Error rate when wrongly infer genotype */*
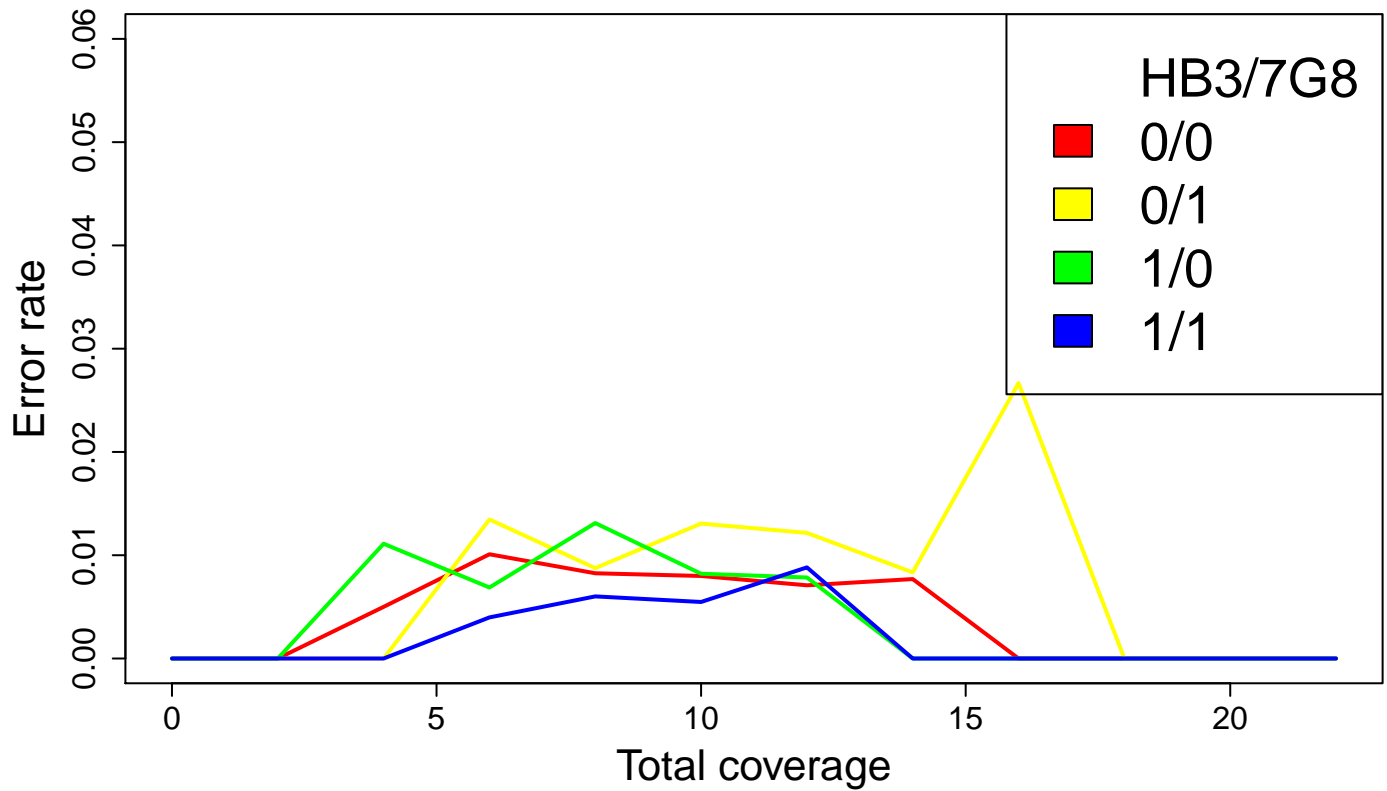
Histogram of coverage