Errata

Over-inking during the printing of the December 1994 issue of the Journal produced unsatisfactory resolution in the following figures: figure 1 of the article by Whaley et al. (the figure was published on page 1094); figure 4 of the article by Kobayashi et al. (the figure was published on page 1107); and figure 2 of the article by Weber et al. (the figure was published on page 1184); all of these figures are reprinted below. The printer apologizes for this error.

Reprinted Figure 1 of the Article by Whaley et al.

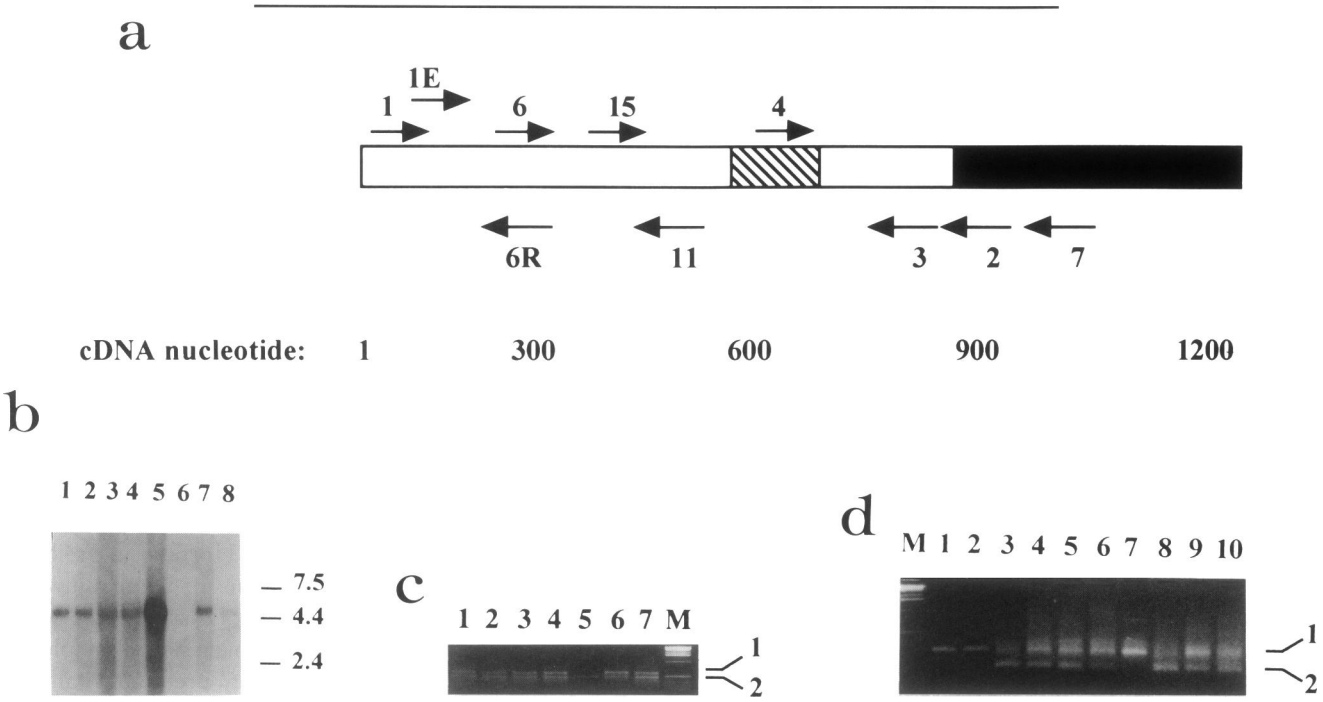

Figure 1 Expression of the VHL gene in normal tissues and in RCC cell lines. *a*, Schematic drawing of the first 1,200 nt of the published partial VHL cDNA and the location of the primers used in RT-PCR. Nt 1–855 represent the open reading frame of the published sequence. The blackened region indicates the 3′ untranslated region, and the hatched region indicates the region corresponding to the alternatively spliced cassette exon 2. *b*, Human multitissue northern blot (2 μg poly-A RNA/lane) hybridized with a RT-PCR product spanning nt 624–954 of the published human VHL cDNA sequence (see Material and Methods). Size markers in kilobases are indicated on the right of the panel. The origins of the tissues are as follows: lane 1, pancreas; lane 2, kidney; lane 3, skeletal muscle; lane 4, liver; lane 5, lung; lane 6, placenta; lane 7, brain; lane 8, heart. *c*, RT-PCR analysis of human VHL mRNA derived from normal tissues. Total RNA was primed with primer 7 and PCR-amplified with primers 6 and 2 in two 30-cycle rounds of amplification. The origins of the tissues are as follows: lane 1, kidney; lane 2, adrenal gland; lane 3, retina; lane 4, pancreas; lane 5, bladder; lane 6, lung; lane 7, cerebellum; lane M, marker lane (1-kb ladder; Gibco/BRL). Band 1 = 622 bp; band 2 = 499 bp. *d*, RT-PCR analysis of VHL mRNA derived from eight sporadic RCC cell lines and normal kidney. RNA was primed and amplified as in *b*, except that the second round of PCR amplification was done with primers 15 and 3. The cell lines are as follows: lane 1, A-498; lane 2, A-704; lane 3, Caki-1; lane 4, Caki-2; lane 5, ACHN; lane 6, 786-O; lane 7, 769-P; lane 8, HS 758T; lanes 9 and 10, normal kidney; lane M, marker lane, as in *b*. Band 1 = 307 bp; band 2 = 184 bp.

Reprinted Figure 4 of the Article by Kobayashi et al.

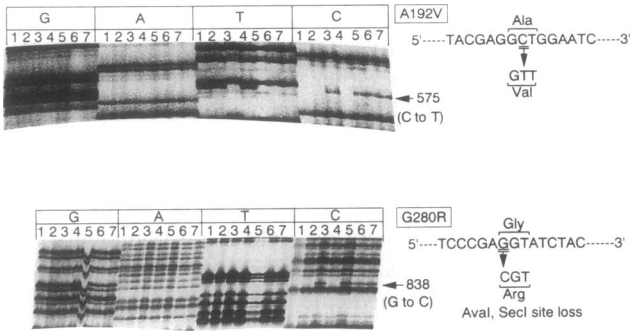

Figure 4 Sequence analysis identifying two different missense mutations in patient N10. Cloning and sequencing were performed for seven clones from patient N10. Counting from the left for each nucleotide, lanes 1, 2, and 4 demonstrate a C-to-T transition at nucleotide 575 (resulting in the A192V mutation), while lanes 3 and 5–7 demonstrate a G-to-C change at nucleotide 838 (resulting in the G280R mutation).