Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:02:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548972.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_SRR1548972 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548972.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:02:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548972.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,232,433
Mapped reads	3,248,879 / 44.92%
Unmapped reads	3,983,554 / 55.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	72,165 / 1%
Duplication rate	1.53%
Clipped reads	283,639 / 3.92%

2.2. ACGT Content

Number/percentage of A's	39,484,220 / 30.74%
Number/percentage of C's	24,496,581 / 19.07%
Number/percentage of T's	39,501,665 / 30.76%
Number/percentage of G's	24,938,489 / 19.42%
Number/percentage of N's	5,983 / 0%
GC Percentage	38.49%

2.3. Coverage

Mean	0.0415
Standard Deviation	0.3167

2.4. Mapping Quality

Mean Mapping Quality	43.64

2.5. Mismatches and indels

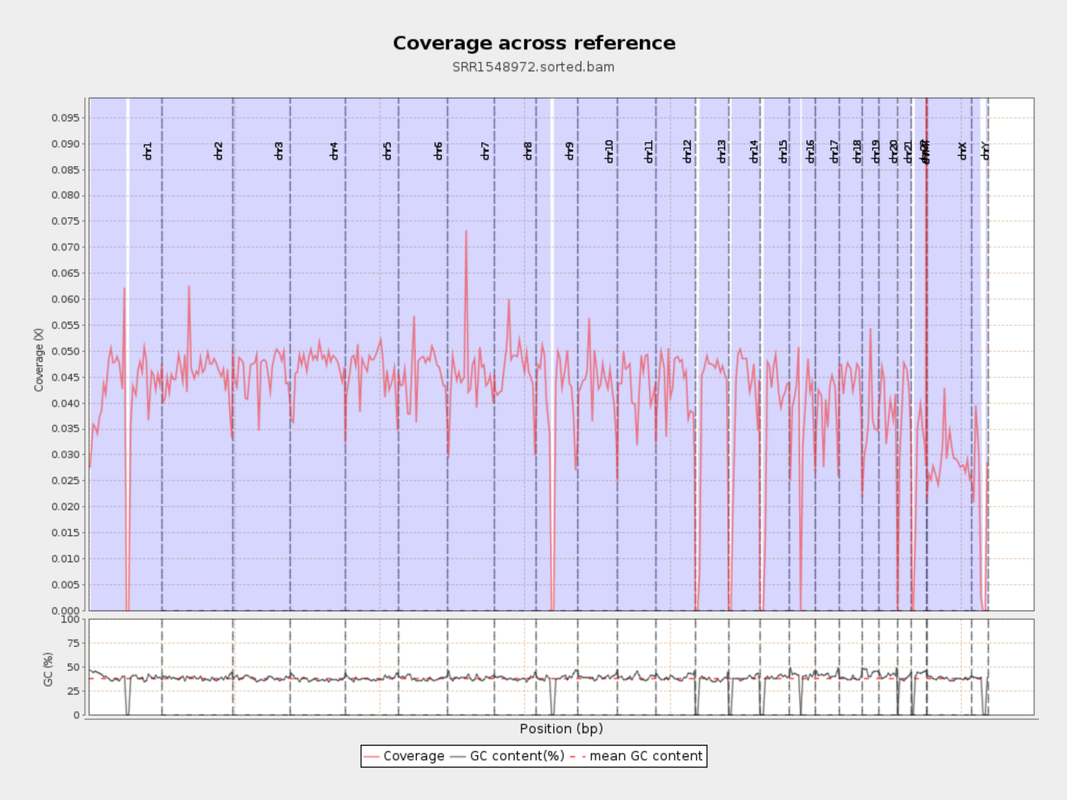
General error rate	0.31%
Mismatches	398,538
Insertions	4,977
Mapped reads with at least one insertion	0.15%
Deletions	12,974
Mapped reads with at least one deletion	0.4%
Homopolymer indels	45.55%

2.6. Chromosome stats

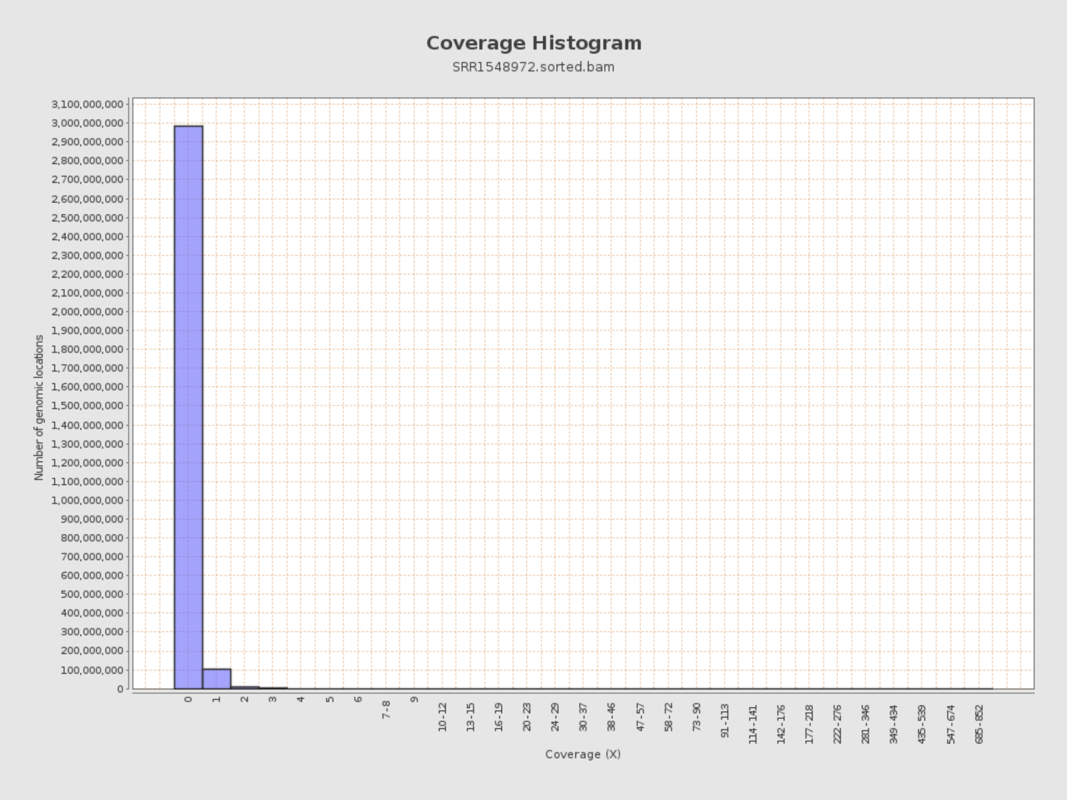
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10221229	0.041	0.5271
chr2	243199373	11154082	0.0459	0.2937
chr3	198022430	9150419	0.0462	0.2381
chr4	191154276	9039520	0.0473	0.2445
chr5	180915260	8384283	0.0463	0.24
chr6	171115067	7849819	0.0459	0.265
chr7	159138663	7300242	0.0459	0.4289
chr8	146364022	6809850	0.0465	0.4909

chr9	141213431	5516588	0.0391	0.2726
chr10	135534747	6009141	0.0443	0.2782
chr11	135006516	5894530	0.0437	0.2831
chr12	133851895	5838118	0.0436	0.2376
chr13	115169878	4459306	0.0387	0.217
chr14	107349540	4073783	0.0379	0.2487
chr15	102531392	3654149	0.0356	0.2083
chr16	90354753	3333945	0.0369	0.2228
chr17	81195210	3094475	0.0381	0.2249
chr18	78077248	3526541	0.0452	0.444
chr19	59128983	2151337	0.0364	0.4811
chr20	63025520	2464172	0.0391	0.2228
chr21	48129895	1737461	0.0361	0.2278
chr22	51304566	1261542	0.0246	0.191
chrMT	16571	3913	0.2361	0.5375
chrX	155270560	4451657	0.0287	0.2161
chrY	59373566	1063142	0.0179	0.1948

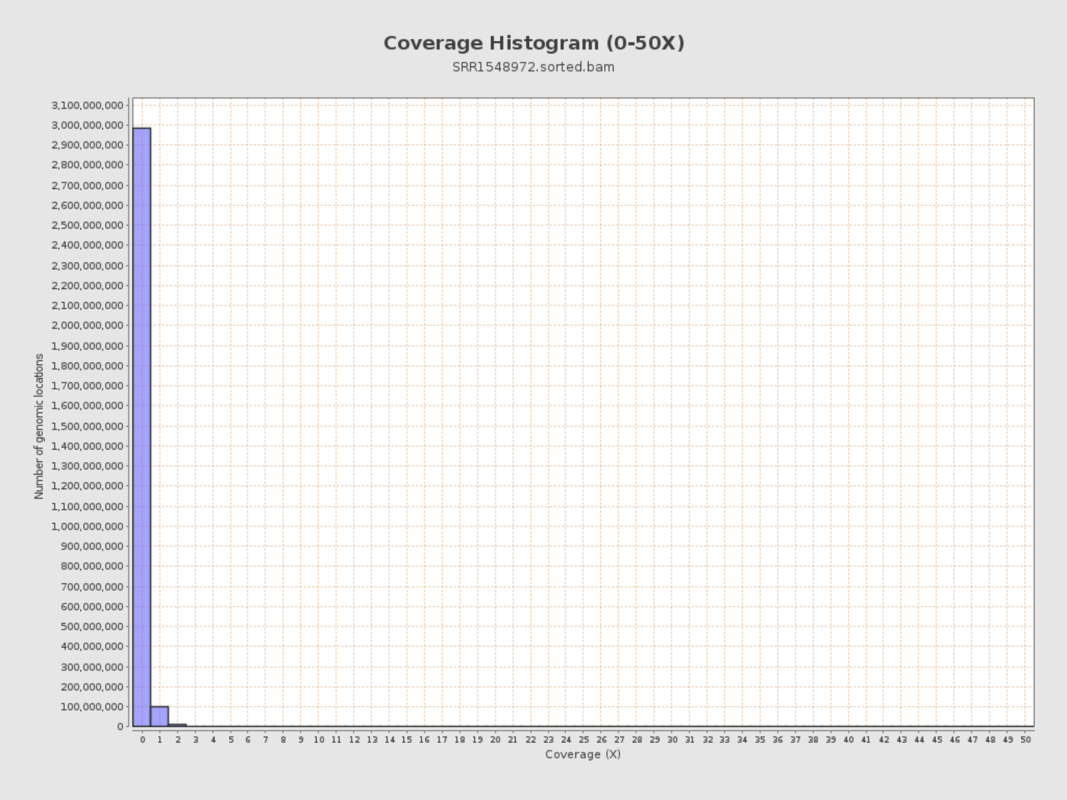
3. Results : Coverage across reference



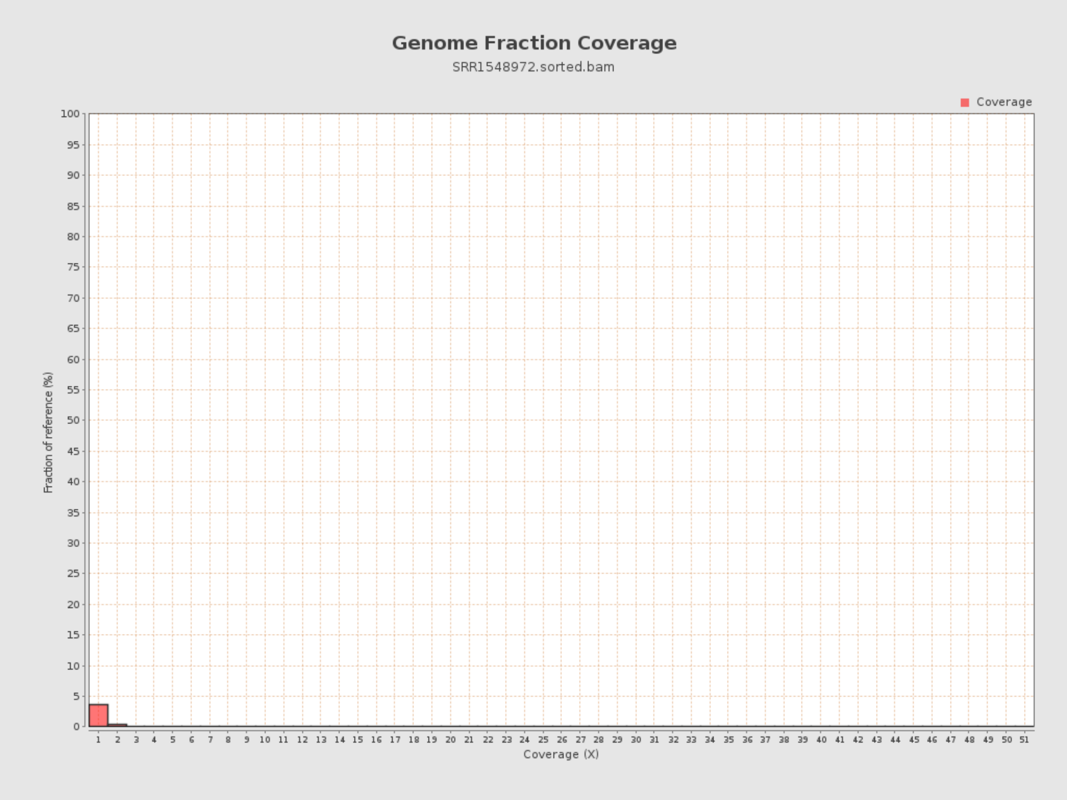
4. Results : Coverage Histogram



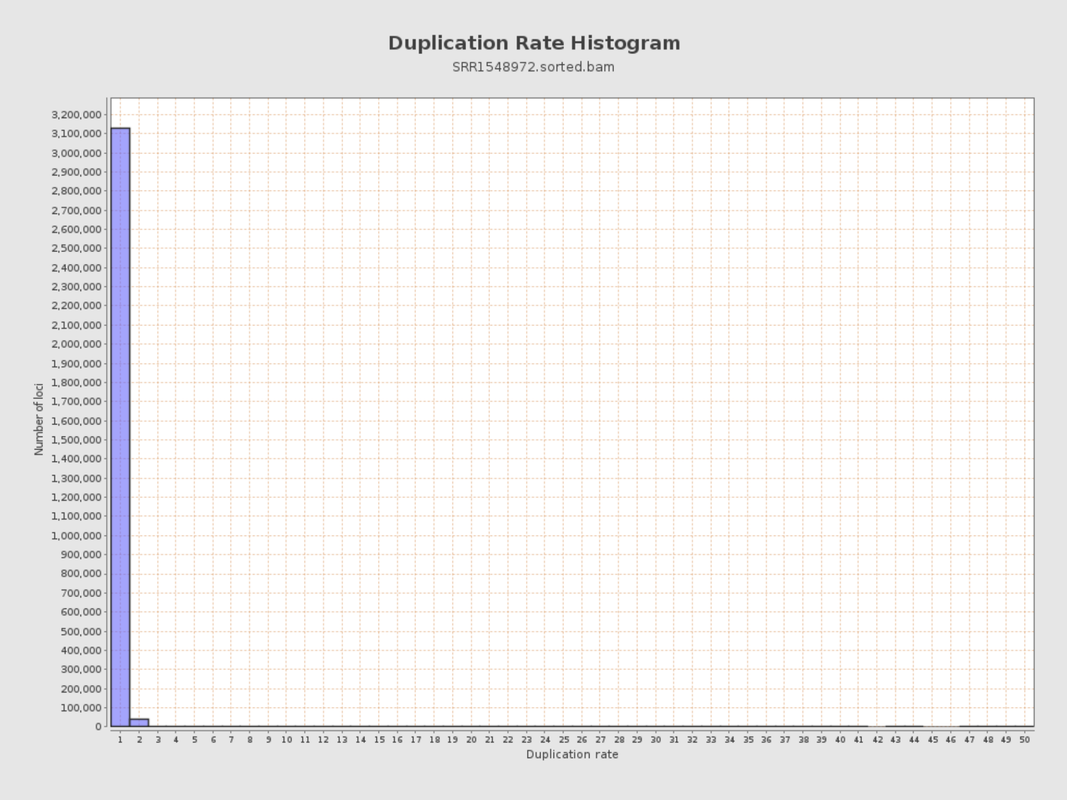
5. Results : Coverage Histogram (0-50X)



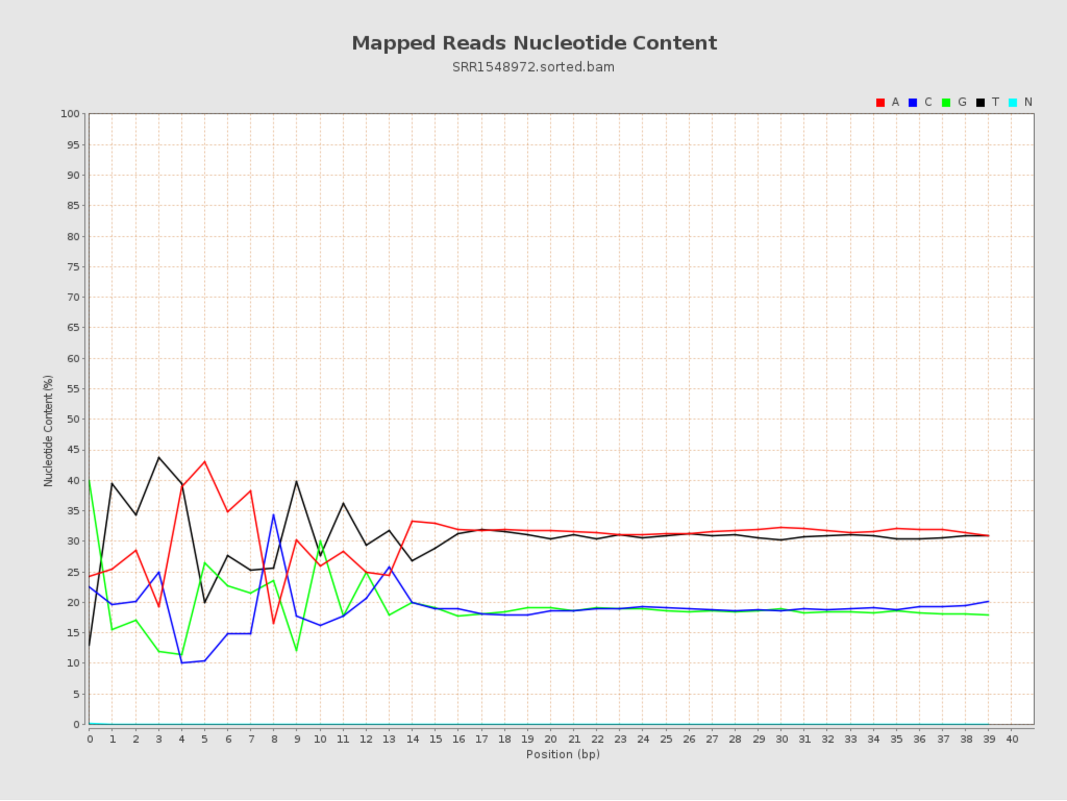
6. Results : Genome Fraction Coverage



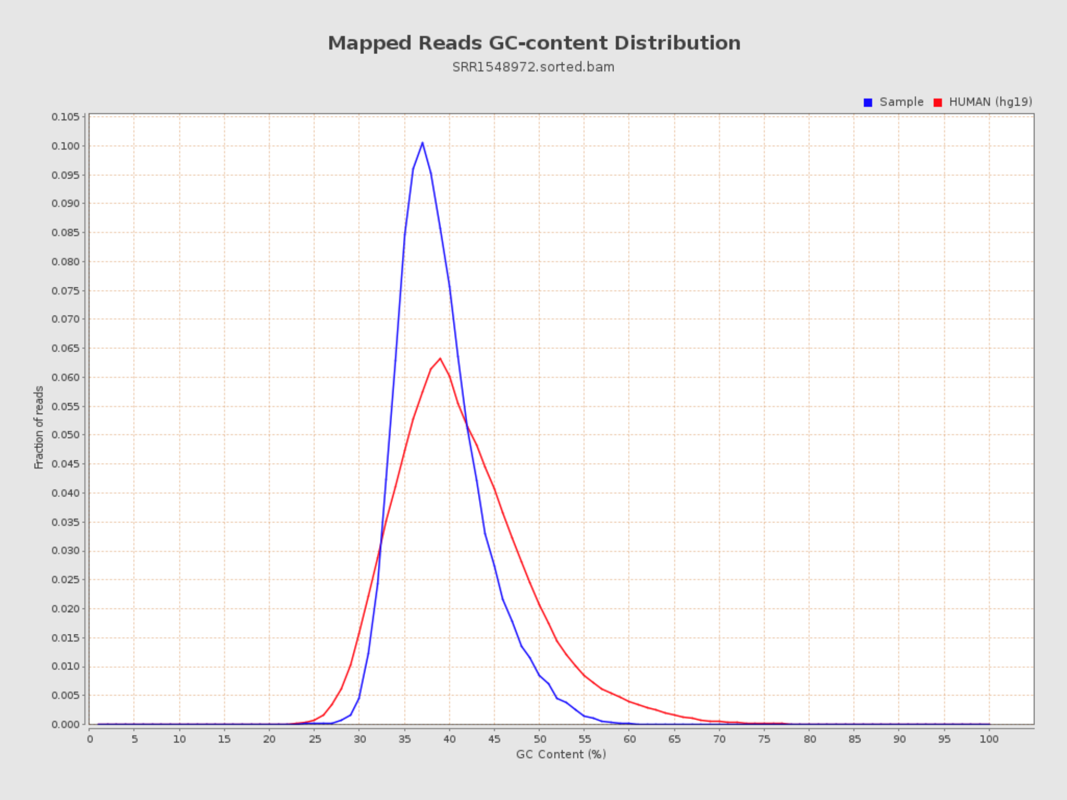
7. Results : Duplication Rate Histogram



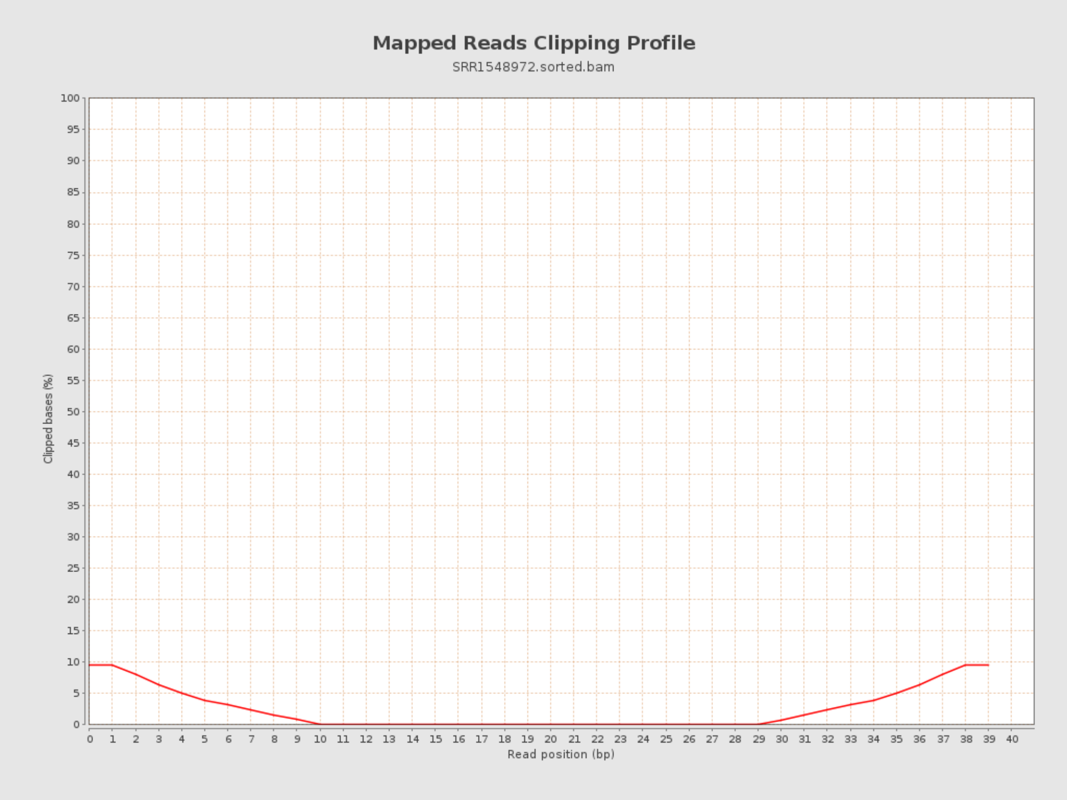
8. Results : Mapped Reads Nucleotide Content



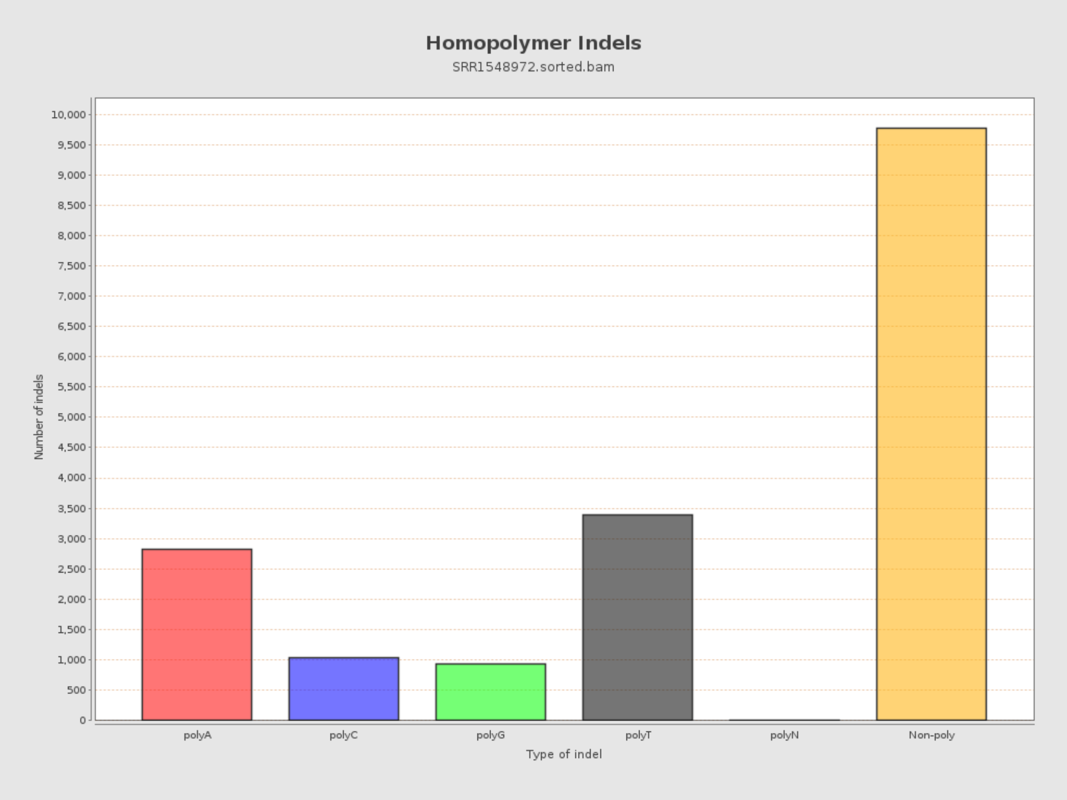
9. Results : Mapped Reads GC-content Distribution



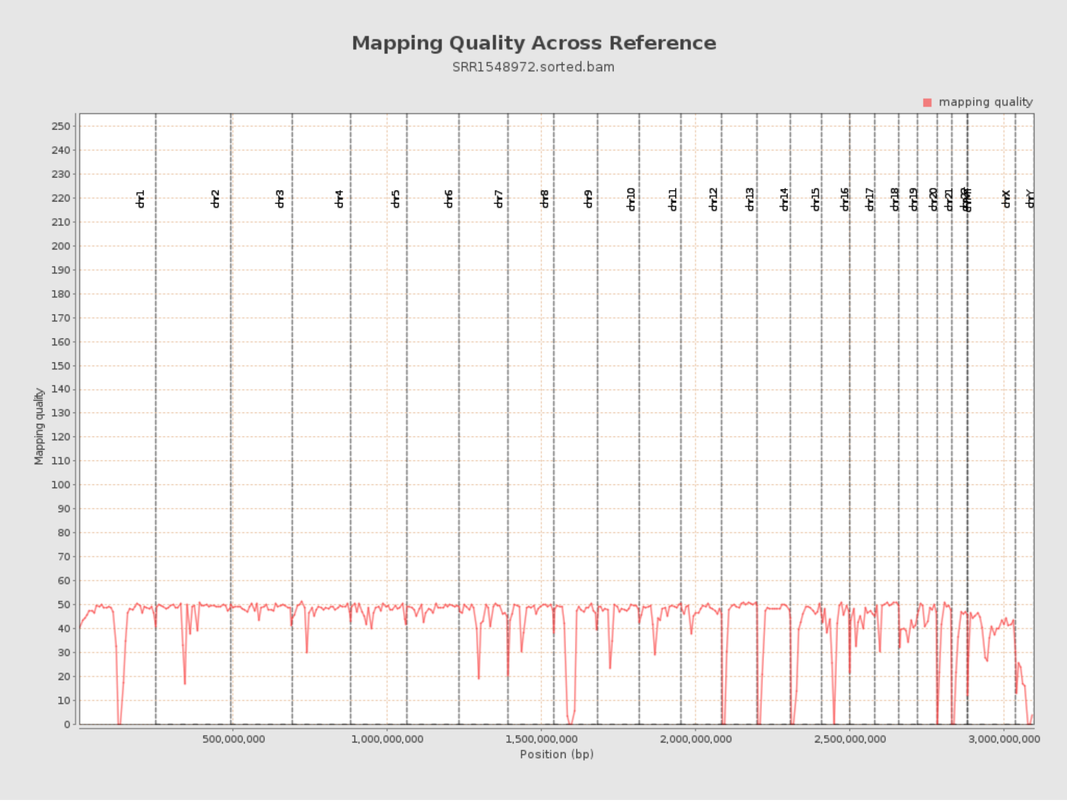
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram