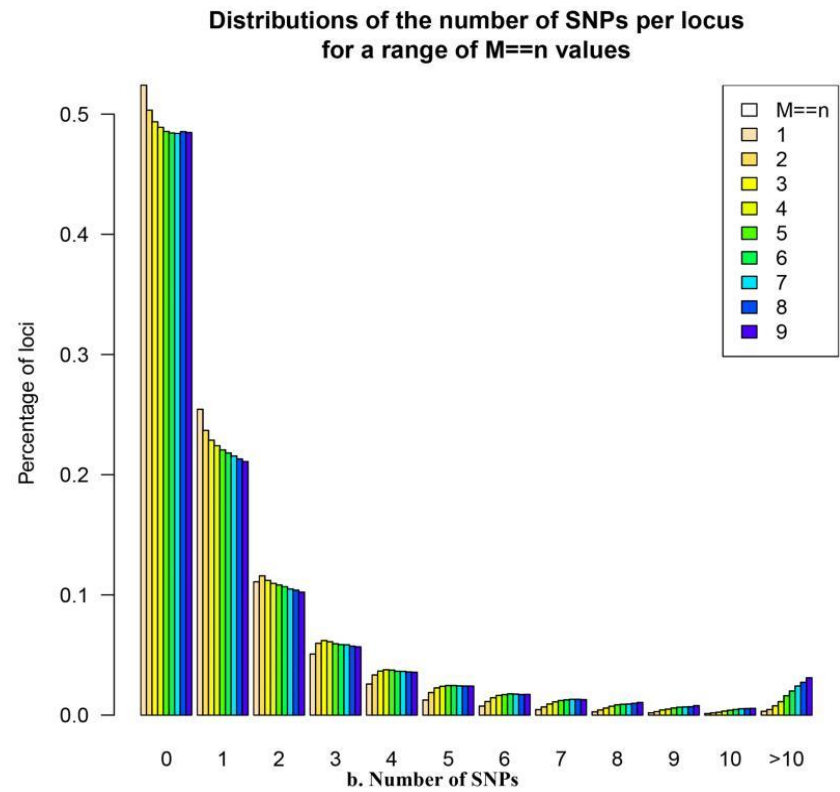
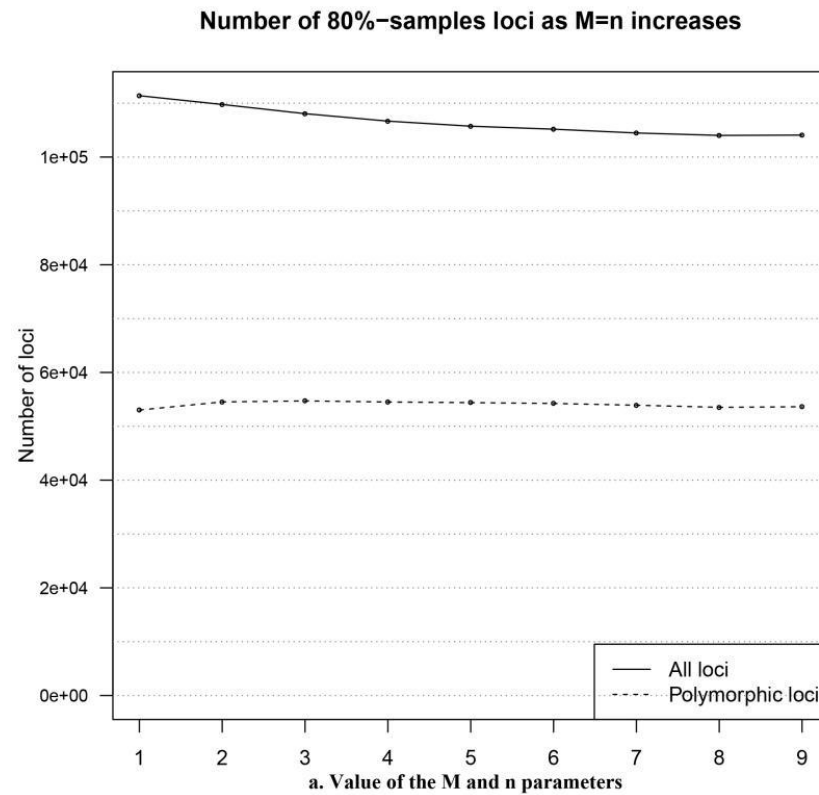


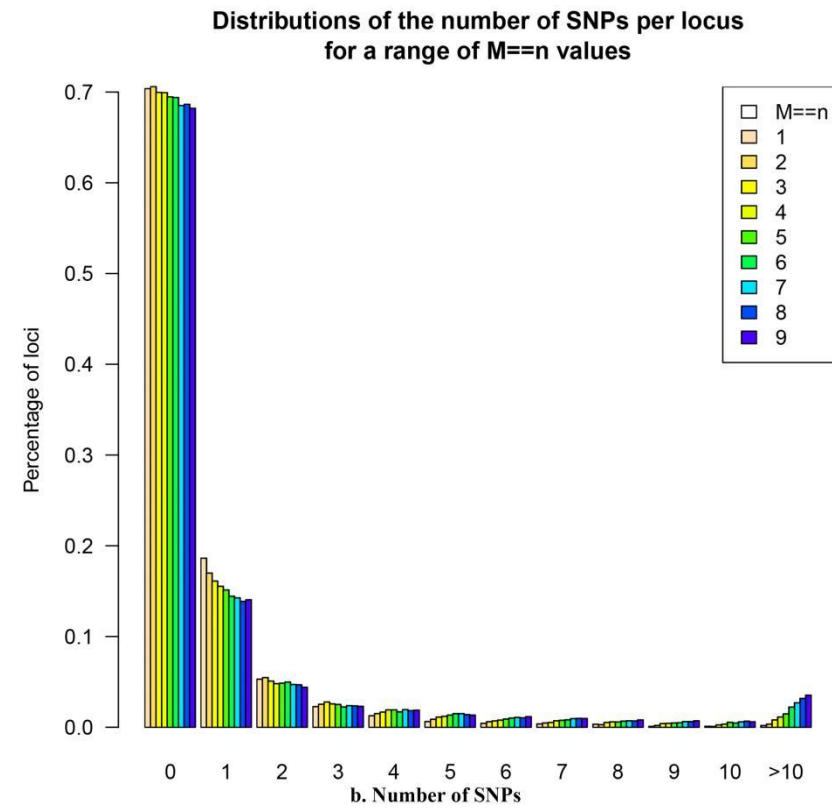
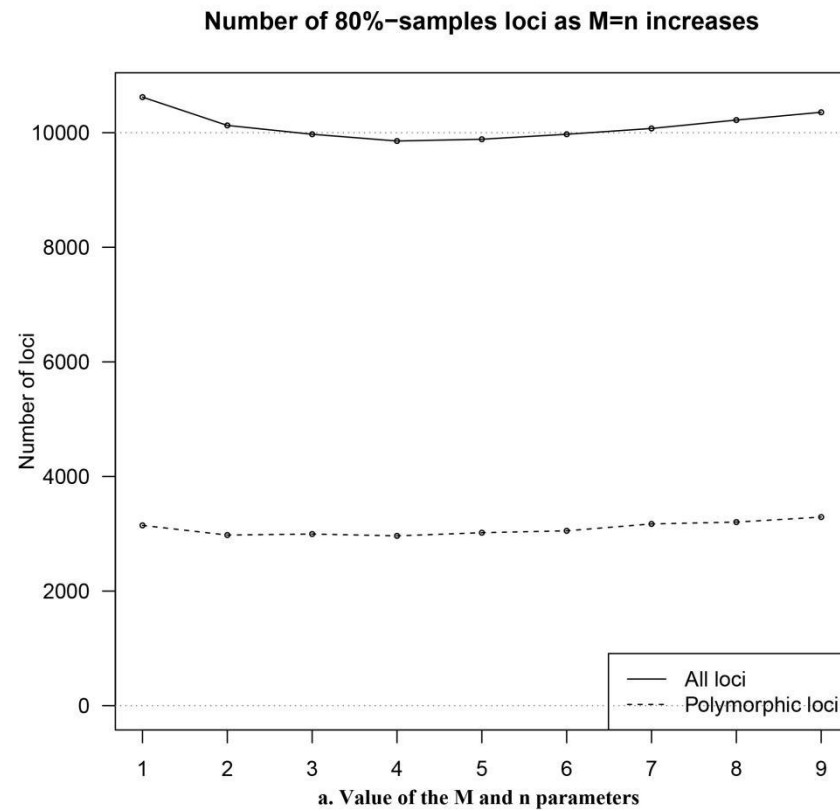
### File S3

Parameter optimization of Stacks *de novo* assembly analysis of *Amolops*. In both maps, we tried to increase  $M=n$  from 1 to 9, ensuring  $M=3$ , and to monitor the number of polymorphic loci found in 80% (r80 locus) or more of the sample, until we find the most stable set of values for  $M$ ,  $n$ , and  $m$  ( $M$  controls the number of mismatches allowed between the two alleles of a heterozygote sample;  $n$  controls the number of mismatches allowed between any two alleles of the population;  $m$  controls the number of identical reads required to initiate a new putative allele). **a.** Number of loci shared by  $\geq 80\%$  of samples. **b.** Number and distribution of snps per locus.

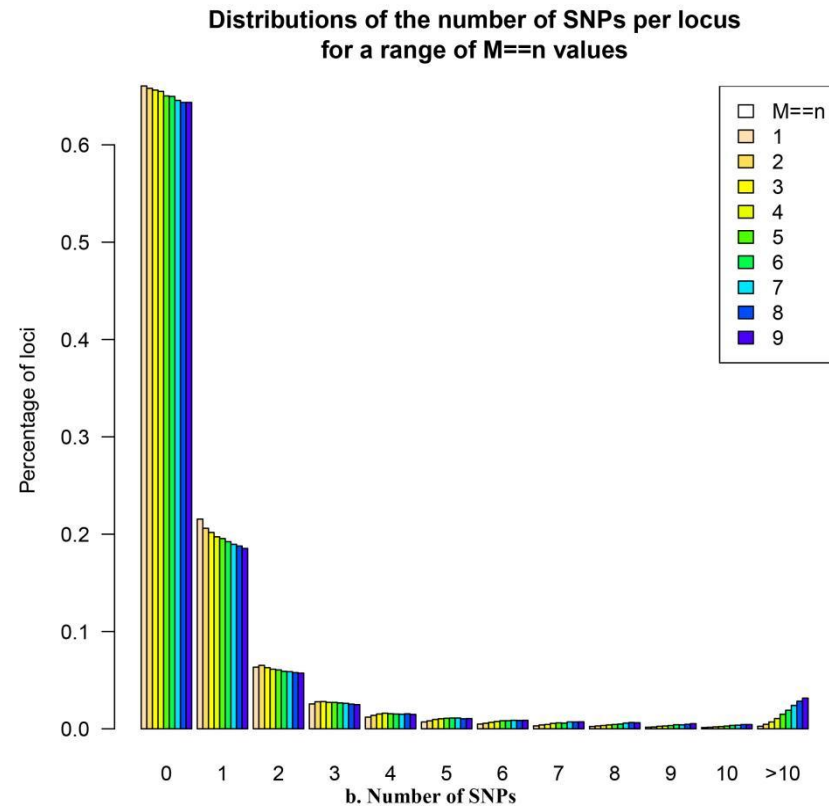
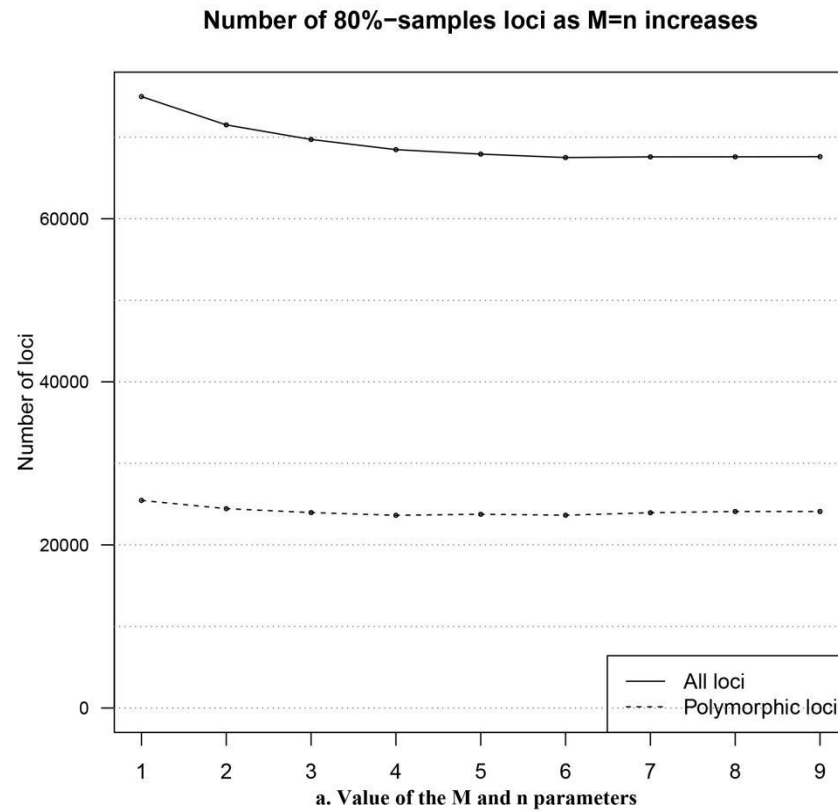
### A. *Chunganensis* (Optimal parameter: $M=n=3, m=3$ .)



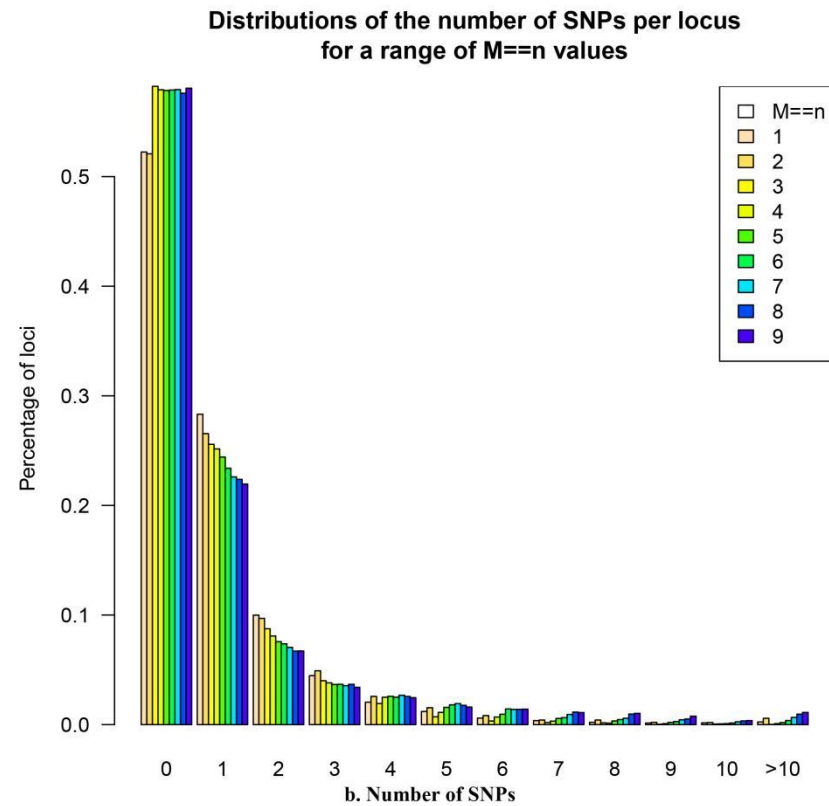
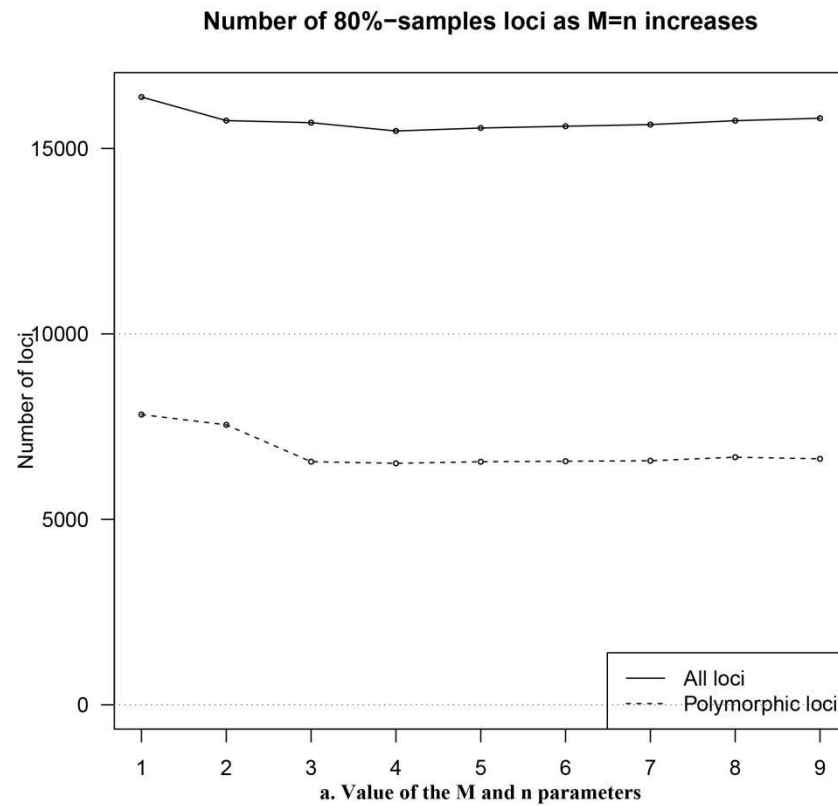
*A. jinjiangensis* (Optimal parameter:  $M=n=2$ ,  $m=3$ .)



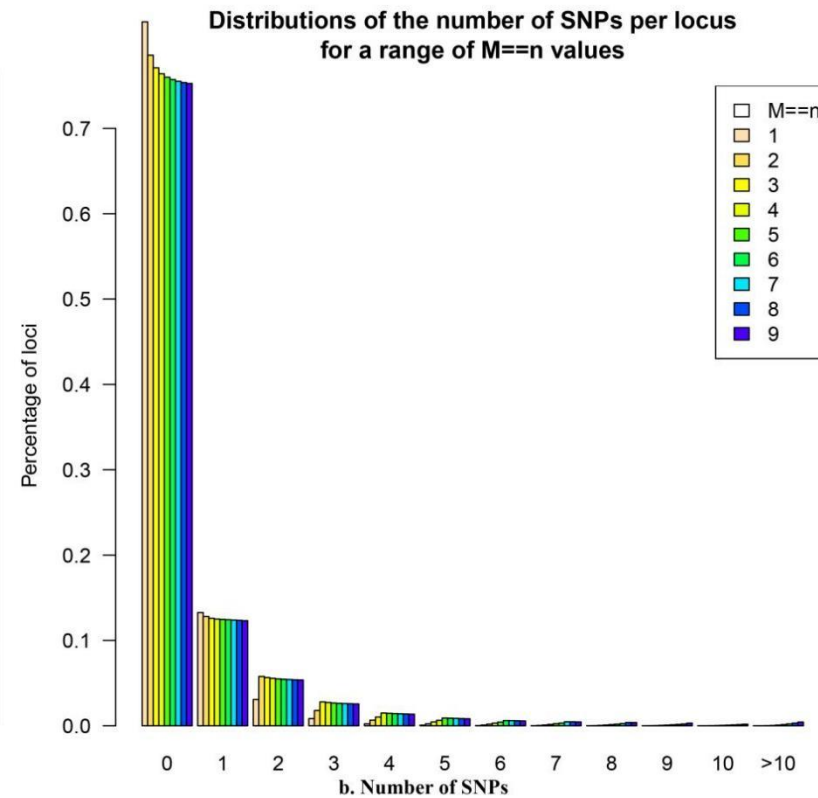
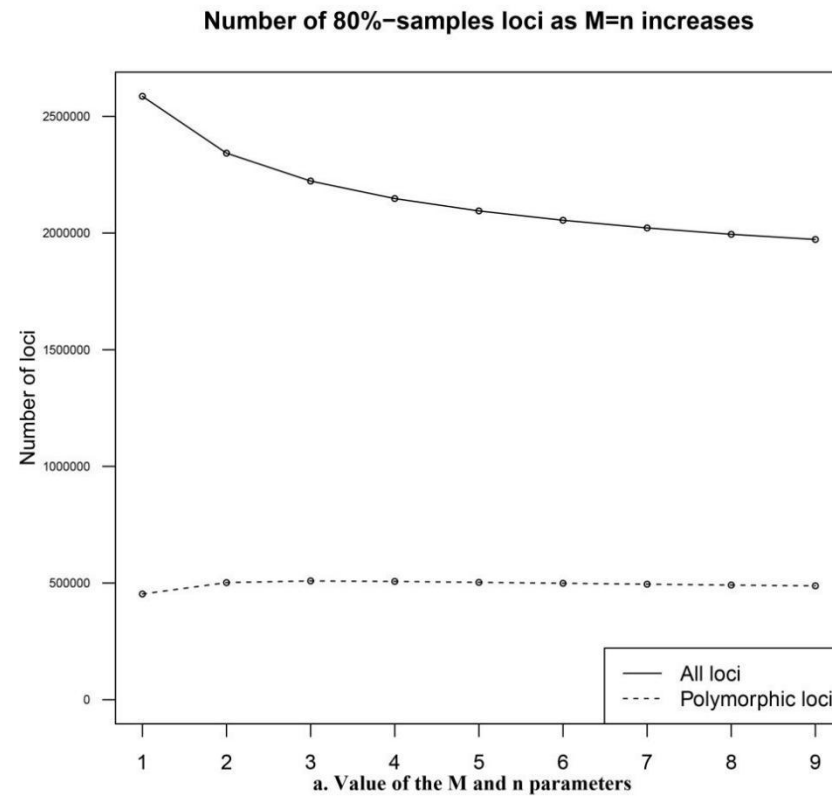
*A. lifanensis* (Optimal parameter:  $M=n=2$ ,  $m=3$ .)



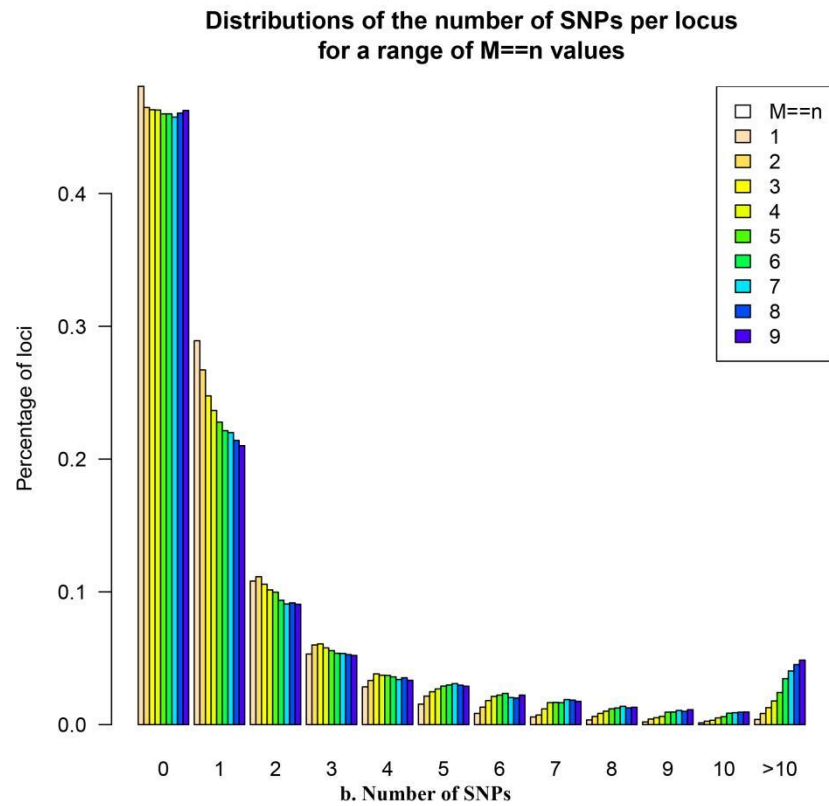
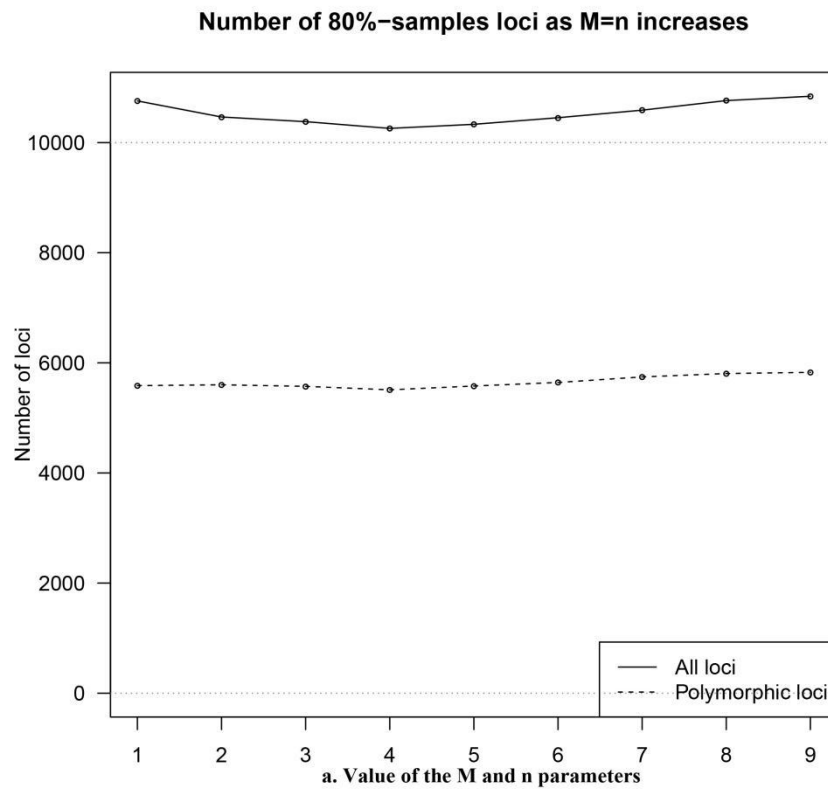
***A. loloensis* (Optimal parameter:  $M=n=3, m=3$ .)**



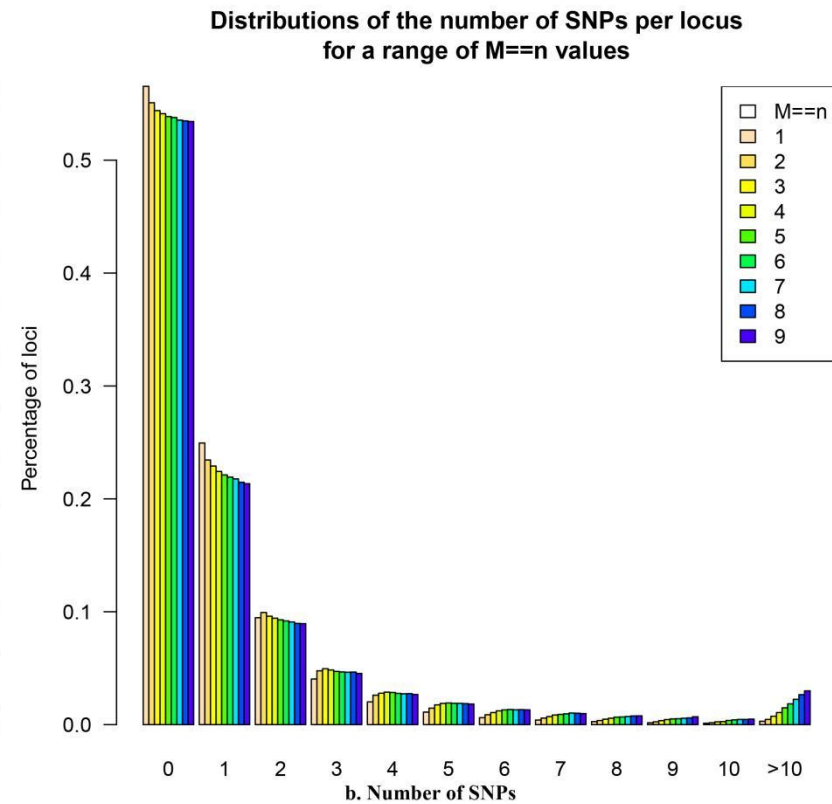
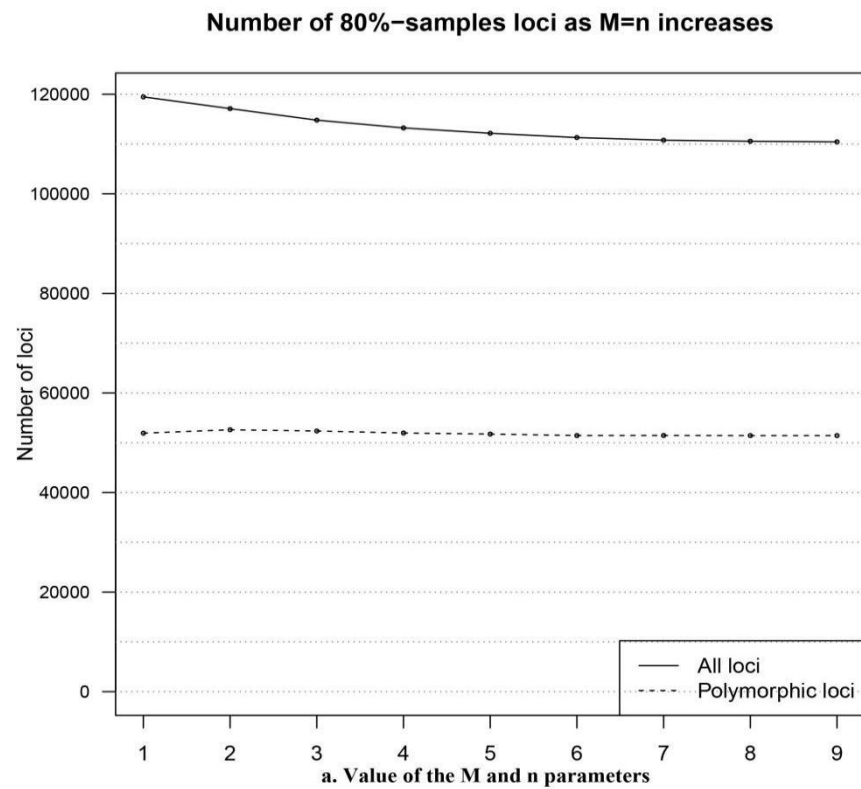
*A. mantzorum* (Optimal parameter:  $M=n=3$ ,  $m=3$ .)



**A. sp. (Optimal parameter:  $M=n=2$ ,  $m=3$ .)**

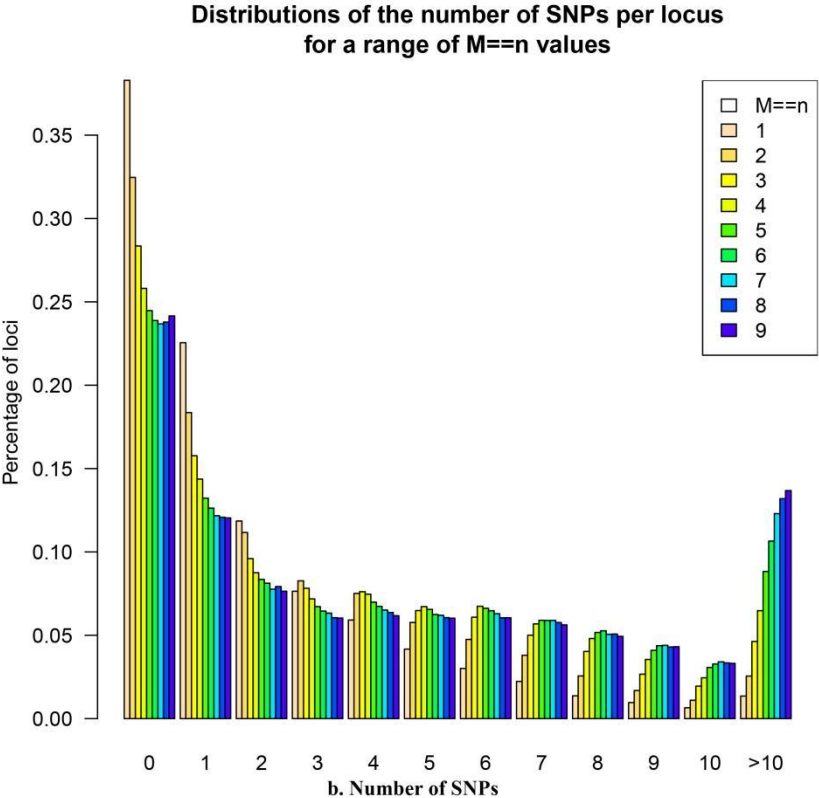
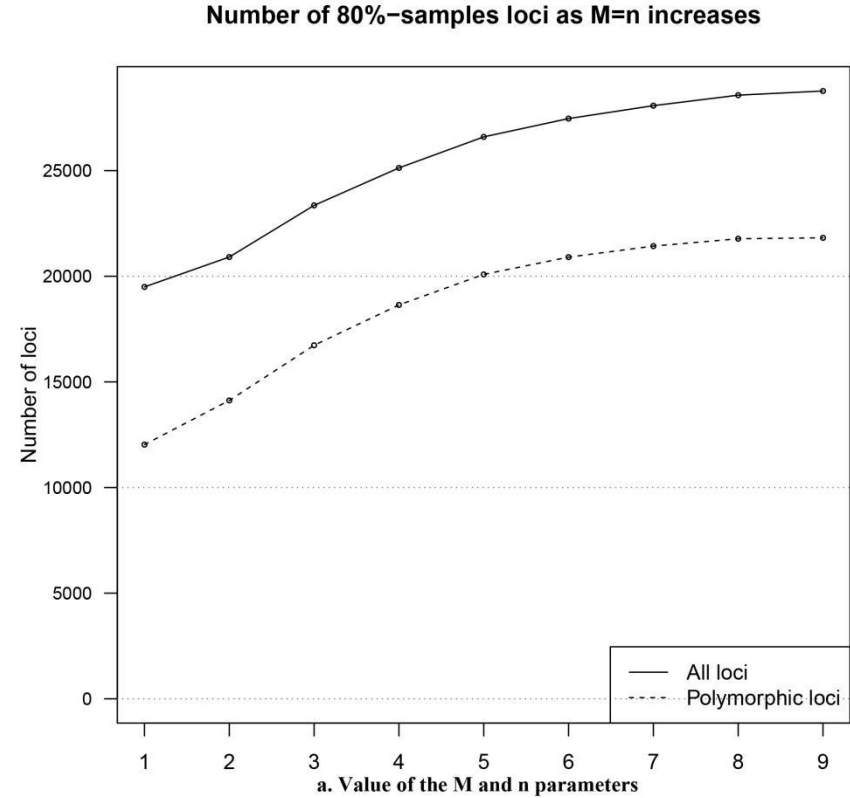


***A. tuberodepressus* (Optimal parameter: M=n=2, m=3.)**





*A. wuyiensis* (Optimal parameter:  $M=n=5$ ,  $m=3$ .)



*A. xinduoqiao* (Optimal parameter:  $M=n=3$ ,  $m=3$ .)

