Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:21:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236096.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_SRR6236096 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236096.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:21:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236096.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,773,762
Mapped reads	1,559,117 / 87.9%
Unmapped reads	214,645 / 12.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,969 / 0.39%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	61,612 / 3.47%
Duplication rate	2.96%
Clipped reads	724,651 / 40.85%

2.2. ACGT Content

Number/percentage of A's	28,457,656 / 27.73%
Number/percentage of C's	18,021,047 / 17.56%
Number/percentage of T's	33,086,882 / 32.24%
Number/percentage of G's	23,006,057 / 22.42%
Number/percentage of N's	44,145 / 0.04%
GC Percentage	39.98%

2.3. Coverage

Mean	0.0332

Standard Deviation	0.3386

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

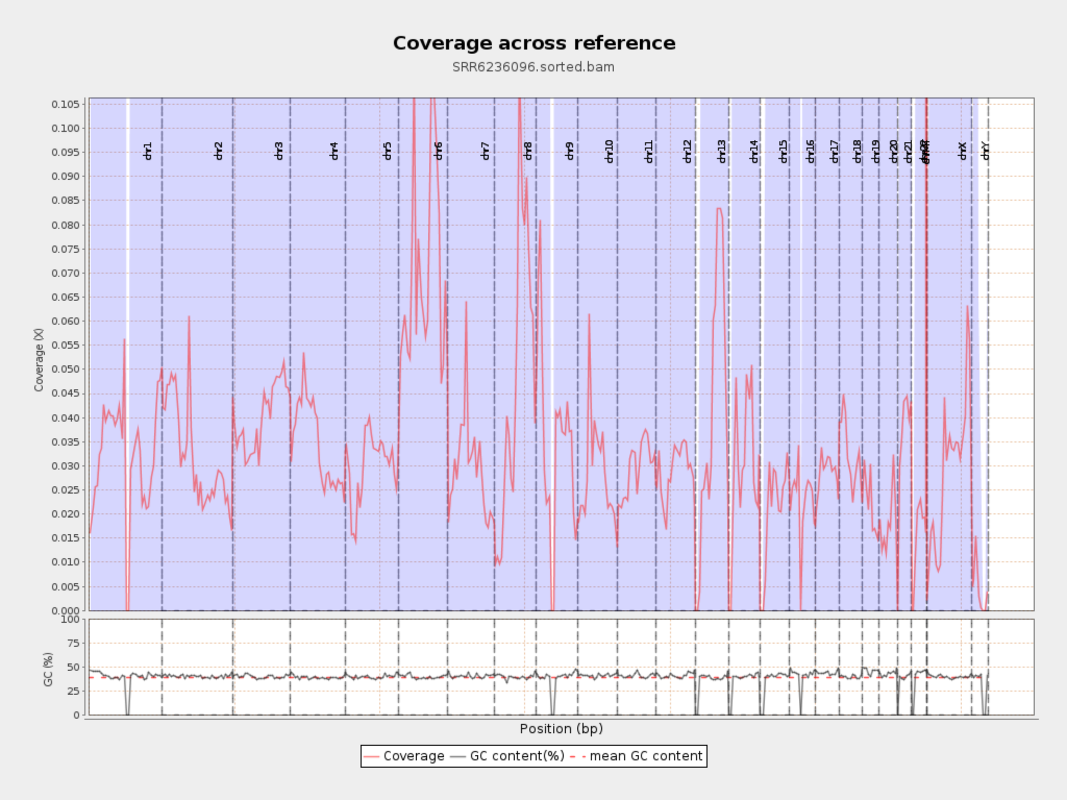
General error rate	0.81%
Mismatches	821,640
Insertions	7,662
Mapped reads with at least one insertion	0.49%
Deletions	29,364
Mapped reads with at least one deletion	1.86%
Homopolymer indels	47.2%

2.6. Chromosome stats

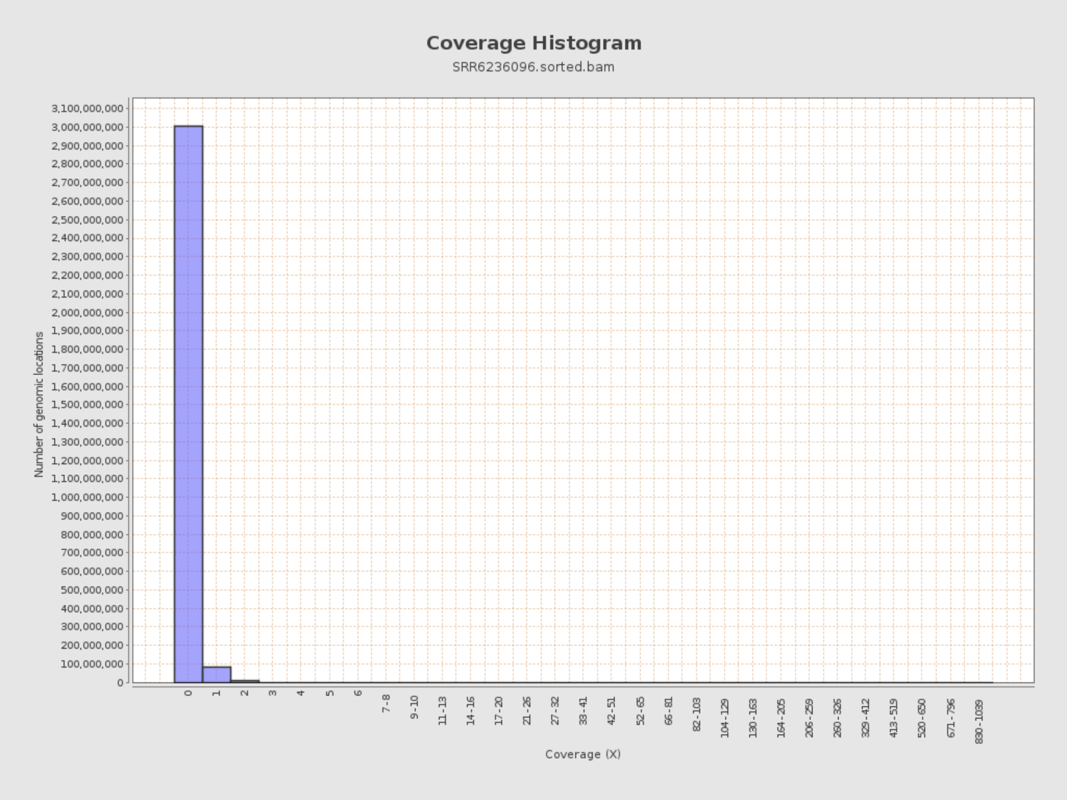
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7975936	0.032	0.524
chr2	243199373	7809504	0.0321	0.3272
chr3	198022430	7972403	0.0403	0.2202
chr4	191154276	6615239	0.0346	0.2211
chr5	180915260	5397177	0.0298	0.1895
chr6	171115067	11961938	0.0699	0.444
chr7	159138663	4721233	0.0297	0.4423

chr8	146364022	6943176	0.0474	0.6727
chr9	141213431	4900247	0.0347	0.3168
chr10	135534747	3888006	0.0287	0.3029
chr11	135006516	3950638	0.0293	0.2604
chr12	133851895	3891517	0.0291	0.1949
chr13	115169878	4743945	0.0412	0.2236
chr14	107349540	3079227	0.0287	0.2088
chr15	102531392	2116471	0.0206	0.1693
chr16	90354753	2056181	0.0228	0.1927
chr17	81195210	2320606	0.0286	0.2097
chr18	78077248	2569432	0.0329	0.5303
chr19	59128983	1313185	0.0222	0.355
chr20	63025520	1138985	0.0181	0.1552
chr21	48129895	1708171	0.0355	0.2259
chr22	51304566	757224	0.0148	0.1299
chrMT	16571	62589	3.777	2.8357
chrX	155270560	4521550	0.0291	0.2119
chrY	59373566	252409	0.0043	0.1159

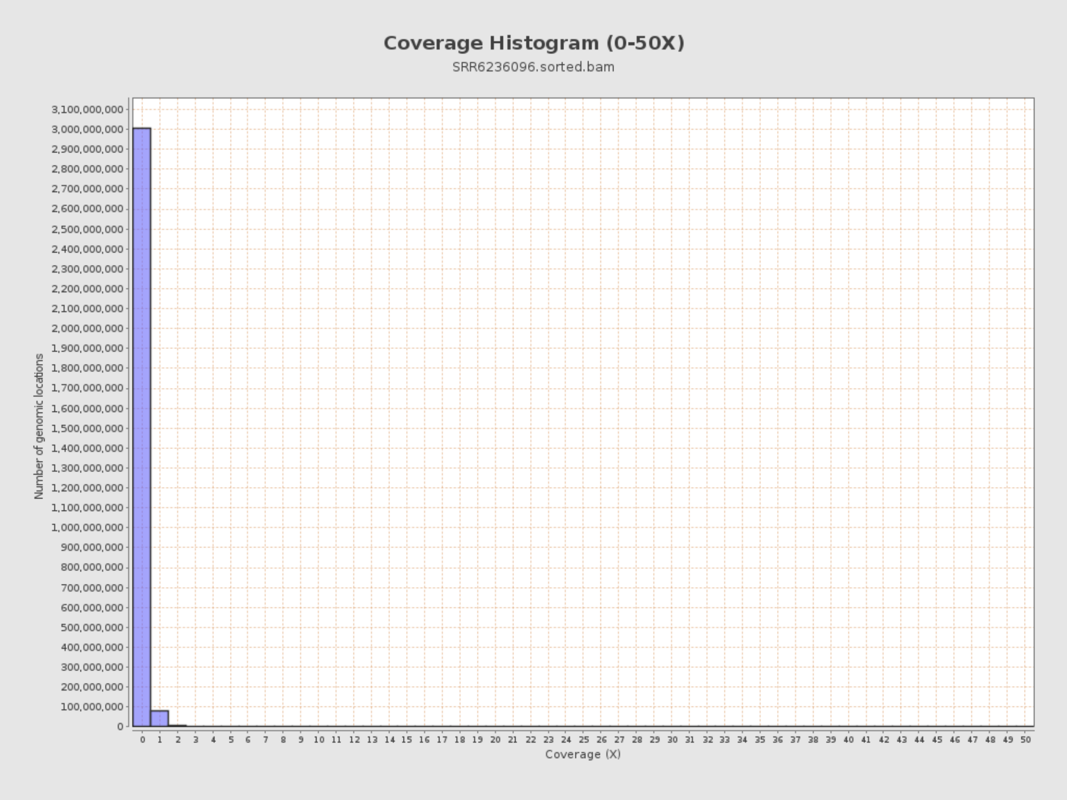
3. Results : Coverage across reference



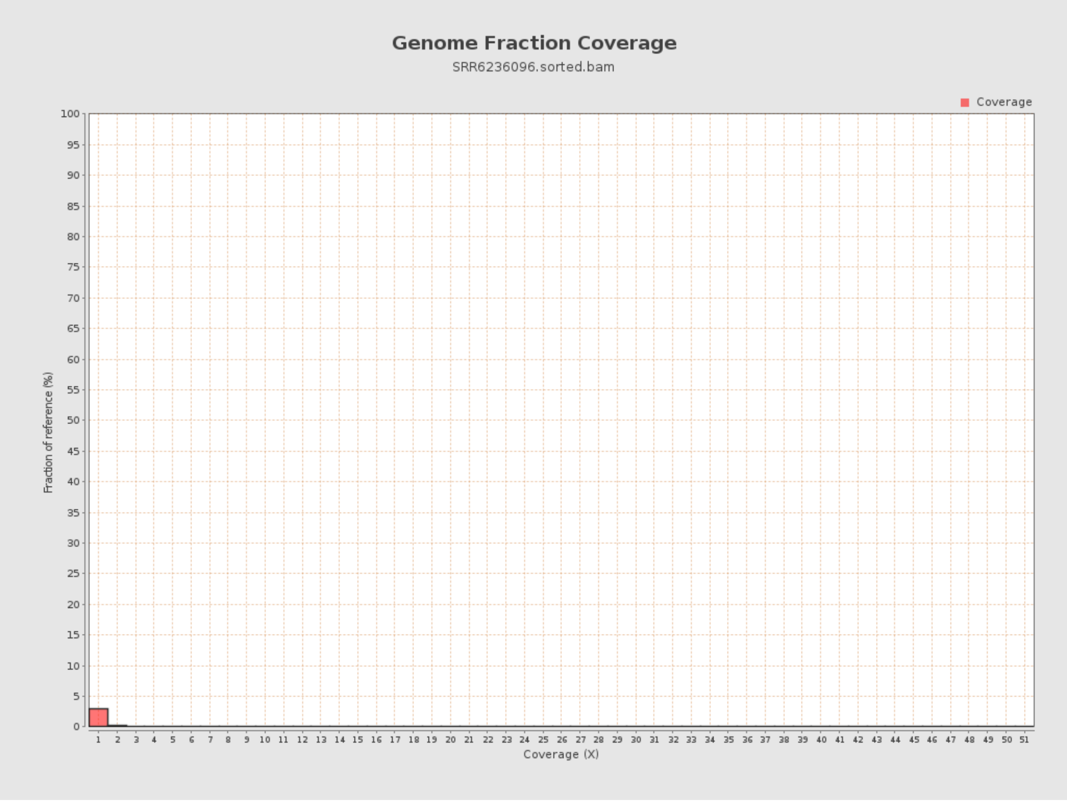
4. Results : Coverage Histogram



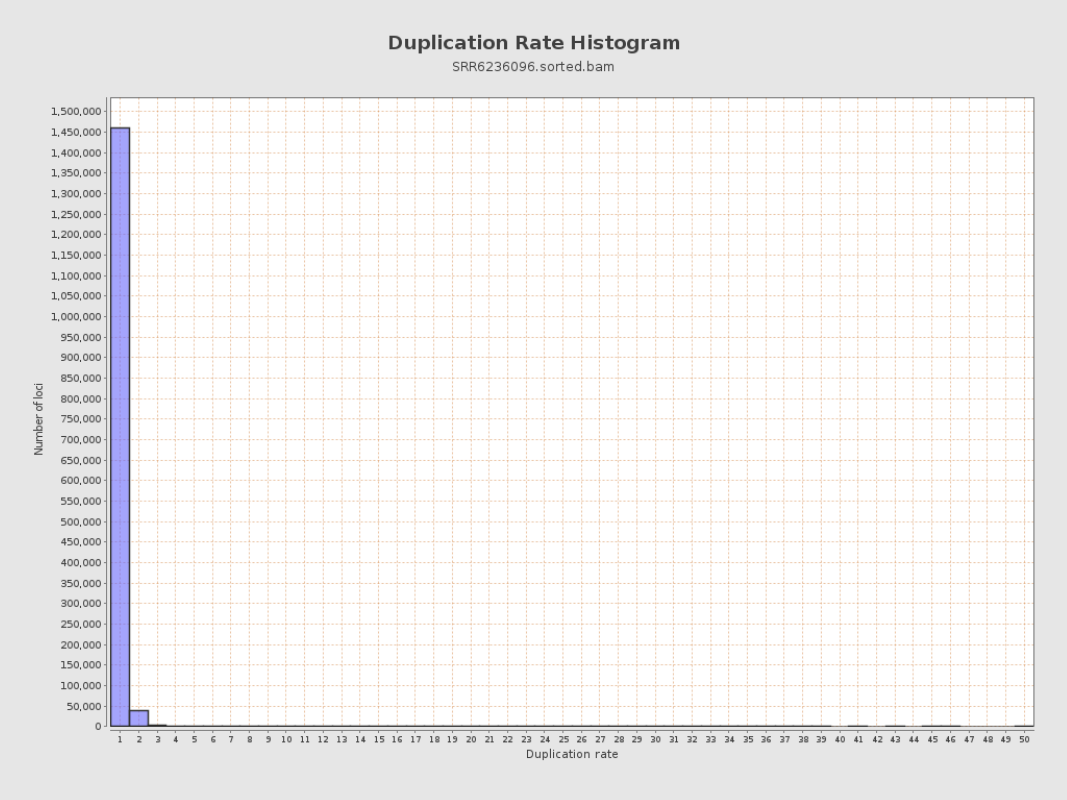
5. Results : Coverage Histogram (0-50X)



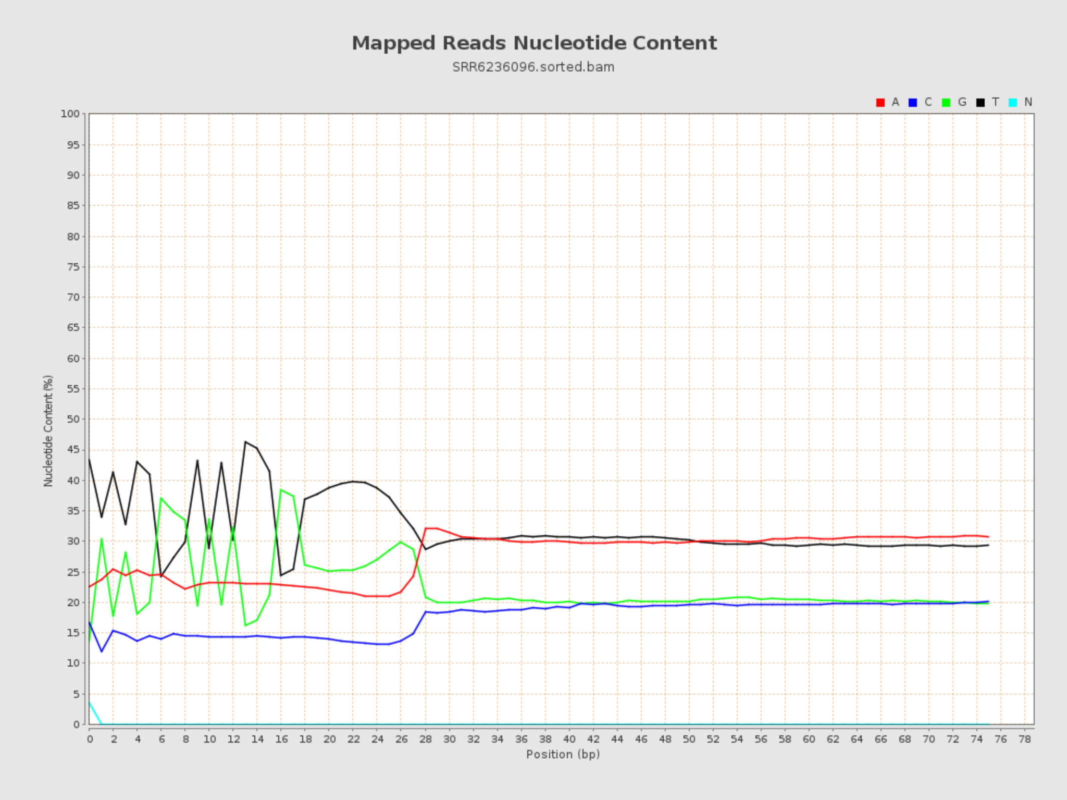
6. Results : Genome Fraction Coverage



7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



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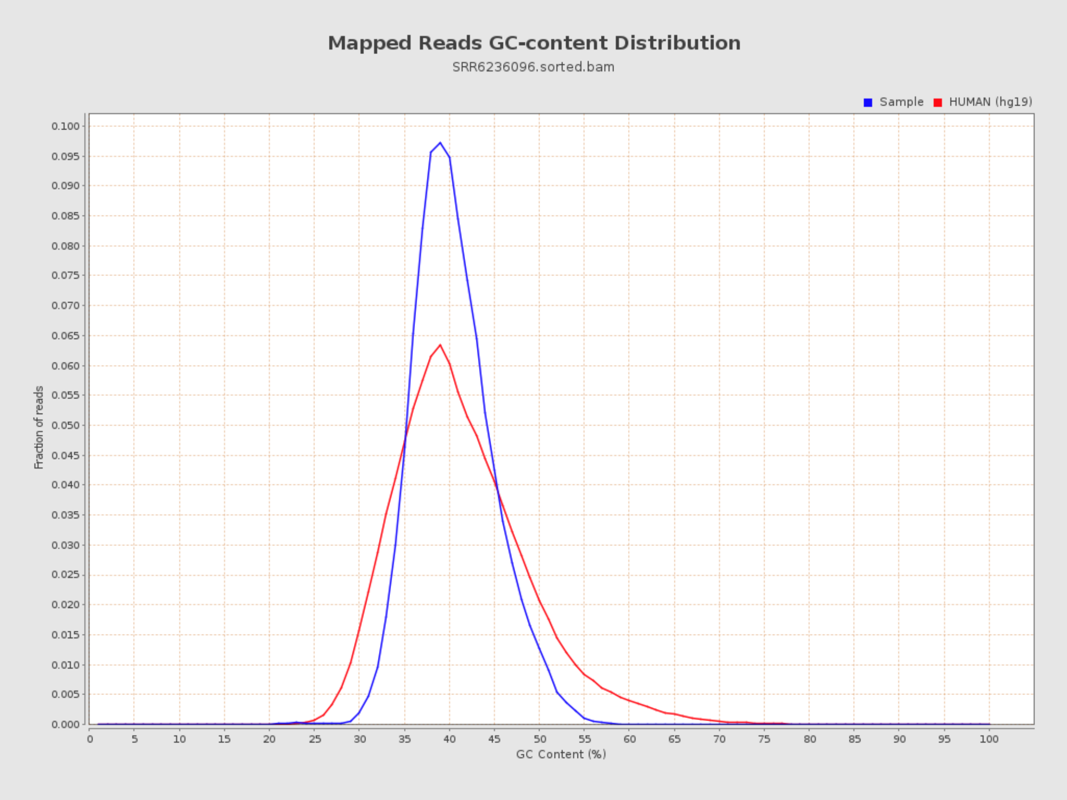
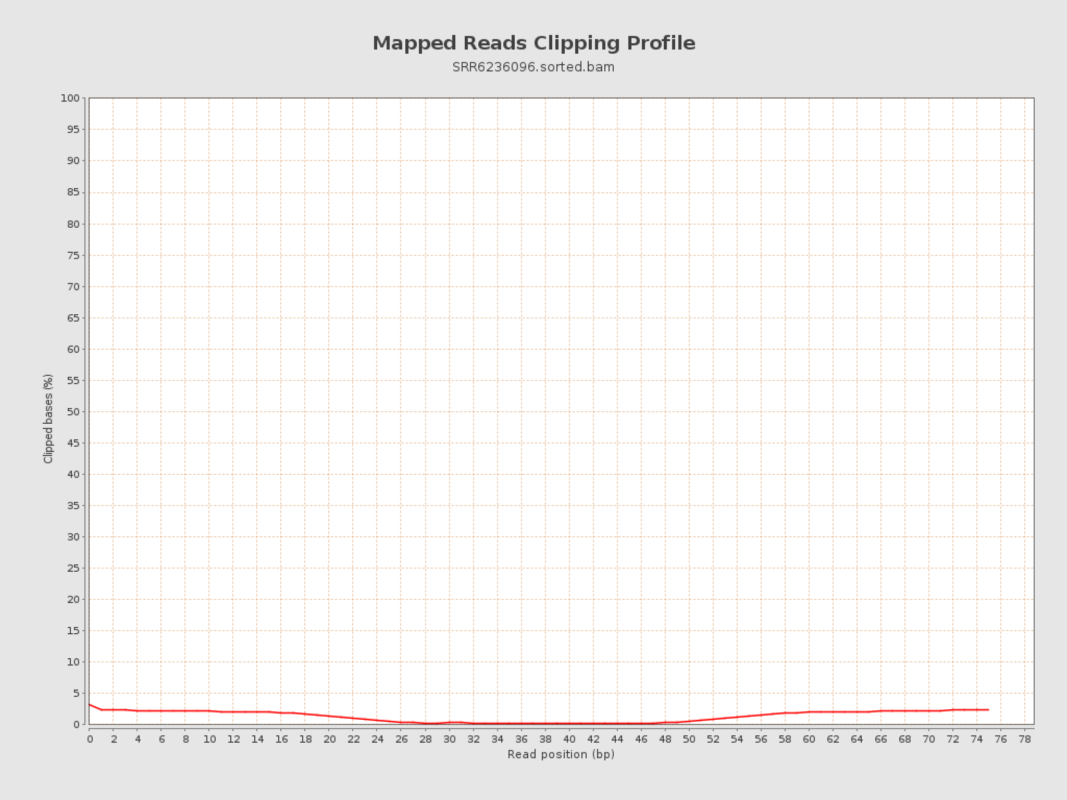
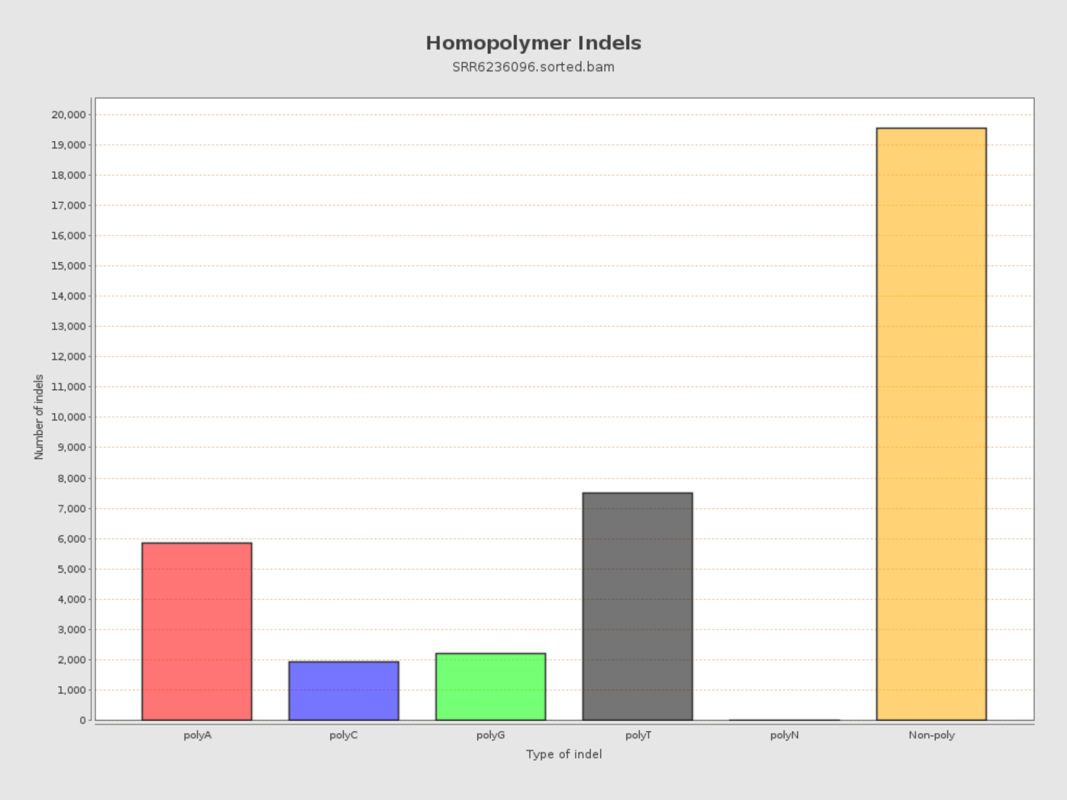
9. Results : Mapped Reads GC-content Distribution



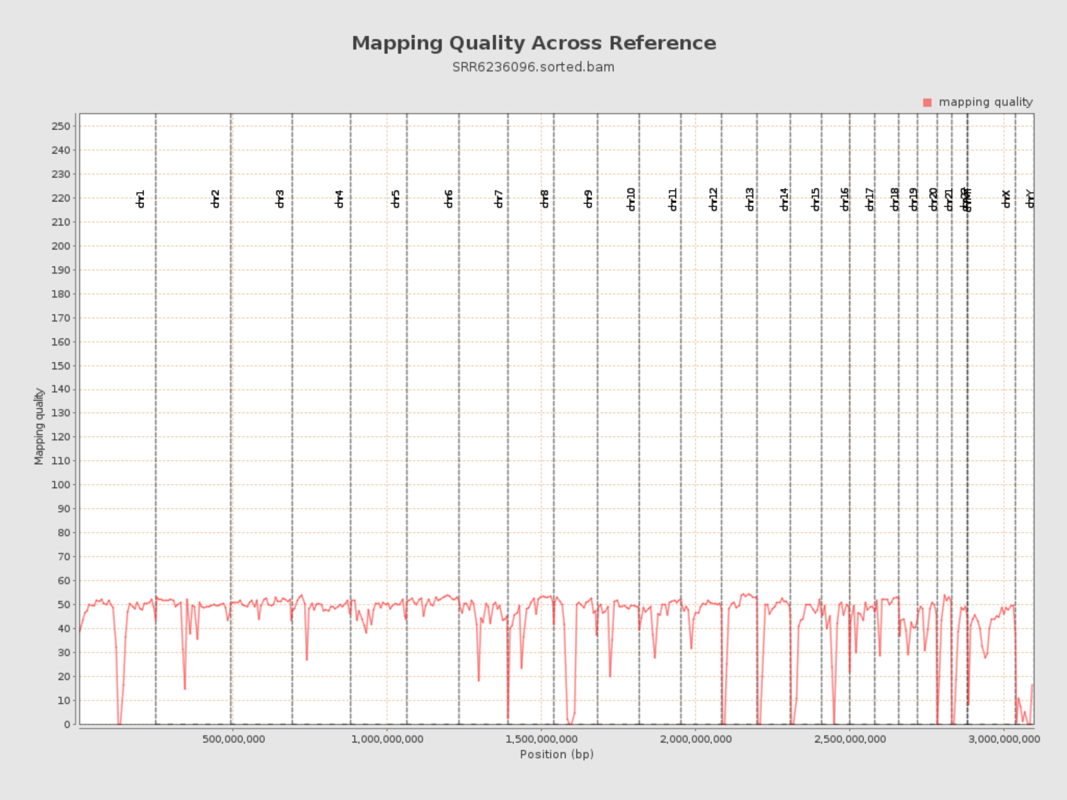
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram