Erratum

Zimprich et al., the authors of "The PARK8 Locus in Autosomal Dominant Parkinsonism: Confirmation of Linkage and Further Delineation of the Disease-Containing Interval" (74:11–19) in the January 2004 issue of the *Journal,* have now identified errors in the data used in the allele scoring of markers D12S291 and D12S1663 for some individuals of families A and D. On the basis of the original allele calling, the 1-LOD support interval had been set between genomic clones AC025253 (56.3 cM, 44.5 Mb) and D12S1701 (59.70 cM/47.7 Mb). Analysis of the corrected data increases that interval to 8 cM (13.4 Mb) between markers D12S345 (50.67 cM/32.2 Mb) and D12S85 (58.42 cM/45.6 Mb). Both family A ($P < .04$) and family D ($P < .007$) remain significant for linkage in that region. For a revised plot of the affected-only LOD score in families A and D (calculated using SIMWALK2 v2.83), see the revised figure 3. The authors apologize for these errors.

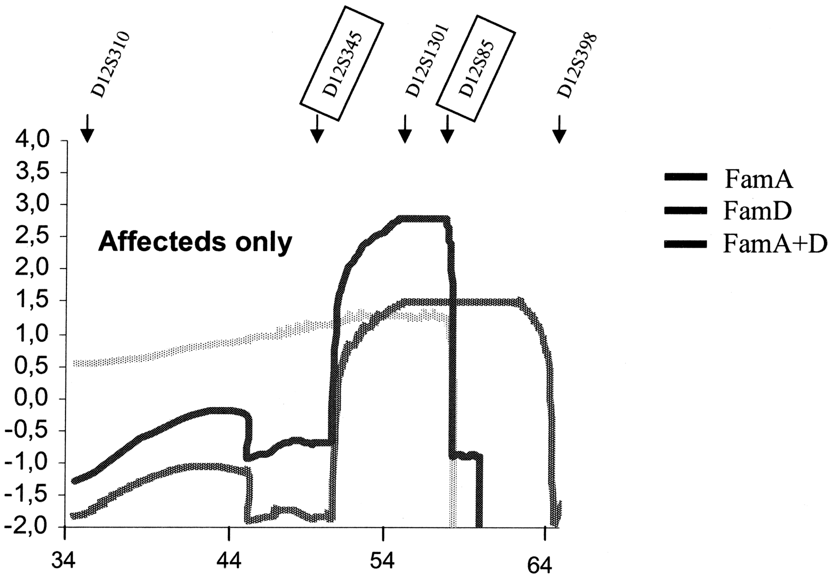

Figure 3 Multipoint LOD score plots for families A and D. The *X*-axis represents location in centimorgans, and the *Y*-axis represents LOD scores. LOD scores are shown for family A, family D, and both families combined (A+D).