

METHODS FOR DE NOVO DISCOVERY OF RNA EDITING EVENTS

IRINA SHCHUKINA

**ALEXANDER KANAPIN, ANASTASIA SAMSONOVA
DEPARTMENT OF ONCOLOGY
UNIVERSITY OF OXFORD**

TYPES OF RNA EDITING

A → I (ADAR)

C → U (APOBEC)

 G G A A
 G G A A
 G A A A
 G A A G
 G G G G
 G G A G
 G A A G
AAGGACTCGTATCACGGATACCGTAGC

Global goal: framework
development

This semester: benchmarking
of existing methods

TOOLS AND DATA

- ▶ REDITools
- ▶ RED
- ▶ ~~GIREMI~~

K-562 cell lines RNA-seq and DNA-seq (ENCODE project)

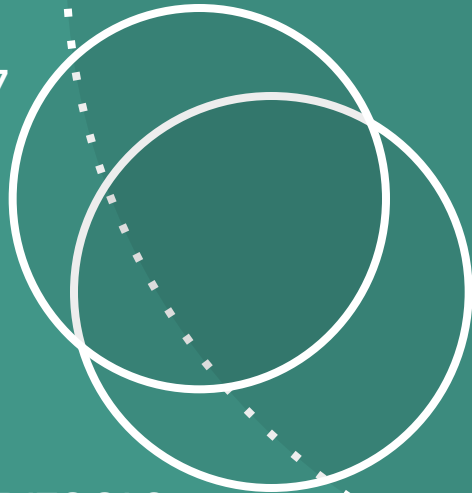
MCF-7 cell lines RNA-seq (hypoxia and normoxia)

**K-562: genome +
transcriptome**

RED
29,927

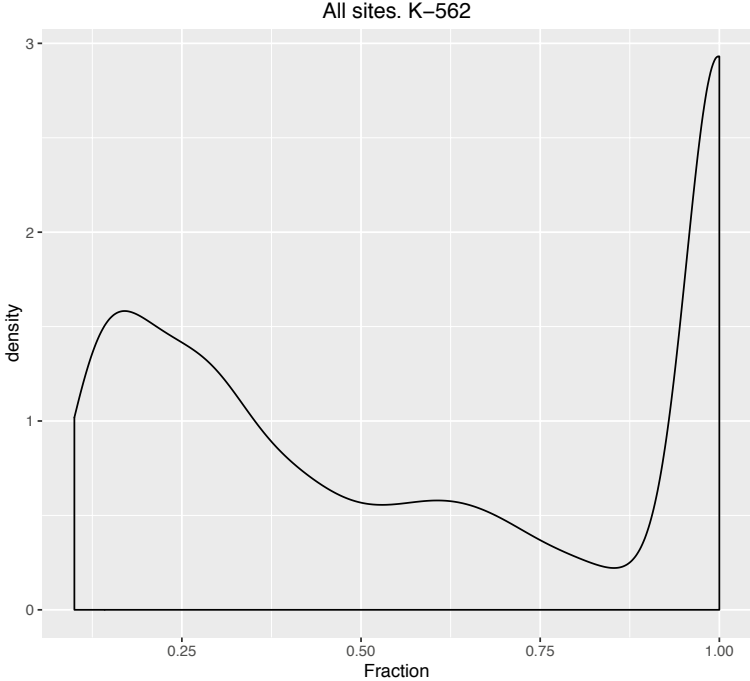
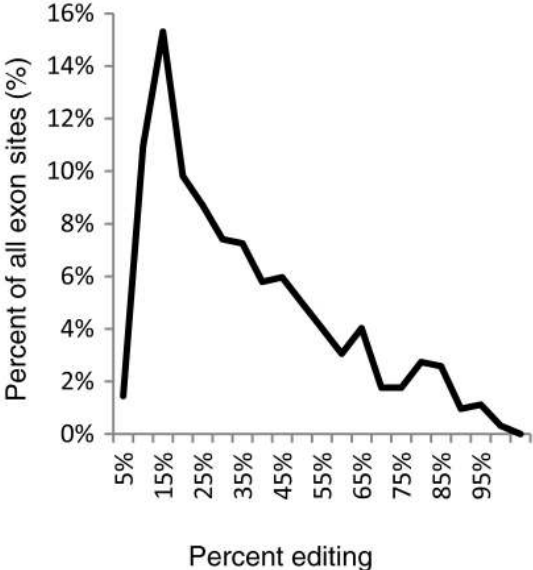
REDITOOLS
31,896

VARSCAN DNA
4,140,928



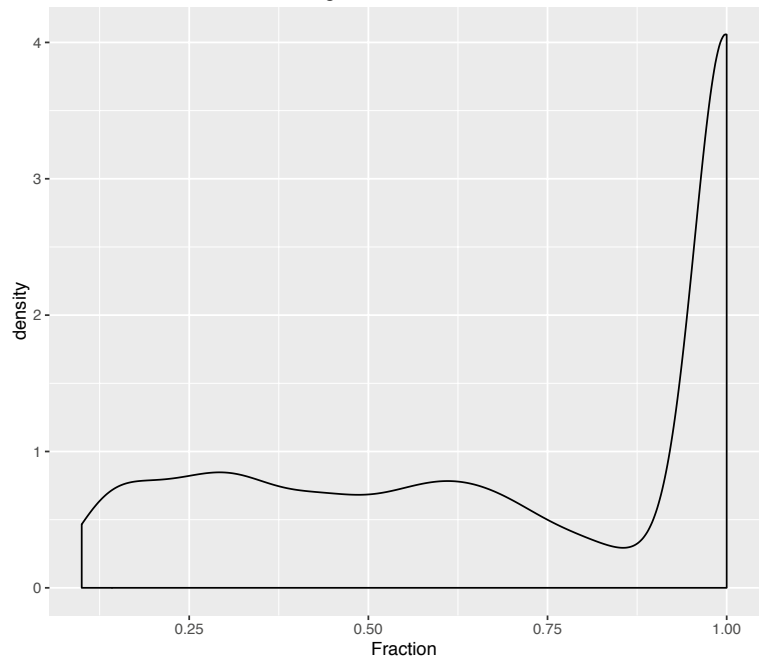
FRACTION DISTRIBUTION (K-562)

C

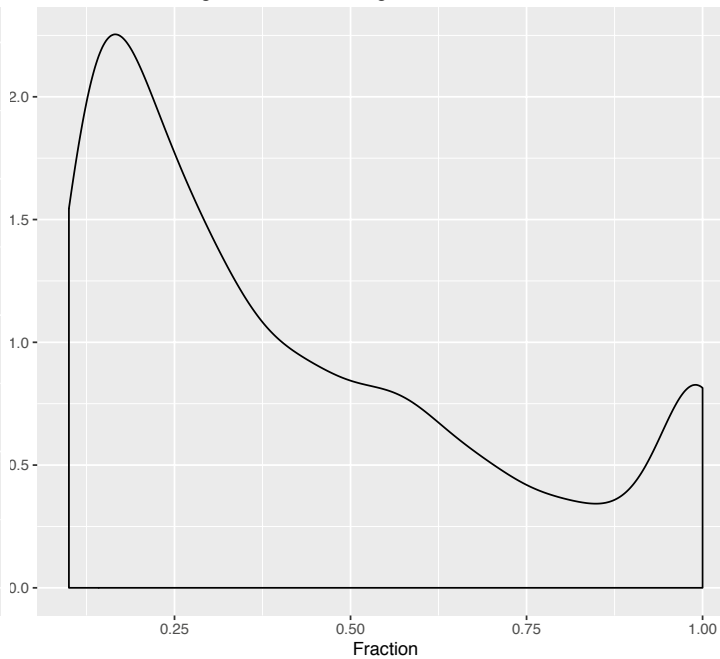


FRACTION DISTRIBUTION (K-562)

All significant sites. K-562



Significant sites. No genome SNPs. K-562



MCF-7

Normoxia



→ Nuclear RNA
→ Cytoplasmic RNA

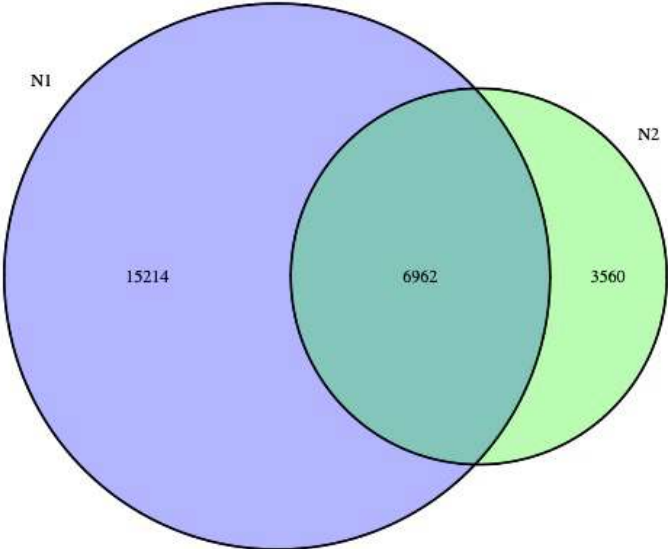
Hypoxia



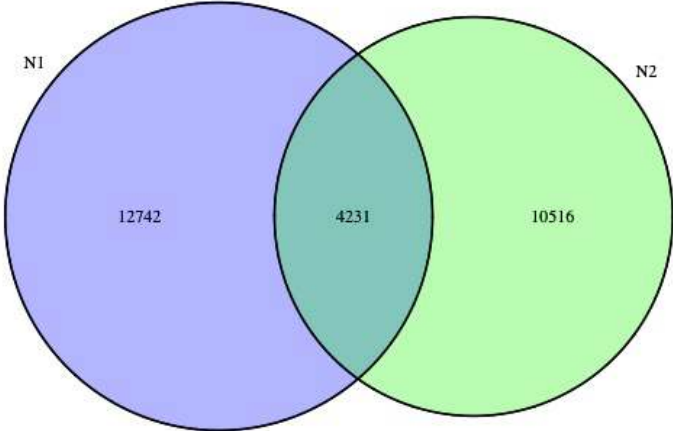
→ Nuclear RNA
→ Cytoplasmic RNA

(2 biological replicates)

REPLICATES COMPARISON

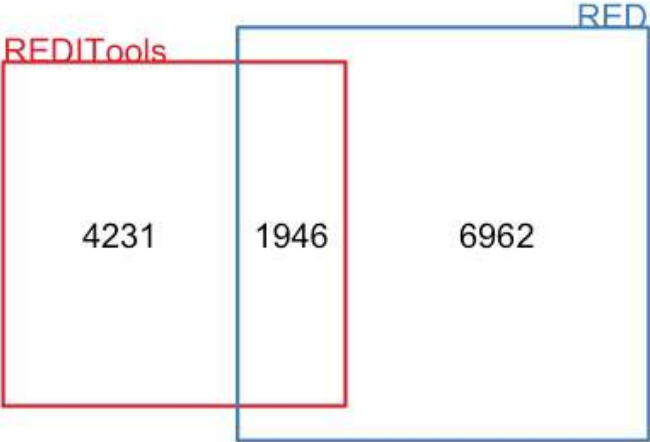


REDITools
(nucleus normoxia)

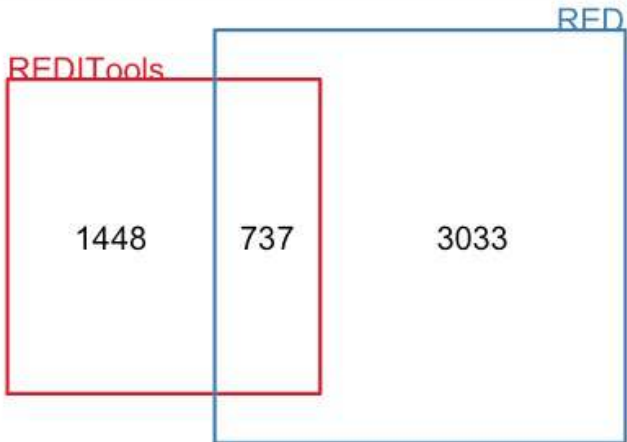


RED
(nucleus normoxia)

REDITTOOLS AND RED RESULTS



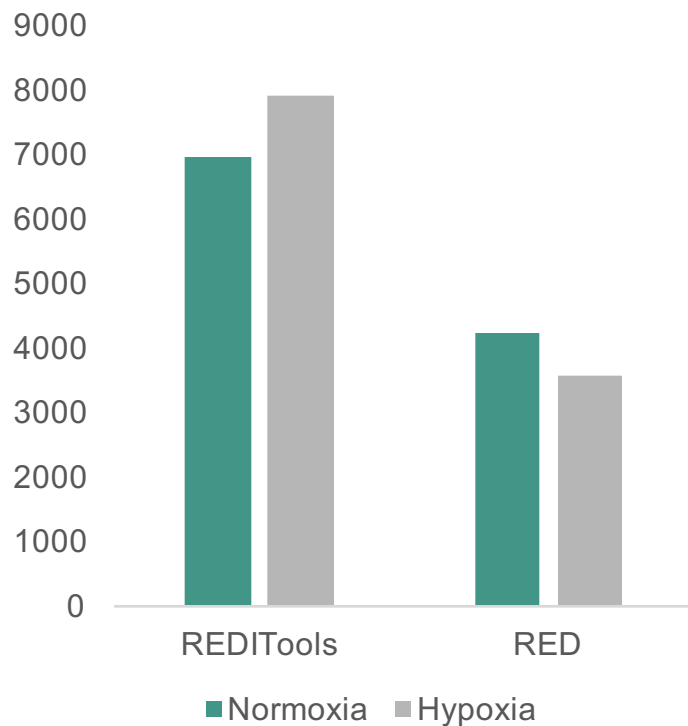
Nucleus
(normoxia)



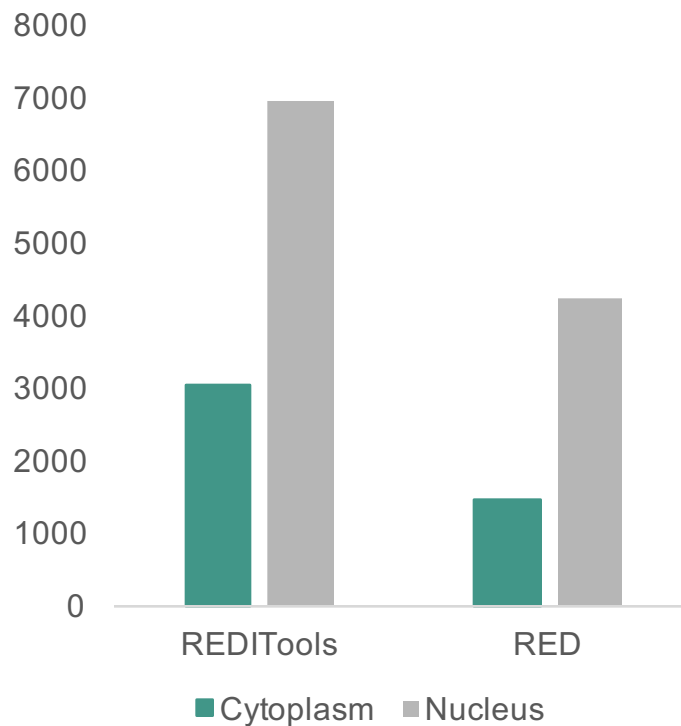
Cytoplasm
(normoxia)

DATA ANALYSIS

Hypoxia vs normoxia




Cytoplasm vs nucleus



RESULTS

- ▶ Bias towards sites with high fraction (SNPs)
- ▶ Poor noise removal
- ▶ Intersection between two methods: 30%
- ▶ Still some biologically relevant results

Future plans: framework development and analysis of total RNA-seq of 10 cancer cell lines (2 conditions)

The image features a teal background with a diagonal split. The upper-left portion is white, while the rest is a solid teal color. The text 'Thank you!' is positioned in the white area.

Thank
you!