Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:07:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230390.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_SRR6230390 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230390.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:07:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230390.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,960,678
Mapped reads	3,271,124 / 82.59%
Unmapped reads	689,554 / 17.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,162 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	160,234 / 4.05%
Duplication rate	3.79%
Clipped reads	1,564,752 / 39.51%

2.2. ACGT Content

Number/percentage of A's	58,421,704 / 27.23%
Number/percentage of C's	37,164,222 / 17.32%
Number/percentage of T's	71,283,767 / 33.23%
Number/percentage of G's	47,260,249 / 22.03%
Number/percentage of N's	416,113 / 0.19%
GC Percentage	39.35%

2.3. Coverage

Mean	0.0693

Standard Deviation	0.5375

2.4. Mapping Quality

Mean Mapping Quality	45.89

2.5. Mismatches and indels

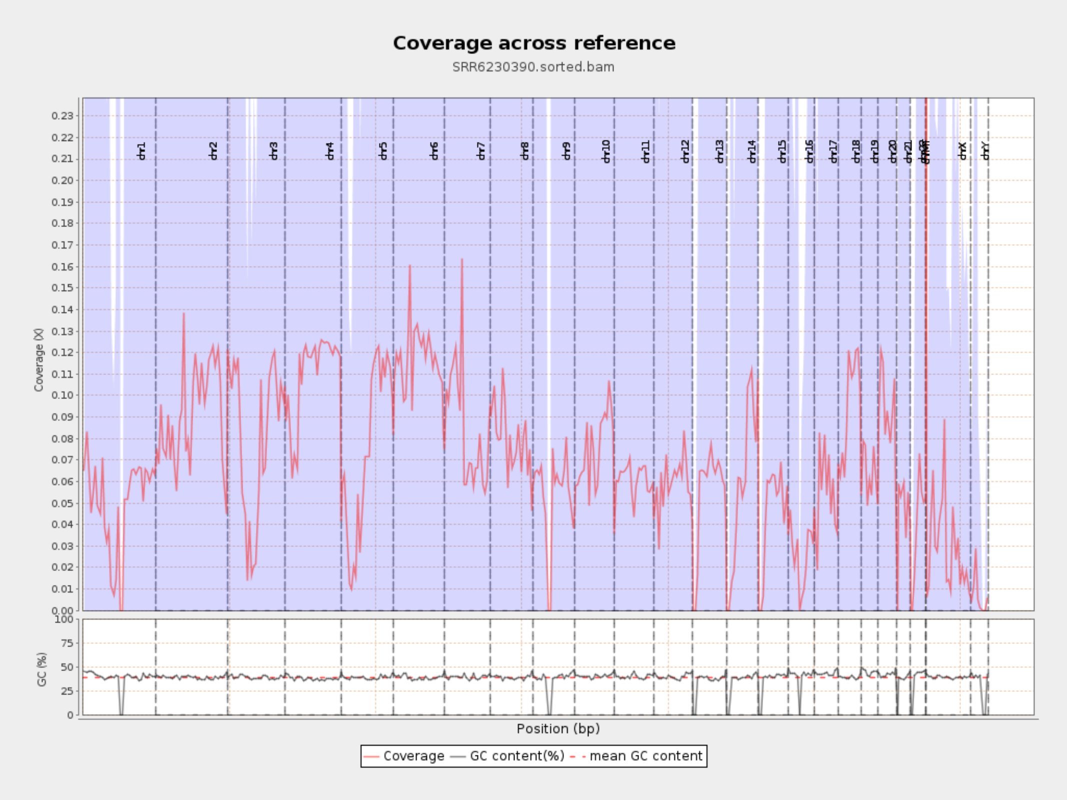
General error rate	0.95%
Mismatches	2,004,025
Insertions	19,318
Mapped reads with at least one insertion	0.59%
Deletions	57,167
Mapped reads with at least one deletion	1.73%
Homopolymer indels	48.14%

2.6. Chromosome stats

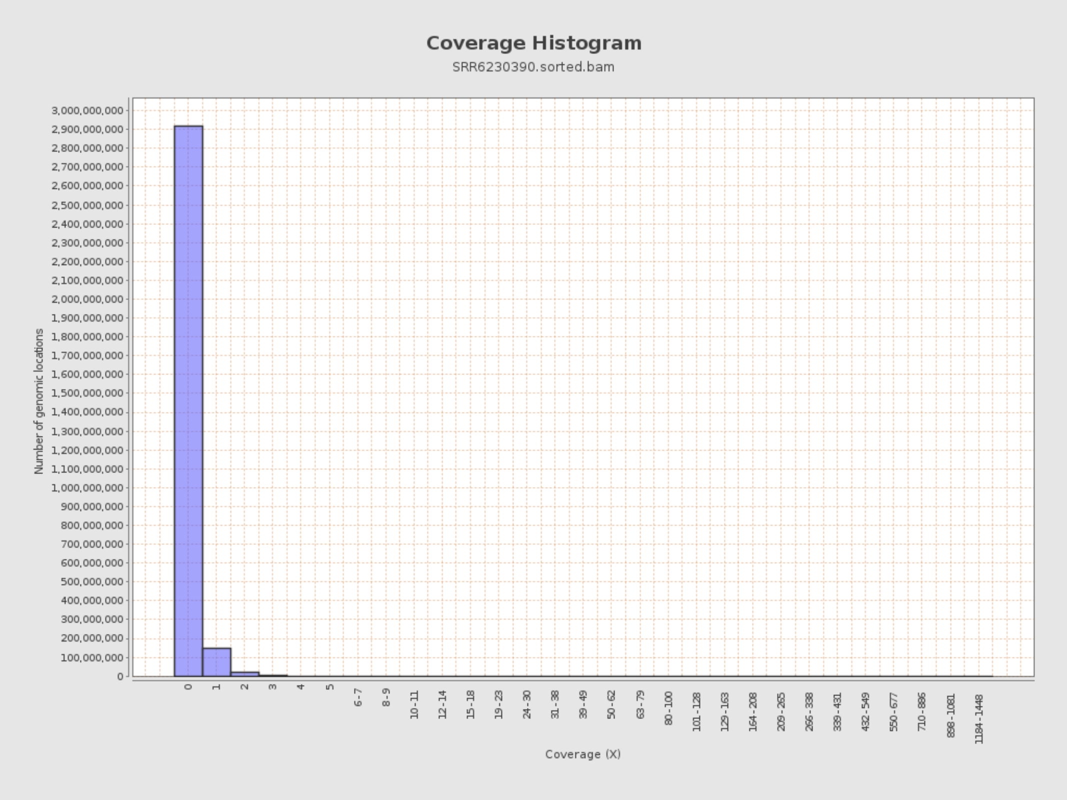
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12452790	0.05	0.6062
chr2	243199373	22297428	0.0917	0.5827
chr3	198022430	15914274	0.0804	0.3274
chr4	191154276	21068786	0.1102	0.4108
chr5	180915260	13362238	0.0739	0.3174
chr6	171115067	20190908	0.118	0.6258
chr7	159138663	13434362	0.0844	1.1589

chr8	146364022	11617430	0.0794	0.9519
chr9	141213431	7577691	0.0537	0.4611
chr10	135534747	10265384	0.0757	0.4681
chr11	135006516	8214289	0.0608	0.4707
chr12	133851895	7939443	0.0593	0.2933
chr13	115169878	6342072	0.0551	0.2694
chr14	107349540	6274634	0.0585	0.311
chr15	102531392	4521370	0.0441	0.2413
chr16	90354753	2285545	0.0253	0.2366
chr17	81195210	4389125	0.0541	0.3537
chr18	78077248	7434232	0.0952	0.8086
chr19	59128983	3745888	0.0634	0.404
chr20	63025520	6038403	0.0958	0.3753
chr21	48129895	2217626	0.0461	0.2899
chr22	51304566	1987714	0.0387	0.2254
chrMT	16571	155028	9.3554	6.0005
chrX	155270560	4488260	0.0289	0.2727
chrY	59373566	425630	0.0072	0.1869

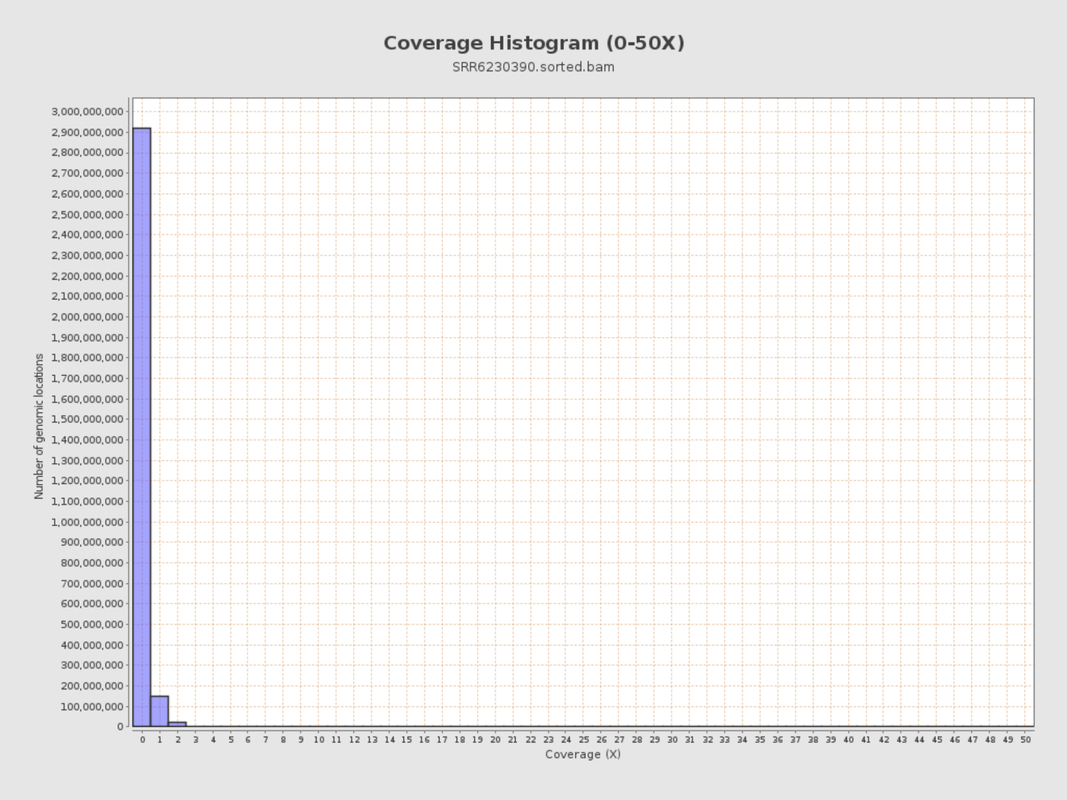
3. Results : Coverage across reference



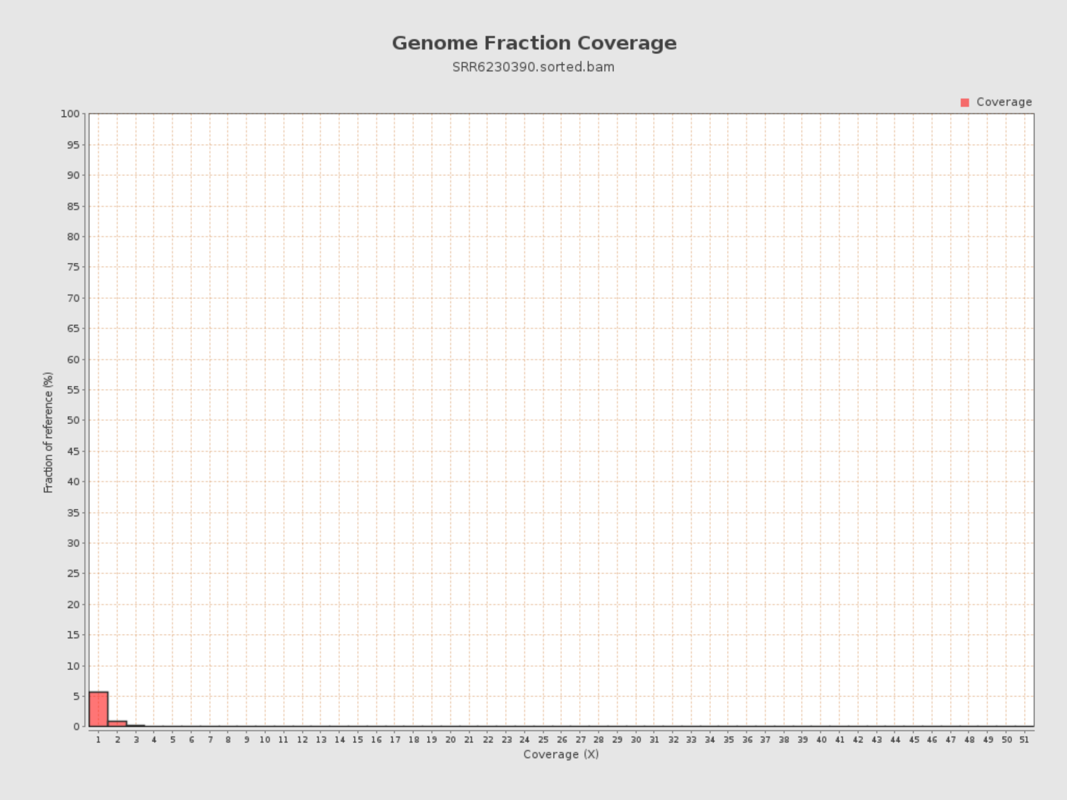
4. Results : Coverage Histogram



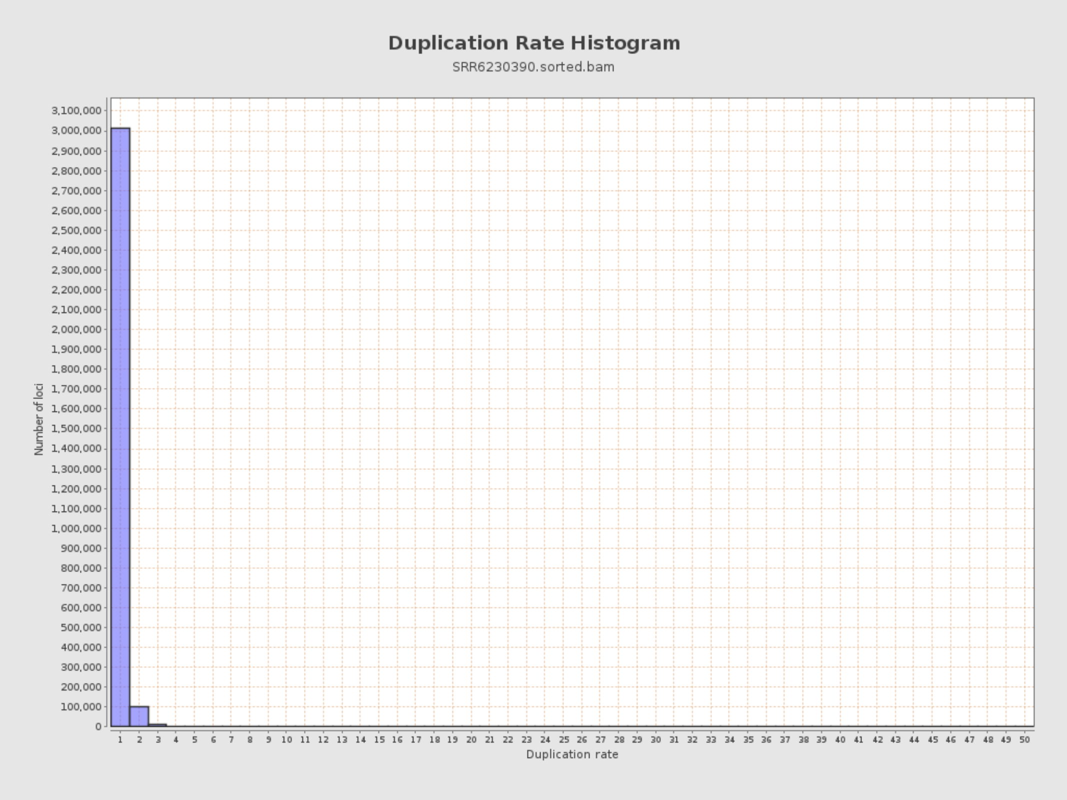
5. Results : Coverage Histogram (0-50X)



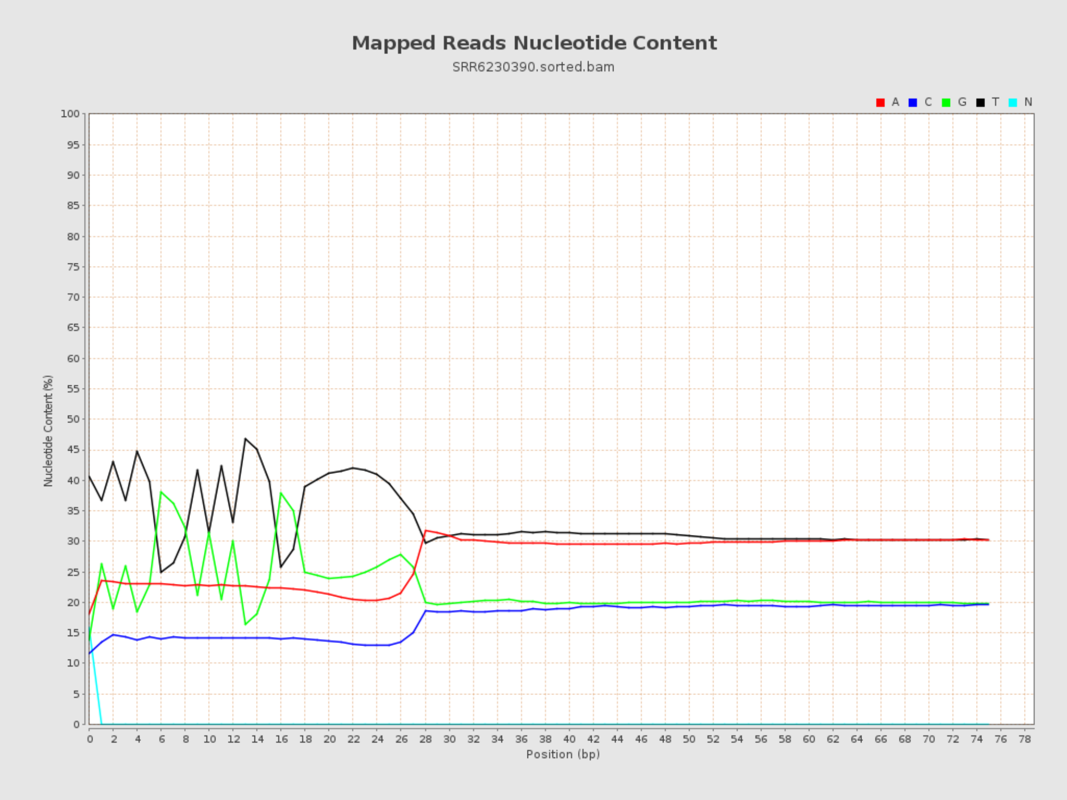
6. Results : Genome Fraction Coverage



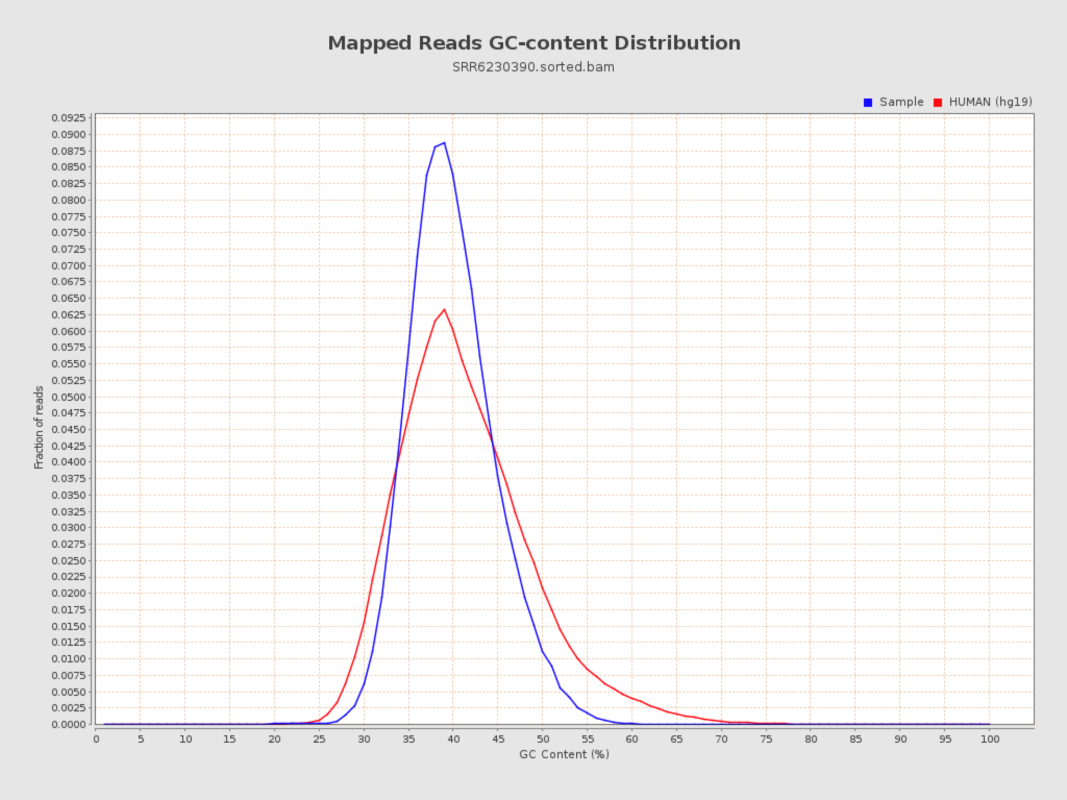
7. Results : Duplication Rate Histogram



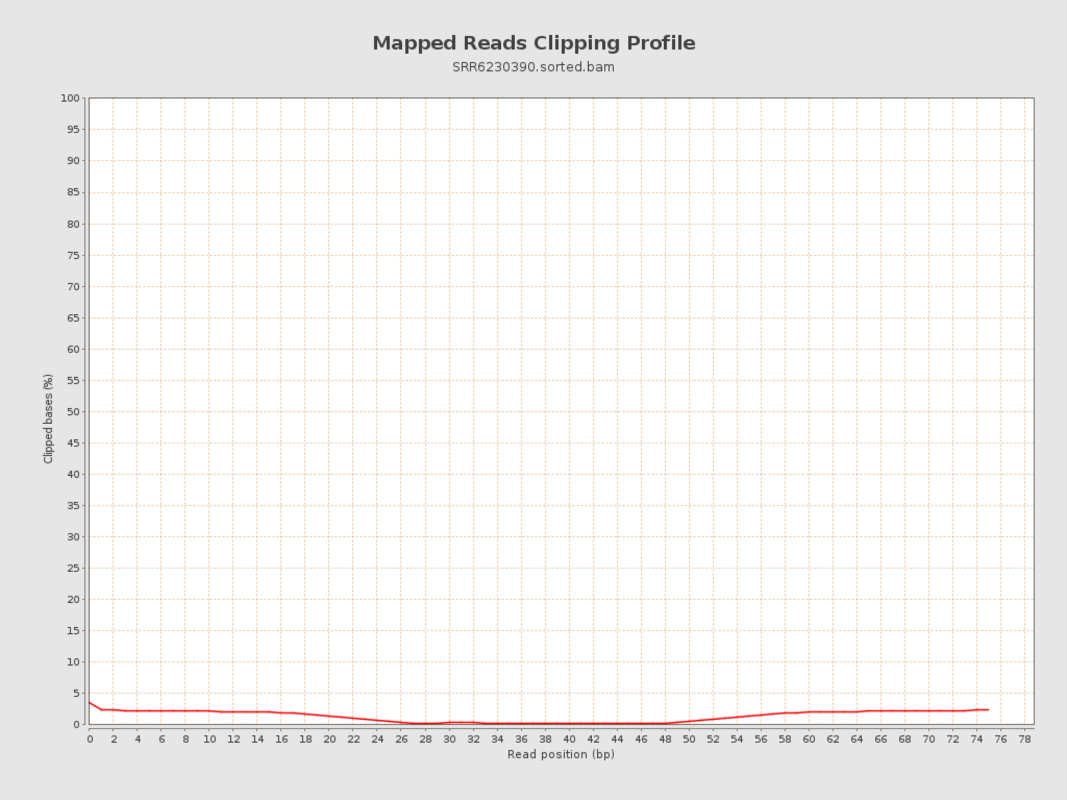
8. Results : Mapped Reads Nucleotide Content



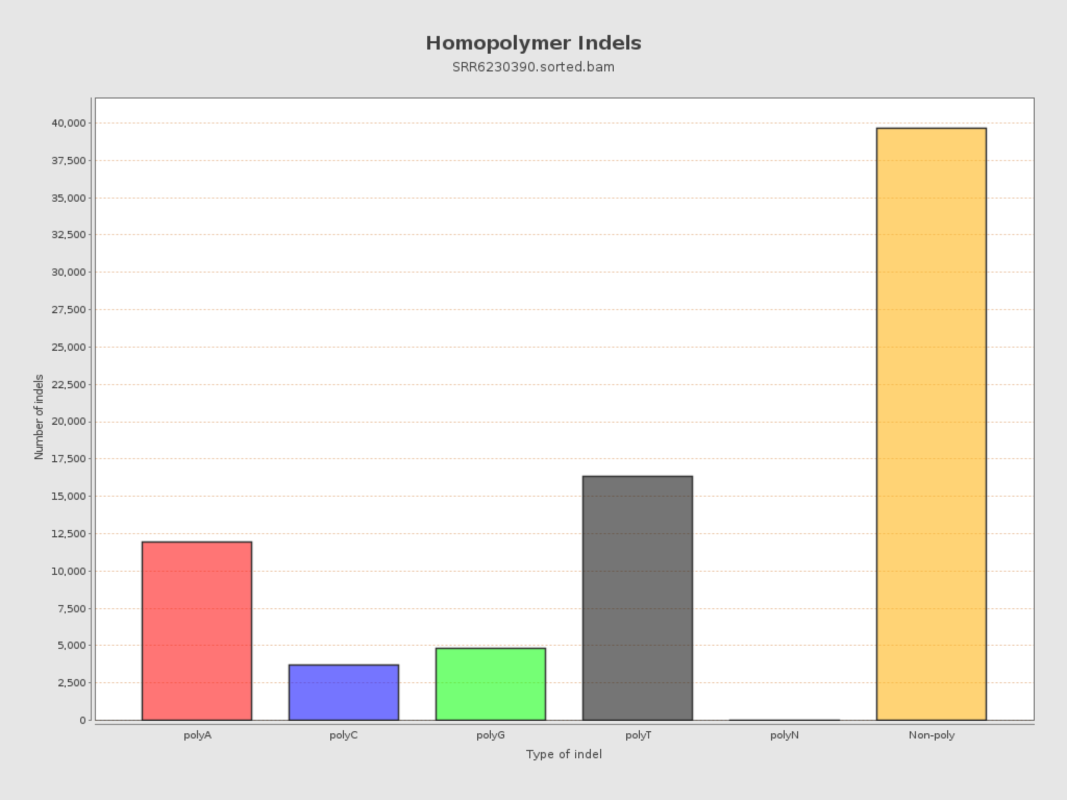
9. Results : Mapped Reads GC-content Distribution



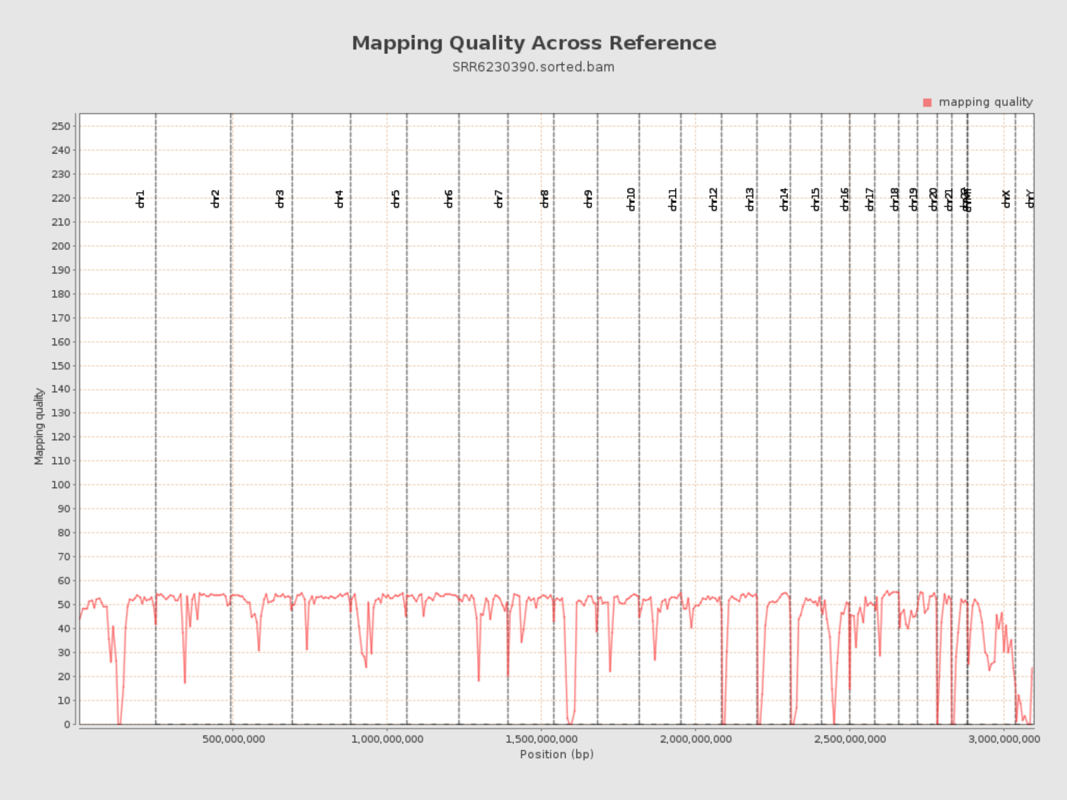
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram