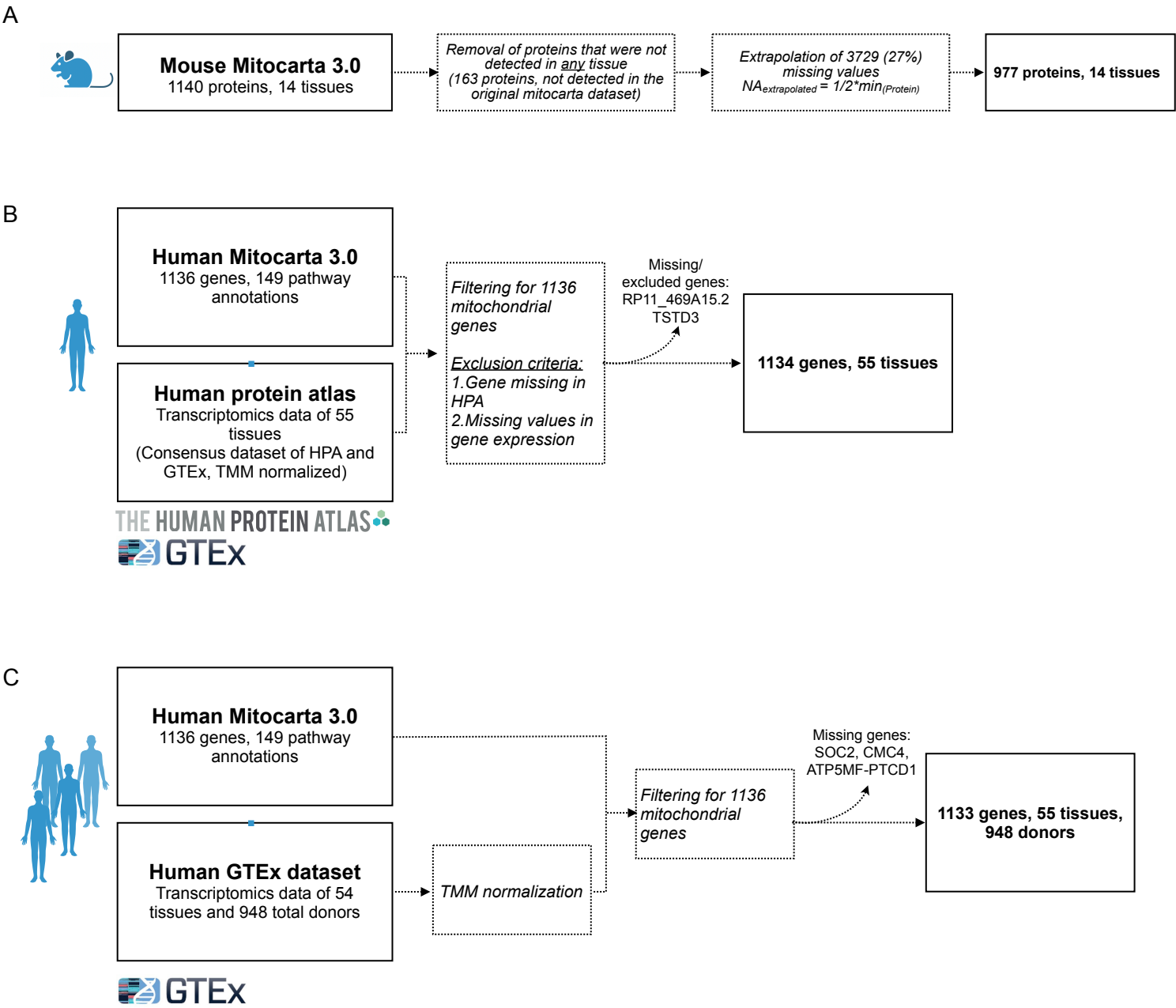
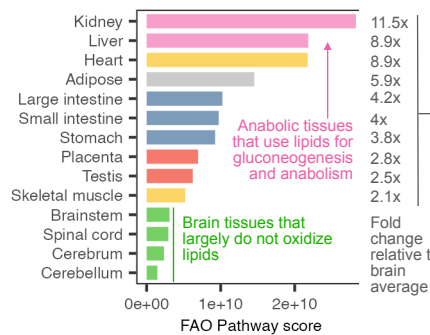


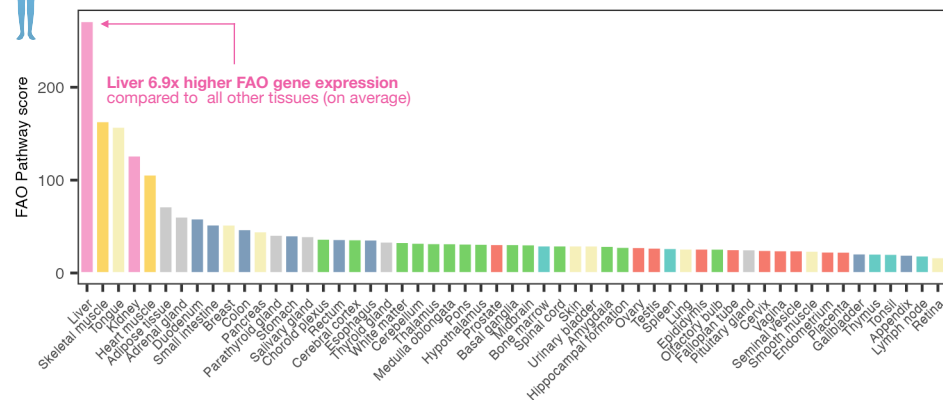


SUPPL FIGURE S2

A  **MOUSE** FAO specialization

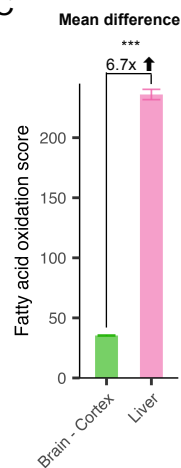


B  **HUMAN** FAO specialization

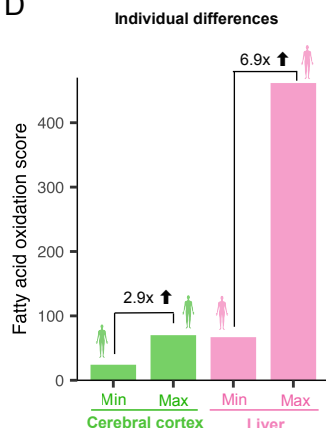


C

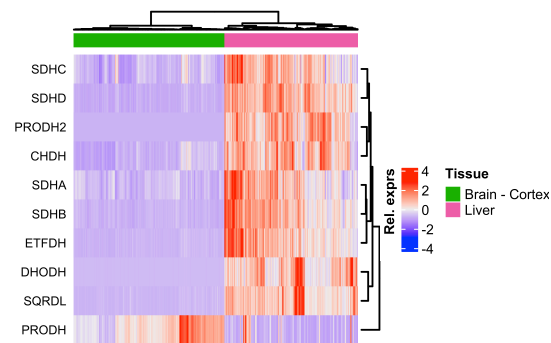
Mean difference



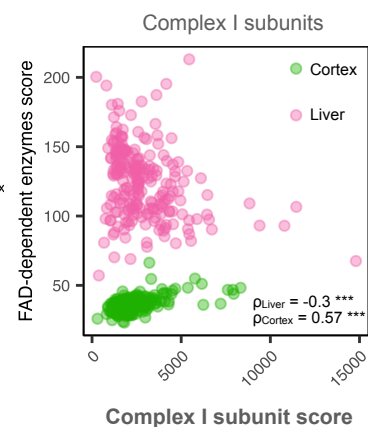
D Individual differences



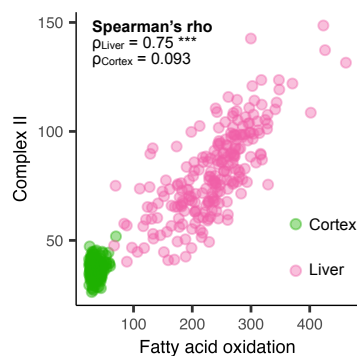
E FAD-DEPENDENT ENZYMES
Gene-level mitotyping



F FAD-DEPENDENT ENZYMES
Pathway-level mitotyping

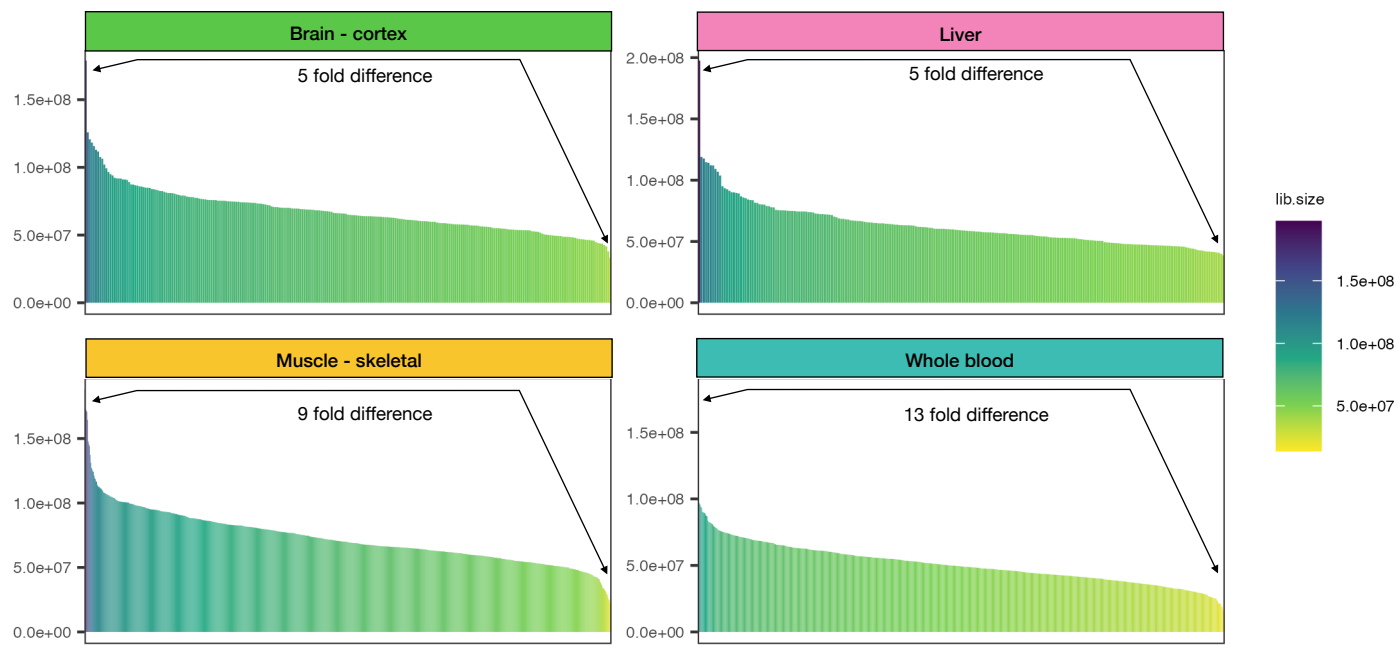


G **FAO and complex II**
across donors

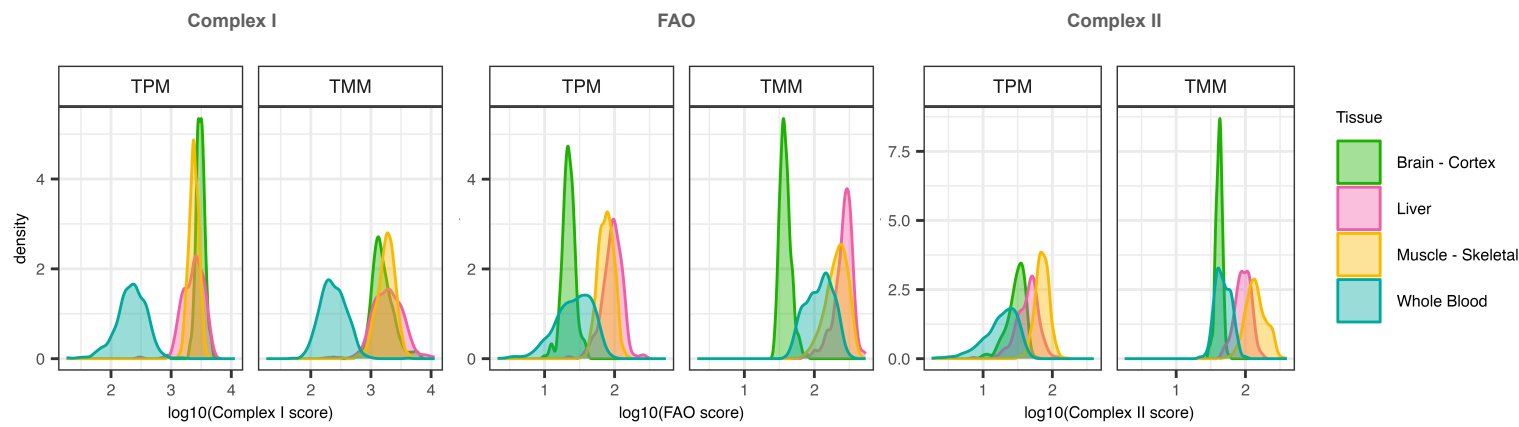


SUPPL FIGURE S3

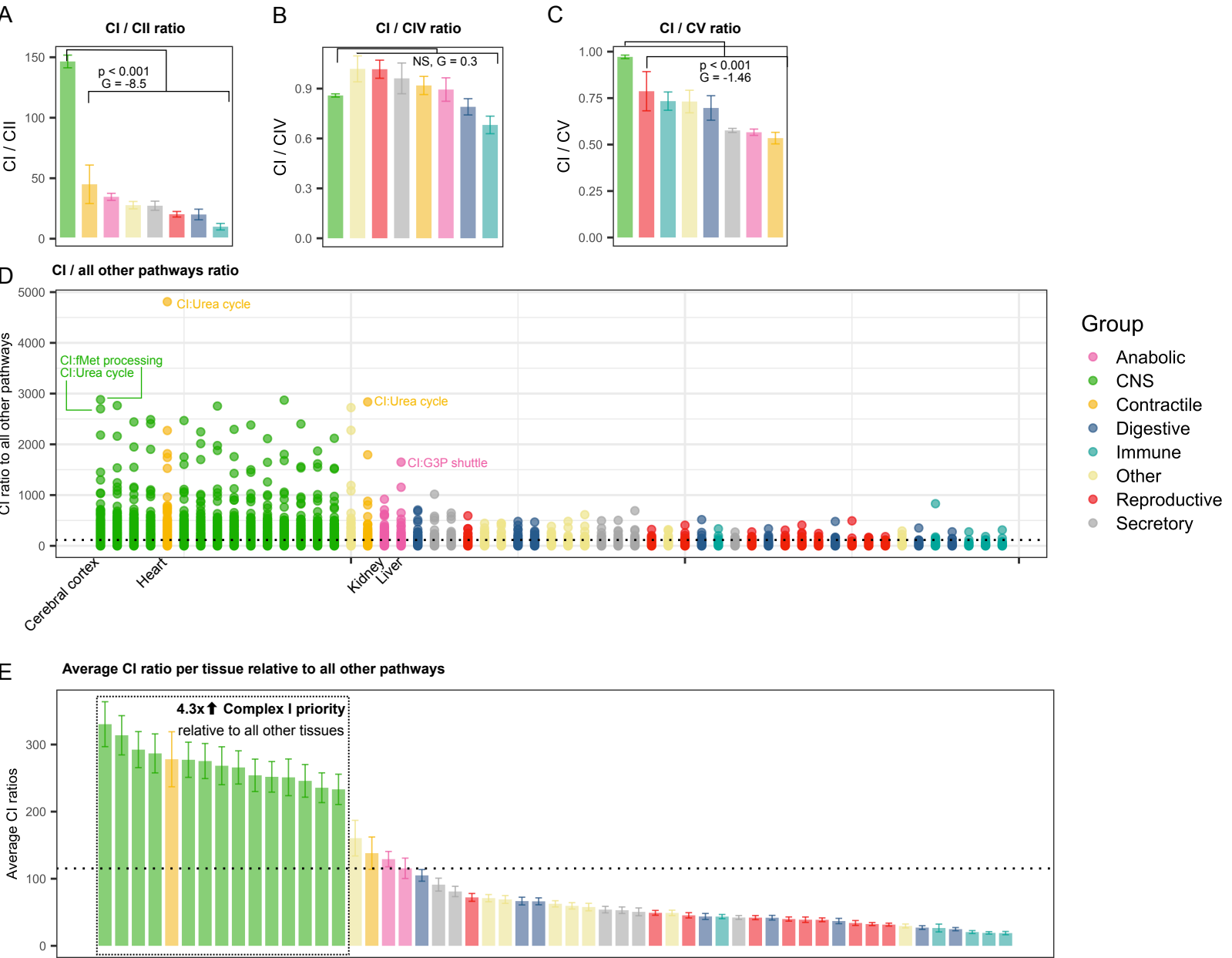
A LIBRARY SIZE PER TISSUE FROM GTEx



B COMPARISON OF NORMALIZATION METHODS

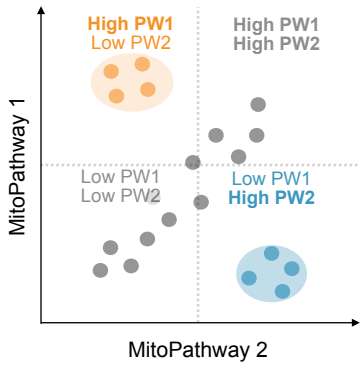


SUPPL FIGURE S4

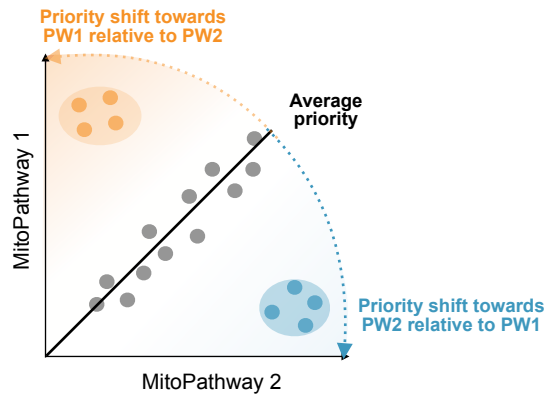


SUPPL FIGURE S5

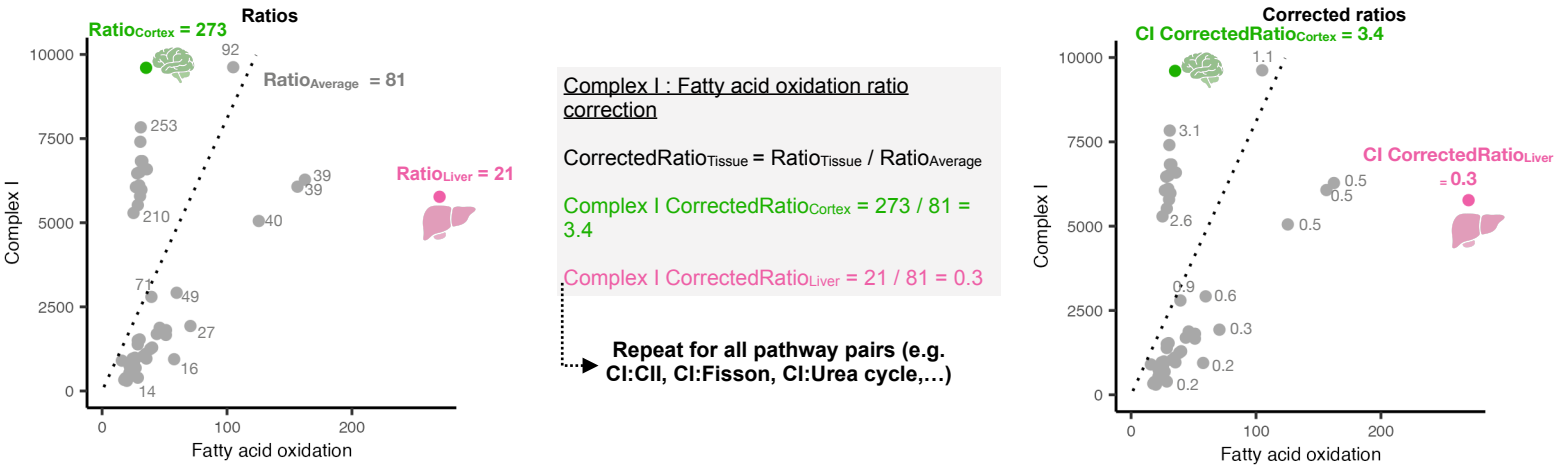
A PATHWAY RATIOS



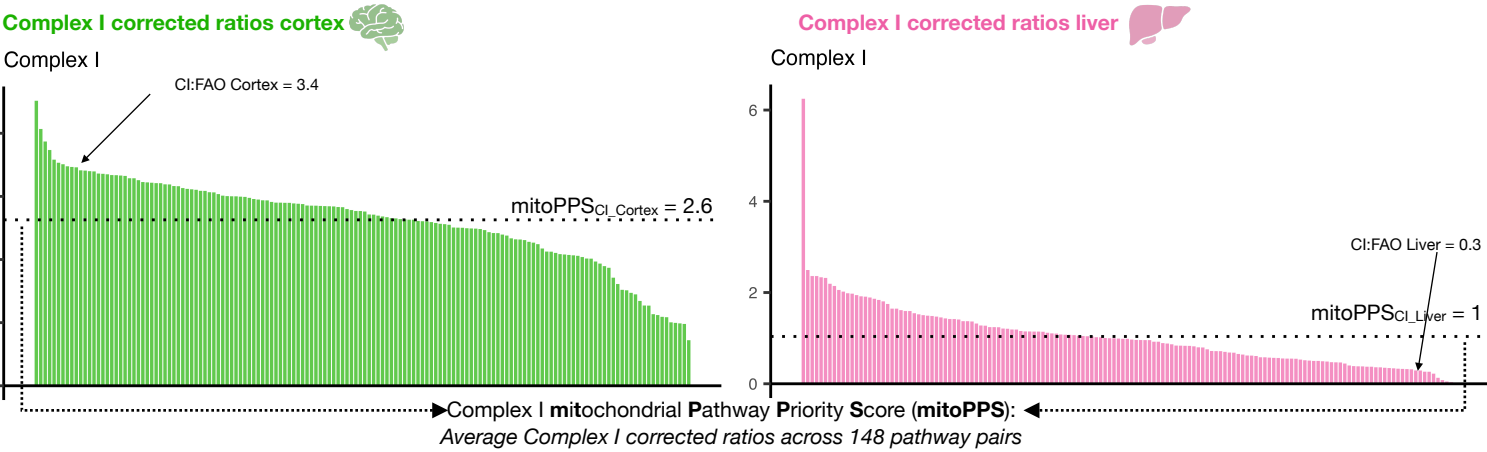
B PATHWAY PRIORITIZATION



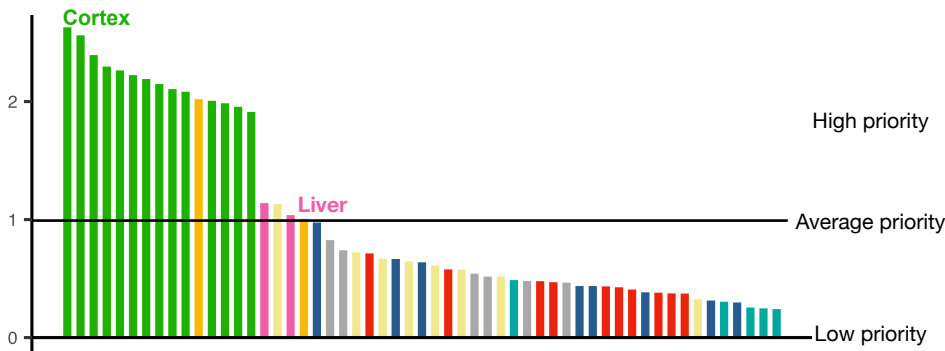
C ESTIMATING PATHWAY PRIORITIZATION FROM CORRECTED PATHWAY RATIOS



D mitoPPS: AVERAGED CORRECTED PATHWAY RATIOS ACROSS 148 PATHWAY PAIRS

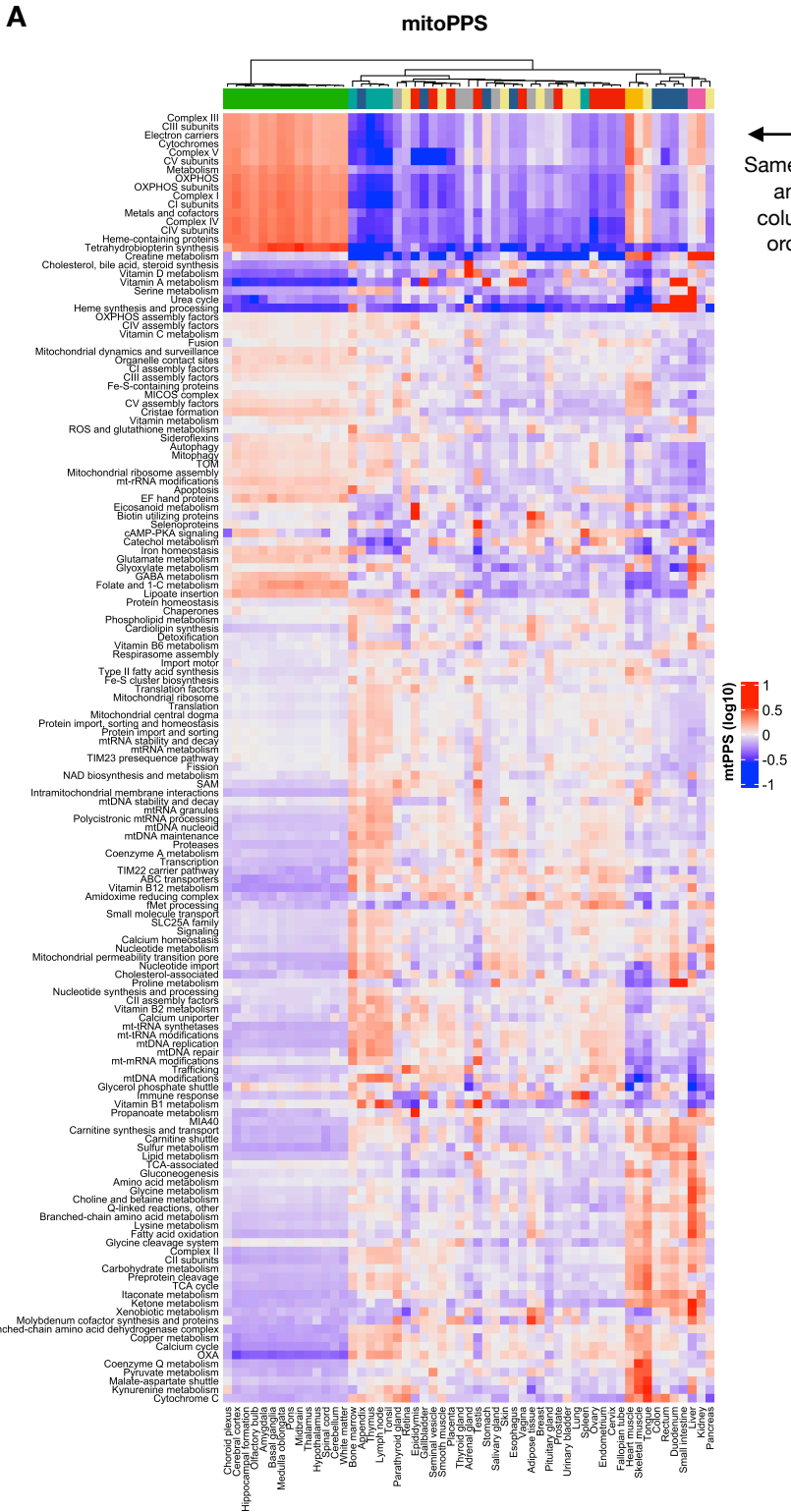


E COMPLEX I mitoPPS ACROSS 55 HUMAN TISSUES

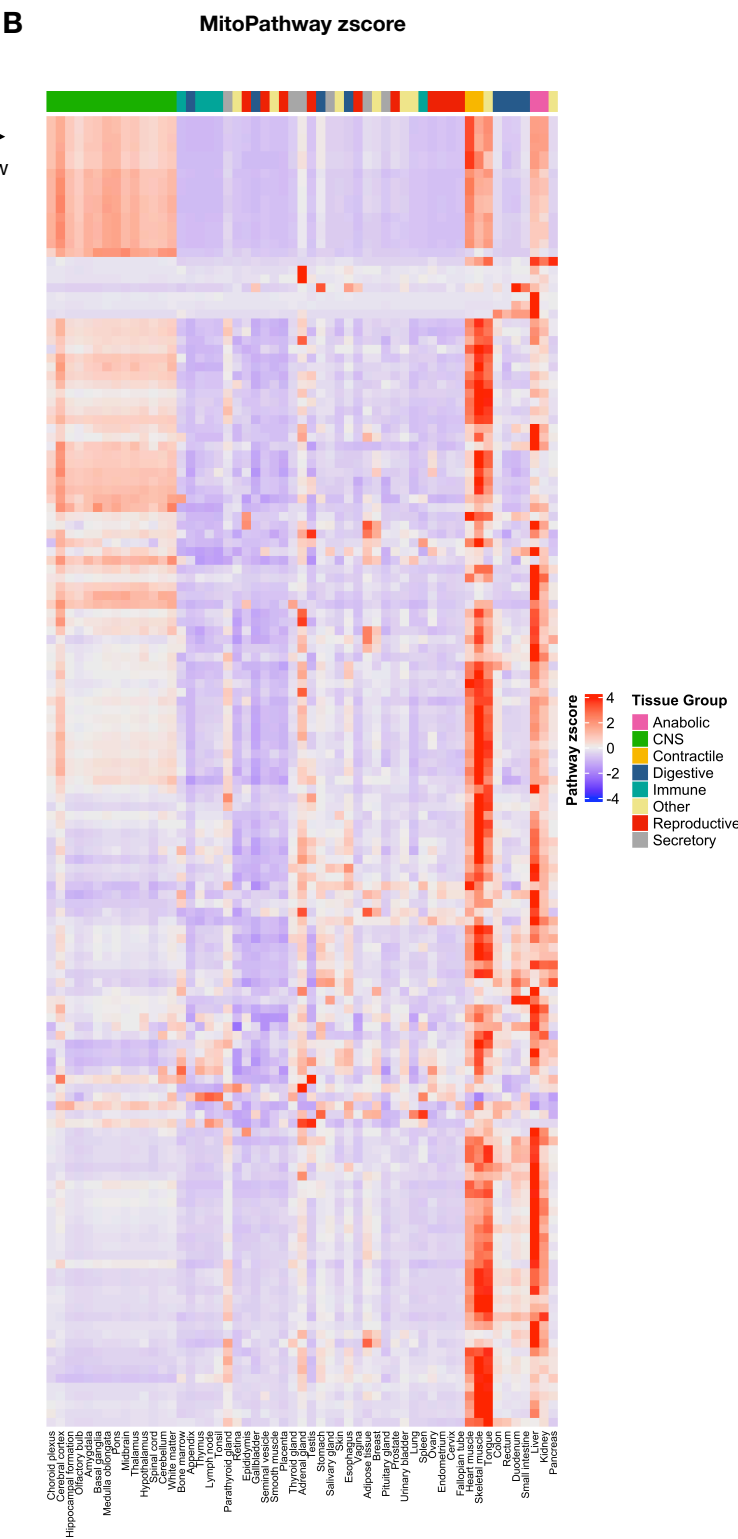


SUPPL FIGURE S6

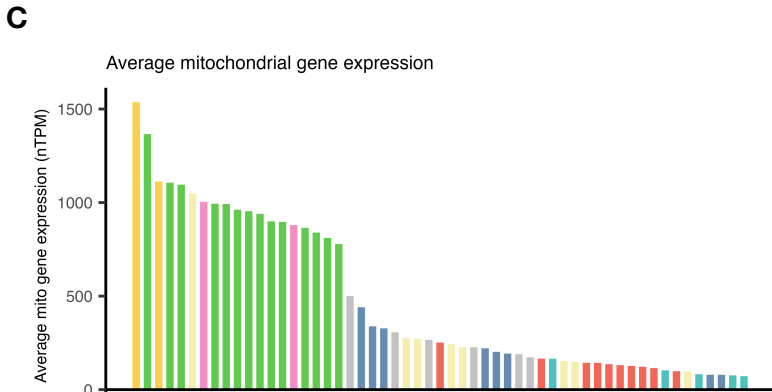
A



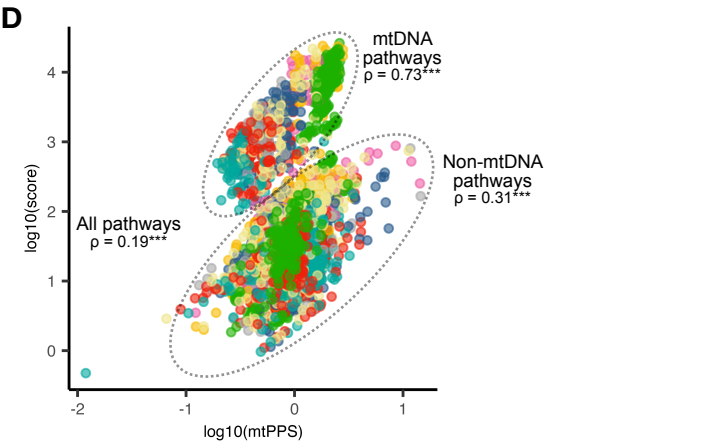
B



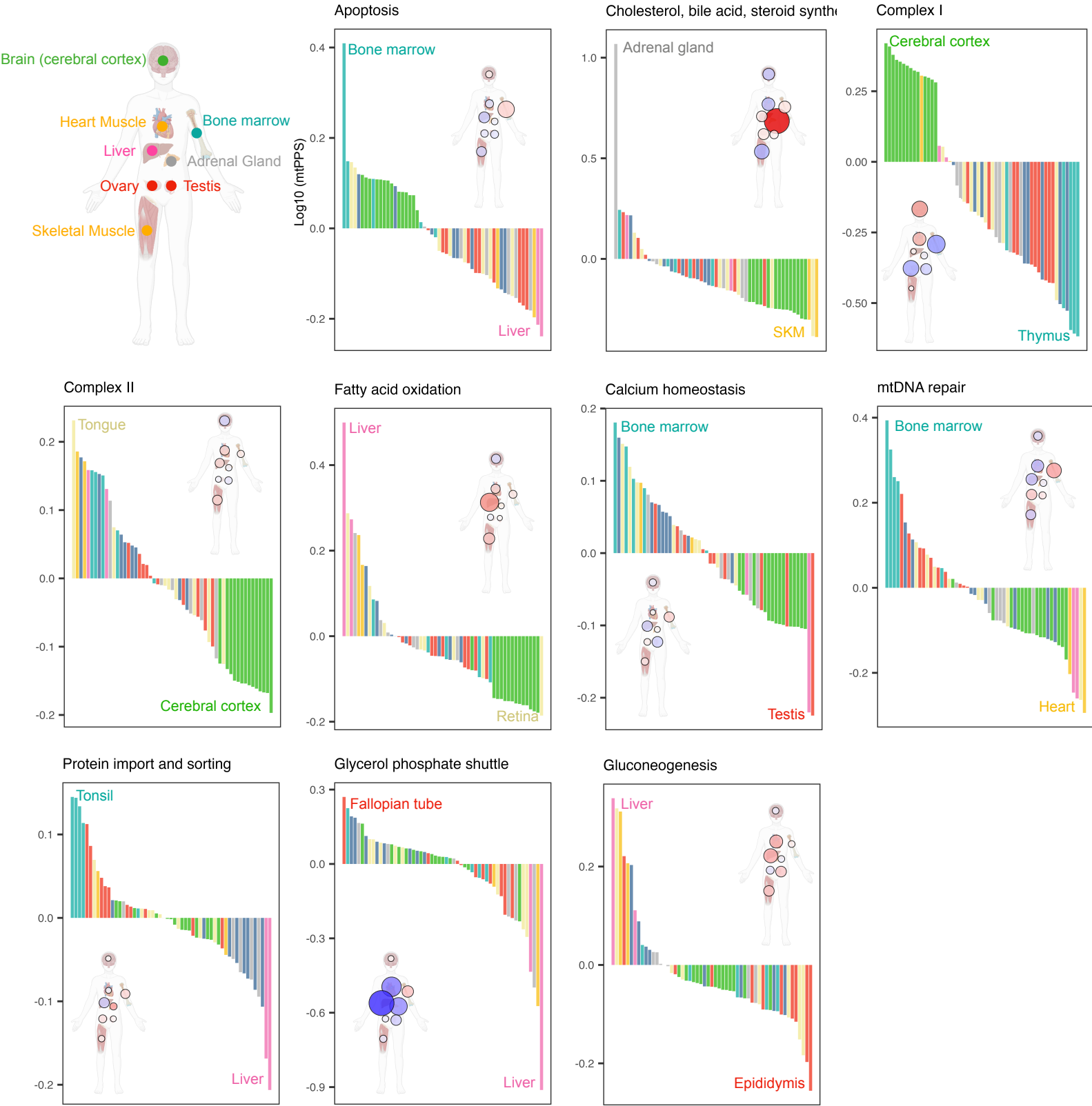
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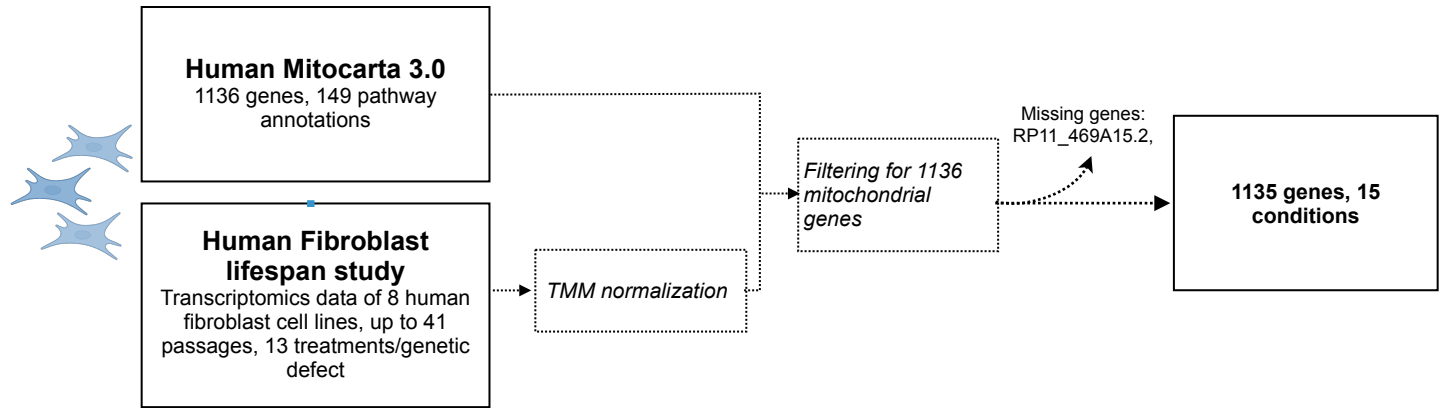
D



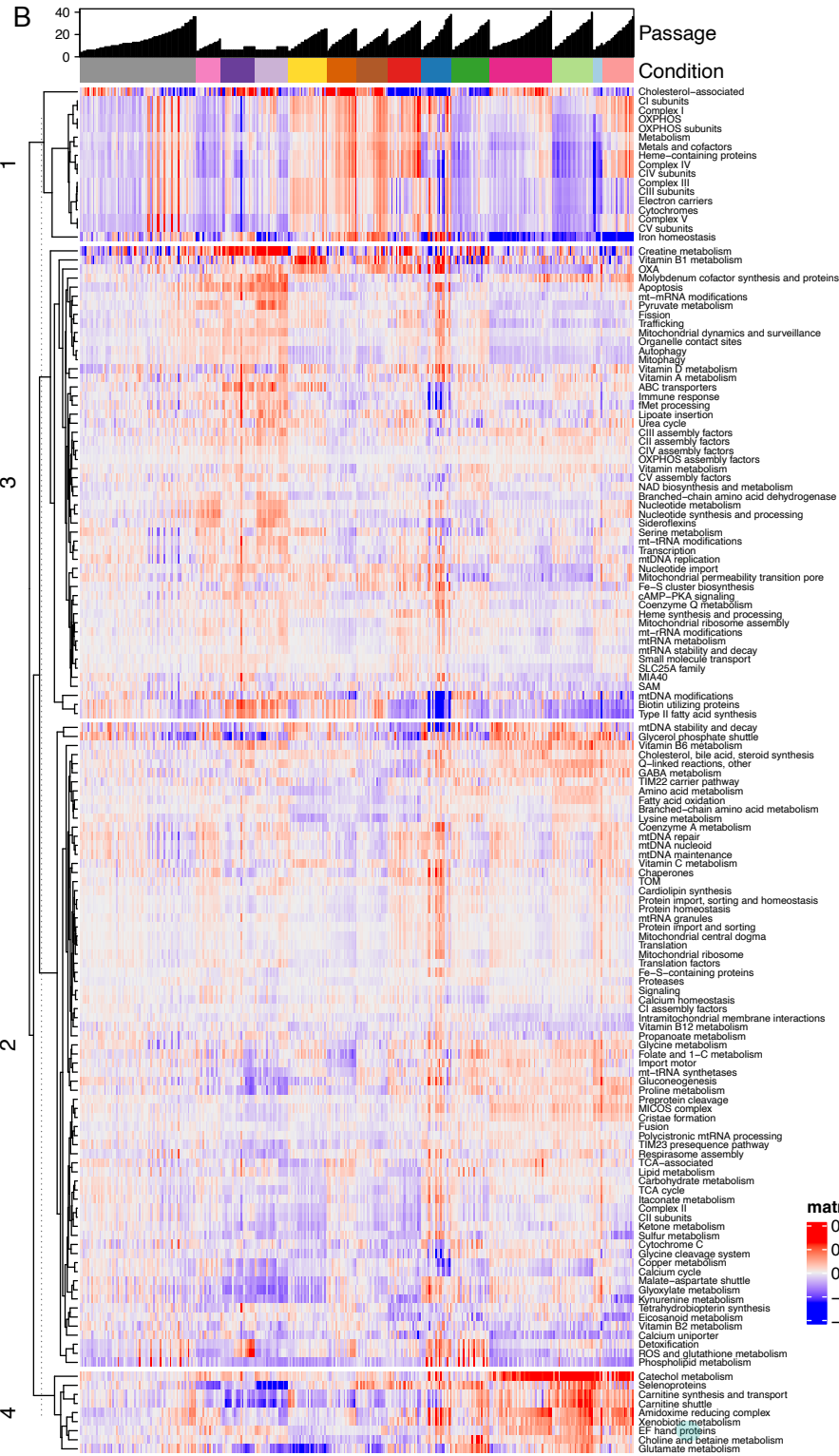
SUPPL FIGURE S7



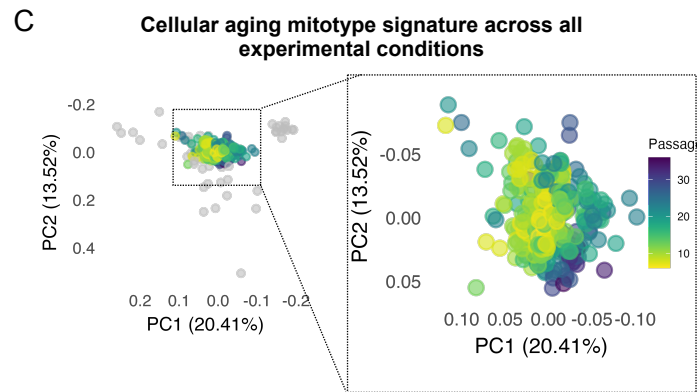
A



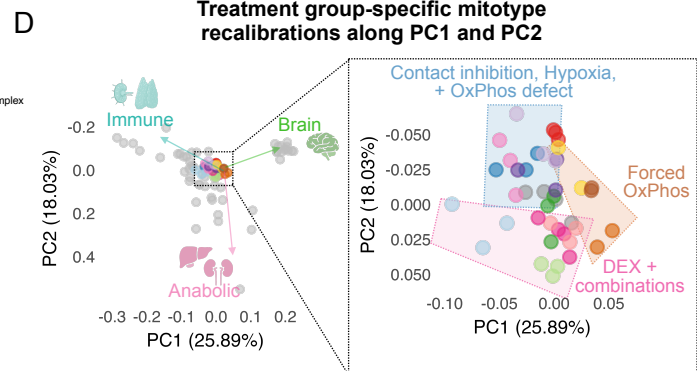
B



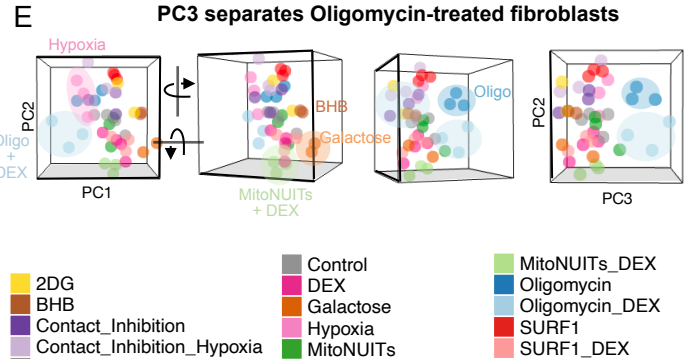
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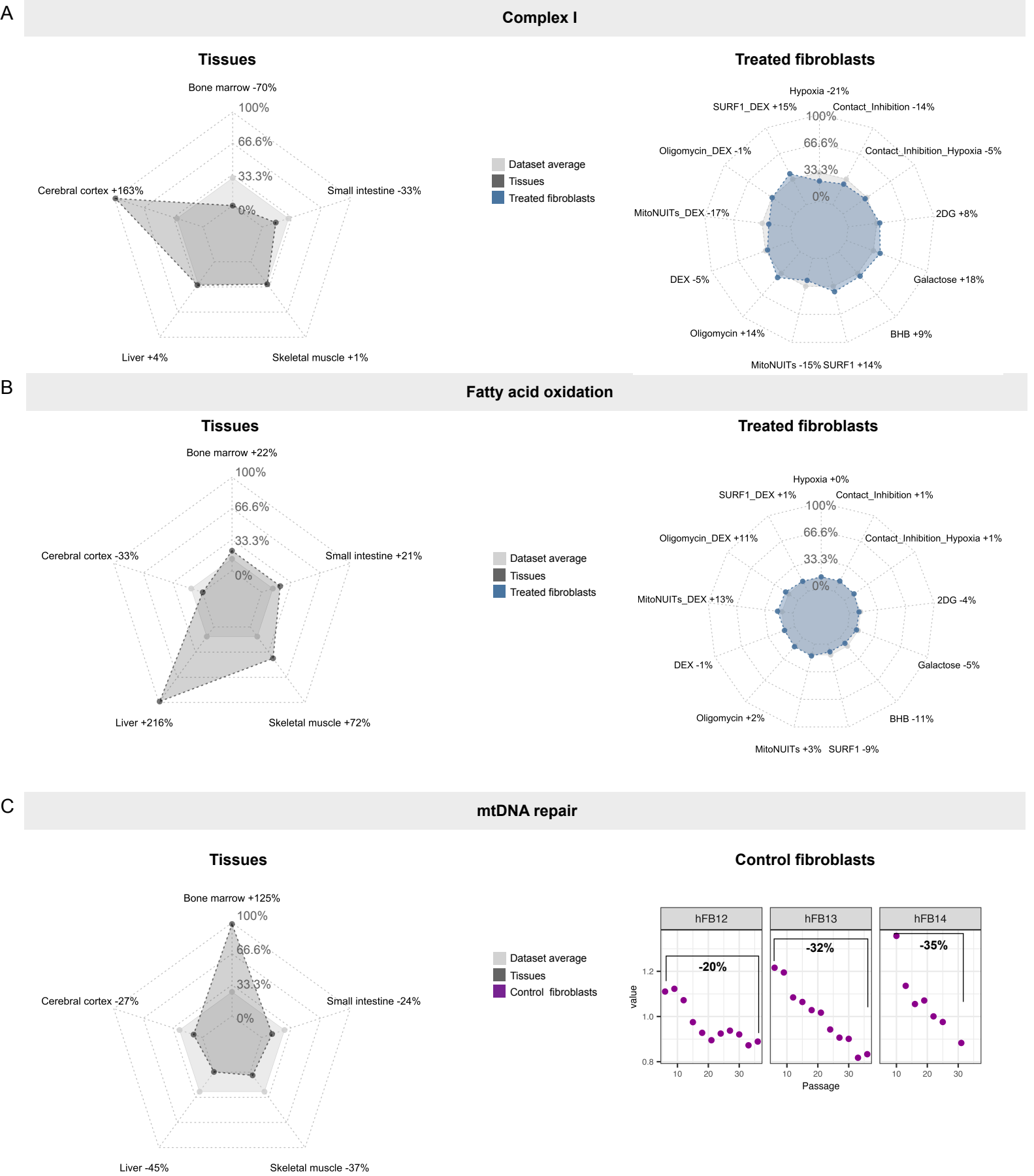


D



E





SUPPL FIGURE S10

