Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:43:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084390.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_SRR3084390 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084390.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:43:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084390.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,551,668
Mapped reads	2,321,930 / 91%
Unmapped reads	229,738 / 9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,215 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	78,757 / 3.09%
Duplication rate	2.96%
Clipped reads	1,049,188 / 41.12%

2.2. ACGT Content

Number/percentage of A's	43,532,131 / 28.04%
Number/percentage of C's	29,859,142 / 19.24%
Number/percentage of T's	47,892,586 / 30.85%
Number/percentage of G's	33,746,994 / 21.74%
Number/percentage of N's	198,834 / 0.13%
GC Percentage	40.98%

2.3. Coverage

Mean	0.0502

Standard Deviation	0.3057

2.4. Mapping Quality

Mean Mapping Quality	46.4

2.5. Mismatches and indels

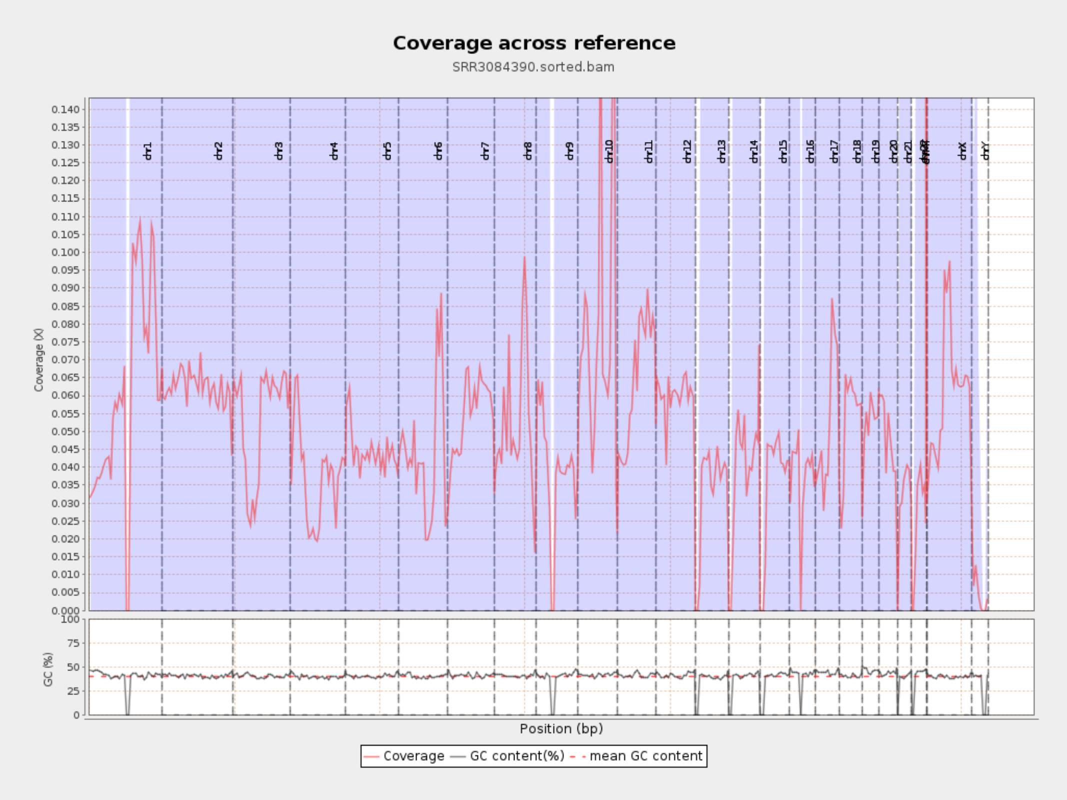
General error rate	1.03%
Mismatches	1,582,001
Insertions	10,930
Mapped reads with at least one insertion	0.47%
Deletions	32,133
Mapped reads with at least one deletion	1.37%
Homopolymer indels	47.99%

2.6. Chromosome stats

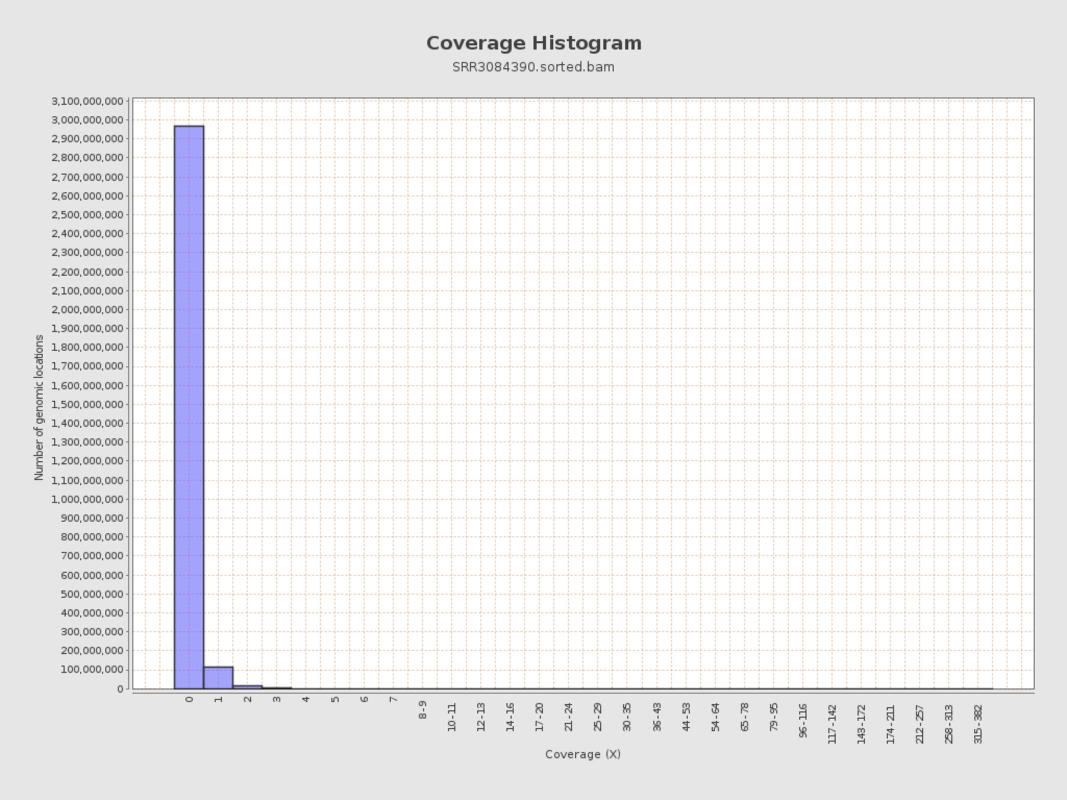
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15092668	0.0606	0.4294
chr2	243199373	15146295	0.0623	0.3427
chr3	198022430	10604240	0.0536	0.2664
chr4	191154276	7158119	0.0374	0.2273
chr5	180915260	8063966	0.0446	0.2417
chr6	171115067	7439128	0.0435	0.2616
chr7	159138663	8767133	0.0551	0.4105

chr8	146364022	7668531	0.0524	0.3164
chr9	141213431	5472914	0.0388	0.256
chr10	135534747	11211651	0.0827	0.407
chr11	135006516	8666027	0.0642	0.3429
chr12	133851895	8001996	0.0598	0.2824
chr13	115169878	3798563	0.033	0.2097
chr14	107349540	4126266	0.0384	0.2302
chr15	102531392	3634035	0.0354	0.2223
chr16	90354753	3364446	0.0372	0.2344
chr17	81195210	4250347	0.0523	0.2767
chr18	78077248	4141923	0.053	0.3869
chr19	59128983	3127950	0.0529	0.3357
chr20	63025520	3024653	0.048	0.253
chr21	48129895	1512944	0.0314	0.2103
chr22	51304566	1269169	0.0247	0.1779
chrMT	16571	68987	4.1631	3.2145
chrX	155270560	9384672	0.0604	0.3025
chrY	59373566	290013	0.0049	0.0956

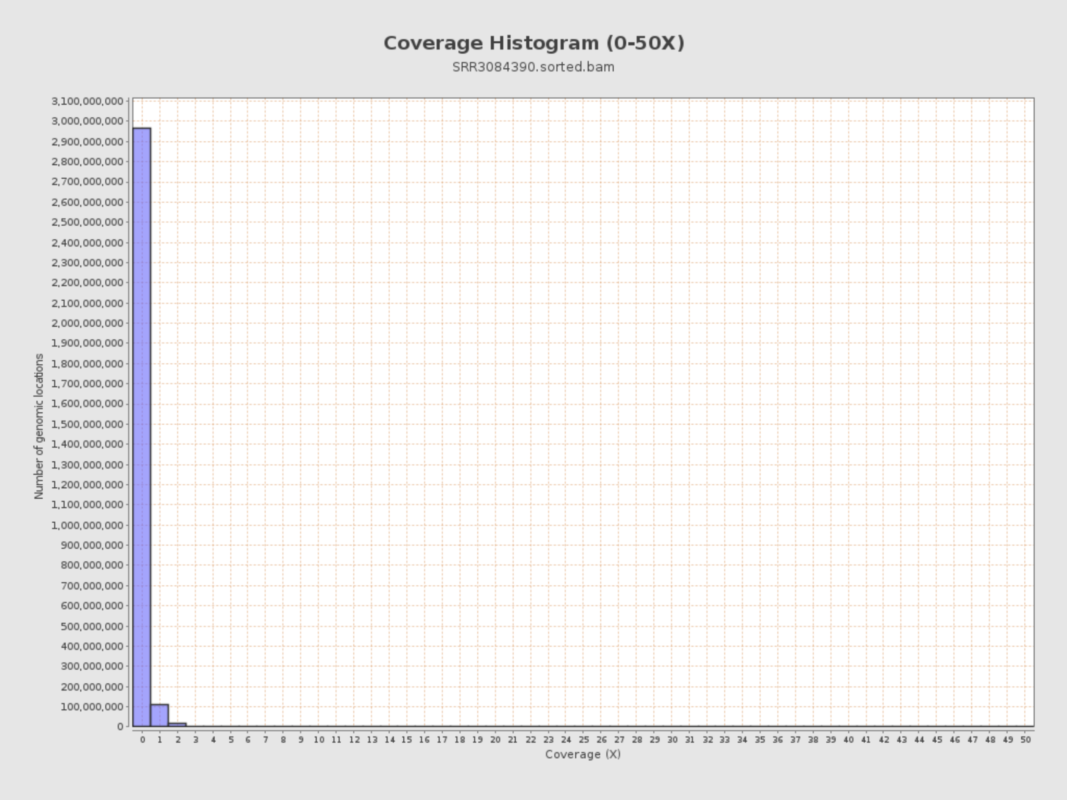
3. Results : Coverage across reference



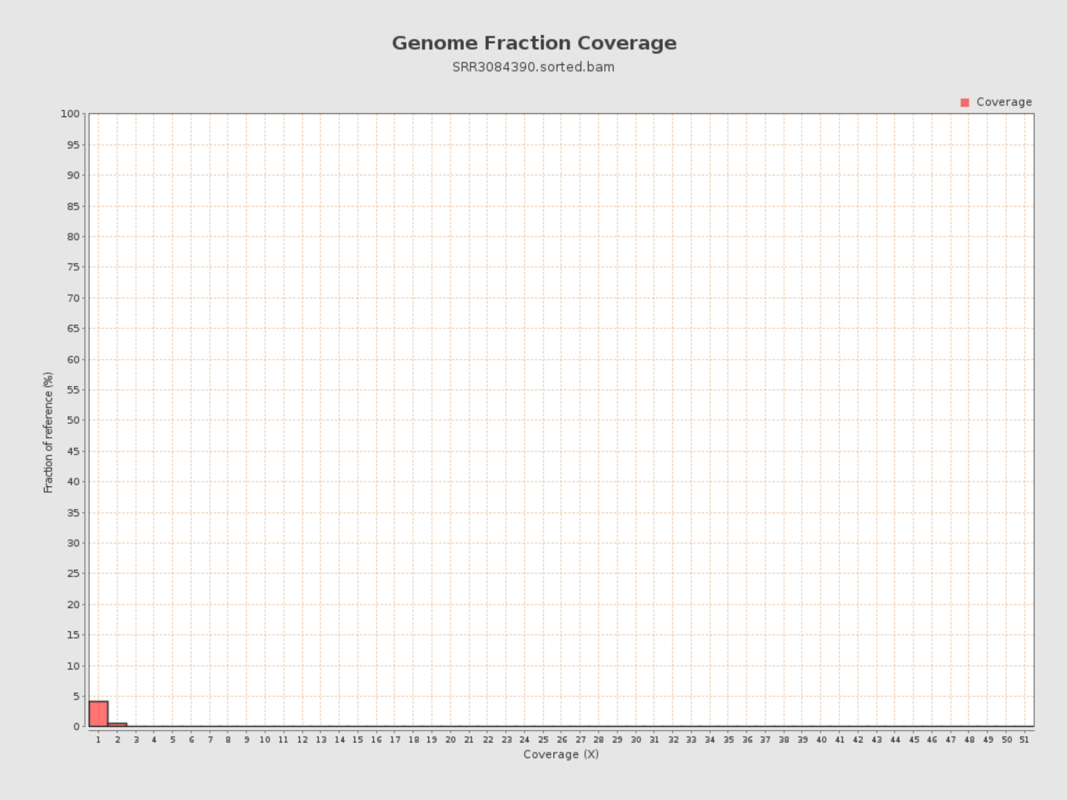
4. Results : Coverage Histogram



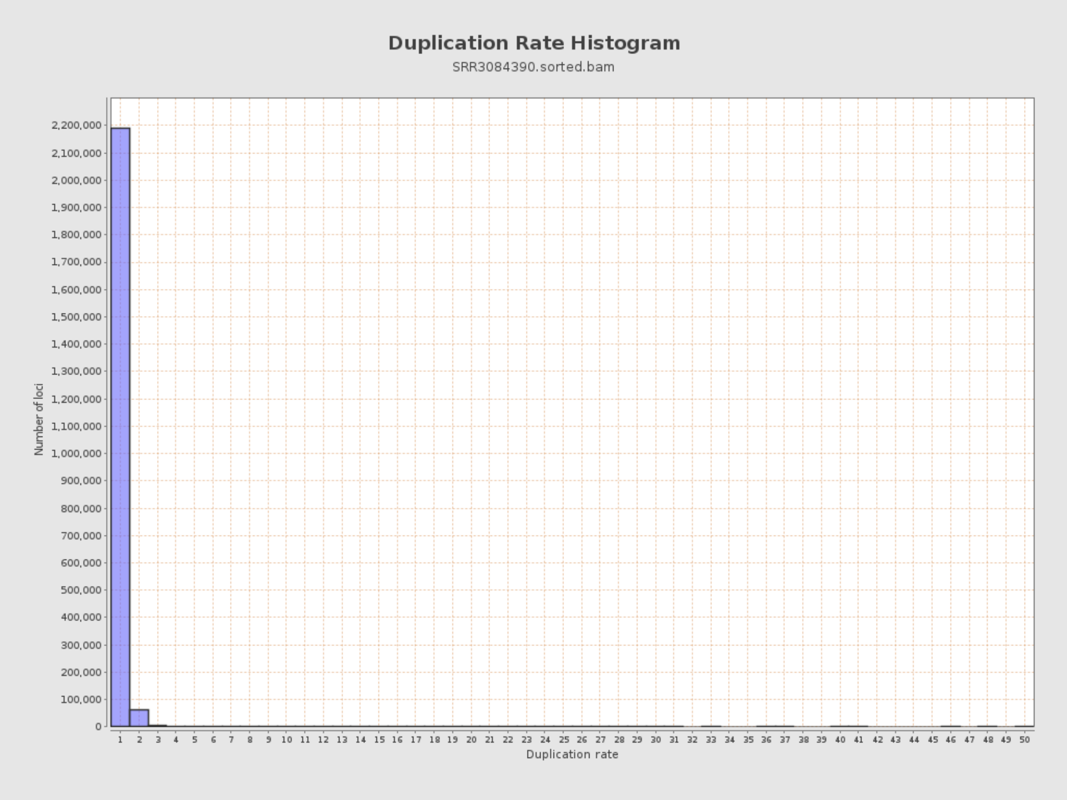
5. Results : Coverage Histogram (0-50X)



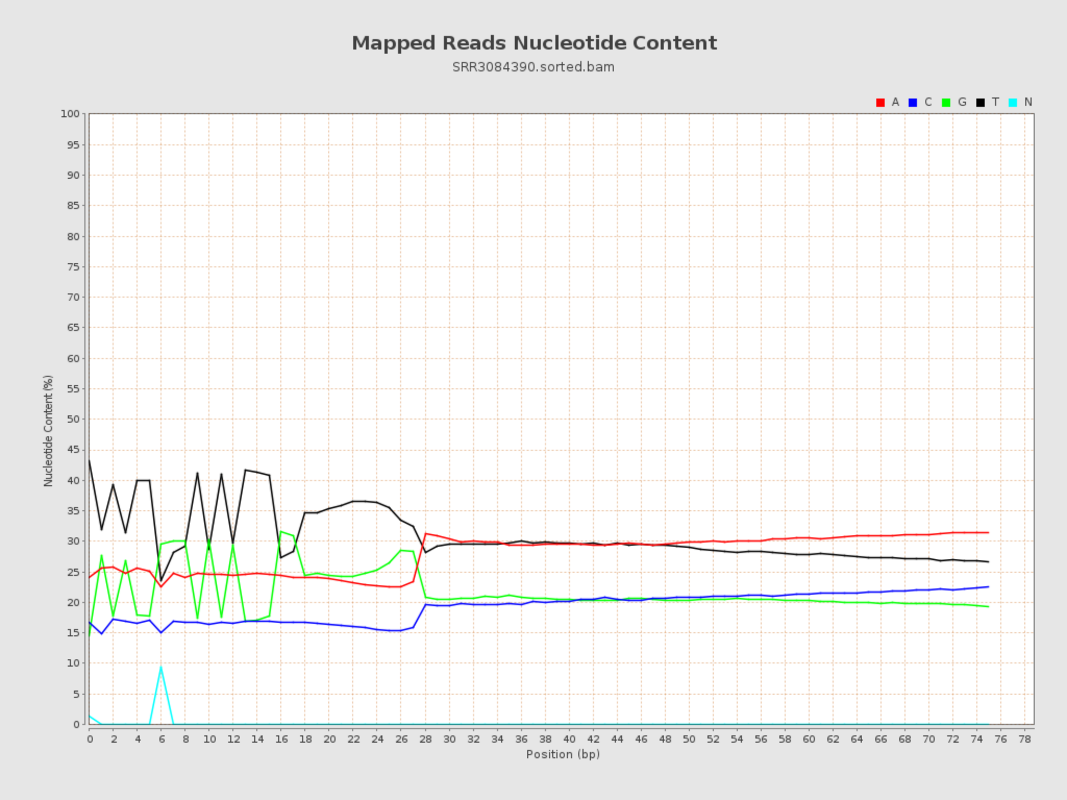
6. Results : Genome Fraction Coverage



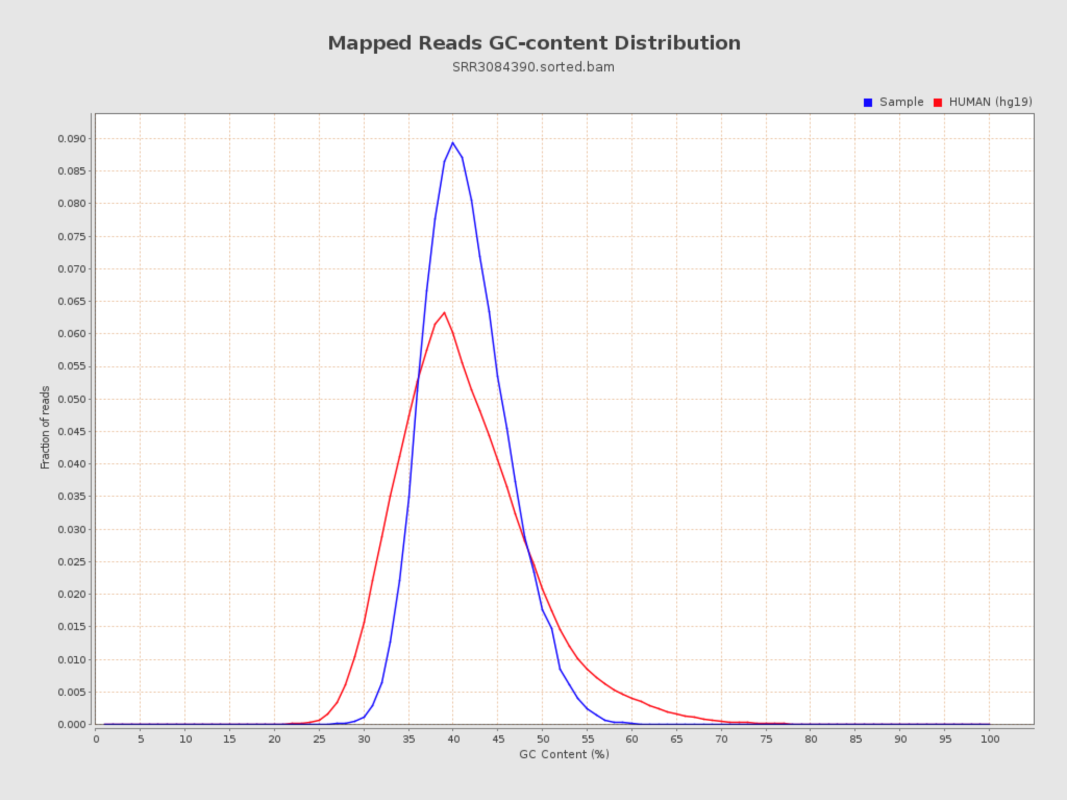
7. Results : Duplication Rate Histogram



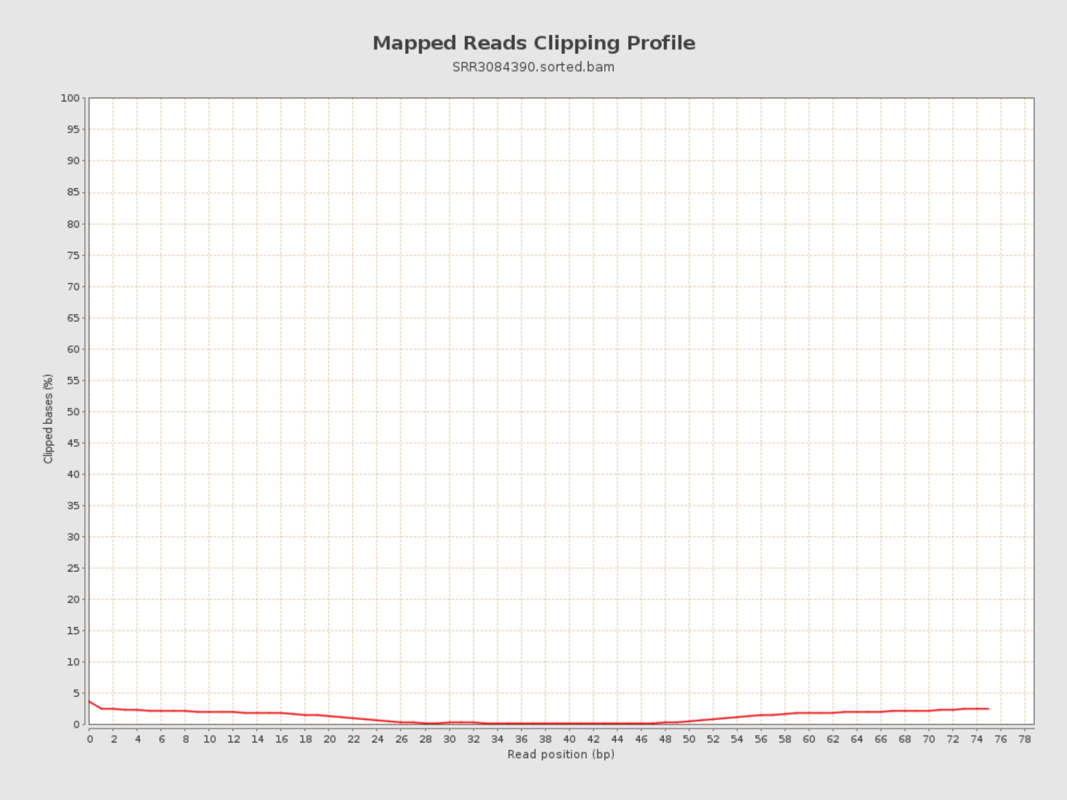
8. Results : Mapped Reads Nucleotide Content



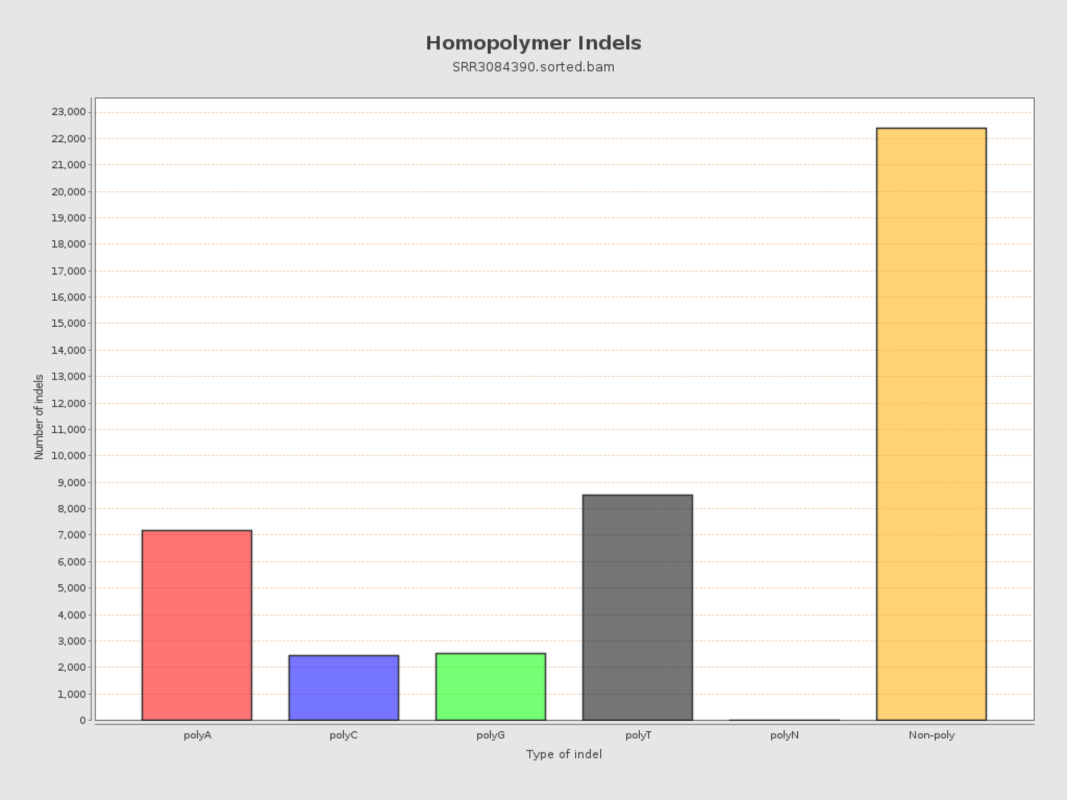
9. Results : Mapped Reads GC-content Distribution



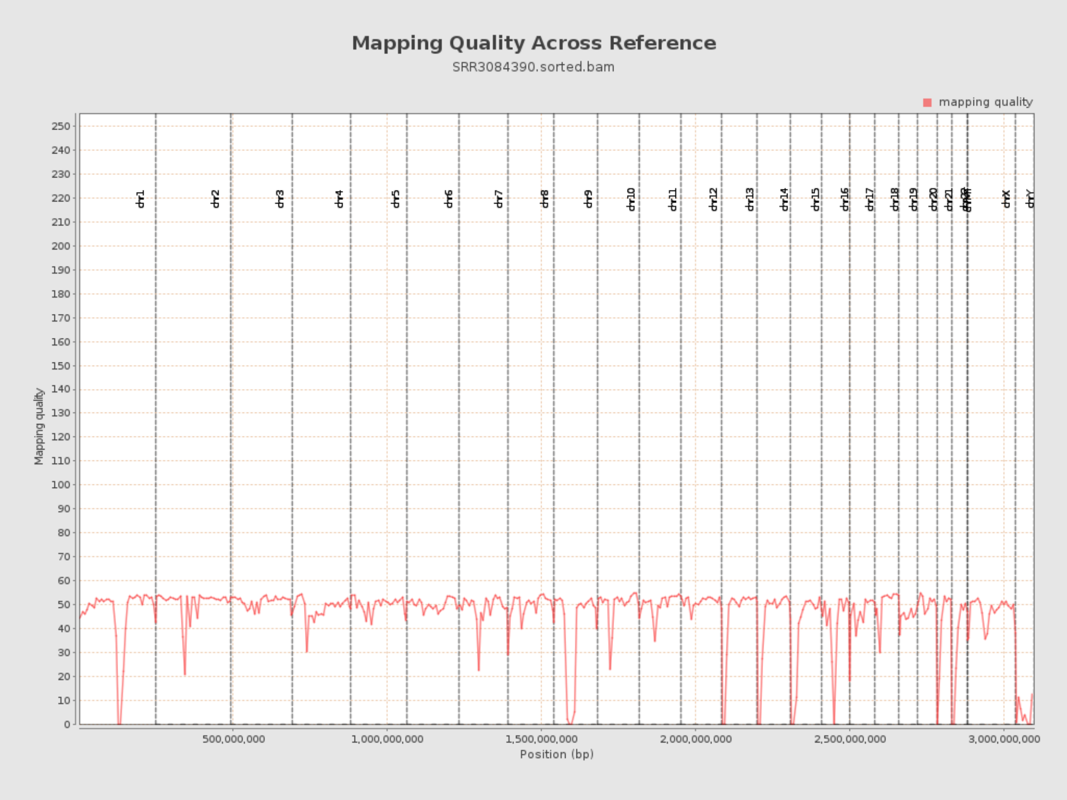
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram