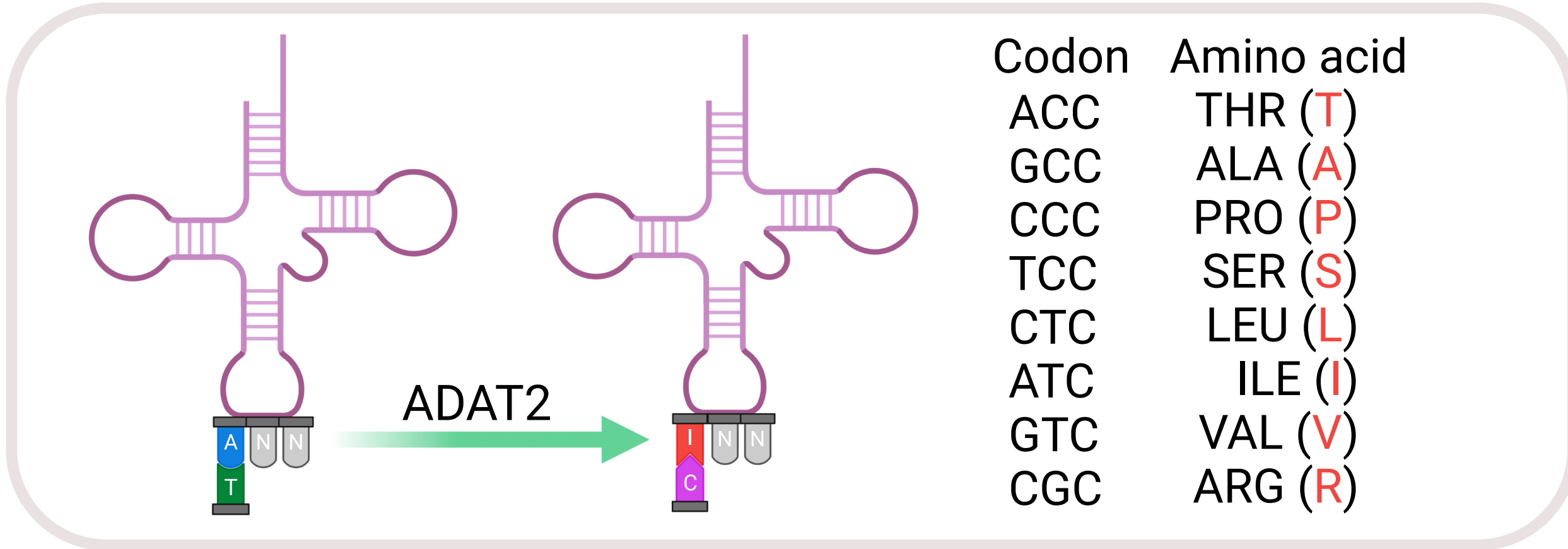


In silico prediction of the impact of tRNA modifications on mRNA translation

Marine Leclercq, Ning An, Coralie Capron, Arnaud Blomme, Pierre Geurts, Francesca Rapino, Pierre Close

ADAT2 - Adenosine Deaminase tRNA-specific 2

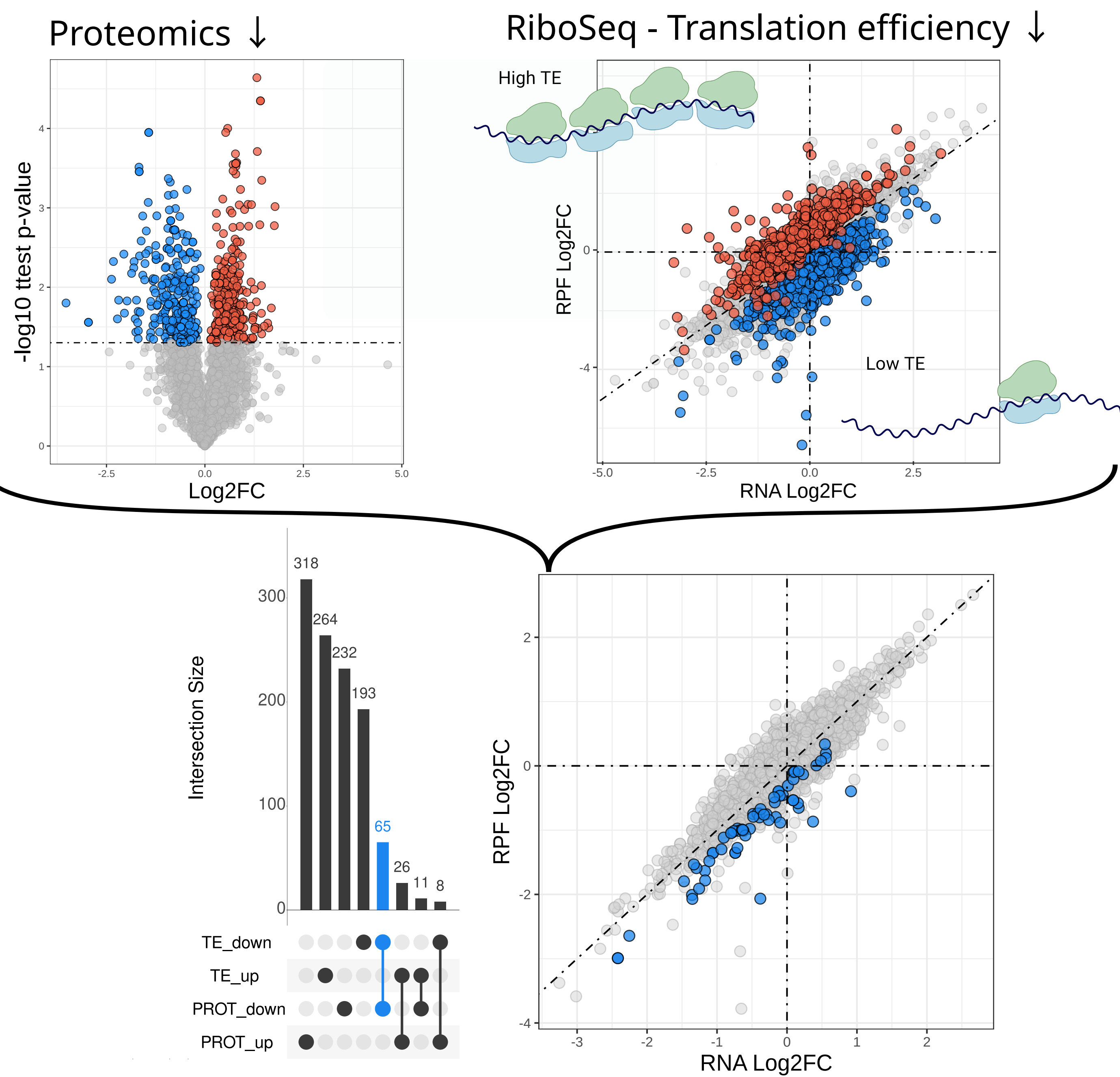


What is the impact of ADAT2 on the proteome? What makes a protein more dependent on ADAT2?

Preliminary data

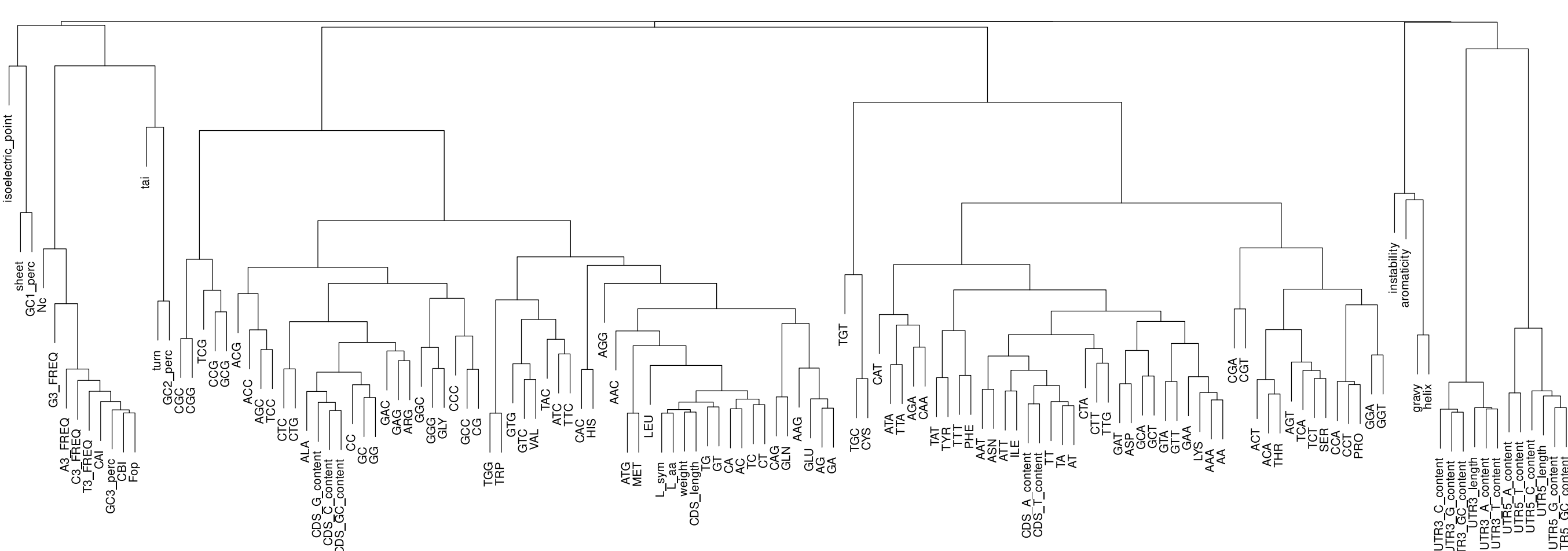
1. Target set

Data from lung cancer cells depleted for ADAT2



By crossing proteomics with RiboSeq, we end up with a list of **65 high-confidence target genes**

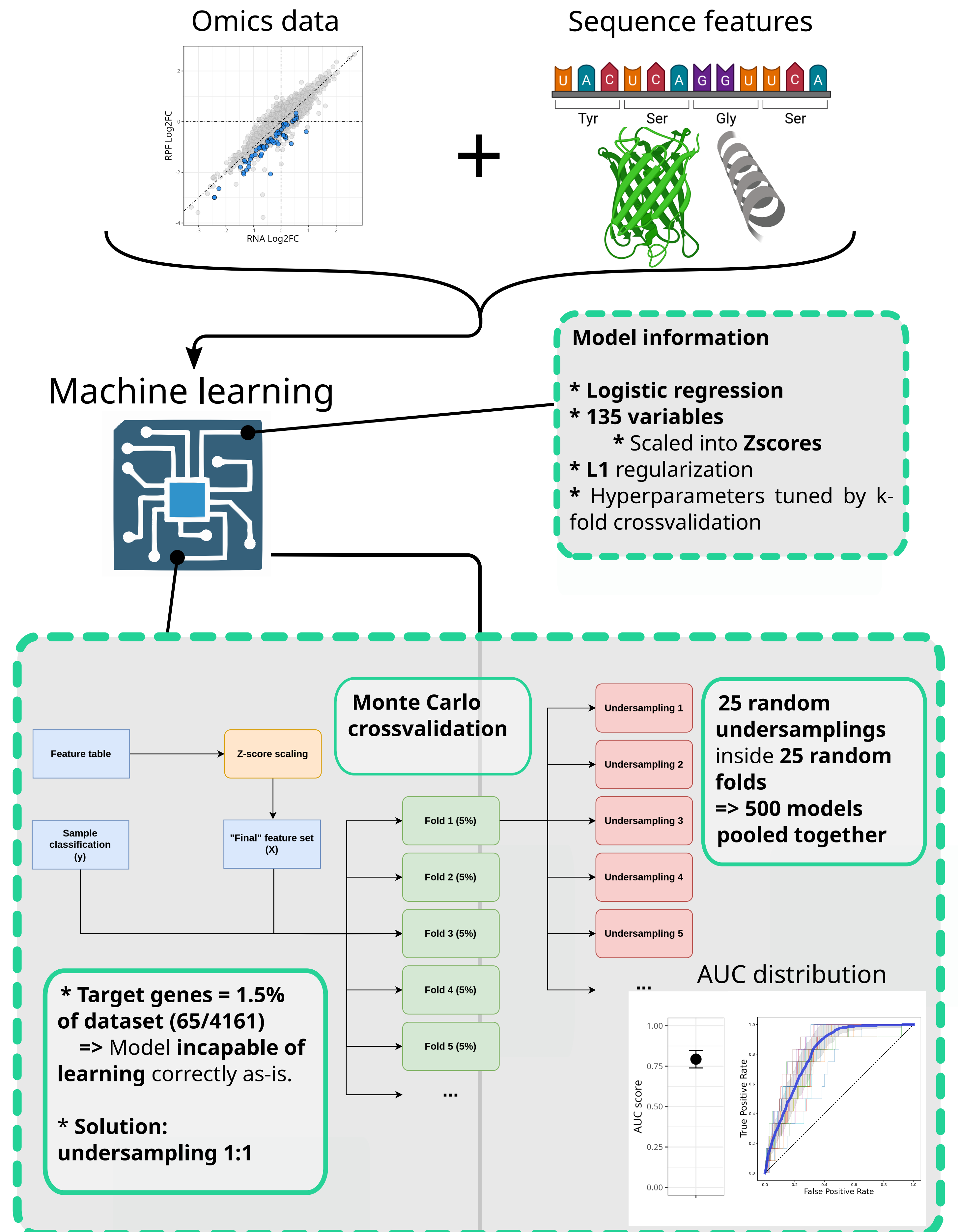
2. Feature set



We created a **database of sequence features** that span the entire consensus CDS of the human genome.

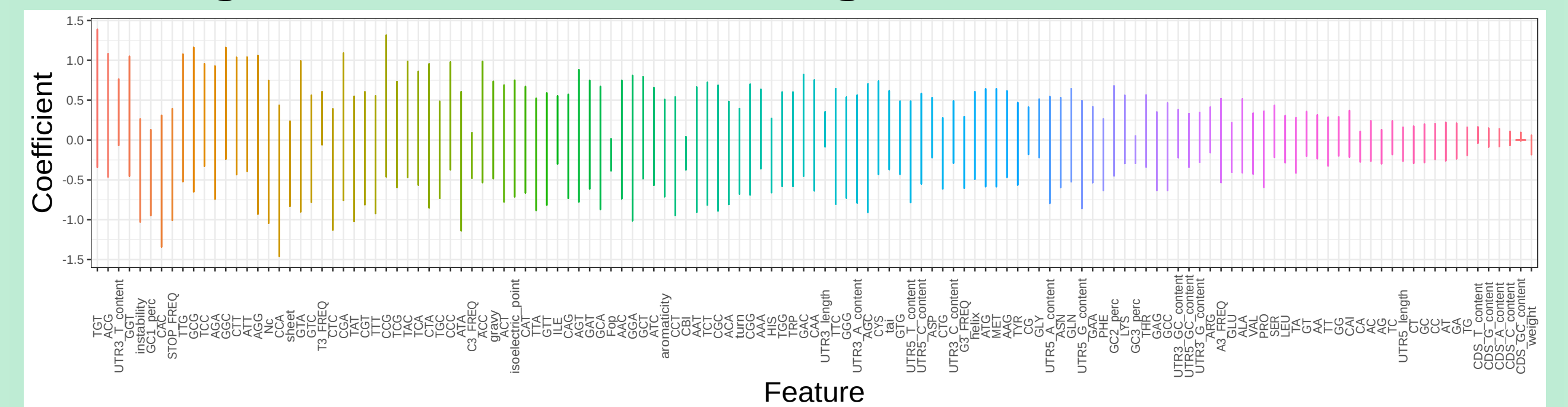
Lower-order features + higher order features

Machine learning pipeline



Feature selection (W.I.P.)

* Resulting distribution of feature weights ↓



* **High variability in weights** between models → yet **really good performance**

Why?

- **Correlation between variables** could be confusing the model

* Tentative **solution**:

- Identify **clusters of correlated variables** → **remove iteratively** to rank

End goal

