Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:29:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716693.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_SRR9716693 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716693.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:29:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716693.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,432,286
Mapped reads	1,281,643 / 89.48%
Unmapped reads	150,643 / 10.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,157 / 1.55%
Read min/max/mean length	30 / 101 / 101.57
Duplicated reads (estimated)	48,947 / 3.42%
Duplication rate	2.16%
Clipped reads	1,301,692 / 90.88%

2.2. ACGT Content

Number/percentage of A's	24,873,180 / 24.98%
Number/percentage of C's	19,451,581 / 19.54%
Number/percentage of T's	30,901,618 / 31.04%
Number/percentage of G's	24,327,608 / 24.44%
Number/percentage of N's	5,262 / 0.01%
GC Percentage	43.97%

2.3. Coverage

Mean	0.0322

Standard Deviation	0.4209

2.4. Mapping Quality

Mean Mapping Quality	42.95

2.5. Mismatches and indels

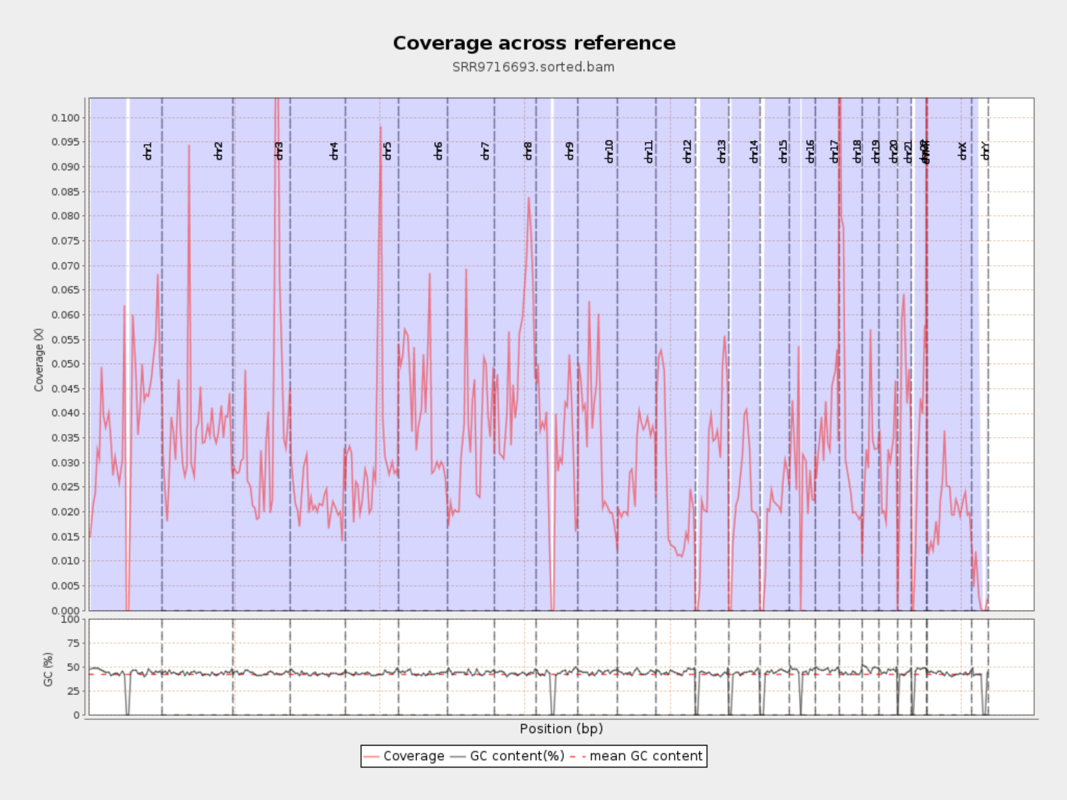
General error rate	0.9%
Mismatches	879,013
Insertions	9,111
Mapped reads with at least one insertion	0.7%
Deletions	24,462
Mapped reads with at least one deletion	1.88%
Homopolymer indels	44.74%

2.6. Chromosome stats

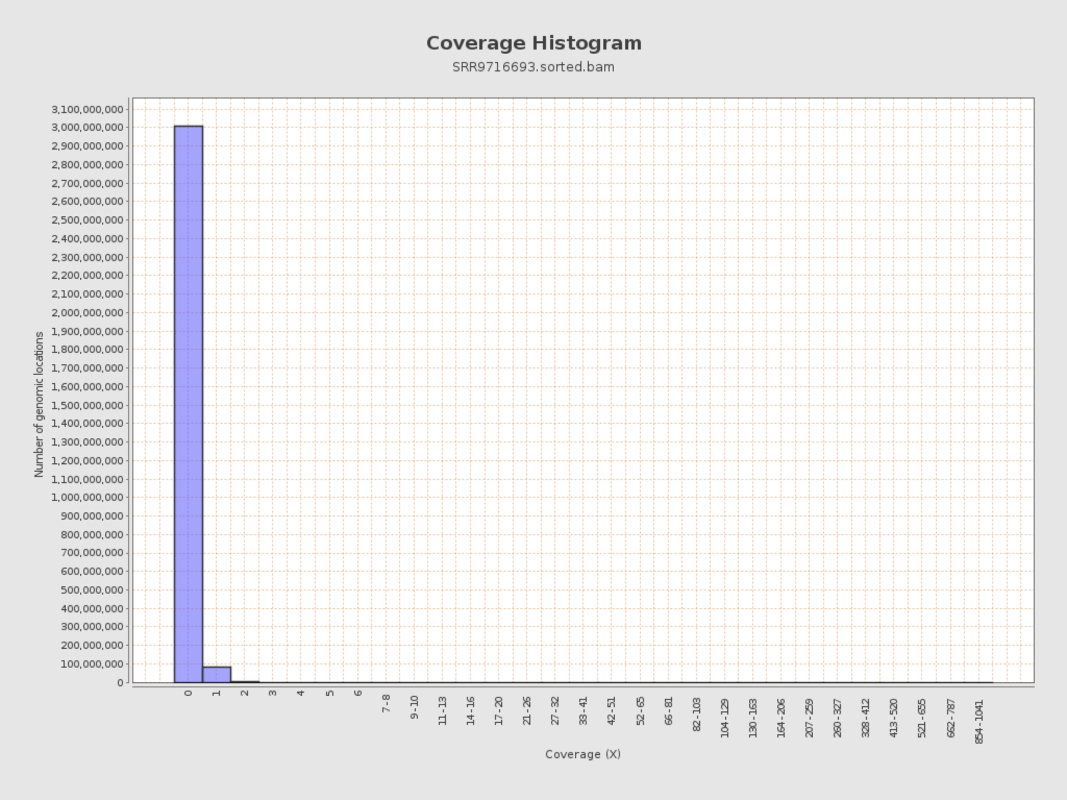
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9312554	0.0374	0.6763
chr2	243199373	8880631	0.0365	0.7512
chr3	198022430	7398952	0.0374	0.2161
chr4	191154276	4266155	0.0223	0.1772
chr5	180915260	5831123	0.0322	0.1999
chr6	171115067	7139123	0.0417	0.2906
chr7	159138663	5565664	0.035	0.5976

chr8	146364022	7486569	0.0512	0.5659
chr9	141213431	4467703	0.0316	0.3876
chr10	135534747	4824679	0.0356	0.3336
chr11	135006516	4021170	0.0298	0.2898
chr12	133851895	3140667	0.0235	0.1749
chr13	115169878	3450925	0.03	0.1903
chr14	107349540	2406307	0.0224	0.2079
chr15	102531392	1946074	0.019	0.159
chr16	90354753	2554063	0.0283	0.214
chr17	81195210	3105566	0.0382	0.2491
chr18	78077248	3066294	0.0393	0.7935
chr19	59128983	1985903	0.0336	0.571
chr20	63025520	1861423	0.0295	0.2209
chr21	48129895	2007572	0.0417	0.2316
chr22	51304566	1498347	0.0292	0.1889
chrMT	16571	3218	0.1942	0.5205
chrX	155270560	3157341	0.0203	0.218
chrY	59373566	223830	0.0038	0.1061

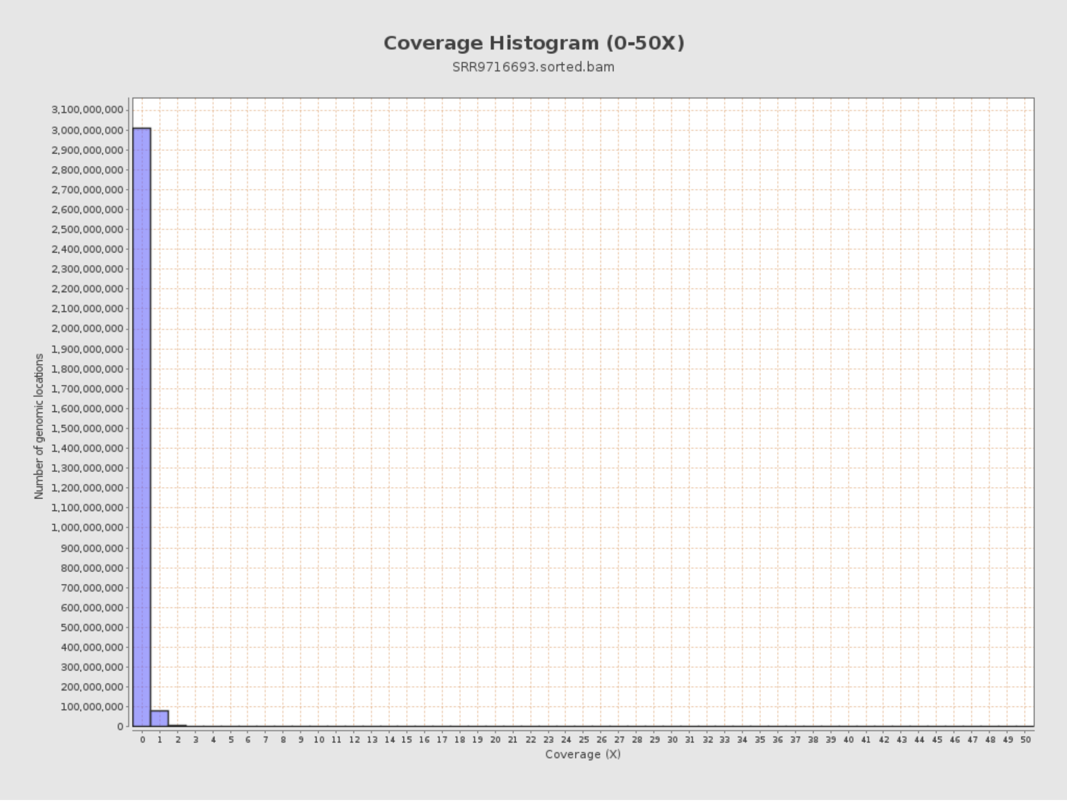
3. Results : Coverage across reference



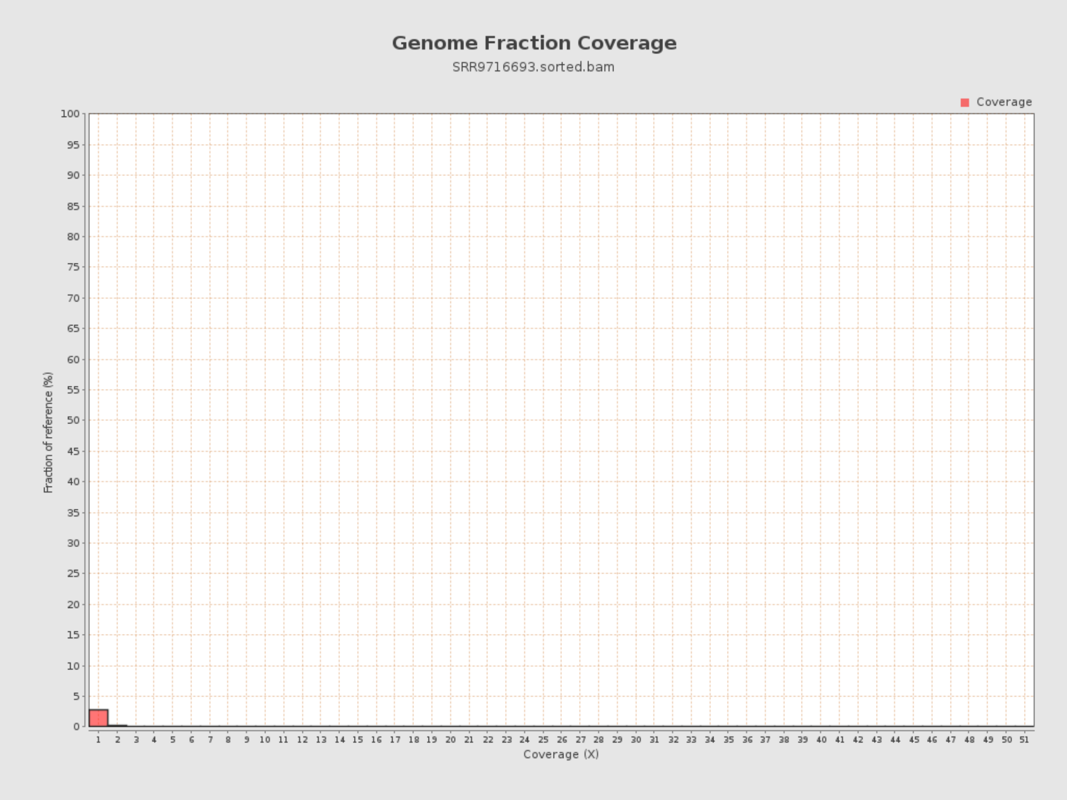
4. Results : Coverage Histogram



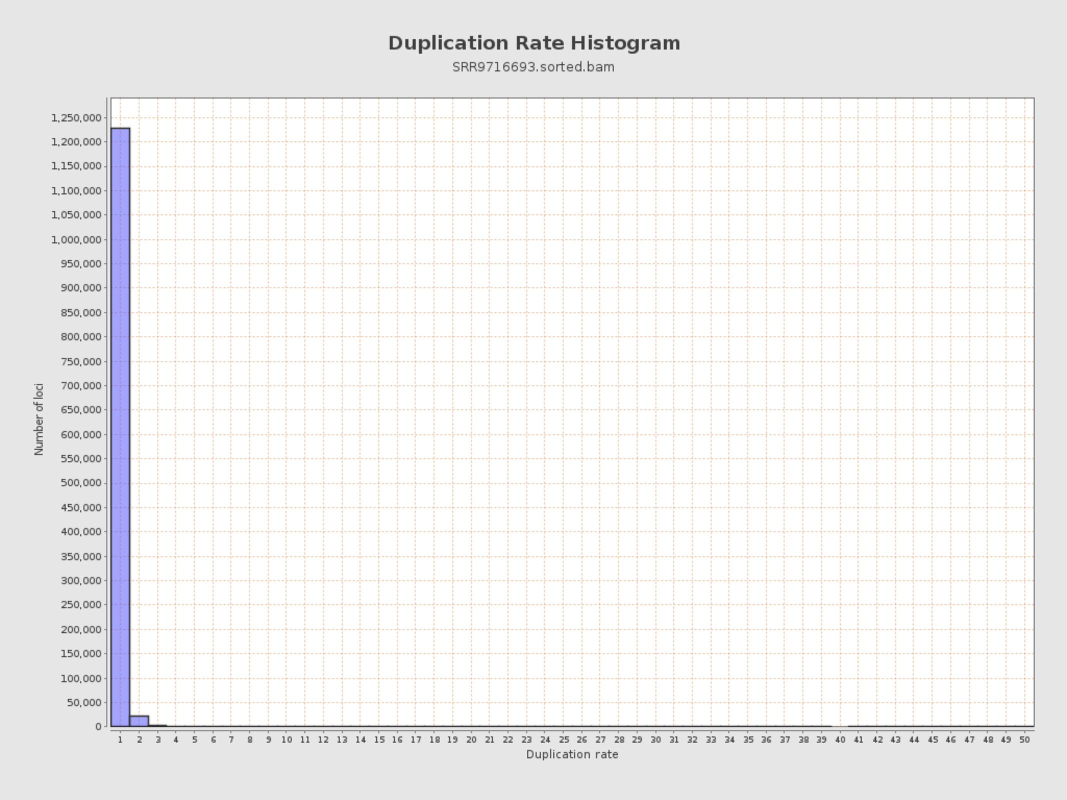
5. Results : Coverage Histogram (0-50X)



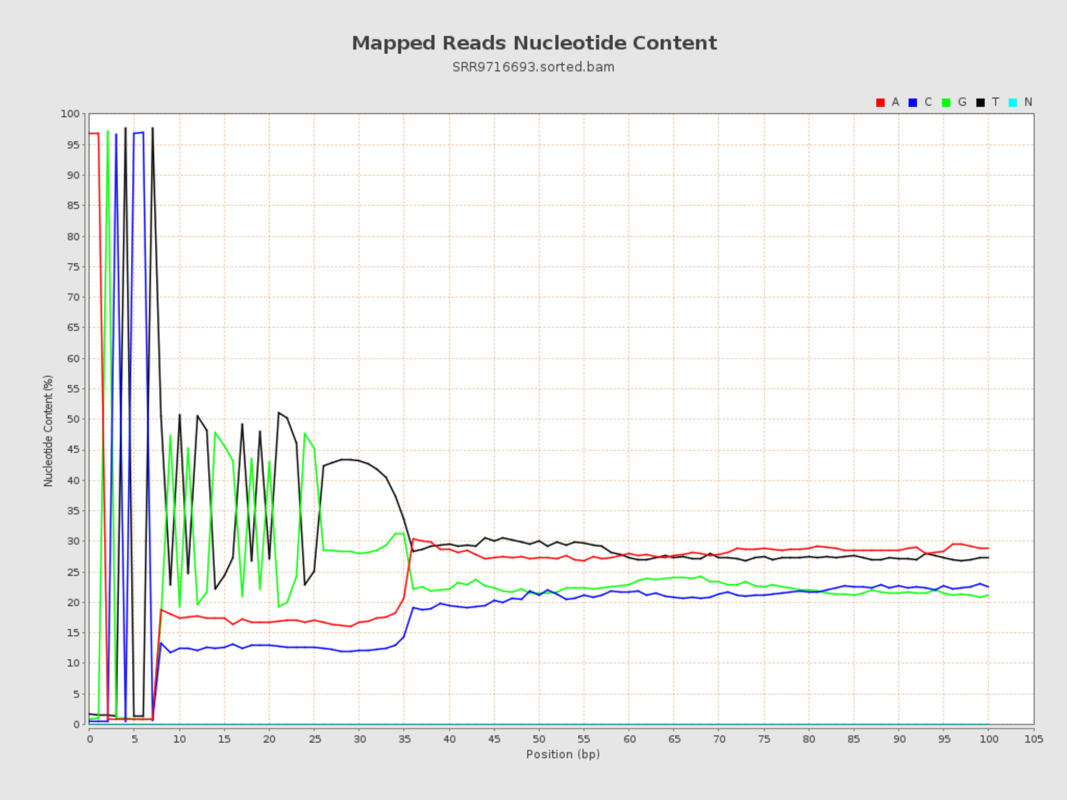
6. Results : Genome Fraction Coverage



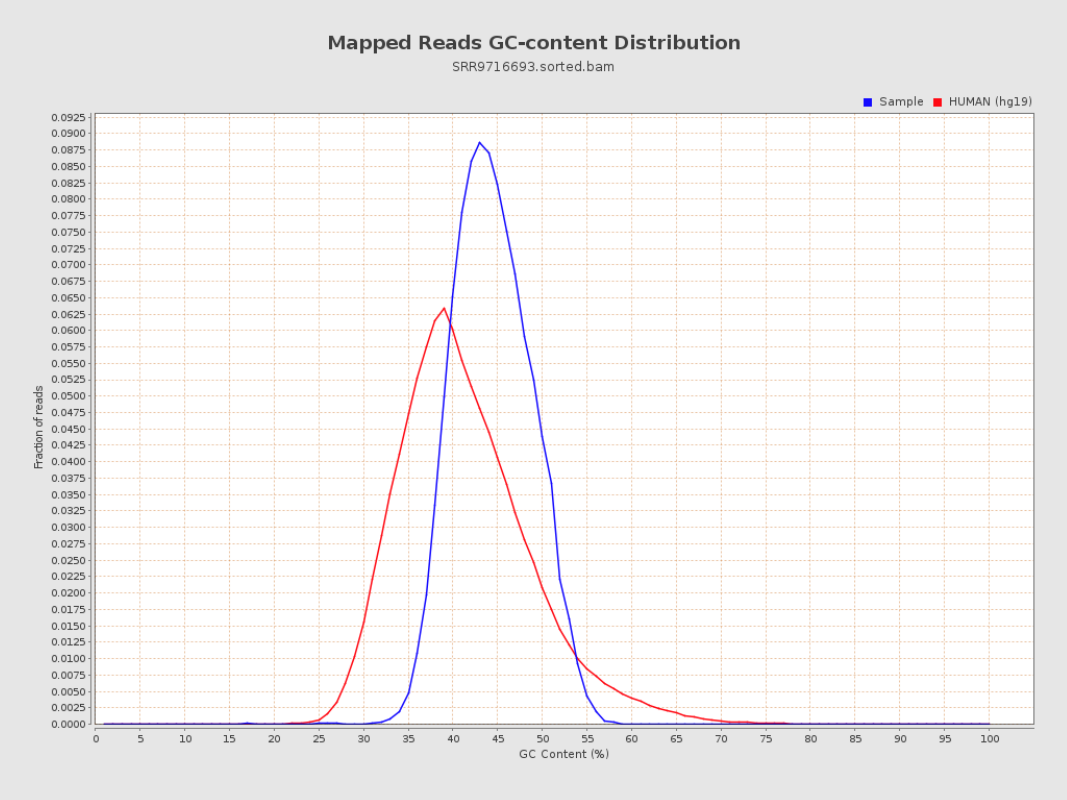
7. Results : Duplication Rate Histogram



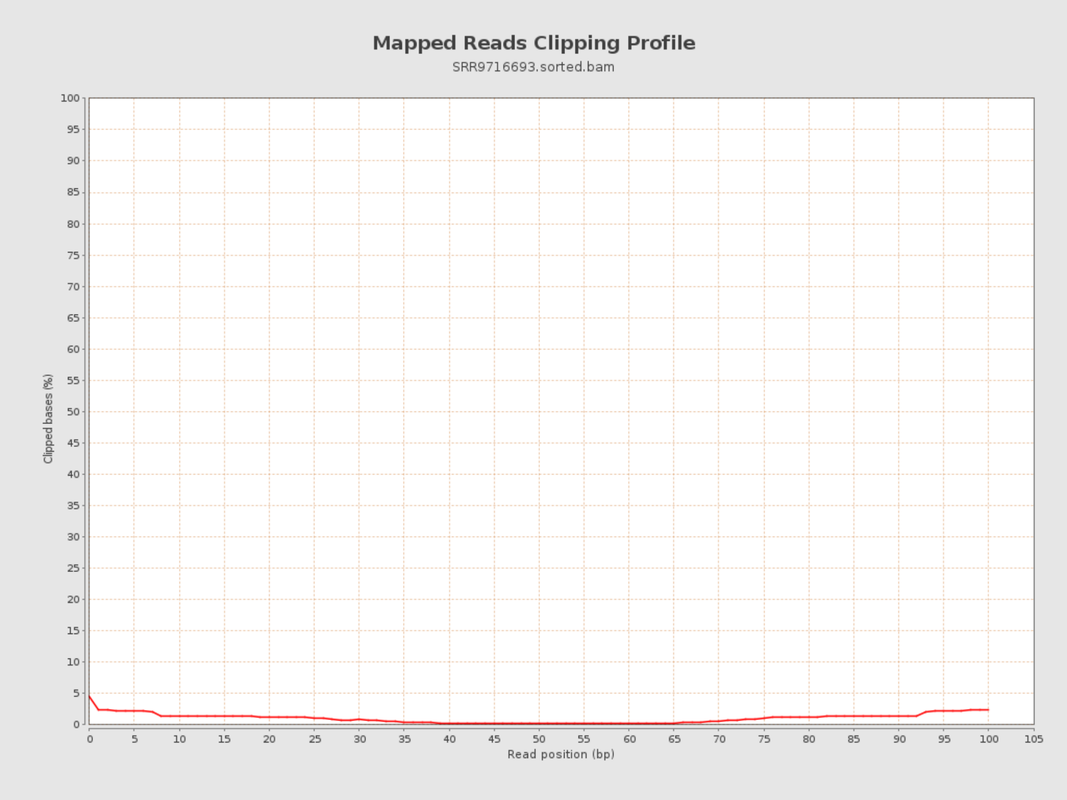
8. Results : Mapped Reads Nucleotide Content



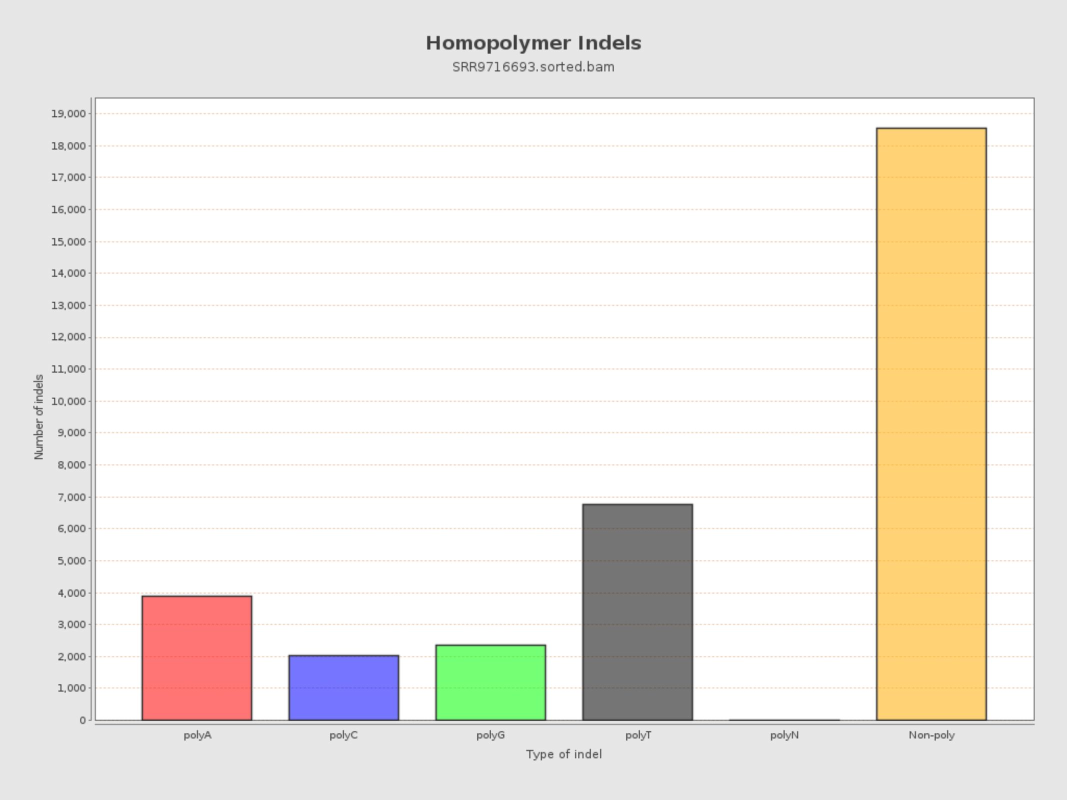
9. Results : Mapped Reads GC-content Distribution



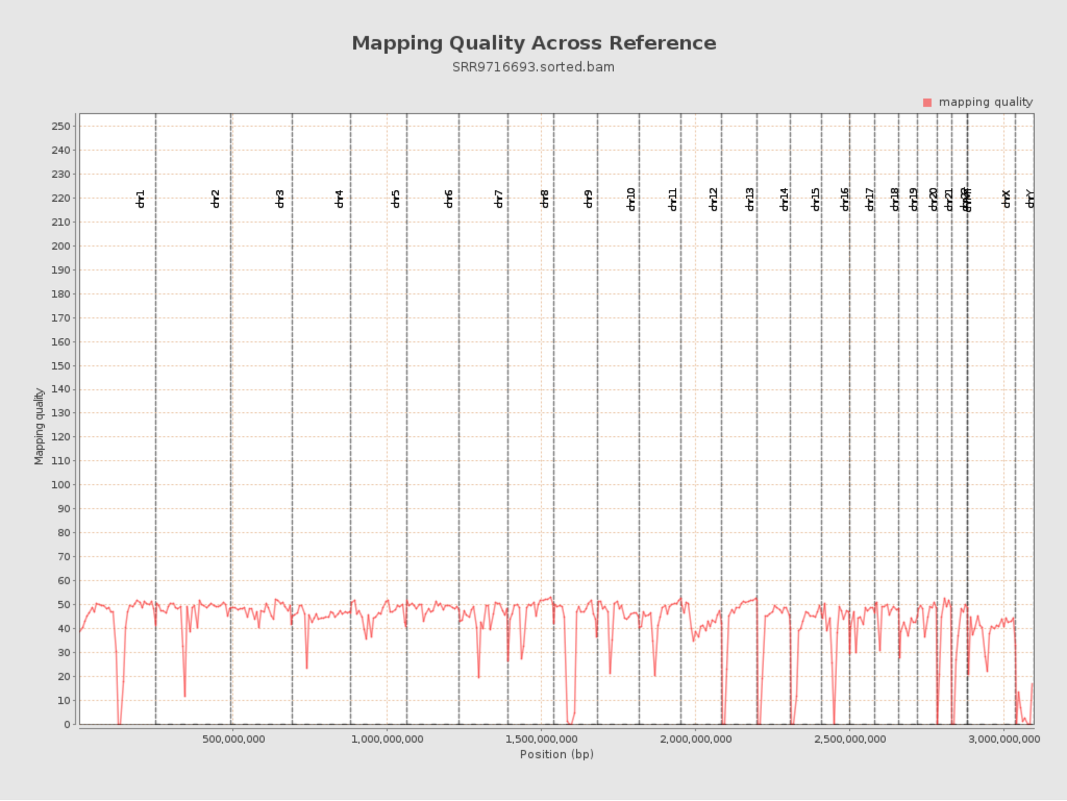
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram