

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:03:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081920.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_SRR3081920 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081920.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:03:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081920.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,126,164
Mapped reads	2,924,016 / 93.53%
Unmapped reads	202,148 / 6.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,701 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	142,232 / 4.55%
Duplication rate	3.63%
Clipped reads	1,020,186 / 32.63%

2.2. ACGT Content

Number/percentage of A's	58,662,916 / 29.05%
Number/percentage of C's	37,447,272 / 18.54%
Number/percentage of T's	63,828,011 / 31.61%
Number/percentage of G's	41,973,307 / 20.79%
Number/percentage of N's	26,514 / 0.01%
GC Percentage	39.33%

2.3. Coverage

Mean	0.0653

Standard Deviation	0.6304
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2.4. Mapping Quality

Mean Mapping Quality	47.3
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2.5. Mismatches and indels

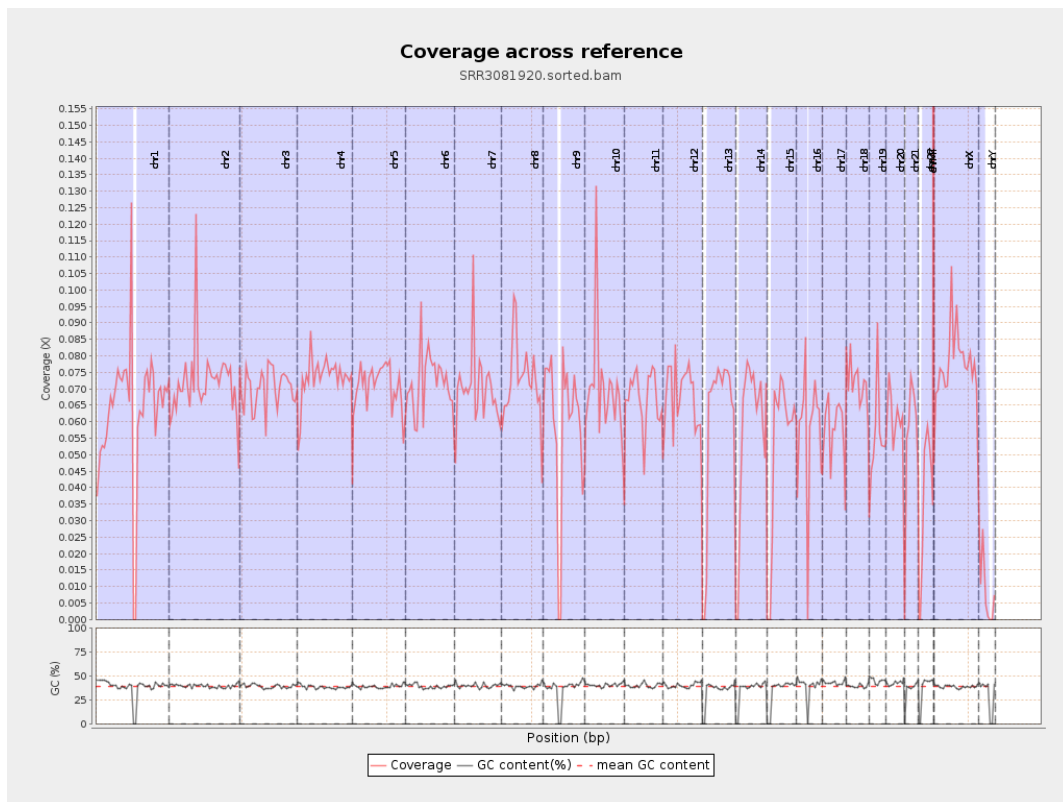
General error rate	0.77%
Mismatches	1,534,756
Insertions	14,712
Mapped reads with at least one insertion	0.5%
Deletions	41,909
Mapped reads with at least one deletion	1.42%
Homopolymer indels	47.75%

2.6. Chromosome stats

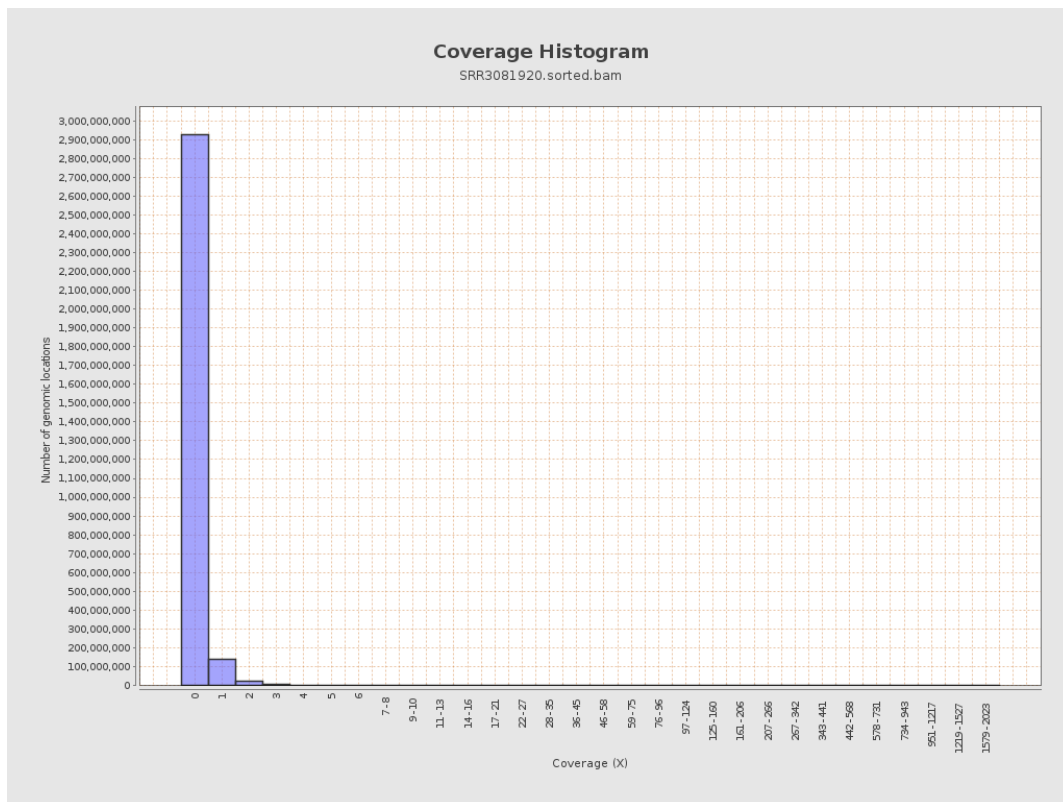
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15856315	0.0636	1.2994
chr2	243199373	17494610	0.0719	0.5853
chr3	198022430	13922580	0.0703	0.3149
chr4	191154276	14038029	0.0734	0.339
chr5	180915260	12828108	0.0709	0.3117
chr6	171115067	12270412	0.0717	0.4052
chr7	159138663	11185803	0.0703	0.7022

chr8	146364022	10534371	0.072	1.2707
chr9	141213431	8420320	0.0596	0.4882
chr10	135534747	9464299	0.0698	0.641
chr11	135006516	9023397	0.0668	0.429
chr12	133851895	9048723	0.0676	0.3128
chr13	115169878	6808958	0.0591	0.2817
chr14	107349540	6143467	0.0572	0.3005
chr15	102531392	5432155	0.053	0.2673
chr16	90354753	5163612	0.0571	0.3427
chr17	81195210	4626638	0.057	0.3105
chr18	78077248	5595666	0.0717	0.941
chr19	59128983	3334366	0.0564	0.8811
chr20	63025520	3819017	0.0606	0.3025
chr21	48129895	2682266	0.0557	0.3025
chr22	51304566	1831432	0.0357	0.2156
chrMT	16571	9467	0.5713	0.8891
chrX	155270560	11969889	0.0771	0.3746
chrY	59373566	508363	0.0086	0.1953

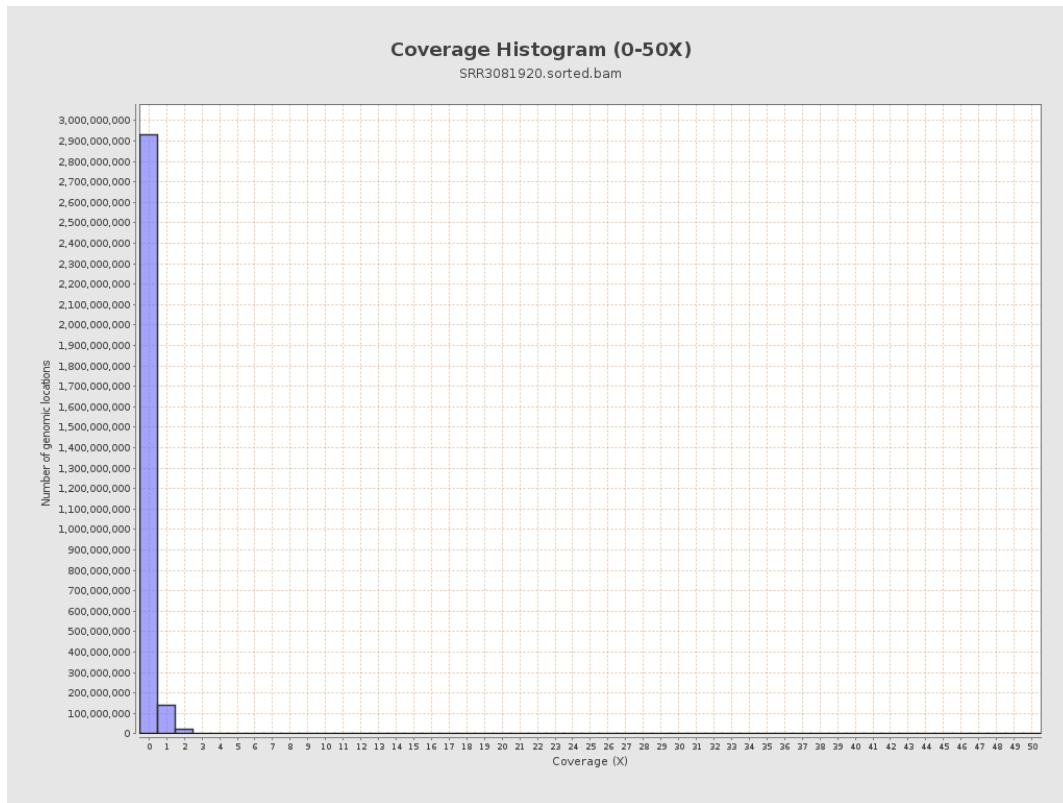
3. Results : Coverage across reference



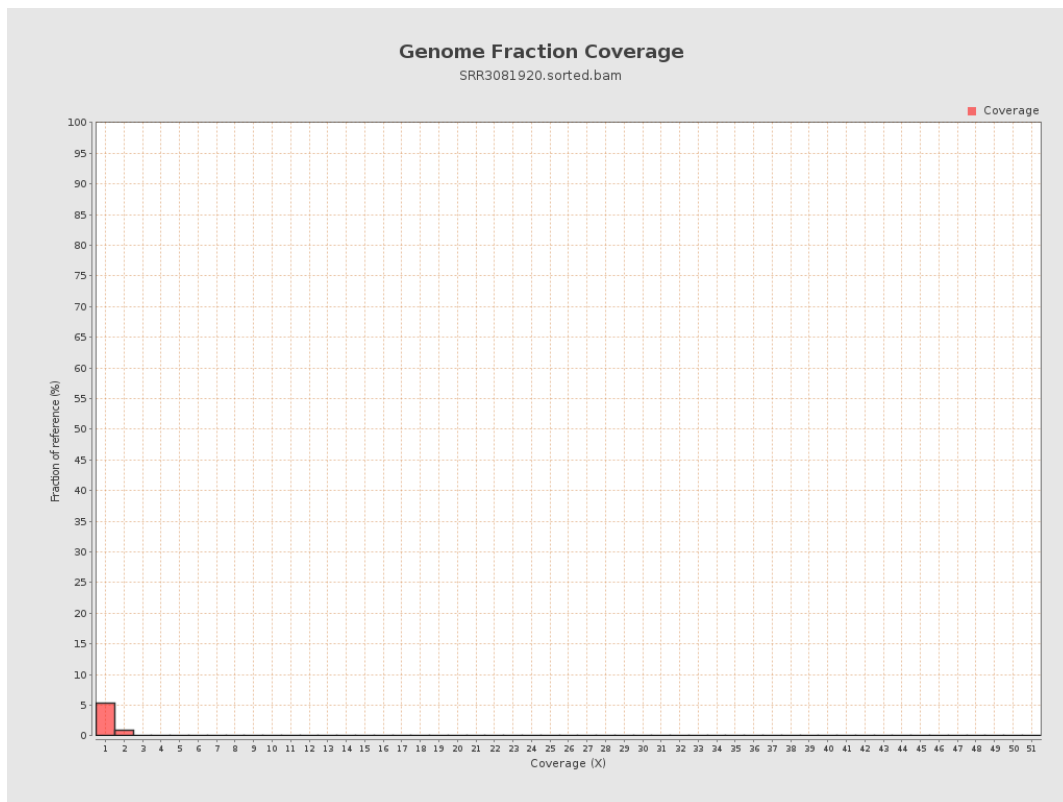
4. Results : Coverage Histogram



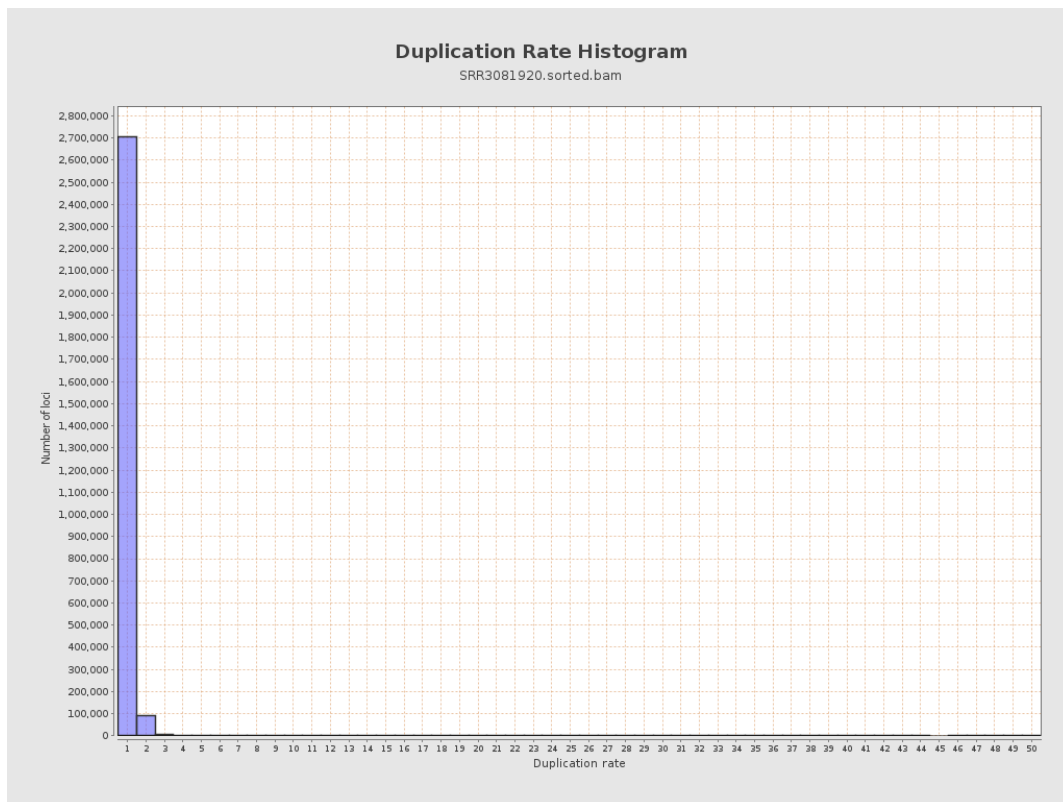
5. Results : Coverage Histogram (0-50X)



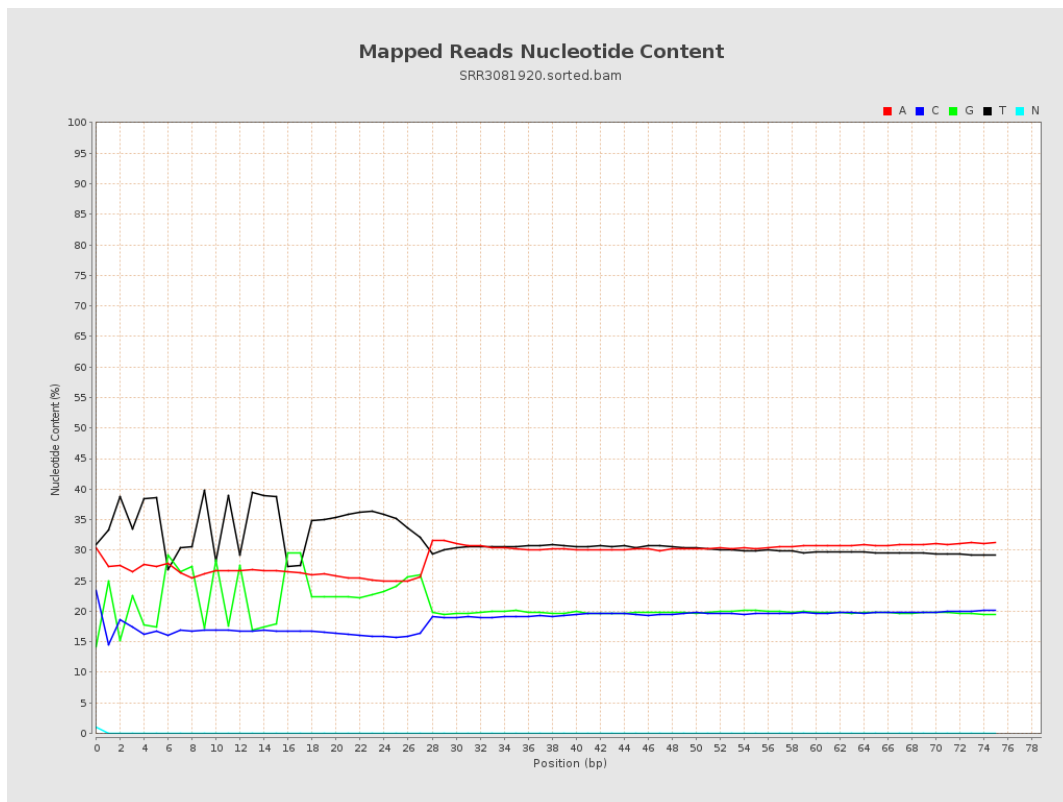
6. Results : Genome Fraction Coverage



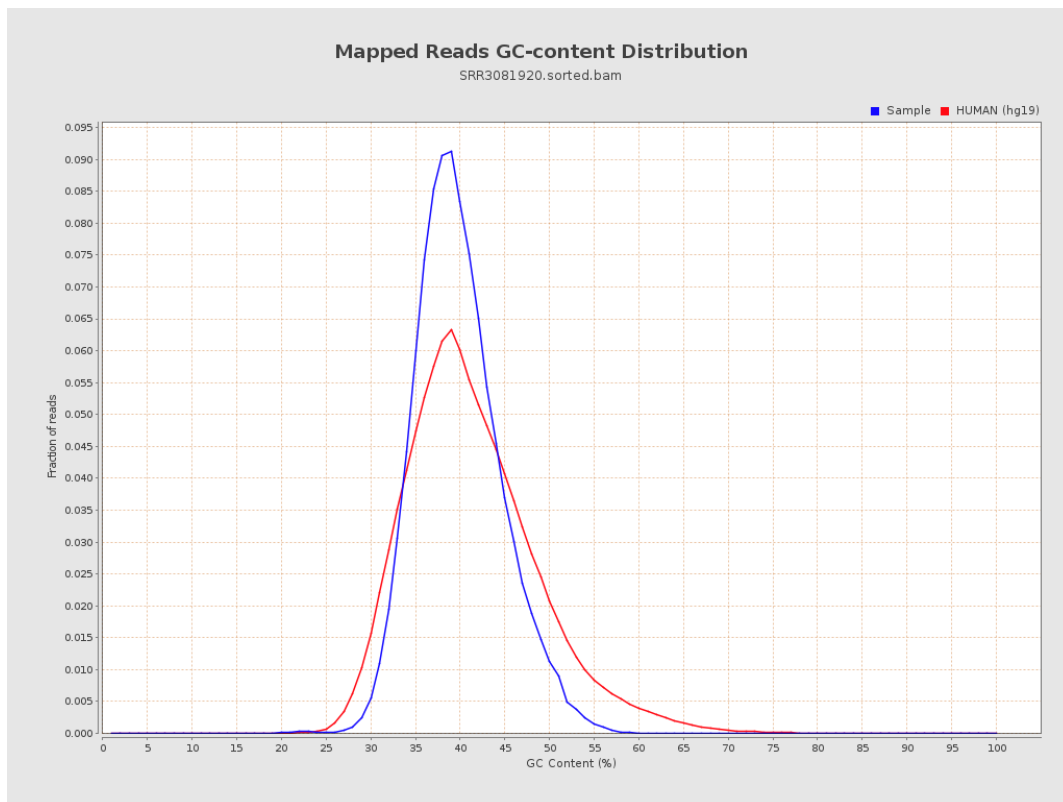
7. Results : Duplication Rate Histogram



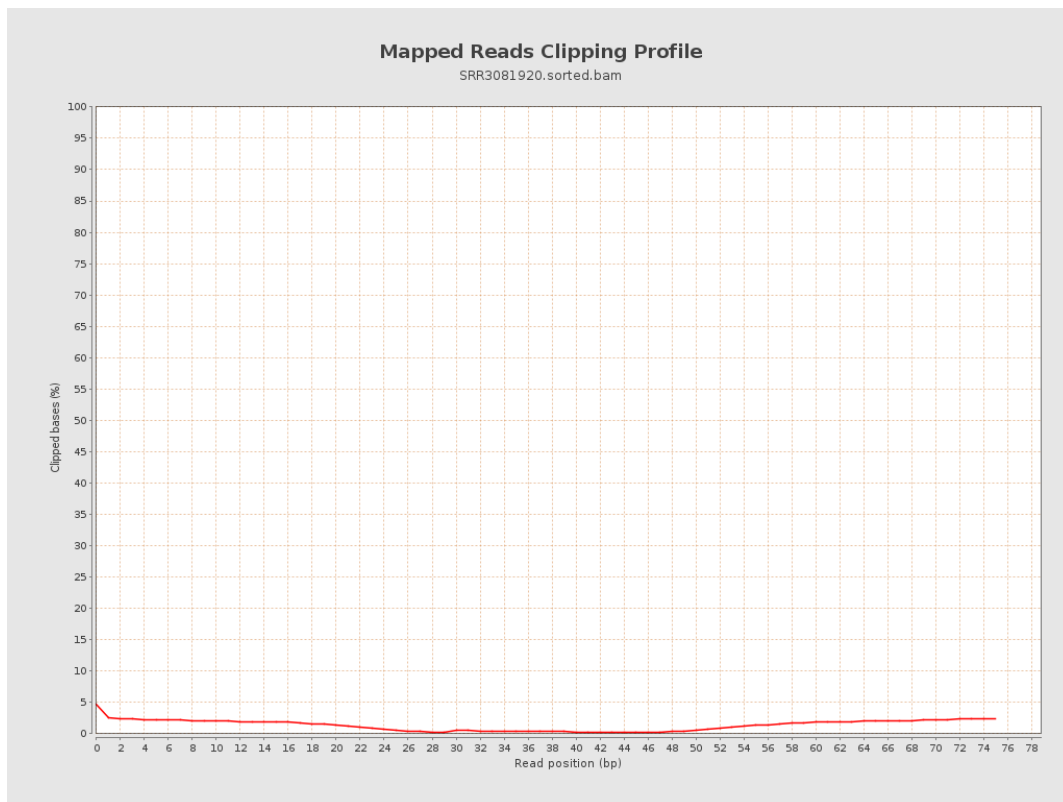
8. Results : Mapped Reads Nucleotide Content



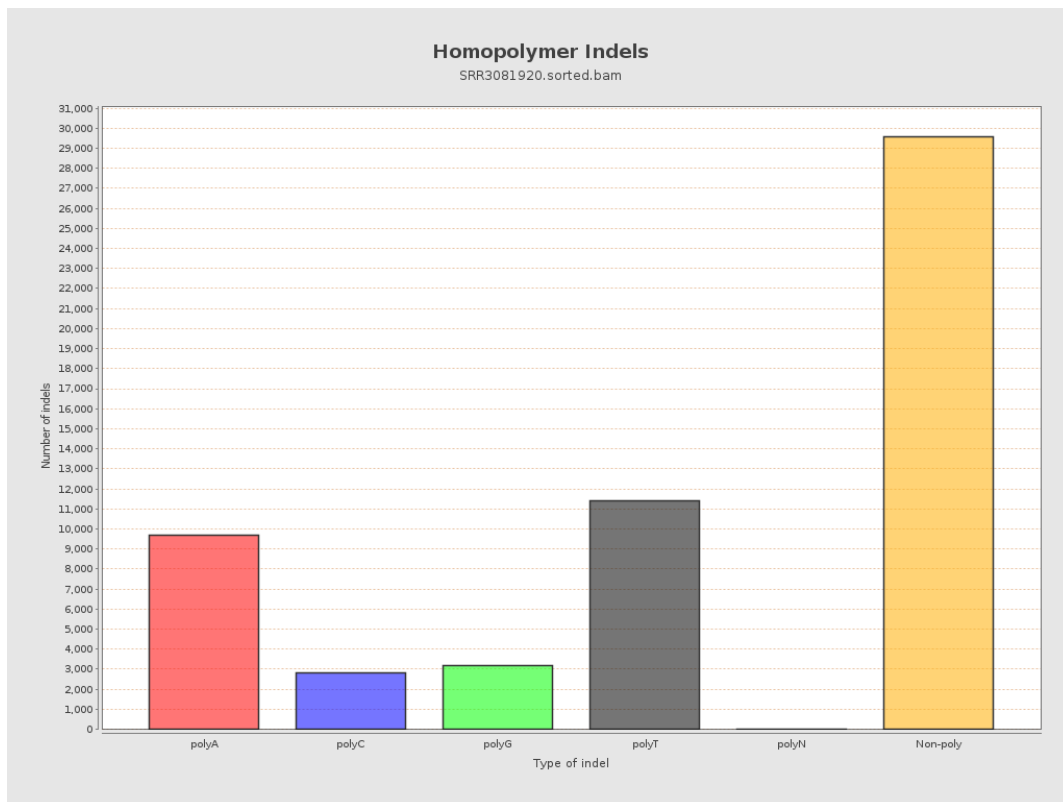
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

