

# Profiling of transcribed cis-regulatory elements in single cells

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# Background

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- GRO-seq - 2008 Dec
- CAGE-Seq - 2012 Feb
  - Riken
  - Piero Carninci
    - Leads the FANTOM project
    - Director of Riken Omics in 2008

# CAGE-Seq



## Pros:

- Measures RNA expression levels and maps TSS in promoter regions
- Provides precise mapping of TSS with single-nucleotide resolution

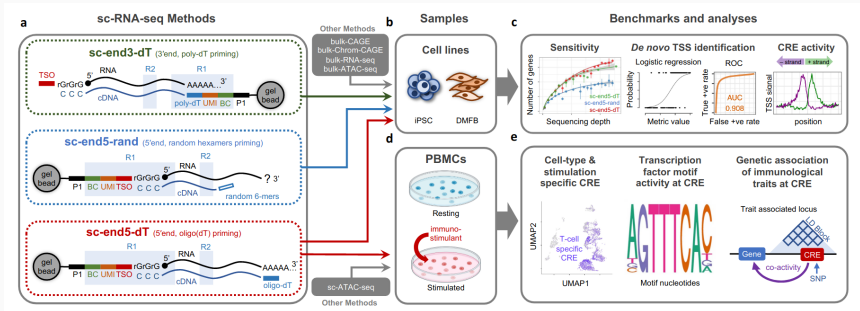
## Cons:

- Only works on total mature RNA
- Detection is biased toward TSS of long-lived transcripts

# Introduction

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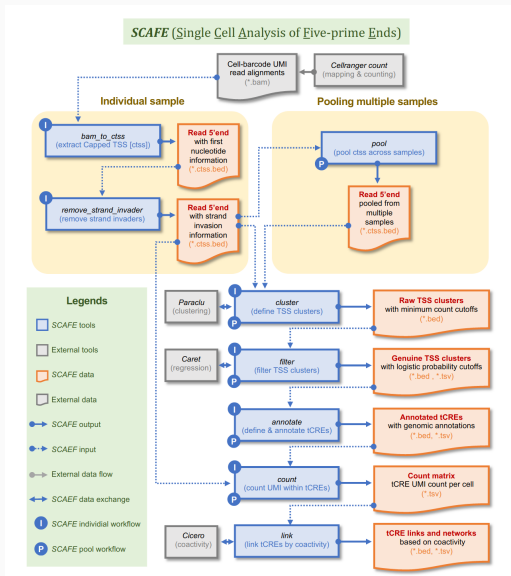
# Overview of the experimental designs and benchmark analysis



# tCRE and aCRE

- tCREs are defined by merging closely located TSS clusters with  $\pm 500$ nt of gene TSS
- aCREs are defined by the ATAC peak ranges



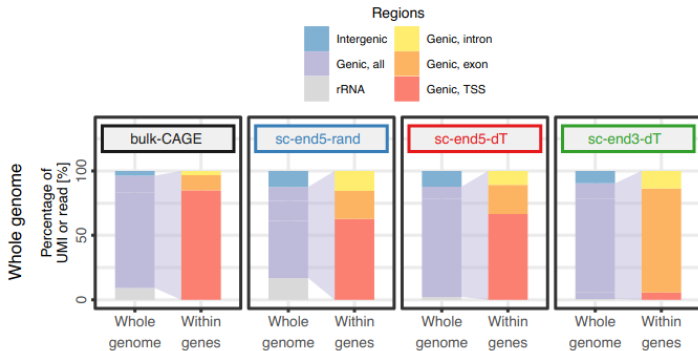


# Results

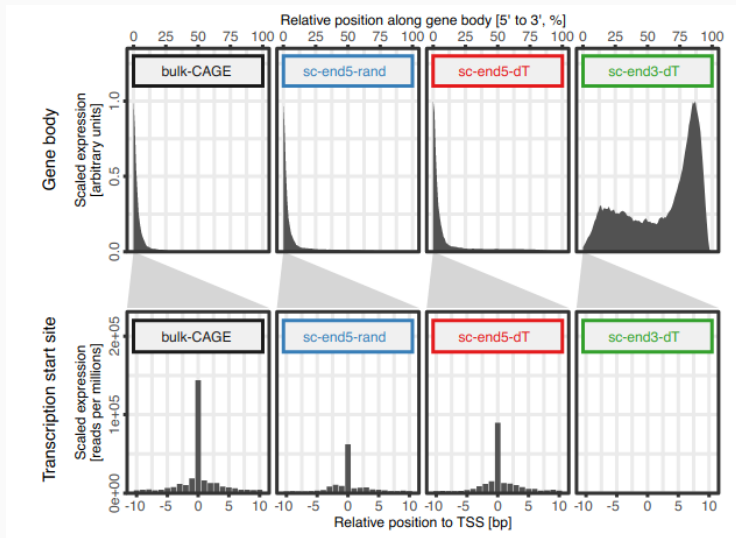
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# Performance of sc-RNA-seq methods

**a**

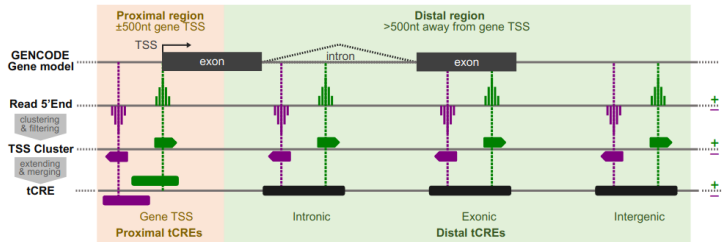


# Performance of sc-RNA-seq methods

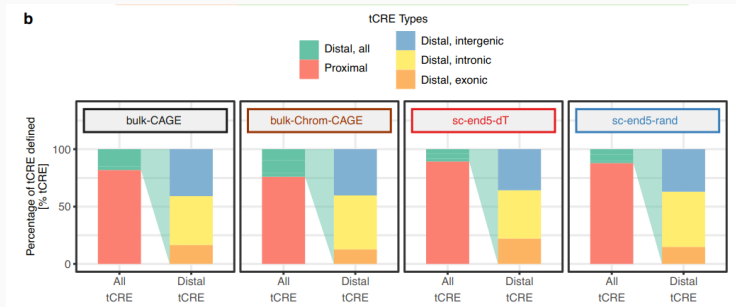


# Definition and properties of tCRE

a



# Definition and properties of tCRE



- Comparison of tCRE and aCRE in PBMCs
- Disease-associated variants attCRE and aCRE in PBMCs

# Discussion

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# Discussion

- Can detect eRNAs with sc-end5-seq, however high level of dropouts
  - Use of meta-cells might fix this
  - Alternative library prep with just nuclei or targeting eRNAs
- sc-end5-seq data can theoretically detect CRE activity with no extra cost
  - Lack of dedicated tools for data analyses prevented the wider adoption