Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:40:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237255.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_SRR6237255 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237255.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:40:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,995,040
Mapped reads	2,684,112 / 89.62%
Unmapped reads	310,928 / 10.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,275 / 1.18%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	972,452 / 32.47%
Duplication rate	22.53%
Clipped reads	1,780,629 / 59.45%

2.2. ACGT Content

Number/percentage of A's	42,695,382 / 25.77%
Number/percentage of C's	28,472,335 / 17.19%
Number/percentage of T's	55,344,471 / 33.41%
Number/percentage of G's	39,117,030 / 23.61%
Number/percentage of N's	17,464 / 0.01%
GC Percentage	40.8%

2.3. Coverage

Mean	0.0535

Standard Deviation	0.8844

2.4. Mapping Quality

Mean Mapping Quality	44.23

2.5. Mismatches and indels

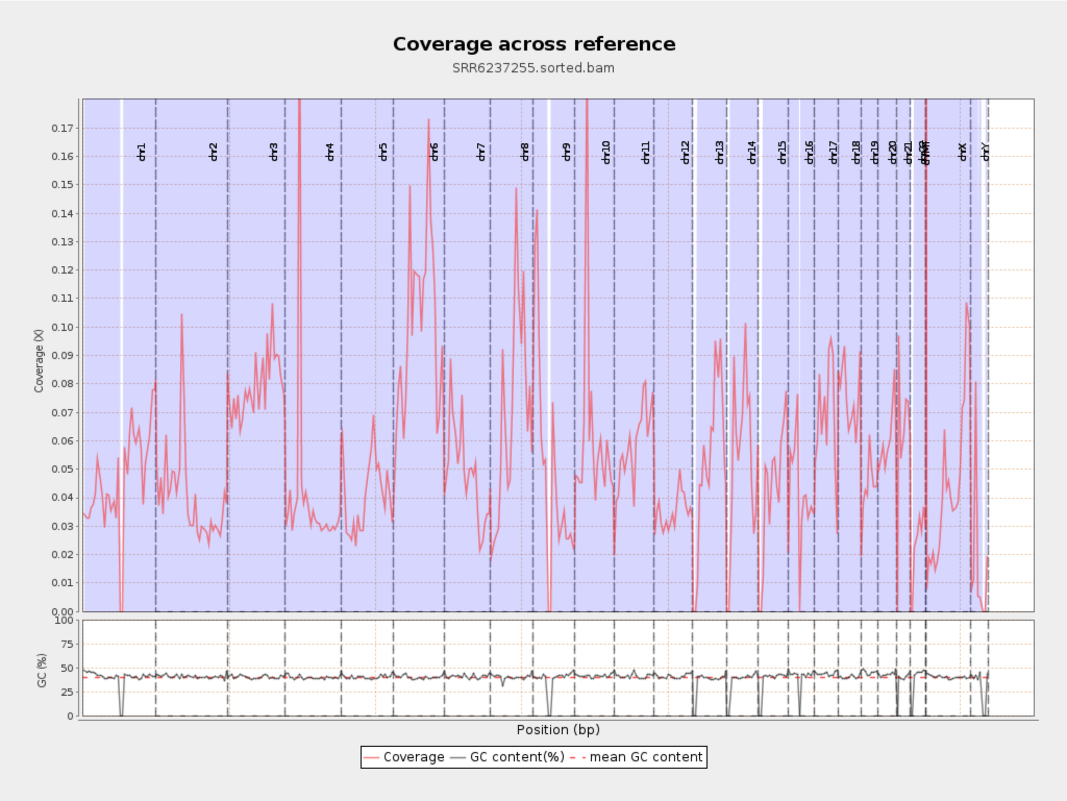
General error rate	0.72%
Mismatches	1,143,858
Insertions	16,922
Mapped reads with at least one insertion	0.62%
Deletions	43,325
Mapped reads with at least one deletion	1.59%
Homopolymer indels	42.66%

2.6. Chromosome stats

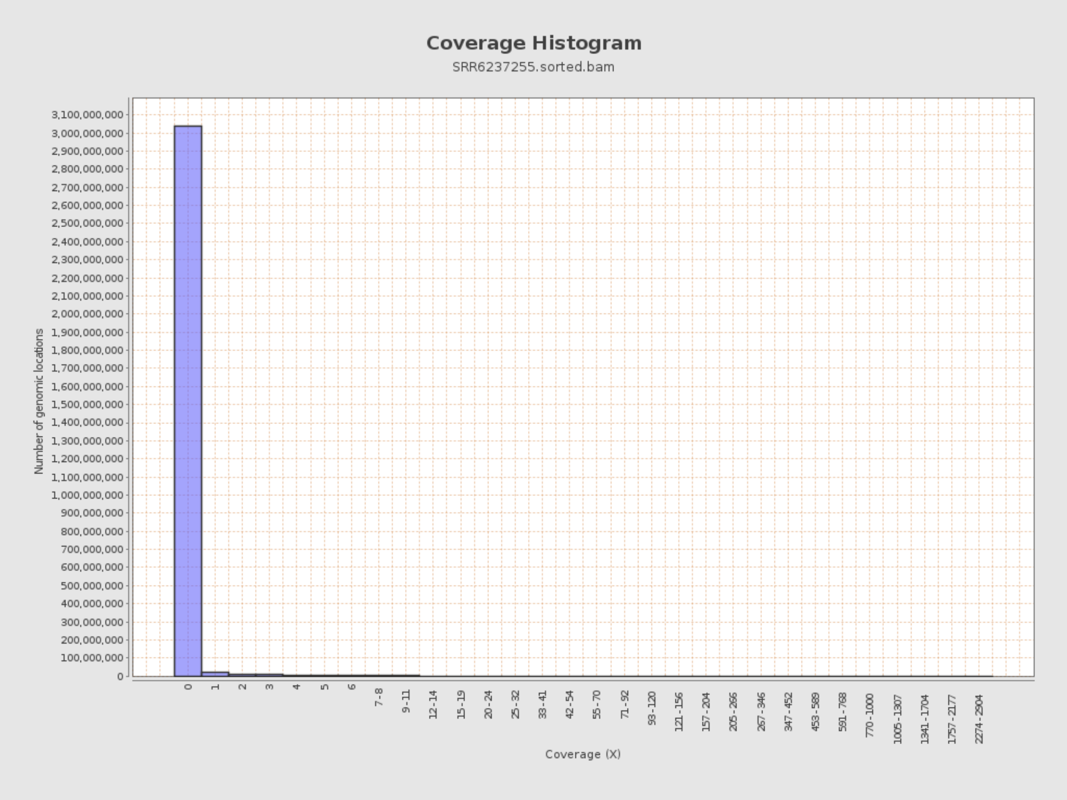
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11547325	0.0463	0.6201
chr2	243199373	9833169	0.0404	1.5256
chr3	198022430	15705879	0.0793	0.6336
chr4	191154276	7963030	0.0417	0.942
chr5	180915260	7433412	0.0411	0.4537
chr6	171115067	17298010	0.1011	0.8395
chr7	159138663	7759938	0.0488	0.5976

chr8	146364022	10294817	0.0703	1.8557
chr9	141213431	6944121	0.0492	0.5898
chr10	135534747	8296674	0.0612	1.2674
chr11	135006516	7861627	0.0582	0.6067
chr12	133851895	4686038	0.035	0.4381
chr13	115169878	6095959	0.0529	0.5524
chr14	107349540	5713356	0.0532	0.5281
chr15	102531392	4358675	0.0425	0.4726
chr16	90354753	3680266	0.0407	0.5296
chr17	81195210	5676443	0.0699	0.6742
chr18	78077248	5920528	0.0758	1.366
chr19	59128983	2653730	0.0449	0.5245
chr20	63025520	3890474	0.0617	0.6061
chr21	48129895	3099591	0.0644	0.7672
chr22	51304566	1206677	0.0235	0.3232
chrMT	16571	7395	0.4463	1.1798
chrX	155270560	6814641	0.0439	0.4964
chrY	59373566	984583	0.0166	0.8307

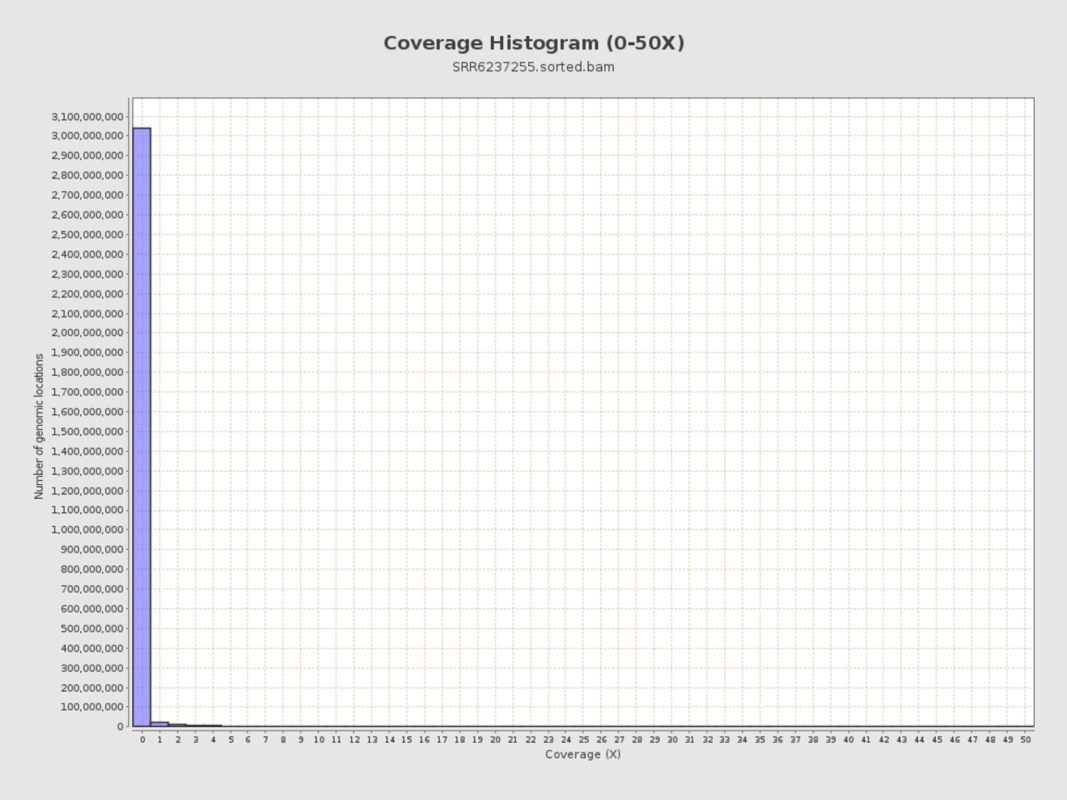
3. Results : Coverage across reference



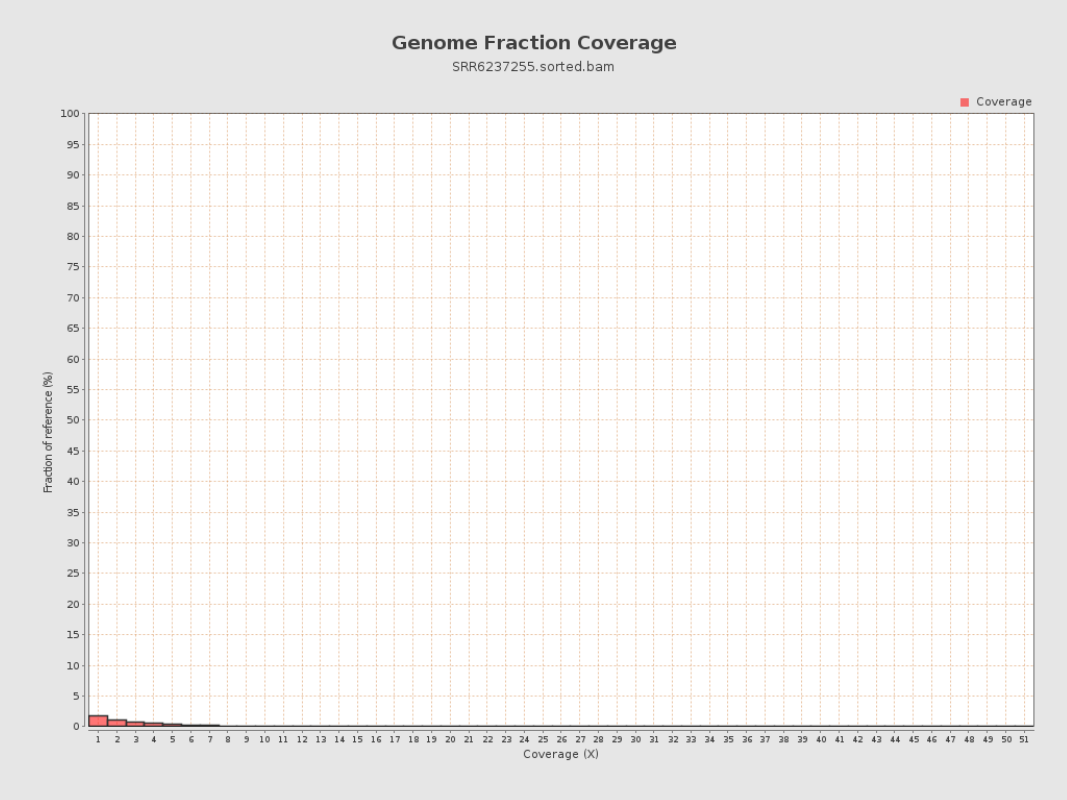
4. Results : Coverage Histogram



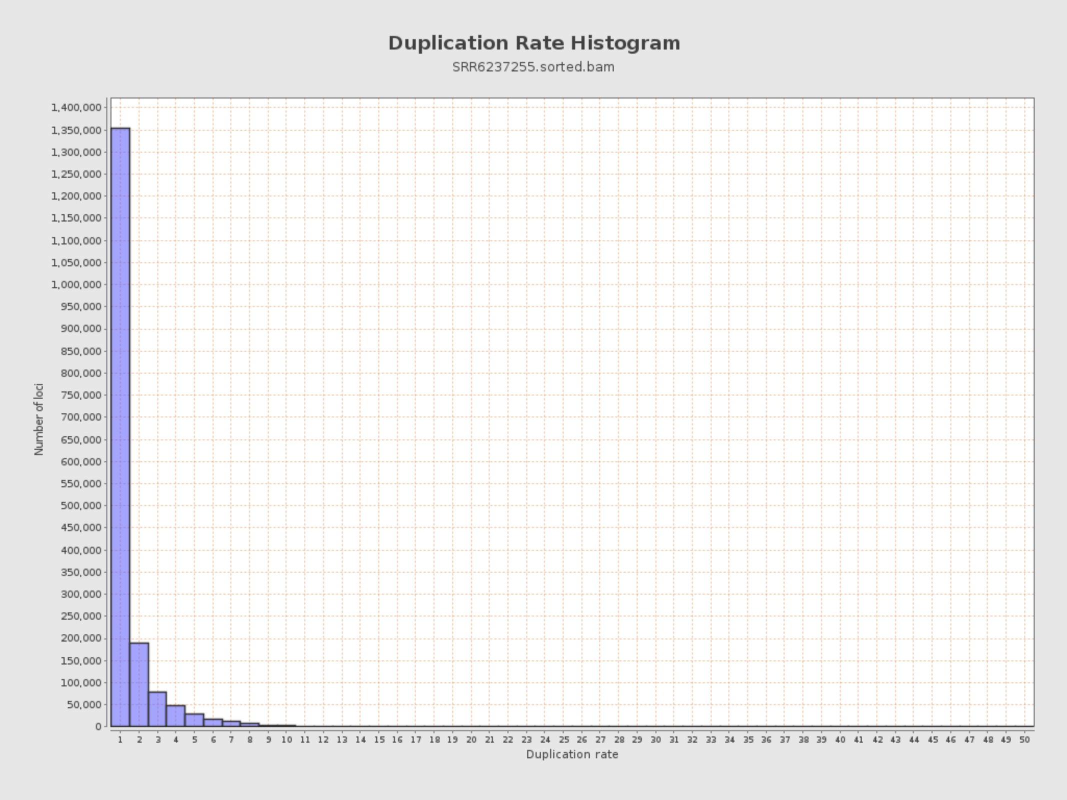
5. Results : Coverage Histogram (0-50X)



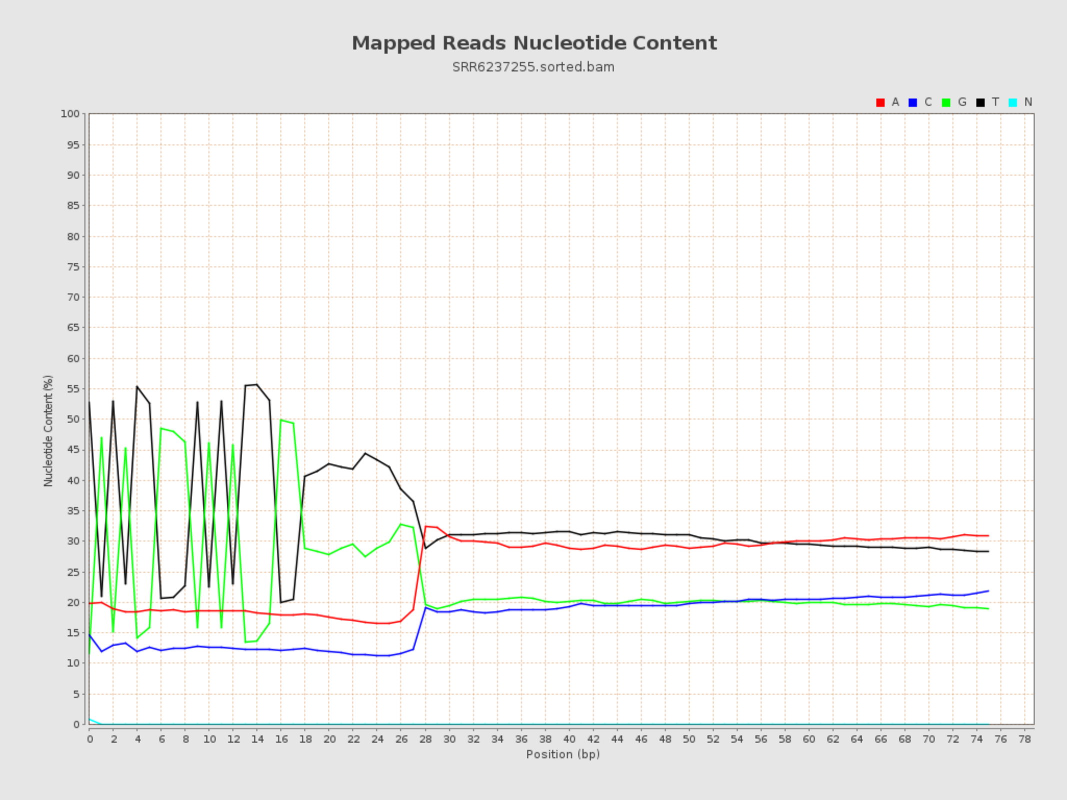
6. Results : Genome Fraction Coverage



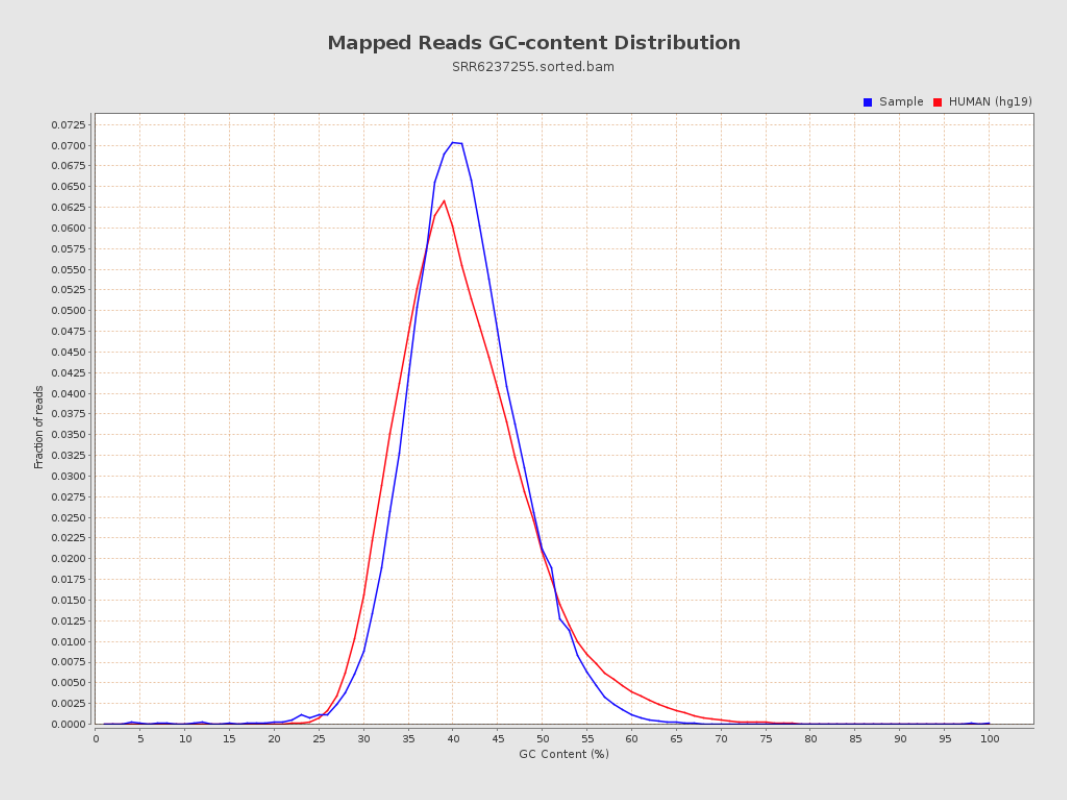
7. Results : Duplication Rate Histogram



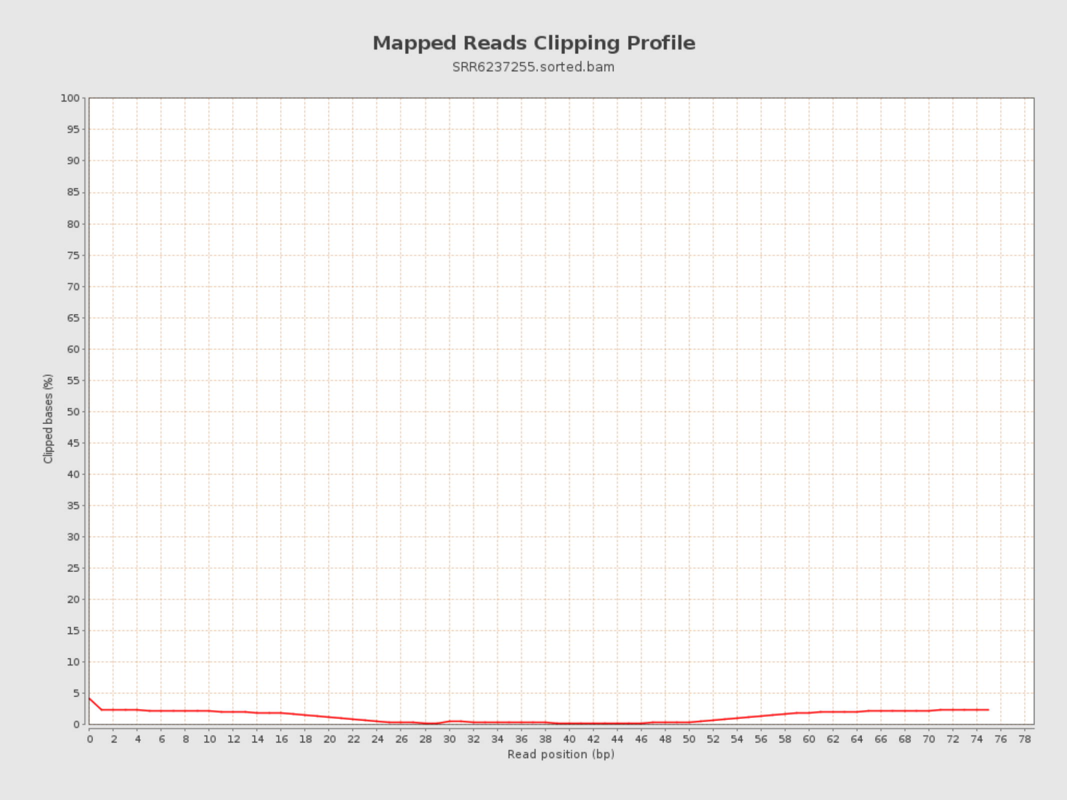
8. Results : Mapped Reads Nucleotide Content



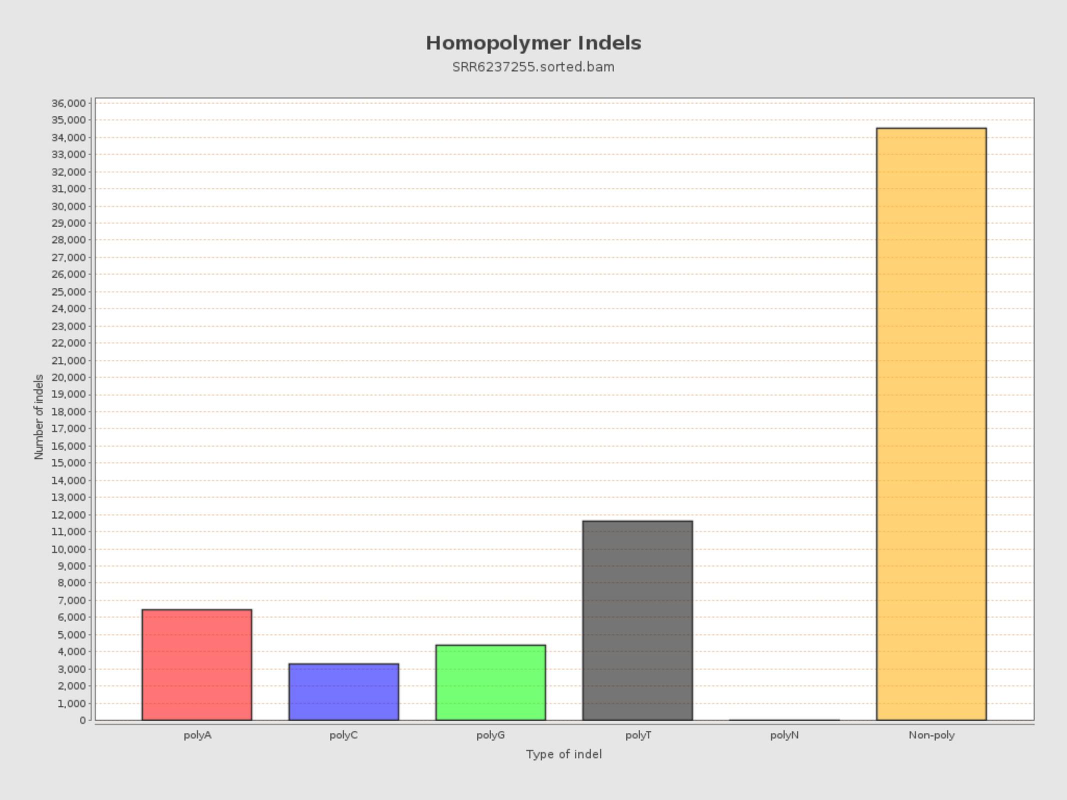
9. Results : Mapped Reads GC-content Distribution



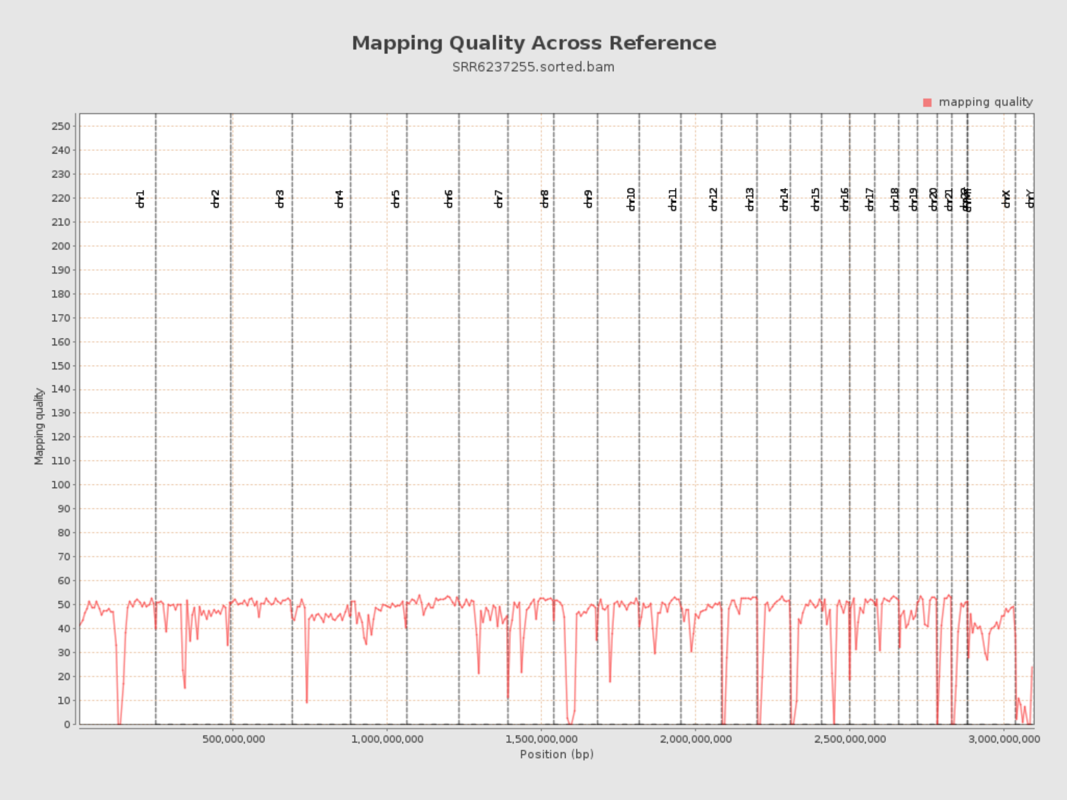
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram