

Orgcode™ Mito 50

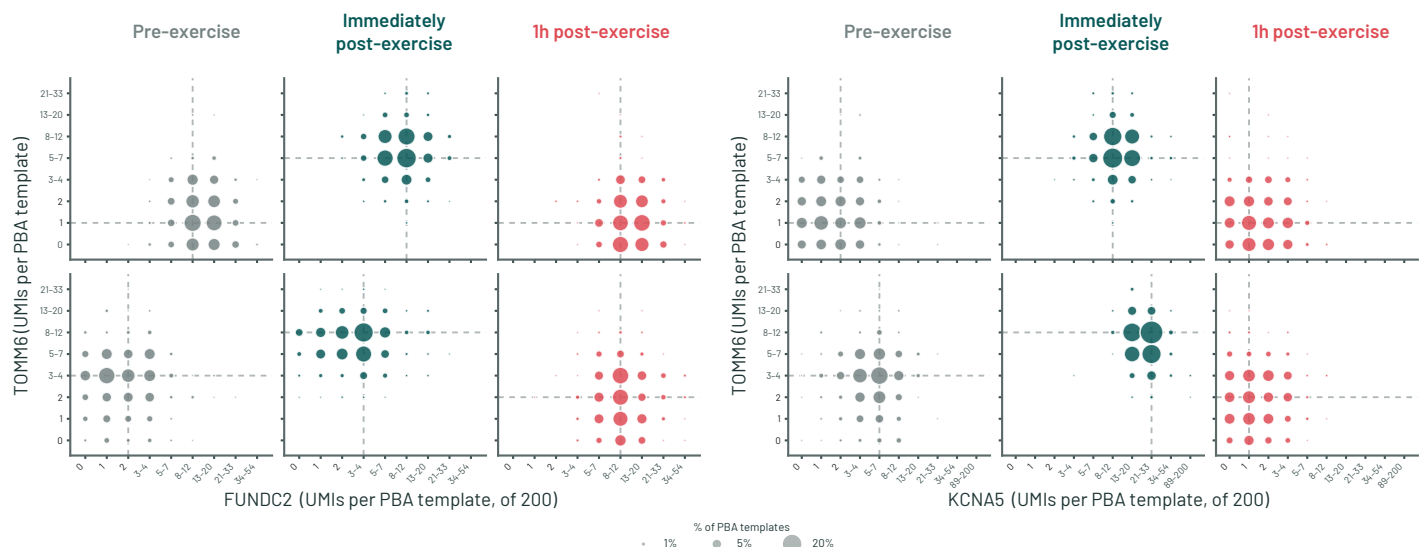
Reveal protein signatures across individual mitochondria

Powered by soPBA™ (single-organelle Proximity Barcoding Assay)

Orgcode™ Mito profiles more than 50 targeted proteins in parallel, revealing relative abundance and proteins detected together on individual mitochondria.

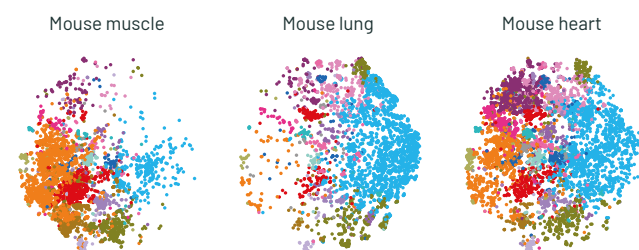
Compare protein abundance • Detect co-localization • Explore heterogeneity

Explore mitochondrial signatures across time and tissue



Mitochondrial protein signatures shift after exercise

The distribution of PBA-template UMI counts for TOMM6/FUNDC2 and TOMM6/KCNA5 changed immediately after exercise and 1h post-exercise, showing time-dependent shifts in mitochondrial protein signatures in plasma-derived samples.



Tissue-associated mitochondrial protein patterns

t-SNE visualization of PBA-template protein profiles from mitochondria isolated from mouse muscle, lung, and heart shows tissue-associated patterns and heterogeneity within each tissue. Colors indicate FlowSOM clusters of profiles with similar protein signatures.

Explore what PBA
can reveal in your research.

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An end-to-end service, from study planning to data report

The Orgcode™ Mito Profiling Service covers the full workflow, from study planning and sample guidance to soPBA™ assay and library preparation, NGS sequencing, and bioinformatics with a data report.

The two key components in soPBA



Orgcode™ Mito workflow

- | | | |
|---------------|---|---|
| Step 1 | Isolate mitochondria | Enrich mitochondria from the sample. |
| Step 2 | Label targets | DNA-barcoded PBA probes bind selected proteins. |
| Step 3 | Link protein IDs on the same mitochondrion | PBA templates capture nearby probes and assign a shared proximity tag. |
| Step 4 | Sequence & analyze | Sequencing and bioinformatics reveal co-localized protein signatures across the targeted panel. |

