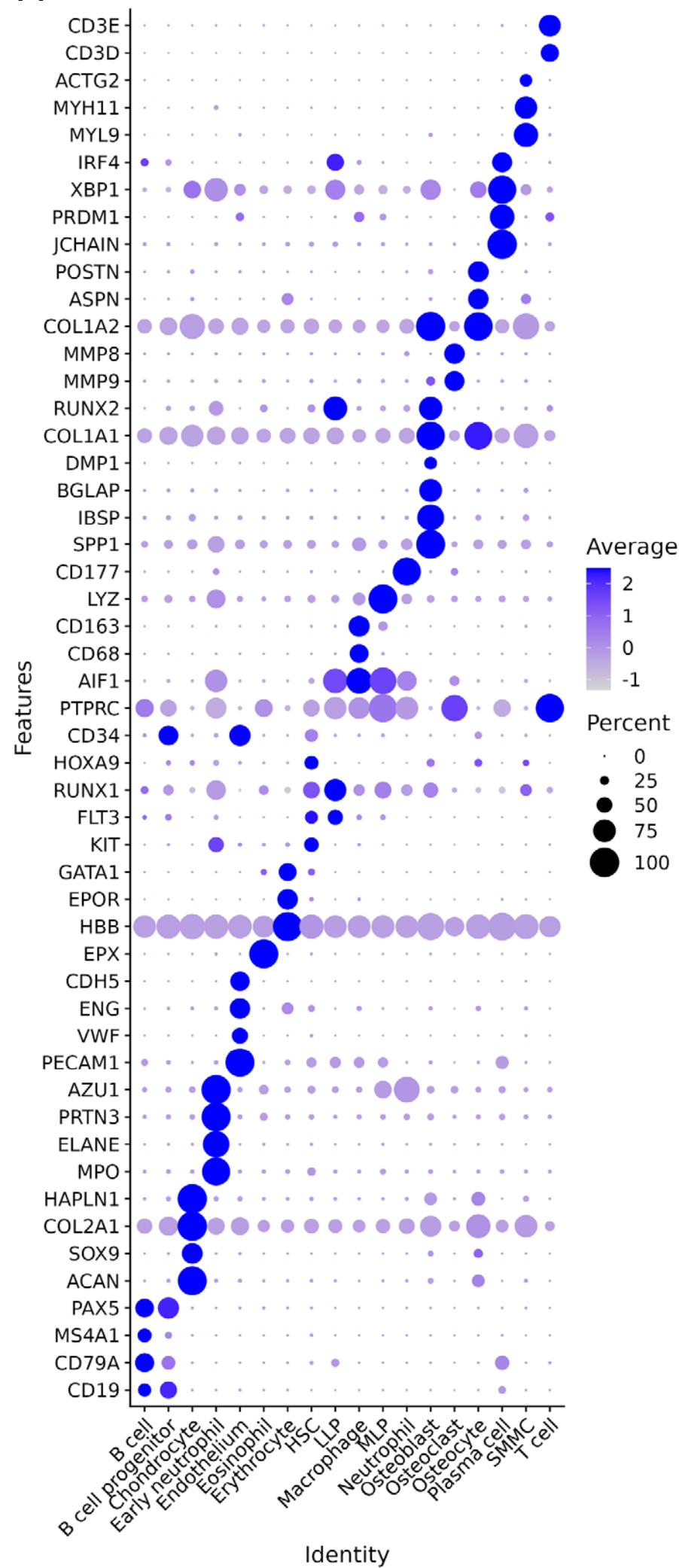
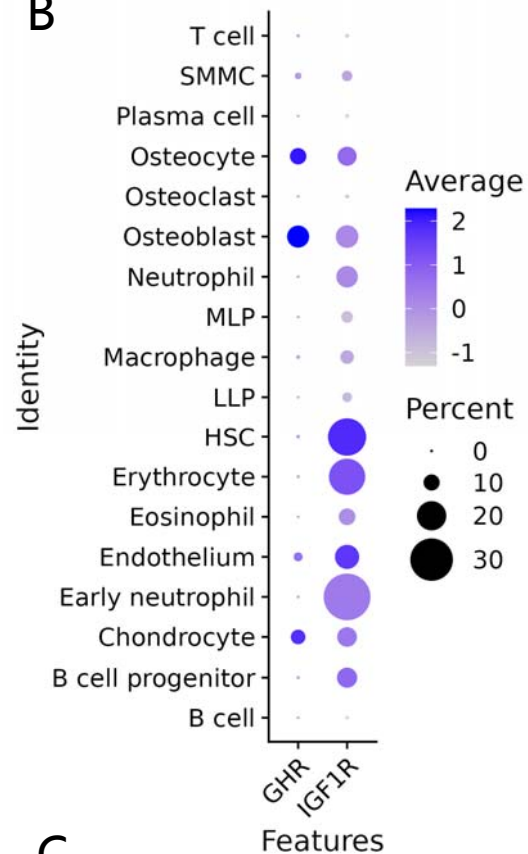


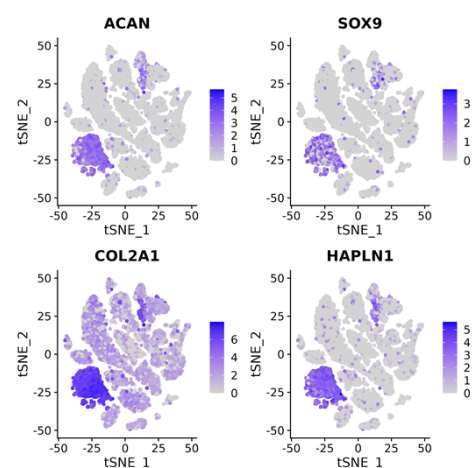
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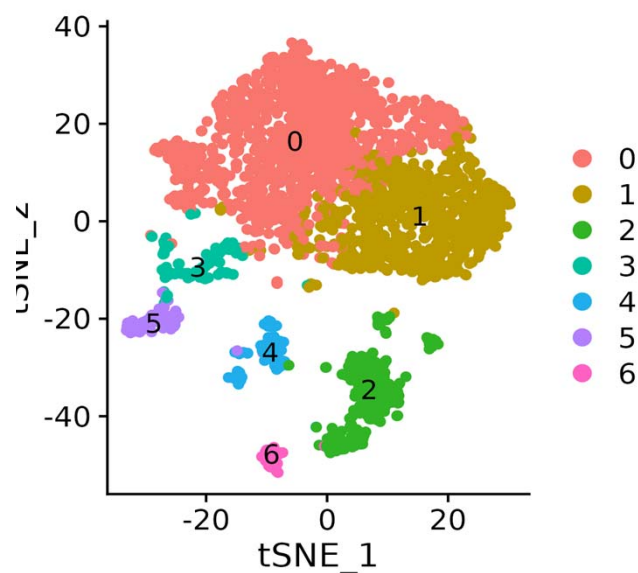
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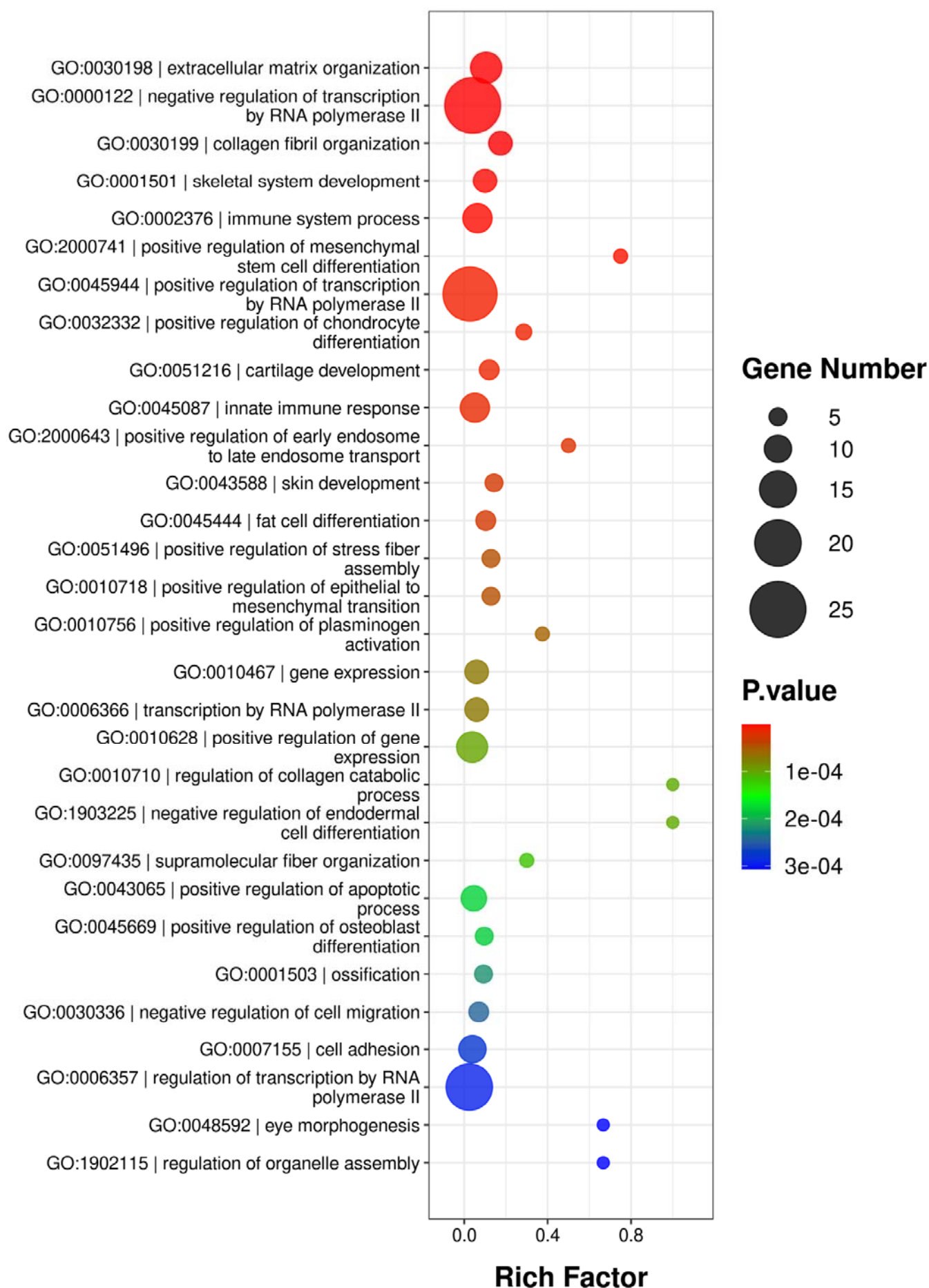
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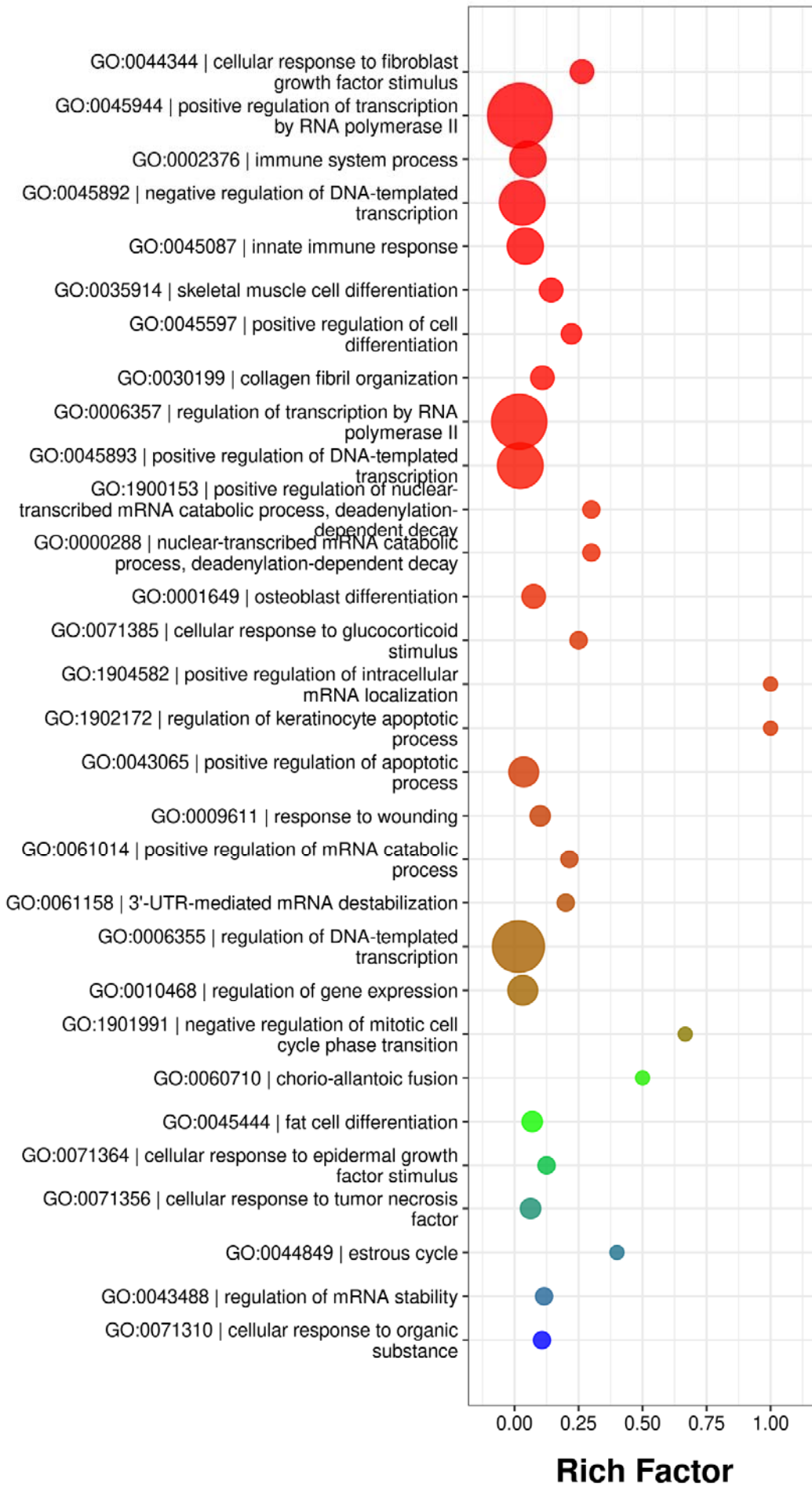
Cluster 0

GO Term

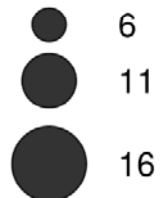


Cluster 1

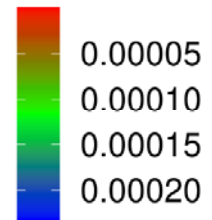
GO Term



Gene Number

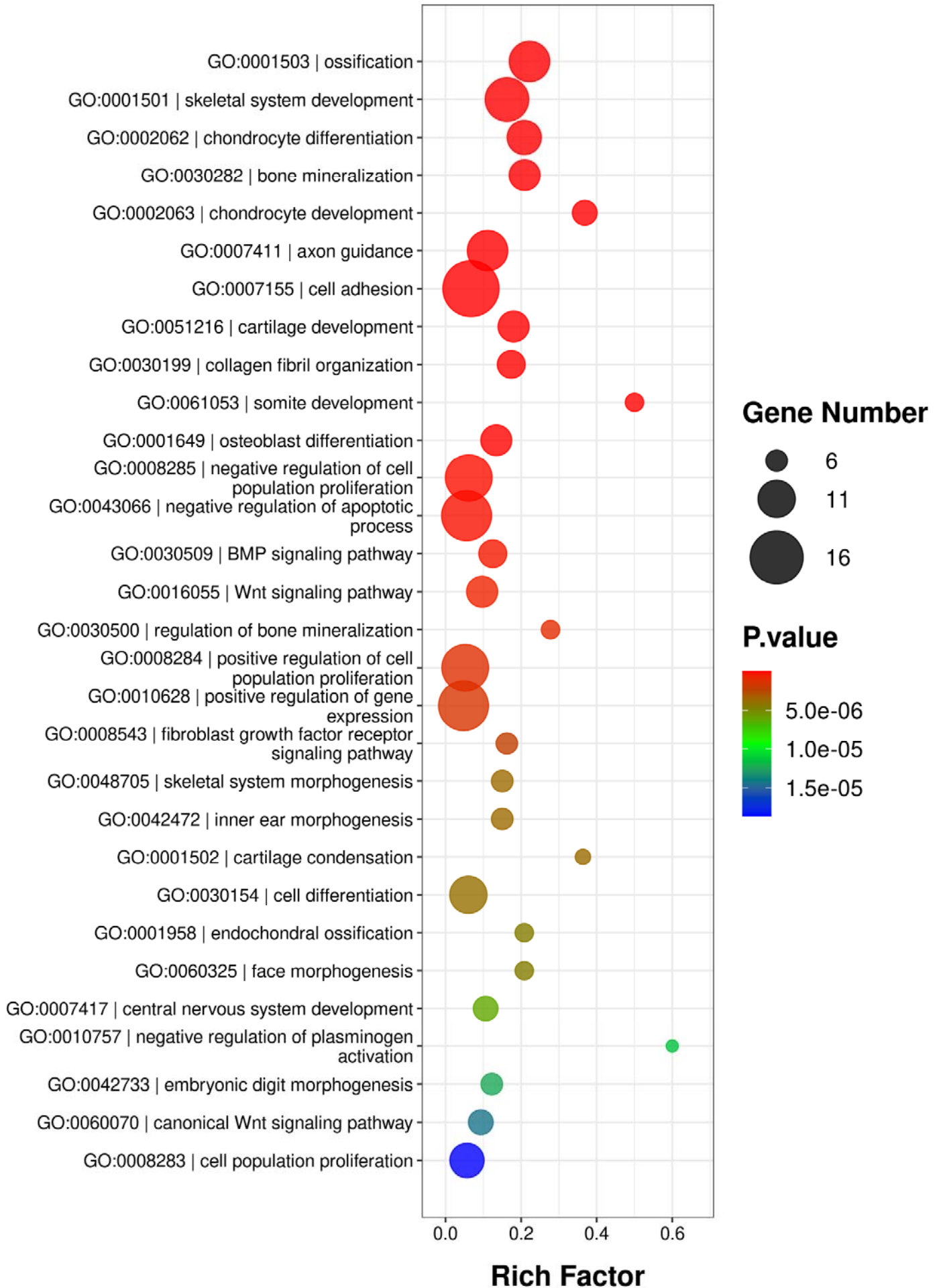


P.value



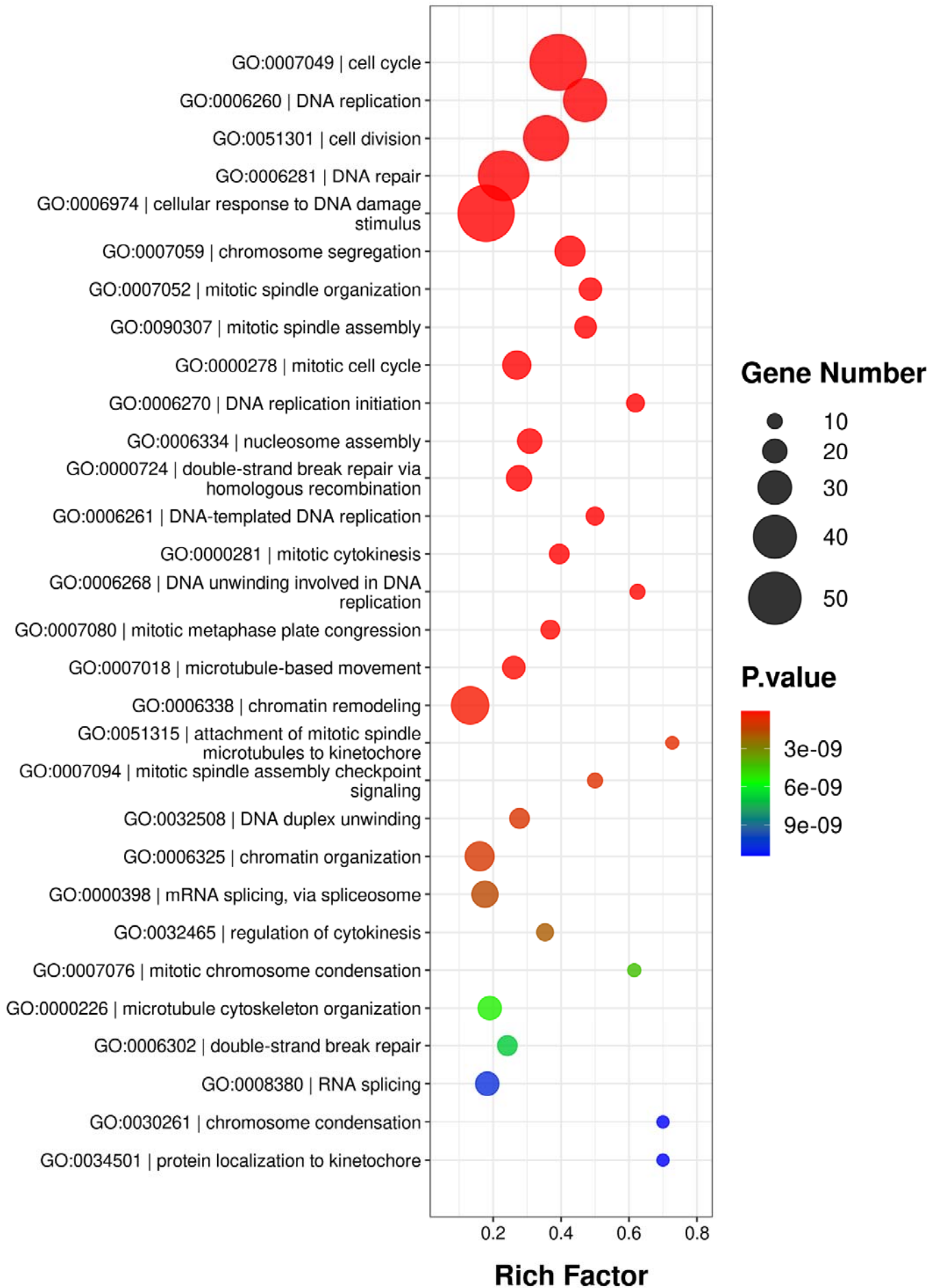
Cluster 2

GO Term



Cluster 3

GO Term

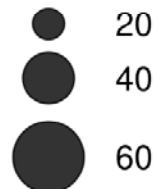


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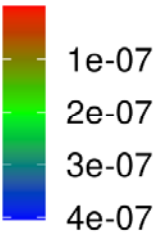
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Gene Number

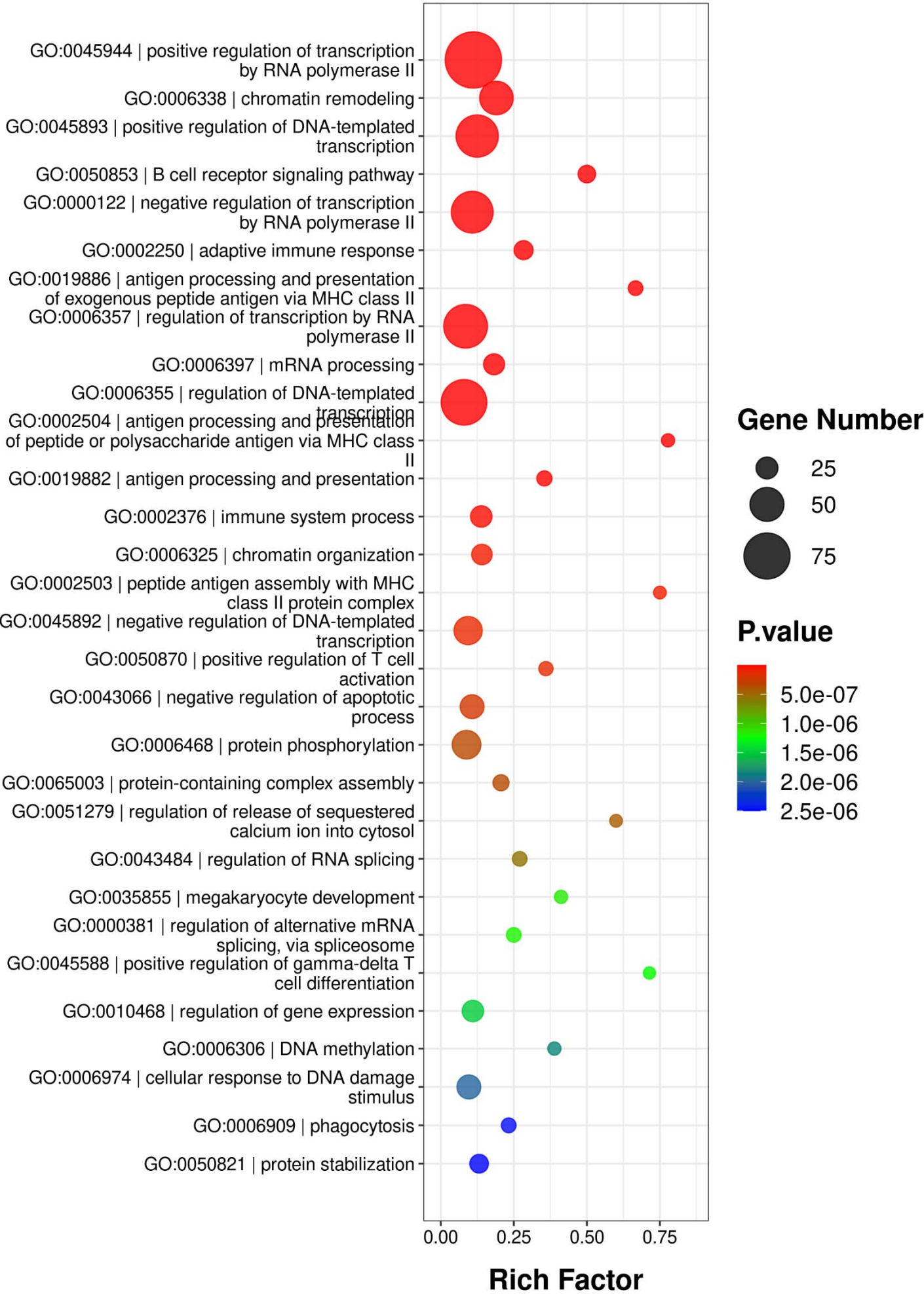


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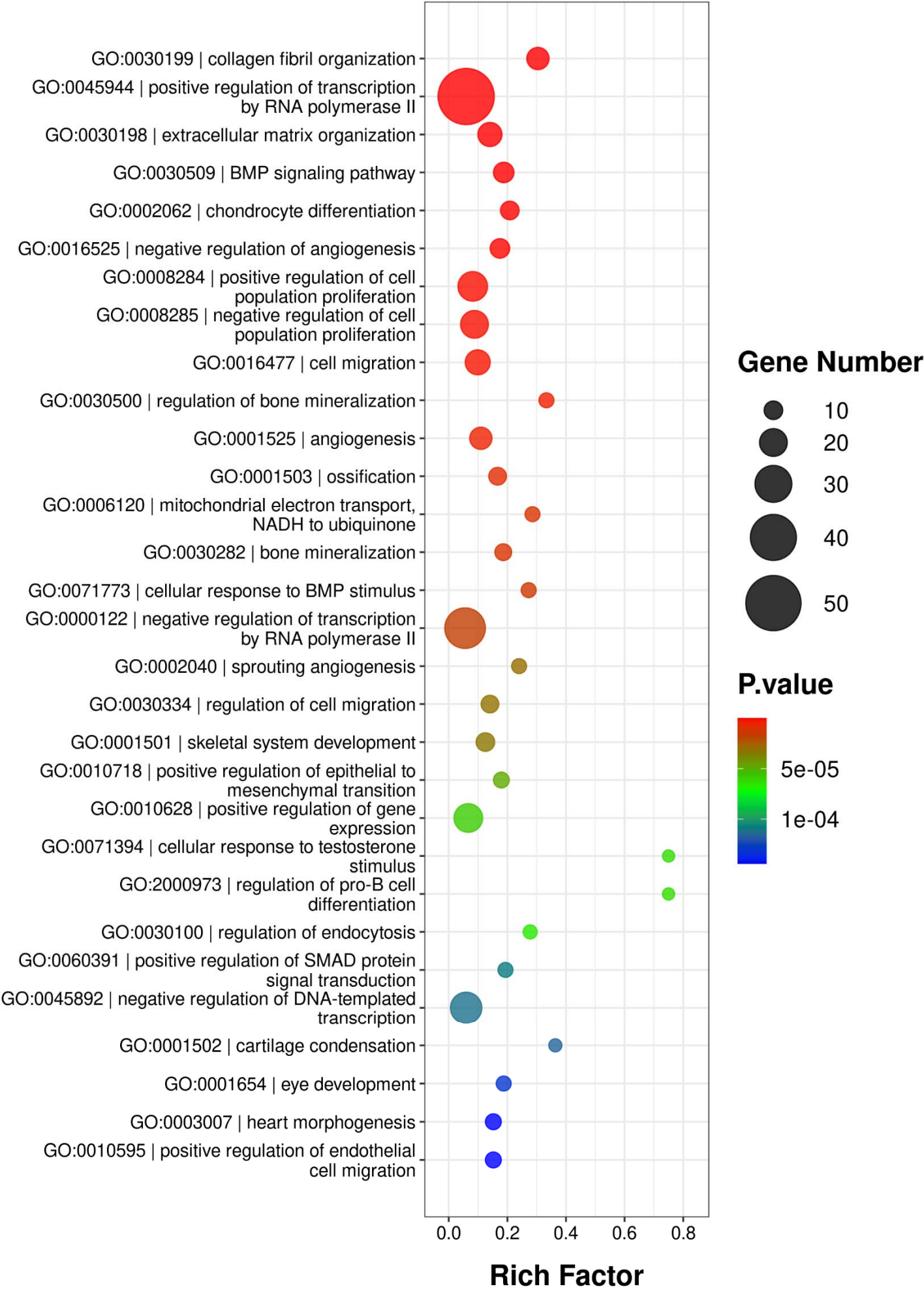
Cluster 5

GO Term

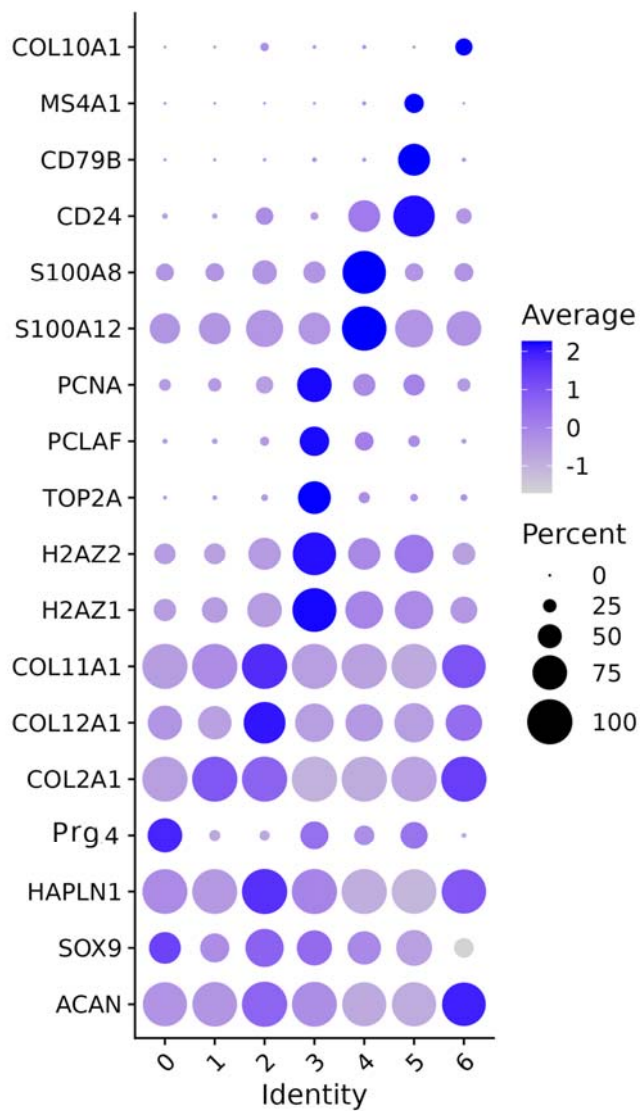


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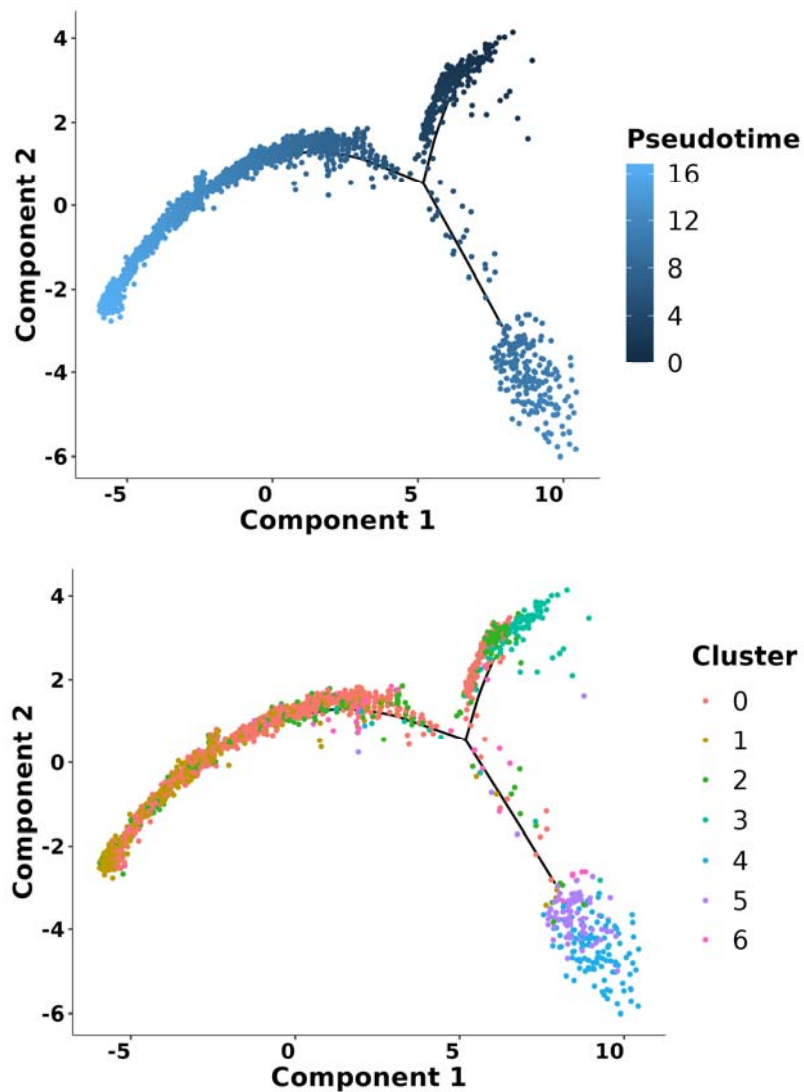
GO Term



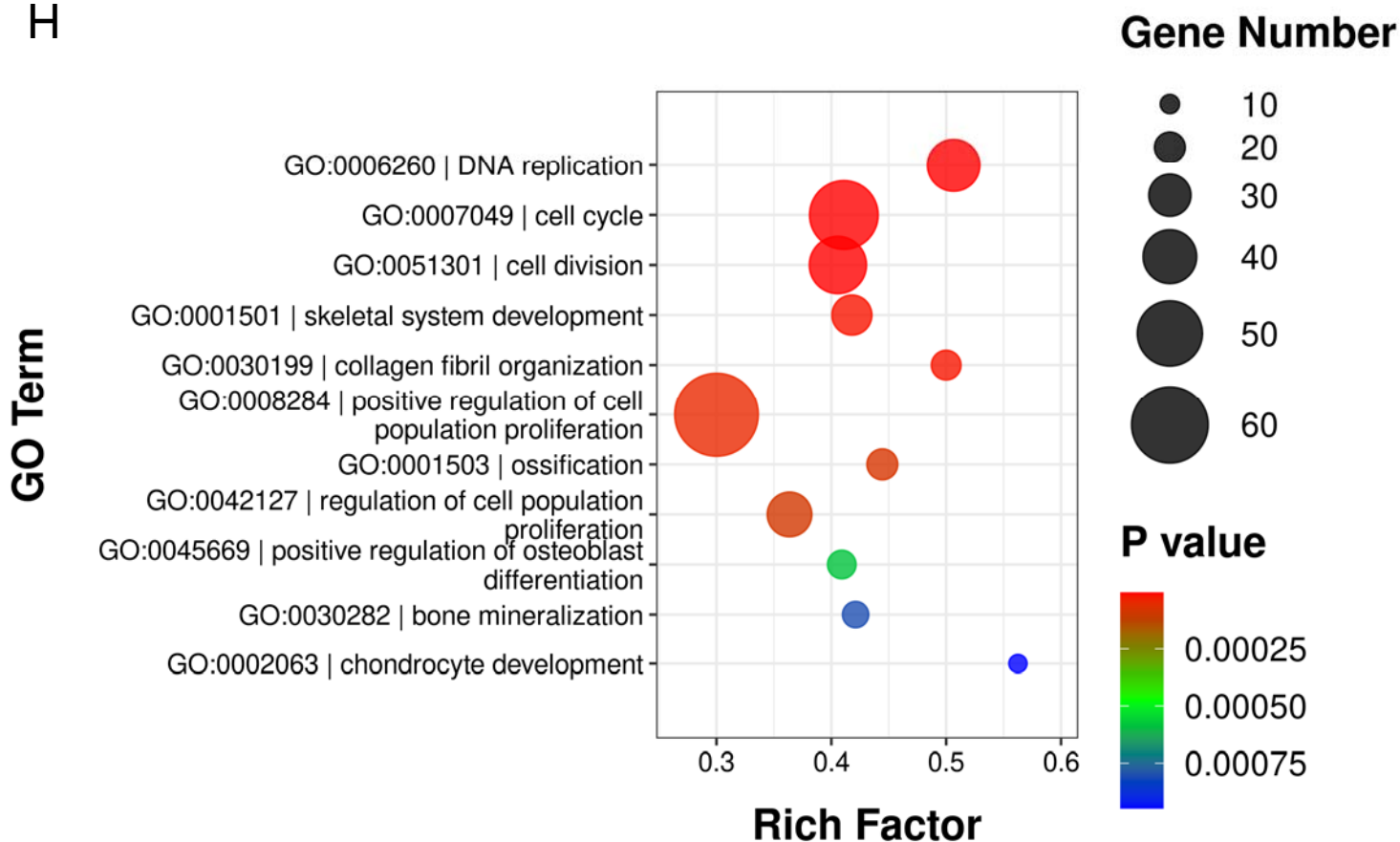
F



G



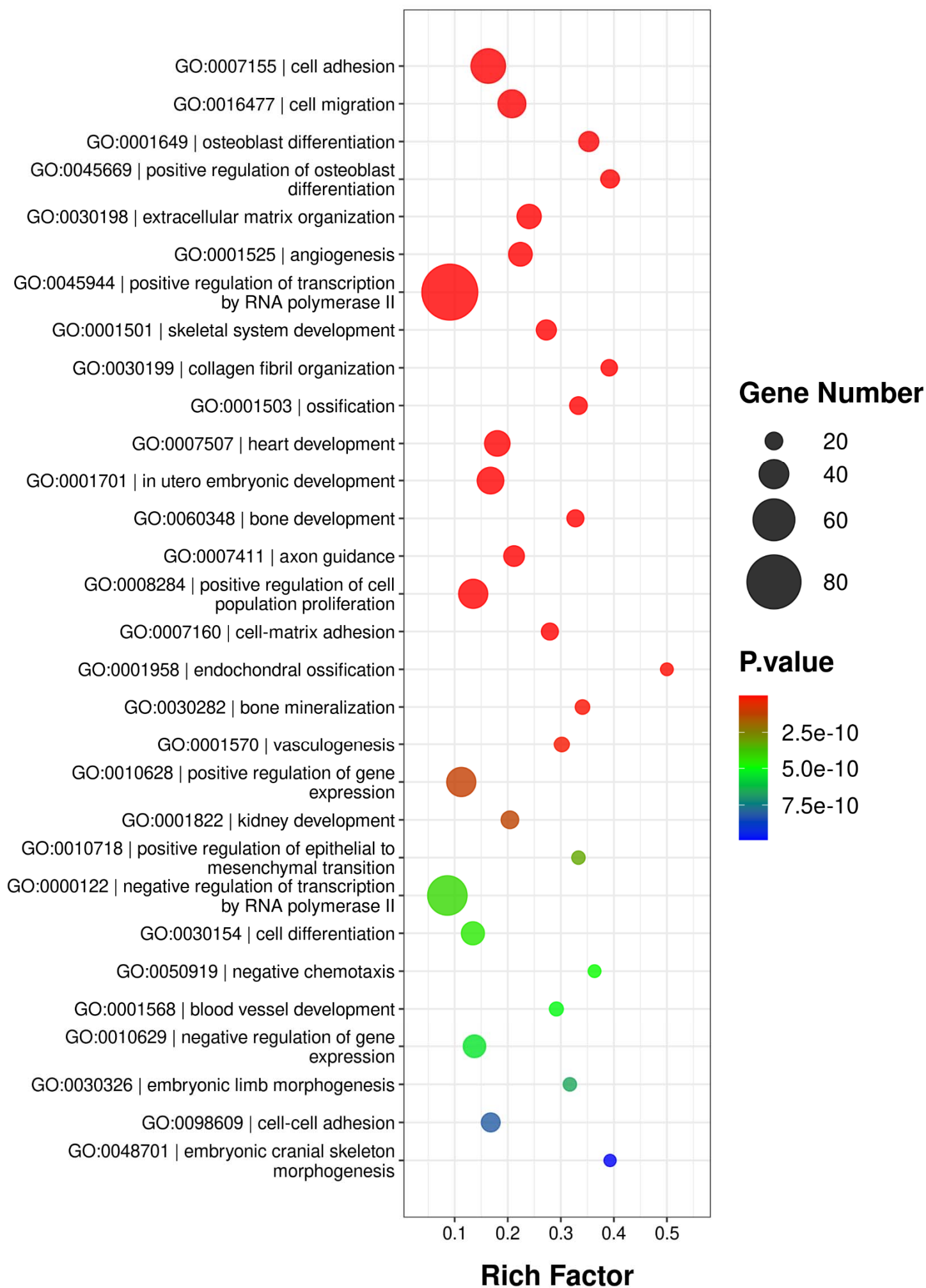
H



I

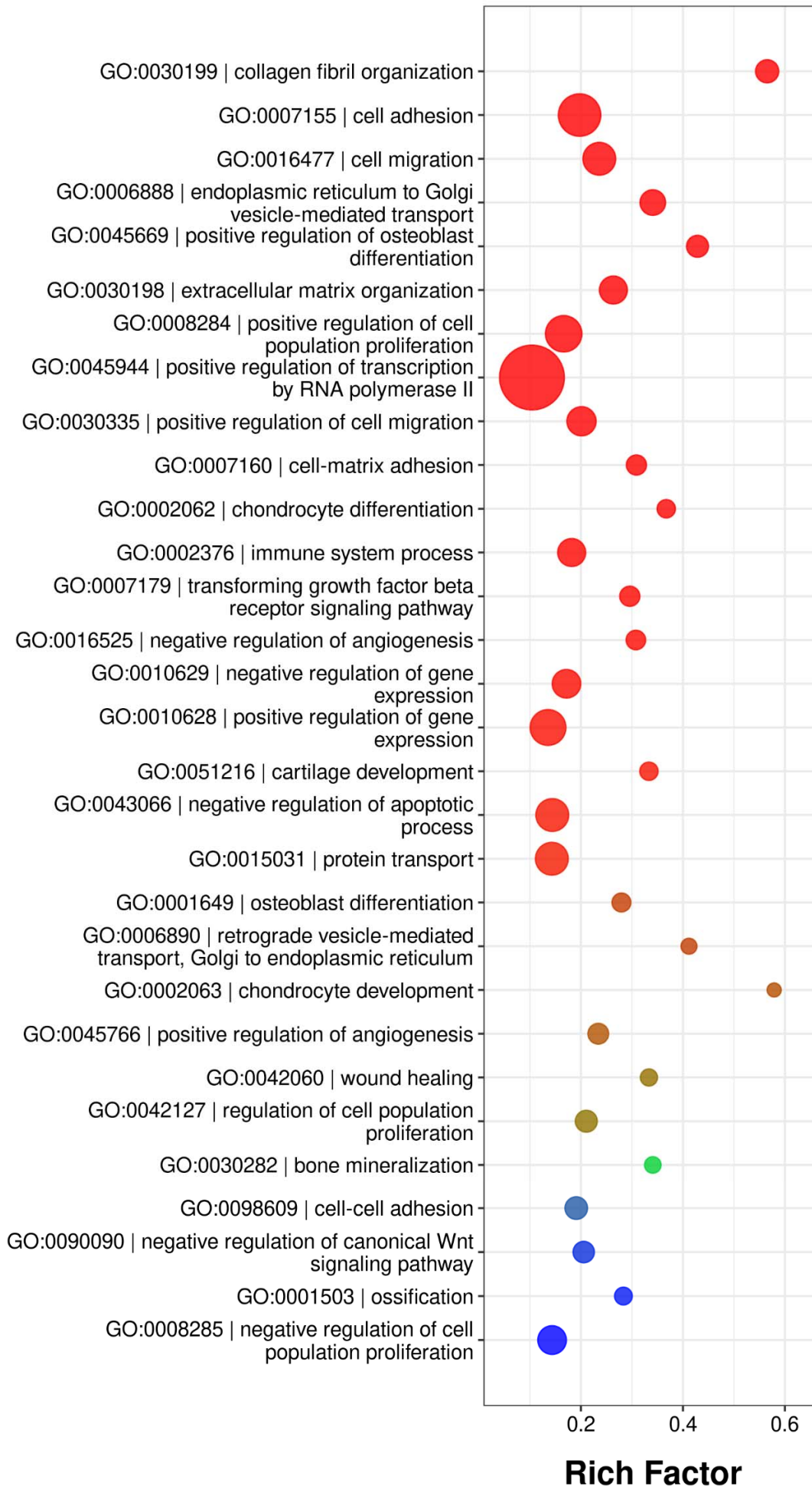
Osteoblast

GO Term

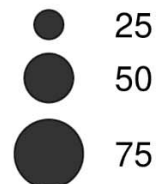


Osteocyte

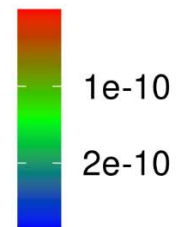
GO Term



Gene Number



P.value



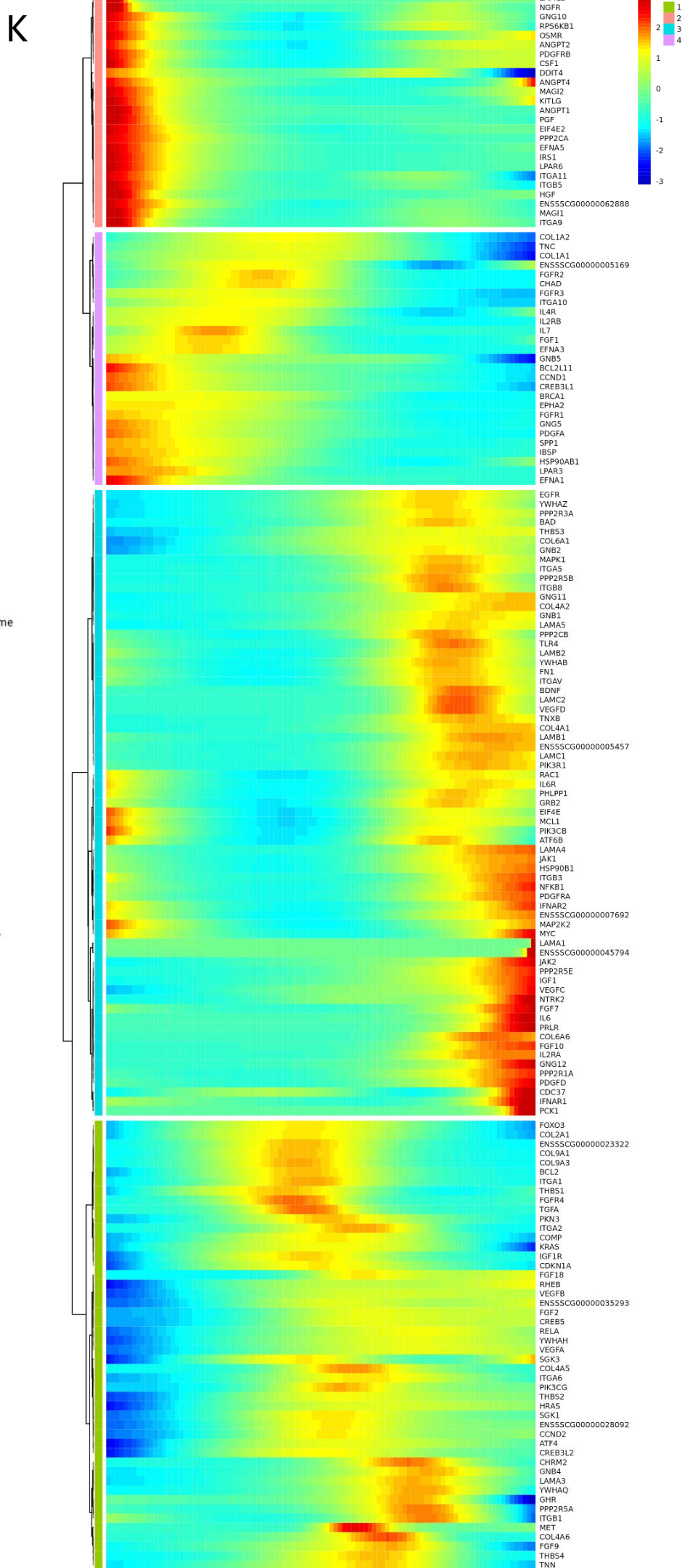
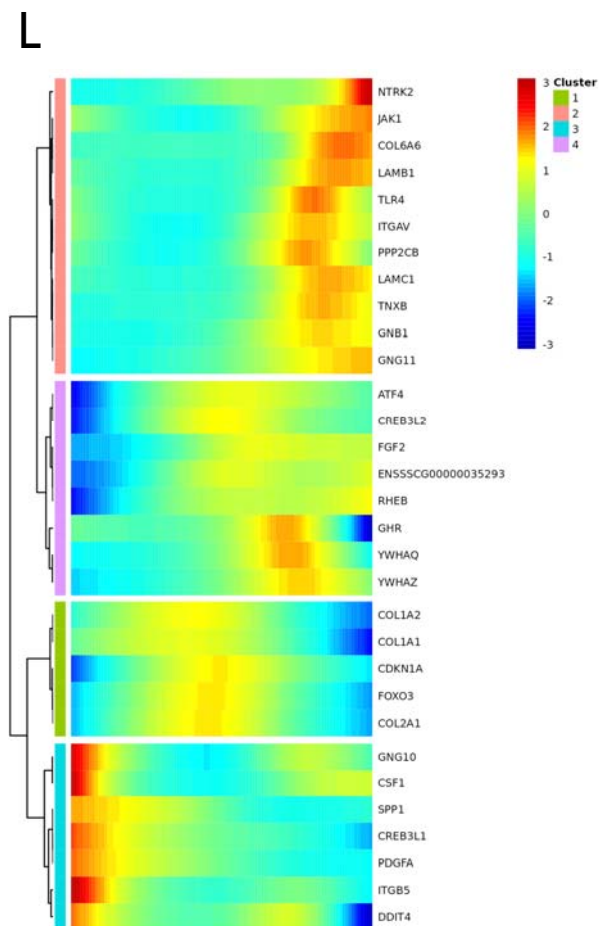
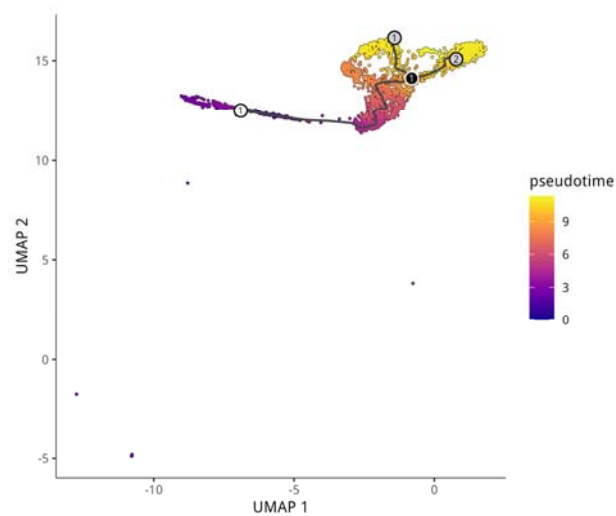
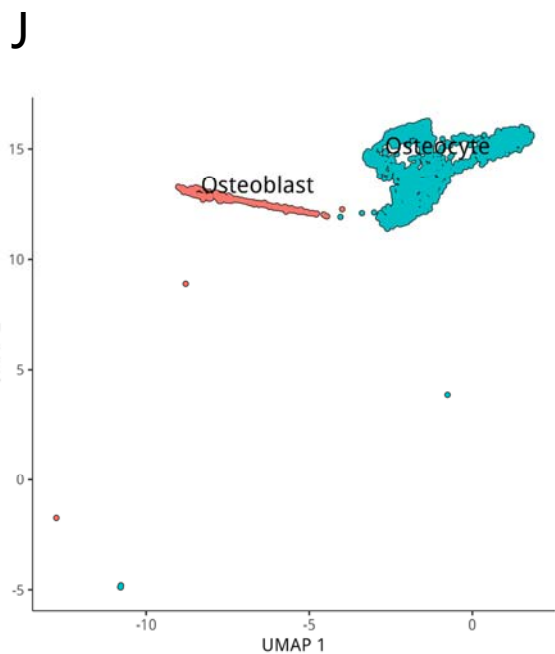


Fig. S3: Single-cell RNA-seq analysis of porcine growth plate transcriptome features contributing to chondrogenesis and osteocytogenesis

A) Dot plot showing the expression of marker genes in distinct growth plate subpopulations.

B) Dot plot showing the expression of GHR and IGF1R in distinct growth plate subpopulations.

C) t-SNE plot showing the expression of chondrocyte-enriched genes, including ACAN, SOX9, COL2A1, and HAPLN1.

D) Graph-based re-clustering of porcine chondrocytes reveals seven distinct subpopulations.

E) GO functional annotation of seven diverse chondrocyte clusters.

F) Dot plot showing the expression of marker genes in seven diverse chondrocyte clusters.

G) Pseudotime single-cell trajectory reconstructed by Monocle2 for seven diverse chondrocyte clusters. Cells are colored by pseudotime and cell type.

H) GO annotation of the branch-dependent genes involved along the chondrogenesis trajectory.

I) GO annotation of the most enriched genes in osteoblasts and osteocytes.

J) Pseudotime single-cell trajectory reconstructed by Monocle3 for osteoblasts and osteocytes.

K) Heatmap showing the branch-dependent genes involved in osteocytogenesis.

L) Heatmap showing the branch-dependent genes that are significantly upregulated in hybrids and involved in osteocytogenesis.