Making Sequencing more Accessible

Next Generation Sequencing Services

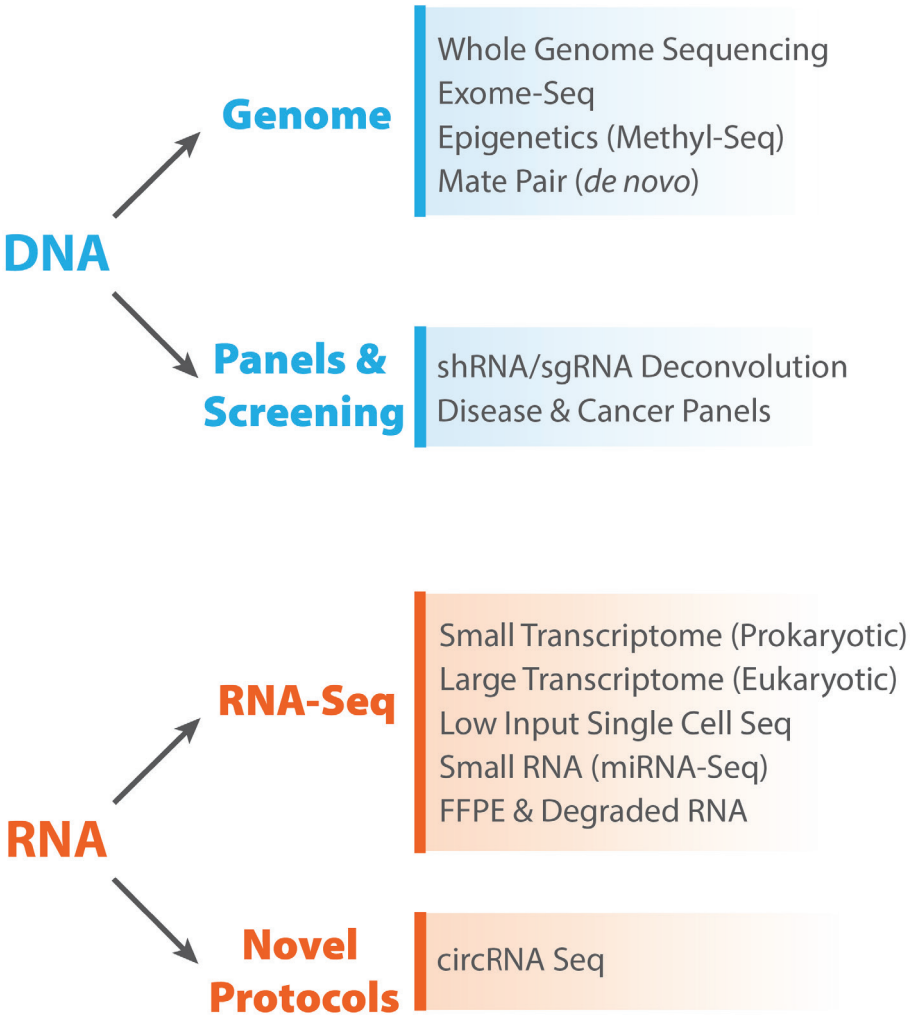
A significant technological advancement, Next Generation Sequencing (NGS), is poised to redefine many aspects of clinical and non-clinical research while setting up the foundation for the upcoming field of personalized medicine. Able to amass utilizable data with sheer magnitude and high precision, NGS provides a wide range of applications such as RNA-Seq for transcriptomes, Exome-Seq for coding regions of the genome, Whole Genome Sequencing, and more!

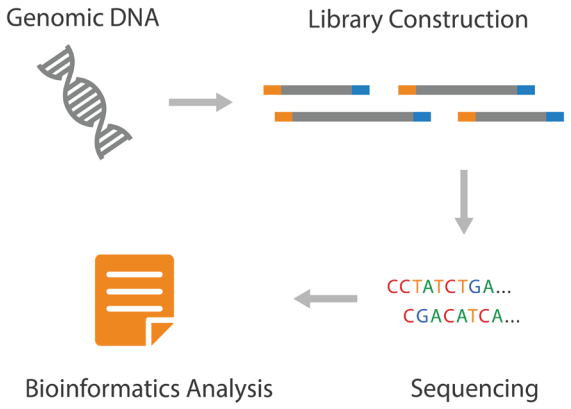
abm® www.abmgood.com

Next Generation Sequencing (NGS) is a significant technological advancement that is redefining many aspects of clinical and non-clinical research and paving the way for personalized medicine. Because of the sheer magnitude, high precision, and applicable nature of its data, NGS is ideal for RNA-Seq, Exome-Seq, Whole Genome Sequencing, and more!

In anticipation of this upcoming era of NGS, **abm**, an Illumina® Certified Service Provider, offers a wide range of sequencing services on the MiSeq, NextSeq, and HiSeq Illumina® platforms at the most affordable prices and with the fastest turnaround times, delivering reliable and comprehensive results for any project.

illumina CSPro® CERTIFIED SERVICE PROVIDER





Whole Genome Sequencing

Whole genome sequencing (WGS) amasses unprecedented levels of comprehensive and detailed information on an individual's genetic make-up, making it pivotal to the understanding of key life processes such as development and major diseases and their impacts on human health. With as little as 50ng of genomic DNA, WGS can provide 30X coverage for any species' genome, a feat that has only recently become achievable.

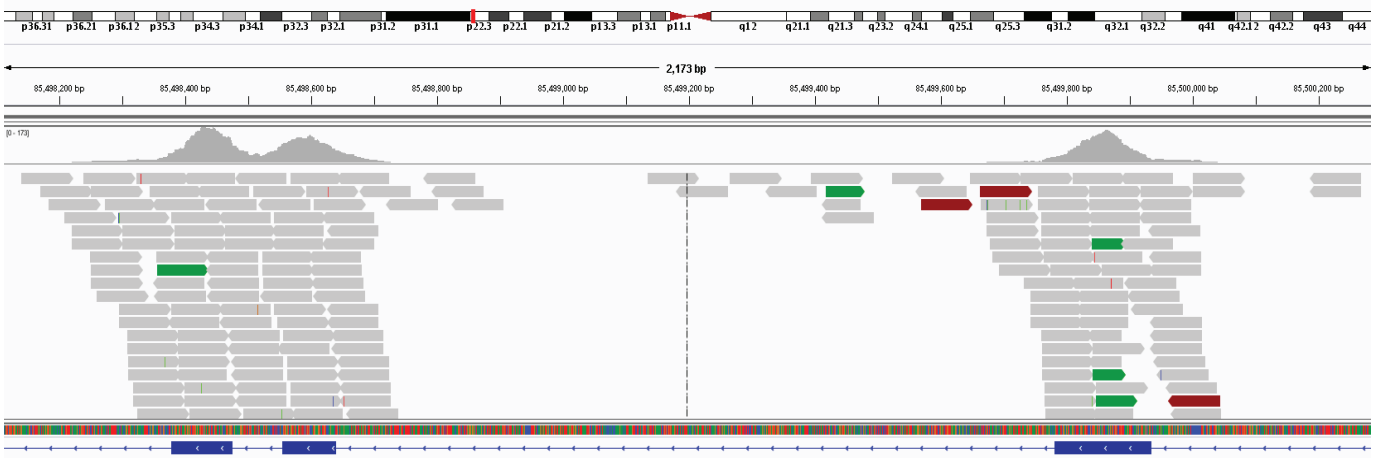
Transcriptome Sequencing/RNA Sequencing

RNA-Seq is an emerging technology that will soon replace conventional methods such as microarrays and comparative genomic hybridization delivering more information at a better value. As a global leader in functional genomics, **abm** offers RNA-Seq services that are tunable to a wide spectrum of custom needs on the MiSeq, NextSeq, and HiSeq Illumina® platforms, with a 2 - 4 week turnaround and options for specialized RNA, low-input, and single-cell sequencing workflows.

Human Exome Sequencing (Exome-Seq)

Exome-Seq uses hundreds of thousands of probes to target exonic protein coding regions, which give rise to ~85% of disease-causing mutations in the human genome. Providing a higher coverage and lower cost option of examining protein coding regions, Exome-Seq is an attractive alternative to Whole Genome Sequencing. Exome-Seq's detailed and iterative data can be used to precisely identify SNVs (single nucleotide variant) and *de novo* mutations associated with Mendelian and common diseases. Its utility in connecting exonic genetic variations to diseases and drug development also make it a powerful tool for the growing field of personalized medicine. **abm**'s industry-leading Exome-Seq services have a 2 - 4 week turnaround and can be tailored for any project.

- 30X coverage - base level of coverage for examining exonic sequences
- 100X coverage - ability to examine rare SNVs while still offering excellent value compared to WGS
- Alternative library capture kits are available at an additional cost for expanded exome (UTRs, miRNAs)



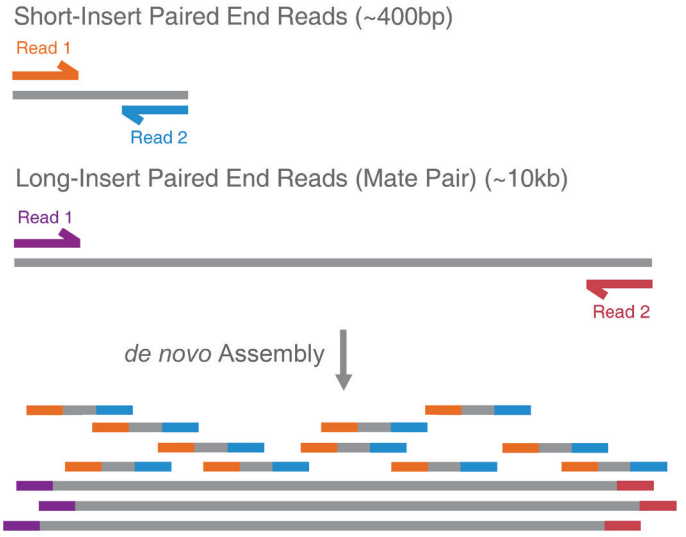
Visualization of Exome-Seq alignment with Integrative Genomics Viewer (IGV). The use of exome capture probes during library prep creates powerful enrichment of exonic sequences, while minimizing the sequencing of intronic and intergenic fragments. This allows for a powerful, focused analysis at a reduced cost compared to WGS.

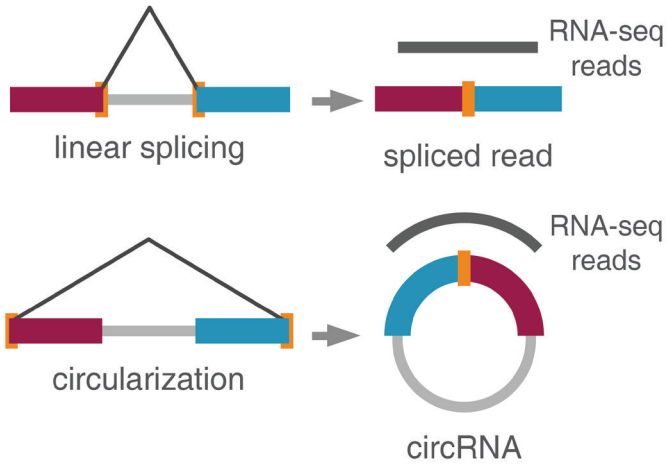
Low Input, Degraded or FFPE Total RNA Sequencing

abm's new ultra low input sequencing now allows researchers to use next generation sequencing with a low quantity of sample or in cases where NGS may mask out the gene expression of a target subgroup of cells. **abm**'s FFPE sequencing unlocks the ability to perform NGS on tissues that have low quality nucleic acids due to histology fixation, such as valuable cancer tumor samples.

Mate Pair Sequencing

The addition of mate pair sequenced reads to a standard paired end project has been demonstrated to help tremendously in improving *de novo* assemblies. Mate Pair Sequencing services offered by **abm** will help researchers gain a more complete and accurate picture of the genome for species lacking suitable reference genomes. By using ultra long insert mate pair reads to link contigs separated by unsequenceable genomic regions, all facets of downstream analyses are improved.



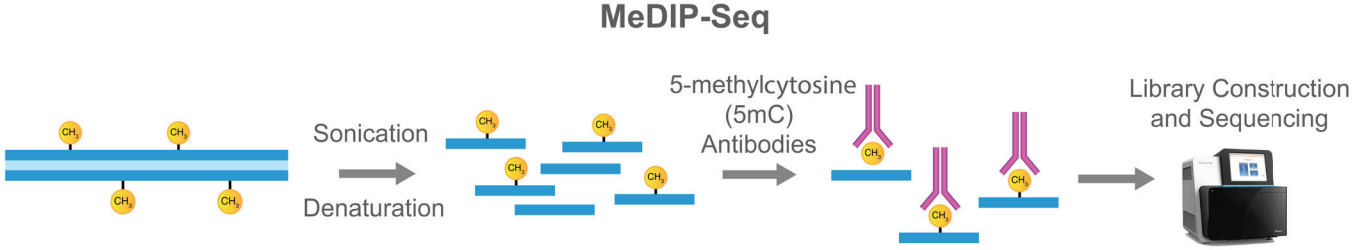


Circular RNA Sequencing (circRNA-Seq)

Interest in the field of circRNA has been growing exponentially since 2013, though its functions are still mostly unknown. **abm**'s new circRNA-Seq service combines RNase R with next generation sequencing for high-throughput sequencing of circular RNA, facilitating new and revolutionary discoveries in this area.

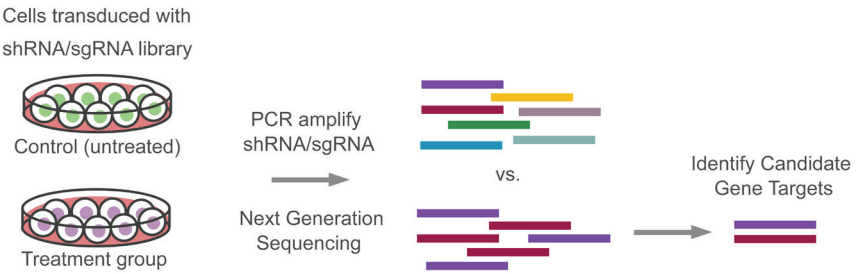
Genomic Methylation Sequencing - RRBS and MeDIP

New services in Genomic Methylation Sequencing now allows researchers to focus on sites of genomic methylation. **abm**'s new Reduced Representation Bisulphite Sequencing (RRBS) service uses the MspI enzyme to capture greater than 70% of all CpG sites of interest while bypassing regions with none or minimal CpG sites. The new Methylated DNA Immunoprecipitation (MeDIP-Seq) service uses the anti-5mC antibody to selectively enrich for DNA fragments with methylated sites, allowing the visualization of relative abundances and genomic locations after alignment.



shRNA/sgRNA/CRISPR Deconvolution

abm is also offering a new service in the area of shRNA or CRISPR sgRNA deconvolution. Using NGS to compare expression gives a much higher throughput readout, enabling a more powerful analysis and more accurate interpretation. This information could be extremely important in discovering new genes that modulate the effects of a novel therapeutic drug or treatment.

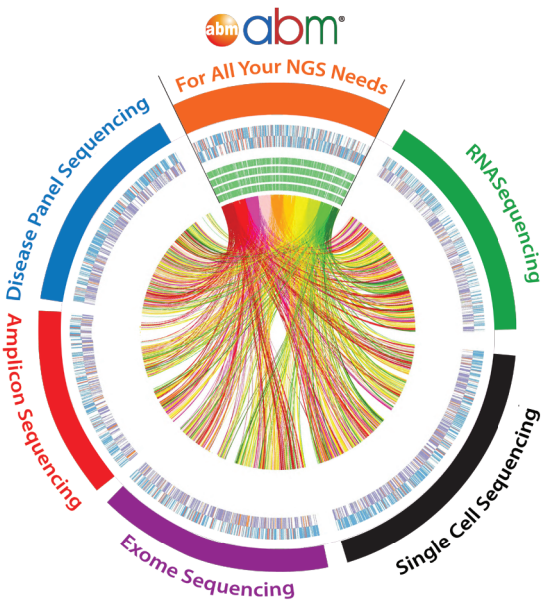


Disease Panels and Pathway Genes

For cost-effective, streamlined, targeted NGS of specific genetic diseases or conditions, **abm** offers Illumina© TruSight sequencing panel services. Designed with recognized health care experts at leading institutions, TruSight panels are comprised of oligo probes targeting genes and regions thought to be relevant for particular diseases or conditions, allowing doctors to conveniently and precisely diagnose and provide personalized treatment plans for each individual.

Data & Bioinformatic Analysis Services

- A concise and comprehensive summary report
- Sequencing results provided in industry standard FASTQ format (BAM available)
- FastQC data analysis to assess the overall quality
- Alignment to the reference (if available)
- Coverage analysis – provides statistics describing the coverage for genomic regions
- Variant analysis – calls SNP and indel variants across a reference
- Comparative analysis between samples available
- Customizable bioinformatics workflows
- Additional analyses available upon request



Next Generation Sequencing Lane Rentals

abm's NGS Lane Rental service allows researchers to construct their own libraries and access the MiSeq, NextSeq and HiSeq systems for low-cost and quick turnaround time for sequencing. Agilent Bioanalyzer library QC and qPCR quantification are also available.

Confidentiality

All customer information is held in strict confidence. All materials and information sent to us and the products produced by us for the order are the property of the customer and will be returned to the customer or discarded in a confidential manner. We only archive customer materials when instructed to.

More Resources

For more information about NGS, visit our Knowledge Base and YouTube Channel!

Knowledge Base

https://www.abmgood.com/marketing/knowledge_base.php

YouTube Channel

www.youtube.com/c/abmgood

Next generation sequencing - Introduction
https://youtu.be/jFCD8Q6qSTM

Next generation sequencing - Sample Preparation
https://youtu.be/-kTcFZxP6kM

Next generation sequencing - Coverage and sample quality control
https://youtu.be/PGAfwSRYv1g

Next generation sequencing - Data analysis
https://youtu.be/l4BAfRekohk

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