Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:47:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084391.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_SRR3084391 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084391.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:47:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084391.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,570,380
Mapped reads	2,344,955 / 91.23%
Unmapped reads	225,425 / 8.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,299 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	80,953 / 3.15%
Duplication rate	2.91%
Clipped reads	1,062,632 / 41.34%

2.2. ACGT Content

Number/percentage of A's	44,528,217 / 28.39%
Number/percentage of C's	29,889,281 / 19.06%
Number/percentage of T's	48,510,497 / 30.93%
Number/percentage of G's	33,698,910 / 21.49%
Number/percentage of N's	205,420 / 0.13%
GC Percentage	40.55%

2.3. Coverage

Mean	0.0507

Standard Deviation	0.332

2.4. Mapping Quality

Mean Mapping Quality	46.15

2.5. Mismatches and indels

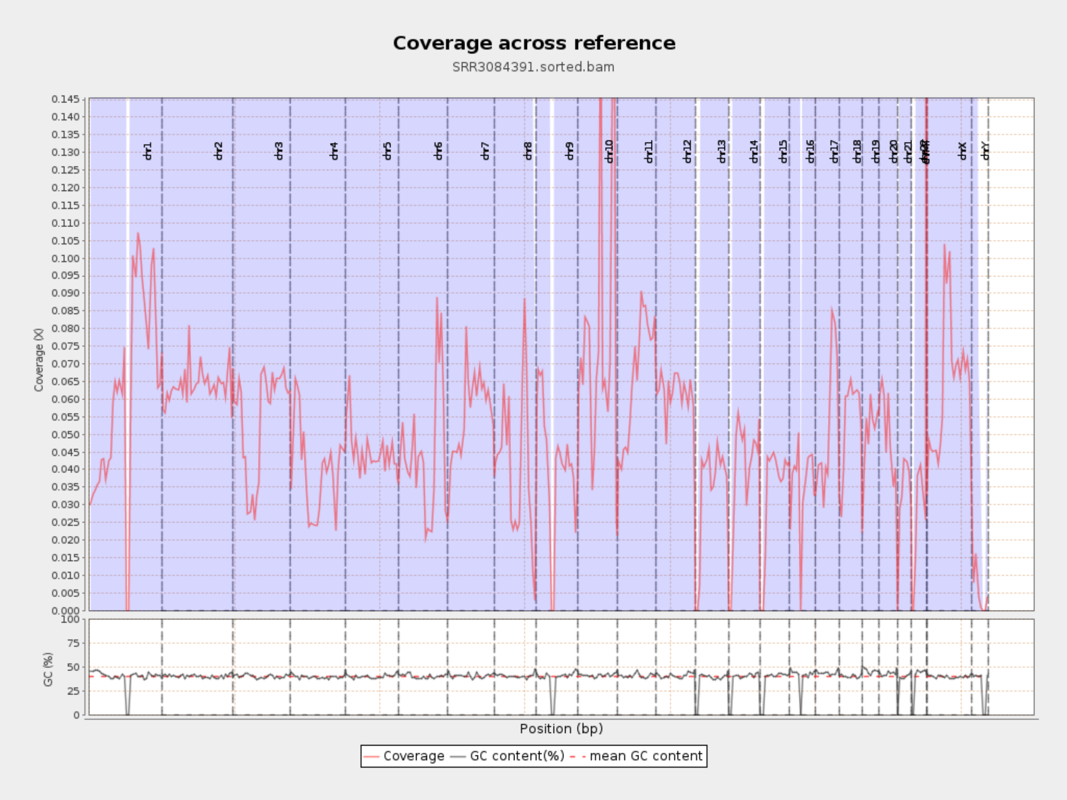
General error rate	1.03%
Mismatches	1,588,783
Insertions	11,310
Mapped reads with at least one insertion	0.48%
Deletions	31,726
Mapped reads with at least one deletion	1.34%
Homopolymer indels	47.77%

2.6. Chromosome stats

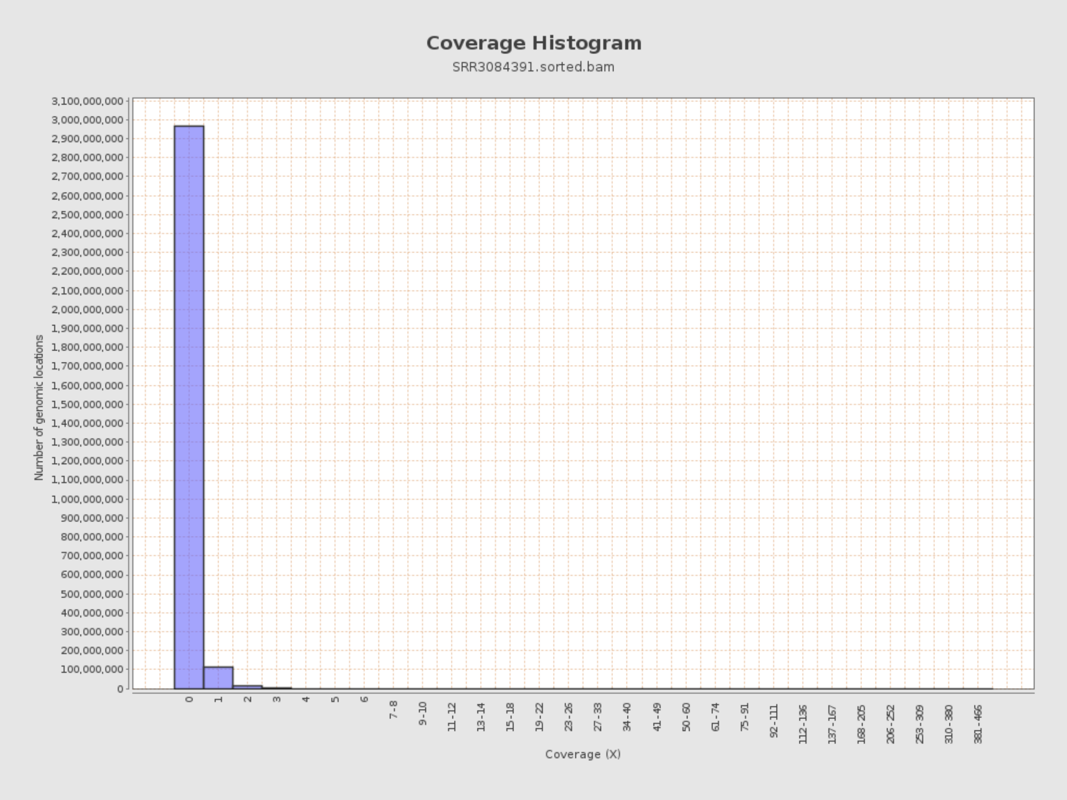
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15445708	0.062	0.5016
chr2	243199373	15599538	0.0641	0.3824
chr3	198022430	10810912	0.0546	0.2698
chr4	191154276	7663450	0.0401	0.2404
chr5	180915260	8193493	0.0453	0.2428
chr6	171115067	7582649	0.0443	0.2641
chr7	159138663	8969099	0.0564	0.4869

chr8	146364022	5964444	0.0408	0.3118
chr9	141213431	5820342	0.0412	0.2796
chr10	135534747	11078104	0.0817	0.4596
chr11	135006516	8884195	0.0658	0.3545
chr12	133851895	8220656	0.0614	0.2863
chr13	115169878	3909566	0.0339	0.2115
chr14	107349540	4163293	0.0388	0.2341
chr15	102531392	3440791	0.0336	0.2164
chr16	90354753	3242395	0.0359	0.233
chr17	81195210	4288491	0.0528	0.2829
chr18	78077248	4242028	0.0543	0.4262
chr19	59128983	3020883	0.0511	0.3739
chr20	63025520	3167609	0.0503	0.26
chr21	48129895	1582147	0.0329	0.2182
chr22	51304566	1264207	0.0246	0.1778
chrMT	16571	20346	1.2278	1.3677
chrX	155270560	9975601	0.0642	0.3201
chrY	59373566	338223	0.0057	0.1226

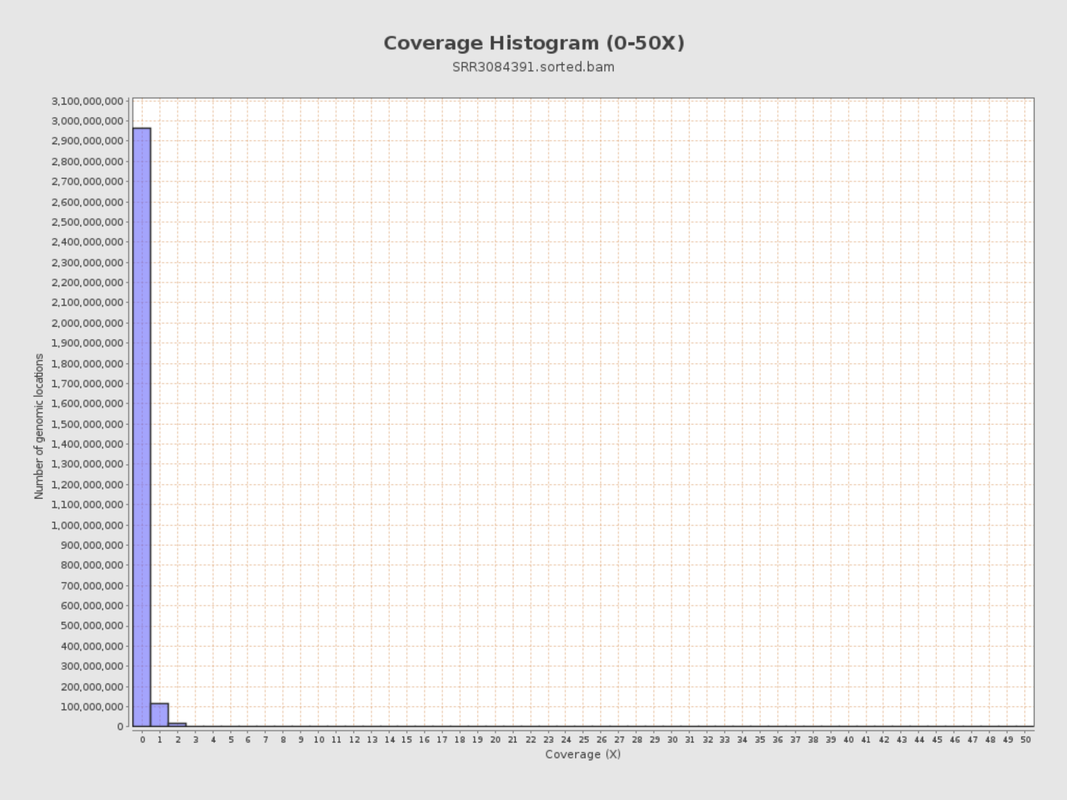
3. Results : Coverage across reference



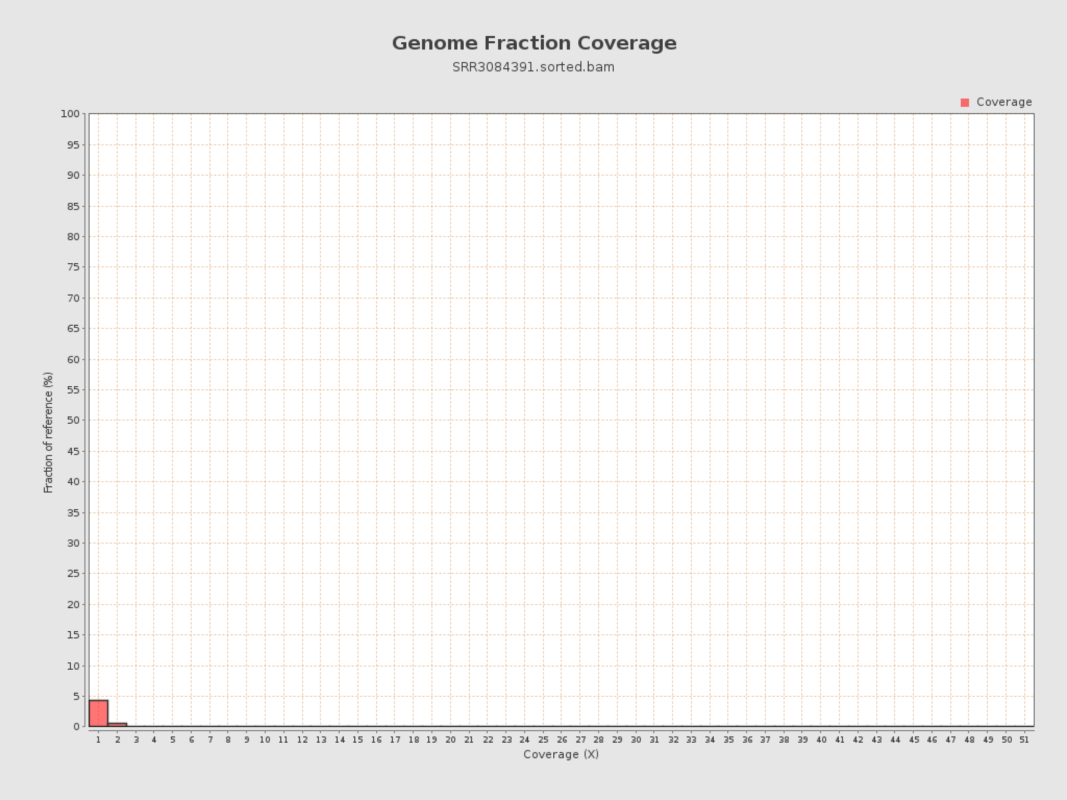
4. Results : Coverage Histogram



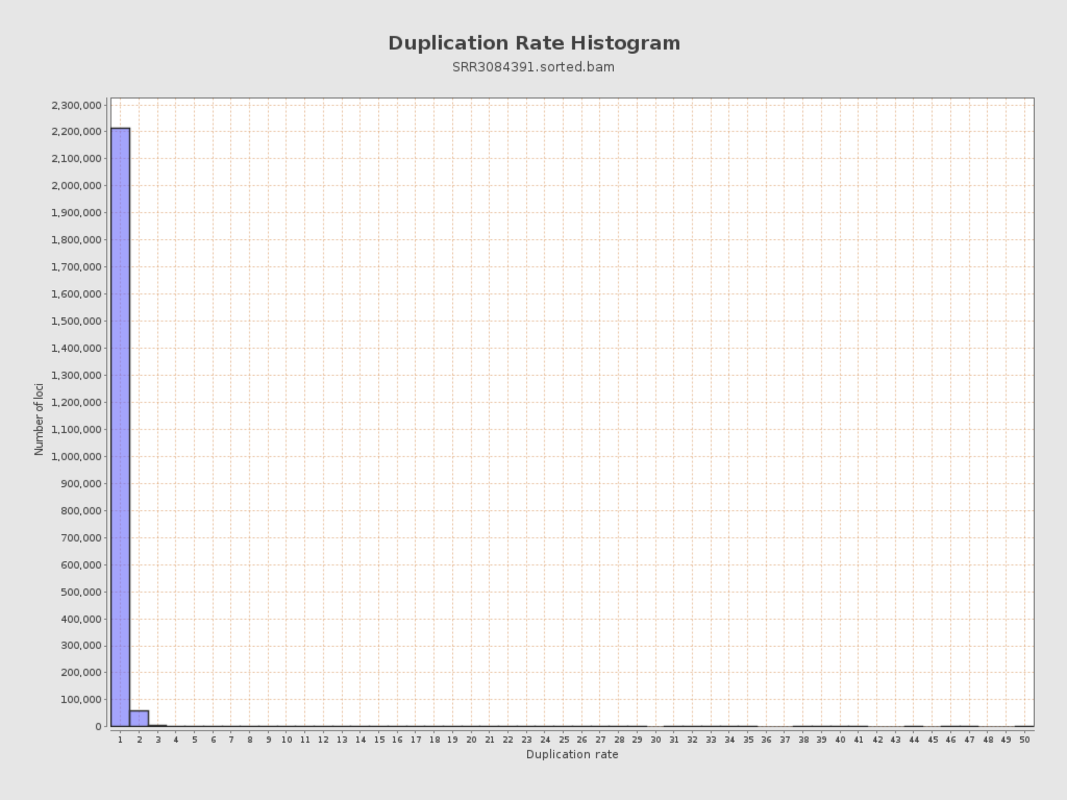
5. Results : Coverage Histogram (0-50X)



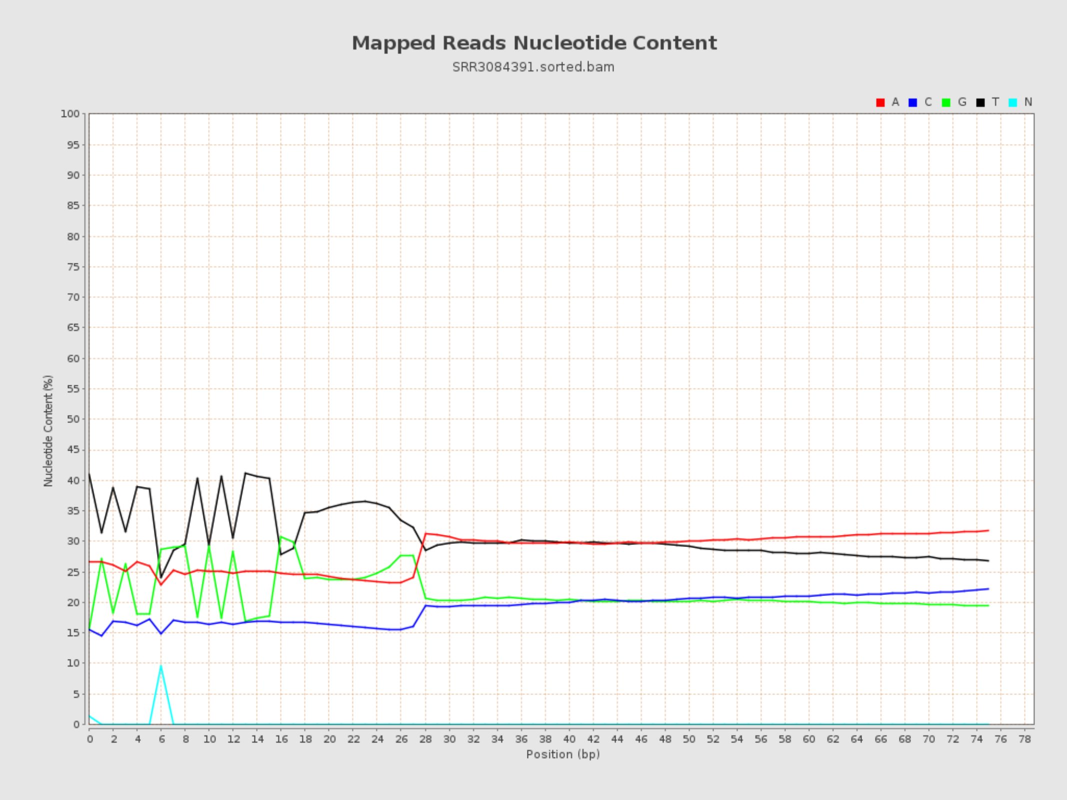
6. Results : Genome Fraction Coverage



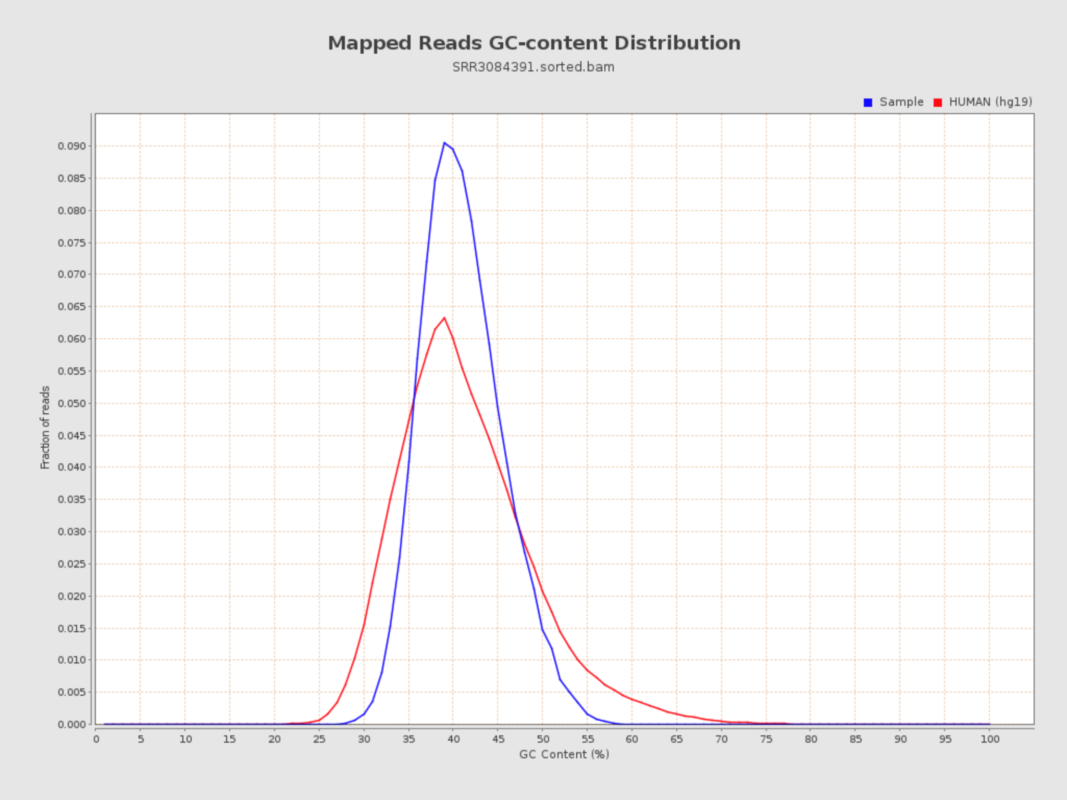
7. Results : Duplication Rate Histogram



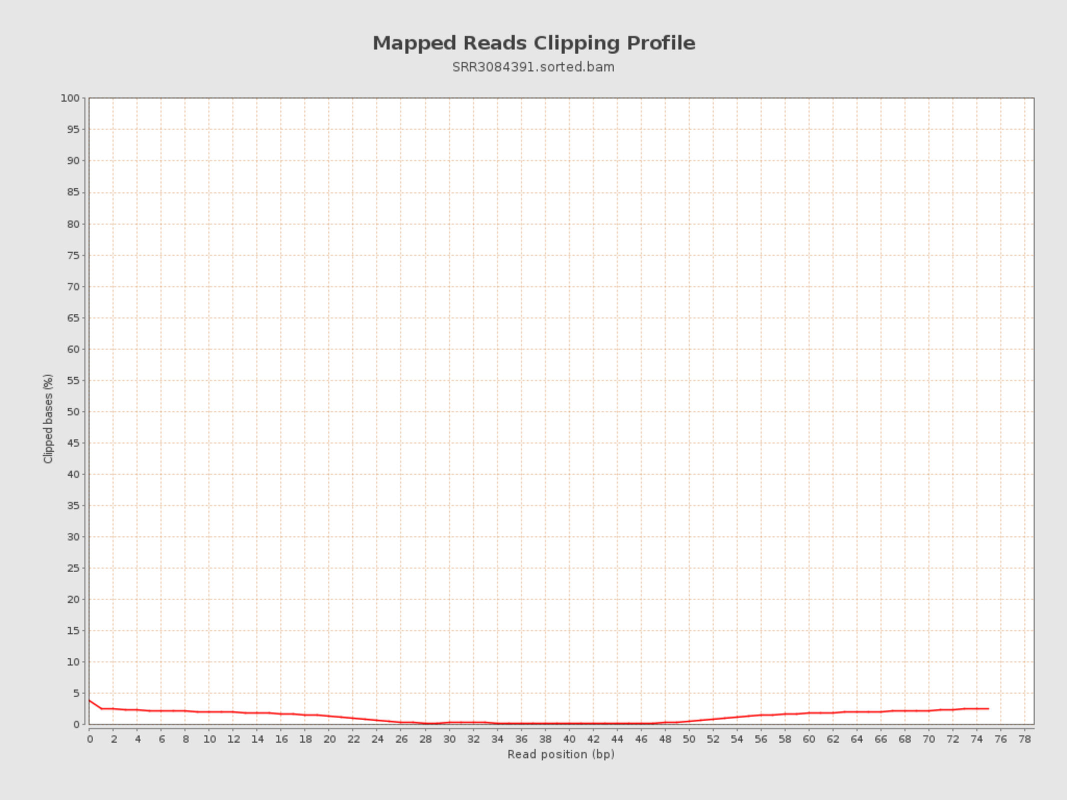
8. Results : Mapped Reads Nucleotide Content



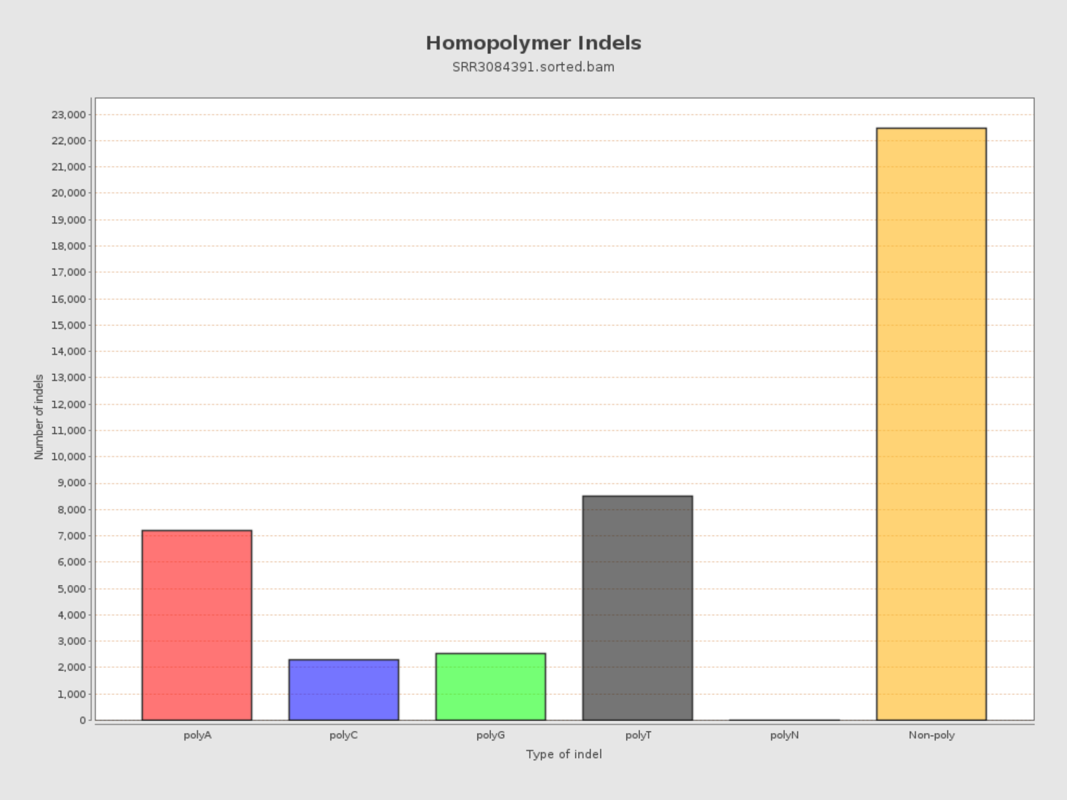
9. Results : Mapped Reads GC-content Distribution



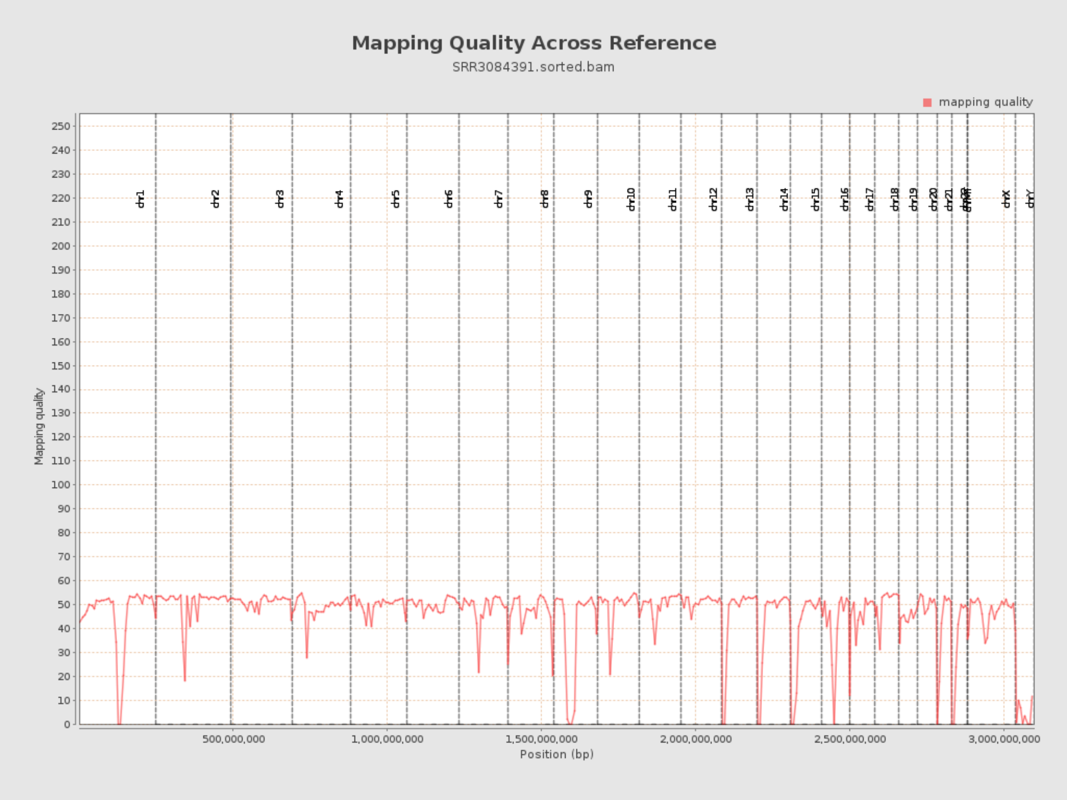
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram