Erratum

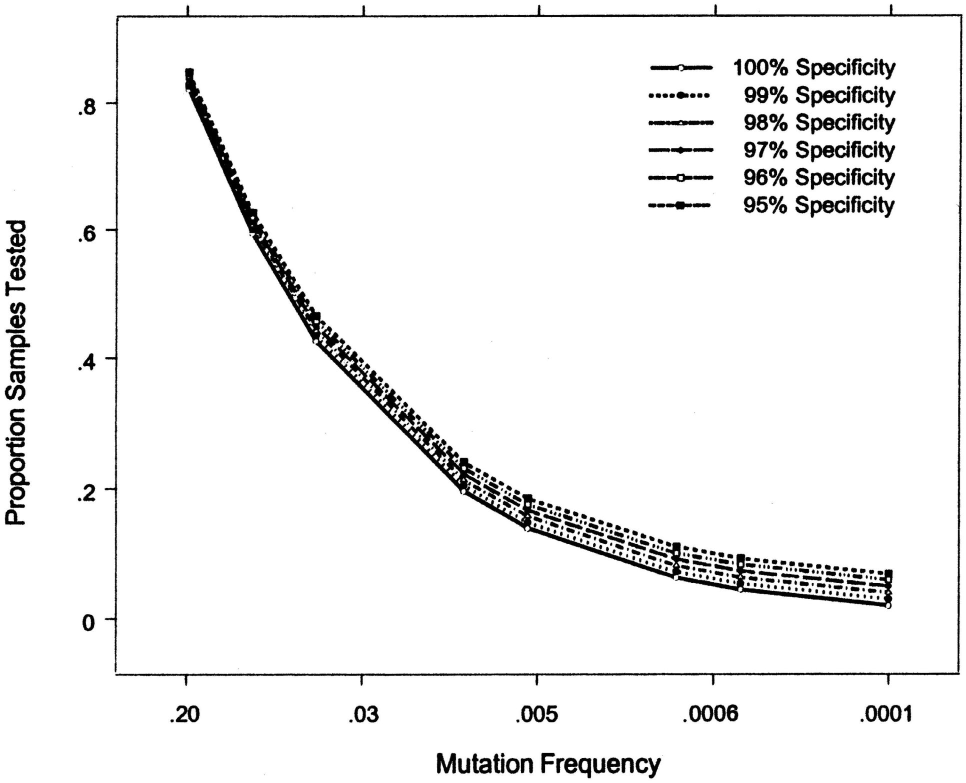

Figure 1 Proportion of tests required when pooled samples are used, with varying specificity of the test

In the May 2000 issue of the *Journal,* in the report "DNA Pooling in Mutation Analysis with Reference to Sequence Analysis," by Amos et al. (66:1689–1692), there was an error in the calculations, which affects both the table and figure 1 of that report. The number of mutations that are detected in pools is $n\gamma/r$ (not $n\gamma$ as reported on the third line from the bottom in the first column of page 1690). As a result, r cancels from all of the right-hand terms for y; for example, the first expression for y, on page 1690, becomes $y = \frac{n}{r} + n\gamma$. The actual proportions of samples under the corrected formulas are smaller than we had reported. The corrected proportions are given both in table 2 of the letter by Gastwirth (2000), which appears in this issue of the *Journal,* and below, in a revised version of figure 1 of our original report. The authors regret this error.