

Analytical validation of the RESOLUTION ctDx FIRST plasma assay as a companion diagnostic for adagrasib and its application to longitudinal monitoring

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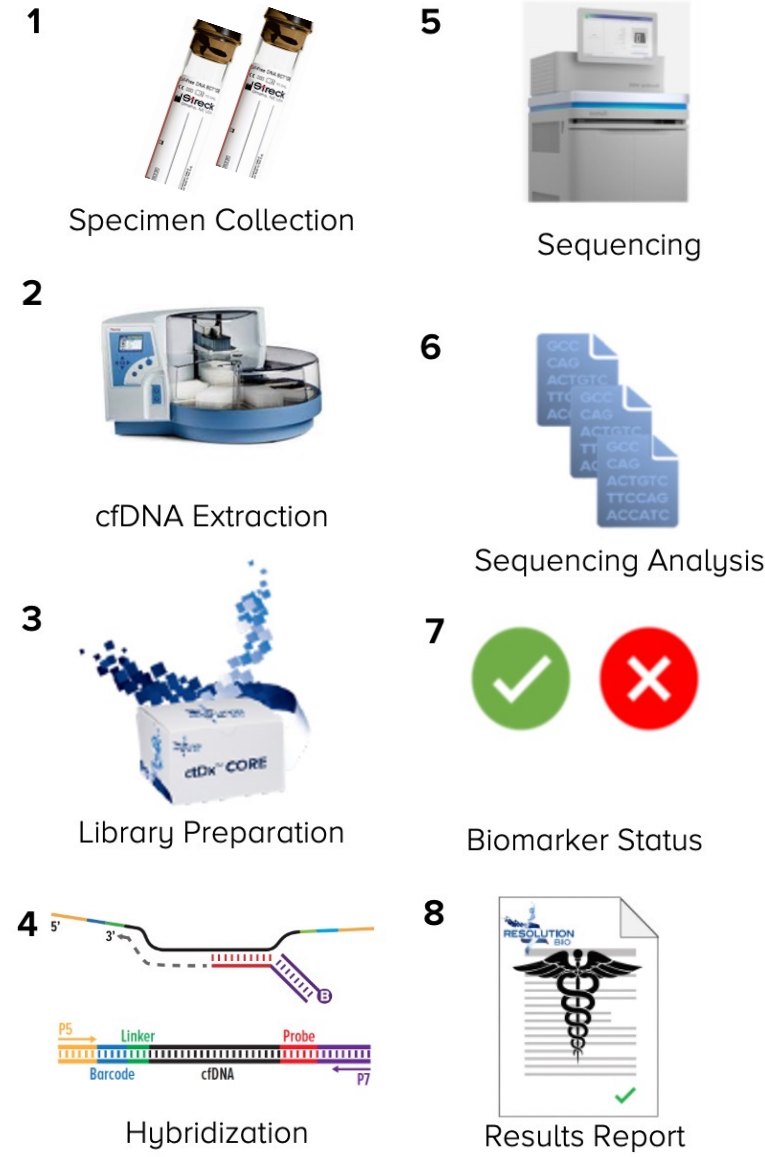
Introduction

RESOLUTION ctDx FIRST (IUO) is a targeted-hybrid capture, next generation sequencing (NGS) liquid biopsy assay which uses circulating cell-free DNA (cfDNA) isolated from plasma.

It is under development as a CDx in the identification of NSCLC patients who may potentially benefit from adagrasib: an investigational, highly selective, oral small molecule inhibitor of KRAS G12C (Mirati Study 849-001).

RESOLUTION ctDx FIRST assay allows sensitive detection of alterations in the genes listed in Fig 1. Isolating cfDNA from blood is minimally invasive and can inform clinical decisions and is of special benefit to NSCLC patients, many without lesions accessible by tissue biopsy testing.

RESOLUTION ctDx FIRST Overview



Specimens are collected in 10 mL Streck cell-free DNA BCT tubes and cfDNA is extracted from 2 - 4 mL plasma. Library preparation is done by a Hamilton Microlab STAR Liquid Handling System. After hybridization, capture, and sequencing, custom software performs bioinformatics, data analysis and reporting.

