Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:56:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236108.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_SRR6236108 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236108.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:56:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236108.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,911,395
Mapped reads	1,736,765 / 90.86%
Unmapped reads	174,630 / 9.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,778 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	84,417 / 4.42%
Duplication rate	3.71%
Clipped reads	658,419 / 34.45%

2.2. ACGT Content

Number/percentage of A's	33,565,348 / 28.42%
Number/percentage of C's	21,509,464 / 18.21%
Number/percentage of T's	37,657,734 / 31.89%
Number/percentage of G's	25,308,402 / 21.43%
Number/percentage of N's	58,276 / 0.05%
GC Percentage	39.64%

2.3. Coverage

Mean	0.0382

Standard Deviation	0.3935

2.4. Mapping Quality

Mean Mapping Quality	45.54

2.5. Mismatches and indels

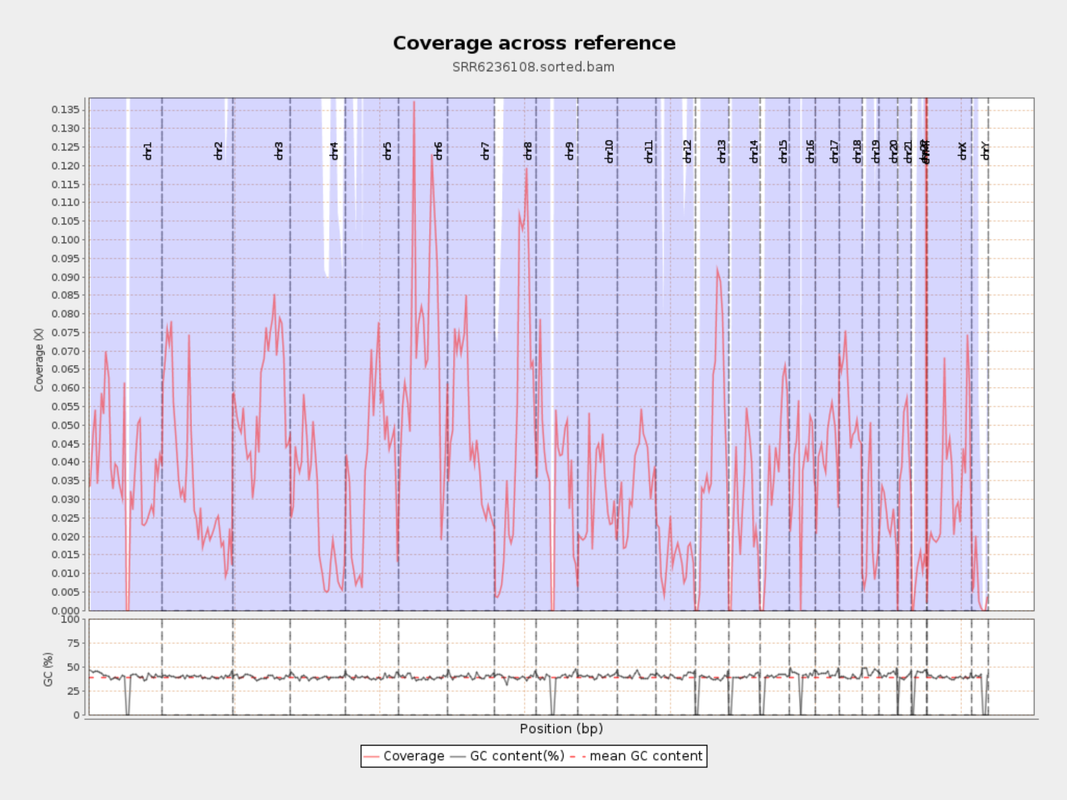
General error rate	0.82%
Mismatches	953,189
Insertions	9,226
Mapped reads with at least one insertion	0.53%
Deletions	33,478
Mapped reads with at least one deletion	1.9%
Homopolymer indels	47.36%

2.6. Chromosome stats

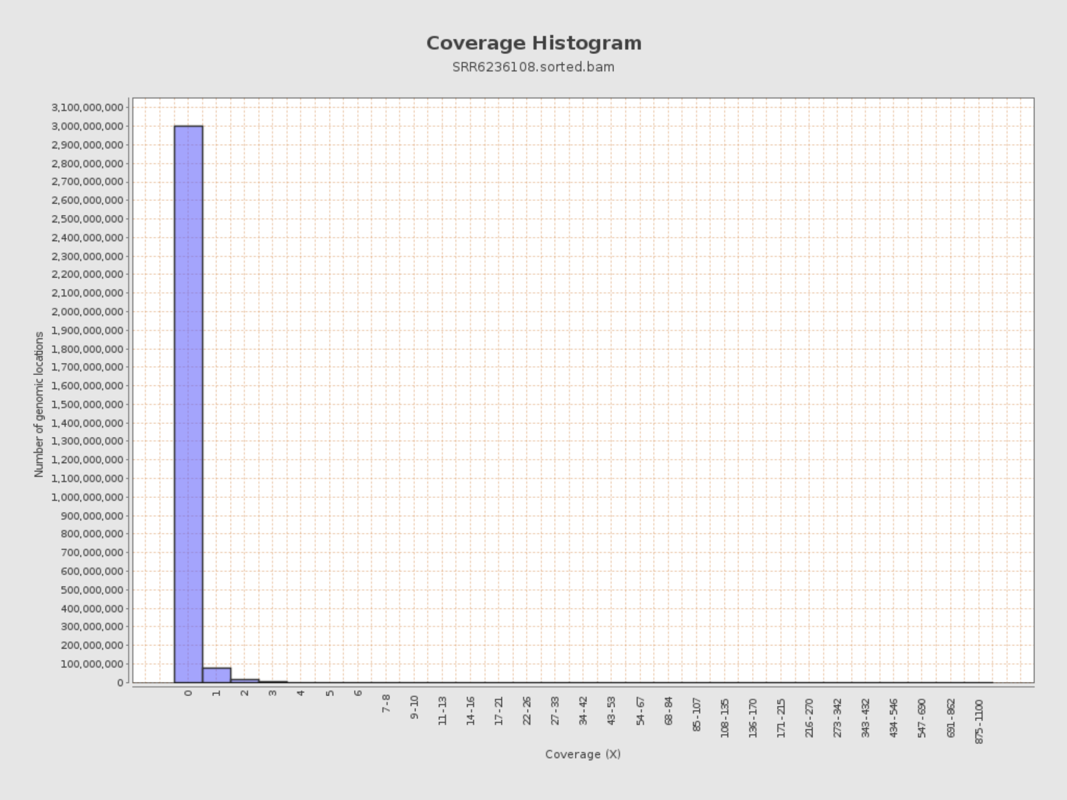
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9398822	0.0377	0.6433
chr2	243199373	8461064	0.0348	0.4092
chr3	198022430	11493498	0.058	0.2843
chr4	191154276	4915947	0.0257	0.2407
chr5	180915260	7133701	0.0394	0.2392
chr6	171115067	12052175	0.0704	0.4264
chr7	159138663	7658529	0.0481	0.5367

chr8	146364022	7167368	0.049	0.7108
chr9	141213431	5272564	0.0373	0.3961
chr10	135534747	4060728	0.03	0.3493
chr11	135006516	4712845	0.0349	0.2613
chr12	133851895	1947584	0.0146	0.1596
chr13	115169878	5125195	0.0445	0.2508
chr14	107349540	2834971	0.0264	0.2197
chr15	102531392	3701127	0.0361	0.2256
chr16	90354753	3466192	0.0384	0.2649
chr17	81195210	3439358	0.0424	0.2934
chr18	78077248	4399755	0.0564	0.6463
chr19	59128983	1177815	0.0199	0.432
chr20	63025520	1597327	0.0253	0.1998
chr21	48129895	1907455	0.0396	0.2764
chr22	51304566	490998	0.0096	0.1112
chrMT	16571	175017	10.5616	6.5272
chrX	155270560	5282529	0.034	0.2472
chrY	59373566	285968	0.0048	0.176

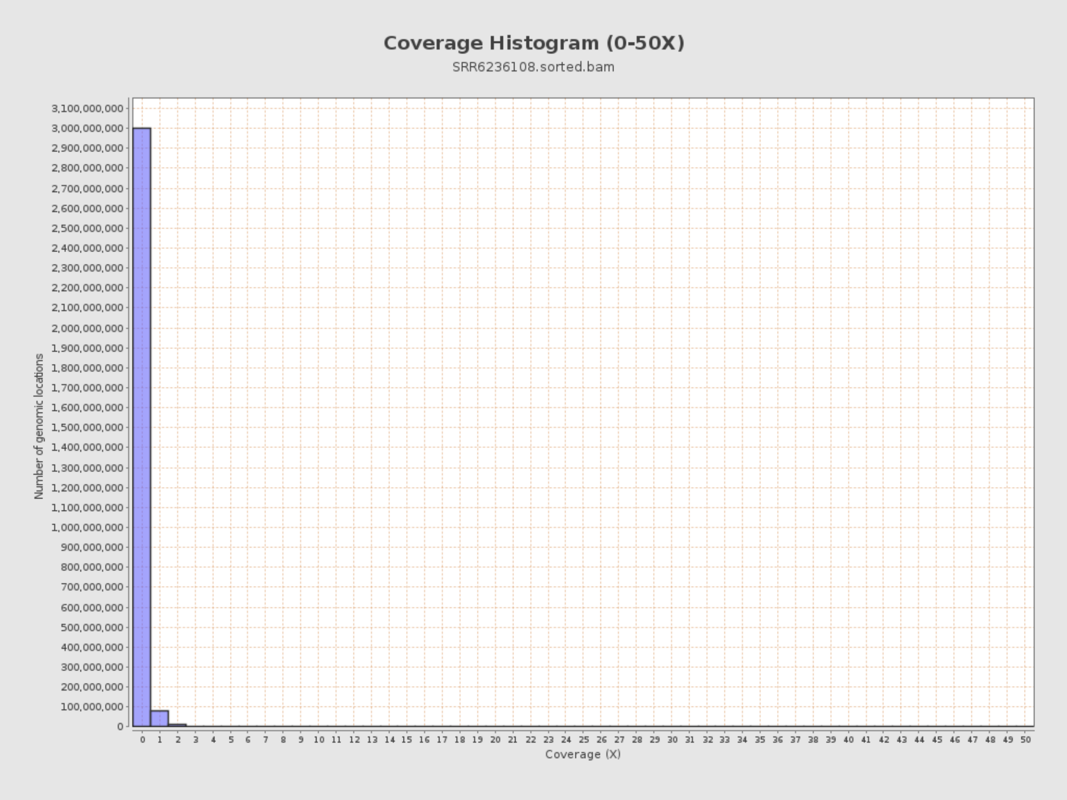
3. Results : Coverage across reference



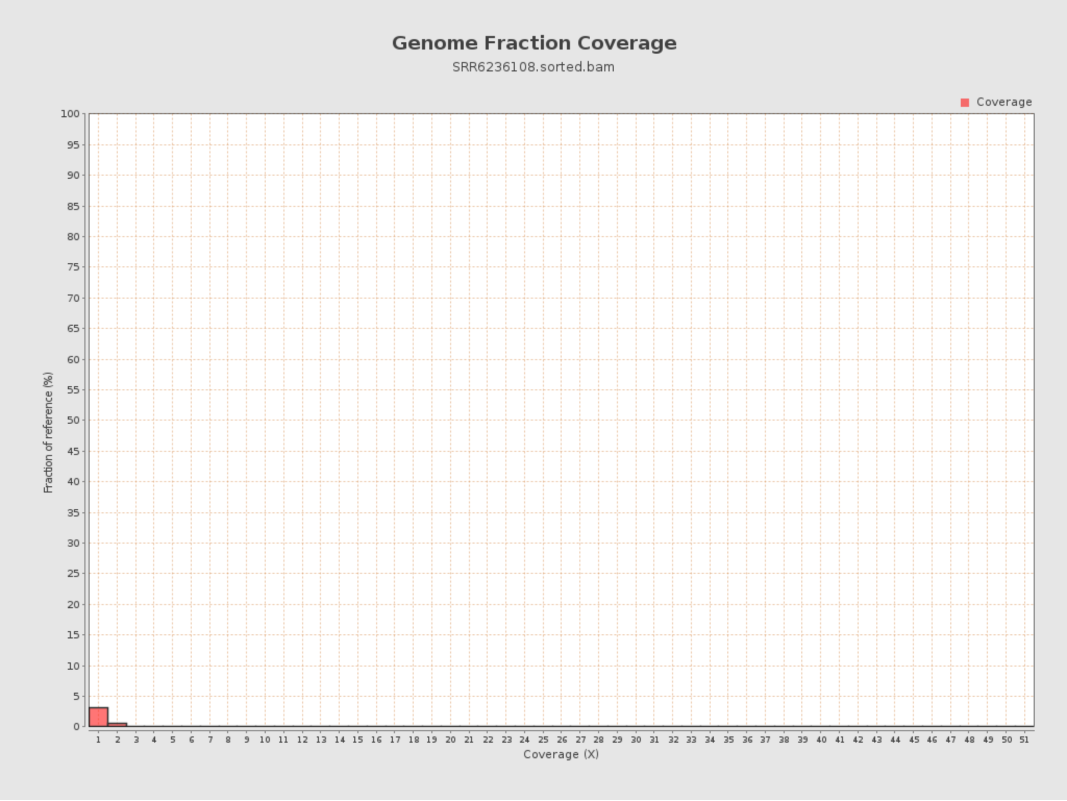
4. Results : Coverage Histogram



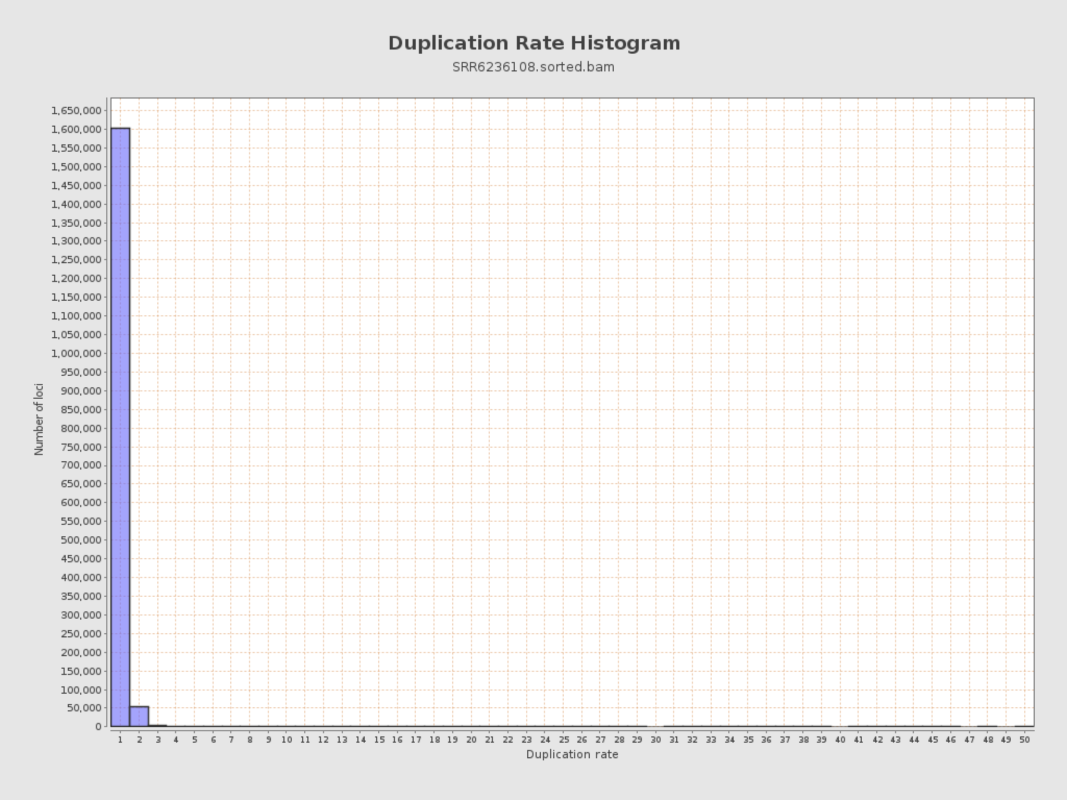
5. Results : Coverage Histogram (0-50X)



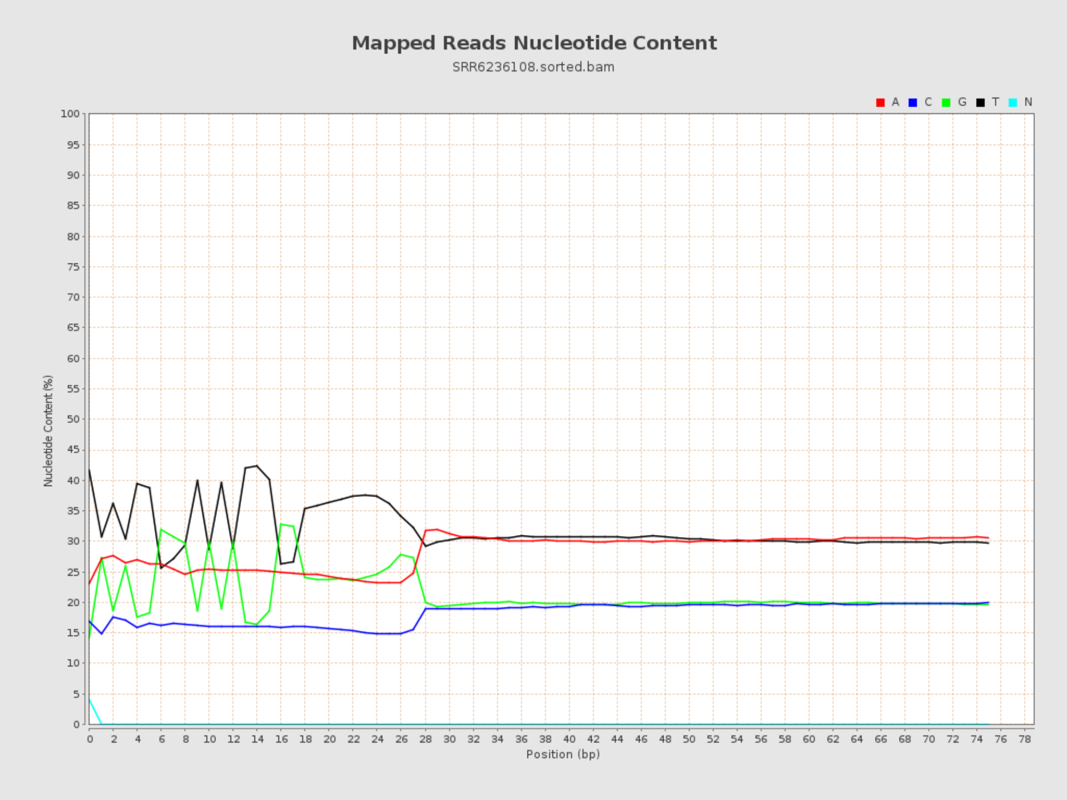
6. Results : Genome Fraction Coverage



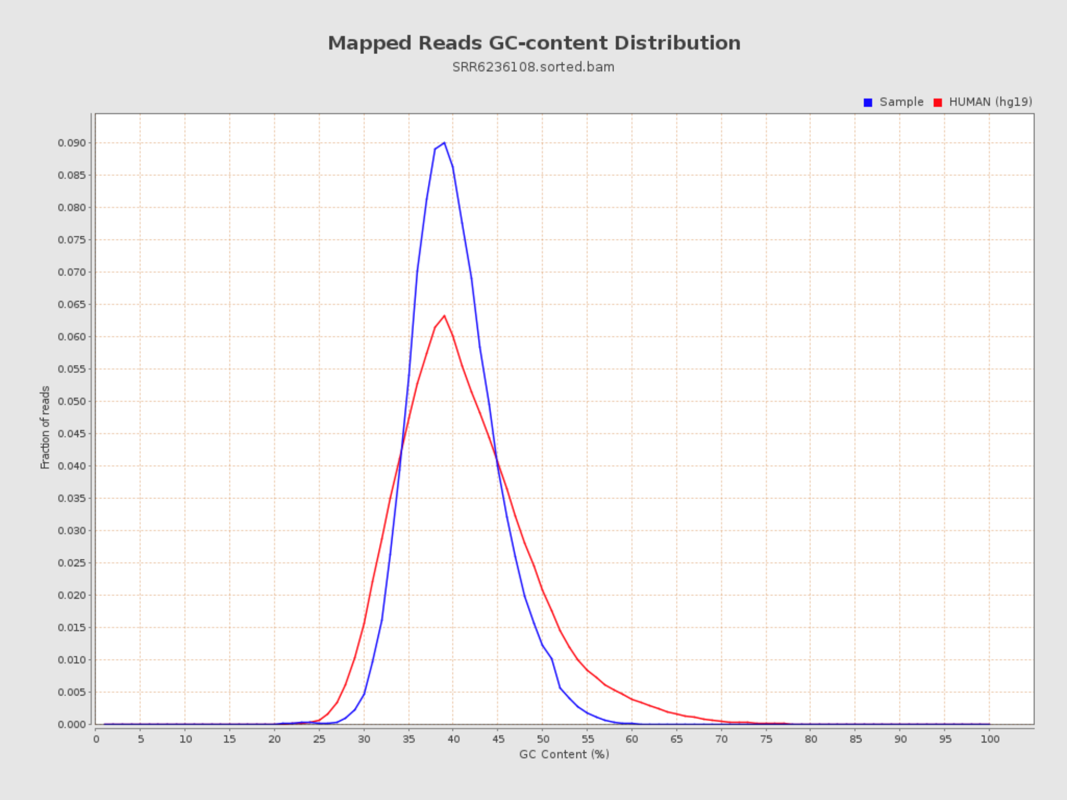
7. Results : Duplication Rate Histogram



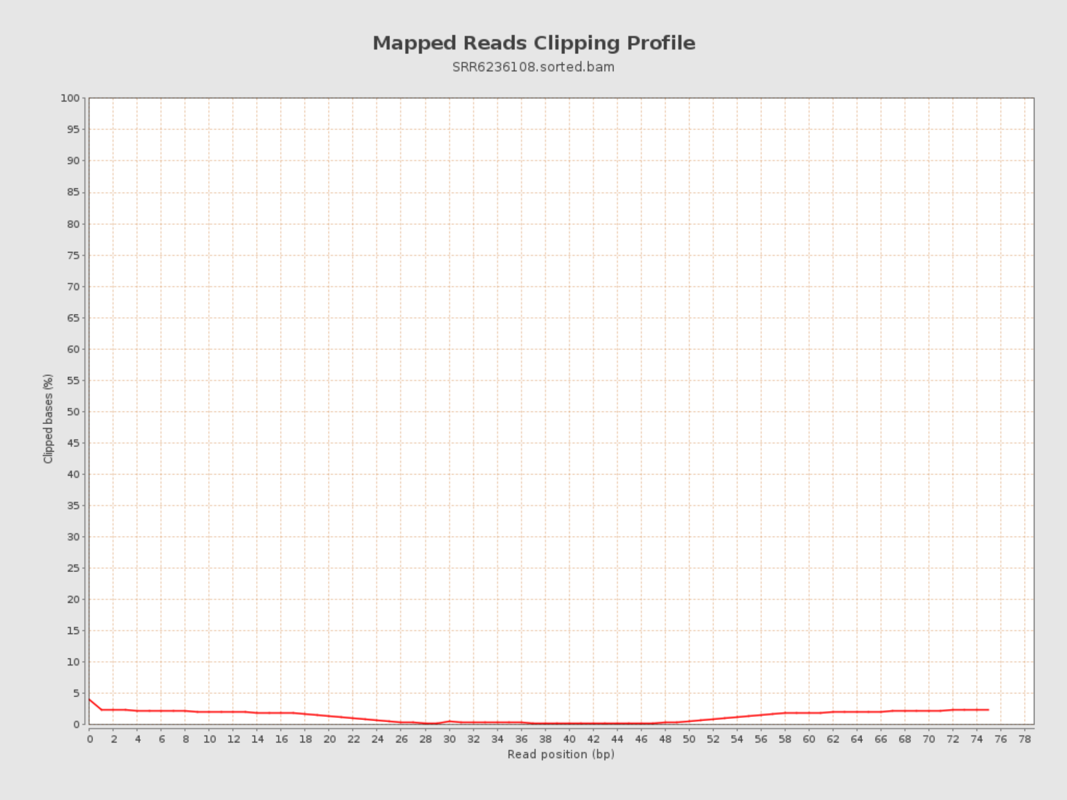
8. Results : Mapped Reads Nucleotide Content



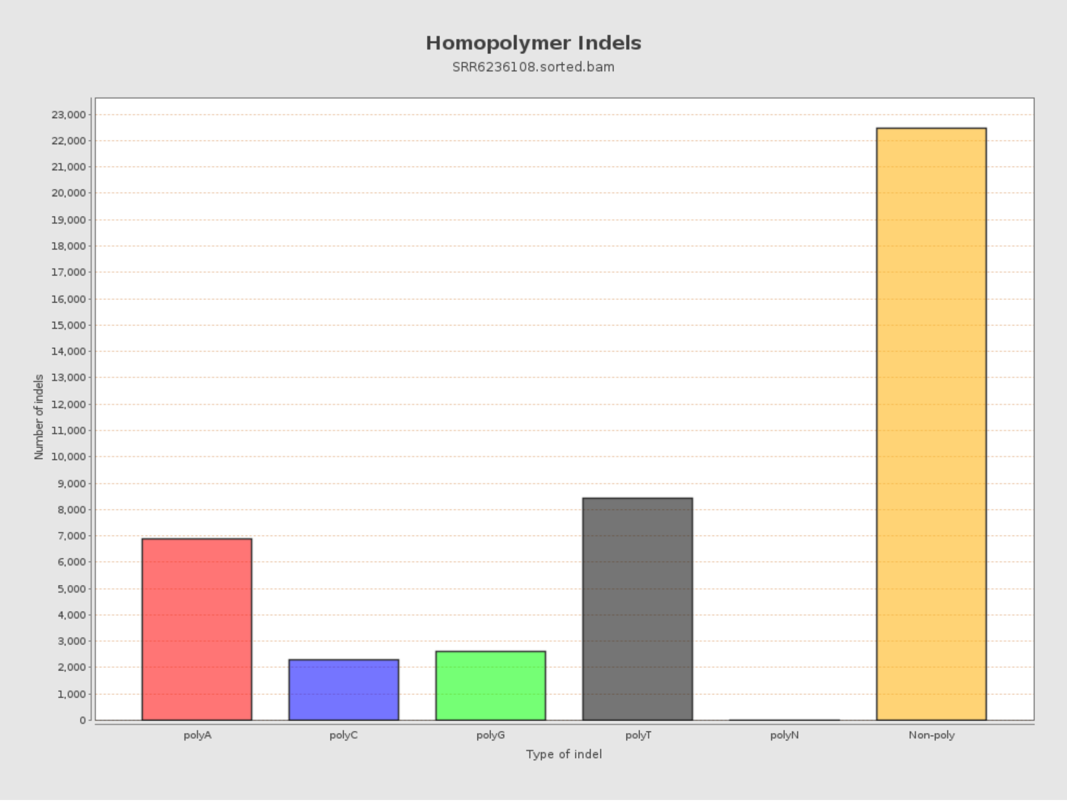
9. Results : Mapped Reads GC-content Distribution



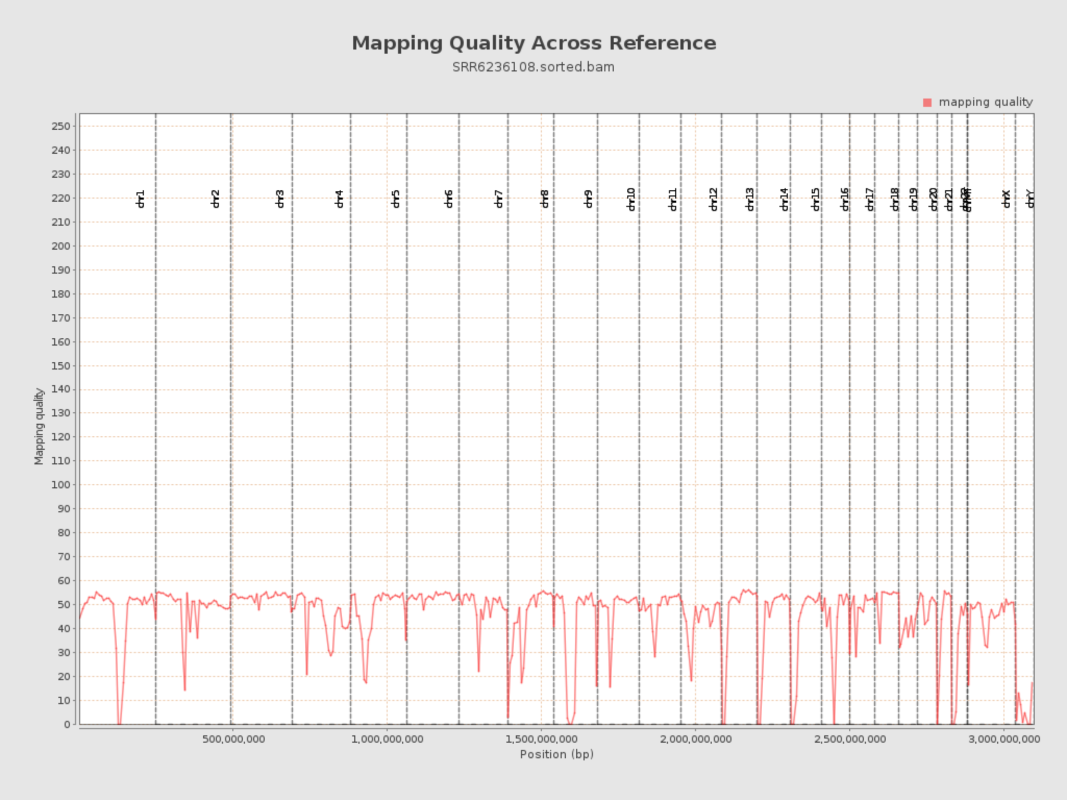
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram