Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:56:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081735.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_SRR3081735 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081735.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:56:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081735.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,770,227
Mapped reads	2,527,122 / 91.22%
Unmapped reads	243,105 / 8.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,866 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	104,978 / 3.79%
Duplication rate	3.13%
Clipped reads	1,063,850 / 38.4%

2.2. ACGT Content

Number/percentage of A's	46,812,509 / 27.54%
Number/percentage of C's	32,668,131 / 19.22%
Number/percentage of T's	52,151,629 / 30.68%
Number/percentage of G's	38,365,148 / 22.57%
Number/percentage of N's	1,964 / 0%
GC Percentage	41.78%

2.3. Coverage

Mean	0.0549

Standard Deviation	0.4522

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

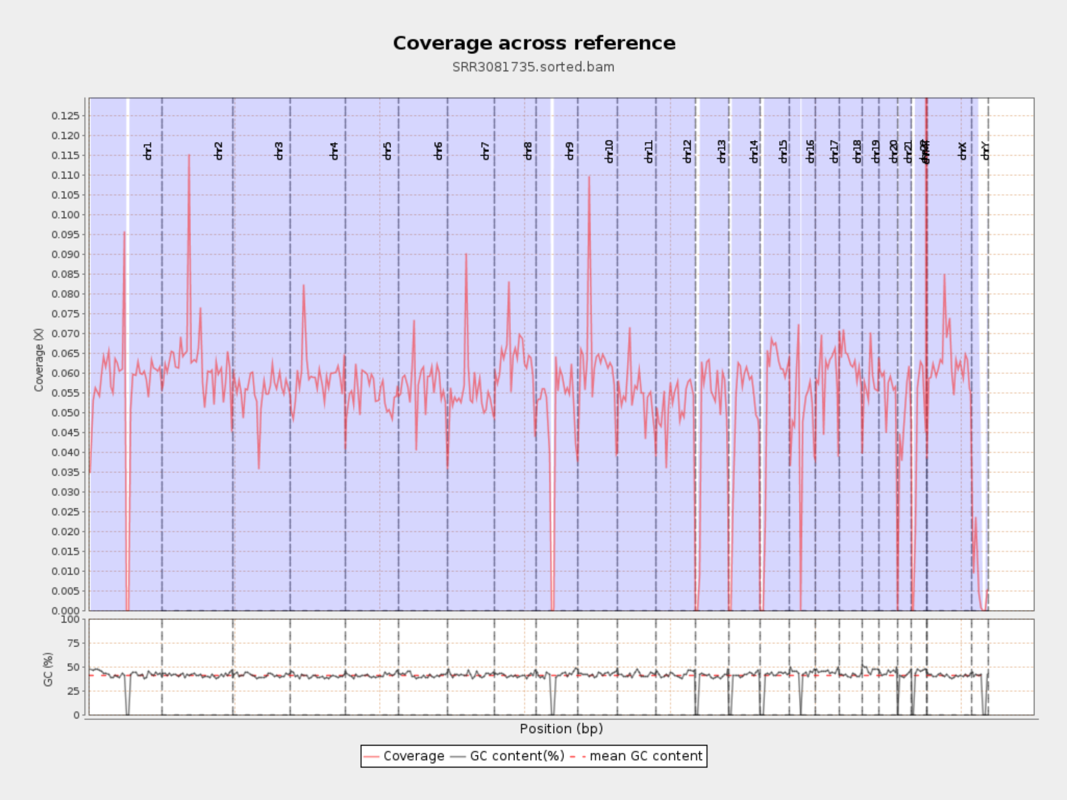
General error rate	0.83%
Mismatches	1,393,254
Insertions	12,117
Mapped reads with at least one insertion	0.48%
Deletions	35,775
Mapped reads with at least one deletion	1.4%
Homopolymer indels	46.23%

2.6. Chromosome stats

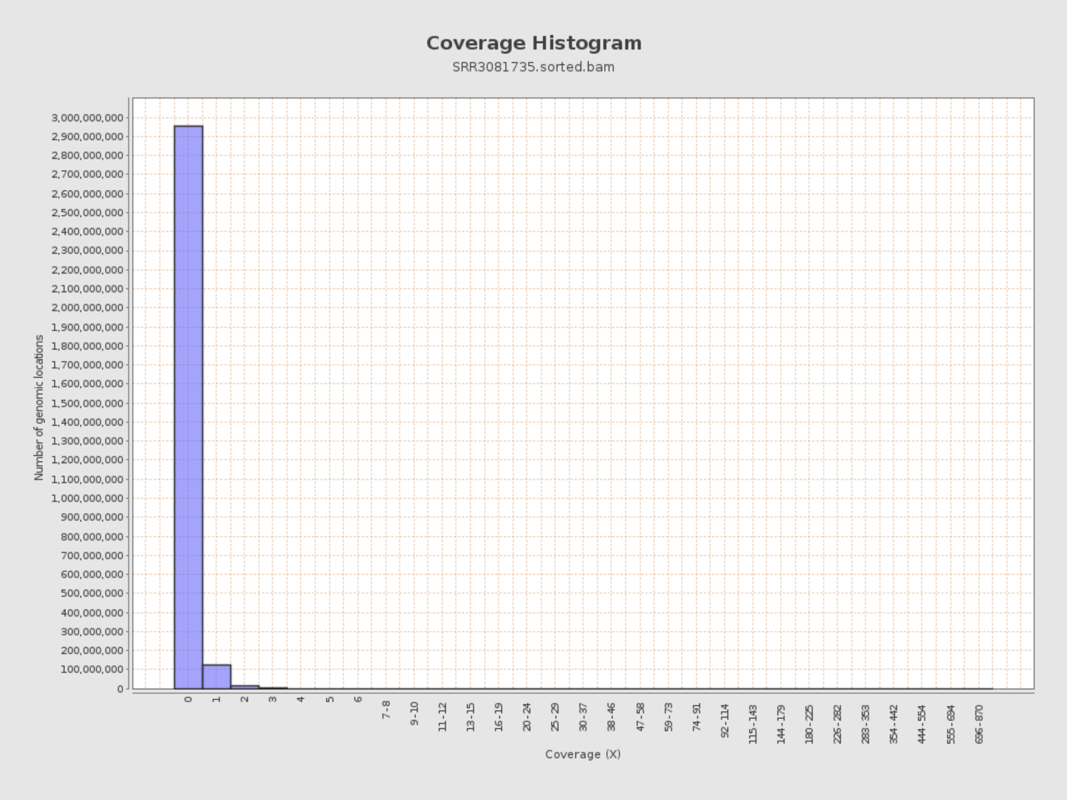
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13955311	0.056	0.805
chr2	243199373	15363724	0.0632	0.5874
chr3	198022430	10992318	0.0555	0.2763
chr4	191154276	11262832	0.0589	0.3025
chr5	180915260	9941926	0.055	0.2683
chr6	171115067	9726250	0.0568	0.3367
chr7	159138663	8833655	0.0555	0.5838

chr8	146364022	9250369	0.0632	0.5132
chr9	141213431	6862183	0.0486	0.4224
chr10	135534747	8532619	0.063	0.5313
chr11	135006516	7345121	0.0544	0.403
chr12	133851895	6898411	0.0515	0.2639
chr13	115169878	5438283	0.0472	0.2477
chr14	107349540	5113136	0.0476	0.2652
chr15	102531392	5274384	0.0514	0.2636
chr16	90354753	4324430	0.0479	0.3006
chr17	81195210	4809688	0.0592	0.3198
chr18	78077248	4944164	0.0633	0.7531
chr19	59128983	3401934	0.0575	0.6149
chr20	63025520	3490518	0.0554	0.2762
chr21	48129895	2160403	0.0449	0.268
chr22	51304566	2024469	0.0395	0.2265
chrMT	16571	47075	2.8408	2.2116
chrX	155270560	9628706	0.062	0.3319
chrY	59373566	441242	0.0074	0.1771

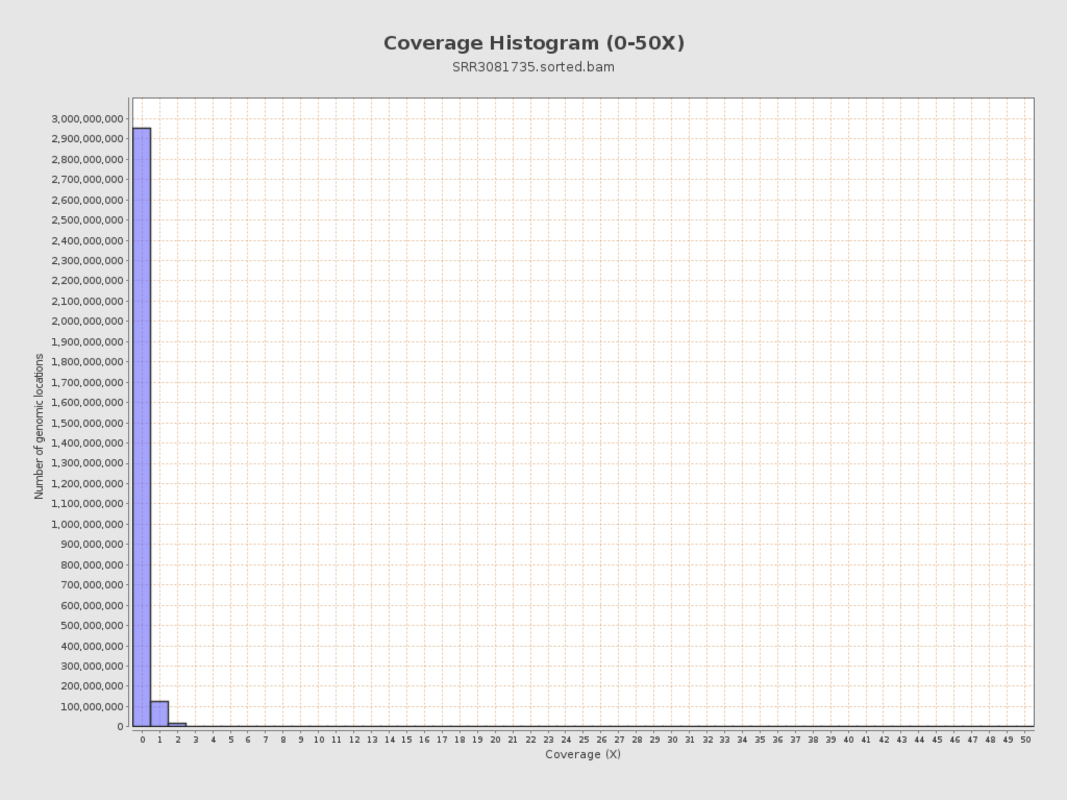
3. Results : Coverage across reference



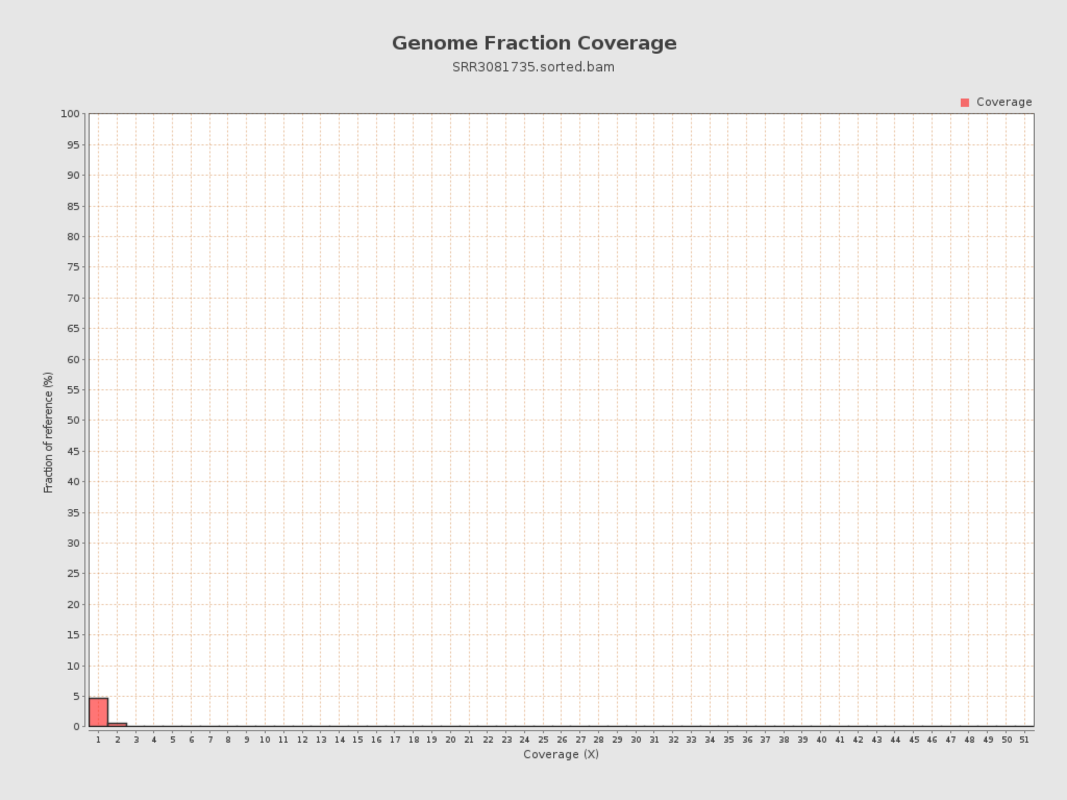
4. Results : Coverage Histogram



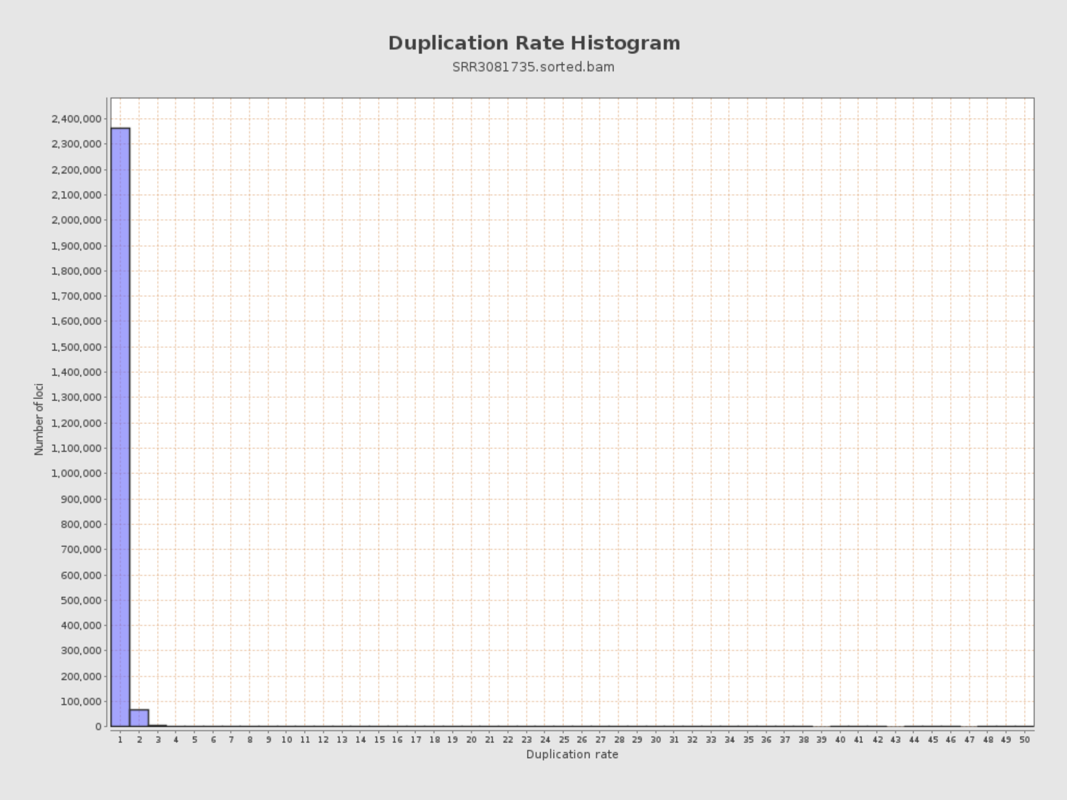
5. Results : Coverage Histogram (0-50X)



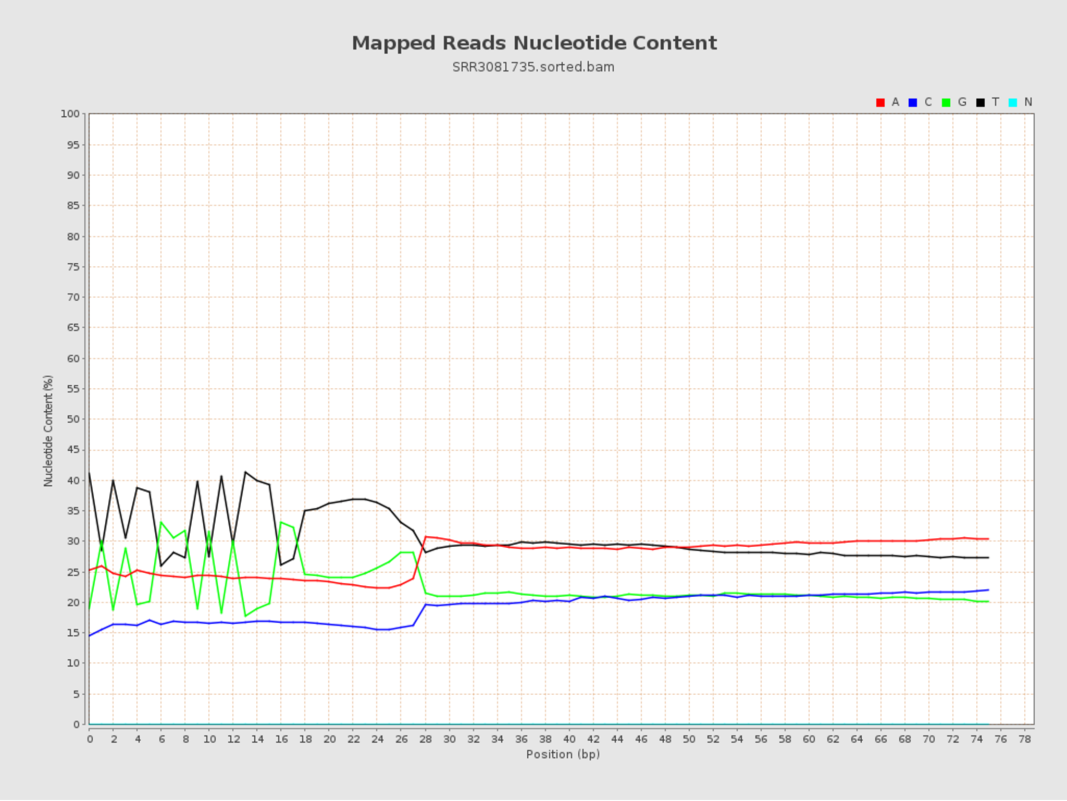
6. Results : Genome Fraction Coverage



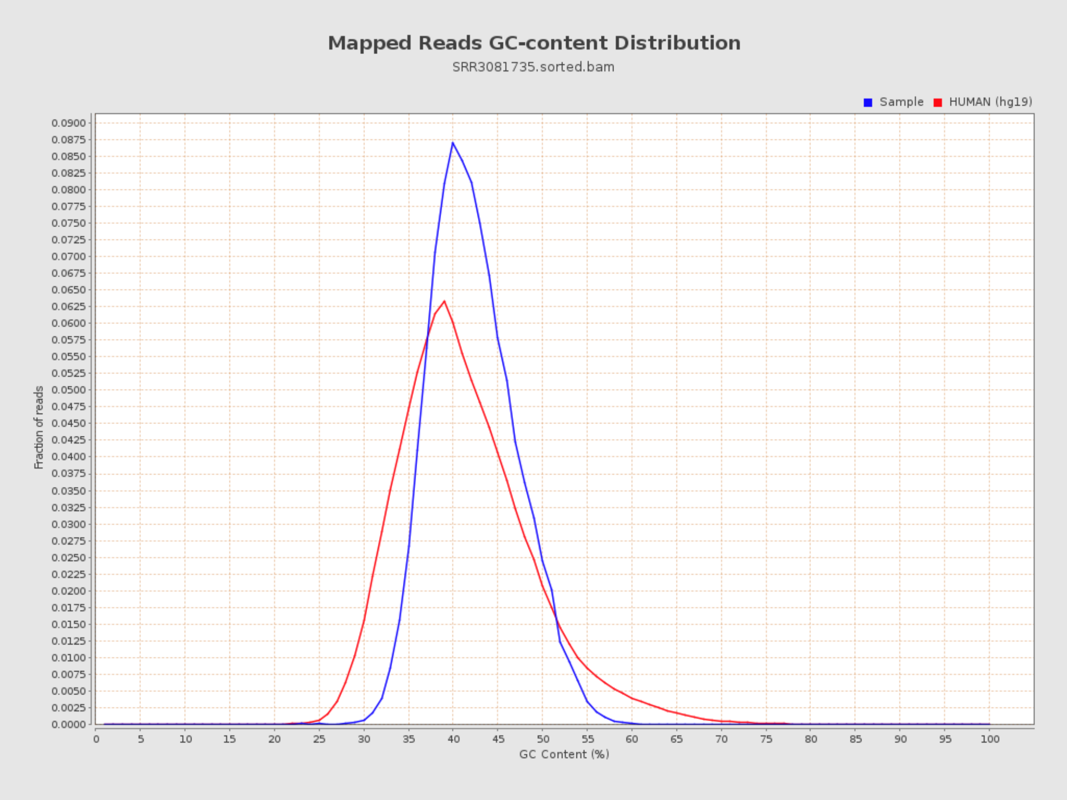
7. Results : Duplication Rate Histogram



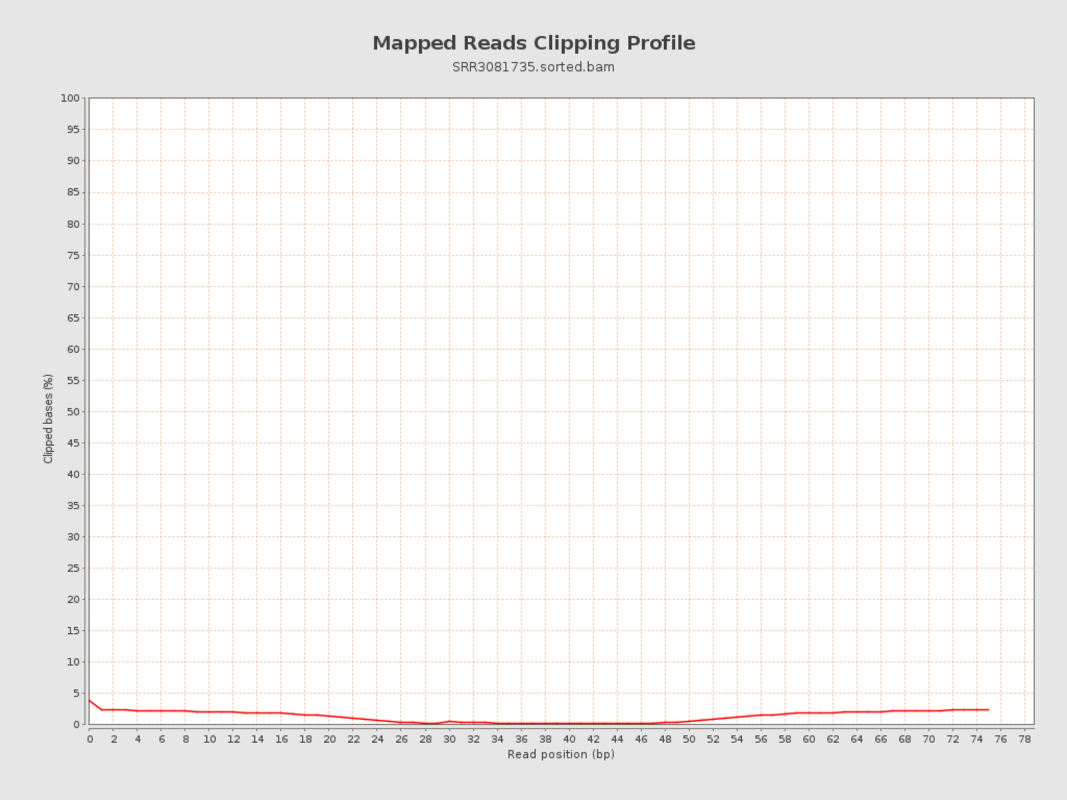
8. Results : Mapped Reads Nucleotide Content



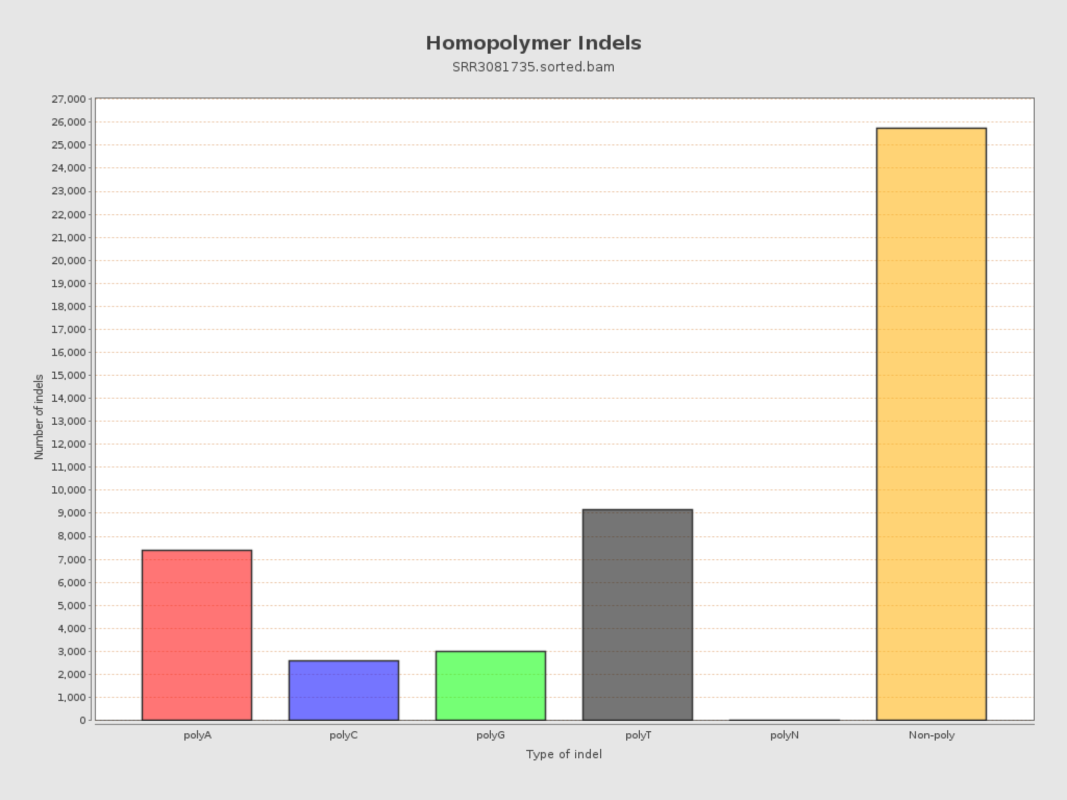
9. Results : Mapped Reads GC-content Distribution



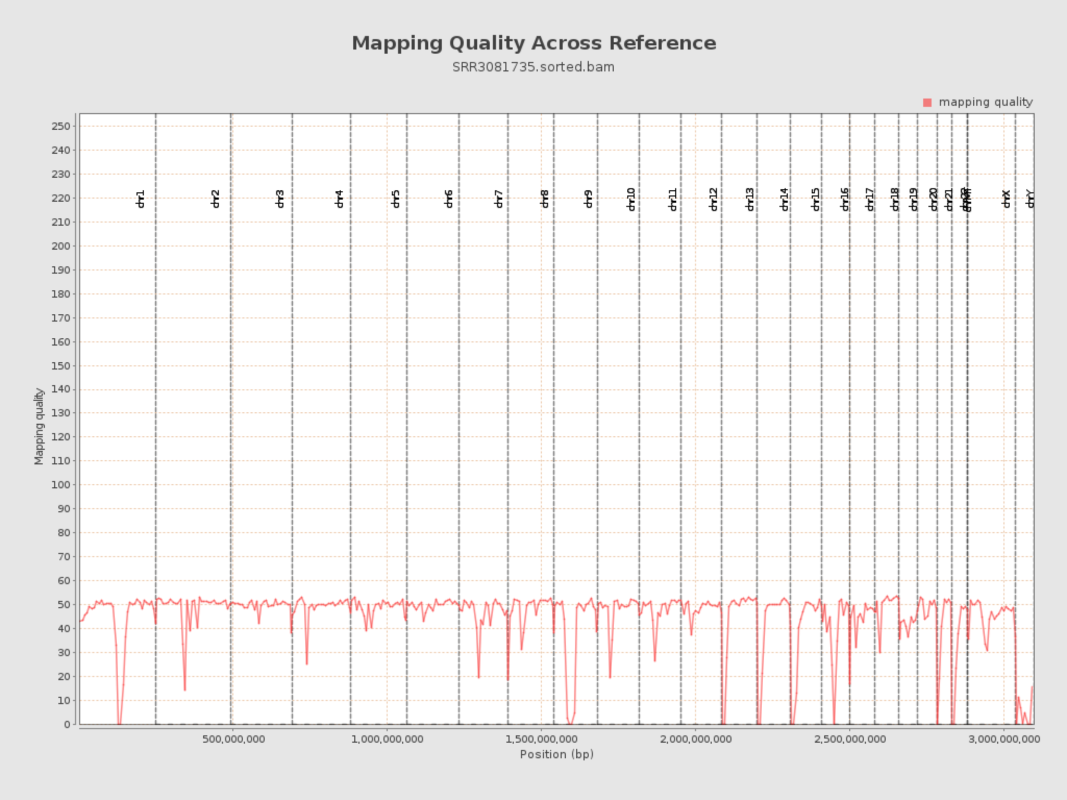
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram