Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:41:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081936.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_SRR3081936 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081936.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:41:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081936.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,921,627
Mapped reads	2,652,370 / 90.78%
Unmapped reads	269,257 / 9.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,837 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	128,803 / 4.41%
Duplication rate	3.36%
Clipped reads	950,202 / 32.52%

2.2. ACGT Content

Number/percentage of A's	51,785,806 / 28.43%
Number/percentage of C's	33,986,592 / 18.66%
Number/percentage of T's	57,076,281 / 31.34%
Number/percentage of G's	39,272,364 / 21.56%
Number/percentage of N's	23,670 / 0.01%
GC Percentage	40.22%

2.3. Coverage

Mean	0.0589

Standard Deviation	0.6235

2.4. Mapping Quality

Mean Mapping Quality	45.11

2.5. Mismatches and indels

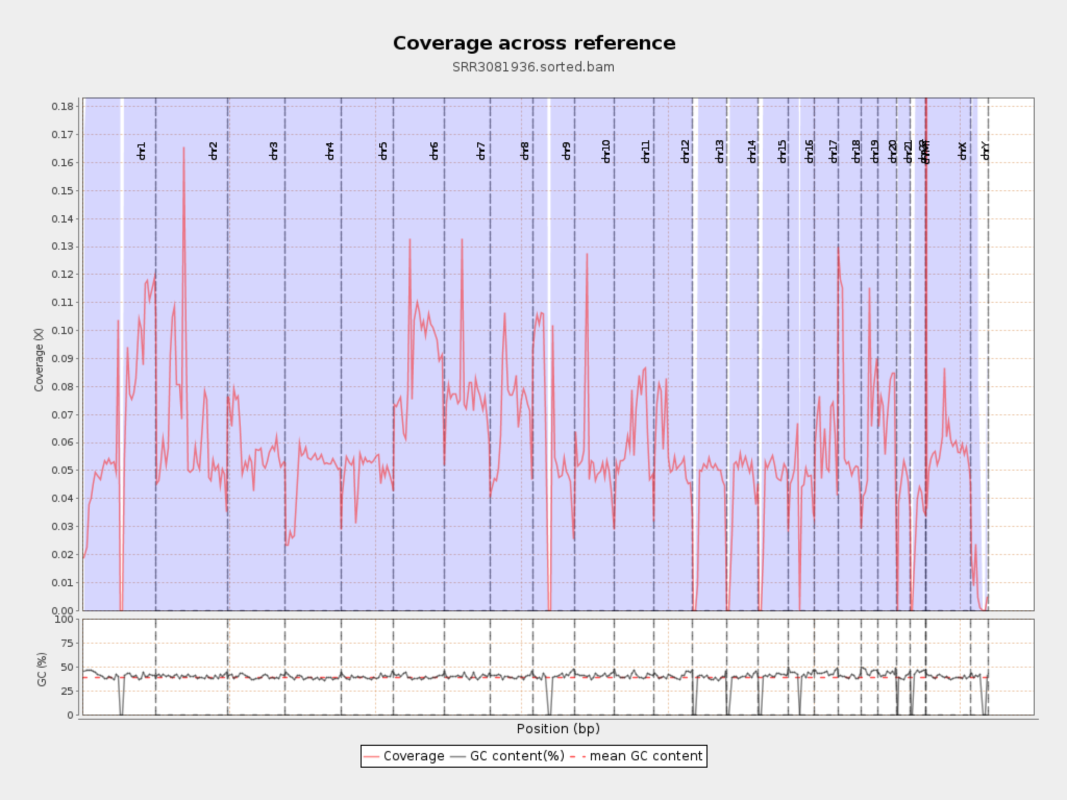
General error rate	0.82%
Mismatches	1,459,362
Insertions	14,083
Mapped reads with at least one insertion	0.53%
Deletions	40,892
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.46%

2.6. Chromosome stats

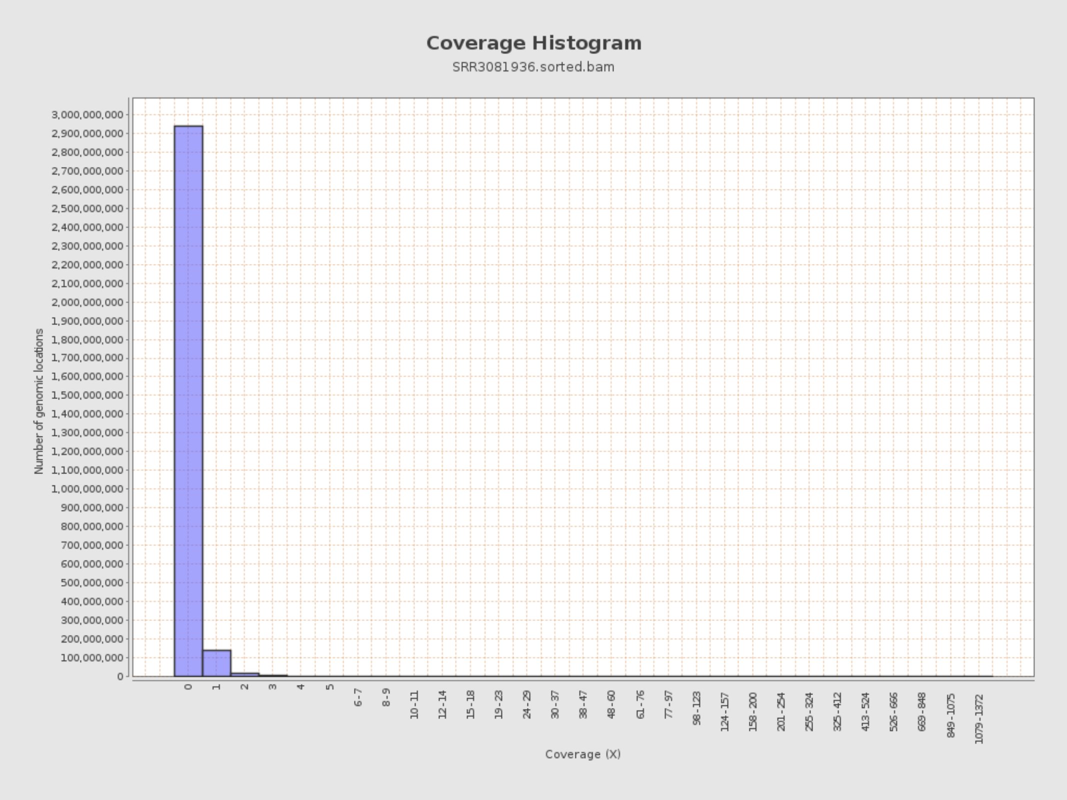
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16522267	0.0663	1.1771
chr2	243199373	15861214	0.0652	0.8485
chr3	198022430	11637273	0.0588	0.2774
chr4	191154276	9256439	0.0484	0.2848
chr5	180915260	9039173	0.05	0.2602
chr6	171115067	15658394	0.0915	0.496
chr7	159138663	12320650	0.0774	0.9237

chr8	146364022	10280227	0.0702	0.8473
chr9	141213431	8799148	0.0623	0.6736
chr10	135534747	7474262	0.0551	0.6018
chr11	135006516	8476897	0.0628	0.4405
chr12	133851895	7700795	0.0575	0.2874
chr13	115169878	4800874	0.0417	0.2288
chr14	107349540	4566330	0.0425	0.2932
chr15	102531392	4232315	0.0413	0.2358
chr16	90354753	3872132	0.0429	0.3212
chr17	81195210	5025211	0.0619	0.3209
chr18	78077248	5271326	0.0675	1.0915
chr19	59128983	3966931	0.0671	0.8307
chr20	63025520	4589033	0.0728	0.3177
chr21	48129895	1984354	0.0412	0.2812
chr22	51304566	1451750	0.0283	0.1856
chrMT	16571	19428	1.1724	1.2831
chrX	155270560	8979889	0.0578	0.3505
chrY	59373566	430649	0.0073	0.2011

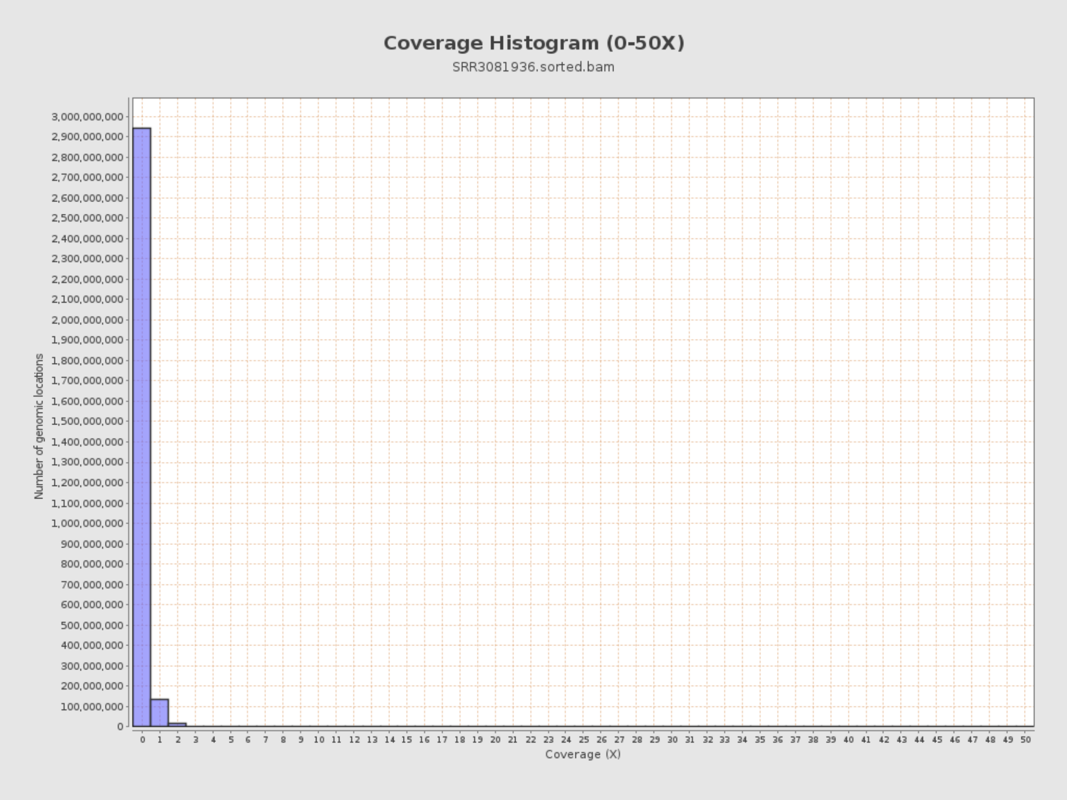
3. Results : Coverage across reference



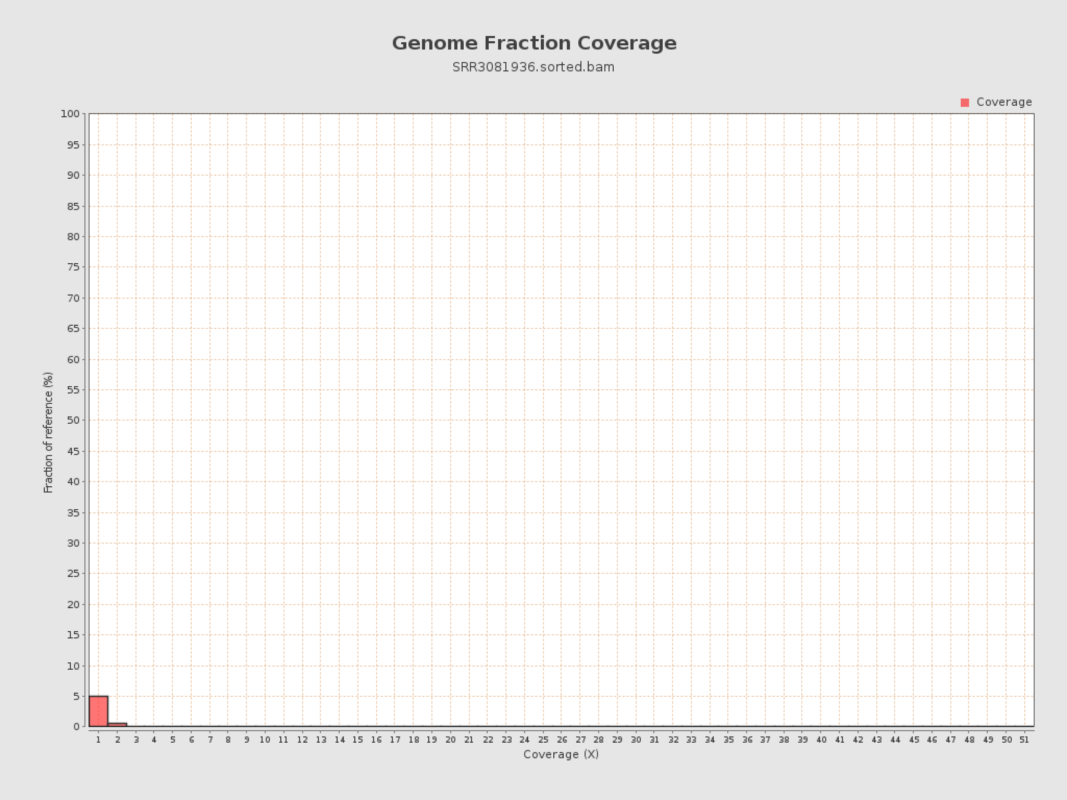
4. Results : Coverage Histogram



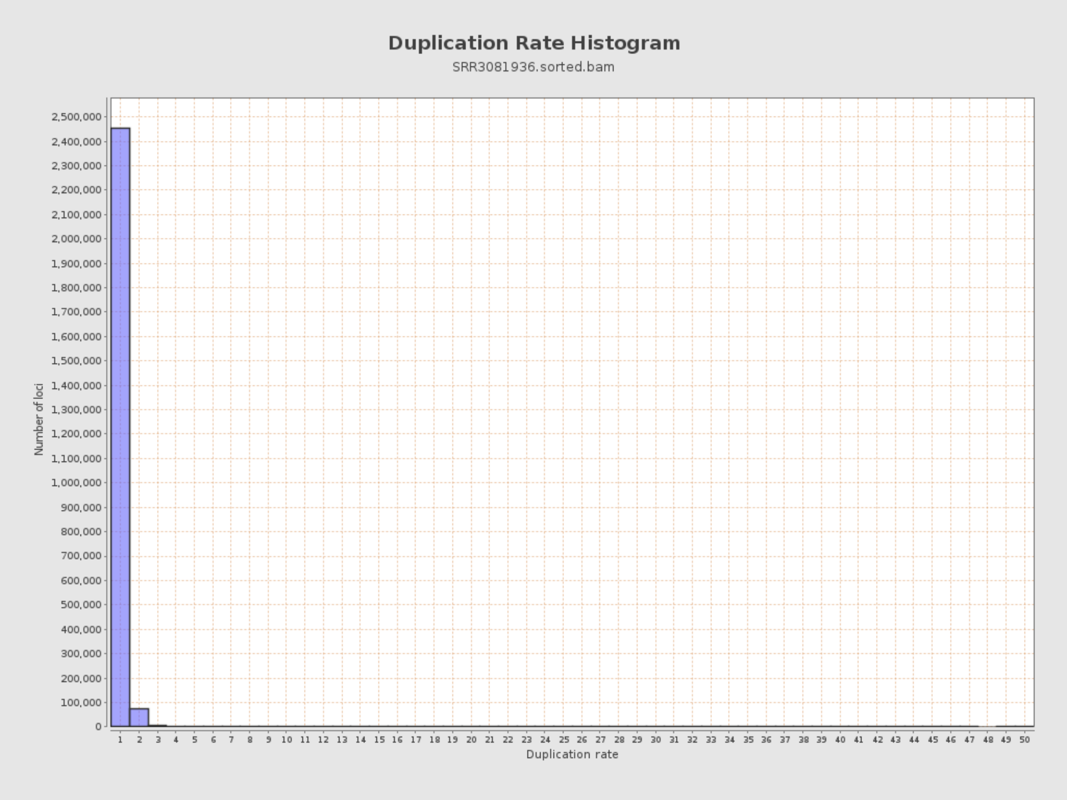
5. Results : Coverage Histogram (0-50X)



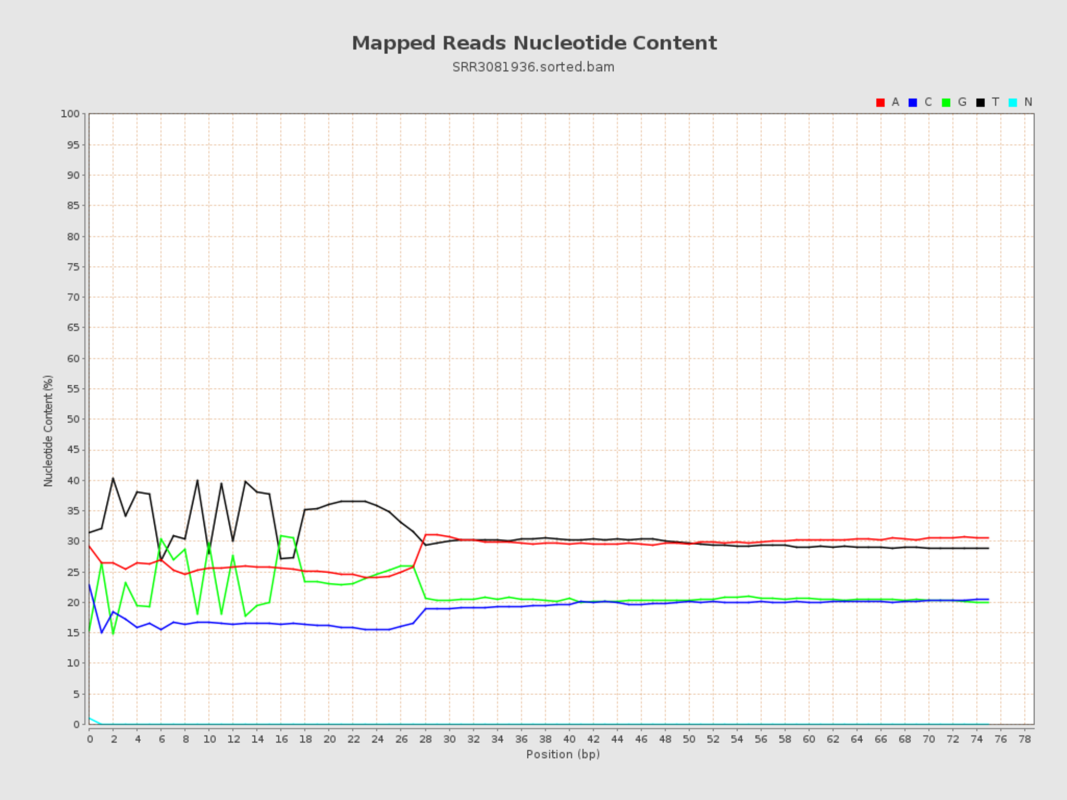
6. Results : Genome Fraction Coverage



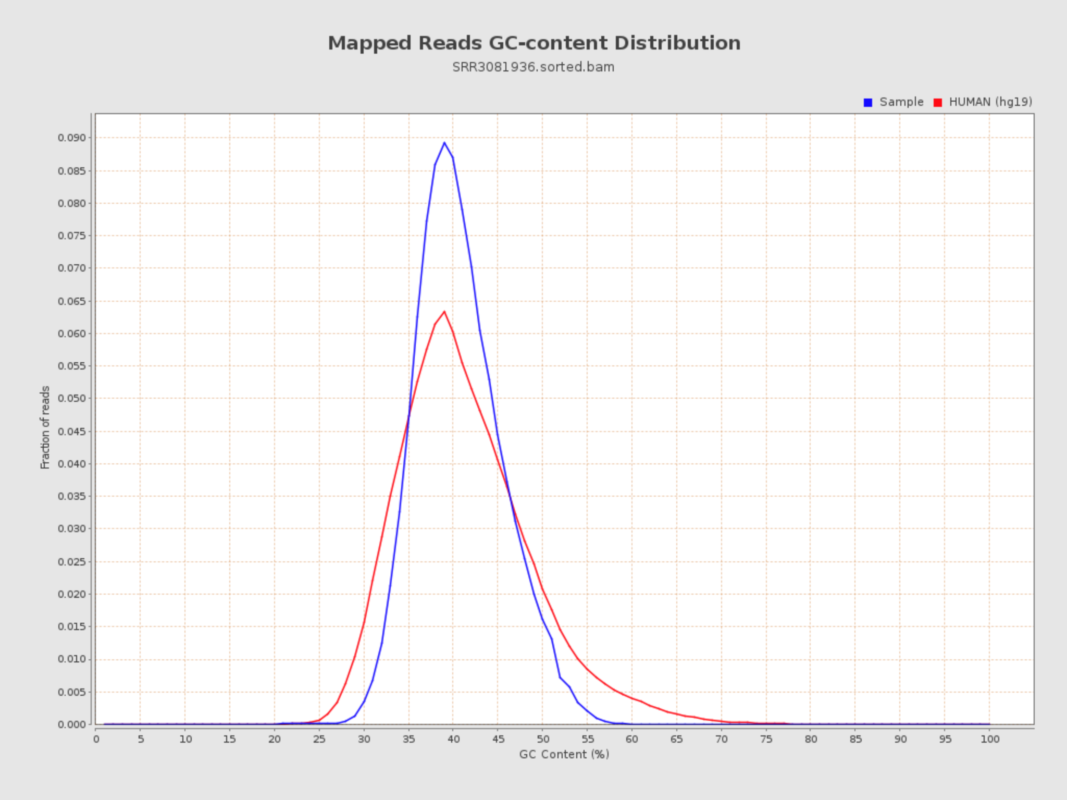
7. Results : Duplication Rate Histogram



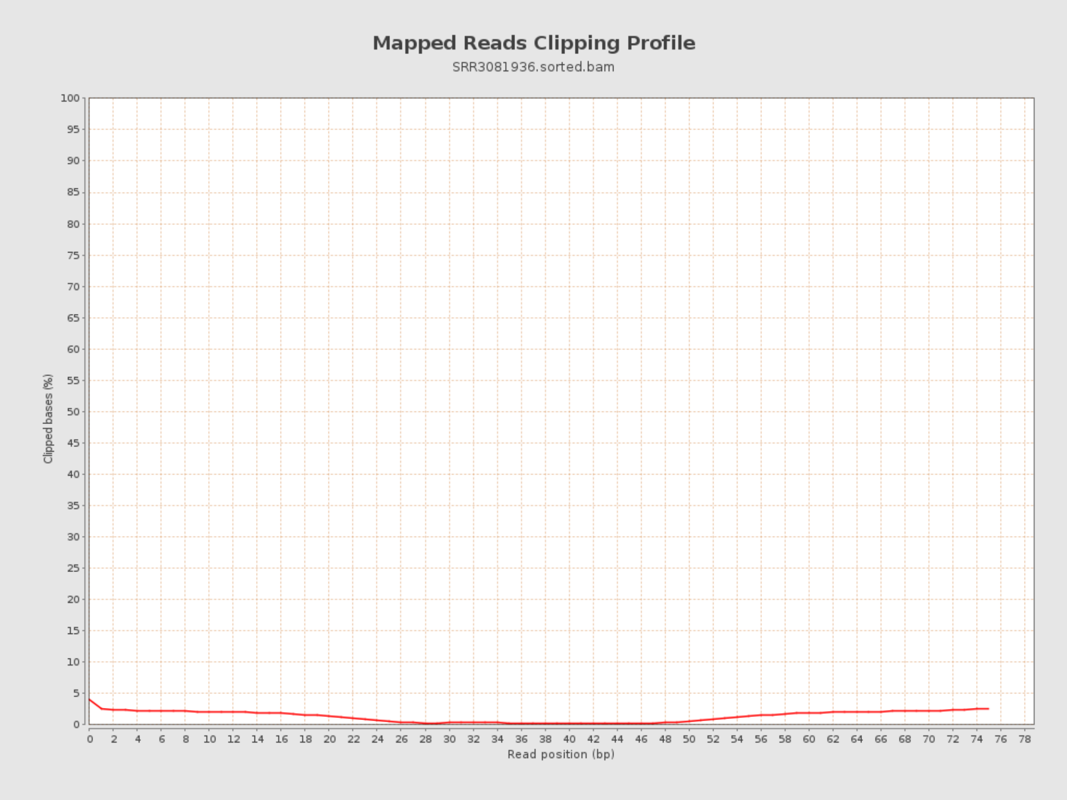
8. Results : Mapped Reads Nucleotide Content



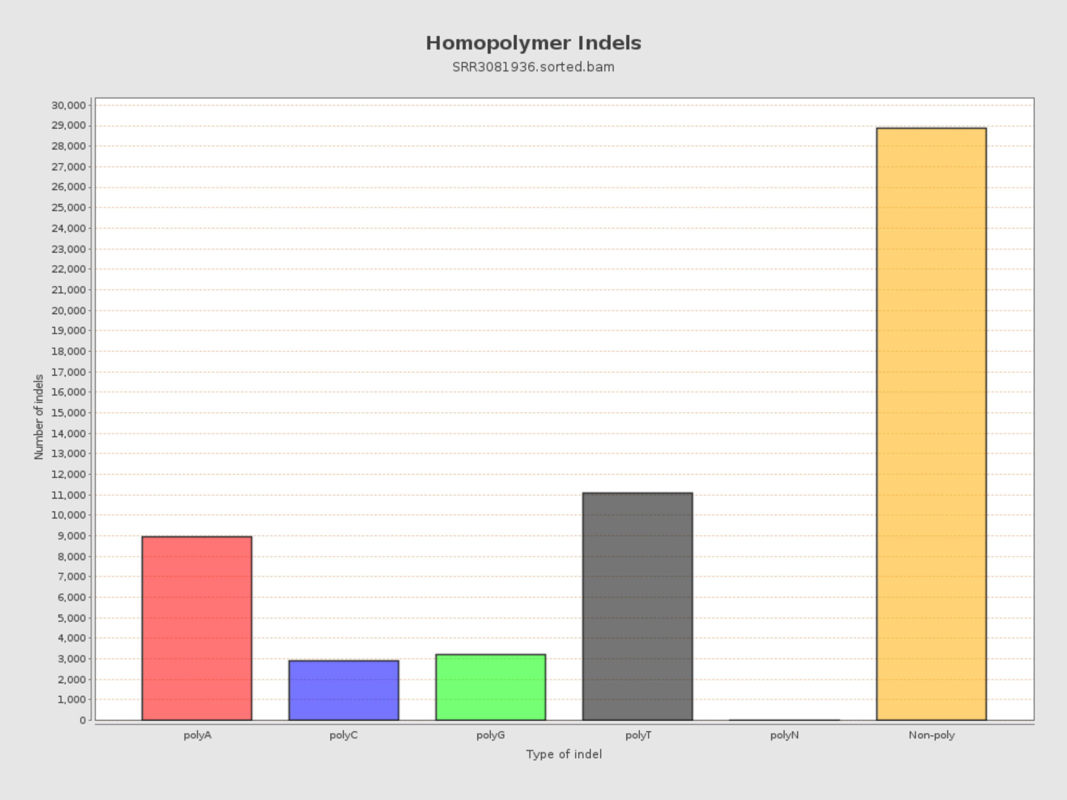
9. Results : Mapped Reads GC-content Distribution



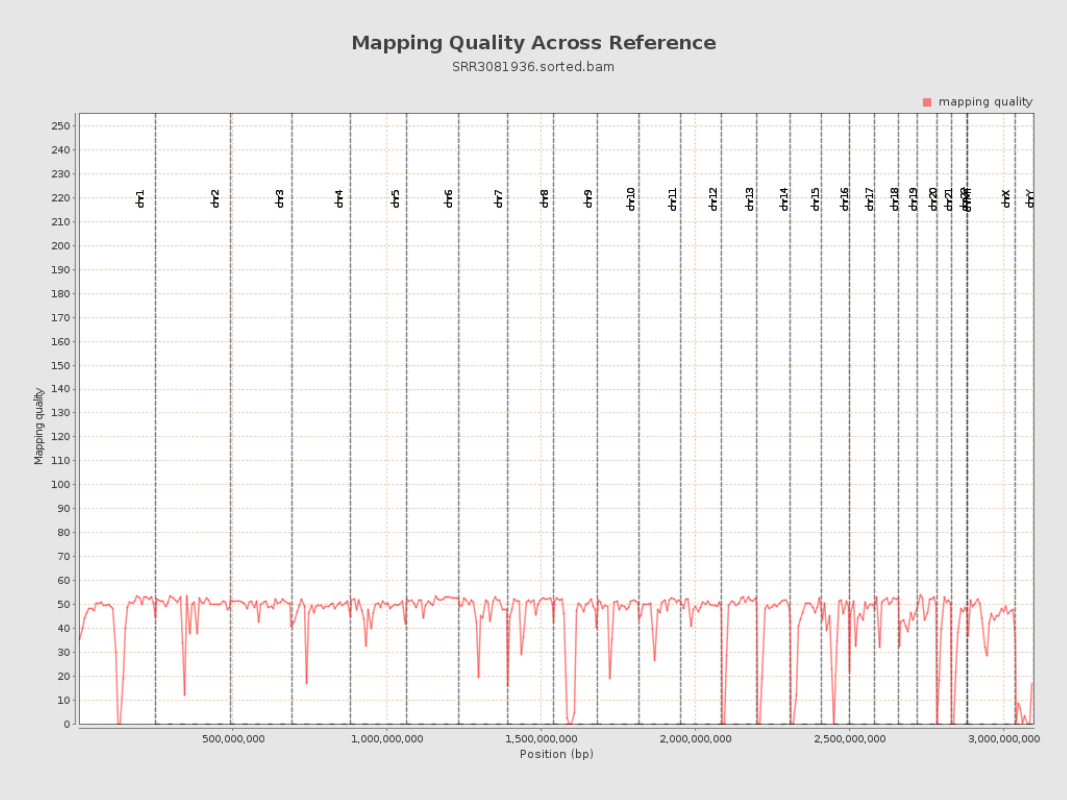
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram