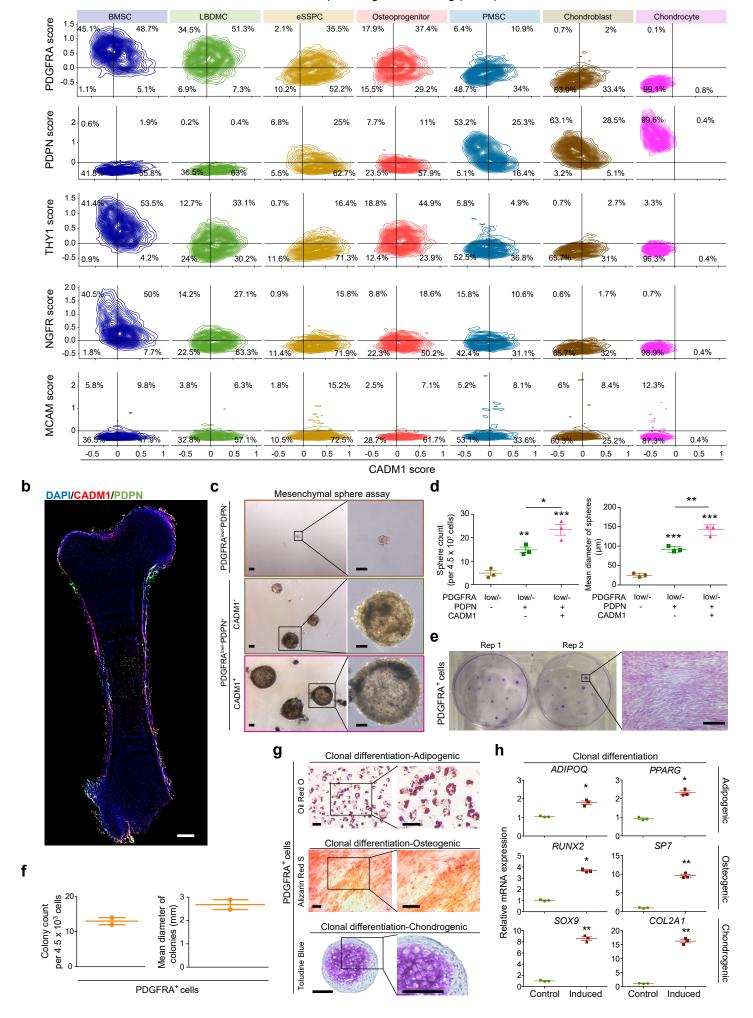
а

## Transcript-averaged cell scoring (TACS)



- **Supplementary Fig. 4.** Further in silico and functional analyses of eSSPCs and PDGFRA+ cells **a**, TACS plots showing the distribution of each OCLC subset between indicated surface marker pairs. Contours outlined regions of increasingly higher cell density. Cell frequencies were shown on the plots.
- **b,** Representative immunofluorescent image of 8 WPC human femur section stained with DAPI (blue), CADM1 (red) and PDPN (green) (n=2 embryos). Scale bar: 200 µm.
- **c,** Representative images showing the mesenchymal spheres formed by the 3 populations sorted as in Fig. 4c (left), with magnified views (right). Scale bars: 25 µm.
- **d,** Quantifications of the number (left) and mean diameter (right) of mesenchymal spheres (n=3 embryos). The statistical significance of differences was determined using one-way ANOVA with multiple comparison tests (LSD). \* P < 0.05; \*\* P < 0.01; \*\*\* P < 0.001. Error bars indicated SEM.
- **e,** Representative crystal violet staining of CFU-F colonies generated by flow cytometrically sorted PDGFRA<sup>+</sup> cells from two independent 8 WPC long bones. Magnified images of the boxed areas were shown on the right. Scale bar: 25 µm.
- **f**, Quantifications of the number (left) and mean diameter (right) of CFU-F colonies generated by flow cytometrically sorted PDGFRA<sup>+</sup> cells (n=2 embryos). Error bars indicated SEM.
- **g** and **h**, Representative oil red O (top), alizarin red (middle) and toluidine blue (bottom) staining after adipogenic, osteogenic and chondrogenic differentiation of clonally expanded PDGFRA<sup>+</sup> cells (**g**) with qPCR quantifications (**h**). Magnified images of the boxed areas were shown on the right (n=2 embryos). Scale bars: 200  $\mu$ m. The statistical significance of differences was determined using Wilcoxon signed rank test. \* P < 0.05; \*\* P < 0.01. Error bars indicated SEM.