Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:10:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237318.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_SRR6237318 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237318.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:10:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237318.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,285,381
Mapped reads	2,090,917 / 91.49%
Unmapped reads	194,464 / 8.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,054 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	74,917 / 3.28%
Duplication rate	2.41%
Clipped reads	801,090 / 35.05%

2.2. ACGT Content

Number/percentage of A's	40,737,675 / 28.54%
Number/percentage of C's	26,861,195 / 18.82%
Number/percentage of T's	44,156,850 / 30.93%
Number/percentage of G's	30,987,173 / 21.71%
Number/percentage of N's	2,199 / 0%
GC Percentage	40.53%

2.3. Coverage

Mean	0.0461

Standard Deviation	0.4548

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

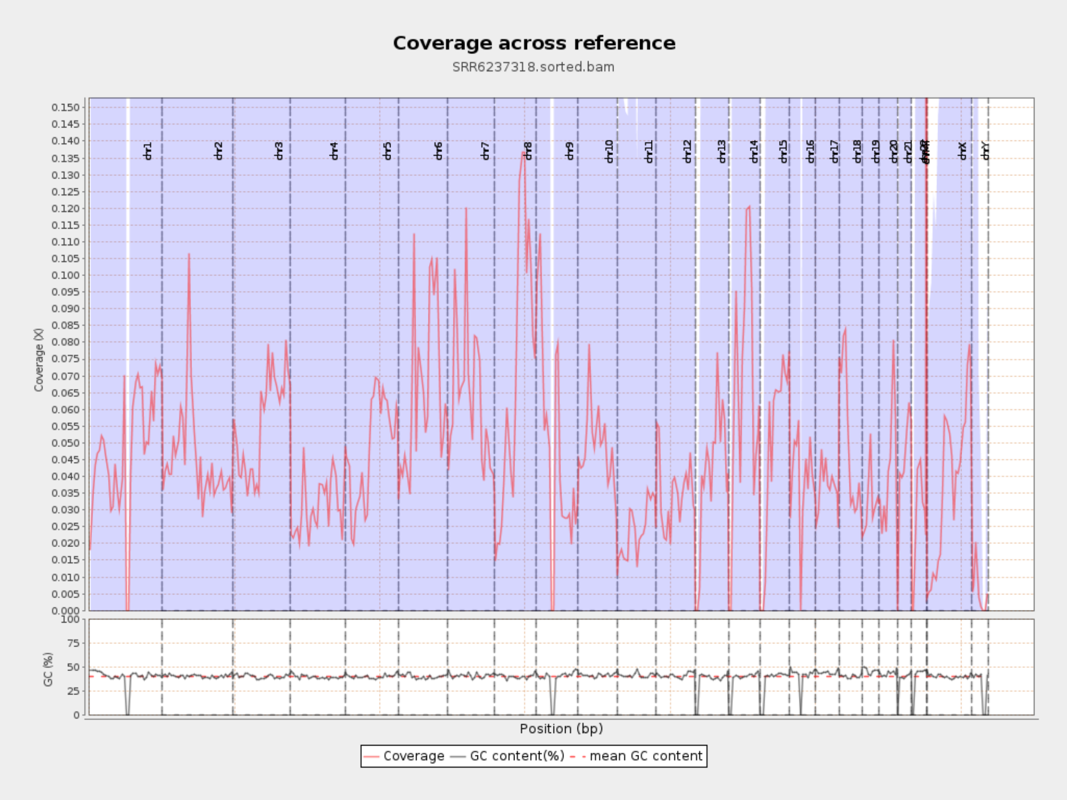
General error rate	0.82%
Mismatches	1,143,811
Insertions	11,524
Mapped reads with at least one insertion	0.55%
Deletions	39,737
Mapped reads with at least one deletion	1.88%
Homopolymer indels	46.94%

2.6. Chromosome stats

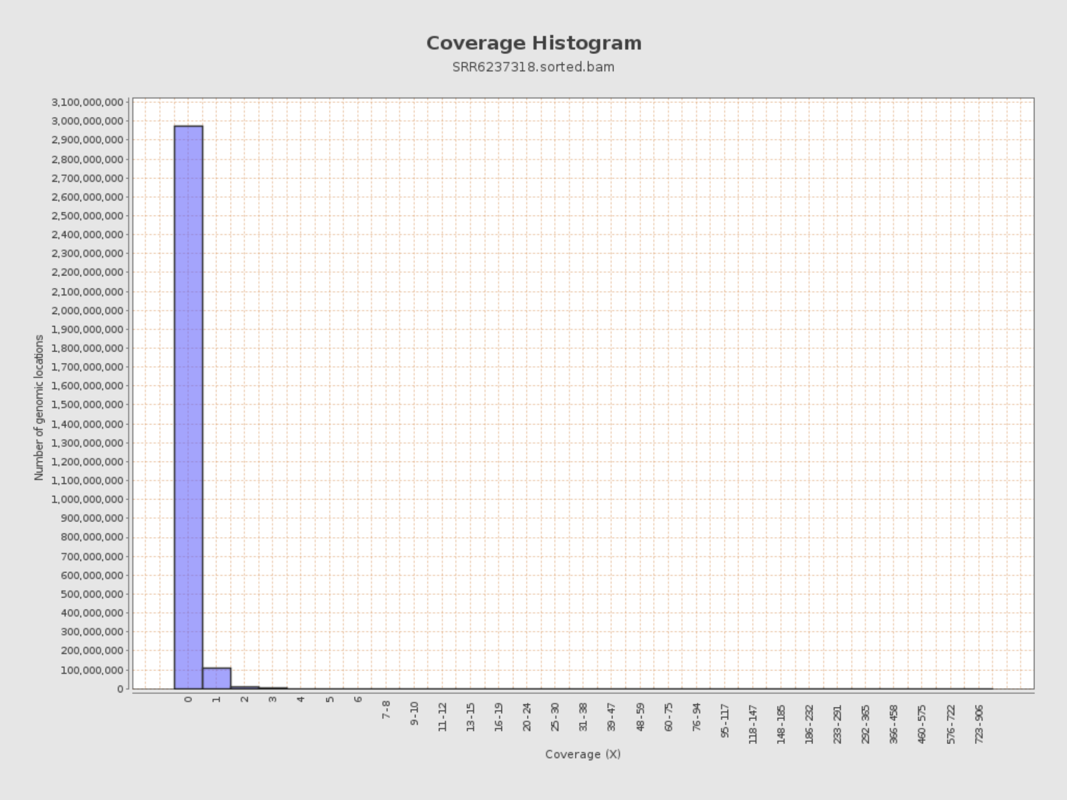
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11888449	0.0477	0.717
chr2	243199373	11096861	0.0456	0.483
chr3	198022430	11040665	0.0558	0.2614
chr4	191154276	5859903	0.0307	0.2308
chr5	180915260	8749865	0.0484	0.249
chr6	171115067	11185550	0.0654	0.4355
chr7	159138663	10297550	0.0647	0.8055

chr8	146364022	10260334	0.0701	0.6817
chr9	141213431	6671885	0.0472	0.4789
chr10	135534747	6674906	0.0492	0.3898
chr11	135006516	3199431	0.0237	0.2971
chr12	133851895	4680829	0.035	0.2212
chr13	115169878	4666134	0.0405	0.2227
chr14	107349540	6856075	0.0639	0.3191
chr15	102531392	4999123	0.0488	0.251
chr16	90354753	3536833	0.0391	0.2907
chr17	81195210	2977635	0.0367	0.2563
chr18	78077248	3957874	0.0507	0.9736
chr19	59128983	1924547	0.0325	0.4842
chr20	63025520	2618866	0.0416	0.2359
chr21	48129895	2126463	0.0442	0.2807
chr22	51304566	1358201	0.0265	0.1776
chrMT	16571	18771	1.1328	1.2571
chrX	155270560	5846375	0.0377	0.2551
chrY	59373566	320881	0.0054	0.1741

