

ESMO 2017 Meet-the-investigator meeting

Disease management and comprehensive genomic profiling in cancer of unknown primary

11 September 2017

IFEMA, Feria de Madrid, Spain

Housekeeping notes

Please remember to fill out the meeting evaluation form before leaving

This meeting is being video recorded

MEETING FEEDBACK FORM

Session 1: Your details (optional)
Name (optional): _____ Institution (optional): _____
Country (optional): _____ Profession (e.g. oncologist): _____

Session 2: Overall
Please rate the following statements (1 = Strongly agree, 2 = Agree, 3 = Disagree, 4 = Strongly disagree)

Statement	Strongly agree	Agree	Disagree	Strongly disagree
Overall standard of care was clinical and evidence based				
Presentations were of high quality				
Presentations were relevant to the topic				
Presentations were of sufficient length				
Presentations were of sufficient depth				
Presentations were of sufficient breadth				
Presentations were of sufficient quality				
Presentations were of sufficient quantity				
Presentations were of sufficient variety				
Presentations were of sufficient interest				
Presentations were of sufficient relevance				
Presentations were of sufficient impact				
Presentations were of sufficient value				
Presentations were of sufficient quality				
Presentations were of sufficient quantity				
Presentations were of sufficient variety				
Presentations were of sufficient interest				
Presentations were of sufficient relevance				
Presentations were of sufficient impact				
Presentations were of sufficient value				

Overall meeting evaluation
Please rate the following statements (1 = Strongly agree, 2 = Agree, 3 = Disagree, 4 = Strongly disagree)

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Presentations were of sufficient relevance				
Presentations were of sufficient impact				
Presentations were of sufficient value				

Agenda



Time	Topic	Presenter/Moderator
09:05 – 09:15	Current standard of care	Alwin Krämer
09:15 – 09:25	Molecular testing: from gene expression profiling to comprehensive genomic profiling	Jeffrey Ross
09:25 – 09:45	Tumor board discussion based on clinical cases	Alwin Krämer / Holger Moch / Jeffrey Ross
09:45 – 09:55	Genomic profiling study for patients with cancers of unknown primary	Alwin Krämer
09:55 – 10:00	Meeting closure	Alwin Krämer

The information contained herein may refer to use of products for indications other than those approved and/or listed in the Summary of Product Characteristics or relating to molecules currently undergoing experimental trials. The issues addressed are not meant to suggest that these products be employed for indications other than those authorised.

Current standard of care

Prof. Alwin Krämer, MD
University of Heidelberg, Germany

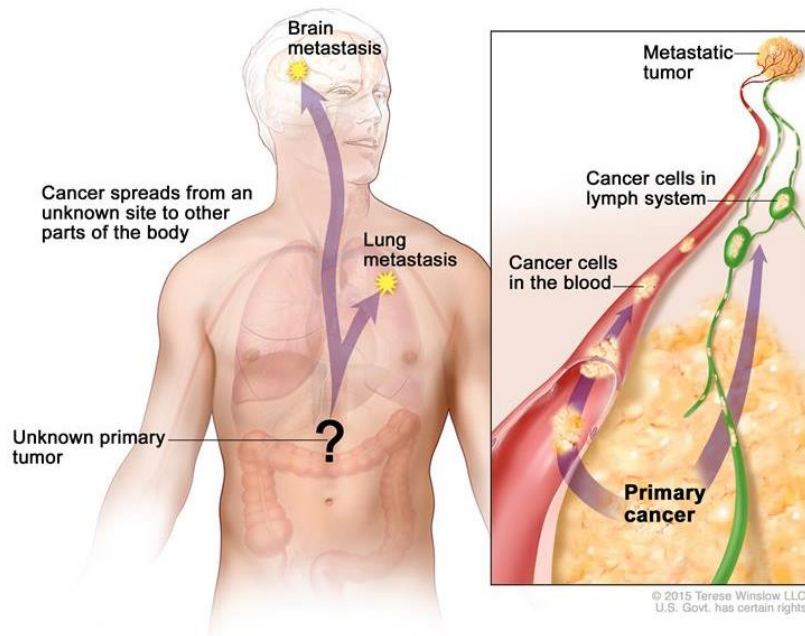
Disclosures



- Prof. Krämer has received research grants from Bayer and Merck, as well as honoraria for lectures or advisory board participation or consulting from Roche, and Novartis.

Cancer of unknown primary site (CUP)

High unmet medical needs



- 2% – 5% of all malignancies¹⁻³
- 12-month overall survival is 23%⁴
- Median overall survival is 9.1 months⁵
- Lack of a definitive primary site often restricts treatment options to **palliative chemotherapy**⁶

Image source: US National Cancer Institute (accessed 15/03/2017)
<https://www.cancer.gov/types/unknown-primary/patient/unknown-primary-treatment-pdq>

1. Stella, G.M., et al. (2012) *J Transl Med* 10:12; 2. Pavlidis, N., et al. (2012) *Lancet* 379:1428; 3. Massard, C., et al. (2011) *Nat Rev Clin Oncol* 8:701; 4. Australian Institute of Health and Welfare. Cancer in Australia 2010: in brief. Canberra: Australian Institute of Health and Welfare, 2010; 5. Greco, F.A., Hainsworth, J.D.: Cancer of unknown primary site, in DeVita VT Jr, Hellman S, Rosenberg SA (eds): *Cancer: Principles and Practice of Oncology* (ed 9). Philadelphia, P.A., J.B. Lippincott, 2011, pp 2033-51. 6. Fizazi, K., et al. (2015) *Ann Oncol* 26(suppl 5):v133.

CUP diagnosis follows ESMO guideline diagnostic work-up

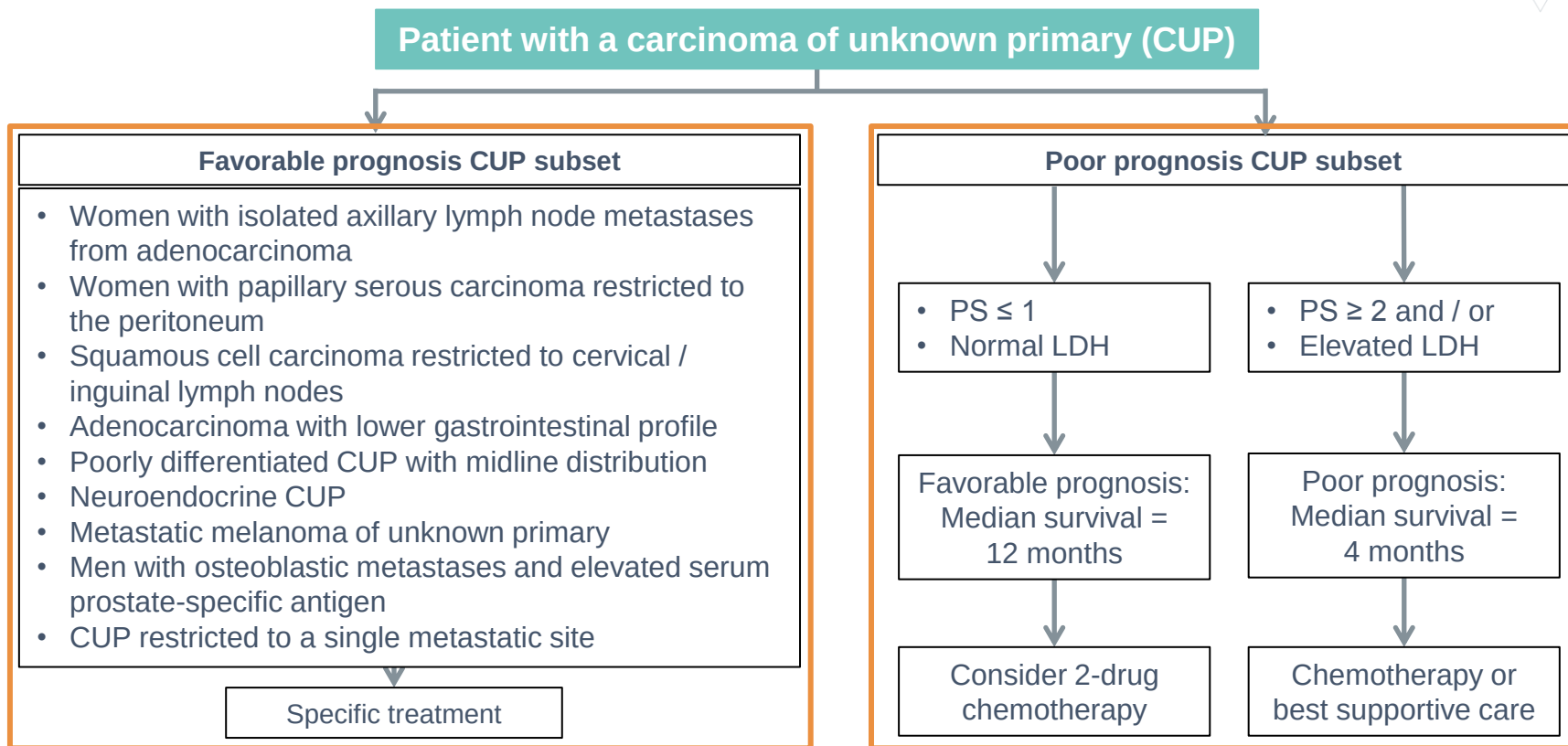
Target patient population	Assessment suggested
All	Thorough medical history and physical examination
All	Basic blood and biochemistry analysis
All	CT scans of thorax, abdomen and pelvis
All	Histology/Immunohistology
All females	Mammography
Females with axillary adenocarcinoma	Breast MRI
Patients with midline metastatic disease	Serum α -fetoprotein and human chorionic gonadotropin
Males with adenocarcinoma bone mets	Serum prostate-specific antigen
Cervical squamous cell carcinoma	Head and neck CT / PET scan
Sign / Symptom / Laboratory oriented	Endoscopies
Patients with neuroendocrine CUP	Octreoscan / Chromogranin A
Sign / Symptom / Laboratory oriented	Additional diagnostic tests

There are many histologies across CUP samples



Histology	Frequency
Adenocarcinoma	
• Well to moderately differentiated	50%
• Poorly or undifferentiated	30%
Squamous cell carcinoma	15%
Undifferentiated neoplasms	5%
• Not specified carcinoma	
• Neuroendocrine tumours	
• Lymphomas	
• Germ cell tumours	
• Melanomas	
• Sarcomas	
• Embryonal malignancies	

The ESMO guideline recognises distinct CUP subsets





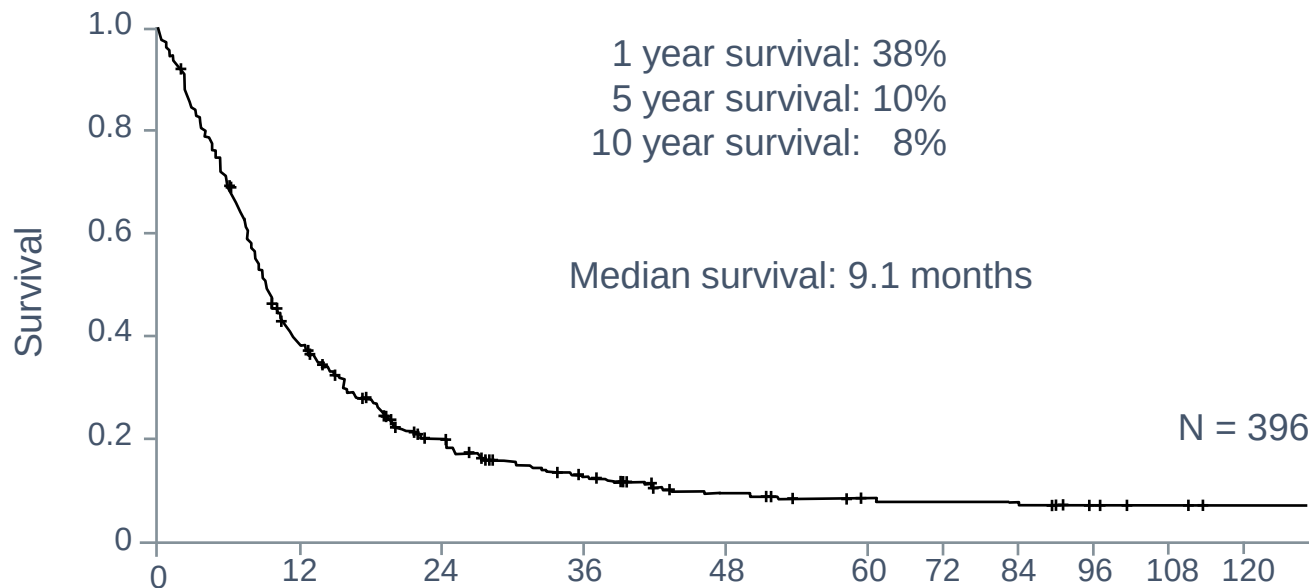
ESMO recommends low-toxicity palliative chemotherapy for poor-prognosis CUP patients

Chemotherapy (mg/m ²)	Time	Interval	Comments
Cisplatin 60-75 + Gemcitabine 1,000	Day 1 Day 1+8	Q3 weeks	Fit patients, adequate hydration
Cisplatin 75 + Etoposide 100	Day 1 Day 1-3	Q3 weeks	Fit patients with neuroendocrine-feature CUP, adequate hydration
Paclitaxel 175 + Carboplatin AUC 5	Day 1	Q3 weeks	Convenient outpatient regimen, monitor neurotoxicity
Docetaxel 75 + Carboplatin AUC 5	Day 1	Q3 weeks	Convenient outpatient regimen, monitor neurotoxicity
Irinotecan 160 + Oxaliplatin 80	Day 1	Q3 weeks	Outpatient regimen, monitor for neurotoxicity and diarrhoea
Oral capecitabine 2,000 ± Oxaliplatin 85-130	Days 1-14 Day 1	Q3 weeks	Outpatient regimen, risk for diarrhoea and neurotoxicity
Gemcitabine 1,000/irinotecan 100	Day 1+8	Q3 weeks	Convenient outpatient regimen, monitor diarrhoea

Patients with poor prognosis have low survival rates, e.g. disseminated adeno- or undifferentiated CUP



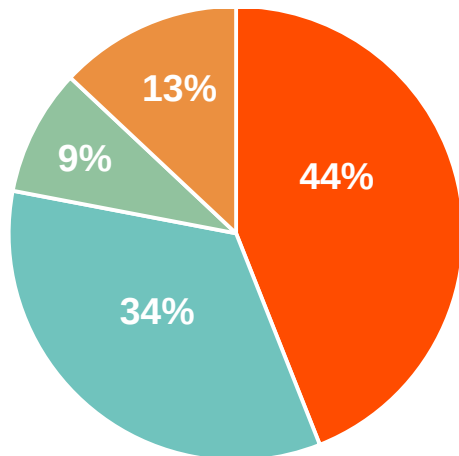
Minnie Pearl Cancer Research Network - 396 CUP Patients Treated in Phase II Studies



Molecular profiling can identify biomarkers associated with a potential drug benefit



Biomarkers found in CUP



- Hotspot variants
- Druggable variants
- Targets with drugs approved and available
- No variants detected

- Molecular profiling was found to identify biomarkers biologically relevant and/or associated with a **potential drug benefit in most CUP cases (87%)¹**
- It included druggable targets in key cancer related genes: BRAF, EGFR and ERBB2¹
- In another study, expression of PD-1 and PD-L1 was observed in 63% and 21% of assessed cases respectively²

Adapted from Clynick, B., et al. ESMO 2017 # 1705-PD.



Molecular testing: From gene expression profiling to comprehensive genomic profiling

Dr. Jeffrey S. Ross, MD

Foundation Medicine, Cambridge, MA USA

Disclosures



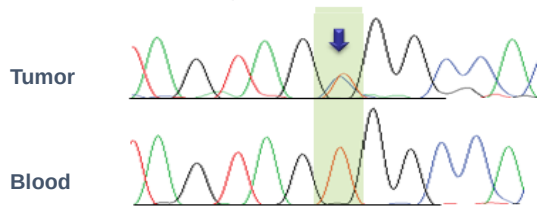
Dr Ross is an employee, holds a leadership position and owns stock in Foundation Medicine, Inc.

FoundationOne® identifies all classes of genomic alterations



Base Substitution

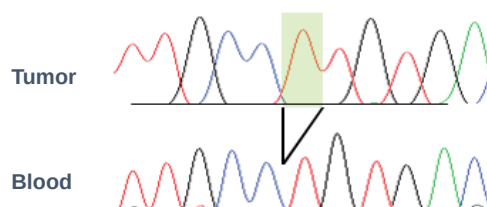
e.g. *BRAF*, *EGFR*



Capillary sequencing, Mass Spectrometry

Short Insertions / Deletion

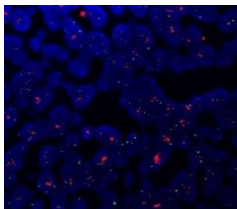
e.g. *EGFR*, *ERBB2*



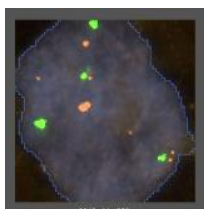
Capillary sequencing, gel size shift assays

Focal Amplification & Homozygous Deletion

e.g. *HER2*, *MET*



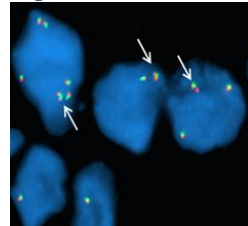
e.g. *PTEN*, *TSC1/2*



Fluorescence *In Situ* Hybridization

Gene Fusion

e.g. *ALK*, *ROS1*, *RET*



Real time-PCR Fluorescence *In Situ* Hybridization

FoundationOne® validation shows the high accuracy and reproducibility required for clinical use

Base Substitutions

(MAF 5-100%)

Sensitivity: > 99% PPV: > 99%

Insertions/Deletions

(1-40bp, MAF $\geq$ 20%)

Sensitivity: 98% PPV: > 99%

Copy Number Alterations

(> 20% tumor content, zero or $\geq$ 8 copies)

Sensitivity: > 95% PPV: > 99%

Gene Fusions

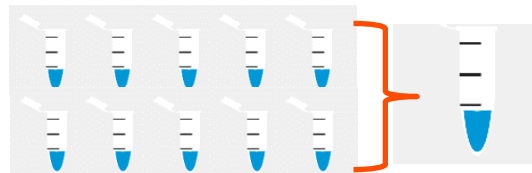
(> 30% tumor content, select introns)

Sensitivity: > 99% PPV: > 99%

Controlled validation studies:

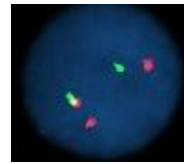
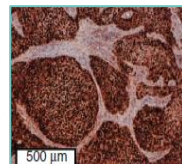
Cell-line pools with known alterations:

- 2,056 subs 227 indels
- 210 CNAs 32 fusions

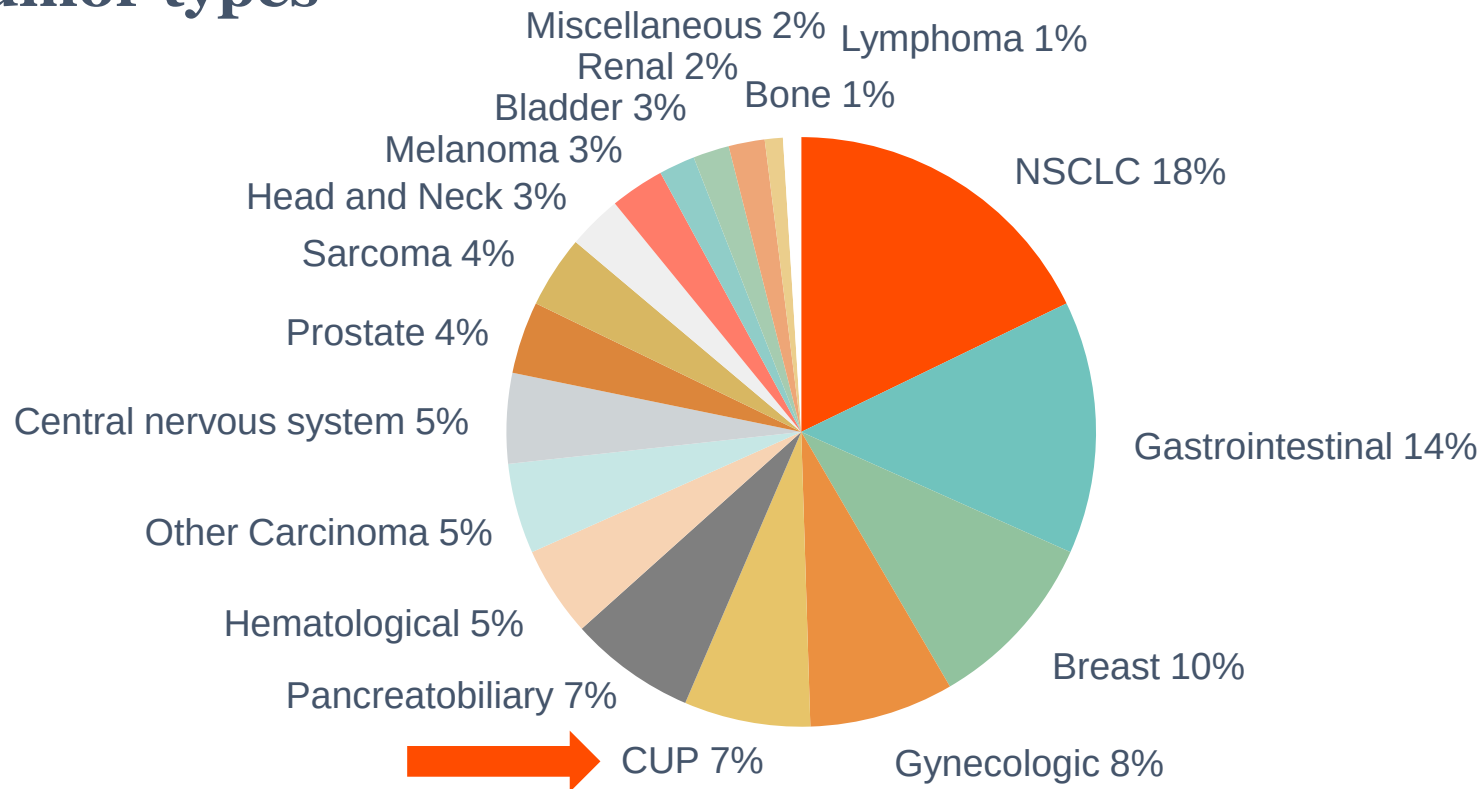


Concordance studies with existing platforms on clinical samples:

- 118 subs/indels: Sequenom, PCR
- 185 CNAs: FISH, IHC
- 43 fusions: break-apart FISH



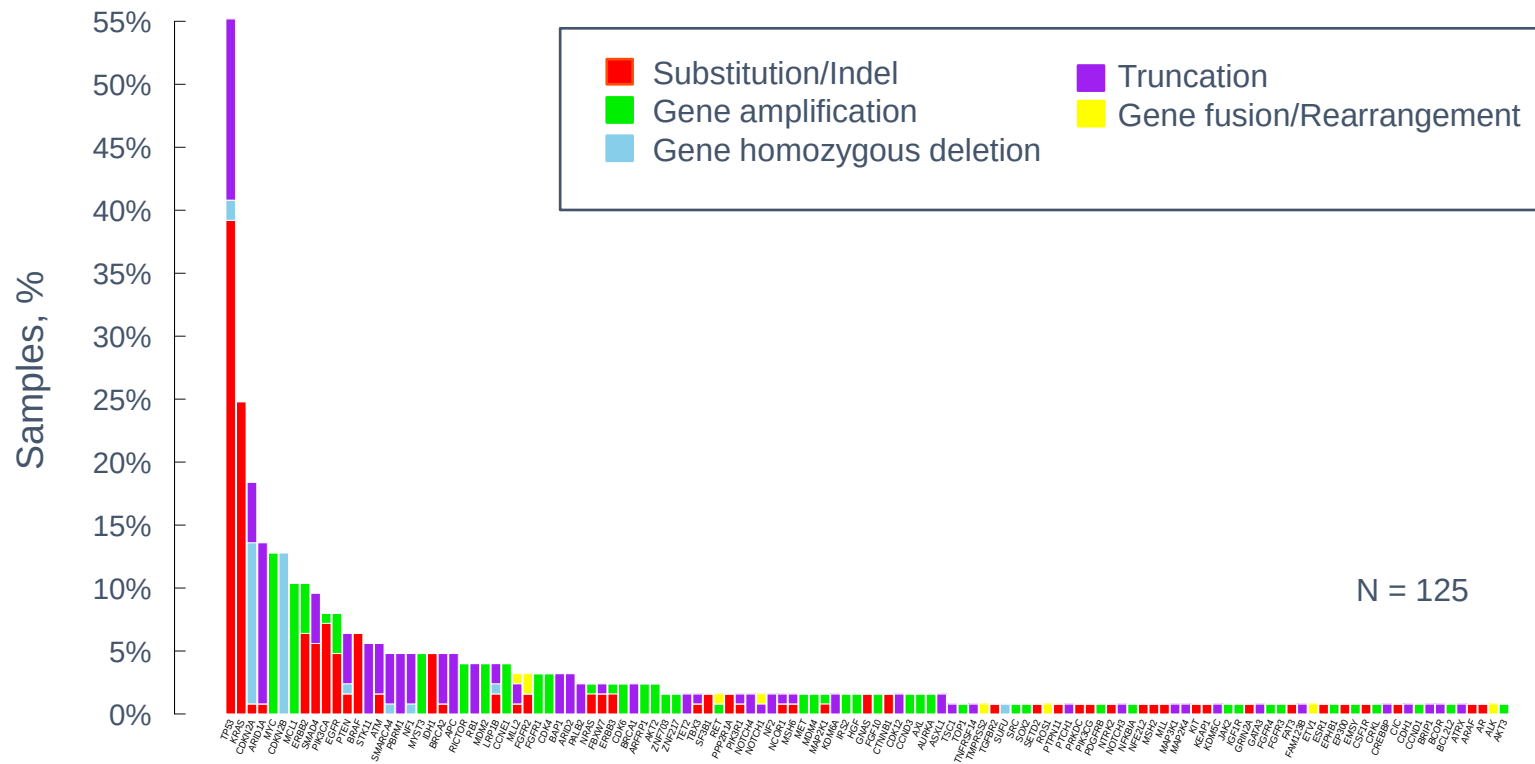
Foundation Medicine has experience across all solid tumor types



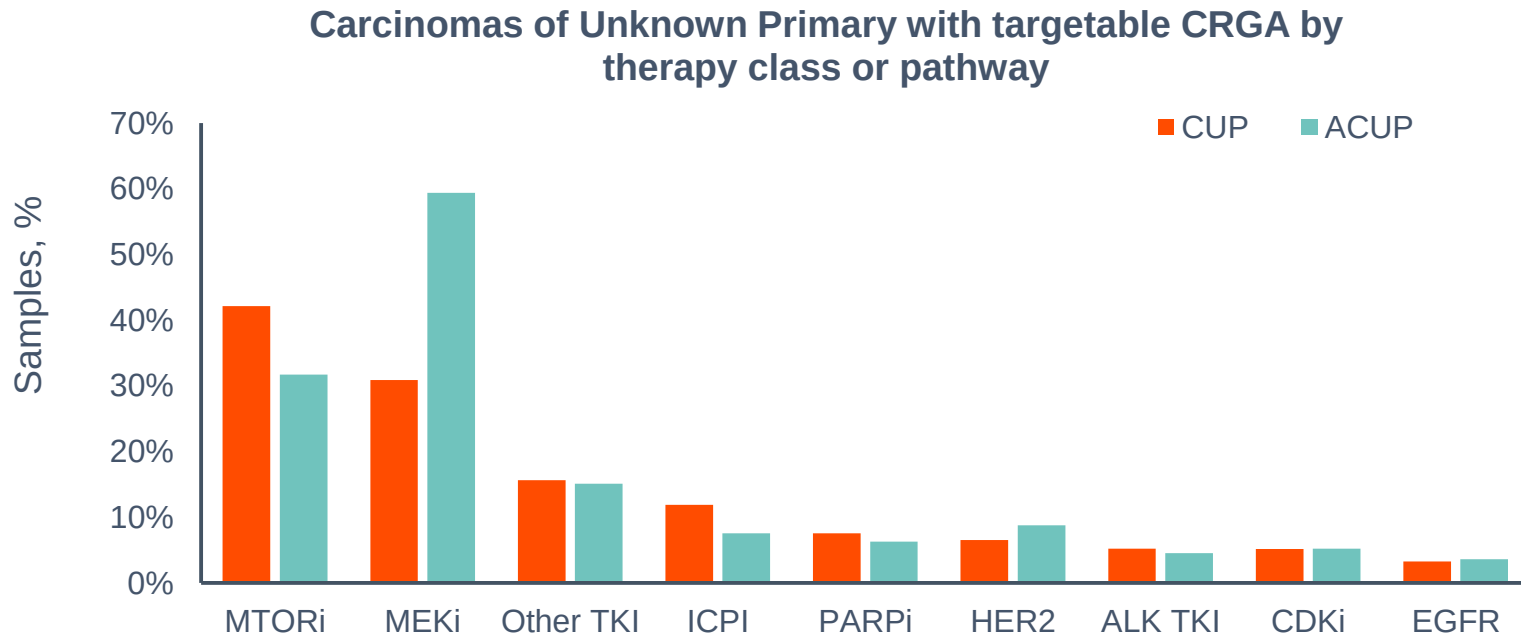
Of 200 cases of CUP, 96% harbored at least one genomic alteration

	ACUP	Non-ACUP
Sample	125	75
Total genomic alterations (GA)	494	347
GA/sample, mean	4.0	4.6
Base substitutions	250 (51%)	151 (44%)
Short insertions and deletions (Indels)	74 (15%)	66 (19%)
Amplifications	119 (24%)	98 (28%)
Homozygous deletions	39 (8%)	27 (8%)
Re-arrangements	12 (2%)	5 (1%)
Samples with no GA detected	0	8

High diversity of genomic alterations and a “long tail” distribution observed across ACUP samples



Most CUP or ACUP samples harbor targetable alterations





Tumor mutational burden (TMB) can help predict benefit from immune checkpoint inhibitors

- Indication of pembrolizumab ▼ for the treatment of patients with unresectable or metastatic solid tumors possessing a microsatellite instability-high (MSI-H) biomarker is the first tissue/site-agnostic approval by the FDA¹
- FoundationOne® TMB high result will detect all MSI-high CUP cases as well as approximately 20-30% more cases where the patients are thus predicted to have a likely long term durable benefit from ICPI therapies²
- CUP in general features a high frequency of TMB high with over 10% of cases featuring ≥ 20 mutations per megabase similar to that seen in NSCLC (not as high as melanoma but higher than bladder cancer)²

1. FDA news release (2017) retrieved from: <https://www.fda.gov/NewsEvents/Newsroom/PressAnnouncements/ucm560167.htm>.

2. FMI data on file.

Therapies marked with ▼ are subject to additional monitoring. Reporting suspected adverse reactions after authorisation of the medicinal product is important. Adverse events should be reported to your local Merck Sharp & Dohme Limited office.

CUP incidence and survival

Latest data from Switzerland

Prof. Holger Moch, MD

University Hospital Zurich, Switzerland

Disclosures

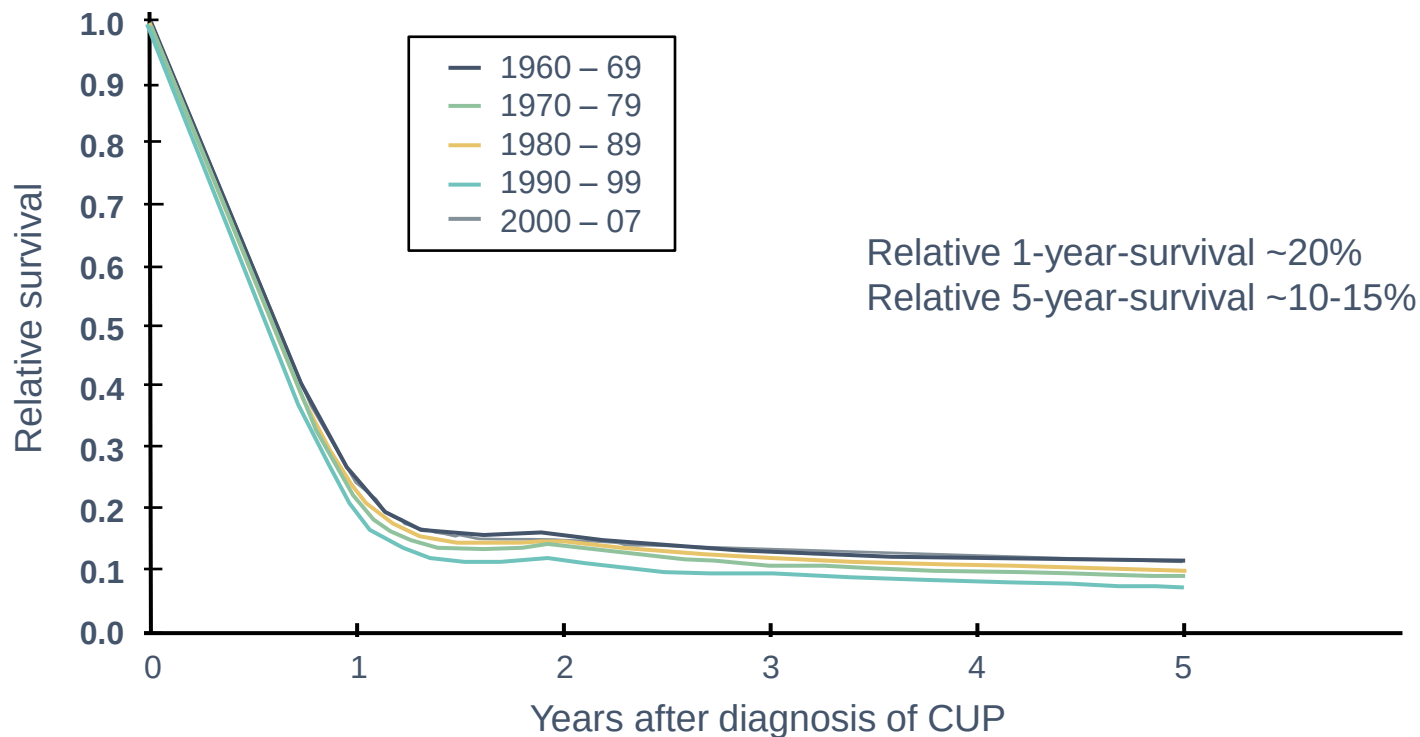
Prof. Moch has received research grants from Roche and Pfizer, as well as honoraria for lectures or advisory board participation or consulting from Roche, and Astra Zeneca



CUP incidence and survival trends in Zurich, Switzerland

- 2,946 CUP patients from 1981 - 2014 (Cancer Registry Zurich)
- Age-standardized incidence:
 - 1981 and 1997: Increase from 10.5 to 17.6 / 100,000
 - 1998 - 2014: Decrease to 5.9 / 100,000
- Mean overall survival:
 - stable at 11.5 months (median 2.3 months)

Survival has not improved in the last 40 years in Disseminated Adeno- or Undifferentiated CUP



Immunohistochemistry work-up in CUP patients



	CK	PSA	ER, PgR	CDX2+, CK20+, CK7-	TTF1, NapsinA, CK7+	Tg, CT	NSE, CG, SNP	AFP, OCT4, hCG, PLAP	LCA	S100, HMB45	Vimentin, Desmin
Undifferentiated carcinoma	+	-	±	-	-	-	-	-	-	-	±
Prostate cancer	+	+	-	-	-	-	-	-	-	-	-
Breast cancer	+	-	±	-	-	-	-	-	-	-	±
Colorectal cancer	+	-	-	+	-	-	-	-	-	-	-
Lung adenocarcinoma	+	-	-	-	+	-	-	-	-	-	-
Thyroid cancer	+	-	-	-	±	+	±	-	-	-	-
Neuroendocrine	+	-	-	-	±	±	+	-	-	-	-
Germ-cell cancer	+	-	-	-	-	-	-	+	-	-	±
Lymphoma	-	-	-	-	-	-	-	-	+	-	-
Melanoma	-	-	-	-	-	-	-	-	-	+	±
Sarcoma	-	-	-	-	-	-	-	-	-	±	+

The table shows general staining patterns but exceptions exist, especially for S100 and vimentin. Thyroid and neuroendocrine cancers often positive with CK7 and TTF1 but not with NapsinA. CK, cytokeratin; PSA, prostate specific antigen; ER, oestrogen receptor; PgR, progesterone receptor; TTF1, thyroid transcription factor 1; Tg, thyroglobulin; CT, calcitonin; NSE, neuron-specific enolase; CG, chromogranin; SNP, synaptophysin; AFP, alpha fetoprotein; hCG, human chorionic gonadotropin; PLAP, placental alkaline phosphatase; LCA, leukocyte common antigen.

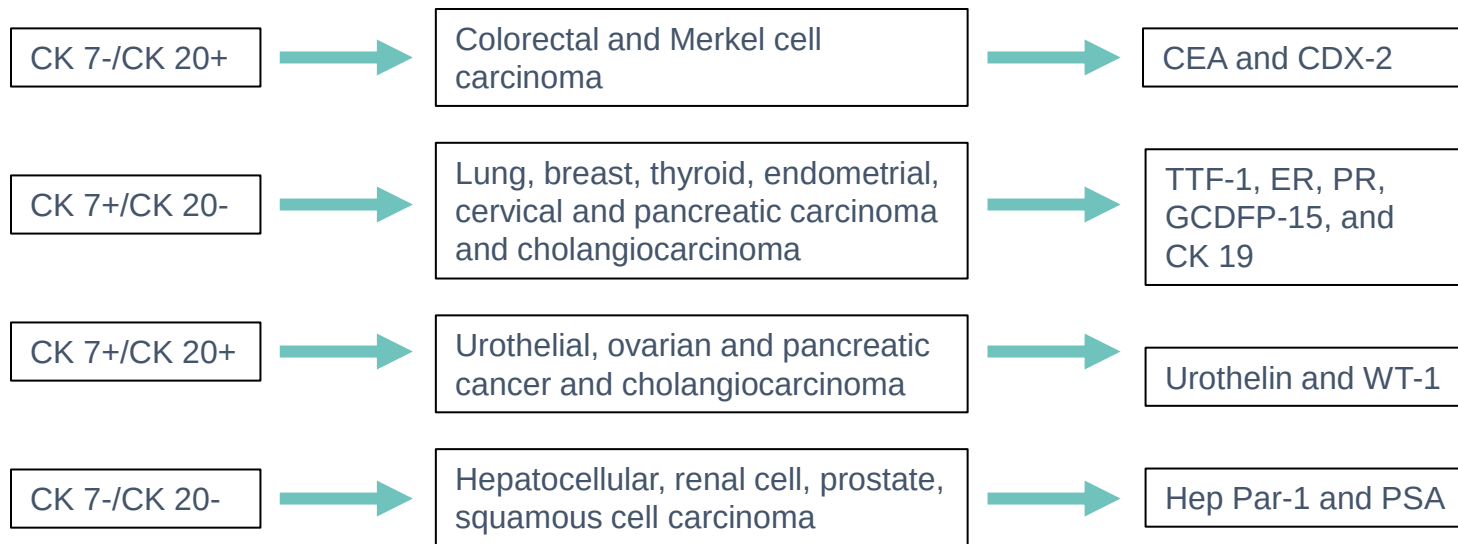
Fizazi, K., et al. (2015) *Ann Oncol* 26(suppl 5):v133-8.

Basic immunohistochemistry work-up of CUP



Primary markers

Additional markers





Tumor board discussion on clinical cases

Dr. Jeffrey S. Ross, MD
Foundation Medicine, Cambridge, MA USA



Clinical case 1

Dr. Jeffrey S. Ross, MD

Foundation Medicine, Cambridge, MA USA

Clinical case 1

Patient medical background



Medical background

- A 53-year old Caucasian female
 - No history of smoking
 - 3-week history of worsening fatigue and severe exertional dyspnea
-

Clinical case 1

Clinical examination



Physical examination

- 3 cm non-tender, hard, subcutaneous, proximal right upper extremity mass with erythematous overlying skin
- 1 cm non-tender, subcutaneous nodule in the left parietal area of the scalp

PET and CT imaging

- Multiple metabolically active masses in the right lung; largest mass in the upper lobe measuring 5.8 x 5.0 cm
- Left lung mass measuring 2.3 x 2.2 cm
- Right hilar and mediastinal lymphadenopathy and subcarinal lymphadenopathy noted
- Extrathoracic, metabolically active lesions noted, including masses in the celiac nodal basin and the anterior right upper arm

Clinical case 1

Laboratory assessment results



Immunohistochemical staining

Positive

Negative

Vimentin

TTF1, Napsin A, AE1/AE3, CK5, CK6, CK7, CAM5.2, and mCEA

Morphologic examination of the biopsy from the right upper extremity mass

Malignant neoplasm of unknown histogenesis

Overall results

Lung origin of tumor could not be confirmed



Based on the initial investigation and laboratory results, what would you advise?

Foundation Medicine report results



FOUNDATIONONE™

Patient Name
 Report Date

Tumor Type
 Unknown primary
 malignant
 neoplasm (NOS)

Date of Birth	Medical Facility	Specimen Received
Sex	Ordering Physician	Specimen Site
FMI Case #	Additional Recipient	Date of Collection
Medical Record #	Medical Facility ID #	Specimen Type
Specimen ID	Pathologist	

ABOUT THE TEST:
 FoundationOne™ is a next-generation sequencing (NGS) based assay that identifies genomic alterations within hundreds of cancer-related genes.

PATIENT RESULTS

3 genomic alterations

1 therapy associated with potential clinical benefit

0 therapies associated with lack of response

6 clinical trials

TUMOR TYPE: UNKNOWN PRIMARY MALIGNANT NEOPLASM (NOS)

Genomic Alterations Identified†
 ALK EML4-ALK fusion
 MCL1 amplification – equivocal‡
 CDKN2A/B loss

†For a complete list of the genes assayed, please refer to the Appendix
 ‡See Appendix for details

THERAPEUTIC IMPLICATIONS

Genomic Alterations Detected	FDA Approved Therapies (in patient's tumor type)	FDA Approved Therapies (in another tumor type)	Potential Clinical Trials
ALK EML4-ALK fusion	None	Crizotinib	Yes, see clinical trials section
MCL1 amplification - equivocal	None	None	Yes, see clinical trials section
CDKN2A/B loss	None	None	Yes, see clinical trials section

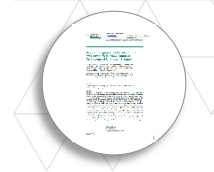




After seeing the Foundation Medicine report results, would you change your treatment strategy?

Clinical case 1

Medical decision



Medical decision

**Crizotinib ▼
(250 mg orally twice daily)**

Reason given

Presence of the EML4-ALK rearrangement,
a known oncogenic driver in a subset of
pulmonary adenocarcinomas

Palma, N.A., et al. (2014) *Case Rep Oncol* 7:503-8.

Therapies marked with ▼ are subject to additional monitoring. Reporting suspected adverse reactions after authorisation of the medicinal product is important. Adverse events should be reported to your local Pfizer Limited office.

Clinical case 1

Therapy results and follow up – CT scan



Pre-treatment



+ 1 month



Computed tomography (CT) scan of the chest before starting crizotinib ▼ and 1 month after starting crizotinib ▼, respectively.

Chung, J.H., et al. (2014) *Case Rep Oncol* 7:628-32.

Therapies marked with ▼ are subject to additional monitoring. Reporting suspected adverse reactions after authorisation of the medicinal product is important. Adverse events should be reported to your local Pfizer Limited office.

Clinical case 2

Dr. Jeffrey S. Ross, MD

Foundation Medicine, Cambridge, MA USA



Clinical case 2

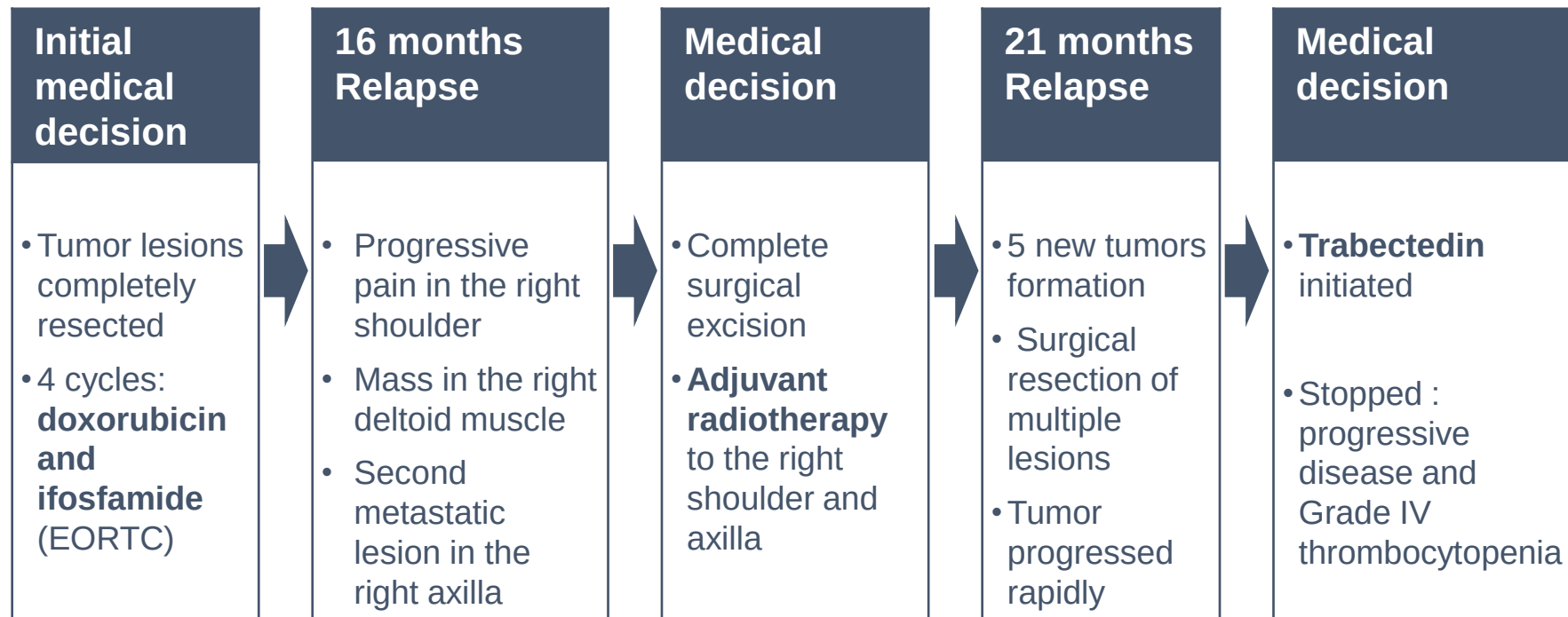
Patient medical background and initial medical investigation



Medical background	Biology	Preliminary diagnosis
44-year-old Caucasian female with metastatic cancer of unknown primary (CUP) Diagnosed with multiple metastatic lesions in the mesentery of the small intestines and the duodenojejunal flexure	Histopathology analyses were inconclusive • High-grade neoplasm with pleomorphic tumor • Positive for vimentin • ~30% of the tumor cells: MIB-1 positive	CUP with sarcomatoid features

Clinical case 2

Patient follow up





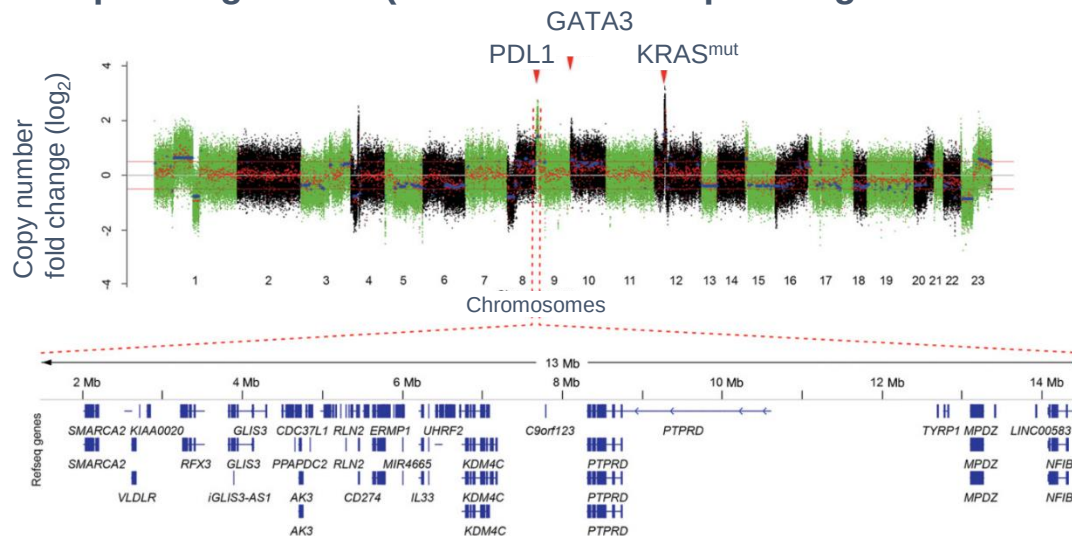
Based on the patient status, what would you advise?

Clinical case 2

Molecular profiling

Enrollment in MASTER (Molecularly Aided Stratification for Tumor Eradication Research), a cross-entity molecular stratification program for advanced-stage cancer and patients with rare tumors (Kordes et al. 2016)

Molecular profiling results (Whole-exome sequencing and RNA-sequencing)





After seeing the profiling results, would you change your treatment strategy?

Clinical case 2

Medical decision



Rationale

- Amplification and overexpression of PDL1
- Hypermutated tumor genome



Medical decision

ICI treatment with the anti-PD1 monoclonal antibody
pembrolizumab ▼



Therapy selected 24 months after initial diagnosis

Pembrolizumab ▼
2 mg/kg
3 week cycles

Gröschel, S., et al. (2016) *Cold Spring Harb Mol Case Stud* 2: a001180.

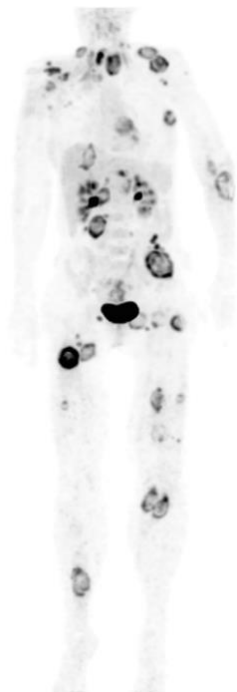
Therapies marked with ▼ are subject to additional monitoring. Reporting suspected adverse reactions after authorisation of the medicinal product is important. Adverse events should be reported to your local Merck Sharp & Dohme office.

Clinical case 2

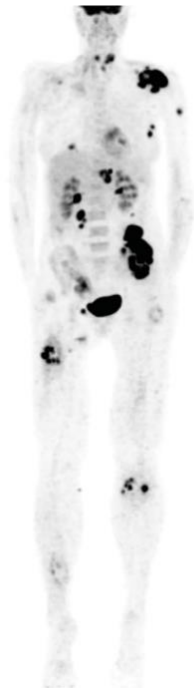
Follow up: PET/CT scans



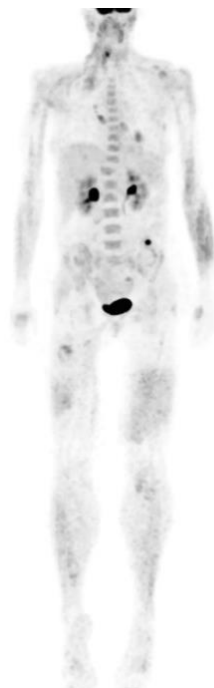
Baseline



+2 months



+6 months



6 months follow up

- Near-complete remission
- Response Evaluation Criteria In Solid Tumors: very good partial remission

14 months follow up

- Remained in continuous **near-complete remission**
- **Free of disease-specific symptoms**



Genomic profiling study for patients with cancers of unknown primary

Prof. Alwin Krämer, MD

University of Heidelberg, Germany

Genomic profiling study for patients with CUP

Rationale



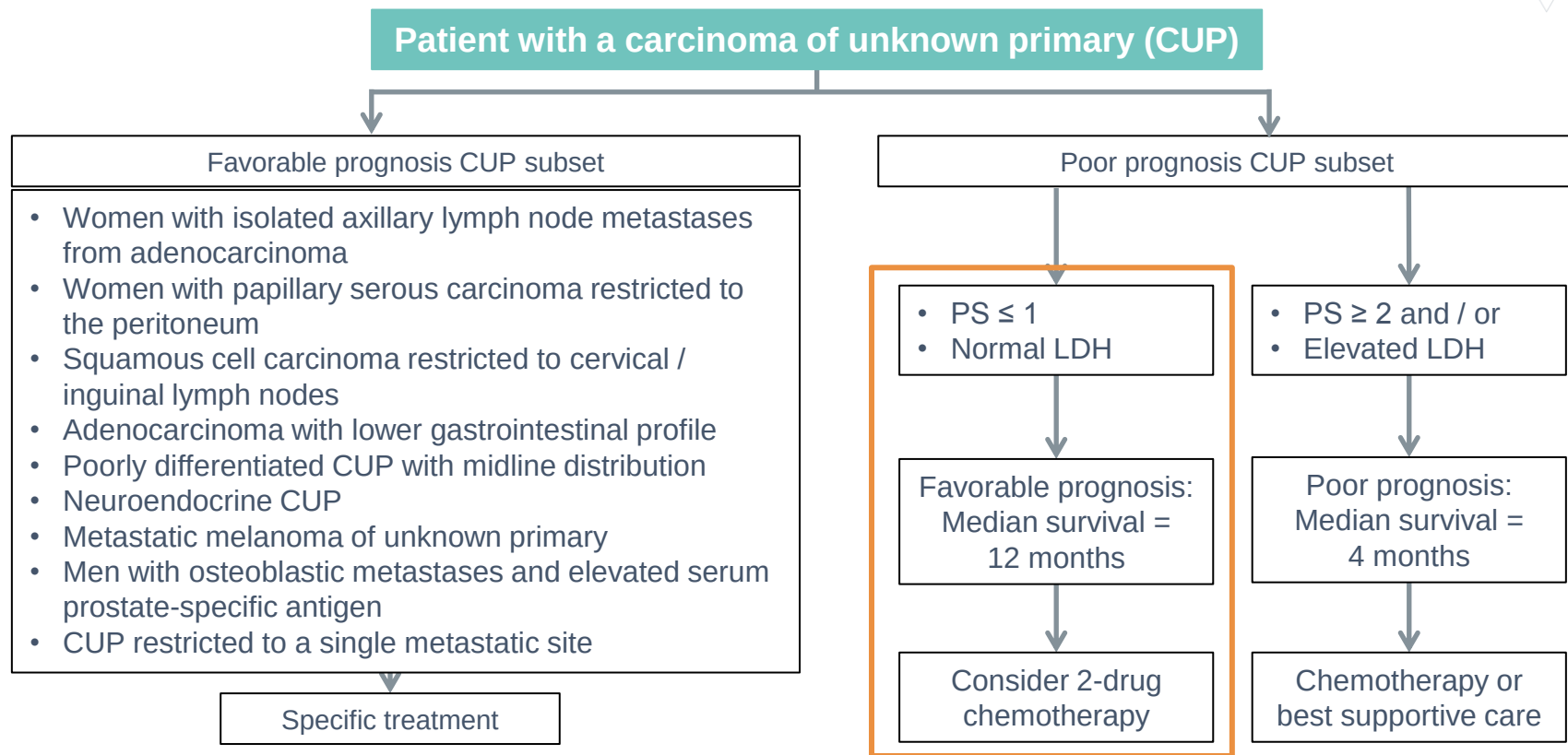
- Current diagnostics can help to identify patients with CUP who have a favourable prognosis
- Treatment options are limited in poor prognosis patients with CUP
- Comprehensive genomic profiling has the potential to identify new treatment options without the need to know the primary tumor site
- Checkpoint inhibitor might be effective in CUP similarly to other tumor types
- Majority of CUP samples harbor targetable alterations

Study objective



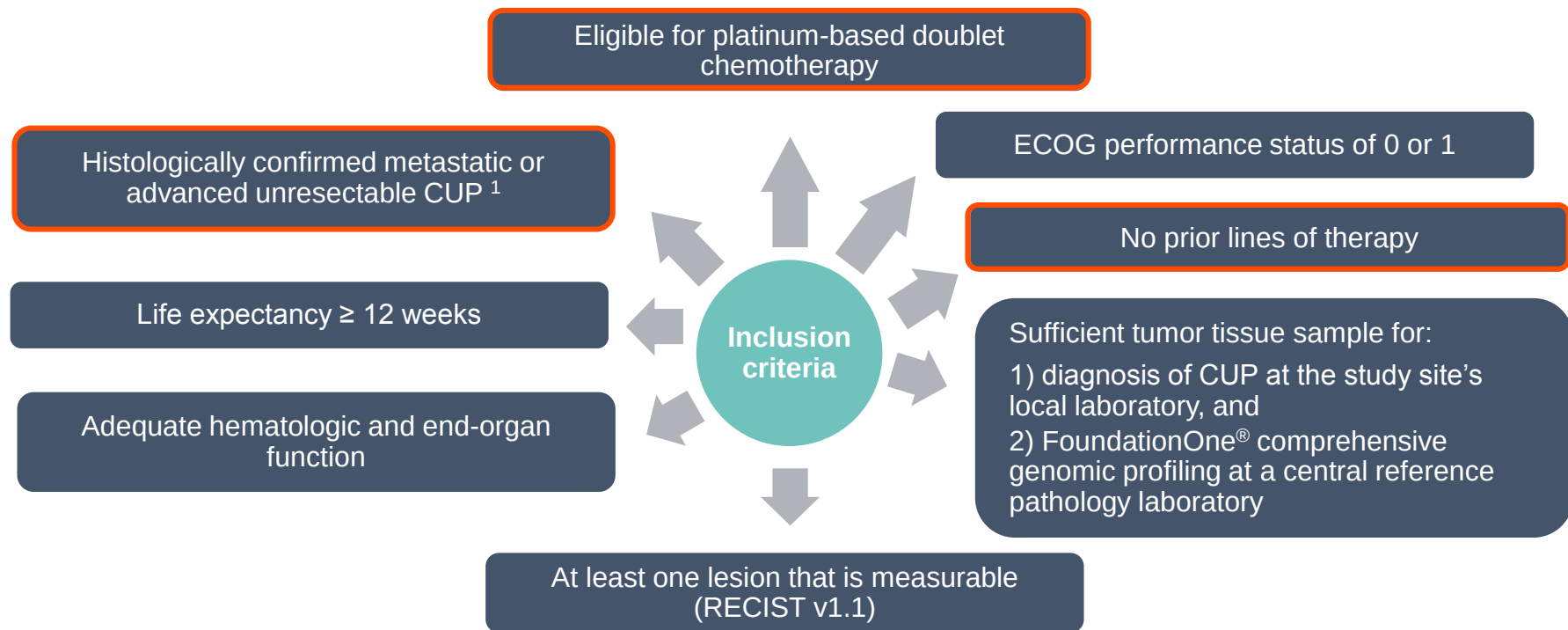
To compare the efficacy and safety of molecularly-guided therapy versus standard platinum-containing chemotherapy in patients with cancer of unknown primary site

Study target population



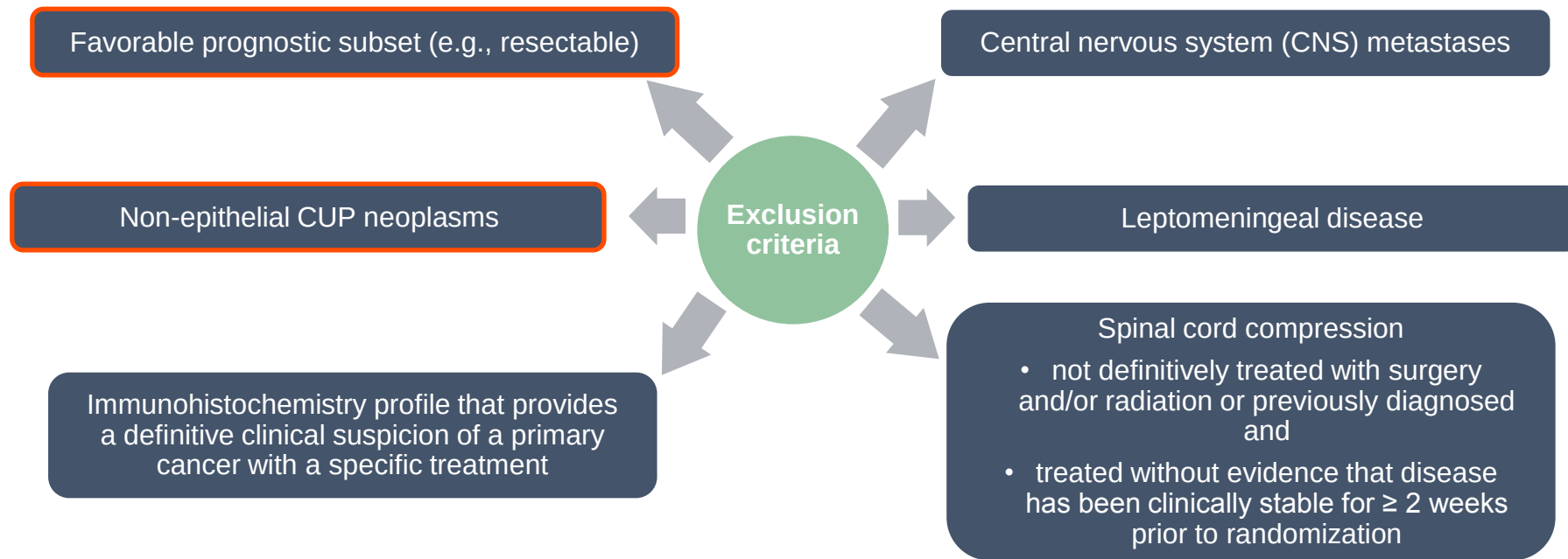
Selected inclusion criteria for the CUP profiling study

Preliminary design



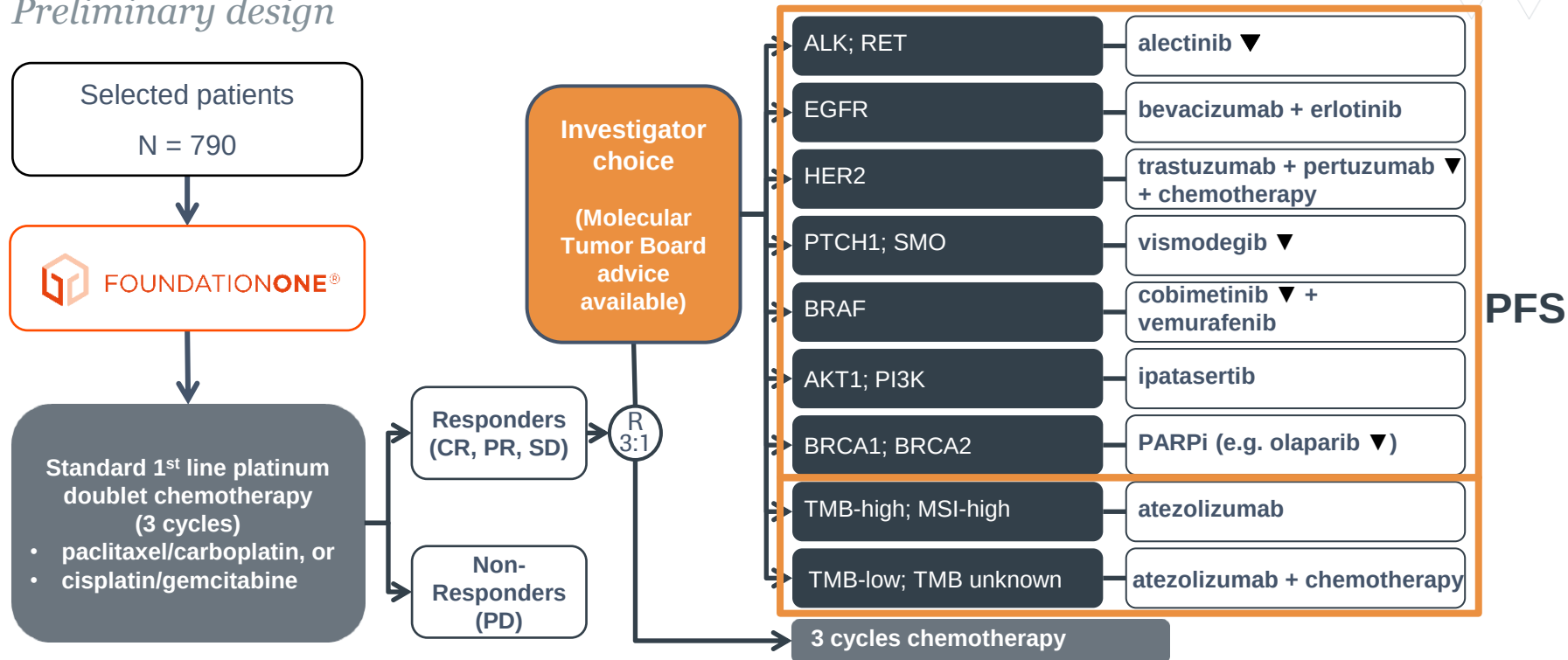
Selected exclusion criteria for the CUP profiling study

Preliminary design



Genomic profiling study for patients with CUP

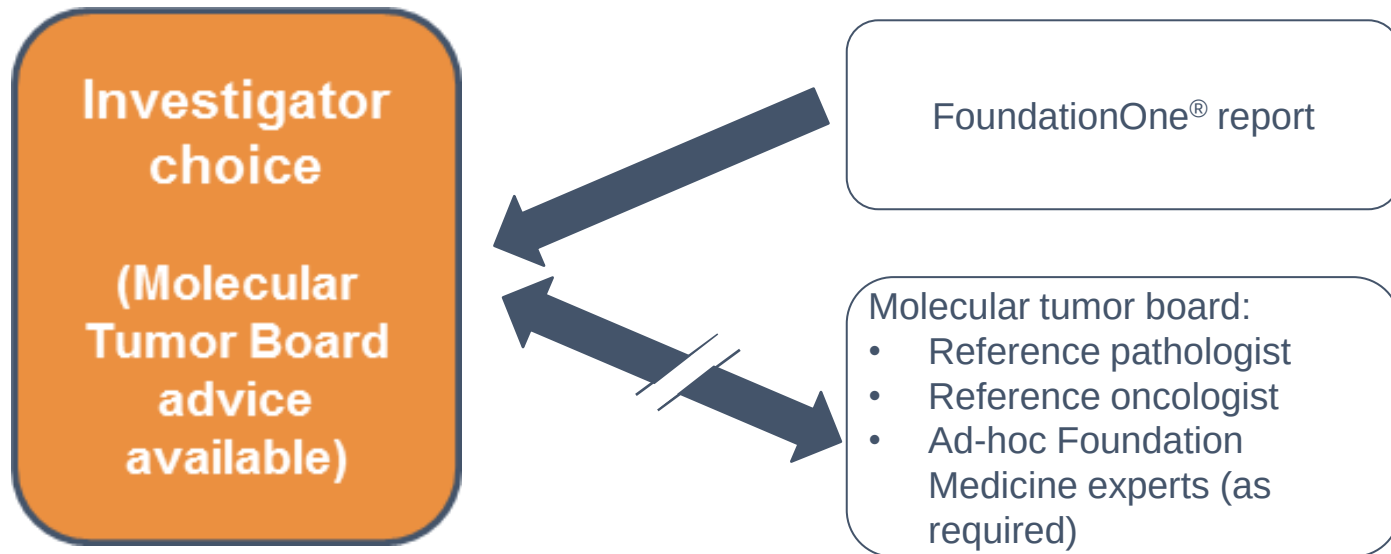
Preliminary design



CR, complete response; PD, progressive disease; PFS, progression-free survival; PR, partial response; SD, stable disease; TMB, tumor mutational burden; MSI: microsatellite instability. Roche data on file, study concept MX39795. Therapies marked with ▼ are subject to additional monitoring. Reporting suspected adverse reactions after authorisation of the medicinal product is important. Adverse events should be reported to your respective local office: AstraZeneca for olaparib; Roche for alectinib, pertuzumab, cobimetinib and vismodegib.

Targeted therapy selection by investigator choice

Preliminary allocation process



A **central molecular tumor board** will be available to **provide advice** on therapy choice and to **ensure consistency** across treatment options

“NAVIFY Tumor Board solution” summarises clinical data for use by molecular tumor board



1. Collect

Gather medical records across specialties



2. Coordinate

Schedule tumor board meetings



3. Prepare

Create presentation of patient data



4. Conduct

Support patient case discussion

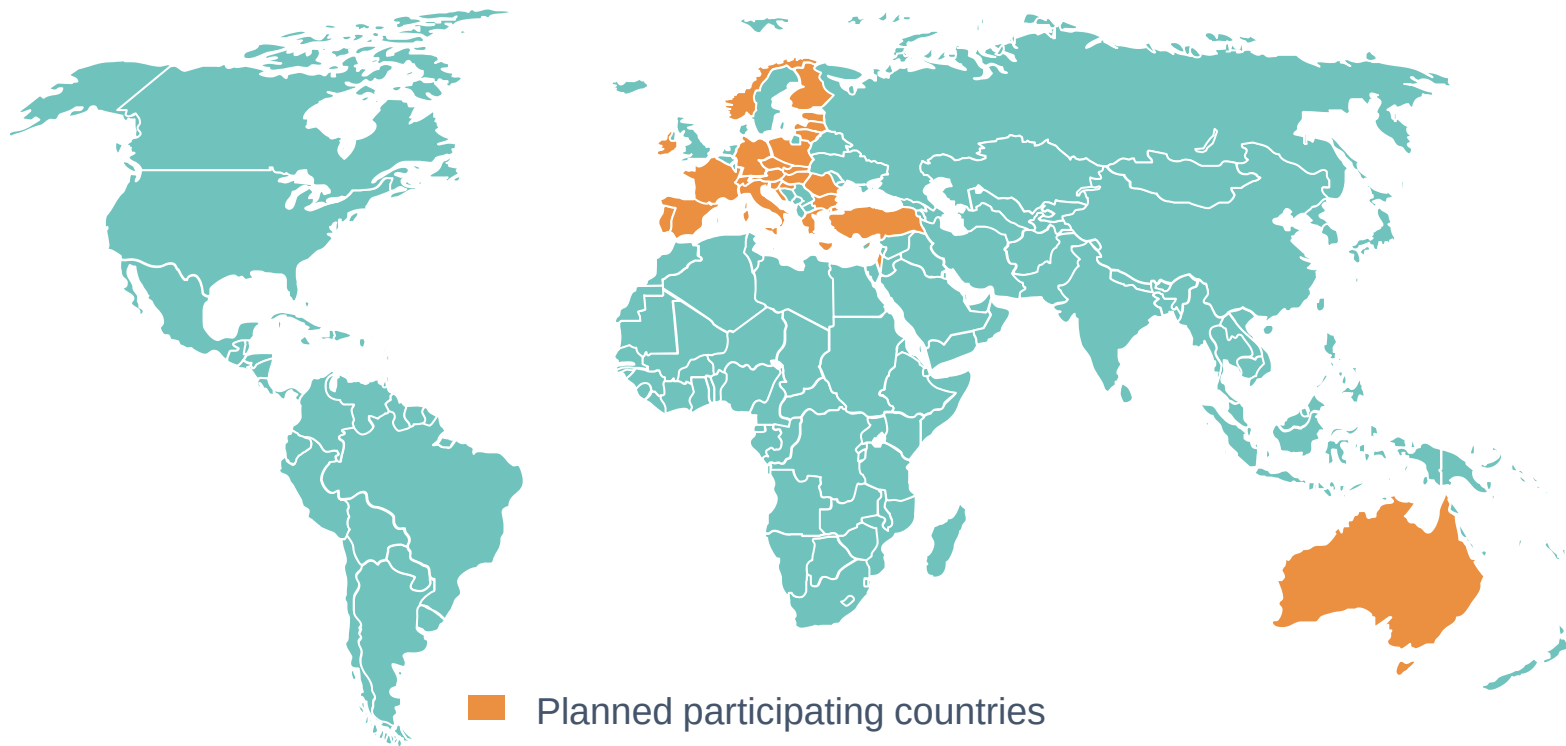


5. Next Steps

Capture and document treatment plan decisions

- For software demonstration, please visit the Roche booth (Hall 7)

Study set-up initiated: 80+ sites planned in 20+ countries



Meeting closure

Prof. Alwin Krämer, MD

University of Heidelberg, Germany





Conclusions

- The ESMO guideline recommends low-toxicity palliative chemotherapy for poor-prognosis CUP patients
- Comprehensive genomic profiling can detect targetable genomic alterations in CUP samples
- The presented genomic profiling CUP study will evaluate the efficacy of molecularly guided therapy versus platinum chemotherapy

Doing now what patients need next