LeXOncofusion (for RNA) Panel

Background

Fusion gene plays an important role as an oncogenic driver in many cancer types. The most common fusion gene targets in solid tumors are tyrosine kinases, such as ALK, ROS1, and RET, which may cause abnormal sequences, functional protein production, or dysregulation of gene expression, thereby causing or promoting tumorigenesis. A number of targeted drugs targeting the corresponding fusion genes such as ALK, RET, ROS1, FGFRs, and NTRKs have been approved for clinical use. Targeted inhibitors of multiple fusion gene targets have significant therapeutic effects in the clinical treatment of tumor and are the main force in the precision medicine . Therefore, the detection of fusion genes is of great significance for clinical diagnosis, treatment, and prognosis.

At present, the conventional methods of fusion gene diagnosis mainly include fluorescence in situ hybridization (FISH), quantitative real-time PCR (RT-PCR), and IHC. Generally, these methods have low resolution and throughput, can only detect a single fusion gene, and cannot identify new fusion gene partners or analyze complex structural reorganizations. Besides, these methods greatly rely on the judgment experience of the technicians and have limited expansion capacity of application.

In recent years, DNA-based targeted capture sequencing technology (DNACap) has been used more and more in clinical testing laboratories because of its various advantages such as independence on prior knowledge of fusion, the ability to discover new fusion subtypes, and high sensitivity. However, DNACap also has certain limitations in the detection of fusion genes, and it is not technically feasible when there are repetitive sequences in the fusion-related region or the intron span is too large. In comparison, RNACap has the following advantages:

- The intron sequence in mRNA has been cleaved, and the reduction of the target regions improves the breadth and sensitivity of fusion analysis;
- Targeted enrichment technology focuses on pivotal fusion-related genes, and RNA library preparation does not require the procedure of ribosomal RNA removal, reducing costs while improving the sensitivity;
- The gene fusion information at the RNA level has more direct clinical significance.

Therefore, LexigenBio takes into account both the breadth and sensitivity of analysis, and has designed and developed a concentrated 105-gene panel specifically for RNA fusion, **LeXOncofusion (for RNA) Panel v1.0**, based on the transcript cDNA sequences.

Product Introduction

LeXOncofusion (for RNA) Panel v1.0 targets 105 genes which are the most common or relevant to clinically significant fusions in solid tumor studies. The probes cover all transcript coding regions and some UTR regions involved in the occurrence of fus- ions which are officially included in RefSeq 109. The panel supports the enrichment of fusion, mutation, and gene expression information at the RNA level.

Gene List

ABL1*†	ABL2	AKT3	ALK	ARHGAP26	AXL	BCL2†	BCOR*	BRAF	BRD3*	BRD4*	CAMTA1
CCNB3*	CCND1	CIC†	COL6A3	CSF1R	DNAJB1	EGFR	EML4	EPC1*	ERBB2†	ERG*	ESR1
ETS1	ETV1*	ETV4	ETV5*	ETV6*	EWSR1	FGFR1	FGFR2	FGFR3	FGR*	FLI1	FLT3
FOSB	FOXO1	FUS	GLI1	HMGA2	INSR	JAK2*	JAK3	JAZF1	KIF5B†	KIT†	KMT2A
MAML2	MAST1	MAST2	MEAF6	MET*	MLLT3	MSH2	MSMB†	MUSK	MYB	MYC	NCOA1*
NCOA2*	NOTCH1	NOTCH2	NOTCH3†	NR4A3*	NRG1	NTRK1	NTRK2	NTRK3	NUMBL	NUTM1	PAX3
PAX7	PDGFB	PDGFRA	PDGFRB†	PHF1*	PIK3CA*	PKN1	PLAG1*	PPARG*	PRKACA	PRKCA	PRKCB
RAF1	RARA*	RELA	RET	ROS1	RSPO2*	RSPO3	SS18	STAT6*	TAF15	TCF12†	TCF3
TERT	TFE3	TFEB	TFG	THADA	TMPRSS2*†	TP53*	USP6*	YWHAE*			

* Covers all 5'-UTRs; † Covers all 3'-UTRs。

Capture Performance

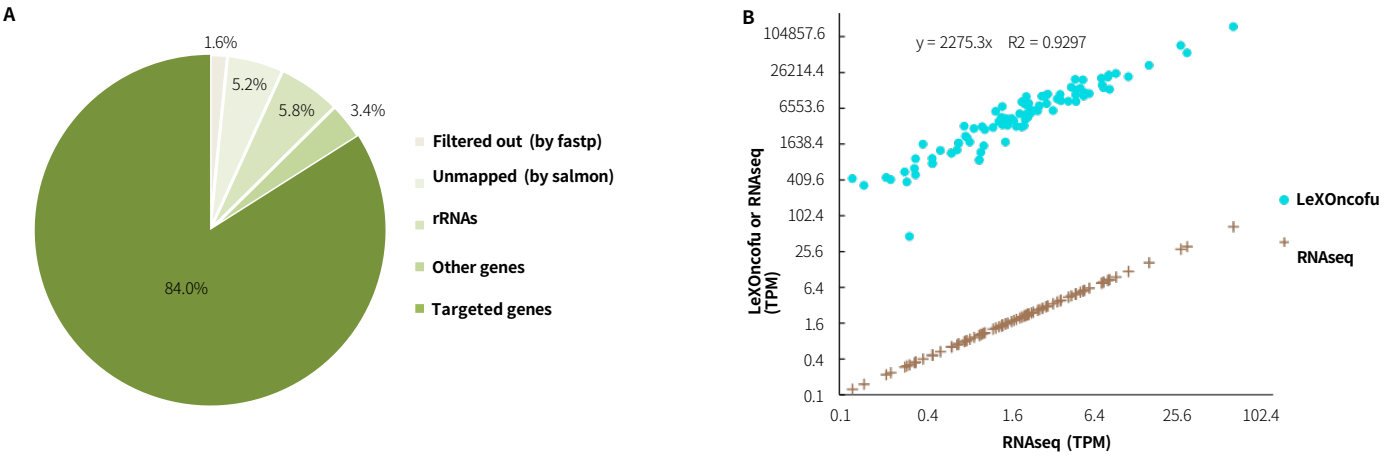

Figure 1. Capture performance of LeXOncofusion (for RNA) Panel v1.0 . A. Typical capture sequencing data; **B.** Comparison of the relative abundance of target genes between capture sequencing and RNAseq. Libraries of Human Brain Total RNA Standards (Clontech, 636530) were prepared using LeXPrep Total RNA-To-DNA Module with LeXPrep DNA Universal Library Preparation Kit Series, and separately carried out the direct sequencing (RNAseq) and LeXOncofusion capture sequencing.

Gene Fusion Detection

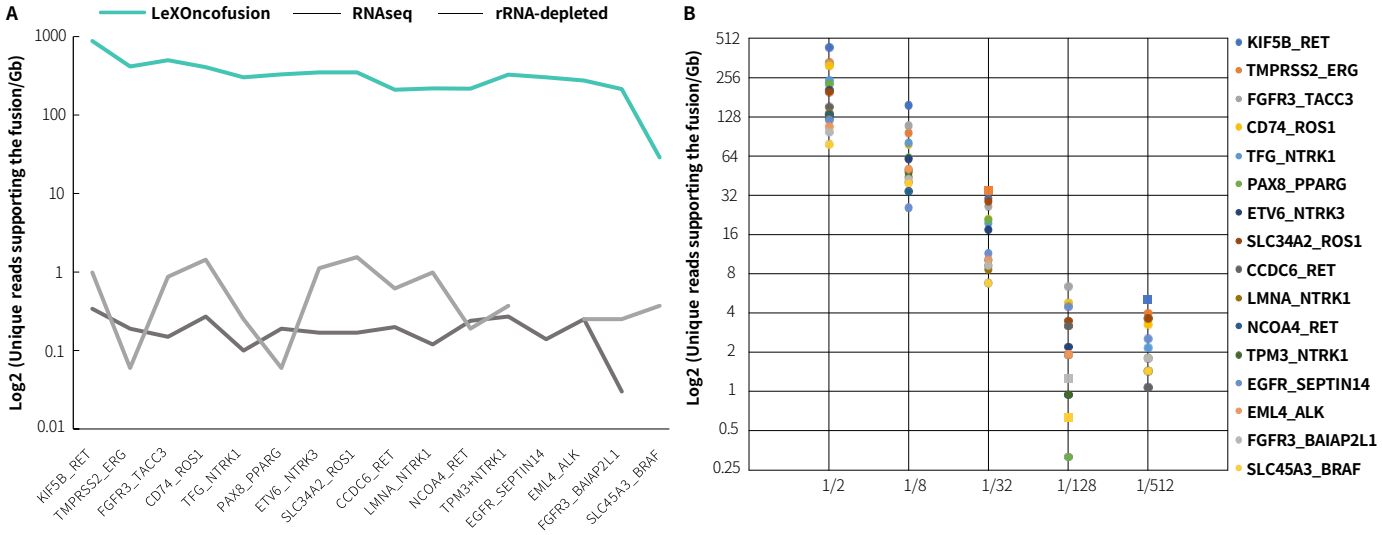

Figure 2. Fusion detection of FFPE fusion RNA standards by LeXOncofusion (for RNA) Panel v1.0. A. Comparison of LeXOncofusion targeted enrichment and RNAseq; **B.** Targeted enrichment performance of LeXOncofusion after multiple dilution of the standards. Libraries of 100 ng Seraseq® FFPE Tumor Fusion RNA v4 Reference Material were prepared using LeXPrep Total RNA-To-DNA Module with LeXPrep DNA Universal Library Preparation Kit Series, separately carried out the direct sequencing (RNAseq), rRNA-depleted RNAseq (NEBNext rRNA Depletion Kit v2), and RNA capture sequencing (LeXOncofusion). 1 Gb data of each library was used for fusion analysis (FusionCatcher v1.10).

Ordering Information

Product	Catalog#
LeXOncofusion (for RNA) Panel v1.0, 16 rxn	LX01512
LeXOncofusion (for RNA) Panel v1.0, 96 rxn	LX01511

For research use only. Not for use in diagnostic procedures.

Statement

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