

CORRECTION

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Correction to: A prototypical non-malignant epithelial model to study genome dynamics and concurrently monitor micro-RNAs and proteins in situ during oncogene-induced senescence

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Following publication of the original article [1], it was reported that earlier versions of Table S4a and Table S4d in Additional file 11 were uploaded. The correct version of Additional file 11 has been included here, and the original article has been corrected.

PED (ESC) HBEC CDC6 Tet-ON cells. **Table S4d.** Down regulated genes in ESCAPED (ESC) HBEC CDC6 Tet-ON cells.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s12864-021-07608-z>.

Additional file 11: Table S4a. Upregulated genes in induced (ON) HBEC CDC6 Tet-ON cells. **Table S4b.** Down regulated genes in induced (ON) HBEC CDC6 Tet-ON cells. **Table S4c.** Upregulated genes in ESCA

The original article can be found online at <https://doi.org/10.1186/s12864-017-4375-1>.

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Reference

1. Komseli ES, Pateras IS, Krejsgaard T, et al. A prototypical non-malignant epithelial model to study genome dynamics and concurrently monitor micro-RNAs and proteins *in situ* during oncogene-induced senescence. *BMC Genomics*. 2018;19:37 <https://doi.org/10.1186/s12864-017-4375-1>.