Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:20:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230394.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_SRR6230394 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230394.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:20:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230394.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,818,103
Mapped reads	2,492,016 / 88.43%
Unmapped reads	326,087 / 11.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,827 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	147,124 / 5.22%
Duplication rate	4.82%
Clipped reads	1,291,417 / 45.83%

2.2. ACGT Content

Number/percentage of A's	44,010,137 / 27.27%
Number/percentage of C's	28,799,543 / 17.84%
Number/percentage of T's	52,102,672 / 32.28%
Number/percentage of G's	36,404,397 / 22.56%
Number/percentage of N's	78,841 / 0.05%
GC Percentage	40.4%

2.3. Coverage

Mean	0.0522

Standard Deviation	0.4055

2.4. Mapping Quality

Mean Mapping Quality	46.33

2.5. Mismatches and indels

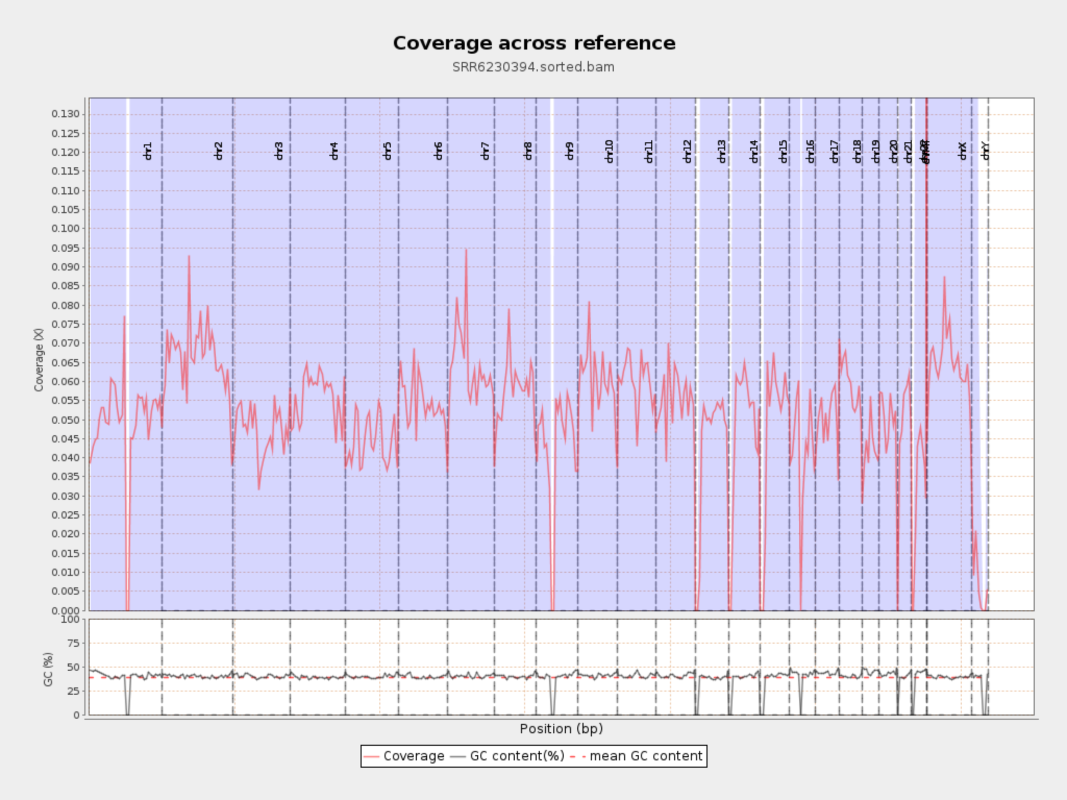
General error rate	0.88%
Mismatches	1,403,777
Insertions	12,322
Mapped reads with at least one insertion	0.49%
Deletions	48,353
Mapped reads with at least one deletion	1.92%
Homopolymer indels	46.66%

2.6. Chromosome stats

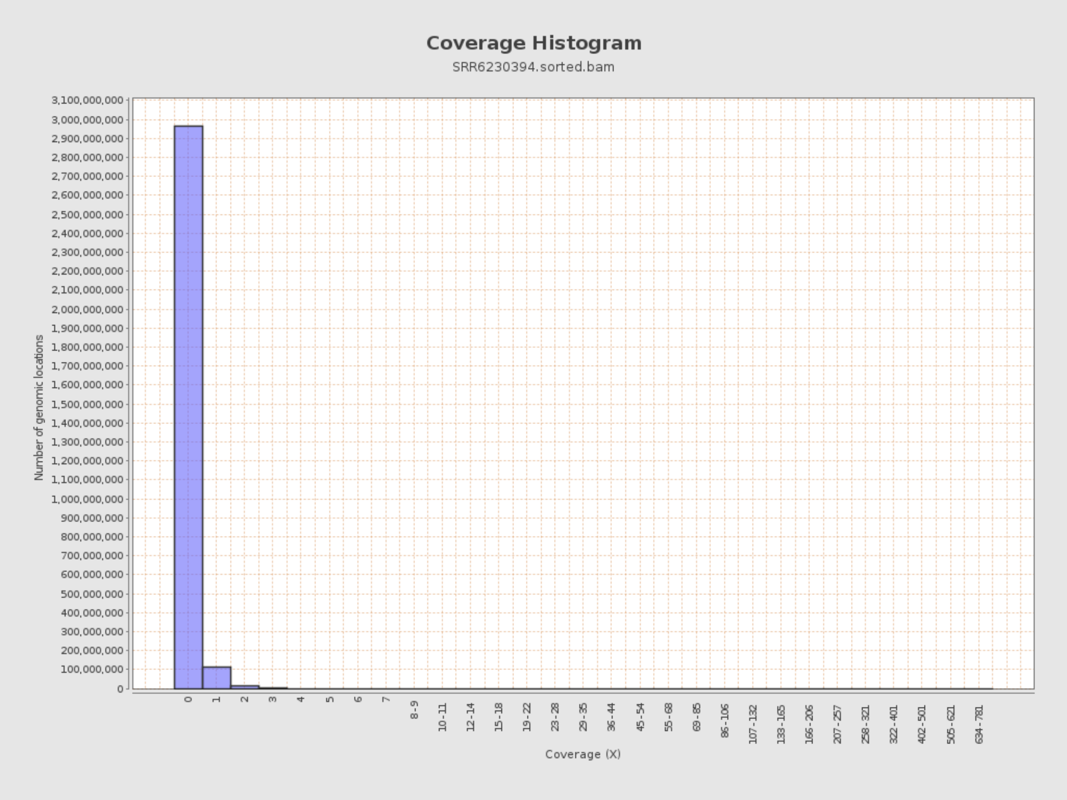
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12206730	0.049	0.624
chr2	243199373	16193328	0.0666	0.5204
chr3	198022430	9297271	0.047	0.2535
chr4	191154276	10709087	0.056	0.2896
chr5	180915260	8013099	0.0443	0.2471
chr6	171115067	9345749	0.0546	0.3339
chr7	159138663	10273789	0.0646	0.6226

chr8	146364022	8484818	0.058	0.5673
chr9	141213431	6053043	0.0429	0.3742
chr10	135534747	8259650	0.0609	0.3801
chr11	135006516	8094061	0.06	0.3962
chr12	133851895	7404093	0.0553	0.2816
chr13	115169878	4878543	0.0424	0.2391
chr14	107349540	4998724	0.0466	0.2631
chr15	102531392	4850248	0.0473	0.2579
chr16	90354753	3769059	0.0417	0.2653
chr17	81195210	4026793	0.0496	0.2898
chr18	78077248	4645123	0.0595	0.6428
chr19	59128983	2520127	0.0426	0.4454
chr20	63025520	3139076	0.0498	0.2707
chr21	48129895	2304202	0.0479	0.2693
chr22	51304566	1530732	0.0298	0.1979
chrMT	16571	4547	0.2744	0.6275
chrX	155270560	10050947	0.0647	0.3354
chrY	59373566	422690	0.0071	0.1489

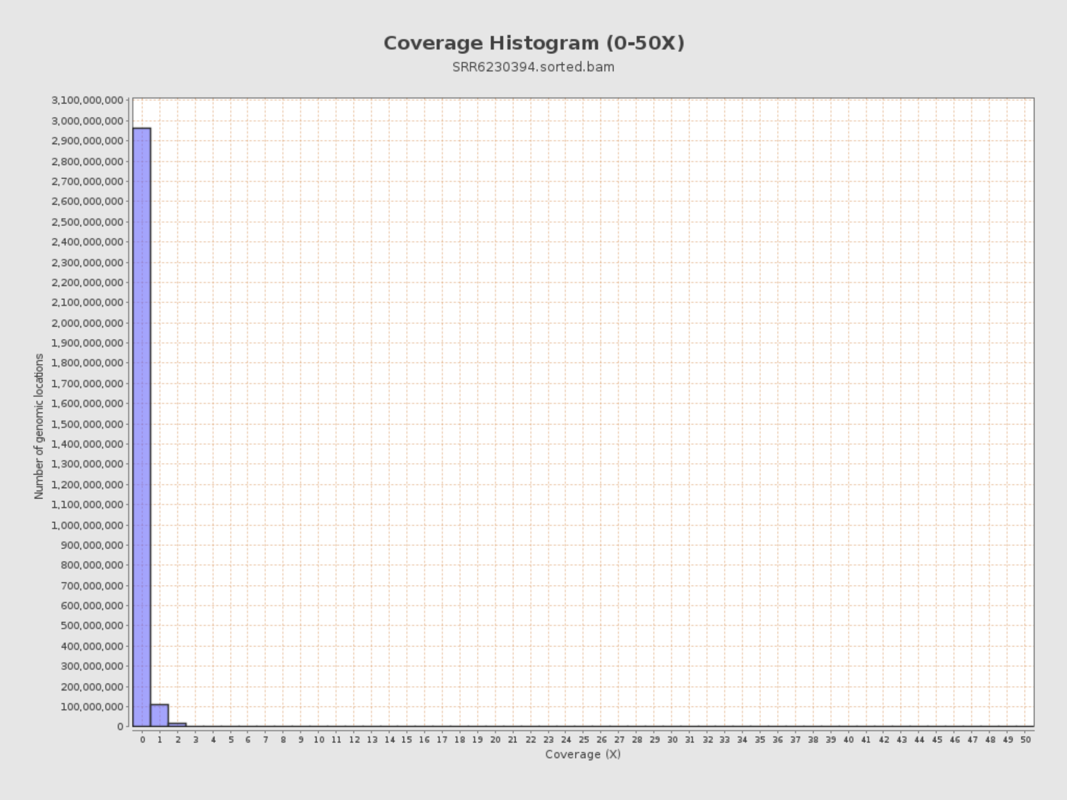
3. Results : Coverage across reference



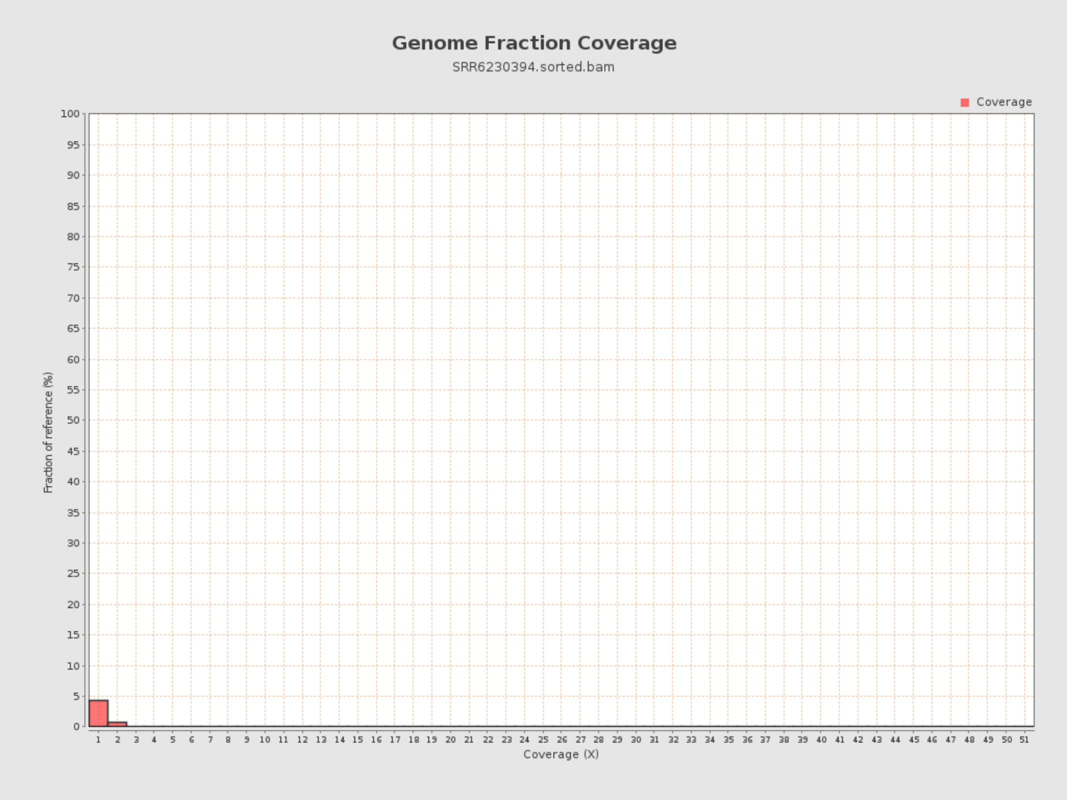
4. Results : Coverage Histogram



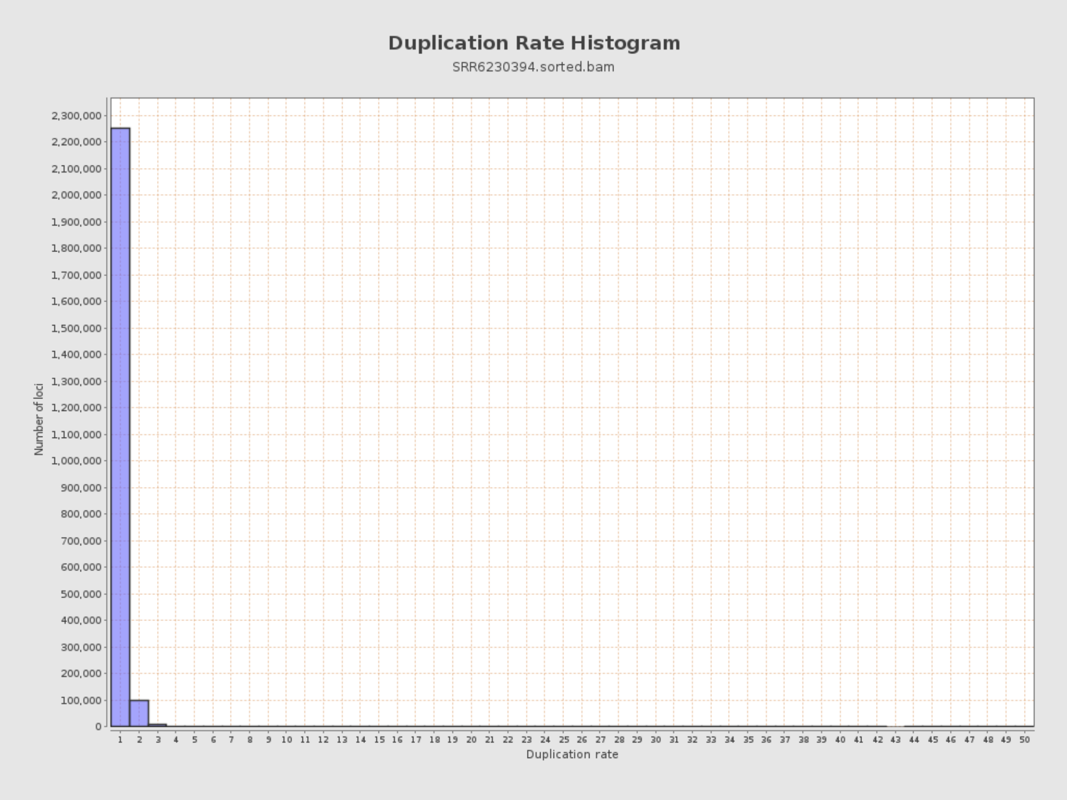
5. Results : Coverage Histogram (0-50X)



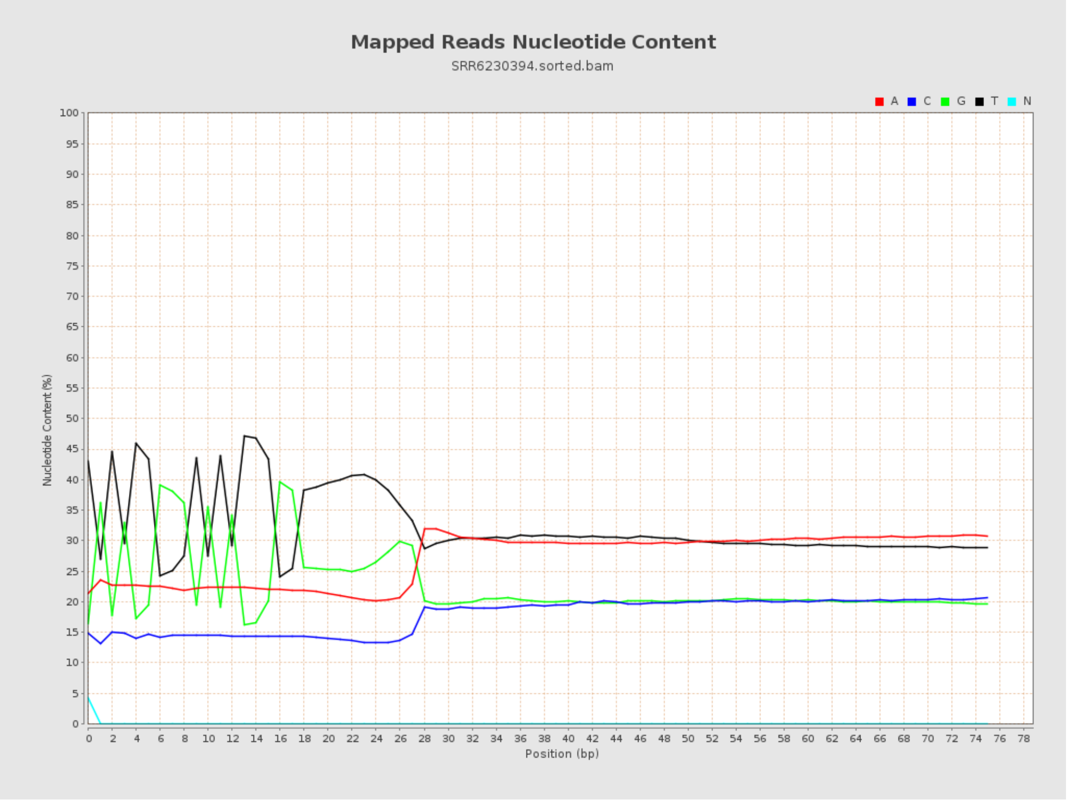
6. Results : Genome Fraction Coverage



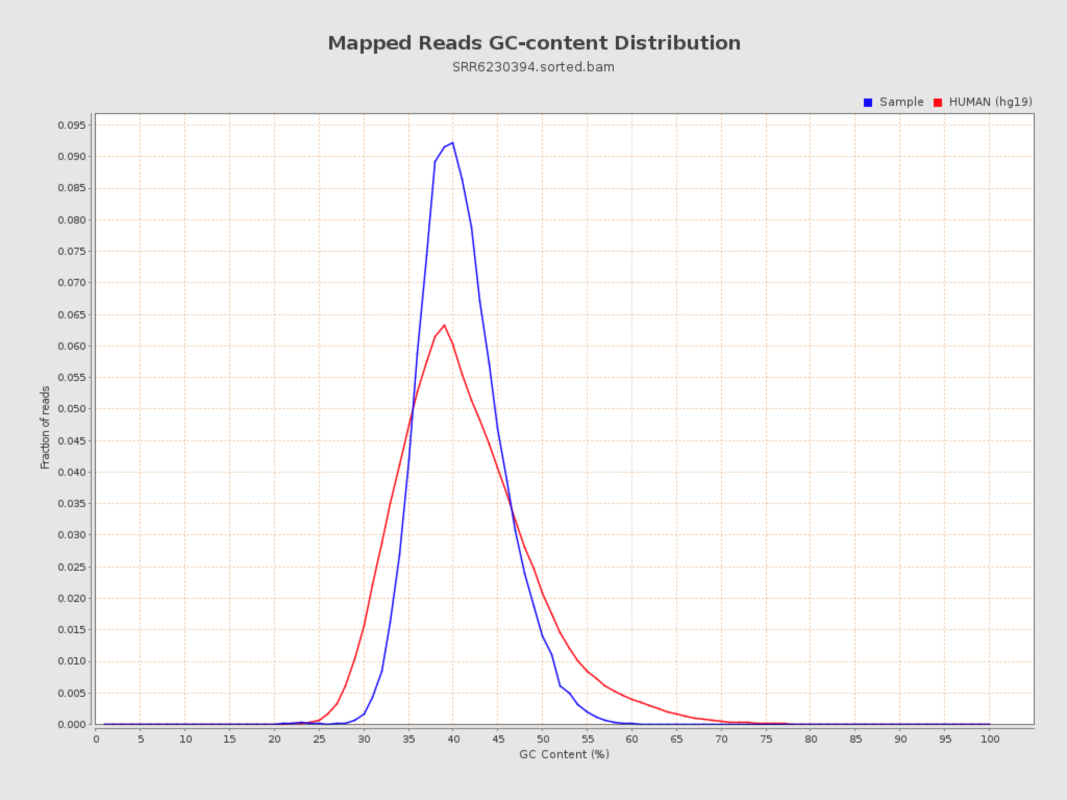
7. Results : Duplication Rate Histogram



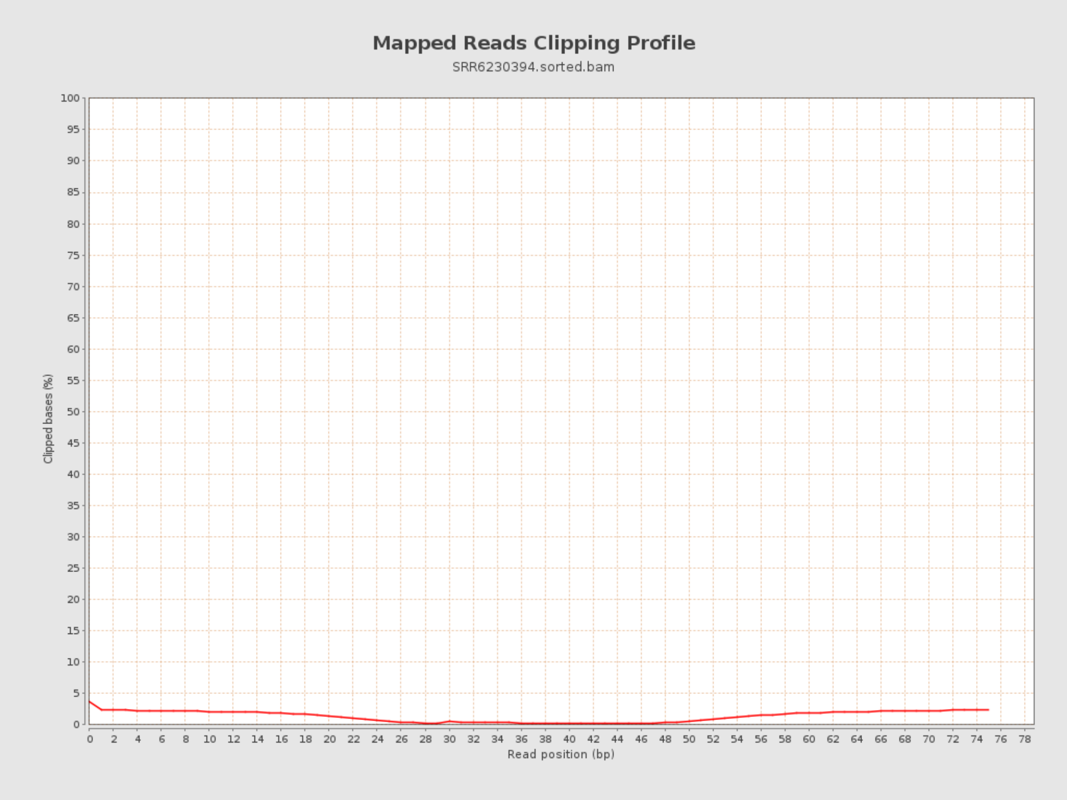
8. Results : Mapped Reads Nucleotide Content



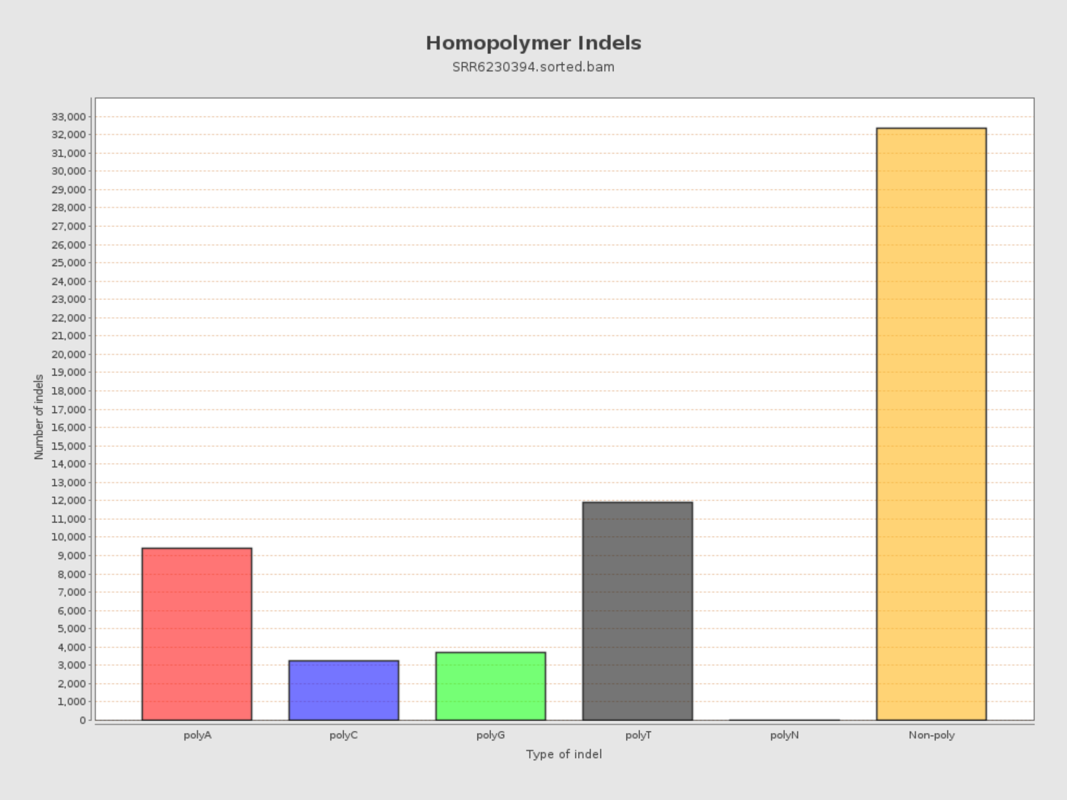
9. Results : Mapped Reads GC-content Distribution



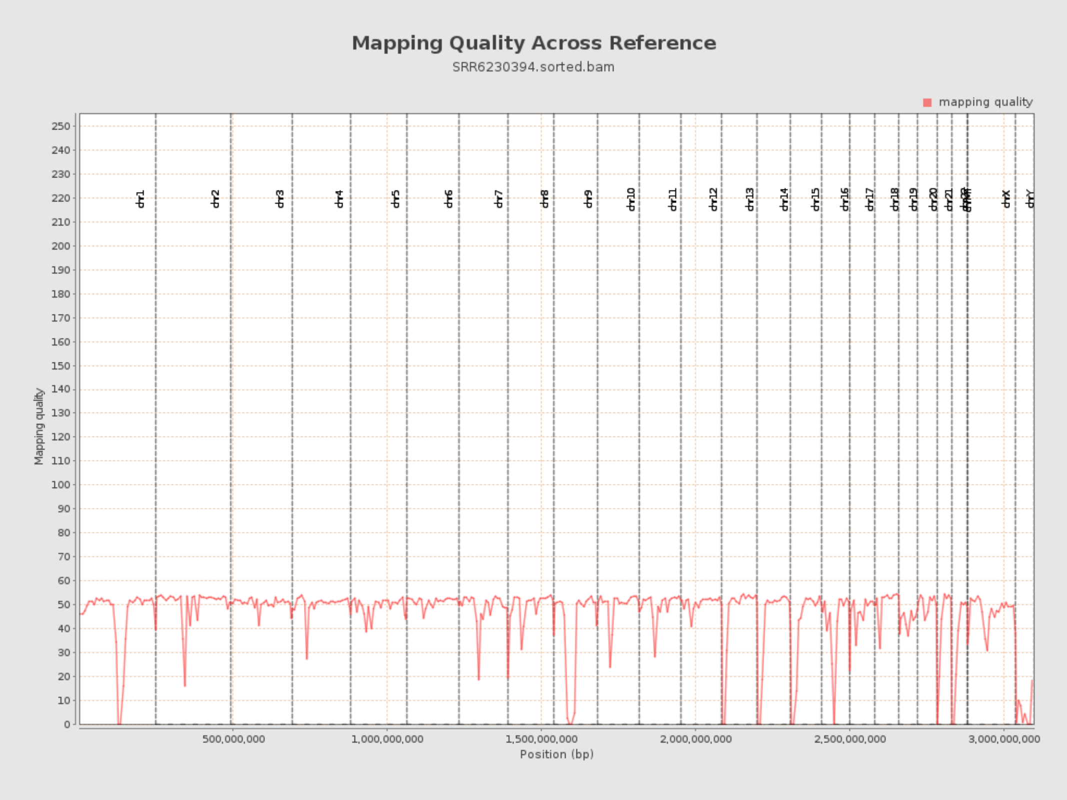
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram