Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:58:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081941.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_SRR3081941 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081941.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:58:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081941.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,119,322
Mapped reads	2,897,107 / 92.88%
Unmapped reads	222,215 / 7.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,206 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	143,152 / 4.59%
Duplication rate	4.08%
Clipped reads	987,026 / 31.64%

2.2. ACGT Content

Number/percentage of A's	57,754,743 / 28.91%
Number/percentage of C's	36,414,504 / 18.23%
Number/percentage of T's	64,141,752 / 32.1%
Number/percentage of G's	41,450,732 / 20.75%
Number/percentage of N's	26,008 / 0.01%
GC Percentage	38.97%

2.3. Coverage

Mean	0.0646

Standard Deviation	0.4575

2.4. Mapping Quality

Mean Mapping Quality	47.53

2.5. Mismatches and indels

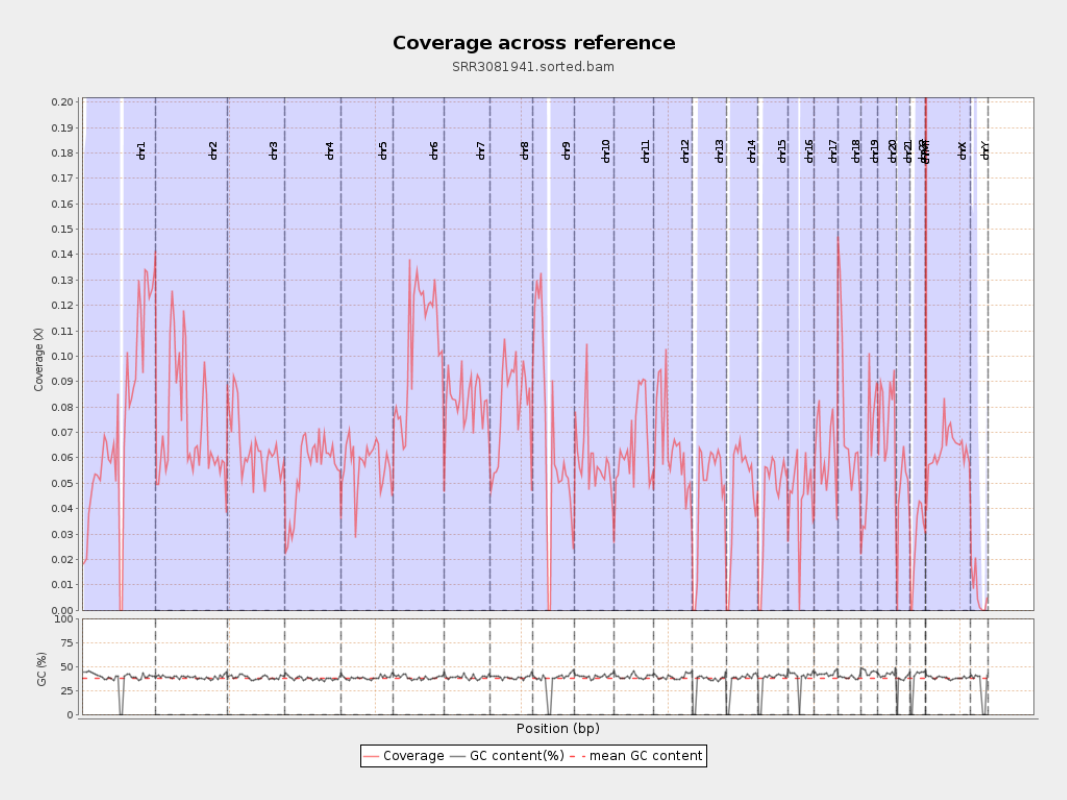
General error rate	0.74%
Mismatches	1,449,012
Insertions	14,048
Mapped reads with at least one insertion	0.48%
Deletions	40,737
Mapped reads with at least one deletion	1.39%
Homopolymer indels	48.88%

2.6. Chromosome stats

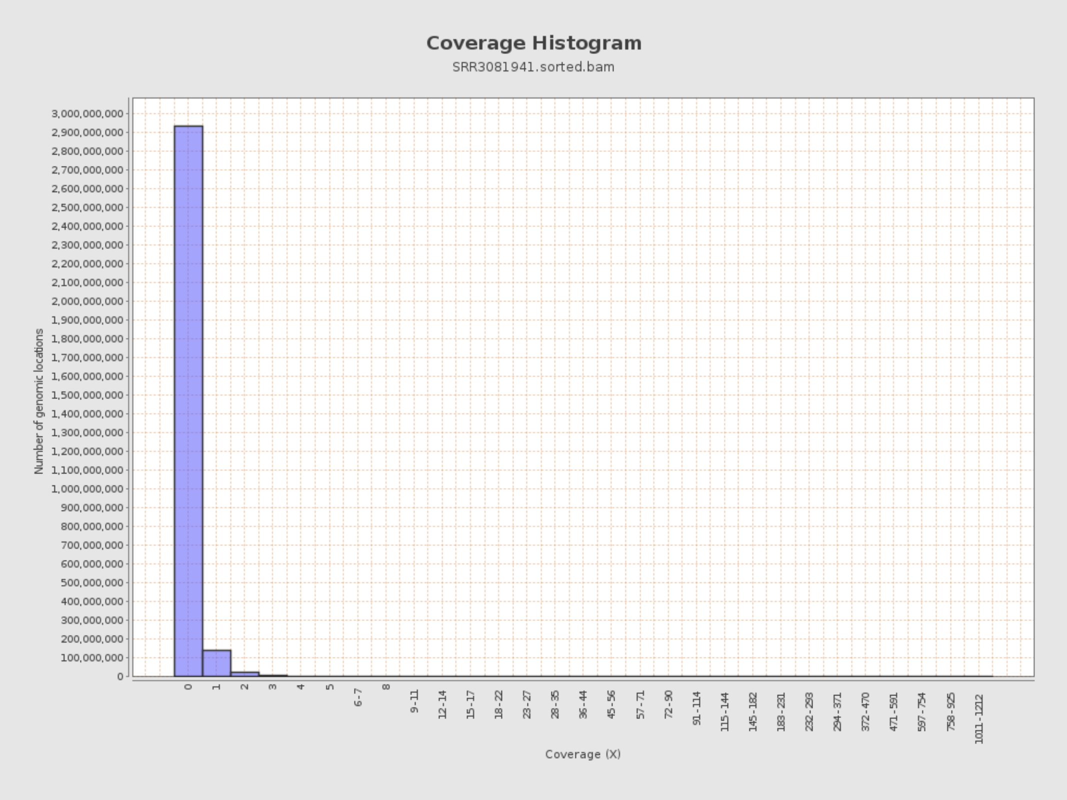
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18374055	0.0737	0.7116
chr2	243199373	17615950	0.0724	0.5507
chr3	198022430	12712794	0.0642	0.2978
chr4	191154276	10499276	0.0549	0.2847
chr5	180915260	10316560	0.057	0.2796
chr6	171115067	17971115	0.105	0.4825
chr7	159138663	13039326	0.0819	0.5238

chr8	146364022	11731990	0.0802	0.8297
chr9	141213431	9616532	0.0681	0.4626
chr10	135534747	8034320	0.0593	0.4516
chr11	135006516	8903253	0.0659	0.3568
chr12	133851895	8692096	0.0649	0.304
chr13	115169878	5436495	0.0472	0.2539
chr14	107349540	5084127	0.0474	0.269
chr15	102531392	4492882	0.0438	0.2442
chr16	90354753	4000368	0.0443	0.2799
chr17	81195210	5089215	0.0627	0.3173
chr18	78077248	5846969	0.0749	0.7525
chr19	59128983	3658737	0.0619	0.5261
chr20	63025520	4862850	0.0772	0.3308
chr21	48129895	2197402	0.0457	0.2688
chr22	51304566	1401105	0.0273	0.1877
chrMT	16571	92106	5.5583	3.5884
chrX	155270560	9791851	0.0631	0.3321
chrY	59373566	397934	0.0067	0.1414

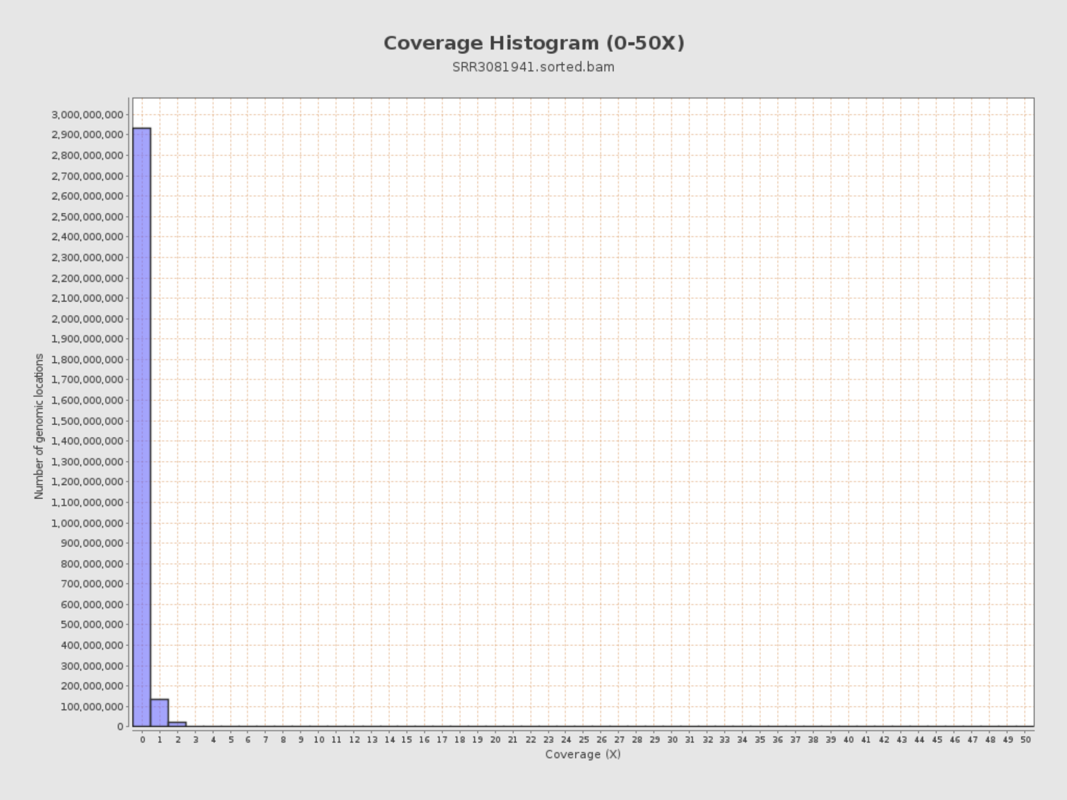
3. Results : Coverage across reference



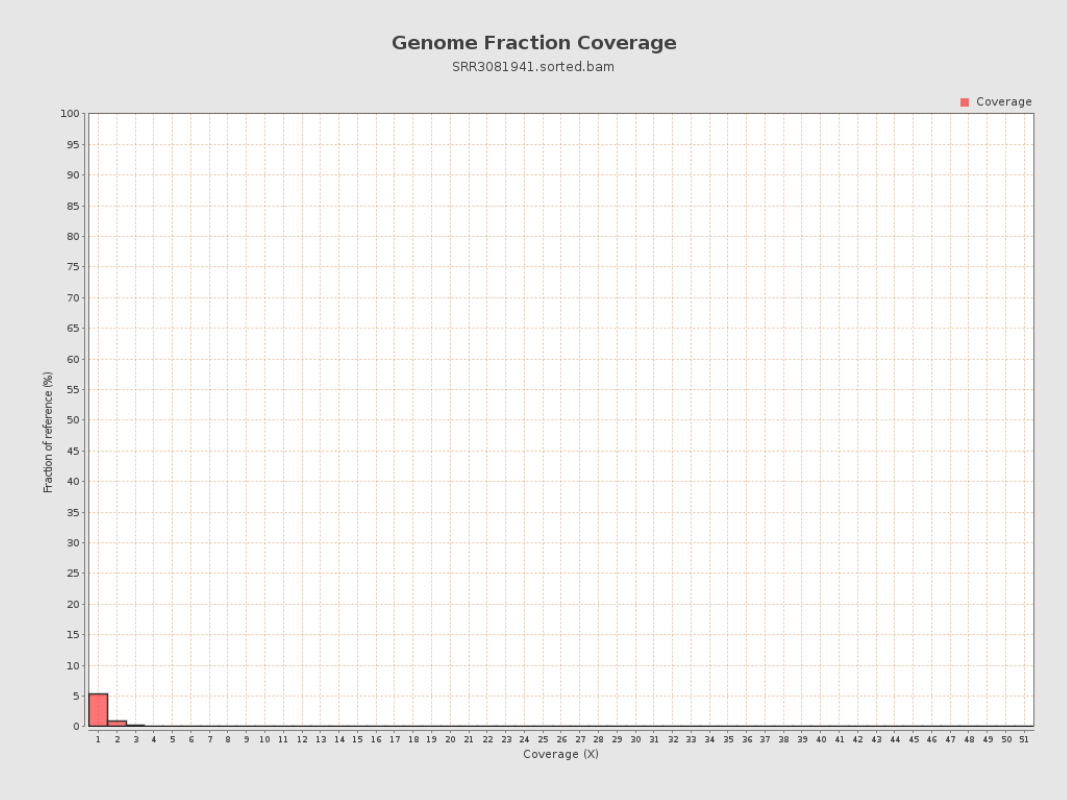
4. Results : Coverage Histogram



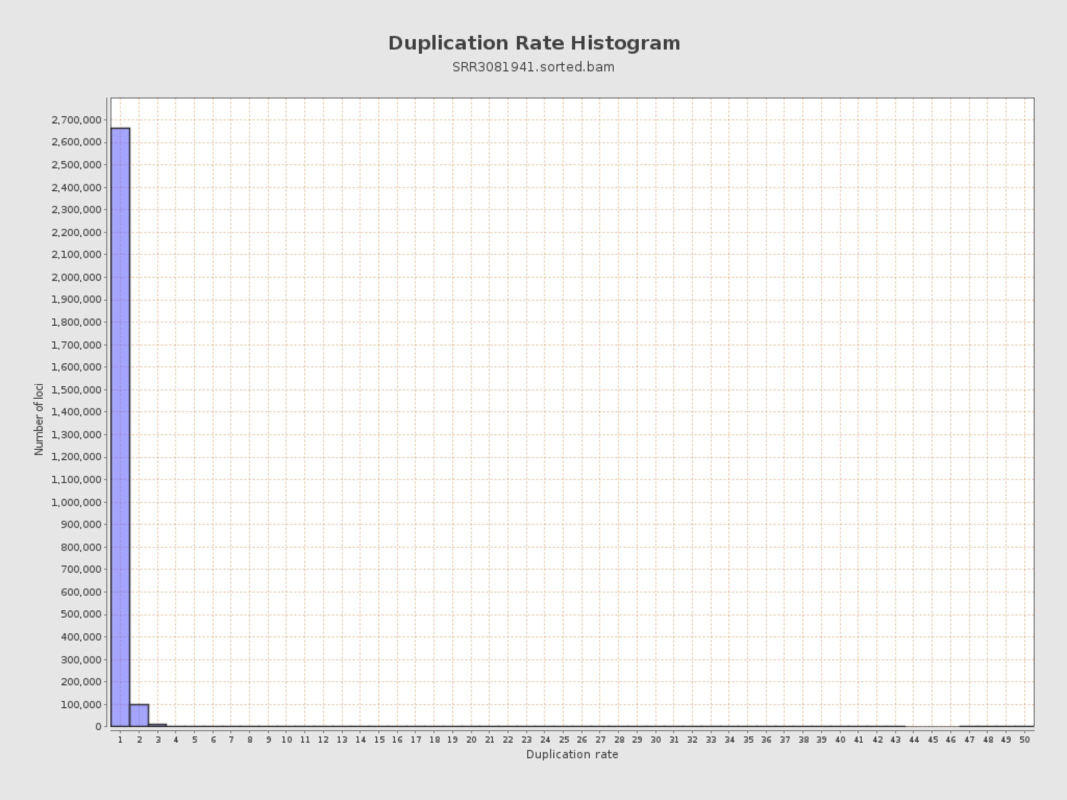
5. Results : Coverage Histogram (0-50X)



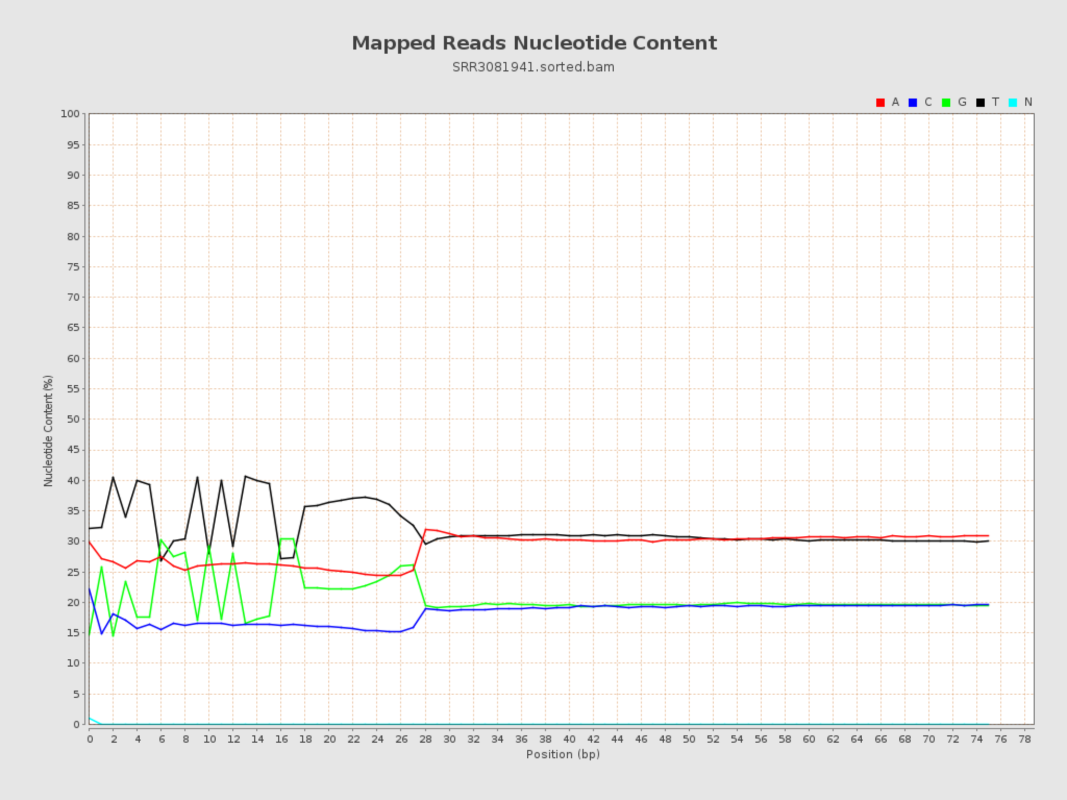
6. Results : Genome Fraction Coverage



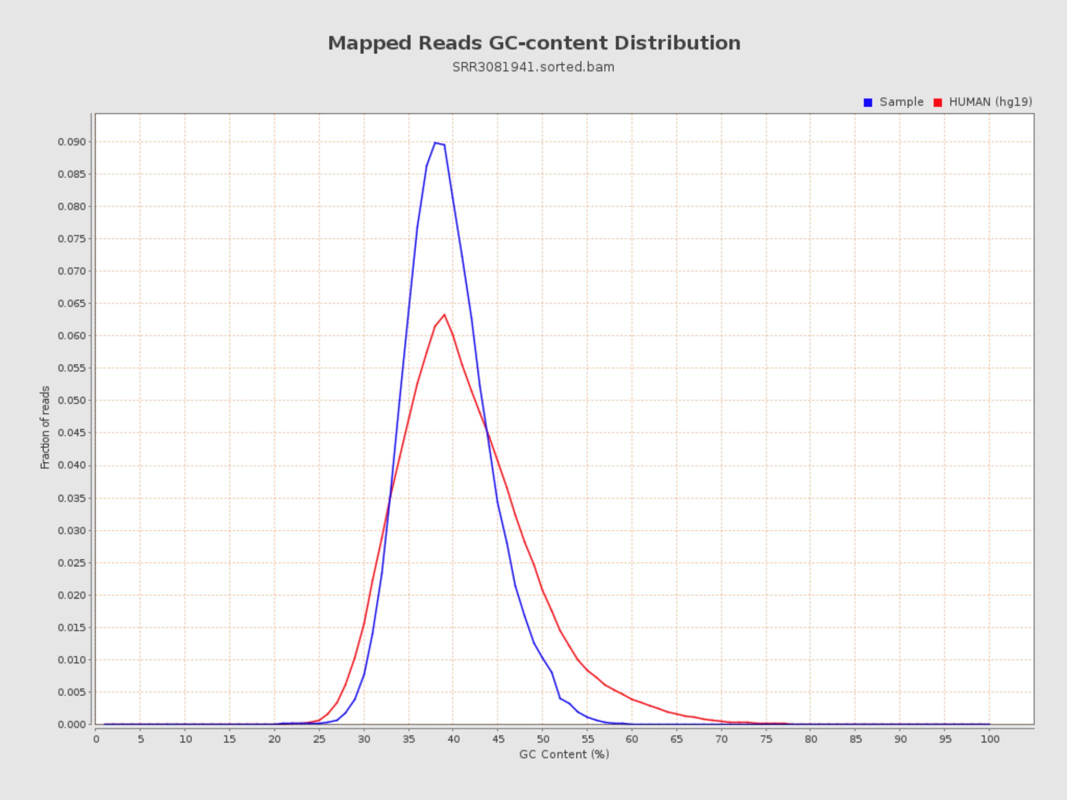
7. Results : Duplication Rate Histogram



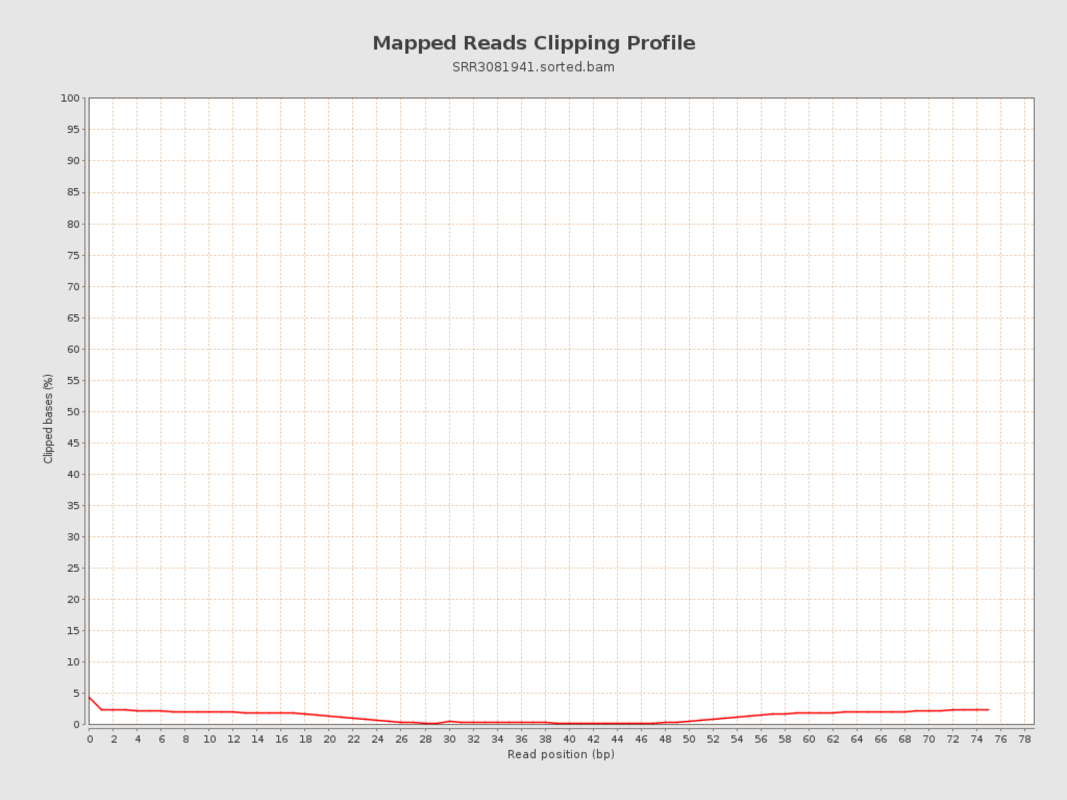
8. Results : Mapped Reads Nucleotide Content



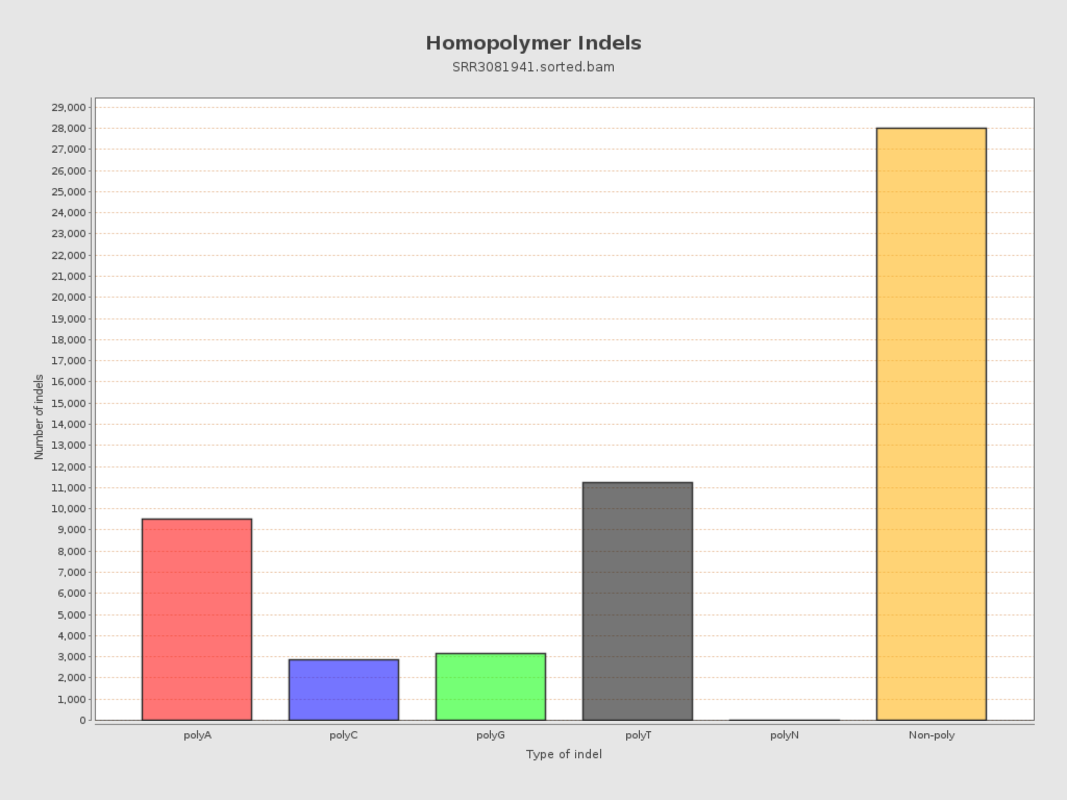
9. Results : Mapped Reads GC-content Distribution



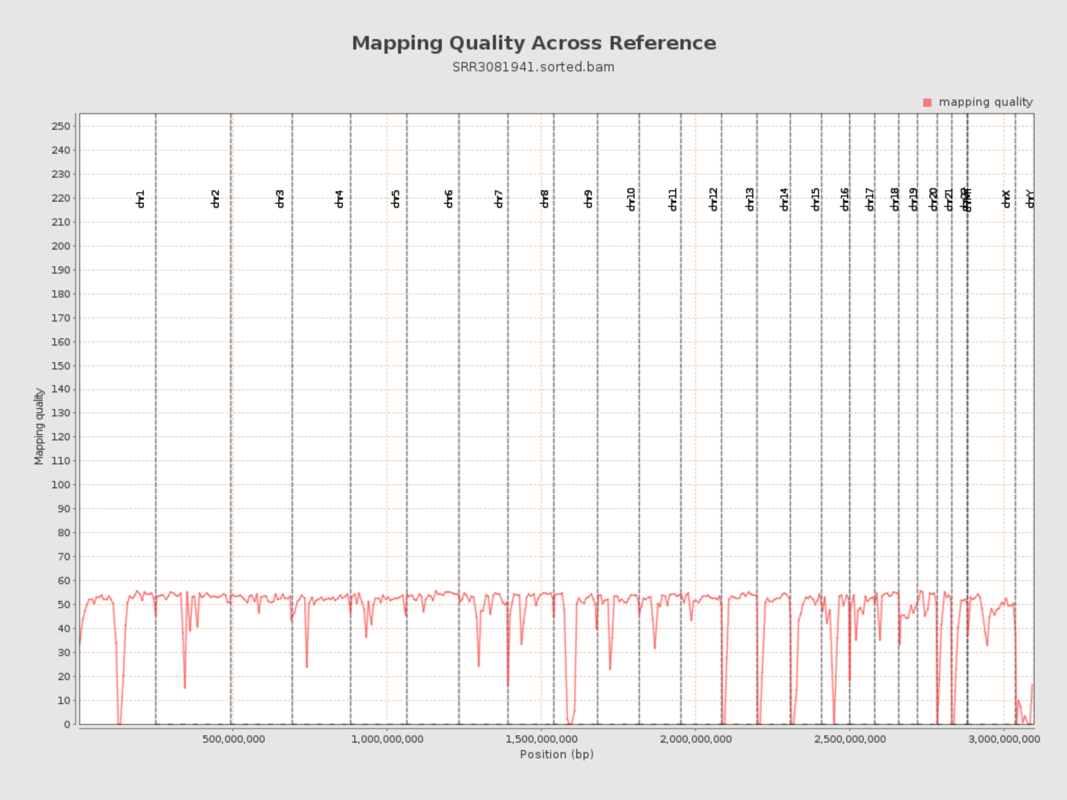
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram