*Insert preparation and data normalization done in Gygi lab.*

Technical replicates from the geometric mean-normalized proteomics data were averaged. Heatmaps were generated by calculating the average value for the GFP replicates and dividing each replicate (experimental and control) by this value for each protein. A list of ETC component proteins was passed into the xpressplot.heatmap() function from XPRESSplot (Berg, PLOS Comp Bio, 2020; Waskom M, et al. seaborn. 2012. doi:Available from: https://doi.org/http://doi.org/10.5281/zenodo).

1313201) and further formatting was performed using Matplotlib (Hunter J, Compting in Science & Engineering, 2007). The volcano plot for the Mecr vs GFP proteomics data was generating by providing lists of Mitocarta (Calvo, Nucl Acids Res, 2015; Pagliarini, Cell, 2008) and ETC proteins and the technical-replicate, geometric-normalized dataframe for both GFP and Mecr replicates to the xpressplot.volcano() function (Berg, PLOS Comp Bio, 2020).

*In case you include the interactive plot, add the following to the end of the paragraph above:*

Interactive volcano plots were generated by outputting log2 Fold Change and -log10 P-value values from the appropriate dataset using xpressplot.volcano() (Berg, PLOS Comp Bio, 2020). Meta-categories were then provided to distringuish ETC and Mitocarta proteins from other entities. Interactive scatterplots of the data were then generated using Plotly Express (Plotly Technologies Inc. Title: Collaborative data science Publisher: Plotly Technologies Inc. Place of publication: Montréal, QC Date of publication: 2015 URL: https://plot.ly), with protein categories being provided.