Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:56:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237279.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_SRR6237279 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237279.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:56:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237279.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,573,920
Mapped reads	2,126,446 / 82.62%
Unmapped reads	447,474 / 17.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,152 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	184,708 / 7.18%
Duplication rate	6.86%
Clipped reads	956,702 / 37.17%

2.2. ACGT Content

Number/percentage of A's	39,750,501 / 28.08%
Number/percentage of C's	25,526,663 / 18.03%
Number/percentage of T's	45,667,943 / 32.26%
Number/percentage of G's	30,614,227 / 21.63%
Number/percentage of N's	2,220 / 0%
GC Percentage	39.66%

2.3. Coverage

Mean	0.0457

Standard Deviation	0.4501

2.4. Mapping Quality

Mean Mapping Quality	45.46

2.5. Mismatches and indels

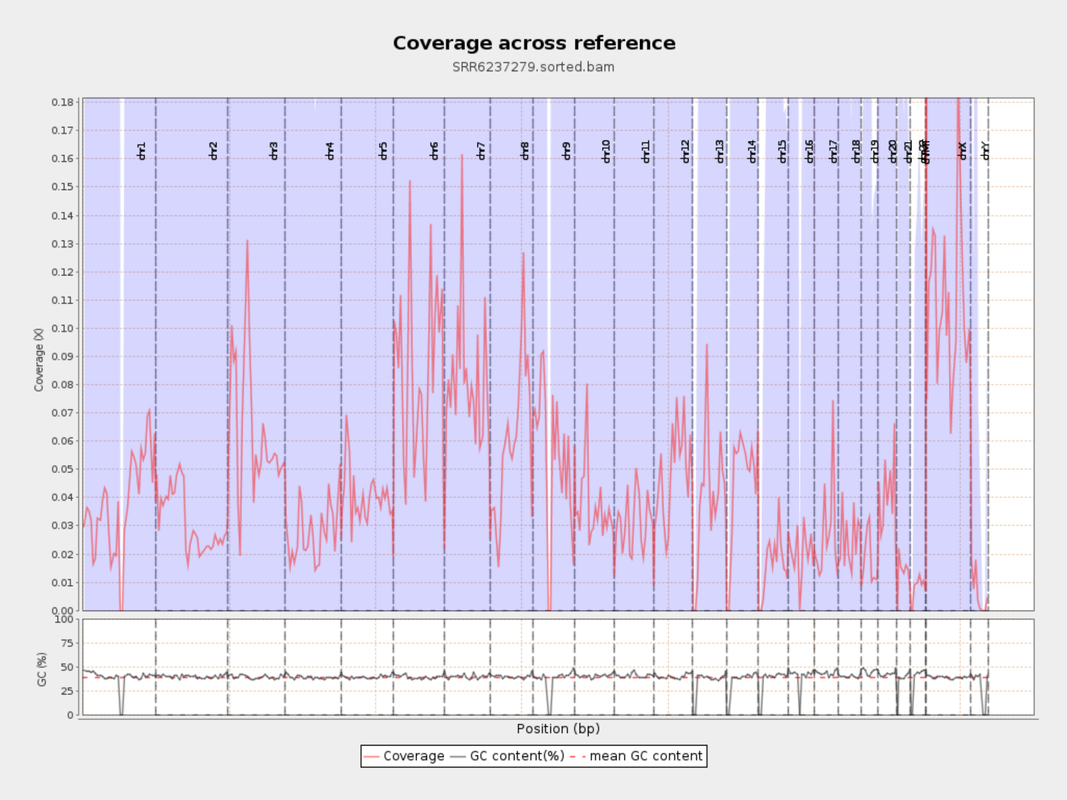
General error rate	0.75%
Mismatches	1,036,512
Insertions	9,941
Mapped reads with at least one insertion	0.46%
Deletions	32,421
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.82%

2.6. Chromosome stats

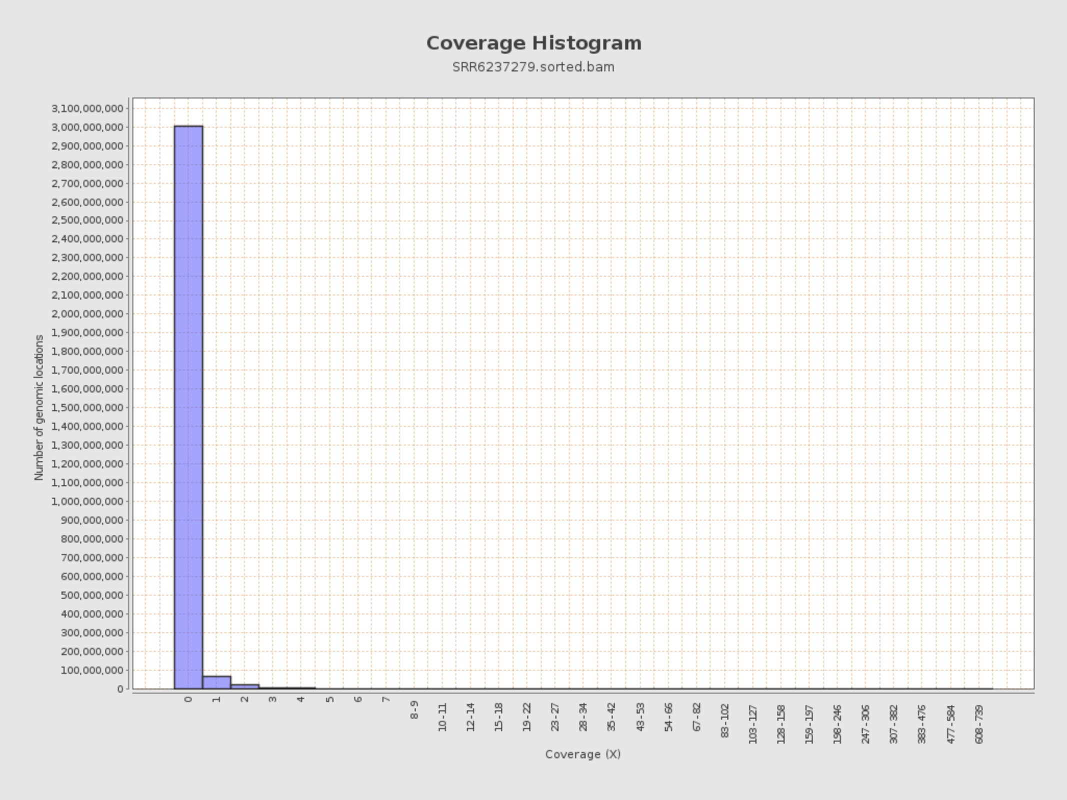
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9420329	0.0378	0.512
chr2	243199373	7639415	0.0314	0.4043
chr3	198022430	12628443	0.0638	0.3534
chr4	191154276	5355692	0.028	0.2777
chr5	180915260	7251440	0.0401	0.2819
chr6	171115067	14801042	0.0865	0.6085
chr7	159138663	12868007	0.0809	1.0005

chr8	146364022	8755564	0.0598	0.4478
chr9	141213431	7704080	0.0546	0.4378
chr10	135534747	4926315	0.0363	0.453
chr11	135006516	4148643	0.0307	0.275
chr12	133851895	6541621	0.0489	0.3223
chr13	115169878	4590300	0.0399	0.2809
chr14	107349540	4912913	0.0458	0.3293
chr15	102531392	1673446	0.0163	0.1793
chr16	90354753	1823409	0.0202	0.2362
chr17	81195210	2243245	0.0276	0.2333
chr18	78077248	1991942	0.0255	0.6658
chr19	59128983	1090028	0.0184	0.4002
chr20	63025520	2631665	0.0418	0.298
chr21	48129895	666369	0.0138	0.2243
chr22	51304566	411291	0.008	0.118
chrMT	16571	95127	5.7406	4.1908
chrX	155270560	17092361	0.1101	0.5468
chrY	59373566	355217	0.006	0.1699

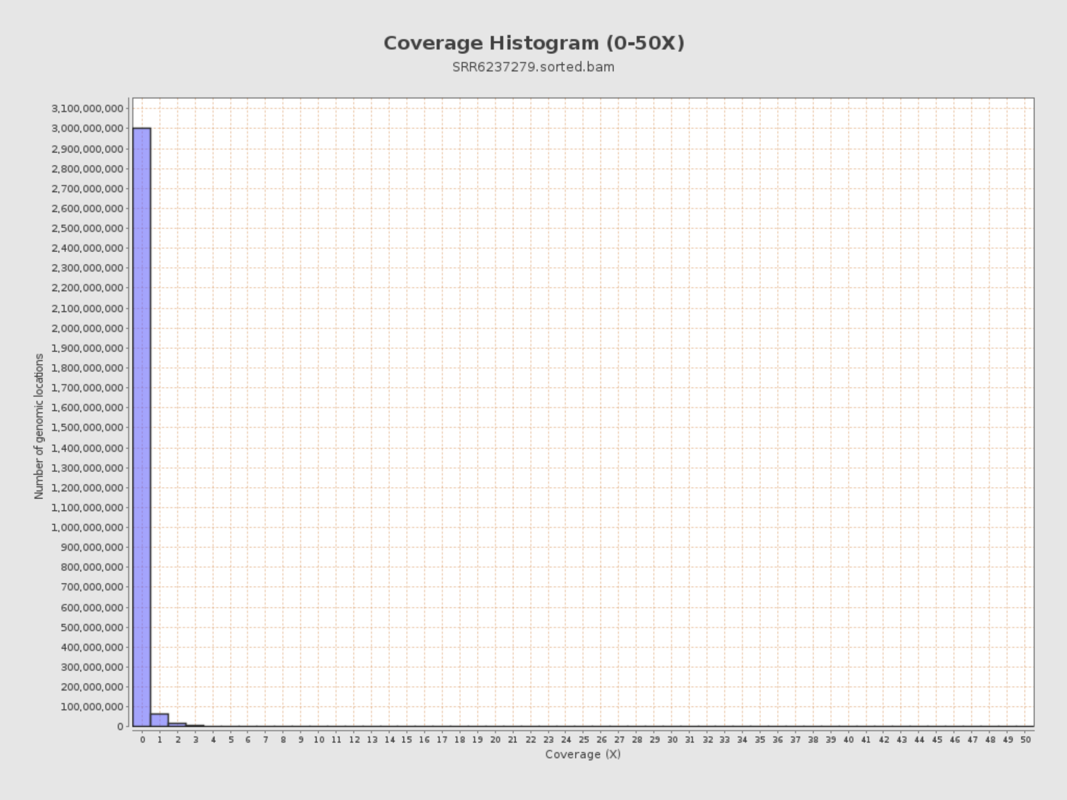
3. Results : Coverage across reference



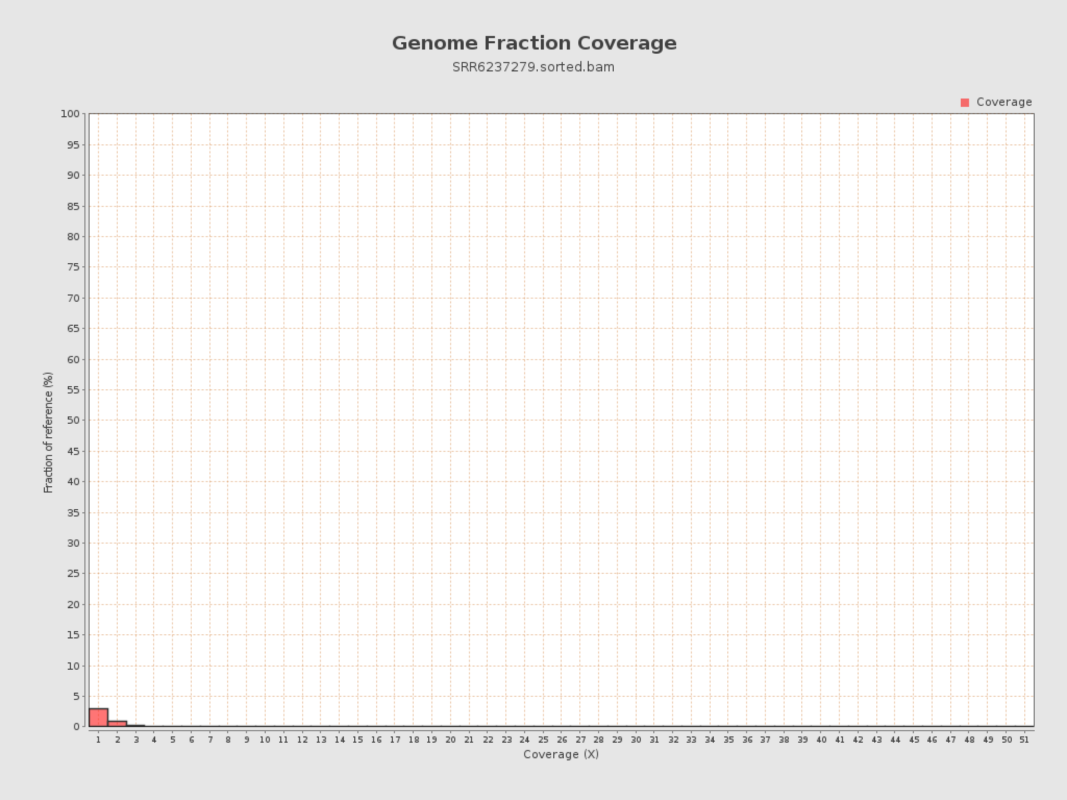
4. Results : Coverage Histogram



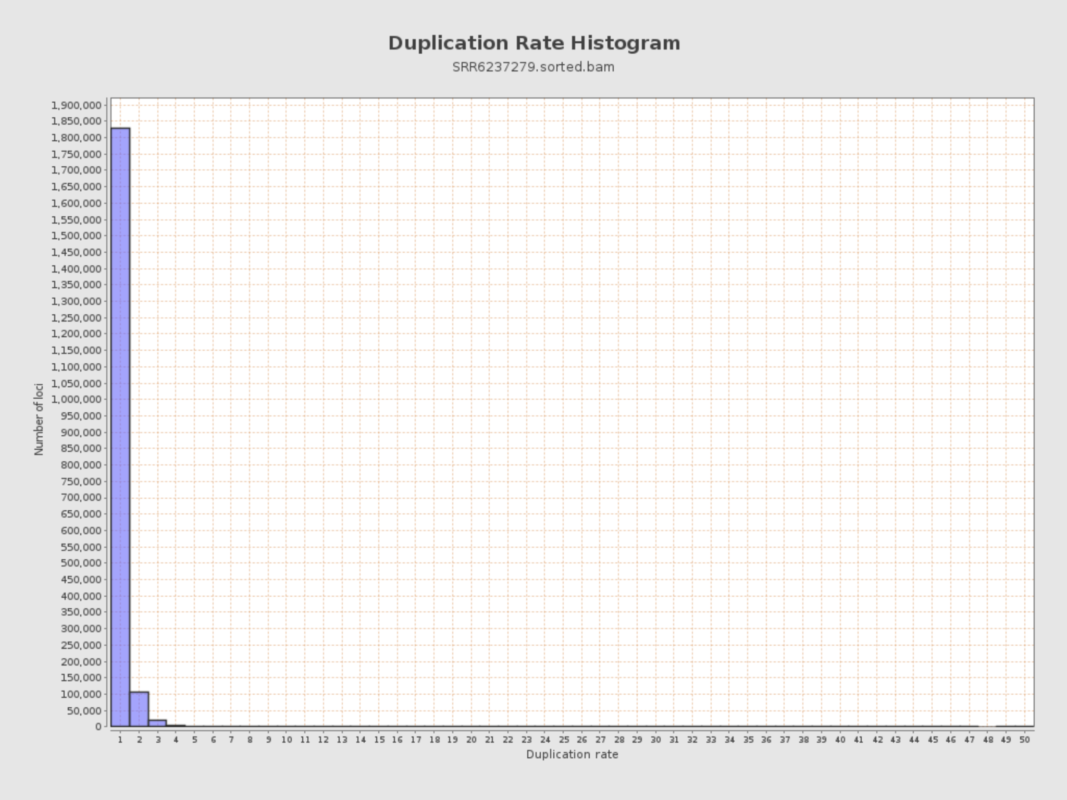
5. Results : Coverage Histogram (0-50X)



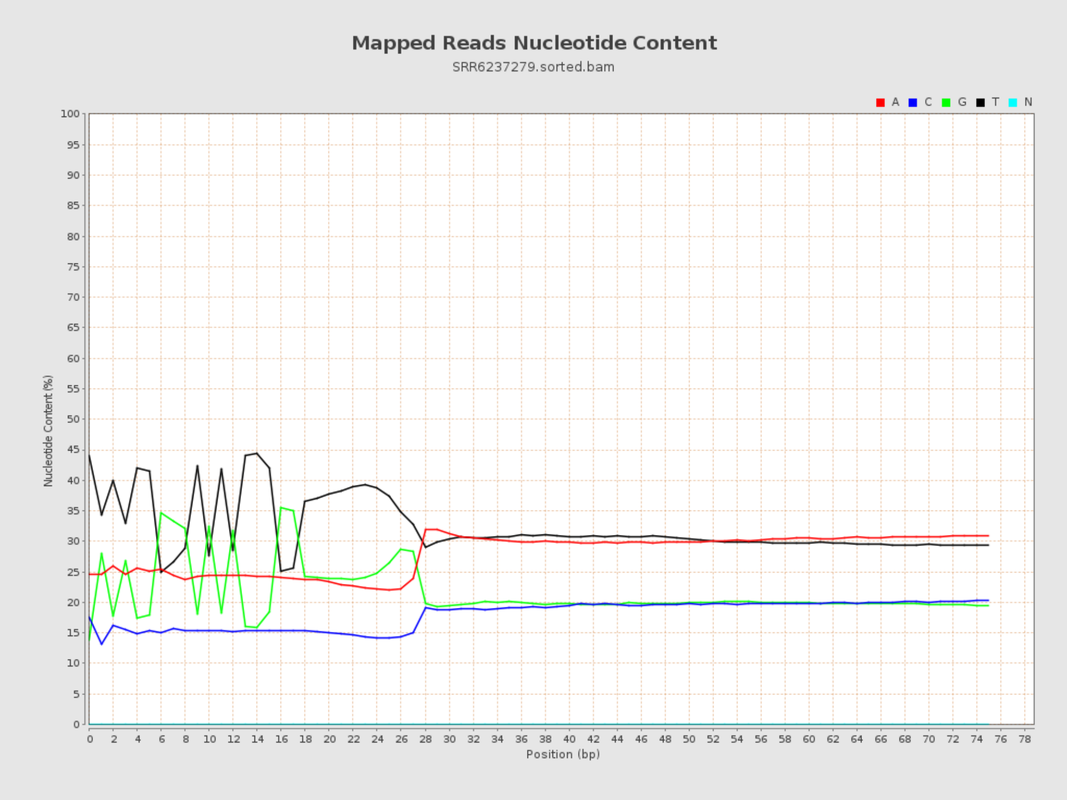
6. Results : Genome Fraction Coverage



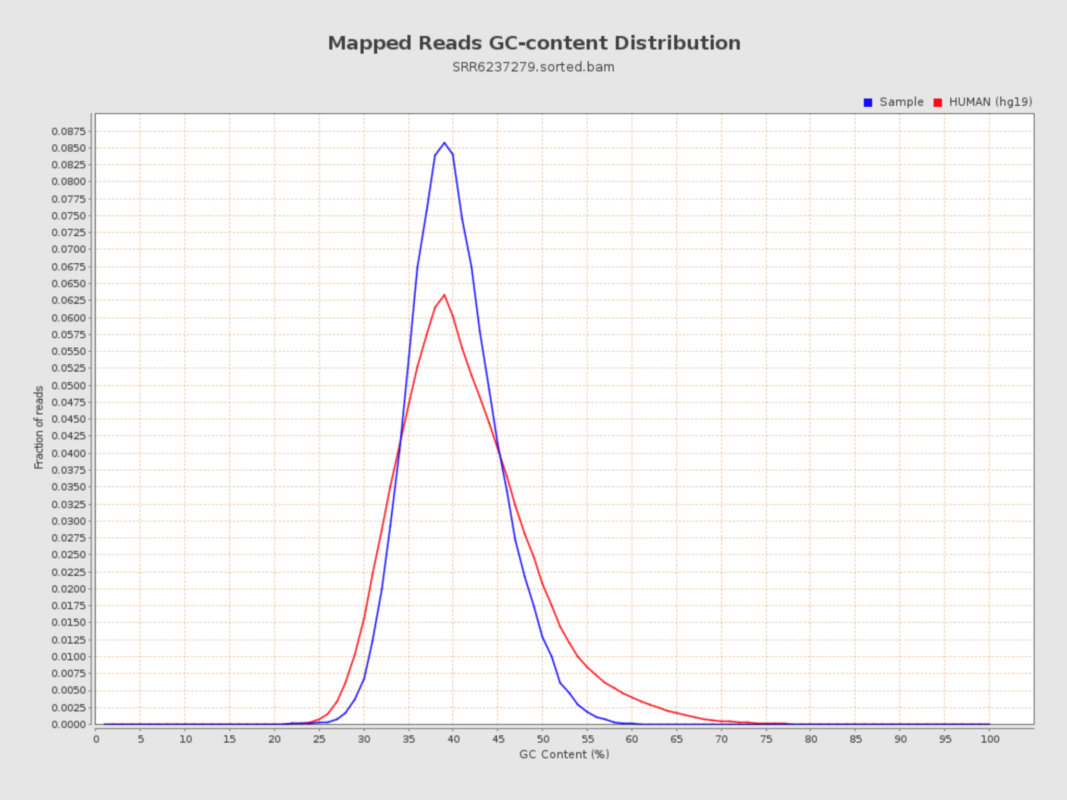
7. Results : Duplication Rate Histogram



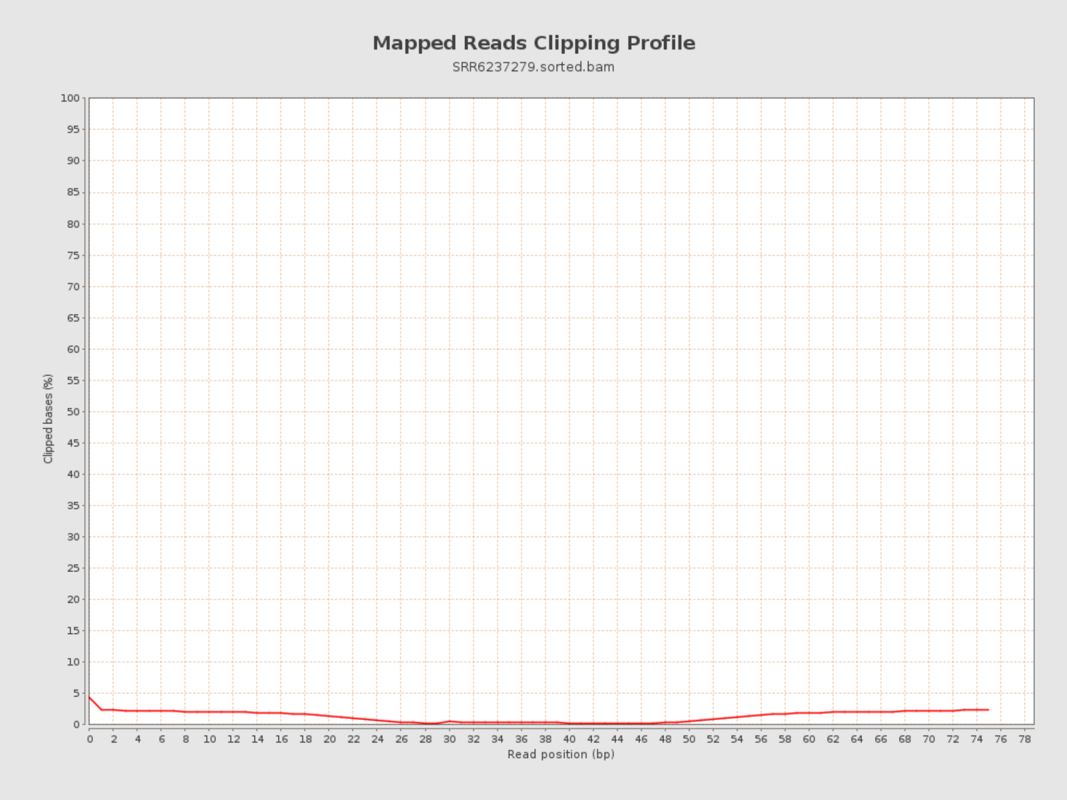
8. Results : Mapped Reads Nucleotide Content



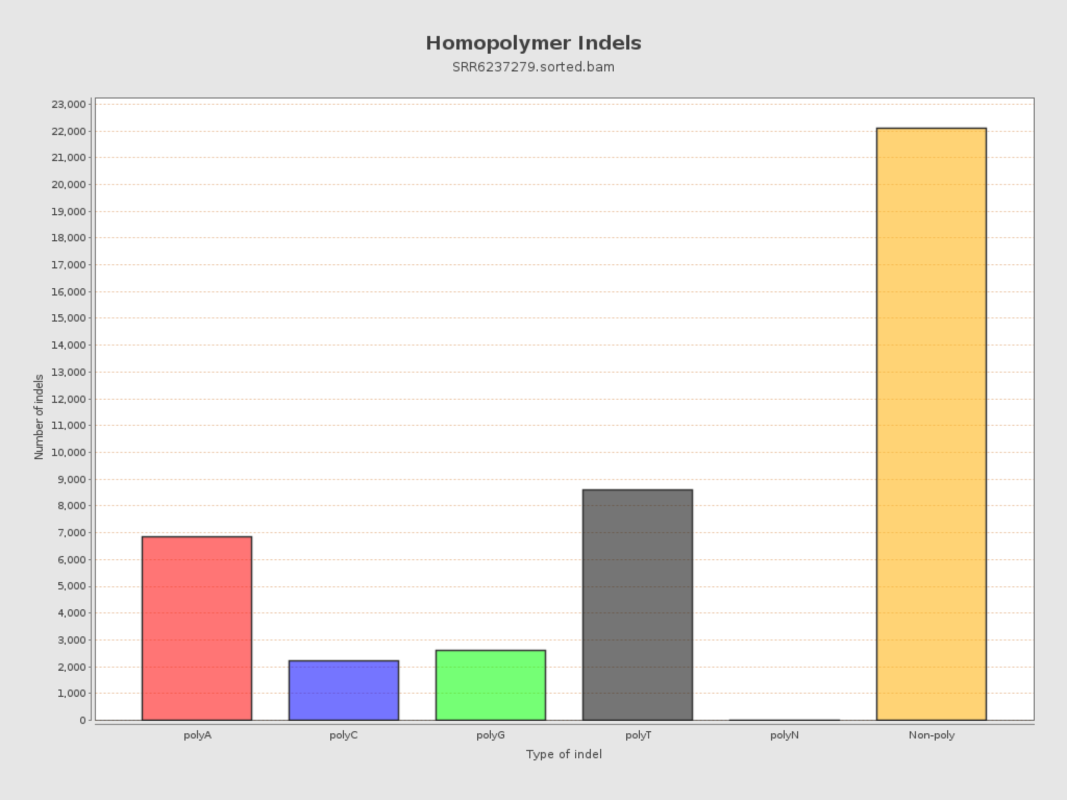
9. Results : Mapped Reads GC-content Distribution



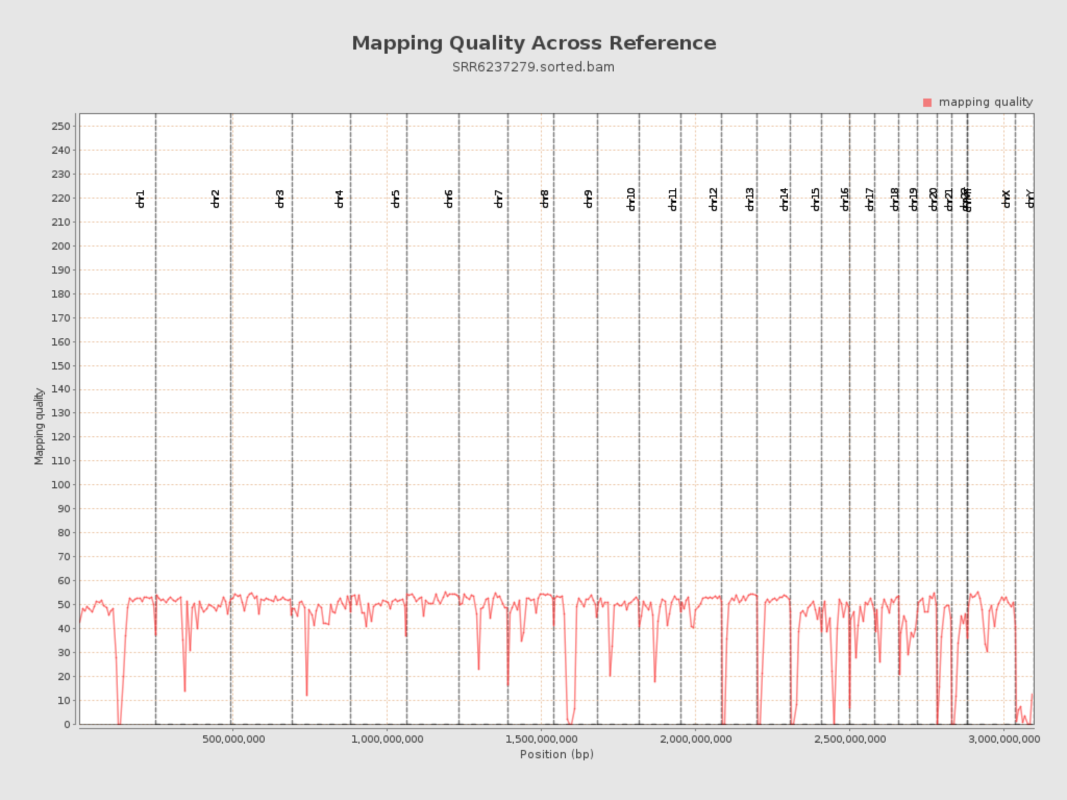
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram