

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 01:52:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506319.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1506319 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506319.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 01:52:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506319.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,062,932
Mapped reads	2,870,940 / 70.66%
Unmapped reads	1,191,992 / 29.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,202 / 0.89%
Read min/max/mean length	30 / 94 / 94.32
Duplicated reads (estimated)	346,153 / 8.52%
Duplication rate	9.51%
Clipped reads	1,742,067 / 42.88%

2.2. ACGT Content

Number/percentage of A's	58,533,238 / 25.7%
Number/percentage of C's	44,104,058 / 19.36%
Number/percentage of T's	67,920,953 / 29.82%
Number/percentage of G's	57,178,377 / 25.1%
Number/percentage of N's	51,097 / 0.02%
GC Percentage	44.46%

2.3. Coverage

Mean	0.0736

Standard Deviation	0.5772
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2.4. Mapping Quality

Mean Mapping Quality	47.81
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2.5. Mismatches and indels

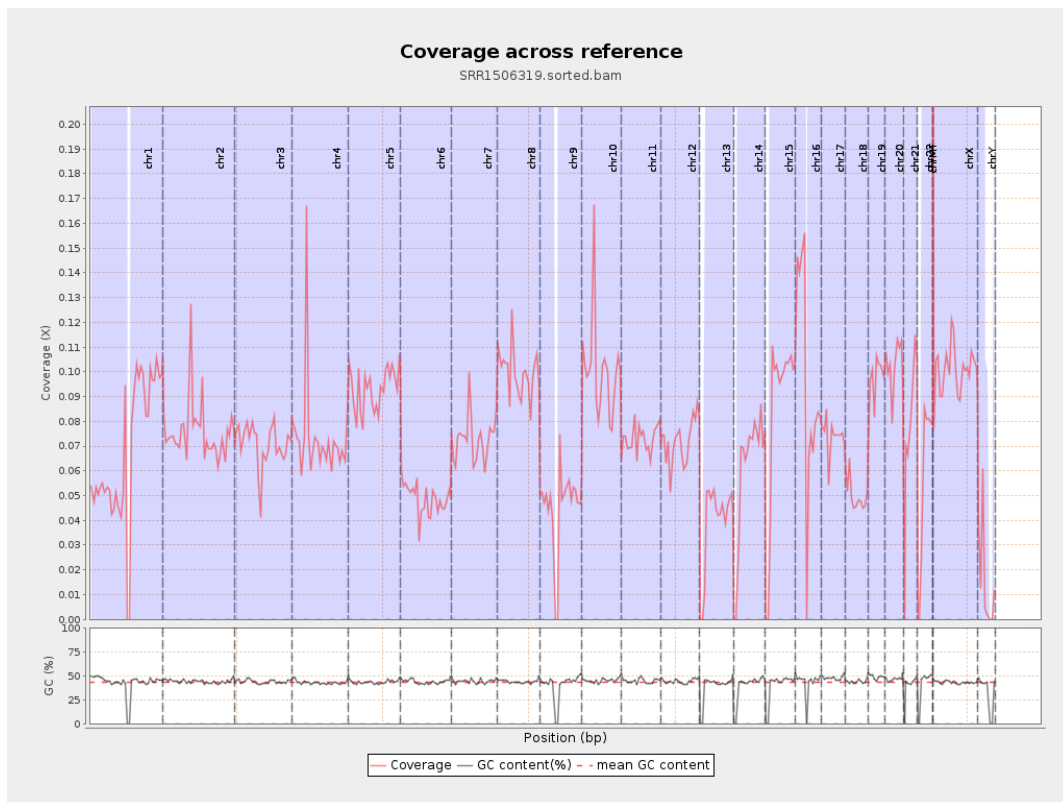
General error rate	0.76%
Mismatches	1,671,951
Insertions	18,409
Mapped reads with at least one insertion	0.62%
Deletions	46,392
Mapped reads with at least one deletion	1.59%
Homopolymer indels	42.2%

2.6. Chromosome stats

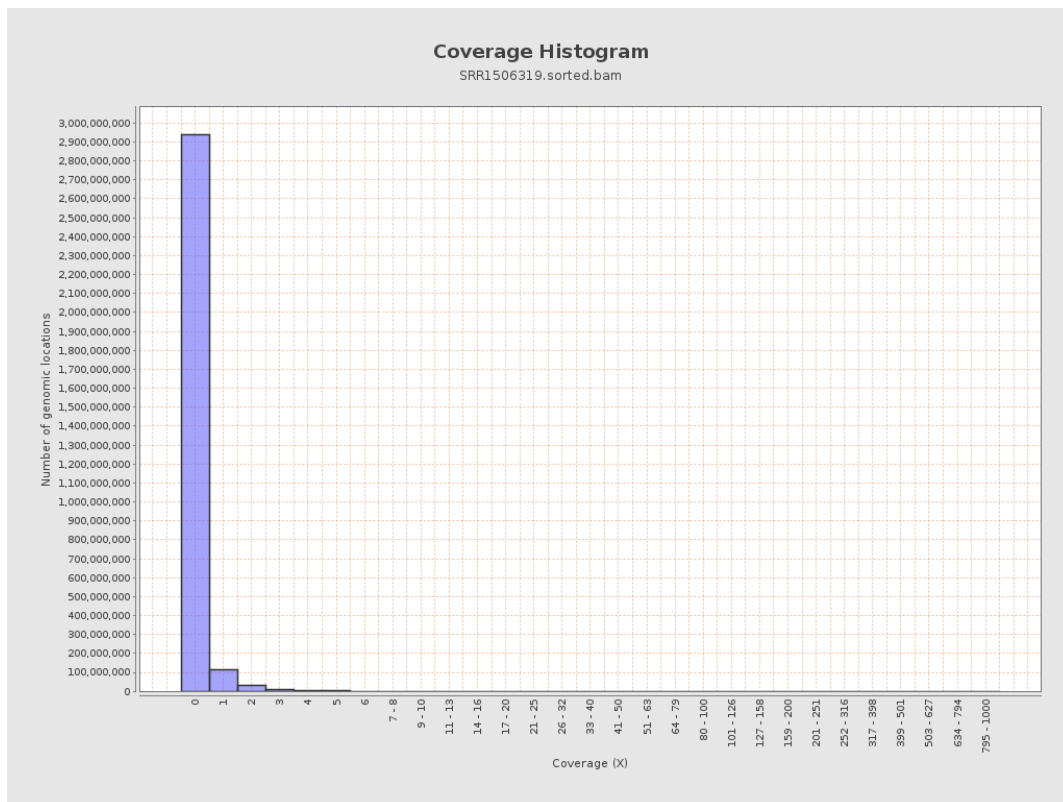
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17022270	0.0683	0.9305
chr2	243199373	18461890	0.0759	0.6639
chr3	198022430	14026886	0.0708	0.3616
chr4	191154276	13997373	0.0732	0.5379
chr5	180915260	16897548	0.0934	0.4222
chr6	171115067	8305141	0.0485	0.3232
chr7	159138663	11628987	0.0731	0.718

chr8	146364022	14536166	0.0993	0.6527
chr9	141213431	6399310	0.0453	0.5904
chr10	135534747	13519210	0.0997	0.7299
chr11	135006516	9816881	0.0727	0.5573
chr12	133851895	9659309	0.0722	0.374
chr13	115169878	4533548	0.0394	0.2628
chr14	107349540	6529713	0.0608	0.3754
chr15	102531392	8504170	0.0829	0.4048
chr16	90354753	8608242	0.0953	0.5007
chr17	81195210	6027744	0.0742	0.4399
chr18	78077248	3900323	0.05	0.7741
chr19	59128983	5763783	0.0975	0.7555
chr20	63025520	6468145	0.1026	0.4722
chr21	48129895	3844470	0.0799	0.4843
chr22	51304566	2886414	0.0563	0.3435
chrMT	16571	6770	0.4085	0.779
chrX	155270560	15638024	0.1007	0.5033
chrY	59373566	901511	0.0152	0.5774

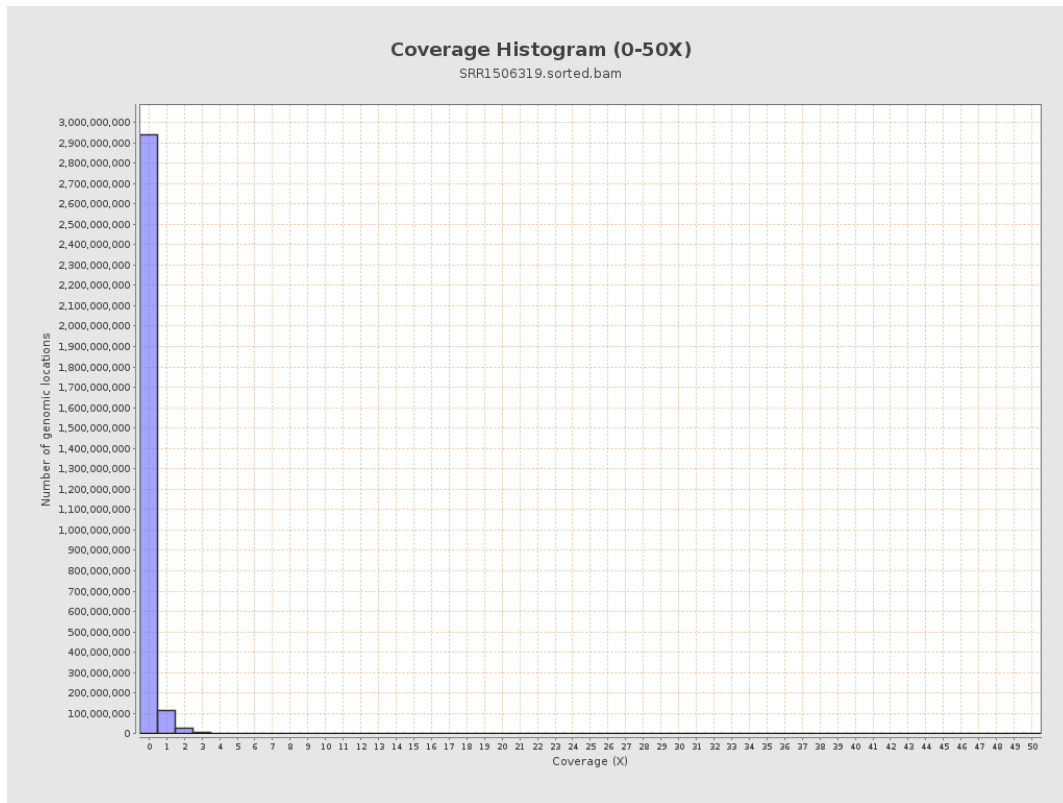
3. Results : Coverage across reference



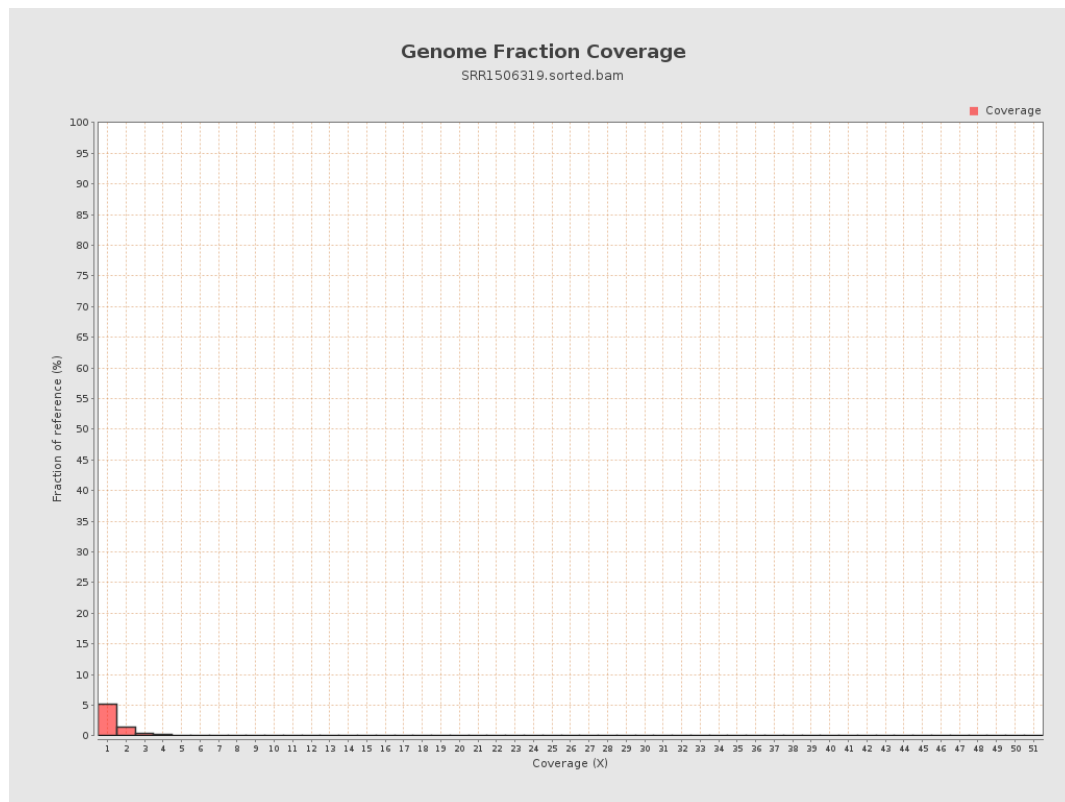
4. Results : Coverage Histogram



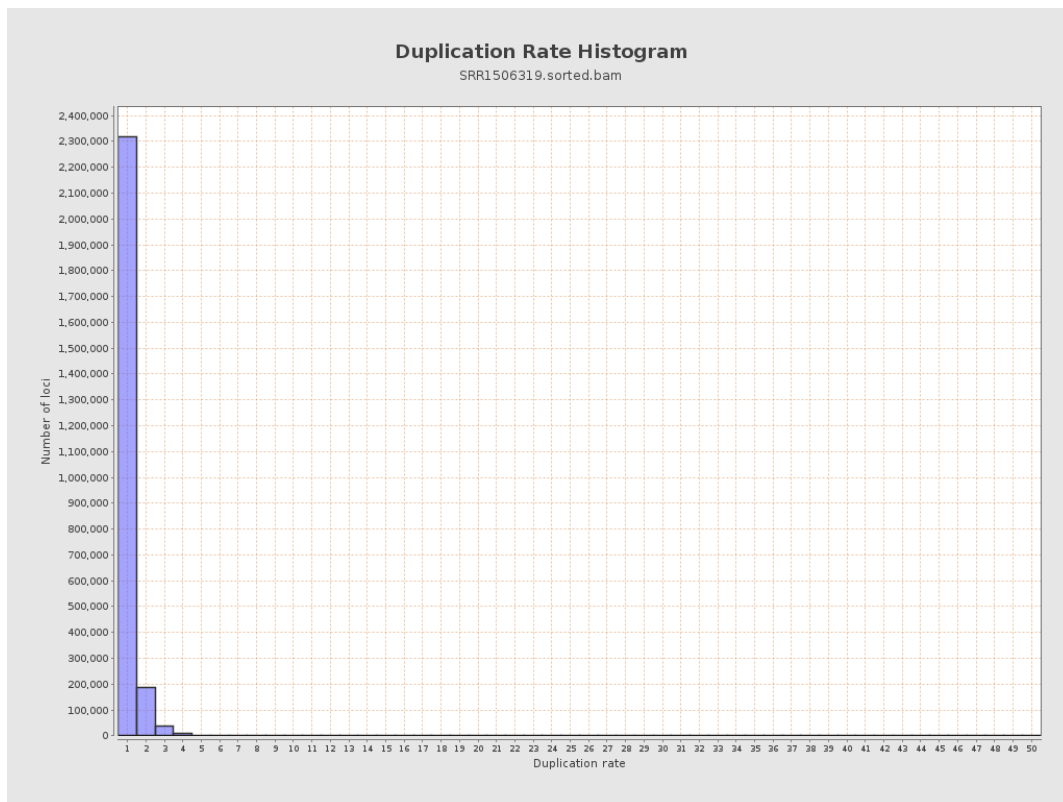
5. Results : Coverage Histogram (0-50X)



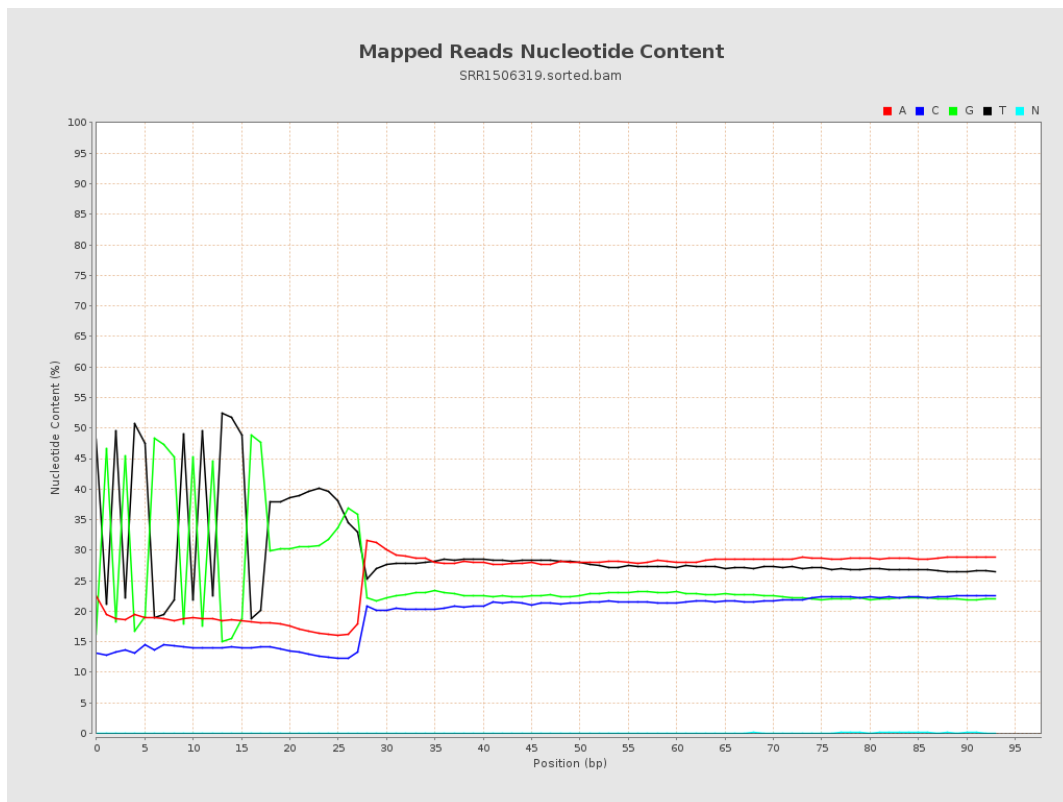
6. Results : Genome Fraction Coverage



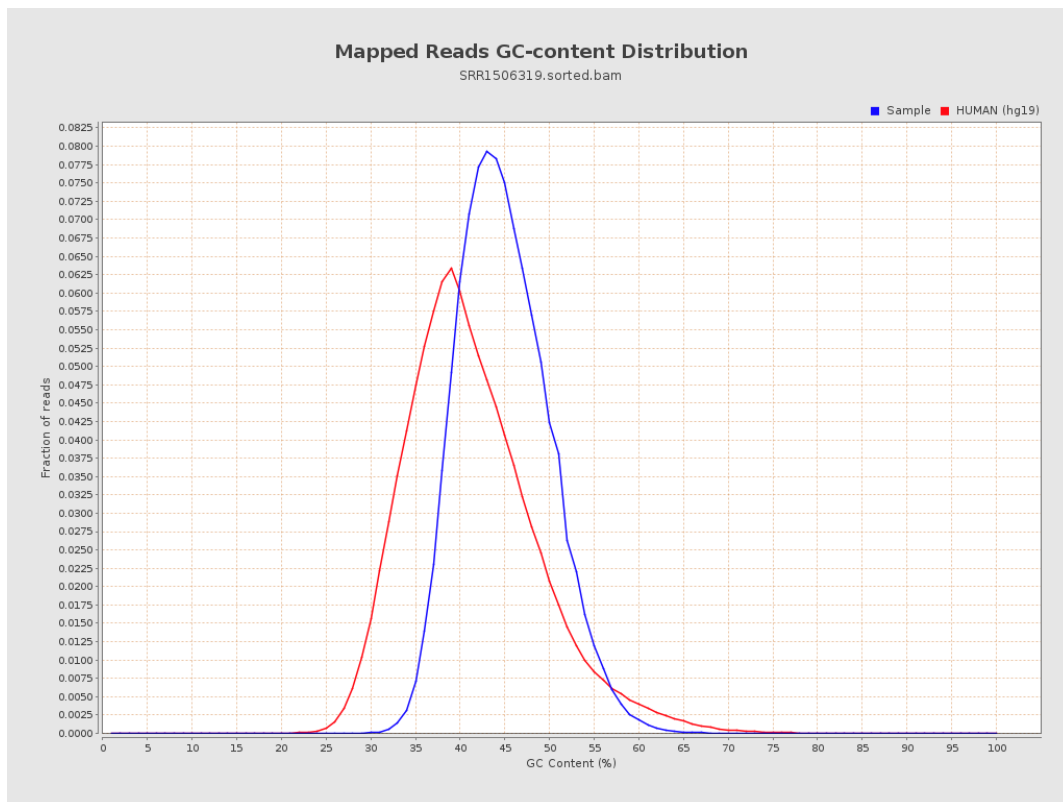
7. Results : Duplication Rate Histogram



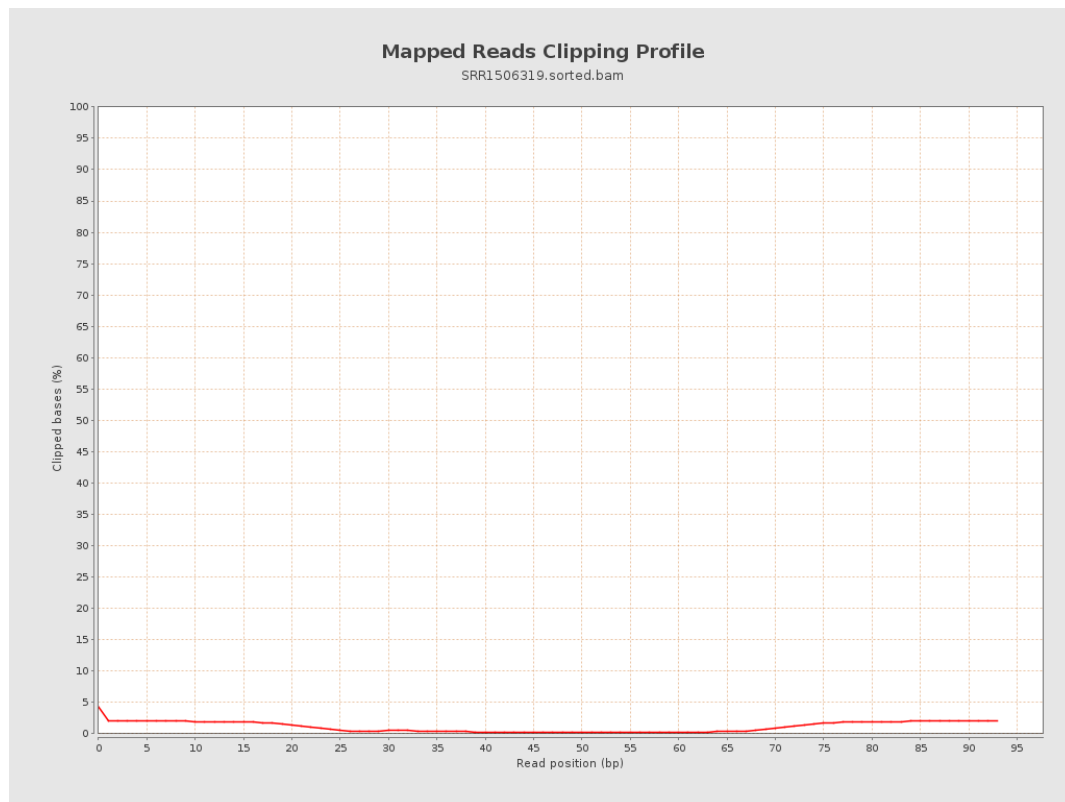
8. Results : Mapped Reads Nucleotide Content



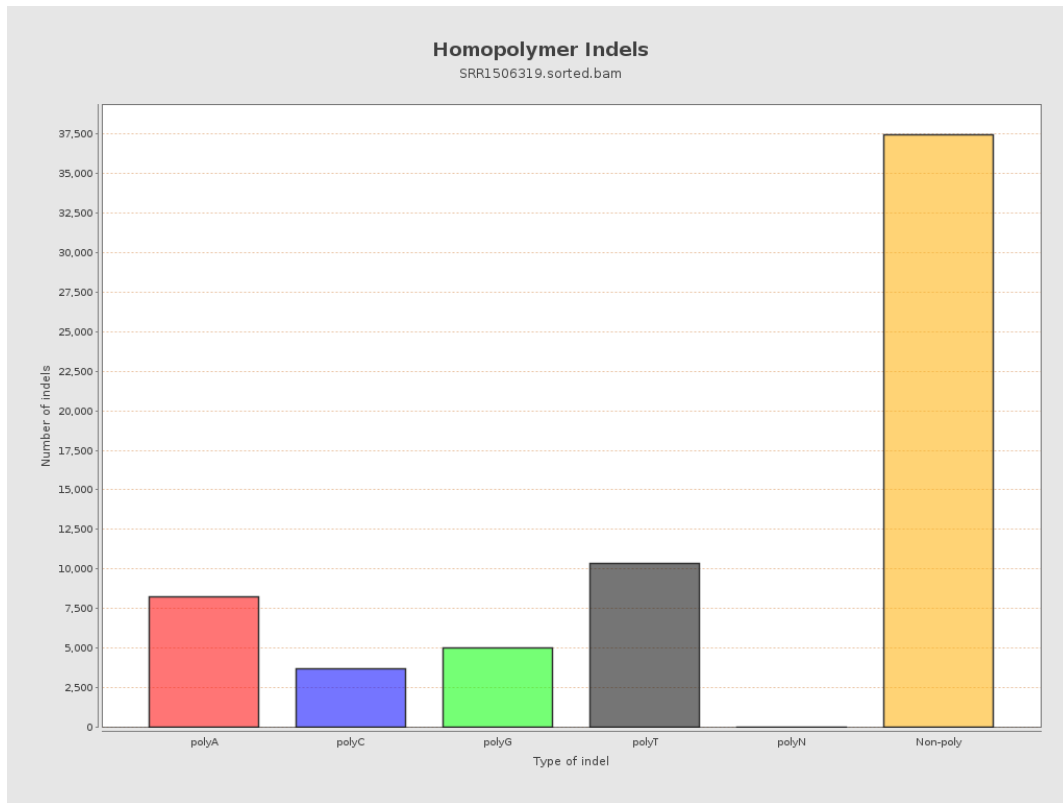
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

