HUDSONALPHA
DISCOVERY
SEQUENCING + BIOINFORMATICS

DISCOVERY LIFE SCIENCE'S NEWEST DIVISION

Academic Innovation at the Speed of Industry

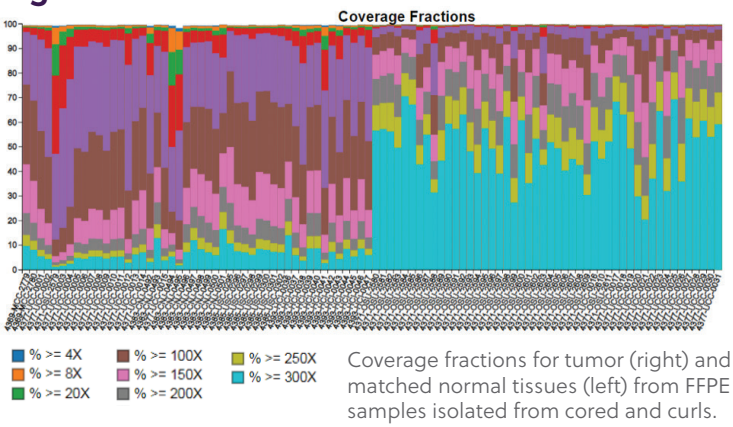
HudsonAlpha Discovery provides comprehensive genomic services to support R&D, translational and pre-clinical drug and diagnostic programs.

DNA Sequencing Services

EXOME

- HudsonAlpha Discovery processes thousands of human exome samples per month
- Several bait sets are available, IDT Exome and Roche EZ Exome are most common
- Multiplexing of exome libraries into hybridization is used to allow extremely high throughput
- Up to 768 exome samples may be processed at once, with sequencing to 100X or 300X exome coverage complete in 2 days
- Protocols are optimized for degraded, low input samples such as FFPE

Figure 1.



Coverage fractions for tumor (right) and matched normal tissues (left) from FFPE samples isolated from cored and curls.

GENOME

- HudsonAlpha Discovery has processed tens of thousands of human whole genomes
- 8 NovaSeq® 6000 sequencers can sequence ~400 human genomes every 2 days
- Optimized library preparation protocols provide even coverage over the genome
- High throughput robotics provide consistent, reproducible results with no batch effects
- Alignment and variant calling of genomic data is available

OncoPanels

- TruSight® Tumor 170, offered by Illumina®, analyzes 170 genes associated with solid tumor indications
- DNA and RNA, isolated from either FFPE or viable cell suspensions, are processed simultaneously and undergo enrichment for the genes of interest
- Identify single nucleotide variants, gene duplications, fusions, splice variants, and mutant allele frequencies as low as 5% can be detected.

COMMONLY REQUESTED MUTATIONS OF INTEREST		
ALK	JAK2	PIK3CA
BRAF	KRAS	PTEN
ERBB	MET	RET
EGFR	MMR Markers	ROS1
FGFR	MYC	ROS2
FLT3	NRAS	

Propel your research with the power of the HudsonAlpha Discovery division; contact us today at

info@dls.com -or learn more at - **dls.com/discovery**

RNA Sequencing Services

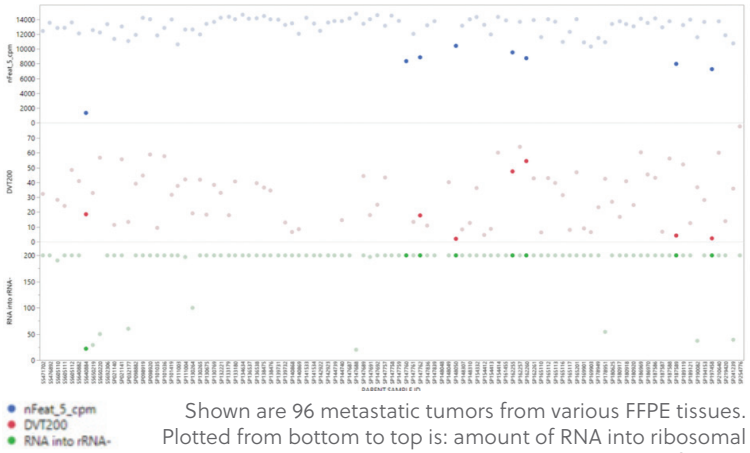
RNA SEQUENCING

HudsonAlpha Discovery has sequenced tens of thousands of human RNAseq samples with a variety of RNAseq protocols using high throughput robotics that provide consistent, reproducible results with no batch effects

RNASeq SERVICES INCLUDE

- Optimized and proprietary protocols:
  - » Library preparation for even coverage over the genome
  - » Ribosomal reduction/globin reduction
  - » Extremely degraded, low-input FFPE samples and urine samples
  - » Sequencing of extracellular RNA sources
- **RNAseq with poly-A selection:** profiles transcribed genes only for a focused view of gene expression
- **microRNAseq:** profiles microRNA expression which is important in cancer and other disease states
- **Low input RNAseq:** allows library construction and sequencing of as little as 1ng of high quality RNA
- Alignment of RNAseq data to the genome and analysis of the transcriptome is available

Figure 2.



Shown are 96 metastatic tumors from various FFPE tissues. Plotted from bottom to top is: amount of RNA into ribosomal RNA reduction protocol; DVT200, and number of genes detected at a threshold of 5 cpm. The samples with the lowest number of genes detected are highlighted.

SINGLE CELL RNASeq

HudsonAlpha Discovery offers the 10XGenomics Chromium Single Cell Gene Expression platform for novel, efficient, and high-throughput RNASeq

- Allows up to 6000 cells per sample profiled
- No normalization bias
- Low cell doublet rates

HUDSONALPHA
DISCOVERY
SEQUENCING + BIOINFORMATICS

Propel your research with the power of the HudsonAlpha Discovery division; contact us today at
info@dls.com -or learn more at - **dls.com/discovery**