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Karolinska Comprehensive Cancer Center

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ABSTRACT BOOKLET

Poster 1

Quality of life and emotional distress in young adults with primary brain tumor – a longitudinal, population-based study

Alexandra Wide 1, Christel Hedman 2,3,4, Roger Henriksson 5, Ingrid Glimelius 6, Lena Wettergren 1,7, Claudia Lampic 7

1 Department of Public Health and Caring Sciences, Uppsala University, Uppsala, Sweden
2 Department of Molecular Medicine and Surgery, Karolinska Institutet, Stockholm, Sweden; R & D Department,
3 Stockholms Sjukhem Foundation, Stockholm, Sweden
4 Department of Clinical Sciences Lund, Lund University, Sweden
5 Department of Radiation Science and Oncology, University Hospital, Umeå, Sweden
6 Department of Immunology, Genetics and Pathology, Uppsala University, Sweden
7 Department of Women's and Children's Health, Karolinska Institutet, Stockholm, Sweden
8 Department of Psychology, Umeå University, Umeå, Sweden

Background
Brain tumors substantially impact those afflicted. The psychosocial impact of a brain tumor in young adulthood, specifically, has yet to be examined. Many studies exclude persons with brain tumors based on supposed cognitive impairment and/or dismal prognosis. The aim of this study is to examine the development over time of health-related quality of life (HRQoL), anxiety, and depression in this population by tumor grade. We further aimed to identify factors associated to change.

Methods
A Swedish population-based cohort with brain tumors at ages 18-39 years answered surveys at 1.5, 3-, and 5-years post-diagnosis. Outcomes were measured using the EORTC QLQ-C30 and the Hospital Anxiety and Depression Scale (HADS). Participants were stratified according to tumor grade (WHO grade I, grade II, and grades III-IV). Descriptive statistics were calculated for each time point. A linear mixed model (LMM) was fit to investigate changes in Global QoL. Similar LMMs are planned for emotional distress and fatigue.

Results
123 (58% response rate), 92, and 83 persons completed the first and last surveys, respectively. Fourteen participants died during the course of the study. About one in three participants had elevated levels of anxiety and about a quarter had elevated HADS-depression scores at all time points. No significant changes in global QoL were observed over time, regardless of tumor grade.

Conclusion
YA:s with brain tumors are an understudied population but many are perfectly able and willing to participate in research. About half experience clinical levels of emotional distress; and anxiety is especially prevalent. Small samples, a heterogeneous diagnosis spectrum, and high mortality rates call for larger studies and meta-analyses.

Keywords: brain tumor, quality of life, young adults

Poster 2

Multi-Omics Profile for Precision Cancer Medicine in Central Nervous System Tumors

Alia Shamikh 1, Emma Tham 1, Zahraa Haider 2, Thomas Sjöberg 1, Christpher Illies 1, Johanna Sandgren3

1 Dept of Molecular Medicine and Surgery, Karolinska Institutet, Sweden
2 Dep of Neuropathology, Dept. of Neuropathology, Heidelberg University Hospital & DKFZ, Germany
3 Barntumörbiobank, Karolinska Institutet

Central nervous system tumors in children represent a highly heterogeneous group of neoplasms, where accurate and timely diagnosis is essential for guiding treatment and improving clinical outcomes. Conventional pathology and molecular diagnostic methods are limited by interobserver variability, tissue sampling challenges, and prolonged turnaround times.

The project aims to integrate multi-omics profiling—including whole-genome sequencing, whole-transcriptome sequencing, methylation analysis, and targeted gene panels—applied to both tumor tissue and liquid biopsy samples. A key focus is nanopore sequencing, a third-generation sequencing platform offering long-read capability, real-time data generation, and rapid turnaround suitable for intra-operative decision-making.

By applying nanopore sequencing to fresh-frozen tumor samples and cerebrospinal fluid-derived cell-free DNA, the project will: (i) evaluate its utility for precision diagnostics in pediatric and adult central nervous system tumors, (ii) establish workflows for ultra-rapid intra-operative molecular diagnosis for brain tumors, and (iii) develop minimally invasive methylation and gene panel analyses as alternatives to traditional biopsies.

The project comprises four interconnected studies:
-Nanopore sequencing of tumor and blood samples to generate methylation and copy number profiles.
-Ultra-rapid intra-operative nanopore analysis to deliver actionable molecular results within hours.
-Methylation and copy number analysis of cell-free DNA from cerebrospinal fluid for minimally invasive diagnostics.
-Targeted gene panel sequencing of cell-free DNA to detect clinically relevant genetic alterations.

Through this multi-omics strategy, the project aims to refine diagnostic workflows in pediatric neuro-oncology, providing more accurate, rapid, and personalized tumor classification. Ultimately, this work seeks to advance precision medicine by reducing diagnostic uncertainty and improving therapeutic stratification, with the goal of enhancing clinical outcomes for children with central nervous system tumors.

Keywords: MultiOmic precision Medicine, CNS tumours, Nanopore

Poster 3

Nitrate and Nitrite Intake from Diet and Drinking Water and Risk of Gastrointestinal Cancers: A Population-based Cohort Study

Ana Rodrigues 1, Jon O Lundberg 2, Eddie Weitzberg 2, Anna Bergström 1, Alicja Wolk 1, Agneta Åkesson 1, Emilie Helte 1

1 Institute of Environmental Medicine, Karolinska Institutet
2 Department of Physiology and Pharmacology, Karolinska Institutet

Background: Dietary exposure to nitrate originates from vegetables, drinking water, and is, together with nitrite, used as food additives in animal products. Both compounds can be converted into N-nitroso compounds of which some are known animal carcinogens. However, the epidemiological evidence of long-term nitrate and nitrite involvement in gastrointestinal (GI) cancer risk is limited.

Methods: Nitrate and nitrite intake was assessed by linking a comprehensive food and drinking water database to food frequency questionnaires completed in 1997, 2009, and 2019 by 82,009 men and women in two population-based cohorts from the Swedish Infrastructure for Medical Population-based Life-course and Environmental Research (SIMPLER). We ascertained incident GI cancers through linkage to the Swedish Cancer Registry from baseline 1998 through 2022. Time-varying Cox proportional hazards regression models were fitted to evaluate exposure-outcome associations, presented as hazard ratios (HR) with 95% confidence intervals (CI).

Results: We ascertained 4,808 total GI cancer cases (621 upper GI cancer and 3,170 colorectal cancer (CRC)). While we observed no associations for nitrate intake and risk of any GI tract cancers, a higher intake of nitrite was associated with a dose-dependent 27% (95%CI: 13-44%; p-trend = 0.00) higher risk of total GI cancer in men but not in women (sex p-interaction = 0.007). When assessing upper and lower GI cancers separately, the HR for upper GI cancer was 1.33 (95%CI: 0.98-1.82) and 1.23 (95%CI: 1.06-1.43) for CRC. Analyses on CRC subsites suggested a higher risk of mainly distal colon cancer (HR 1.50; 95%CI: 1.13-1.98). No associations of nitrite with GI cancers were observed among women.

Conclusion: A higher intake of nitrite was associated with a higher risk of total GI cancer and CRC in men, but not in women. The increased CRC risk was attributed to a higher risk of distal colon cancer. Dietary nitrate intake was not associated with the risk of cancer.

Keywords: Nitrate and nitrite intake, Gastrointestinal cancer, Epidemiological study

Poster 4

VHIO Academy: Building a Culture of Collaboration and Professional Growth to Advance Translational Cancer Research

Ana Martins Ribeiro 1, Alba Echarte Ventura 1, Maria Yubero Gomez 1, Carme Harris Amoros 1, Paula Rodriguez Ocaña 1, Eva Navarrete Espuña 1, Imma Falero 1

1 Vall d'Hebron Institute of Oncology

Established in 2021, the VHIO Academy was conceived as a driving force in fostering a collaborative and sustainable research culture within the Vall d'Hebron Institute of Oncology (VHIO). Guided by the principles of interdisciplinarity, scientific creativity, collaboration, communication, and mentoring, the department acts as a central hub for promoting ethical, inclusive, and patient-centered scientific practices that enhance career development and biomedical innovation. VHIO Academy's mission is to foster an environment where scientific excellence and professional wellbeing coexist as part of a coherent institutional culture, ensuring the continuous delivery of responsible, high-quality, and impactful cancer research.

VHIO Academy coordinates a broad portfolio of actions that include community building initiatives, institutional fellowship calls, and cancer research-focused educational programs for researchers, clinicians, and other VHIO professionals. Its activities include the design and delivery of seminars, workshops, and complementary courses that strengthen intellectual, technical, and transferable skills across all career stages, as well as structured mentoring schemes that support career progression. Through strategic design and curation of tailored actions that respond to the needs of the different VHIO professionals, the department enhances the capacity of VHIO's scientific, clinical and research administration communities. By consolidating international collaborations and facilitating the mobility of researchers and clinicians, the VHIO Academy amplifies opportunities for professional networking, shared learning, and cross-border cooperation, which plays a pivotal role in the global exchange of knowledge and best practices in oncology and cancer research.

Through these coordinated actions designed to attract and support talented professionals, the VHIO Academy positions scientific education and professional development as central pillars of VHIO's mission of conducting excellent preclinical and clinical research practices that ensure tangible benefits for patients and society.

Keywords: Scientific Education, Research Culture, Professional Development

Poster 5

Personalised Tumour-Trained Lymphocytes – A neoantigen targeted T-cell therapy product for treatment of colorectal cancer

Anne-Laure Joly 1,2, Vilma Urbonaviciute 1,2, Huqiao Luo 1,2, Sofia Berglund 1,2, Erwan Le Maître 1,2, Kelly Day 1,2, Katarína Bankóová 1, Luigi Notari 1, Andreas Kaiser 1, Claudia Carvalho-Queiroz 1, Kristine Bylund 1, Alejandro Fernandez Woodbridge 1,Birce Akpinar 1,2, Long Jiang 1,2, Ahmed Salim Tarfy 3, Per J Nilsson 4, Abbas Chabok 5, Maziar Nikberg 3, Maximilian Kordes* 6, Mattias Carlsten 7*, Ola Nilsson 1, Per Norlén 1, Andrea Salmén 1, Samuel Svensson 1, Guro Gafvelin 1,2, Hans Grönlund 1,2

1 NEOGAP Therapeutics AB, Cancer Center Karolinska, Stockholm, Sweden
2 Dept. of Clin. Neuroscience, Karolinska Institutet, Stockholm, Sweden
3 Dept. of Surgery, Section for Colorectal Surgery, Västmanland Hospital Västerås, Sweden
4 Dept. of Pelvic Cancer, Karolinska University Hospital, Stockholm, Sweden
5 Dept. of Surgery, Danderyd Hospital, Stockholm, Sweden
6 Phase 1 unit, Theme Cancer, Karolinska University Hospital, Stockholm, Sweden
7 Medical Unit Cell Therapy and Allogeneic Stem cell Transplantation, Karolinska University Hospital, Huddinge, Sweden
* Contributed equally

Background

Adoptive T-cell therapy utilising precision neoantigen targeting is a promising concept for the treatment of solid tumours. Personalised tumour-trained lymphocytes (pTTL) form an autologous T cell product derived from regional lymph nodes (RLN) that targets patient-specific neoantigens. A phase I/II First in Human (FIH) clinical trial of pTTL in Stage IV colorectal cancer (CRC) patients is ongoing.

Methods

pTTL is an in vitro expanded T-cell product derived from tumour-adjacent RLNs. The T cells are stimulated with a patient-specific array of neoantigens utilising the proprietary EpiTCer® technology. Immunogenic mutations are identified from next generation sequencing data obtained from tumour and normal tissue samples. Personal neoantigen epitopes are then selected and ranked using the bioinformatic software PIOR®. The 36 highest ranked neoantigen epitopes are included in in-house produced proteins linked to paramagnetic micro-particles, forming patient-specific EpiTCer® beads. These are used as raw material for tumour-selective T-cell expansion in pTTL manufacturing.
pTTL are characterised by typing of T-cell differentiation and activation markers (flow cytometry, single-cell RNA sequencing). T-cell clonality of RLN cells and corresponding pTTL are determined by TCR sequencing. Neoantigen specificity is assessed by recall assays i.e. restimulation of pTTL with EpiTCer® beads using e.g. fluorospot (IFNγ, TNFα) or CellTrace™ dilution.

Results

The pTTL manufacturing process generates a T-cell product with individually varying CD4/CD8 ratios and minor proportions of other cells, such as NK cells. It is mainly composed of memory T cells with limited percentages of terminally differentiated T cells, indicating functionality. Functionality is also supported by elevated expression of cytotoxic and tumour-homing molecules, while maintaining a non-exhausted phenotype. TCR sequencing shows that pTTL is oligoclonal, indicating antigen-specific expansion during manufacturing from polyclonal RLNs. Finally, proliferation and secretion of pro-inflammatory cytokines IFN-γ and TNF-α in response to EpiTCer® beads restimulation demonstrate enrichment in neoantigen-specific T cells.

In the ongoing FIH trial, up to 16 patients with Stage IV CRC are treated with a single dose pTTL after lymphodepletion regimen with cyclophosphamide and fludarabine. The primary endpoint is safety. Secondary outcomes include objective response, overall survival, and progression-free survival. Biomarkers for tumour burden, pTTL persistence, and pTTL characteristics in terms of reactivity and specificity, will be evaluated.

The study is approved according to EU:s Clinical Trials Regulation (EU) 536/2014, including review via CTIS by the Swedish Ethical Review Authority.
Trial Registration EU CT #2024-512296-13-00
Clinicaltrials.gov Identifier #NCT05908643

Keywords: personalised T-cell therapy, neoantigens, colorectal cancer

Poster 6

Design Principles for Multi-Analyte Companion Diagnostics in Translational Oncology

Christer Ericsson 1

1 SOMA Genomics AB (Karolinska Institutet spin-off, KI Science Park)

Precision oncology has traditionally relied on single-biomarker companion diagnostics to guide targeted therapies. However, many solid tumors are characterized by interacting molecular drivers, co-drivers, pathway redundancy, and context-dependent signaling that collectively shape therapeutic response. As next-generation modalities increasingly target complex biological states rather than isolated genomic events, diagnostic frameworks may benefit from approaches that capture treatment-relevant tumor complexity within a single clinical decision structure.

This poster outlines conceptual design principles for multi-analyte, single-diagnosis companion diagnostics in translational oncology. The proposed framework integrates biologically related signals — including DNA alterations, RNA expression patterns, and protein-level context — into a structured evaluation aligned with therapeutic mechanism of action. Rather than expanding multiplex breadth across unrelated targets, the approach emphasizes biological coherence within a defined disease setting.

A central principle is the use of therapeutic index considerations as a diagnostic design parameter. By aligning analyte selection with mechanism-informed sensitivity and resistance pathways, diagnostic architecture can support more precise patient stratification and more efficient clinical trial design. This perspective is particularly relevant within Comprehensive Cancer Centres, where integration of molecular pathology, translational research, and early-phase clinical trials provides an opportunity to harmonize biological insight with implementation.

The framework also considers regulatory alignment within EU IVDR and FDA companion diagnostic pathways, as well as the role of structured data integration in supporting reproducibility and clinical usability.

By focusing on biologically integrated, disease-specific decision models, multi-analyte companion diagnostics may contribute to improved translational coherence between tumor biology, therapeutic strategy, and clinical evaluation. The poster aims to stimulate discussion on how diagnostic design can evolve in parallel with emerging targeted and next-generation therapies within European cancer centre networks.

Keywords: Translational oncology, Companion diagnostics, Multi-analyte integration

Poster 7

Mechanical Control of mRNA Translation in Breast Cancer

Christos Vogiatzakis 1, Solenne Bleuse 2, Arash Darzian Rostami 2, Sara Göransson 3, Ola Larsson 2, Staffan Strömblad 4

1 Department of Medicine Huddinge, Karolinska Institutet, Huddinge, SE-141 83, Sweden.
2 Department of Oncology-Pathology, Science for Life Laboratory, Karolinska Institutet, Solna, Sweden
3 Clinical Trials Office, Centrum för Kliniska Cancerstudier, Tema Cancer, Karolinska Universitetssjukhuset, Stockholm, SE-171 76, Sweden.
4 Department of Medicine Huddinge, Karolinska Institutet, Huddinge, SE-141 83, Sweden.

Introduction
Breast cancer ranks amongst the malignancies with the highest incidence and mortality. Extracellular matrix stiffness is a hallmark of breast tumors and is actively involved in promoting cell proliferation and invasion and progression of the disease. However, the way that malignant cells respond to external mechanical cues remains poorly defined. Emerging data suggest that mRNA translation regulates cellular plasticity, promoting tumor aggressiveness. This project aims to provide mechanistic understanding on how extracellular stiffness can reprogram mRNA-translation to drive breast tumor malignancy.

Methods
Breast cancer cell lines have been cultured on matrix-coated hydrogels with tunable stiffnesses to recapitulate the mechanical and matrix features of the breast tissue in healthy and malignant states. We analyzed the differential gene expression between the two conditions through total and polysome-associated mRNA sequencing, to decouple transcriptional and translational changes. We performed further bioinformatics characterization to elucidate stiffness-dependent alterations of mRNA-translation components. Additionally, a subset of translationally regulated genes has been tested for their function for the malignant phenotype and functional changes.

Results
Integrated data analysis has unveiled a substantial rewiring of the mRNA-translation promoted by increased extracellular stiffness. Features such as the length size of the 5'UTRs, the presence of uORFs and the codon/dicodon usage have emerged as regulators of translation efficiency in the malignant state. Interestingly, analysis of the transcription start sites has shown that different mRNA-variants are favored between the tested conditions. By in vitro silencing the expression of a subset of genes that are more efficiently translated upon stiffness, candidate genes have emerged with the potential to reverting cancer cells to a non-malignant phenotype.

Conclusions
In summary, the current findings define the importance of mRNA-translation as an downstream effector of mechanotransduction, which is currently overlooked in the context of cancer progression.

Keywords: breast cancer, mechanotransduction, mRNA translation

Poster 8

TETRIS WP2: development of a framework for predicting adverse events after breast cancer radiotherapy

Filippo Schiavo 1, Giovanna Gagliardi 1, Mattias Hedman 1, Andri Papakonstantinou 1, **Eva Onjukka 1**

1 Karolinska University Hospital

Purpose
Breast cancer accounts for the majority of female cancers in the world, leading to a large number being recommended treatment with adjuvant radiotherapy (RT). Major improvements have been made in the techniques of radiatherapy delivery, but the impact of long-term side effects has not been systematically and routinely accounted for, yet.
The TETRIS consortium, including six hospitals and oncological institutes and two companies, distributed in four European countries, was instituted in sight of this purpose. The aim of work package 2, led by Karolinska University Hospital (KUH), is to develop a prediction model framework, based on dosimetric and clinical predictors, to be used in personalised follow-up of breast cancer patients. Thereof, patients at higher risk of rare severe cardiac and respiratory side effects, or secondary cancer, can be informed and followed up effectively.

Material and Methods
The dosimetric and clinical data from a retrospective cohort of 2400 breast cancer patients, treated between 2010 and 2013 with 3D-conformal RT at KUH, were obtained for the initial modelling phase. In parallel, models for radiation-induced cardiac and respiratory late adverse reactions, as well as for secondary cancers, were retrieved from the literature and analysed in terms of their applicability to the KUH cohort and the full TETRIS cohort, as well as their statistical power.

Results
The KUH dataset includes data from the Swedish national health registries, namely the breast cancer-, cancer-, cause of death-, medicinal-, outpatient-, and inpatient registries. Core information regarding pre-existing conditions, comorbidities, side effects from RT, and cause of death (if applicable), retrievable either directly from the registries, or indirectly (e.g. through the medicinal records) are currently being extracted and processed for further stratification and testing of the models. The literature review revealed 8 and 16 potentially applicable models for cardiac and respiratory side effects at a given time after RT, respectively. Moreover, a larger number of survival models for all endpoints of interest was identified. The models vary widely in terms of features, such as type of cancer, adverse events considered (single or composite endpoints), RT modality, dose delivered, cohort size and incidence, dosimetric and clinical predictors, and performance metrics used

Conclusion
The KUH cohort presents a rich dataset to pilot the testing of multiple prediction models which can be implemented in the TETRIS model framework. In the next phase, selected models will be tested on the full TETRIS cohort, including other real-world cohorts in combination with prospective trial cohorts.

Keywords: Breast cancer, Radiotherapy, Side effects modelling

Poster 9

Phase I Trial of a Heat-Conditioned Tumor Lysate Vaccine (TRIMELVax) in Anti-PD-1 Refractory Melanoma: Safety and Immunological Aspects (NCT06556004)

Flavio Salazar-Onfray 1,2, Roberto Estay 3, Adnane Achour 1,4, Mercedes N. López 5, Andrés Tittarelli 6

1 Department for Basic and Clinical Oncology, Faculty of Medicine, Universidad de Chile.
2 Science for Life Laboratory, Department of Medicine, Karolinska Institutet, Stockholm, Sweden
3 Oncology Department, Hospital del Salvador, Santiago, Chile
4 Division of Infectious Diseases, Karolinska University Hospital, Stockholm, Sweden
5I nterdisciplinary Nucleus of Pharmacology and Immunology, Institute of Biomedical Sciences, Faculty of Medicine, Universidad de Chile, Santiago, Chile
6 University Institute for Research and Technology Development (UIRTD), Universidad Tecnológica Metropolitana, Santiago, Chile

Background: TRIMELVax is a cancer vaccine prototype derived from heat-conditioned melanoma cell lysates combined with a natural adjuvant. Preclinical studies demonstrated robust antitumor immune responses and tumor regression. We conducted a Phase I clinical trial to evaluate the safety, tolerability, immunogenicity, and preliminary efficacy of TRIMELVax in patients with unresectable stage IV melanoma who had progressed after first-line anti-PD-1 therapy.

Methods: Eligible patients had stage IV melanoma with documented progression or unacceptable toxicity following anti-PD-1 treatment. TRIMELVax was administered intradermally every four weeks for a total of four doses. The primary endpoints of the study were safety and feasibility, which were assessed according to CTCAE v5.0. Secondary endpoints included efficacy as assessed by RECIST 1.1, overall survival (OS), progression-free survival (PFS), and immunogenicity, evaluated by peripheral blood immune cell responses and delayed-type hypersensitivity (DTH) reactions.

Results: Seventeen patients received ≥1 dose; 13 completed all four doses. Treatment-related adverse events occurred in 9 patients, with a grade 1 or 2 severity. Two patients experienced manageable grade 3 events. No grade 4-5 toxicities were observed. No complete responses were observed in this cohort. Notably, a partial response was observed in 1 patient, stable disease in 6 patients, yielding a 41% disease control rate; 10 patients progressed. Median OS was 14 months, and median PFS was 5.2 months. DTH positivity was observed in six of the nine patients tested, correlating with the induction of memory T cells in peripheral blood after treatment. Immunomonitoring revealed increased CXCR3 expression in $CD8^+$ T cells and decreased CD39 expression in both $CD4^+$ and $CD8^+$ subsets in patients with disease control. One case with lung metastasis regression exhibited a significant expansion of $TCF1^+PD\text{-}1^+$ $CD4^+$ and $CD8^+$ T cell populations, and an enriched $perforin^+granzyme\ B^+$ $CD8^+$ T cell compartment, consistent with vaccine-associated immune activation.

Conclusions: TRIMELVax demonstrated acceptable safety and early signs of clinical activity in anti-PD-1 refractory melanoma patients. These findings support its immunogenic potential and warrant further evaluation in larger, controlled studies. CLINICALTRIAL.GOV: NCT06556004.

Keywords: cancer vaccine, melanoma, immunotherapy

Poster 11

Identifying and Targeting the tumorigenic Functions of Oncometabolites in Colon Cancer

Hanna Hjärpsgård 1, Amir Ata Saei 1

1 MTC Karolinska

Colorectal cancer (CRC) is one of the deadliest cancers, claiming 9.2% of all cancer-related deaths. Metastatic cases are associated with poor prognosis, and therefore new therapeutic strategies are needed. A key feature of CRC is its dependence on polyamines—essential metabolites that fuel tumor growth and metastasis. Both APC and KRAS, drivers of CRC progression, enhance polyamine synthesis. Despite their critical role, the targets and functions of polyamines in CRC remains unclear.

We investigated the proliferation of CRC cells in the presence and absence of polyamines, using specific inhibitors such as DFMO and 4MCHA. We use PISA (Proteome Integral Stability Alteration) assay, a technique for detection of protein-ligand interactions, to identify the protein targets of polyamines in primary and metastatic CRC cells, including SW480 and SW620.

Using PISA assay, we identified several putative targets that are engaged by polyamines in CRC cell lines. We then shortlisted the top targets based on their expression in CRC tumours vs. healthy tissue, and their association with survival. We aim to validate the binding of polyamines to the top targets using orthogonal techniques. We will also comprehensively validate the downstream effects upon polyamine binding to the targets, e.g., by modulating the expression of the targets in CRC cells.

This project will reveal the mechanisms by which polyamines support CRC progression. Our comprehensive study will identify the protein targets of polyamines in CRC cells and establish their role as druggable targets in cancer. We hope that these findings will pave the way for the development of novel therapeutics targeting polyamine-related pathways in CRC and other cancers.

Keywords: Colon cancer, Metabolites, Proteomics

Poster 11

Targeting vulnerabilities in metabolism and DNA repair sensitizes cancers to MTHFD1/2 inhibitor

Hannah Stigsdotter 1, Helge Gad 1, Christina Chalkiadaki 1, Petra Marttila 2, Elisée Wiita 1, Ana Slipicevic 3, Thomas Helleday 1

1 Karolinska Institutet
2 Luxembourg Institute of Health
3 One-carbon Therapeutics

The one-carbon folate metabolic protein methylenetetrahydrofolate dehydrogenase 2 (MTHFD2) has been identified among the most consistently overexpressed protein in cancer compared to normal tissue. The protein regulates mitochondrial formate release and supports thymidine biosynthesis, central to the supply of nucleotides for DNA replication and repair. Given the absence of MTHFD2 in normal tissue, this presents an attractive strategy for developing a cancer-specific therapy. We have developed TH9619, a first-in-class MTHFD1/2 inhibitor that selectively kill cancer cells. Mechanistically, TH9619 prevents thymidine production leading to misincorporation of uracil into DNA, induction of DNA damage and replication stress, as well as death of MTHFD2-expressing cells. Here, we conducted a genome-wide CRISPR-Cas9 drug screen in colorectal cancer (CRC) cells and identify genes involved in nucleotide biosynthesis and DNA repair to be associated with TH9619 response. The base excision repair DNA glycosylase UNG, responsible for excising misincorporated uracil from DNA, was found to provide resistance to TH9619, whereas depletion of UNG hypersensitized CRC cells to TH9619. The toxicity could be rescued through addition of external thymidine and inhibition and/or depletion of dUTPase led to further sensitization to TH9619 and Floxuridine in UNG-KO cells. Moving forward, our studies will focus on detailing the mechanisms underlaying cancers vulnerability to targeting thymidine levels and identification of biomarkers to predict TH9619 response. Overall, TH9619 offers a unique cancer-specific approach to target cancers and has received approval for testing in clinical trials.

Poster 12

From Plasma to Precision: A Next-Gen Bead-Based Approach for EV Biomarker Discovery

Hema Saranya Ilamathi 1,2, Mariana Castañeda Mesa 1,2, Srinidhi Rangarajan 1,2, Metoboroghene Mowoe 1,3, Doste Rashid Mamand 1,2, Oliver Hayes 1,3, Malgorzata Honcharenko 1,3, Samir EL Andaloussi 1,3, André Görgens 1,3, Daniel Hagey 1,3, Oscar P.B Wiklander 1,2

1 Division of Biomolecular and Cellular Medicine, Department of Laboratory Medicine, Karolinska Institutet, Huddinge, Sweden
2 Breast Center, Karolinska Comprehensive Cancer Center, Karolinska University Hospital, Stockholm, Sweden
3 Center for Cell Therapy and Allogeneic Stem Cell Transplantation (CAST), Karolinska University Hospital, Stockholm, Sweden

Introduction
Extracellular vesicles (EVs) circulating in biological fluids have emerged as powerful, minimally invasive biomarkers for disease detection and monitoring. Cancer-derived EVs carry molecular signatures reflective of their cell of origin, making them an attractive source for oncological profiling. However, current commercial bead-based EV capture technologies face critical limitations, including non-specific background binding, rigid pre-designed kits, and suboptimal sensitivity. To address these challenges, we developed a fully customizable bead-based platform with enhanced sensitivity and specificity for EV protein biomarker detection.

Methods
Our in-house platform enables surface functionalization of beads with user-selected antibodies, allowing tailored EV capture. We employed fluorescent-tagged commercial and clinical-grade antibodies to validate the system using EVs derived from cancer cells. Further, the platform was tested on human plasma samples to assess real-world applicability.

Results
The platform operates via a dual-antibody approach: capture antibodies immobilized on beads and detection antibodies for signal amplification, enabling multiplexed and customizable biomarker profiling. Protocol optimization significantly improved antibody conjugation efficiency and minimized background binding, confirming system specificity. Spiking experiments demonstrated robust detection of cancer-derived EVs in healthy plasma at concentrations as low as 10^7 EVs/mL. Importantly, the platform successfully distinguished HER2-high from HER2-low breast cancer EVs, validating its clinical relevance for stratifying tumor subtypes.

Conclusion
Our bead-based system overcomes key limitations of existing commercial platforms by offering improved sensitivity, specificity, and flexibility for multiplexed EV biomarker detection. The ability to directly analyze plasma without prior processing reduces turnaround time, making this approach highly feasible for clinical screening. This customizable platform holds strong potential for rapid, scalable, and cost-effective EV-based diagnostics, paving the way for personalized cancer monitoring and early detection.

Keywords: Liquid biopsy, Extracellular Vesicles, Biomarker

Poster 13

OVERDRIVE: overcoming cancer cell resistance to drugs by supplementary nontoxic molecule predicted by a machine learning tool

Hezheng Lyu 1, Hassan Gharibi 1, Liang He 1, Xuepei Zhang 1, Massimiliano Gaetani 1, Amir Ata Saei 1, Alexander Kel 2, Daria Stelmashenko 2, Galina Selivanova 1, Roman A. Zubarev 1.

1 Karolinska Institutet
2 geneXplain

Here we aim to test the notion that overcoming cancer cells' acquired resistance to chemotherapy drugs may be achieved by administrating together with the main drug a molecule that is not toxic by itself but enhances the drug efficacy in killing the resistant cells. Finding such a supplementary molecule is a nontrivial task. Our algorithmic approach, named OVERcoming Drug Resistance by In Vitro cell Exposure (OVERDRIVE), involves exposing drug-sensitive cancer cells to increasing drug concentrations for several weeks followed by a comprehensive proteomic analysis of both the exposed and sensitive cells. Applying a machine learning tool Genome Enhancer to the proteomic data reveals the protein network accounting for the differences between the exposed and naïve cells and predicts molecules that may shift the exposed cell phenotypes to the sensitive one. Experimental validation of the top predicted nontoxic molecules confirmed that the combined treatment of the experimental drug LTCA2940 that targets redox pathways with identified supplementary molecule restored the sensitivity of LTCA2940-resistant cells. The OVERDRIVE approach may pave a way for a strategy to overcoming anticancer resistance to chemotherapy in clinic.

Keywords: proteomics, drug resistance, machine learning

Poster 14

The Swedish Childhood Tumor Biobank - A national omics and tissue research resource for pediatric cancers

Díaz de Ståhl T 1, Prochazka G 1, Somarajan PR 1, Basmaci E 1, Zielinska-Chomej K 1, von Salomé J 1, Ardalan A 1, Cao D 1, Wessman S 1,2, Illies C 1,2, Ljungman G 3 and **Sandgren J 1,2**

1 Department of Oncology-Pathology, Karolinska Institutet, Stockholm, Sweden
2 Clinical Pathology and Cancer Diagnostics, Karolinska University Hospital, Stockholm, Sweden
3 Department of Women´s and Children's Health, Uppsala University, Uppsala, Sweden

Introduction:
In Sweden, around 350 children are diagnosed with cancer annually. Despite an 85% survival rate, cancer remains a leading cause of childhood death. Survivors often suffer treatment related sequelae, underscoring the need for deeper biological insights to improve survival and quality of life. The Swedish Childhood Tumor Biobank (Barntumörbanken, BTB) enhances understanding of pediatric solid tumors by providing infrastructure, biological samples, and molecular/genomic data for research.

Material & Methods:
BTB collaborates with the six university hospitals treating pediatric cancer nationwide. Fresh frozen tumors, blood samples, CSF, viable tumor cells, digital pathology slides and parental blood are collected. BTB registers, processes, and stores samples with linked clinical information, and performs whole genome and transcriptome sequencing, proteomics and methylation profiling. BTB partners with SciLifeLab for comprehensive molecular characterization and developing bioinformatic pipelines. Internal variant databases and data portals support secure data organization, traceability, and visualization.

Results:
Over 2600 cases are registered and 60,000 samples collected/prepared. About 1600 cases have been genomically characterized, with BTB managing the resulting data, including for the Genomic Medicine Sweden Childhood Cancer study. BTB has shared samples and data with over 20 approved research projects, governed by medicolegal review and access agreements. BTB also supports clinical studies with logistics, regulatory guidance, and data interpretation.

Conclusions:
BTB systematically collects specimens and informed consent from over 90% of Swedish pediatric patients with solid tumors, generating structured high quality molecular data. Continued use of these samples and omics datasets in approved studies is expected to improve future clinical care for children with cancer.

Keywords: pediatric cancer, biobanking, precision medicine

Poster 15

Input Resolution Drives Performance in Deep Learning-Based Mammographic Prediction of Breast Cancer Clinical Subtypes

Jose Luis Diaz Resendiz 1, Fernando Cossio Ramirez 2, Taeyang Choi 1, Michael Nercessian 3, Adam Yala 3, Apostolia Tsirikoglou 1, Fredrik Strand 1

1 Karolinska Institutet
2 KTH
3 UC Berkeley

Purpose:
Clinical subtype of breast cancer may change over the course of preoperative treatment, necessitating a renewed needle biopsy. Our aim was to optimize an interpretable deep learning framework for clinical subtype prediction (Luminal vs. Non-Luminal) applicable to sequential mammography images ('virtual biopsy'), by systematically evaluating network architecture and input resolution.

Methods:
This retrospective study included 9,057 breast cancer patients (22,256 mammograms) diagnosed between 2007 and 2021, with clinical subtypes assigned from the Swedish National Breast Cancer Register. Data were split at patient level into a development set (training: 5,323 patients; validation: 1,315 patients) and an independent held-out test set (2,419 patients) that remained unused during model development and hyperparameter selection. We benchmarked ResNet18, ResNet50, and EfficientNetV2-Small using mammograms resized to 224×224, 384×384, and 512×512 pixels using aspect-ratio-preserving downscaling with black padding. Models were trained on single-view inputs and evaluated at study level by fusing CC and MLO predictions via max selection. Performance was measured using Area Under the Curve (AUC) and Matthews Correlation Coefficient (MCC), with 95% confidence intervals estimated via stratified study-level bootstrapping (1000 iterations). Model behavior was examined using Integrated Gradients attribution maps.

Results:
The optimal configuration was ResNet50 at 512×512 achieved MCC of 0.228 (95% CI: 0.191–0.263) and the highest AUC of 0.710 (95% CI: 0.684–0.736). Across all architectures, increasing input resolution from 224×224 to 512×512 consistently improved discrimination. Attribution maps confirmed focus on clinically relevant tumor regions.

Conclusion:
In this study we demonstrate that increasing input image size significantly improves mammography-based clinical subtype prediction. Interpretability analyses support the presence of resolution-dependent breast cancer tumor phenotypes.

Keywords: Breast Cancer Subtyping, Deep Learning , Virtual Biopsy

Poster 16

An adaptive multi-agent reasoning framework for clinical decision support in sarcoma

Julien Vibert 1, Hakim Benkirane 2, Maud Kamal 3, Semih Dogan 3, Paul-Henry Cournède 2, Fabrice André 1

1 Gustave Roussy, Inserm U981, IHU PRISM
2 Centrale Supélec, IHU PRISM
3 IHU PRISM

Background: Sarcomas are rare and heterogeneous malignancies requiring highly specialized expertise for optimal management. Decision-making is often complex, particularly outside expert centers, due to the need to integrate diverse clinical, pathological, radiological, and molecular data. Multidisciplinary tumor boards (MTBs) are essential but resource-intensive, motivating the development of computational frameworks that emulate expert reasoning while adapting dynamically to case-specific features.

Methods: We designed an adaptive multi-agent architecture in which domain-specialized agents (general oncologist, pathologist, radiologist, molecular biologist) interact through a structured reasoning layer formalized as a graph. This reasoning layer integrates multimodal data with curated knowledge sources (guidelines, scientific literature, trial registries) and governs the deliberation process by dynamically adjusting task sequencing, evidence weighting, and agent contributions according to the characteristics and uncertainties of each case. Sixteen synthetic sarcoma cases were generated for evaluation, with treatment recommendations reviewed by a senior sarcoma oncologist for concordance with international standards of care.

Results: Across synthetic sarcoma scenarios, the framework produced treatment recommendations consistently aligned with guideline-based expert assessments. The adaptive reasoning layer improved transparency by making explicit the factors shaping deliberation and ensured robust integration of multimodal evidence through structured multi-agent interactions.

Conclusions:
This study introduces the first adaptive multi-agent reasoning framework dedicated to sarcoma, combining structured graph-based deliberation with dynamic case-specific adaptation. Beyond reproducing guideline-concordant decisions, the system models the logic of MTB discussions, adjusts reasoning to the clinical context, and provides transparent justifications. Such an approach lays the groundwork for decision-support platforms capable of scaling expert-level reasoning to non-expert centers, while preserving interpretability and auditability.

Keywords: Artificial intelligence agents, Sarcomas, Precision oncology

Poster 17

Longitudinal evaluation of cognitive functioning and wellbeing after thyroid surgery - a prospective trial

Karin Lind 1, Maria Wiklander 2, Catharina Ihre Lundgren 1, Renske Altena 3

1 Department of Molecular Medicine and Surgery (MMK)
2 Department of Neurobiology, Care Sciences and Society (NVS)
3 Department of Oncology-Pathology (onk-pat)

Differentiated thyroid cancer (DTC) incidence has increased worldwide while mortality remains low, shifting focus toward survivorship outcomes. DTC survivors commonly report reduced health-related quality of life (HR-QoL) and cognitive complaints (e.g., impaired attention, memory, and executive function). However, prior studies are limited by cross-sectional designs, heterogeneous assessments, and lack of pretreatment testing and benign surgical controls. This prospective, longitudinal study aims to objectively evaluate cognitive functioning after thyroid surgery using the Amsterdam Cognition Scale (ACS), an online neuropsychological test.
Consecutive adults scheduled for thyroid surgery for Bethesda III–VI nodules at Karolinska University Hospital (the only thyroid surgery unit in the Stockholm region) are invited, supporting population-based inclusion and minimizing selection bias. After informed consent, participants complete baseline assessments preoperatively and follow-up assessments at I year post-surgery (with a planned 36-month follow-up). Assessments include ACS, HR-QoL (SF-36 and thyroid-specific questionnaires), physical activity (Modified Godin Questionnaire), and demographics. Blood samples are collected to measure thyroid hormones (routine clinical sampling when feasible; local laboratory sampling for groups 1 and 2 at follow-up). Postoperative pathology defines three groups: (1) benign disease (including follicular adenomas/no malignancy), (2) extreme low-risk DTC (pT1a pN0/x M0 and selected follicular profiles), and (3) all other DTC risk groups. The primary outcome is the difference in change in ACS total score from baseline to 12 months between groups 1 and 3. Secondary and exploratory analyses compare groups 2 and 3, and examine relationships between objective and subjective cognition, HR-QoL, thyroid hormones, physical activity, and lifestyle factors.
Status update: To date, 180 patients have been included, of whom 113 were classified in group 3. Accrual is expected to be completed when 120 patients in group 3 have completed the longitudinal data collection (2027).

Keywords: Differentiated Thyroid Cancer, Cognitive function, Surgery

Poster 18

Di-codon organization orchestrates the malignant proteome

Kiana H. Moghaddam1, Clelia Timpone2, Laasya Naga Gowda2, Candani A. Tutuka2, Gail P. Risbridger2, Joel R. Steele3, Ralf B. Schittenhelm3, Eric P. Kusnadi2,*,# Luc Furic2,*,# and Ola Larsson1,*,#

1 Department of Oncology-Pathology, Karolinska Institutet, Science for Life Laboratory, 17165 Solna, Sweden
2 Prostate Cancer Translational Research Laboratory, Peter MacCallum Cancer Centre, Melbourne, VIC, 3000, Australia
3 Monash Proteomics & Metabolomics Platform, Department of Biochemistry and Molecular Biology, Biomedicine Discovery Institute, Monash University, Melbourne, Victora 3800, Australia
E. P. Kusnadi, L. Furic and O. Larsson are co-senior authors of this study

Aberrant mRNA translation is a hallmark of prostate cancer, yet the codon-level mechanisms that shape this deregulation remain understudied. We previously showed that U34 tRNA-modifying enzymes ELP3, ALKBH8 and CTU2 coordinate transcriptional and translational programs within the ERα network in prostate cancer. Here, we show that loss of U34 tRNA modifications impairs translation elongation at specific dicodon contexts, whose cumulative presence and spatial distribution within the ORF independently explained ELP3-dependent changes in protein levels. This disrups the codon-biased translation of mRNAs critical for cancer cell proliferation and survival.
We first demonstrated that CRISPR/Cas9-mediated depletion of ELP3 significantly decreases proliferation and clonogenic potential in prostate cancer cell lines DU145 and LNCaP, but not in the non-transformed, prostate-derived cell line PNT1A. Importantly, integration of translatomic and proteomics datasets suggested that mRNAs encoding downregulated proteins were highly associated with polysomes. While single-codon analysis was insufficient to explain this pattern, we identified six codon pairs significantly associated with reduced protein output despite increased ribosome association which indicates ribosome stalling. This highlights that combination of codons provides unique information not captured by individual codons alone. Functionally, enrichment analysis and subsequent validation experiments demonstrated that ELP3 depletion caused mitotic defects, including lagging chromosomes and micronuclei formation. Furthermore, although the Integrated Stress Response (ISR) pathway was activated, as indicated by increased p-eIF2α, its typical translational program was suppressed. This suggests that ELP3 loss-dependant dicodons decouples ISR signalling due to the absence of tRNA modifications required to translate mRNAs encoding downstream ISR effectors.
Together, we showed that the identified di-codons act as translational traps, slowing down elongation and thereby affecting protein fate under ELP3 depletion. Our data identify U34 tRNA modification as a cancer-selective, targetable vulnerability that links coding features to translational control, mitotic fidelity and cellular stress response.

Keywords: hormone-dependant cancer, mRNA translation, codon usage

Poster 19

DKFZ Cancer Research Academy

Lindsay Murrells 1, Mariana Schulte-Sasse 1

1 German Cancer Research Center (DKFZ)

The German Cancer Research Center (DKFZ) is committed to advancing innovative cancer research that translates scientific discovery into meaningful clinical benefit for patients. To support this mission, the DKFZ Cancer Research Academy serves as an institutional framework for the structured training and professional development of early-career cancer researchers across disciplinary and career-stage boundaries.

Under the umbrella of the Cancer Research Academy, the DKFZ coordinates dedicated programs to support the next generation of cancer researchers. Within the International Master´s Program 'Molecular Biosciences' at Heidelberg University, the DKFZ organizes the Major Cancer Biology Master´s Program. The dedicated International PhD and Postdoc Programs host and provide support for over 600 PhD students and approximately 450 postdoctoral fellows respectively. Further, to promote the translation of research findings into clinical applications, the Clinician Scientist Program offers physicians early during their residency protected time to conduct research, and the Junior Group Leader and Junior Clinical Cooperation Unit programs support new group leaders to establish their independent research profiles.

The Cancer Research Academy helps its fellows to achieve scientific independence by customized training, rigorous mentoring and a diverse spectrum of education opportunities, including the portfolio of the H3 Health Hub, a Helmholtz transfer academy for entrepreneurial tracks. Furthermore, career development support is provided to scientists at all career stages through the DKFZ Career Center and a comprehensive alumni network. The resources offered through the Cancer Research Academy are complemented by strong national partnerships, such as the National Center for Tumor Diseases and the German Cancer Consortium (DKTK), as well as with international partners and networks around the globe, including Cancer Core Europe.

By empowering early-career researchers (ECRs) to develop independent research profiles, drive innovation, and translate discovery into clinical impact, the DKFZ Cancer Research Academy cultivates a globally connected community committed to advancing the future of cancer research and improving outcomes for patients worldwide.

Find out more about the DKFZ Cancer Research Academy on our website:
https://www.dkfz.de/en/career/cancer-research-academy.

Upcoming application deadlines:

- 21 April 2026: PhD Program Summer Selection (www.dkfz.de/phd)
- NEW: May 2026: Collaborative Seed Funding Grants for ECRs (details on our PhD and Postdoc webpages)
- 15 June 2026: Junior Group Leader Program (www.dkfz.de/en/career/junior-research-groups)
- 15 September 2026: Postdoctoral Fellowships Program (www.dkfz.de/postdoc)
- 15 March 2027: Clinician Scientist Fellowship Program (www.dkfz.de/clinicianscientist)
- 15 March 2027: Major Cancer Biology Master’s Program (www.dkfz.de/major)

Keywords: PhD students, Postdocs, Training

Poster 20

Characterizing ILC2 dynamics during bone marrow fibrosis progression

Maria Angeles Piñero Garasa 1, Lixin Gong 1, Jonathan Coquet 2, Johanna Ungerstedt 3, Itziar Martinez-Gonzalez 1, Sergio Martinez-Høyer 1

1 Dept. Microbiology, Tumor and Cell Biology (MTC), Karolinska Institutet
2 Dept. Immunology and Microbiology, University of Copenhagen
3 Biomedical and Clinical Science (BKV), Linköping University

Background
Primary myelofibrosis (PMF) is a subtype of myeloproliferative neoplasm (MPN) that leads to progressive and irreversible bone marrow fibrosis. Recent evidence from mouse models of PMF show that type 2 inflammation contributes to disease pathogenesis, as blockade of IL-4 and IL-13 signaling delayed fibrotic onset. However, the cellular players originating such signals are still poorly defined. Group 2 innate lymphoid cells (ILC2) are innate lymphocytes present throughout the organism that do not react against specific antigens but instead are highly responsive to alarmins released upon damage, such as IL-33. Upon activation, ILC2s produce large amounts of type 2 cytokines, including IL-13 and IL-4, and therefore are considered key initiators and orchestrators of type 2 immune responses. Remarkably, ILC2-derived IL-13 has been shown to be involved in fibrotic responses in different tissues.
Aims
Our work aims to understand the contribution of ILC2s to the inflammatory response that promotes the progression of PMF.
Methods
We transplanted primary bone marrow cKIT+ cells transduced with a retrovirus expressing MPL W515L (or MPL WT as control) into sublethally irradiated recipients. Peripheral blood, spleen, and bone marrow were harvested at different time points after transplantation to study immune cell populations using high dimensional flow cytometry.
Results
At early disease stages, we observed a significant increase in mature KLRG1+ ILC2s in peripheral blood. Concomitantly, KLRG1+ ILC2s were reduced in the bone marrow suggesting local activation and egress into circulation. As disease progressed and transplanted animals developed splenomegaly, we observed accumulation of CD25+ ILC2s in the spleen. CD25 encodes for the receptor of IL-2, which is an activating factor for ILC2s. At late stages, when fibrosis is present, ILC2s exhibited markedly elevated expression of the inhibitory receptor PD-1, both in the bone marrow and spleen. In contrast, although splenic T cell subsets also expressed PD-1, they did not display a comparable accumulation.
Furthermore, analysis of peripheral blood mononuclear cells from patients in early stages of the disease showed a shift towards an ILC2 phenotype within the ILC compartment, suggesting that the disease development promotes ILC2s in circulation. In addition, functional analyses of purified ILC2s from MPN patients showed their competence to produce the type 2 cytokines.
Conclusion
Together, our findings suggest a stage specific involvement of ILC2s in the pathogenesis of MPN, switching from an activated state in pre-fibrosis towards an exhausted phenotype at fibrosis onset. Our study may uncover previously unrecognized features of the lymphoid microenvironment in MPN progression, emphasizing the potential contribution of ILC2s to the development of bone marrow fibrosis in myeloid malignancies.

Keywords: myelofibrosis, ILC2, Inflammation

Poster 21

A multifeature liquid biopsy for integrated microbial profiling and tumor copy number analysis

Mariano A. Molina 1, Juan Du 2, Daniel W. Hagey 1

1 Department of Laboratory Medicine, Karolinska Institutet
2 Department of Microbiology, Tumor and Cell Biology, Karolinska Institutet

Early cancer detection remains a major unmet clinical need, as most solid tumors are still diagnosed at advanced stages when therapeutic options are limited. Liquid biopsy approaches based on circulating tumor DNA have shown promise, yet their sensitivity in early disease remains constrained and largely ignores the contribution of microbial signals to systemic cancer biology. Increasing evidence suggests that bacterial extracellular vesicles (BEVs), nanosized vesicles released by bacteria and capable of translocating into the bloodstream, represent a stable and biologically meaningful carrier of microbial information in human plasma. Here, we present a multifeature liquid biopsy framework for the integrated analysis of BEV-associated microbial DNA and host genomic alterations from a single low-input assay. Using differential centrifugation to enrich extracellular vesicle subpopulations followed by tagmentation-based shallow whole-genome sequencing (sWGS), we demonstrate that small extracellular vesicle fractions are enriched for non-human DNA while simultaneously retaining detectable tumor-derived copy number variation (CNV) signals. This enables parallel extraction of microbial profiles and host genomic features from the same sequencing library, overcoming the need for separate assays. An in-house broad-range 16S rRNA PCR assay confirms robust detection of bacterial DNA across vesicle fractions, with the strongest and most reproducible signals observed in small EVs from cancer patients. Applying this workflow to plasma samples from esophageal cancer patients reveals distinct microbial signatures, visualized as patient-specific microbial heatmaps, highlighting inter-individual heterogeneity. Importantly, these microbial signals are detected alongside CNV profiles derived from the same sequencing data, illustrating the feasibility of a convergent host-microbial readout. Together, this work establishes a unified plasma-centric liquid biopsy pipeline that captures bacterial and tumor signals in a single assay. By integrating microbial and host genomic information within one workflow, this approach provides a scalable foundation for multifeature cancer profiling and supports the development of BEV-based biomarkers for multi-cancer early detection (MCED) and translational diagnostics.

Keywords: Bacterial extracellular vesicles, Cancer biomarkers, Sequencing

Poster 22

Variables influencing biopsy adherence: Lessons from the Cancer Core Europe (CCE) clinical trial Basket of Baskets

Marta Rotxes Costa 1, F. Opdam 2, M. Vlasov 3, C. Massard 4, R. D. Baird 5, L. De Petris 6, R.F. Schlenk 7, C. Vernieri 8, J. Jimenez 9, R. Fasani 9, E. Chavarria 10, A. Romero Tamarit 10, F. Gallego 9, J.-Y. Scoazec 11, G. Pruneri 12, E. Provenzano 13, J. Rodon Ahnert 14, I. Braña 15, J. Carmona Sanz 10, P. Nuciforo 9

1 Early Drug Development (UITM) Unit, VHIO - Vall d'Hebron Institute of Oncology, Barcelona, Spain
2 Medical Oncology Department, NKI-AVL - Netherlands Cancer Institute/Antoni van Leeuwenhoek Hospital, Amsterdam, Netherlands
3 Biostatistics Unit, VHIO - Vall d'Hebron Institute of Oncology, Barcelona, Spain
4 Department of Therapeutic Innovation and Early Trials (DITEP), Gustave Roussy - Cancer Campus, Villejuif, France
5 Department of Oncology, Cancer Research UK Cambridge Centre, Cambridge, United Kingdom
6 Department of Oncology-Pathology, Karolinska Comprehensive Cancer Center, Stockholm, Sweden
7 Clinical Trial Center, NCT - Nationales Zentrum für Tumorerkrankungen, Heidelberg, Germany
8 Department of Medical Oncology, Fondazione IRCCS - Istituto Nazionale dei Tumori, Milan, Italy
9 Molecular Oncology Laboratory, VHIO - Vall d'Hebron Institute of Oncology, Barcelona, Spain;
10 Scientific Managment Area, VHIO - Vall d'Hebron Institute of Oncology, Barcelona, Spain;
11 Department of Pathology and Translational Research, Institut Gustave Roussy, Villejuif, France
12 Pathology department, Fondazione IRCCS - Istituto Nazionale dei Tumori, Milan, Italy
13 Department of Histopathology, Addenbrooke's Hospital, Cambridge, United Kingdom
14 Department of Drug Development, The University of Texas MD Anderson Cancer Center - Main Building, Houston, United States of America
15 Early Drug Development (UITM) Unit, VHIO - Vall d'Hebron Institute of Oncology, Barcelona, Spain

Paired biopsies provide insights into tumor dynamics, supporting biomarker discovery. Although biopsies are frequently considered in oncology trial protocols, not all patients undergo these procedures. Multiple factors can influence adherence to biopsy requirements, impacting biomarker research, and trial outcomes.

We analyzed 101 patients from Module 1 of the academic platform CCE Basket of Baskets trial (NCT03767075). Clinical variables- age, tumor type, baseline ECOG, adverse events, comorbidities, concomitant medications, baseline tumor size [primary tumor or metastatic site, defined as sum of target lesions], and tumor response- were correlated with biopsy performance. Logistic regression models were fitted to assess factors associated with biopsy procedures. Additionally, Random Forest models explored non-linear relationships.

Among 101 patients, 62 underwent tumor biopsies (39 paired). Baseline tumor size and tumor type were the strongest predictors of biopsy likelihood. Smaller tumors reduced biopsy probability, while larger tumors markedly increased the chance of baseline biopsy (OR=1.0175 per unit increase; $p<0.001$). When grouped by tumor type, breast cancer accounted for the highest percentage of patients with biopsies (86.7% vs. 13.3% without biopsy), while genitourinary showed the lowest proportion (46.7% vs. 53.3% without biopsy).

Among patients who underwent a baseline biopsy, statistical modeling aimed to predict the likelihood of completing an on-treatment biopsy. The most influential factors identified are the change in tumor size in the first radiology assessment (6 weeks after treatment start), baseline ECOG and the tumor type, all three of them displaying a non-linear pattern.

Baseline tumor size emerged as the strongest predictor of biopsy performance, driving the likelihood of completing both baseline and on-treatment biopsies. Other clinical variables—including tumor type, ECOG performance status, and previous medical history—showed a secondary influence. These findings suggest that clinical and functional status play a role in biopsy adherence, which impacts translational research outcomes.

Keywords: Biopsy compliance, Baseline tumor size, Tumor type

Poster 23

First in Human Evaluation of ELC 301, a CD20 CAR T Cell Therapy Engineered With Neutrophil Activating Protein (NAP)

Mats Hellström 1, Gunilla Enblad 1, Jamal El-Mosleh 2, Margareth Jorvid 2, Di Yu 1, Magnus Essand 1

1 Uppsala University, Dept. Immunology, Genetics, Pathology and Uppsala Comprehensive Cancer Center, Sweden
2 Elicera Therapeutics AB, Gothenburg, Sweden

Background:
CD19 directed CAR T therapy has improved outcomes in relapsed/refractory B cell lymphomas, but resistance and relapse remain major challenges. ELC 301 is a CD20 targeted CAR T cell product engineered with the Helicobacter pylori neutrophil activating protein (NAP) to address antigen loss resistance and modulate the tumor microenvironment. ELC 301 entered clinical evaluation in the Phase I CARMA 01 study in 2024.

Methods:
CARMA 01 is a first in human, dose escalation trial assessing safety of ELC 301 at three dose levels (2×10^5, 6×10^5, 20×10^5 CAR+ T cells/kg) following standard Cy/Flu lymphodepletion. Primary endpoints are DLTs and adverse events (AEs). This report includes the first six patients from dose levels 1 and 2 with ≥1 month follow up.

Results:
All six patients experienced grade ≥3 AEs considered possibly related to treatment, mainly neutropenia (6/6), thrombocytopenia (5/6), and anemia (2/6). One case each of grade 1 CRS and grade 2 hypotension occurred. No grade 5 toxicity was observed, and all events resolved without additional supportive care.
At one month, the overall response rate was 83%, with four patients (67%) achieving complete remission, including one previously treated with CD19 CAR T therapy. The longest ongoing response is 12 months.

Conclusion:
ELC 301 demonstrated manageable toxicity and encouraging early efficacy, with a high rate of complete remissions. These findings support continued clinical development and evaluation in larger patient cohorts.

Keywords: CAR-T, Lymphoma, First in man

Poster 24

Live-remote träning efter behandling för cancer: resultat från den randomiserade studien EX-MED Cancer Sweden

Melissa Kotte[1,2], Kate Bolam[3], Prue Cormie[4], Renske Altena[5,6], Sara Mijwel[1], Yvonne Wengström[1,2]

[1]Institutionen för neurobiologi, vårdvetenskap och samhälle, Karolinska Institutet, Stockholm, Sverige
[2]Tema Cancer, Karolinska Comprehensive Cancer Centre, Stockholm, Sverige
[3]Cardiometabolic Health and Exercise Physiology Lab, Baker Heart and Diabetes Institute, Melbourne, Australia
[4]Sir Peter MacCallum Department of Oncology, The University of Melbourne, Melbourne, Australia
[5]Institutionen för onkologi-patologi, Karolinska Institutet, Stockholm, Sverige
[6]Docrates Cancersjukhus, Stockholm, Sverige

Bakgrund
Fysisk träning kan ge viktiga hälsofördelar för cancerdrabbade, men deltagandet är lågt på grund av hinder som tidsbrist, reseavstånd och begränsad tillgång till anpassade träningsinsatser. Virtuellt ledarledd träning som levereras live på distans kan minska dessa hinder och samtidigt ge professionellt stöd.

Syfte
Att utvärdera effekterna av en 12-veckors ledarledd live-remote träningsintervention på hälsorelaterad livskvalitet (HRQoL) och andra patientrapporterade samt fysiologiska utfall hos personer som behandlats för bröst-, prostata- eller kolorektalcancer.

Material och metod
200 deltagare (medelålder 58,5 ± 10,4 år; 62 % kvinnor) randomiserades till en träningsintervention eller sedvanlig vård. Interventionen bestod av två 60-minuters virtuella gruppträningspass per vecka under 12 veckor, ledda av särskilt utbildade personliga tränare. Mätningar gjordes vid baseline, vid 3 månader och 6 månader. Primärt utfall var övergripande HRQoL (EORTC QLQ-C30 summary score). Sekundära utfall inkluderade patientrapporterad fysisk funktion, VO_2max, styrka och fysisk aktivitetsnivå.

Resultat
Median träningsnärvaro var 75 % och inga allvarliga händelser rapporterades. Ingen signifikant mellan-gruppsskillnad sågs för övergripande HRQoL. Vid 3 månader visade interventionsgruppen signifikanta förbättringar jämfört med sedvanlig vård i fysisk funktion, VO_2max, styrka och fysisk aktivitet (alla $p < 0,05$). De flesta effekter var inte kvar vid 6 månader. Explorativa analyser antydde större effekter för kvinnor, deltagare med pågående endokrinbehandling samt deltagare med lägre hälsostatus vid baseline.

Slutsats
Ledarledd live-remote träning förbättrade fysisk funktion, kondition, styrka och aktivitetsnivå, men inte övergripande HRQoL. Vissa undergrupper kan ha särskilt nytta av den typ av träningen.

Poster 25

Profiling of B cell Dynamics Identifies Prognostic Immune Niches in Soft Tissue Sarcoma

Yanhong Su 1, Panagiotis Tsagkozis 2, Lennart Linke 1, Andri Papakonstantinou 3, Elisabeth Wetzer 4, Cecilia Haglund 1, Haoyang Mi 5, Peng Sun 6, Nicholas P. Tobin 1, Christina L. Stragliotto 2, Aleksander S. Popel5,Yanxia Shi 6, Felix Haglund de Flon 1, **Monika Ehnman** 1

1 Department of Oncology-Pathology, Karolinska Institutet, BioClinicum J6:20, Visionsgatan 4, 171 64 Solna, Sweden
2 Department of Molecular Medicine and Surgery, Karolinska Institutet and Muskuloskeletal Tumor Service, Karolinska University Hospital, 171 76 Stockholm, Sweden
3 Department of Breast Cancer, Endocrine Tumors and Sarcoma, Karolinska University Hospital, 171 76 Stockholm, Sweden
4 Department of Physics and Technology, University of Tromsø, Siva Innovasjonssenter Tromsø, Norway
5 Department of Biomedical Engineering, Johns Hopkins University School of Medicine, Baltimore, Maryland
6 Department of Oncology, Sun Yat-sen University Cancer Center, 510000, Guangzhou, China

Soft tissue sarcomas, including undifferentiated pleomorphic sarcoma (UPS), remain clinically challenging due to the lack of robust immune biomarkers for prognosis and predicting immunotherapy response.

In this cross-continental study of independent UPS cohorts, we systematically characterized B-cell dynamics within the tumor microenvironment. Using multiplex immunofluorescence and spatial analysis, we found that tumors with lymphoid aggregates (LA) displayed more fragmented B-cell desert areas, indicating enhanced local immune activation. We developed a novel “B-index” that integrates B-cell abundance and maturation, outperforming LA assessment in predicting patient survival. Notably, the B-index offers mechanistic insights from routine pathology samples and remains informative even in the absence of tertiary lymphoid structures.

These findings deepen our understanding of B cell-mediated immunity in sarcoma, bridge molecular pathology with clinical oncology, and support the development of universal immune-based scoring systems and therapeutic stratification strategies for personalized medicine in sarcoma.

Keywords: sarcoma, lymphoid aggregates, spatial profiling

Poster 26

Real-world prospective study on compassionate use and off-label novel anticancer therapies in children, adolescents, and young adults: the SACHA-INTERNATIONAL ITCC Study

Pablo Berlanga 1, Gerard Millen 2, Antonio Juan-Ribelles 3, Johannes Gojo 4, Ruta Tuckuviene 5, Nicoletta Bertorello 6, **Lee Aymar Ndounga-Diakou 1**, Salim Laghouati 1, Gilles Vassal 1

1 Gustave Roussy Cancer Campus, Villejuif, France
2 Birmingham Children's Hospital, Birmingham, United Kingdom
3 Hospital U i P La Fe, Valencia, Spain
4 Medical University of Vienna
5 Rigshospitalet, Copenhagen, Denmar
6 Regina Margherita Children's Hospital, Turin, Italy

Novel anticancer therapies are regularly prescribed outside their marketing authorization or through compassionate use programs to children, adolescents and young adults. Until recently, safety and efficacy data on those prescriptions were neither prospectively nor systematically collected and pharmacovigilance declarations were largely underreported.
SACHA-INTERNATIONAL (NCT04477681) is a prospective international non-interventional study developed within the Innovative Therapies for Children and adolescents with Cancer (ITCC) Consortium, which documents safety and efficacy data of compassionate and off-label innovative anticancer therapies administered to patients aged ≤ 25 years. SACHA-INTERNATIONAL is built up on the SACHA-France study developed by the French Society of Pediatric Oncology (SFCE) (Berlanga et al. JAMA Netw Open 2023), opened in Q1 2020. SACHA-INTERNATIONAL is adapted to each national regulation with common study objectives and eligibility criteria. Data are collected in a common central database. Since Q3 2023, SACHA-INTERNATIONAL is open in UK, Spain, Denmark, Austria and Ireland. In Q4 2024, Italy has joined the study. From 14/10/2023 to 01/10/2025 (cut-off to be updated), 811 compassionate or off-label prescriptions were registered for 698 patients across 66 centers in 6 countries (32 in France, 15 in the UK, 14 in Spain, 2 in Denmark, 1 in Austria and 1 in Italy). Before 14/10/2023, 552 prescriptions in 393 patients had been reported in the SACHA-France study. The median number of patients enrolled per center was 8 (range: 2–93). Median age at enrolment was 10.7 years (range: 0.2-24.9), and 79 different drugs were prescribed. Study enrollment increased progressively over time reflecting both the international expansion of the study, but also the increase off-label use following closure of trial recruitment. Detailed information on yearly inclusions, diagnostic groups and adverse drug reactions is summarized (figures).
Prospective real-world data collection on compassionate and off-label anticancer therapies is feasible at multicenter and international level. By expanding across multiple countries, the SACHA-INTERNATIONAL study ensures that critical safety and efficacy information is adequately collected and shared with the scientific community.

Keywords: Pediatric malignancies, Compassionate use/Off-label therapies, Real-World evidence

Poster 27

Diagnostic plasma biomarkers for lung adenocarcinoma using in-depth proteomics and machine learning

Noora Sissala 1, Irene Villanueva Sanz 1, Xiaofang Cao 1, Jenny Forshed 1, Lukas M. Orre 1, Lars E. Eriksson2,3, Maria Pernemalm 1, Haris Babačić 1, Janne Lehtiö 1

1 Department of Oncology-Pathology, Karolinska Institutet & Science for Life Laboratory, Stockholm, Sweden
2 Department of Neurobiology, Care Sciences and Society, Karolinska Institutet, Huddinge, Sweden
3 School of Health and Medical Sciences, City St George's, University of London, London, United Kingdom

Lung cancer remains the leading cause of cancer-related death worldwide, primarily due to late diagnosis and the lack of reliable methods for early detection. In this study, we aimed to identify plasma protein biomarkers for diagnosis of lung adenocarcinoma (LUAD) by analyzing pre-diagnostic plasma samples from two retrospective cohorts of LUAD patients and matched non-cancer controls (LCP1: 93 stage I-IV LUAD and controls, LCP2: 57 stage III-IV LUAD and controls) using two complementary proteomics platforms: global mass-spectrometry based proteomics (HiRIEF LC-MS) and targeted antibody-based proteomics (Olink Explore). Several thousand proteins quantified in LCP1 were analyzed through a machine learning pipeline involving feature selection and model training on small sets of the most frequently selected proteins. Model performance was estimated in LCP1 through cross validation and validated in LCP2 based on area under the receiver operating characteristic curve (AUC). The analysis revealed multiple signatures of 3-50 proteins that accurately differentiated LUAD cases from controls, achieving AUCs > 0.8 in LCP2. These findings highlight the potential of plasma proteomics for advancing early detection of lung cancer.

Keywords: Lung cancer, Proteomics, Biomarker discovery

Poster 28

Human Epidermal growth factor Receptor 2 (HER2)-targeted PET-imaging with [68Ga]Ga-ABY-025 to predict targeted-therapy response in HER2-expressing metastatic breast cancer: a multicentre, prospective, open-label trial

Nour Susaeg Romdhani 1*, Renske Altena 1*, Oscar P.B. Wiklander 2,3, Anna Kistner 4,5, Marie Klintman 6, Ida Skarping 6,7, Henrik Lindman 8, Veronica Sanchez Rodriguez 9, Oskar Frisell 10,11, Peter Lindgren 10,11, Klas Bratteby 1,5, Emma Jussing 1,5, Joachim Feldwisch 1,2, Fredrik Y. Frejd 12,13, Helena Silva Cascales 5, Jonathan Siikanen 1,5, Cecilia Hindorf 4,5, Thuy A. Tran 1,5

1. Department of Oncology-Pathology, Karolinska Institutet, Stockholm, Sweden.
2. Department of Laboratory Medicine, Karolinska Institutet, Stockholm, Sweden
3. Breast Center, Karolinska Comprehensive Cancer Center, Karolinska University Hospital, Stockholm, Sweden
4. Department of Molecular Medicine and Surgery, Karolinska Institutet, Stockholm, Sweden
5. Theranostics Trial Center, Department of Nuclear Medicine and Medical Physics, Karolinska University Hospital, Stockholm, Sweden
6. Division of Oncology, Department of Clinical Sciences, Lund University, and Skåne University Hospital, Lund, Sweden.
7. Department of Clinical Physiology and Nuclear Medicine, Skane University Hospital, Lund, 8. Sweden.
8. Department of Oncology, Uppsala University hospital, Uppsala, Sweden
9. Division of Radiology and Nuclear Medicine, Department of Surgical Sciences, Uppsala University, Uppsala, Sweden.
10. The Swedish Institute for Health Economics, Stockholm, Sweden
11. Department of Learning, Informatics, Management and Ethics, Karolinska Institutet, Solna, Sweden
12. Affibody AB, Stockholm, Sweden
13. Department of Immunology, Genetics and Pathology, Uppsala University, Sweden
*Equal contribution

Background
Trastuzumab deruxtecan (T-DXd) is effective in HER2-expressing metastatic breast cancer (mBC), yet inter-patient benefit varies. The current reference biomarker—HER2 immunohistochemistry (IHC) on tumour biopsies—is insufficient as a sole predictor of response. HER2-targeted PET/CT offers non-invasive, whole-body, real-time assessment of target expression. We hypothesize that HER2-targeted PET with [68Ga]Ga-ABY-025 improves prediction of T-DXd outcomes and supports individualized treatment planning.

Methods
HER2-Ex PET is a multicentre, phase II open-label diagnostic trial enrolling patients with HER2-non-amplified mBC who are candidates for T-DXd under current approvals (EU CT 2024-512721-89-00; NCT06830382). All participants undergo baseline HER2-PET with [68Ga]Ga-ABY-025 and a tumour biopsy. Patients with biopsy-confirmed HER2 expression (IHC 1–3+; Cohort 1) receive T-DXd and repeat HER2-PET after 3–4 cycles; others receive physician's-choice systemic therapy (Cohort 2).
The primary endpoint is the association between baseline HER2-PET signal—defined as the mean SUVmax across the five most avid lesions—and objective response per RECIST v1.1 after 3–4 cycles of T-DXd. A total sample size of 70 provides 80% power (α=0.05), allowing for attrition and technical failures. Secondary endpoints include health-economic outcomes and translational analyses of tumour biology and heterogeneity. The study is open at Karolinska University Hospital (Stockholm, Sweden), with Uppsala and Skåne University Hospitals planned for activation in Q1 2026.

Discussion

Demonstrating a robust correlation between HER2-PET signal and early radiologic response would validate imaging-based patient selection for T-DXd, facilitate adaptive treatment decisions, and enhance biological understanding of intra- and inter-patient HER2 heterogeneity. Key considerations include standardization of imaging protocols across sites, potential temporal discordance between biopsy and imaging, and the non-randomized design. Positive results would justify incorporation of HER2-targeted PET into clinical pathways and inform the design of subsequent randomized trials testing PET-guided T-DXd strategies.

Trial registration

EU CT 2024-512721-89-00; ClinicalTrials.gov NCT06830382 (registration date February 11th 2025; https://clinicaltrials.gov/study/NCT06830382)

Keywords: Metastatic HER2-low breast cancer, HER2-targeted PET, [68Ga]Ga-ABY-025

Poster 29

The effect of prior proton pump inhibitor use on gastric cancer survival: A population-based cohort study in the five Nordic countries

Onyinyechi Duru 1, Giola Santoni 1, Dag Holmberg 1, Helgi Birgisson 2, Joonas H. Kauppila 1,3, My von Euler-Chelpin 4, Eivind Ness-Jensen 5, Jesper Lagergren 1,6

1 Upper Gastrointestinal Surgery, Department of Molecular medicine and Surgery, Karolinska Institutet, and Karolinska University Hospital, Stockholm, Sweden
2 The Icelandic Cancer Registry, Reykjavik, Iceland
3 Oulu University Hospital and University of Oulu, Oulu, Finland
4 Department of Public Health, University of Copenhagen, Copenhagen, Denmark
5 HUNT Research Center, Department of Public Health and Nursing, NTNU, Norwegian University of Science and Technology, Trondheim/Levanger, Norway, Medical Department, Levanger Hospital, Nord-Trøndelag Hospital Trust, Levanger, Norway
6 Pharmaceutical Sciences, King's College London, United Kingdom

Objectives: Proton pump inhibitors (PPI) might mask gastric cancer symptoms, leading to delayed diagnosis and worse oncological outcomes. However, current evidence is sparse and underpowered. This study aimed to elucidate if PPI-use influences oncological outcomes of gastric cancer in a well-powered study.

Methods: This population-based cohort study included patients with gastric non-cardia adenocarcinoma from the five Nordic nations (Denmark, Finland, Iceland, Norway, Sweden). Multiple nationwide registries provided prospectively collected data. The patients were grouped into non-users, light users, or heavy PPI-users during the 2-year period before diagnosis. The outcomes 5-year disease-specific mortality (primary) and 5-year all-cause mortality were analyzed using Cox regression, providing hazard ratios (HR) with 95% confidence intervals (CI). The outcomes metastatic disease and advanced tumor stage at diagnosis were analyzed using logistic regression, providing odds ratios (OR) with 95% CI. The risk estimates were adjusted for age, sex, country, year, comorbidity, and Helicobacter pylori treatment.

Results: Among 21,433 gastric non-cardia adenocarcinoma patients, PPI-users had no increased risk of 5-year disease-specific mortality. Compared to non-users, heavy and light users demonstrated rather decreased risks (HR=0.90, 95% CI 0.86-0.94 and HR=0.87, 95% CI 0.84-0.91, respectively), with similar results for 5-year all-cause mortality. PPI-users had no increased risks of presenting with metastatic disease (OR=0.70, 95% CI 0.64-0.76, comparing heavy-users with non-users) or advanced tumor stage (OR=0.71, 95% CI 0.56-0.89, comparing heavy users with non-users). The results were similar for PPI-use during the 12-month and 6-month periods before diagnosis.

Conclusion: PPI-use before gastric non-cardia adenocarcinoma diagnosis may not result in poorer oncological outcomes.
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Keywords: gastric adenocarcinoma, proton pump inhibitor, mortality

Poster 30

From Unstructured Text to Clinical-Grade Information Extraction from Breast MRI Reports Using Large Language Models

Parishad Mokhber 1, Rony Dahdal 2, Annika Gerigoorian 3, Dimitra Ntoula 1, Reihaneh Baniasadi 4, Taeyang Choi 1, Fredrik Strand 1,5, Apostolia Tsirikoglou 1

1 Karolinska Institutet
2 Elon University
3 KTH Royal Institute of Technology
4 Stockholm County Health Care Area
5 Karolinska University Hospital

Purpose: Breast MRI radiology reports contain detailed descriptions of lesion characteristics, laterality, assessment categories, and malignancy indicators, and other key clinical and quantitative parameters. However, this clinically meaningful information remains embedded in unstructured free text, rendering large-scale secondary analysis labor-intensive and practically infeasible.
Methods: To unlock this latent value, we present a privacy-preserving framework, based on open-source models that extracts structured variables from typed or dictated reports using locally deployed, fine-tuned Large Language Models (LLMs). We evaluated seven open-source models on Swedish and English corpora, specifically addressing the challenge of extracting variables like lesion size from numerically dense contexts where multiple plausible numeric candidates appear but only one is the correct target output.
Results: Our results indicates that language-dependent top performance after fine-tunning, Mistral-7B-Instruct achieved the highest accuracy in English (89.2%), while BioMistral-7B proved superior in Swedish (85.6%).
Conclusion: These findings demonstrate that fine-tuned open-source models can parse heterogeneous reporting styles within secure infrastructure, enabling the scalable transformation of expert-authored unstructured text into machine-readable data without compromising patient privacy.

Keywords: Artificial intelligence, Breast MRI Report, Large Language Model

Poster 31

The tumour microenvironment influences long-term tamoxifen benefit in postmenopausal ER+/HER2- breast cancer patients

Paula Camargo-Romera 1,2, Miguel Castresana-Aguirre 1,2, O. Danielsson 1,2, Huma Dar 1,2, Arne Östman1, Kamila Czene 3, L. S. Lindström 1,2, Nicholas P. Tobin 1,2

1 Department of Oncology and Pathology, BioClinicum, Karolinska Institutet and University Hospital, Visionsgatan 4, 171 64 Stockholm, Sweden
2 Breast Center, Karolinska Comprehensive Cancer Center, Karolinska University Hospital, Stockholm, Sweden
3 Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden.

Background: The tumour microenvironment (TME) influences breast cancer progression and treatment response. We investigated whether TME composition predicts tamoxifen benefit in postmenopausal women with oestrogen receptor-positive, HER2-negative (ER+HER2-) breast cancer.
Methods: This study included 513 patients from the Stockholm Tamoxifen (STO-3) trial, which randomised postmenopausal, lymph node–negative women to tamoxifen or no endocrine therapy. Bulk tumour transcriptomes were deconvoluted with the ConsensusTME algorithm to estimate the relative abundance of 18 immune and stromal cell types. A summary score of combined immune cells was created on a per patient basis and evaluated alongside fibroblast and endothelial stromal compartments. Patients were categorised into immune and stromal tertiles on the basis of these scores. Associations between TME composition and tumour characteristics were evaluated using Spearman correlations and Fisher's exact test. Tamoxifen benefit was analysed by univariable Kaplan-Meier (log-rank) and multivariable Cox proportional hazards adjusting for age, tumour size, grade, progesterone receptor, Ki-67, and radiotherapy. Differential expression was assessed with limma and pathway enrichment with fgsea using Hallmark gene sets from MSigDB.
Results: Low immune abundance was significantly associated with higher ER expression (Fisher's exact test $p < 0.001$). Among tamoxifen-treated patients, those with low immune scores showed improved distant recurrence-free interval (DRFI) relative to untreated patients (log-rank $p < 0.001$). Similarly, intermediate endothelial ($p < 0.001$) and low/intermediate fibroblast abundances ($p = 0.042$, $p = 0.009$) were associated with favourable DRFI. In multivariable models, low immune (aHR = 0.17, 95% CI 0.08–0.40), intermediate endothelial (aHR = 0.21, 95% CI 0.09–0.51), and low/intermediate fibroblast tertiles (aHR = 0.50, 95% CI 0.27–0.93; aHR = 0.36, 95% CI 0.17–0.77) retained significance. Transcriptomic analysis revealed enrichment of oestrogen-response, MYC-target, and oxidative-phosphorylation pathways in low-immune and low-fibroblast tumours, while interferon-γ response and allograft rejection pathways were downregulated.
Conclusions: TME composition modulates tamoxifen benefit in postmenopausal ER+HER2- breast cancer. Low immune, intermediate endothelial, and low/intermediate fibroblast abundances are associated with improved benefit from tamoxifen, suggesting that both immune and stromal compartments influence endocrine treatment efficacy.

Keywords: TME, breast cancer, omics approach

Poster 32

Glycolysis-associated stratification delineates immune microenvironment heterogeneity and clinical outcomes following immunotherapy in lung squamous cell carcinoma

Qiaofeng Zhong 1, Yuequan Shi 2, Mingci Huang 3, Weijin Xiao 3

1 Karolinska Institutet
2 Peking Union Medical College Hospital
3 Fujian Cancer Hospital

Background
Glycolysis plays a crucial role in tumor progression and immune modulation. However, the clinical relevance of glycolysis-associated molecular heterogeneity in lung squamous cell carcinoma (LUSC) remains insufficiently characterized.
Methods
Gene expression and clinical data from TCGA (502 LUSC patients and 51 healthy controls) were used as the training cohort, with external validation in the GSE30219 dataset (n = 61) and an independent Fujian Cancer Hospital cohort (n = 48); the IMvigor210 cohort was further analyzed to evaluate outcomes following immune checkpoint blockade. Glycolysis-related pathways were identified using gene set enrichment analysis, and key candidate genes were further screened to construct a glycolysis-associated prognostic signature based on univariate, LASSO, and multivariate Cox regression analyses. The prognostic performance of the signature was evaluated using survival analyses and time-dependent receiver operating characteristic curves. Functional enrichment and immune infiltration analyses were performed to characterize biological pathways and immune microenvironment differences between risk groups.
Results
A glycolysis-associated gene signature comprising 13 genes was developed to stratify patients with LUSC into distinct risk groups. Patients in the high-risk group exhibited significantly poorer overall survival (OS) in the TCGA training cohort, with AUCs of 0.667, 0.726, and 0.710 for 1-, 3-, and 5-year OS, respectively, and these findings were consistently validated in independent GEO and Fujian Cancer Hospital cohorts. Multivariate Cox regression confirmed the risk score as an independent prognostic factor (HR = 3.652, $P < 0.001$), outperforming conventional clinical characteristics. Functional enrichment analyses indicated that high-risk tumors were associated with tumor-promoting pathways, whereas low-risk tumors were enriched in metabolic and translational processes. Immune profiling further revealed marked heterogeneity in the tumor immune microenvironment, with high-risk tumors characterized by increased infiltration of immunosuppressive macrophages, particularly M2 macrophages, and broad alterations in immune-related functions, consistent with an immunosuppressive immune landscape. Notably, in the IMvigor210 immune checkpoint blockade–treated cohort, patients classified as high risk by the glycolysis-associated signature experienced significantly shorter OS compared with low-risk patients ($P = 0.006$), supporting the clinical relevance of glycolysis-associated immune heterogeneity in predicting outcomes following immunotherapy.
Conclusion
We developed and validated a glycolysis-associated stratification that delineates heterogeneity of the immune microenvironment and is associated with differences in prognosis and clinical outcomes following immunotherapy in LUSC.

Keywords: glycolysis-related gene, lung squamous carcinoma, immunotherapy

Poster 33

An internet-delivered intervention (Fex-Can 2.0) for sexual problems and fertility-related distress following cancer in young adulthood

Rebecca Skog 1, Erik Olsson 2, Jessica Gorman 3, Sharon Bober 4, Claudia Lampic 5, Lena Wettergren 1

1 Department of Public Health and Caring Sciences, Uppsala university
2 Department of Women's and Children's Health, Uppsala university
3 College of Health, Oregon State University
4 Department of Supportive Oncology, Dana-Farber Cancer Institute, Department of Psychiatry, Harvard Medical School
5 Department of Psychology, Umeå university

Objective: Fertility-related distress and sexual dysfunction following a cancer diagnosis during young adulthood is a major threat to quality of survivorship. Evidence-based interventions to alleviate such challenges are however lacking. The Fex-Can 2.0 is an internet-delivered intervention aiming to reduce sexual problems and fertility-related distress among young adult (18-39 years) cancer survivors. Fex-Can 2.0 is a psychoeducational, guided self-help intervention, developed in collaboration with patient research partners and grounded in self-determination theory. Participants receive a personal set of modules throughout the 12-week program, and modules include educational and behavior change content, self-management tools, and feedback support.

Methods: The Fex-Can 2.0 will be evaluated in a two-armed superiority randomized controlled trial with an internal pilot phase. The primary objective is to determine the efficacy of the intervention in alleviating sexual problems and/or fertility-related distress, as compared to a standard care control group. In the internal pilot trial, feasibility of the Fex-Can 2.0 is assessed, determined according to progression criteria focusing on recruitment, attrition, adherence, and resources needed.

Primary and secondary outcomes will be assessed at baseline, 6-weeks into the intervention, at end of the intervention, and 12 weeks later. Primary outcomes are sexual function and satisfaction (PROMIS® SexFS v2.0) and fertility distress (RCAC). Following the internal pilot trial, intervention group participants will further be interviewed about their experiences of the program.

Conclusion and implications: Findings from this study will determine the feasibility and efficacy of the Fex-Can 2.0 intervention. If proven efficacious, the Fex-Can 2.0 intervention may have significant clinical implications through improving care provided to young adults diagnosed with cancer.

Keywords: Internet-delivered interventions, Sexual and reproductive health, Cancer

Poster 34

Decoding CAPRIN1's RNA interactome in anti-cancer-drug-treated liver cancer

Riccardo Mosca 1, Claudia Kutter 1
1 Karolinska Institutet

Hepatocellular carcinoma (HCC) presents persistent therapeutic challenges due to high recurrence rates and limited efficacy to current treatments. Our research focuses on how RNA regulation influences drug response in HCC, particularly upon Sorafenib treatment - a clinically approved tyrosine kinase inhibitor (TKI) used as first-line therapies that target cell cycle and stress response pathways.
RNA regulation occurs at both transcriptional and post-transcriptional levels, with RNA binding proteins (RBPs) playing a central role in post-transcriptional regulation by interacting with regulatory RNA molecules to modulate cellular processes (1).

We have linked Sorafenib to the formation of stress granules (SGs) in liver cancer cells that potentially contribute to drug resistance and reduced treatment efficacy. We recently identified CAPRIN1 as a critical player in Sorafenib-driven SG maturation. CAPRIN1 is reactivated in HCC and may help cancer cells adapt to drug-induced stress, contributing to drug resistance.

The identification of CAPRIN1 RNA targets is crucial for the understanding of CAPRIN1 regulatory function, both in physiological and stress conditions.
At this purpose we developed a novel, in vitro, RBP-centric technology that discovers and quantifies RBP binding sites in any given transcriptome/species of interest. RAPseq is an in vitro binding assay between a recombinant purified RBP and native total chemically fragmented RNA. The bound RNA molecules are recovered and sequenced on an NGS platform. Our custom NGS data processing pipelines then deconvolute the RBP binding sites.
With RAPseq we have identified the potential targets of CAPRIN1 in vitro, with a high enrichment for cell-cycle and stress-response RNAs.

To define the CAPRIN1 RNA neighborhood in living cells during therapy, we are applying APEX-seq (2) under sorafenib exposure. Integrating RAPseq (direct binding) with APEX-seq (in-cell proximity) will reveal stress-condition sequestration of CAPRIN1-associated RNAs and drug-specific differences between different stressors. We hypothesize that CAPRIN1 partitions key cell-cycle and integrated-stress-response transcripts into SGs to transiently repress translation and foster TKI tolerance. These data nominate CAPRIN1-dependent RNA circuits as biomarkers of TKI responsiveness and highlight CAPRIN1/SG modulation as a potential co-therapy to resensitize HCC to TKI.

(1) Gebauer F et al. Nature Reviews Genetics 22.3 (2021): 185-198.
(2) Fazal, Furqan M., et al. "Atlas of subcellular RNA localization revealed by APEX-Seq." Cell 178.2 (2019): 473-490.

Keywords: Therapy resistance, RNA regulation, RNA binding proteins

Poster 35

Feasibility of multimodal data generation in cancer for clinical trials

Rikard Fred1, Richard Rosenquist Brandell2, Maria Creignou3, Thoas Fioretos4, Åsa Johansson5, Anna Martling2, Jeffrey Yachnin6, Janne Lehtiö7, Päivi Östling1

1 Dept. Of Oncology-Pathology, Karolinska Institutet, Stockholm
2 Dept. of Molecular Medicine and Surgery, Karolinska Institutet, Stockholm
3 Center for Clinical Cancer Studies, Karolinska University Hospital, Stockholm
4 Dept. of Laboratory Medicine, Lund University, Lund
5 Dept. of Immunology, Genetics and Pathology, Uppsala University, Uppsala
6 Karolinska Comprehensive Cancer Center, Karolinska University Hospital, Stockholm
7 Clinical Proteomic Mass Spectrometry Facility, Karolinska University Hospital, Stockholm

The rapid development of technologies for molecular profiling paves the way for novel diagnostic approaches to match patients with effective treatment. This project aims to increase access for translational research to SciLifeLab's technology platforms to support future academic and industry-initiated clinical trials. Our goal was to identify mature diagnostic methods to be evaluated in observational clinical studies and test feasibility of maximizing data generation on clinical samples. This meant supporting cross-platform data generation with sample and analysis flows and testing timelines and quality for compliance with clinical trials are needed. The feasibility testing was done on five pilot projects, four in cancer (uveal melanoma, breast cancer, lung cancer and CLL) that were identified through an open call. Important learnings from these projects includes setting up a recuring, temperature controlled, transportation chain directly from surgeries performed at the Karolinska University hospital to sample preparation labs at SciLifeLab. This include establishing the necessary contacts with the hospital transportation unit and on the importance of handling the sample flow without increasing the workload of the surgery coordinator.

These pilot projects have also shown the importance of support in data provenance and interoperability including the need for unique sample identifiers to track samples throughout the process of data generation at SciLifeLab. Similarly, today metadata is often customized and collected project-by-project often without adhering to technology-based nor clinical data standards nor semantic vocabulatries. The lack of identifiers and meta-data standards leads to to unnecessary fragmentation and hinders further data integration for large-scale data-driven studies, and dimished the FAIRness. Our goal is to increase our ability to provide for molecular data including good data management practices for translational research projects, clinical studies and trials .

Keywords: Multimodal data generation, Translational research, Data management

Poster 36

Facilitating Access to Precision Oncology in France: Real-World Results from Over 8,000 Liquid Biopsy Analyses

V. Suybeng , E. Turlotte, M Ngocamus, C Nicotra, R. Tang, J Tran, M. Degaud, M Laetitia, N Vungbo, L. Drouard, C Badoual, L. Lacroix, E Angevin, M. Morfouace, A Italiano, **E. Rouleau**

Gustave Roussy

The FRESH program was launched at Gustave Roussy to provide nationwide access to comprehensive genomic profiling (CGP) using circulating tumor DNA (ctDNA) for patients with advanced solid tumors. Operational since July 11, 2024, the program centralizes testing within a dedicated Liquid Biopsy Genomic Profiling Laboratory (PGBL) and integrates molecular results into Molecular Tumor Board (MTB) discussions to guide therapeutic decisions.
Using the CE-IVD FoundationOne® Liquid CDx assay (324 genes), more than 9,100 prescriptions were received between July 2024 and January 2026. The median turnaround time was 12.5 days, with fewer than 7% of results delivered beyond 15 days. The overall analytical performance demonstrated high robustness in a real-world national setting.
Among 8,427 analyzed samples, 77% harbored at least one pathogenic or likely pathogenic single nucleotide variant (SNV), 24% presented copy number variations (CNV), and 22% showed gene fusions or rearrangements. Tumor mutational burden (TMB) was >10 mutations/Mb in 14% of cases and >20 mutations/Mb in 4%. Importantly, 48% of samples showed tumor fraction <1%, emphasizing tumor fraction as a critical quality and interpretative parameter, especially when discussing sub-1% Limit of Detection (LOD) performance claims.
Molecular Tumor Boards recommended matched therapies in 72% of evaluable cases (estimation a part of the cohort related to Gustave Roussy), with treatment decisions based exclusively on liquid biopsy findings in a significant subset of patients, highlighting its clinical added value.
Clonal hematopoiesis (CHIP) was detected in 51% of samples, with a mean variant allele frequency of 6%. Potential incidental findings suggestive of germline predisposition were identified in 4.2% of cases, supporting systematic oncogenetic referral pathways.
The FRESH program demonstrates the feasibility of implementing large-panel ctDNA testing at a national scale within an accredited ISO 15189 framework. It provides rapid, equitable access to precision oncology, generates standardized real-world molecular data, and supports therapeutic orientation through TMB. The model is scalable for reimbursement integration and can be leveraged for trial screening and dedicated precision oncology studies.

Keywords: ctDNA, tumor molecular board, technique performance in real world data

Poster 37

The perceptions of a home-based blood flow restriction training program during and after treatment for hepatopancreatobiliary cancer

Malin Backman 1, Melissa Kotte 2, Berit Sunde 1, Truls Raastad 3, **Sara Mijwel 2**

1 Karolinska Univerity Hospital
2 Karolinska Institutet
3 The Norwegian School of Sport Sciences

Purpose
Blood-flow restricted resistance training (BFR-T), which uses low loads, may reduce mechanical stress and support faster muscle recovery compared with heavy-load training. Delivered at home, it may also improve exercise accessibility for cancer survivors, yet limited research has explored their experiences. This study aimed to qualitatively examine participants' perspectives of a home-based BFR-T program, focusing on barriers and facilitators to participation and adherence, and experiences with the activity tracker and protein supplement used in the intervention.

Methods
Individual interviews were conducted with nine participants between October and November 2024. All had completed a two-armed randomized controlled trial evaluating whether BFR-T could preserve skeletal muscle mass and enhance functional capacity and mental health in patients with pancreatic, biliary tract, or liver cancer. Interviews were transcribed verbatim and analyzed using reflexive thematic analysis with an inductive approach.

Results
Three themes were developed: From uncertainty to understanding BFR-T (instructions for BFR-T, adherence to BFR-T, expectations vs experience, willingness to recommend BFR-T, cuff experiences); Feeling the change—in body and beyond (perceived effects of BFR-T and its influence on continued exercise); and Beyond the cuffs—additional components shaping engagement (home-based format, activity tracker, protein supplement).

Conclusions and Implications
Participants progressed from initial uncertainty to growing confidence and acceptance of home-based BFR-T, supported by clear instructions, increasing familiarity, and perceived physical and mental benefits. Early challenges included cuff discomfort and skepticism, while the activity tracker, protein supplement, and home-based delivery offered mixed but generally supportive value. Successful implementation should emphasize clear guidance, comfortable equipment, and flexible use of supplementary elements. With appropriate support, home-based BFR-T appears feasible, acceptable, and potentially helpful in promoting sustained exercise participation among cancer survivors.

Keywords: Patient experience, Blood-flow restricted resistance training, Hepatopancreatobiliary cancer

Poster 38

High-Throughput, Multiplexed, Quantitative Epigenetic Profiling of Cancer Cells, Tissues, and Liquid Biopsies

Showgy Ma'ayeh 1, Alisa Alekseenko 1, Qian Li 1, Simon Elsässer 2

1 Epigenica AB
2 Karolinska Institute

Epigenetic changes drive cancer progression and appear in presymptomatic phases, offering early detection potential. Combined histone posttranslational modifications (hPTMs) and DNA methylation analyses reveal tumor origins and subtypes, help stratify patients, and identify epigenetic alterations in gene regulatory elements that fuel therapy resistance—yet existing methods fall short on throughput, multiplexing and quantitative precision for scalable insights.

EpiFinder™ GenomePro delivers multiplexed ChIP-seq for up to 8 hPTMs across 24 samples in one streamlined workflow. Its pool-split design slashes technical noise while enabling spike-in-free, quantitative comparisons between conditions. Compatible with native/formalin-fixed cells and frozen tissues, it integrates DNA methylation profiling for holistic multi-layer epigenomic analysis.

EpiFinder™ cNUC pioneers high-throughput, multiplexed, quantitative epigenomics from plasma/serum nucleosomes—no extraction needed. This first-of-its-kind platform profiles hPTMs and DNA methylation simultaneously across liquid biopsies, unlocking novel biomarker signatures for cancer monitoring. The utility of EpiFinder™ cNUC as one of a kind tool in liquid biopsy research is demonstrated with its ability to detect highest tumor DNA (i.e., nucleosomes) is detected in the plasma of patients with colorectal cancer (CRC) compared to healthy control. The enrichment of H3K4me3, H3K27ac, H3K9me3 and 5mC together with the genes regulated by each epigenetic mark as well as promoter and enhancer regions could be identified for all epigenetics marks simultaneously. Gene Ontology analysis underpinned important biological functions associated with CRC, including epithelium development, transcription regulation, and immune and white blood cells pathways. Overall, the results show that EpiFinder™ cNUC provided great insights into the CRC biology when looking at both hPTMs and DNA methylation simultaneously.

EpiFinder's high-throughput, multiplexed, quantitative platforms revolutionize epigenetic profiling of cancer cells, tissues, and liquid biopsies—accelerating diagnostics, precision therapies, and drug discovery.

Keywords: Multiplex ChIP-Seq, Epigenetic Profiling, Histone modifications

Poster 39

Can preoperative functional capacity predict length of stay and post-discharge daily step count after radical cystectomy for urinary bladder cancer?

Simon Torikka Suua 1, Andrea Porserud 1, Malin Nygren-Bonnier 1, Maria Hagströmer 1

1 Karolinska Institutet, Department of Neurobiology, Care Sciences and Society, Division of Physiotherapy

Introduction
Higher levels of physical function have been associated with an enhanced recovery after surgery in different cancer types. However, similar associations have not been tested in patients undergoing radical cystectomy. This study aimed to evaluate whether preoperative functional capacity, a component of physical function, can predict two postoperative early recovery measures: length of stay and post-discharge daily step count.

Methods
In total, 105 patients undergoing robot-assisted radical cystectomy were included, based on preoperative and baseline measurements from a randomised controlled trial. Functional capacity was measured using the Six-minute walk test. Length of stay (n days) was collected from medical records. Daily step count was measured for seven consecutive days after discharge using an accelerometer (activPAL3 micro activity monitor). Multiple regression analysis was used, adjusting for age, sex, and American Society of Anaesthesiologists score.

Results
Analysis included 73 participants with valid measurements for both functional capacity, length of stay and daily step count. Functional capacity did not predict length of stay (β = .004; 95% CI: -.015-.007). However, functional capacity was a significant predictor of post-discharge daily steps, with a higher preoperative walking distance (by 100 metres) associated with approximately 600 more steps per day (β = 5.92; 95% CI: 0.53–11.29).

Conclusions
The findings indicate that preoperative functional capacity can predict post-discharge daily step counts, but not length of stay, both of which are indicators of postoperative recovery. Interventions aimed at improving functional capacity before robot-assisted radical cystectomy may enhance recovery.

Keywords: Abdominal cancer surgery, Activity monitor, Recovery

Poster 40

Lesion-Level Diagnostic Accuracy of Human Epidermal Growth Factor Receptor 2 (HER2)-Targeted PET/CT Compared to Pathology: A Systematic Review

Siri af Burén 1, Nour Susaeg Romdhani 2, Antonios Tzortzakakis 1, Gary Ulaner 3, Randy Yeh 4, Thuy A. Tran2, Rimma Axelsson 5, Renske Altena 2

1 KI CLINTEC
2 Department of Oncology-Pathology, Karolinska Institutet, Stockholm, Sweden.
3 Molecular Imaging and Therapy, Hoag Family Cancer Institute, Irvine, California, USA
4 Nuclear Medicine and Molecular Imaging, Department of Diagnostic, Molecular and Interventional Radiology, Mount Sinai Health System, New York, USA
5 Department of Molecular Medicine and Surgery, Karolinska Institutet, Stockholm, Sweden.

Purpose: Human Epidermal growth factor Receptor 2 (HER2)-targeted PET/CT enables whole-body, noninvasive assessment of HER2 status in breast cancer (BC). We performed a systematic review to evaluate its lesion-level diagnostic accuracy for detecting HER2-positive disease compared to pathology.

Materials and Methods: PubMed, EMBASE, and Web of Science were searched through January 27, 2026, for clinical studies of HER2-targeted PET/CT in BC reporting lesion-level results with biopsy verification. Sensitivity, specificity, and risk of bias (QUADAS-2) were assessed.

Results: Ten reports from seven prospective trials (209 patients, 195 lesions) met inclusion criteria. Both affinity protein- and monoclonal antibody (mAb)-based tracers detected HER2-positive lesions. Sensitivity estimates were similar (affinity proteins: 75% [95% CI, 65–83%]; mAbs: 100% [95% CI, 59–100%]), although between-class comparisons were limited by heterogeneity, small mAb sample size, and differences in study design. Specificity for affinity proteins was 79% (95% CI, 68–87%); it was not estimable for mAbs. Across tracers, most false positives (≥86%) corresponded to HER2-low lesions. QUADAS-2 identified concerns regarding patient selection, incomplete lesion sampling, and post hoc SUV thresholds.

Conclusion: HER2-targeted PET/CT shows promising lesion-level sensitivity for detecting HER2-positive BC, with affinity protein and mAb tracers demonstrating broadly comparable performance relative to pathology. Frequent uptake in HER2-low lesions suggest potential predictive utility for therapy selection, but this remains unproven. Current evidence is constrained by small, heterogeneous studies and nonstandardized thresholds. Larger prospective trials with prespecified SUV cutoffs and systematic verification of PET-non-avid lesions are needed to establish HER2-targeted PET/CT as a complement to pathology in clinical practice.

Keywords: HER2, Breast cancer, PET/CT

Poster 41

Lifestyle patterns in cancer survivors – a cross-sectional descriptive analysis from the Swedish CArdioPulmonary BioImage study (SCAPIS)

Therese Christensson 1, Philip von Rosen 1, Andrea Porserud 2,3, Maria Hagströmer 2, 4

1 Department of Neurobiology, Care Sciences and Society, Karolinska Institutet, Stockholm, Sweden
2 Division of Physiotherapy, Department of Neurobiology, Care Sciences and Society, Karolinska Institutet, Stockholm, Sweden
3 Women's Health and Allied Health Professionals Theme, Medical Unit Occupational Therapy & Physiotherapy, Karolinska University Hospital, Stockholm, Sweden
4 Department of Health Promoting Science, Sophiahemmet University, Stockholm, Sweden

Earlier detection and improved treatment have led to a growing population living with and beyond cancer. Following a cancer diagnosis, survivors have an increased risk of CVD, cancer recurrence, and mortality. To reduce the risk of these adverse events, the World Cancer Research Fund (WCRF) encourages cancer survivors to be physically active, maintain a healthy diet, and reduce alcohol consumption. Secondary prevention aimed at modifiable lifestyle factors is important for cancer survivors. To tailor these intervention strategies, it is important to understand how adherence in cancer survivors is distributed.

The primary aim of this study was to describe the distribution of lifestyle factors—including physical activity, diet, smoking, alcohol consumption, and sleep quality—among Swedish cancer survivors, stratified by sex and age. The secondary aim was to examine the distribution of combinations of these lifestyle factors.

A descriptive cross-sectional study was performed using data from the Swedish CArdioPulmonary BioImage study (SCAPIS). The cohort consists of a sample of 30 000 individuals between the ages of 50 and 64. Data on lifestyle factors were collected through questionnaires, and accelerometers were used to collect information on physical activity. Data were linked to the Swedish in- and out-patient registry to identify cancer survivors, and descriptive statistics were used to describe lifestyle factors stratified by different cancer diagnoses. Adherence to lifestyle factors was dichotomized into adhering vs not adhering based on national recommendations.

In total, 2576 individuals were identified as cancer survivors in the SCAPIS-cohort. The median age was 59 years, the majority were women (57%), and the median time since diagnosis was 13 years. The most common cancer type was malignant melanoma, accounting for 50% of the cases. Most cancer survivors in the sample adhered to at least one lifestyle recommendation, whereas 17% adhered to all five. Diet was the least adhered to lifestyle, followed by alcohol consumption.

In this study of cancer survivors, we found that few adhered to guidelines for diet and alcohol consumption. These findings suggest that cancer survivors might benefit from secondary prevention strategies targeting lifestyle factors in general and diet and alcohol consumption in particular.

Keywords: Prevention, Cancer survivors,Health behaviour

Poster 42

Uncovering the hidden rules tuning peptide immunogenicity

Tom Resink 1, Renhua Sun 1, Xiao Han 1, Evren Alici 2, Hans-Gustaf Ljunggren 3, Adnane Achour 1

1 Structural and Biophysical Immunobiology, SciLifeLab & Department of Medicine Solna, Karolinska Institute
2 Center for Hematology and Regenerative Medicine, Department of Medicine Huddinge, Karolinska Institute & Hematology Center, Karolinska University Hospital
3 Center for Infectious Medicine, Department of Medicine Huddinge, Karolinska Institute

The mechanisms of T cell receptor (TCR)-dependent recognition of cognate peptide-major histocompatibility complexes (pMHCs) are central to understanding T lymphocyte biology. In addition to being one of the three required signals for the productive activation of naïve T cells, the TCR-pMHC interaction alone is sufficient to direct effector CD8+ T cell-mediated cytotoxicity. Despite their importance, these interactions are often reduced to a simplified comparison of affinities, with current predictive models of TCR-pMHC affinity or immunogenicity, or overall immunogenicity, relying on sequence, single static structures, and other macroscopic biophysical information. Such approaches struggle to generalize beyond sequence and structural similarity and frequently fail to capture the impact of single-point mutations at the TCR-pMHC interface. By neglecting further microscopic information, such as local residue flexibility, the mechanisms of TCR-pMHC binding and recognition reliant on conformational dynamics can be overlooked. Fully leveraging all available structural and dynamic parameters is therefore important for the effective identification of immunogenic peptides or TCR-pMHC pairings from high-throughput mass spectrometry or sequencing experiments. We demonstrate that a network-based description of pMHC interfacial dynamics can yield mechanistic insights that were previously inaccessible through conventional sequence- or structure-based methods. Specifically, we identify paths of long-range dynamic perturbation following the introduction of a mutation in the peptide. We further exemplify how these methods can be employed in partially characterized systems to generate actionable hypotheses. Overall, these numerical representations of protein dynamics could be readily integrated into existing predictive models. Thus, our work represents a promising step towards an integrative understanding and prediction of peptide immunogenicity.

Keywords: Immunogenicity, Major Histocompatibility Complex (MHC), T cell receptor (TCR)

Poster 43

Selective PERK inhibition induces ER stress-mediated apoptosis in non-small cell lung cancer cells

Wioletta Rozpędek-Kamińska 1, Ireneusz Majsterek 1

1 Department of Clinical Chemistry and Biochemistry, Medical University of Lodz, 90-419 Lodz, Poland

Chronic activation of endoplasmic reticulum (ER) stress conditions and the PERK-dependent unfolded protein response (UPR) signaling pathway contribute to tumor progression and therapy resistance in non-small cell lung cancer (NSCLC). The PERK-eIF2α-ATF4 pathway is a central regulator of adaptive stress responses that promote cancer cell survival and therefore represents a potential therapeutic target. This study evaluated the biological effects of the selective PERK inhibitor NCI 159456 in an in vitro model of NSCLC.
Both A549 NSCLC cells and normal human pulmonary fibroblasts (HPF) were treated with the investigated PERK inhibitor under basal and thapsigargin-induced ER stress conditions. Gene expression of ATF4, DDIT3, BAX, and Bcl-2 was assessed by RT-qPCR method. Cytotoxicity was evaluated using the XTT assay, DNA damage by alkaline comet assay, apoptosis by caspase-3 activity assay, and oxidative stress by intracellular reactive oxygen species (ROS) measurement.
Treatment with 50 µM tested compound significantly upregulated ATF4, DDIT3, and BAX and downregulated Bcl-2 in A549 cells under both normal and ER stress conditions. PERK inhibition reduced cancer cell viability in a time- and concentration-dependent manner, increased DNA damage, and significantly elevated caspase-3 activity, confirming induction of apoptosis. Additionally, the inhibitor markedly increased intracellular ROS levels, indicating disruption of redox homeostasis. These effects were further enhanced under ER stress conditions. In contrast, no significant cytotoxic, genotoxic, apoptotic, or oxidative alterations were observed in HPF cells within the entire concentration range examined.
Taken together, these results demonstrate that PERK inhibition disrupts adaptive UPR signaling and promotes apoptotic cell death selectively in NSCLC cells, while sparing normal pulmonary fibroblasts. These findings support PERK as a promising therapeutic target and suggest that modulation of ER stress signaling may represent an effective strategy in lung cancer treatment.
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Keywords: PERK inhibition, Endoplasmic reticulum stress, non-small cell lung cancer

Poster 44

Menopausal hormone therapy and risk of liver cancer in a Swedish population-based cohort study

Yongying Huang 1, Giola Santoni 1, Jessica L. Petrick 2, Victoria Wocalewski 1, Ernesto Sparrelid 1, Shao-Hua Xie 1

1 Karolinska Institutet
2 Boston University

Background: Previous studies have suggested a potential role of sex hormones in the development of liver cancer. This study aimed to examine whether menopausal hormone therapy (MHT) is associated with a decreased risk of liver cancer by histological type.
Method: This Swedish population-based cohort study included 217,878 women who received MHT in 2006-2023 and an age-matched comparison group of 1,089,390 women who did not receive MHT. Cox regression assessed the associations between use of MHT and the risk of two main subtypes of liver cancer, i.e., hepatocellular carcinoma and intrahepatic cholangiocarcinoma, with adjustment for smoking- and alcohol-related diagnoses, non-alcoholic fatty liver disease, diabetes or obesity, hysterectomy, use of non-steroidal anti-inflammatory drugs or aspirin, and use of statins.
Results: MHT users had a decreased risk of hepatocellular carcinoma (hazard ratio [HR] 0.45, 95% confidence interval [CI] 0.29 to 0.70). Decreased HRs of hepatocellular carcinoma were indicated both in users of estrogen only (HR 0.42, 95% CI 0.21 to 0.86) and estrogen combined with progestogen (HR 0.49, 95% CI 0.28 to 0.85). The risk reduction in hepatocellular carcinoma was apparently more pronounced in users aged 60 years or older (HR 0.37, 95% CI 0.19 to 0.75). Use of MHT was not associated with the risk of intrahepatic cholangiocarcinoma (HR 0.99, 95% CI 0.72 to 1.36).
Conclusions: MHT in women may decrease the risk of hepatocellular carcinoma, but not intrahepatic cholangiocarcinoma.

Keywords: Menopausal hormone therapy, Hepatocellular carcinoma, Intrahepatic cholangiocarcinoma

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