Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:51:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081256.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_SRR3081256 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081256.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:51:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081256.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,227,156
Mapped reads	2,632,838 / 81.58%
Unmapped reads	594,318 / 18.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,923 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	139,100 / 4.31%
Duplication rate	4.27%
Clipped reads	1,113,808 / 34.51%

2.2. ACGT Content

Number/percentage of A's	48,789,716 / 27.64%
Number/percentage of C's	31,787,000 / 18.01%
Number/percentage of T's	57,090,449 / 32.34%
Number/percentage of G's	38,810,634 / 21.99%
Number/percentage of N's	44,756 / 0.03%
GC Percentage	39.99%

2.3. Coverage

Mean	0.057

Standard Deviation	0.4643

2.4. Mapping Quality

Mean Mapping Quality	47.39

2.5. Mismatches and indels

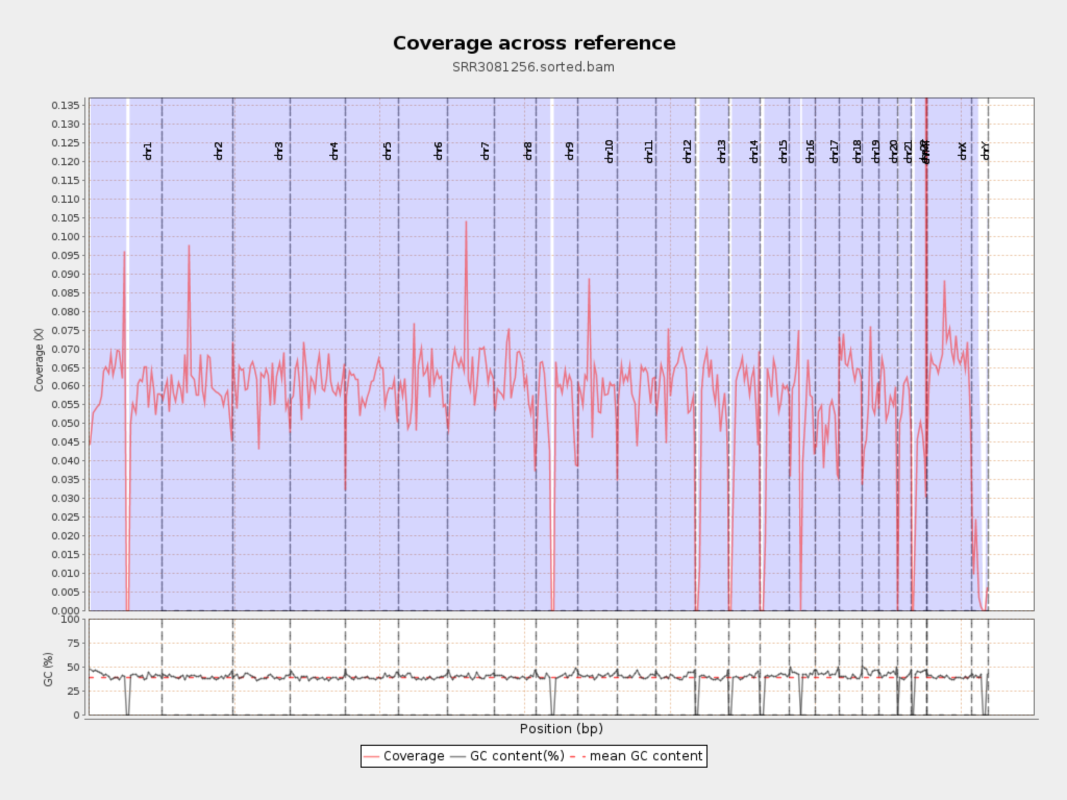
General error rate	0.88%
Mismatches	1,526,876
Insertions	14,984
Mapped reads with at least one insertion	0.56%
Deletions	41,060
Mapped reads with at least one deletion	1.54%
Homopolymer indels	49.37%

