Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:41:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237571.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_SRR6237571 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237571.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:40:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237571.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,994,201
Mapped reads	1,557,204 / 78.09%
Unmapped reads	436,997 / 21.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,771 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	90,648 / 4.55%
Duplication rate	4.8%
Clipped reads	769,196 / 38.57%

2.2. ACGT Content

Number/percentage of A's	28,688,576 / 28.15%
Number/percentage of C's	18,342,720 / 18%
Number/percentage of T's	32,858,158 / 32.25%
Number/percentage of G's	21,820,427 / 21.41%
Number/percentage of N's	190,385 / 0.19%
GC Percentage	39.41%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.3396

2.4. Mapping Quality

Mean Mapping Quality	46.75

2.5. Mismatches and indels

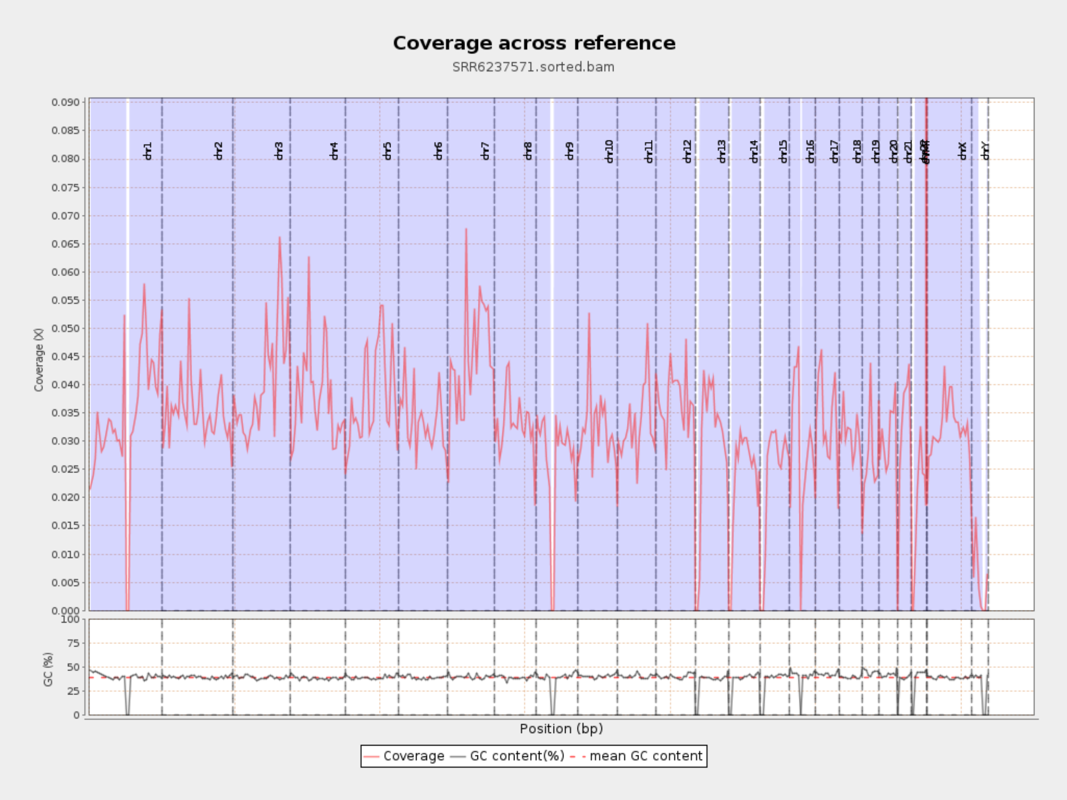
General error rate	0.98%
Mismatches	985,104
Insertions	8,669
Mapped reads with at least one insertion	0.55%
Deletions	37,952
Mapped reads with at least one deletion	2.4%
Homopolymer indels	46.55%

2.6. Chromosome stats

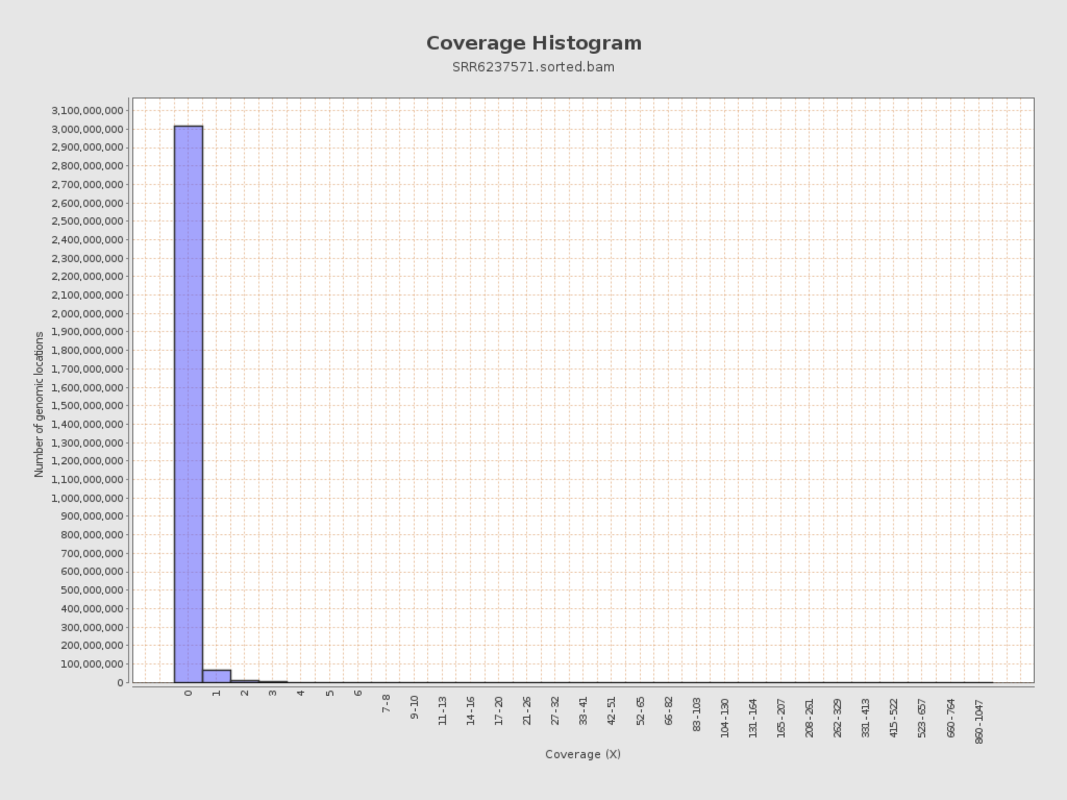
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8536376	0.0342	0.5753
chr2	243199373	8613882	0.0354	0.3332
chr3	198022430	8044332	0.0406	0.2454
chr4	191154276	7257815	0.038	0.247
chr5	180915260	6917114	0.0382	0.2389
chr6	171115067	5736881	0.0335	0.2623
chr7	159138663	7236055	0.0455	0.4735

chr8	146364022	4806046	0.0328	0.6459
chr9	141213431	3713224	0.0263	0.2644
chr10	135534747	4409925	0.0325	0.3042
chr11	135006516	4417469	0.0327	0.2661
chr12	133851895	4983727	0.0372	0.2407
chr13	115169878	3327885	0.0289	0.2091
chr14	107349540	2481165	0.0231	0.2029
chr15	102531392	2406772	0.0235	0.1862
chr16	90354753	2633328	0.0291	0.2181
chr17	81195210	2710705	0.0334	0.2426
chr18	78077248	2428405	0.0311	0.4809
chr19	59128983	1604281	0.0271	0.3827
chr20	63025520	1935099	0.0307	0.2219
chr21	48129895	1506824	0.0313	0.2249
chr22	51304566	907789	0.0177	0.1586
chrMT	16571	49687	2.9984	2.5786
chrX	155270560	4983625	0.0321	0.2335
chrY	59373566	314068	0.0053	0.1172

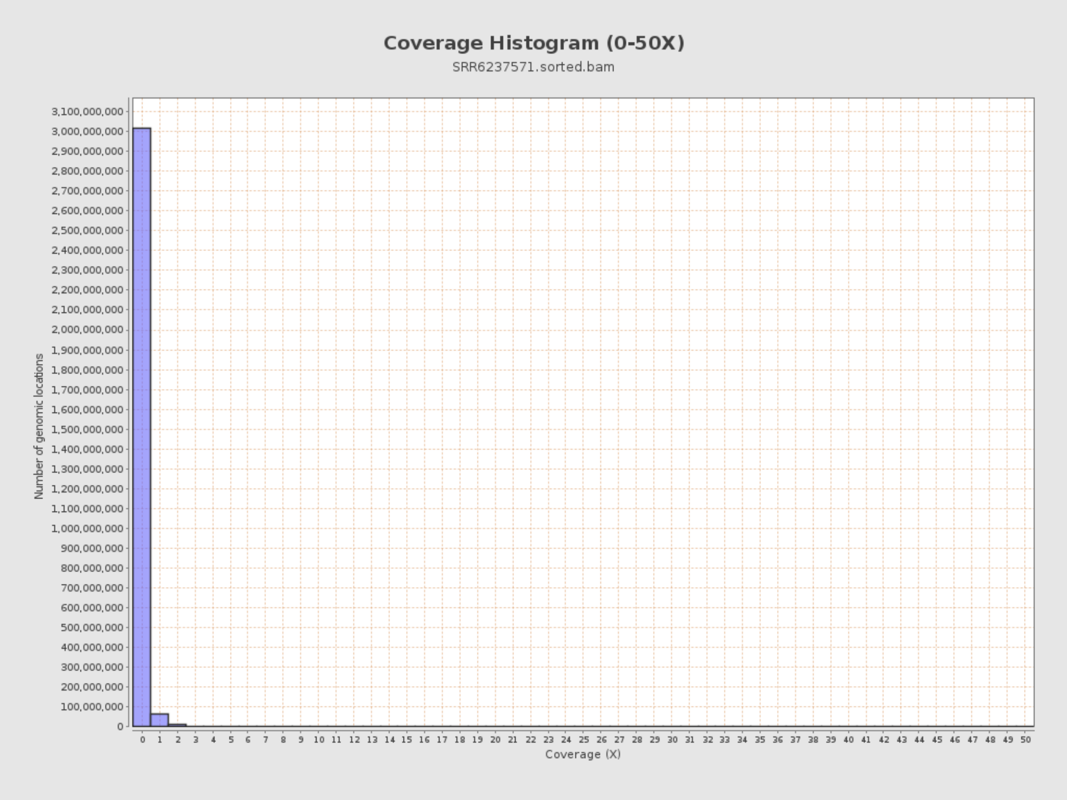
3. Results : Coverage across reference



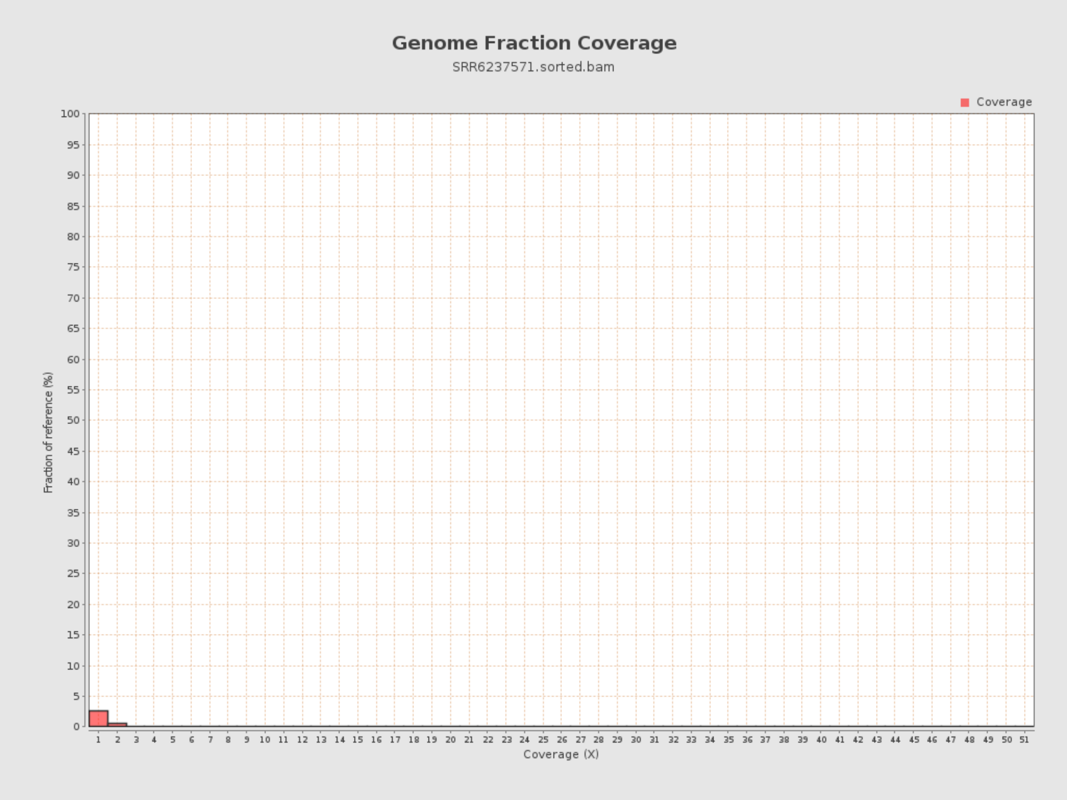
4. Results : Coverage Histogram



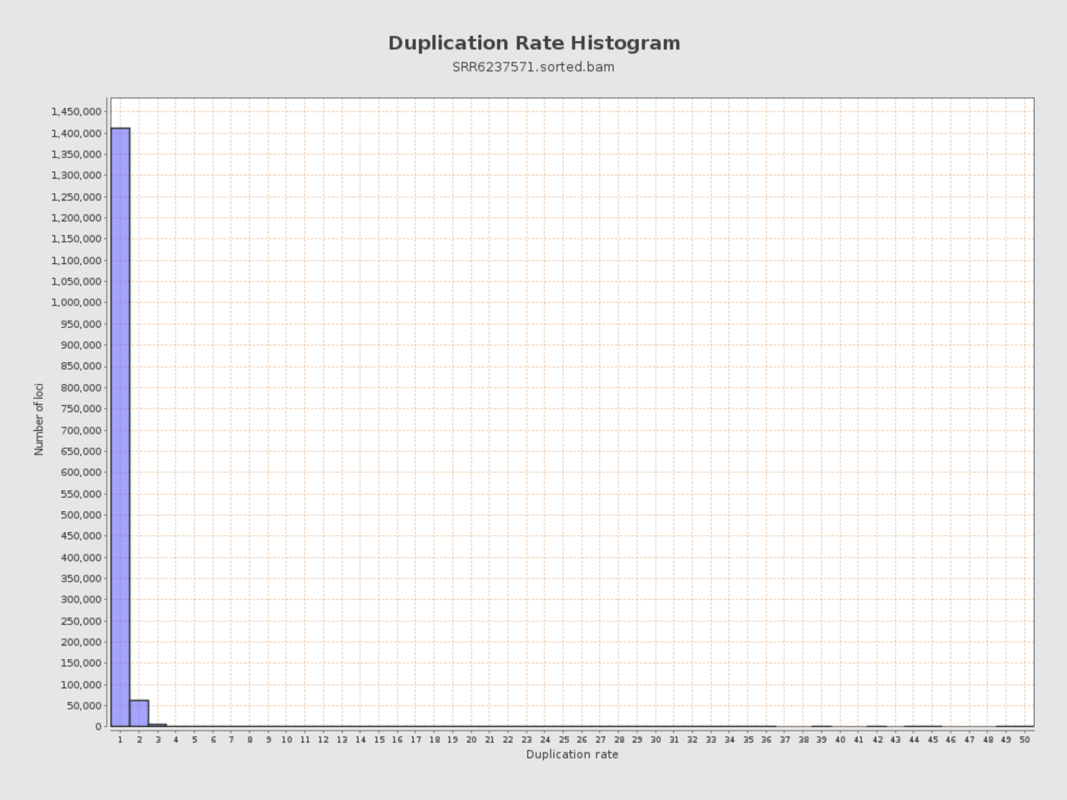
5. Results : Coverage Histogram (0-50X)



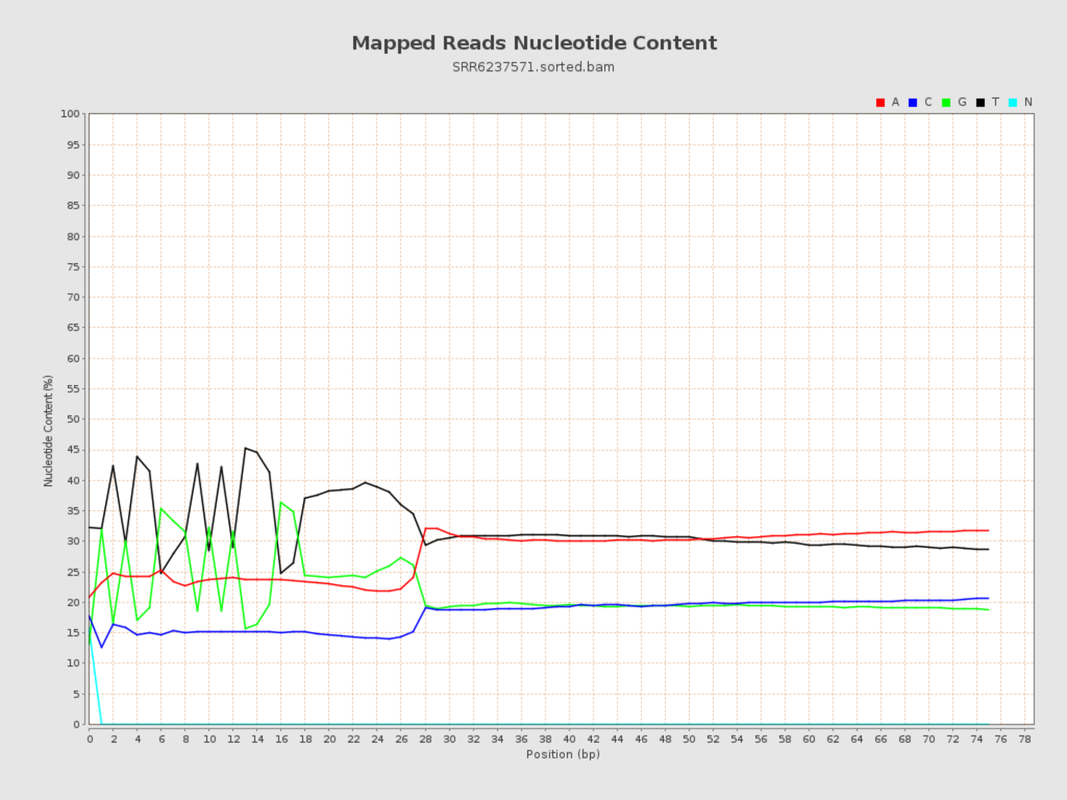
6. Results : Genome Fraction Coverage



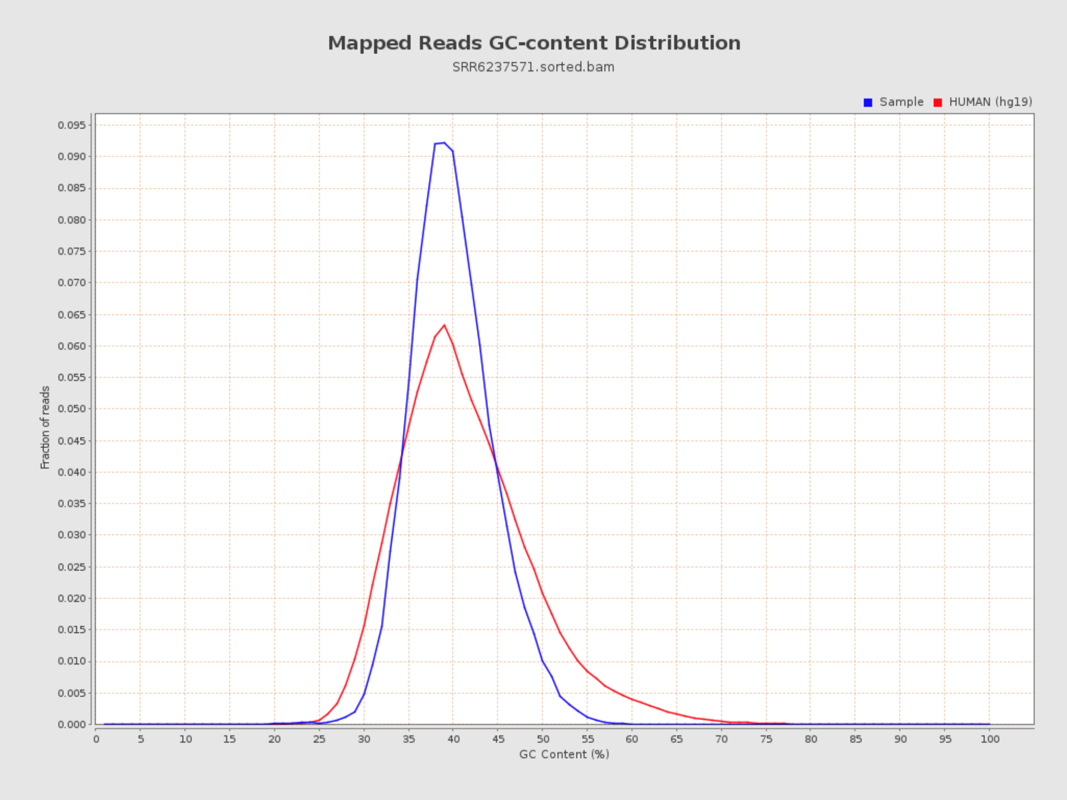
7. Results : Duplication Rate Histogram



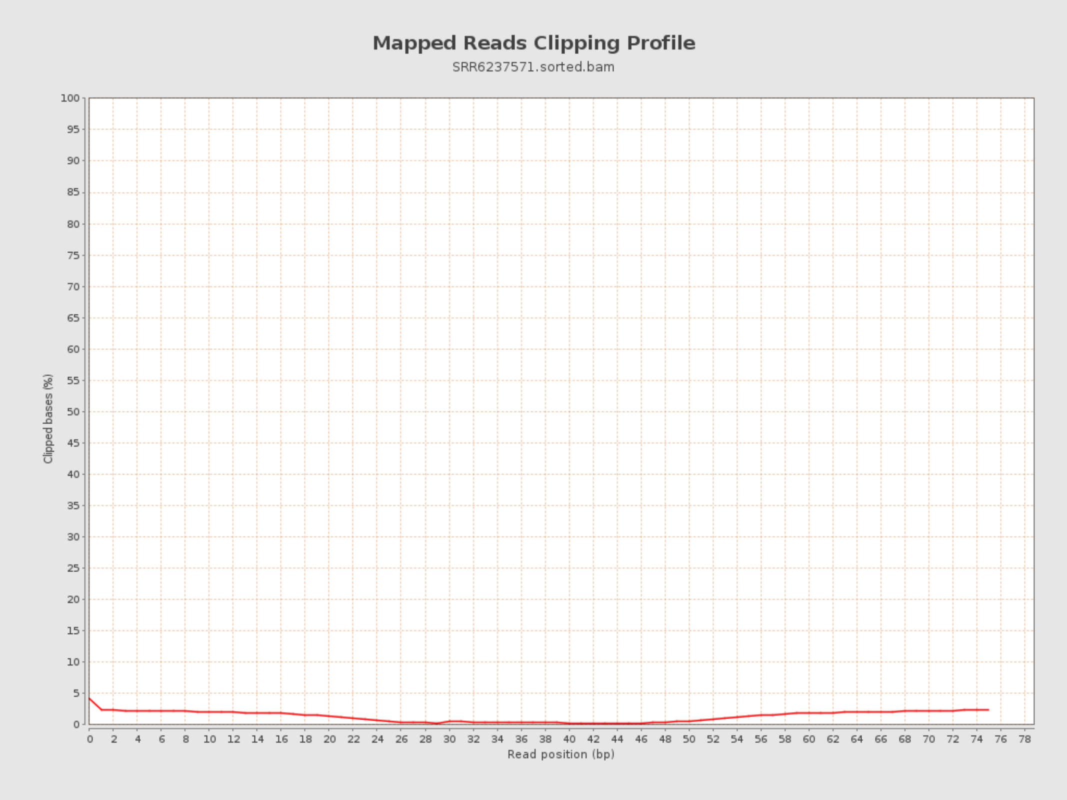
8. Results : Mapped Reads Nucleotide Content



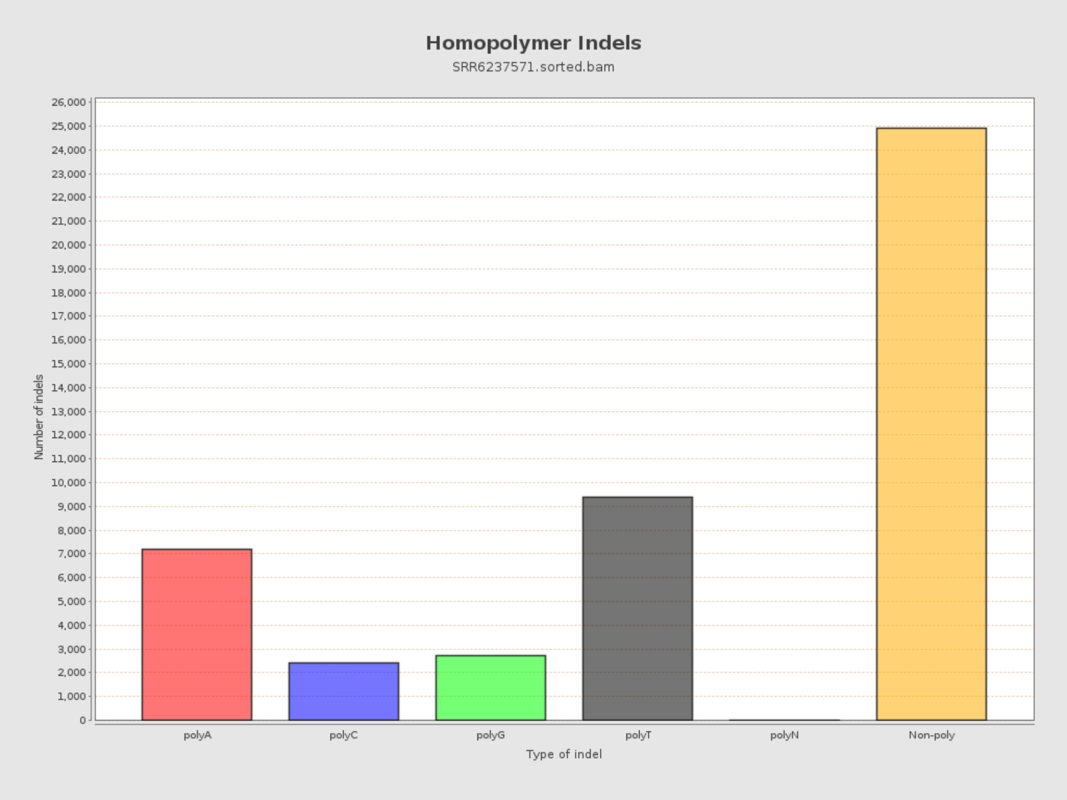
9. Results : Mapped Reads GC-content Distribution



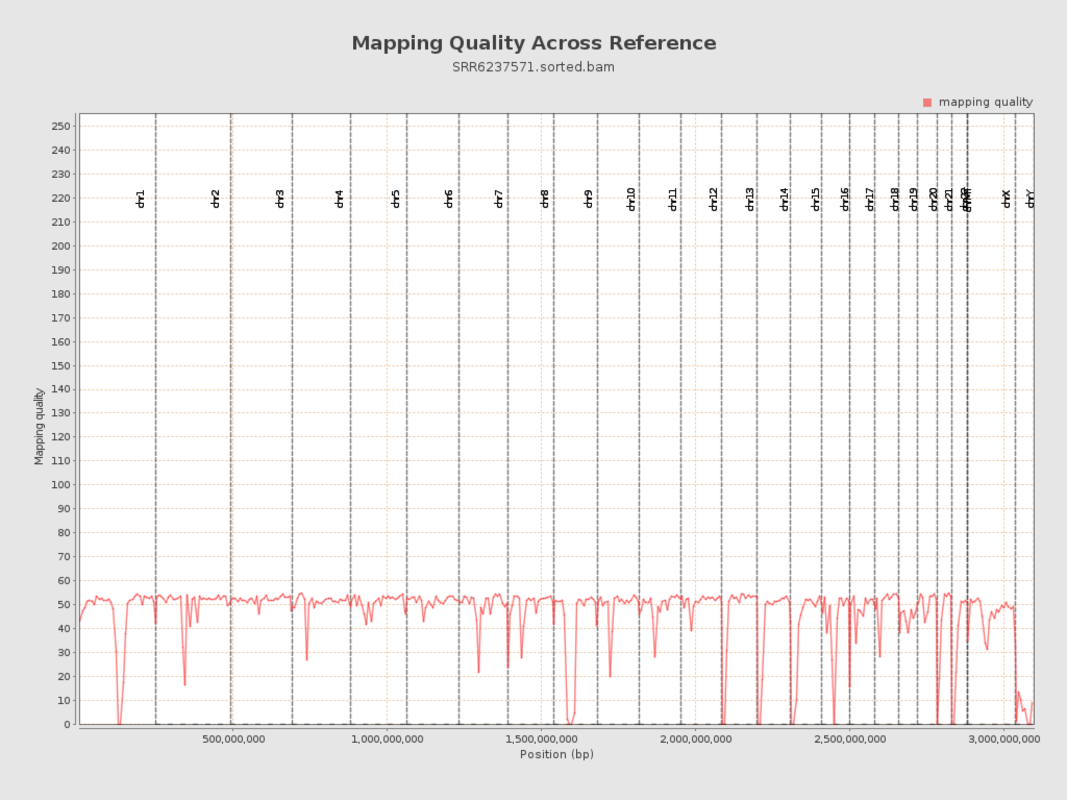
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram