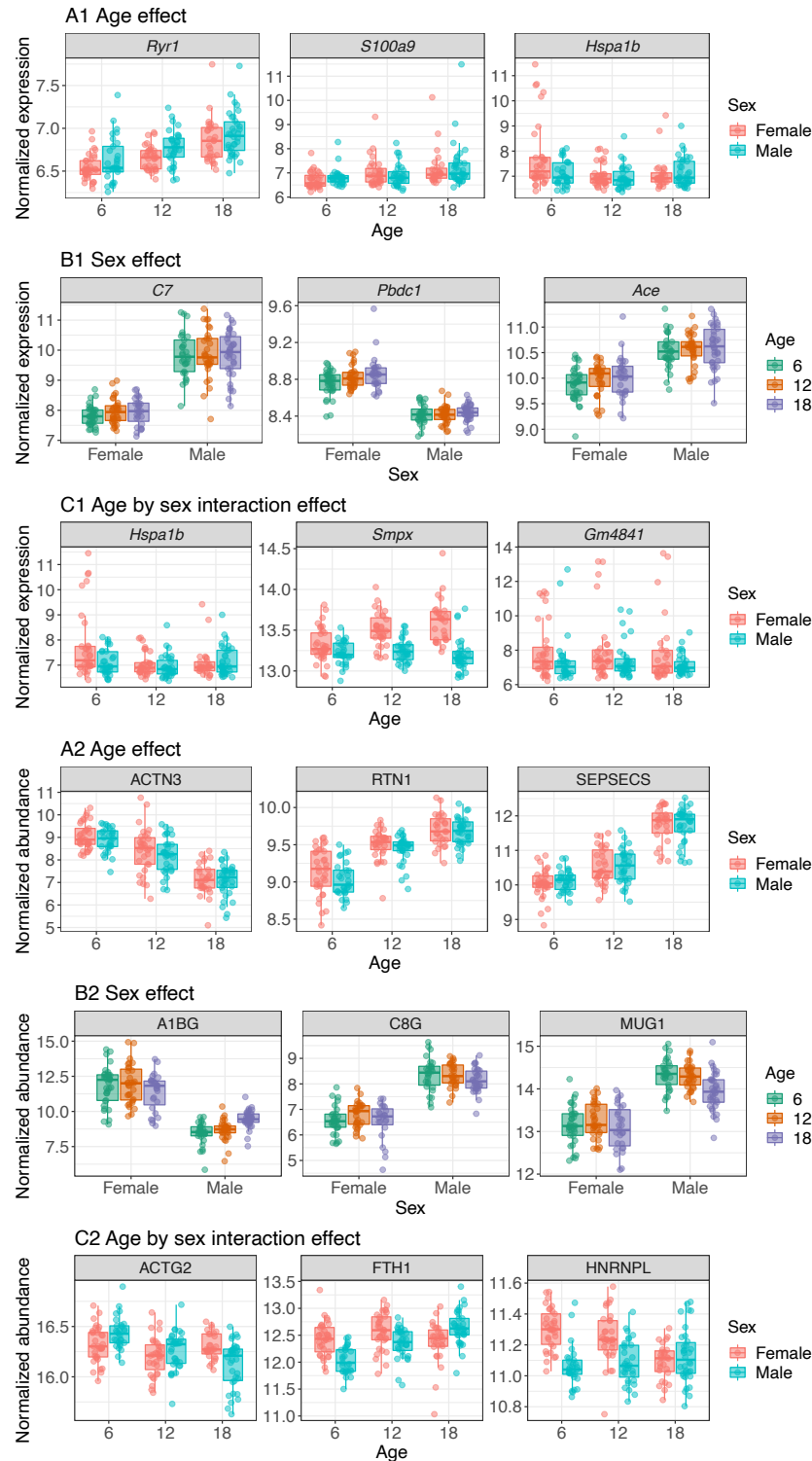
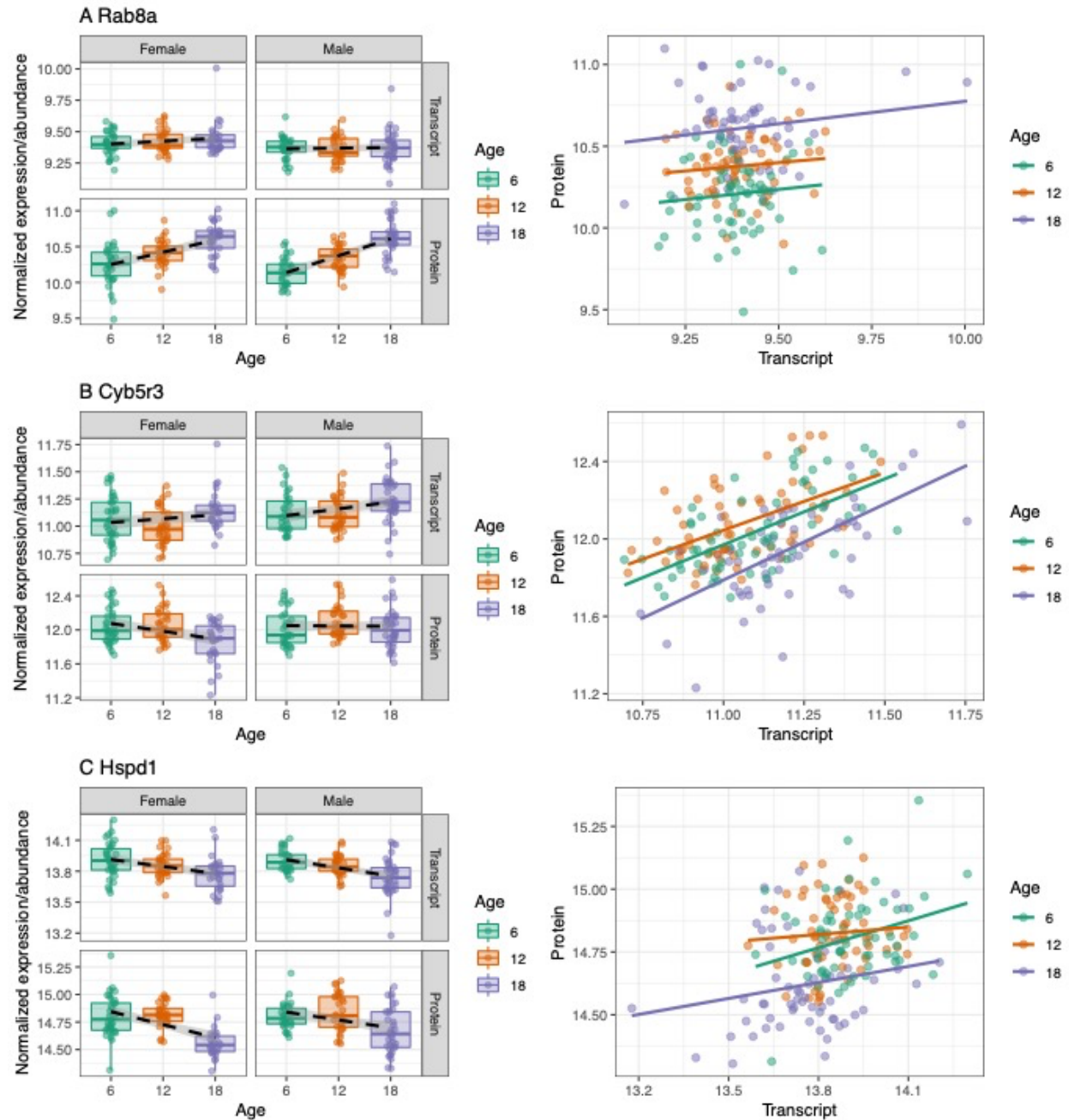


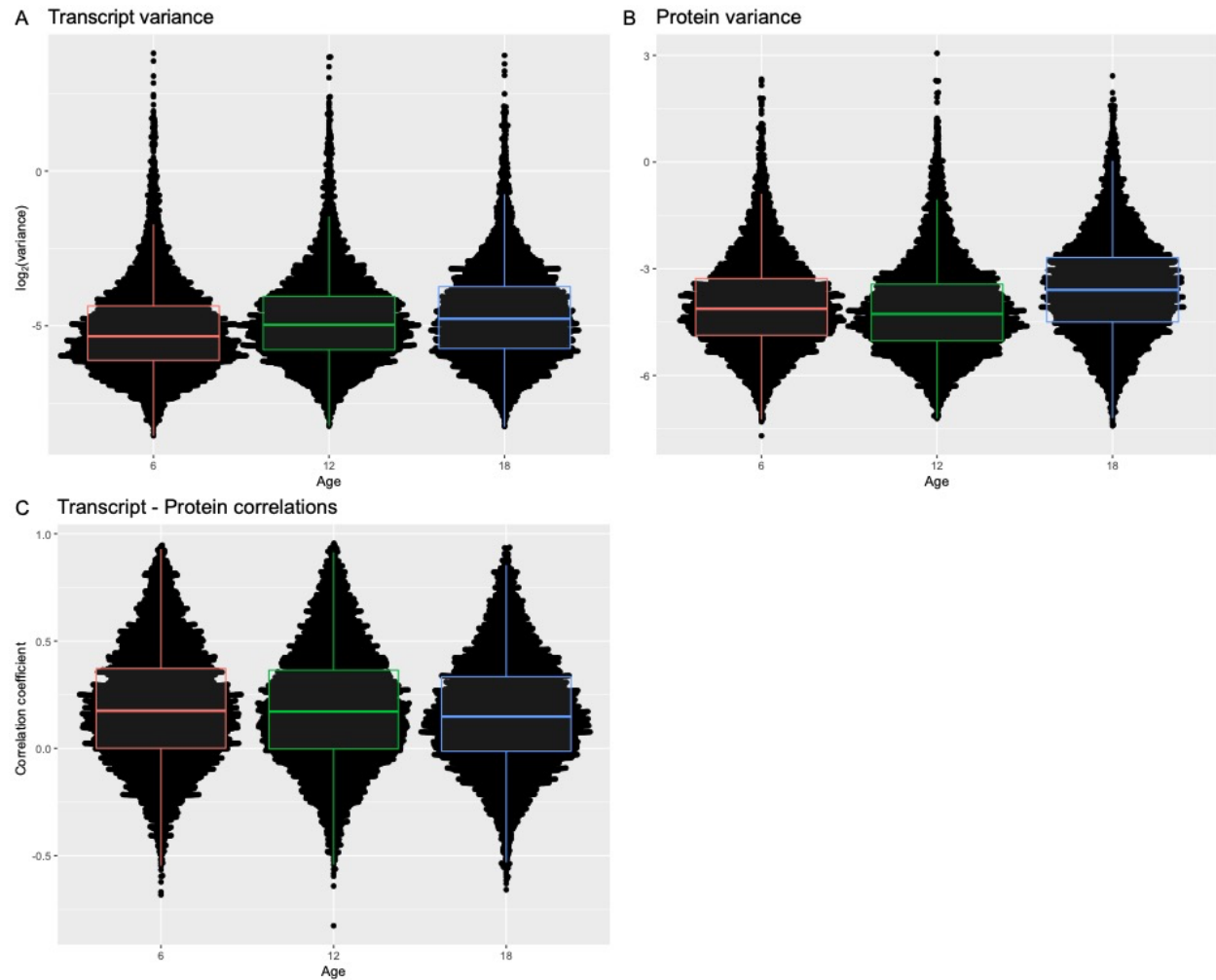


Supplemental Figure S1: Examples of age, sex, and age-by-sex effects on transcripts and proteins.

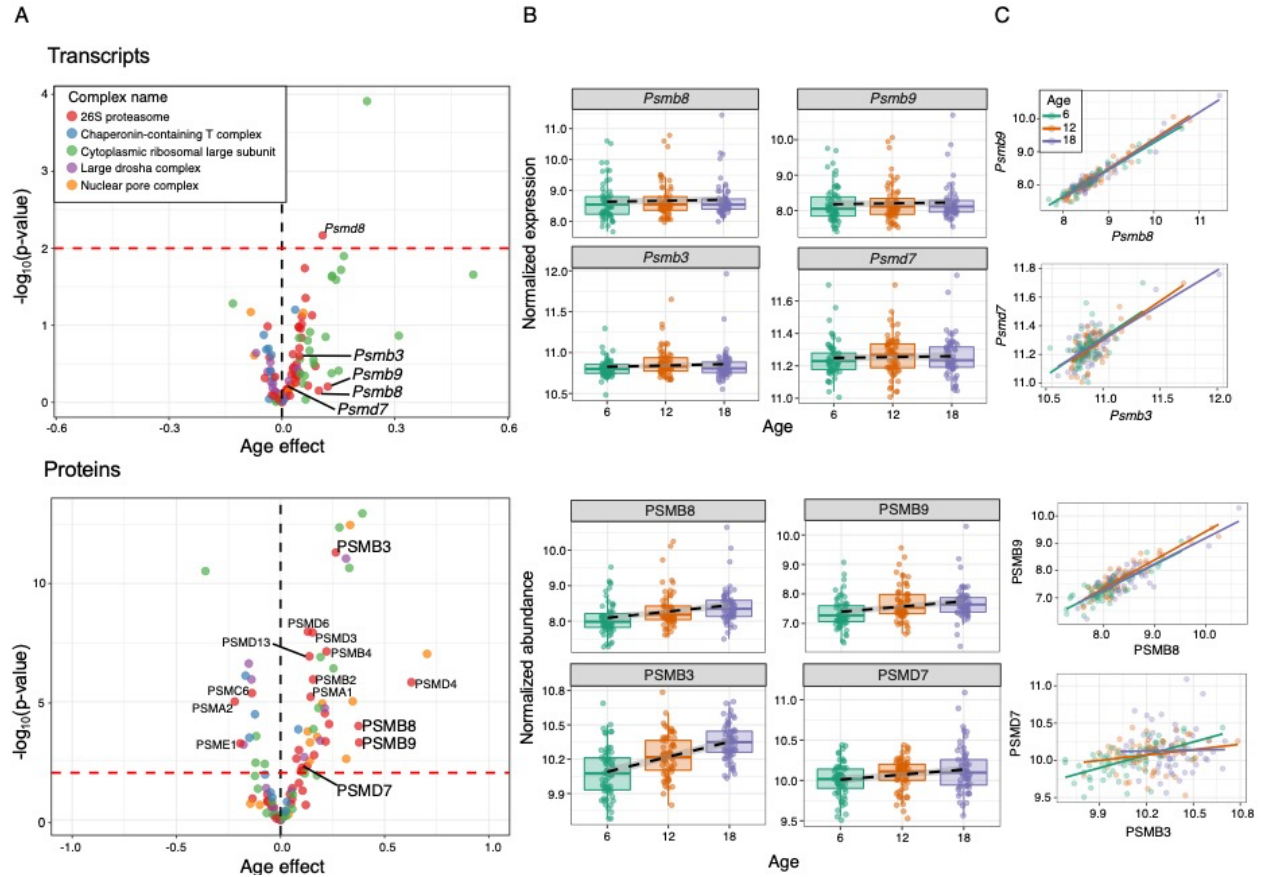
Normalized expression (y-axis) of transcripts (1) or normalized abundance (y-axis) of proteins (2) demonstrating a significant ($FDR < 0.01$) age effect (A), sex effect (B) and age by sex interaction effect (C). In A) and C) the data are plotted by age on the x-axis and stratified and colored according to sex. In B) the data are plotted by sex on the x-axis and stratified and colored according to age group.



Supplemental Figure S2: Examples of genes with age effects, highlighted through functional enrichment analysis. Normalized (top) gene expression and (bottom) protein abundance (y-axis) by age (x-axis), stratified by sex on the left, and normalized protein abundance (y-axis) by normalized transcript expression (x-axis) on the right for the genes (A) *Rab8a*, (B) *Cyb5r3* and (C) *Hspd1*. Points are colored according to age group. Best fit regression lines for each age group included to highlight trends.

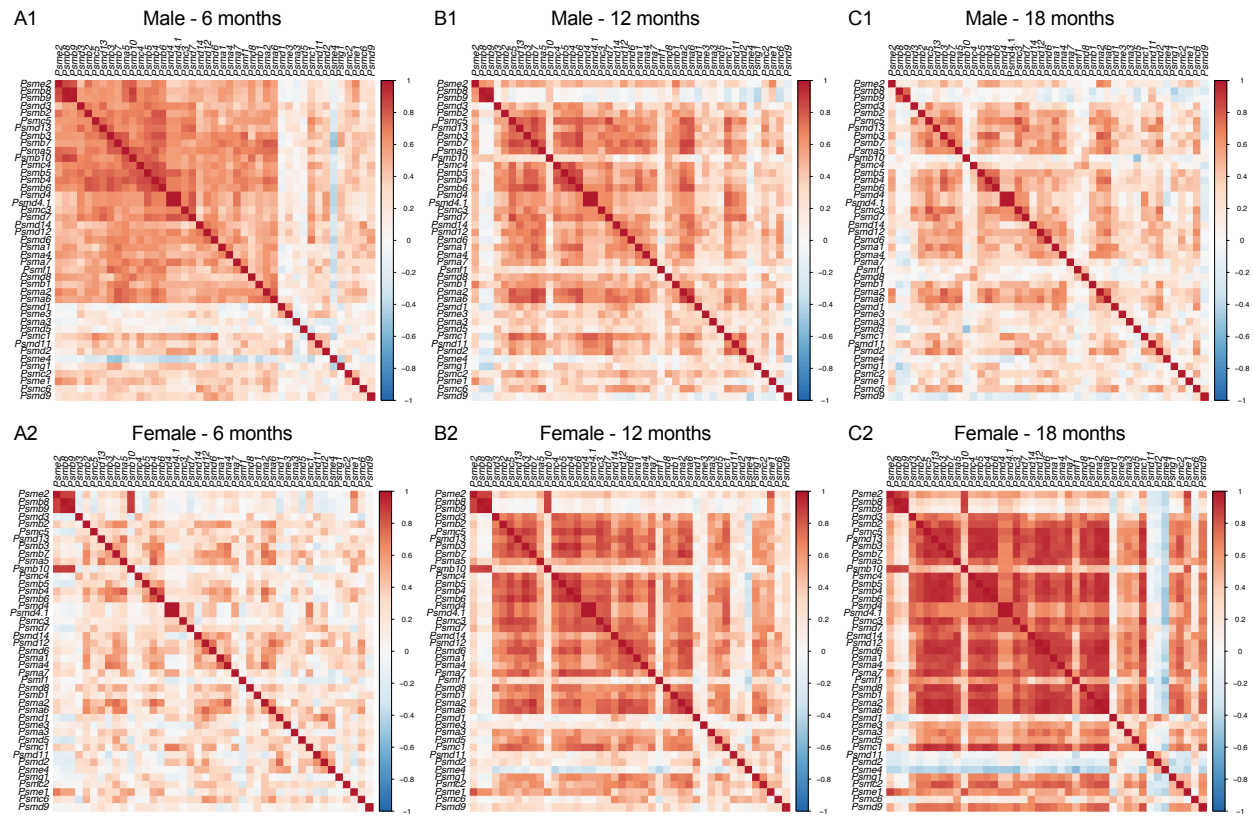


Supplemental Figure S3: Variances and correlation of proteins and transcripts across age groups. Log₂ variances for (A) transcripts and (B) proteins, stratified by age group. Each point represents a transcript or protein. C) Pearson correlation coefficients for transcript-protein pairs, stratified by age group. Each point represents a transcript-protein pair for a given age group.

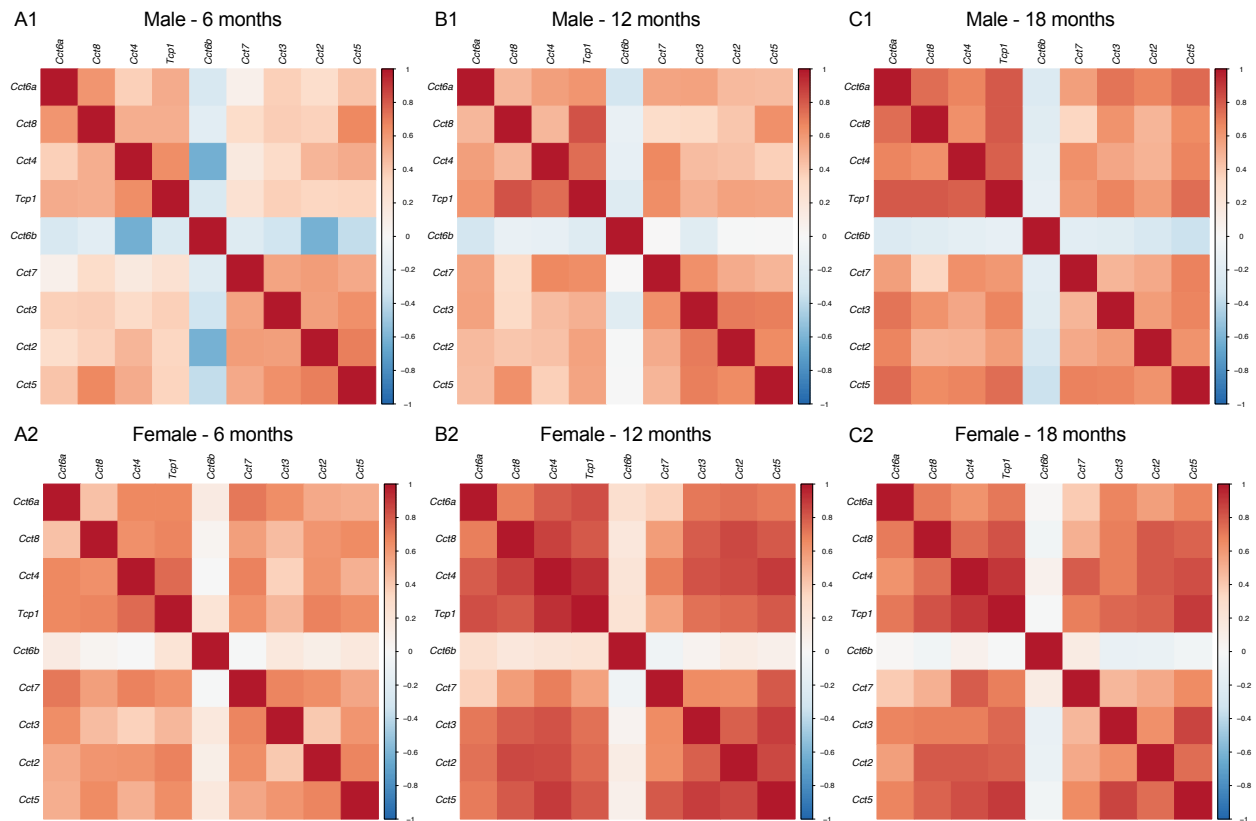


Supplemental Figure S4: Age effects on transcripts and proteins that form protein complexes. A) Volcano plots show the $-\log_{10}(\text{p-value})$ (y-axis) by age effects (x-axis) for members of protein complexes at the transcript (top) and protein (bottom) levels. The horizontal red line represents the significance cut-off at $\text{FDR} < 0.01$. Age effects are reported as $\log_2$ change in abundance per year. Included genes represent the 26S proteasome, chaperonin-containing T complex, cytoplasmic ribosomal large subunit, large drosha complex and nuclear pore complex (indicated by colors), which are the protein complexes most affected by age based on correlation. Genes from the 26S proteasome are highlighted. Many members have significant age effects on the proteins, but much less so on transcripts. Vertical line at zero included for reference. B) Normalized abundance (y-axis) for transcripts (top) and proteins (bottom) across age (x-axis) for the genes *Psmb8*, *Psmb9*, *Psmb3* and *Psmd7*. These genes tend to increase with age at both transcript and protein levels. Best fit lines included to highlight trends. C) Correlation between the *Psmb8* (x-axis) and *Psmb9* (y-axis) and the *Psmb3* (x-axis) and *Psmd7* (y-axis) for both transcripts (top) and proteins (bottom) across age groups (indicated by color). The correlation between *Psmb8* and *Psmb9* is maintained across age groups for both transcript and protein. Even though *Psmb3* and *Psmd7* change in the same direction with age, their correlation is reduced with age in proteins.

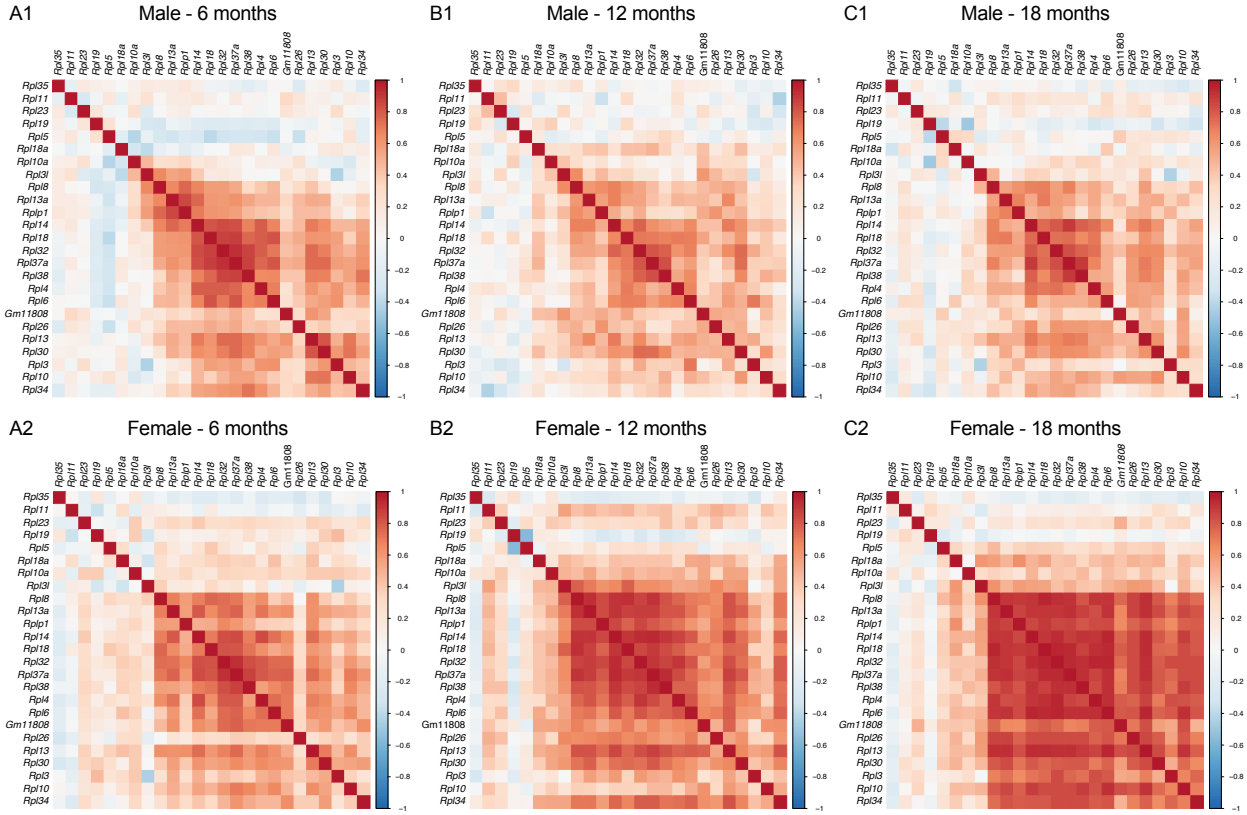
26S proteasome



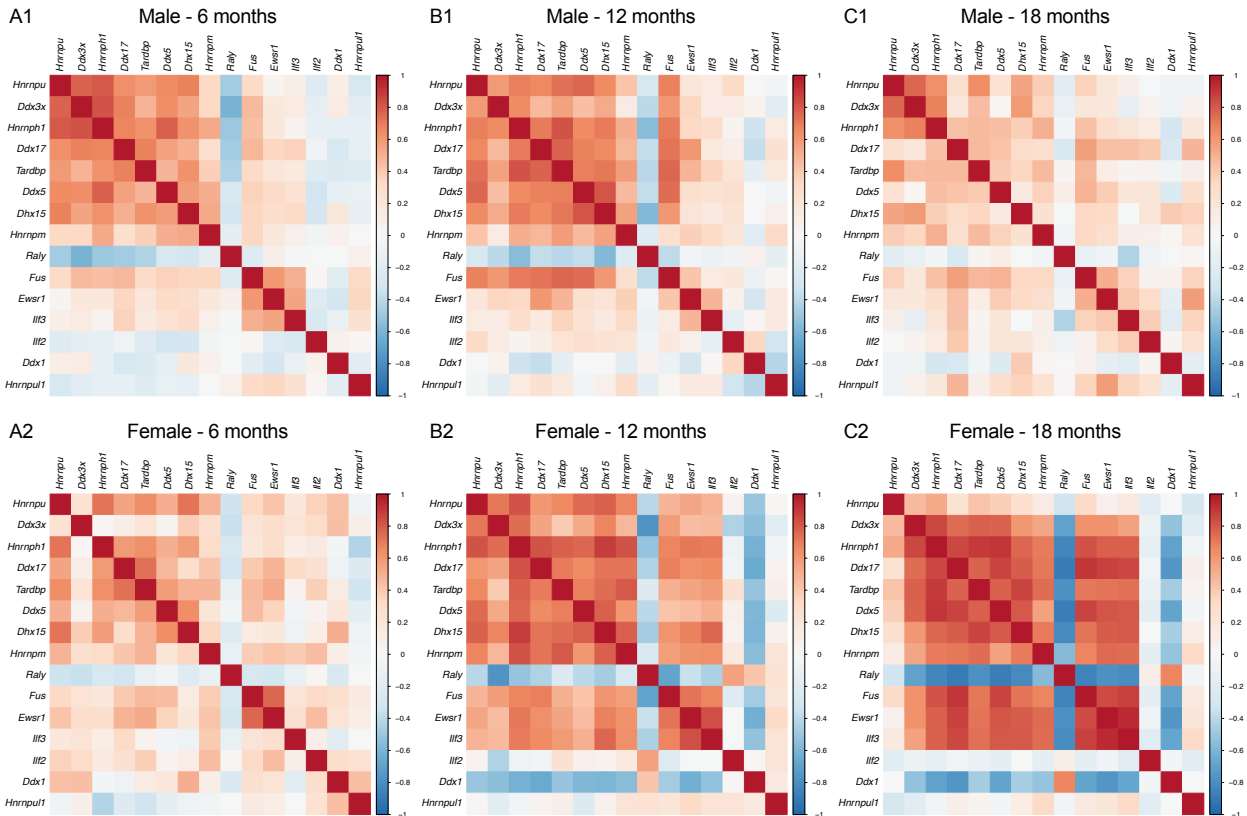
Chaperonin-containing T complex



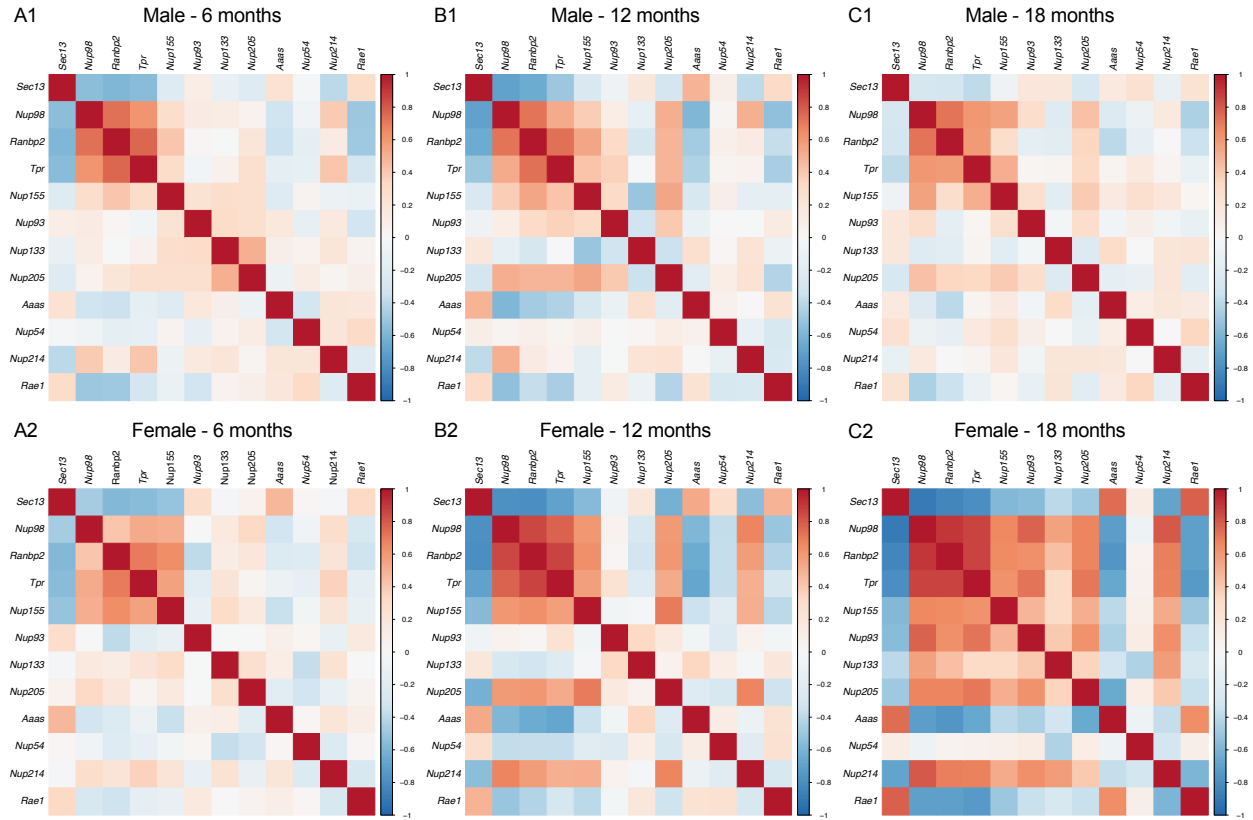
Cytoplasmic ribosomal large subunit



Large drosha complex

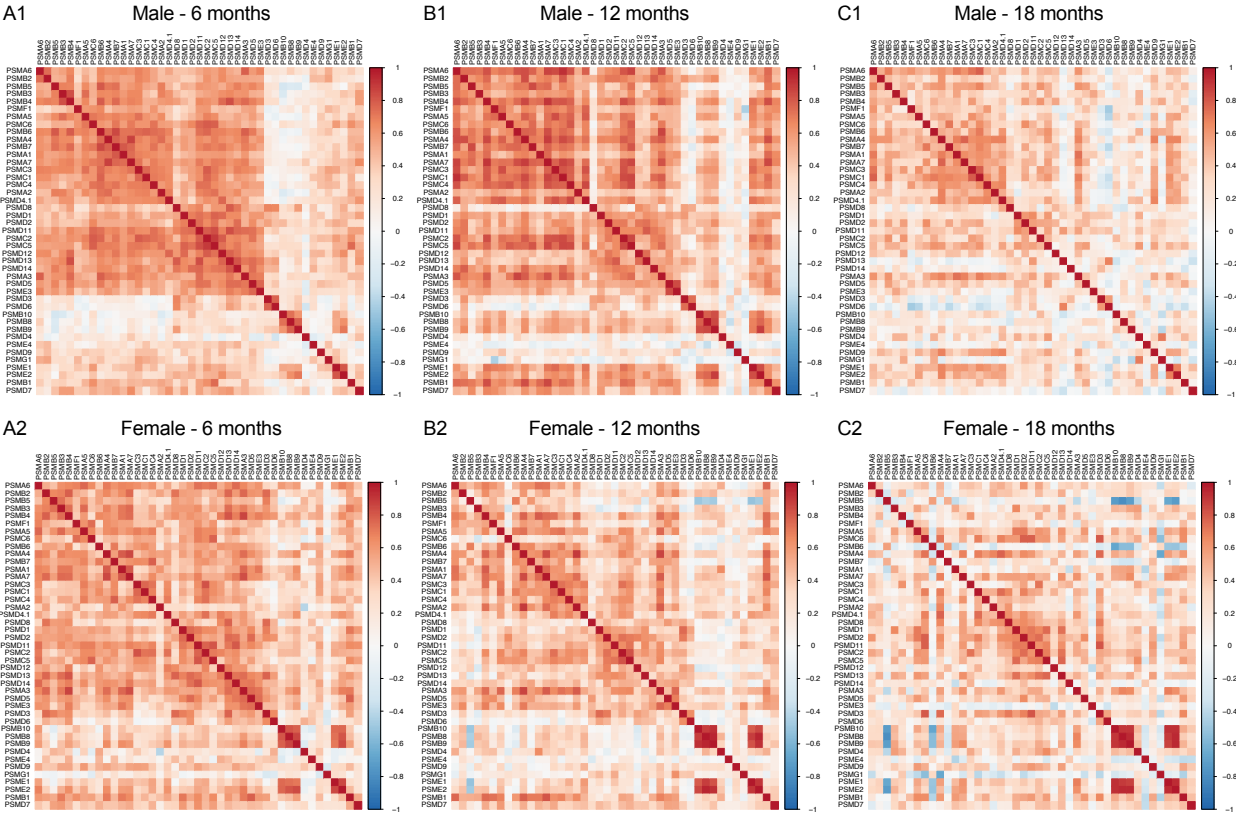


Nuclear pore complex

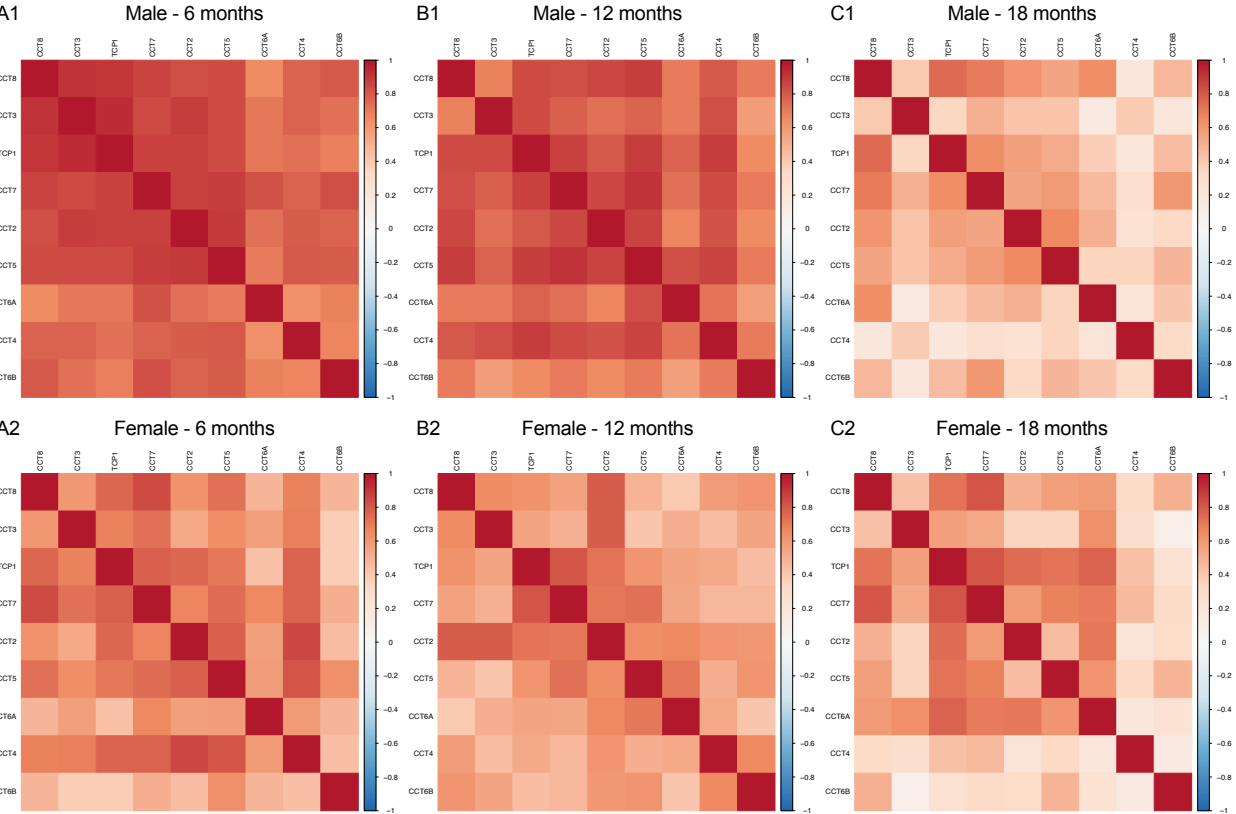


Supplemental Figure S5: Correlations for transcripts from protein complexes, stratified by age and sex. Heatmaps represent the correlation coefficients for transcript expression between members of the protein complexes that were most affected by age (26S proteasome, chaperonin-containing T complex, cytoplasmic ribosomal large subunit, large drosha complex and nuclear pore complex). Each column represents a heatmap for the age groups of 6 (A), 12 (B) and 18 months (C). The top row (1) represents males, and the bottom row (2) represents females.

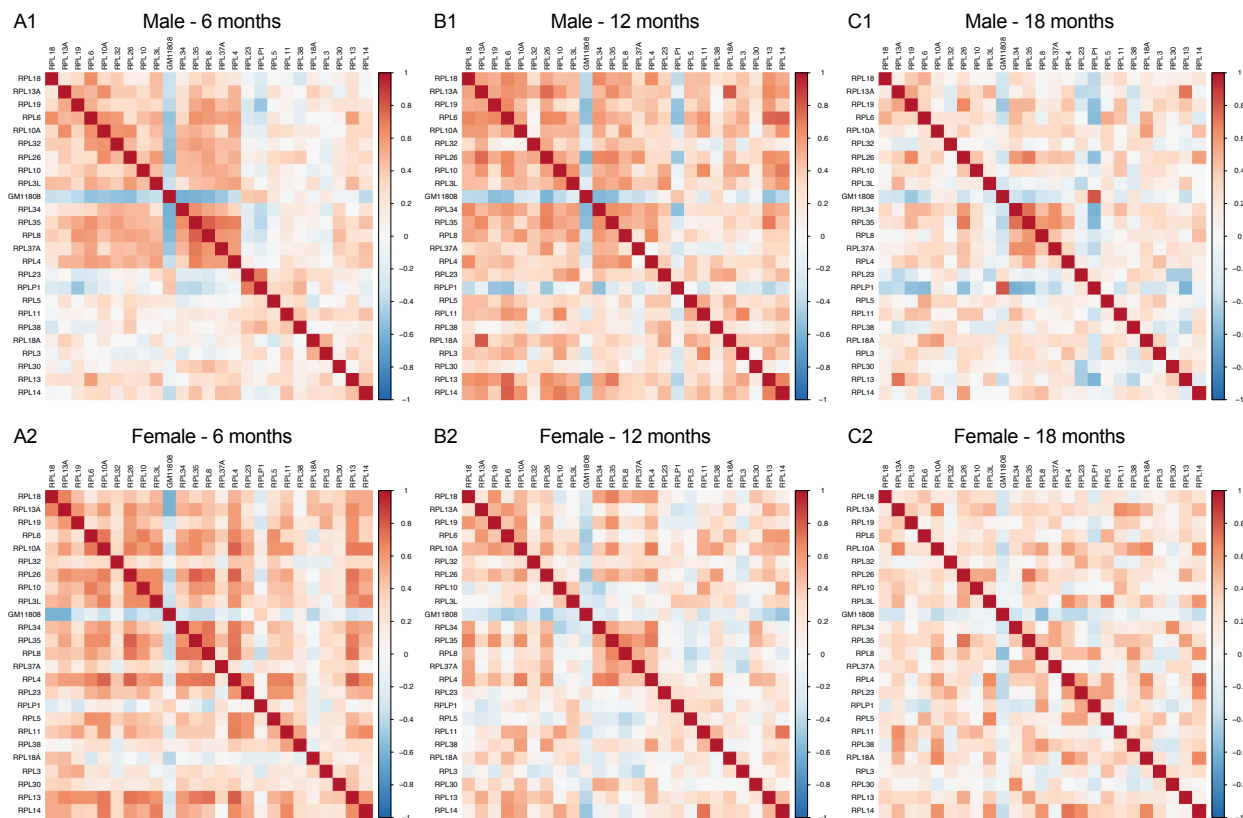
26S proteasome



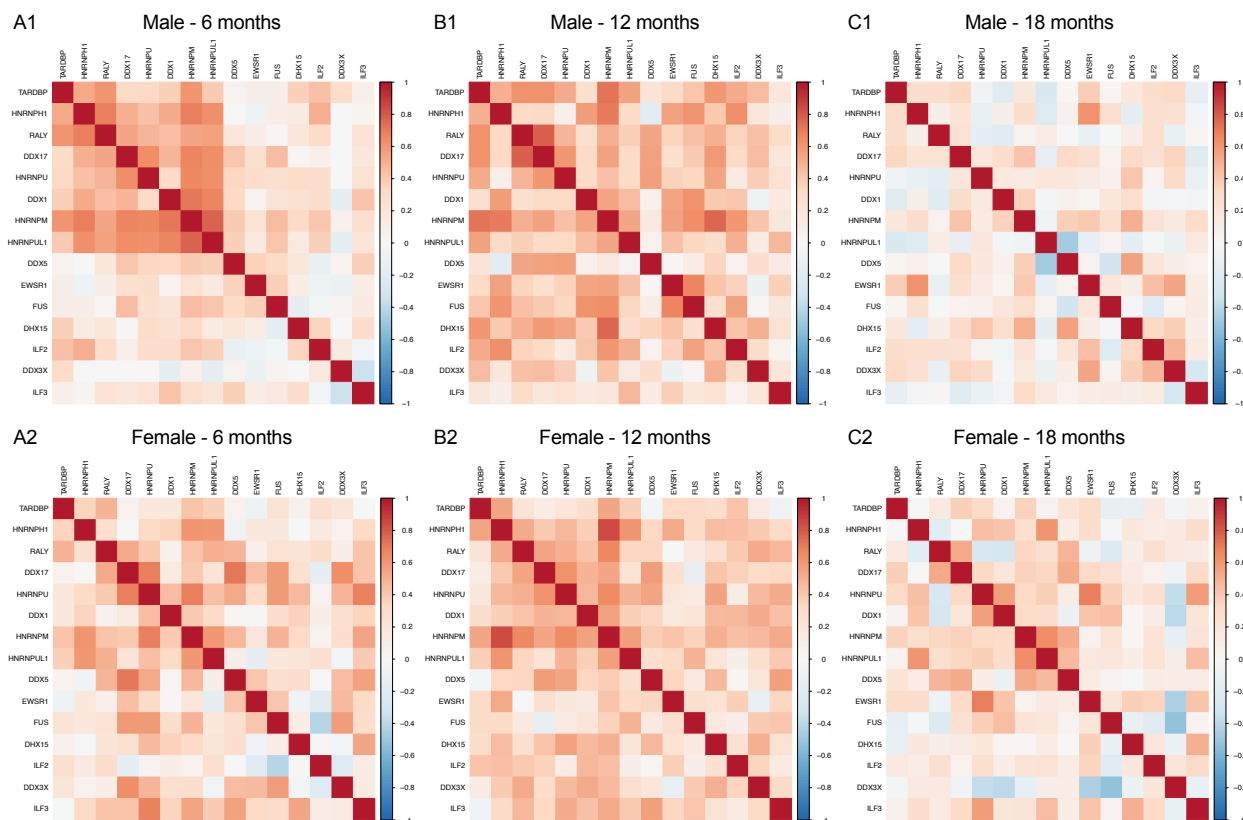
Chaperonin-containing T complex



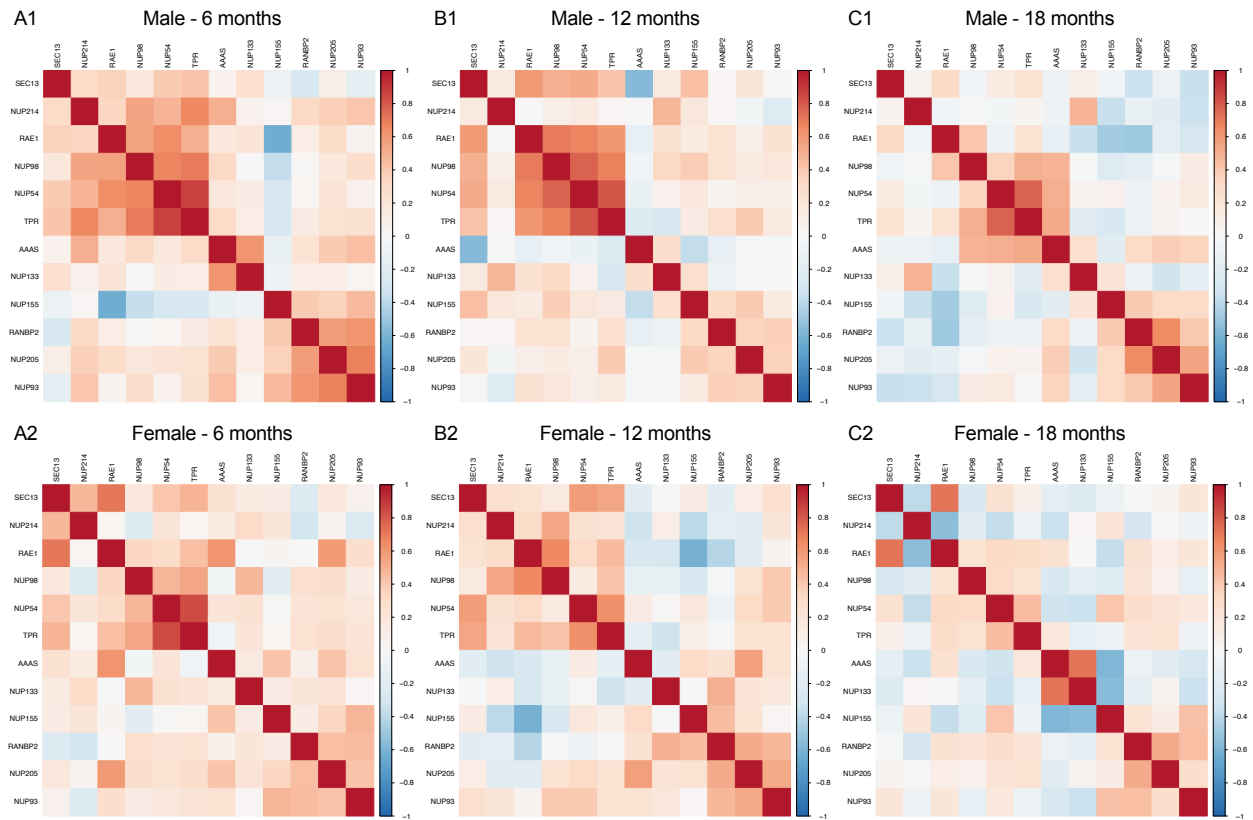
Cytoplasmic ribosomal large subunit



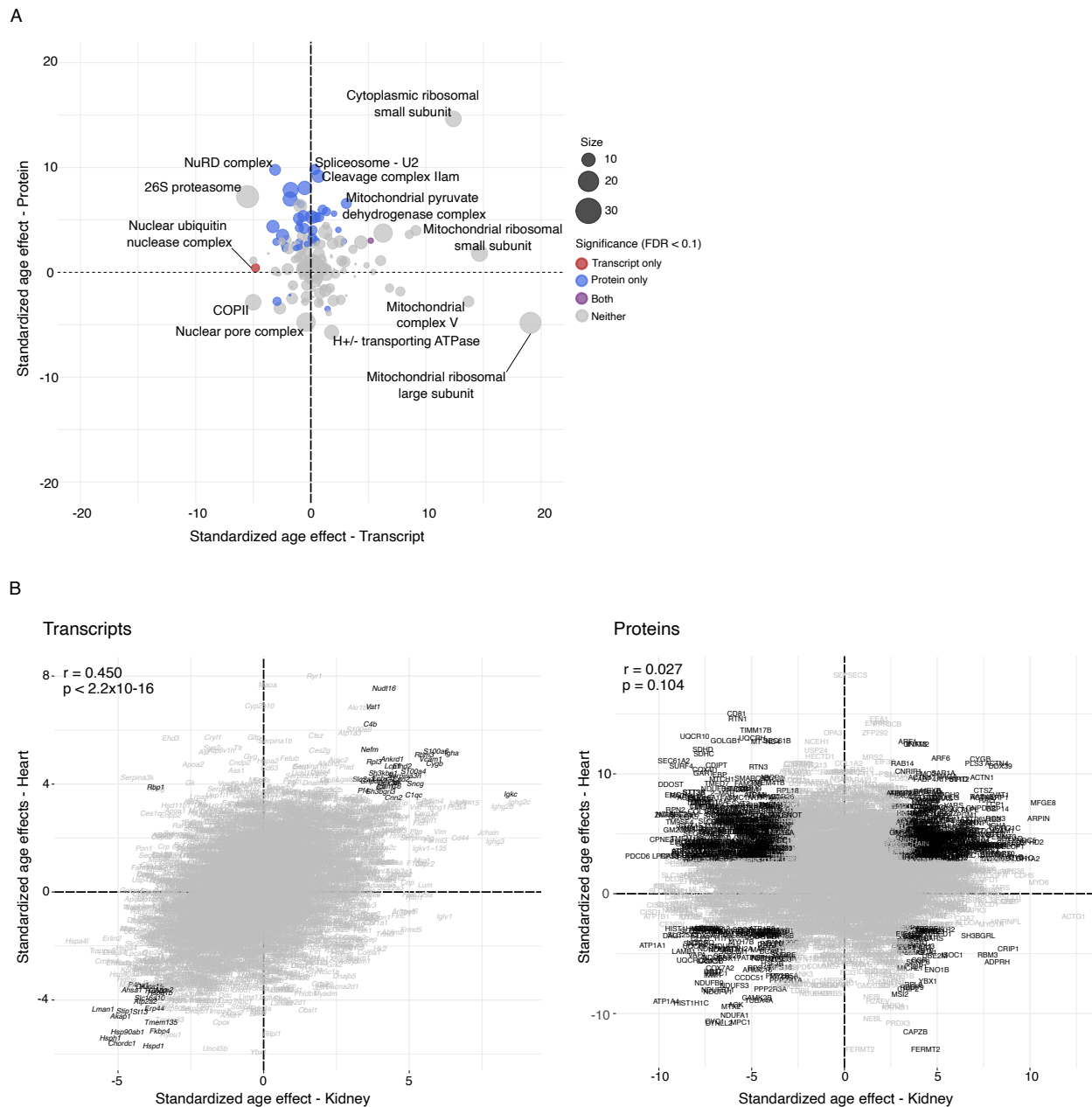
Large drosha complex



Nuclear pore complex

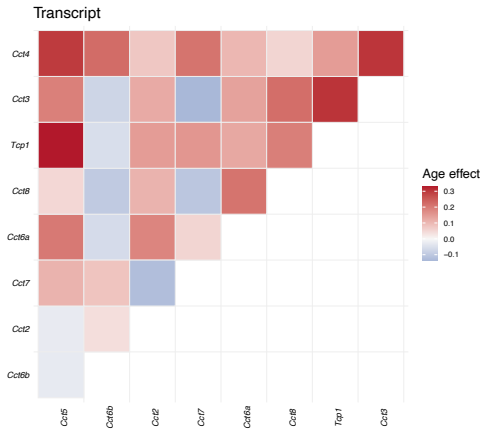


Supplemental Figure S6: Correlations for proteins from protein complexes, stratified by age and sex. Heatmaps represent the correlation coefficients for protein abundance between members of the protein complexes that were most affected by age (26S proteasome, chaperonin-containing T complex, cytoplasmic ribosomal large subunit, large drosha complex and nuclear pore complex). Each column represents a heatmap for the age groups of 6 (A), 12 (B) and 18 months (C). The top row (1) represents males, and the bottom row (2) represents females.

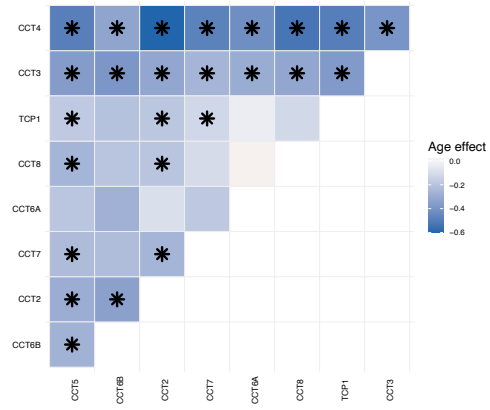


Supplemental Figure S7: Comparison of age effects between heart and kidney tissues. A) Standardized age effects on protein complex correlation in the kidney on proteins (y-axis) by transcripts (x-axis). Protein complex correlations mostly increase with age for proteins in kidney, unlike in the heart where they decrease (Figure 4A). Red points indicate a significant ($FDR < 0.1$) age effect for transcripts only, blue points for proteins only, purple points for both transcripts and proteins, and grey points indicate non-significant age effects for either. Size of points represents the total number of subunits in the complex for which we have data. Horizontal and vertical lines at 0 included for reference. B) Comparisons of standardized age effects between kidney (x-axis) and heart (y-axis) for transcripts (left) and proteins (right) reveal that there is reduced correlation between the tissues for proteins compared to transcripts. Age effects are reported as change in expression or abundance per year. Black labels represent genes with significant ($FDR > 0.01$) age-related changes for transcript and protein in both tissues.

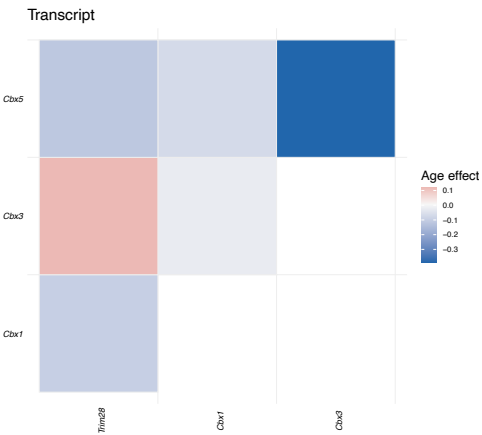
Chaperonin-containing T complex



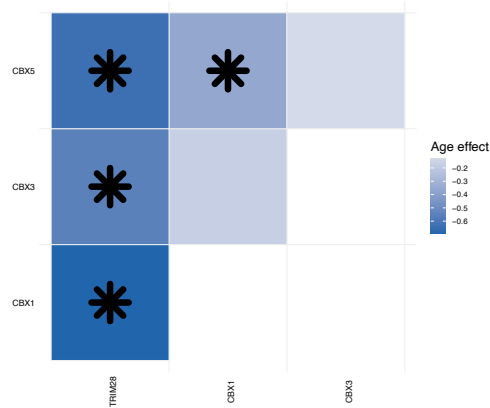
Protein



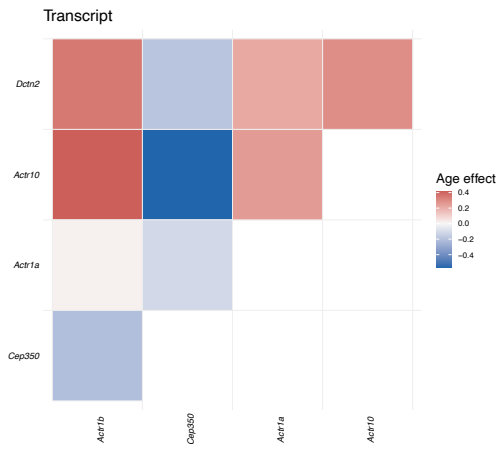
Suv39h1



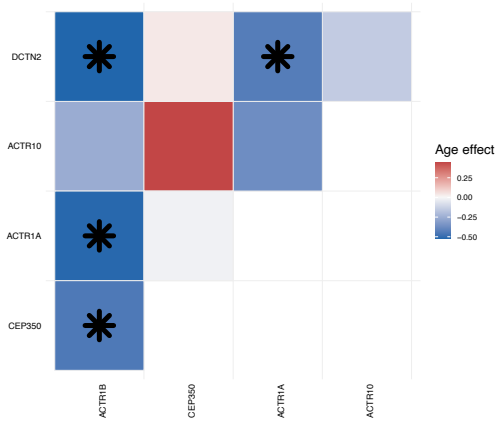
Protein



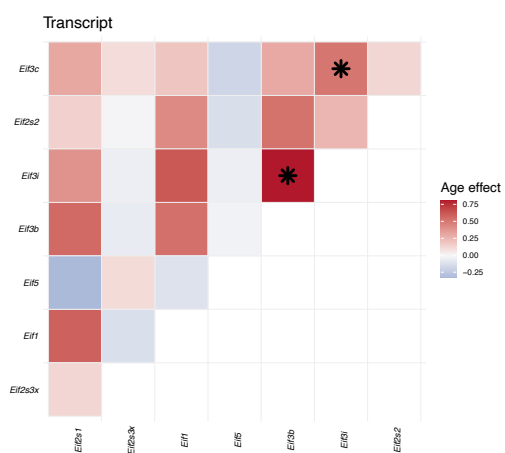
Dynactin complex



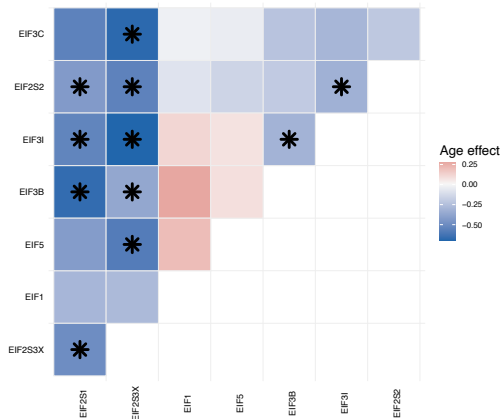
Protein



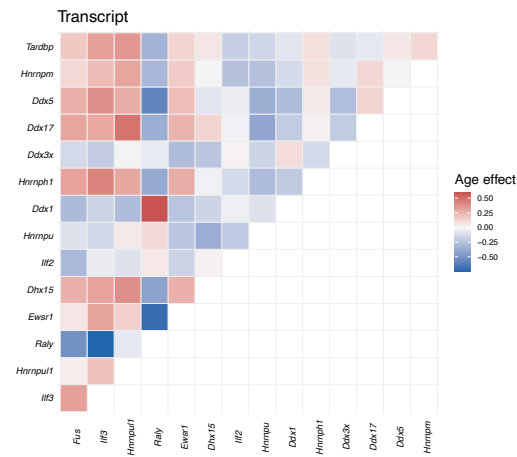
Multi-eLF complex



Protein



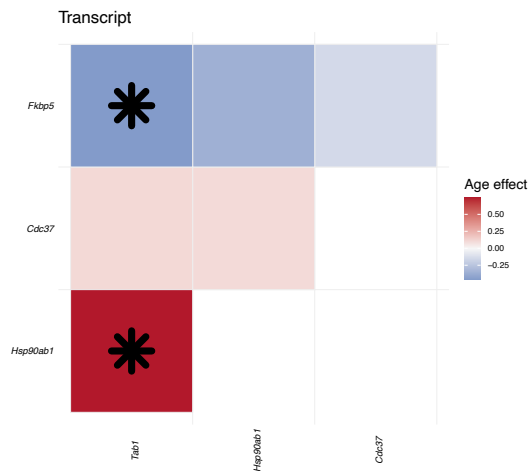
Large drosha complex



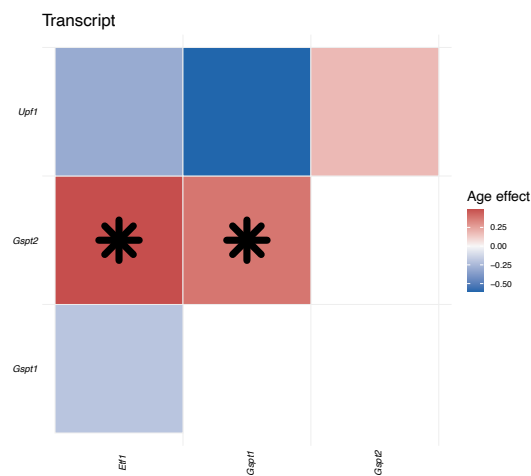
Ubiquitin-proteasome complex



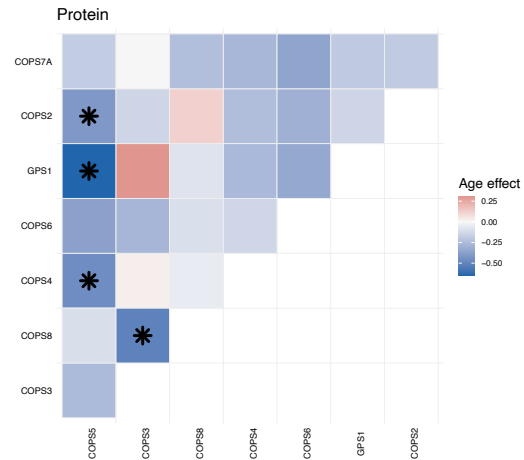
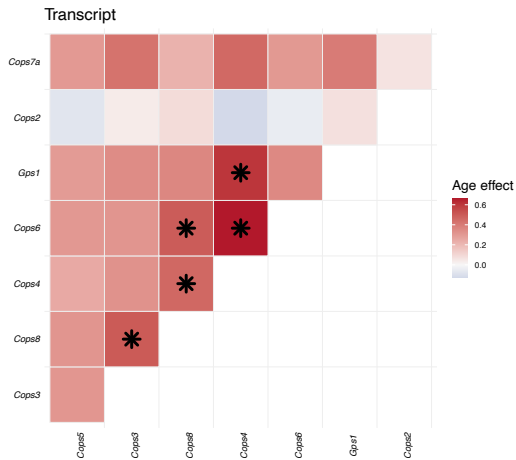
TNF-alpha/NF-kappa B signaling complex 7



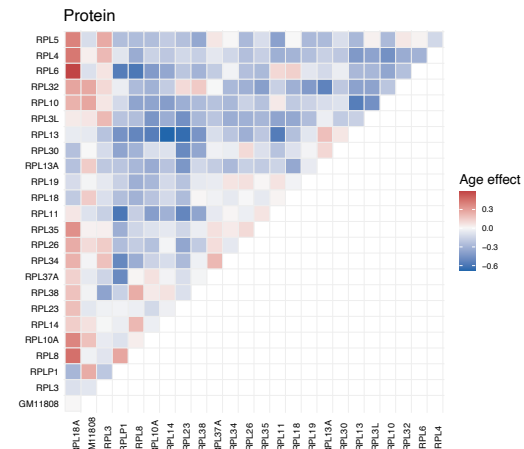
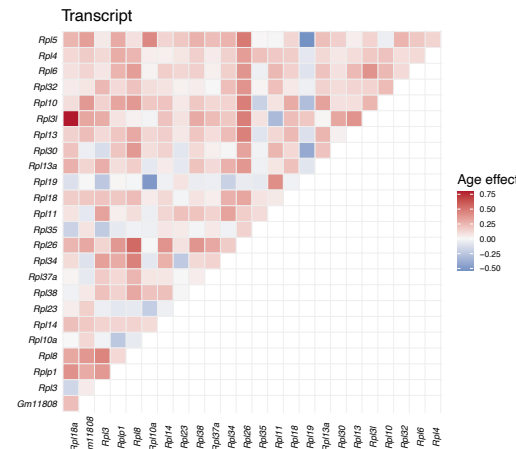
SMG-1-Upf1-eRF1-eRF3 (SURF) complex



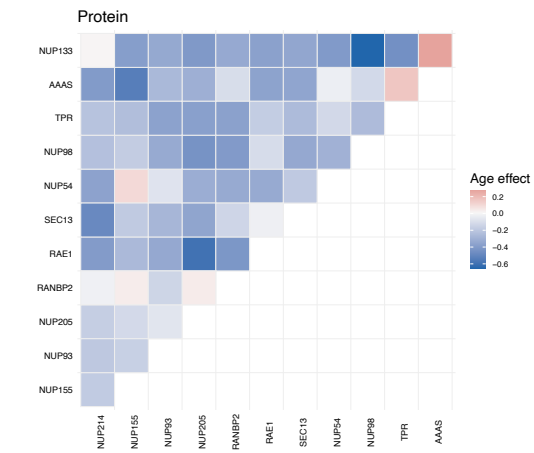
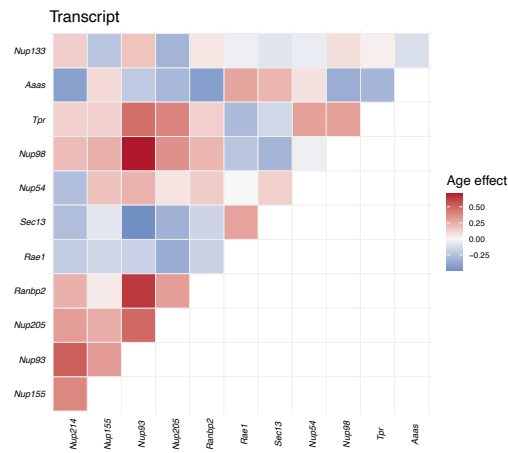
COP9 signalosome



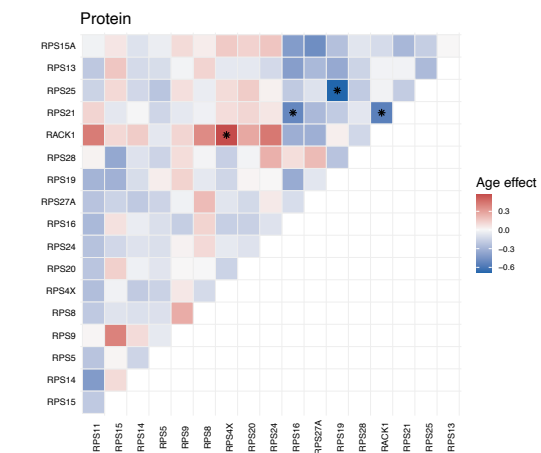
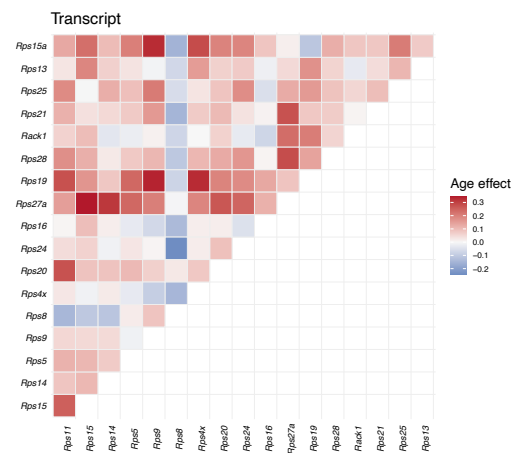
Cytoplasmic ribosomal large subunit

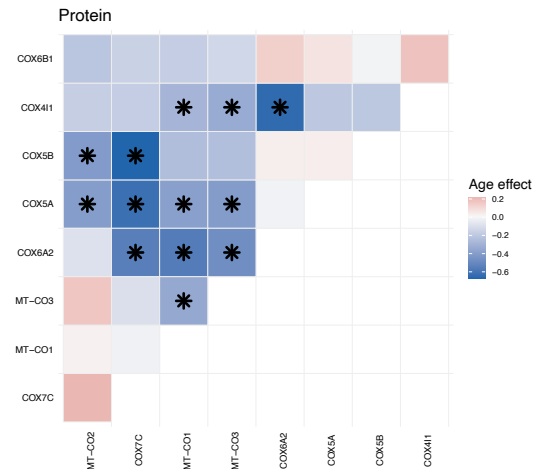
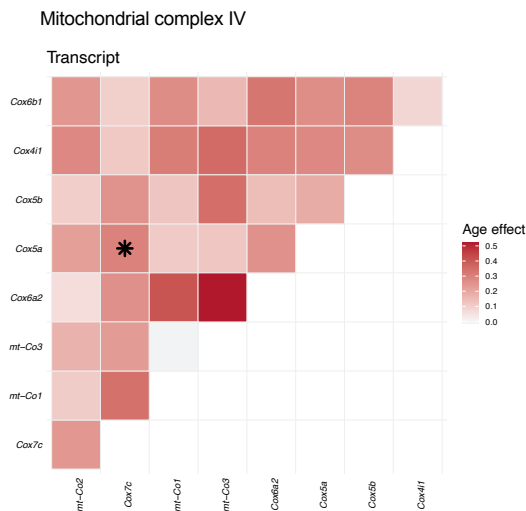
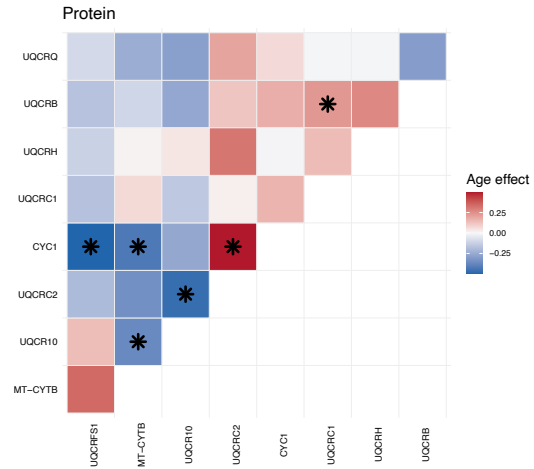
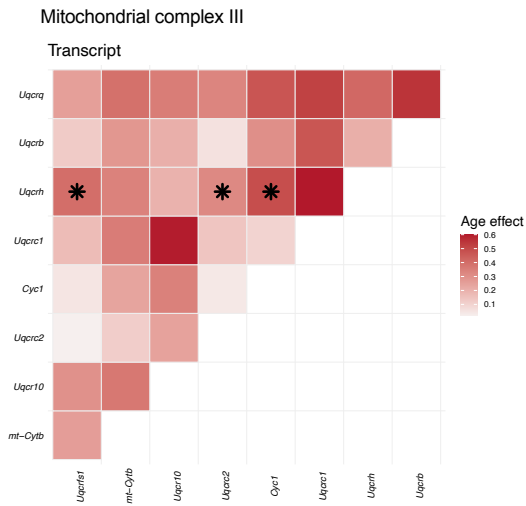
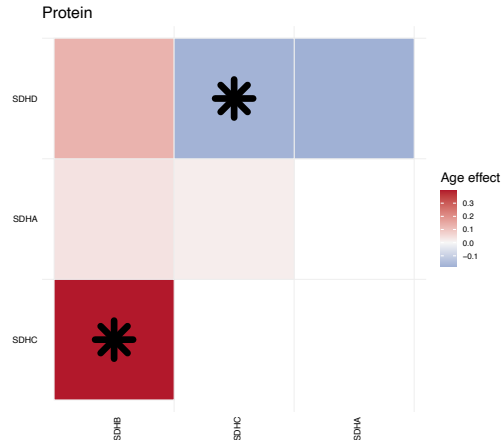
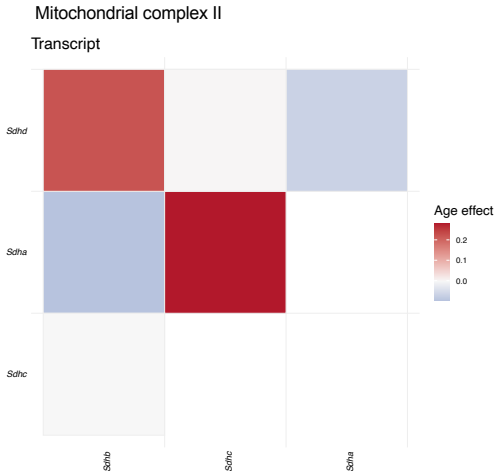
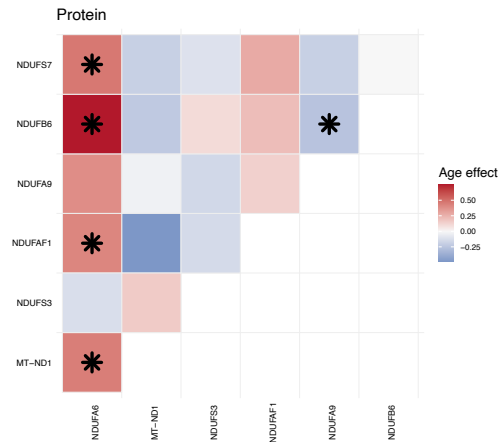
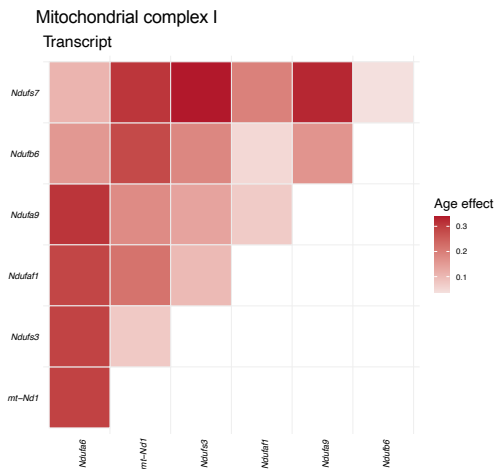


Nuclear pore complex (NPC)

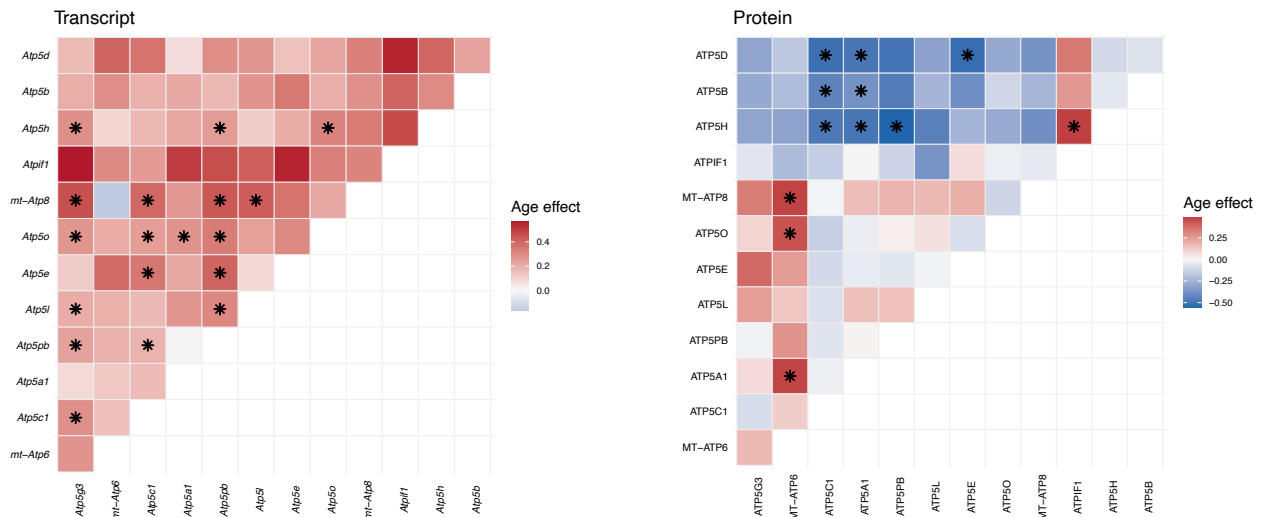


Cytoplasmic ribosomal small subunit





Mitochondrial complex V



Supplemental Figure S8: Age effects on protein complex correlations. Heatmaps represent the age-related change in correlations between gene pairs for members of 17 protein complexes (Chaperonin-containing T complex, Suv39h1, Dynactin complex, Multi-eLF complex, Large drosha complex, Ubiquitin-proteasome complex, TNF-alpha/NF-kappa B signaling complex 7, SURF complex, COP9 signalosome, Cytoplasmic ribosomal large subunit, NPC, Cytoplasmic ribosomal small subunit, and mitochondrial respiratory chain complexes I-V). Age effects on transcripts are shown on the left and age effects on proteins are shown on the right. These protein complexes were detected by either having a strong overall age effect or by presenting a high proportion of pairwise correlations with significant changes due to age. Asterisks highlight gene pairs with significant (FDR < 0.1) changes in correlation.

