Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:32:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237271.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_SRR6237271 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237271.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:32:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237271.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,894,514
Mapped reads	2,662,528 / 91.99%
Unmapped reads	231,986 / 8.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,093 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	102,733 / 3.55%
Duplication rate	3.1%
Clipped reads	919,950 / 31.78%

2.2. ACGT Content

Number/percentage of A's	53,642,133 / 29.09%
Number/percentage of C's	35,060,519 / 19.01%
Number/percentage of T's	57,179,079 / 31%
Number/percentage of G's	38,545,040 / 20.9%
Number/percentage of N's	3,129 / 0%
GC Percentage	39.91%

2.3. Coverage

Mean	0.0596

Standard Deviation	0.4578

2.4. Mapping Quality

Mean Mapping Quality	47.27

2.5. Mismatches and indels

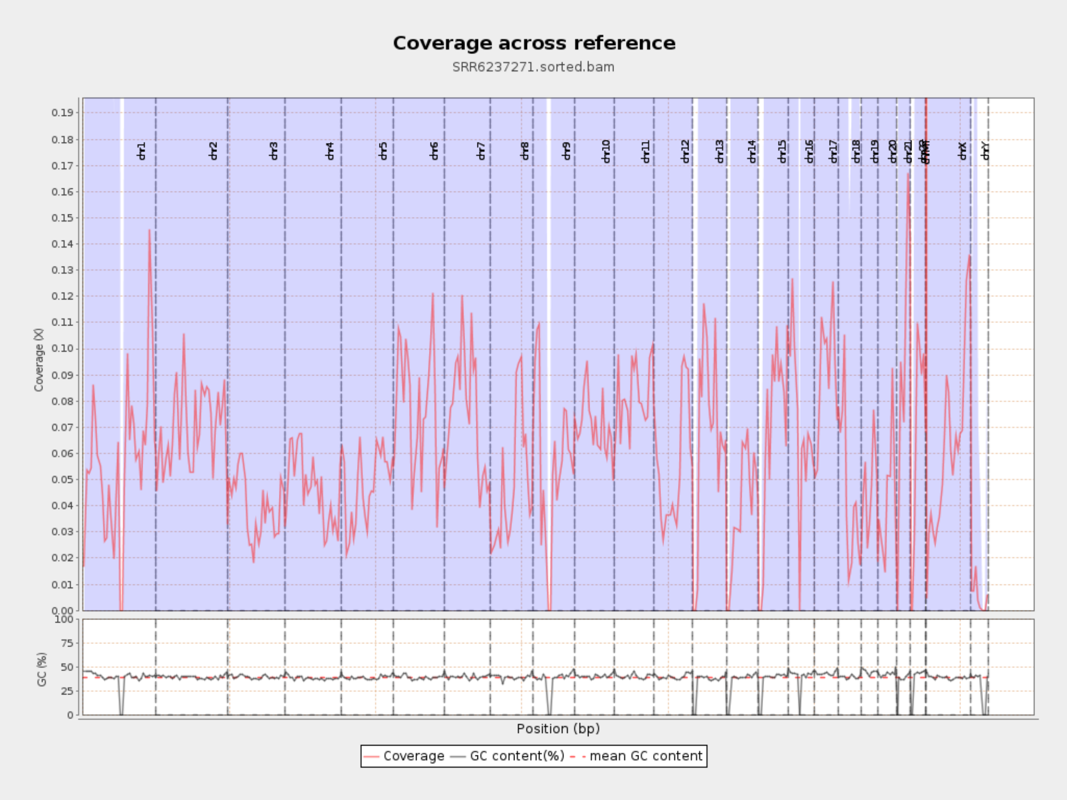
General error rate	0.82%
Mismatches	1,493,155
Insertions	13,427
Mapped reads with at least one insertion	0.5%
Deletions	73,386
Mapped reads with at least one deletion	2.71%
Homopolymer indels	45.2%

