Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:55:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716971.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_SRR9716971 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716971.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:55:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716971.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,855,075
Mapped reads	3,347,817 / 86.84%
Unmapped reads	507,258 / 13.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,167 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	150,859 / 3.91%
Duplication rate	3.14%
Clipped reads	3,351,088 / 86.93%

2.2. ACGT Content

Number/percentage of A's	48,563,205 / 25.59%
Number/percentage of C's	37,182,401 / 19.6%
Number/percentage of T's	59,635,630 / 31.43%
Number/percentage of G's	44,355,322 / 23.38%
Number/percentage of N's	3,027 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0613

Standard Deviation	0.4817

2.4. Mapping Quality

Mean Mapping Quality	42.84

2.5. Mismatches and indels

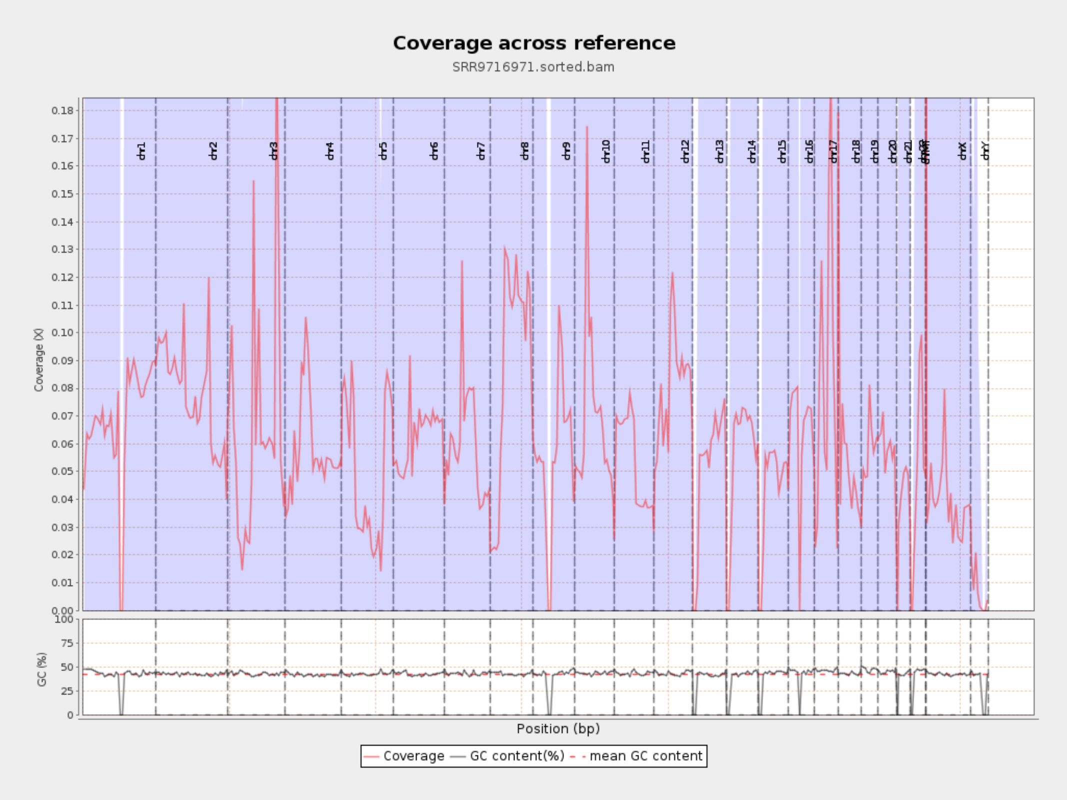
General error rate	0.53%
Mismatches	978,242
Insertions	12,600
Mapped reads with at least one insertion	0.37%
Deletions	37,474
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.28%

2.6. Chromosome stats

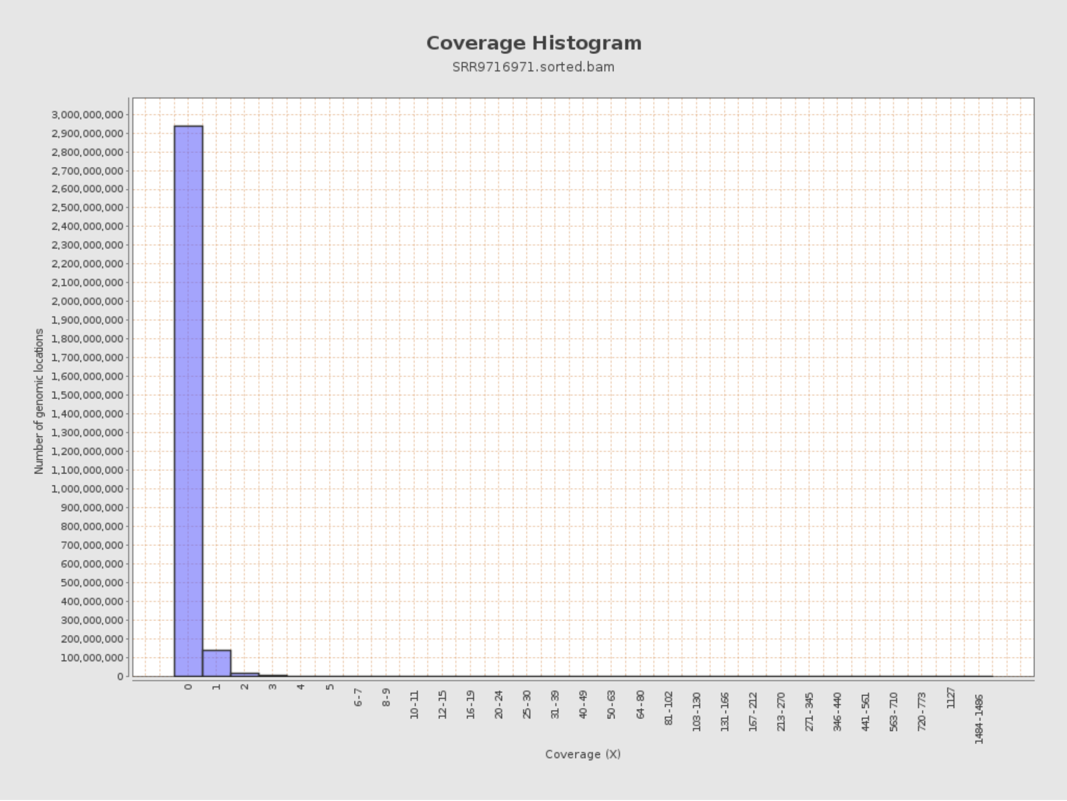
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17066621	0.0685	0.6258
chr2	243199373	18972892	0.078	0.7228
chr3	198022430	13186054	0.0666	0.3526
chr4	191154276	11203403	0.0586	0.3006
chr5	180915260	9001638	0.0498	0.2655
chr6	171115067	10776307	0.063	0.3609
chr7	159138663	9579106	0.0602	0.8276

chr8	146364022	13002134	0.0888	0.4881
chr9	141213431	7799050	0.0552	0.3737
chr10	135534747	9432894	0.0696	0.7606
chr11	135006516	7314592	0.0542	0.3871
chr12	133851895	10964654	0.0819	0.391
chr13	115169878	5982706	0.0519	0.2667
chr14	107349540	6083593	0.0567	0.2943
chr15	102531392	4410381	0.043	0.2581
chr16	90354753	5718762	0.0633	0.3475
chr17	81195210	6955577	0.0857	0.3787
chr18	78077248	4255412	0.0545	0.6067
chr19	59128983	3412164	0.0577	0.6457
chr20	63025520	3705750	0.0588	0.3257
chr21	48129895	1867212	0.0388	0.2481
chr22	51304566	2574839	0.0502	0.2634
chrMT	16571	15521	0.9366	1.21
chrX	155270560	6121258	0.0394	0.3455
chrY	59373566	395488	0.0067	0.1443

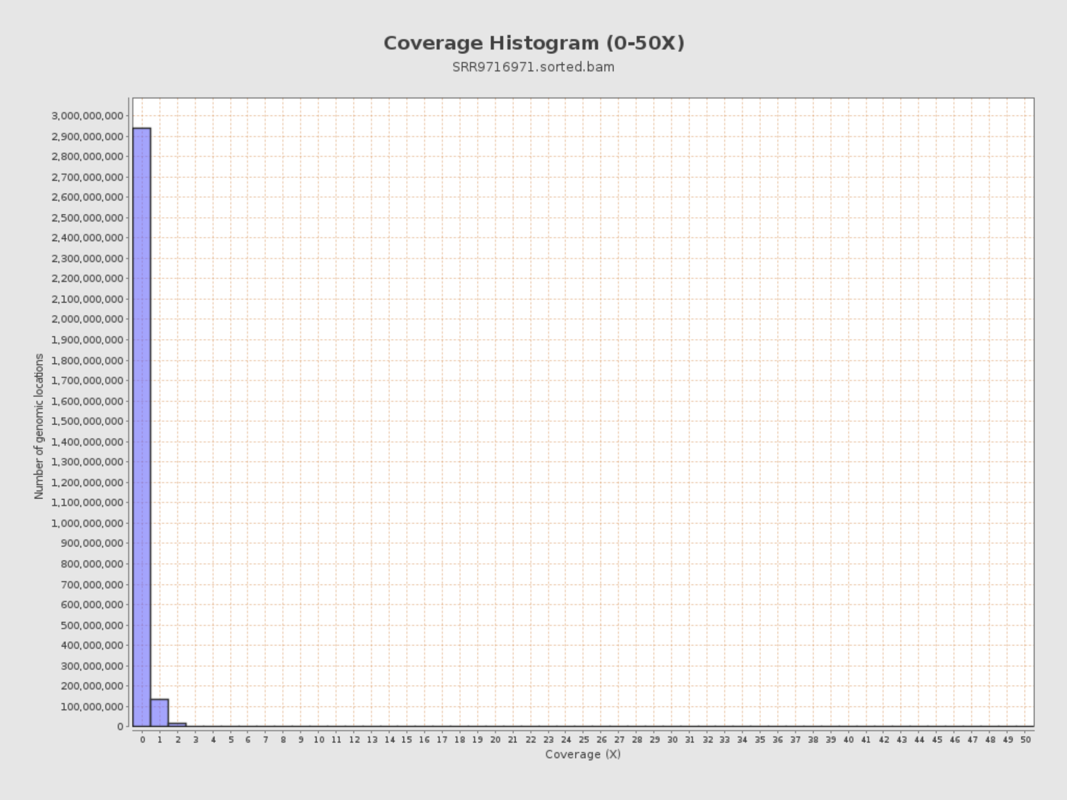
3. Results : Coverage across reference



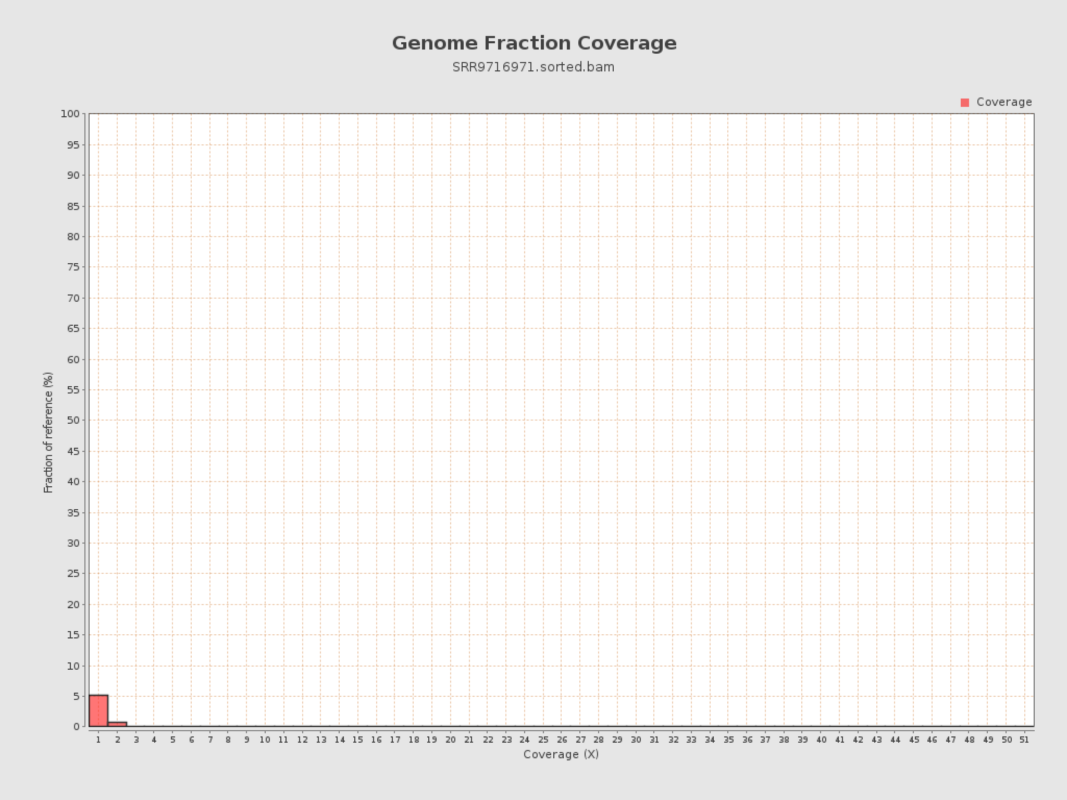
4. Results : Coverage Histogram



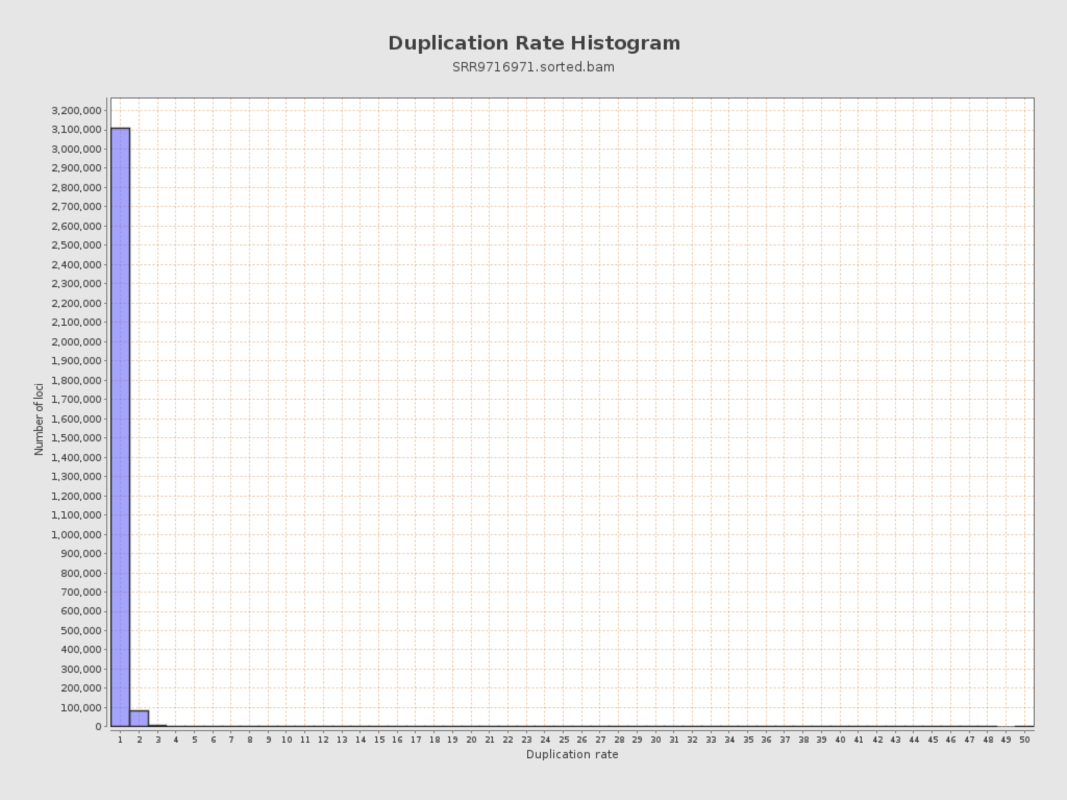
5. Results : Coverage Histogram (0-50X)



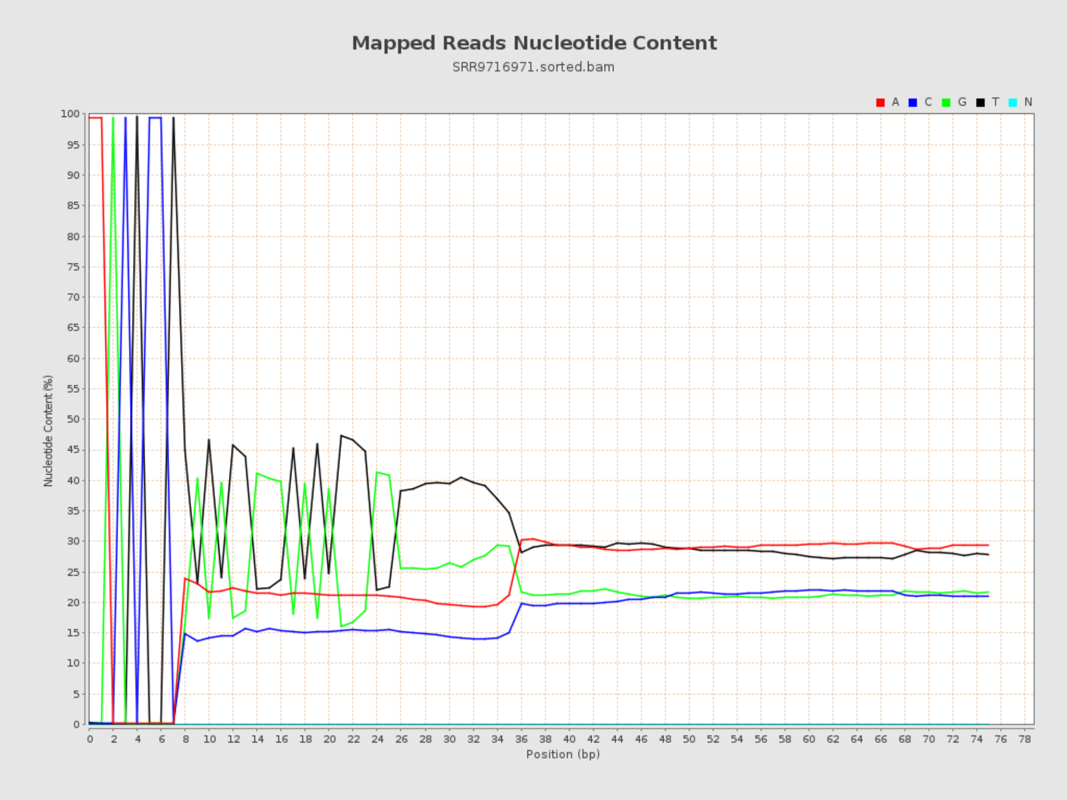
6. Results : Genome Fraction Coverage



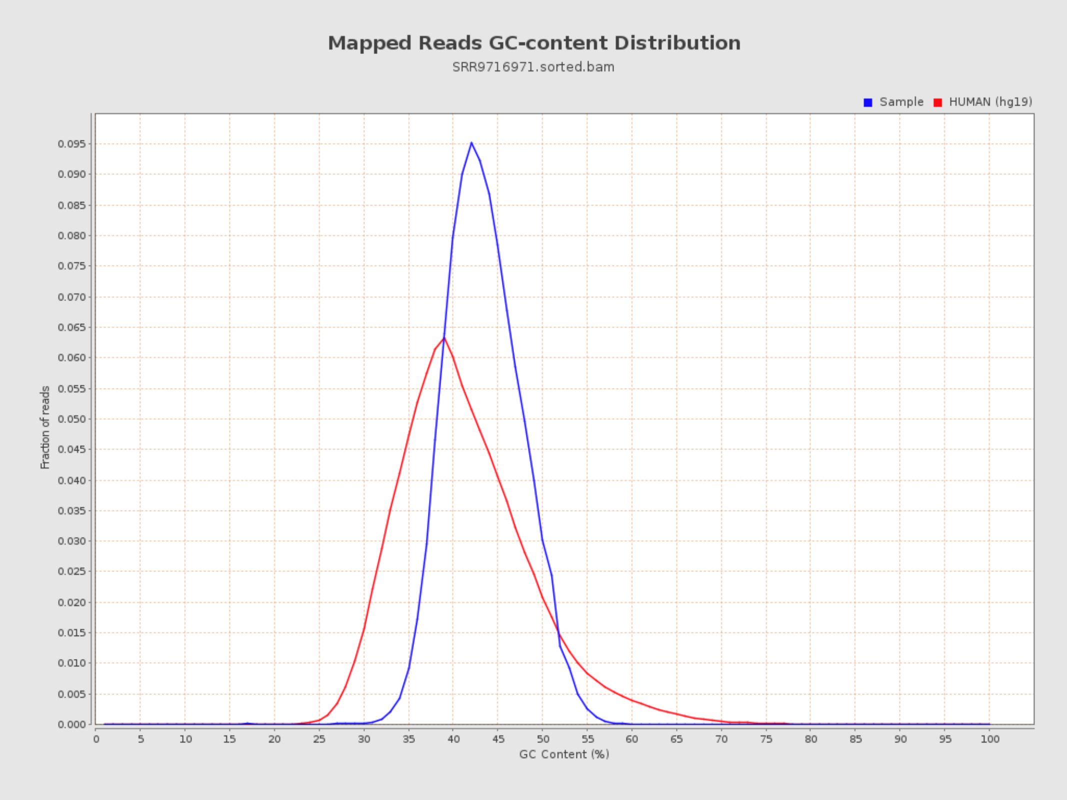
7. Results : Duplication Rate Histogram



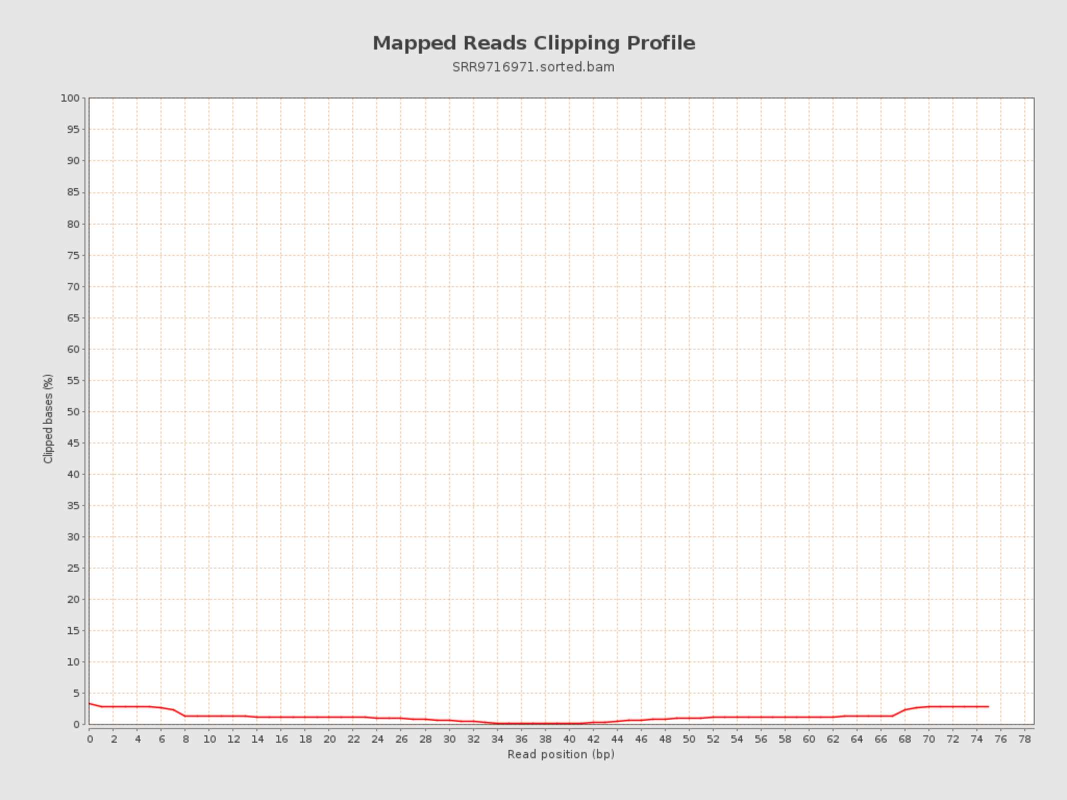
8. Results : Mapped Reads Nucleotide Content



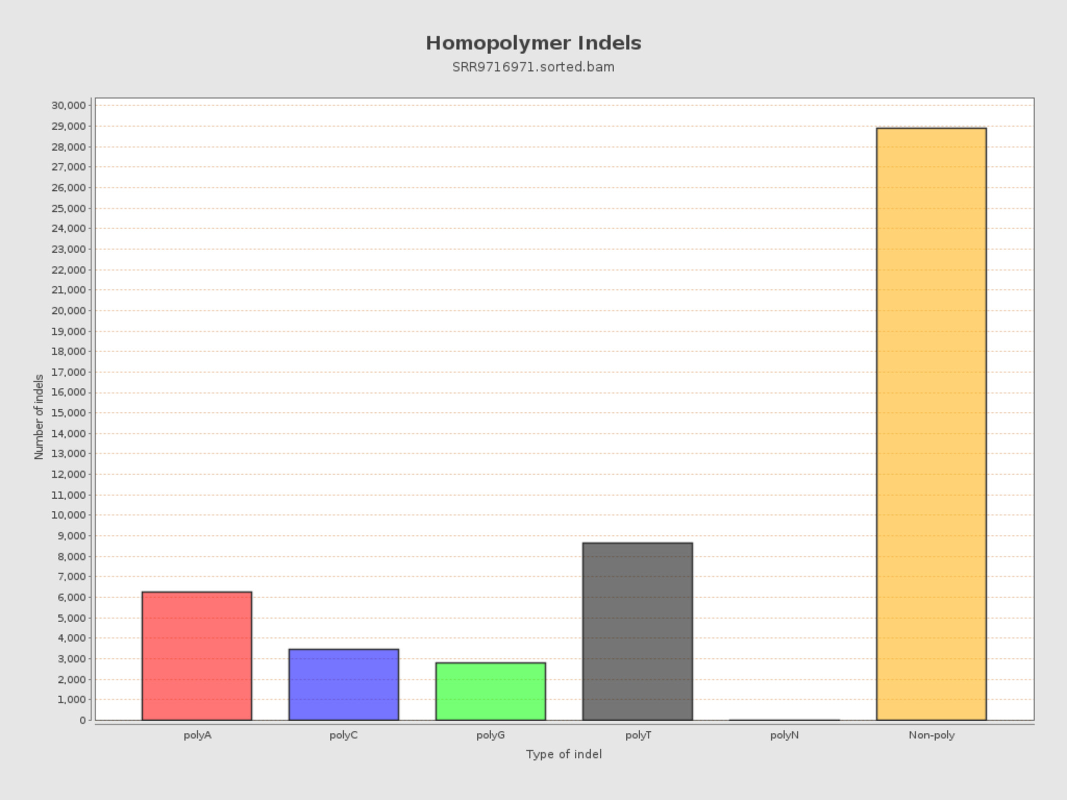
9. Results : Mapped Reads GC-content Distribution



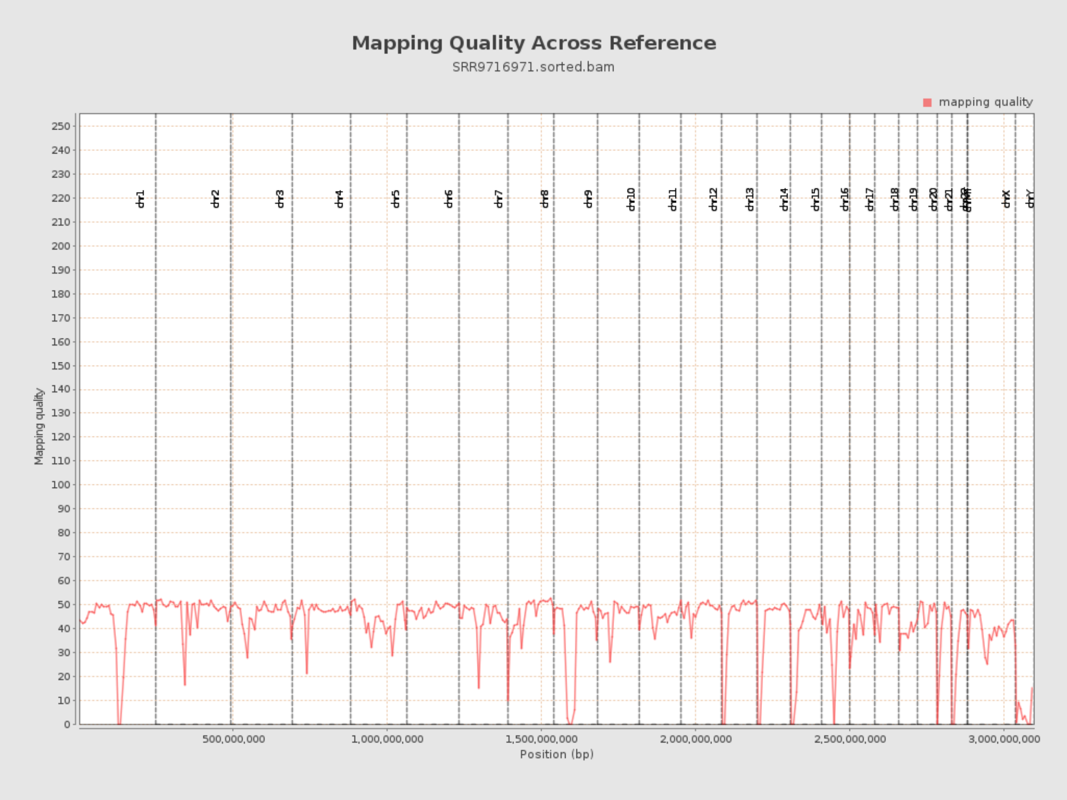
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram