Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 10:20:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472841.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_SRR3472841 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472841.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 10:20:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472841.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,840,474
Mapped reads	2,362,010 / 83.16%
Unmapped reads	478,464 / 16.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,041 / 0.71%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	74,343 / 2.62%
Duplication rate	2.41%
Clipped reads	1,253,662 / 44.14%

2.2. ACGT Content

Number/percentage of A's	41,333,122 / 27.15%
Number/percentage of C's	29,811,815 / 19.59%
Number/percentage of T's	45,577,787 / 29.94%
Number/percentage of G's	35,489,972 / 23.32%
Number/percentage of N's	3,860 / 0%
GC Percentage	42.9%

2.3. Coverage

Mean	0.0492

Standard Deviation	0.34

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Mismatches and indels

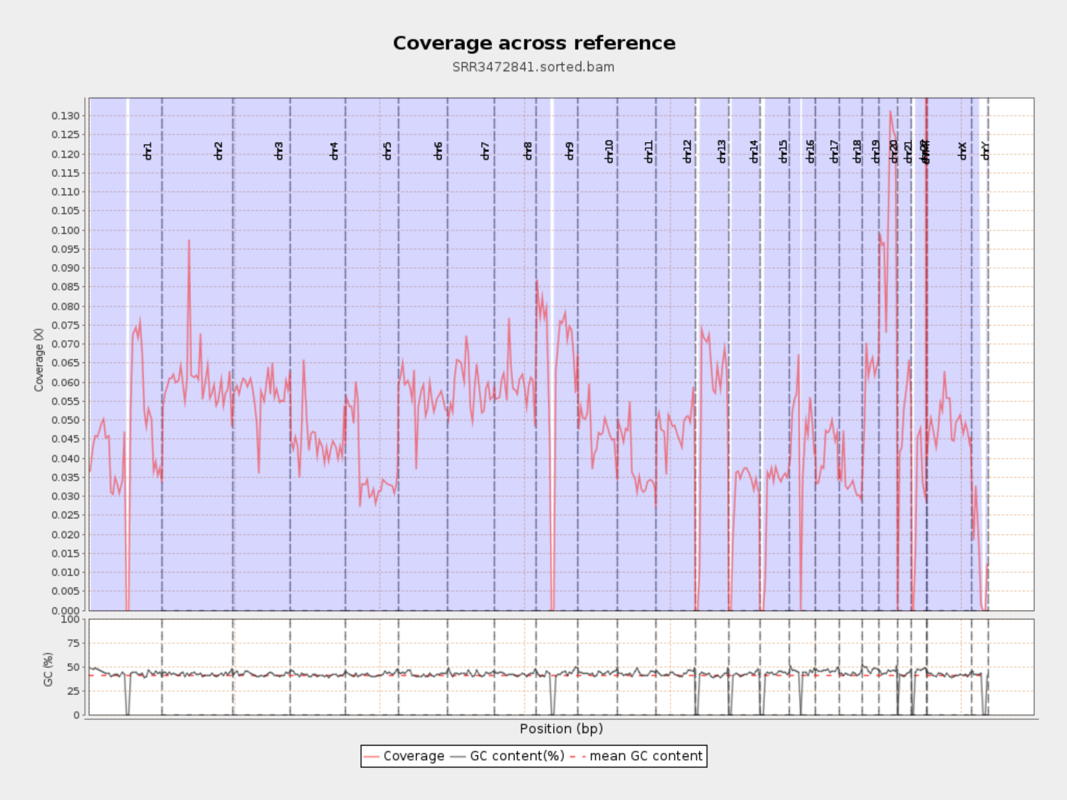
General error rate	0.83%
Mismatches	1,248,388
Insertions	11,993
Mapped reads with at least one insertion	0.5%
Deletions	34,549
Mapped reads with at least one deletion	1.45%
Homopolymer indels	46.17%

2.6. Chromosome stats

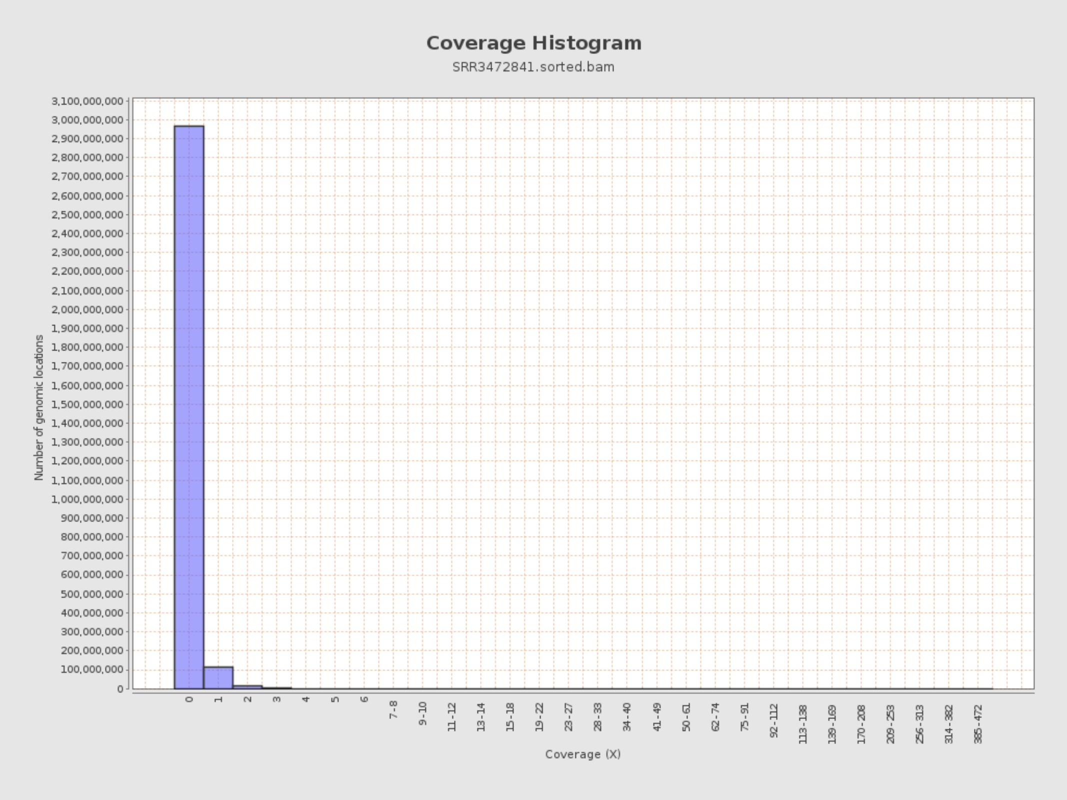
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11040780	0.0443	0.4145
chr2	243199373	14727229	0.0606	0.4925
chr3	198022430	11304373	0.0571	0.2678
chr4	191154276	8503260	0.0445	0.2628
chr5	180915260	6853022	0.0379	0.22
chr6	171115067	9638835	0.0563	0.2886
chr7	159138663	9377721	0.0589	0.441

chr8	146364022	8668950	0.0592	0.3569
chr9	141213431	9060921	0.0642	0.4101
chr10	135534747	6400562	0.0472	0.3029
chr11	135006516	5203226	0.0385	0.3318
chr12	133851895	6494302	0.0485	0.2544
chr13	115169878	6271653	0.0545	0.2702
chr14	107349540	3173173	0.0296	0.2289
chr15	102531392	2927282	0.0286	0.2055
chr16	90354753	4162088	0.0461	0.2701
chr17	81195210	3426782	0.0422	0.251
chr18	78077248	2640150	0.0338	0.6005
chr19	59128983	3628166	0.0614	0.373
chr20	63025520	6629152	0.1052	0.3928
chr21	48129895	2310817	0.048	0.2879
chr22	51304566	1392019	0.0271	0.1915
chrMT	16571	27522	1.6609	1.8141
chrX	155270560	7650825	0.0493	0.2775
chrY	59373566	765693	0.0129	0.1688

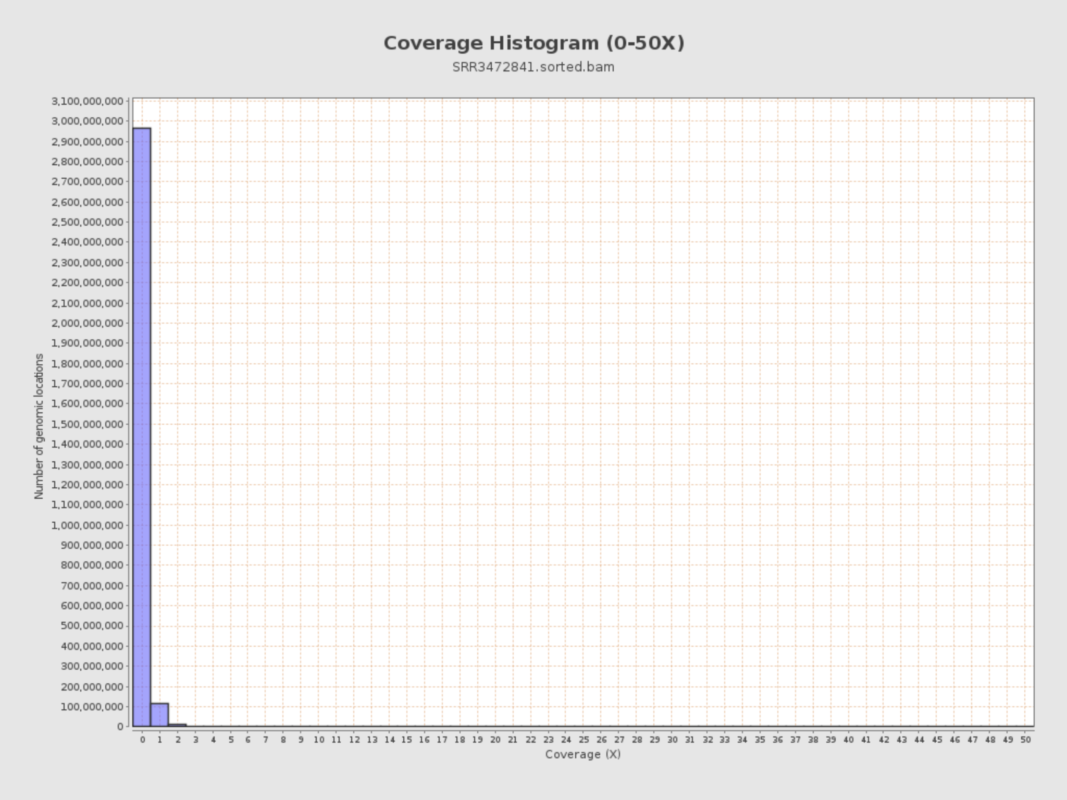
3. Results : Coverage across reference



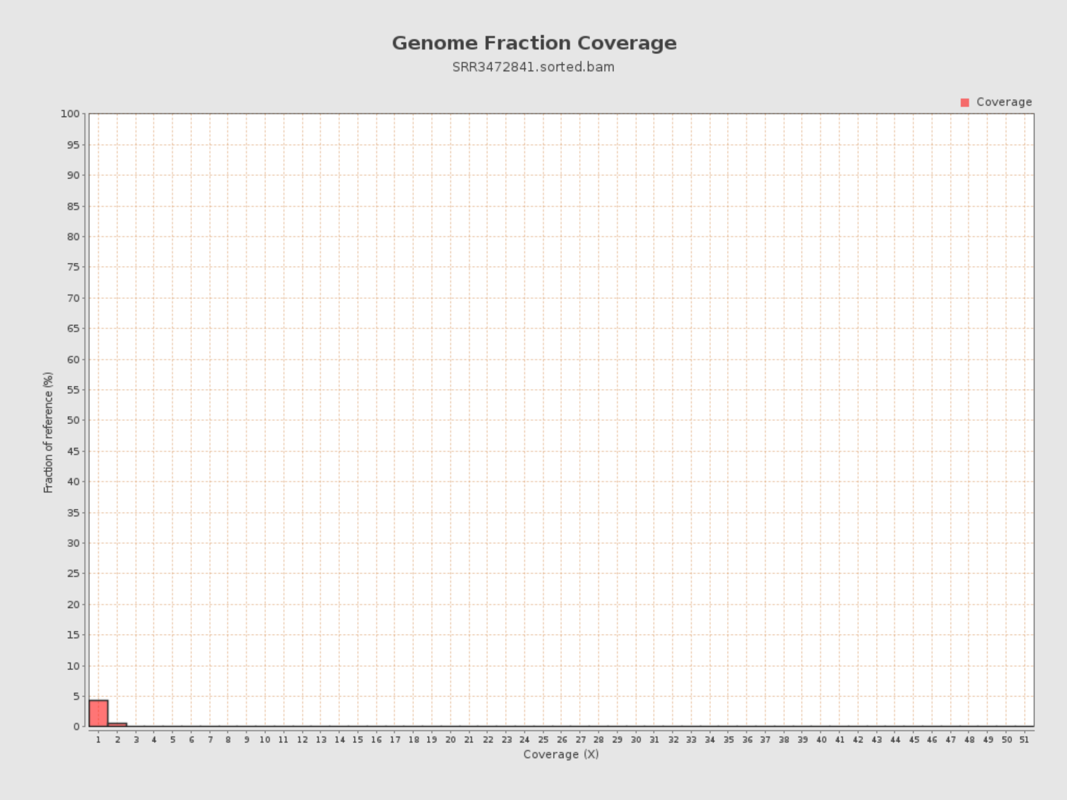
4. Results : Coverage Histogram



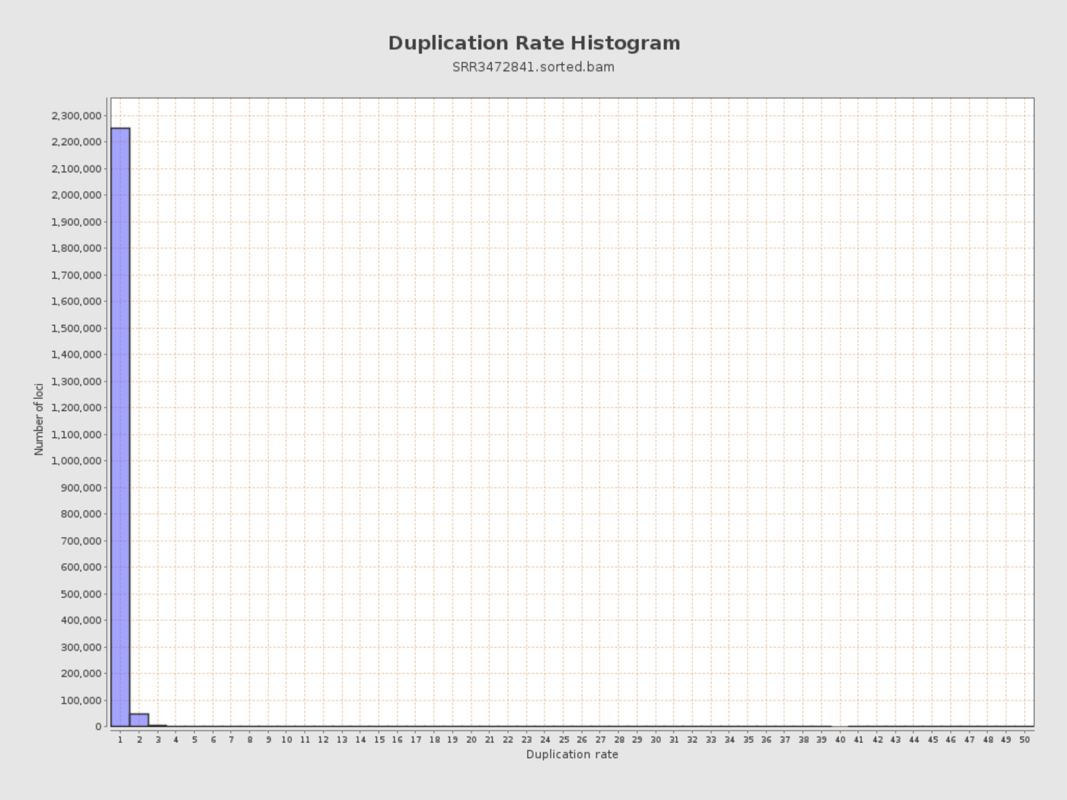
5. Results : Coverage Histogram (0-50X)



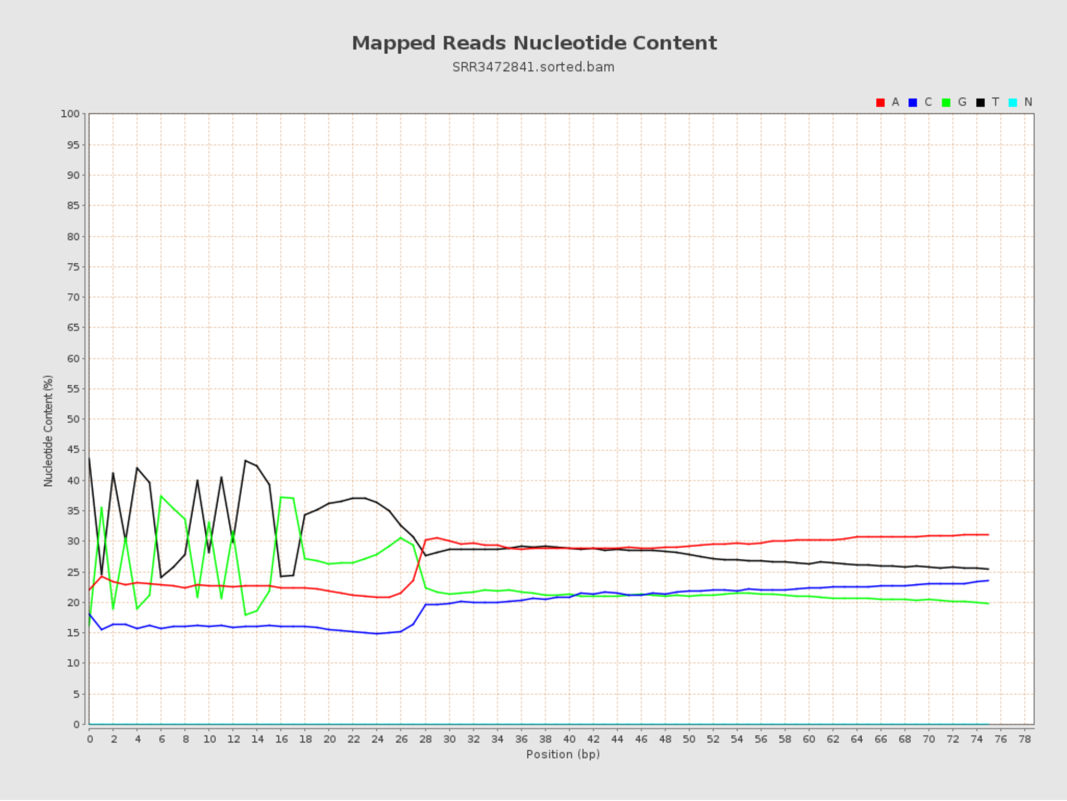
6. Results : Genome Fraction Coverage



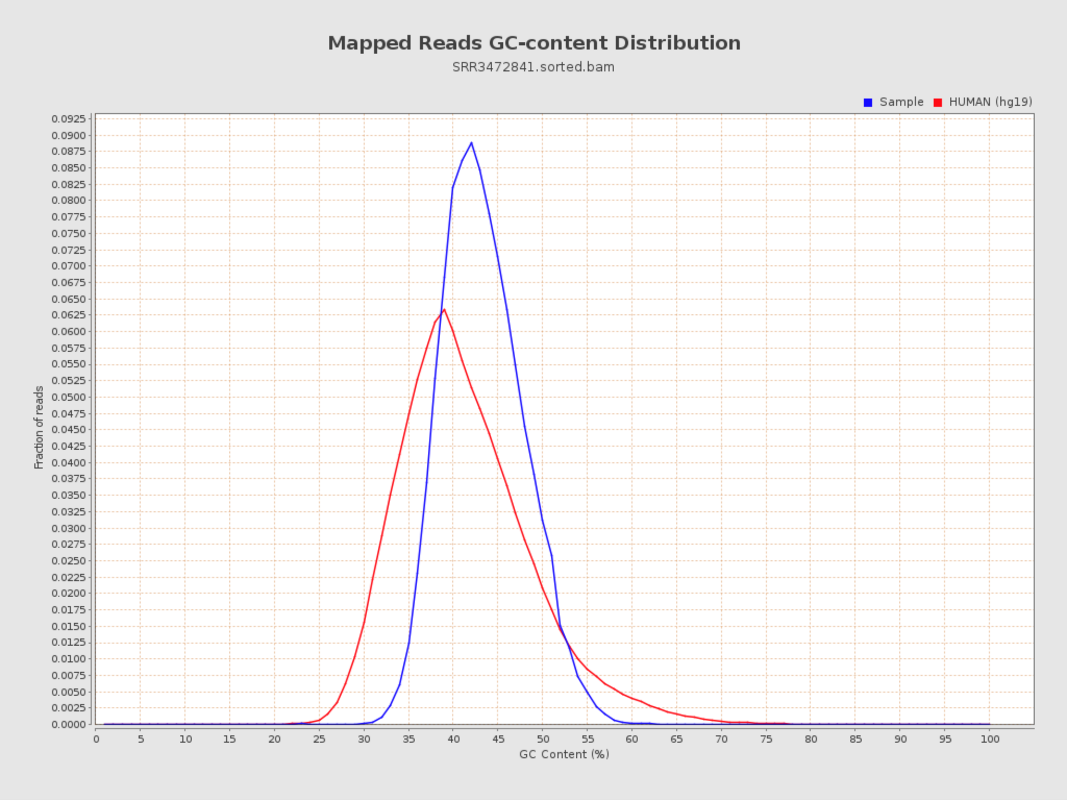
7. Results : Duplication Rate Histogram



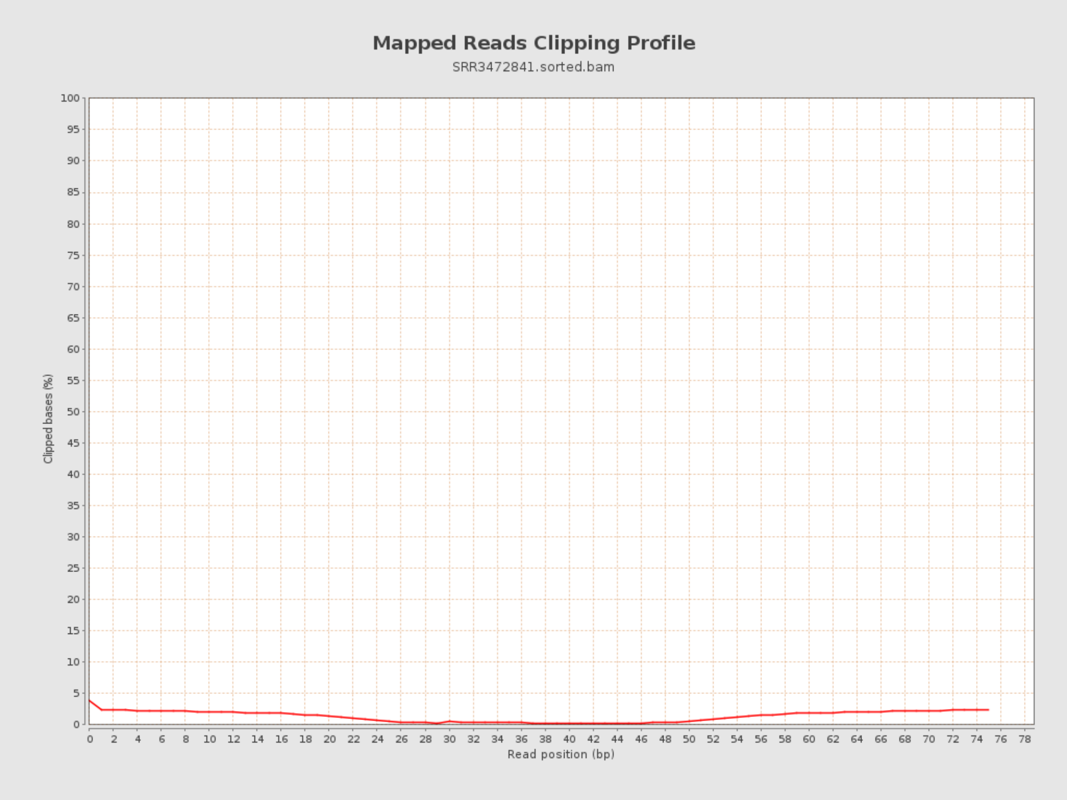
8. Results : Mapped Reads Nucleotide Content



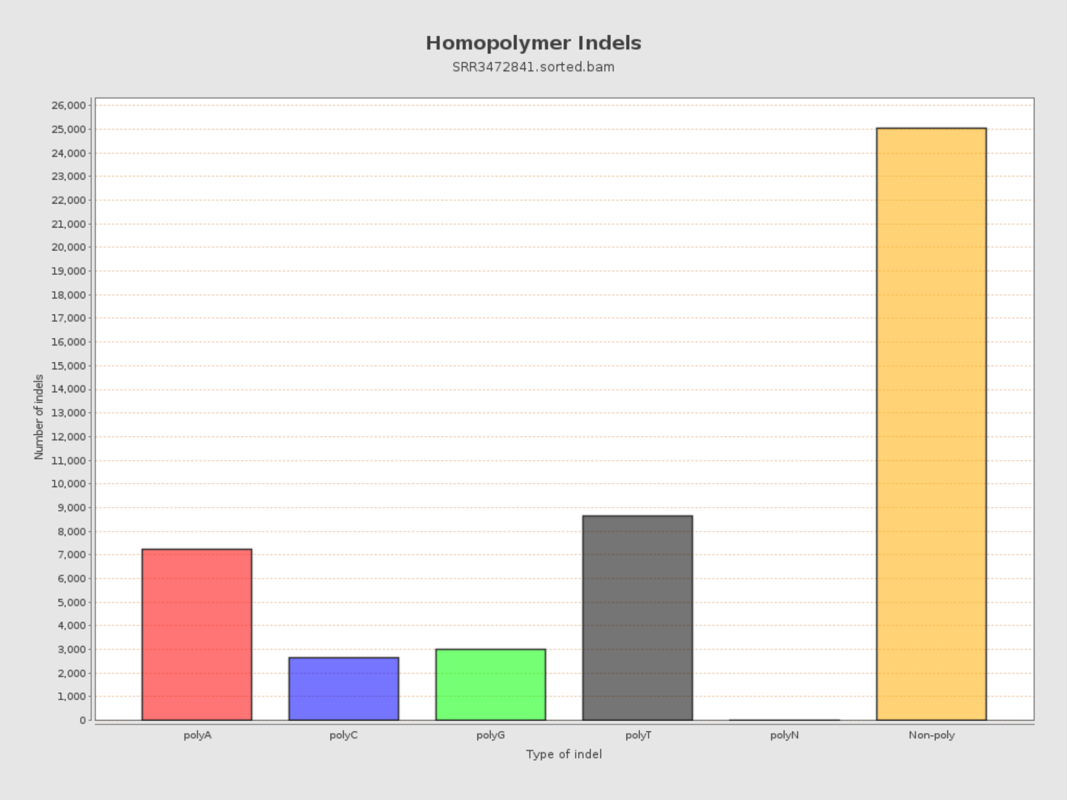
9. Results : Mapped Reads GC-content Distribution



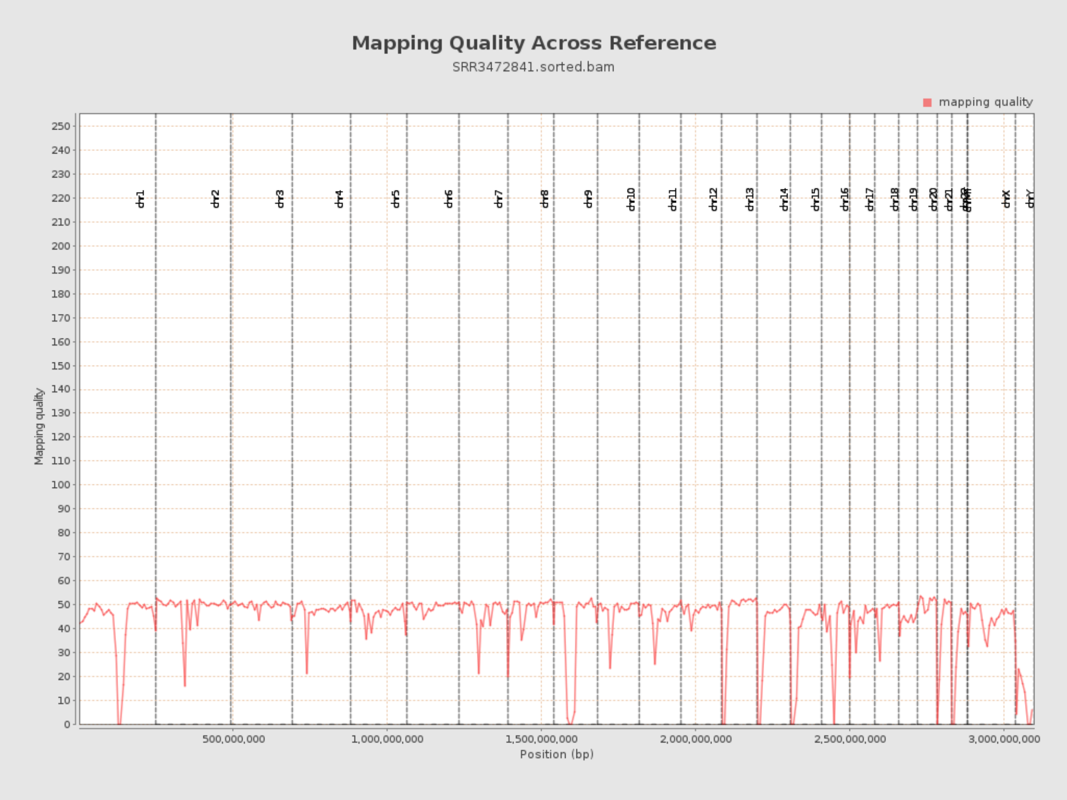
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram