Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:27:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081252.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_SRR3081252 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081252.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:27:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081252.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,932,470
Mapped reads	2,408,032 / 82.12%
Unmapped reads	524,438 / 17.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,436 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	104,550 / 3.57%
Duplication rate	3.45%
Clipped reads	1,010,633 / 34.46%

2.2. ACGT Content

Number/percentage of A's	44,944,482 / 27.79%
Number/percentage of C's	29,217,096 / 18.07%
Number/percentage of T's	52,095,181 / 32.21%
Number/percentage of G's	35,416,452 / 21.9%
Number/percentage of N's	41,844 / 0.03%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0523

Standard Deviation	0.4284

2.4. Mapping Quality

Mean Mapping Quality	46.85

2.5. Mismatches and indels

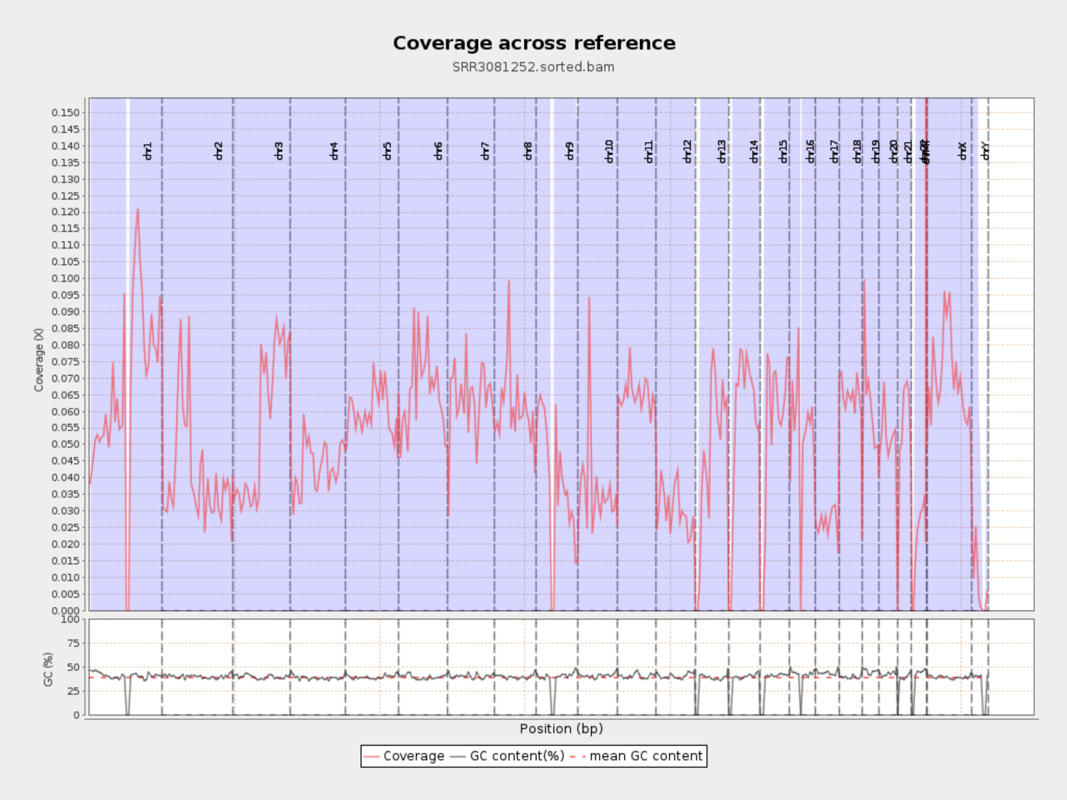
General error rate	0.86%
Mismatches	1,372,351
Insertions	12,850
Mapped reads with at least one insertion	0.53%
Deletions	41,253
Mapped reads with at least one deletion	1.69%
Homopolymer indels	49.71%

2.6. Chromosome stats

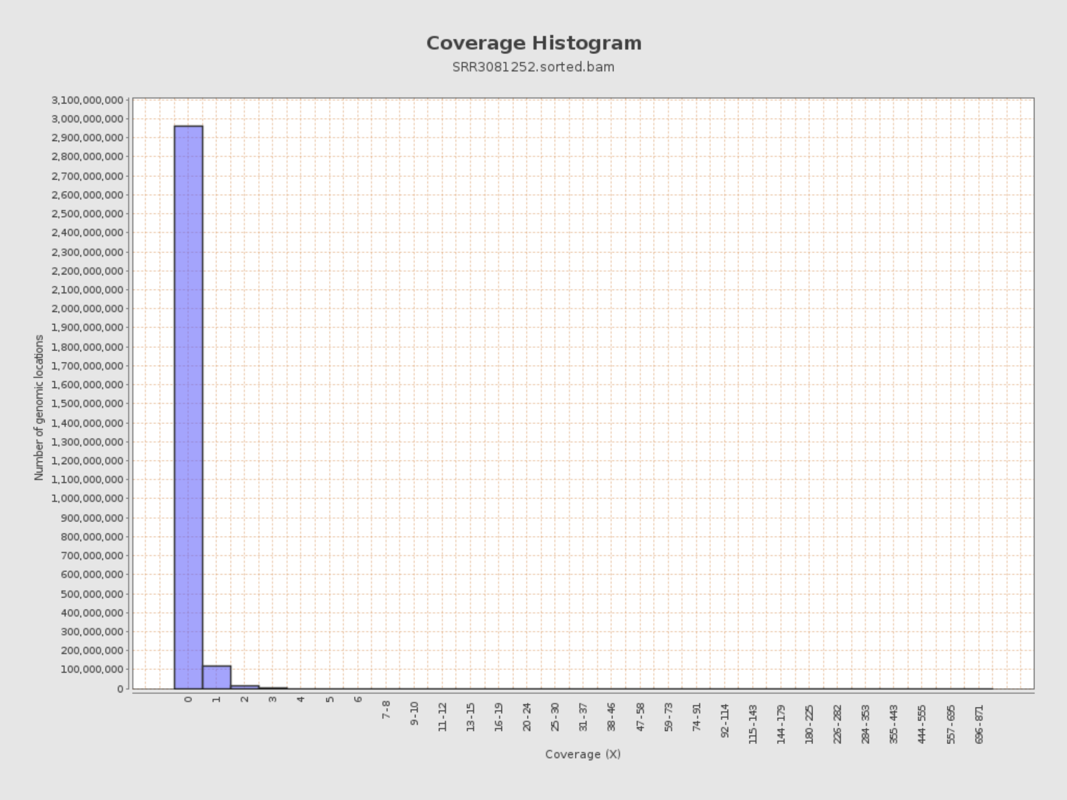
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16819747	0.0675	0.8122
chr2	243199373	10059824	0.0414	0.4438
chr3	198022430	11067249	0.0559	0.282
chr4	191154276	8270714	0.0433	0.2575
chr5	180915260	10883570	0.0602	0.2814
chr6	171115067	11332788	0.0662	0.3571
chr7	159138663	10263143	0.0645	0.4811

chr8	146364022	8968246	0.0613	0.6274
chr9	141213431	5448895	0.0386	0.3556
chr10	135534747	4987206	0.0368	0.5324
chr11	135006516	8697632	0.0644	0.4218
chr12	133851895	4015284	0.03	0.2037
chr13	115169878	5380114	0.0467	0.2444
chr14	107349540	6121036	0.057	0.2793
chr15	102531392	5481964	0.0535	0.2624
chr16	90354753	4836734	0.0535	0.2968
chr17	81195210	2132316	0.0263	0.227
chr18	78077248	5089719	0.0652	0.5744
chr19	59128983	3651302	0.0618	0.594
chr20	63025520	3311049	0.0525	0.2673
chr21	48129895	2536694	0.0527	0.2799
chr22	51304566	1076817	0.021	0.1623
chrMT	16571	44202	2.6674	2.1083
chrX	155270560	10851677	0.0699	0.3374
chrY	59373566	456075	0.0077	0.168

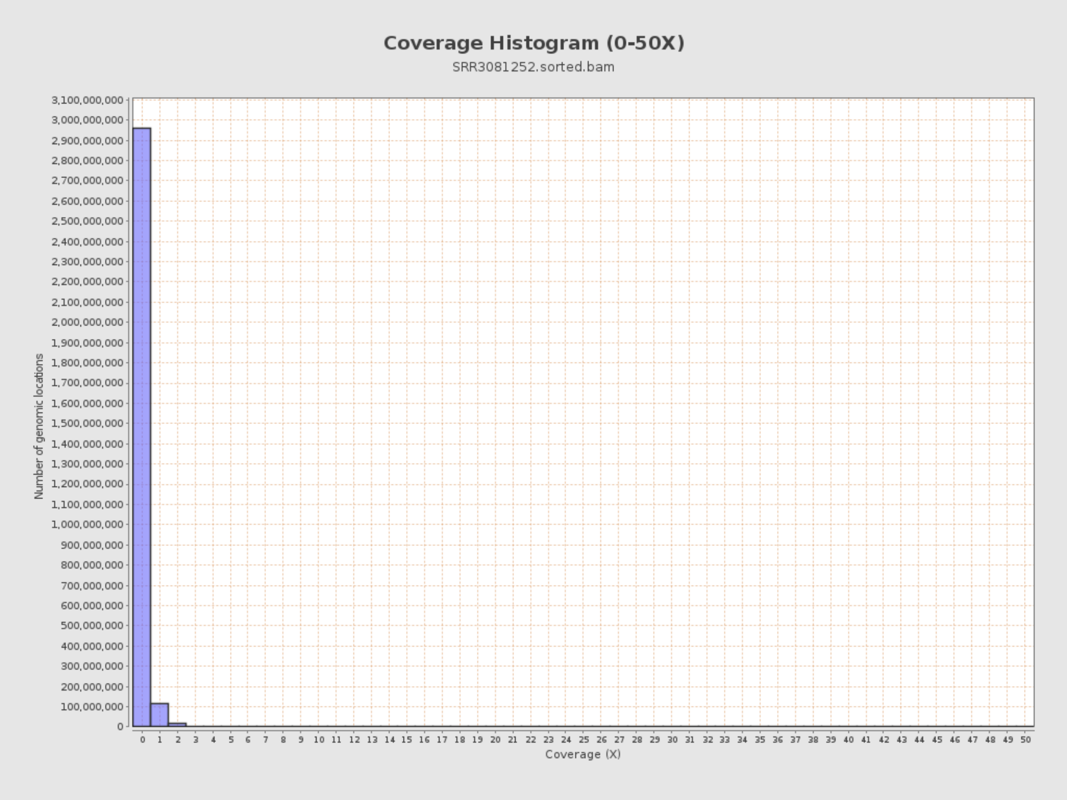
3. Results : Coverage across reference



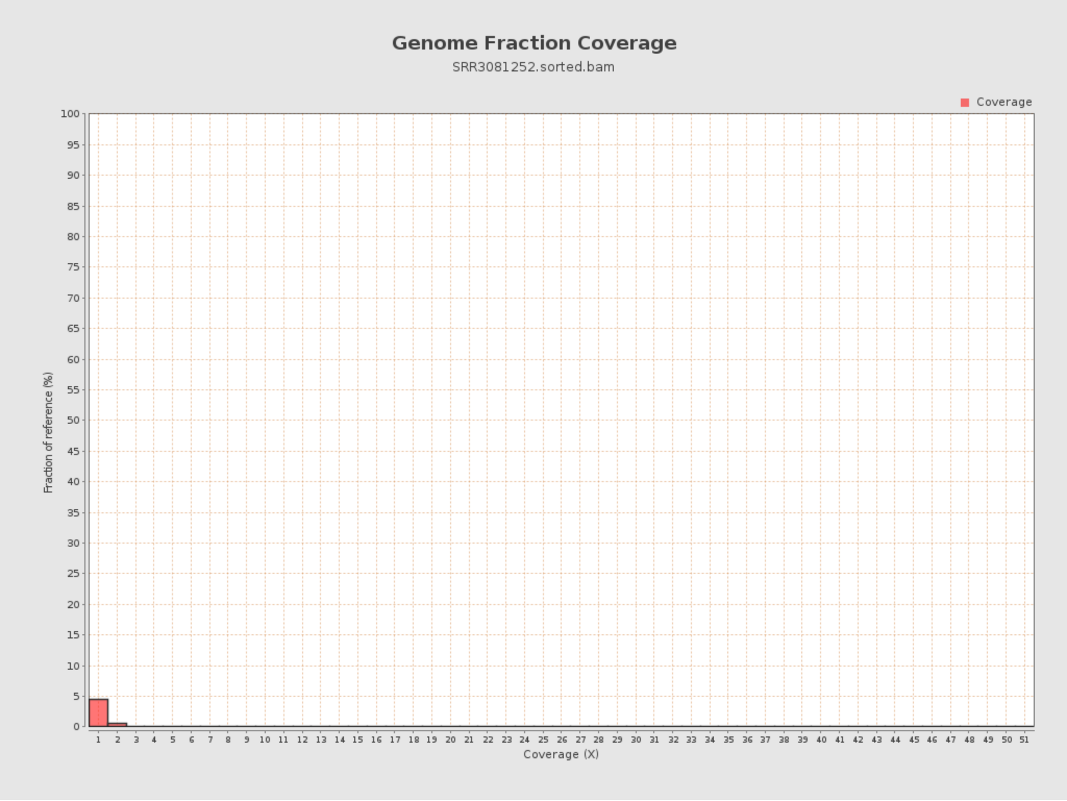
4. Results : Coverage Histogram



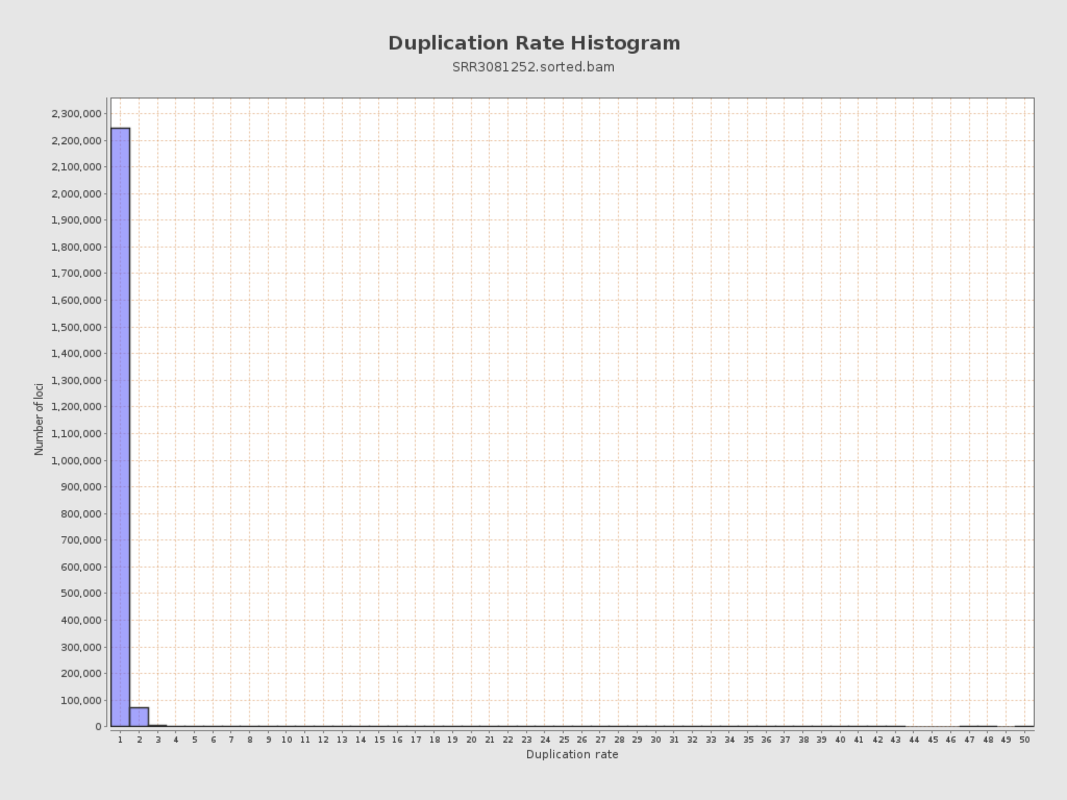
5. Results : Coverage Histogram (0-50X)



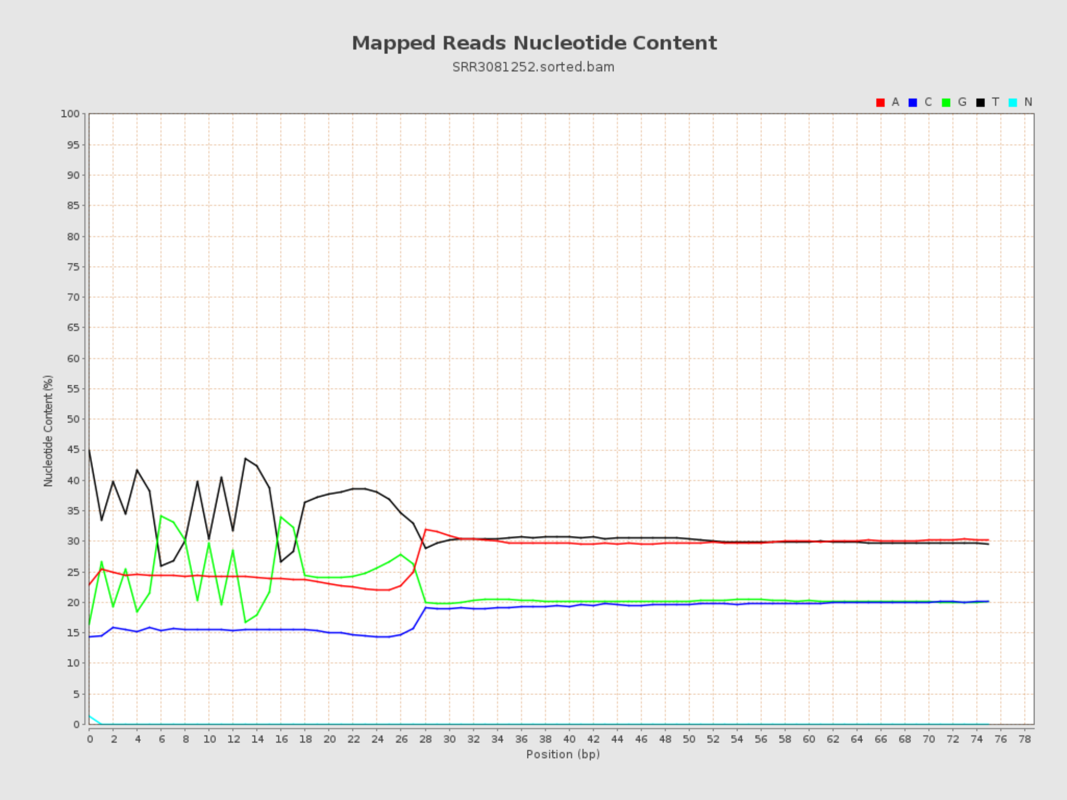
6. Results : Genome Fraction Coverage



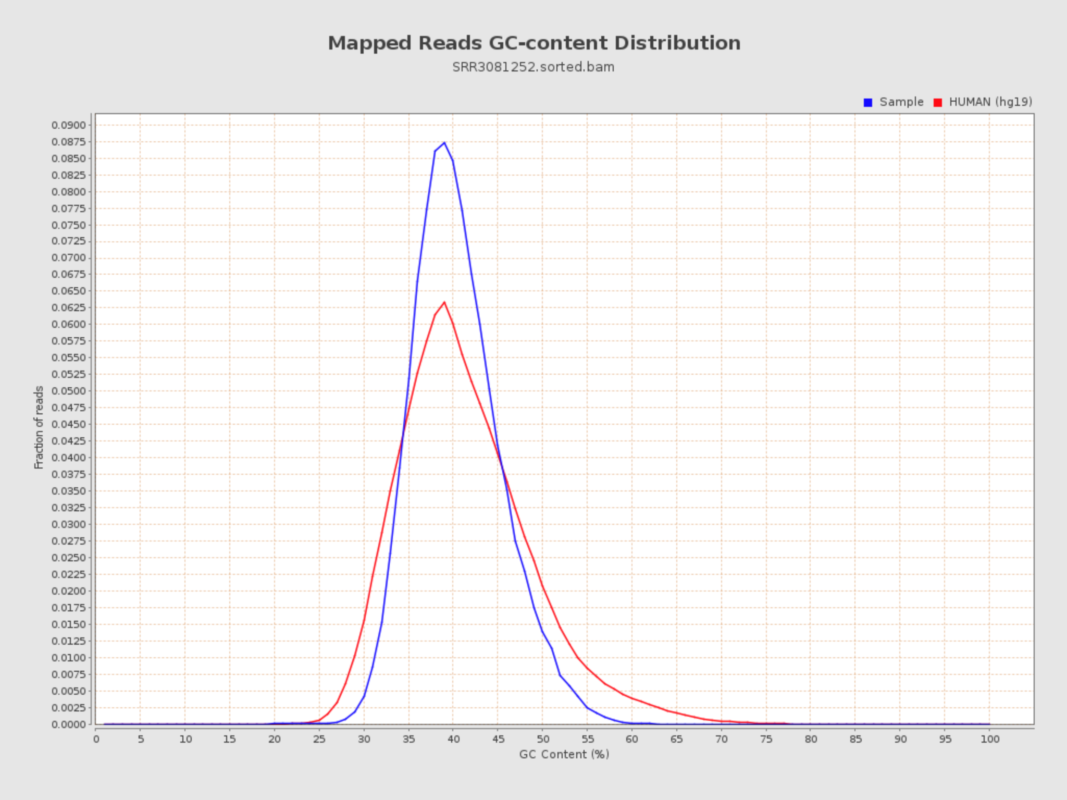
7. Results : Duplication Rate Histogram



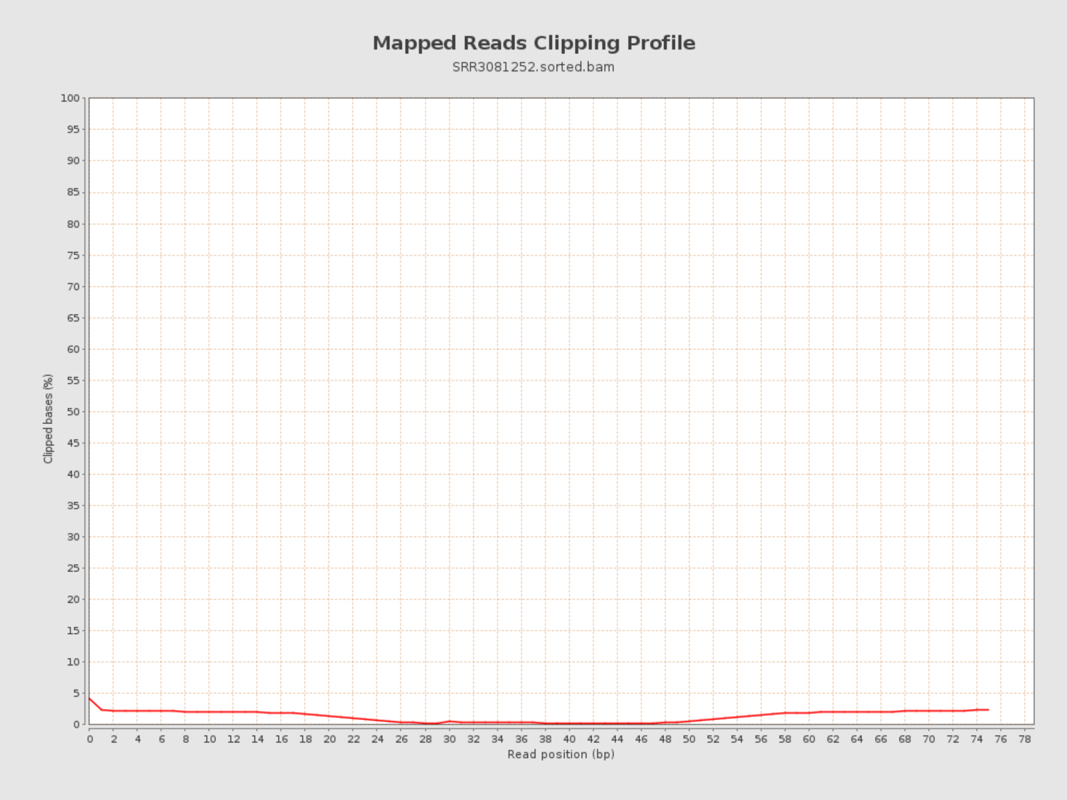
8. Results : Mapped Reads Nucleotide Content



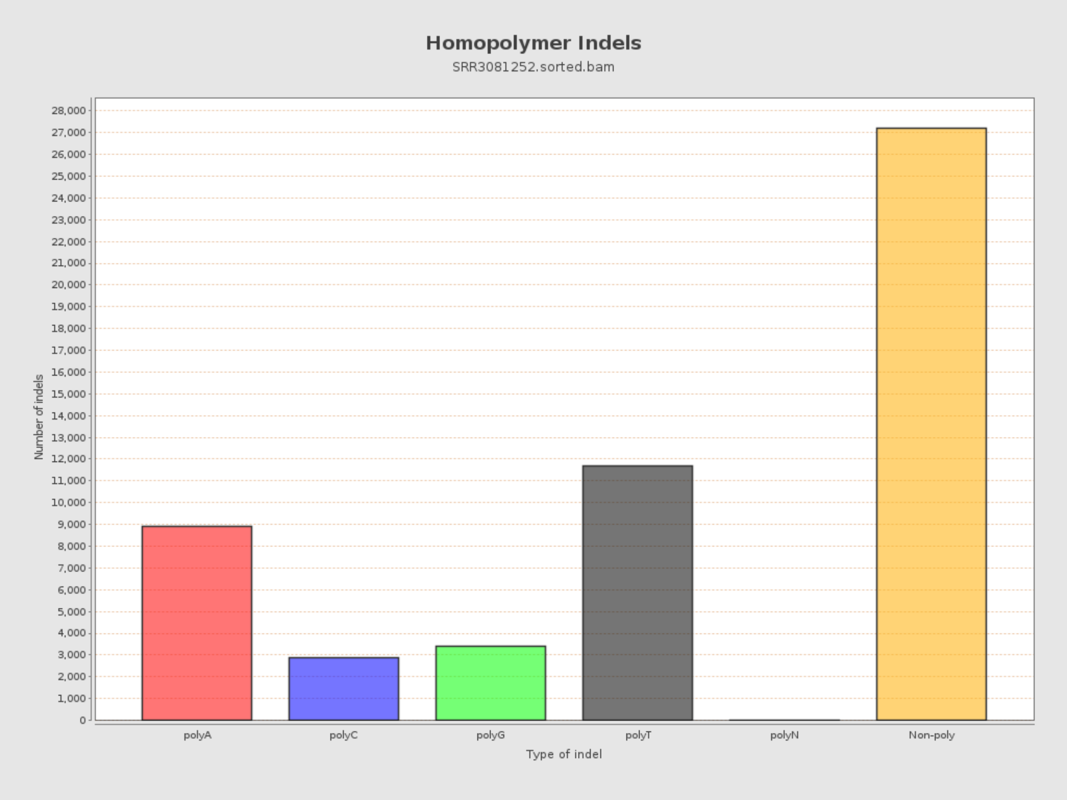
9. Results : Mapped Reads GC-content Distribution



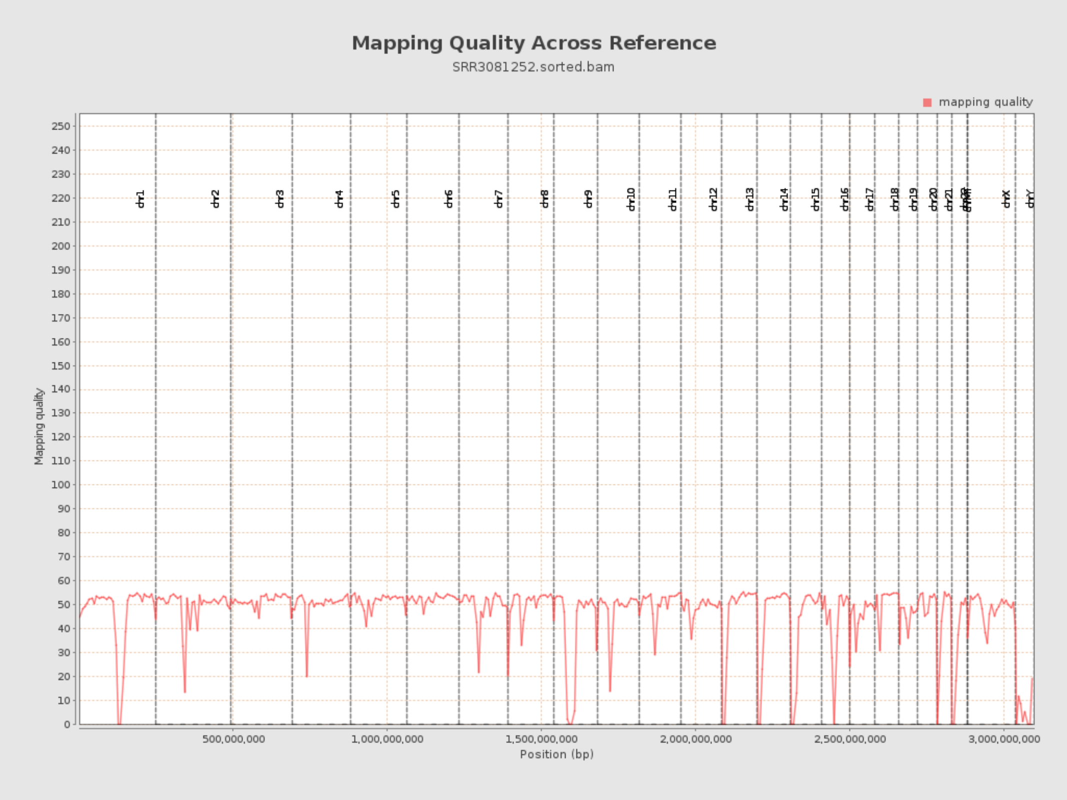
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram