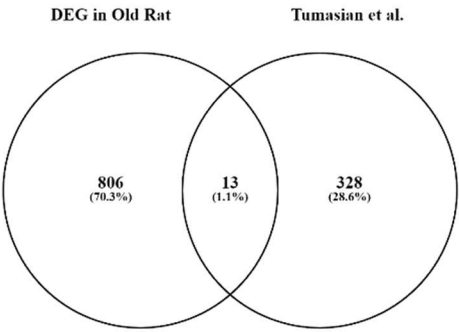
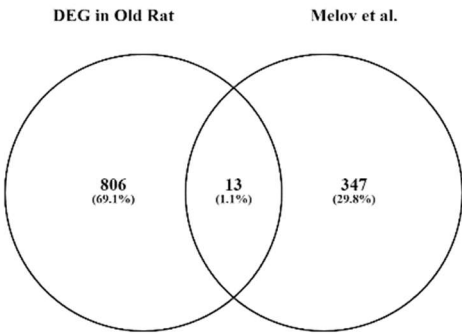


Figure S1. Comparing the DEG with previously published studies on muscle ageing or CR.

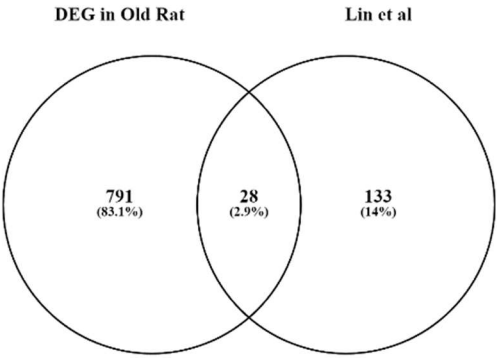
A



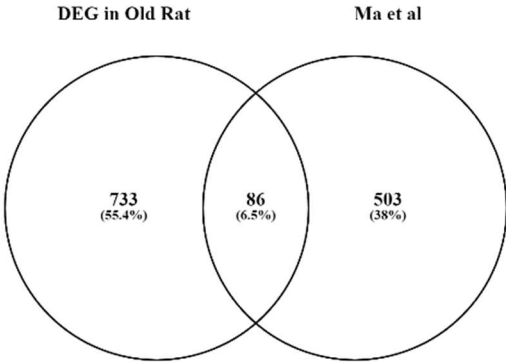
B



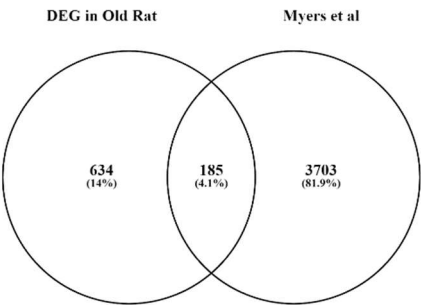
C



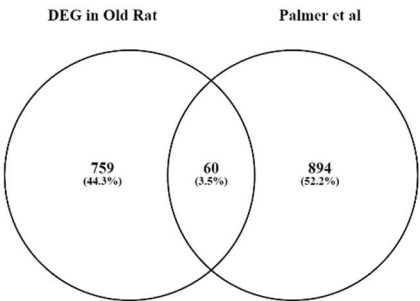
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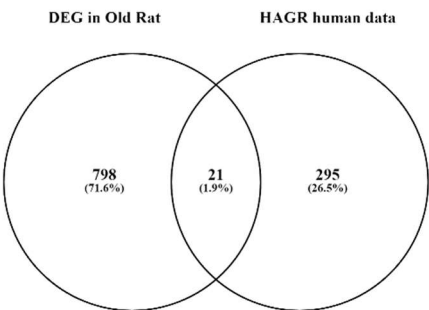
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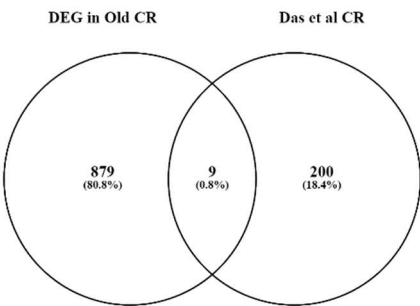
F



G



H



I

J

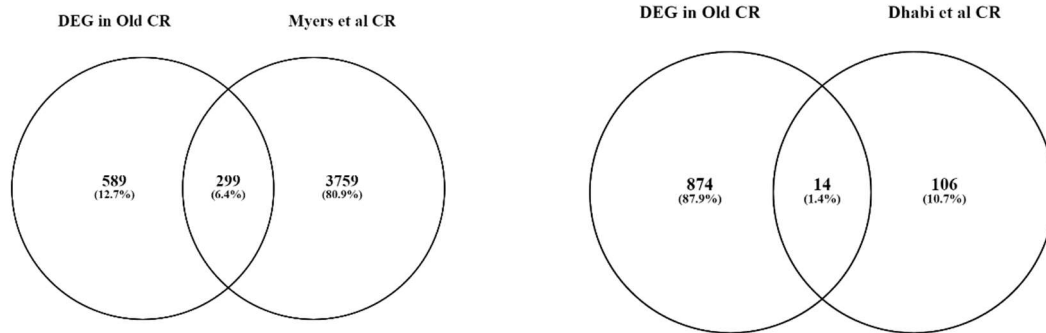


Figure S1. A. Thirteen DEGs were present in both our study and a human study by Tumasian et al. (2021). **B.** Thirteen DEGs were present in both our study and a human study by Melov et al. (2007). **C.** Twenty-eight DEGs were present in both our study and a mouse muscle ageing study by Lin et al. (2018). **D.** Comparing our study with a single-cell RNA-seq study in *Rattus norvegicus*, 86 DEGs were present in both studies (Ma et al., 2020b). **E.** Comparing to a study on muscle ageing by Myers et al. (2021), we found 185 DEGs were present in both studies. **F.** Comparing our study with a meta-analysis of the ageing transcriptome (including muscle data) by Palmer et al. (2021), we found 60 DEGs present in both studies. **G.** Examining DEGs in relation to the Human Ageing Genomic Resources (HAGR) database (Tacutu et al., 2018), 21 DEGs were present in both our study and the database. **H.** Nine DEGs were present in both our DEGs found in old calorie-restricted rat muscle and previous human CR-associated DEGs (Das et al., 2023). **I.** Two hundred ninety-nine DEGs were present in both our study and another rat CR study on muscle ageing (Myers et al., 2021). **J.** Fourteen DEGs were present in both our study and a previous CR-treated study on muscle ageing (Dhahbi et al., 2012). Venn diagram was created using: <https://bioinfogp.cnb.csic.es/tools/venny/>.

Figure S2. RNA quality analysis.

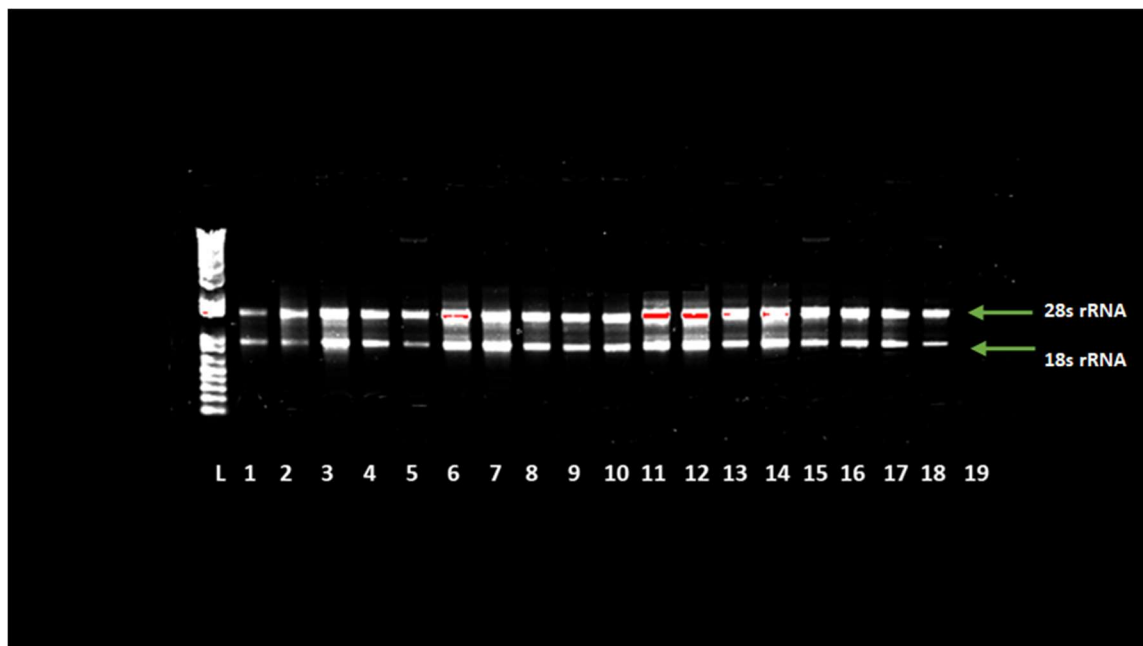


Figure S2. Quality analysis of RNA samples as observed in 1% agarose gel. All RNAs from all samples were intact and good quality. Lane L represents DNA ladder, Lanes 1-18 represents RNA samples and Lane 19 represents negative control.