

Lentiviral Integration Sites Analysis

Advantages

- Multiplex samples for cost-effective results
- · Effective workflow and fast turnaround time
- · Multiple approaches to meet different goals
- Qualitative and quantitative analysis
- Comprehensive bioinformatics analysis



The Introduction of Lentiviral Integration Sites Analysis

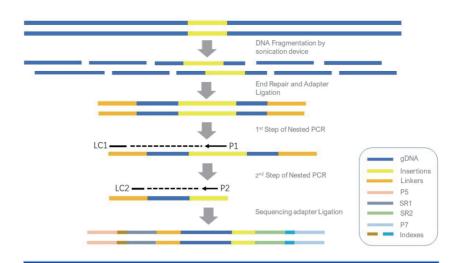
Lentiviral vectors are the most common gene delivery vehicles used for stable genetic modification in cells. These vectors are integrated into the host genome to express therapeutic transgenes. Although this integration appears random, literature has suggested that there are in fact hotspots for lentiviral integration. To avoid deleterious effects on cellular functions (e.g., integration near oncogenes or within key genes), it is important to identify the exact integration sites of lentiviral vectors after cells have been infected. Integration site analysis is the key tool to assess the biosafety of vectors for gene therapy and the clonal tracking fate of genetically modified cells *in vivo*.

CD Genomics has developed a comprehensive set of tools for viral integration site analysis by combining PCR and sequencing-based approaches with proprietary bioinformatics pipelines. We are able to identify the position of integration sites and determine the integration frequency of viral vectors with unmatched precision and sensitivity. Through our end-to-end services, we are committed to providing the highest quality data and the most reliable analysis.

Method	Sample Requirement	Sequencing Strategy	Data Output	Application	
LM-PCR	1x10^6 cells	Illumina PE150	1 Gb	For CAR-T cell genome	
Whole genome sequencing	or >500 ng gDNA	illuriiria PE130	≥150 Gb	For monoclonal cell line	

Workflow

A. Schematic diagram of LM-PCR library construction



Bioinformatic Workflow

Data Quality Control Mapping IS Detection IS Annotation Advanced Analysis

Raw Data Clean Data Mapping Integration Site Basic Annotation Preference Analysis

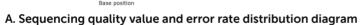
#Date Size #Base Quality #Base Content #Mapping Rate #Coverage #Peak Dist.

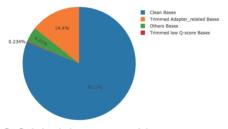
Statistics of Annotation Advanced Analysis

B. Bioinformatics analysis flow chart

Demo Results

Base Quality and Error Rate Distribution Plot(coh003_Data_L1)

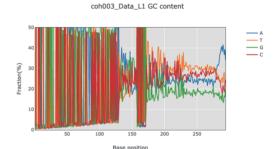




C. Original data composition

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4	chrl	971676	971722	LTR:26	intronio	AGRN				LTR:733jchr1:971717	16174	1439
6	chr1	974070	974370	LTR:35	intronio	AGRN			- 4	LTR:733(chr1:974277	18568	1127
8	chr1	976521	976821	LTR:5	expric	AGRN		Name=CpG: 351		LTR:733jchr1:976560	21019	0
7	chr1	1048199	1048499	LTR:32	intronic	Ctorf159				LTR:733 chr1:1046261	3237	1860
8	chrl	1074221	1074521	LTR:4	noRNA_intronio	LINO01342				LTR:733johr1:1074414	1825	1375
9	chr1	1066968	1086988	LTR:30	interponio	LINC01342;MIR200B	dist=7234;dist=15516			LTR:733jdhr1:1086833	14272	6244
10	chr1	1101030	1101330	LTR:5	interpenic	LINC01342;MIR200B	dist=21598;dist=1154	-		LTR:753(ehr1:1101135	1153	447

E. Integration site detection and annotation results



B. Base content distribution diagram

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D. Distribution plot of mapped reads in chromosomes

