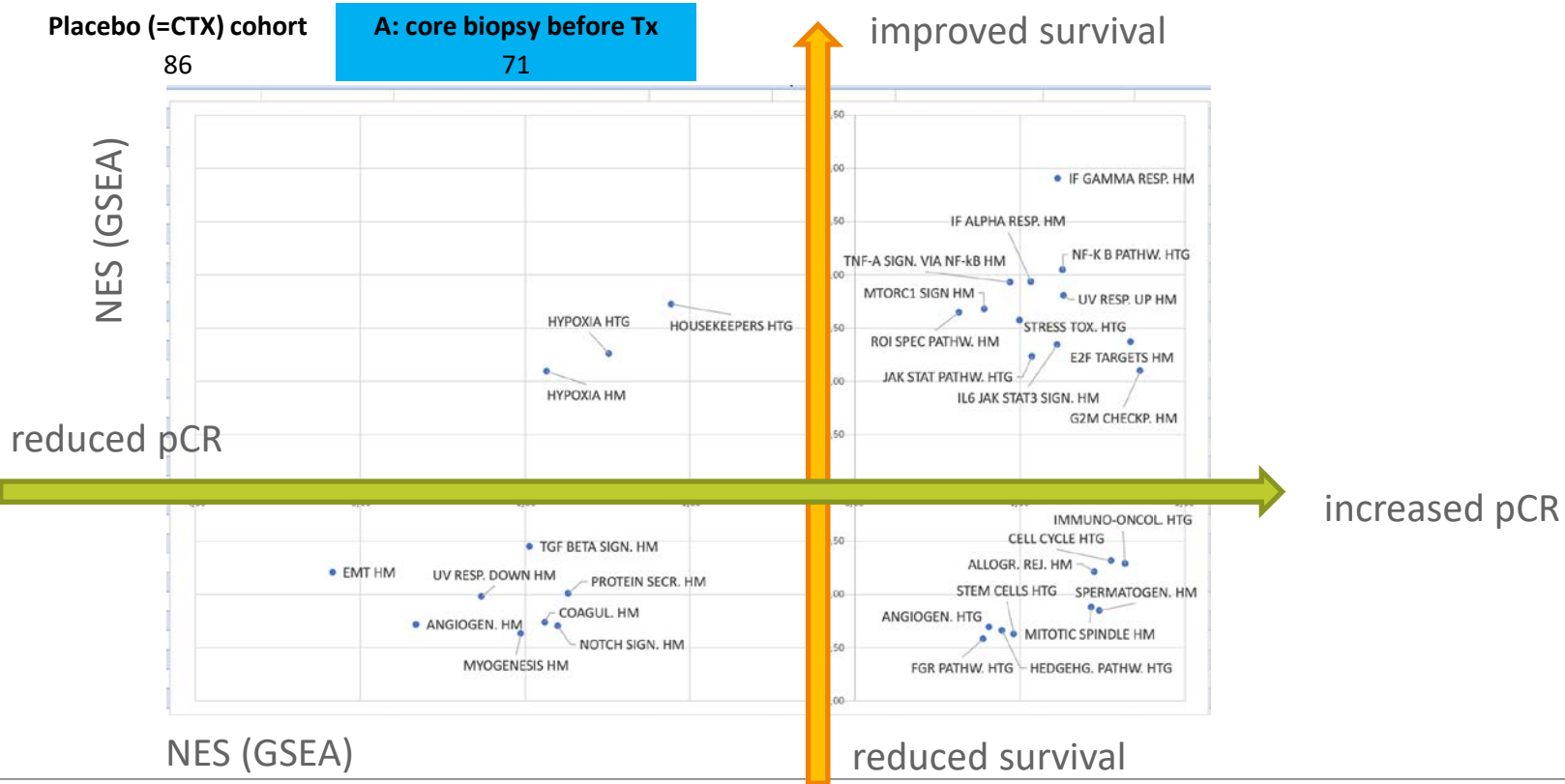
Time (months)	Placebo	Durvalumab
0	71	77
12	65	69
24	56	65
36	48	59
48	12	18
60	0	0



Time (months)	Placebo, without pCR	Durvalumab without pCR	Placebo, with pCR	Durvalumab, with pCR
0	35	34	36	42
12	31	30	34	39
24	25	26	31	39
36	19	24	29	35
48	4	4	8	14
60	0	0	0	0

DDFS, months

Placebo (=CTX) arm– prognostic vs predictive signatures



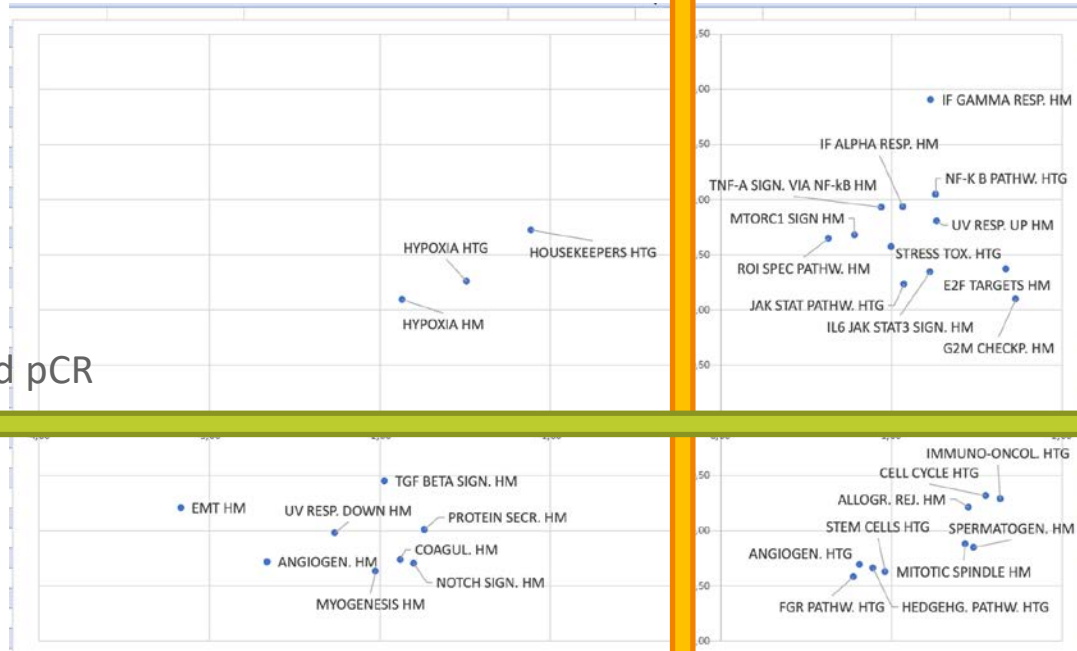
Placebo (=CTX) arm– prognostic vs predictive signatures

Placebo (=CTX) cohort
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A: core biopsy before Tx
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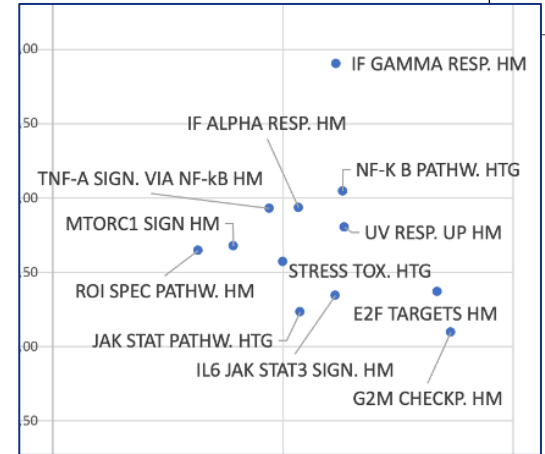
NES (GSEA)

reduced pCR

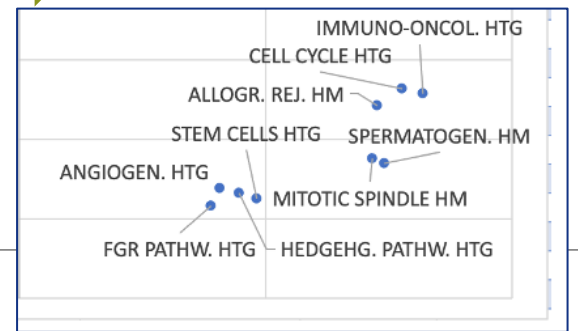


NES (GSEA)

reduced survival

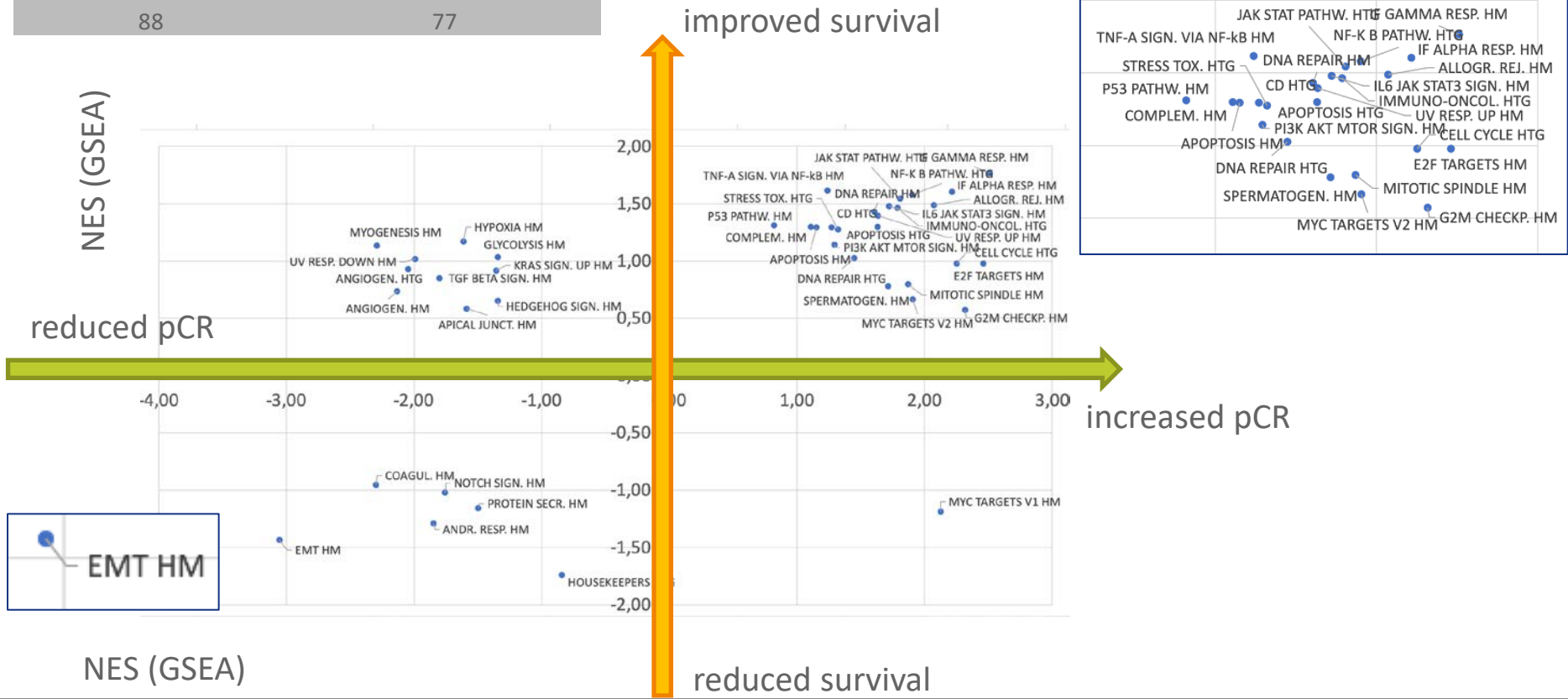


increased pCR

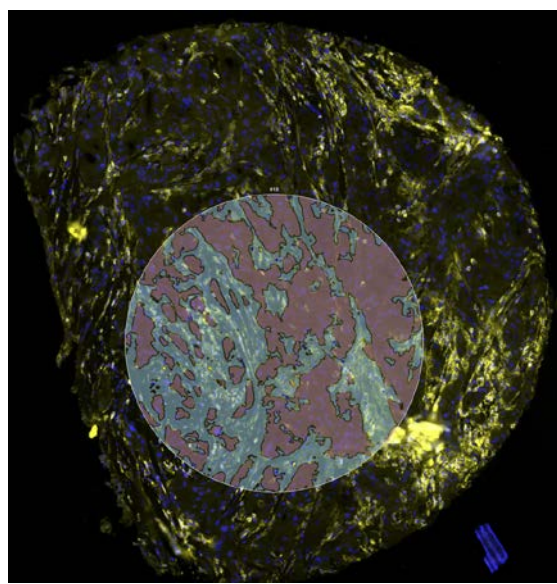
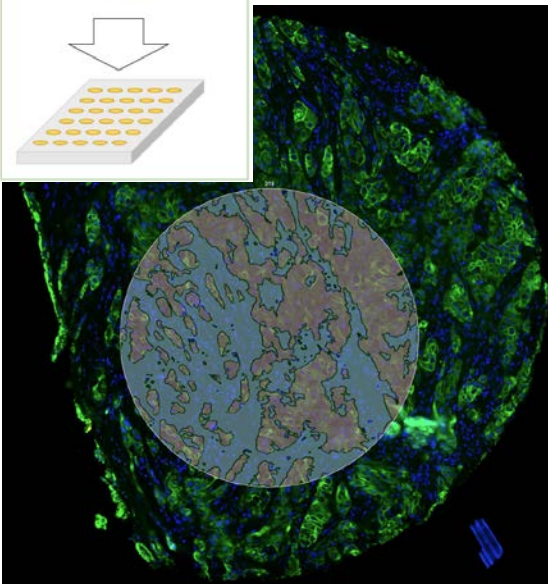
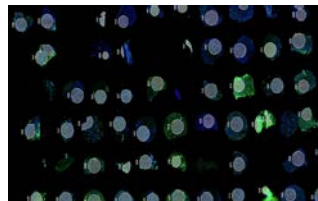
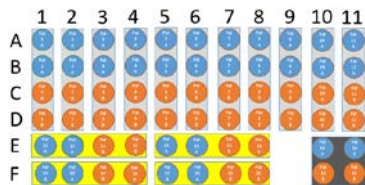
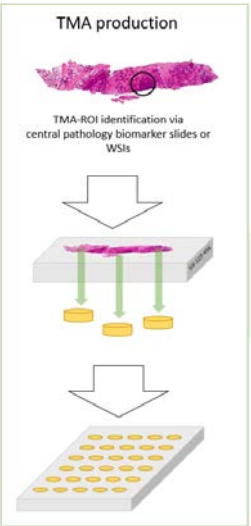


Durvalumab (+CTX) arm– prognostic vs predictive signatures

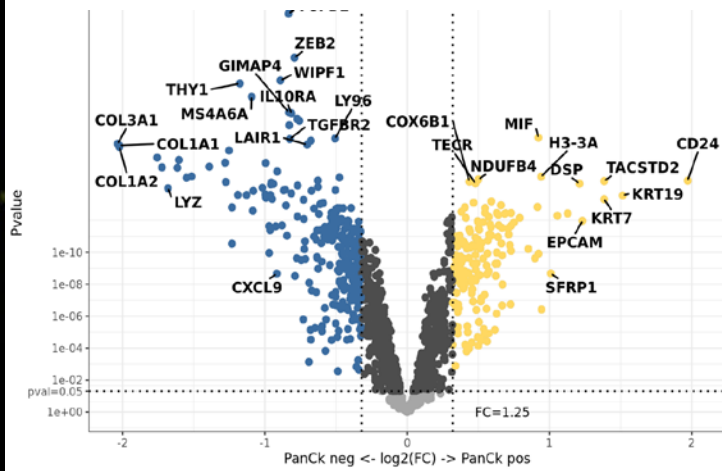
Durvalumab cohort 88
 A: core biopsy before Tx 77



Nanostring GeoMx spatial profiling in the GeparNuevo trial



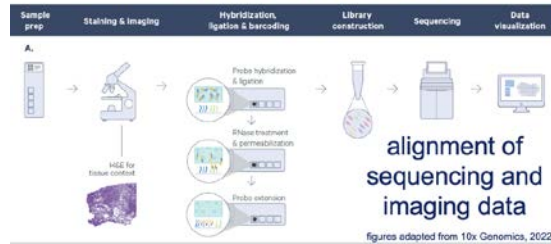
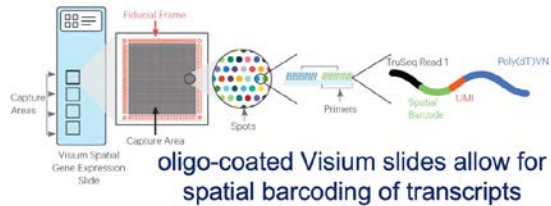
Spatial heterogeneity in tumor regions:
Tumor cell areas vs. stromal areas (GeoMx spatial RNA analysis)



Technologies to evaluate tumor heterogeneity in FFPE tissue

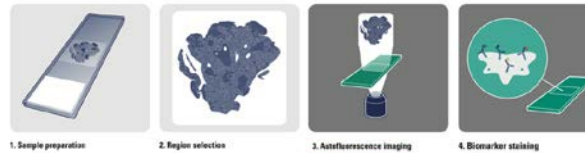
Visium 10x spatial RNA profiling in FFPE tissue from clinical trials

(Julia Teply-Szymanski)

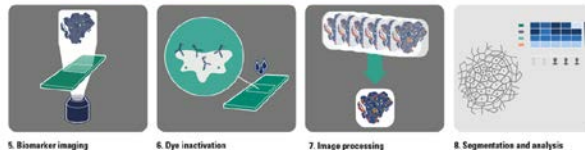


Leica CellDive multiplex imaging up to 60 antibodies

(Paul Jank, Maxime Schmitt, Moritz Jesinghaus)



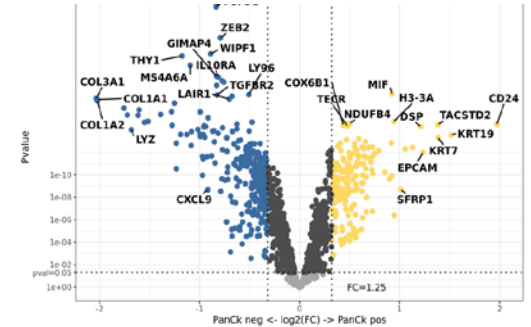
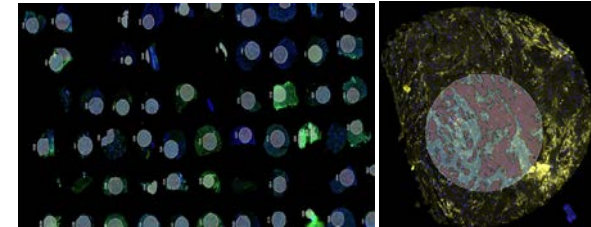
4 antibodies per cycle
&
up to 15 cycles validated



figures adapted from Leica Microsystems, 2022

Nanostring GeoMx spatial sequencing

(Paul Jank, Akira Hattesoehl)



Tumorheterogenität - GBG translationale Forschung

longitudinale und räumliche Heterogenität

- **Penelope:**
 - Vergleich von Stanze und Resektat
- **GeparNuevo:**
 - Vergleich von Stanzen vor und nach dem Window
 - Vergleich von Stanzen vor und nach der Chemotherapie
 - Vergleich von verschiedenen Regionen im Tumor
- **Klassifikation der molekularen Response im Residualtumor**

Methoden

- **HTG EdgeSeq Genexpressionsanalyse**
 - 2500 Gene in einem Schnitt
 - geeignet für kleine Proben
 - keine räumliche Auflösung
 - >2500 GBG Proben gemessen
- **Räumliche Auflösung**
 - Nanostring GeoMx
 - 10X Visium
 - Leica CellDive

Vielen Dank an das Team der Zentralpathologie Marburg

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Subboard Trafo of GBG

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Andrew Tutt

Wilko Weichert

TIL working group



Microbiota against cancer
International research program

European Commission
H2020



Central Repository for Digital
Pathology

