



## Correction to: Co-expression network analysis identified key genes in association with mesenchymal stem cell osteogenic differentiation

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### Correction to: Cell Tissue Res (2019)

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The authors regret that in our published paper entitled “Co-expression network analysis identified key genes in association with mesenchymal stem cell osteogenic differentiation” Cell Tissue Res (2019). <https://doi.org/10.1007/s00441-019-03071-1>; there is a typo in the text that appears in the “Material and method\_ Co-expression network construction”. We mistakenly wrote GSE58919 as GSE658919.

The error in the Table 2 was that the Table 2 was not fully displayed.

The authors would like to apologize for any inconvenience made by this mistake.

### Therefore, in our article we make the following corrigendum in the text:

- 1) Page 2, Material and method, (“Co-expression network construction”), last paragraph. Consequently, the text has the following changes (for the changes, see underlined text).  
“In this study, the soft threshold in GSE658919 is 16 while the soft threshold in GSE18043 is 14”. GSE658919 should be corrected to GSE58919.
- 2) Page 12, Table 2, (“Characteristics of potential key genes in MSC osteogenic differentiation”). Replacement for Table 2 showing the correct information is displayed below.

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**Table 2** Characteristics of potential key genes in MSC osteogenic differentiation

Symbol	Description	GO-Biological Process and KEGG pathway	Function	Reference
<b>CCT2</b>	T-complex protein 1 subunit beta	NA	Cell cycle and osteoblast differentiation	(Minegishi, et al., 2018, Alves, et al., 2010)
<b>NOP58</b>	Nucleolar protein 58	Ribosome biogenesis in eukaryotes	Influence 2'-O-methylation of rRNAs to regulated the proliferation	(Qin, et al., 2017)
<b>FBL</b>	Fibrillarin		Influence 2'-O-methylation of rRNAs to regulated the proliferation and regulate differentiation	(Bouffard, et al., 2018, Watanabe-Susaki, et al., 2014, Shubina, et al., 2016)
<b>PSMC6</b>	Proteasome 26S subunit, ATPase 6	Wnt signaling pathway, amino acid metabolic process and proteasome	Participate in stem cell differentiation and self-renewal	(Vilchez, et al., 2012, Koyuncu, et al., 2018, Saez, et al., 2018)
<b>PSMB7</b>	Proteasome subunit beta 7			
<b>EXOSC8</b>	exosome component 8	NA	Correct neuronal differentiation	(Giunta, et al., 2016, Lloret-Llinares, et al., 2018, Makino, et al., 2013)
<b>SNRPD1</b>	small nuclear ribonucleoprotein D1 polypeptide	NA	Interacts with cajal body to regulate transcription	(Smolinski and Kolowierz, 2012)

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