



Sequencing By Binding (SBB) Shows Superior Sensitivity and Specificity of Detection of Low Frequency Variants from ctDNA

AGTA 2022 | Sunshine Coast

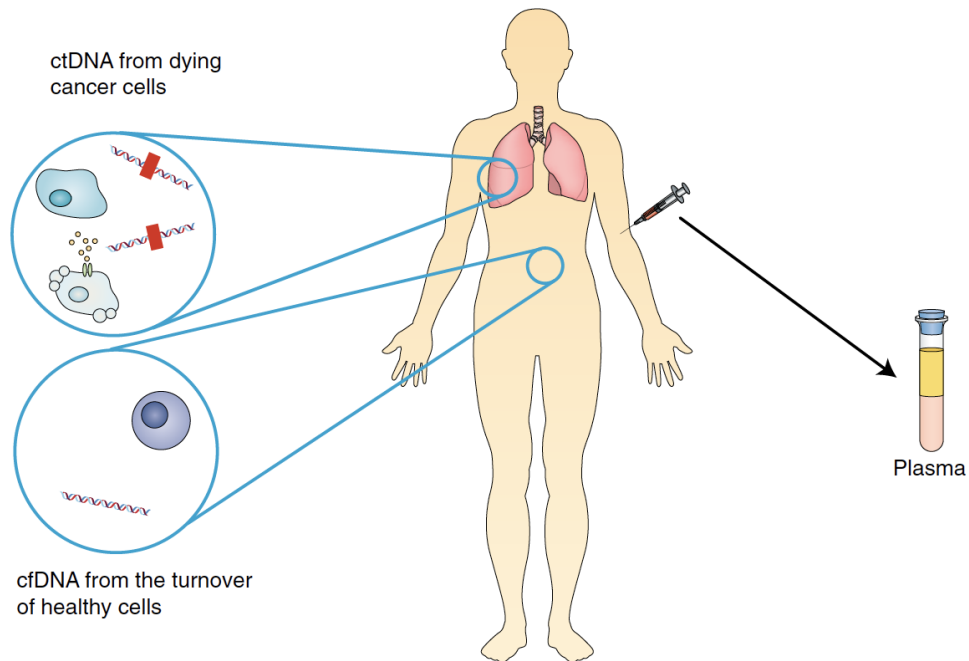
Rob Linder, Daniel Nasko, Christopher Kingsley, **James Miller**, Zuwei Qian, Jonathan Bibliowicz

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Liquid biopsies and the challenges of "needle in a haystack"

Only a small fraction of cell-free DNA (cfDNA) is circulation tumor DNA (ctDNA)

Amount of cfDNA shed by solid tumors depends on cancer stage and tumor size



Song et al, Nature Biomed Engineering, 2021

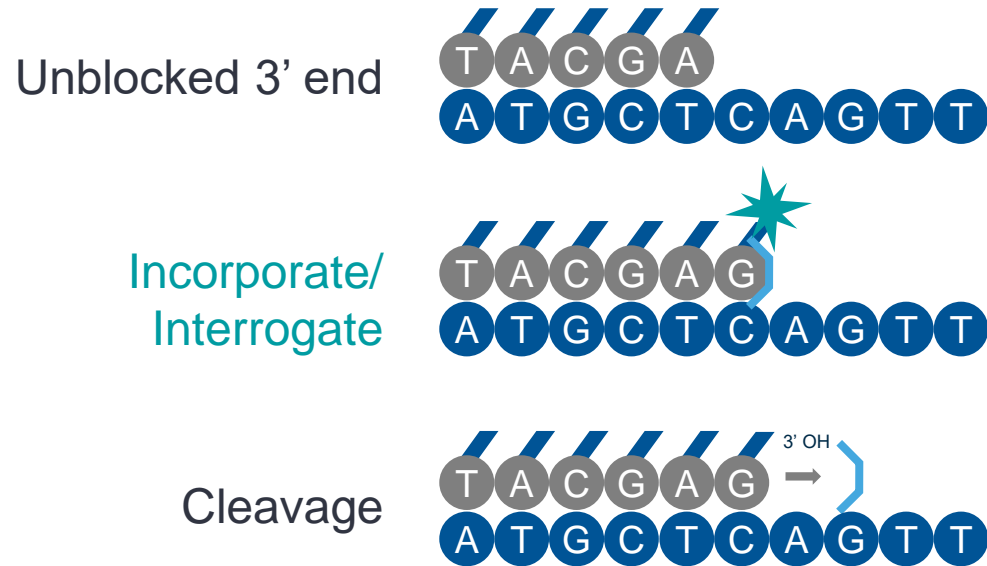
Tumor diameter	Number of genomes per <u>10ml of blood</u>	Likelihood of detection by ctDNA
27mm	6	High
12.5mm	~1	Moderate/Low
6mm	<<1	Unlikely

Improve the sequencing
Sequencing By Binding (SBB)

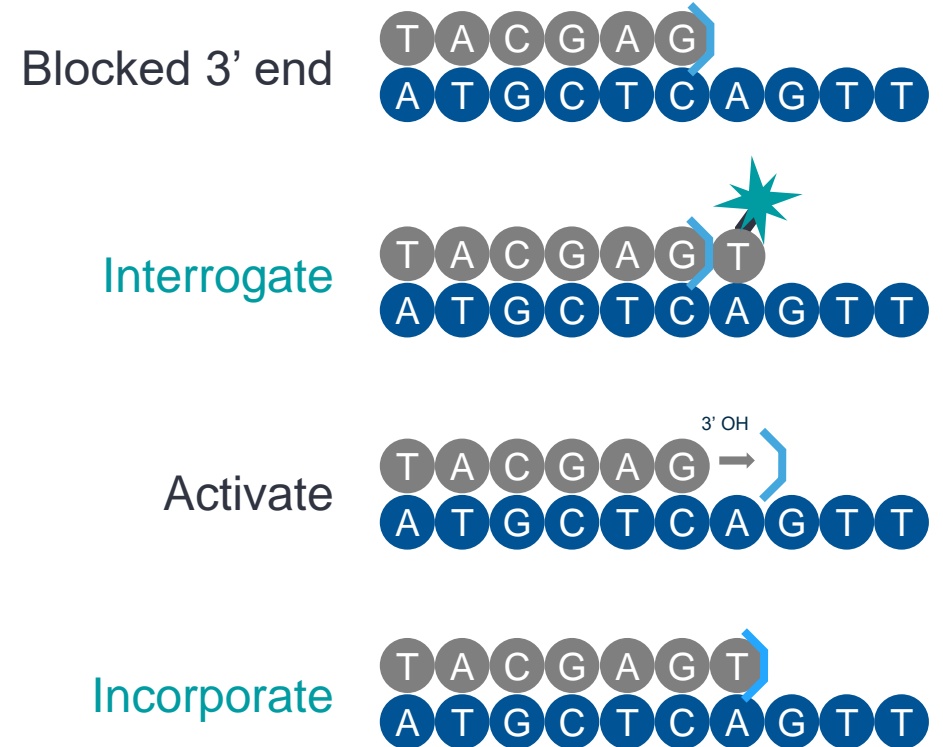
SBB advantages: Incorporates native nucleotides, produces unmodified DNA

No base modifications, no molecular scarring

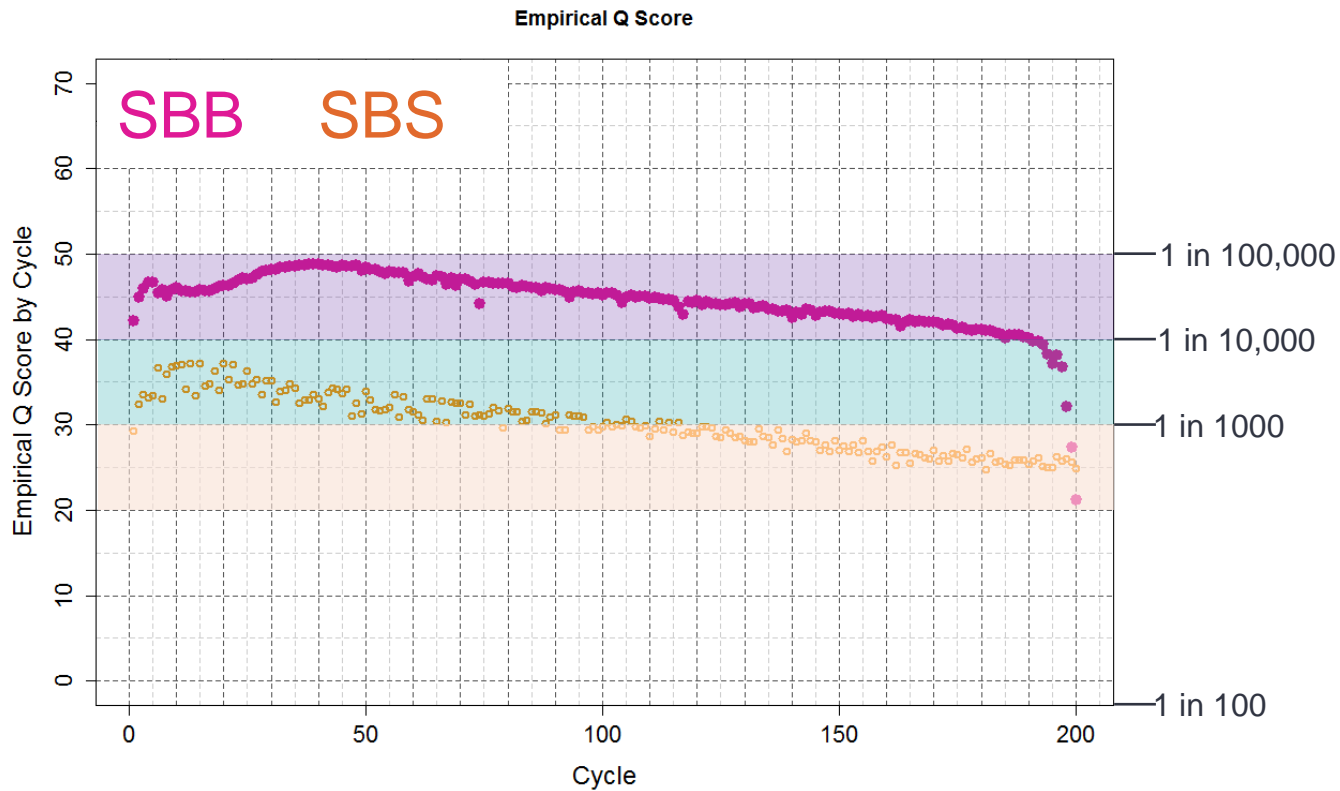
Sequencing by synthesis (SBS)



Sequencing by binding (SBB)



SBB accuracy - >90% of bases Q40+



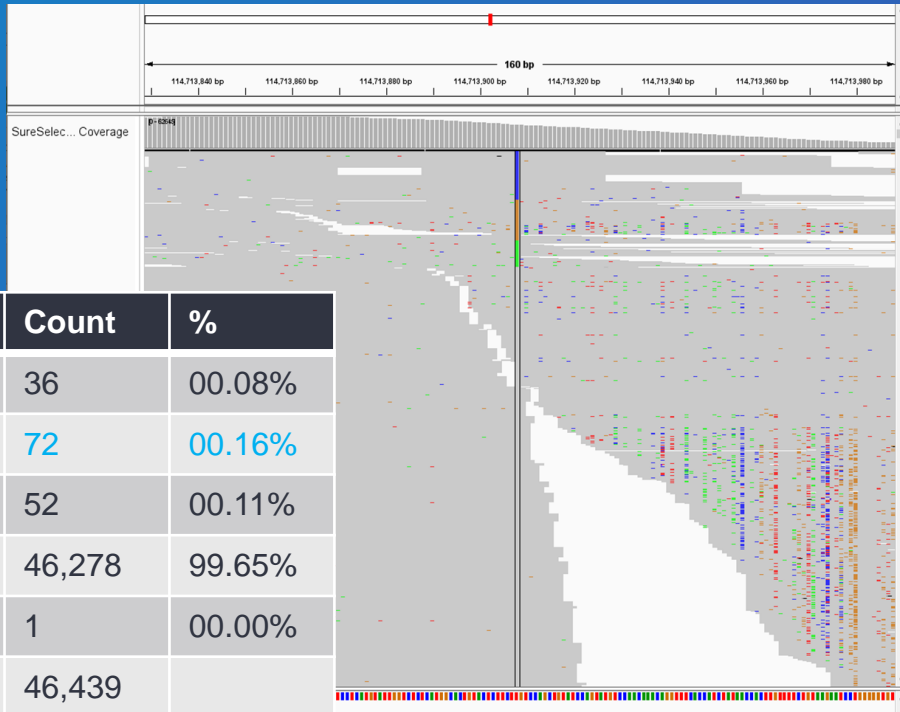
SBB error rates ~15x lower at any given cycle, between 1:10,000 to 1:100,000

- Attain **near-perfect accuracy** in sequencing, changing standard parameters for multiple applications
- SBB error rates mean **not having to sequence at unnecessary depth**
- Reduces level of uncertainty
- Identify biological events that have critical implications

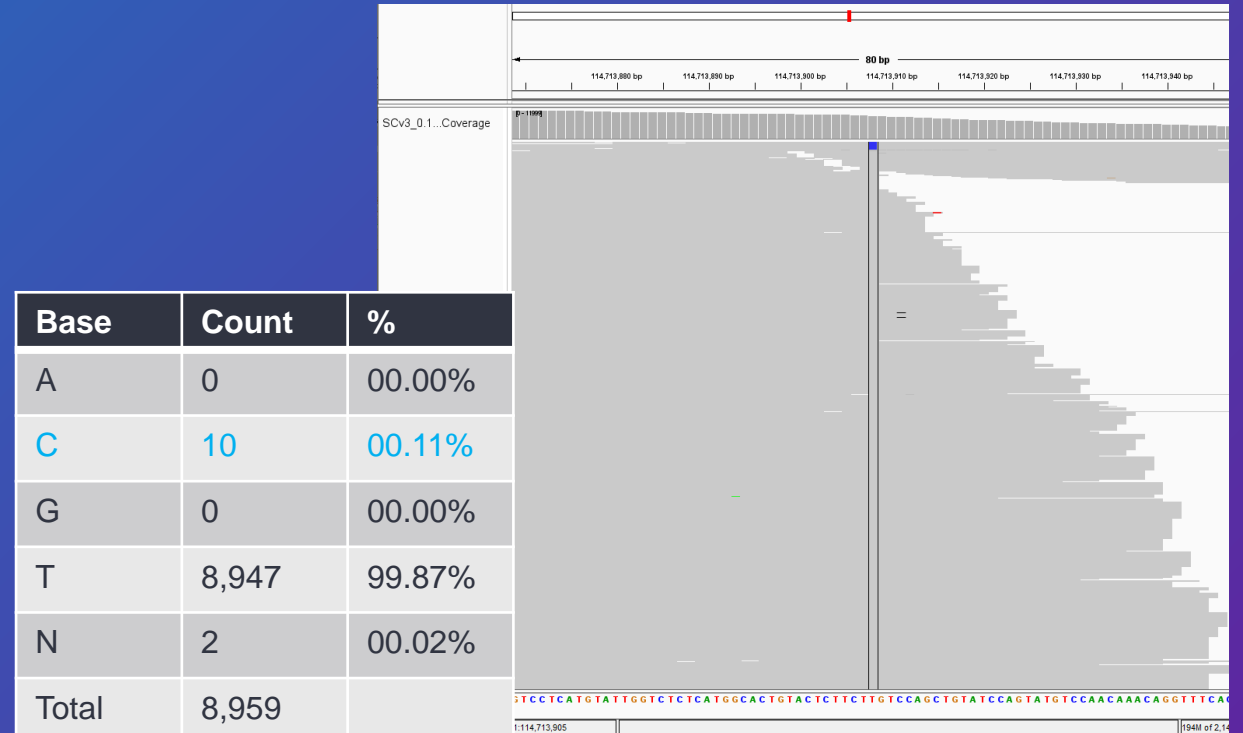
Sequencing of true variant sample SBB vs SBS

0.1% VAF NRAS Q61R

SBS 48,000x



SBB 12,000x



Revio™ system

1,300

WGS / Year

1- 4

SMRT Cells
in parallel

24 hr

Run time

50%

Fewer
consumables

>3x

Output per
SMRT Cell



\$995 USD* / human genome (30x HiFi)

*U.S. list price is \$995 for sequencing reagents for one Revio SMRT Cell, which has an expected yield of 90 Gb, equivalent to a 30X human genome. Your local sales representative can provide detailed pricing in your currency.

Onso™ system

400-500M

Reads

200 + 300

Cycle kits

48 hr

Run time

≥ 90%

Bases Q40+

