Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:37:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971296.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_SRR2971296 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971296.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:37:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971296.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,646,085
Mapped reads	8,488,234 / 79.73%
Unmapped reads	2,157,851 / 20.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	549,927 / 5.17%
Duplication rate	5.37%
Clipped reads	654,686 / 6.15%

2.2. ACGT Content

Number/percentage of A's	97,725,359 / 29.12%
Number/percentage of C's	68,182,459 / 20.32%
Number/percentage of T's	99,561,134 / 29.67%
Number/percentage of G's	70,083,814 / 20.89%
Number/percentage of N's	5,777 / 0%
GC Percentage	41.2%

2.3. Coverage

Mean	0.1084
Standard Deviation	0.7698

2.4. Mapping Quality

Mean Mapping Quality	41.8

2.5. Mismatches and indels

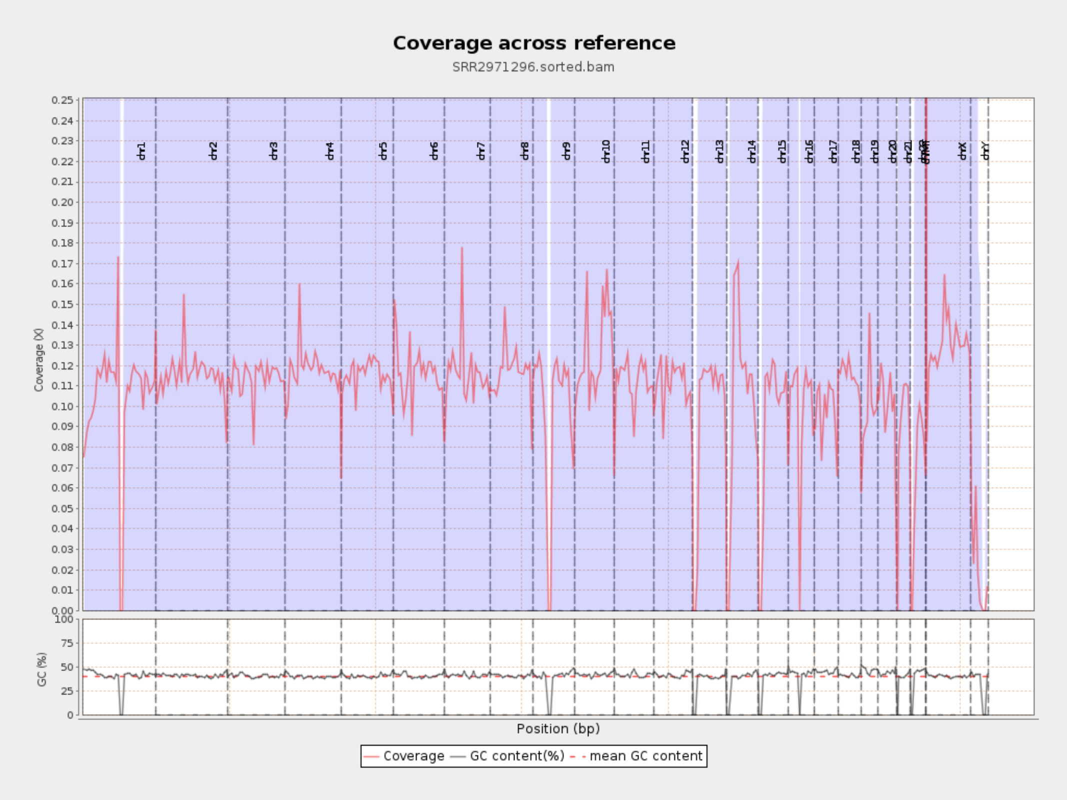
General error rate	0.26%
Mismatches	854,131
Insertions	9,412
Mapped reads with at least one insertion	0.11%
Deletions	22,386
Mapped reads with at least one deletion	0.26%
Homopolymer indels	41.03%

2.6. Chromosome stats

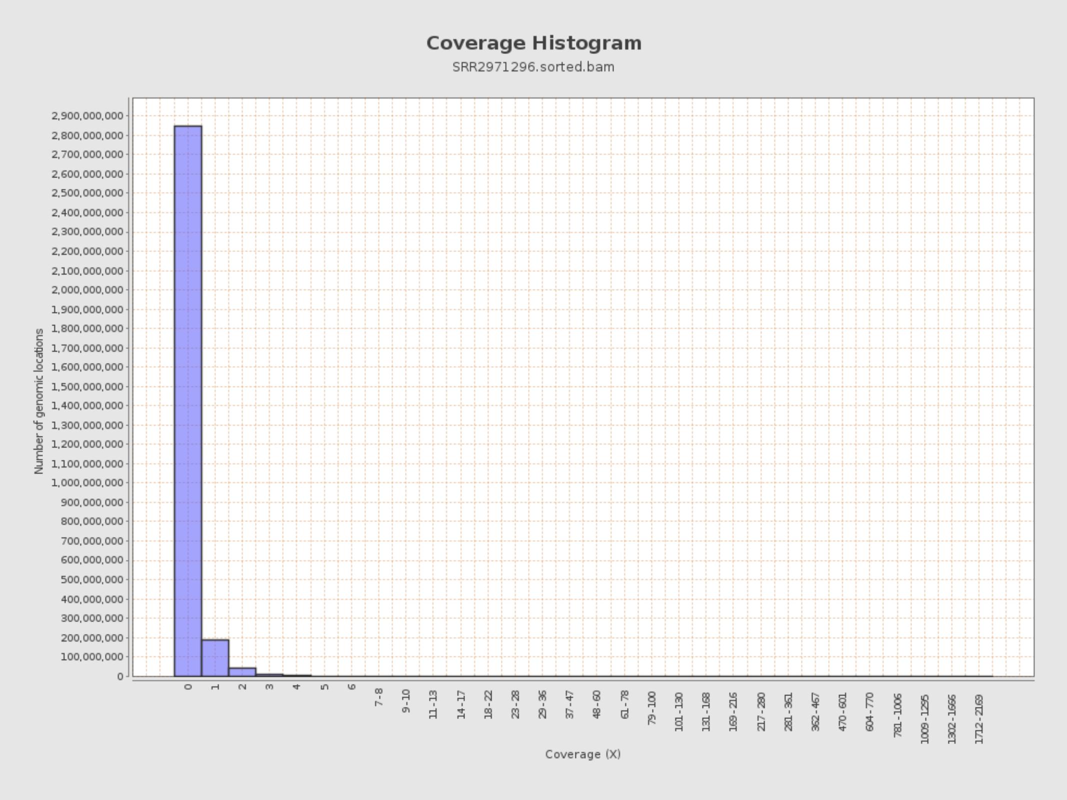
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26061853	0.1046	1.499
chr2	243199373	28149084	0.1157	0.6486
chr3	198022430	22612896	0.1142	0.438
chr4	191154276	22631714	0.1184	0.5016
chr5	180915260	20871384	0.1154	0.4489
chr6	171115067	19983743	0.1168	0.5205
chr7	159138663	18518753	0.1164	1.0065
chr8	146364022	17110955	0.1169	1.1653

chr9	141213431	13892526	0.0984	0.6198
chr10	135534747	17137655	0.1264	0.6949
chr11	135006516	15167796	0.1123	0.6244
chr12	133851895	14926846	0.1115	0.4491
chr13	115169878	10932922	0.0949	0.3944
chr14	107349540	11371044	0.1059	0.5068
chr15	102531392	9298820	0.0907	0.3881
chr16	90354753	8666286	0.0959	0.4616
chr17	81195210	8000710	0.0985	0.4637
chr18	78077248	9022361	0.1156	1.4178
chr19	59128983	5875639	0.0994	1.3266
chr20	63025520	6495049	0.1031	0.4417
chr21	48129895	4274916	0.0888	0.4692
chr22	51304566	3319932	0.0647	0.3741
chrMT	16571	37047	2.2357	2.4883
chrX	155270560	20065438	0.1292	0.5555
chrY	59373566	1162824	0.0196	0.3204

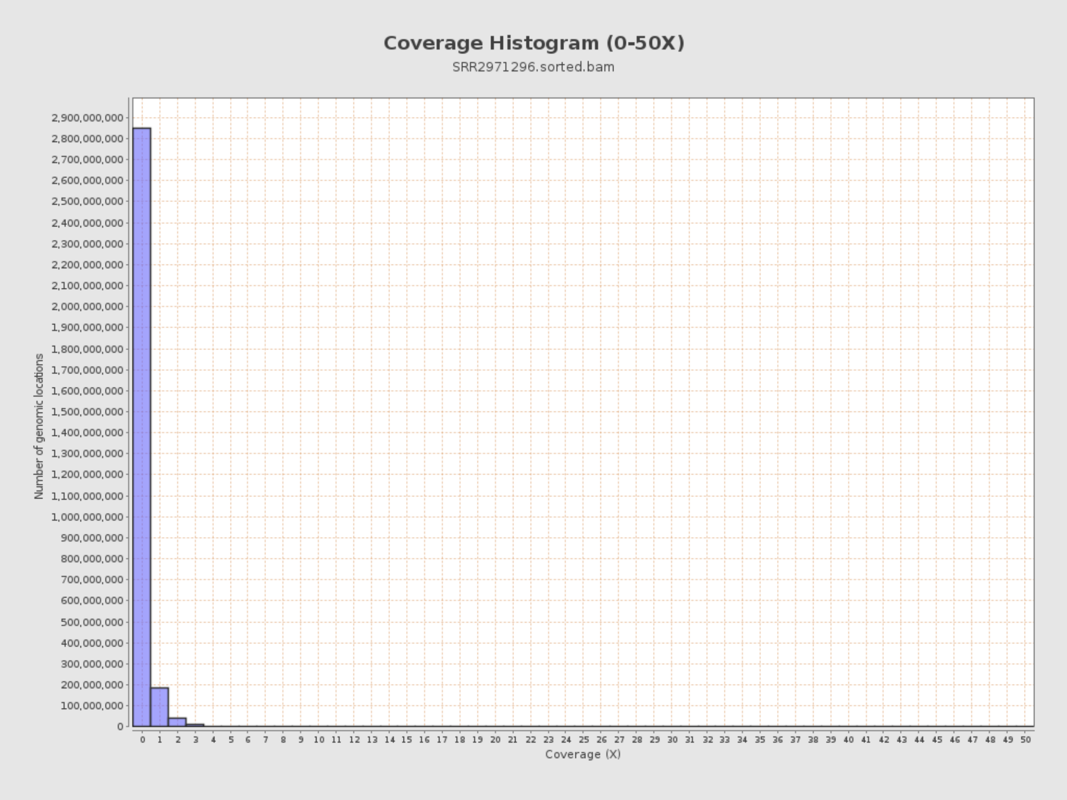
3. Results : Coverage across reference



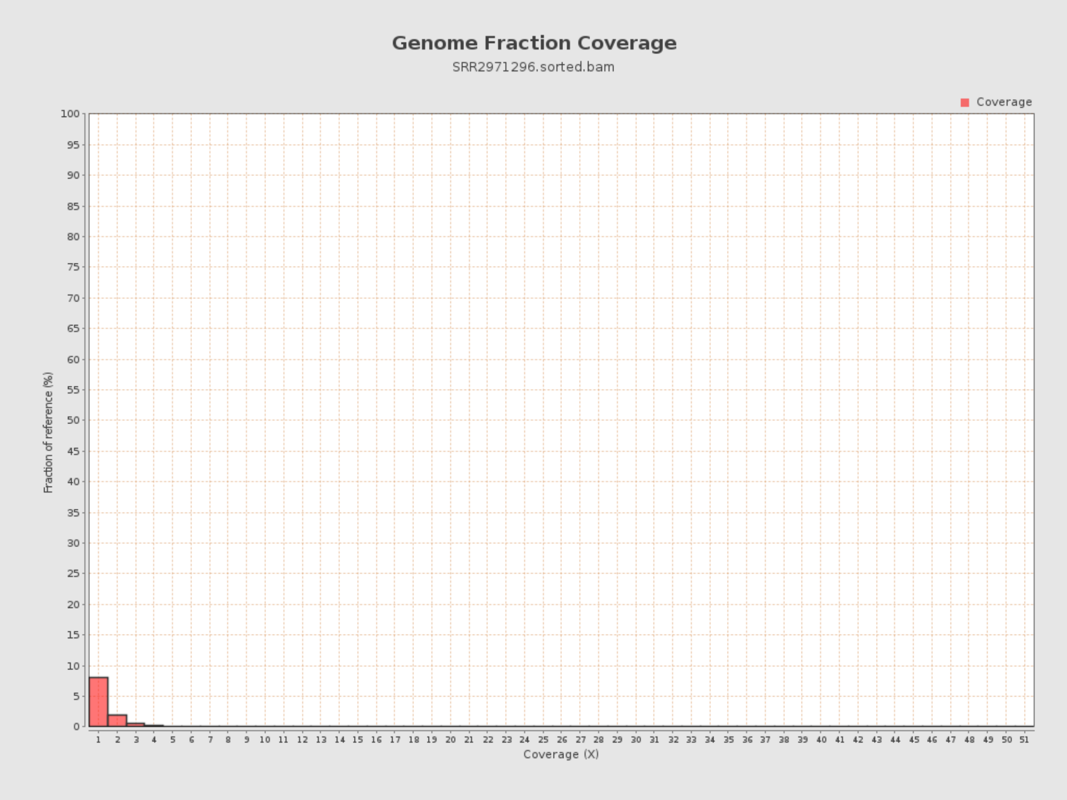
4. Results : Coverage Histogram



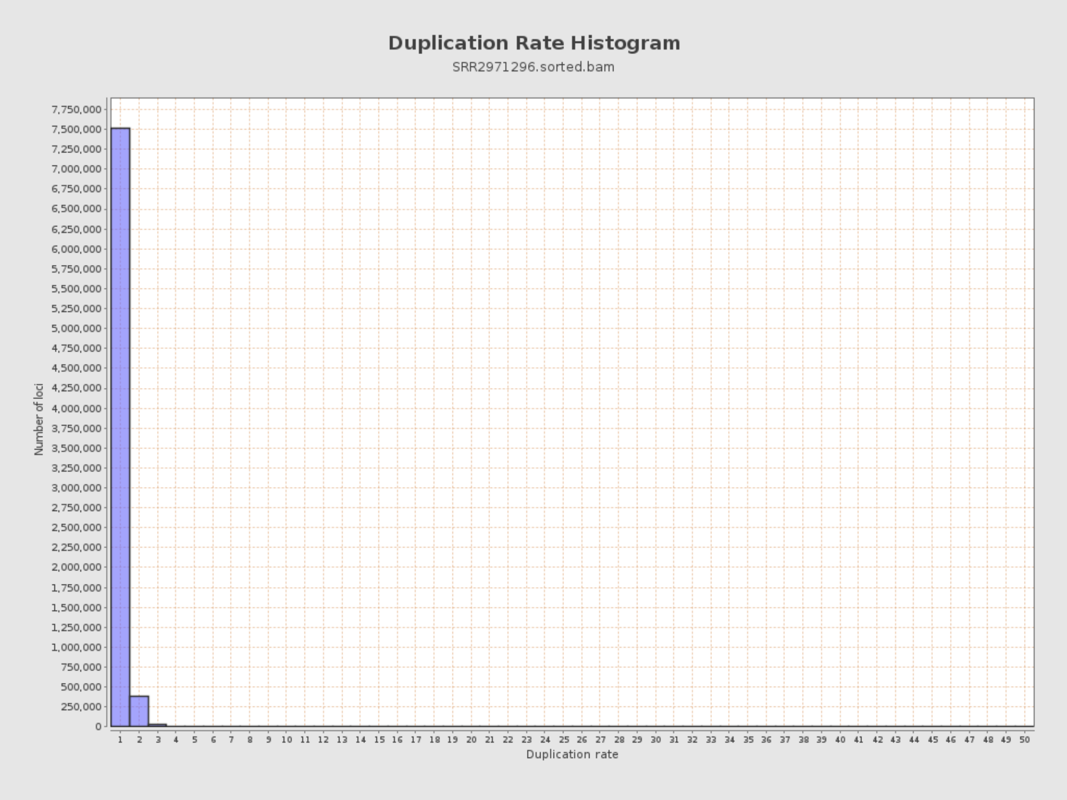
5. Results : Coverage Histogram (0-50X)



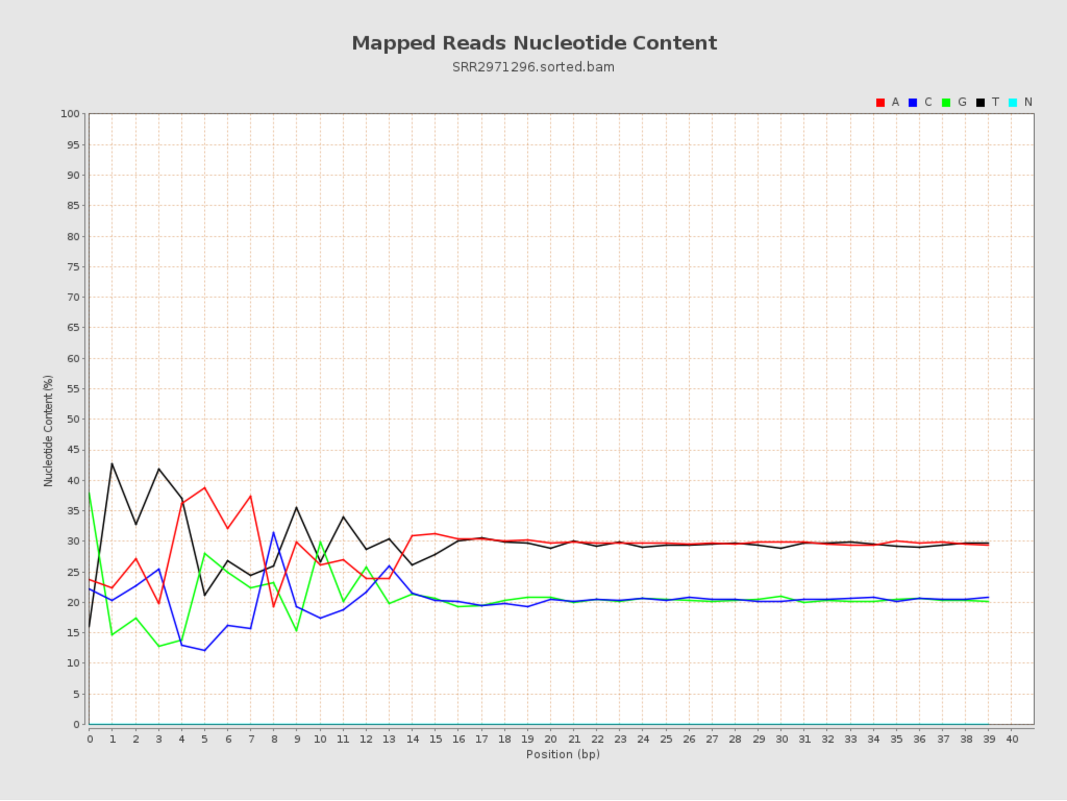
6. Results : Genome Fraction Coverage



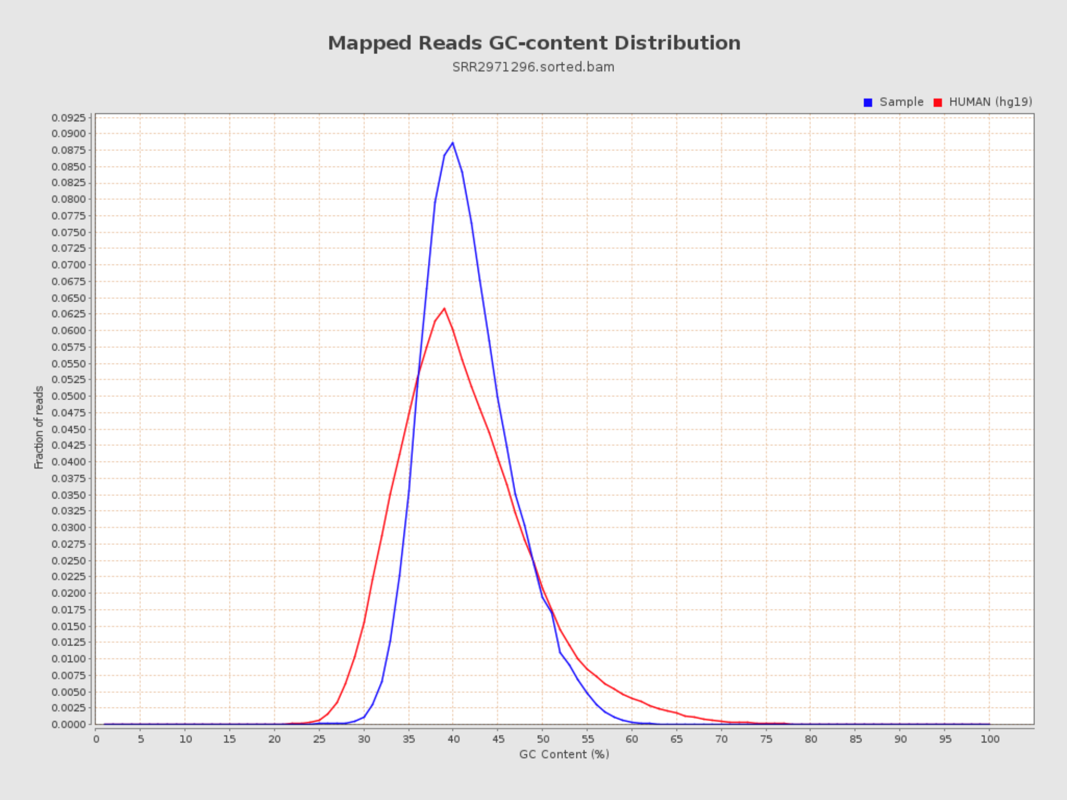
