Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:15:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237247.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_SRR6237247 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237247.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:15:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237247.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,726,720
Mapped reads	2,457,844 / 90.14%
Unmapped reads	268,876 / 9.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,999 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	121,233 / 4.45%
Duplication rate	3.47%
Clipped reads	987,507 / 36.22%

2.2. ACGT Content

Number/percentage of A's	47,108,192 / 28.41%
Number/percentage of C's	30,805,919 / 18.58%
Number/percentage of T's	51,821,411 / 31.26%
Number/percentage of G's	36,061,483 / 21.75%
Number/percentage of N's	2,874 / 0%
GC Percentage	40.33%

2.3. Coverage

Mean	0.0536

Standard Deviation	0.5462

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

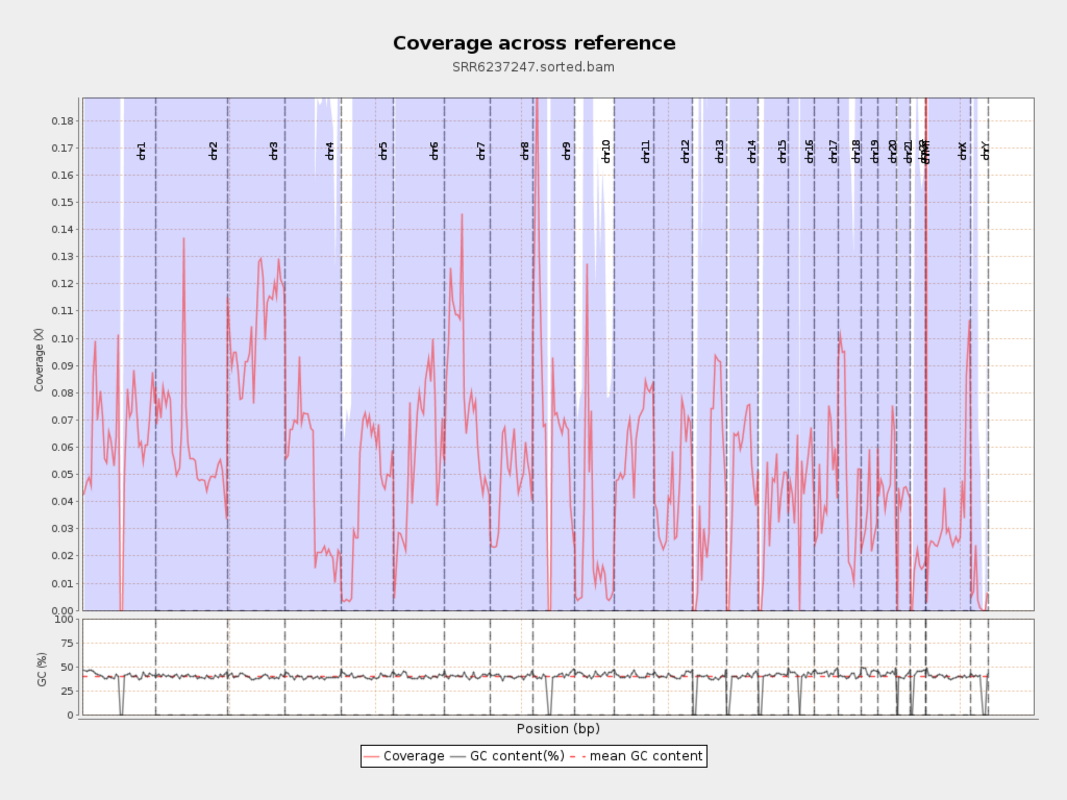
General error rate	0.86%
Mismatches	1,402,001
Insertions	13,309
Mapped reads with at least one insertion	0.54%
Deletions	60,692
Mapped reads with at least one deletion	2.43%
Homopolymer indels	44.83%

2.6. Chromosome stats

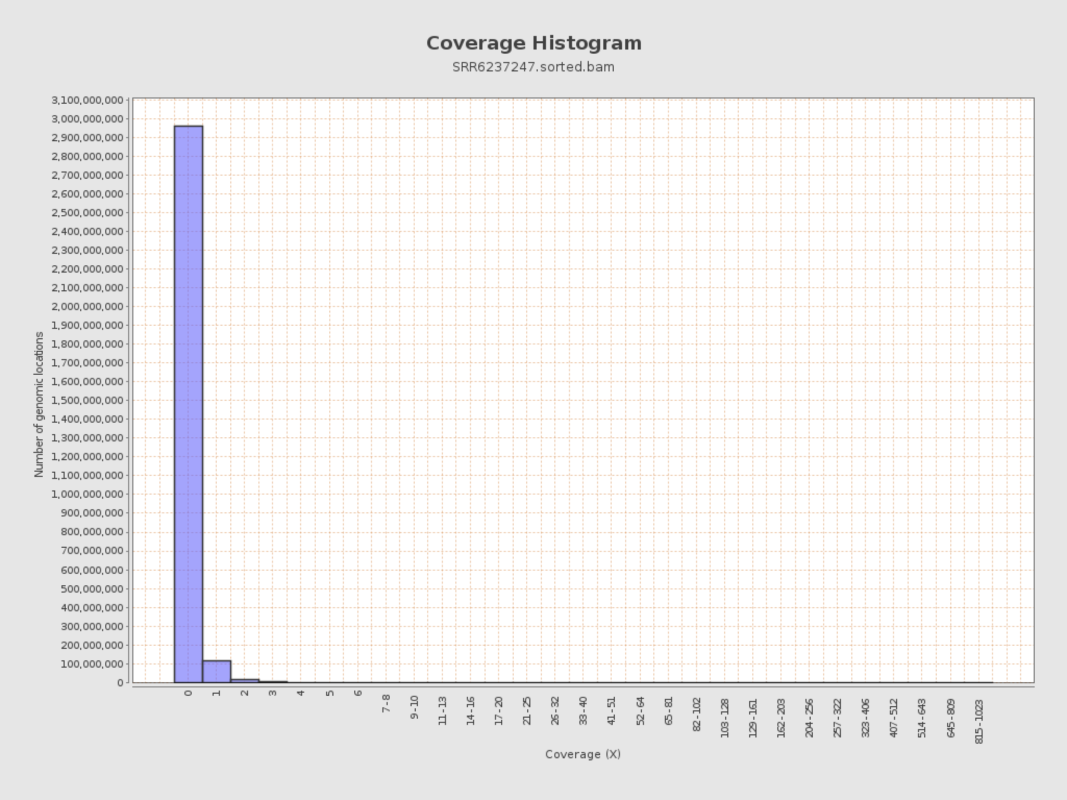
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15785822	0.0633	0.9088
chr2	243199373	14681681	0.0604	0.616
chr3	198022430	20768799	0.1049	0.3961
chr4	191154276	8684988	0.0454	0.3058
chr5	180915260	7874739	0.0435	0.2521
chr6	171115067	9718800	0.0568	0.3284
chr7	159138663	12892969	0.081	1.0246

chr8	146364022	7002649	0.0478	0.678
chr9	141213431	10552337	0.0747	0.584
chr10	135534747	3148520	0.0232	0.6649
chr11	135006516	8577773	0.0635	0.4542
chr12	133851895	6085660	0.0455	0.2825
chr13	115169878	5340170	0.0464	0.2509
chr14	107349540	5530738	0.0515	0.3488
chr15	102531392	3672888	0.0358	0.2198
chr16	90354753	4086809	0.0452	0.3371
chr17	81195210	3762861	0.0463	0.3654
chr18	78077248	4177784	0.0535	0.9363
chr19	59128983	1972574	0.0334	0.6247
chr20	63025520	3143956	0.0499	0.2761
chr21	48129895	1877231	0.039	0.3236
chr22	51304566	702238	0.0137	0.1344
chrMT	16571	15396	0.9291	1.2081
chrX	155270560	5494563	0.0354	0.2837
chrY	59373566	353112	0.0059	0.2283

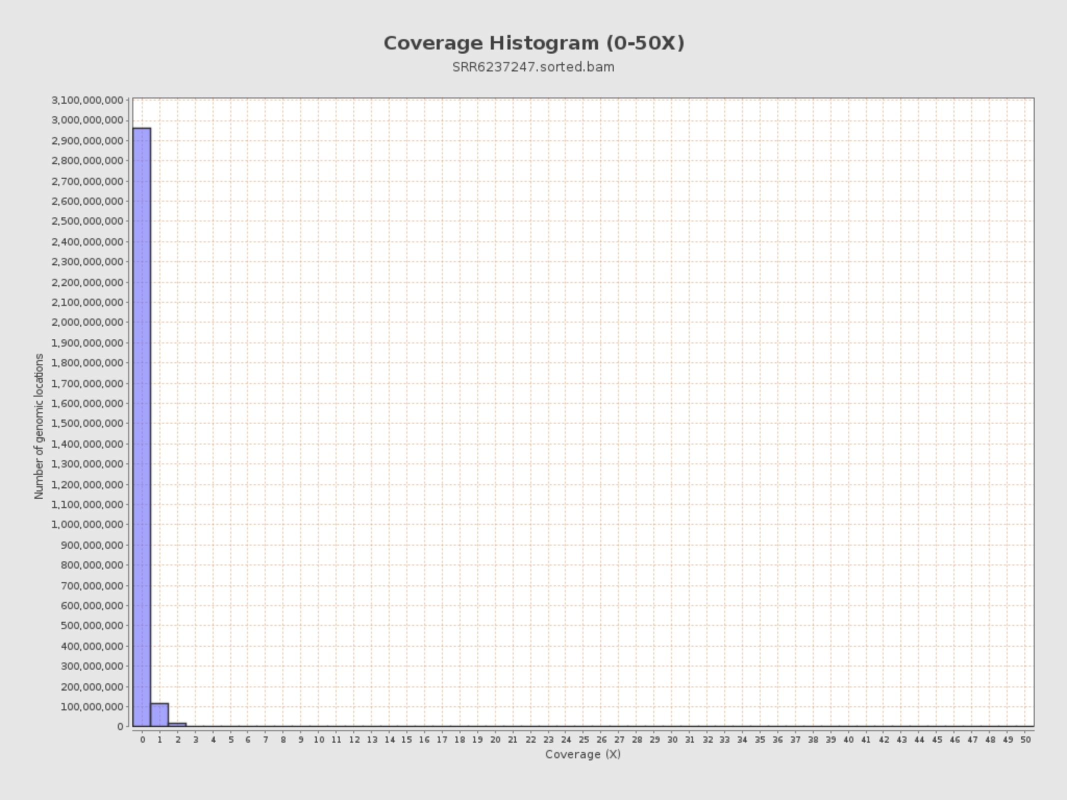
3. Results : Coverage across reference



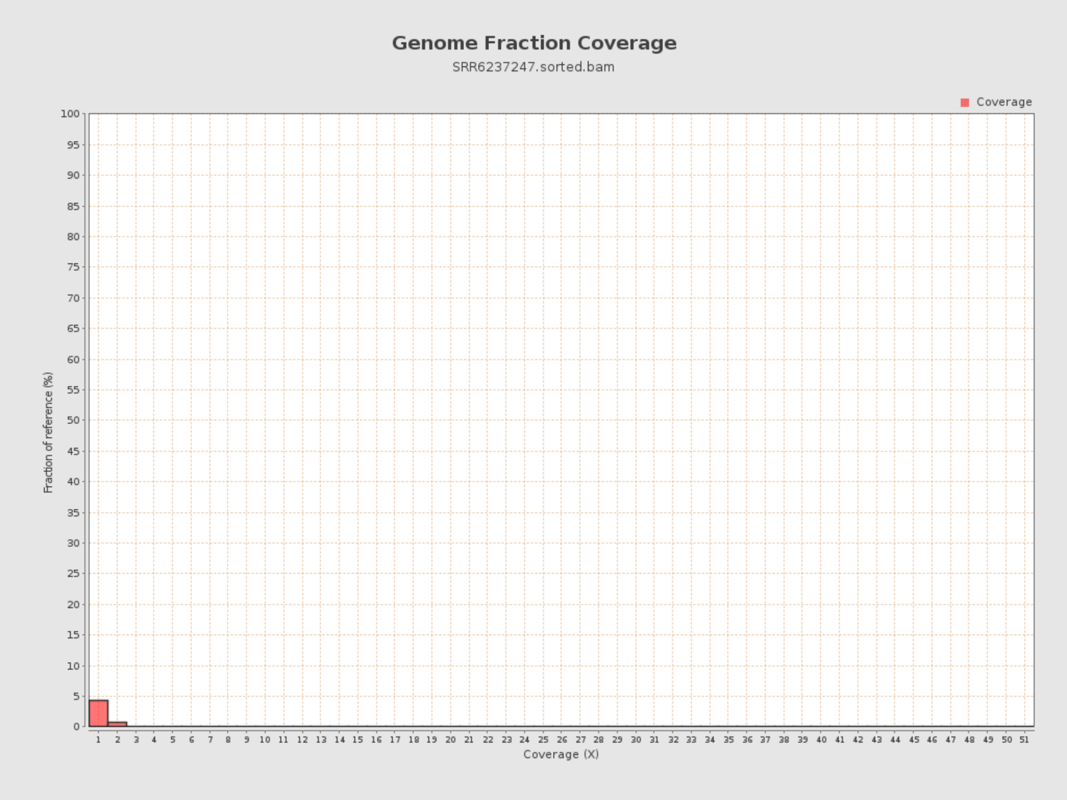
4. Results : Coverage Histogram



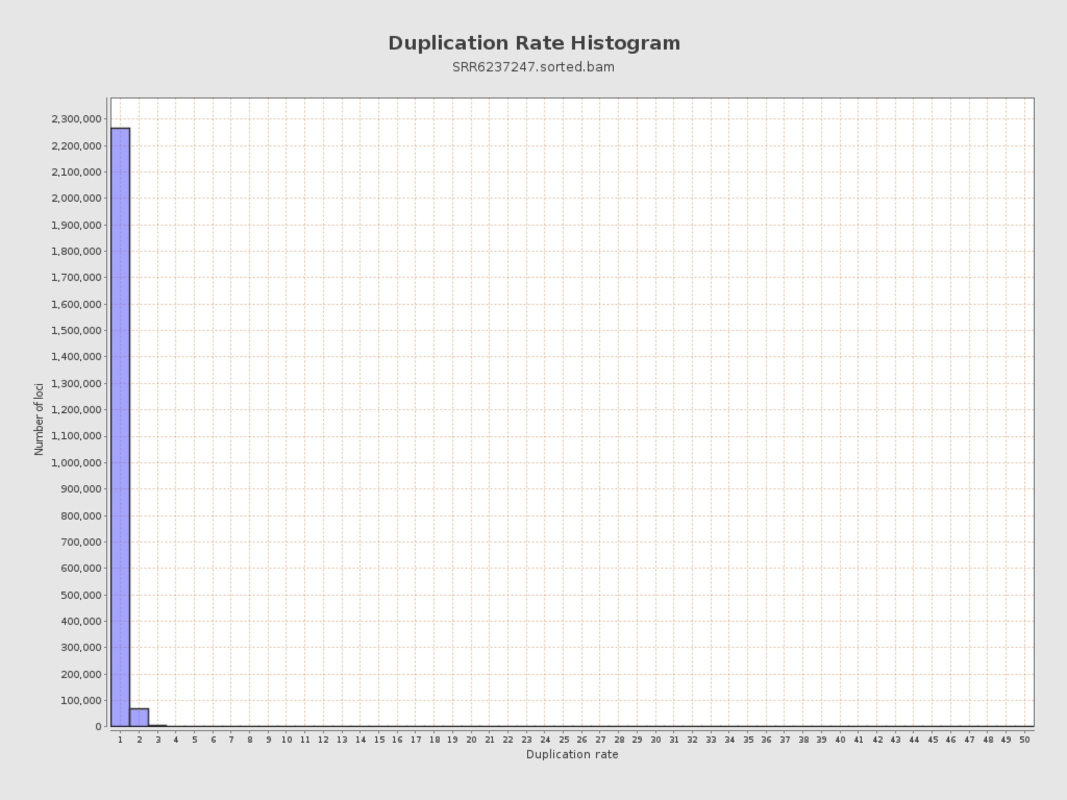
5. Results : Coverage Histogram (0-50X)



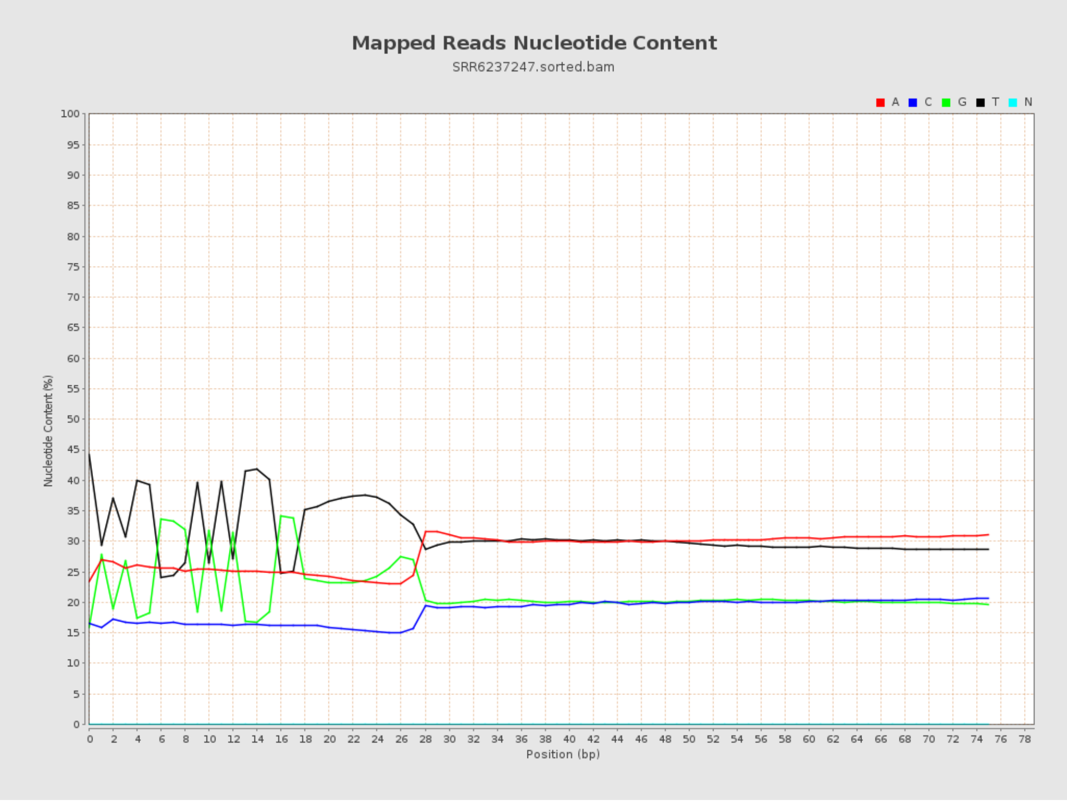
6. Results : Genome Fraction Coverage



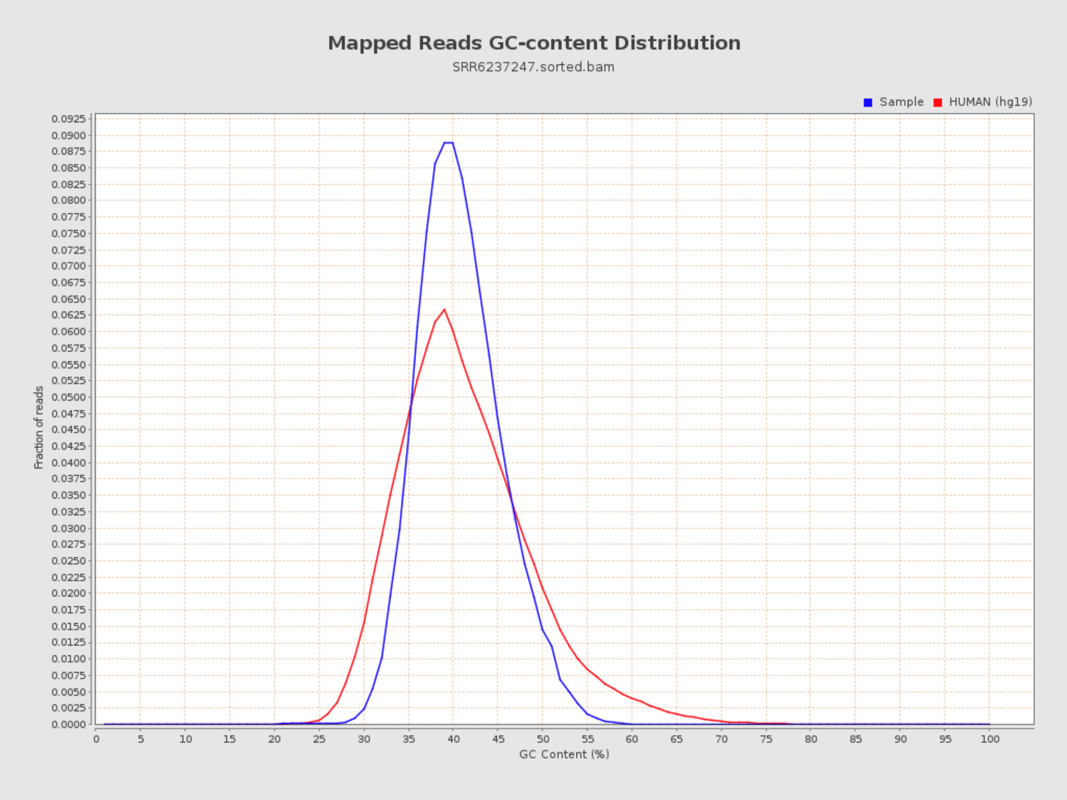
7. Results : Duplication Rate Histogram



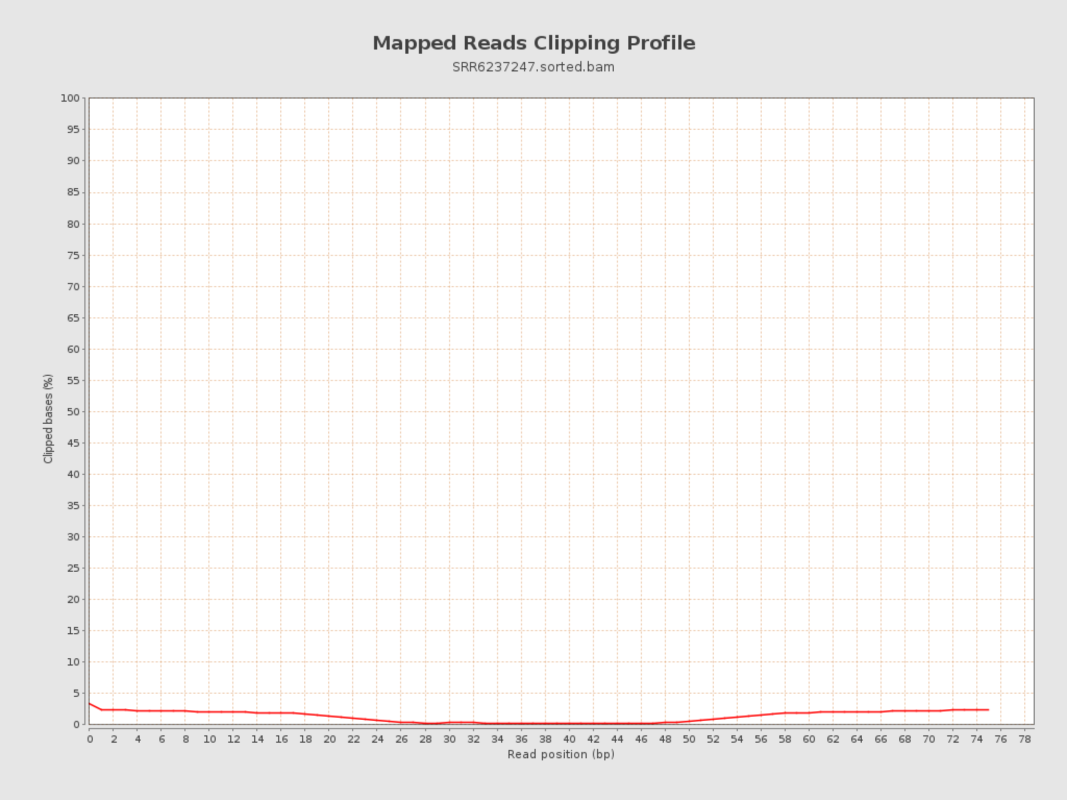
8. Results : Mapped Reads Nucleotide Content



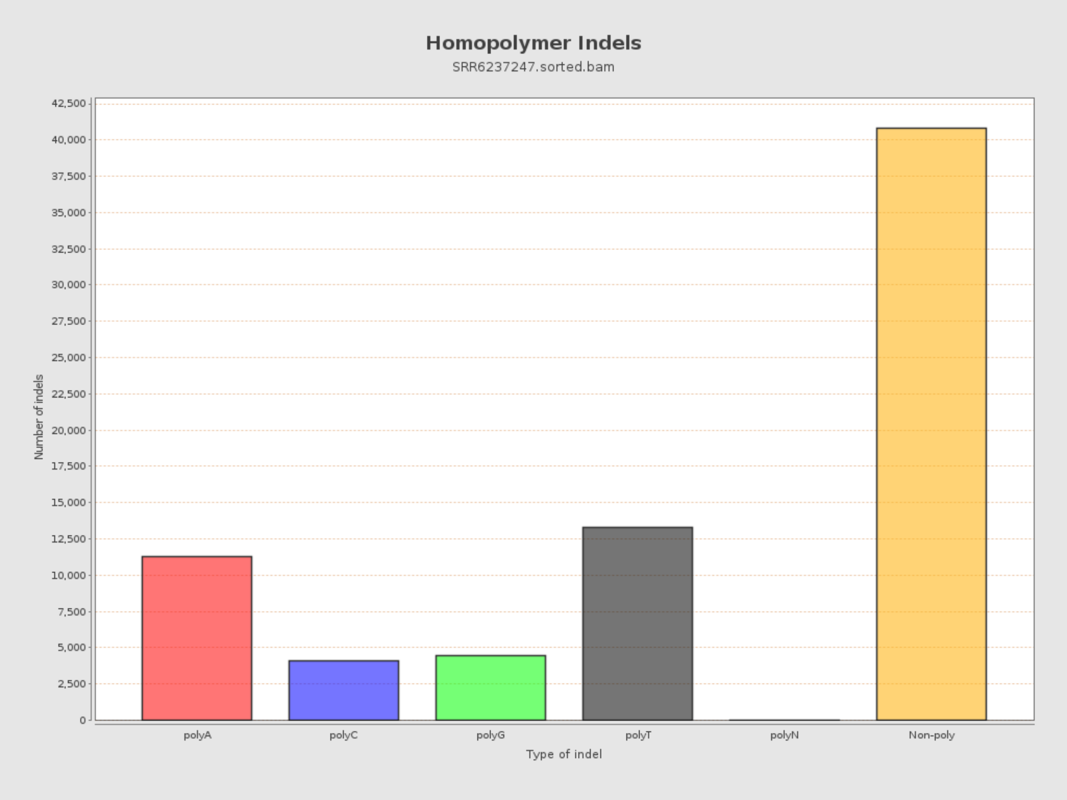
9. Results : Mapped Reads GC-content Distribution



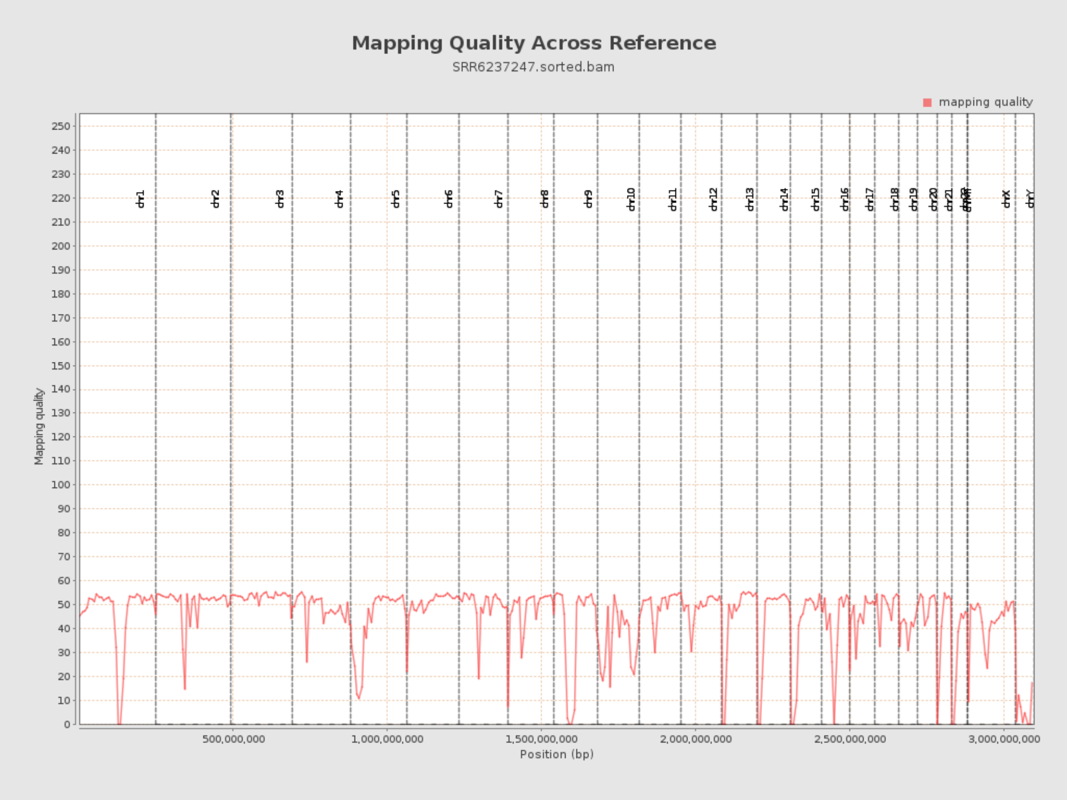
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram