Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:30:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230397.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_SRR6230397 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230397.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:30:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230397.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	129,893
Mapped reads	114,870 / 88.43%
Unmapped reads	15,023 / 11.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	934 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	2,096 / 1.61%
Duplication rate	1.65%
Clipped reads	46,831 / 36.05%

2.2. ACGT Content

Number/percentage of A's	2,283,556 / 29.32%
Number/percentage of C's	1,428,503 / 18.34%
Number/percentage of T's	2,478,332 / 31.82%
Number/percentage of G's	1,593,871 / 20.46%
Number/percentage of N's	4,261 / 0.05%
GC Percentage	38.81%

2.3. Coverage

Mean	0.0025

Standard Deviation	0.0544

2.4. Mapping Quality

Mean Mapping Quality	46.52

2.5. Mismatches and indels

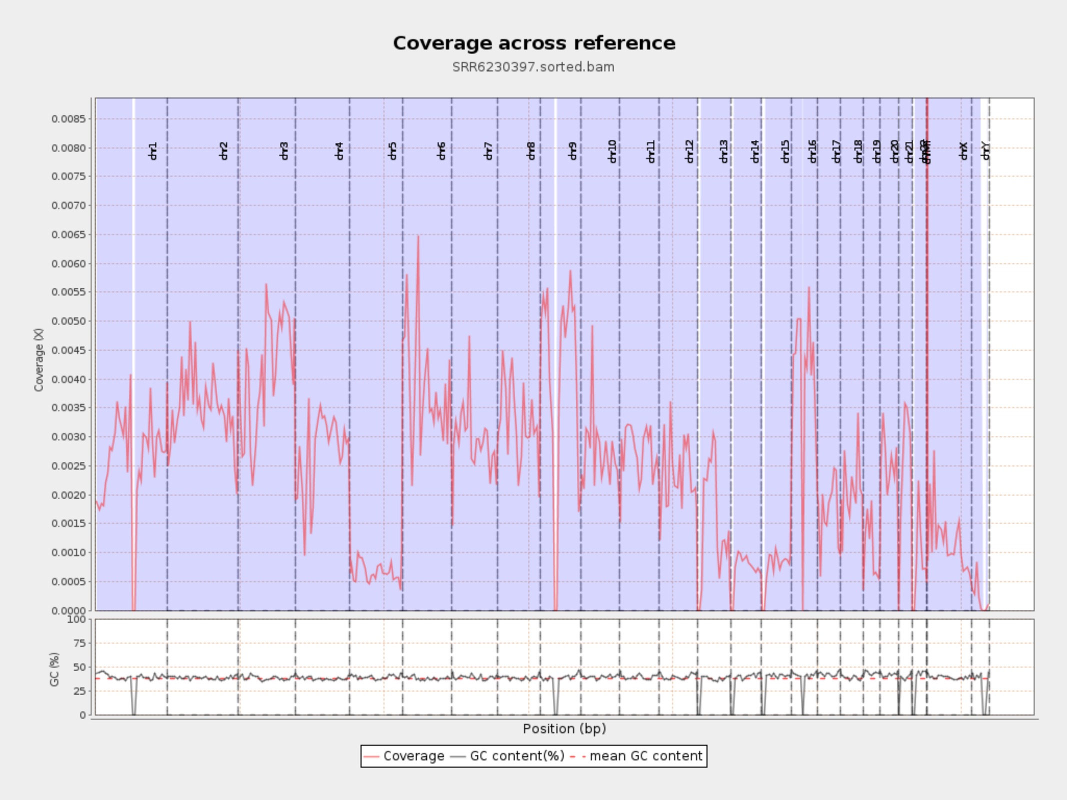
General error rate	0.88%
Mismatches	67,227
Insertions	681
Mapped reads with at least one insertion	0.59%
Deletions	2,029
Mapped reads with at least one deletion	1.74%
Homopolymer indels	49.04%

2.6. Chromosome stats

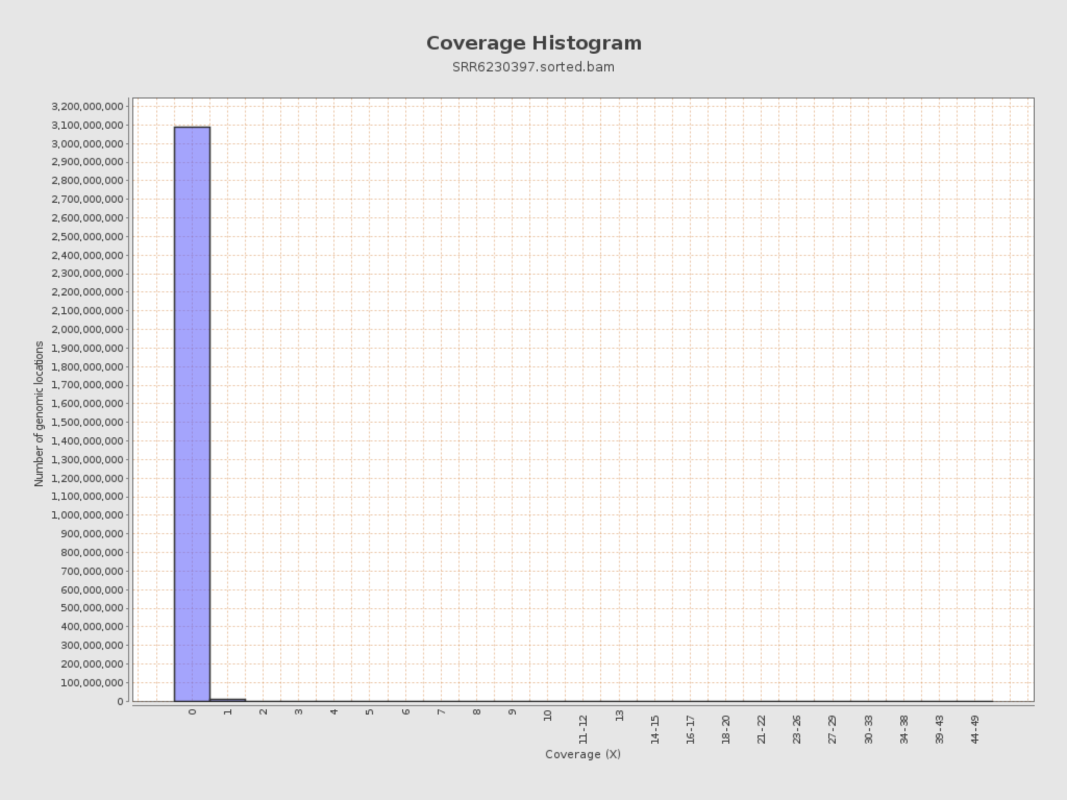
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	646091	0.0026	0.0621
chr2	243199373	851829	0.0035	0.0635
chr3	198022430	814892	0.0041	0.066
chr4	191154276	522889	0.0027	0.0544
chr5	180915260	119954	0.0007	0.0275
chr6	171115067	664131	0.0039	0.0653
chr7	159138663	469700	0.003	0.0602

chr8	146364022	480518	0.0033	0.0665
chr9	141213431	578750	0.0041	0.0673
chr10	135534747	370668	0.0027	0.0567
chr11	135006516	372157	0.0028	0.0562
chr12	133851895	316945	0.0024	0.0502
chr13	115169878	175017	0.0015	0.04
chr14	107349540	77070	0.0007	0.0283
chr15	102531392	74319	0.0007	0.0279
chr16	90354753	356989	0.004	0.0656
chr17	81195210	137281	0.0017	0.0424
chr18	78077248	163564	0.0021	0.0603
chr19	59128983	65305	0.0011	0.0421
chr20	63025520	162121	0.0026	0.0522
chr21	48129895	121962	0.0025	0.0522
chr22	51304566	46260	0.0009	0.0309
chrMT	16571	5364	0.3237	0.6303
chrX	155270560	184719	0.0012	0.0361
chrY	59373566	13389	0.0002	0.0171

