

## **Nanopore read binning**

```
canu 'corMhapOptions=--threshold 0.8 --ordered-sketch-size 1000 --ordered-kmer-size 14' saveOverlaps=true correctedErrorRate=0.105 'stageDirectory=$TMPDIR' -p  
BisonSimmental -d assembly genomesize=2.7g -haplotypeBison_sire bison_sire.fastq -  
haplotypeSimmental_dam Simmental_dam.fq -nanopore-raw  
bison_simmental.ul.ont.fasta.gz
```

## **Meryl Hi-C read binning**

```
meryl-lookup -exclude -mers simmental_dam.only.meryl -sequence hic_R1.fastq.gz -  
sequence2 hic_R2.fastq.gz -r2 Bison_sire_hic-dam-excluded.R2.fastq.gz | pigz -c >  
Bison_sire_hic-dam-excluded.R1.fastq.gz
```