Lymphoma DNA Panel

HoopBio

Panel of 60 genes created for and by experts in clinical diagnosis.
Allows the analysis of key biomarkers (including NOTCH1 3'UTR) applicable for the study of a range of lymphoid neoplasms, including both B and T cell lymhpomas.

Determination of lymhphoid neoplasms by massive sequencing

GENES STUDIED IN THE PANEL

Leukemia Chronic Lymphocytic	Intravascular Large B-Cell Lymphoma	High-Grade B Cell Lymhpoma Double-Hit/ Triple-Hit	B-Cell Expansion With Nfkb And T-Cell Anergy	Other Genes to analyze according comparative criteria
RPS15	BCL6	BCL2	CARD11	KRAS
TP53				HRAS
SAMHD1				
MEF2B				
SF3B1				
XPO1				
Non-Hodgkin B cell Lymphoma	**Follicular Lymhpoma**	**Leukemia Lymphoblastic**	**Myeloproliferative Neoplasm**	**Diffuse large B cell lymphoma**
EP300	EZH2	PAX5	PIM1	CXCR4
ID3	MAP2K1	ETV6	DIS3	CDKN2A
SMARCA4	BTK		PRDM1	B2M
	ARID1A			SOCS1
Angioimmunoblastic T-cell lymphoma		**Acute myeloid leukemia**	**Acute lymphoblastic leukemia**	STAT6
IDH2		DIS3	CCND3	FOXO1
		STAT5B		

Categorization of lymphoid malignancy samples (including both B and T cell lymphomas) across 60 key DNA targets

Technical informations

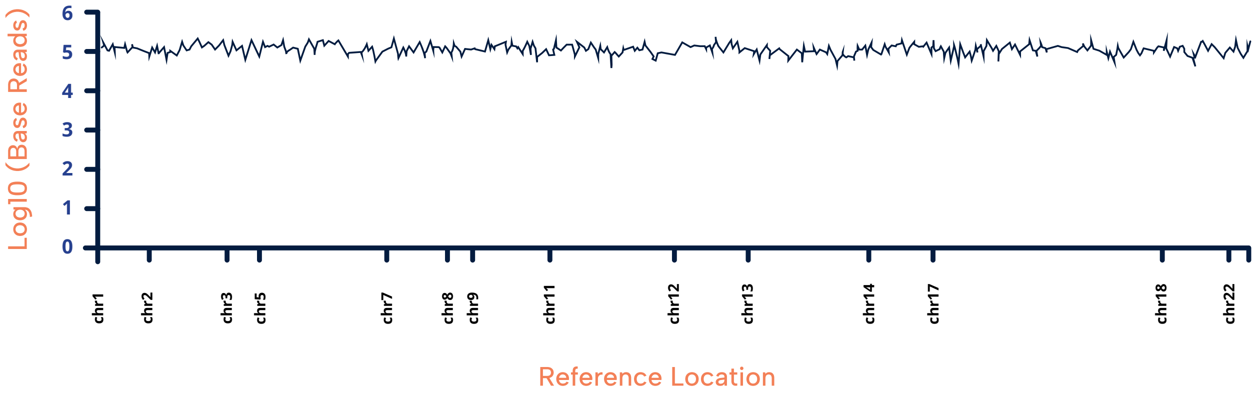
- Starting sample: blood
- 1M readings per sample
- 119bp medium amplicon size
- Covers the exonic region of 60 genes
- + 10bp of intronic region
- Great uniformity of readings
- Starting quantity: 10ng

Study of:

- Mutations
- Insertions
- Deletions
- CNVs (It allows to develop a specific laboratory baseline for CNV detection)

www.hoopbio.com

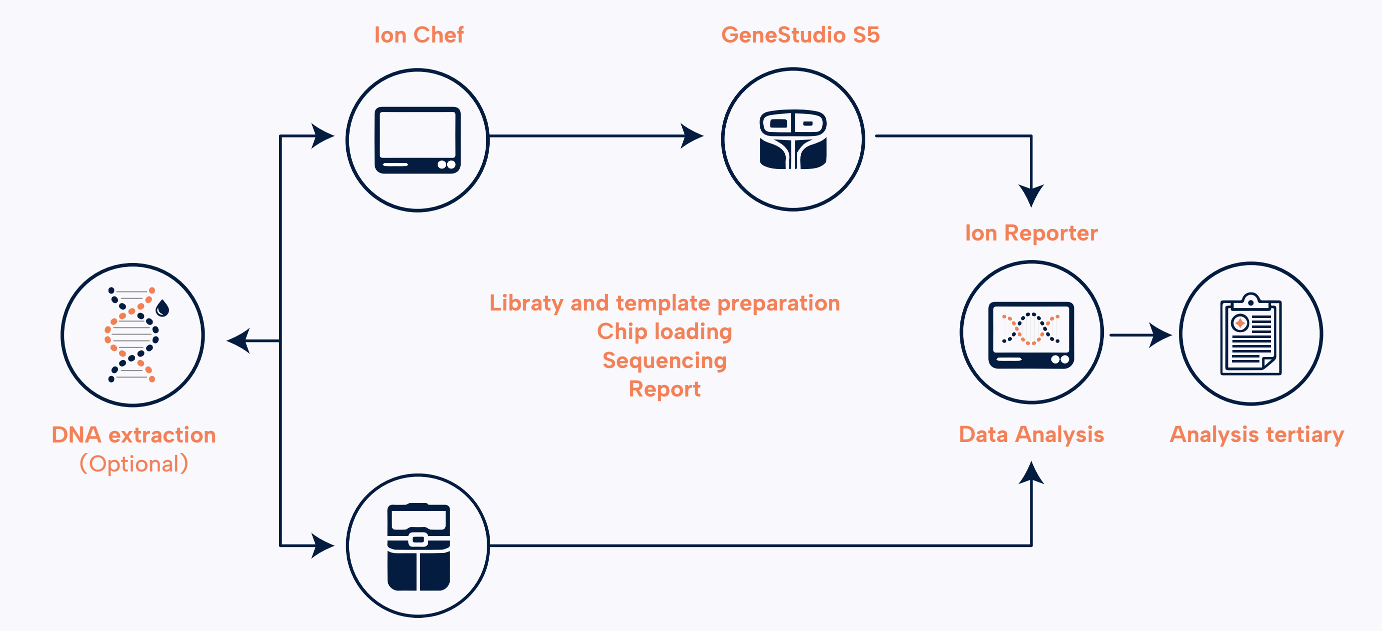
CE RUO ISO 13485



Coverage Overview

The perfect combination of EasyNGS HC + Ion Torrent

- **From DNA to variants call:**
- 3 days with S5+Ion Chef
- 1 day with Genexus
- **Automated library prepartion**
- Consistant results
- Error limitation
- **Workfow validated with tertiary Software**
- **Panel and workfow verified by end users**
- **Flexibility with 5 diferent chips** (from 2M to 130M reads)



Ion Chef

GeneStudio S5

Ion Reporter

Libraty and template preparation
Chip loading
Sequencing
Report

DNA extraction
(Optional)

Data Analysis

Analysis tertiary

- Amplicon insert length: 199pb (67-140b)
- Panel size: 158,2 kB
- Average mean uniformity: 92.43%
- Average mean depth: 2347X
- Average mean coverage: 2200X
- % Amplicons > 100X: 97,75%
- % Amplicons > 500X: 90,47%
- Number of reads per sample: 3M

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