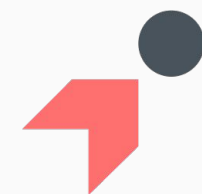


#3072 - Clinical validation of Northstar Select, a novel liquid biopsy assay for comprehensive genomic profiling of solid tumors



NORTHSTAR

BY BILLIONTOONE

Xavier Bower¹, Jan Wignall¹, Joyce Zhu¹, Michael O’Sullivan¹, Naomi Searle¹, Lenny Hong¹, Matthew Varga¹, Jason Luong¹, Esther Lin¹, Marie Simon¹, John ten Bosch¹, Ajeet Gajra², Chanh Huynh³, David Tsao^{1*}, Wen Zhou^{1†}

¹ BillionToOne, Inc., Menlo Park, CA. ² Hematology Oncology Associates of Central New York, East Syracuse, NY. ³ Cancer Care Associates of York, York, PA.

david@billiontoone.com*, wzhou@billiontoone.com†

BACKGROUND

The field of oncology has increasingly embraced comprehensive genomic profiling (CGP) to enhance treatment decision-making for late-stage solid tumor cancer patients. In particular, *liquid biopsy CGP assays*:

- Detect clinically actionable somatic mutations via circulating tumor DNA.
- Alleviate issues with sample availability, tumor heterogeneity, and turnaround time in tissue-based CGP testing.

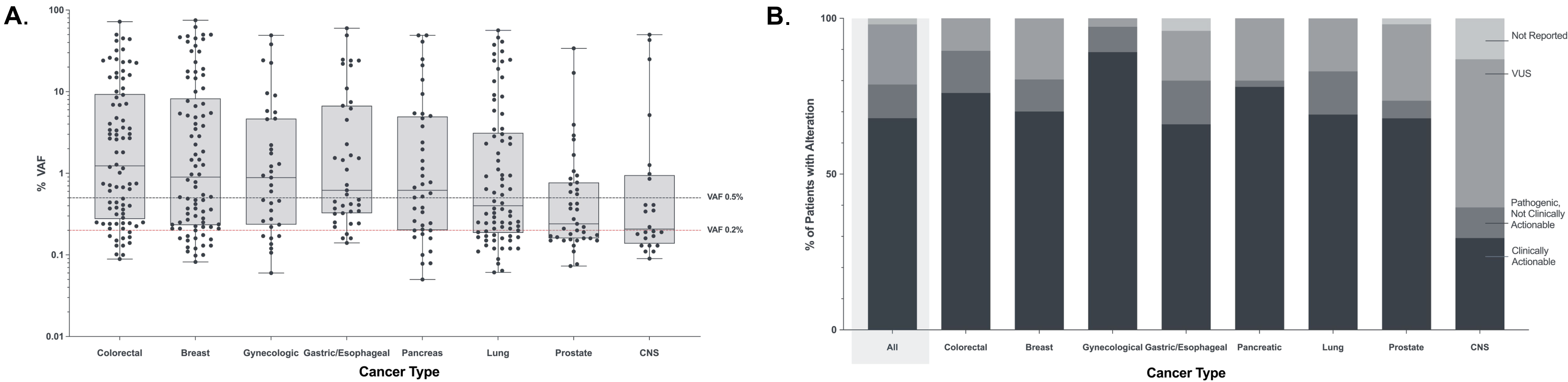
However, **current liquid biopsies are generally unreliable** for the detection of variants **below 0.5% variant allele fraction (VAF)**¹, leading to an **unmet clinical need for a highly sensitive liquid biopsy**:

- Many cancers shed little ctDNA - ½ of SNVs are <0.5%, ¼ <0.25% VAF.²
- Patients are similarly likely to respond to targeted therapy regardless of driver mutation VAF level in blood.²⁻⁵

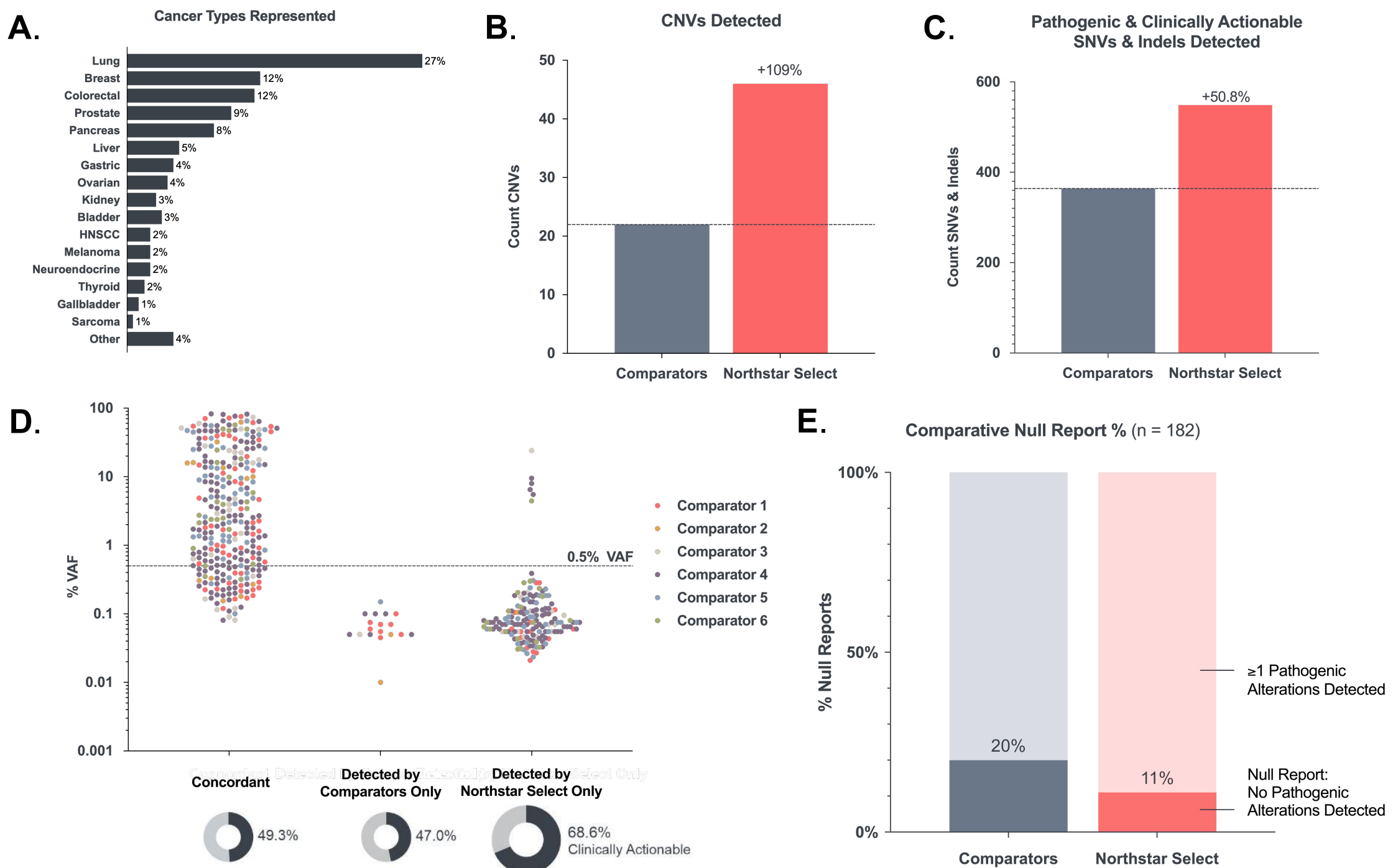
Northstar Select is a CGP assay that leverages Quantitative Counting Template™ (QCT) technology and innovations in chemistry, panel design, and bioinformatics **for greatly increased sensitivity**. Here, we present:

- The clinical relevance of variants called by Northstar Select and their indication of ctDNA shedding rates, across cancer types.
- Head-to-head comparison of results against on-market liquid biopsies.

CTDNA SHEDDING & CLINICAL ACTIONABILITY



HEAD-TO-HEAD COMPARISON TO ON-MARKET LIQUID BIOPSIES



Alteration Type	# Detected by Northstar Select	# Detected by Comparators	% Detected by Northstar Select Over Comparators
CNV			
ERBB2 (amplification)	4	4	0%
MET (amplification)	1	1	0%
PIK3CA (amplification)	3	1	200%
PTEN (loss)	5	0	+
CNV Sum	13	6	116%
SNV / Indels			
ALK	1	0	+
BRAF	8	6	33%
BRCA1/2	15	11	36%
HRR Genes*	42	18	133%
EGFR	6	4	50%
ERBB2	6	5	20%
ESR1	6	4	50%
FGFR3	3	2	50%
IDH1	3	1	200%
KIT	2	0	+
KRAS	44	38	16%
MET	2	2	0%
NRAS	4	3	33%
PIK3CA	37	27	37%
PTEN	30	18	67%
VHL	2	1	100%
SNV / Indels Sum	211	140	51%

Table 1. Variants with FDA-approved therapies detected by Northstar Select vs. comparators.

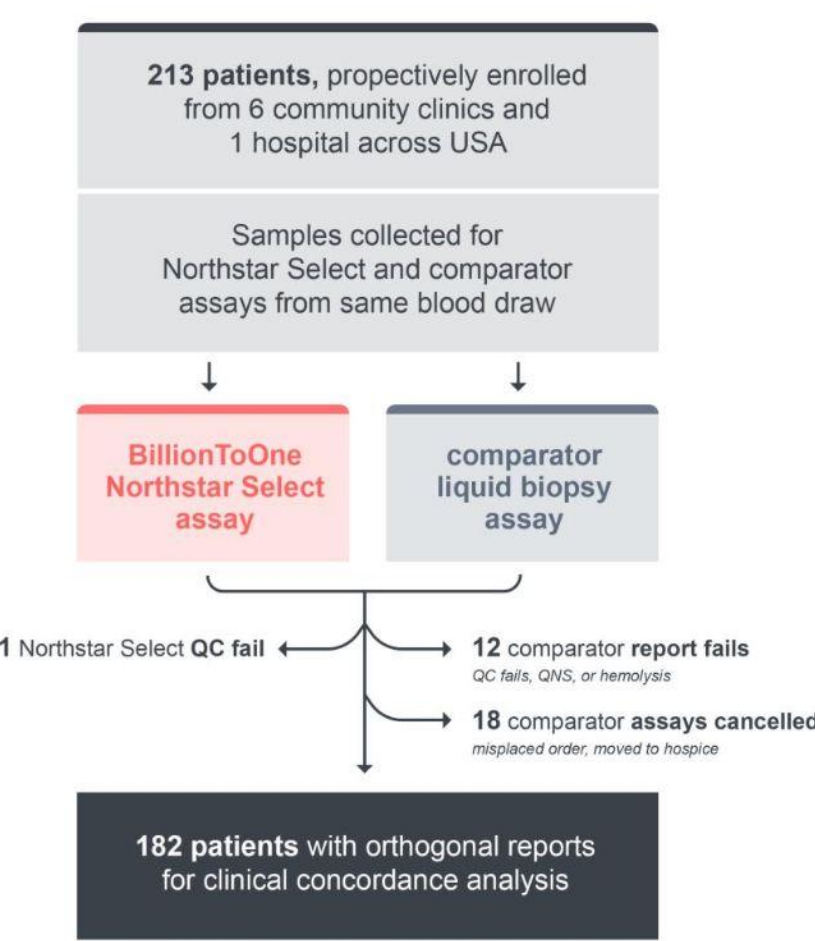
Assay	# CHIP	# Somatic	Percent CHIP (CI)
Northstar Select	22	66	25.0% (± 9.0%) †
Comparators	13	40	24.5% (± 13.3%) †

† - NS (p > .05) by Fisher's Exact (odds ratio = 1.02, p > 0.9999)

Table 2. CHIP variant rate comparison.

METHODS

- ctDNA Shedding & Clinical Actionability
 - 674 unique samples spanned a multitude of cancer types.
 - Blood specimens were assayed by at BillionToOne in Menlo Park, CA.
 - ctDNA shedding level was estimated as the average VAF of pathogenic SNVs and Indels for each patient.
 - Clinically actionable variants include those associated with targeted therapy, clinical trial and/or diagnostic/prognostic relevance.
- Comparison to On-Market Liquid Biopsies
 - Blood specimens were concurrently assayed by Northstar Select and the physician's choice of commercially available comparator CGP liquid biopsy as part of standard of care (n=182 patients).
 - Buffy coat genomic DNA was used to identify variants due to clonal hematopoiesis of indeterminate potential (CHIP) (n=28 patients).
 - All procedures were carried out in accordance with the Declaration of Helsinki and protocols approved by WCG IRB #20230250.



Acknowledgements

We thank the patients for their participation in these studies.

References

1. Mack PC, Banks KC, Espenschied CR, et al. Cancer. 2020; 126(14):3219-3228.
2. Deveson IW, Gong B, Lai K, et al. Nat Biotechnol. 2021; 39(9):1115-1128.
3. Tran HT, Lam VK, Elamin YY, Hong L, et al. JCO Precis Oncol. 2021; 5:1241-1249.
4. Jacobs MT, Mohindra NA, Shantzer L, et al. JCO Precis Oncol. 2018; 2:1-10.
5. Abida W, Armenia J, Gopalan A, et al. JCO Precis Oncol. 2017; 2017: 1:1-26.