Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:04:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081234.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_SRR3081234 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081234.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:04:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081234.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,445,032
Mapped reads	2,108,895 / 86.25%
Unmapped reads	336,137 / 13.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,350 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	121,419 / 4.97%
Duplication rate	4.75%
Clipped reads	1,120,306 / 45.82%

2.2. ACGT Content

Number/percentage of A's	39,010,079 / 28.45%
Number/percentage of C's	26,255,101 / 19.15%
Number/percentage of T's	42,354,045 / 30.89%
Number/percentage of G's	29,486,993 / 21.5%
Number/percentage of N's	17,184 / 0.01%
GC Percentage	40.65%

2.3. Coverage

Mean	0.0443

Standard Deviation	0.3633

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

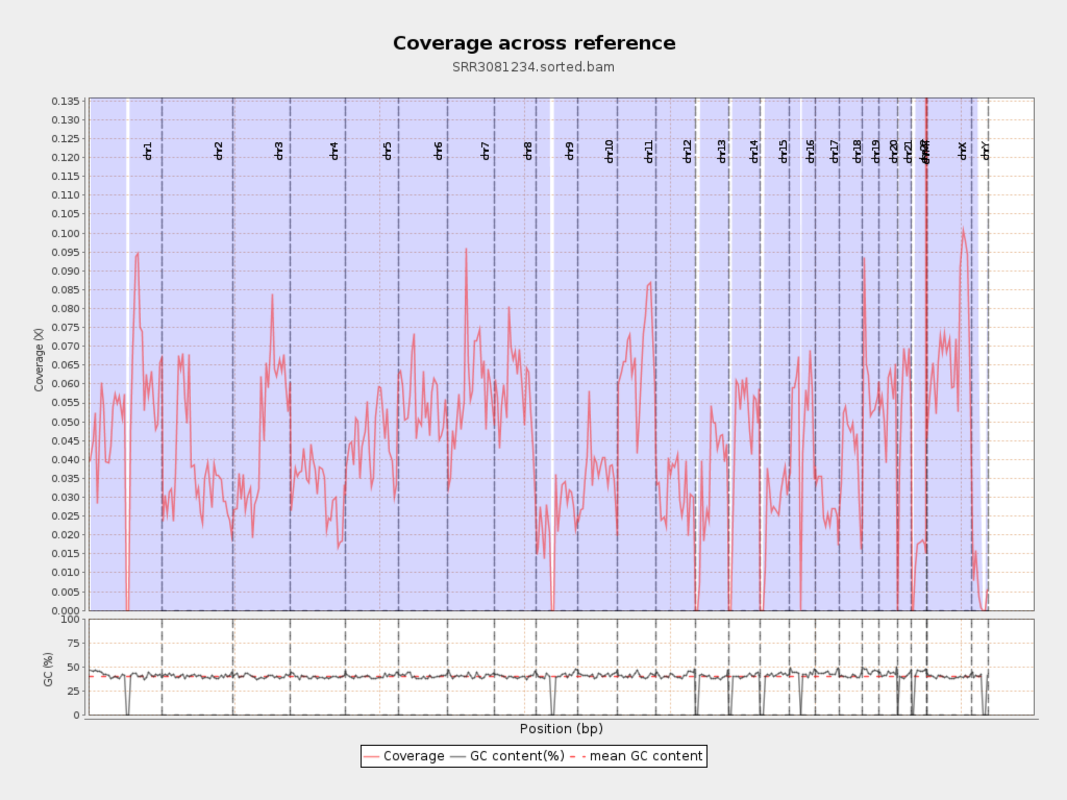
General error rate	0.93%
Mismatches	1,255,594
Insertions	10,222
Mapped reads with at least one insertion	0.48%
Deletions	30,720
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.9%

2.6. Chromosome stats

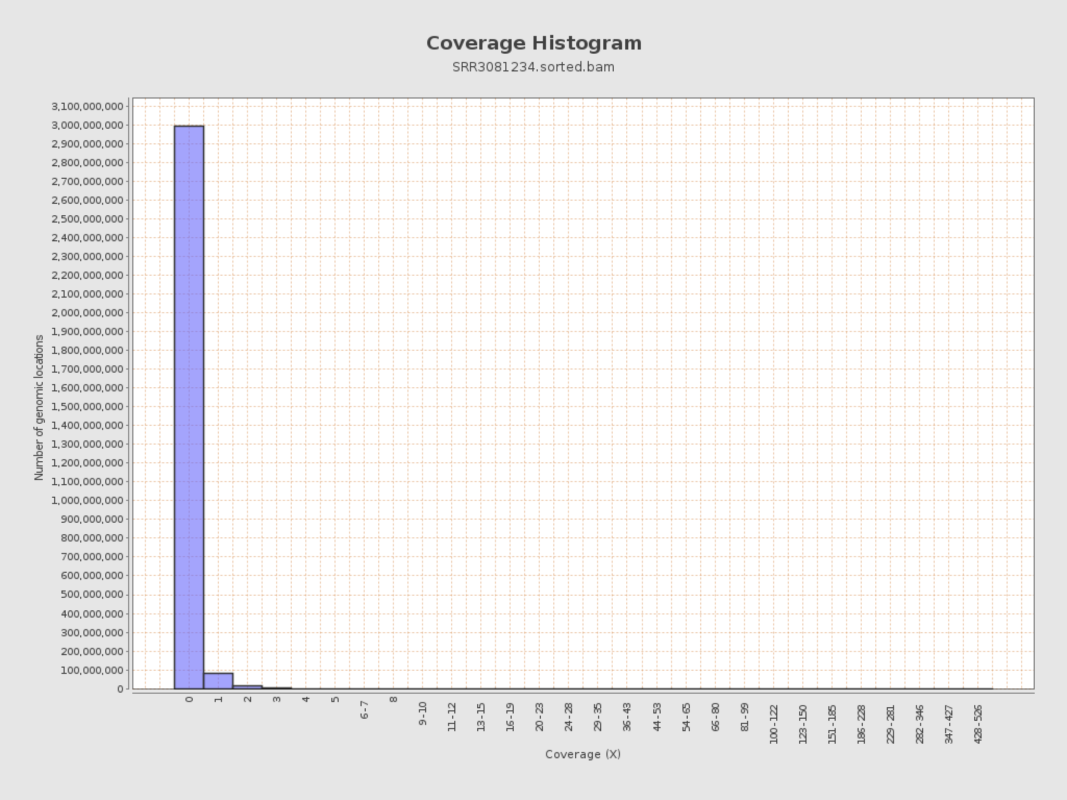
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13168699	0.0528	0.5318
chr2	243199373	8977337	0.0369	0.4044
chr3	198022430	9253619	0.0467	0.2735
chr4	191154276	6093020	0.0319	0.2244
chr5	180915260	8075598	0.0446	0.2637
chr6	171115067	9468690	0.0553	0.3462
chr7	159138663	9275307	0.0583	0.6201

chr8	146364022	8529749	0.0583	0.457
chr9	141213431	3299053	0.0234	0.2582
chr10	135534747	4925596	0.0363	0.3248
chr11	135006516	8909704	0.066	0.4514
chr12	133851895	4177361	0.0312	0.2224
chr13	115169878	3838043	0.0333	0.2304
chr14	107349540	4933917	0.046	0.2732
chr15	102531392	2597319	0.0253	0.2047
chr16	90354753	4549370	0.0504	0.2894
chr17	81195210	2212841	0.0273	0.2328
chr18	78077248	3311800	0.0424	0.4351
chr19	59128983	3561449	0.0602	0.46
chr20	63025520	3464747	0.055	0.2964
chr21	48129895	2536735	0.0527	0.296
chr22	51304566	678951	0.0132	0.1386
chrMT	16571	138610	8.3646	6.3235
chrX	155270560	10835987	0.0698	0.355
chrY	59373566	359721	0.0061	0.1126

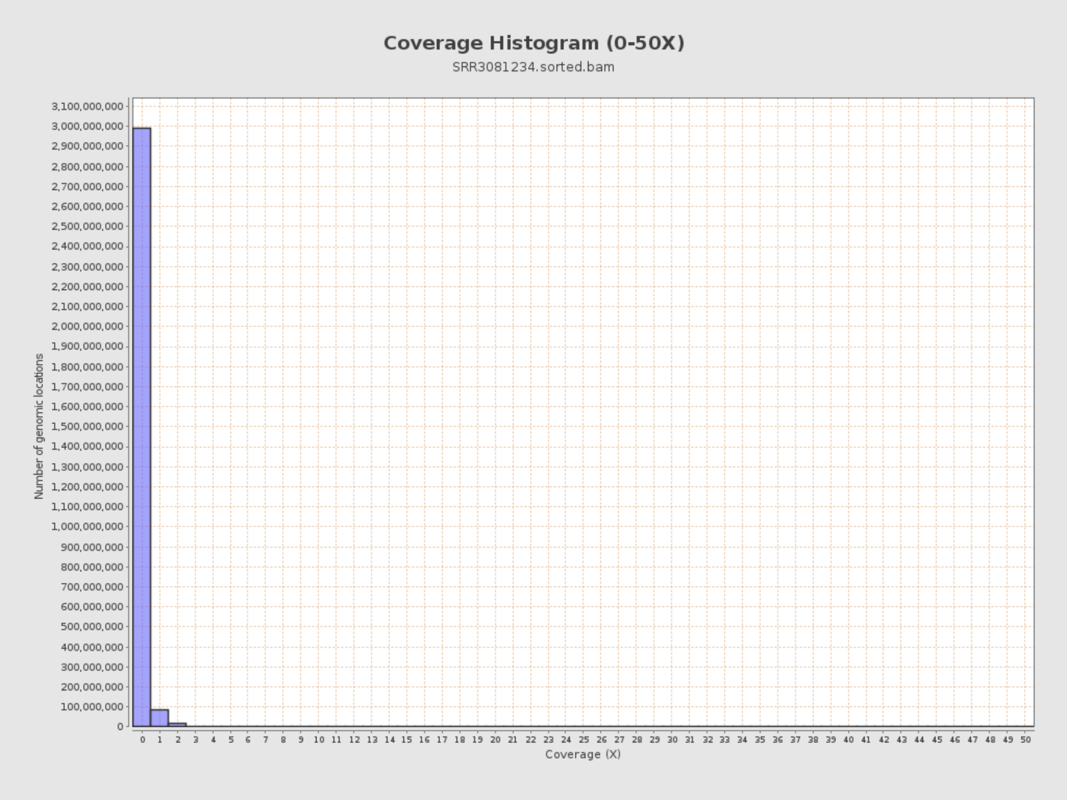
3. Results : Coverage across reference



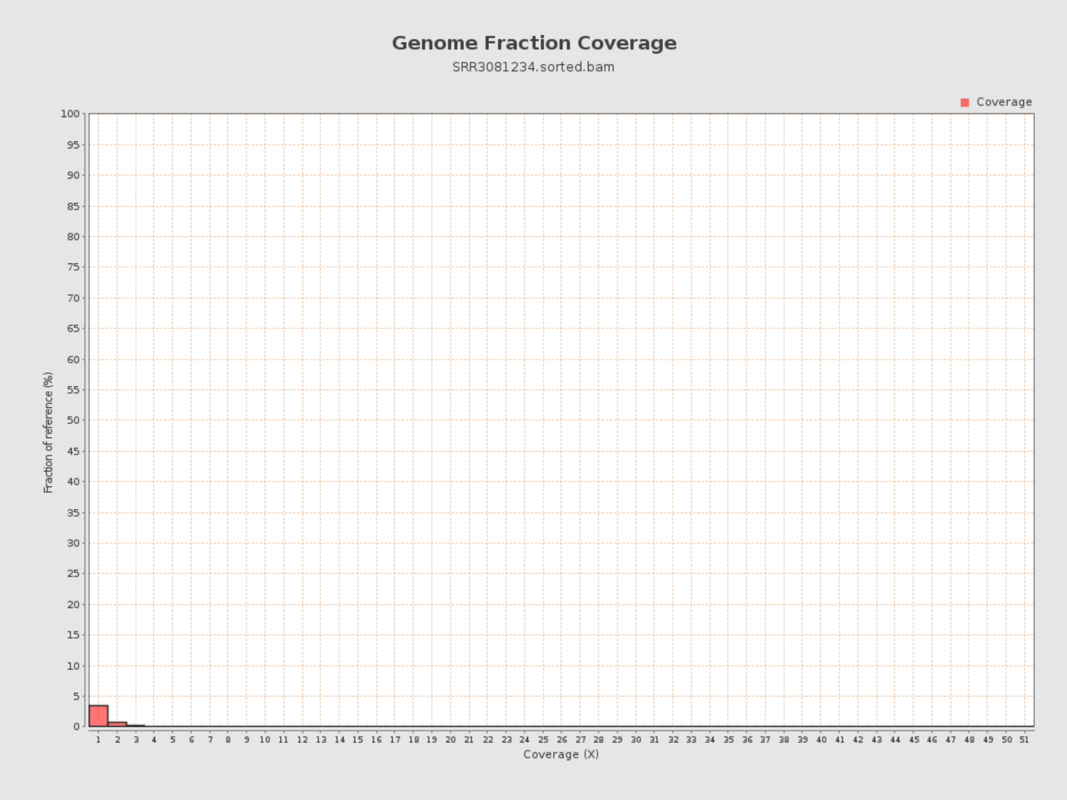
4. Results : Coverage Histogram



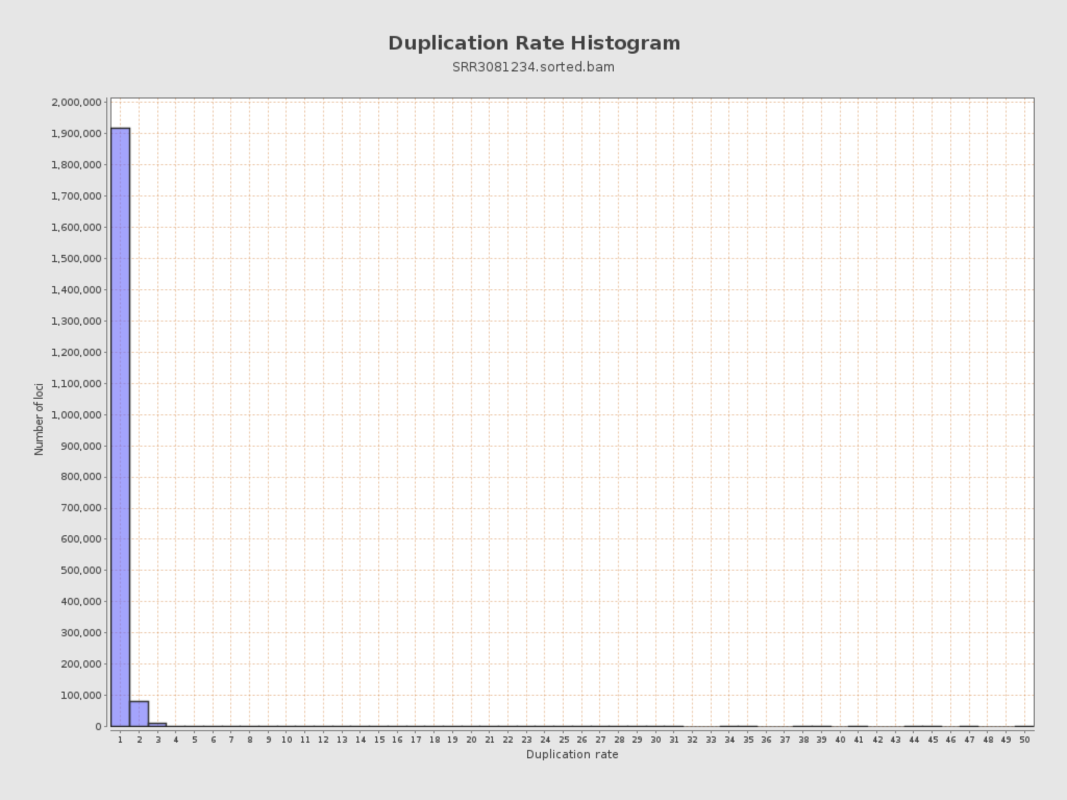
5. Results : Coverage Histogram (0-50X)



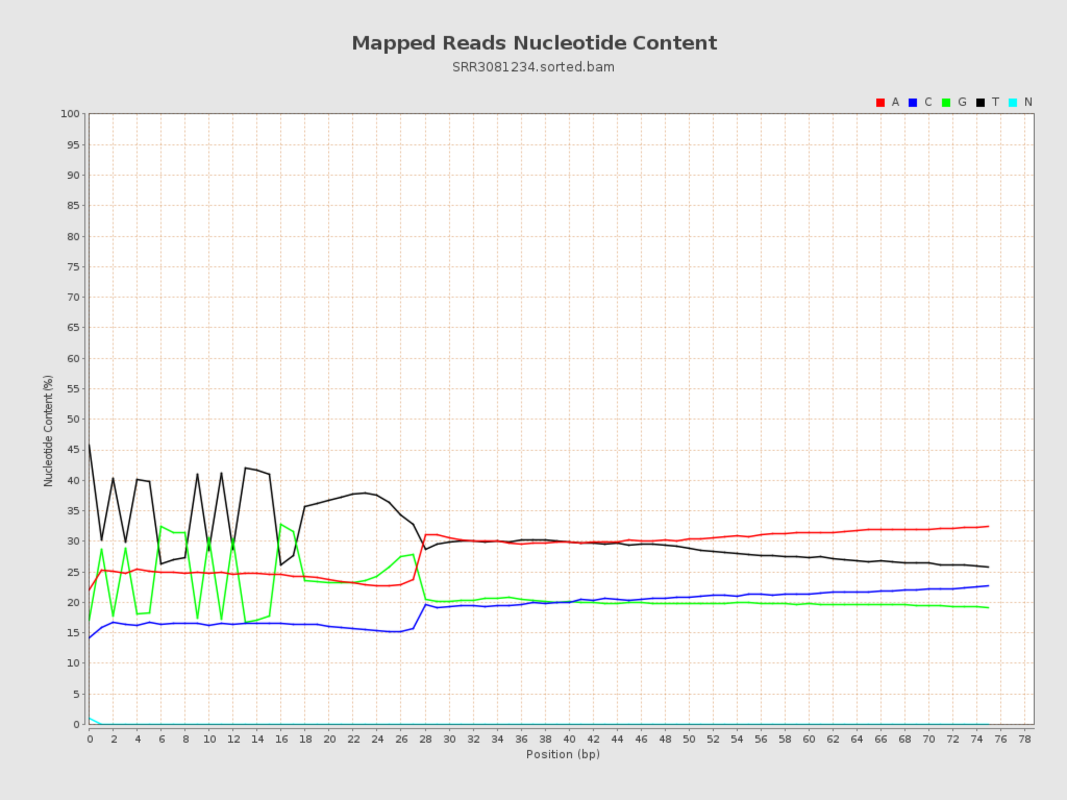
6. Results : Genome Fraction Coverage



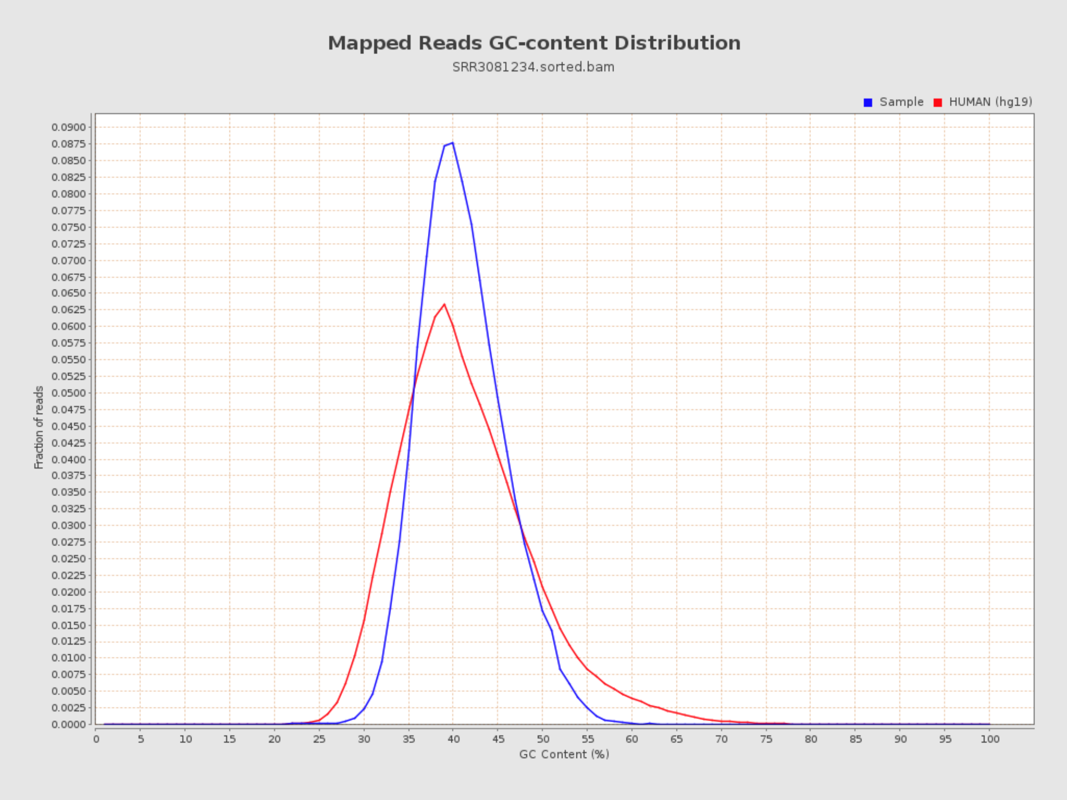
7. Results : Duplication Rate Histogram



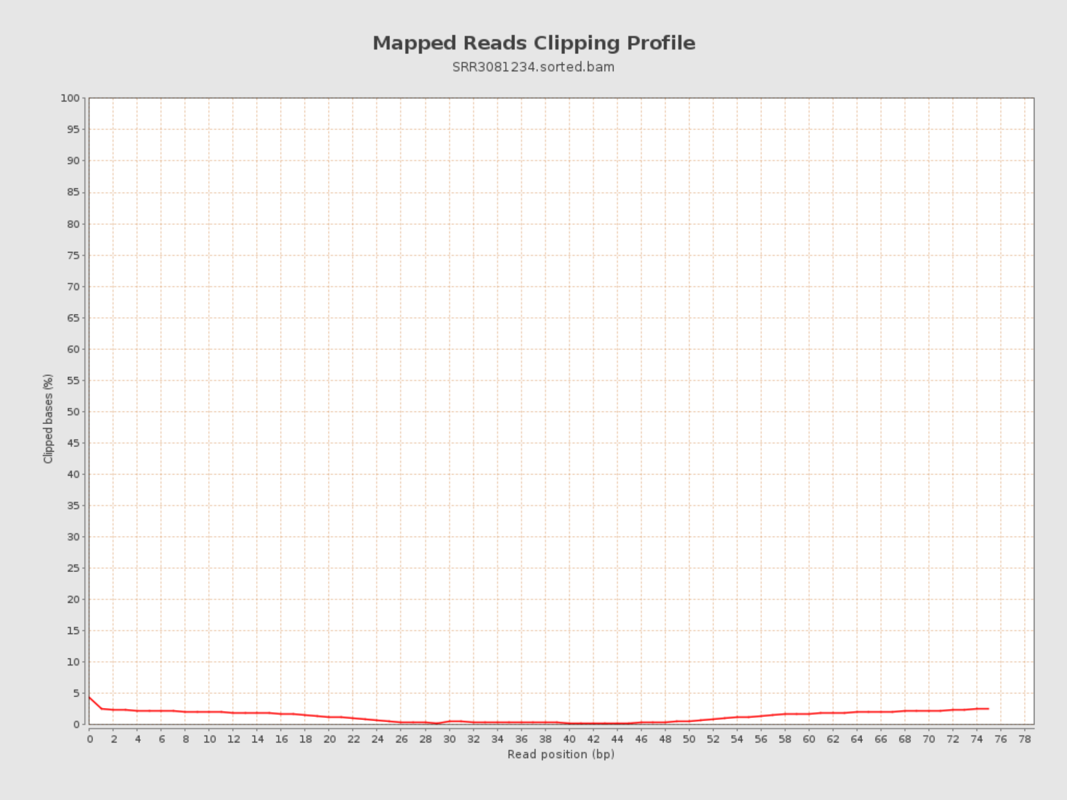
8. Results : Mapped Reads Nucleotide Content



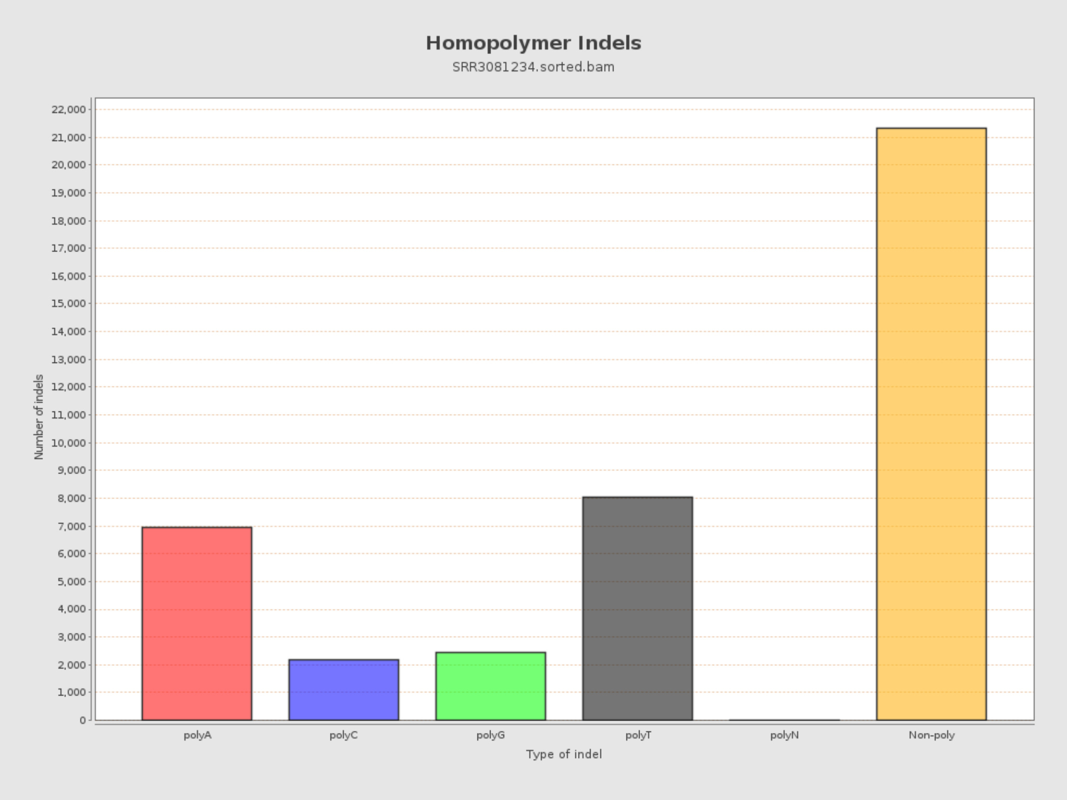
9. Results : Mapped Reads GC-content Distribution



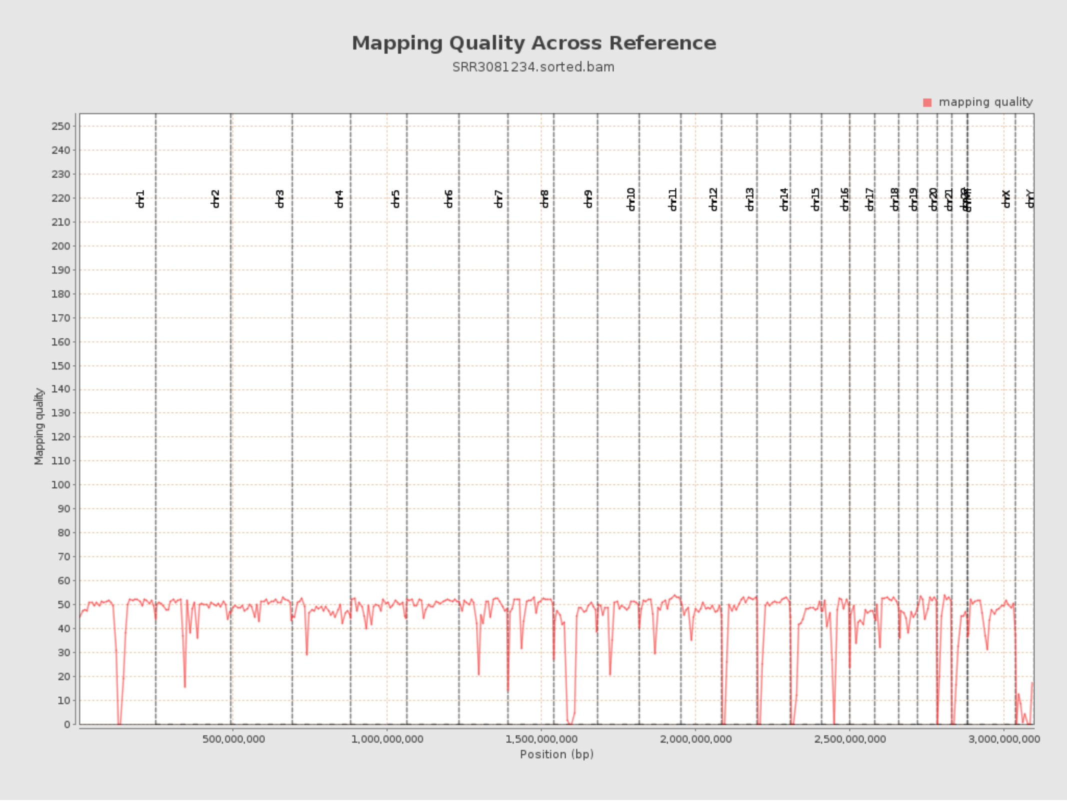
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram