

EACR

European Association
for Cancer Research

CONFERENCES

www.eacr.org

EACR Conference Cancer Genomics, Multiomics and Computational Biology

12-14 May 2026 | Essen, Germany

Scientific Programme Committee

Carlos Caldas
Nuria Lopez-Bigas
Elaine Mardis

Yardena Samuels
Nicholas McGranahan

Scan the QR code to access online conference
resources, including poster abstracts



Tag us   @helloeacr | Wi-Fi: EACR Password: GEN2026!

EACR onsite team



Chris Iliffe
Conference Officer



Kathryn Wass
Conferences Manager



Dr. Alexandra Boitor
Scientific Manager



Catherine Burns
Programmes and Membership Officer

Conference dinner

Optional ticketed event (sold out) Wednesday 13 May, 20:00

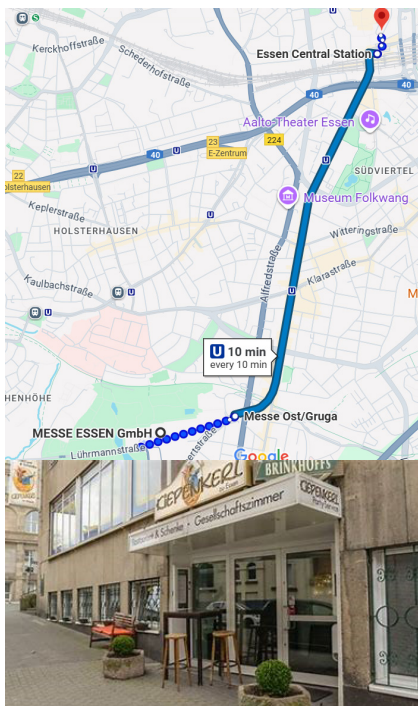
The conference dinner will take place on the Wednesday night at the Kiepenkerl restaurant. It will be an excellent opportunity for participants and speakers to get to know each other in a relaxed and informal environment.

It is important that you bring your participant badge with you for entry to the dinner.

KIEPENKERL, Teichstraße 1, 45127 Essen | www.kiepenkerl-zu-essen.de

Getting to the restaurant from Messe Essen:

- Walk 2 minutes to the Underground U11 Gelsenkirchen Buerer Str.
- Travel 6 minutes (4 stops) to Essen Central Station
- Walk about 3 minutes to Restaurant Kiepenkerl



15 top speakers including:

Mette Agerbæk Ellen Heitzer
Angela DeMichele An Hendrix
Maximilian Diehn David Lyden
Remond Fijneman Nikolas Stoecklein

Showcasing pioneering research and clinical applications that are transforming precision oncology

- Liquid insights at the earliest stage
- Tracking the unseen
- Frontiers in liquid biopsy technology
- Unveiling the biology beneath the biomarkers

EACR Conference

LIQUID BIOPSIES

22 - 24 September 2026, Lyon

eacr.org/conferences



EACR Conference

CANCER METABOLISM

06 - 08 October 2026, Bilbao



eacr.org/conferences

16 top speakers including:

Arkaitz Carracedo Christian Frezza
Ilaria Elia Marcia Haigis
Ayelet Erez Luca Scorrano
Sarah M Fendt Alpaslan Tasdogan

It is essential to understand the role that metabolism plays in the different clinical scenarios

- Undocumented metabolic alterations in cancer
- Cancer - host metabolic communication
- Metabolite-based regulation of cellular responses

EACR Conference CHROMOSOMES IN CRISIS:

From Chromosomal
Instability to Catastrophes
in Cancer Genomes

3 - 5 November 2026, Berlin

eacr.org/conferences



16 top speakers including:

Christina Curtis	John Maciejowski
Daniele Fachinetti	Sarah McClelland
Jan Korbel	Serena Nik-Zainal
Susanne Lens	Ofer Shoshani

**Uncover how chromosomal
chaos shapes cancer
biology and opens new
avenues for clinical
intervention**

- Genetics & genomics of chromosomal catastrophes
- Emerging technologies & model systems to measure and study chromosomal instability
- Therapeutic vulnerabilities & clinical opportunities
- Various chromosomal alterations, their formation and cellular consequences

14 top speakers including:

Chiara Ambrogio	Alfredo Gimenez Cassina
Alberto Bardelli	Marta Puyol
Rene Bernards	Giulia Siravegna
Alejo Efeyan	Alexia-Ileana Zaromytidou

Professional development for cancer researchers

Information, insight and strategies to develop a successful career in cancer research.

- Career opportunities after a PhD
- Equality, inclusion and diversity
- Grant writing
- Ethical and productive use of AI

EACR European Association
for Cancer Research

CAREER MASTERCLASS

FOR EARLY CAREER
CANCER RESEARCHERS

Virtual event | 17 - 18 November 2026

eacr.org/conferences



Cancer Genomics, Multiomics and Computational Biology

Tag us   @helloeacr | Wi-Fi: EACR Password: GEN2026!

Day 1 | Tuesday 12 May 2026

From 11:30

REGISTRATION

Session 1
posters can
be put up

12:00-13:00

 WELCOME REFRESHMENTS

A chance to meet fellow attendees and enjoy a light buffet

13:00-13:10

CONFERENCE WELCOME

Scientific Programme Committee

13:10-13:40

SESSION 1 Chair: Carlos Caldas

EMBO YOUNG INVESTIGATOR OPENING KEYNOTE

Q&A: 13:40-13:55

Nick McGranahan University College London, UK

'Somatic evolution and cancer plasticity'

13:55-14:05

Fatemeh Ahmadimoghari Institute of Cancer Research, UK

Q&A: 14:05-14:10

Proffered Paper 1: 'Distinct Hypoxia and Rho Epigenetic Cell States Drive Therapy Resistance in Triple-Negative Breast Cancer'

14:10-14:30

Itay Tirosh Weizmann Institute of Science, Israel

Q&A: 14:30-14:40

'Cell states and their spatial organization in head and neck cancer''

14:40-14:50

EXHIBITOR INTRODUCTIONS

14:50-15:20

 COFFEE, EXHIBITION AND SOLO MEET-UP

Solo travellers are invited to meet up at the EACR banner to connect with fellow adventurers

15:20-15:30

Marnix Koops Erasmus Medical Center, Netherlands

Q&A: 15:30-15:35

Proffered Paper 2: 'Spatial profiling identifies a distinct and topographically-defined tumor microenvironment that emerges during multiple myeloma evolution'

15:35-15:45

Veronique Calleja HAWK Biosystems, Spain

Q&A: 15:45-15:50

Proffered Paper 3: 'Spatial Immune Checkpoint Biology Reveals Functional CTLA-4/CD80 and PD-1/PD-L1 Interactions Associated with Immunotherapy Response in NSCLC'

15:50-16:10 Q&A: 16:10-16:20	Francesca Ciccarelli QMUL & The Francis Crick Institute, UK 'Understanding the functional consequences of cancer drivers from initiation to therapy response'
16:20-16:30	POSTER SPOTLIGHTS <i>Posters 1, 25 and 50 will be presented in 3-minute 'flash talks'</i>
16:30-17:00	NETWORKING QUIZ
17:00-18:00	 WELCOME BUFFET AND DRINKS
18:00-19:30	POSTER DISCUSSION SESSION 1 <i>Presenters of posters 1-52 should stand by their boards.</i>

Day 2 | Wednesday 13 May

08:15-08:45	 EARLY POSTER VIEWING WITH COFFEE
08:45-09:00	Chair: Elaine Mardis BIOMOL INDUSTRY SPOTLIGHT Felipe Oliveira Navinci 'The Next Generation of Spatial Interactomics'
09:00-09:20 Q&A: 09:20-09:30	SESSION 2 SOCIETY FOR FUNCTIONAL PRECISION MEDICINE SPEAKER Jesse Boehm Massachusetts Institute of Technology, USA 'Accelerating prediction of tumor vulnerabilities using precision functional genomics'
09:30-09:40 Q&A: 09:40-09:45	Luuk Harbers VIB-KU Leuven, Belgium Proffered Paper 4: 'Long-read single-cell genome, transcriptome and open chromatin profiling links genotype to phenotypes in B-cell acute lymphoblastic leukaemia'
09:45-10:05 Q&A: 10:05-10:15	Mor Nitzan The Hebrew University of Jerusalem, Israel 'Decoding layers of spatial and temporal organization in multicellular systems'
10:15-10:35 Q&A: 10:35-10:45	Jessica Zucman Rossi University Paris Descartes, France 'Germline-somatic alterations interplay in liver tumors'
10:45-11:15	 COFFEE BREAK & EXHIBITION
11:15-11:35 Q&A: 11:35-11:45	Yardena Samuels (<i>pre-recorded talk</i>) Weizmann Institute of Science, Israel 'Challenges and solutions in effectively targeting neoantigens'

Take down session 1 posters

Session 2 posters can be put up

11:45-11:55 Q&A: 11:55-12:00	Hou Wang Lam University College London, UK Proffered Paper 5: 'Spatiotemporal Mapping of Proton Beam Radioresistance in Colorectal Cancer Liver Metastasis'
12:00-12:10	POSTER SPOTLIGHTS <i>Posters 60, 80 and 100 will be presented in 3-minute 'flash talks'</i>
12:10-12:25	CELL SIGNALING TECHNOLOGY SPOTLIGHT Yannick Nossin Cell Signaling Technology 'InTraSeq™ Single Cell Analysis: Seq What You've Been Missing'
12:25-12:40	TAKARA BIO EUROPE SPOTLIGHT Matthieu Pesant Takara Bio Europe 'Enabling true single-cell spatial (multi)omics of the tumor microenvironment with a new class of spatial technology'
12:40-13:30	 LUNCH BREAK <i>light refreshments will be served</i>
13:30-15:00	POSTER DISCUSSION SESSION 2 <i>Presenters of posters 53-105 should stand by their boards.</i>
15:00-15:20 Q&A: 15:20-15:30	SESSION 3 Chair: Nick McGranahan Nuria Lopez-Bigas IRB, Spain 'Cancer driver mutations in normal tissues and their relation to cancer'
15:30-15:40 Q&A: 15:40-15:45	Erik Schüftan UKM, Germany Proffered Paper 6: 'Beyond Cell States: Spatial Organisational Complexity as a Predictor of Patient Outcome Across Primary Brain Tumours'
15:45-15:55 Q&A: 15:55-16:00	Haia Khoury Tel-Aviv University, Israel Proffered Paper 7: 'Pan-cancer analysis reveals genomic fidelity and evolution of patient-derived organoids'
16:00-16:20 Q&A: 16:20-16:30	Elaine Mardis Institute for Genomic Medicine, USA 'PEDIA-BRAIN: An emerging research resource of tissue-specific human brain development'
16:30-17:00	 COFFEE BREAK & EXHIBITION
17:00-17:20 Q&A: 17:20-17:30	Jamie Blundell University of Cambridge, UK 'In vivo lineage tracing using methylation barcodes in the PCDH gene cluster'
17:30-17:50 Q&A: 17:50-18:00	Andrea Sottoriva Human Technopole, Italy 'Single cell multi-omics quantifies epigenetic evolution and plasticity of colorectal cancer and its microenvironment'

18:00-18:45

MEET THE SCIENTIFIC PROGRAMME COMMITTEE

Reflections on the conference so far and insights from their personal and professional experiences.

20:00

OPTIONAL CONFERENCE DINNER [SOLD OUT]

The conference dinner will be held at Kiepenkerl in central Essen (separate ticketed event).

Day 3 | Thursday 14 May

08:15-09:00

EARLY POSTER VIEWING WITH COFFEE

09:00-09:20

SESSION 4 Chair: Nuria Lopez-Bigas

Raza Ali CRUK Cambridge Institute, UK

Q&A: 09:20-09:30

'Spatial predictors of response to neoadjuvant IO therapy'

09:30-09:50

Ewa Szczurek Helmholtz Munich, Germany

Q&A: 09:50-10:00

'Who Lives Next to Whom? AI Reveals Spatial Neighborhoods in Cancer'

10:00-10:10

Archana Verma UKM, Germany

Q&A: 10:10-10:15

Proffered Paper 8: 'Transcriptional Divergence and Tumor Cell Lineage States in Pediatric Low-Grade Glioma Revealed by Single-Cell Transcriptomics'

10:15-10:45

COFFEE BREAK & EXHIBITION

10:45-11:05

Eduard Porta IJC, Spain

Q&A: 11:05-11:15

'From Spatial Maps to Clinical Decisions: Building the Next Diagnostic Layer'

11:15-11:45

EMBO CLOSING KEYNOTE LECTURE

Carlos Caldas Hebrew University of Jerusalem, Israel, and University of Cambridge, UK

Q&A: 11:45-12:00

'Breast cancers at bulk, single cell and spatial levels'

12:00

SUMMARY, AWARDS AND DEPART

GET
UPDATES:
eacr.org/congress

Annual Congress of the

EACR 2026

08 - 11 June | Budapest

Innovative Cancer Science

European Association for Cancer Research

**OUTSTANDING
SCIENCE IN A
WELCOMING
ENVIRONMENT**

**GREAT NETWORKING
OPPORTUNITIES
WITH 2000+ CANCER
RESEARCHERS**

**98% OF
PARTICIPANTS
WOULD
RECOMMEND**

SESSION TOPICS INCLUDE:

- Advances in Clinical Trial Design
- Cancer and RNA modifications
- Cancer Immunology and Immunotherapy
- Cancer Initiation
- Cancer Prevention
- Cell Cycle Regulation
- Cell Death Mechanisms
- Functional Genomics
- Genomic Instability
- Immune Activation beyond T cells
- Mechanisms of Tumour Metastasis
- Novel Cancer Models
- Plasticity and Non-genetic Cancer Evolution
- Spatial Tumour Biology / Tumour Heterogeneity at the Single Cell Level
- Tumors are Ecosystems: New insights on the Tumor Microenvironment
- Tumour Innervation
- Tumour Macroenvironment (cachexia, metabolics)

Travel grants

More information about EACR grants: eacr.org/travel-grant

EACR-Worldwide Cancer Research Travel Grants provide funds to help early-career EACR members and researchers based in low- or middle-income economy countries to participate in our conferences.

Congratulations to the recipients of the Travel Grants for this conference. Each recipient received a full registration free of charge and funds to assist with travel and accommodation costs.

- **ELLA REED** UK
- **PAULA ZICKLER** GERMANY
- **BRYAN ÔRTERO PEREZ GONÇALVES** BRAZIL
- **IKA NURLAILA** INDONESIA

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Supporters

We give our thanks to the following grant providers:

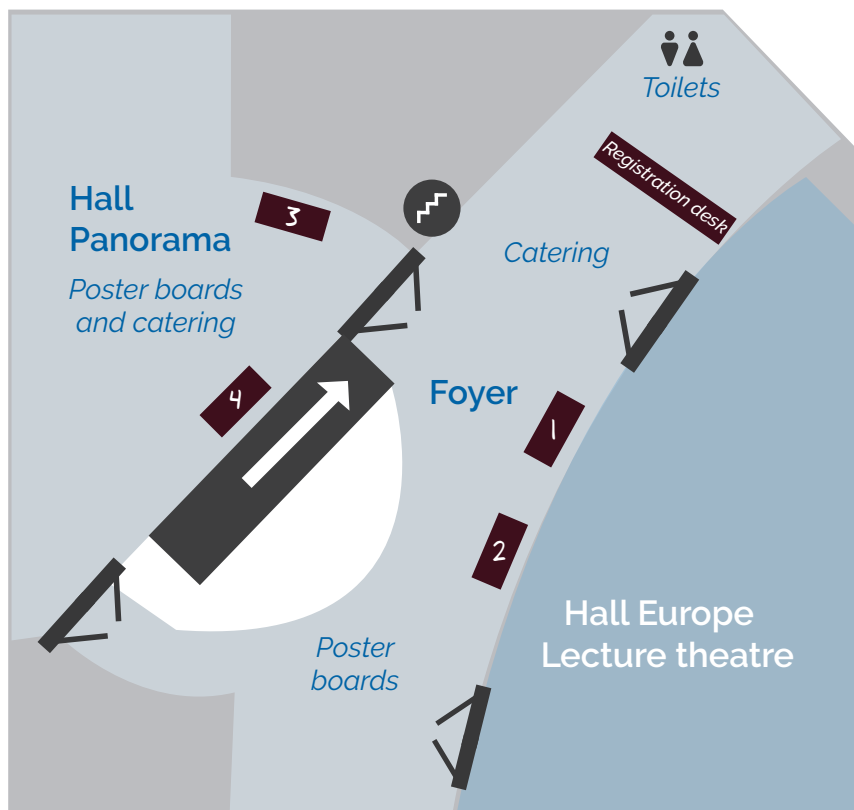


We would also like to thank the following partners for supporting us in promoting this conference:



Venue floor plan

Messe Essen - west entrance



Exhibitors

1. Cell Signaling Technology
2. Takara Bio Europe
3. IDEXX BioAnalytics
4. Biomol

Meet the exhibitors

Cell Signaling Technology Stand: 1

Website: www.cellsignal.com

Represented at the conference by:
Timo Herrenkind, Yannick Nossin



Spotlight: Wednesday 13 May | 12:10-12:45

Yannick Nossin, Senior Field Application Scientist, Cell Signaling Technology
'InTraSeq™ Single Cell Analysis: Seq What You've Been Missing'

Takara Bio Europe Stand: 2

Website: www.takarabio.com

Represented at the conference by:
Matthieu Pesant, Sascha Deppermann



Spotlight: Wednesday 13 May | 12:25-12:40

Matthieu Pesant, Sr Market Strategy Manager Translational Genomics, Takara
'Enabling true single-cell spatial (multi)omics of the tumor microenvironment with a new class of spatial technology'

IDEXX BioAnalytics Stand: 3

Website: idexxbioanalytics.eu

Represented at the conference by:
Adaobi Udobi, Christina Back

IDEXX BioAnalytics

Biomol Stand: 4

Website: www.biomol.com

Represented at the conference by:
Felipe Oliveira, Michael Hofmeister



Spotlight: Wednesday 13 May | 08:45-09:00

Felipe Oliveira, Sales Area Manager, Navinci
'The Next Generation of Spatial Interactomics'

Poster spotlights and poster index

View abstracts when logged in at www.eacr.org/conference/cancergenomics2026

Poster Spotlight session 1: Tuesday, 16:20 | Also as posters on Tuesday

1 Estimating tumour microenvironment cellular states from bulk RNA-seq reveals biomarkers of clinical outcome in Non Small Cell Lung Cancer (NSCLC) across disease stages Presented by [Marcelo Hurtado](#), [Université de Toulouse](#), FRANCE

25 Medium-Throughput Bioprinted Spatially Recapitulated Triple-Droplet Organoids Reveal Stroma-Barrier-Driven Therapeutic Resistance Presented by [Chenqin Le](#), [Charité - Universitätsmedizin Berlin](#), GERMANY

50 Transcriptomics-Guided Drug Repositioning Uncovers Therapeutic Vulnerabilities in Osteosarcoma Presented by [Mariangela Morelli](#), [Fondazione Pisana per la Scienza ONLUS](#), Pisa, ITALY

Poster Spotlight session 2: Wednesday, 12:00 | Also as posters on Wednesday

60 Unveiling the heterogeneity of pancreatic cancer initiation: a novel perspective on epithelial-immune cell-cell Interactions Presented by [Ella Reed](#), [Cardiff University](#), UK

80 Large-scale single-cell spatial transcriptomics reveals immune evasion in hepatocellular carcinoma Presented by [Yi Yin](#), [University of Cambridge](#), UK

100 Peritumoral tissue transcriptomics reveals reproducible prognostic subtypes in clear cell renal cell carcinoma Presented by [Laurent Guyon](#), [IRIG \(CEA/INSERM/UGA\)](#), [Grenoble](#), FRANCE

Poster presentations session 1: Tuesday, 18:00 - 19:30

1 [POSTER SPOTLIGHT] Estimating tumour microenvironment cellular states from bulk RNA-seq reveals biomarkers of clinical outcome in Non Small Cell Lung Cancer (NSCLC) across disease stages Presented by [Marcelo Hurtado](#), [Université de Toulouse](#), FRANCE

2 Single-cell phylogenetics reveals rapid late-stage expansions in colorectal cancer Presented by [Joao Alves](#), [Universidade de Vigo](#), and [IIS Galicia Sur](#), Vigo, SPAIN

3 Single-nucleus multiomic profiling reveals cellular composition and inter-sample heterogeneity in BCOR-ITD embryonal brain tumors. Presented by [Guillaume Appé](#), [Institut Curie](#), [PSL University](#), Paris, FRANCE

4 COSMIC v103 - Curating Somatic Variants in Colorectal Cancers with a Focus on Early-Onset Disease Presented by [David Armstrong](#), [Wellcome Sanger Institute](#), Cambridge, UK

5 Benchmarking and clinical application of cell-free RNA deconvolution for non-invasive early cancer detection Presented by [Giovanni Asole](#), [Flomics Biotech SL](#), and [Centre for Genomic Regulation](#), Barcelona, SPAIN

6 p63 sustains proliferation of bladder cancer cells through epigenetic regulation Presented by [Damiano Barnaba](#), [University of Rome Tor Vergata](#), ITALY

7 Evolutionary Trajectories of Breast Cancer during Neoadjuvant Chemotherapy Presented by [Lucrezia Berton](#), [University of Bergen](#), and [Haukeland University Hospital](#), Bergen, NORWAY

8 H3K27 and H2BK120 acetylation enhance chromatin accessibility at cis-regulatory elements under the pruning activity coordinated by HDAC4 Presented by [Alessio Bertozzo](#), [University of Udine](#), Friuli - Venezia Giulia, ITALY

9 PIK3CA Mutant Allelic Expression Imbalance as a biomarker in precision oncology
Presented by André Duarte, expressTEC, and Universidade do Algarve, Faro,
PORTUGAL

10 Leveraging machine learning to tackle tumor heterogeneity with a pan-cancer
approach Presented by Luisa Bresadola, TRON gGmbH, Mainz, GERMANY

11 AI tool for the classification of variants of uncertain significance (VUS) in cancer
Presented by Dido Carrero, CNIO, Madrid, SPAIN

12 Towards a nested classification approach for determining tissue-of-origin in cancers
of unknown primary from cell-free DNA methylation profiles Presented by Holly
Cassell, Cancer Research UK National Biomarker Centre, Manchester, UK

13 Clonal and spatial evolution reveal homologous recombination deficiency dynamics
in breast cancer Presented by Emma Champneys, University College London, UK

14 Mutagenesis Driven by IncBART-NuRD-Base Excision Repair Chromatin Architecture
and KDM5B-Associated Open Enhancers in EBV-Positive Nasopharyngeal Carcinoma
Presented by Lai Shun Dittman Chung, The University of Hong Kong, HONG KONG

15 Germline BRCA1/2-dependent multiomic landscape in High Grade Serous
Ovarian Cancer (HGSOC): insights from the PowerOMICS study Presented by Karolina
Chwialkowska, Medical University of Białystok, POLAND

16 Urinary miRNAs and beyond: multi-cancer detection enhanced by integrated small
RNA profiling Presented by Akira Arakawa, Craif Inc, Nagoya, JAPAN

17 MetaboDynamics reveals changes in metabolite dynamics that are linked to DNA
repair in irradiated cancer cells Presented by Katja Danielzik, University of Duisburg-
Essen, GERMANY

18 Quantitative modeling integrates and decomposes multiplexed measurements
of treatment responses in gastrointestinal stromal tumors Presented by Mohammad
Darbalaei, University of Duisburg-Essen, GERMANY

19 Reannotation of cancer mutations based on expressed RNA transcripts reveals
functional non-coding mutations in melanoma Presented by Dylan De Groote, KU
Leuven, BELGIUM

20 Proteomic profiling identifies response-associated pathways in immunotherapy-
treated melanoma Presented by Renan de Jesus Teixeira, Barretos Cancer Hospital,
São Paulo, BRAZIL

21 Dissecting ferroptosis regulation in recurrent glioblastoma multiforme at the glial
cell type level using machine learning and network analysis
reveals ZFP36 as a therapeutic target in astrocytes Presented by Sainitin Donakonda,
TUM Hospital, Munich, GERMANY

22 Spatially Resolved Transcriptomics Reveals Microenvironment-Driven Heterogeneity
in Cutaneous T-Cell Lymphoma Presented by Alireza Dostmohammadi, University of
Duisburg-Essen, GERMANY

23 Lineage tracing reveals therapeutic targets in drug-resistant cell populations of
high-grade serous carcinoma Presented by Kyriaki Driva, University of Copenhagen,
DENMARK

24 Proteome-wide analysis reveals an oncogenicity – HLA-I presentability trade-off
shaping missense variants in cancer genomes Presented by Ana Dueso-Barroso, VHIO,
Barcelona, SPAIN

25 [POSTER SPOTLIGHT] Medium-Throughput Bioprinted Spatially Recapitulated
Triple-Droplet Organoids Reveal Stroma-Barrier-Driven Therapeutic Resistance
Presented by Chenqin Le, Charité - Universitätsmedizin Berlin, GERMANY

26 Integrative Multiomic Reconstruction of TBXT-Driven Regulatory Networks Reveals
Actionable Dependencies in Chordoma Presented by Cihan Erkut, DKFZ, and National
Center for Tumor Diseases, Heidelberg, GERMANY

- 27 Clonal origins of CTCs during metastatic progression in breast cancer xenografts Presented by Nuria Estévez Gómez, Universidade de Vigo, and IIS Galicia Sur, Vigo, SPAIN
- 28 A rare population of hybrid cells drives escape from therapy-induced senescence Presented by Itai Fabian, Tel Aviv University, ISRAEL
- 29 Epigenetics-Informed Multi-Omics Prediction of Synthetic Lethality in Gastrointestinal Cancers Presented by Maria Fariña-Morillas, VHIO, Barcelona, SPAIN
- 30 Prediction of the origin of cancers of unknown primary using chromatin-informed mutation patterns Presented by Annika Föhr, Charité - Universitätsmedizin Berlin, GERMANY
- 31 MIZ1/MYC Complexes at Enhancers Regulate Neuroendocrine Differentiation in Small Cell Lung Cancer Presented by Lisa Marie Fröhlich, LMU University Hospital, Munich, GERMANY
- 32 Unravelling Pancreatic Tumour-Stroma Crosstalk Shaping Therapy Outcomes Through Integrated Approaches Presented by Xiao Fu, CRUK Scotland Institute, Glasgow, UK
- 33 Benchmarking copy-number feature representations for signature analysis Presented by Keshav Gandhi, University of Cologne, GERMANY
- 34 PhytClust: Efficient and Optimal Partitioning of Rooted Phylogenetic Trees Presented by Katyayni Ganesan, University of Cologne, GERMANY
- 35 Ensemble Machine Learning Identifies a 17-Gene Transcriptomic Signature Predicting Neoadjuvant Chemotherapy Response in Breast Cancer Presented by Styliana Georgiou, AnaBioSi-Data, and University of Cyprus, Nicosia, CYPRUS
- 36 Routine isolation and single-cell molecular profiling of circulating tumor cells to guide personalized cancer therapy Presented by Debora Meijer, Tzu Cancer Therapeutics, Amsterdam, NETHERLANDS
- 37 Inferring cell state transitions through chromatin accessibility with CREPE Presented by Prahalad Varadan Giridhar, Wellcome Sanger Institute, Hinxton, UK
- 38 Integrative Methylome and Transcriptome Analysis Reveals miR-770-5p-Associated Epigenomic Remodeling in TNBC Presented by Bala Gur Dedeoglu, Ankara University Biotechnology Institute, TURKEY
- 39 SOX4-associated regulatory program in prostate cancer anti-androgen resistance Presented by Sini Hakkola, Tampere University Hospital, FINLAND
- 40 Multimodal integration reveals tumour ecosystem heterogeneity in colorectal cancer Presented by Emmi Hämäläinen, Tampere University, and University of Helsinki, FINLAND
- 41 Integrated Genomic and Transcriptomic Profiling Delineates the Molecular Landscape of Cancer of Unknown Primary Presented by Waqar Hussain, NCT/UCC, and University Hospital Carl Gustav Carus, TUD Dresden University of Technology, Dresden, GERMANY
- 42 Computing tumor-specificity of cancer antigen targets by k-mer indexing of healthy tissue transcriptomes Presented by Jonas Ibn-Salem, Johannes Gutenberg University Mainz, GERMANY
- 43 Multiomics Study Reveals a Metastasis-Prone Epigenomic Subtype in EBV-Associated Nasopharyngeal Carcinoma Presented by Kazi Anisha Islam, University of Hong Kong, HONG KONG
- 44 Transcriptional programs of metastasis across cancer types and their clinigenomic associations Presented by Manuel Jara, VHIO, Barcelona, SPAIN

- 45 Deciphering the epigenetic landscape of Osimertinib persister cells through integrated ATAC, RNA, and CTCF ChIP sequencing in PCg models Presented by Jae Kyun Jeong, Sungkyunkwan University, Suwon, SOUTH KOREA
- 46 Fusion gene heterogeneity and kinase enrichment in high-grade serous carcinomas Presented by Bjarne Johannessen, Oslo University Hospital, NORWAY
- 47 Comparative Clinical and Molecular Profiling of Papillary Thyroid Carcinomas with Unilateral and Bilateral Lateral Lymph Node Metastasis Presented by Young-Hoon Joo, The Catholic University of Korea, Seoul, SOUTH KOREA
- 48 Liver Metastasis Atlas Links Tumor Invasion Programs to Invasive Trophoblast Signatures Presented by Costerwell Khyriem, University of Freiburg, GERMANY
- 49 Risk of skin cancer and response to immune checkpoint therapy is influenced by HLA-DRB1 peptide breadth Presented by Gergely Koppany, UN-REN Biological Research Centre, and University of Szeged, Szeged, HUNGARY
- 50 [POSTER SPOTLIGHT] Transcriptomics-Guided Drug Repositioning Uncovers Therapeutic Vulnerabilities in Osteosarcoma Presented by Mariangela Morelli, Fondazione Pisana per la Scienza ONLUS, Pisa, ITALY
- 51 Multimodal Representation Learning for Pan-Cancer Type Classification Using Attention-Based Set Encoding and Contrastive Pre-Training Presented by Fabian Janosch Krüger, Max Delbrück Center for Molecular Medicine, Berlin, GERMANY
- 52 ESRP1-Driven Mesenchymal-to-Epithelial Transition Coupled with Proliferative Reprogramming: A Novel Mechanism for Malignant Transformation of Endometriosis to Ovarian Cancer Presented by Aicha Lakhssassi, Abdelmalek Essaadi University, Tétouan, MOROCCO

