Uncovering new translational targets in cancer

SCAN ME

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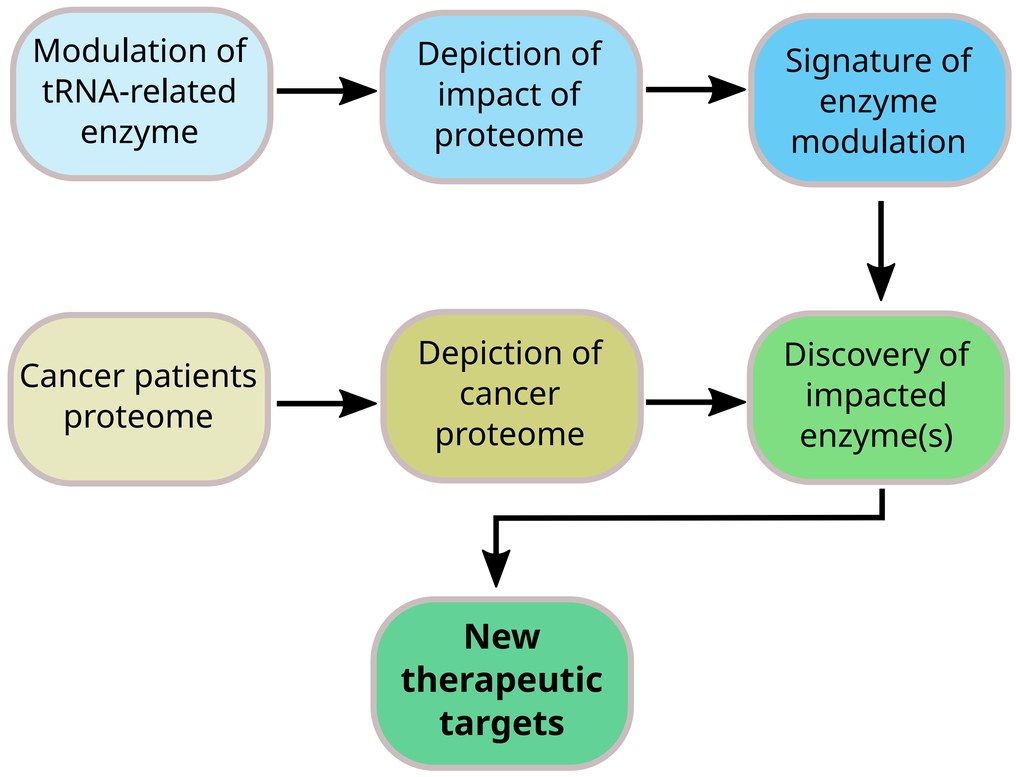
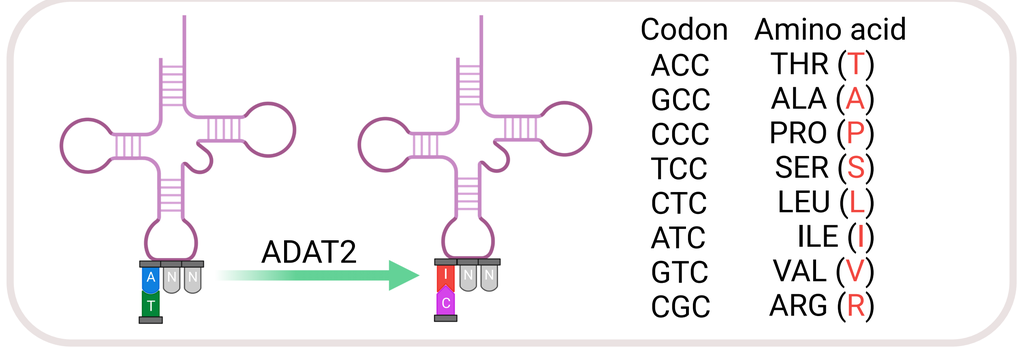
Our aim

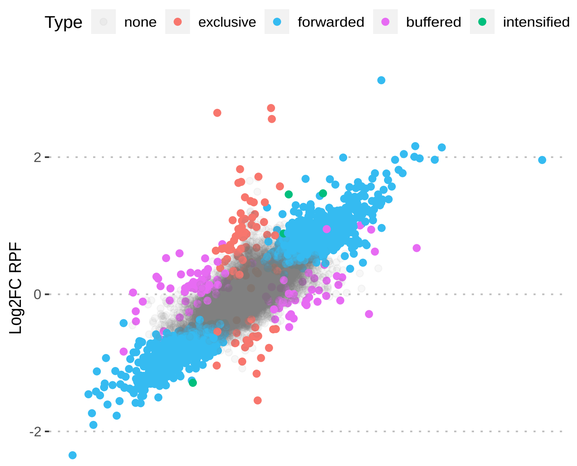
In this project, we are developing **a method to circumvent the difficulties of studying perturbations of translation in cancer**.

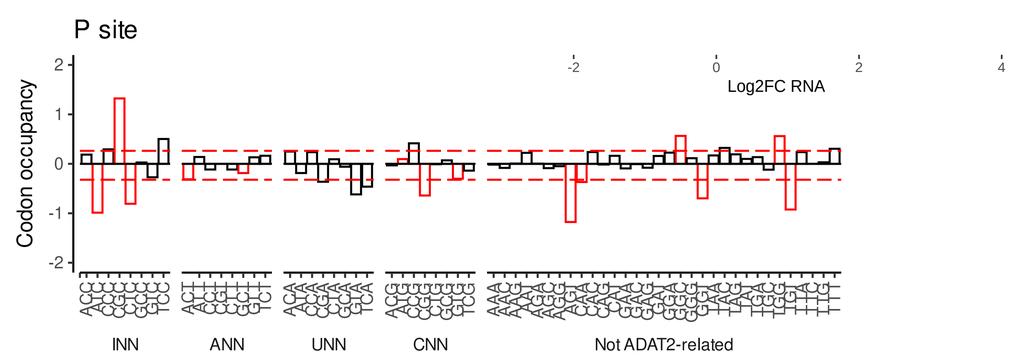


How to predict the impact of tRNA enzymes modulation on the proteome?



Riboseq experiments indicate that **the loss of ADAT2 has a limited impact on global translation**. Codon occupancy analysis indicates that **3 specific codons are the most affected** by ADAT2 loss (ATC, CGC, CTC).



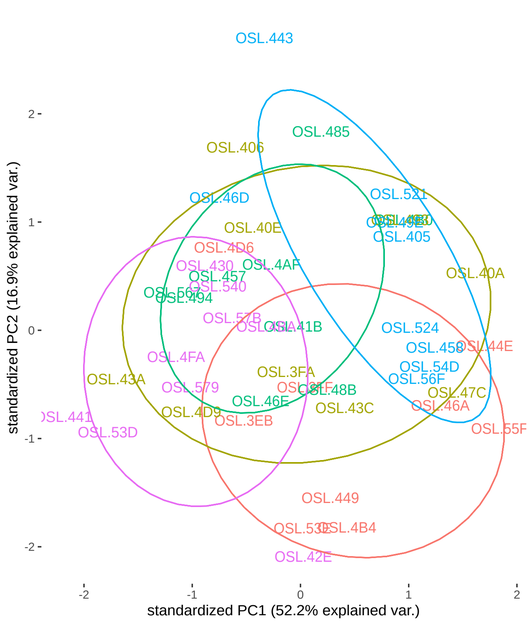


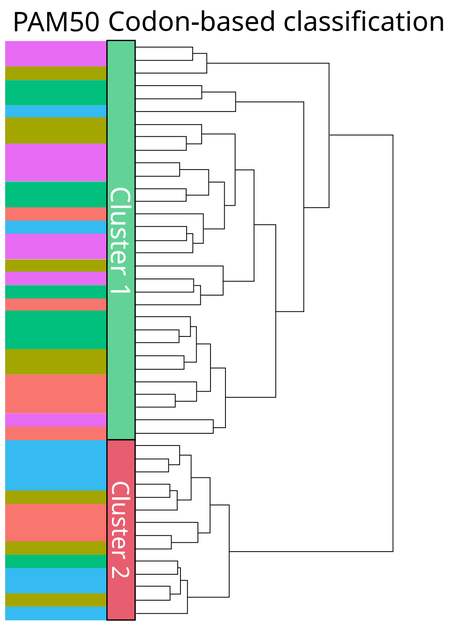
How to characterize translation modulation in cancer patients?

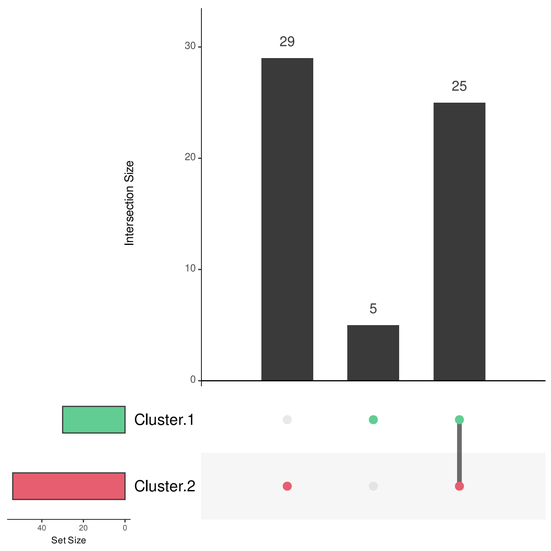
We used a **breast cancer proteomics** dataset of **patient** samples from every PAM50 subtype.

Basal-like	Luminal A	Luminal B	HER2	Normal-like
9	9	9	9	9

Codon content analysis is **unable to recapitulate PAM50** clustering **but highlights two novel codon-dependent clusters.**



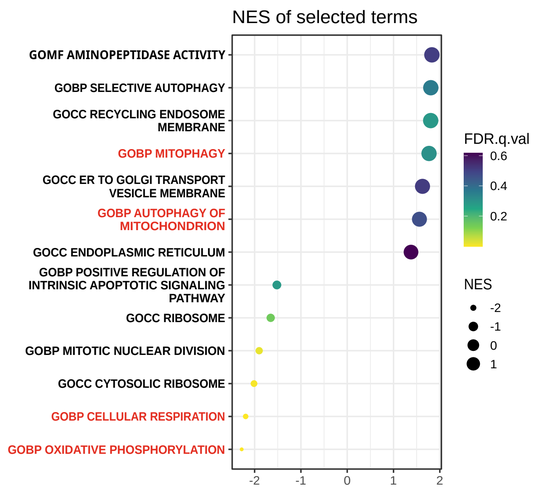


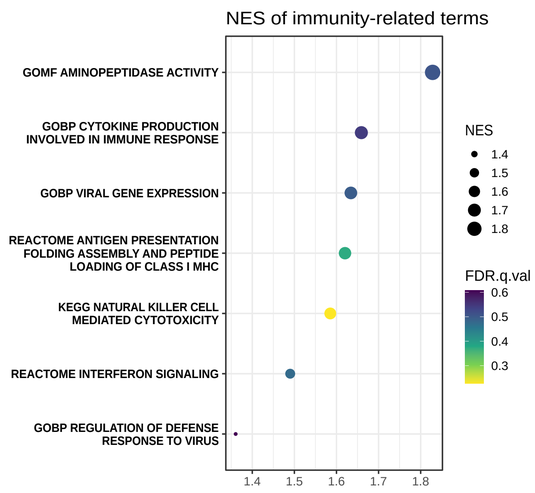


The 2 clusters are characterized by **mutually exclusive codons (cluster 1: 29 | cluster 2: 5).**

We are currently investigating the **biological and clinical features** of these **novel codon-dependent clusters** of breast cancer patients.

Loss of ADAT2 leads to **increased immunogenicity of cancer cells**, as shown by **proteomics** data analysis.





We derived an **ADAT2 proteomic signature** (n = 82) and show that it **negatively correlates with CD4+ T-cell infiltration** across a panel of cancers (using TCGA & TIMER databases).

Future analyses will focus on **refining the ADAT2 signature** by adding more information, such as **tRNA sequencing**, and then **assessing the predictivity of this signature in relation to immune regulation.**