Errata

Hirpara JL, Seyed MA, Loh KW, Dong H, Kini RM, Pervaiz S. Induction of mitochondrial permeability transition and cytochrome C release in the absence of caspase activation is insufficient for effective apoptosis in human leukemia cells. *Blood*. 2000;95(5):1773-1780.

On page 1777 in the 1 March 2000 issue, there is an error in the Figure 2 legend. The legend omits the final sentence, which should read, "The mitochondrial swelling measurements were done concomitantly with 2 other drugs, namely C1 and C2, and therefore the upper 2 control panels are the same as in Figure 6A of Ref. 19." On page 1777, Figure 3B includes incorrect flow histograms. On page 1778, Figure 5B includes an incorrect blot. The interpretation of the data and the message in the figures remain unchanged. The corrected Figures 3B and 5B are shown.

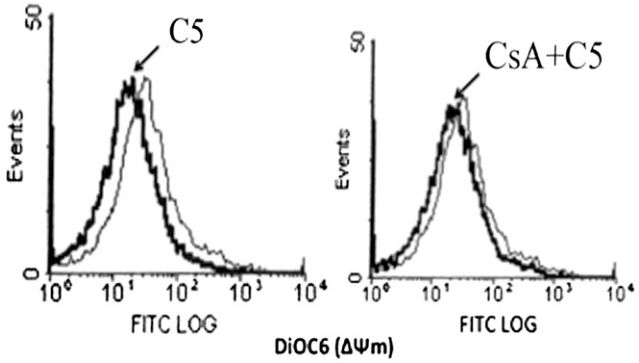

Figure 3. C5-triggered Cyt C release and drop in mitochondrial $\Delta\Psi_m$ is dependent on opening of the MPT pore. (A) 0.5 mg purified rat liver mitochondria was exposed to 150 μg/mL C5 in the presence or absence of CsA (10 μmol/L) for 30 minutes at 30°C. Mitochondria were then pelleted, and supernatants were subjected to SDS-PAGE and western blot analysis for Cyt C, as described in Materials and methods. (B) Mitochondria were treated with C5 in the presence or absence of CsA as above and stained with membrane potential–sensitive dye $DiOC_6$ (40 nmol/L) at 37°C for 30 minutes, washed, and analyzed by flow cytometry for $\Delta\Psi_m$.

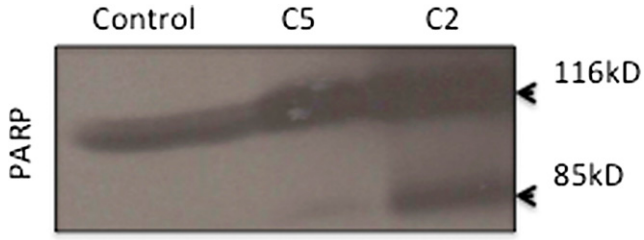

Figure 5. C5 does not activate caspase 8, 2, or 9. (A) HL60 cells were treated with 150 μg/mL C5 or 100 μg/mL C2 for 12 hours, and lysates were analyzed for caspase 8, 2, or 9 activation by fluorometric assays designed to detect cleavage of the AFC-conjugated specific substrate (IETD-AFC for caspase 8, VDVAD-AFC for caspase 2, and LEHD-AFC for caspase 9), as described in Materials and methods. Caspase activity is expressed as fold increase (*x* increase) over the activity obtained in untreated cells, shown here as 1 X. (B) Lysates obtained from C5- and C2-treated HL60 cells were also analyzed by SDS-PAGE and western blotting for cleavage of PARP (85-kd fragment) using a monoclonal anti-PARP antibody.

Kanduri M, Cahill N, Göransson H, et al. Differential genome-wide array-based methylation profiles in prognostic subsets of chronic lymphocytic leukemia. *Blood*. 2010;115(2):296-305.

On page 298 in the 14 January 2010 issue, the average difference in methylation index (MI) value applied between the immunoglobulin heavy-chain variable (IGHV) mutated and IGHV unmutated subgroups, 0.45, is incorrect. The correct MI value is 0.40. In "Methods," the last sentence under the heading "Methylation array analysis" reads, "Consequently, an average difference in MI of 0.45 between the IGHV mutated and IGHV unmutated subgroups, 0.35 between the IGHV3-21 and IGHV mutated subgroups, and 0.35 between IGHV3-21 and IGHV unmutated subgroups was applied." The sentence should have read, "Consequently, an average difference in MI of 0.40 between the IGHV mutated and IGHV unmutated subgroups, 0.35 between the IGHV3-21 and IGHV mutated subgroups, and 0.35 between IGHV3-21 and IGHV unmutated subgroups was applied."

Furthermore, the number of genes identified as significantly differentially methylated between IGHV mutated and unmutated chronic lymphocytic leukemia (CLL) as well as the number of genes identified in the comparison between IGHV unmutated versus IGHV3-21 CLL and IGHV mutated versus IGHV3-21 CLL, respectively, are incorrect. The correct total number of genes identified as significantly differentially methylated between IGHV mutated and unmutated CLL is 96; the correct numbers of genes identified in the comparison between IGHV unmutated versus IGHV3-21 CLL and IGHV mutated versus IGHV3-21 CLL are 59 and 51, respectively. In "Results," the fourth and fifth sentences under the heading "Methylation profiling of different prognostic subgroups of CLL" read, "Using highly stringent selection criteria (as detailed in "Methylation array analysis"), a total of 64 genes were identified as significantly differentially methylated between IGHV mutated and unmutated CLL (Figure 2A). Similarly, 60 and 31 genes were identified in the comparison between IGHV unmutated versus IGHV3-21 CLL and IGHV mutated versus IGHV3-21 CLL, respectively (Figure 2B-C)." The sentences should have read, "Using highly stringent selection criteria (as detailed in "Methylation array analysis"), a total of 96 genes (99 CpG sites) were identified as significantly differentially methylated between IGHV mutated and unmutated CLL (Figure 2A). Similarly, 59 genes (61 CpG sites) and 51 genes (52 CpG sites) were identified in the comparison between IGHV unmutated versus IGHV3-21 CLL and IGHV mutated versus IGHV3-21 CLL, respectively (Figure 2B-C)."