Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:03:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082972.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_SRR3082972 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082972.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:03:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082972.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,399,781
Mapped reads	2,826,077 / 83.13%
Unmapped reads	573,704 / 16.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,985 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	103,837 / 3.05%
Duplication rate	2.67%
Clipped reads	1,327,296 / 39.04%

2.2. ACGT Content

Number/percentage of A's	54,845,942 / 29.16%
Number/percentage of C's	34,226,106 / 18.2%
Number/percentage of T's	58,572,337 / 31.14%
Number/percentage of G's	40,431,551 / 21.5%
Number/percentage of N's	18,119 / 0.01%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0608

Standard Deviation	0.4965

2.4. Mapping Quality

Mean Mapping Quality	45.52

2.5. Mismatches and indels

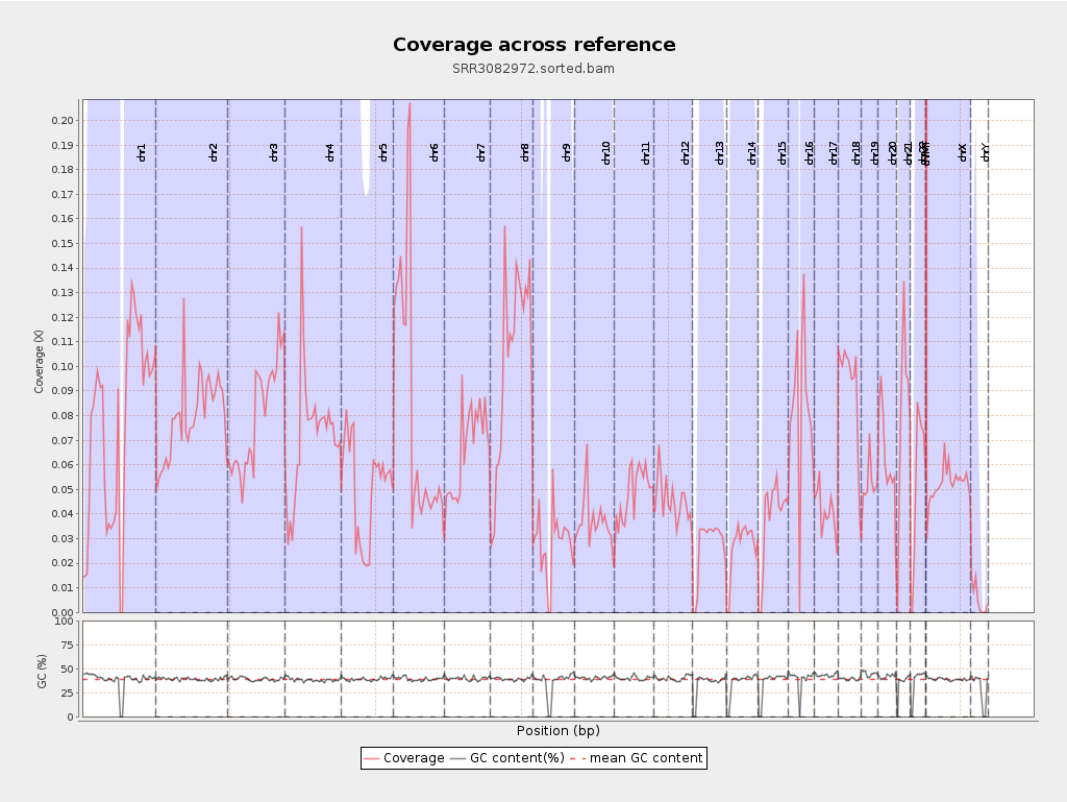
General error rate	0.95%
Mismatches	1,754,628
Insertions	15,841
Mapped reads with at least one insertion	0.56%
Deletions	44,169
Mapped reads with at least one deletion	1.55%
Homopolymer indels	46.71%

2.6. Chromosome stats

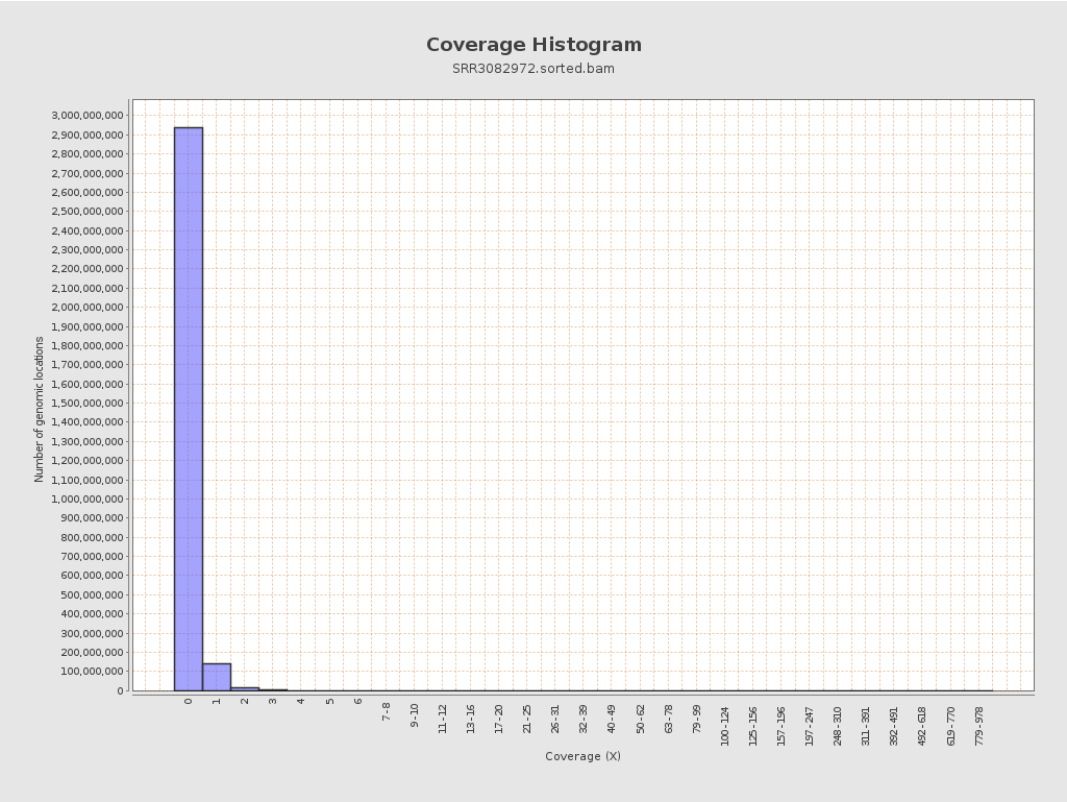
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19105356	0.0767	0.9125
chr2	243199373	19363553	0.0796	0.6657
chr3	198022430	15632307	0.0789	0.317
chr4	191154276	13862738	0.0725	0.3066
chr5	180915260	9123848	0.0504	0.2534
chr6	171115067	13866821	0.081	0.473
chr7	159138663	10506910	0.066	0.6333

chr8	146364022	15041107	0.1028	0.6346
chr9	141213431	4013273	0.0284	0.4262
chr10	135534747	5009088	0.037	0.3569
chr11	135006516	6548896	0.0485	0.3829
chr12	133851895	6120061	0.0457	0.2475
chr13	115169878	3102527	0.0269	0.1815
chr14	107349540	2885338	0.0269	0.2451
chr15	102531392	3857417	0.0376	0.2198
chr16	90354753	7367954	0.0815	0.3694
chr17	81195210	3361321	0.0414	0.2773
chr18	78077248	7306198	0.0936	0.9923
chr19	59128983	3092675	0.0523	0.6249
chr20	63025520	4061609	0.0644	0.3094
chr21	48129895	3776874	0.0785	0.3289
chr22	51304566	2722314	0.0531	0.2584
chrMT	16571	44008	2.6557	2.3588
chrX	155270560	8078764	0.052	0.3187
chrY	59373566	319041	0.0054	0.1029

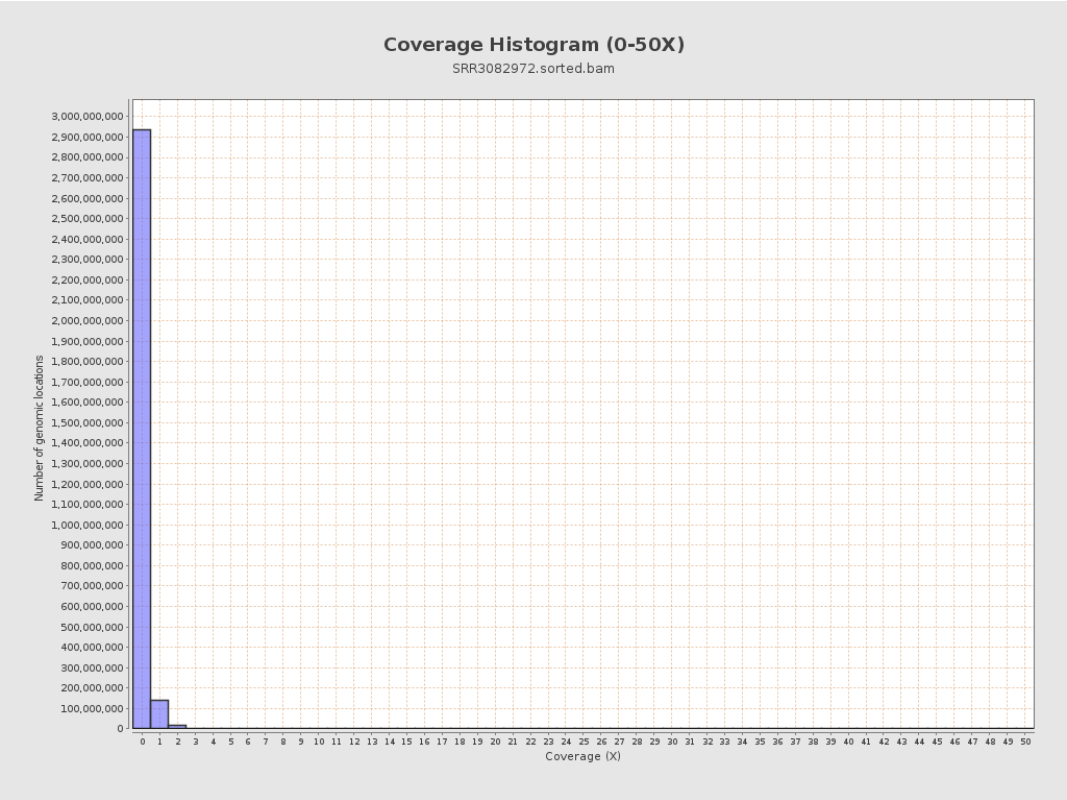
3. Results : Coverage across reference



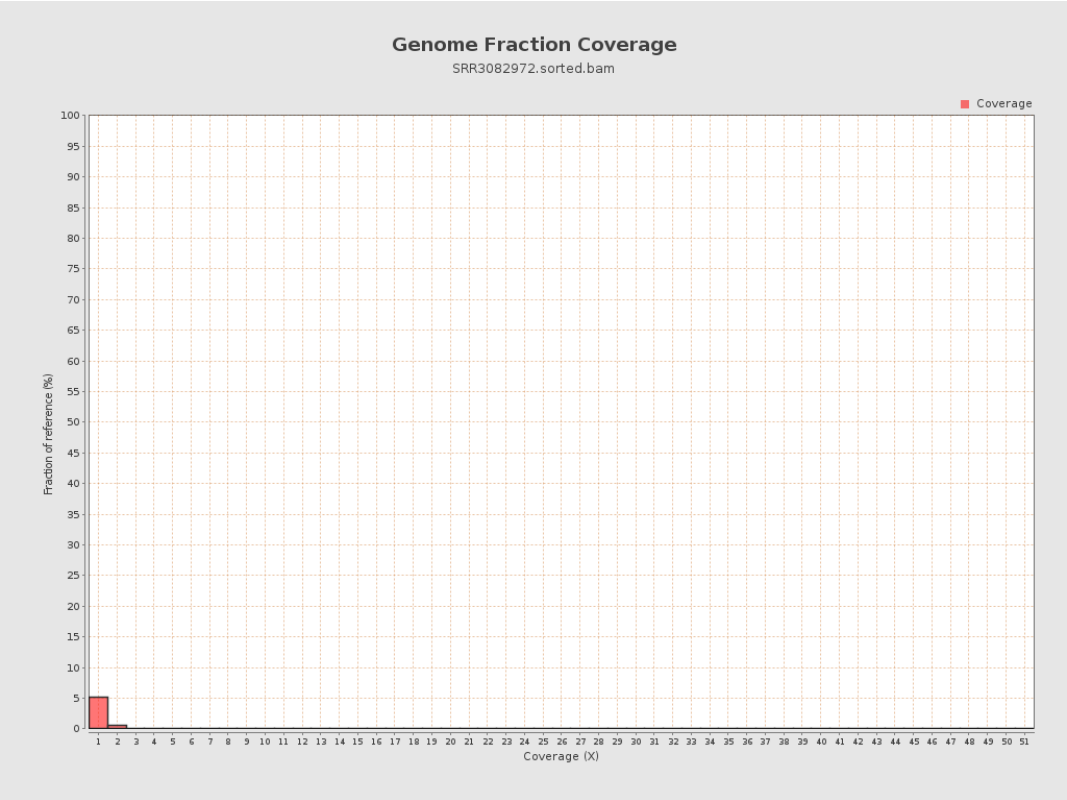
4. Results : Coverage Histogram



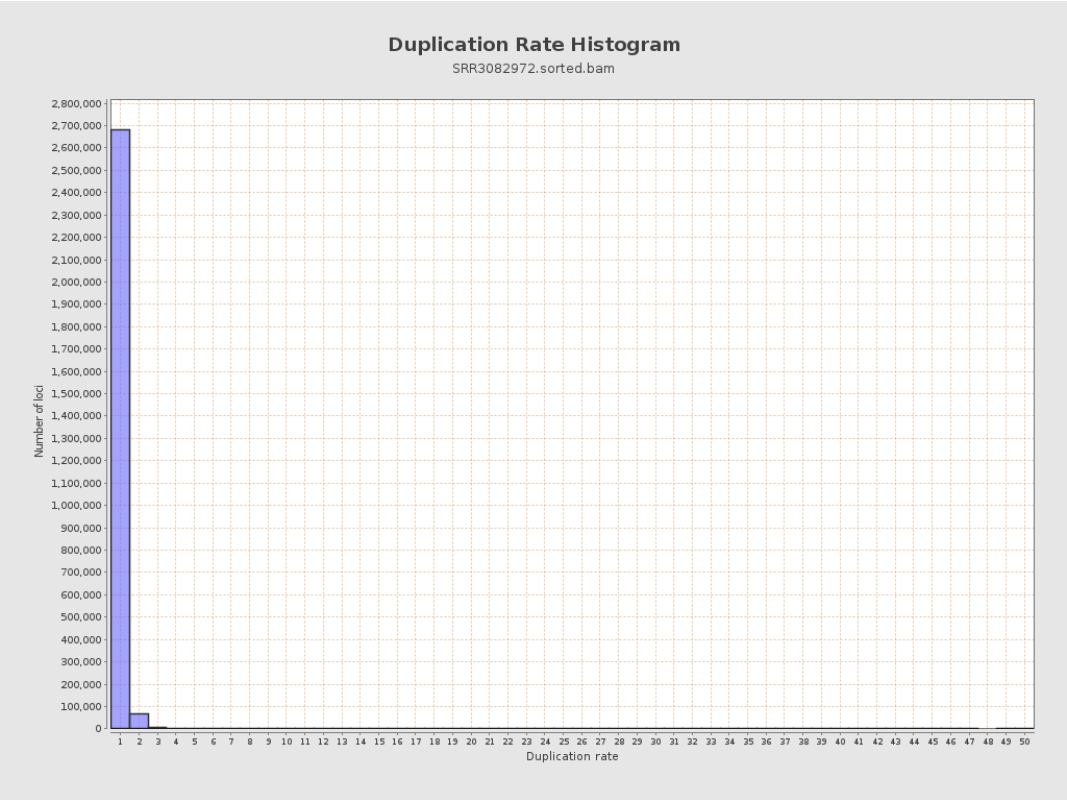
5. Results : Coverage Histogram (0-50X)



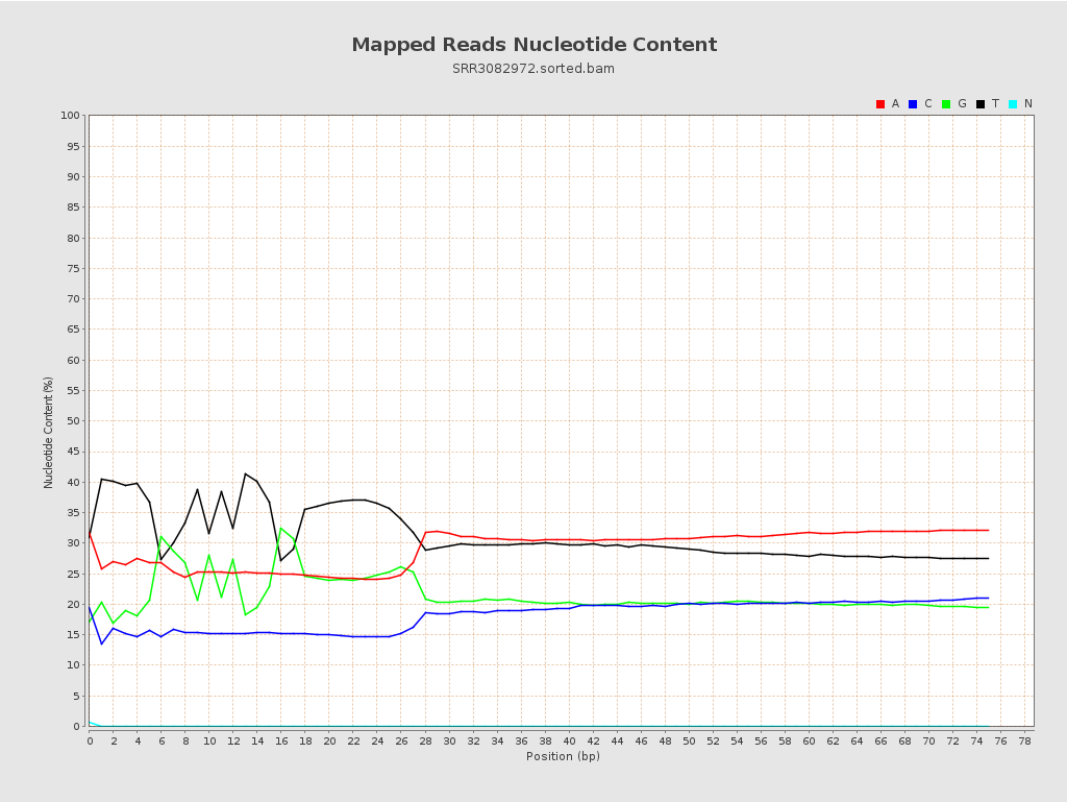
6. Results : Genome Fraction Coverage



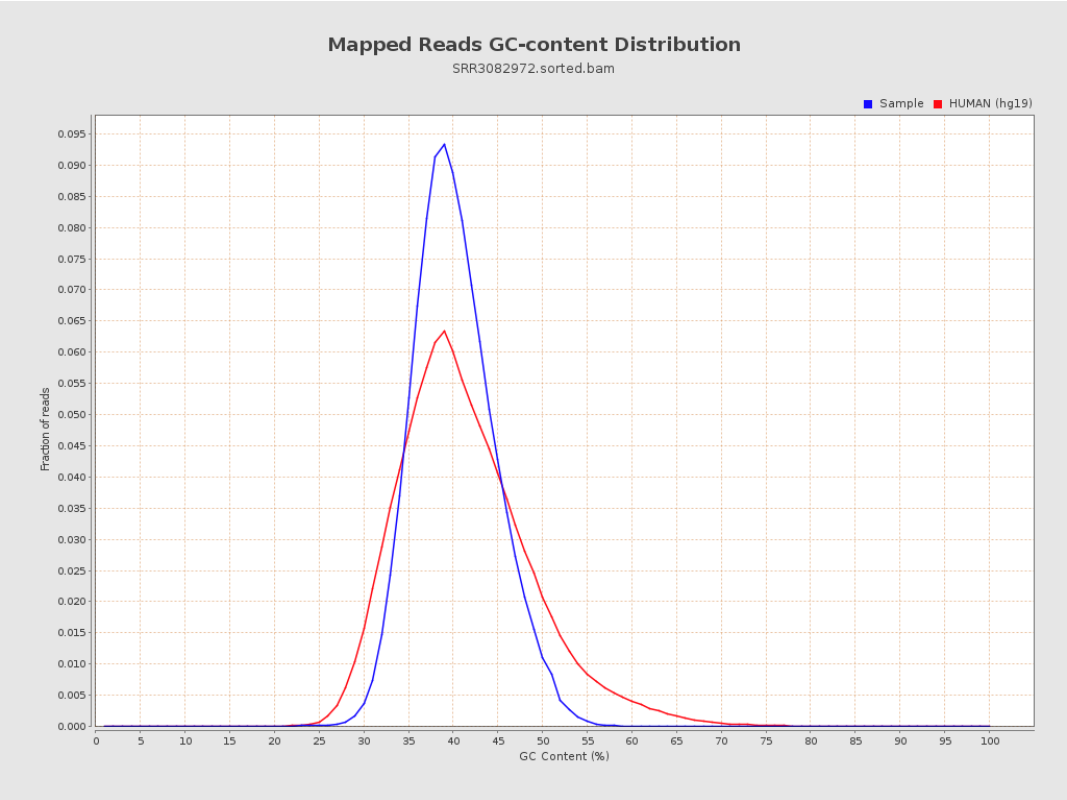
