

Nonlinear dynamics of multi-omics profiles during human aging

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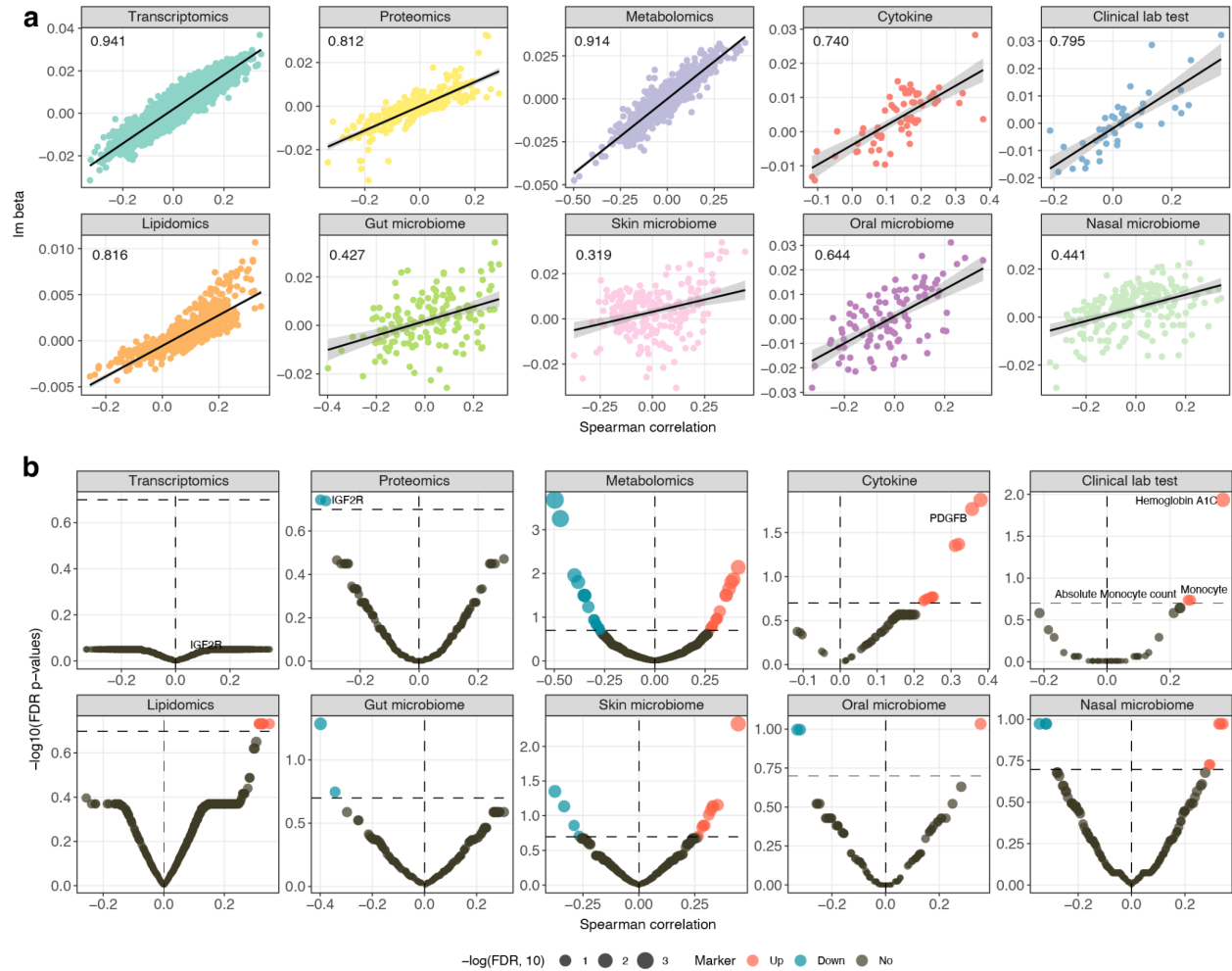
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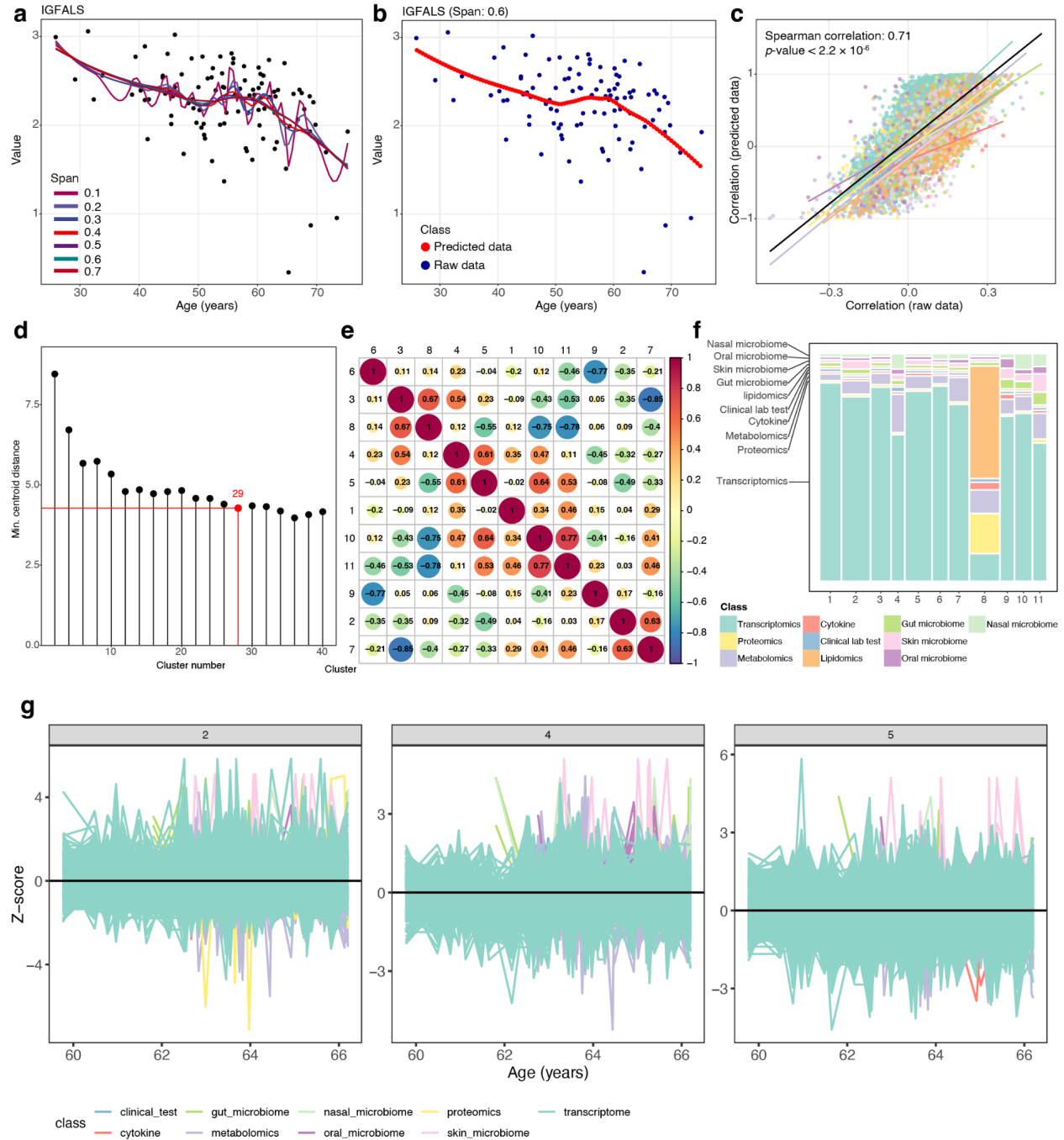
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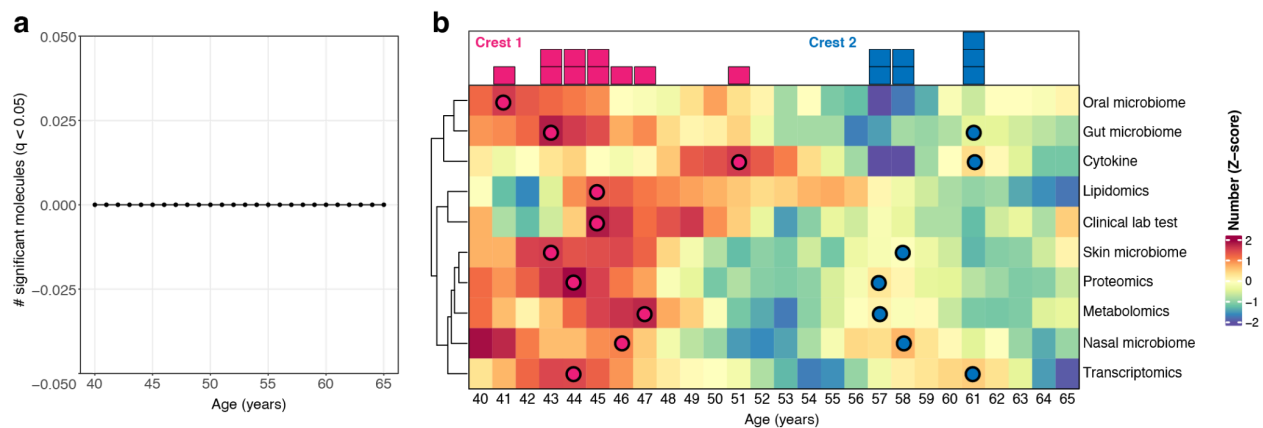
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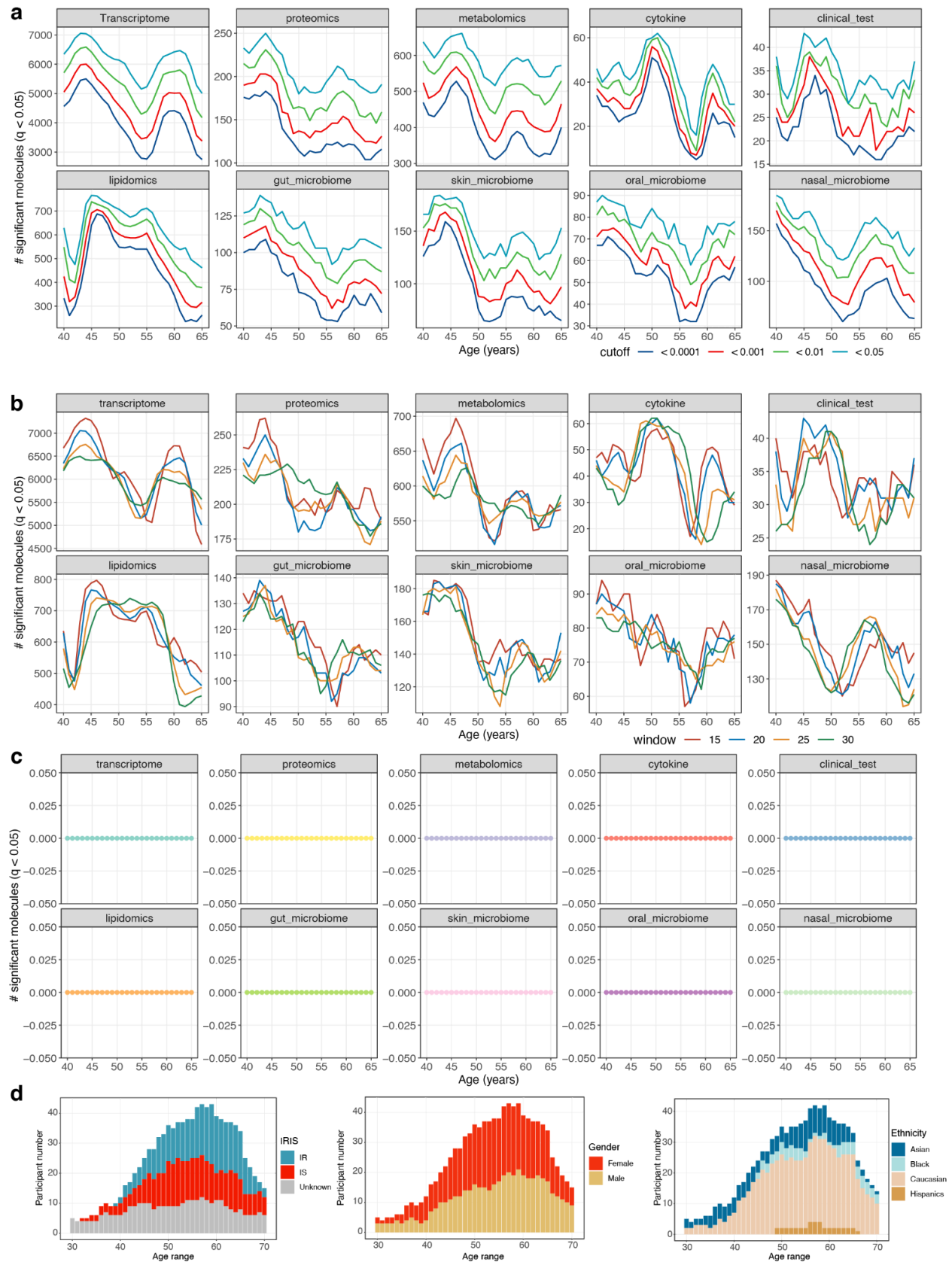
Supplementary Figure 1. Linear changing molecules during human aging. **a**, The Spearman correlations highly correlate with the beta coefficients from linear regression models for each type of omics data. The shaded area around the regression line represents the 95% confidence interval. **b**, Linear changing molecules for different types of omics data using the Spearman correlation approach (FDR-adjusted p -values < 0.05).



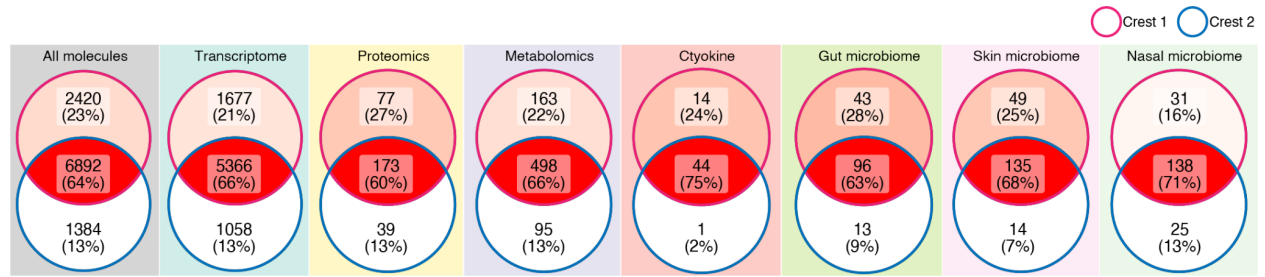
Supplementary Figure 2. LOESS smoothing for omics data and Fuzzy C-clustering. **a**, LOESS smoothing for protein IGFALS with parameter Span from 0.1 to 0.7 (step = 0.1). **b**, LOESS smoothing for protein IGFALS with best span 0.6. **c**, The predicted data and raw data have high correlations for all the omics data (Spearman correlation: 0.71, p -value < 2.2×10^{-6}). **d**, The optimization of the number of clusters. **e**, The correlation matrix of 11 clusters for all the omics data. **f**, The classes of all the molecules in all the clusters. **g**, The molecules in clusters 2, 4, and 5 at individual levels.



Supplementary Figure 3. Waves of molecules and microbes during aging. **a**, The waves disappeared when the phenotypes of the individuals were randomly permuted. **b**, The waves for different types of omics data across the human lifespan.



Supplementary Figure 4. DE-SWAN age effect for multiple q -values cutoffs, windows size, and after phenotypes permutations. **a**, Different q -value cutoffs are used for each type of omics data, respectively. **b**, Different windows are used for each type of omics data. **c**, The crests disappeared when the sample labels were randomly shifted for each type of omics data respectively. **d**, The distribution of insulin sensitivity, gender, and ethnicity across ages.



Supplementary Figure 5. The overlap of all types of omics data between crests 1 and 2.

Supplementary Note

R Packages used in the study

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loaded via a namespace (and not attached):

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