Erratum

Sequence, Organization, and Evolution of Rh50 Glycoprotein Genes in Nonhuman Primates

Cheng-Han Huang,¹ Zhi Liu,¹ Pol-André Aupois,² Antoine Blancher²

¹ Laboratory of Biochemistry and Molecular Genetics, Lindsley F. Kimball Research Institute, New York Blood Center, New York, NY 10021, USA

² Laboratoire d'Immunogénétique Moléculaire, Université Paul Sabatier, Pavillon Charles Lefebvre, Hôpital Purpan, Toulouse, France

Re: J Mol Evol (2000) 51:76–87. Due to a production error, an incorrect version of Fig. 3A (missing the bottom three lines) appeared in this article (p. 79). The corrected Fig. 3, along with its caption, is shown on page 304.

Fig. 3. Deduced amino acid sequences and variability index of Rh50 homologs. **A** Rh50 sequences of nonhuman primates (AF177621 to 177626 and AF132980) are aligned to the human and mouse counterparts. *Dashes* denote deletions and *dots* identical amino acids. In *Cebus apella* (capuchin monkey), *question marks* denote polymorphic positions or unknown amino acids at the N- and C-termini. **B** Hydrophilic-

ity and membrane topology between humans and nonhuman primate Rh50. Hydroplicity of human Rh50 is calculated in Kyte and Doolittle scale. The variability index was based on the sequences shown in **A**. The 12-TM topology of human Rh50 is shown. The *gray line* denotes the middle point of either exo- and endloops. Exon limits are those of human *RHAG* gene.