7. Results : Duplication Rate Histogram



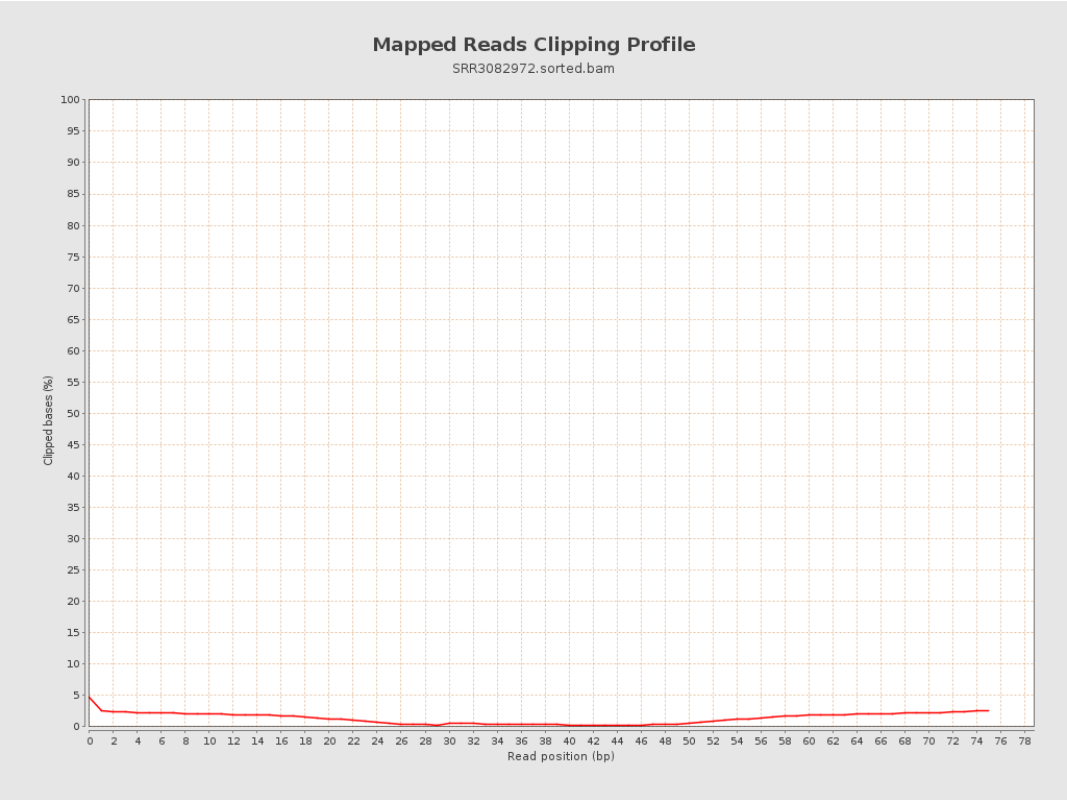
8. Results : Mapped Reads Nucleotide Content



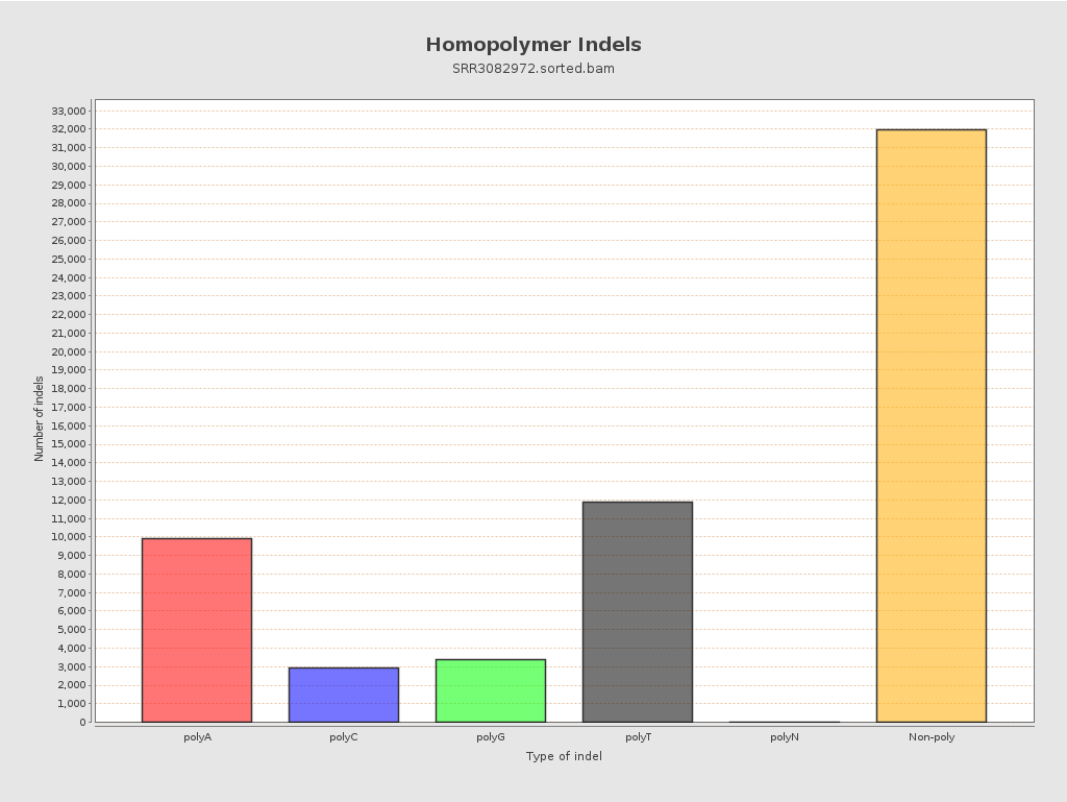
9. Results : Mapped Reads GC-content Distribution



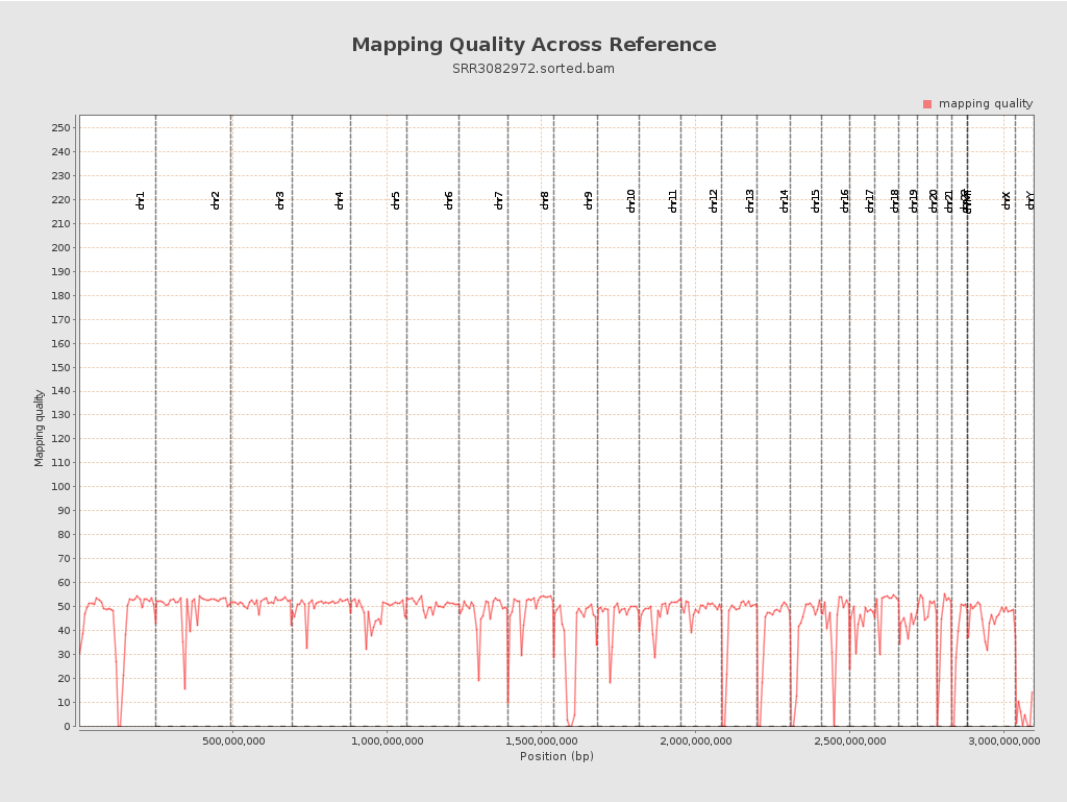
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram