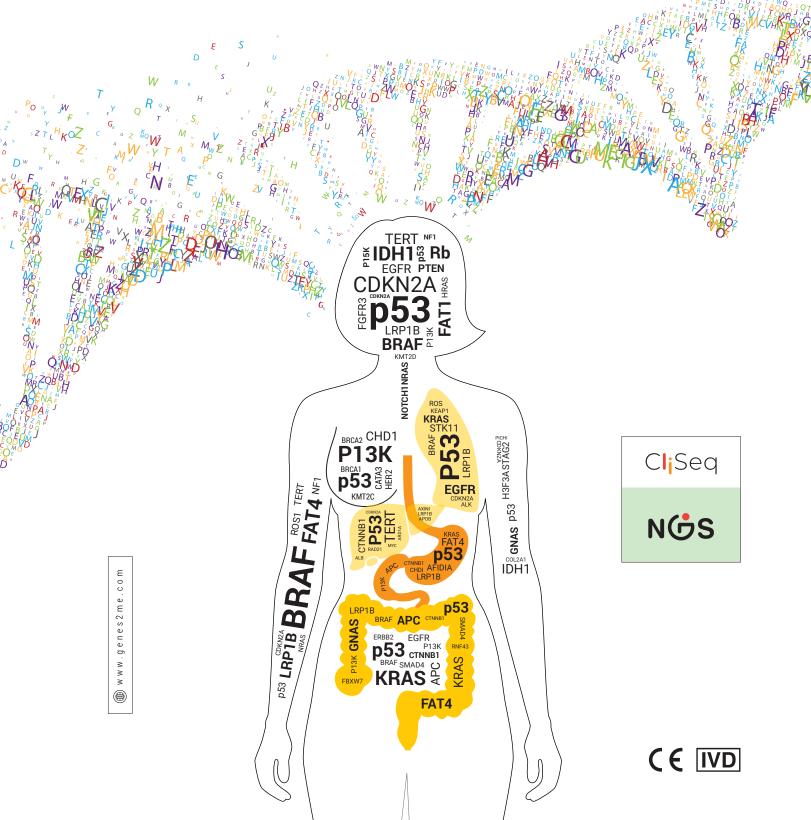




Cancer GenomicProfiling









PAN Cancer Panel





Pan Cancer Panel is an NGS panel aimed to screen a range of cancer causing genes to identify somatic mutations in DNA & RNA from human clinical samples like FFPE and fresh tissue targeting 681 genes covering all the coding sequences enriched by Hybridization capture-based target enrichment.

Genes are selected based on ACMG, AMP, NCCN and ASCO guidelines to uncover the coding region to screen a range of cancer types. The genomic DNA & RNA from the FFPE or fresh tissue is considered for library preparation and enrichment that further can be sequenced on NGS sequencer. This panel detects all variant types and immune-oncology markers (TMB, MSI, HRR) which are crucial for cancer immunotherapy.

This panel covers major mutation types like SNVs, Indels, CNV and covers the DNA and RNA fusions as well. Results of the assay are used as an aid in identifying related cancer variants in combination with a patient's clinical indications. The panel is also designed to detect Epstein-Barr virus (EBV) & Human Papilloma Viruses (HPV), allowing for the comprehensive analysis of cancer-associated genes



Cancer-associated Biomarkers

- TMB, MSI, HRR & Fusion genes
- Uniform Depth Coverage
- Best On-Target Ratio
- Low Bias Base Call
- Less duplication rates
- Short Hybridization time of approx 4 hours
- Rigorously engineered to target hard to capture regions

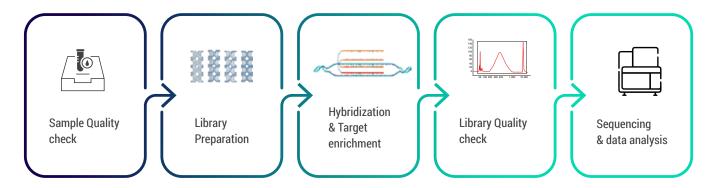
No. of Genes	681 (DNA) + 105 (RNA)
Gene Count / Family	524
Covered Region	Whole CDS, Hotspots, Fusion Genes
Target Size	~1.7 Mb
Mutation Type	SNV/ InDels / CNV
Biomarkers	TMB, MSI, HRR Genes
Sample Type	FFPE & Fresh Frozen Tissue

no

PROCESS WORKFLOW

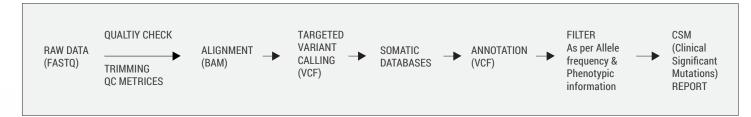
Platform Agnostic

Compatible on multiple platforms (Illumina, Thermo Fisher, Element Biosciences, MGI)



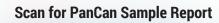
Bioinformatics Solution

Data Analysis and Interpretation using Genes 2Me Cliseq Interpreter plaftform



After raw data generation, we follow the GATK best practices framework for identification of variants in the sample, starting with raw data quality check using the FastQC followed by BWA read aligner for mapping/aligning to human reference genome GRCh38. After the alignment, GATK Mutect2 algorithm is used for variant calling. Annotation of the variants is performed using open-source available software SnpEff.

Further relevant mutations are annotated using published variants in literature and set of diseases databases – ClinVar, OMIM, COSMIC and HPO. The 1000Genome, gnomAD, dbSNP databases are used for annotation of variants for their minor allele frequency. The dbNSFP database is used for annotation and functional prediction of all potential non-synonymous variants.









- Cloud based (CPU) analysis Software
- Global Software Access
- Strong customer Data Security

PANEL PERFORMANCE

Features	Illumina	мді	Thermo Fisher
Coverage uniformity (%)	>98	>98	>84
Precision (%)	>95	>96	>89
Reproducibility (%)	97	97	95
On Target Ratio (%)	86-95	85-95	74-85
*Analytical sensitivity (%)	98.6	96	93
*Analytical specificity (%)	99	100	98
*Repeatability (%)	96	96	94
*Limits of detection and VAF (%)	1	1	1

*Note :- This data has been calculated from a sample number size of 92 samples

VAF - Variant Allele Frequency

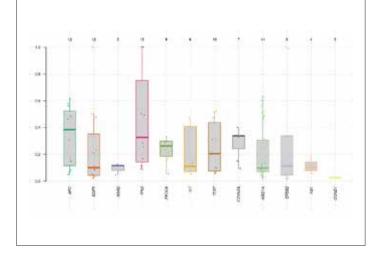
Number of Genes covered in G2M CGP panel vs the Competitor CGP panels



The above illustration shows a Venn diagram comparison for number of genes covered by G2M vs by other competitor companies in their CGP panels. For instance, in figure (a), G2M covers 378 unique genes when compared to 18 unique genes of the competitor company. They both have an overlap of 303 genes.

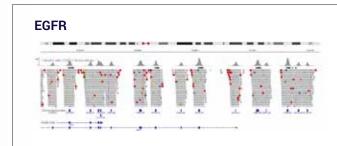
VAF PLOT

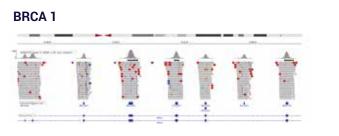
VAF is the percentage of sequence reads observed matching a specific DNA variant divided by the overall coverage at that locus. This VAF plots shows, the top 8 out of 12 genes that were detected under median value 1-20% VAF.



Coverage across Genes

The below mentioned plots showcase the coverage across the exonic regions of BRCA 1 and EGFR genes, two most important genes in Cancer. The plots show how uniformly our panel covers the exonic regions of the EGFR and BRCA1 gene.







	l	<u> </u>	<u> </u>	2	<u> </u>
Colorectal Cancer	Breast Cancer	Ovarian Cancer	Bladder Cancer	Lung Cancer	Oesophagus Cancer
→RAS →EGFR →TGF →ATM	→BRCA 1 →BRCA 2 →PTEN →TP53	→CHEK2 →TP53 →BARD1 →KRAS	→TP53 →RB1 →HRAS →PIK3CA	→EGFR →KRAS →ALK →RET	→ERBB2 →EGFR →RB1
→BRAF →CHEK2 →NRAS →PIK3CA →PTEN →TP53	→ CHEK2 → BRIP1 → ATM → PALB2 → PIK3CA → PMS2 → ESR1	→RAD51 →BRIP1 →PALB2 →BRAF →ERBB2 →PTEN →PIK3CA	→FGFR3 →ATM →MTOR	→PIK3CA →EGFR →KRAS →MET →PTEN →RET →BRAF	
<u> </u>	→FGFR1	→BRCA1	Q	→ERBB2 →ALK	0
Prostate Cancer	Pancreatic Cancer	Thyroid Cancer	Cervical Cancer	Liver Cancer	Gastric Cancer
→BRCA 1 →HOXB13 →AR →ATM →MYC →PTEN	→BRCA 1 →BRCA 2 →EGFR →HRAS →KRAS →PALB2	→BRAF →RAS →RET →TP53 →PTEN	→DICER1 →MED1 →HLA-A →PI3K →MAPK	→TP53 →CDKN2A	→APC →MLH1 →MSH2 →MSH6 →EPCAM

^{*}Limited Cancer Gene list presented here

→BRCA2

The Genes2Me Pan Cancer Panel screens broad range of cancer causing genes to identify somatic mutations in the tumor tissue.

It provides comprehensive detail of the cancer and recommendations regarding the FDA approved drugs, helps to decide the best course of treatment.



Scan for PanCan Gene List

Gene & Drug Recommendations

TYPE OF CANCER*	GENE	DRUG
Gilioma, Acute Myeloid Leukemia	IDH1	Olutasidenib
Breast Cancer, Ovarian Cancer	BRCA1	Olaparib
NSCLC, Colorectal Cancer	EGFR	Osimertinib
Colorectal Cancer, NSCLC	KRAS	Cetuximab
NSCLC, Melanoma, Metastatic Colorectal Cancer	BRAF	Encorafenib
Follicular Lymphoma Tumor	EZH2	Tazemetostat
Medullary Thyroid Cancer, Thyroid Cancer	RET	Selpercatinib
Prostate Cancer	BRCA2	Niraparib
Breast Cancer, Gastroesophageal Cancer	ERBB2	Trastuzumab
Non-Small Cell Lung Cancer	ALK	Alectinib
Esophageal, colorectal, Lung cancer	TP53	Venetoclax
Breast Cancer, Ovary, stomach cancer	PIK3CA	Alpelisib
Gastrointestinal Stromal Tumors, glioblastoma, melanoma	PDGFRA	Avapritinib
Urothelial Cancer, multiple myeloma, bladder cancer	FGFR3	Erdafitinib
NSCLC, Metastatic cancer	MET	Capmatinib
Myeloma , lung adenocarcinoma, colon adenocarcinoma, nelanoma, breast carcinoma	PDGFRB	Imatinib Mesylate
Acute Myelogenous Leukemia, Bone Marrow cancer	FLT3	Quizartinib
Aggressive Systemic Mastocytosis, lung adenocarcinoma,	KIT	Imatinib
colon adenocarcinoma	ESR1	Elacestrant
Breast Cancer, endometrial and prostate cancer Solid Tumors, lung cancer, colorectal cancer	NTRK1	Entrectinib

^{*}Limited cancer type details mentioned

ORDERING INFORMATION

Commercial Name	Cat No.
PAN Cancer Panel	G2MPC06001-ill; G2MPC06001-TF; G2MPC06001-MG

06

Automate your

NGS Libraries with

EZY-AutoPrep-48

Construct upto 48 sample libraries in one run

Construct upto 48 Sample Libraries in one run



Built to streamline the intricate process of sample preparation for NGS, our platform combines state-of-the-art technology with user friendly design to empower your library preparation experience



Flexible Matching Experiment Needs



Multiple Functional Modules



Efficient Contamination Prevention



Simple Operation, Get Started Quickly



Simple Operation, Get Started Quickly



Precise Pipetting



Genes2Me Pvt. Ltd.

1105, 11th Floor, Tower B, SAS Tower, Medicity, Sector - 38, Gurgaon - 122 001, Haryana, India

Tel: + 91 18001 214030 / + 91 88000 23600 E-mail: contact@genes2me.com

www.genes2me.com