7. Results : Duplication Rate Histogram



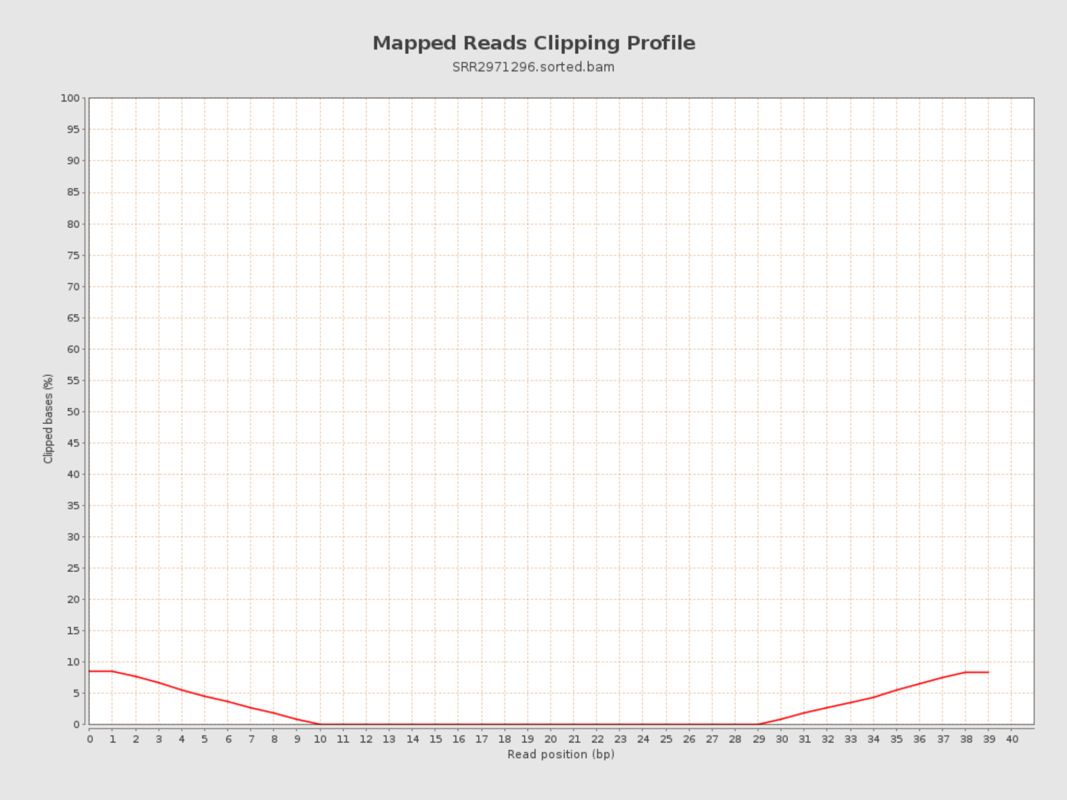
8. Results : Mapped Reads Nucleotide Content



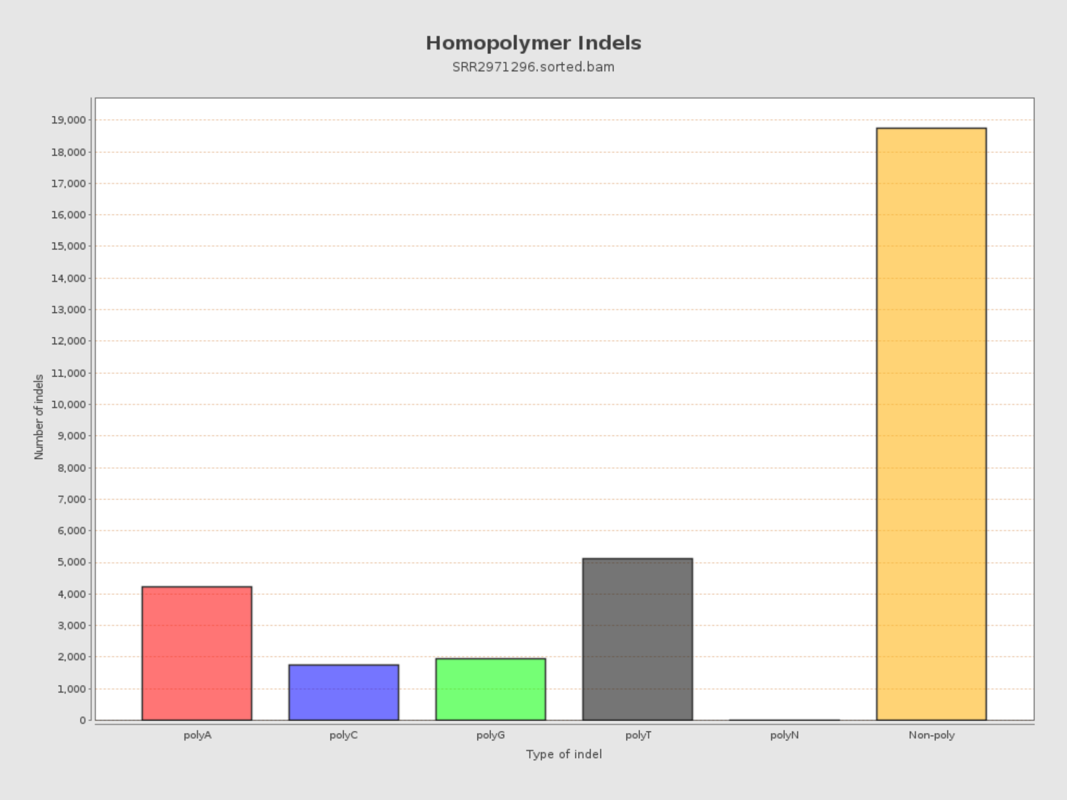
9. Results : Mapped Reads GC-content Distribution



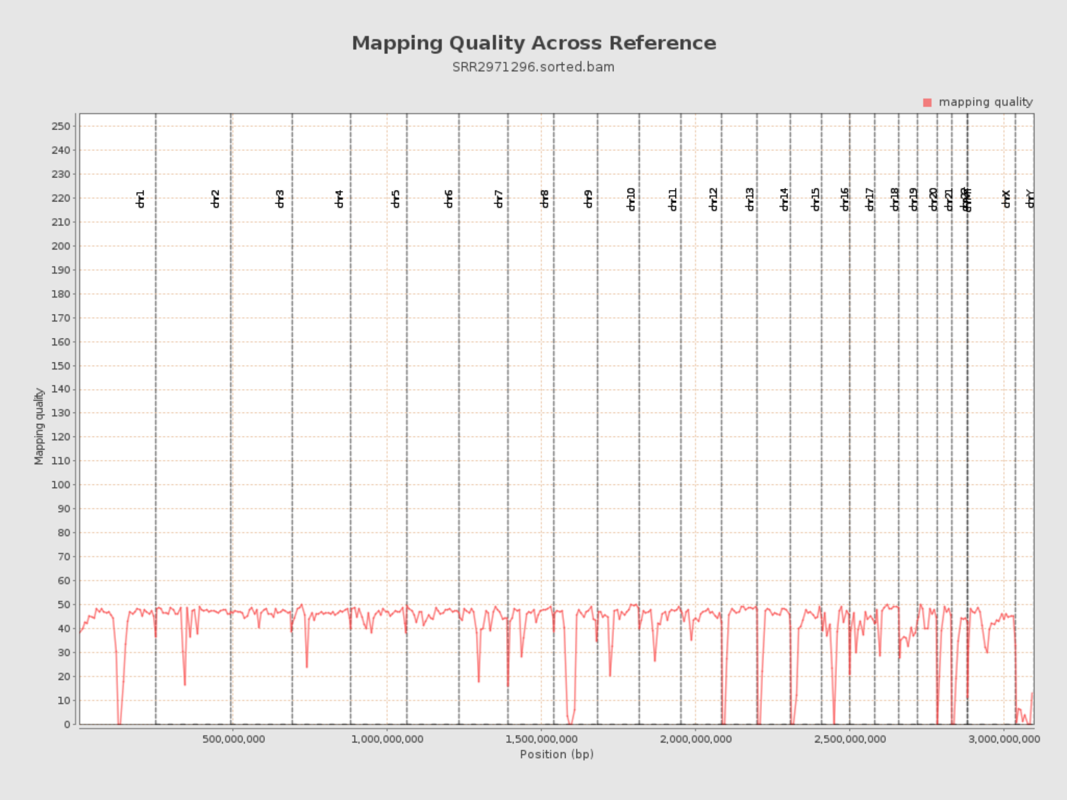
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram