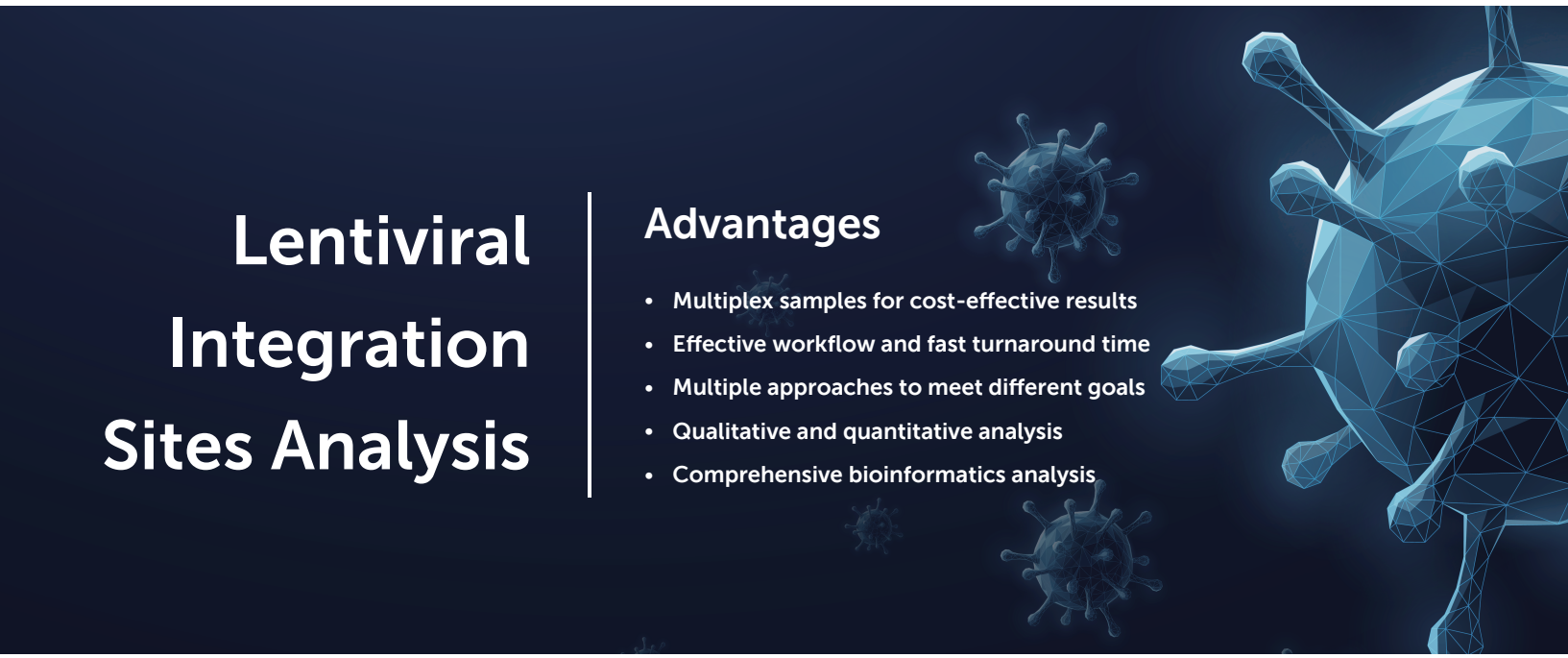
CD Genomics
The Genomics Services Company

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



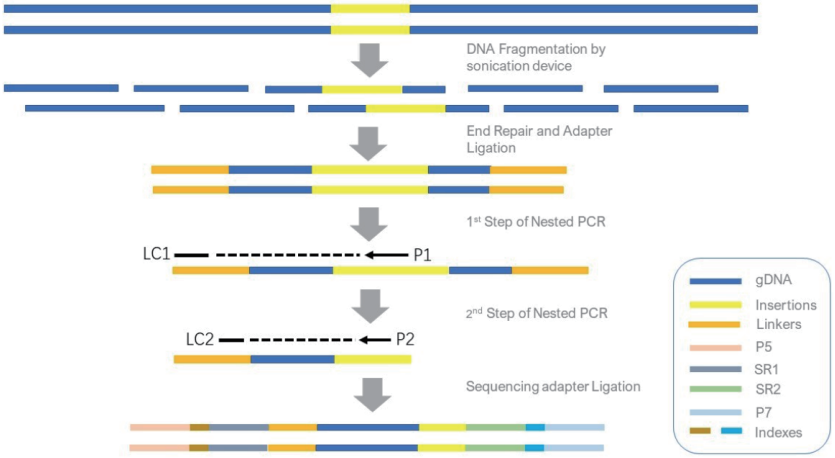
The Introduction of Lentiviral Integration Sites Analysis

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*.

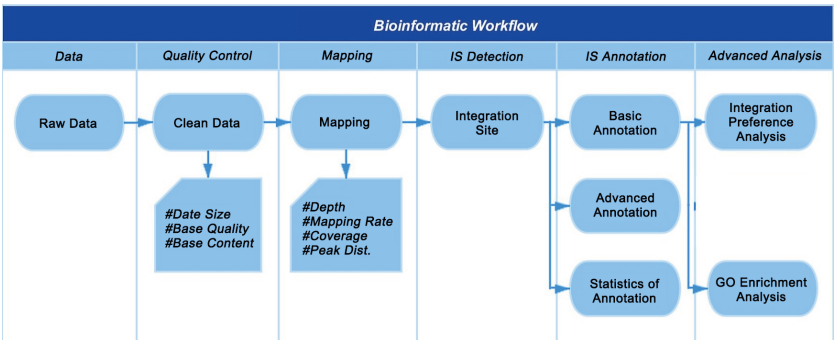
CD Genomics has developed a comprehensive set of tools for viral integration site analysis by combining PCR and sequencing-based approaches with proprietary bioinformatics pipelines. We are able to identify the position of integration sites and determine the integration frequency of viral vectors with 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 or >500 ng gDNA	Illumina PE150	1 Gb	For CAR-T cell genome
Whole genome sequencing			⩾150 Gb	For monoclonal cell line

Workflow



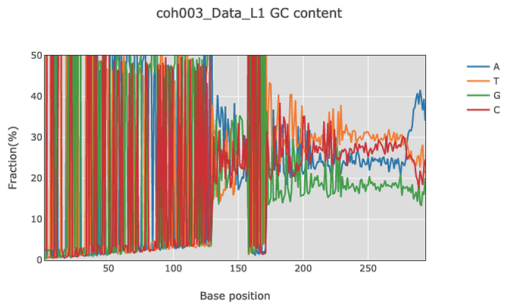
A. Schematic diagram of LM-PCR library construction



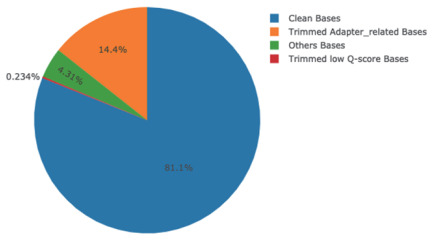
B. Bioinformatics analysis flow chart

Demo Results

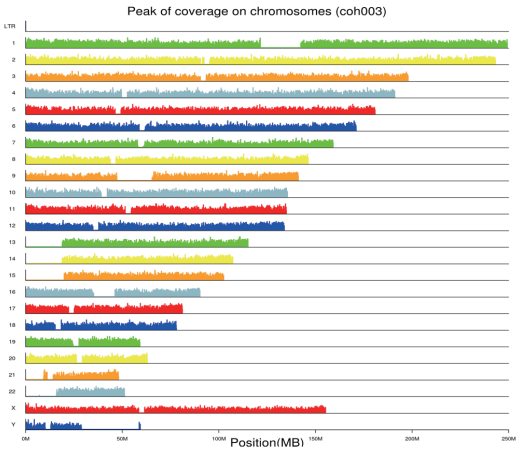
A. Sequencing quality value and error rate distribution diagram



B. Base content distribution diagram



C. Original data composition



D. Distribution plot of mapped reads in chromosomes

Index	Chr	Start	End	SupportReads	Func.refGene	Gene.refGene	GeneDetail.refGene	cpgIslandExt	coemic79	BreakPoint	Distance2TSS	Distance2CpG
1	chr1	885774	886074	LTR:4	intronic	NOC2L	.	.	.	LTR:733|chr1:886045	8605	283
2	chr1	915794	916094	LTR:6	exonic	PERM1	.	.	.	LTR:733|chr1:915811	1379	2642
3	chr1	960620	961220	LTR:5	intergenic	ISG15;AGRN	dist=1001;dist=4280	.	.	LTR:733|chr1:961016	2074	1070
4	chr1	971676	971722	LTR:26	intronic	AGRN	.	.	.	LTR:733|chr1:971717	16174	1439
5	chr1	974070	974370	LTR:35	intronic	AGRN	.	.	.	LTR:733|chr1:974277	18568	1127
6	chr1	976521	976821	LTR:5	exonic	AGRN	.	Name=CpG: 351	.	LTR:733|chr1:976560	21019	0
7	chr1	1048189	1048489	LTR:32	intronic	C1orf159	.	.	.	LTR:733|chr1:1048281	3237	1860
8	chr1	1074221	1074521	LTR:4	ncRNA_intronic	LINC01342	.	.	.	LTR:733|chr1:1074414	1825	1375
9	chr1	1086668	1086968	LTR:30	intergenic	LINC01342;MIR2008	dist=7234;dist=19516	.	.	LTR:733|chr1:1086832	14272	6244
10	chr1	1101030	1101330	LTR:5	intergenic	LINC01342;MIR2008	dist=21596;dist=1154	.	.	LTR:733|chr1:1101133	1153	447

E. Integration site detection and annotation results