We use out peak-calling to determine the clonally variant genes in our ChIP-Seq samples.

We assume as variant any gene having a heterochromatin peak in any sample.

We use MACS2(v2.2.5) to call the peaks with the following parameters:

* -f BAMPE -B
* -g 2.41e7
* --keep-dup all
* --fe-cutoff 1.5
* --nomodel
* --extsize 150

We only consider a gene heterochromatic if it’s coding region overlaps with at least one peak.