Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:41:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472825.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_SRR3472825 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472825.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:41:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472825.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,709,141
Mapped reads	2,263,084 / 83.54%
Unmapped reads	446,057 / 16.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,974 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	67,137 / 2.48%
Duplication rate	2.3%
Clipped reads	1,150,711 / 42.48%

2.2. ACGT Content

Number/percentage of A's	40,139,929 / 27.29%
Number/percentage of C's	29,440,486 / 20.02%
Number/percentage of T's	43,482,485 / 29.56%
Number/percentage of G's	34,011,737 / 23.12%
Number/percentage of N's	3,154 / 0%
GC Percentage	43.14%

2.3. Coverage

Mean	0.0475

Standard Deviation	0.3264

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

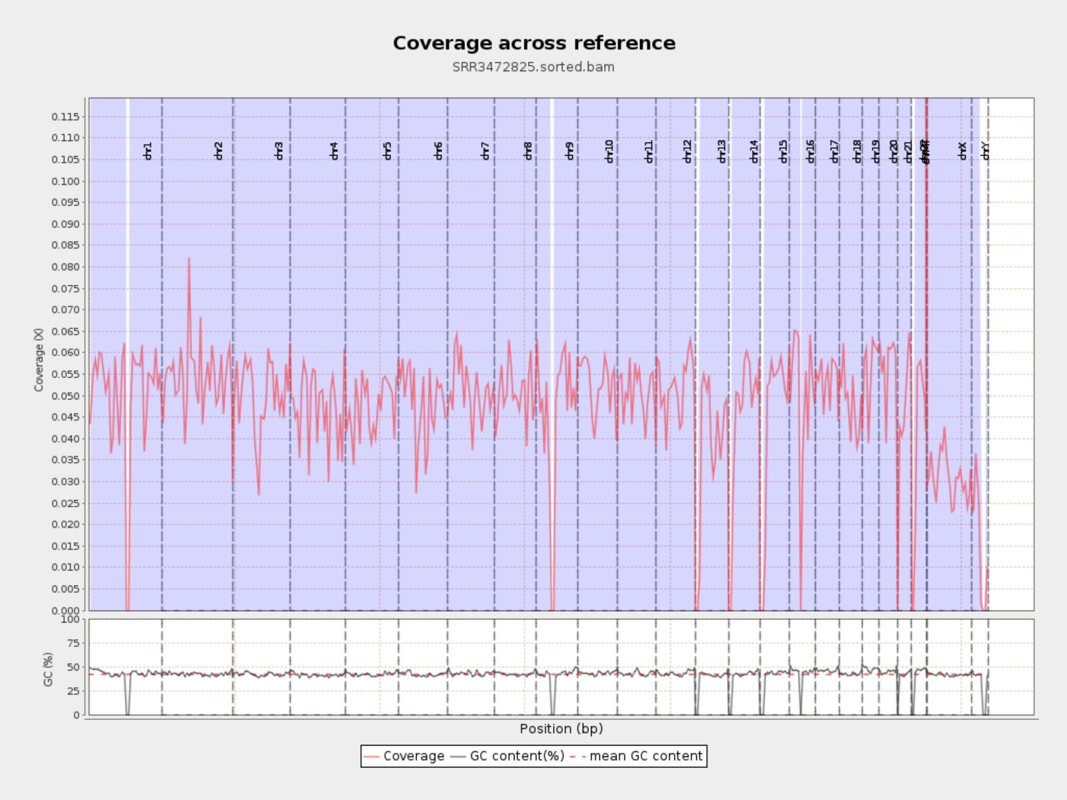
General error rate	0.85%
Mismatches	1,223,120
Insertions	11,226
Mapped reads with at least one insertion	0.49%
Deletions	32,327
Mapped reads with at least one deletion	1.41%
Homopolymer indels	45.55%

2.6. Chromosome stats

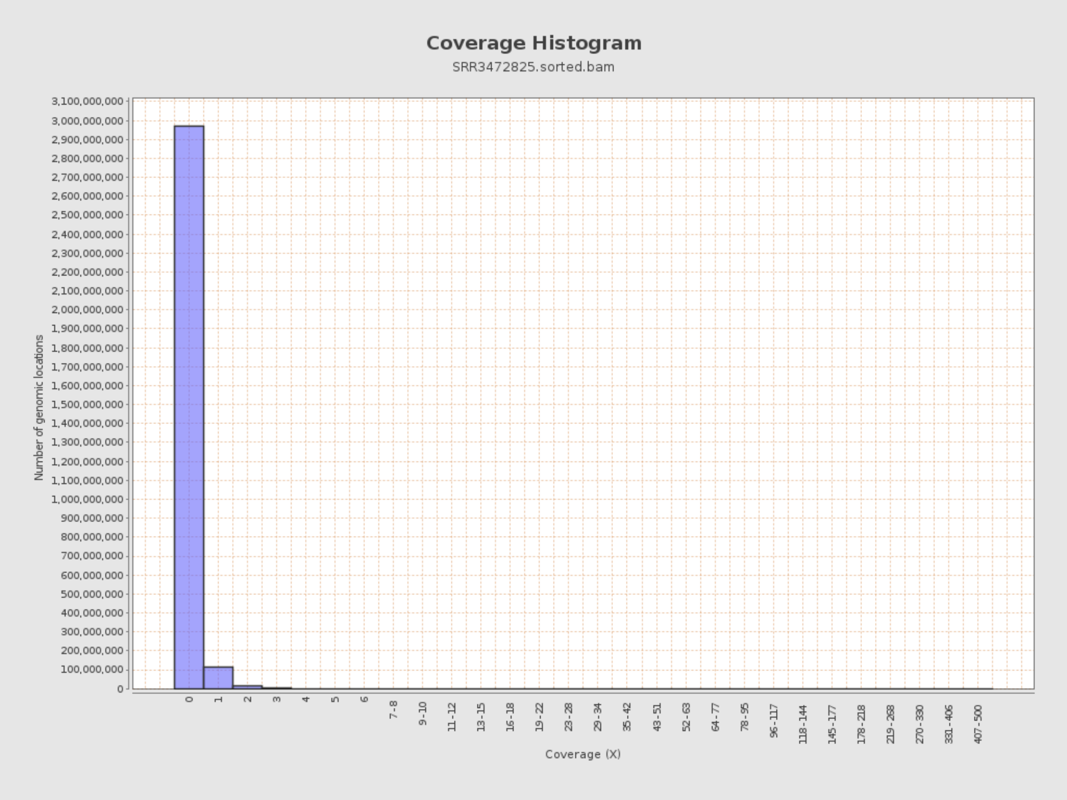
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12385484	0.0497	0.4314
chr2	243199373	13296895	0.0547	0.4488
chr3	198022430	9863638	0.0498	0.2485
chr4	191154276	8983228	0.047	0.2579
chr5	180915260	8569034	0.0474	0.2436
chr6	171115067	8292656	0.0485	0.2723
chr7	159138663	8159396	0.0513	0.3498

chr8	146364022	7402274	0.0506	0.3447
chr9	141213431	6346439	0.0449	0.3434
chr10	135534747	7138188	0.0527	0.3051
chr11	135006516	6820711	0.0505	0.3696
chr12	133851895	6995556	0.0523	0.2598
chr13	115169878	4296143	0.0373	0.2251
chr14	107349540	4709870	0.0439	0.2552
chr15	102531392	4498188	0.0439	0.2438
chr16	90354753	4530833	0.0501	0.2809
chr17	81195210	4361540	0.0537	0.2805
chr18	78077248	3786767	0.0485	0.6343
chr19	59128983	3310116	0.056	0.3546
chr20	63025520	3569944	0.0566	0.2789
chr21	48129895	2190085	0.0455	0.2741
chr22	51304566	1914520	0.0373	0.2293
chrMT	16571	21780	1.3143	1.3844
chrX	155270560	4820688	0.031	0.2286
chrY	59373566	871875	0.0147	0.1672

