



A spatiotemporal single-cell atlas of porcine development reveals regulatory dynamics and cellular targets of domestication

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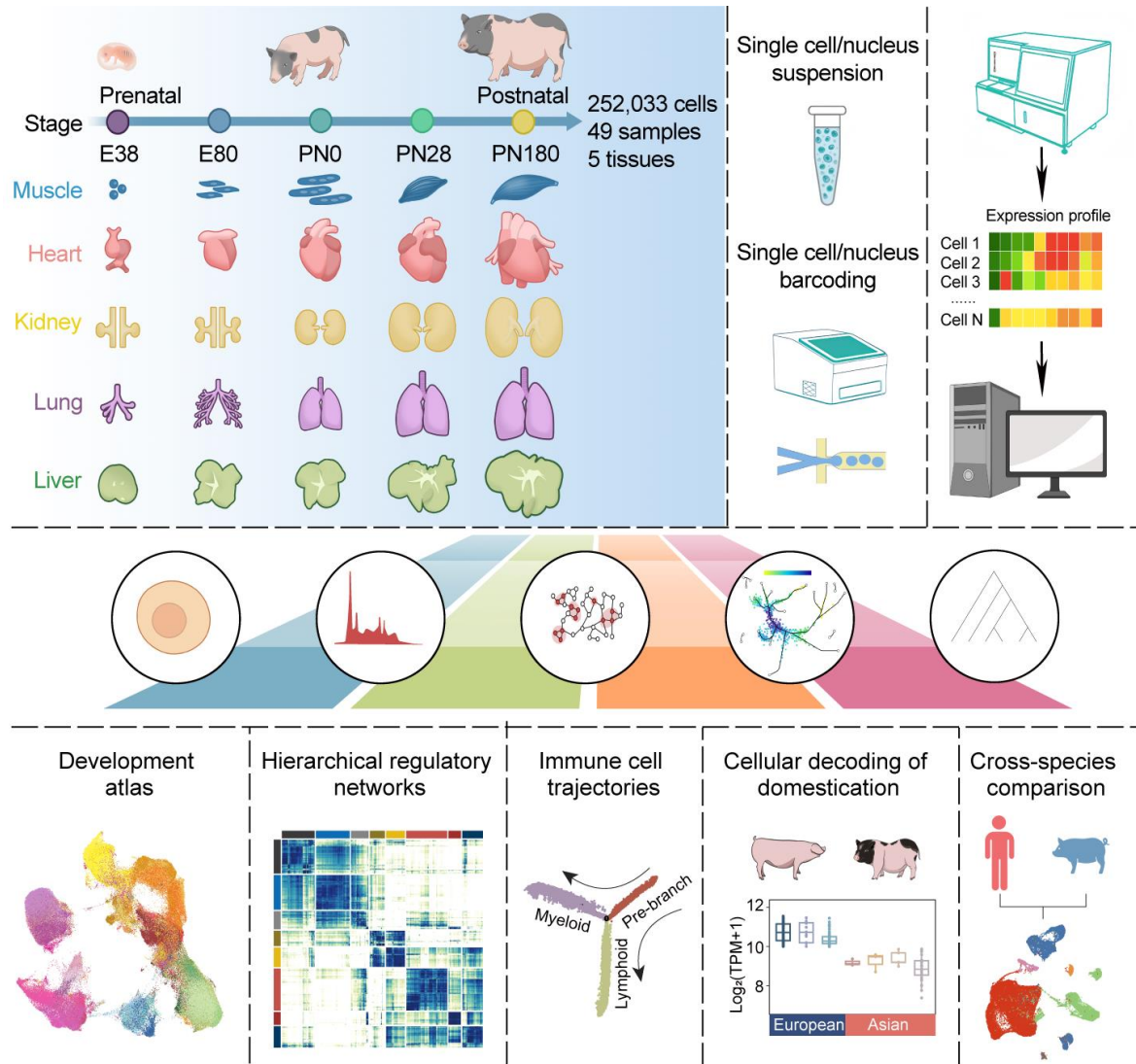
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Highlights



- ❑ A dynamic single-cell atlas of pig development maps 83 cell types across five tissues and developmental stages.
- ❑ Key transcription factors driving lineage specification and functional tissue maturation are identified, and a conserved bifurcated transcriptional trajectory of immune cells was reconstructed.
- ❑ Integrative multi-omic and single-cell data analysis identifies a muscle-specific enhancer of the *MYOT* gene as a target of artificial selection that underlies meat quality divergence between Asian and European pig breeds.
- ❑ Cross-species comparison between pig and human reveals conserved cell types and underscores the value of the reference pig cell atlas as a resource for biomedical research.

