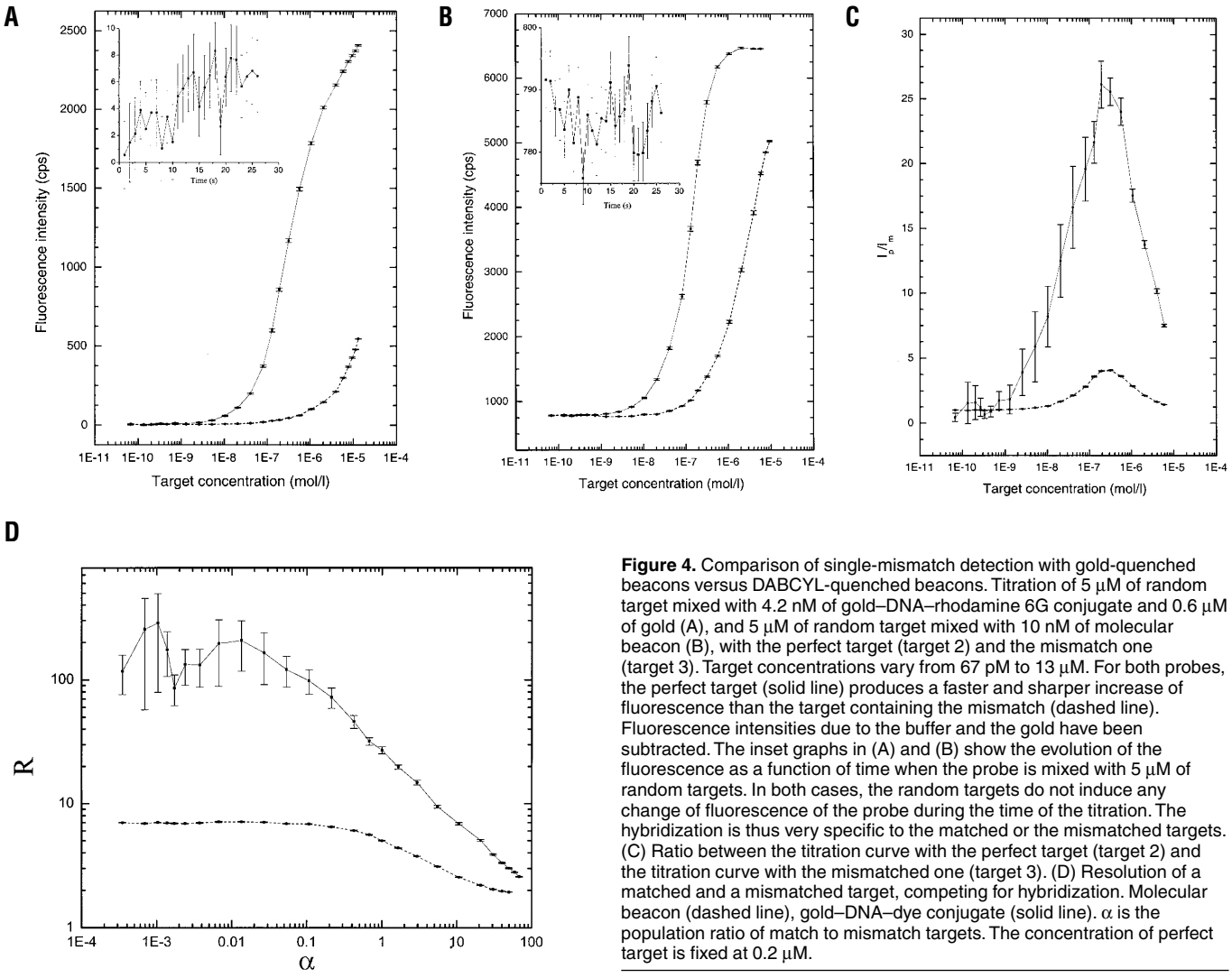

Figure 4. Comparison of single-mismatch detection with gold-quenched beacons versus DABCYL-quenched beacons. Titration of 5 μM of random target mixed with 4.2 nM of gold–DNA–rhodamine 6G conjugate and 0.6 μM of gold (A), and 5 μM of random target mixed with 10 nM of molecular beacon (B), with the perfect target (target 2) and the mismatch one (target 3). Target concentrations vary from 67 pM to 13 μM. For both probes, the perfect target (solid line) produces a faster and sharper increase of fluorescence than the target containing the mismatch (dashed line). Fluorescence intensities due to the buffer and the gold have been subtracted. The inset graphs in (A) and (B) show the evolution of the fluorescence as a function of time when the probe is mixed with 5 μM of random targets. In both cases, the random targets do not induce any change of fluorescence of the probe during the time of the titration. The hybridization is thus very specific to the matched or the mismatched targets. (C) Ratio between the titration curve with the perfect target (target 2) and the titration curve with the mismatched one (target 3). (D) Resolution of a matched and a mismatched target, competing for hybridization. Molecular beacon (dashed line), gold–DNA–dye conjugate (solid line). α is the population ratio of match to mismatch targets. The concentration of perfect target is fixed at 0.2 μM.

Research Corrigenda

An antisense-based functional genomics approach for identification of genes critical for growth of *Candida albicans*

Marianne D. De Backer, Bart Nelissen, Marc Logghe, Jasmine Viaene, Inge Loonen, Sandy Vandoninck, Ronald de Hoogt, Sylviane Dewaele, Fermin A. Simons, Peter Verhasselt, Greet Vanhoof, Roland Contreras, and Walter H.M.L. Luyten
Nat. Biotechnol. **19**, 235–241 (2001).

The URL given for sequence information on the *Candida albicans* genome is incorrect. The correct URL is as follows:
http://www-sequence.stanford.edu/group/candida/
The authors regret the error.

Rapid discrimination among individual DNA hairpin molecules at single-nucleotide resolution using an ion channel

Wenonah Vercoutere, Stephen Winters-Hilt, Hugh Olsen, David Deamer, David Haussler, and Mark Akeson
Nat. Biotechnol. **19**, 248–252 (2001).

The URL given for the DNA mfold server in Table 1 (p. 249) and in the text (p. 251) is incorrect. The correct URL is
http://bioinfo.math.rpi.edu/~mfold/dna/form1.cgi
The authors regret the error.