Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:27:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081742.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_SRR3081742 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081742.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:27:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081742.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,259,137
Mapped reads	2,027,086 / 89.73%
Unmapped reads	232,051 / 10.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,643 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	76,857 / 3.4%
Duplication rate	3.11%
Clipped reads	865,047 / 38.29%

2.2. ACGT Content

Number/percentage of A's	37,569,730 / 27.65%
Number/percentage of C's	25,561,609 / 18.81%
Number/percentage of T's	42,617,357 / 31.36%
Number/percentage of G's	30,133,649 / 22.18%
Number/percentage of N's	1,597 / 0%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0439

Standard Deviation	0.3236

2.4. Mapping Quality

Mean Mapping Quality	46.18

2.5. Mismatches and indels

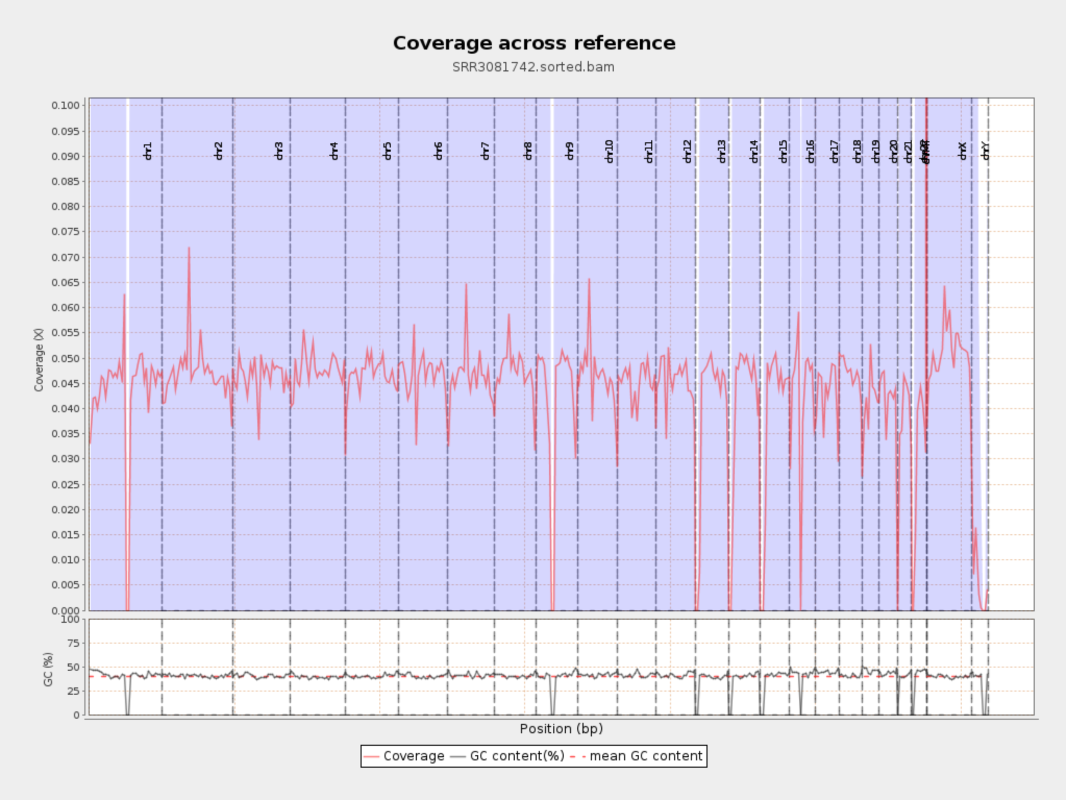
General error rate	0.79%
Mismatches	1,058,676
Insertions	9,299
Mapped reads with at least one insertion	0.45%
Deletions	26,710
Mapped reads with at least one deletion	1.3%
Homopolymer indels	47.77%

2.6. Chromosome stats

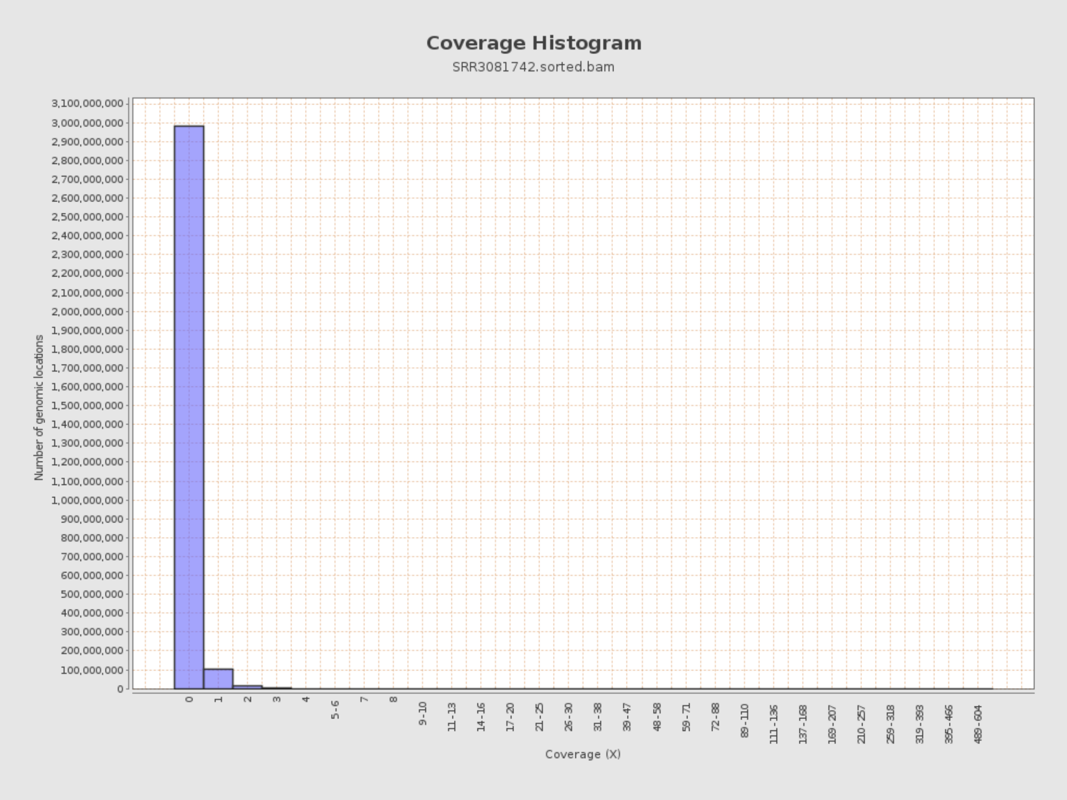
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10738920	0.0431	0.482
chr2	243199373	11511597	0.0473	0.3923
chr3	198022430	9209543	0.0465	0.2441
chr4	191154276	9122866	0.0477	0.2577
chr5	180915260	8472779	0.0468	0.2447
chr6	171115067	8017824	0.0469	0.2759
chr7	159138663	7411553	0.0466	0.39

chr8	146364022	6913254	0.0472	0.4496
chr9	141213431	5814144	0.0412	0.3065
chr10	135534747	6346602	0.0468	0.3404
chr11	135006516	6093477	0.0451	0.2898
chr12	133851895	6126023	0.0458	0.2431
chr13	115169878	4469509	0.0388	0.2233
chr14	107349540	4260386	0.0397	0.2343
chr15	102531392	3909962	0.0381	0.2266
chr16	90354753	3810817	0.0422	0.2544
chr17	81195210	3462638	0.0426	0.2475
chr18	78077248	3696610	0.0473	0.5204
chr19	59128983	2468202	0.0417	0.3917
chr20	63025520	2655423	0.0421	0.236
chr21	48129895	1740862	0.0362	0.2301
chr22	51304566	1419251	0.0277	0.1868
chrMT	16571	7747	0.4675	0.6998
chrX	155270560	7920378	0.051	0.2735
chrY	59373566	330358	0.0056	0.1232

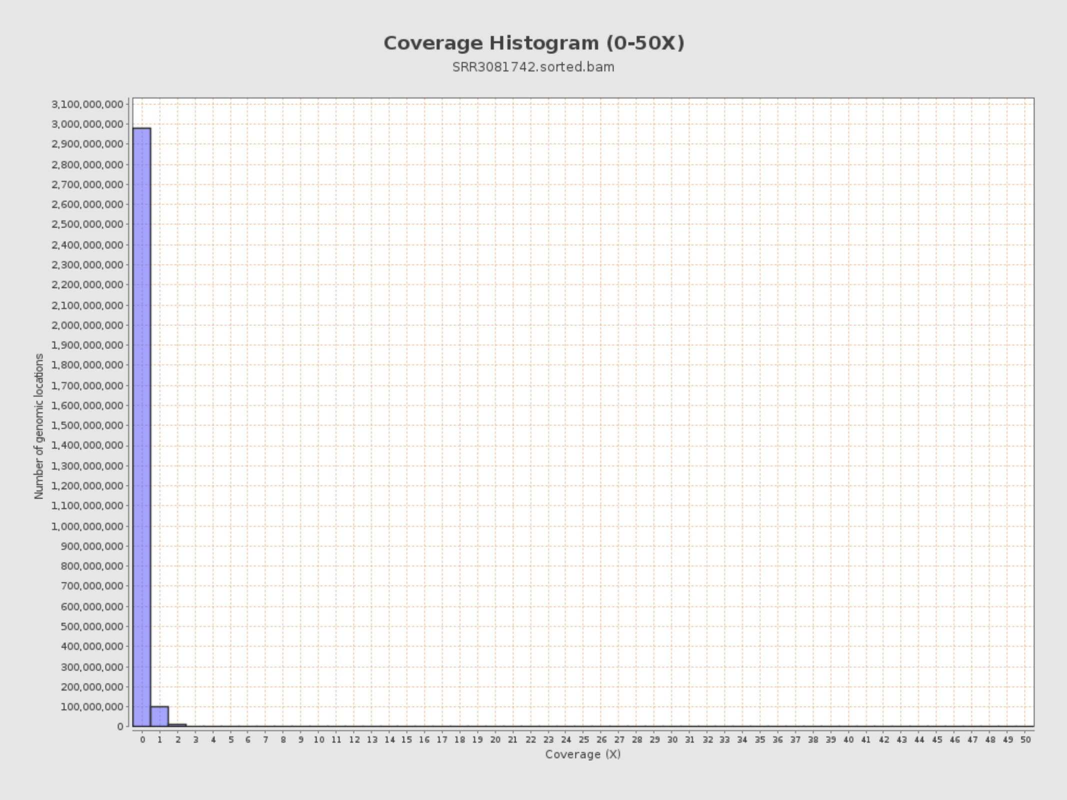
3. Results : Coverage across reference



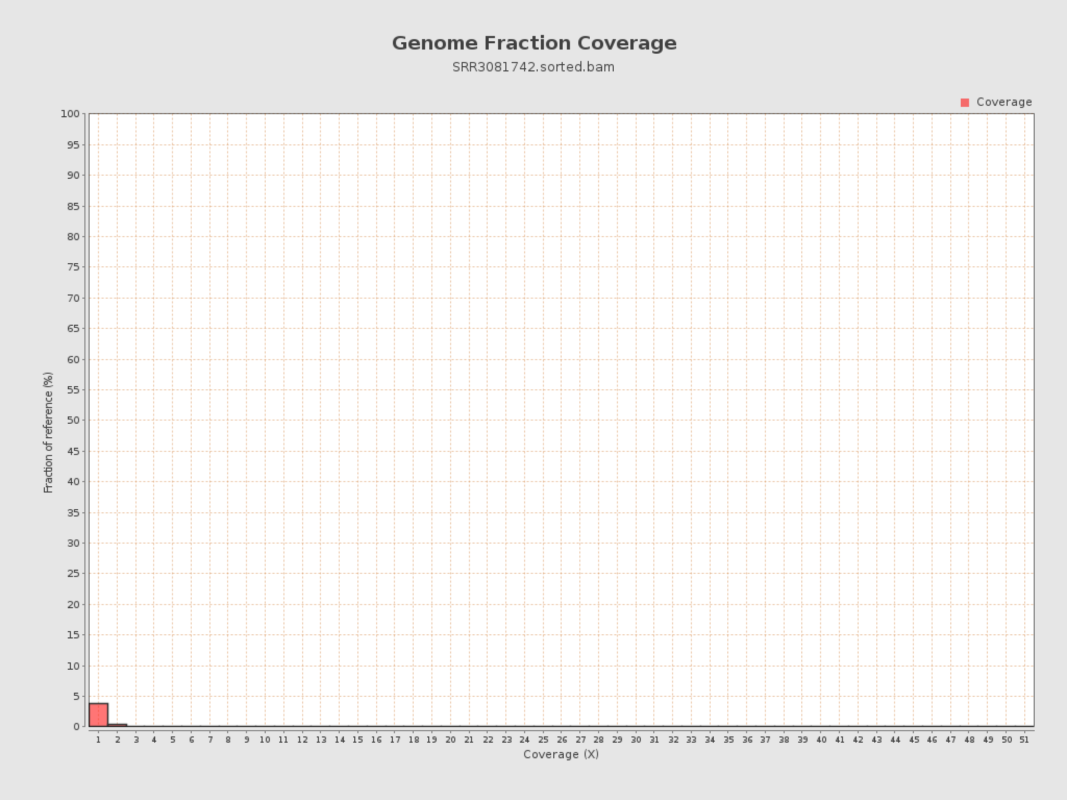
4. Results : Coverage Histogram



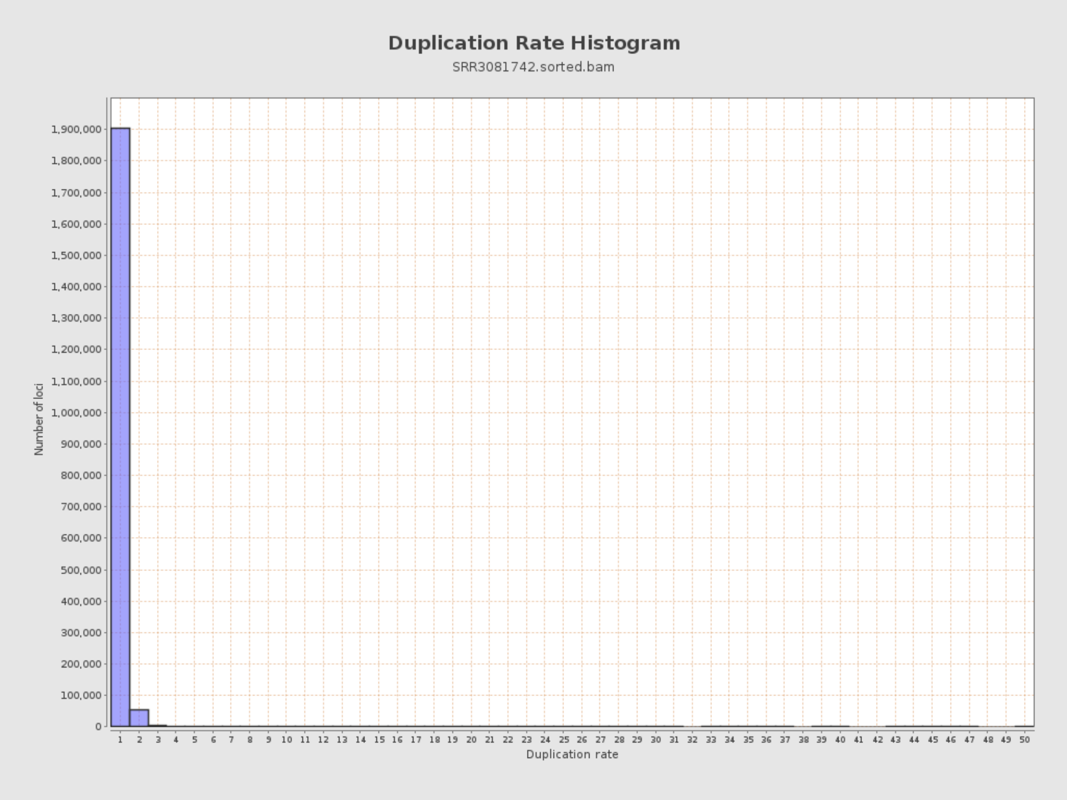
5. Results : Coverage Histogram (0-50X)



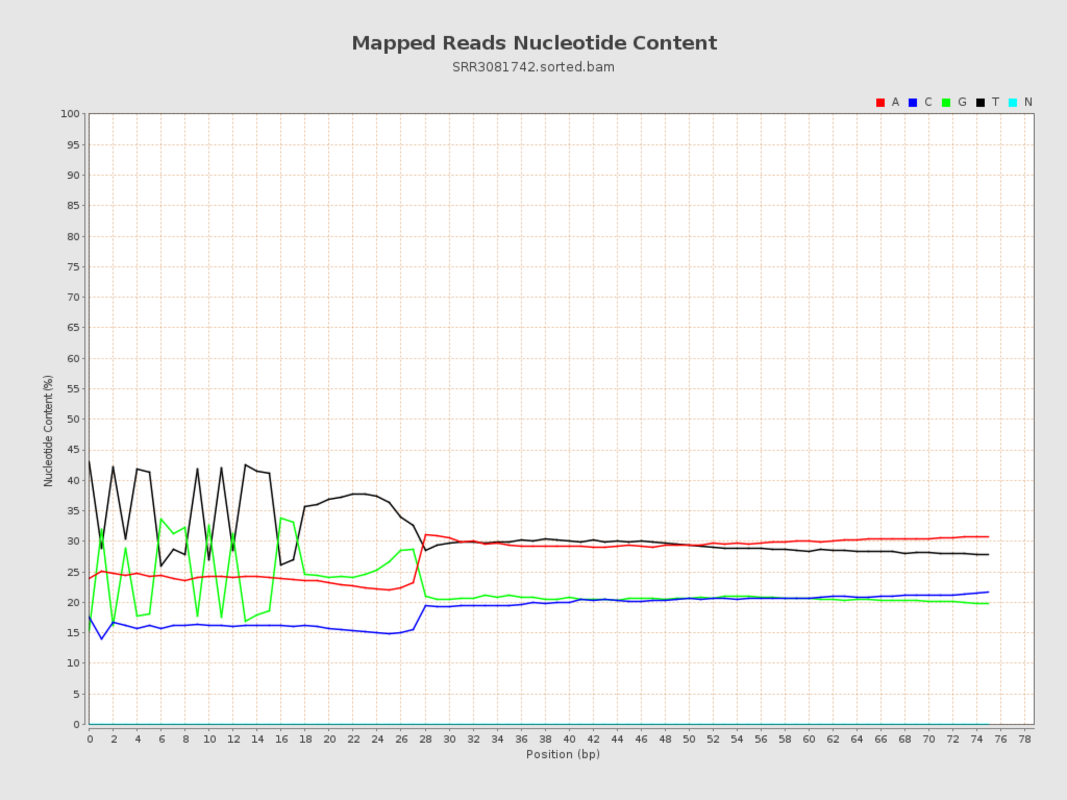
6. Results : Genome Fraction Coverage



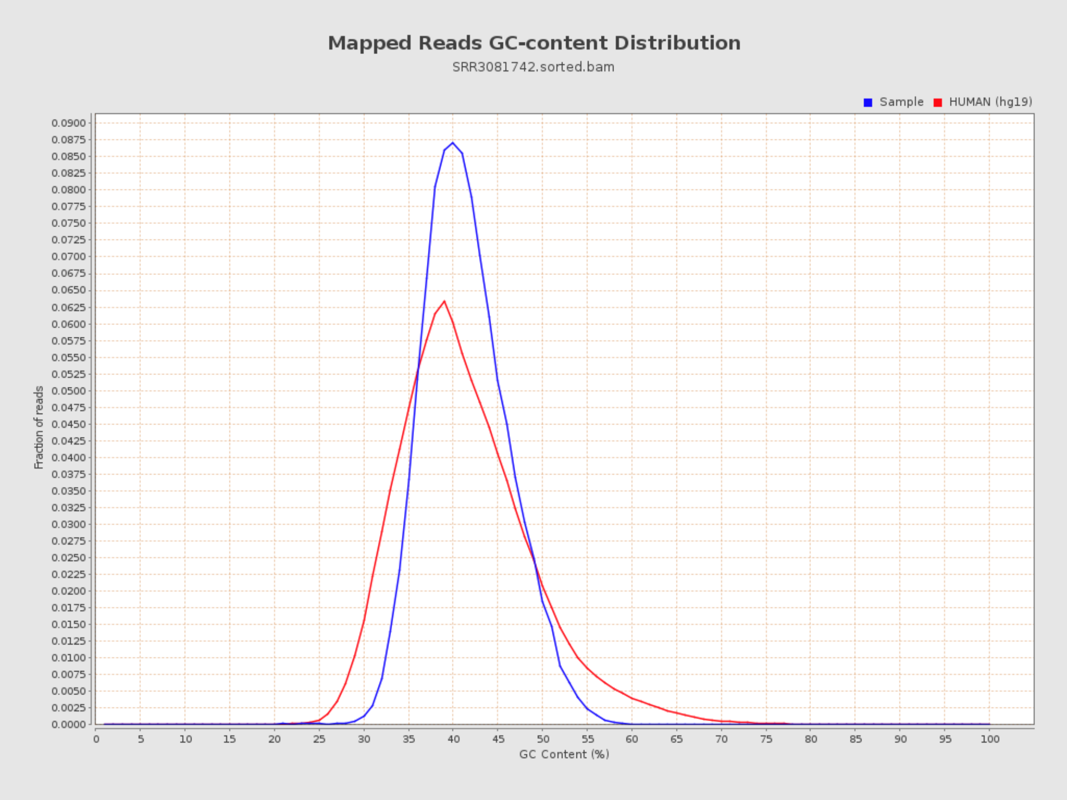
7. Results : Duplication Rate Histogram



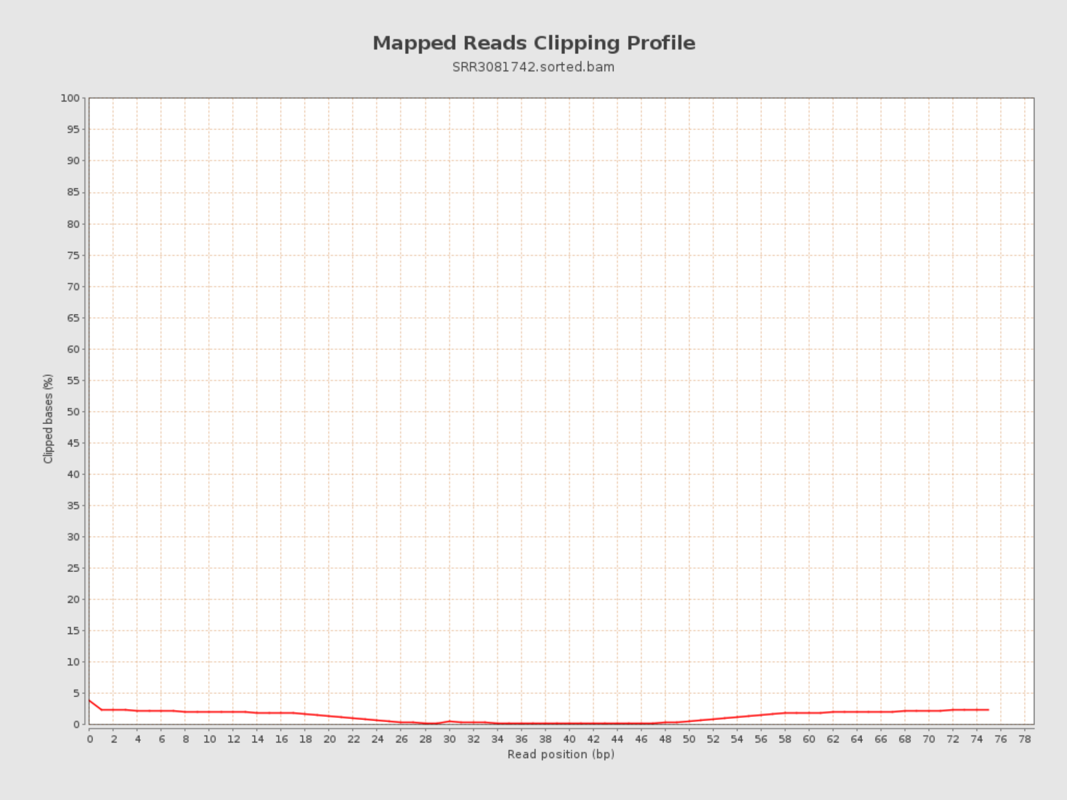
8. Results : Mapped Reads Nucleotide Content



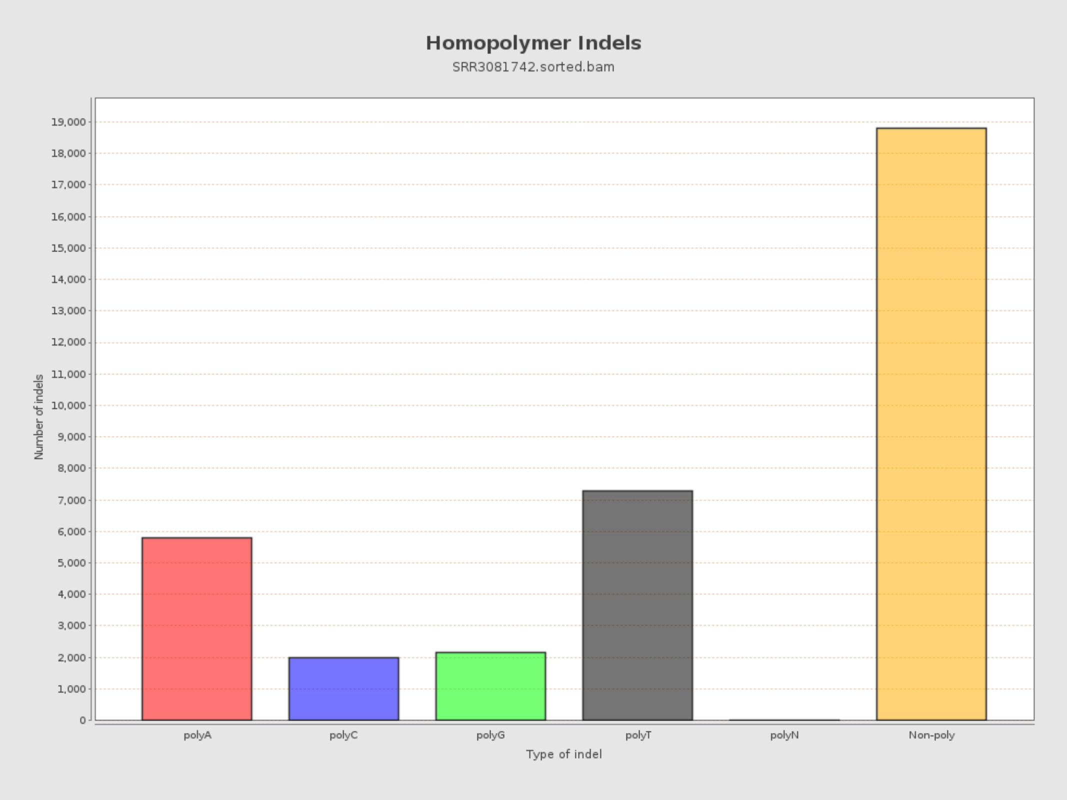
9. Results : Mapped Reads GC-content Distribution



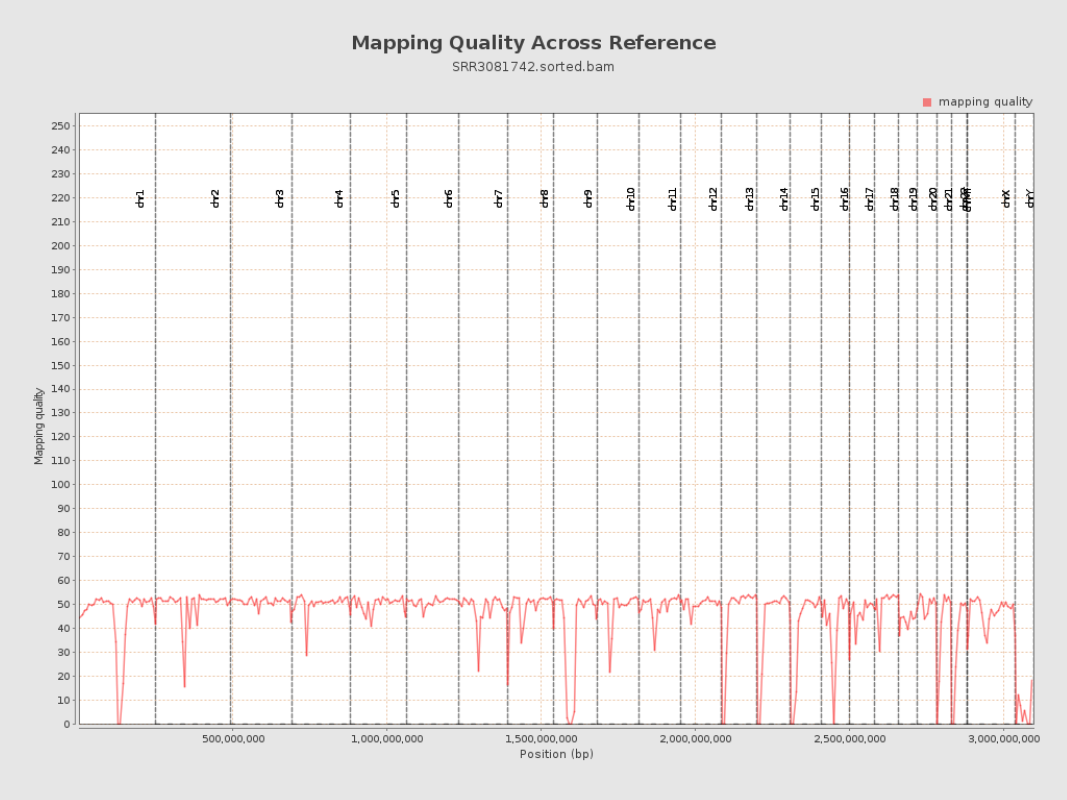
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram