CellPress
OPEN ACCESS

Correction

CD177, a specific marker of neutrophil activation, is associated with coronavirus disease 2019 severity and death

Yves Lévy,* Aurélie Wiedemann, Boris P. Hejblum, Mélany Durand, Cécile Lefebvre, Mathieu Surénaud, Christine Lacabaratz, Matthieu Perreau, Emile Foucat, Marie Déchenaud, Pascaline Tisserand, Fabiola Blengio, Benjamin Hivert, Marine Gauthier, Minerva Cervantes-Gonzalez, Delphine Bachelet, Cédric Laouénan, Lila Bouadma, Jean-François Timsit, Yazdan Yazdanpanah, Giuseppe Pantaleo, Hakim Hocini, Rodolphe Thiébaut,* and the French COVID cohort study group

*Correspondence:
yves.levy@aphp.fr (Y.L.),
rodolphe.thiebaut@u-bordeaux.fr (R.T.)
https://doi.org/10.1016/j.isci.2022.105715

(iScience 24, 102711; July 23, 2021)

The authors declare that in their original article, there was an error in the calculation of the library size for the normalization of some gene expression data. As a result, several figures, Table S1, and sentences associated with these were incorrect. This has now been corrected, and the discussion and conclusions of this paper remain unchanged. The authors apologize for any confusion caused.
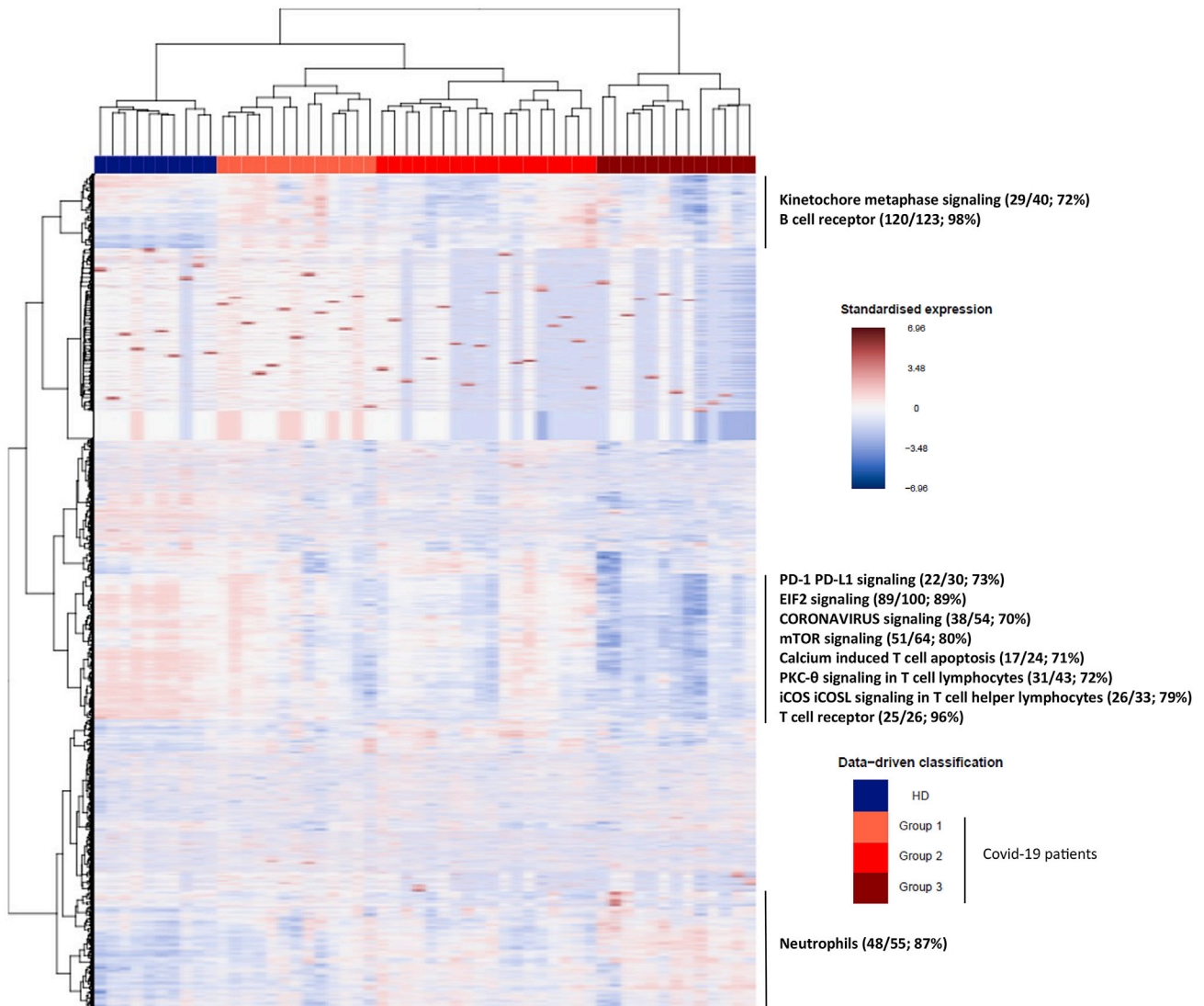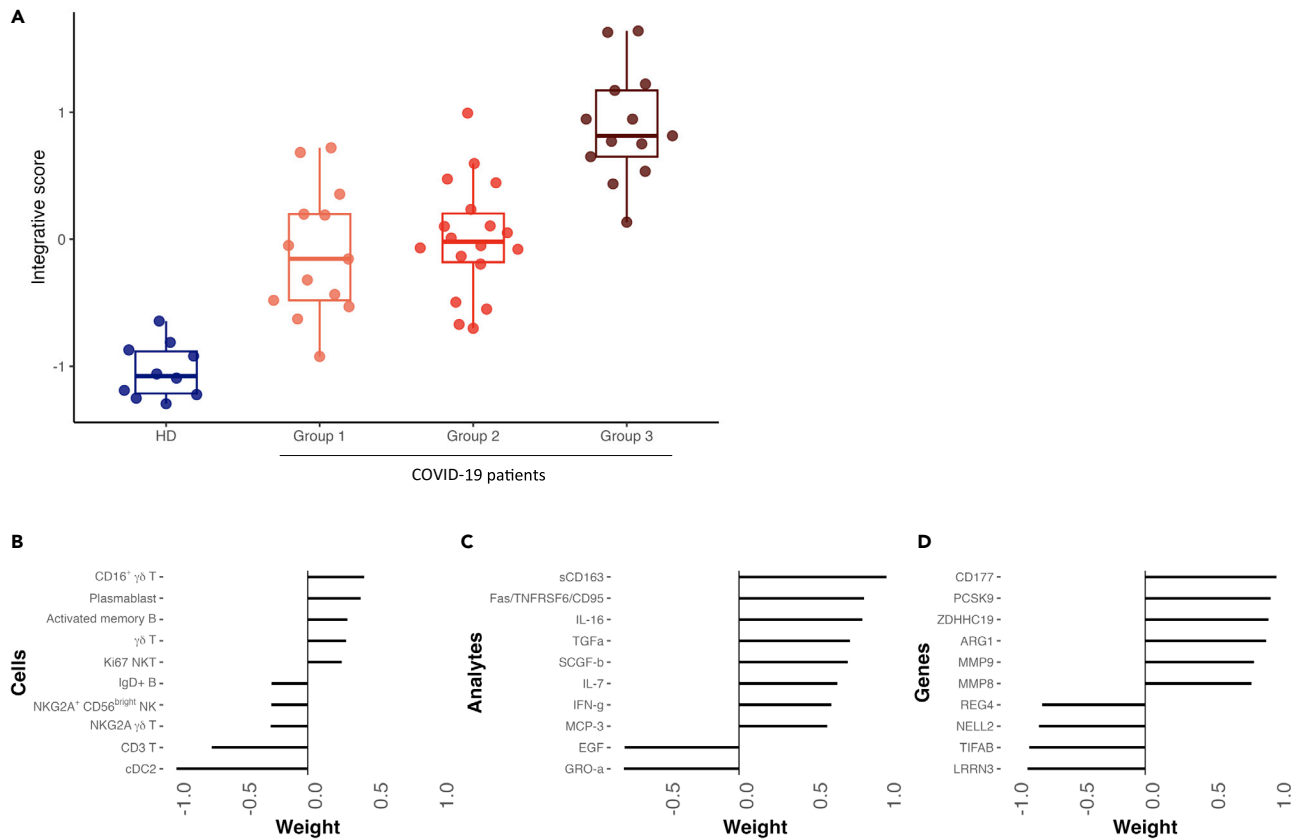
Figure 4. Heatmap of standardized gene expression (corrected)

Figure 5. Integrative analysis of the data of RNA-seq (30,185 genes) from 44 patients with COVID-19, cell phenotype (52 types) from 45 patients with COVID-19, and serum analytes (71 analytes) from 33 patients with COVID-19 using a sparse principal component analysis approach, MOFA v2 (corrected)
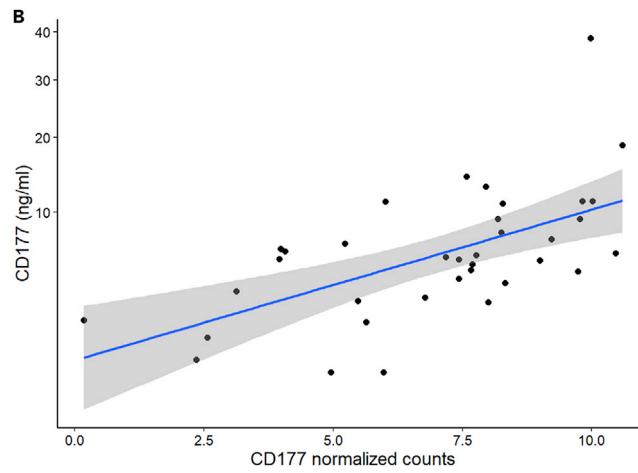
Figure 6B. Distribution of the CD177 marker and association with clinical outcomes of patients with COVID-19 (corrected)
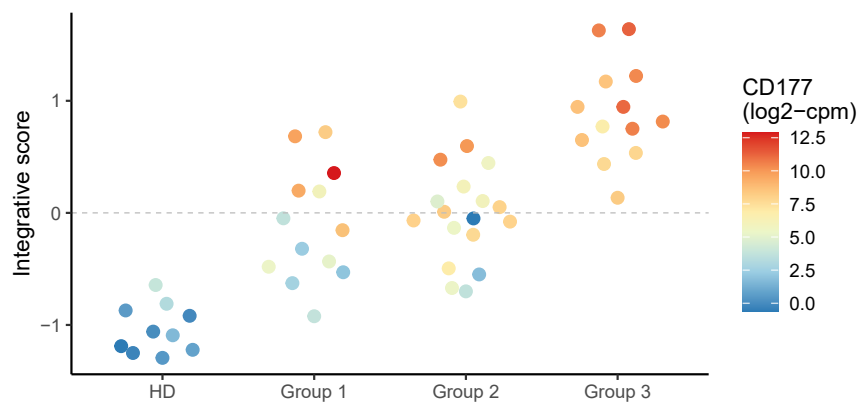

Figure S5. Integrative analysis from COVID-19 patients (corrected)

Document S1. Figures S1–S6 and Tables S1–S3 (corrected)