Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:46:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237276.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_SRR6237276 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237276.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:46:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237276.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	613,846
Mapped reads	457,344 / 74.5%
Unmapped reads	156,502 / 25.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,583 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	8,565 / 1.4%
Duplication rate	1.54%
Clipped reads	200,912 / 32.73%

2.2. ACGT Content

Number/percentage of A's	8,772,772 / 28.66%
Number/percentage of C's	5,612,535 / 18.34%
Number/percentage of T's	9,515,410 / 31.09%
Number/percentage of G's	6,709,652 / 21.92%
Number/percentage of N's	453 / 0%
GC Percentage	40.25%

2.3. Coverage

Mean	0.0099

Standard Deviation	0.1214

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

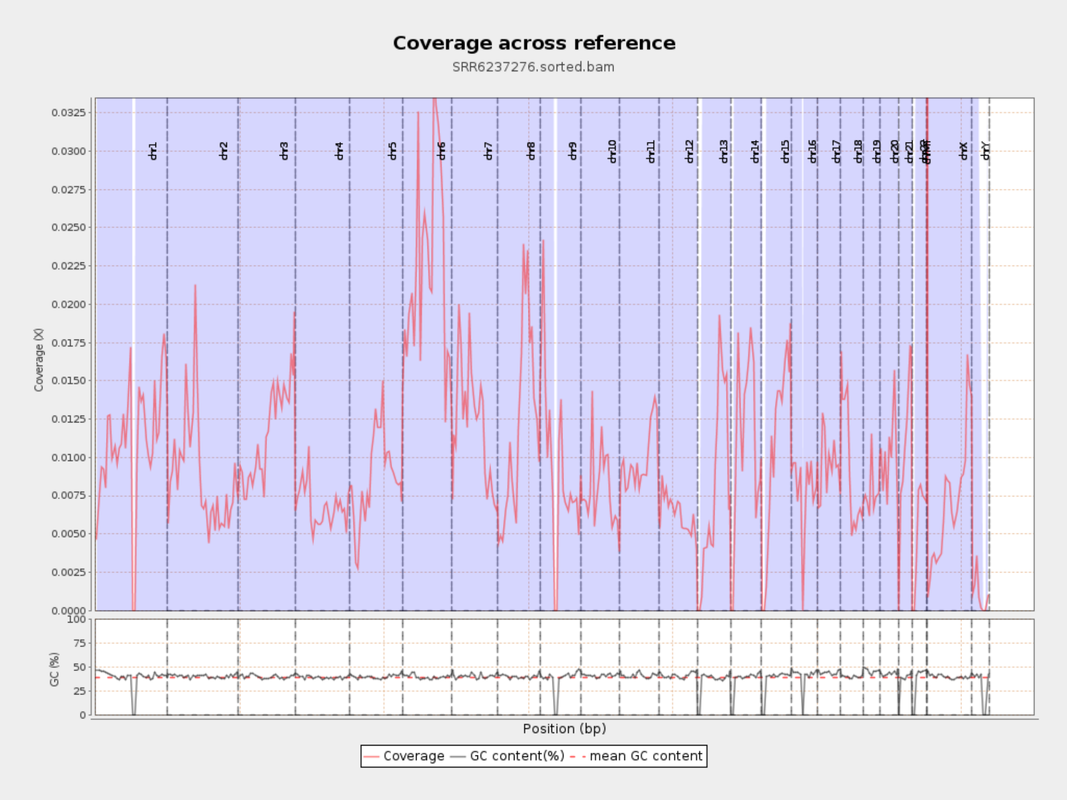
General error rate	0.96%
Mismatches	289,786
Insertions	2,615
Mapped reads with at least one insertion	0.57%
Deletions	9,002
Mapped reads with at least one deletion	1.94%
Homopolymer indels	45.47%

2.6. Chromosome stats

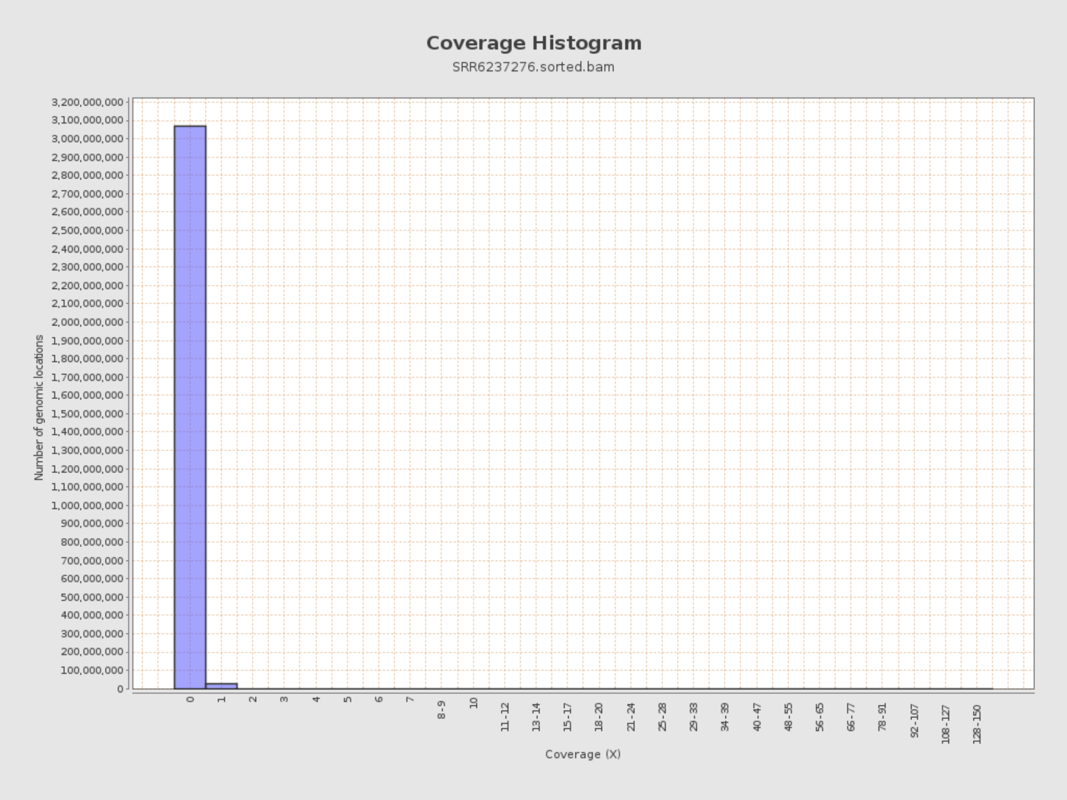
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2741894	0.011	0.1634
chr2	243199373	2157397	0.0089	0.125
chr3	198022430	2270389	0.0115	0.1103
chr4	191154276	1302399	0.0068	0.0882
chr5	180915260	1579700	0.0087	0.0966
chr6	171115067	3853384	0.0225	0.1842
chr7	159138663	1944730	0.0122	0.1514

chr8	146364022	1764915	0.0121	0.1493
chr9	141213431	1316268	0.0093	0.1142
chr10	135534747	1077229	0.0079	0.107
chr11	135006516	1340932	0.0099	0.1142
chr12	133851895	849352	0.0063	0.0823
chr13	115169878	922574	0.008	0.0923
chr14	107349540	1166801	0.0109	0.109
chr15	102531392	1087171	0.0106	0.1066
chr16	90354753	699587	0.0077	0.0956
chr17	81195210	769637	0.0095	0.105
chr18	78077248	708837	0.0091	0.155
chr19	59128983	458983	0.0078	0.1159
chr20	63025520	636515	0.0101	0.1041
chr21	48129895	521872	0.0108	0.1098
chr22	51304566	277344	0.0054	0.0755
chrMT	16571	26965	1.6272	1.6719
chrX	155270560	1089670	0.007	0.0888
chrY	59373566	62284	0.001	0.0405

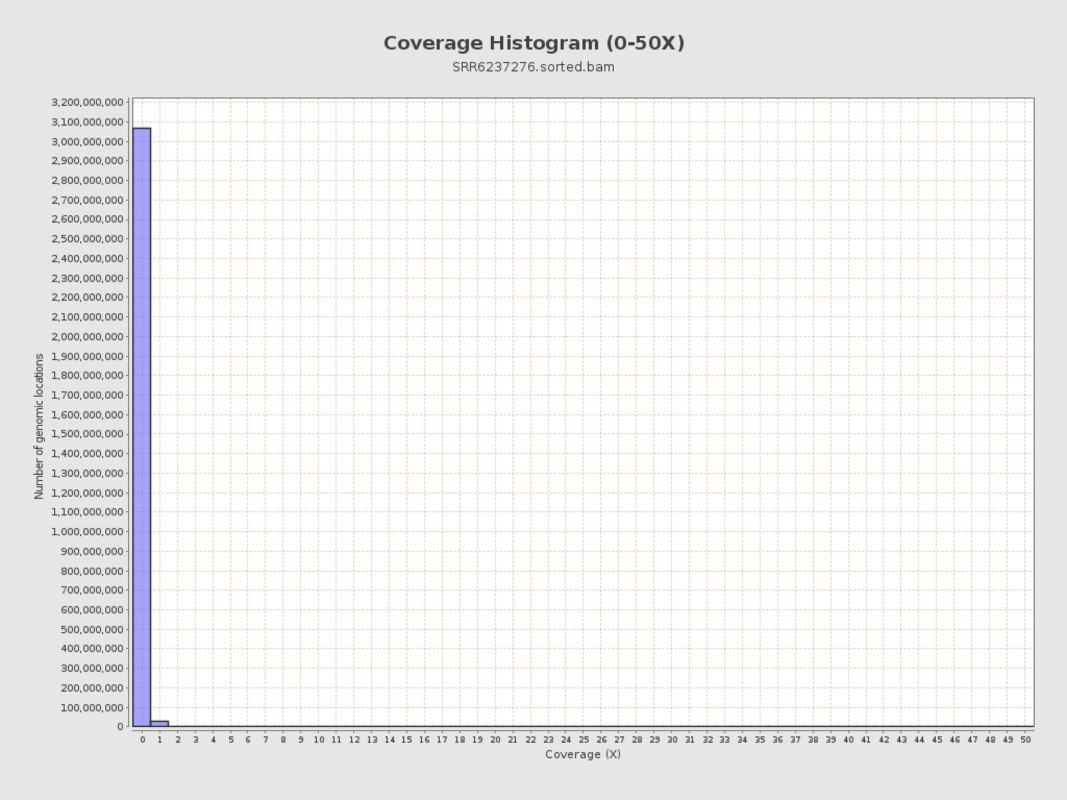
3. Results : Coverage across reference



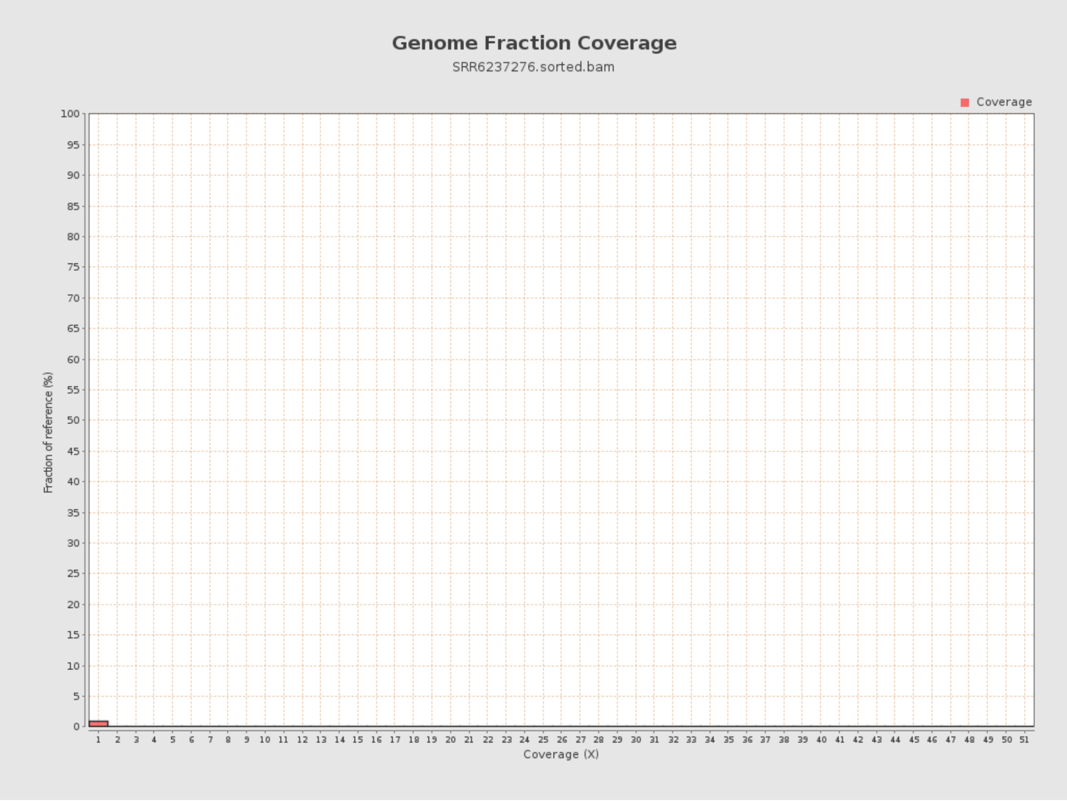
4. Results : Coverage Histogram



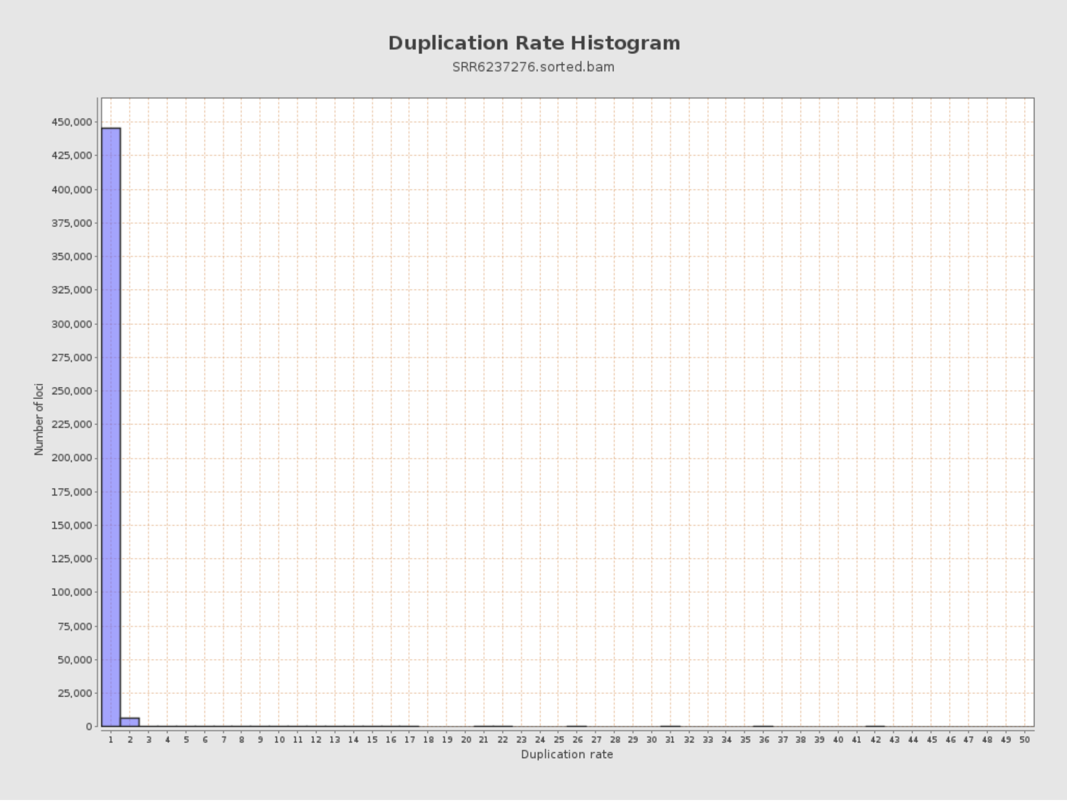
5. Results : Coverage Histogram (0-50X)



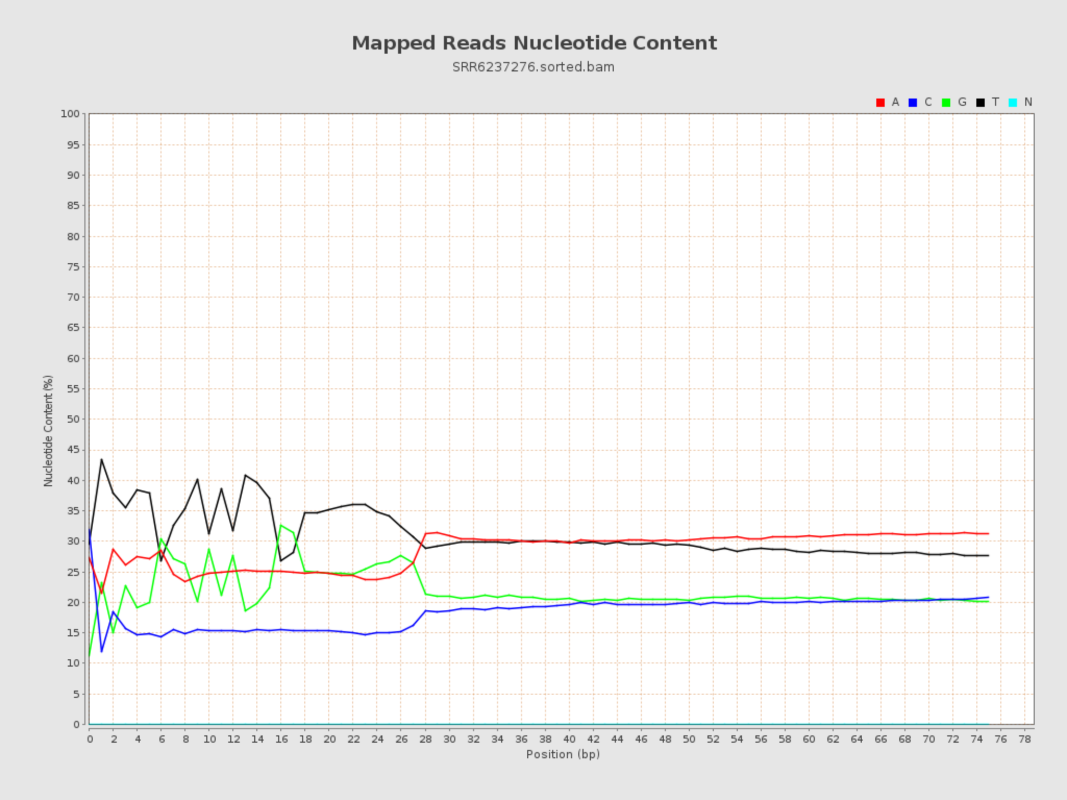
6. Results : Genome Fraction Coverage



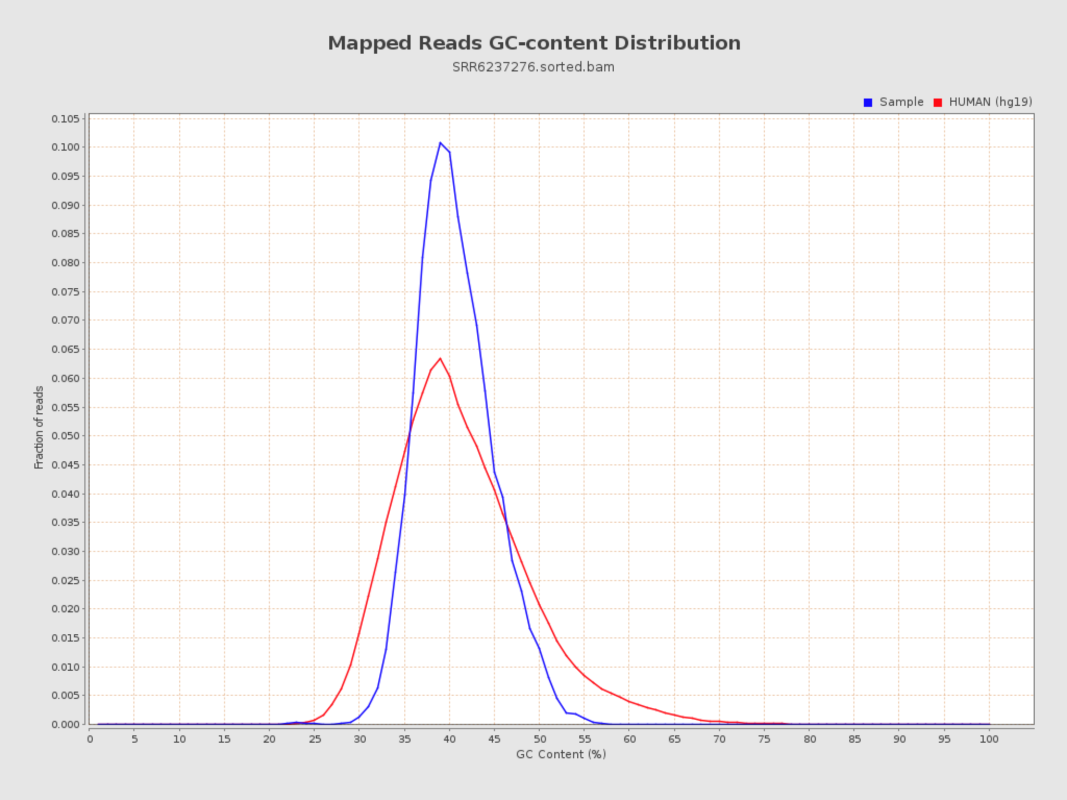
7. Results : Duplication Rate Histogram



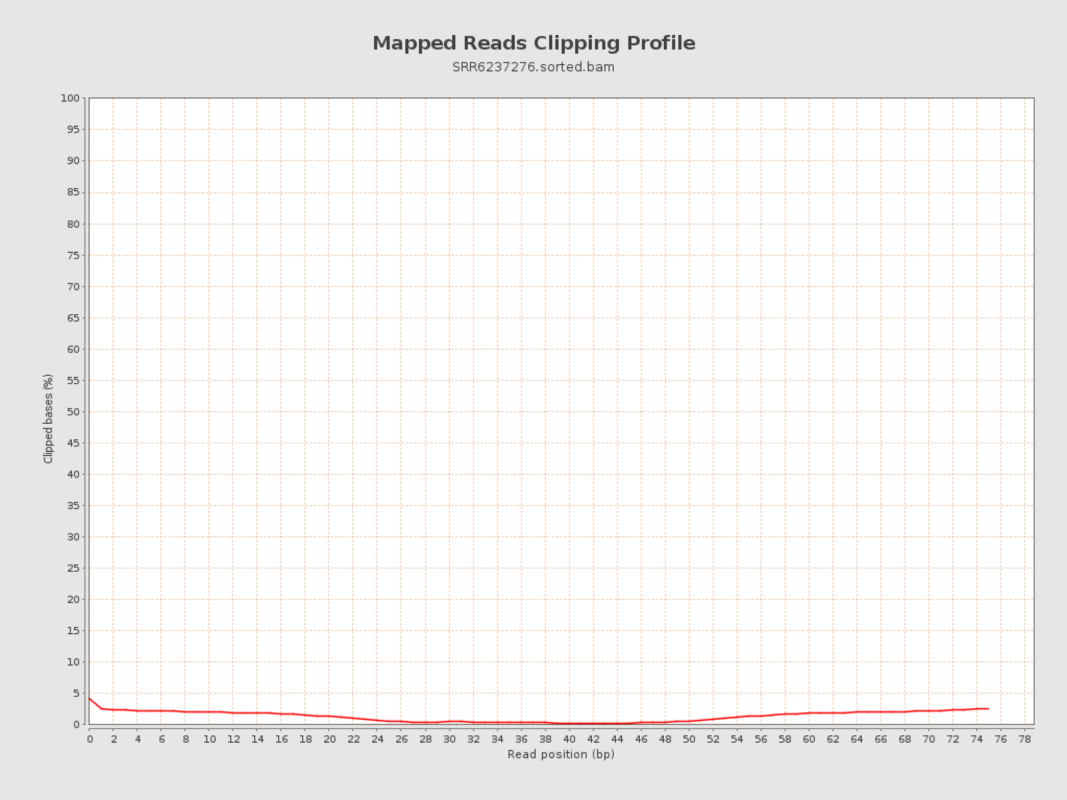
8. Results : Mapped Reads Nucleotide Content



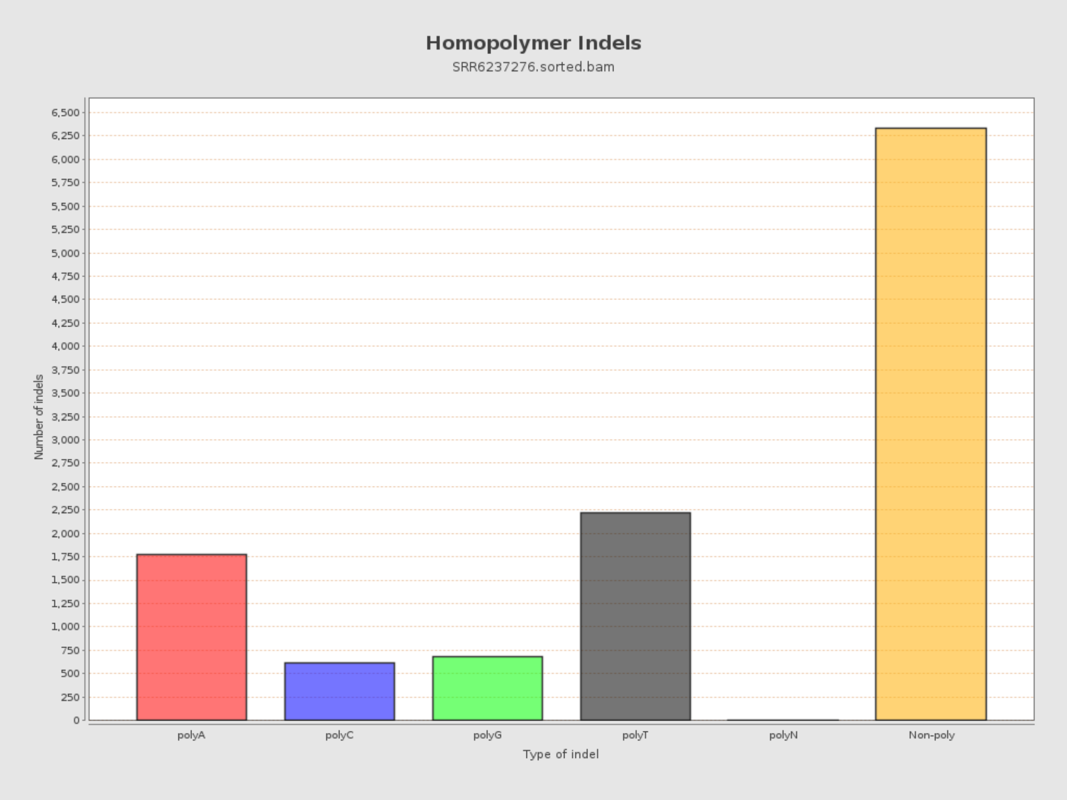
9. Results : Mapped Reads GC-content Distribution



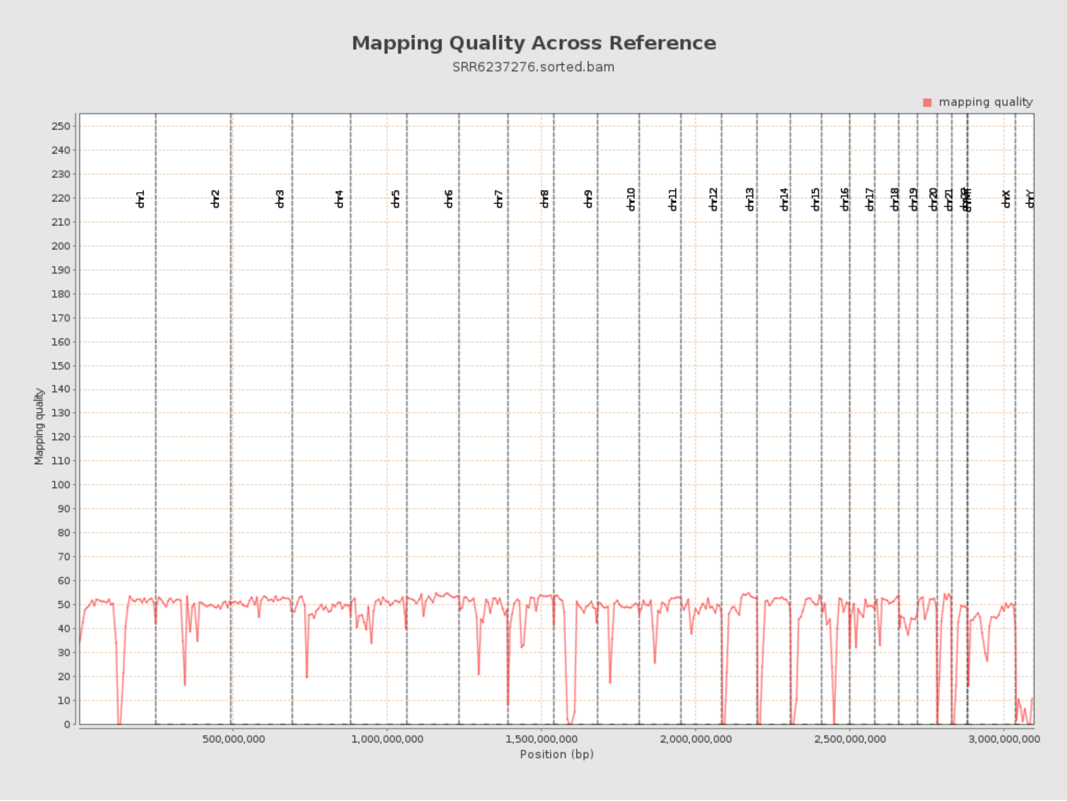
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram