Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:33:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236099.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_SRR6236099 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236099.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:33:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,808,501
Mapped reads	2,391,386 / 85.15%
Unmapped reads	417,115 / 14.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,244 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	307,545 / 10.95%
Duplication rate	9.99%
Clipped reads	1,447,582 / 51.54%

2.2. ACGT Content

Number/percentage of A's	43,892,726 / 29.05%
Number/percentage of C's	27,273,256 / 18.05%
Number/percentage of T's	48,404,338 / 32.04%
Number/percentage of G's	31,506,298 / 20.85%
Number/percentage of N's	1,293 / 0%
GC Percentage	38.91%

2.3. Coverage

Mean	0.0488

Standard Deviation	0.4991

2.4. Mapping Quality

Mean Mapping Quality	40.46

2.5. Mismatches and indels

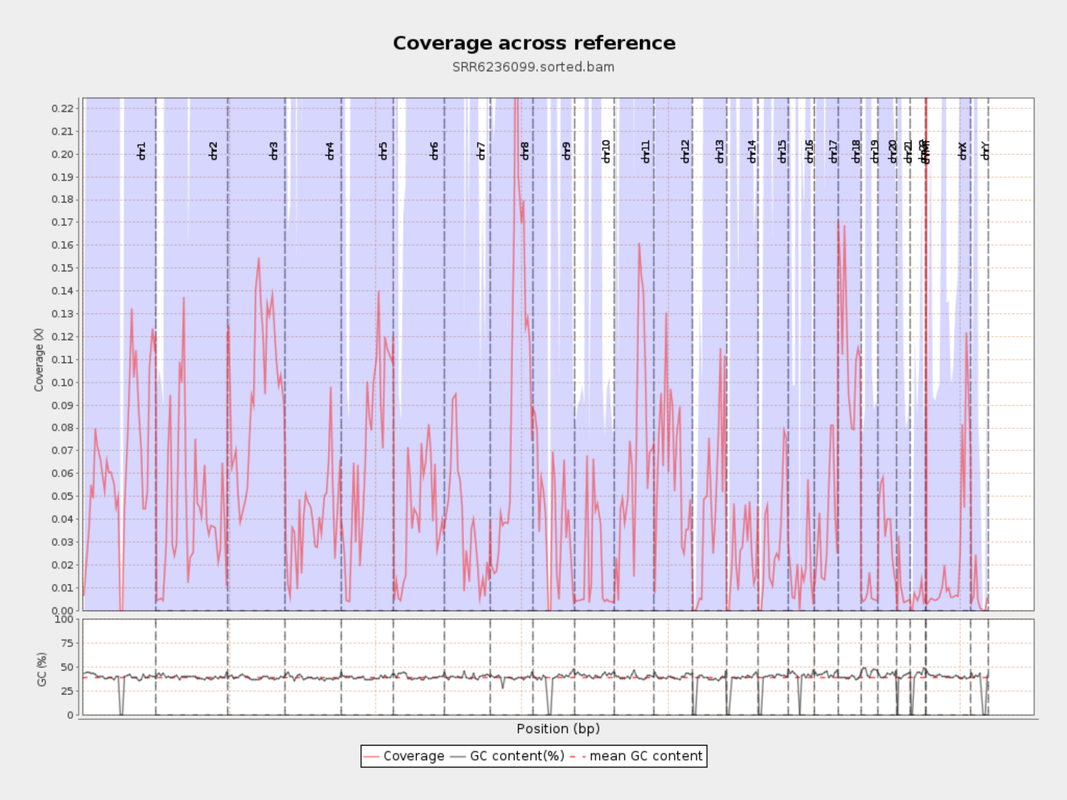
General error rate	0.79%
Mismatches	1,166,414
Insertions	11,701
Mapped reads with at least one insertion	0.49%
Deletions	41,944
Mapped reads with at least one deletion	1.73%
Homopolymer indels	45.29%

2.6. Chromosome stats

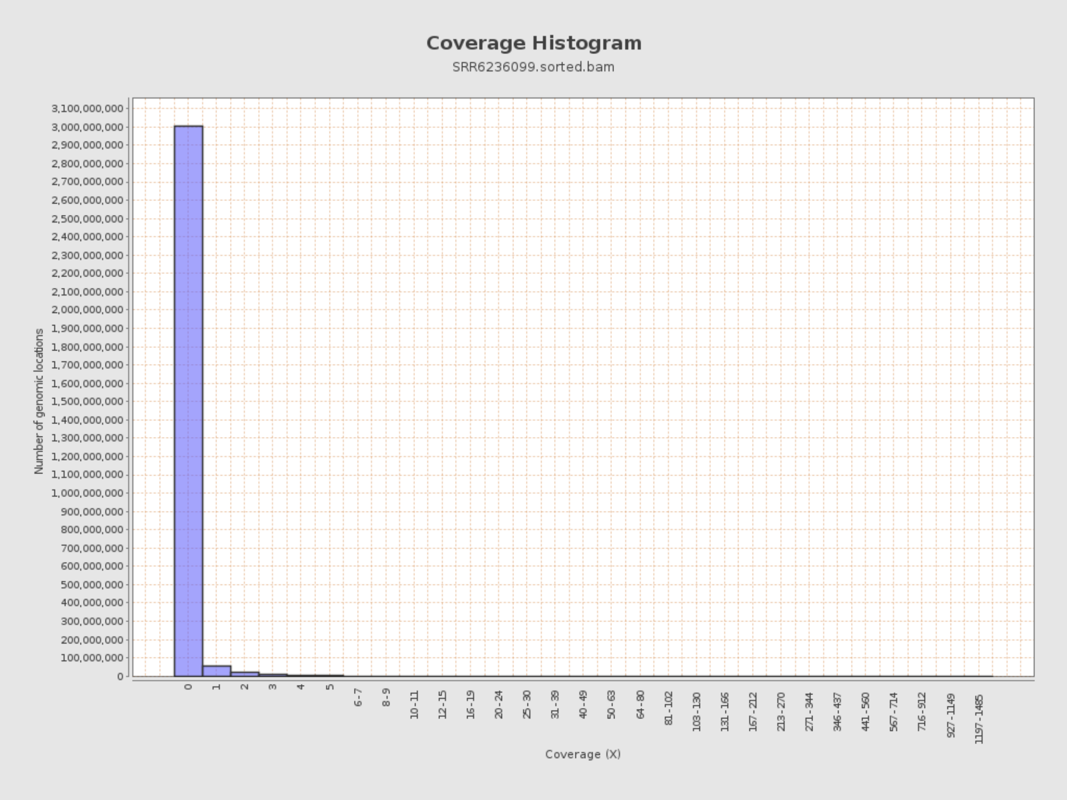
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16061004	0.0644	0.4497
chr2	243199373	10582013	0.0435	0.7432
chr3	198022430	18966638	0.0958	0.4803
chr4	191154276	7654156	0.04	0.3736
chr5	180915260	12821620	0.0709	0.4106
chr6	171115067	6991818	0.0409	0.3342
chr7	159138663	5879829	0.0369	0.4063

chr8	146364022	14256640	0.0974	1.0913
chr9	141213431	5643362	0.04	0.4871
chr10	135534747	2506246	0.0185	0.5269
chr11	135006516	9133219	0.0677	0.6117
chr12	133851895	8292907	0.062	0.3992
chr13	115169878	5171311	0.0449	0.327
chr14	107349540	2568826	0.0239	0.2481
chr15	102531392	3150539	0.0307	0.2676
chr16	90354753	1484792	0.0164	0.2255
chr17	81195210	3155646	0.0389	0.3557
chr18	78077248	9178729	0.1176	0.7737
chr19	59128983	399845	0.0068	0.3406
chr20	63025520	2356038	0.0374	0.2934
chr21	48129895	452880	0.0094	0.2095
chr22	51304566	293263	0.0057	0.1007
chrMT	16571	59526	3.5922	3.6229
chrX	155270560	3747802	0.0241	0.2822
chrY	59373566	339376	0.0057	0.2225

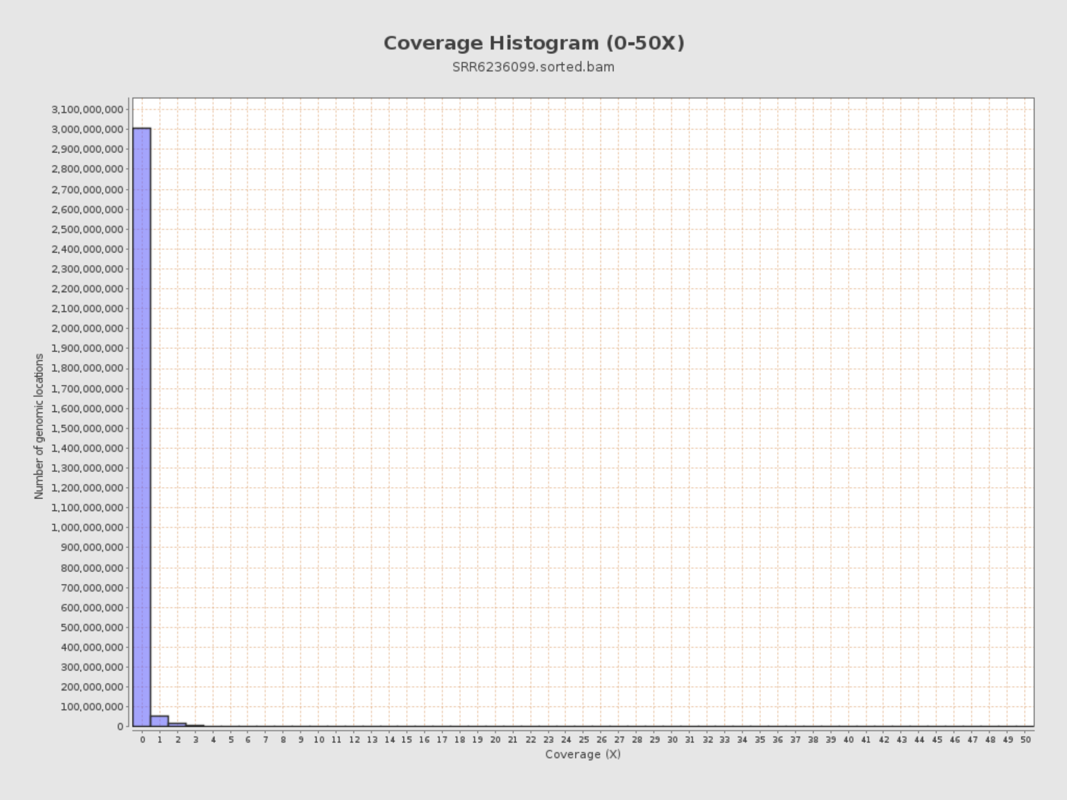
3. Results : Coverage across reference



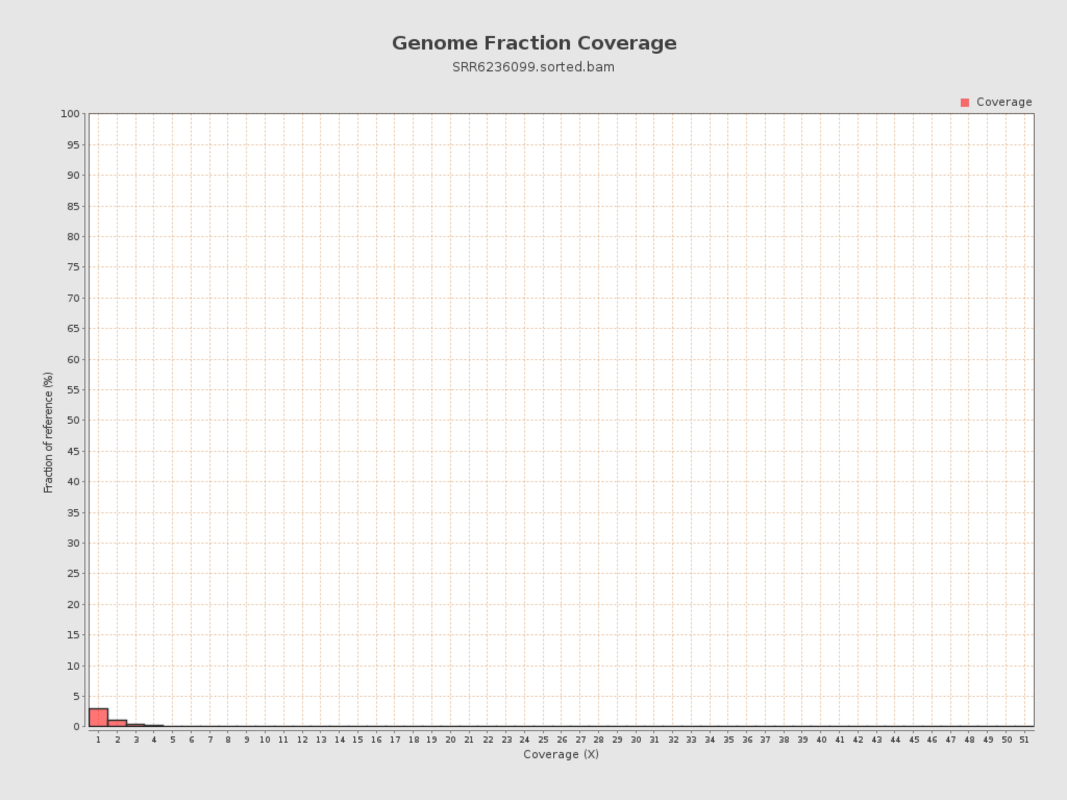
4. Results : Coverage Histogram



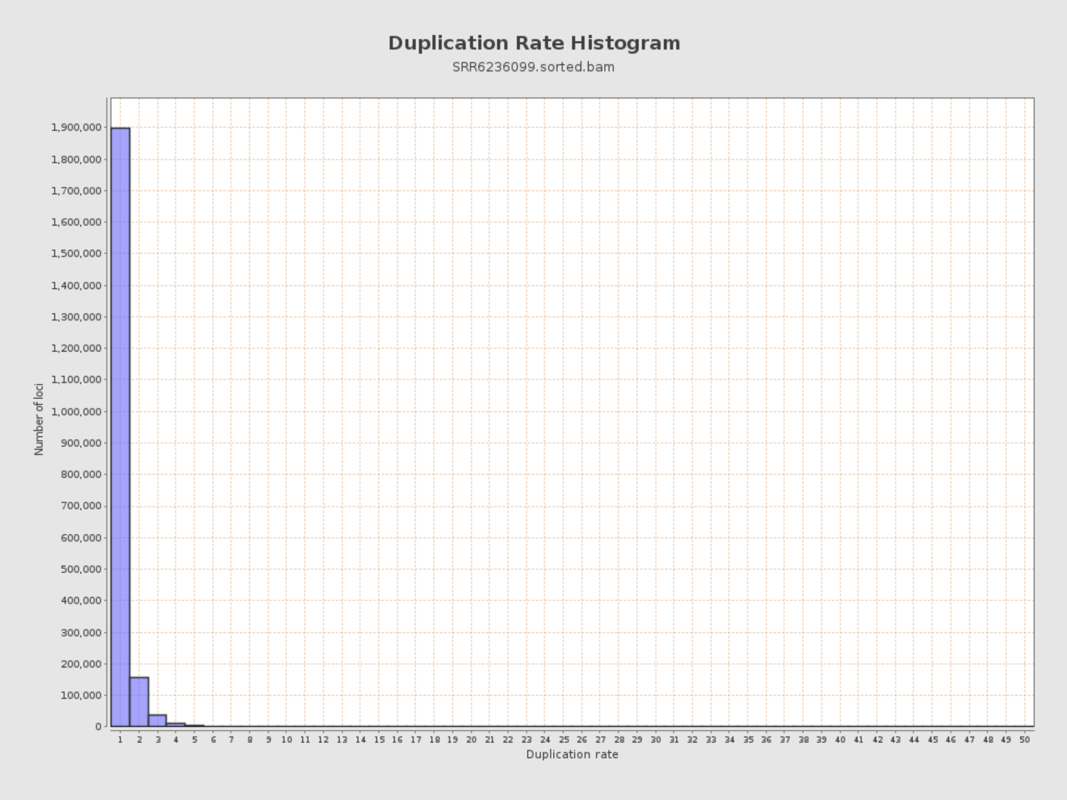
5. Results : Coverage Histogram (0-50X)



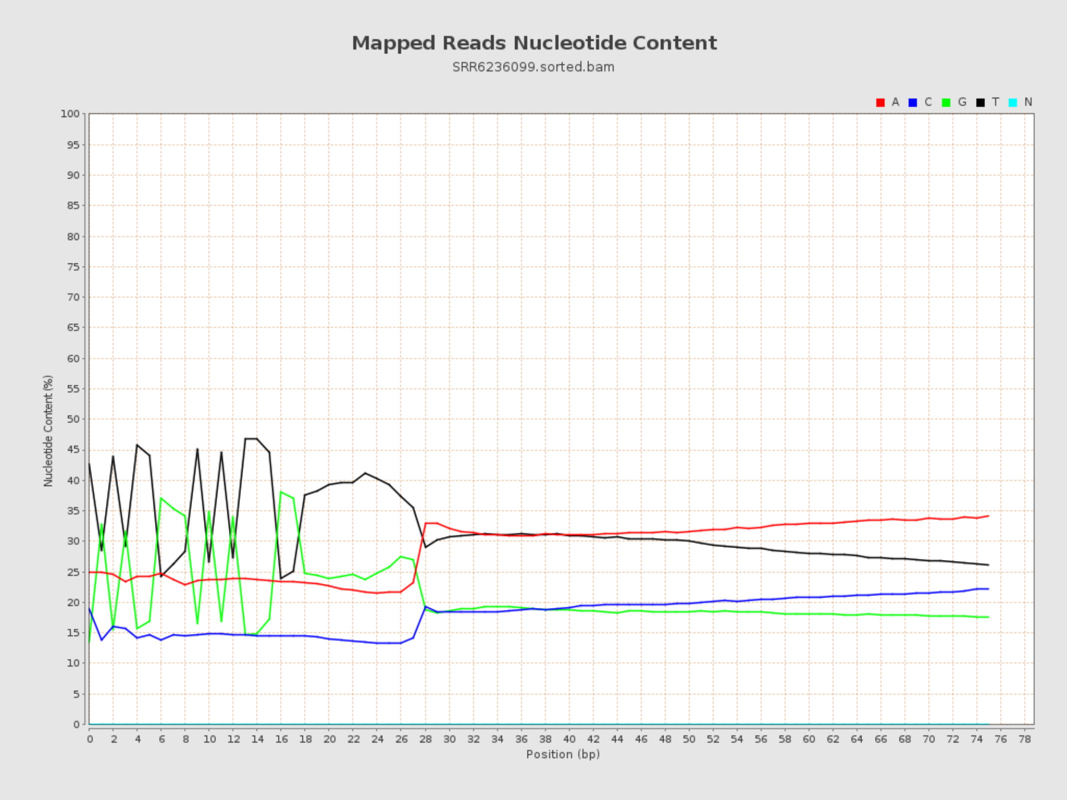
6. Results : Genome Fraction Coverage



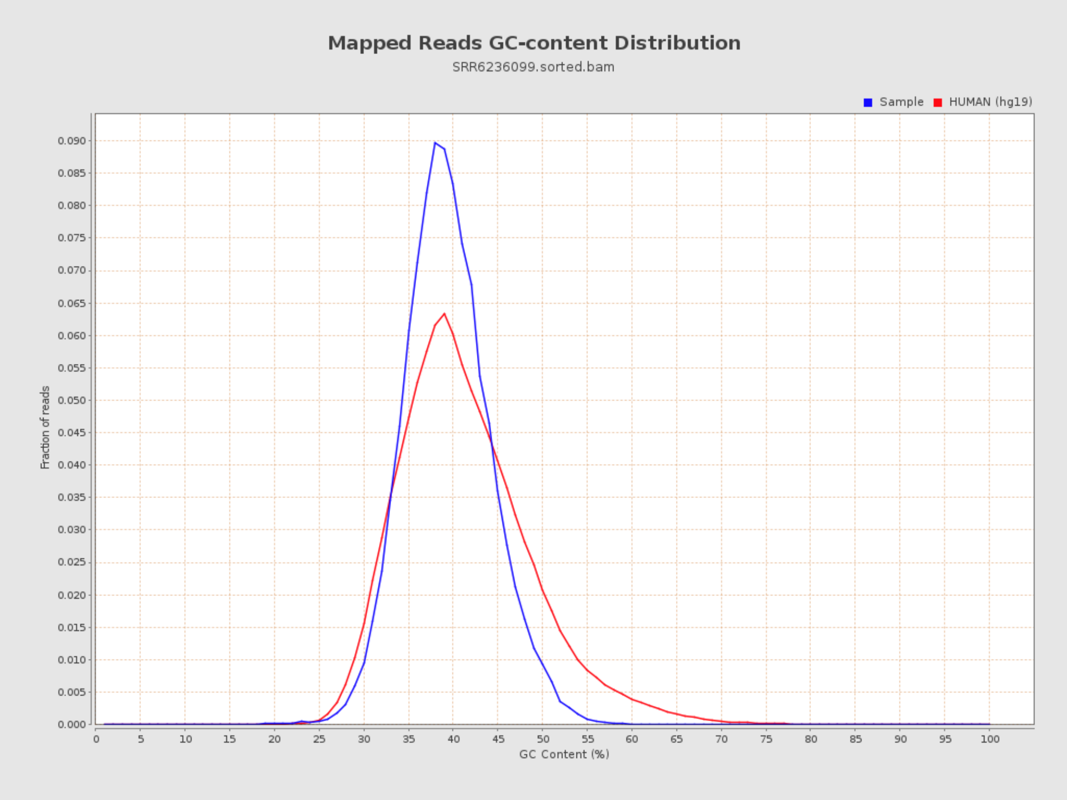
7. Results : Duplication Rate Histogram



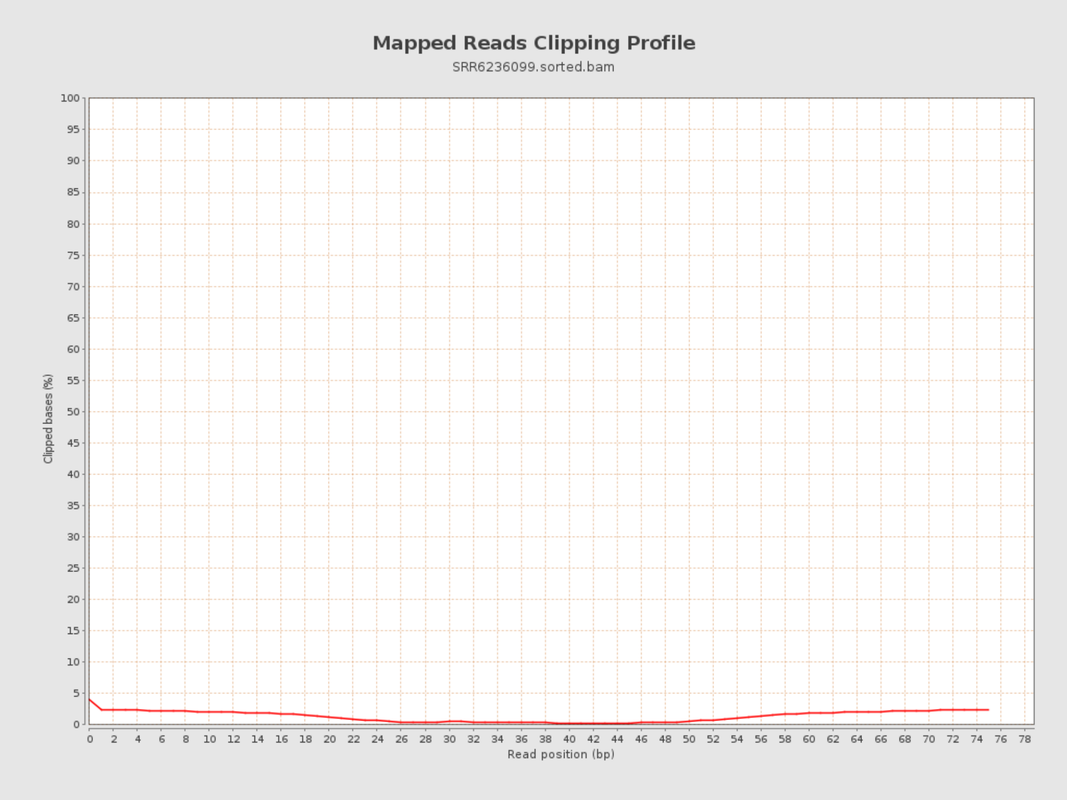
8. Results : Mapped Reads Nucleotide Content



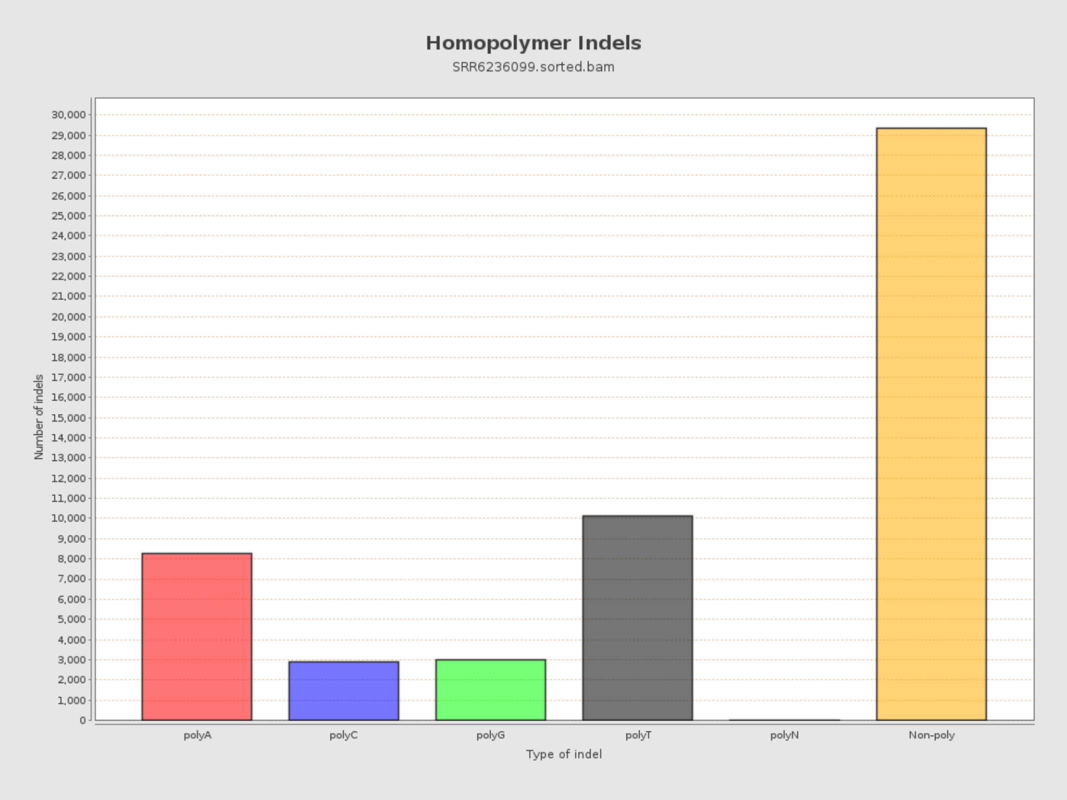
9. Results : Mapped Reads GC-content Distribution



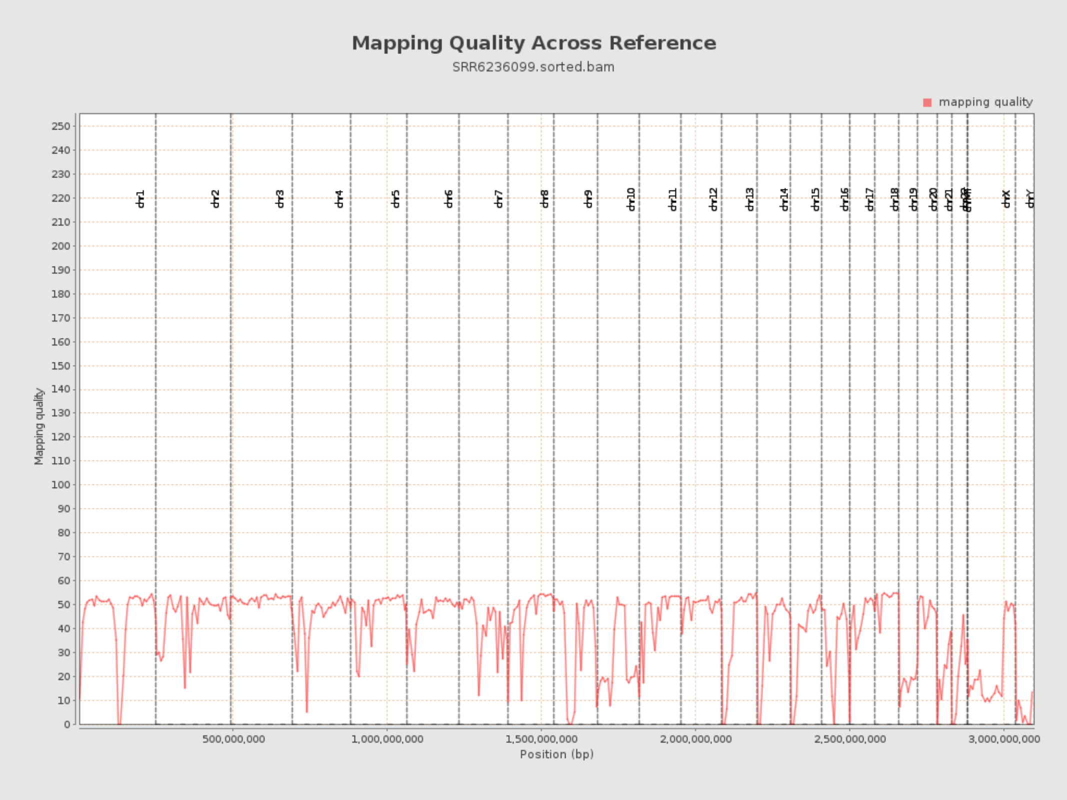
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram