

HotSpot Detection | LeXso HotSpot Panel v1.0

Introduction

LeXso HotSpot Panel v1.0 targets the “hotspot” regions of tumor mutation, involving 49 genes related to carcinogenesis and tumor suppressor, with probes covering approximately 25 Kb of the genome.

This Panel is designed for use with the LeXso Hybrid Capture System. Based on the novel LeXso targeted enrichment system, the **LeXso HotSpot Panel v1.0** delivers improved capture efficiency, consistent and excellent capture performance, and significantly reduces experimental time, enabling more efficient sequencing and cost savings.

Gene list

<i>AKT1</i>	<i>ALK</i>	<i>APC</i>	<i>AR</i>	<i>ARAF</i>	<i>ATM</i>	<i>BRAF</i>	<i>CDKN2A</i>	<i>CHEK2</i>	<i>CTNNB1</i>
<i>DDR2</i>	<i>EGFR</i>	<i>ERBB2</i>	<i>ERBB3</i>	<i>ESR1</i>	<i>FBXW7</i>	<i>FGFR1</i>	<i>FGFR2</i>	<i>FGFR3</i>	<i>FGFR4</i>
<i>FLT3</i>	<i>GNA11</i>	<i>GNAQ</i>	<i>GNAS</i>	<i>HRAS</i>	<i>IDH1</i>	<i>IDH2</i>	<i>KIT</i>	<i>KRAS</i>	<i>MAP2K1</i>
<i>MAP2K2</i>	<i>MET</i>	<i>MTOR</i>	<i>NRAS</i>	<i>NTRK1</i>	<i>NTRK3</i>	<i>PDGFRA</i>	<i>PIK3CA</i>	<i>PTCH1</i>	<i>PTEN</i>
<i>RAF1</i>	<i>RET</i>	<i>ROS1</i>	<i>SF3B1</i>	<i>SMAD4</i>	<i>SMO</i>	<i>STK11</i>	<i>TP53</i>	<i>TSC1</i>	

Performance

Capture performance

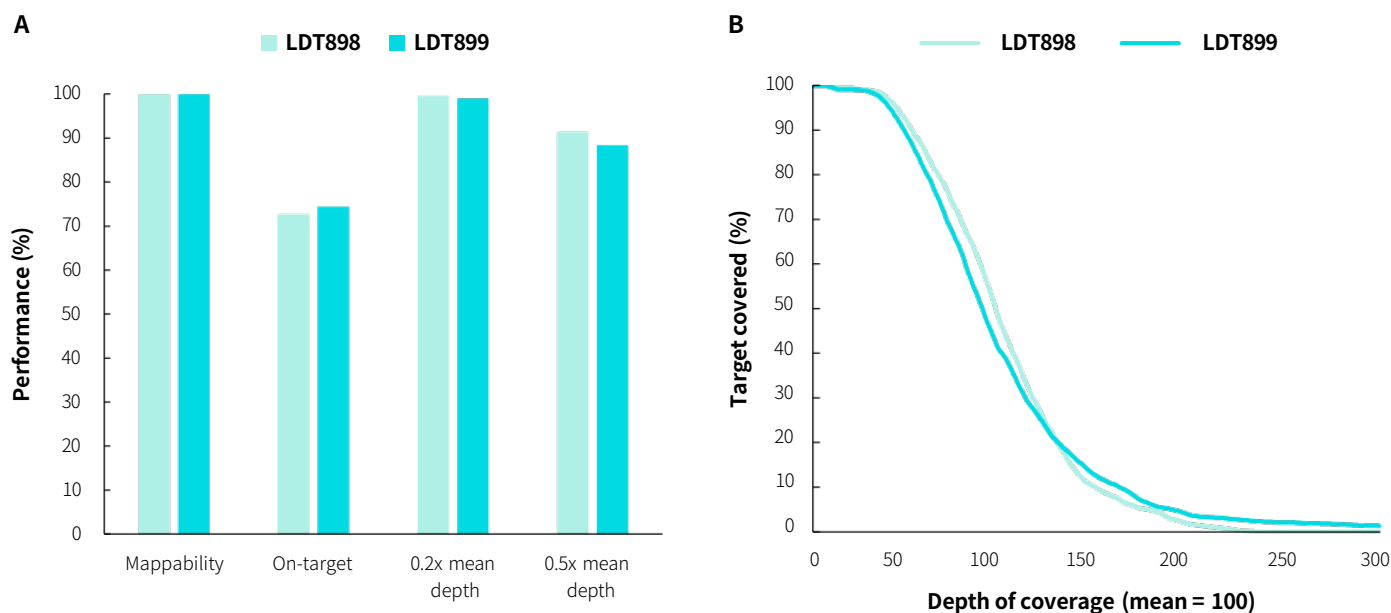


Fig 1. Capture performance of LeXso HotSpot Panel v1.0. LDT OncoOne Pan-tumor gDNA Standard (LDT Bioscience, LDT900) was used for pre-library preparation with LeXPrep® EZ DNA Library Preparation Kit v2 paired with LeXPrep® Universal Stubby Adapter (UDI) Module; 500 ng/pre-library (1-plex) input was used, following the user manual of LeXso hybrid capture. Sequencing was performed using Illumina Novaseq 6000, PE150. The BWA was used for alignment to the reference genome hg38 and On-target rate was calculated by the number of reads. **A.** Mappability, On-target rate and Target covered; **B.** Coverage uniformity. **Note:** OncoOne Pan-cancer gDNA Standard (LDT Bioscience, LDT900) include a negative control (LDT Bioscience, LDT898) and a positive control (LDT Bioscience, LDT899). Sequencing platform: Illumina Novaseq 6000, PE150.

Variant analysis

Variant	Allele frequency for reference(%)	Observed allele frequency (%)	
		LDT898	LDT899
NRAS_Q61H	5	0.0	3.8
NRAS_G12D	5	0.0	3.9
KRAS_Q61H	12	0.0	9.7
KRAS_G13D	5	0.0	3.8
KRAS_G12A	6	0.0	4.4
PIK3CA_E545K	5	0.0	4.5
PIK3CA_H1047R	6	0.0	6.1
EGFR_G719S	5	0.0	3.6
EGFR_delE746_A750	2.5	0.0	1.7
EGFR_T790M	4	0.0	2.9
EGFR_L858R	4	0.0	3.2
BRAF_V600E	5	0.0	4.1
MET_EXON14SKIPPING	50	0.0	50.2

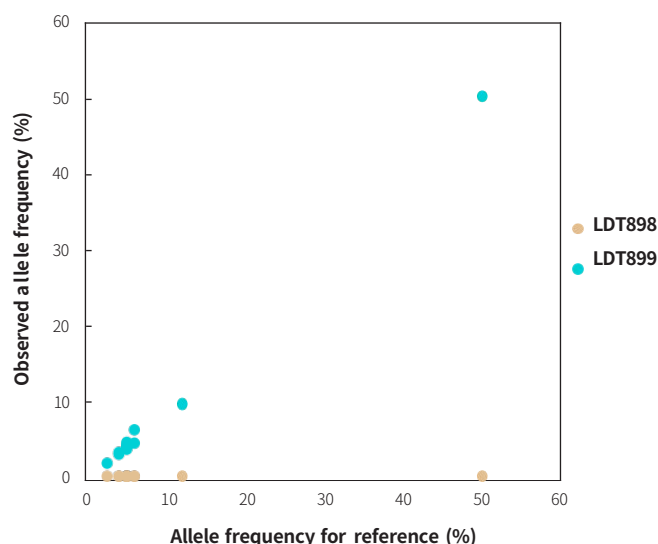


Fig 2. Consistency of the allele frequency in LeXso HotSpot Panel v1.0 capture data with the reference frequency of the standards. Pre-libraries were prepared using the LeXPrep EZ DNA Library Preparation Kit v2, LeXso HotSpot Panel v1.0 was used to complete hybridization capture. Sequencing was performed using Illumina Novaseq 6000, PE150.

Note: The samples were: OncoOne Pan-cancer gDNA Standard (LDT Bioscience, LDT900).

Ordering Information

Product	Catalog#
LeXso HotSpot Panel v1.0, 16 rxn	LX11402
LeXso HotSpot Panel v1.0, 96 rxn	LX11401

Statement

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

Without the written permission of LexigenBio, no other individual or organization may reproduce, copy, edit, expand, reduce or translate the contents of this document in any form into other languages for any purpose. In case of improper use, LexigenBio Inc. reserves all rights.