Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:11:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080639.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_SRR3080639 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080639.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:11:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080639.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,231,563
Mapped reads	2,541,760 / 78.65%
Unmapped reads	689,803 / 21.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,200 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	107,086 / 3.31%
Duplication rate	3.34%
Clipped reads	1,295,332 / 40.08%

2.2. ACGT Content

Number/percentage of A's	45,650,206 / 27.12%
Number/percentage of C's	29,859,793 / 17.74%
Number/percentage of T's	54,467,496 / 32.36%
Number/percentage of G's	38,188,835 / 22.69%
Number/percentage of N's	132,883 / 0.08%
GC Percentage	40.43%

2.3. Coverage

Mean	0.0544

Standard Deviation	0.4146

2.4. Mapping Quality

Mean Mapping Quality	45.69

2.5. Mismatches and indels

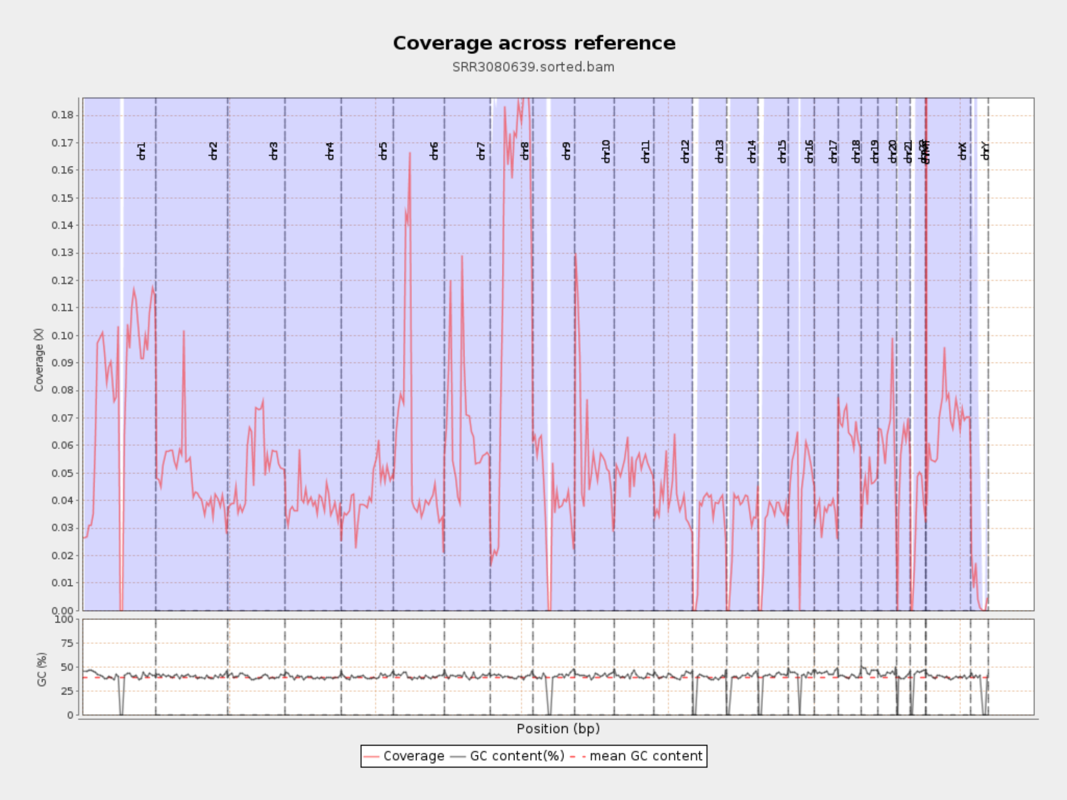
General error rate	0.93%
Mismatches	1,532,821
Insertions	14,740
Mapped reads with at least one insertion	0.58%
Deletions	41,128
Mapped reads with at least one deletion	1.6%
Homopolymer indels	46.97%

2.6. Chromosome stats

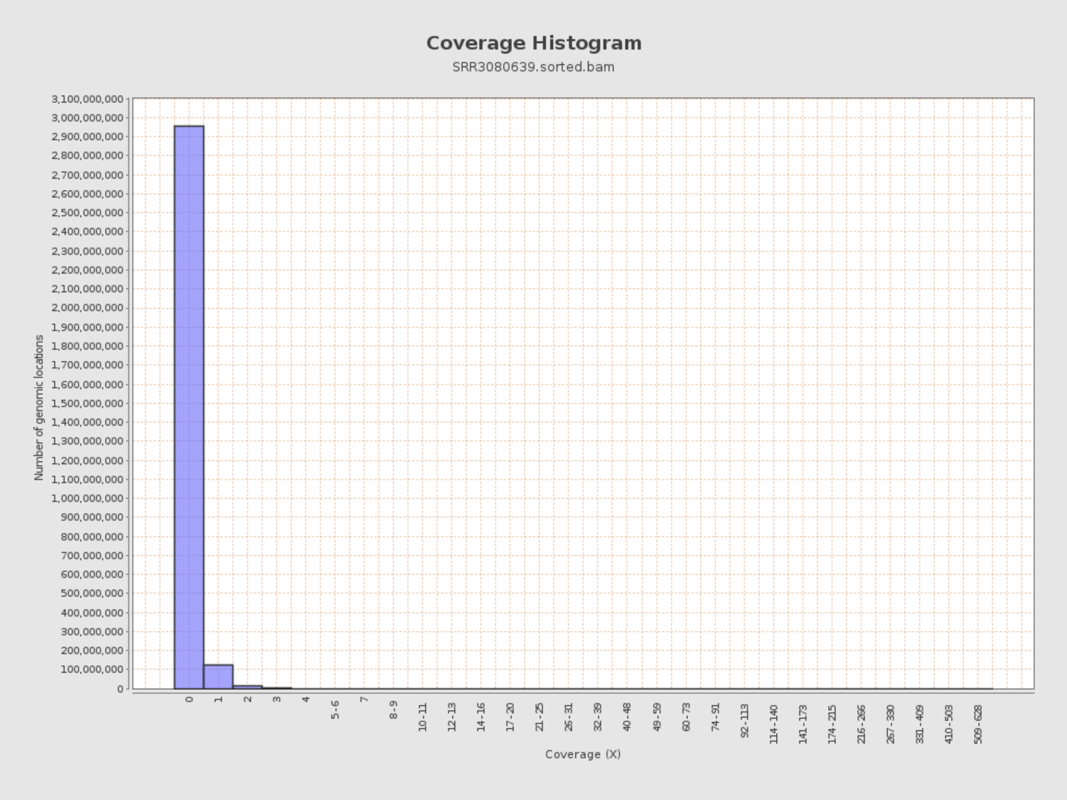
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19831818	0.0796	0.5596
chr2	243199373	11723828	0.0482	0.4813
chr3	198022430	10463226	0.0528	0.2634
chr4	191154276	7495080	0.0392	0.2459
chr5	180915260	7655581	0.0423	0.2336
chr6	171115067	10252690	0.0599	0.4505
chr7	159138663	10555718	0.0663	0.8684

chr8	146364022	19437185	0.1328	0.6035
chr9	141213431	5657658	0.0401	0.3709
chr10	135534747	8193554	0.0605	0.4124
chr11	135006516	7032153	0.0521	0.3055
chr12	133851895	5428997	0.0406	0.2367
chr13	115169878	3740992	0.0325	0.2016
chr14	107349540	3438160	0.032	0.2295
chr15	102531392	3046447	0.0297	0.1944
chr16	90354753	4348036	0.0481	0.272
chr17	81195210	2913369	0.0359	0.2253
chr18	78077248	5208740	0.0667	0.5521
chr19	59128983	2718256	0.046	0.4124
chr20	63025520	4143065	0.0657	0.307
chr21	48129895	2531248	0.0526	0.2774
chr22	51304566	1625992	0.0317	0.1993
chrMT	16571	30883	1.8637	2.7245
chrX	155270560	10516506	0.0677	0.3441
chrY	59373566	377537	0.0064	0.1343

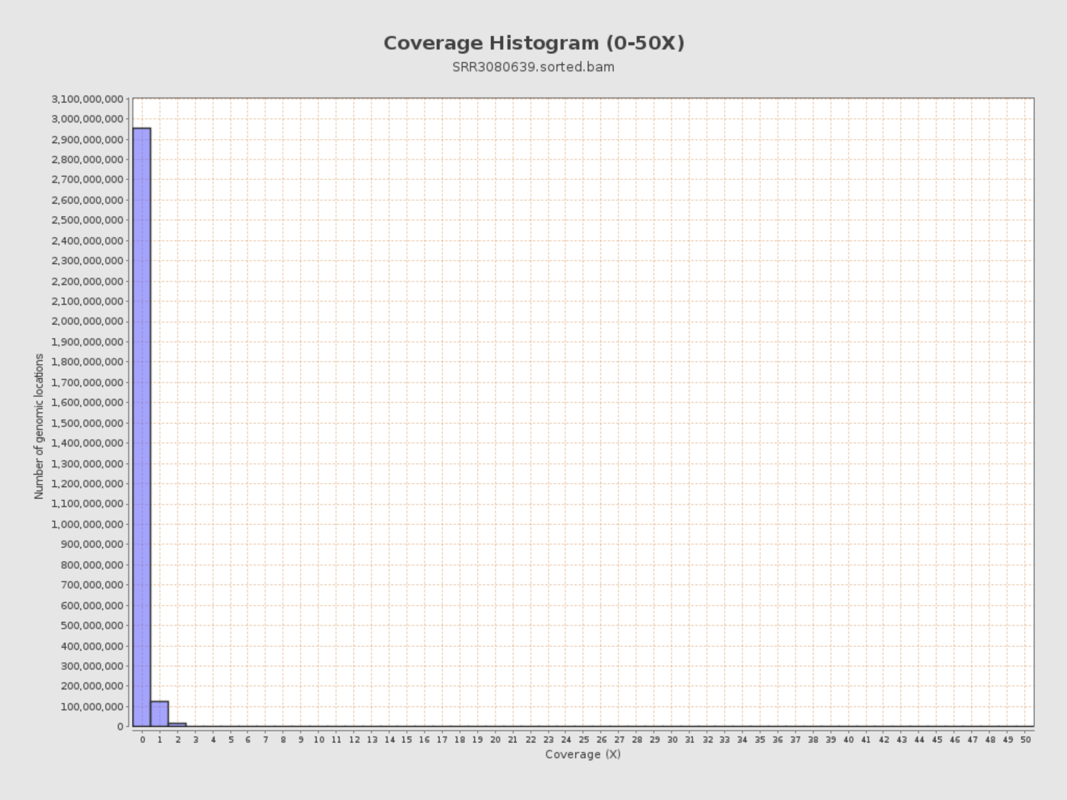
3. Results : Coverage across reference



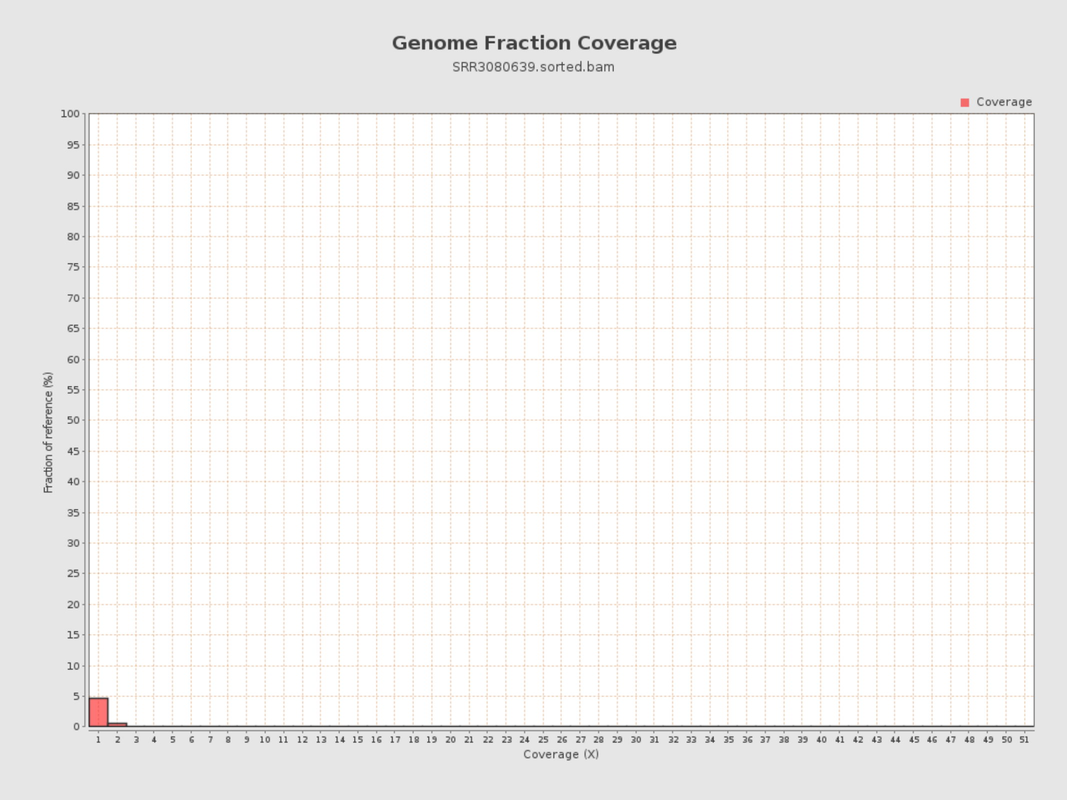
4. Results : Coverage Histogram



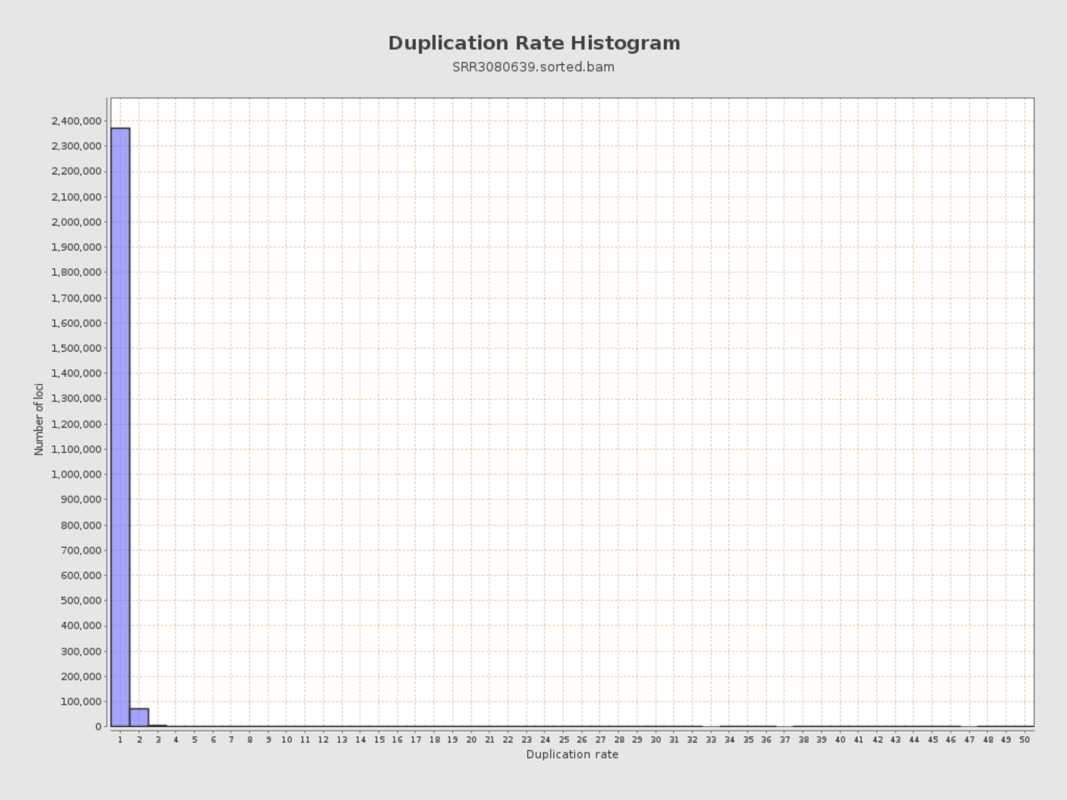
5. Results : Coverage Histogram (0-50X)



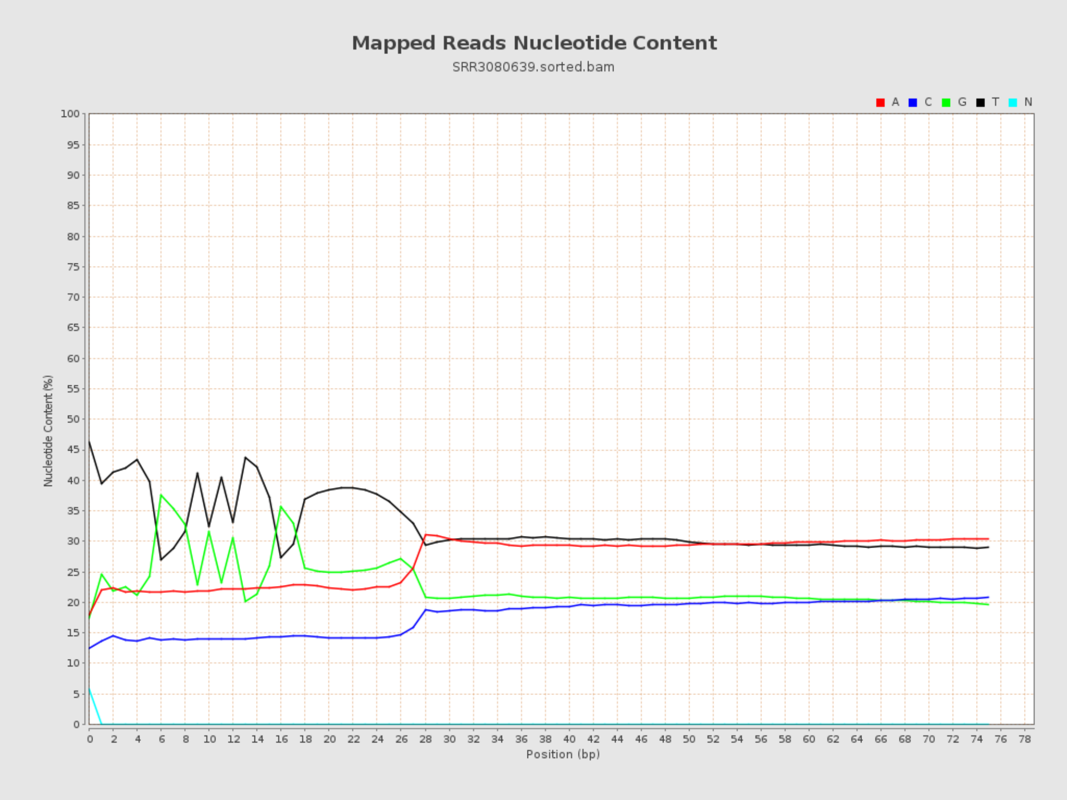
6. Results : Genome Fraction Coverage



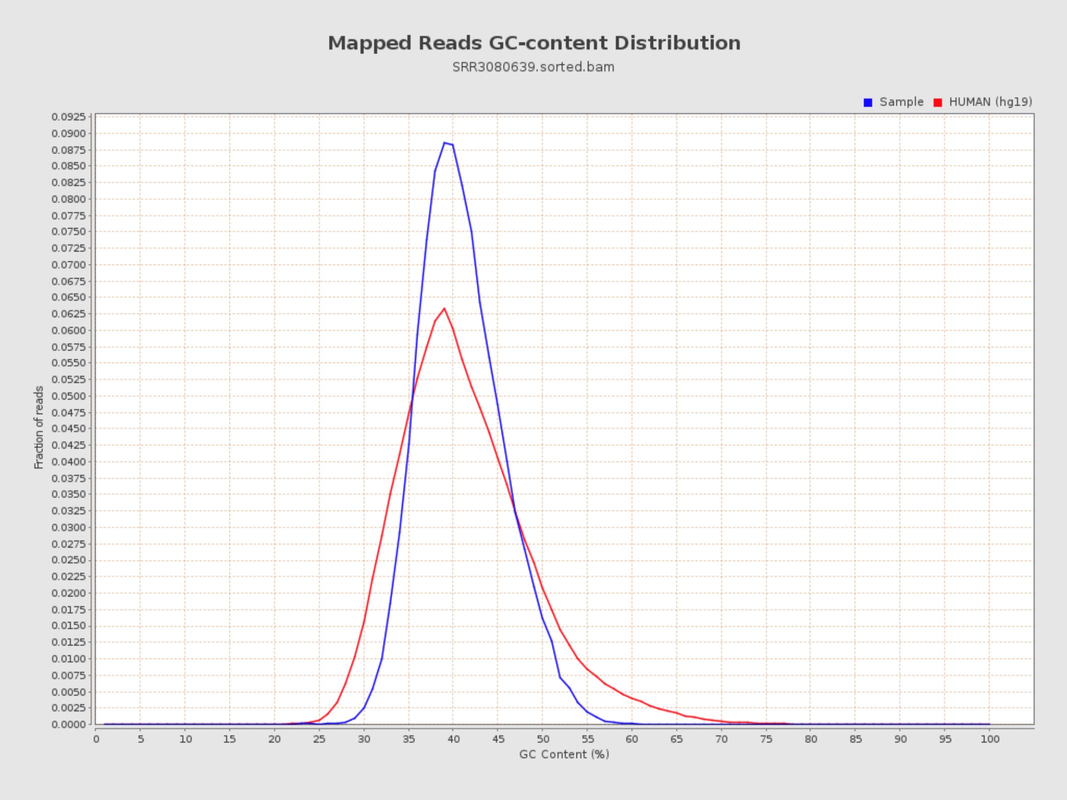
7. Results : Duplication Rate Histogram



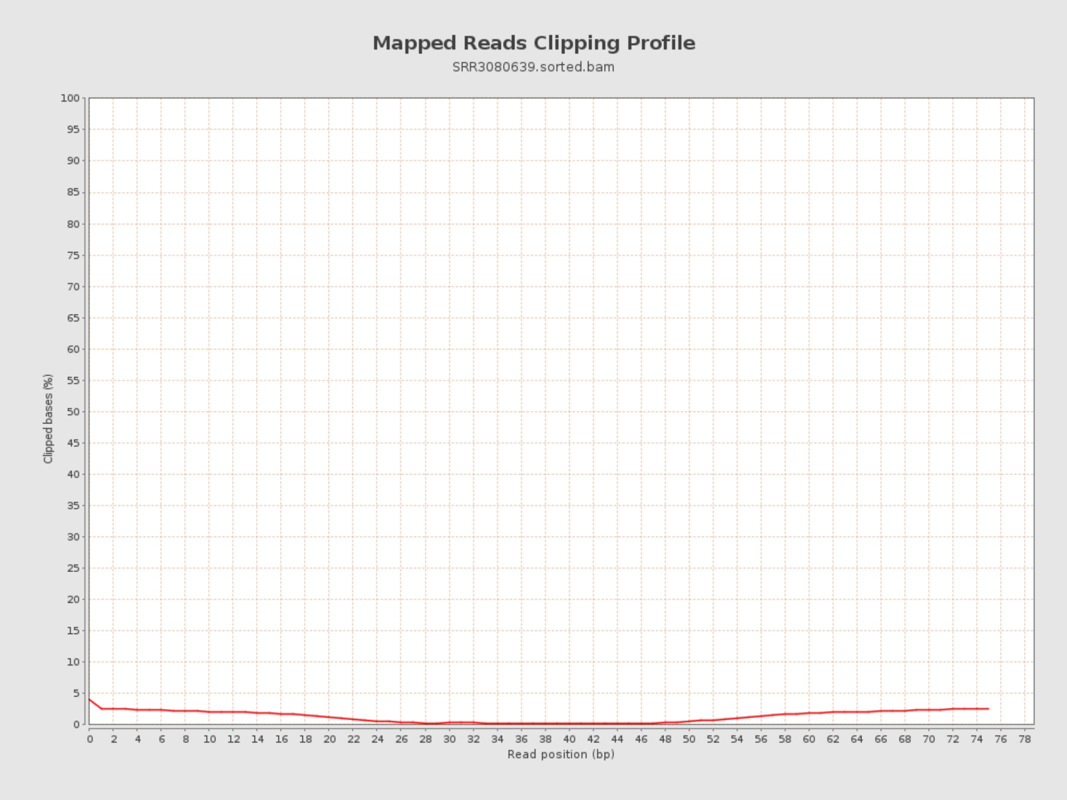
8. Results : Mapped Reads Nucleotide Content



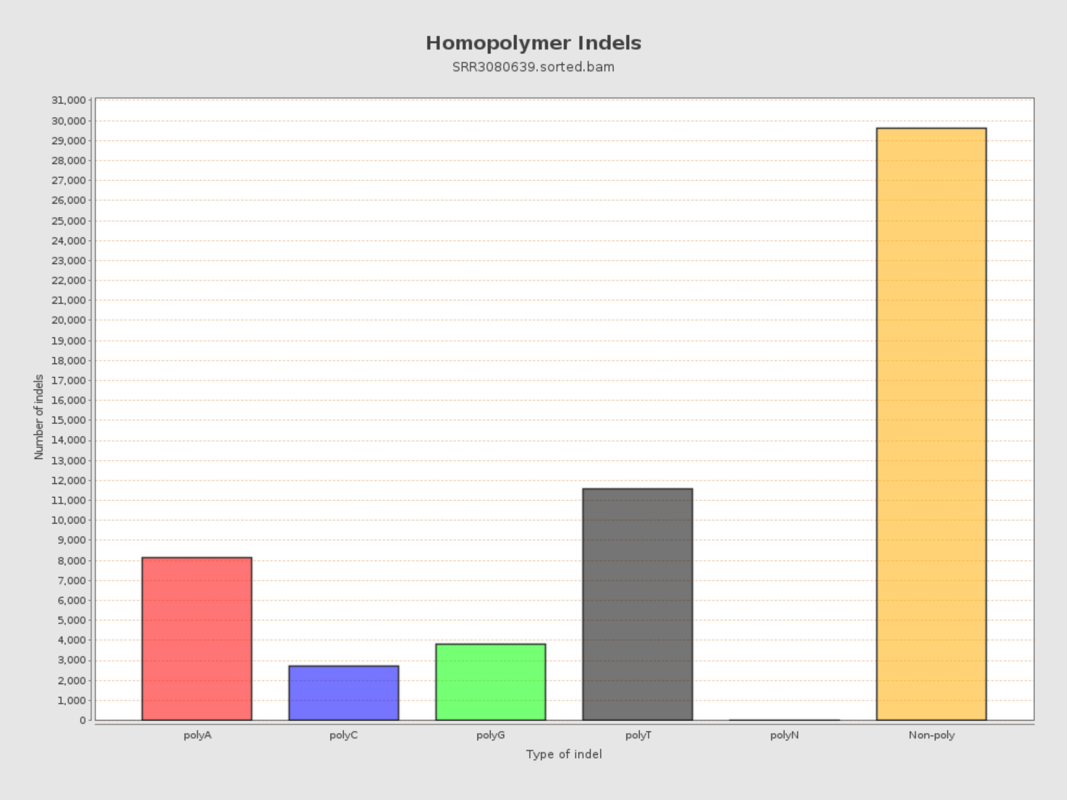
9. Results : Mapped Reads GC-content Distribution



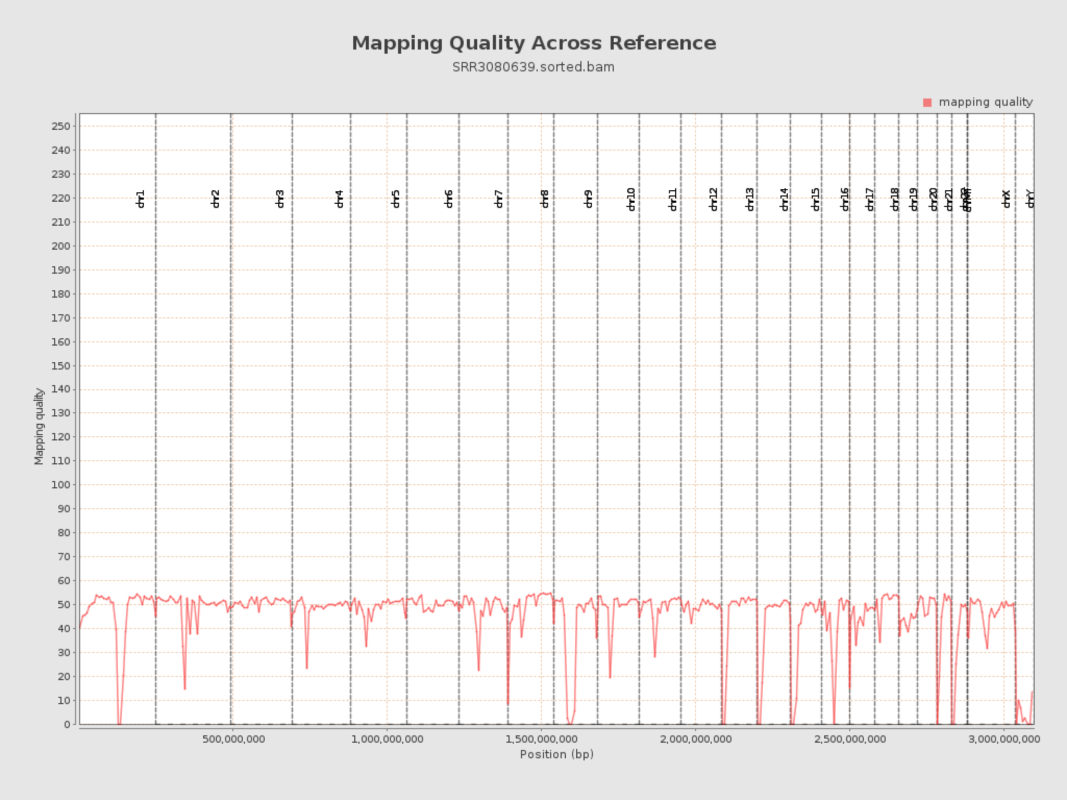
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram