Phalanx
Biotech Group

The Expert in High Throughput Analysis

- Next Generation Sequencing Services
- Bioinformatics & Big Data Services

The Expert in High Throughput Analysis

Genetic Test Platform Development, Lab Services
Bioinformatics and Big Data Analytics

Over the last 14 years Phalanx Biotech has serviced more than 3,000 high throughput cases, and has been cited in over 376 international scientific journals. We understand that it can be daunting to navigate genomics data. Our bioinformatics services contain a "personal touch" that has resonated with our clients and has led to many long-term partnerships. We are trusted, experienced partners to scientists and companies around the world with offices in the United States and Asia.

Please read on to learn about our NGS and Bioinformatics services, and Contact Us to discuss your project!

DNA-Seq

Exome Sequencing

Exome sequencing targets protein-coding and untranslated regions within expressed transcripts. This approach often focuses on the confirmation and annotation of various mutations, such as SNPs, indels, and rare somatic mutations involved in cancer.

Advantages

- Cost effective - targets only exome regions
- High coverage - 99% of SNPs can be detected
- Customizable - target protein coding regions only or include non-coding regions

Applications

- Genome-wide association study (GWAS)
- Cancer research
- Personalized medicine

Bioinformatics

- Data QC & filtering
- Align reads to the human reference genome
- SNP calling and annotation
- SNP validation and comparison
- Functionality prediction of SNPs
- InDel calling and annotation
- InDel validation and comparison

RNA-Seq

Gene Expression Analysis

Gene expression, or transcriptomics, has become a cornerstone of modern biomedical research. RNA sequencing, or RNA-Seq, is the NGS approach to precisely sequence all RNA molecules in an organism. RNA-seq data is compared to a reference genome in order to calculate the expression level of all RNA transcripts along with a wealth of additional information. This approach is useful for research applications in physiology, cell biology, biomarker discovery, pathology, drug screening, and other fields. We have extensive experience in RNA-Seq, and our services include library generation, transcript sequencing, and complete data analysis according to your custom requirements.

Advantages

- Digitized signals - directly determine each RNA fragment sequence at single nucleotide resolution without crosstalk and background clutter common in traditional microarray hybridization
- Precise gene expression levels are calculated by the RPKM method
- High throughput - more than 10 million reads can be acquired in a single experiment
- RNA-seq approaches offer good reproducibility across experiments

Applications

- Identify an organism's entire transcriptome
- Identify differentially expressed genes following treatment
- Identify mechanisms of pathogenicity

Bioinformatics

- Data QC & filtering
- Gene expression analysis
- Differential gene expression analysis
- Gene ontology enrichment analysis of DEGs
- Pathway enrichment analysis of DEGs
- PCA analysis

RNA-Seq

Small RNA Analysis

Small RNAs include microRNA (miRNA), small interfering RNA (siRNA), and piwi-interacting RNA (piRNA). These small RNAs are about 18-30 nt in length, and are involved in the regulation of gene expression. Our Small RNA sequencing services include total RNA prep, isolation of small RNAs, library prep, sequencing, and data analysis. Data analysis can include novel miRNA prediction, miRNA expression analysis, target gene prediction, and functional annotation of gene targets.

Advantages

- High throughput: suitable for analysis of multiple samples
- High resolution: single base resolution
- Novel miRNAs can be discovered

Bioinformatics

- Data QC & filtering
- Length distribution of small RNA
- Explore small RNA distribution across selected genome
- Identify rRNAs, tRNAs, snRNAs, etc.
- Identify known miRNAs
- Annotate small RNAs
- Analyze the expression pattern of known miRNAs
- Target genes prediction of novel and known miRNA
- GO and KEGG pathway analysis of known and novel miRNA Target genes
- Differential expression analysis and cluster analysis of known miRNA
- Differential expression analysis and cluster analysis of novel miRNA
- Target genes prediction of differential miRNA
- GO and KEGG pathway analysis of differential miRNA Target genes

RNA-Seq

lncRNA Analysis

Long non-coding RNAs (lncRNAs) are RNA molecules greater than 200 nt that do not code for a protein. lncRNAs are involved in X chromosome inactivation, genomic imprinting, chromatin modifications, and transcriptional regulation, yet lncRNA research is only in its infancy. NGS promises to accelerate lncRNA discovery and allow for studies looking at lncRNA expression levels during treatment.

By reducing ribosomal RNAs first and then using strand-specific primers during library preparation, our NGS pipeline is targeted to lncRNA molecules, and we can provide directional information in the final data analysis. Our final reports will also include lncRNA expression levels, differential expression during treatment, and novel lncRNA discovery.

Advantages

- High reproducibility: repeated testing of the same sample shows Pearson correlation greater than 0.993
- A single NGS experiment can reveal nearly all lncRNA information in your sample
- Data are not limited to known lncRNAs, novel lncRNA prediction is also available
- LncRNA analysis of non-model organisms is also available - we can collaborate with you on all your custom research needs

Applications

- Biomarker identification
- Mechanisms of gene regulation

Bioinformatics

- Data QC & filtering
- Transcripts assembly
- Known and novel transcripts identification
- Novel lncRNA prediction
- Quantification and differential expression analysis of lncRNA
- Up/down stream lncRNA of a gene
- Pre-miRNA prediction

RNA-Seq

Transcriptome *de novo* Assembly

Transcriptome de novo assembly is designed to generate sequence data of your samples under different conditions, including the transcripts of coding and non-coding RNAs. This approach allows for a gene expression analysis as discussed previously, but it also facilitates the discovery of novel transcripts, detection of alternative splice variants, and detection of low-expressing transcripts. SNP detection is also available if you are working with a species that has a reference genome sequence. Transcriptome assembly is possible with rare cell populations, stem cells, circulating tumor cells (CTCs), ancient DNA samples, and samples that require difficult RNA extraction methods.

Advantages

- Complete coverage: sequences all RNA transcripts in your sample.
- Wide range of detection: detects both rare transcripts and highly expressed transcripts.
- High resolution: detects alternative splice variants of a gene and homologous sequences within a gene family.

Applications

- Transcriptome assembly for non-model organisms
- Detection of alternative splice variants
- Novel transcript variants underlying cancer
- Non-coding RNA analysis

Bioinformatics

- Data QC & filtering
- Transcriptome de novo assembly
- Unigene annotation (COG and GO classification)
- Unigene pathway analysis
- Protein coding region (CDS) prediction
- Unigene differential expression analysis
- Gene ontology classification of differentially expressed unigene
- SNP analysis

Epigenetics

ChIP-Seq

Histones are proteins involved in the maintenance and regulations of chromatin structure. Histone modifications affect chromatin structure which thereby affects gene expression. Similarly, transcription factors are proteins that bind DNA and directly regulate the expression of downstream genes. Chromatin immunoprecipitation followed by NGS (ChIP-Seq) targets regions of DNA bound by chromatin or transcription factors. ChIP-Seq is used to confirm/discover, 1) transcription factor binding sites, and 2) various posttranslational modifications of histones, such as lysine acetylation, lysine and arginine methylation, serine and threonine phosphorylation, and lysine ubiquitination and sumoylation.

Advantages

- High throughput: suitable for analysis of multiple samples
- High resolution: single base resolution

Bioinformatics

- Data QC & filtering
- Align reads to the reference genome
- Peak analysis (peak length and depth)
- Peak annotation (peak distribution, GO and pathway analysis of peak related gene)
- Identify differential peaks between samples
- Differential peaks annotation (differential peaks distribution, GO and pathway analysis of differential peak related gene)
- Motif analysis

Metagenomics

16S Sequencing

16S ribosomal RNA is a component of the prokaryotic ribosome and is the target widely used in microbial genomics. By targeting 16S, you can determine species composition and abundance in environmental samples. Compared to the traditional microbial identification techniques, 16S NGS approaches offer a high throughput and precise solution to metagenomics research.

Advantages

- Unbiased: microbial identification without strain isolation and culture
- High throughput: suitable for the analysis of multiple samples
- Rapid results: no strain isolation and culture = you get your microbial diversity data fast

Bioinformatics

- Data QC & filtering
- Species composition and abundance analysis
- Complexity of a single sample (alpha diversity)
- Complexity differences among different samples (beta diversity, samples ≥ 2)
- Principal components analysis (samples ≥ 3)
- Clustering of species composition among samples (Samples ≥ 3)

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