

| SPHN-PHRT Symposium | Zurich | 28.08.25 |

SPO-NDS: Fueling Precision Oncology in Switzerland

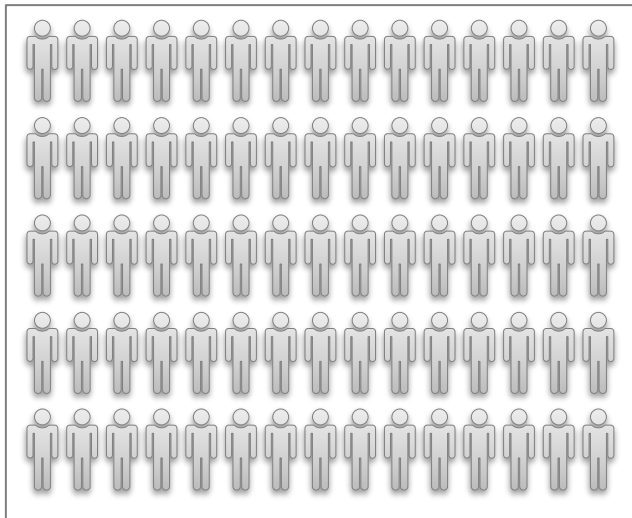
Olivier Michielin, MD-PhD

Head of Department of Oncology and
Precision Oncology Service,
Geneva University Hospital – Geneva
Co-Director of Swiss Cancer Center Lemman,
Agora – Lausanne
Professor at the Swiss Federal Institute of
Technology, EPFL – Lausanne

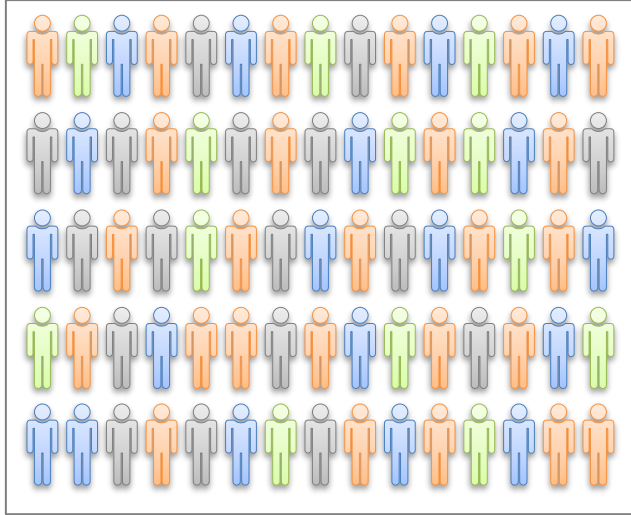
Introduction: precision oncology, a new paradigm



Personalization

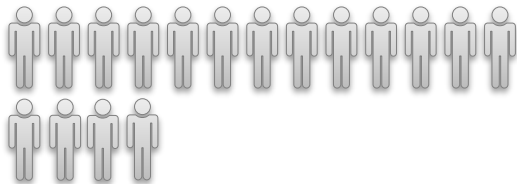


Personalization

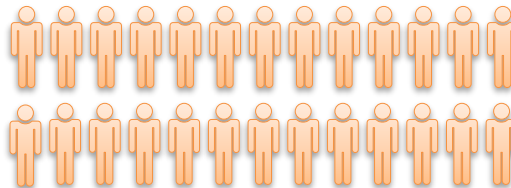


Personalization

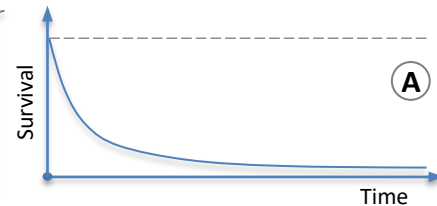
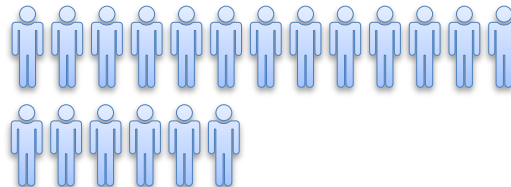
No treatment!



Treatment A



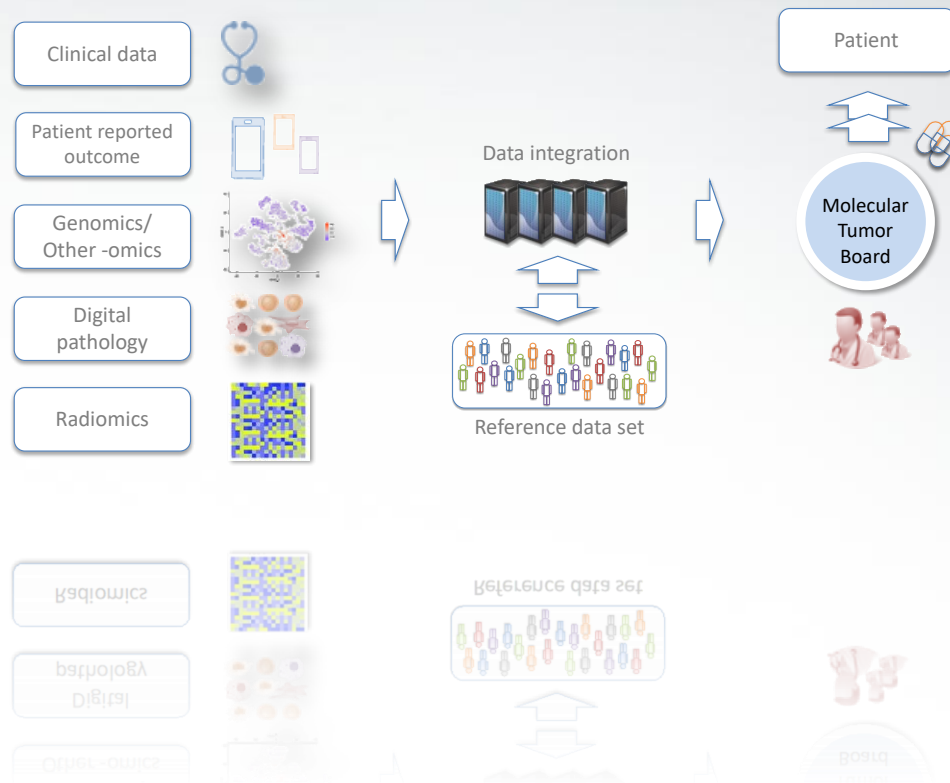
Treatment B



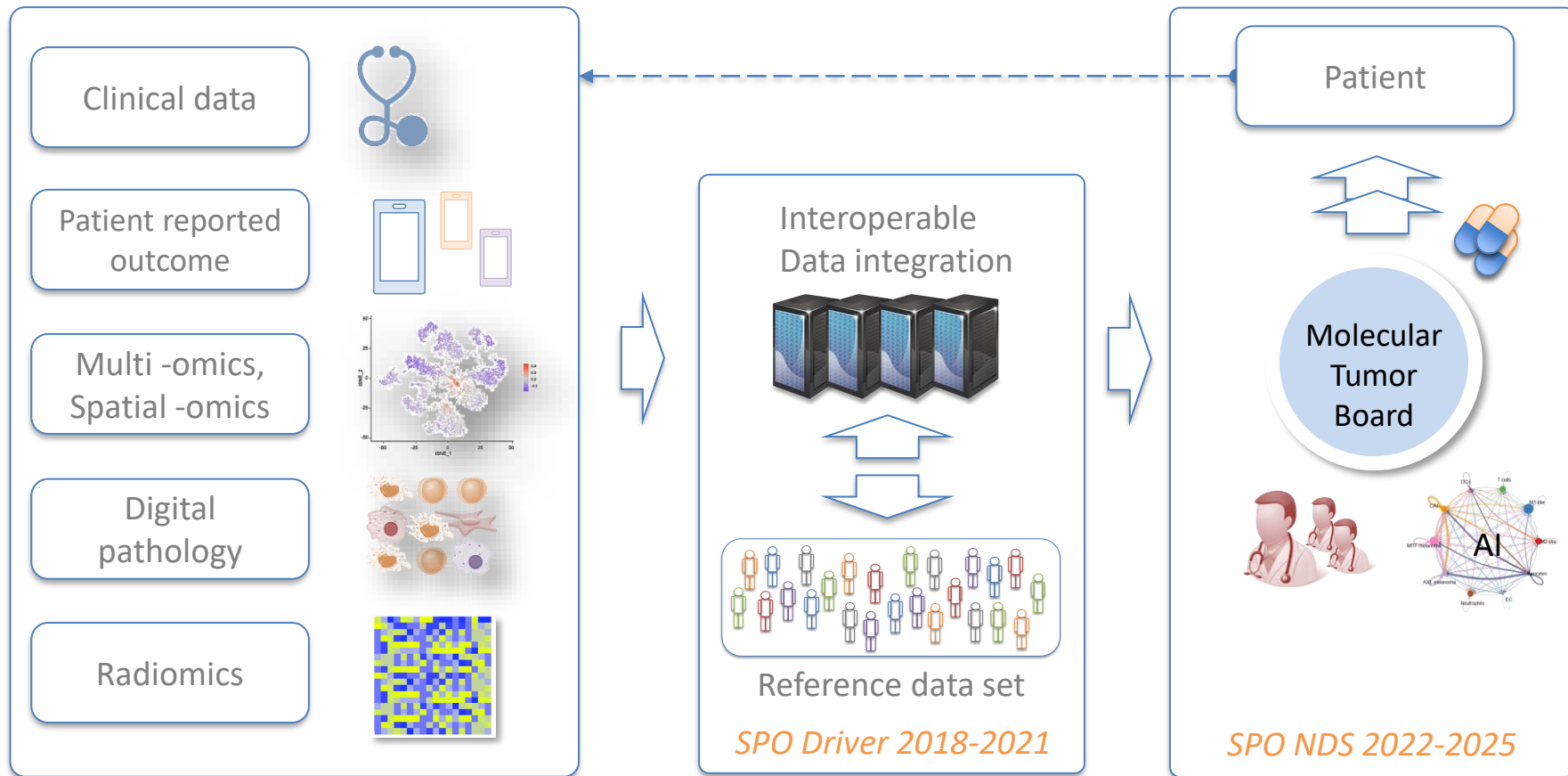
Treatment C



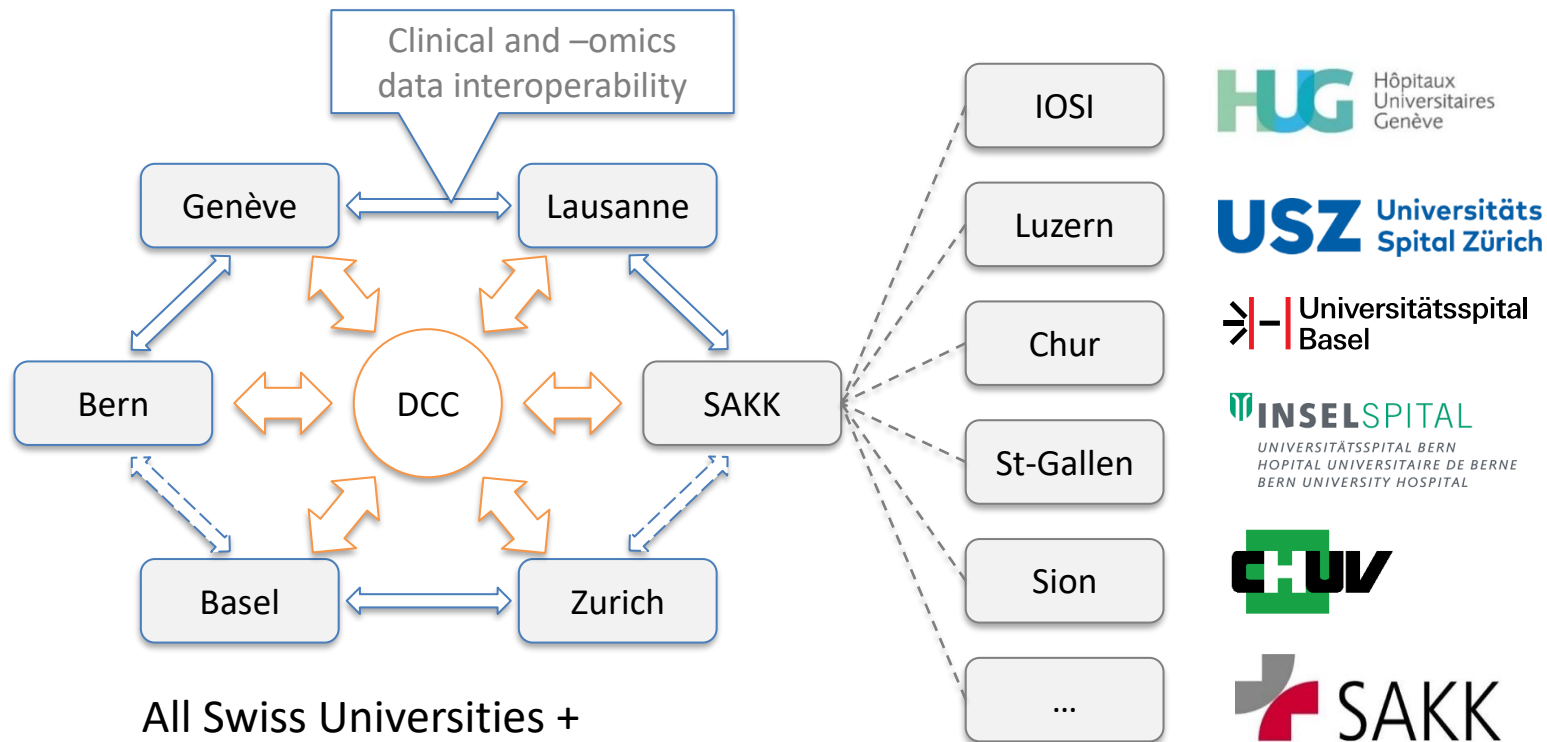
Key data streams in precision oncology



Precision oncology: integrating multiple data streams



The Swiss Personalized Oncology (SPO) network



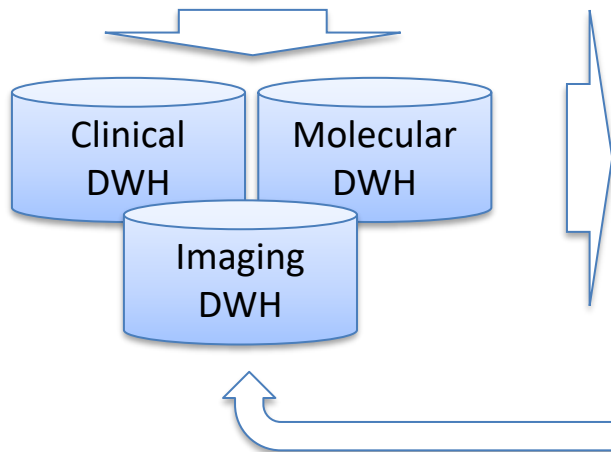
All Swiss Universities +

EPFL

ETH zürich

Data strategy for SPHN SPO-Driver and SPO-NDS

Electronic Patient Record



#	Group	Data Category	Required Single Data Point
1	DEMOGRAPHIC	Demographic	Year of birth
2			Gender
3	1st DIAGNOSIS	Classification	First date of diagnosis (Biopsy or Main Tumor)
4			CIM 10
5			ICD-O3 / Morphology
6			ICD-O3 / Topography
7		Staging	Free text diagnosis
8			TNM classification
9			TNM Version
10			Stage
11			Staging system
12			Grade
13			Grading system
14	TREATMENT	Therapy	Type of treatment
15			Date of treatment
16			Treatment specification
17	RESPONSE	Outcome	Method of assessment
18			Date of assessment
19			Results from the assessment (RECIST 1.1)
20			Updated stage
21			Staging system
22	SURVIVAL	PFS	Follow-up event
23		OS	Date of follow-up event
24			Date of event
25			Event type

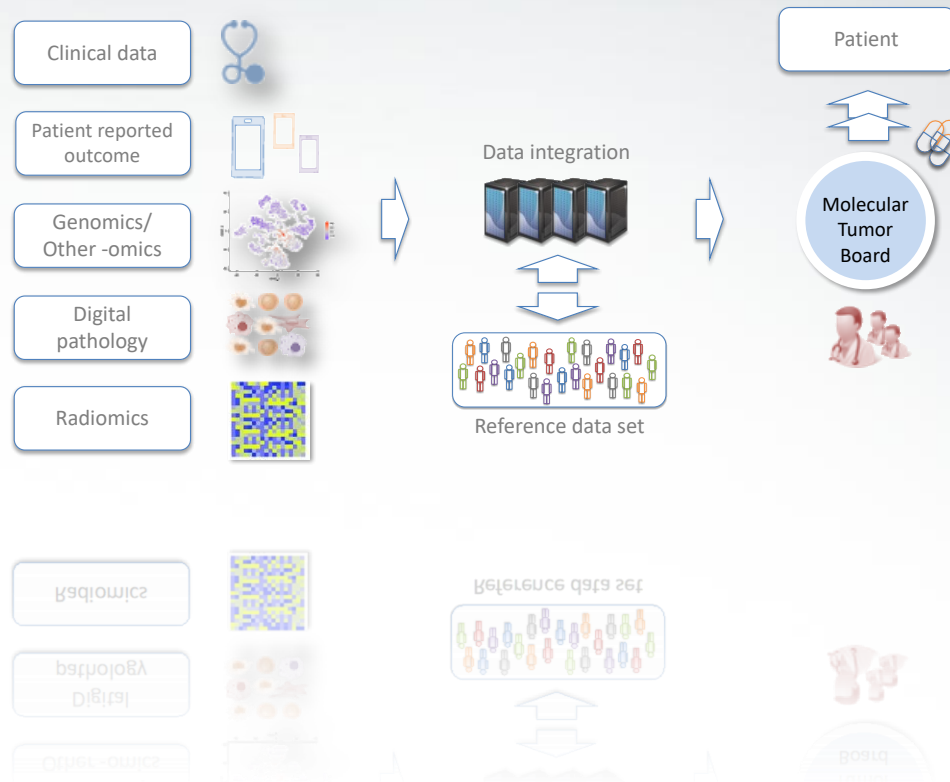


Local infrastructure @ Hospital X:
heterogeneous

Standardised dataset @ Hospital X:
fully interoperable

Centralisation &
mutualisation: SPHN

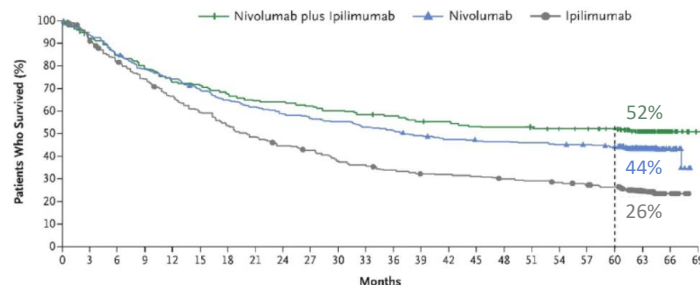
SPO Driver: exploiting clinical data



Clinical data: real-world data vs Checkmate-067 – 1st line

A

CM-067 OS¹

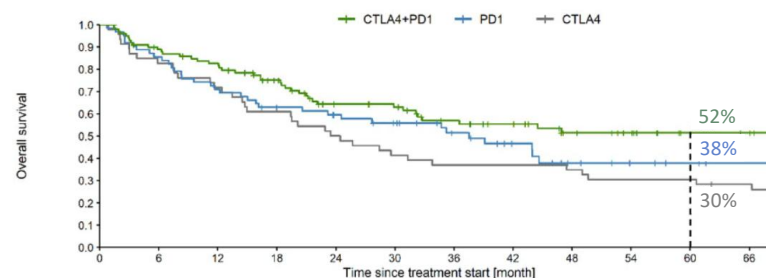


No. at Risk

Nivolumab plus ipilimumab	314	292	265	248	227	222	210	201	199	193	187	181	179	172	169	164	163	159	157	155	150	92	14	0
Nivolumab	316	292	266	245	231	214	201	191	181	175	171	164	158	150	145	142	141	139	137	135	130	78	14	0
Ipilimumab	315	285	253	227	203	181	163	148	135	128	113	107	100	95	94	91	87	84	81	77	73	36	12	0

B

RWD OS²

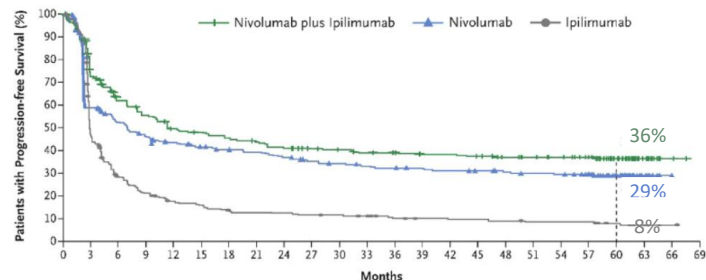


Number at risk

CTLA4	46	38	33	28	23	19	17	16	14	14	12
PD1	62	53	44	37	33	29	22	16	7	5	3
CTLA4+PD1	100	86	79	65	49	45	36	31	23	11	10

C

CM-067 PFS¹

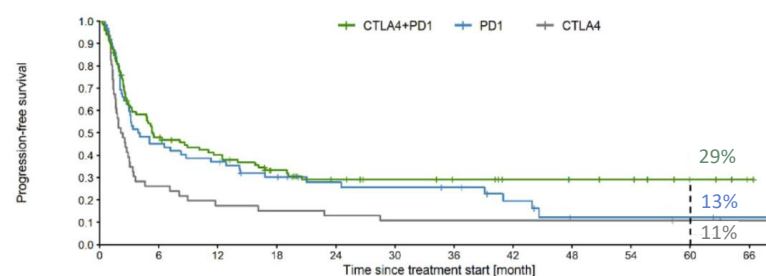


No. at Risk

Nivolumab plus ipilimumab	314	218	174	155	136	131	124	117	110	104	101	97	95	91	90	88	82	79	76	69	45	19	2	0
Nivolumab	316	177	151	132	120	112	106	103	97	88	84	80	78	76	73	71	68	66	65	60	40	13	1	0
Ipilimumab	315	136	78	58	46	42	34	32	31	29	28	26	21	19	18	18	17	15	15	11	8	1	0	

D

RWD PFS²



Number at risk

CTLA4	46	12	8	7	6	5	5	5	5	4	3
PD1	62	28	23	17	12	11	10	6	2	2	1
CTLA4+PD1	100	40	36	25	19	16	14	11	10	9	2

¹Larkin, NEJM 2019;

²Wicky, Frontiers 2023



Strategic Focus Area
Personalized Health
and Related Technologies

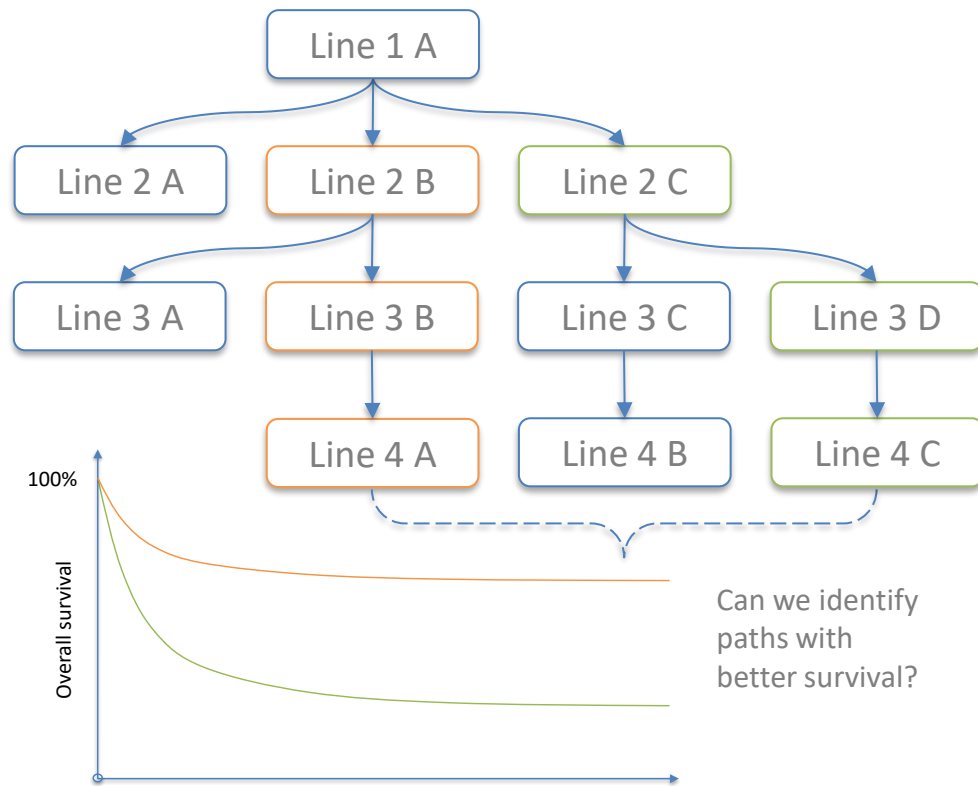


Analyzing sequence of events: Process mining

- Clinical data -> sequence of events:
 - Treatments
 - Evaluation Scanners
 - ...
- SPO can capture all these events as data extraction originates from the hospital data warehouses (DWH)



- Process mining approaches can be used to detect preferred therapeutic pathways as well as outliers
- Important information can be projected onto these pathways, including PFS or OS

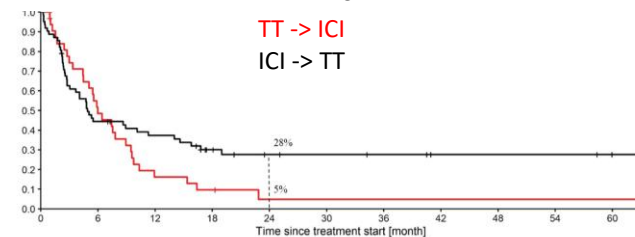


Melanoma real-world data analysis using process mining¹



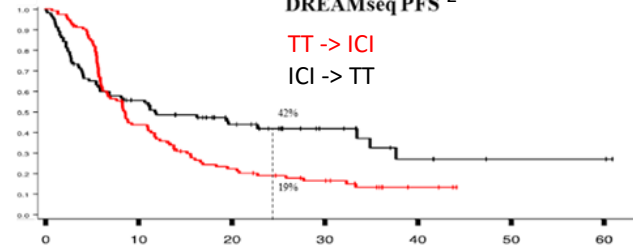
RWD PFS¹

TT -> ICI
ICI -> TT



DREAMseq PFS²

TT -> ICI
ICI -> TT



¹Wicky, *Frontiers* 2023

SPO: Example of nation-wide data extraction – BRAF mutations

- The first nation-wide studies are now being conducted¹

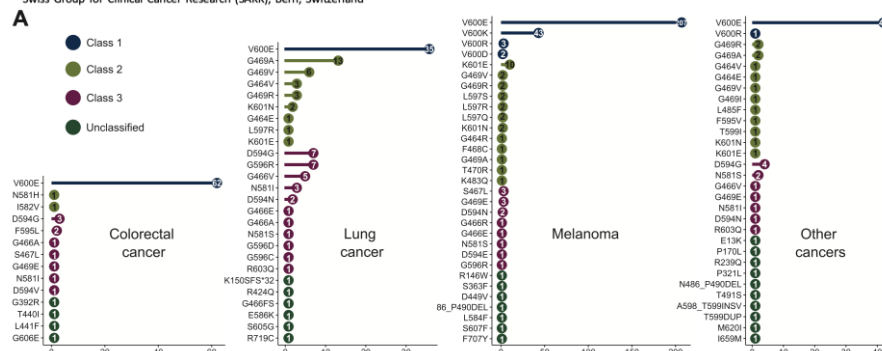


ORIGINAL ARTICLE

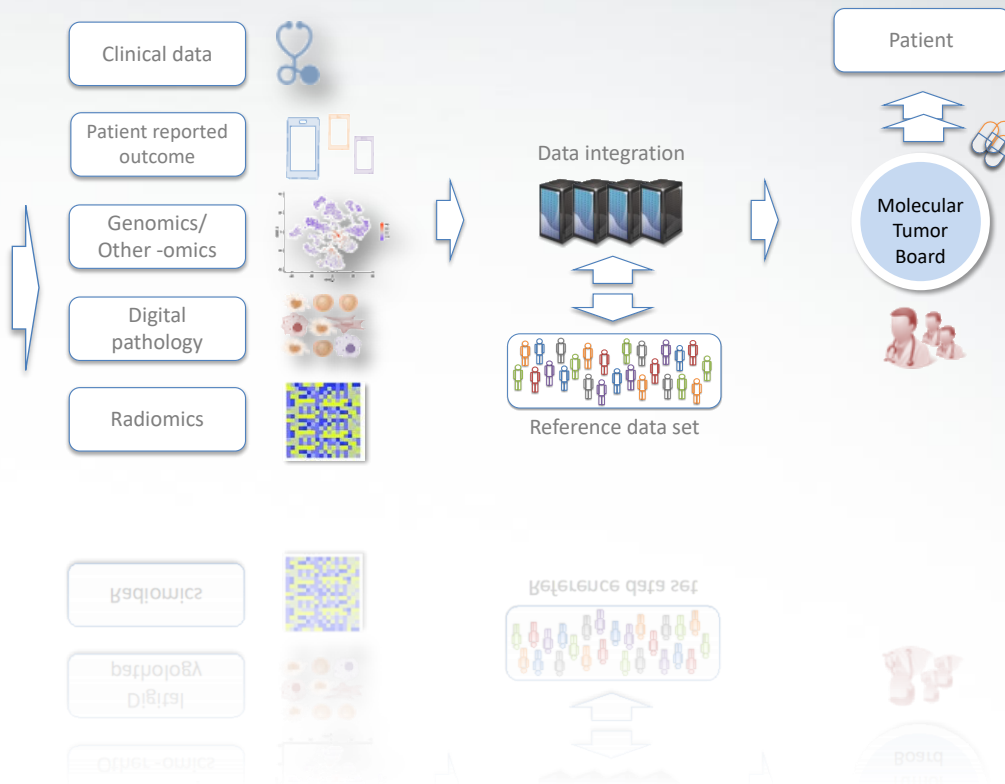
Real-world occurrence, therapy, and outcome of patients with class 2 or 3 BRAF compared with class 1 BRAF-mutated cancers

S. Pradervand¹, N. Freund¹, B. Gosztonyi², L. Roncoroni², R. Achermann³, T. Schwenk⁴, G. de Fraipont⁵, J. Garesius¹, S. Haefliger⁶, A. B. Leichte⁷, M. K. Kiessling⁷, T. Mueller-Focke⁸, F. S. Krebs⁸, V. Zoete^{8,9}, P. Tsantoulis⁵, O. Michielin^{5,1}, C. Britschgi^{10,11} & A. Wicki^{12,13}

¹Centre Hospitalier Universitaire Vaudois – CHUV, Department of Oncology, Lausanne; ²Department of Medical Oncology and Hematology, University Hospital Zurich, University of Zurich; ³Department of Medical Informatics, Universitätsspital Basel – USB, Basel; ⁴Oncology, Hematology and Transfusion Medicine, Kantonsspital Aarau, Aarau; ⁵Geneva University Hospitals – HUG, Geneva; ⁶Department of Medical Oncology, Inselspital, Bern University Hospital, University of Bern; ⁷Department of Clinical Chemistry, Inselspital – Bern University Hospital and Center for Artificial Intelligence, University of Bern, Bern; ⁸Computer-Aided Molecular Engineering Group, Department of Oncology UNIL-CHUV, Ludwig Institute for Cancer Research Lausanne, Lausanne; ⁹Molecular Modelling Group, Swiss Institute of Bioinformatics, Lausanne; ¹⁰Swiss Group for Clinical Cancer Research (SAKK), Bern, Switzerland



Precision oncology: omics & spatial -omics



Spatiomomics as a new way to design predictive biomarkers

npj | precision oncology

Published in partnership with The Hormel Institute, University of Minnesota

Review article



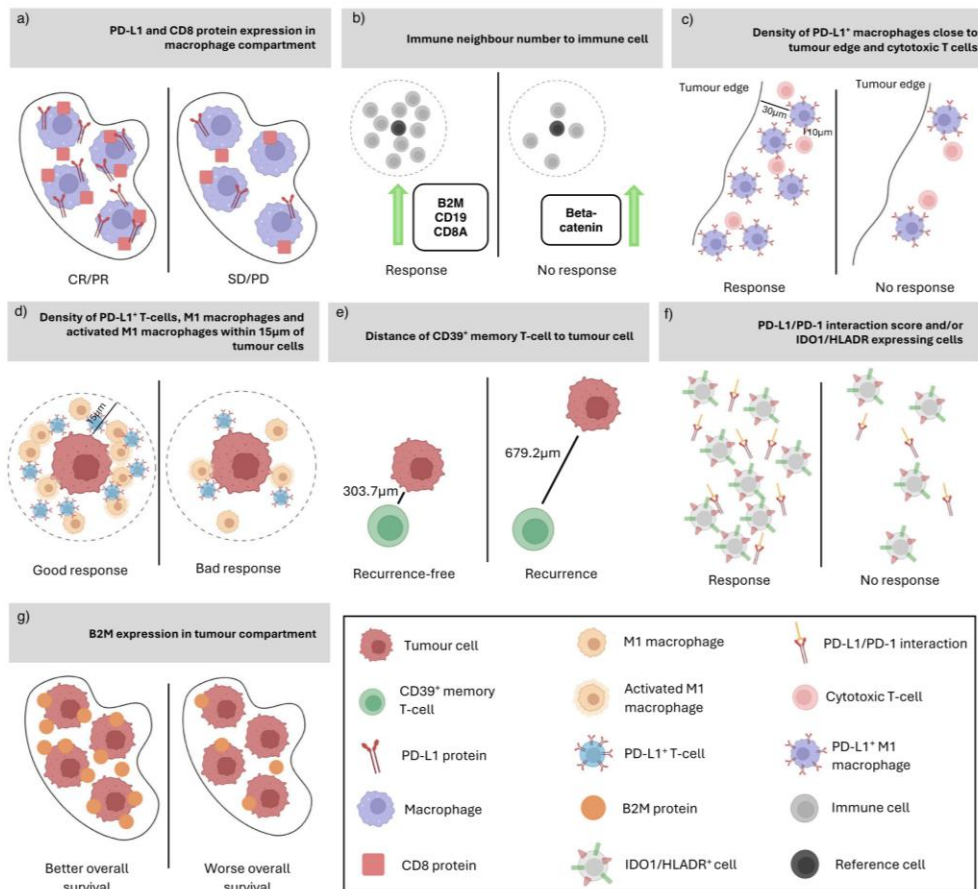
<https://doi.org/10.1038/s41698-024-00671-1>

The current landscape of spatial biomarkers for prediction of response to immune checkpoint inhibition

Check for updates

Hannah L. Williams^{1,7}✉, Ana Leni Frei^{1,2,7}, Thibaud Koessler^{3,4,6}, Martin D. Berger⁶, Heather Dawson¹, Olivier Michielin^{3,4,5} & Inti Zlobec¹

- **Spatial information** provided by spatial proteomics and/or spatial transcriptomics can be leveraged to **build predictive biomarkers**
- This work has started in many IO sensitive tumor types including melanoma and lung cancer
- Our national program plans to make **extensive use of these technologies** and data to develop predictive biomarkers for precision oncology



QuPath v3.11.0

File Edit Tools View Objects TMA Measure Automate Analyze Classify Extensions Help

Project Image Annotations Hierarchy Workflow

None
 ■ None
 ■ Other
 ■ Lymphocyte

Single measurement classifier (3N1c.tif)

Object filter: Detections (all)

Channel filter: No filter (allow all channels)

Measurement: Prediction

Threshold: -7.0052

Above threshold: Lymphocyte

Below threshold: Other

☒ Live preview

Classifier name: Enter object classifier name Save

Annuler Appliquer

Key	Value
Image	3N1c.tif
Name	Image
Num Detections	970
Num Lymphocyte	966
Num Other	4

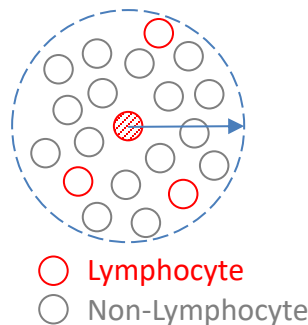
3702x 74415px
 244 221 230

Visualization with different classification thresholds on a ROI in QuPath
(lymphocytes in green, other cells in yellow)

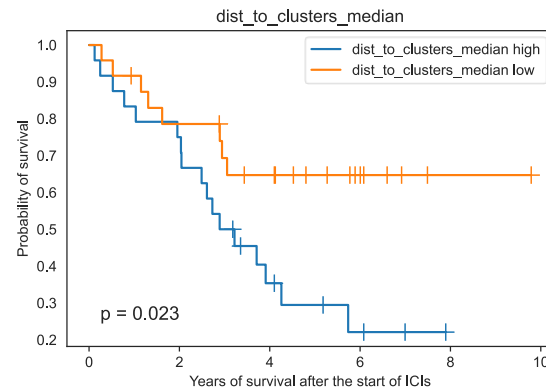
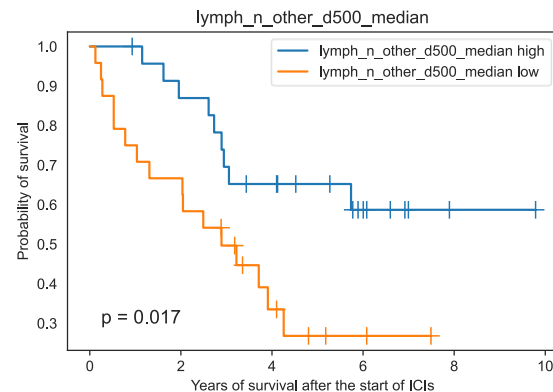
Example of abstract features

- We can stratify PD-1 benefit with sophisticated higher-order features, available only via computational pathology
- Multiple features are promising, 2 examples:

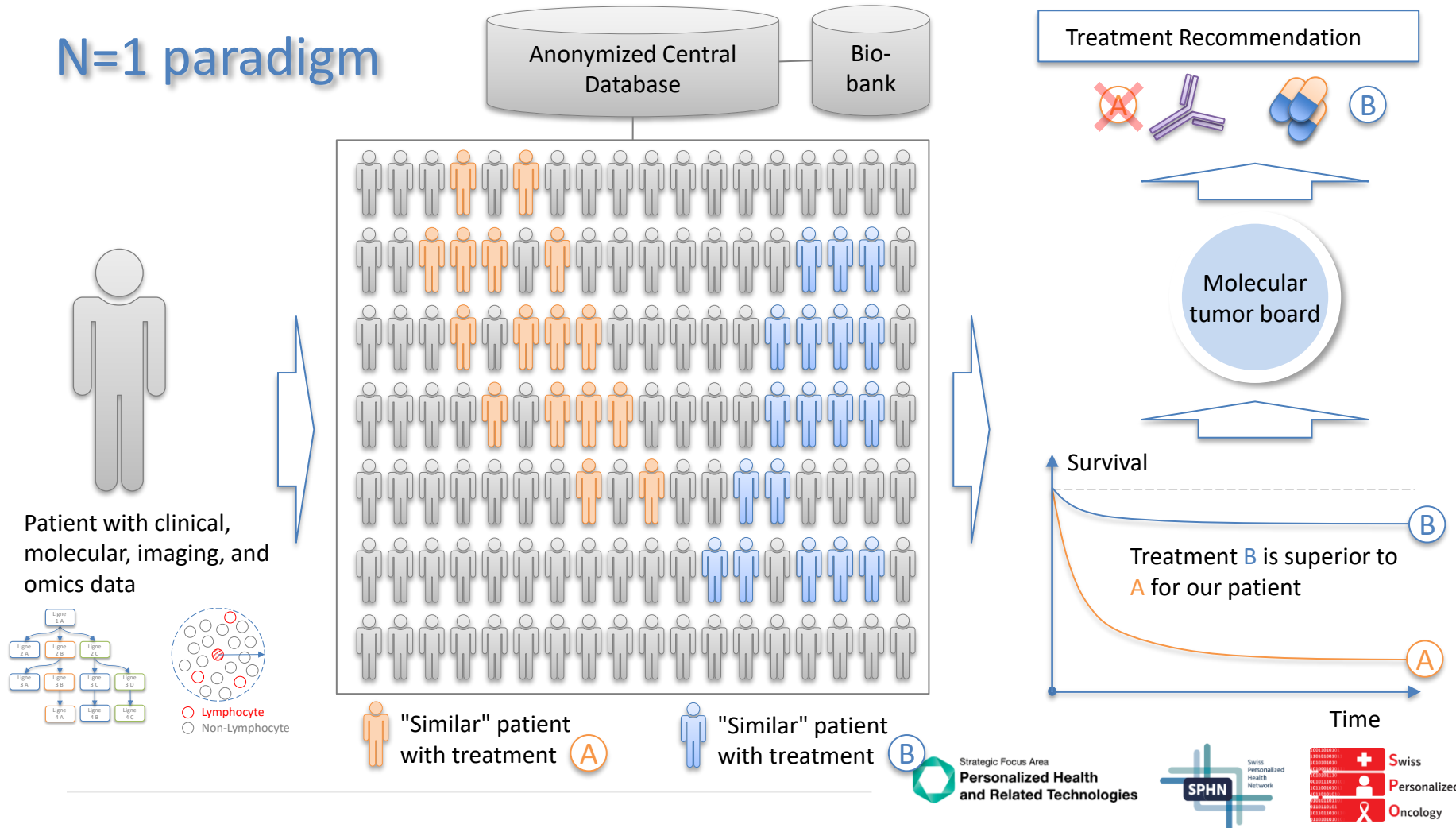
- Median number of non-lymphocyte cells within 500 pixels of each lymphocyte (lymph_notherd500_median)
- Median distance between each non-lymphocyte cell to the nearest lymphocyte cluster (dist_to_clusters_median)



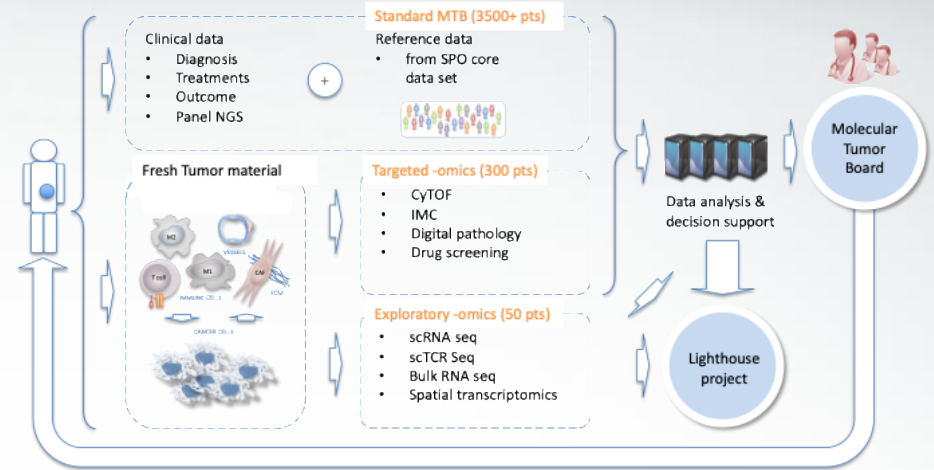
- Importantly: neither of these features are visually discernable in routine practice and require computer aided approaches!

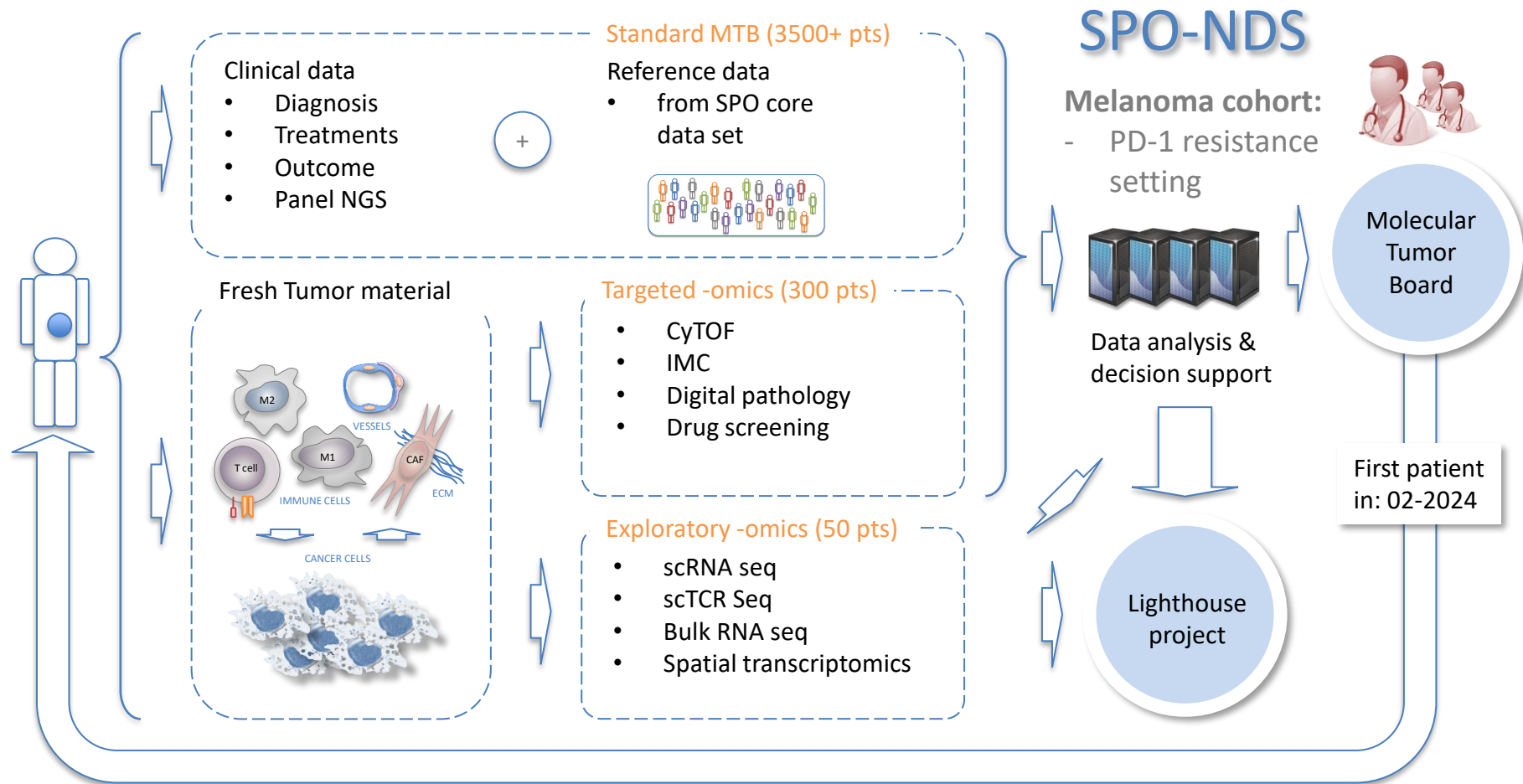


N=1 paradigm



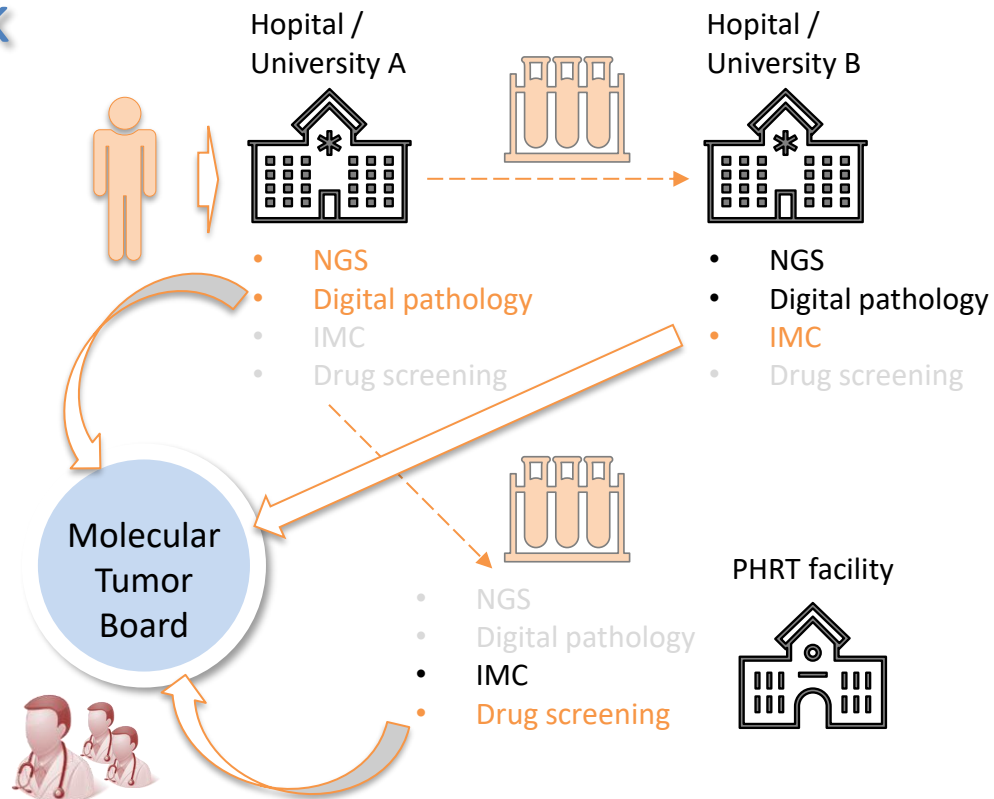
Prospective multi-omics: SPO - NDS



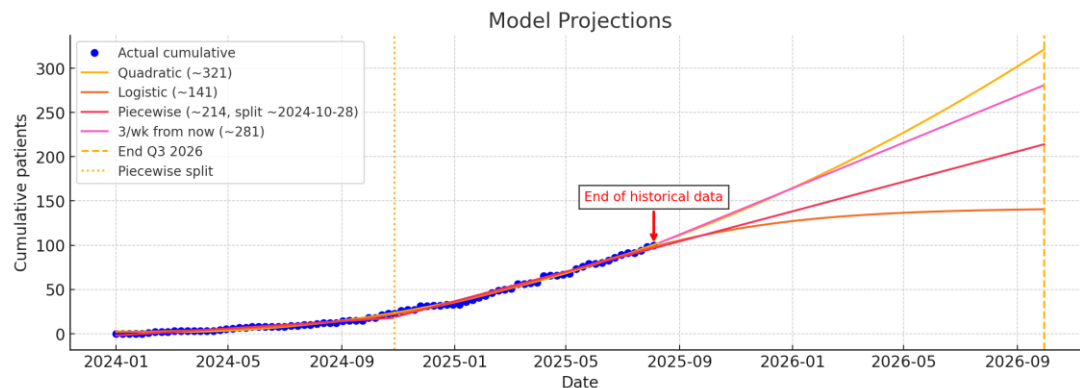
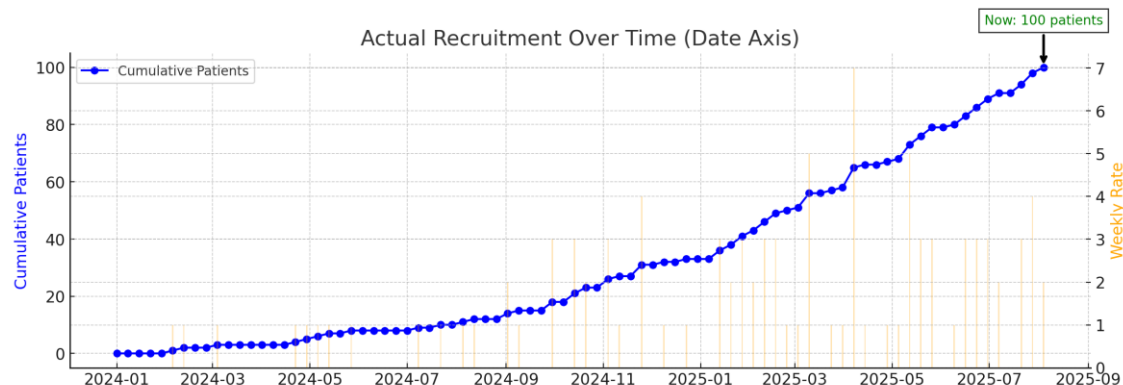


National –omics network

- We have built a decentralized program that allows recruitment of patients at all sites, multi-omics analyses in specific locations, yet central data integration
- New sites can be onboarded if they develop one of the multi-omics technology locally
- The multi-omics platforms are tumor specific (different anti-body panels, normalization, ...)
- QC programs are in place within the –omics facilities



SPO-NDS: current recruitment rates



Upper panel:

Cumulative recruitment (blue circles) and weekly inclusion rate (orange bars) are shown from February 2024 to present (top).

Lower panel:

Model-based projections to 30 September 2026 are shown (bottom) using four approaches: quadratic, logistic, piecewise linear (change point ~28 Oct 2024), and fixed rate (3 patients/week).

Projected totals on 30 Sept 2026 are shown in the legend.

Current recruitment rate:
3-5 patients / week!

SPO-NDS: Prospective study data collection

Legend:

B = Breast cancer

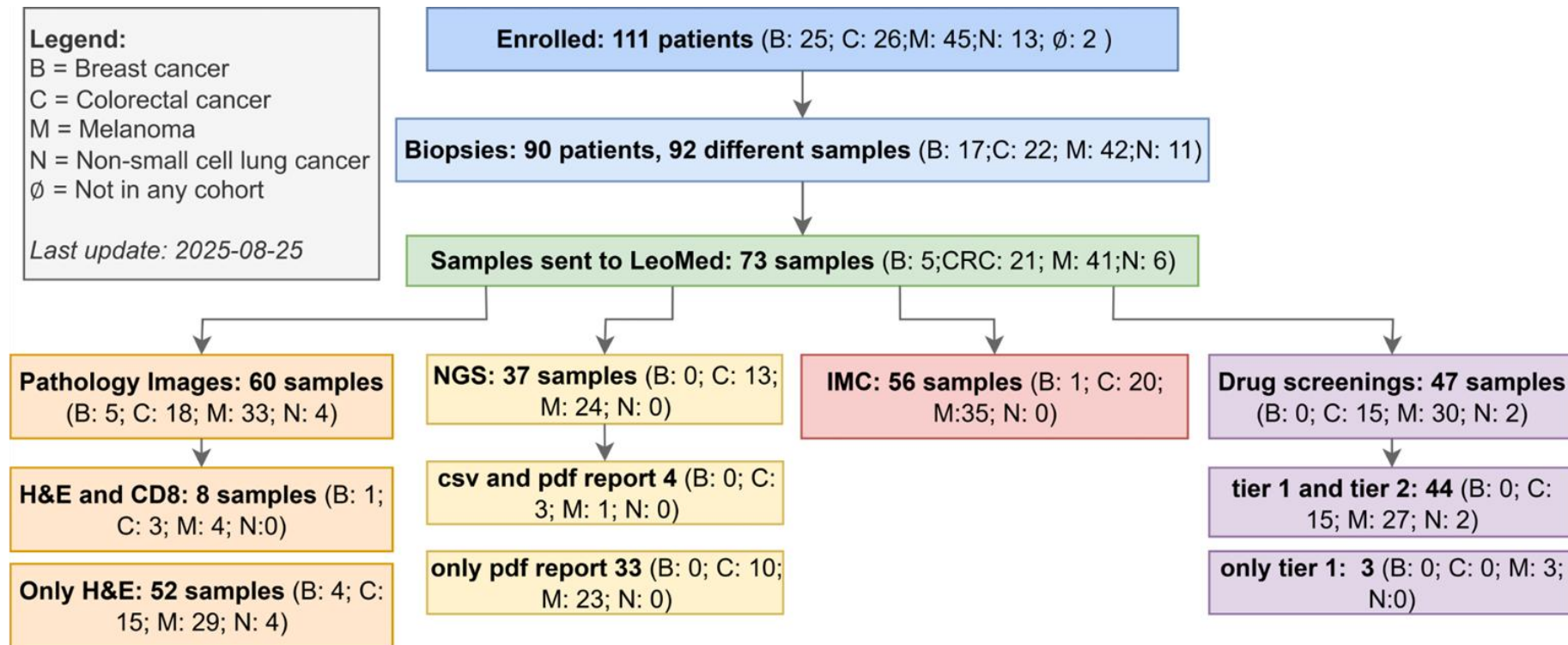
C = Colorectal cancer

M = Melanoma

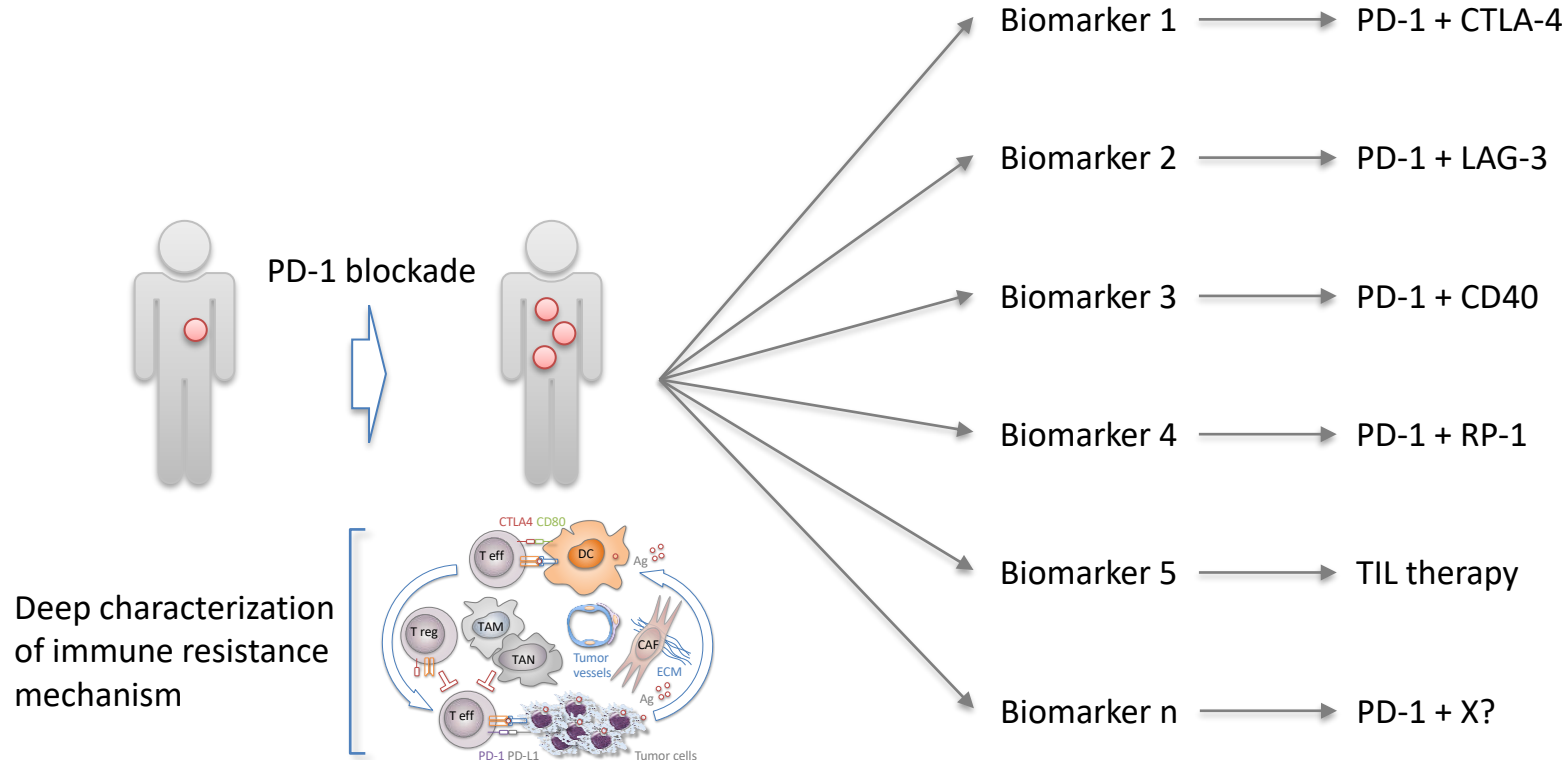
N = Non-small cell lung cancer

∅ = Not in any cohort

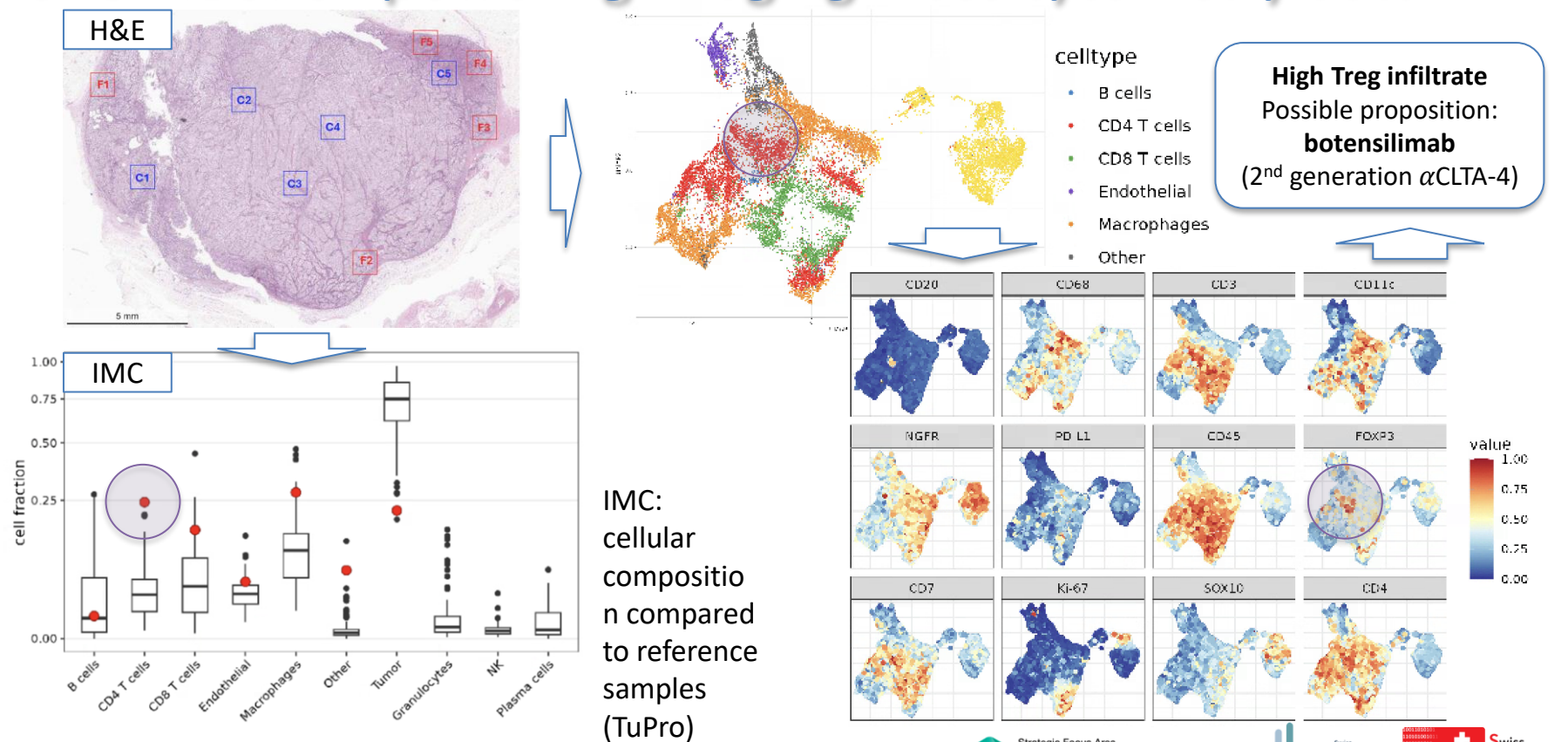
Last update: 2025-08-25



SPO-NDS: melanoma cohort – resistance to PD-1



SPO-NDS: empowering imaging mass cytometry data



Bringing data back to the molecular tumor boards

Patient
Therapies
Gene dependencies
Tumor landscape
Selected therapies 2
Reports
New submission

Patient
Name: Example 8
Cancer type: Melanoma (NCI:C3224, OncoTree:MEL)

		Allele frequency	TumorScreen	Druggable	OncoKB	Interact	Mutation frequency (GENIE)
BRAF	L485W	61.9%					37.91%
PIK3CA	E545K	34.2%					4.19%
KRAS	G12A	57.5%					2.64%
NF1	Q282*	33.9%					16.91%
KIT	D816V	3.2%					6.62%
FANCA	G501S	17.1%					3.57%
JAK1	V865M	35.9%					2.89%
TP53	P72R	91.7%					20.56%
TP53	P72A	7.4%					20.56%
TET1	W710L	51.9%					3.84%

- Example 8_presentation 2024-12-03 11:11:55 remove Open presentation
- Test histological image 2024-11-11 15:05:39 remove histological image is uploaded
- Diagnosis 2024-11-06 14:42:18 remove Melanoma (OncoTree:MEL)
- Patient registration 2024-11-06 13:42:18 remove

Add new note or image
Create new PPT presentation
Highlighted alterations: 2
Selected therapies: 2

Last histological image
Histopathological image has uploaded on 2024-11-11 15:05:39:

Disadvantage
Neutral
Dependency
Evidence at variant level
Evidence at gene level

by: ☐ Variant ☒ Gene
in: ☒ Melanoma ☐ Pan-cancer

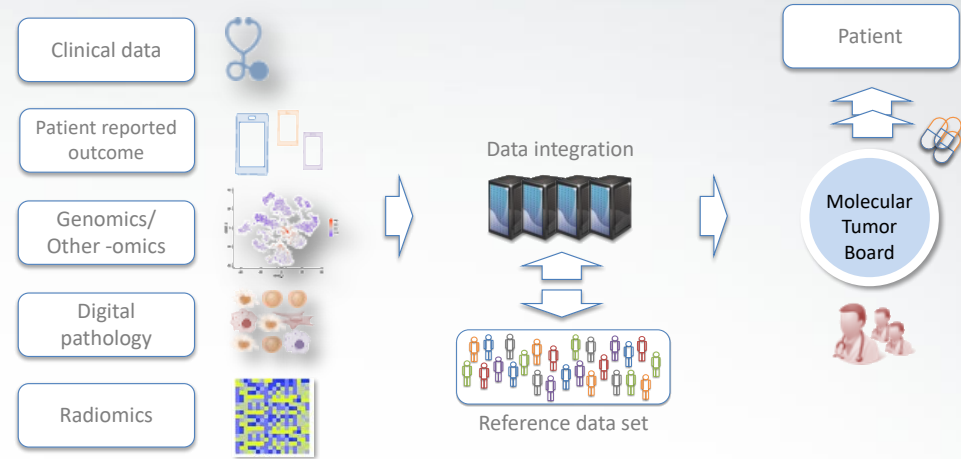
Somatic Mutations 10
Copy Number Alterations 1
Structural Variants 1

1 - 10 of 10

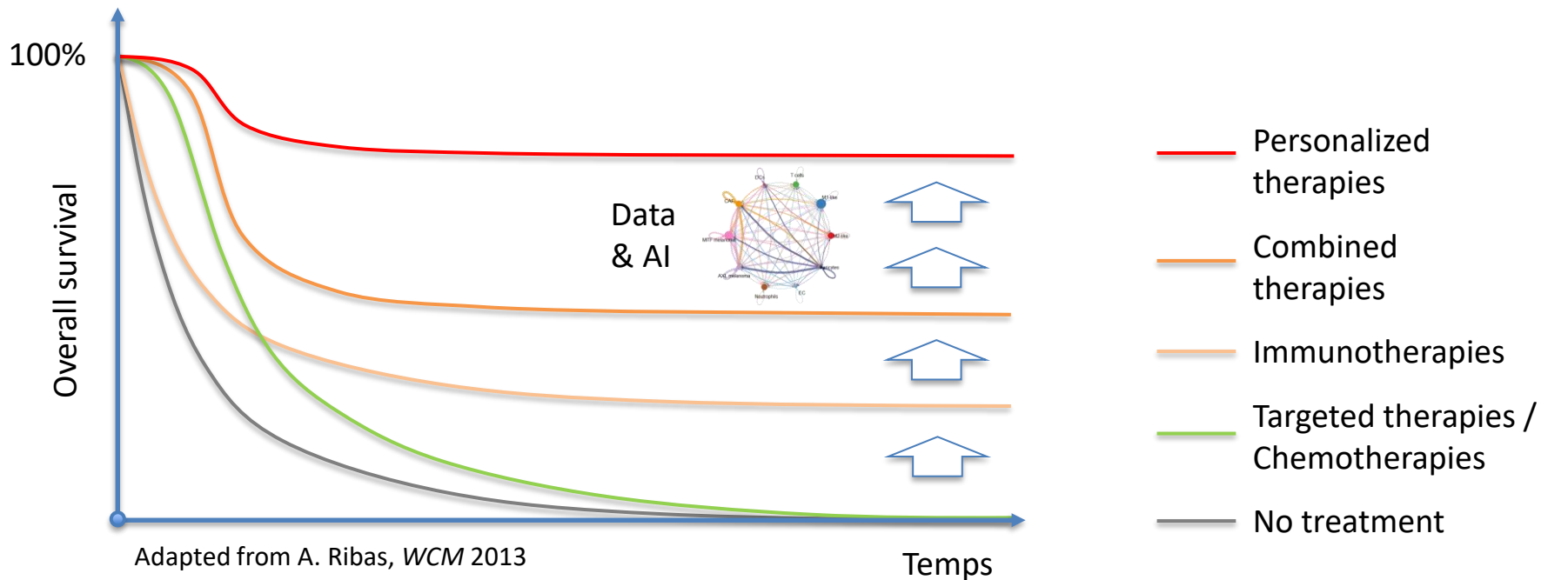
Variant: BRAF L485W Actionable alteration
TumorScreen: Likely-Dependency
Interpretation: Likely Oncogenic (Likely Gain-of-function), SIFT deleterious_low_confidence(0), Polyphen probably_damaging(0.979)
Therapies: GENIE
Variant frequency 0.08 %, Gene mutation frequency 37.91 %

Remove selection
More details

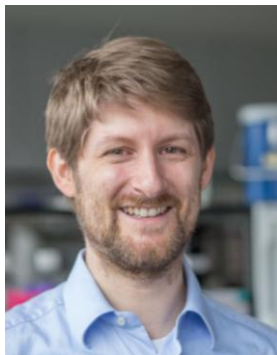
Conclusion and Outlook



Expected benefit from personalized strategies



Many thanks to a fantastic team!



Prof. Bernd Bodenmiller
Main co-PI



Prof. Andreas Wicki



Prof. Mitchel
Levesque



Prof. Mohamed
Bentires-Alj



Dr. Sylvain Pradervand



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Miklos Pless (SAKK)
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Bettina Sobottka-Brillout (USZ)
Deborah Stroka (UniBern)
Petros Tsantoulis (HUG)
Markus Vetter (KSBL)

... and many more
collaborators across
CHUV, EPFL, ETHZ,
HES-SO, HUG, INSEL,
KISPI, KSBL, SAKK,
SDSC, UNIBAS, UNIBE,
UNIGE, UNIL, USB,
USZ, and UZH.

| SPHN-PHRT Symposium | Zurich | 28.08.25 |

**THANK YOU FOR
YOUR ATTENTION!**