In this Letter, we reported the detection and replication of epistatic interactions between common single nucleotide polymorphisms (SNPs) that influence gene expression in peripheral blood, including both cis–cis and cis–trans interactions. We applied a statistical method widely used to detect epistasis. Wood et al. (2014) replicated these findings statistically in an additional whole-genome sequencing dataset but found that a large fraction of these epistatic effects could be explained by tagging sequence variants that were not genotyped in our study. They suggested that the interactions arose owing to haplotypes that tag single additive variants. In our response [BN1], we argued that such a mechanism could not explain cis–trans interactions. We have since undertaken further analyses to try to understand the mechanism that gives rise to cis–trans associations (Hemani et al. 2020). We find that in the presence of imperfectly tagged cis-expression quantitative trait loci with large additive effects, the F-test statistic used to detect interactions can result in an inflated false positive rate. As a result, we voice concern over whether our reported epistatic associations arose owing to biological mechanisms or from inflated test statistics caused by imperfectly tagged additive effects. All authors agree with the revised interpretation of the original findings and [Authors A. Smith, B. Jones…] agree with the retraction. [Authors C. Brown and D. Mills] do not agree with the retraction.