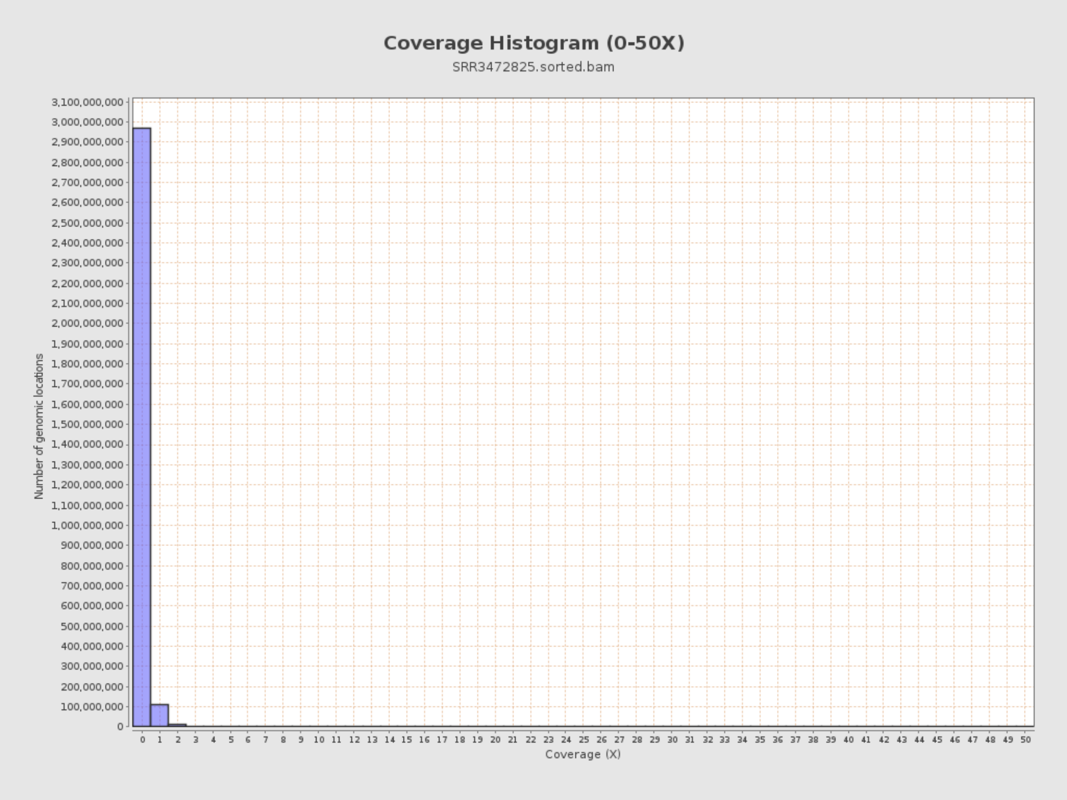
3. Results : Coverage across reference



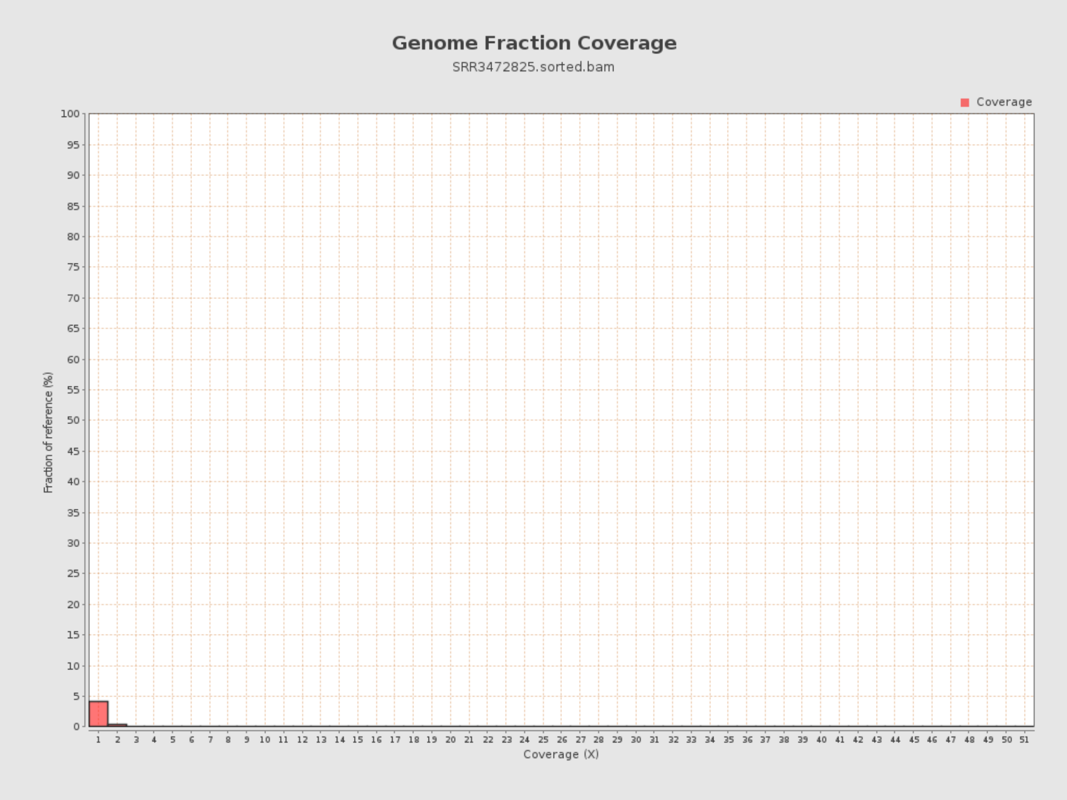
4. Results : Coverage Histogram



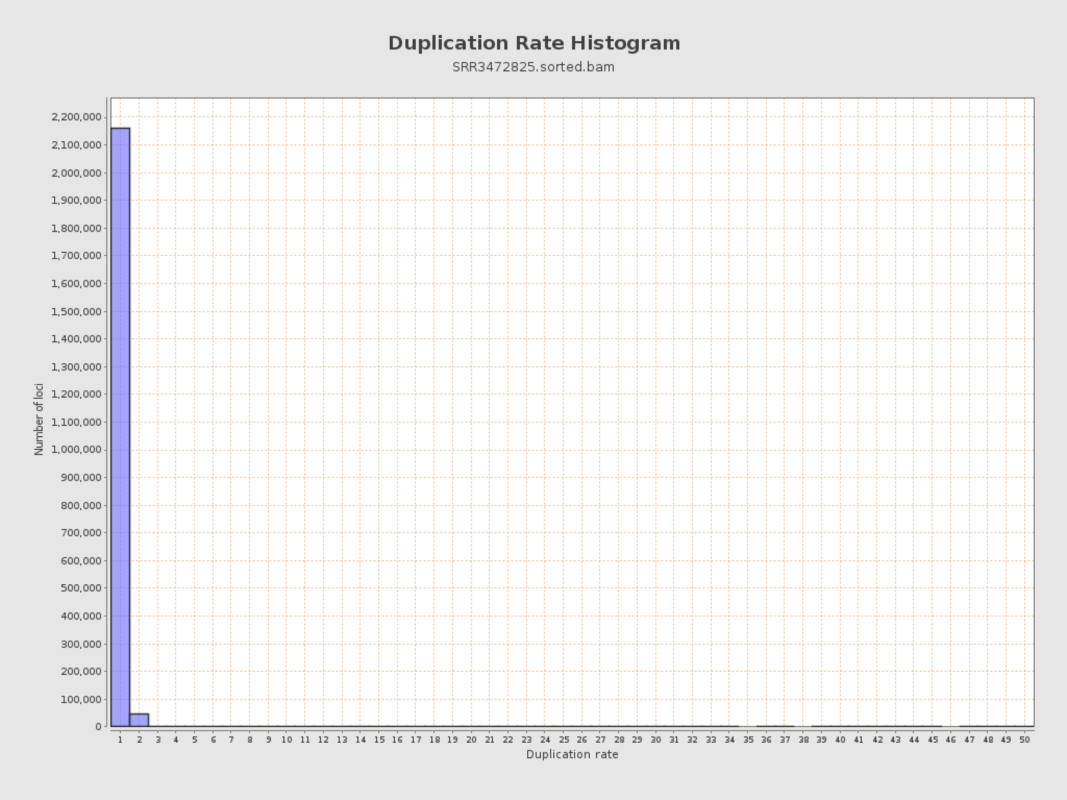
5. Results : Coverage Histogram (0-50X)



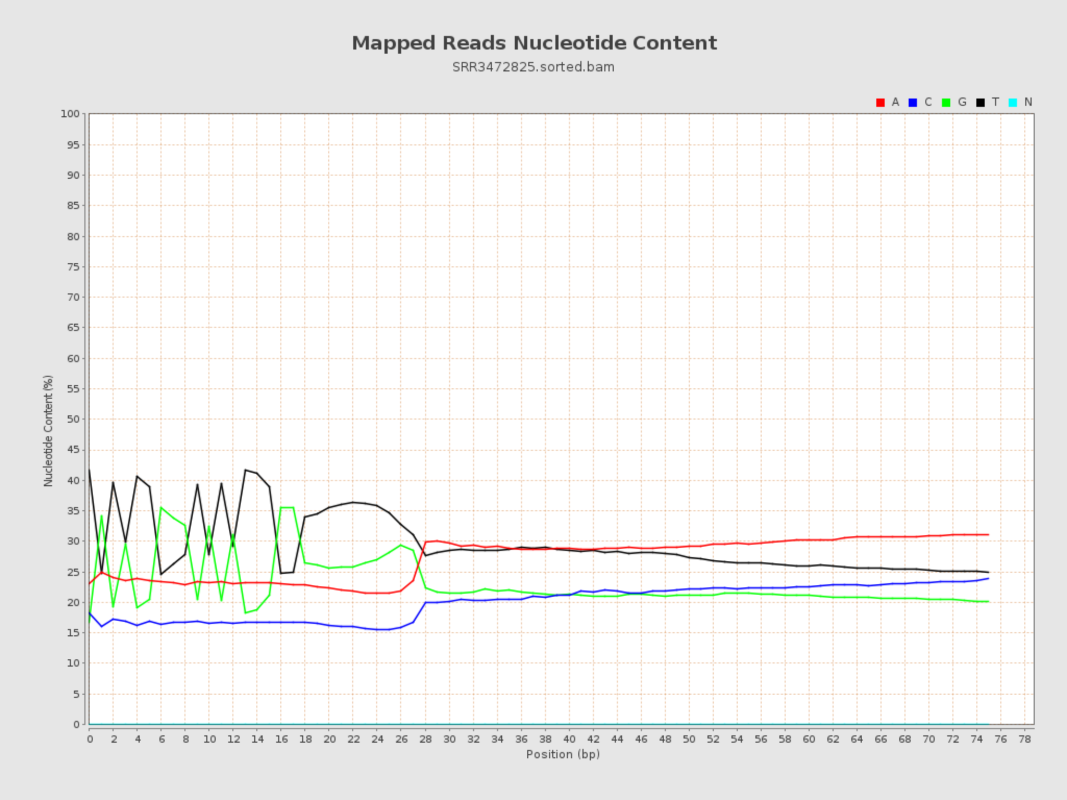
6. Results : Genome Fraction Coverage



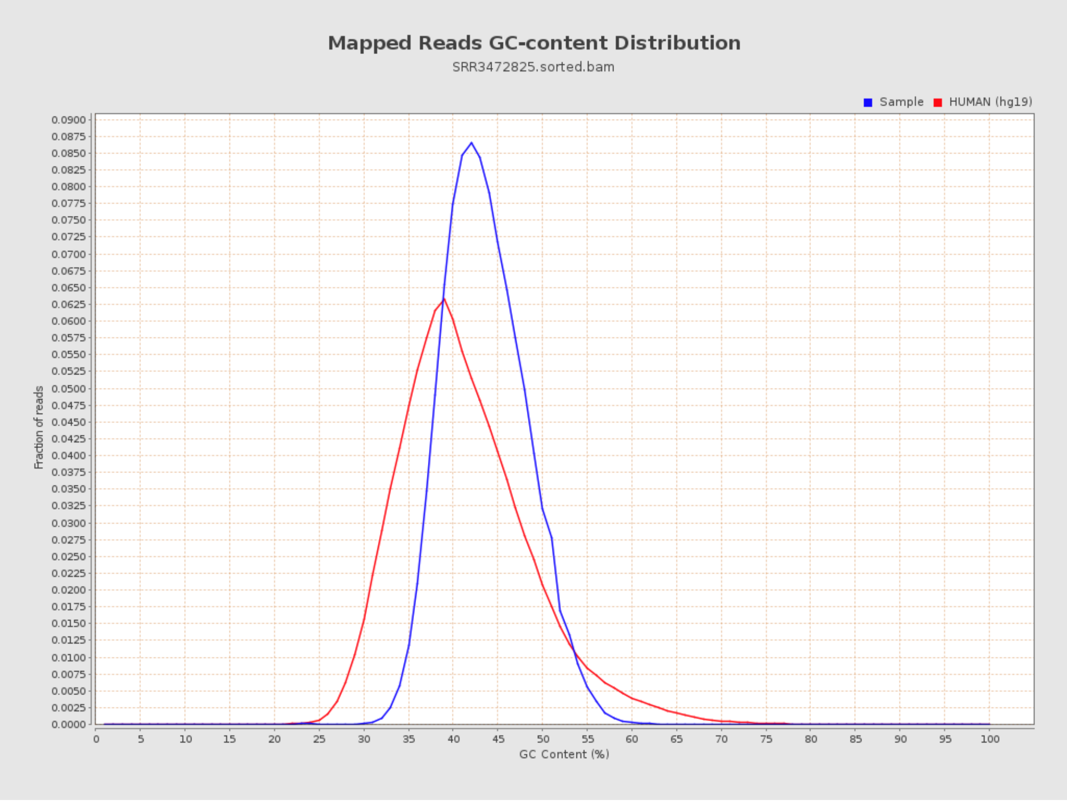
7. Results : Duplication Rate Histogram



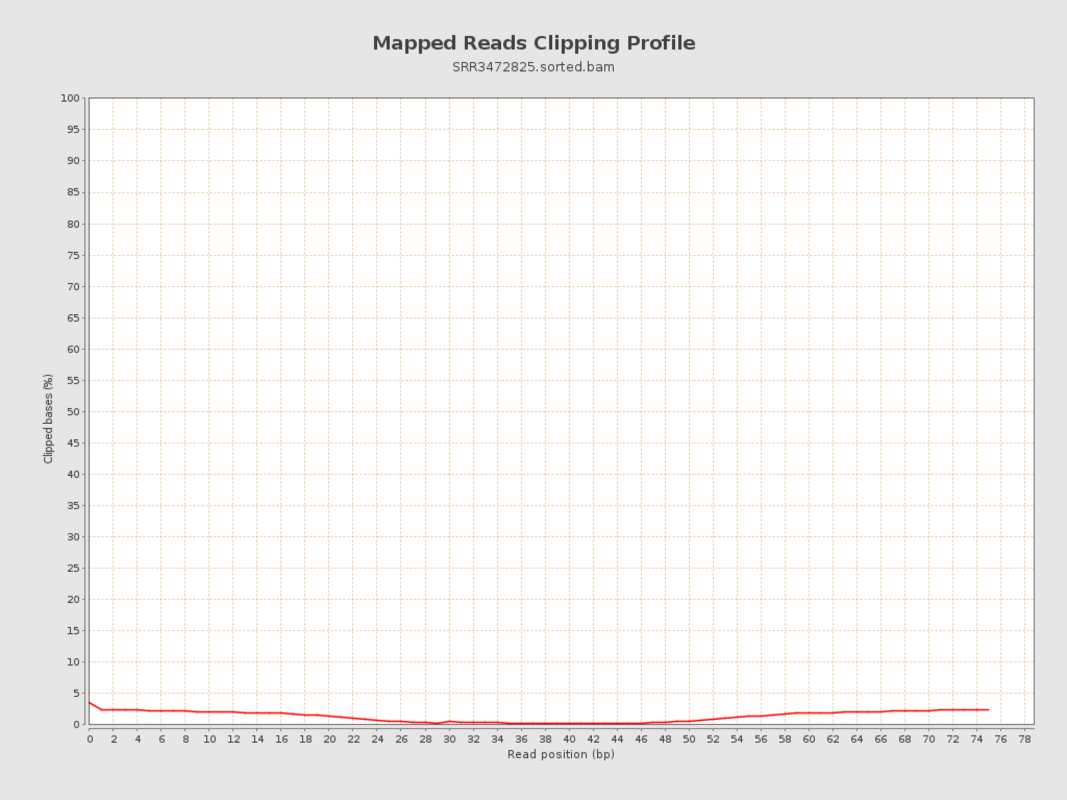
8. Results : Mapped Reads Nucleotide Content



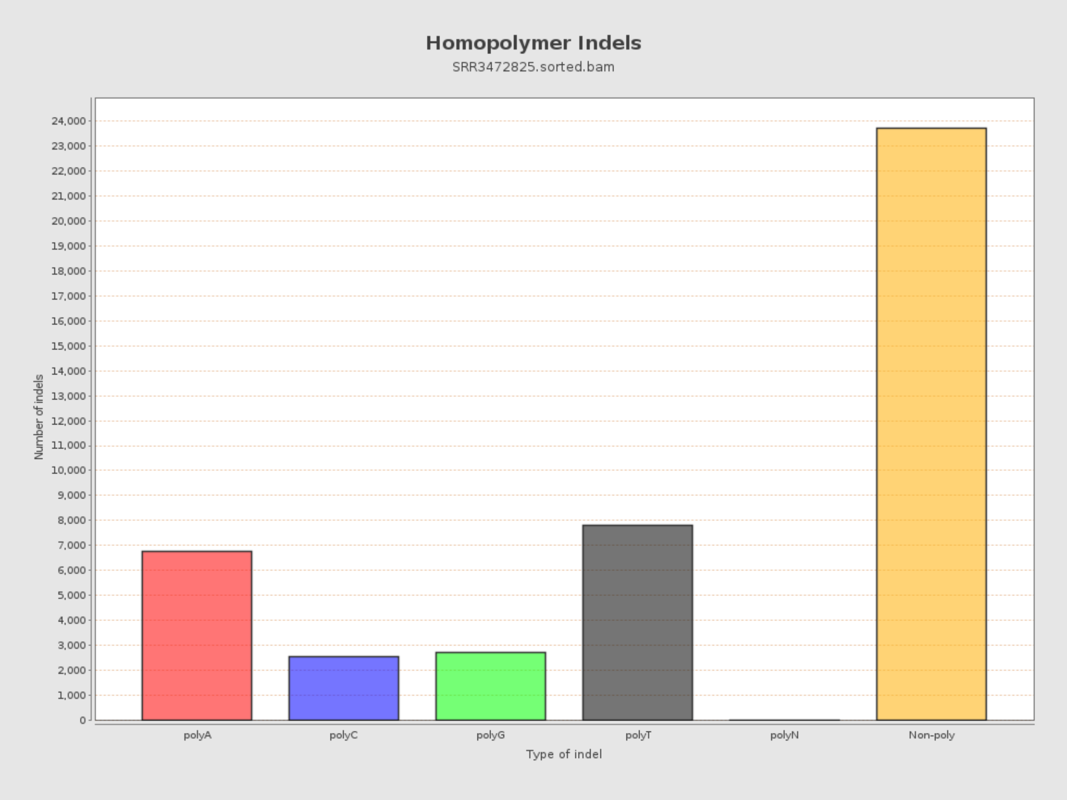
9. Results : Mapped Reads GC-content Distribution



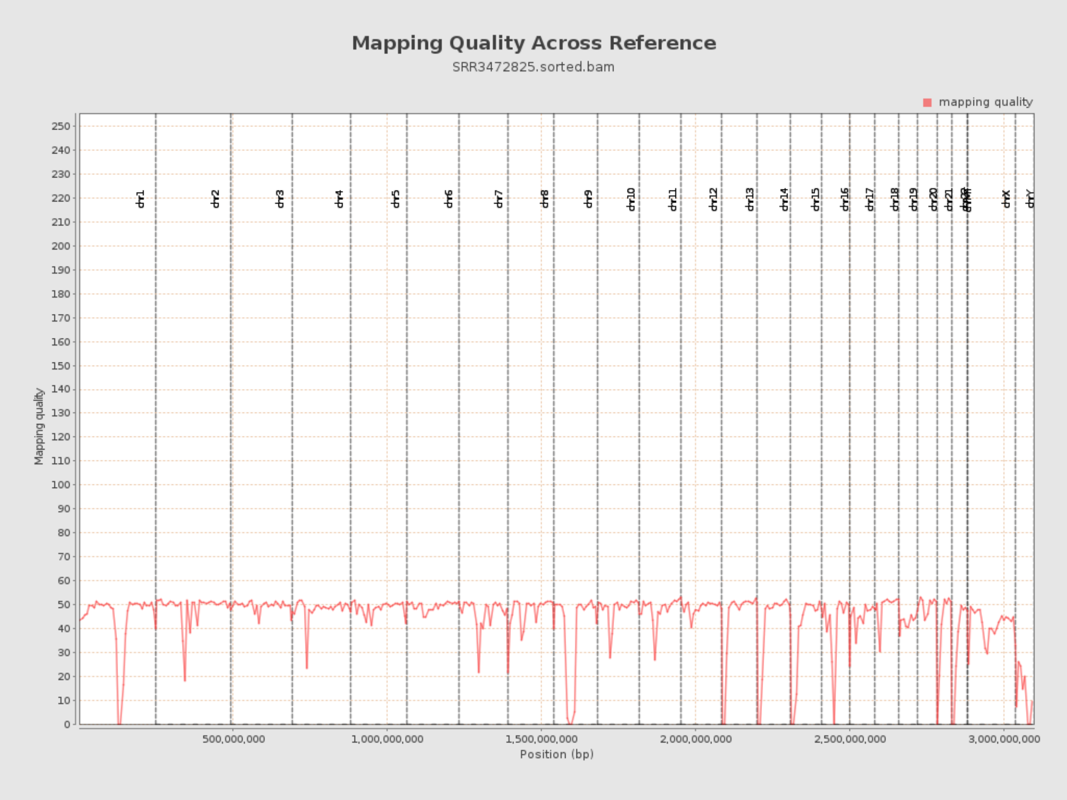
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram