

Erratum

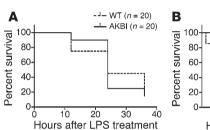
$I\kappa B\alpha$ and $I\kappa B\beta$ possess injury context-specific functions that uniquely influence hepatic NF- κB induction and inflammation

Chenguang Fan, Qiang Li, Yulong Zhang, Xiaoming Liu, Meihui Luo, Duane Abbott, Weihong Zhou, and John F. Engelhardt

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Citation for this erratum: J. Clin. Invest. 115:477 (2005). doi:10.1172/JCI200517337E1.

During preparation of this manuscript for publication, an error was introduced into Figure 5B. The correct figure appears below. We regret this error.



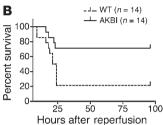


Figure 5

AKBI mice have improved survival following I/R injury. AKBI or WT littermates either (**A**) received a lethal dose of LPS (4 μ g/g body weight, i.v.) or (**B**) underwent partial lobar liver I/R. Survival was assessed for 14 days. Only times of survival are given for which deaths occurred. No deaths occurred past the plotted times. Survival curves were significantly different between AKBI and WT mice (P < 0.05) as assessed using the log-rank test.

Erratum

Folate pathway gene expression differs in subtypes of acute lymphoblastic leukemia and influences methotrexate pharmacodynamics

Leo Kager, Meyling Cheok, Wenjian Yang, Gianluigi Zaza, Qing Cheng, John C. Panetta, Ching-Hon Pui, James R. Downing, Mary V. Relling, and William E. Evans

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During preparation of this manuscript for publication, errors were introduced into the abstract and introduction. The second sentence of the abstract incorrectly included the phrase "fewer than." The sentence should read:

"We measured in vivo MTXPG accumulation in leukemia cells from 101 children with acute lymphoblastic leukemia (ALL) and established that B-lineage ALL with either *TEL-AML1* or *E2A-PBX1* gene fusion, or T-lineage ALL, accumulates significantly lower MTXPG compared with B-lineage ALL without these genetic abnormalities or compared with hyperdiploid (greater than 50 chromosomes) ALL."

The third sentence of the introduction also incorrectly stated "fewer than." This sentence should read:

"Subtypes with a relatively unfavorable prognosis on many treatment protocols include T-lineage ALL (T-ALL) and ALL with rearranged *MLL* genes or with *BCR-ABL* gene fusion, whereas ALL with either *TEL-AML1* or *E2A-PBX1* gene fusions, or hyperdiploid karyotypes (greater than 50 chromosomes), have a relatively good prognosis with most treatment protocols . . ."

We regret these errors.