Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:47:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237257.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_SRR6237257 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237257.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:47:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237257.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,893,304
Mapped reads	2,668,818 / 92.24%
Unmapped reads	224,486 / 7.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,826 / 1.07%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	482,057 / 16.66%
Duplication rate	14.79%
Clipped reads	1,604,425 / 55.45%

2.2. ACGT Content

Number/percentage of A's	43,368,049 / 25.75%
Number/percentage of C's	29,873,347 / 17.74%
Number/percentage of T's	55,359,425 / 32.87%
Number/percentage of G's	39,810,417 / 23.64%
Number/percentage of N's	18,554 / 0.01%
GC Percentage	41.37%

2.3. Coverage

Mean	0.0544

Standard Deviation	0.7057

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

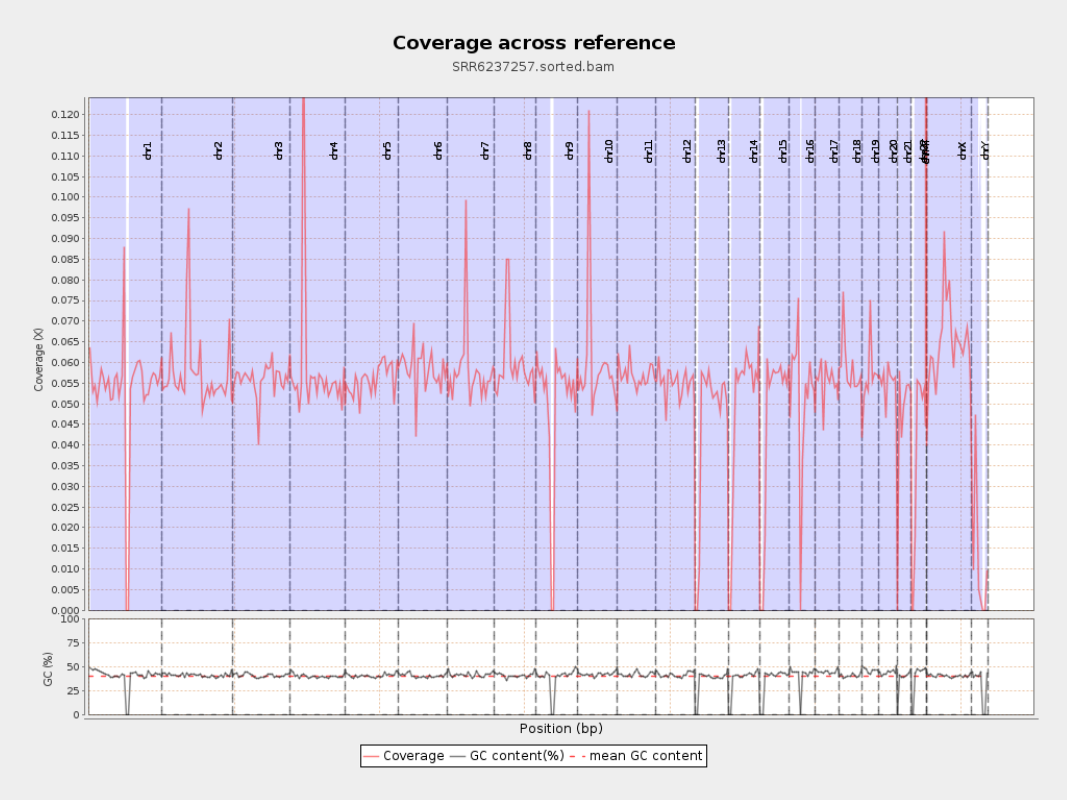
General error rate	0.61%
Mismatches	998,214
Insertions	13,860
Mapped reads with at least one insertion	0.51%
Deletions	38,113
Mapped reads with at least one deletion	1.41%
Homopolymer indels	43.85%

