Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:53:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716986.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_SRR9716986 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716986.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:53:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716986.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,913,888
Mapped reads	1,759,774 / 91.95%
Unmapped reads	154,114 / 8.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,920 / 0.57%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	64,778 / 3.38%
Duplication rate	2.61%
Clipped reads	1,766,034 / 92.27%

2.2. ACGT Content

Number/percentage of A's	26,484,699 / 25.78%
Number/percentage of C's	20,896,526 / 20.34%
Number/percentage of T's	31,299,676 / 30.46%
Number/percentage of G's	24,065,463 / 23.42%
Number/percentage of N's	1,207 / 0%
GC Percentage	43.76%

2.3. Coverage

Mean	0.0332

Standard Deviation	0.3148

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

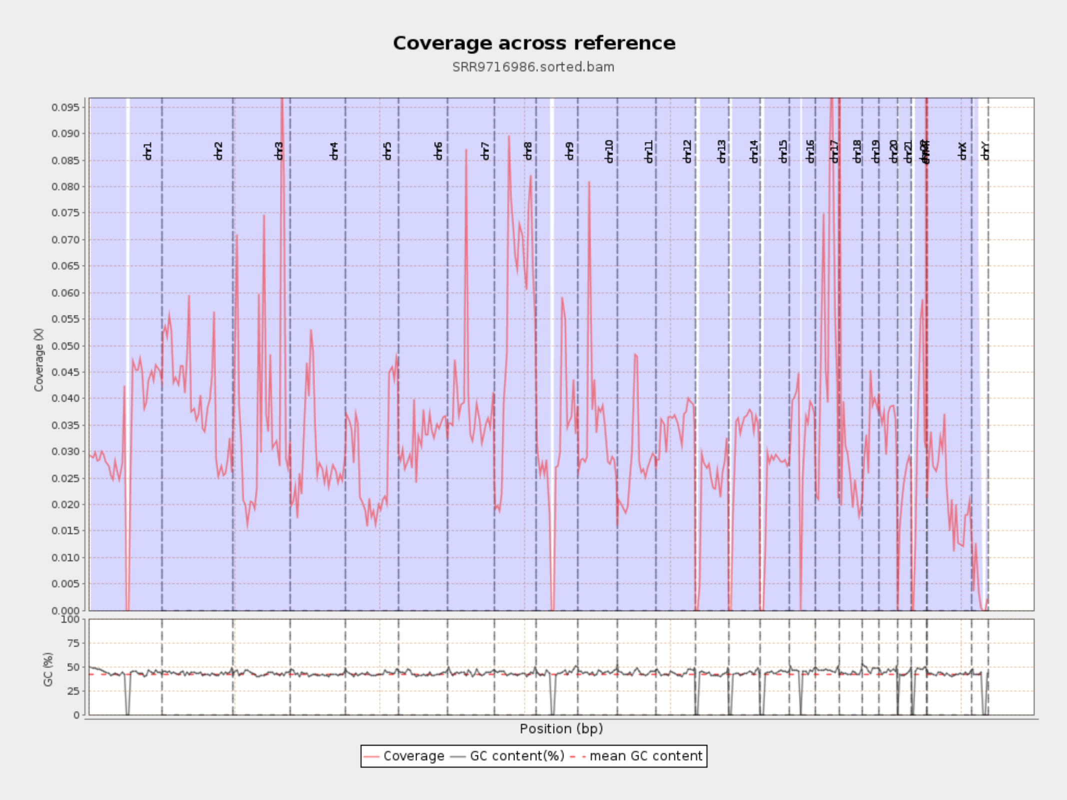
General error rate	0.51%
Mismatches	513,610
Insertions	6,588
Mapped reads with at least one insertion	0.37%
Deletions	19,124
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.43%

2.6. Chromosome stats

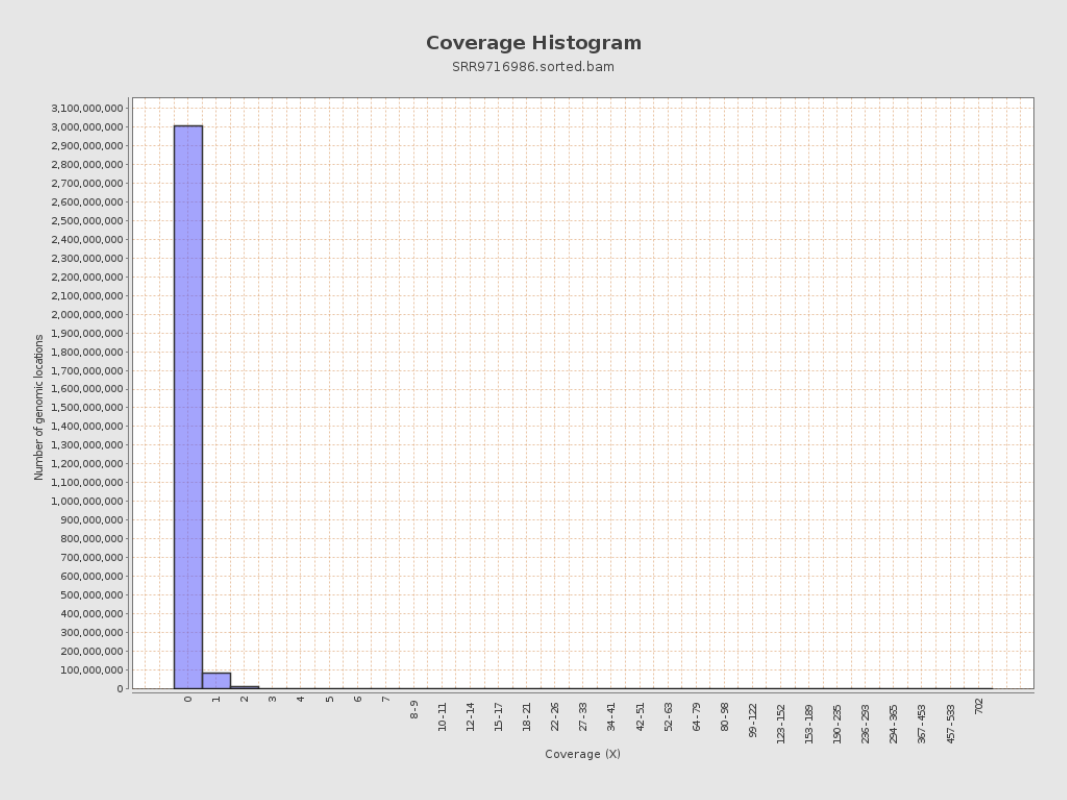
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8302996	0.0333	0.4137
chr2	243199373	9849698	0.0405	0.3735
chr3	198022430	7630471	0.0385	0.2304
chr4	191154276	5529419	0.0289	0.2088
chr5	180915260	5097407	0.0282	0.1854
chr6	171115067	5560776	0.0325	0.2163
chr7	159138663	6266982	0.0394	0.7053

chr8	146364022	8363942	0.0571	0.3509
chr9	141213431	4226038	0.0299	0.2205
chr10	135534747	4736588	0.0349	0.4126
chr11	135006516	3694966	0.0274	0.2181
chr12	133851895	4709691	0.0352	0.2291
chr13	115169878	2552663	0.0222	0.1623
chr14	107349540	3230649	0.0301	0.1963
chr15	102531392	2374573	0.0232	0.1713
chr16	90354753	3092141	0.0342	0.2133
chr17	81195210	4317903	0.0532	0.2645
chr18	78077248	2325799	0.0298	0.3426
chr19	59128983	2082313	0.0352	0.3777
chr20	63025520	2265068	0.0359	0.22
chr21	48129895	1036690	0.0215	0.1699
chr22	51304566	1543388	0.0301	0.1899
chrMT	16571	273560	16.5084	10.2102
chrX	155270560	3486535	0.0225	0.1894
chrY	59373566	227289	0.0038	0.1066

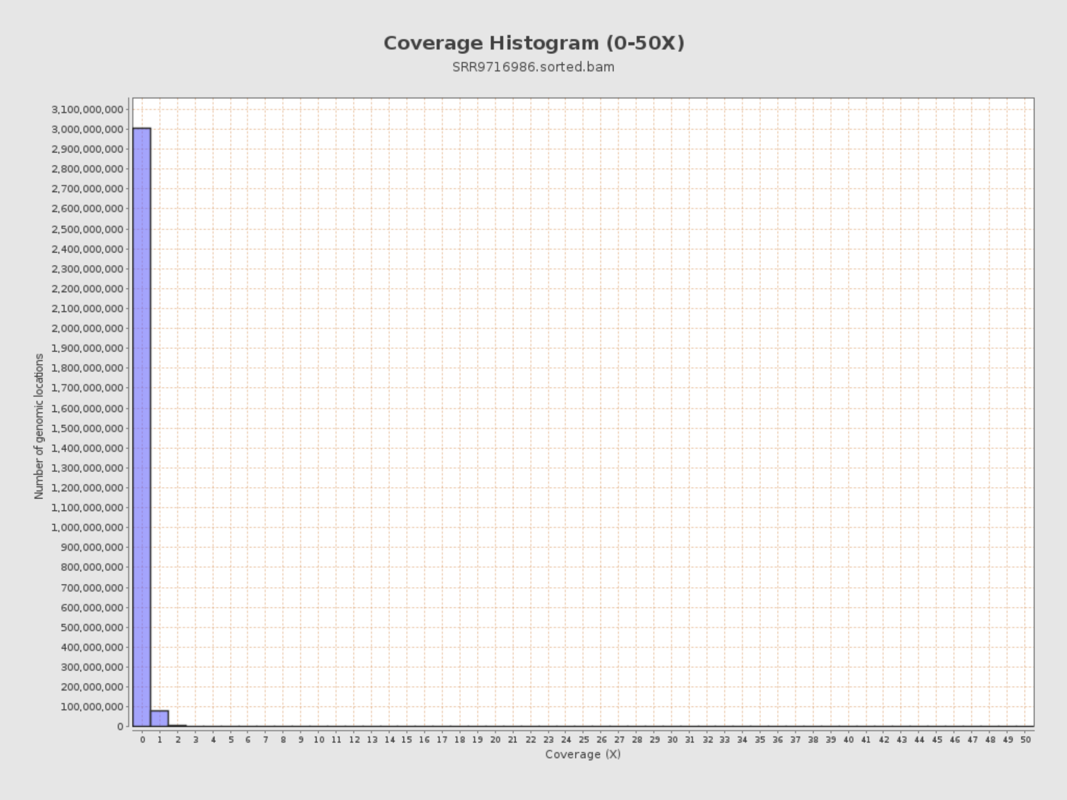
3. Results : Coverage across reference



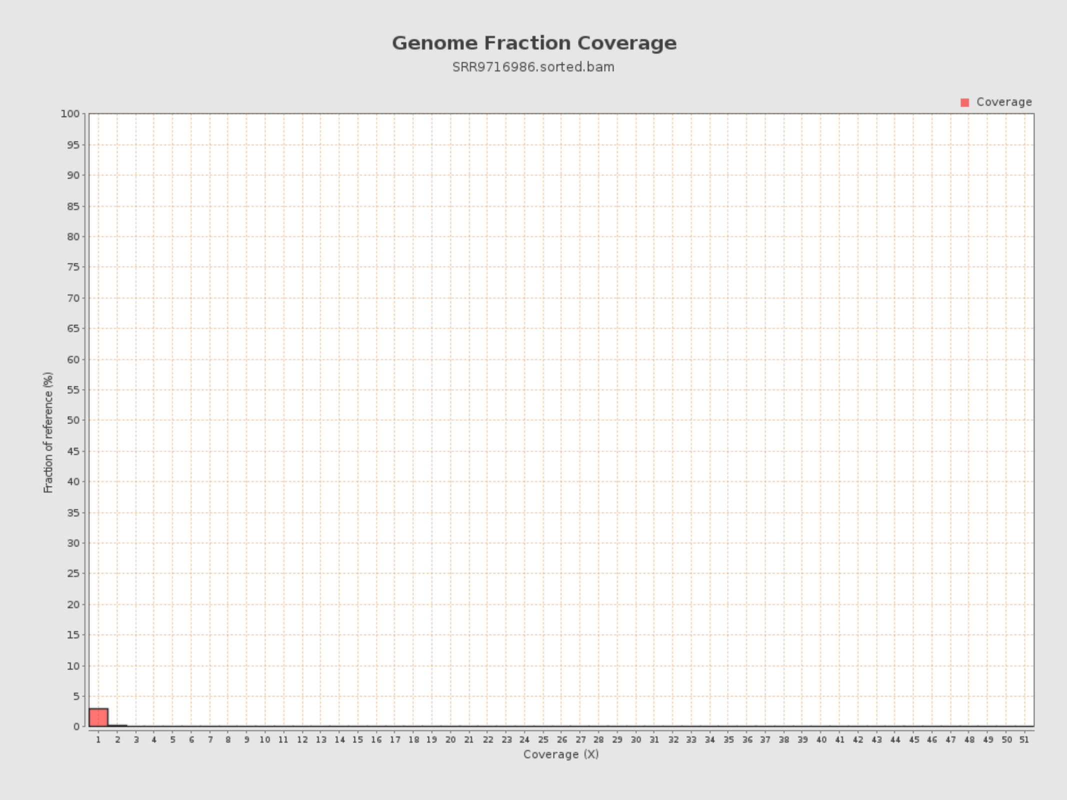
4. Results : Coverage Histogram



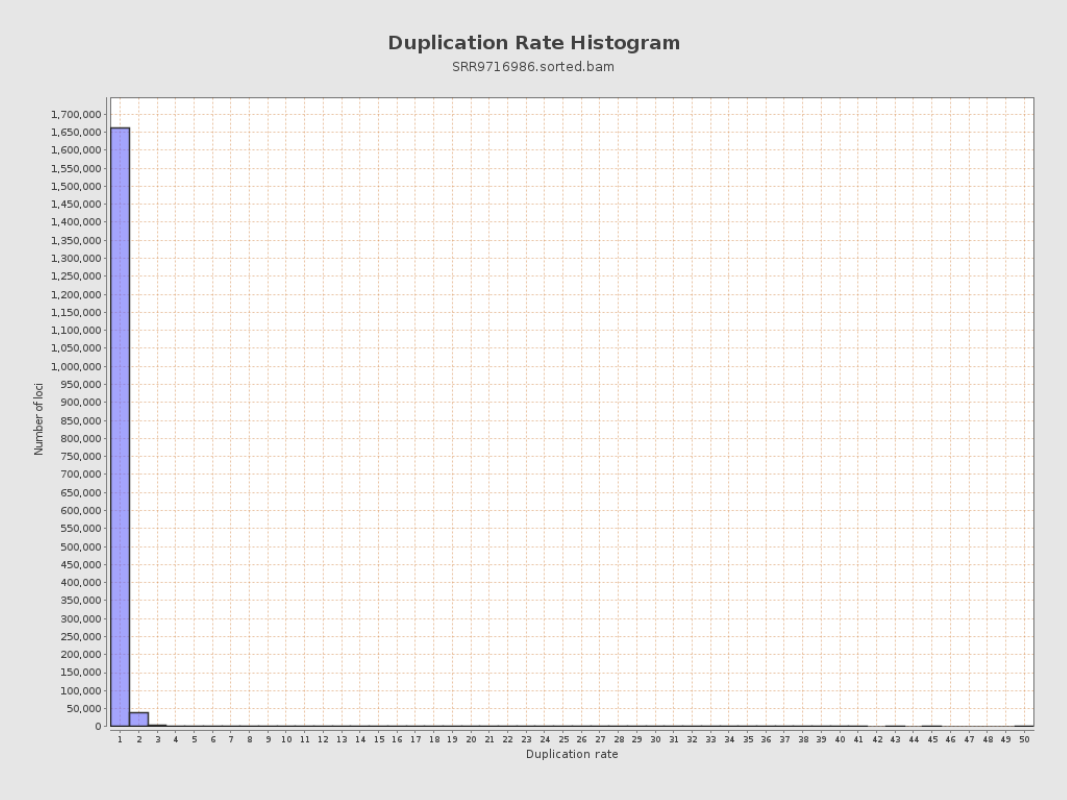
5. Results : Coverage Histogram (0-50X)



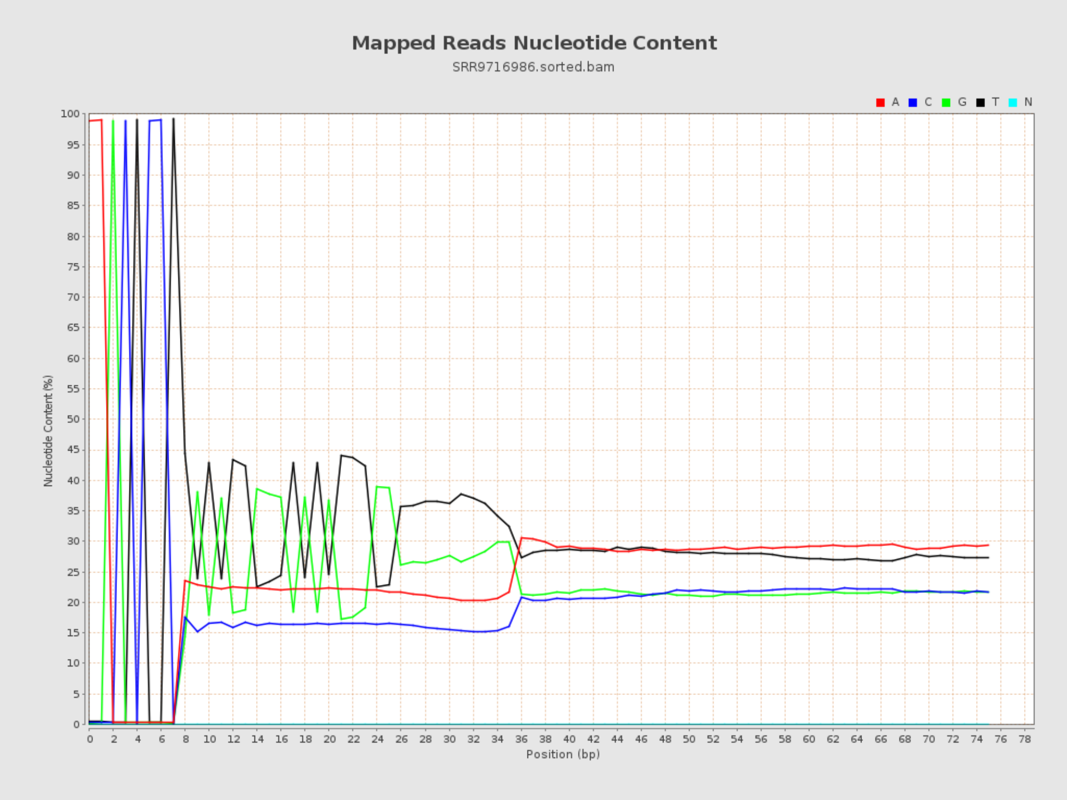
6. Results : Genome Fraction Coverage



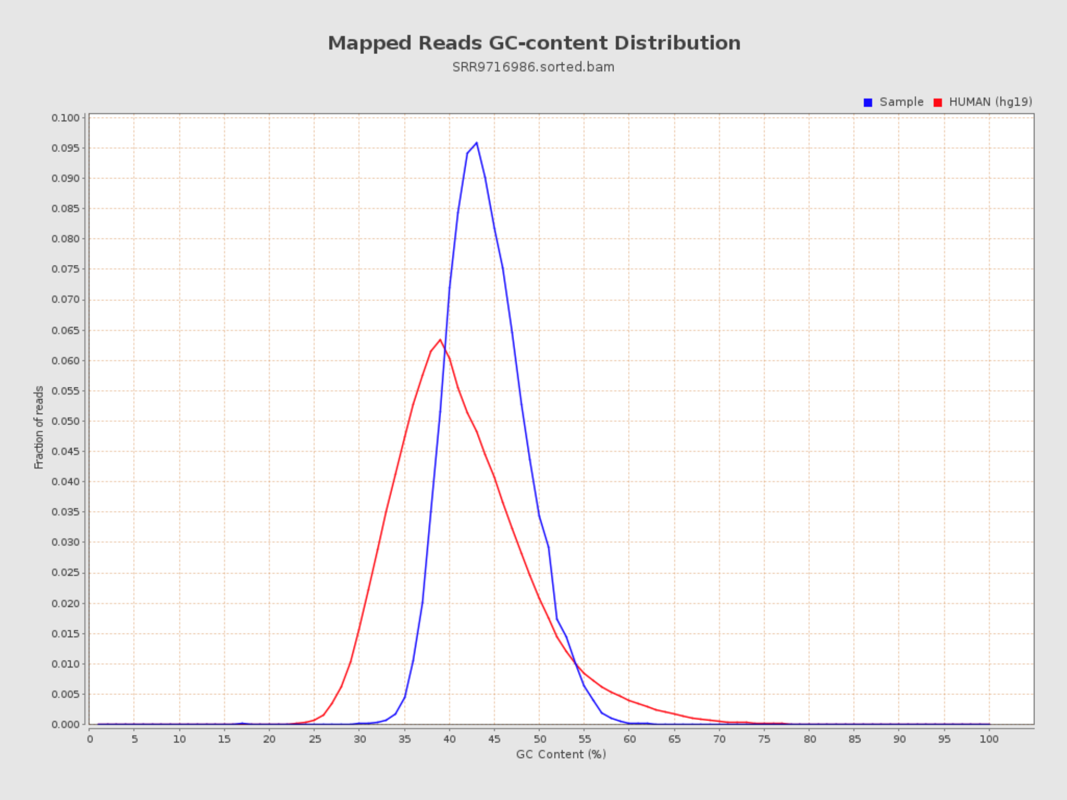
7. Results : Duplication Rate Histogram



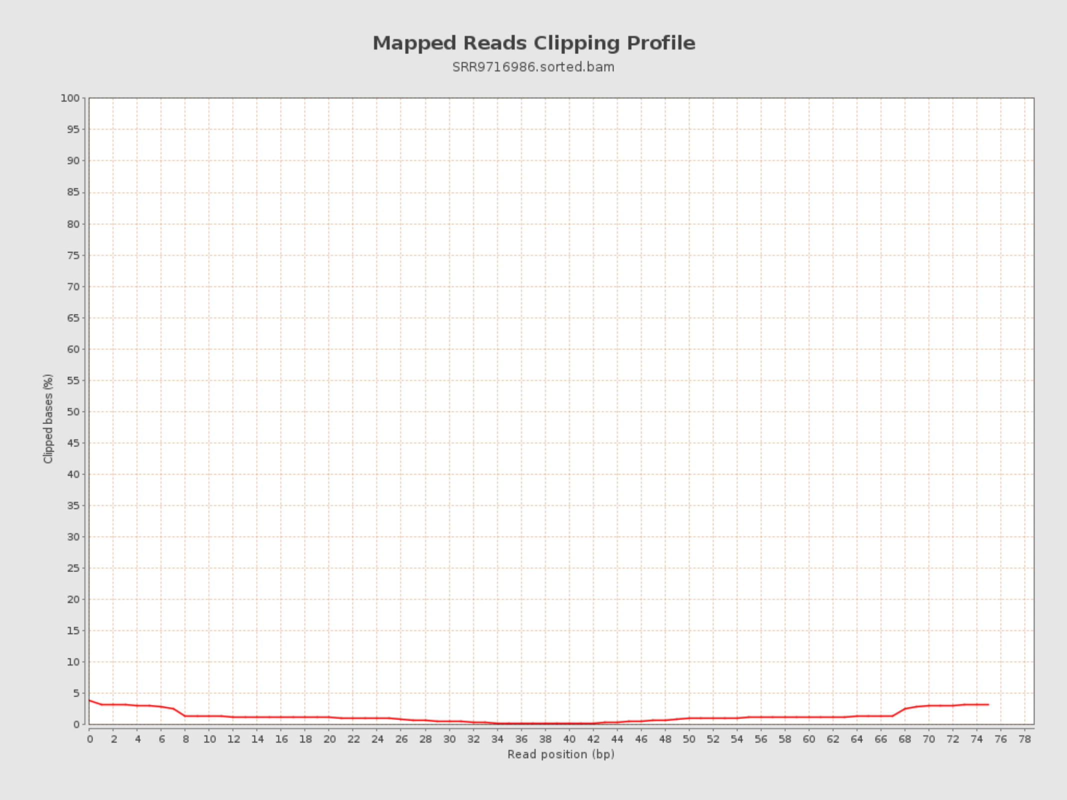
8. Results : Mapped Reads Nucleotide Content



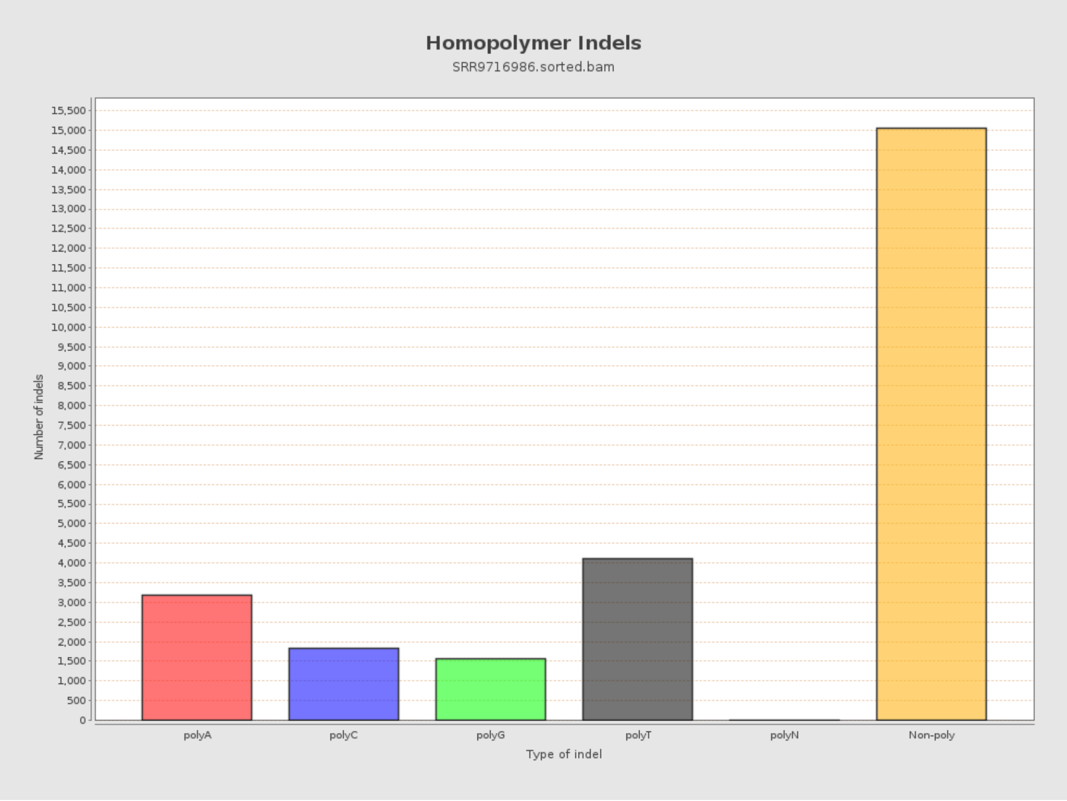
9. Results : Mapped Reads GC-content Distribution



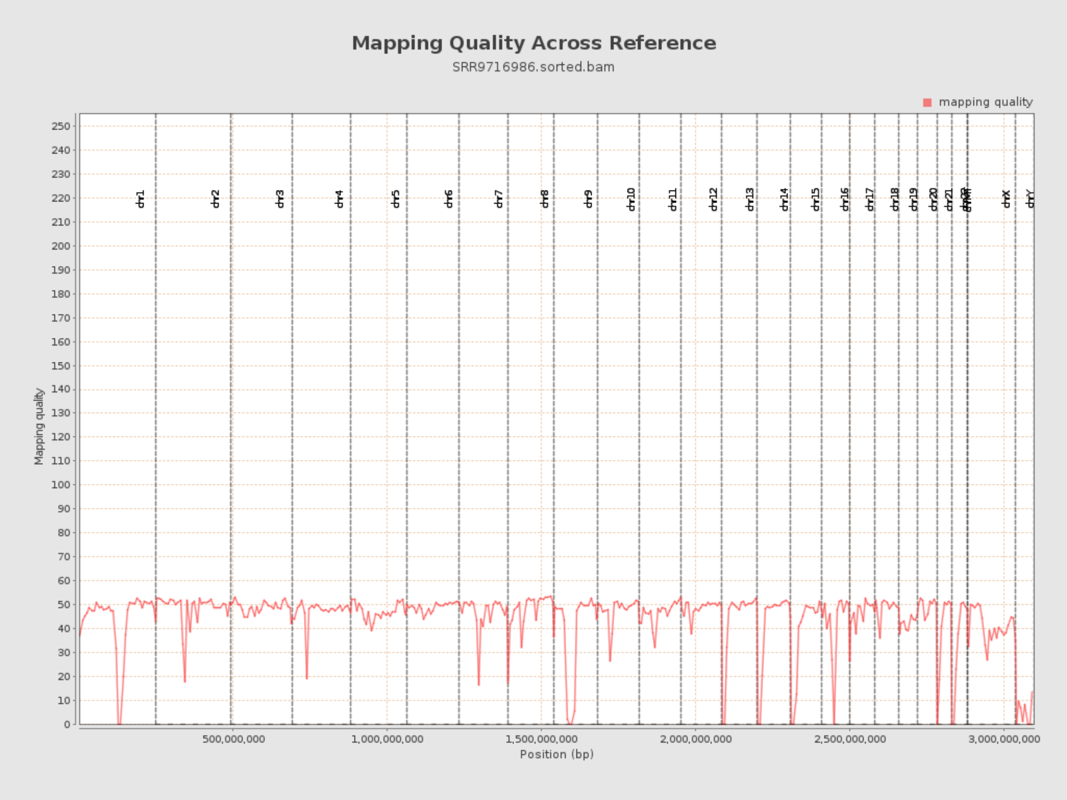
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram