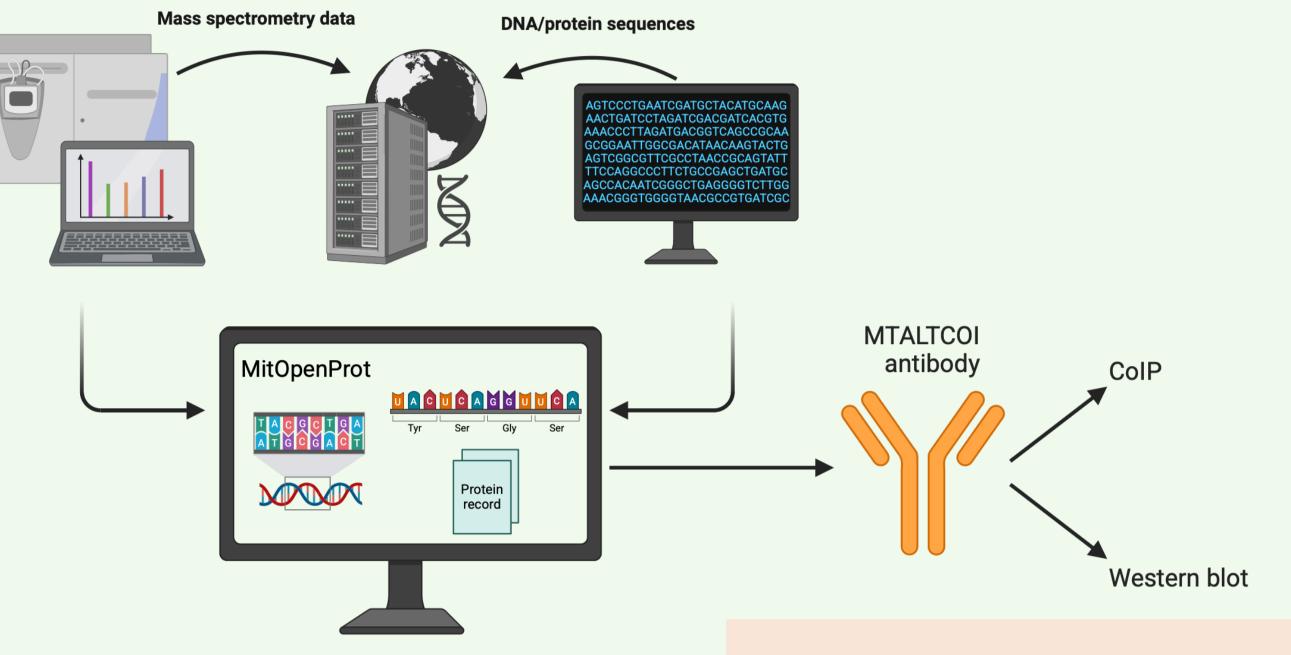
# Unraveling the mitochondrial alternative proteome: systematic identification and evolutionary insights into altORFs

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# What is MitOpenProt?

Based on mass spectrometry data, DNA/protein sequences, MitOpenProt predict protein and DNA sequence of proteins localized in the alternative open reading frames of mitochondrial DNA.

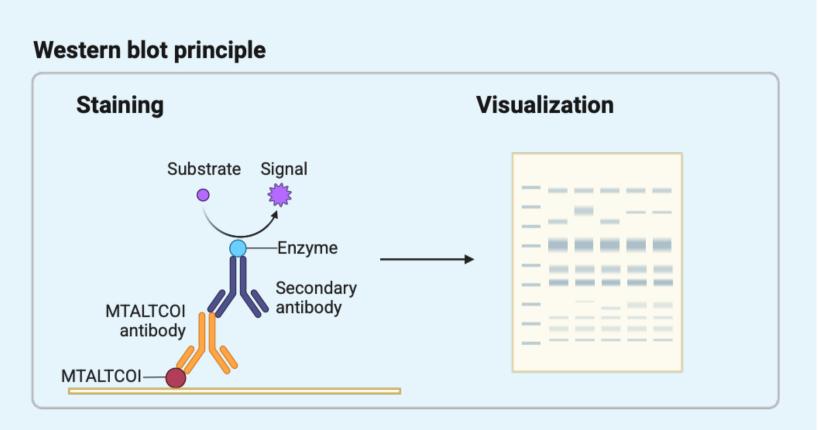


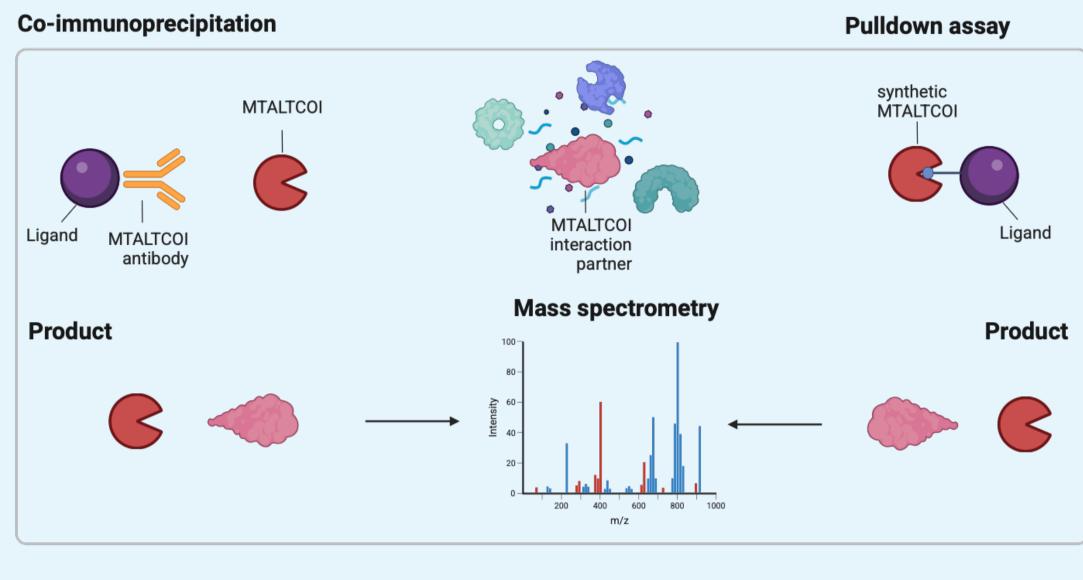
Develop a bioinformatic pipeline to allow alternative protein discovery in human mitogenome

# MitOpenProt Wetlab Application

Antibodies designed with MitOpenProt are useful to:

- Identify proteins with Western Blot;
- Identify interaction partners with co-immunoprecipitation.





# MitOpenProt Development

Conservation analyses

mtaltORFs DNA sequence

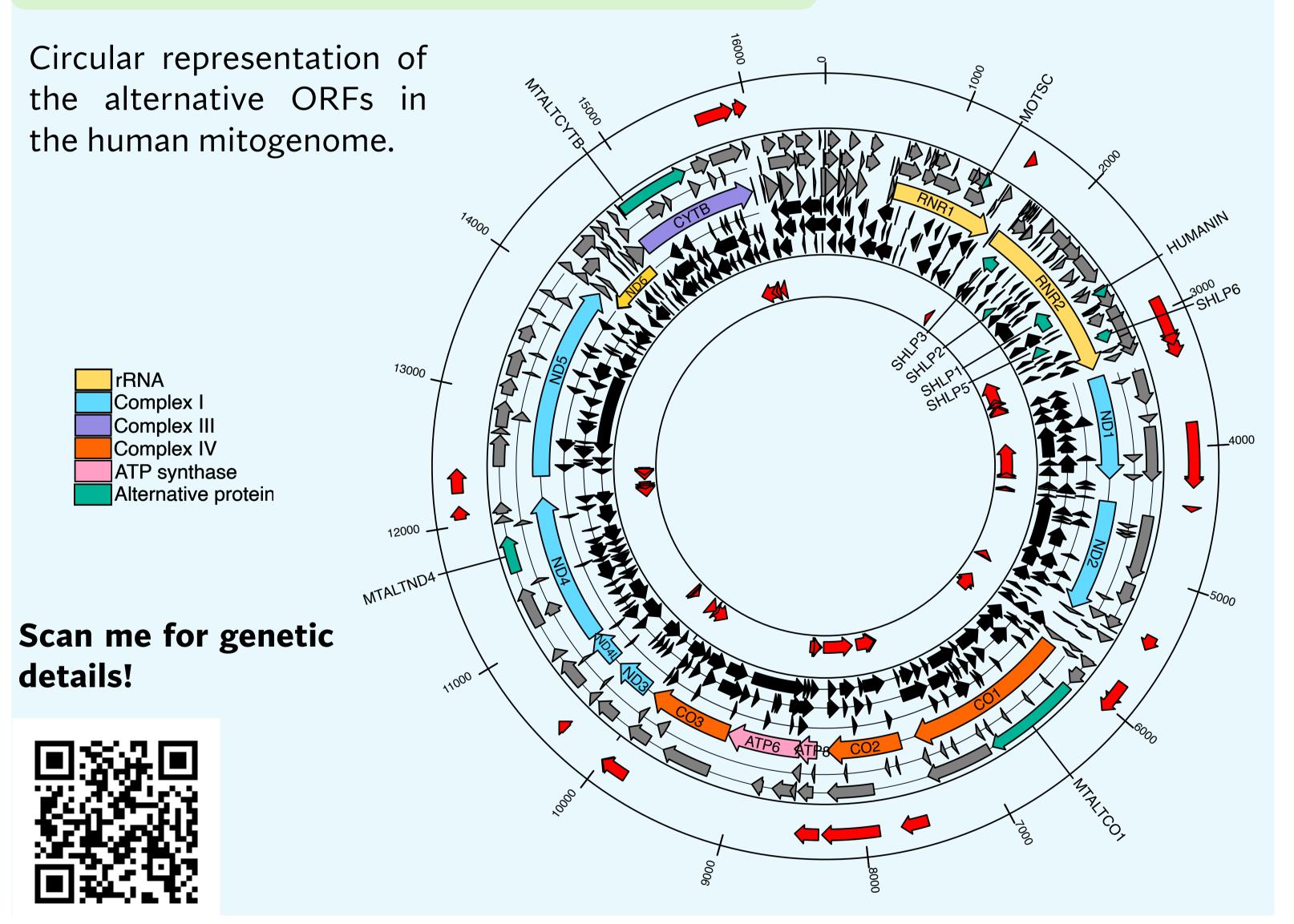
Gene expression

Translation

Degeneracy

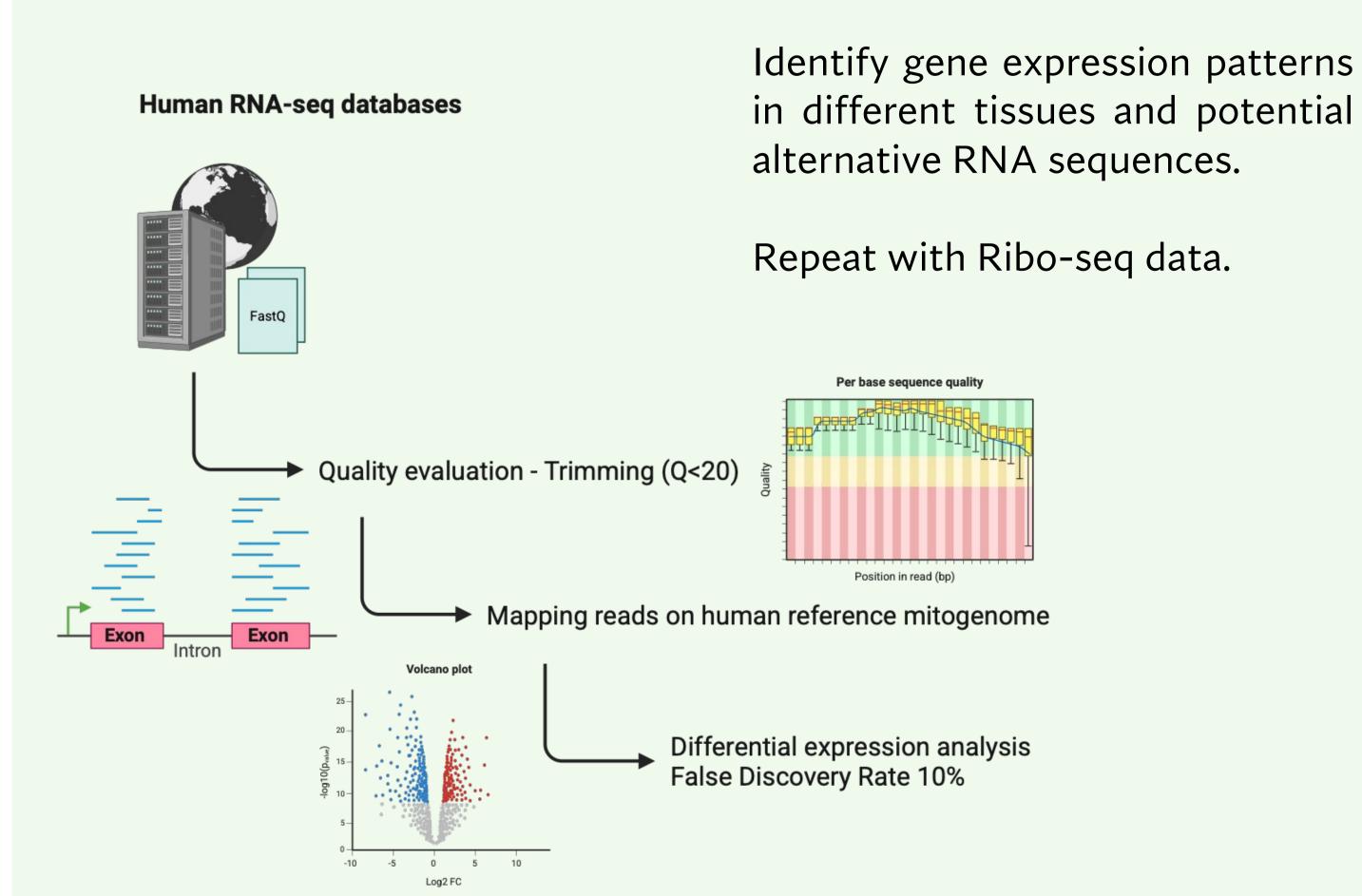
Conservation

# MtaltORFs Human Map



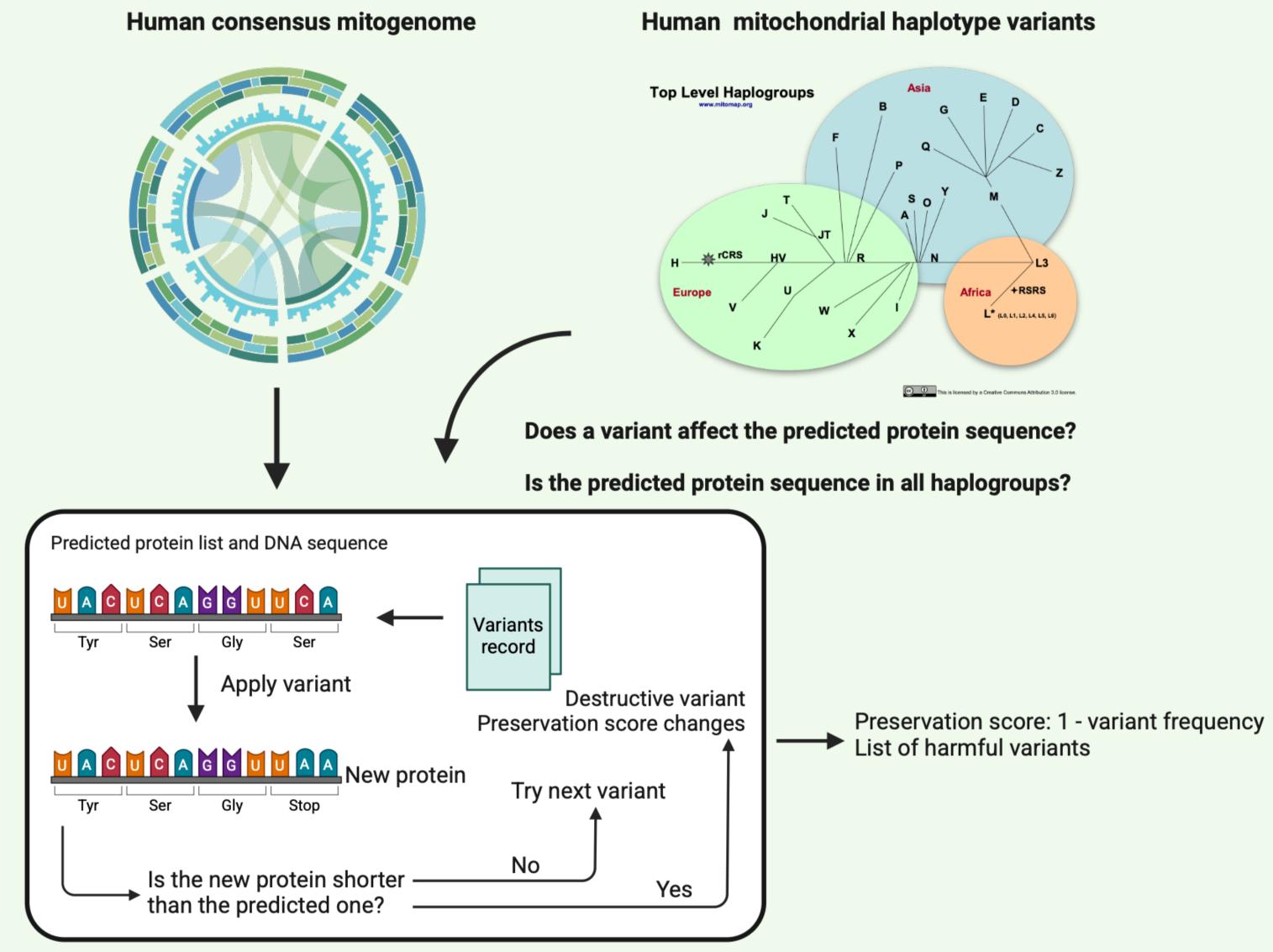
# Where are MtaltORFs Expressed?

To identify sources of alternative proteins in the organism, a meta-analysis of existing complete cell lysate RNA-seq data will be performed.



# **Mitogenomic Diversity**

Based on the human reference mitochondrial genome, the predictions need to take the haplogroup diversity into account. Here, we simulated the impact of common genetic variants on proteins sequences, variants are considered destructive when affecting it.



# Take-Home Message

- Alternative proteins need to be discovered
- MitOpenProt facilitates the designing process of antibodies
- It takes genetic diversity and context dependent expression into account

#### References

Robitaille *et al*. 2024 Kienzle *et al*. 2023 Biorender.com Mitomap.org