2.6. Chromosome stats

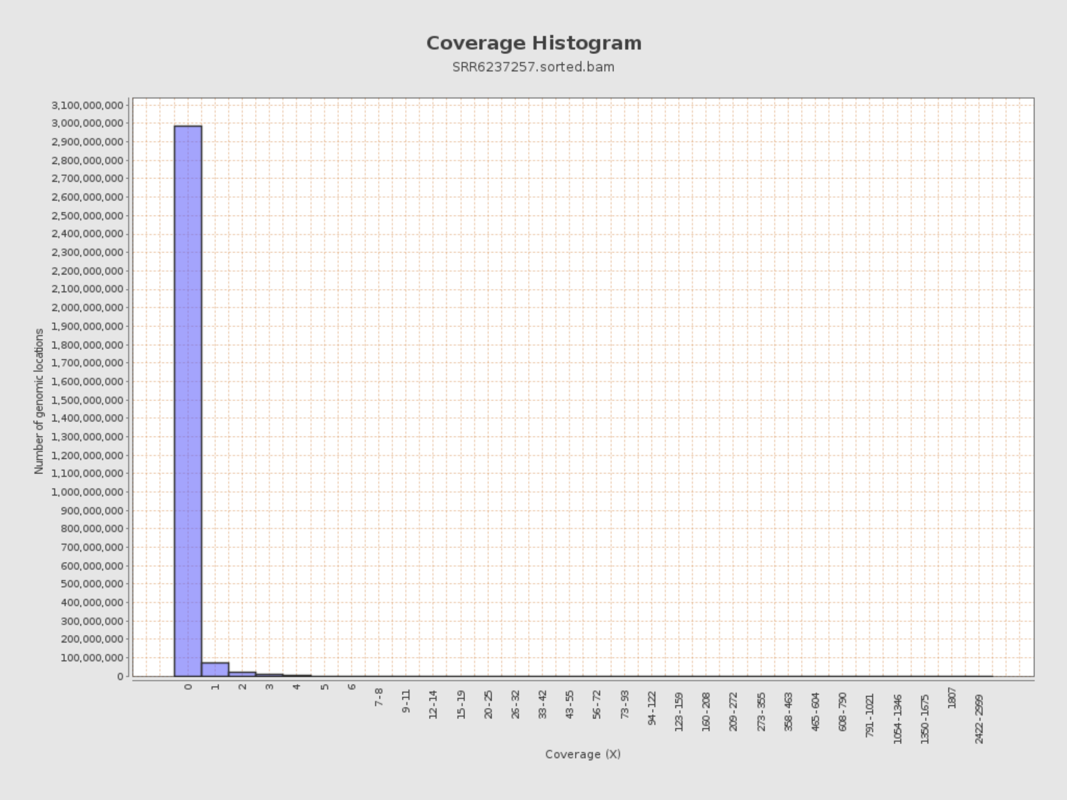
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13221078	0.053	0.9328
chr2	243199373	14045798	0.0578	1.4294
chr3	198022430	11030435	0.0557	0.3417
chr4	191154276	11051105	0.0578	0.5298
chr5	180915260	10103948	0.0558	0.344
chr6	171115067	9988361	0.0584	0.5477
chr7	159138663	9225929	0.058	0.688

chr8	146364022	8739040	0.0597	1.075
chr9	141213431	6956443	0.0493	0.4659
chr10	135534747	8041700	0.0593	0.6696
chr11	135006516	7677691	0.0569	0.4627
chr12	133851895	7373574	0.0551	0.3502
chr13	115169878	5172968	0.0449	0.3745
chr14	107349540	5162569	0.0481	0.3379
chr15	102531392	4733702	0.0462	0.3392
chr16	90354753	4666095	0.0516	0.3669
chr17	81195210	4495138	0.0554	0.3793
chr18	78077248	4606579	0.059	1.2862
chr19	59128983	3371413	0.057	0.6278
chr20	63025520	3468313	0.055	0.3946
chr21	48129895	2257612	0.0469	0.3895
chr22	51304566	1895271	0.0369	0.2657
chrMT	16571	479169	28.9161	21.7166
chrX	155270560	10046655	0.0647	0.4228
chrY	59373566	686662	0.0116	0.4148

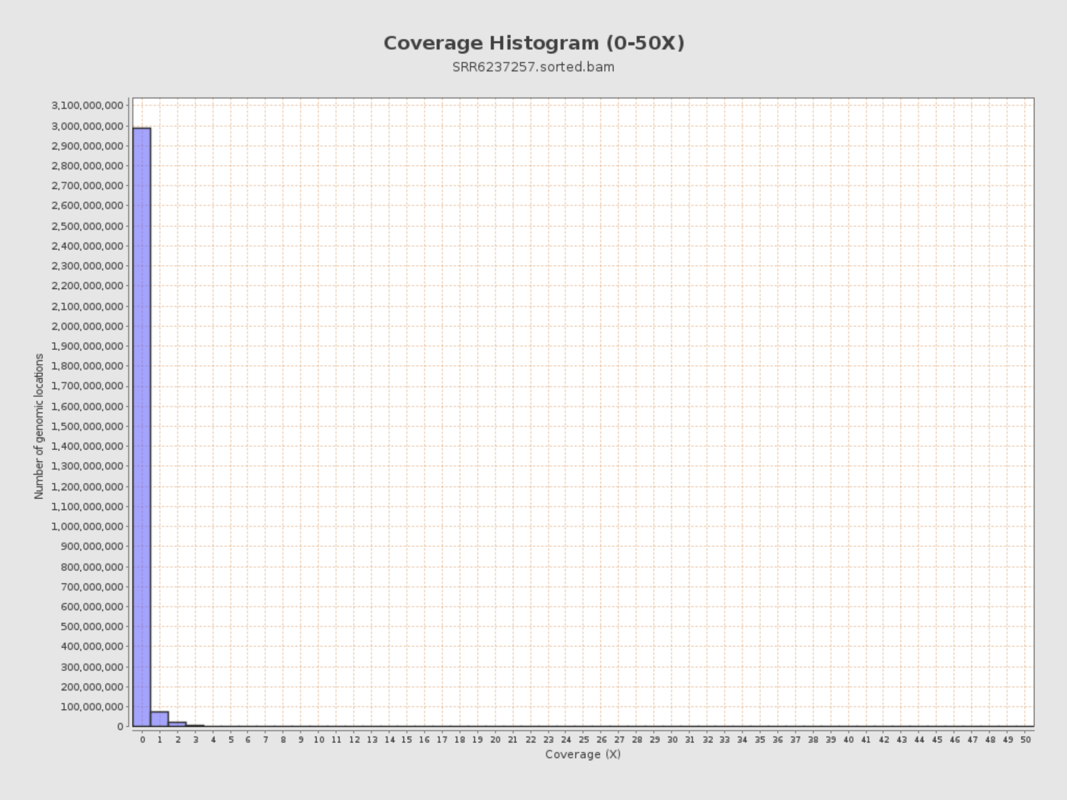
3. Results : Coverage across reference



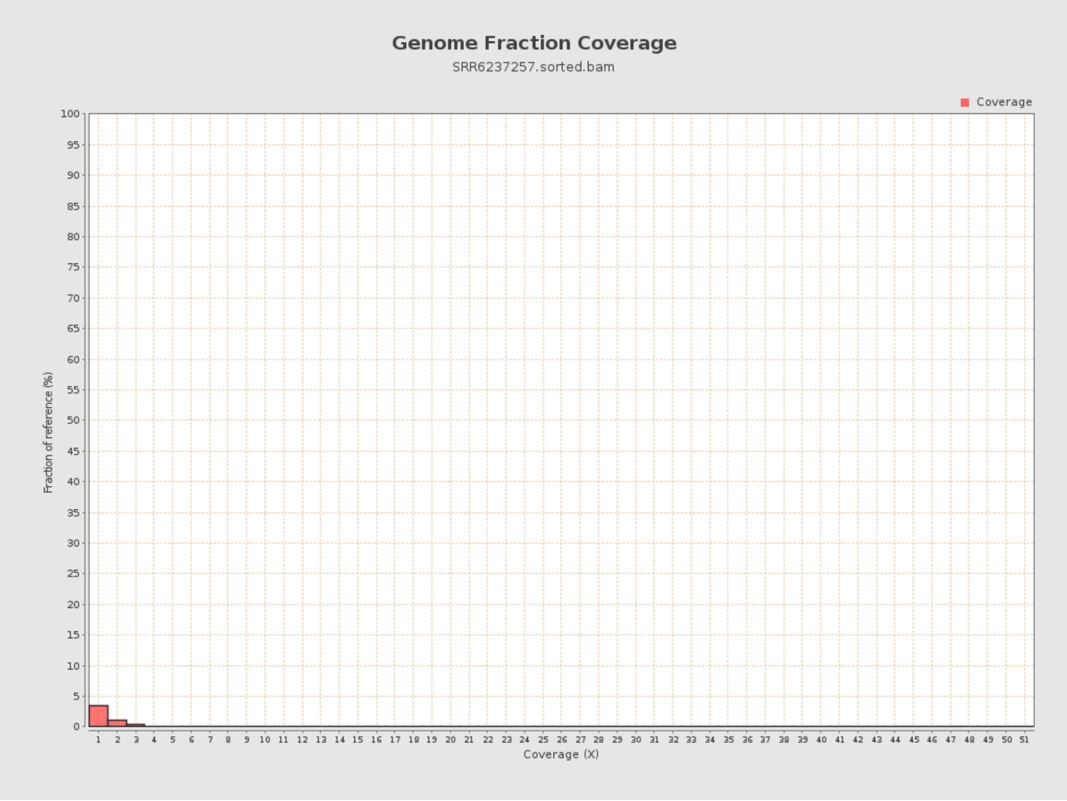
4. Results : Coverage Histogram



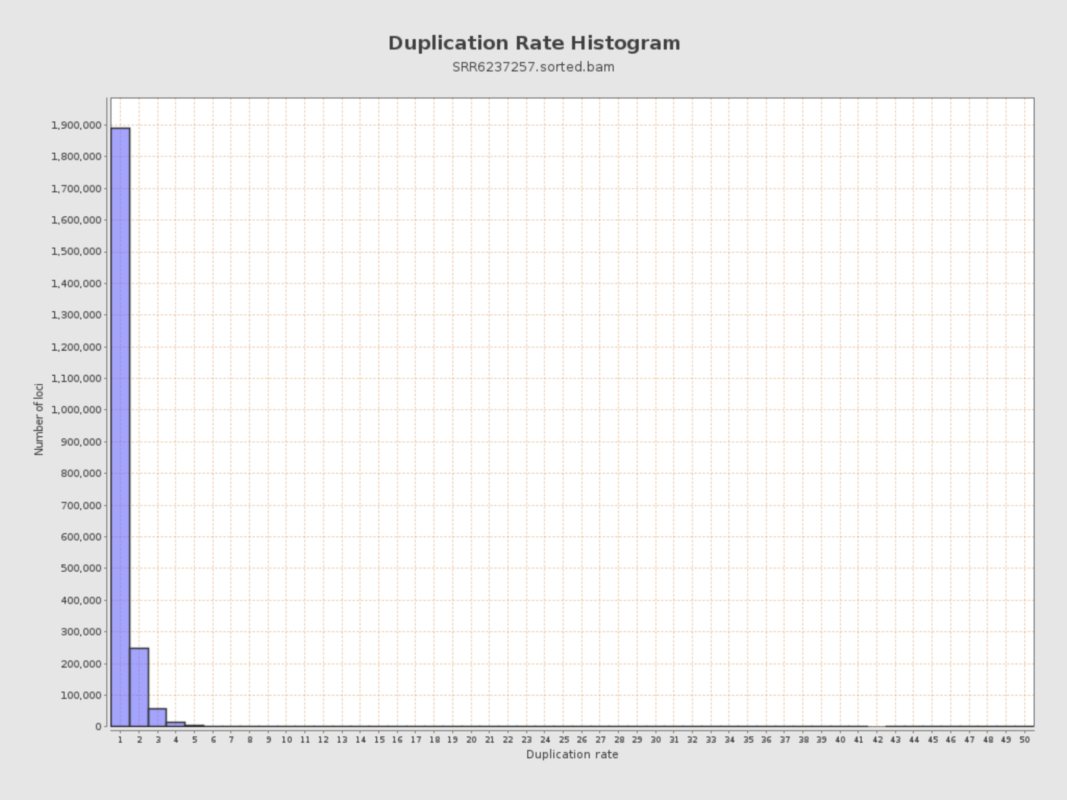
5. Results : Coverage Histogram (0-50X)



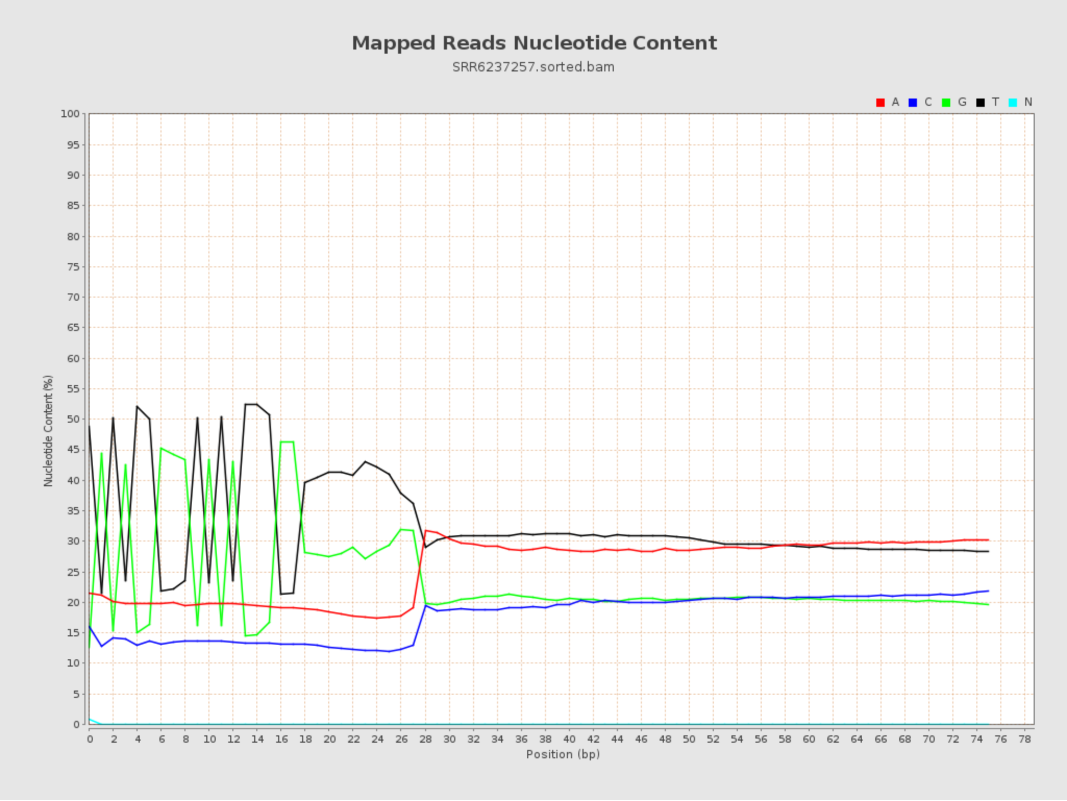
6. Results : Genome Fraction Coverage



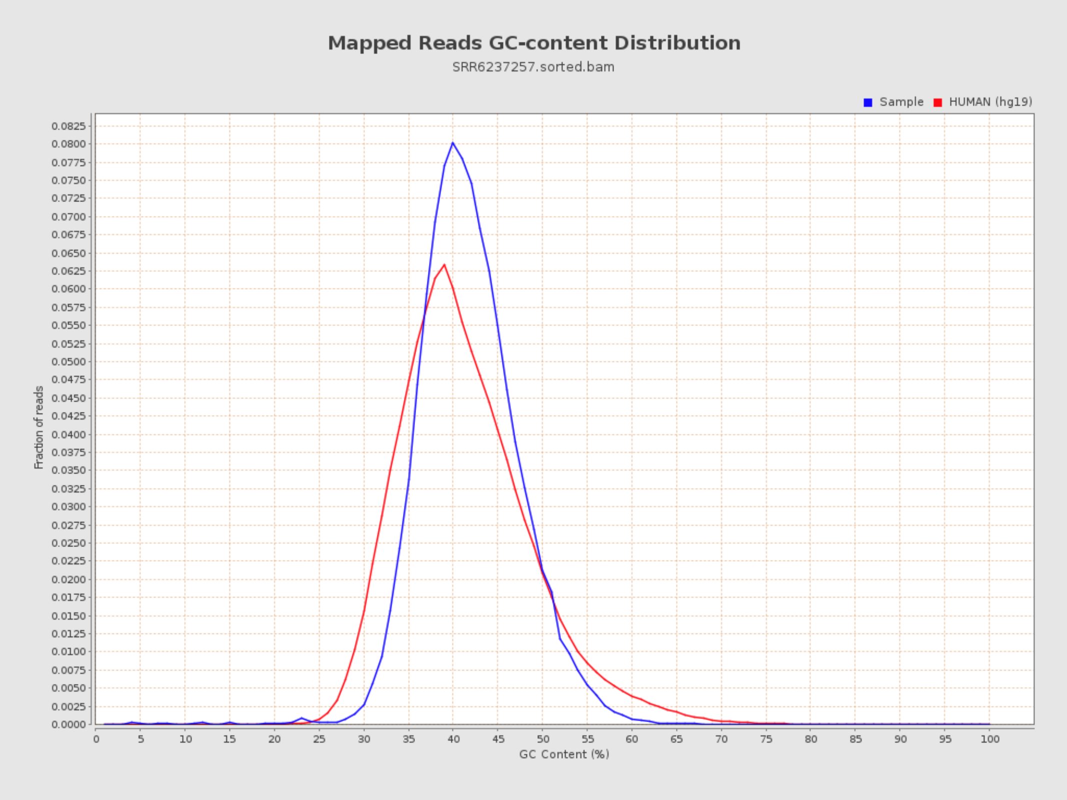
7. Results : Duplication Rate Histogram



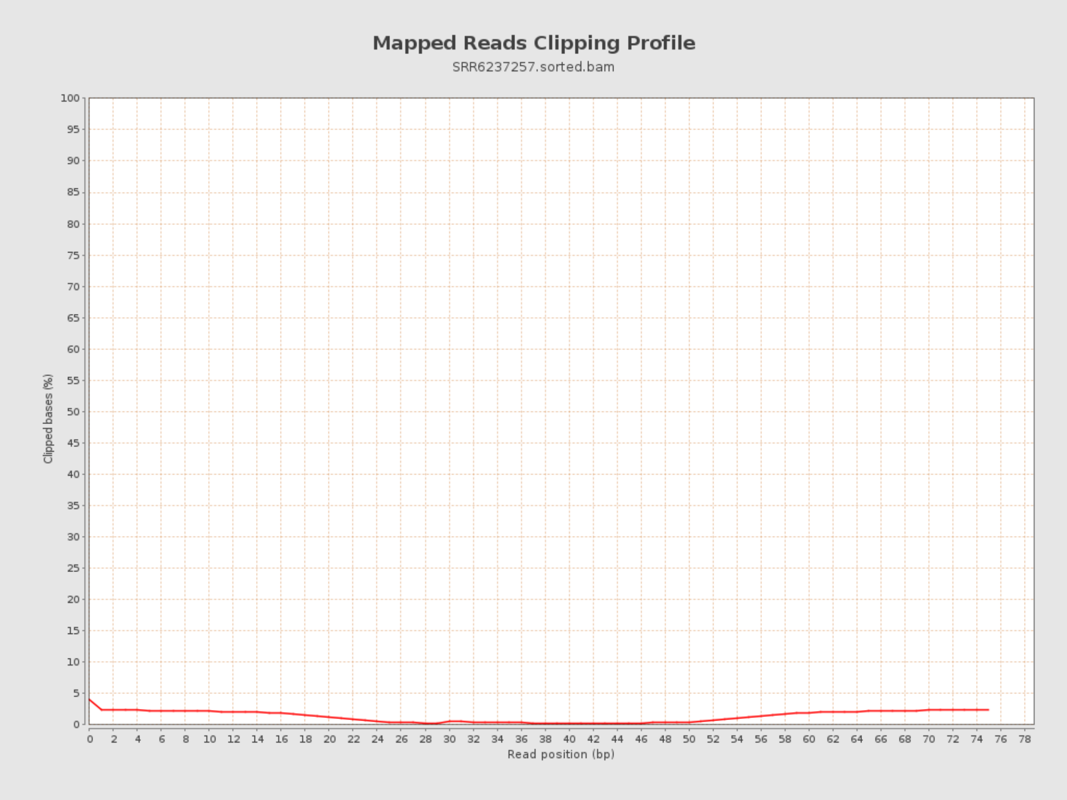
8. Results : Mapped Reads Nucleotide Content



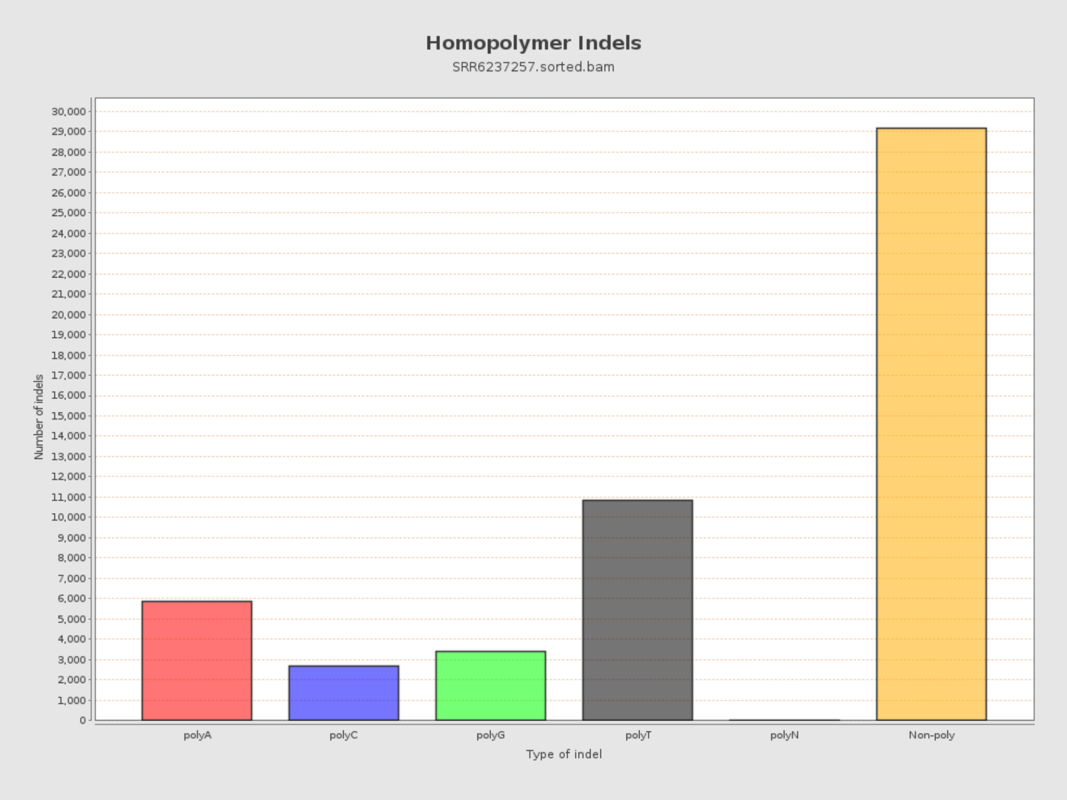
9. Results : Mapped Reads GC-content Distribution



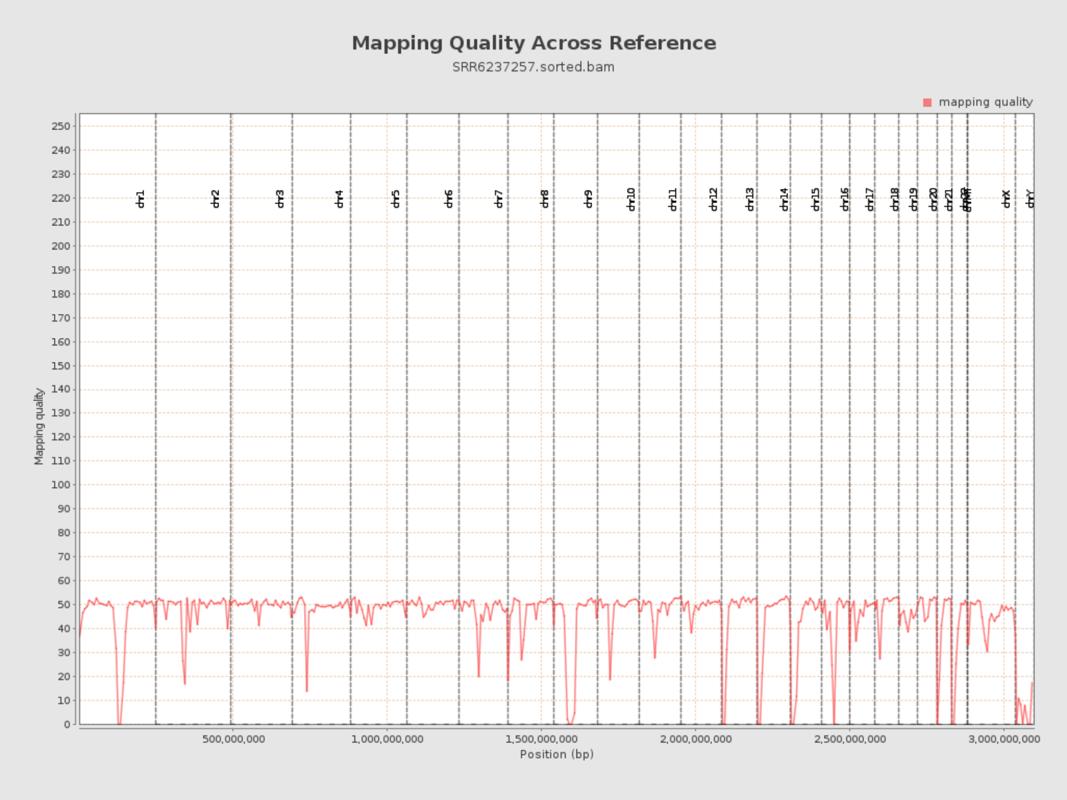
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram