

## To remember

- \* Hifiasm is not always the perfect tool
- \* Need to test at least two assemblers
- \* Need an optimal coverage (between 15 and 70X according to the technology)
- \* Known your genome (heterozygosity, size genome...)
- \* If possible, sequencing in long reads
- \* Check your assembly ! (reads mapping, BUSCO, D-GENIES, kmer content...)