Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:02:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084272.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_SRR3084272 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084272.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:02:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084272.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,334,734
Mapped reads	1,114,010 / 83.46%
Unmapped reads	220,724 / 16.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,628 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	23,500 / 1.76%
Duplication rate	1.51%
Clipped reads	452,079 / 33.87%

2.2. ACGT Content

Number/percentage of A's	22,757,598 / 30.21%
Number/percentage of C's	14,109,685 / 18.73%
Number/percentage of T's	22,062,133 / 29.29%
Number/percentage of G's	16,393,441 / 21.76%
Number/percentage of N's	799 / 0%
GC Percentage	40.5%

2.3. Coverage

Mean	0.0243

Standard Deviation	0.2316

2.4. Mapping Quality

Mean Mapping Quality	46.34

2.5. Mismatches and indels

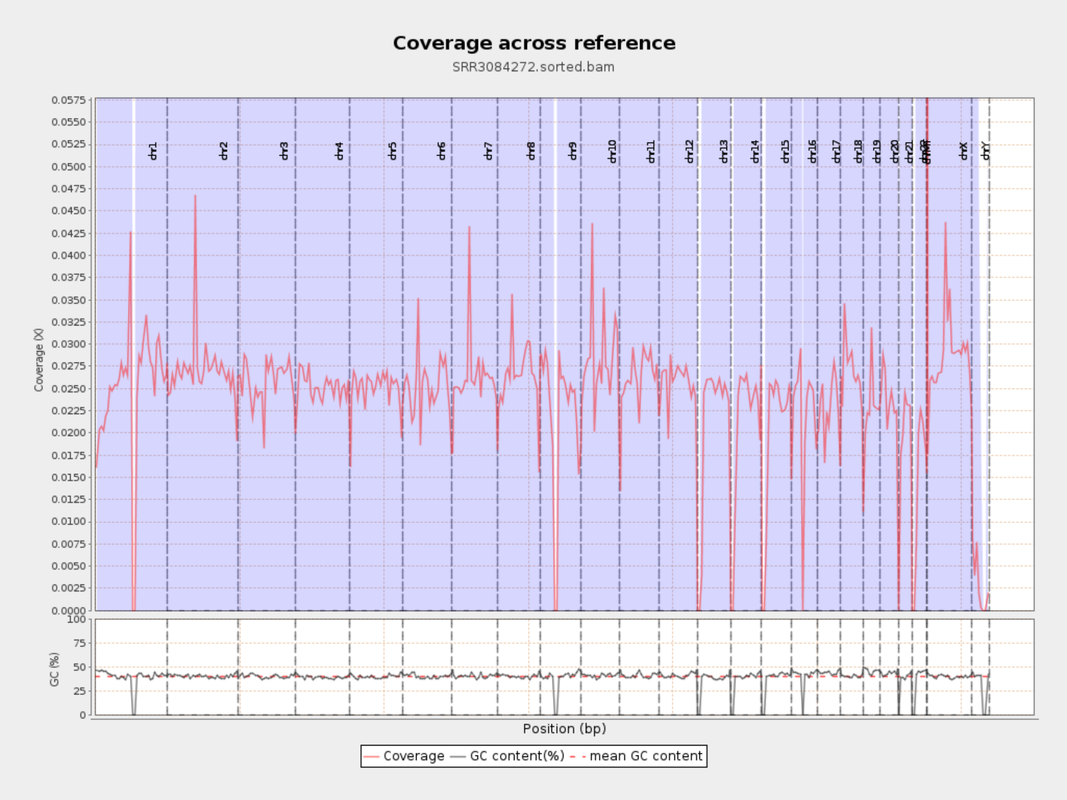
General error rate	0.84%
Mismatches	620,005
Insertions	5,779
Mapped reads with at least one insertion	0.51%
Deletions	13,947
Mapped reads with at least one deletion	1.24%
Homopolymer indels	43.32%

2.6. Chromosome stats

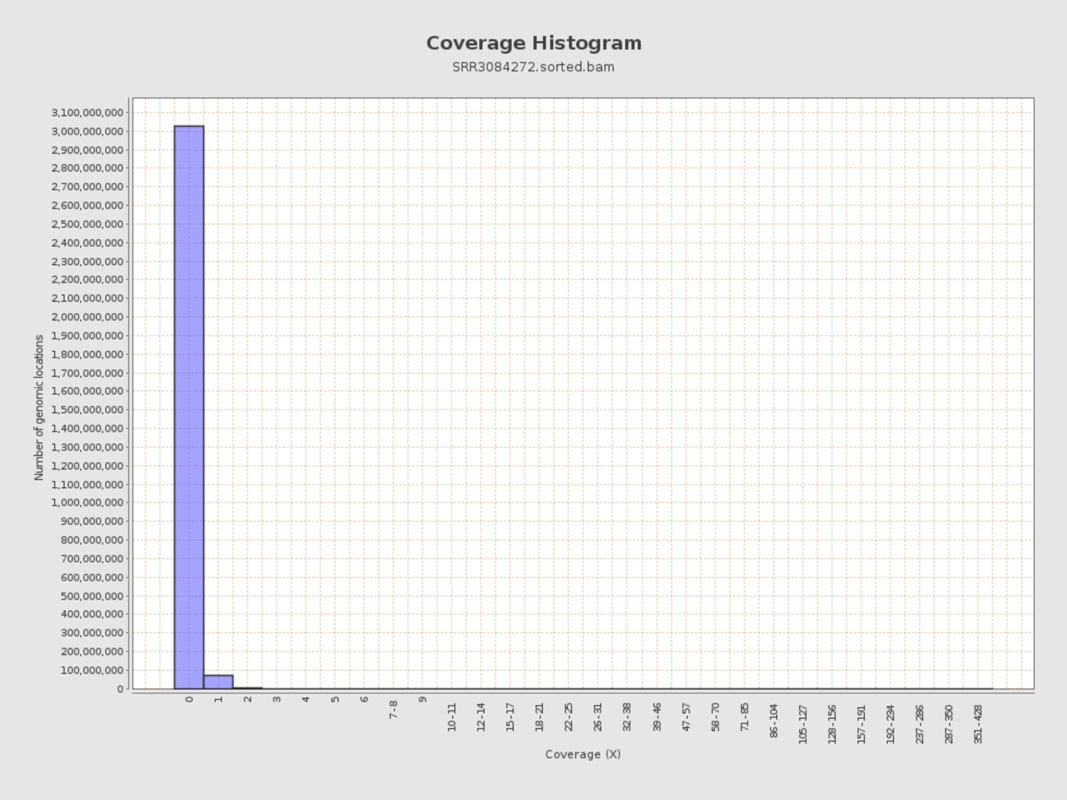
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6190995	0.0248	0.3937
chr2	243199373	6606231	0.0272	0.2585
chr3	198022430	5131551	0.0259	0.1663
chr4	191154276	4790758	0.0251	0.1663
chr5	180915260	4572393	0.0253	0.1643
chr6	171115067	4303249	0.0251	0.1949
chr7	159138663	4203073	0.0264	0.3043

chr8	146364022	3887934	0.0266	0.2183
chr9	141213431	3125610	0.0221	0.2113
chr10	135534747	3823964	0.0282	0.2523
chr11	135006516	3557439	0.0264	0.2135
chr12	133851895	3437108	0.0257	0.1662
chr13	115169878	2398532	0.0208	0.1485
chr14	107349540	2194609	0.0204	0.1625
chr15	102531392	2022560	0.0197	0.1502
chr16	90354753	1951307	0.0216	0.1719
chr17	81195210	1853352	0.0228	0.1773
chr18	78077248	2116299	0.0271	0.4359
chr19	59128983	1355293	0.0229	0.2856
chr20	63025520	1481595	0.0235	0.1628
chr21	48129895	919662	0.0191	0.1489
chr22	51304566	725117	0.0141	0.1225
chrMT	16571	33738	2.036	1.8441
chrX	155270560	4499761	0.029	0.197
chrY	59373566	164281	0.0028	0.0668

