Errata

In the December 2000 issue of the *Journal,* in the article "Ascertainment Adjustment: Where Does It Take Us?" (67:1505–1514), by Burton et al., there is an error in the WinBUGS code used to generate two of the estimates in Example 2, on page 1510. The relevant code was not part of the paper. The code that generated these particular estimates failed to properly incorporate information from the fifth member of each cluster in the ascertainment adjustment. This coding error affects no other results reported in the article and makes no substantive difference to the its conclusions; however, for anyone trying to replicate the original analysis by using the correct code, the reported estimates, $\tilde{\alpha} = -2.39$ (standard error [SE] 0.12) and $\tilde{\sigma}_C^2 = 2.45$ (SE 0.36), should be replaced by $\tilde{\alpha} = -2.15$ (SE 0.11) and $\tilde{\sigma}_C^2 = 1.98$ (SE 0.32). Both the incorrect and correct versions of the code are available from the corresponding author (Dr. Paul Burton), on request. The authors apologize for this error.

In the August 2001 issue of the *Journal,* in the report "A Genomewide Screen for Autism Susceptibility Loci" by Liu et al. (69:327–340), a grant acknowledgment was omitted. The following sentence should be included in the Acknowledgments section: "Support by National Institute for Mental Health grant MH44292 (to J.O.) is gratefully acknowledged." The authors regret this omission.

In the July 2001 issue of the *Journal,* in the article "High-Resolution Multipoint Linkage-Disequilibrium Mapping in the Context of a Human Genome Sequence" (69: 159–178), by Rannala and Reeve, the haplotype frequencies shown in table 2 are incorrect. All analyses were performed with the correct data, and the description of table 2 in the text refers to the correct version, which is provided below. The authors apologize for this error.

Table 2

Frequency of Marker Haplotypes on Disease Chromosomes

No. of Copies	*Eco*RI	TAGA	*Sty*I	CA	CCTT
	Haplotype[a]				
79	0	0	0	0	0
31	0	0	0	0	1
18	0	0	0	1	1
5	0	0	0	1	0
5	1	1	1	1	0
4	0	1	0	0	0
2	0	1	0	0	1
1	1	1	1	0	1
1	1	1	1	1	1
1	1	0	1	0	1
1	1	0	0	0	0
	P_0[b]				
	.088	.361	.256	.161	.049

NOTE.—Data are those reported by Hästbacka et al. (1992) and include unpublished frequencies provided to the authors by J. Hästbacka.

[a] Only the putative ancestral (represented by 0) and derived (represented by 1) alleles are shown.

[b] Frequency of ancestral allele at each locus in the sample of normal individuals.