scientific reports

Check for updates

OPEN

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

Published online: 14 September 2023

Xu Zhang, Jihyun Song, Binal N. Shah, Jin Han, Taif Hassan, Galina Miasniakova, Adelina Sergueeva, Sergei Nekhai, Roberto F. Machado, Mark T. Gladwin, Santosh L. Saraf, Josef T. Prchal & Victor R. Gordeuk

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.

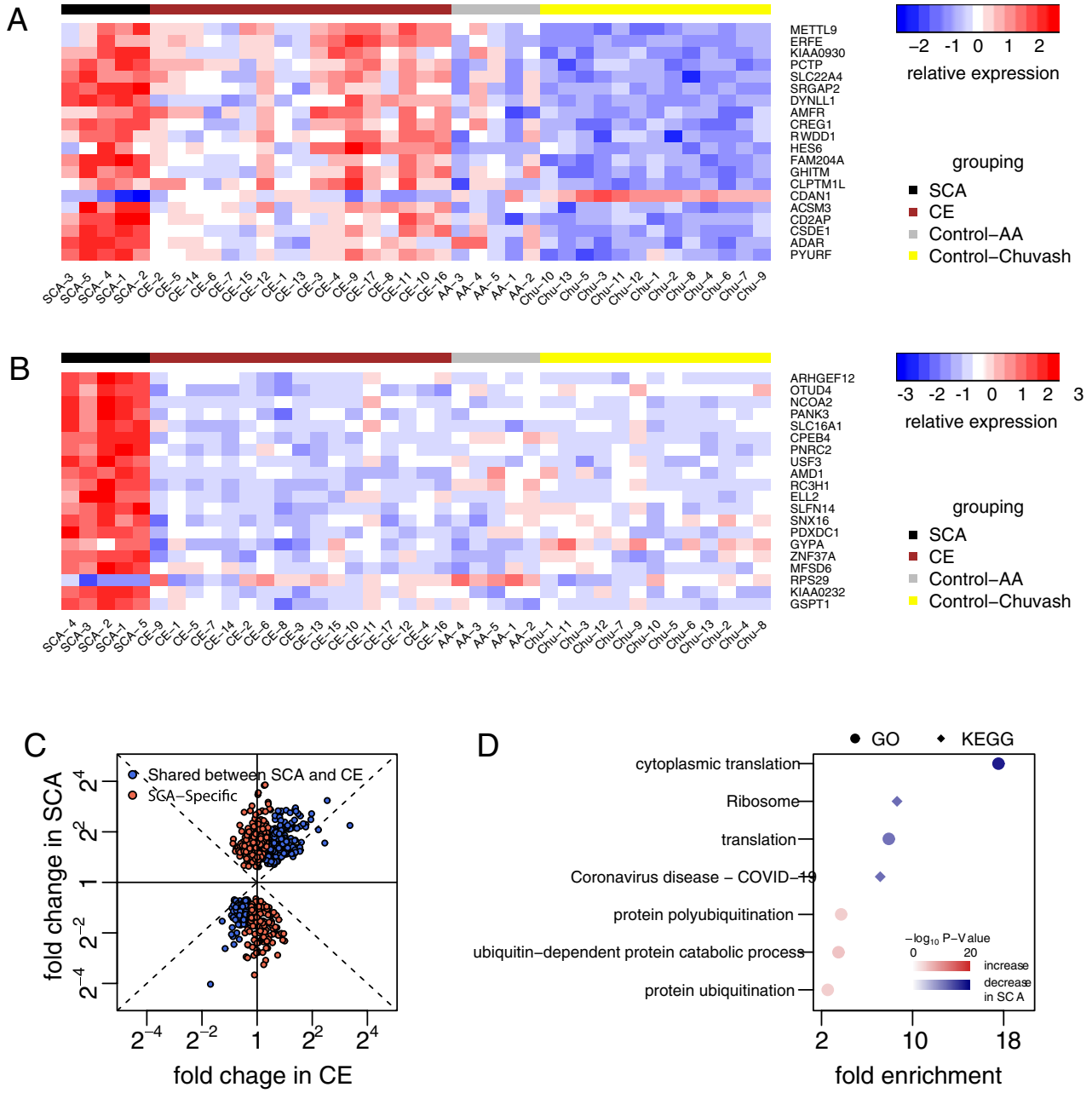

Figure 3. SCA-specific expression changes. (**A,B**) Hierarchical clustering of individuals within groups, using Euclidean distance of gene expression levels of (**A**) the top 20 most significant differential genes in CE whose expression changes were shared in SCA and (**B**) the top 20 most significant 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.