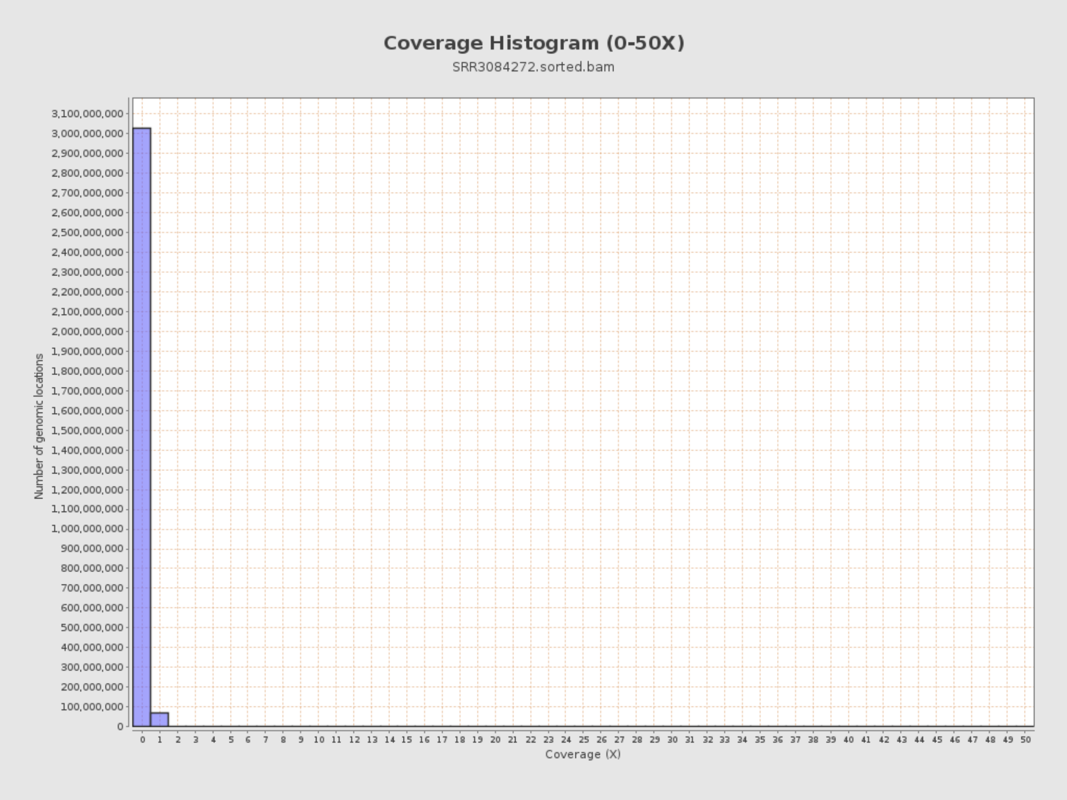
3. Results : Coverage across reference



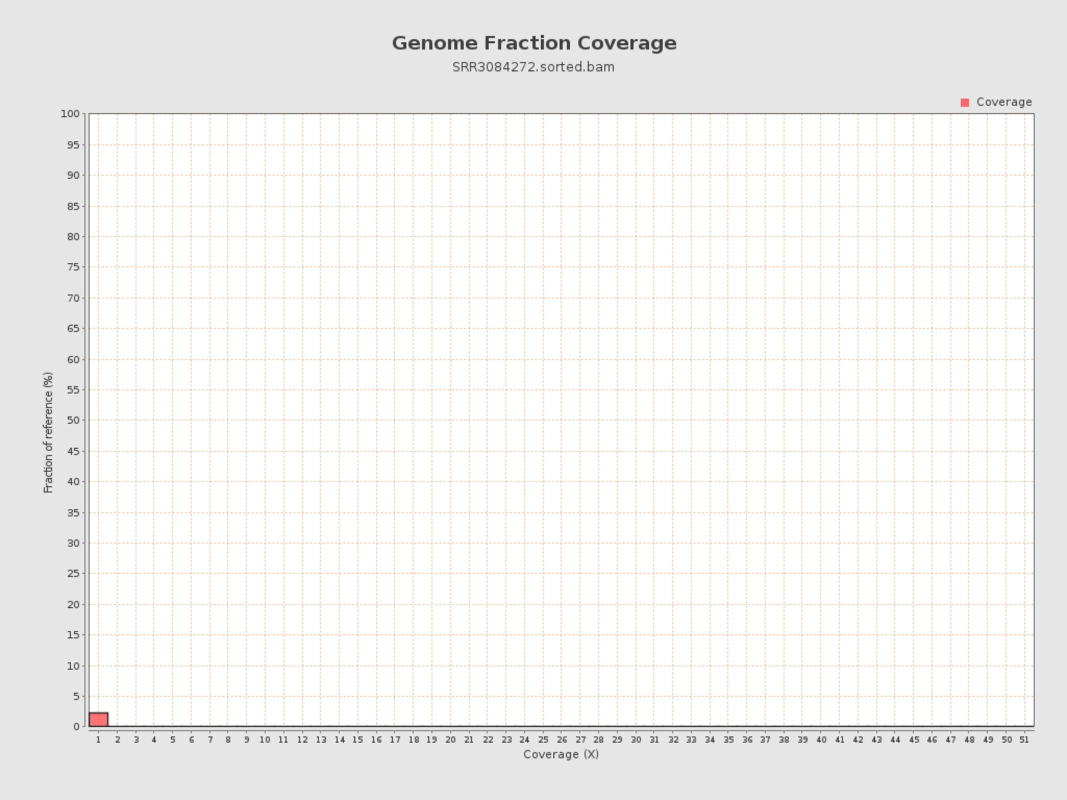
4. Results : Coverage Histogram



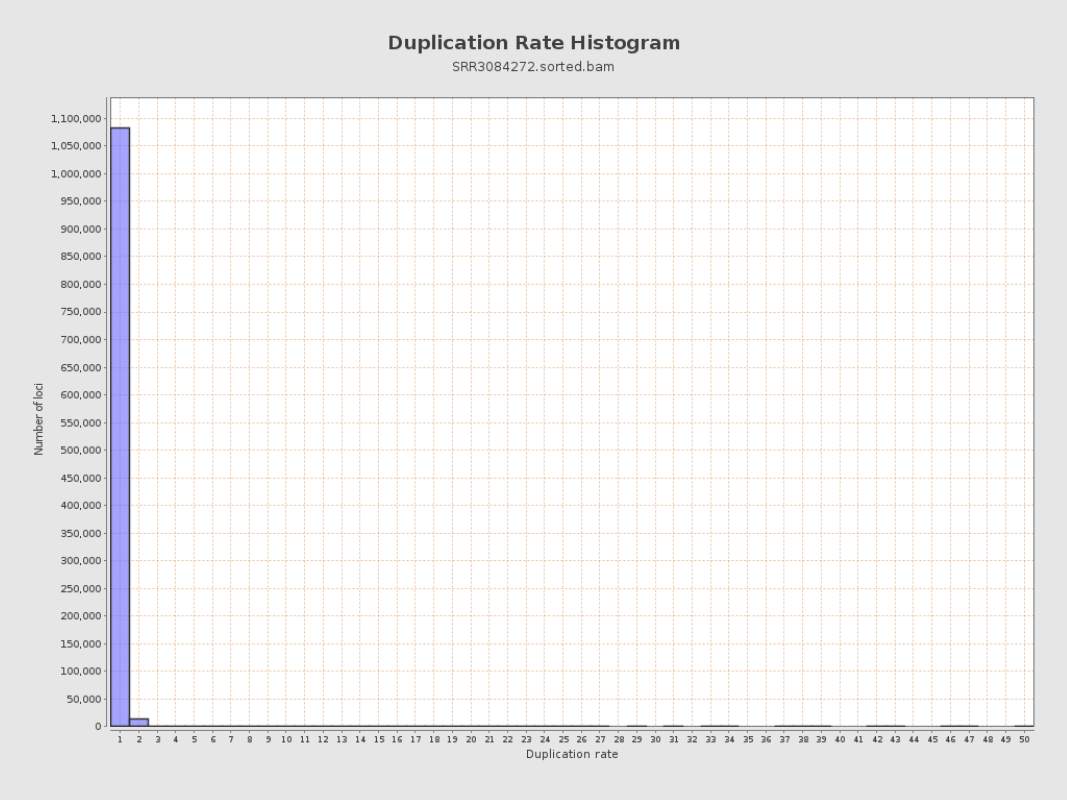
5. Results : Coverage Histogram (0-50X)



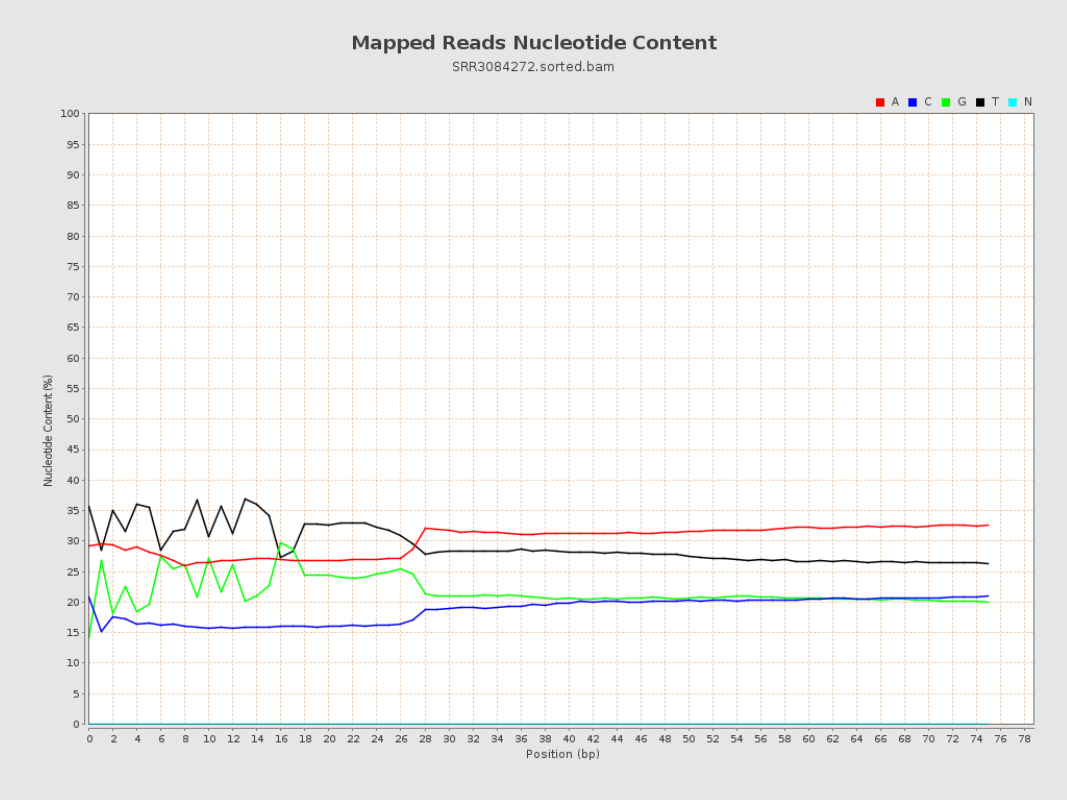
6. Results : Genome Fraction Coverage



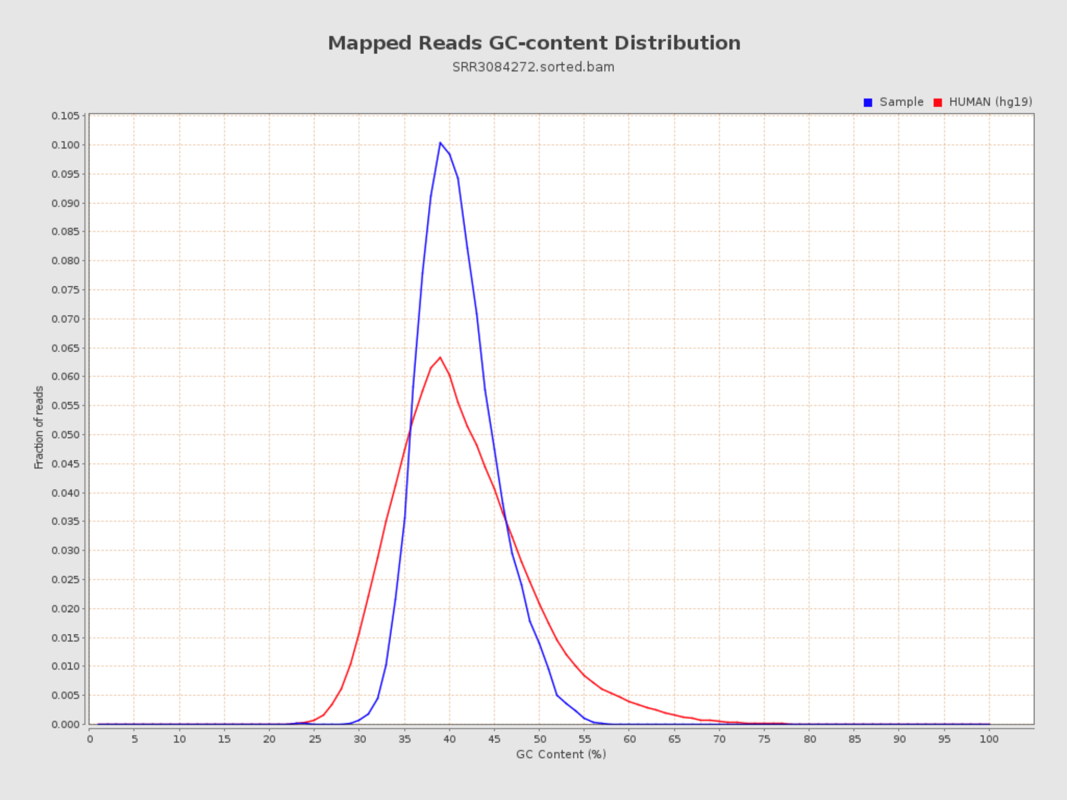
7. Results : Duplication Rate Histogram



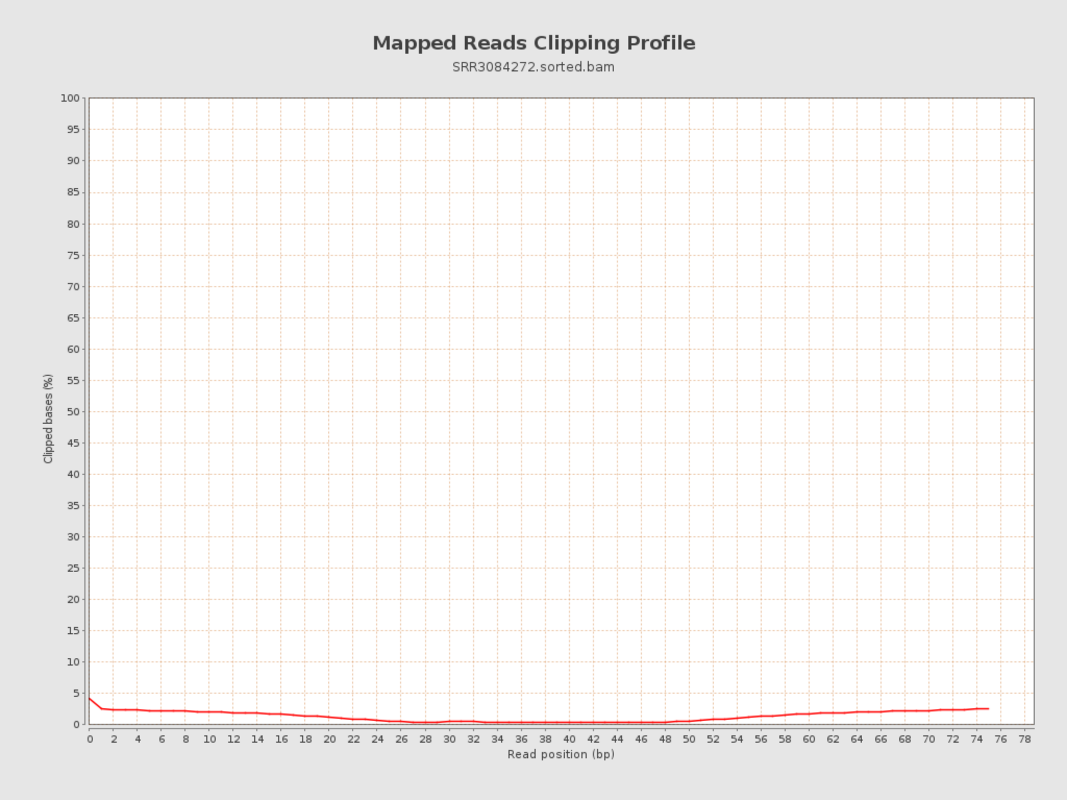
8. Results : Mapped Reads Nucleotide Content



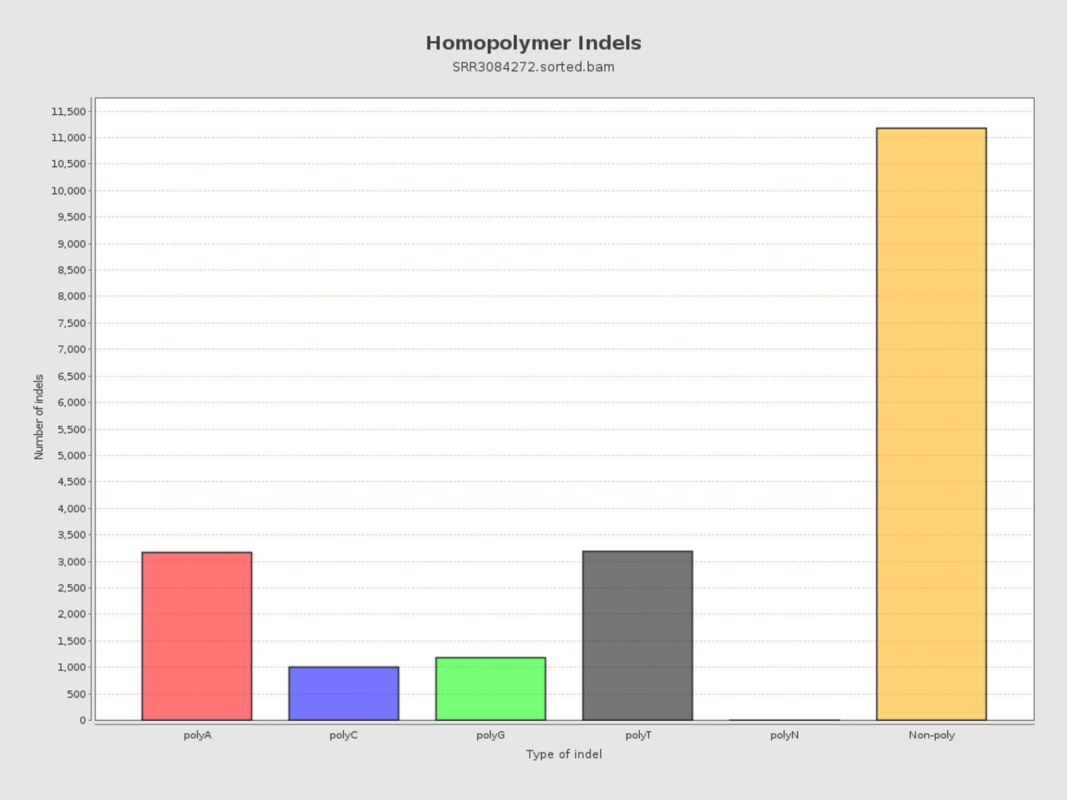
9. Results : Mapped Reads GC-content Distribution



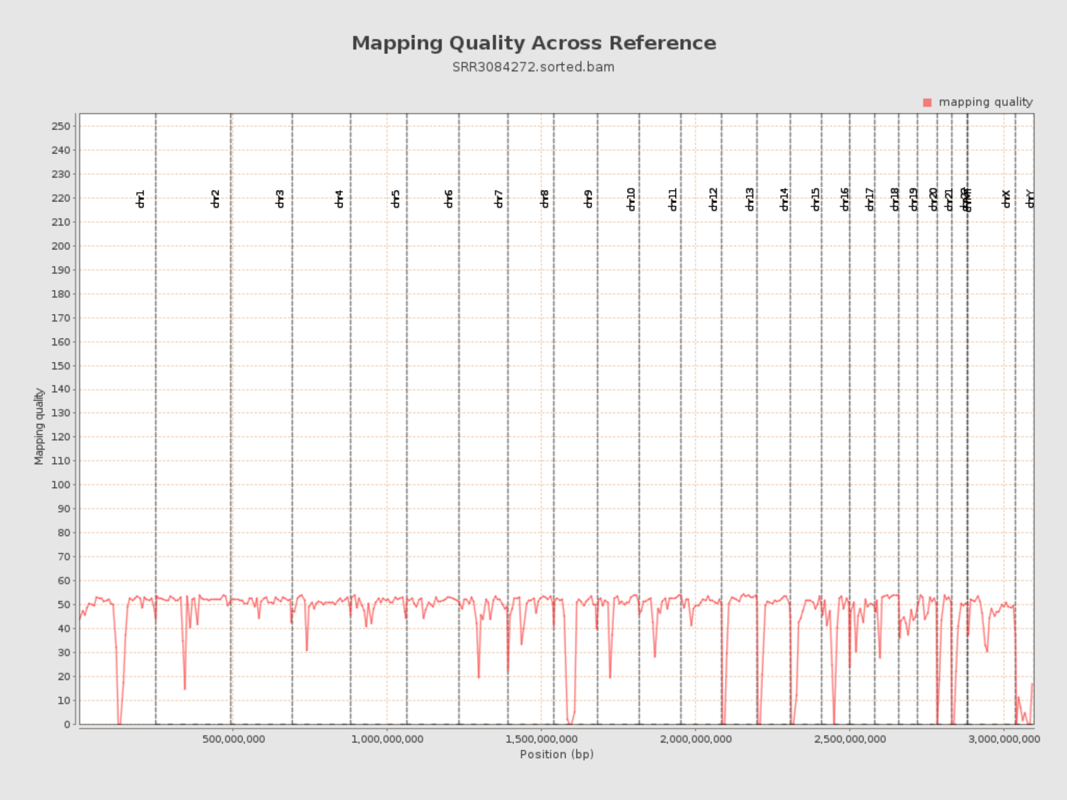
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram