

Correction

High Incidence of Amplifications in Pancreatic Cancer

In the article on high incidence of amplifications in pancreatic cancer the July 1, 2004 issue of *Cancer Research* (1), there is an error in the symbol key to Figure 3B. The corrected figure appears below.

- Holzmann K, Kohlhammer H, Schwaenen C, Wessendorf S, Kestler HA, Schwoerer A, Rau B, Radlwimmer B, Döhner H, Lichter P, Gress T, Bentz M. Genomic DNA-chip hybridization reveals a higher incidence of genomic amplifications in pancreatic cancer than conventional comparative genomic hybridization and leads to the identification of novel candidate genes. *Cancer Res* 2004;64:4428–33.

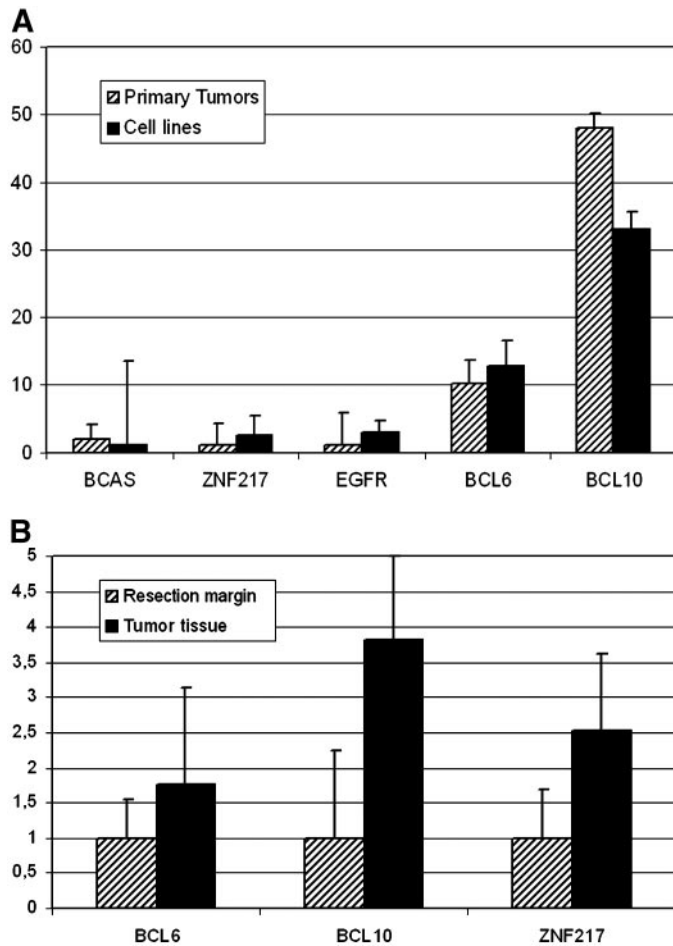


Fig. 3. *A*, mean relative expression levels for selected genes in eight pancreatic cancer cell lines and four primary tumor samples. Note the similar expression levels in cell lines and tumor samples. The *error bars* indicate 1 SD. *B*, mean relative expression levels for *BCL6*, *BCL10*, and *ZNF217* in three primary tumor tissues compared with three nontumorous pancreatic tissues obtained from resection margins. The *error bars* indicate 1 SD.