Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:28:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080781.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_SRR3080781 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080781.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:28:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080781.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,940,243
Mapped reads	2,601,818 / 88.49%
Unmapped reads	338,425 / 11.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,699 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	91,105 / 3.1%
Duplication rate	2.77%
Clipped reads	1,190,564 / 40.49%

2.2. ACGT Content

Number/percentage of A's	49,326,253 / 28.39%
Number/percentage of C's	33,592,392 / 19.33%
Number/percentage of T's	53,027,916 / 30.52%
Number/percentage of G's	37,789,827 / 21.75%
Number/percentage of N's	3,656 / 0%
GC Percentage	41.09%

2.3. Coverage

Mean	0.0561

Standard Deviation	0.4018

2.4. Mapping Quality

Mean Mapping Quality	46.04

2.5. Mismatches and indels

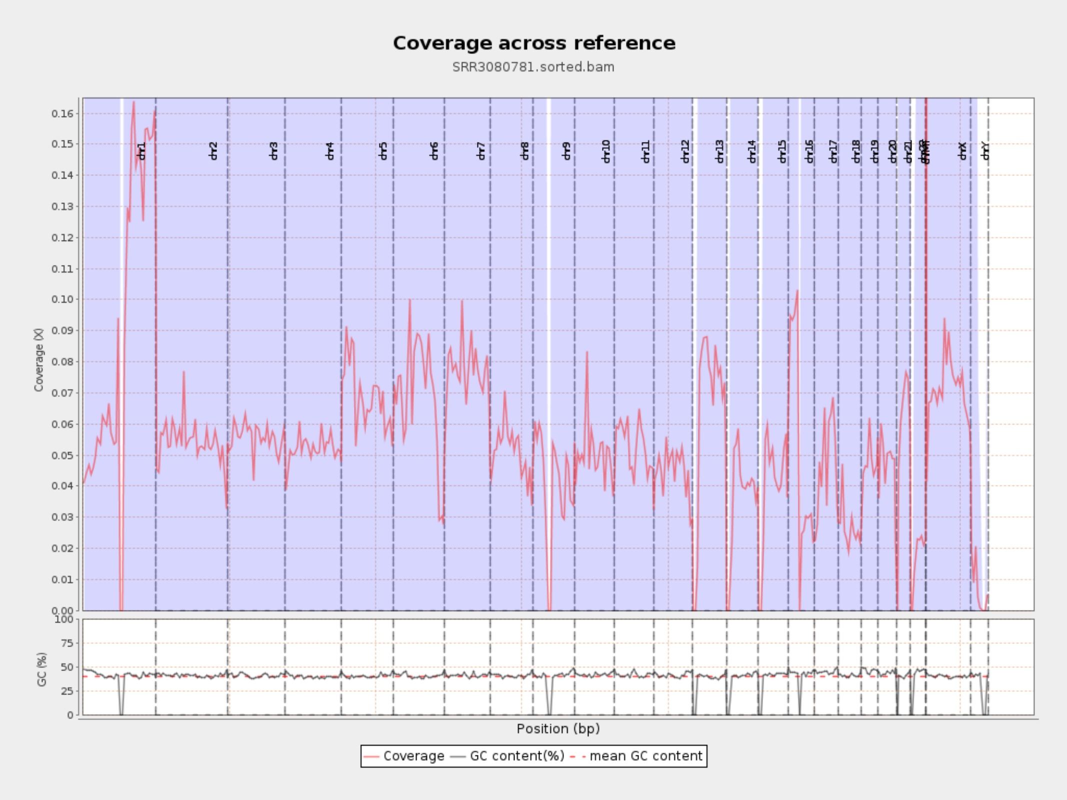
General error rate	0.77%
Mismatches	1,309,028
Insertions	13,027
Mapped reads with at least one insertion	0.5%
Deletions	36,851
Mapped reads with at least one deletion	1.4%
Homopolymer indels	47.12%

2.6. Chromosome stats

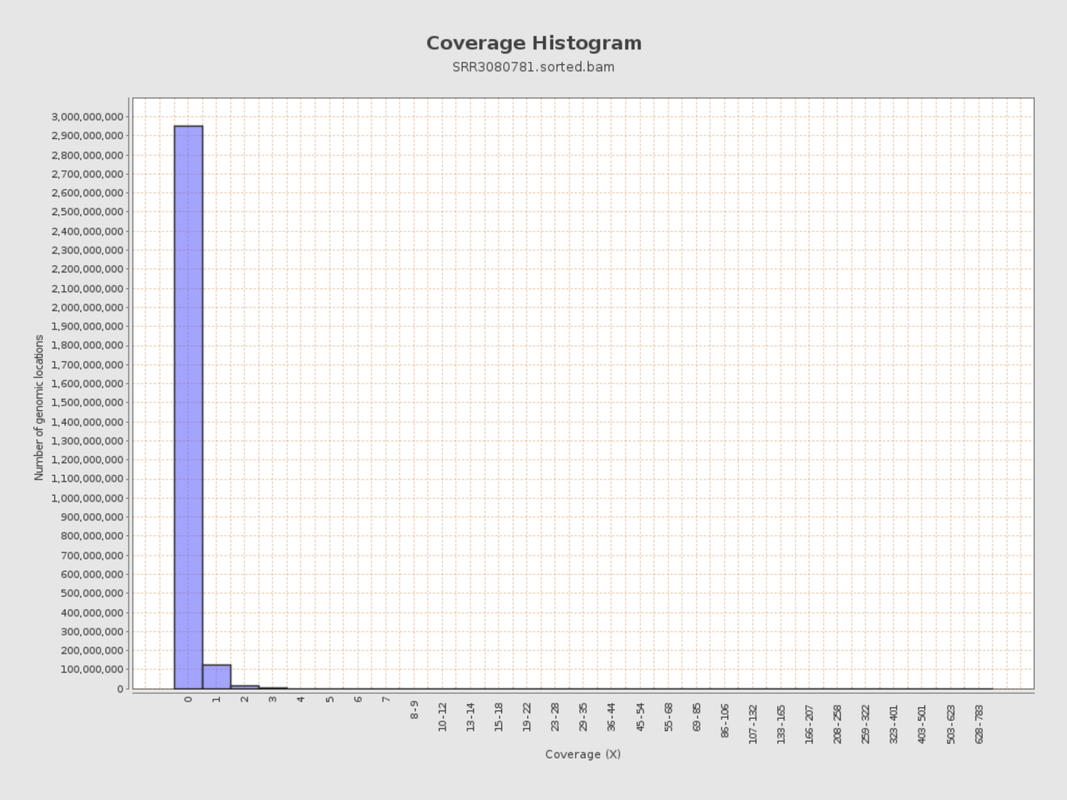
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22519064	0.0903	0.7253
chr2	243199373	13166682	0.0541	0.4587
chr3	198022430	11018956	0.0556	0.2697
chr4	191154276	9980071	0.0522	0.2715
chr5	180915260	12402978	0.0686	0.2988
chr6	171115067	12009337	0.0702	0.4284
chr7	159138663	12309270	0.0773	0.5382

chr8	146364022	7461205	0.051	0.4935
chr9	141213431	5805182	0.0411	0.3134
chr10	135534747	6850352	0.0505	0.392
chr11	135006516	7144179	0.0529	0.3155
chr12	133851895	6026151	0.045	0.2444
chr13	115169878	7478068	0.0649	0.2918
chr14	107349540	3977868	0.0371	0.2408
chr15	102531392	4020152	0.0392	0.2322
chr16	90354753	4575004	0.0506	0.2802
chr17	81195210	3892156	0.0479	0.2607
chr18	78077248	2111845	0.027	0.5713
chr19	59128983	2809054	0.0475	0.5164
chr20	63025520	3015165	0.0478	0.2613
chr21	48129895	2829452	0.0588	0.2869
chr22	51304566	846102	0.0165	0.1432
chrMT	16571	35377	2.1349	1.7414
chrX	155270560	11105542	0.0715	0.3273
chrY	59373566	410154	0.0069	0.1437

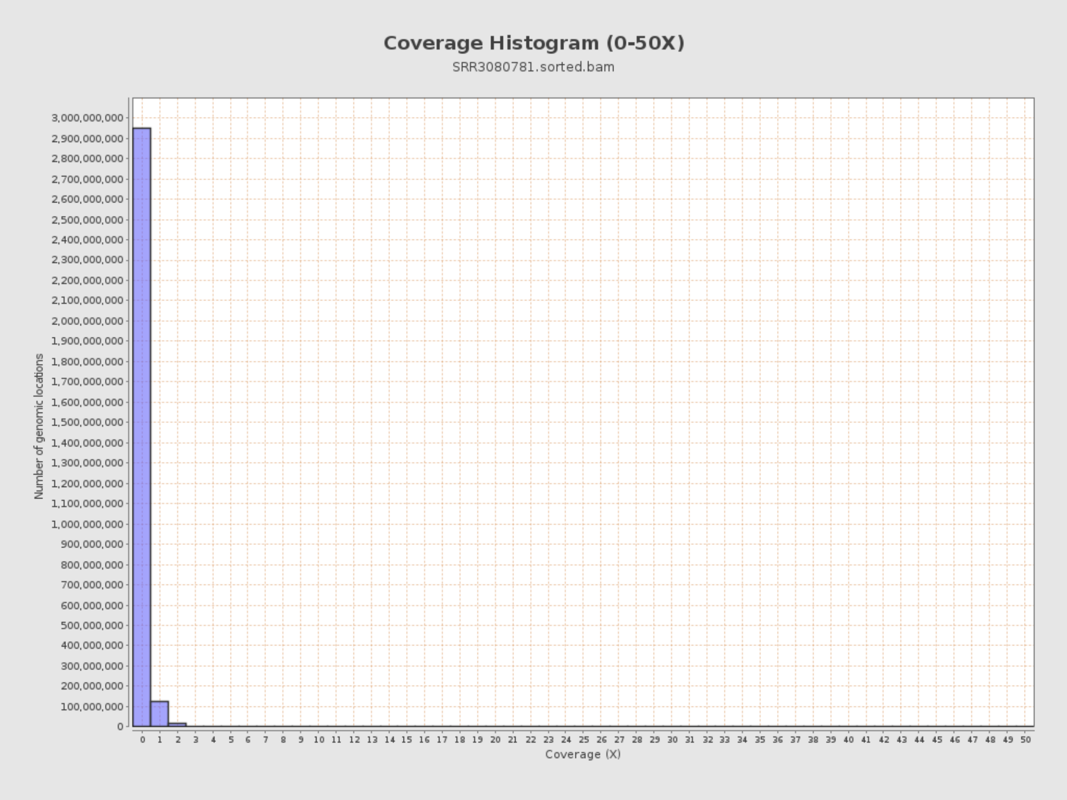
3. Results : Coverage across reference



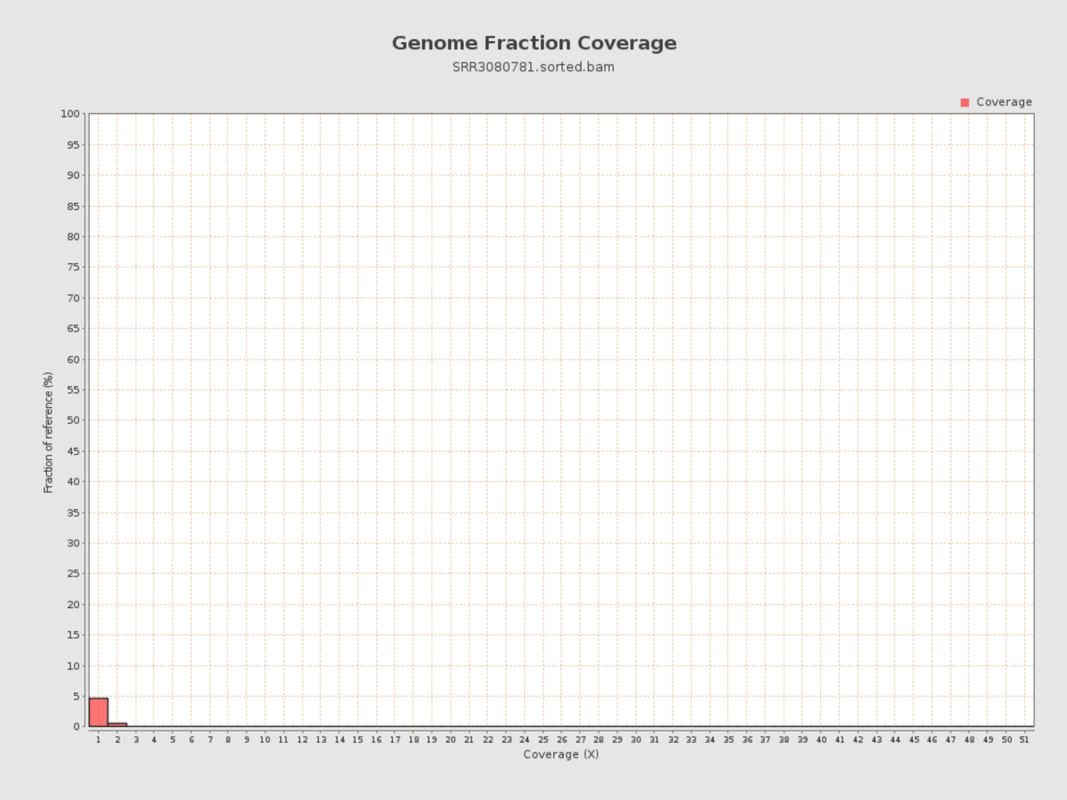
4. Results : Coverage Histogram



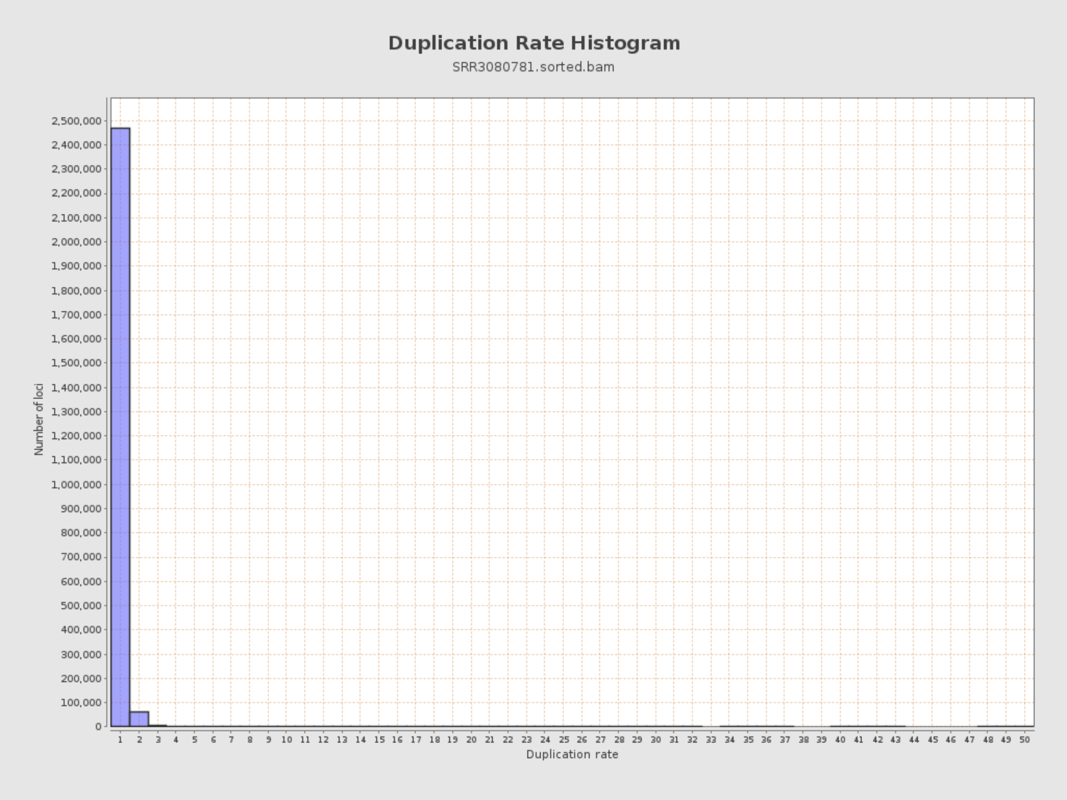
5. Results : Coverage Histogram (0-50X)



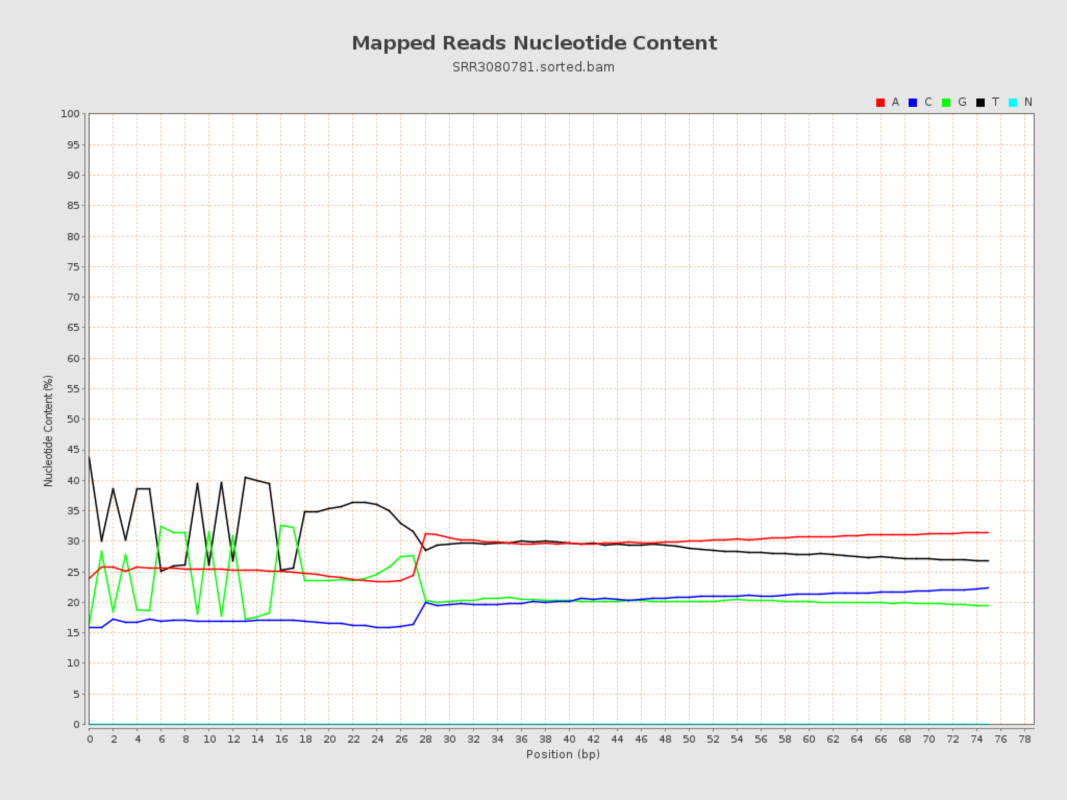
6. Results : Genome Fraction Coverage



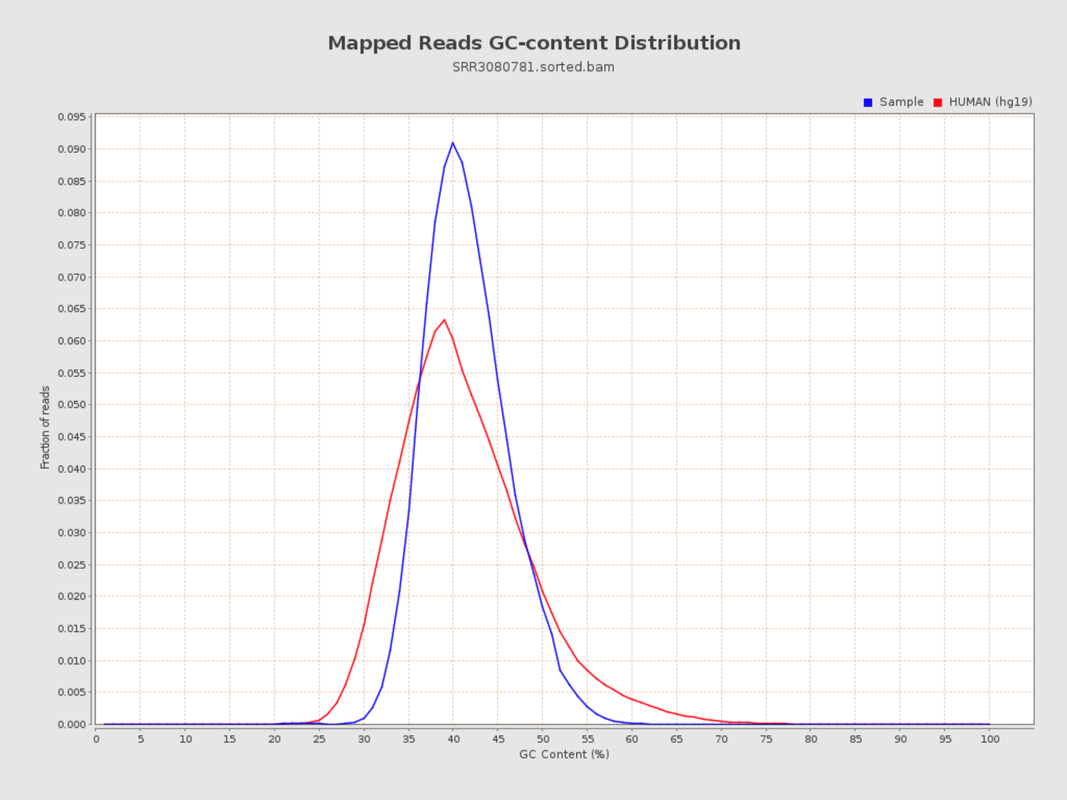
7. Results : Duplication Rate Histogram



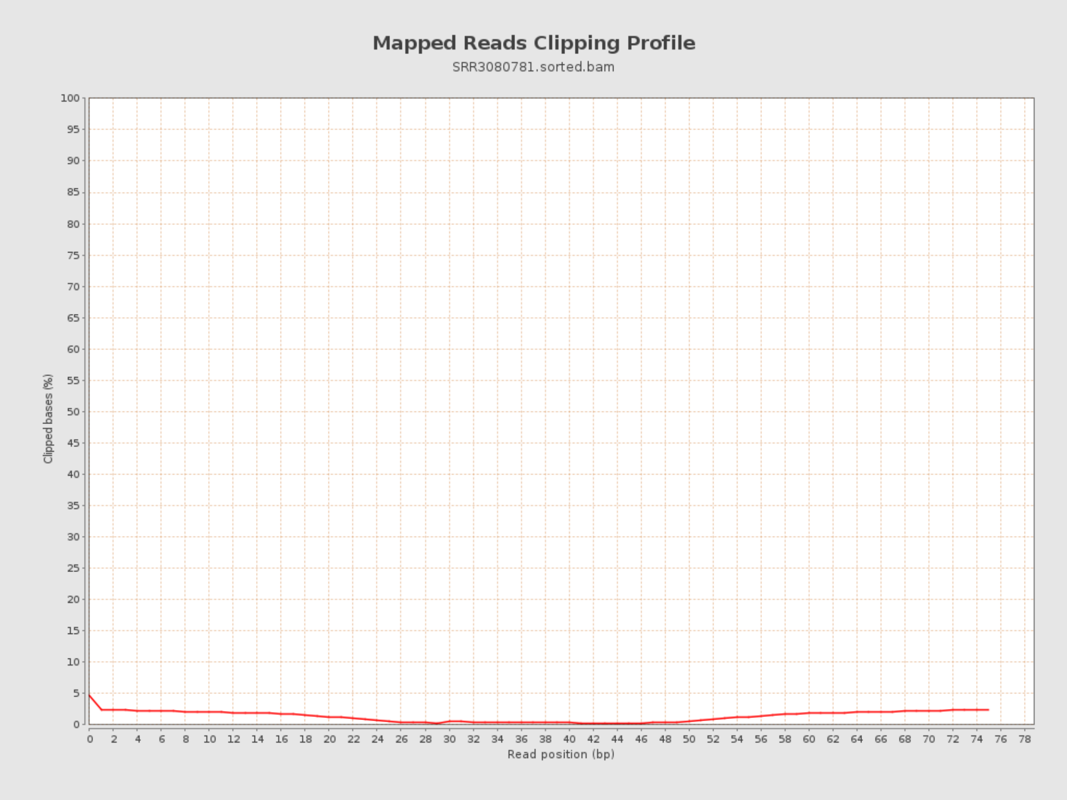
8. Results : Mapped Reads Nucleotide Content



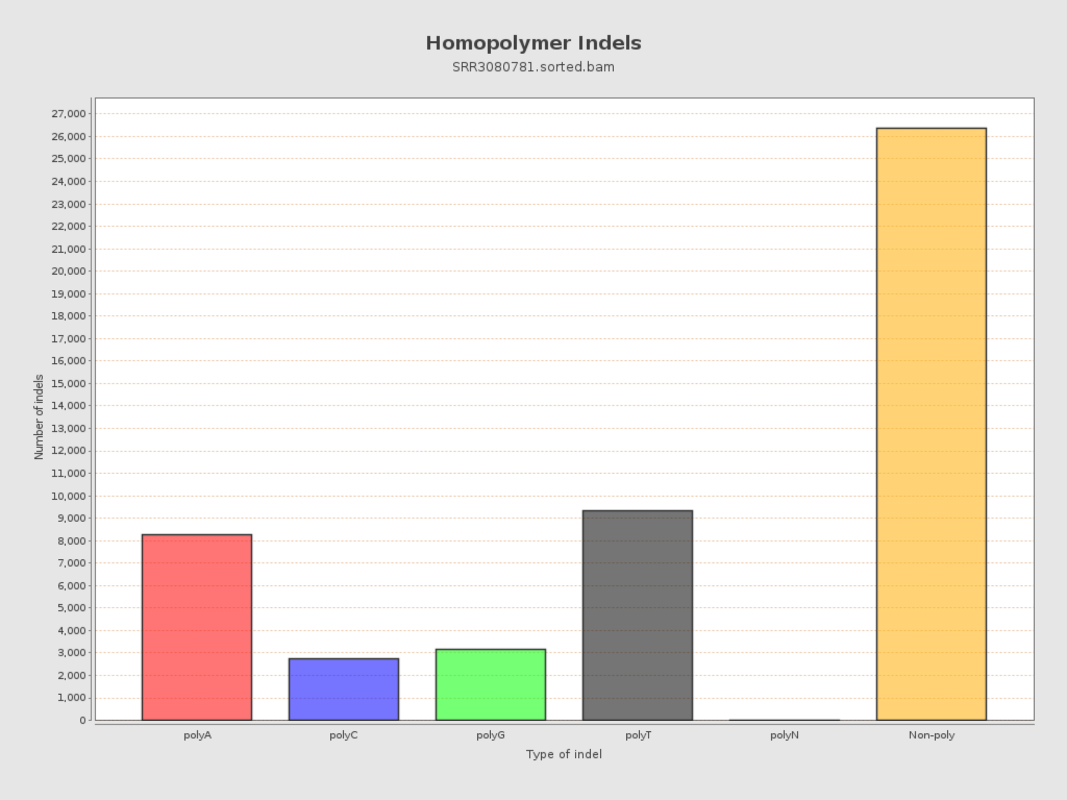
9. Results : Mapped Reads GC-content Distribution



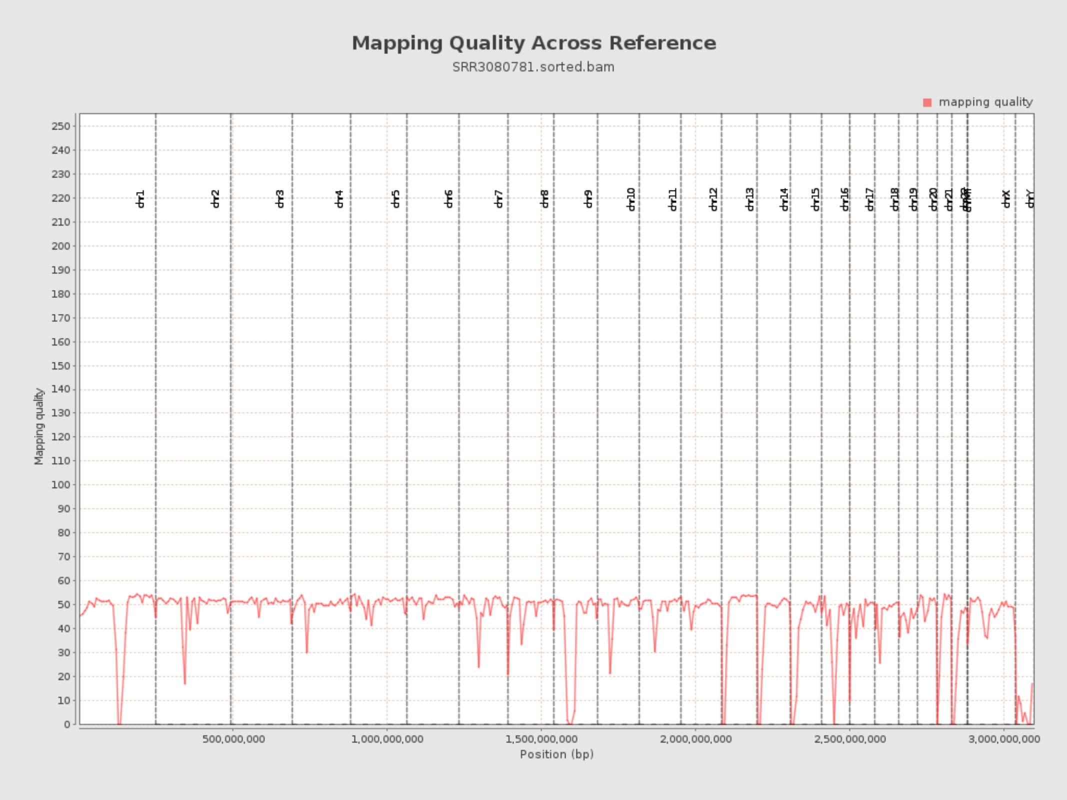
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram