Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:40:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237274.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_SRR6237274 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237274.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:40:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237274.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,965,445
Mapped reads	2,683,014 / 90.48%
Unmapped reads	282,431 / 9.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,955 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	124,385 / 4.19%
Duplication rate	3.32%
Clipped reads	1,085,984 / 36.62%

2.2. ACGT Content

Number/percentage of A's	51,655,862 / 28.47%
Number/percentage of C's	33,614,629 / 18.52%
Number/percentage of T's	56,860,053 / 31.33%
Number/percentage of G's	39,329,161 / 21.67%
Number/percentage of N's	3,149 / 0%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0586

Standard Deviation	0.5628

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

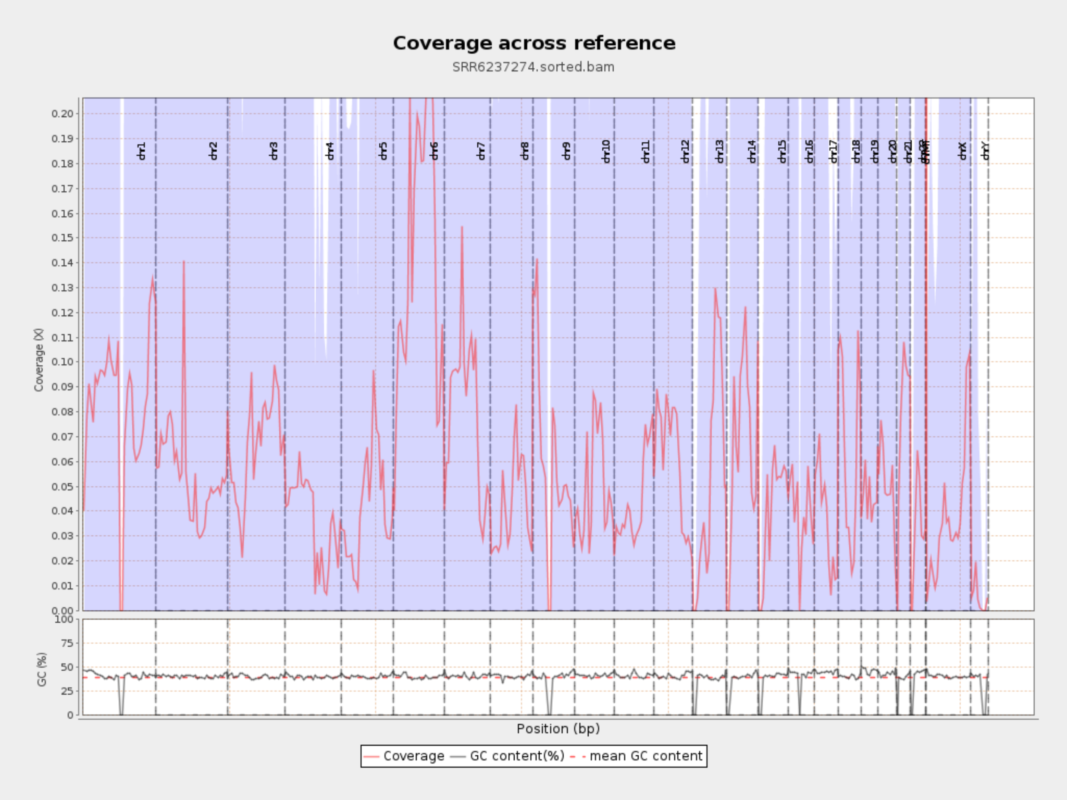
General error rate	0.79%
Mismatches	1,408,230
Insertions	13,561
Mapped reads with at least one insertion	0.5%
Deletions	50,621
Mapped reads with at least one deletion	1.87%
Homopolymer indels	47.18%

