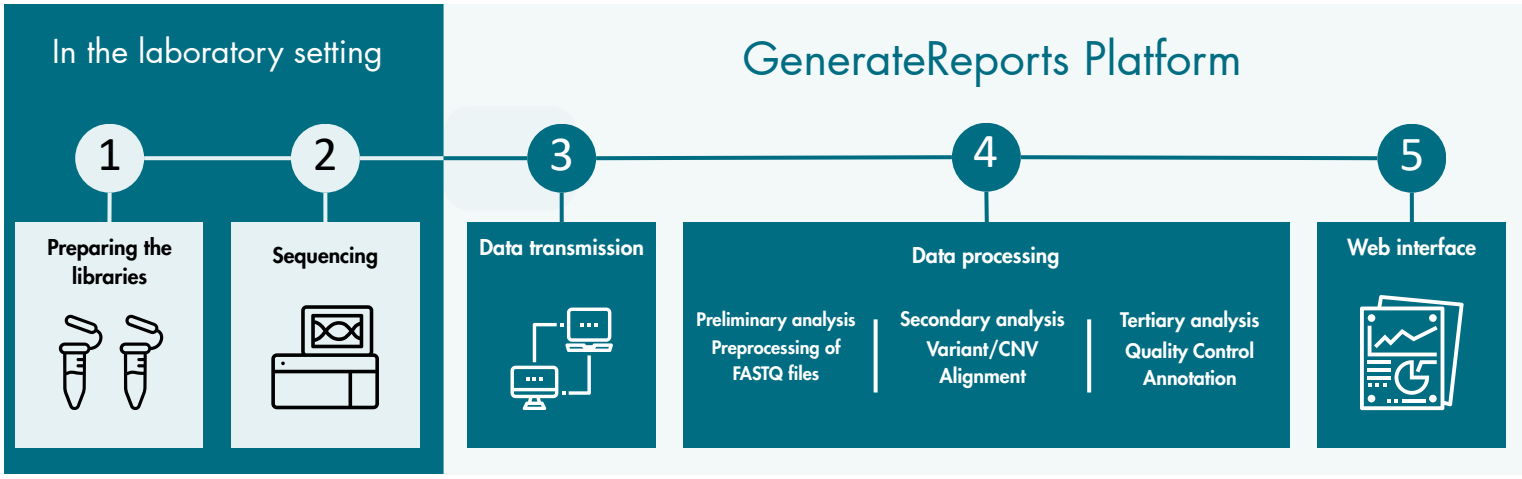
G&R | GENERATE REPORTS

Genexpath

For the analysis of your new generation sequencing data

The GenerateReports bioinformatics platform analyzes and interprets high-throughput sequencing data derived from raw inputs. The processing encompasses data **quality control, variant** detection and annotation, as well as **gene copy** estimation**.**
For enhanced monitoring, elements of **experimental traceability** are maintained on the platform.
For each generated sample, the main results are **accessible and interpretable.**

A comprehensive bioinformatics solution



Analytical instruments

GenerateReports' web interface facilitates daily sample analysis and enables retrospective exploration of sequencing data. This exploration can occur at multiple levels: project, patient cohort, run, sample, gene, or variant.

The capacity to generate **lists of variants** facilitates **automated analyses** that enable comparisons of results from multiple samples, from a diagnosis/relapse pair, or the execution of differential analyses between healthy and tumor tissue.

Library Compatibility	QIAseq (QIAGEN) AmpliSeq (Illumina) For inquiries regarding other libraries, please reach out to us.		SureSelect (Agilent), Twist (Twist Biosciences)	
Sequenced data type	Genes panels Whole Exome Sequencing (WES) Whole Genome Sequencing (WGS)			
Type of variants identified	Single Nucleotide Polymorphisms (SNPs) Insertion and Deletion (INDEL) Mid-sized INDEL (~100 bp) Panel/exome/whole genome Copy Number Variants (CNVs)			
Sequencer compatibility	Illumina® Sequencers Thermo Fisher ION S5 Sequencers			
Supported data formats	FASTQ format			
Databases used	1000G ExAC ESP6500siv2 CG46			
Prediction scores utilized	ADA Score RF Score Score SIFT Score PolyPhen	LRT MutationTaster MutationAssessor FATHMM	PROVEAN VEST3 MetaSVM MetaLR	MCAP CADD fathmm_MKL_coding GERP InterPro_domain

Benefits

- Examination of your areas of interest
- Analyzing libraries utilizing UMI
- Extensive array of compatible kits
- Downloadable datasets
- Comprehensive bioinformatics analysis
- Utilization of advanced algorithms
- Automated analysis modules
- No supplementary computer hardware

Communications

- Delfau-Larue MH et al., P1123: Early ctDNA clearance following CAR T-cell infusion predicts outcomes in patients with large B-cell lymphoma: results from ALYCANTE, a phase 2 LYSA study. Hemasphere. 2023 PMCID: PMC10430960.
- Camus V et al. High expression of PDL1/PDL2 genes correlates with poorer outcomes in primary mediastinal large B-cell lymphoma. Blood Adv. 2023 PMID: 37862676
- Camus V et al. Circulating tumor DNA in primary mediastinal large B-cell lymphoma compared to classical Hodgkin lymphoma: a retrospective study. Leuk Lymphoma. 2022 PMID: 35075971
- Bohers E et al., Non-invasive monitoring of diffuse large B-cell lymphoma through high-throughput targeted sequencing of cell-free DNA: analysis of a prospective cohort. Blood Cancer J. 2018 PMID: 30069017

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