Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:24:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230395.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_SRR6230395 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230395.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:24:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230395.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,980,111
Mapped reads	2,600,925 / 87.28%
Unmapped reads	379,186 / 12.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,690 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	161,267 / 5.41%
Duplication rate	4.93%
Clipped reads	1,387,799 / 46.57%

2.2. ACGT Content

Number/percentage of A's	45,399,289 / 27.13%
Number/percentage of C's	29,853,975 / 17.84%
Number/percentage of T's	53,725,521 / 32.1%
Number/percentage of G's	38,289,071 / 22.88%
Number/percentage of N's	85,085 / 0.05%
GC Percentage	40.72%

2.3. Coverage

Mean	0.0541

Standard Deviation	0.461

2.4. Mapping Quality

Mean Mapping Quality	45.89

2.5. Mismatches and indels

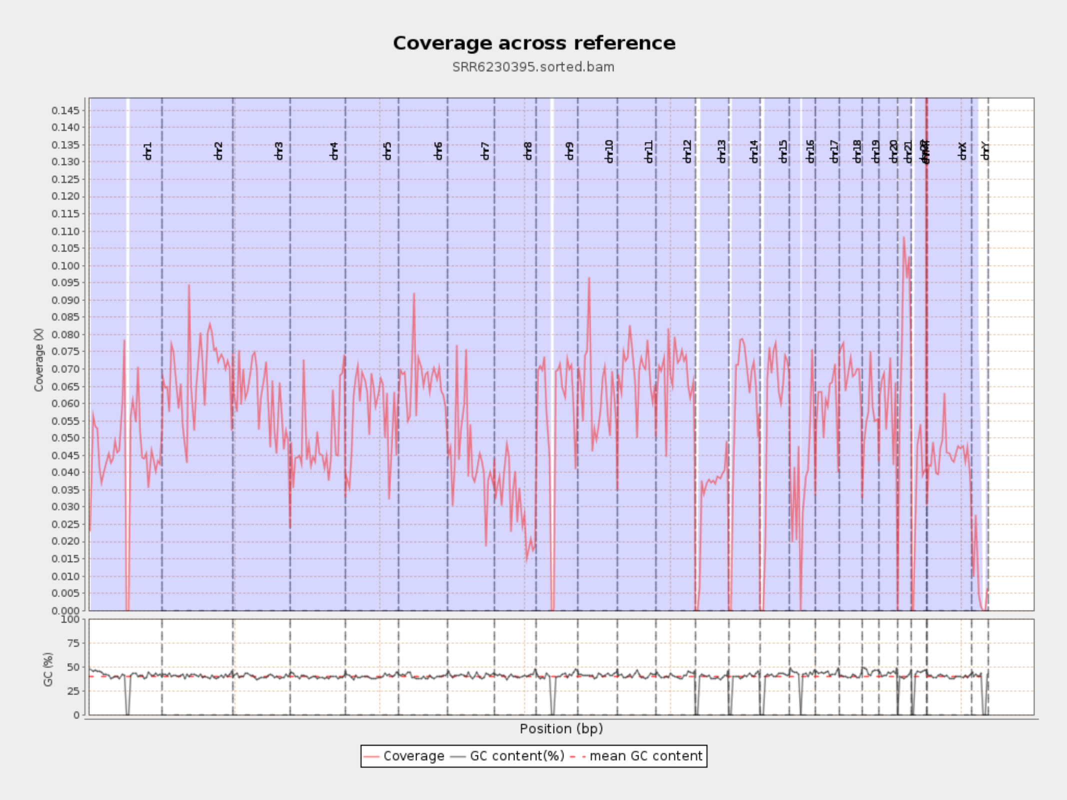
General error rate	0.9%
Mismatches	1,476,545
Insertions	13,029
Mapped reads with at least one insertion	0.5%
Deletions	50,062
Mapped reads with at least one deletion	1.9%
Homopolymer indels	45.51%

2.6. Chromosome stats

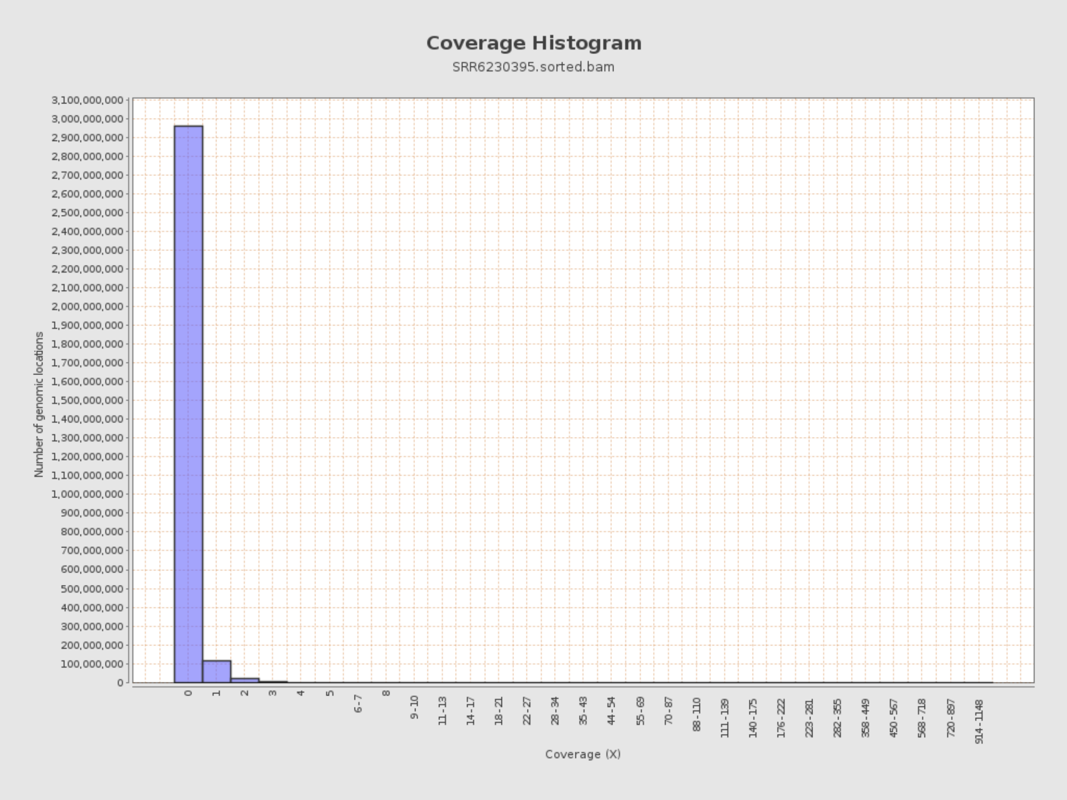
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11222716	0.045	0.8506
chr2	243199373	16646311	0.0684	0.5442
chr3	198022430	12144665	0.0613	0.2922
chr4	191154276	9382860	0.0491	0.2937
chr5	180915260	10416369	0.0576	0.2864
chr6	171115067	11404935	0.0667	0.3972
chr7	159138663	7151519	0.0449	0.5825

chr8	146364022	4411624	0.0301	0.4876
chr9	141213431	8145000	0.0577	0.4571
chr10	135534747	8514060	0.0628	0.4317
chr11	135006516	9273591	0.0687	0.4835
chr12	133851895	9198172	0.0687	0.3189
chr13	115169878	3725948	0.0324	0.2117
chr14	107349540	6277505	0.0585	0.306
chr15	102531392	5763156	0.0562	0.2849
chr16	90354753	3441030	0.0381	0.2825
chr17	81195210	4834426	0.0595	0.3215
chr18	78077248	5464108	0.07	0.848
chr19	59128983	3324518	0.0562	0.5089
chr20	63025520	3804877	0.0604	0.3081
chr21	48129895	3748716	0.0779	0.3576
chr22	51304566	1685241	0.0328	0.2111
chrMT	16571	8278	0.4995	0.8821
chrX	155270560	6991446	0.045	0.2974
chrY	59373566	455081	0.0077	0.1889

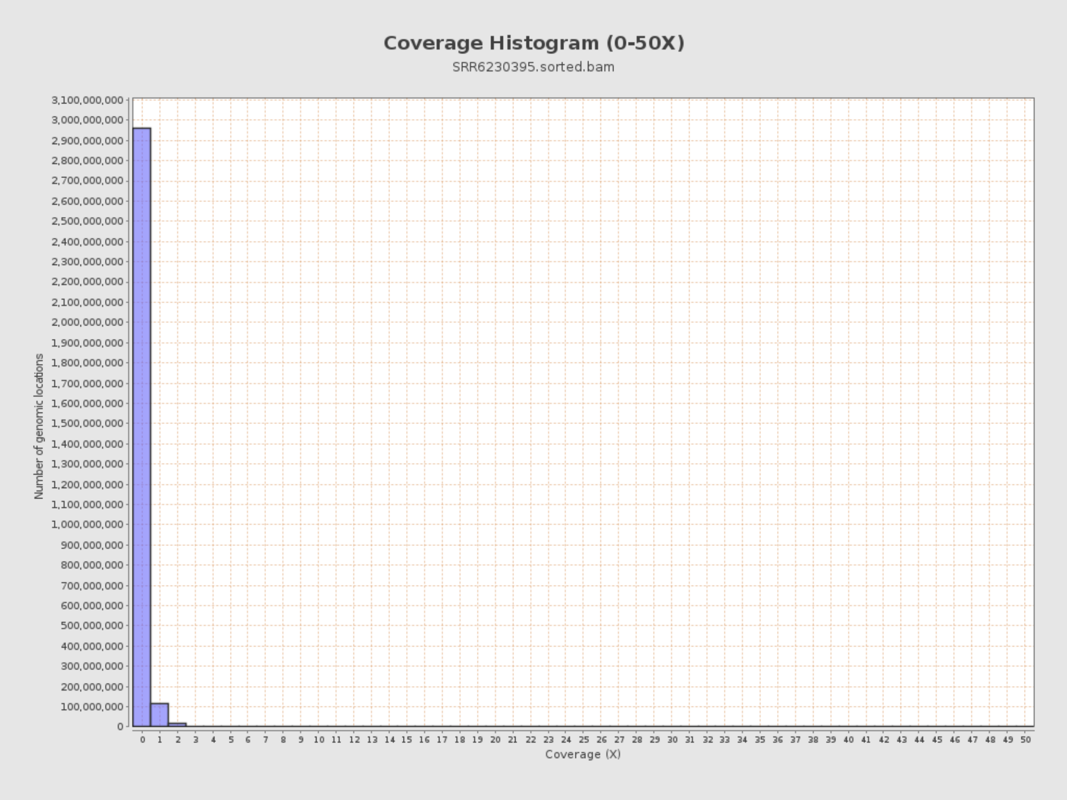
3. Results : Coverage across reference



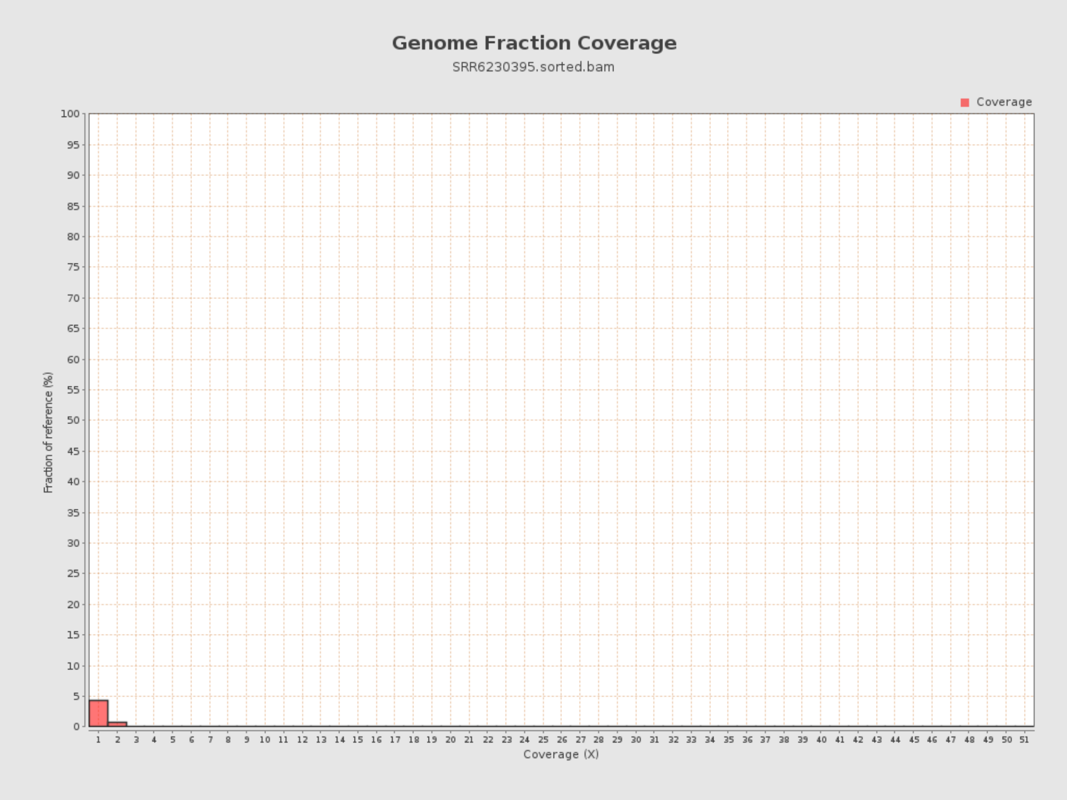
4. Results : Coverage Histogram



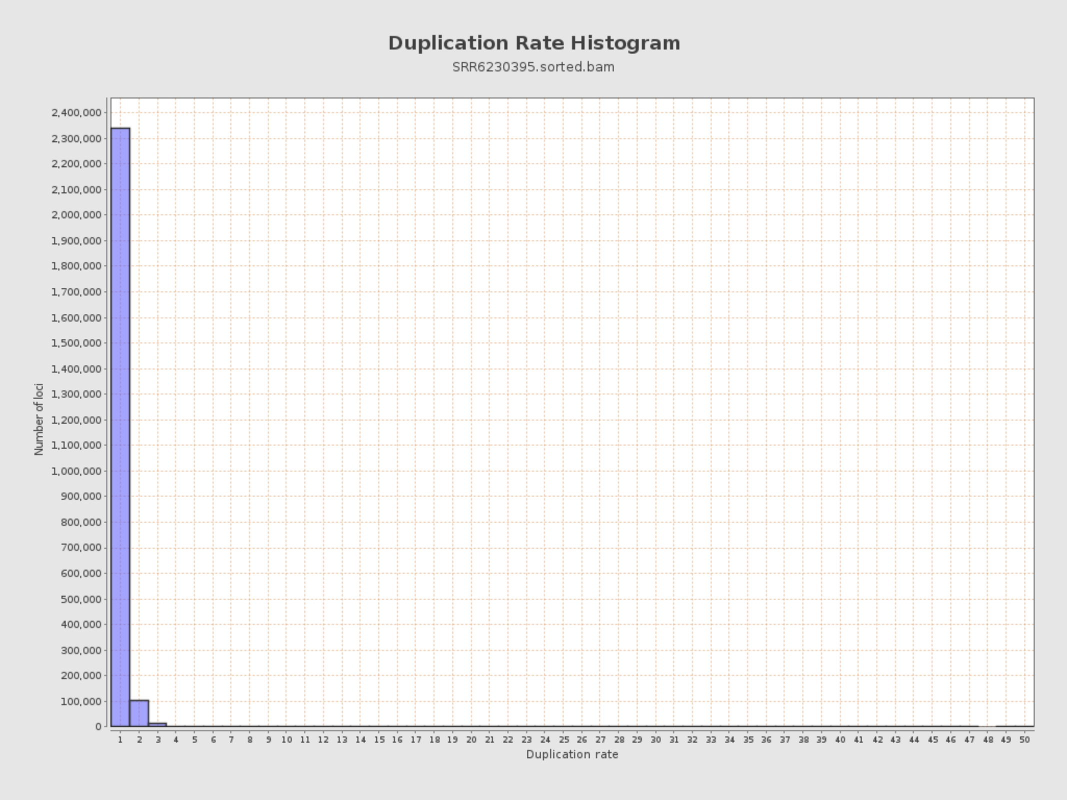
5. Results : Coverage Histogram (0-50X)



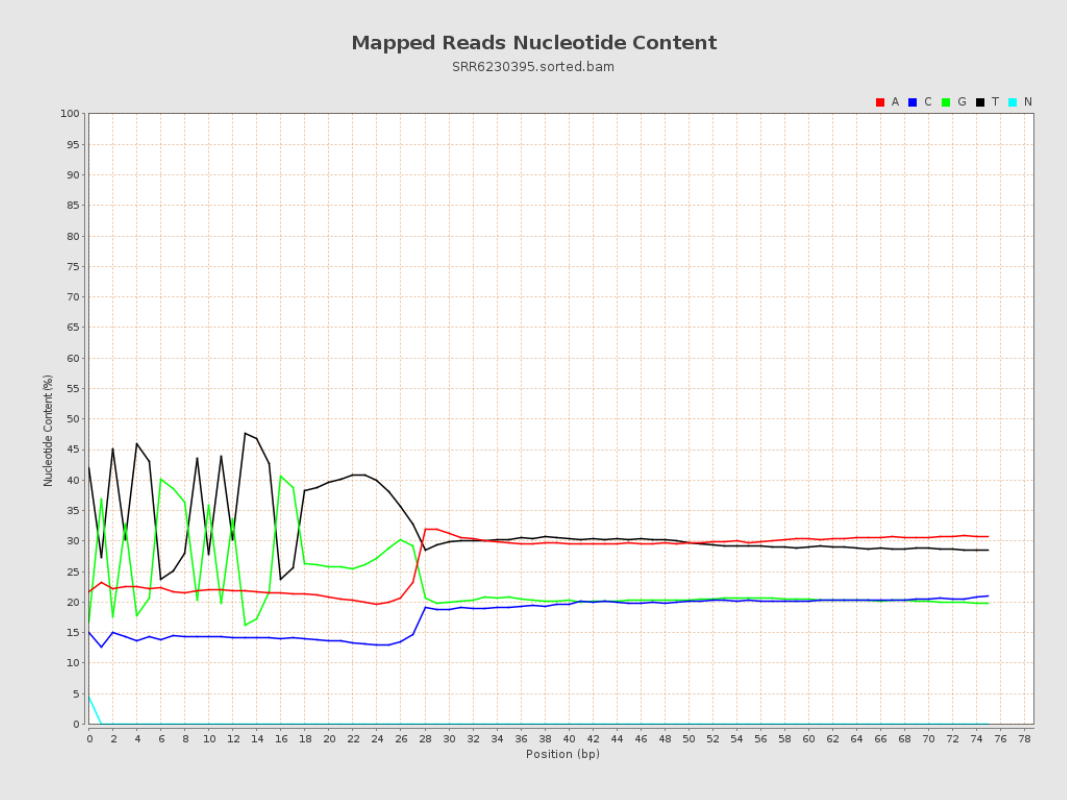
6. Results : Genome Fraction Coverage



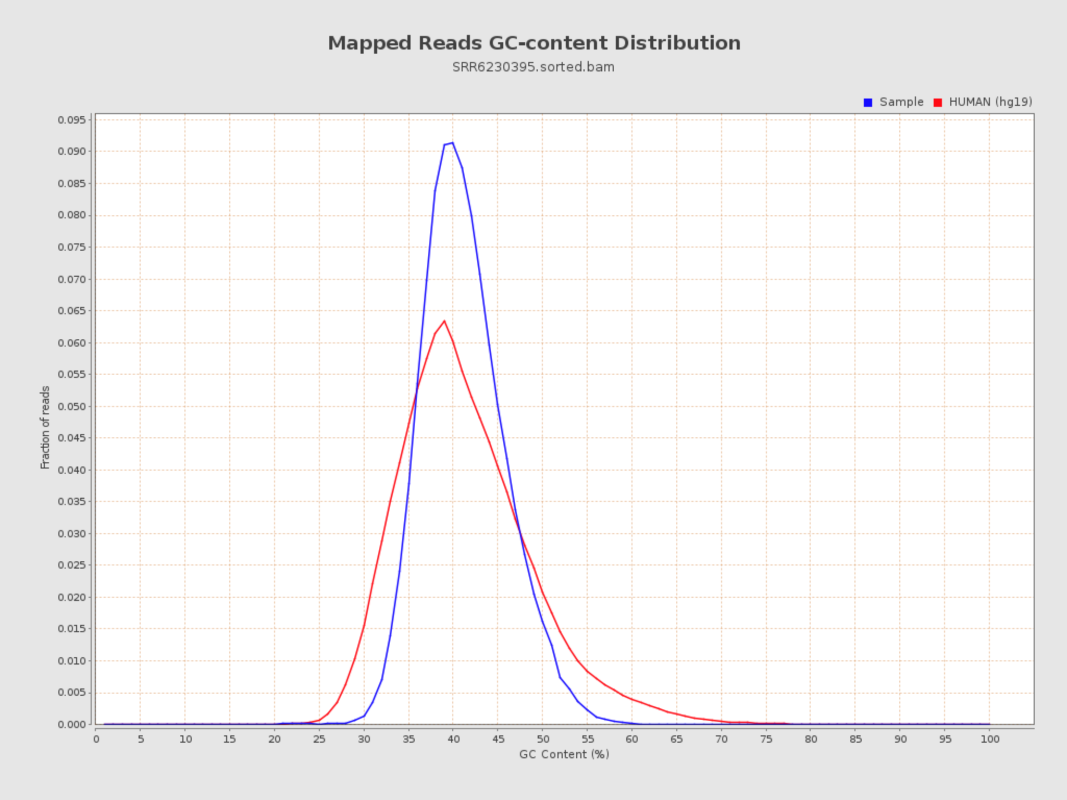
7. Results : Duplication Rate Histogram



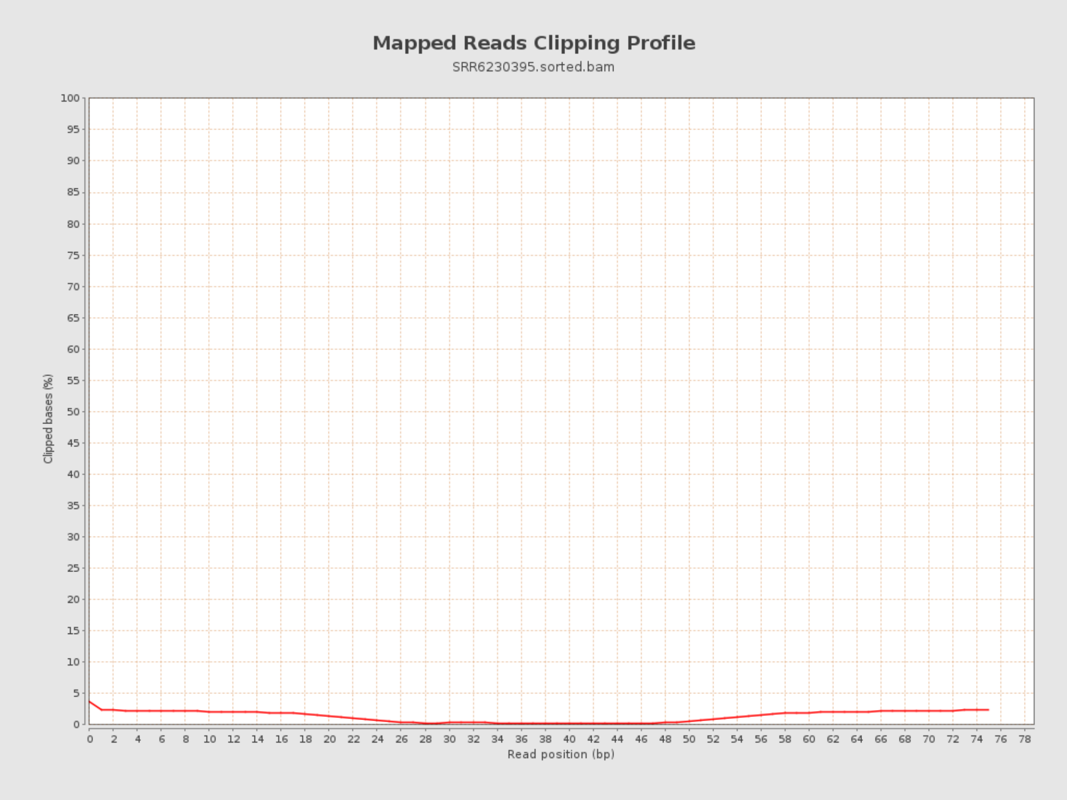
8. Results : Mapped Reads Nucleotide Content



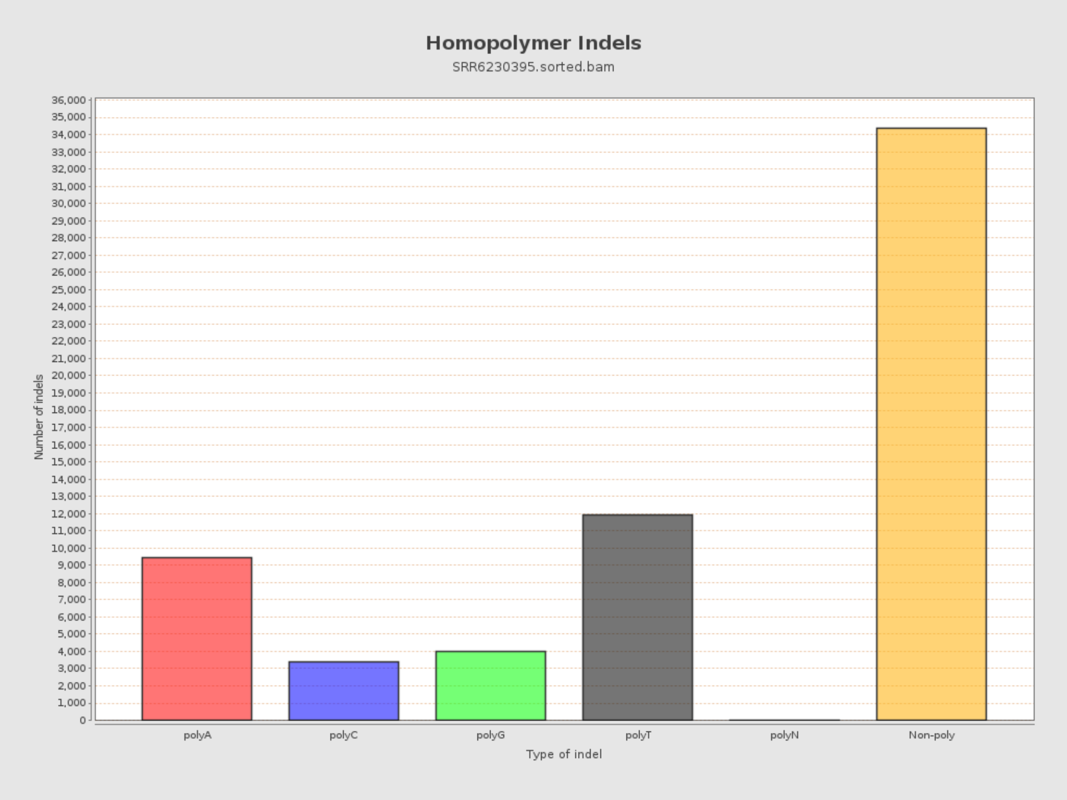
9. Results : Mapped Reads GC-content Distribution



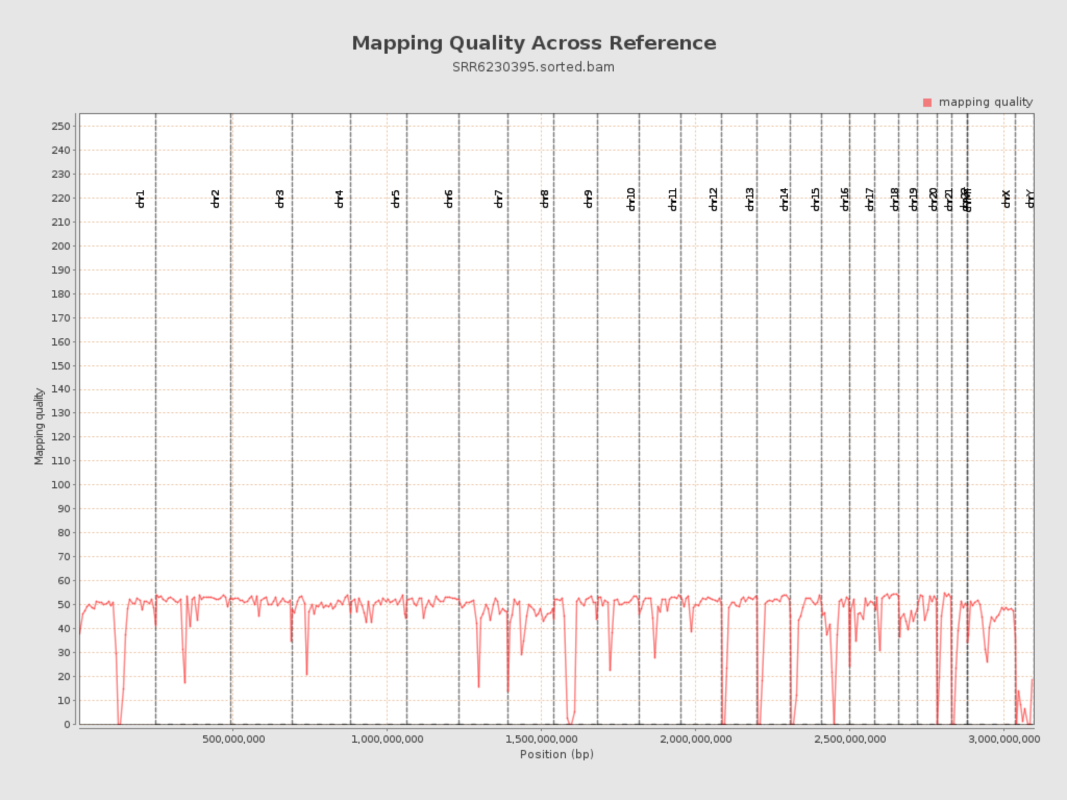
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram