TOMA OS-SEQ™ REAGENT

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Comprehensive analysis of mutations including copy number alterations for 131 cancer genes

The TOMA OS-Seq™ reagent is a comprehensive oncology-focused gene analysis solution that enables researchers to evaluate each gene in its panel for all mutation types including copy number alterations (CNAs). Our simplified highly efficient single stranded library preparation method reduces sample loss and minimizes dependence on polymerase chain reaction (PCR) while taking only 8 hours to complete. With the TOMA OS-Seq cancer panel, researchers can analyze precious tumor samples from fresh frozen, paraffin embedded archival tissues (including FFPE), and circulating tumor DNA (coming soon) out of plasma – using less material while maintaining excellent data quality.

	TOMA OS-SEQ	OTHER COMMERCIAL REAGENTS	TOMA OS-SEQ ADVANTAGE
CANCER GENE COVERAGE	Comprehensive – complete sequencing of every gene in the panel (end to end coverage)	Limited – "Hot spot" methods miss 90% of each gene and are not capable of reporting all mutation types	Detects all mutation types single nucleotide variations (SNV's), insertions and deletions (indels), translocations, select fusions and rearrangements and copy number alterations
COPY NUMBER ALTERATIONS	Complete – 100% of copy number alterations	No Amplifications – misses HALF of actionable genomic alterations	Dramatically increases actionable alterations
EFFICIENCY	High – double digit yield from ultra efficient ligation	Low Yield – less than 0.3% yield creates high dependency on PCR to generate sufficient library for sequencing	Highly efficient library preparation method enables a simple count of copy number changes
PCR USED IN DNA PREPARATION	Minimal – Library preparation method eliminates "whole genome" PCR and only amplifies targets of interest	High – amplifies "whole genome" PCR creating artifacts and errors, reducing specificity and causing analysis issues	No "whole genome," PCR dramatically reducing errors common to other methods
SEQUENCING DEPTH	500X – significant average coverage depth to identify alterations even in highly heterogenous samples	LOW – misses key mutations and significantly increases false negatives	Minimize false negatives
TIMING	Fast – DNA library preparation in as little as 8 hours	Slow – takes 2-3 days	Generate a sequencing library in a single day
ANALYSIS	Simple and streamlined – fewest number of artifacts and off target reads	Requires additional steps – including use of complex algorithms and the removal of PCR artifacts, duplicates and off target sequencing	Simplifies informatics workflow to provide straightforward annotation

TOMA BIOSCIENCES™

TOMA OS-SEQTM CANCER PANEL GENE LIST

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	

The TOMA OS-Seq™ sequencing solution is a highly efficient and streamlined library preparation method that minimizes the sample distortion common to other methods. The sample DNA bases damaged by chemicals during tissue fixation and storage are excised rather than repaired in order to prevent the introduction of errors arising from misincorporated bases.

Our highly efficient ligation method completely eliminates “whole genome” PCR, to provide a more accurate representation of the original sample in the final sequencing library. Complete within one hour, target enrichment with TOMA OS-Seq probes is complete within 1 hr, and enables detection of mutant alleles down to a 2% mutant allele frequency (MAF). The TOMA OS-Seq sequencing solution therefore offers a fast, simple approach to generating reliable sequencing data in a short amount of time.

To Order TOMA OS-Seq Reagents
Call TOMA Customer Service at 877-840-8662 (TOMA)
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