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Supplemental File

Human umbilical cord mesenchymal stem cell derived exosomes encapsulated in functional peptide hydrogel promote cardiac repair

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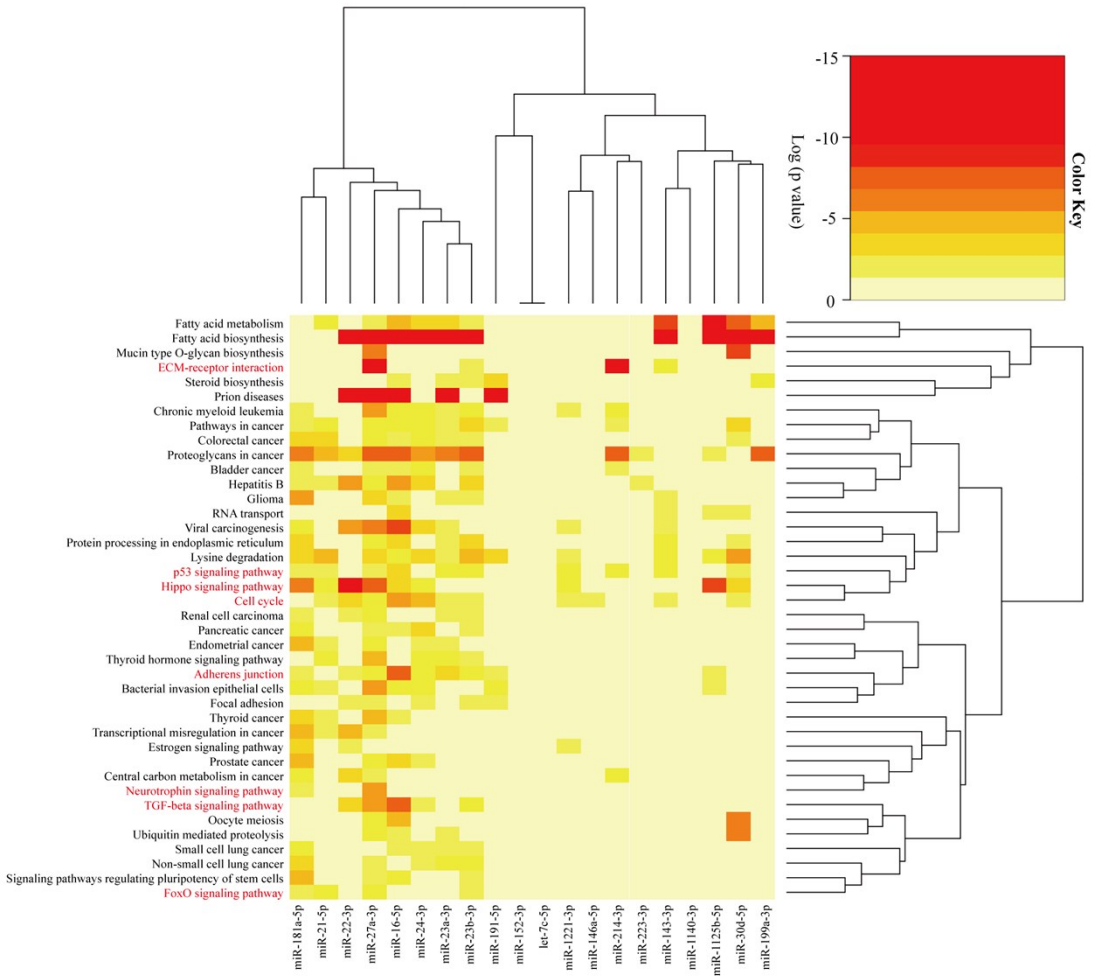
Materials and methods

miRNA sequencing and analysis

Total RNA from UMSC derived exosomes was extracted using Qiagen miRNeasy Mini Kit. The sequence was analyzed by HiSeq 2500 (Novel Bioinformatics Co., Ltd,Shanghai, China). Fast-QC software (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) was used to assess the quality of acquired data roundly. Subsequently, RNA-seq data was mapped to miRNA, Rfam and Genome database respectively by MapSplice software, which was used for reads of short (< 75 bp) or long sequence (>75 bp). MiRNA expression was quantified by read per kilobases per millionreads (RPKM). Top 20 highly expressed miRNA in UMSC exosomes was used to analysis the possible pathway by TarBase v7.0 for target gene prediction and KEGG analysis for gene pathway prediction. The p-value threshold was set at 0.05 and the Enrichment analysis method was used Fisher's exact test (Hypergeometric Distribution), and the heatmap was drawn by DIANA-miRPath v3.0 (http://www.microrna.gr/miRPathv3) as described previously[1].

Supplemental Figure Legends



Supplemental Figure 1. The potential pathways of the top 20 miRNAs in the UMSC exosomes.

Reference

1. I. S. Vlachos, K. Zagganas, M. D. Paraskevopoulou, G. Georgakilas, D. Karagkouni, T. Vergoulis, T. Dalamagas and A. G. Hatzigeorgiou, *Nucleic acids research*, 2015, **43**, W460-466.