

We have wrapped up the code and will publish it with the manuscript (**S8 File**)^[1].

[[Alex: In my previous paper retrodups were discovered per population because coverage was really shallow. In my previous publication there were less than 1 retrodup per person when using population data. Here we are discovering significantly more per person, and counts are comparable (?) to those when using high coverage data. You can actually check how many of those found from high coverage analysis are found by population study and by this approach. High coverage calls for 2 individuals are given in my previous paper. Similar arguments can probably be made with respect to other previous publications.]]