Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:43:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237572.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_SRR6237572 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237572.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:43:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237572.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,979,267
Mapped reads	1,671,244 / 84.44%
Unmapped reads	308,023 / 15.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,690 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	85,416 / 4.32%
Duplication rate	3.82%
Clipped reads	917,316 / 46.35%

2.2. ACGT Content

Number/percentage of A's	29,942,515 / 27.9%
Number/percentage of C's	18,491,477 / 17.23%
Number/percentage of T's	34,868,012 / 32.49%
Number/percentage of G's	23,850,897 / 22.22%
Number/percentage of N's	182,349 / 0.17%
GC Percentage	39.45%

2.3. Coverage

Mean	0.0347

Standard Deviation	0.4091

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

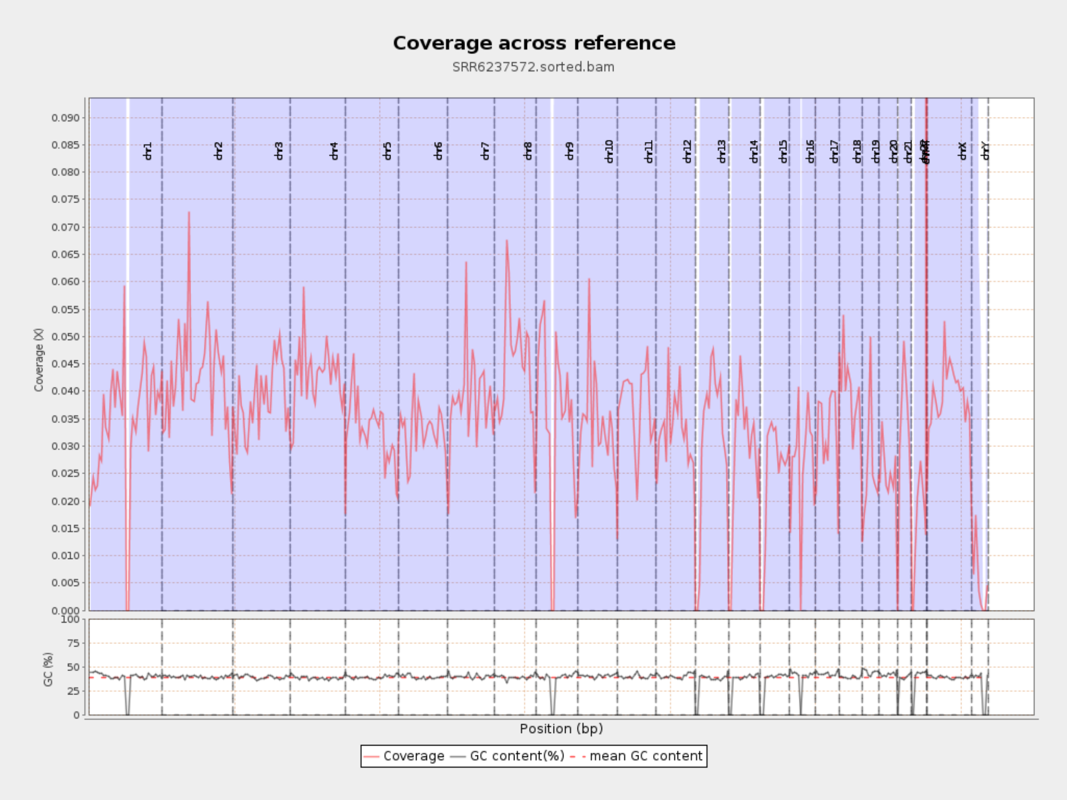
General error rate	0.95%
Mismatches	1,001,136
Insertions	9,573
Mapped reads with at least one insertion	0.57%
Deletions	36,952
Mapped reads with at least one deletion	2.18%
Homopolymer indels	46.72%

2.6. Chromosome stats

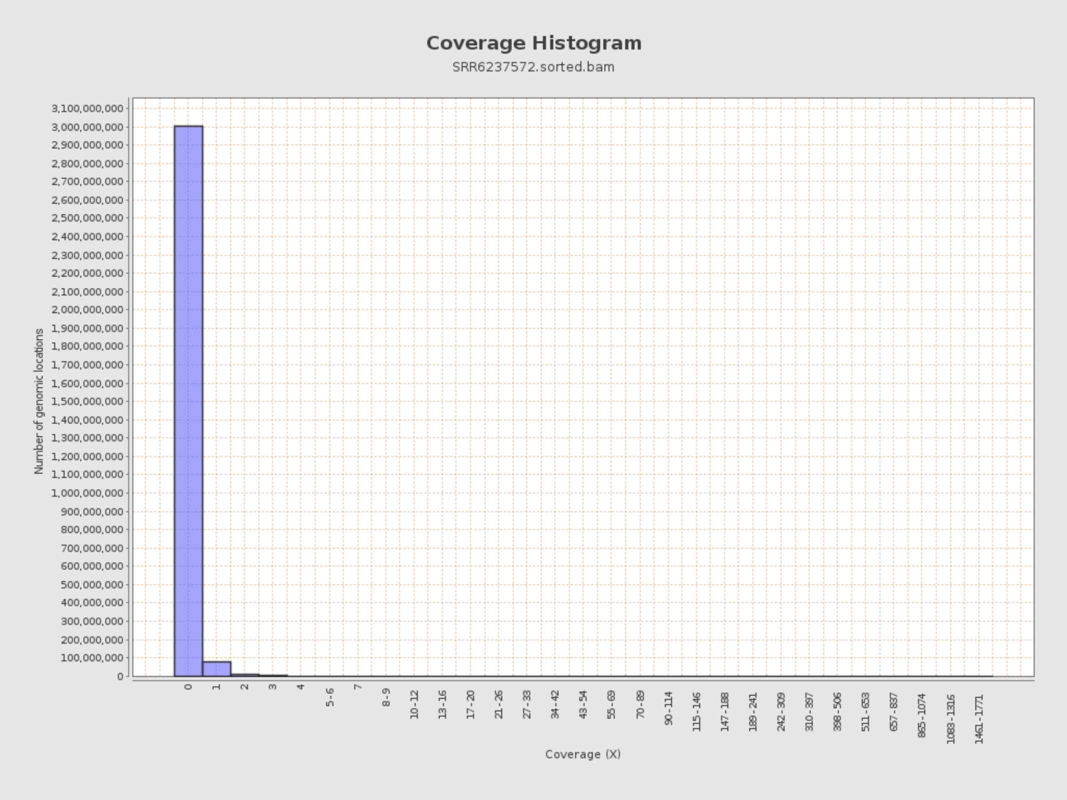
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8518346	0.0342	0.6302
chr2	243199373	10366611	0.0426	0.4068
chr3	198022430	7681854	0.0388	0.2255
chr4	191154276	8210712	0.043	0.2552
chr5	180915260	5987447	0.0331	0.2106
chr6	171115067	5624843	0.0329	0.2338
chr7	159138663	6233411	0.0392	0.4393

chr8	146364022	6498149	0.0444	1.0559
chr9	141213431	5051388	0.0358	0.3638
chr10	135534747	4653989	0.0343	0.3153
chr11	135006516	5023124	0.0372	0.3104
chr12	133851895	4399773	0.0329	0.2201
chr13	115169878	3536889	0.0307	0.2003
chr14	107349540	3056232	0.0285	0.2272
chr15	102531392	2507505	0.0245	0.1855
chr16	90354753	2458664	0.0272	0.2183
chr17	81195210	2579115	0.0318	0.2319
chr18	78077248	3114778	0.0399	0.7352
chr19	59128983	1563119	0.0264	0.428
chr20	63025520	1586226	0.0252	0.1973
chr21	48129895	1543642	0.0321	0.2328
chr22	51304566	801920	0.0156	0.1418
chrMT	16571	38921	2.3487	2.2256
chrX	155270560	6046105	0.0389	0.2564
chrY	59373566	312969	0.0053	0.1532

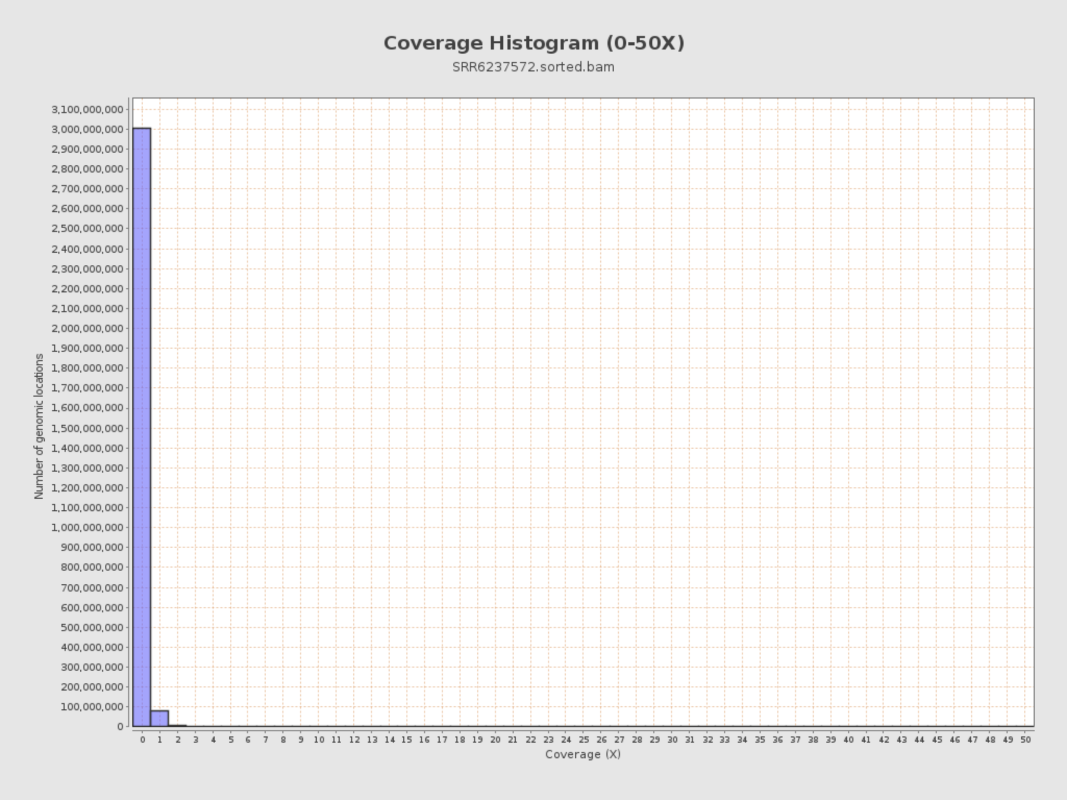
3. Results : Coverage across reference



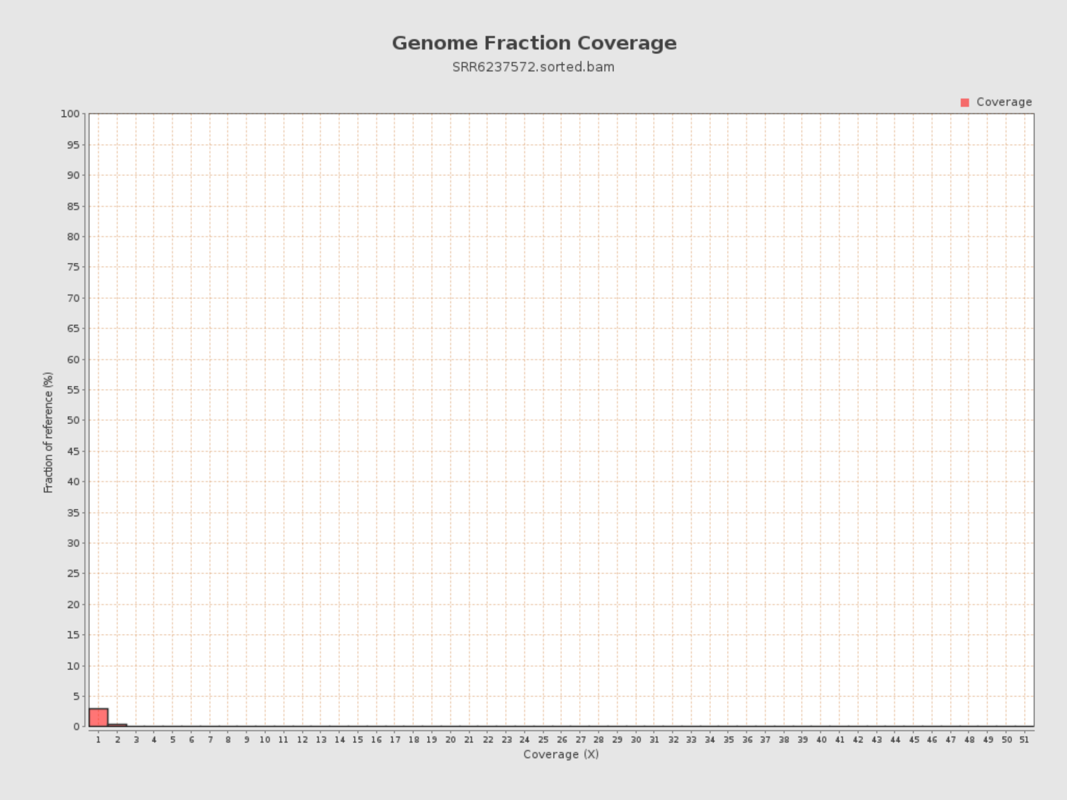
4. Results : Coverage Histogram



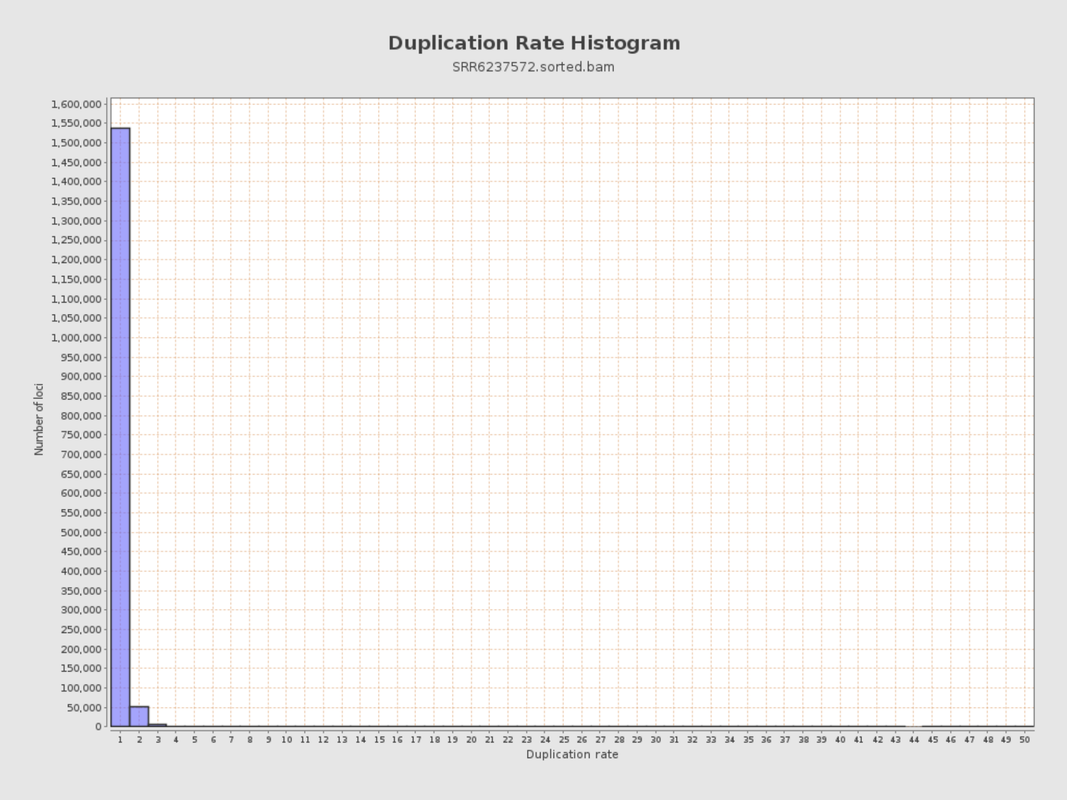
5. Results : Coverage Histogram (0-50X)



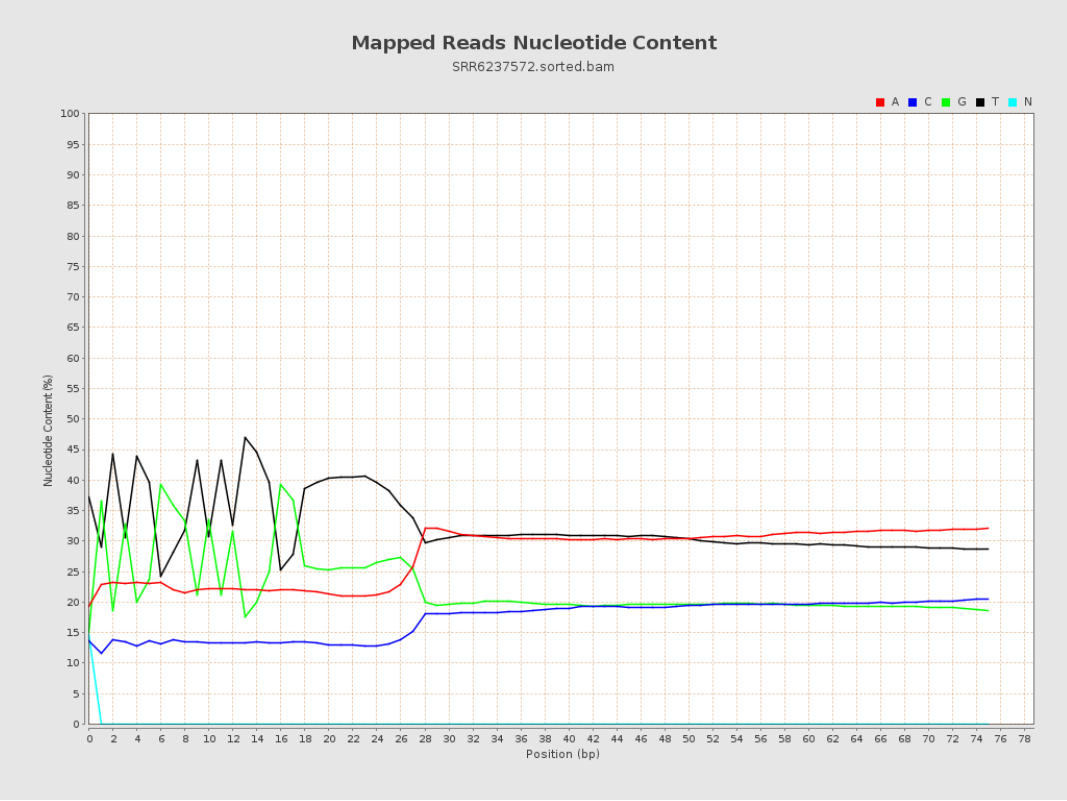
6. Results : Genome Fraction Coverage



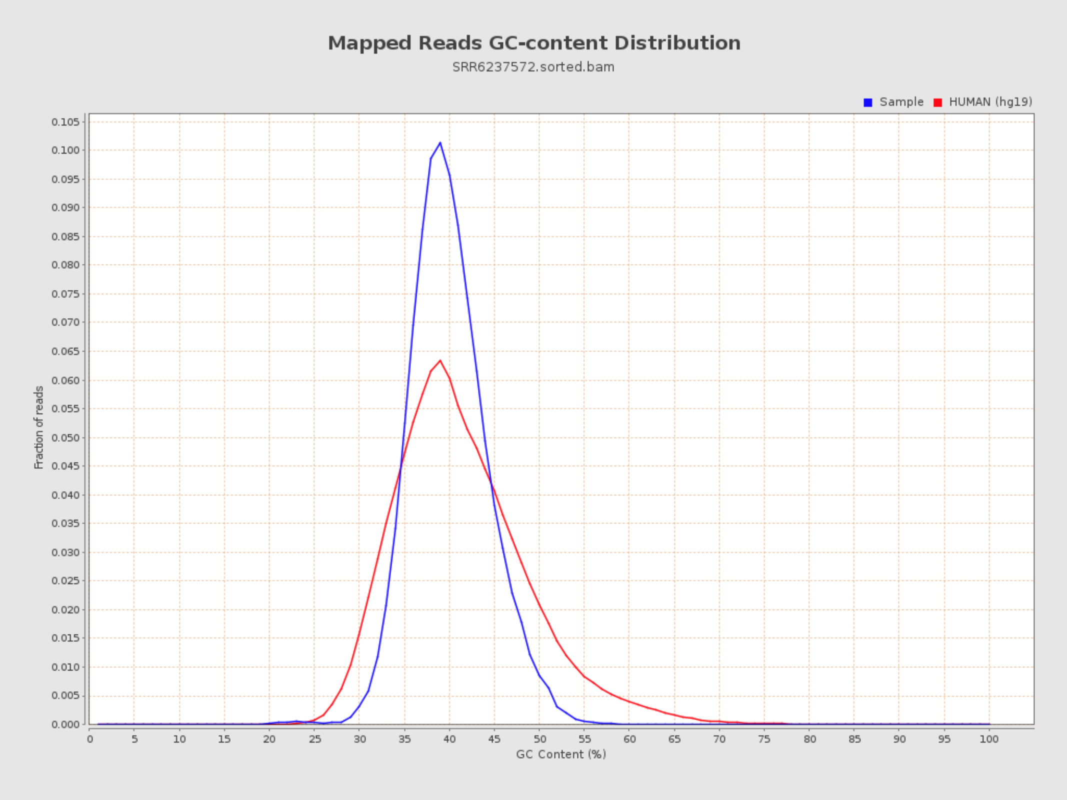
7. Results : Duplication Rate Histogram



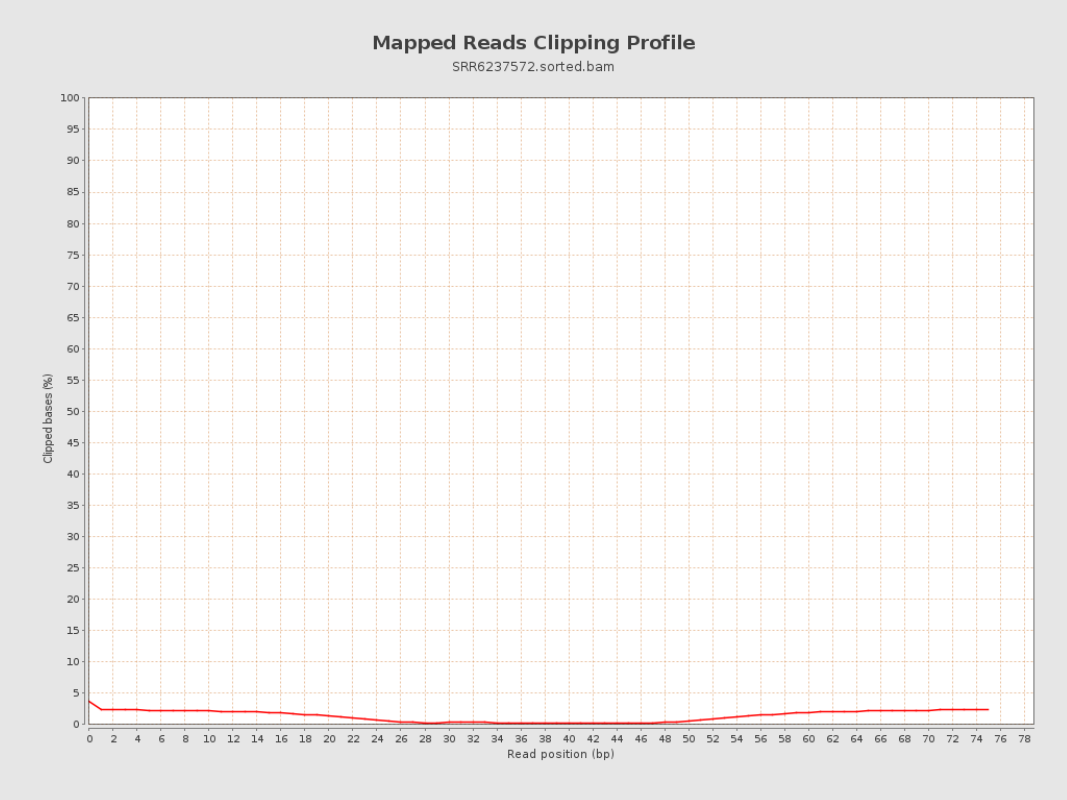
8. Results : Mapped Reads Nucleotide Content



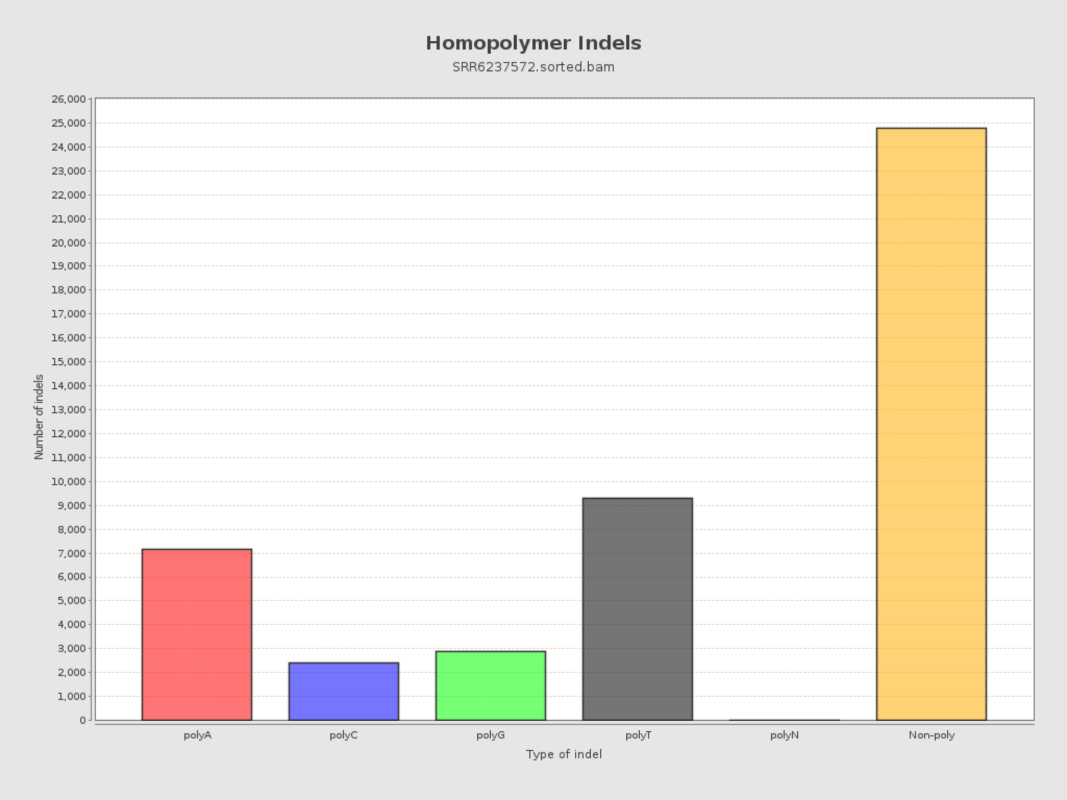
9. Results : Mapped Reads GC-content Distribution



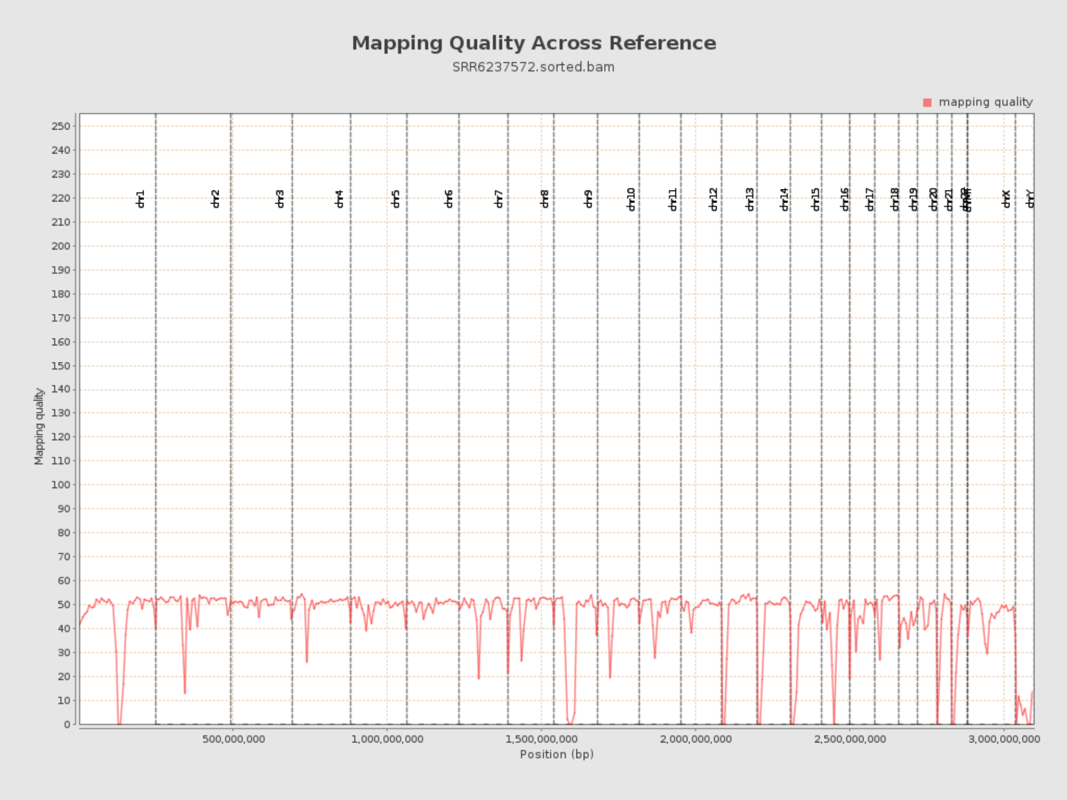
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram