List of Current Services Offered by the Core

Service Name	Description
Whole Genome Sequencing (WGS) data analysis	Analyzing whole genomic DNA-seq data, calling genomewide variants, and anotating the variants
Whole Exome Sequencing (WES) data analysis	Analyzing exome DNA-seq data, calling exome variants, and anotating the variants
RNA-seq data analysis	Analysis for RNA-seq data to profile total RNA expression level in biological samples
miRNA-seq data analysis	Analysis for miRNA-sseq data to profile miRNA expression level in biological samples
16s metagenomics data analysis	Analyzing 16s rRNA-seq data to decipher taxomomic microbiome knowledge of biological samples
WGS metagenomics data analysis	Analyzing metageomic DNA-seq data to decipher taxomomic microbiome knowledge of biological samples
ChIP-seq data analysis	Aanlysis of chromatin immunoprecipitation data followed by sequencing (ChIP-seq)
10x Genomics scRNA-seq data analysis	Single-cell transcriptomie sequencing data analysis from 10X Genomics technolgy
De novo genome-assembly and annotation	De novo genome-assembly and annotation for eukaryotic species
ATAC-seq data analyiss	Analysis for the Array for Transposase-Accesible Chromatin (ATAC) sequencing data to investigate the chromatin accessibility landscape
Single-cell ATAC-seq data analyiss	Analysis for the scATAC sequencing data to investigate the chromatin accessibility landscape and epigenomic regulation at the single-cell level
Nucleotide analysis to calculate percentages of A/T/G/C in ORF frames	Nucleotide analysis to calculate percentages of A/T/G/C in ORF frames
Identification of ribosome binding sites (RBS) within the whole genome	Identification of ribosome binding sites (RBS) within the whole genome
Polygenetic risk score (PRS) analysis	Polygenetic risk score calculation and analysis for DNAseq GWAS data
Proteomics data analysis	Proteomics data analysis to understand protein profiling levels in biological samples
GEO data submission	Submitting RNA-seq data to NIH Gene Expression Omnibus (GEO) repository databases

Detection of exogenous DNA integration sites	Using detectIS pipeline to rapidly detect exogenous DNA integration sites using DNA or RNA paired-end sequencing data
GWAS analysis	Genome Wide Association Study (GWAS) analysis for DNA-seq data
Alternative splicing RNA-seqe data analysis	Alternative splicing analysis for RNA-seq data using rMATs tool
Codon analysis	Analysis to decipher codon information for microbial RNA-seq data
Targeted DNA-seq data analysis	Targeted DNA-seq data analysis for targeted DNA-seq data including mapping, variant calling and variant annotation
Fixed scRNAseq data analysis	Analyzing 10x Genomics fixed scRNAseq data, which use different color bar codes to label RNA samples for different samples and missed the samples together for scRNAseq by cell ranger tool
Bulk ATAC-seq data analysis	Analyzing bulk ATAC-seq (Assay of Transposase Accessible Chromatin sequencing) data of chromatin accessibity profiling by HOMER (Hypergeometric Optimization of Motif EnRichment) tool
ScRNA spatial data analysis	Analyzing scRNA spatial data for classifying tissue or cell types based on total mRNA using 10x Genomics Visium tool
CUT&RUN data analysis	Analysis for CUT&RUN (Cleavage Under Targets and Release Using Nuclease) data, a new chromatin profiling that performs antibody-targeted controlled cleavage with micrococcal nuclease to release DNA fragments for sequencing, using HOMER and other general tools
CUT&TAG data analysis	Analysis for CUT&TAG (Cleavage Under Targets and Tagmentation) data by HOMER and other general tools. It provides an advanced approach to investigate the correlationshipcorrelation between chromatin structure and protein-DNA interactions, combining the benefits of precision and simplicity.
DNA methylation data analysis for Illumina EpicV2 array	Analysis for Illumnia EpicV2 array the most new format of DNA methylation data using minfi and other R packages
Parse Biosciences scRNA data analysis	Analysis for scRNAseq data from libray kit of Parse Biosciences by Parse Biosciences pipeline
IPA analyses	Functional pathway and network analyses using Ingenuity Pathway Analysis software and database from QIAGEN
DAVID analysis	Performing various functional pathway analysis using NIH Database for Annotation, Visulization fn Integrated Discovery (DAVID) tool
KEGG analysis	Ananlysis of functional pathway enrichment using Kyoto Encyclopedia of Genes and Genomes (KEGG) database resource

GO analysis	Performing enrichment analysis on gene sets using Gene Ontology (GO) terms and databases
GSEA analysis	Gene Set Enrichment Analysis (GSEA) using NIH supported GSEA software and Molecular Signature Database (MSigDB)
CNV analyis for CGH arrays	Identifying DNA Copy Number Variations by analyzing Comparative Genomic Hybridization (CGH) array data
DNA methylation array analysis	Identifying DNA genomics hyper- or hypo-methylation loci by analyzing DNA methylation array data
TCGA data analysis	Extracting specific cancer genomic data and performing statistical analyses from The Cancer Genome Atlas (TCGA) databases
NCBI/GEO data analysis	Extracting specific cancer genomic data and performing statistical analyses from NIH GEO repository databases
SNP association analysis	SNP association analysis for SNP array data using PLINK tool
Venn diagrams and Upset plots	Analysis of overlapped genes in different comparisons and plotting Venn diagram
2D&3D PCA	Principal Component Analysis (PCA) and plotting in 2D and 3D levels
Heatmap anad volcano plots	Heatmap and volcano analysis and plotting
Survial analysis	Survial analysis and plotting
Oncomine and cBioPortal data analyses	Extracting and data analyses for data from Oncomine and cBioPortal databases
Metabolomic pathway analysis	Functional pathway enrichment analysis for metabolomic data
Intergrated metabolomic pathway analysis	Ingegrated functional pathway enrichment analysis for metabolomic data and genomic/proteomic data
miRNA-seq target gene pathway analysis	miRNA-seq target gene pathway analysis and figures
Interaction analysis of lncRNAs with gene promoters and mRNA	Interaction analysis of lncRNAs with gene promoters and mRNA
All-Of-Us GWAS analysis	GWAS analysis for NIH All of Us (AoU) databases data
Development of web sites and web applications	Development of web sites and web applications to publish research data
Development of searchable relational databases	Development of searchable relational databases for complex research data
Clustering and modeling experimental data using machine learning	Clustering and modeling experimental data using machine learning
Development of custom programs	Development of custom programs to analyze complex data

Motifs/pattern discovery from large datasets	Motifs/pattern discovery from large datasets
Analysis of patient data from wearable devices like pedometers	Analysis of patient data from wearable devices like pedometers
Experimental data submission to public repositories	Multiple mechanisms of sharing data via ftp, depositing data into SRA/NCBI resources
Customized BLAST server setup to run BLAST on their own datasets	Providing customized BLAST servers to run BLAST on their own datasets
RNA-seq data analysis using a new R package, NBBt-test	Development of a new R package, NBBtest, for RNAseq differential and alternative splicing statistical analyses
Pre-grant consultation	Pre-grant consultation, support letters, collaborations
Consultation on the NGS/Bioinformatics experimental design and budget quotes	Consultation on the NGS/Bioinformatics experimental design and budget quotes
Generate figures to represent high-dimensional data	Generate figures to represent high-dimensional data
Consultation on Data Management and Sharing (DMS) Plans	Consultation on Data Management and Sharing (DMS) Plans
Molecular docking and prediction of interaction sites	Molecular docking using known or predicted crystallographic structures to identify potential protein-protein or ligand-protein interaction sites
Virtual screening of ultra-large (billion compound) ligand libraries against drug targets	In silico drug discovery using virtual screening of ultra-large drug compound libraries against drug targets