2.6. Chromosome stats

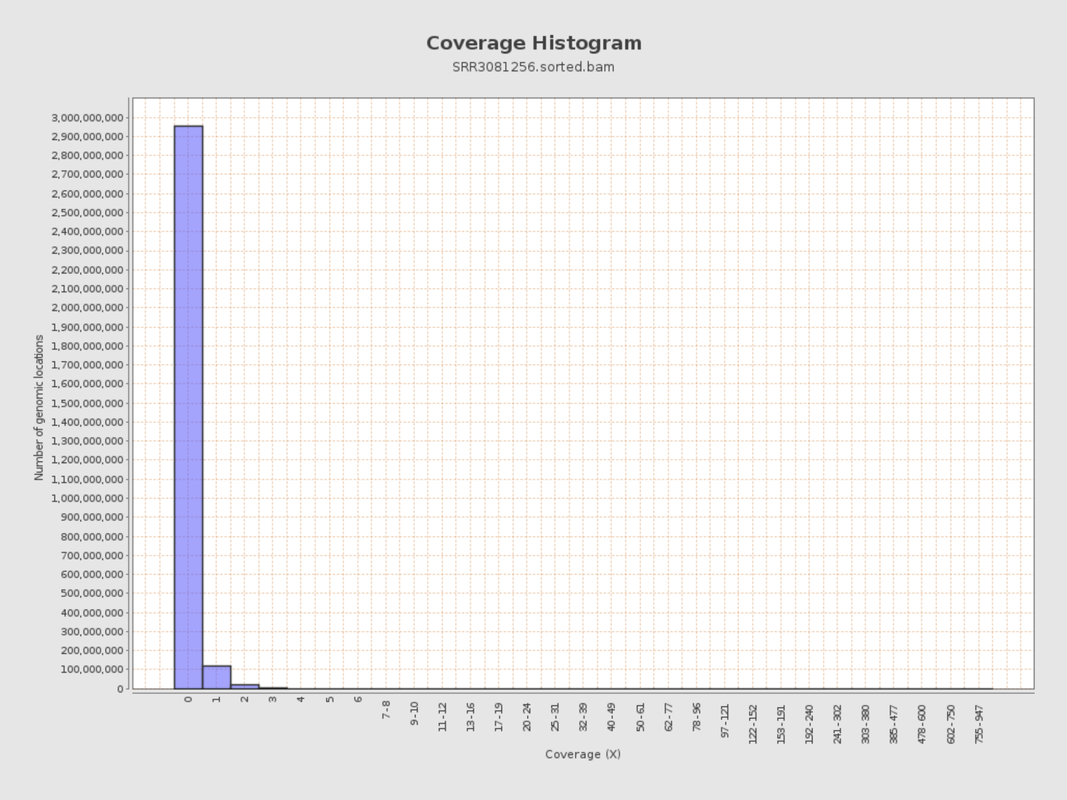
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14204724	0.057	0.8481
chr2	243199373	14693489	0.0604	0.4665
chr3	198022430	12139895	0.0613	0.2923
chr4	191154276	11742034	0.0614	0.3171
chr5	180915260	10819776	0.0598	0.2902
chr6	171115067	10334889	0.0604	0.3636
chr7	159138663	10502513	0.066	0.6621

chr8	146364022	8827184	0.0603	0.6484
chr9	141213431	7302913	0.0517	0.4243
chr10	135534747	8140988	0.0601	0.4483
chr11	135006516	8056753	0.0597	0.4174
chr12	133851895	8194627	0.0612	0.2977
chr13	115169878	5662778	0.0492	0.2613
chr14	107349540	5456603	0.0508	0.286
chr15	102531392	4980632	0.0486	0.2572
chr16	90354753	4665657	0.0516	0.2974
chr17	81195210	3894216	0.048	0.3013
chr18	78077248	5183332	0.0664	0.7899
chr19	59128983	3208336	0.0543	0.6165
chr20	63025520	3613102	0.0573	0.2892
chr21	48129895	2436849	0.0506	0.2984
chr22	51304566	1646363	0.0321	0.2079
chrMT	16571	25528	1.5405	1.5794
chrX	155270560	10417884	0.0671	0.3387
chrY	59373566	438349	0.0074	0.1747

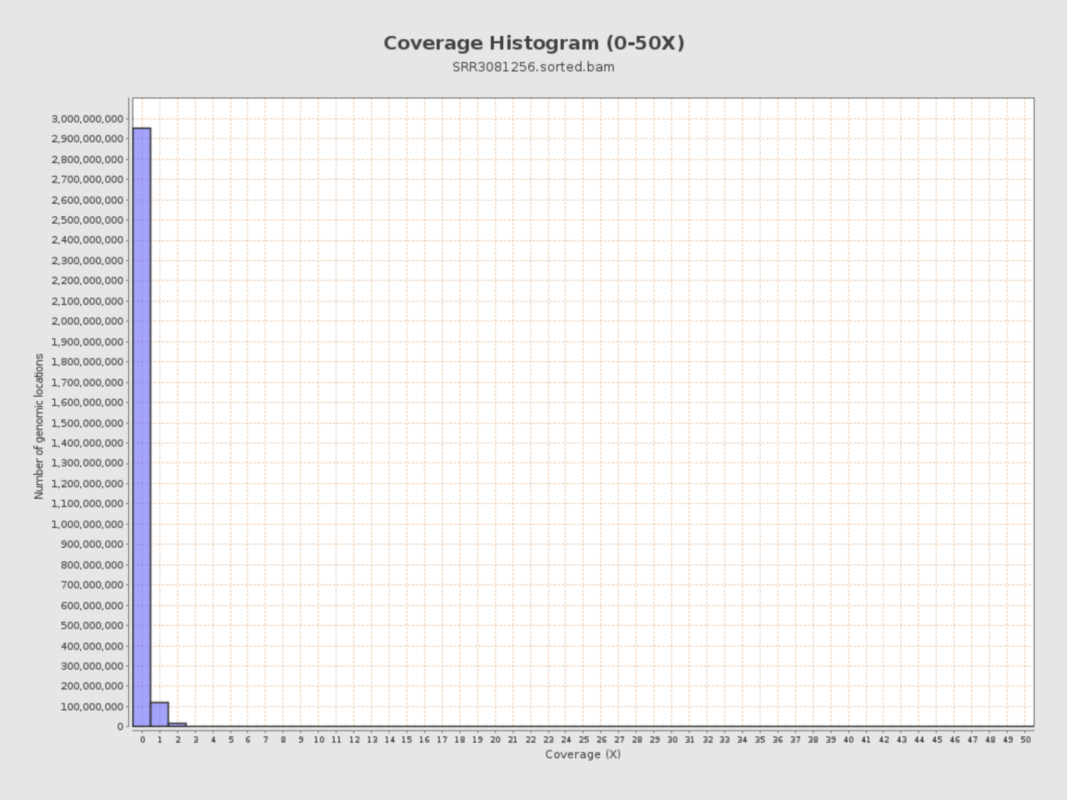
3. Results : Coverage across reference



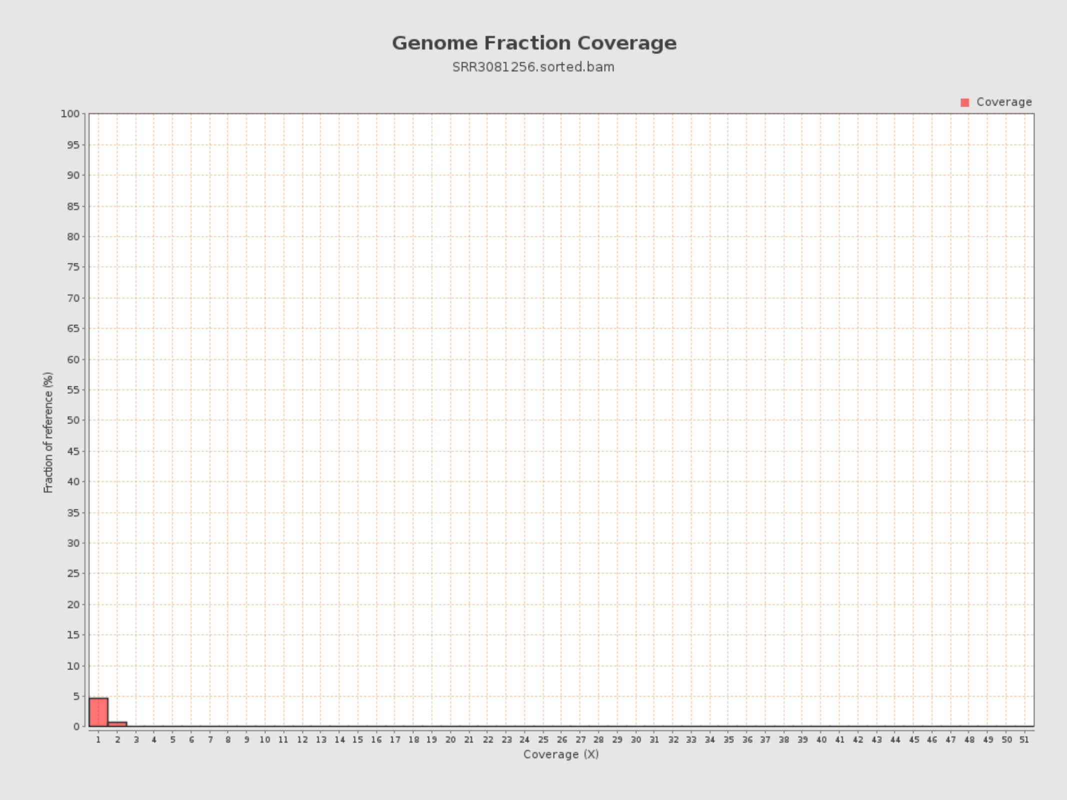
4. Results : Coverage Histogram



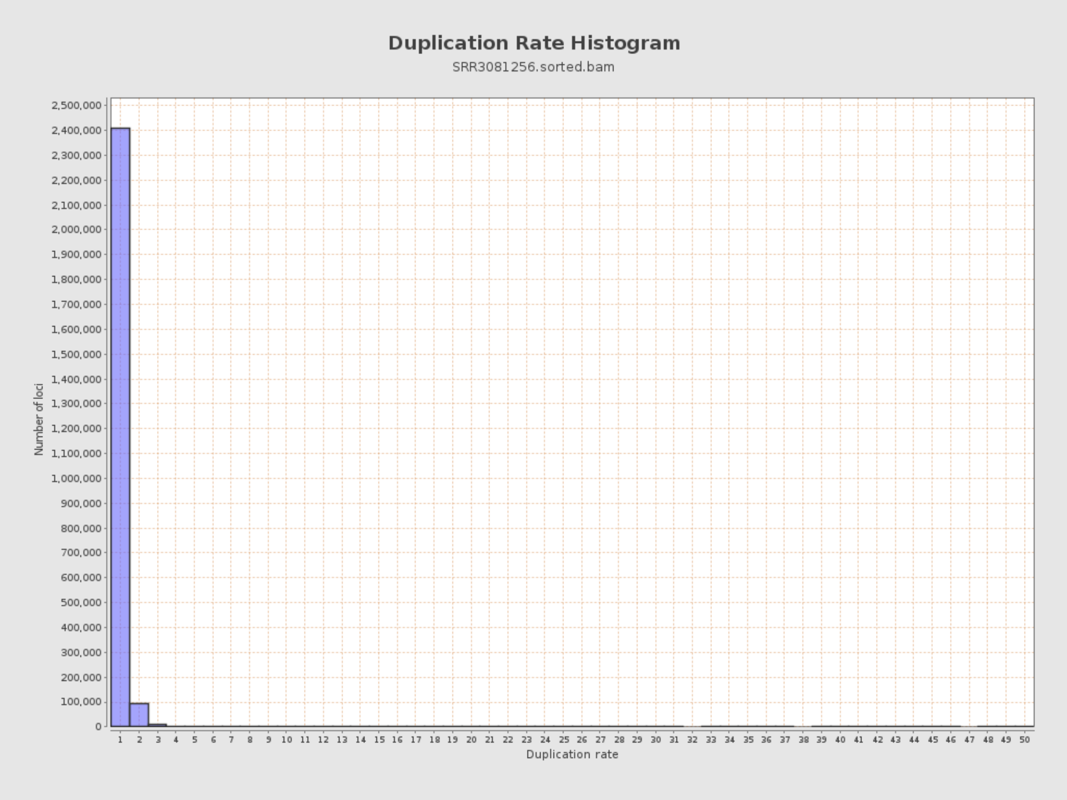
5. Results : Coverage Histogram (0-50X)



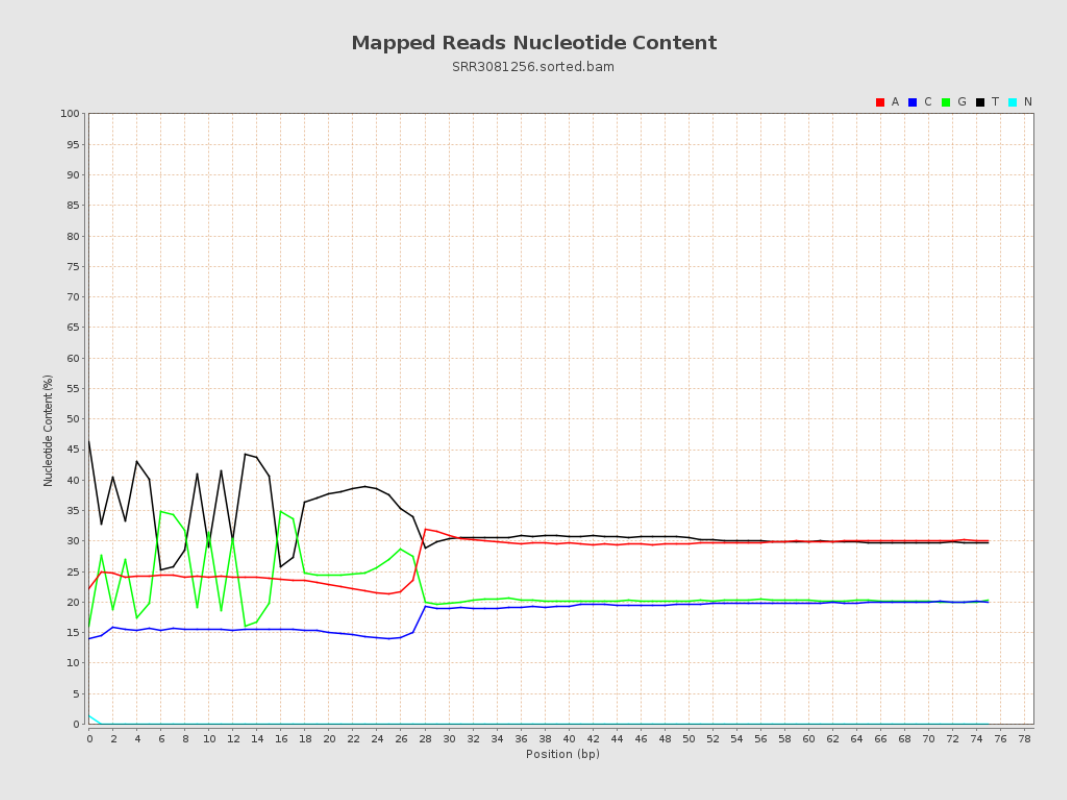
6. Results : Genome Fraction Coverage



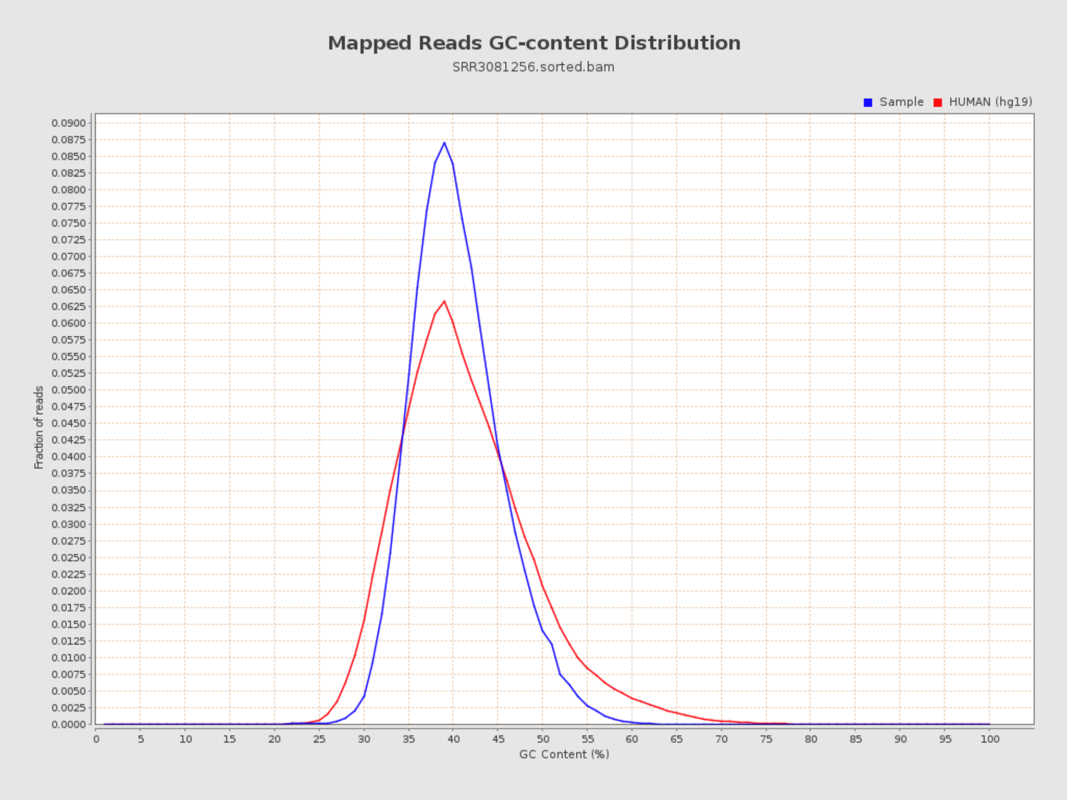
7. Results : Duplication Rate Histogram



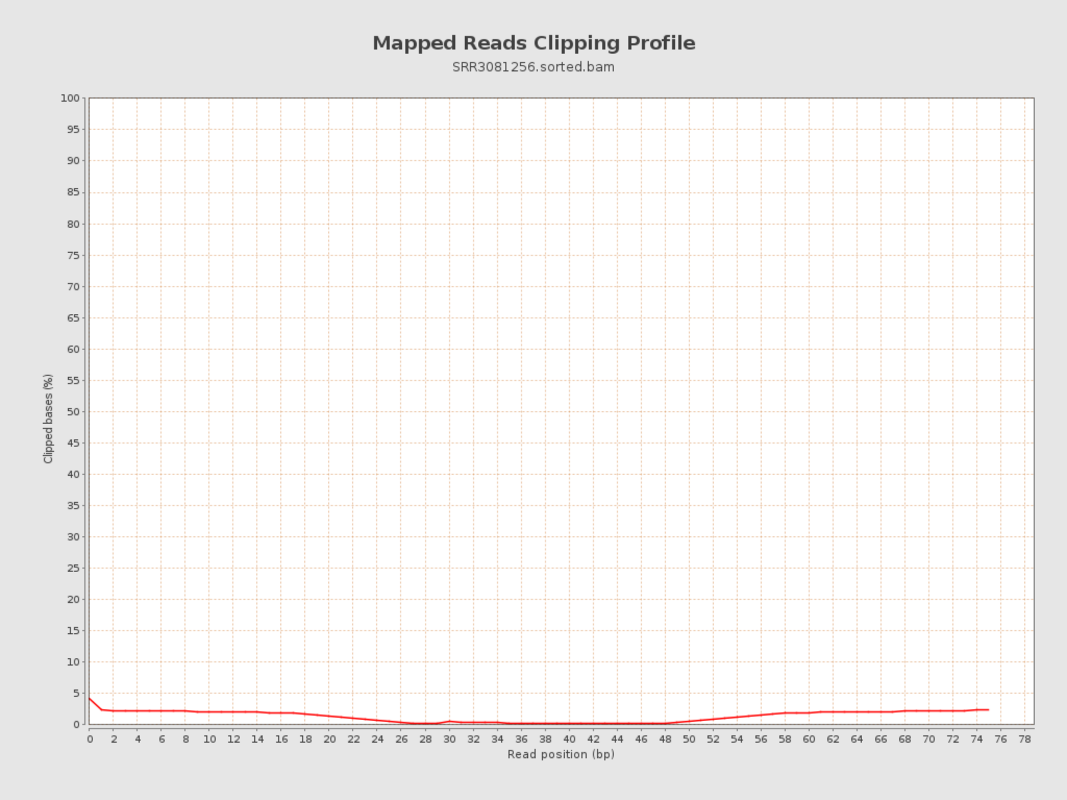
8. Results : Mapped Reads Nucleotide Content



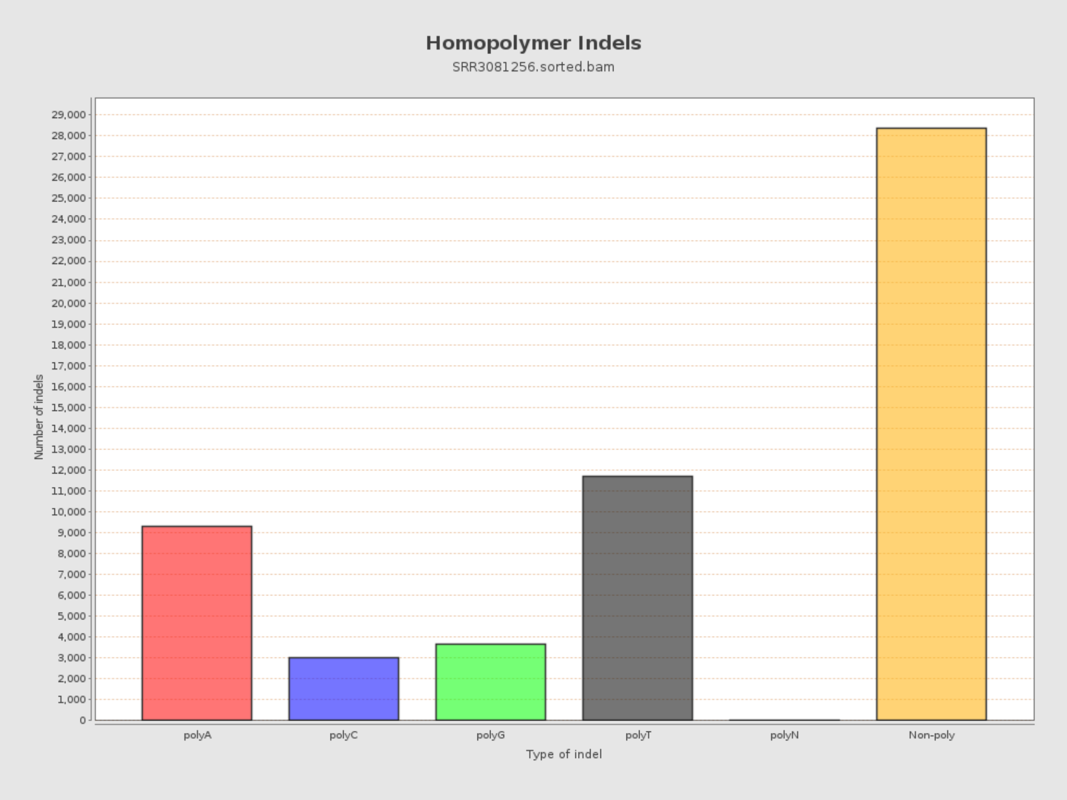
9. Results : Mapped Reads GC-content Distribution



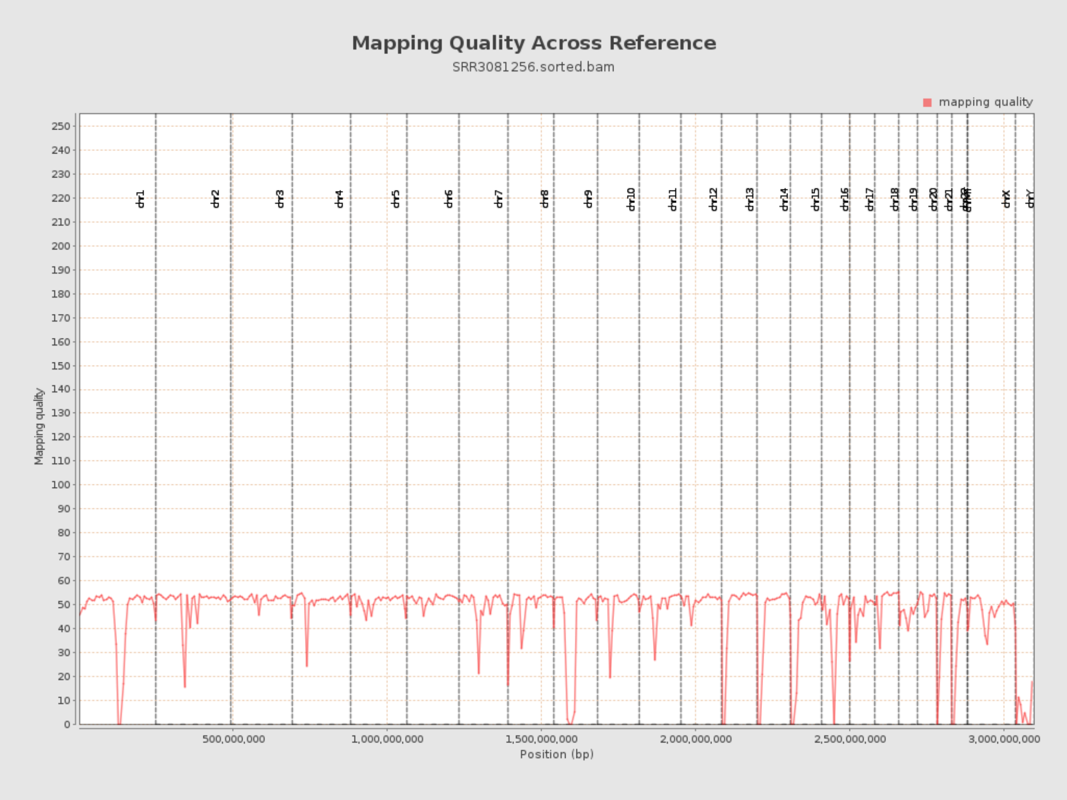
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram