Correction: Direct Comparison of Dll1- and Dll4-Mediated Notch Activation Levels Shows Differential Lymphomyeloid Lineage Commitment Outcomes

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Corrections


In Materials and Methods, under the heading \textit{OP9-DL1(lo/med/hi) and OP9-DL4(lo/med/hi) cells}, in both the penultimate sentence and the last sentence, “GP” and E86” and “GP and E86” should be “GP+E86”. In addition, under the heading \textit{Western blot analysis}, in the first sentence, “0.5% doxycycline” should be “0.5% Na deoxycholate”.

In Results, under the heading \textit{Generation of OP9 cells expressing different levels of Dll1 and Dll4}, in the fourth sentence of the first paragraph, “GPF” should be “GFP”. In the fifth sentence of the third paragraph, “immunobloted” should be “immunoblotted”.

In Figs. 3C, 5A, and 5C, the labels for the immunoblots and flow cytometry plots were mistakenly duplicated as OP9-DL1. The labels on the left are correct as “OP9-DL1”, but the labels on the right should be “OP9-DL4”. The results and the conclusions in the article remain unchanged. The corrected figures are shown below. The published figure legends are correct but are shown below for reference.

The online version of this article has been corrected and now differs from the print version as originally published.

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{figure3.png}
\caption{Generation of OP9 cells expressing discrete and comparable levels of Dll1 and Dll4. A, OP9 cells were retrovirally transduced and then sorted based on different levels of GFP fluorescence. Flow cytometric analysis for GFP expression is shown for OP9-DL1 (lo/med/hi) or OP9-DL4 (lo/med/hi), parental OP9 cells (OP9), and the originally described OP9-DL1 (Ori) and OP9-DL4 (Ori) cells. B, Flow cytometric analysis is shown for cell surface expression of Dll1 and Dll4 on OP9-DL1 (lo/med/hi), OP9-DL4 (lo/med/hi), and parental OP9 cells. C, Immunoblot analysis of OP9-DL1 (lo/med/hi), OP9-DL4 (lo/med/hi), parental OP9 cells, E16 total thymus, and purified TEC samples probed for the expression Dll4 and β-tubulin. Blots were stripped and reprobed for HA-tagged Dll1 and Dll4 expression. Anti-β-tubulin Ab was used to detect equal loading per lane for the immunoblot. The blot shown is representative of four independent experiments. D, Flow cytometric analysis is shown for E16 TECs and OP9-DL4 (med) cells for Dll4 and Dll1 (TEC only) expression, with cells not stained with primary Ab shown as Ctrl.}
\end{figure}
FIGURE 5. Different levels of Dll1 and Dll4 expressed on OP9 cells support the generation of diverse cell fates from HPCs. A, Flow cytometric analysis for the expression of CD19 at days 6 and 9 of coculture, with different OP9 cell lines, as indicated. B, The average percentage of CD19⁺ cells present at days 6 and 9 of cocultures with the indicated OP9 cell lines is shown from three independent experiments (error bars represent SEM; lo [l], med [m], hi [h], OP9-DL1 [DL1], OP9-DL4 [DL4]). C, Flow cytometric analysis for the expression of CD11b at days 6 and 9 of coculture, with different OP9 cell lines, as indicated (top two rows). Bottom row shows cells from OP9, OP9-DL1med, and OP9-DL4med cocultures that were electronically gated as CD11b⁻ or CD11b⁺ (dashed lines within histogram) and further analyzed for the expression of CD45R (B220) and CD11c as indicated by dashed arrows. D, The average percentage of CD11b⁺ cells present at days 6 and 9 of cocultures with the indicated OP9 cell lines is shown from three independent experiments (error bars represent SEM; lo [l], med [m], hi [h], OP9-DL1 [DL1], OP9-DL4 [DL4]). E, The average total cellularity of pDCs (CD11b⁻ CD11c⁺ CD45R⁻) measured at day 9 of cocultures with the indicated OP9 cell lines is shown from three independent experiments (error bars represent SEM).