

Fig. S1. Calibration of alternate LPM lineage topologies

Influence of k-mean values on lineage topologies throughout the LPM. Various K-mean values were sequentially applied until lineages recapitulated known IRX3/FOXF1 marker gene expression patterns in Figure 3. k4 produced a biologically relevant branch between somatic and splanchnic cell clusters (arrow), whereas k5 produced a relevant branch between the limb and non-limb somatic LPM (arrow). Neither branch structure was represented within a single graph.

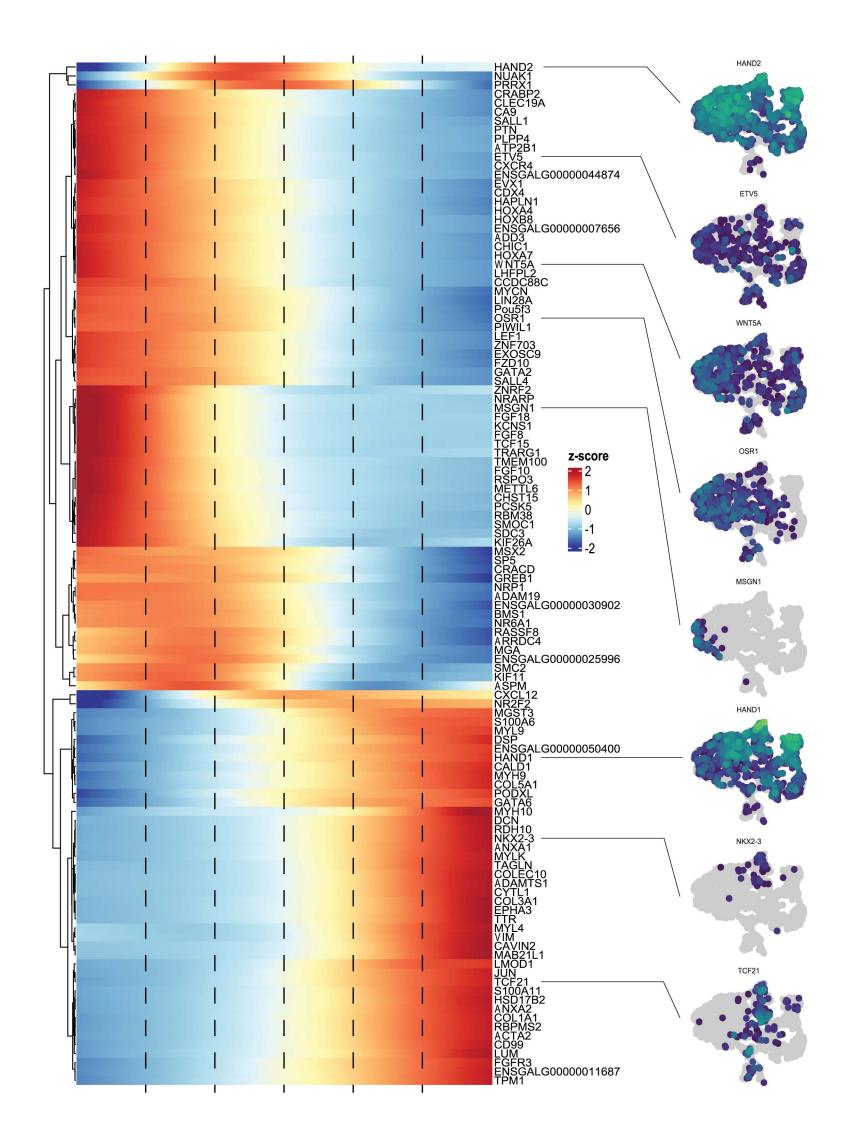


Fig. S2. Splanchnic LPM expression dynamics.

Extended pseudotime heatmap of significant differentially regulated genes along the splanchnic LPM lineage, with select expression plots. Bottom half of the heatmap revealed modules of genes that are specifically activated during splanchnic LPM specification and subsequent differentiation. The full list of significant genes are found in table S3.

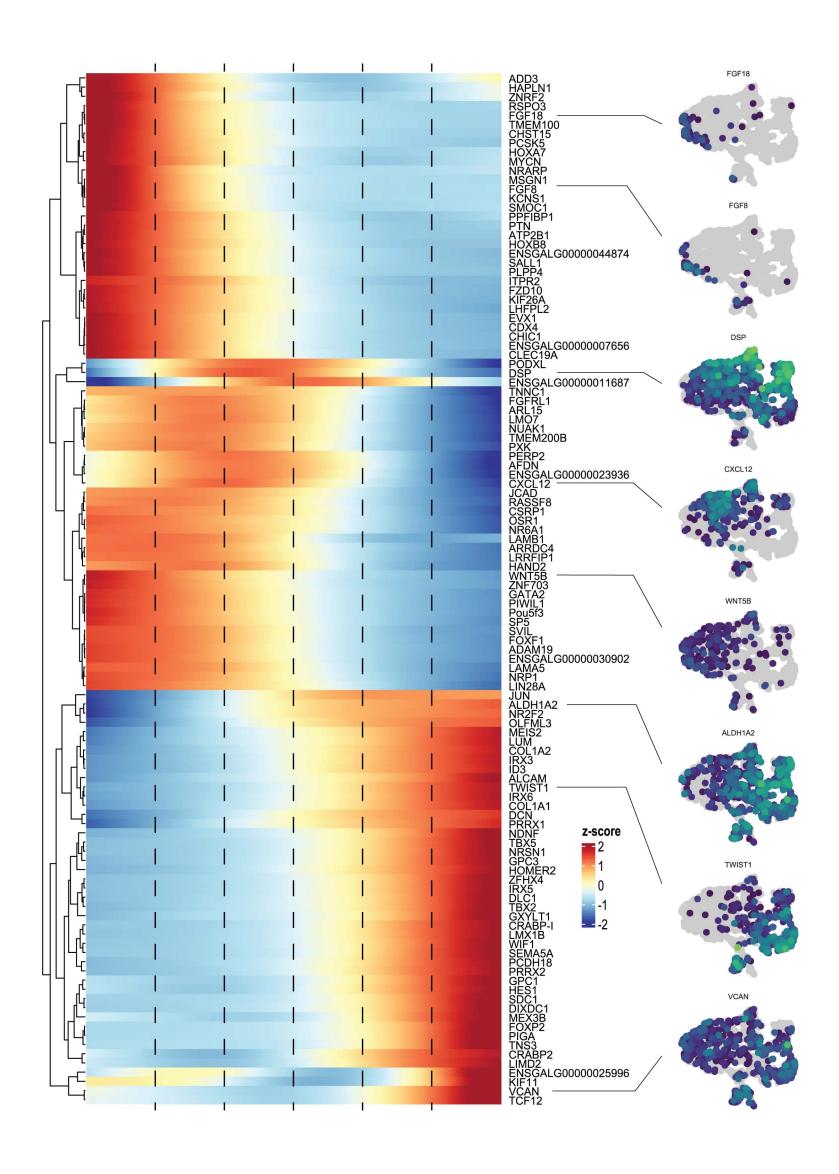


Fig. S3. Somatic LPM expression dynamics.

Extended pseudotime heatmap of significant differentially regulated genes along the somatic LPM lineage, with select expression plots. Bottom half of the heatmap revealed modules of genes that are specifically activated during somatic LPM specification and subsequent limb bud differentiation. The full list of significant genes are found in table S4.

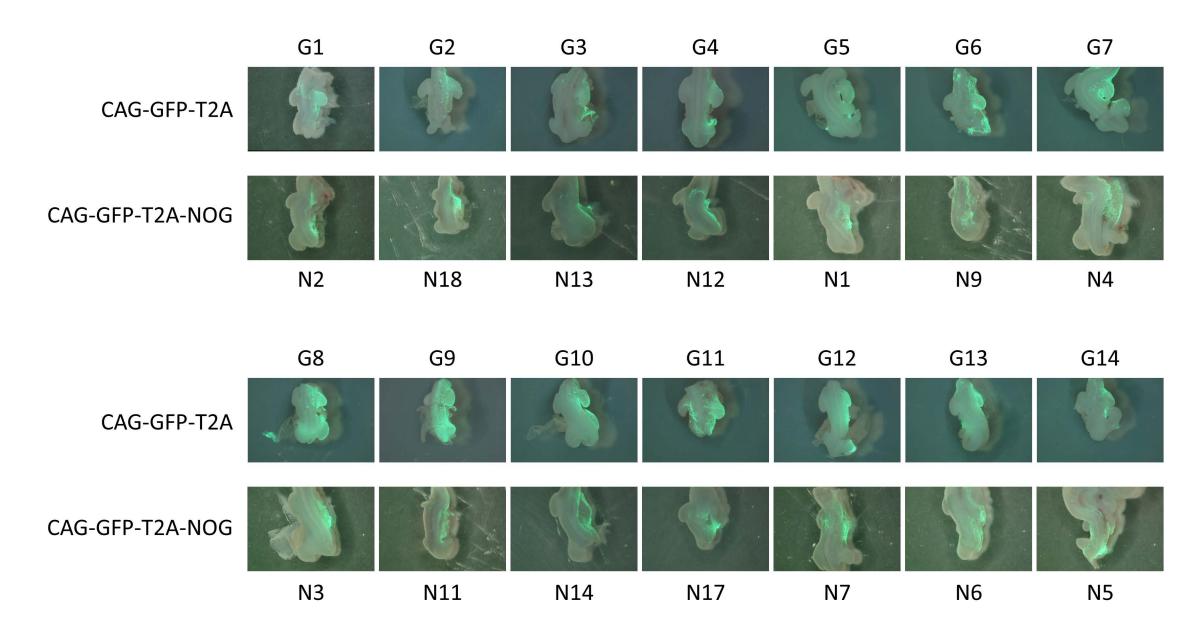


Fig. S4. BMP antagonism inhibits forelimb outgrowth.

Extended images from Figure 5, showing the effect of Noggin on limb development compared with GFP controls. Note, in instances where GFP-T2A-NOG field is extended posteriorly, hindlimbs additionally fail to develop.

Table S1. Global limb field cluster differentially expressed genes.

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Table S2. LPM-specific cluster differentially expressed genes.

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Table S3. Splanchnic LPM lineage significant spatially correlated genes.

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Table S4. Somatic LPM lineage significant spatially correlated genes.

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Table S5. Antibodies and plasmids used in the study.

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