Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:22:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237337.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_SRR6237337 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237337.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:22:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237337.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,601,237
Mapped reads	2,253,431 / 86.63%
Unmapped reads	347,806 / 13.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,317 / 1.09%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	893,374 / 34.34%
Duplication rate	23.19%
Clipped reads	1,616,997 / 62.16%

2.2. ACGT Content

Number/percentage of A's	35,125,704 / 26.09%
Number/percentage of C's	23,012,974 / 17.09%
Number/percentage of T's	45,590,309 / 33.86%
Number/percentage of G's	30,881,777 / 22.94%
Number/percentage of N's	13,257 / 0.01%
GC Percentage	40.03%

2.3. Coverage

Mean	0.0435

Standard Deviation	1.0234

2.4. Mapping Quality

Mean Mapping Quality	42.99

2.5. Mismatches and indels

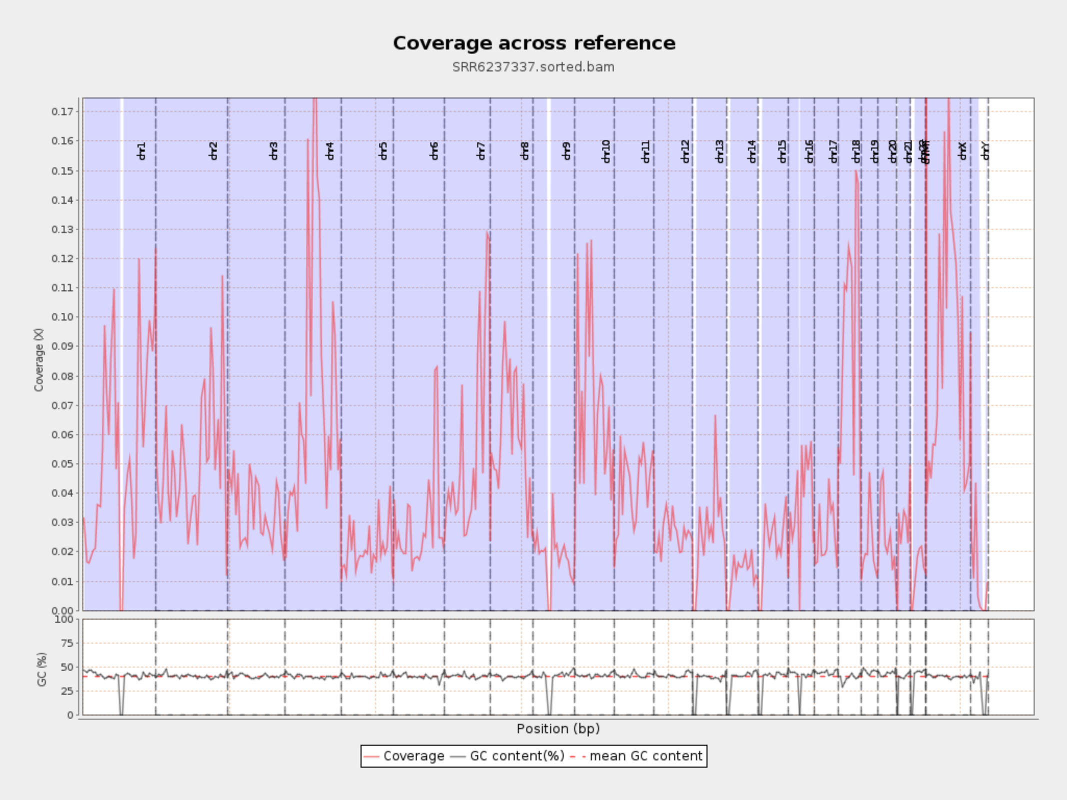
General error rate	0.69%
Mismatches	917,359
Insertions	8,795
Mapped reads with at least one insertion	0.39%
Deletions	52,742
Mapped reads with at least one deletion	2.31%
Homopolymer indels	40.24%

2.6. Chromosome stats

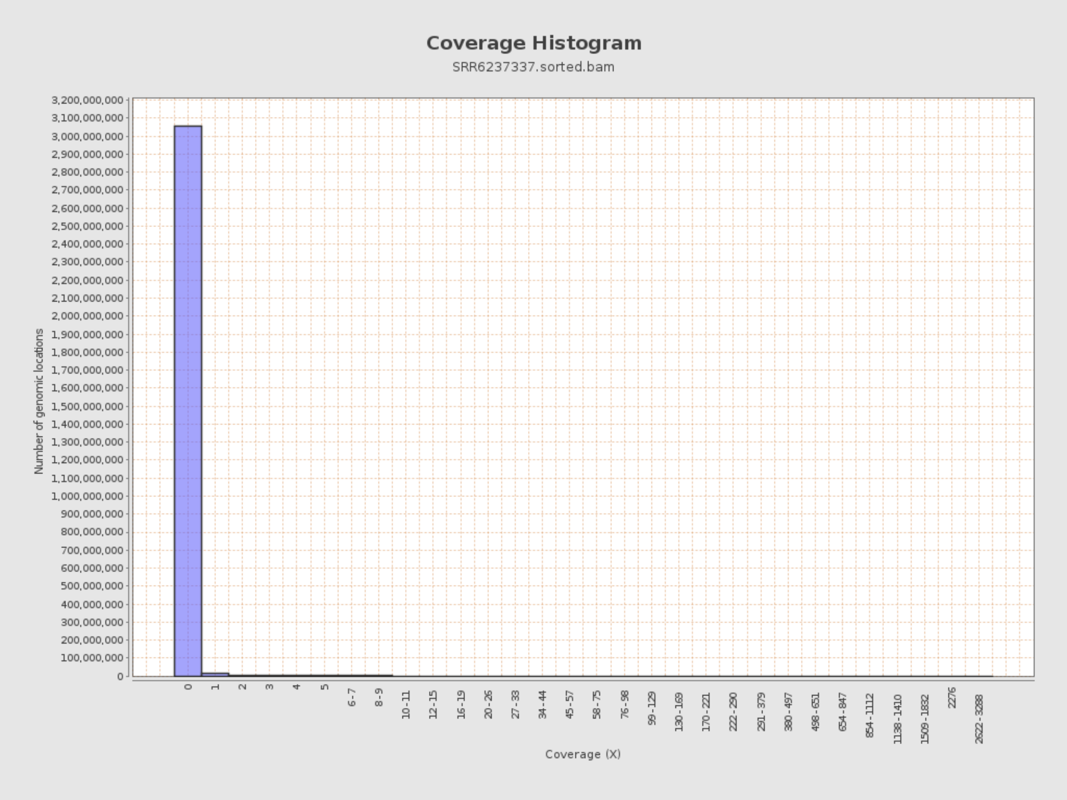
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13461294	0.054	0.9092
chr2	243199373	12412178	0.051	1.533
chr3	198022430	6684729	0.0338	0.4886
chr4	191154276	14759843	0.0772	0.7704
chr5	180915260	3807456	0.021	0.3687
chr6	171115067	5182683	0.0303	0.7897
chr7	159138663	8927499	0.0561	0.8884

chr8	146364022	8817031	0.0602	1.2457
chr9	141213431	2583355	0.0183	0.3812
chr10	135534747	9658503	0.0713	0.7955
chr11	135006516	5704395	0.0423	0.5526
chr12	133851895	3467044	0.0259	0.4139
chr13	115169878	3059880	0.0266	0.6878
chr14	107349540	1392881	0.013	0.2942
chr15	102531392	2354415	0.023	0.4274
chr16	90354753	3279255	0.0363	0.5395
chr17	81195210	2120690	0.0261	0.4116
chr18	78077248	7679030	0.0984	4.1699
chr19	59128983	1305169	0.0221	0.5938
chr20	63025520	1658527	0.0263	0.414
chr21	48129895	1365831	0.0284	0.45
chr22	51304566	673254	0.0131	0.2708
chrMT	16571	16469	0.9938	3.1857
chrX	155270560	13671640	0.0881	0.8096
chrY	59373566	671042	0.0113	0.5868

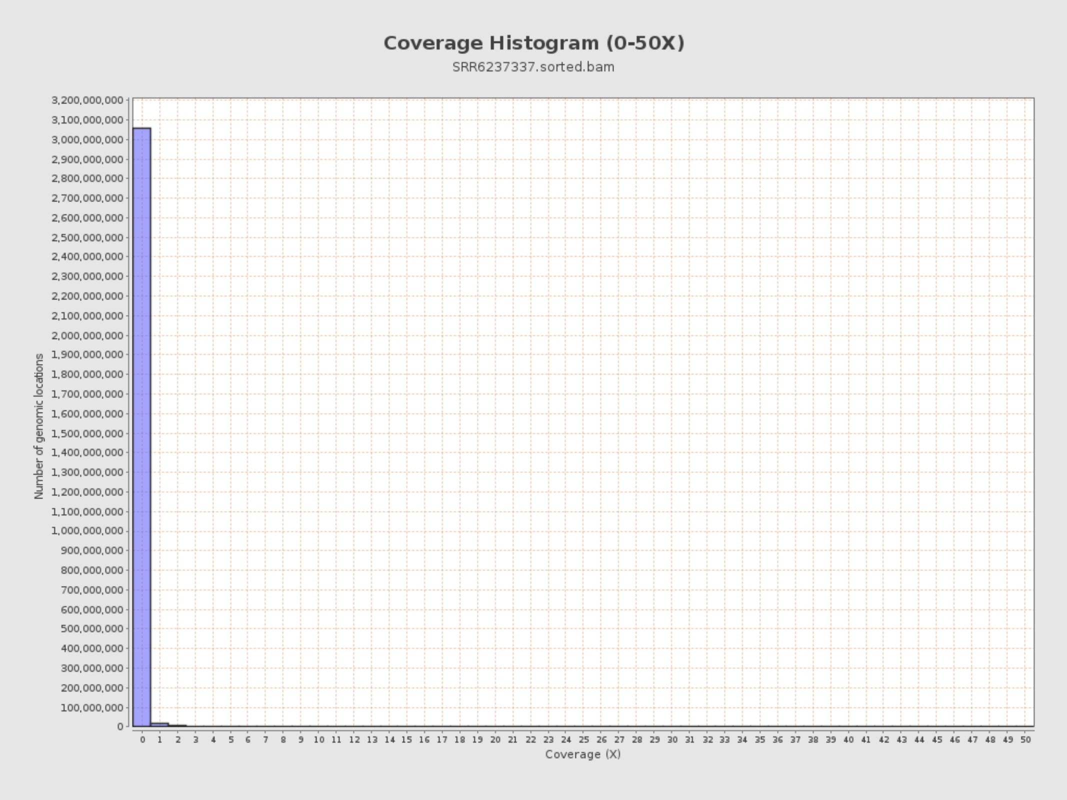
3. Results : Coverage across reference



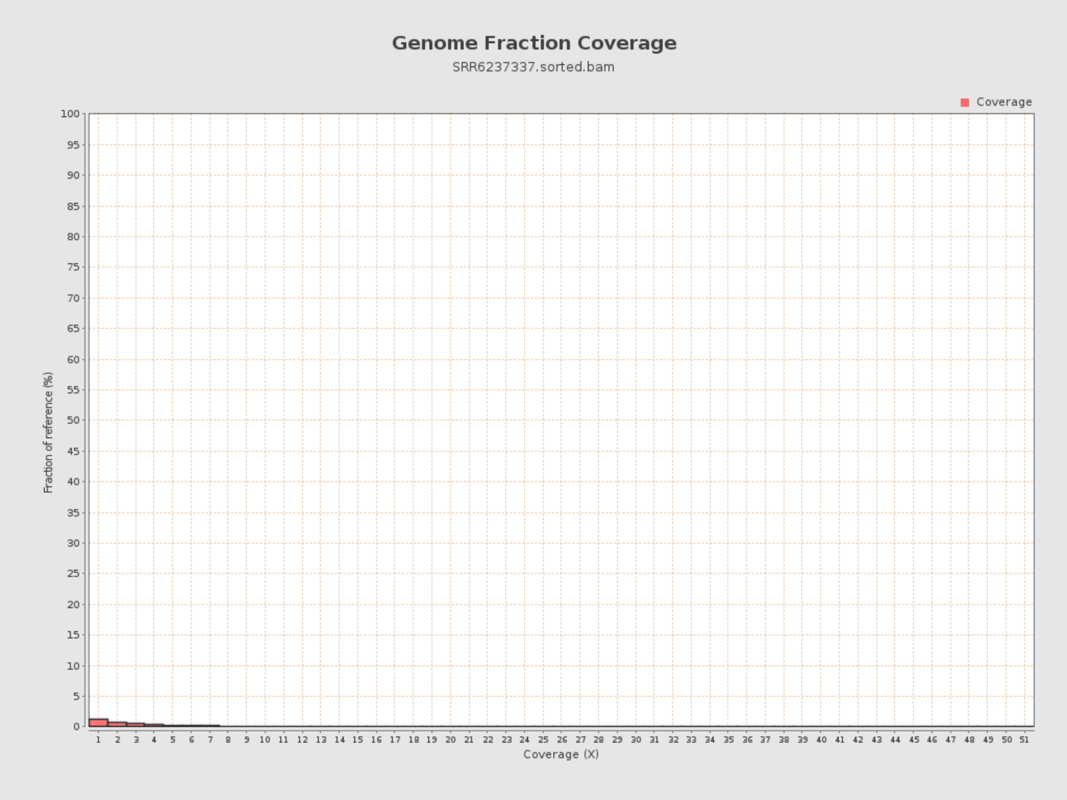
4. Results : Coverage Histogram



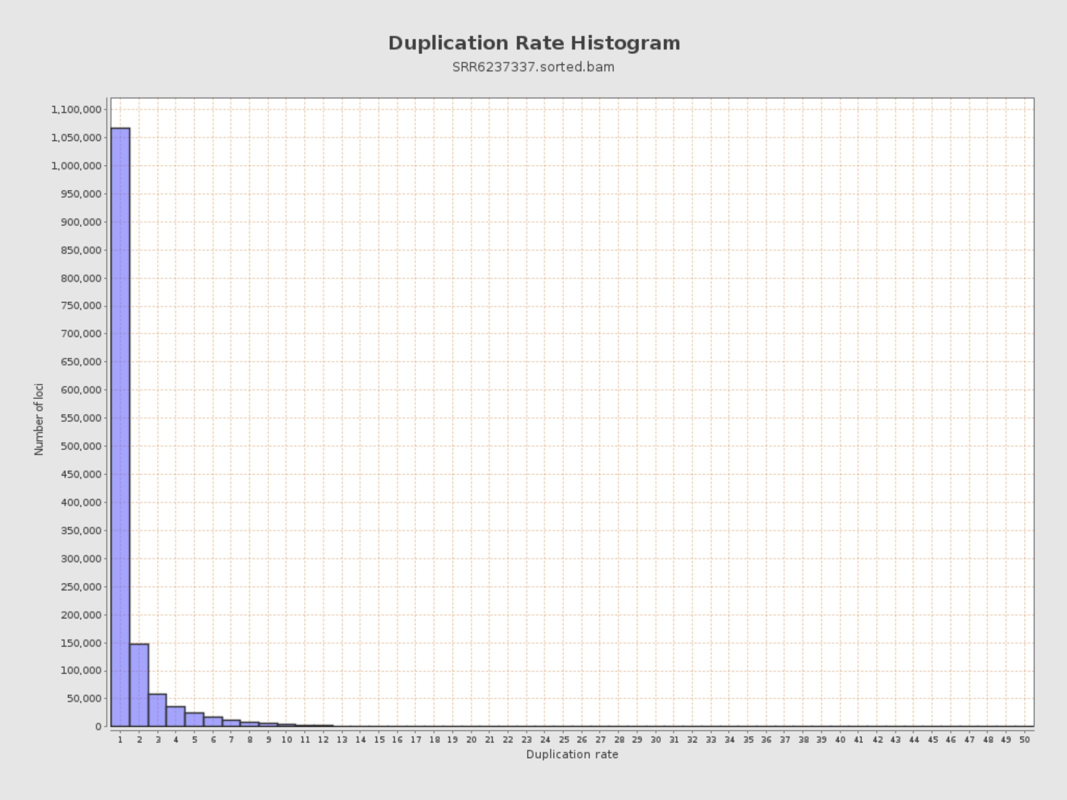
5. Results : Coverage Histogram (0-50X)



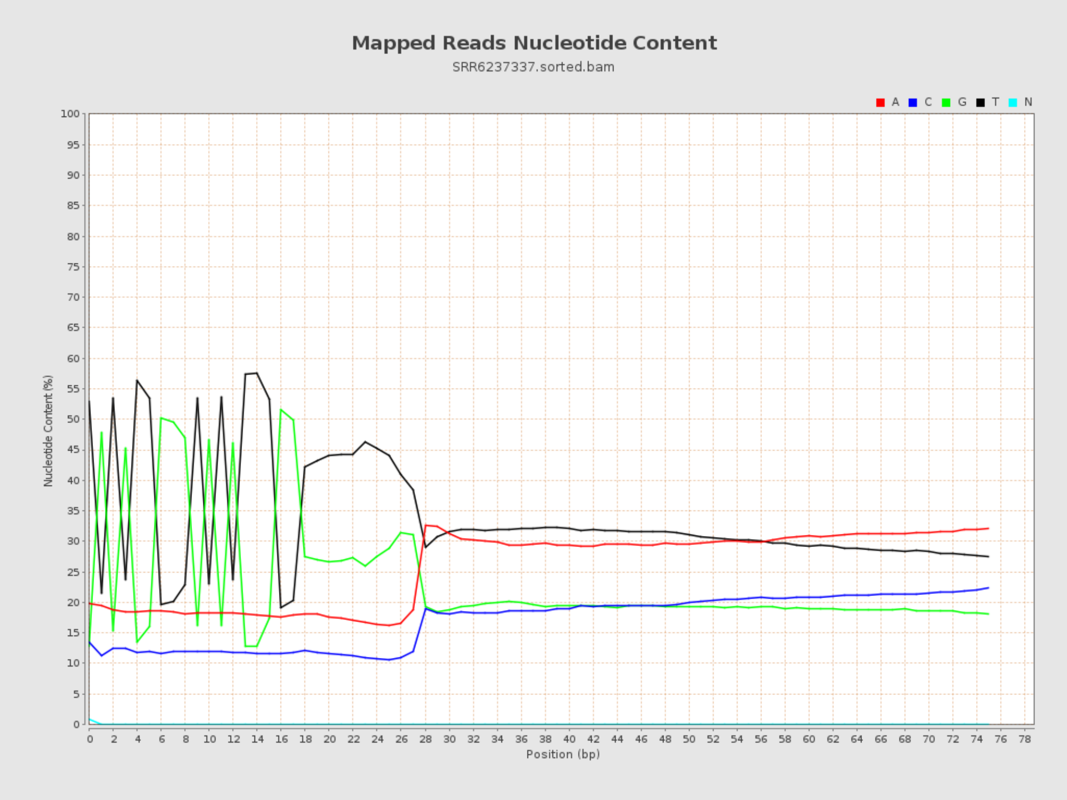
6. Results : Genome Fraction Coverage



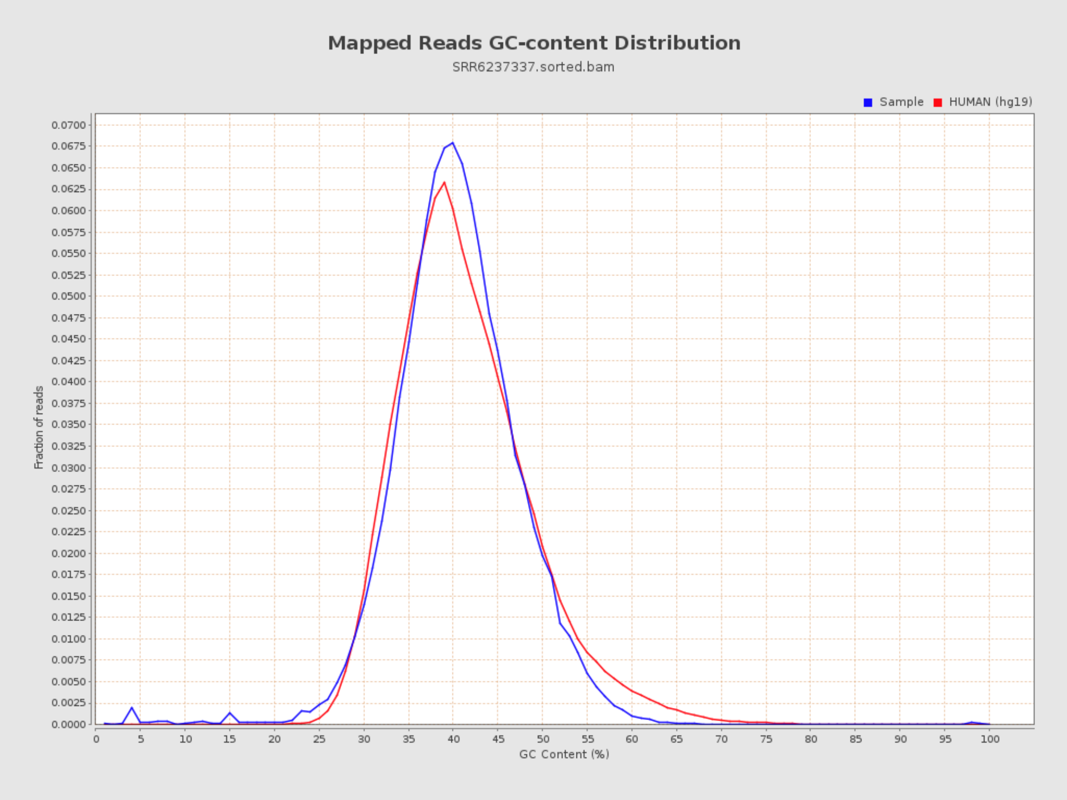
7. Results : Duplication Rate Histogram



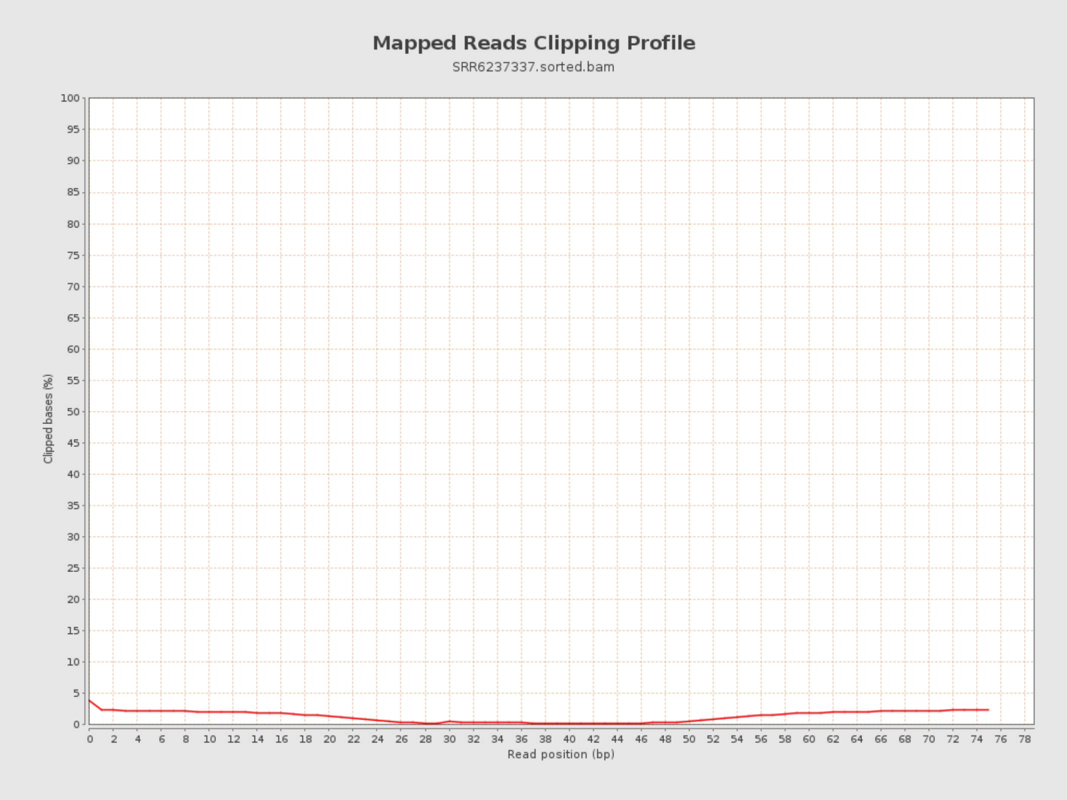
8. Results : Mapped Reads Nucleotide Content



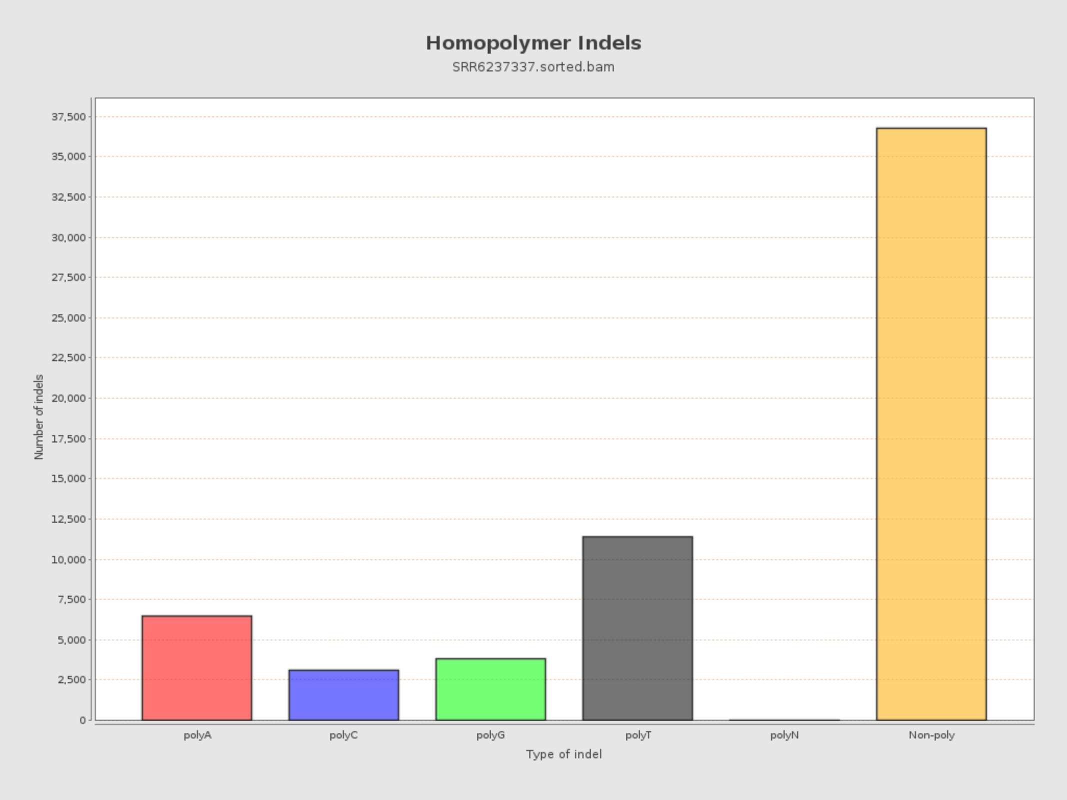
9. Results : Mapped Reads GC-content Distribution



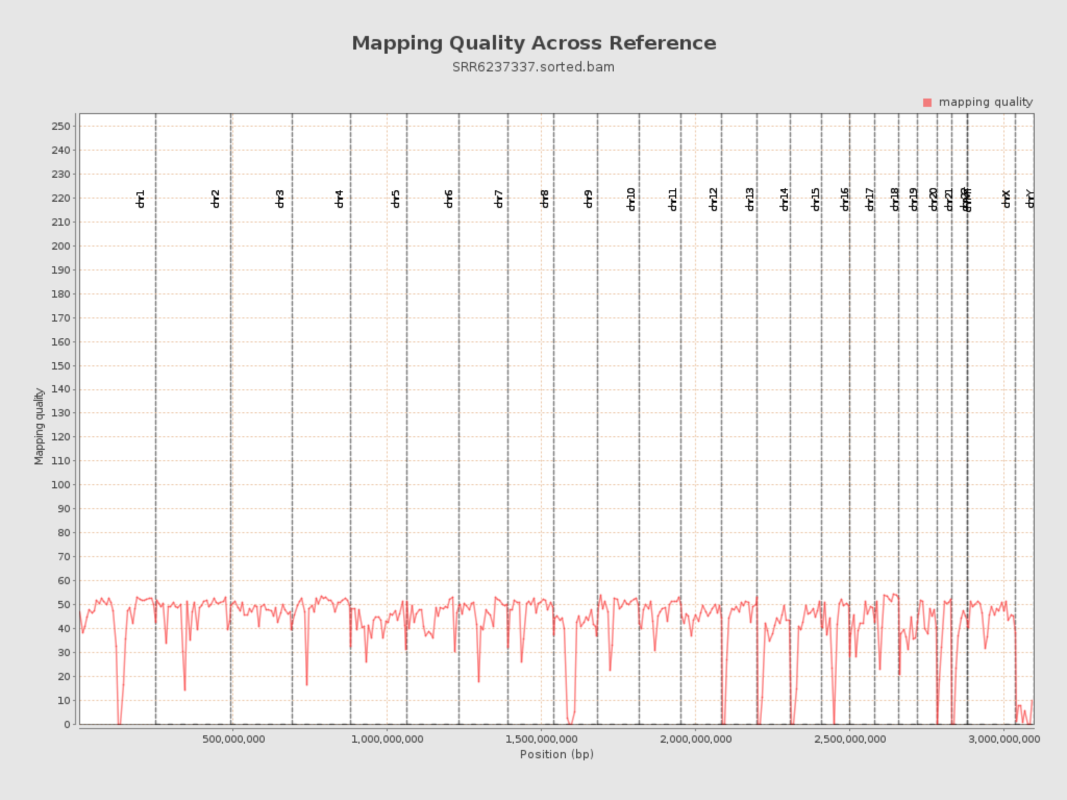
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram