Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 22:29:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237252.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_SRR6237252 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237252.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 22:29:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237252.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,844,093
Mapped reads	2,577,986 / 90.64%
Unmapped reads	266,107 / 9.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,666 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	118,496 / 4.17%
Duplication rate	2.9%
Clipped reads	1,063,244 / 37.38%

2.2. ACGT Content

Number/percentage of A's	49,824,376 / 28.49%
Number/percentage of C's	31,923,742 / 18.25%
Number/percentage of T's	55,188,778 / 31.56%
Number/percentage of G's	37,952,048 / 21.7%
Number/percentage of N's	2,945 / 0%
GC Percentage	39.95%

2.3. Coverage

Mean	0.0565

Standard Deviation	0.6187

2.4. Mapping Quality

Mean Mapping Quality	44.12

2.5. Mismatches and indels

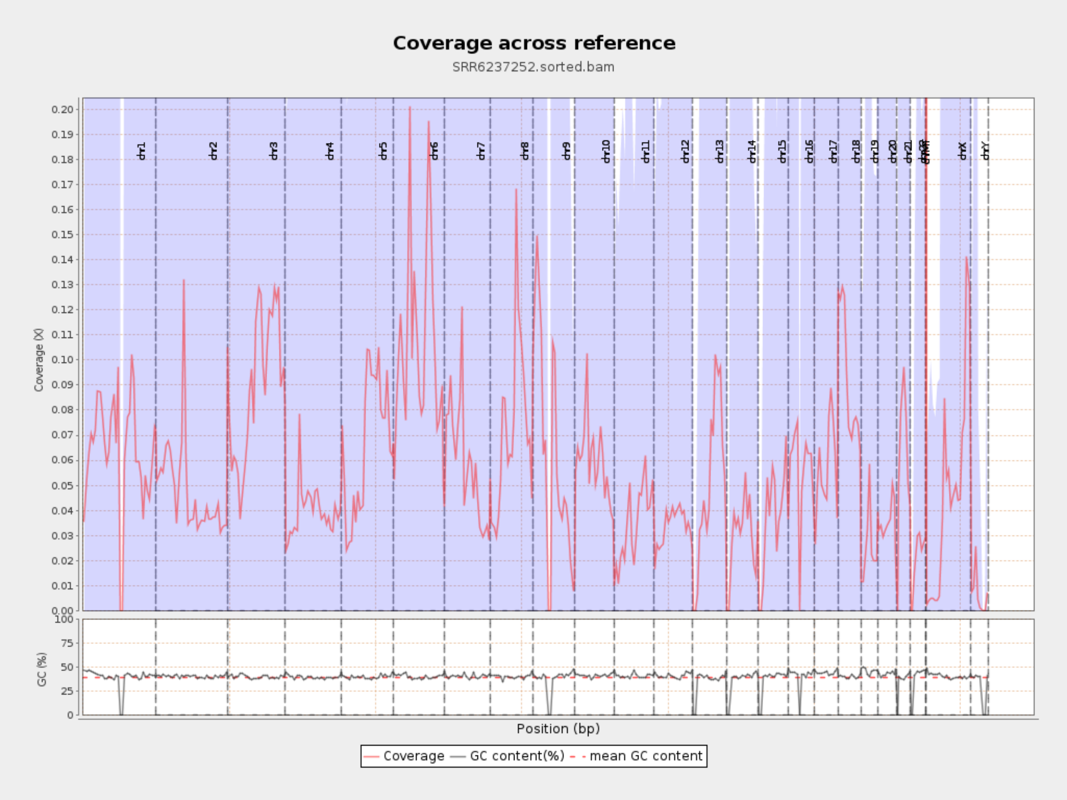
General error rate	0.82%
Mismatches	1,410,426
Insertions	15,219
Mapped reads with at least one insertion	0.59%
Deletions	43,922
Mapped reads with at least one deletion	1.68%
Homopolymer indels	47.02%

2.6. Chromosome stats

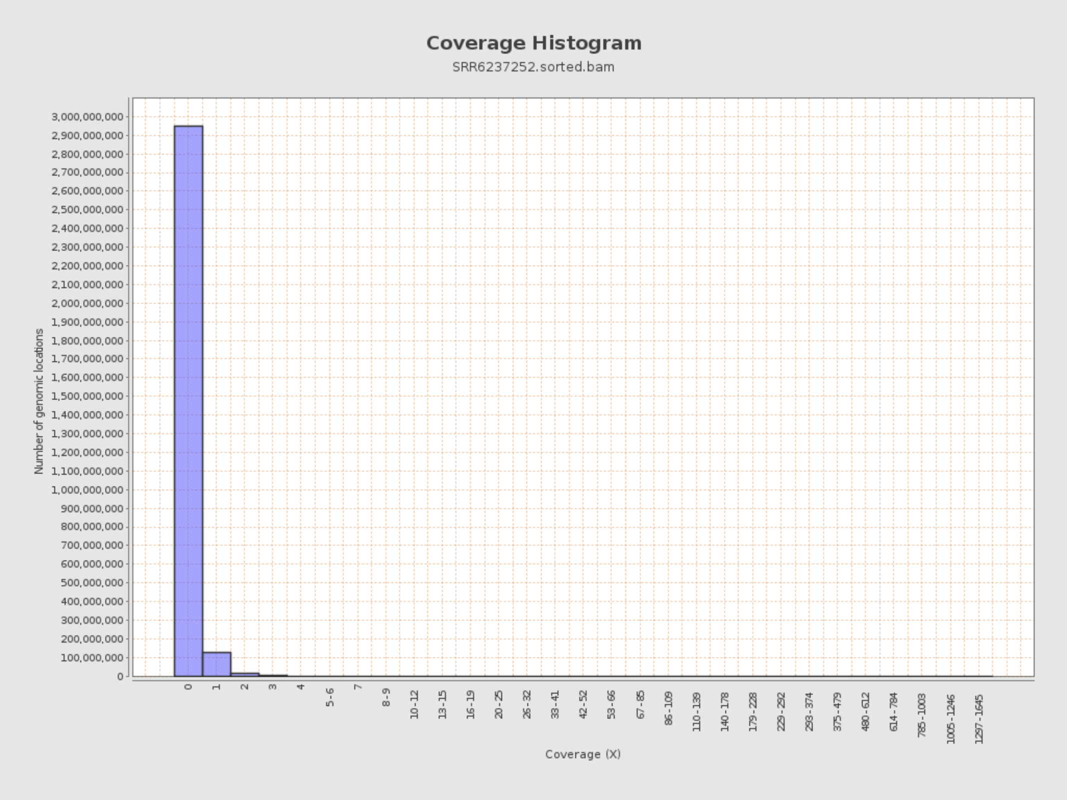
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15847151	0.0636	0.7776
chr2	243199373	11652778	0.0479	0.8033
chr3	198022430	17856472	0.0902	0.3481
chr4	191154276	7582346	0.0397	0.3237
chr5	180915260	12175110	0.0673	0.3063
chr6	171115067	18522221	0.1082	0.8534
chr7	159138663	9341826	0.0587	0.9322

chr8	146364022	10581035	0.0723	1.1169
chr9	141213431	8945108	0.0633	0.7307
chr10	135534747	8046200	0.0594	0.5517
chr11	135006516	4703209	0.0348	0.4295
chr12	133851895	4478700	0.0335	0.2575
chr13	115169878	5876196	0.051	0.2583
chr14	107349540	3146602	0.0293	0.3413
chr15	102531392	3740807	0.0365	0.2335
chr16	90354753	4941265	0.0547	0.3608
chr17	81195210	4714104	0.0581	0.387
chr18	78077248	7297466	0.0935	1.1895
chr19	59128983	1553812	0.0263	0.6268
chr20	63025520	2274510	0.0361	0.2549
chr21	48129895	2959439	0.0615	0.3948
chr22	51304566	1037881	0.0202	0.1568
chrMT	16571	113298	6.8371	5.0355
chrX	155270560	7172137	0.0462	0.3456
chrY	59373566	405320	0.0068	0.2271

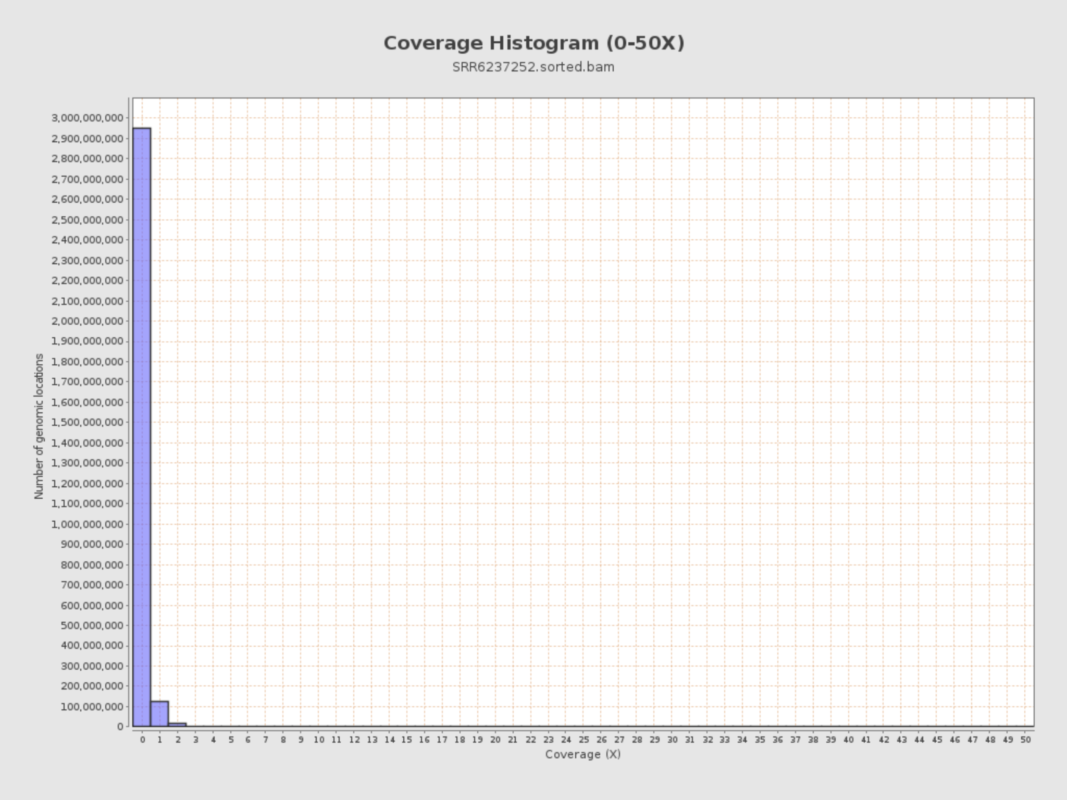
3. Results : Coverage across reference



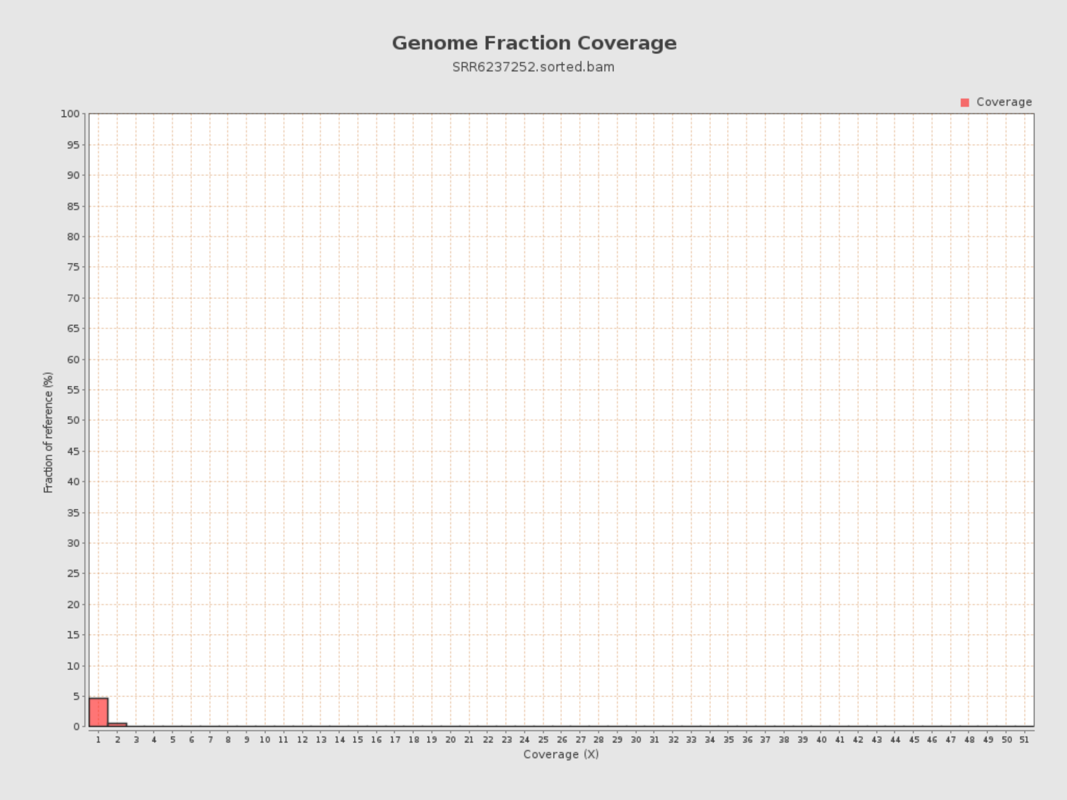
4. Results : Coverage Histogram



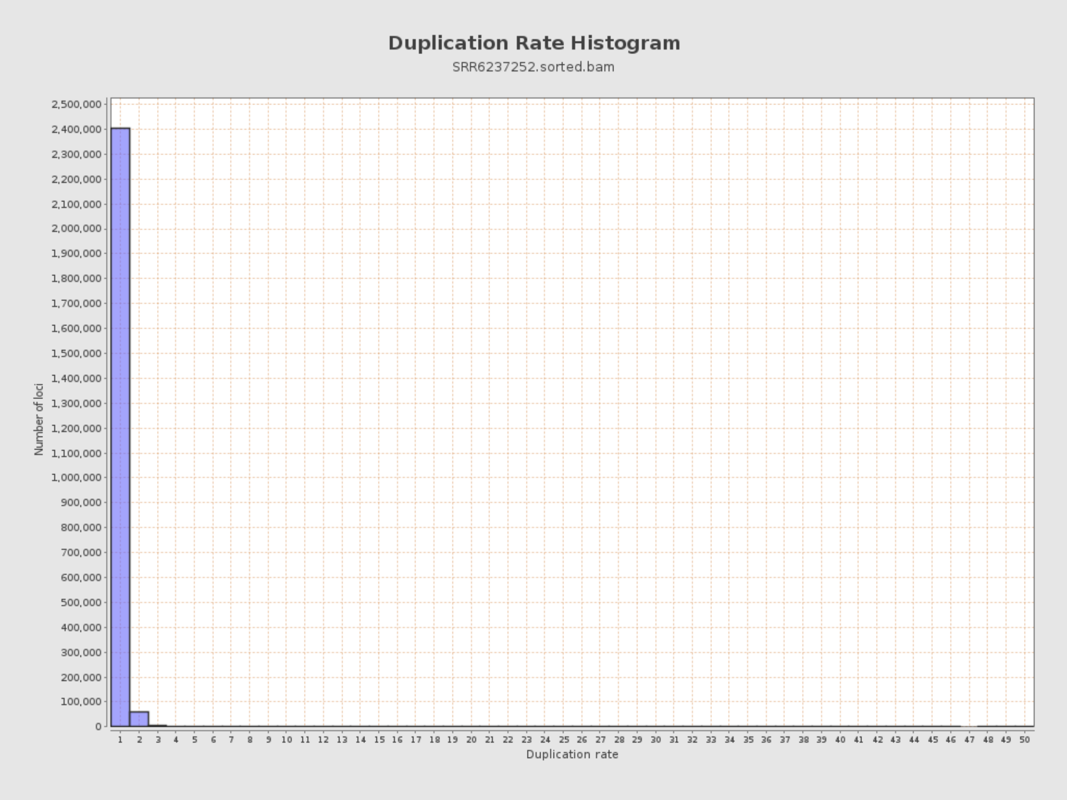
5. Results : Coverage Histogram (0-50X)



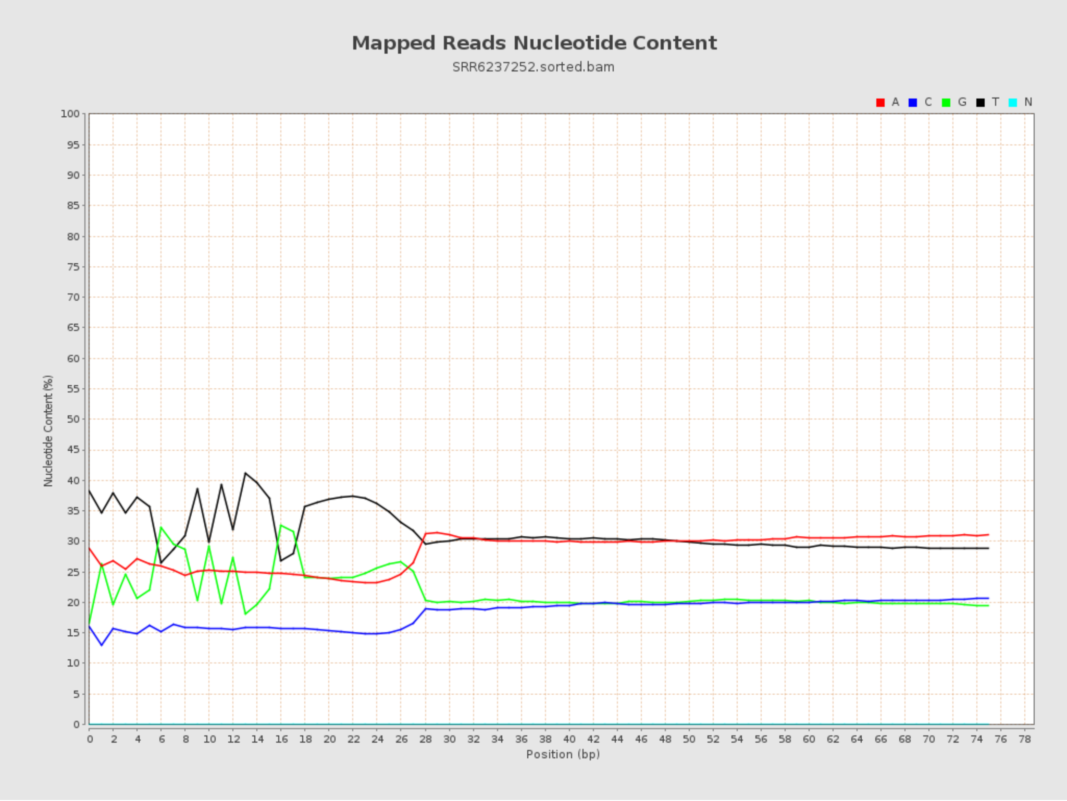
6. Results : Genome Fraction Coverage



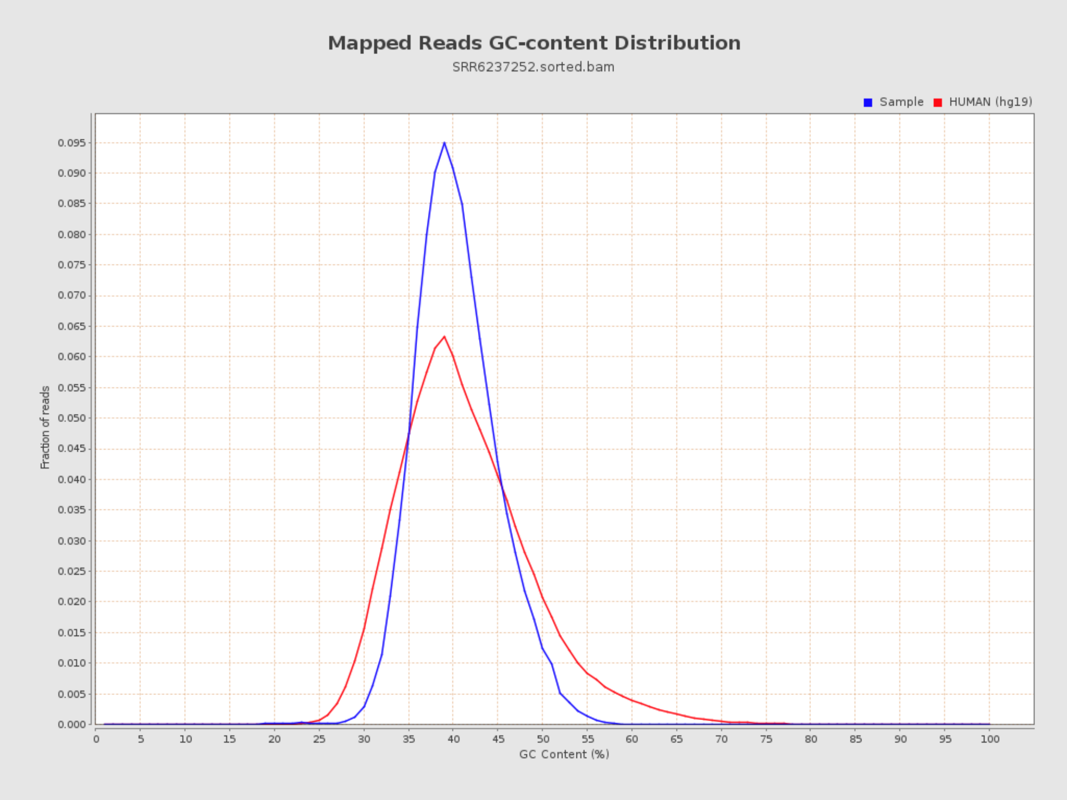
7. Results : Duplication Rate Histogram



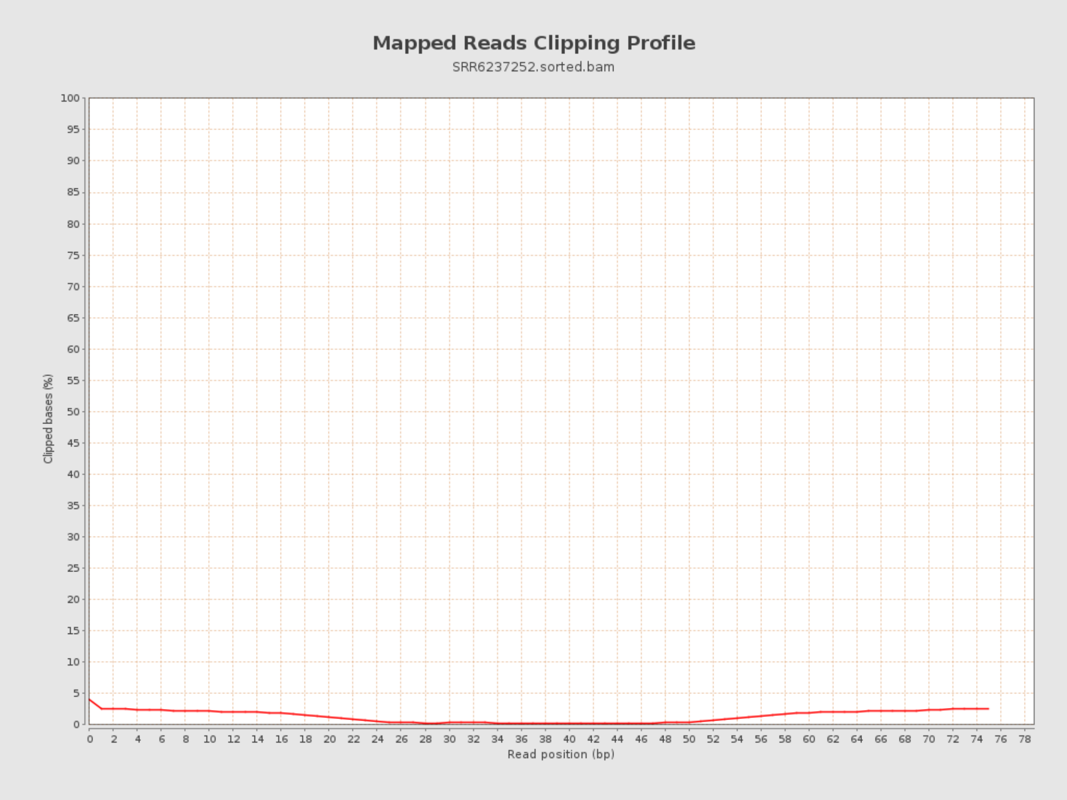
8. Results : Mapped Reads Nucleotide Content



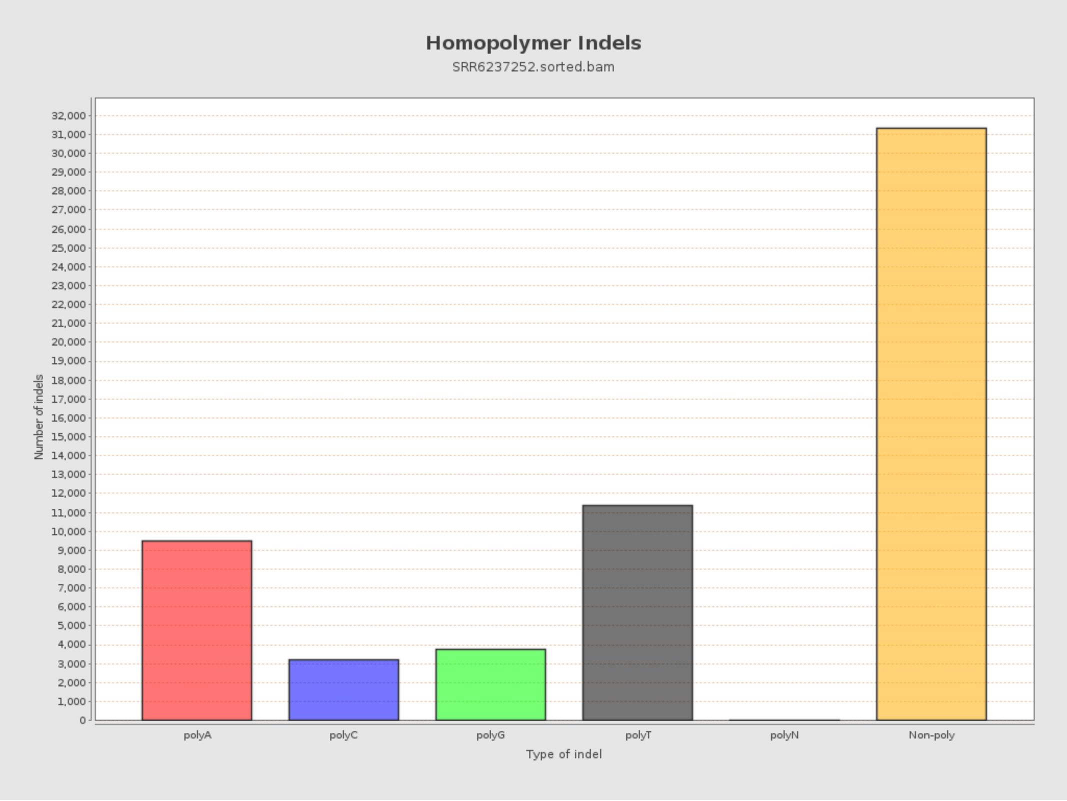
9. Results : Mapped Reads GC-content Distribution



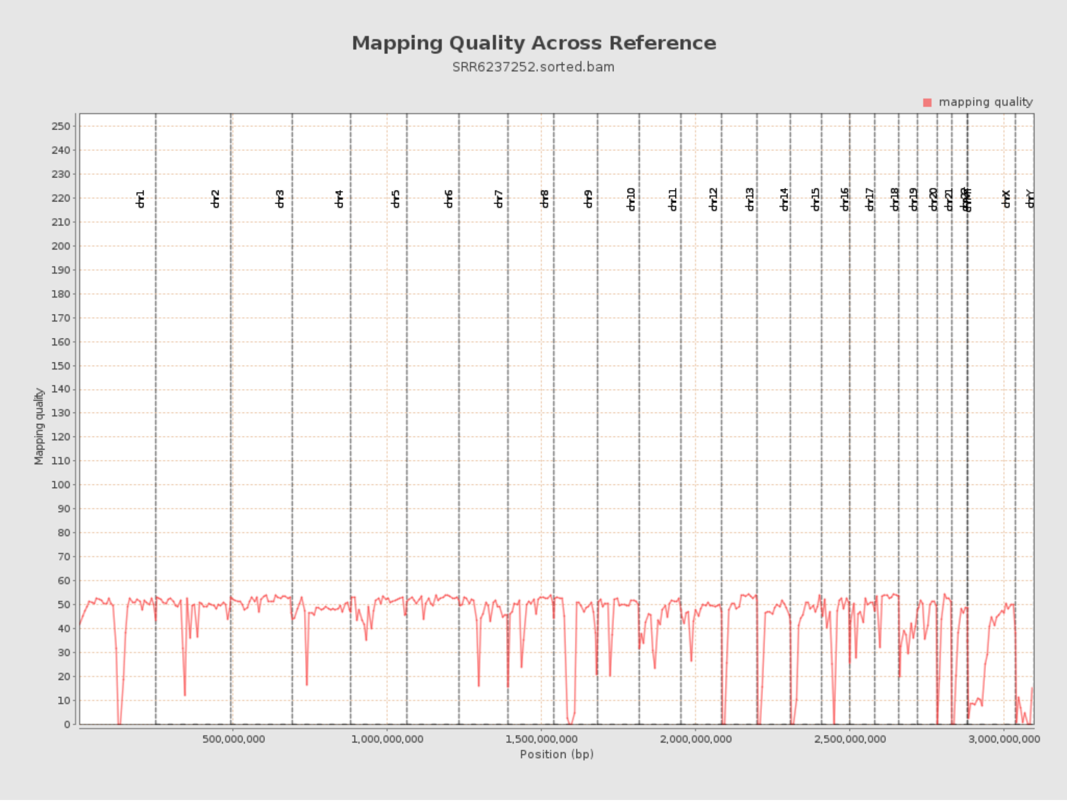
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram