Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:50:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971307.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_SRR2971307 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971307.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:50:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971307.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,268,394
Mapped reads	4,419,343 / 83.88%
Unmapped reads	849,051 / 16.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	183,115 / 3.48%
Duplication rate	3.28%
Clipped reads	380,474 / 7.22%

2.2. ACGT Content

Number/percentage of A's	51,651,024 / 29.6%
Number/percentage of C's	34,612,615 / 19.83%
Number/percentage of T's	52,919,676 / 30.32%
Number/percentage of G's	35,328,636 / 20.24%
Number/percentage of N's	10,358 / 0.01%
GC Percentage	40.08%

2.3. Coverage

Mean	0.0564
Standard Deviation	0.4473

2.4. Mapping Quality

Mean Mapping Quality	42.82

2.5. Mismatches and indels

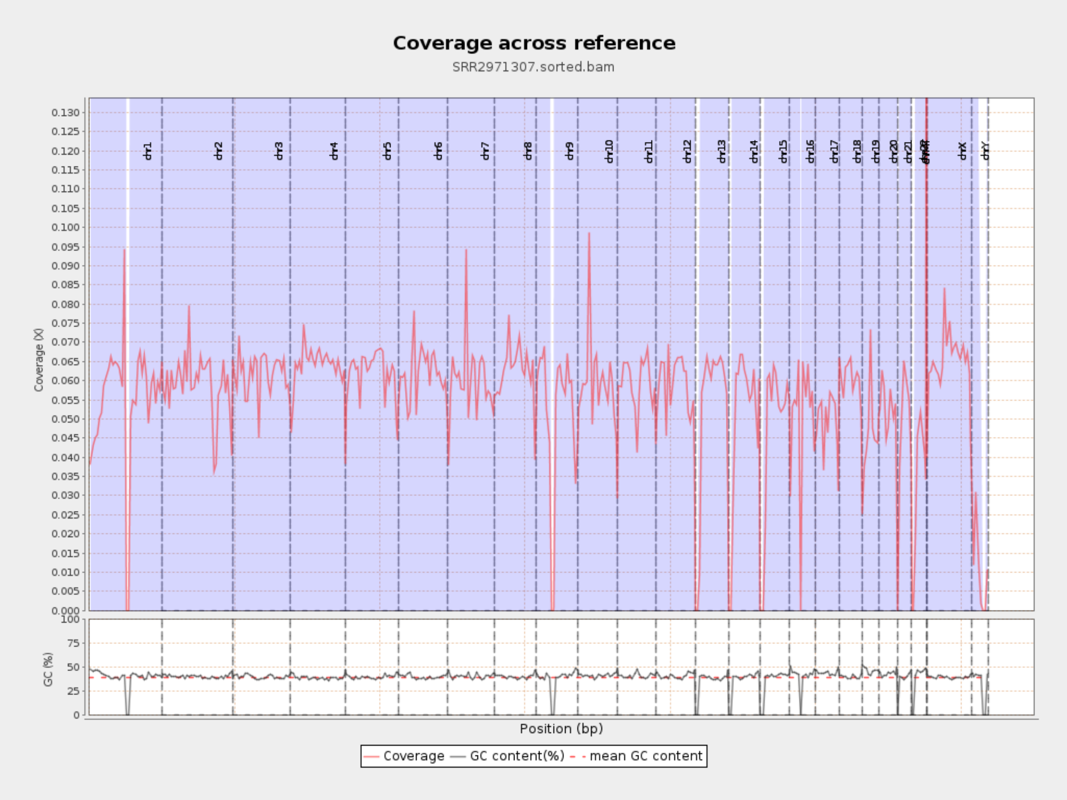
General error rate	0.27%
Mismatches	473,085
Insertions	5,691
Mapped reads with at least one insertion	0.13%
Deletions	13,237
Mapped reads with at least one deletion	0.3%
Homopolymer indels	40.88%

2.6. Chromosome stats

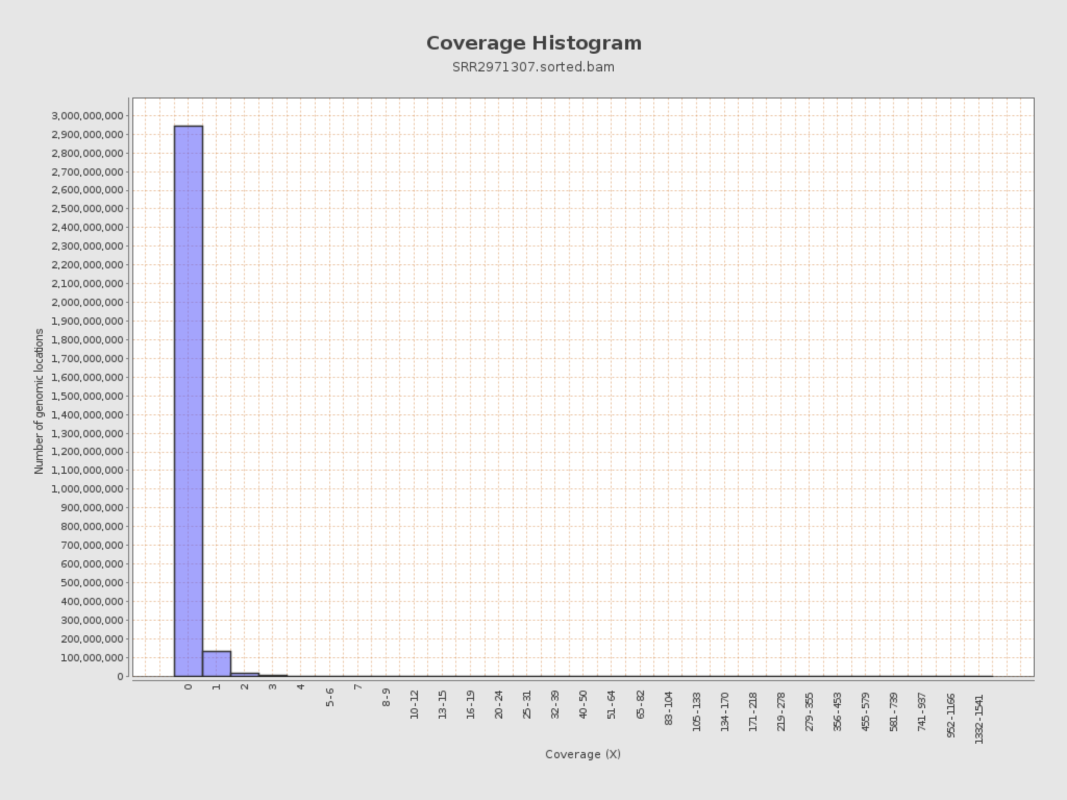
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13706703	0.055	0.8476
chr2	243199373	14344674	0.059	0.3574
chr3	198022430	12257930	0.0619	0.2789
chr4	191154276	12263193	0.0642	0.294
chr5	180915260	11258669	0.0622	0.2808
chr6	171115067	10575449	0.0618	0.3256
chr7	159138663	9644928	0.0606	0.5658
chr8	146364022	9157435	0.0626	0.8068

chr9	141213431	7266898	0.0515	0.3588
chr10	135534747	8141033	0.0601	0.4338
chr11	135006516	7953066	0.0589	0.3615
chr12	133851895	7902952	0.059	0.2777
chr13	115169878	5945942	0.0516	0.251
chr14	107349540	5300744	0.0494	0.2959
chr15	102531392	4773319	0.0466	0.2382
chr16	90354753	4534165	0.0502	0.3078
chr17	81195210	3981237	0.049	0.2772
chr18	78077248	4742390	0.0607	0.608
chr19	59128983	2781259	0.047	0.7473
chr20	63025520	3305186	0.0524	0.2609
chr21	48129895	2269515	0.0472	0.2679
chr22	51304566	1638615	0.0319	0.1998
chrMT	16571	6652	0.4014	0.749
chrX	155270560	10144243	0.0653	0.3229
chrY	59373566	642699	0.0108	0.1659

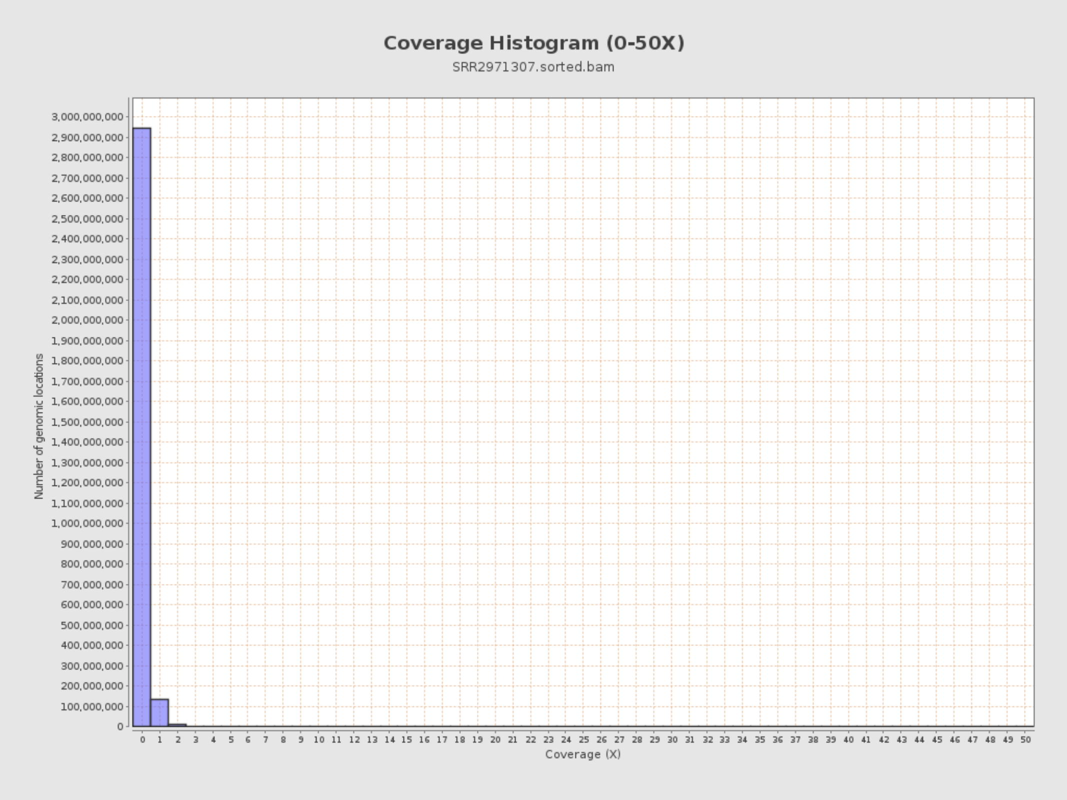
3. Results : Coverage across reference



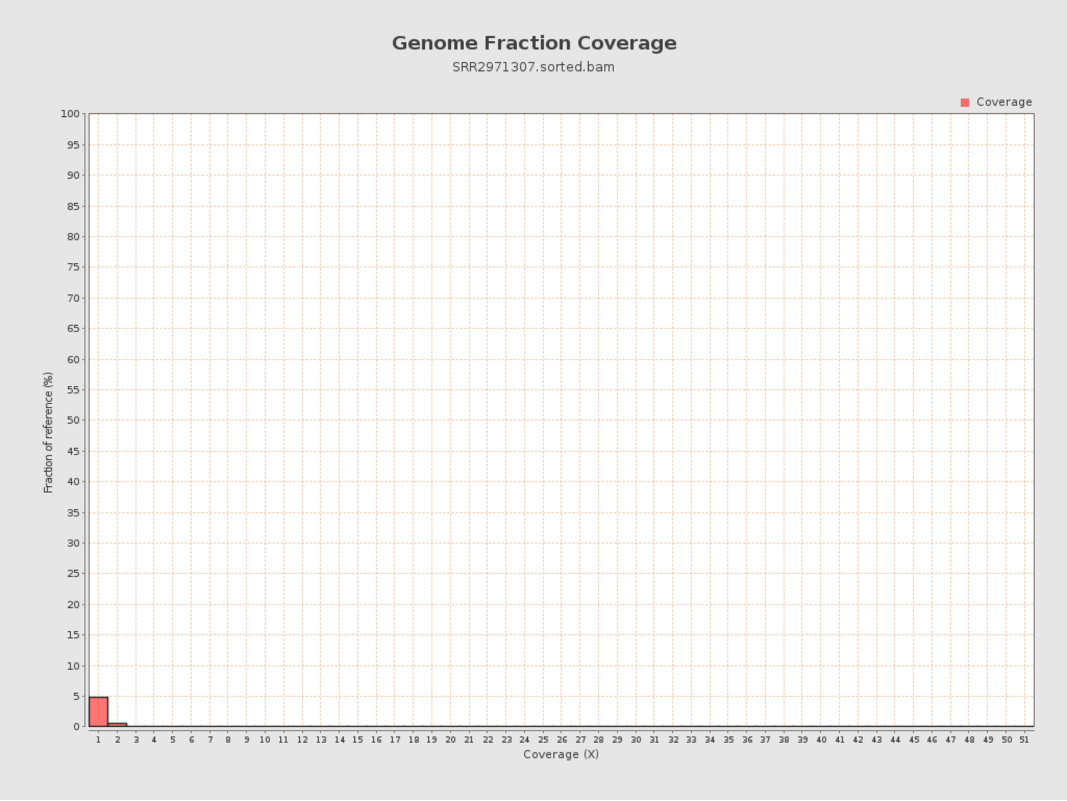
4. Results : Coverage Histogram



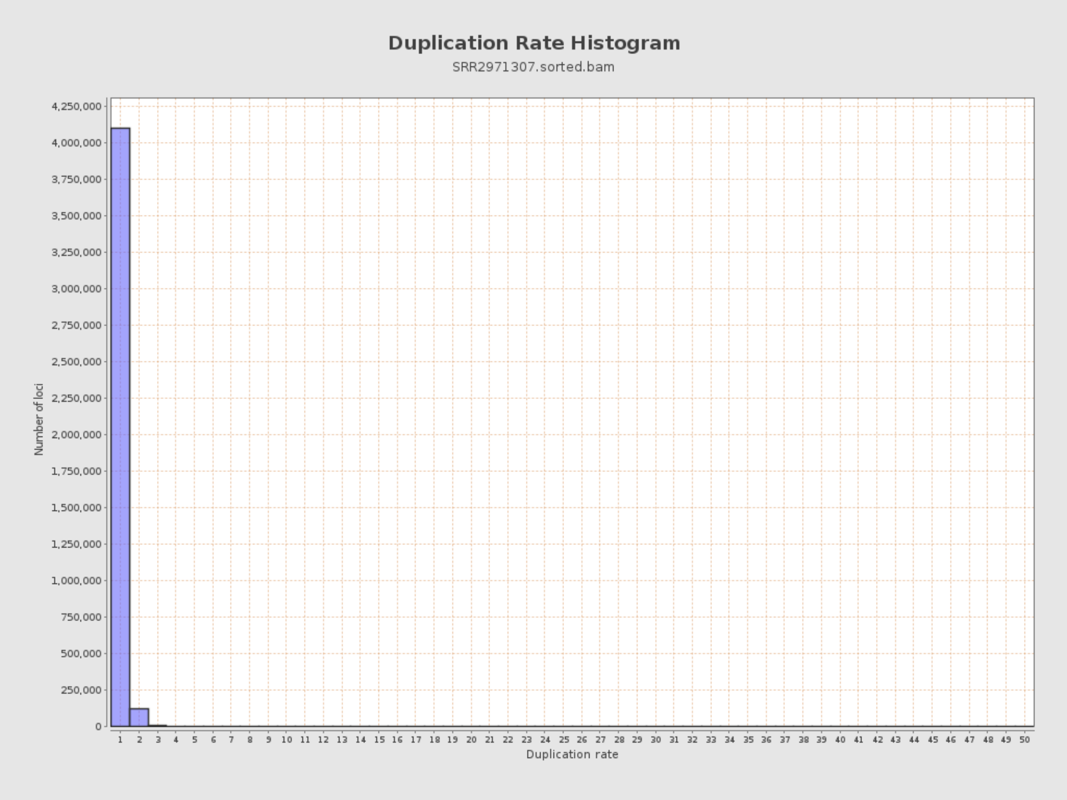
5. Results : Coverage Histogram (0-50X)



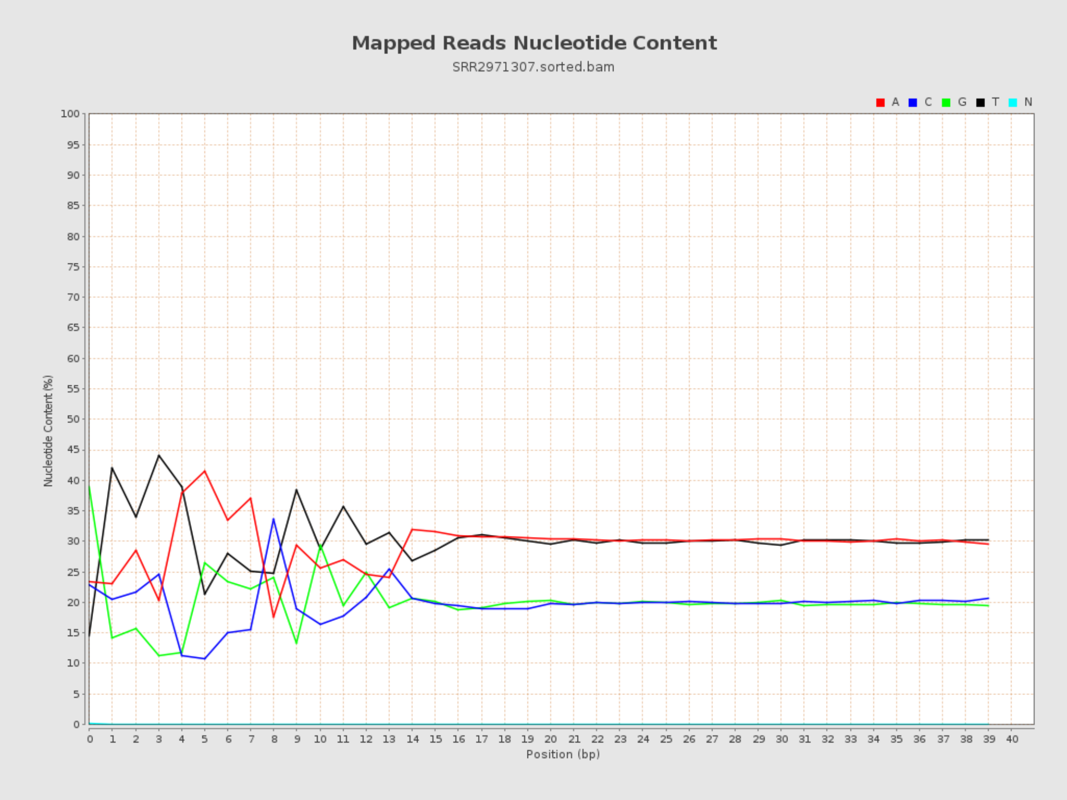
6. Results : Genome Fraction Coverage



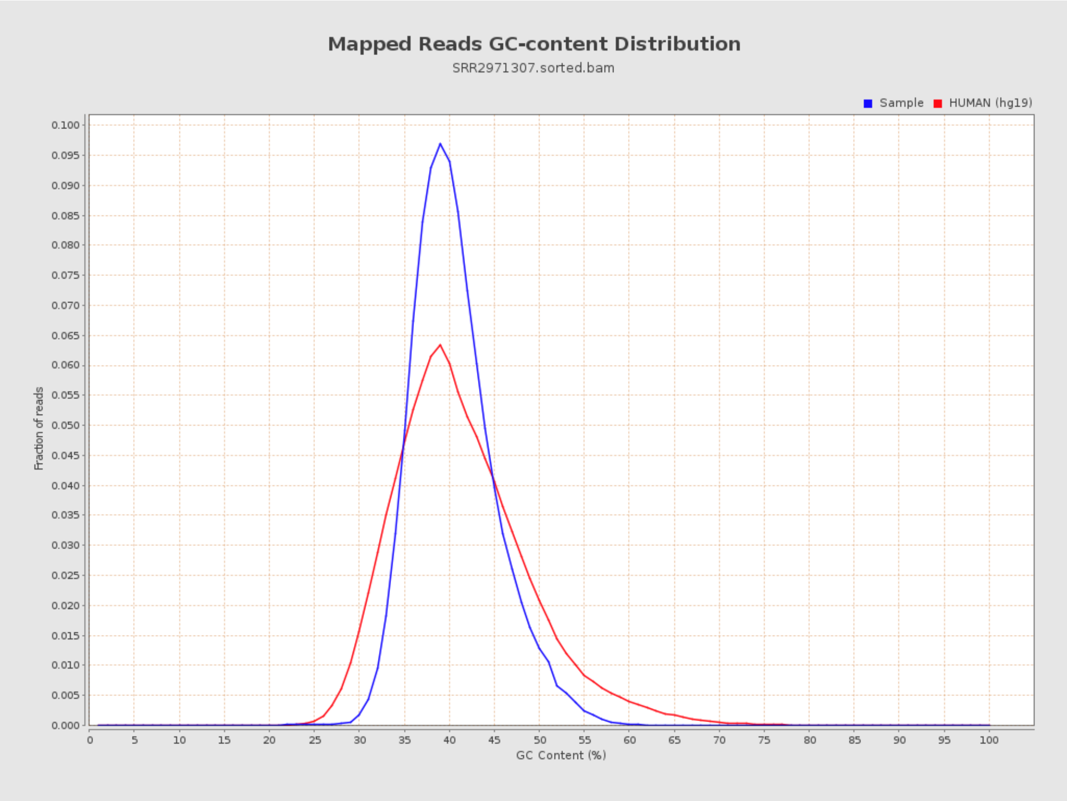
7. Results : Duplication Rate Histogram



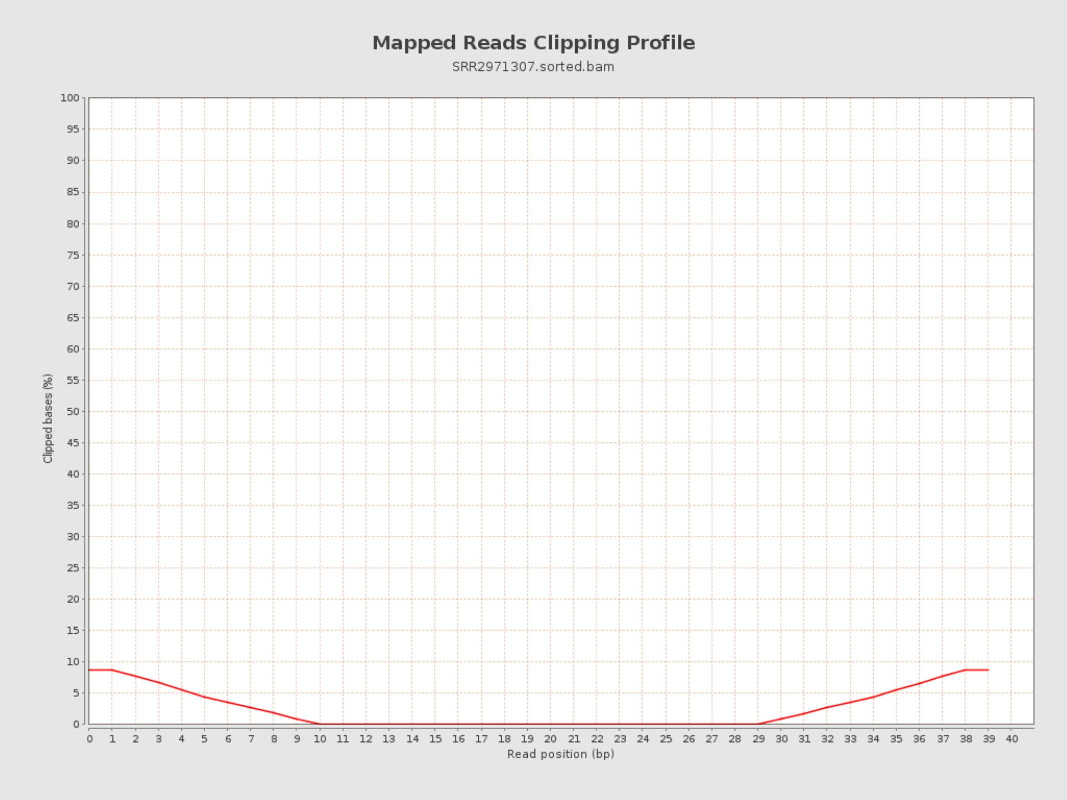
8. Results : Mapped Reads Nucleotide Content



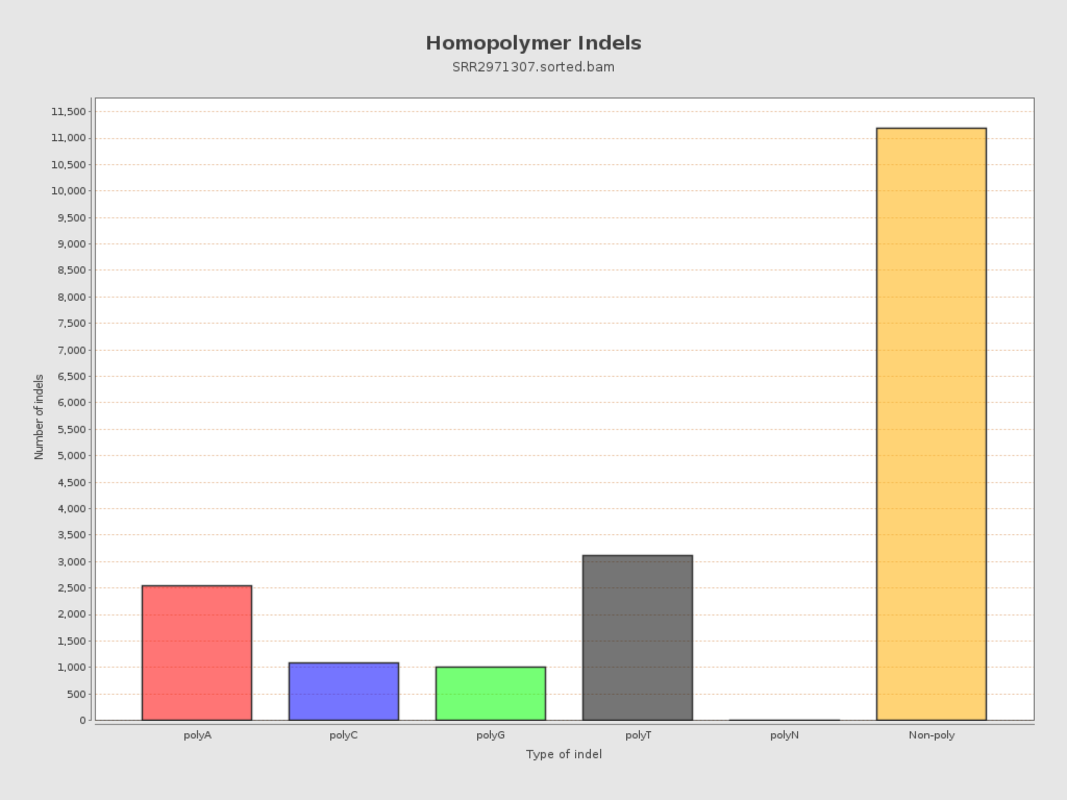
9. Results : Mapped Reads GC-content Distribution



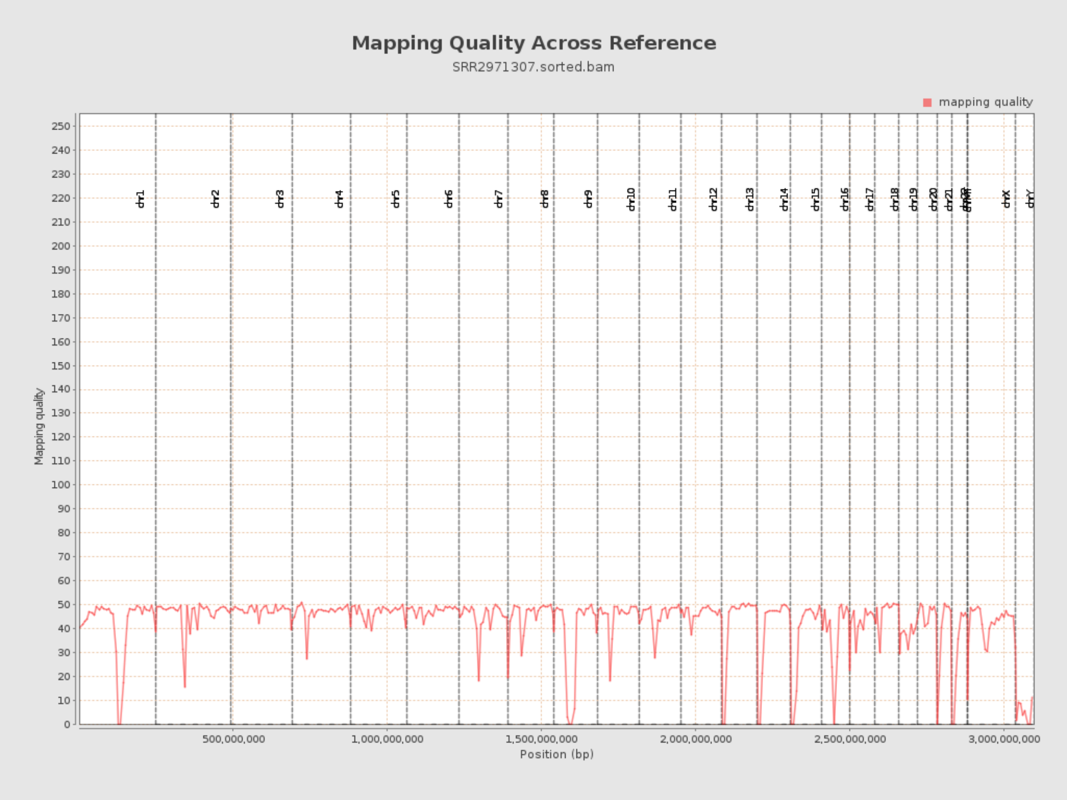
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram