We offer preclinical sequencing options and cutting-edge bioinformatics services to investigate clinically relevant mutations and expression profiles in patient-derived xenograft (PDX) tumors before and after therapy. Bioinformatic solution services specifically delineate mouse from human reads, resulting in clean data analysis.

COMPREHENSIVE SOLUTIONS FOR YOUR PRECLINICAL OR CLINICAL TUMOR PROFILING NEEDS.

DiscoverSeq: Targeted Exome Sequencing
Whole Exome Sequencing
Whole Transcriptome Sequencing
**DISCOVERSEQ - TARGETED EXOME SEQUENCING**

A next generation sequencing (NGS)-based assay of 358 cancer-associated genes (Full gene list here: jax.org/ctp)

Testing can be integrated into your preclinical study plan or it can be used opportunistically to query unique biological events.

- Compare vehicle and reference compound arms to experimental treatment arms
- Evaluate the differences between non-responsive and responsive tumors in a single study arm

The pipeline is able to detect multiple molecular alternations of and allele frequency of ≥5%. The alteration types include:

- Single nucleotide variations (SNVs) at ≥5% allele frequency
- Insertions and deletions (Indels) up to 50-bp in length at ≥5% allele frequency
- Gene-level copy number variations (CNVs)

**WHOLE EXOME SEQUENCING**

Sequencing of the whole exome for a comprehensive assessment of coding variation

Testing can be integrated into your preclinical study plan or it can be used opportunistically to query unique biological events.

- Compare vehicle and reference compound arms to experimental treatment arms
- Evaluate the differences between non-responsive and responsive tumors in a single study arm

The pipeline is able to detect multiple molecular alternations including:

- Single nucleotide variations (SNVs)
- Insertions and deletions (indels)

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**WHOLE TRANSCRIPTOME SEQUENCING**

RNA-seq based transcriptome analysis of cancer progression and response to pharmaceuticals

Testing can be integrated into your preclinical study plan or it can be used opportunistically to query unique biological events.

- Compare vehicle and reference compound arms to experimental treatment arms
- Evaluate the differences between non-responsive and responsive tumors in a single study arm

**DATA PROCESSING**

To aid functional interpretation, detailed annotations of variants based on a number of genomic, functional, and population datasets including dbSNP, COSMIC, Ensembl, UCSC, the 1000 Genomes project, NHLBI Exome Sequencing Project (ESP), the Exome Aggregation Consortium (ExAC), PolyPhen, SIFT, PhyloP, and many more will be provided.

**ASK US ABOUT OUR PDX TUMORS**

Over 400 additional PDX Tumors

400+ characterized models are annotated and available for review.

Search our database for the right model (tumor.informatics.jax.org).

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**JAX® MICE, CLINICAL & RESEARCH SERVICES**

1-800-422-6423 (US, CANADA & PUERTO RICO)
1-207-288-5845 (FROM ANY LOCATION)

jax.org/pdxseq