Poster presentations session 2: Wednesday, 13:30 - 15:00

- 53 Genomic characterization of DEK::NUP214 rearranged acute myeloid leukemia reveals specific additional genetic alterations Presented by Lisa Latzko, DKTK, and LMU Munich, Munich, GERMANY
- 54 Decoding the Spatial Interface of Resistance and Dedifferentiation in Anaplastic Thyroid Cancer Presented by Han Sai Lee, Seoul National University, SOUTH KOREA
- 55 DOMINO: Diffusion-optimised graph contrastive learning framework for domain detection in spatial transcriptomic Presented by Nora Liu, Adelaide University, AUSTRALIA
- 56 PatientProfiler, from multi-omic data to clinical insight: patient-specific models to derive signalling-based biomarkers Presented by Veronica Lombardi, Sapienza University of Rome, ITALY
- 57 Comparing Homologous Recombination Deficiency Scoring Methods in Multisite High Grade Serous Ovarian Cancer. Presented by Marc Lorentzen, Imperial College London, UK
- 58 Multi-omic characterization of therapeutic resistance in ex vivo models of glioblastoma recurrence Presented by Salma Mahmoudi, FPO-IRCCS, and University of Turin, Turin, ITALY
- 59 Beyond apoptosis: A transcriptomic analysis of non-canonical TRAIL signalling in tumour cells Presented by Pumla Manyatsi, Dokuz Eylül University, Izmir, TURKEY
- 60 [POSTER SPOTLIGHT] Unveiling the heterogeneity of pancreatic cancer initiation: a novel perspective on epithelial-immune cell-cell Interactions Presented by Ella Reed, Cardiff University, UK
- 61 Single-cell multiomic characterization of pediatric glioma evolution under targeted therapy Presented by Alvaro Martinez Rubio, Institut Curie, PSL University, Paris, FRANCE

- 62 Predicting therapy response in breast cancer patients using spatial biomarkers of metastatic lymph nodes Presented by [Andrea Mock, University of Basel, and Swiss Institute of Bioinformatics, Lausanne, SWITZERLAND](#)
- 63 SWI/SNF as a therapeutic target in B-Acute Lymphoblastic Leukemia Presented by [Fernando Montenegro Elvira, University of Granada, and ibs.GRANADA, SPAIN](#)
- 64 An Integrated Multi-Omics AI-Driven Pipeline for Immunogenic Cancer Neopeptide Identification Presented by [Marmar Moussa, University of Oklahoma, Norman, USA](#)
- 65 Loss of MCPIP1 triggers sex-dependent inflammatory microenvironment remodeling during early hepatocarcinogenesis revealed by single-cell transcriptomics Presented by [Rafat Myrczek, Jagiellonian University, Kraków, POLAND](#)
- 66 Functional states of the tumor microenvironment shape prognostic landscapes in cervical cancer Presented by [Shiva Najjary, Amsterdam UMC, NETHERLANDS](#)
- 67 An Accurate Microsatellite Instability Classification Using NGS From Ultima Genomics UG 100 Platform Across Diverse Tumor Types Presented by [Stav Naky, Technion - Israel Institute of Technology, Haifa, ISRAEL](#)
- 68 Integrated multi-omics dissection of proteostasis in hepatobiliary cancers identifies druggable heat shock protein hubs Presented by [Manju Nidagodu Jayakumar, BITS Pilani, Dubai, UNITED ARAB EMIRATES](#)
- 69 Weighted Gene Co-expression Network Analysis identifies a survival-associated miRNA module in high-grade serous ovarian cancer: the PowerOMICS study Presented by [Wiktorja Turska-Skrodzka, Medical University of Bialystok, POLAND](#)
- 70 Antigen Processing Machinery (APM) Dysregulation Reveals Immune Vulnerabilities in an Under-Represented Indonesian Breast Cancer Population Presented by [Ika Nurlaila, National Research and Innovation Agency \(BRIN\), South Tangerang, INDONESIA](#)
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