Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:30:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080971.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_SRR3080971 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080971.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:30:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080971.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,900,942
Mapped reads	6,112,071 / 88.57%
Unmapped reads	788,871 / 11.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	63,087 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	500,298 / 7.25%
Duplication rate	6.48%
Clipped reads	2,614,685 / 37.89%

2.2. ACGT Content

Number/percentage of A's	115,520,108 / 28.11%
Number/percentage of C's	72,379,485 / 17.61%
Number/percentage of T's	133,834,754 / 32.57%
Number/percentage of G's	88,373,943 / 21.51%
Number/percentage of N's	811,763 / 0.2%
GC Percentage	39.12%

2.3. Coverage

Mean	0.1328

Standard Deviation	0.8357

2.4. Mapping Quality

Mean Mapping Quality	47.03

2.5. Mismatches and indels

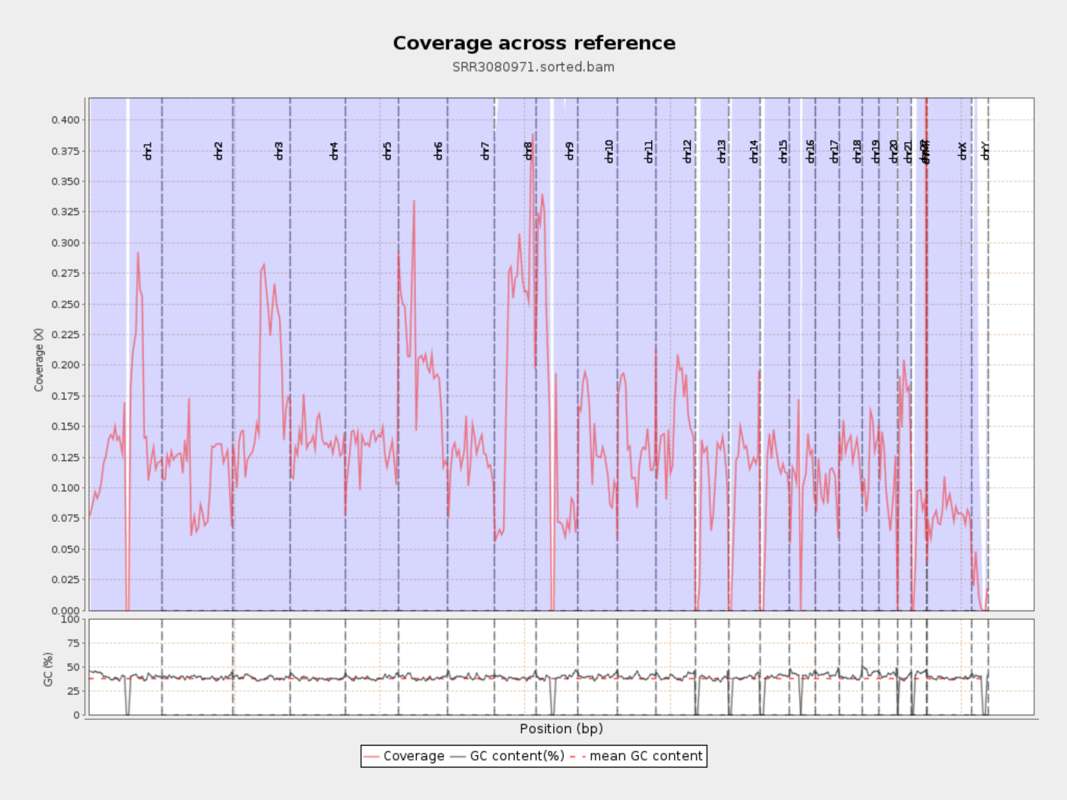
General error rate	1.01%
Mismatches	4,077,421
Insertions	32,332
Mapped reads with at least one insertion	0.53%
Deletions	91,362
Mapped reads with at least one deletion	1.48%
Homopolymer indels	49.22%

2.6. Chromosome stats

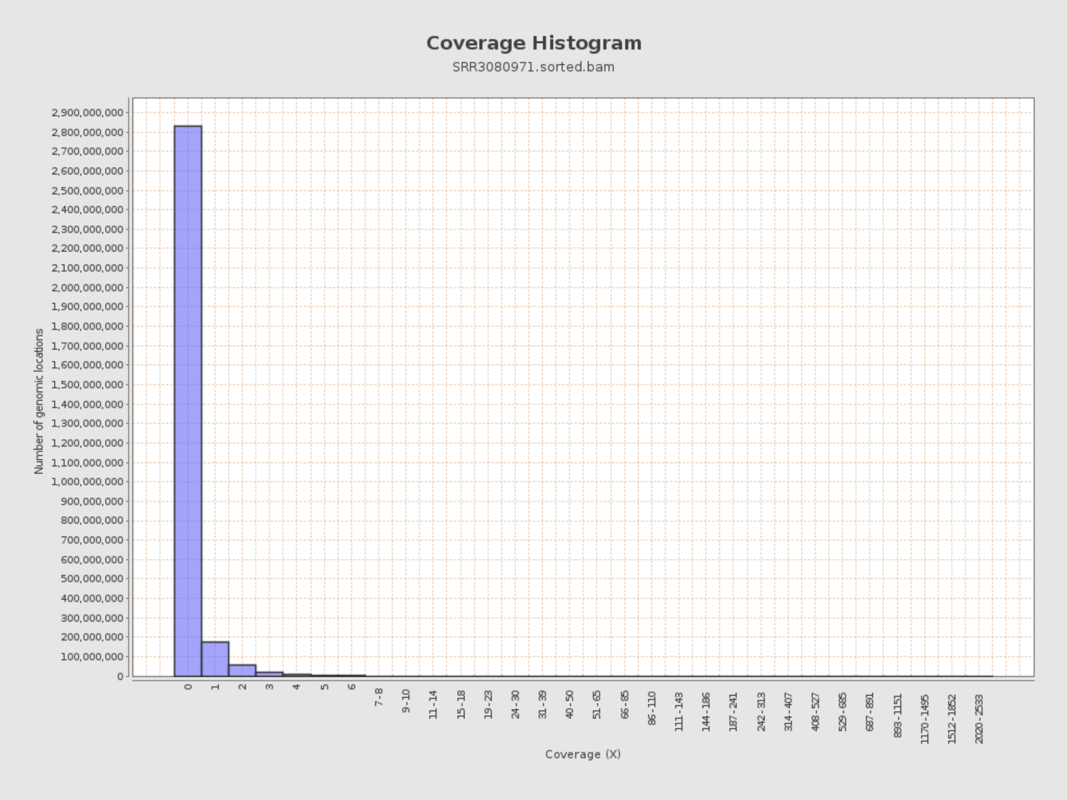
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34187355	0.1372	1.1218
chr2	243199373	26978328	0.1109	0.788
chr3	198022430	35957079	0.1816	0.611
chr4	191154276	26208982	0.1371	0.5558
chr5	180915260	23927419	0.1323	0.516
chr6	171115067	35483115	0.2074	0.9662
chr7	159138663	20163862	0.1267	0.8296

chr8	146364022	32079926	0.2192	1.6833
chr9	141213431	20128172	0.1425	1.0156
chr10	135534747	18467090	0.1363	0.7036
chr11	135006516	18312721	0.1356	0.6826
chr12	133851895	20205287	0.151	0.5804
chr13	115169878	11218673	0.0974	0.4412
chr14	107349540	11490437	0.107	0.5961
chr15	102531392	10375197	0.1012	0.4528
chr16	90354753	9687410	0.1072	0.5808
chr17	81195210	7977274	0.0982	0.467
chr18	78077248	10316813	0.1321	1.7734
chr19	59128983	7371878	0.1247	0.8951
chr20	63025520	6536078	0.1037	0.488
chr21	48129895	7606323	0.158	0.6903
chr22	51304566	3229823	0.063	0.3463
chrMT	16571	202494	12.2198	6.7836
chrX	155270560	12071019	0.0777	0.4565
chrY	59373566	888373	0.015	0.2692

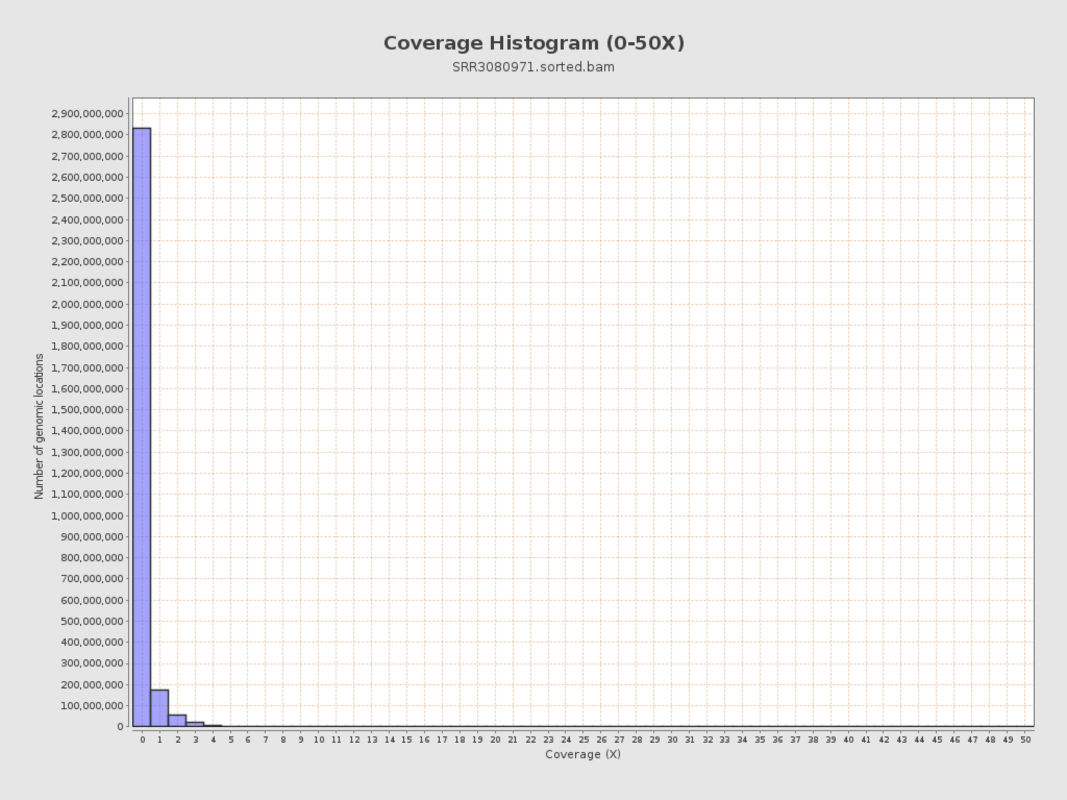
3. Results : Coverage across reference



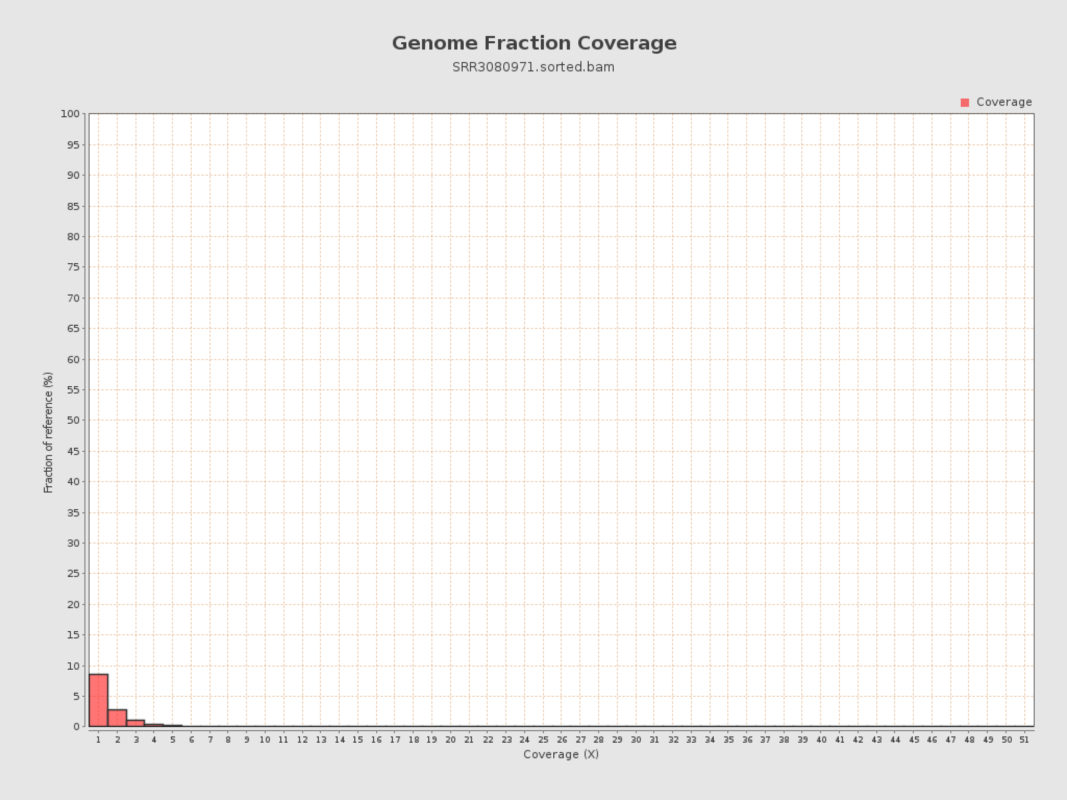
4. Results : Coverage Histogram



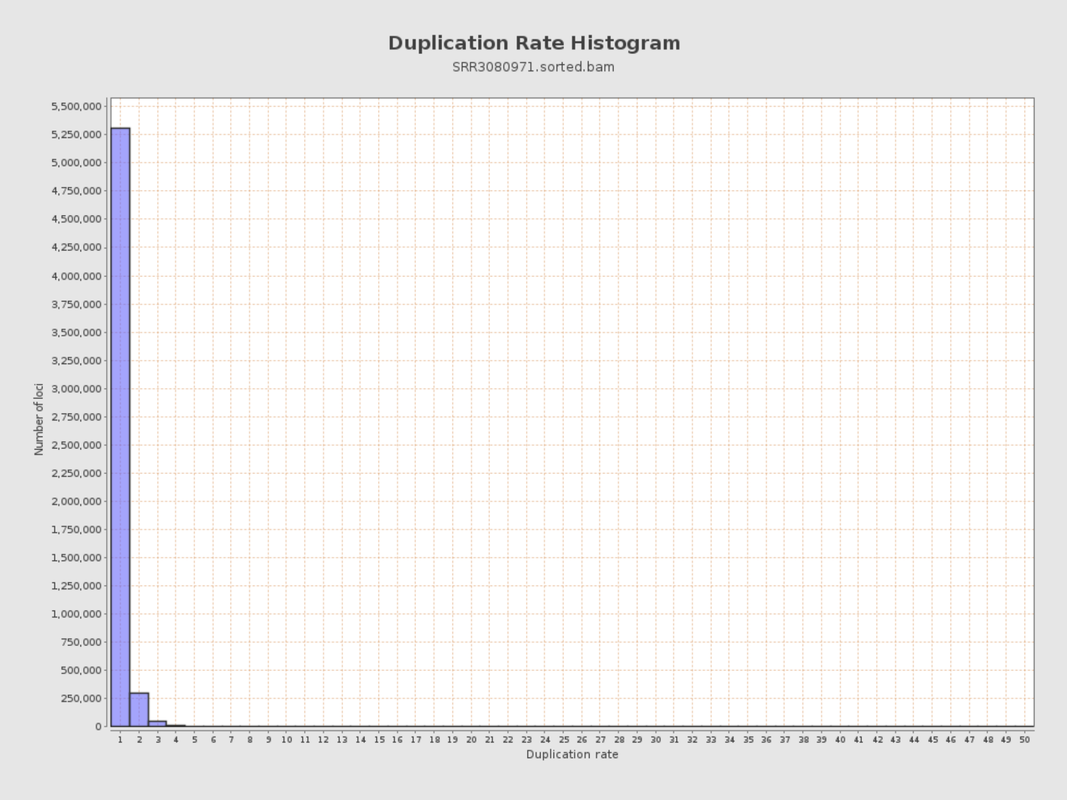
5. Results : Coverage Histogram (0-50X)



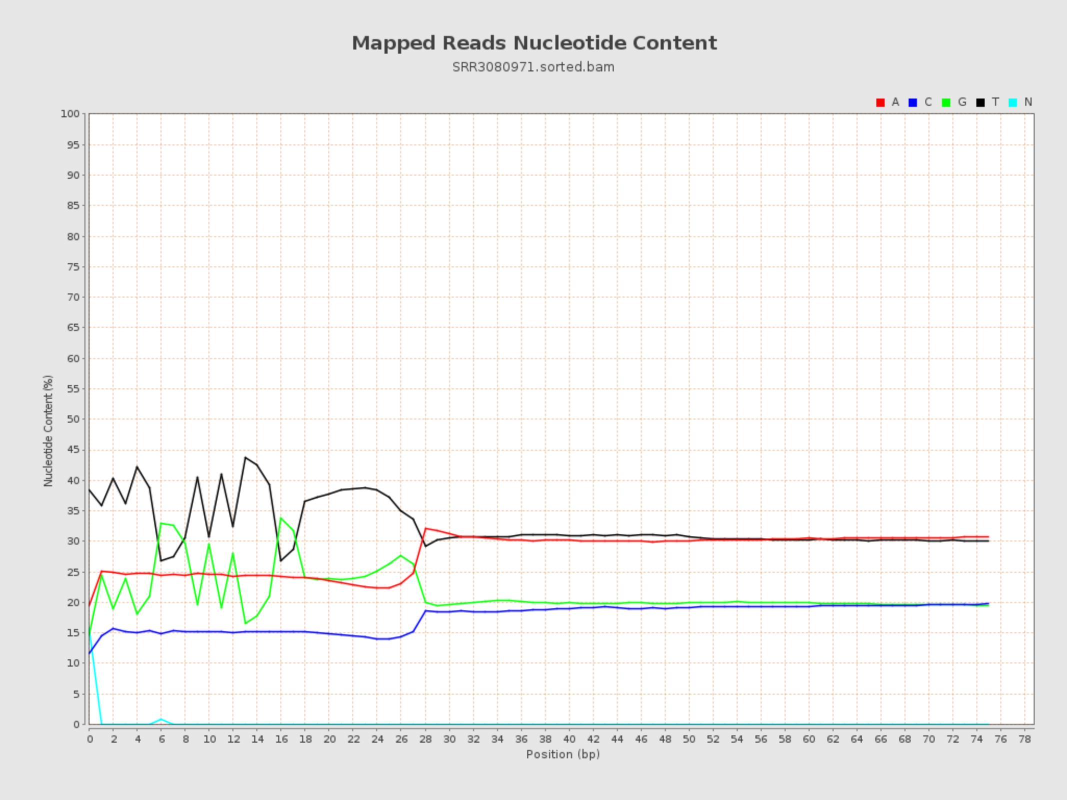
6. Results : Genome Fraction Coverage



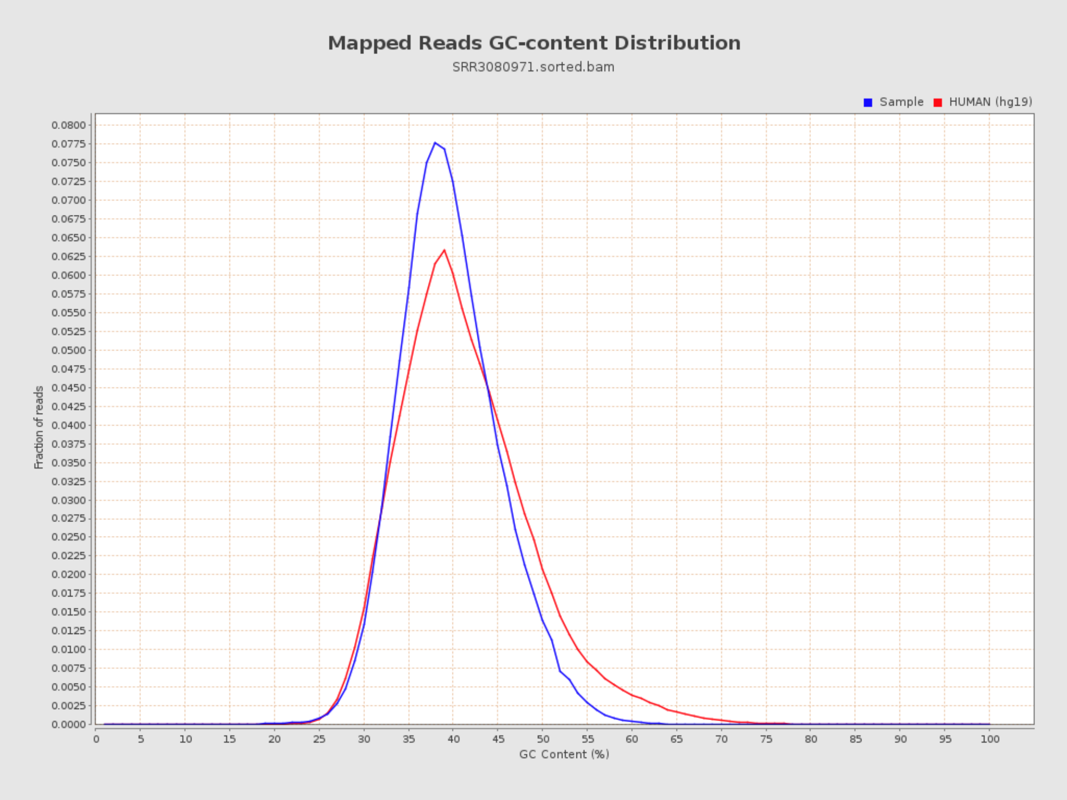
7. Results : Duplication Rate Histogram



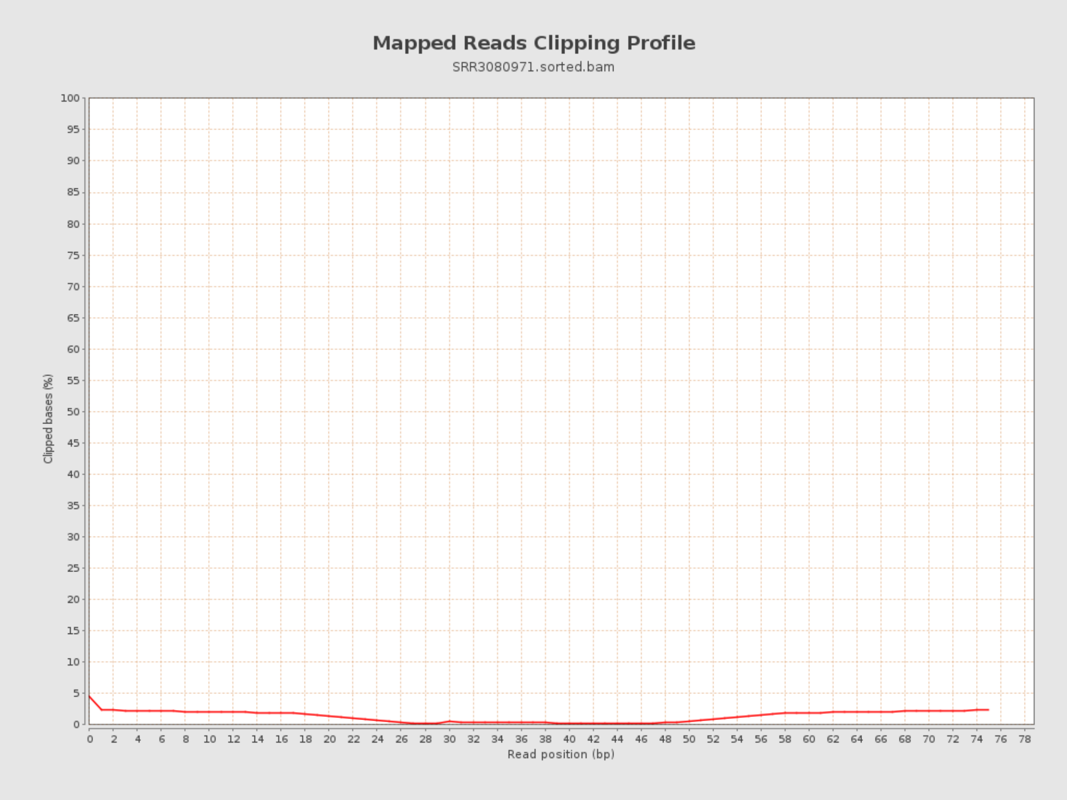
8. Results : Mapped Reads Nucleotide Content



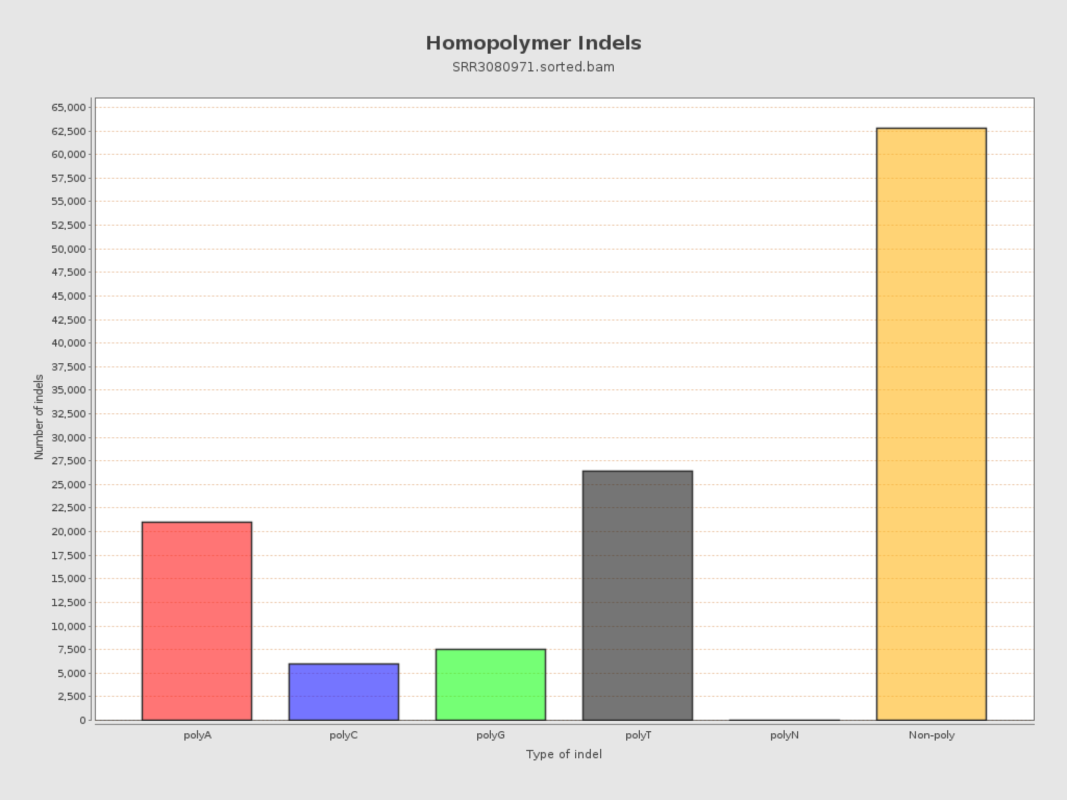
9. Results : Mapped Reads GC-content Distribution



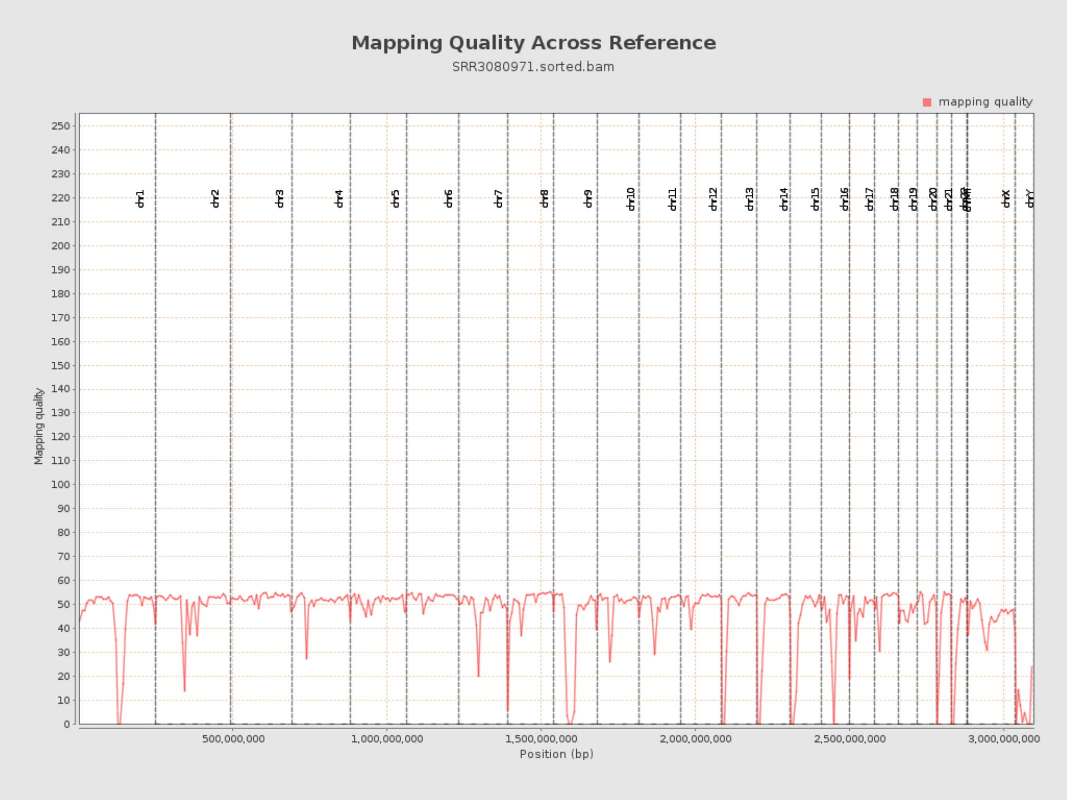
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram