

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:43:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080635.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_SRR3080635 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080635.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:43:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080635.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,322,126
Mapped reads	2,914,576 / 87.73%
Unmapped reads	407,550 / 12.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,506 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	129,016 / 3.88%
Duplication rate	3.66%
Clipped reads	1,247,085 / 37.54%

2.2. ACGT Content

Number/percentage of A's	55,265,411 / 28.06%
Number/percentage of C's	35,316,708 / 17.93%
Number/percentage of T's	62,993,712 / 31.98%
Number/percentage of G's	43,212,857 / 21.94%
Number/percentage of N's	167,047 / 0.08%
GC Percentage	39.87%

2.3. Coverage

Mean	0.0636

Standard Deviation	0.4533
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2.4. Mapping Quality

Mean Mapping Quality	47.11
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2.5. Mismatches and indels

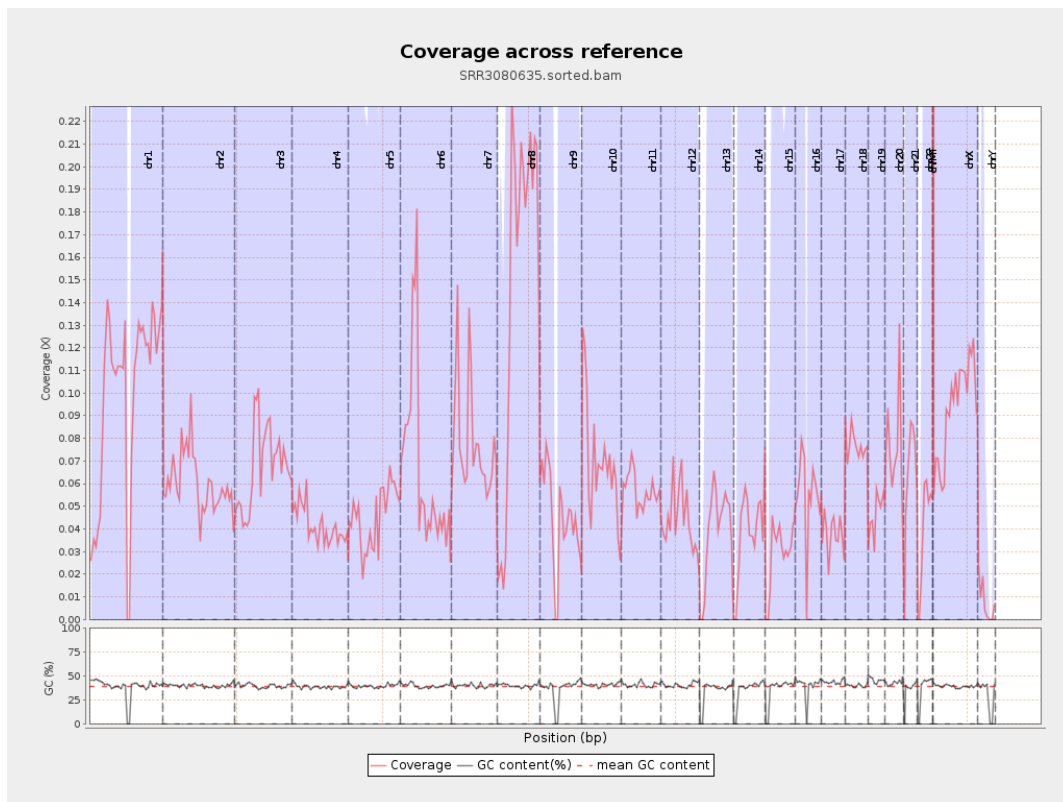
General error rate	0.92%
Mismatches	1,776,274
Insertions	16,483
Mapped reads with at least one insertion	0.56%
Deletions	49,666
Mapped reads with at least one deletion	1.69%
Homopolymer indels	48.35%

2.6. Chromosome stats

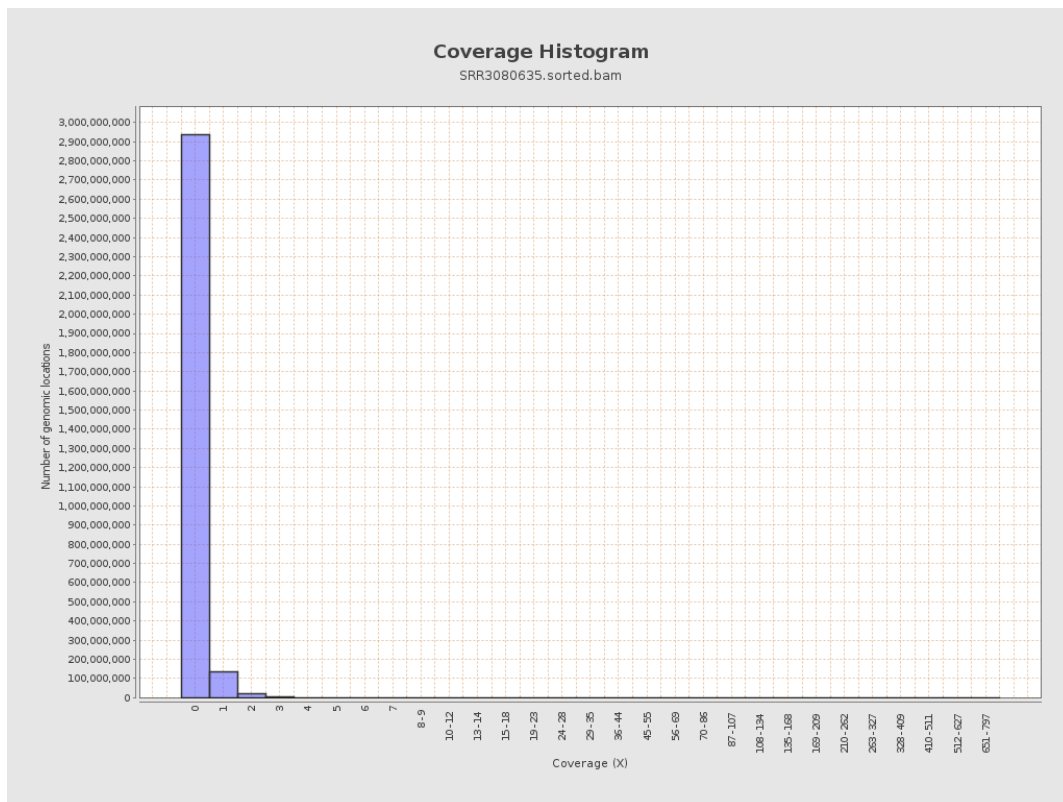
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24627968	0.0988	0.6003
chr2	243199373	14631540	0.0602	0.4452
chr3	198022430	13341710	0.0674	0.3022
chr4	191154276	7953009	0.0416	0.2546
chr5	180915260	8166173	0.0451	0.2462
chr6	171115067	11522435	0.0673	0.4992
chr7	159138663	12555519	0.0789	1.0581

chr8	146364022	21702981	0.1483	0.6453
chr9	141213431	6364624	0.0451	0.3734
chr10	135534747	9526204	0.0703	0.425
chr11	135006516	7633212	0.0565	0.3403
chr12	133851895	5882302	0.0439	0.2489
chr13	115169878	4463607	0.0388	0.2262
chr14	107349540	4108526	0.0383	0.25
chr15	102531392	2962448	0.0289	0.1973
chr16	90354753	4933296	0.0546	0.2988
chr17	81195210	3067759	0.0378	0.2436
chr18	78077248	6007491	0.0769	0.5856
chr19	59128983	2774606	0.0469	0.4197
chr20	63025520	4861754	0.0771	0.3294
chr21	48129895	3066197	0.0637	0.3247
chr22	51304566	2013460	0.0392	0.229
chrMT	16571	39065	2.3574	2.8617
chrX	155270560	14392257	0.0927	0.374
chrY	59373566	439926	0.0074	0.1448

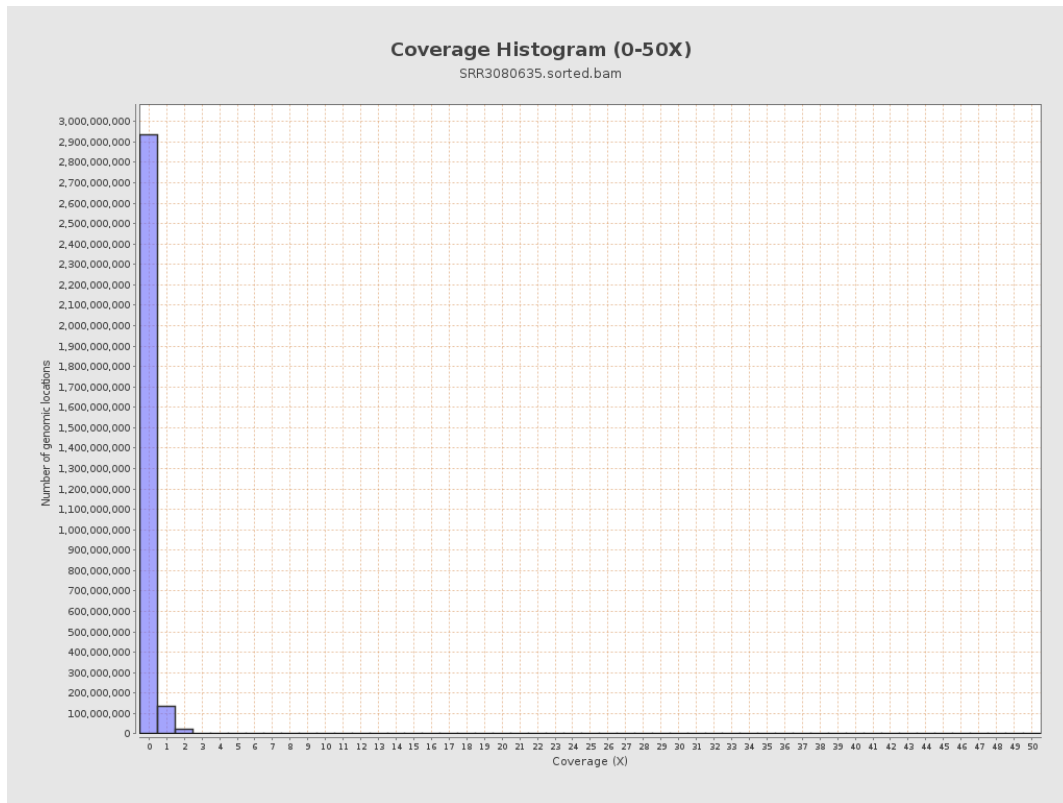
3. Results : Coverage across reference



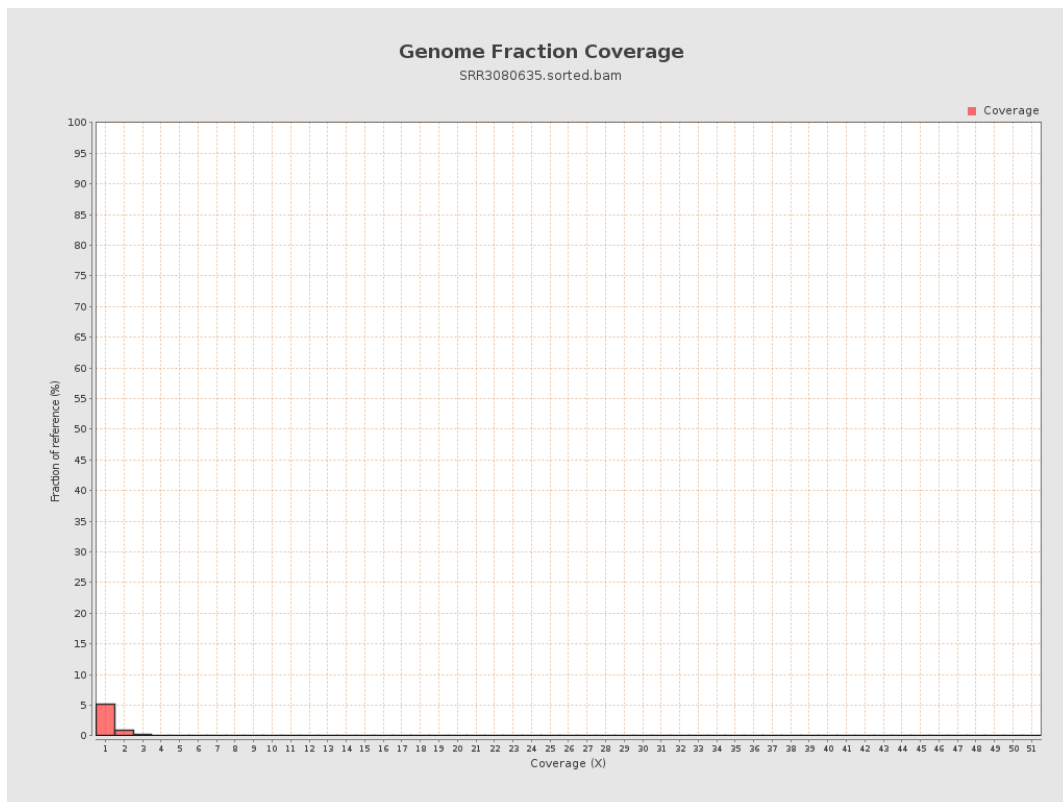
4. Results : Coverage Histogram



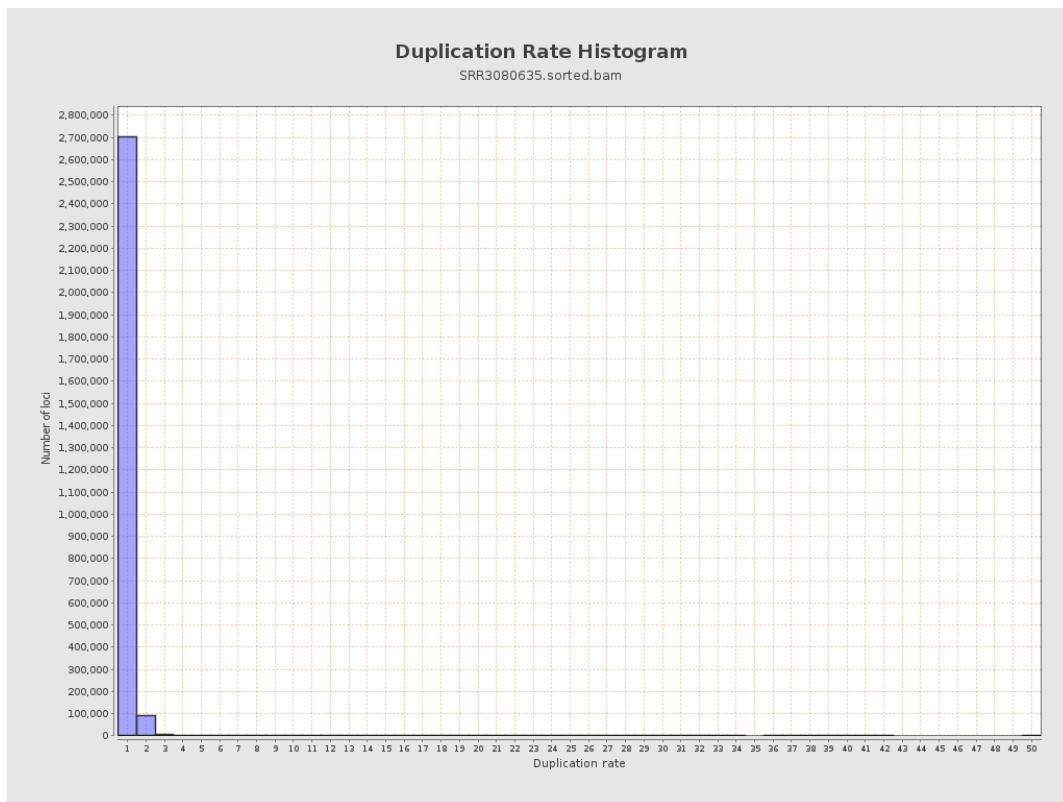
5. Results : Coverage Histogram (0-50X)



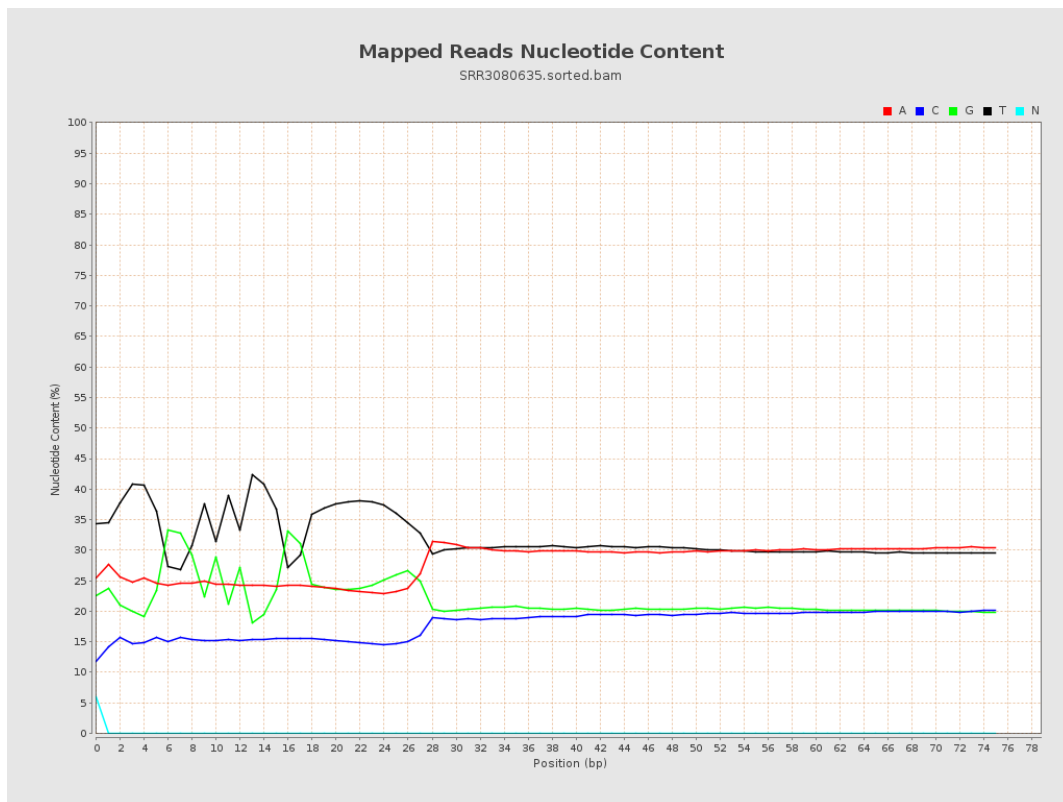
6. Results : Genome Fraction Coverage



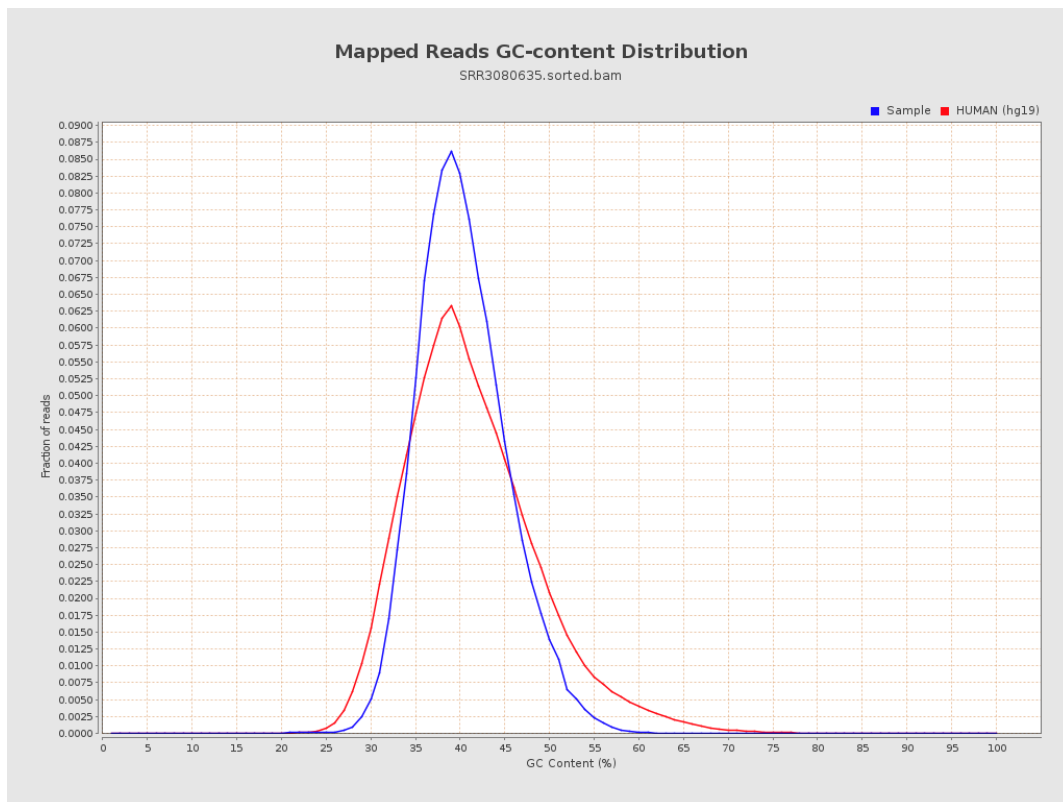
7. Results : Duplication Rate Histogram



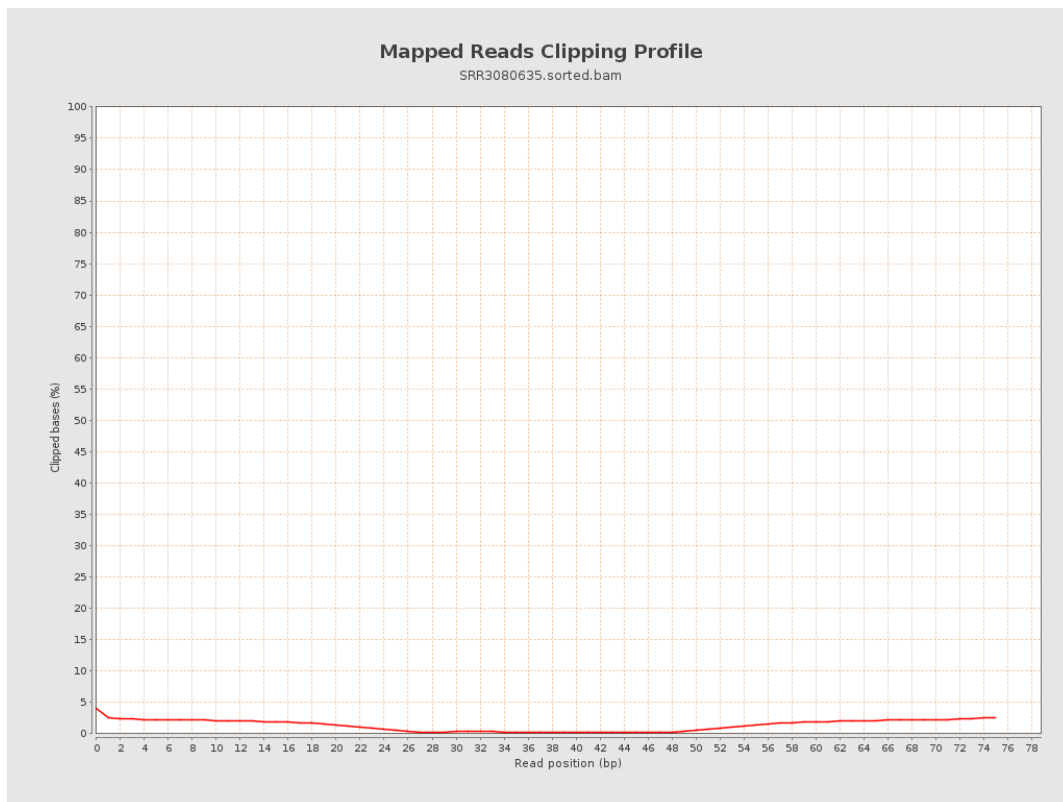
8. Results : Mapped Reads Nucleotide Content



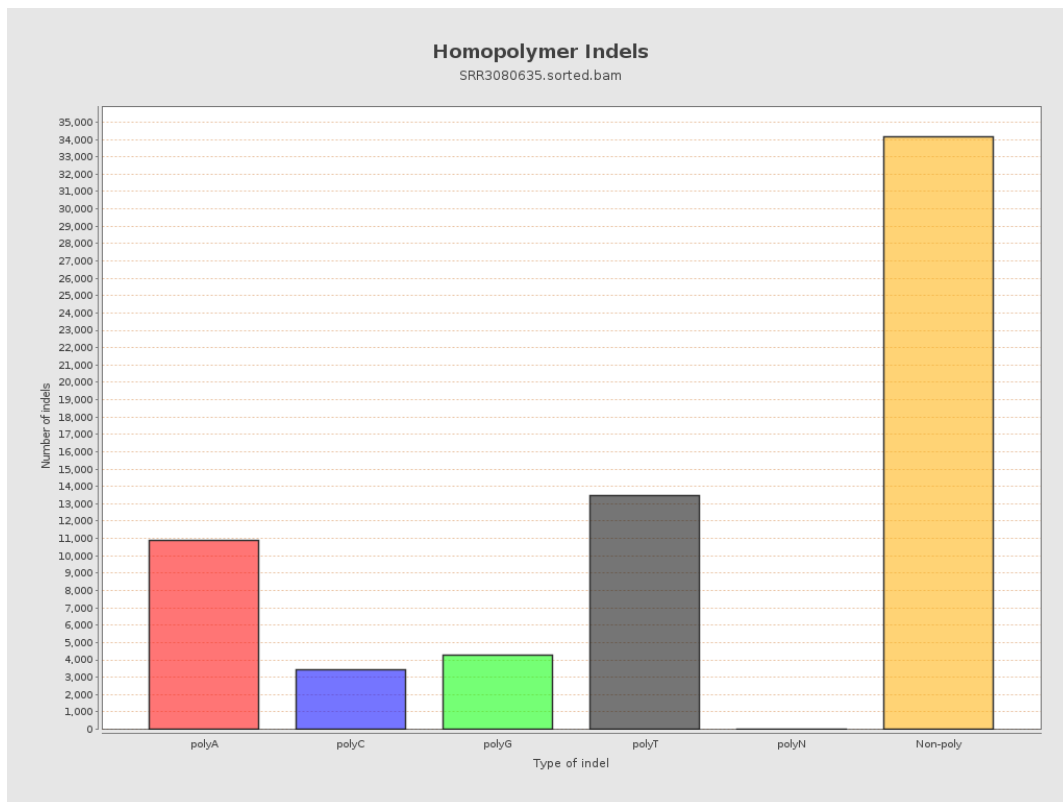
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