Single-cell spatiotemporal maps reveal the patterns of dynamic transitions in pig cell lineage development

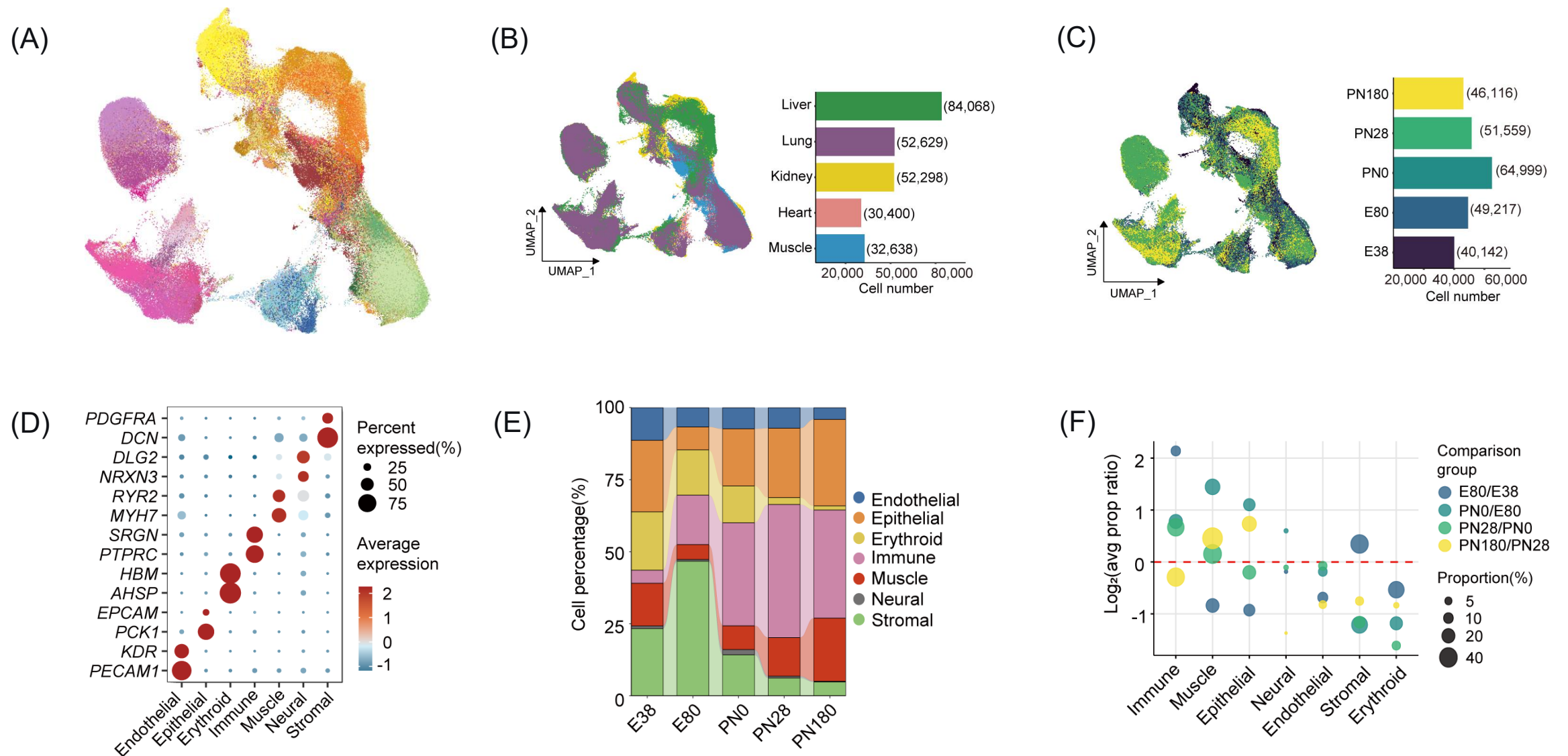


Figure 1. Construction of a spatiotemporal cell atlas during pig development.



