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Melo *et al.* reply:

We are satisfied to learn that the presence of *TARBP2* mutations in human primary colorectal tumors within the context of putative hereditary non-polyposis colorectal cancer (HNPCC) cases that we initially reported in 2009[1] has been confirmed in the correspondence by Garre *et al.*[2]. The difference between their findings and our initial observation was the frequency of this event. In Garre *et al.*[2], the authors used a technique based on fragment length differences that we do not consider acceptable to detect a 1-nucleotide change in a pool of normal contaminating material that biases against the amplification and detection of a longer allele. We recommend the cloning and sequencing of 12 PCR products from each sample, as we did, to accurately detect the presence of the mutant allele in each case. Interestingly enough, reanalysis of their data excluding HNPCC cases in which bona fide germline mutations in mismatch repair genes were not identified ($n = 27$) doubles the incidence of *TARBP2* mutations.

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