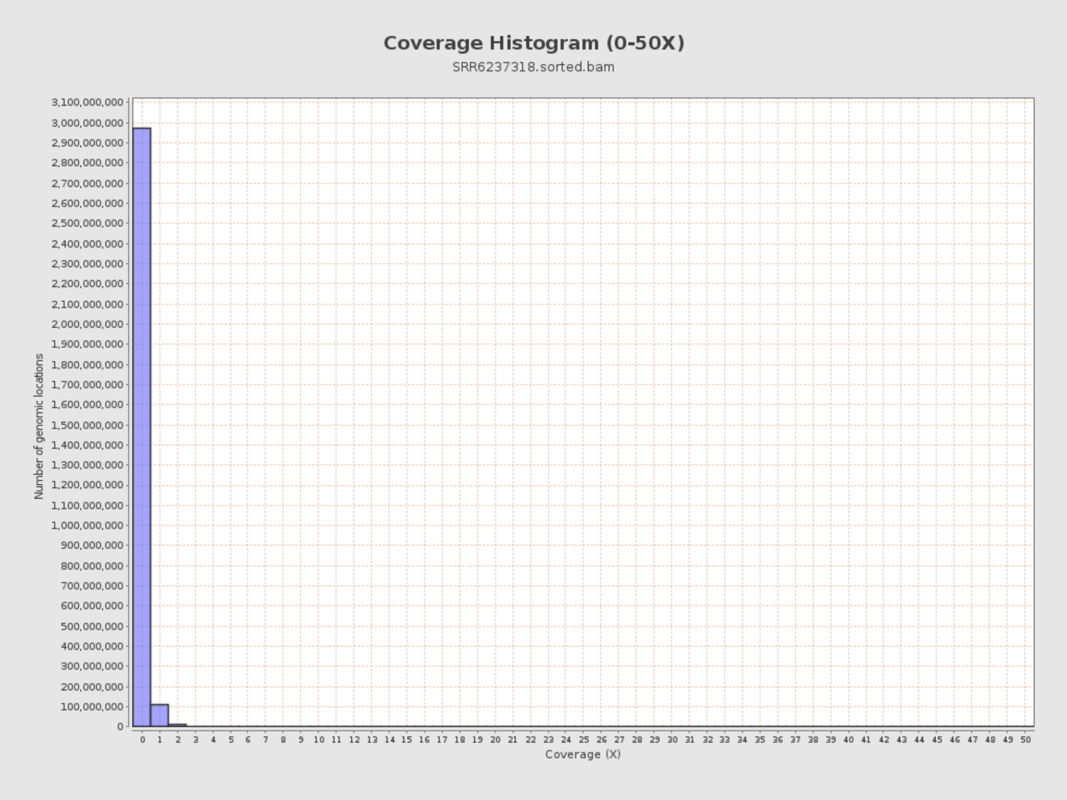
3. Results : Coverage across reference



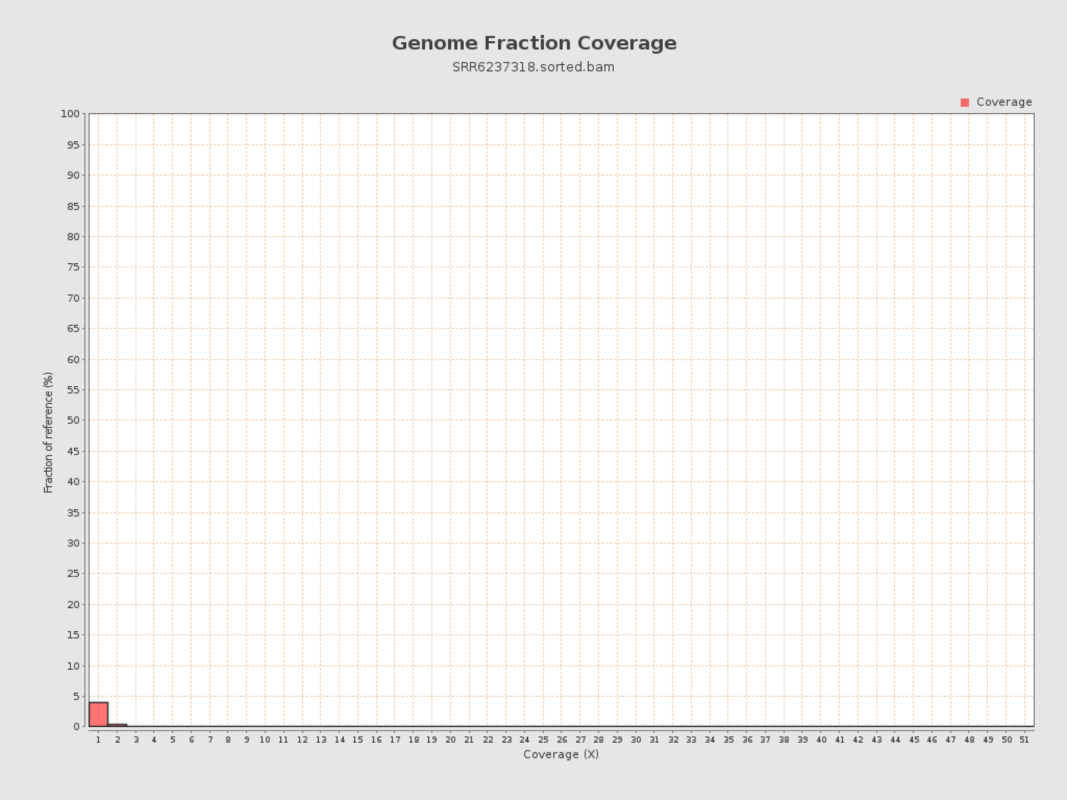
4. Results : Coverage Histogram



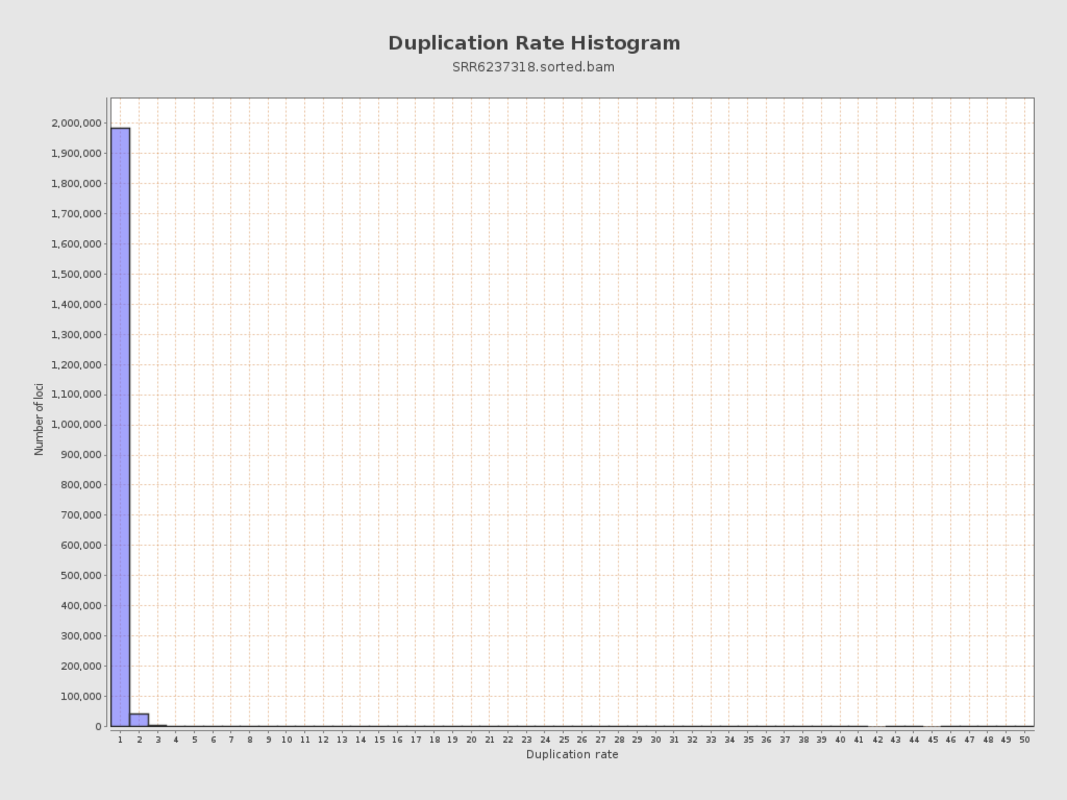
5. Results : Coverage Histogram (0-50X)



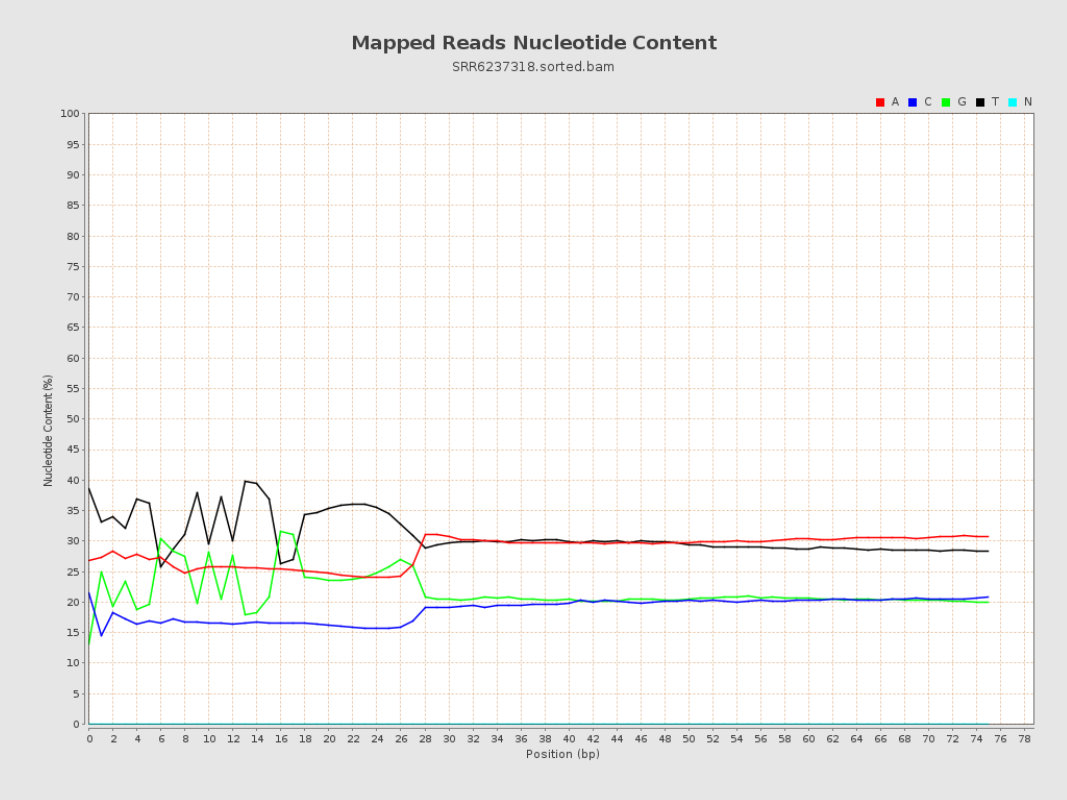
6. Results : Genome Fraction Coverage



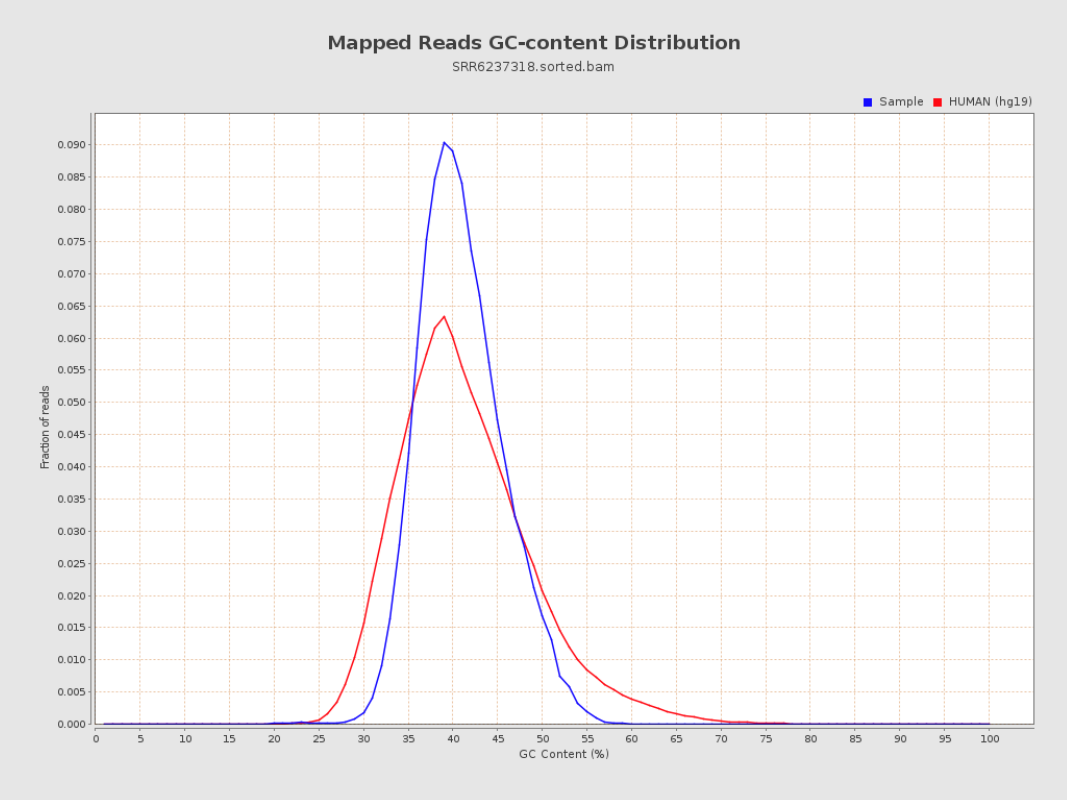
7. Results : Duplication Rate Histogram



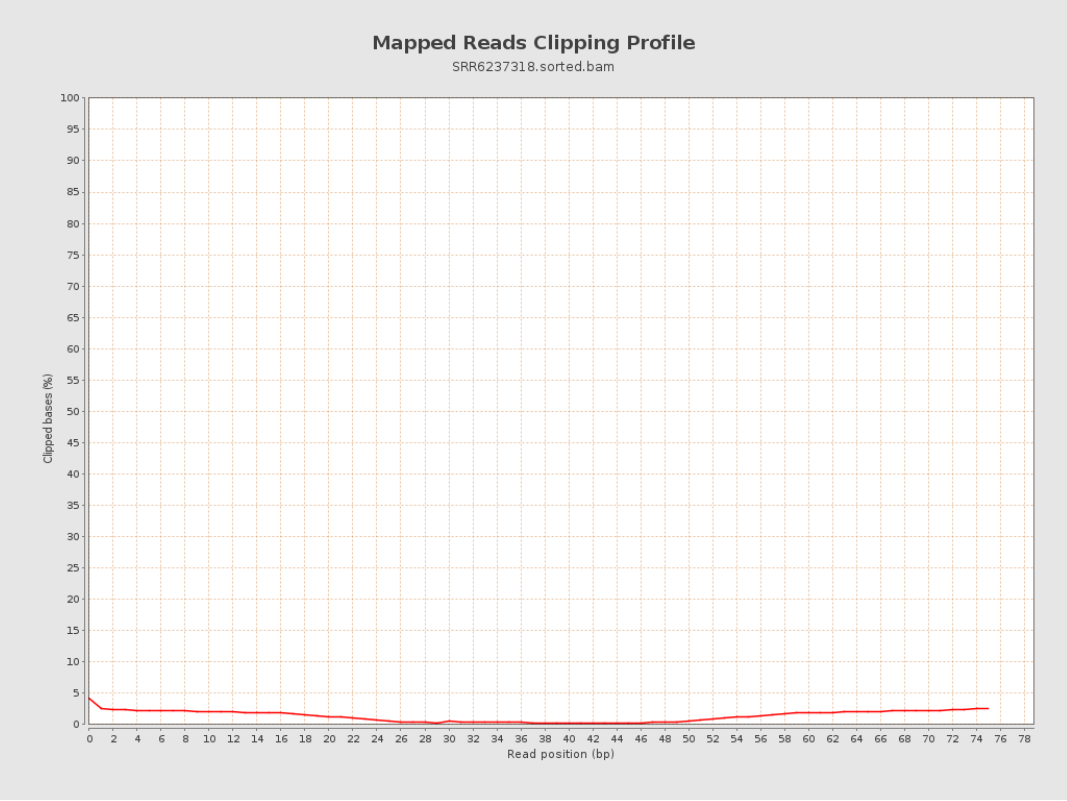
8. Results : Mapped Reads Nucleotide Content



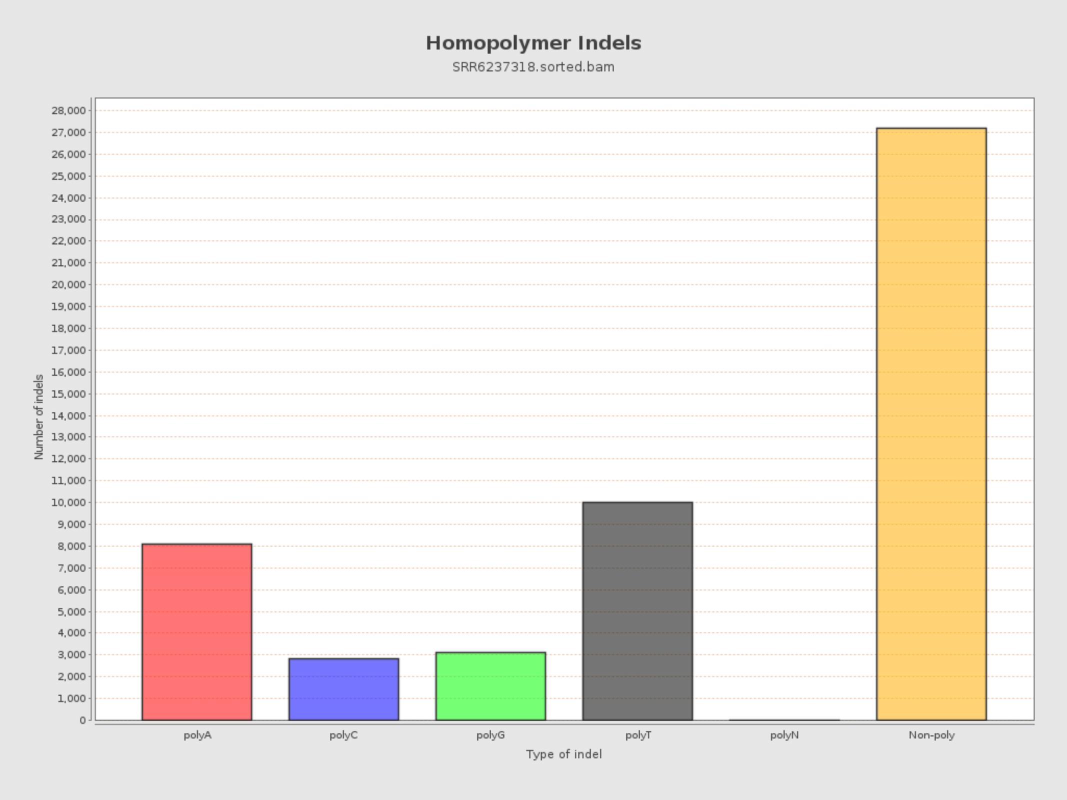
9. Results : Mapped Reads GC-content Distribution



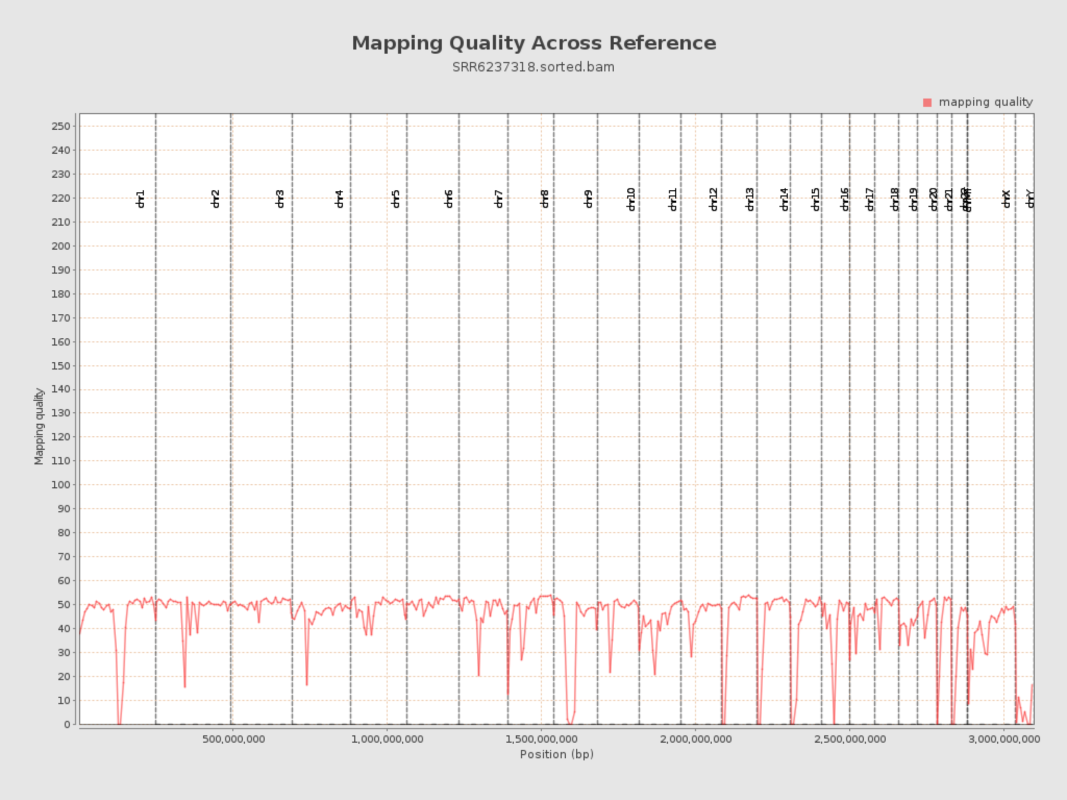
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram