Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:17:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236094.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_SRR6236094 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236094.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:17:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236094.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	250,752
Mapped reads	211,512 / 84.35%
Unmapped reads	39,240 / 15.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,367 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	4,814 / 1.92%
Duplication rate	2.02%
Clipped reads	103,939 / 41.45%

2.2. ACGT Content

Number/percentage of A's	3,761,278 / 27.21%
Number/percentage of C's	2,460,188 / 17.8%
Number/percentage of T's	4,478,923 / 32.4%
Number/percentage of G's	3,118,089 / 22.55%
Number/percentage of N's	6,596 / 0.05%
GC Percentage	40.35%

2.3. Coverage

Mean	0.0045

Standard Deviation	0.0765

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

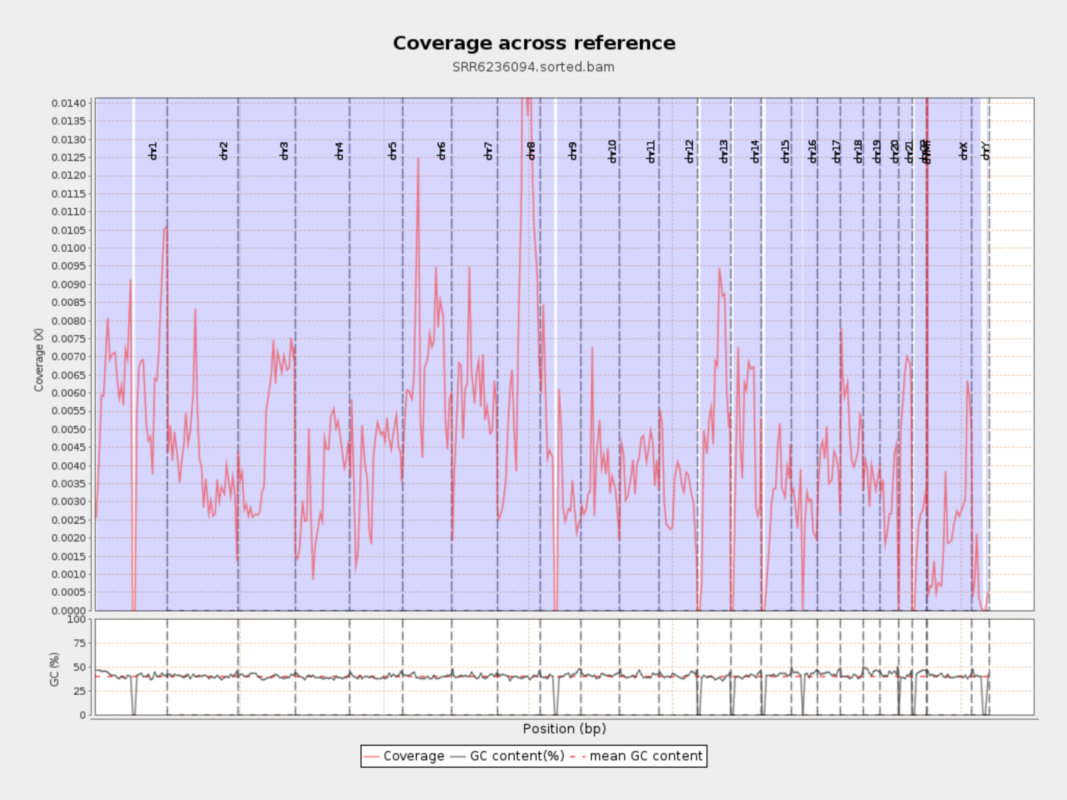
General error rate	0.85%
Mismatches	115,682
Insertions	953
Mapped reads with at least one insertion	0.45%
Deletions	4,254
Mapped reads with at least one deletion	1.99%
Homopolymer indels	46%

