Integrated Solution for Predefined Tumor Profiling Products

August, 2025

About iGenetech

iGeneTech Bioscience is a high-tech enterprise in Beijing founded in 2014, focusing on the development and supply of target gene " reading" and "writing" solutions with three self-developed core technology platforms: NGS hybridization capture, multiplex PCR and high-throughput DNA synthesis. We provide catalog and customized NGS target enrichment panels, NGS reagents and kits, OEM and CDMO services and large-cale DNA synthesis services to 1000+ customers from various fields including healthcare, agriculture, micro-biology, and academic research. We've set high quality standards to our NGS products, and our quality management system has received ISO 13485: 2016 and ISO 9001: 2015 certifications.

Catalog

CONTENTS

Predefined Products for Tumor Genomics

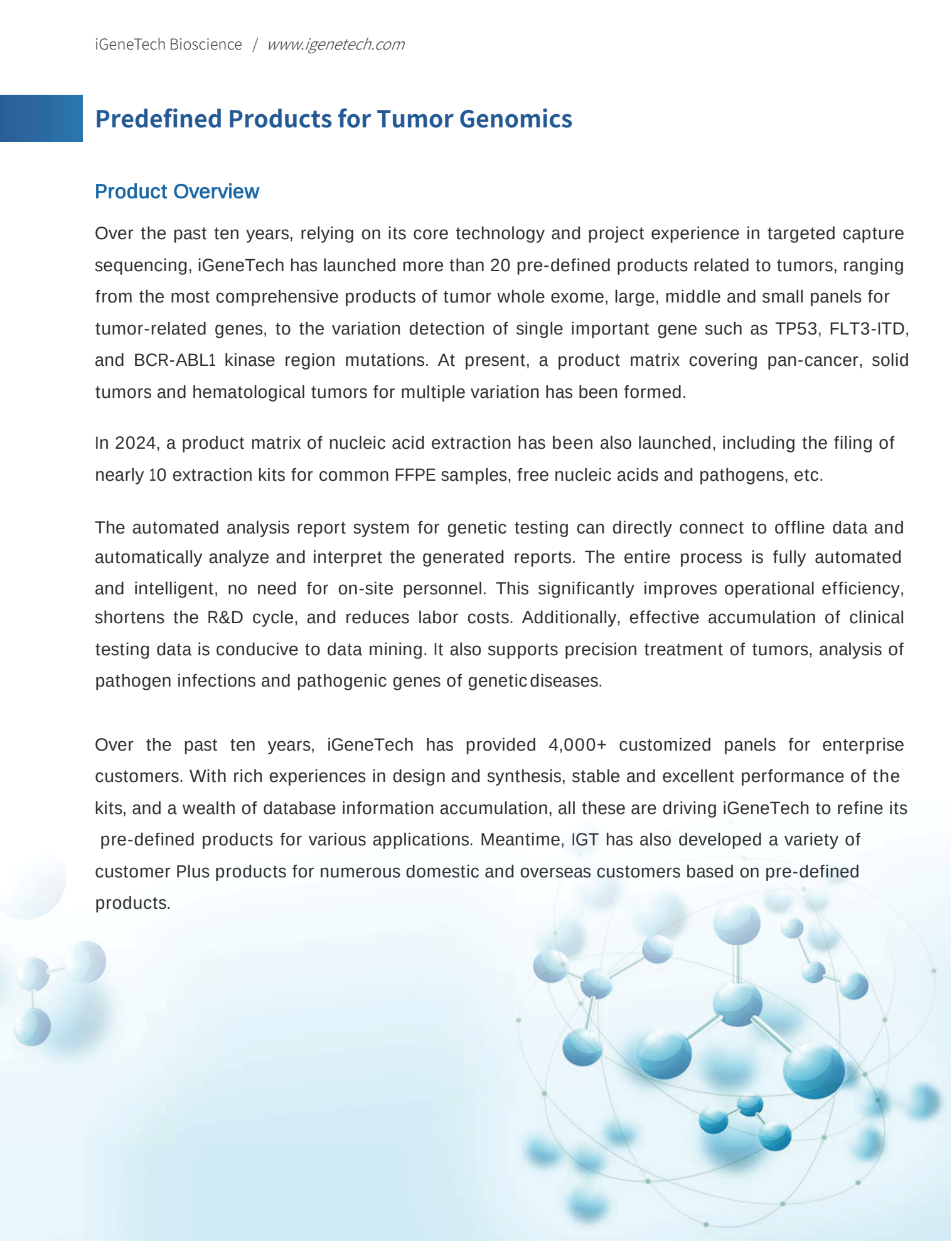
Product Overview

Over the past ten years, relying on its core technology and project experience in targeted capture sequencing, iGeneTech has launched more than 20 pre-defined products related to tumors, ranging from the most comprehensive products of tumor whole exome, large, middle and small panels for tumor-related genes, to the variation detection of single important gene such as TP53, FLT3-ITD, and BCR-ABL1 kinase region mutations. At present, a product matrix covering pan-cancer, solid tumors and hematological tumors for multiple variation has been formed.

In 2024, a product matrix of nucleic acid extraction has been also launched, including the filing of nearly 10 extraction kits for common FFPE samples, free nucleic acids and pathogens, etc.

The automated analysis report system for genetic testing can directly connect to offline data and automatically analyze and interpret the generated reports. The entire process is fully automated and intelligent, no need for on-site personnel. This significantly improves operational efficiency, shortens the R&D cycle, and reduces labor costs. Additionally, effective accumulation of clinical testing data is conducive to data mining. It also supports precision treatment of tumors, analysis of pathogen infections and pathogenic genes of genetic diseases.

Over the past ten years, iGeneTech has provided 4,000+ customized panels for enterprise customers. With rich experiences in design and synthesis, stable and excellent performance of the kits, and a wealth of database information accumulation, all these are driving iGeneTech to refine its pre-defined products for various applications. Meantime, IGT has also developed a variety of customer Plus products for numerous domestic and overseas customers based on pre-defined products.



Pre-defined panels

AIExome® Human Exome Panel V5 - Tumor

Product Overview

Coverage Size	35.3 Mb
Coverage	On the coverage basis of full exome, the depth of 641 tumor-related genes were increased to three times that of other regions. Additionally, hot spot fusion regions, MSI loci, SNP skeletons, HLA typing probes and the full length of mitochondria were added separately.
Detection Range	SNV/InDel、Fusion、CNV、MSI、TMB、HRD/HRR、HLA、mtDNA
Recommonded Sequencing data	20 Gb/200×
Applications	Targeted therapy, immunotherapy guidance, MRD detection

Advantages

- Fully cover the detection needs of tumor-related variations and markers;
- Deep differentiation adjustment, deepening depth of tumor-related area and no additional increase of overall data cost
- Depends on self-developed TargetSeq One® v3.0 hybrid capture system, flexible and efficient capture, support multiple hyb, fast hyb
- Support customized servicesfor different research purposes, increase and encryption probe area upondemand.

Performance

Excellent Data Capture Performance

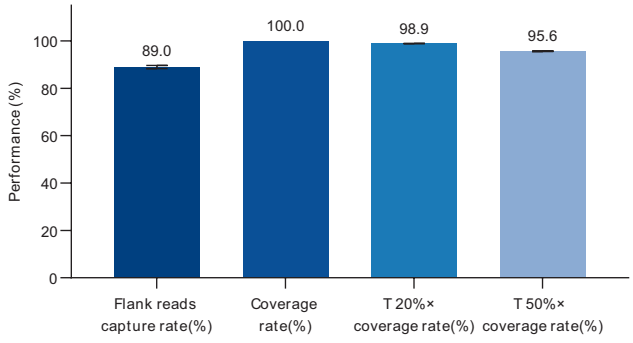


Figure 1. **Capture data performance test ofgDNA standard product**

Use gDNA standard for test, the library was constructed at an input of 100 ng, hybrid capture by TargetSeq One® Hyb & Wash Kit v3.0, sequenced on Illumina with NovaSeq 6000 PE150.

In-depth optimization in different regions

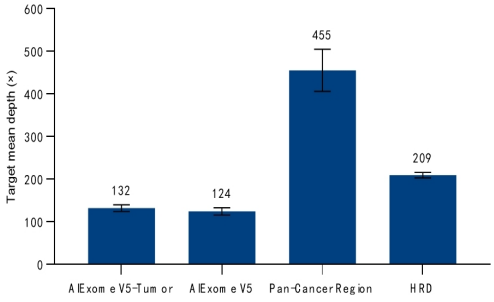


Table1. Depth summary of special areas

Special Region	Target mean depth（×）
mtDNA	6040×
HLA-A	426×
HLA-B	652×
HLA-C	683×
HLA-DRB1	452×
HLA-DQB1	397×
HLA-DPB1	586×

Figure 2. Use gDNA standard（Progema G3041）for test, the library was constructed at an input of 100 ng, hybrid and capture by TargetSeq One® Hyb & Wash Kit v3.0 for overnight hybridization and sequenced by Illumina NovaSeq 6000 PE150 with 13 G raw bases.

High sensitivity and accuracy of mutation detection

Table 2. Detection of gDNA standard product variations

Gene	Variant	Expected Allelic Frequency	Reported Allelic Frequency		
			Repeat 1	Repeat 2	Repeat 3
BRAF	p.V600E	5.0%	4.0%	4.0%	4.7%
EGFR	p.G719S	5.0%	4.0%	4.2%	4.8%
EGFR	p.L858R	5.0%	4.0%	5.4%	3.6%
EGFR	p.T790M	5.0%	5.0%	4.7%	4.7%
EGFR	p.E746_A750del	5.0%	2.7%	3.1%	1.7%
KRAS	p.G12A	5.0%	7.1%	4.7%	5.8%
KRAS	p.G13D	5.0%	5.0%	3.4%	5.1%
KRAS	p.Q61H	10.0%	10.0%	10.2%	10.7%
NRAS	p.G12D	5.0%	8.0%	3.3%	6.5%
NRAS	p.Q61H	5.0%	6.4%	6.2%	6.6%
MET	Exon 14 Skipping	50.0%	53.0%	52.5%	54.0%
PIK3CA	p.H1047R	5.0%	5.0%	4.3%	2.0%
PIK3CA	p.E545K	5.0%	6.0%	5.6%	6.6%

Note：Analysis of the mutation sites detection of positive standard products. Use gDNA standard product (Shuimujiheng PSC500) with an input of 100 ng for library prep. Sequenced by Illumina NovaSeq 6000 PE150 with 20 Gb raw bases. All positive mutation sites were detected, with consistent results as expected.

Product Information

Product Name	Spec.	Cat.
AIExome® Human Exome Panel V5 - Tumor	24/96 rxn	PH2007385/PH2007382
IGT® Enzyme Plus Library Prep Kit V3	96 rxn	C11112
IGT® Adapter & UDI Primer 1-96*	96 rxn	C10042
TargetSeq One® Hyb & Wash Kit v3.0*	24/96 rxn	C11534/C11532
TargetSeq® Eco Universal Blocking Oligo*	24/96 rxn	C80504/C80502
TargetSeq® Cap Beads & Nuclease-Free Water*	5 mL each	C10422

*IGT® can provide kits compatible with Illumina, MGI etc., as well as universal reagents corresponding to each platform.

Pan-Cancer Panel V2

Product overview

Coverage Size	2.1 Mb
Coverage	Covers 641 genes related to targeted drugs for solid tumors and tumor genetic susceptibility related, also additionally adds 38 hot spot fusion intron regions and 15 classic microsatellite loci
Detection Range	SNV、InDel、Fusion、CNV、MSI、TMB
Recommended Sequencing Data	3Gb/500×，7Gb/1000×
Applications	Targeted therapy, immunotherapy guidance, MRD detection

Advantages

- Full detection of tumor-related genes, covering multi genes and microsatellite loci, the TMB and MSI value can be calculated;
- Flexible and efficient capture depending on self-developed TargetSeq One® hybrid & capture system;
- High sensitivity and accuracy of mutation detection;
- Customized services for different research purposes, increase and encrypt probes of target area upon demand.

Performance

Excellent Capture Data Performance

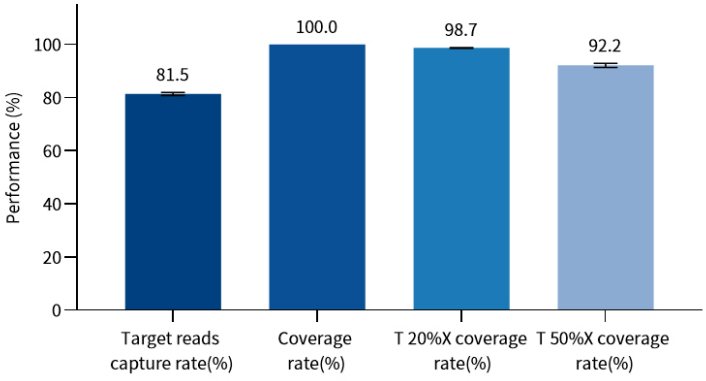


Figure 3. **Capture data performance test of gDNA standard product**

Use gDNA positive standard product for test, the library was constructed at an input of 50 ng, hybrid and capture by TargetSeq One® Pan-Cancer Panel V2, and sequenced by Illumina NovaSeq 6000 PE150.

High sensitivity and accuracy of mutation detection

Table 3. Mutation detection of gDNA standard product

Gene	Variant	Expected Allelic Frequency	Reported Allelic Frequency
EGFR	p.L858R	1.0%	0.9%
KRAS	p.A146T	1.0%	1.4%
NRAS	p.Q61K	1.0%	0.9%
EGFR	p.T790M	2.0%	1.9%
EGFR	p.E746_A750del	2.0%	1.5%
FLT3	p.I836del	2.0%	1.8%
KIT	p.D816V	2.0%	2.3%
KRAS	p.G12D	2.0%	1.6%
EGFR	p.A767_V769dup	3.0%	1.9%
EGFR	p.G719S	4.0%	4.5%
KRAS	p.G13D	4.0%	3.3%
EML4-ALK	Fusion	5.0%	3.6%
CD74-ROS1	Fusion	6.0%	2.1%
BRAF	p.V600E	7.0%	4.7%
PIK3CA	p.H1047R	7.0%	7.1%

Note：Analysis results of the mutation sites detection of positive standard products. Use gDNA standard product (Jingliang, cat. GW-OPSM003) with an input of 50 ng for library prep. Sequenced by Illumina NovaSeq 6000 PE150, depth after deduplication ~1,000× time (7 Gb raw bases). All positive mutation sites were detected with consistent results as expected.

Accurate detection of low-frequency mutations

Table 4. Detection result of ctDNA standard product

Gene	Variant	Expected Allelic Frequency	Reported Allelic Frequency	
			Repeat 1	Repeat 2
EGFR	p.L858R	0.50%	0.56%	0.66%
EGFR	p.ΔE746_A750	0.50%	0.15%	0.58%
EGFR	p.T790M	0.50%	0.31%	0.60%
EGFR	p.V769_D770insASV	0.50%	0.26%	0.40%
KRAS	p.G12D	0.50%	0.36%	0.11%
NRAS	p.Q61K	0.50%	0.71%	0.55%
NRAS	p.A59T	0.50%	1.11%	0.56%
PIK3CA	E545K	0.50%	0.43%	0.40%

NOTE：ctDNA efficiency assessment. Mix the ctDNA standard reference product of mutation frequency of 1% and wild-type (Horizon, Cat. HD780) in equal proportions to 0.5% ctDNA standard reference product. Input 10 ng for library prep in combination with UMI analysis tag technology, MGI-T7 PE150 sequencing. Extract same data for UMI analysis built by iGeneTech, the results showed that all mutation sites could be detected under low input and low sequencing data volume (8000×), and the variation ratio in two repeated detections was consistent as expected.

Gene list

641 gene - full coverage of CDS region

ABCB1	*ABCC3*	*ABL1*	*ABL2*	*ACVR1*	*ACVR1B*	*AGO2*	*AKT1*	*AKT2*	*AKT3*	*ALK*	*ALOX12B*	*AMER1*
ANKRD11	*APC*	*APEX1*	*AR*	*ARAF*	*ARFRP1*	*ARID1A*	*ARID1B*	*ARID2*	*ARID5B*	*ASNS*	*ASXL1*	*ASXL2*
ATIC	*ATM*	*ATR*	*ATRX*	*AURKA*	*AURKB*	*AXIN1*	*AXIN2*	*AXL*	*B2M*	*BABAM1*	*BAP1*	*BARD1*
BBC3	*BCL10*	*BCL2*	*BCL2L1*	*BCL2L11*	*BCL2L2*	*BCL6*	*BCOR*	*BCORL1*	*BCR*	*BIRC3*	*BIRC7*	*BLM*
BMPR1A	*BRAF*	*BRCA1*	*BRCA2*	*BRD4*	*BRIP1*	*BTG1*	*BTG2*	*BTK*	*C11orf30*	*C8orf34*	*CALR*	*CARD11*
CARM1	*CASP7*	*CASP8*	*CBFB*	*CBL*	*CBR3*	*CCND1*	*CCND2*	*CCND3*	*CCNE1*	*CD22*	*CD274*	*CD276*
CD3EAP	*CD44*	*CD70*	*CD79A*	*CD79B*	*CDA*	*CDC42*	*CDC73*	*CDH1*	*CDK12*	*CDK4*	*CDK6*	*CDK8*
CDKN1A	*CDKN1B*	*CDKN2A*	*CDKN2B*	*CDKN2C*	*CEBPA*	*CENPA*	*CHD2*	*CHD4*	*CHEK1*	*CHEK2*	*CIC*	*CREBBP*
CRKL	*CRLF2*	*CSDE1*	*CSF1R*	*CSF3R*	*CTCF*	*CTLA4*	*CTNNA1*	*CTNNB1*	*CTTN*	*CUL3*	*CUL4A*	*CXCR4*
CYLD	*CYP17A1*	*CYP19A1*	*CYP1B1*	*CYP2C8*	*CYP2D6*	*CYP4B1*	*CYSLTR2*	*DAXX*	*DCUN1D1*	*DDR1*	*DDR2*	*DDX43*
DICER1	*DIS3*	*DNAJB1*	*DNMT1*	*DNMT3A*	*DNMT3B*	*DOT1L*	*DPYD*	*DROSHA*	*DUSP4*	*DYNC2H1*	*E2F3*	*EED*
EGFL7	*EGFR*	*EIF1AX*	*EIF4A2*	*EIF4E*	*ELF3*	*EP300*	*EPAS1*	*EPCAM*	*EPHA2*	*EPHA3*	*EPHA5*	*EPHA7*
EPHB1	*EPHB4*	*ERBB2*	*ERBB3*	*ERBB4*	*ERCC1*	*ERCC2*	*ERCC3*	*ERCC4*	*ERCC5*	*ERF*	*ERG*	*ERRFI1*
ESR1	*ESR2*	*ETV1*	*ETV6*	*EWSR1*	*EXT1*	*EZH1*	*EZH2*	*FADD*	*FAM175A*	*FAM46C*	*FAM58A*	*FANCA*
FANCC	*FANCD2*	*FANCE*	*FANCF*	*FANCG*	*FANCL*	*FANCM*	*FAS*	*FAT1*	*FAT3*	*FBXW7*	*FCGR2A*	*FCGR3A*
FGF10	*FGF12*	*FGF14*	*FGF19*	*FGF23*	*FGF3*	*FGF4*	*FGF6*	*FGFR1*	*FGFR2*	*FGFR3*	*FGFR4*	*FH*
FLCN	*FLT1*	*FLT3*	*FLT4*	*FOXA1*	*FOXL2*	*FOXO1*	*FOXP1*	*FRS2*	*FSHR*	*FUBP1*	*FYN*	*GAB2*
GABRA6	*GALNT12*	*GATA1*	*GATA2*	*GATA3*	*GATA4*	*GATA6*	*GGH*	*GID4*	*GLI1*	*GNA11*	*GNA13*	*GNAQ*
GNAS	*GPR124*	*GPS2*	*GREM1*	*GRIN2A*	*GRM3*	*GSK3B*	*GSTA1*	*GSTM1*	*GSTP1*	*H3F3A*	*H3F3B*	*H3F3C*
HAS3	*HDAC1*	*HDAC6*	*HGF*	*HIST1H1C*	*HIST1H2BD*	*HIST1H3A*	*HIST1H3B*	*HIST1H3C*	*HIST1H3D*	*HIST1H3E*	*HIST1H3F*	*HIST1H3G*
HIST1H3H	*HIST1H3I*	*HIST1H3J*	*HIST2H3C*	*HIST2H3D*	*HIST3H3*	*HLA-A*	*HLA-B*	*HMMR*	*HNF1A*	*HOXB13*	*HRAS*	*HSD3B1*
HSP90AA1	*HSPB1*	*ICOSLG*	*ID3*	*IDH1*	*IDH2*	*IFNGR1*	*IGF1*	*IGF1R*	*IGF2*	*IKBKE*	*IKZF1*	*IL10*
IL1A	*IL4*	*IL7R*	*IL8*	*INHA*	*INHBA*	*INPP4A*	*INPP4B*	*INPPL1*	*INSR*	*IRF2*	*IRF4*	*IRS1*
IRS2	*JAK1*	*JAK2*	*JAK3*	*JUN*	*KAT6A*	*KDM3B*	*KDM5A*	*KDM5C*	*KDM6A*	*KDR*	*KEAP1*	*KEL*
KIT	*KLF4*	*KLHL6*	*KMT2A*	*KMT2B*	*KMT2C*	*KMT2D*	*KNSTRN*	*KRAS*	*LATS1*	*LATS2*	*LIG4*	*LIMK1*
LIN28B	*LMO1*	*LRP1B*	*LTK*	*LYN*	*LZTR1*	*MAF*	*MAGI2*	*MALT1*	*MAP2K1*	*MAP2K2*	*MAP2K4*	*MAP3K1*
MAP3K13	*MAP3K14*	*MAPK1*	*MAPK3*	*MAPKAP1*	*MAX*	*MCL1*	*MDC1*	*MDM2*	*MDM4*	*MECOM*	*MED12*	*MEF2B*
MEN1	*MERTK*	*MET*	*MGA*	*MGMT*	*MITF*	*MKNK1*	*MLH1*	*MLH3*	*MPL*	*MRE11A*	*MSH2*	*MSH3*
MSH6	*MSI1*	*MSI2*	*MST1*	*MST1R*	*MTAP*	*MTHFR*	*MTOR*	*MTRR*	*MUTYH*	*MXI1*	*MYC*	*MYCL*
MYCN	*MYD88*	*MYO3B*	*MYOD1*	*NBN*	*NCOA3*	*NCOR1*	*NDRG1*	*NEGR1*	*NEIL1*	*NF1*	*NF2*	*NFE2L2*
NFKBIA	*NKX2-1*	*NKX3-1*	*NOS2*	*NOTCH1*	*NOTCH2*	*NOTCH3*	*NOTCH4*	*NPM1*	*NQO1*	*NQO2*	*NRAS*	*NSD1*
NT5C2	*NTHL1*	*NTRK1*	*NTRK2*	*NTRK3*	*NUF2*	*NUP93*	*OPRM1*	*P2RY8*	*PAK1*	*PAK3*	*PAK7*	*PALB2*
PARK2	*PARP1*	*PARP2*	*PARP3*	*PAX5*	*PBRM1*	*PDCD1*	*PDCD1LG2*	*PDGFRA*	*PDGFRB*	*PDK1*	*PDPK1*	*PGR*
PHB	*PHOX2B*	*PIK3C2B*	*PIK3C2G*	*PIK3C3*	*PIK3CA*	*PIK3CB*	*PIK3CD*	*PIK3CG*	*PIK3R1*	*PIK3R2*	*PIK3R3*	*PIM1*
PLAT	*PLCG2*	*PLK2*	*PMAIP1*	*PMS1*	*PMS2*	*PNRC1*	*POLD1*	*POLE*	*PON1*	*PPARG*	*PPM1D*	*PPP2R1A*
PPP2R2A	*PPP4R2*	*PPP6C*	*PRDM1*	*PRDM14*	*PREX2*	*PRKAA1*	*PRKAR1A*	*PRKCI*	*PRKD1*	*PRKDC*	*PRSS8*	*PTCH1*
PTEN	*PTP4A1*	*PTPN11*	*PTPRD*	*PTPRO*	*PTPRS*	*PTPRT*	*QKI*	*RAB35*	*RAC1*	*RAC2*	*RAD21*	*RAD50*
RAD51	*RAD51B*	*RAD51C*	*RAD51D*	*RAD52*	*RAD54L*	*RAF1*	*RANBP2*	*RARA*	*RASA1*	*RB1*	*RBM10*	*RECQL*
RECQL4	*REL*	*RET*	*RFWD2*	*RHBDF2*	*RHEB*	*RHOA*	*RICTOR*	*RIT1*	*RNF43*	*ROS1*	*RPS6KA4*	*RPS6KB2*
RPTOR	*RRAGC*	*RRAS*	*RRAS2*	*RRM1*	*RSF1*	*RTEL1*	*RUNX1*	*RUNX1T1*	*RXRA*	*RYBP*	*SDHA*	*SDHAF2*
SDHB	*SDHC*	*SDHD*	*SEMA3C*	*SESN1*	*SESN2*	*SESN3*	*SETD2*	*SETD8*	*SF3B1*	*SGK1*	*SH2B3*	*SH2D1A*
SHOC2	*SHQ1*	*SLCO1B1*	*SLCO1B3*	*SLIT1*	*SLIT2*	*SLX4*	*SMAD2*	*SMAD3*	*SMAD4*	*SMARCA4*	*SMARCB1*	*SMARCD1*
SMO	*SMYD3*	*SNCAIP*	*SOCS1*	*SOD2*	*SOS1*	*SOX10*	*SOX17*	*SOX2*	*SOX4*	*SOX9*	*SPEN*	*SPOP*
SPRED1	*SPTA1*	*SRC*	*SRSF2*	*STAG2*	*STAT3*	*STAT4*	*STAT5A*	*STAT5B*	*STK11*	*STK19*	*STK40*	*SUFU*
SUZ12	*SYK*	*TAF1*	*TAP1*	*TAP2*	*TBX3*	*TCEB1*	*TCF3*	*TCF7L2*	*TDG*	*TEK*	*TERC*	*TERT*
TET1	*TET2*	*TGFB1*	*TGFBR1*	*TGFBR2*	*TIPARP*	*TLR2*	*TMEM127*	*TMPRSS2*	*TNF*	*TNFAIP3*	*TNFRSF14*	*TNFSF11*
TOP1	*TOP2A*	*TP53*	*TP53BP1*	*TP63*	*TRAF2*	*TRAF7*	*TRRAP*	*TSC1*	*TSC2*	*TSHR*	*TSHZ2*	*TSHZ3*
TTF1	*TXN*	*TXNRD2*	*TYMS*	*TYRO3*	*U2AF1*	*UGT1A1*	*UGT1A4*	*UMPS*	*UPF1*	*VEGFA*	*VHL*	*VTCN1*
WHSC1	*WHSC1L1*	*WISP3*	*WT1*	*WWTR1*	*XIAP*	*XPC*	*XPO1*	*XRCC1*	*XRCC2*	*XRCC3*	*YAP1*	*YES1*
ZBTB2	*ZFHX3*	*ZNF217*	*ZNF703*									

List of 38 DNA rearrangement

NOTCH2	*NTRK1*	*ALK*	*MSH2*	*RAF1*	*ETV5*	*FGFR3*	*SLC34A2*	*PDGFRA*	*KIT*	*CD74*	*ROS1*
MYB	*EZR*	*EGFR*	*BRAF*	*FGFR1*	*MYC*	*NTRK2*	*RET*	*FGFR2*	*KMT2A*	*ETV6*	*BRCA2*
NUTM1	*RARA*	*BRCA1*	*ETV4*	*SDC4*	*TMPRSS2*	*BCR*	*EWSR1*	*BCL2*	*RSPO2*	*MET*	*ETV1*
PPARγ	*TERT*										

List of 15 MSI

BAT40	Mono-27	BAT26	D2S123	NR24	BAT25	D5S346	D8S554	Penta C	NR27	NR21	D17S250
D18S69	D18S64	Penta D									

214 Chemotherapy sites

rs8175347	*rs13181*	*rs2207396*	*rs3211371*	*rs10426377*	*rs602950*	*rs3740066*	*rs7194667*
rs2070676	*rs1051640*	*rs2231137*	*rs544093*	*rs17626122*	*rs17376848*	*rs17583889*	*rs879207*
rs10981694	*rs11615*	*rs717620*	*rs55886062*	*rs4149015*	*rs1517114*	*rs12210538*	*rs34743033*
rs11045585	*rs1736557*	*rs2849380*	*rs139887*	*rs885004*	*rs4646487*	*rs4148950*	*rs4148945*
rs2301159	*rs2292954*	*rs2238472*	*rs2227291*	*rs1871450*	*rs1799931*	*rs12960*	*rs2228001*
rs1042522	*rs1799735*	*rs25487*	*rs3212986*	*rs3957357*	*rs60369023*	*rs2740574*	*rs9561778*
rs1695	*rs2032582*	*rs2075252*	*rs316019*	*rs1056892*	*rs8133052*	*rs3892097*	*rs3918290*
rs9514091	*rs1801158*	*rs1801265*	*rs1801159*	*rs2297595*	*rs1801133*	*rs1045642*	*rs9024*
rs67376798	*rs9394992*	*rs2234693*	*rs1052536*	*rs7319981*	*rs4694362*	*rs7779029*	*rs934635*
rs7176005	*rs9936750*	*rs7325568*	*rs7853758*	*rs2291767*	*rs1801160*	*rs1061472*	*rs1799793*
rs11692021	*rs2070959*	*rs11563250*	*rs2269577*	*CYP3A4 *1, CYP3A4 *20, CYP3A4 *8*	*rs1056836*	*rs310786*	*rs75017182*
rs11479	*rs9351963*	*rs442767*	*rs12046844*	*rs1650697*	*rs11545078*	*rs12022243*	*rs2612091*
rs2741171	*rs12132152*	*rs9825762*	*rs6900017*	*rs879825*	*rs3594*	*rs1801249*	*rs4550690*
rs76387818	*rs1872328*	*rs10937158*	*rs2292997*	*rs225440*	*rs3749438*	*rs1934951*	*rs1113129*
rs7699188	*rs2229774*	*rs4880*	*rs6493497*	*rs183205964*	*rs2813543*	*rs12659*	*rs2227310*
rs17574269	*rs2494752*	*rs1979277*	*rs3740556*	*rs2306283*	*rs16950650*	*rs1051266*	*rs1801368*
rs25648	*rs1128503*	*rs1800566*	*rs1127687*	*rs4353229*	*rs1760217*	*rs17091162*	*rs12721655*
rs12613732	*rs1048943*	*rs6413432*	*rs1130214*	*rs430397*	*rs861539*	*rs861539*	*rs7921977*
rs12415607	*rs7769719*	*rs730720*	*rs6922548*	*rs4148947*	*rs4148943*	*rs3734254*	*rs2016520*
rs1883322	*rs1402467*	*rs12418*	*rs3212986*	*rs1799983*	*rs2070744*	*rs532545*	*rs4646*
rs9981861	*rs9597*	*rs9679162*	*rs34489327*	*rs4444903*	*rs396991*	*rs698*	*rs1142345*
rs1801131	*rs7851395*	*rs17655*	*rs2010963*	*rs11942466*	*rs1570360*	*rs662*	*rs699947*
rs144854329	*rs7984870*	*rs3213239*	*rs34489327*	*rs2231142*	*rs371194629*	*rs9380142*	*rs17179108*
rs3738948	*rs1800975*	*rs1799801*	*rs4413407*	*rs35864111*	*rs4244285*	*rs3917412*	*rs944050*
rs1563828	*rs11023197*	*rs9535828*	*rs9996584*	*rs712829*	*rs13104811*	*rs1353295*	*rs9535826*
rs61734430	*rs1051298*	*rs3788189*	*rs914232*	*rs2293347*	*rs1047840*	*rs9369421*	*rs17109924*
rs12819505	*rs10878232*	*rs11868547*	*rs4541111*	*rs1052555*	*rs13207351*	*rs1801274*	*rs7958904*
rs619586	*rs2839698*	*rs6983267*					

Product Information

Product Name	Spec.	Cat.
Pan-Cancer Panel V2	24/96 rxn	PT1011715/PT1011712
IGT® Enzyme Plus Library Prep Kit V3	96 rxn	C11112
IGT® Fast Library Prep Kit v2.0	96 rxn	C10022
IGT® Adapter & UDI Primer 1-96*	96 rxn	C10042
TargetSeq One® Hyb & Wash Kit v3.0*	24/96 rxn	C11534/C11532
TargetSeq® Eco Universal Blocking Oligo*	24/96 rxn	C80504/C80502
TargetSeq® Cap Beads & Nuclease-Free Water*	5 mL each	C10422

*IGT® can provide kits compatible with Illumina, MGI etc., as well as universal reagents corresponding to each platform.

Solid Tumor Fusion RNA Panel

Product overview

Coverage size	1.2 Mb
Coverage	All coding regions of transcripts from 298 main genes related to solid tumors and the UTR regions of selected genes.
Detection Range	Fusion, transcript variation and expression, etc.
Recommended Sequencing Data	4 Gb
Applications	Adjuvant diagnosis, medication guidance, prognostic indication

Advantages

- **Comprehensive and precise**— Design target capture regions across all transcripts, based on RNA-level samples.
- **Sensitive and efficient**— Efficient capture of target regions, cost-saving and sensitive detection.
- **Stable and superior** — Stable and excellent performance relying on iGeneTech® TargetSeq® probe hybridization capture sequencing technology.
- **Flexible customization**— Customized and semi-customized services (e.g., probe encryption, target region expansion) based on client needs, meeting personalized requirements.

Performance

Capture performance

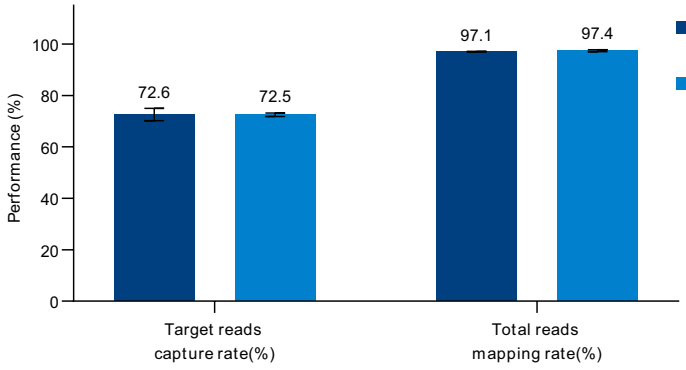


Figure 4. **Capture performance test of RNA standard product.**

Total RNA was extracted from Seraseq® FFPE fusion RNA Reference Material v4. Using RNA library prep kits at an input of 50 ng for library prep. Sequencing on Illumina NovaSeq 6000 PE150 after hybridization capture.

Validation of fusion standard product

Table 5. Detection results of fusion standard product

Fusion Gene	50 ng Input		100 ng Input	
	Repeat 1	Repeat 2	Repeat 1	Repeat 1
	(Junction/Spanning reads)		(Junction/Spanning reads)	
TMPRSS2 - ERG	112	54	74	84
KIF5B - RET	146	102	149	191
SLC45A3 - BRAF	108	77	66	109
FGFR3 - TACC3	166	124	137	154
FGFR3 - BAIAP2L1	130	107	140	172
LMNA - NTRK1	87	69	59	96
TPM3 - NTRK1	130	75	117	122
CD74 - ROS1	166	104	187	185
NCOA4 - RET	105	58	46	52
ETV6 - NTRK3	65	35	35	47
CCDC6 - RET	20	31	28	35
TFG - NTRK1	41	44	48	46
EML4 - ALK	55	40	51	71
SLC34A2 - ROS1	55	45	54	47
EGFR - SEPT14	39	32	42	61
PAX8 - PPARG	136	78	117	106
MET exon14 skipping	408	408	351	405
EGFR Variant III	167	106	88	134

NOTE：Detection comparison analysis of fusion events in positive standard products shows that, under the same data volume (~4G) but with different input amounts, all fusion events could be detected with consistent results as expected.

Gene List

Cover all transcripts of the main genes

ABL1 †*	*ABL2*	*ACKR3*	*ACTB*	*AFF1*	*AFF3*	*AHRR*	*AKAP9*	*AKT3*	*ALK*
ARHGAP26	*ASPSCR1*	*ATF1*	*ATIC*	*AXL*	*BAG4*	*BAIAP2L1*	*BCAS3*	*BCAS4*	*BCL11A*
BCL2 †	*BCL3*	*BCOR* †*	*BIRC3*	*BIRC6*	*BRAF*	*BRD3*	*BRD4**	*C11orf95*	*CAMTA1*
CANT1	*CARS1*	*KNL1*	*CASP7*	*CCAR2*	*CCDC6*	*CCNB1IP1*	*CCNB3*	*CCND1*	*CCND3*
CD74	*CDH11*	*CDKN2D*	*CDX1*	*CHCHD7*	*CIC †*	*CLTC*	*COL1A1*	*COL1A2*	*COL4A5*
COL6A3	*CREB1*	*CREB3L1*	*CREB3L2*	*CRLF2*	*CRTC1*	*CRTC3*	*CSF1*	*CSF1R*	*CTNNB1*
CUX1	*DDIT3*	*DDX5*	*DEK*	*SLC49A4*	*DNAJB1*	*DUX4*	*EBF1*	*EGFR*	*EIF3E*
EIF4A2	*ELK4*	*EML4*	*EP300*	*EPC1*	*EPCAM*	*ERBB2 †*	*ERC1*	*ERG**	*ERLIN2*
ESR1	*ESRRA*	*ETS1*	*ETV1**	*ETV4*	*ETV5**	*ETV6**	*EWSR1*	*EZR*	*TAFA2*
FEV	*FGF8*	*FGFR1*	*FGFR2*	*FGFR3*	*FGR**	*FHIT*	*FLI1*	*FLT3*	*FOSB*
FOXO1	*FOXO4*	*FRYL*	*FUS*	*GLI1*	*GOLGA5*	*GOPC*	*GPC3*	*GRID1*	*HAS2*
HERPUD1	*HEY1*	*HIP1*	*HJURP*	*HMGA1*	*HMGA2*	*HMGN2P46*	*HNRNPA2B1*	*HOOK3*	*HPR*
INSR	*IRF2BP2*	*JAK2**	*JAK3*	*JAZF1*	*KAT6B*	*RELCH*	*KIAA1549*	*KIF5B †*	*KIT †*
KLF17	*KLK2*	*KLK4*	*KLKP1*	*KMT2A*	*KRAS*	*KTN1*	*LHFPL6*	*LIFR*	*LMO1*
LPP	*LRIG3*	*LRP1*	*MAML2*	*MAST1*	*MAST2*	*MBTD1*	*MEAF6*	*MET**	*OGA*
MIPOL1	*MRTFB*	*MLLT11*	*MLLT3*	*MN1*	*MSH2*	*MSMB*	*MUSK*	*MUTYH*	*MYB*
MYC	*MYH11*	*MYH9*	*NAB2*	*NCOA1**	*NCOA2**	*NCOA4*	*NDRG1*	*NFATC2*	*NFIB*
NIPBL	*NONO*	*NOTCH1*	*NOTCH2*	*NOTCH3 †*	*NR4A3**	*NRG1*	*NSD1*	*NTRK1*	*NTRK2*
NTRK3	*NUMA1*	*NUMBL*	*NUP98*	*NUTM1*	*NUTM2A*	*NUTM2B*	*NUTM2E*	*OMD*	*PAFAH1B2*
PATZ1	*PAX3*	*PAX5*	*PAX7*	*PAX8*	*PBX1*	*PBX3*	*PCM1*	*PCSK7*	*PDGFB*
PDGFRA	*PDGFRB †*	*PHF1*	*PIK3CA**	*PKN1*	*PLAG1**	*PLPP3*	*POU5F1*	*PPARG**	*PPFIBP1*
PRCC	*PRKACA*	*PRKAR1A*	*PRKCA*	*PRKCB*	*PSPC1*	*PTGFRN*	*PTPRK*	*RAD51B*	*RAF1*
RANBP2	*RARA**	*RELA*	*RET*	*RGS17*	*RMI2*	*ROS1*	*RPS10*	*RSPO2**	*RSPO3*
RUNX1	*SDC4*	*SDHA*	*SDHB*	*SDHD*	*SEC16A*	*SEC22B*	*SEC31A*	*SEPTIN14*	*SEPTIN9*
SFPQ	*SLC34A2*	*SLC45A3*	*SMARCB1*	*SMARCE1*	*SP3*	*SRGAP3*	*SS18*	*SS18L1*	*SS18L2*
SSX1	*SSX2*	*SSX4*	*STAT6*	*STRN*	*SUZ12*	*TACC1*	*TACC3*	*TAF15*	*TBL1XR1*
TCEA1	*TCF12 †*	*TCF3*	*TCF7L2*	*TEC*	*TENM4*	*TERT*	*TET1*	*TFE3*	*TFEB*
TFG	*TGFBR3*	*THADA*	*THRAP3*	*TMPRSS2* †*	*TP53**	*TPM3*	*TPM4*	*TPR*	*TRIM24*
TRIM27	*TRIM33*	*USP6**	*VTI1A*	*WASF2*	*WCDP*	*WDFY2*	*NSD2*	*WIF1*	*WT1*
WWTR1	*YAP1*	*YWHAE**	*YY1*	*ZC3H7B*	*ZDHHC7*	*ZNF331*	*ZNF444*		

*NOTE：*Cover all 5'-UTR，†cover all 3'-UTR*

Product Information

Product Name	Spec.	Cat.
Solid Tumor Fusion RNA Panel	24/96 rxn	PT1009785/PT1009782
IGT® Fast Stranded RNA Library Prep Kit v2.0	96 rxn	C10032
IGT® Adapter & UDI Primer 1-96*	96*1 rxn	C10042
TargetSeq One® Hyb & Wash Kit v3.0*	24/96 rxn	C11534/C11532
TargetSeq® Eco Universal Blocking Oligo*	24/96 rxn	C80504/C80502
TargetSeq® Cap Beads & Nuclease-Free Water*	5 mL each	C10422

*IGT® can provide kits compatible with Illumina, MGI etc., as well as universal reagents corresponding to each platform.

Pan-Cancer DNA+RNA Research Assay

Product Overview

Coverage Size	2.1 Mb (DNA) +1.2 Mb (RNA)
Coverage	Panels of DNA level cover 641 genes related to targeted medication for solid tumors and tumor genetic susceptibility, also with an addition of 38 hot spot fusion intron regions & 15 classic microsatellite sites. Panels of RNA level cover all coding regions of transcripts from 298 main genes related to solid tumors and the UTR regions of selected genes.
Detection Range	SNV、InDel、Fusion、CNV、MSI、TMB；fusion, transcript variation and expressions, etc.
Recommended Sequencing Data	7 Gb (DNA)；4 Gb (RNA)

Advantages

- Regarding to the DNA and RNA dual detection requirements in solid tumors, this product is fully equipped with reagents for library construction of DNA and RNA samples, hybridization capture reagents, DNA + RNA probes for Pan-cancer,

- While achieving the detection of mutations, copy number amplification, insertion/deletion, fusion and other variants at DNA level, it also conducts auxiliary verification of fusion mutations and exon jumping at RNA level. With DNA + RNA dual detection, this product enables precise fusion detection, assists clinical decision-making and benefits patients.

Product Information

Product Name	Spec.	Cat.
Pan-Cancer DNA+RNA Research Assay*	96 rxn	C11252

**IGT® shipping list includes library prep kits, adapter kits, capture kits, universal reagents and pre-defined products.*

**IGT® can provide kits compatible with Illumina, MGI etc., as well as universal reagents corresponding to each platform.*

Solid Tumor Mid Panel

Product Overview

Coverage Size	438.3 kb
Coverage	Covers 122 genes related to targeted medication for solid tumors, also with an addition of 25 hot spot fusion intron regions & 19 classic microsatellite sites, 219 chemotherapy sites.
Detection Range	SNV、InDel、Fusion、CNV、MSI
Recommended Sequencing Data	1.5 Gb/ 1000×
Applications	Targeted therapy, immunotherapy guidance

Advantages

- Selected 122 genes related to pan-cancer
- Multiple variation detection, MSI and etc.

Performance

Capture Performance

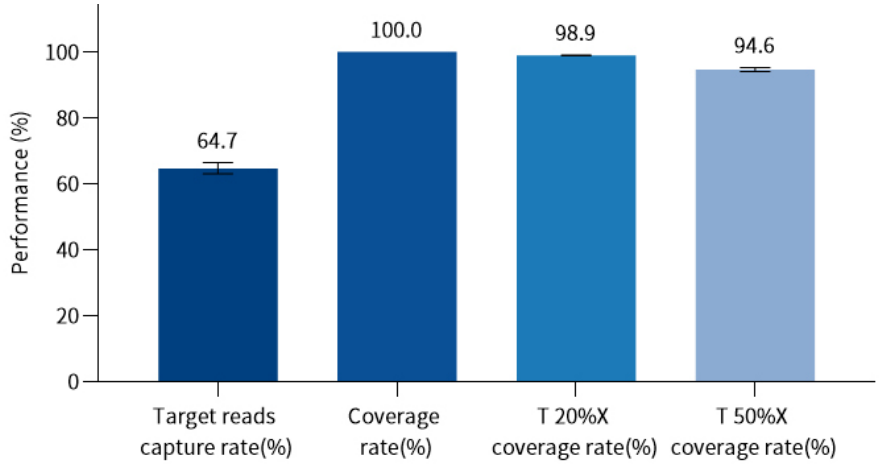


Figure 5. Capture data performance test of gDNA standard product. Use gDNA positive standard product for test, input of 50 ng for library prep, hybrid and capture, sequenced by Illumina NovaSeq 6000 PE150.

Variation detection

Table 6. Detection results of gDNA positive standard product mutation sites

Gene	Variant	Expected Allelic Frequency	Reported Allelic Frequency
EGFR	p.L858R	1.0%	0.9%
KRAS	p.A146T	1.0%	1.4%
NRAS	p.Q61K	1.0%	0.9%
EGFR	p.T790M	2.0%	1.9%
EGFR	p.E746_A750del	2.0%	1.5%
FLT3	p.I836del	2.0%	1.8%
KIT	p.D816V	2.0%	2.3%
KRAS	p.G12D	2.0%	1.6%
EGFR	p.A767_V769dup	3.0%	1.9%
EGFR	p.G719S	4.0%	4.5%
KRAS	p.G13D	4.0%	3.3%
EML4-ALK	p.Fusion	5.0%	3.6%

Note: Analysis of the mutation sites detection of positive standard products. Use gDNA standard product (Jingliang, cat. GW-OPSM003) with an input of 50 ng for library prep. Sequenced by Illumina NovaSeq 6000 PE150, depth after deduplication ~1,000× time (7 Gb raw bases). All positive mutation sites were detected with consistent results as expected.

Table 7. Detection results of ctDNA positive standard product mutation sites

Gene	Variant	Expected Allelic Frequency	Reported Allelic Frequency
EGFR	p.L858R	1.0%	0.9%
KRAS	p.A146T	1.0%	1.4%
NRAS	p.Q61K	1.0%	0.9%
EGFR	p.T790M	2.0%	1.9%
EGFR	p.E746_A750del	2.0%	1.5%
FLT3	p.I836del	2.0%	1.8%
KIT	p.D816V	2.0%	2.3%
KRAS	p.G12D	2.0%	1.6%
EGFR	p.A767_V769dup	3.0%	1.9%

Note：Analysis of the mutation sites detection of positive standard products. Use cfDNA standard product (Jingliang, cat. GW-OPSM003) with an input of 50 ng for library prep. Sequenced by Illumina NovaSeq 6000 PE150, depth after deduplication ~1,000×time (7 Gb raw bases). All positive mutation sites were detected with consistent results as expected.

Gene List

Full Coverage of CDS Region

AKT1	*ABL1*	*ABL2*	*AKT3*	*ALK*	*APC*	*AR*	*ARAF*	*ARID1A*	*ATM*	*ATR*	*BAP1*	*BRAF*
BRCA1	*BRCA2*	*CCND1*	*CDH1*	*CDK12*	*CDK4*	*CDK6*	*CDKN2A*	*CDX2*	*CTNNB1*	*DDR2*	*EGFR*	*EPCAM*
ERBB2	*ERBB3*	*ERBB4*	*ERCC2*	*ESR1*	*EZH2*	*FBXW7*	*FGFR1*	*FGFR2*	*FGFR3*	*FGFR4*	*FLT3*	*FOXA1*
FOXL2	*GATA3*	*GNA11*	*GNAQ*	*GNAS*	*HNF1A*	*HRAS*	*IDH1*	*IDH2*	*JAK2*	*KDM5C*	*KDM6A*	*KEAP1*
KIT	*KRAS*	*MAP2K1*	*MAPK1*	*MDM2*	*MET*	*MLH1*	*MPL*	*MSH2*	*MSH6*	*MTOR*	*MYC*	*MYCN*
MYD88	*NF1*	*NF2*	*NOTCH1*	*NPM1*	*NRAS*	*NRG1*	*NTRK1*	*NTRK2*	*NTRK3*	*PBRM1*	*PDGFRA*	*PDGFRB*
PIK3CA	*PMS2*	*POLD1*	*POLE*	*PTCH1*	*PTEN*	*PTPN11*	*RAF1*	*RB1*	*RET*	*RHEB*	*RHOA*	*RIT1*
ROS1	*SETD2*	*SMAD4*	*SMO*	*SPOP*	*STK11*	*TERT*	*TP53*	*TSC1*	*TSC2*	*VHL*	*BARD1*	*CHEK2*
DICER1	*FH*	*FLCN*	*SDHA*	*SMARCA4*	*BRIP1*	*MUTYH*	*PALB2*	*PMS2*	*RAD51C*	*RAD51D*	*SDHAF2*	*SDHB*
SDHC	*SDHD*	*TMEM127*	*SMAD3*	*SUFU*	*SMARCB1*							

25 Hot Spot Fusion Intron Region

NTRK1	*ALK*	*FGFR3*	*CD74*	*ROS1*	*FGFR1*	*NTRK2*	*RET*	*FGFR2*	*ETV6*

19 MSI Region

BAT40	Mono-27	BAT26	D2S123	NR24	BAT25	D5S346	D8S554	Penta C	NR27	NR21	D17S250
D18S69	D18S64	Penta D	NR22	D17S261	D17S520	D18S34					

219 Chemotherapy sites

rs8175347	*rs13181*	*rs2207396*	*rs3211371*	*rs10426377*	*rs602950*	*rs3740066*	*rs7194667*	*rs2070676*	*rs1051640*
rs2231137	*rs544093*	*rs17626122*	*rs17376848*	*rs17583889*	*rs879207*	*rs10981694*	*rs11615*	*rs717620*	*rs55886062*
rs4149015	*rs1517114*	*rs12210538*	*rs34743033*	*rs11045585*	*rs1736557*	*rs2849380*	*rs139887*	*rs885004*	*rs4646487*
rs4148950	*rs4148945*	*rs2301159*	*rs2292954*	*rs2238472*	*rs2227291*	*rs1871450*	*rs1799931*	*rs12960*	*rs2228001*
rs1042522	*rs1799735*	*rs25487*	*rs3957357*	*rs60369023*	*rs2740574*	*rs9561778*	*rs1695*	*rs2032582*	*rs2075252*
rs316019	*rs1056892*	*rs8133052*	*rs3892097*	*rs3918290*	*rs9514091*	*rs1801158*	*rs1801265*	*rs1801159*	*rs2297595*
rs1801133	*rs1045642*	*rs9024*	*rs67376798*	*rs9394992*	*rs2234693*	*rs1052536*	*rs7319981*	*rs4694362*	*rs7779029*
rs934635	*rs7176005*	*rs9936750*	*rs7325568*	*rs7853758*	*rs2291767*	*rs1801160*	*rs1061472*	*rs1799793*	*rs11692021*
rs2070959	*rs11563250*	*rs2269577*	*CYP3A4 *1, CYP3A4 *20, CYP3A4 *8*	*rs1056836*	*rs310786*	*rs75017182*	*rs11479*	*rs9351963*	*rs442767*
rs12046844	*rs1650697*	*rs11545078*	*rs12022243*	*rs2612091*	*rs2741171*	*rs12132152*	*rs9825762*	*rs6900017*	*rs879825*
rs3594	*rs1801249*	*rs4550690*	*rs76387818*	*rs1872328*	*rs10937158*	*rs2292997*	*rs225440*	*rs3749438*	*rs1934951*
rs1113129	*rs7699188*	*rs2229774*	*rs4880*	*rs6493497*	*rs183205964*	*rs2813543*	*rs12659*	*rs2227310*	*rs17574269*
rs2494752	*rs1979277*	*rs3740556*	*rs2306283*	*rs16950650*	*rs1051266*	*rs1801368*	*rs25648*	*rs1128503*	*rs1800566*
rs1127687	*rs4353229*	*rs1760217*	*rs17091162*	*rs12721655*	*rs12613732*	*rs1048943*	*rs6413432*	*rs1130214*	*rs430397*
rs7921977	*rs12415607*	*rs7769719*	*rs730720*	*rs6922548*	*rs4148947*	*rs4148943*	*rs3734254*	*rs2016520*	*rs1883322*
rs1402467	*rs12418*	*rs1799983*	*rs2070744*	*rs532545*	*rs4646*	*rs9981861*	*rs9597*	*rs9679162*	*rs4444903*
rs396991	*rs698*	*rs1142345*	*rs1801131*	*rs7851395*	*rs17655*	*rs2010963*	*rs11942466*	*rs1570360*	*rs662*
rs699947	*rs144854329*	*rs7984870*	*rs3213239*	*rs2231142*	*rs371194629*	*rs9380142*	*rs17179108*	*rs3738948*	*rs1800975*
rs1799801	*rs4413407*	*rs35864111*	*rs4244285*	*rs3917412*	*rs944050*	*rs1563828*	*rs11023197*	*rs9535828*	*rs9996584*
rs712829	*rs13104811*	*rs1353295*	*rs9535826*	*rs61734430*	*rs1051298*	*rs3788189*	*rs914232*	*rs2293347*	*rs1047840*
rs9369421	*rs17109924*	*rs12819505*	*rs10878232*	*rs11868547*	*rs4541111*	*rs1052555*	*rs13207351*	*rs1801274*	*rs7958904*
rs619586	*rs2839698*	*rs6983267*							

Product Information

Product Name	Spec.	Cat.
Solid Tumor Mid Panel	24/96 rxn	PH2002105/PH2002102
IGT® Enzyme Plus Library Prep Kit V3	96 rxn	C11112
IGT® Adapter & UDI Primer 1-96*	96 rxn	C10042
TargetSeq One® Hyb & Wash Kit v3.0*	24/96 rxn	C11534/C11532
TargetSeq® Eco Universal Blocking Oligo*	24/96 rxn	C80504/C80502
TargetSeq® Cap Beads & Nuclease-Free Water*	5 mL each	C10422

Core Genes Fusion RNA Panel

Product Overview

Coverage Size	582.6 kb
Coverage	Select 90 core main genes related to solid tumors, including all coding regions of transcripts and the UTR regions of selected genes.
Detection Range	Fusion, transcript variation and expression, etc.
Recommended Sequencing Data	3 Gb
Applications	Adjuvant diagnosis, medication guidance, and prognostic indication

Advantages

- **Comprehemsive and precise**—— Design target capture regions across all transcripts, based on RNA-level samples.
- **Sensitive and efficient**—— Efficient capture of target regions, cost-saving and sensitive detection.
- **Stable and superior**—— Stable and excellent performance relying on iGeneTech® TargetSeq® probe hybrid capture sequencing technology.
- **Flexible customization**—— Customized and semi-customized services (e.g. probe encryption, target region expansion) based on client needs, meeting personalized requirements.

Performance

Capture performance

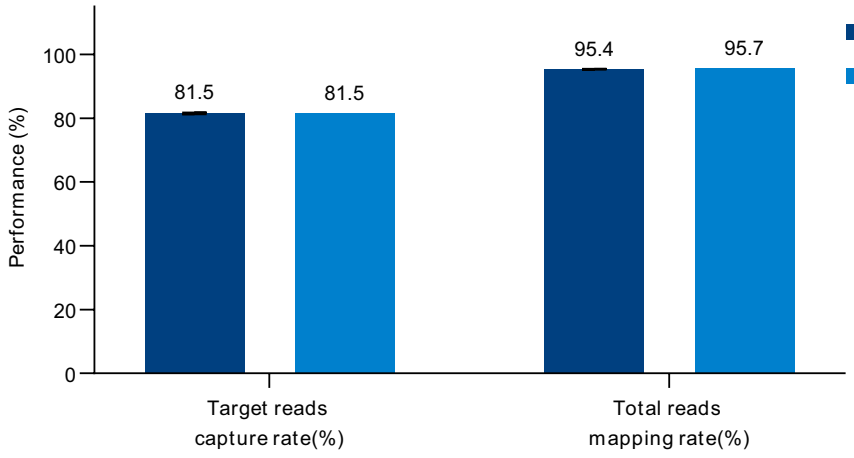


Figure 6. Capture performance testing of RNA standard product.

Extract total RNA from Seraseq® FFPE fusion RNA Reference Material v4, use RNA library prep kits at an input of 50 ng for library construction. Sequence on Illumina NovaSeq 6000 PE150 after hybridization capture.

Verification of fusion standard product

Table 8. Detection Results of fusion standard product

Fusion Gene	50 ng Input		100 ng Input	
	Repeat 1	Repeat 2	Repeat 1	Repeat 2
	(Junction/Spanning reads)		(Junction/Spanning reads)	
TMPRSS2 - ERG	352	141	274	281
KIF5B - RET	456	212	463	266
SLC45A3 - BRAF	370	188	291	253
FGFR3 - TACC3	439	252	384	247
FGFR3 - BAIAP2L1	366	225	408	195
LMNA - NTRK1	269	163	230	171
TPM3 - NTRK1	277	125	262	163
CD74 - ROS1	219	128	246	130
NCOA4 - RET	265	101	178	126
ETV6 - NTRK3	208	84	135	103
CCDC6 - RET	134	84	103	68
TFG - NTRK1	162	118	151	62
EML4 - ALK	198	101	182	52
SLC34A2 - ROS1	106	88	135	51
EGFR - SEPT14	112	63	113	18
PAX8 - PPARG	335	142	305	6
MET exon14 skipping	1360	1357	1327	975
EGFR Variant III	606	432	436	470

Gene List

Cover all the transcripts of 90 main genes

ABL1 †*	*ALK*	*BCL2 †*	*BCOR* †*	*BRAF*	*BRD4**	*CCDC6*	*CCND1*	*CIC †*	*COL1A1*
CRTC1	*DDIT3*	*DNAJB1*	*EGFR*	*EML4*	*EPC1*	*ERBB2 †*	*ERG**	*ETV1**	*ETV4*
*ETV6**	*EWSR1*	*EZR*	*FGFR1*	*FGFR2*	*FGFR3*	*FGR**	*FLI1*	*FLT3*	*FOXO1*
FUS	*GLI1*	*HMGA2*	*JAK2**	*JAZF1*	*KIAA1549*	*KMT2A*	*LPP*	*MAML2*	*MAST1*
MAST2	*MET**	*MLLT3*	*MYB*	*MYC*	*NAB2*	*NCOA1**	*NCOA2**	*NCOA4*	*NOTCH1*
NOTCH2	*NR4A3**	*NRG1*	*NTRK1*	*NTRK2*	*NTRK3*	*NUTM1*	*PAX3*	*PAX5*	*PAX7*
PAX8	*PBX1*	*PDGFB*	*PDGFRA*	*PDGFRB †*	*PHF1*	*PIK3CA**	*PLAG1**	*PPARG**	*PRKACA*
RAF1	*RARA**	*RET*	*ROS1*	*RUNX1*	*SLC45A3*	*SS18*	*SSX1*	*SSX2*	*STAT6*
SUZ12	*TAF15*	*TCF3*	*TFE3*	*TFEB*	*TFG*	*TMPRSS2* †*	*TP53**	*USP6**	*YWHAE**

* Cover all 5'-UTR， † cover all 3'-UTR

Product Information

Product Name	Spec.	Cat.
Core Genes Fusion RNA Panel	24/96 rxn	PH2000595/PH2000592
IGT® Fast Stranded RNA Library Prep Kit v2.0	96 rxn	C10032
IGT® Adapter & UDI Primer 1-96*	96*1 rxn	C10042
TargetSeq One® Hyb & Wash Kit v3.0*	24/96 rxn	C11534/C11532
TargetSeq® Eco Universal Blocking Oligo*	24/96 rxn	C80504/C80502
TargetSeq® Cap Beads & Nuclease-Free Water*	5 mL each	C10422

**IGT® can provide kits compatible with Illumina, MGI etc., as well as universal reagents corresponding to each platform.*

NSCLC Panel V2

Product Overview

Coverage Size	170 kb
Coverage	Targeting on 23 genes related to NSCLC treatment recommended by NCCN, covering the whole exome regions of 23 genes and hot spot fusion regions rela ted to BRAF, ALK, RET, ROS1 , MET Exon 14 Skipping Mutation etc.
Detection range	Detection of mutation, fusion, copy number variation and insertion/deletion, etc.
Recommended Sequencing Data	1 Gb/1000×
Applications	Auxiliary diagnosis, medication and prognosis indication

Advantages

- **Comprehensive and precise**— Targeting CDS and intron regions of 23 genes related to NSCLC, multiple variation detection.
- **Sensitive and efficient**— Efficient capture of target regions, cost-saving and sensitive detection.
- **Stable and superior**— Stable and excellent performance relying on iGeneTech® TargetSeq® probe hybrid capture sequencing technology.
- **Flexible customization**— Customized and semi-customized services (e.g., probe encryption, target region expansion) based on client needs, meeting personalized requirements.

Performance

Capture performance testing

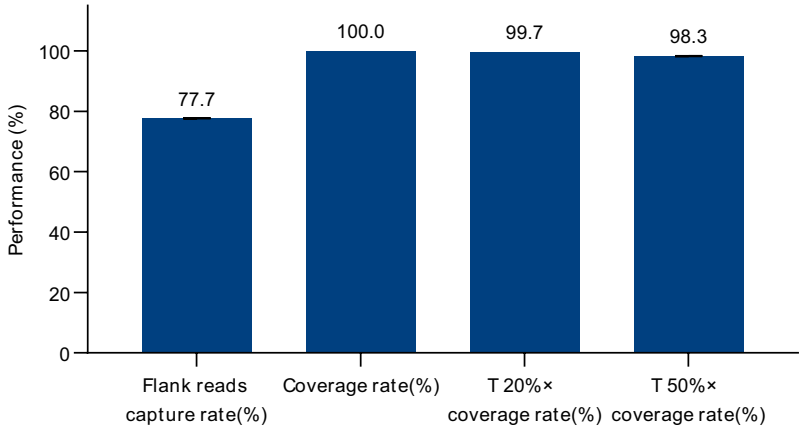


Figure 7. Capture performance testing of gDNA standard product

Note：Use gDNA standard product for testing, IGT® Fast Library Prep Kit v2.0 for library construction, matched with Target Seq One® Hyb & Wash Kit v3.0, and sequencing on Illumina NovaSeq 6000 PE150.

Variation detection

Table 9. Detection results of gDNA positive standard product mutation sites

Gene	Variant	Expected Allelic Frequency	Reported Allelic Frequency
EGFR	p.L858R	1.0%	1.7%
KRAS	p.A146T	1.0%	0.7%
NRAS	p.Q61K	1.0%	0.9%
EGFR	p.T790M	2.0%	2.3%
EGFR	p.ΔE746_A750	2.0%	1.1%
KRAS	p.G12D	2.0%	1.3%
EGFR	p.V769_D770insASV	3.0%	1.4%
EGFR	p.G719S	4.0%	4.3%
KRAS	p.G13D	4.0%	3.3%
EML4-ALK	Fusion	5.0%	2.4%
CD74-ROS1	Fusion	6.0%	2.9%
BRAF	p.V600E	7.0%	6.3%
PIK3CA	p.H1047R	7.0%	4.7%

Notes: Analysis of the mutation sites detection of positive standard products. Use gDNA standard product (Jingliang, cat. GW-OPSM003) with an input of 50 ng for library prep. Sequenced by Illumina NovaSeq 6000 PE150, depth after deduplication ~1,000 × time (1 Gb raw bases). All positive mutation sites were detected with consistent results as expected.

Table 10. Detection results of ctDNA positive standard product mutation sites

Gene	Variant	Expected Allelic Frequency	Reported Allelic Frequency
NRAS	Q61K	0.5%	0.6%
NRAS	A59T	0.5%	0.8%
PIK3CA	E545K	0.5%	0.7%
EGFR	ΔE746 - A750	0.5%	0.6%
EGFR	V769 - D770insASV	0.5%	0.6%
EGFR	T790M	0.5%	0.6%
EGFR	L858R	0.5%	0.6%
KRAS	G12D	0.6%	0.8%
EGFR	p.G719S	4.0%	4.5%

Note：Analysis of the mutation sites detection of positive standard products. Use cfDNA standard product (Horizon，cat. HD780) with an input of 10 ng forlibrary prep. Sequenced by Illumina NovaSeq 6000 PE150, depth after deduplication ~1,000 × time (4 Gb raw bases). All positive mutation sites were detected with consistent results as expected.

Gene List

Cover CDS regions of 23 genes

*ALK**	*BRAF**	*CDKN2A*	*EGFR**	*ERBB2*	*KRAS*	*MAP2K1*	*MET**	*NRAS*	*NRG1*
PIK3CA	*RET**	*ROS1**	*TP53*	*NTRK1**	*NTRK2**	*NTRK3*	*NF1*	*STK11*	*PTEN*
*FGFR1**	*FGFR2**	*FGFR3**							

Product Information

Product name	Spec.	Cat.
NSCLC Panel V2	24/96 rxn	PH2000165/PH2000162
IGT® Enzyme Plus Library Prep Kit V3	96 rxn	C11112
IGT® Fast Library Prep Kit v2.0	96 rxn	C10022
IGT® Adapter & UDI Primer 1-96*	96 rxn	C10042
TargetSeq One® Hyb & Wash Kit v3.0*	24/96 rxn	C11534/C11532
TargetSeq® Eco Universal Blocking Oligo*	24/96 rxn	C80504/C80502
TargetSeq® Cap Beads & Nuclease-Free Water*	5 mL each	C10422

**IGT® can provide kits compatible with Illumina, MGI etc., as well as universal reagents corresponding to each platform.*

MultipSeq® BRCA1/2 Research Assay V2

Product Overview

Coverage Size	19.5 kb
Coverage	Includes all exon regions of BRCA1 & BRCA2 genes, and at least 10 bp and UTR regions of the upstream and downstream, as well as 228 pathogenic sites, suspected pathogenic sites, and sites of unknown clinical significance located in non-exon regions from the ClinVar database.
Detection range	SNV、InDel
Recommend Sequencing Data	0.2 Gb/5000×
Applications	Health screening, risk assessment

Advantage

- **Highly optimized workflow——** Based on self-developed MultipSeq® multiplex amplicon sequencing technology, enables highly specific targeted enrichment.
- **Comprehensive coverage——** Fully covers the regions to be tested.
- **Excellent performance——** Stable and superior metrics in coverage, capture efficiency, and uniformity.
- **Convenient and efficient——** Short experimental cycle (3-4 hours) and simple operation.

Performance

Stable and superior capture performance across multiple sample types

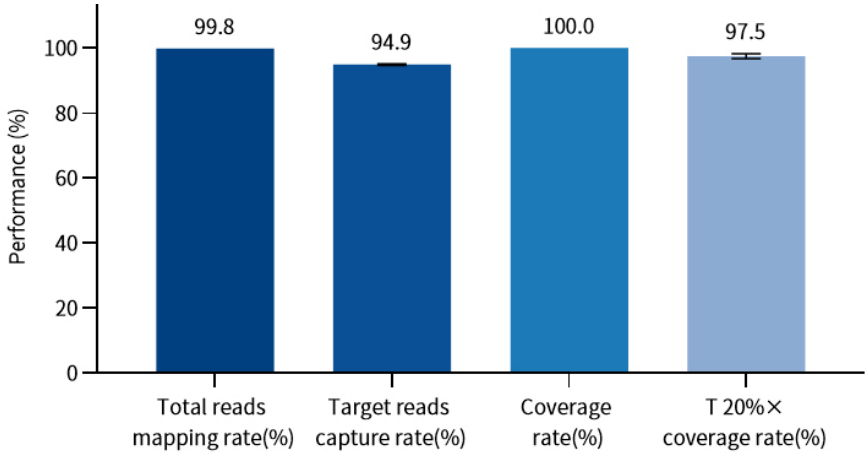


Figure 8. Performance in different sample types.
gDNA extracted from blood samples, gDNA from saliva (female & male) , with 40 ng of each input for library prep. Sequencing on NovaSeq 6000 platform using PE150, sequencing data approximately 120 Mb.

High sensitivity and accuracy in mutation detection

Table 11. Detection results of standard product mutation

Gene	Variant	Expected Allelic Frequency	Observed by ddPCR	Reported Allelic Frequency
BRCA1	p.S1634G	5.0%	4.6%	4.5±0.4%
BRCA1	p.K1183R	5.0%	4.7%	4.8±0.4%
BRCA1	p.P871Q	45.0%	46.8%	48.3±2.7%
BRCA1	p.K820E	5.0%	4.9%	5.1±0.1%
BRCA1	p.S694S	5.0%	4.5%	4.7±0.3%
BRCA1	p.D435Y	5.0%	4.2%	4.9±0.4%
BRCA2	p.N289D	5.0%	5.2%	5.3±0.3%
BRCA2	p.H743H	5.0%	4.9%	4.5±0.4%
BRCA2	p.N991D	5.0%	4.7%	5.2±0.9%
BRCA2	p.S1172S	5.0%	5.1%	5.2±0.5%
BRCA2	p.V1269V	5.0%	5.9%	5.3±0.3%
BRCA2	p.L1521L	100.0%	100.0%	100.0±0.0%
BRCA2	p.N1784fs	10.0%	10.4%	11.3±0.9%
BRCA2	p.V2171V	100.0%	100.0%	100.0±0.0%
BRCA2	p.V2466A	100.0%	100.0%	100.0±0.0%
BRCA1	p.R1443*	1.0%	1.0%	0.74±0.0%
BRCA2	p.K1132K	45.0%	47.2%	44.1±2.0%
BRCA2	p.D1420Y	5.0%	4.8%	5.1±0.4%
BRCA2	p.K1691fs	5.0%	4.7%	7.6±0.9%
BRCA2	p.S455S	5.0%	5.6%	5.6±0.7%

Note: iGeneTech MultipSeq® BRCA1/2 Research Assay V2 (for Illumina) was used to test Cobio BRCA standard products: 100% detection rate for 21 locus, and the detected frequencies were essentially consistent with the theoretical mutation frequencies.

Product information

Product Name	Spec.	Cat.
MultipSeq® BRCA1/2 Research Assay V2*	96 rxn	M62232
IGT® UDI Primer 1-96 (10 μM each, for Illumina, plate)	96* 1 rxn	C80202

**IGT® can provide kits compatible with Illumina, MGI etc., as well as universal reagents corresponding to each platform.*

HRD & HRR Panel

Product Overview

Product name	HRR Panel	HRD Panel	HRD & HRR Panel V2
Target/ Coverage size	177.9 kb	4.0 Mb	4.2 Mb
Coverage	39 core genes in the HRR pathway, including BRCA1/2.	37,000 SNP locus within whole genome.	Cover the core genes of HRR pathway and SNP loci across whole genome.
Detection range	SNV, InDel	LOH, TAI, LST	SNV, InDel; LOH, TAI, LST
Sequencing Data	0.5 Gb/1000× (Recommended)	6 Gb/500×	4 Gb/HRR 1200×; HRD 300×
Applications	HRD Score	Detection of HRR pathway gene mutations (BRCA 1/2, etc.)	One test with two results (HRD and HRR)

Advantages

- Suitable for Chinese population, the HRD detection product was designed on the basis of population genetic background and the therapeutic effect data. Self-developed HRD Scoremodel is on the basis of a large number of clinical samples and Chinese population database, reflecting the HRD status objectively.
- **Flexible customization**：Customized sites detetion according to customer requirements, also can be used in combination with any CDS Panel.
- **Double excellence in joint detection**：HRD & HRR co-detection kit, optimize the regional depth ratio on a single test to save the sequencing data volume.
- **Wide population for applications**：Patients with solid tumors such as newly diagnosed or recurrent breast cancer, ovarian cancer, prostate cancer, pancreatic cancer, and bladder cancer etc.

Performance

Excellent Capture data

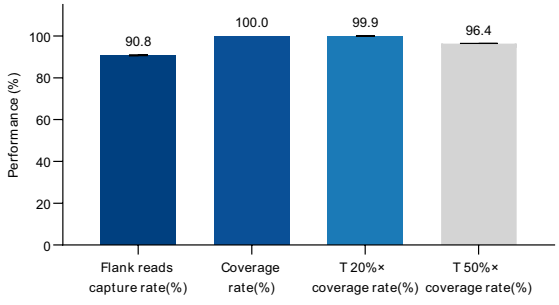


Figure 9. Capture performance testing of HRR Panel.

Use gDNAstandard product，matched withTargetSeq One® Hyb & Wash Kit v3.0，sequencing by Illumina NovaSeq 6000 PE150.

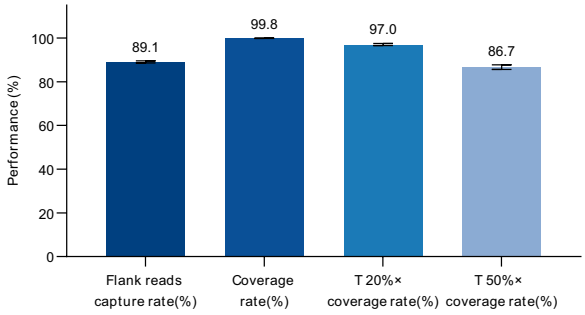


Figure10. Capture performance testing of HRD Panel.

Use gDNA kit for library construction, matched with TargetSeq One® Hyb & Wash Kit v3.0，sequencing by Illumina NovaSeq 6000 PE150.

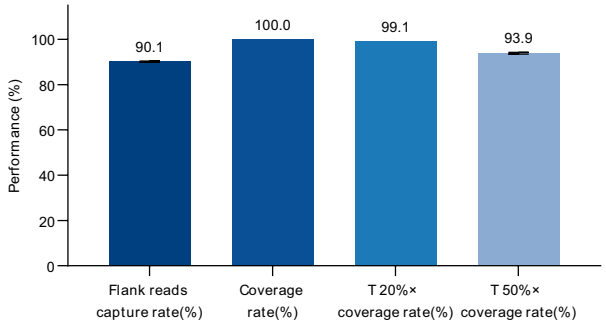


Figure 11. Capture performance testing of HRD & HRR Panel.
Use gDNA kit for library construction, matched with TargetSeq One® Hyb & Wash Kit v3.0，sequencing by Illumina NovaSeq 6000 PE150.

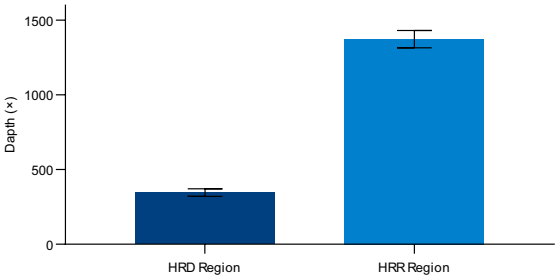


Figure 12. Testing of HRD & HRR Panel 1:4 Depth difference.
Use gDNA kit for library construction, matched with TargetSeq One® Hyb & Wash Kit v3.0，sequencing by Illumina NovaSeq 6000 PE150.

Precise analysis on HRD Score

Table 12. HRD standard product testing results

Sample	LOH	TAI	LST	HRD-sum	Result(⩾ 43)
Positive-High Ref	18	32	40	90	/
HRD-P9-T-Repeat 1	17	23	26	66	HRD-H
HRD-P9-T-Repeat 2	18	24	31	73	HRD-H
Negative-Low Ref	5	10	10	25	/
HRD-P13-T-Repeat 1	5	12	10	27	HRD-L
HRD-P13-T-Repeat 2	5	11	10	26	HRD-L
Critical Value-Median Ref	16	20	9	45	/
HRD-P15-T-Repeat 1	18	19	13	50	HRD-H
HRD-P15-T-Repeat 2	16	21	15	52	HRD-H

Note: Use 3 groups of Cobio HRD standard product（HRD-P9, HRD-P13, HRD-P15）for testing，combining the HRD analysis process and threshold value of iGeneTech, calculate the HRD score and determine the HRD status.

Gene List

CDS region of 39 core genes on HRR pathway

ABRAXAS1	*ATM*	*ATR*	*BARD1*	*BLM*	*BRCA1*	*BRCA2*	*BRIP1*	*CDK12*	*CHEK1*
CHEK2	*EMSY*	*FANCA*	*FANCC*	*FANCD2*	*FANCE*	*FANCF*	*FANCI*	*FANCL*	*FANCM*
MDC1	*MRE11*	*NBN*	*PALB2*	*PPP2R2A*	*PTEN*	*RAD50*	*RAD51*	*RAD51B*	*RAD51C*
RAD51D	*RAD52*	*RAD54L*	*RBBP8*	*RPA1*	*SLX4*	*TP53*	*WRN*	*XRCC2*	

Product Information

Product Name	Spec.	Cat.
HRD Panel	24/96 rxn	PH2000975/PH2000972
HRR Panel	24/96 rxn	PH2003715/PH2003712
HRD & HRR Panel V2	24/96 rxn	PH2003805/PH2003802
TargetSeq One® Hyb & Wash Kit v3.0*	24/96 rxn	C11534/C11532
TargetSeq® Eco Universal Blocking Oligo*	24/96 rxn	C80504/C80502
TargetSeq® Cap Beads & Nuclease-Free Water*	5 mL each	C10422

**IGT® can provide kits compatible with Illumina, MGI etc., as well as universal reagents corresponding to each platform.*

Tumor-informed MRD Research Kit

Product Overview

Based on Tumor-informed assays, combined with self-developed hybrid capture system and high-throughput MRD Panel, iGeneTech has launched a complete set of MRD hybrid capture reagents including hybrid capture reagents, blocking sequences and capture magnetic beads. Combined with the MRD Panel free customized to form a cost-effective and highly stable MRD detection solution, promoting the popularization of clinical application of MRD detection.

Advantages

- Full-process matching reagent- ensure stable and efficient reagent flow throughout the entire process
- Highly compatible hybrid capture reagents - compatible with multi-hybrid and fast-hybrid of all probe types
- Customization of high-throughput MRD Panel - Zero cost to meet the demand for large sample volumes
- More personalized MRD Panel monitoring sites - the higher the detection sensitivity.

Performance

Capture performance of MRD Panels of different sizes

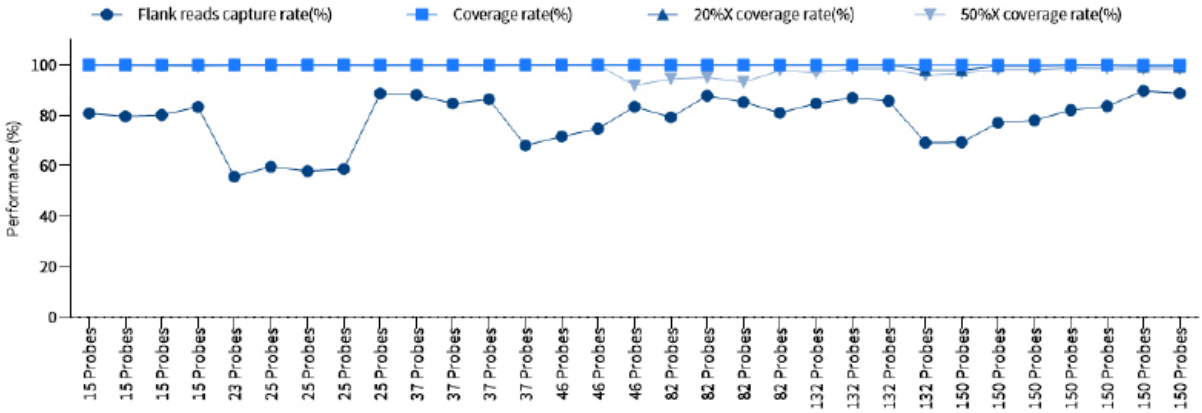


Figure 13. **Statistic results of MRD Panel test with different probe numbers.**

Based on the overall solution of iGeneTech MRD Panel, different 33 synthetic MRD panel (including 15 ~ 150 loci) were collected for capture performance testing. All the MRD Panels tested have presented excellent capture performance.

Test of probe preservation stability

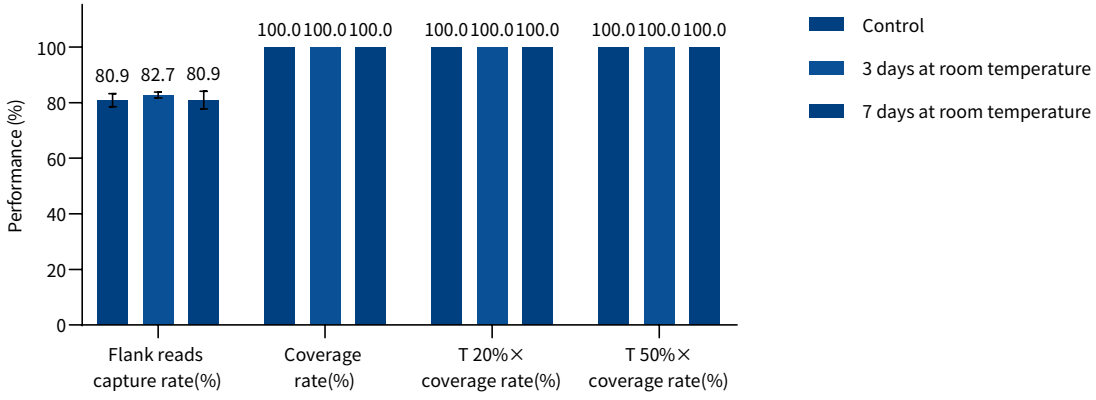


Figure 14. Data performance of probe preservation stability of MRD panel Use MRD Panel with 34 loci for testing. The input of the single-hybrid library was 750 ng, PE150 sequencing on NovaSeq 6000 platform. The probes of the MRD Panel were stored at room temperature for 3 days and 7 days before capture tests, while the control probes were stored at -20 ℃. Test data indicate that the capture effect of the MRD Panel remains stable after being stored at room temperature for 3 ~ 7 days.

Test of probe preservation stability

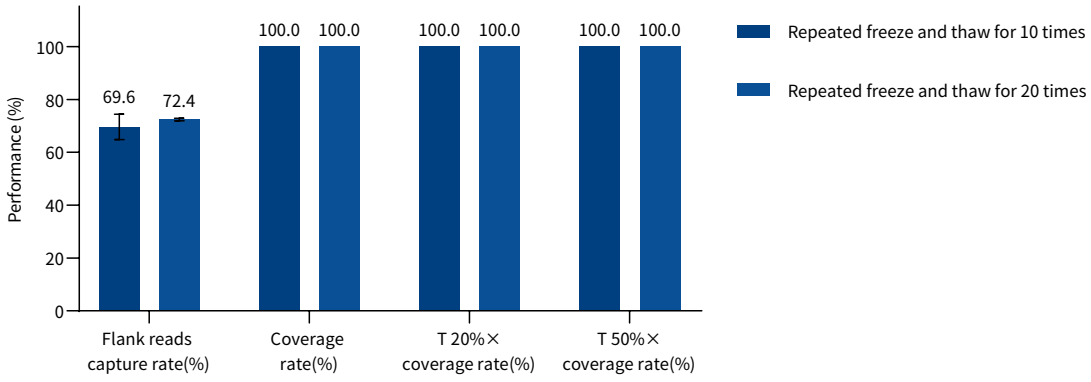


Figure 15. Data performance of probe frozen-thawed stability of MRD Panel. Use MRD Panel with 25 loci for testing. The input of the single-hybrid library was 750 ng, PE150 sequencing on NovaSeq 6000 platform. The probes of the MRD Panel were repeatedly frozen and thawed for 10 and 20 times before capture testing. The control probes were stored at -20℃. The test data indicate that the capture performance of the MRD Panel remains stable after repeated freezing and thawing for 10 and 20 times.

Product Information

Product Name	Spec.	Cat.
Tumor-informed MRD Research Kit (for Illumina)*	16 rxn	C81171
	96 rxn	C81172

* The shipping list includes hybrid capture reagents, blocking sequences and capture beads.

Hema Tumor Fusion RNA Panel

Product Overview

Coverage Size	851.1 kb
Coverage	Covering all transcript regions of 141 main genes related to hematological tumor fusion
Detection range	Fusion, transcript variation and expression, etc.
Sequencing volume	3 Gb (Recommended)
Applications	Adjuvant diagnosis, medication guidance, and prognostic indication

Advantages

- **Sensitive and precise**– Design all the transcripts in the target area, target capture of aimed regions, detect with low cost, high depth and sensitivity.
- **Efficient and uniform**– Stable and excellent performance relying on iGeneTech® TargetSeq® probe hybrid capture sequencing technology.
- **Stable and superior**– Stable and excellent performance relying on iGeneTech® TargetSeq® probe hybridization capture sequencing technology.
- **Flexible customization**– Customized and semi-customized services (e.g., probe encryption, target region expansion) based on client needs, meeting personalized requirements.

Performance

Capture performance testing

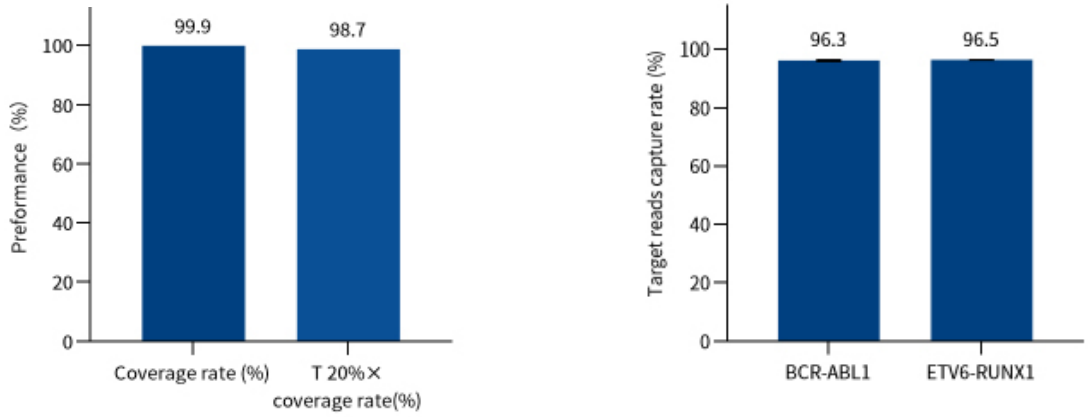


Figure 16. Probe performance testing with gDNA、RNAdual-sample

Use gDNA standard product G304A、Fusion genes RNA standard product BCR(E14)-ABL(E2)-P210 Fusion (Cobio，CBP20031R) and ETV6-RUNX1 Fusion (Cobio，CBP20091R) each 100 ng for library construction, sequencing after hybrid capture. The data comparison rate, capture efficiency and coverage of the two RNA fusion standards of gDNA in two replicates are all stable and excellent.

Expression consistency testing

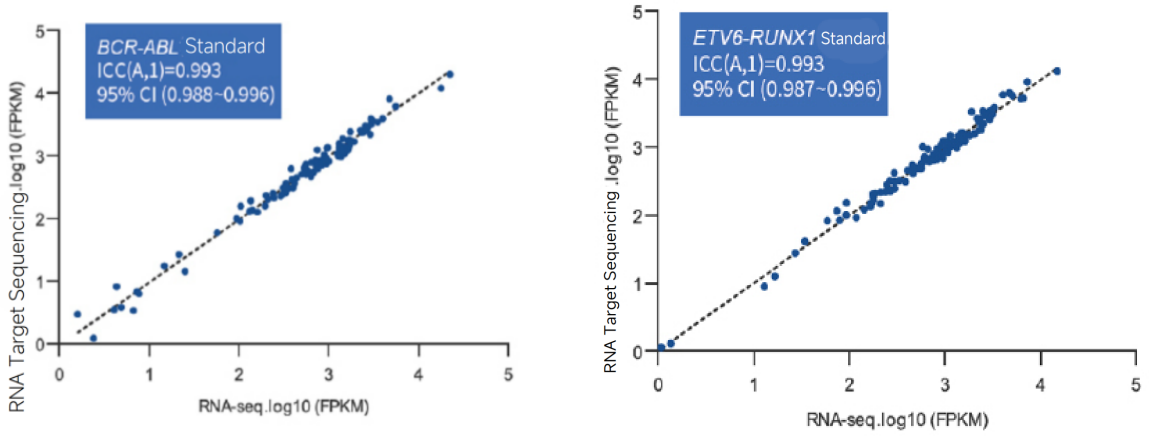


Figure 17. Comparison of RNA-targeted sequencing and amount of RNA-Seq gene expression.

Two RNA standards of fusion genes were respectively used for 100 Gb RNA-seq library prep sequencing, meantime, Hema Tumor Fusion RNA Panel was used for hybridization capture. Work out the Read count and calculate the FPKM, remove the genes with zero expression and conduct the consistency analysis. RNA targeted sequencing was highly consistent with the results of high-depth RNA-Seq expression amount.

Higher sensitivity in detecting fusion genes

Table 13. Detection results of fusion standards on different gradient

Sequencing method	Dilution rate	BCR - ABL1 Fusion			ETV6 - RUNX1 Fusion		
		Input copy number	Average Unique Reads	Conclusion	Input copy number	Average Unique Reads	Conclusion
RNA target sequencimg	1 time	13400	890.3	Detection	8800	250.5	Detected
	2 times	6700	407.5	Detected	4400	132.0	Detected
	4 times	3350	214.0	Detected	2200	79.5	Detected
	32 times	419	63.5	Detected	275	12.5	Detected
	128 times	105	24.5	Detected	68	3.5	Detected
	256 times	52	11.0	Detected	34	2.5	Detected
	512 times	26	2.5	Detected	17	0	Not Detected
RNA-Seq	4 times	3350	0	Not Detected	2200	0	Not Detected

Note：The fusion detection results of RNA fusion standards under gradient dilution. Introduce the Fusion gene RNA standard BCR(E14)-ABL(E2)-P210 Fusion (Cobio, CBP20031R, ddPCR reference value 134 copies/ng) and ETV6-RUNX1 Fusion (Cobio, CBP20091R, ddPCR reference value 88 copies/ng) 100 ng for library construction, Illumina NovaSeq 6000 PE150 sequencing after hybridization capture, 3 Gb raw bases, 2000×. When diluted to 256 times, the TargetSeq® Hema Tumor Fusion RNA Panel can still detect fusions stably.

Gene List

Cover transcripts of 141 major genes

ABL1	*ABL2*	*AFDN*	*AFF1*	*ALK*	*AP2A2*	*ARID1B*	*ATF7IP*	*BCL11A*	*BCL2*	*BCL6*	*BCL9*
BCOR	*BCR*	*BCS1L*	*BIRC3*	*BMP2K*	*CALM2*	*CBFA2T3*	*CBFB*	*CDK5RAP2*	*CD28*	*CHD6*	*CPSF6*
CREBBP	*CRLF2*	*CSF1R*	*CTLA4*	*DAZAP1*	*DEK*	*EBF1*	*ELL*	*EP300*	*EPOR*	*EPS15*	*ERG*
ETV6	*EWSR1*	*FGFR1*	*FIP1L1*	*FOXJ2*	*FOXO4*	*FUS*	*GLIS2*	*GTF2I*	*HLF*	*HNRNPUL1*	*HOXA11*
HOXA13	*HOXA9*	*HOXC11*	*HOXD13*	*HRASLS5*	*IKZF1*	*IL2RB*	*IQGAP2*	*IRF2BP2*	*ITK*	*JAK2*	*KDM5A*
KDM6A	*KIF5B*	*KMT2A*	*KMT6A*	*LMBRD1*	*MBTD1*	*MECOM*	*MEF2D*	*MLF1*	*MLLT1*	*MLLT10*	*MLLT11*
MLLT3	*MLLT6*	*MNX1*	*MRTFA*	*MYB*	*MYC*	*MYH11*	*MYH9*	*NABP1*	*NCOA3*	*NID2*	*NPM1*
NSD1	*NTRK3*	*NUMA1*	*NUP214*	*NUP98*	*P2RY8*	*PAX5*	*PBX1*	*PDGFRA*	*PDGFRB*	*PHF21B*	*PMEL*
PML	*PPFIBP1*	*PRDM16*	*PRDX1*	*PRKAR1A*	*PRRX1*	*PTK2B*	*RANBP2*	*RARA*	*RARG*	*RBM15*	*RCSD1*
RPL22	*RPN1*	*RUNX1*	*RUNX1T1*	*SEPTIN6*	*SET*	*SNX2*	*SS18*	*SSBP2*	*STAG2*	*STAT3*	*STAT5B*
STIL	*STRN*	*STRN3*	*SYK*	*SYNRG*	*TAF15*	*TAL1*	*TBL1XR1*	*TCF3*	*TERF2*	*TNIP1*	*TPR*
TRIM24	*TSLP*	*TYK2*	*ZBTB16*	*ZC3HAV1*	*ZEB2*	*ZMIZ1*	*ZMYND11*	*ZNF384*			

Product Information

Product Name	Spec.	Cat.
Hema Tumor Fusion RNA Panel	24/96 rxn	PH2008285/PH2008282
IGT® Fast Stranded RNA Library Prep Kit v2.0	96 rxn	C10032
IGT® Adapter & UDI Primer 1-96*	96 rxn	C10042
TargetSeq One® Hyb & Wash Kit v3.0*	24/96 rxn	C10332
TargetSeq® Eco Universal Blocking Oligo*	24/96 rxn	C80502
TargetSeq® Cap Beads & Nuclease-Free Water*	5 mL each	C10422

**IGT® can provide kits compatible with Illumina, MGI etc., as well as universal reagents corresponding to each platform.*

Lymphoma SV Panel

Product Overview

Coverage Size	7.7 Mb
Coverage	This product replaces the traditional FISH method with probe capture technology, encompassing IGH category conversion area involved in common structural variations and providing encryption coverage of the MTC regions of genes such as MYC, BCL2, and BCL6.
Detection range	SV
Data	1 Gb raw bases (Recommended)
Applications	In high-grade B-cell lymphomas, recombination of genes such as MYC, BCL2, or BCL6 with the super-enhancer (IGH) lead to oncogene overexpression and/or amplification, giving rise to a distinct subgroup characterized by high aggressiveness and poor prognosis.

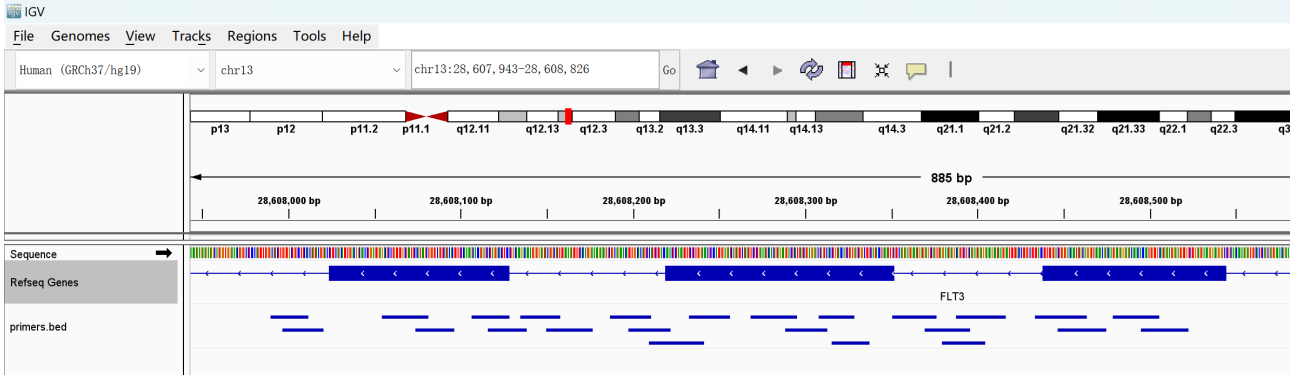
Product Information

Product Name	Spec.	Cat.
Lymphoma SV Panel	24/96 rxn	PH2001705/PH2001702

**IGT® can provide kits compatible with Illumina, MGI etc., as well as universal reagents corresponding to each platform.*

FLT3-ITD Primer Pool

The FLT3-ITD mutation is one of the common pathogenic mutations in AML, playing a crucial role in prognosis and targeted therapy guidance for hematological tumor. To address this, our approach utilizes multiplex amplicon sequencing technology combined with a unique primer design strategy, incorporating the entire region from intron 13 to exon 15 into the target area. By enabling random amplification, this method enhances detection sensitivity to accurately identify both known and unknown ITD mutations occurring on exons 14-15.



Product Information

Product Name	Spec.	Cat.
MultipSeq® Library Prep Kit (200)*	96 rxn	M61022
IGT® UDI Primer 1-96 (10 μM each, for Illumina, plate)	96*1 rxn	C80202
MultipSeq® FLT3-ITD Primer Pool (for Illumina TS)	24/96 rxn	PA6004125/PA6004122

* There are multiple different versions of the MultipSeq® Library Prep Kit. Only 200 versions are directly sold. The version selection is up to the Panel, etc. The customized version and the standard product of the MultipSeq® Library Prep Kit may be different. Please select according to the Panel.

TP53 Primer Pool

As a critical tumor suppressor gene in humans, TP53 not only prevents tumor cell division, induces apoptosis but also repairs damages of normal DNA. By detecting TP53 genotypes, this test can assess the individual's genetic predisposition to cancer, provide personalized guidance, and help reduce the risk of cancer development. Therefore, this product targets the CDS region of TP53 gene and uses multiplex amplicon sequencing technology combined with NGS to enable efficient, convenient, and rapid detection of TP53 gene mutations.

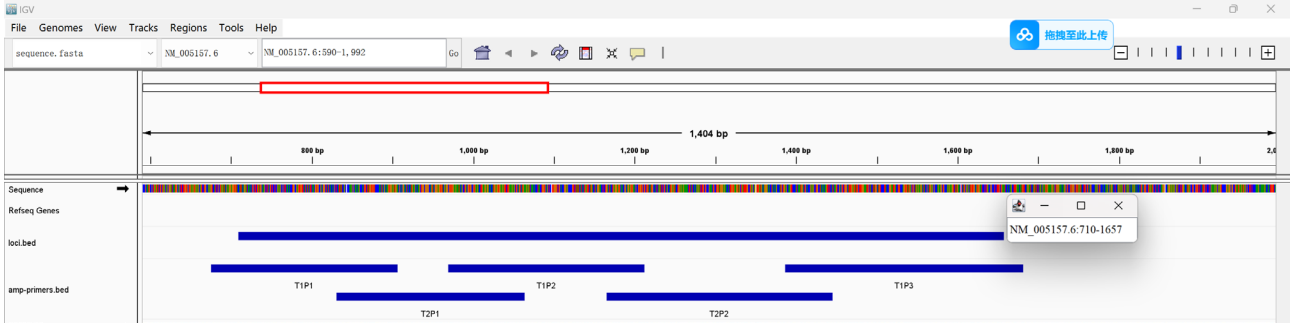
Product Information

Product Name	Spec.	Cat.
MultipSeq® Library Prep Kit (200)*	96 rxn	M61022
IGT® UDI Primer 1-96 (10 μM each, for Illumina, plate)	96*1 rxn	M80202
TP53 Primer Pool (for Illumina TS)	96 rxn	PA6005332

* There are multiple different versions of the MultipSeq® Library Prep Kit. Only 200 versions are directly sold. The version selection is up to the Panel, etc. The customized version and the standard product of the MultipSeq® Library Prep Kit may be different. Please select according to the Panel.

BCR-ABL1 Primer Pool

Tyrosine kinase inhibitors (TKIs) have become a critical component of first-line treatment for chronic myeloid leukemia (CML). However, some patients still develop primary or secondary resistance, with BCR-ABL1 kinase domain mutations being the main mechanism of resistance. Studies show that more than half of CML patients resistant to imatinib, nilotinib, or dasatinib test positive for BCR-ABL1 kinase domain mutations. Consequently, both ELN and NCCN guidelines recommend mutation testing when CML patients exhibit suboptimal response or treatment failure.



Product Information

Product Name	Spec.	Cat.
MultipSeq® Library Prep Kit (200)*	96 rxn	M61022
IGT® UDI Primer 1-96 (10 μM each, for Illumina, plate)	96*1 rxn	M80202
BCR-ABL1 Primer Pool (for Illumina TS)	96 rxn	PA6006592

* There are multiple different versions of the MultipSeq® Library Prep Kit. Only 200 versions are directly sold. The version selection is up to the Panel, etc. The customized version and the standard product of the MultipSeq® Library Prep Kit may be different. Please select due to the Panel.

Extraction Kit

Product Name	Spec.	Cat.
Magnetic Beads Based Large Vomule Circulating Free DNA Extraction Kit	20/50 rxn	E10018/E10011
Magnetic Beads Based Universal Nucleic Acid Extraction Kit	50/200 rxn	E10211/E10212
Magnetic Beads Based FFPE DNA/RNA Co-extraction Kit	50/200 rxn	E10061/E10062
Magnetic Beads Based FFPE RNA Extraction Kit	50/200 rxn	E20031/E20032
Magnetic Beads Based Tissue & Nucleic Acid Co-extraction Kit	50/200 rxn	E20041/E20042
Magnetic Beads Based DNA/RNA Product Recycle and Purification Kit	50/200 rxn	E10131/E10132
Magnetic Beads Based Blood Nucleic Acids Fast Extraction Kit	50/200 rxn	E10151/E10152
Magnetic Beads Based Formaldehyde Tissue Nucleic Acid Extraction Kit	50/200 rxn	E10161/E10162
Magnetic Beads Based Blood RNA Extraction Kit	50 rxn	E20021

References

Cancer gDNA Reference Standard

Cancer gDNA Reference Standard uses human-derived cell lines as raw material with a single, well-characterized genomic background, covering the drug target of common solid tumors, including 15 hot spot mutations (11 SNV, 1 InDel, 1 copy number amplification, 1 fusion and 1 MET Exon 14 Skipping Mutation), precisely quantified by digital PCR. This product can be used to establish and improve the somatic mutation detection and indoor quality control of NGS method.

Product Name	Form	Spec.	Cat.
Cancer gDNA Reference Standard	gDNA	30 ng/μL，1 μg/tube	PCS500

RNA Fusion Mix 3.0

The main component of RNA Fusion Mix 3.0 is a mixture of purified RNA fragments and cell line-derived RNA, including 23 fusion forms, fully covering the fusion genes appliable to targeted drug, multiple breakpoints and partner genes. Since RNA-NGS has shown excellent performance in fusion variant detection, it has been included in *NCCN Clinical Practice Guidelines for NSCLC*, *NCCN Clinical Practice Guidelines for Colon Cancer*, *Chinese Expert Consensus on NGS of Bone & Soft Tissue Tumors* etc. DNA + RNA co-detection is gradually becoming a trend, accurate detection of gene fusion is of great significance for the treatment and comprehensive understanding of tumor. This product can be used to validate fusion variant detection performance of RNA-NGS and indoor quality control.

Product Name	Form	Spec.	Cat.
RNA Fusion Mix 3.0	RNA	50 ng/μL, 1 μg/tube	MD07361

Hematologic tumor gDNA standard quality control products

Hematologic tumor gDNA standard uses human-derived cell line as raw materials, the quality control products contain 34 hotspot genetic variations (18 SNVs，15 Indel and FLT3-ITD variation). Precise quantification through digital PCR, applying to the assessment and verification of various variant forms. This product can be used to establish and improve the performance of somatic mutation detection by NGS methods as well as indoor quality control.

Product Name	Form	Spec.	Cat.
Hematologic tumor gDNA standard	gDNA	1 μg/tube	MD030064

MRD ctDNA reference standard

MRD ctDNA reference standard uses human-derived cell line as raw material, obtaining four variation levels (0.5%, 0.05%, 0.005%, 0%) via manual fragmentation of mixed DNA, simulation and dilution of ctDNA, quantified by NGS panel or digital PCR. This product covers common drug targets of lung cancer, colorectal cancer and breast cancer, including total 26 hotspot mutations: 18 SNV, 5 InDel (del1bp/2 bp/15bp; ins9bp/12bp), 2 fusions and 1 MET Exon 14 Skipping mutation. This product can be used to validate MRD detection and indoor quality control of NGS method.

Product Name	Form	Spec.	Cat.
MRD ctDNA reference standard	cfDNA	20 ng/μL，500 ng/tube	MD080719

Bioinformatic analysis of data and interpretation solution

The automated analysis report system for genetic testing can directly connect to offline data and automatically analyze and interpret the generated reports. The entire process is fully automated and intelligent, no need for on-site personnel. This significantly improves operational efficiency, shortens the R&D cycle, and reduces labor costs. Additionally, effective accumulation of clinical testing data is conducive to data mining. It also supports precision treatment of tumors, analysis of pathogen infections and pathogenic genes of genetic diseases.

Advantages

Multi-functional：Compatible with main sequencing platforms, covering multiple modules such as bioinformatic analysis etc., rich in annotation and clinical reporting functions.

Flexible workflow customization：Pre-set workflows for multiple research fields, which can be flexibly optimized or locked without advanced professional skills.

Simple and efficient operation：One-stop report with one-click generation, fully automated process, easy operation, and supports customization

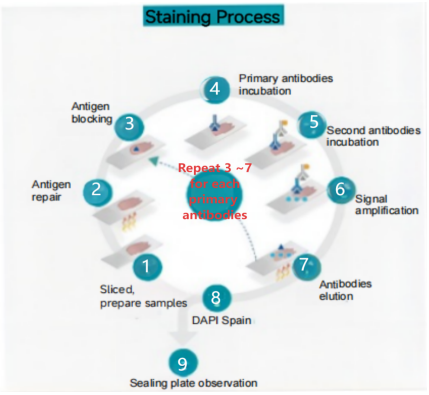
Safety specification guarantee：Locally generated and stored report, with third-level information security protection, strict permission control, and real-time monitoring throughout the entire process.

mIHC Integrated Solution

Multiplex fluorescence immunohistochemical technique (mIHC) can perform staining of multiple markers in a single FFPE section, meantime, conduct parallel detection of cells from multiple biological tissue samples, and collect information such as cell types, density, and spatial positional relationships in each tissue region. The mIHC integrated solution is based on the Krast automatic staining machine and KR-HTS scanner. It can customize detection plans according to different biological tissue samples, verify the target genes obtained from the customer's existing multi-omics data, and achieve high-throughput immunofluorescence quantitative analysis of 3 ~ 9 colors.

3 color/4 color/5 color/6 color/7 color/8 color/9 color fluorescence chromogenic kit

3 color/ 4 color/ 5 color/6 color/ 7 color/8 color/9 color fluorescence chromogenic kit



Fully automatic immunohistochemical staining machine

* Compatible with both traditional mmunohistochemistry and multiplex fluorescence immunohistochemistry staining
* One click completion of the entire process from baking, dewaxing, antigen remediation to re-staining
* 1-30/60 pieces operate flexibly
* Different slide slots are independently programmed and operated on their own
* Patented technology ensures thorough reaction and cleaning, better staining effect
* Minimum sample input can be reduced to 80 μL, cost-saving

High-throughput fluorescence digital pathology scanner

* Certified: A multispectral scanner independently developed in China and led in obtaining the registration certificate for Class II medical devices
* Precise: Accurately subtract the autofluorescence of the tissue and spectral spliting the staining signal of 9-color image
* Efficient: Simultaneously detect 7-9 biomarkers on a single slice to save precious samples
* Intelligent: Fully automatic unattended operation, 80 pieces of high-throughput ultra-high-speed scanning
* Fast: A full-frame scan completed within 12-15 mins

Innovative Gene-industry Turbo-engine

iGeneTech Bioscience Co., Ltd.
Website: www.igenetech.com
Email: sales@igenetech.com
Tel: 010-89146623
Add of Head Quarter: F7, Building 1, No.1A Chaoqian Rd, Science and Technology Park, Changping District, Beijing 100000, CN
Add of Jiaxing Subsidiary: Building 2, No. 371 Hongye Road, Dayun Town, Jiashan County, Jiashan City, Zhejiang 314100, CN

Follow us on Wechat

For Research Use Only. Not for use in diagnostic procedure.

Copyright: This brochure is the copyright of iGeneTech Bioscience Co., Ltd. and its subsidiaries. No other person or organization may reproduce, copy, edit or translate the contents of this brochure into other languages in any form without the written permission of iGeneTech Bioscience Co., Ltd. All trademarks or logos in this brochure are the property of iGeneTech Bioscience Co., Ltd.

Doc. NO.：PMM250702
Version：A.0