Errata

In the July 2002 issue of the *Journal,* in the review article "Splitting p63," by van Bokhoven and Brunner (71:1–13), there were inconsistencies in the annotation of mutations, because of the use of different template sequences. According to the reference sequence reported by Yang et al. (Mol Cell 2:305–316, 1998; GenBank accession number AF075430), the following corrections should be introduced in table 2 and figure 3: 1689InsA should be 1572InsA, 1693-1694DelTT should be 1576-1577DelTT, 1859DelC should be 1742DelC, 1860-1861DelAA should be 1743-1744DelAA, L518F should be L514F, L518V should be L514V, C526W should be C522W, C526G should be C522G, G534V should be G530V, T537P should be T533P, Q540L should be Q536L, and I541T should be I537T. The authors regret these errors and apologize for any confusion.

In the January 2003 issue of the *Journal,* in the article entitled "Distribution Patterns of Postmortem Damage in Human Mitochondrial DNA," by Gilbert et al. (72: 32–47), an incorrect version of table 4, "Standardized Mutation and Damage Rates" (p. 41), was submitted by the authors. The table contained errors in the standardized mutation rates estimated from the two data sets published elsewhere (Excoffier and Yang 1999; Meyer et al. 1999). The corrected table is presented here. As a result, the paragraph containing the sentences

> Of the 30 sites that can be compared for postmortem-damage and in vivo mutation rates, 15 show very similar rates, and only 6 (sites 16110, 16144, 16148, 16204, 16242, and 16325) completely disagree (i.e., are not observed to mutate in vivo but experience fast postmortem damage). Of these six, at least three have mutation-rate estimates, in the two modern studies, that also disagree, and this may relate to sampling stochasticity or the standardization approach. If so, further sampling may provide evidence for elevated mutation rates at these sites.

should have read

> Of the 34 sites that can be compared for postmortem-damage and in vivo mutation rates, 6 show very similar rates in all three studies, 23 show similar rates in this and at least one of the other studies, and only 7 (sites 16129, 16172, 16189, 16192, 16293, 16309, and 16362) completely disagree (i.e., are not observed to mutate in vivo but experience fast postmortem damage, or vice versa). However, at least 11 sites from the two modern studies also disagree with each other. Thus, these findings may relate to sampling stochasticity or the standardization approach. If so, further sampling may provide more-accurate estimates of mutation rates at these sites.

The authors regret this error and would like to thank Dr. Peter Forster for drawing their attention to this mistake.

Table 4

Standardized Mutation and Damage Rates

HVR1 Base Position	E99	M99	TG03
16093	4	3	4
16126	0	4	3
16129[a]	4	4	1
16148	0	3	1
16163	2	3	3
16172[a]	4	3	1
16182	4	0	1
16183	4	3	2
16187	0	3	1
16189[a]	4	4	1
16192[a]	4	3	1
16209	4	0	1
16219	0	3	1
16223	4	4	4
16230	0	4	1
16234	3	0	2
16265	4	2	1
16270	4	3	4
16274	0	3	2
16278	4	4	2
16290	2	2	3
16291	4	2	1
16293[a]	4	4	1
16294	4	4	2
16298	0	2	4
16304	4	0	1
16309[a]	4	4	1
16311	4	4	2
16319	0	3	2
16320	3	2	1
16327	0	2	3
16343	3	2	1
16355	3	2	2
16362[a]	4	4	1

NOTE.— Site-specific in vivo mutation rates taken from two previous studies (Excoffier and Yang 1999 [E99]; Meyer et al. 1999 [M99]) were standardized into quartiles and were compared with the standardized postmortem-damage rates from the present study (TG03).

[a] Seven sites where major disagreement is observed between rates of occurrence of modern mutations and ancient damage.

In the October 2002 issue of the *Journal,* in the article "Functional Analysis of *RUNX2* Mutations in Japanese Patients with Cleidocranial Dysplasia Demonstrates Novel Genotype-Phenotype Correlations," by Yoshida et al. (71:724–738), the reference cited as "Yoshida et al., in press" should be supplemented with two related references: Kundu et al. (2002) and Miller et al. (2002). ("Yoshida et al., in press" was cited at two places in the text, the last line in the first paragraph of p. 725 and the last line in the second paragraph of p. 735.) The updated full data of these three references are as follows:

Kundu M, Javed A, Jeon JP, Horner A, Shum L, Eckhaus M, Muenke M, Lian JB, Yang Y, Nuckolls GH, Stein GS, Liu PP (2002) Cbfβ interacts with Runx2 and has a critical role in bone development. Nat Genet 32:639–644

Miller J, Horner A, Stacy T, Lowrey C, Lian JB, Stein GS, Nuckolls GH, Speck NA (2002) The core-binding factor β subunit is required for bone formation and hematopoietic maturation. Nat Genet 32:645–649

Yoshida CA, Furuichi T, Fujita T, Fukuyama R, Kanatani N, Kobayashi S, Satake M, Takada K, Komori T (2002) Core-binding factor β interacts with Runx2 and is required for skeletal development. Nat Genet 32:633–638