Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:35:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716983.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_SRR9716983 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716983.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:35:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716983.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,423,235
Mapped reads	1,084,644 / 76.21%
Unmapped reads	338,591 / 23.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,309 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	70,559 / 4.96%
Duplication rate	5.64%
Clipped reads	1,084,016 / 76.17%

2.2. ACGT Content

Number/percentage of A's	11,687,097 / 20.37%
Number/percentage of C's	10,126,161 / 17.65%
Number/percentage of T's	19,125,070 / 33.34%
Number/percentage of G's	16,428,050 / 28.64%
Number/percentage of N's	1,010 / 0%
GC Percentage	46.29%

2.3. Coverage

Mean	0.0185

Standard Deviation	0.1807

2.4. Mapping Quality

Mean Mapping Quality	43.1

2.5. Mismatches and indels

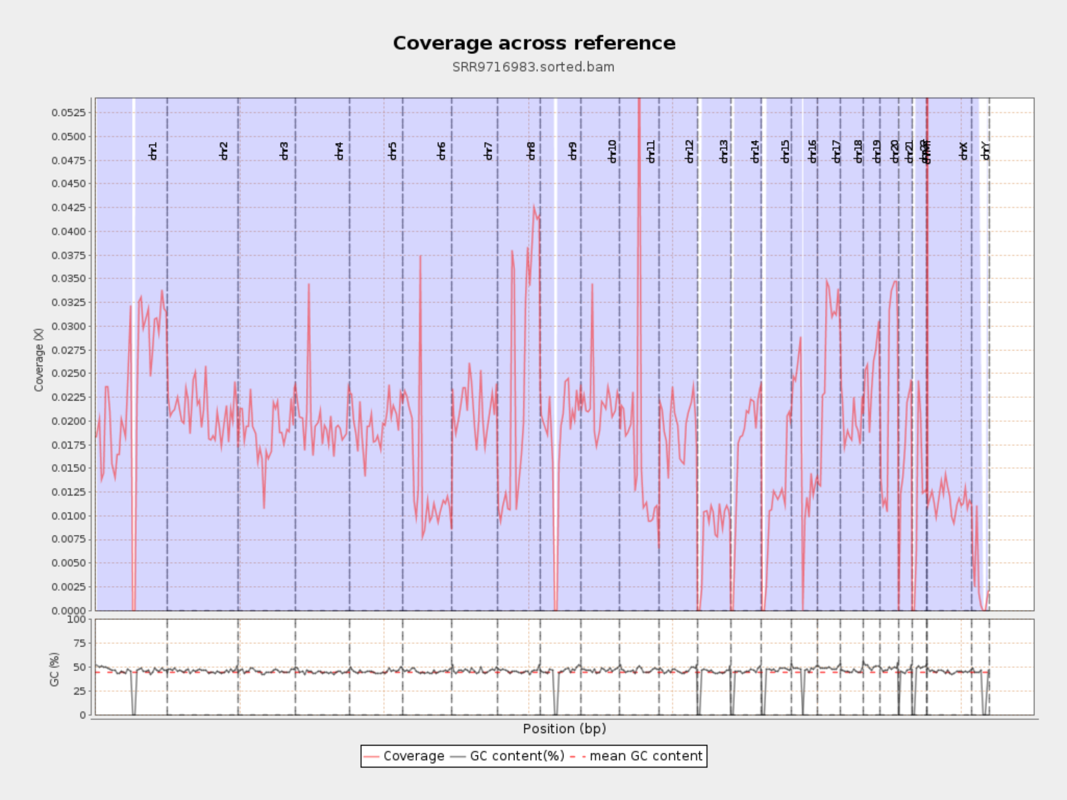
General error rate	0.72%
Mismatches	404,434
Insertions	3,260
Mapped reads with at least one insertion	0.3%
Deletions	9,373
Mapped reads with at least one deletion	0.86%
Homopolymer indels	40.8%

2.6. Chromosome stats

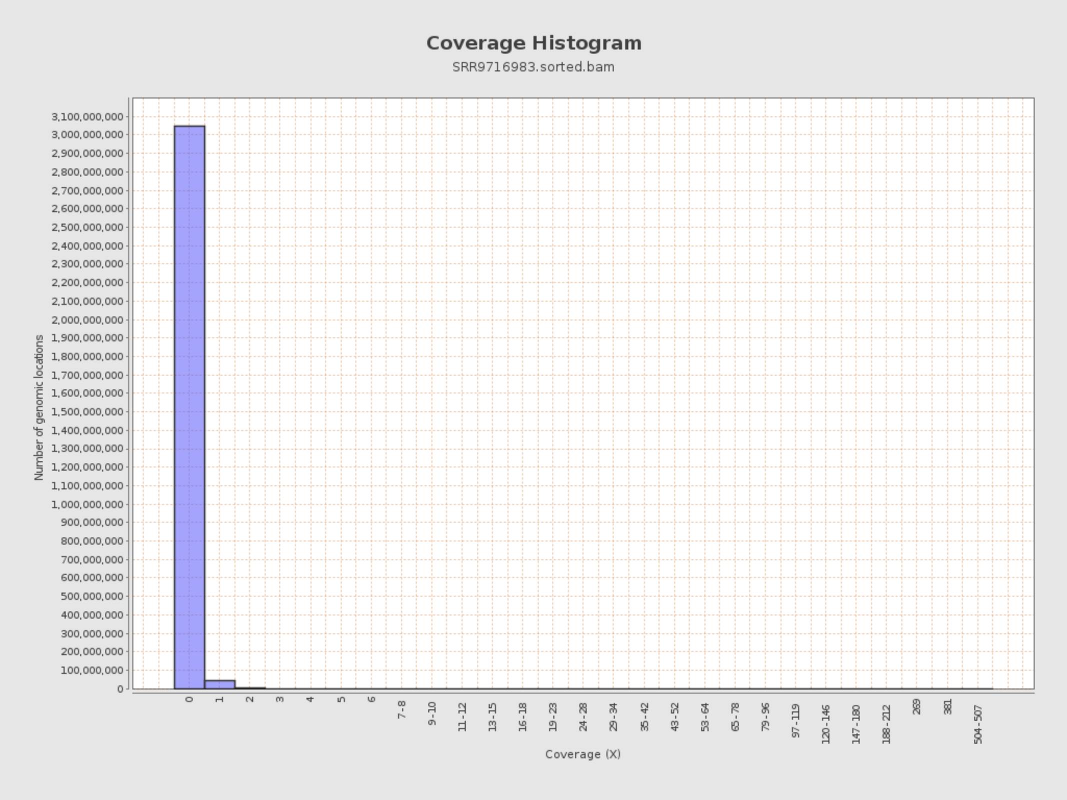
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5705902	0.0229	0.2284
chr2	243199373	5085133	0.0209	0.2674
chr3	198022430	3728091	0.0188	0.1557
chr4	191154276	3834756	0.0201	0.1699
chr5	180915260	3569668	0.0197	0.1587
chr6	171115067	2421882	0.0142	0.1541
chr7	159138663	3406129	0.0214	0.1999

chr8	146364022	3584566	0.0245	0.1856
chr9	141213431	2565759	0.0182	0.1667
chr10	135534747	2976016	0.022	0.205
chr11	135006516	2418075	0.0179	0.1728
chr12	133851895	2607613	0.0195	0.1581
chr13	115169878	960698	0.0083	0.1043
chr14	107349540	1817673	0.0169	0.149
chr15	102531392	1126067	0.011	0.1202
chr16	90354753	1468319	0.0163	0.1571
chr17	81195210	2196442	0.0271	0.1925
chr18	78077248	1536954	0.0197	0.1919
chr19	59128983	1482678	0.0251	0.2215
chr20	63025520	1476147	0.0234	0.1816
chr21	48129895	808451	0.0168	0.1567
chr22	51304566	615007	0.012	0.1248
chrMT	16571	8733	0.527	0.8995
chrX	155270560	1812152	0.0117	0.1274
chrY	59373566	170395	0.0029	0.0915

