General comments

This revision is much better. Sections 1.1–1.2 of the supplement, which I criticized in previous reviews, are now beautifully clear.

I'm willing to recommend this manuscript without modification, but I want to raise one issue (mentioned first in my first review), in case the authors would prefer to address it. On p. 1 of the supplement, the authors write

$$p(O_{mnc}|a_y) = \begin{cases} 1 - \epsilon_{mnc} & \text{if } O_{mnc} = a_y \\ \frac{\epsilon_{mnc}}{3} & \text{otherwise} \end{cases}$$

I finally understand what this equation means, and I think it would be correct were it not for the fact that the method excludes nucleotide sites at which the sample contains more than two alleles. After conditioning on this fact, I think the "3" in the denominator will disappear. (If the observed allele is not the true one, there is only one alternative—not three.)

As I said above, I am happy to recommend this paper as it stands. The numerical results demonstrate that the method compares favorably with competitors, especially when coverage is low. This suggests that the issue just raised has no large effect. On the other hand, addressing it might improve the method.

Minor comments

- 100: Should state that F is the frequency **of the genotype**.
- page 1 of Supplement: In the definitions of a_i and O_{mnc}, the authors should state what "0" and "1" represent. Is "0" the reference allele and "1" the alternate?