Erratum

Page 9, Section 1.3, 2nd Paragraph:

Original: We note that the variants identified in this study did not overlap with variants reported by the Applicant. This could be due to potential differences in the in-silico analysis algorithms used, or insufficient sampling of variant information within each dataset, leading to disparate findings between the two studies.

Corrected: The Applicant notes that the CPS1 locus reported in Cancellieri *et al*. was nominated in their in silico study because it met the homology criteria for an alternative PAM even in the absence of the variant allele. The in silico nomination methods or sampling of variant information may contribute to differences in these studies.