

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

#15CongressGeCP

# How to treat uncommon EGFR mutations

Xabier Mielgo-Rubio, MD

*Unidad de Oncología*

*Hospital Universitario Fundación Alcorcón, Madrid*



## Disclosures

- **Speaker or educational material:** Astra Zeneca, Bristol Myers Squibb, Merck Sharp and Dohme, Novartis, Roche, Pfizer
- **Consultant or Advisory Role:** Astra Zeneca, Boehringer, Pfizer
- **Research support:** Bristol Myers Squibb



## OUTLINE

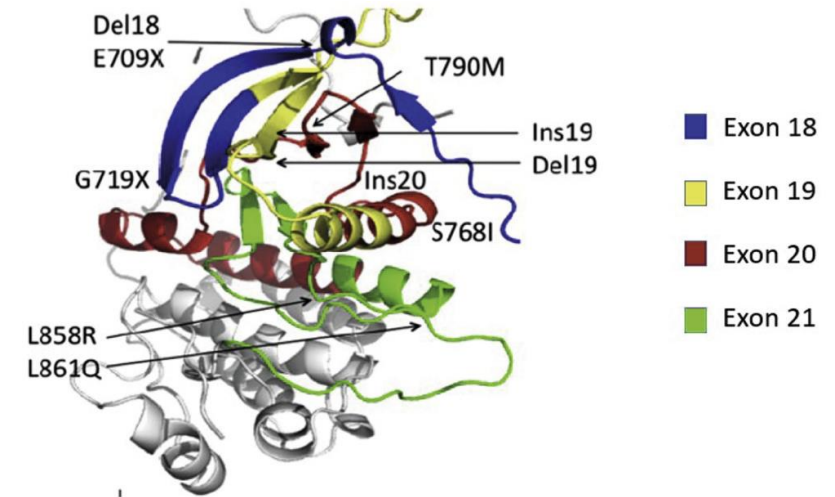
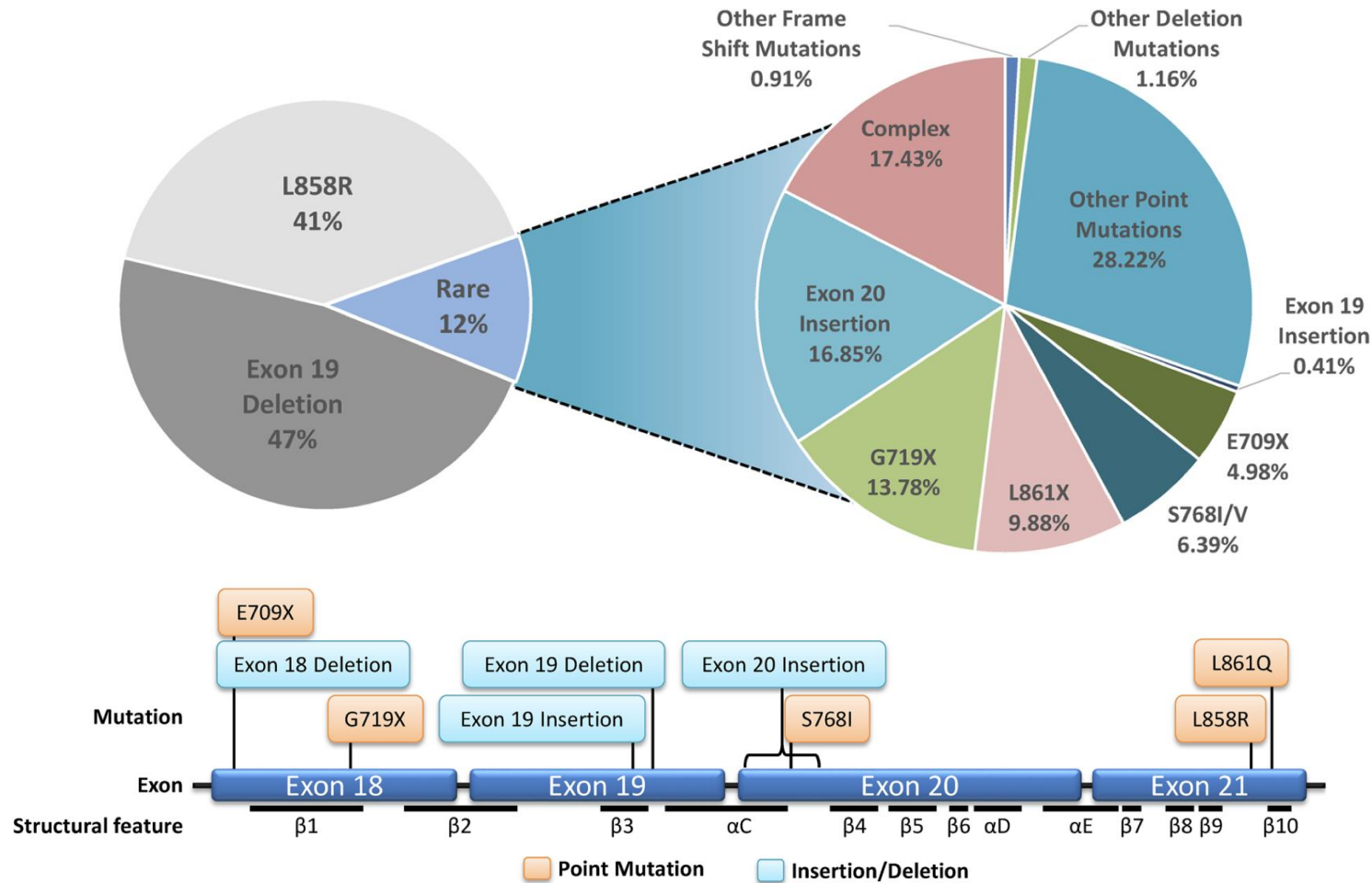
1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions



## OUTLINE

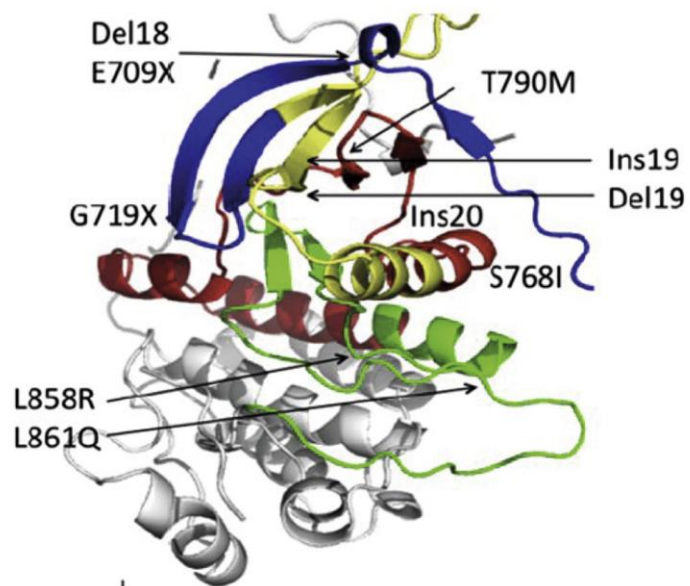
1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions

## EGFR kinase domain mutations are heterogeneous

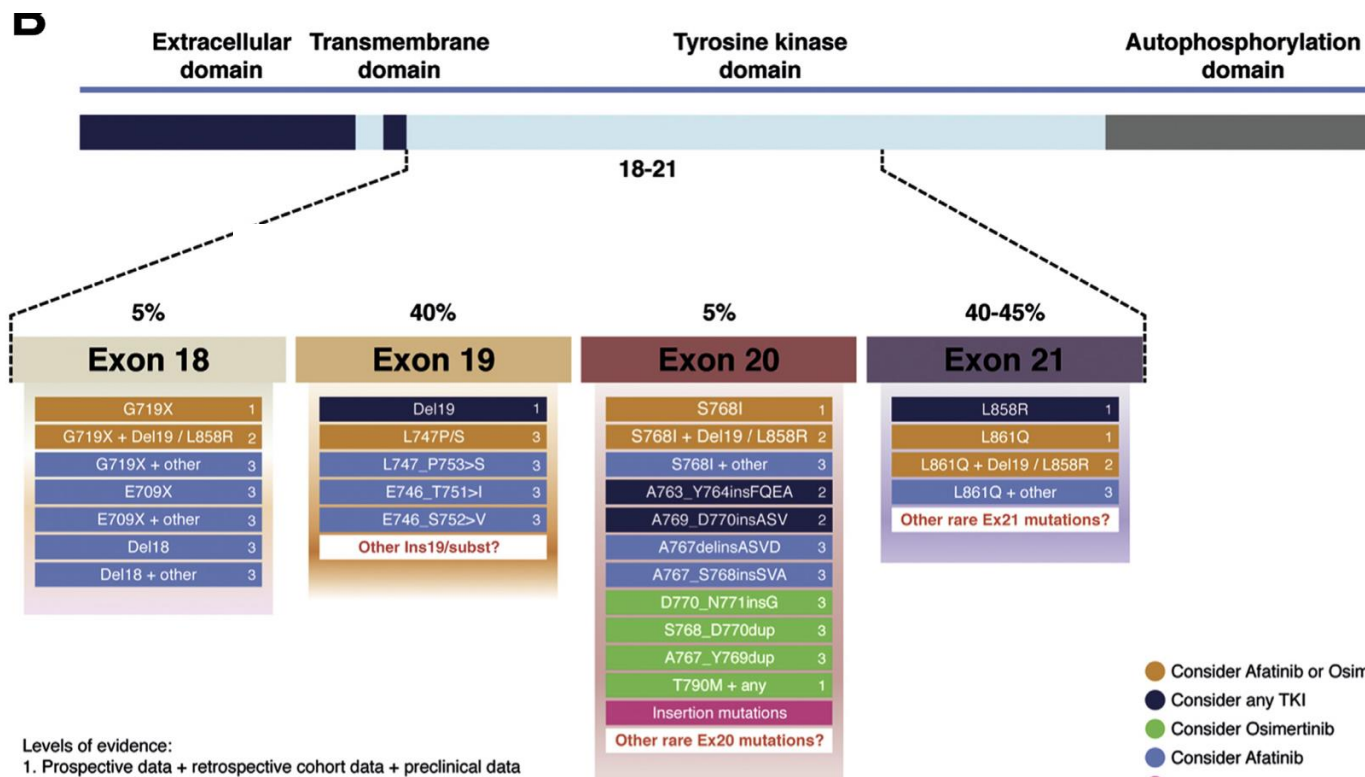




# EGFR kinase domain mutations classification by exon location

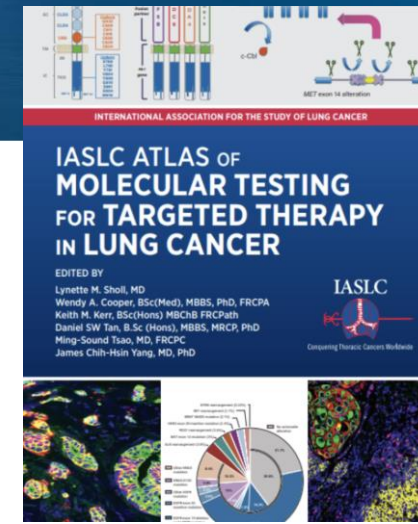


- Exon 18
- Exon 19
- Exon 20
- Exon 21



## Types of **uncommon** EGFR mutations

*Uncommon EGFR mutations: ANYTHING NOT COMMON OR T790M*



### Exon 20 insertions

- The most common of the uncommon (~ 12%)
- Very heterogenous
- NGS recommended

### Compound EGFR mutations

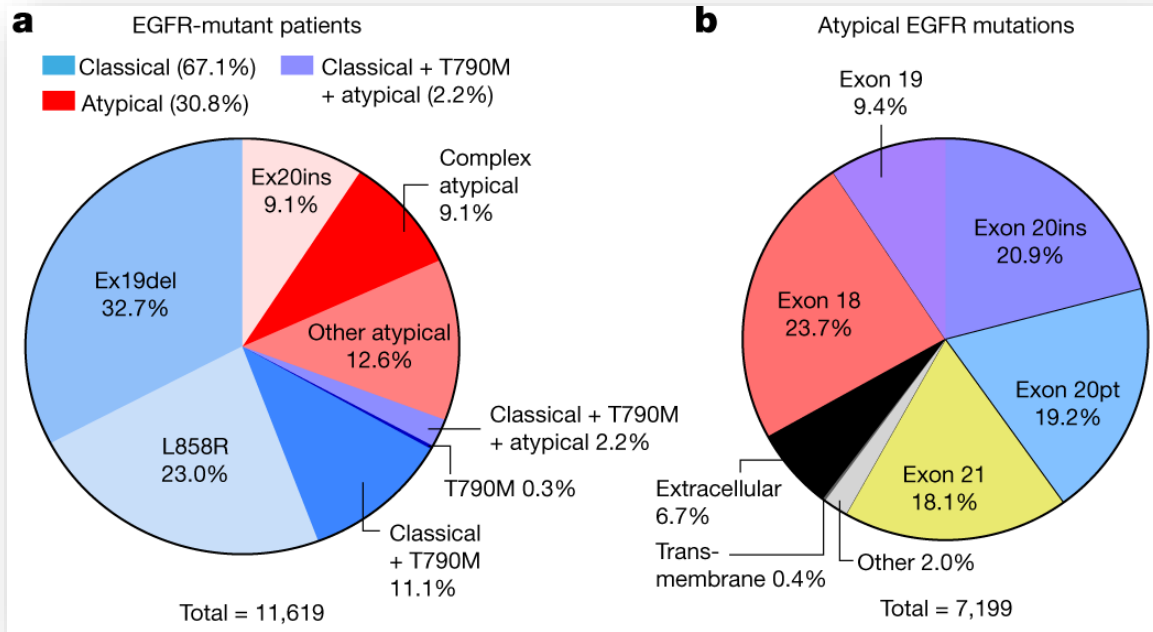
- Any type of combination
- 4-26% of all EGFR mutations

### Other uncommon (or atypical) simple mutations

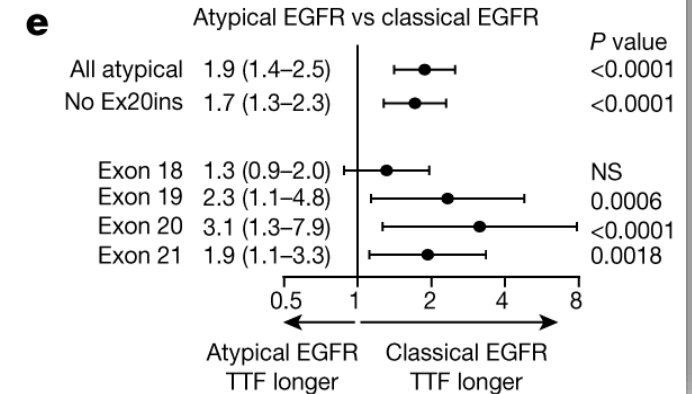
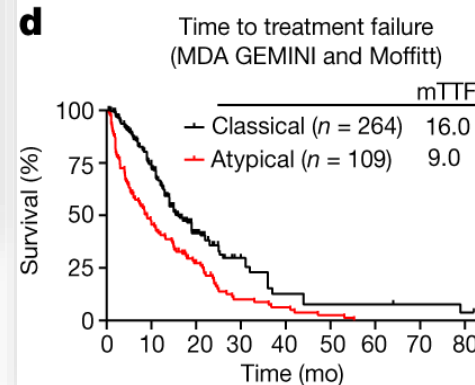
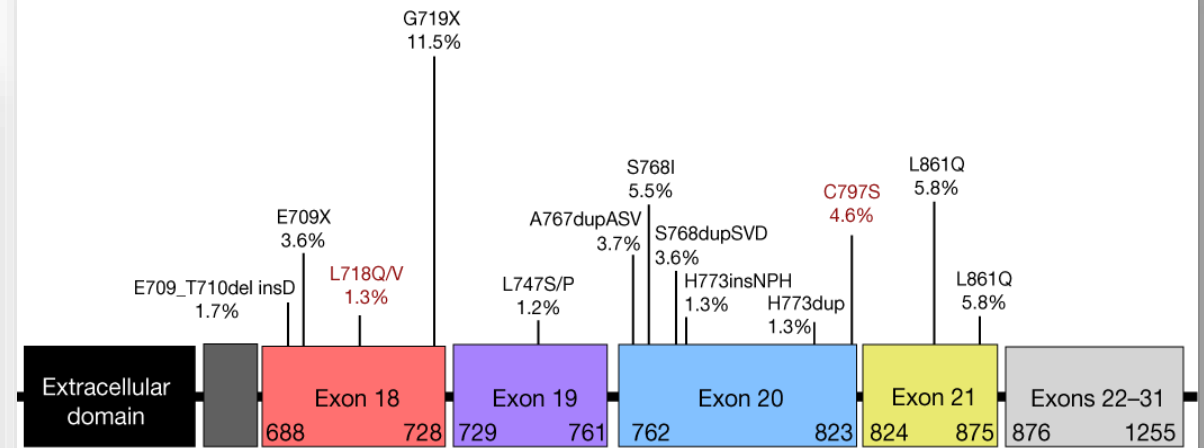
- All mutations except exon 19 deletions, L858R, and T790M mutations.
- G719X (ex18) > L861X (ex21) > S768I (ex20)
- Can be sensitive to EGFR TKIs

# Types of uncommon EGFR mutations

MD Anderson work: 5 patient databases with genomic profiling; 16715 EGFR-mutant patients



**c** Frequency of atypical EGFR mutations >1% (n = 7,199)

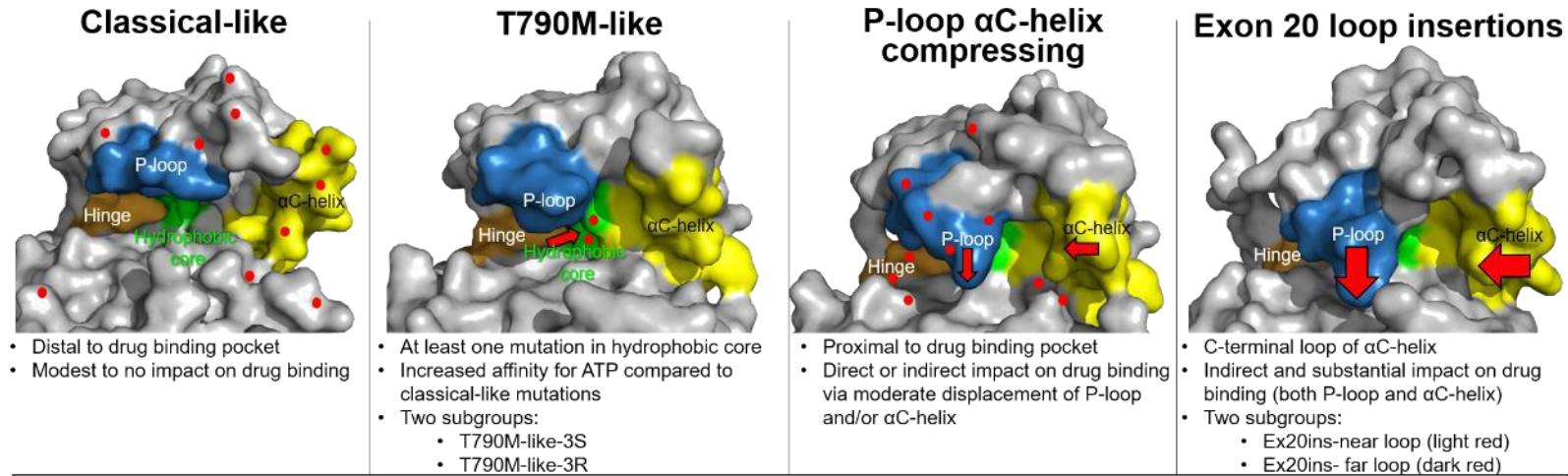








# Structure/function classification predicts drug response in EGFR mutant NSCLC



Mutation resulted structural change



Function



Drug sensitivity

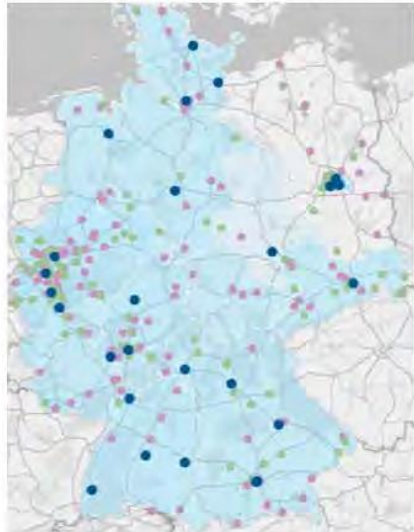
Representative Mutations									
L858R	K754E	T790M-3S		T790M-3R		Primary	Acquired	Ex20ins-NL	Ex20ins-FL
Exon 19 deletions	T725M	Classical/T790M		Ex19del/T790M/L792H		G719X	C797S	S768dupSVD	H773insNPH
S720P	L833F/V	G719X/T790M		L858R/T790M/L718X		S768I	L792H	A767dupASV	H773dupH
L861Q/R	A763insFQEA	L747_K745delinsATSPE		Classical/T790M/C797S		L747P/S	G724S	D770insNPG	V774insAV
S811F	A763insLQEA	S768I/T790M				E709_T710del insD	L718X	D770del insGY	V774insPR
						V769L	T854I		
Drug Sensitivity/Selectivity									
Sensitive & Selective		T790M-3S		T790M-3R				Ex20ins-NL	Ex20ins-FL
		Third-generation		PKi		Second-generation		Ex20ins-specific	Ex20ins-specific
		Second-generation		ALKi		First-generation		Second-generation	
		First-generation		Third-generation		Ex20ins-specific		Third-generation	Third-generation
		Exon20ins-specific		Second-generation		Third-generation		First-generation	First-generation
Resistant		First-generation		First-generation					

# ANALYSIS OF CLINICAL ACTIONABILITY OF ATYPICAL EGFR MUTATIONS

nNGM

## National Network Genomic Medicine Lung Cancer

Funded by the German Cancer Aid since 2018 and the health insurance companies



● 24 University nNGM centers at 26 sites

359 regional partners:  
● 170 practices / MVZs  
● 189 hospitals

2022:  
NGS of ca. 17.000 pts. with newly diagnosed advanced NSCLC  
= ca. 50% of cases in Germany

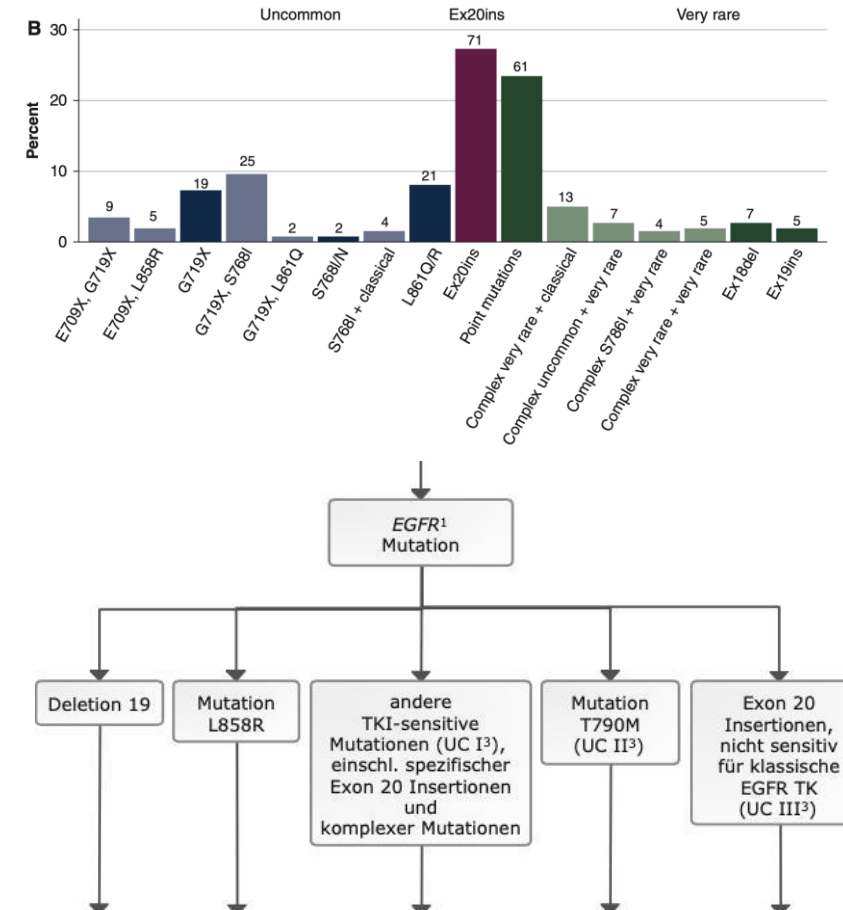


nNGM

1 nNGM UC1 TKI-sensitive EGFR mutations	
<b>A</b>	G719X, S768X, L861X mutations, alone or in complex with other uncommon mutations such as E709X or classical L858R or exon19 deletions (group 1 in nNGM clinical FUP cohort)
<b>B</b>	complex mutations containing classical EGFR mutations L858R or exon19 deletions with very rare EGFR mutations
<b>C</b>	exon 19 insertions
<b>D</b>	Specific exon 20 insertions
	Y763_V764insFQEV EGFR-TKI naïve
	A767_V769dup EGFR-TKI naïve
	N771_H773dup 2 <sup>nd</sup> EGFR-TKI, switch from gefitinib due to toxicities
	H773_V774insGHPH EGFR-TKI naïve
	H773_V774insAH EGFR-TKI naïve
<b>E</b>	Specific very rare single point mutations
	E711Q EGFR-TKI naïve
	P733Q EGFR-TKI naïve
	L747P EGFR-TKI naïve
	EGFR-TKI naïve
	P753L 5L (1L gefitinib PFS 2.0 months, 2L erlotinib PFS 3.0 months, 4L & 5L chemo)
	E758G EGFR-TKI naïve
	R776H EGFR-TKI naïve
	Q791H EGFR-TKI naïve
<b>F</b>	Specific complex mutations: uncommon with very rare
	G719A, P753Q EGFR-TKI naïve
<b>G</b>	Specific complex mutations: very rare with very rare
	L833V, H835L EGFR-TKI naïve

Novel classification of clinical actionability

Janning, Ann Oncol 2022



Uptake into national NSCLC guideline 2022



# NOVEL NNGM CLASSIFICATION OF RARE EGFR MUTATIONS

UC1: TKI-sensitive

UC2: de Novo T790M

UC3: Exon20 Insertions

UC4: Ultrarare Point/Compound Mutations

<b>A</b>	<b>G719X, S768X, L861X</b> mutations, alone or in complex with other uncommon mutations such as E709X or classical L858R or exon19 deletions (group 1 in nNGM clinical FUP cohort)	
<b>B</b>	<b>complex mutations containing</b> classical <i>EGFR</i> mutations <b>L858R or exon19 deletions</b> with very rare <i>EGFR</i> mutations	
<b>C</b>	<b>exon 19 insertions</b>	
<b>D</b>	<b>Specific exon 20 insertions</b>	
	Y763_V764insFQEV	EGFR-TKI naïve
	A767_V769dup	EGFR-TKI naïve
	N771_H773dup	2 <sup>nd</sup> EGFR-TKI, switch from gefitinib due to toxicities
	H773_V774insGHPH	EGFR-TKI naïve
	H773_V774insAH	EGFR-TKI naïve
<b>E</b>	<b>Specific very rare single point mutations</b>	
	E711Q	EGFR-TKI naïve
	P733Q	EGFR-TKI naïve
	L747P	EGFR-TKI naïve
		EGFR-TKI naïve
	P753L	5L (1L gefitinib PFS 2.0 months, 2L erlotinib PFS 3.0 months, 4L & 5L chemo)
	E758G	EGFR-TKI naïve
	R776H	EGFR-TKI naïve
	Q791H	EGFR-TKI naïve
<b>F</b>	<b>Specific complex mutations: uncommon with very rare</b>	
	G719A, P753Q	EGFR-TKI naïve
<b>G</b>	<b>Specific complex mutations: very rare with very rare</b>	
	L833V, H835L	EGFR-TKI naïve

- Very rare single point mutations\*
- Complex mutations: uncommon with very rare\*
- Complex mutations: very rare with very rare\*

\*except those mentioned in nNGM UC1

EGFR TKI (Afa, Osi)

Osimertinib

Amivantamab

Preclinical testing/MTB



## OUTLINE

1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions



## OUTLINE

1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions

## Finding the needle in the haystack

### *UNMET MEDICAL NEED*

1-3% OF NSCLC patients with rare/atypical EGFR mutations

0,7-2% w/o Exon20 Insertions and T790M

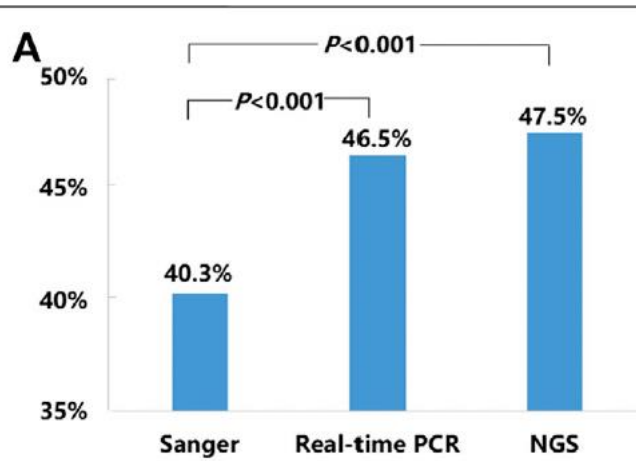


Significant subgroup of patients with unmet medical need: > 2000 newly diagnosed patients in EU/Y

## Uncommon EGFR mutations testing – What’s best?

*Mutation spectrum of EGFR from 21324 chinese NSCLC patients tested by multiple methods - CAP accredited lab*

Mutation detection rates of EGFR



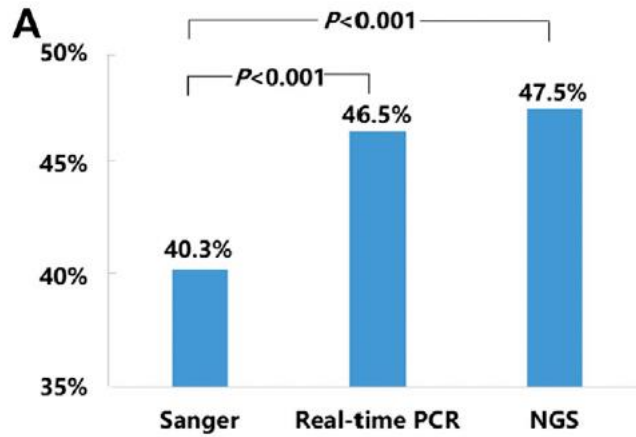




# Uncommon EGFR mutations testing – What’s best?

Mutation spectrum of EGFR from 21324 chinese NSCLC patients tested by multiple methods - CAP accredited lab

Mutation detection rates of EGFR



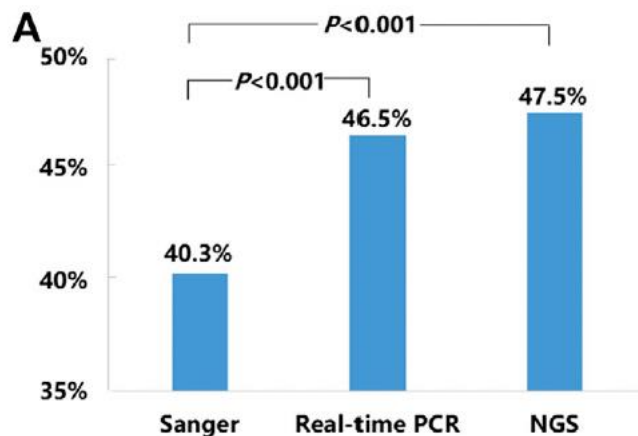
Specimens	Sanger sequencing	Real-time PCR	NGS
Number of samples	5,244	13,329	2,751
EGFR mutation rate	40.3%	46.5%	47.5%
EGFR mutation types	46%	36%	76%
Covered regions of EGFR	18-21 exons	18-21 exons hotspots <sup>a</sup>	All coding sequencing <sup>b</sup>
Covered non-EGFR	No	No	Yes <sup>c</sup>
Technical sensitivity	20%	1%	1%
Recommended TCC	≥40%	≥1%	≥1%
Mean TAT (days)	5	4	8



## Uncommon EGFR mutations testing – What’s best?

Mutation spectrum of EGFR from 21324 chinese NSCLC patients tested by multiple methods - CAP accredited lab

Mutation detection rates of EGFR



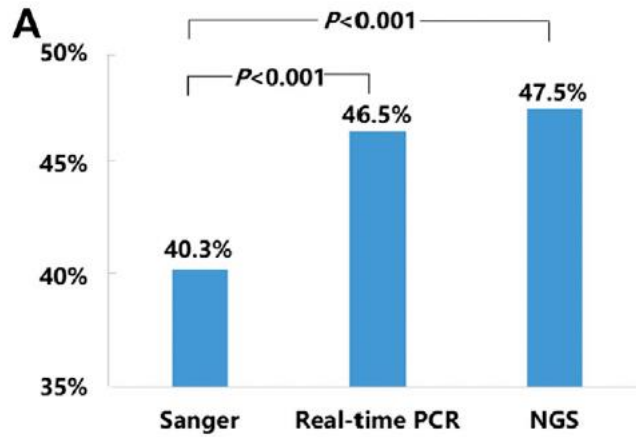
Specimens	Sanger sequencing	Real-time PCR	NGS
Number of samples	5,244	13,329	2,751
EGFR mutation rate	40.3%	46.5%	47.5%
EGFR mutation types	46%	36%	76%
Covered regions of EGFR	18-21 exons	18-21 exons hotspots <sup>a</sup>	All coding sequencing <sup>b</sup>
Covered non-EGFR	No	No	Yes <sup>c</sup>
Technical sensitivity	20%	1%	1%
Recommended TCC	≥40%	≥1%	≥1%
Mean TAT (days)	5	4	8



# Uncommon EGFR mutations testing – What’s best?

Mutation spectrum of EGFR from 21324 chinese NSCLC patients tested by multiple methods - CAP accredited lab

Mutation detection rates of EGFR



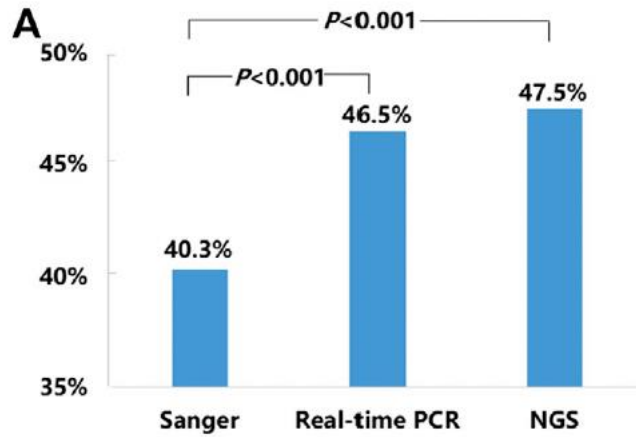
Specimens	Sanger sequencing	Real-time PCR	NGS
Number of samples	5,244	13,329	2,751
EGFR mutation rate	40.3%	46.5%	47.5%
EGFR mutation types	46%	36%	76%
Covered regions of EGFR	18-21 exons	18-21 exons hotspots <sup>a</sup>	All coding sequencing <sup>b</sup>
Covered non-EGFR	No	No	Yes <sup>c</sup>
Technical sensitivity	20%	1%	1%
Recommended TCC	≥40%	≥1%	≥1%
Mean TAT (days)	5	4	8



# Uncommon EGFR mutations testing – What’s best?

Mutation spectrum of EGFR from 21324 chinese NSCLC patients tested by multiple methods - CAP accredited lab

Mutation detection rates of EGFR



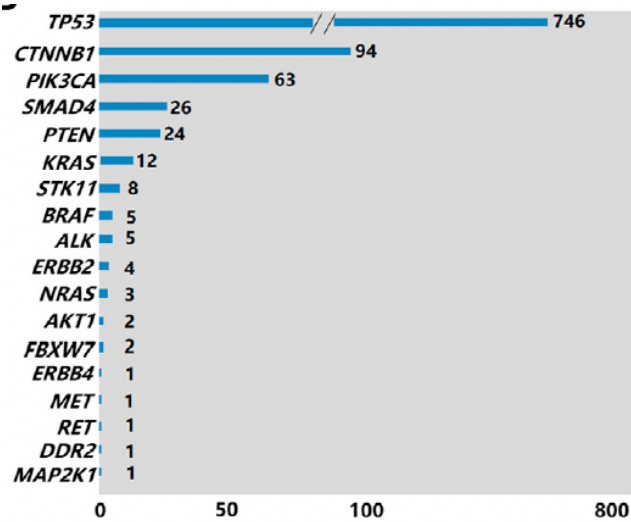
Specimens	Sanger sequencing	Real-time PCR	NGS
Number of samples	5,244	13,329	2,751
EGFR mutation rate	40.3%	46.5%	47.5%
EGFR mutation types	46%	36%	76%
Covered regions of EGFR	18-21 exons	18-21 exons hotspots <sup>a</sup>	All coding sequencing <sup>b</sup>
Covered non-EGFR	No	No	Yes <sup>c</sup>
Technical sensitivity	20%	1%	1%
Recommended TCC	≥40%	≥1%	≥1%
Mean TAT (days)	5	4	8



# Uncommon EGFR mutations testing – What’s best?

Mutation spectrum of EGFR from 21324 chinese NSCLC patients tested by multiple methods - CAP accredited lab

Non-EGFR co-mutations detected in EGFRm



Of the 1,308 cases with EGFR mutations found by NGS, **65.3%** of the cases (854/1,308) harbored **non-EGFR mutations** in 18 tumor-related genes, with TP53 being the most frequently mutated

Specimens	Sanger sequencing	Real-time PCR	NGS
Number of samples	5,244	13,329	2,751
EGFR mutation rate	40.3%	46.5%	47.5%
EGFR mutation types	46%	36%	76%
Covered regions of EGFR	18-21 exons	18-21 exons hotspots <sup>a</sup>	All coding sequencing <sup>b</sup>
Covered non-EGFR	No	No	Yes <sup>c</sup>
Technical sensitivity	20%	1%	1%
Recommended TCC	≥40%	≥1%	≥1%
Mean TAT (days)	5	4	8





# Uncommon EGFR testing- What's best?

## NGS Is More Comprehensive Than PCR for Testing EGFR Exon 20 Insertions

- Due to the heterogeneity, exon 20 insertions are not uniformly detected across commonly used PCR testing methods for EGFR
- For detection of EGFR Exon 20 Insertions, NGS is more comprehensive than PCR





## OUTLINE

1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions



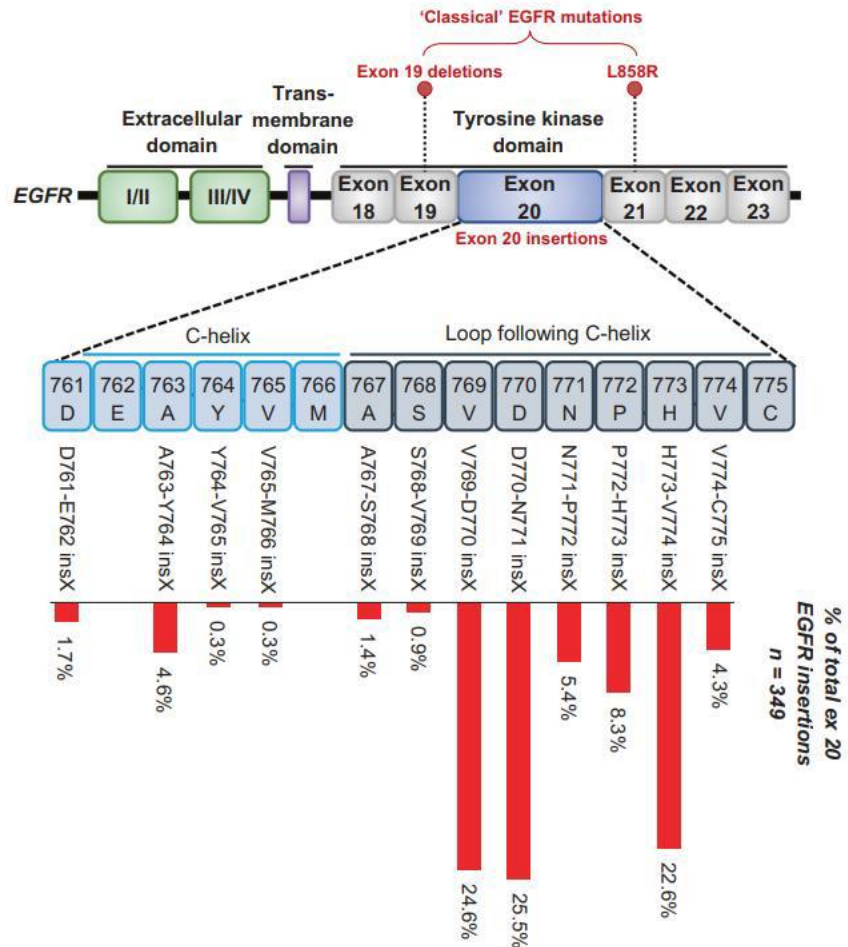


## OUTLINE

1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions



# EXON 20 INSERTIONS



Ins 20 variant Parental BaF3	Erlotinib IC50 values	Gefitinib	Afatinib	Osimertinib	Mobocertinib	Pozotinib	Amivantamab	BAY2576568	BLU-451	Oric-114	Furmonertinib	Tarloxitinib
WT EGFR	71.0	55.5	3.8	350.5	34.5	6.49	0.9	273	921	2.3	109.9	N/A
A763_Y764insFQEA	21.0	90.0	0.4	51.1	3.1	1.90	N/A	N/A	61	0.9	N/A	15.2
V769_D770insASV	80.0	287.4	10.3	61.1	2.1	2.13	0.6	15.3	78	N/A	14	675.9
D770_N771insNPG	469.0	941.0	9.0	27.2	1.3	0.73	N/A	N/A	7	2.7	11	N/A
D770_N771insSVD	528.0	918.4	41.3	226.7	6.5	1.5	1.4	11.1	53	N/A	N/A	990.1
H773_V774insNPH	191.2	1132.8	18.9	153.6	2.6	31.93	N/A	67.9	75	N/A	20	714.0

■ IC50 >100 ■ IC50 < 10 to ≤ 100 ■ IC50 ≤ 10



# RWD: EXON21Ins - worse prognosis

### Real-world overall survival



**75% increased risk of death with EGFR exon20ins compared with cEGFR; (Adj HR, 1.75 [95% CI, 1.45–2.13]; p<0.0001)**

### Real-world PFS



**170% increased risk of progression or death on TKI treatment with EGFR exon20ins compared with cEGFR; (Adj HR, 2.7 [95% CI, 2.06–3.55]; p<0.0001)**



## RWD response and outcomes in Exon20Ins

- Platin-based chemo alone or in combination with other therapy was the most common 1L therapy
- **IO therapy** was associated with poor confirmed rwORR and survival, consistently in the 1L and  $\geq 2L$
- **EGFR TKIs** had limited clinical benefit with a poor confirmed rwORR in 1L and  $\geq 2L$

**Table 3.** Confirmed rwORR and survival outcomes by therapy

Cohort	N	Confirmed rwORR (95% CI)	Median OS (95% CI), months	Median rwPFS (95% CI), months
1L: Platinum	41	19.5% (8.8%, 34.9%)	17.0 (10.5, 33.2)	5.7 (3.0, 10.9)
1L: IO + Platinum	16	18.8% (4.0%, 45.6%)	11.3 (5.6, NR)	4.5 (1.2, 10.3)
1L: IO monotherapy	11	9.1% (0.2%, 41.3%)	11.0 (1.2, NR)	3.1 (1.1, 5.2)
1L: EGFR TKI	37	2.7% (0.1%, 14.2%)	10.7 (3.4, 22.3)	3.3 (2.2, 6.6)
$\geq 2L$ post-platinum: IO monotherapy	20	5.0% (0.1%, 24.9%)	7.1 (2.5, 10.1)	2.2 (1.7, 3.0)
$\geq 2L$ post-platinum: EGFR TKI	10	10.0% (0.3%, 44.5%)	12.2 (1.3, 17.8)	3.4 (0.0, 5.9)

1L, first line; CI, confidence interval; IO, immuno-oncology; mOS, median overall survival; mPFS, median progression-free survival; NR, not reached; rwORR, real-world overall response rate.



# 3<sup>rd</sup> G EGFR TKIs: Efficacy Results in Patients With *EGFR* Exon 20 Insertions

A Retrospective Study in  
*EGFR* Exon 20 Insertion+ NSCLC:  
 Response to Osimertinib<sup>1,a</sup>

A Phase 2 Study in  
*EGFR* Exon 20 Insertion+ NSCLC:  
 Response to Osimertinib<sup>2,b</sup>: POSITION 20

Mutation	ORR, %	PFS, Median, months	OS, Median, months
Exon 20 mutations (n=21)	5% (1 PR)	3.6 (95% CI, 2.6-4.5)	8.7 (95% CI, 1.1-16.4)

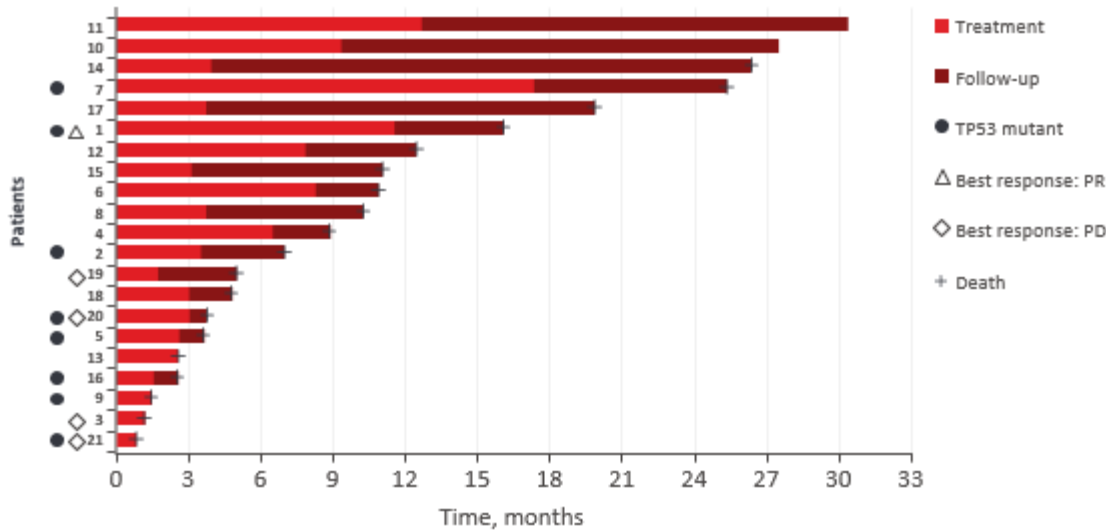
Osimertinib in Treating Patients With Stage IIIB-IV or Recurrent Non-small Cell Lung Cancer With *EGFR* Exon 20 Insertion Mutations

ClinicalTrials.gov Identifier: NCT03191149

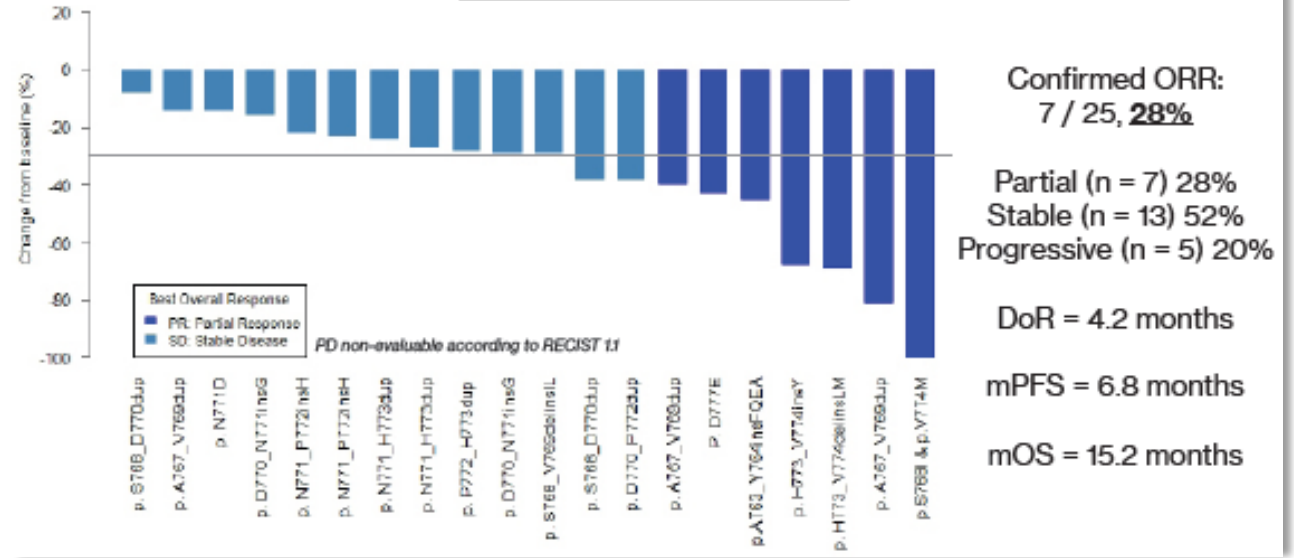
The safety and scientific validity of this study is the responsibility of the study sponsor and investigators. Listing a study does not mean it has been evaluated by the U.S. Federal Government. Read our [disclaimer](#) for details.

Recruitment Status: Suspended (Other - response analysis)  
 First Posted: June 19, 2017  
 Last Update Posted: February 2, 2022

Swimmer Plot of PFS and OS After Osimertinib<sup>1,a</sup>



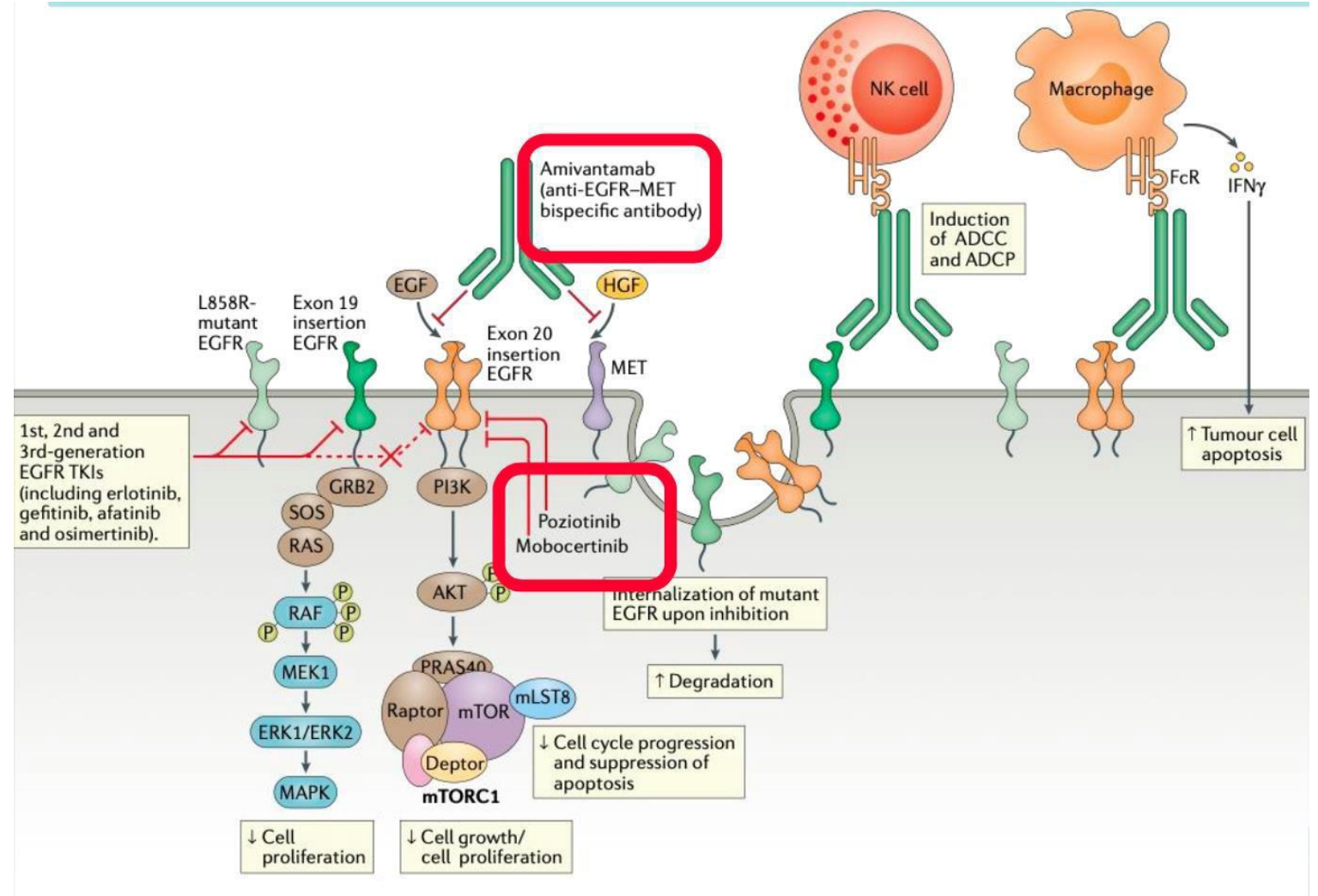
## OVERALL EFFICACY





## Exon20Ins: new therapeutic options

- Amivantamab (bispecific c-MET-EGFR antibody)
- Exon20Ins specific TKI
  - Mobocertinib
  - Poziotinib
  - Others

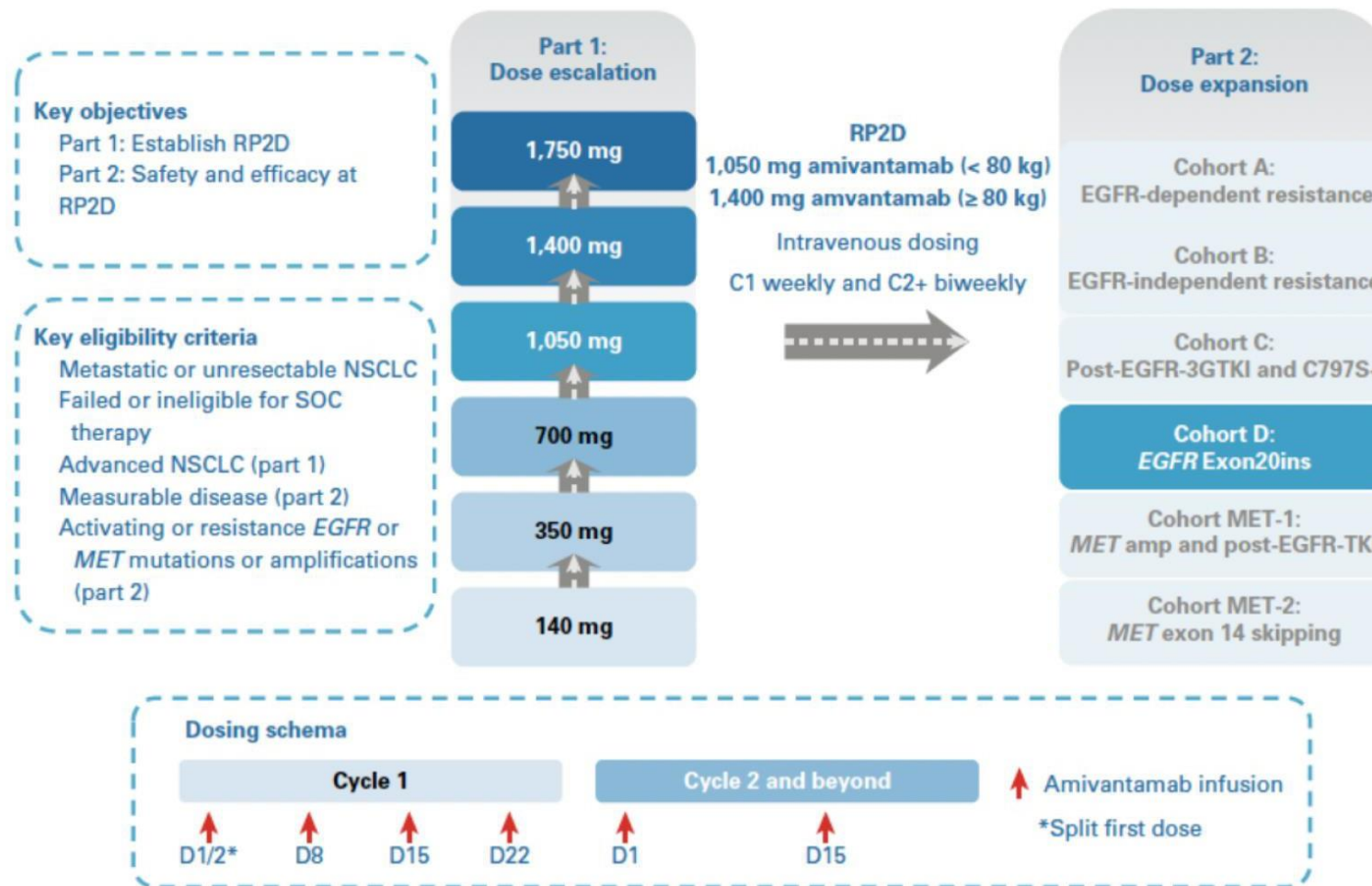




# Exon20Ins - AMIVANTAMAB

## CHRYSALIS 1: Amivantamab (tras varias líneas de tratamiento)

Phase I/II





# Exon20Ins- AMIVANTAMAB in PRETREATED- Chrysalis

## Phase I/II

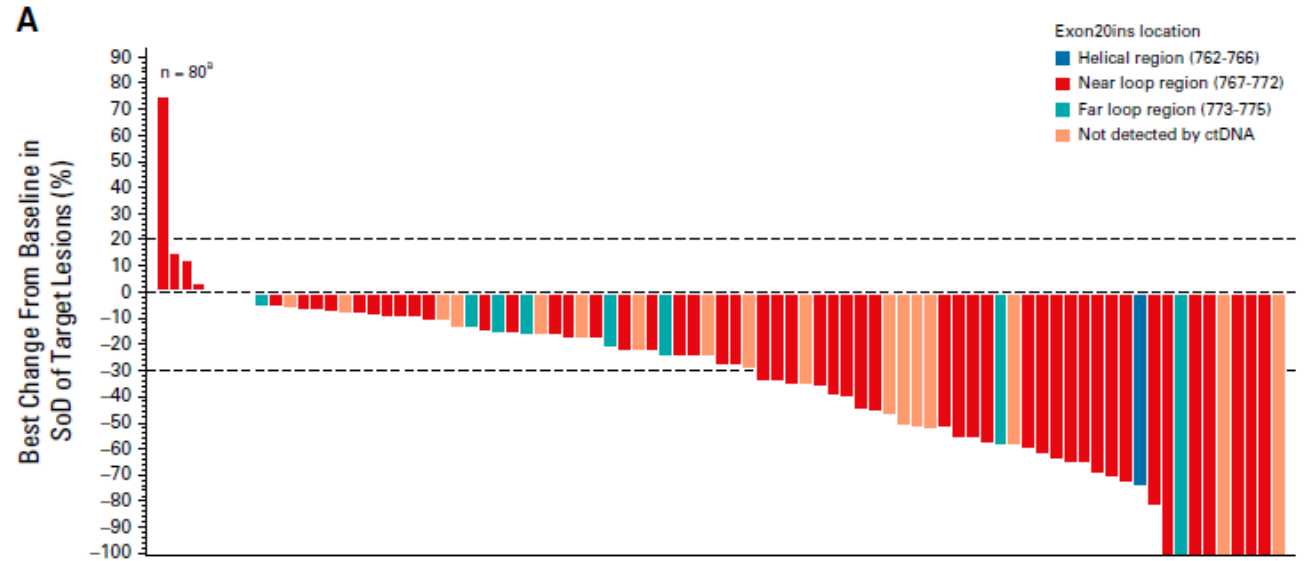
Median PFS was 8.3 months (95% CI, 6.5 to 10.9) by BICR and investigator (95% CI, 5.5 to 10.6)

Median OS was 22.8 months (95% CI, 14.6 to not reached)

**TABLE 3.** Response as Assessed by Blinded Independent Central Review

Response per RECIST	Efficacy Population (n = 81)
ORR, % (95% CI) <sup>a</sup>	40 (29 to 51)
CBR, % (95% CI) <sup>b</sup>	74 (63 to 83)
Best response, No. (%)	
CR	3 (4)
PR	29 (36)
SD	39 (48)
PD	8 (10)
NE	2 (2)

Median Follow Up: 9,7m (range, 1,1-29.3 m)



762 E (n = 0)	763 A (n = 1)	764 Y (n = 0)	765 V (n = 0)	766 M (n = 0)	767 A (n = 19)	768 S (n = 13)	769 V (n = 1)	770 D (n = 9)	771 N (n = 9)	772 P (n = 3)	773 H (n = 8)	774 V (n = 0)	775 C (n = 0)
Helical region (n = 1) ORR = 100% CBR = 100%					Near loop (n = 54) ORR = 41% CBR = 70%						Far loop (n = 8) ORR = 25% CBR = 75%		
Not detected by ctDNA (n = 18) ORR = 39% CBR = 83%													





# Exon20Ins- AMIVANTAMAB in PRETREATED- Chrysalis

Phase I/II

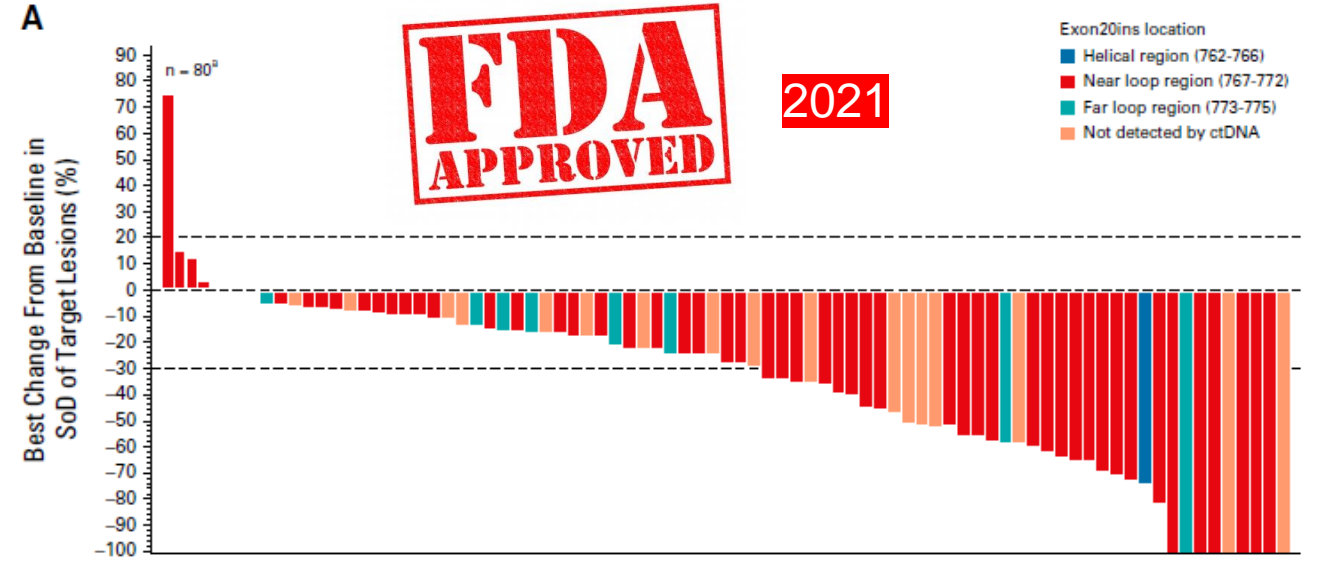
Median PFS was 8.3 months (95% CI, 6.5 to 10.9) by BICR and investigator (95% CI, 5.5 to 10.6)

Median OS was 22.8 months (95% CI, 14.6 to not reached)

**TABLE 3.** Response as Assessed by Blinded Independent Central Review

Response per RECIST	Efficacy Population (n = 81)
ORR, % (95% CI) <sup>a</sup>	40 (29 to 51)
CBR, % (95% CI) <sup>b</sup>	74 (63 to 83)
Best response, No. (%)	
CR	3 (4)
PR	29 (36)
SD	39 (48)
PD	8 (10)
NE	2 (2)

Median Follow Up: 9,7m (range, 1,1-29.3 m)



762 E (n = 0)	763 A (n = 1)	764 Y (n = 0)	765 V (n = 0)	766 M (n = 0)	767 A (n = 19)	768 S (n = 13)	769 V (n = 1)	770 D (n = 9)	771 N (n = 9)	772 P (n = 3)	773 H (n = 8)	774 V (n = 0)	775 C (n = 0)
Helical region (n = 1) ORR = 100% CBR = 100%					Near loop (n = 54) ORR = 41% CBR = 70%						Far loop (n = 8) ORR = 25% CBR = 75%		
Not detected by ctDNA (n = 18) ORR = 39% CBR = 83%													



# Exon20Ins- AMIVANTAMAB in PRETREATED- Chrysalis

## Safety profile (dose-escalation)

Treatment-related dose reductions occurred in 15 patients (13%):

- Rash (11 [10%]) being most frequently reported.

Five patients (4%) had treatment-related discontinuation:

- Rash and IRR in two (1.8%) each
- Paronychia in one (1%).

There were no treatment-related grade 5 events.

Median Follow Up: 5,1 m (range, 0,2-29,3 m)

Most Common AE (≥ 10%)	Safety Population (n = 114), No. (%)				Patients Treated at the RP2D (n = 258), No. (%)			
	Total, No. (%)	Grade 1, No. (%)	Grade 2, No. (%)	Grade ≥ 3, No. (%)	Total, No. (%)	Grade 1, No. (%)	Grade 2, No. (%)	Grade ≥ 3, No. (%)
Rash <sup>a</sup>	98 (86)	43 (38)	51 (45)	4 (4)	202 (78)	101 (39)	94 (36)	7 (3)
Infusion-related reaction	75 (66)	9 (8)	63 (55)	3 (3)	167 (65)	21 (8)	140 (54)	6 (2)
Paronychia	51 (45)	28 (25)	22 (19)	1 (1)	104 (40)	50 (19)	51 (20)	3 (1)
Hypoalbuminemia	31 (27)	6 (5)	22 (19)	3 (3)	63 (24)	21 (8)	38 (15)	4 (2)
Constipation	27 (24)	18 (16)	9 (8)	0	58 (23)	36 (14)	22 (9)	0
Nausea	22 (19)	17 (15)	5 (4)	0	55 (21)	40 (16)	14 (5)	1 (0.4)
Dyspnea	22 (19)	12 (11)	8 (7)	2 (2)	52 (20)	28 (11)	13 (5)	11 (4)
Stomatitis	24 (21)	11 (10)	13 (11)	0	50 (19)	33 (13)	17 (7)	0
Peripheral edema	21 (18)	20 (18)	1 (1)	0	50 (19)	43 (17)	5 (2)	2 (1)
Pruritus	19 (17)	11 (10)	8 (7)	0	49 (19)	40 (16)	9 (4)	0
Fatigue	21 (18)	15 (13)	4 (4)	2 (2)	47 (18)	29 (11)	16 (6)	2 (1)
Cough	16 (14)	11 (10)	5 (4)	0	40 (16)	25 (10)	15 (6)	0
Decreased appetite	16 (14)	7 (6)	9 (8)	0	39 (15)	23 (9)	16 (6)	0
Dry skin	18 (16)	18 (16)	0	0	33 (13)	32 (12)	1 (0.4)	0
Increased alanine aminotransferase	17 (15)	15 (13)	1 (1)	1 (1)	30 (12)	22 (9)	5 (2)	3 (1)
Vomiting	12 (11)	10 (9)	2 (2)	0	29 (11)	22 (9)	6 (2)	1 (0.4)
Myalgia	14 (12)	12 (11)	2 (2)	0	28 (11)	23 (9)	5 (2)	0
Dizziness	9 (8)	8 (7)	0	1 (1)	28 (11)	24 (9)	3 (1)	1 (0.4)
Headache	8 (7)	4 (4)	3 (3)	1 (1)	28 (11)	17 (7)	8 (3)	3 (1)

TABLE 2. Summary of AEs

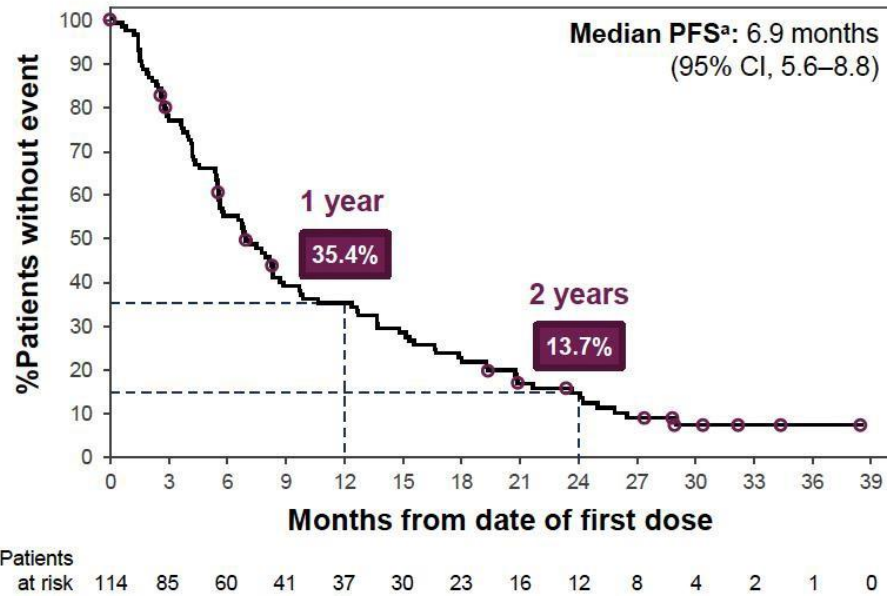
Event	Safety Population (n = 114), No. (%)	Patients Treated at the RP2D (n = 258), No. (%)
Any AE	113 (99)	257 (100)
Grade ≥ 3 AE	40 (35)	101 (39)
Serious AE	34 (30)	79 (31)
AE leading to death	8 (7)	13 (5)
AE leading to discontinuation	11 (10)	17 (7)
AE leading to dose reduction	15 (13)	26 (10)
AE leading to dose interruption <sup>a</sup>	40 (35)	88 (34)



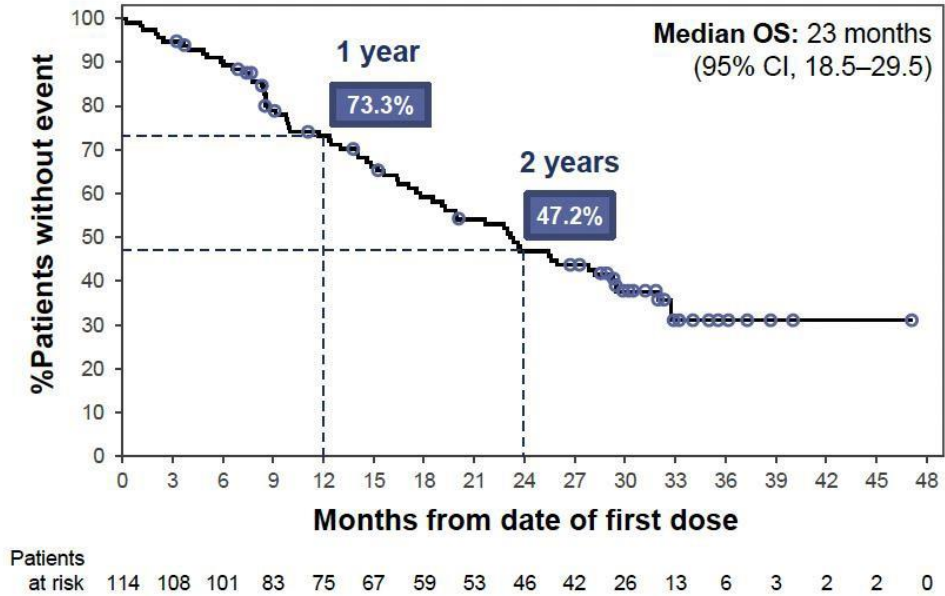
# Exon20Ins- AMIVANTAMAB in PRETREATED- Chrysalis

Long-term outcomes

**Progression-free Survival**



**Overall Survival**



- Better if no alterations in RAS/RAF/MEK
- Better if Partial Response

- As of 12 Sept 2022, the median follow-up was 19.2 months and median duration of treatment was 7.5 months, with 48 of 114 (42%) patients alive

# Amivantamab Plus Chemotherapy vs Chemotherapy as First-line Treatment in EGFR Exon 20 Insertion–mutated Advanced Non-small Cell Lung Cancer (NSCLC)

## Primary Results From PAPILLON, a Randomized Phase 3 Global Study

Nicolas Girard,<sup>1</sup> Keunchil Park,<sup>2,\*</sup> Ke-Jing Tang,<sup>3</sup> Byoung Chul Cho,<sup>4</sup> Luis Paz-Ares,<sup>5</sup> Susanna Cheng,<sup>6</sup> Satoru Kitazono,<sup>7</sup> Muthukkumaran Thiagarajan,<sup>8</sup> Jonathan W. Goldman,<sup>9</sup> Joshua K. Sabari,<sup>10</sup> Rachel E. Sanborn,<sup>11</sup> Aaron S. Mansfield,<sup>12</sup> Jen-Yu Hung,<sup>13</sup> Sanjay Papat,<sup>14</sup> Josiane Mourão,<sup>15</sup> Archan Bhattacharya,<sup>16</sup> Trishala Agrawal,<sup>17</sup> S. Martin Shreeve,<sup>18</sup> Roland E. Knoblach,<sup>17</sup> Caicun Zhou<sup>19</sup>

<sup>1</sup>Institut Curie, Institut du Thorax Curie-Montsouris, Paris, France and Paris Saclay University, UVSQ, Versailles, France; <sup>2</sup>Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, Republic of Korea; <sup>3</sup>The First Affiliated Hospital of Sun Yat-sen University, Guangzhou, China; <sup>4</sup>Division of Medical Oncology, Yonsei Cancer Center, Yonsei University College of Medicine, Seoul, Republic of Korea; <sup>5</sup>Hospital Universitario 12 de Octubre, Madrid, Spain; <sup>6</sup>Sunnybrook Odette Cancer Centre, Toronto, ON, Canada; <sup>7</sup>Cancer Institute Hospital, Japanese Foundation for Cancer Research, Tokyo, Japan; <sup>8</sup>General Hospital Kuala Lumpur, Kuala Lumpur, Malaysia; <sup>9</sup>David Geffen School of Medicine, University of California Los Angeles, Los Angeles, California, USA; <sup>10</sup>NYU Langone Health, New York, NY, USA; <sup>11</sup>Earle A. Chiles Research Institute, Providence Cancer Institute, Portland, OR, USA; <sup>12</sup>Mayo Clinic, Rochester, MN, USA; <sup>13</sup>Department of Internal Medicine, Kaohsiung Medical University Hospital, Kaohsiung Medical University, Kaohsiung, Taiwan; <sup>14</sup>Royal Marsden Hospital NHS Foundation Trust, London, UK and The Institute of Cancer Research, London, UK; <sup>15</sup>Barretos Cancer Hospital, Barretos, Brazil; <sup>16</sup>Janssen R&D, High Wycombe, UK; <sup>17</sup>Janssen R&D, Spring House, PA, USA; <sup>18</sup>Janssen R&D, San Diego, CA USA; <sup>19</sup>Shanghai Pulmonary Hospital, Tongji University School of Medicine, Shanghai, China.

\*Current Affiliation: MD Anderson Cancer Center, Houston, TX, USA.



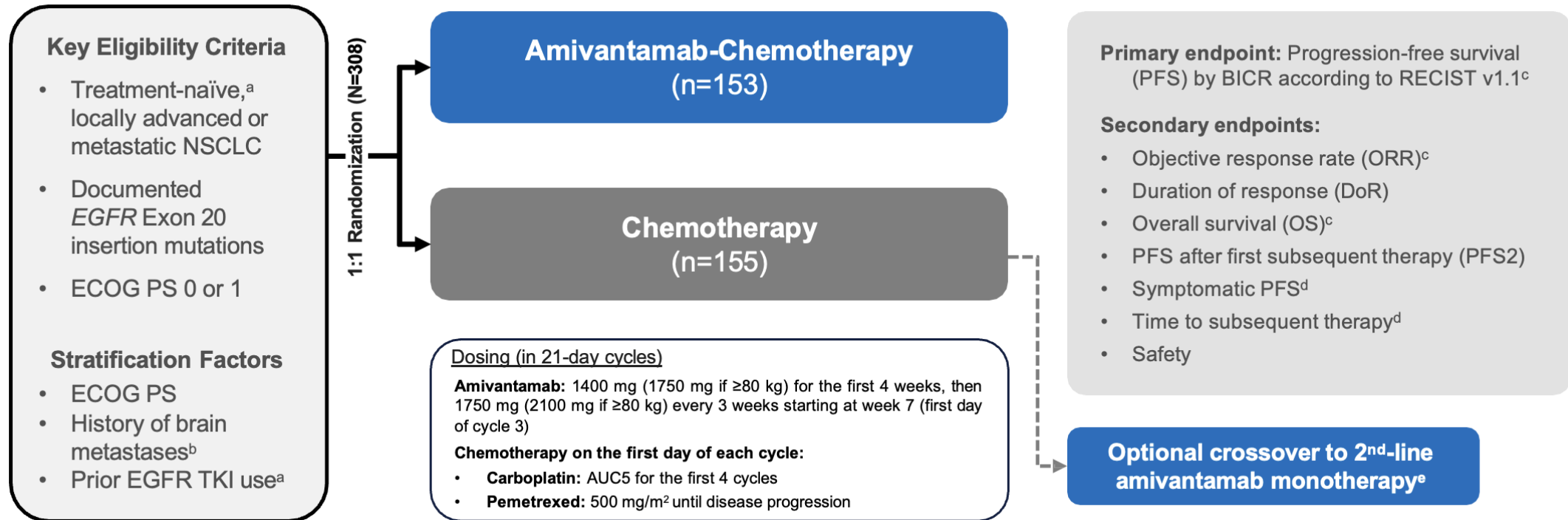
Copies of this presentation obtained through QR code are for personal use only and may not be reproduced without written permission of the authors





# Exon20Ins – AMIVANTAMAB 1L - PAPILLON

## Study design



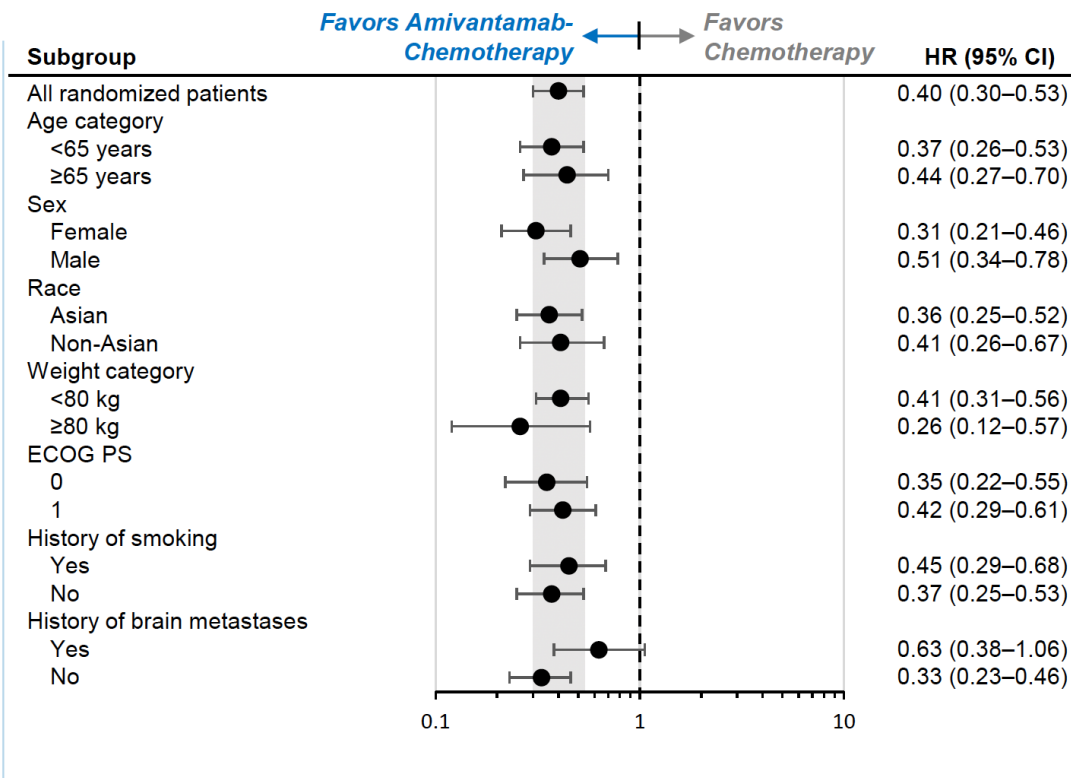
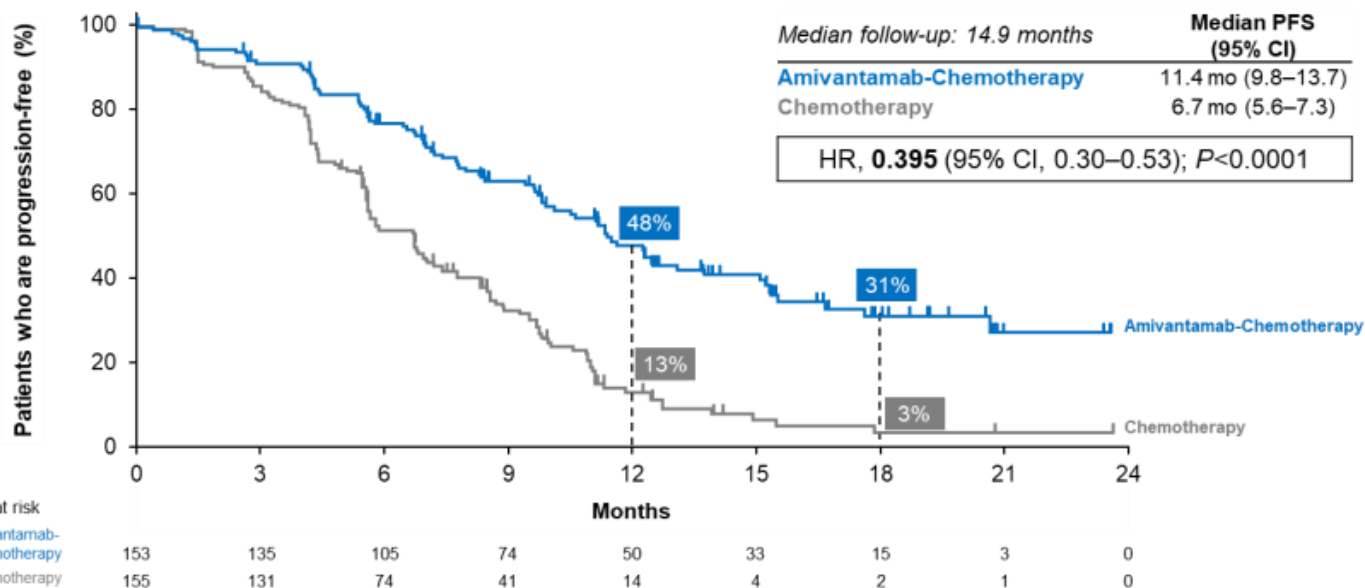


# Exon20Ins – AMIVANTAMAB 1L - PAPILLON

Primary objective of the study: PFS by BICR

## Primary Endpoint: Progression-free Survival by BICR

Amivantamab-chemotherapy reduced risk of progression or death by 60%



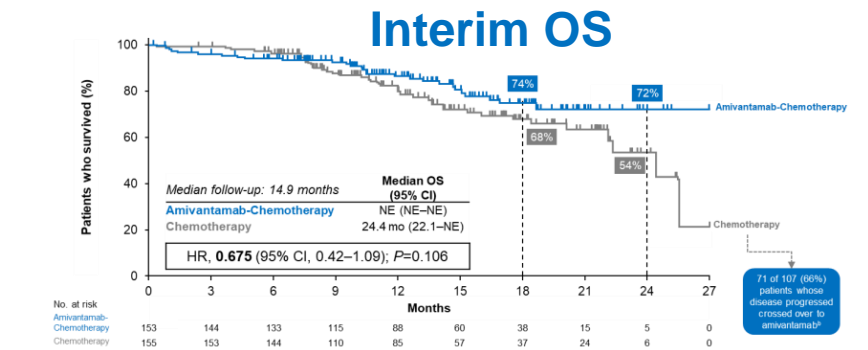
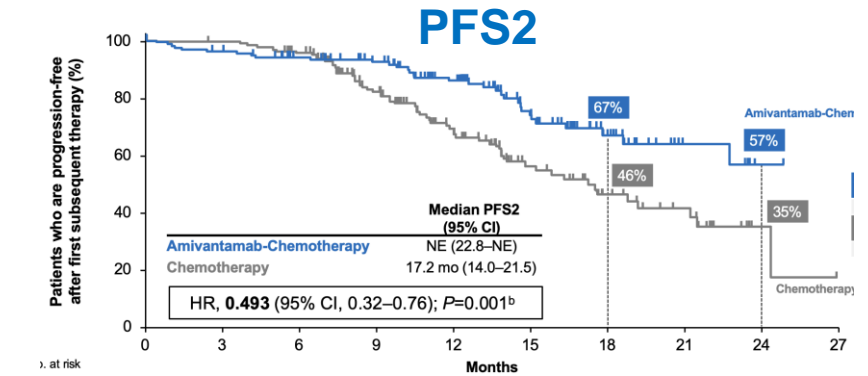
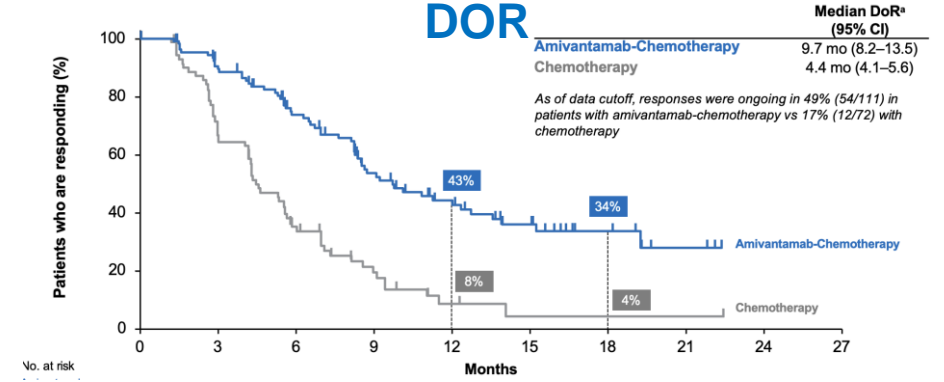
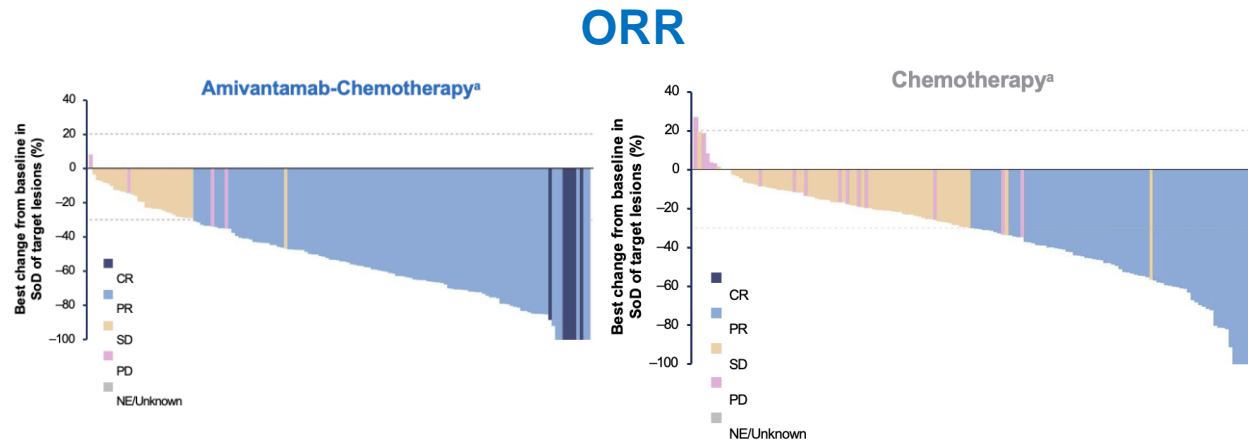
Consistent PFS benefit by investigator: 12.9 vs 6.9 mo(HR, 0.38; 95% CI, 0.29-0.51; P<0.0001a)



# Exon20Ins – AMIVANTAMAB 1L - PAPILLON

## Efficacy data

BICR-assessed response <sup>b</sup>	Amivantamab-Chemotherapy (n=153)	Chemotherapy (n=155)
Mean percent change of SoD	-53% <sup>c</sup>	-34%
ORR	73% (95% CI, 65–80)	47% (95% CI, 39–56)
Odds ratio	3.0 (95% CI, 1.8–4.8); $P < 0.0001$	
Best response, n (%)		
Complete response	6 (4)	1 (1)
Partial response	105 (69)	71 (47)
Stable disease	29 (19)	62 (41)
Progressive disease	4 (3)	16 (11)
NE/Unknown	8 (5)	2 (1)
Median time to response	6.7 wk (range, 5.1–72.5)	11.4 wk (range, 5.1–60.2)





# Exon20Ins – AMIVANTAMAB 1L - PAPILLON

## Safety data

	Amivantamab-Chemotherapy (n=151)	Chemotherapy (n=155)
Median treatment duration, months (range)	9.7 (0.1–26.9)	6.7 (0–25.3)
No. of chemotherapy cycles, median (range)		
Carboplatin	4 (1–4)	4 (1–5)
Pemetrexed	13 (1–34)	10 (1–37)

Treatment-emergent AEs, n (%)	Amivantamab-Chemotherapy (n=151)	Chemotherapy (n=155)
Any AEs	151 (100)	152 (98)
Grade ≥3 AEs	114 (75)	83 (54)
Serious AEs	56 (37)	48 (31)
AEs leading to death	7 (5)	4 (3)
Any AE leading to treatment:		
Interruptions of any agent	104 (69)	56 (36)
Related interruptions of amivantamab	63 (42)	–
Reductions of any agent	73 (48)	35 (23)
Related reductions of amivantamab	54 (36)	–
Discontinuations of any agent	36 (24)	16 (10)
Related discontinuations of amivantamab	10 (7)	–
Discontinuations of all study agents due to AEs	12 (8)	12 (8)

- Similar rate of serious AEs, AEs leading to death and discontinuation due to AEs.
- Treatment-related discontinuations of amivantamab were low (7%)

Most common AEs of any cause by preferred term (≥20%, n (%))	Amivantamab-Chemotherapy (n=151)		Chemotherapy (n=155)	
	All grades	Grade ≥3	All grades	Grade ≥3
<b>Associated with EGFR inhibition</b>				
Paronychia	85 (56)	10 (7)	0	0
Rash	81 (54)	17 (11)	12 (8)	0
Dermatitis acneiform	47 (31)	6 (4)	5 (3)	0
Stomatitis	38 (25)	2 (1)	9 (6)	0
Diarrhea	31 (21)	5 (3)	20 (13)	2 (1)
<b>Associated with MET inhibition</b>				
Hypoalbuminemia	62 (41)	6 (4)	15 (10)	0
Peripheral edema	45 (30)	2 (1)	16 (10)	0
<b>Other</b>				
Neutropenia	89 (59)	50 (33)	70 (45)	35 (23)
Anemia	76 (50)	16 (11)	85 (55)	19 (12)
Infusion-related reaction	63 (42)	2 (1)	2 (1)	0
Constipation	60 (40)	0	47 (30)	1 (1)
Leukopenia	57 (38)	17 (11)	50 (32)	5 (3)
Nausea	55 (36)	1 (1)	65 (42)	0
Thrombocytopenia	55 (36)	15 (10)	46 (30)	16 (10)
Decreased appetite	54 (36)	4 (3)	43 (28)	2 (1)
Alanine aminotransferase increased	50 (33)	6 (4)	56 (36)	2 (1)
Aspartate aminotransferase increased	47 (31)	1 (1)	51 (33)	1 (1)
COVID-19	36 (24)	3 (2)	21 (14)	1 (1)
Hypokalemia	32 (21)	13 (9)	13 (8)	2 (1)
Vomiting	32 (21)	5 (3)	29 (19)	1 (1)

- EGFR- and MET-related AEs were increased, primarily grade 1-2
- CT-associated hematologic and GI toxicities were comparable except neutropenia
- Neutropenia was transient; majority of events were not serious, low discontinuations
- Pneumonitis was reported in 4 (3%) Amivantamab + CT





# Exon20Ins – AMIVANTAMAB 1L - PAPILLON

## Safety data

	Amivantamab-Chemotherapy (n=151)	Chemotherapy (n=155)
Median treatment duration, months (range)	9.7 (0.1–26.9)	6.7 (0–25.3)
No. of chemotherapy cycles, median (range)		
Carboplatin	4 (1–4)	4 (1–5)
Pemetrexed	13 (1–34)	10 (1–37)

Most common AEs of any cause by preferred term (≥20%, n (%))	Amivantamab-Chemotherapy (n=151)		Chemotherapy (n=155)	
	All grades	Grade ≥3	All grades	Grade ≥3
<b>Associated with EGFR inhibition</b>				
Paronychia	85 (56)	10 (7)	0	0
Rash	81 (54)	17 (11)	12 (8)	0
Dermatitis acneiform	47 (31)	6 (4)	5 (3)	0
Stomatitis	38 (25)	2 (1)	9 (6)	0
Diarrhea	31 (21)	5 (3)	20 (13)	2 (1)
<b>Associated with MET inhibition</b>				

**Amivantamab-chemotherapy represents the new standard of care for first-line *EGFR* Ex20ins advanced NSCLC**

	Amivantamab-Chemotherapy (n=151)	Chemotherapy (n=155)
Interruptions of any agent	104 (69)	56 (36)
Related interruptions of amivantamab	63 (42)	–
Reductions of any agent	73 (48)	35 (23)
Related reductions of amivantamab	54 (36)	–
Discontinuations of any agent	36 (24)	16 (10)
Related discontinuations of amivantamab	10 (7)	–
Discontinuations of all study agents due to AEs	12 (8)	12 (8)

	Amivantamab-Chemotherapy (n=151)	Grade ≥3	Chemotherapy (n=155)	Grade ≥3
Nausea	58 (38)	1 (1)	58 (37)	0
Thrombocytopenia	55 (36)	15 (10)	46 (30)	16 (10)
Decreased appetite	54 (36)	4 (3)	43 (28)	2 (1)
Alanine aminotransferase increased	50 (33)	6 (4)	56 (36)	2 (1)
Aspartate aminotransferase increased	47 (31)	1 (1)	51 (33)	1 (1)
COVID-19	36 (24)	3 (2)	21 (14)	1 (1)
Hypokalemia	32 (21)	13 (9)	13 (8)	2 (1)
Vomiting	32 (21)	5 (3)	29 (19)	1 (1)

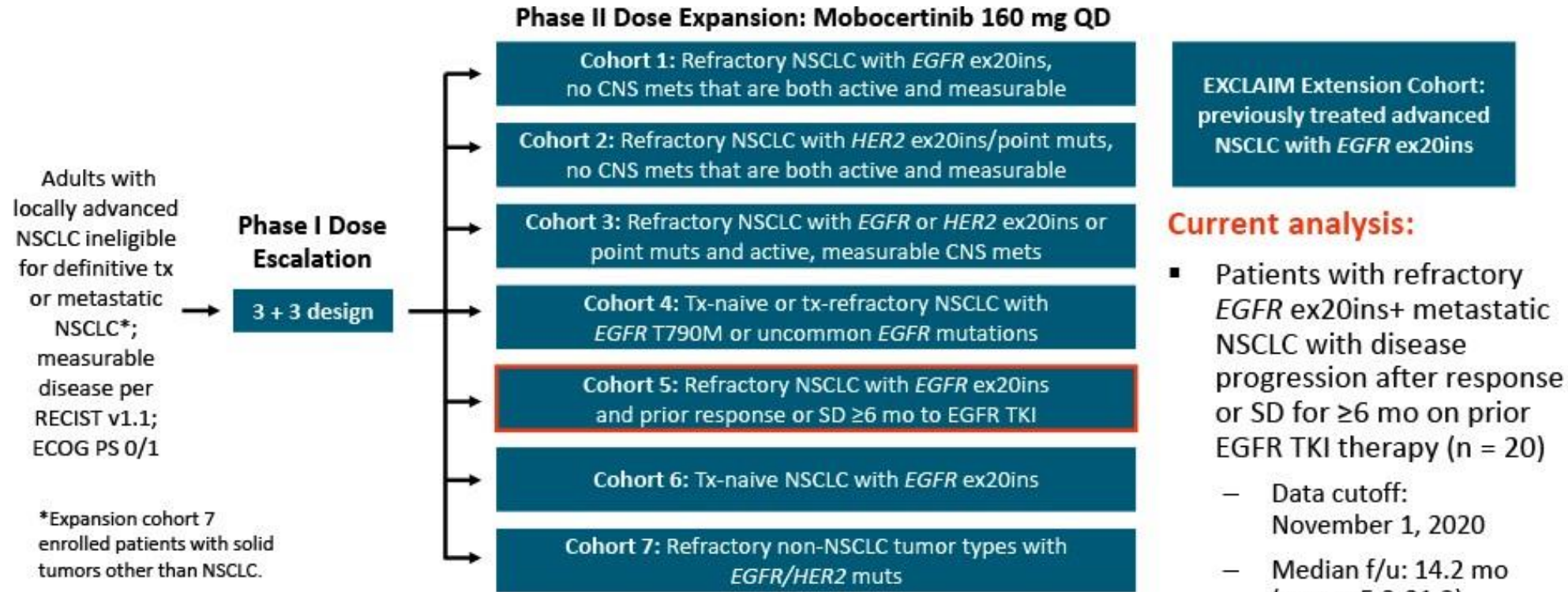
- Similar rate of serious AEs, AEs leading to death and discontinuation due to AEs.
- Treatment-related discontinuations of amivantamab were low (7%)

- EGFR- and MET-related AEs were increased, primarily grade 1-2
- CT-associated hematologic and GI toxicities were comparable except neutropenia
- Neutropenia was transient; majority of events were not serious, low discontinuations
- Pneumonitis was reported in 4 (3%) Amivantamab + CT



# Exon20Ins – MOBOCERTINIB in PRETREATED – EXCLAIM Trial

## Exclaim Trial



- **Primary endpoint (phase II):** ORR by RECIST v1.1
- **Select secondary endpoints (phase II):** ORR by IRC, BOR, DCR, DoR, TTR, PFS, OS, safety/tolerability

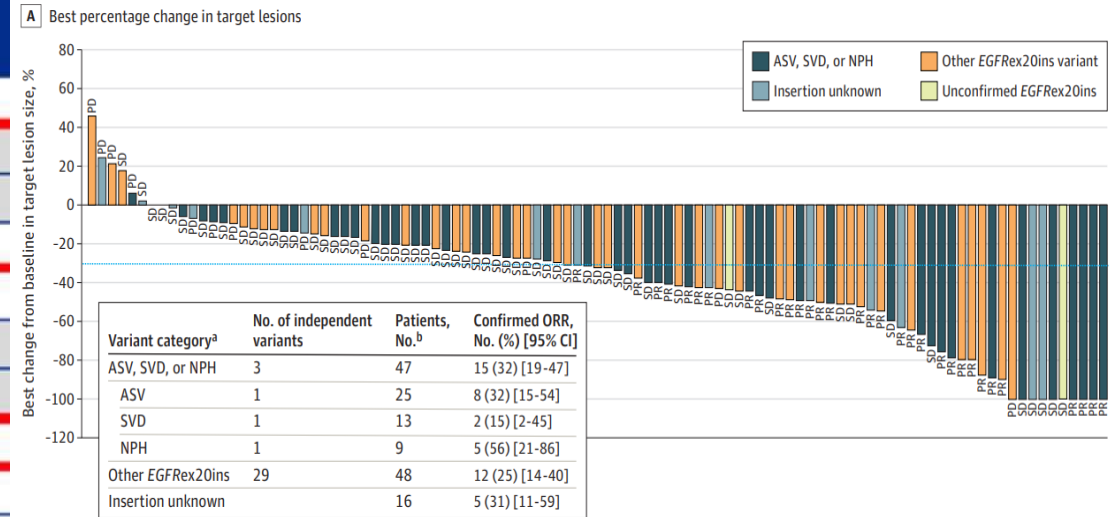


# Exon20Ins – MOBOCERTINIB in PRETREATED – EXCLAIM Trial

## Mobocertinib efficacy

Parameter	PPP Cohort (N=114)	EXCLAIM Cohort (N=96)
Median time on treatment, mo (range)	7.0 (0–31)	6.5 (0–14)
Confirmed ORR per IRC, n (%) [95% CI]	30 (26) [19–35]	22 (23) [15–33]
Confirmed ORR per investigator, n (%) [95% CI]	40 (35) [26–45]	31 (32) [23–43]
Median DOR per IRC, mo [95% CI] <sup>a</sup>	17.5 (8.3–NE)	NE (8.3–NE)
Median DOR per investigator, mo [95% CI] <sup>a</sup>	13.9 (5.6–NE)	NE (5.5–NE)
DCR per IRC, n (%) [95% CI] <sup>b</sup>	89 (78) [69–85]	73 (76) [66–84]
DCR per investigator, n (%) [95% CI] <sup>b</sup>	89 (78) [69–85]	72 (75) [65–83]
Median PFS per IRC, mo [95% CI]	7.3 (5.5–10.2)	7.3 (5.5–10.2)
Median PFS per investigator, mo [95% CI]	7.3 (5.5–8.1)	7.1 (5.6–7.8)

- 78% and 84% of patients had DOR >6 months in PPP and EXCLAIM cohorts, respectively (per IRC)
- At the time of data cutoff, over 50% of responses were ongoing in both cohorts



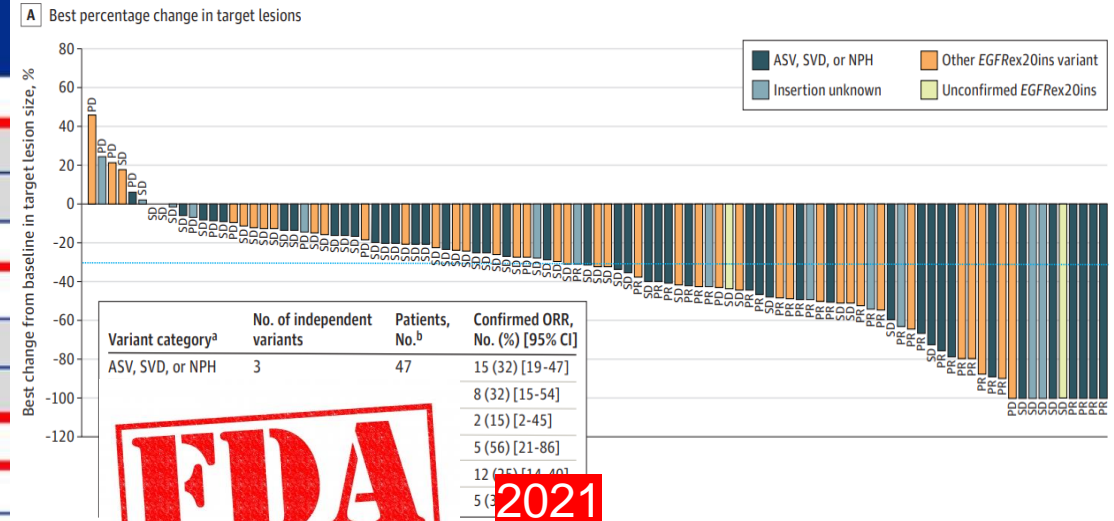


# Exon20Ins – MOBOCERTINIB in PRETREATED – EXCLAIM Trial

## Mobocertinib efficacy

Parameter	PPP Cohort (N=114)	EXCLAIM Cohort (N=96)
Median time on treatment, mo (range)	7.0 (0–31)	6.5 (0–14)
Confirmed ORR per IRC, n (%) [95% CI]	30 (26) [19–35]	22 (23) [15–33]
Confirmed ORR per investigator, n (%) [95% CI]	40 (35) [26–45]	31 (32) [23–43]
Median DOR per IRC, mo [95% CI] <sup>a</sup>	17.5 (8.3–NE)	NE (8.3–NE)
Median DOR per investigator, mo [95% CI] <sup>a</sup>	13.9 (5.6–NE)	NE (5.5–NE)
DCR per IRC, n (%) [95% CI] <sup>b</sup>	89 (78) [69–85]	73 (76) [66–84]
DCR per investigator, n (%) [95% CI] <sup>b</sup>	89 (78) [69–85]	72 (75) [65–83]
Median PFS per IRC, mo [95% CI]	7.3 (5.5–10.2)	7.3 (5.5–10.2)
Median PFS per investigator, mo [95% CI]	7.3 (5.5–8.1)	7.1 (5.6–7.8)

- 78% and 84% of patients had DOR >6 months in PPP and EXCLAIM cohorts, respectively (per IRC)
- At the time of data cutoff, over 50% of responses were ongoing in both cohorts



2021



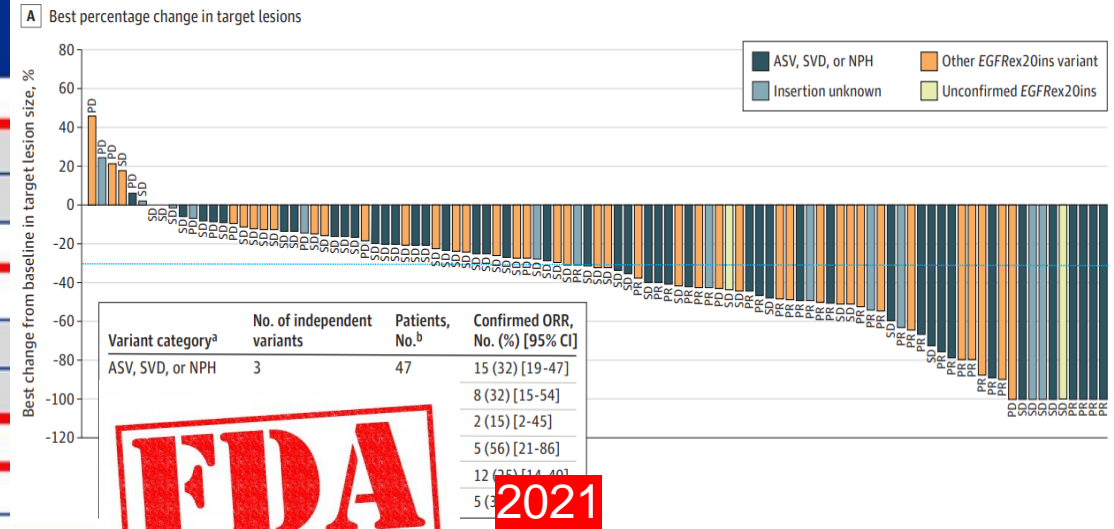
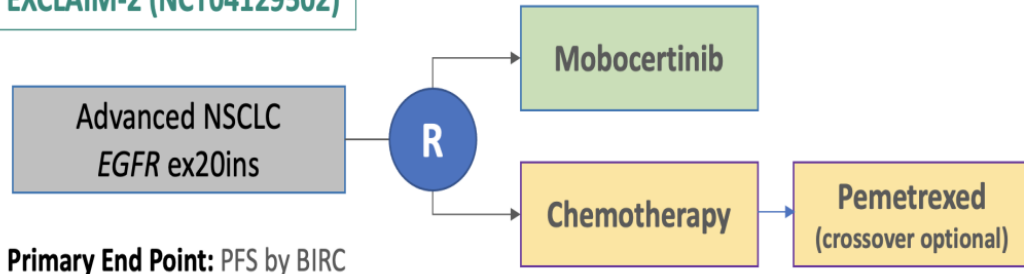
# Exon20Ins – MOBOCERTINIB in PRETREATED – EXCLAIM Trial

## Mobocertinib efficacy

Parameter	PPP Cohort (N=114)	EXCLAIM Cohort (N=96)
Median time on treatment, mo (range)	7.0 (0–31)	6.5 (0–14)
Confirmed ORR per IRC, n (%) [95% CI]	30 (26) [19–35]	22 (23) [15–33]
Confirmed ORR per investigator, n (%) [95% CI]	40 (35) [26–45]	31 (32) [23–43]
Median DOR per IRC, mo [95% CI] <sup>a</sup>	17.5 (8.3–NE)	NE (8.3–NE)
Median DOR per investigator, mo [95% CI] <sup>a</sup>	13.9 (5.6–NE)	NE (5.5–NE)
DCR per IRC, n (%) [95% CI] <sup>b</sup>	89 (78) [69–85]	73 (76) [66–84]
DCR per investigator, n (%) [95% CI] <sup>b</sup>	89 (78) [69–85]	72 (75) [65–83]
Median PFS per IRC, mo [95% CI]	7.3 (5.5–10.2)	7.3 (5.5–10.2)
Median PFS per investigator, mo [95% CI]	7.3 (5.5–8.1)	7.1 (5.6–7.8)

- 78% and 84% of patients had DOR >6 months in PPP and EXCLAIM cohorts, respectively (per IRC)
- At the time of data cutoff, over 50% of responses were ongoing in both cohorts

EXCLAIM-2 (NCT04129502)



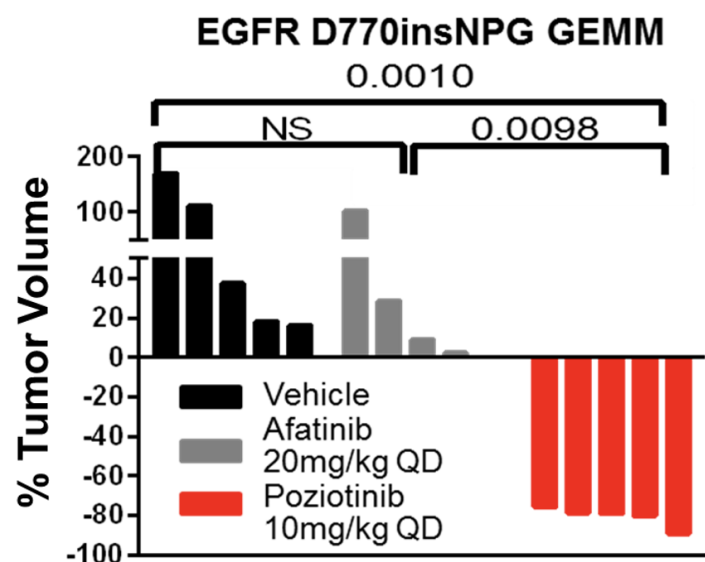
Press release on Oct. 02, 2023

Voluntary withdrawal of mobocertinib in the U.S. based on the outcome of the Phase 3 EXCLAIM-2 which did not meet its primary endpoint.



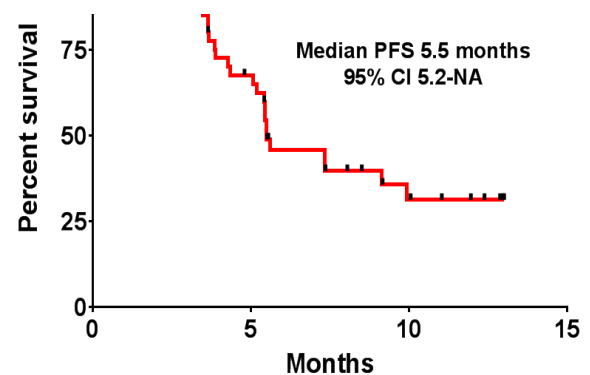
# Exon20Ins – POZIOTINIB in PRETREATED – ZENITH20 (multicohort phase II)

ZENITH20 Poziotinib efficacy in cohort 1 EGFR Exon20ins



## Poziotinib efficacy in EGFR Exon 20 mutant NSCLC

(Evaluable patients n=44)





## Exon20Ins-directed therapies in pretreated pts: efficacy and toxicity summary

Drug	Study	N	Efficacy		Toxicity		
			ORR	mPFS	Rash all/G3	Diarrhoea	Other
Mobocertinib	II	114	28%	7,3 mo	45%/0%	91%/21%	
Poziotinib	II	42	31%	5,5 mo	90%/34%	92%/22%	
Sunvozertinib	II	104	61%	NR	80%/1%	20%/3%	
Zipalertinib	I/IIa	73	38,4%	10 mo	80%/1%	30%/3%	
Furmonertinib	II	26	46%	NR	21%/0%	86%/0%	



## OUTLINE

1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions





## OUTLINE

1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions



## OTHER UNCOMMON MUTATIONS

### *1st Generation TKIs*

- Not included in pivotal trials
- Retrospective and case reports

### *2nd Generation TKIs*

- Lux-lung 2/3/6 included 11% patients with uncommon mutations (100 uncommon, 75 receiving afatinib)
- AFANDA ambispective cohort study with dacomitinib or afatinib

### *3rd Generation TKIs*

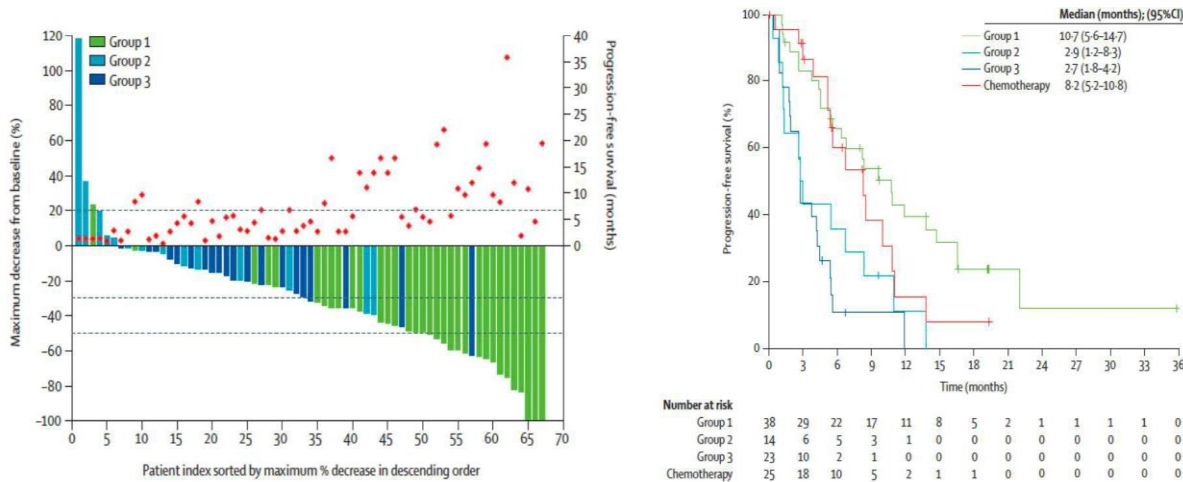
- Retrospective multicenter UNICORN study: 60 pts treated with osimertinib
  - Group A: uncommon.
  - Group B: common + uncommon
- Phase II UNICORN study with osimertinib: 40 pts
- Phase II *KCSG-LU15-09* study with osimertinib: 35 pts



# OTHER UNCOMMON MUTATIONS: AFATINIB 1L

## 2nd Generation TKIs: AFATINIB Lux-Lung 2/3/6 pool

838 pts randomly assigned LL2/3/6 → 100 uncommon EGFRm → 75 receiving afatinib



Genotypes	ORR, n (%)	Median PFS, months (95% CI)	Median OS, months (95% CI)
<b>G719X</b> (n=18) G719X (n=8) G719X + T790M (n=1) G719X + S768I (n=5) G719X + L861Q (n=3) G719X + T790M + L858R (n=1)	14 (78)	13.8 (6.8-NE)	26.9 (16.4-NE)
<b>L861Q</b> (n=16) L861Q (n=12) L861Q + G719X (n=3) L861Q + Del19 (n=1)	9 (56)	8.2 (4.5-16.6)	16.9 (15.3-22.0)
<b>S768I</b> (n=8) S768I (n=1) S768I + G719X (n=5) S768I + L858R (n=2)	8 (100)	14.7 (2.6-NE)	NE (3.4-NE)

Note: A patient may be presented in more than 1 category.

	Objective response	Duration of response (months)	Disease control	Progression-free survival (months)	Overall survival (months)
Group 1 (n=38)*	27 (71.1%, 54.1-84.6)	11.1 (4.1-15.2)	32 (84.2%, 68.7-94.0)	10.7 (5.6-14.7)	19.4 (16.4-26.9)
Group 2 (n=14)†	2 (14.3%, 1.8-42.8)	8.2 (4.1-12.4)	9 (64.3%, 35.1-87.2)	2.9 (1.2-8.3)	14.9 (8.1-24.9)
Group 3 (n=23)‡	2 (8.7%, 1.1-28.0)	7.1 (4.2-10.1)	15 (65.2%, 42.7-83.6)	2.7 (1.8-4.2)	9.2 (4.1-14.2)

Data are n (%; 95% CI) or median (95% CI). \* Consists of patients with all point mutations or duplications in exons 18-21 (Leu861Gln, Gly719Ser, Gly719Ala, Gly719Cys, Ser768Ile, and rare others). † Consists of patients with de-novo Thr790Met mutations. ‡ Consists of patients with exon 20 insertions.



# OTHER UNCOMMON MUTATIONS: AFATINIB 1L

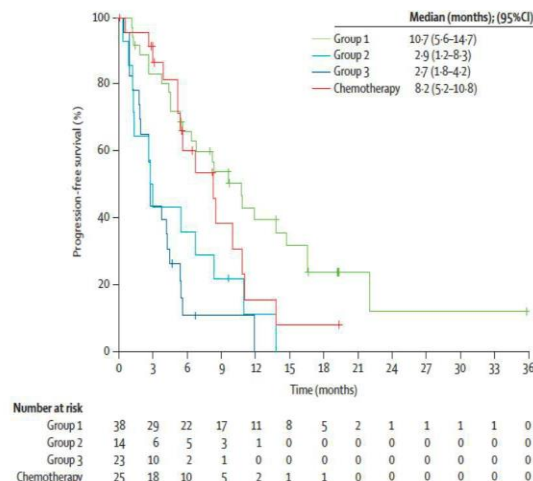
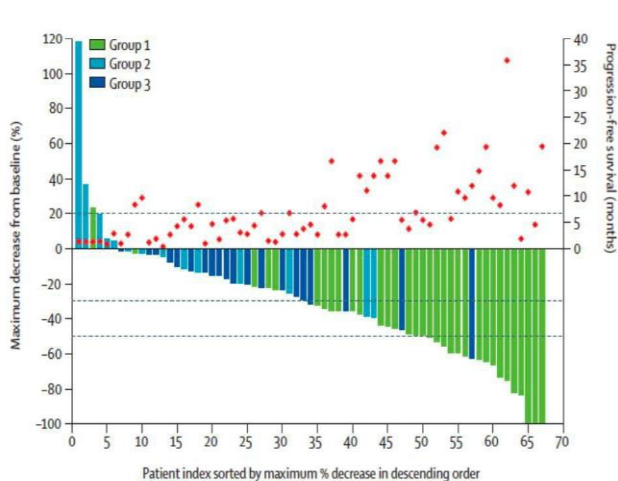


2018

## 2nd Generation TKIs: AFATINIB Lux-Lung 2/3/6 pool

L861Q, G719X and S768I.

838 pts randomly assigned LL2/3/6 → 100 uncommon EGFRm → 75 receiving afatinib



Group	38	29	22	17	11	8	5	2	1	1	1	1	0
Group 1	38	29	22	17	11	8	5	2	1	1	1	1	0
Group 2	14	6	5	3	1	0	0	0	0	0	0	0	0
Group 3	23	10	2	1	0	0	0	0	0	0	0	0	0
Chemotherapy	25	18	10	5	2	1	1	0	0	0	0	0	0

Genotypes	ORR, n (%)	Median PFS, months (95% CI)	Median OS, months (95% CI)
<b>G719X</b> (n=18) G719X (n=8) G719X + T790M (n=1) G719X + S768I (n=5) G719X + L861Q (n=3) G719X + T790M + L858R (n=1)	14 (78)	13.8 (6.8-NE)	26.9 (16.4-NE)
<b>L861Q</b> (n=16) L861Q (n=12) L861Q + G719X (n=3) L861Q + Del19 (n=1)	9 (56)	8.2 (4.5-16.6)	16.9 (15.3-22.0)
<b>S768I</b> (n=8) S768I (n=1) S768I + G719X (n=5) S768I + L858R (n=2)	8 (100)	14.7 (2.6-NE)	NE (3.4-NE)

Note: A patient may be presented in more than 1 category.

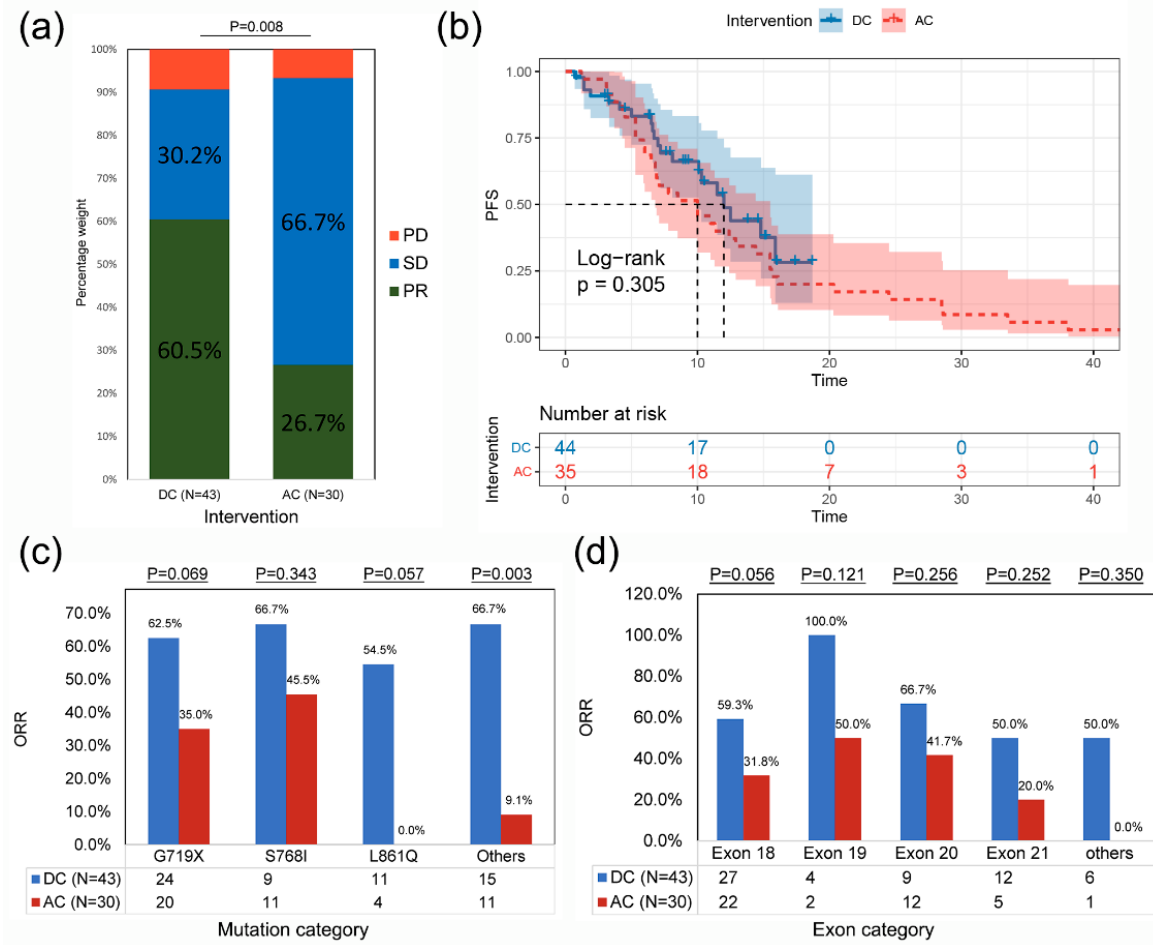
	Objective response	Duration of response (months)	Disease control	Progression-free survival (months)	Overall survival (months)
Group 1 (n=38)*	27 (71.1%, 54.1-84.6)	11.1 (4.1-15.2)	32 (84.2%, 68.7-94.0)	10.7 (5.6-14.7)	19.4 (16.4-26.9)
Group 2 (n=14)†	2 (14.3%, 1.8-42.8)	8.2 (4.1-12.4)	9 (64.3%, 35.1-87.2)	2.9 (1.2-8.3)	14.9 (8.1-24.9)
Group 3 (n=23)‡	2 (8.7%, 1.1-28.0)	7.1 (4.2-10.1)	15 (65.2%, 42.7-83.6)	2.7 (1.8-4.2)	9.2 (4.1-14.2)

Data are n (%; 95% CI) or median (95% CI). \* Consists of patients with all point mutations or duplications in exons 18-21 (Leu861Gln, Gly719Ser, Gly719Ala, Gly719Cys, Ser768Ile, and rare others). † Consists of patients with de-novo Thr790Met mutations. ‡ Consists of patients with exon 20 insertions.



# OTHER UNCOMMON MUTATIONS: DACOMITINIB 1L

2nd Generation TKIs: DACOMITINIB - AFANDA ambispective cohort study in China







## OTHER UNCOMMON MUTATIONS – OSIMERTINIB 1L

3rd Generation TKIs: UNICORN phase II (Tokyo Cooperative Oncology Group)

Solitary mutations (n = 22)		Compound mutations (n = 18)	
Overall response rate, % (90% CI)	45.5 (26.9-65.3)	Overall response rate, % (90% CI)	66.7 (43.7-83.7)
Disease control rate, % (95% CI)	81.8 (61.5-92.7)	Disease control rate, % (95% CI)	100.0 (82.4-100)
Progression-free survival, median (95% CI), mo	5.4 (3.6-22.7)	Progression-free survival, median (95% CI), mo	9.8 (5.1-NR)
Overall survival, median (95% CI), mo	23.0 (12.3-NR)	Overall survival, median (95% CI), mo	NR
Duration of response, median (95% CI), mo	22.7 (3.6-22.7)	Duration of response, median (95% CI), mo	NR (5.7-NR)



# OTHER UNCOMMON MUTATIONS – OSIMERTINIB 1L

3rd Generation TKIs: UNICORN phase II (Tokyo Cooperative Oncology Group)

Solitary mutations (n = 22)		Compound mutations (n = 18)	
Overall response rate, % (90% CI)	45.5 (26.9-65.3)	Overall response rate, % (90% CI)	66.7 (43.7-83.7)
Disease control rate, % (95% CI)	81.8 (61.5-92.7)	Disease control rate, % (95% CI)	100.0 (82.4-100)
Progression-free survival, median (95% CI), mo	5.4 (3.6-22.7)	Progression-free survival, median (95% CI), mo	9.8 (5.1-NR)
Overall survival, median (95% CI), mo	23.0 (12.3-NR)	Overall survival, median (95% CI), mo	NR
Duration of response, median (95% CI), mo	22.7 (3.6-22.7)	Duration of response, median (95% CI), mo	NR (5.7-NR)

Uncommon and uncommon mutations (n = 11)		Common and uncommon mutations (n = 7)	
Overall response rate, % (90% CI)	54.5 (28.0-78.7)	Overall response rate, % (90% CI)	85.7 (54.8-96.7)
Disease control rate, % (95% CI)	100.0 (74.1-100.0)	Disease control rate, % (95% CI)	100.0 (64.6-100.0)
Progression-free survival, median (95% CI), mo	9.7 (3.7-NR)	Progression-free survival, median (95% CI), mo	15.2 (2.9-NR)
Overall survival, median (95% CI), mo	NR (9.8-NR)	Overall survival, median (95% CI), mo	NR (9.7-NR)
Duration of response, median (95% CI), mo	NR (5.6-22.7)	Duration of response, median (95% CI), mo	NR (5.8-NR)

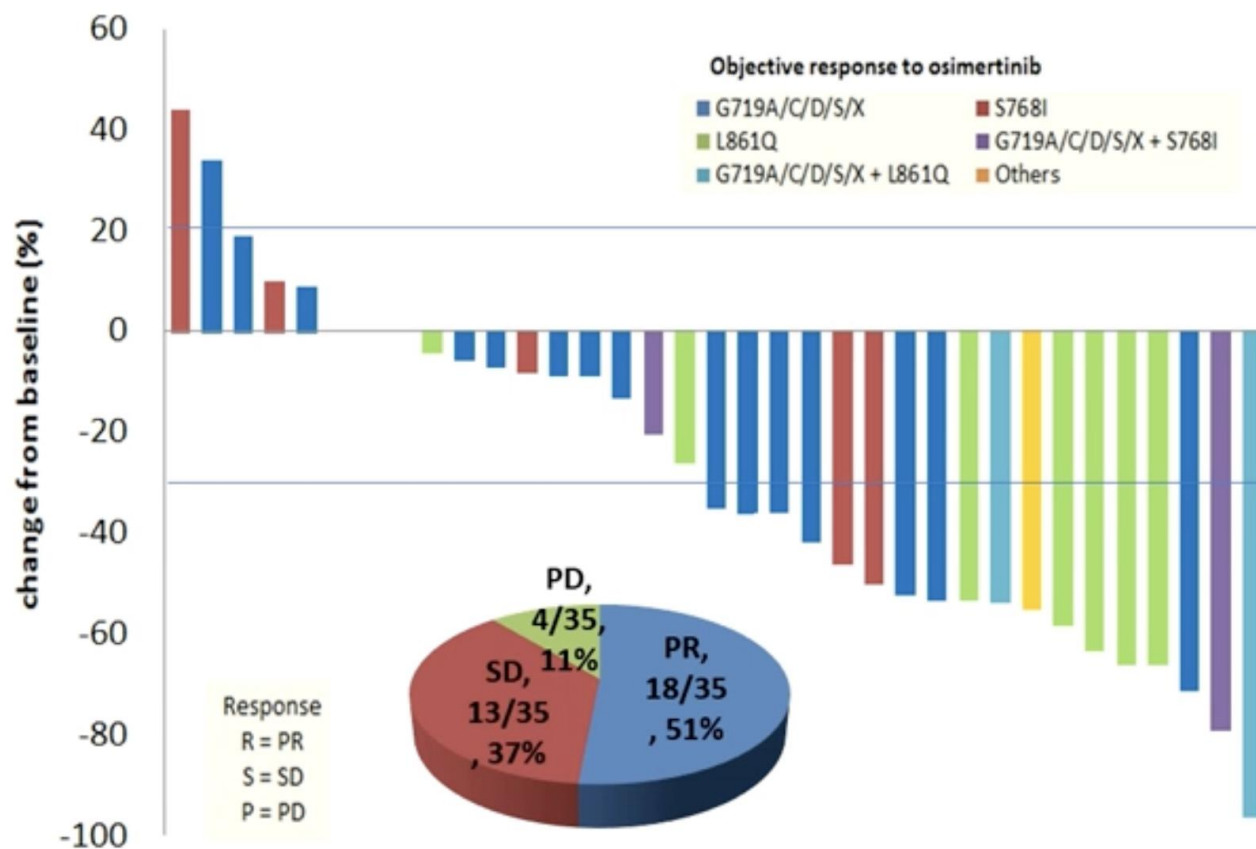




# OTHER UNCOMMON MUTATIONS – OSIMERTINIB 1L

3rd Generation TKIs: KCSG-LU15-09 phase II

**L861Q: RR 78%**



Clinical response	Osimertinib (n=35)
Objective response rate (95% CI)	51% (34, 68)
Disease control rate (95% CI)	89% (78, 99)
Median progression-free survival, months (95% CI)	8.0 (5.7, 10.3)
Median overall survival, months (95% CI)	27.0 (19.3, 34.7)
Median duration of response, months (95% CI)	13.0 (9.1, 16.9)
Median progression-free survival 2, months (95% CI)	16.0 (8.5, 23.5)

•Median follow-up duration: 61.0 months



## OUTLINE

1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions



## OUTLINE

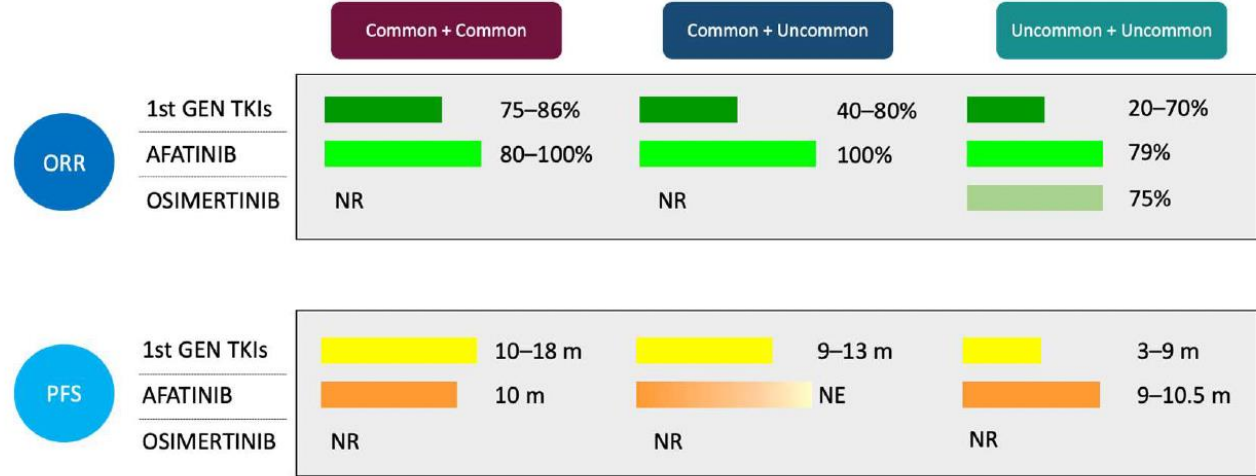
1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. **Compound mutations**
6. How to treat uncommon mutations algorithm
7. Conclusions



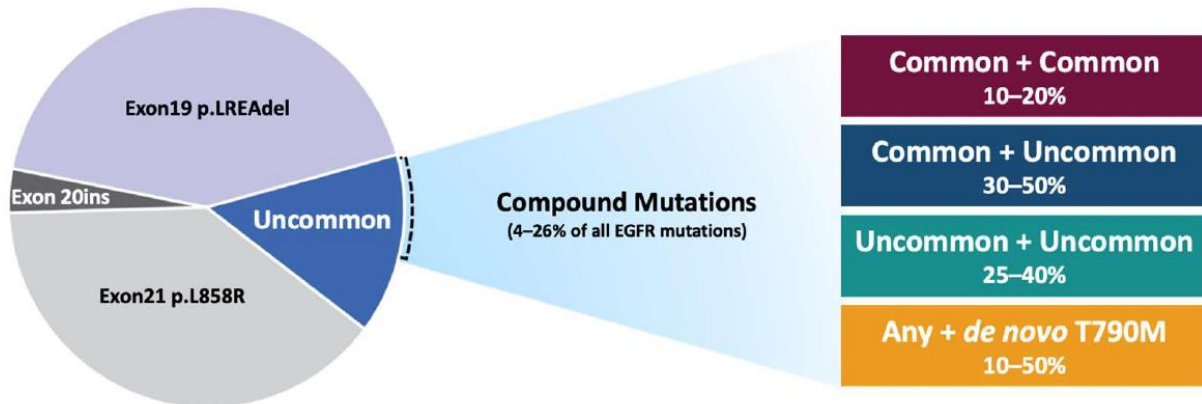
# COMPOUND EGFR MUTATIONS

Frequency and subtypes according to a 2022 Systematic Review

Study	Region	Patients Screened (N)	Testing Method	EGFR Mut Rate (N, %)	EGFR Compound Mut Rate (N, % of EGFR Mut)
Syahrudin et al., 2018 [7]	Indonesian	1779	PCR HRM RFLP	791 (44.4)	154 (19.5)
Zaini et al., 2019 [8]	Indonesian	116	PCR HRM RFLP	69 (63.2)	18 (26)
Jing et al., 2018 [9]	China	112	NGS	58 (51.8)	11 (18.9)
Mao et al., 2021 [11]	China	21,324	NGS + qPCR + Sanger	9,621 (47.5)	642 (6.7)
Wen et al., 2019 [14]	China	1200	NGS	571(47.6)	87 (15.3)
Zhou et al., 2021 [12]	SW China (Q vs. non-Q)	2146	ARMS-PCR	346 (46) Q 710 (51) non-Q	151 (43.6) Q 74 (10.4) non-Q
Namba et al., 2019 [10]	Japan	531	MBS	64 (n.e.) <sup>1</sup>	8 (12.5)
Shi et al., 2013 [13]	Malaysia	484	ARMS + HRM	221 (45.7)	9 (4)
Evans et al., 2019 [15]	EU	17,782	qPCR	1,737 (10.7)	79 (4.9)
Sousa et al., 2020 [17]	EU	1228	Sanger	252 (20.5)	19 (7.5)
Martin et al., 2019 [16]	EU	2906	Sanger	408 (14)	22 (5.4)



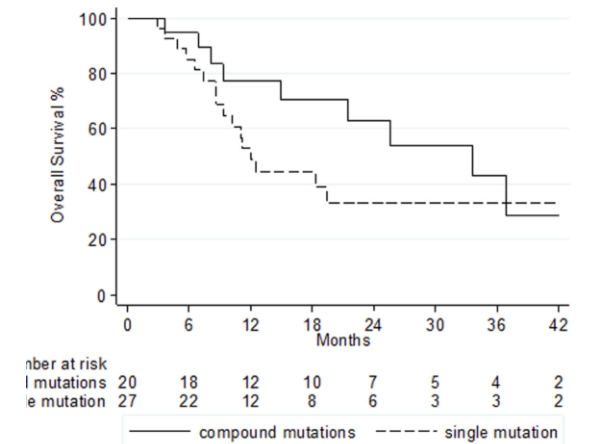
\*Sensitivity of the co-mutation drivers the overall response to different TKIs



**Potential activity**

3rd G\* > 2nd G > 1st G  
 2nd G > 3rd G\* > 1st G  
 2nd G > 3rd G  
 3rd G

\*lacking data





## OUTLINE

1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions

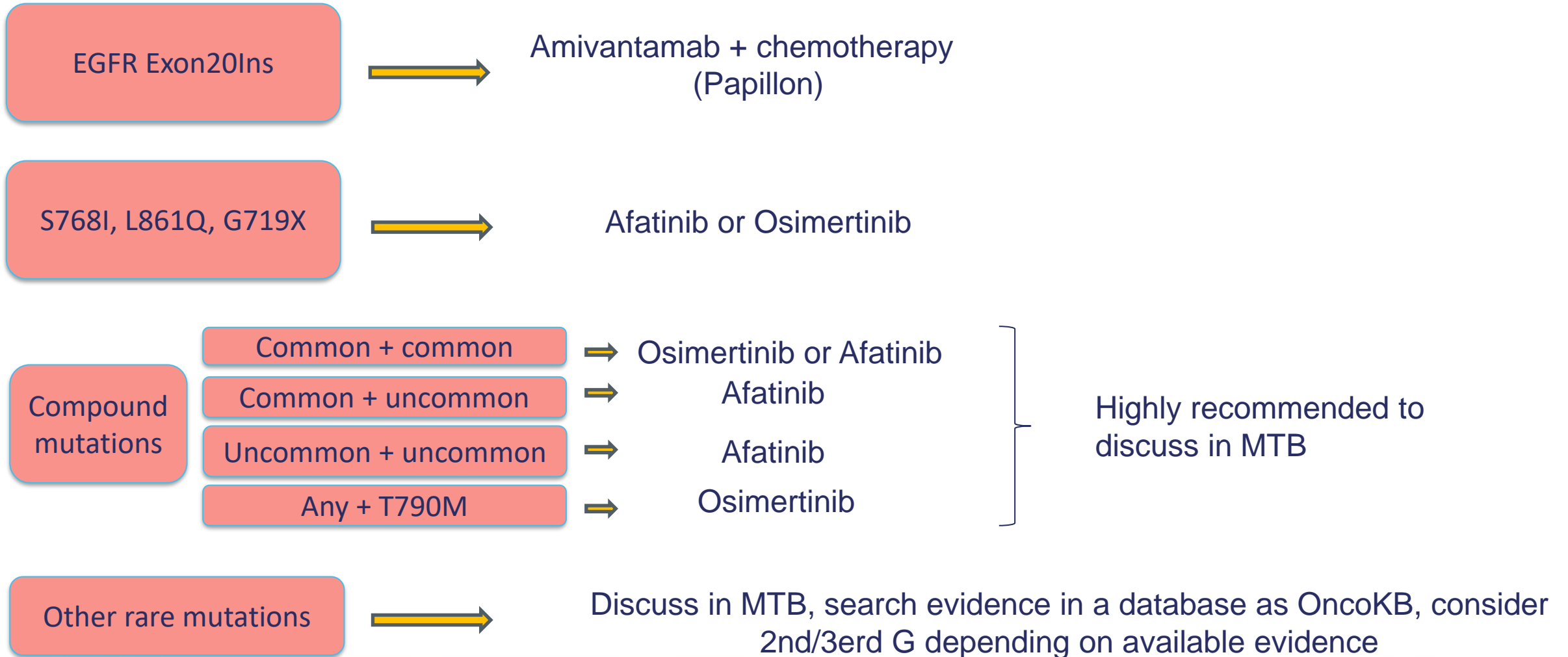


## OUTLINE

1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions



## So...how to treat uncommon EGFR mutations?





## OUTLINE

1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions





## OUTLINE

1. Uncommon EGFR mutation subtypes and classification
2. Molecular testing options
3. Exon 20 Insertions
4. Other uncommon EGFR point mutations
5. Compound mutations
6. How to treat uncommon mutations algorithm
7. Conclusions



## TAKE HOME MESSAGES

- Sensitive methods sequencing the entire EGFR gene is recommended to identify and characterize uncommon mutations, NGS preferred.
- Exon20Ins is a distinct entity with low activity of classical TKIs
  - Amivantamab + chemotherapy significantly improved PFS vs chemo in 1st line (new SoC)
  - Several promising specific TKIs in development
- EGFR TKIs should be considered in frontline treatment of G719X, L861X and S768I
  - Available evidence suggest better outcomes with 2nd G TKIs (afatinib) in G719X and S768I and 3rd G in L861Q
- Few clinical data in compound mutations
  - Sensitivity of the co-mutation drivers the overall response to different TKIs
- Further research is needed

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

#15CongressGeCP

**Muchas Gracias**