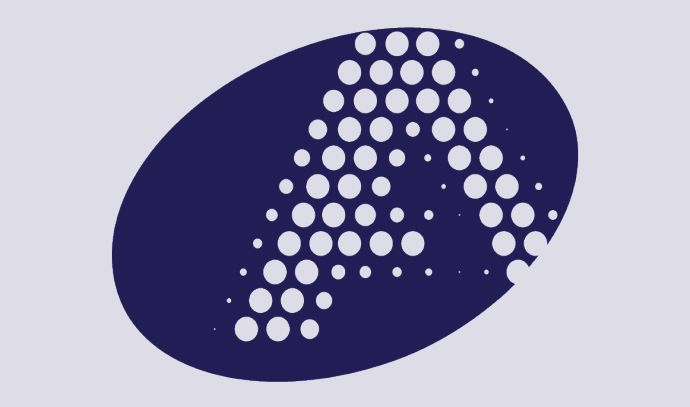


# ATCC® Cell Line Land: An RNA-seq Reference Database for Authenticated Materials



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## Abstract

Biomedical research has struggled with reproducibility issues, often due to the use of poorly documented cell lines. To address this, ATCC has partnered with QIAGEN® to create a reference database of whole transcriptome data for over 3,000 authenticated ATCC human and animal cell lines. Here, we describe our standardized laboratory and bioinformatics workflows, and we present highlights from our initial profiling of ~200 cell lines.

## Introduction

- An estimated 15-20% of all experiments found in the literature are using misidentified cell lines.<sup>1</sup>
- In order to combat negative authentication results, ATCC is completing RNA-seq analysis on their broad selection of cells using well-established protocols and stringent quality metrics (described below).
- All fully authenticated data will be available through the ATCC Cell Line Land (ACLL). For more information: <https://digitalinsights.qiagen.com/atcc-cell-line-land>.

## Materials & Methods

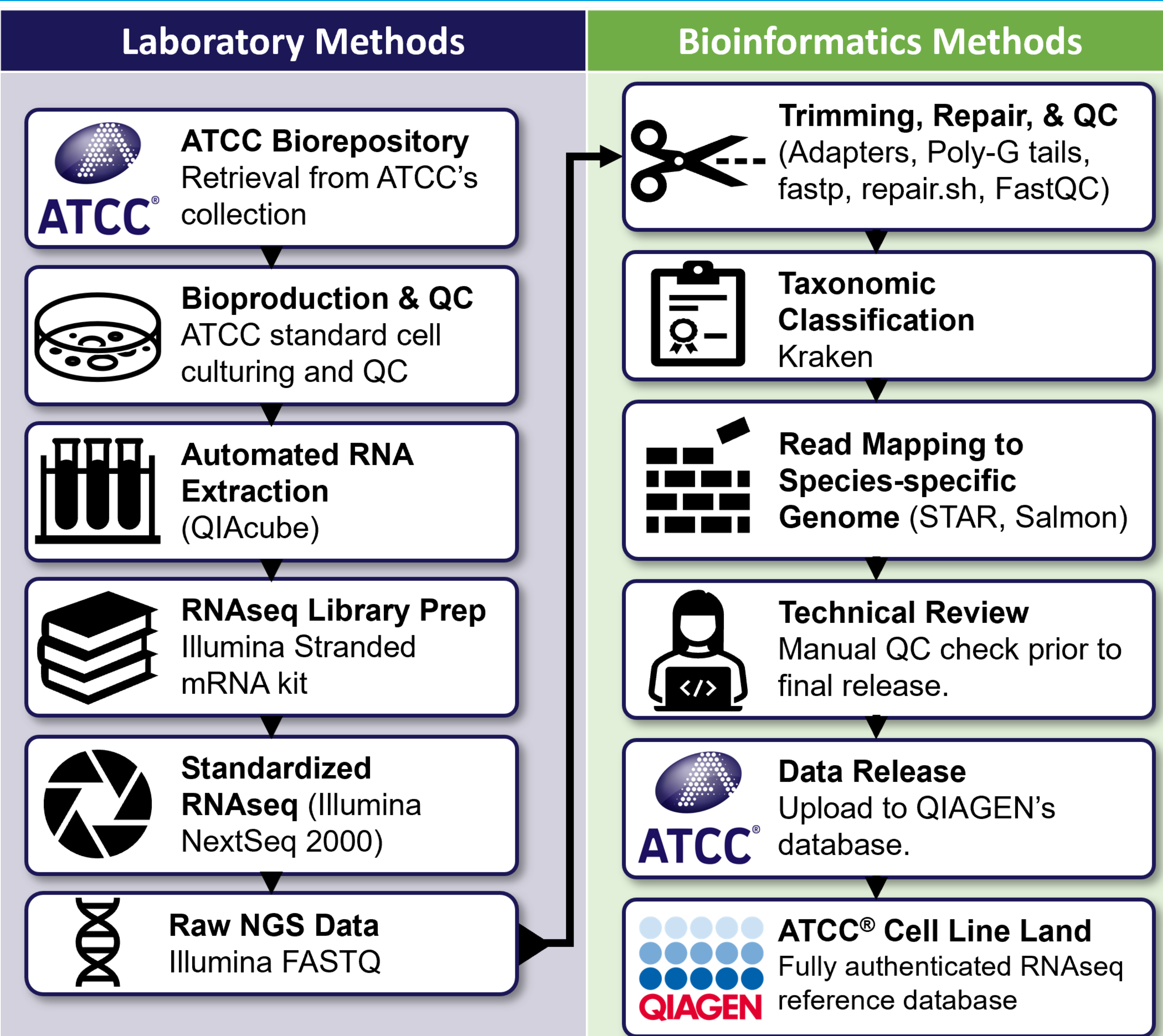


Figure 1: Schematic of experimental workflow.

Table 1: QC metrics used for data approval and examples of metadata in the ACLL.

QC Metrics	Average Values	Metadata Available
RNA Integrity Number (RIN)	>6.5	Passage # Disease
260/280 Value	>1.8	Sex Tissue/cell type
Input Read Number	>18x10 <sup>6</sup>	Age Growth media
% Uniquely Mapped Reads	>70%	Ethnicity Culture condition Demography Cryopreservation

## Results

Gene expression results for human tissue by available metadata in the ACLL.

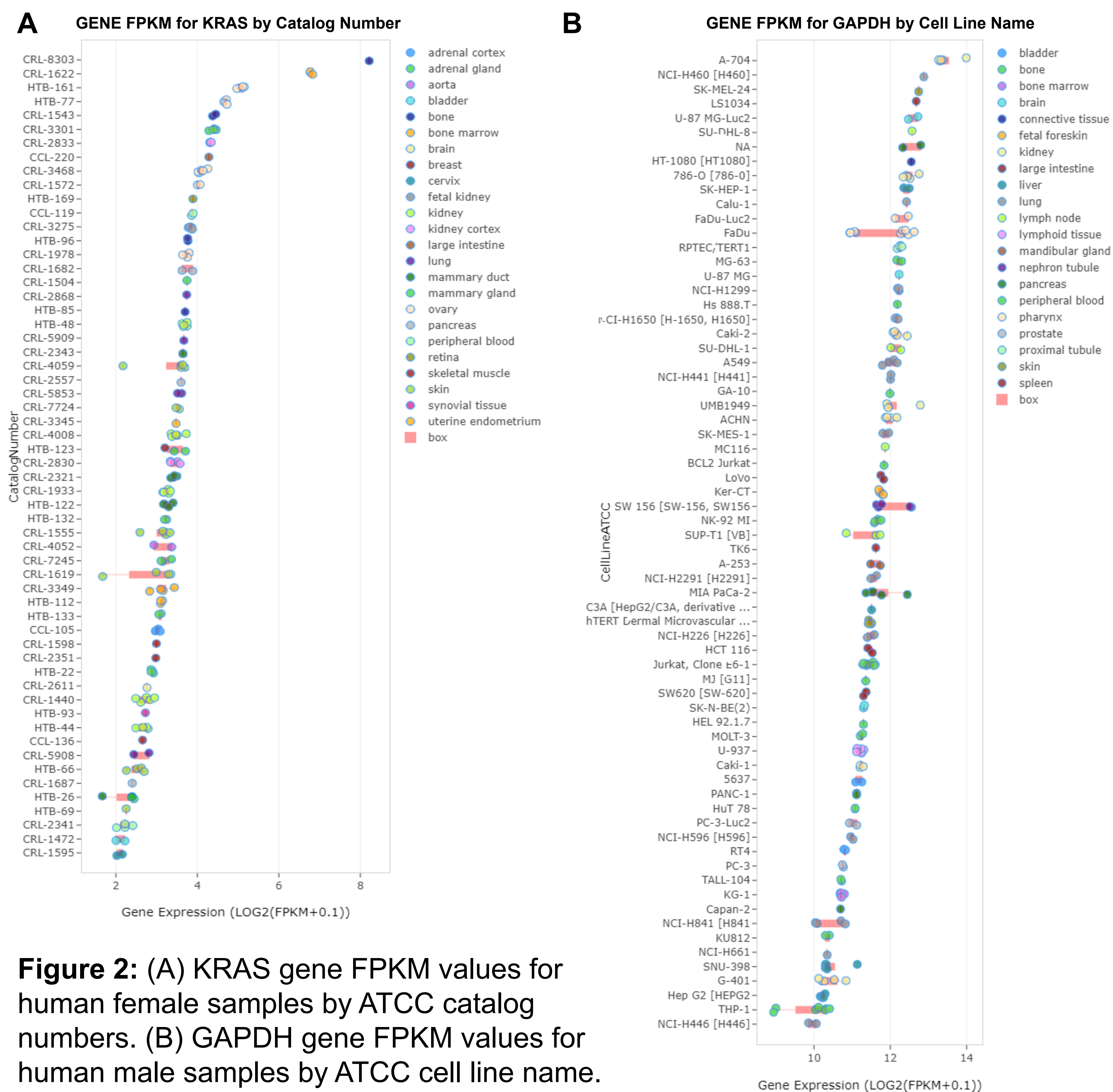


Figure 2: (A) KRAS gene FPKM values for human female samples by ATCC catalog numbers. (B) GAPDH gene FPKM values for human male samples by ATCC cell line name.

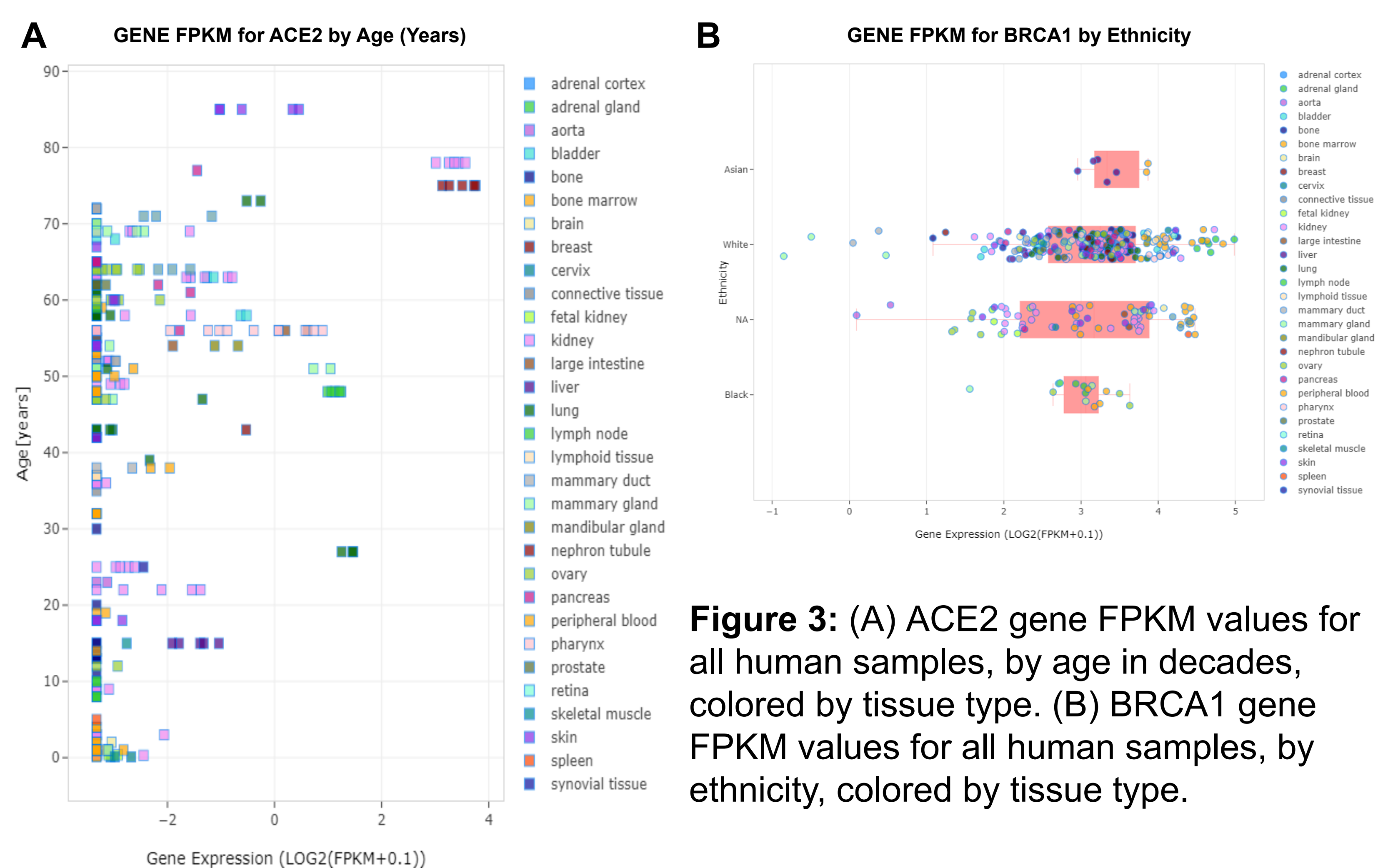


Figure 3: (A) ACE2 gene FPKM values for all human samples, by age in decades, colored by tissue type. (B) BRCA1 gene FPKM values for all human samples, by ethnicity, colored by tissue type.

## Summary

ATCC's extensive, ISO-certified quality control cell culture and sequencing metrics combined with a standardized bioinformatic analysis pipeline leads to the creation of reliable, reproducible, fully-authenticated RNA-seq data.

<https://digitalinsights.qiagen.com/atcc-cell-line-land>

### References

- Freshney, R. Ian. "Database of misidentified cell lines." International journal of cancer 126.1 (2010): 302-302..

