1) Simple bootstrapping to compare proportion of ROH in genome for 4 lengths and 4 regions. Sampled 1000 times from each group with replacement, compared distribution of means with CIs.

2) Same.

3) Modelled proportion of ROH remaining as a function of rescue pairs using a generalized linear model separately considering Ranthambore and Wayanad populations. Assumed a quasi-binomial error distribution and used ‘contrasts’ to determine how much better each rescue population is from the Ranthambore-Ranthambore and Wayanad-Wayanad pairs. Plotted predicted values with CIs.

4-5) Simple visualizations of mean and CI.