### For ATACseq

## Convert BAM file to a BED file, then run MACS2 o "call peaks" in the aligned reads

## sample SRR13169286

bedtools bamtobed -i SRR13169286.pruned.bam | sort -k1,1 -k2,2n > SRR13169286.pruned.bed

macs2 callpeak -t SRR13169286.pruned.bed -f BED -n SRR13169286.broad -g hs -q 0.05 --nomodel --shift -100 --extsize 200 -B --broad --keep-dup all

## sample SRR13169287

bedtools bamtobed -i SRR13169287.pruned.bam | sort -k1,1 -k2,2n > SRR13169287.pruned.bed

macs2 callpeak -t SRR13169287.pruned.bed -f BED -n SRR13169287.broad -g hs -q 0.05 --nomodel --shift -100 --extsize 200 -B --broad --keep-dup all

## sample SRR13169288

bedtools bamtobed -i SRR13169288.pruned.bam | sort -k1,1 -k2,2n > SRR13169288.pruned.bed

macs2 callpeak -t SRR13169288.pruned.bed -f BED -n SRR13169288.broad -g hs -q 0.05 --nomodel --shift -100 --extsize 200 -B --broad --keep-dup all

## sample SRR13169289

bedtools bamtobed -i SRR13169289.pruned.bam | sort -k1,1 -k2,2n > SRR13169289.pruned.bed

macs2 callpeak -t SRR13169289.pruned.bed -f BED -n SRR13169289.broad -g hs -q 0.05 --nomodel --shift -100 --extsize 200 -B --broad --keep-dup all