DNBSEQ™ SERVICE OVERVIEW
Whole Exome Sequencing

Service Description

For many applications, Whole Exome Sequencing is gaining popularity as a viable and cost-effective alternative for Whole Genome Sequencing. We provide expert exome sequencing services to aid in small- and large-scale clinical trials, pharmaceutical drug development initiatives, human and animal (rodents and monkeys) research.

Besides raw sequencing data output, we offer standard and custom bioinformatics services to suit your specific research needs.

Sequencing Service Specification

Our Human Exome Sequencing Service are performed with the DNBSEQ sequencing technology, featuring cPAS and DNA Nanoballs(DNB™) for superior data quality.

Sample Preparation and Services

- Agilent Sureselect or IDT xGen exome kit for library construction and enrichment，100/150bp paired-end sequencing options available
- Clean data and advanced bioinformatics analysis are available in standard file formats
- Standard and custom bioinformatics data analysis
- Available data storage and bioinformatics applications

Sequencing Quality Standard

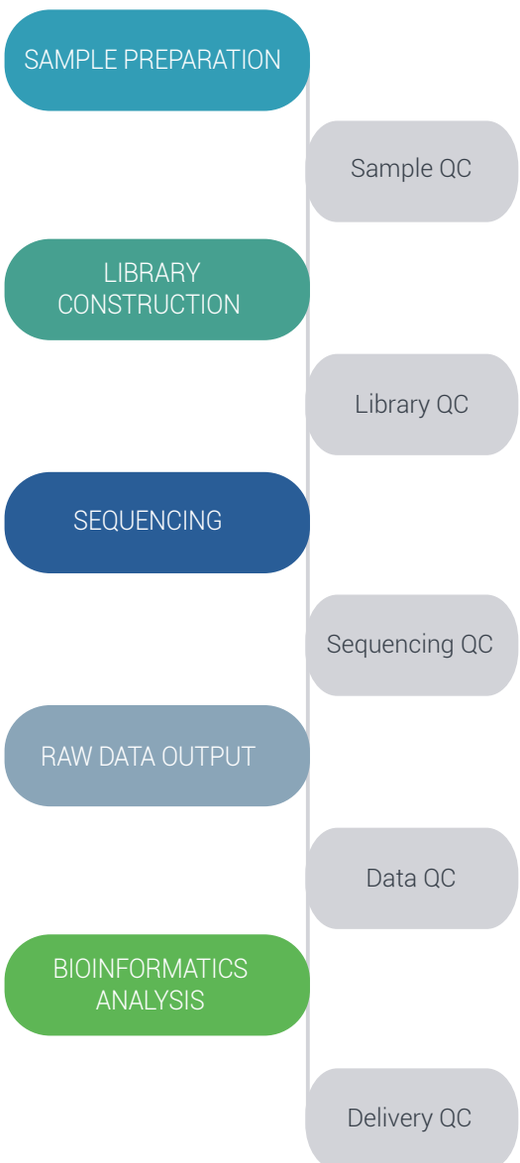
- Guaranteed ≥80% of bases with quality score of ≥Q30
- Standard sequencing coverage ≥50X; ≥100x is recommended for cancer samples

Turn Around Time

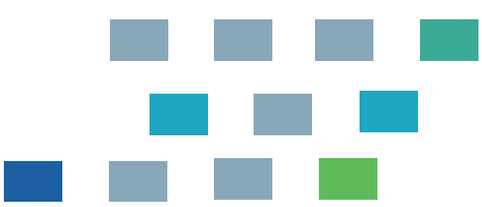
- Typical 18 days after sample acceptance for data delivery
- Rapid delivery service available

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 the integrity of your results.



Quality Data | Fast TAT | Cost Effective



Data Analysis

Besides clean data output, we offer a range of standard and customized bioinformatics pipelines for your whole exome sequencing project.

Reports and output data files are delivered in industry standard file formats: BAM, VCF, .xls, .png

CANCER MUTATION ANALYSIS

- Data Filtering and QC
- Align reads to the human reference genome
- Germline SNP/InDel detection
- Somatic SNV detection
- Somatic InDel detection
- Somatic CNV detection
- Tumor purity and ploidy analysis
- Verification of homology of paired samples
- Susceptibility gene screening
- Drug Targeted Annotation
- Driving gene prediction
- Identifying Significant Mutated Genes
- Deciphering Mutational Signature
- CN-neutral Loss of Heterozygosity
- Hyper-mutated Sample Classification
- Clone Analysis

HUMAN- MENDELIAN DISORDERS ANALYSIS

- Data filtering
- Align reads to the human reference genome
- Variants calling
- VEP annotation
- Public group AF annotation
- Harmful or conservative prediction tools
- Signaling pathway annotation
- OMIM annotation
- Normal tissue protein expression annotation
- Data screening and interpretation
- Screening according to ACMG genetic variation classification criteria and guidelines
- Screening by threshold
- *De novo* mutation screening
- Analysis of family co-separation
- RoH analysis

OTHER AVAILABLE ADVANCED ANALYSIS

- Population genetics analysis
- Complex disease analysis
- *De novo* mutation analysis for family samples
- Tumor neoantigen prediction

CUSTOMIZED ANALYSIS

Further customization of Bioinformatics analysis to suit your unique project is available:
Please contact our technical representative

Sample Requirements

We can process your gDNA, Blood, Cell line, Fresh frozen tissue samples from a variety of species, with the following general requirements:

Sample type	Mass	Concentration	Integrity (AGE)	Sample Purity
Genomic DNA	≥500ng	≥12.5ng/μL	The band shown on gel electrophoresis has little degradation, or of fragment size greater than 20kb.	No contamination with RNA, protein or salt ions; colorless and transparent; non-sticky.

Tissue Type	Requirements
Fresh Cell Culture (Number of Cell or Net Weight)	≥5×10^6 cells
Fresh Animal Tissue (Net Weight)	≥50mg
Whole Blood (Mammals)	≥0.5 mL
FFPE	≥ 10 slides, unstained, 100 mm^2 area, 5 ~ 10μm thickness, tumor content≥70%

DNBSEQ Sequencing Technology

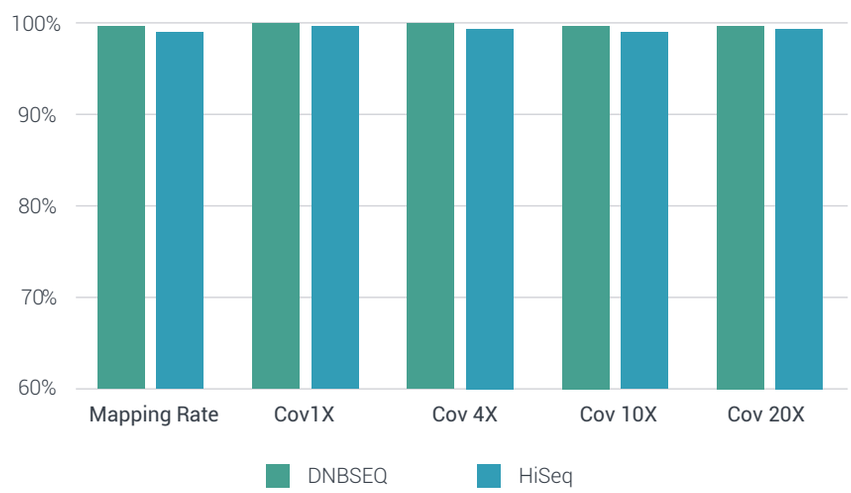
DNBSEQ system is an industry leading high-throughput sequencing solution, powered by combinatorial Probe-Anchor Synthesis (cPAS) and improved DNA Nanoballs (DNB™) technology. The cPAS chemistry works by incorporating a fluorescent probe to a DNA anchor on the DNB™, followed by high-resolution digital imaging. This combination of linear amplification and DNB™ technology reduces the error rate while enhancing the signal. In addition, the size of the DNB™ is controlled in such a way that only one DNB™ is bound per active site. This patterned array technology not only provides sequencing accuracy, but it also increases the chip utilization and sample density.

Sequencing Technology References

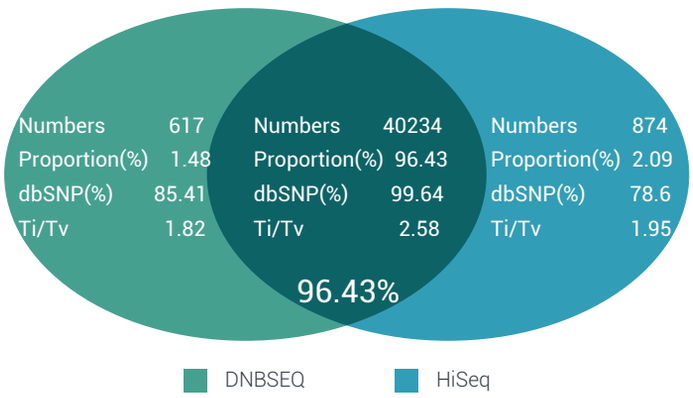
Drmanac R, Sparks AB, Callow MJ,Halpern AL, Burns NL, Kermani BG, Carnevali P et al. Human genome sequencing using unchained base reads on selfassembling DNA nanoarrays. Science. 2010;327(5961):78–81.

Data Performance

Following is an example of typical DNBSEQ data output for a 100X WES project with standard sample NA12878, compared with data from the Illumina HiSeq 4000 system.

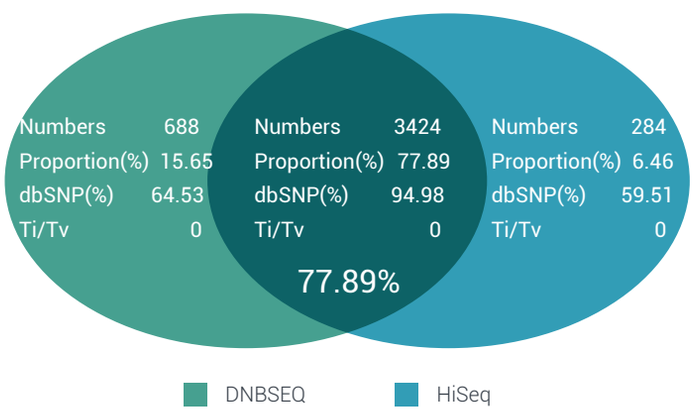


Bar-Graph showing the mapping rate and sequencing coverage of the samples using DNBSEQ and Illumina HiSeq 4000 platform of 100X WES.



SNP calling performance from the NA12878 standard sample demonstrates good concordance between platforms

SNP ANALYSIS	DNBSEQ	HiSeq
PRECISION	76.95%	76.44%
SENSITIVITY	95.53%	95.50%



InDel calling performance from the NA12878 standard sample demonstrates good concordance between platforms.

InDel ANALYSIS	DNBSEQ	HiSeq
PRECISION	74.04%	79.77%
SENSITIVITY	87.60%	84.93%

*Full demonstration data reports are available through our account representative.

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