

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:13:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068135.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_SRR6068135 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068135.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:13:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068135.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,180,170
Mapped reads	1,977,456 / 90.7%
Unmapped reads	202,714 / 9.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,359 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	120,360 / 5.52%
Duplication rate	4.81%
Clipped reads	884,595 / 40.57%

2.2. ACGT Content

Number/percentage of A's	36,719,594 / 27.81%
Number/percentage of C's	24,427,261 / 18.5%
Number/percentage of T's	41,864,239 / 31.71%
Number/percentage of G's	29,020,347 / 21.98%
Number/percentage of N's	2,581 / 0%
GC Percentage	40.48%

2.3. Coverage

Mean	0.0427

Standard Deviation	0.4409
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2.4. Mapping Quality

Mean Mapping Quality	41.8
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2.5. Mismatches and indels

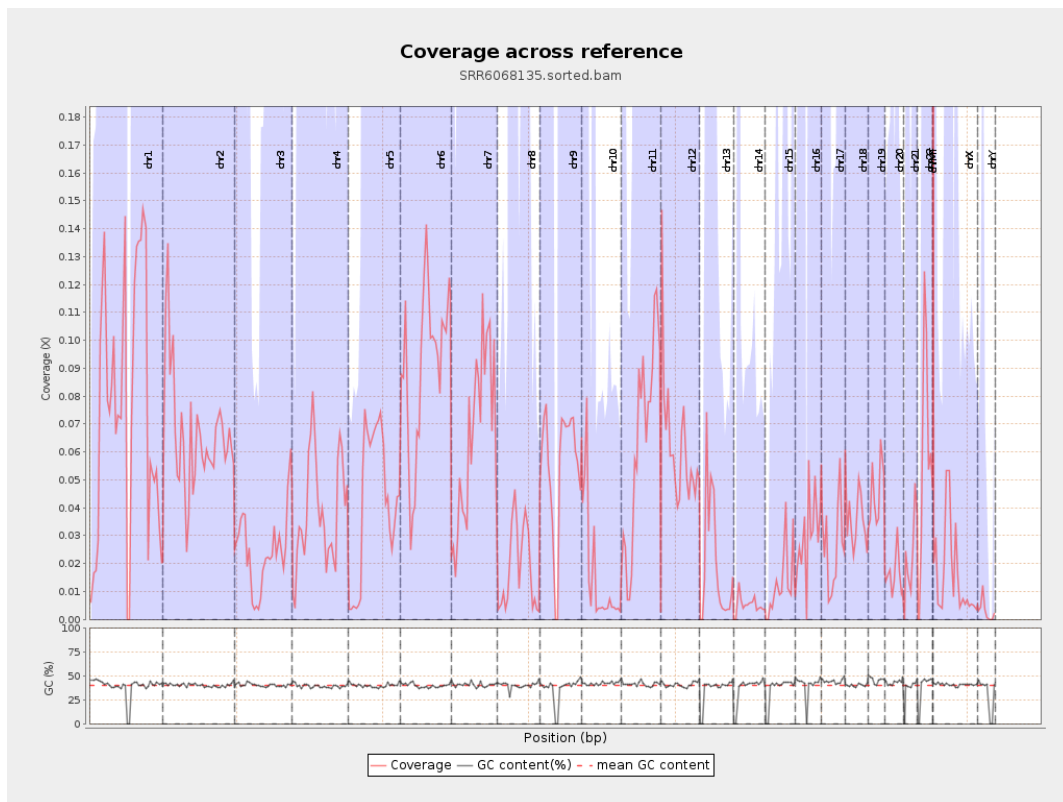
General error rate	0.77%
Mismatches	995,605
Insertions	10,607
Mapped reads with at least one insertion	0.53%
Deletions	34,630
Mapped reads with at least one deletion	1.73%
Homopolymer indels	47.49%

2.6. Chromosome stats

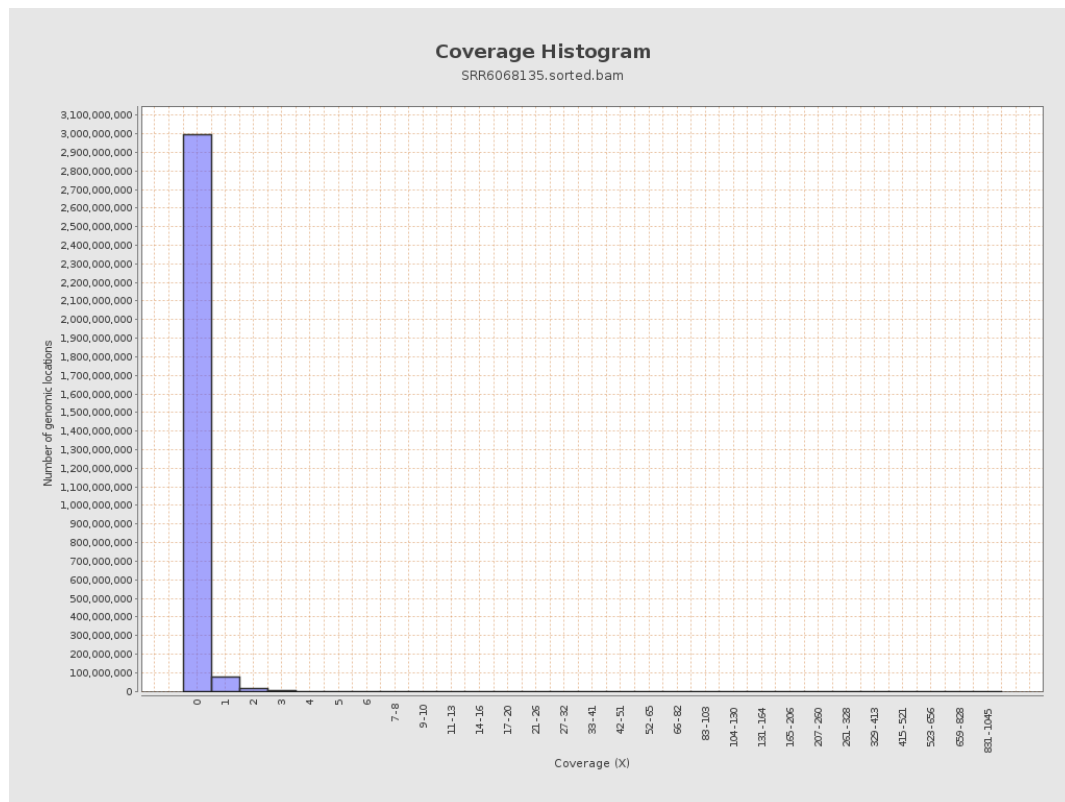
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18602223	0.0746	0.9096
chr2	243199373	16130708	0.0663	0.4873
chr3	198022430	4862289	0.0246	0.1927
chr4	191154276	7435767	0.0389	0.2602
chr5	180915260	7594548	0.042	0.2574
chr6	171115067	15648522	0.0915	0.4116
chr7	159138663	10263310	0.0645	0.4524

chr8	146364022	2644959	0.0181	0.62
chr9	141213431	7836908	0.0555	0.4402
chr10	135534747	2070837	0.0153	0.2553
chr11	135006516	8572454	0.0635	0.4934
chr12	133851895	8309804	0.0621	0.3221
chr13	115169878	2191362	0.019	0.1725
chr14	107349540	550544	0.0051	0.1857
chr15	102531392	1381542	0.0135	0.1487
chr16	90354753	2673617	0.0296	0.2475
chr17	81195210	2161616	0.0266	0.2381
chr18	78077248	2800985	0.0359	0.7168
chr19	59128983	2613823	0.0442	0.6851
chr20	63025520	1001225	0.0159	0.1667
chr21	48129895	1155716	0.024	0.2118
chr22	51304566	2961200	0.0577	0.2956
chrMT	16571	10332	0.6235	1.2683
chrX	155270560	2421313	0.0156	0.2031
chrY	59373566	194132	0.0033	0.1017

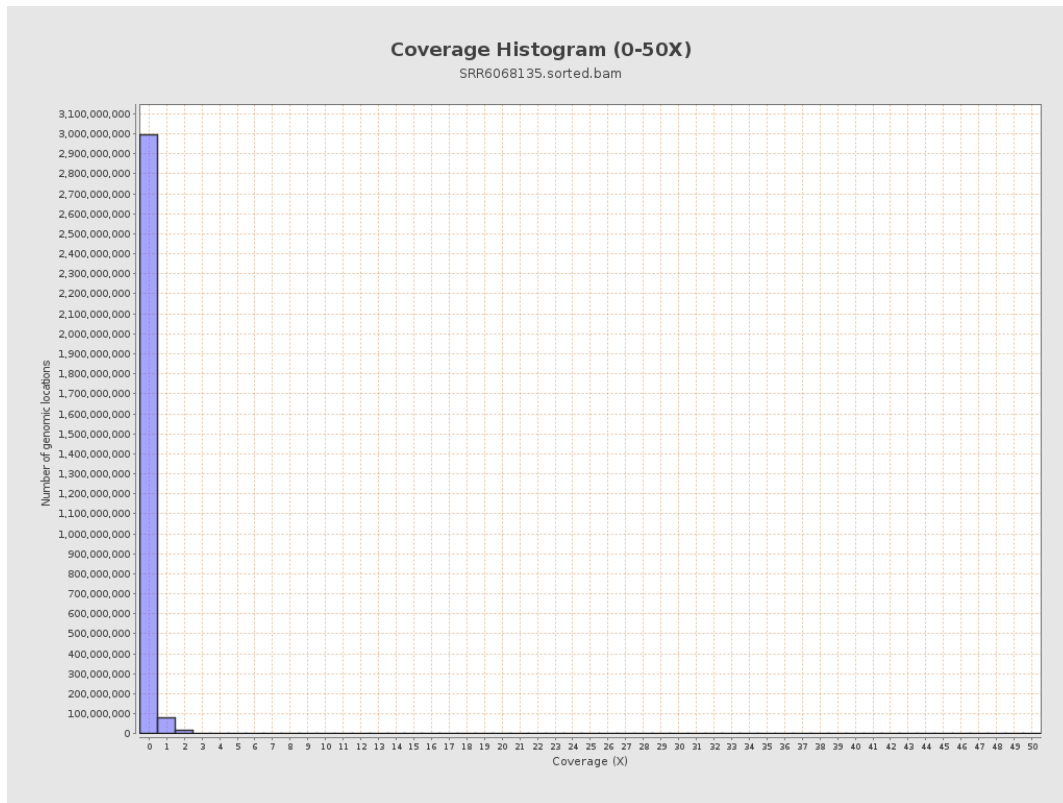
3. Results : Coverage across reference



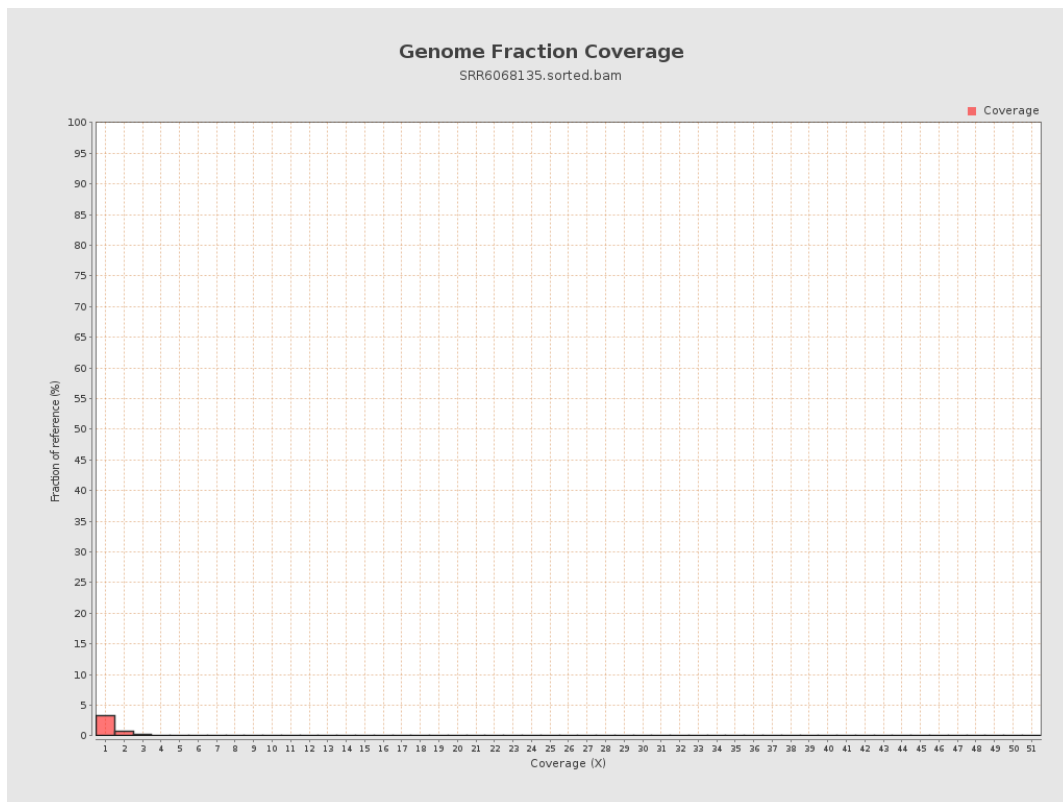
4. Results : Coverage Histogram



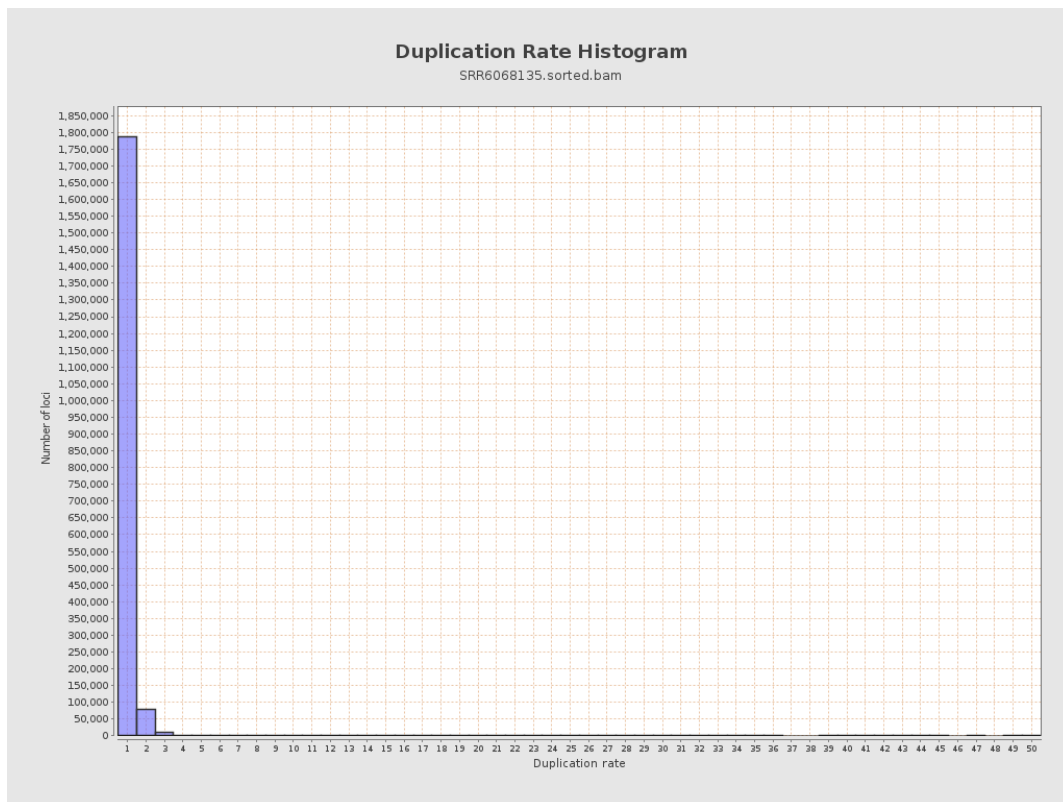
5. Results : Coverage Histogram (0-50X)



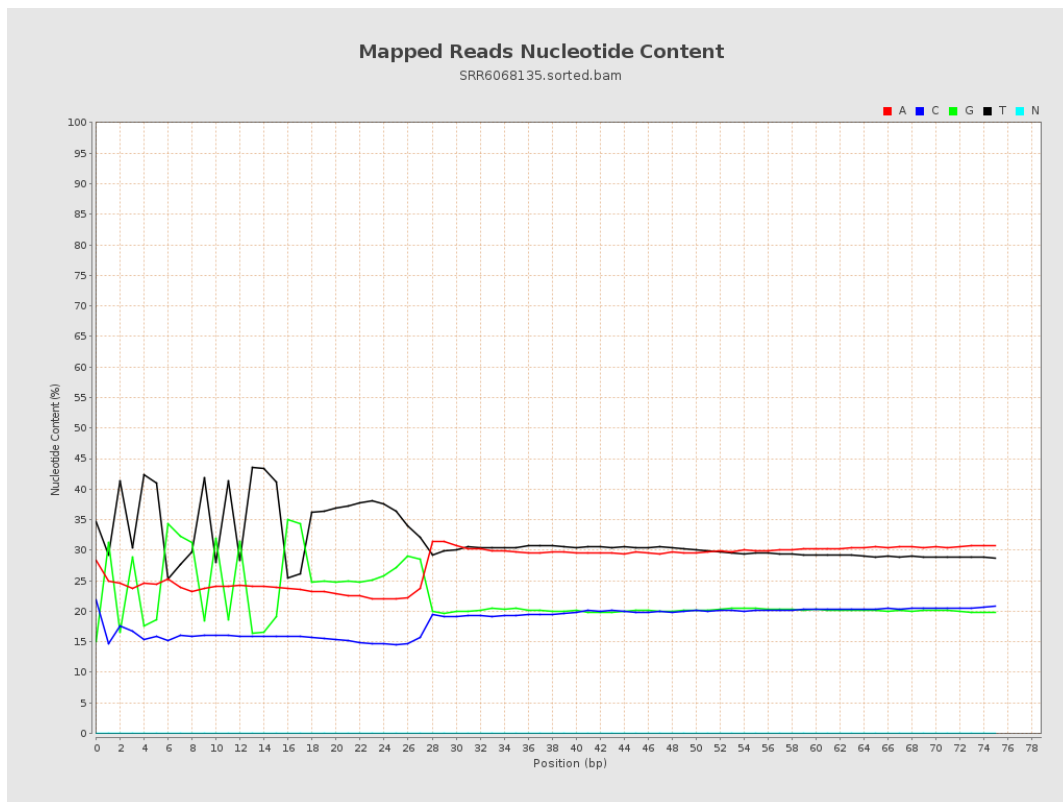
6. Results : Genome Fraction Coverage



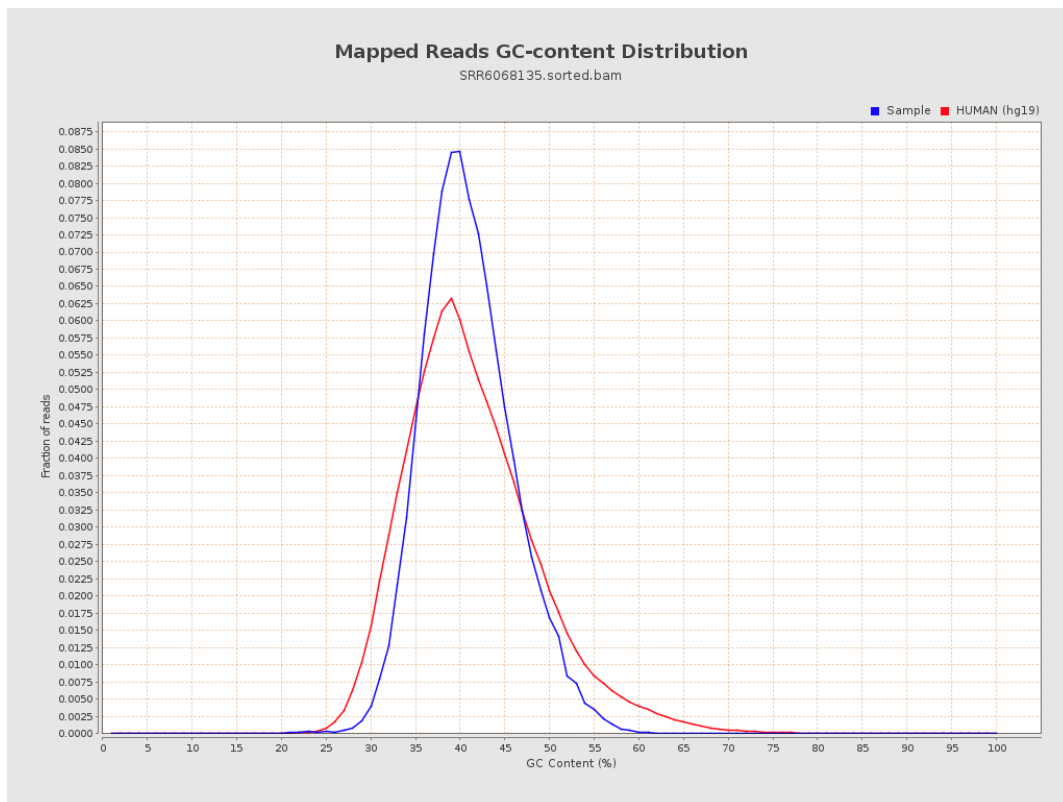
7. Results : Duplication Rate Histogram



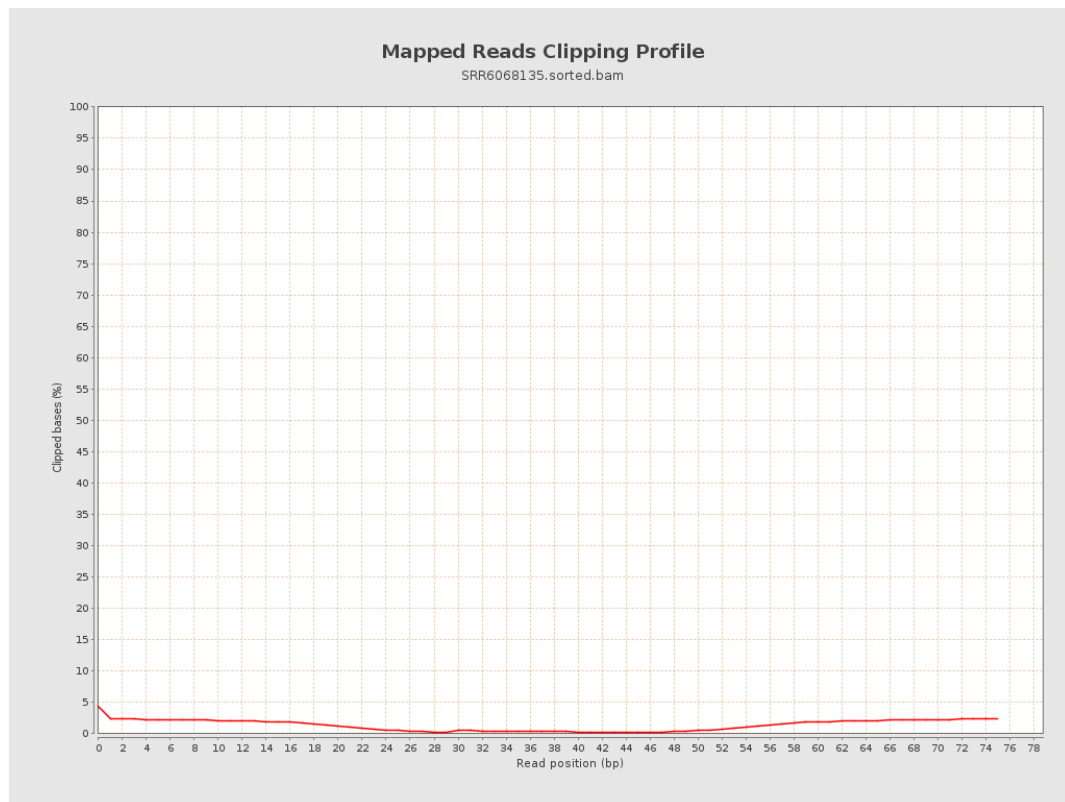
8. Results : Mapped Reads Nucleotide Content



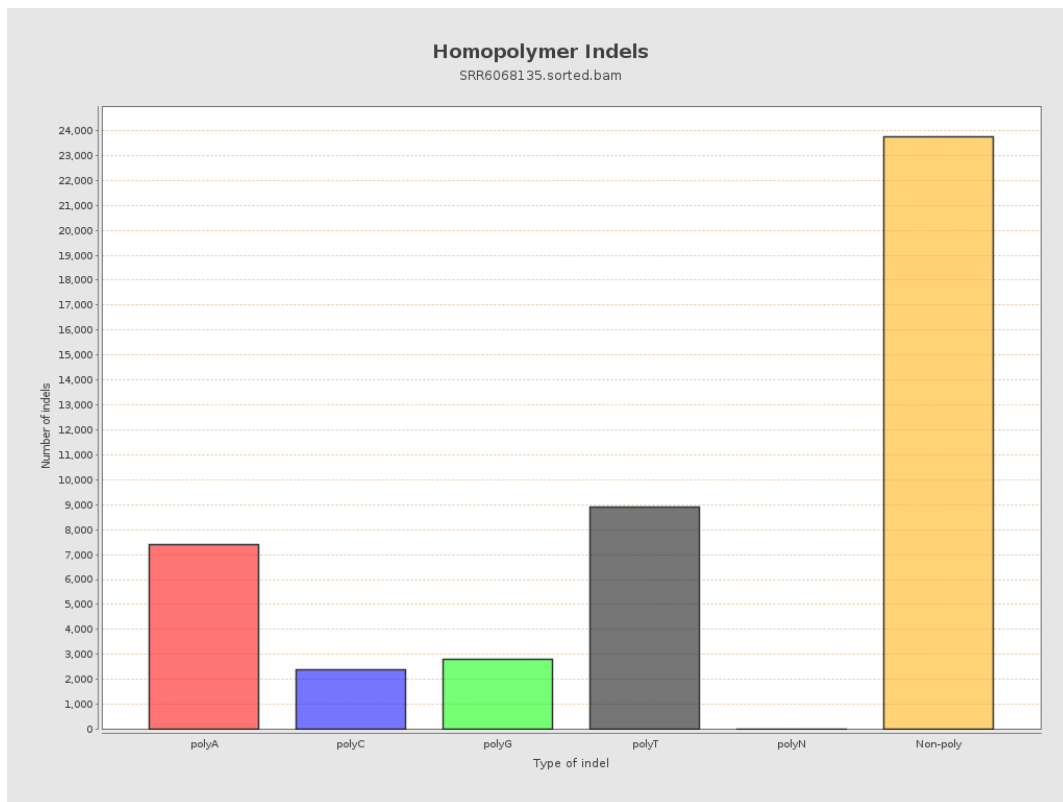
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

