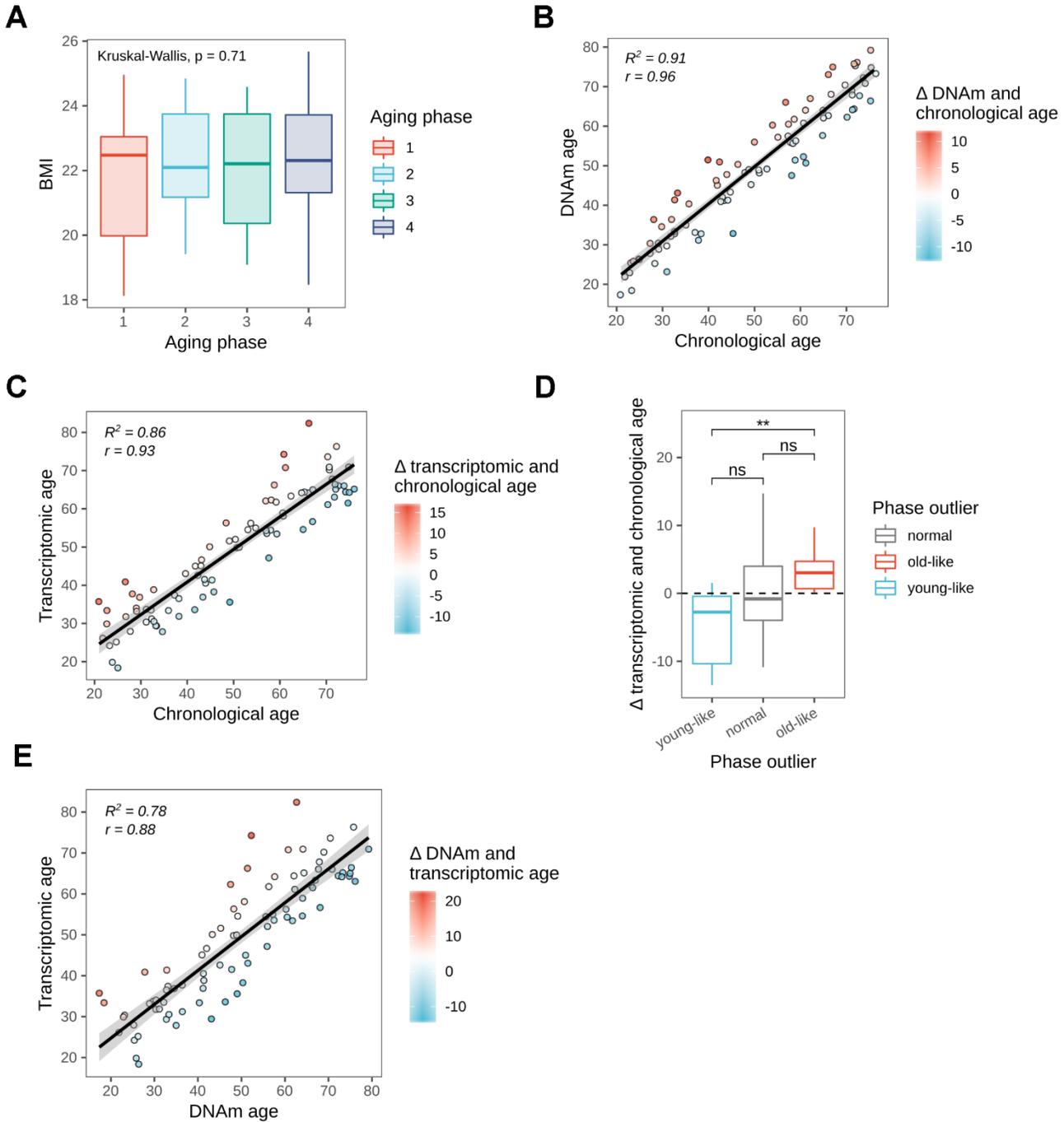
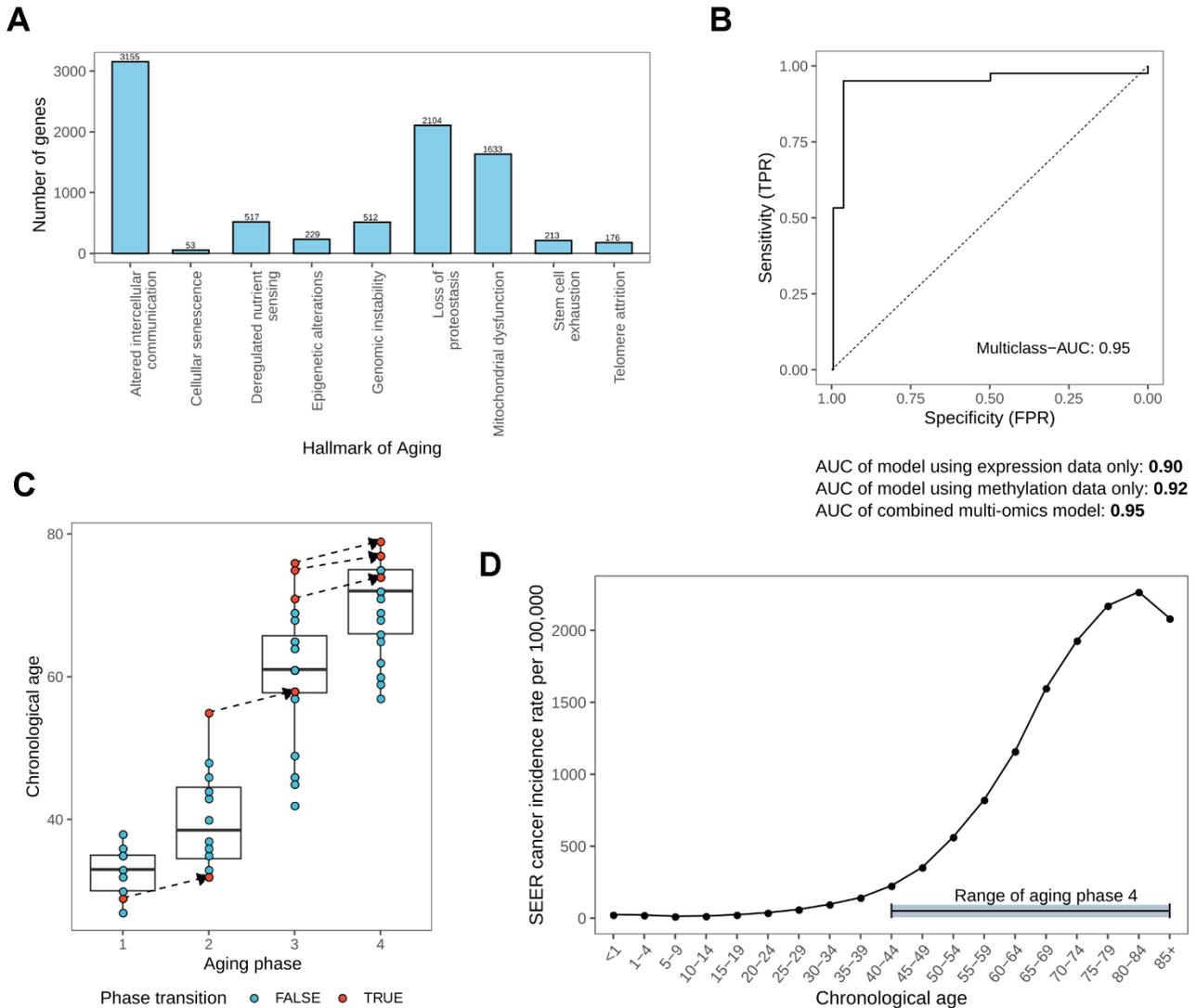


SUPPLEMENTARY FIGURES



Supplementary Figure 1. (A) Boxplots showing the distribution of BMI within the identified aging phases, with no apparent bias detectable. (B) Relationship between chronological and DNAm age. (C) Relationship between chronological and transcriptomic age. (D) Boxplot showing the deviation of transcriptomic from chronological age based on aging phase outlier status. Statistical significance determined using pairwise T-tests. (E) Relationship between DNAm and transcriptomic age.



Supplementary Figure 2. (A) Sizes of the Hallmark of Aging gene sets generated from GO and Reactome pathways. (B) Receiver operating characteristic curve, showing the accuracy of classification of the random forest model trained on expression and methylation features to predict aging phases of the re-invited subjects at the longitudinal second time point. TPR and FPR rates were determined using 5 x 5-fold repeated cross-validation on the original data. (C) Classification of re-invited subjects into the respective aging phases, with transitioning subjects marked in red, distributed along their chronological age. Only re-invited subjects are shown. (D) Cancer incidence rate (aggregated SEER statistics from 1976-2016 for the United States of America), with the observed chronological age range of aging phase 4 in this study marked in blue.