Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:18:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472819.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_SRR3472819 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472819.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:18:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472819.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,722,878
Mapped reads	2,256,717 / 82.88%
Unmapped reads	466,161 / 17.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,056 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	69,755 / 2.56%
Duplication rate	2.36%
Clipped reads	1,128,760 / 41.45%

2.2. ACGT Content

Number/percentage of A's	39,626,776 / 26.9%
Number/percentage of C's	29,493,271 / 20.02%
Number/percentage of T's	43,664,177 / 29.64%
Number/percentage of G's	34,515,096 / 23.43%
Number/percentage of N's	2,988 / 0%
GC Percentage	43.45%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.3351

2.4. Mapping Quality

Mean Mapping Quality	44.21

2.5. Mismatches and indels

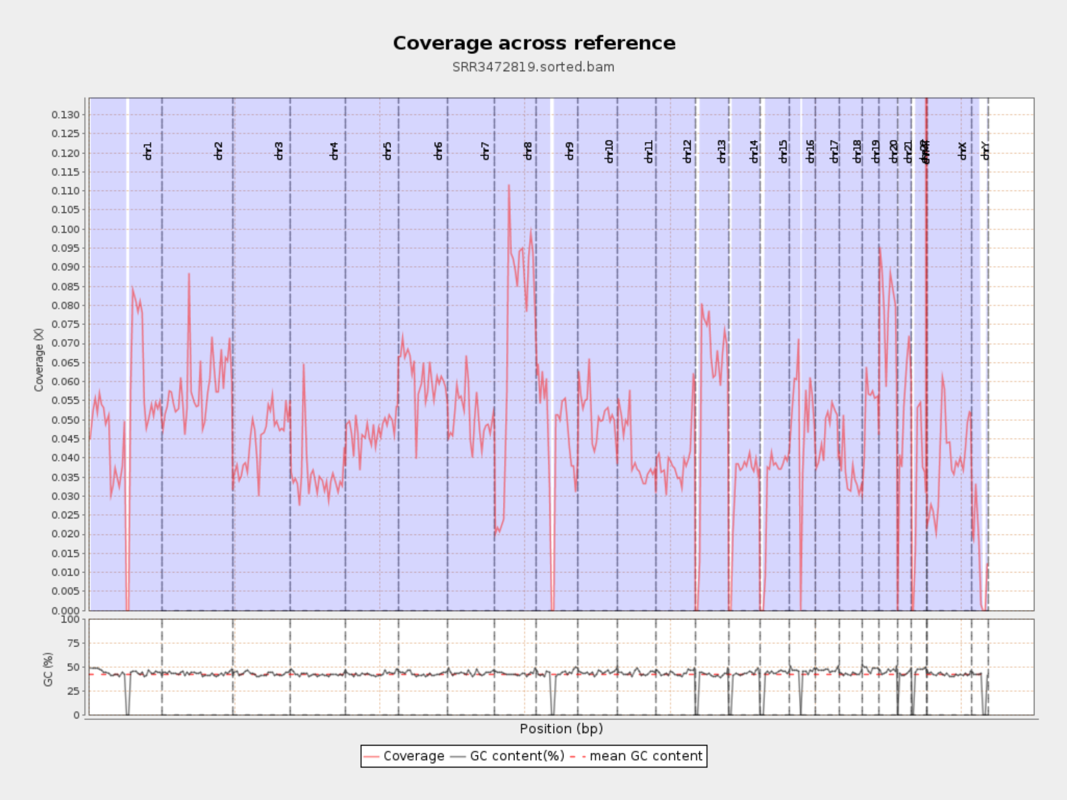
General error rate	0.86%
Mismatches	1,245,409
Insertions	11,360
Mapped reads with at least one insertion	0.5%
Deletions	34,073
Mapped reads with at least one deletion	1.49%
Homopolymer indels	45.26%

2.6. Chromosome stats

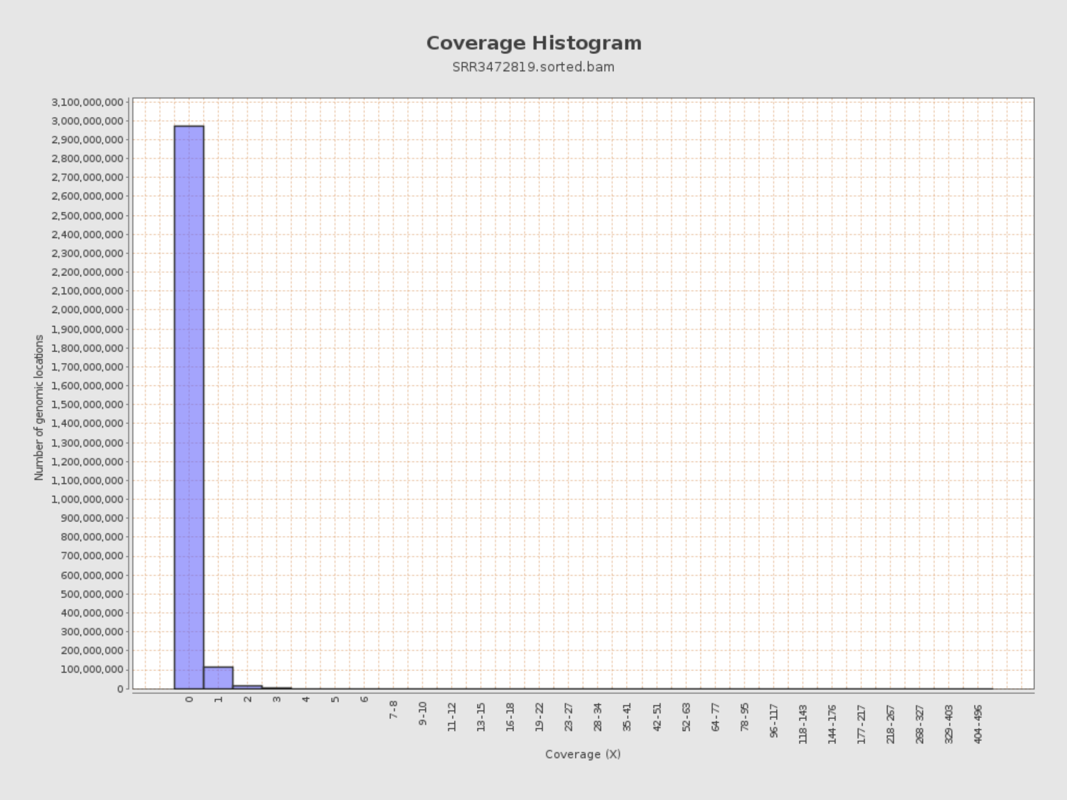
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12497280	0.0501	0.4011
chr2	243199373	14223701	0.0585	0.4774
chr3	198022430	8847998	0.0447	0.2366
chr4	191154276	6723474	0.0352	0.2445
chr5	180915260	8529212	0.0471	0.2438
chr6	171115067	10454229	0.0611	0.3011
chr7	159138663	8078590	0.0508	0.4141

chr8	146364022	10434578	0.0713	0.3928
chr9	141213431	6228467	0.0441	0.3548
chr10	135534747	7001337	0.0517	0.327
chr11	135006516	5583353	0.0414	0.3445
chr12	133851895	5271410	0.0394	0.2288
chr13	115169878	6702991	0.0582	0.2799
chr14	107349540	3443058	0.0321	0.234
chr15	102531392	3170301	0.0309	0.2116
chr16	90354753	4517271	0.05	0.2734
chr17	81195210	3785033	0.0466	0.2674
chr18	78077248	2806160	0.0359	0.6399
chr19	59128983	3175123	0.0537	0.3471
chr20	63025520	5038700	0.0799	0.3332
chr21	48129895	2390589	0.0497	0.3081
chr22	51304566	1587109	0.0309	0.2091
chrMT	16571	78867	4.7593	3.5912
chrX	155270560	6042220	0.0389	0.2587
chrY	59373566	752694	0.0127	0.1676

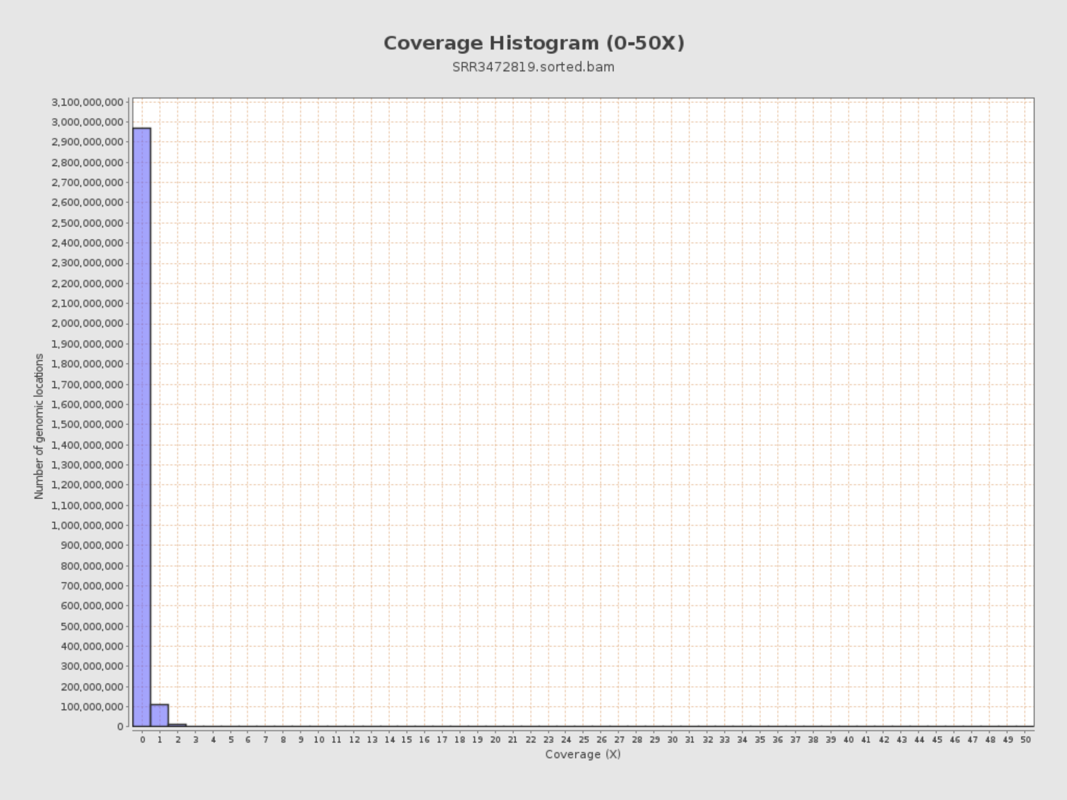
3. Results : Coverage across reference



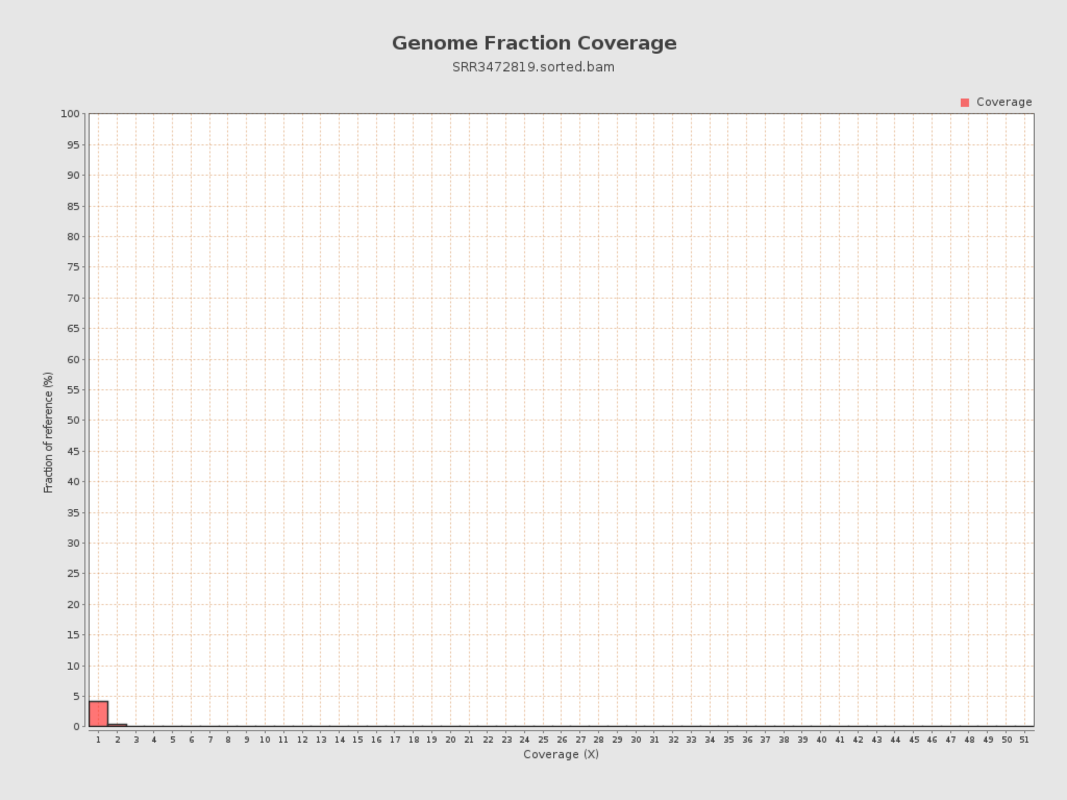
4. Results : Coverage Histogram



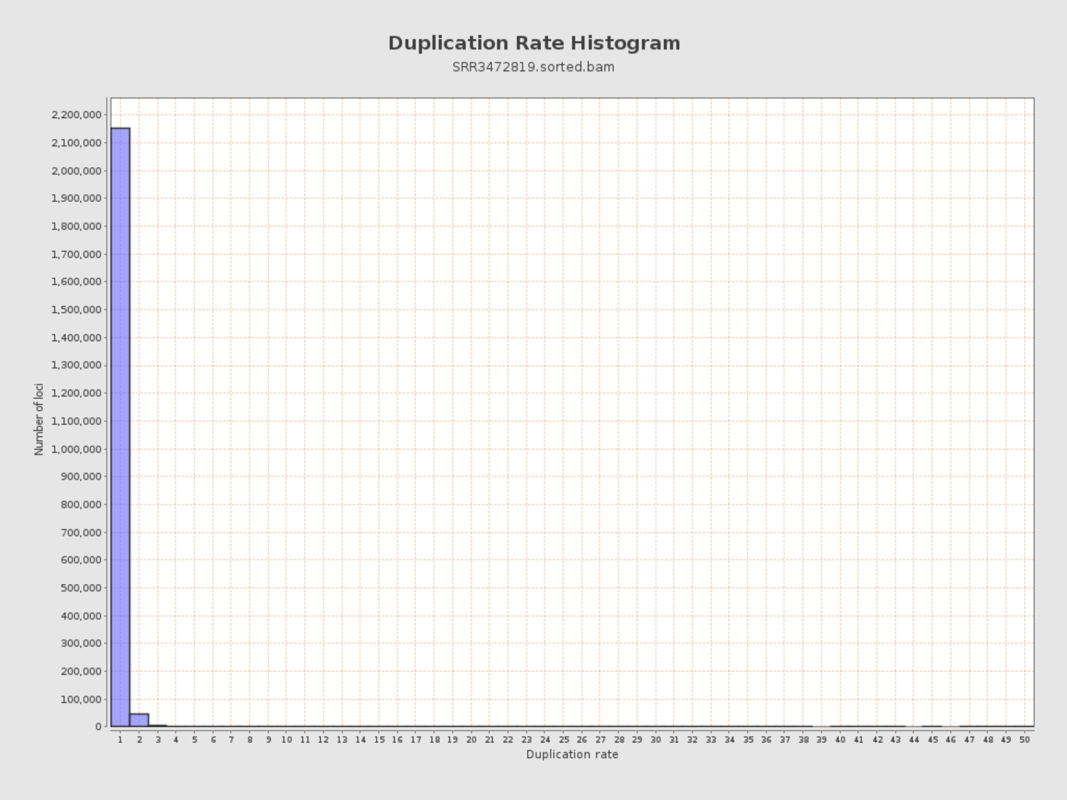
5. Results : Coverage Histogram (0-50X)



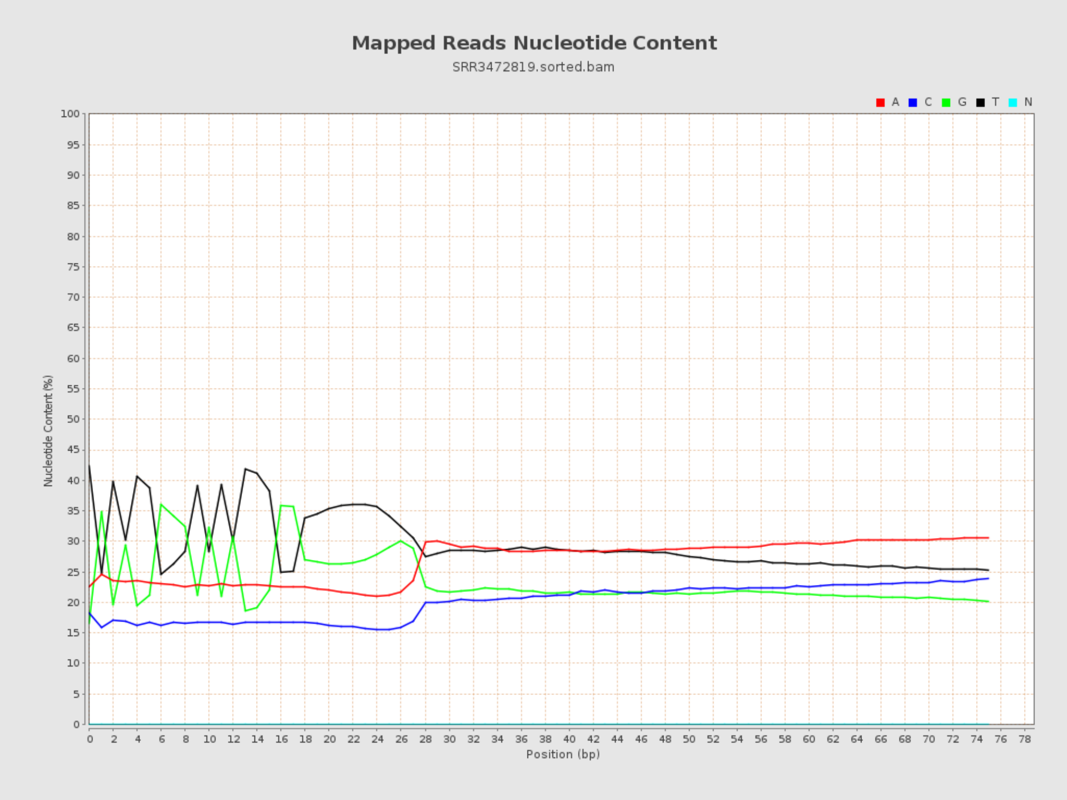
6. Results : Genome Fraction Coverage



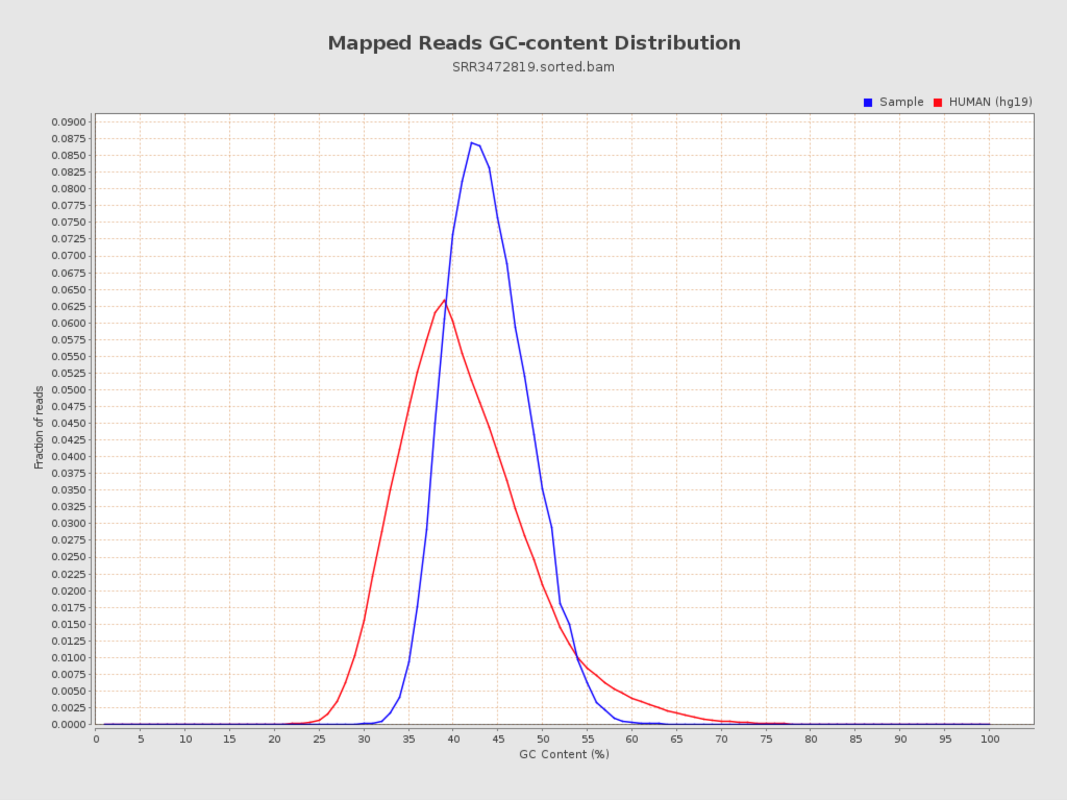
7. Results : Duplication Rate Histogram



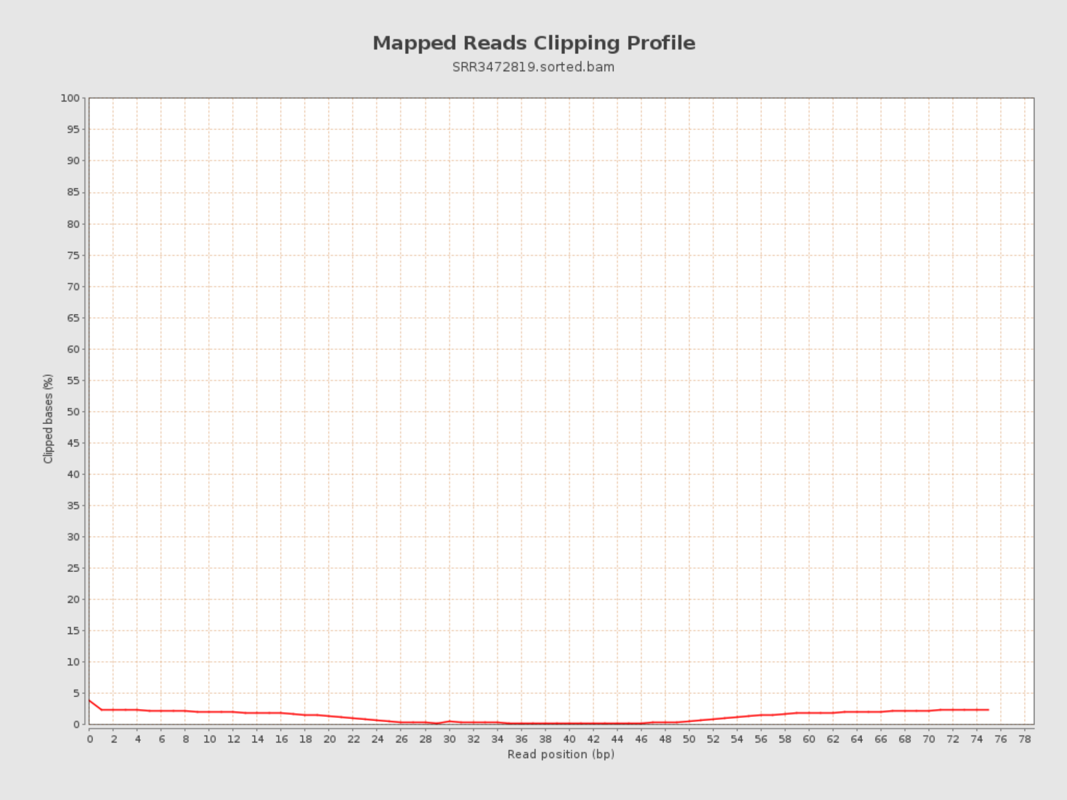
8. Results : Mapped Reads Nucleotide Content



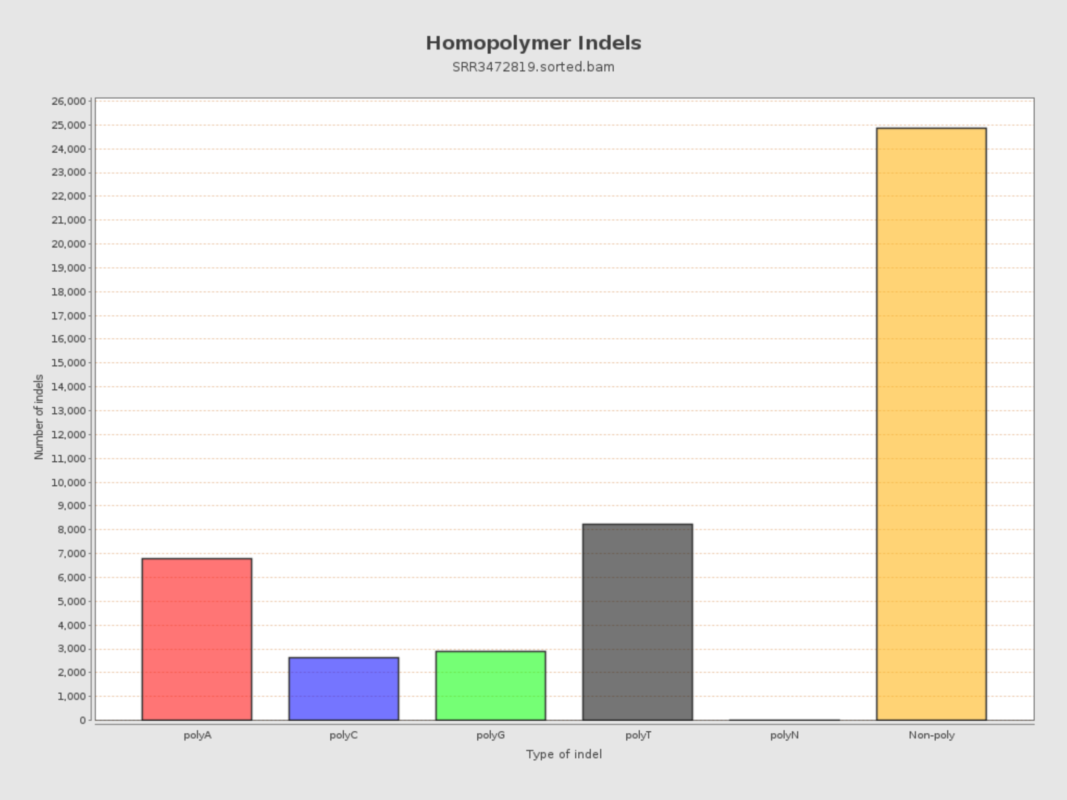
9. Results : Mapped Reads GC-content Distribution



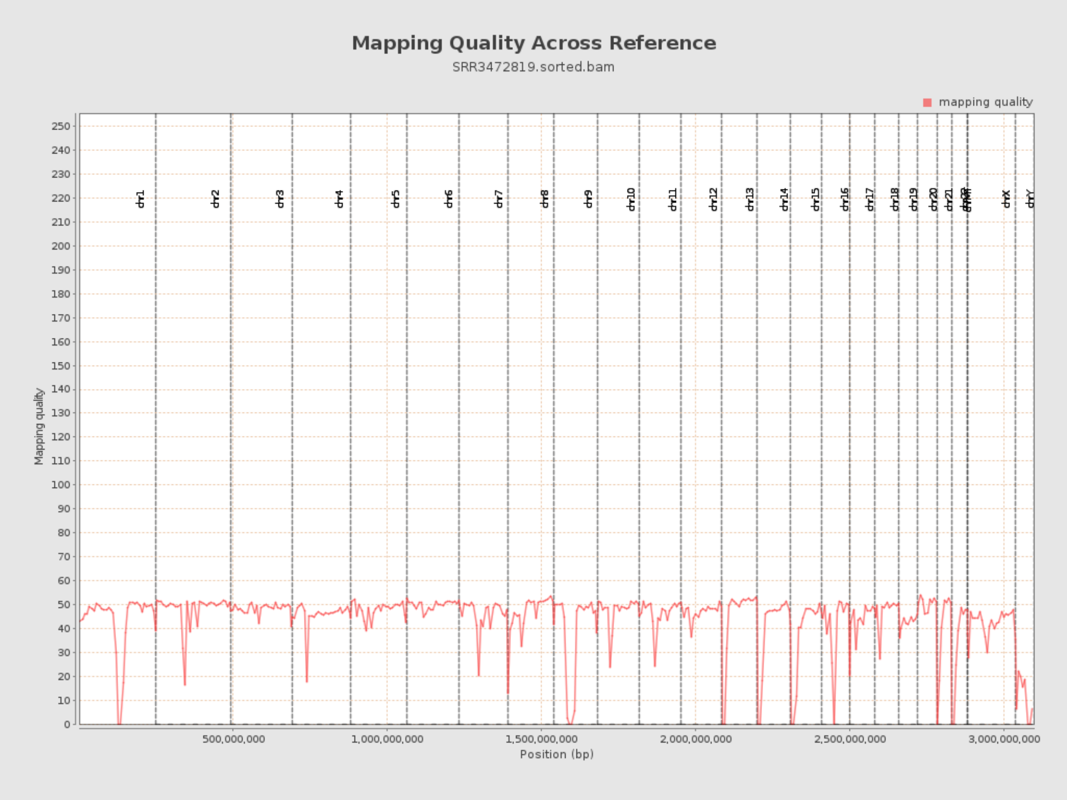
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram