TOMA BIOSCIENCES

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TOMA OS-SEQ™ CANCER ASSAY

Comprehensive detection of cancer somatic variants

The TOMA OS-Seq™ Cancer Assay is a beginning-to-end cancer gene variant profiling assay that delivers a complete, comprehensive solution for cancerous somatic variant detection. The assay evaluates genes for all types of sequence variants, including copy number alterations (CNAs). Its simplified, highly efficient library preparation method reduces sample loss, minimizes dependence on PCR, and reduces preparation time.

Using the TOMA OS-Seq™ Cancer Assay, researchers can quickly interrogate precious tumor samples from FFPE samples using less material while maintaining excellent data quality. Final results are generated in Stratus™, our easy-to-use, cloud-based genomic data analysis tool that delivers the latest methods in somatic variant analysis without expensive computing infrastructure.

	TOMA OS-SEQ	OTHER COMMERCIAL REAGENTS	TOMA OS-SEQ ADVANTAGE
CANCER GENE COVERAGE	**Comprehensive** – complete sequencing of every exon interrogated	**Limited** – "Hot Spot" methods exclude up to 90% of each gene and are not able to report all variant types	Detects all mutation types: single nucleotide variations, short indels, and copy number alterations
SAMPLE - EFFICIENT	**Highly** – accepts DNA inputs as low as 10 ng from **FFPE** (formalin-fixed paraffin embedded tissue)	**Requires large quantities of DNA input** – exhausts precious oncology patient samples - high rate of rejection (quantity not sufficient QNS)	**Preserves precious patient samples** – accept DNA inputs as low as 10ng
SENSITIVE VARIANT DETECTION	**Complete** – High sensitivity for all variant types, down to 2% for single nucleotide variants (SNVs) and 94% concordance to FISH for copy number (CNAs)	**False Negatives** – misses majority of copy number alterations, the largest class of actionable genomic alterations in cancer	Dramatically **increases clinically significant findings**
EFFICIENCY	**High Yield** – from ultra efficient adaptor ligation	**Low Yield** – highly dependant upon PCR to generate sufficient library for sequencing	**Highly efficient** library preparation method preserves precious sample
PCR USED IN DNA PREPARATION	**Minimal** – library preparation method only amplifies targets of interest; eliminates whole genome PCR	**High** – amplifies "whole genome" PCR creating artifacts and errors, reducing specificity and causing analysis issues	**No "whole genome," PCR** dramatically reduces errors common to other methods
SEQUENCING DEPTH	**500X** – up to 6 concurrent samples on an Illumina MiSeq	**LOW** – misses key mutations and significantly increases false negatives	**Minimizes false negatives**
ANALYSIS	**Simple** – TOMA Stratus™ easy, accurate calling of somatic alterations, including CNAs	**None** – limited assay specific bioinformatics; not designed for somatic alteration detection	**Simple** – Stratus provides the easiest, high accuracy variant calls
TIMING	**Fast** – DNA library complete in **16 hours** (3 hrs hands on time)	**Slow** – takes **2-3 days**	Generates a sequencing library in a **single day**

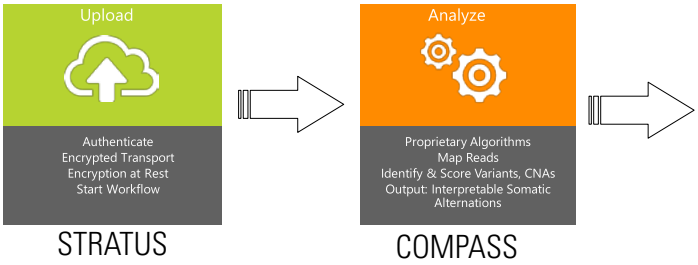
For Research Use Only. Not for use in diagnostic procedures.

TOMA OS-SEQ™ CANCER ASSAY

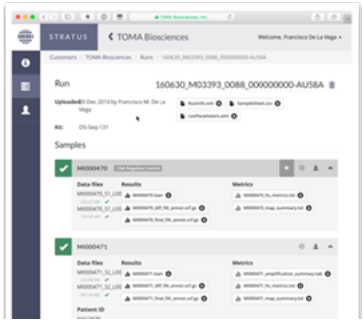
TOMA OS-SEQ™ 131 CANCER GENE PANEL							
ABL1	BRCA1	CDKN2B	FGFR1	KIT	NBN	PTPN11	SYK
ABL2	BRCA2	CEBPA	FGFR2	KRAS	NF1	RAD50	TERT
AKT1	BTK	CSF1R	FGFR3	MAP2K1	NFE2L2	RB1	TET2
AKT3	CALR	CTNNB1	FGFR4	MAP2K2	NOTCH1	RET	TP53
ALK	CCND1	CYP2D6	FLT3	MAPK1	NPM1	RICTOR	TPMT
APC	CCND2	DDR2	GNA11	MCL1	NRAS	RNF43	TSC1
AR	CCND3	DNMT3A	GNAQ	MDM2	NTRK1	ROS1	TSC2
ARAF	CD274	DPYD	GNAS	MET	NTRK2	RPTOR	U2AF1
ASXL1	CDH1	EGFR	H3F3A	MLH1	NTRK3	RUNX1	UGT1A1
ATM	CDK12	EMSY	HNF1A	MPL	PALB2	SF3B1	VEGFA
ATR	CDK2	ERBB2	HRAS	MRE11A	PARP1	SLCO1B1	VHL
ATRX	CDK4	ERBB3	IDH1	MSH2	PARP2	SMAD4	WT1
AURKA	CDK5	ERBB4	IDH2	MSH6	PDGFRA	SMARCB1	
AURKB	CDK6	ERCC2	IGF1R	MTOR	PIK3CA	SMO	
AXL	CDK8	ESR1	JAK2	MUTYH	PMS2	SRC	
BCL2	CDK9	ETV6	JAK3	MYC	PTCH1	SRSF2	
BRAF	CDKN2A	EZH2	KDR	MYD88	PTEN	STK11	

TOMA's cloud based data analysis tools:

- Simple
- Complete
- Meaningful



STRATUS COMPASS



SEQUENCING PERFORMANCE METRICS - 6 CONCURRENT SAMPLES ON ILLUMINA MISEQ						
Mean Coverage	On - Target	Fold Enrichment	Fold 80 Base Penalty	% ROI Bases 2X	% ROI Bases 50X	% ROI Bases 100X
> 500 X	50-80%	1200-2300	1.9 - 3.5	99.5%	98.5%	98.1%

The TOMA OS-Seq Cancer Assay is a highly efficient ligation method completely eliminates "whole genome" PCR, to provide a more accurate representation of the original sample in the final sequencing library. TOMA OS-Seq target enrichment is complete within an hour, and enables detection of mutant alleles down to a 2% variant allele frequency (VAF). The TOMA OS-Seq sequencing solution integrated with STRATUS data analysis tool offers a fast, simple approach to generating reliable sequencing data in a short time.

To Order TOMA OS-Seq Reagents
Call TOMA Customer Service at 877-840-8662 (TOMA)
Email: orderTOMAOSSeq@tomabio.com

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