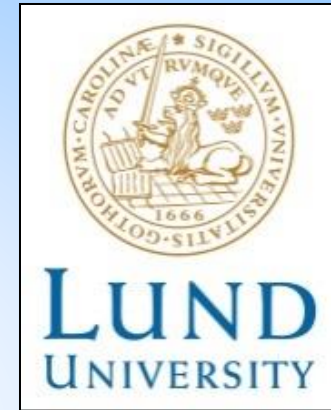


Cancer Moonshot LUND



GYORGY MARKO-VARGA

**Lund University Hospital*

**Division of Clinical Protein Science & Imaging, Dep. BioMedical Engineering, Lund University, Lund, Sweden,*

**First Department of Surgery, Tokyo Medical University, Tokyo, Japan*

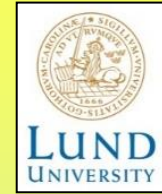
Lecture Content

1. European Cancer Moonshot Lund Center
2. Functional Cancer Impact
3. Clinical Studies
4. Drug Imaging
5. Targeting Tumor Clones

European Cancer Moonshot Lund TEAM



European Cancer Moonshot Lund Center



MAX IV Laboratories



LU-Institute of Technology Structure Labs



EU-Spallation Source “ESS”



“EU Spallation Center-Lund Univ”

Interreg

Öresund-Kattegat-Skagerrak
European Regional Development Fund



EUROPEAN UNION



REGION
SKÅNE



LUND
UNIVERSITY



ESS & MAX IV:
Cross Border
Science and Society

European Spallation Source

The European Spallation Source (ESS) is a European Research Infrastructure Consortium (ERIC), a multi-disciplinary research facility based on the world's most powerful neutron source. Our vision is to build and operate the world's most powerful neutron source, enabling scientific breakthroughs in research related to materials, energy, health and the environment, and addressing some of the most important societal challenges of our time.

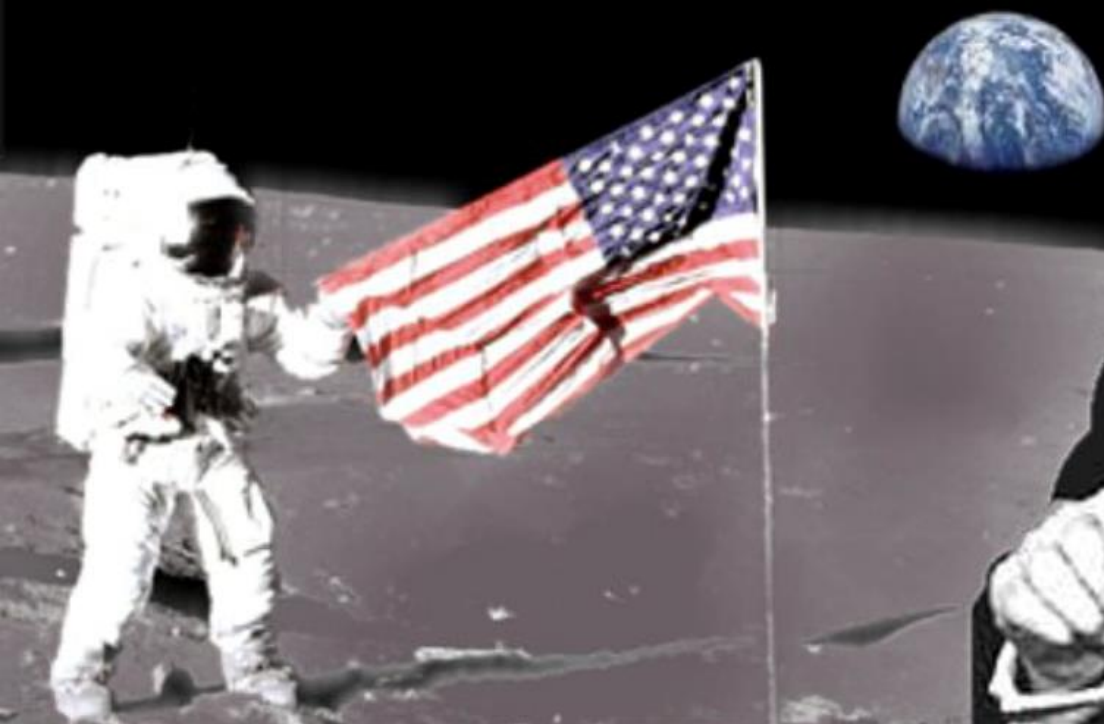


Cancer Moonshot Program Biggest Cancer Initiative EVER..



Phase 2 - 2022-2027

I believe that this Nation should commit itself to achieving the goal, before this decade is out, of landing a man on the moon and returning him safely to earth.

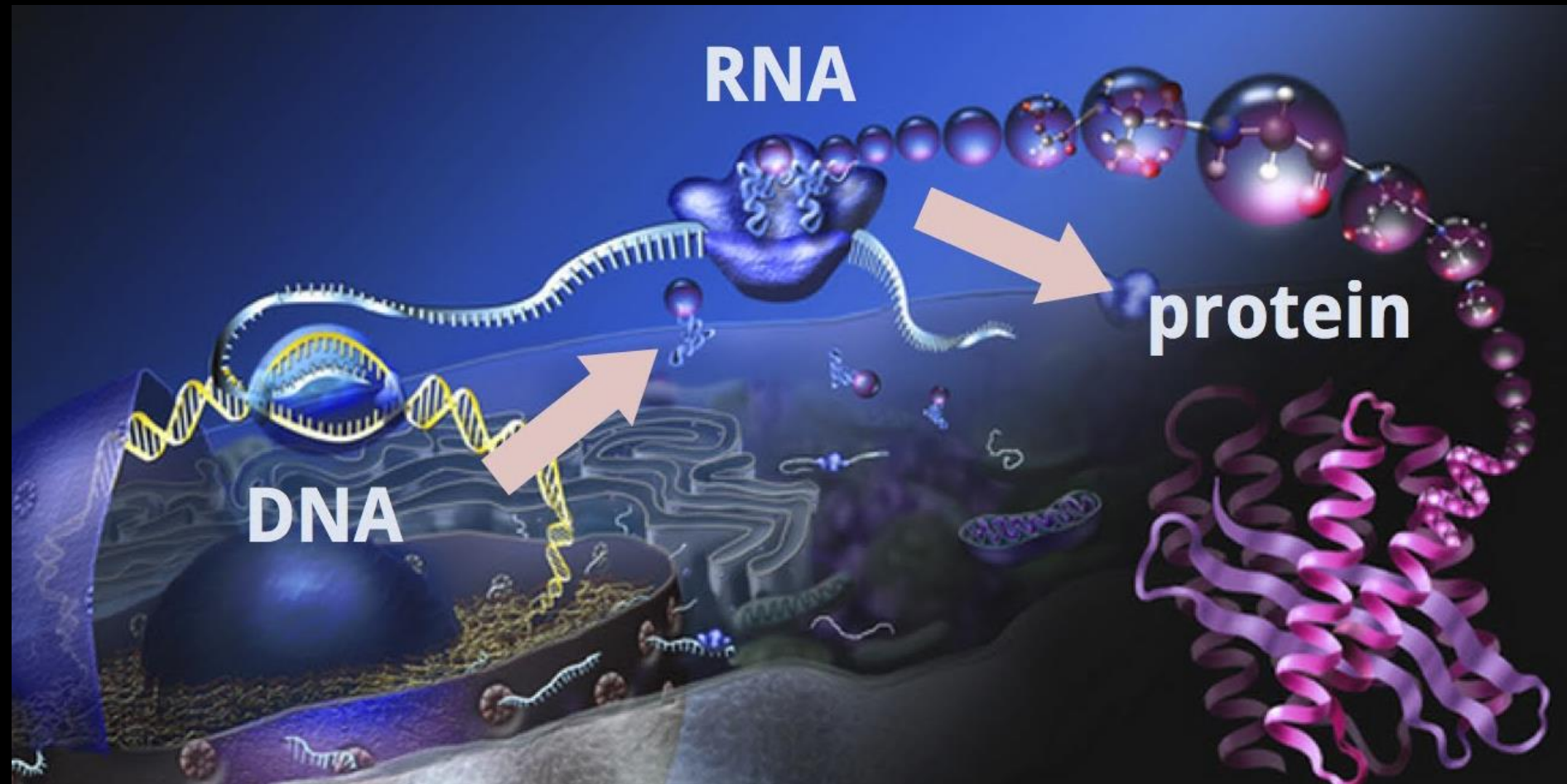




CANCER MOONSHOT

- Catalyse/Unleash Proteogenomic Big Data Breakthroughs
- Detect Cancer Earlier
- Accelerate Trials of New Cancer Therapies/PHARMA
- Better Match Patients to Drugs/PHARMA

Central Dogma of Life





The Human Proteome Blueprint-2020

The Human Genome



In - 2000

nature COMMUNICATIONS

PERSPECTIVE Check for updates

<https://doi.org/10.1038/s41467-020-19045-9> OPEN

A high-stringency blueprint of the human proteome

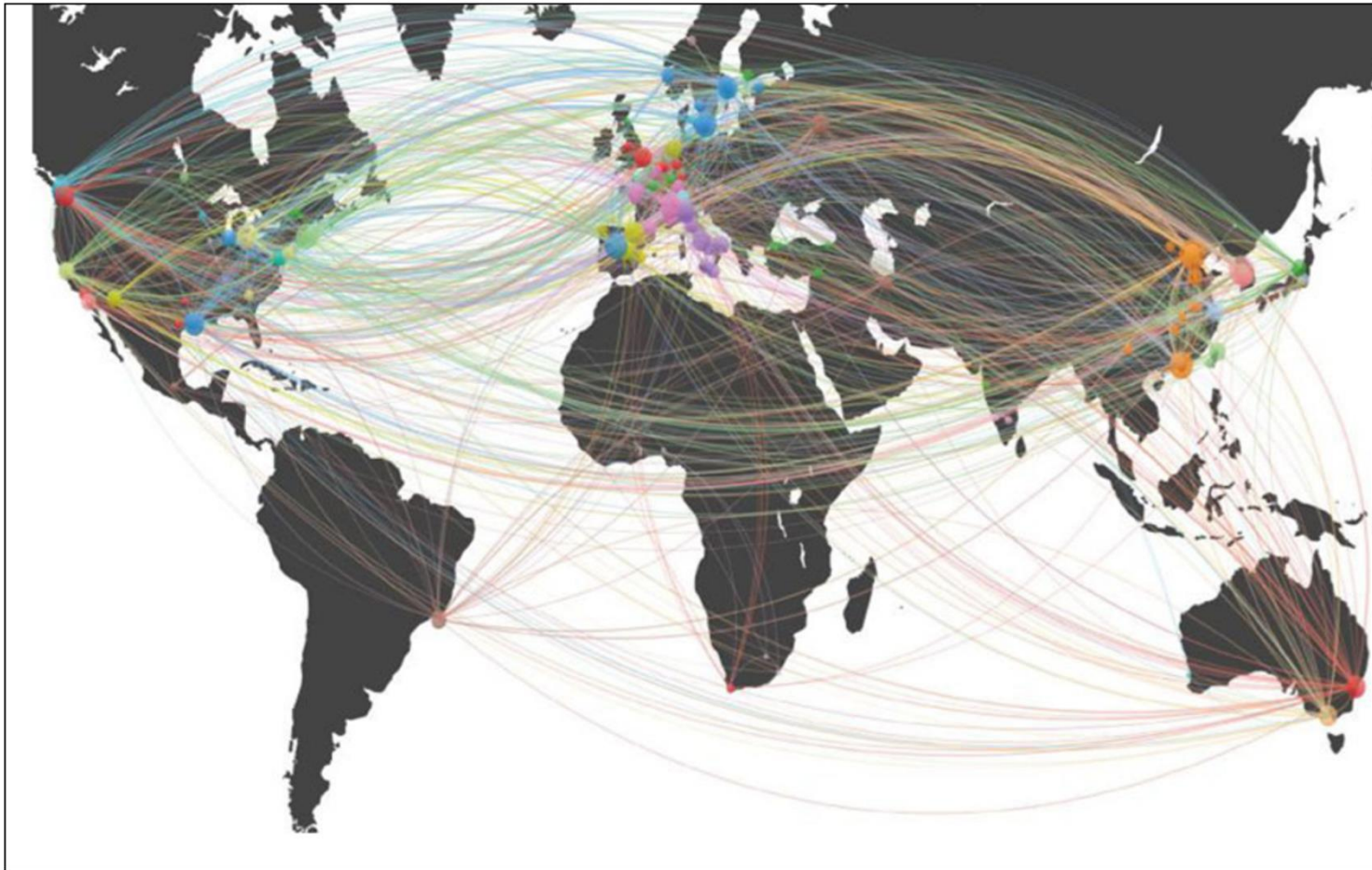
Subash Adhikari et al.[#]

“Nov 2020”

The Human Proteome Organization (HUPO) launched the Human Proteome Project (HPP) in 2010, creating an international framework for global collaboration, data sharing, quality assurance and enhancing accurate annotation of the genome-encoded proteome. During the subsequent decade, the HPP established collaborations, developed guidelines and metrics, and undertook reanalysis of previously deposited community data, continuously increasing the coverage of the human proteome. On the occasion of the HPP's tenth anniversary, we here report a 90.4% complete high-stringency human proteome blueprint. This knowledge is essential for discerning molecular processes in health and disease, as we demonstrate by highlighting potential roles the human proteome plays in our understanding, diagnosis and treatment of cancers, cardiovascular and infectious diseases.

A decade after the release of the draft Human Genome Project (HGP), the Human Proteome Organization (HUPO) leveraged this genomic encyclopedia to launch a visionary international scientific collaboration called the Human Proteome Project (HPP)¹⁻⁴. Utilizing substantial community data, the HPP connects scientists, clinicians, industry, institutions and

Building Human Global Libraries



Adhikari et al, Nature com., 2020,

The European Cancer Moonshot Center Labs



- MultiPlexing Deep Mining
- Quantitation of 14.000 proteins
- 200.000 Peptides



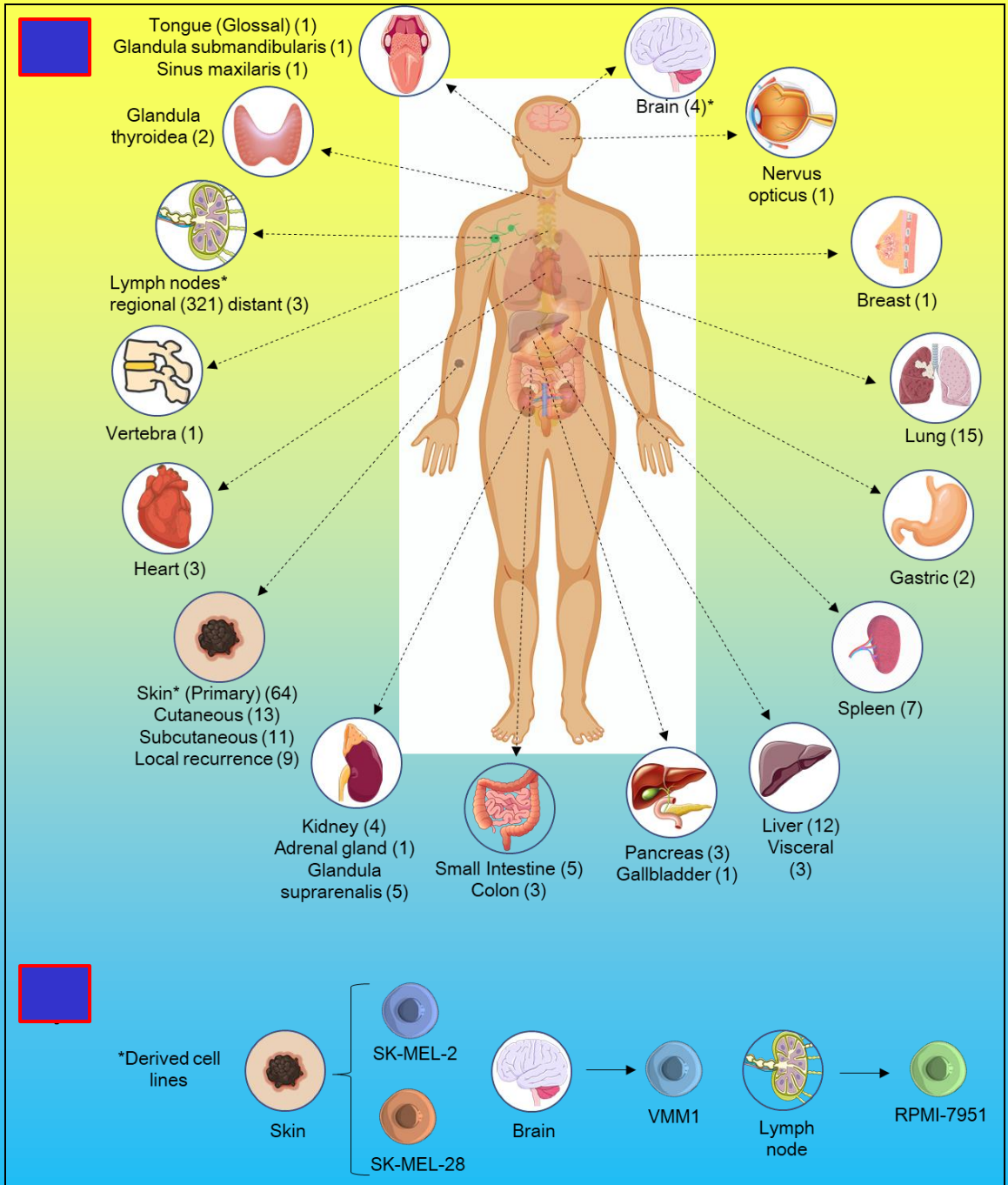
Fully Automated Biobank -80°C
Robotic Processing
Electronic Surveillance
2D-Barcoding
LINKED TO
Sothern SWEDISH HEALTHCARE



BIOBANKING
Capacity: 6 Mill
Currently: 2 Mill Samples

Fully Automated Biobank -80°C
Robotic Processing
Electronic Surveillance
2D-Barcoding
LINKED TO
Sothern SWEDISH HEALTHCARE

Melanoma Proteome Atlas





Human Melanoma Protein Atlas

DOI: 10.1002/ctm2.451

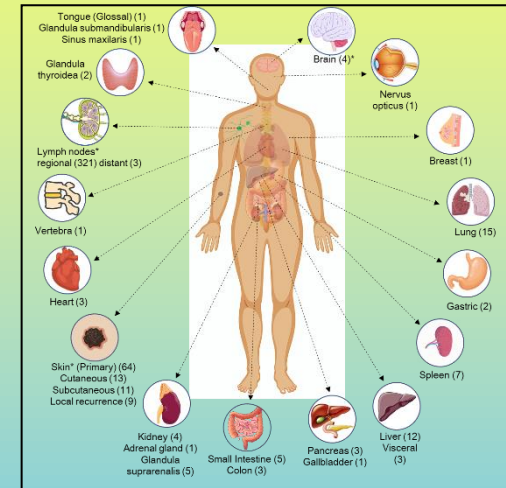
RESEARCH ARTICLE

CLINICAL AND TRANSLATIONAL MEDICINE

WILEY

The Human Melanoma Proteome Atlas—Complementing the melanoma transcriptome

Lazaro Hiram Betancourt¹ | Jeovanis Gil¹ | Aniel Sanchez² | Viktória Doma^{3,4}



Received: 12 March 2021 | Revised: 3 June 2021 | Accepted: 8 June 2021 | Published online: 1 July 2021

DOI: 10.1002/ctm2.473

RESEARCH ARTICLE

CLINICAL AND TRANSLATIONAL MEDICINE

WILEY

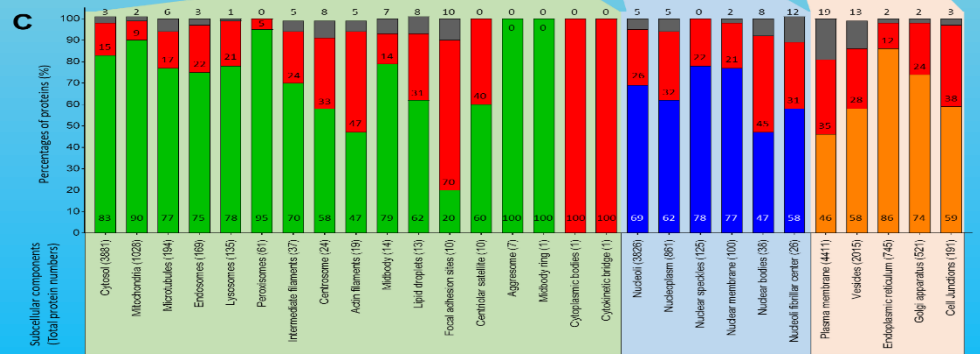
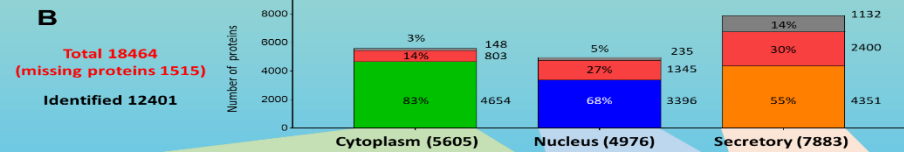
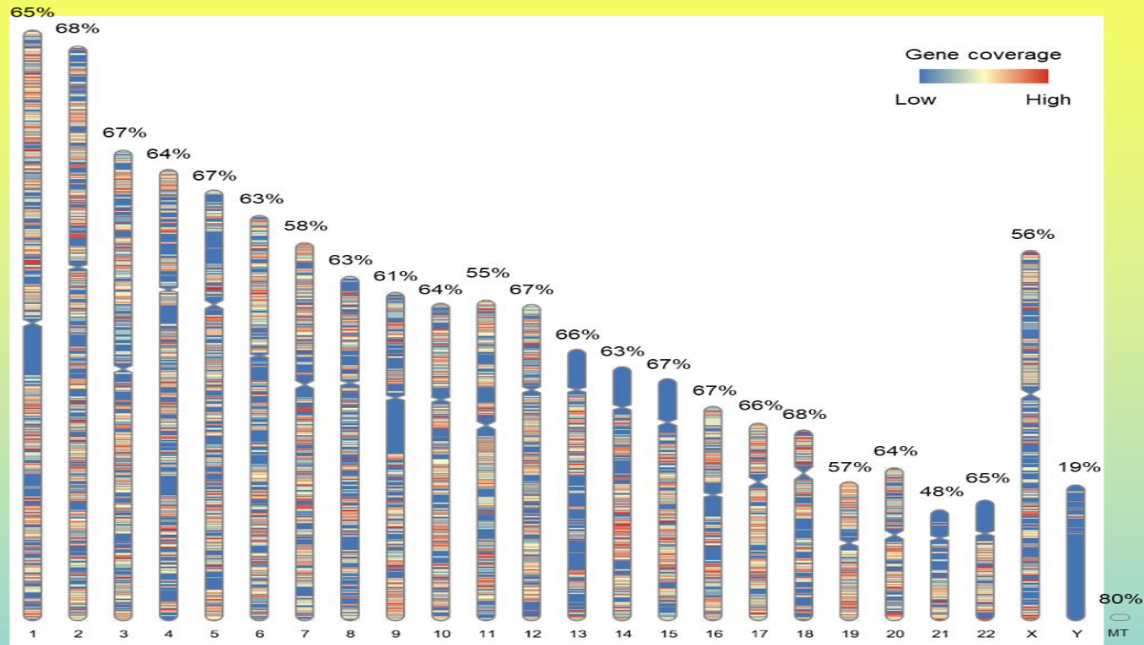
The human melanoma proteome atlas—Defining the molecular pathology

Lazaro Hiram Betancourt¹ | Jeovanis Gil¹ | Yonghyo Kim¹ | Viktória Doma^{2,3}

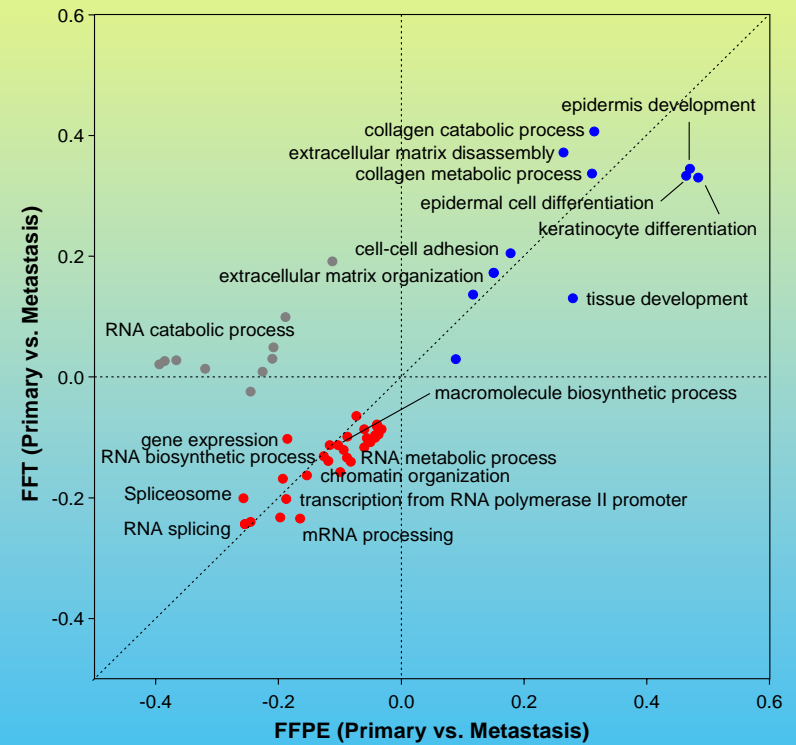
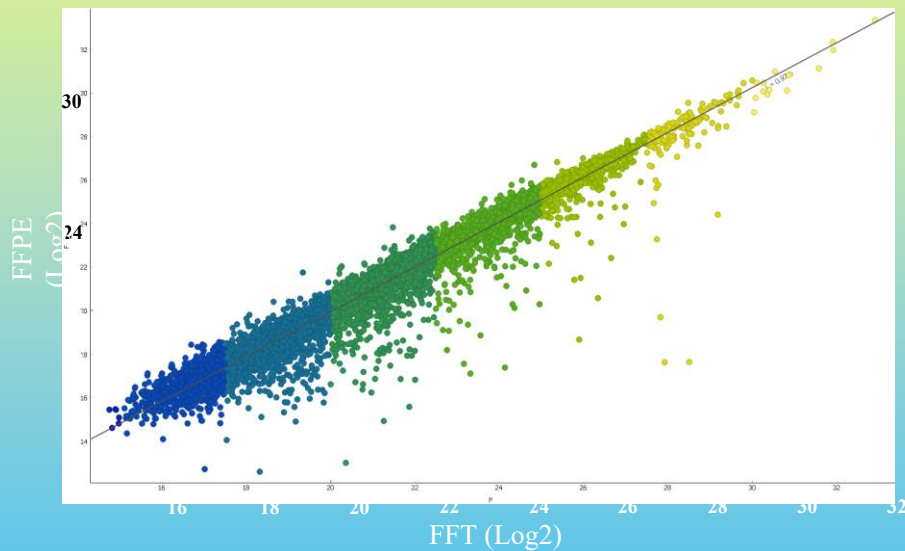
8 Global Medical Centers

Lazaro Hiram Betancourt¹ | Jeovanis Gil¹ | Aniel Sanchez² | Viktória Doma^{3,4}
 Magdalena Kuras² | Jimmy Rodriguez Murillo⁵ | Erika Velasquez⁶ |
 Ugur Cakir⁴ | Yonghyo Kim¹ | Yutaka Sugihara⁷ | Indira Pla Parada² |
 Beata Szeitz⁸ | Roger Appelqvist¹ | Elisabet Wieslander¹ | Charlotte Welinder¹
 Natália Pinto de Almeida^{7,8} | Nicole Woldmar^{7,8} | Matilda Marko-Varga¹ |
 Jonatan Eriksson¹ | Krzysztof Pawlowski^{4,9,10} | Bo Baldetorp¹ |
 Christian Ingvar^{11,12} | Håkan Olsson¹¹ | Lotta Lundgren¹¹ | Henrik Lindberg¹ |
 Henriett Oskolas¹ | Boram Lee¹ | Ethan Berge¹ | Marie Sjögren¹ |
 Carina Eriksson¹ | Dasol Kim¹³ | Ho Jeong Kwon¹³ | Beatrice Knudsen¹⁴ |
 Melinda Rezeli³ | Johan Malm³ | Runyu Hong¹⁵ | Peter Horvath¹⁶ |
 A. Marcell Szász^{17,18} | József Timár³ | Sarolta Kárpáti⁴ | Peter Horvatovich¹⁹ |
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 Madalina Oppermann²³ | Ken Miller²³ | Francesco Florindi²⁴ | Quimin Zhou²⁵ |
 Gilberto B. Domont⁷ | Luciana Pizzatti⁷ | Fábio C. S. Nogueira⁷ |
 Leticia Szadai²⁶ | István Balázs Németh²⁶ | Henrik Ekedahl¹¹ | David Fenýő¹⁵ |
 György Marko-Varga^{8,13,22}

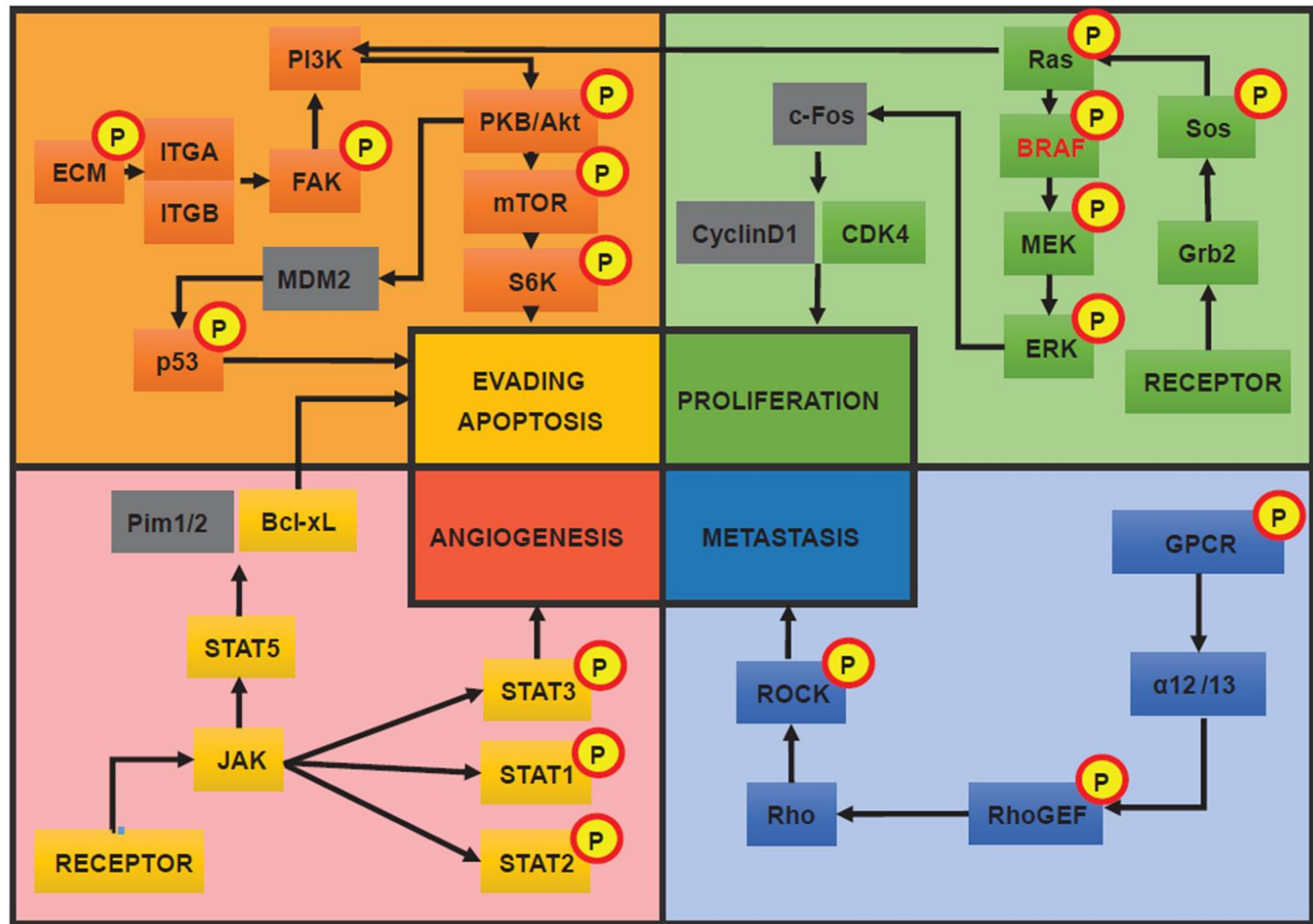
Melanoma Protein Expression & Localisation



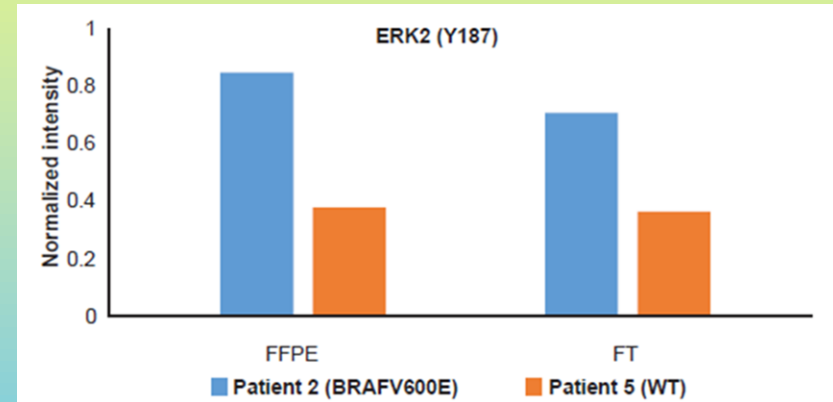
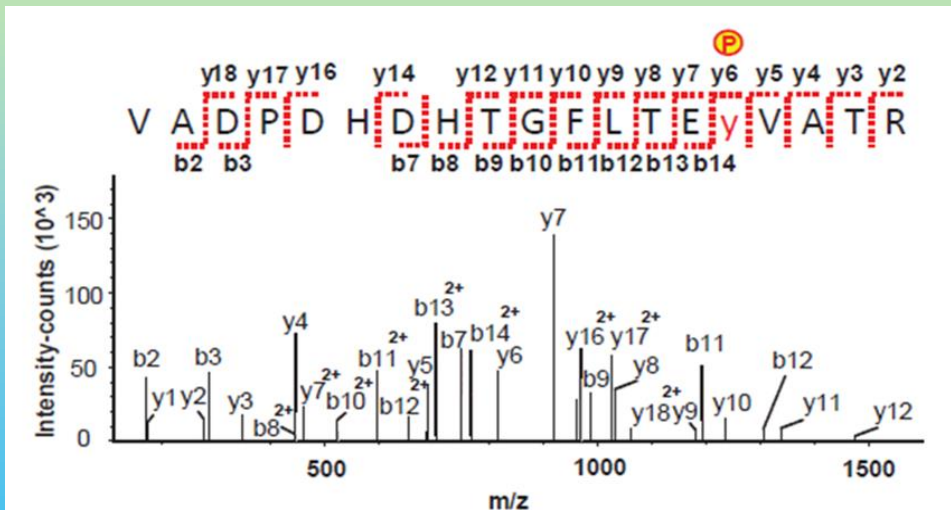
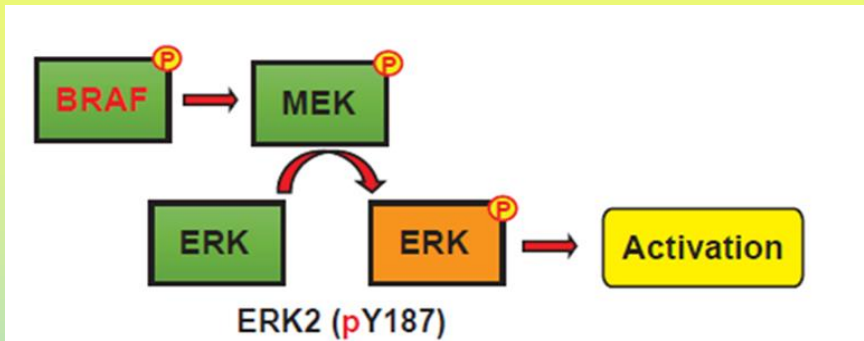
Global proteome analysis of FFPE and FFT



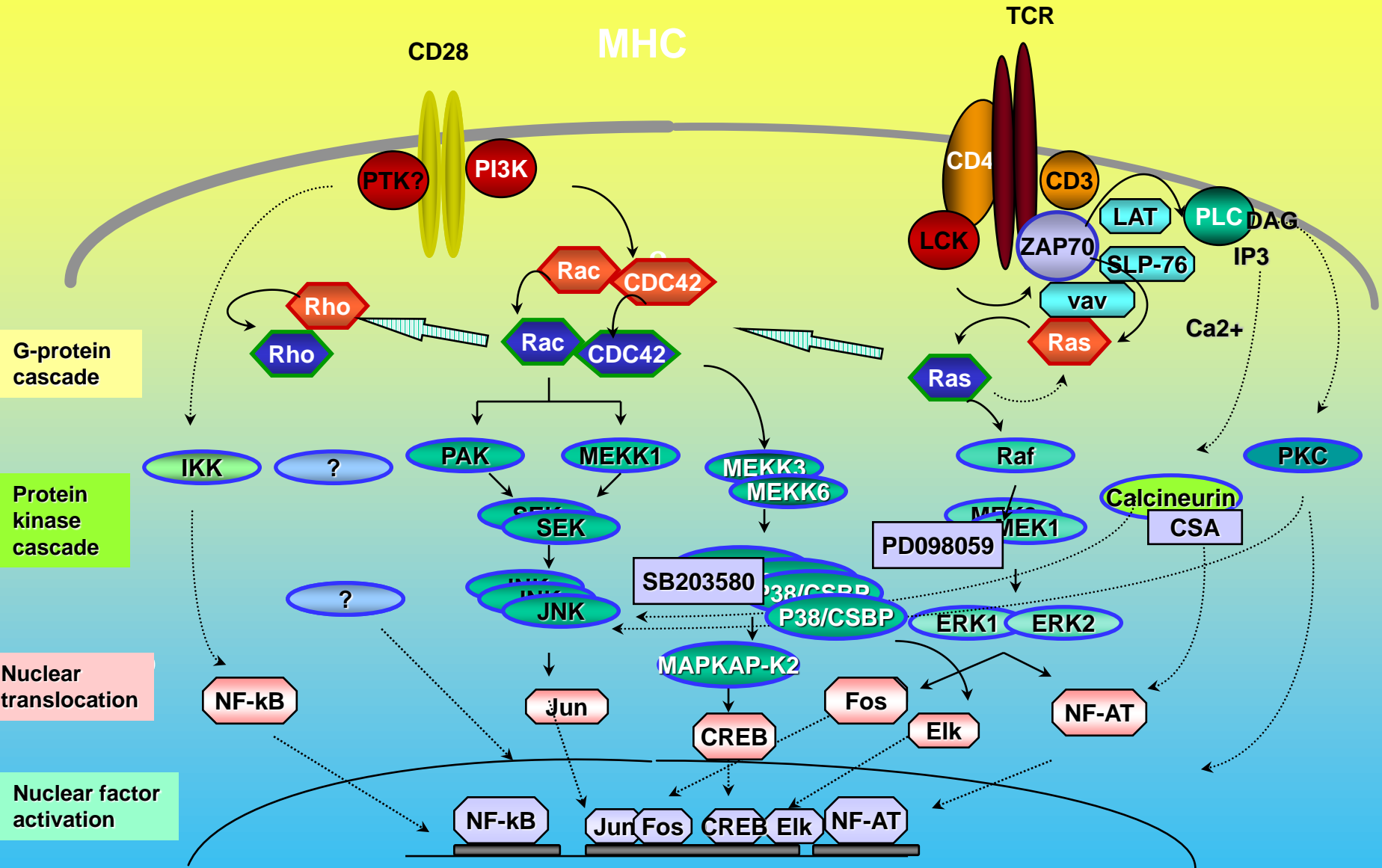
Mapping Cancer-Specific Pathways



Personalized Treatment Monitoring

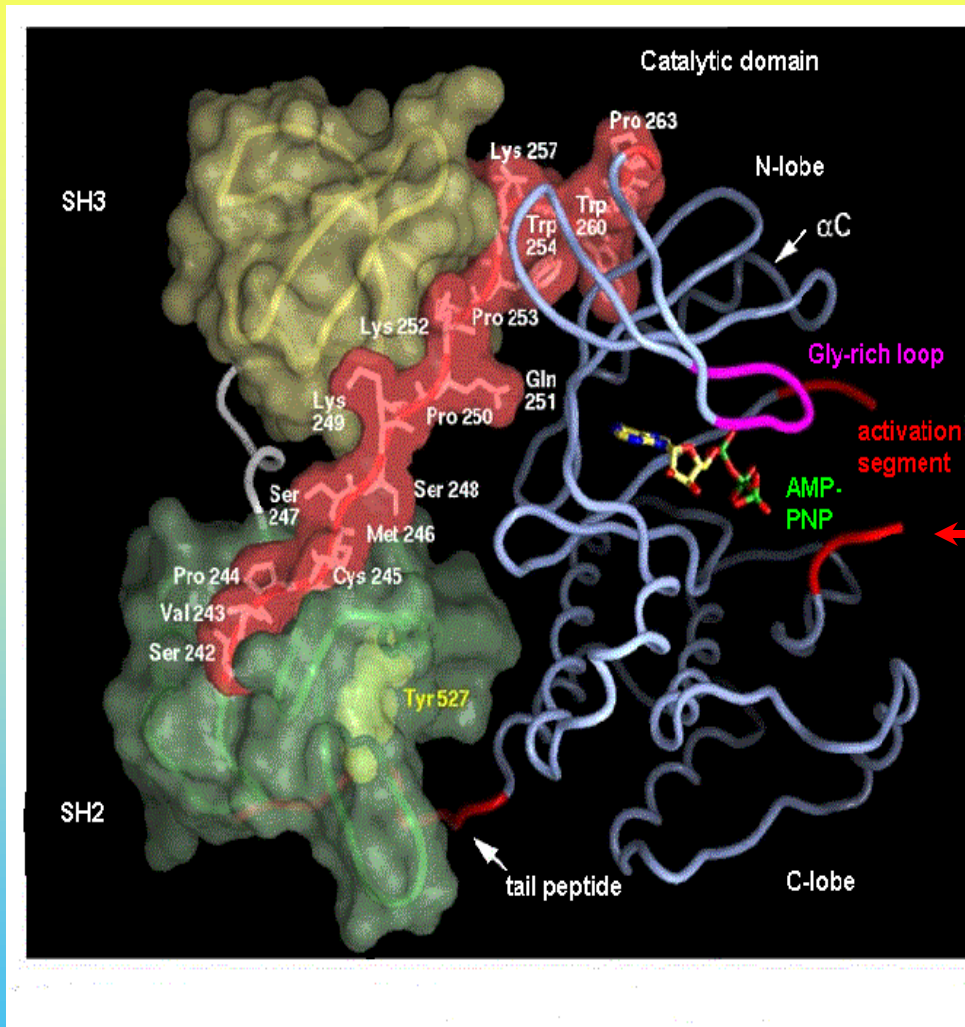


Components of Signaling Pathways Through TCR and CD28



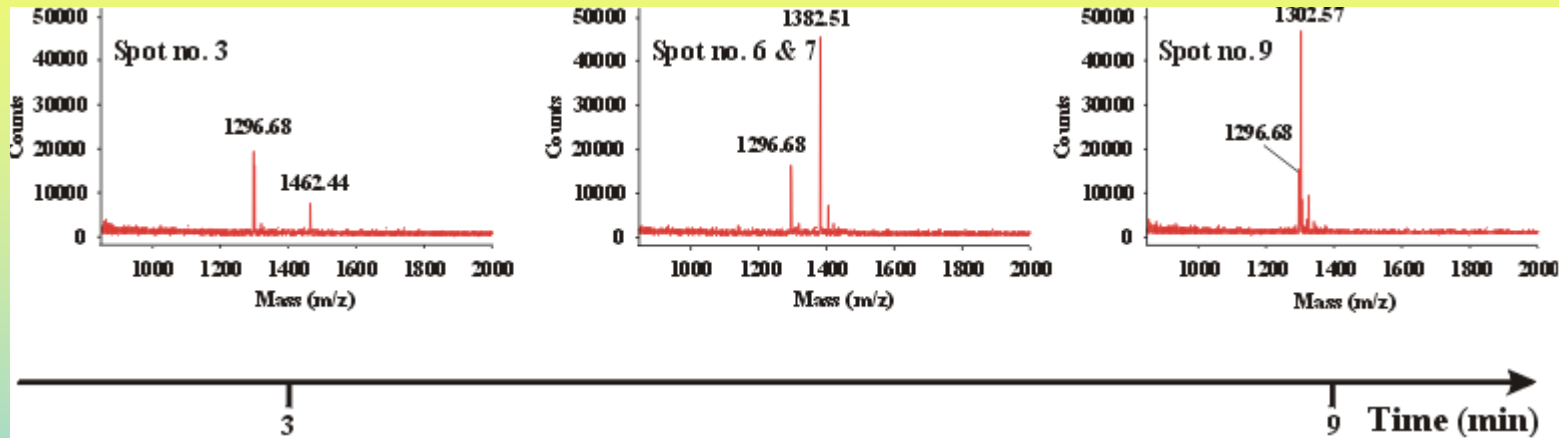
Jacinto et al *Immunity* 8, 31-41, 1998, Kaga et al *J Immunol* 160, 4182-89, 1998, Cantrell *Annu Rev Immunol* 14, 259-74, 1996, Cohen *Trends in Cell Biology* 7, 353-361, 1997

Phosphorylation of Y493 in the activation loop



Autophosphorylation-site Y493

Capillary LC coupled to MALDI-TOF MS



- Detection of; **ALGADDSY^{PP}TAR** its phosphorylation states
- Fractions correspond to 5 fmol - sensitivities down to 50 attomoles achieved

Mass Spectrometry Imaging

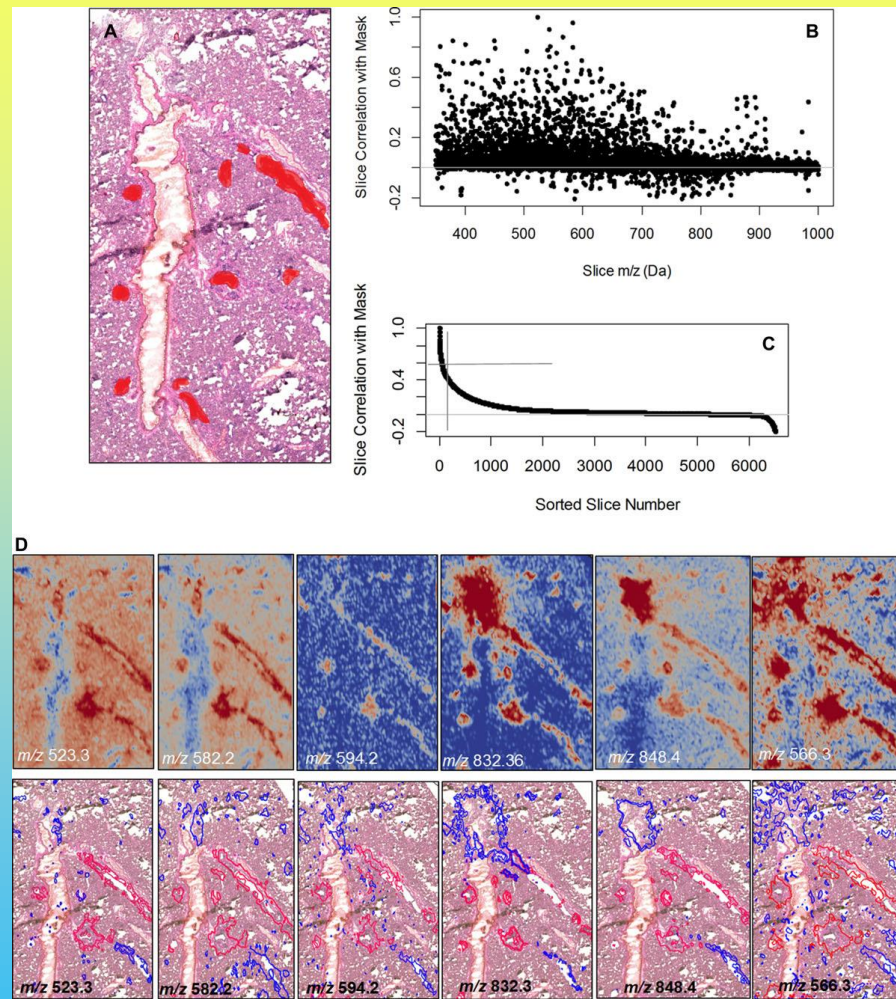
CROSS-OVER HISTOLOGY & MS-IMAGING

ID-of specific metabolites Lung Cancer Function



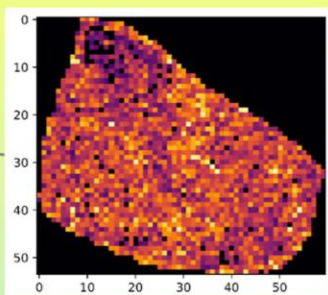
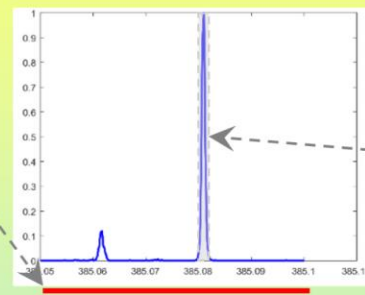
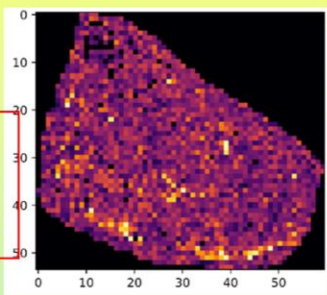
Fehniger, Marko-Varga

- *Mask location (red) on H&E image showing bronchioles
- *Pearson's correlation index of individual m/z values
- *Pearson's correlation sorted according to Pearson's correlation.
- *Upper row: representative m/z distribution associated with the mask
- *Lower row: H&E image with m/z intensity contour of the mask (red) and other locations (blue)



Detection of Vemurafenib in human Melanoma Lung Metastasis

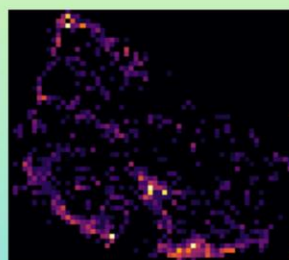
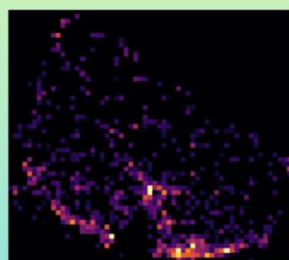
Single Cell spatial resolution



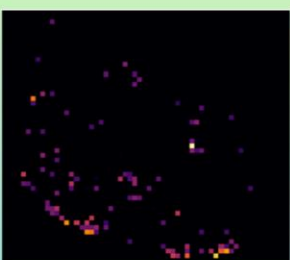
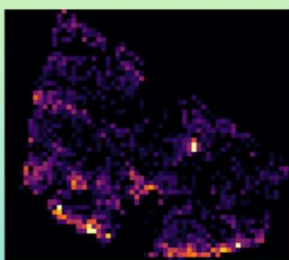
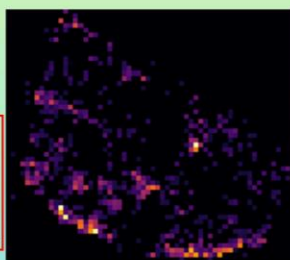
Isotopes and fragments.

KDE peak cluster 385 Da

Binning



binning
0.05 Da width



357.125 Da

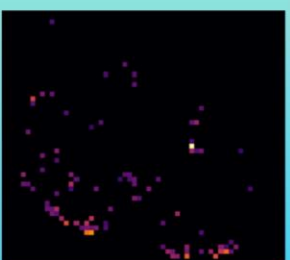
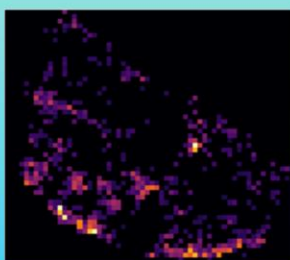
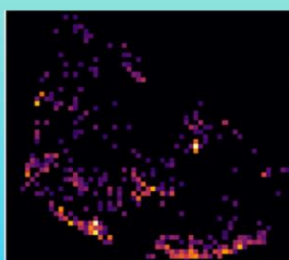
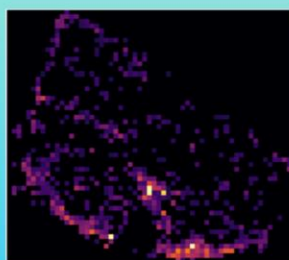
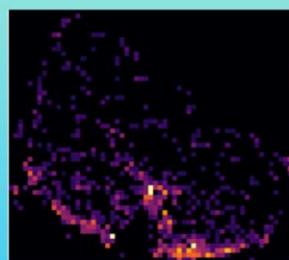
371.175 Da

491.075 Da

492.075 Da

493.075 Da

Cluster wise



357.148 Da

371.164 Da

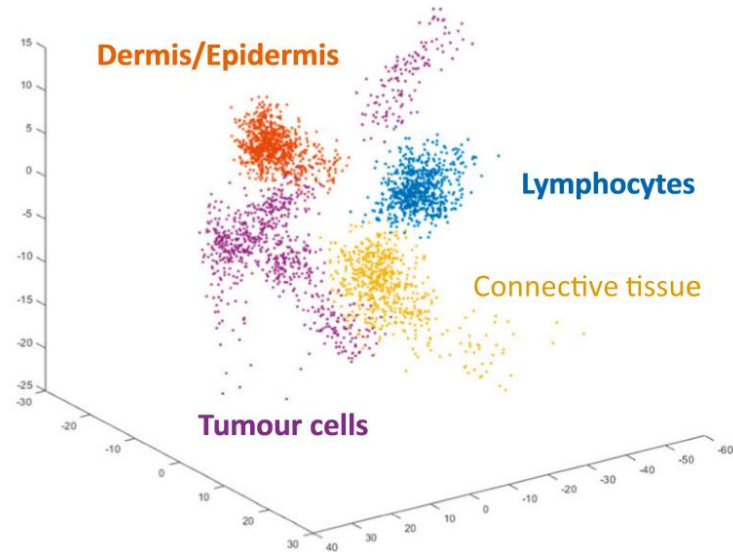
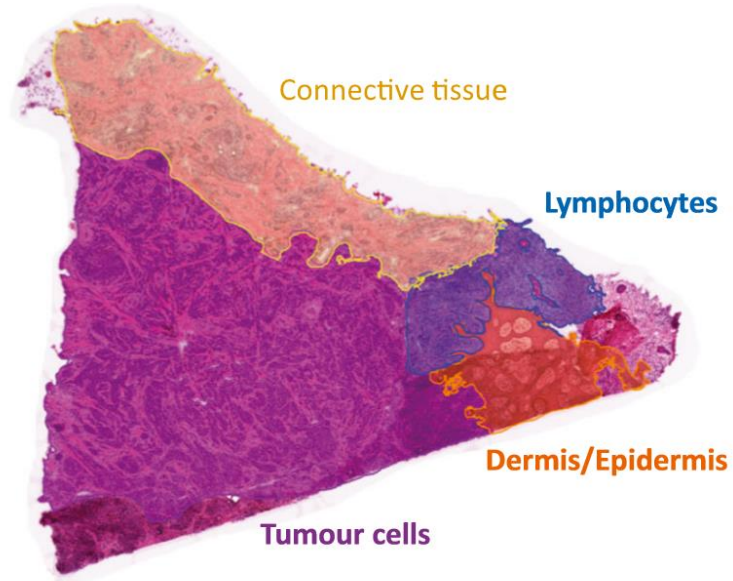
385.062 Da

491.085 Da

492.078 Da

493.082 Da

Mass Spec IMAGING - Surgically Isolated Tumor



H&E-stained Tumor from Cancer Patient

Principal Component analysis - MALDI Spectra - Compartments

BIG3 Study AstraZeneca & Region Skåne -2022

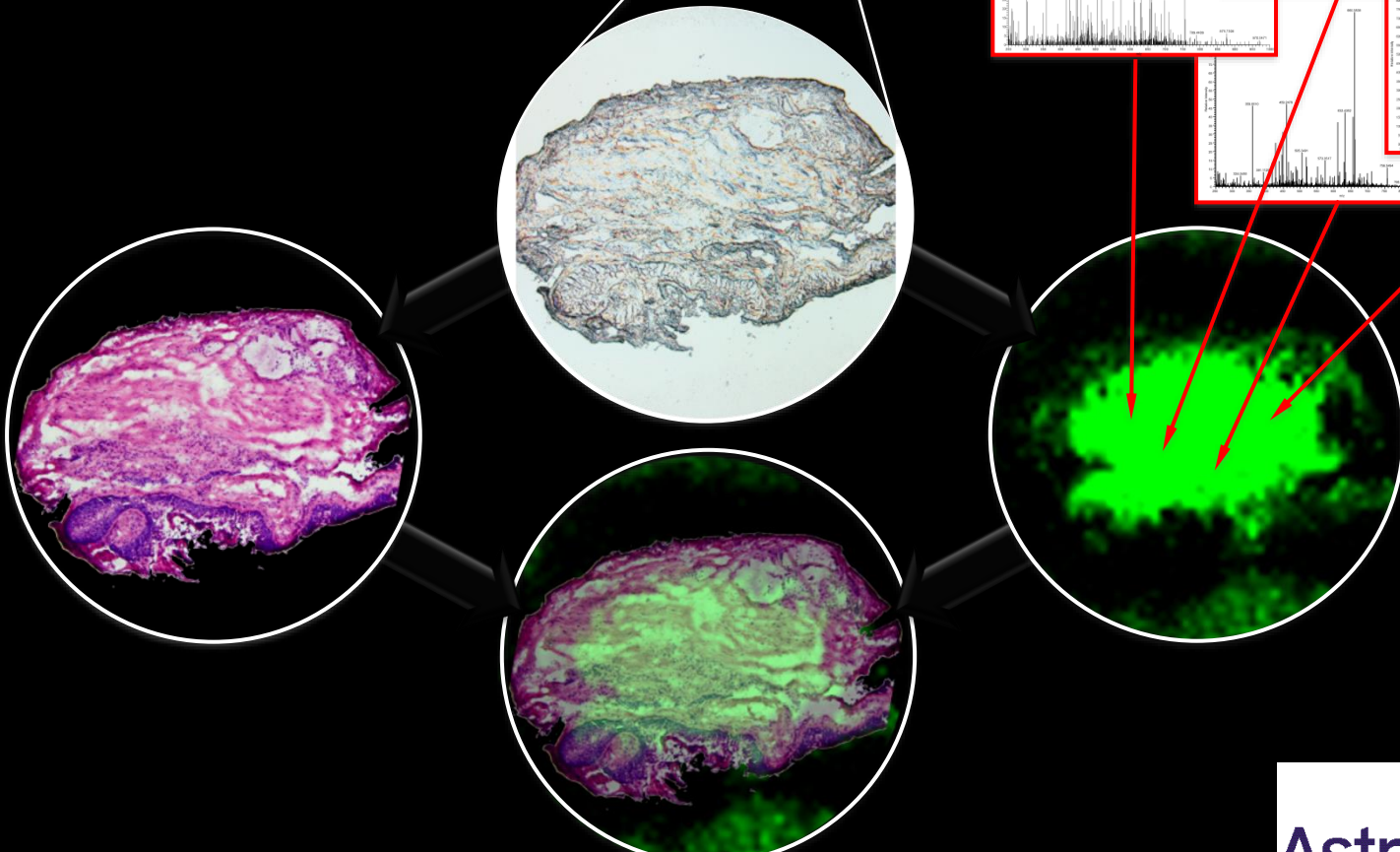
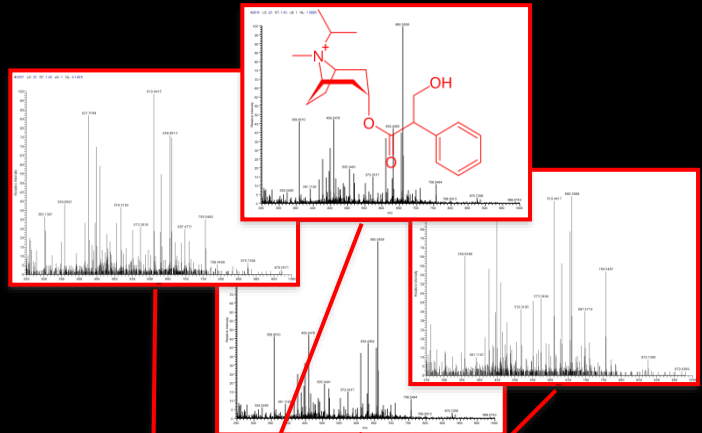
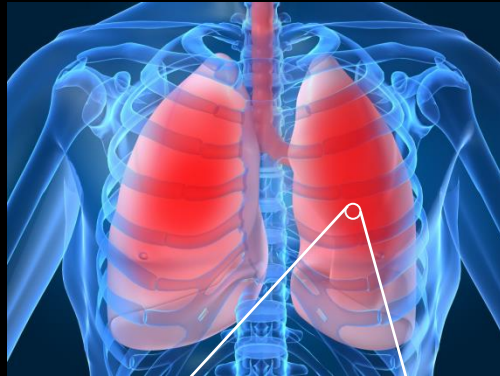
Lung Cancer/COPD/Cardiovascular



BIG3

- * Contacted more than 60.000 Patients**
- * 10.000 passed Questionnaire**
- * 5.000 Patients Heart & Lung test**
- * 2300 passed CT Imaging**
- * 3.7 Million Blood Samples**

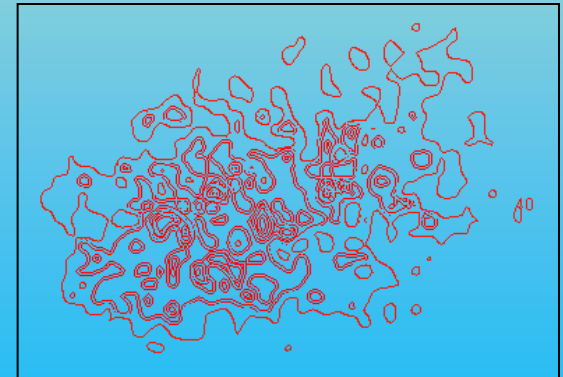
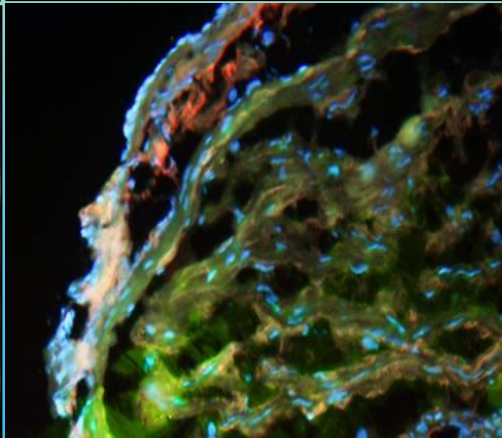
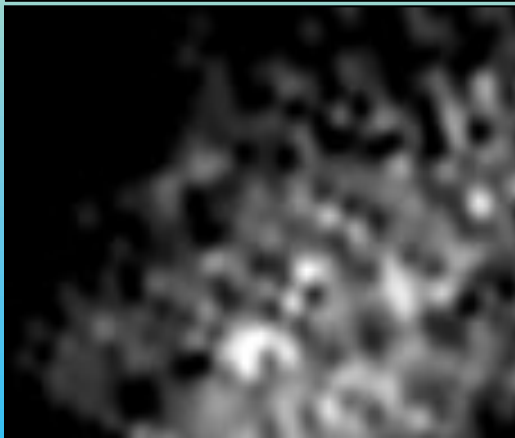
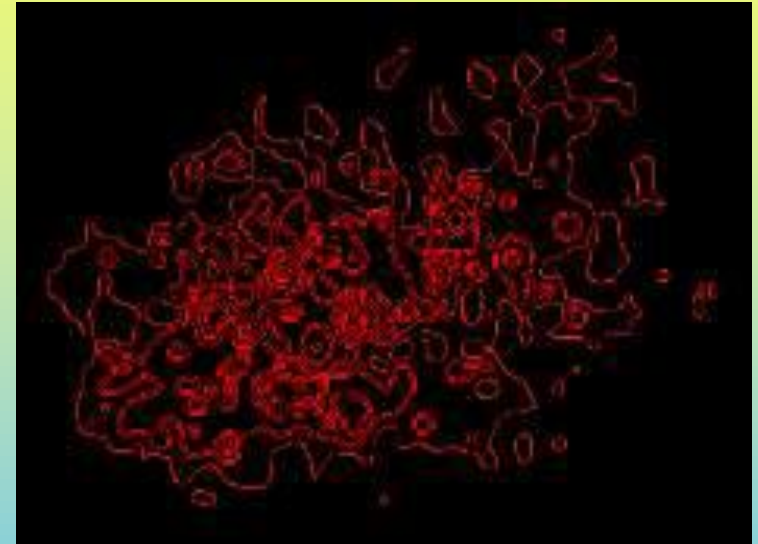
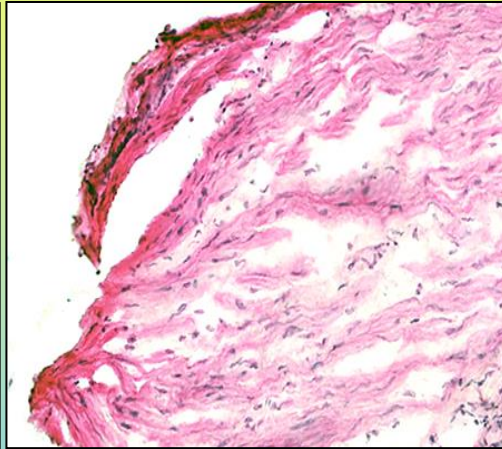
First LUNG CANCER /COPD Drug Imaging Study - Single Cell View



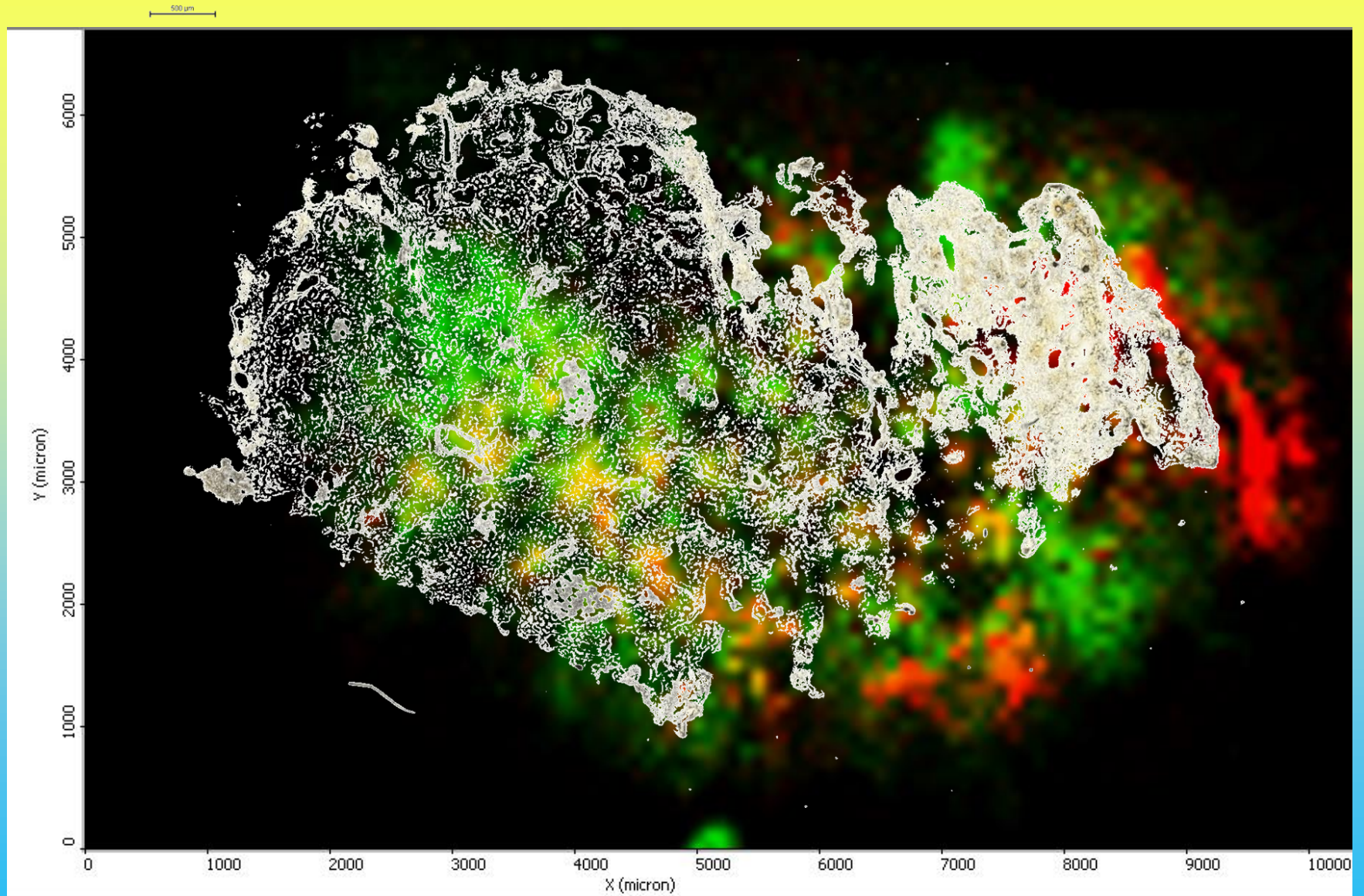
Co-Localization Drug and Protein Target Study



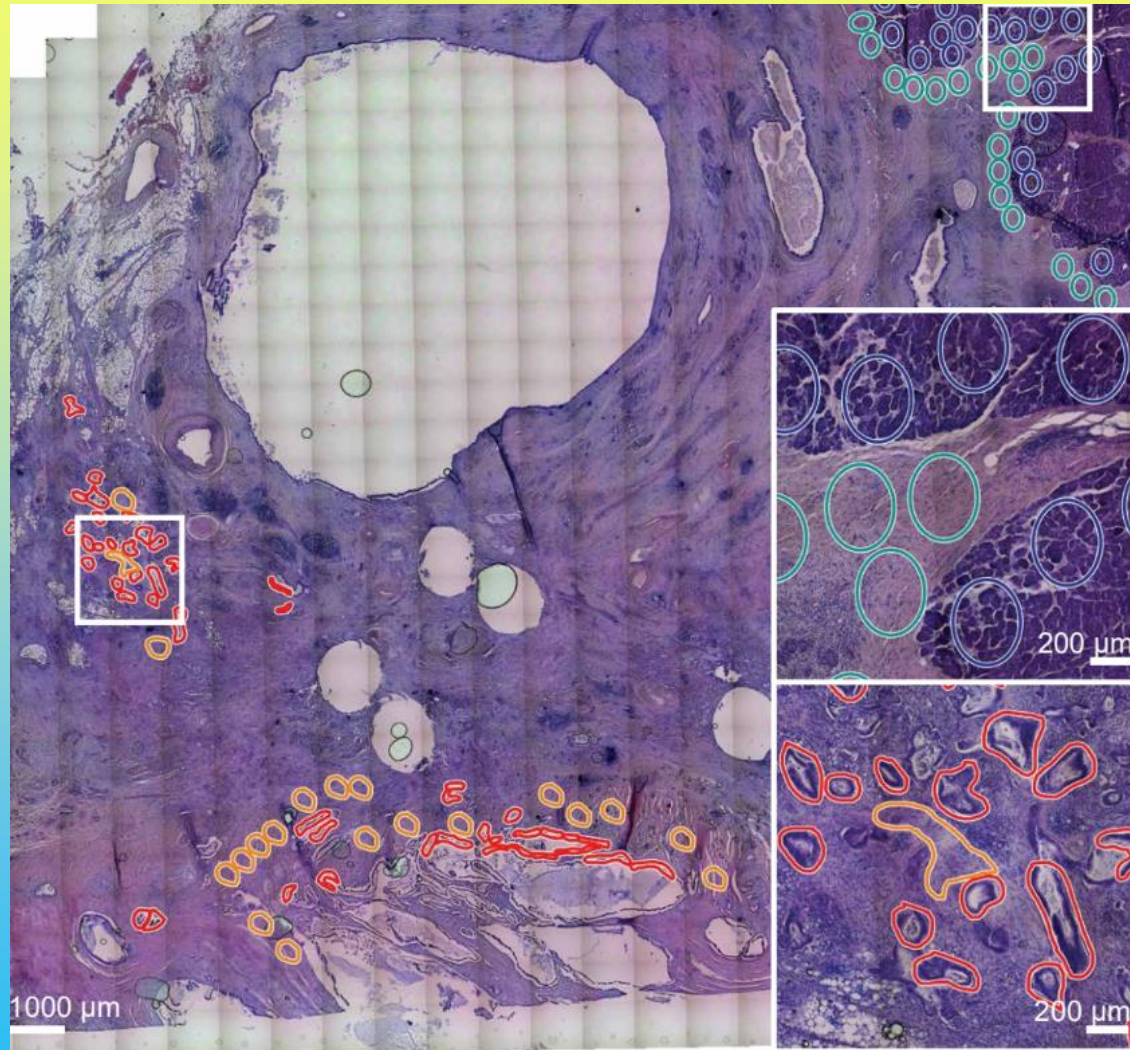
Study



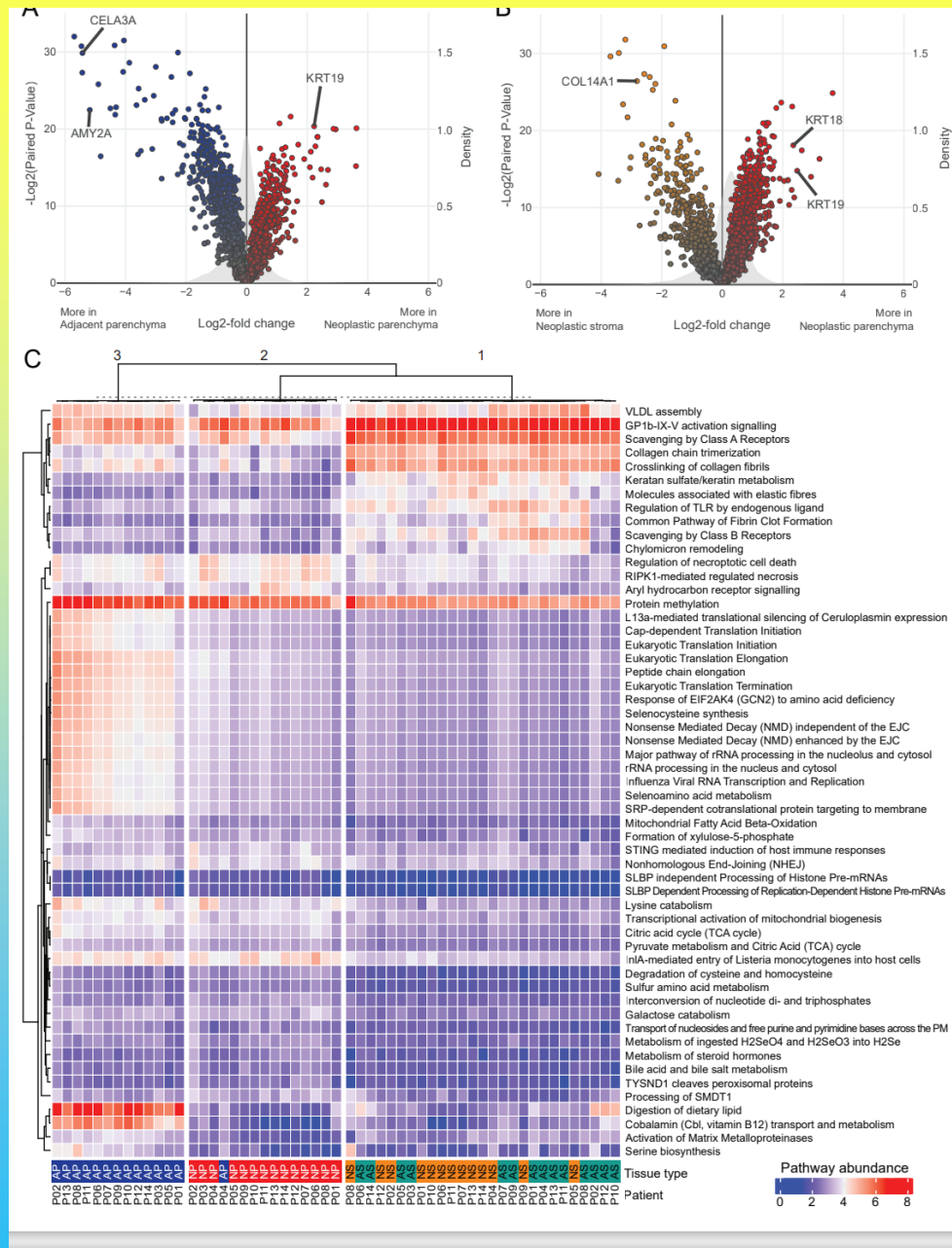
Localization of Gefitinib "IRESSA" & Ipratropium



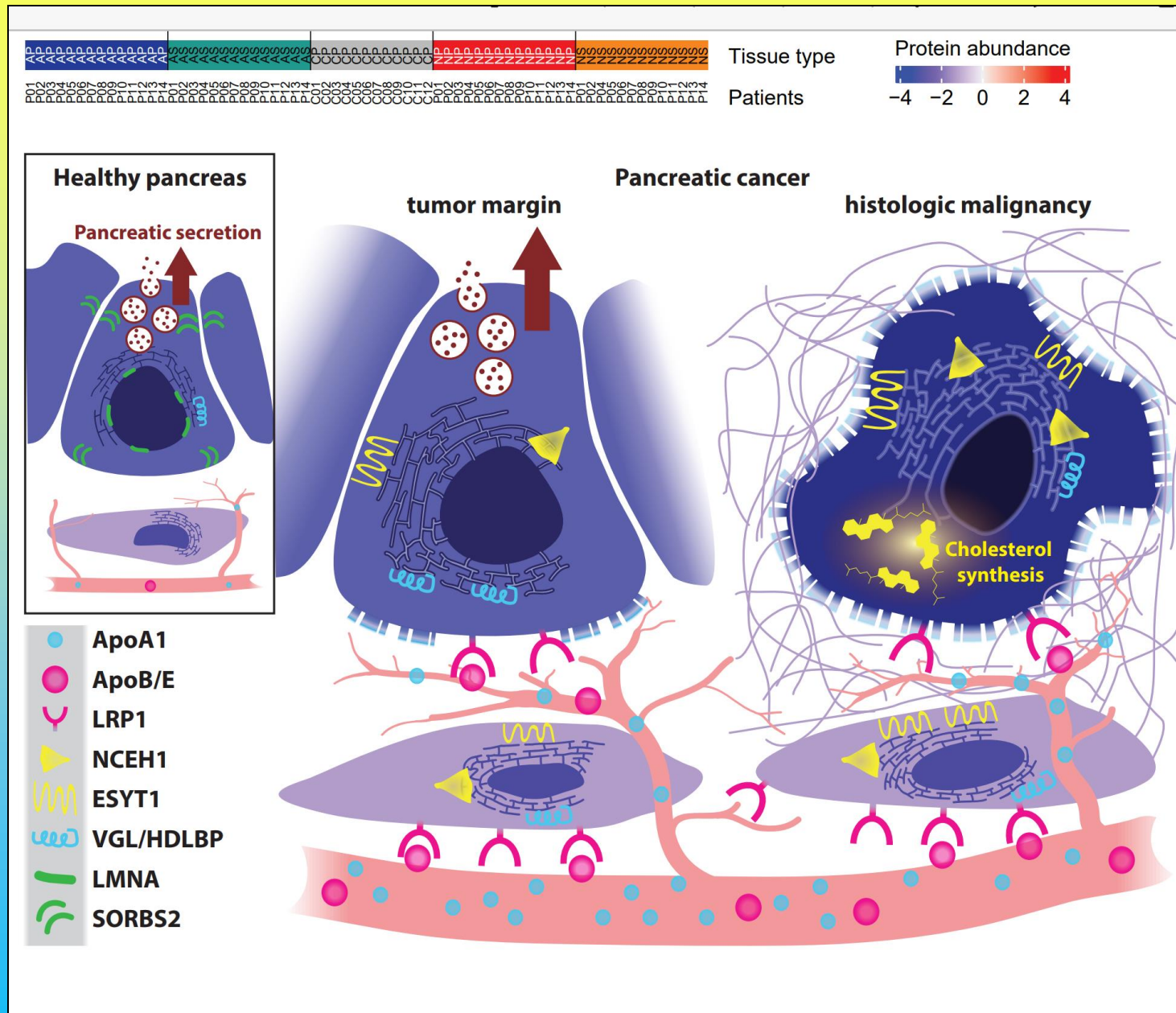
Pancreatic Cancer - Targeting Single Cell isolations



Regions Distant from malignant cells already display Protein Expression Changes Related to lipid transport and metabolism



Pancreatic Metabolic Cross-Talks with its Environment



Discovery within the Study with Impact *NOVELTY*

***Deep Proteomic Analyses from diagnostic specimens of operable, treatment naïve PDAC patients**

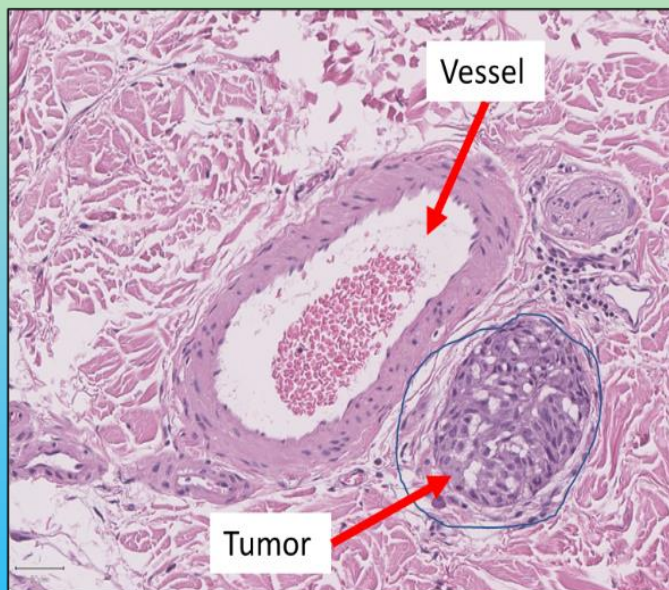
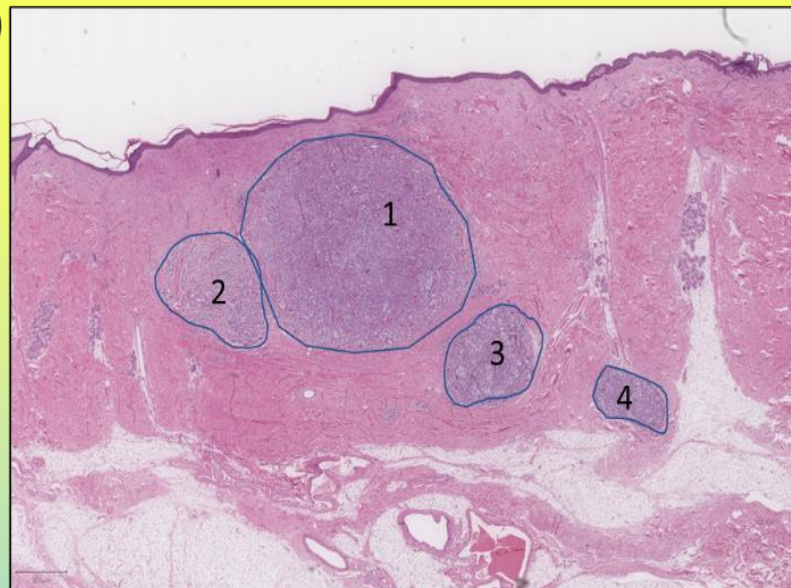
***Widespread Downregulation of Pancreatic Secretory Functions Paralleled by High Cholesterol Biosynthetic activity**

***Lack of Prominent Lipid Storage in the Neoplastic Cells**

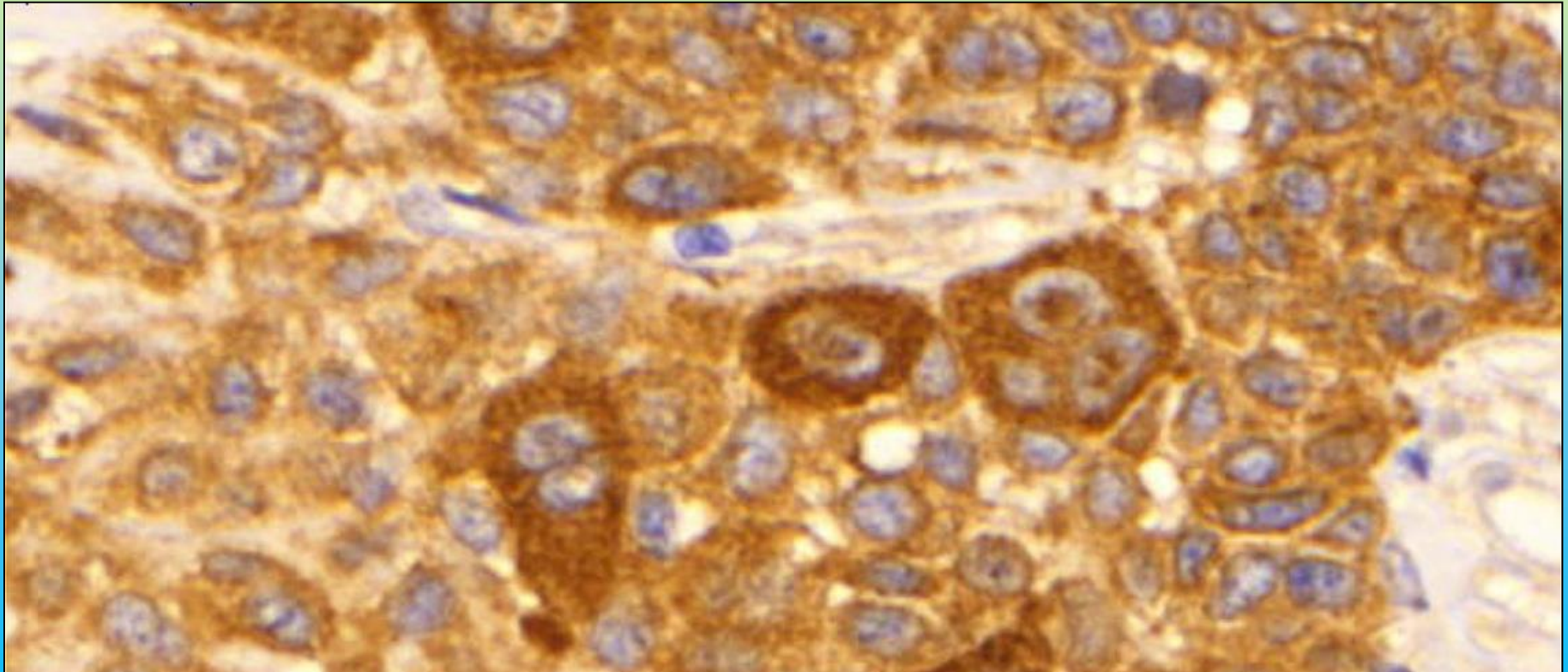
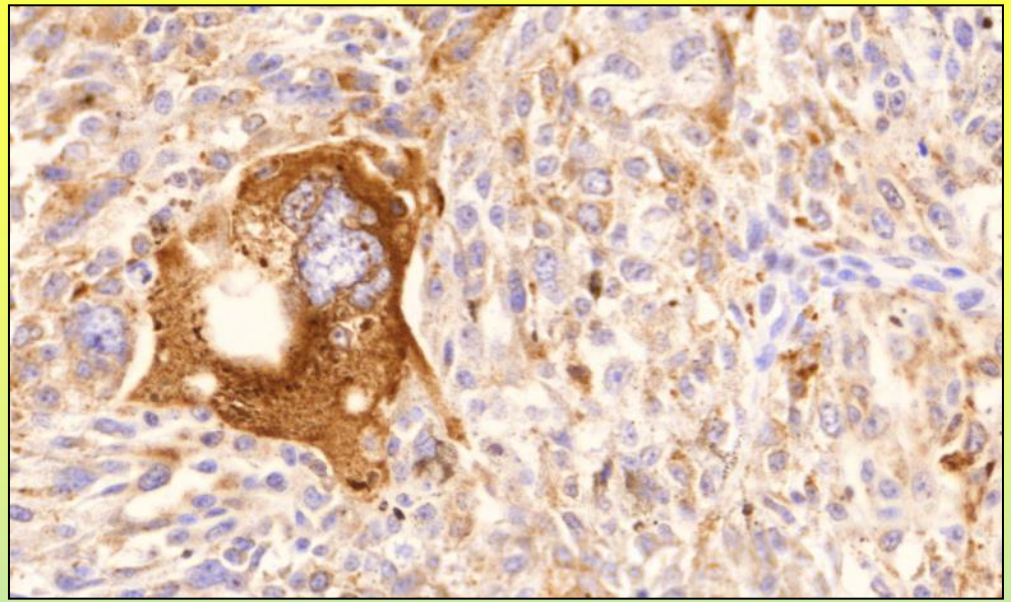
TARGETING Clone Heterogeneity – Melanoma Primary Tumor

“Our New Direction”

Followig Patient Relapses



**Tumor
Heterogeneity
Addressing
Single Cells/Clones**



In Summary

- Protein Functionality and variants thereof is KEY in Cancer treatment
- Drug Imaging by MS and Single Cell resolution – FDA standard
- Tumor Clone disposition is a Future focus for improved patient outcome
- Current work: adding digital pathology layers and AI-based characterization – provide complement understanding – improved treatment



@europeancancermoonshotlund



@europeancancermoonshot



@CancerLund

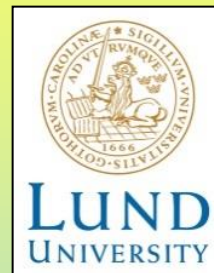
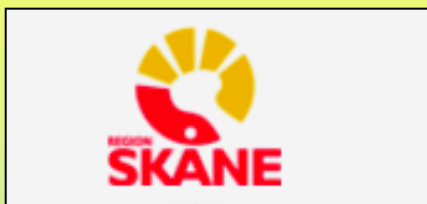


European Cancer Moonshot Lund

www.cancermoonshotlund.com



Funding & Support







Coal's Decline Spreads Far Beyond Appalachia



Democrats Seek Upset in South Carolina Special Election



Senate GOP Plans Health-Care Vote Next Week



BREAKING NEWS

U.K. charges Barclays, four former executives with fraud related to crisis-era fundraising with Qatar



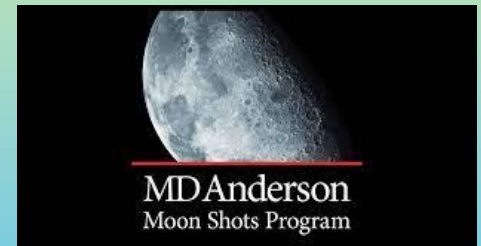
THE EXPERTS

Why the 'Moon Shot' to Cure Cancer Might Work

Feb 17, 2016 7:00 am ET

ATUL GROVER: Widespread praise for Vice President Joseph Biden's "Moon Shot to Cure Cancer" is another positive development

Recommended Videos



Thank You
For
Your attention

