```
BLMTfil = {
	exec "samtools view -b -L hg19Whitelist.bed -q 10 -o $output.bam $input.sam"
}

sort = {
	exec "samtools sort -o $output.bam $input.bam"
}

rmdup = {
	exec "MarkDuplicates.sh I=$input.bam O=$output.bam M=$output.txt REMOVE_DUPLICATES=true
VALIDATION_STRINGENCY=SILENT"
}

csort = {
	exec "samtools sort -o $output.bam $input.bam"
}

index = {
	exec "samtools index $input.bam"
}

tdf = {
	exec "igvtools count $input.bam $output mm10"
}

nsort = {
	exec "samtools sort -n -o $output.bam $input.bam"
}

bed = {
	exec "bedtools bamtobed -bedpe -i $input.bam > $output"
}

peaks = {
	exec "macs2 callpeak -t $input.bam --nomodel --nolambda --keep-dup all -f BAMPE -g hs -
n $input.bam"
}

Bpipe.run {
	trim + align + BLMTfil + sort + rmdup + [index + tdf, peaks]
}
```

-b Output in the BAM format.

-L *FILE* Only output alignments overlapping the input BED *FILE* [null]

-q *INT* Skip alignments with MAPQ smaller than *INT* [0].

-o *FILE* Output to *FILE [stdout]*

-n Sort by read names (i.e., the **QNAME** field) rather than by chromosomal coordinates.

Bamtobed converting bam fles to bed file for input for MACS2

MACS2:

Fundamental commands

callpeak call the peaks in the data

nomodel no shifting model of peaks used (used for ChipSeq data not required for ATAC-seq)

nolambda by default MACS uses local noise –backfgrpund reads to call peaks

keep-dup all if a set parameter is defined MACS will ingore read counts that exceed the specified parameter.