RESOLUTION ctDx FIRST	
Main Features	Intended Use
113 Genes	Identify NSCLC patients with KRAS G12C mutations as candidates for treatment with adagrasib
74 genes with full CDS coverage	
Targeting ~2096 pathogenic hotspots	
LPWG	
MSI	
dMMR	
23 genes with deletion detection	

ABL1	DDR2	JAK1	PMS2	AKT1	ERBB3	NTRK1	ALK
AKT1	DNMT3A	JAK2	POLE	AKT2	ERBB4	PALB2	BRAF
AKT2	EGFR	KEAP1	PTCH1	AR	ERCC2	PDGFRA	EGFR
ALK	ERBB2	KIT	PTEN	ARAF	ESR1	PDGFRB	ETV6
AR	ERBB3	KRAS	PTPNH1	ARID1A	EZH2	PIK3CA	FGFR1
ARAF	ERBB4	MAP2K1	RAC1	ATM	FANCA	PMS2	FGFR2
ARID1A	ERCC2	MAP2K2	RAD50	ATR	FBXW7	PTEN	FGFR3
ATM	ESR1	MDM2	RAD51B	B2M	FGF19	RAC1	NRG1
ATR	EZH2	MET	RAD51C	BAP1	FGF3	RAD51C	NTRK1
ATRX	FANCA	MLH1	RAD51D	BRAF	FGF4	RAF1	NTRK2
B2M	FANCC	MSH2	RAD54L	BRCA1	FGFR1	RB1	NTRK3
BAP1	FANCL	MSH6	RAF1	BRCA2	FGFR2	RET	RAF1
BARD1	FBXW7	MTOR	RB1	BRD4	FGFR3	RICTOR	RET
BRAF	FGF3	MYC	RET	BRIP1	FGFR4	ROS1	ROS1
BRCA1	FGFR1	MYD88	RICTOR	CCND1	FLT3	SMARCA4	
BRCA2	FGFR2	NF1	ROS1	CCND2	HGF	SMARCB1	ALK
BRD4	FGFR3	NF2	SMARCA4	CCNE1	JAK2	SMO	BRAF
BRIP1	FGFR4	NPM1	SMARCB1	CD274	KIT	STK11	EGFR
CCND1	FLT3	NRAS	SMO	CDK12	KRAS	TERT	FLT3
CD274	GNA11	NTRK1	STAG2	CDK4	MDM2	TP53	KIT
CDK12	GNAQ	NTRK2	STK11	CDK6	MET	TSC2	
CDK4	GNAS	NTRK3	TERT	CDKN2A	MYC	VEGFA	
CDKN2A	HGF	PALB2	TP53	CDKN2B	NF1	VHL	
CHEK1	HRAS	PDGFRA	TSC1	CHEK2	NF2		
CHEK2	IDH1	PDGFRB	TSC2	EGFR	NPM1		
CTNNB1	IDH2	PIK3CA	VHL	ERBB2	NRAS		

Full CDS Coverage

Hotspot Coverage

Gene Amplification

Gene Deletion

Amplification & Deletion

Gene Fusions

Rearrangements

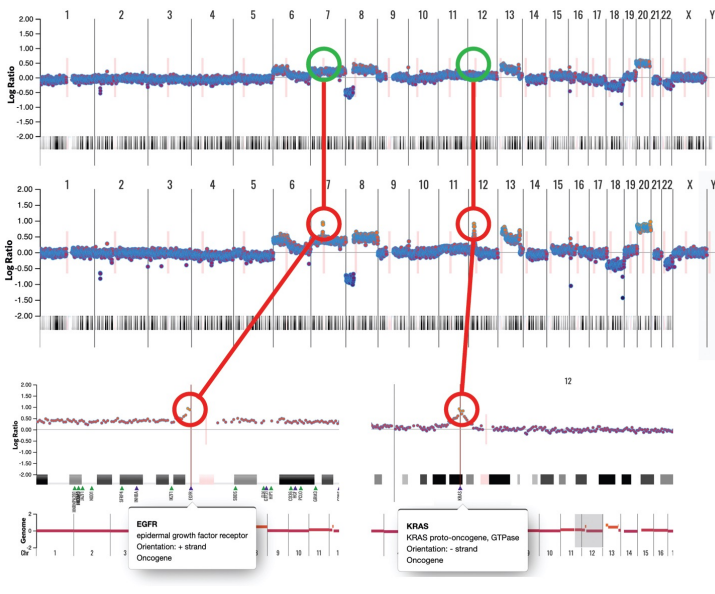
Figure 1. Alterations detected by RESOLUTION ctDx FIRST

Longitudinal Monitoring: CRC Patients at progression developed resistance and new driver mutations

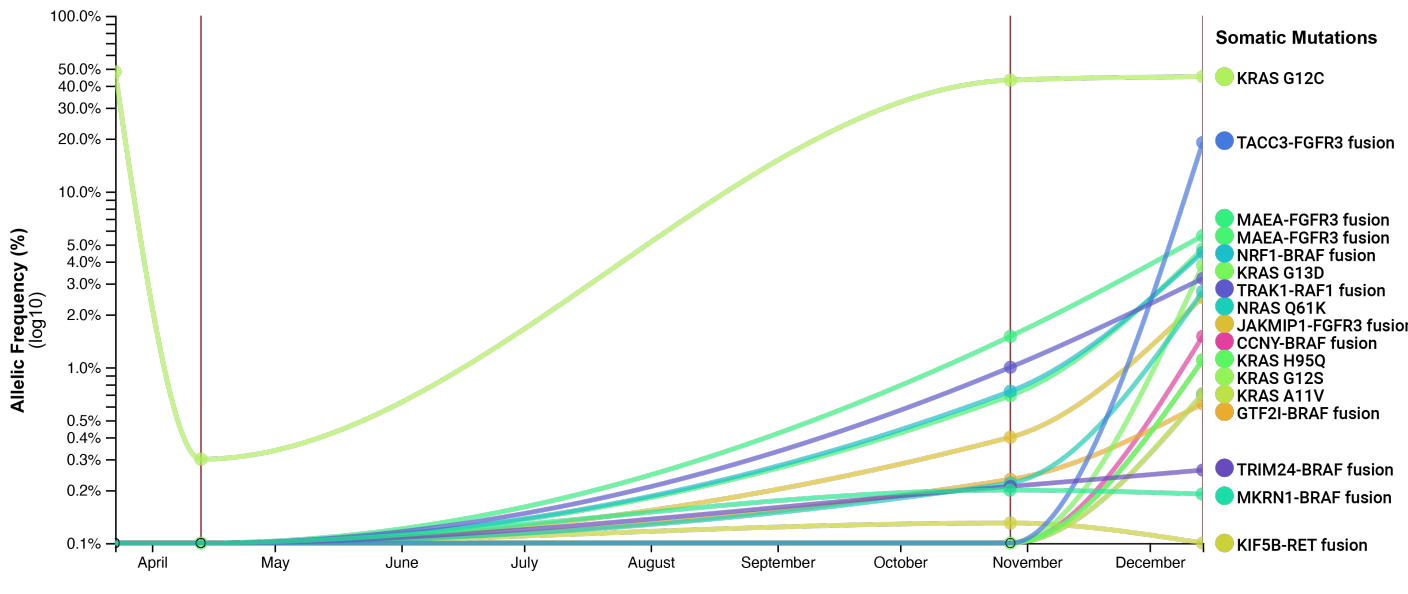
Patient 1 developed emergent high-level copy gain of KRAS and EGFR which can potentially enable a treatment decision at progression for the initiation of an EGFR inhibitor (e.g. cetuximab).

Patient 2 developed resistance (KRAS H95Q) as well as multiple new drivers including 11 functional gene fusions in multiple genes.

Patient 1: EGFR/KRAS Amplifications



Patient 2: Resistance and Emerging Drivers



Limit of Blank (LOB)

False positive rate was 0% for KRAS G12C, EGFR exon 19 deletions, EGFR L858R, and EGFR T790M.

LOB was established by profiling plasma from 30 individual risk-matched healthy donors, tested 6 times each for a total of 180 results, with multiple lots of reagents, instruments, and operators. Libraries were prepared from 50 ng cfDNA input.

Precision from DNA

PPA: 97.2%-100%. NPA/ANA: 100%

LOD study data were evaluated across multiple reagent lots, sequencers, and operators.

For each variant, the MAF level that was closest to 1.5X and 2–3X LOD was assessed for variant agreement. PPA for all variants and LOD levels: 97.2%-100%. PPAs for each level of the experimental components along with the average percent agreements (APAs) between the different components ranged from 96.7%-100%.

NPA and average negative agreement (ANA) were analyzed from the LOB study. There were no false positives in any of the variant positions, therefore, no evidence of differences between operators, reagent lots or sequencers. Therefore, the best estimates of ANA matched the NPA estimates = 100%.

cfDNA Input

Assay Input Range: 15 – 50 ng cfDNA

6 NSCLC clinical cfDNA sample blends with KRAS G12C, EGFR L858R or EGFR exon 19 deletions.

Each sample was tested 2X below assay minimum input (7.5 ng) to 1.5X above maximum input (75 ng), 50 ng was used as reference condition.

For all variants tested, PPA and NPA was 100% at each input level.

Limit of Detection (LOD)

LOD: Analytical Sensitivity

LOD values were established using NSCLC clinical samples with KRAS G12C, EGFR exon 19 deletions, EGFR L858R, and EGFR T790M variants in cfDNA from healthy donor plasma. Samples were serially diluted to six MAF levels: 0.0375 – 4.0% MAF. Each level was tested with 35-36 replicates at input of 15 ng. LoD estimates are listed in Table 1.

Table 1. LOD Estimation

Variant	LOD95 (%MAF)	95% CI (%MAF)
KRAS G12C	0.503%	0.379%, 0.667%
EGFR exon 19 deletions	0.339%	0.241%, 0.476%
EGFR L858R	0.377%	0.289%, 0.493%
EGFR T790M	0.820%	0.680%, 0.989%

Plasma Concordance (Analytical Accuracy)

KRAS G12C: PPA 98.1%, NPA 96.4%

Variant detection of 230 NSCLC plasma samples compared against an externally validated ddPCR assay.

- 76 KRAS G12C+ from Mirati Study 849-001 (enrolled with tissue result).
- 154 commercially procured and representative of trial population.

Table 2. Concordance of KRAS G12C Between RESOLUTION ctDx FIRST and ddPCR Assays

Variant	PPA (N) [95% CI]	NPA (N) [95% CI]
KRAS G12C	98.1% (53/54) [90.1, 99.9]	96.4% (163/169*) [92.4, 98.7]

*Variants observed in the RESOLUTION ctDx FIRST but not in the ddPCR assay were very low frequency (< 0.4% MAF) and enrolled with a tissue result.

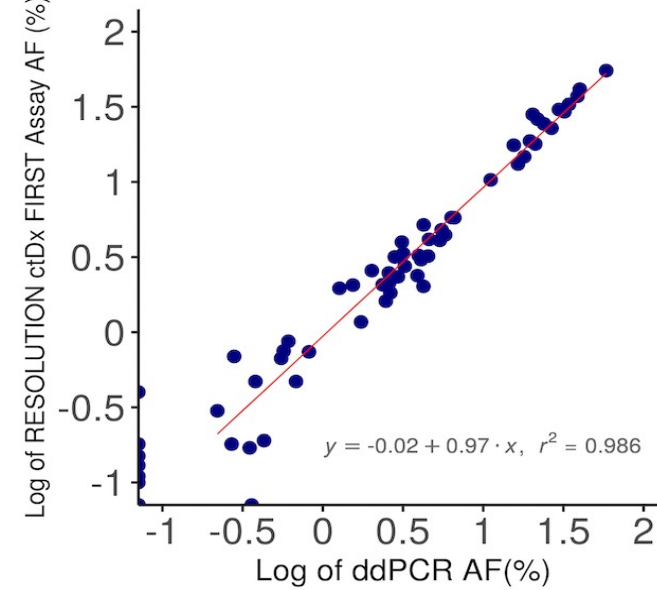


Figure 2. MAF correlation between RESOLUTION ctDx FIRST assay and ddPCR assay for KRAS G12C

Tissue Concordance

KRAS G12C Concordance: PPA 71.8%, NPA 100%

Variant detection of NSCLC plasma samples compared against tissue results.

- 71 KRAS G12C+ from Mirati Study 849-001 with previous tissue result.
- 74 commercially procured and representative of trial population.

CAUTION:

Investigational device. Limited by Federal (or United States) law to investigational use.

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EGFR: PPA 88.9 – 100%, NPA 97.8 – 100%

Detection of EGFR exon 19 deletions, L858R, and T790M variants was compared against the results of the externally validated ddPCR assay.

- 178 NSCLC plasma samples generated a total of 330 comparative valid results.

Table 3. Concordance of EGFR variants Between RESOLUTION ctDx FIRST and ddPCR Assays

Variant	PPA (N) [95% CI]	NPA (N) [95% CI]
EGFR L858R	100% (29/29) [88.1, 100]	97.8% (88/90*) [92.2, 99.7]
EGFR T790M	88.9% (8/9) [51.8, 99.7]	100% (89/89) [95.9, 100]
EGFR exon 19 Deletions	92.9% (26/28) [76.5, 99.1]	100% (85/85) [95.8, 100]

*Variants observed in the RESOLUTION ctDx FIRST but not in the ddPCR assay were very low frequency (< 0.3% MAF).

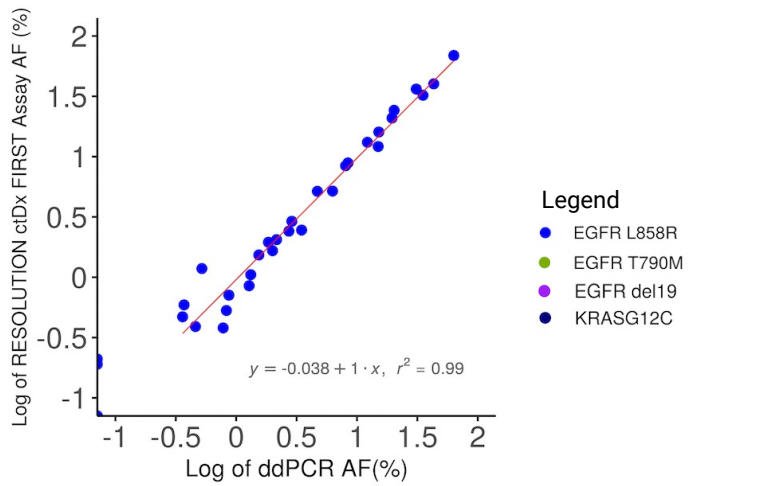
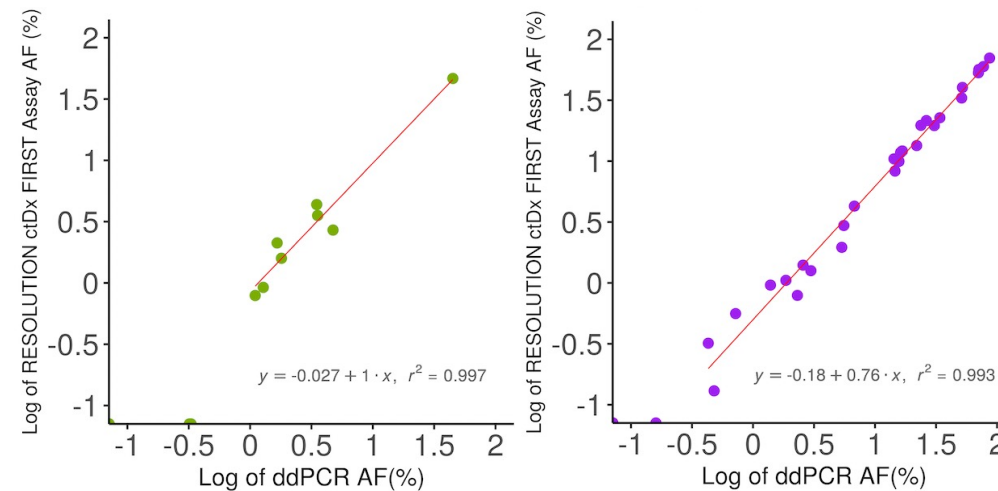


Figure 3. MAF correlation between RESOLUTION ctDx FIRST assay and ddPCR assay for EGFR variants

Conclusions

The analytical performance of the RESOLUTION ctDx FIRST assay offers highly sensitive, specific, and robust test results and meets analytical requirements for the intended use.