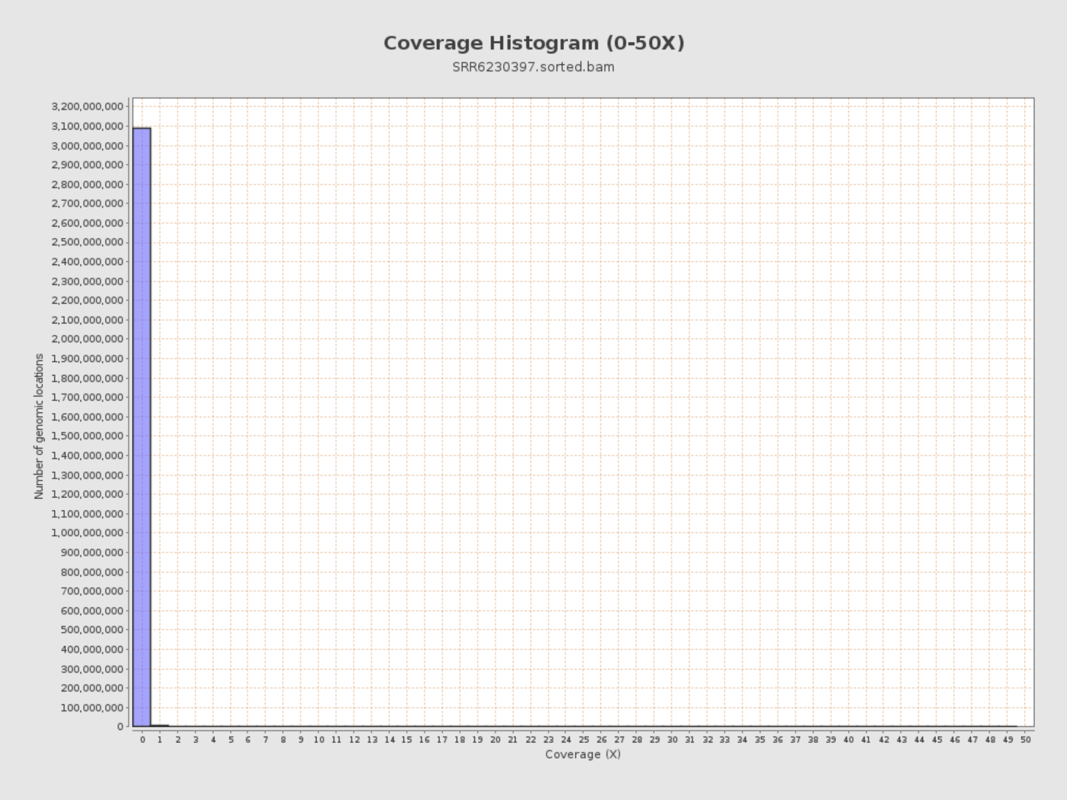
3. Results : Coverage across reference



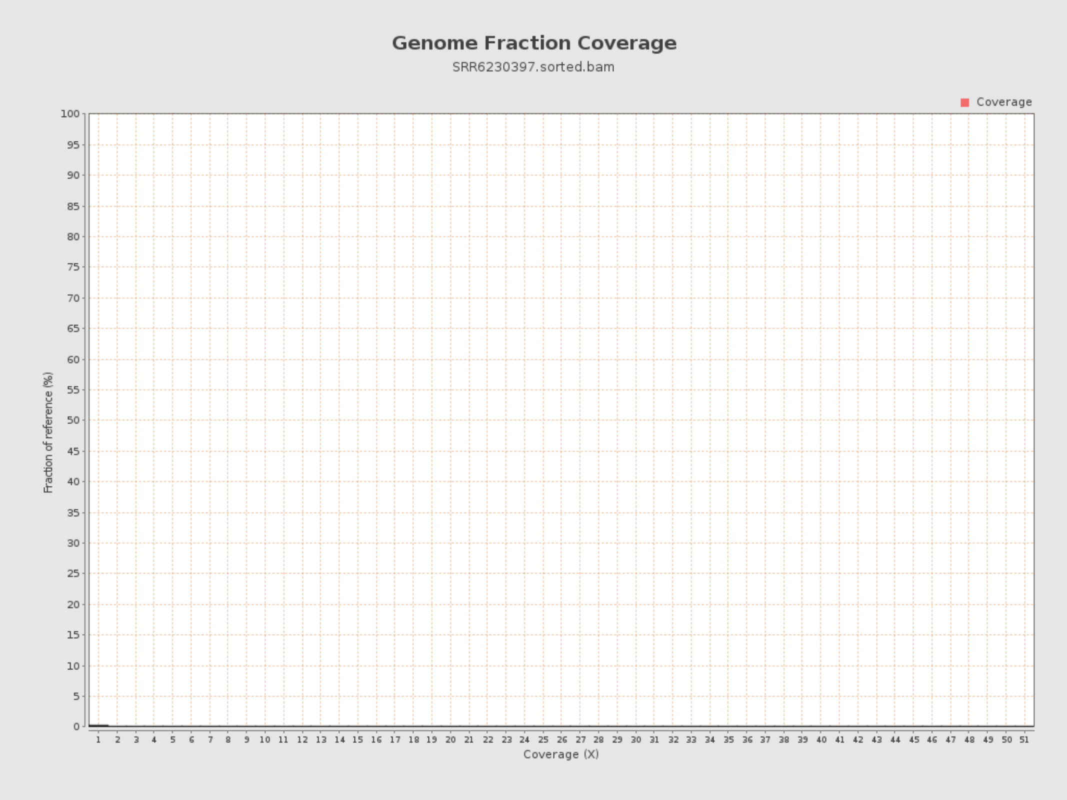
4. Results : Coverage Histogram



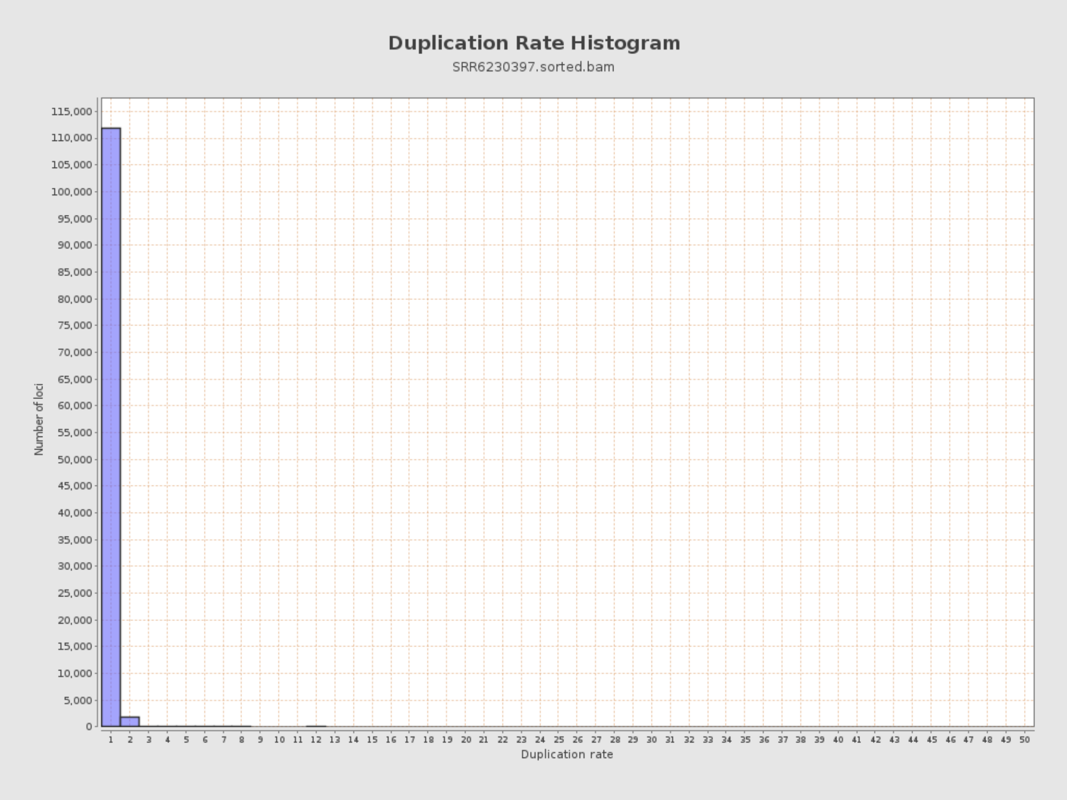
5. Results : Coverage Histogram (0-50X)



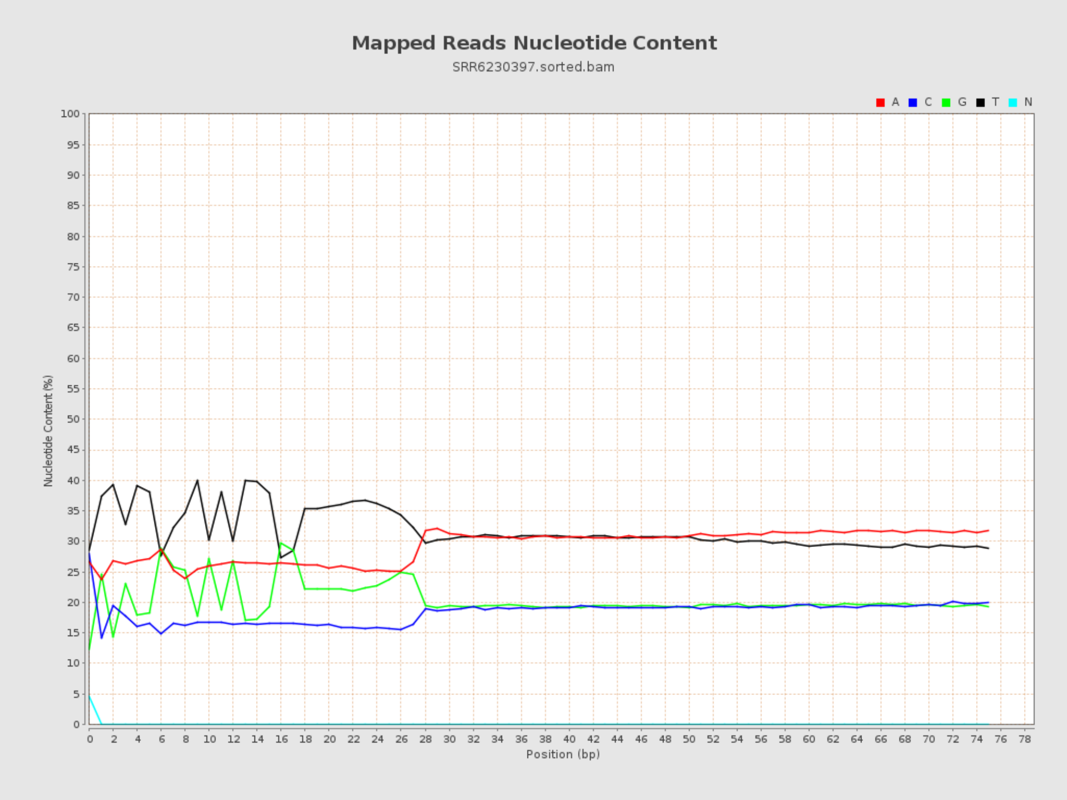
6. Results : Genome Fraction Coverage



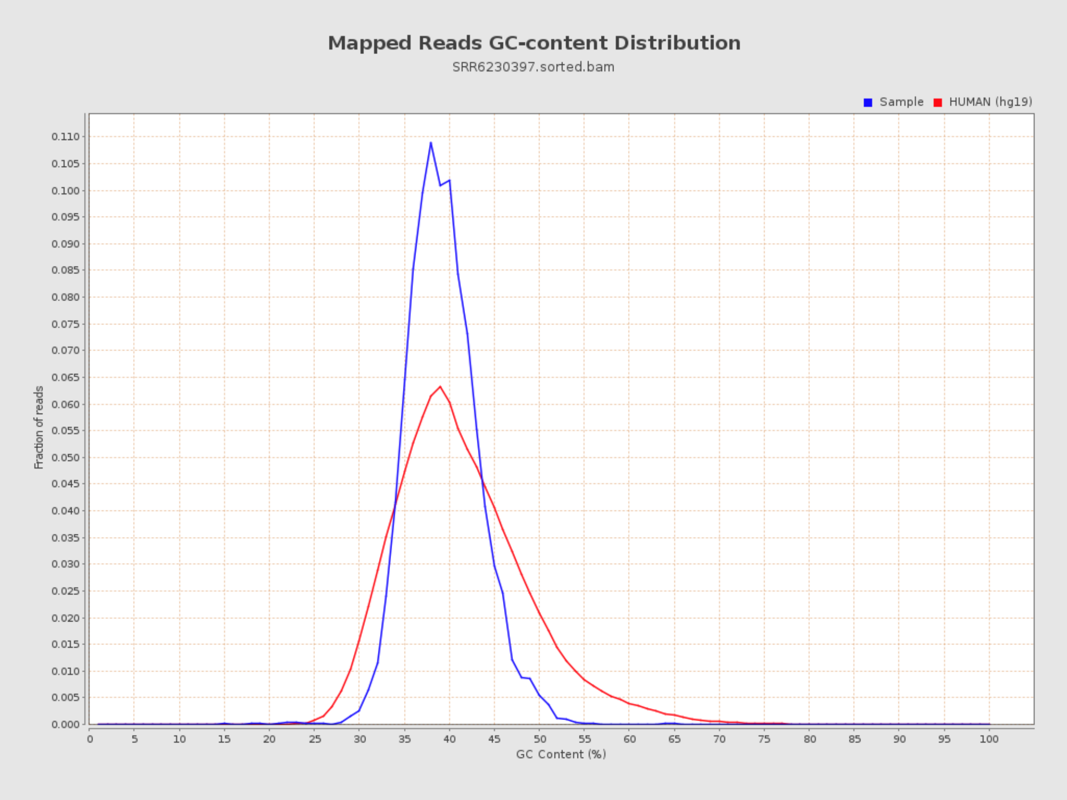
7. Results : Duplication Rate Histogram



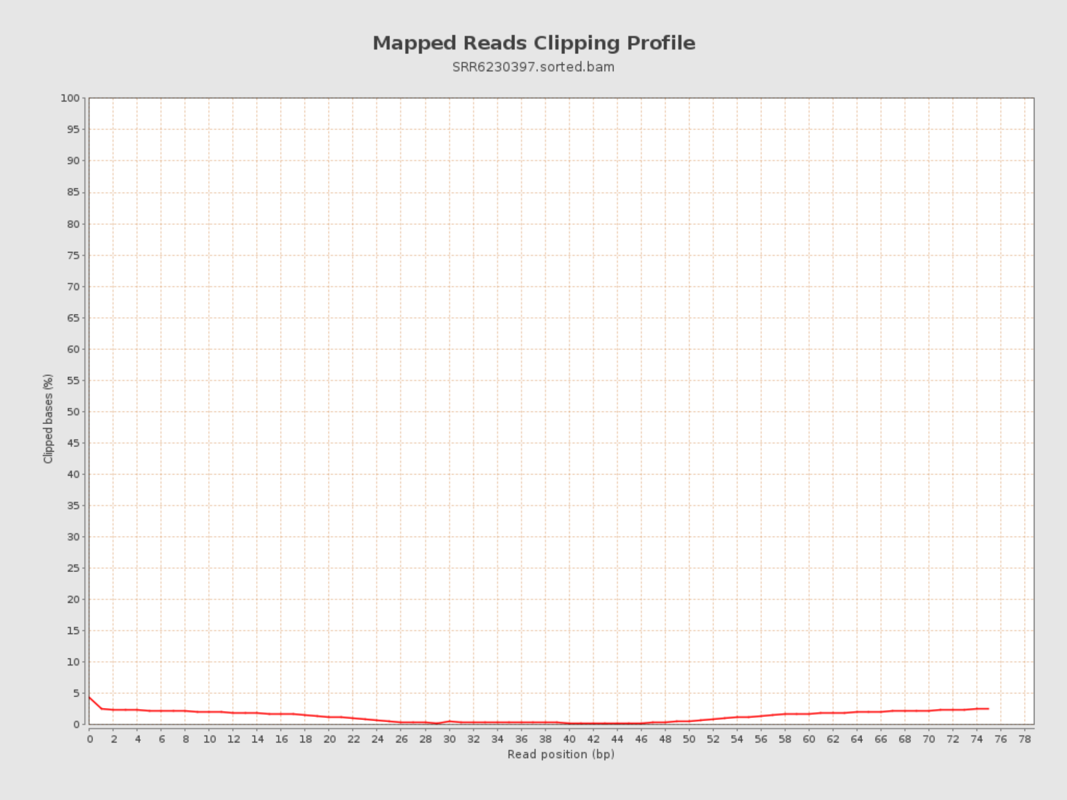
8. Results : Mapped Reads Nucleotide Content



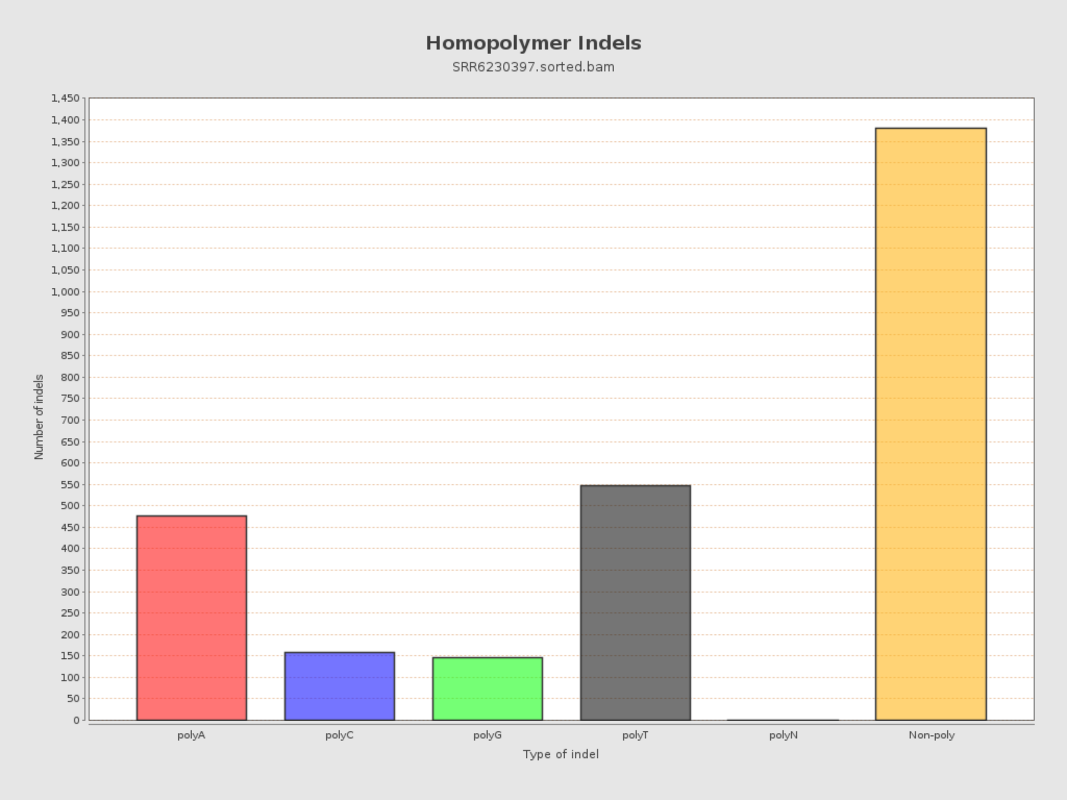
9. Results : Mapped Reads GC-content Distribution



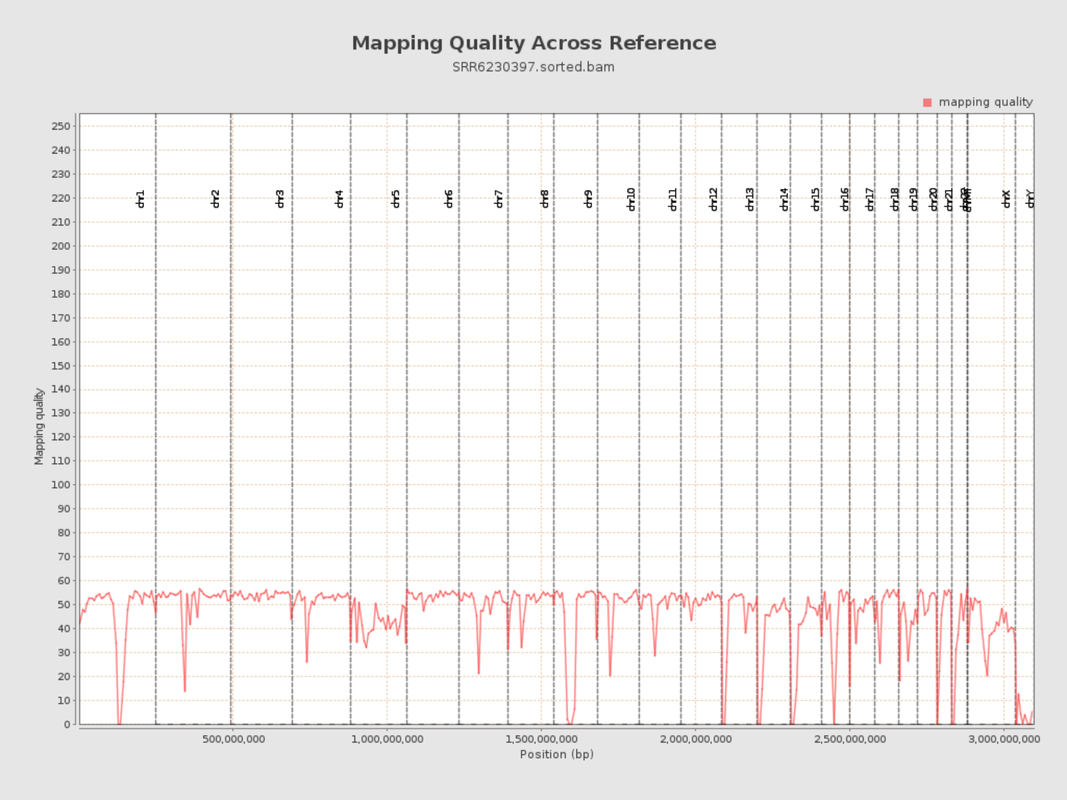
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram