Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 17:27:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716893.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_SRR9716893 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716893.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 17:27:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716893.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,936,333
Mapped reads	3,674,213 / 93.34%
Unmapped reads	262,120 / 6.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	81,046 / 2.06%
Read min/max/mean length	30 / 101 / 101.74
Duplicated reads (estimated)	174,448 / 4.43%
Duplication rate	3.39%
Clipped reads	3,752,851 / 95.34%

2.2. ACGT Content

Number/percentage of A's	70,165,878 / 25.99%
Number/percentage of C's	56,857,426 / 21.06%
Number/percentage of T's	77,076,231 / 28.54%
Number/percentage of G's	65,890,666 / 24.4%
Number/percentage of N's	30,436 / 0.01%
GC Percentage	45.46%

2.3. Coverage

Mean	0.0873

Standard Deviation	0.6095

2.4. Mapping Quality

Mean Mapping Quality	45.96

2.5. Mismatches and indels

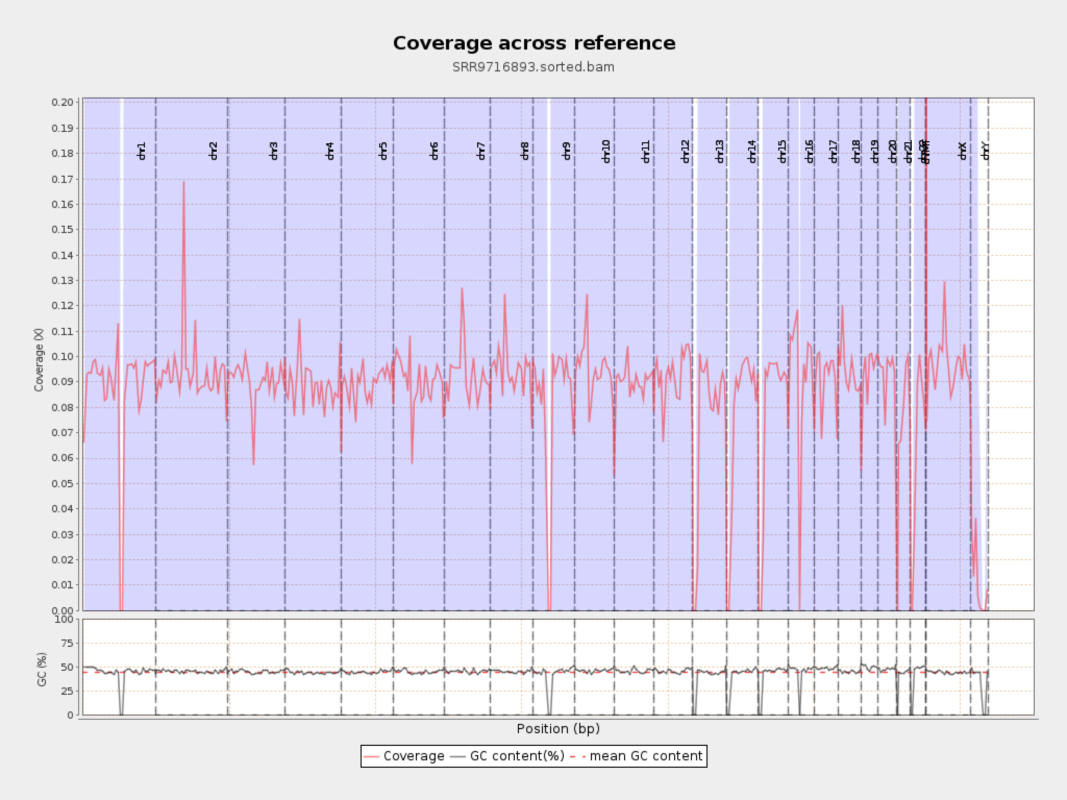
General error rate	0.75%
Mismatches	1,973,445
Insertions	19,624
Mapped reads with at least one insertion	0.53%
Deletions	52,261
Mapped reads with at least one deletion	1.41%
Homopolymer indels	41.56%

2.6. Chromosome stats

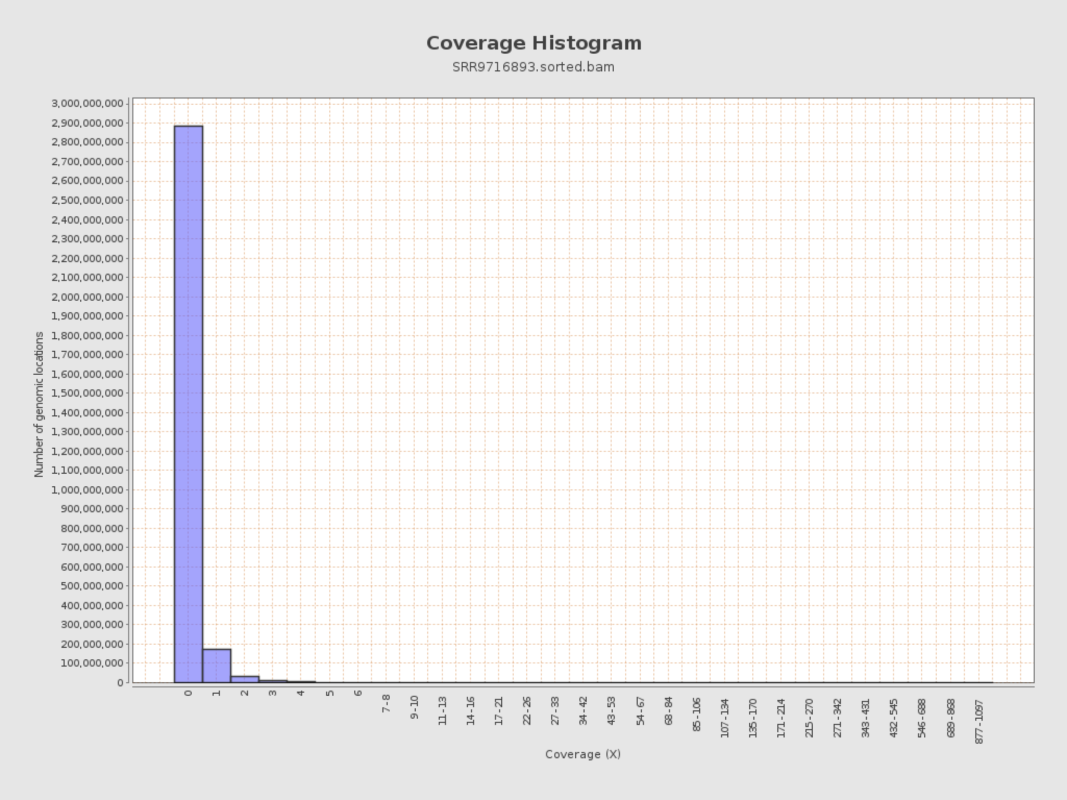
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21661423	0.0869	0.7061
chr2	243199373	22995715	0.0946	0.9047
chr3	198022430	17881528	0.0903	0.3648
chr4	191154276	17017758	0.089	0.4078
chr5	180915260	16189636	0.0895	0.3711
chr6	171115067	15460951	0.0904	0.4486
chr7	159138663	14818536	0.0931	0.7897

chr8	146364022	13855062	0.0947	0.8392
chr9	141213431	11339732	0.0803	0.663
chr10	135534747	12876947	0.095	0.5863
chr11	135006516	12156829	0.09	0.6715
chr12	133851895	12466228	0.0931	0.3848
chr13	115169878	8550231	0.0742	0.3309
chr14	107349540	8216328	0.0765	0.4485
chr15	102531392	7789617	0.076	0.3388
chr16	90354753	8091179	0.0895	0.4339
chr17	81195210	7481039	0.0921	0.4207
chr18	78077248	7423373	0.0951	1.3548
chr19	59128983	5577283	0.0943	0.6628
chr20	63025520	5795992	0.092	0.3966
chr21	48129895	3554703	0.0739	0.3796
chr22	51304566	3189250	0.0622	0.3068
chrMT	16571	13452	0.8118	1.2214
chrX	155270560	15032236	0.0968	0.532
chrY	59373566	674792	0.0114	0.2836

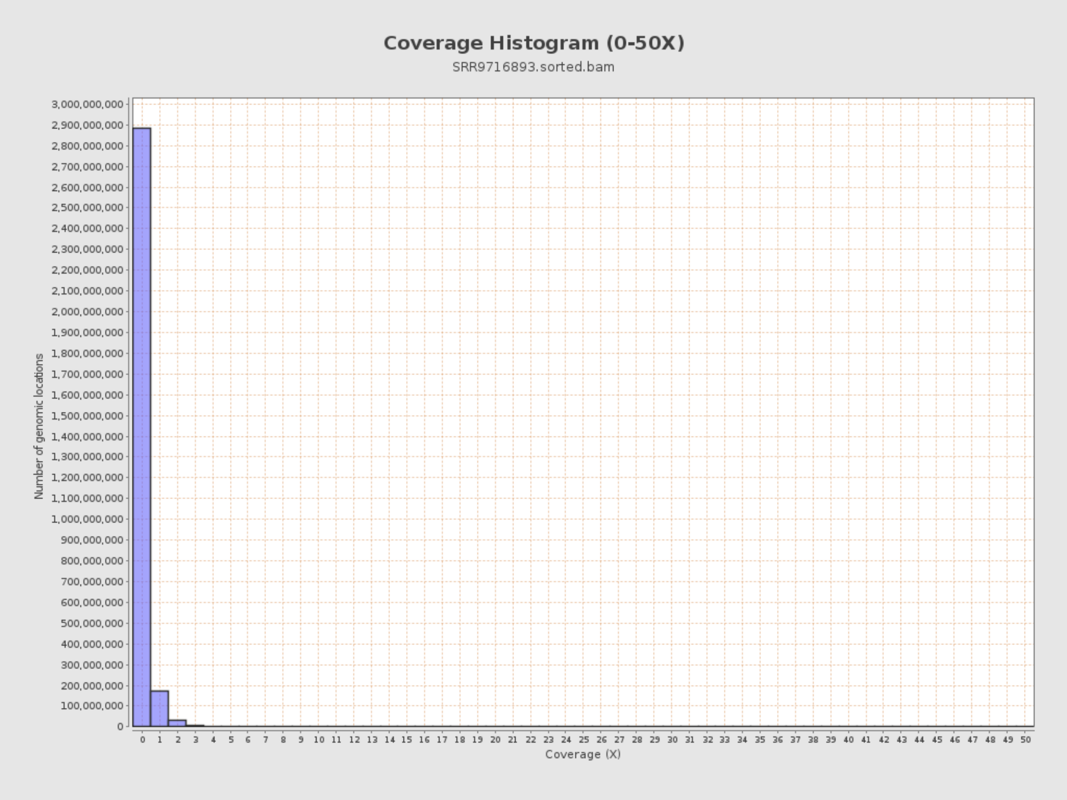
3. Results : Coverage across reference



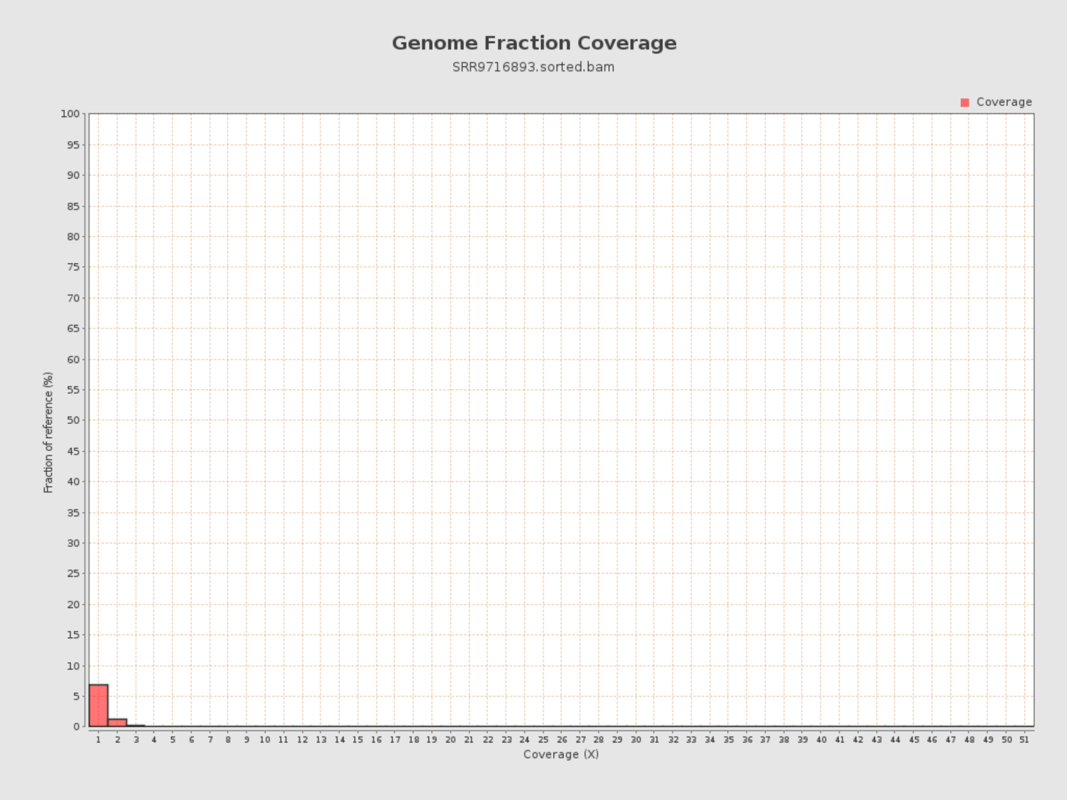
4. Results : Coverage Histogram



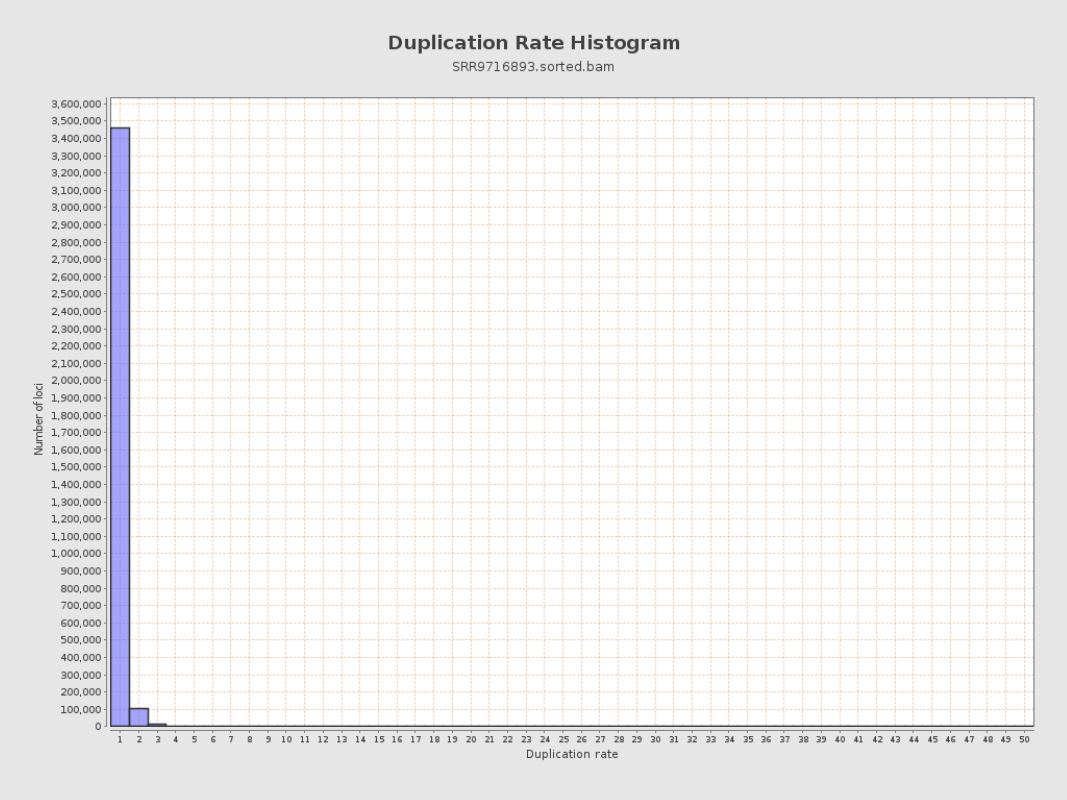
5. Results : Coverage Histogram (0-50X)



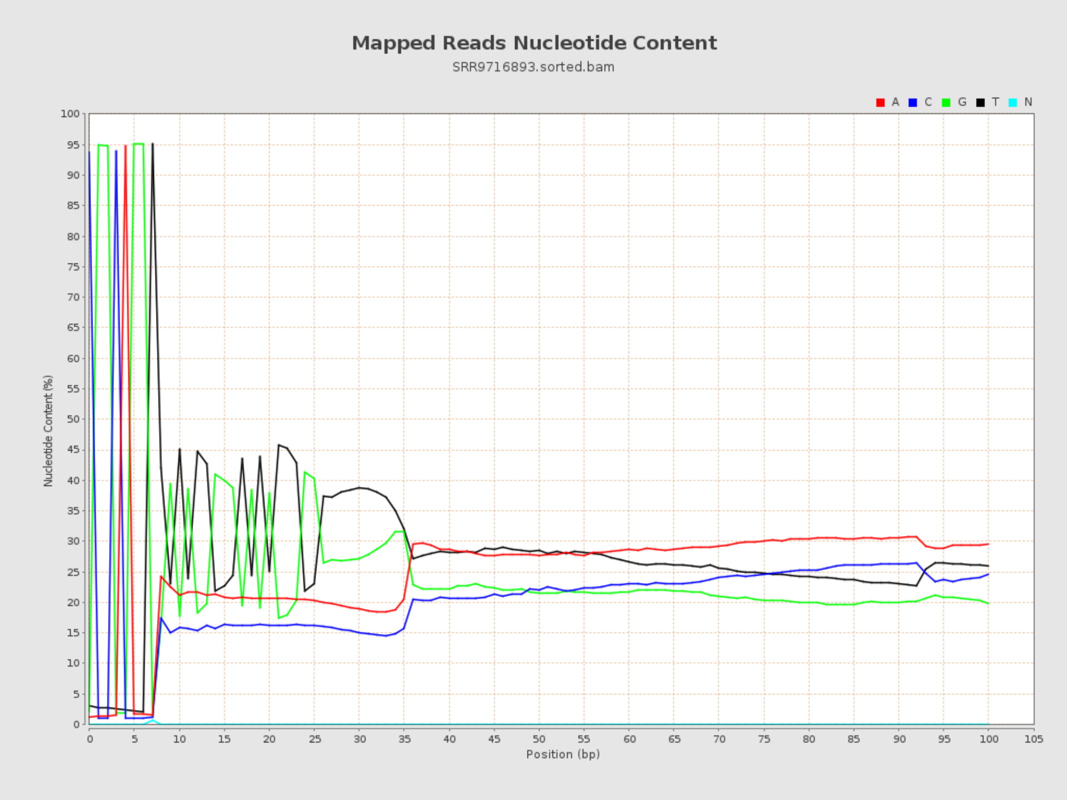
6. Results : Genome Fraction Coverage



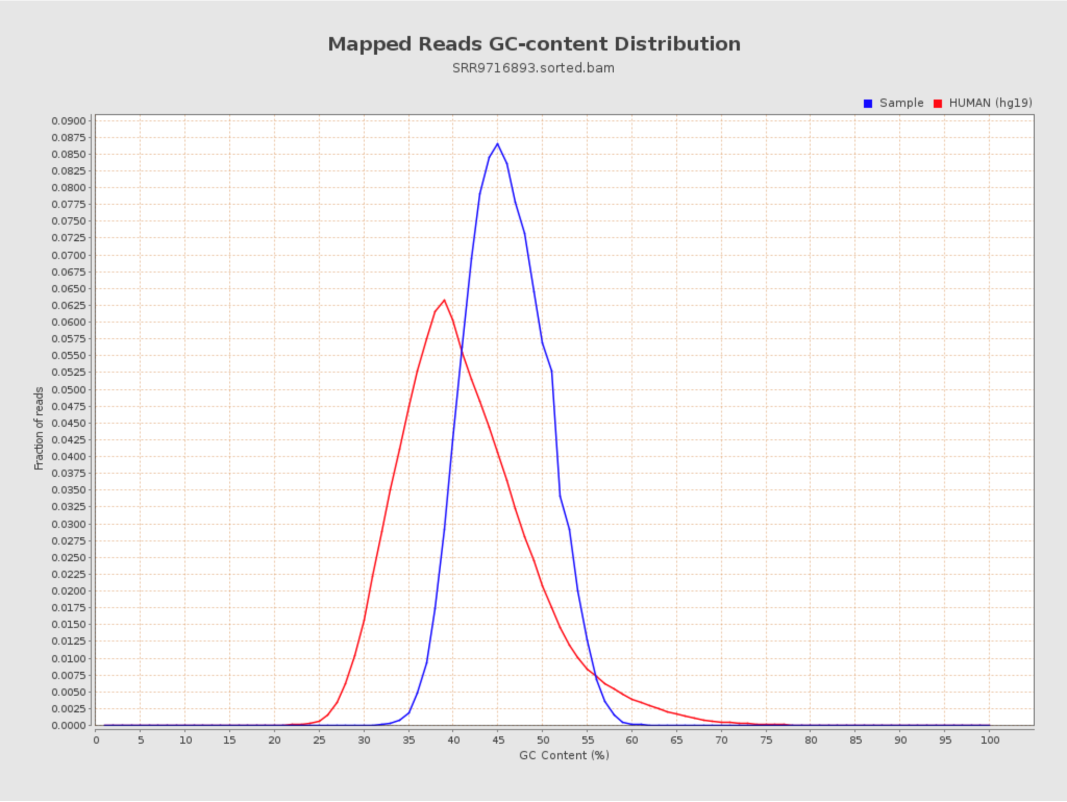
7. Results : Duplication Rate Histogram



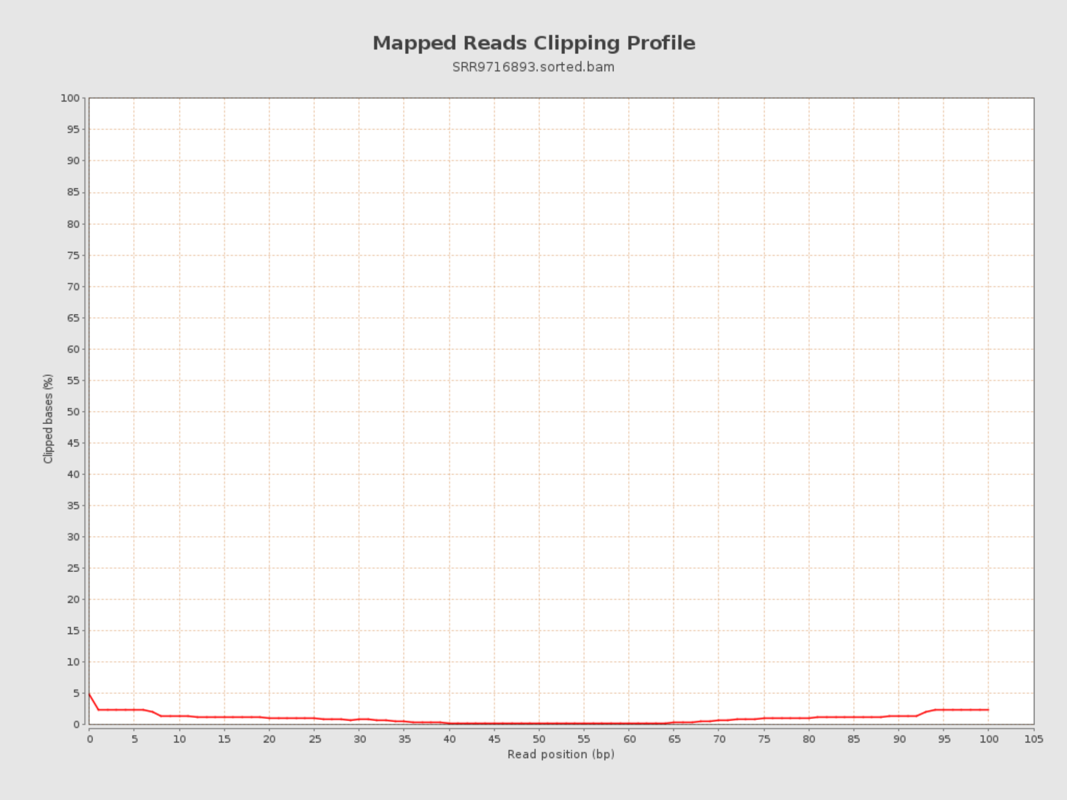
8. Results : Mapped Reads Nucleotide Content



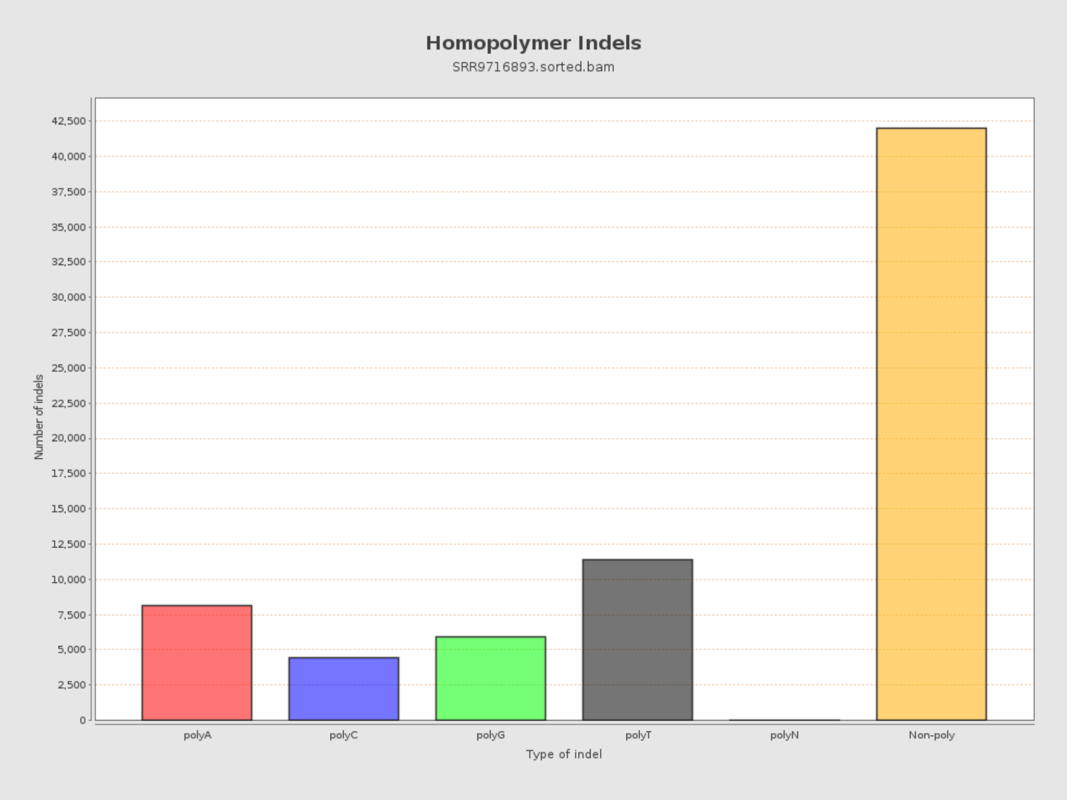
9. Results : Mapped Reads GC-content Distribution



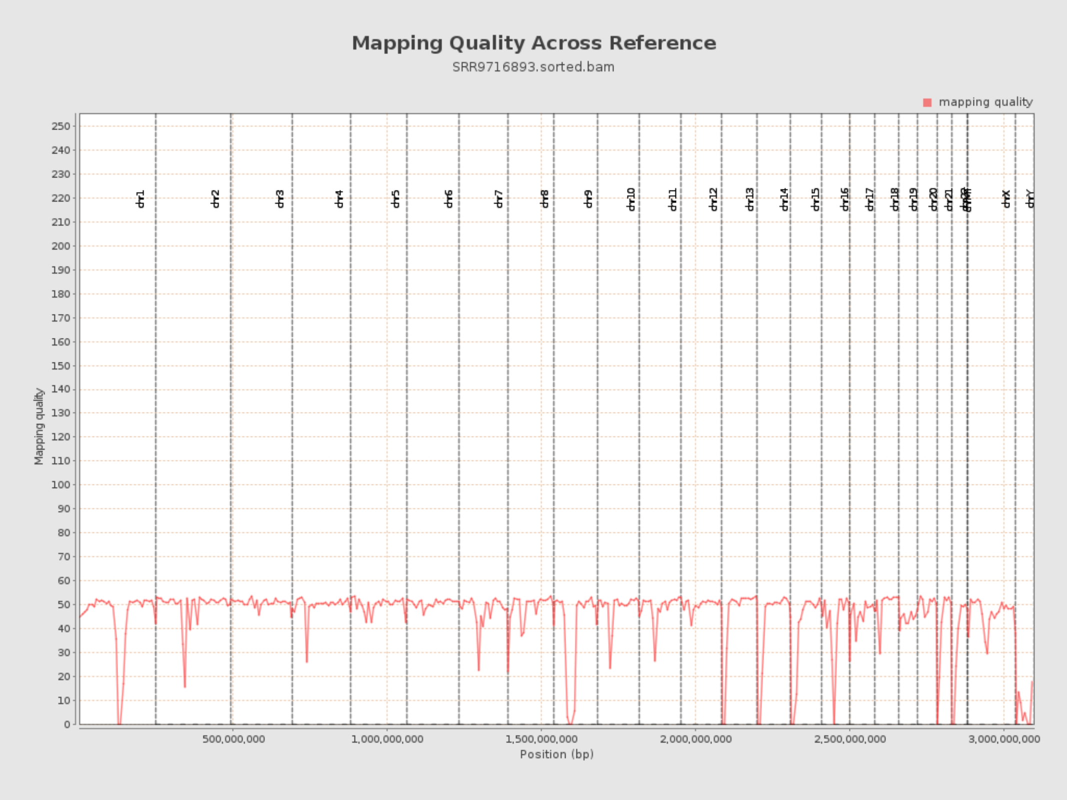
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram