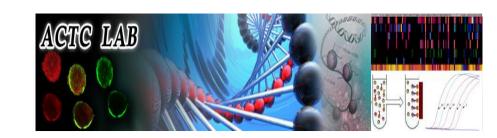


Detection of EGFR Mutations in Plasma cfDNA and Paired CTCs of NSCLC Patients before and after Osimertinib Therapy Using Crystal Digital PCR



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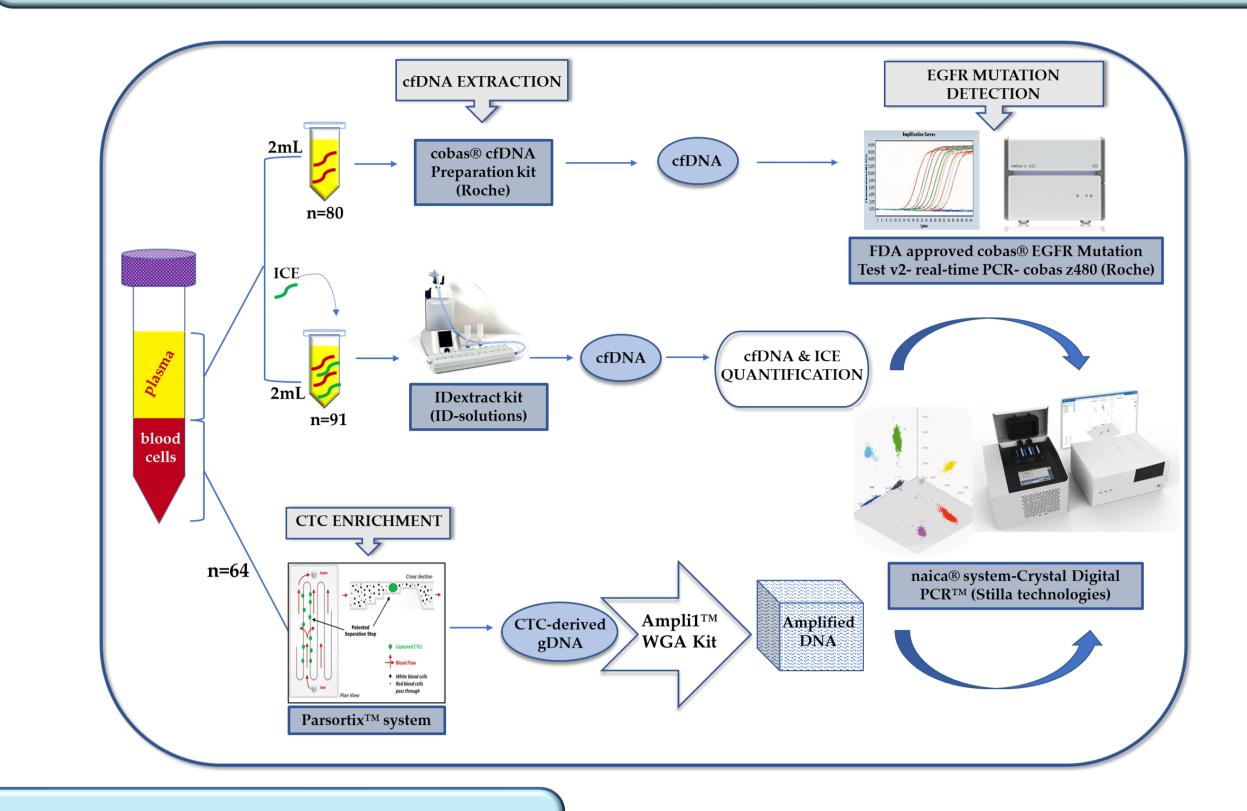
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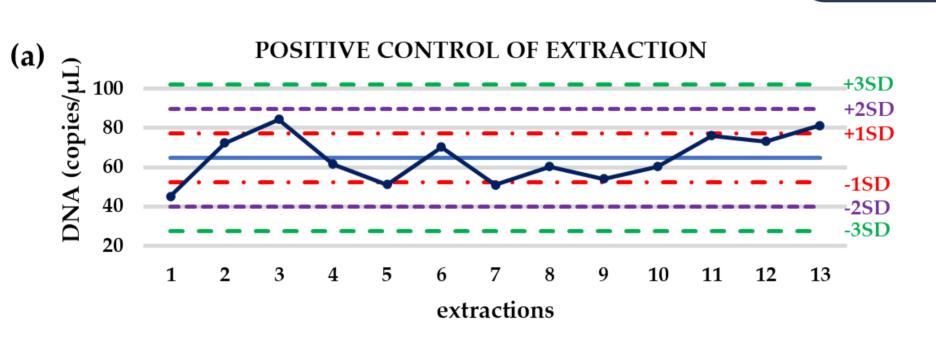


- **Osimertinib** is administered as 2nd line treatment in NSCLC patients resistant to 1st and 2nd generation EGFR TKIs.
- **Liquid biopsy as a minimally invasive method consists a more** feasible approach to track tumor evolution during therapy
- **Digital PCR consists a breeding ground for molecular analysis in the** field of oncology by providing improved precision, increased dynamic range and analytical sensitivity while detecting rare events.

Experimental Flowchart



Our our aim was to use crystal digital PCR technology to detect the presence and %MAF of EGFR mutations in plasma cfDNA and matched CTC fractions of 48 NSCLC patients before and after osimertinib therapy in the context of a Phase II multicenter clinical study (NCT02771314)



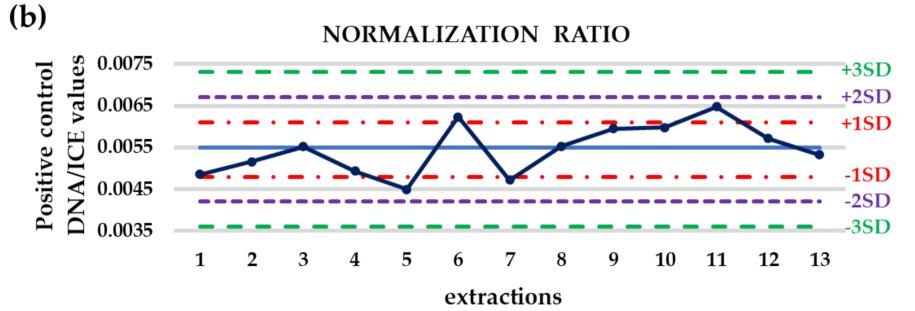


Figure 1. Levey-Jennings graphs for the evaluation of extraction process based on a) DNA con-centration (copies/µL) of the target positive control of extraction and on b) normalized positive control DNA/ICE values

During cfDNA extraction, internal extraction control (ICE) was added in every sample to assess the efficiency of the extraction

Results

Levey-Jennings graphs showed that most of the positive control either values presented as concentrations or as normalized DNA values were within ±1SD (Fig.1)

cases, plasma cfDNA some In levels were significantly increased at PD compared to baseline (Fig.2)

p=0.006

Months

before treatment with osimertinib and at PD

30.00

20.00

- GROUP A

- GROUP B

40.00

- GROUP A-censored

- GROUP B-censored

50.00

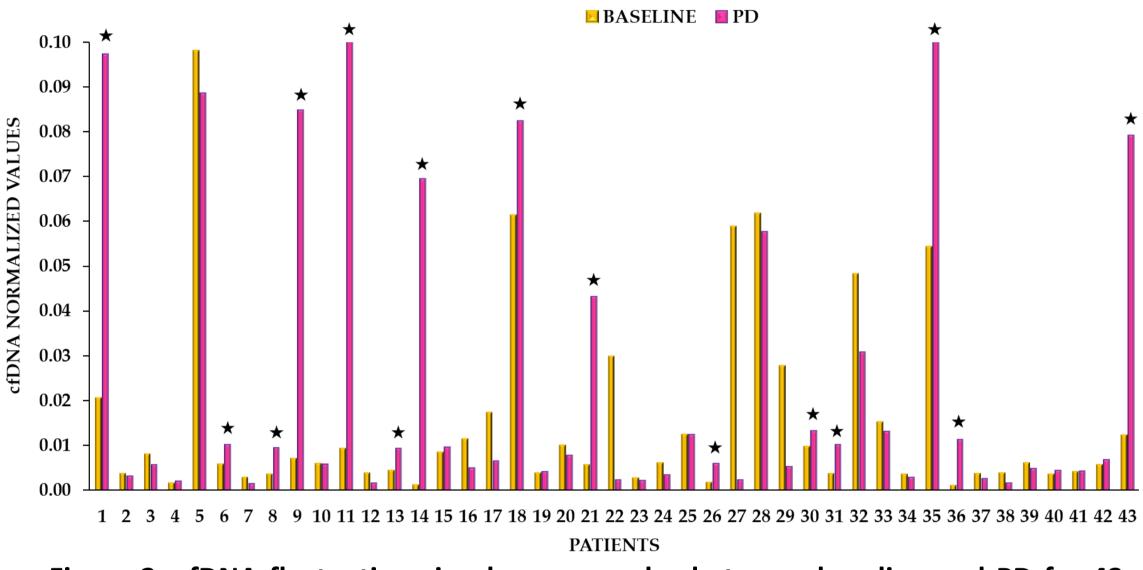
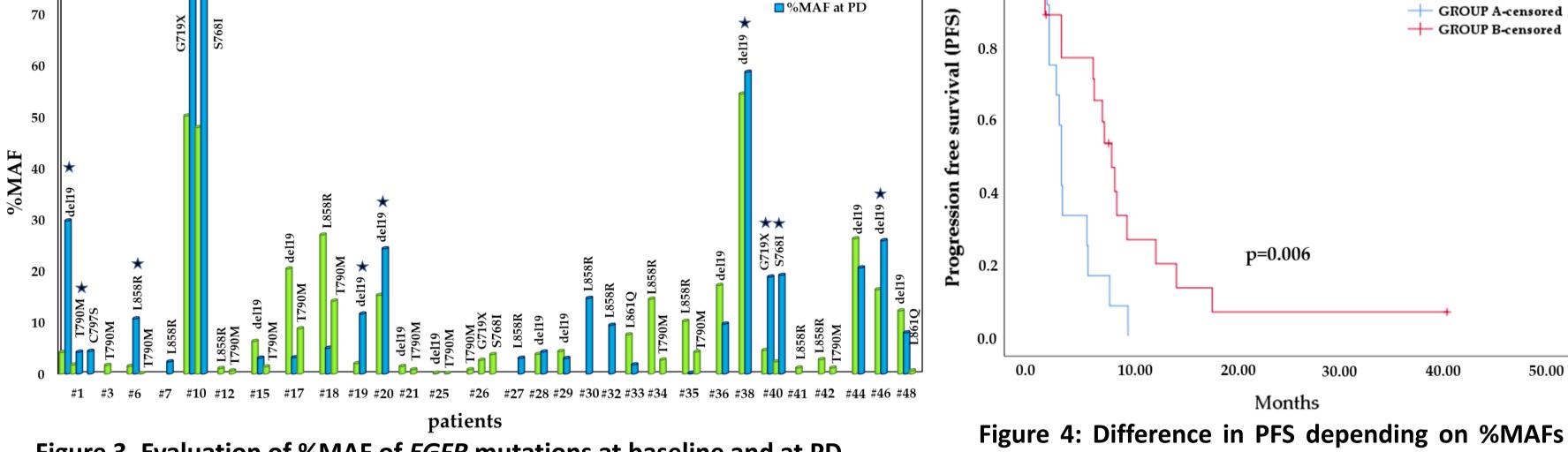


Figure 2. cfDNA fluctuations in plasma samples between baseline and PD for 43 patients based on normalized cfDNA values, \star : cases where normalized cfDNA values are higher in PD than at the baseline

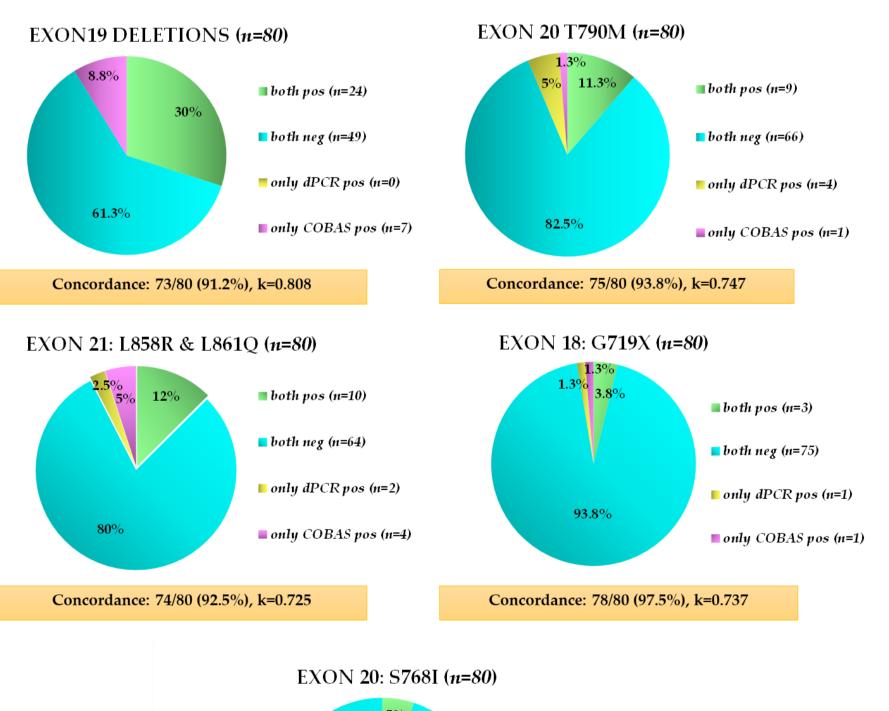
□ We compared the % MAFs of each type of *EGFR* mutation in plasma between baseline and PD. In some patients, mutations disappear at PD and in others are maintained or reemerge. In patients #1, #6, #10, #19, #20, #38, #40, #46, %MAFs for various EGFR mutations were significantly increased at PD (Fig.3). Patients with higher %MAFs at PD (Group A) presented significantly lower PFS compared to those that lost EGFR mutations after osimertinib therapy (Group B) (Fig.4).



■ %MAF at baseline

1.0

Figure 3. Evaluation of %MAF of EGFR mutations at baseline and at PD, \star : cases where %MAF are higher in PD than at the baseline



between group A and group B comparison of crystal **Direct** dPCR and the FDA approved cobas[®] EGFR Mutation test in identical plasma samples 80 from both time points revealed high concordance rates for all EGFR mutations (Fig.5) In some cases, crystal dPCR was more sensitive in detecting the

- key resistance EGFR mutation, T790M.
- **U** Direct comparison of EGFR genotyping between primary

						_
ntients	primary tissue	crystal dPCR				🗧 : exon19 deletion
		plasma			ved gDNA	🗧 : T790M
		baseline	PD	baseline	PD	:C797S
#1	••			\otimes	\otimes	: L858R
#2	••	\otimes	\otimes	\otimes	\otimes	:L861Q
#3	••	•		\otimes		Exon 20 In sertion
=4		\otimes	\otimes	\otimes	\otimes	• : G719X
#5	•	\otimes	\otimes	\otimes	\otimes	• :5768I
#6	•	•	•	NA	\otimes	-
#7	•	\otimes	•	•	\otimes	⊗ :wild type NA :not available
#8	•	\otimes	\otimes	NA	\otimes	: under therapy
<i>=</i> 9	•	\otimes	•	\otimes	\otimes	, runner uner up y
<i>=</i> 10	• •		• •	• •		
#11	•	\otimes	\otimes	•	\otimes	
#12	•	•	\otimes	\otimes	•	
#13		\otimes		NA		
#14	•	\otimes	\otimes	\otimes	\otimes	
#15	••	••		\otimes	NA	
#16		\otimes	\otimes	NA	\otimes	
<i>=</i> 17	••	••		NA	•	
#18	🔵 🔴	0 🔴	•	0	•	EGF
#19	•		•	NA	NA	
#20	••		•	•	NA	fror
#21	••	•	\otimes	NA	NA	
#22	••	\otimes		0	ļ	
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<i>=</i> 26	• •		\otimes	NA	\otimes	
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#31	••	\otimes	\otimes	\otimes	\otimes	[e]]
#32	•	\otimes	•	NA	\otimes	
#33	0	0	0	NA	\otimes	aha

- 64 matched **CTC-derived** gDNA samples were analyzed for the detection of EGFR mutations using crystal dPCR.
- **.1** samples were found positive for EGFR mutations with %MAF ranging from 0.2 to 2.25%.
- Differences in EGFR genotyping petween plasma and CTCs might reflect tumor heterogeneity that characterizes NSCLC and also the

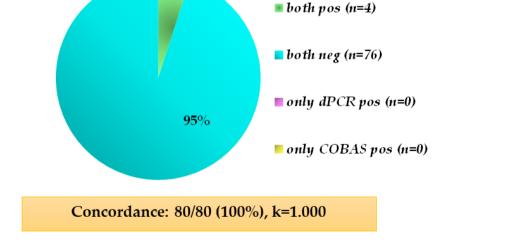
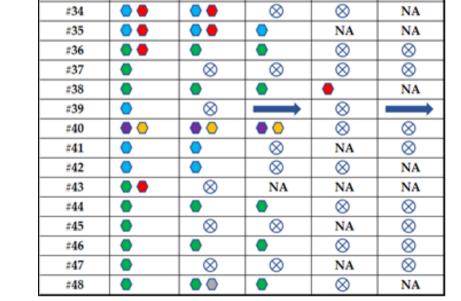


Figure 5. Direct comparison of EGFR mutations detected with

crystal dPCR and FDA-approved cobas[®] EGFR mutation test v2

cfDNA and plasma tissue samples revealed high rates of concordance for the EGFR the mutations.



presence of resistance mechanisms that occur under selective therapy pressure due to dominance of T790M wild type clones.

Conclusions

- Crystal dPCR, a highly sensitive technology, allowed to track tumor evolution through the detection of low abundance EGFR mutations in cfDNA and CTCs predictive for the treatment outcomes of NSCLC patients under osimertinib treatment.
- **Crystal dPCR exhibited high concordance rates in correlation with** the FDA-approved cobas technology.
- □ In some cases, crystal dPCR was more sensitive in detecting the T790M mutation.
- □ For the first time, crystal dPCR was applied to detect EGFR mutations in CTC-derived gDNA samples of NSCLC patients under osimertinib.
- **Discrepancies found between CTCs and tumor or** cfDNA genotyping, confirmed previous evidence about tumor heterogeneity and clonal evolution in NSCLC.

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Reference

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