Errata

In the paper entitled "Feedback Control of Mitosis in Budding Yeast" by Li and Murray (Cell *66*, 519–531, 1991), we previously reported the sequence of a gene that we believed complemented the budding yeast *mad2-1* mutation that inactivates the spindle assembly checkpoint. Further analysis has shown that the reported gene, which encodes the β subunit of a geranylgeranyl transferase (Li et al., Nature *366*, 82–84, 1993; Jiang et al., Nature *366*, 84–86, 1993), is not *MAD2* but the gene adjacent to the bona fide *MAD2* gene. The geranylgeranyl transferase–encoding gene has been renamed *BET4* since one of the other subunits of the geranylgeranyl transferase is the product of the previously identified *BET2* gene. The newly identified *MAD2* gene (GenBank accession number U14132) lacks homology to known genes and encodes an 196 amino acid open reading frame upstream of and divergently transcribed from *BET4*. The *mad2-1* mutation is a G to A change that converts Trp-94 to a stop codon, and disruption of the *MAD2* gene produces a phenotype identical to that of *mad2-1*. In addition, we have discovered two errors in the previously reported *BET4* sequence: in the upstream sequence, there is an additional T between positions 71 and 72, and within the coding sequence, position 799 is a C rather than an A, changing Pro-131 to Thr (all numbers refer to Figure 7A of our original paper). We apologize for our mistake and deeply regret any inconvenience it has caused.

The paper entitled "Mxi1, a Protein That Specifically Interacts with Max to Bind Myc–Max Recognition Sites" by Zervos et al. (Cell *72*, 223–232, 1993) reported the sequence of cDNA from HeLa cells encoding the human Max-interacting protein Mxi1. Careful examination of the original data and resequencing of a GC-rich stretch near the 5′ end of the coding sequence revealed two errors in the reported sequence. The correct sequence differs from the published sequence at two positions: at 294, where a CG is replaced by GGC, and at 891–892, where TA is deleted. The errors affect both the amino and carboxyl termini of the predicted protein. The correct Mxi1 protein sequence is 228 rather than 220 residues; compared with the published sequence, it lacks 28 amino acids at the carboxyl terminus but contains 36 new residues at the amino terminus. The corrected Mxi1 sequence contains at its extreme amino terminus another stretch of amino acids with similarity to the Max-interacting protein Mad (Ayer et al., Cell *72*, 211–222, 1993). Moreover, at least one commercially available anti-Mxi1 antiserum was raised against a peptide that matches the published carboxyl terminus and is unlikely to recognize Mxi1. A corrected version of Figure 3c of Zervos et al., which aligns Mxi1 and Mad, is shown below. The authors are mortified by these errors and apologize for the inconvenience they have caused. The corrected Mxi1 sequence has been deposited in GenBank (accession number L07648).