

# Improvements to single-cell mRNA sequencing

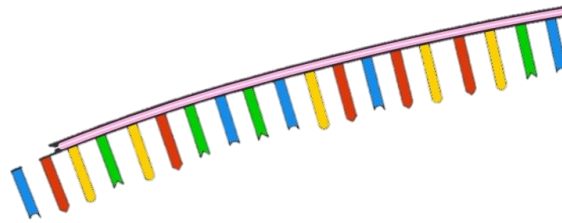
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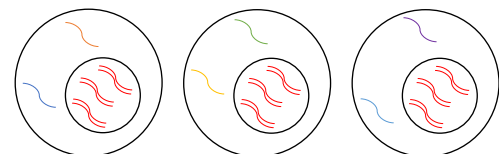
Funding sources:



**GORMAN**  
RESEARCH SCHOLARS

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## RNA Sequencing Shows Cell Functionality



heart cell

kidney cell

skin cell

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# Single-Cell Sequencing Reveals Rare Cell Types

- RNA sequencing conducted in bulk conceals the information gained from single cells

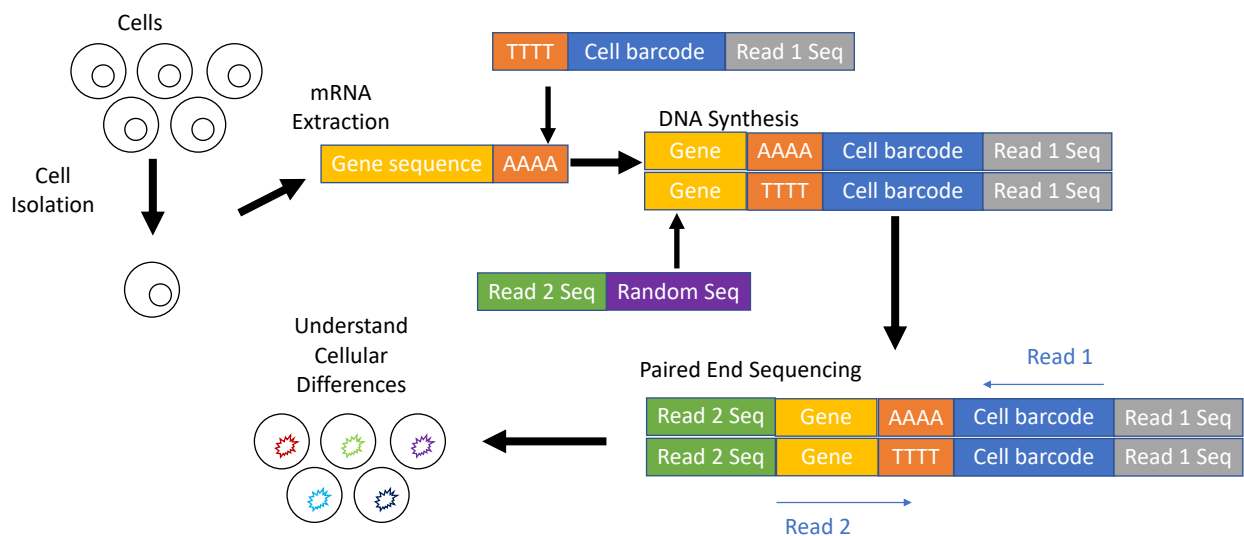


Bulk Sequencing



Single-Cell Sequencing

# Current Method For Single-Cell mRNA-Seq



## Project Aims

### Overall Goals:

1. Lower Costs
2. Maintain sensitivity

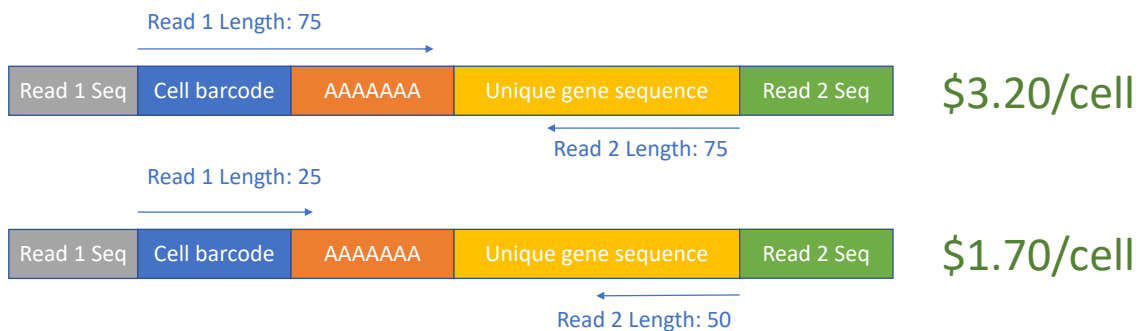
### Accomplished By:

1. Sequencing Less Nucleotides
2. Reversing The Current Method

Sensitivity: the ability to accurately identify a sequence as being unique to a gene

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## Currently 150 Bases are Read During Paired-End Sequencing But a 75 Base Kit Is Available

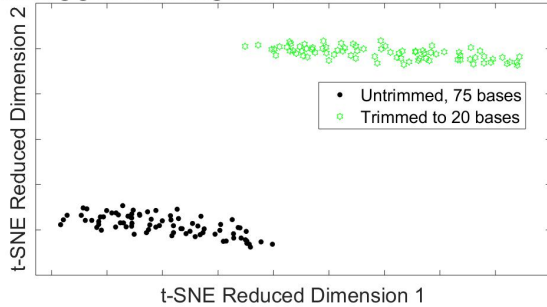


It is unclear if 50 base pairs of gene sequence is enough to uniquely identify a gene

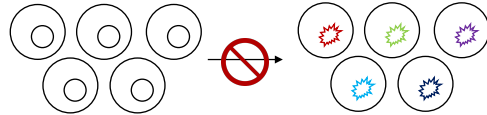
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# Moving To A 75 Base Kit Does Not Affect Cell Type Identification

Trimming gene read length to 20 bases effects cell identification

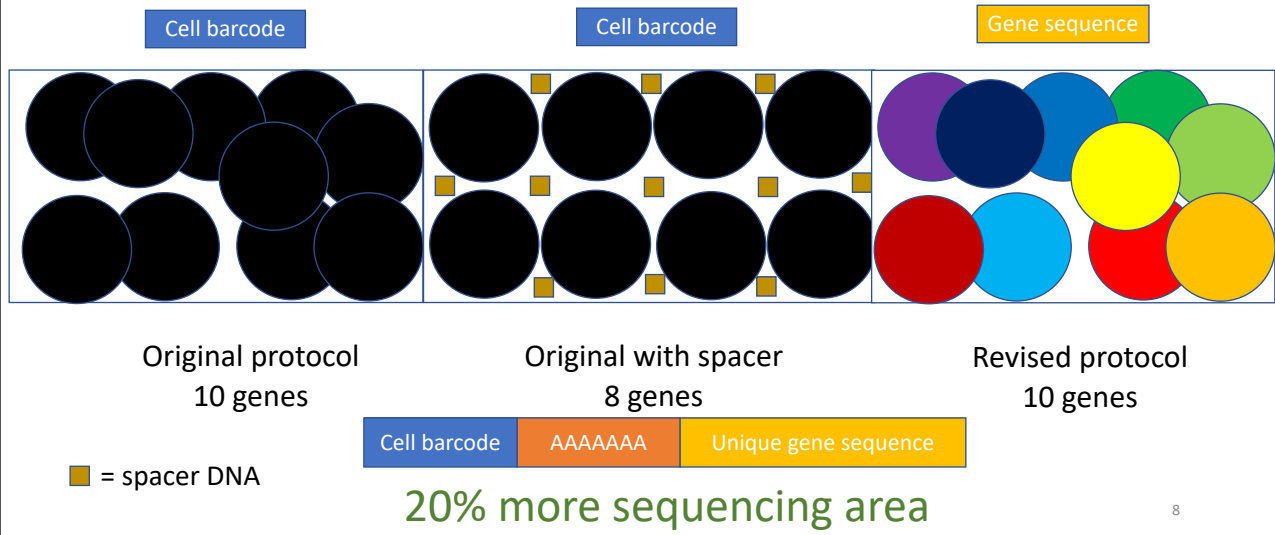


- Created artificial reduction of sequencing data in a simulation
- ~~Simulation with 50 to 25 bases unique gene sequences that is indistinguishable from the real (75 base) run~~

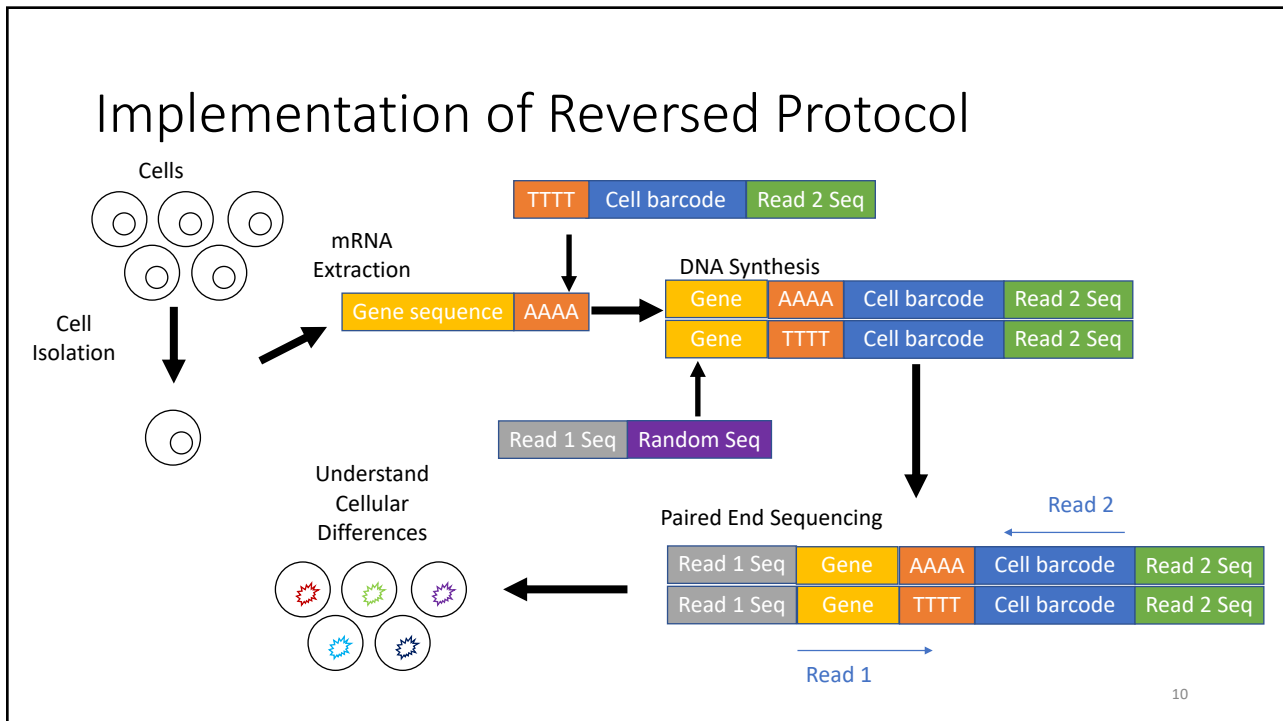
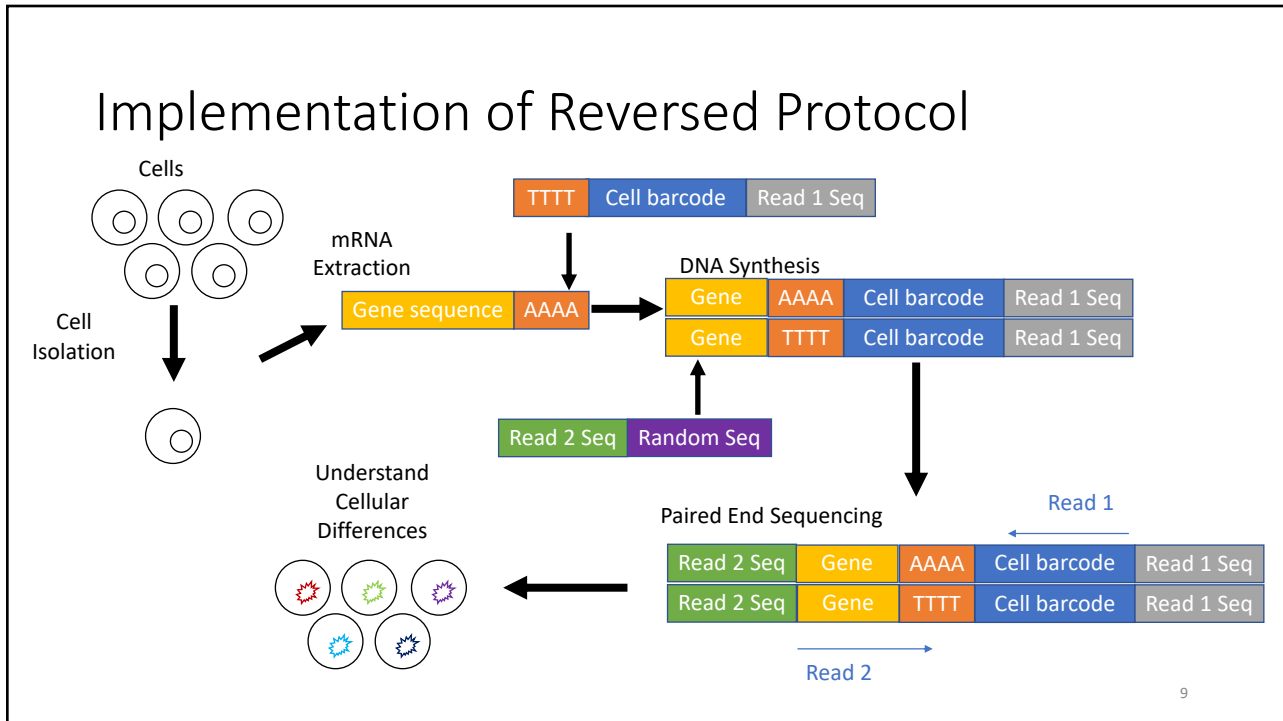


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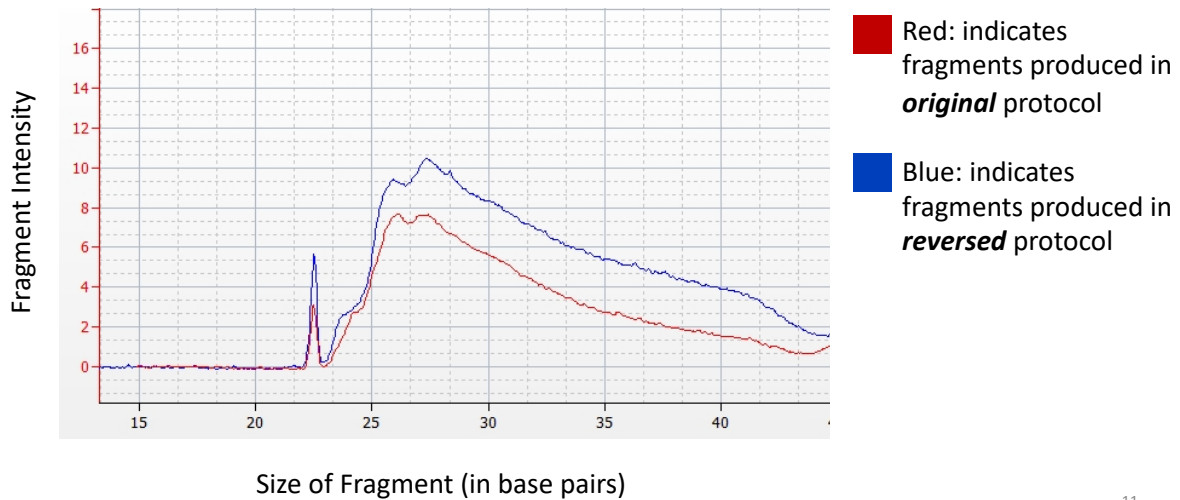
# Current Lack of Diversity in Read 1 Necessitates the Addition of Spacer DNA During Sequencing



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## Testing for RNA in reversed protocol shows to be effective



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## Costs Reduced for Protocol

- Original Cost: \$3.20/cell
- ✓ Sequencing Less Nucleotides → \$1.70/cell
  - ✓ Reversing The Current Method → \$1.36/cell (20%)

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## The Dey group

### Graduate students

Alex Chialastri  
Chad Wangsanuwat  
Matthew Smith (not pictured)

### Undergrad

Rob Jones  
Estella Liu (not pictured)  
Yash Nagpal

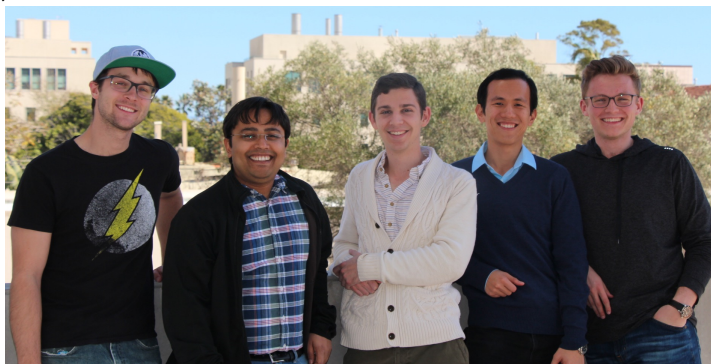
### Former graduate students

Sam Wilson (rotating)  
Nicole Chan (rotating)

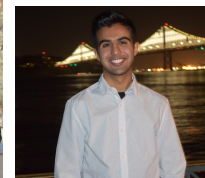


CHEMICAL ENGINEERING  
UC SANTA BARBARA

## Acknowledgements



PI: Prof. Sid  
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