Cell lineage is the primary determinant of transcriptional heterogeneity

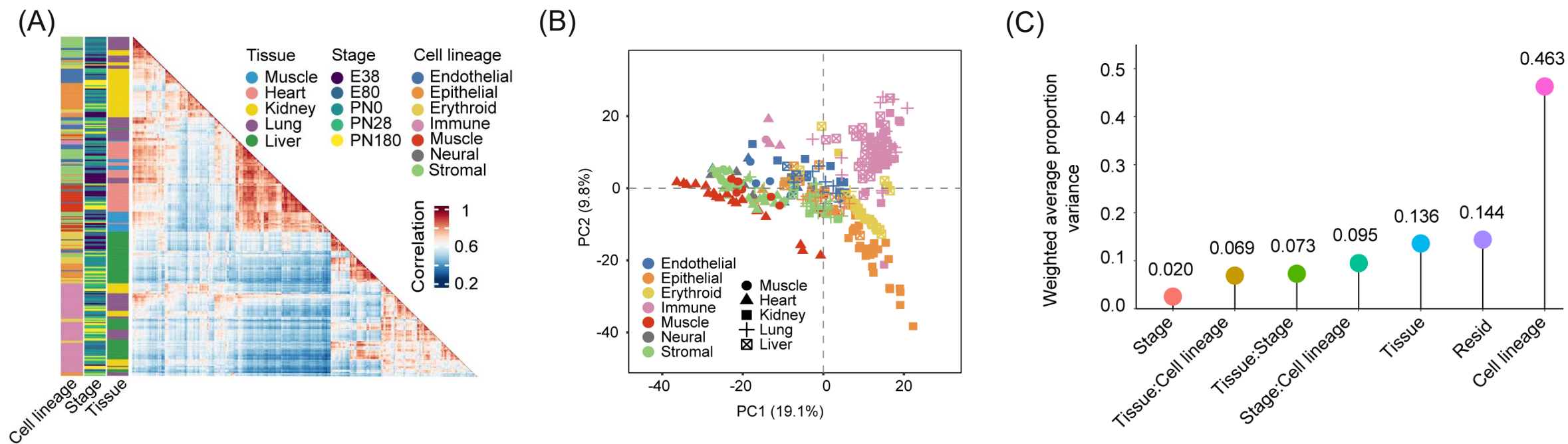


Figure 2. Dynamics of differential gene expression and transcriptional variability across developmental stages in pig.

The period from embryogenesis to birth is a critical turning point in cellular transcriptional remodeling

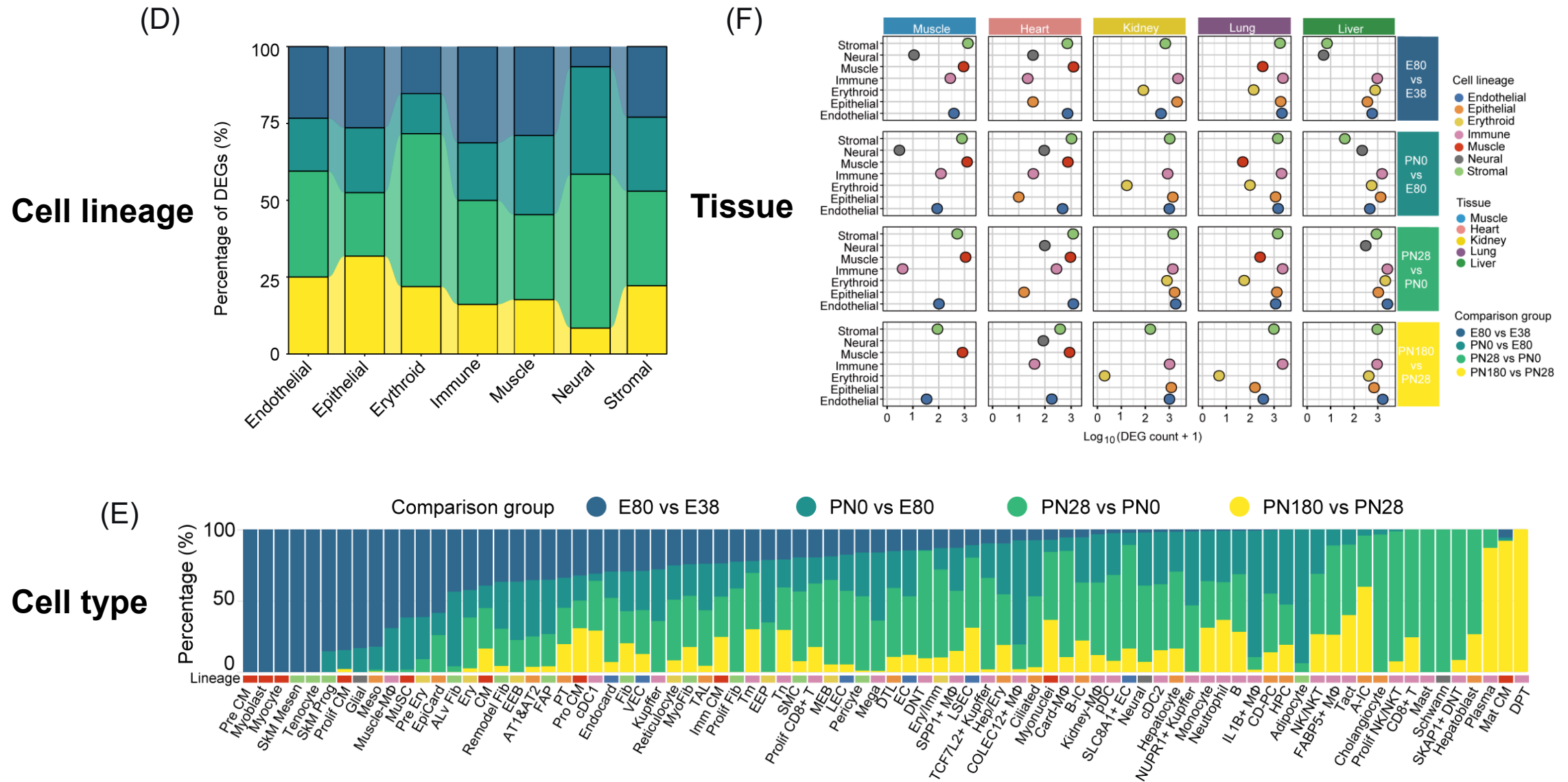


Figure 2. Dynamics of differential gene expression and transcriptional variability across developmental stages in pig.



A developmental regulatory network in pigs reveals the heterogeneity of lineage differentiation and mechanisms of cross-tissue coordination

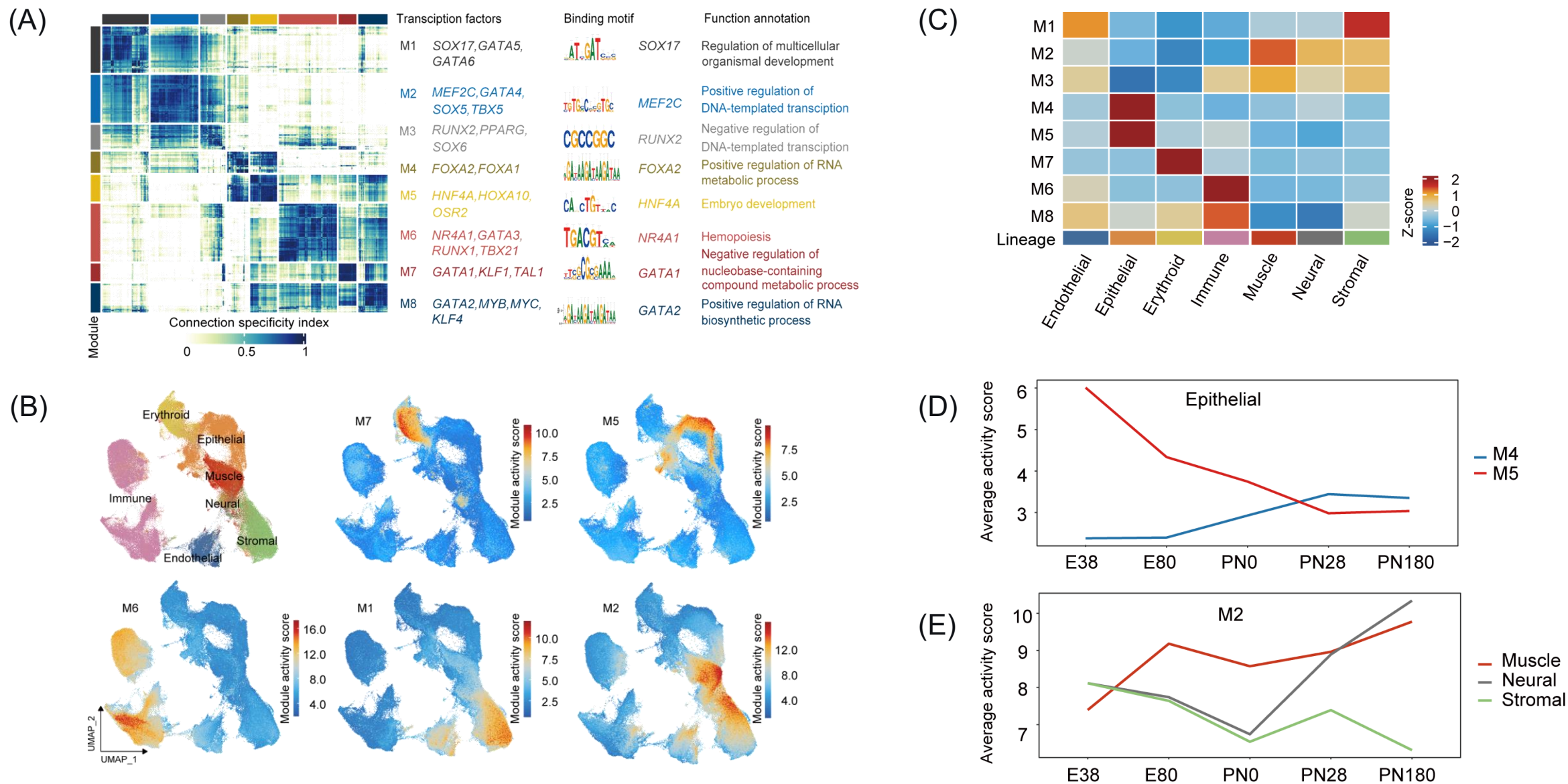


Figure 3. Transcriptional regulon modules orchestrate pig development through temporally ordered and lineage-specific programs.

The differentiation of immune cell lineages across multiple tissues follows a conserved two-branch regulatory mechanism

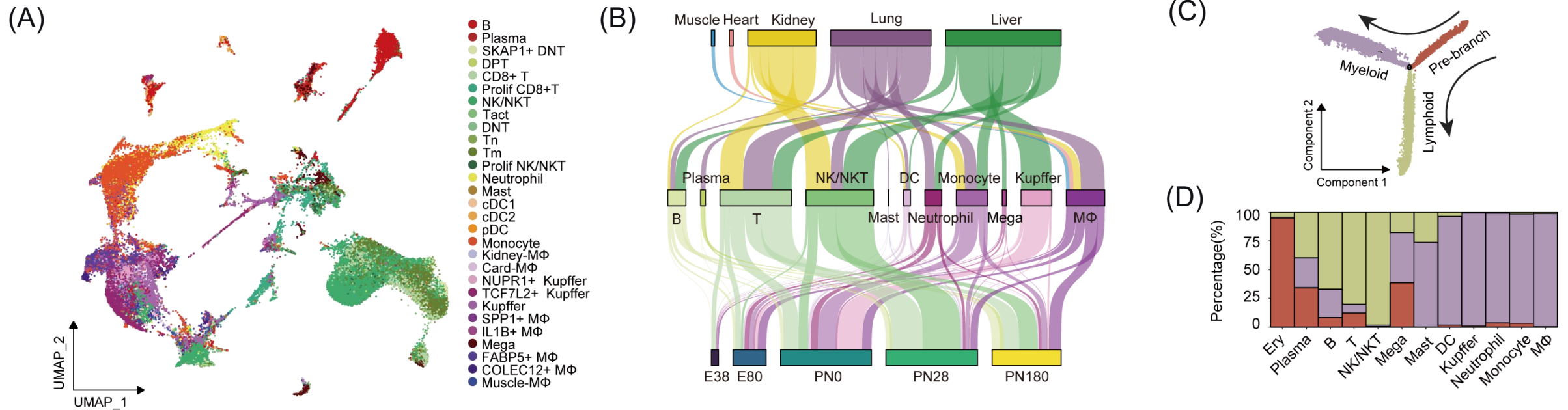


Figure 4. Developmental trajectories reveal the temporal and regulatory coordination of immune lineage differentiation during pig development.

The differentiation of immune cell lineages across multiple tissues follows a conserved two-branch regulatory mechanism

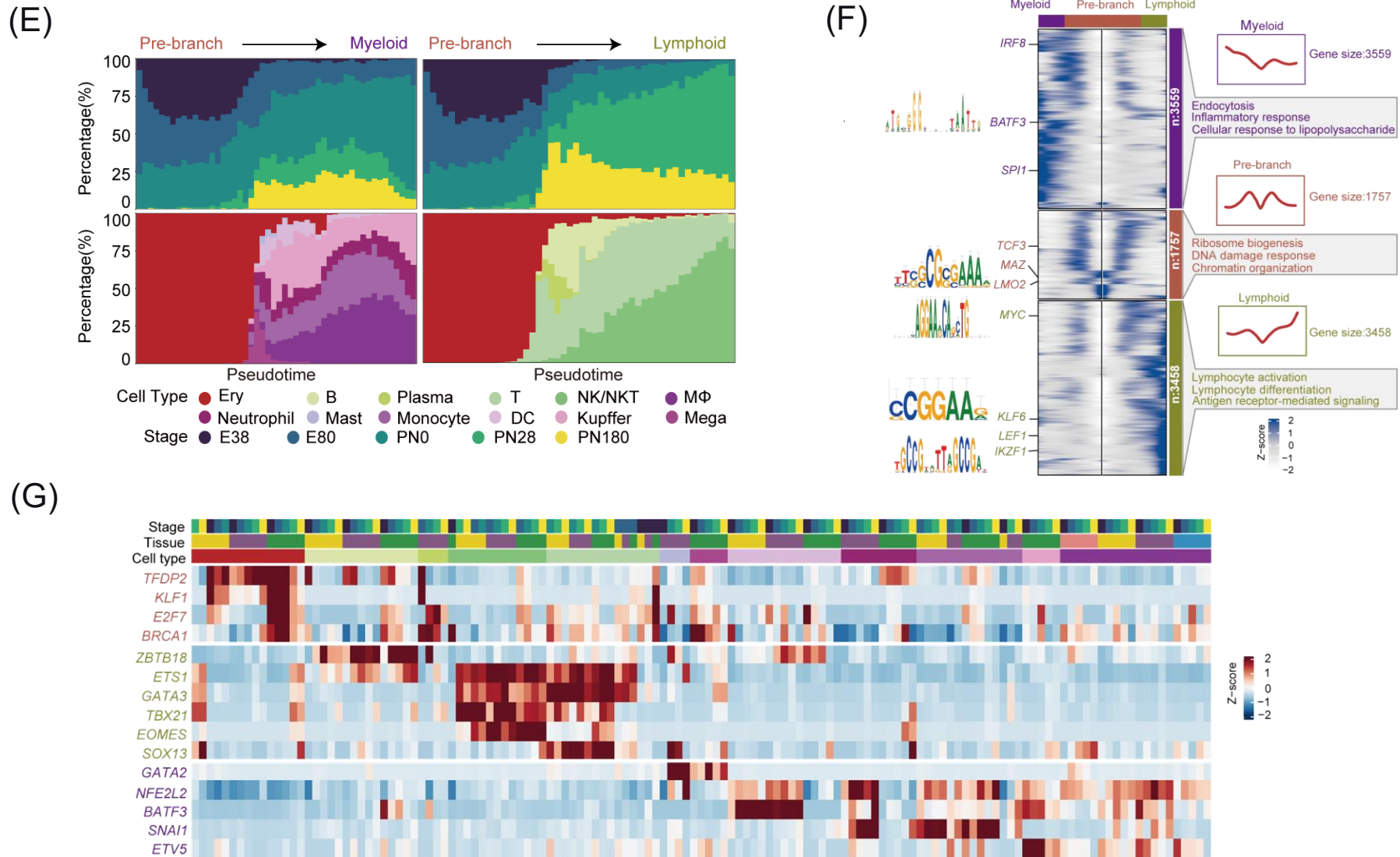


Figure 4. Developmental trajectories reveal the temporal and regulatory coordination of immune lineage differentiation during pig development.

Analysing the mechanisms of differential selection for muscle traits in Eurasian pig breeds at the single-cell level

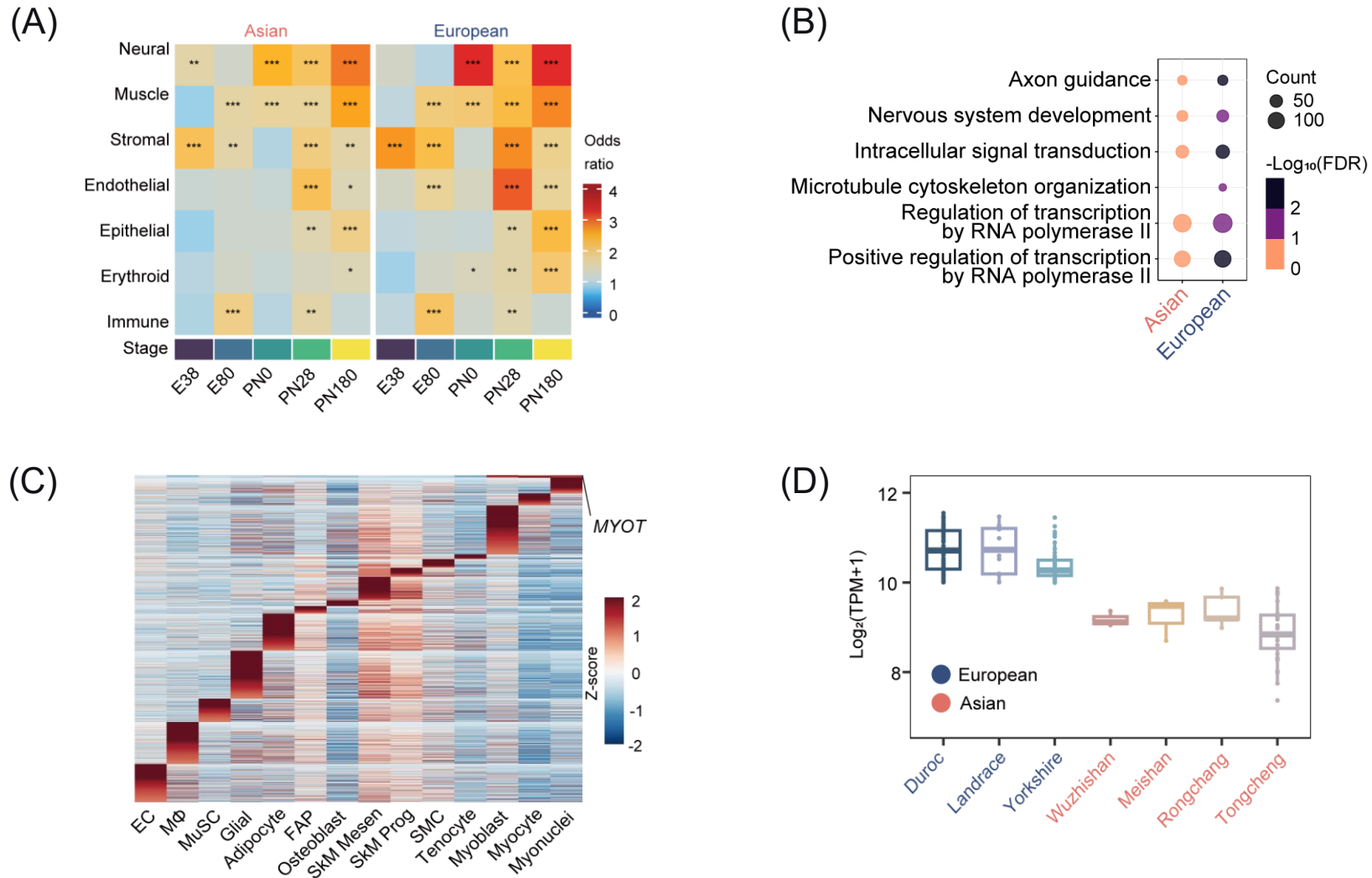


Figure 5. Single-cell mapping of domestication-associated regulatory programs highlights *MYOT* as a muscle-specific target in European pigs.

Analysing the mechanisms of differential selection for muscle traits in Eurasian pig breeds at the single-cell level

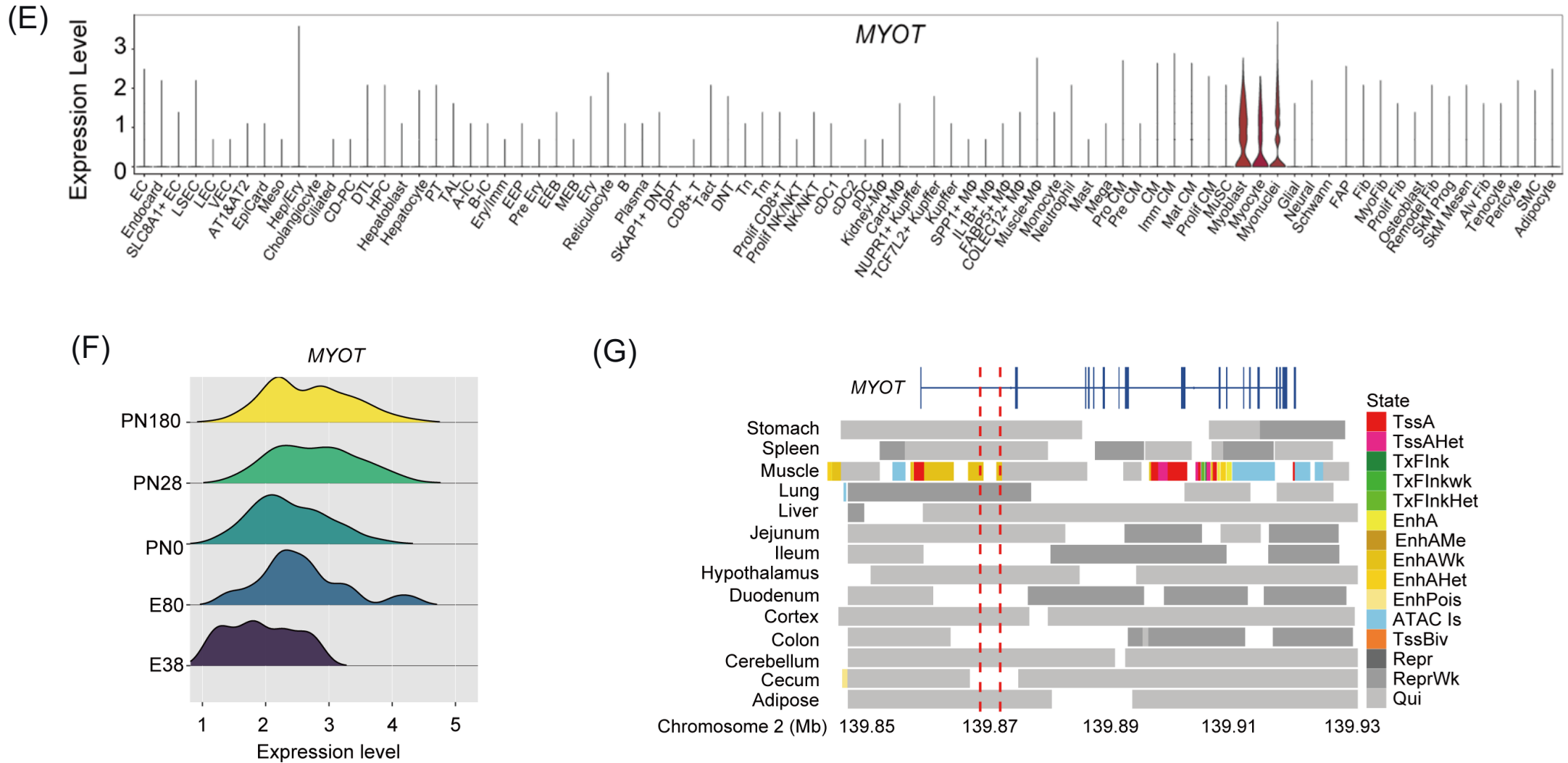


Figure 5. Single-cell mapping of domestication-associated regulatory programs highlights *MYOT* as a muscle-specific target in European pigs.

Cross-species comparisons between pigs and humans reveal transcriptional conservation

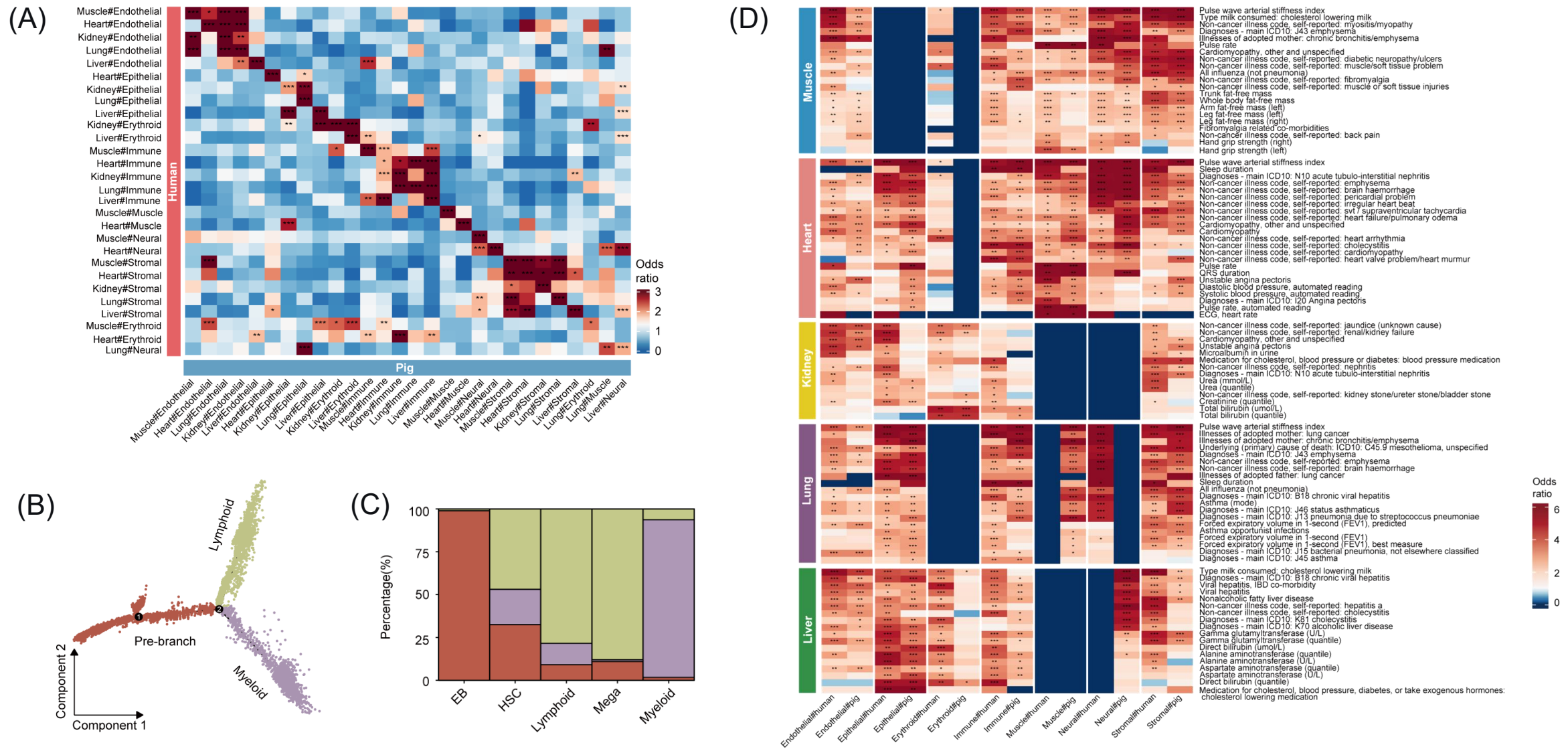


Figure 6. Cross-species single-cell mapping reveals conserved lineage specification and disease relevance.



Summary

- ❑ This study constructed a single-cell/single-nucleus transcriptomic atlas of five key pig tissues—liver, lung, kidney, heart, and longissimus dorsi—across five developmental stages from embryonic to adult life, comprising 252,033 cells. This fills an important gap in foundational resources for spatiotemporal multi-tissue developmental atlases in pigs.
- ❑ Based on this resource, the study systematically characterized the transcriptional regulatory mechanisms underlying cell lineage differentiation and tissue maturation. In particular, it revealed immune cell developmental trajectories at the whole-organism level, as well as their co-activated regulatory programs with endothelial and stromal cells.
- ❑ By integrating population genomic analyses, the study uncovered how domestication genetically shaped key cell types, such as muscle and neural cells, and associated genes, including *MYOT*.
- ❑ This work provides an important data resource and theoretical framework for livestock developmental biology, precision breeding, and human disease modeling.

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