

Supplementary Figures

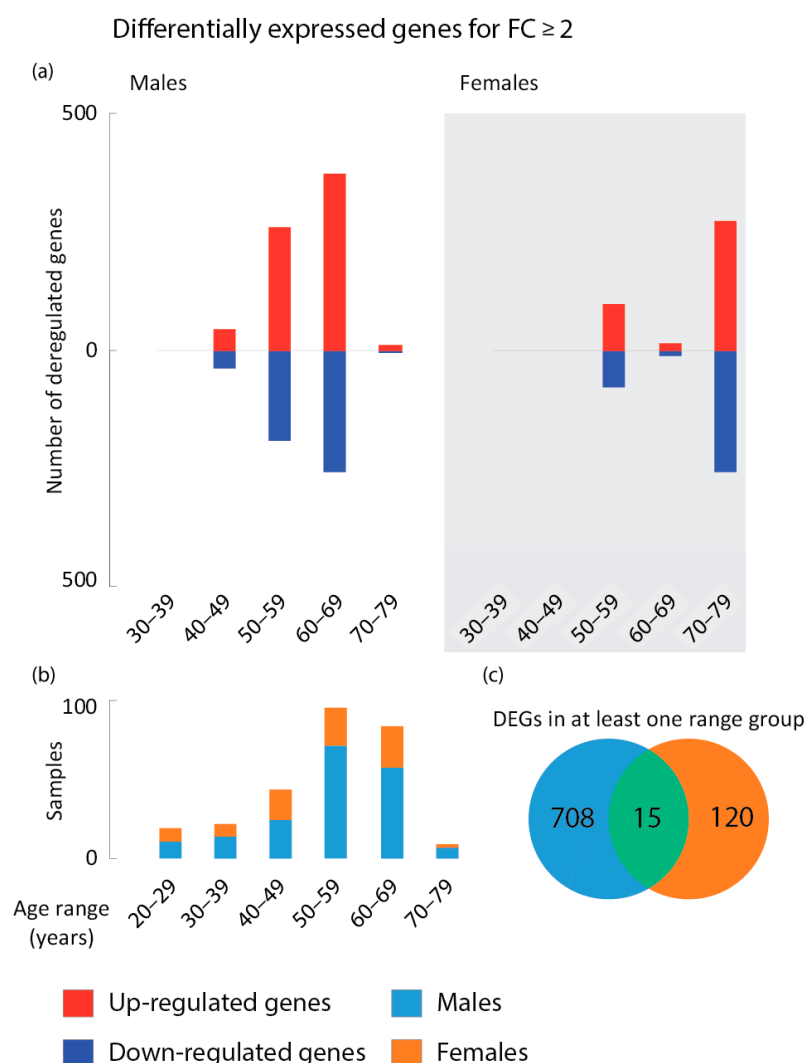


Figure S1. Differentially expressed genes (DEGs) of each age range from the oldest group to the youngest group (a). The youngest group (20–29 years old) was used as a common reference using the Genotype-Tissue Expression database. Differences were only observed for the proposed cutoff ($FC \geq |2|$, $FDR < 0.05$) after the 40–49 age range for males and 50–59 age range for females. Comparatively, there were fewer DEGs in 70–79-year-old males, and the opposite occurred in 70–79-year-old females. This could be due to smaller sample sizes of 70–79-year-olds (b). Quantitative representation of common and specific DEGs for males, females, and between the groups are represented by Venn diagram (c).

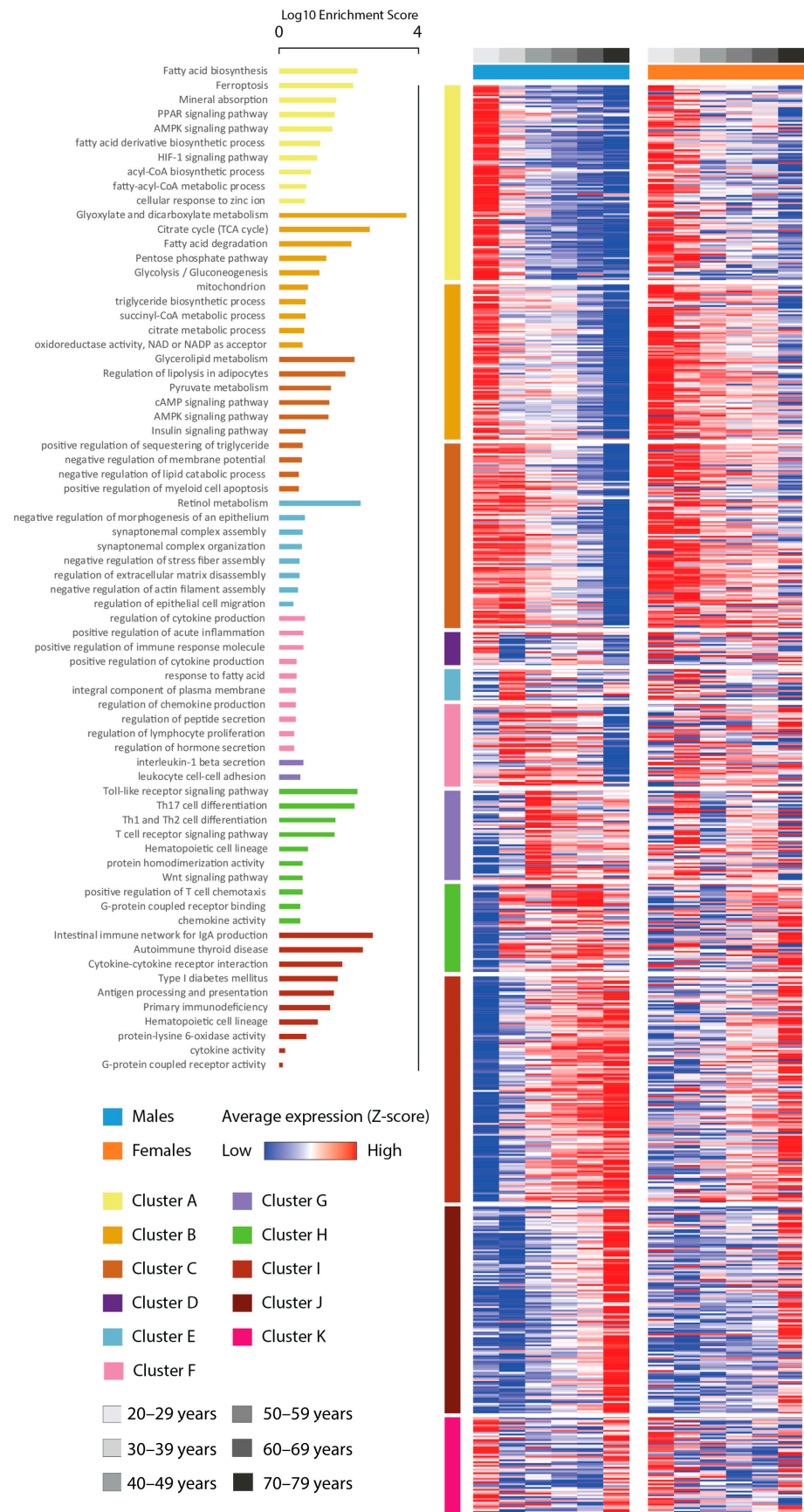


Figure S2. Heatmap of the mean expression of differentially expressed genes (DEGs) in at least one age group clustered with K means = 11. The expression of some genes progressively increases with aging at different rates (clusters A, B, and C), while others decrease (clusters I and J). In addition, some do not form gradients and have overall lower enrichment scores (D, E, F, G, H, J, and K).

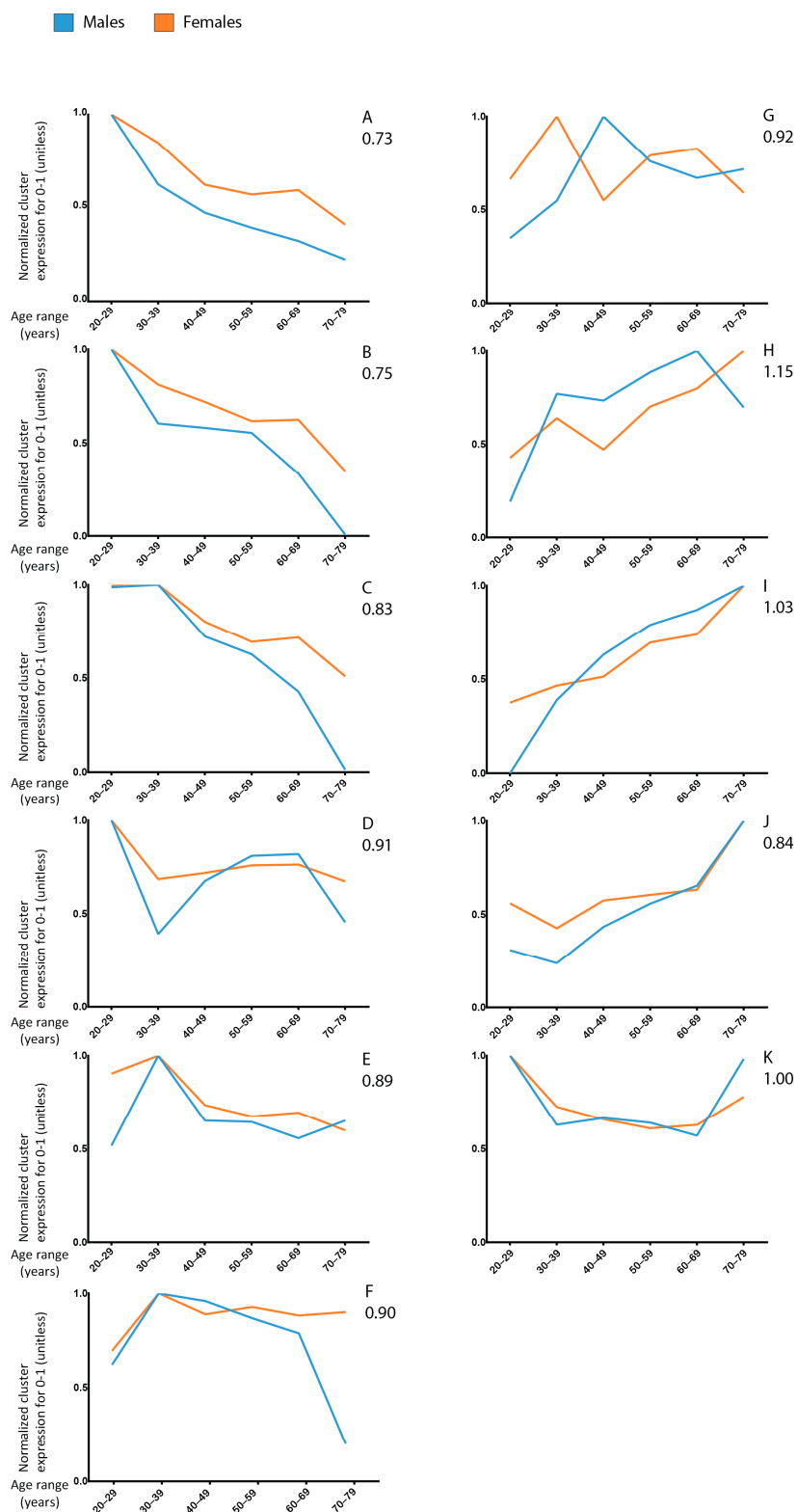


Figure S3. Unitless (0, 1) and normalized mean expression of each cluster for males and females and the ratio of the AUC between males and females (upper right corner of each graph). The closer to 1, the higher the similarity between males and females. In clusters A, B and C we can see a downward trend, while in cluster I and J, a growing trend.

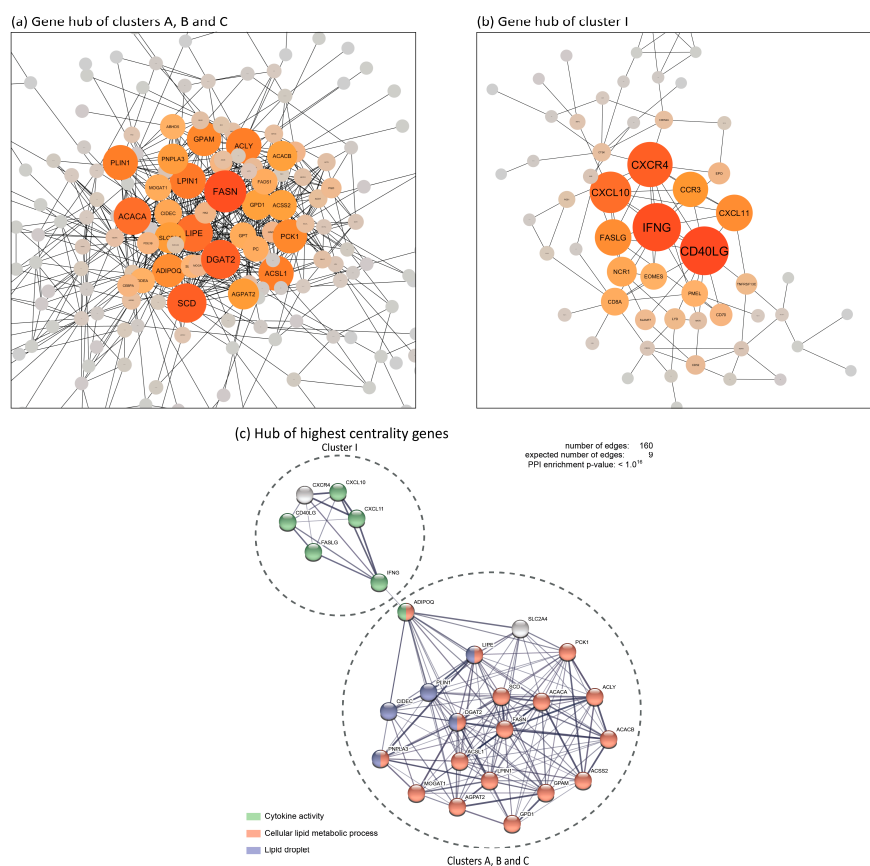


Figure S4. Gene-gene interaction analysis concerning physical protein-protein expression, text mining, and co-expression connectivity between clusters. Node sizes correspond to eigenvector centrality (a) in genes whose expression increase gradually with age and (b) decrease with age. Finally, (c) the interaction between the genes with the highest centrality of all clusters.