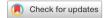
## scientific reports



## **OPEN** Publisher Correction: Gene expression changes in sickle cell reticulocytes and their clinical associations

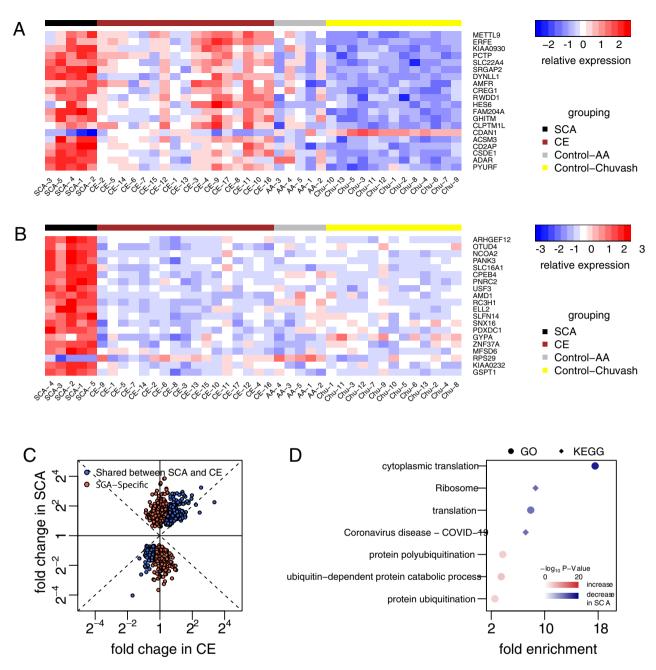
Published online: 14 September 2023

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Correction to: Scientific Reports https://doi.org/10.1038/s41598-023-40039-2, published online 08 August 2023

The original version of this Article contained errors in Figure 3. The numbers in the colour bar of Figure 3B '-3, -2, -1, 0, 1, 2, 3' did not align correctly with the gradients of the colour bar, the two characters "va" within the word "Control-Chuvash" in the legends of grouping annotation of Figure 3A, B overlapped and "Coronavirus disease - Covid-19" in the y-axis labelling in Figure 3D did not align correctly. The original Figure 3 and accompanying legend appear below.

The original Article has been corrected.



**Figure 3.** SCA-specific expression changes. (**A,B**) Hierarchical clustering of individuals within groups, using Euclidean distance of gene expression levels of (**A**) the top 20 most significant differential genes in CE whose expression changes were shared in SCA and (**B**) the top 20 most significant genes whose expression changes differed between SCA and CE. Individuals are grouped as SCA, CE, African American controls (Control-AA), and Chuvash controls (Control-Chuvash). (**C**) Scatter plot of fold change in CE (x-axis) and SCA (y-axis). (**D**) GO biological processes and KEGG pathways enriched with SCA-specific differential genes.

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