DNBSEQ™ SERVICE OVERVIEW
ChIP Sequencing

Service Description

ChIP Sequencing is widely used to analyze protein interactions with DNA. It combines chromatin immunoprecipitation (ChIP) with massively parallel DNA sequencing to identify binding sites of DNA-associated proteins,and can be used to precisely map global binding sites for any protein of interest. ChIP sequencing offers higher resolution and more precise and abundant information in comparison with array-based ChIP-chip.Besides clean sequencing data output, we offer standard, advanced and customized bioinformatics services to suit your specific research needs.

Low input: As low as 5 ng ChIP-ed DNA/sample for human sample.
Comprehensive analysis:
Correlation analysis between ChIP-Seq and RNA-Seq.

Sequencing Service Specification

Our ChIP-Seg Service will be performed with DNBSEQ sequencing technology, featuring combinatorial probe-anchor synthesis (CPAS) and DNA Nanoballs (DNB) technology[1] for superior data quality.

ACTGACT
TACTACT
GACTAC
CTGAGGT

Sample Preparation and Services

- 50 bp Single-end sequencing reads
- Standard output 20 million reads per sample
- Clean data and bioinformatics analysis are available in standard file formats
- Available data storage and bioinformatics applications
- Cloud-based data storage and delivery system

24/7

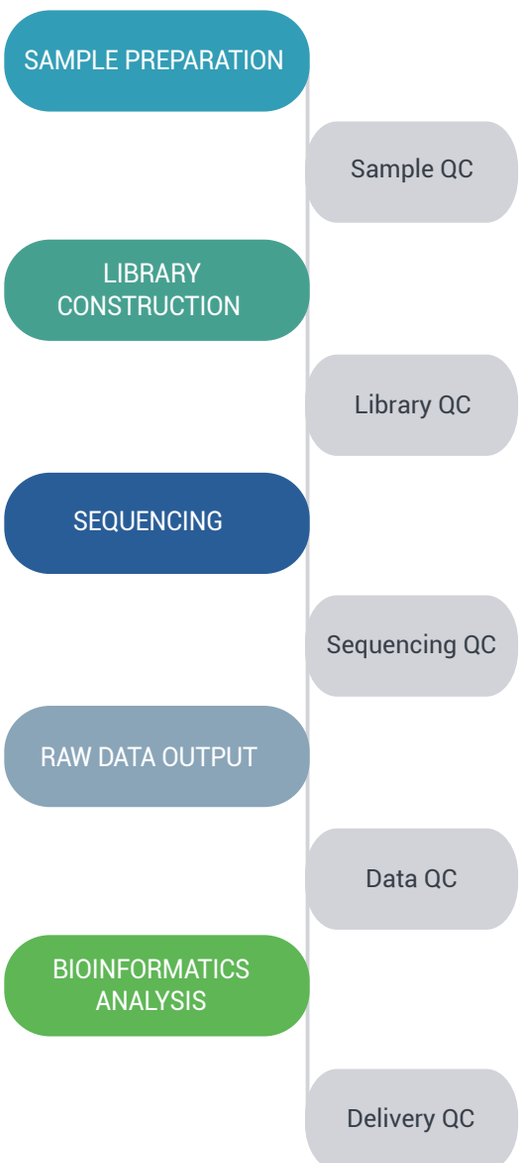
Turn Around Time

- Typical 26 working days from sample QC acceptance to final data delivery
- Expedited services are available, contact our specialist for details

Quality Data | Fast TAT | Cost Effective

Project Workflow

We care for your samples from the start through to the result reporting. Highly experienced laboratory professionals follow strict quality procedures to ensure high quality results.



Data Analysis

In addition to clean data output, we offer a range of standard, advanced and customized bioinformatics pipelines for your ChIP-Seq analysis project, including the correlation analysis of differential expression genes and peak-related genes.

Reports and output data files are delivered in industry standard FASTQ, and Excel file formats with publication-ready tables and figures.

STANDARD BIOINFORMATICS ANALYSIS

- Data filtering
- Alignment to the reference genome
- Peak scanning and annotation
- Identification of differential peaks between samples
- Differential peaks annotation

ADVANCED BIOINFORMATICS ANALYSIS

- Motif Analysis

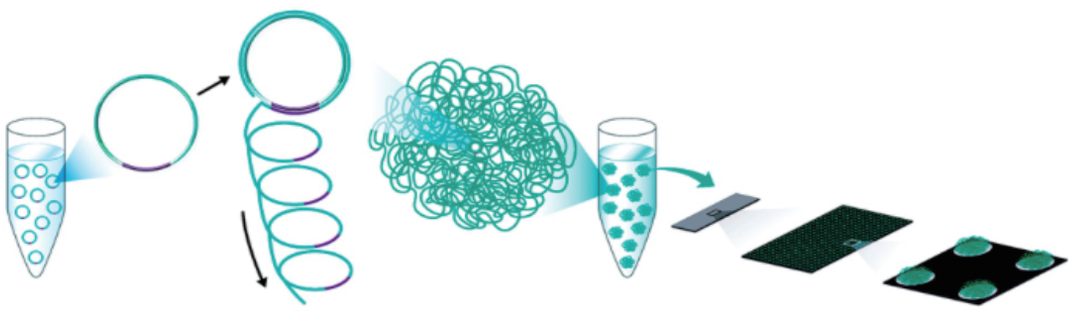
CUSTOMIZED BIOINFORMATICS ANALYSIS

- Statistics of the epigenetic modification level and mRNA expression level of related genes
- The distribution of epigenetic modification level in different gene categories
- Overall connection of epigenetic modification level and the mRNA expression level in different gene categories
- The relationship of the ratio of epigenetic modification and the ratio of mRNA expression in a pair of samples
- Clustering analysis based on epigenetic modification level and mRNA expression level
- Calculate different level of epigenetic modification when mRNA expression level is different
- GO, Pathway analysis, related functional excavation and verification of the genes that differences exist in both epigenetic modification and mRNA expression
- Further customization of Bioinformatics analysis to suit your unique project is available:
- Please contact our technical representative.

DNBSEQ Sequencing Technology

DNBSEQ is an innovative high-throughput sequencing solution, developed by Innomics's Complete Genomics subsidiary in Silicon Valley. The system is powered by combinatorial Probe-Anchor Synthesis (cPAS), linear isothermal Rolling-Circle Replication and DNA Nanoballs (DNB™) technology, followed by high-resolution digital imaging.

The combination of linear amplification and DNB technology reduces the error rate while enhancing the signal. The size of the DNB is controlled in such a way that only one DNB is bound per active site on the DNBSEQ flow cell. This densely patterned array technology provides optimal sequencing accuracy and increases flow cell utilization.



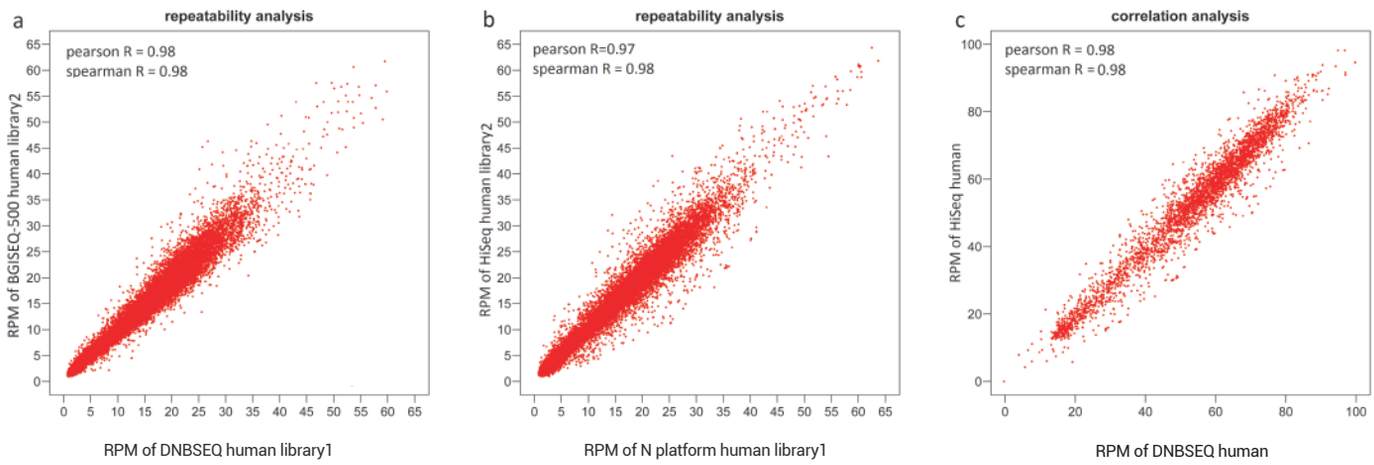
Sequencing Data Performance

Excellent agreement of data quality between N platform and DNBSEQ

The plot below shows the high sequencing data quality of human HeLa cell libraries and mouse libraries on DNBSEQ as compared to the N platform. By applying the same filtering criteria, the clean rate and unique mapping rate from the same samples are consistent on both platforms.

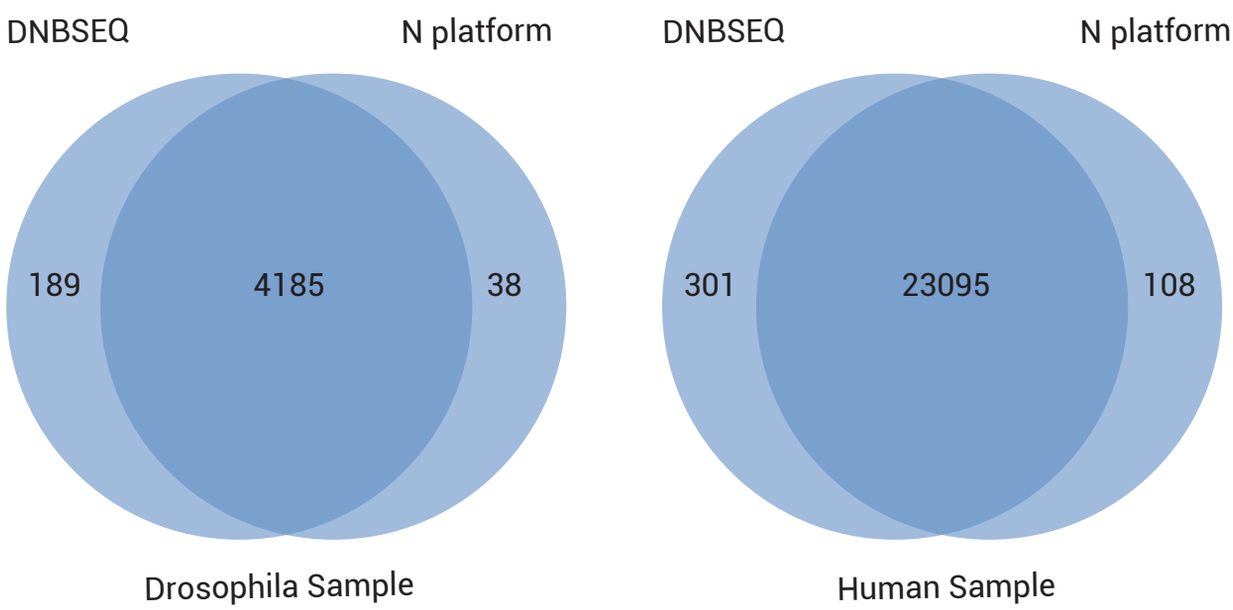
Excellent agreement of reads per million(RPM) between N platform and DNBSEQ

The scatterplots below compare thereads per million PPMvalues of human Hela cell sample sequenced on the DNBSEC and N platform. The coefficients of sequencing repeatabilty on both platforms are high (Figures a, b). There is a high correlation between DNBSEQ and N platform as well (Fiqure c).



Excellent agree ment of peak number detection between N platform and DNBSEQ

The fiqures below show the comparison of detected peak numbers on both N platform and DNBSEQ from the same samples[2]. The common peak detection rate of both drosophila and human HeLa cell sample are higher than 99%, while both platforms have a small amount of their own uniquely detected peaks.



Sample Requirements

We can process DNA samples of human, plant, animal and microbial samples, with the following general requirements:

	DNA Amount and Concentration	Minimum Volume
ChIP-ed DNA	Amount ≥ 10 ng, Concentration ≥ 1 ng/μL	15 μL
ChIP-ed DNA (human sample only)	Amount ≥ 5 ng, Concentration ≥ 1 ng/μL	15 μL

References

[1] Human genome sequencing using unchained base reads on self-assembling DNA nanoarrays Drmanac R, Sparks AB, Callow MJ, Halpern AL, Bums NL, Kermani BG, Carnevali P, Nazarenko l, Nilsen GB, Yeung G,.et al Science (2010) 327(5961):78-81 doi:10.1126/science.1181498

http://science.sciencemag.org/content/327/5961/78.full

[2] ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia Stephen G. Landt,Georgi K. Marinov,Anshul Kundaje, et al. *Genome Res*.2012 Sep;22(9):1813-31.doi: 10.1101/gr.136184.111
https://www.ncbi.nlm.nih.gov/pubmed/22955991

To Learn More

If you have any questions or would like to discuss how our services can help you with your research, please don't hesitate to contact us at P_contact@innomics.com. We look forward to hearing from you!

Innomics Inc.
750 N. Pastoria Ave
Sunnyvale, CA 94085
USA

www.innomics.com