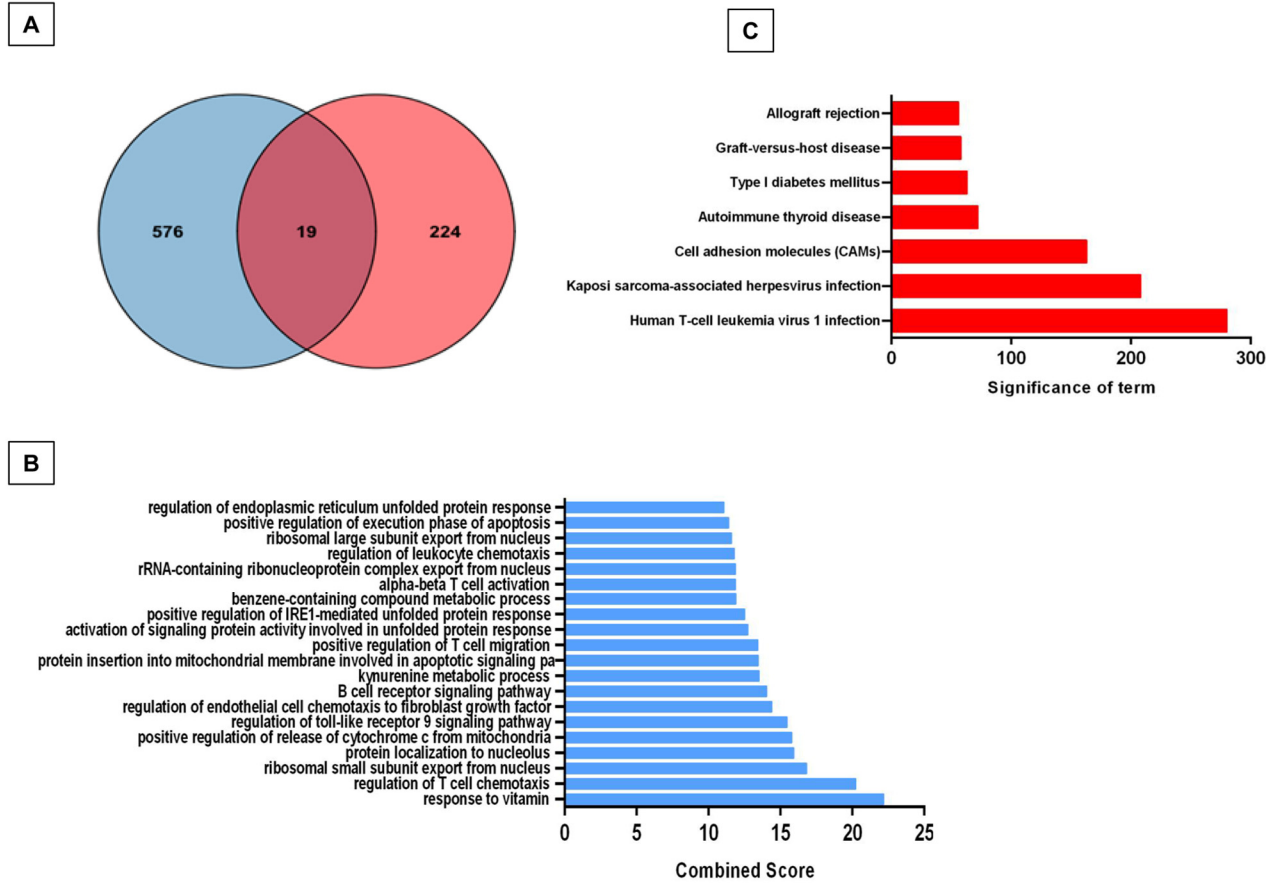
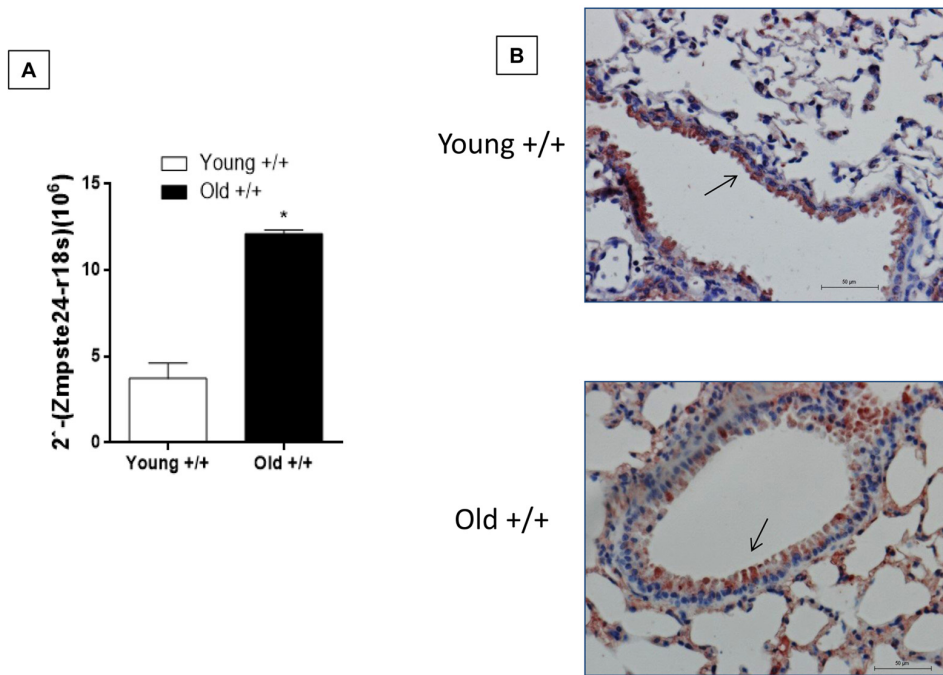


SUPPLEMENTARY FIGURES



Supplementary Figure 1. Bioinformatic analysis of changes associated to accelerated lung aging compared to normal lung aging. (A) Venn diagram of dysregulated genes in natural aging (old WT vs young WT) in blue circle, and dysregulated genes in accelerated aging (old *Zmpste24*^{-/-} vs young *Zmpste24*^{-/-}) in red circle. Light purple circle shows overlapping genes between both groups. (B and C) Gene ontology (B) and KEGG (C) functional analysis. Threshold criteria considered for the analysis are log fold-change > 1 or < -1 and p-value < 0.05 for genes, and >0.5 or < -0.5 for miRnas.



Supplementary Figure 2. Lung expression and localization of *Zmpste24* in old and young WT mice. (A) qPCR of *Zmpste24* in lungs of old and young WT mice under basal conditions. Results are shown as mean \pm SD. Statistical significance was determined by Student's t-test (* $p < 0.05$). (B) Representative photomicrographs of immunohistochemical staining performed with specific primary antibody against *Zmpste24* in lungs from old and young WT mice under basal conditions. Positive signal is observed in bronchoalveolar epithelial cells (black arrows). All sections were counterstained with hematoxylin. Scale bar: 50 μ m.