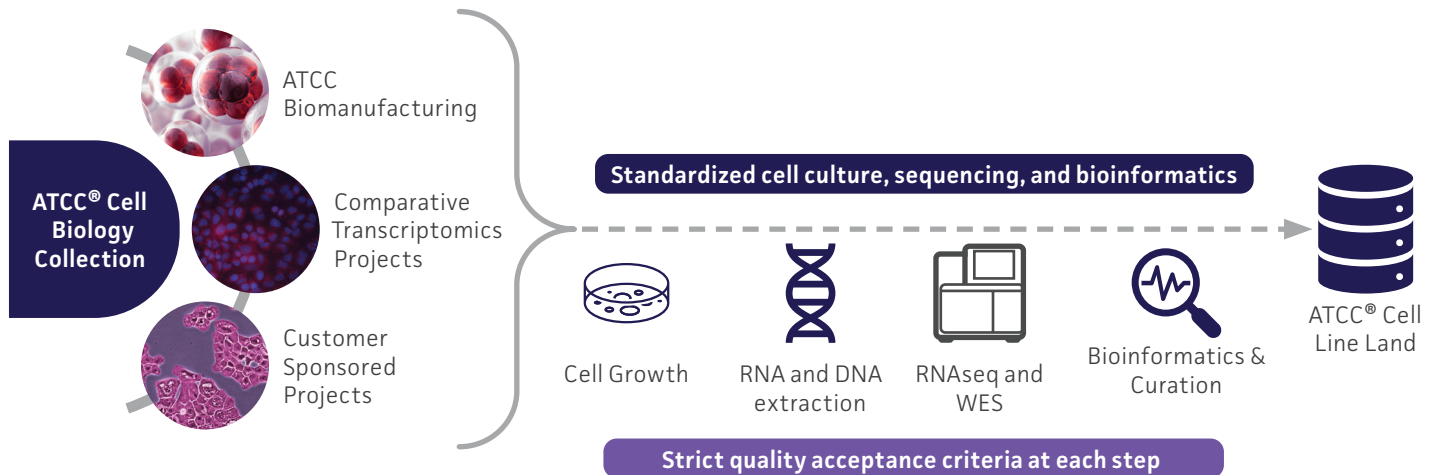# ATCC CELL LINE LAND

Combining the power of ATCC's gold-standard cell lines with QIAGEN's best-in-class bioinformatics solutions, we have developed ATCC Cell Line Land—a curated, ISO 9000-compliant database of RNA-seq and whole-exome sequencing datasets derived from ATCC's authenticated human and mouse cell lines. This digital resource allows researchers to efficiently identify suitable cell models based on gene expression and mutation profiles for specific applications.

- Use as a reference control in your experimental setting
- Build hypotheses and design experiments
- Access carefully curated metadata
- Compare gene expression across or within cell lines
- Explore precomputed differential gene expression

- Analyze pathway and gene interactomes
- Discover biomarkers and therapeutic targets
- Predict drug treatment responses
- Investigate molecular mechanism of disease pathogenesis
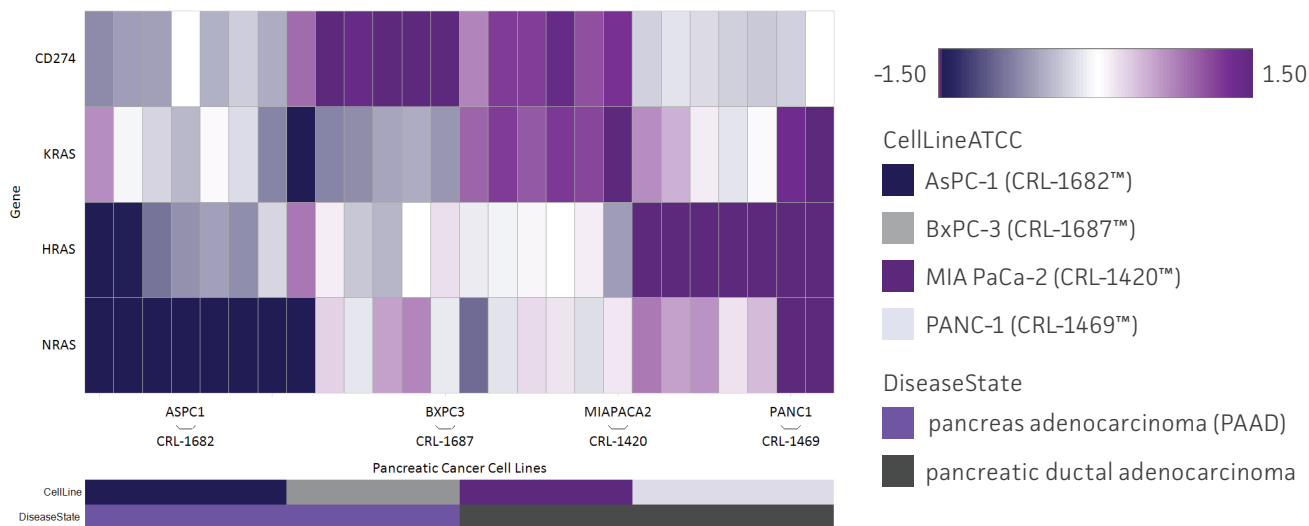- Purchase the authenticated ATCC source material

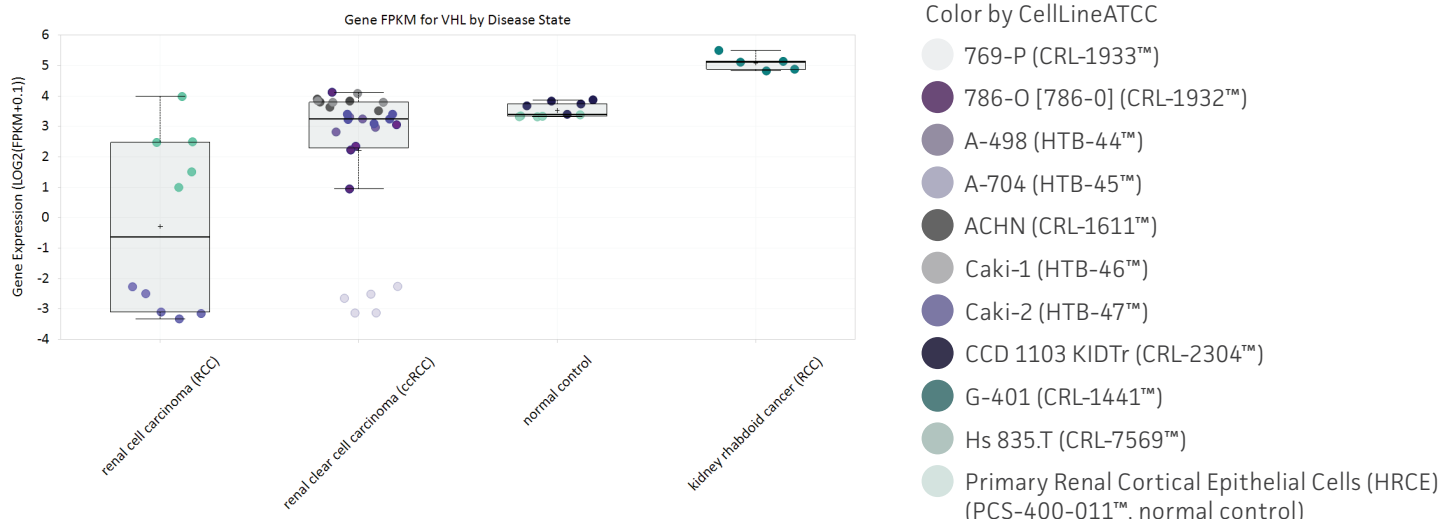**Over 1,000 new datasets are added to ATCC Cell Line Land every year**

LEARN MORE AT WWW.ATCC.ORG/TRANSCRIPTOMICS

EXAMPLES OF ATCC CELL LINE LAND APPLICATIONS

-1.50 ▬ 1.50

CellLineATCC
■ AsPC-1 (CRL-1682™)
■ BxPC-3 (CRL-1687™)
■ MIA PaCa-2 (CRL-1420™)
■ PANC-1 (CRL-1469™)

DiseaseState
■ pancreas adenocarcinoma (PAAD)
■ pancreatic ductal adenocarcinoma

Predict drug sensitivity and optimize cell line selection

You can evaluate the baseline gene expression levels in various cancer cell lines. These data can be used for selecting appropriate models for drug screening against a candidate target gene. Each cell line's gene expression profile is analyzed to identify those with expression patterns most relevant to the target gene. In this example, the x-axis indicates the number of RNA sequencing datasets produced from biological replicates of the respective cell line, each containing a minimum of three biological replicates. Purple indicates induction while dark blue indicates reduction.

Color by CellLineATCC
○ 769-P (CRL-1933™)
● 786-O [786-0] (CRL-1932™)
● A-498 (HTB-44™)
○ A-704 (HTB-45™)
● ACHN (CRL-1611™)
○ Caki-1 (HTB-46™)
● Caki-2 (HTB-47™)
● CCD 1103 KIDTr (CRL-2304™)
● G-401 (CRL-1441™)
○ Hs 835.T (CRL-7569™)
○ Primary Renal Cortical Epithelial Cells (HRCE) (PCS-400-011™, normal control)

Evaluate the differential expression patterns of specific genes in normal and cancerous tissues

In this figure, the mRNA expression of the VHL gene shows significant differences between normal kidney tissue and kidney cancer tissue, particularly in clear cell renal cell carcinoma (ccRCC). In ccRCC, the VHL gene is often inactivated due to mutations, leading to reduced mRNA expression compared to normal kidney tissue.

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