CORRIGENDUM

doi:10.1038/nature05812

Pluripotency of mesenchymal stem cells derived from adult marrow

Yuehua Jiang, Balkrishna N. Jahagirdar, R. Lee Reinhardt, Robert E. Schwartz, C. Dirk Keene, Xilma R. Ortiz-Gonzalez, Morayma Reyes, Todd Lenvik, Troy Lund, Mark Blackstad, Jingbo Du, Sara Aldrich, Aaron Lisberg, Walter C. Low, David A. Largaespada & Catherine M. Verfaillie

Nature 418, 41–49 (2002); doi:10.1038/nature00870; published online 20 June 2002

In response to questions raised recently about flow cytometry data reported in Fig. 1 of this Article, we had the flow cytometry data for Fig. 1 and the experimental approach used to generate them reviewed by flow cytometry experts.

The flow cytometry data in the original Fig. 1b were found to be flawed in that corresponding IgG isotype control tracings for several of the plots differ by 1 log in fluorescence intensity, even though the same IgG subtype was used. The plots for these antigens (CD19, CD34, Sca-1, Thy-1 and MHC II) in the original Fig. 1b should therefore not be relied upon as an accurate representation of MAPC surface marker profiles. Details of the specific flaws are individually listed as Supplementary Information to this Corrigendum. A corrected version of Fig. 1b is now provided as Fig. 1 below.

The FACS plots in the original Fig. 1b were obtained from the ROSA26 cell line also used for the blastocyst injection studies and the postnatal transplantation in NOD-SCID mice. In Fig. 1 we now provide additional FACS analysis data for these specific antigens from the GFP transduced mouse MAPC line we described in the original Article at population doubling 120 (this line was also used to demonstrate the single-cell origin of endothelium-like, hepatocyte-like and neuroectoderm-like cell differentiation *in vitro*). These data appear not to be subject to the same technical problem. On the basis of this analysis, we have summarized the FACS phenotype of MAPC in Table 1 below. The phenotype of MAPC isolated subsequently and published by our group[1,2] are also not affected by the same flaws in the plots published in the original Article. It should also be noted that

Table 1 | Cell surface characteristics of MAPC

Phenotype	The original Article	This Corrigendum*	References 1 and 2
CD45	NEG	NEG	NEG
CD44	NEG	NEG	NEG
MHC I	NEG† (incorrect plot inserted)	NEG	NEG
MHC II	NEG†,‡	NEG	NEG
Sca-1	NEG/DIM‡	NEG	NEG
Thy-1	DIM‡	DIM	NEG
c-Kit	NEG	NEG	POS
CD34	NEG‡	NEG	NEG
Flk-1	DIM	DIM	Not tested
SSEA-1	DIM/POS	DIM/POS	Not tested
CD3	NEG	NEG	NEG
Mac-1	NEG	NEG	NEG
CD19	NEG‡	NEG	NEG
CD13	POS	POS	Not tested

* Corrections based on data provided in Fig. 1.
† The superscripts 'k' in MHC II (I-A^k) and MHC I (H-$2K^k$) should be 'b'.
‡ Erroneous IgG control stains.
NEG, negative; DIM, minimally positive; POS, positive.

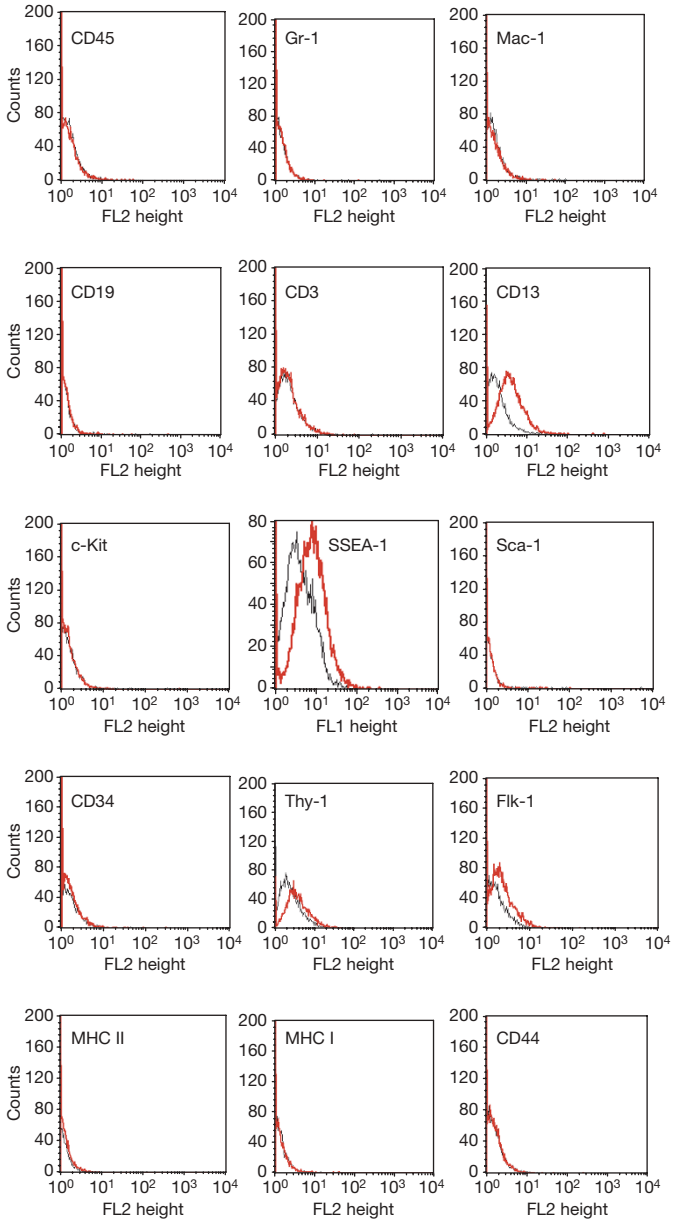

Figure 1 | This is the corrected version of the original Fig. 1b. Single cell derived GFP transduced MAPC were collected after 120 population doublings and stained with a PE-coupled antibody against MHC II (I-A^b) and MHC I (H-$2K^b$) (mIgG2a); CD19, and Sca-1 (rIgG2a); Gr-1, Mac-1, CD3, CD44, CD45, Thy-1 and c-Kit (rIgG2b); CD13 (rIgG1); or with an unconjugated IgG2a antibody directed at CD34 or Flk-1 followed by a secondary PE-coupled antibody. For each sample an individual tube of cells was stained with a control IgG antibody of the correct IgG subtype either directly coupled to PE, or followed by a secondary PE-coupled antibody. All antibodies were from Becton Dickinson. For SSEA-1, ROSA26 mouse-derived MAPC were collected after 120 population doublings and stained with an unconjugated anti-SSEA-1 antibody (mIgM, obtained from Iowa Hybridoma Bank) followed by a FITC-coupled secondary antibody. Cells were analysed using a FACScan (Becton Dickinson). Black line, isotype control; red line, specific antibody stain.

©2007 Nature Publishing Group

in the original Fig. 1b, the plot for MHC I was a duplication of the FACS plot for Mac-1, although the correct FACS plot acquisition data for MHC I was presented in the original Supplementary Fig. 1 of the original Article.

Although problems with these specific FACS plots (as published in Fig. 1) undermine their utility as markers of the MAPC surface phenotype, the specific errors in these FACS plots do not alter the conclusions of the Article. Nevertheless, we wish to inform other scientists of the problems with these published FACS profiles, and provide an accurate representation of the phenotype of MAPC we described.

We submitted some minor corrections to *Nature* in 2002, but owing to administrative errors by the authors and *Nature* these were not seen through to publication. The three changes requested are as follows.

(1) In the legend to Fig. 1b, the superscripts 'k' in MHC II (I-A^k) and MHC I (H- $2K^k$) should be 'b'.

(2) In the Methods under 'Differentiation culture and analysis', the concentration of 10^9 M dexamethasone should be 0.05 μM.

(3) In the Supplementary Information, the sequence of the primers rex-1 and oct-4 should correctly read as follows. Mrexa: aag cgt ttc ctg gat ttc; Mrexb: ttt gcg tgg gtt agg atg tg; Moct4a: gaa gcc gac aac aat gag aac; Moct4b: aca gaa cca tac tcg aac cac a.

1. Serafini, M, *et al.* Long-term lymphohematopoietic reconstitution from nonhematopoietic cells. *J. Exp. Med.* **129–139,** 129–139 (2007).
2. Breyer, A, *et al.* Multipotent adult progenitor cell (MAPC) isolation and culture procedures. *Exp. Hematol.* **34,** 1596–1601 (2006).

Supplementary Information is linked to the online version of this Corrigendum at www.nature.com/nature.

©2007 Nature Publishing Group