2.6. Chromosome stats

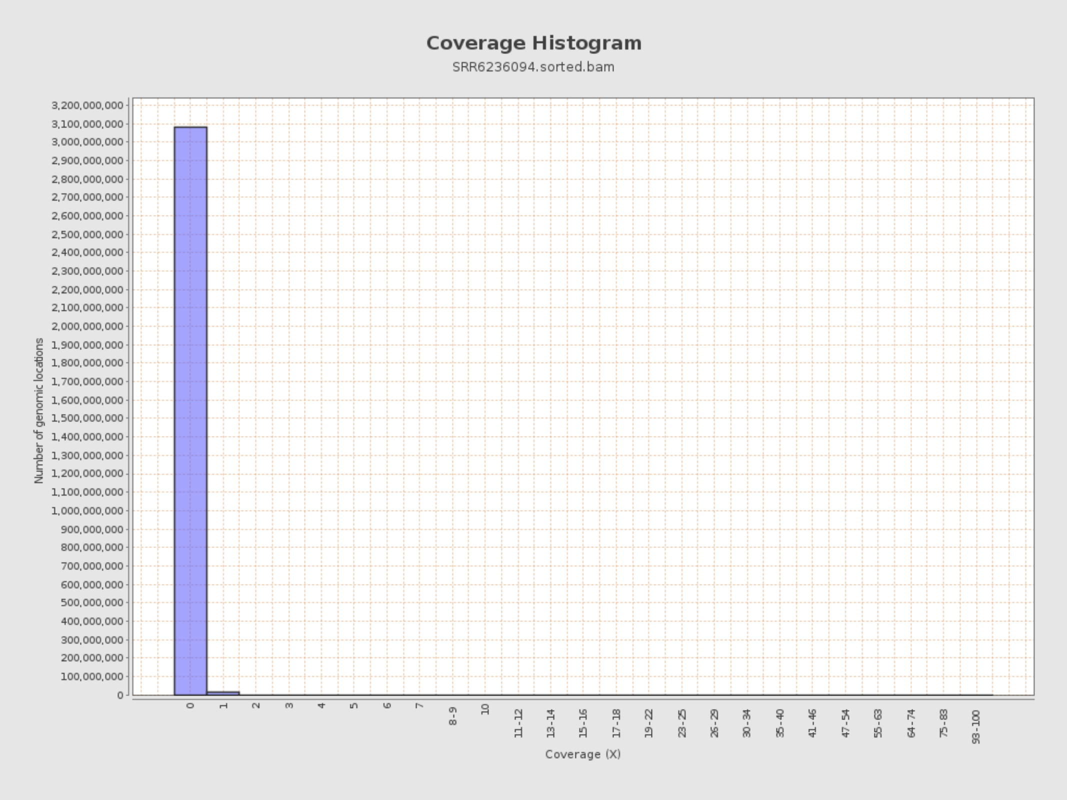
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1542673	0.0062	0.1037
chr2	243199373	978405	0.004	0.0738
chr3	198022430	976692	0.0049	0.0725
chr4	191154276	669329	0.0035	0.0632
chr5	180915260	742569	0.0041	0.0663
chr6	171115067	1175421	0.0069	0.0914
chr7	159138663	932001	0.0059	0.0955

chr8	146364022	1247155	0.0085	0.1142
chr9	141213431	522682	0.0037	0.0684
chr10	135534747	500541	0.0037	0.069
chr11	135006516	553050	0.0041	0.068
chr12	133851895	443223	0.0033	0.06
chr13	115169878	608199	0.0053	0.0751
chr14	107349540	466118	0.0043	0.0683
chr15	102531392	292554	0.0029	0.0551
chr16	90354753	235842	0.0026	0.0544
chr17	81195210	331579	0.0041	0.0668
chr18	78077248	406541	0.0052	0.0946
chr19	59128983	217181	0.0037	0.0751
chr20	63025520	193789	0.0031	0.0577
chr21	48129895	271935	0.0057	0.079
chr22	51304566	101968	0.002	0.0455
chrMT	16571	31557	1.9044	1.8169
chrX	155270560	359449	0.0023	0.0505
chrY	59373566	32117	0.0005	0.0272

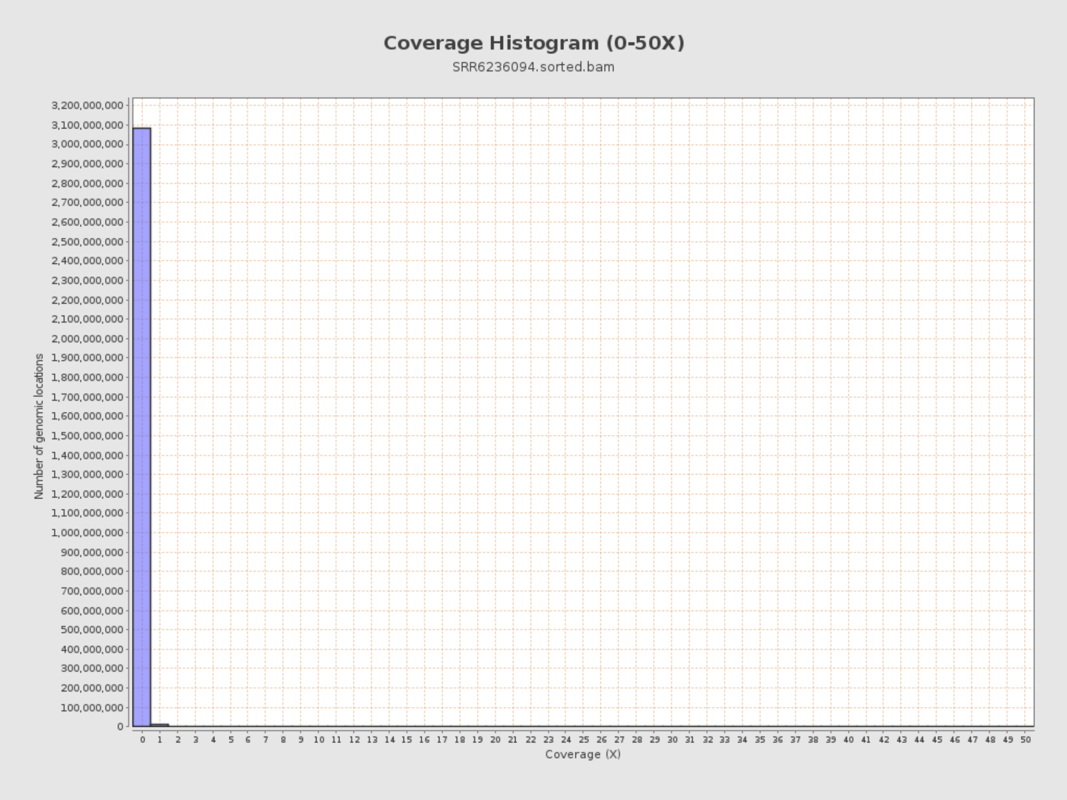
3. Results : Coverage across reference



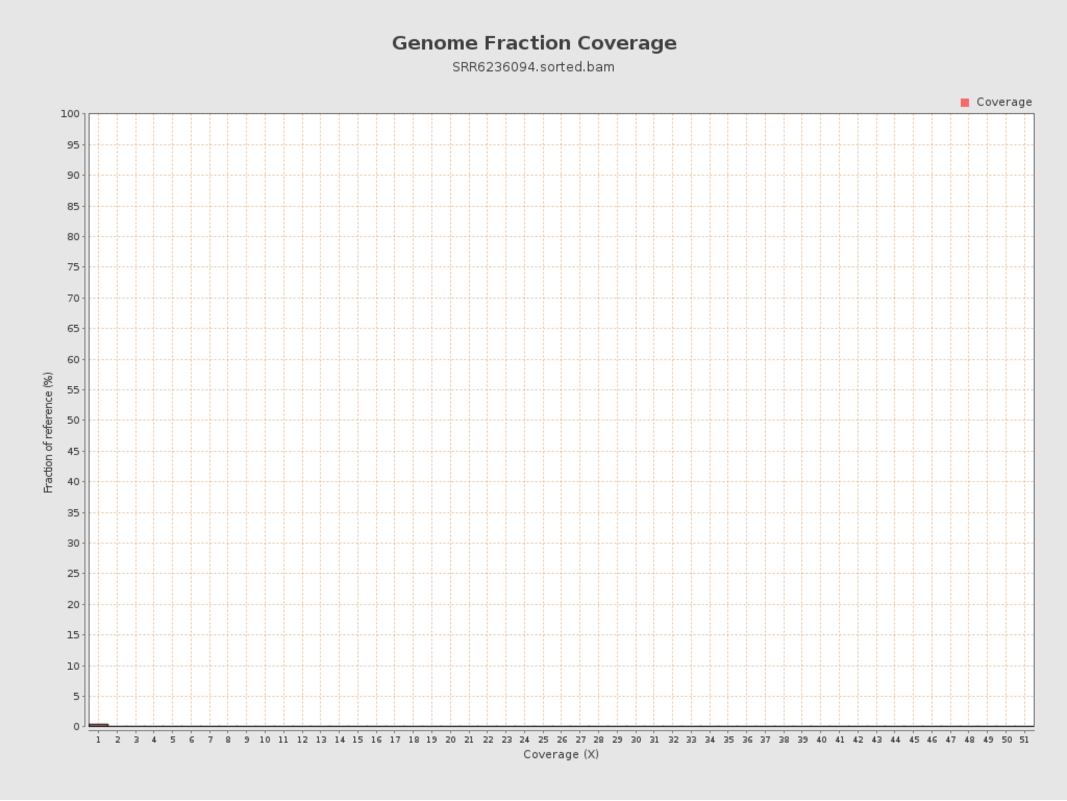
4. Results : Coverage Histogram



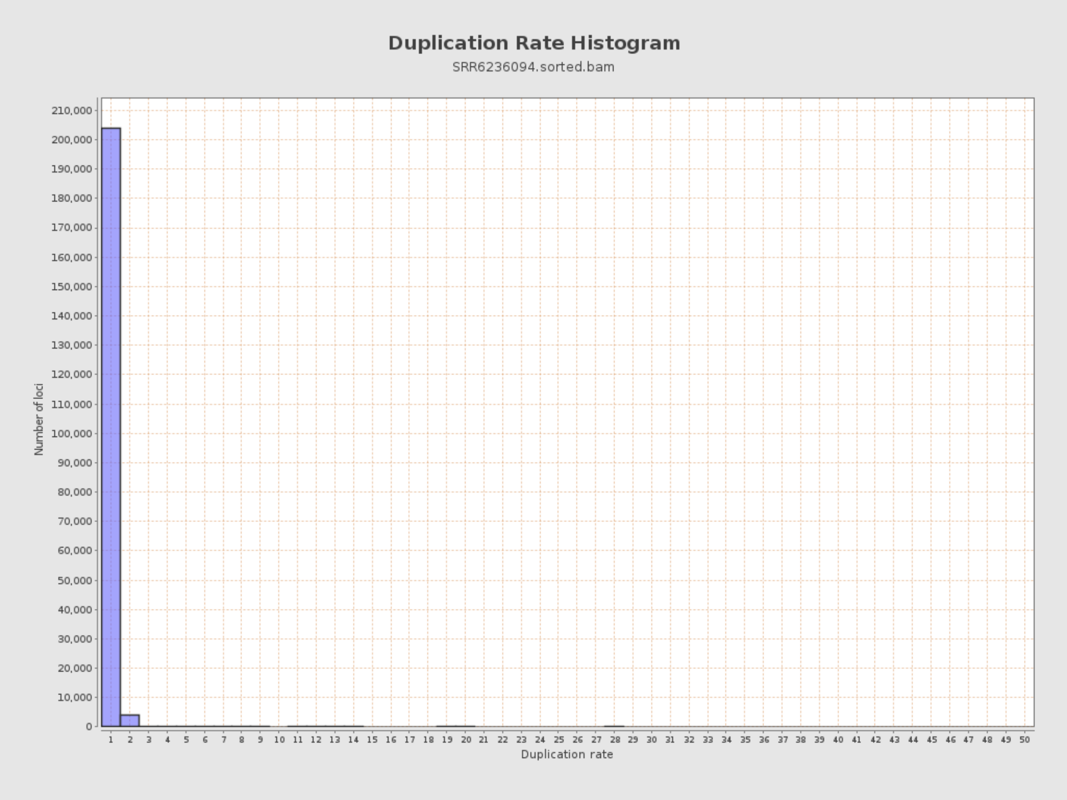
5. Results : Coverage Histogram (0-50X)



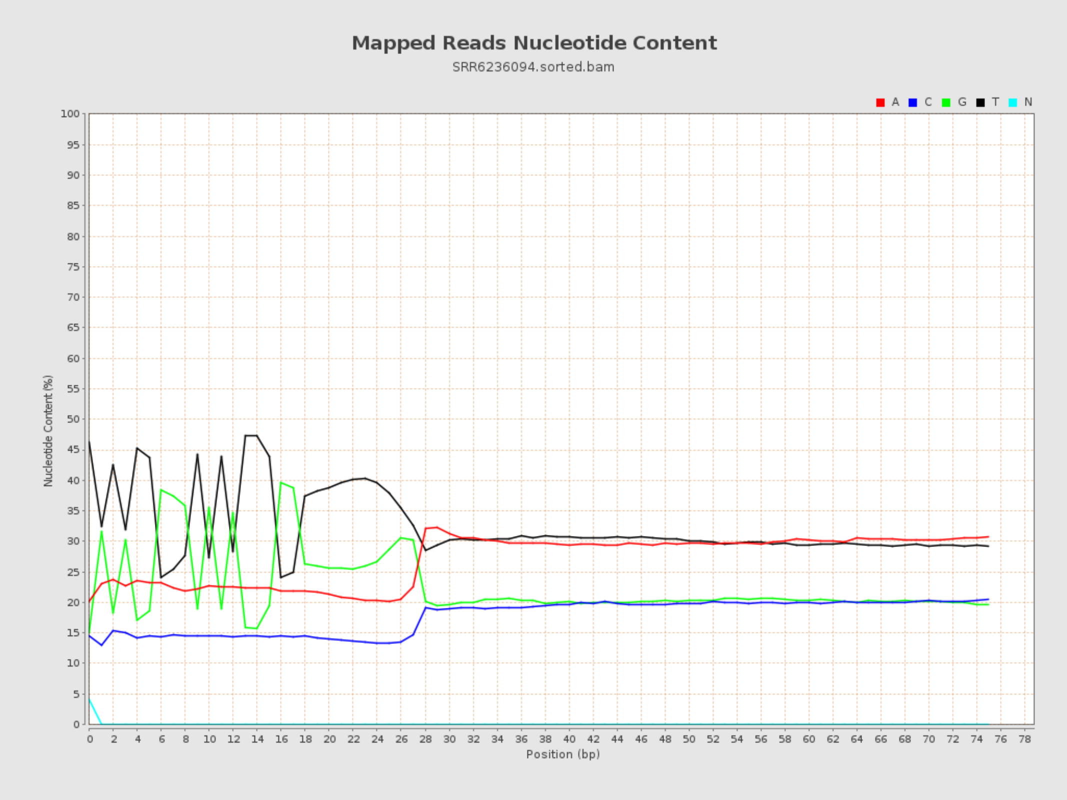
6. Results : Genome Fraction Coverage



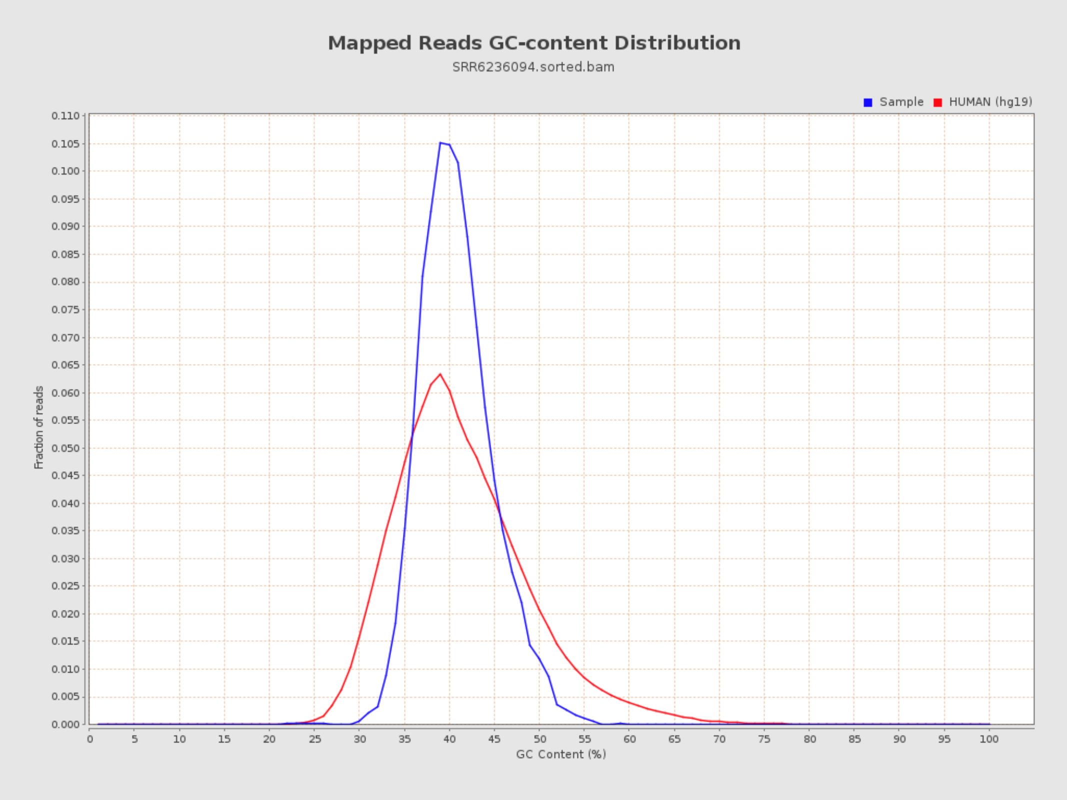
7. Results : Duplication Rate Histogram



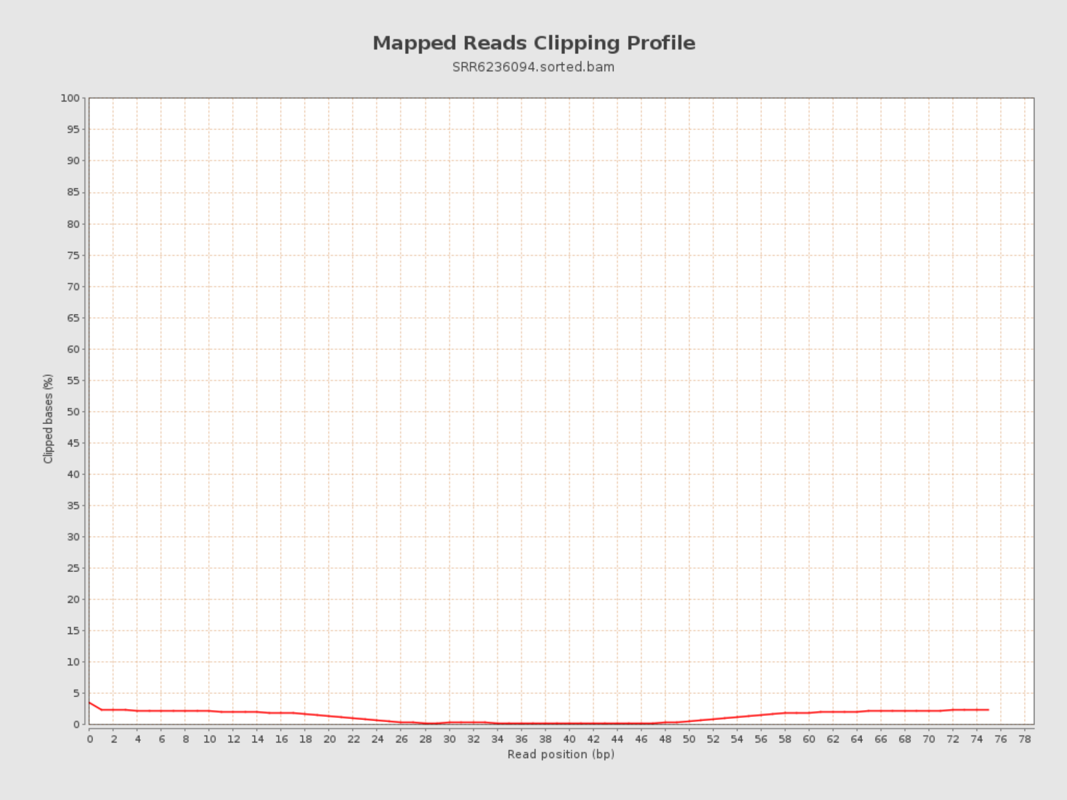
8. Results : Mapped Reads Nucleotide Content



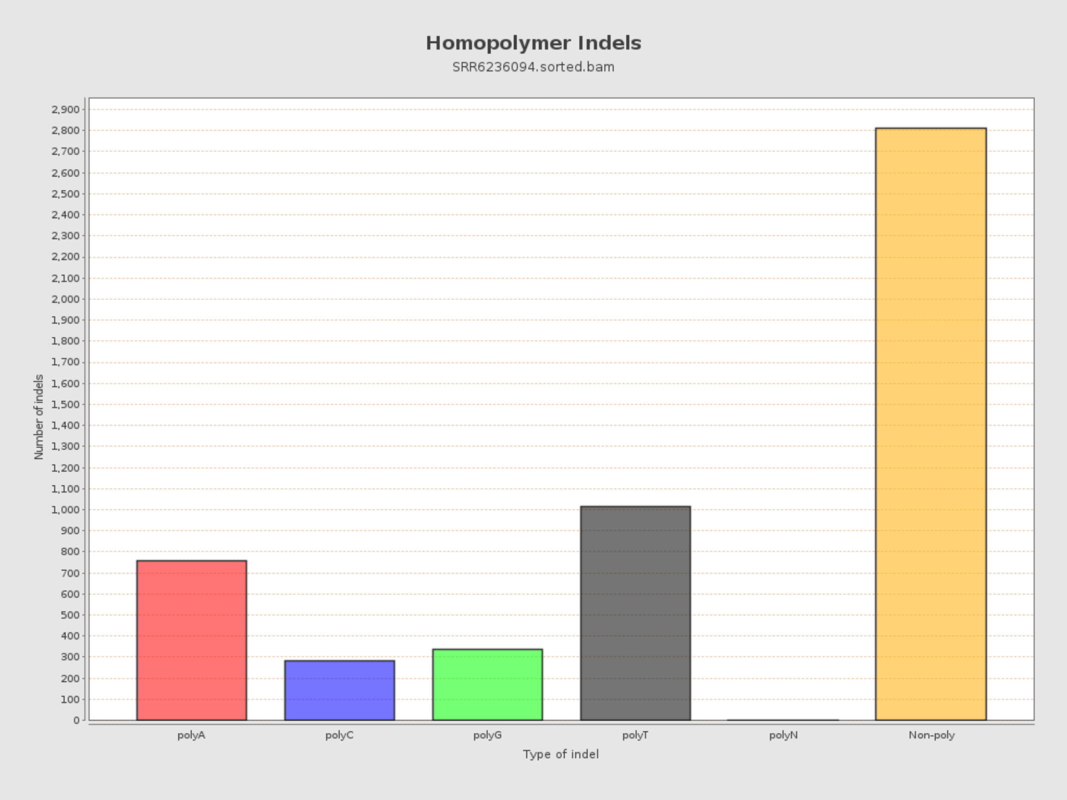
9. Results : Mapped Reads GC-content Distribution



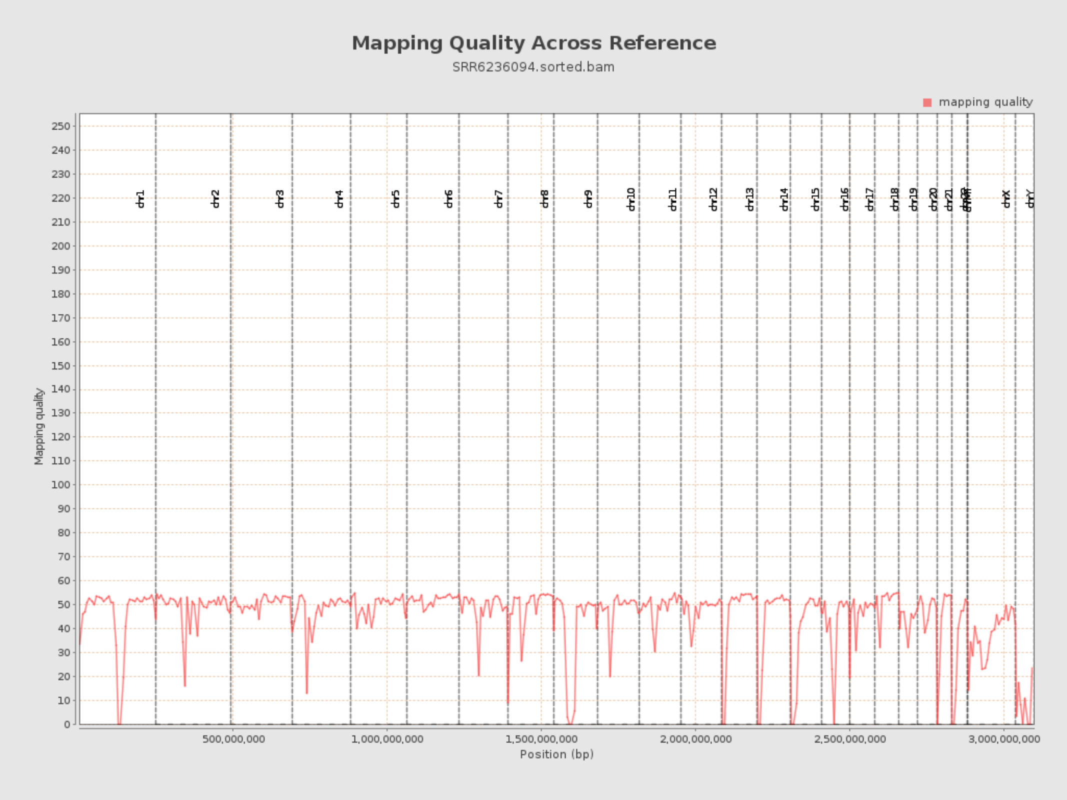
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram