

15<sup>th</sup> MADRID  
on **Lung** CONGRESS  
CANCER  
23&24  
November 2023

#15CongressGECp

**DUAL USE OF MALIGNANT EFFUSIONS FOR  
GENOTYPING AND DRUG SCREENING IN  
PERSONALIZED THERAPY OF LUNG CANCER PATIENTS**

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## DISCLOSURES

I do not have any financial relationships to disclose

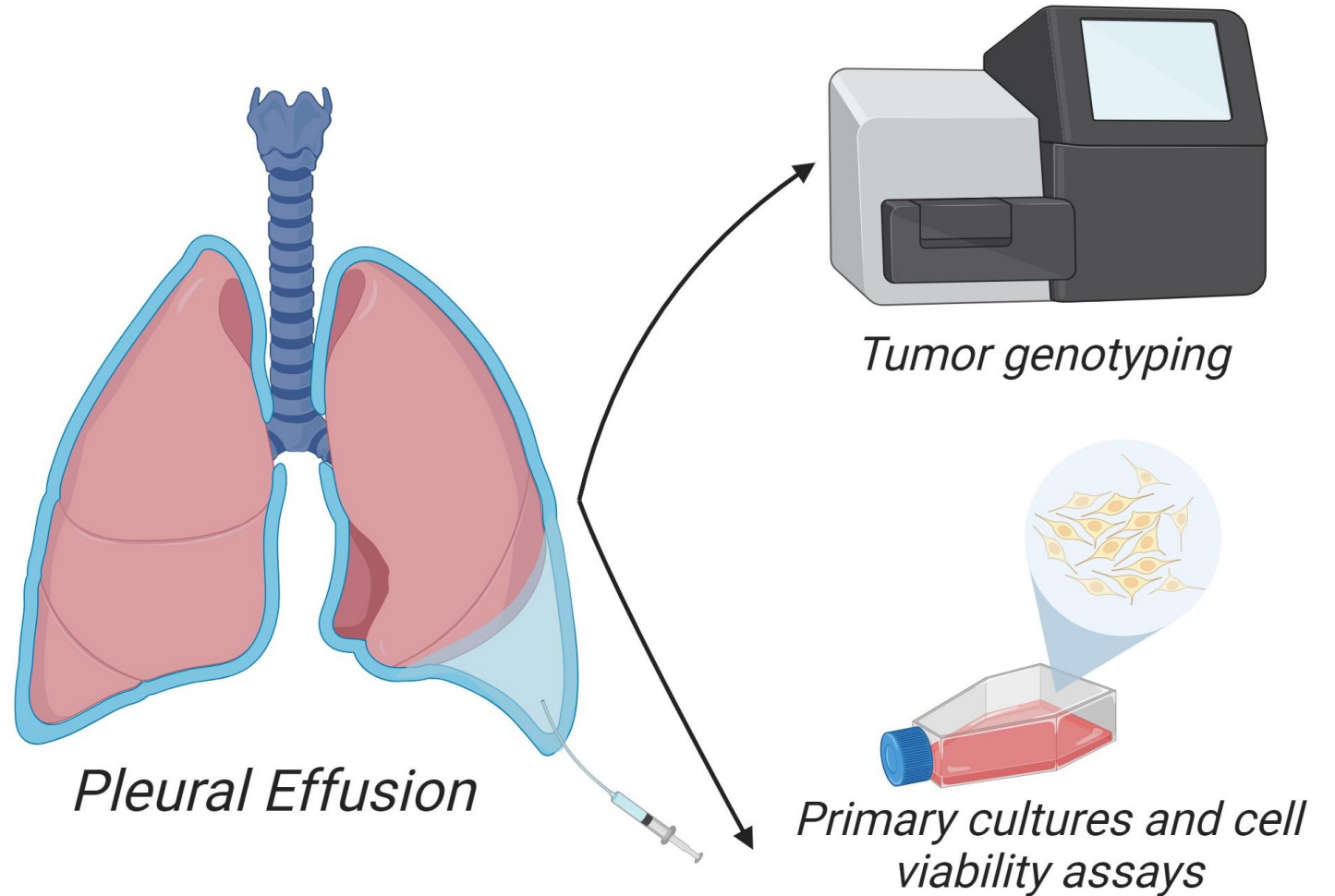


## BACKGROUND

Malignant effusions (ME's) are a good source for genetic testing in lung cancer patients



Results from MEs could be used for treatment decision





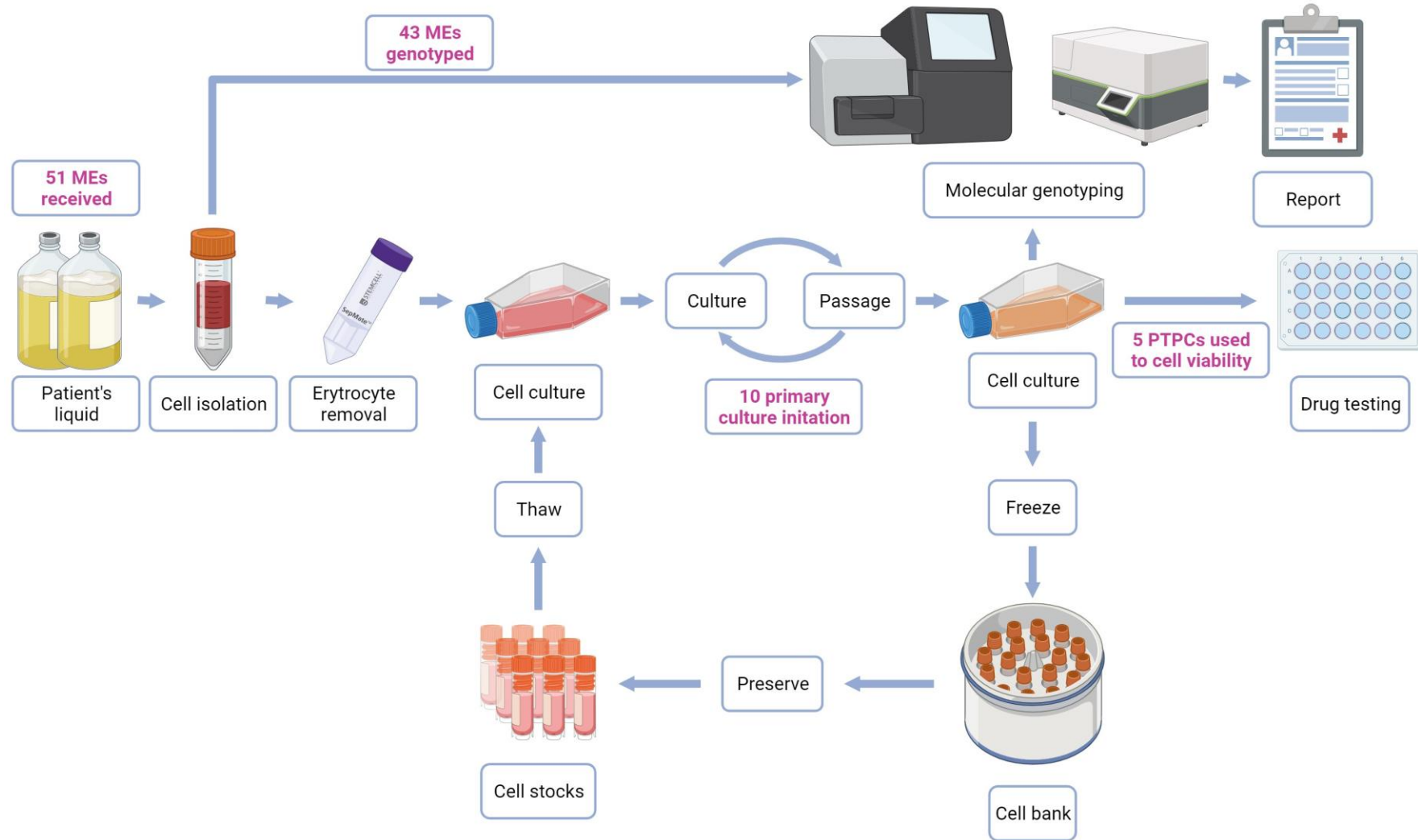
## OBJECTIVES

- Incorporate MEs collection into the routine clinical practice for:
  - Determination of relevant genetic alterations
  - Initiation of primary cultures and cell viability assays with anticancer drugs



# METHODS

Volumes of MEs ranged from 5 to 5,000 mL



PTPCs: Pure Tumor Primary Cultures

Data cut off May 2023



## CHARACTERISTICS OF THE MEs GENOTYPED AND CULTURED

Fluid Characteristics	Total of samples n=43	PTPCs n=10
<b>Type of fluid</b>		
Pleural effusion (MPE)	40 (93 %)	10 (100.0 %)
Ascites	3 (7 %)	0 (0.0 %)
<b>Cytology (presence of tumor cells)</b>		
Positive	6 (14.0 %)	3 (30 %)
Negative	0 (0.0 %)	0 (0.0 %)
ND	37 (86.0%)	7 (70.0 %)
<b>Histology</b>		
Adenocarcinoma	42 (97.7 %)	10 (100.0 %)
Squamous Cell Carcinoma	1 (2.3 %)	0 (0.0 %)
<b>Paired blood or FFPE samples</b>		
Yes	10 (23.3 %)	7 (70.0 %)
No	33 (76.7 %)	3 (30 %)
<b>Collection time</b>		
Baseline	17 (39.5 %)	5 (50.0 %)
Progression	17 (39.5 %)	4 (40.0 %)
ND	9 (20.9 %)	1 (10.0 %)
<b>Clinically relevant alterations</b>		
Detected	38 (88.4 %)	9 (90.0 %)
Not detected	5 (11.6 %)	1 (10.0 %)



# MEs GENOTYPING





# GENOTYPE OF THE MEs (I)

Most common alterations detected, mutations in *TP53* (n=23); *EGFR* (n=13); *KRAS* (n=10)

Alterations	Gene	PO-1	PO-2	PO-3	PO-4	PO-5	PO-6	PO-7	PO-8	PO-9	PO-10	PO-11	PO-12	PO-13	PO-14	PO-15	PO-16	PO-17	PO-18	PO-19	PO-20	PO-21	PO-22	PO-23	PO-24	PO-25	PO-26	PO-27	PO-28	PO-29	PO-30	PO-31	PO-32	PO-33	PO-34	PO-35	PO-36	PO-37	PO-38	PO-39	PO-40	PO-41	PO-42	PO-43															
Mutations	KRAS																																																										
	EGFR																																																										
	BRAF																																																										
	TP53																																																										
	ARID1																																																										
	STK11																																																										
	FAT1																																																										
	MET																																																										
	FGFR1																																																										
	RET																																																										
	KEAP1																																																										
	PIK3CA																																																										
	POLE																																																										
	ERBB4																																																										
	SETD2																																																										
Fusions	EML4-ALK:E6:A20																																																										
	SDC4-ROS1:S2:R32																																																										
Amplifications	MET																																																										
	MYC																																																										
	BRAF																																																										
	NRAS																																																										
	EGFR																																																										
	CDK4																																																										

In red tissue and MEs paired samples





## GENOTYPE OF THE MEs (II)

	Alterations in tissue	Alterations in MEs
PO-10	<i>BRAF</i> p.V600E; <i>TP53</i> c.97-2A>T	<i>BRAF</i> p.V600E; <i>TP53</i> c.97-2A>T
PO-16	<i>TP53</i> p.G266E	<i>TP53</i> p.G266E
PO-17	<i>FAT1</i> p.D4244E; <i>FGFR1</i> c.936+86G>C; <i>KEAP1</i> p.G571V; <i>TP53</i> p.G266R and p.E68; amp <i>FGFR1</i>	<i>FAT1</i> p.D4244E; <i>FGFR1</i> c.936+86G>C; <i>KEAP1</i> p.G571V; <i>TP53</i> p.G266R and p.E68; amp <i>FGFR1</i>
PO-19	<i>KRAS</i> p.G12C; <i>TP53</i> p.V157F	<i>KRAS</i> p.G12C; <i>TP53</i> p.V157F
PO-23	<i>KRAS</i> p.G12D; <i>MET</i> p.H1174Y; <i>TP53</i> p.G245C	<i>KRAS</i> p.G12D; <i>MET</i> p.H1174Y; <i>TP53</i> p.G245C
PO-26	<i>PIK3CA</i> p.H1047R; <i>TP53</i> p.Y163C	<i>PIK3CA</i> p.H1047R; <i>TP53</i> p.Y163C
PO-27	<i>EGFR</i> p.E746_A750del; <i>FAT1</i> p.G855R; <i>TP53</i> p.C176Y	<i>EGFR</i> p.E746_A750del; <i>FAT1</i> p.G855R; <i>TP53</i> p.C176Y
PO-31	<i>EGFR</i> p.L747_P753delins	<i>EGFR</i> p.L747_P753delins
PO-35	<i>KEAP1</i> [NM_203500.2:g.10486720_10486721insACTC...]; <i>KEAP1</i> [NM_203500.2:g.10486720_10486721insACTC...]; <i>KRAS</i> G12A; <i>STK11</i> E165*	<i>KEAP1</i> [NM_203500.2:g.10486720_10486721insACTC...]; <i>KEAP1</i> [NM_203500.2:g.10486720_10486721insACTC...]; <i>KRAS</i> G12A; <i>STK11</i> E165*
PO-42	<i>EGFR</i> p.E746_A750del; <i>MET</i> p.D1228N; <i>TP53</i> p.C135Y; amp <i>MET</i>	<i>EGFR</i> p.E746_A750del; <i>MET</i> p.D1228N; <i>TP53</i> p.C135Y; amp <i>MET</i>

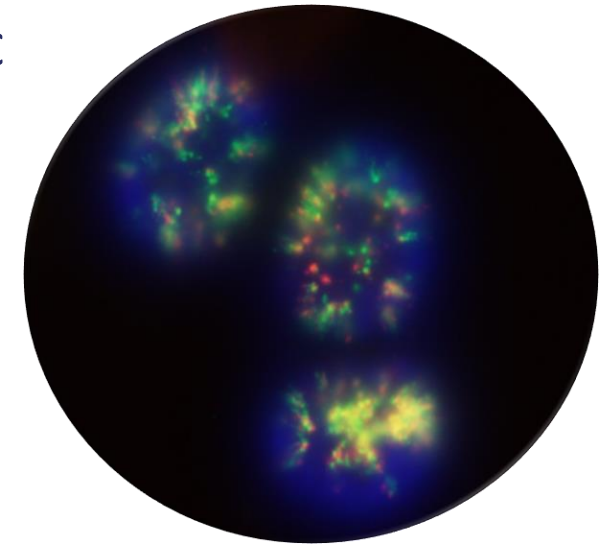
Paired tissue and MEs samples  $\longrightarrow$  100% concordance



# CONCORDANT RESULTS OF PAIRED ME AND PTPC SAMPLES: CASE PO-6

Patient PO-6: Female, 59 y.o, smoker, diagnosed with stage IIIA. Tumor biopsy was not possible. Pleural effusion was collected. PTPC and supernatant were genotyped by NGS showing in both cases a *TP53* mutation and copy number gain in *MYC* (A, B). Additionally, FISH using ZytoLight® SPEC MYC Dual Color Break Apart Probe was performed in viable tumoral cells, further confirming copy number gain of *MYC* gene (C).

C



A

Biomarker	Alteration	Function	Impact	Case - Quantity
<i>MYC</i> 2C Pathogenic	amplification	gain	-	57.92 copies
<i>TP53</i> 2C Pathogenic	c.216delC p.V73fs*50	loss	Frameshift	85% (of 170 reads)

PTPC

B

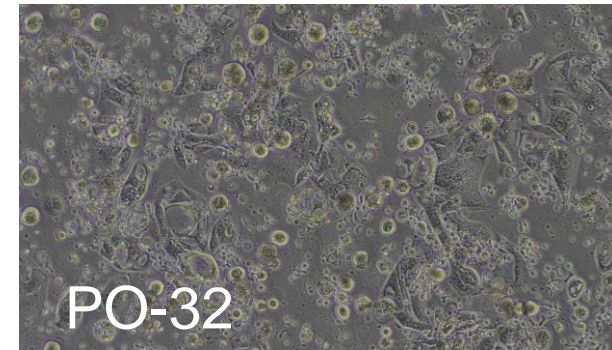
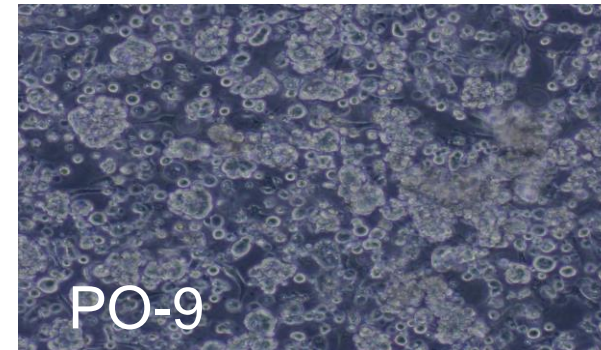
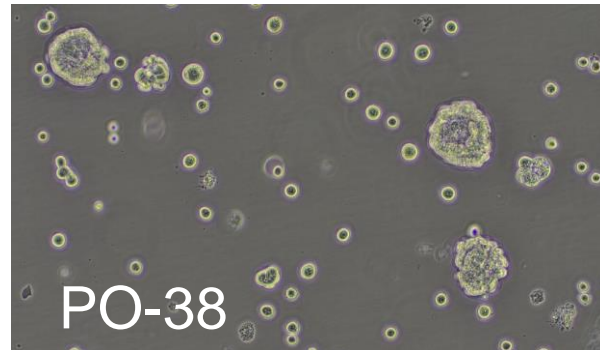
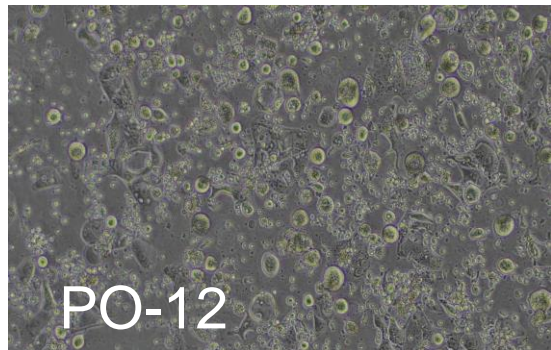
Biomarker	Alteration	Function	Impact	Case - Quantity
<i>MYC</i> 2C Pathogenic	amplification	gain	-	32.70 copies
<i>TP53</i> 2C Pathogenic	c.216delC p.V73fs*50	loss	Frameshift	86% (of 1057 reads)

Fluid supernatant



## PTPCs

Sample	Fluid	Primary tumor	Basal/Progression	Treatment	Alterations
PO-12	Pleural	Lung ADC	Basal		<i>MET</i> polisomy
PO-38	Pleural	Lung ADC	Basal		<i>EGFR</i> p.S768_D770dup
PO-9	Pleural	Lung ADC	Progression	Tepotinib	<i>MET</i> amp <i>MET</i> p.D1228N/H and p.Y1230H
PO-11	Pleural	Lung ADC	Progression	Tepotinib	<i>MET</i> amp; <i>NRAS</i> amp
PO-32	Pleural	Lung ADC	Progression	Osimertinib	<i>EGFR</i> p.L858R

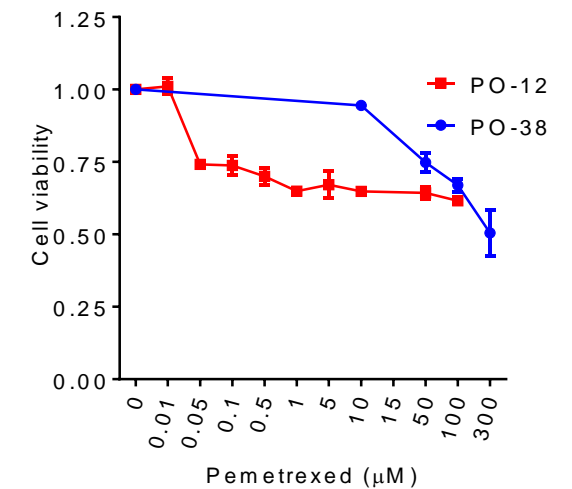
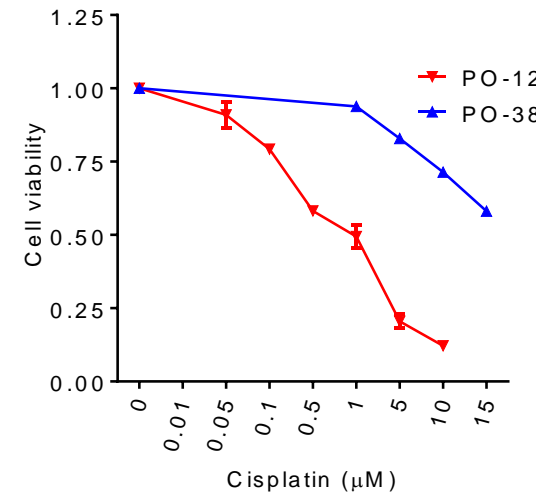




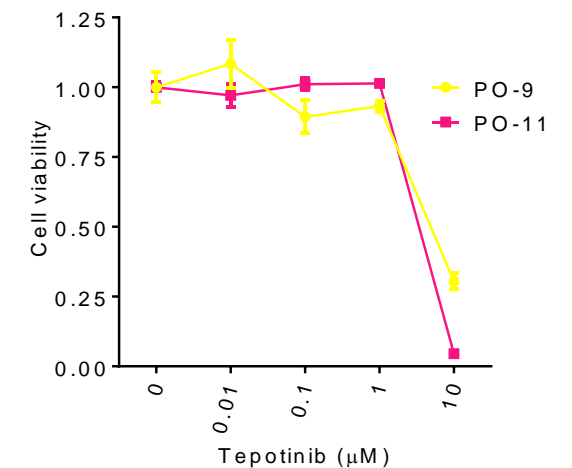
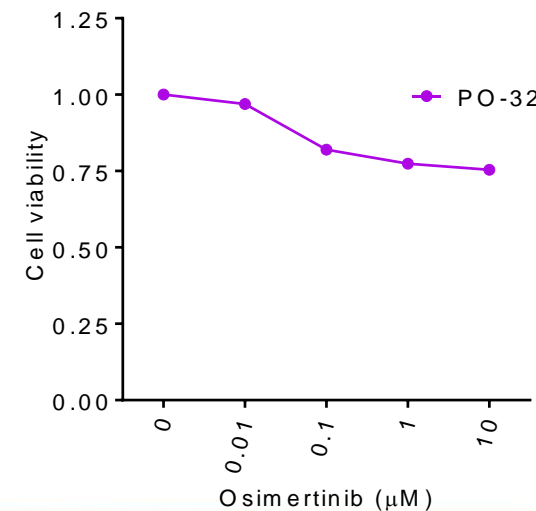
# RESPONSE TO ANTITUMOR DRUGS OF PTPCs

## Baseline PTPCs treated with chemotherapeutic agents

Sample	IC <sub>50</sub> (μM)	Maximum plasmatic concentration (μM)
PO-12	0.8 (cisplatin) > 300.0 (pemetrexed)	14.4 306.0
PO-38	15.0 (cisplatin) 300.0 (pemetrexed)	14.4 306.0
PO-9	4.7 (tepotinib)	0.9
PO-11	4.5 (tepotinib)	0.9
PO-32	> 10 (osimertinib)	0.2

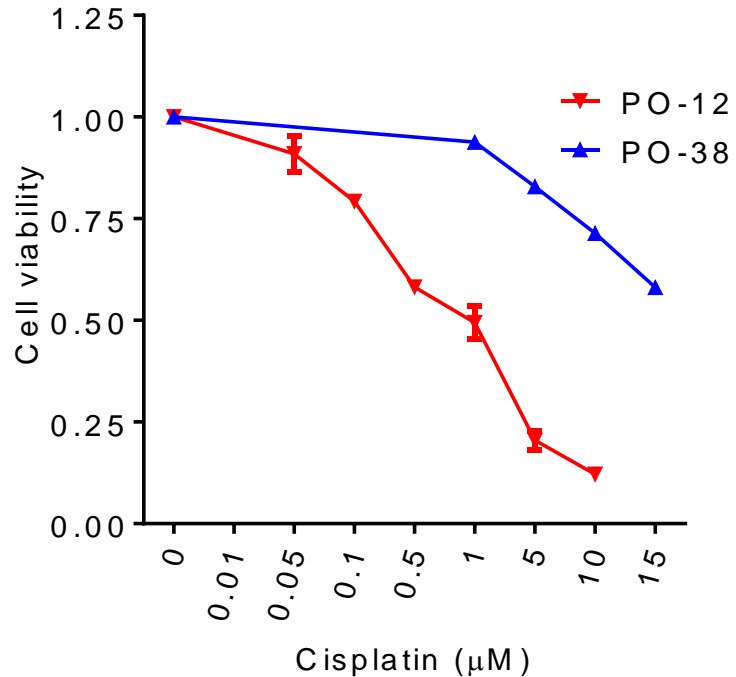


## PTPCs at progression treated with targeted therapies





## PTPCs AS A POSSIBLE TOOL IN TREATMENT SELECTION (I)



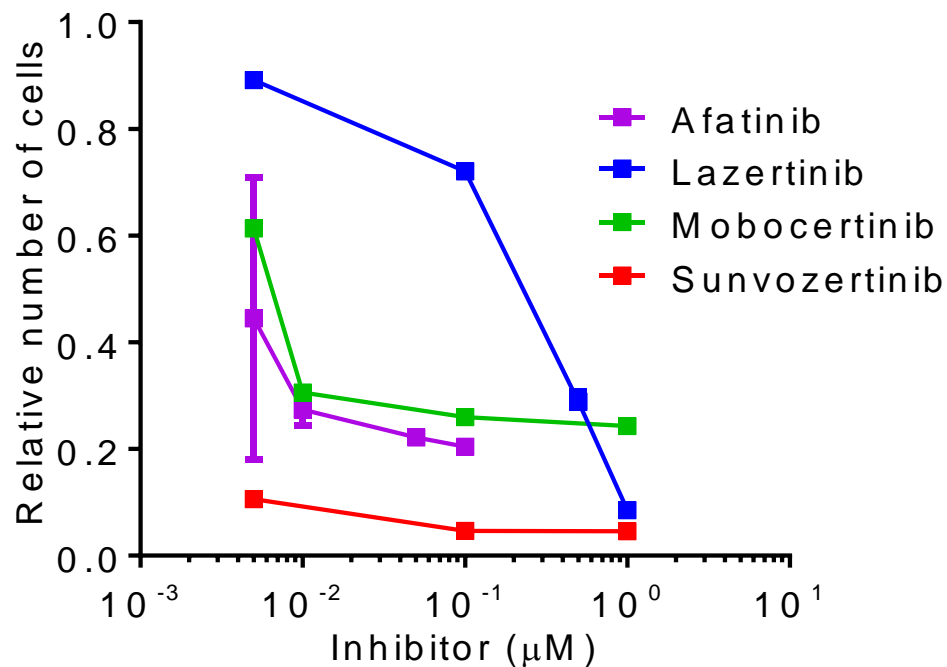
Patient PO-12, partial response to platin-based chemotherapy

Patient PO-38, stable disease to platin-based chemotherapy



## PTPCs AS A POSSIBLE TOOL IN TREATMENT SELECTION (II)

Patient PO-38: Female, 67 y/o, non-smoker, diagnosed with stage IV NSCLC. Pleural effusion was genotyped and cultured showing *EGFR* p.S768\_D770dup and CDK4 amplification.



	IC <sub>50</sub> (μM)
<b>Afatinib</b>	< 0.005
<b>Lazertinib</b>	0.300
<b>Mobocertinib</b>	0.007
<b>Sunvozertinib</b>	< 0.005



## CONCLUSIONS

MEs can be prospective collected in the clinical setting and used for a **dual purpose**:

- **Genotyping**
- **Culturing** and cell viability assays

Drug testing in primary cultures could be of help in **treatment selection**

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**Muchas Gracias**