Correction. In the article "Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure of a glycoprotein immunologically crossreactive with carcinoembryonic antigen" by Yuji Hinoda, Michael Neumaier, Stanley A. Hefta, Zofia Drzeniek, Christoph Wagener, Louise Shively, Laura J. F. Hefta, John E. Shively, and Raymond J. Paxton, which appeared in number 18, September 1988, of *Proc. Natl. Acad. Sci. USA* (**85**, 6959–6963), the authors request that the following corrections be noted. In Fig. 2, the nucleotide at position 1401 should be changed from C to AG. In addition, we have determined that the final 350 nucleotides of the 3′ untranslated region—i.e., nucleotides 1540–1889—is an artificially fused gene fragment corresponding to nucleotides 13197–13538 of the human mitochondrial genome plus 8 unrelated nucleotides. By isolating two new cDNA clones from this region, we determined the correct sequence for nucleotides 1541–2116. A corrected version of Fig. 2 is shown below. Due to these changes, the size of the predicted cytoplasmic domain of biliary glycoprotein I increased from 35 to 74 amino acids, and a potential glycosylation site at residue 441 was revealed. Furthermore, the results in Figs. 3*B* and 4, which were obtained by hybridizing RNAs and DNA to a probe from the incorrect 3′ untranslated region, should be corrected as follows. Hybridization of a probe corresponding to nucleotides 1605–2000 of the correct 3′ untranslated region to RNAs from colon cancer cell line HT29 and lung cancer cell line Calu3 revealed a single 3.9-kilobase (kb) message. This message was also observed when the hybridization was performed with a 159-bp coding region probe from A′ domain. This 3.9-kb message corresponds to the 4.1-kb message previously identified by hybridization of the 159-bp coding region probe to normal human liver RNA (Fig. 3*A*, lane 4). Hybridization of this new 3′ untranslated probe to genomic DNA digested with four different restriction enzymes revealed single bands in each case. The sizes of these bands were 9.1 kb for *Bam*HI, 4.7 kb for *Eco*RI, 8.3 kb for *Hin*dIII, and 3.7 kb for *Xba* I.

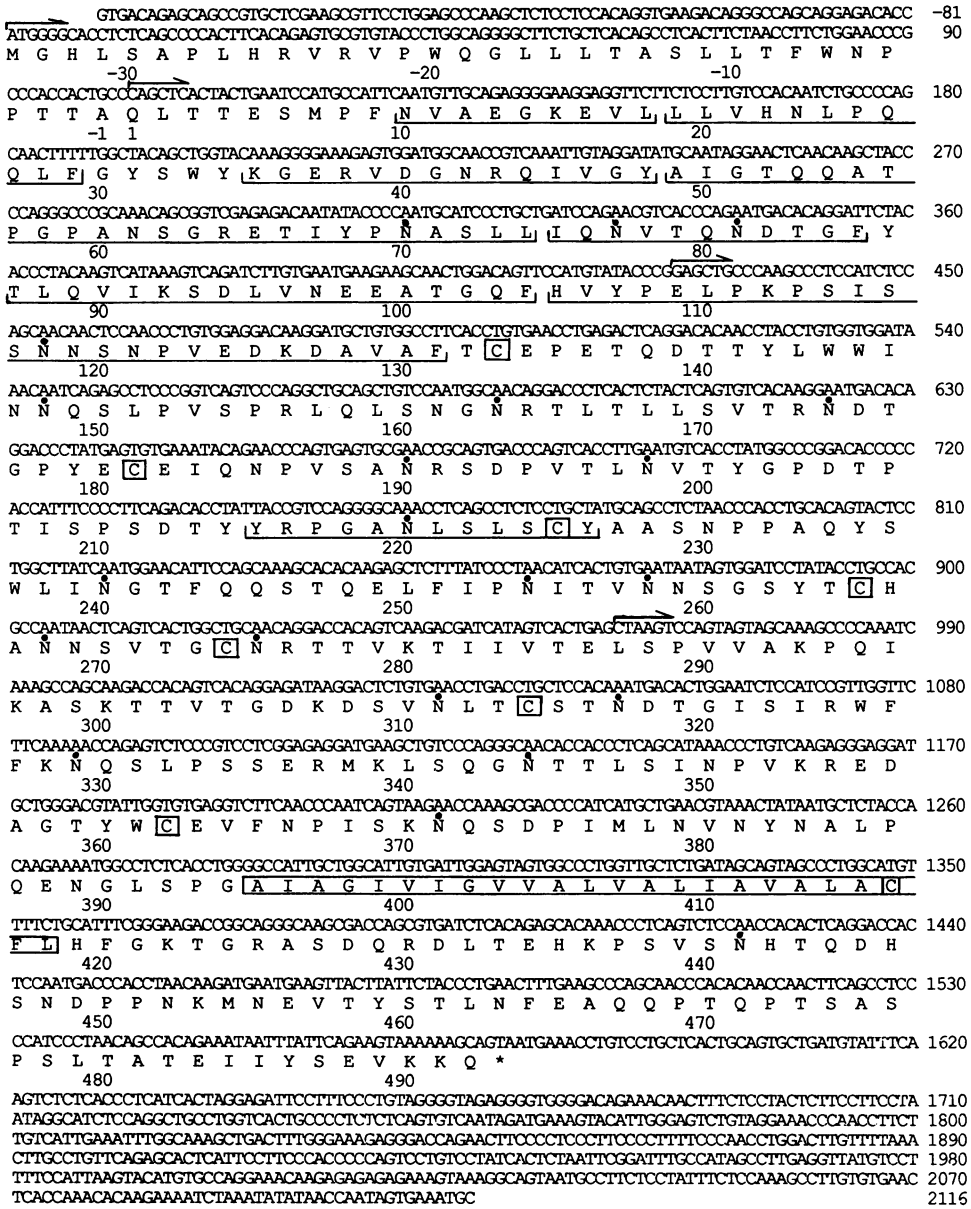

FIG. 2. Nucleotide and deduced amino acid sequence of the BGP I cDNA. The open reading frame begins at nucleotide 1 and contains a leader peptide region (102 bp), an N-terminal domain (324 bp), an immunoglobulin-like domain (534 bp) consisting of two subdomains A and B, a BGP I-specific domain (324 bp) (domain A′), a membrane-spanning domain (72 bp), and a cytoplasmic domain (222 bp). The lengths of 5′ and 3′ untranslated regions are 81 and 538 bp, respectively. The boundaries of the domains are represented by the arrows. The amino acid sequences underlined show chymotryptic peptides that were analyzed. Cysteine residues and potential asparagine glycosylation sites are indicated by boxed letters and dots, respectively. The membrane-spanning domain is boxed.