Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:36:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080695.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_SRR3080695 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080695.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:36:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080695.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,790,695
Mapped reads	2,481,044 / 88.9%
Unmapped reads	309,651 / 11.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,479 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	127,331 / 4.56%
Duplication rate	4.2%
Clipped reads	709,304 / 25.42%

2.2. ACGT Content

Number/percentage of A's	53,253,827 / 30.33%
Number/percentage of C's	32,393,755 / 18.45%
Number/percentage of T's	55,031,310 / 31.34%
Number/percentage of G's	34,921,290 / 19.89%
Number/percentage of N's	2,701 / 0%
GC Percentage	38.33%

2.3. Coverage

Mean	0.0567

Standard Deviation	0.5575

2.4. Mapping Quality

Mean Mapping Quality	48.17

2.5. Mismatches and indels

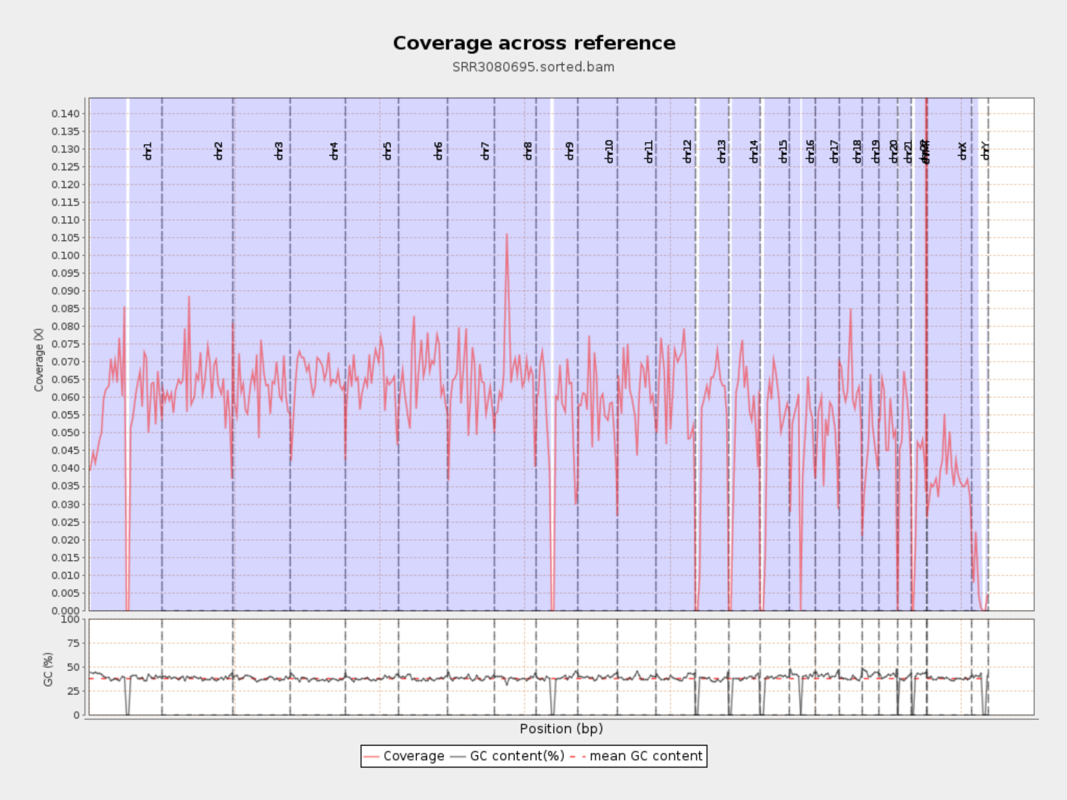
General error rate	0.8%
Mismatches	1,374,410
Insertions	14,143
Mapped reads with at least one insertion	0.56%
Deletions	36,600
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.94%

2.6. Chromosome stats

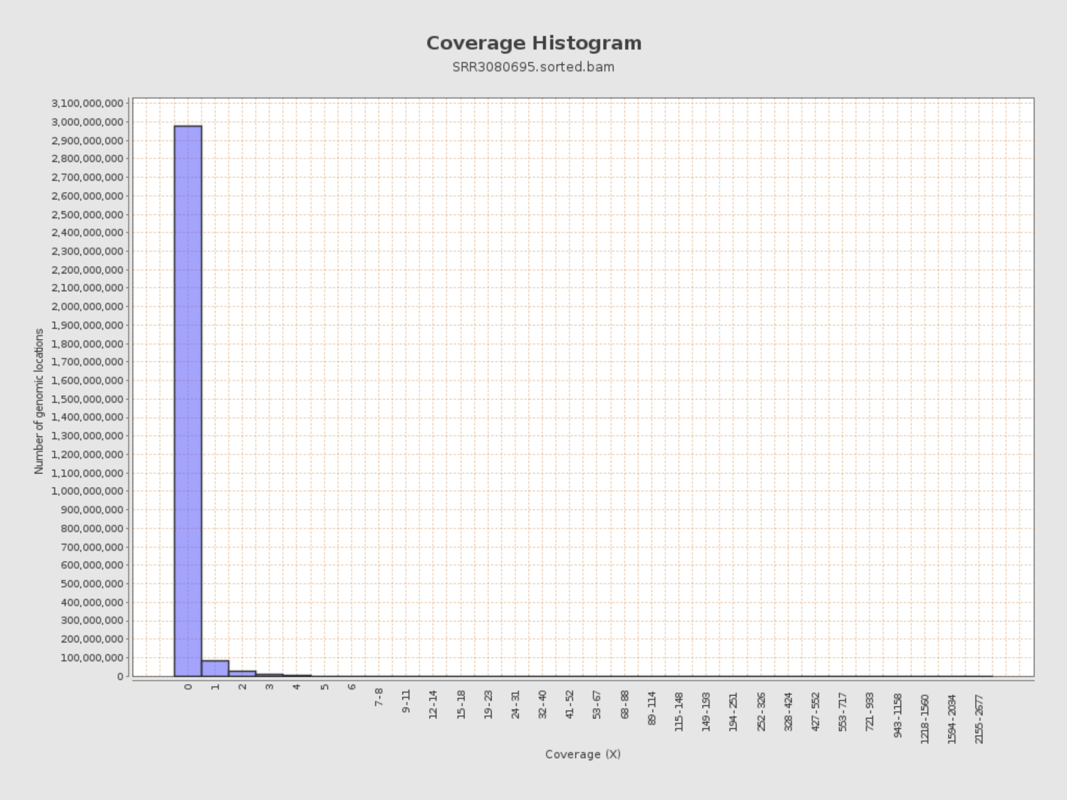
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14069950	0.0564	0.7853
chr2	243199373	15482199	0.0637	0.4419
chr3	198022430	12491903	0.0631	0.3485
chr4	191154276	12553234	0.0657	0.3675
chr5	180915260	11789626	0.0652	0.3568
chr6	171115067	11400362	0.0666	0.3754
chr7	159138663	10046496	0.0631	0.4886

chr8	146364022	9831981	0.0672	1.6774
chr9	141213431	7389998	0.0523	0.407
chr10	135534747	7889270	0.0582	0.4277
chr11	135006516	8321283	0.0616	0.3961
chr12	133851895	8424462	0.0629	0.3498
chr13	115169878	6013162	0.0522	0.3221
chr14	107349540	5445410	0.0507	0.3254
chr15	102531392	4912706	0.0479	0.3002
chr16	90354753	4298232	0.0476	0.3132
chr17	81195210	4013588	0.0494	0.3281
chr18	78077248	4964508	0.0636	0.6303
chr19	59128983	2695556	0.0456	0.5137
chr20	63025520	3295438	0.0523	0.3196
chr21	48129895	2318127	0.0482	0.3207
chr22	51304566	1612556	0.0314	0.2384
chrMT	16571	176536	10.6533	6.874
chrX	155270560	5872609	0.0378	0.2822
chrY	59373566	360011	0.0061	0.1725

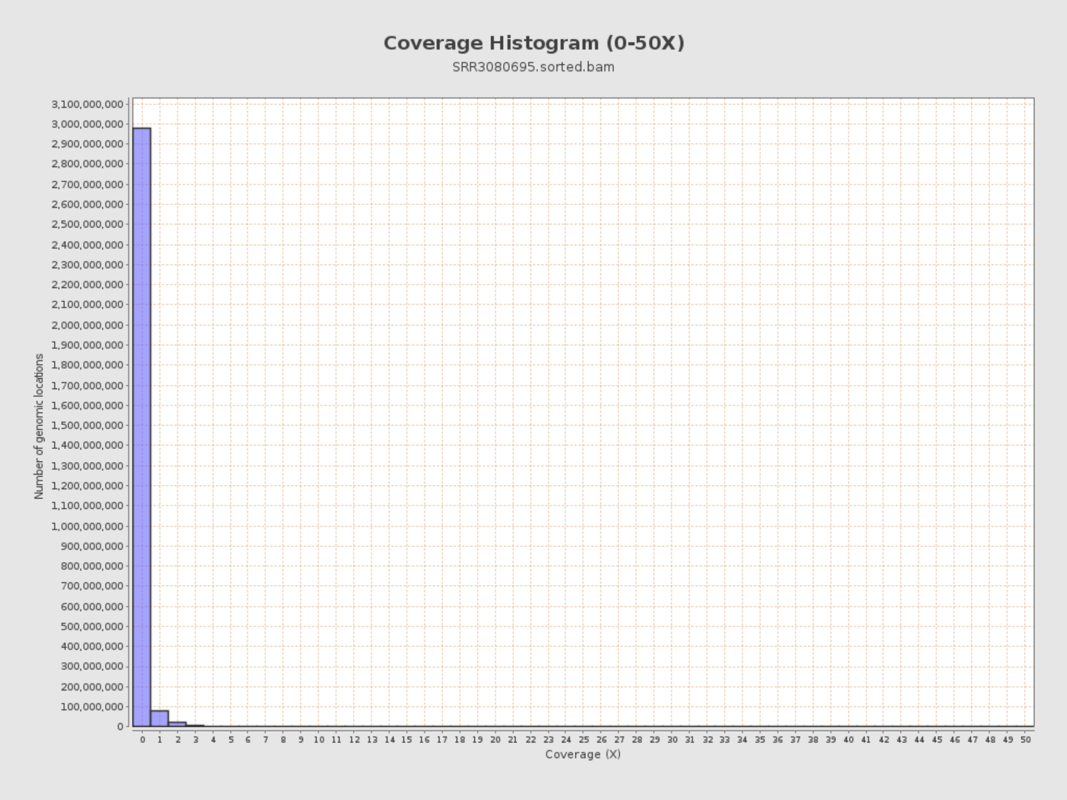
3. Results : Coverage across reference



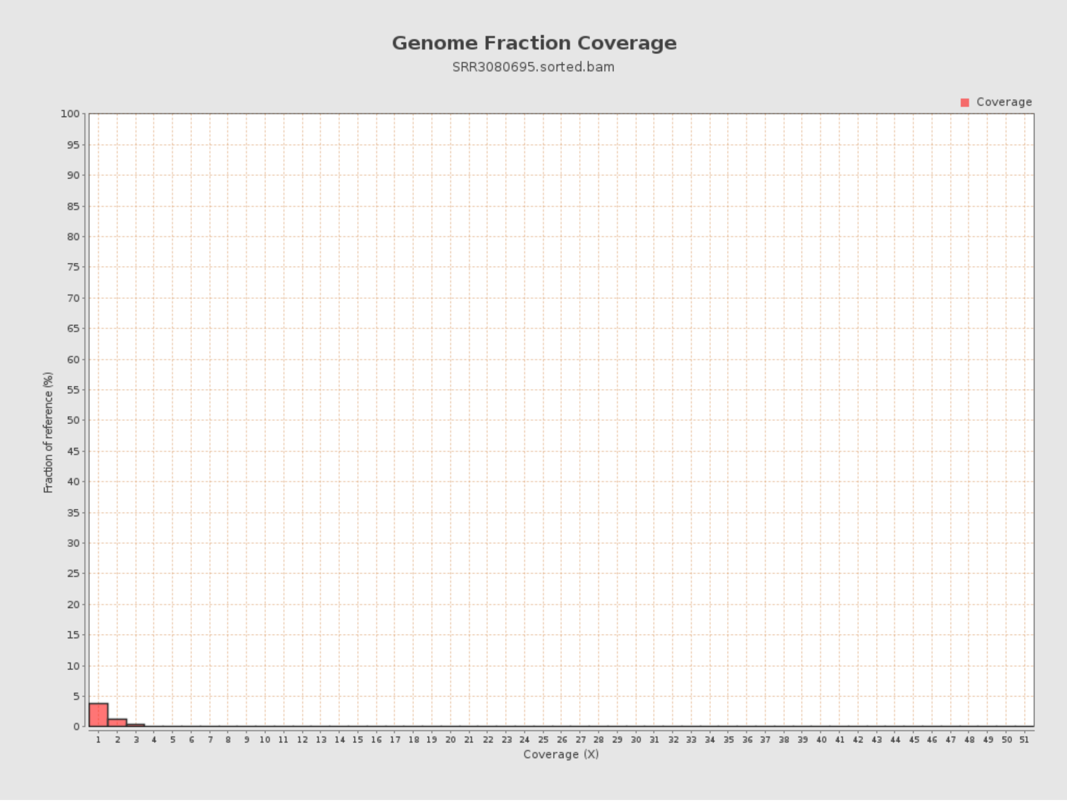
4. Results : Coverage Histogram



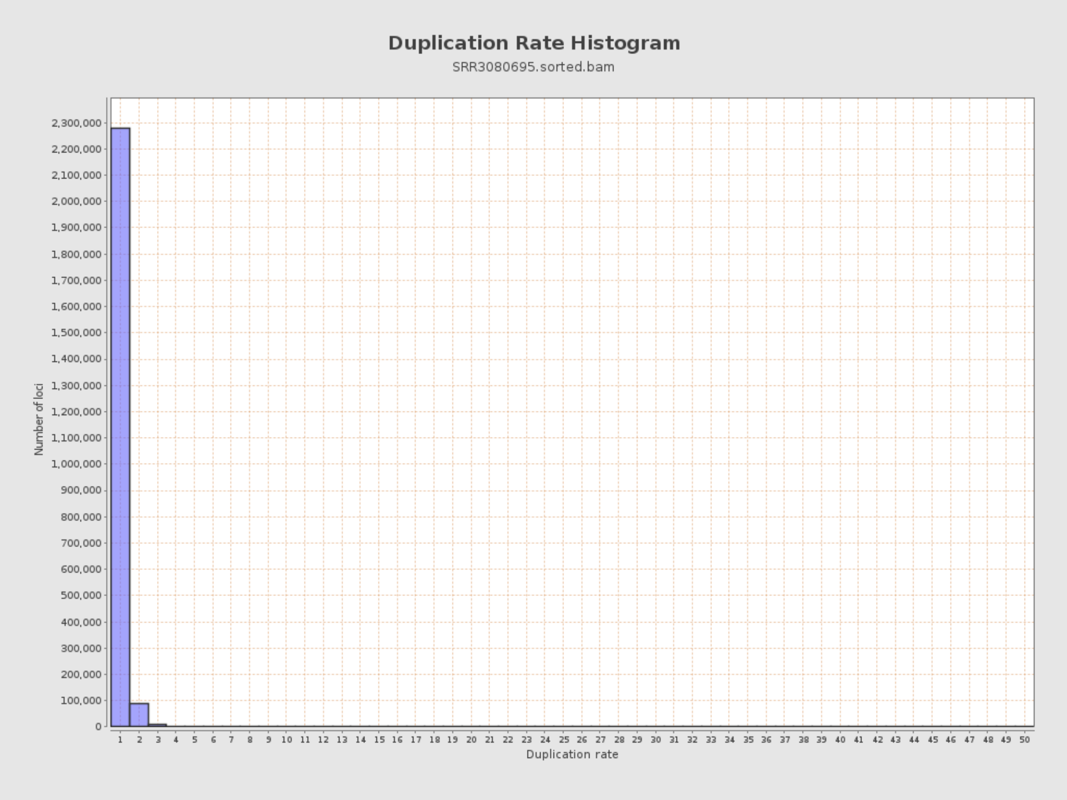
5. Results : Coverage Histogram (0-50X)



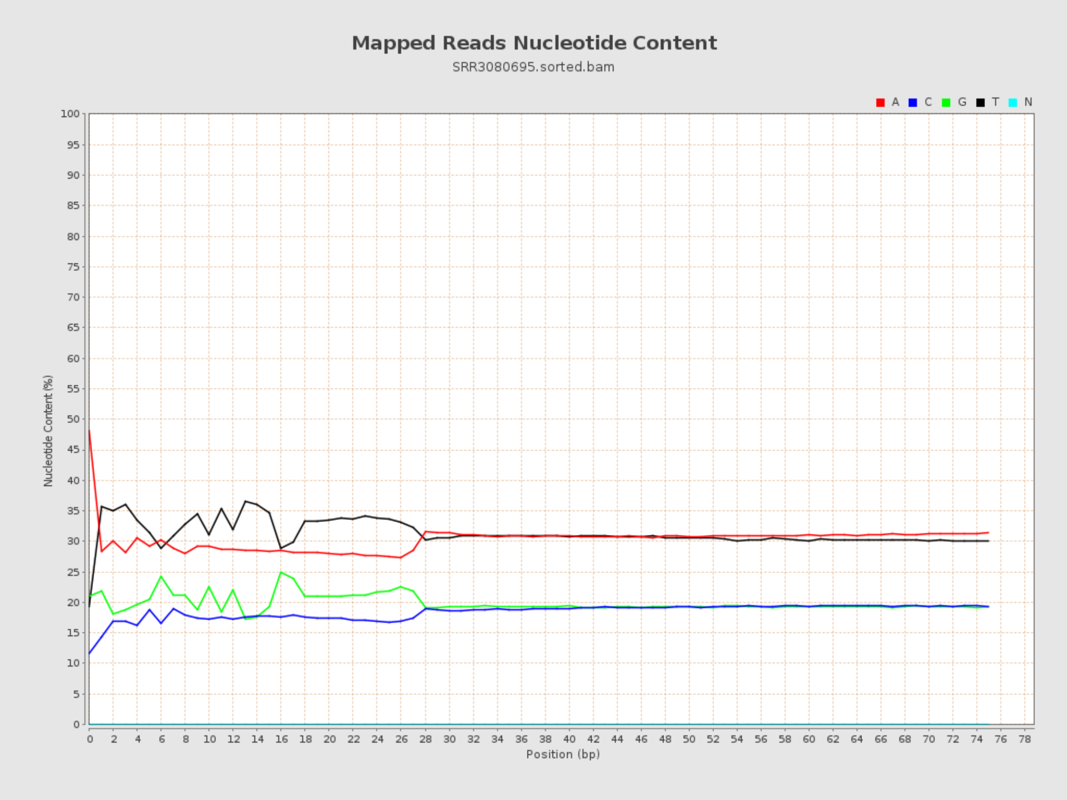
6. Results : Genome Fraction Coverage



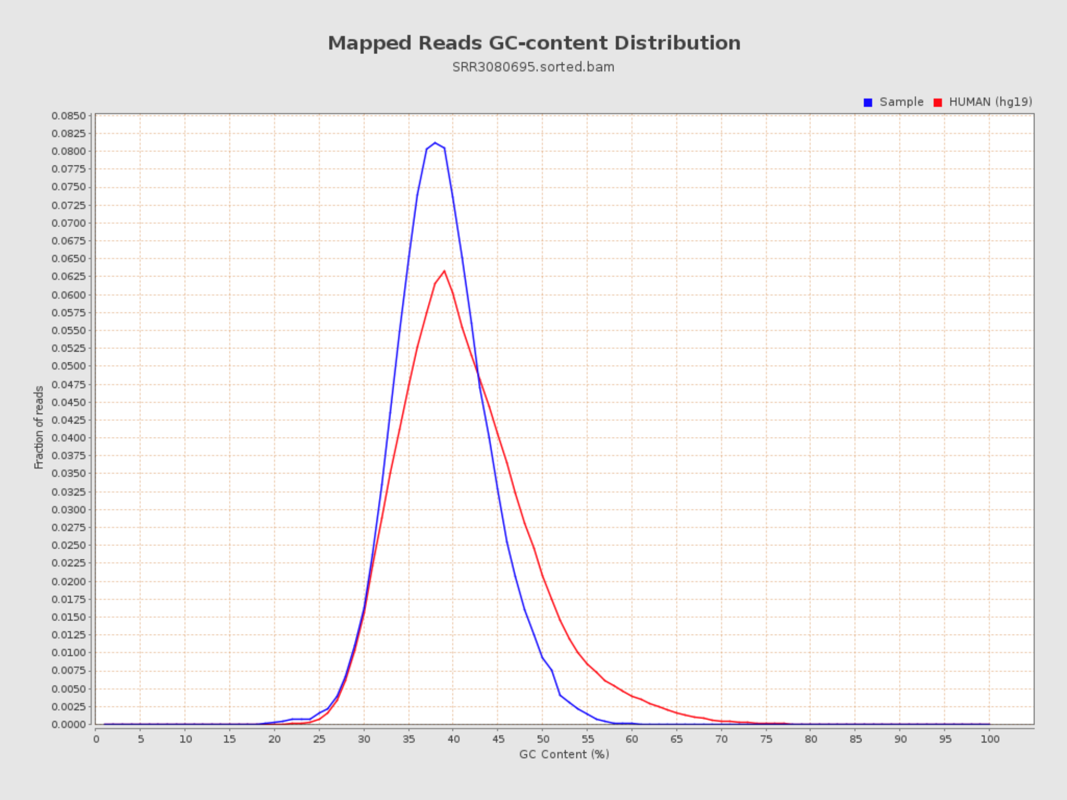
7. Results : Duplication Rate Histogram



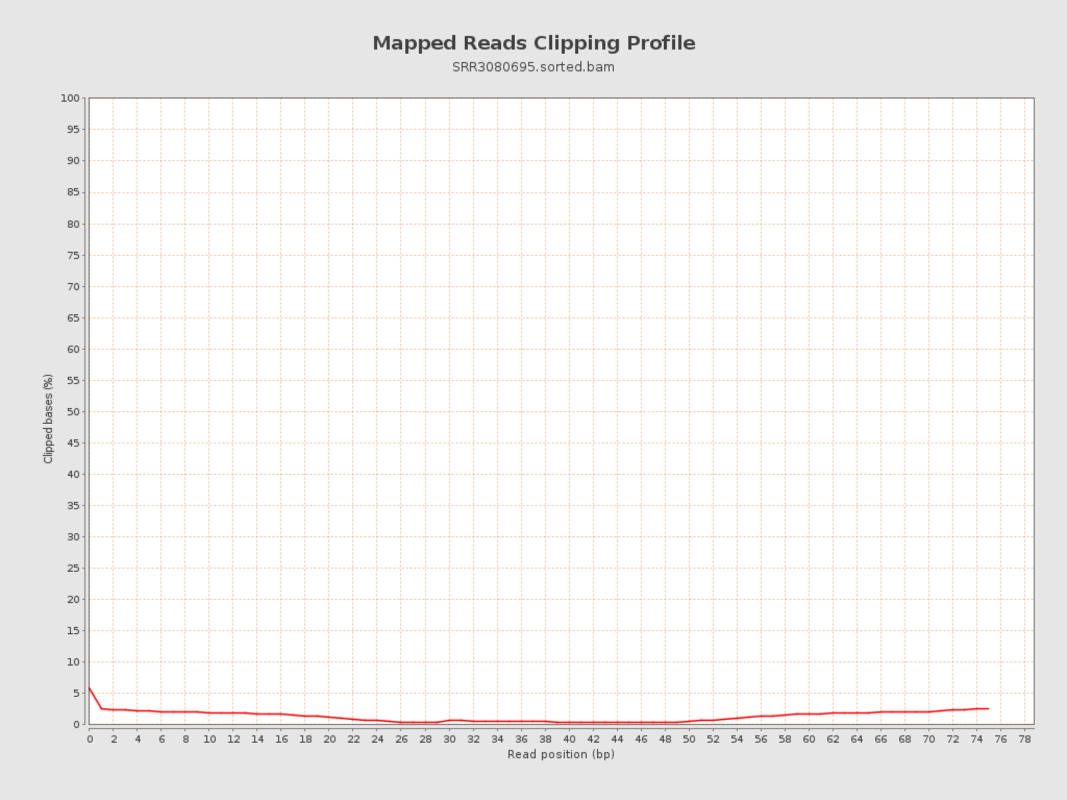
8. Results : Mapped Reads Nucleotide Content



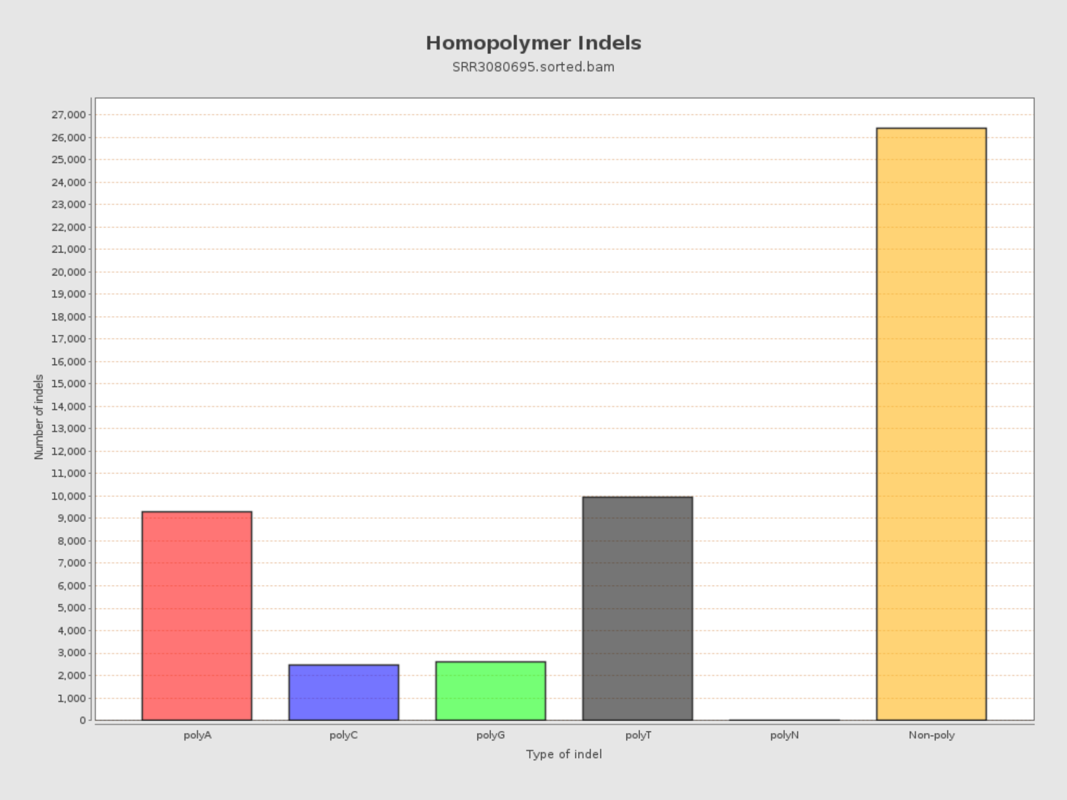
9. Results : Mapped Reads GC-content Distribution



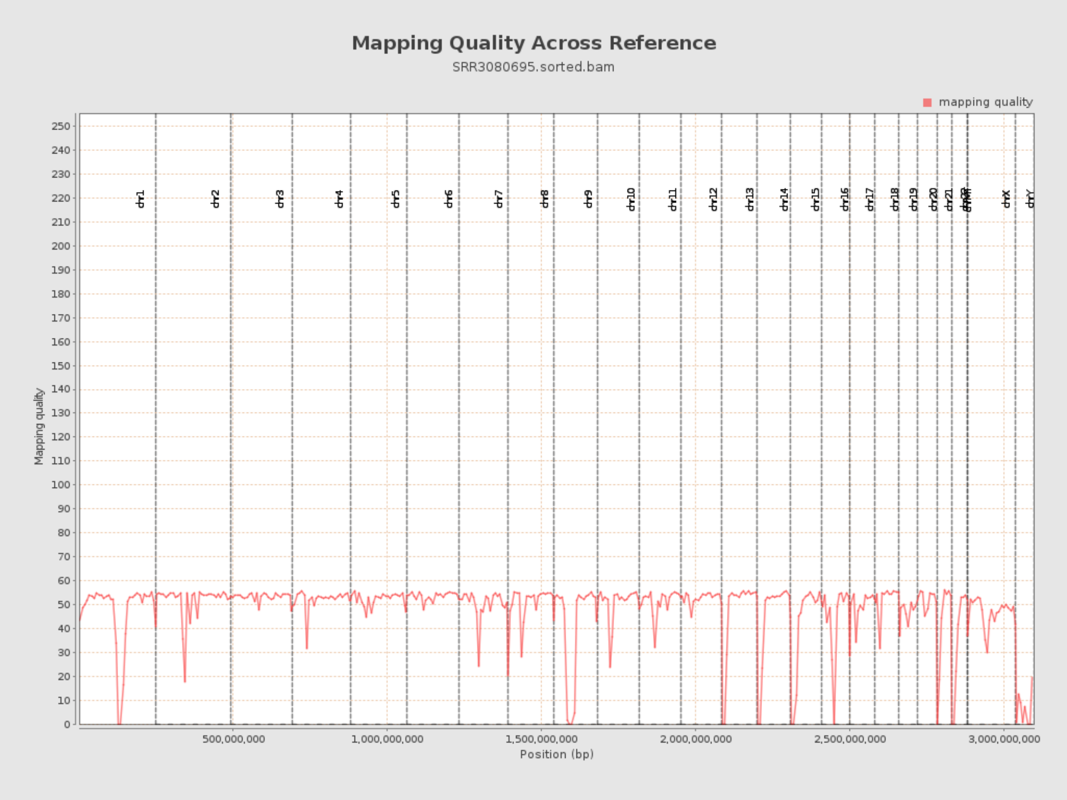
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram