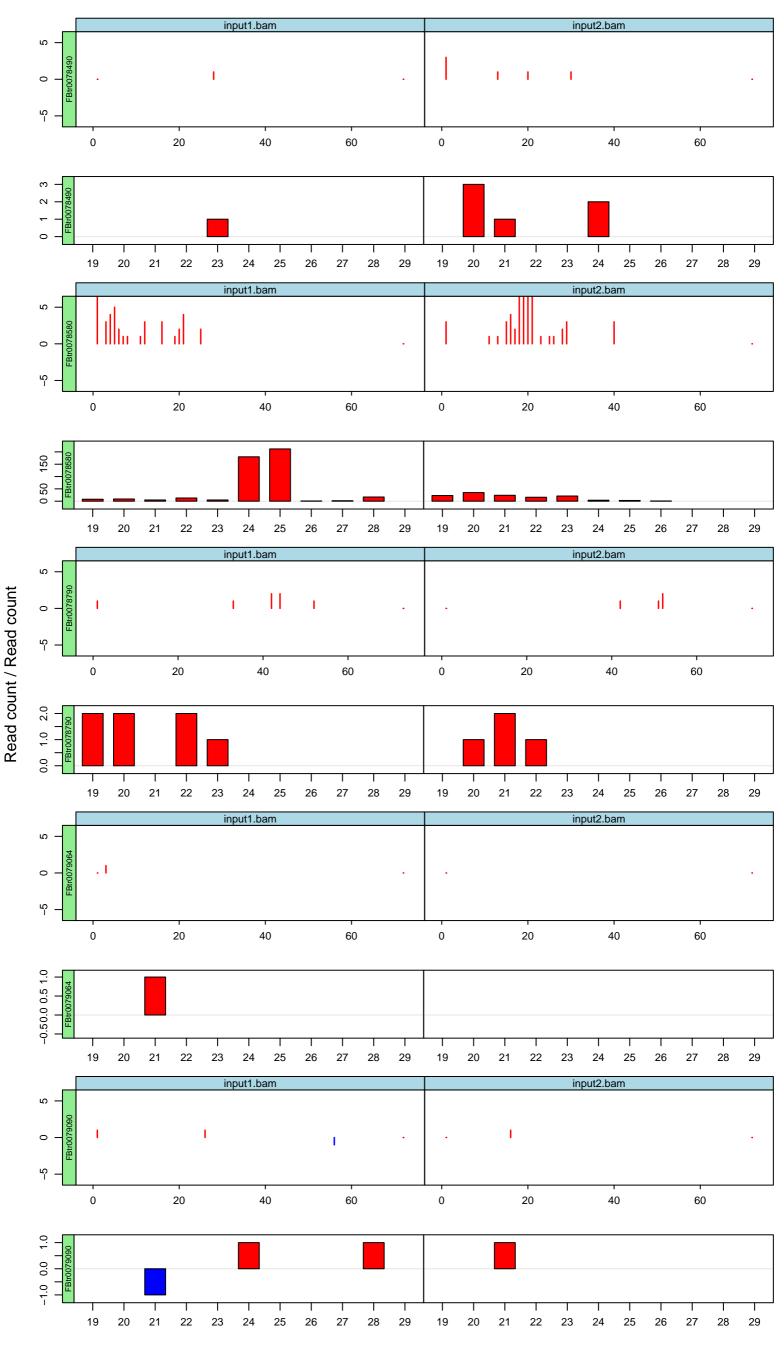
#### Read Counts and Size Distributions input1.bam input2.bam -5 input2.bam input1.bam input2.bam input1.bam 10 15 input2.bam input1.bam input1.bam input2.bam

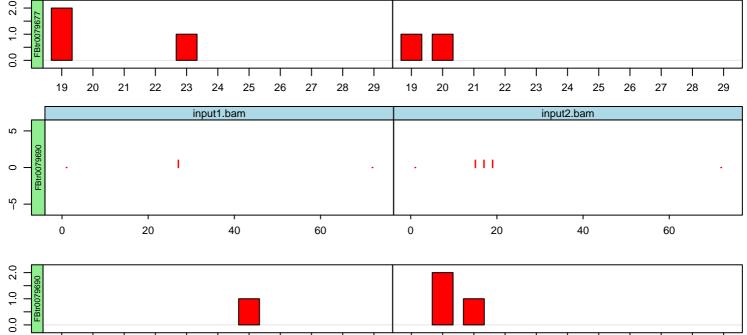
Read count / Read count

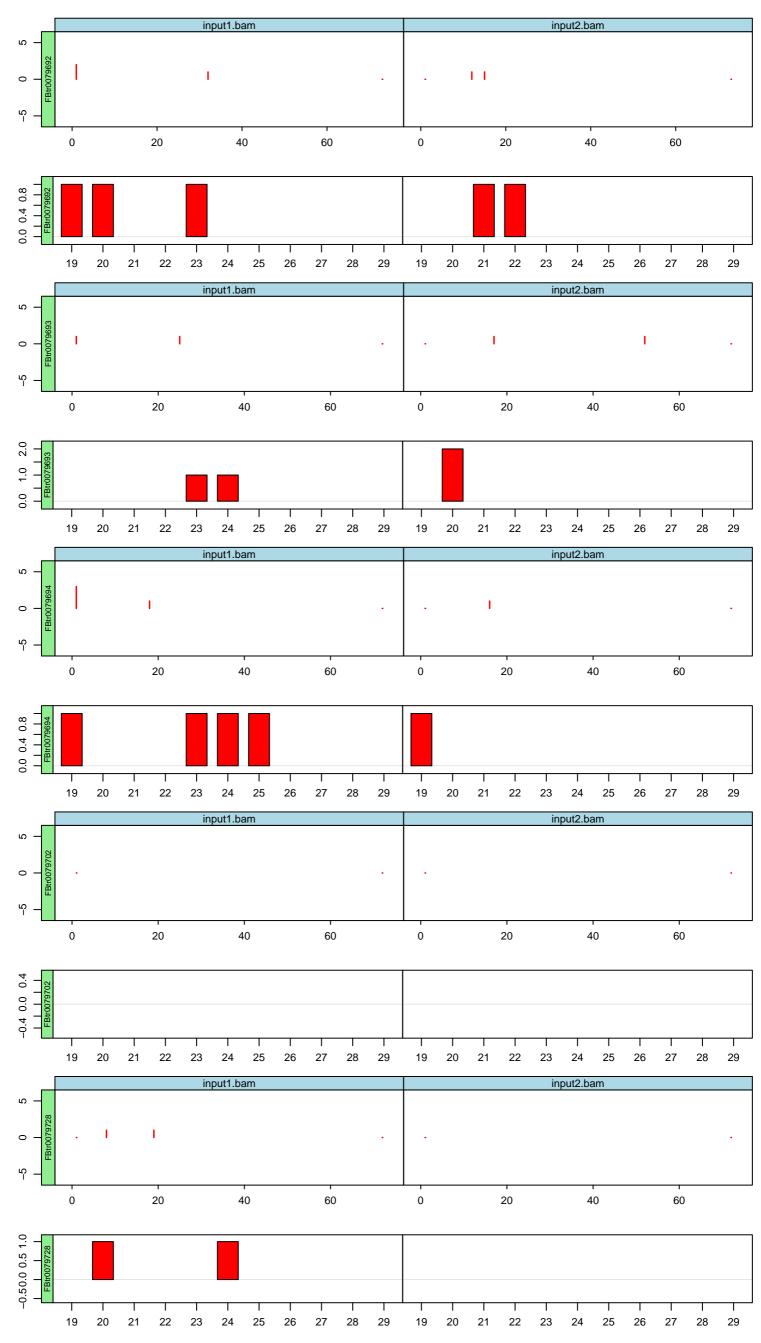


Coordinates (nucleotides) / Sizes of reads

#### Read Counts and Size Distributions input1.bam input2.bam h -5 input1.bam input2.bam 0 10 20 30 40 input2.bam input1.bam اا 010 30 input1.bam input2.bam

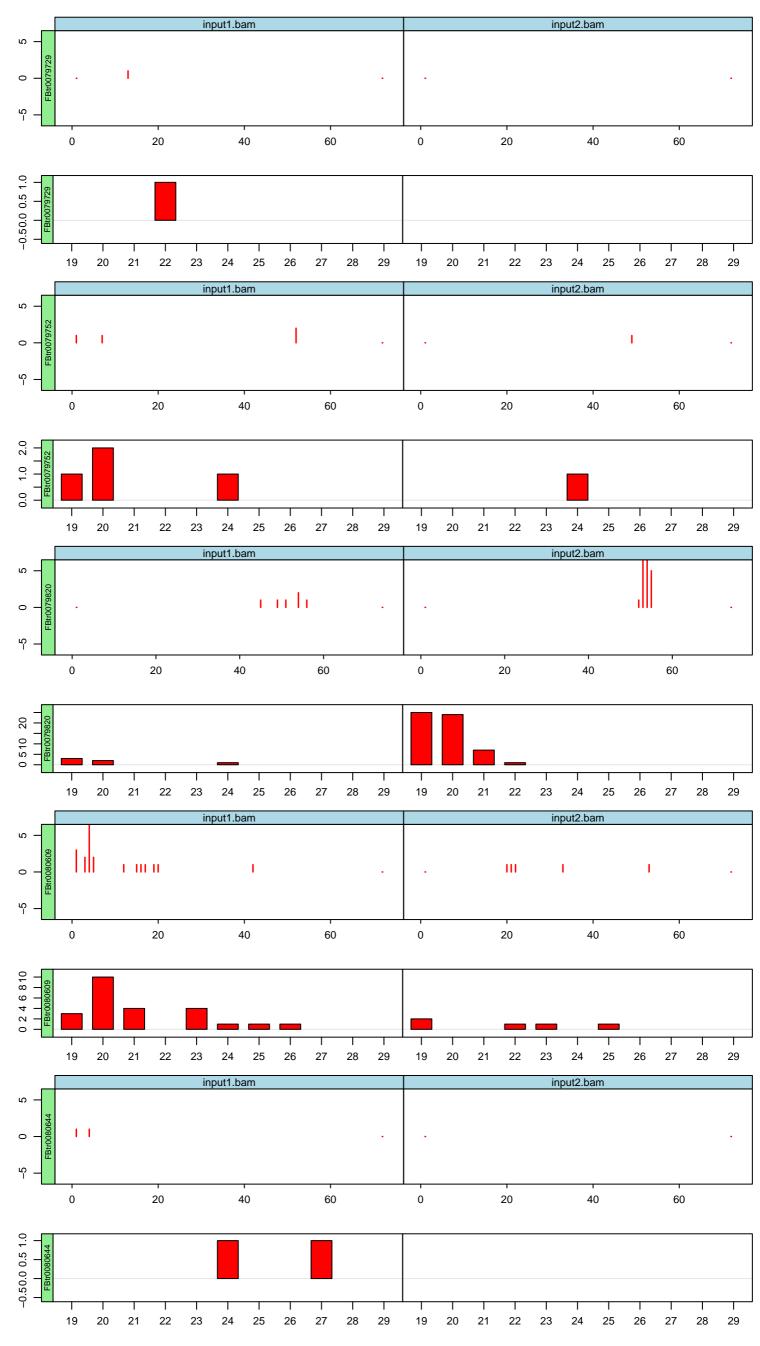
Read count / Read count





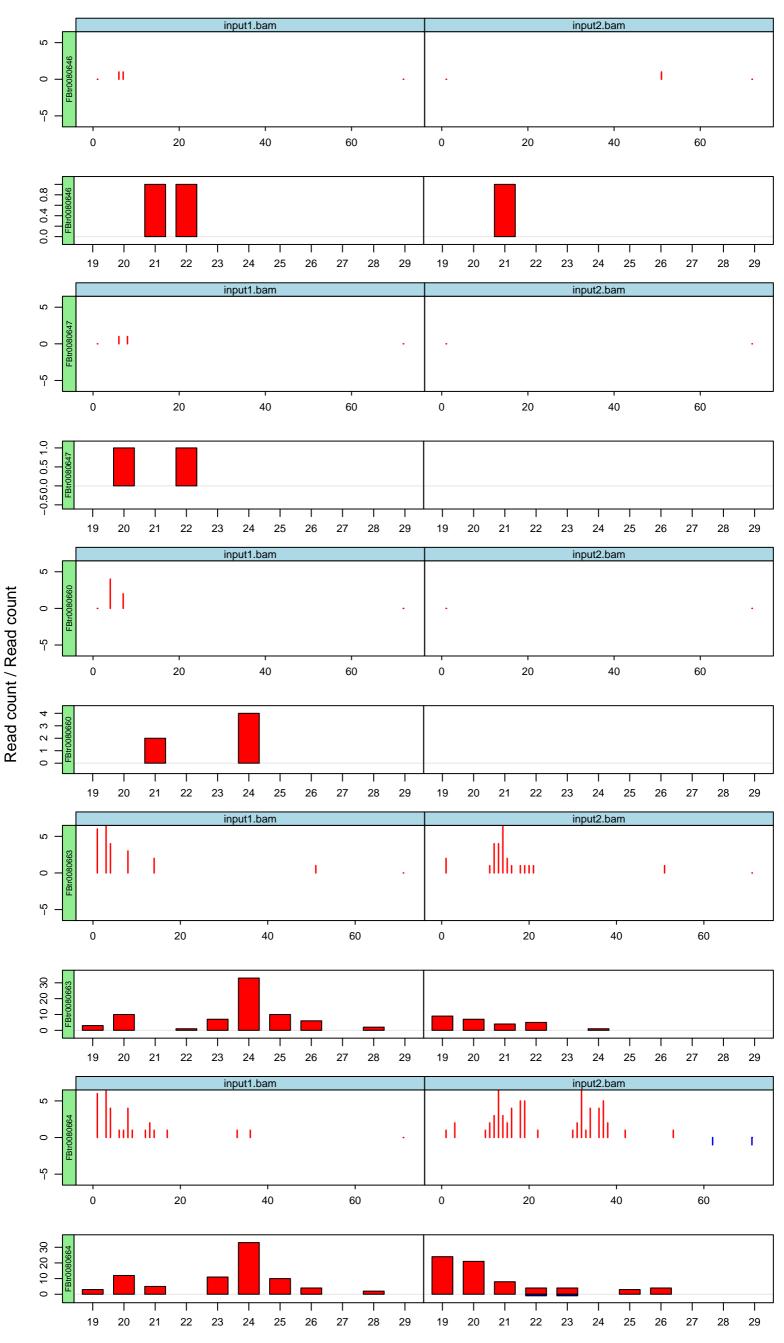
Read count / Read count

Coordinates (nucleotides) / Sizes of reads



Read count / Read count

Coordinates (nucleotides) / Sizes of reads



Coordinates (nucleotides) / Sizes of reads