2.6. Chromosome stats

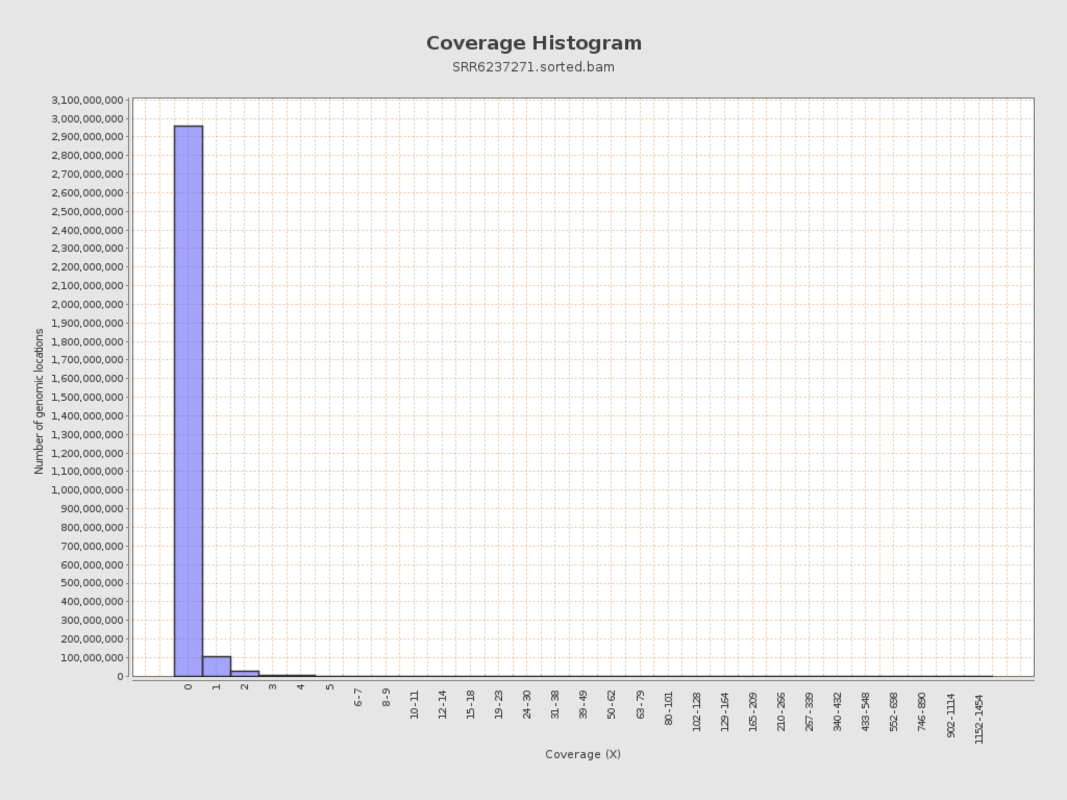
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14170726	0.0569	0.5293
chr2	243199373	17145283	0.0705	0.4914
chr3	198022430	7815187	0.0395	0.2518
chr4	191154276	8956458	0.0469	0.2947
chr5	180915260	8668605	0.0479	0.2798
chr6	171115067	13218374	0.0772	0.3758
chr7	159138663	12048488	0.0757	0.6872

chr8	146364022	7024006	0.048	0.9823
chr9	141213431	7911988	0.056	0.3807
chr10	135534747	9566808	0.0706	0.4318
chr11	135006516	11032722	0.0817	0.4986
chr12	133851895	7485334	0.0559	0.3082
chr13	115169878	7693428	0.0668	0.3352
chr14	107349540	4192549	0.0391	0.2626
chr15	102531392	6691156	0.0653	0.3292
chr16	90354753	6446245	0.0713	0.3634
chr17	81195210	7383723	0.0909	0.4502
chr18	78077248	3622681	0.0464	0.6157
chr19	59128983	2692945	0.0455	0.507
chr20	63025520	2740673	0.0435	0.2744
chr21	48129895	4512441	0.0938	0.4123
chr22	51304566	3438113	0.067	0.3293
chrMT	16571	68734	4.1478	3.1323
chrX	155270560	9719427	0.0626	0.3489
chrY	59373566	312428	0.0053	0.1409

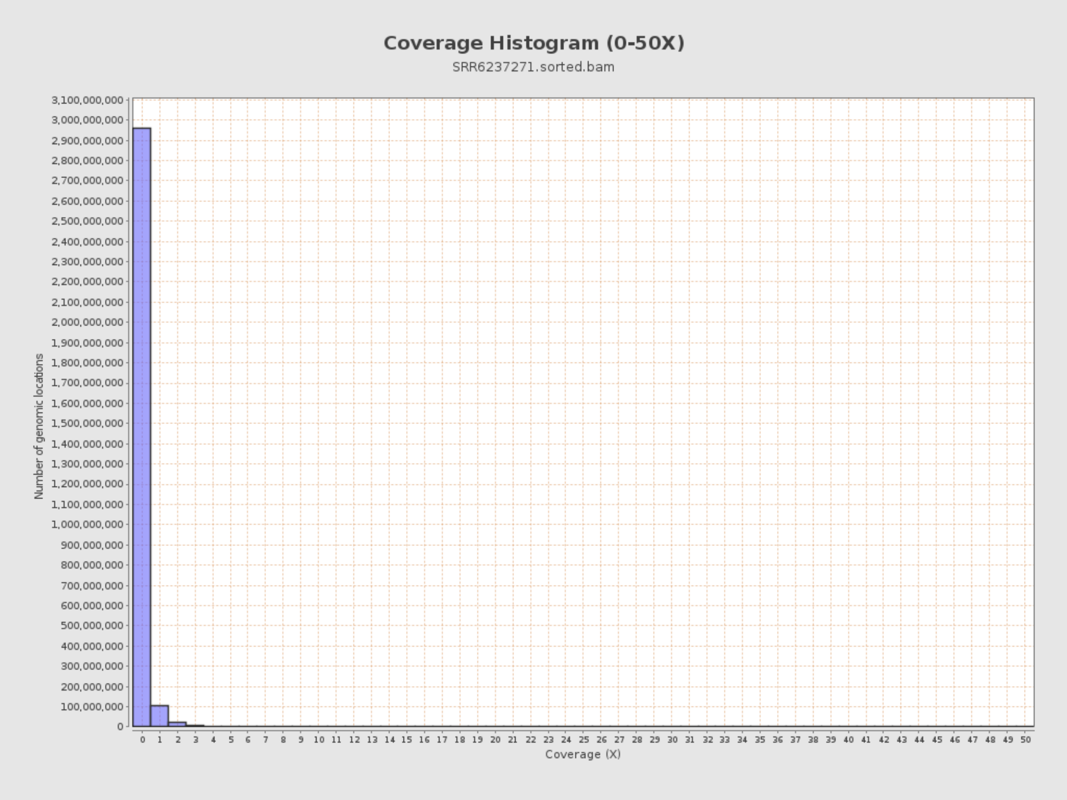
3. Results : Coverage across reference



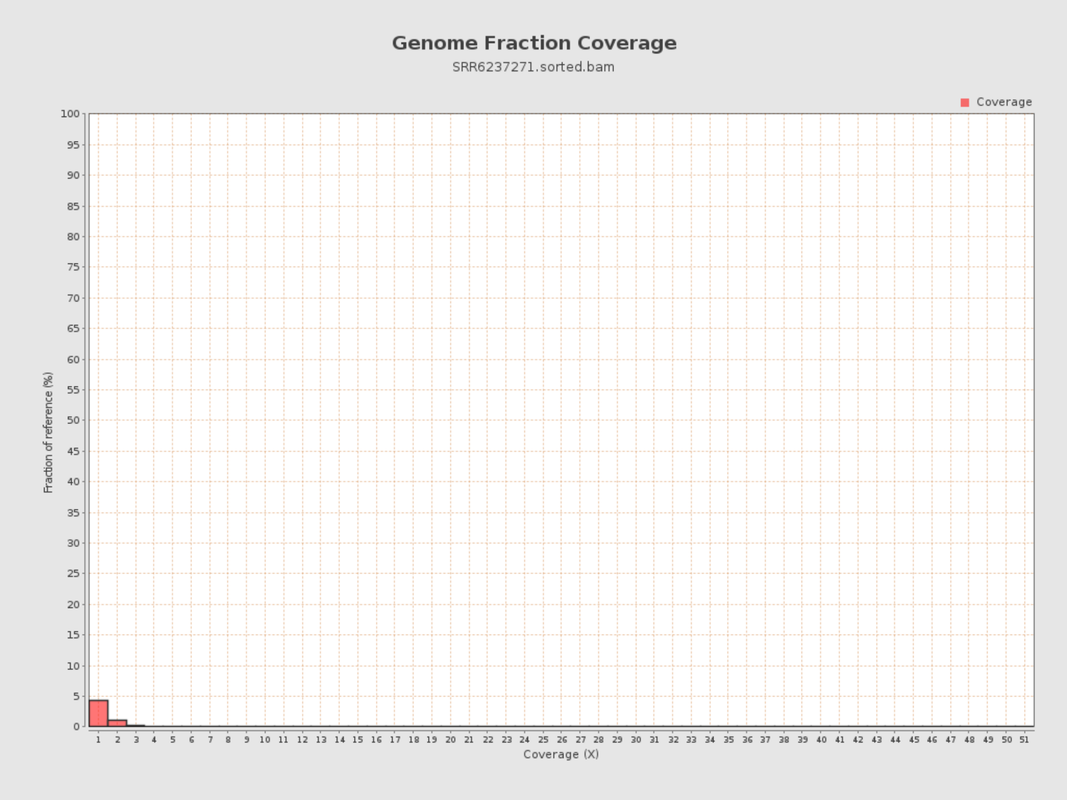
4. Results : Coverage Histogram



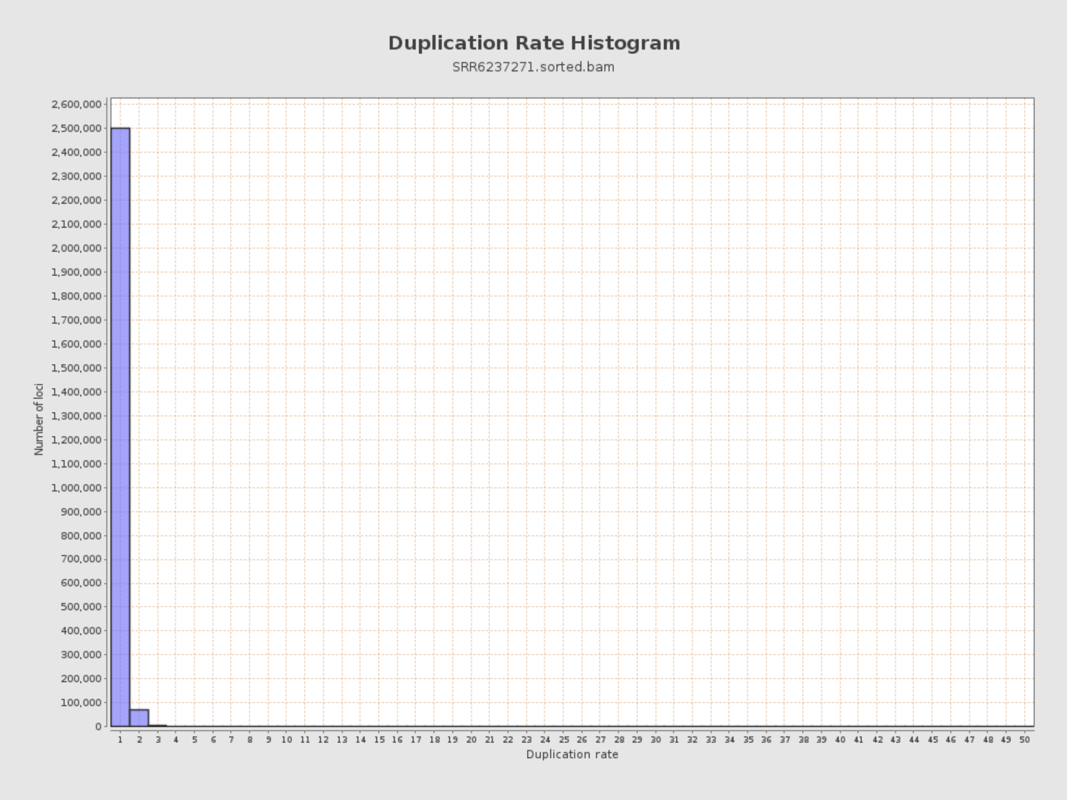
5. Results : Coverage Histogram (0-50X)



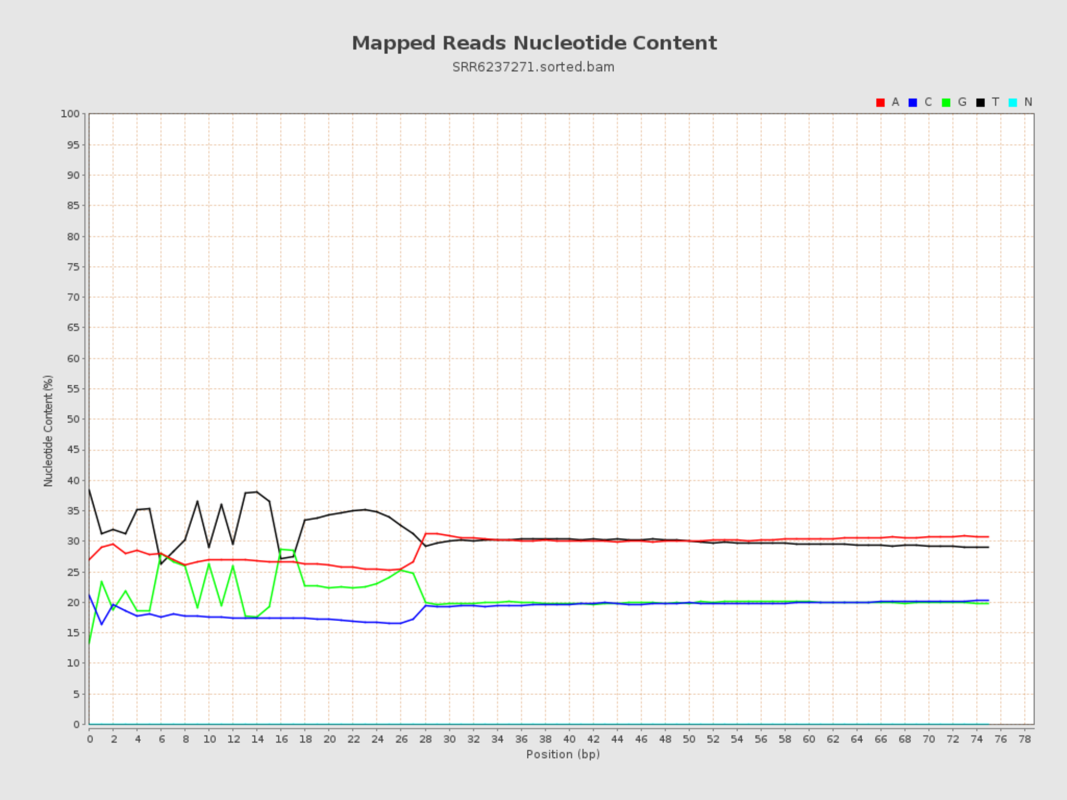
6. Results : Genome Fraction Coverage



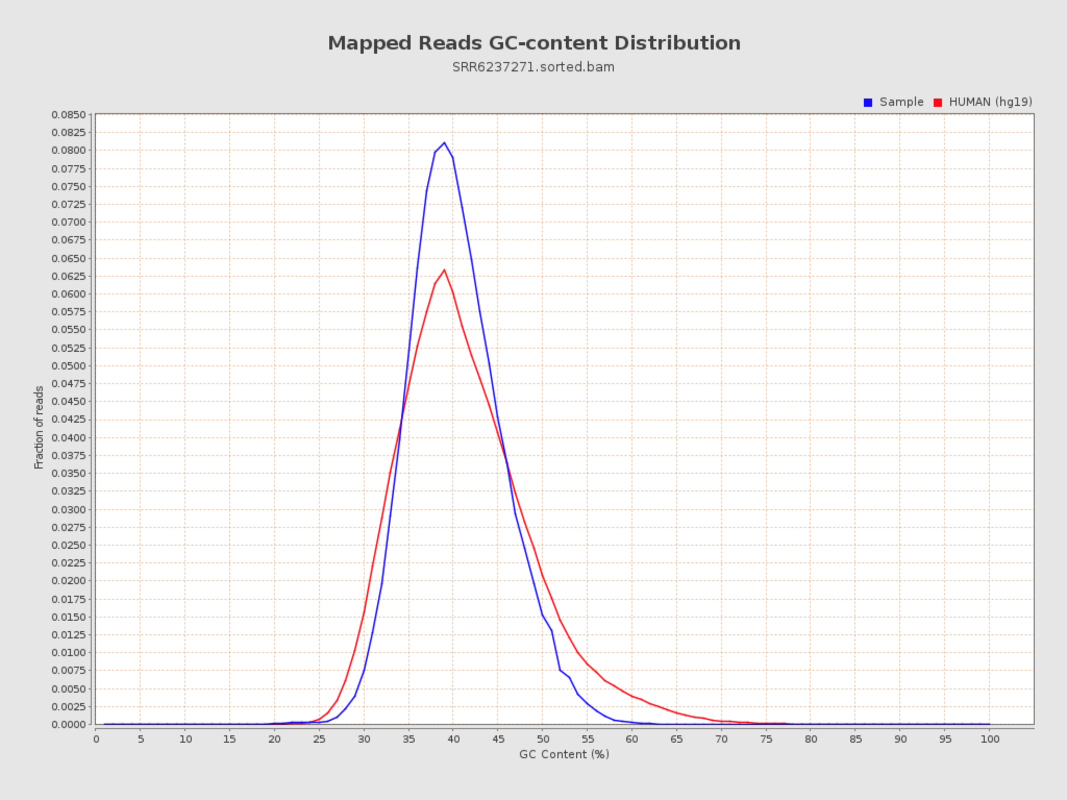
7. Results : Duplication Rate Histogram



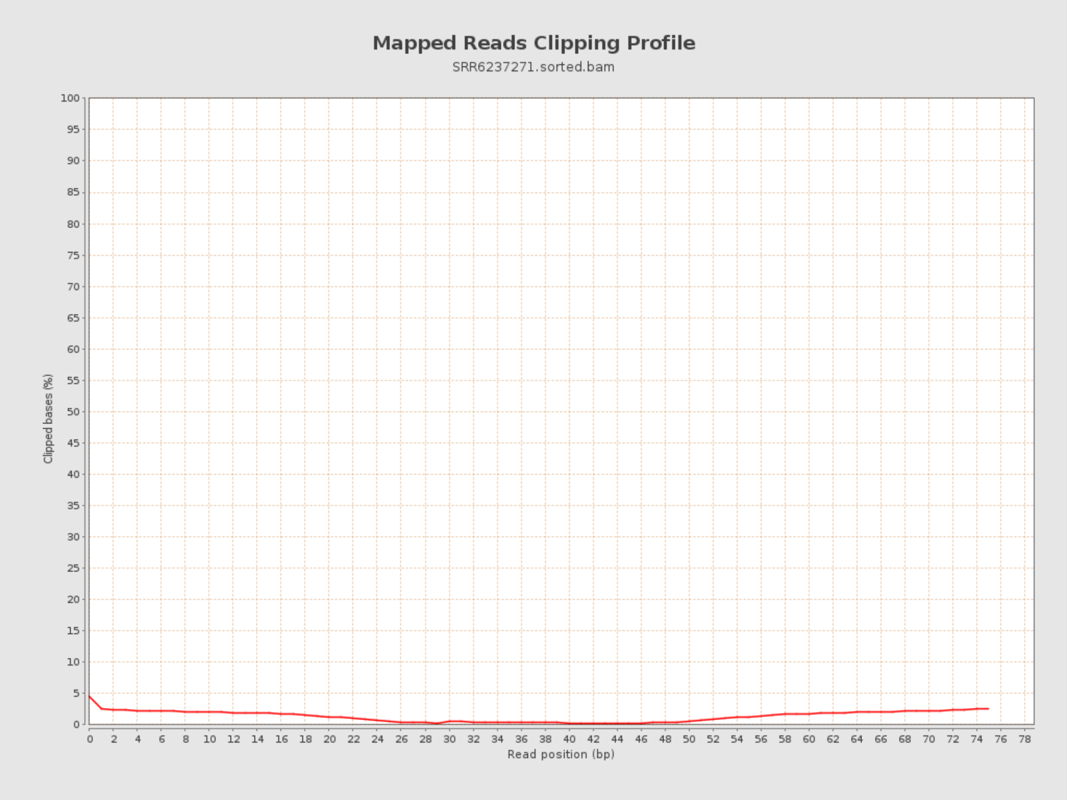
8. Results : Mapped Reads Nucleotide Content



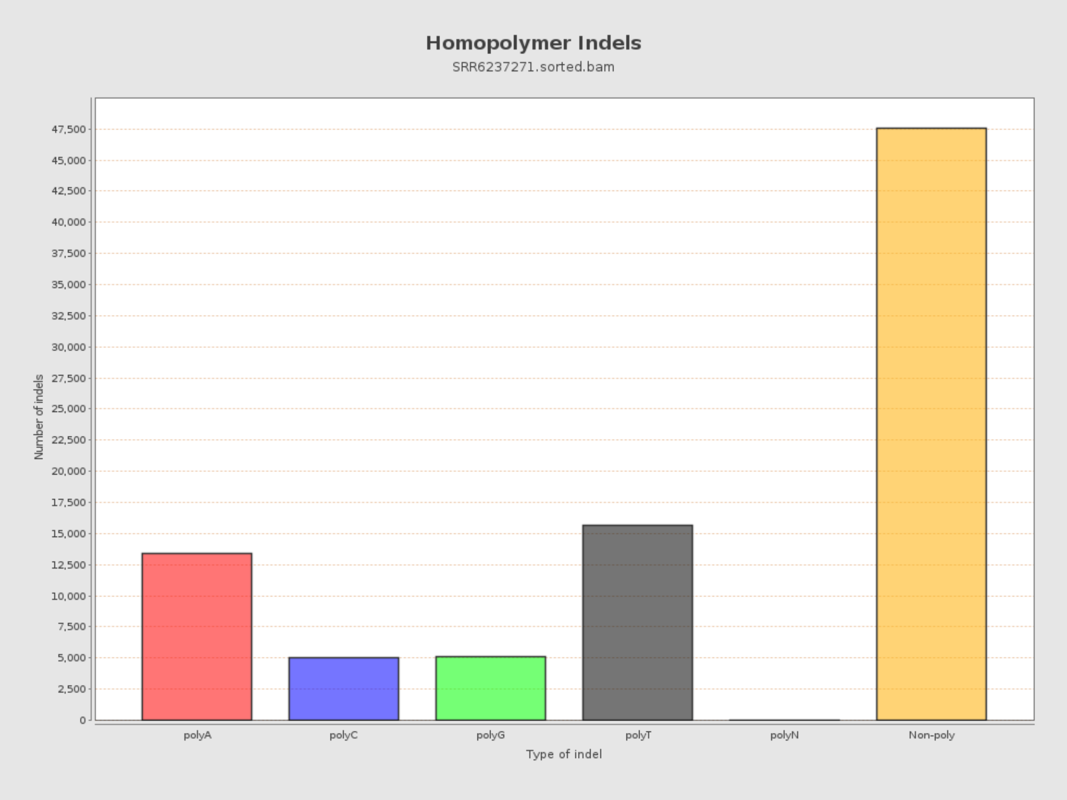
9. Results : Mapped Reads GC-content Distribution



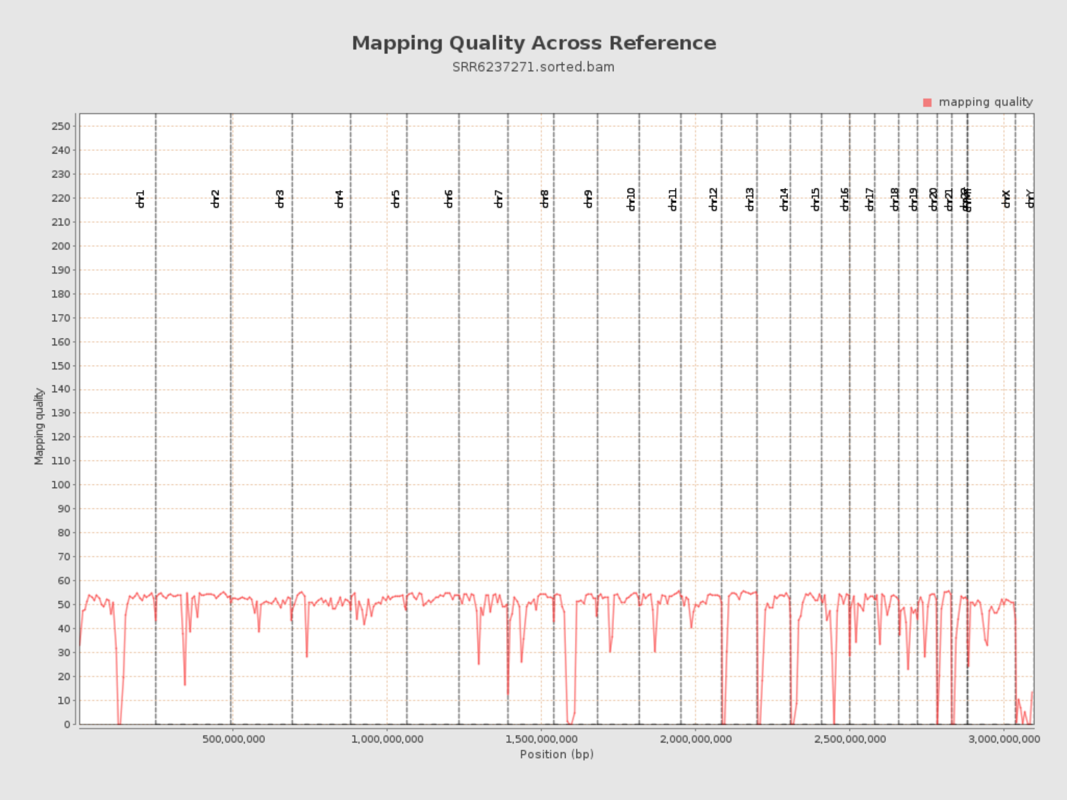
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram