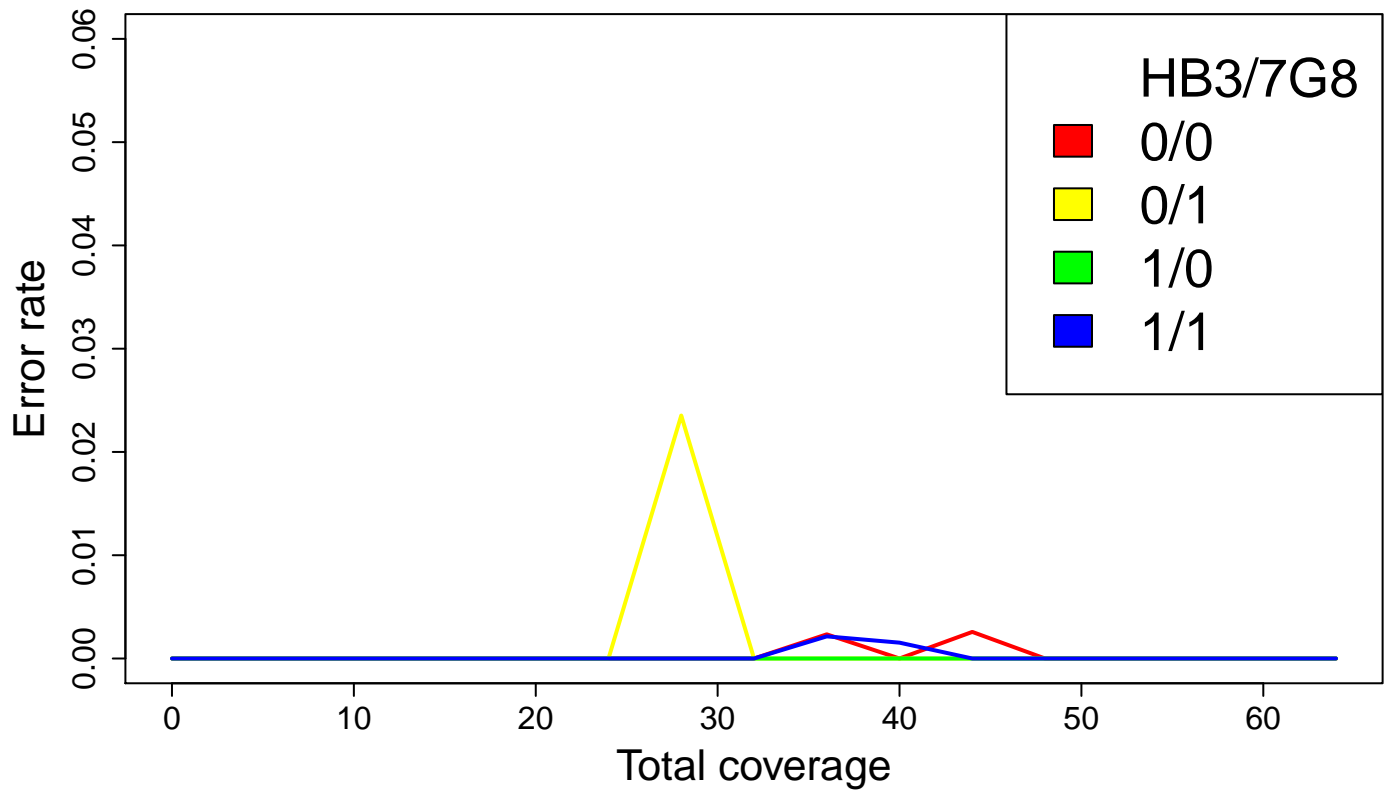


Error rate when wrongly infer genotype */*



Histogram of coverage