2.6. Chromosome stats

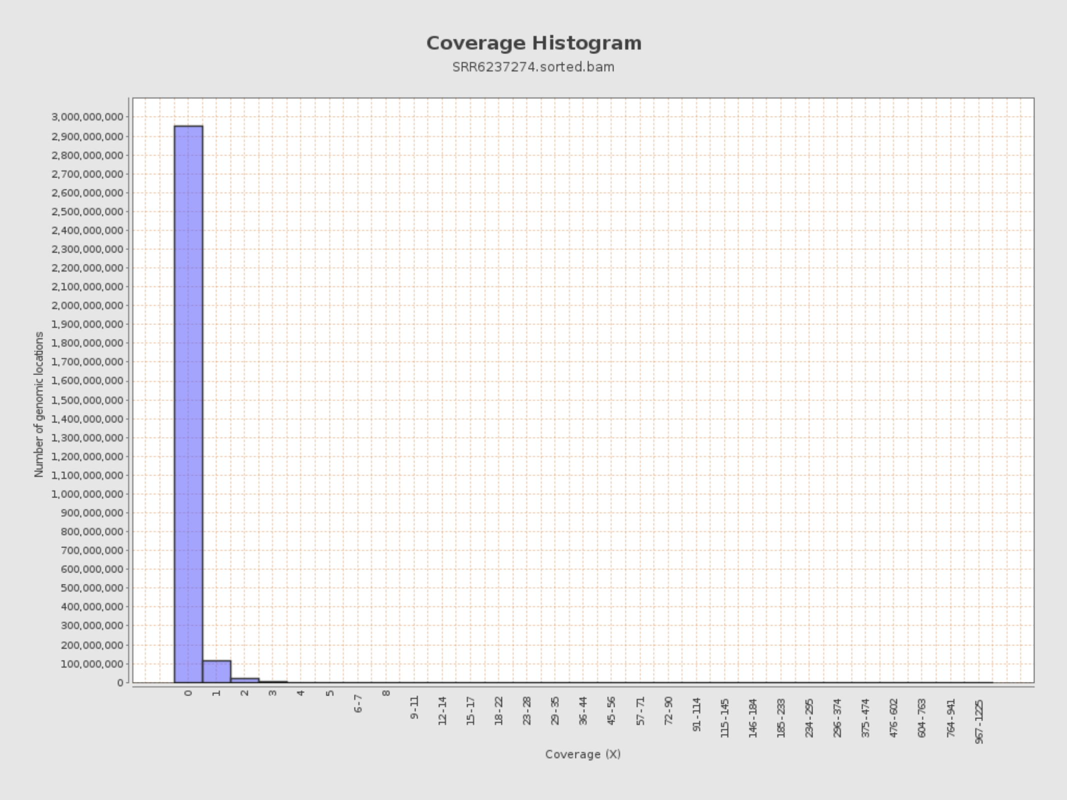
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20898954	0.0838	0.8038
chr2	243199373	13465161	0.0554	0.6537
chr3	198022430	13285664	0.0671	0.3092
chr4	191154276	6909671	0.0361	0.2494
chr5	180915260	7546042	0.0417	0.25
chr6	171115067	25177184	0.1471	0.8024
chr7	159138663	12802713	0.0805	1.0385

chr8	146364022	6144191	0.042	0.8305
chr9	141213431	8225821	0.0583	0.5757
chr10	135534747	6741276	0.0497	0.4743
chr11	135006516	5949022	0.0441	0.3931
chr12	133851895	8123719	0.0607	0.3089
chr13	115169878	6238499	0.0542	0.2806
chr14	107349540	6973749	0.065	0.3547
chr15	102531392	4082217	0.0398	0.2429
chr16	90354753	3457626	0.0383	0.3002
chr17	81195210	2987680	0.0368	0.31
chr18	78077248	4986406	0.0639	1.0597
chr19	59128983	2723949	0.0461	0.5202
chr20	63025520	3244933	0.0515	0.2849
chr21	48129895	3749796	0.0779	0.3675
chr22	51304566	1637108	0.0319	0.2112
chrMT	16571	130637	7.8835	5.0618
chrX	155270560	5746071	0.037	0.2859
chrY	59373566	323507	0.0054	0.1416

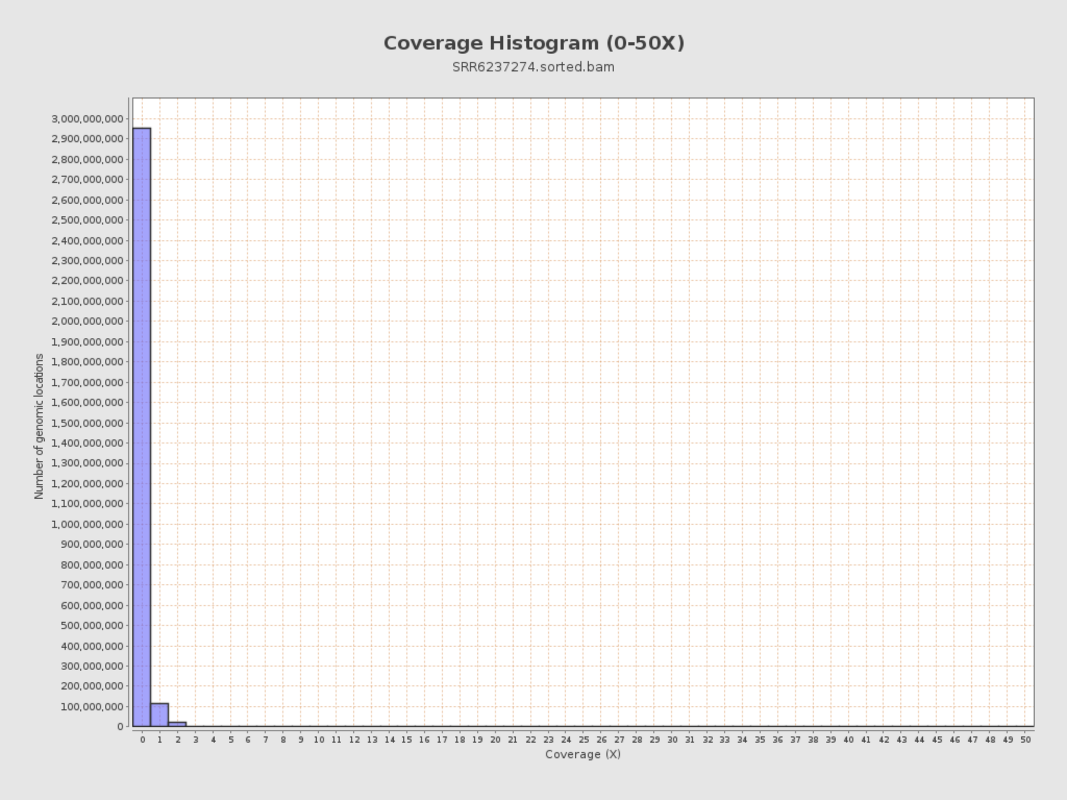
3. Results : Coverage across reference



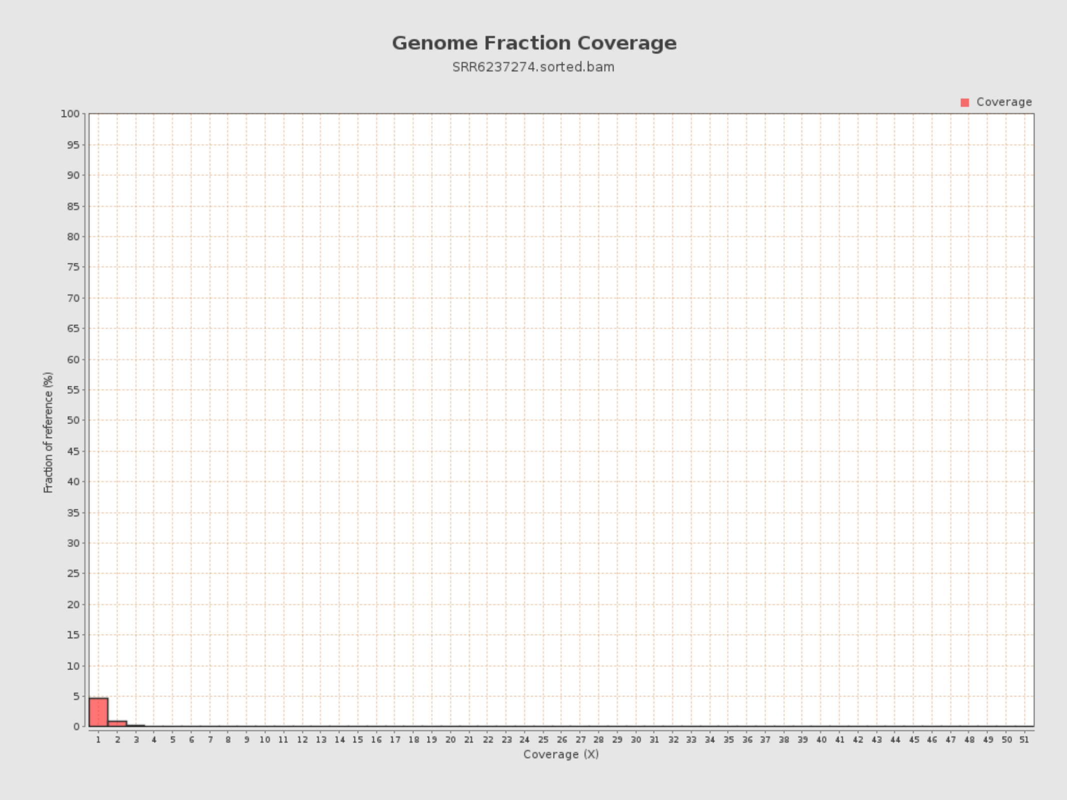
4. Results : Coverage Histogram



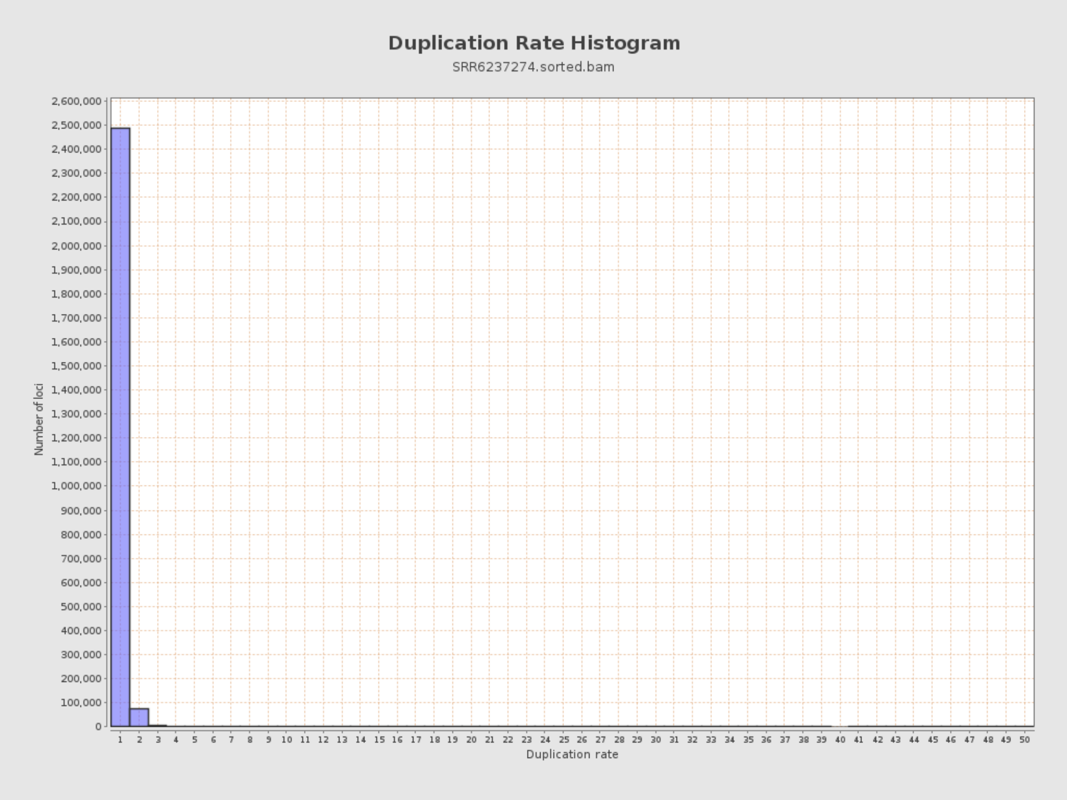
5. Results : Coverage Histogram (0-50X)



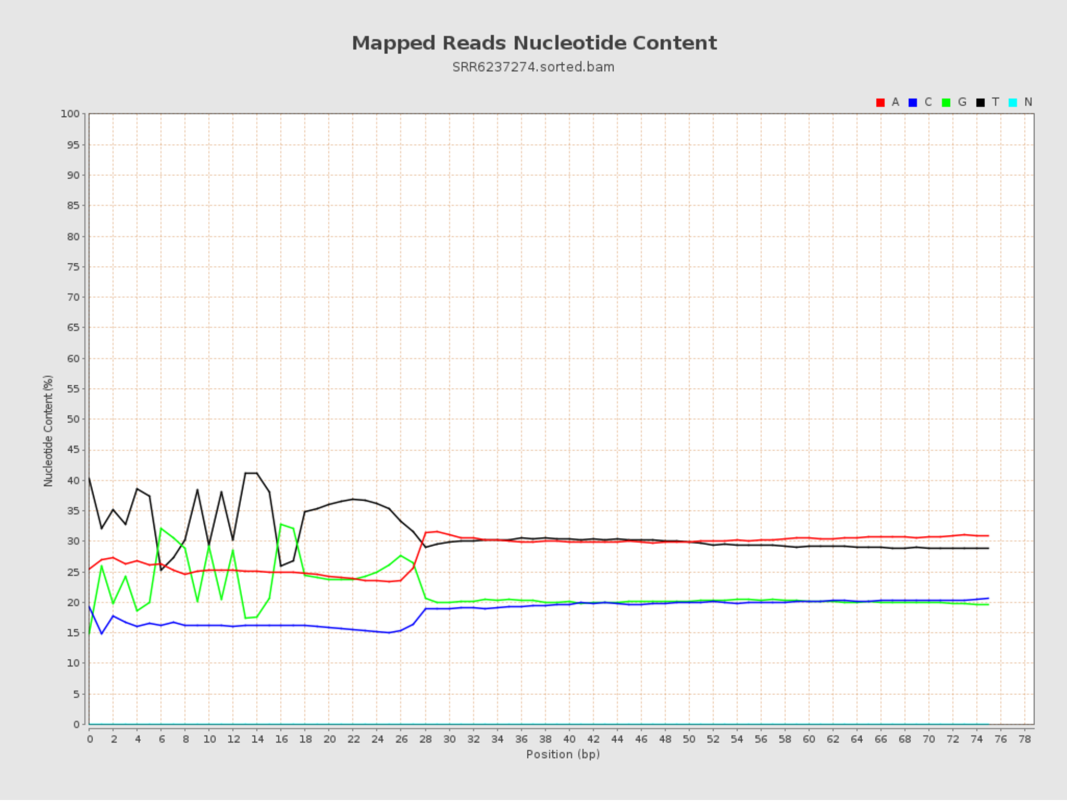
6. Results : Genome Fraction Coverage



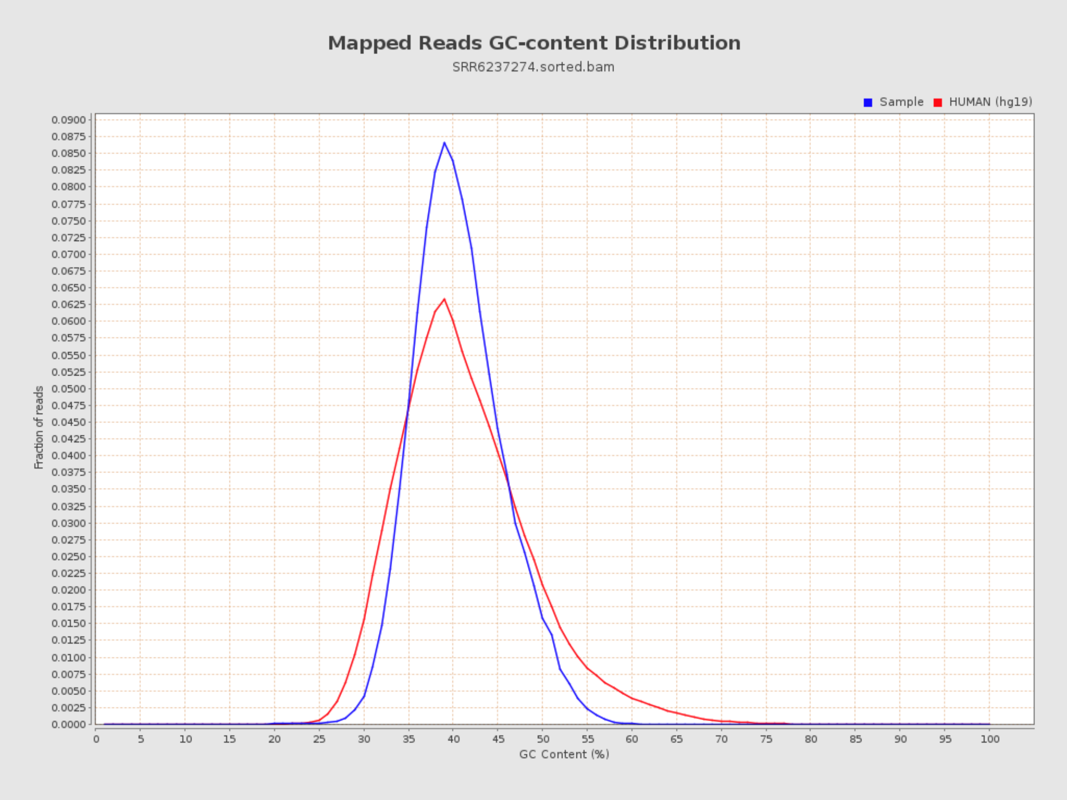
7. Results : Duplication Rate Histogram



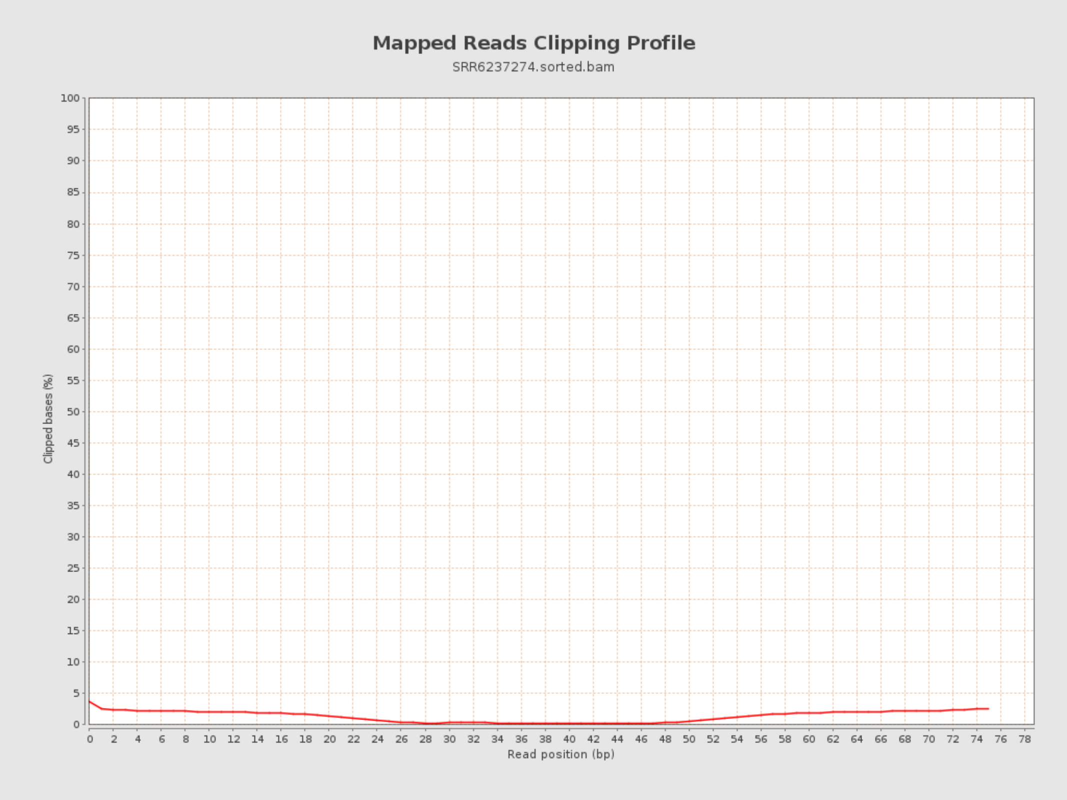
8. Results : Mapped Reads Nucleotide Content



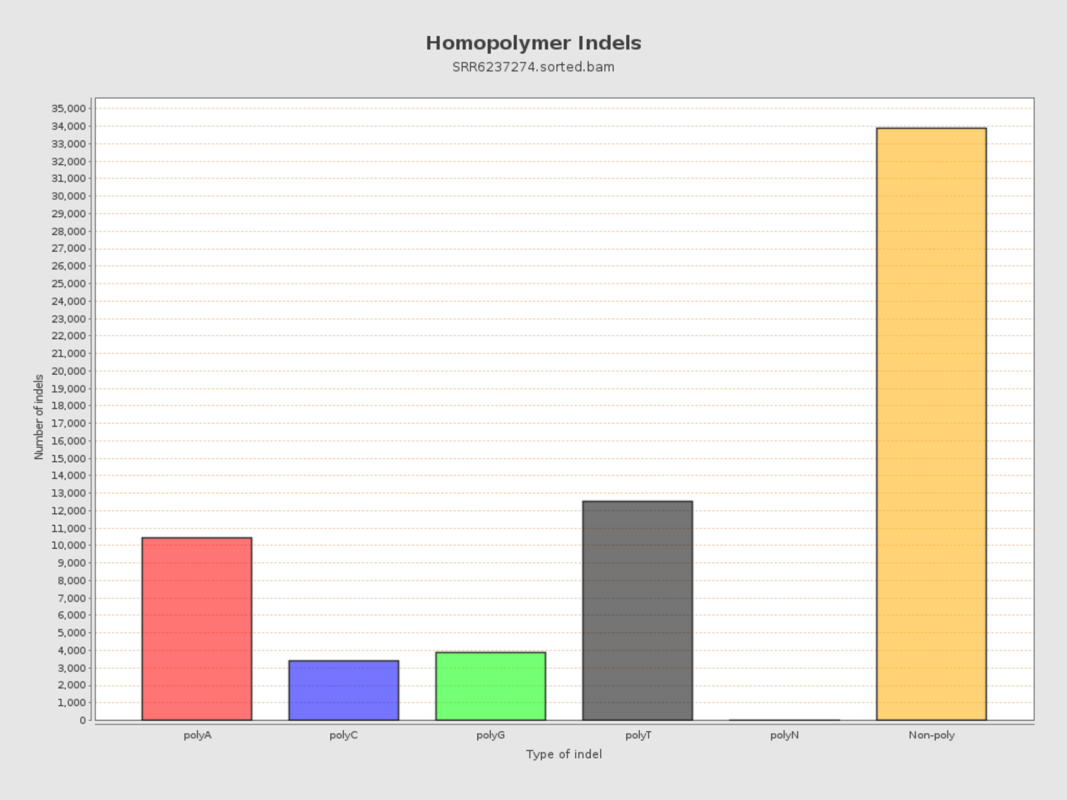
9. Results : Mapped Reads GC-content Distribution



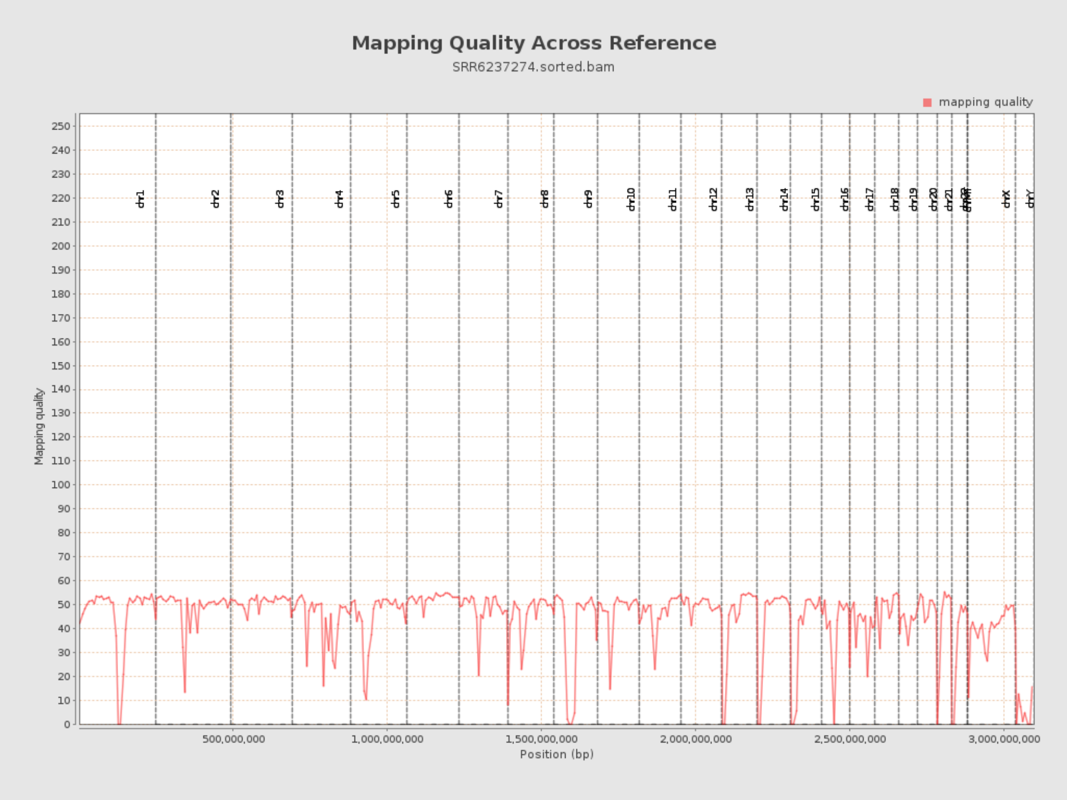
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram