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SIGNALS FOR LIFE

Discovery of Variants & Polymorphisms

Applications

Genetic variation forms the foundation of phenotypic diversity, trait inheritance, and adaptive evolution. Theracues' Variant and Polymorphism Discovery service enables comprehensive identification of single nucleotide polymorphisms (SNPs), simple sequence repeats (SSRs), and repeat elements using high-throughput sequencing technologies, supporting applications in genomics, breeding, population genetics, and molecular marker development.

Pros

- Genome-wide detection of SNPs, SSRs, and repeats
- High sensitivity and accuracy
- Supports population and comparative studies
- Enables marker-assisted selection
- Applicable across multiple species

Notes

- Requires adequate sequencing depth
- Reference genome improves accuracy
- Complex genomes may need higher coverage
- Validation recommended for functional use

Input

Genomic DNA

DNA Quantity:≥200 ng (recommended)

Sample Types

Blood/ PBMC | Tissue | Plant tissues (leaf, root, stem) | Bacterial Cultures

Platform

Illumina/ ONT Long-read sequencing platforms

Process Map

Sample DNA Extraction → DNA QC → Library Prep → NGS Data Acquisition → Data QC → Read Alignment → Variant calling (SNPs, InDels, SSRs, repeats) → Variant annotation

Standard Deliverables

Download Sample Report

References

- Ellegren, H. (2004). Microsatellites: simple sequences with complex evolution. Nature Reviews Genetics.
- Nielsen, R. et al. (2011). Genotype and SNP calling from next-generation sequencing data. Nature Reviews Genetics.

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Discovery of Variants & Polymorphisms

Applications

Rapid Molecular Diversity Analysis enables quick and reliable assessment of genetic variation within and between populations. By leveraging molecular markers and high-throughput sequencing or targeted genotyping approaches, this service supports diversity studies, germplasm characterization, breeding programs, and evolutionary research. This service focuses on evaluating genetic diversity, population structure, and relatedness using molecular marker data. It enables rapid comparison of multiple samples to identify genetic similarities and differences, supporting applications in breeding selection, conservation genetics, and population-level studies.
Analyses can be performed using SNPs, SSRs, or other polymorphic markers, depending on study goals and turnaround requirements.

Pros

- Rapid turnaround time
- Efficient population-level analysis
- High reproducibility
- Supports breeding and conservation studies
- Scalable across sample sizes

Notes

- Marker choice impacts resolution
- Reference data improves interpretation
- Limited functional inference
- Best suited for comparative analysis

Input

Genomic DNA

DNA Quantity: ≥ 100 ng (recommended)

Sample Types

Blood/ PBMC | Tissue | Plant tissues (leaf, root, stem) | Bacterial Cultures

Platform

Illumina sequencing platforms

Process Map

Sample DNA Extraction → DNA QC → Library Prep → NGS Data Acquisition → Data QC → Read Alignment → Variant calling (SNPs, InDels, SSRs, repeats) → Variant annotation → Diversity and population analysis

Standard Deliverables

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References

- Ellegren, H. (2004). Microsatellites: simple sequences with complex evolution. Nature Reviews Genetics.
- Nielsen, R. et al. (2011). Genotype and SNP calling from next-generation sequencing data. Nature Reviews Genetics.

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Cell line characterization - clonality analysis

Applications

Cell line authentication is essential to ensure research validity, reproducibility, and data integrity. ' Cell Line Typing – Amplicon service provides accurate genetic profiling of cell lines using targeted amplicon sequencing, enabling reliable identification, authentication, and detection of cross-contamination. This service uses amplicon-based sequencing to analyze specific genetic loci for cell line identification and verification. It supports routine authentication, quality control, and validation of cell lines used in research and translational studies.
The workflow enables comparison against reference profiles to confirm identity and detect misidentification or contamination, ensuring experimental reliability.

Pros

- High accuracy and reproducibility
- Rapid and cost-effective
- Detects cross-contamination
- Suitable for routine QC
- Low DNA input required

Notes

- Limited to targeted loci
- Reference profiles required
- Not genome-wide
- Periodic testing recommended

Input

Genomic DNA

DNA Quantity: ≥ 100 ng (recommended)

Sample Types

Human Cell-lines | Animal Cell-lines | Fresh or frozen cell pellets

Platform

Illumina Sequencing Platforms

Process Map

Standard Deliverables

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References

- Ellegren, H. (2004). Microsatellites: simple sequences with complex evolution. Nature Reviews Genetics.
- Nielsen, R. et al. (2011). Genotype and SNP calling from next-generation sequencing data. Nature Reviews Genetics.

Hybridoma sequencing

Applications

This service focuses on sequencing antibody variable domains (VH and VL) from hybridoma-derived samples. By combining targeted amplification with next-generation sequencing, it enables reliable recovery of functional antibody sequences for cloning, expression, humanization, and intellectual property protection.
Hybridoma sequencing ensures long-term preservation of antibody sequence information independent of cell line stability.

Pros

- Accurate VH/VL sequence recovery
- Supports antibody cloning
- Preserves antibody IP
- High sensitivity and specificity
- Suitable for R&D workflows

Notes

- Requires high-quality RNA/DNA
- Targets variable regions only
- Mixed clones may complicate analysis
- Confirmation recommended

Input

Total RNA or Genomic DNA

- RNA: ≥500 ng
- DNA: ≥200 ng

Sample Types

Hybridoma cell pellets

Cultured hybridoma cells

Platform

Illumina/ ONT Long-read sequencing platforms

Process Map

Standard Deliverables

Download Sample Report

References

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- Nielsen, R. et al. (2011). Genotype and SNP calling from next-generation sequencing data. Nature Reviews Genetics.

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Bulk Immune Repertoire Sequencing (B-cell / T-cell)

Applications

This service profiles B-cell receptors (BCRs) and T-cell receptors (TCRs) using long-read sequencing technologies to recover full-length receptor sequences in bulk samples. It enables detailed analysis of:

- Immune diversity and clonotype composition
- Clonal expansion and dominance
- Isotype and chain pairing (BCR)
- Immune responses in disease, vaccination, and therapy

Long-read sequencing eliminates assembly ambiguity associated with short reads, ensuring accurate repertoire reconstruction.

Pros

- Full-length BCR/TCR sequences
- Accurate clonotype resolution
- Reduced assembly bias
- Captures V(D)J and CDR regions
- Suitable for complex repertoires

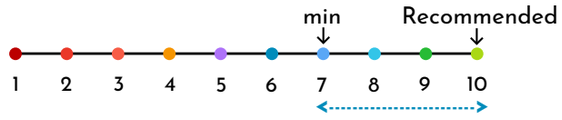
Notes

- Requires high-quality RNA
- Bulk-level resolution only
- Higher input recommended
- Data interpretation is specialized

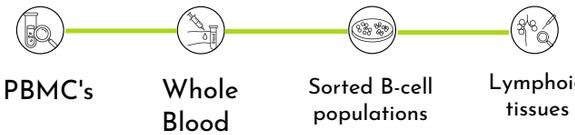
Input

Total RNA Input Amount: ≥1 µg

RNA Integrity (RIN)



Sample Types



Platform

ONT Long-read sequencing platforms

Process Map

Standard Deliverables

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- Nielsen, R. et al. (2011). Genotype and SNP calling from next-generation sequencing data. Nature Reviews Genetics.

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BCR Sequencing

Applications

This service focuses on sequencing immunoglobulin heavy and light chain regions to analyze B-cell repertoires in bulk samples. It enables assessment of:

- B-cell diversity and clonotype distribution
- Clonal expansion and dominance
- V(D)J gene usage and CDR characteristics
- Immune responses in infection, vaccination, and disease

The workflow supports both short-read and long-read sequencing strategies, depending on resolution requirements.

Pros

- High-resolution BCR profiling
- Sensitive detection of clonal expansion
- Supports immunology and vaccine studies
- Flexible sequencing strategies
- Reproducible and scalable

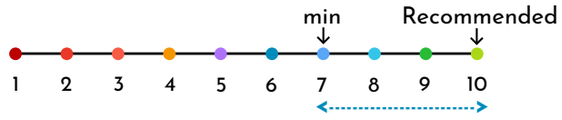
Notes

- Bulk-level analysis only
- RNA quality is critical
- Chain pairing limited with short reads
- Specialized interpretation required

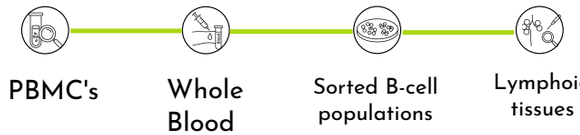
Input

Total RNA Input Amount: ≥500 ng

RNA Integrity (RIN)



Sample Types



Platform

ONT Long-read sequencing platforms

Process Map

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TCR Sequencing

Applications

This service sequences TCR α, β (and optionally ɣ, δ) chains to analyze T-cell repertoires in bulk samples. It enables assessment of:

- T-cell diversity and clonotype composition
- Clonal expansion and immune dominance
- V(D)J gene usage and CDR3 diversity
- Immune monitoring in disease, vaccination, and therapy

The workflow supports short-read or long-read sequencing, depending on resolution and pairing requirements.

Pros

- High-resolution TCR profiling
- Sensitive clonotype detection
- Supports immuno-oncology studies
- Scalable across cohorts
- Reproducible workflows

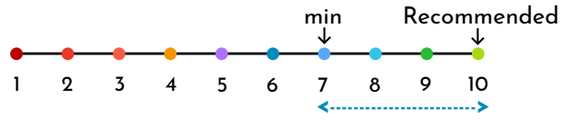
Notes

- Bulk-level analysis only
- RNA quality is critical
- Chain pairing limited with short reads
- Expert interpretation required

Input

Total RNA Input Amount: ≥1 µg

RNA Integrity (RIN)



Sample Types

PBMC's | Whole Blood | Sorted B-cell populations | Lymphoid tissues

Platform

ONT Long-read sequencing platforms

Process Map

Standard Deliverables

Download Sample Report

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- Nielsen, R. et al. (2011). Genotype and SNP calling from next-generation sequencing data. Nature Reviews Genetics.