

## Reviewer Report

**Title:** Population-wide Sampling of Retrotransposon Insertion Polymorphisms Using Deep Sequencing and Efficient Detection

**Version:** Revision 1      **Date:** 6/5/2017

**Reviewer name:** Adam Ewing

### Reviewer Comments to Author:

This manuscript is much improved, thank you for careful consideration and incorporation of my questions and suggestions at last review. I am satisfied that this can be published following a few minor issues being resolved, largely around improving clarity:1. When specific algorithms are mentioned e.g. "Maximal Valid Clusters" (line 117-8), and "Asynchronism Scanning" (line 136), these are not cited or clearly defined. It would be helpful to include either a reference if they were developed previous to this work, or a reference to where in the supplemental material these specific algorithms are described (I could not locate specific headings for these).2. Define "AFS" where it is first used (line 314).3. I'm not sure that the claim, "This study is the first to evaluate the natural selection effect on retrotransposon insertions at the population level" is justified. For instance, Stewart et al (PLoS Genetics 2011) evaluate the allele frequency spectra of different populations using a similar approach.

### Level of Interest

Please indicate how interesting you found the manuscript: An article whose findings are important to those with closely related research interests

### Quality of Written English

Please indicate the quality of language in the manuscript: Acceptable

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