

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:31:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004064.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_SRR6004064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004064.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:31:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,875,645
Mapped reads	2,067,542 / 71.9%
Unmapped reads	808,103 / 28.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,236 / 0.7%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	367,625 / 12.78%
Duplication rate	12.38%
Clipped reads	1,077,272 / 37.46%

2.2. ACGT Content

Number/percentage of A's	37,439,097 / 27.96%
Number/percentage of C's	24,253,120 / 18.11%
Number/percentage of T's	42,857,072 / 32.01%
Number/percentage of G's	29,235,299 / 21.84%
Number/percentage of N's	102,092 / 0.08%
GC Percentage	39.95%

2.3. Coverage

Mean	0.0433

Standard Deviation	0.5248
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2.4. Mapping Quality

Mean Mapping Quality	43.57
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2.5. Mismatches and indels

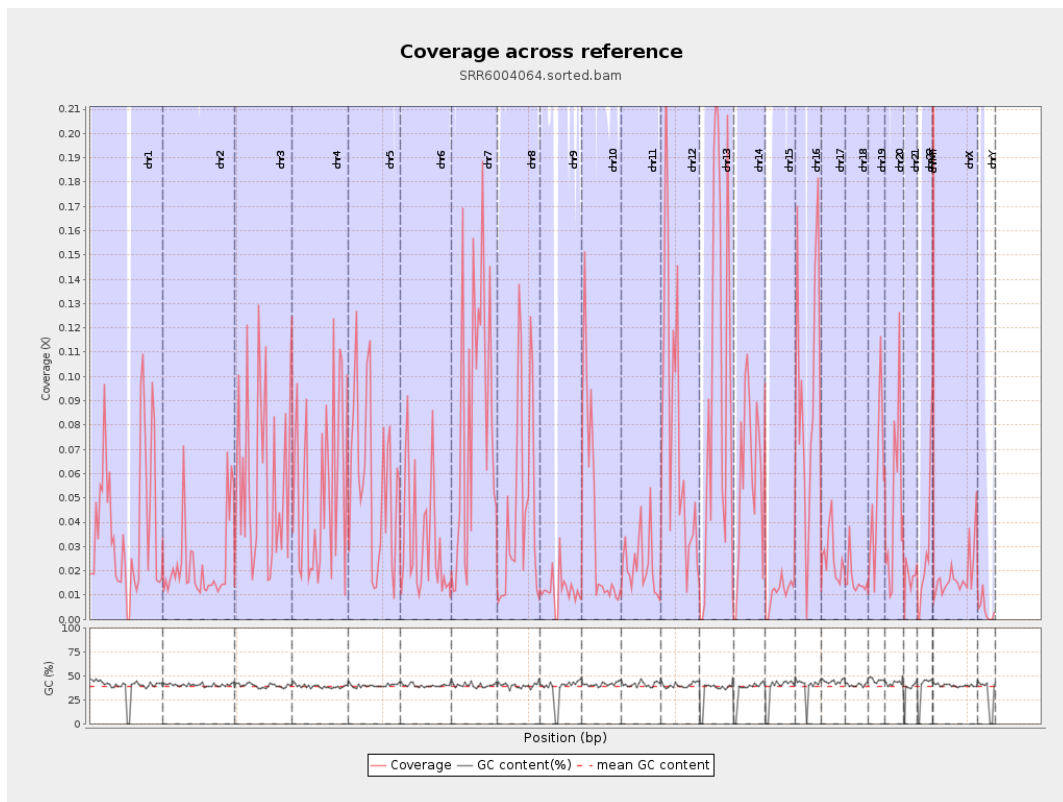
General error rate	0.86%
Mismatches	1,138,283
Insertions	9,915
Mapped reads with at least one insertion	0.48%
Deletions	35,348
Mapped reads with at least one deletion	1.69%
Homopolymer indels	46.67%

2.6. Chromosome stats

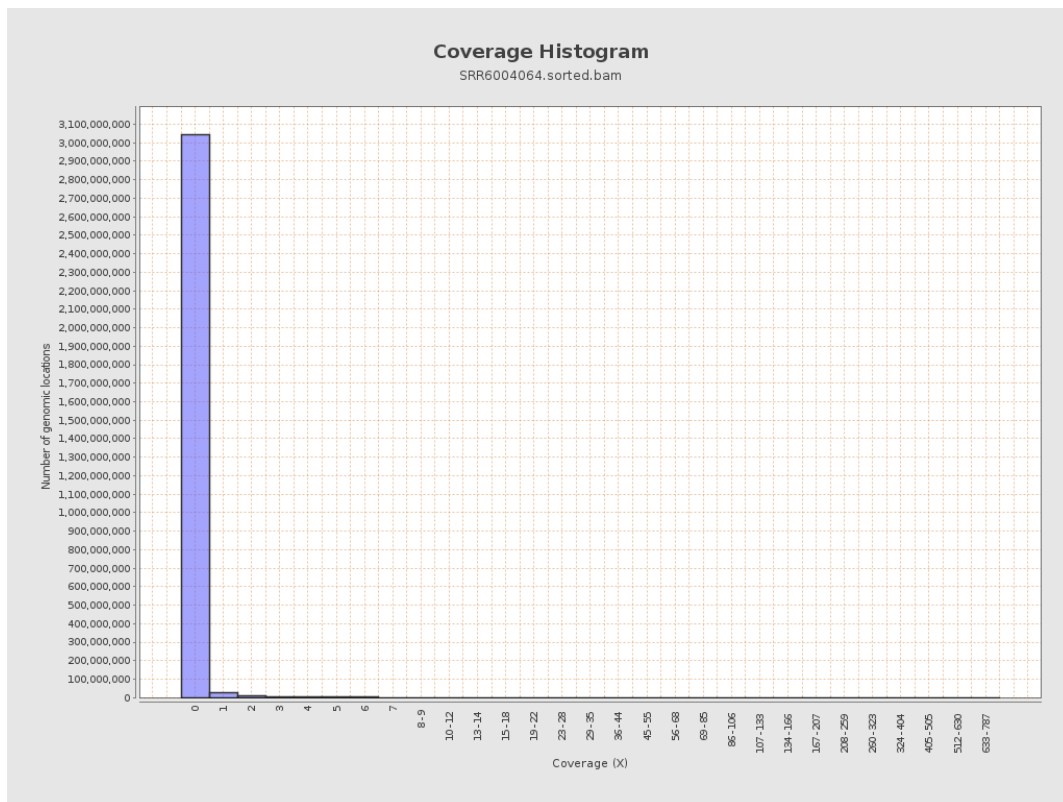
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9667441	0.0388	0.4805
chr2	243199373	5555563	0.0228	0.4196
chr3	198022430	11416512	0.0577	0.514
chr4	191154276	10412133	0.0545	0.5304
chr5	180915260	9898997	0.0547	0.5055
chr6	171115067	5490736	0.0321	0.3918
chr7	159138663	12863039	0.0808	1.1173

chr8	146364022	6843380	0.0468	0.6037
chr9	141213431	1712768	0.0121	0.2519
chr10	135534747	5266167	0.0389	0.4417
chr11	135006516	3125497	0.0232	0.335
chr12	133851895	10132913	0.0757	0.5856
chr13	115169878	11301609	0.0981	0.6929
chr14	107349540	6382384	0.0595	0.5357
chr15	102531392	1123133	0.011	0.4052
chr16	90354753	7923781	0.0877	0.6404
chr17	81195210	2076222	0.0256	0.3336
chr18	78077248	1294159	0.0166	0.5346
chr19	59128983	3133344	0.053	0.4999
chr20	63025520	2956392	0.0469	0.4544
chr21	48129895	846089	0.0176	0.277
chr22	51304566	1445926	0.0282	0.3362
chrMT	16571	57698	3.4819	4.0783
chrX	155270560	2779605	0.0179	0.2844
chrY	59373566	240529	0.0041	0.1734

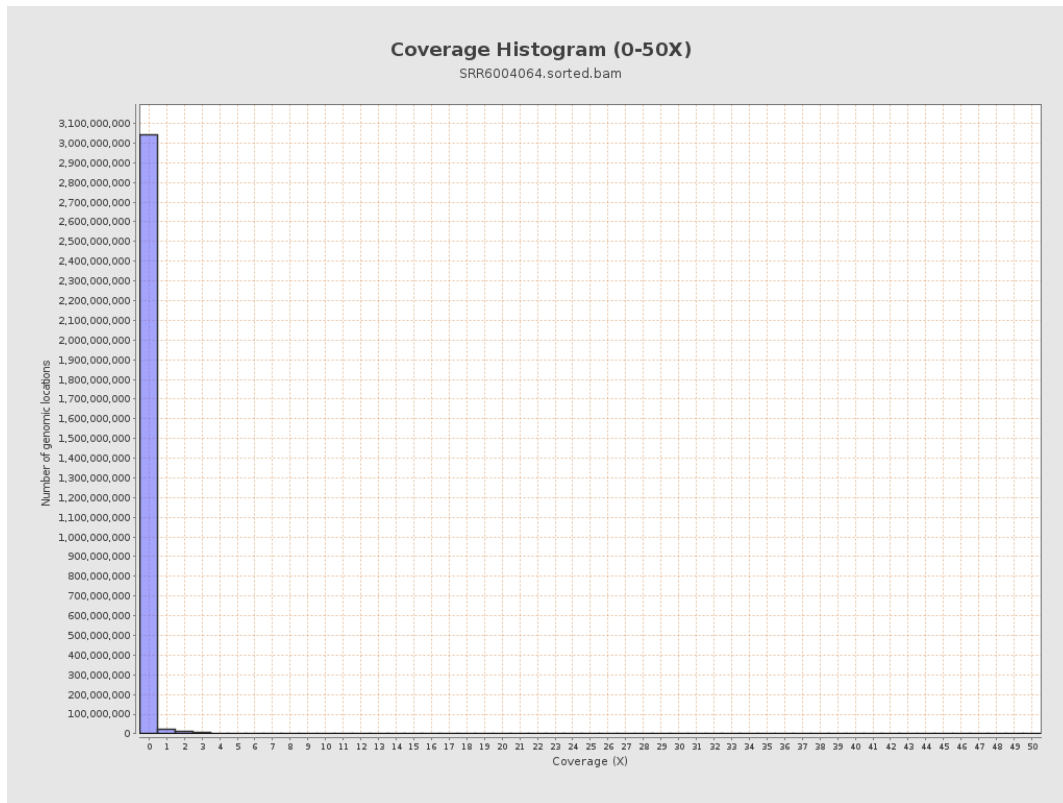
3. Results : Coverage across reference



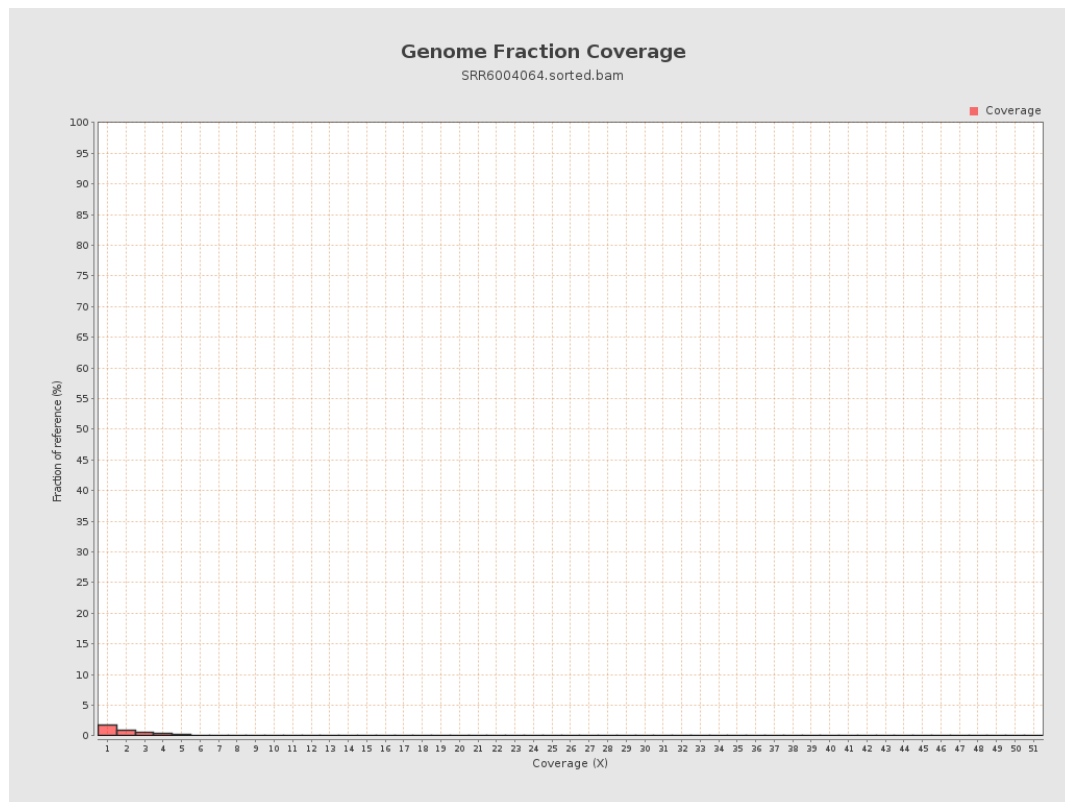
4. Results : Coverage Histogram



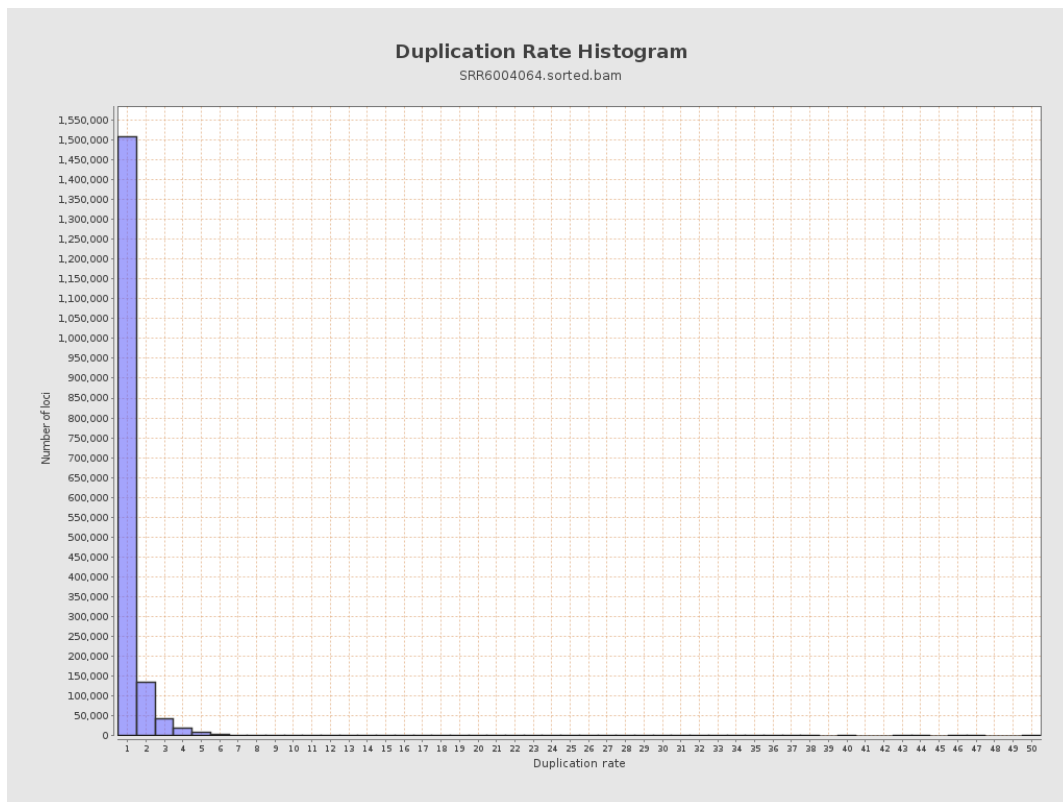
5. Results : Coverage Histogram (0-50X)



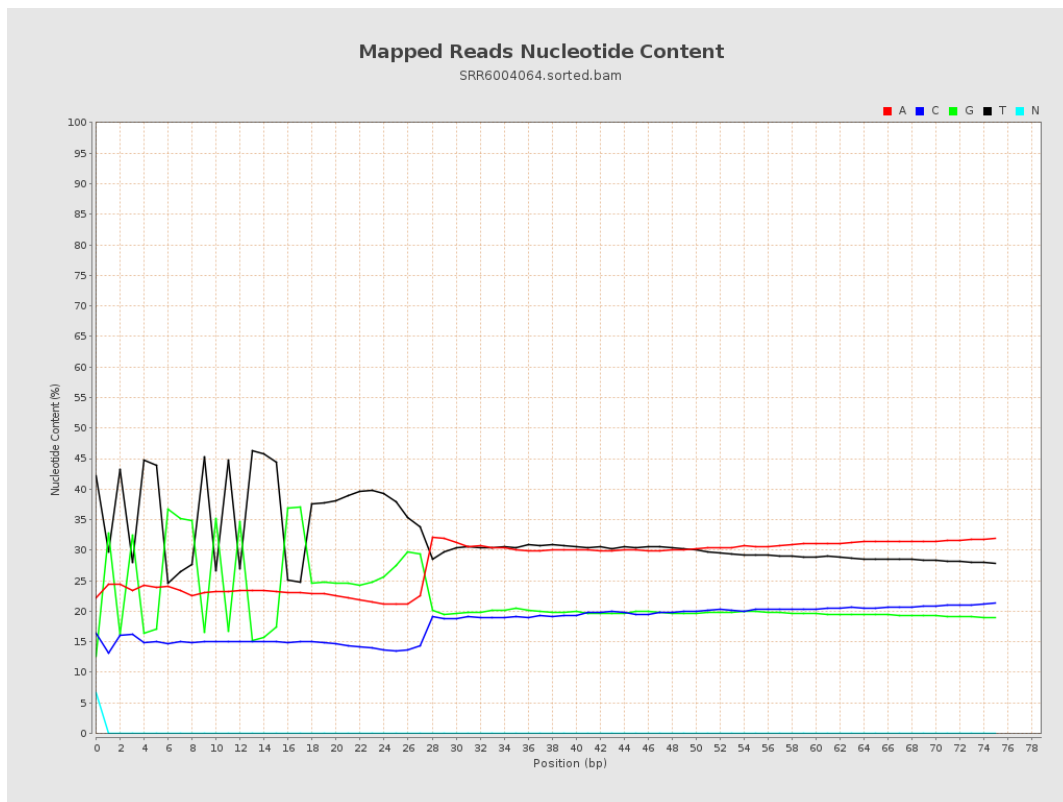
6. Results : Genome Fraction Coverage



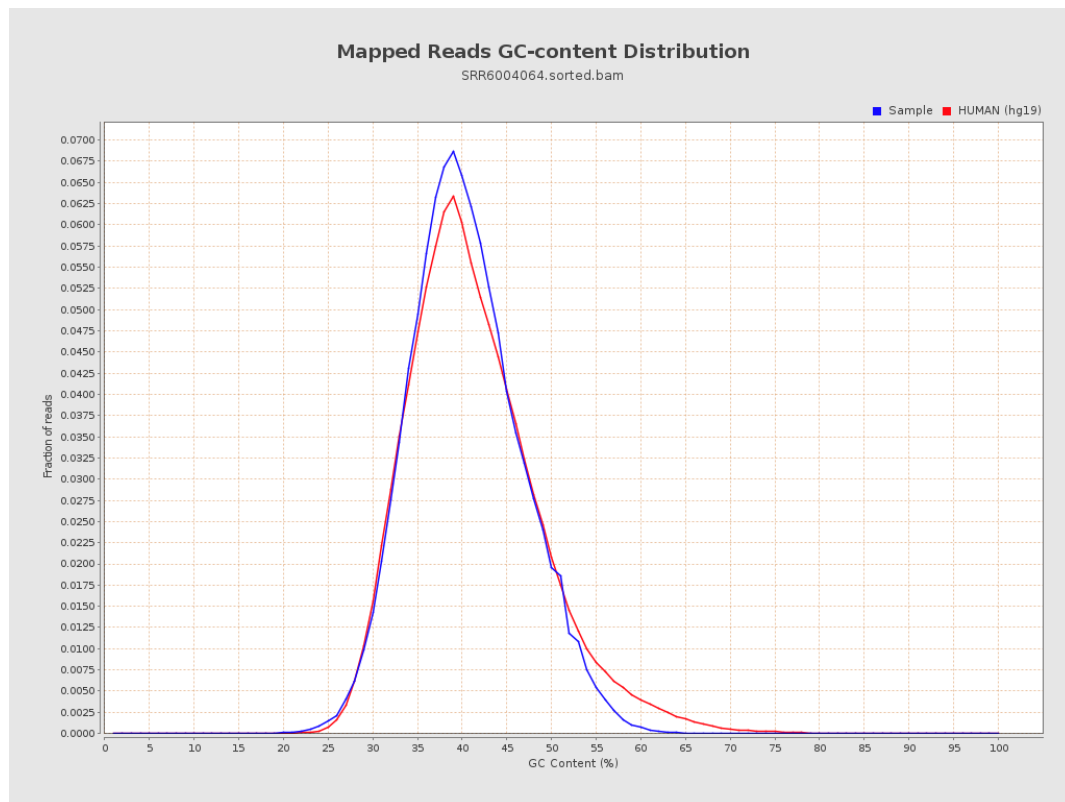
7. Results : Duplication Rate Histogram



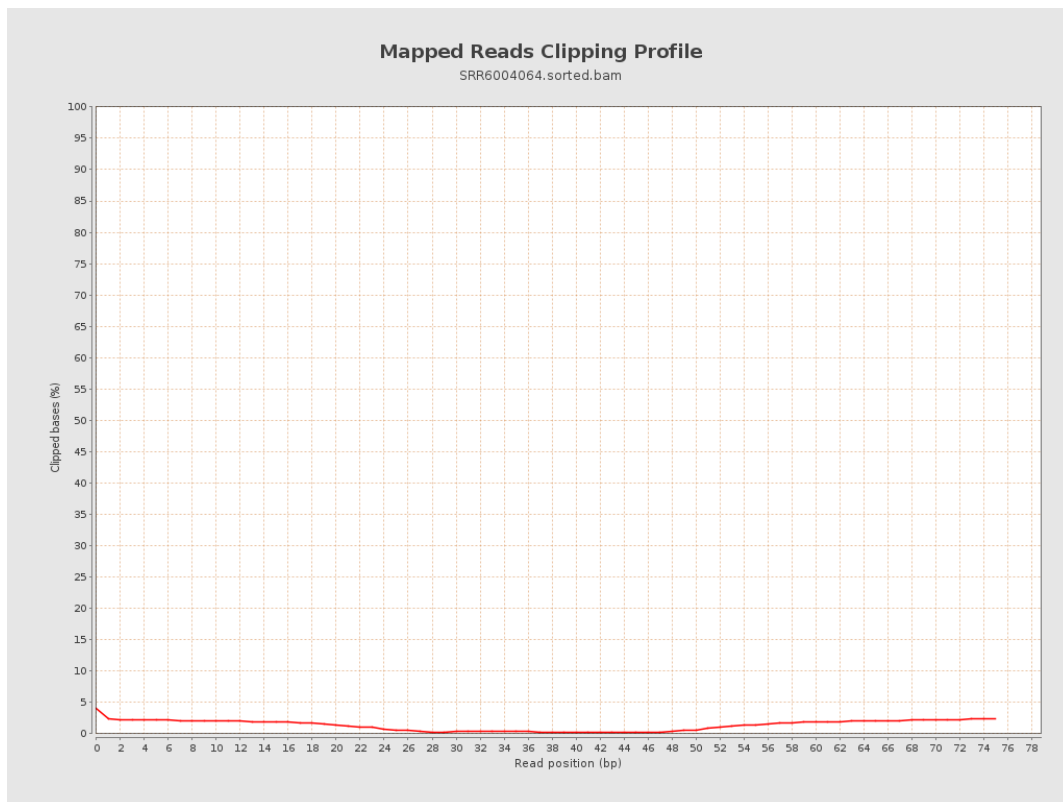
8. Results : Mapped Reads Nucleotide Content



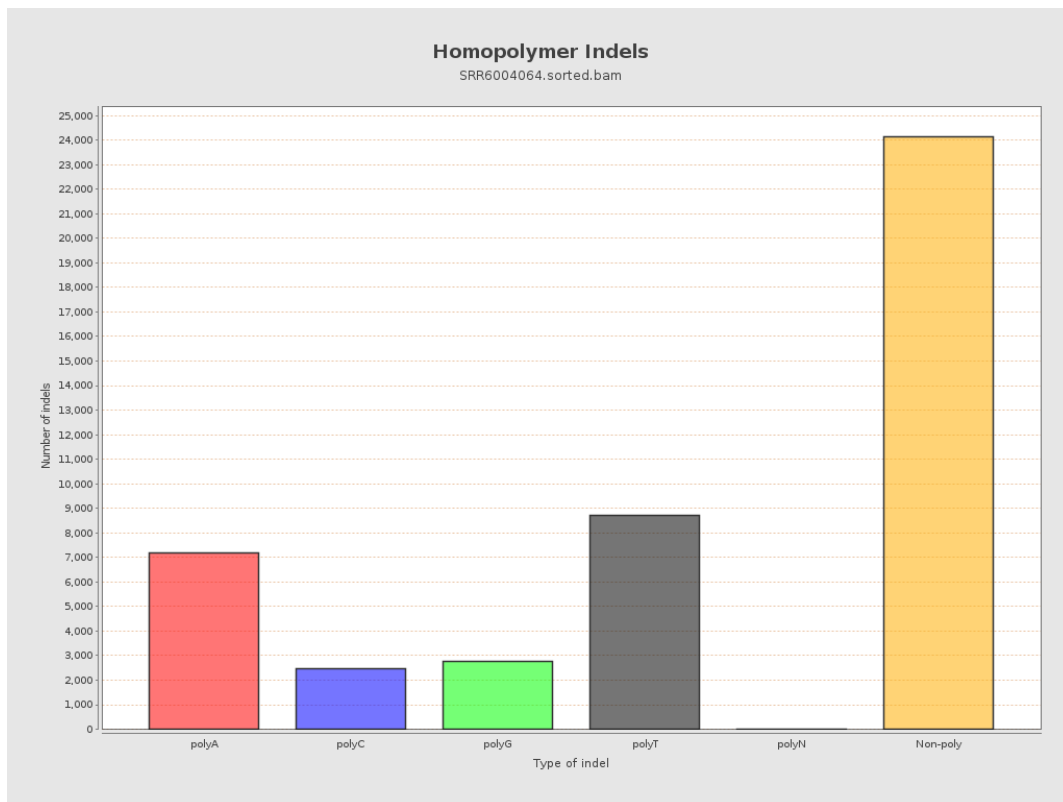
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

