

CORRECTION

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# Correction: Macrophage polarization toward M1 phenotype through NF- $\kappa$ B signaling in patients with Behcet's disease

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Following publication of the original article [1], the authors have identified an error in Figs. 1, 2, 3 and 4. The correct figures are given below.

The original article [1] has been updated.

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The original article can be found online at <https://doi.org/10.1186/s13075-022-02938-z>.

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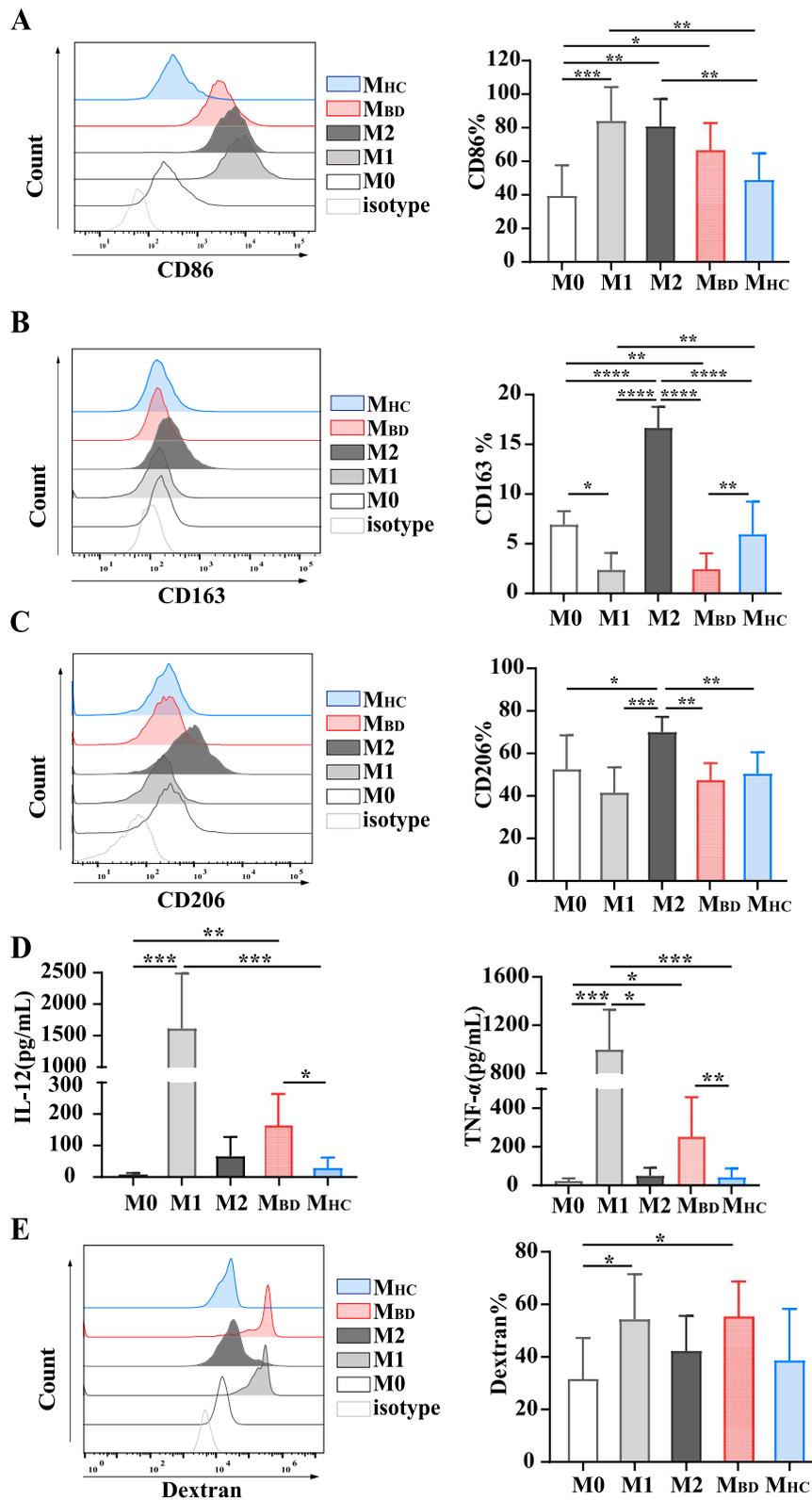
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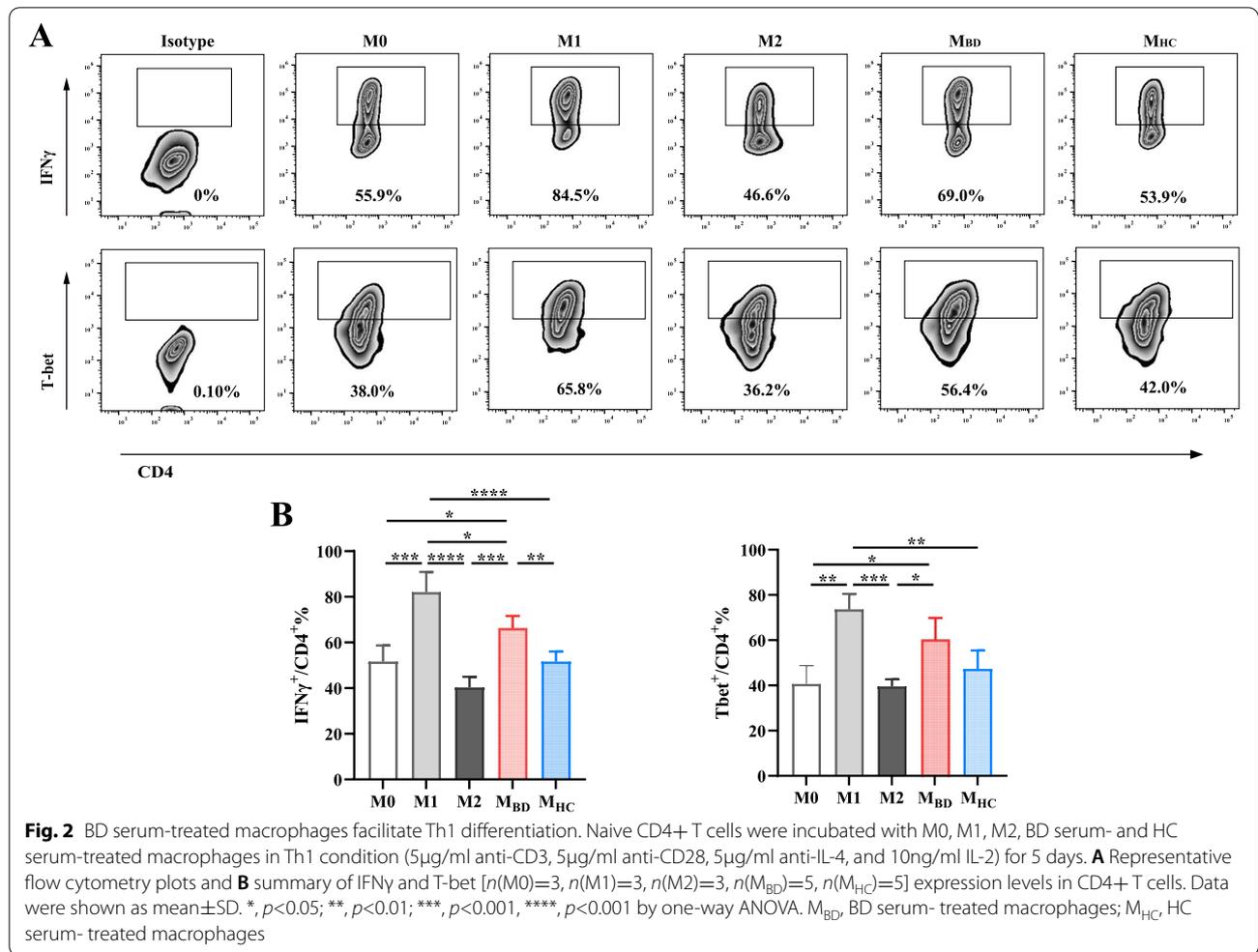
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(See figure on next page.)

**Fig. 1** BD serum promotes M1-like macrophage polarization. Resting macrophages (M0) were stimulated with M1 condition (100ng/ml LPS+ 20ng/ml IFN $\gamma$ ), M2 condition (20ng/ml IL-4+ 20ng/ml IL-13), BD serum or HC serum for 48 h. **A–C** Representative histograms (left) and summary (right) of CD86, CD163 and CD206 expression level of macrophages stimulated with M0 ( $n=6$ ), M1 ( $n=6$ ), and M2 ( $n=6$ ) conditions, as well as BD ( $n=12$ ) serum and HC ( $n=12$ ) serum. Data were expressed as mean $\pm$ SD and were analyzed using one-way ANOVA. **D** IL-12 and TNF- $\alpha$  production by macrophages stimulated with M0 ( $n=6$ ), M1 ( $n=6$ ), and M2 ( $n=6$ ) conditions, as well as BD ( $n=12$ ) serum and HC ( $n=12$ ) serum. Data were expressed as mean $\pm$ SD and were analyzed using Kruskal-Wallis test. **E** Representative histograms (left) and summary (right) of dextran uptake by macrophages stimulated with M0 ( $n=7$ ), M1 ( $n=7$ ), M2 ( $n=7$ ) conditions, and BD ( $n=9$ ) serum and HC ( $n=9$ ) serum. Data were expressed as mean $\pm$ SD and were analyzed using one-way ANOVA. \*,  $p<0.05$ ; \*\*,  $p<0.01$ ; \*\*\*,  $p<0.001$ , \*\*\*\*,  $p<0.001$ . M<sub>BD</sub>, BD serum-treated macrophages; M<sub>HC</sub>, HC serum-treated macrophages

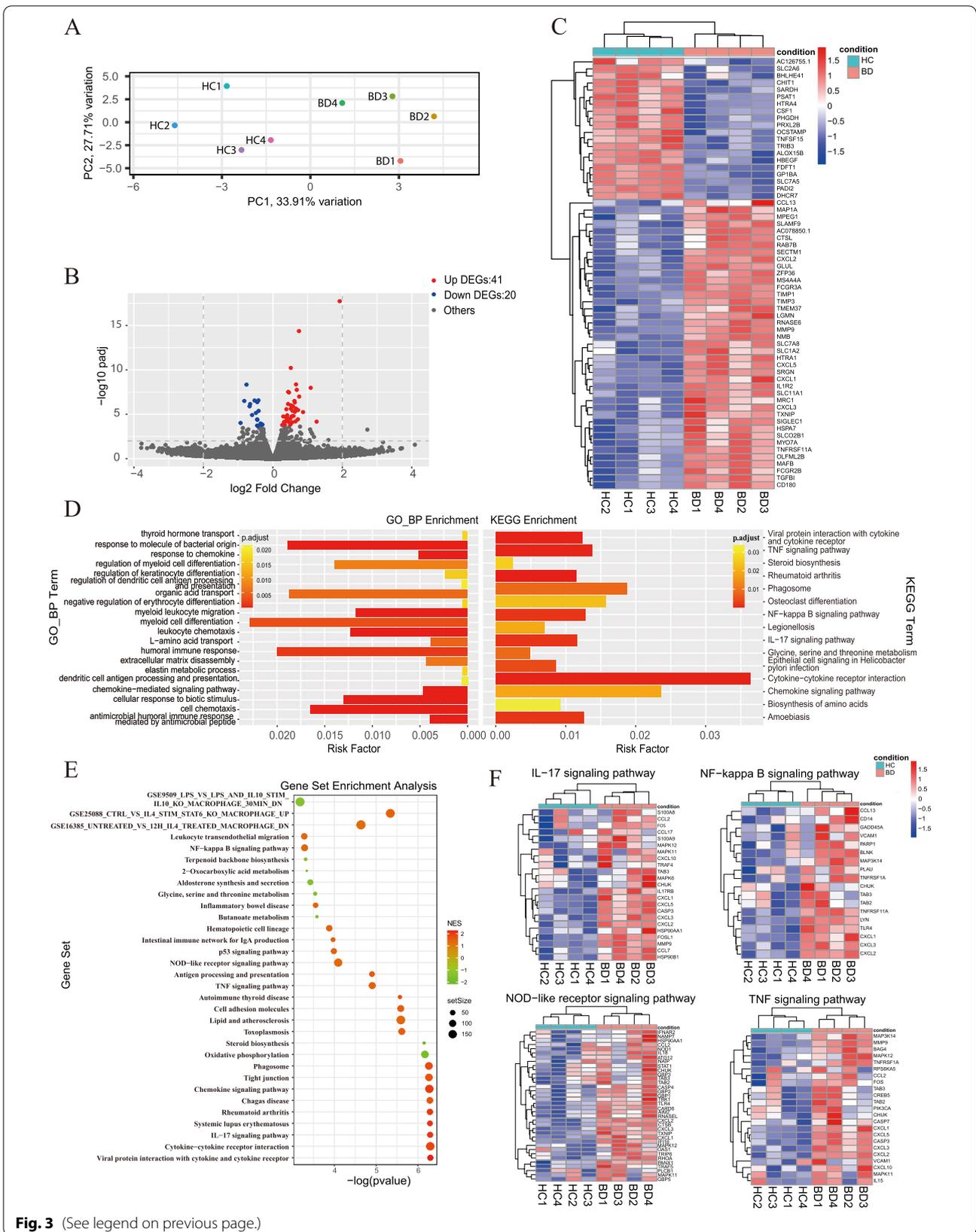


**Fig. 1** (See legend on previous page.)

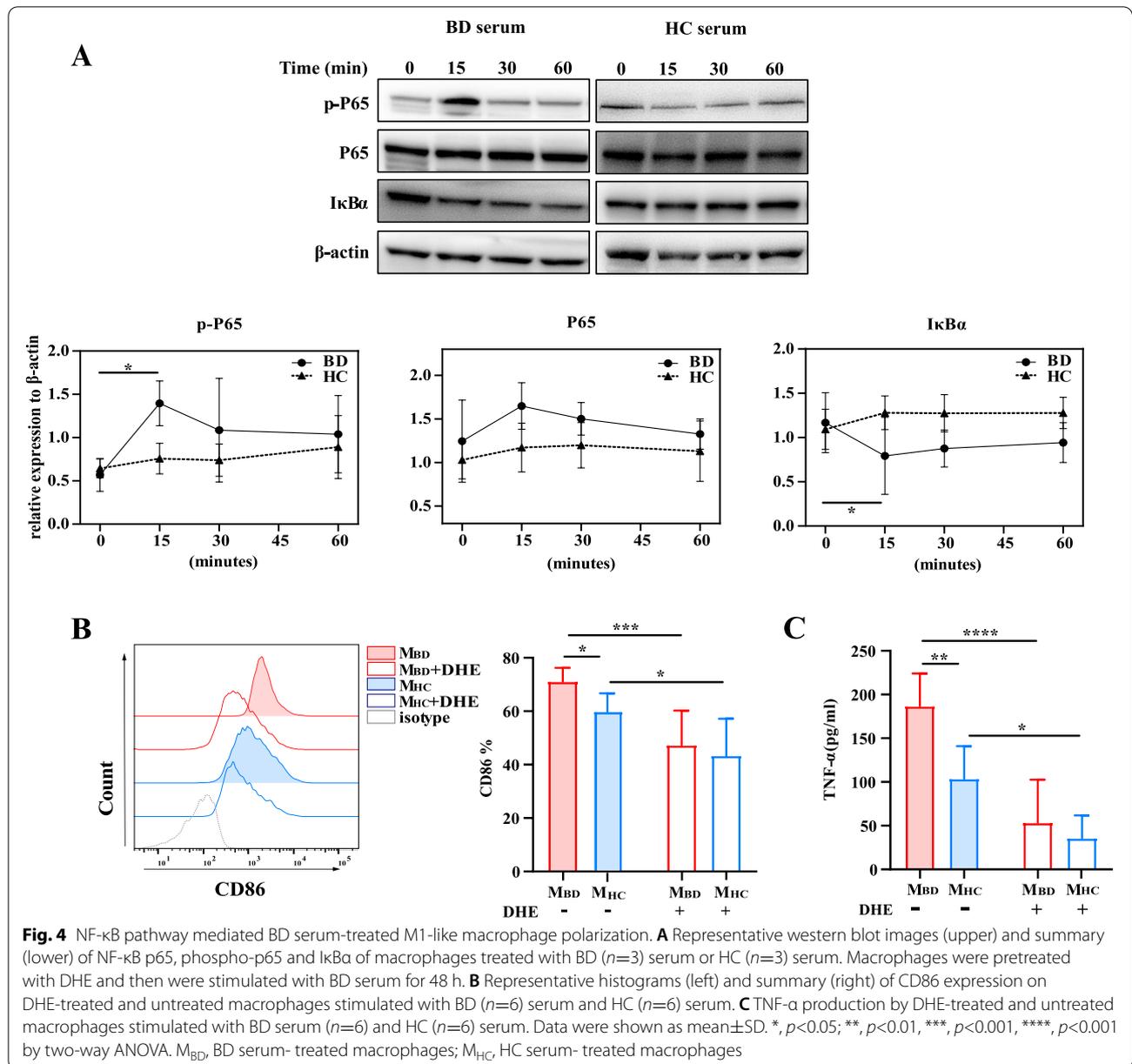


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**Fig. 3** Transcriptome analysis of BD serum- and HC serum-treated macrophages. HMDMs were stimulated with serum from four treatment-naïve active BD patients and matched healthy volunteers for 48 h, and total RNA was extracted for RNA-seq analysis. **A** Principal component analysis (PCA) of BD serum-treated and HC serum-treated macrophages. **B** Volcano plot of upregulated (red, n=41) and downregulated (blue, n=20) DEGs in BD serum-treated macrophages compared with HC serum-treated macrophages. **C** Heatmap of DEGs between BD serum- and HC serum-treated macrophages. **D** GO biological process enrichment analysis and KEGG enrichment analysis between BD serum- and HC serum-treated macrophage. **E, F** Dot plots (left) showed Gene Set Enrichment Analysis (GSEA) of BD serum- and HC serum-treated macrophage. Representative enriched gene sets were illustrated by heatmap (right). DEGs, differentially expressed genes; GO, gene ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes



**Fig. 3** (See legend on previous page.)



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**Reference**

1. Wu X, Wang Z, Shi J, et al. Macrophage polarization toward M1 phenotype through NF-κB signaling in patients with Behçet's disease. *Arthritis Res Ther.* 2022;24:249. <https://doi.org/10.1186/s13075-022-02938-z>.