Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:15:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081167.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_SRR3081167 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081167.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:15:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081167.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,524,152
Mapped reads	2,245,749 / 88.97%
Unmapped reads	278,403 / 11.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,973 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	95,330 / 3.78%
Duplication rate	3.44%
Clipped reads	1,023,655 / 40.55%

2.2. ACGT Content

Number/percentage of A's	41,731,547 / 27.87%
Number/percentage of C's	27,495,239 / 18.36%
Number/percentage of T's	47,292,522 / 31.59%
Number/percentage of G's	33,166,368 / 22.15%
Number/percentage of N's	44,362 / 0.03%
GC Percentage	40.51%

2.3. Coverage

Mean	0.0484

Standard Deviation	0.3617

2.4. Mapping Quality

Mean Mapping Quality	46.52

2.5. Mismatches and indels

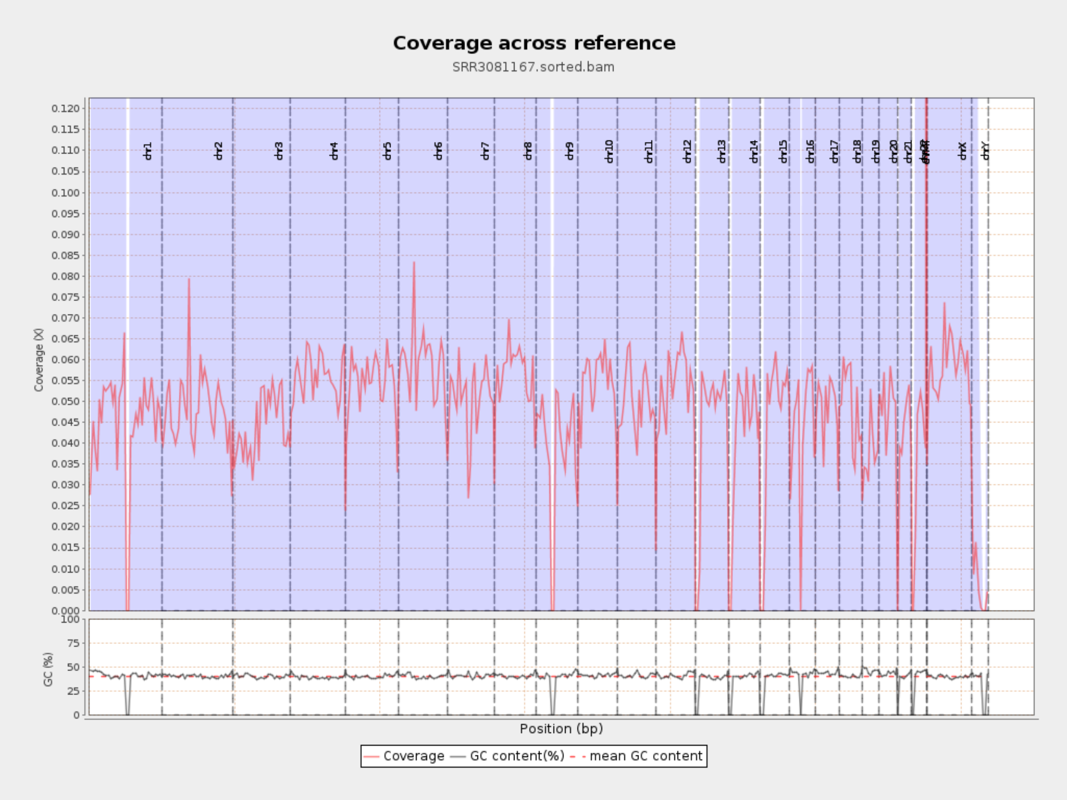
General error rate	0.84%
Mismatches	1,235,217
Insertions	11,507
Mapped reads with at least one insertion	0.51%
Deletions	33,511
Mapped reads with at least one deletion	1.48%
Homopolymer indels	46.95%

2.6. Chromosome stats

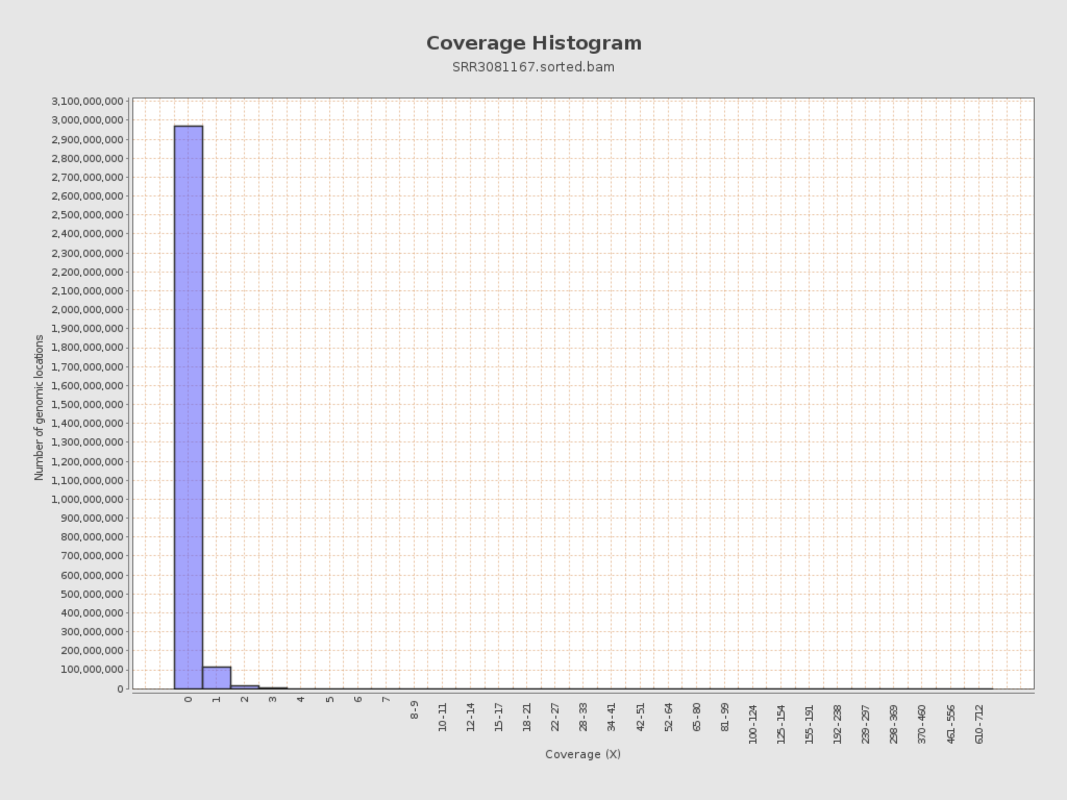
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11137013	0.0447	0.5222
chr2	243199373	11788760	0.0485	0.482
chr3	198022430	8715471	0.044	0.2361
chr4	191154276	10710501	0.056	0.274
chr5	180915260	9909108	0.0548	0.2641
chr6	171115067	10133932	0.0592	0.3819
chr7	159138663	8121807	0.051	0.413

chr8	146364022	8314687	0.0568	0.4871
chr9	141213431	5484715	0.0388	0.338
chr10	135534747	7459532	0.055	0.3321
chr11	135006516	6724992	0.0498	0.3603
chr12	133851895	7266541	0.0543	0.266
chr13	115169878	5018049	0.0436	0.2349
chr14	107349540	4434393	0.0413	0.2423
chr15	102531392	4521096	0.0441	0.2431
chr16	90354753	3966625	0.0439	0.2593
chr17	81195210	3905847	0.0481	0.2752
chr18	78077248	3846394	0.0493	0.6454
chr19	59128983	2257347	0.0382	0.4163
chr20	63025520	3057872	0.0485	0.2517
chr21	48129895	1944055	0.0404	0.2433
chr22	51304566	1674331	0.0326	0.2019
chrMT	16571	21797	1.3154	1.4146
chrX	155270560	9010278	0.058	0.2998
chrY	59373566	358843	0.006	0.1133

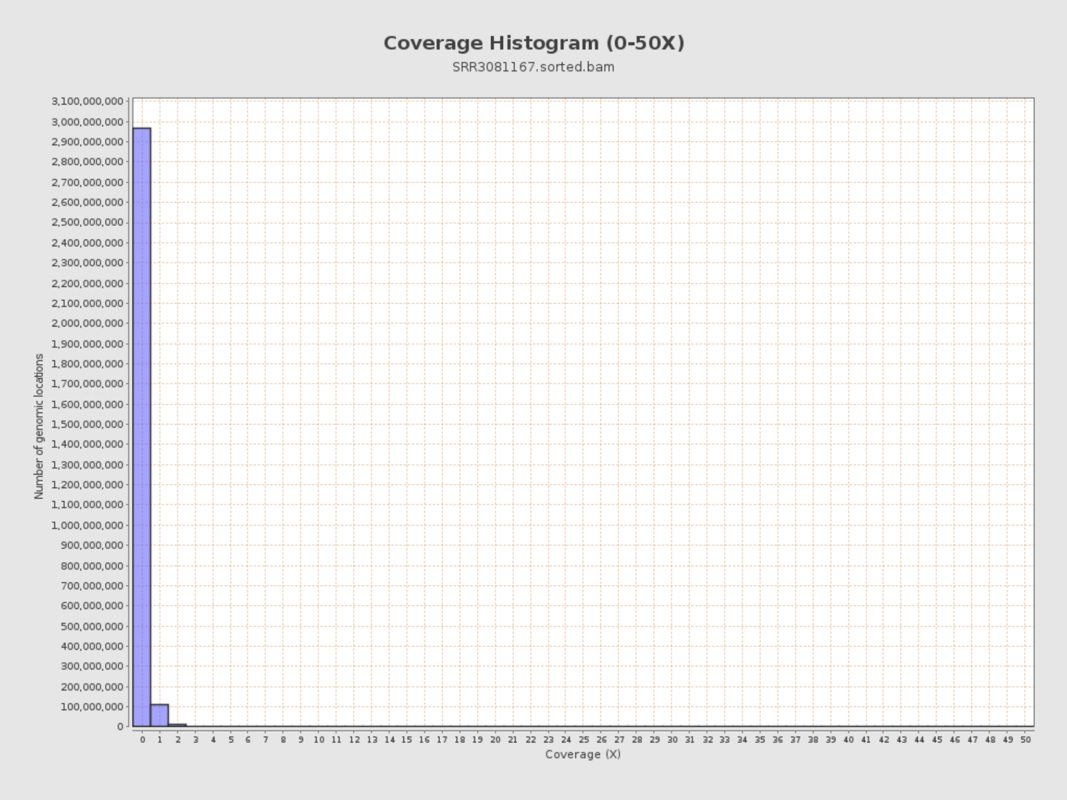
3. Results : Coverage across reference



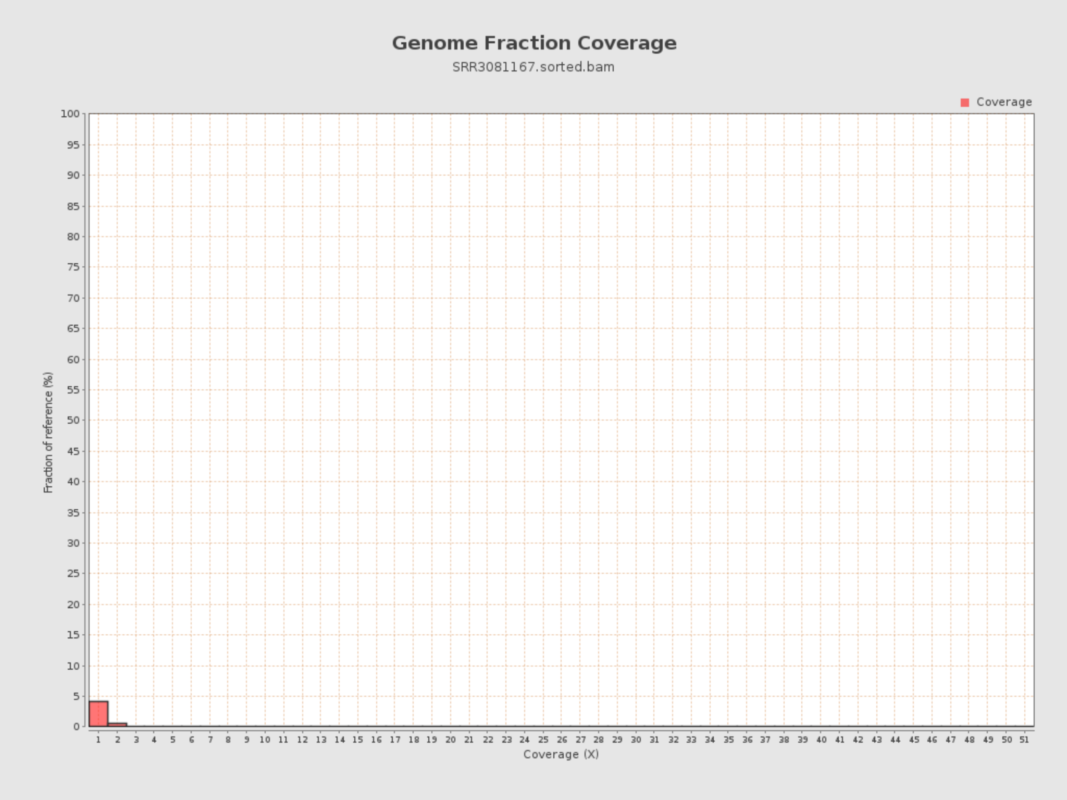
4. Results : Coverage Histogram



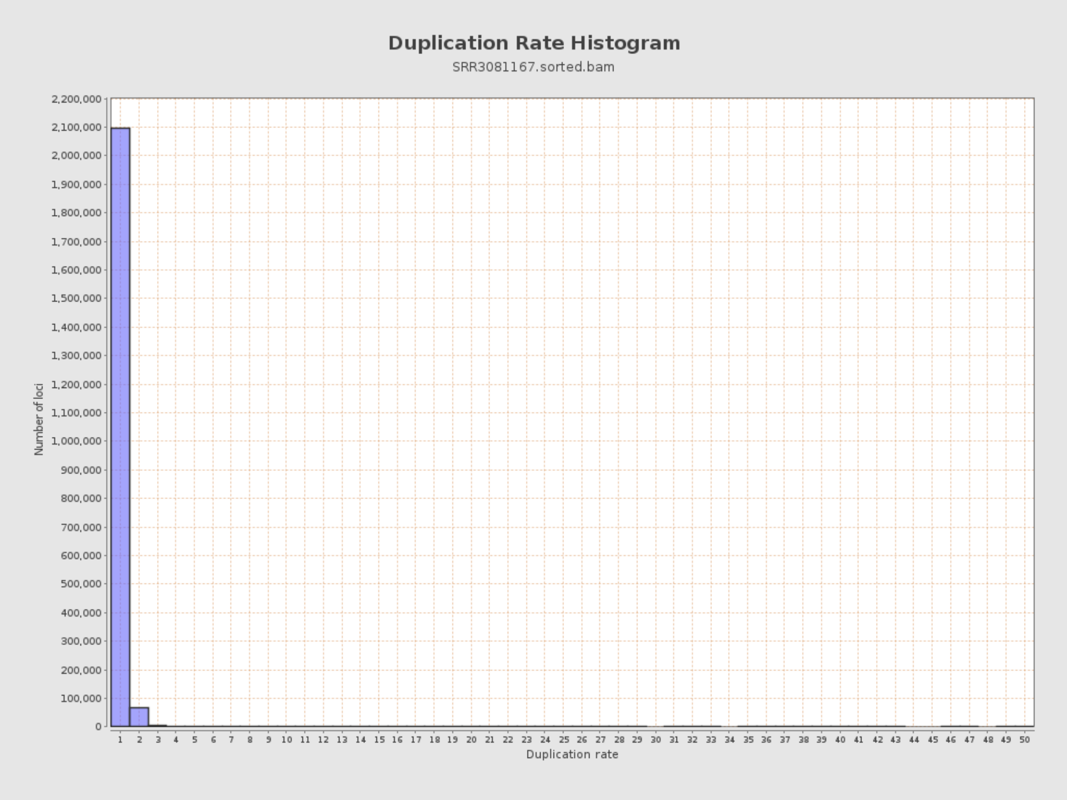
5. Results : Coverage Histogram (0-50X)



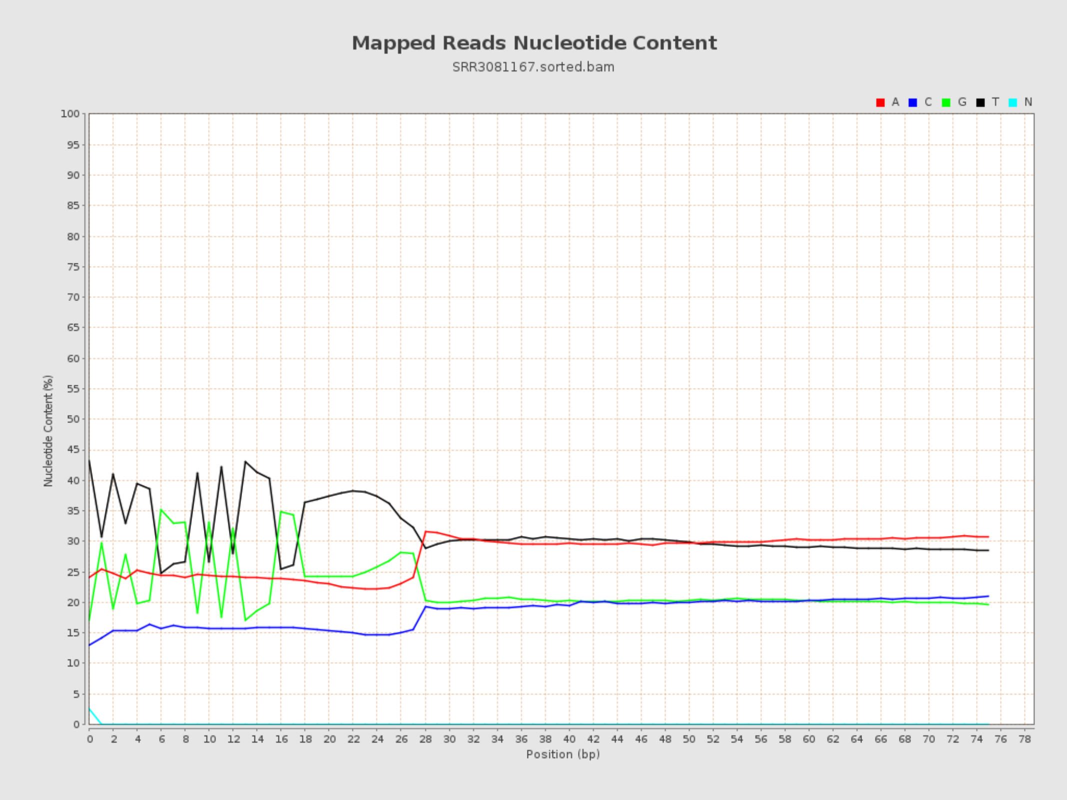
6. Results : Genome Fraction Coverage



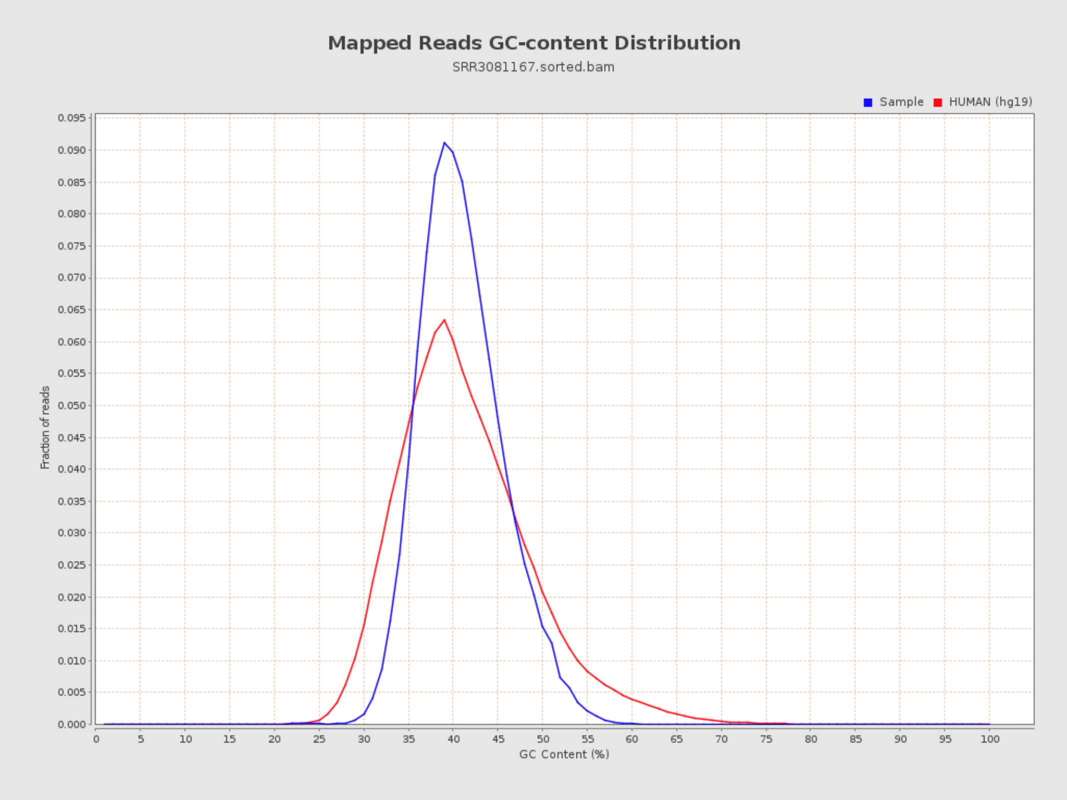
7. Results : Duplication Rate Histogram



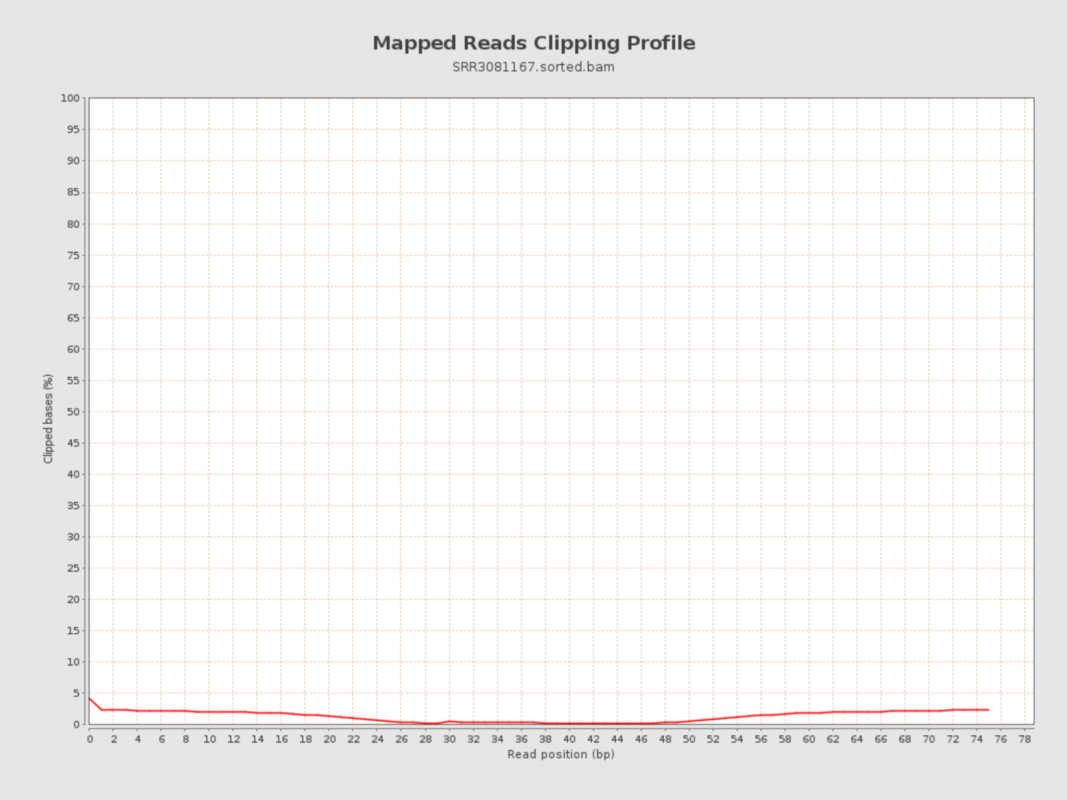
8. Results : Mapped Reads Nucleotide Content



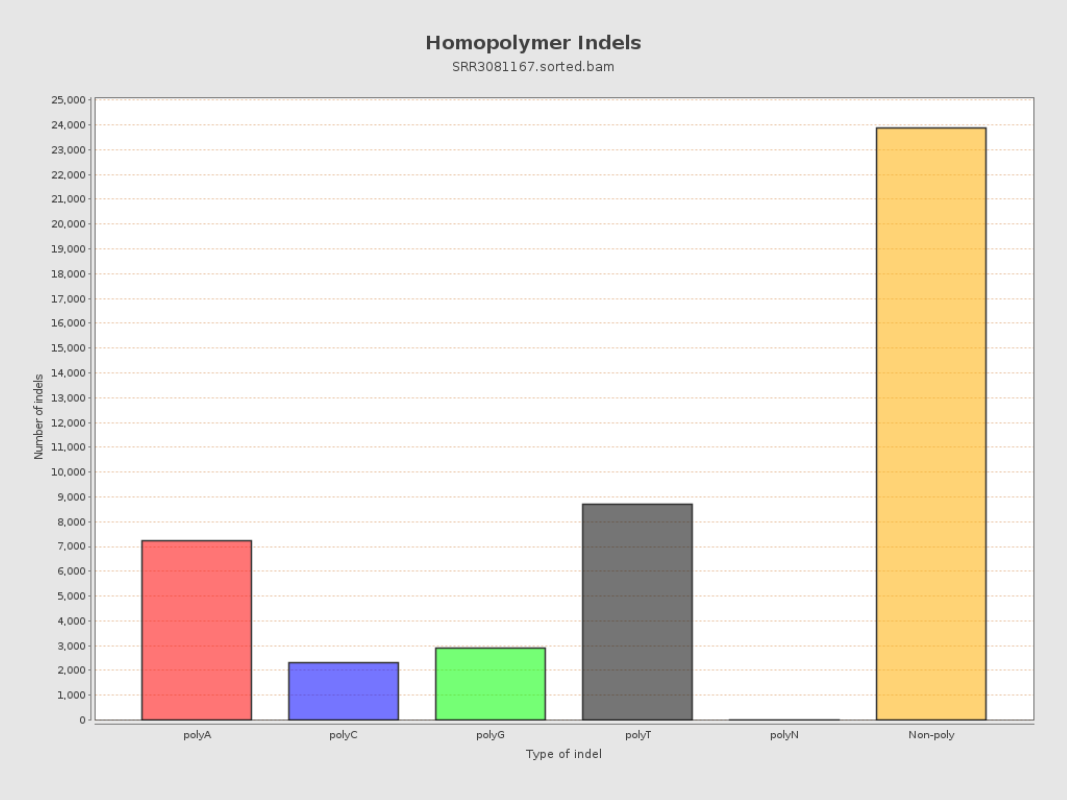
9. Results : Mapped Reads GC-content Distribution



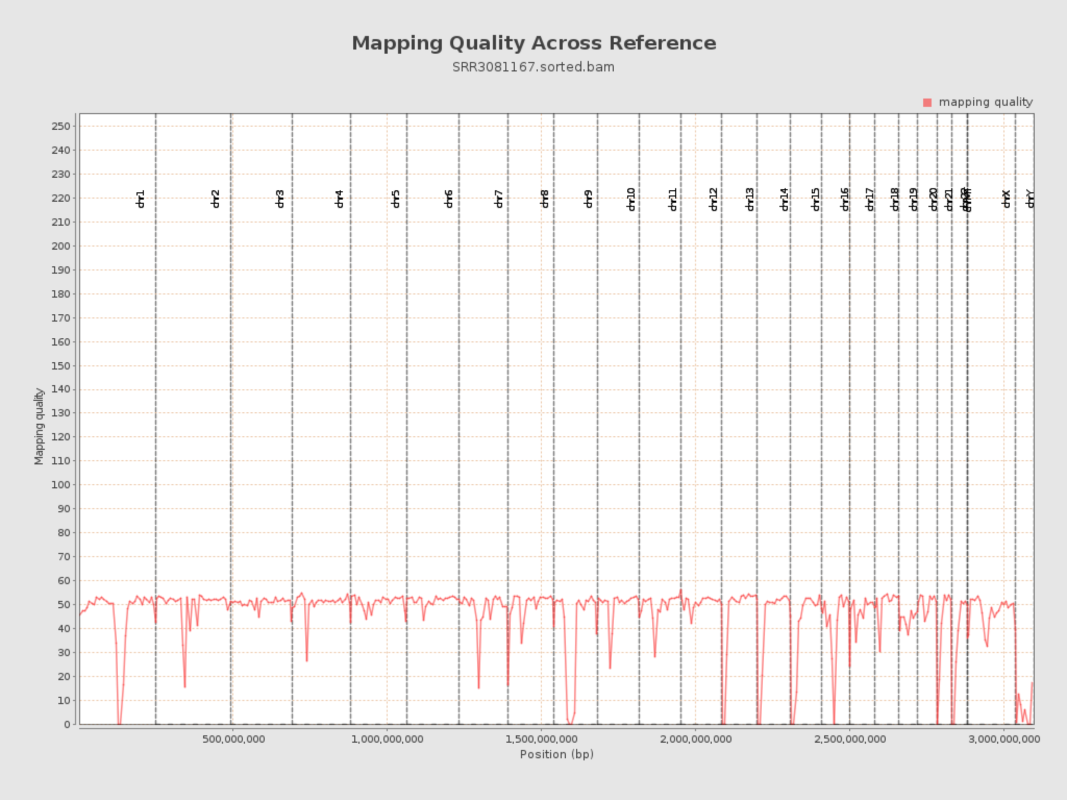
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram