

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:46:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068095.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_SRR6068095 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068095.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:46:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068095.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,287,651
Mapped reads	2,911,313 / 88.55%
Unmapped reads	376,338 / 11.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,395 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	296,416 / 9.02%
Duplication rate	7.6%
Clipped reads	1,444,587 / 43.94%

2.2. ACGT Content

Number/percentage of A's	53,998,512 / 28.14%
Number/percentage of C's	36,220,478 / 18.88%
Number/percentage of T's	59,958,929 / 31.25%
Number/percentage of G's	41,701,863 / 21.73%
Number/percentage of N's	3,960 / 0%
GC Percentage	40.61%

2.3. Coverage

Mean	0.062

Standard Deviation	0.8154
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2.4. Mapping Quality

Mean Mapping Quality	42.11
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2.5. Mismatches and indels

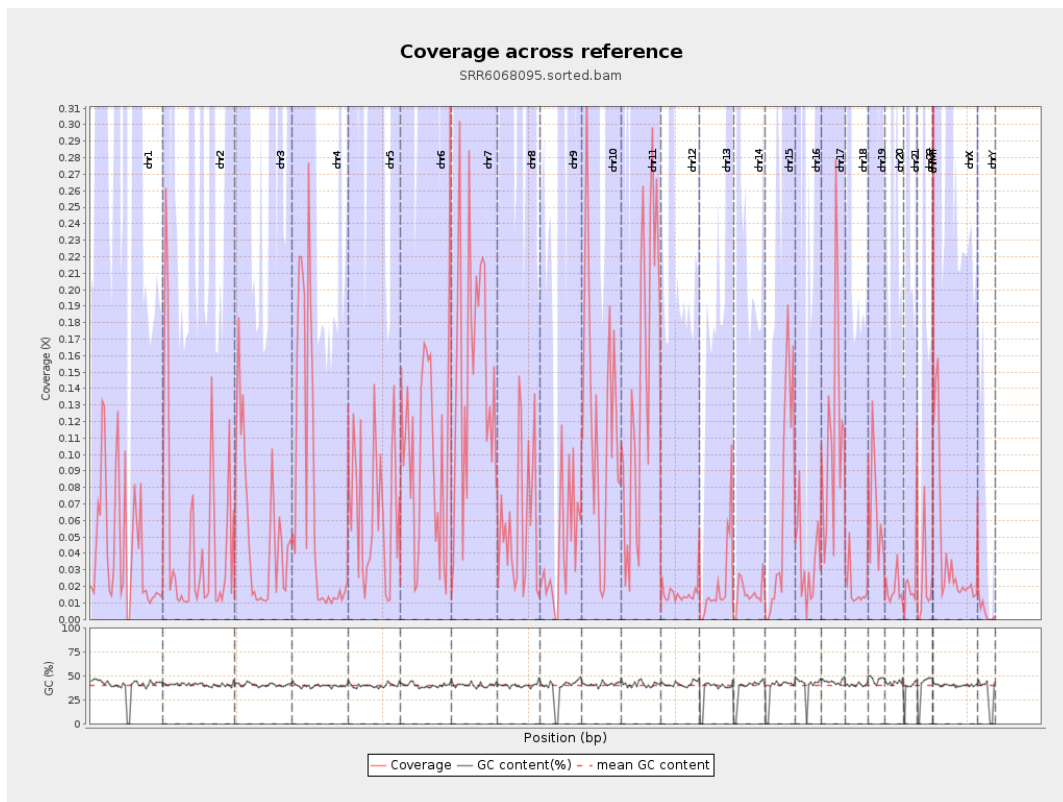
General error rate	0.77%
Mismatches	1,455,841
Insertions	14,244
Mapped reads with at least one insertion	0.49%
Deletions	50,781
Mapped reads with at least one deletion	1.73%
Homopolymer indels	46.47%

2.6. Chromosome stats

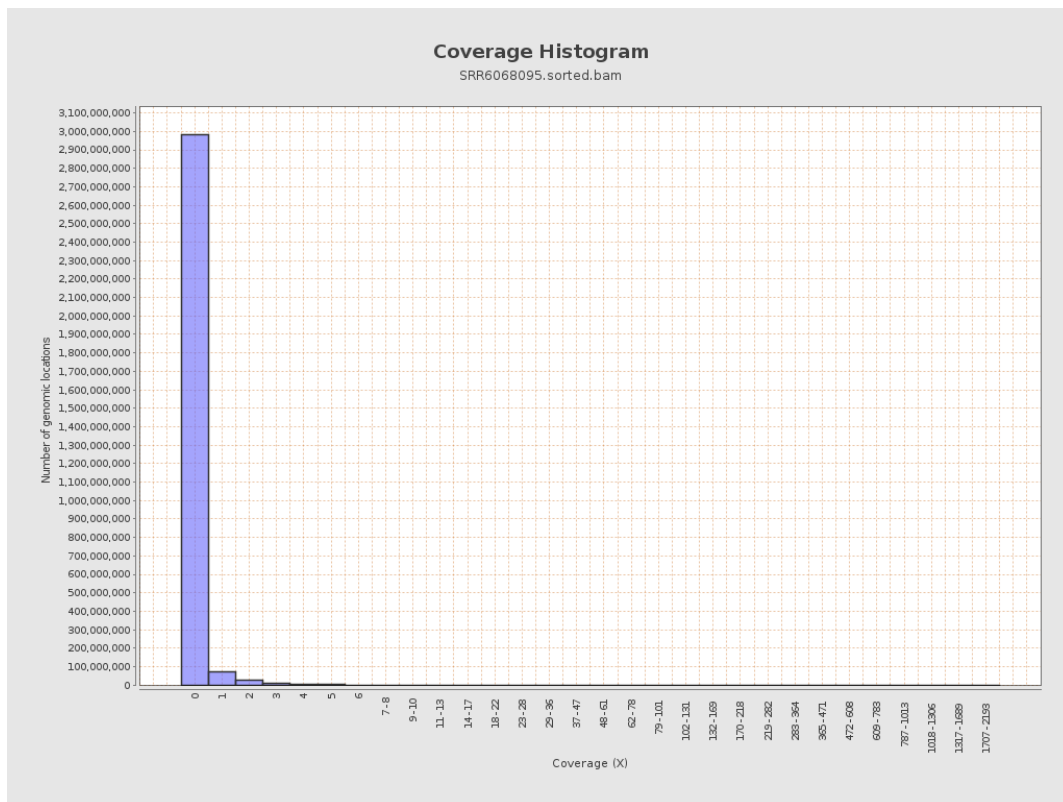
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10589272	0.0425	1.7428
chr2	243199373	11839457	0.0487	0.5974
chr3	198022430	10293165	0.052	0.3547
chr4	191154276	13631149	0.0713	0.4311
chr5	180915260	11733317	0.0649	0.4002
chr6	171115067	17798686	0.104	0.5142
chr7	159138663	24170150	0.1519	1.7174

chr8	146364022	8674575	0.0593	0.752
chr9	141213431	6082220	0.0431	0.6692
chr10	135534747	16756862	0.1236	0.6018
chr11	135006516	19215740	0.1423	0.7873
chr12	133851895	2137738	0.016	0.3108
chr13	115169878	2652717	0.023	0.2365
chr14	107349540	1702699	0.0159	0.4733
chr15	102531392	6715033	0.0655	0.4147
chr16	90354753	3150172	0.0349	0.3707
chr17	81195210	9261659	0.1141	0.543
chr18	78077248	1437980	0.0184	1.2149
chr19	59128983	3910362	0.0661	1.1377
chr20	63025520	1136122	0.018	0.2614
chr21	48129895	1278246	0.0266	0.3123
chr22	51304566	1024340	0.02	0.2063
chrMT	16571	58736	3.5445	3.0153
chrX	155270560	6433499	0.0414	0.4043
chrY	59373566	282217	0.0048	0.0986

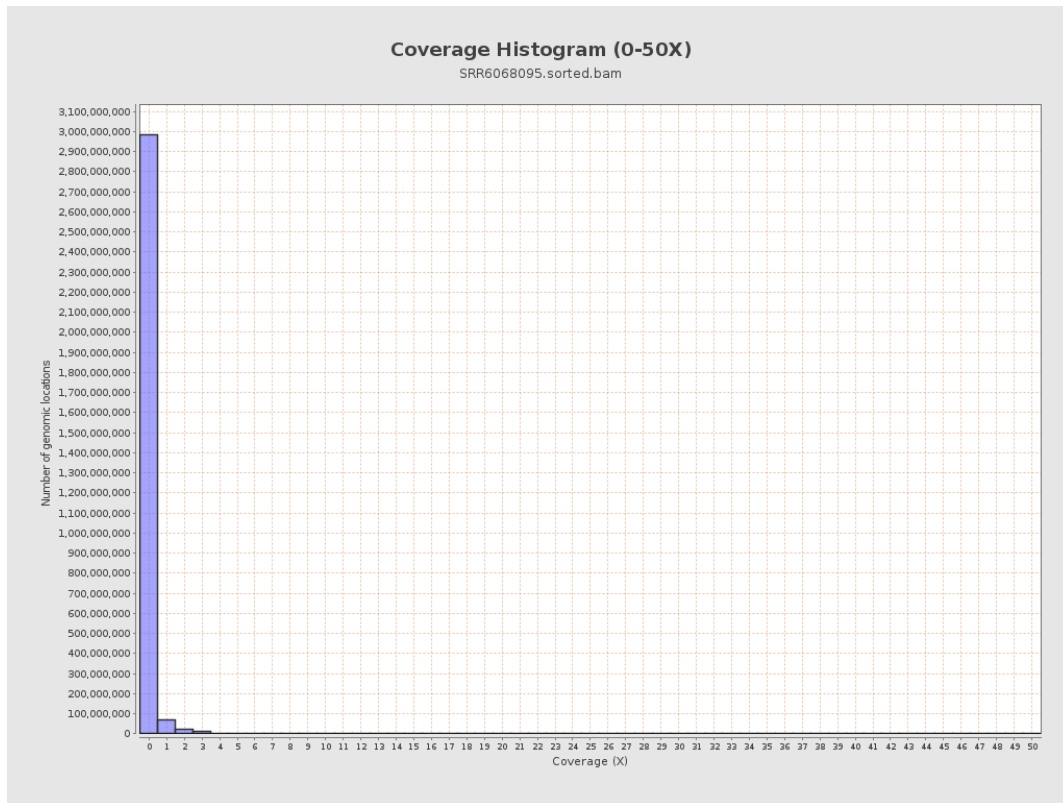
3. Results : Coverage across reference



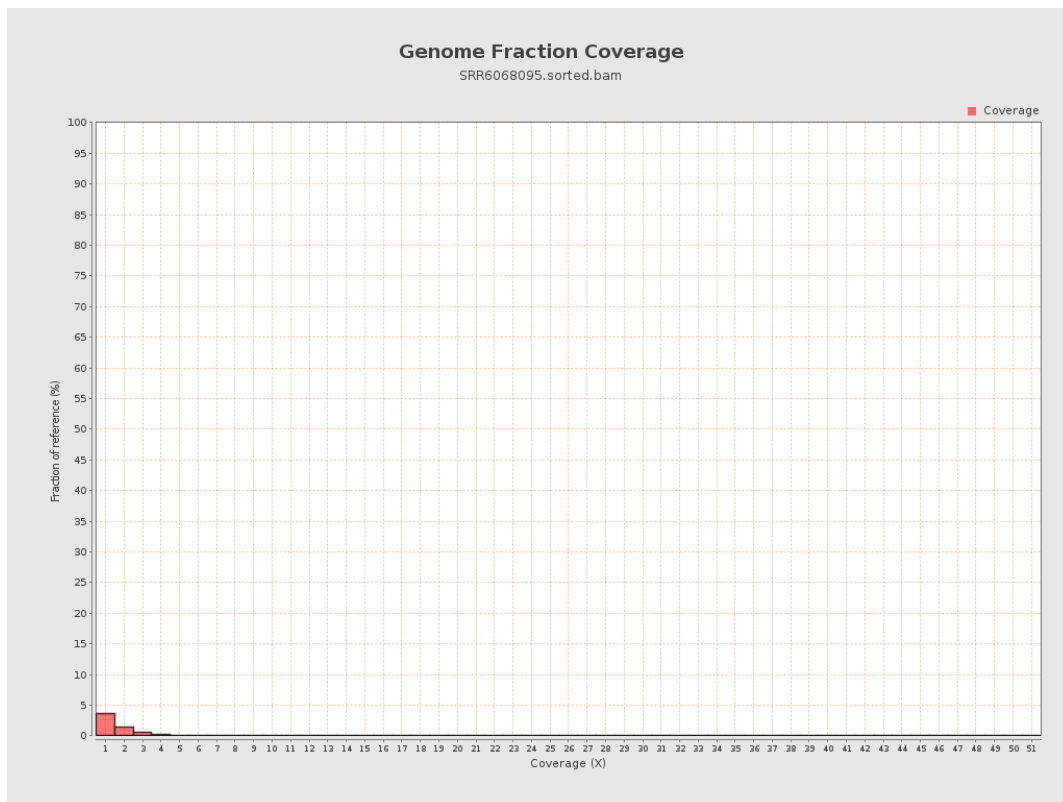
4. Results : Coverage Histogram



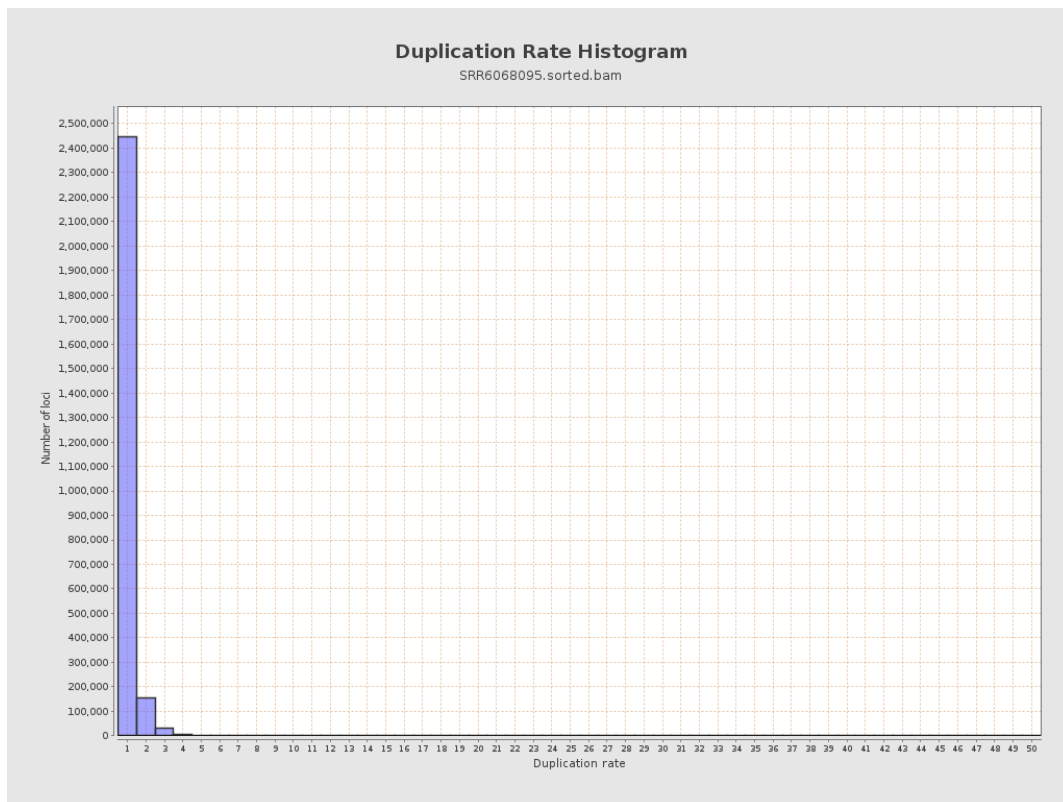
5. Results : Coverage Histogram (0-50X)



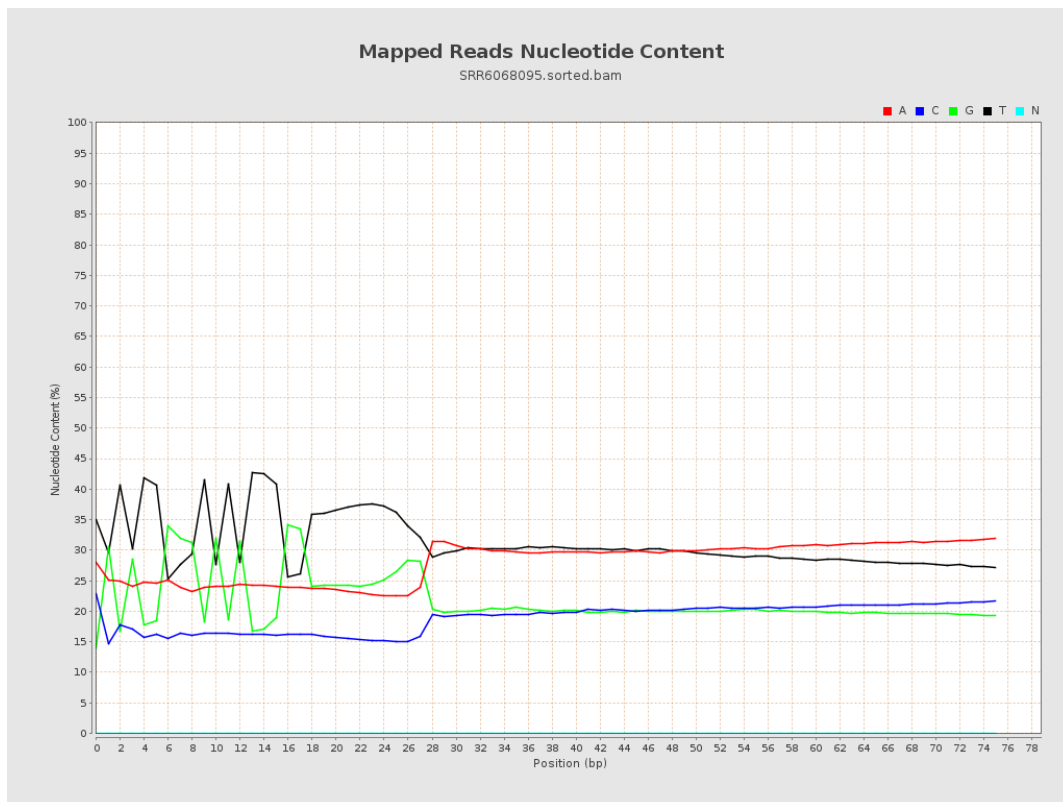
6. Results : Genome Fraction Coverage



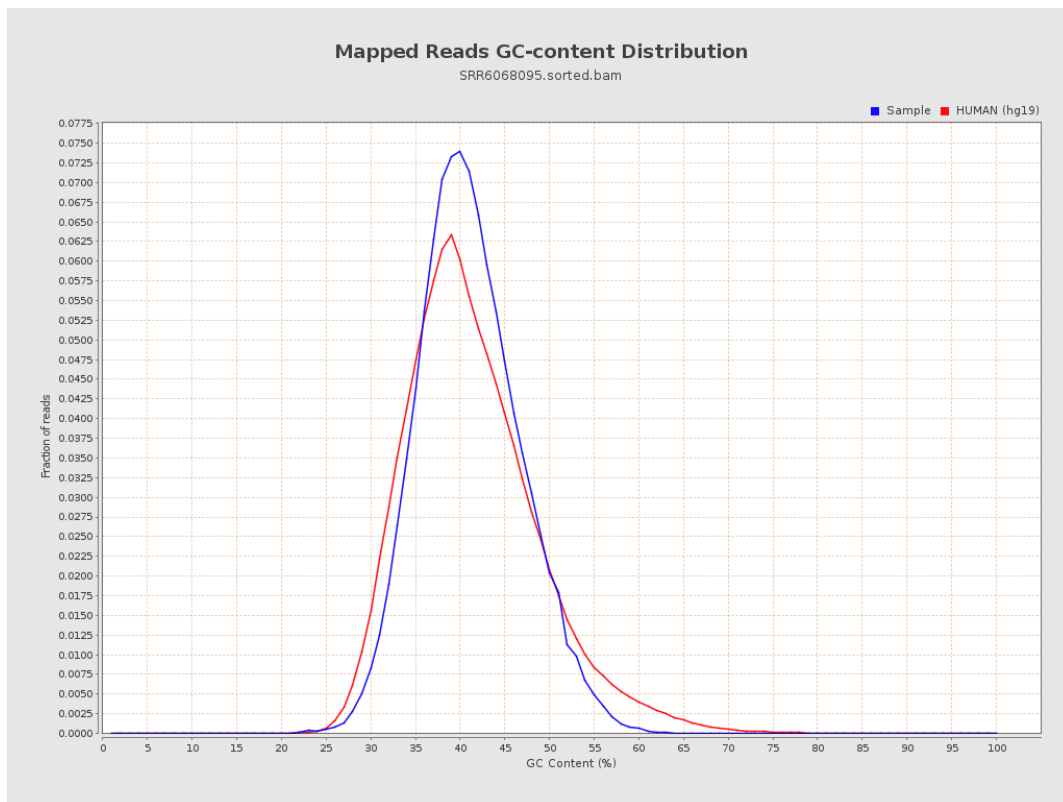
7. Results : Duplication Rate Histogram



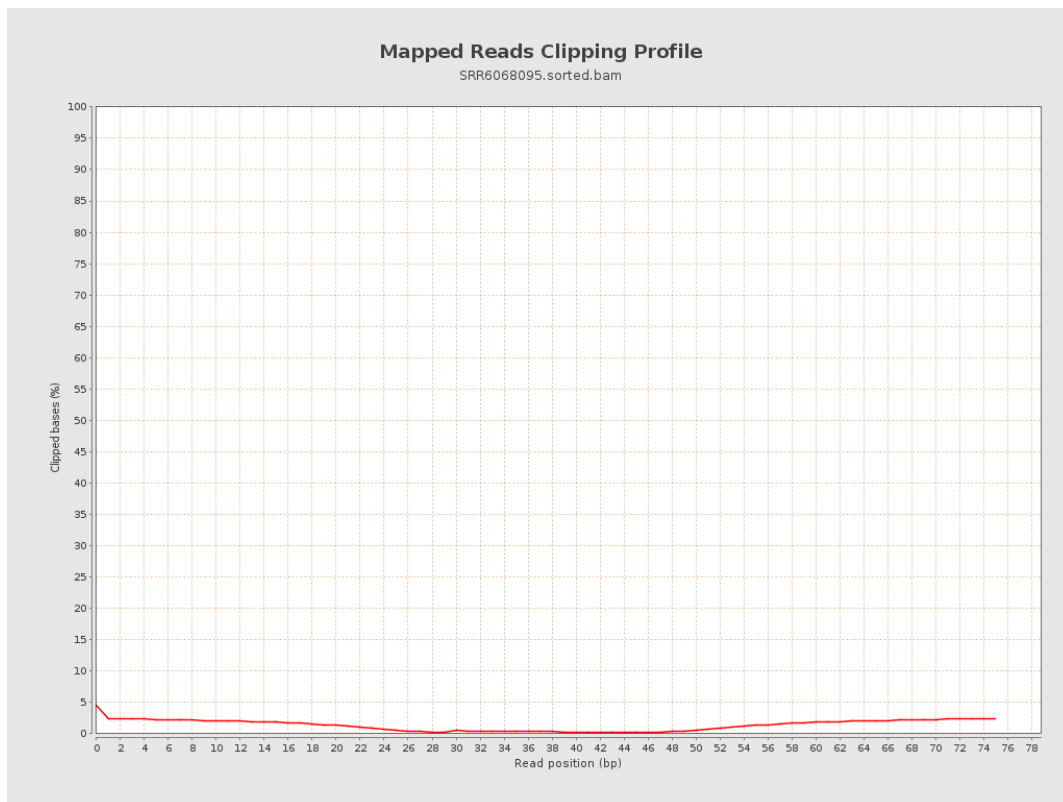
8. Results : Mapped Reads Nucleotide Content



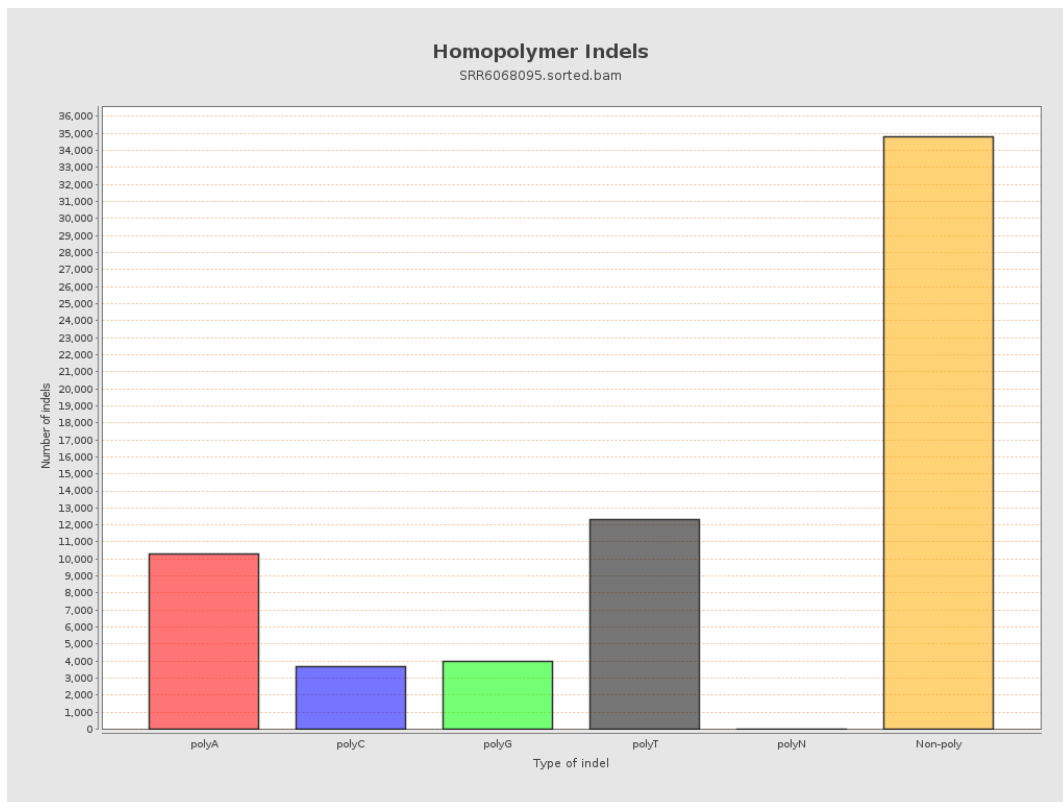
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

