NGS Disease Research Panels

ClearSeq Comprehensive Cancer

Next Generation Comprehensive Cancer Profiling

Key Benefits

Disease-Associated Targets

- Content provided by researchers from Washington University in St Louis
- Simultaneously targets 151 key genes associated with a wide range of cancers

Confident Answers

- Deep coverage of targets enabling accurate variant detection, even in FFPE tissue
- Have sequencing-ready libraries in as little as one day with robust SureSelect workflows

Comprehensive Solution

- Simplify NGS data analysis with SureCall software
- Easily QC samples and automate library prep with industry-leading tools

Overview

Identification of DNA mutations in cancer provides important insights into clonal evolution, disease progression and pathogenesis. Whilst complementary methods such as cytogenetic analysis, fluorescence in situ hybridization (FISH) and single gene amplification assays have been commonly used to characterize cancer samples, in research there is a need to perform deep molecular profiling of cancers in order to gain more complete genetic characterization. Targeted capture of key cancer genes followed by next generation sequencing is an efficient method for comprehensive analysis of both solid tumours and hematological malignancies.

The ClearSeq Comprehensive Cancer, developed in collaboration with researchers at the Washington University in St Louis, targets 151 disease-associated genes that have been implicated in studies of a wide range of cancers (eg. breast, lung, colorectal, AML). All coding exons, exon-intron boundaries and selected introns of these genes are targeted (Table 1).

Table 1. Targeted genes

ABL1	BRCA1	EGFR	JAK2	MYC	PIK3CA	RUNX1
AKT1	BRCA2	ESR1	KRAS	MYD88	PTCH1	SMO
ALK	CDKN2A	FGFR2	KIT	NF1	PTEN	STK11
APC	CEBPA	FLT3	MAP2K2	NOTCH1	PTPN11	TET2
ASXL1	CTNNB1	HRAS	MET	NPM1	NRAS	TP53
ATM	DNMT3A	IDH1	KMT2A	MTOR	RB1	VHL
BRAF	ERBB2	IDH2	MPL	PDGFRA	RET	WT1
ABCB1	CYP19A1	FBXW7	IL2RB	MLH1	ROS1	SMARCB1
ABCC2	CYP2A6	FGFR1	IL2RG	MST1R	RPS6KB1	SNCAIP
ABL2	CYP2B6	FGFR3	INPP4B	NELL2	RXRA	SOS1
AKT2	CYP2C19	FGFR4	JAK1	PDGFRB	RXRB	SPRED1
AKT3	CYP2C9	FLT1	JAK3	PHF6	RXRG	SRC
ATRX	CYP2D6	FLT4	KDM6A	PIK3R1	SHH	SUFU
CBL	DDR1	FSTL5	KDR	PSMB1	SHOC2	TAS2R38
CDA	DDR2	GNA11	LAMA2	PSMB2	SLC22A1	TRRAP
CDH1	DDX3X	GNAQ	LCK	PSMB5	SLC22A2	TYK2
CDKN2B	DPYD	GNAS	LTK	PSMD1	SLC31A1	UGT1A1
CHD7	ERBB3	GSTP1	MAP2K1	PSMD2	SLC34A2	YES1
CHIC2	ERBB4	H3F3A	MAP2K4	RAF1	SLC45A3	ZMYM3
CREBBP	ERG	HNF1A	MAP3K1	RARA	SLCO1B1	
CRLF2	ESR2	IKZF1	MAPK1	RARB	SMAD4	
CSF1R	EZH2	IL2RA	MED13	RARG	SMARCA4	

ClearSeq Comprehensive Cancer

Confident Answers

The ClearSeq Comprehensive Cancer was designed for deep coverage of target bases and high on-target specificity, ensuring that variants are detected accurately with minimal sequencing (Figure 1). The research panel provides excellent performance even with challenging samples like formalin-fixed, paraffin-embedded (FFPE) DNA, which is important given that many solid tumor samples are available only as FFPE tissue (Figure 2). ClearSeq Comprehensive Cancer is compatible with the SureSelect Target Enrichment System and the combination of an optimized design and robust capture protocols allows the cancer researcher to confidently identify disease-associated somatic variants. The panel can also be easily customized by the addition of genes using SureDesign.

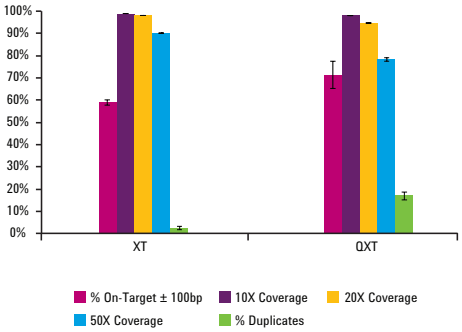

Figure 1. Excellent coverage of target bases when enriching HapMap cell line DNA with different SureSelect library preparation protocols (*XT – post-capture library pooling; QXT – transposase-based library prep*). Data is representative of eight replicates per protocol and each sample was sequenced to 300X depth (240 Mb).

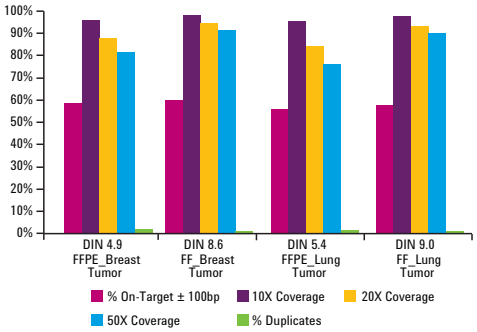

Figure 2. Sequencing performance of SureSelect^{XT} libraries from FFPE and fresh-frozen (FF) breast and lung tumor samples enriched using ClearSeq Comprehensive Cancer (240 Mb sequencing/sample). The level of DNA degradation is indicated by the DNA Integrity Number (DIN) provided by the 2200 Tapestation System, where a DIN of 10 and 1 indicate intact gDNA and completely degraded gDNA respectively.

Comprehensive Solution

Sequence data generated from libraries enriched by ClearSeq Comprehensive Cancer are ideally suited for analysis using SureCall, an NGS data analysis software developed to address the critical bioinformatics needs of clinical researchers. Using guided cancer analysis workflows, identify known variants of interest within minutes, greatly reducing time-to-results. Together with robust sample QC and throughput scalability by automation, ClearSeq Comprehensive Cancer accelerates the profiling of many genes associated with cancer.

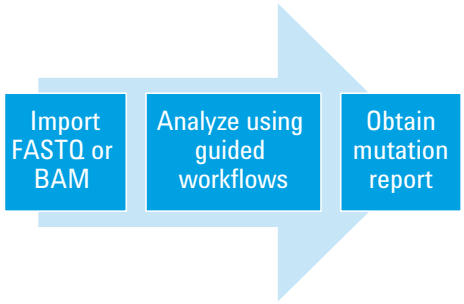

Figure 3. Accelerate time-to-results with a simplified 3-step analysis workflow using SureCall. Starting from FASTQ or BAM files, obtain a report of categorized variants within minutes.

Ordering Information:

Part Number	Description
5190-8011	ClearSeq Comprehensive Cancer, 16, XT
5190-8012	ClearSeq Comprehensive Cancer, 96, XT
5190-8013	ClearSeq Comprehensive Cancer, 96 auto, XT
5190-8014	ClearSeq Comprehensive Cancer Plus, 16, XT
5190-8015	ClearSeq Comprehensive Cancer Plus, 96, XT
5190-8016	ClearSeq Comprehensive Cancer Plus, 96 auto, XT
5190-8017	ClearSeq Comprehensive Cancer, 16, XT2
5190-8018	ClearSeq Comprehensive Cancer, 96, XT2
5190-8019	ClearSeq Comprehensive Cancer, 96 auto, XT2
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5190-8021	ClearSeq Comprehensive Cancer Plus, 96, XT2
5190-8022	ClearSeq Comprehensive Cancer Plus, 96 auto, XT2

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