

Figure 1. Quality check plots. **A, B, C.** MA plots showing that the quality of the samples is fairly good, p adjusted cutoff 0.001, absolute fold change cutoff 2. **D.** Expression matrices show good quality with sharp peaks for unexpressed, lowly expressed, and highly expressed genes across all samples.

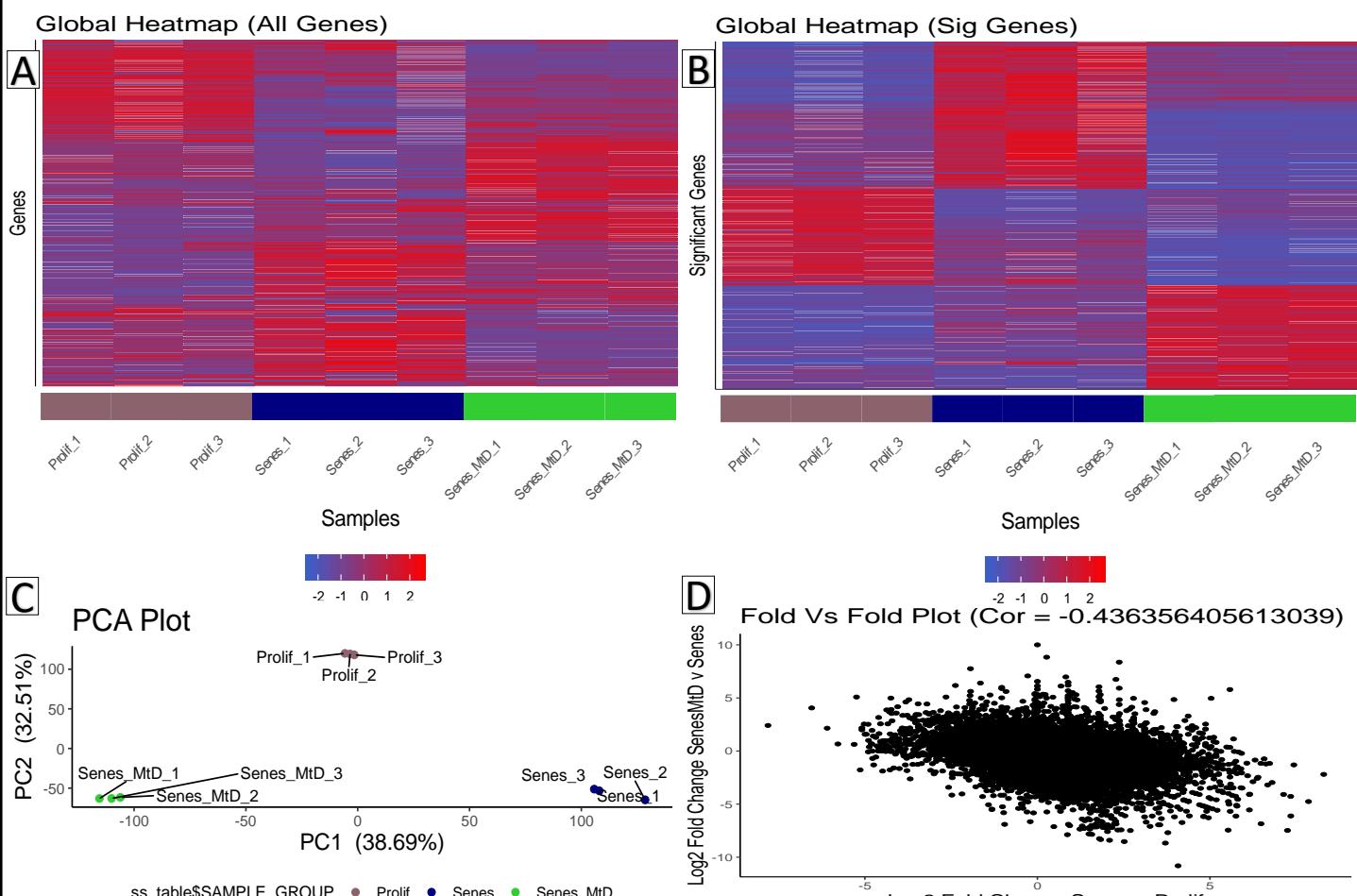


Figure 2. Global Plots **A.** and **B.** heatmaps depicting overall variation in expression; clear differences in the three sample groups (significant = $p.\text{adj} < 0.001$ & absolute log2 fold change > 2). **C.** PCA plot depicts clear clustering of sample groups with distinct variation between them. **D.** SenesMtD v Senes and Senes v Prolif are negatively correlated.

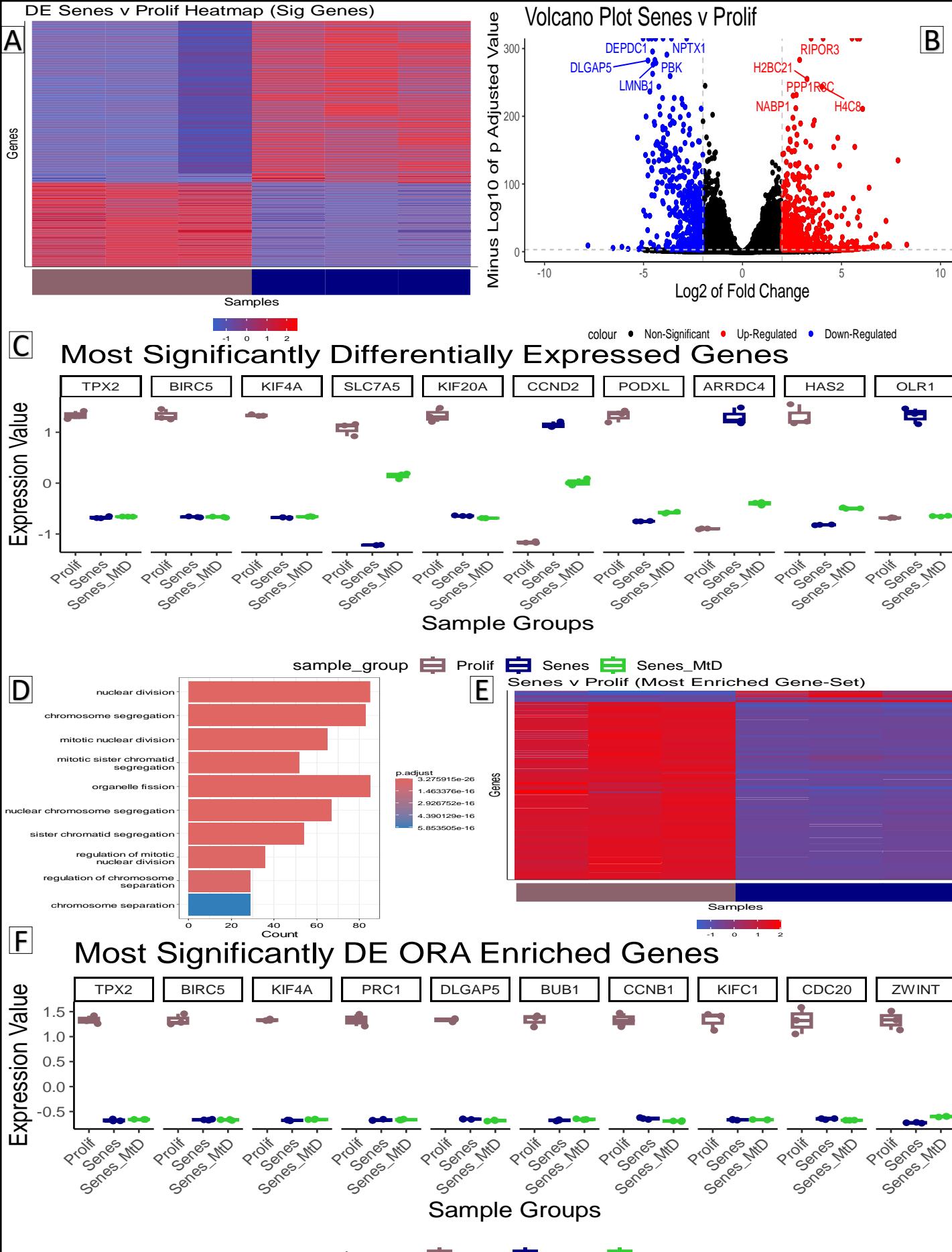


Figure 3. Differential Expression Senescent vs Proliferating **A.** and **B.** showing the overall pattern of differential expression of the 1291 significant genes. **C.** a boxplot showing the expression of the top 10 most differentially expressed genes, 7 are downregulated and 3 are upregulated. **D.** shows that proliferation related pathways are overrepresented. **E.** showing gene expression of the most enriched pathway 'nuclear division' containing 85 DE genes **F.** shows the 10 most significant of these 85 genes in the 'nuclear division' geneset.

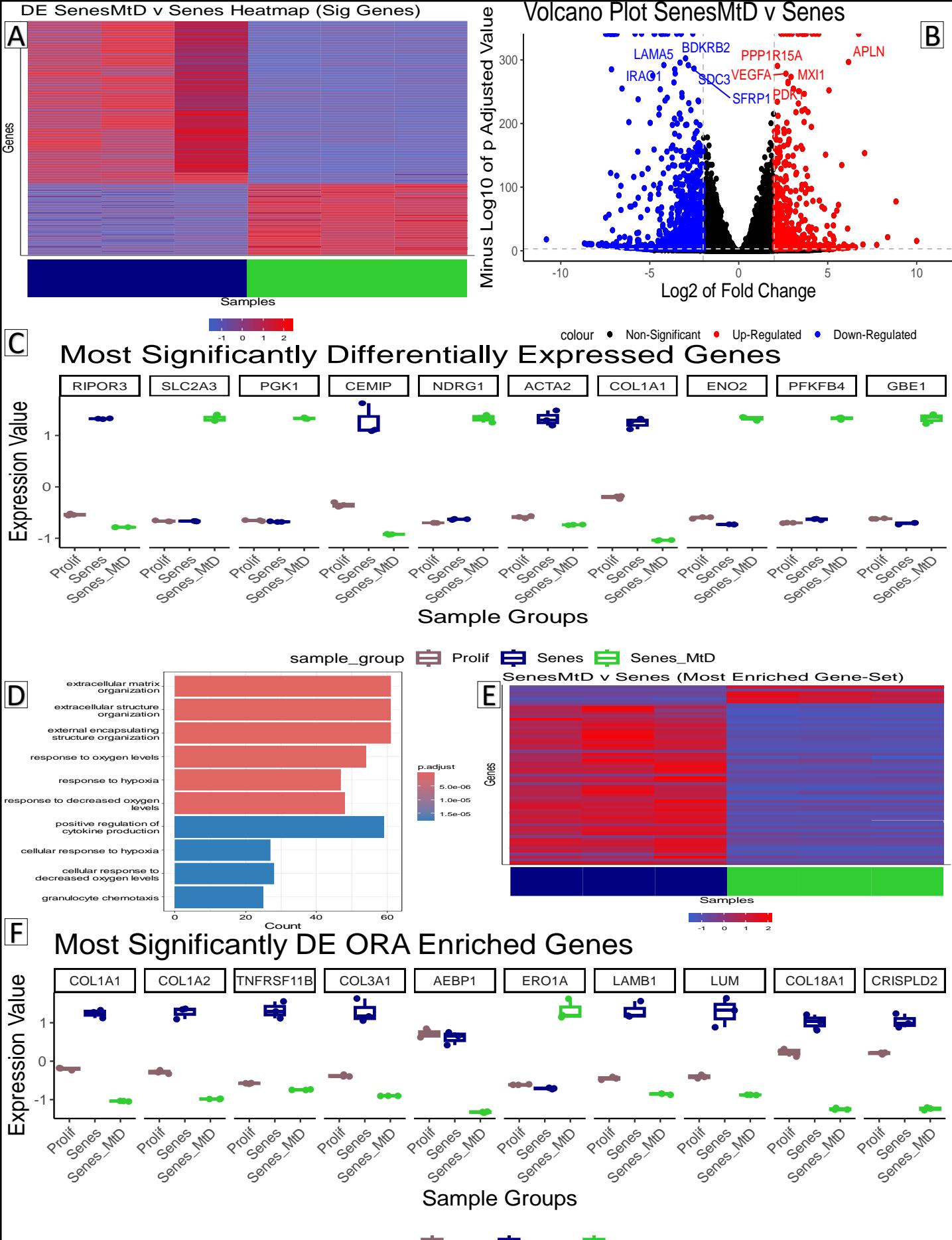


Figure 4. Differential Expression Senescent-MtD vs Senescent **A.** and **B.** showing the overall pattern of differential expression of the 1572 significant genes. **C.** a boxplot showing the expression of the top 10 most differentially expressed genes, 4 are downregulated and 6 are upregulated. **D.** shows that extra-cellular matrix related pathways are over-represented. **E.** showing gene expression of the most enriched pathway 'extracellular matrix organization' containing 61 DE genes **F.** shows the 10 most significant of these 61 genes in the 'extra-cellular matrix' geneset.

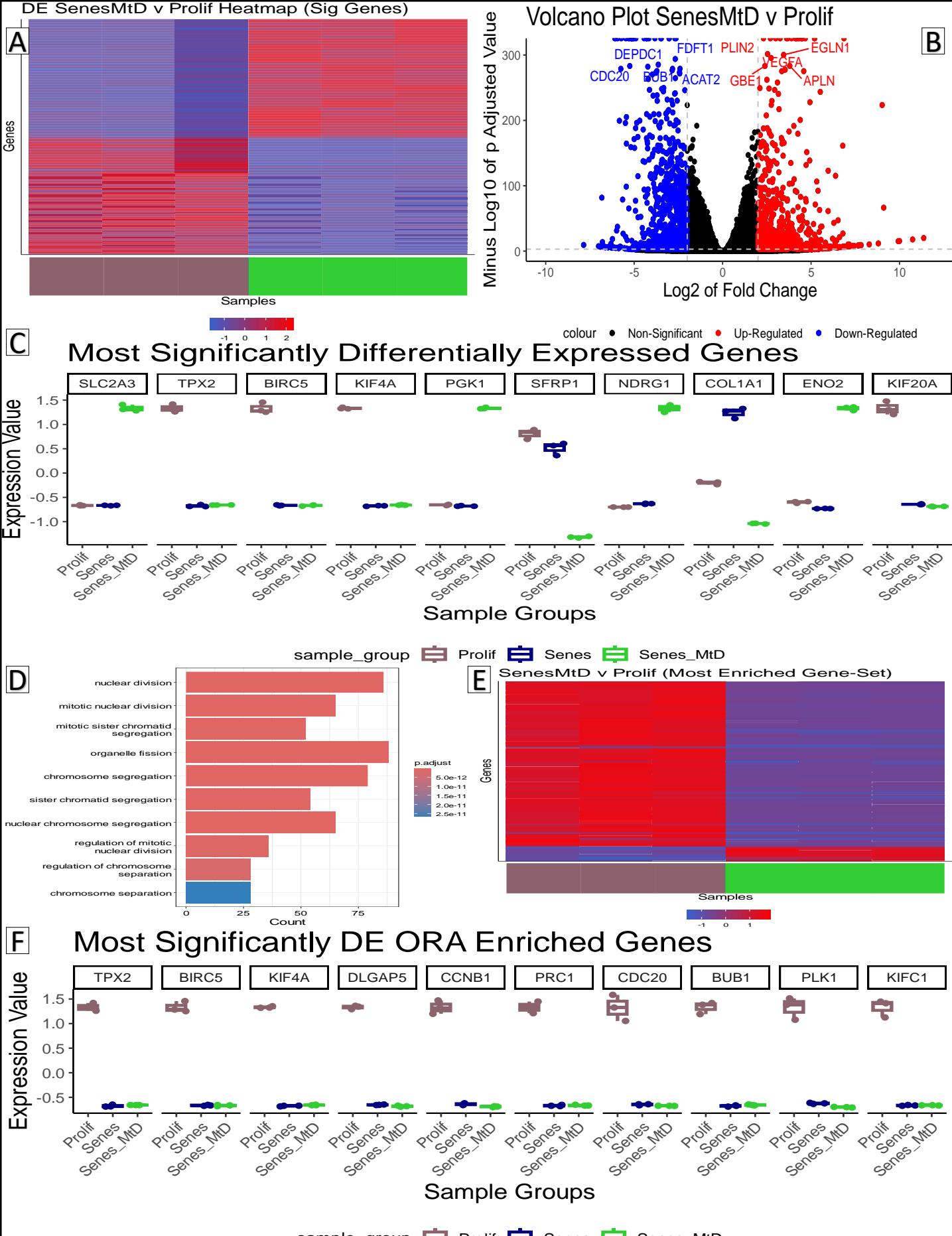


Figure 5. Differential Expression Senescent-MtD vs Prolif **A.** and **B.** showing the overall pattern of differential expression of the 1798 significant genes. **C.** a boxplot showing the expression of the top 10 most differentially expressed genes, 6 are downregulated and 4 are upregulated. **D.** shows that cell division related pathways are overrepresented. **E.** showing gene expression of the most enriched pathway 'nuclear division' containing 86 DE genes **F.** shows the 10 most significant of these 86 genes in the 'nuclear division' geneset.

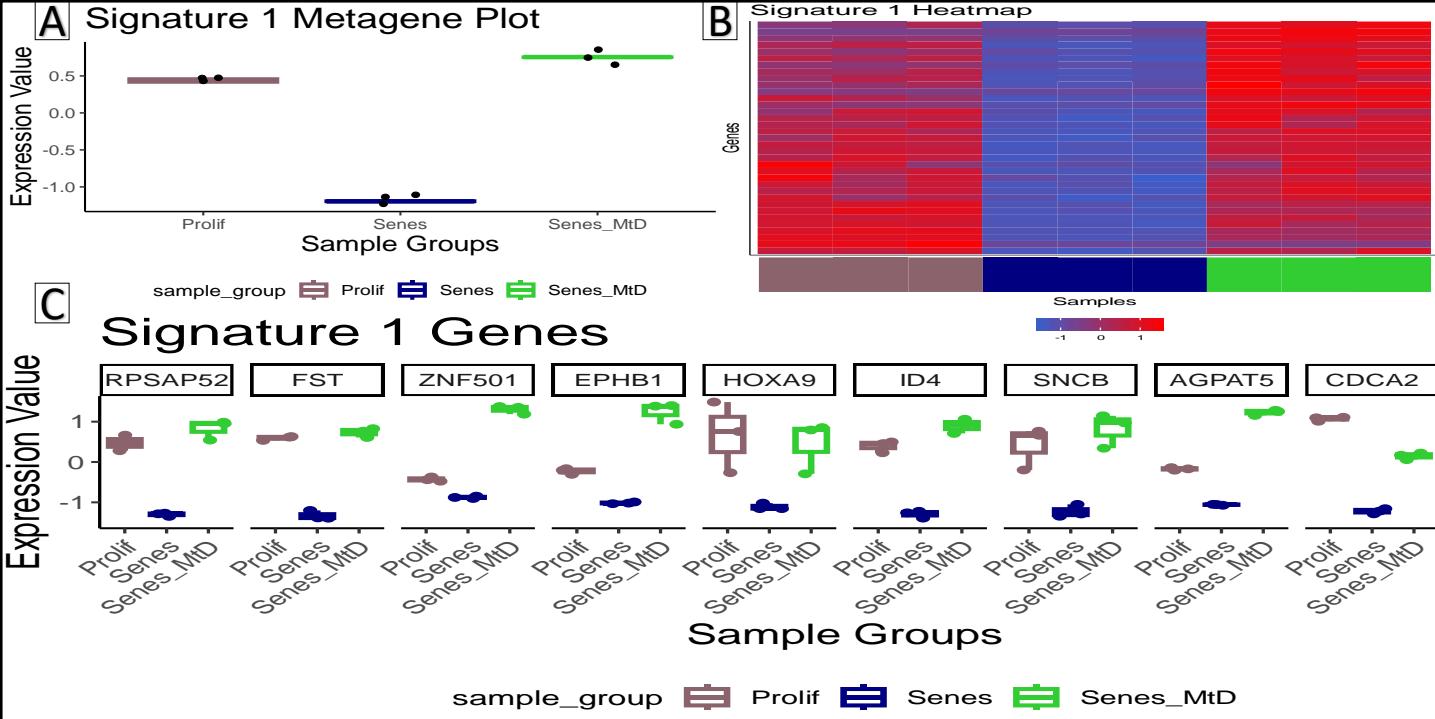


Figure 6. Signature 1 Analysis **A.** and **B.** show the global trend of expression in the signature containing 39 genes, going down while senescent, and up after depleting mitochondria. **C.** boxplot of random subset of 9 genes.

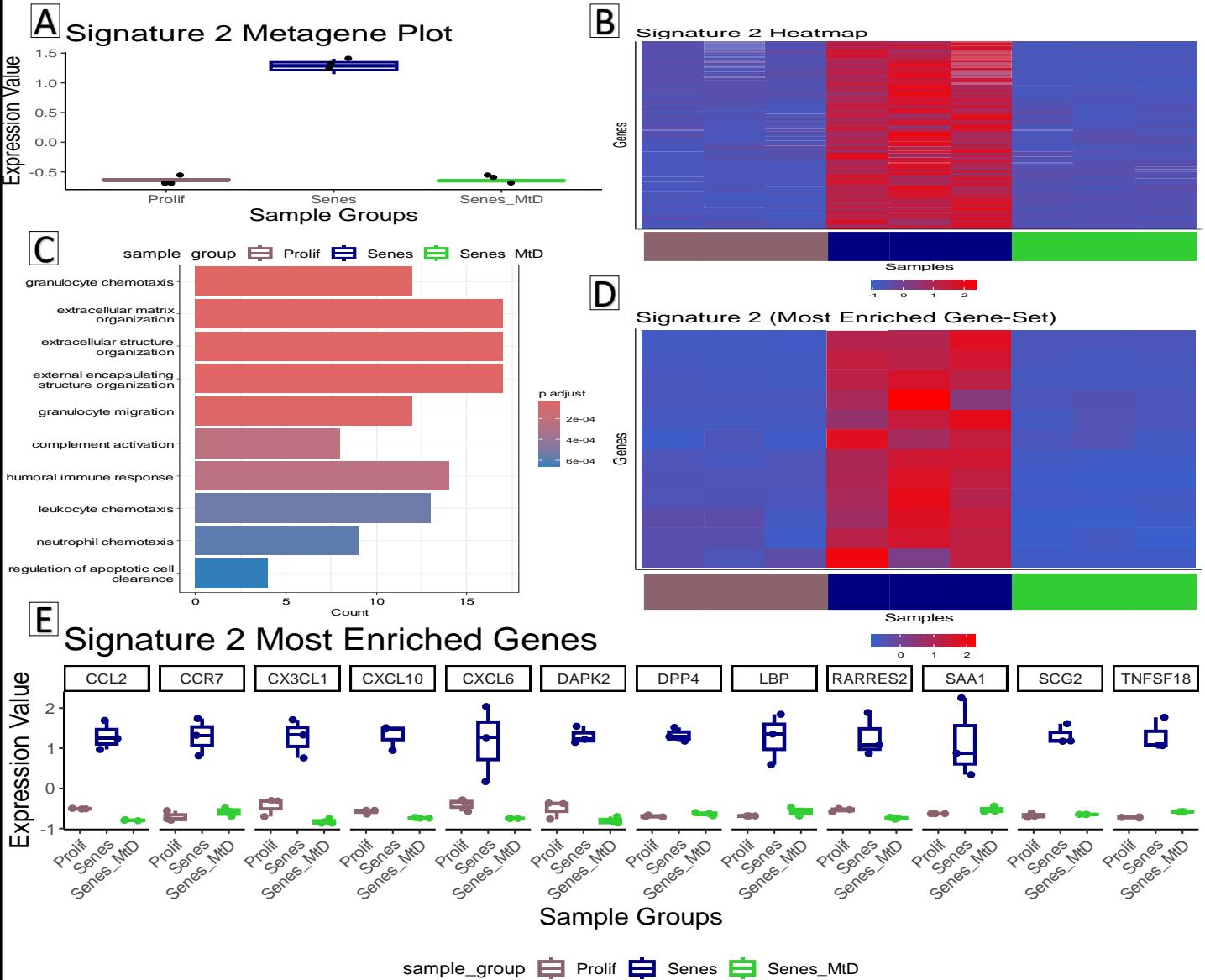


Figure 7. Signature 2 Analysis **A.** and **B.** show the global trend of expression in the signature containing 283 genes, going up while senescent, and down after depleting mitochondria. **C.** ORA barplot showing that immune response pathways are over-represented. **D.** and **E.** showing expression of the 12 'granulocyte chemotaxis' genes