Circulating tumor DNA: Disruptive Technology in Medicine

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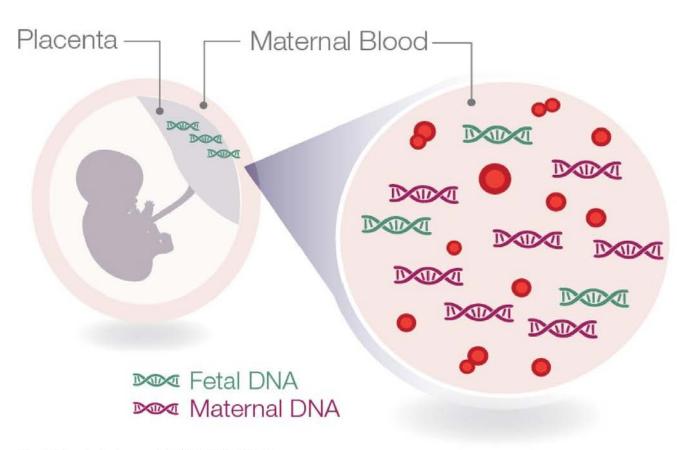


# A revolution in cancer: ctDNA: liquid biopsy

Cancer sheds mutated DNA into blood



### Cell-Free Fetal DNA in Maternal Circulation



Discovery of cell-free fetal DNA in the maternal circulation in 1997\*

2008 publications drove implementation of this new technology into clinical practice

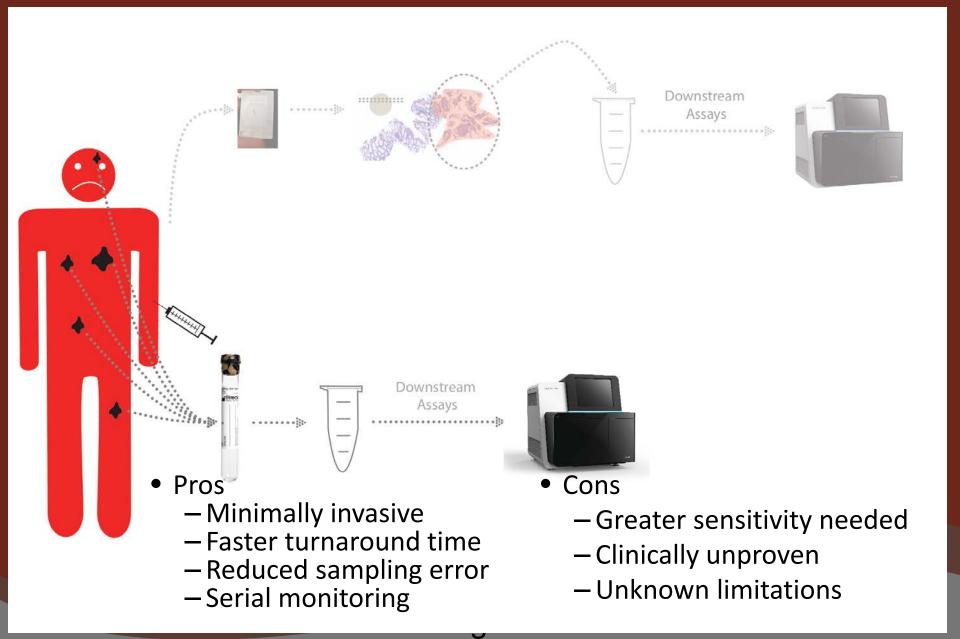
\* Lo YM, et al., Lancet 1997; 350:485-7

Paternal SNPsunique to fetus

Tumor genomic changeunique from germline



### Circulating free DNA (cfDNA) workflow



# ctDNA: Financial World

•NYT front page business section articles

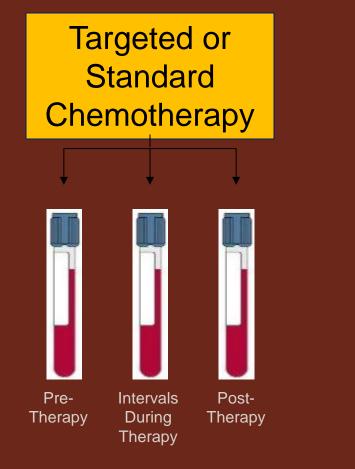
- Guardant Health: Stanford spin off, \$10M
  Sequoia venture capital investment
- •Personal Genome Dx: JHU spin off
- •Natera: NIPT to ctDNA
- Roche \$1Billion purchase of 56% FM



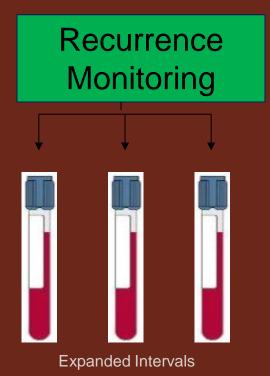
# ctDNA: Disrupting Oncology

- Replace \$\$ biopsy, surgery, imaging
- Targeted real-time resistance and recurrence detection
- Perfusion sampling of entire tumor and body
- Targeted therapy

### Treatment & Recurrence Monitoring



### **Digital PCR or NGS**

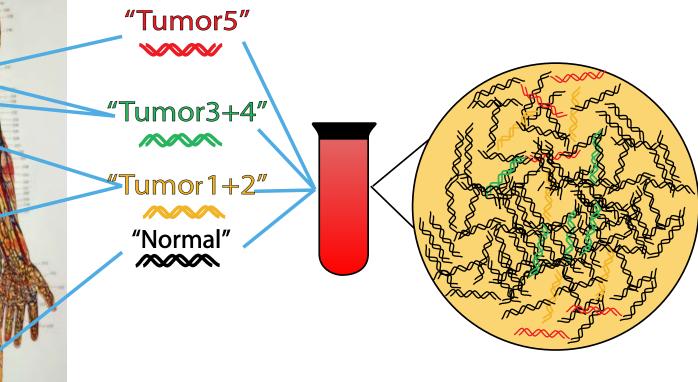


Replace imaging/bx/surgery, actionable genomic targets

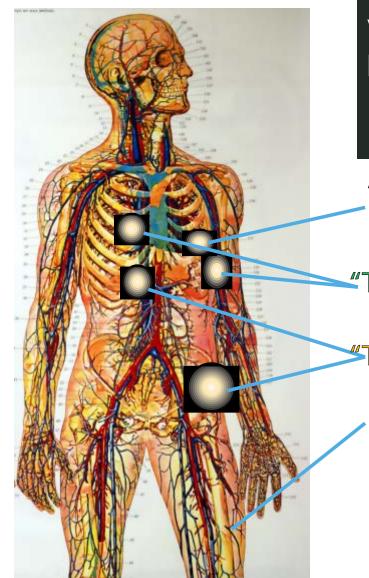


ctDNA reduces tumor sampling error by analyzing the entire tumor burden via perfusion sampling: primary, mets, heterogeneous clones

Blood is the "window to the body"







## ctDNA Methodologies

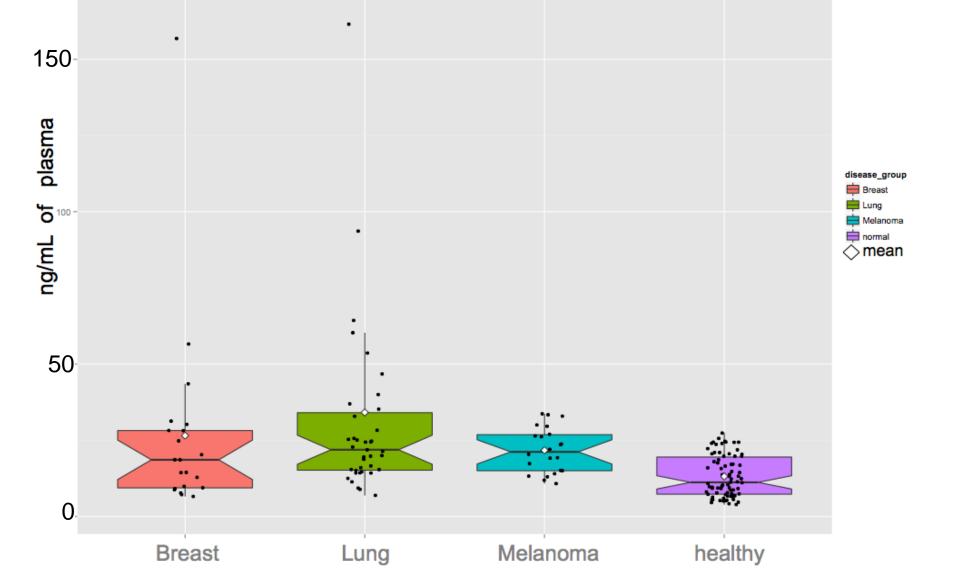


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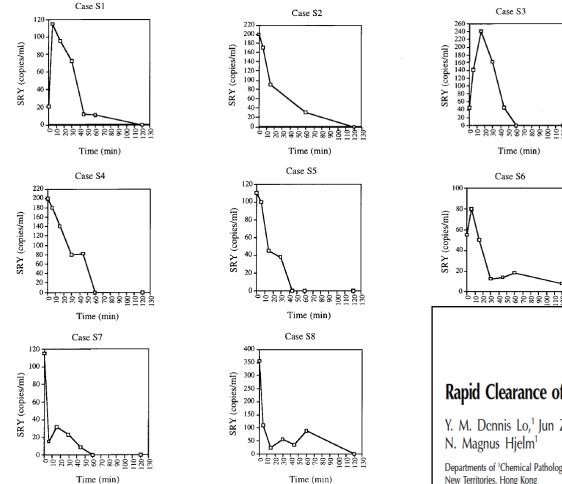
### How much cfDNA is present in plasma?



### cfDNA kinetics

• Fetal cfDNA from maternal plasma with male fetus

Clearance of SRY (chrY) gene: 1-2 hours!



# 

Am. J. Hum. Genet. 64:218-224, 1999

### Rapid Clearance of Fetal DNA from Maternal Plasma

Y. M. Dennis Lo,<sup>1</sup> Jun Zhang,<sup>1</sup> Tse N. Leung,<sup>2</sup> Tze K. Lau,<sup>2</sup> Allan M. Z. Chang,<sup>2</sup> and N. Magnus Hjelm<sup>1</sup>

Departments of <sup>1</sup>Chemical Pathology and <sup>2</sup>Obstetrics and Gynecology, Chinese University of Hong Kong, Prince of Wales Hospital, Shatin, New Territories, Hong Kong ctDNA by BMF Capture NGS

**Goal:** ctDNA gene panel with <1% sensitivity for low-level cancer variants & translocations diluted by circulation

Keith Gligorich, Daniel Baker, Brett Kennedy



ctDNA Mutation and Translocation Detection by BMF Capture NGS

- 5-20 ng of DNA input (1 BCT blood tube)
- Flexible capture method
- Barcodes
- High depth sequencing
- Analysis & variant calling by ARUP's BMF software

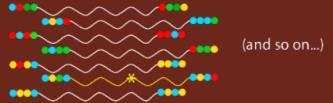


### Digital Next Generation Sequencing (NGS)

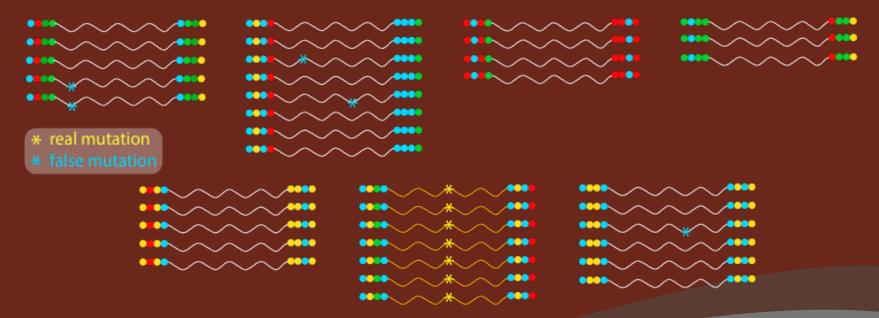
1. Sample with low (<0.1%) frequency mutation (x); a needle in a haystack



2. "Barcode" each molecule with a unique "Nmer" tag during library generation



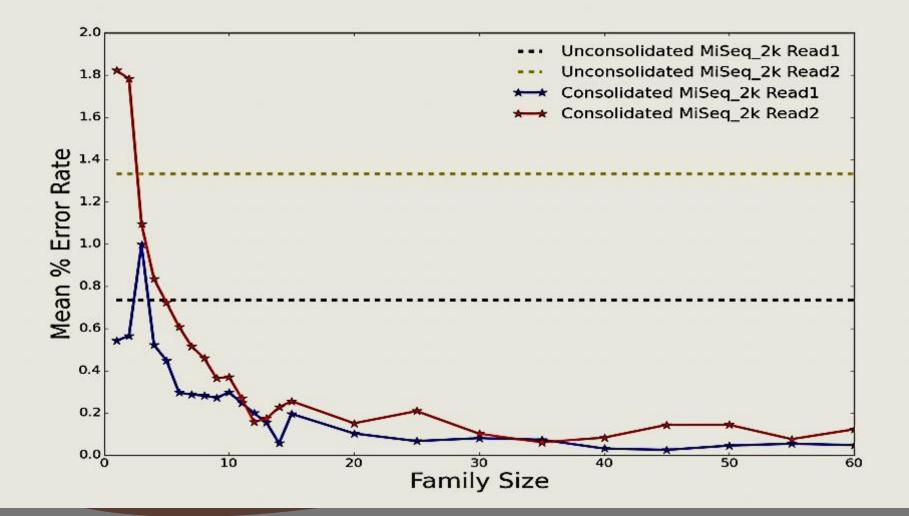
3. PCR amplify molecules, capture regions of interest, redundant sequencing (50million reads)



4. Bioinformatic processing to separate "signal (\*)" from "noise (\*)" (sequencing errors, PCR errors)

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# NGS error reduction via BMF bioinformatics 2000 Copy Read Depth



### Targeted Hot Spot ctDNA Panel:

ABL1 AKT1 ALK\* APC ATM BRAF CDH1 CDKN2A CTNNB1 DDR2 EGFR\*\*

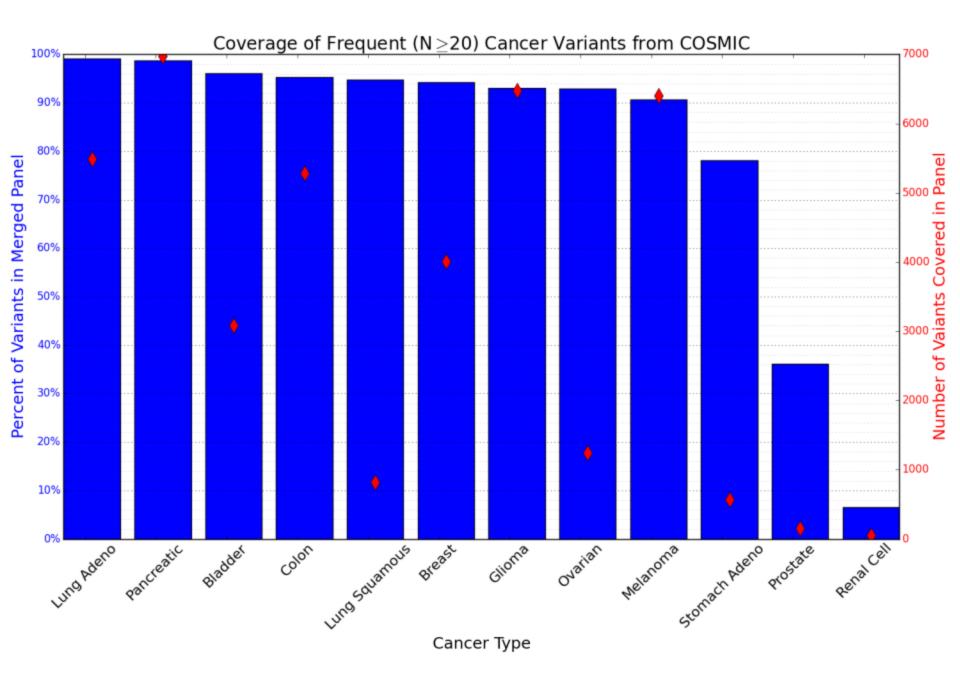
ERBB2/4 FBXW7 FGFR1 FGFR2 FGFR3 GNA11 GNAQ **GNAS** HRAS **IDH1** IDH2

**JAK2/3 KDR** KIT **KRAS** MAP2K1 MET MTOR NOTCH1 NRAS NTRK1 **PDGFRA** 

PIK3CA PTEN\*\* RB1 RET ROS1 SMAD4 **SMO** STK11 TERT **TP53\*\*** VHL

\*Intron 19 coverage for translocations, \*\*Full exon coverage





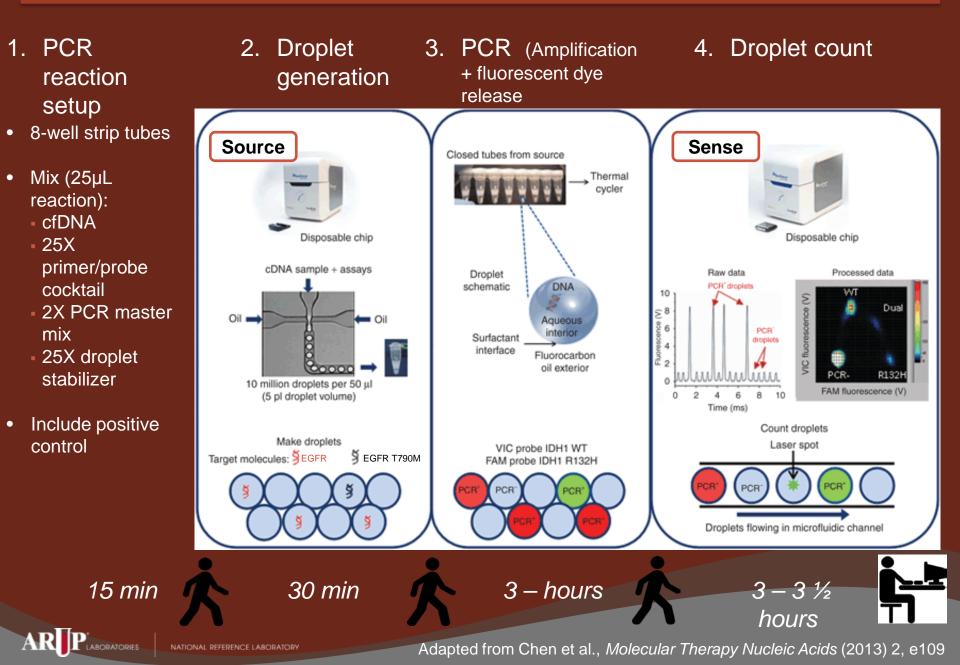
# ctDNA testing by digital droplet PCR (ddPCR): EGFR T790M mutation

## Sabine Hellwig, PhD

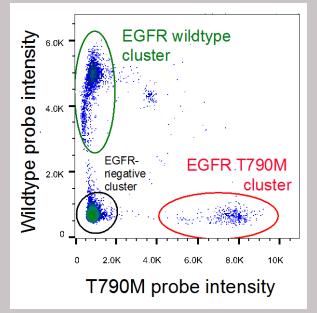


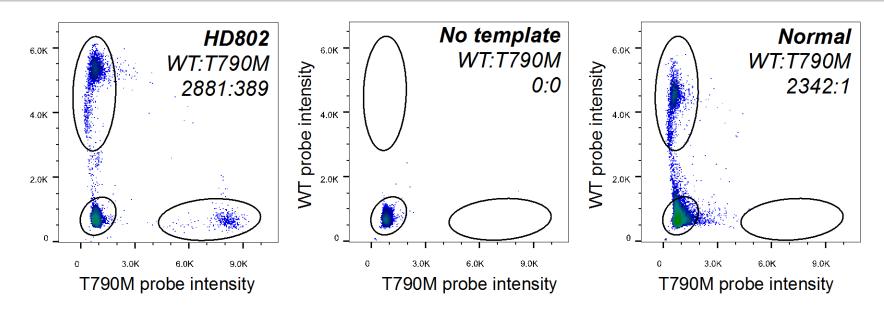
#### EGFR targeted therapy in lung cancer Estimated new US lung CA's 2015: 220,000 Estimated US lung CA deaths 2015: 158,000 (27% all CA) **Biopsy** 85% NSCLC Liquid TKI 10-20% EGFRm<sup>+</sup> Biopsy (exon 19 del or L858R) (gefitinib, erlotinib) ~ 11 months Scan x3 Serial monitoring Scan x3 of ctDNA for Scan x3 **T790M** ✓ Non-invasive **Biopsy 100% Progression** ✓ Whole body tumor burden Next gen TKI ✓ Remote 2/3's: T790M+ (Rociletinib, sampling いい possible AZD9291) Scan x3 ✓ Sensitive Scan x3

### EGFR T790M ddPCR Assay

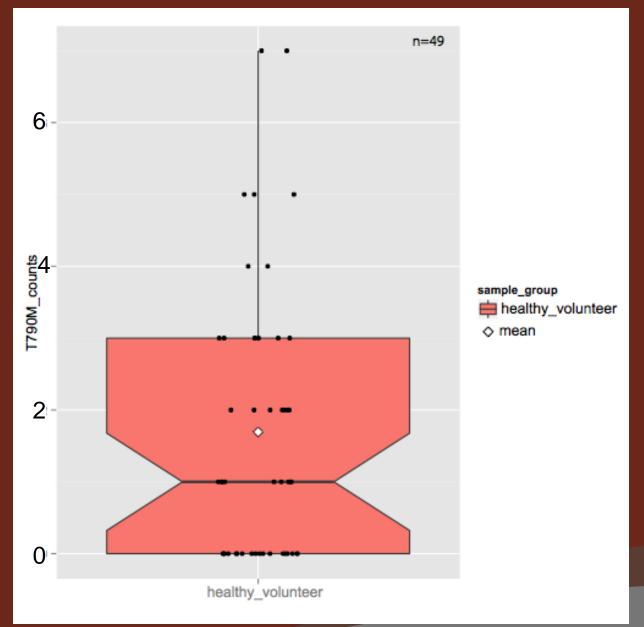


### EGFR T790M ddPCR Assay – Data Analysis





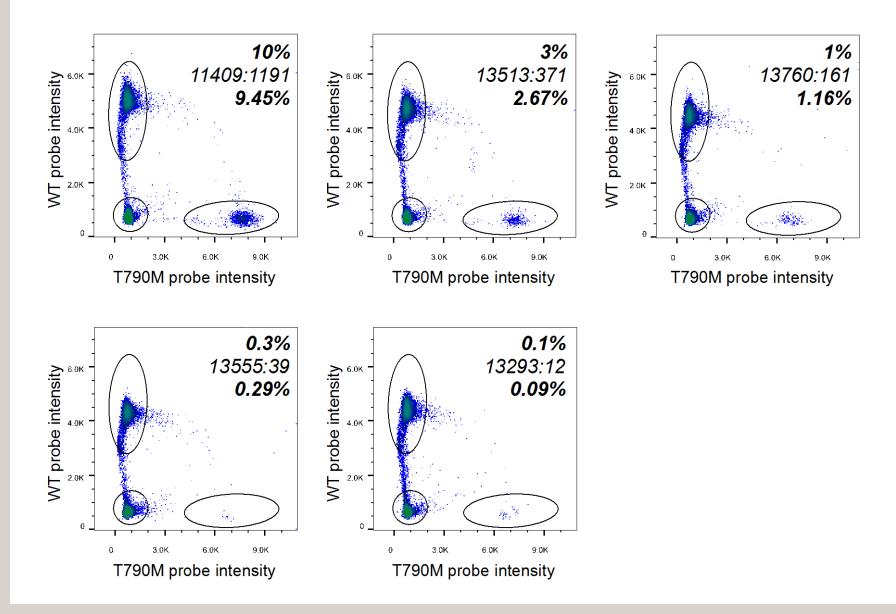
### Background (noise) in healthy cfDNA?



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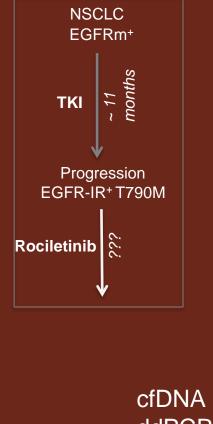
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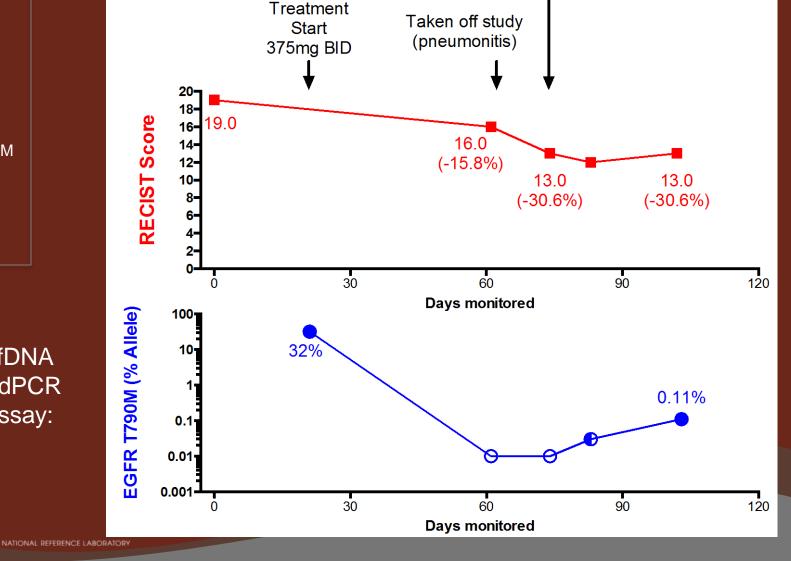
### Quantitative accuracy: DNA standards



### The power of serial monitoring by ctDNA

NZHGFL (VB)



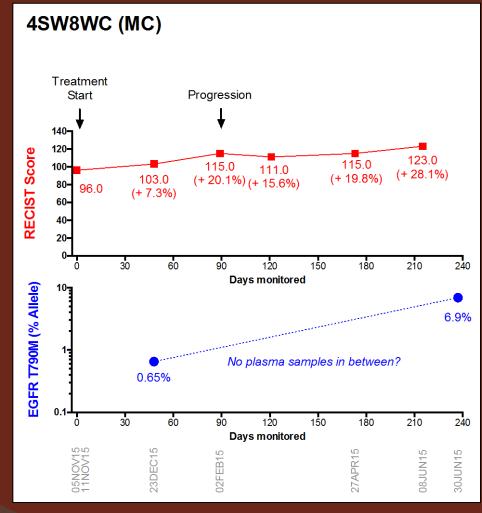


Restart at lower dose

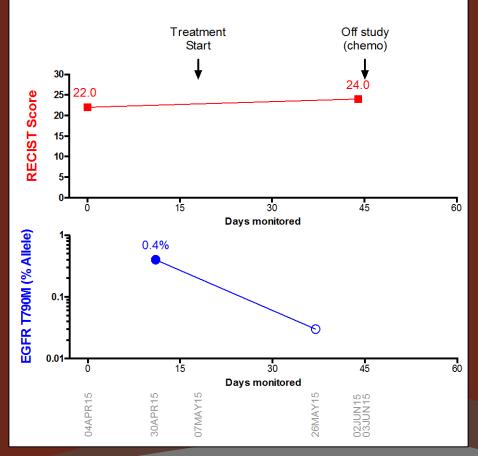
250mg BID

**ddPCR** assay:

### The power of serial monitoring by ctDNA



KUD7H9 (CS)



# Summary

- Duplex adapters in capture NGS
- BMF tools: new bioinformatic pipeline
  - -Powerful NGS error reduction
  - -Target sensitivity (0.05-0.1% MAF)



# Summary

• ddPCR

-Cost effective-Highly sensitive-Focused mutations



Many thanks to ARUP, D. Baker, K. Gligorich, S. Hellwig, W. Akerley, K. Grossman!!

