

Expression and regulation of long noncoding RNAs during the osteogenic differentiation of periodontal ligament stem cells in the inflammatory microenvironment

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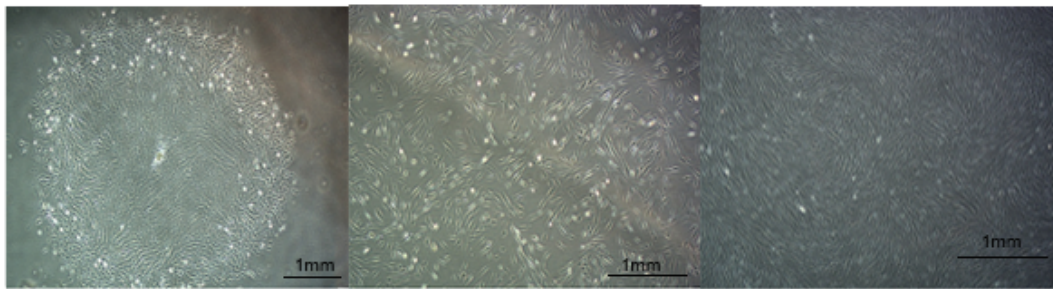
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A

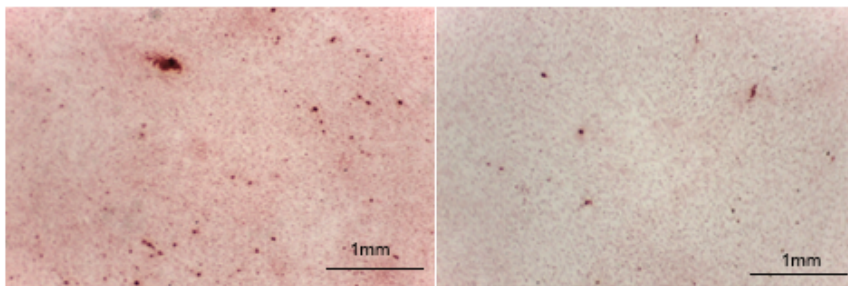


cells primarily culture in 7 days

cells subculture in 1 day

cells subculture in 3 days

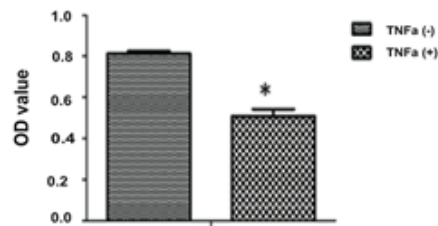
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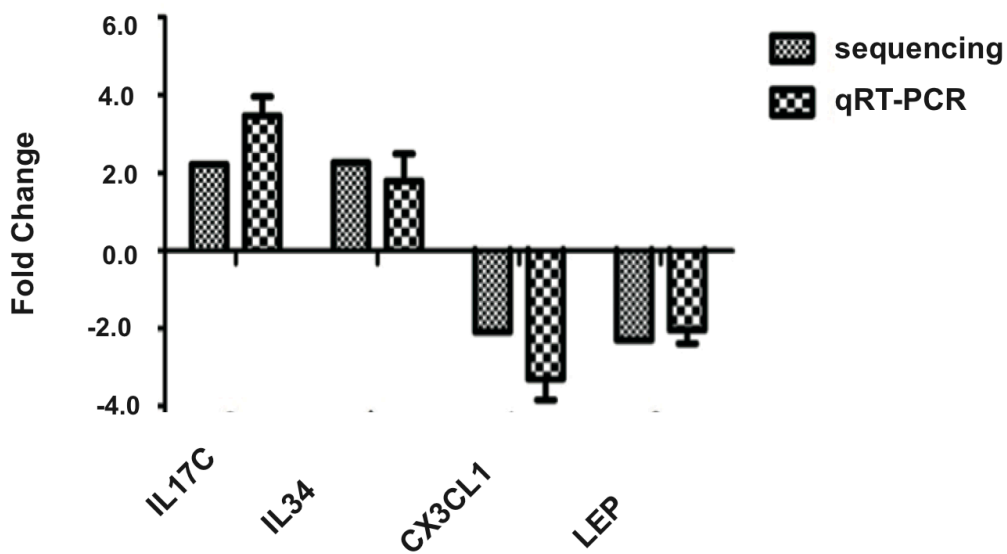
TNF- α (-)

TNF- α (+)

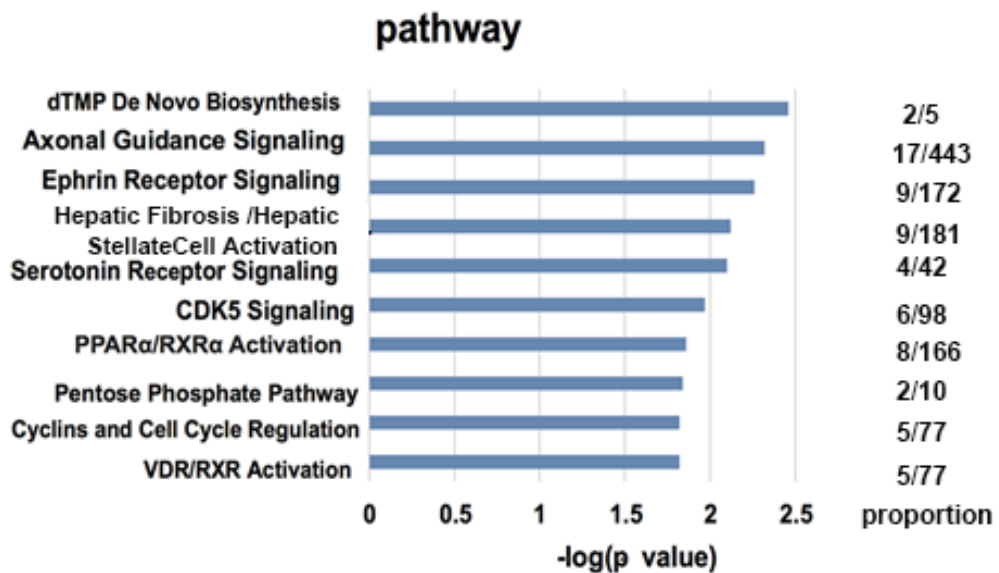
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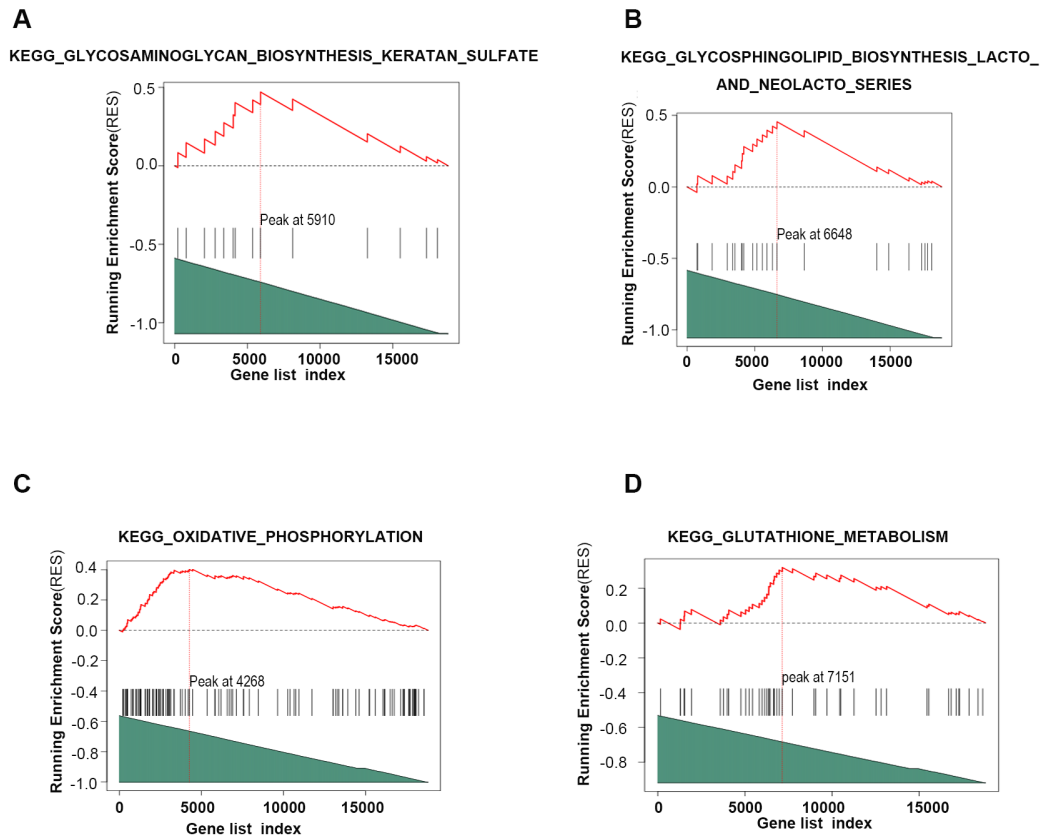
Supplementary Fig. 1: Clone-like appearance of PDLSCs. (A) From left to right: cells primarily cultured for 7 days, cells subcultured for 1 day and cells subcultured for 3 days. (B) Alizarin red staining of dPDLSCs (left) and TNF- α -PDLSCs (right). (C) Quantitative analysis of Alizarin red staining.



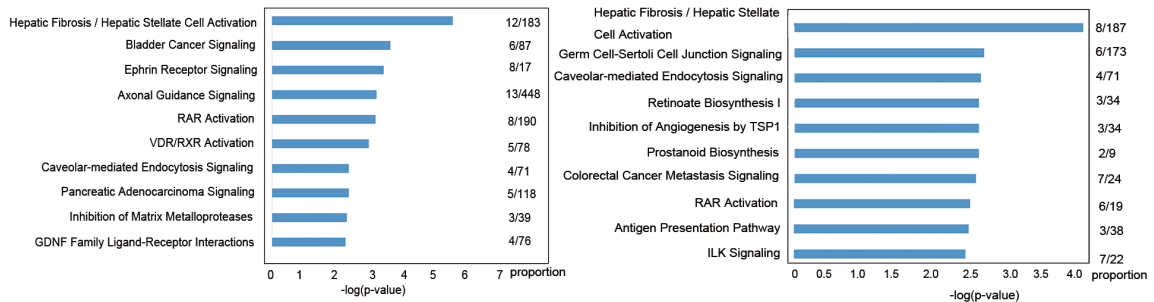
Supplementary Fig. 2: The expression change of four protein-coding genes validated by RT-PCR.



Supplementary Fig. 3: Significantly enriched pathways for neighboring protein-coding genes for DE lncRNAs between uPDLSCs and dPDLSCs.



Supplementary Fig. 4: (A) (B) The top two significantly enriched pathways for DE lncRNAs between uPDLSCs and dPDLSCs via LncRNAs2Pathways. (C) (D) The top two significantly enriched pathways for DE lncRNAs between dPDLSCs and TNF- α -dPDLSCs via LncRNAs2Pathways.



Supplementary Fig. 5: The significantly enriched pathways for mRNAs involved in ceRNA networks via IPA.

Supplementary Table 1: The final lncRNA reference consisted of 31,822 previously identified lncRNAs and 63 novel lncRNAs not annotated in lncRNA databases.

Supplementary Table 2: Differentially expressed lncRNAs identified by DESeq2 and EdgeR in dPDLSCs compared to uPDLSCs.

Supplementary Table 3: Differentially expressed lncRNAs identified by DESeq2 and EdgeR in TNF- α -dPDLSCs compared to dPDLSCs.

Supplementary Table 4: Differentially expressed protein-coding genes identified by DESeq2 and EdgeR in dPDLSCs compared to uPDLSCs.

Supplementary Table 5: Differentially expressed protein-coding genes identified by DESeq2 and EdgeR in TNF- α -dPDLSCs compared to dPDLSCs.

Supplementary Table 6: A. Significantly enriched pathways for DE lncRNAs between uPDLSCs and dPDLSCs via LncRNAs2Pathways analysis. B. Significantly enriched pathways for DE lncRNAs between dPDLSCs and TNF- α -dPDLSCs via LncRNAs2Pathways analysis.

Supplementary Table 7: A. the lncRNAs, mRNAs and shared miRNAs of lncRNA-mRNA ceRNA interactions in the DE lncRNAs between dPDLSCs and uPDLSCs. B. the lncRNAs, mRNAs and shared miRNAs of lncRNA-mRNA ceRNA interactions in the DE lncRNAs between TNF- α -dPDLSCs and dPDLSCs.