Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:26:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237251.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_SRR6237251 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237251.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:26:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237251.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,389,023
Mapped reads	1,753,829 / 73.41%
Unmapped reads	635,194 / 26.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,368 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	210,227 / 8.8%
Duplication rate	9.27%
Clipped reads	833,833 / 34.9%

2.2. ACGT Content

Number/percentage of A's	31,284,749 / 26.98%
Number/percentage of C's	21,505,389 / 18.55%
Number/percentage of T's	36,708,328 / 31.66%
Number/percentage of G's	26,438,560 / 22.8%
Number/percentage of N's	1,663 / 0%
GC Percentage	41.35%

2.3. Coverage

Mean	0.0375

Standard Deviation	0.4112

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

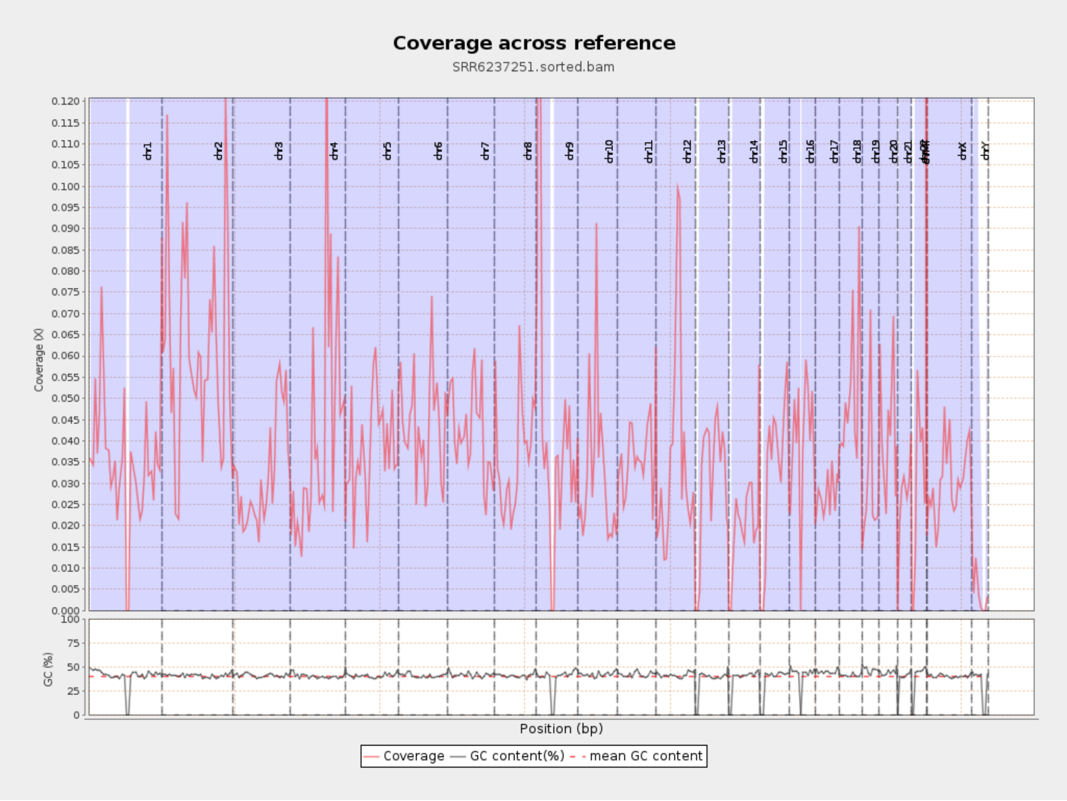
General error rate	0.83%
Mismatches	948,401
Insertions	8,973
Mapped reads with at least one insertion	0.51%
Deletions	26,353
Mapped reads with at least one deletion	1.49%
Homopolymer indels	46.61%

2.6. Chromosome stats

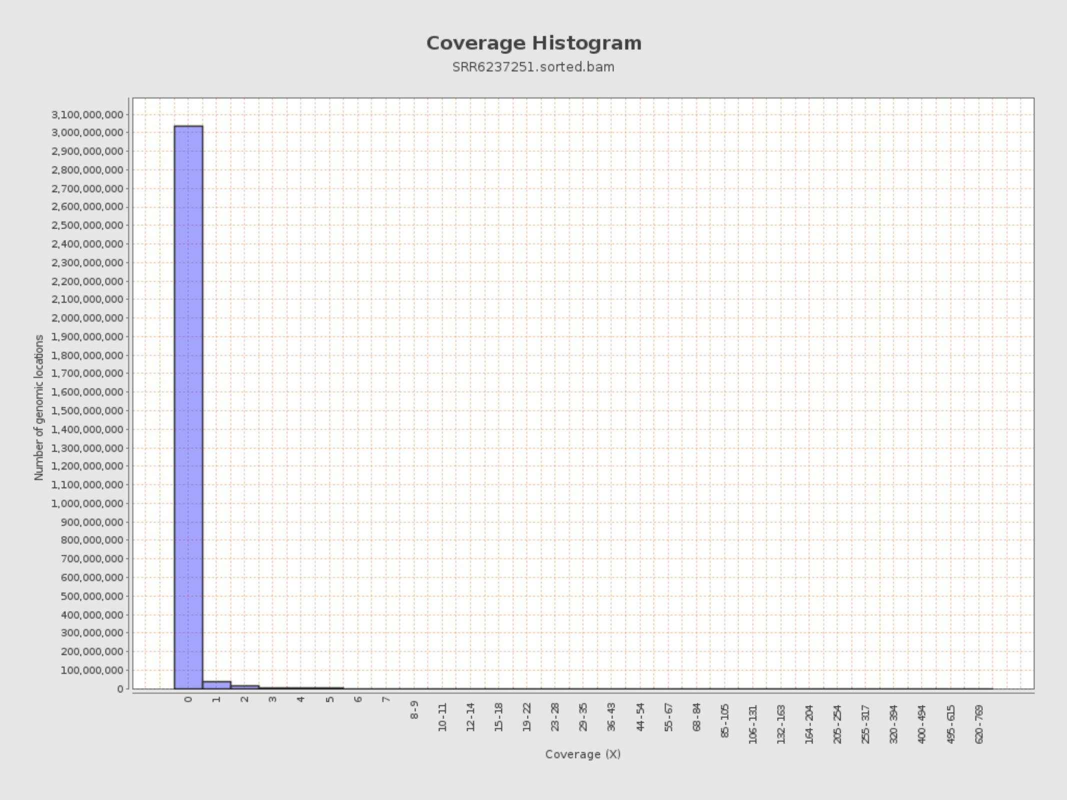
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8711334	0.035	0.677
chr2	243199373	15218754	0.0626	0.5683
chr3	198022430	6334769	0.032	0.3094
chr4	191154276	8018605	0.0419	0.3749
chr5	180915260	6936038	0.0383	0.3438
chr6	171115067	7519925	0.0439	0.4139
chr7	159138663	6725898	0.0423	0.4207

chr8	146364022	5283056	0.0361	0.3683
chr9	141213431	6165926	0.0437	0.3913
chr10	135534747	4419176	0.0326	0.3678
chr11	135006516	4755880	0.0352	0.3441
chr12	133851895	4768698	0.0356	0.3271
chr13	115169878	3528452	0.0306	0.3052
chr14	107349540	2056914	0.0192	0.2485
chr15	102531392	3405811	0.0332	0.3485
chr16	90354753	3628983	0.0402	0.3605
chr17	81195210	2222327	0.0274	0.2883
chr18	78077248	3996917	0.0512	0.4939
chr19	59128983	1782871	0.0302	0.4292
chr20	63025520	2631769	0.0418	0.3722
chr21	48129895	1273742	0.0265	0.2822
chr22	51304566	1426482	0.0278	0.2948
chrMT	16571	176481	10.65	7.2249
chrX	155270560	4747329	0.0306	0.3274
chrY	59373566	246077	0.0041	0.1163

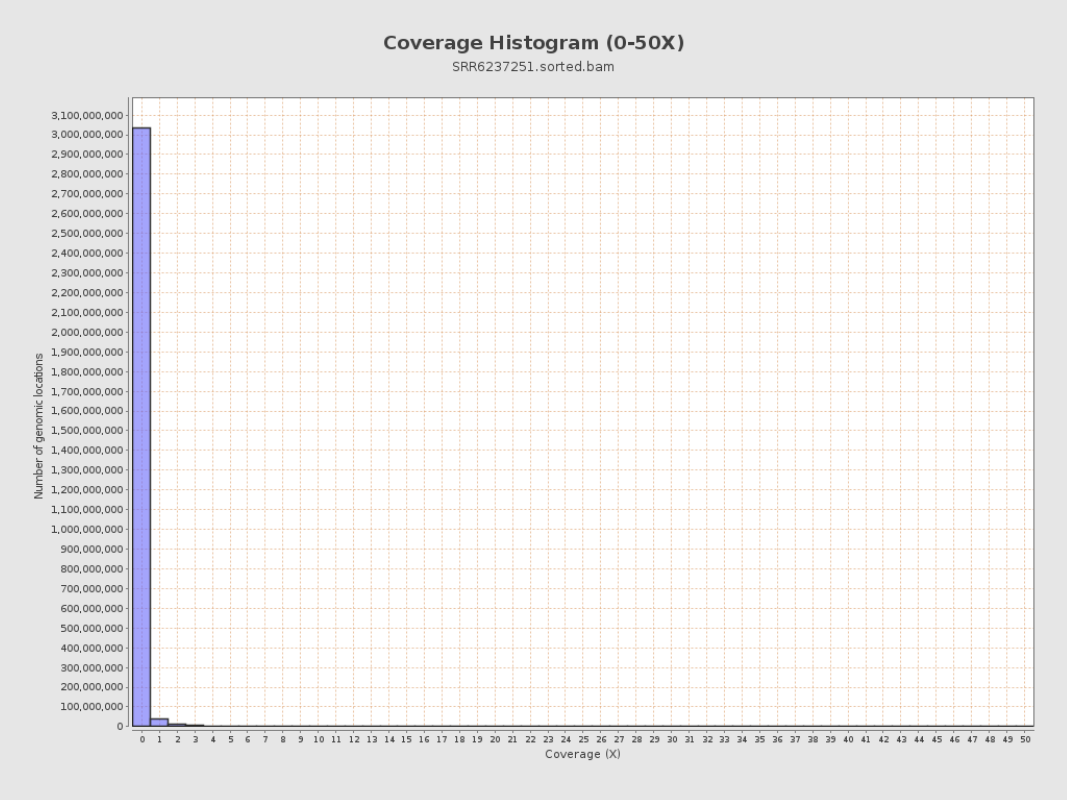
3. Results : Coverage across reference



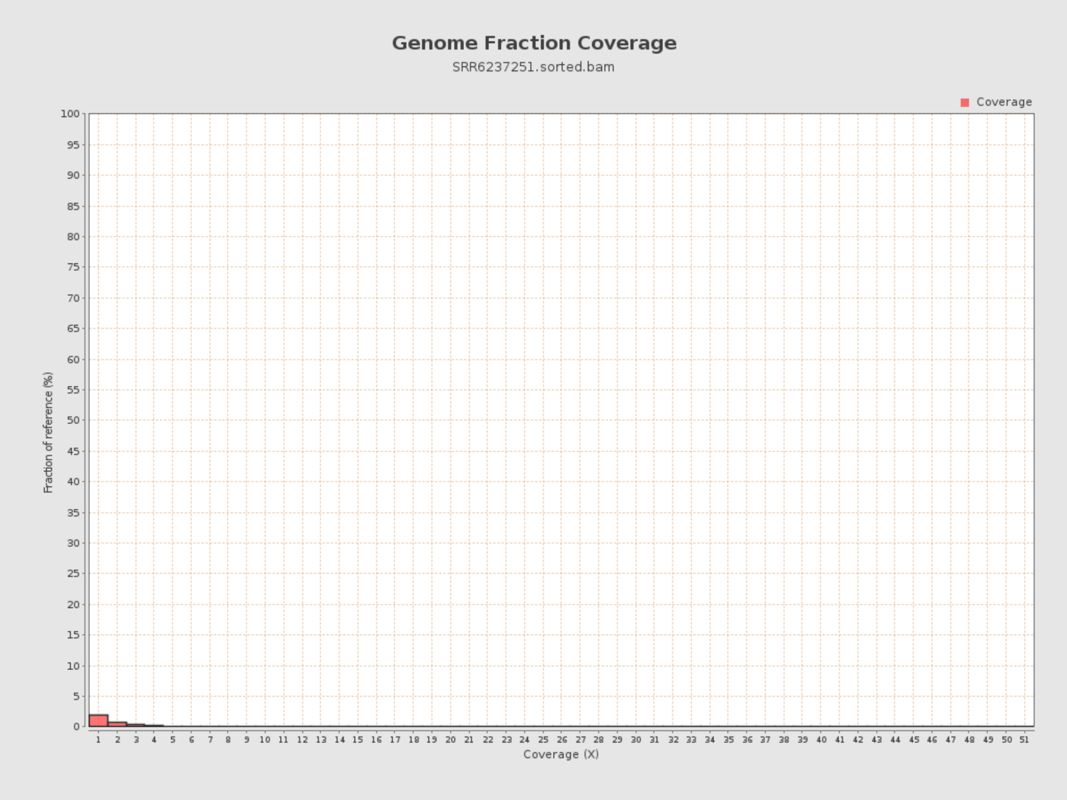
4. Results : Coverage Histogram



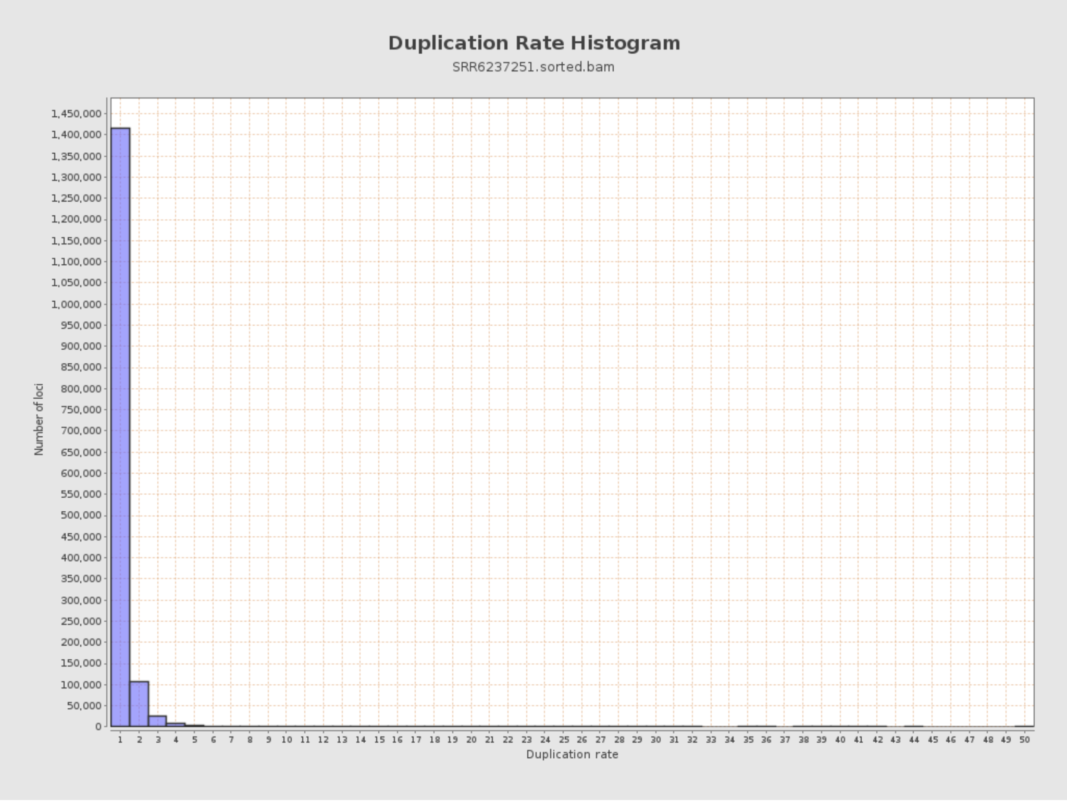
5. Results : Coverage Histogram (0-50X)



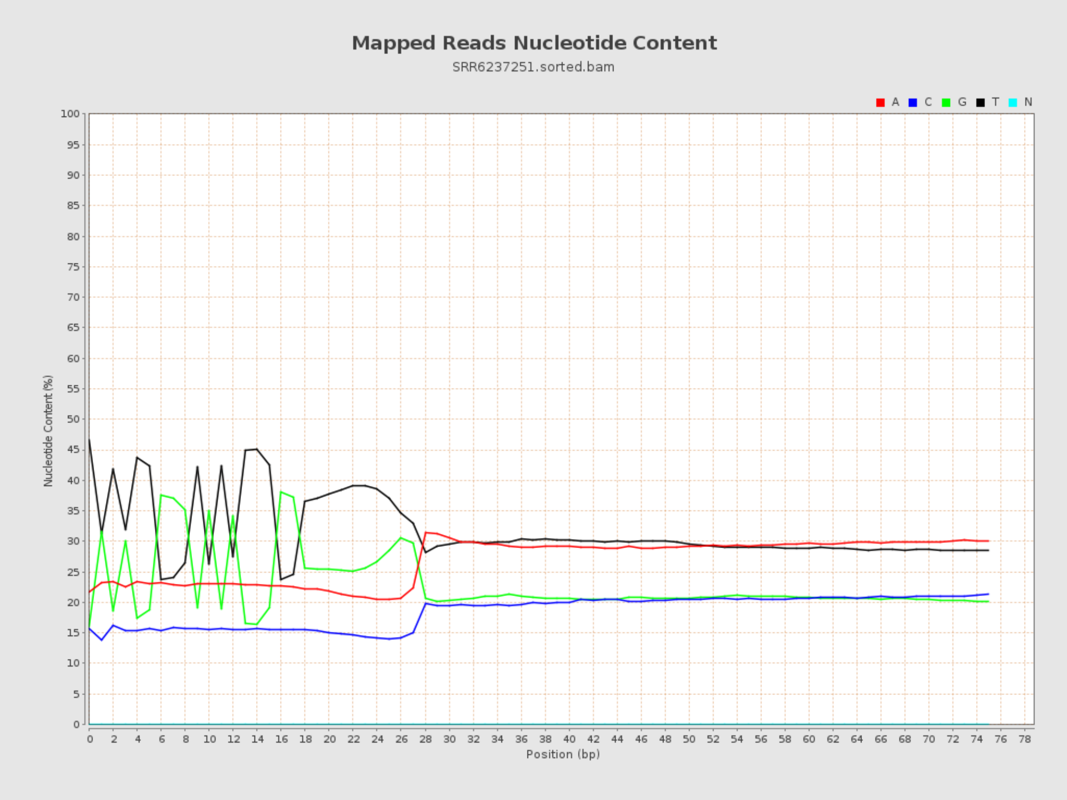
6. Results : Genome Fraction Coverage



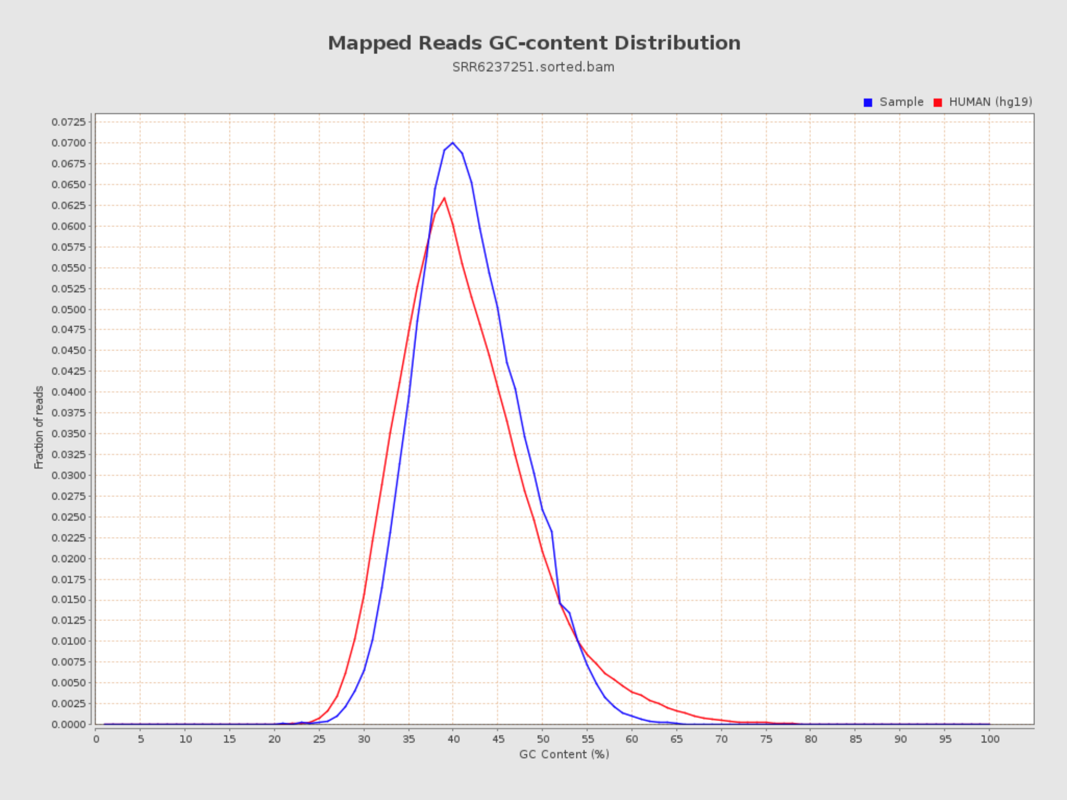
7. Results : Duplication Rate Histogram



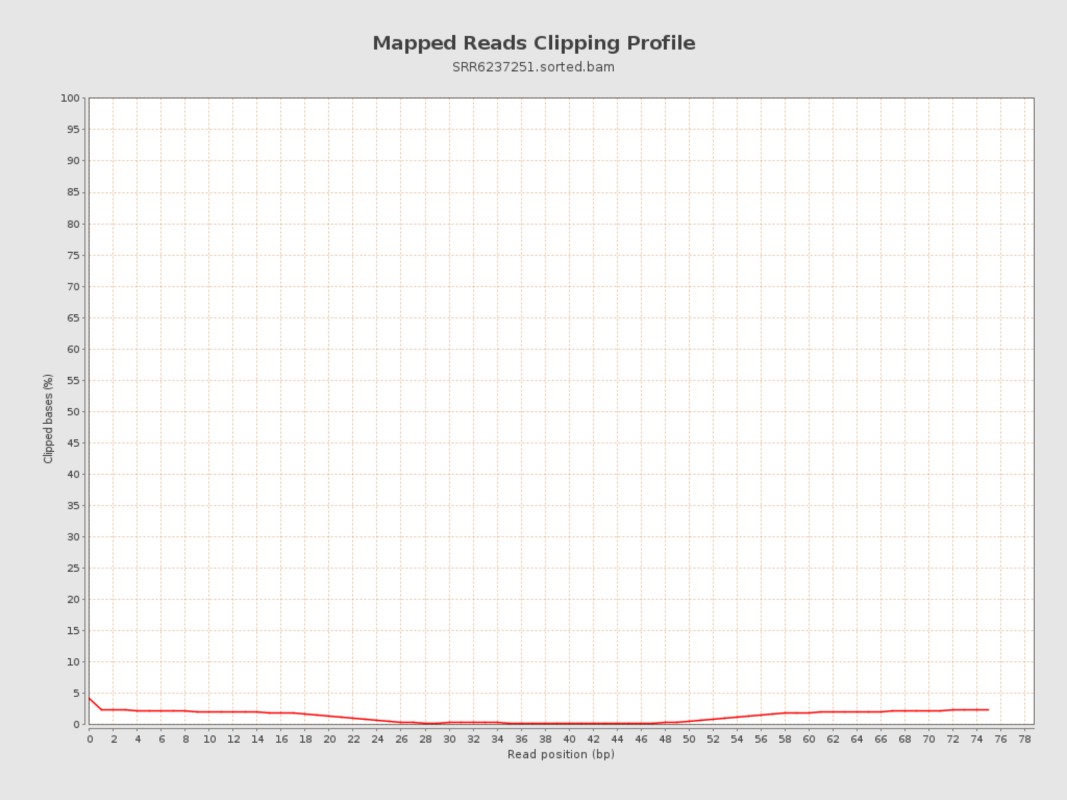
8. Results : Mapped Reads Nucleotide Content



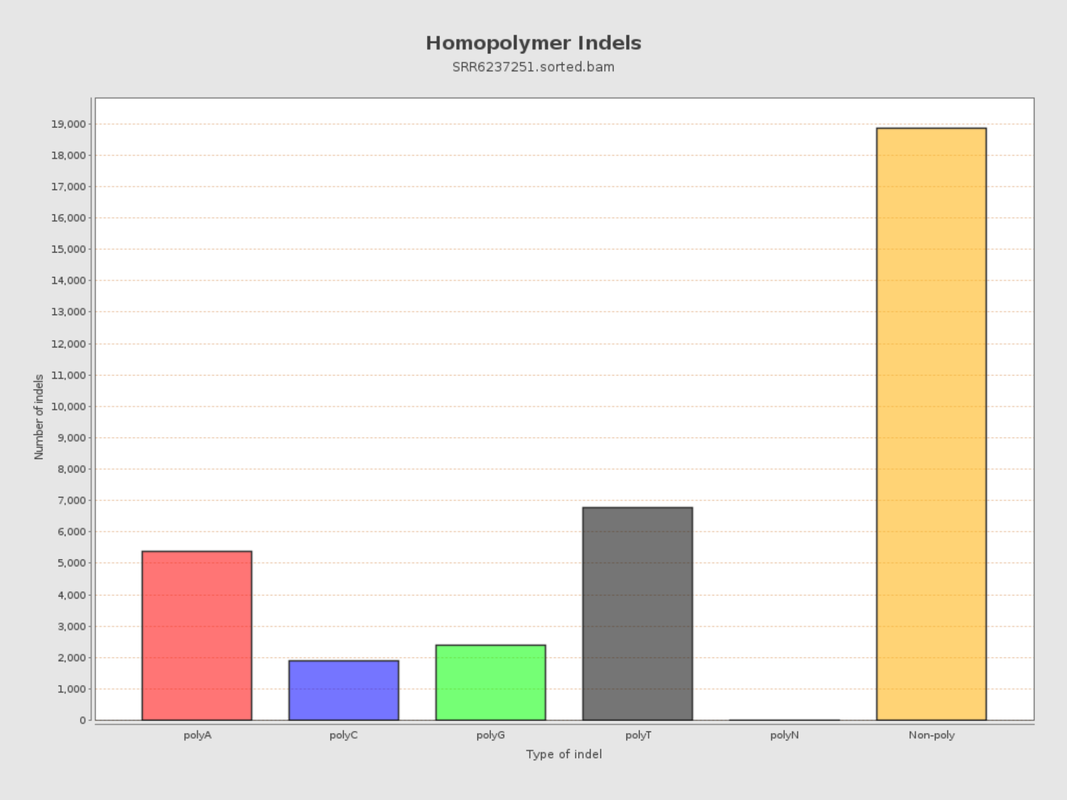
9. Results : Mapped Reads GC-content Distribution



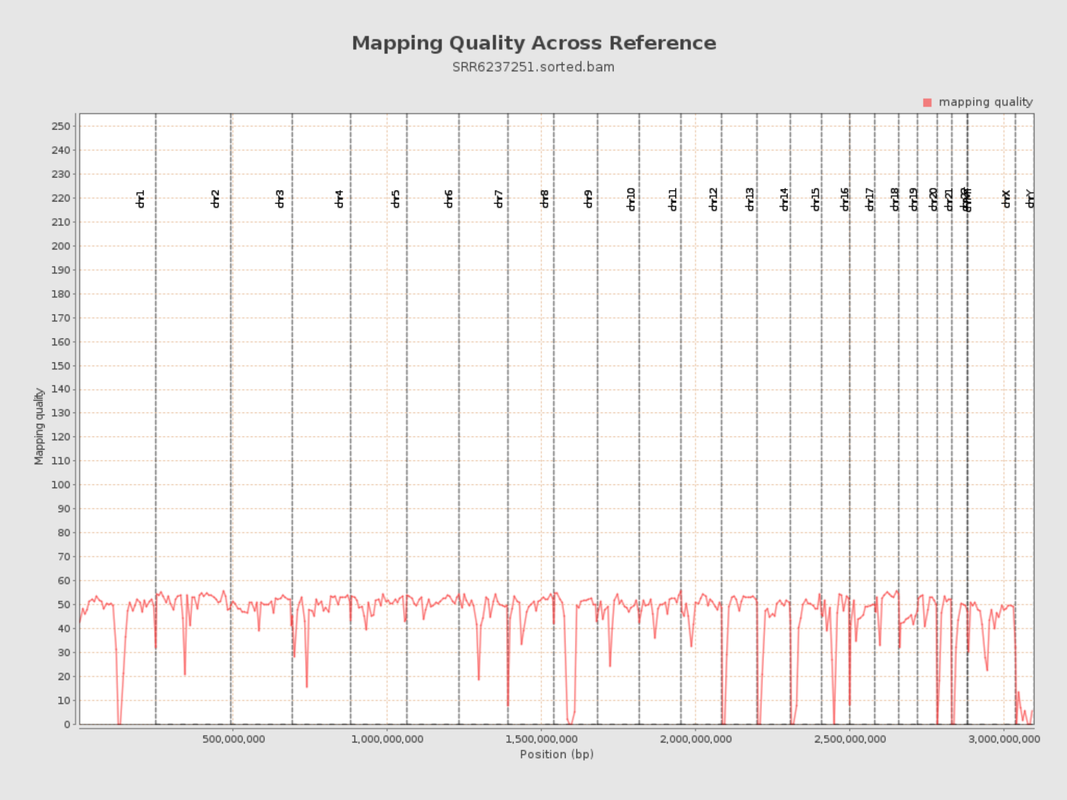
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram