

Introduction to NGS data: experimental design

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Experimental design

You discovered a new species!



Experimental design

You have access to many samples!



Experimental design



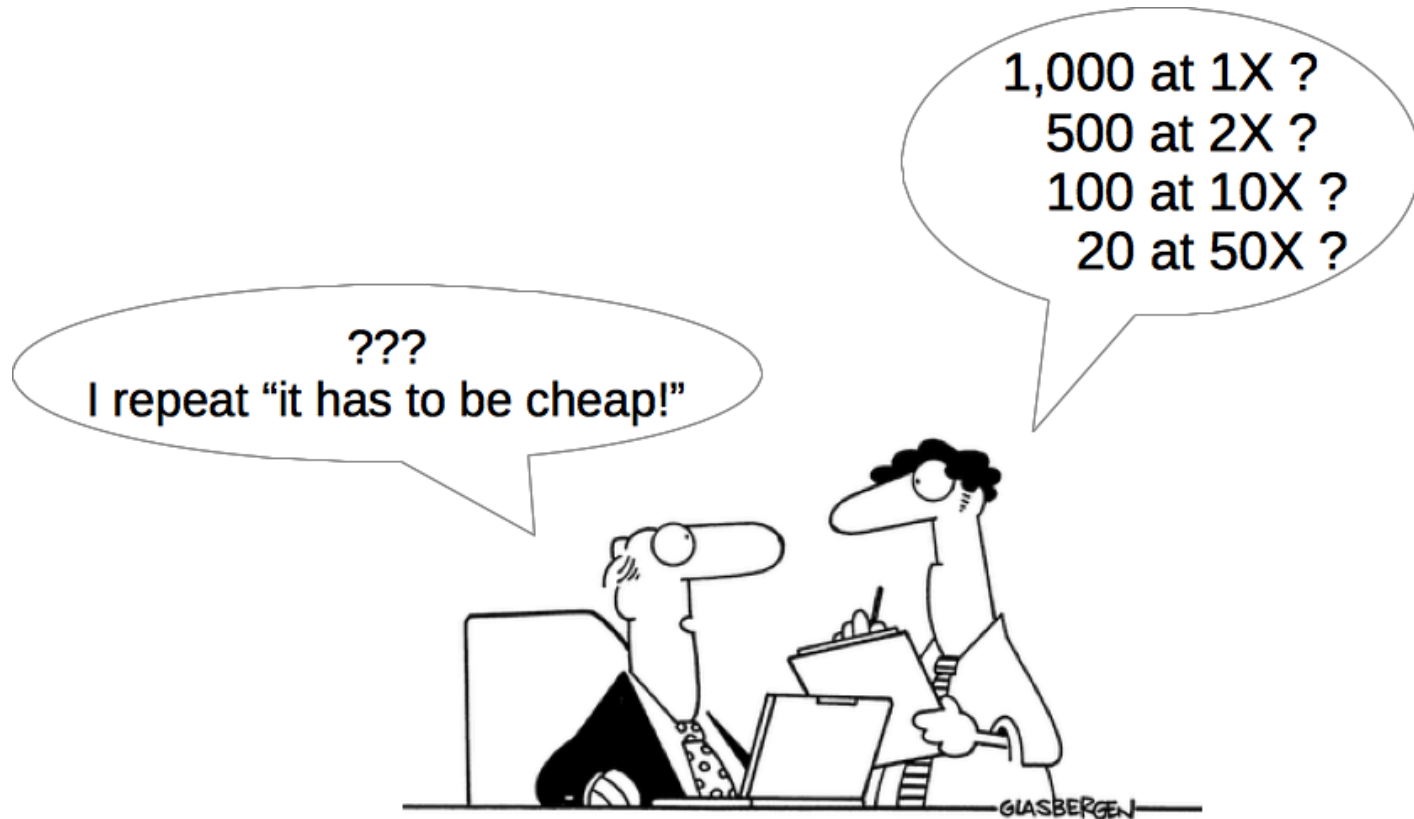
Experimental design



Experimental design

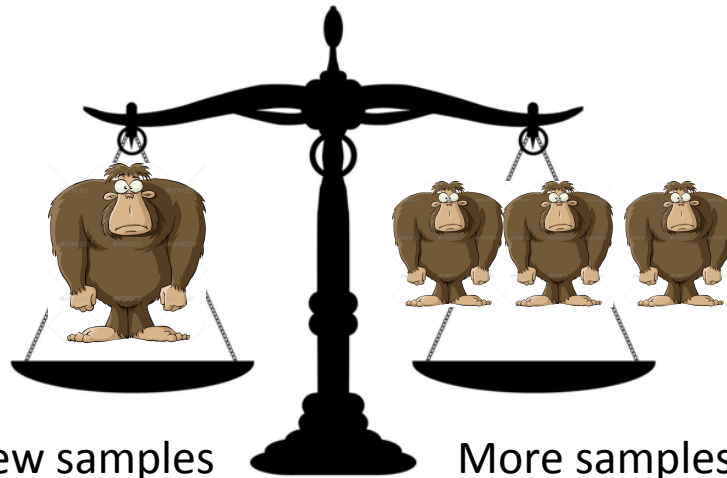


Experimental design



Experimental design

At a fixed budget...




Few samples
at higher quality

More samples
at lower quality

Simulations design

The sequencing strategy can easily be modeled in terms of the number of sequenced samples and the per-sample sequencing depth.

Sample size	Per-sample depth
1,000	1X
500	2X
100	10X
20	50X

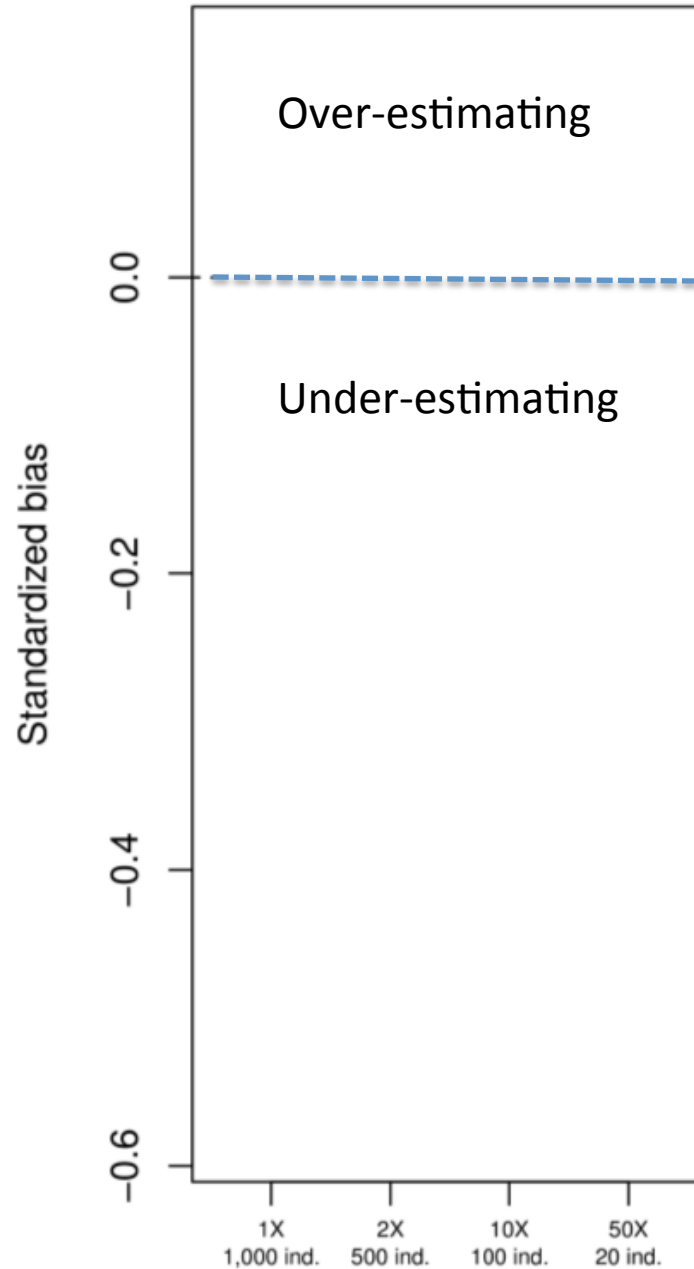


total depth is
1,000X

Number of segregating sites

$$Bias(S) = \frac{\hat{S} - S}{S}$$

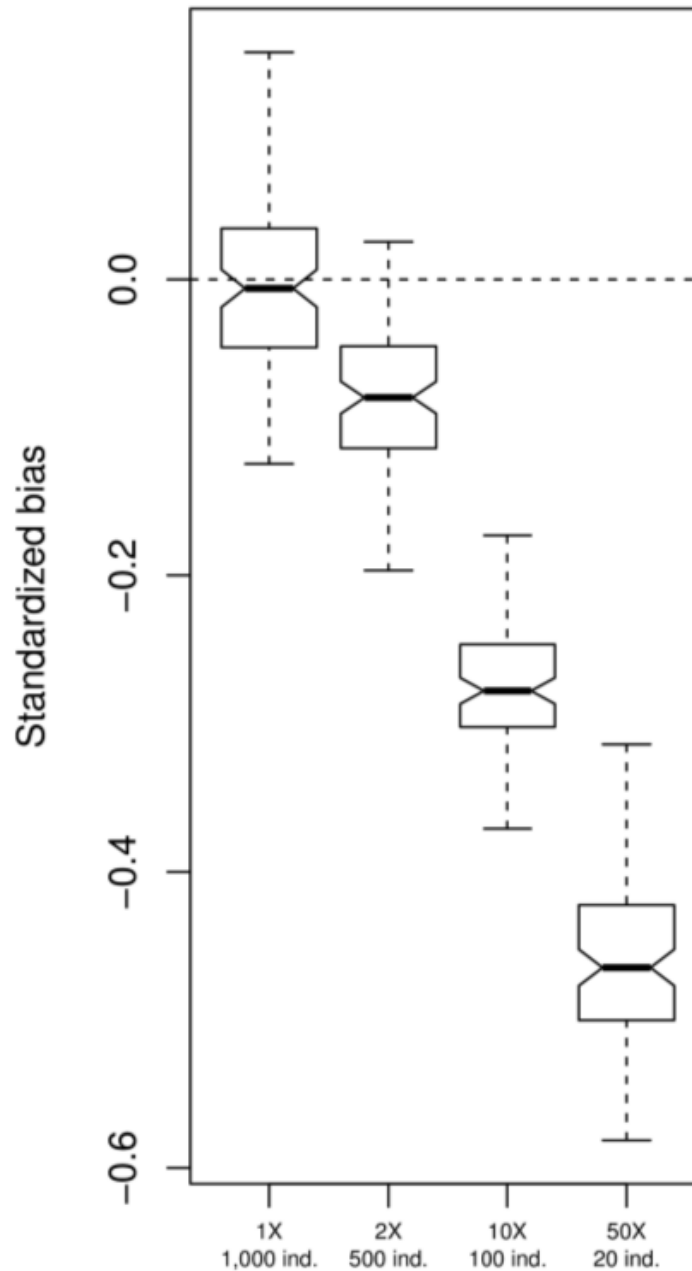
Compared against the
whole **population!**



Number of segregating sites

$$\text{Bias}(S) = \frac{\hat{S} - S}{S}$$

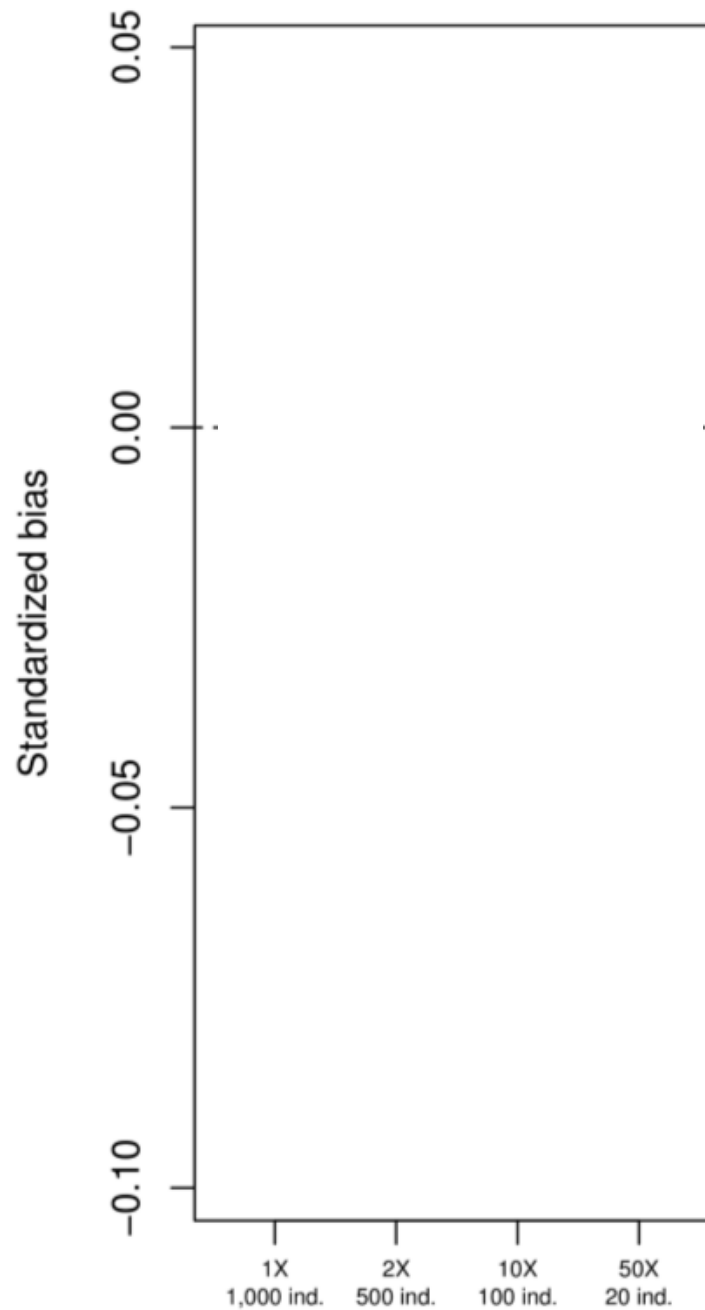
Compared against the
whole **population!**



Expected heterozygosity

$$\text{Bias}(S) = \frac{\hat{S} - S}{S}$$

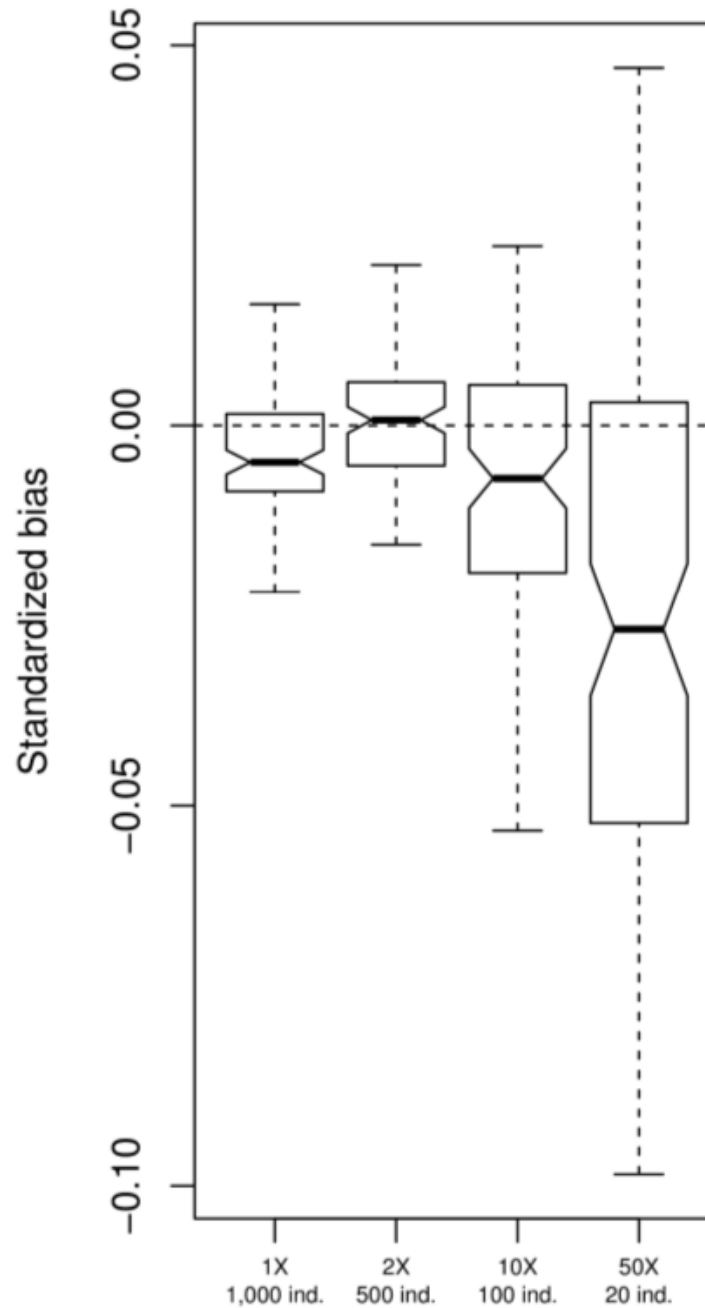
Compared against the
whole **population!**



Expected heterozygosity

$$\text{Bias}(S) = \frac{\hat{S} - S}{S}$$

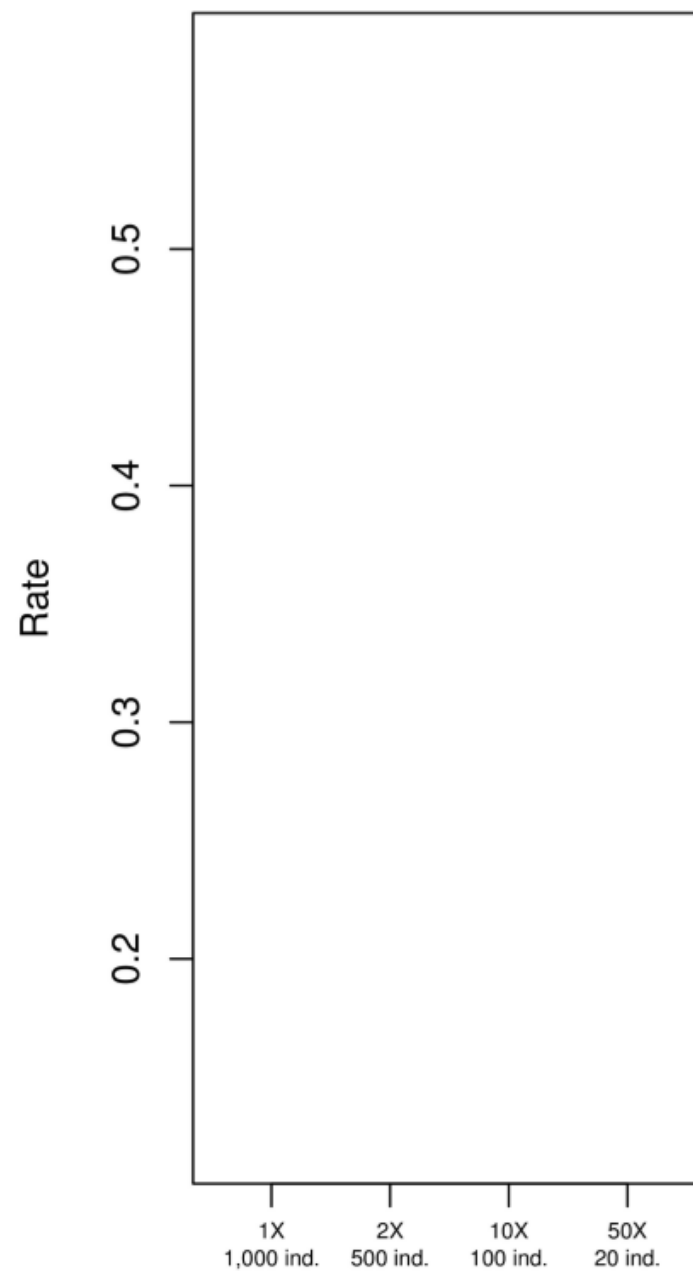
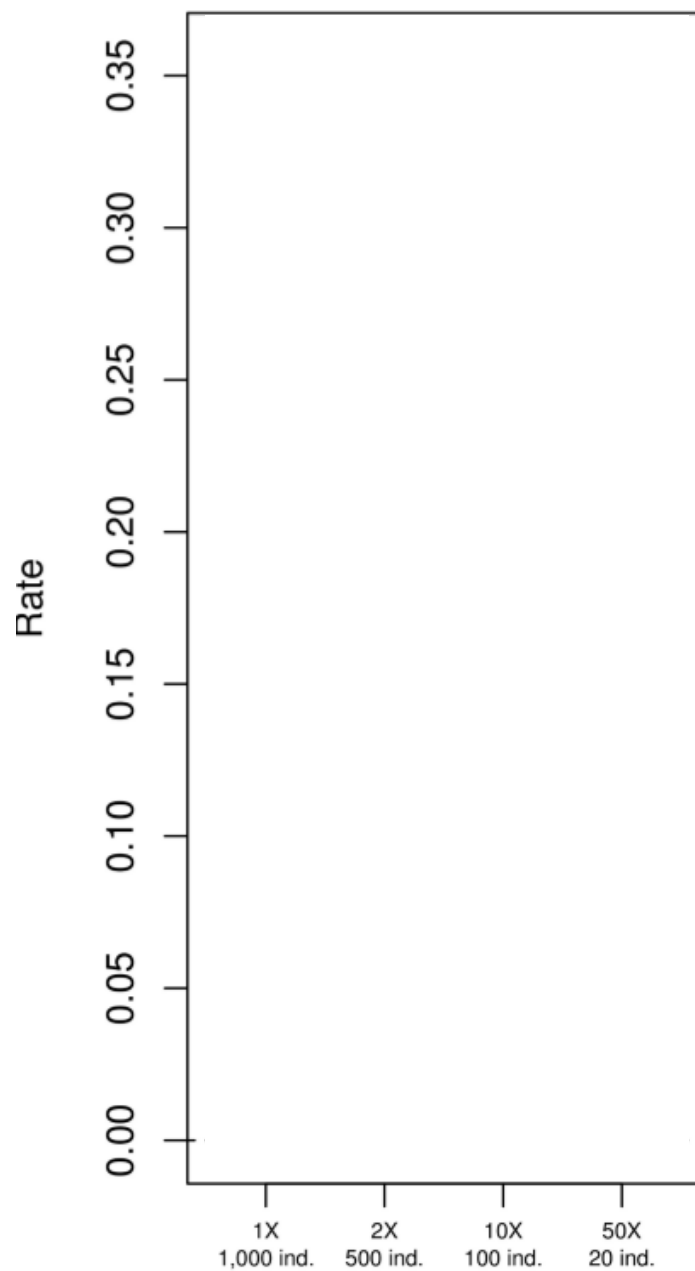
Compared against the
whole **population!**



False Positive

SNP calling

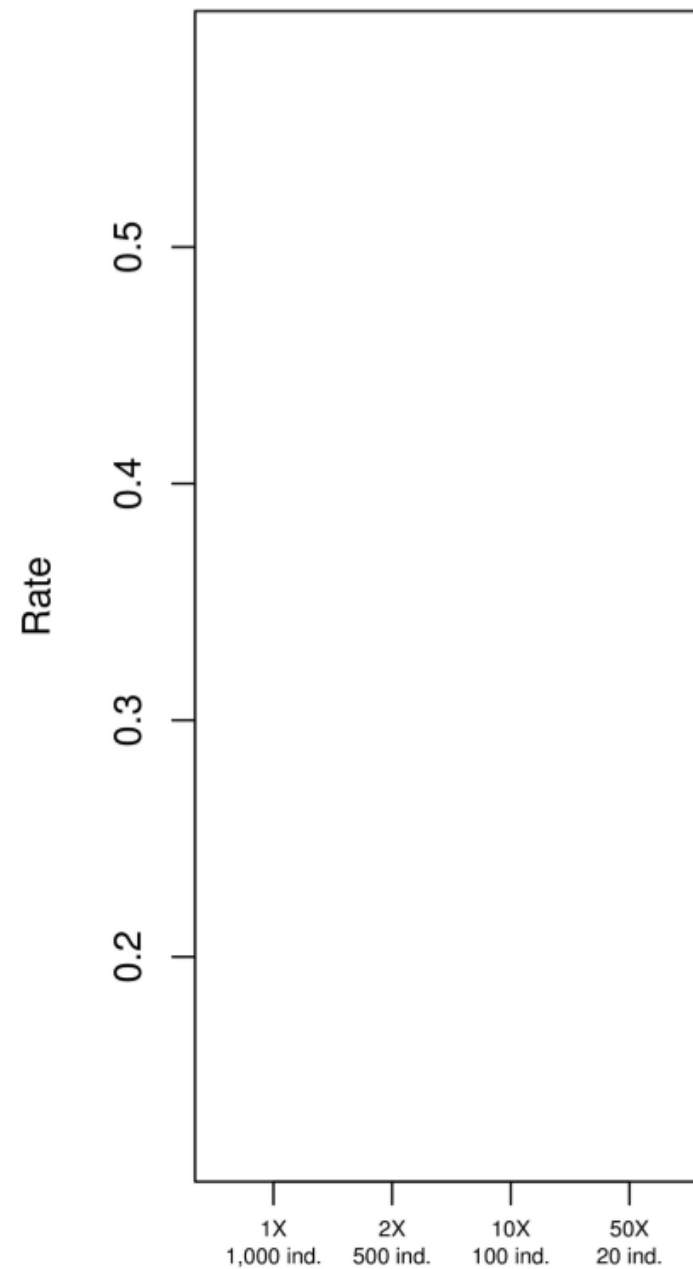
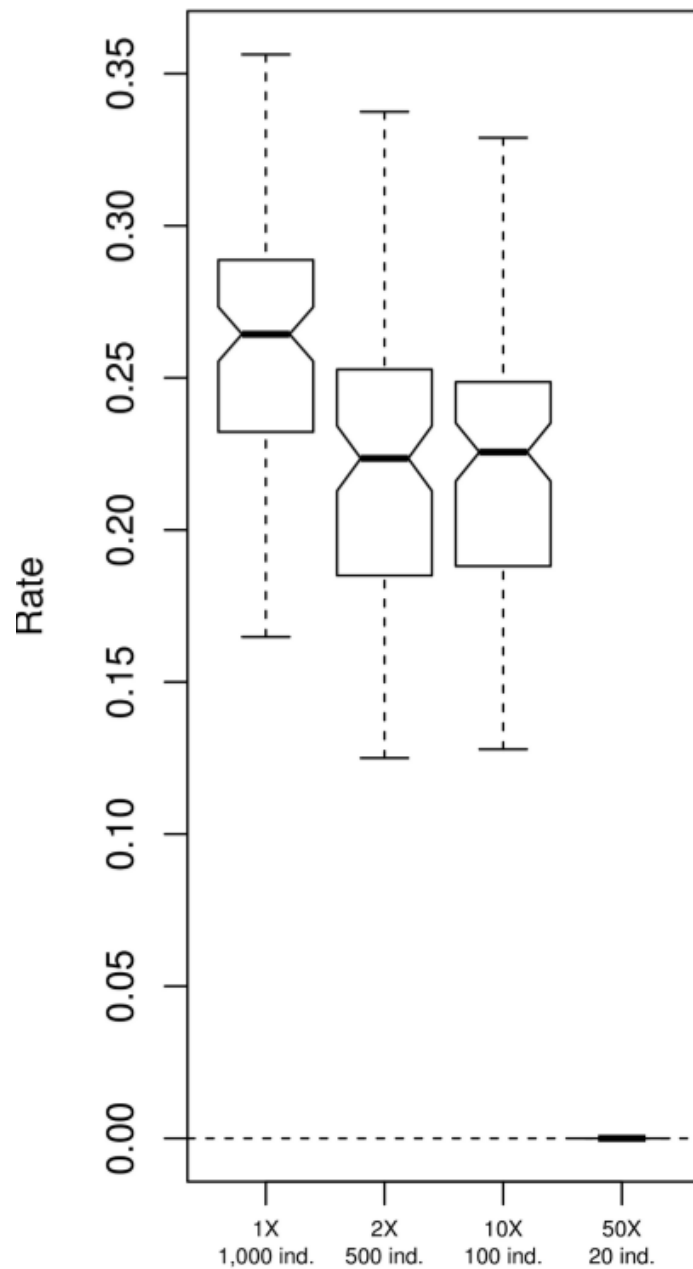
False Negative



False Positive

SNP calling

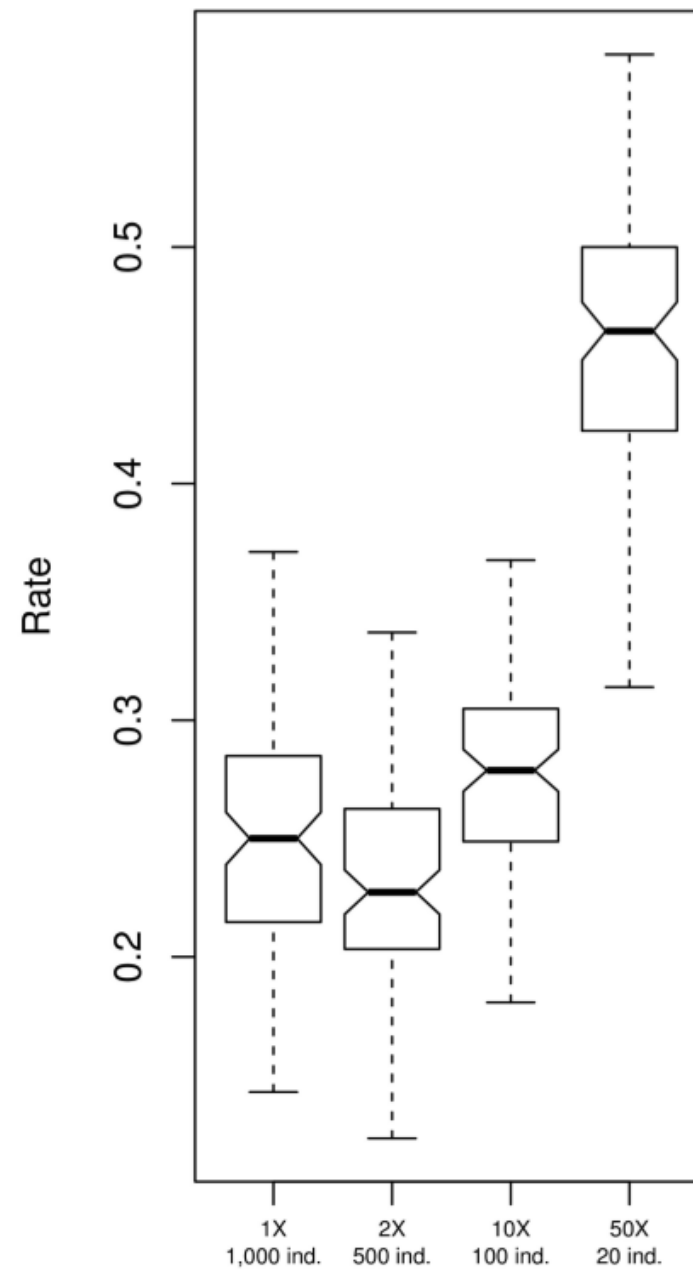
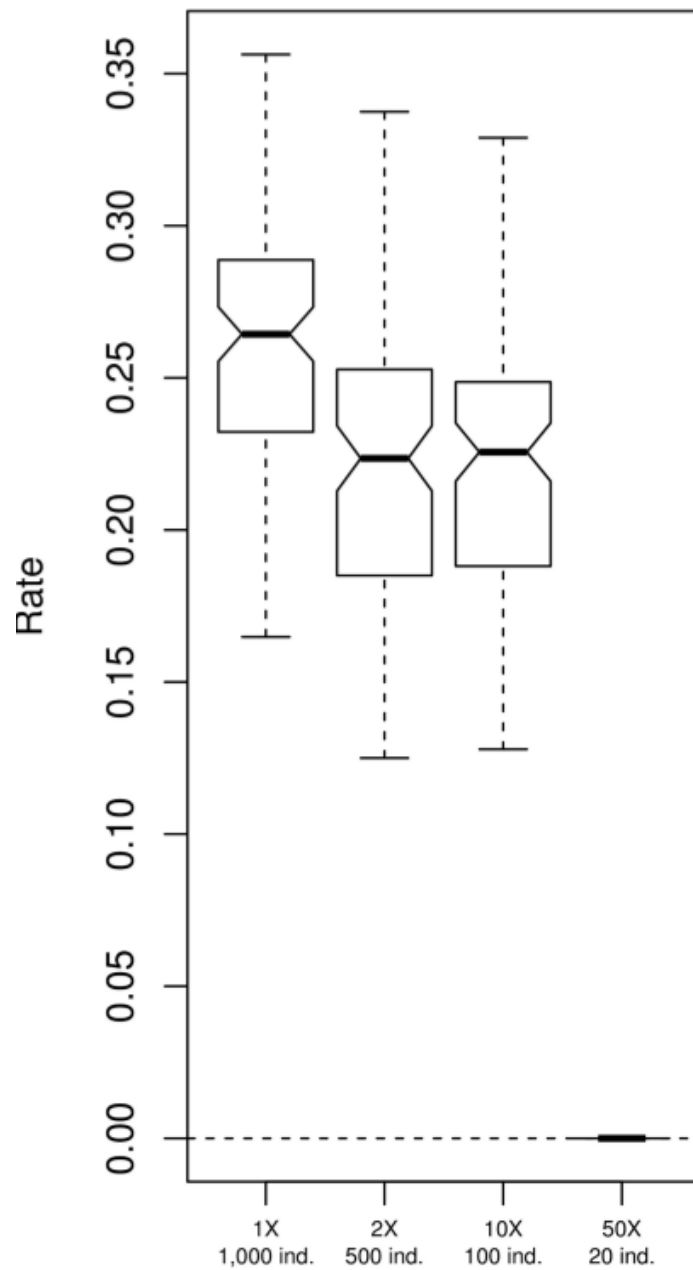
False Negative



False Positive

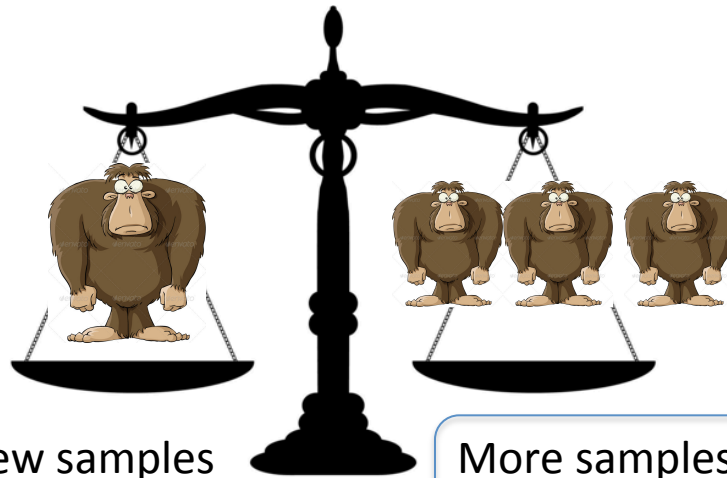
SNP calling

False Negative



Experimental design

At a fixed budget...



Few samples
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at lower quality

**For population
genetics**

Sample allele
frequencies will be a
better representation
of population variation