Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:23:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081741.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_SRR3081741 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081741.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:23:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081741.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,182,253
Mapped reads	1,963,090 / 89.96%
Unmapped reads	219,163 / 10.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,052 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	62,335 / 2.86%
Duplication rate	2.3%
Clipped reads	731,602 / 33.53%

2.2. ACGT Content

Number/percentage of A's	38,819,969 / 28.89%
Number/percentage of C's	25,476,673 / 18.96%
Number/percentage of T's	41,453,727 / 30.85%
Number/percentage of G's	28,630,630 / 21.31%
Number/percentage of N's	1,573 / 0%
GC Percentage	40.26%

2.3. Coverage

Mean	0.0434

Standard Deviation	0.3698

2.4. Mapping Quality

Mean Mapping Quality	45.99

2.5. Mismatches and indels

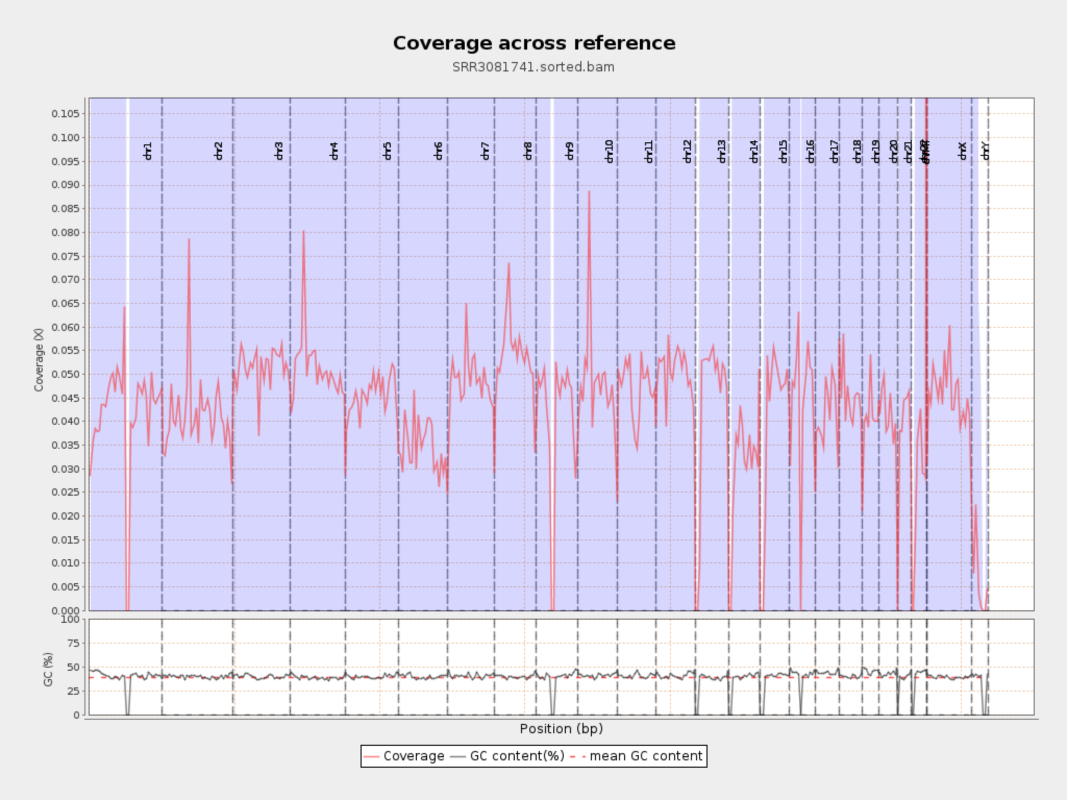
General error rate	0.84%
Mismatches	1,103,245
Insertions	11,025
Mapped reads with at least one insertion	0.55%
Deletions	29,272
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.04%

2.6. Chromosome stats

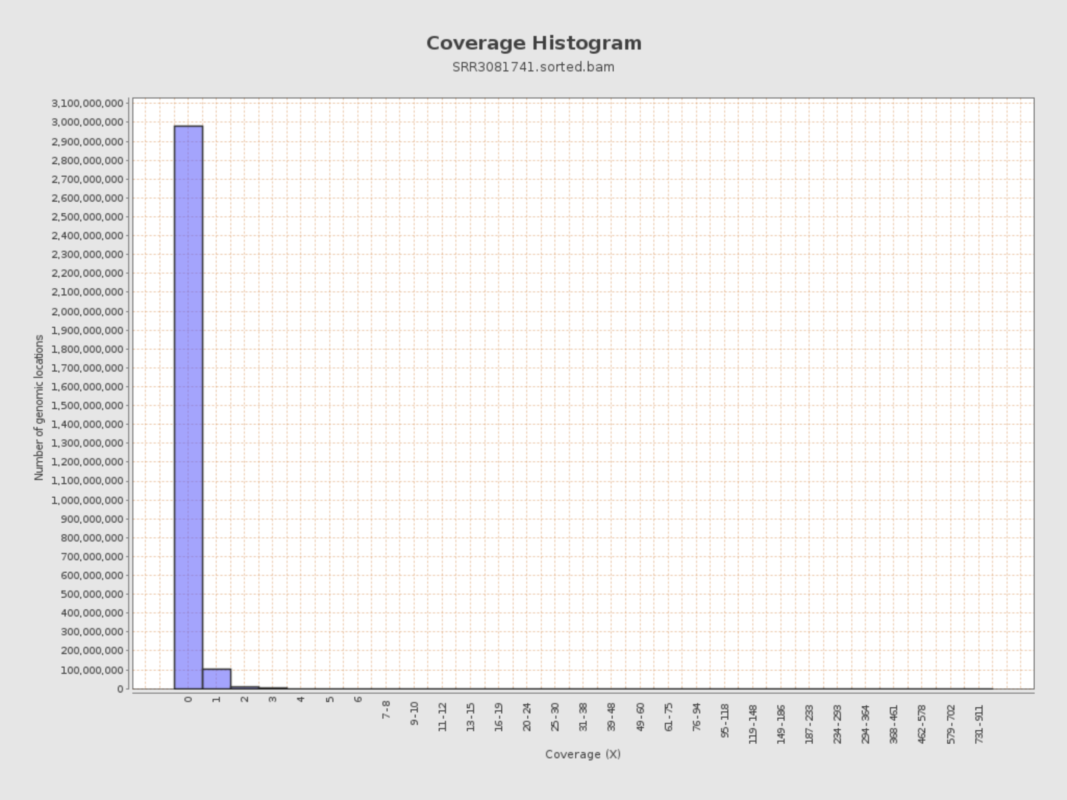
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10385905	0.0417	0.5803
chr2	243199373	10066263	0.0414	0.4407
chr3	198022430	10220929	0.0516	0.2532
chr4	191154276	9836986	0.0515	0.2929
chr5	180915260	8243514	0.0456	0.2357
chr6	171115067	5925314	0.0346	0.2254
chr7	159138663	7804168	0.049	0.4288

chr8	146364022	7895331	0.0539	0.6446
chr9	141213431	5720480	0.0405	0.3454
chr10	135534747	6571508	0.0485	0.4404
chr11	135006516	6305650	0.0467	0.3141
chr12	133851895	6768620	0.0506	0.2513
chr13	115169878	4958357	0.0431	0.228
chr14	107349540	3179586	0.0296	0.2092
chr15	102531392	4143135	0.0404	0.2233
chr16	90354753	4007737	0.0444	0.2803
chr17	81195210	3352463	0.0413	0.2302
chr18	78077248	3565495	0.0457	0.6236
chr19	59128983	2435731	0.0412	0.4296
chr20	63025520	2594369	0.0412	0.2331
chr21	48129895	1783601	0.0371	0.2466
chr22	51304566	1232187	0.024	0.1706
chrMT	16571	13844	0.8354	1.0715
chrX	155270560	7051579	0.0454	0.2608
chrY	59373566	372339	0.0063	0.1959

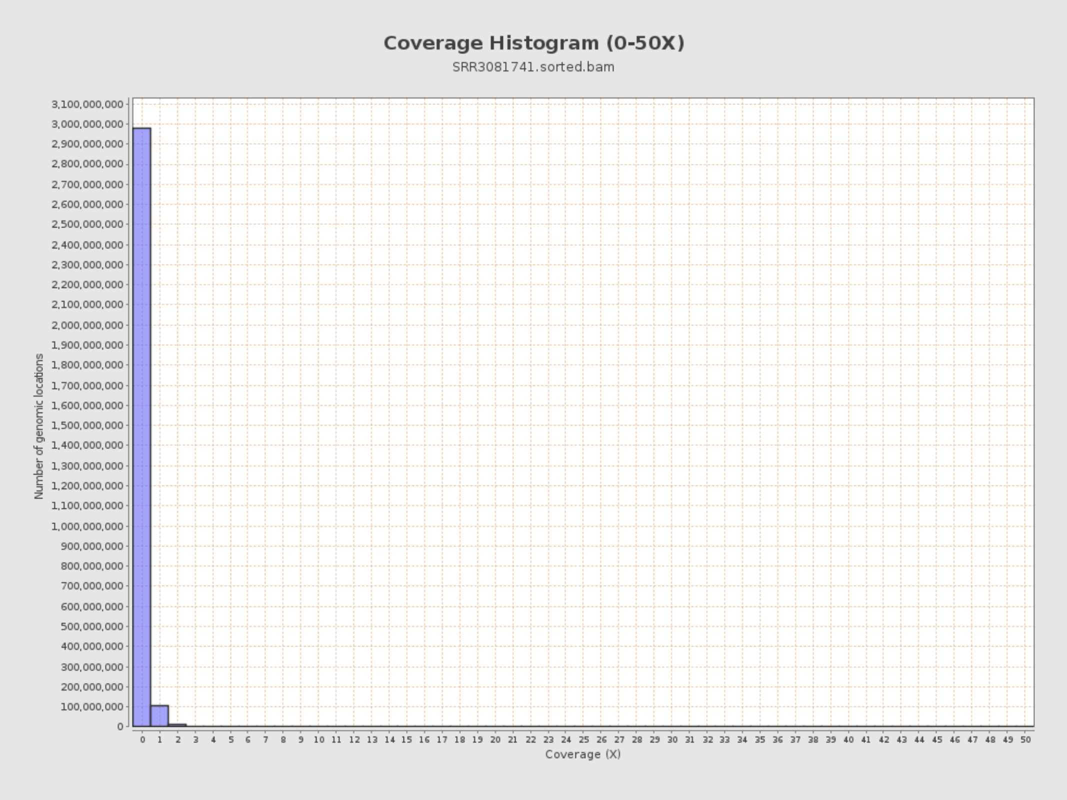
3. Results : Coverage across reference



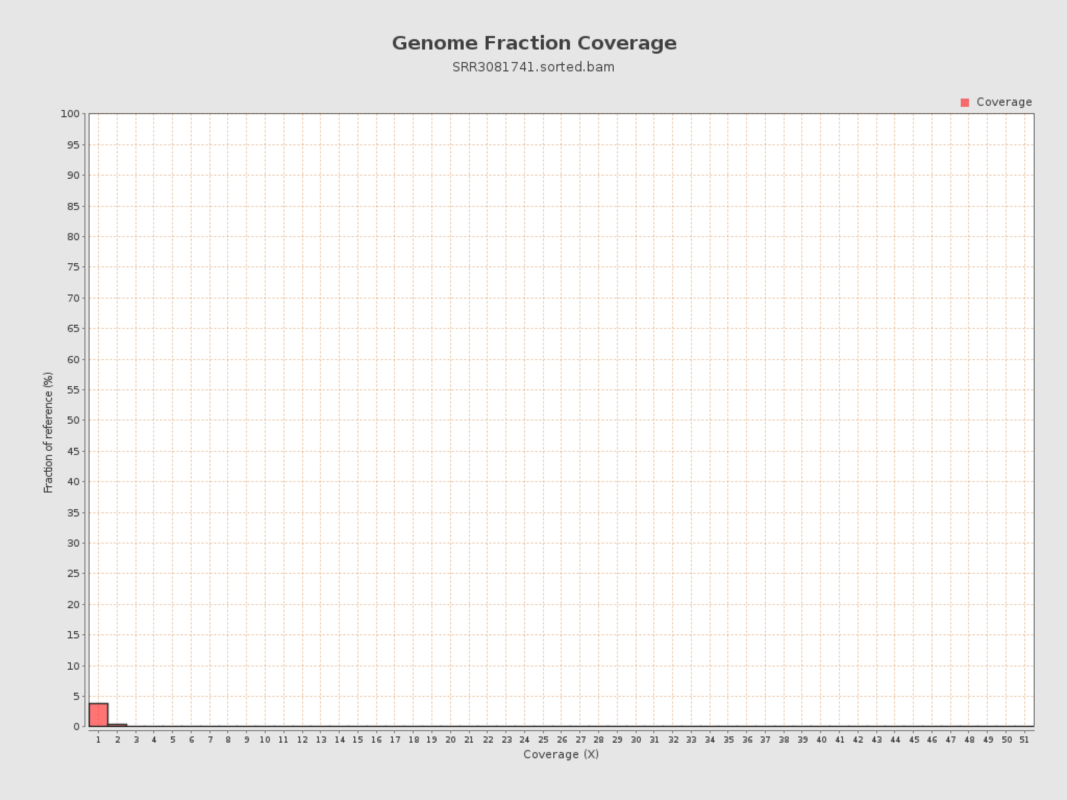
4. Results : Coverage Histogram



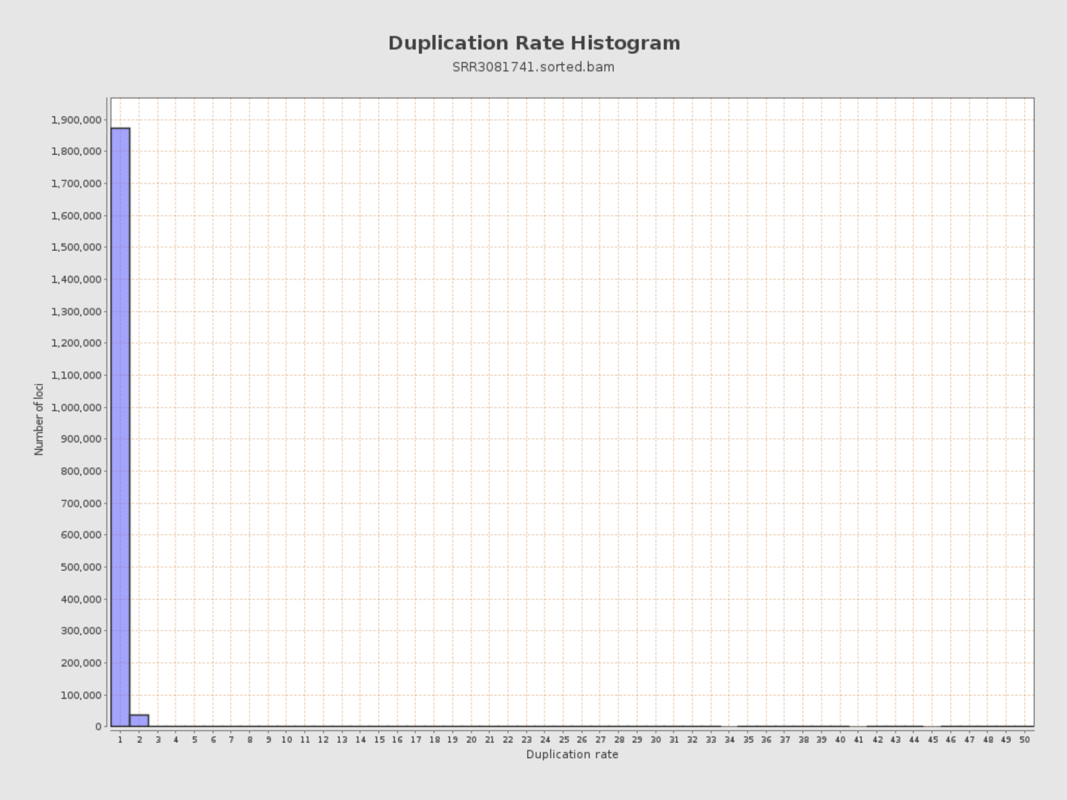
5. Results : Coverage Histogram (0-50X)



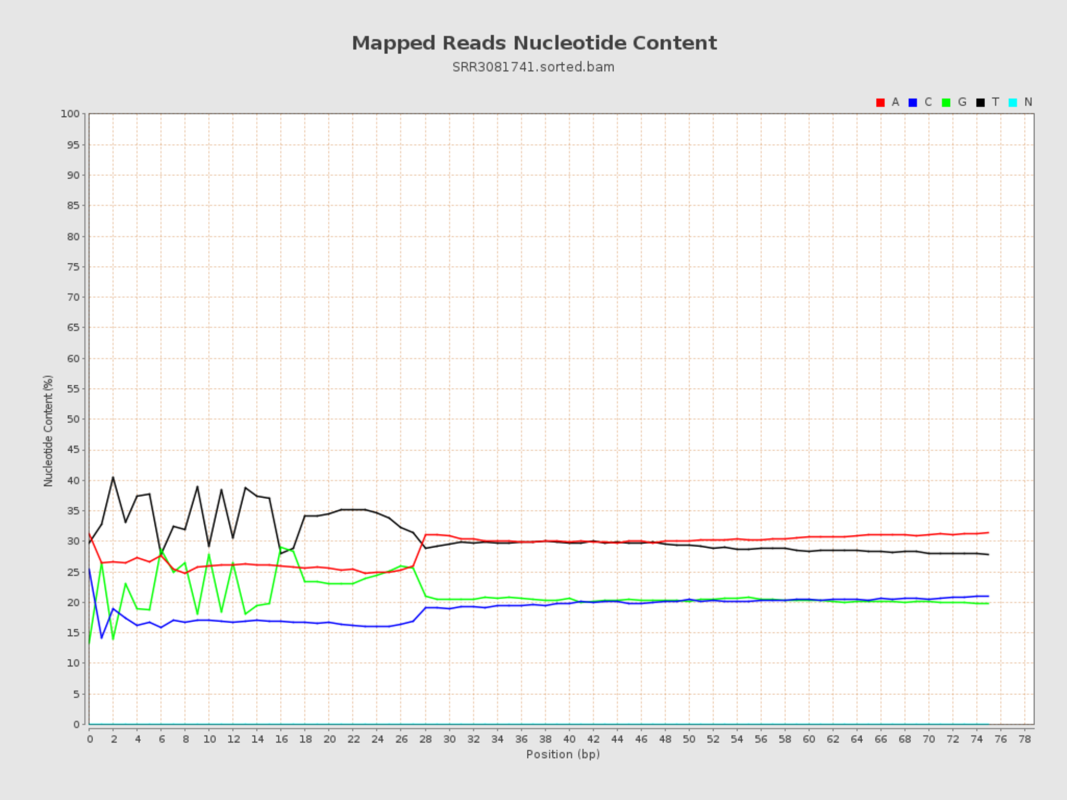
6. Results : Genome Fraction Coverage



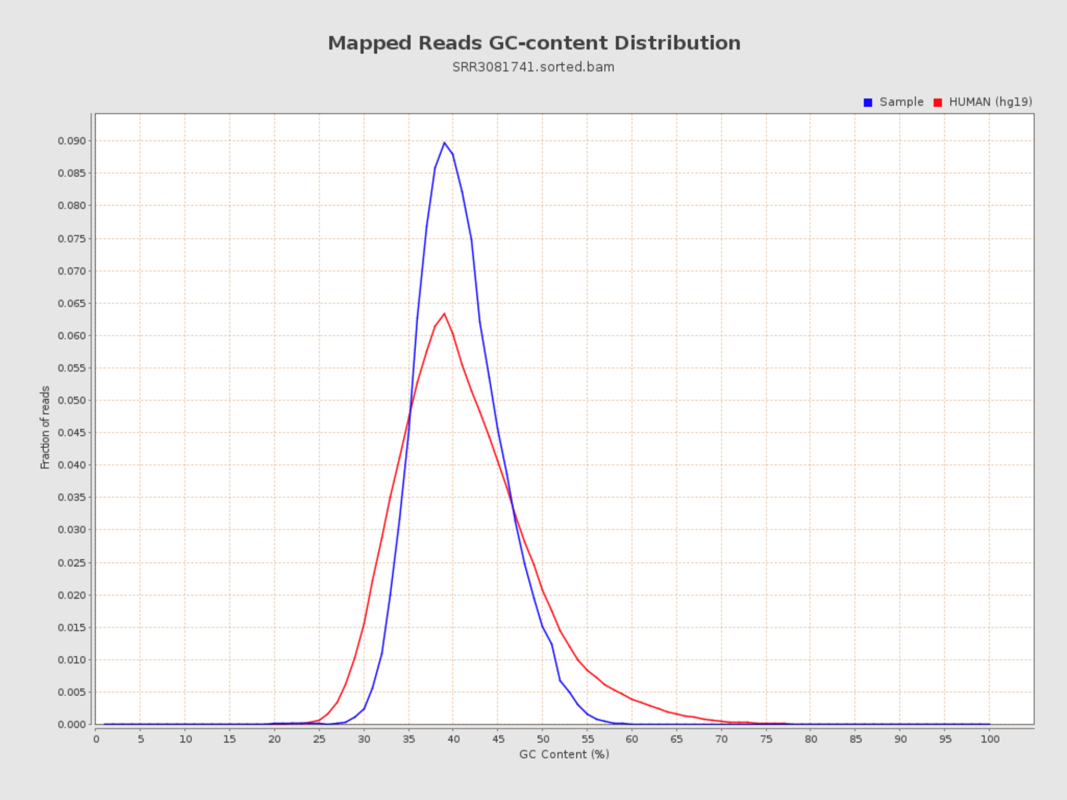
7. Results : Duplication Rate Histogram



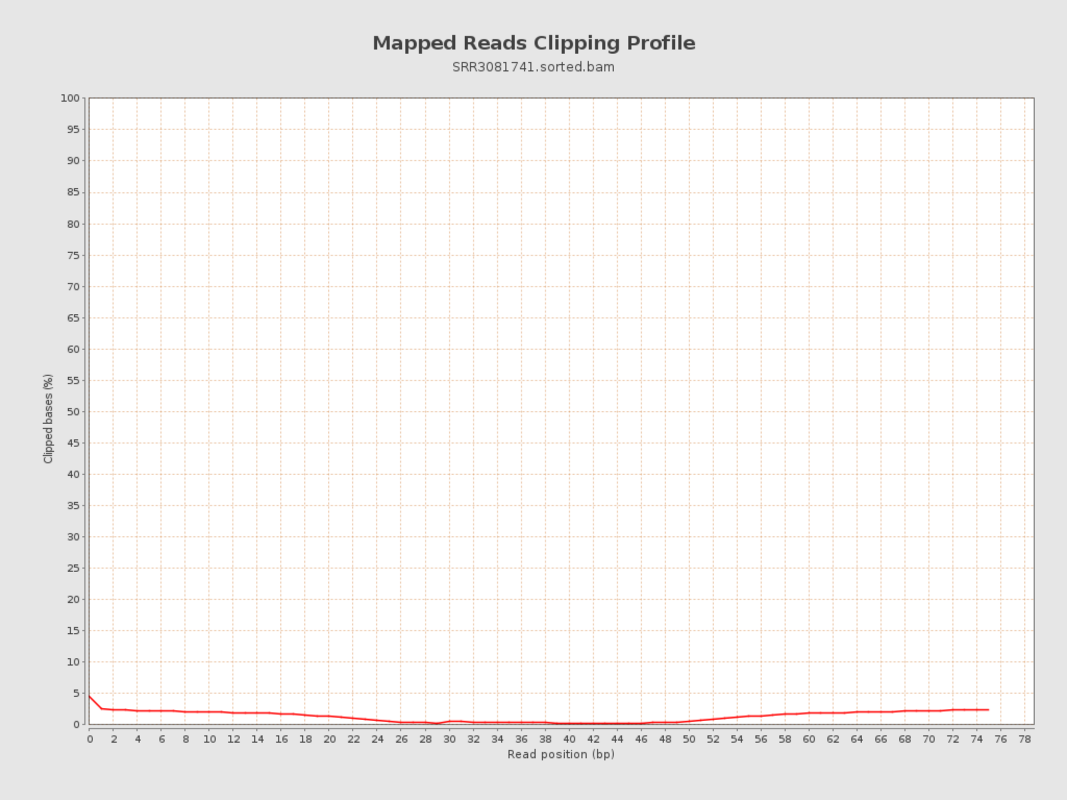
8. Results : Mapped Reads Nucleotide Content



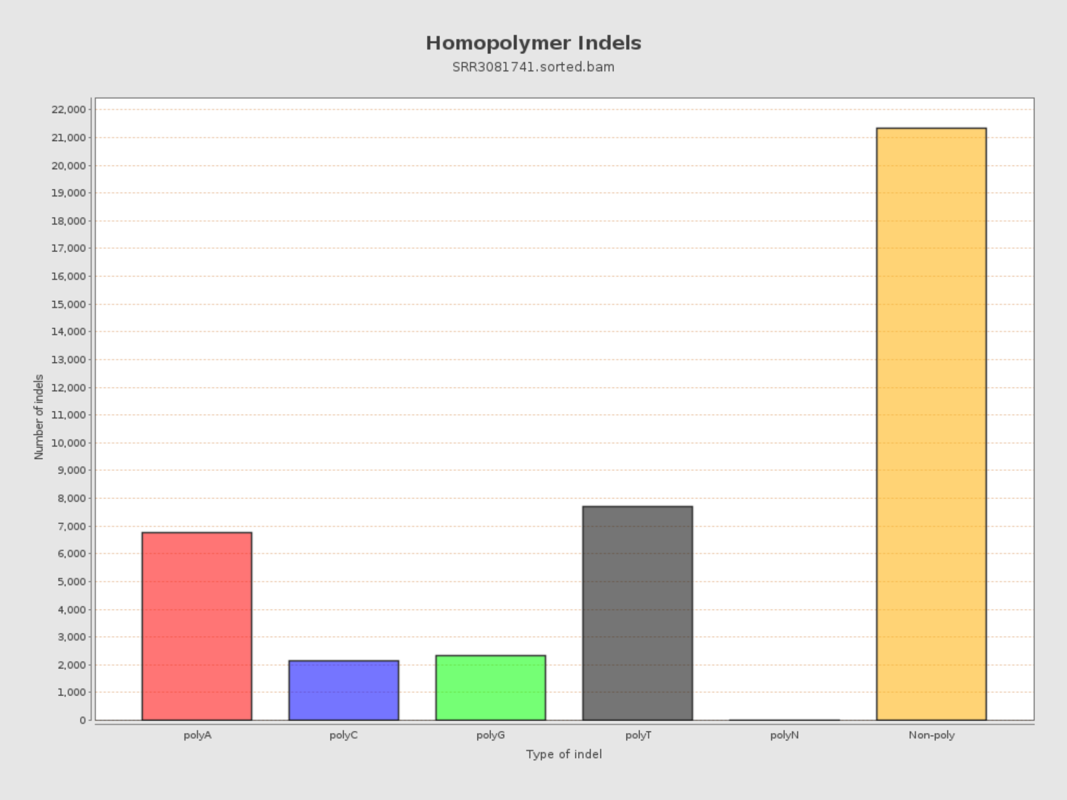
9. Results : Mapped Reads GC-content Distribution



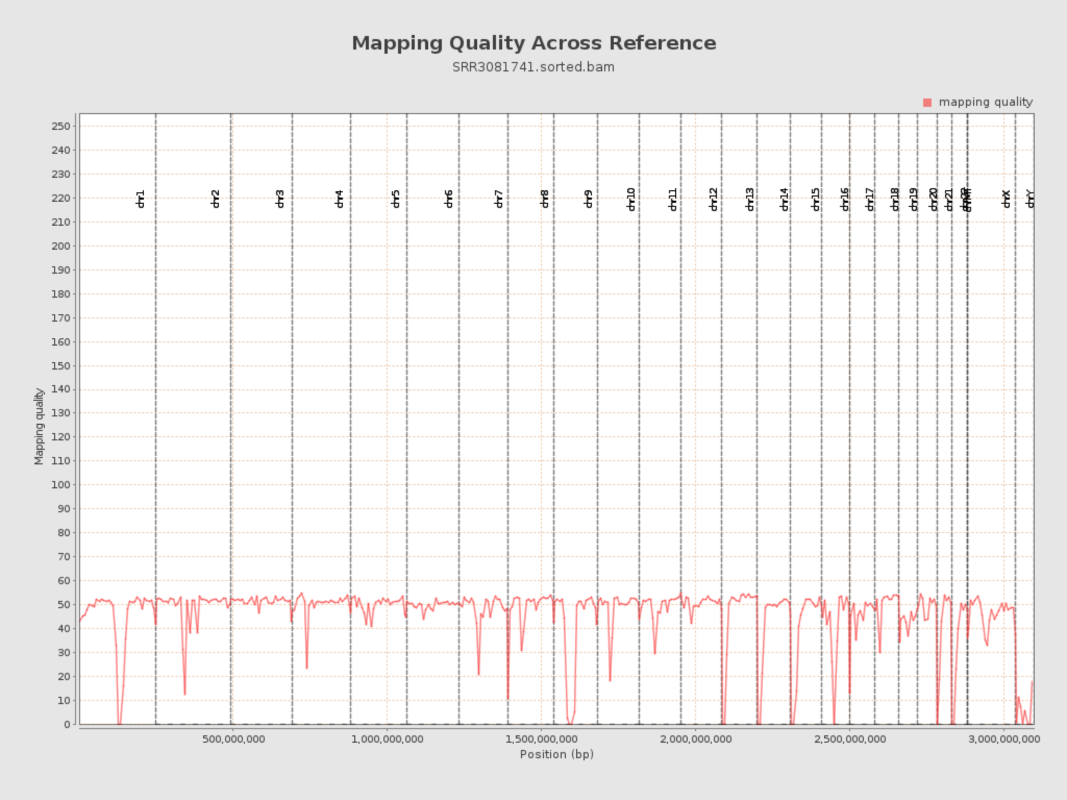
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram