LeXome XP Panel

Introduction

LeXome XP Panel v1.0 is an enhanced extended whole exome capture panel. On the basis of LeXome Core Panel, it provides expanded coverage of clinically relevant variants in non-coding genomic regions, and includes the GENCODE annotation of protein-coding regions, and provides a comprehensive coverage of immunoglobulins (IG) and T cell receptors (TR) coding genes, and extends the target regions to SNP skeleton of whole genome, intronic regions related to common gene fusion in solid tumors and classical microsatellite loci, which spans a 45.9 Mb region of human genome.

- **Clinvar variants in non-coding region**

  LeXome XP Panel v1.0 provides expanded coverage of clinically relevant variants in non-coding genomic regions.

Table 1. The number of loci with the mean coverage depth of non-coding region in ClinVar less than 0.05x captured by LeXome XP Panel v1.0.

Clinical significance value	NO. of loci (mean depth< 0.05x)			All
	LeXome XP Panel v1.0	LeXome Core Panel	VendorA	
Pathogenic	145	725	954	105,597
Likely_pathogenic	32	177	325	44,113
Drug_response	6	566	570	2,020
Risk_factor	2	65	56	451
Affect	0	6	6	154
Protective	0	8	7	34

The libraries were prepared using LeXPrep DNA Universal Library Preparation Kit (for Illumina®) from Human Female Genomic DNA (Promega-female, G1521). The whole exome panels from different vendors were respectively used to complete hybridization capture with the mean coverage depth of approximately 100x, and then counted the number of different clinical significance loci with mean depth of coverage < 0.05x.

- **Expanded coding region coverage**

  LeXome XP Panel v1.0 further includes the GENCODE annotation of protein-coding regions, and provides a comprehensive coverage of IG and TR coding genes.

Table 2. The coverage rate of different database in LeXomeXP Panel v1.0.

Product	CCDS (22)	Refseq (109 all)	Refseq (109 NM)	GENCODE (38)
LeXome Core Panel	99.91%	95.82%	99.77%	95.26%
VendorA	100.00%	96.17%	99.63%	97.08%
Vendor B	99.73%	94.73%	98.64%	94.38%
LeXome XP Panel v1.0	**99.92%**	**96.75%**	**99.85%**	**98.81%**

- **SNP skeleton of whole genome**

  Based on the 1000 Genomes database, we mainly select > 9,000 loci with high MAF values and high heterozygosity population, covering the entire human genome at approximately 300 Kb intervals. It provides richer and more evenly distributed information on the genomic composition based on the whole exome, and can be used for detection of CNVs and loss of heterozygosity.

- **Common gene fusion in solid tumors**

  Contains intron regions and non-coding regions related to common fusions and can be used to analyze fusion loci in solid tumors.

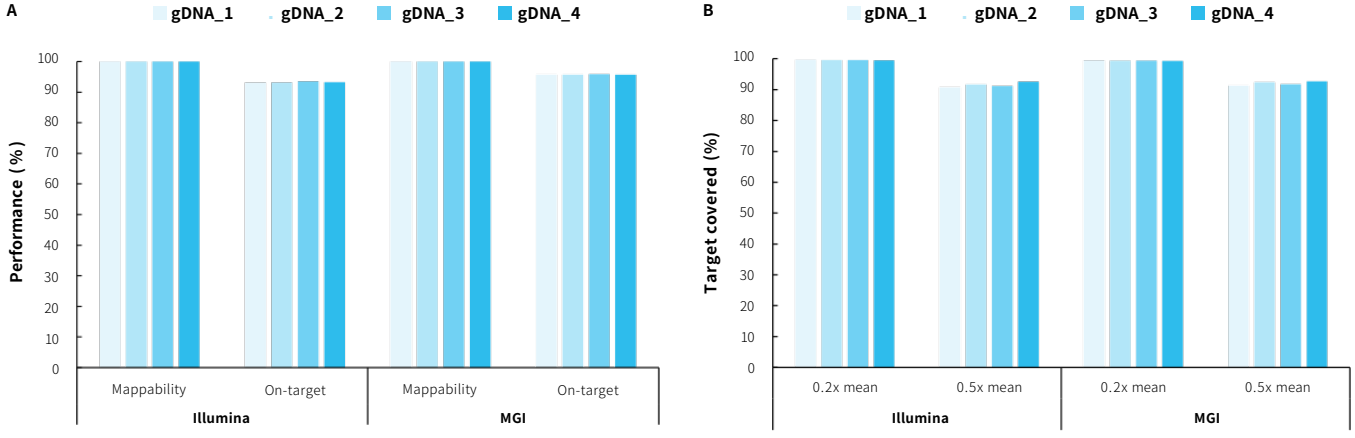
ALK intron 18 - 19	*BCL2* 3'UTR	*BCR* intron 8,13 - 14	*BRAF* intron 7-10	*BRCA1* intron2,7 - 8,12,16,19 - 20	*BRCA2* intron 2	*CD74* intron 6-8	*EGFR* intron 7,15,24-27	*ETV4* intron 5 - 6	*ETV5* intron 6 - 7	*ETV6* intron 5 - 6
EWSR1 intron 6-13	*EZR* intron 9-12	*FGFR1* intron 1,5,17	*FGFR2* intron 1,17	*FGFR3* intron 17	*FLI1* intron 3-8	*KIT* intron 16	*KMT2A* intron 6-11	*MET* intron 1,14	*MSH2* intron 5	*MYB* intron 14
MYC intron 1	*NOTCH2* intron 26	*NTRK1* intron 8-10	*NTRK2* intron 12,15	*NTRK3* intron 13 - 14	*NUTM1* intron 1	*PDGFB* intron 1	*PDGFRA* intron 7,9,11	*RAF1* intron 4-9	*RARA* intron 2	*RET* intron 7-11
ROS1 intron 31-35	*RSPO2* Upstream,5'UTR, exon 1 - 2, intron 1		*SDC4* intron 2	*SLC34A2* intron 4	*TMPRSS2* intron 1-3					

- **Classical microsatellite loci**

  The **LeXome Core Panel** itself covers a large number of microsatellite loci, and the addition of 15 optimally designed MSI classical loci facilitates the comparison between different microsatellite instability analytical methods as well as the optimization and calibration of the analytical process.

BAT-25	*BAT-26*	*BAT-40*	*BAT-RII*	*NR-21*	*NR-22*	*NR-24*	*NR-27*	*MONO-27*	*D2S123*	*D5S346*	*D17S250*	*D17S261*	*D17S20*	*D18S34*

Capture Performance



(Continued)

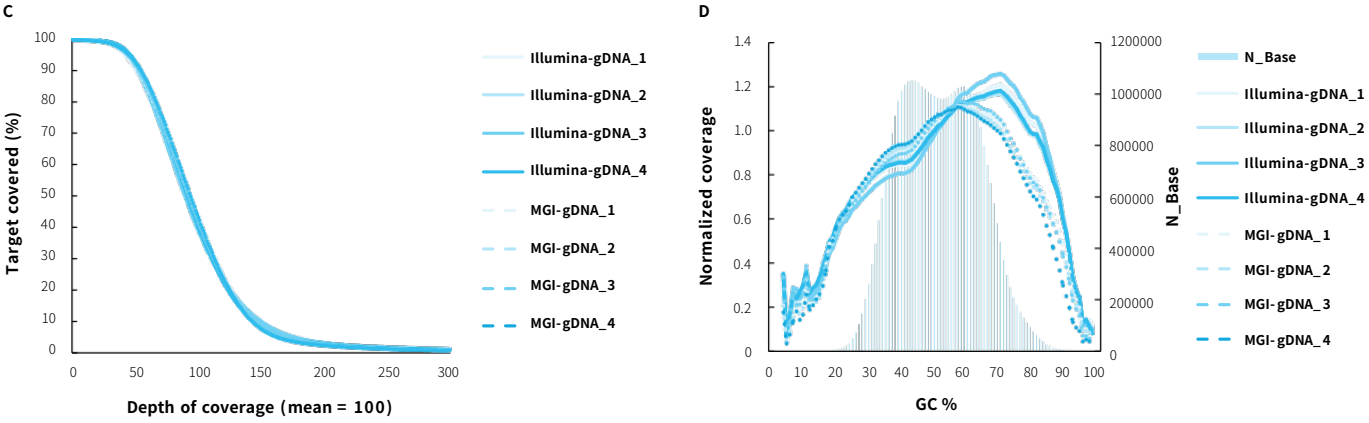


Fig 1. Capture performance of LeXome XP Panel v1.0 in different gDNA libraries. The libraries were prepared using LeXPrep DNA Universal Library Preparation Module Series coupled with LeXPrep Universal Stubby Adapter (UDI) Module and LeXPrep Universal Adapter (MDI) Module (for MGI) from different gDNA. LeXome XP Panel v1.0 were respectively used to complete hybridization capture. The BWA was used for alignment of raw reads to the reference genome (hg38). **A.** Mappability and On-target rate; **B.** Targeted covered; **C.** Coverage uniformity and consistency; **D.** The unbiased of GC coverage.

Note: The gDNA_1-4 samples were: Human Male Genomic DNA (Promega-male, G1471); Human Female Genomic DNA (Promega-female, G1521); PancancerLight 800 gDNA Reference Standard with 100 ng (Genewell, GW-OGTM800); Cell Line gDNA Standard (Coriell, NA12878), respectively. Sequencing platform: Illumina Novaseq 6000，PE150；DNBSEQ-G400，PE150.

Variant Analysis

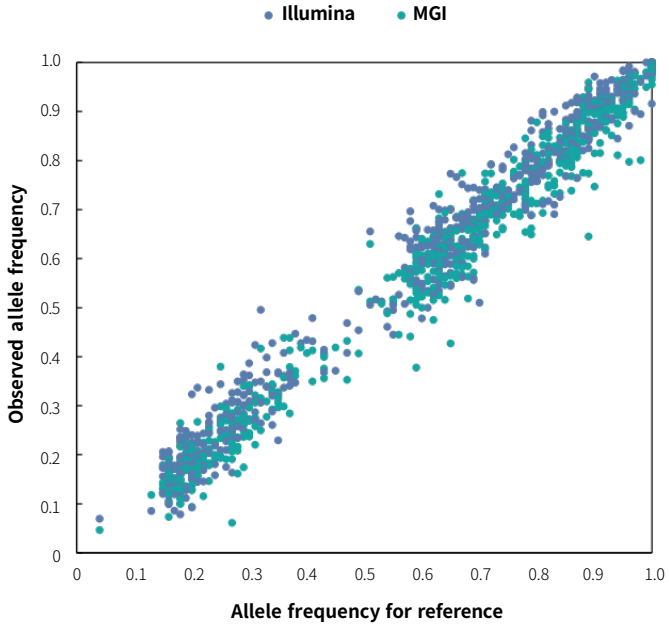


Fig 2. Consistency of the allele frequencies in LeXome XP Panel v1.0 capture data with the nominal frequencies of the standards. The libraries were prepared using LeXPrep DNA Universal Library Preparation Kit Series and LeXome XP Panel v1.0 were respectively used to complete hybridization capture. VarDict was used for variant calling. Sequencing platform: Illumina Novaseq 6000，PE150；DNBSEQ-G400，PE150.

Note: Sample type: PancancerLight 800 gDNA Reference Standard with 100 ng (Genewell, GW-OGTM800).

High Confidence Variant Calls

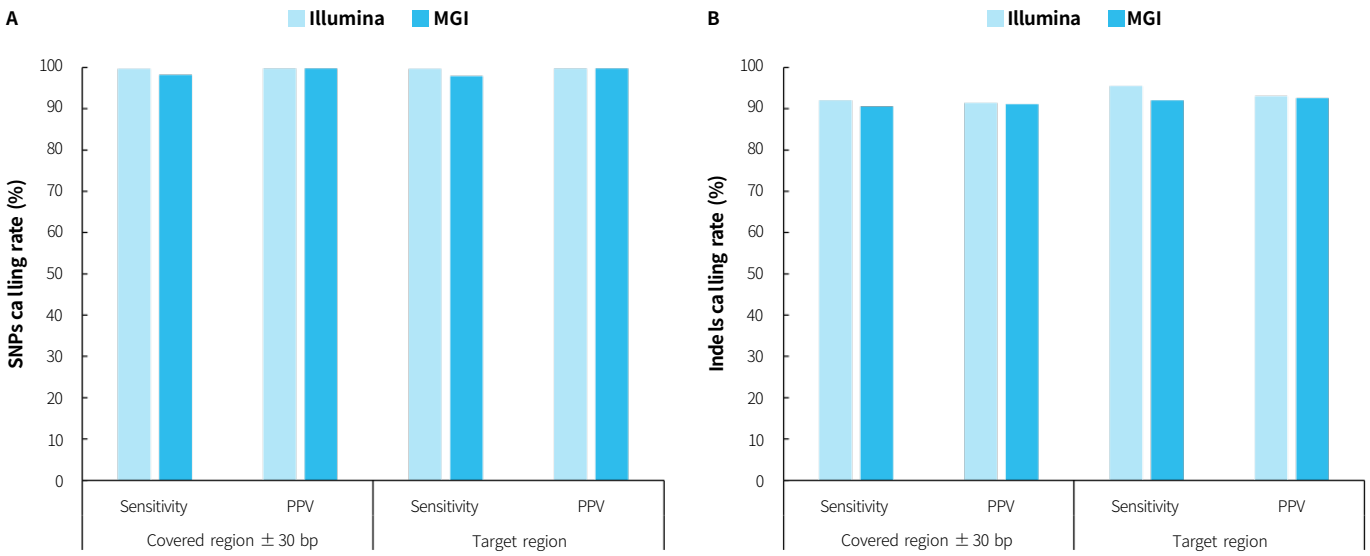


Fig 3. Sensitivity and positive predictive value (PPV) of LeXome XP Panel v1.0 for NA12878 mutation identification. A. SNPs; **B.** Indels.

Note: Sample type: Cell Line gDNA Standard (Coriell, NA12878). Sequencing platform: Illumina Novaseq 6000，PE150；DNBSEQ-G400，PE150.

Ordering Information

Product	Catalog #
LeXome XP Panel v1.0, 16 rxn	LX01872
LeXome XP Panel v1.0, 96 rxn	LX01871

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

LexigenBio Inc.
support@lexigenbio.com
www.lexigenbio.com
521 Cottonwood Dr Suite 121, Milpitas, CA 95035

Version202506