ERRATA

In the May 2005 issue of the *Journal,* in the article entitled "A Novel *STX16* Deletion in Autosomal Dominant Pseudohypoparathyroidism Type Ib Redefines the Boundaries of a *cis*-Acting Imprinting Control Element of *GNAS*" by Linglart et al. (76:804–814), sequences of primers E and F were given incorrectly in table 1; however, the position of the 5′ end of each primer with respect to AL139349 was indicated correctly (nucleotides 4938 and 5190, respectively). The correct sequences are (for E) 5′-GGGAGGGCACCAAGATAGTT-3′ and (for F) 5′-GCCAGCAGAGGAAGTGTTTC-3′. The authors regret the error.

In the May 2007 issue of the *Journal,* in the article entitled "Hypomorphic Mutations in the Gene Encoding a Key Fanconi Anemia Protein, FANCD2, Sustain a Significant Group of FA-D2 Patients with Severe Phenotype" by Kalb et al. (80:895–910), there were errors in the text and in table 3.

On page 897, in the "Retroviral Complementation" section, the text should read "In addition, cDNAs of the enhanced green fluorescent protein (*GFP*) and *FANCA* genes were separately cloned into the vector S11IN…." On page 900, in the "Mutations Affecting Pre-mRNA Splicing" section, "splec" should be "splice." On page 905, in the "Residual FANCD2 Protein" section, "(data not shown)" should be "(fig. 8*B,* right panel)." Therefore, in figure 8, the description of panel B should be "*B*, Blood-derived cells from nonmosaic FA-D2 patients (exemplified 13, 5, 1, 21, 2, 6, 11, and 28) and fibroblasts from mosaic FA-D2 patients (exemplified 3, 14, and 26) show faint but conspicuous FANCD2 bands of both species in response to MMC exposure exclusively on overexposed immunoblots, as indicated by the very intense FANCD2 signals of the normal control LCLs (CON) (patient 13, stimulated PBL; patients 5, 1, 21, 2, 6, 11, and 28, LCLs; patients 3, 14, 26, cultured fibroblasts; loading control, RAD50)." In the figure 6 legend, two reference numbers were incorrect. The sentence should be "Mutations identified in the present study are shown above, mutations reported elsewhere[26,27] are indicated below the schematic display of FANCD2 cDNA."

The revised table 3 contains seven superamplicons that were actually used in the study. Their numbering corresponds to their order shown in figure 4*C*. The table has been modified accordingly.

The authors and the *Journal* regret these errors.

Table 3. *FANCD2* Superamplicon Primers

		Forward		Reverse		PCR Product
Superamplicon	Containing Exons	Designation	Sequence (5′→3′)	Designation	Sequence (5′→3′)	Size (bp)
I	1 and 2	hFANCD2_exon1_F	TATGCCCGGCTAGCACAGAA	hFANCD2_super_7_15_R	GGCCCACAGTTTCCGTTTCT	4,346
II	10, 11, 12, 13, 14, and 15	hFANCD2_exon10_F	GCCCAGCTCTGTTCAAACCA	hFANCD2_super_7_15_R	TTAAGACCCAGCGAGGTATTC	5,635
III	13, 14, 15, 16, and 17	hFANCD2_super_13_17_F	CATGGCAGGAACTCCGATCTTG	hFANCD2_super_13_17_R	CTCCCTTAAAAGCTCAAAGCTCAAGTTC	8,858
IV	19 and 20	hFANCD2_super_19_22_F	ACGTAATCACCCCTGTAATCC	hFANCD2_exon20_R	TGACAGAGCGAGACTCTCTAA	2,749
V	21, 22, and 23	hFANCD2_21_23_F	GCTTCTAGTCACTGTCAGTTCACCAG	hFANCD2_21_23_R	ACGTTGGCCAGAAAGTAATCTCAG	2,518
VI	22, 23, 24, 25, and 26	hFANCD2_super_22_29_F	GGCCTTGTGCTAAGTGCTTTT	hFANCD2_exon26_R	TCAGGGATATTGGCCTGAGAT	3,252
VII	27, 28, and 29	hFANCD2_exon27_F	GCATTCAGCCATGCTTGGTAA	hFANCD2_super_22_29_R	CACTGCAAACTGCTCACTCAA	3,371