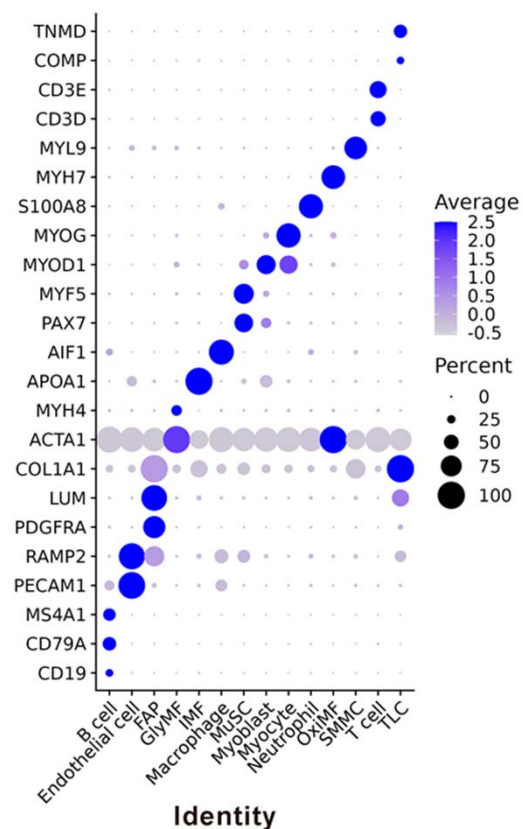
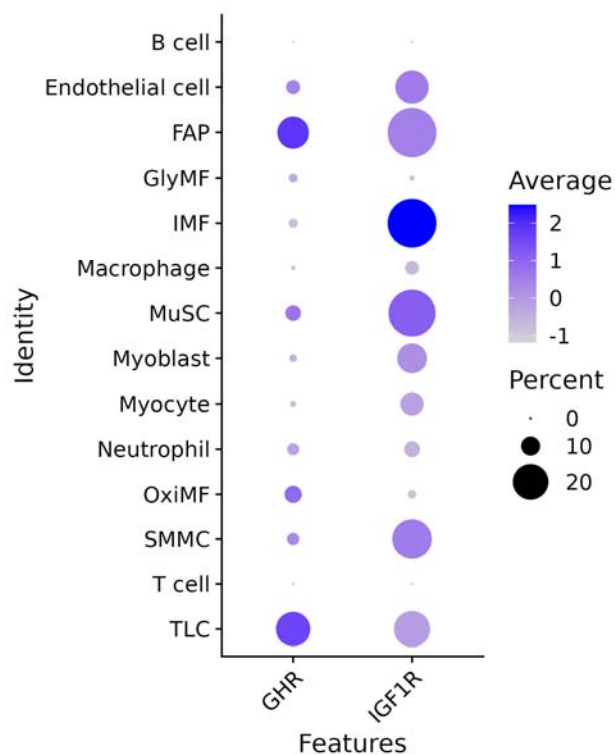


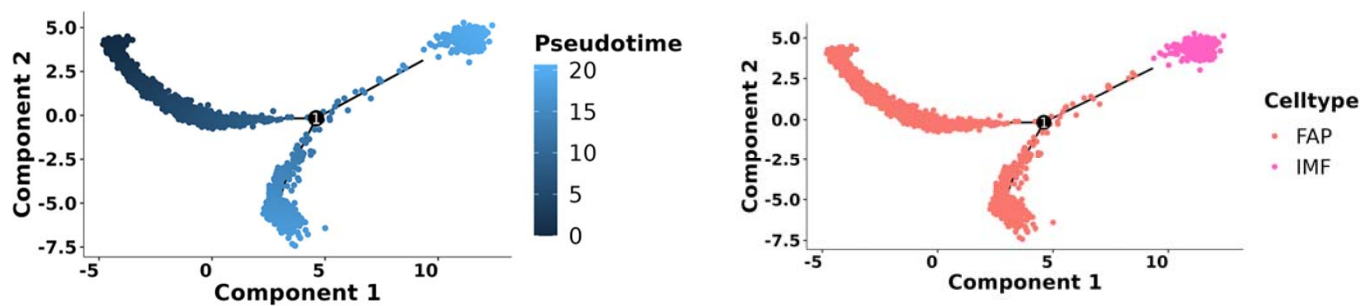
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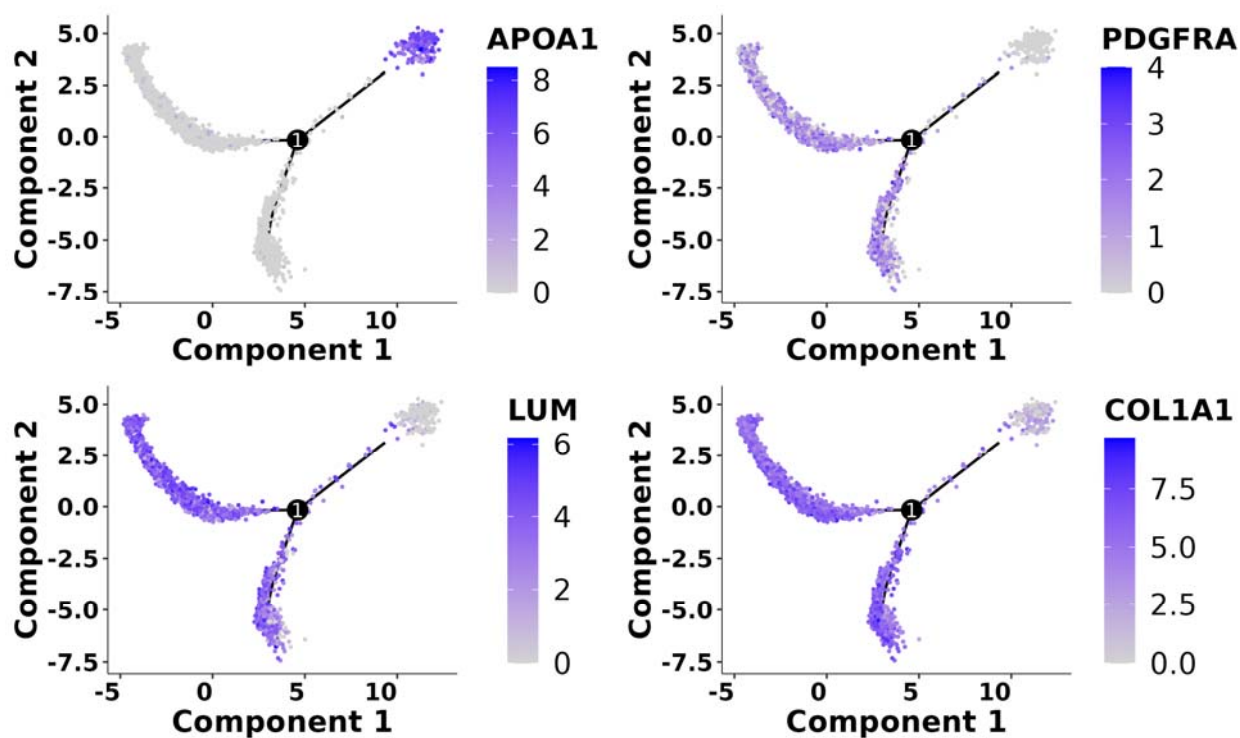
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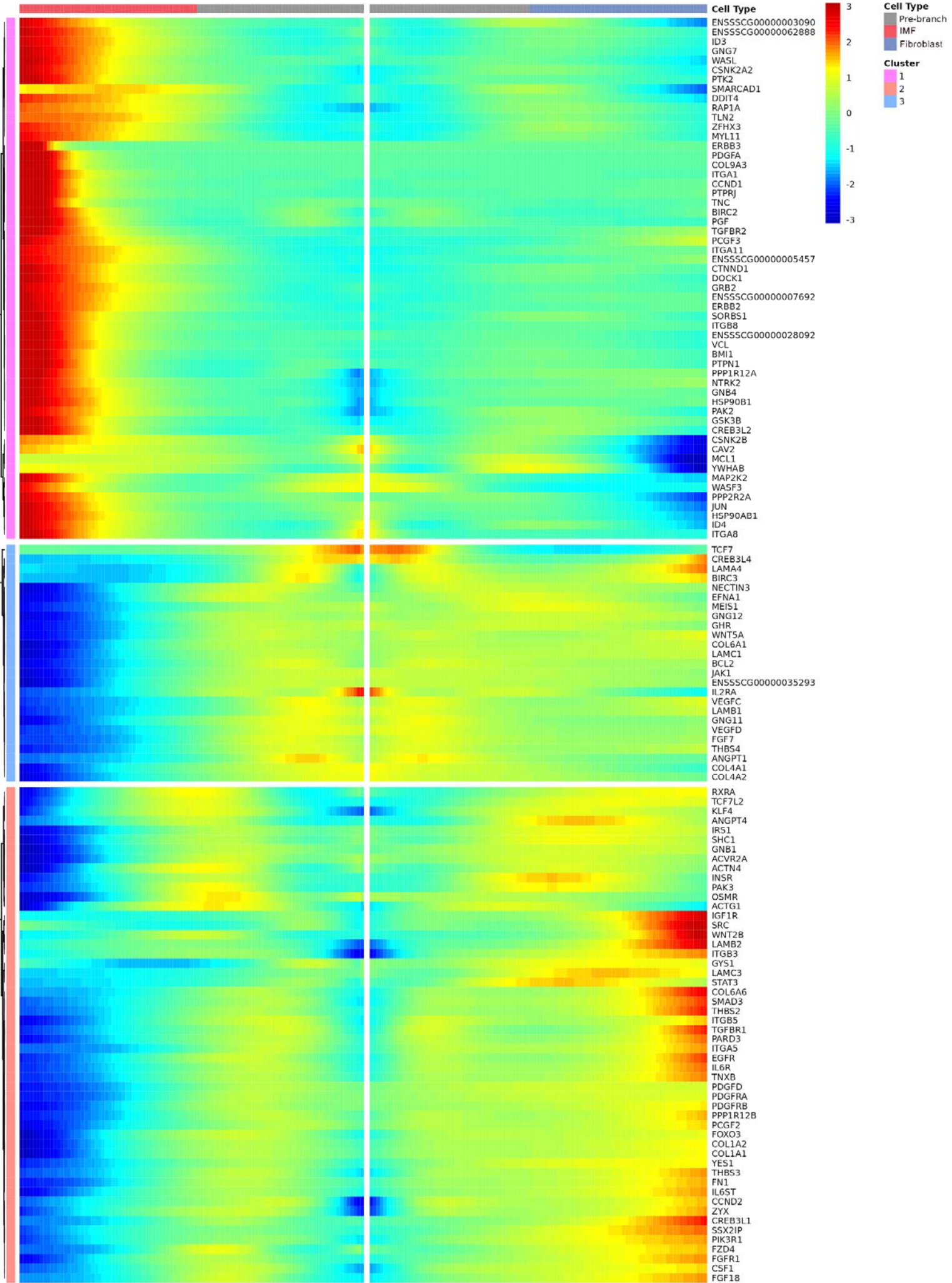
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D

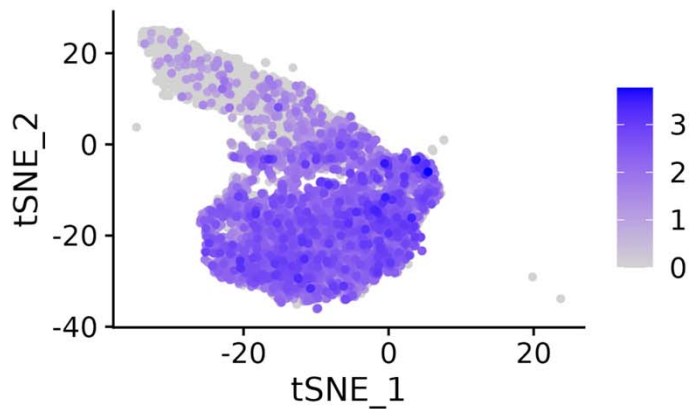


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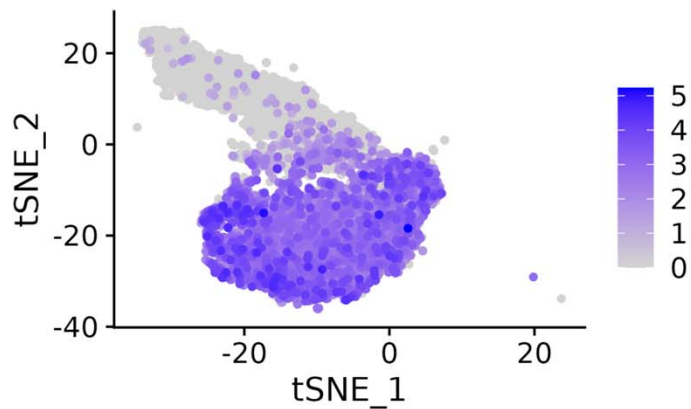


F

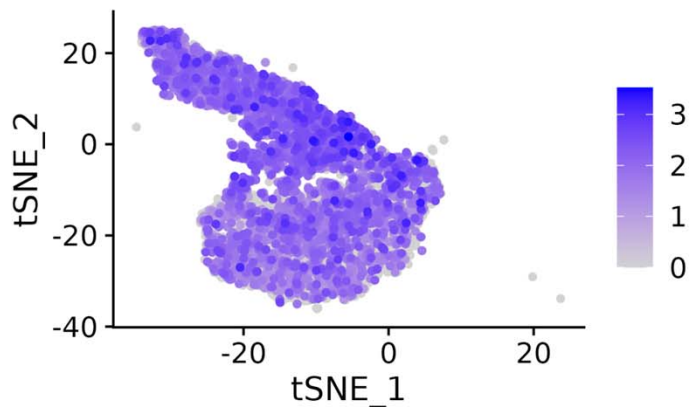
PAX7



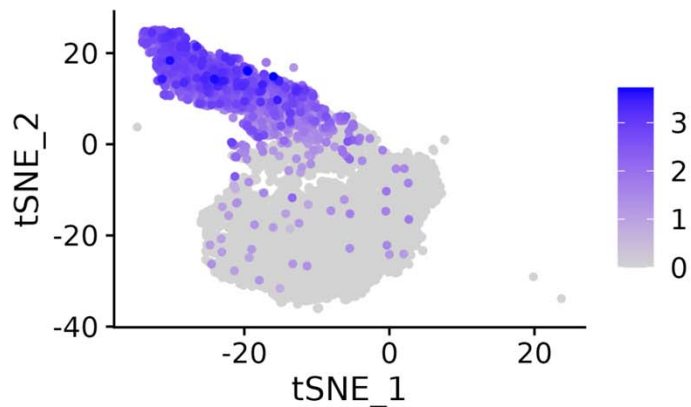
MYF5



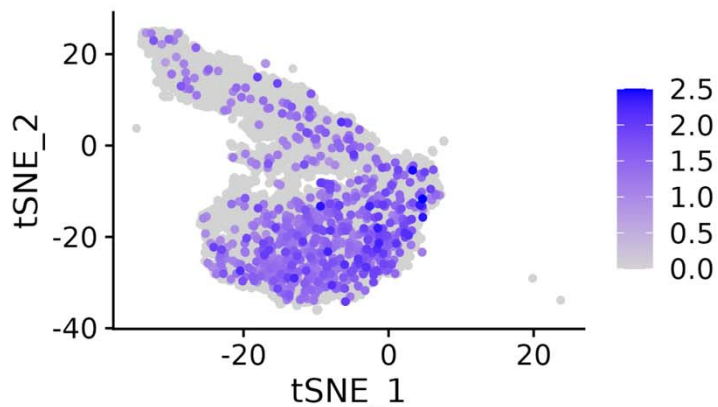
MYOD1



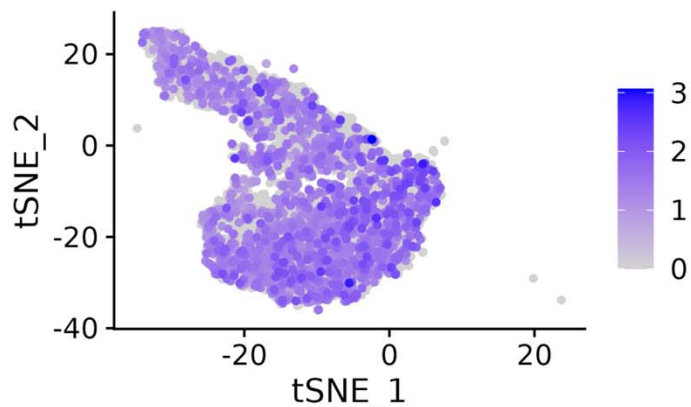
MYOG



GHR



IGF1R



G

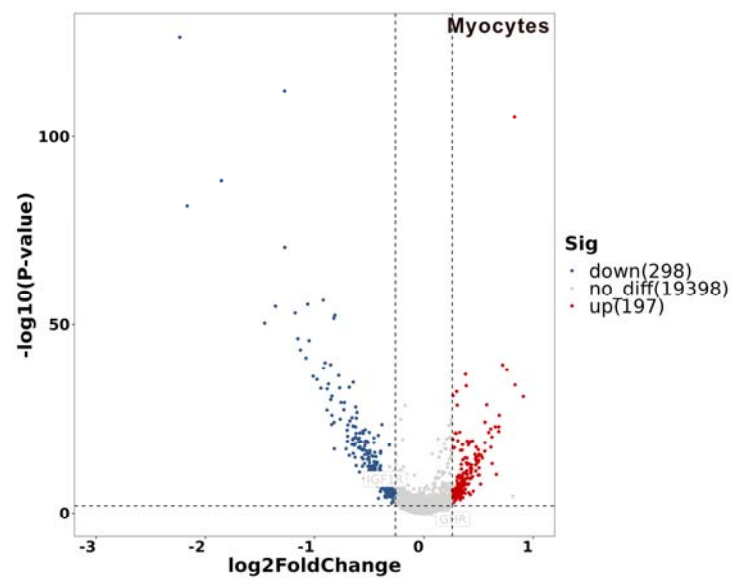
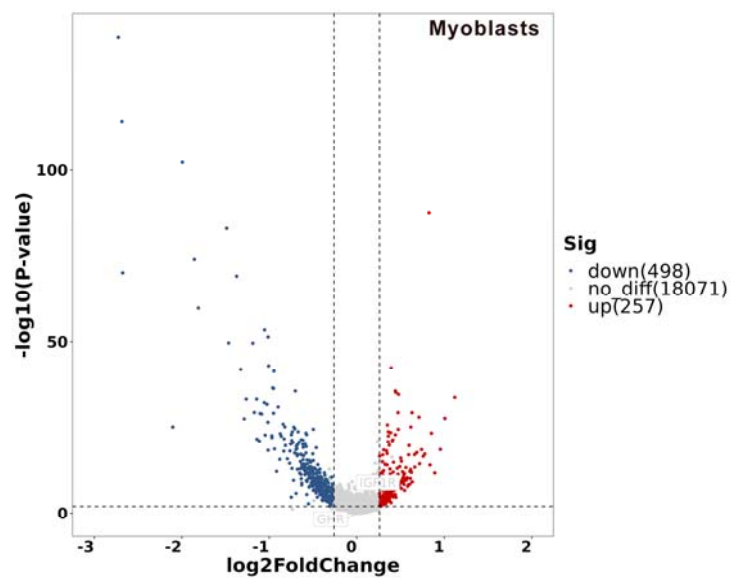


Fig. S4: Single-cell RNA-seq analysis of porcine longissimus dorsi transcriptome features responsible for adipogenesis and myogenesis

- A) Dot plot showing the expression of marker genes in distinct longissimus dorsi subpopulations.
- B) Dot plot showing the expression of GHR and IGF1R in distinct longissimus dorsi subpopulations.
- C) Pseudotime single-cell trajectory reconstructed by Monocle2 for FAP and IMF cells. Cells are colored by pseudotime and cell type.
- D) Tree diagram showing the expression of APOA1, PDGFRA, LUM, and COL1A1 in a pseudotime manner from FAP to IMF transition.
- E) Heatmap showing branch-dependent genes enriched in KEGG pathways activated by GHR and/or IGF1R, governing IMF progression.
- F) t-SNE plot showing the expression of myogenesis-related genes, including PAX7, MYF5, MYOD1, MYOG, GHR, and IGF1R.
- G) Volcano plot showing differentially expressed genes between small-ear spotted pigs and their hybrids in the myoblast and myocyte populations, respectively.