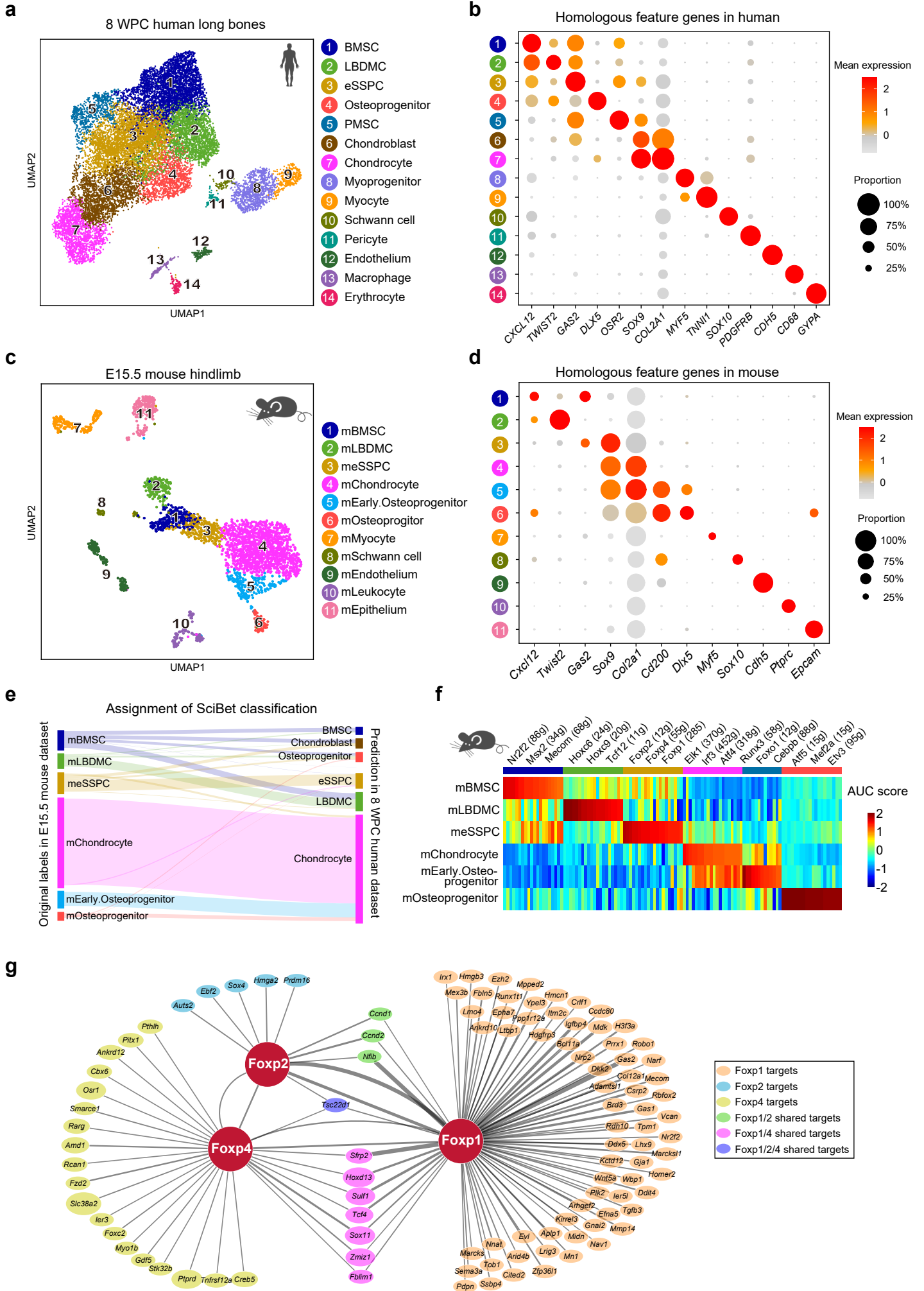


Figure S3



Supplementary Fig. 3. Cross-species comparison between human and mouse embryonic long bones during POC formation

a, UMAP plot of the 14 subsets in 8 WPC human long bones.

b, Dot plots showing the expression of human homologous feature genes in the 14 subsets indicated in **(a)**.

c, UMAP plot of the 11 subsets in re-processed E15.5 mouse hindlimb dataset.

d, Dot plots showing the expression of mouse homologous feature genes in the 11 mouse hindlimb subsets indicated in **(c)**.

e, Sankey diagram for assigning mouse E15.5 hindlimb datasets to human 8 WPC long bone datasets.

f, Heatmap showing the AUC scores of regulons enriched in mouse OCLC subsets. Z-score (column scaling) was calculated. Representative regulons were shown on the top.

g, The *Foxp1/2/4* regulon networks in mouse OCLC subsets. Lines thickness indicated the level of GENIE3 weights. Dot size indicated the number of enriched TF motifs.