Quantification of human sexual dimorphism with the dimorphism index in subcutaneous adipose tissue

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- 1 Abstract
- 2 Introduction
- 3 Methods
- 4 Results
- 4.1 Descriptive Analysis

Correlation between the continuous variables:

- 4.2 Differential Gene Expression Analysis
- 4.3 Interpretation of the DI-associated transcriptome
- 4.3.1 Hormone Receptors Associated with the Dimorphism Indices and with Sex
- 4.3.2 Gene Set Enrichment Analysis
- 5 Discussion and Conclusion

Annexes

Session Information

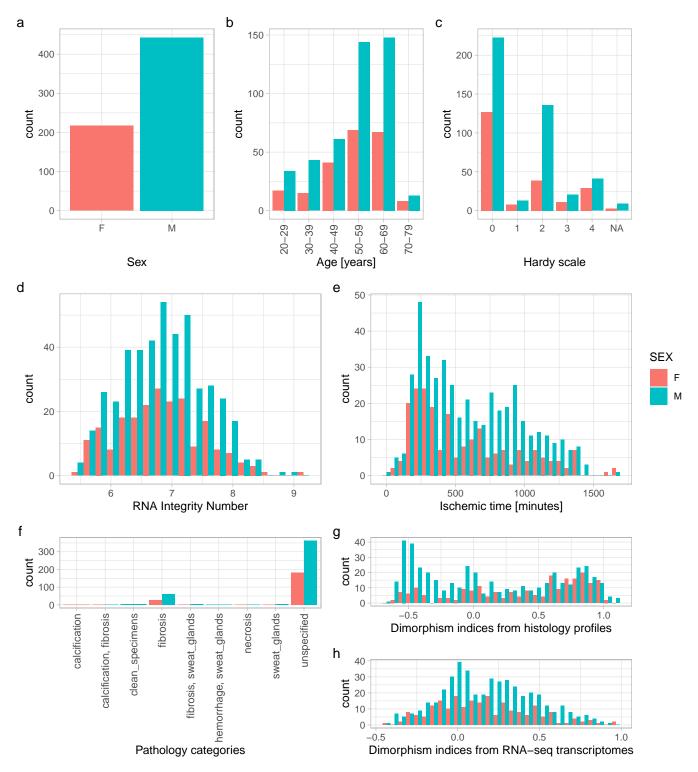


Figure 1: Distribution of the clinical and technical variables, and the dimorphism indices of the samples separated by sex (F = Female, M = Male). (a) Number of Female and Male subcutaneous adipose tissue sample donors. (b) Distribution of ages (in decades) of the donors. (c) Death classification of the samples' donors with the Hardy scale. (d) Distribution of the samples' RNA integrity numbers. (e) Distribution of the samples' ischemic time. (f) Medical conditions diagnosed post-mortem from histology slides. (g) Distribution of the transcriptional dimorphism indices computed from whole RNA-seq transcriptomes. (h) Distribution of the dimorphism indices computed from AI-based histology profiles.

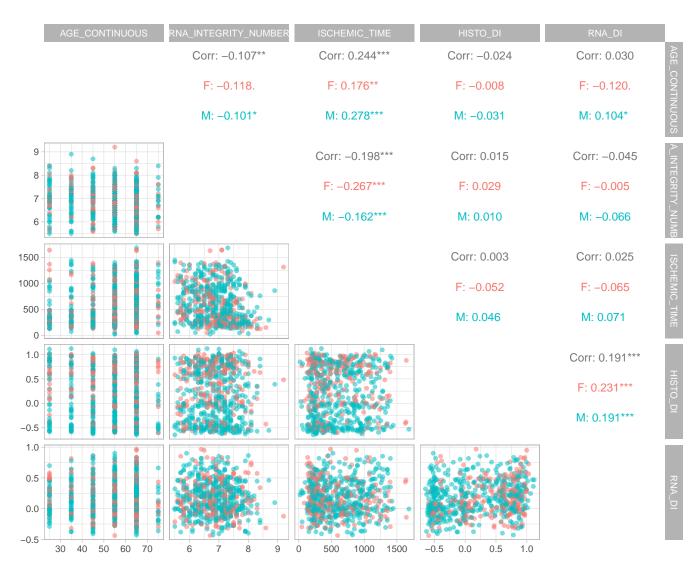


Figure 2: Pairs plot of the continuous clinical and technical covariates for the samples separated by sex. The lower diagonal shows the scatter plots of each pair of variables. The upper diagonal indicates the Pearson correlation coefficients of the variables considering all the samples (grey), or for the samples separated by sex (F = Female, M = Male). Statistical significance of the correlation is indicated by an asterisk (*** for p-value p < 0.001, ** for p < 0.01, * for p < 0.05, and . for p < 0.10).