



# Hands-on Workshop

## CMCexplorer for sncRNA Data Analysis

CMCexplorer allows you to explore small non-coding RNA (sncRNA) molecules and profiles from thousands of datasets across the Sequence Read Archive (SRA), the International Nucleotide Sequence Database Collaboration (INSDC), and others. Explore within or across one or more samples, and investigate specific isoforms such as isomiRs, tRFs, rRFs, and yRFs.

### CMCexplorer at a glance

- 61,904** datasets
- 8,625,844** molecules  $\geq 10$  RPM
- 69,244** isomiRs
- 256,918** rRFs
- 67,181** tRFs
- 9,280** yRFs
- 8,219,349** unk
- 3,872** multiclass

### Molecule Explorer

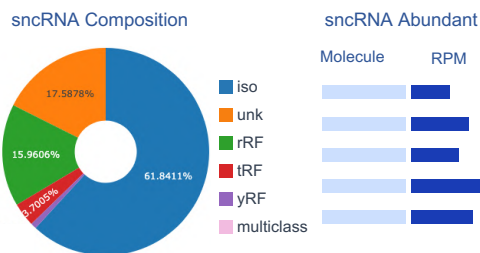
TCTCACTGTAGCCTCGAACCCC

isomiR tRF rRF

yRF other

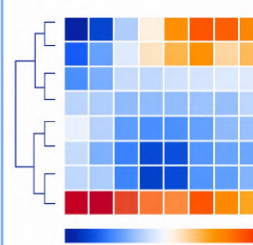
Explore molecules and isoforms across datasets

### sncRNA Profile Overview



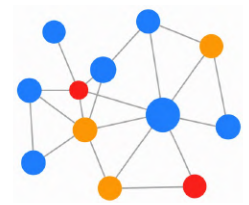
Inspect the composition of sncRNA types and identify the most abundant sncRNAs

### Heatmaps



Visualize expression patterns across samples

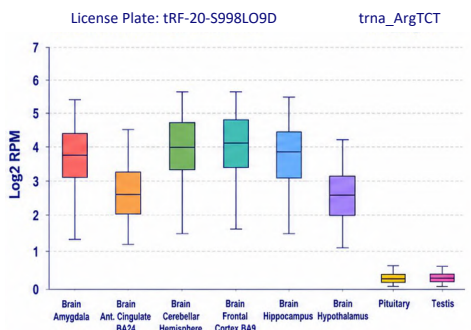
### Networks



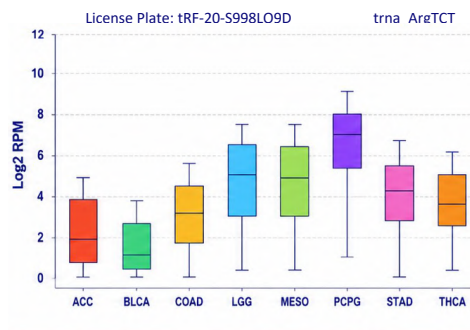
Explore relationships between molecules

## Evidence in action: Explore sncRNA data

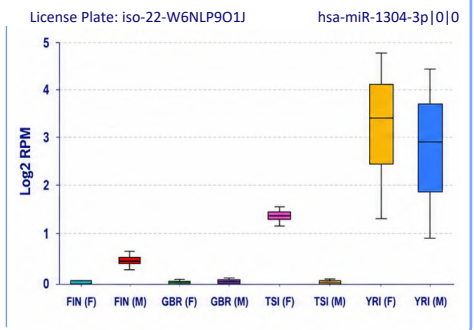
### Expression across tissues



### Expression across cancer



### Population-level comparison



### What you will do in the workshop

- ✓ Explore sncRNA composition in samples
- ✓ Find top-expressed sncRNAs
- ✓ Inspect specific molecules such as isomiRs across tissues
- ✓ Compare expression across tissues or populations
- ✓ Use heatmaps and networks to interpret patterns

Participants should bring a laptop

### Workshop details

- Date:** Wednesday, July 8
- Time:** 09:00-12:00
- Location:** Hamilton Building, TJU
- Registration:** [Click here to complete the registration form](#) ↗

**Seats are limited** - Apply by Wednesday, July 1, 2026



SCAN ME



**Accelerate Discovery**  
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