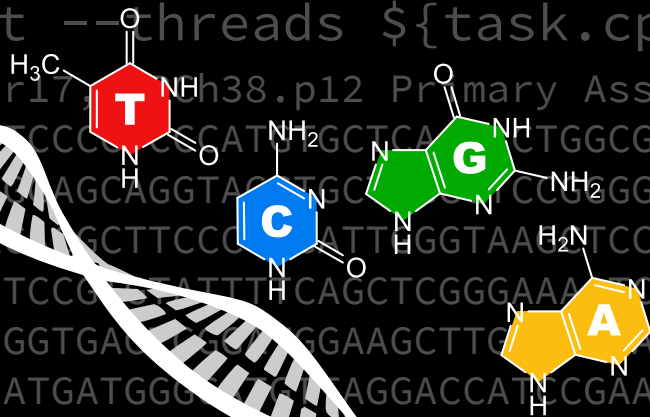


```
bwa mem -R \"${readGroup}\" ${extra} -t ${task.cpus}
${genomeFile} ${fastqFile1} ${fastqFile2} | \
samtools sort --threads ${task.cpus} -m 2G - > ${id}
```



>Homo sapiens chr17:10,380,000-10,380,038.p12 Primary Assembly

TGGGATTGGTCTCCCGCCCATGCTCACTGGCGCTAAAAGGAGCCTCAAAA
 ACCACCGTCCAGCAGGTATGCTCCCGGGAATTTGCGTTCCGGGGAGC
 CACTACGACGGTGAAGCTTCCCGATTGGTAAATCCTGAACCTGATGAGTCCTCTC
 GTCAGCTCTCGGCTCCCGATTTCAGCTCGGGAAAAGCTGGGGCTGGTGGGAGTG
 ACTTAGCAGTTTGGGGGTGACGCGGAAGCTTGGGGATCATCTGGAGTCTTG
 GGAGACCTGCTGTAGATGATGGGCTTAGGACCATTCGAACTCAAAGTTGAACGCCTAGCCAGA

