Addressing the Challenges of NGS Assays with Seraseq® Oncology Controls

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February 7, 2022

Standards division:

Mission-critical tools for quality assurance applications

Quality control materials

Reference materials and analytical standards

Supply chain assurance solutions (SCA)

Some of our products

Some of our outcomes

We develop and produce quality control materials for clinical and molecular diagnostic customers to support the delivery of consistently accurate measurements in clinical laboratories.

Our proficiency testing schemes provide a framework for regular independent assessment of laboratory performance.

Our reference materials and analytical standards enable the development, validation and quality control of analytical testing methods, from applied research and discovery through to analytical testing laboratories and the final manufacturing of drug products.

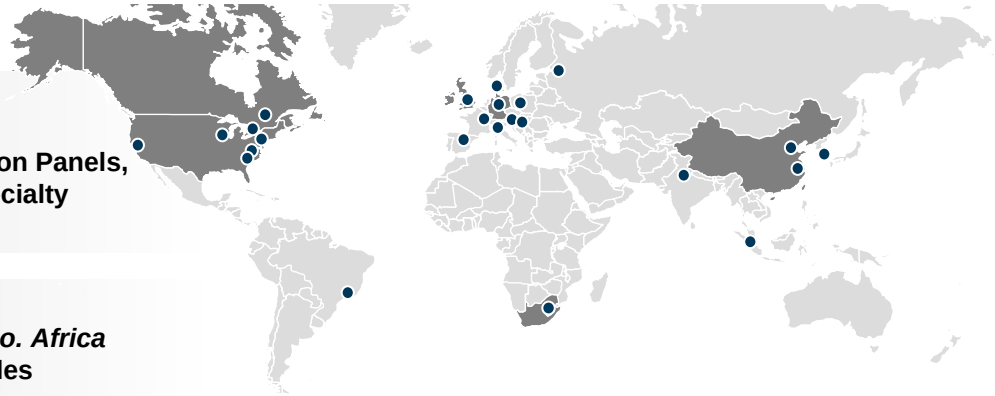
Our products are used primarily in the pharmaceutical and the applied market segments.

Our SCA solutions support consistent quality criteria through the supply chain. This includes management system standards used by food manufacturing sites, proficiency testing schemes, consumer facing endorsement marks and provision of digital supply chain management solutions.

Our solutions are critical to customers in the food, beverage and consumer safety market segments.

LGC Clinical Diagnostics Centers of Excellence

7 Sites, ~500 Employees



Serology & Infectious Disease
Milford, Massachusetts (USA)
- Develop, manufacture IVD/RUO IQC, Verification Panels, PT/EQA samples, bulk serum, plasma and specialty biologics

Proficiency Testing Hubs
Traverse City, Michigan (USA) & Johannesburg, So. Africa
- Provision and distribution of clinical PT samples

Molecular & NGS
Gaithersburg, Maryland (USA)
- Design, develop and manufacture catalog and custom reference materials for molecular and NGS assays
- RUO products, EQA samples, QC testing

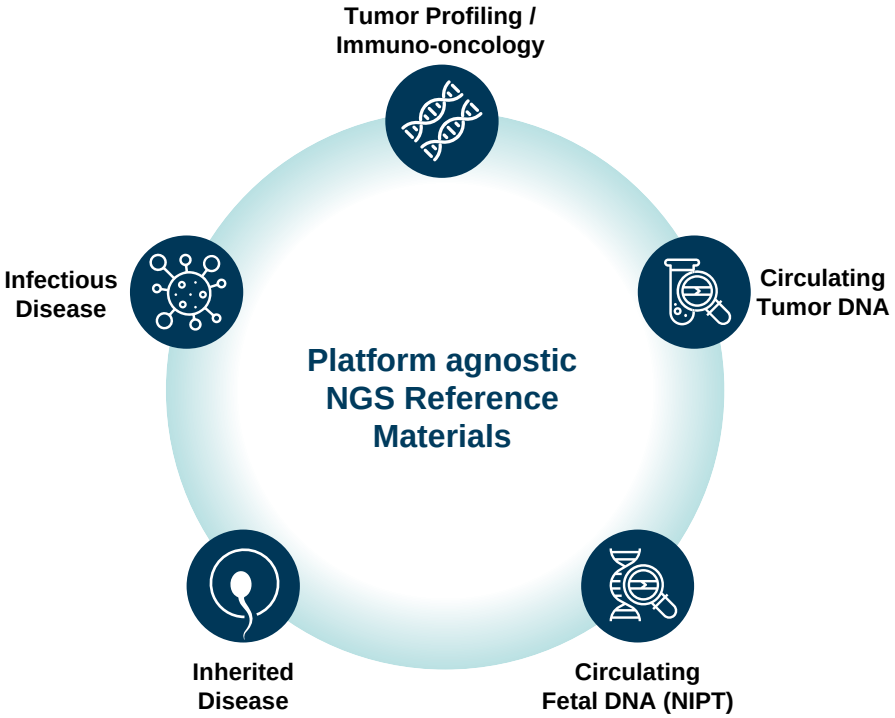
Antigens & Antibodies
Oxford, England
- Manufacture viral and bacterial Ag/Ab
- Develop and utilize proprietary mammalian expression system

Clinical Biochemistry & Immunoassay
Tipperary, Ireland
- Design, develop, manufacture multi-constituent IVD IQC

Clinical Biochemistry & Immunoassay
Portland, Maine (USA)
- Design, development, manufacture of IVD Linearity & CalVer, PT/EQA samples & custom floor standards
- World-class laboratory for clinical diagnostics (800+ validated assays on automated platforms)

Seraseq® Products for Clinical Genomics

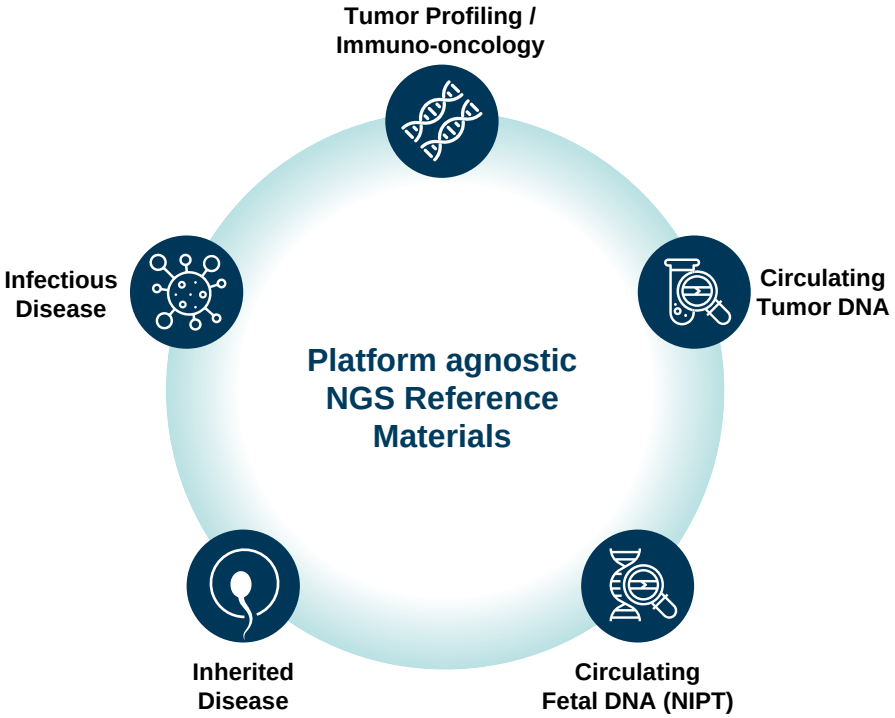
Flexible, Highly-Multiplexed Reference Materials to Expedite NGS Assay Development and Validation



Seraseq® Products for Clinical Genomics

- ✓ **Biosynthetic spike-in technology**
  Any clinically relevant variant and variant types: SNV, INDEL, CNV, SV or RNA fusion
- ✓ **Multiplex controls**
  Provide a rich source of data in a single run at low cost
- ✓ **Patient-like material**
  Performance similar to clinical samples in multiple formats (gDNA/RNA in buffer, cfDNA sizing, plasma, FFPE)
- ✓ **Highly customizable**
  Expedite assay development, validation, QC and Proficiency testing (EQA)

Unique I-O reference portfolio supports patient stratification based on complex signatures: TMB, MSI, bTMB



NIPT reference materials for autosomal and sex chromosome aneuploidies and microdeletions

Solutions for Clinical Oncology NGS Applications

Disease profiling

Solid Tumors

- Tumor DNA/FFPE
- Fusion RNA/FFPE
- CNVs DNA/FFPE
- NTRK RNA/FFPE
- Whole Transcriptome RNA-Seq

Heme Disorders

- Myeloid DNA/RNA
- Lymphoma DNA/FFPE

Immuno-Oncology

Tumor Mutational Burden

- Tissue TMB gDNA/FFPE
- Blood TMB (ctDNA)
- TMB Reference Panel (gDNA)

Microsatellite Instability

- MSI Reference Panels
- MSI-High gDNA/FFPE

Disease monitoring

Liquid Biopsy

- ctDNA v2 ctDNA / plasma
- ctDNA Complete™ ctDNA / plasma
- ctDNA MRD Panel

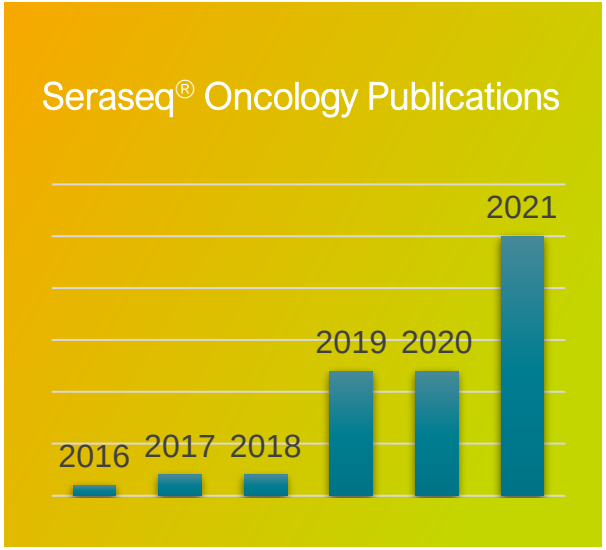
New release

Coming soon

Industry-first

Increasing adoption of NGS reference materials

Supporting clinical and commercial NGS assay development and approval to realize the promise of precision medicine



Regulatory validation requirements

Accuracy, precision, reproducibility and sensitivity (LoD)

CGPs moving towards clinical use

Broad variant content necessitates use of multiplexed samples for clinical validation

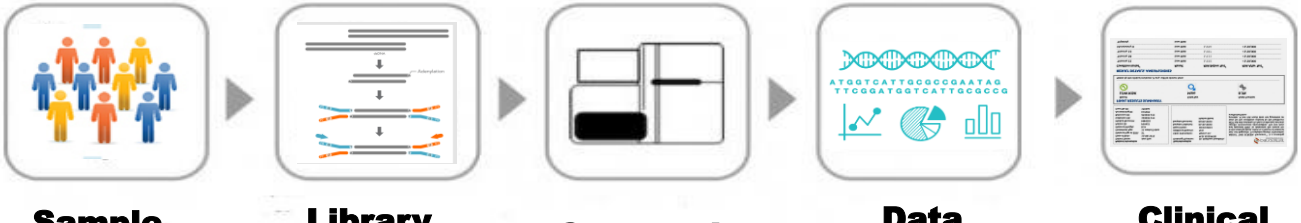
Expansion of testing focus

As diagnostics and therapies target rare and cancer agnostic events, representative patient samples are difficult to source

Detecting challenging variants in limited samples

Biosynthetic reference materials in patient-like FFPE and plasma formulas can test the assay limits to ensure accurate reporting

Next Gen Sequencing needs Next Gen Quality Controls



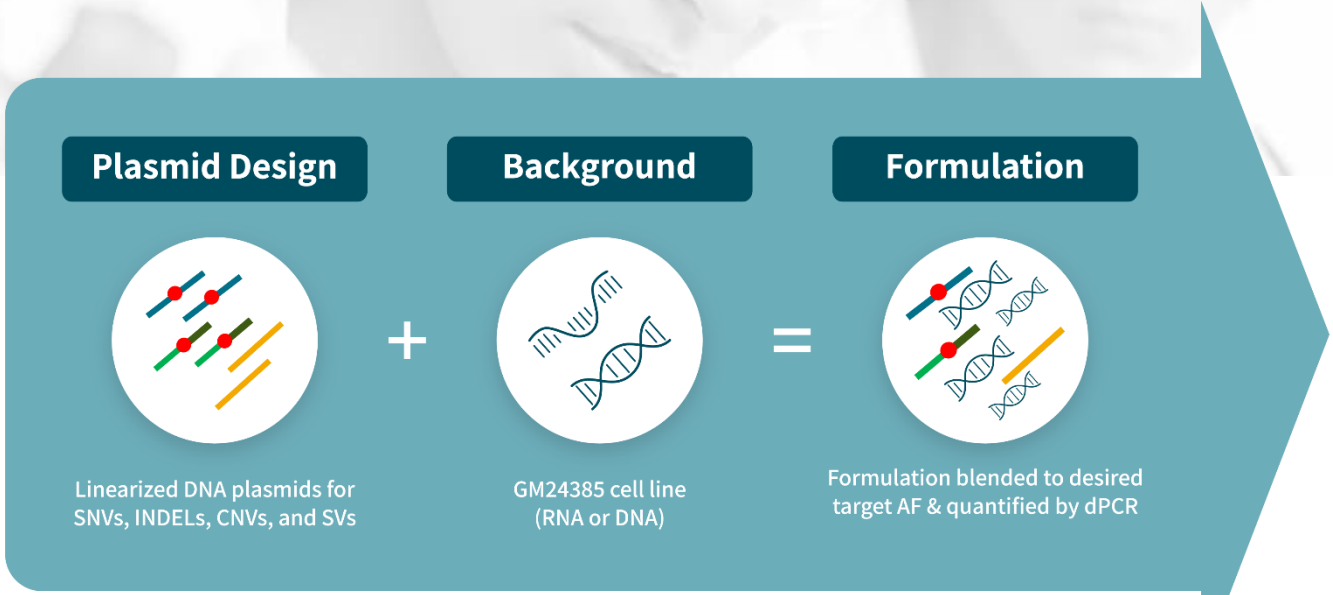
Seraseq® FFPE/Plasma

Seraseq® DNA/RNA/ctDNA

Positive reference ensures genomic changes in patient tests are correctly identified & reported.

- ✓ Developed specifically for NGS platforms
- ✓ Well-characterized GIAB GM24385 genomic background
- ✓ cGMP manufactured to ISO 13485 standards
- ✓ US-FDA audited manufacturing facilities
- ✓ Global IVD product manufacturer for >30 years

Seraseq® Reference Material Design Process



FFPE: DNA / IVT RNA transfected into the cell line

- Typical construct length is 800 bp
- In vitro transcribed plasmids for variant transcripts and fusions
- Final product tested by ddPCR and NGS assays

Seraseq® Oncology Focus on Cancer Biomarkers of Clinical Utility in Targeted Therapies

Disease	Targeted Biomarker(s)	Drug	Pharma	Rel. Year	Seraseq Product
CML	BCR-ABL1	Imatinib	Genentech	2001	Myeloid RNA Fusion RNA v4 Whole Transcriptome RNA Seq
NSCLC/Pancreas	EGFR L858R	Gefitinib Erlotinib	AZ Osi	2003 2004	Pan Cancer DNA ctDNA v2 ctDNA Complete™
Thyroid Cancer, Renal cancer	VEGFR1/2/3 BRAF KIT FLT3 RET MET	Sorafenib Cabozantinib	Bayer Exelixis	2005 2012	Pan Cancer DNA Myeloid DNA ctDNA v2
CML	BCR-ABL1; Ph+	Dasatinib	BMS	2006	Myeloid RNA Fusion RNA v4 Whole Transcriptome RNA Seq
Breast Cancer	EGFR ERBB2	Lapatinib	GSK	2007	Pan Cancer DNA ctDNA Complete™
NSCLC	ALK-EML4 CD74-ROS1	Crizotinib Ceritinib Alectinib Lorlatinib	Hoffman-LaRoche Pfizer Novartis	2011 2014 2015 2018	Pan Cancer DNA Fusion RNA v4 ctDNA v2 ctDNA Complete™
Melanoma	BRAF V600E	Vemurafenib Encorafenib	Genentech Hoffman-LaRoche	2011 2018	Pan Cancer DNA ctDNA v2 ctDNA Complete™
NSCLC	EGFR ERBB2 ERBB4	Afatinib	Boehringer-Ingelheim	2013	Pan Cancer DNA ctDNA Complete™
Pan-Cancer	TMB	Nivolumab	BMS	2014 2021	FFPE TMB ctDNA TMB FFPE MSI
Pan-Cancer	TMB (Score>10)	Pembrolizumab	Merck	2014 2020	FFPE TMB ctDNA TMB FFPE MSI
NSCLC	EGFR T790M	Osimertinib	AZ	2015	Pan Cancer DNA ctDNA v2 ctDNA Complete™

Disease	Targeted Biomarker(s)	Drug	Pharma	Rel. Year	Seraseq Product
NSCLC	ALK, ROS1, FLT3, EGFR	Brigatinib	Ariad	2017	Pan Cancer DNA ctDNA v2
EGFR-mutant NSCLC	EGFR family	Dacomitinib	Pfizer	2018	Pan Cancer DNA ctDNA v2 ctDNA Complete™
AML	FLT3	Gilteritinib	Astellas	2018	Myeloid DNA Pan Cancer DNA ctDNA v2
Melanoma	BRAF	Benimetinib	Array Bio	2018	Pan Cancer DNA ctDNA v2 ctDNA Complete™
Solid Tumors/NTRK	NTRK; ROS1	Larotrectinib	Loxo/Bayer	2018	FFPE NTRK Fusion RNA v4
Solid Tumors/NTRK	NTRK; ROS1	Entrectinib	Igynta	2019	FFPE NTRK Fusion RNA v4
NSCLC	MET ex14	Capmatinib	Novartis	2020	Fusion RNA v4 Whole Transcriptome RNA Seq
GIST	PDGFR	Avapritinib	Blueprint	2020	Pan Cancer DNA ctDNA v2
NSCLC	RET	Praseltinib	Blueprint	2020	Pan Cancer DNA ctDNA v2 ctDNA Complete™
Cholangicarcinoma	FGFR2	Pemigatinib	Incyte	2020	Pan Cancer DNA ctDNA v2
NSCLC	MET	Tepotinib	EMD Serono	2021	Pan Cancer DNA

Seraseq® Oncology Products

Disease profiling: Solid Tumor DNA and RNA

Seraseq® Tumor DNA Products

Pan-Cancer Tumor DNA AF7 / 10

- 28 pan-cancer genes; 40 variants
- SNVs, INDELs, SVs
- All variants at AF7% or AF10%
- Purified gDNA

AKT1*	GNA11*	PIK3CA*#
APC*#	GNAQ*	PTEN#
ATM#	GNAS*	RET*
BRAF*	IDH1*	SMAD4*
CTNNB1*	JAK2*	TP53*#
EGFR*#	KIT*	NRAS/CSDE1¥
ERBB2#	KRAS*	TPR-ALK¥
FGFR3*	MPL*	NCOA4-RET¥
FLT3#	NPM1*#	
FOXL2*	PDGFRA*	

* SNVs; ¥ Fusions; # INDELs

Tri-Level Tumor DNA AF4 / 7 / 10

- 28 pan-cancer genes; 40 variants
- SNVs, INDELs, SVs
- AF4% (13), AF7% (13), AF10% (14)
- Purified gDNA

AKT1*	GNA11*	PIK3CA*#
APC*#	GNAQ*	PTEN#
ATM#	GNAS*	RET*
BRAF*	IDH1*	SMAD4*
CTNNB1*	JAK2*	TP53*#
EGFR*#	KIT*	NRAS/CSDE1¥
ERBB2#	KRAS*	TPR-ALK¥
FGFR3*	MPL*	NCOA4-RET¥
FLT3#	NPM1*#	
FOXL2*	PDGFRA*	

* SNVs; ¥ Fusions; # INDELs

Compromised FFPE Tumor DNA

- 15 solid tumor genes; 34 variants
- SNVs (18), CNVs (3), INDELs (10), SVs (3)
- 10 uM FFPE curl

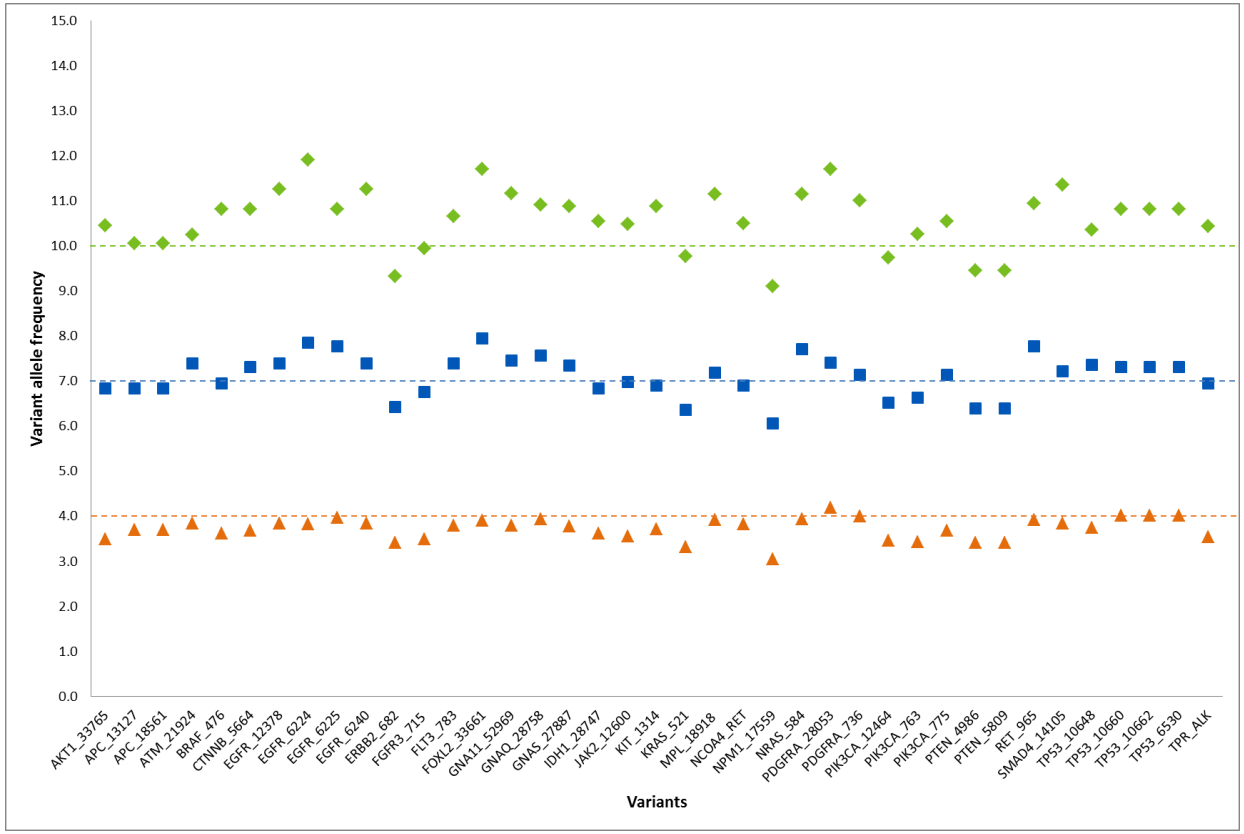
Industry-first

AKT1*	METγ
ALK*	MYCγ
BRAF*#	NRAS*
BRCA1#	PIK3CA*
BRCA2#	TP53*#
EGFR*#	CD74-ROS1¥
ERBB2#γ	NCOA4-RET¥
KIT*	EML4-ALK¥
KRAS*	

* SNVs; ¥ Fusions; γ CNVs; # INDELs

- **Quantified by ddPCR and NGS**
- **Suitable for amplicon and hybrid capture NGS assays**

Precise Control of Tumor DNA VAF by dPCR



AF10
Mean = 10.6%

AF7
Mean = 7.1%

AF4
Mean = 3.7%

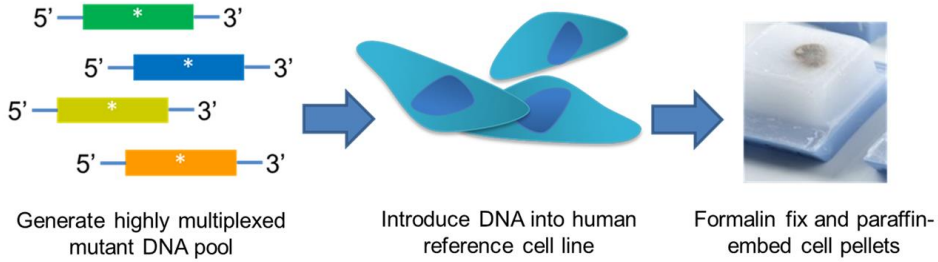
Seraseq Tumor DNA & Tri-Level Mixes

Compromised FFPE Product Development

FFPE Process

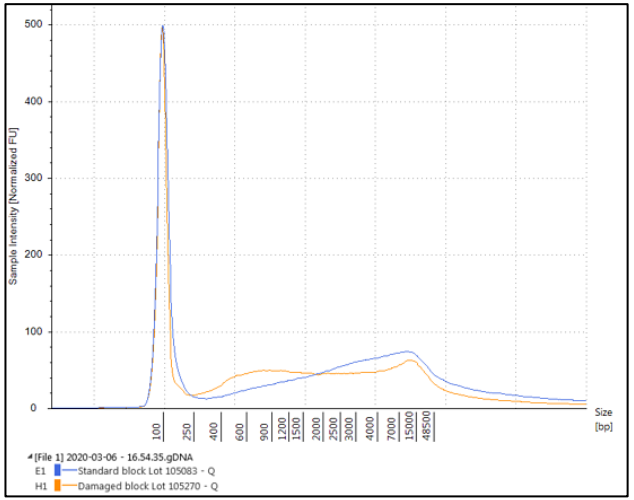
- Light fixation (standard)
- Moderate fixation (new)
  - ➢ More damaged, patient-like FFPE
  - ➢ DIN ~3.9 & 4.3* (*patient ~3.3-3.5)*

**Maxwell kit: 4.0; QIAamp kit = 4.3*



Extraction Efficiencies

- QIAamp FFPE Tissue DNA
  - ➢ 130-240 ng / 10 µm curl
- Maxwell FFPE Tissue DNA
  - ➢ 320-445 ng / 10 µm curl



DNA quality

Compromised (orange) = less intact DNA

Light fixation (blue) = more intact DNA

Compromised FFPE Tumor DNA

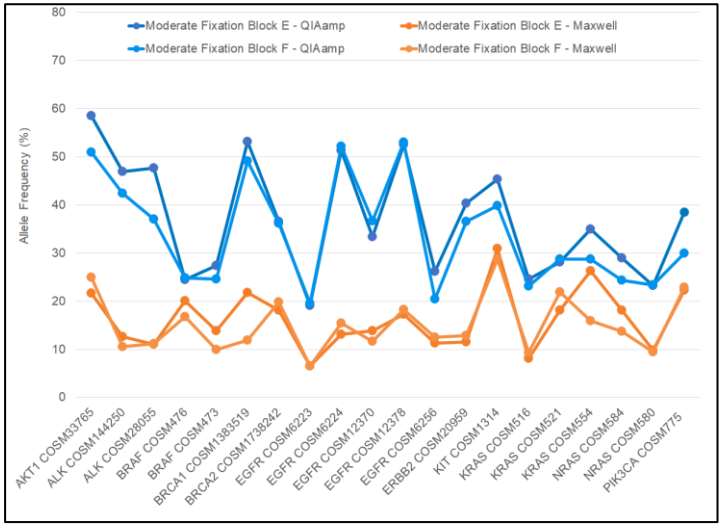
#	Gene	COSMIC ID	AA change	AA Mutation	Variant Type
1	AKT1	COSM33765	p.E17K	c.49G>A	SNV
2	ALK	COSM144250	p.G1202R	c.3604G>A	
3	ALK	COSM28055	p.F1175L	c.3522C>A	
4	BRAF	COSM476	p.V600E	c.1799T>A	
5	EGFR	COSM6240	p.T790M	c.2369C>T	
6	EGFR	COSM6224	p.L858R	c.2573T>G	
7	EGFR	COSM6493937	p.C797S	c.2389T>A	
8	KIT	COSM1314	p.D816V	c.2447A>T	
9	KRAS	COSM521	p.G12D	c.35G>A	
10	KRAS	COSM516	p.G12C	c.34G>T	
11	KRAS	COSM554	p.Q61H	c.183A>C	
12	NRAS	COSM584	p.Q61R	c.182A>G	
13	NRAS	COSM580	p.Q61K	c.181C>A	
14	PIK3CA	COSM775	p.H1047R	c.3140A>G	
15	PIK3CA	COSM765	p.E545D	c.1635G>T	
16	TP53	COSM10648	p.R175H	c.524G>A	
17	TP53	COSM10660	p.R273H	c.818G>A	
18	TP53	COSM10662	p.R248Q	c.743G>A	
19	BRAF	COSM473	p.V600K	c.1798_1799delinsAA	Del
20	BRCA1	COSM1383519	p.K654fs*47	c.1961del	
21	BRCA2	COSM1738242	p.R2645fs*3	c.7934del	
22	EGFR	COSM6223	p.E746_A750 del ELREA	c.2235_2249del	
23	EGFR	COSM12370	p.L747_P753>S	c.2240_2257del	
24	EGFR	COSM6256	p.S752_I759 del SPANKEI	c.2254_2277del	
25	TP53	COSM6530	p.C242fs*5	c.723delC	
26	TP53	COSM18610	p.S90fs*33	c.263delC	
27	EGFR	COSM12378	p.D770_N771insG	c.2310_2311insGGT	Ins
28	ERBB2	COSM20959	p.Y772_A775dup	c.2313_2324dup	
29	ERBB2	N/A	Amplification	N/A	CNV
30	MET	N/A	Amplification	N/A	
31	MYC	N/A	Amplification	N/A	
32	CD74-ROS1	N/A	translocation	N/A	SV
33	NCOA4-RET	N/A	Gene Fusion	N/A	
34	EML4-ALK	N/A	translocation	N/A	

Highly multiplexed (34 variants in 15 genes)

- All variant types: SNVs (18), INDELs (10), CNVs (3), SVs (3)
- Clinically-actionable (drivers, etc.)

Qualitative control = mutation-positive

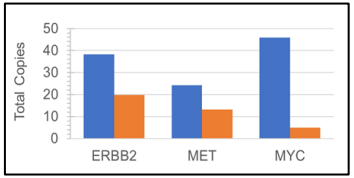
- AF ≥10%, range of AF ~10-50%



Kit = 1x 10 µm FFPE curl

Quant by dPCR & NGS (TSO500

CNVs

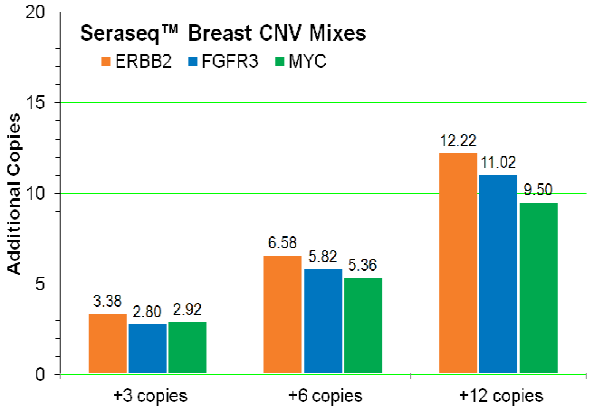


Seraseq® CNV Mix Products

Breast CNV Mix

- 3 Genes: ERBB2, FGFR3, MYC
- Clinically-relevant whole genes
- +3, +6 or +12 amplifications
- 200 ng purified gDNA
- dPCR Quantitation, NGS validated

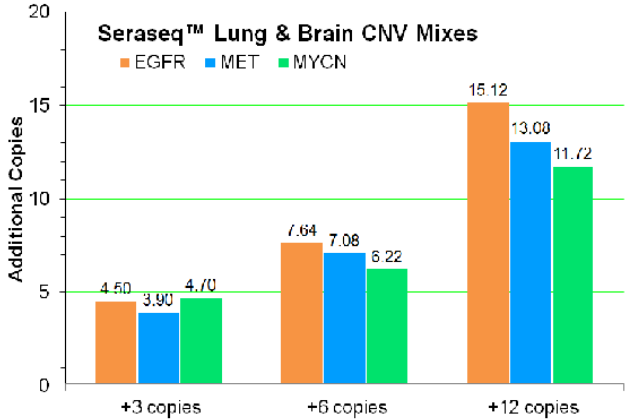
External NGS validation:



Lung & Brain CNV Mix

- 3 Genes: EGFR, MYCN, MET
- Clinically-relevant whole genes
- +3, +6 or +12 amplifications
- 200 ng Purified gDNA
- dPCR Quantitation, NGS validated

External NGS validation:



Seraseq® Fusion RNA Products

- 18 solid tumor fusion genes
- ~1500 copies / µl
- Targeted AMP and Hyb-Cap NGS assays

Pan-Cancer RNA & FFPE

RNA Fusion	5' Partner	3' Partner
CCDC6-RET	CCDC6 ex 1	RET ex 12
CD74-ROS1	CD74 ex 6	ROS1 ex 34
EGFR Variant III	EGFR ex 1	EGFR ex 8
EGFR-SEPT14	EGFR ex 24	SEPT14 ex 10
EML4-ALK	EML4 ex 13	ALK ex 20
ETV6-NTRK3	ETV6 ex 5	NTRK3 ex 15
FGFR3-BAIAP2L1	FGFR3 ex 17	BAIAP2L1 ex 2
FGFR3-TACC3	FGFR3 ex 17	TACC3 ex 11
KIF5B-RET	KIF5B ex 24	RET ex 11
LMNA-NTRK1	LMNA ex 2	NTRK1 ex 10
MET ex 14 Skipping	MET ex 13	MET ex 15
NCOA4-RET	NCOA4 ex 8	RET ex 12
PAX8-PPARG1	PAX8 ex 9	PPARG1 ex 3
SLC34A-ROS1	SLC34A2 ex 4	ROS1 ex 34
SLC45A3-BRAF	SLC45A3 ex 1	BRAF ex 8
TFG-NTRK1	TFG ex 5	NTRK1 ex 9
TMPRSS2-ERG	TMPRSS2 ex 1 (5' UTR)	ERG ex 2
TPM3-NTRK1	TPM3 ex 7	NTRK1 ex 9

- 22 pan-cancer fusion genes
- >20,000 copies / µl
- Whole Transcriptome RNA-Seq NGS assays

Whole Transcriptome RNA Seq

RNA Fusion	5' Partner	3' Partner
BCR-ABL1	BCR exon 14	ABL1 exon 2
CCDC6-RET	CCDC6 exon 1	RET exon 12
CD74-ROS1	CD74 exon 6	ROS1 exon 34
EML4-ALK	EML4 exon 14	ALK exon 20
ETV6-ABL1 (transcript 1)	ETV6 exon 4	ABL1 exon 2
ETV6-ABL1 (transcript 2)	ETV6 exon 5	ABL1 exon 2
ETV6-NTRK3	ETV6 exon 5	NTRK3 exon 13
FGFR3-TACC3	FGFR3 exon 17	TACC3 exon 11
KIF5B-RET	KIF5B exon 24	RET exon 11
LMNA-NTRK1	LMNA exon 2	NTRK1 exon 10
LMNA-NTRK1	LMNA exon 11	NTRK1 exon 10
MEF2D-CSF1R	MEF2D exon 7	CSF1R exon 12
MET ex 14 Skipping	MET exon 13	MET exon 15
NACC2-NTRK2	NACC2 exon 5	NTRK2 exon 11
NCOA4-RET	NCOA4 exon 8	RET exon 12
PML-RARA	PML exon 6	RARA intron 2
RUNX1-RUNX1T1	RUNX1 exon 5	RUNX1T1 exon 2
SLC34A2-ROS1	SLC34A2 exon 4	ROS1 exon 34
SLC45A3-BRAF	SLC45A3 exon 1	BRAF exon 8
TCF3-PBX1	TCF3 exon 16	PBX1 exon 3
TMPRSS2-ERG	TMPRSS2 exon 1 (5' UTR)	ERG exon 2
TPM3-NTRK1	TPM3 exon 8	NTRK1 exon 9

- 15 NTRK1/2/3 fusion genes
- >1000 copies / µl
- Support for LDT/CDx NGS assay validation for patient stratification

Industry-first

NTRK RNA & FFPE

NTRK Fusion Gene	5' Partner	3' Partner
TPM3-NTRK1	TPM3 ex 7	NTRK1 ex 10
LMNA-NTRK1	LMNA ex 11	NTRK1 ex 11
IRF2BP2-NTRK1	IRF2BP2 ex 1	NTRK1 ex 10
SQSTM1-NTRK1	SQSTM1 ex 5	NTRK1 ex 10
TFG-NTRK1	TFG ex 5	NTRK1 ex 10
AFAP1-NTRK2	AFAP1 ex 14	NTRK2 ex 12
NACC2-NTRK2	NACC2 ex 4	NTRK2 ex 13
QKI-NTRK2	QKI ex 6	NTRK2 ex 16
TRIM24-NTRK2	TRIM24 ex 12	NTRK2 ex 15
PAN3-NTRK2	PAN3 ex 1	NTRK2 ex 17
ETV6-NTRK3	ETV6 ex 5	NTRK3 ex 14
ETV6-NTRK3	ETV6 ex 5	NTRK3 ex 15
ETV6-NTRK3	ETV6 ex 4	NTRK3 ex 15
ETV6-NTRK3	ETV6 ex 4	NTRK3 ex 14
BTBD1-NTRK3	BTBD1 ex 4	NTRK3 ex 14

Seraseq Fusion RNA v4 Multi-Lab Testing

RNA Mix
6 Evaluation Labs

RNA FFPE
5 Evaluation Labs

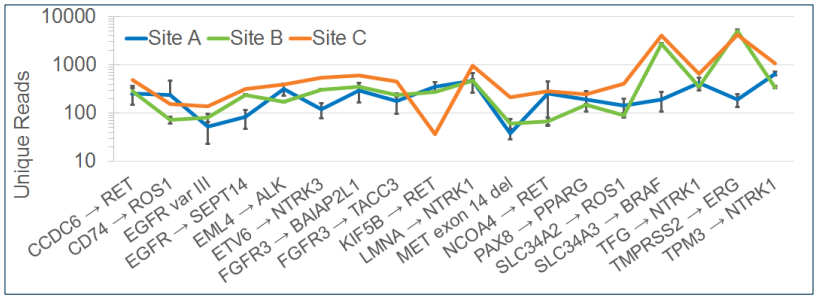
NGS Platforms/Assays

- Illumina TST170
- Archer FusionPlex
- Oncomine Focus (FFPE)

Result Highlights:

- High sequencing efficiencies (% on-target)
- Detection of all 18 fusions: compatible with multiple platforms and FFPE extraction kits
- Performance at RNA input as low 40 ng
- **FFPE**: 3 kits tested
  - *Qiagen AllPrep FFPE DNA/RNA* ■
  - *Promega Maxwell FFPE RNA* ▼
  - *Agencourt Formapure FFPE RNA* ▲

Site	NGS Assay	RNA Input (ng)	Library Yield (nM)	Read Depth	On Target (%)
A	AST	200	2666	10.59 M	81
		100	1219	5.00 M	74
		50	1395	7.21 M	73
B	AST	200	359		97
		20	430	0.5 M	97
B	AL	200	532		94
		20	609	1 M	94
C	AST	200	33.8 (ng/µL)	Not Reported	92
C	ACTL	200	63.8 (ng/µL)	Not Reported	93
D	AC	250 (dilution series)	408	1.35 M	92.1
E	TST170	40	883	16 M	79.8



Multi-lab study results presented at 2019 AACR Meeting (#:4899), and 2019 AMP Global meeting (Poster#:P096)

Seraseq® NTRK Fusion RNA Products

- ✓ NTRK fusions are rare events, cancer type agnostic, require NGS testing for identification
- ✓ Developed in collaboration with Bayer/Loxo to support patient stratification for treatment with Larotrectinib
- ✓ 15 NTRK gene fusions (NTRK1, NTRK2, NTRK3) in GM24385 WT background
- ✓ Purified total RNA (500 ng) or FFPE reference material (10 µm curl)
- ✓ Fusions quantified by dPCR & NGS
- ✓ Fusion analysis by NGS: FFPE ~ RNA Mix

#	NTRK Fusion Gene	5' Partner	3' Partner	Unique Start Sites (NGS)	
				Mix	FFPE
1	TPM3-NTRK1	TPM3 exon 7	NTRK1 exon 10	66	82
2	LMNA-NTRK1	LMNA exon 11	NTRK1 exon 11	182	249
3	IRF2BP2-NTRK1	IRF2BP2 exon 1	NTRK1 exon 10	430	467
4	SQSTM1-NTRK1	SQSTM1 exon 5	NTRK1 exon 10	314	330
5	TFG-NTRK1	TFG exon 5	NTRK1 exon 10	361	533
6	AFAP1-NTRK2	AFAP1 exon 14	NTRK2 exon 12	334	423
7	NACC2-NTRK2	NACC2 exon 4	NTRK2 exon 13	188	270
8	QKI-NTRK2	QKI exon 6	NTRK2 exon 16	143	218
9	TRIM24-NTRK2	TRIM24 exon 12	NTRK2 exon 15	68	82
10	PAN3-NTRK2	PAN3 exon 1	NTRK2 exon 17	130	226
11	ETV6-NTRK3	ETV6 exon 5	NTRK3 exon 14	101	114
12	ETV6-NTRK3	ETV6 exon 5	NTRK3 exon 15	168	230
13	ETV6-NTRK3	ETV6 exon 4	NTRK3 exon 15	167	197
14	ETV6-NTRK3	ETV6 exon 4	NTRK3 exon 14	306	290
15	BTBD1-NTRK3	BTBD1 exon 4	NTRK3 exon 14	143	136

Fusion RNA control used in a clinical setting for NSCLC patient diagnosis and care management

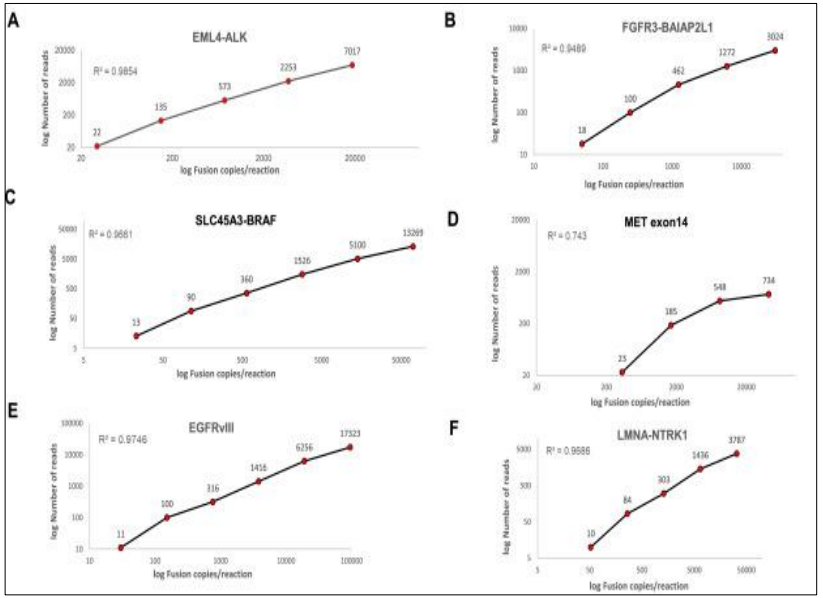
Key considerations for comprehensive validation of an RNA fusion NGS panel

Subit Barua [1], Gary Wang [1], Mahesh Mansukhani, Susan Hsiao, Helen Fernandes [*]

Department of Pathology and Cell Biology, Columbia University Medical Center, New York, USA

- ✓ NYSDOH-certified CLIA lab running a 47-gene NGS assay for NSCLC
- ✓ Reflex to fusion RNA testing for tumors lacking DNA driver mutations
- ✓ RNA panel covering 17 fusion genes validated using Seraseq Fusion RNA mix v3
- ✓ Seraseq samples used for LoD, reproducibility, precision and performance monitoring
- ✓ Reflex fusion test led to 10% increase in diagnostic yield with minimal additional testing/processing time
- ✓ Reducing the number of tests performed

Practical Laboratory Medicine



Barua S., et. al., *Pract. Lab. Med.*, 2020 Jun 8;21:e00173. doi: 10.1016/j.plabm.2020.e00173.

Seraseq® Whole Transcriptome Reference

Why Whole Transcriptome RNA-Seq?

- ✓ Targeted RNA-seq NGS panels do not analyze all exons/transcripts
- ✓ Whole Transcriptome RNA-Seq: qualitative and quantitative
- ✓ Identify full catalog of transcripts (~20,000 genes), define gene structures and determine gene expression levels.
- ✓ New fusion RNA biomarker discovery: emerging drugs targeting fusions, e.g. in NTRK, RET (NSCLC), MET
- ✓ Exome-wide Dx tumor profiling: improved diagnostic yield when paired with targeted DNA-Seq assays

Seraseq Whole Transcriptome RNA-Seq Mix

- ✓ 22 Fusion RNA targets (pan-cancer)
- ✓ >20,000 copies/µl per target
- ✓ RNA size ~ 1kb, poly-A extension ~100 bp
- ✓ 1 µg Purified RNA

#	Fusion RNA Targets	dPCR cp/µl	NGS (reads)*
1	BCR-ABL1	43680	120
2	CCDC6-RET	48000	177
3	CD74-ROS1	41493	100
4	EML4-ALK	49267	158
5	ETV6-ABL1 (transcript 1)	34640	144
6	ETV6-ABL1 (transcript 2)	40107	88
7	ETV6-NTRK3	52747	194
8	FGFR3-TACC3	33227	193
9	KIF5B-RET	25800	191
10	LMNA-NTRK1 (transcript 1)	21387	180
11	LMNA-NTRK1 (transcript 2)	41013	71
12	MEF2D-CSF1R	30133	47
13	MET ex 14 Skipping	59040	103
14	NACC2-NTRK2	39040	303
15	NCOA4-RET	34027	133
16	PML-RARα	35893	28
17	RUNX1-RUNX1T1	28000	178
18	SLC34A2-ROS1	45280	77
19	SLC45A3-BRAF	35147	231
20	TCF3-PBX1	29013	69
21	TMPRSS2-ERG	30453	186
22	TPM3-NTRK1	37760	427

**NGS data generated using a custom IDT xGen Exome Panel (>19,000 genes) – Tempus Labs*

Seraseq® Oncology Products

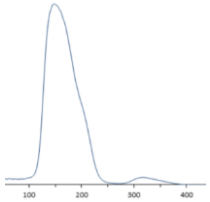
Liquid Biopsy (ctDNA)

Seraseq® ctDNA Products

ctDNA v2 MM & RM

- 28 pan-cancer genes; 40 variants
- SNVs, INDELs, & SVs
- VAFs: 0.125%, 0.25%, 0.5%, 1%, 2%, WT

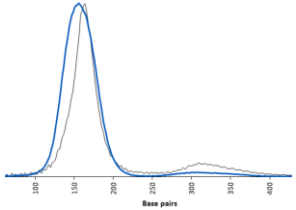
AKT1	JAK2
APC	KIT
ATM	KRAS
BRAF	MPL
CTNNB1	NCOA4-RET
EGFR	NPM1
ERBB2	NRAS
FGFR3	PDGFRA
FLT3	PIK3CA
FOXL2	PTEN
GNA11	RET
GNAQ	SMAD4
GNAS	TP53
IDH1	TPR-ALK



ctDNA Complete™ MM & RM

- 16 solid tumor genes; 25 variants
- SNVs, INDELs, CNVs, & SVs
- VAFs: 0.1%, 0.5%, 1%, 2.5%, 5%, WT

AKT1
ALK
BRAF
EGFR
KIT
KRAS
NRAS
PIK3CA
BRCA1
BRCA2
ERBB2
MET
MYC
CD74-ROS1
EML4-ALKv1
NCOA4-RET

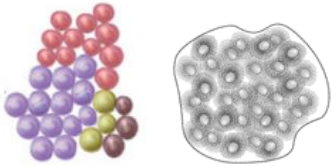


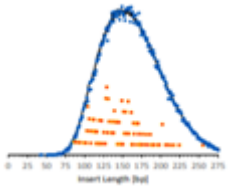
Quantified by ddPCR and NGS

ctDNA MRD Panel Mix

- >600 variants (solid tumor cell line + synthetic variants)
- SNVs, INDELs, CNVs
- Tumor fractions: 0%, 0.5%, 0.05% and 0.005%

Industry-first



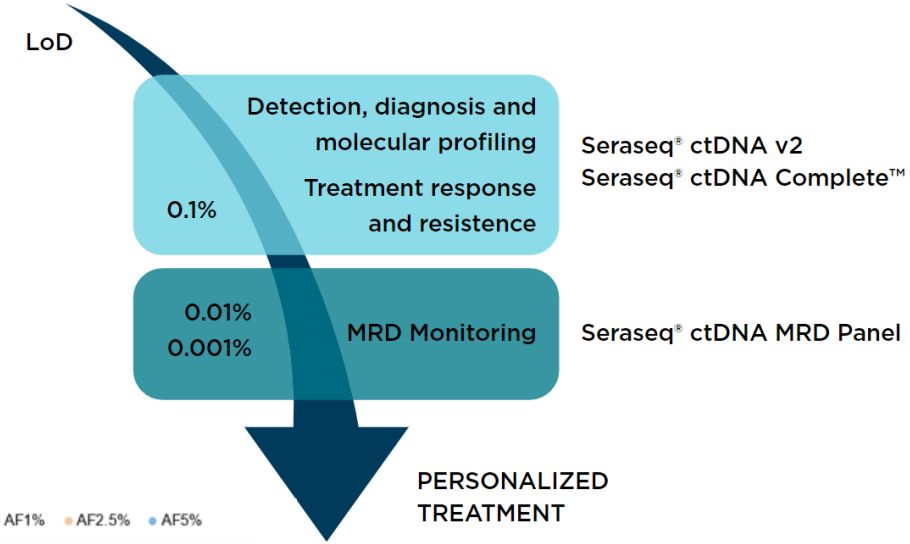


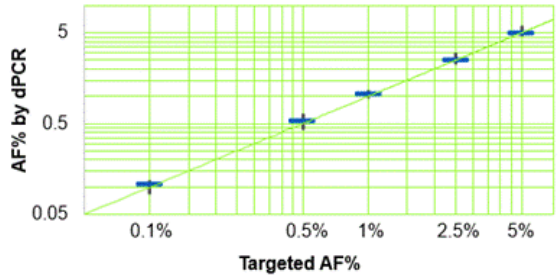
AKT1
ALK
BRAF
EGFR
KIT
KRAS
NRAS
PIK3CA
BRCA1
BRCA2
ERBB2
MET
MYC
CD74-ROS1
EML4-ALKv1
NCOA4-RET

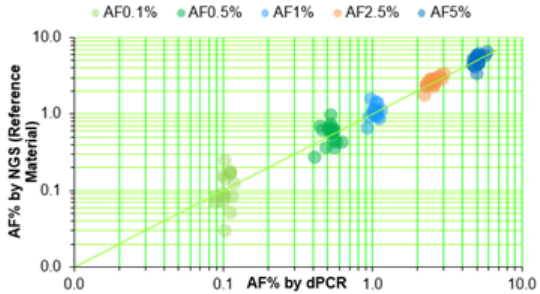
Seraseq® ctDNA in liquid biopsy applications

Product Highlights and Options:

- ✓ Purified ctDNA (MM): no extraction needed
- ✓ ctDNA in plasma (RM): extraction required
- ✓ ctDNA sizing ~**160-170 bp**
- ✓ VAF range:
  - **ctDNA v2:** 0.125%, 0.25%, 0.5%, 1%, 2%, WT
  - **ctDNA Complete™:** 0.1%, 0.5%, 1%, 2.5%, 5%, WT
- ✓ ddPCR and NGS quantitation

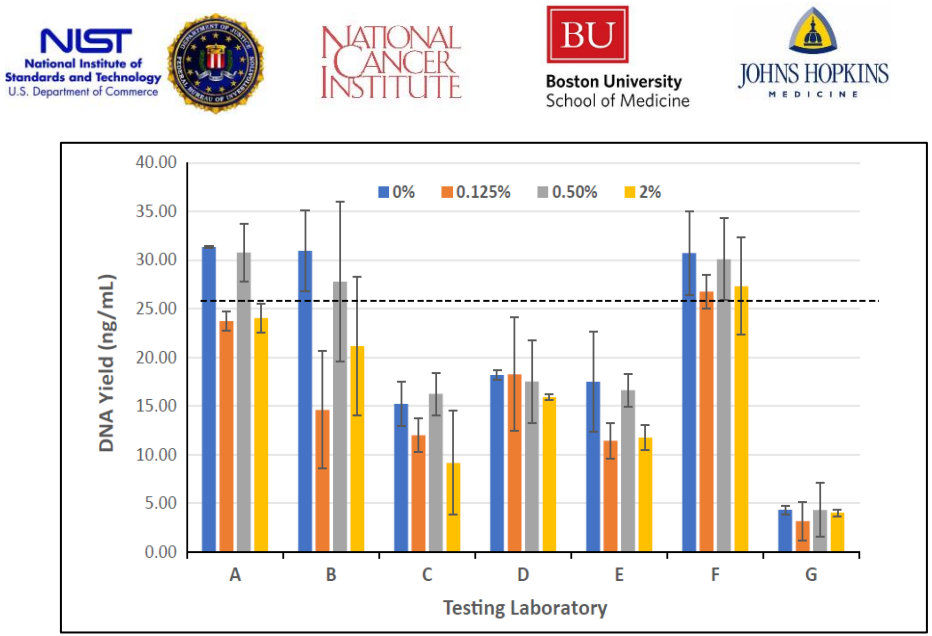




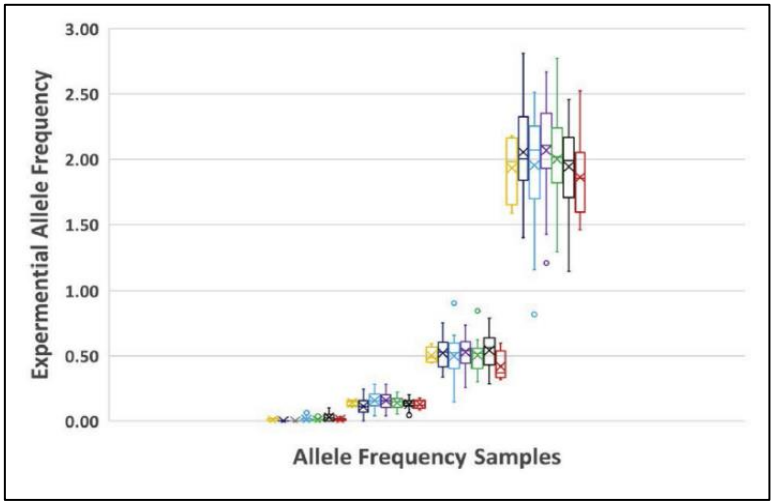


Ideal for LoD and precision validation of the most sensitive clinical assays

Seraseq ctDNA v2 Multi-Lab Assessment



DNA Yields for Reference Material Samples



Comparison of NGS results of analysis of blended AF versus observed AF values

Cole, KD, et. al., J. Mol. Diag., 2019, Vol 21, No 4, 658-676

Multi-Lab/Platform Evaluation Study using Seraseq ctDNA Complete™

CANCER ID

EU Liquid Biopsy Consortium

- Industry experts in biomarker validation, assay dev, clinical sciences, and bioinformatics

Multi-lab study to investigate:

- Utility of contrived materials across clinical oncology assays, primarily solid tumor
- Compare various platform chemistries against a common reference material

Conclusions:

- Biosynthetic reference materials are useful for assessment of mutation analysis platforms
- Variability of NGS assays highlights importance of extensive validation before implementing in clinical practice

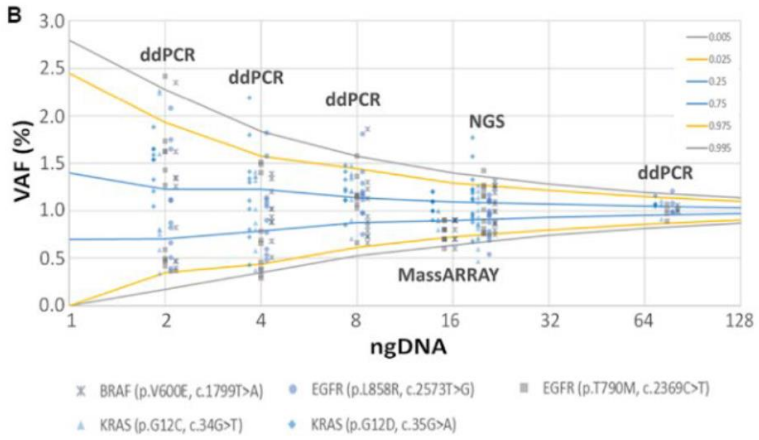
cancers

Weber, S, Heitzer, E. et al ., DOI: 10.3390/cancers12061588

MDPI

Article

Technical Evaluation of Commercial Mutation Analysis Platforms and Reference Materials for Liquid Biopsy Profiling



Use of Seraseq ctDNA reference materials in validation of MSK-ACCESS cfDNA panel

ARTICLE
https://doi.org/10.1038/s41467-021-24109-5 OPEN

nature COMMUNICATIONS

Enhanced specificity of clinical high-sensitivity tumor mutation profiling in cell-free DNA via paired normal sequencing using MSK-ACCESS

Precision & Reproducibility: 7 clinical cfDNA samples and Seraseq ctDNA Complete™ AF1% and AF2.5%

LoD assessment: 19 mutations (SNVs and INDELs) in Seraseq ctDNA Complete™ AF 5%, AF2.5%, AF 1%, AF 0.5%, and AF 0.1%

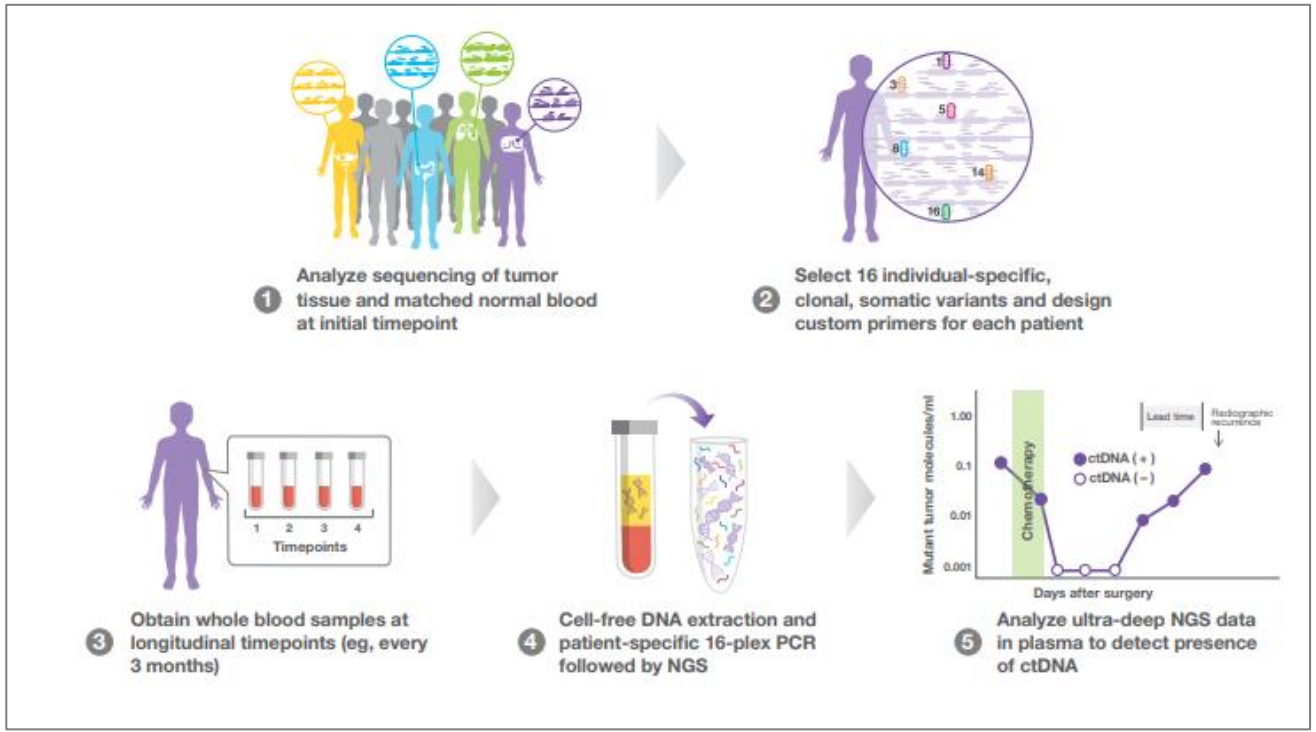
Developed in Memorial Sloan Kettering Cancer Cetre

- Based on FDA-approved MSK-IMPACT tissue NGS panel
- Comprehensive NGS assay for detection of low frequency somatic alterations in 129 genes
- Validated as a clinical test for detection of somatic variants in cfDNA, NYSDH-approved in 2019

Reproducibility for 19 ctDNA Complete variants	LoD
VAF 1%: av. measured VAF = 0.98%, CV 22.1% **VAF 2.5%:** av. measured VAF = 2.33%, CV 20.4%	92% sensitivity @ VAF 0.5% (de-novo) 99% sensitivity for known mutations

Rose Brannon, A. *et al. Nat Comm.,* **12,** 3770 (2021). https://doi.org/10.1038/s41467-021-24109-5

Natera Signatera™ MRD Assay validated using the Seraseq® ctDNA v2 Mutation Mix



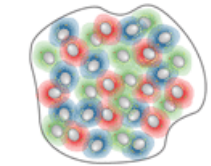
- First assay designed for detecting MRD
- Sensitivity at VAF <0.1% of cfDNA from plasma
- Analytical validation was performed using Seraseq ctDNA v2 MM AF 0.5%, titrated down to AF 0.005%
- Sensitivity threshold: able to detect at least two clonal mutations per panel

Natera MRD White paper

Magbanua MJM et al. ***Circulating tumor DNA in neoadjuvant-treated breast cancer reflects response and survival****, Annals of Oncology (2020), doi: https://doi.org/10.1016/j.annonc.2020.11.007.*

Seraseq® ctDNA MRD Panel Mix Development

Intended Use: Develop, validate and monitor the performance of patient-informed MRD assays in cancer patients undergoing therapy



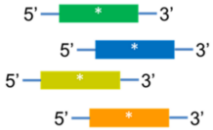
Tumor cell line (gDNA)

WES

>600 variants

Variant Calls (VCF)

0.5% tumor



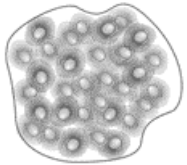
DNA constructs

Targeted panel

22 variants

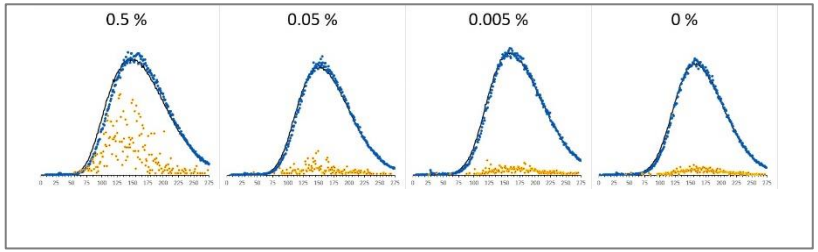
Variant Calls (VCF)

0.25% AF variants



Matched normal cell line (gDNA)

0.5% tumor blend is diluted to 0.05% and 0.005%, all TF including 0% are fragmented & sized



Blends (bulk mix) of tumor-derived ctDNA MRD variants

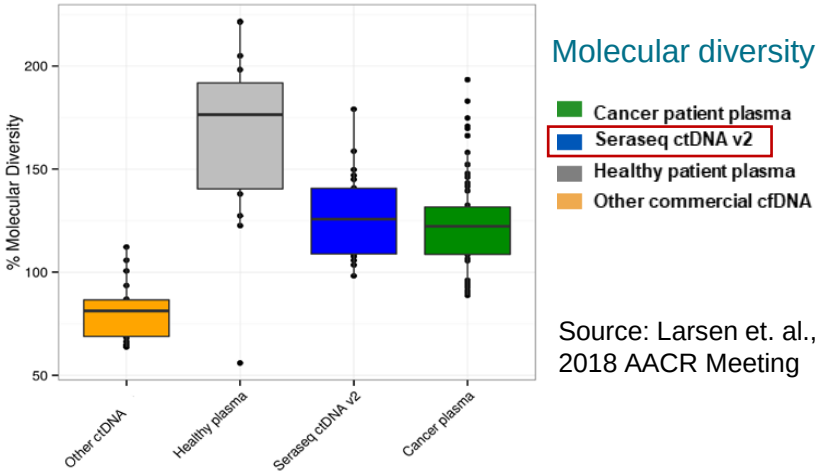
Targeted panel for 100 tumor variants

Variant Calls (VCF)

MRD Assay using a subset of tumor and synthetic variants – mix & match

Seraseq® ctDNA and FFPE reference materials are patient-like samples

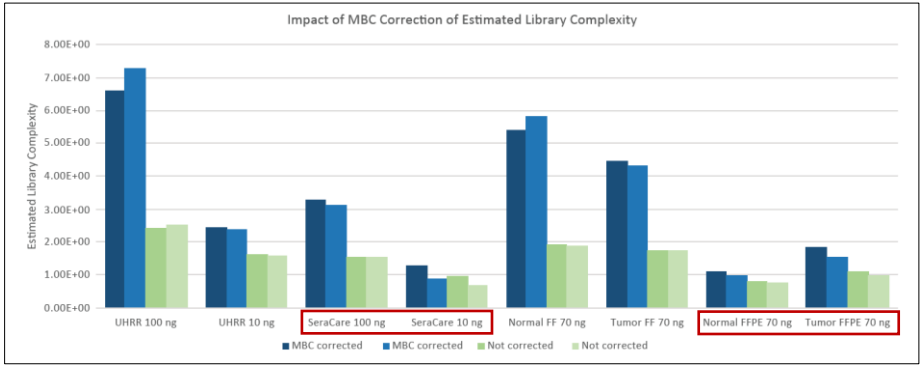
ctDNA



Source: Larsen et. al., 2018 AACR Meeting

Seraseq ctDNA Mutation Mix v2 reference standards and cancer patient plasma samples have comparable post-sequencing molecular diversity

FFPE

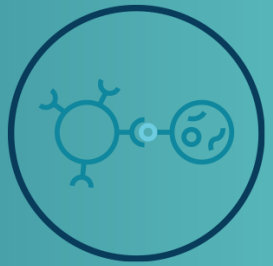


Matched tumor and normal FFPE samples, Agilent UHRR and Seraseq FFPE tumor fusion RNA reference material v2. Source: Agilent application note

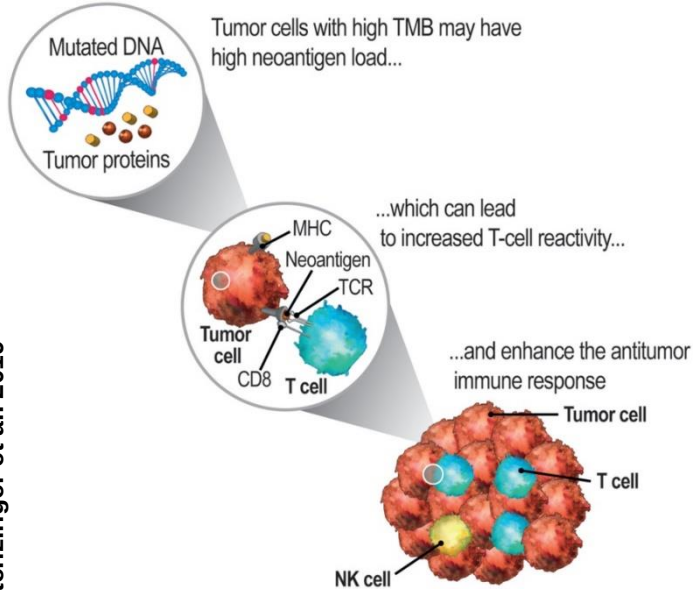
- ✓ Agilent SureSelect XT HS RNA library prep, target enrichment with Human V7 exome
- ✓ Seraseq sample Seraseq FFPE Fusion RM has similar library complexity to clinical FFPE samples: represents idealized FFPE input

Seraseq® Oncology Products

Immuno-Oncology



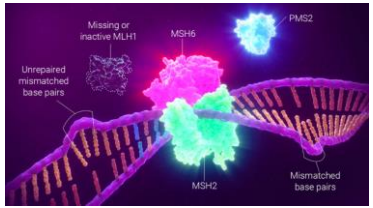
TMB and MSI in immuno-oncology



Stenzinger et al. 2019

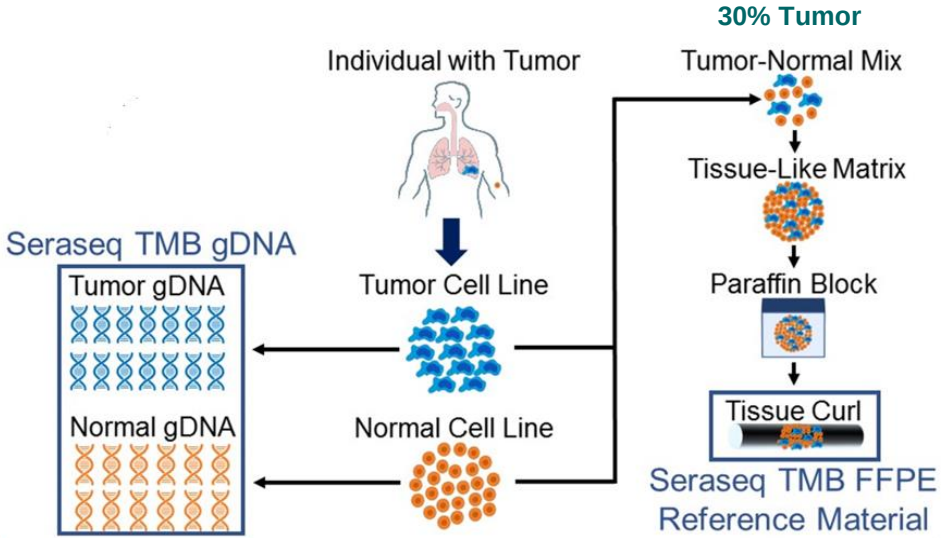
Immune checkpoint inhibitors (CPIs) unleash patient's own T cells to kill tumors

- ✓ TMB = tumor mutational burden (# of somatic mutations / Mb)
- ✓ Clinical data shows patients with TMB-H have positive response to CPIs
- ✓ Both WES and targeted panels are used for TMB measurements – calculated scores vary!
- ✓ There is a need for reference standards to align TMB scores determined by NGS panels and WES



- ✓ Microsatellites (MS) are short tandem repeat DNA sequences prone to replication errors → shortening of repeats
- ✓ MSI = microsatellite instability status is predictive of Lynch syndrome and also correlates with positive response to CPI

TMB Reference Material Development & Analysis



TMB Reference Standards	TMB Scores (gDNA)	TMB Scores (FFPE)
Seraseq® TMB Score 7	7.2 ± 0.2	7.15 ± 0.4
Seraseq® TMB Score 9	9.5 ± 0.4	7.52 ± 1.3
Seraseq® TMB Score 13 #	12.6 ± 0.02	12.1 ± 0.3
Seraseq® TMB Score 20	20.1 ± 0.2	18.59 ± 0.5
Seraseq® TMB Score 26	25.8 ± 0.5	22.8 ± 3.6

WES-based TMB Scores were derived using NGS enrichment kit (Agilent/SureSelect All Exon V6), Illumina Novaseq sequencer and NGS bioinformatics pipeline filters/settings following the recommendations of FoCR harmonization project*
Filters: non-synonymous variants, VAF >5%

mutagenized healthy cell line

Merino, D., et. al., Poster #268, 2019 ASCO Meeting, Chicago, USA; https://meetinglibrary.asco.org/record/172797/abstract

Tumor Mutational Burden (TMB) Collaborations

- **Global Partnerships on TMB**
  - FoCR TMB Harmonization Project → gDNA TMB
  - IQN-Path TMB Proficiency Pilot → FFPE TMB
  - SeraCare TMB Working Group → gDNA/FFPE/ctDNA

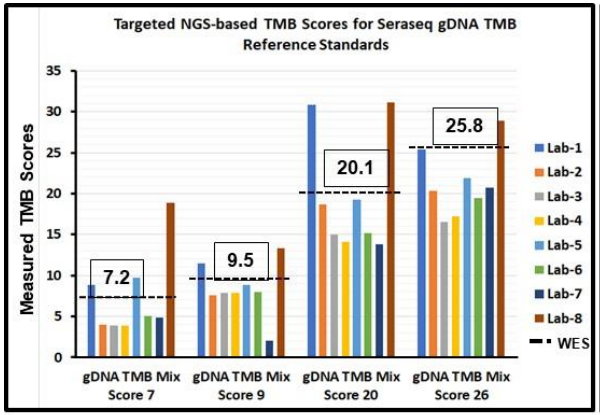
- **TMB reference standards**
  - 100% Tumor-Normal paired **gDNA** TMB standards
  - 30% Tumor **FFPE** TMB standards
  - 0%, 0.5% & 2% tumor **ctDNA** TMB (bTMB) standards

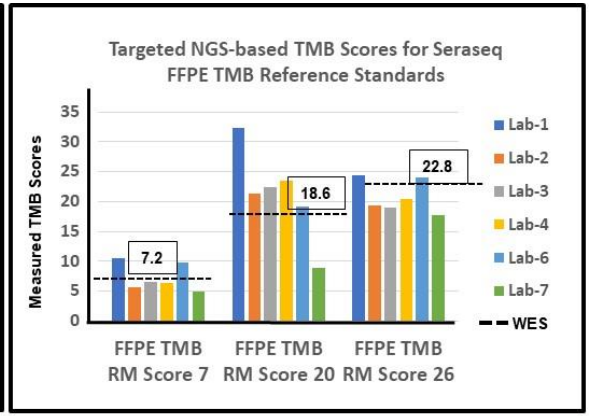
- **TMB Scoring by WES and Targeted Panels**
  - Tissue TMB = WES; ctDNA TMB = Targeted Panel
  - WES TMB Scoring pipeline (SeraCare proprietary)
  - Extensive evaluation on targeted NGS panels

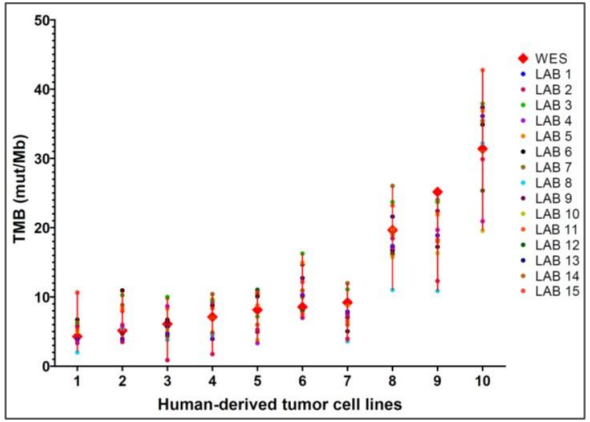
Seraseq TMB Reference Standards

Support Validation of TMB Measurements by NGS Panels

There is a need for reference standards to validate, harmonize and improve the precision of TMB measurements by targeted NGS panels for clinical applications.







illumina · BROAD INSTITUTE · Memorial Sloan Kettering Cancer Center · new oncology · sema4 · Roche · Intermountain PRECISION GENOMICS

FoCR TMB Consortium of 16 clinical laboratories

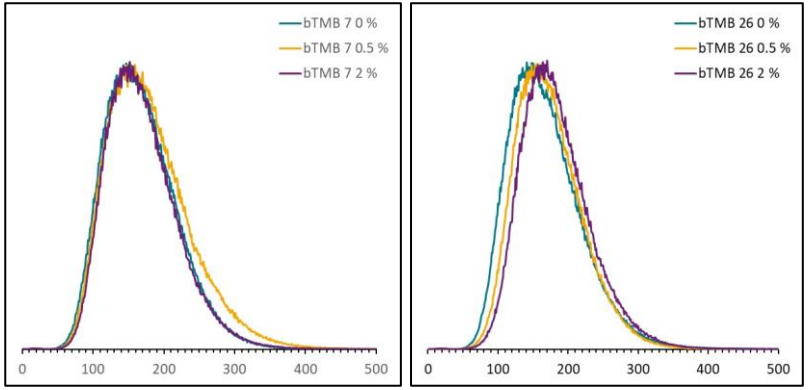
Vega D.M. et al. Annals of Oncology 2021 https://doi.org/10.1016/j.annonc.2021.09.016

Blood TMB – An Emerging Biomarker

- Blood TMB (bTMB) scores correlate with tissue TMB (tTMB), however they tend to be higher so there is a need for ctDNA TMB assay validation and identification of optimal clinical cut-offs.
- Assessing TMB scores in liquid biopsy samples combine challenges of ctDNA assays with challenges of measuring TMB by targeted gene panels.

New Seraseq patient-like Blood TMB products:

- ✓ Derived from tumor and their SNP-matched normal cell lines with **TMB 7,13,20 and 26**
- ✓ Provided in ctDNA format at 0%, 0.5% and 2% tumor fractions
- ✓ TMB Scores determined by a targeted NGS assay (TSO500 plasma/TMB pipeline)
- ✓ Analytical workflow require analyzing 0% tumor blend as a filter for somatic TMB variants



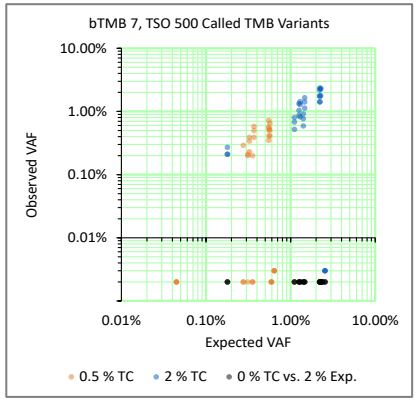
ctDNA size profiles for Seraseq® Blood TMB Score 7 and Score 26 @ 0%, 0.5% and 2% tumor fractions.

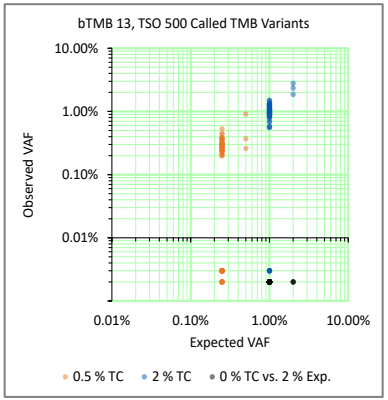
Eun-Ang Raiber-Moreau, et al, 2022 Genes, Chromosomes and Cancer (submitted) -collaboration with AZ
Butler, et al, Abstract #1982, 2020 AACR Virtual II

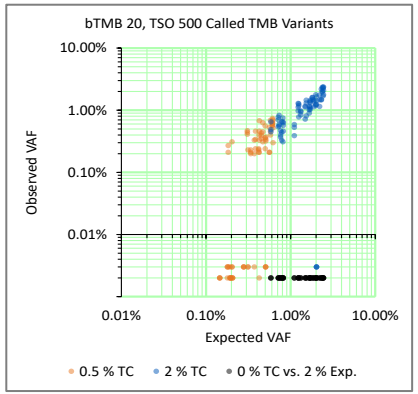
Seraseq Blood TMB Analysis by TSO500 ctDNA

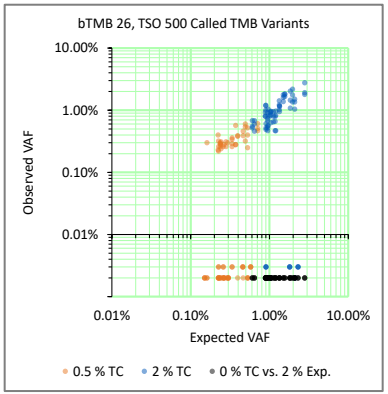
NGS Assay Platform: TSO500 ctDNA || NovaSeq 6000
bTMB Analysis: DRAGEN TSO500 Analysis Software v1.1
Filters: VAF >0.2%; Min Variant Coverage = 1000X

Sample	%Tumor Fraction	Conc (ng/ul)*	Input (ng)	Reps	Ave Blood TMB Score**	Adjusted Blood TMB Scores***
Seraseq Blood TMB Mix Score 7	0%	41	30	3	7.5 ± 1.7	**0**
	0.5%	57.6	30	3	13.1 ± 2.6	**5.6 ± 2.1**
	2%	41.2	30	3	17.9 ± 1.3	**10.4 ± 1.7**
Seraseq Blood TMB Mix Score 13	0%	21.7	30	3	4.6 ± 0.5	**0**
	0.5%	31.9	30	3	18.7 ± 2.1	**14.1 ± 2.2**
	2%	33.7	30	3	24.6 ± 0.8	**20.0 ± 0.9**
Seraseq Blood TMB Mix Score 20	0%	17	30	3	7.5 ± 1.4	**0**
	0.5%	21.7	30	3	26.0 ± 2.3	**18.5 ± 2.7**
	2%	24.5	30	3	35.6 ± 1.0	**28.1 ± 1.7**
Seraseq Blood TMB Mix Score 26	0%	64.8	30	3	6.0 ± 0.5	**0**
	0.5%	11	30	3	20.7 ± 5.5	**14.7 ± 2.4**
	2%	11.9	30	3	30.4 ± 1.8	**24.4 ± 1.5**









****Adjusted Score subtracts somatic contributions from 0% background of ~5-7 mut/Mb*

Seraseq® MSI Products

MSI Reference Panel AF5% & AF20%

- 5 clinically approved Bethesda MSI markers
- 5% or 20% VAF plus matched normal
- ddPCR and Promega MSI tested
- **Purified DNA mix**
- For qPCR/CE, dPCR, NGS assays

Marker	Gene	Chromosome	Position (hg19 based)	Comment
BAT-25	KIT (intron16)	chr4	55598211	25T -> 19T
BAT-26	MSH2 (intron5)	chr2	47641559	27A -> 17A
NR-21	SLC7A8 (5'UTR)	chr14	23652346	21A -> 13A
NR-24	ZNF2 (3'UTR)	chr2	95849361	23T -> 17T
MONO-27[1]	MAP4K3 (intron 3)	chr2	39573062	27A -> 21A
	MAP4K3 (intron13)		39536690	

MSI Classification by Promega:

- ≥2/5 unstable = MSI-H
- 1/5 unstable = MSI-L
- 0/5 unstable = MS-S

qPCR		
AF5%	AF20%	WT (0%)
Unstable	Unstable	Stable
Unstable	Unstable	Stable
Stable	Unstable	Stable
Unstable	Unstable	Stable
Unstable	Unstable	Stable

MSI-High FFPE & gDNA

- MSI-High human diseased cell line
- Multiple MSI loci present including 5 clinical ones
- MSI-H status confirmed with 2 NGS assays
- **Purified DNA Mix & FFPE formats**
- For NGS assay validation and MSI measurements

Industry-first

Illumina TSO500:

Product Name	NGS Assay	Av. MSI Sites Detected*	Av. Unstable MSI sites*	Av. MSI Score*	MSI Call
Seraseq® gDNA MSI-High Mix	TSO500	106	81	77.1	High
Seraseq® FFPE MSI-High RM	TSO500	119 105	90 75	75.6 71.4	High High

**MSI measurements from replicate TSO500 runs. MSI score is the percentage ratio of unstable MSI sites to the total number of MSI sites detected. The value must be >20% for an MSI-High determination.*

Sophia STS MSI Module:

Local score*	Global score*	MS status
37.4	37.1	MSI-HC

**Average MSI distance scores from replicate runs with Sophia Genetics STS Library Prep Kit and MSI module of Sophia DDM software. Minimum overall distance score >14 is required for an MSI-HC (high confidence) status..*

Seraseq® Oncology Products

Heme Malignancies

Seraseq® Heme Disorder Products

Leukemia / Lymphoma

- 22 Myeloid (AML/MDS) genes
- SNVs & INDELs including ITDs
- VAF 5-15%
- Purified DNA mix format

- 9 Myeloid (AML/MDS) fusion genes
- >1,000 copies / µl
- Purified RNA mix format

Industry-first

- 26 Lymphoid (HL/NHL) genes
- SNVs, INDELs, SVs
- VAF 5-15%, gDNA & FFPE formats

Industry-first

Myeloid DNA Mix

Gene ID	COSMIC ID	HGVS	Protein variant	AF
CSF3R	COSM1737962	c.1853C>T	p.T618I	5%
FLT3		c.1759_1800dup		5%
IDH1	COSM28747	c.394C>T	p.R132C	5%
JAK2	COSM12600	c.1849G>T	p.V617F	5%
CALR	COSM1738055	c.1092_1143del52	p.L367fs*46	5%
MPL	COSM18918	c.1544G>T	p.W515L	5%
NPM1	COSM17559	c.863_864insTCTG	p.W288fs*12	5%
SF3B1	COSM84677	c.2098A>G	p.K700E	5%
SF3B1	COSM131557	c.1998G>T	p.K666N	5%
SRSF2	COSM146289	c.284_307del24	p.P95_R102del	5%
ABL1	COSM12560	c.944C>T	p.T315I	10%
ASXL1	COSM36165	c.1900_1922del23	p.E635fs*15	10%
ASXL1	COSM34210	c.1934_1935insG	p.G646fs*12	10%
BRAF	COSM476	c.1799T>A	p.V600E	10%
CBL	COSM34055	c.1139T>C	p.L380P	10%
CBL	COSM34077	c.1259G>A	p.R420Q	10%
FLT3	N/A	duplication of chr13:28,608,250-28,608,277 (hg19) insGCCCC between duplicated and native seq		10%
FLT3	COSM783	c.2503G>T	p.D835Y	10%
JAK2	COSM24440	c.1624_1629delAATGAA	p.N542_E543del	10%
MYD88	COSM85940	c.794T>C	p.L265P	10%
CEBPA	COSM18922	c.68_69insC	p.H24fs*84	15%
CEBPA	COSM18099	c.939_940insAAG	p.K313_V314insK	15%

Myeloid Fusion RNA Mix

Fusion Gene	HGVS	Fusion Copies/µL
BCR-ABL1	BCR{NM_004327.3}:r.1_2782_ABL{NM_005157.3}:r.c.80_3393	1970
ETV6-ABL1 (transcript 1)	ETV6{NM_001987.4}:r.1_463_ABL1{NM_007313.2}:r.137-3450	2112
ETV6-ABL1 (transcript 2)	ETV6{NM_001987.4}:r.1_1009_ABL1{NM_007313.2}:r.137-3450	NA*
FIPIL1-PDGRFA	FIP1L1{NM_030917.3}:r.1_923_PDGFRA{NM_006206.5}:r.1698_3270	1035
MYST3-CREBBP	MYST3{NM_006766.4}:r.1_3352_CREBBP{NM_004380.2}:r.86_7329	2208
PCM1-JAK2	PCM1{NM_006197.3}:r.1_3943_JAK2{NM_004972.3}:r.1514_3399	2661
PML-RARα	PML{NM_033238.2}:r.1_1646_ins134bp_RARA{NM_000964.3}:r.179_1389	1125
TCF3-PBX1	TCF3{NM_003200.3}:r.1_1450_PBX1{NM_002585.3}:r.266_1293	1208
RUNX1-RUNX1T1	RUNX1 {NM_001754.4}: r.1-613_RUNX1T1 {NM_004349.3}:r.419-2145	1245

Lymphoma DNA & FFPE

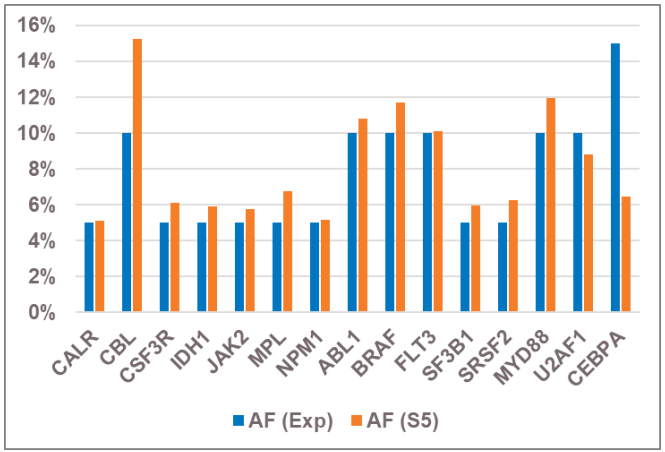
#	5' partner	3'partner	Variant Type
1	NPM1	ALK	Translocation
2	HSP90AA1	BCL6	Translocation
3	CCND1	CDC42BPB	Translocation
4	BIRC3	MALT1	Translocation
5	MYC	IGH	Translocation
6	TBL1XR1	TP63	Translocation

#	Gene	NA change	A_A Change	Variant Type
7	BCL2	c.302G>C	p.G101A	SNV
8	BRAF	c.1799T>A	p.V600E	SNV
9	DNMT3A	c.2645G>A	p.R882H	SNV
10	EZH2	c.1922A>T	Y641F	SNV
11	IDH2	c.515G>A	p.R172K	SNV
12	MYD88	c.794T>C	p.L265P	SNV
13	CXCR4	c.1013C>G	p.S338X	SNV
14	CXCR4	c.1013C>A	p.S338X	SNV
15	NOTCH1	c.7541_7542del	p.P2514Rfs*4	Del
16	NOTCH2	c.7198C>T	p.R2400*	SNV
17	RHOA	c.50G>T	p.G17V	SNV
18	SF3B1	c.2098A>G	p.K700E	SNV
19	STAT3	c.1919A>T	p.Y640F	SNV
20	STAT3	c.1982A>T	p.D661V	SNV
21	STAT3	c.1940A>T	p.N647I	SNV
22	STAT5B	c.1994A>T	p.Y665F	SNV
23	STAT5B	c.1924A>C	p.N642H	SNV
24	TP53	c.743G>A	p.R248Q	SNV
25	TP53	c.820del	p.V274Ffs*71	Del
26	TP53	c.818G>A	p.R273H	SNV

Quantified by ddPCR and NGS

Seraseq® Myeloid DNA Validation Examples

Oncomine validation by Thermo Fisher R&D



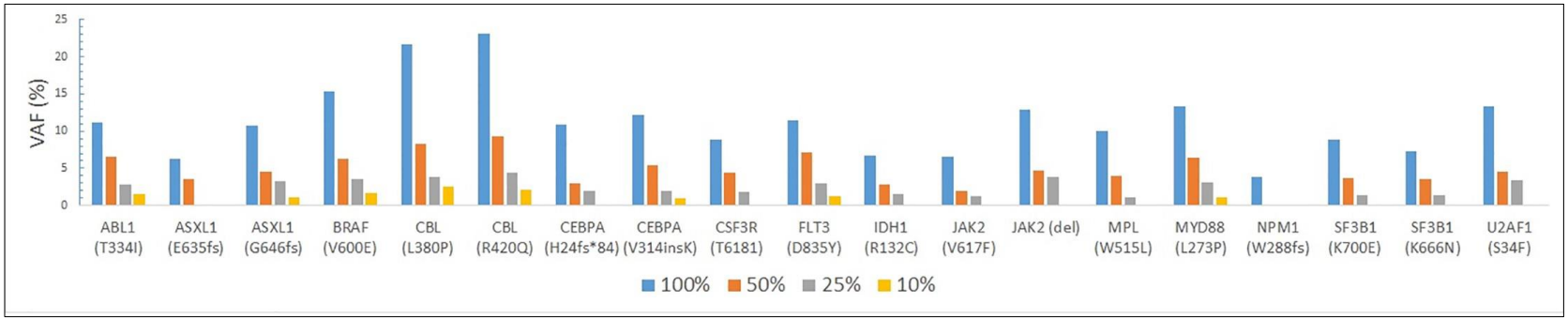
Validation of TSO500 panel by Medical College of Georgia

Reproducibility and LOD studies were performed using dilutions of Seraseq Myeloid DNA Mix.

- ✓ SNVs: detection at 25%-10% dilution, LoD ~1%
- ✓ indels/ITDs: variable detection at 100%-10%, LoD >1%
- ✓ FlT3 ITD variants and CALR 52 bp del were **not detected** in Seraseq Myeloid DNA mix or clinical samples

Highlighting limitations in detecting large INDELs with NGS

Sahajpal NS, et al. (2020). PLoS ONE 15(10). https://doi.org/10.1371/journal.pone.0240976



VariantFlex Custom Workflow

Flexible, Scalable, Bespoke

A simplified process to rapidly develop customized solutions

Assay Development → **Validation** → **QC Release / Launch** → **Regulatory Approval**

Sample Format:
DNA, RNA, ctDNA, ctRNA

Matrix:
Buffer, plasma, FFPE

Type of Variants:
SNVs, INDELs, CNVs, SVs, and RNA fusions

Seraseq
Custom Solutions
Flexible. Scalable. Bespoke

QC Testing Methods:
dPCR and NGS to confirm AFs and copy numbers

QA Level:
From lab notebook to full batch record

Background DNA:
GM24385 cell line, SNP-matched normal cell lines, or customer-provided

Partnerships and Collaborations Advancing Development and Adoption

National Cancer Institute	CRADA, Biosynthetic solid tumor, MATCH, ctDNA
Brown Alpert Medical School	PDX, ctDNA, Exosomes
Dartmouth-Hitchcock	Solid tumor, Fusions, Interlab, iQ NGS software, QC metrics
NIST	CRADA, ctDNA performance testing, dPCR vs NGS, DNA methylation
genosity	Assay validation, CAP CLIA certification
BloodPAC	ctDNA NGS assay standardization & data commons
The European Liquid Biopsy Society	
Stanford Medicine	ccfDNA amplification and analysis
CancerID	ctDNA standardization, CTC reference materials
Friends of Cancer Research	Tumor mutational burden, NGS assay harmonization
FNIH The biomarkers Consortium	ctDNA reference material commutability, NGS analytical validation, clinical validation of 14 biomarkers, FDA
LGC	TMB Working Group, NGS assay standardization, validation, clinical support

Seraseq® Oncology Product Summary

Best-in-class reference materials

- Designed with industry and clinical collaborations, NGS-focused, highly multiplexed reference samples for disease profiling, disease monitoring, and immuno-oncology biomarker validation
- Most patient-like reference standards covering all genomic events: SNVs, INDELs, CNVs, structural rearrangements/gene fusions
- Allow standardization, analytical and clinical validation of NGS assays across all phases of the laboratory and analysis workflow
- The industry leader in positive and negative sample controls for the broadest range of cancer patient testing assays.
- Innovative first-to-market products such as TMB, Blood TMB, Whole Transcriptome RNA-Seq, Lymphoma, ctDNA MRD
- Manufactured in cGMP and ISO13485 complaint facilities

Outcomes

Clinical

Operational

Financial

Support Resources

- Product Management
  - Omo Clement, PhD
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    - Omoshile.Clement@lgcgroup.com
  - Indira Chivukula, PhD
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    - Field Applications Scientist (EMEAI)
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Thank you!

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