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Corrigendum: Single-cell transcriptomics reveals the complexity of the tumor microenvironment of treatment-naïve osteosarcoma

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single-cell RNA sequencing, tumor microenvironment, naïve osteosarcoma, heterogeneity, osteolysis

A Corrigendum on

Single-Cell Transcriptomics Reveals the Complexity of the Tumor Microenvironment of Treatment-Naïve Osteosarcoma

By Liu Y, Feng W, Dai Y, Bao M, Yuan Z, He M, Qin Z, Liao S, He J, Huang Q, Yu Z, Zeng Y, Guo B, Huang R, Yang R, Jiang Y, Liao J, Xiao Z, Zhan X, Lin C, Xu J, Ye Y, Ma J, Wei Q and Mo Z (2021) *Front. Oncol.* 11:709210. doi: 10.3389/fonc.2021.709210

In the published article, there was an error in Figure 1D as published. The labels of feature plots in Figure 1D were misleadingly described. The original labels for “osteoblastic OS cells” should switch with “CAFs”, as well as “Osteoclasts” should switch with “Plasmocytes”. The corrected Figure 1D and its caption appear below.

In the published article, there was an error in Figure 1E as published. The label of “Patient 1” in Figure 1E was incorrectly described, which should be changed to “Patient 3”. The corrected Figure 1E and its caption appear below.

In the published article, there was an error in Supplementary Figure 1A as published. The labels of

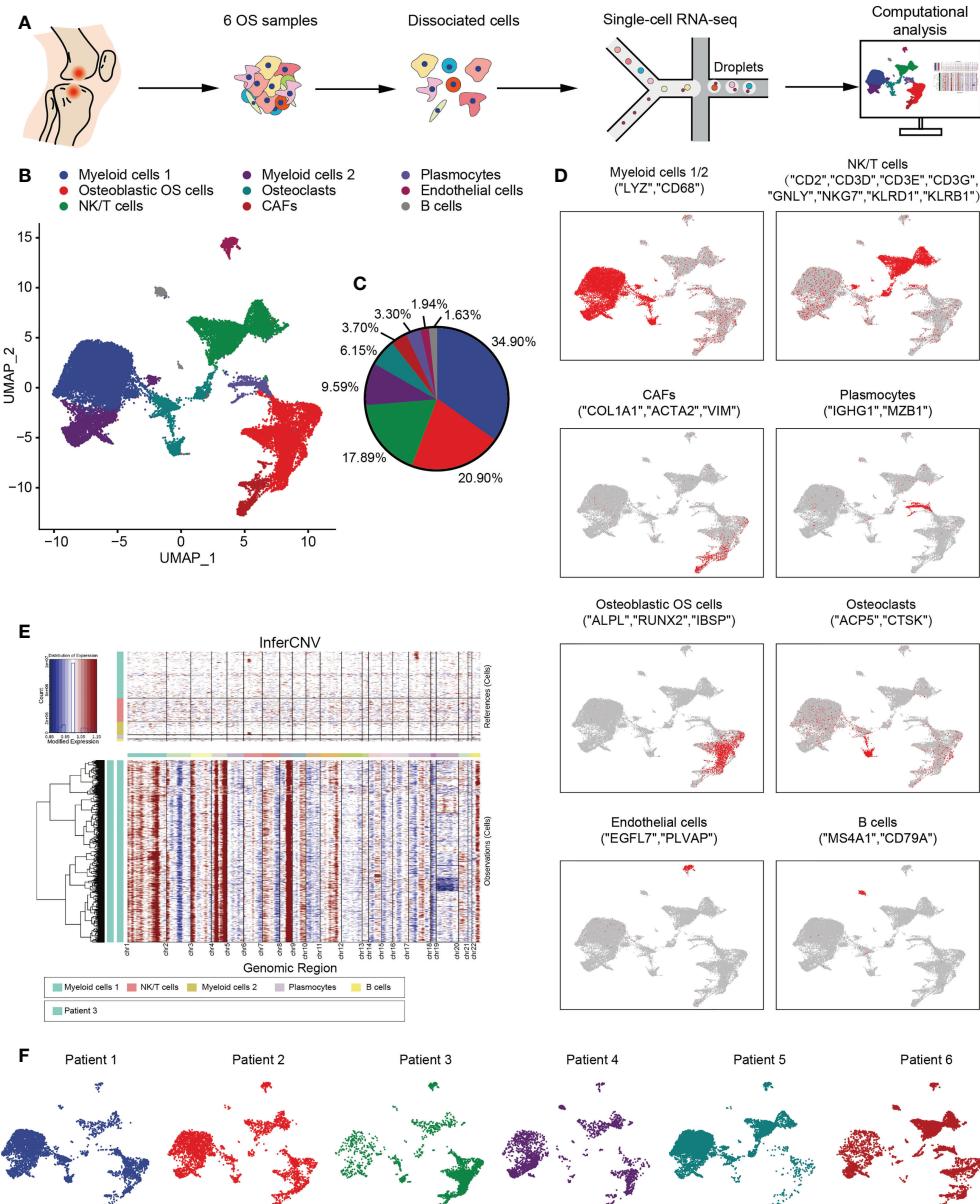


FIGURE 1

Overview of single cells derived from OS tissues. (A) Workflow depicting collection and processing of specimens of OS tumors for scRNA-seq. (B) UMAP plot of all the single cells, with each color-coded for the 9 major cell types. (C) Pie chart, indicating the cell composition of OS. (D) UMAP plots of the normalized marker expression of the 9 major cell types. (E) The large-scale chromosomal landscape in patient 3 was calculated using reference cells (myeloid cells 1/2, NK/T cells, plasmocytes and B cells); the red color represents an increased copy number, whereas the blue color represents a decreased copy number. (F) UMAP plot of all the single cells, with each cell color-coded for different patients. OS, osteosarcoma; UMAP, uniform manifold approximation and projection; scRNA-seq, single-cell RNA sequencing; NK, natural killer.

“Patient 1” in **Supplementary Figure 1A** were incorrectly described. The six “Patient 1” in inferCNV of **Supplementary Figure 1A** should need to be corrected in order.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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