

CORRECTION

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Correction to: RNA-sequencing reveals positional memory of multipotent mesenchymal stromal cells from oral and maxillofacial tissue transcriptomes

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Following publication of the original article [1], the authors identified an error in Figs. 4, 5, 6. In these figures the label for I-MSCs was incorrectly given as I-MCs. The correct figures are given below and the original article has been updated.

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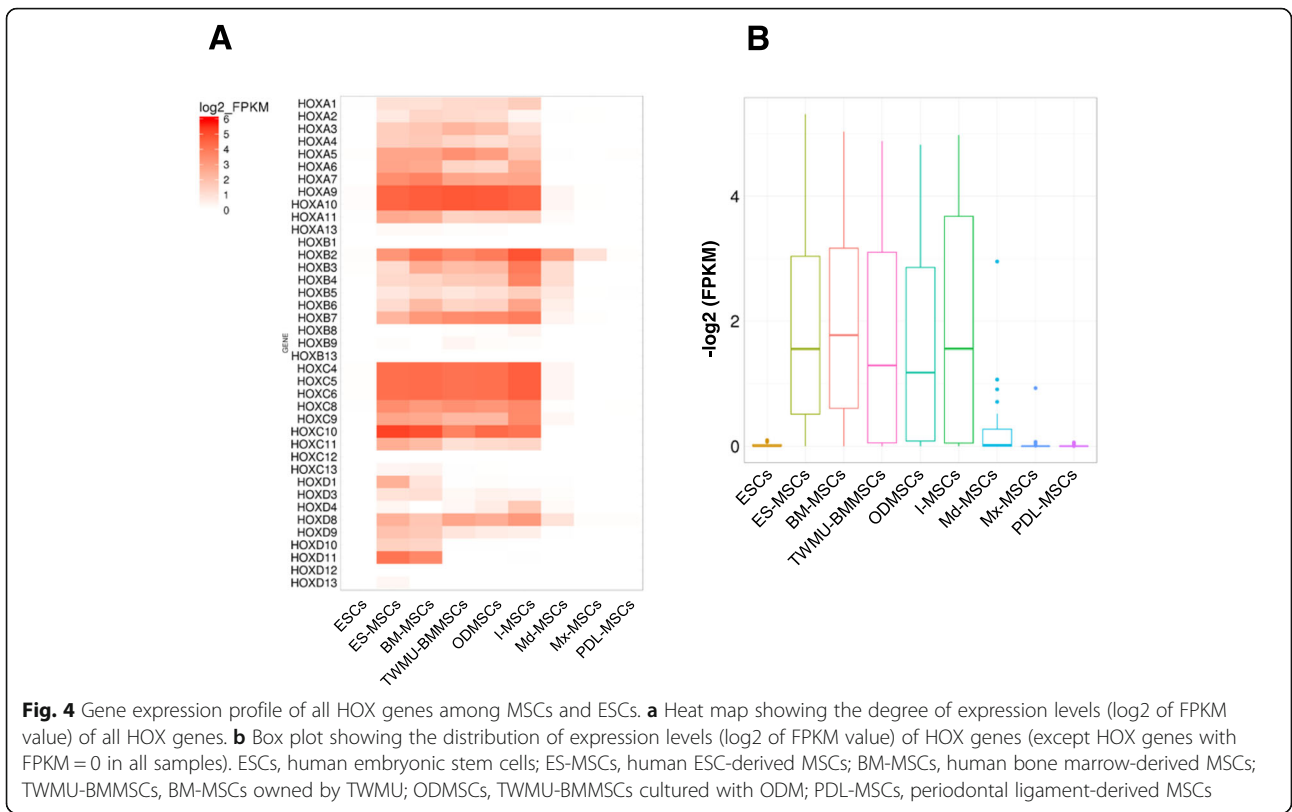
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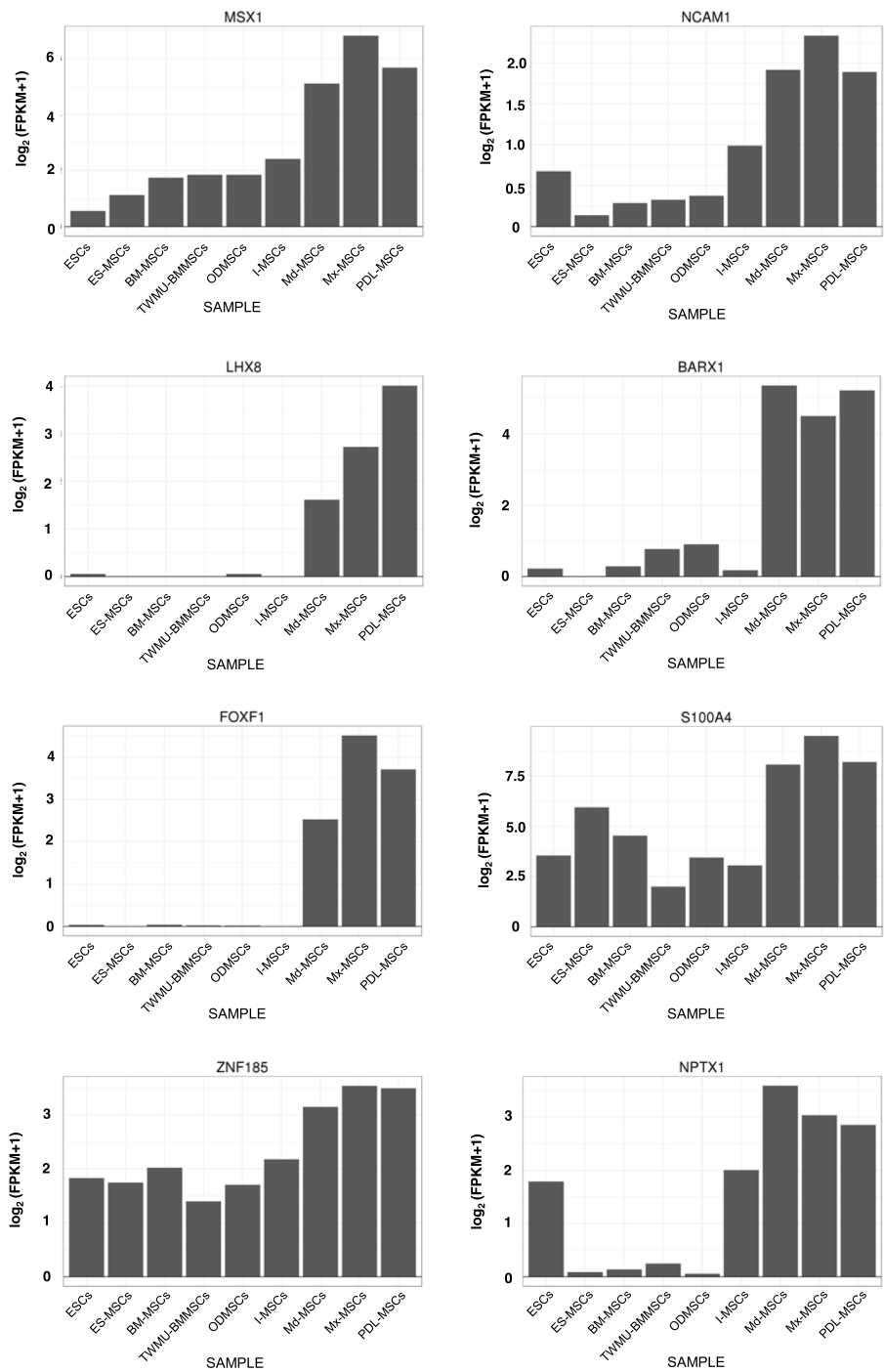


Fig. 5 Specific up-regulated DEGs in oral and maxillofacial tissue-derived MSCs. The vertical axis represents gene expression levels with log₂ of [FPKM + 1]

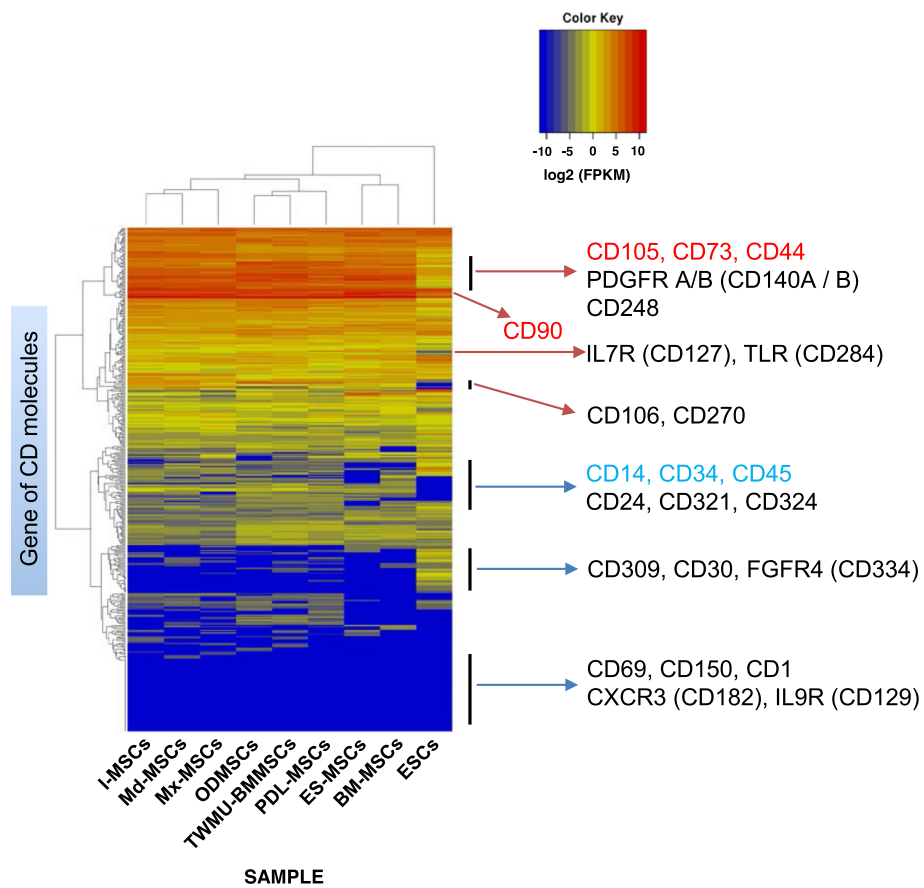


Fig. 6 Gene expression profile of CD molecules in each sample. Heatmap showing the degree of expression levels (log₂ of FPKM value) of all CD genes. Scaled expression values are color-coded according to the legend on the left. Genes are hierarchically clustered by the similarity of their expression profiles over the set of samples, and the samples are hierarchically clustered by the similarity of expression patterns over their expression profile. The described genes (right side of heatmap) are representative CD molecules. Red letters represent positive markers for MSCs, and blue letters represent negative markers for MSCs