

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:03:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068084.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_SRR6068084 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068084.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:03:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,892,466
Mapped reads	2,503,801 / 86.56%
Unmapped reads	388,665 / 13.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,609 / 0.99%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	188,218 / 6.51%
Duplication rate	6.27%
Clipped reads	1,135,511 / 39.26%

2.2. ACGT Content

Number/percentage of A's	46,982,946 / 28.18%
Number/percentage of C's	30,250,534 / 18.14%
Number/percentage of T's	53,560,928 / 32.12%
Number/percentage of G's	35,930,378 / 21.55%
Number/percentage of N's	3,752 / 0%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0539

Standard Deviation	0.4407
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2.4. Mapping Quality

Mean Mapping Quality	42.18
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2.5. Mismatches and indels

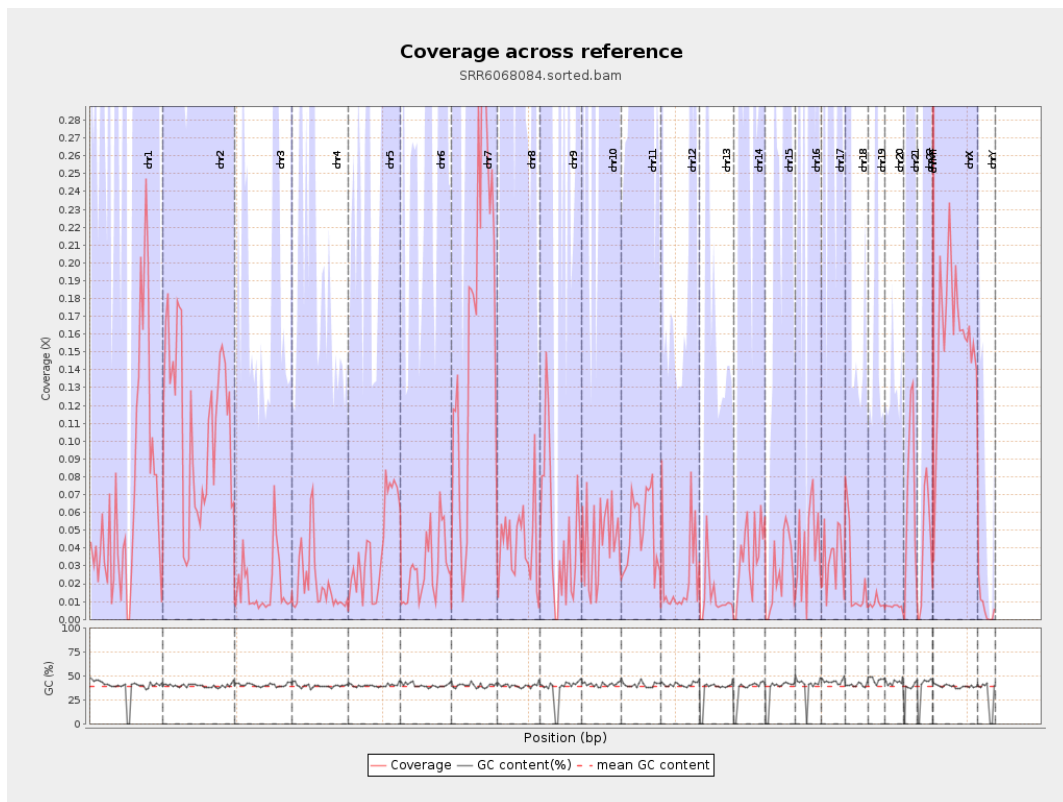
General error rate	0.72%
Mismatches	1,173,762
Insertions	11,854
Mapped reads with at least one insertion	0.47%
Deletions	40,747
Mapped reads with at least one deletion	1.61%
Homopolymer indels	47.66%

2.6. Chromosome stats

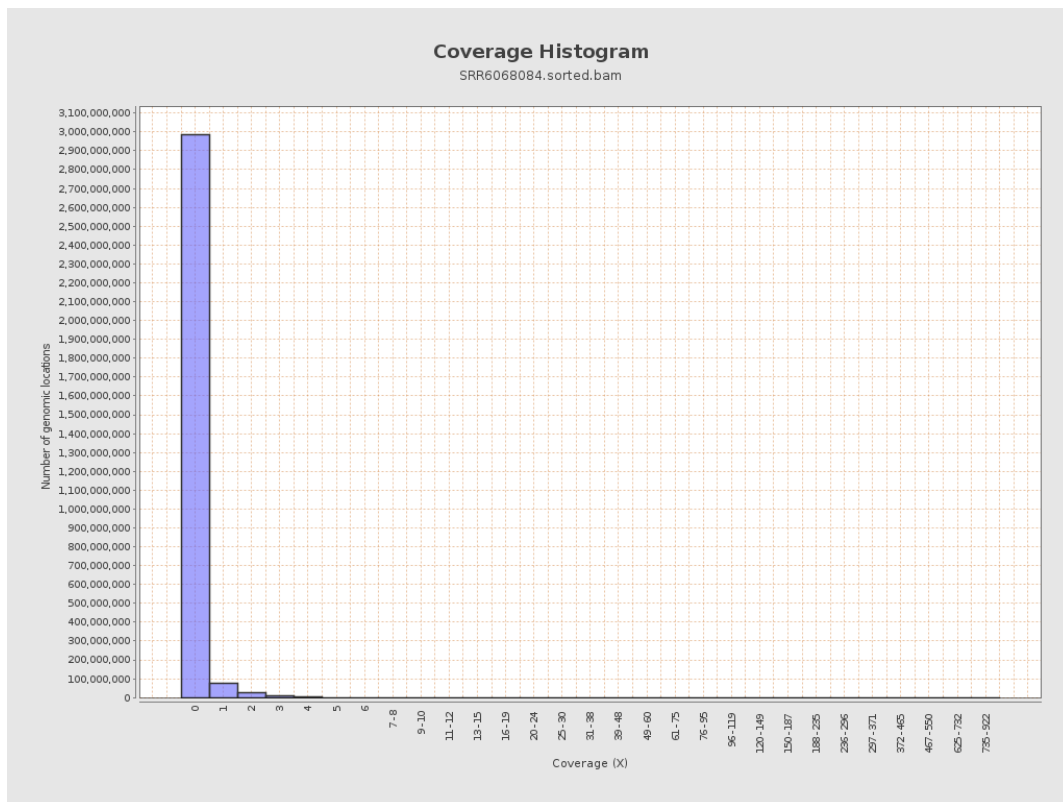
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16791481	0.0674	0.4023
chr2	243199373	26566500	0.1092	0.6079
chr3	198022430	3575096	0.0181	0.1889
chr4	191154276	3833169	0.0201	0.1954
chr5	180915260	7199557	0.0398	0.2694
chr6	171115067	5044195	0.0295	0.249
chr7	159138663	26986934	0.1696	1.1596

chr8	146364022	6207338	0.0424	0.3897
chr9	141213431	6886073	0.0488	0.3194
chr10	135534747	5974374	0.0441	0.4166
chr11	135006516	6716785	0.0498	0.4543
chr12	133851895	3207521	0.024	0.2122
chr13	115169878	1545210	0.0134	0.1585
chr14	107349540	3790393	0.0353	0.2569
chr15	102531392	2667158	0.026	0.2238
chr16	90354753	3697892	0.0409	0.2784
chr17	81195210	2745636	0.0338	0.27
chr18	78077248	1854283	0.0237	0.3776
chr19	59128983	529122	0.0089	0.2043
chr20	63025520	464205	0.0074	0.1261
chr21	48129895	3216238	0.0668	0.3605
chr22	51304566	2203426	0.0429	0.2763
chrMT	16571	52315	3.157	2.9484
chrX	155270560	24658172	0.1588	0.6465
chrY	59373566	380551	0.0064	0.1012

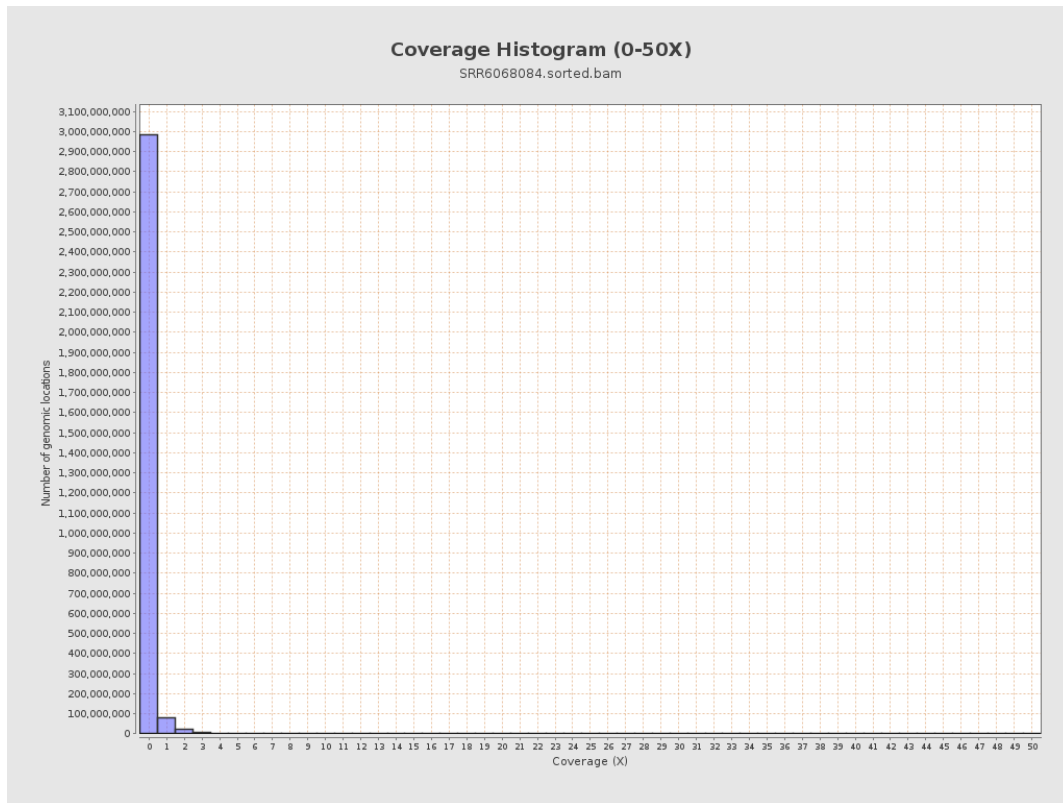
3. Results : Coverage across reference



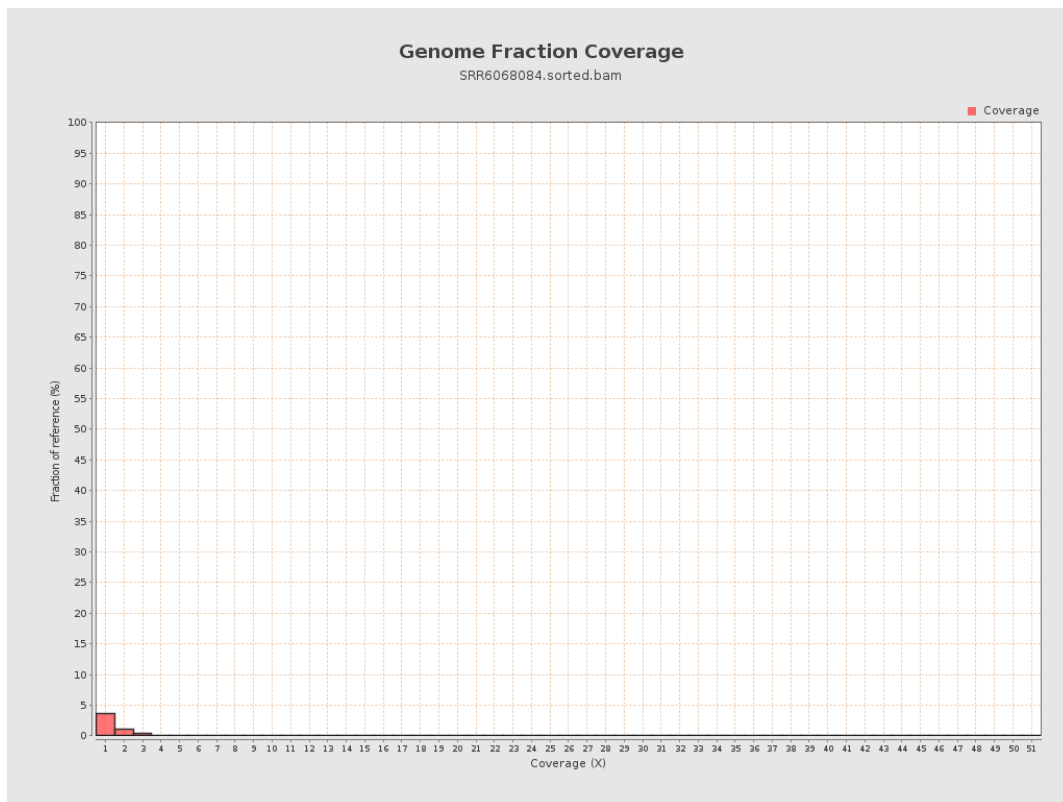
4. Results : Coverage Histogram



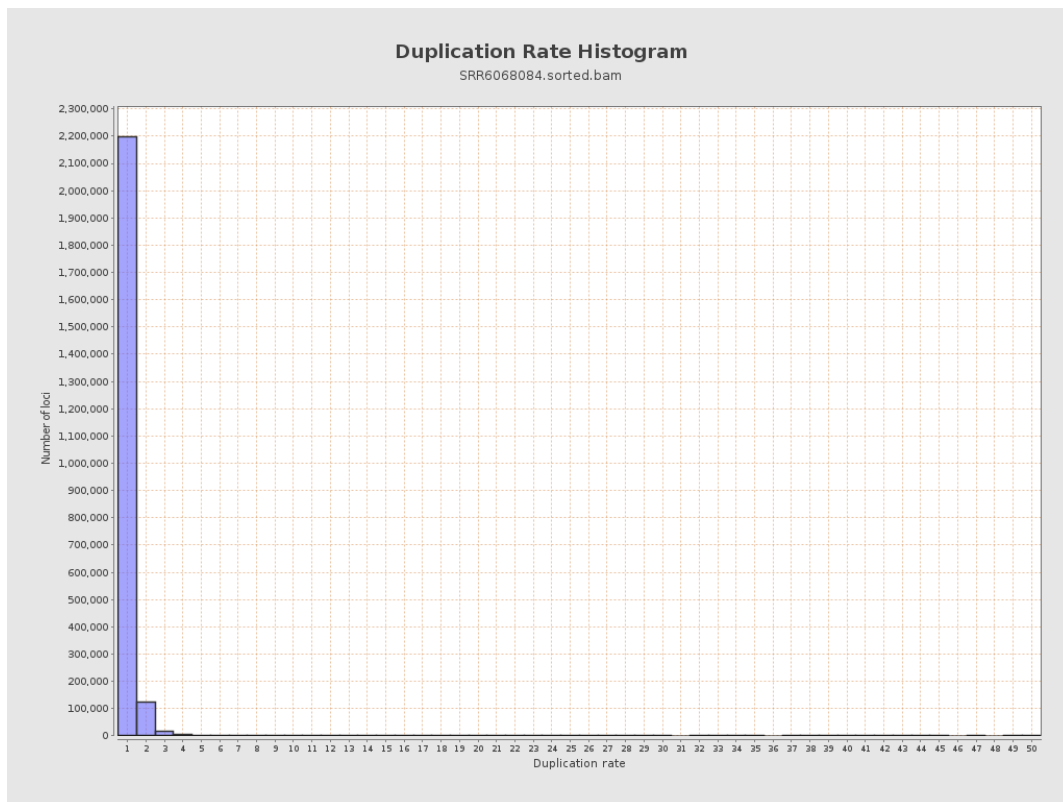
5. Results : Coverage Histogram (0-50X)



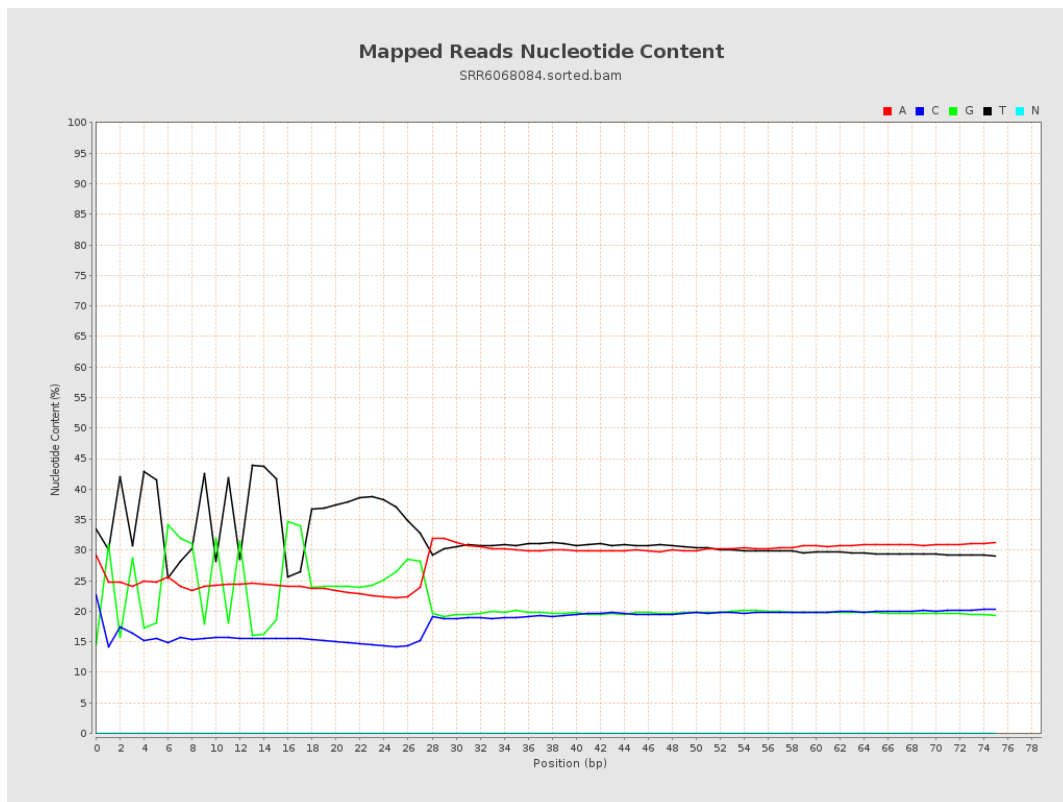
6. Results : Genome Fraction Coverage



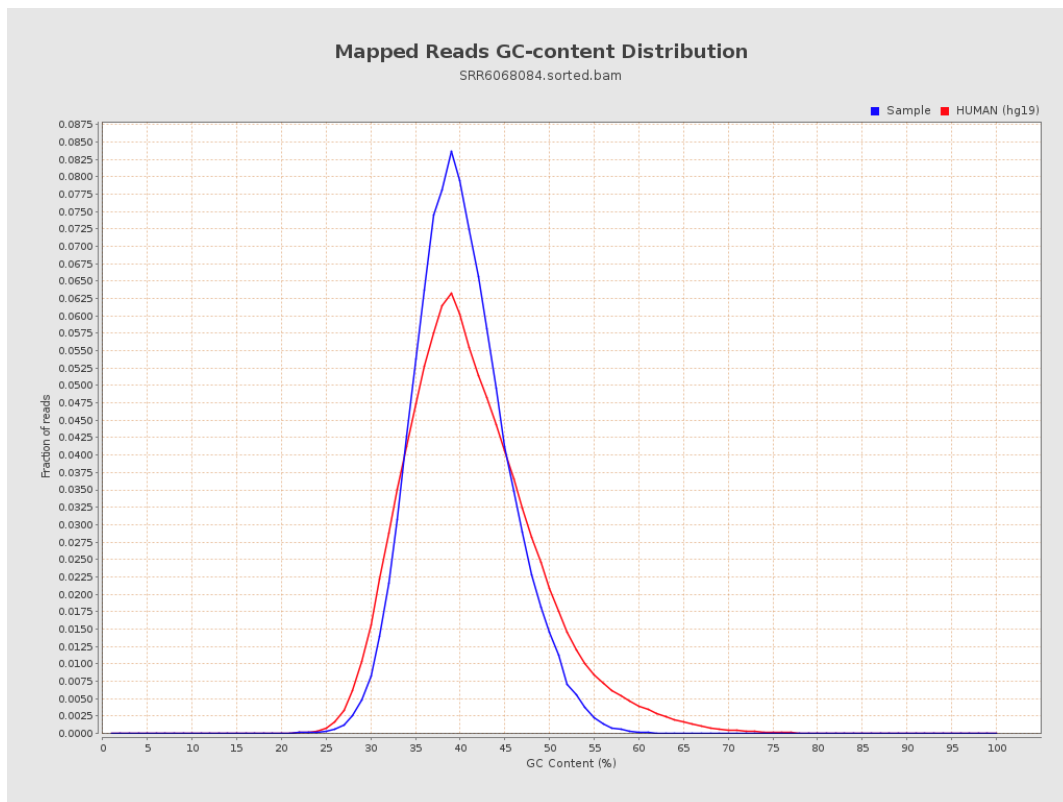
7. Results : Duplication Rate Histogram



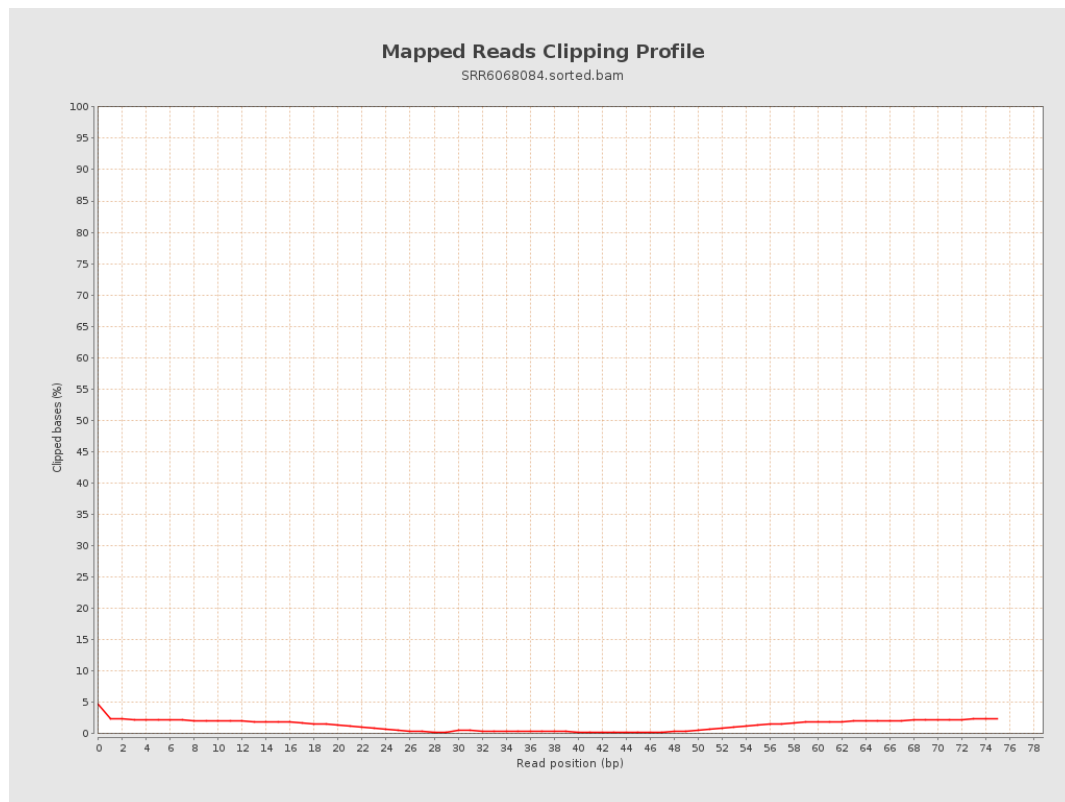
8. Results : Mapped Reads Nucleotide Content



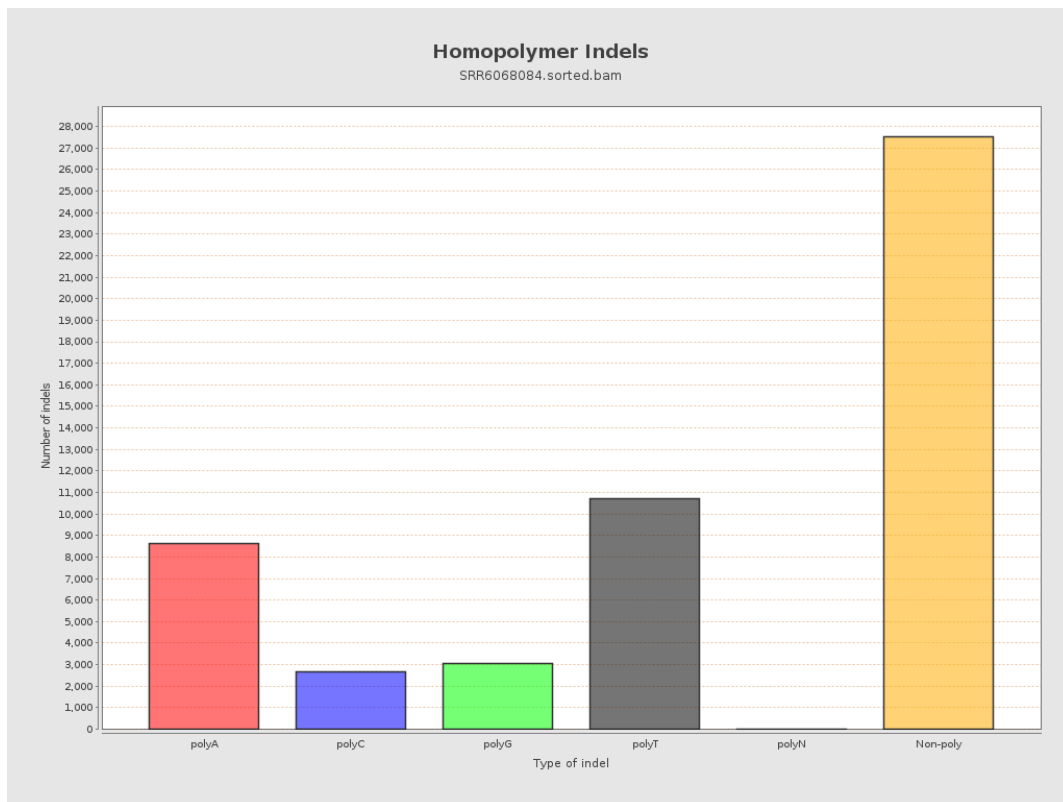
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

