

Review of: "The genomic landscape of contemporary western Remote Oceanians"

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Potential competing interests: The author(s) declared that no potential competing interests exist.

This paper presents the population genomic structure of a very interesting population, and should complement the migration and peopling history of modern human from global perspective.

- (i) how many SNPs from the Omni2.5 array were being called, and subsequently being included in the analysis? I understand that the authors also used the previously published WGS data for sex-biased analysis. The process of pooling the datasets and the SNPs remained should be clarified. Was there an imputation performed on the pooled datasets? If yes, then how was it done?
- (ii) Did the authors pooled the Omni2.5 data (X-chr, Y-chr and mtDNA) with the WGS data? If yes, how many SNPs were remained for the downstream analysis? I understand that the SNP array has rather limited density on the X-chr, Y-chr, so I am not quite sure how many SNPs would remained in the analysis. I am not quite clear how the data processing were being carried out in this section.
- (iii) Very comprehensive analysis performed with appropriate interpretation.
- (iv) ROH analysis could be considered as supporting evidence to the levels of inbreeding of ni-Vanuatu.
- (v) Although natural selection analysis had been performed in the previous paper, considering the large sample size collected, with considerably isolated environment, I feel that it is worth performing an analysis of natural selection in this study, in a more detail manner. Estimating the time of selection may provide some further insights to the genetic history of ni-Vanuatu (for example, see Pierron et al., 2018 - Nat Comm).