Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:45:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084772.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_SRR3084772 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084772.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:45:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084772.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,710,993
Mapped reads	2,431,651 / 89.7%
Unmapped reads	279,342 / 10.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,754 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	109,549 / 4.04%
Duplication rate	3.47%
Clipped reads	1,032,106 / 38.07%

2.2. ACGT Content

Number/percentage of A's	44,665,678 / 27.3%
Number/percentage of C's	30,881,227 / 18.88%
Number/percentage of T's	51,091,443 / 31.23%
Number/percentage of G's	36,900,684 / 22.56%
Number/percentage of N's	63,648 / 0.04%
GC Percentage	41.43%

2.3. Coverage

Mean	0.0529

Standard Deviation	0.4286

2.4. Mapping Quality

Mean Mapping Quality	46.62

2.5. Mismatches and indels

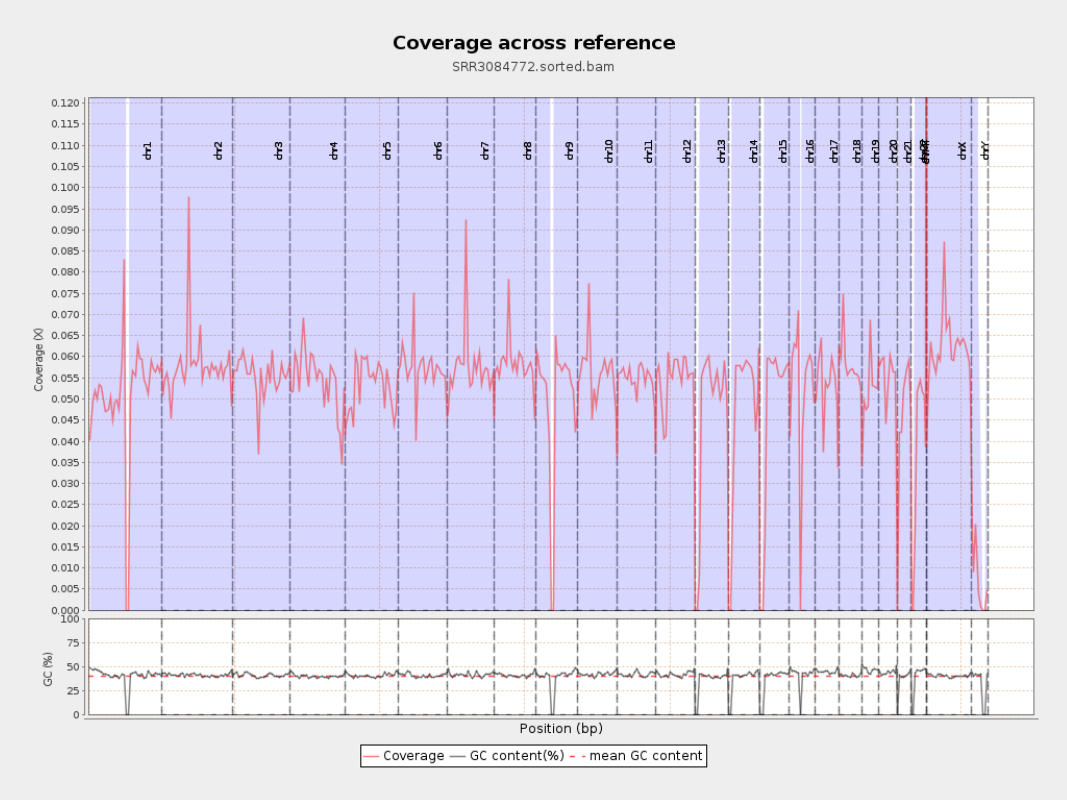
General error rate	0.9%
Mismatches	1,447,754
Insertions	12,541
Mapped reads with at least one insertion	0.51%
Deletions	42,219
Mapped reads with at least one deletion	1.72%
Homopolymer indels	46.48%

2.6. Chromosome stats

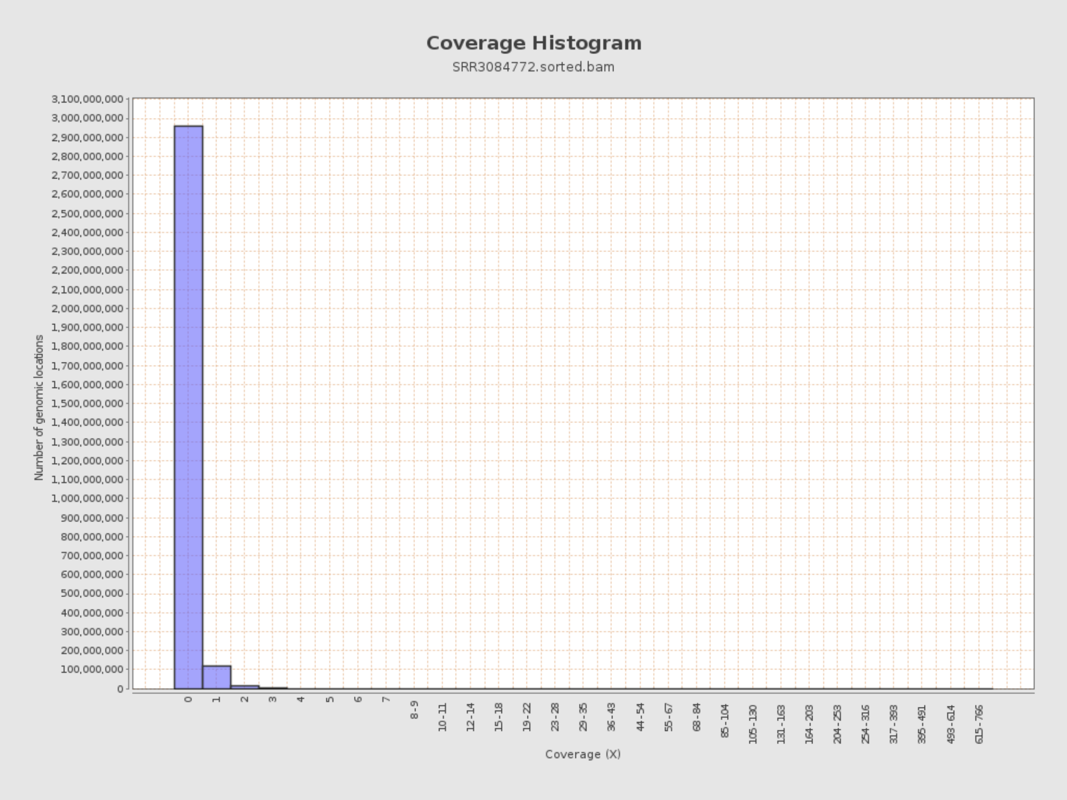
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12611010	0.0506	0.6888
chr2	243199373	14078008	0.0579	0.5501
chr3	198022430	10995536	0.0555	0.2663
chr4	191154276	10370247	0.0543	0.2858
chr5	180915260	9602417	0.0531	0.2648
chr6	171115067	9795379	0.0572	0.3524
chr7	159138663	9240292	0.0581	0.604

chr8	146364022	8542730	0.0584	0.4315
chr9	141213431	6903017	0.0489	0.4332
chr10	135534747	7633375	0.0563	0.3982
chr11	135006516	7365490	0.0546	0.4029
chr12	133851895	7329703	0.0548	0.2713
chr13	115169878	5269560	0.0458	0.2453
chr14	107349540	4968803	0.0463	0.2719
chr15	102531392	4770256	0.0465	0.2587
chr16	90354753	4729046	0.0523	0.3
chr17	81195210	4267238	0.0526	0.3177
chr18	78077248	4578809	0.0586	0.8975
chr19	59128983	3108134	0.0526	0.5447
chr20	63025520	3456089	0.0548	0.2815
chr21	48129895	2187951	0.0455	0.2615
chr22	51304566	1835004	0.0358	0.2136
chrMT	16571	4915	0.2966	0.6461
chrX	155270560	9634375	0.062	0.3365
chrY	59373566	394582	0.0066	0.1426

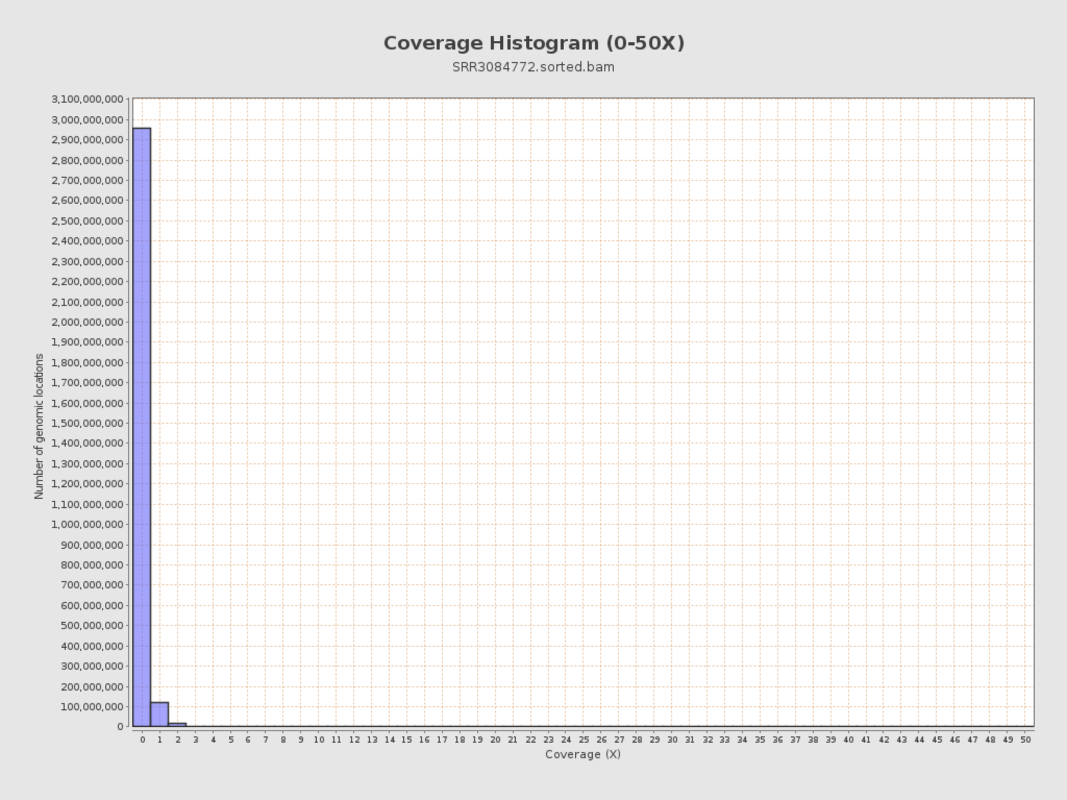
3. Results : Coverage across reference



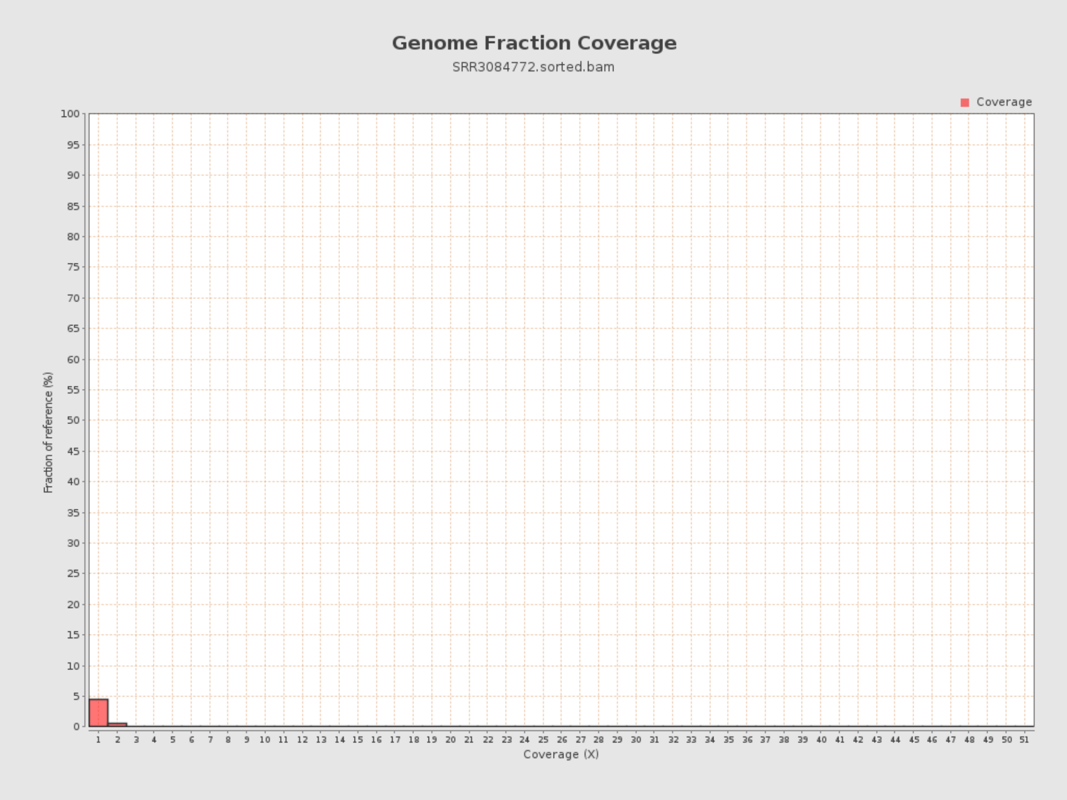
4. Results : Coverage Histogram



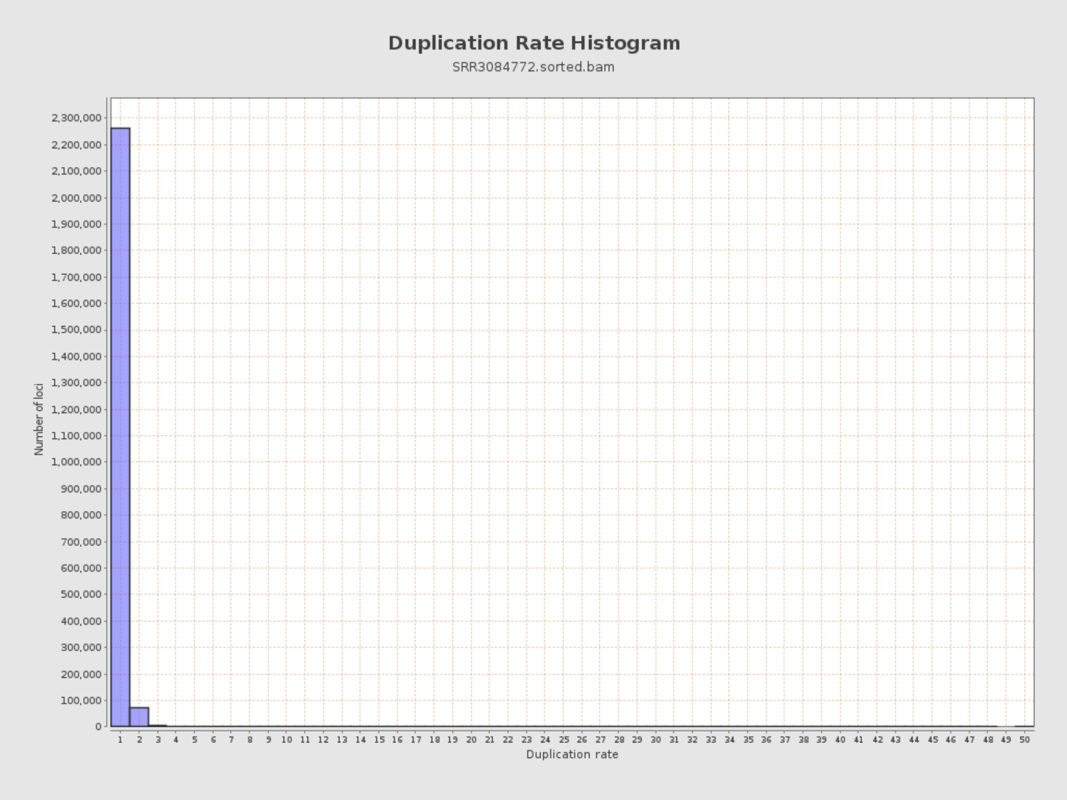
5. Results : Coverage Histogram (0-50X)



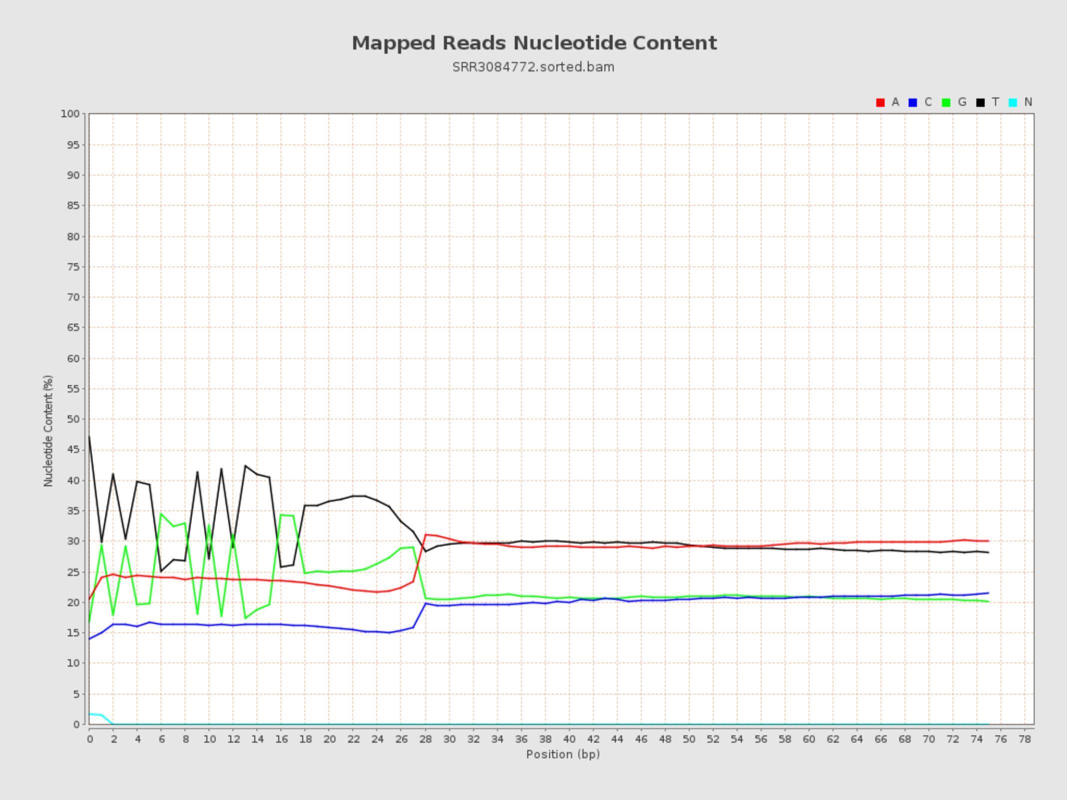
6. Results : Genome Fraction Coverage



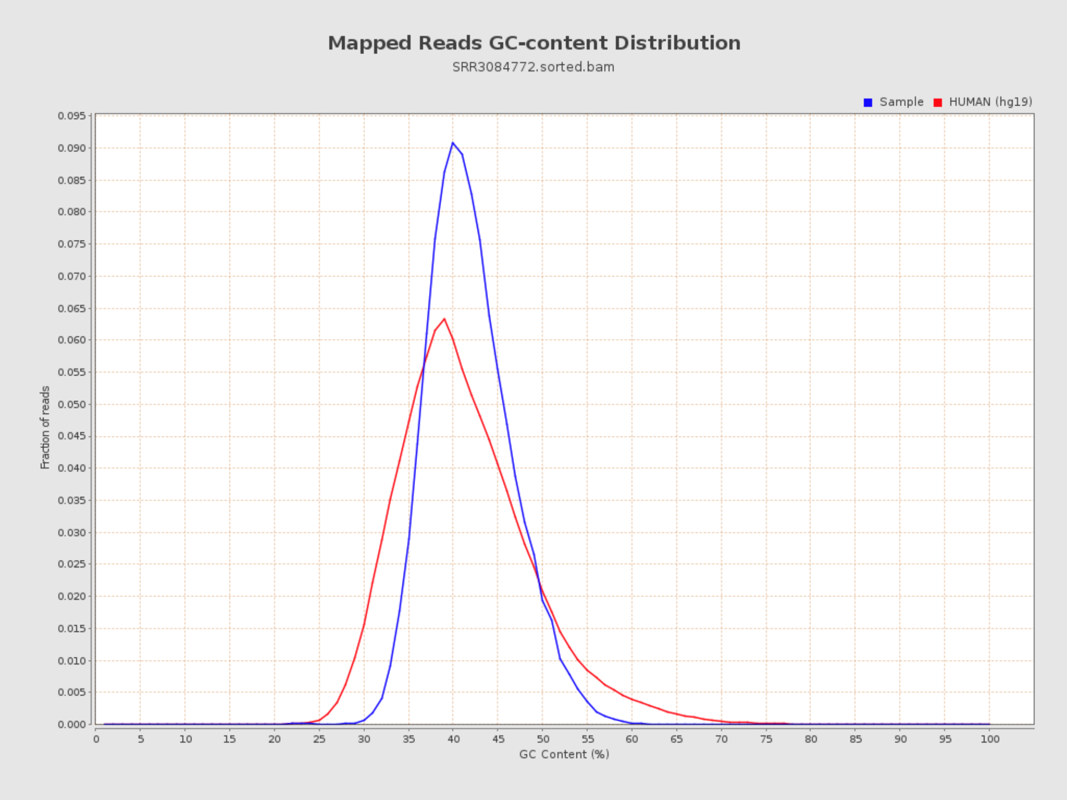
7. Results : Duplication Rate Histogram



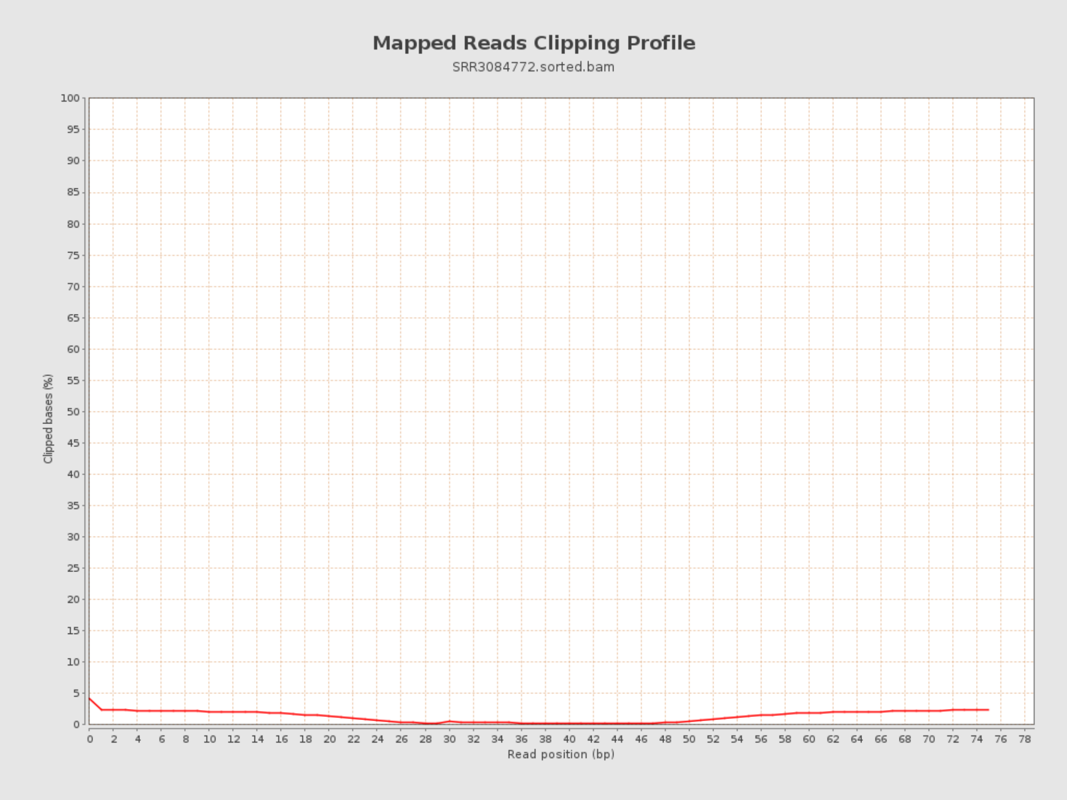
8. Results : Mapped Reads Nucleotide Content



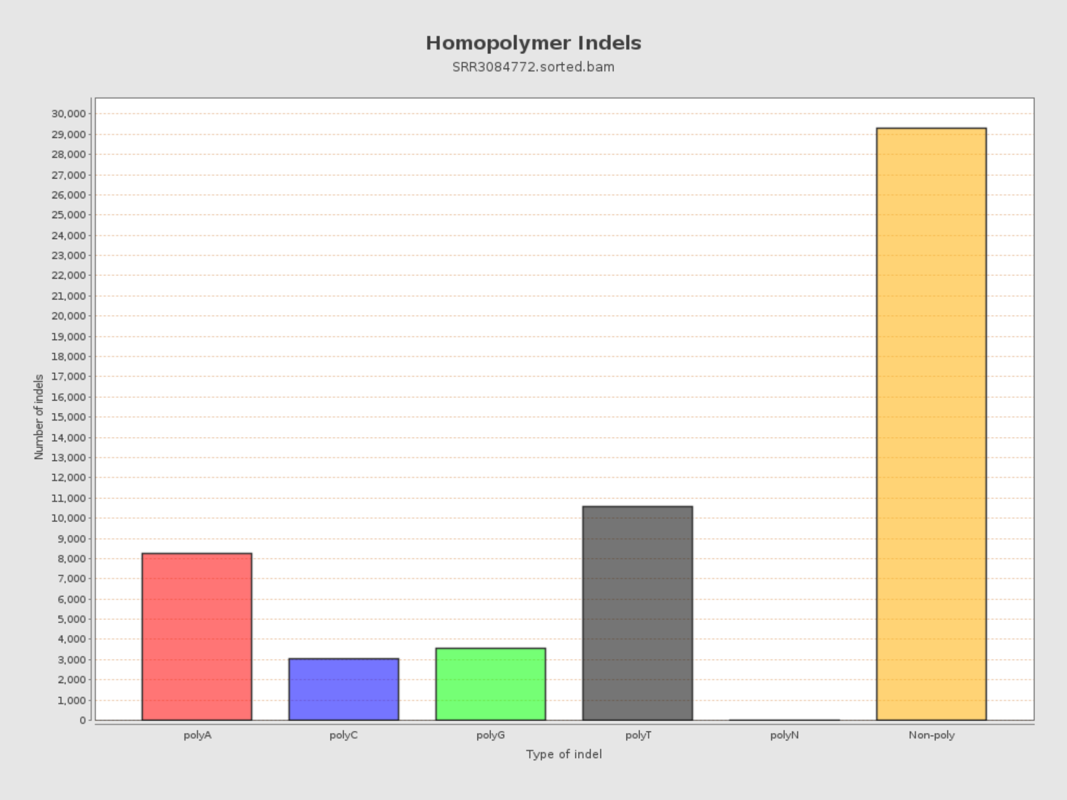
9. Results : Mapped Reads GC-content Distribution



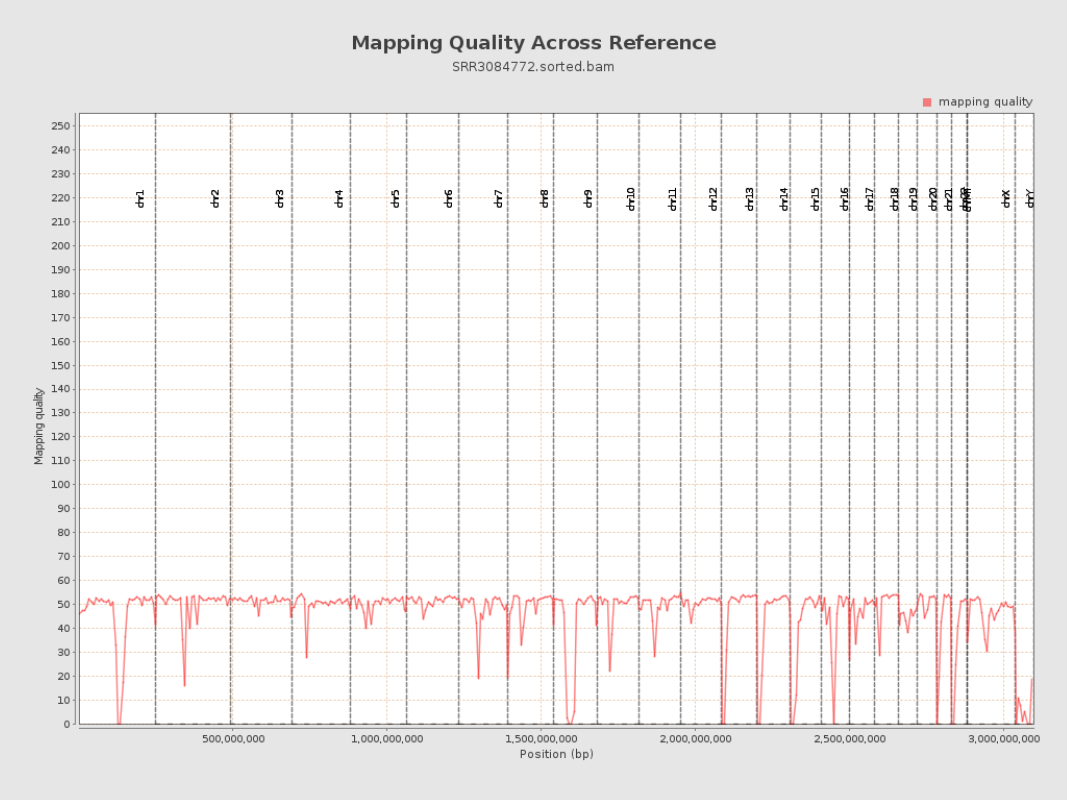
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram