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Supplemental Information

Defining the Substrate Spectrum

of the TIM22 Complex Identifies Pyruvate

Carrier Subunits as Unconventional Cargos

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Figure S1. Carrier protein import is reduced in temperature sensitive Tim22 mutant, Related to Figure 1. (A) Wild type (WT) and *tim22-14* yeast cells expressing GFP-Mir1 were grown at 25°C or shifted to 37°C for 25 h. Cells were co-stained with MitoTracker Orange and analyzed by fluorescence microscopy. Merged green and red fluorescence images are shown (yellow/orange). (Scale bar: 5 μ m). (B) Purified mitochondria from wild type (WT) and *tim22-14* cells grown at the permissive temperature (25°C) or shifted to the non-permissive temperature (37°C) for 14 h were analyzed by SDS-PAGE and western blotting. *: non-specific band. (C) Proteomic analyses of *tim22-14 versus* WT mitochondria. log₂ ratio-intensity plots showing the effect of loss of Tim22 function on the abundance of mitochondrial carrier proteins (red) and MPC subunits (blue) after 15 h (i), 25 h (ii) and 40 h (iii) at 37°C. Filled circles indicate proteins significantly altered in abundance in each dataset.



Figure S2. Presequence-containing precursor import is normal in tim22-14 mitochondria, Tom70/71-dependent import of carrier proteins Crc1 and Hem25, and uncharacterized proteins Yfr045w and Ypr011c are required for mitochondrial activity, Related to Figure 2. (A) [³⁵S]-labelled Su9-DHFR and Atp5 were imported into purified wild type (WT) and tim22-14 mitochondria in the presence or absence of a membrane potential. Samples were analyzed by SDS-PAGE and digital autoradiography. p: precursor; m: mature. (B) [³⁵S]-labelled Atp5 was imported in the presence or absence of a membrane potential into wild type (WT) and tim22-14 mitochondria. After Proteinase K treatment, assembly of Atp5 into complex V was analyzed by BN-PAGE followed by digital autoradiography. (C) [35S]-labelled Crc1 and Hem25 were imported into purified wild type (WT) and $tom 70/71 \Delta \Delta$ mitochondria in the presence or absence of a membrane potential. After Proteinase K treatment and solubilization of the samples, proteins were separated by BN-PAGE followed by digital autoradiography. (D) (top) Representation of the predicted transmembrane organization of Yfr045w and Ypr011c. Membrane topology prediction (bottom) based on the typical six transmembrane span arrangement of the carrier family. (E) Growth test of wild type (WT), $yfr045w\Delta$, and $ypr011c\Delta$ cells on glucose (YPD), glycerol (YPG), or lactate (YPL) medium. N: N-terminus; C: C-terminus; aa: amino acid; IMM: inner mitochondrial membrane; IMS: intermembrane space; Matr.: matrix; dil.: dilution; $\Delta \psi$: membrane potential.