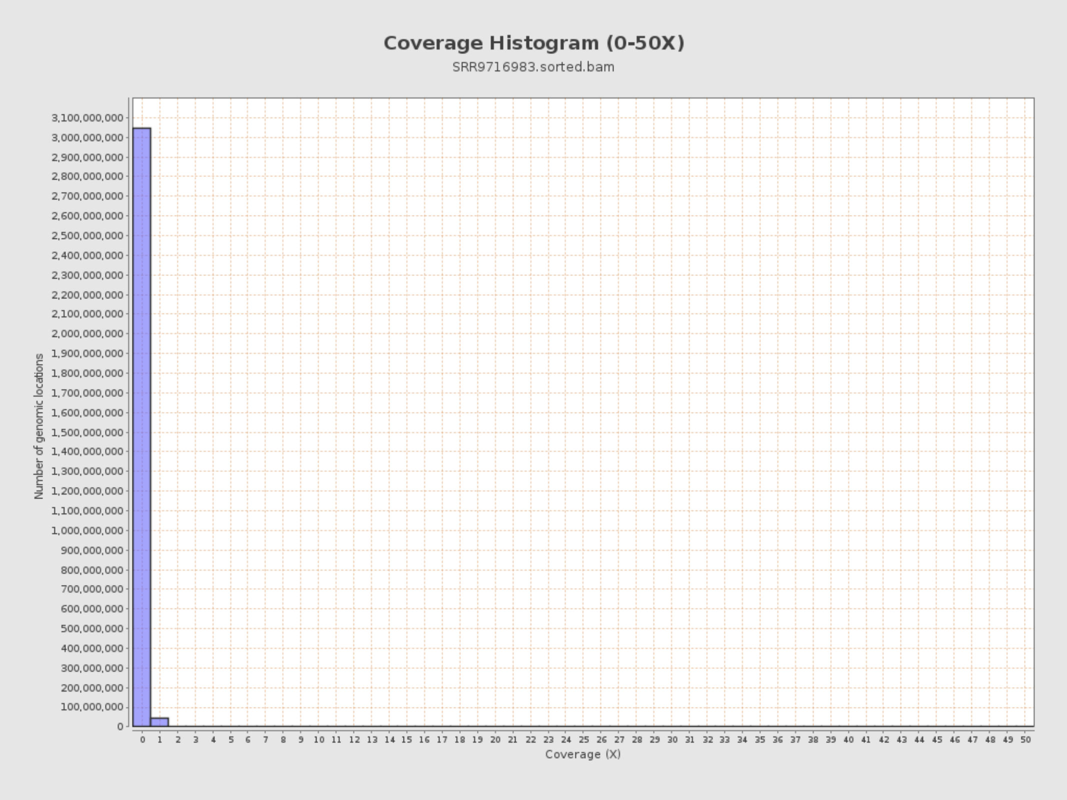
3. Results : Coverage across reference



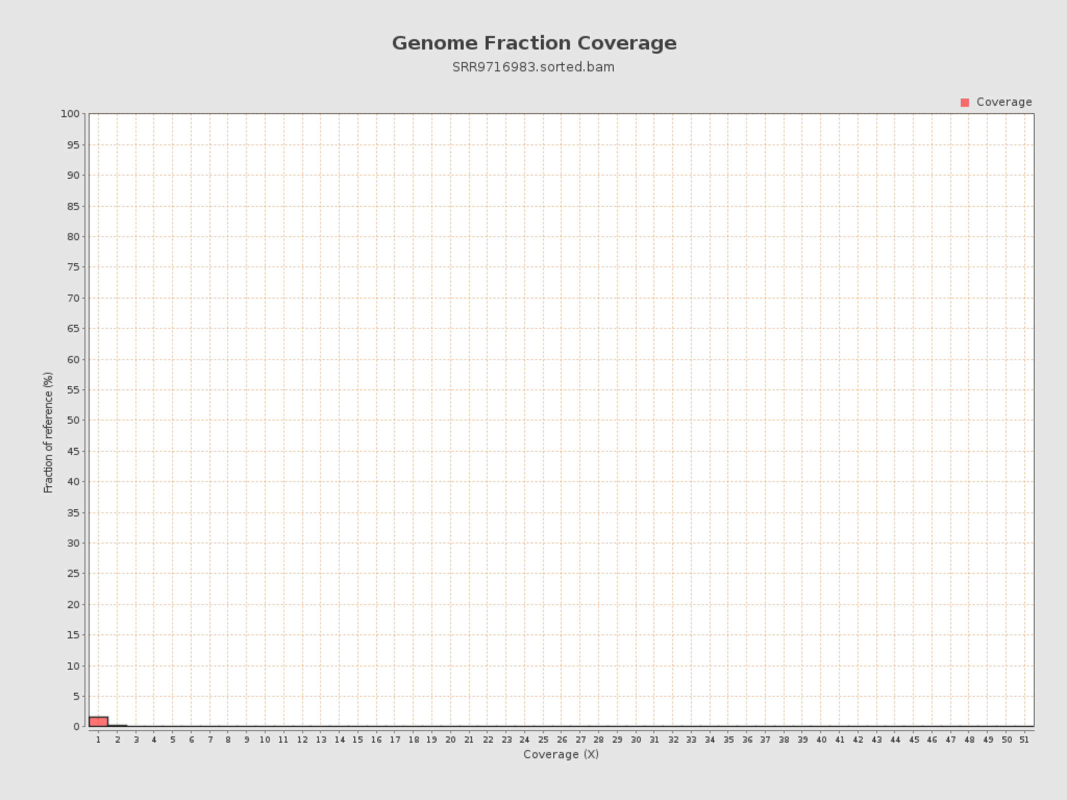
4. Results : Coverage Histogram



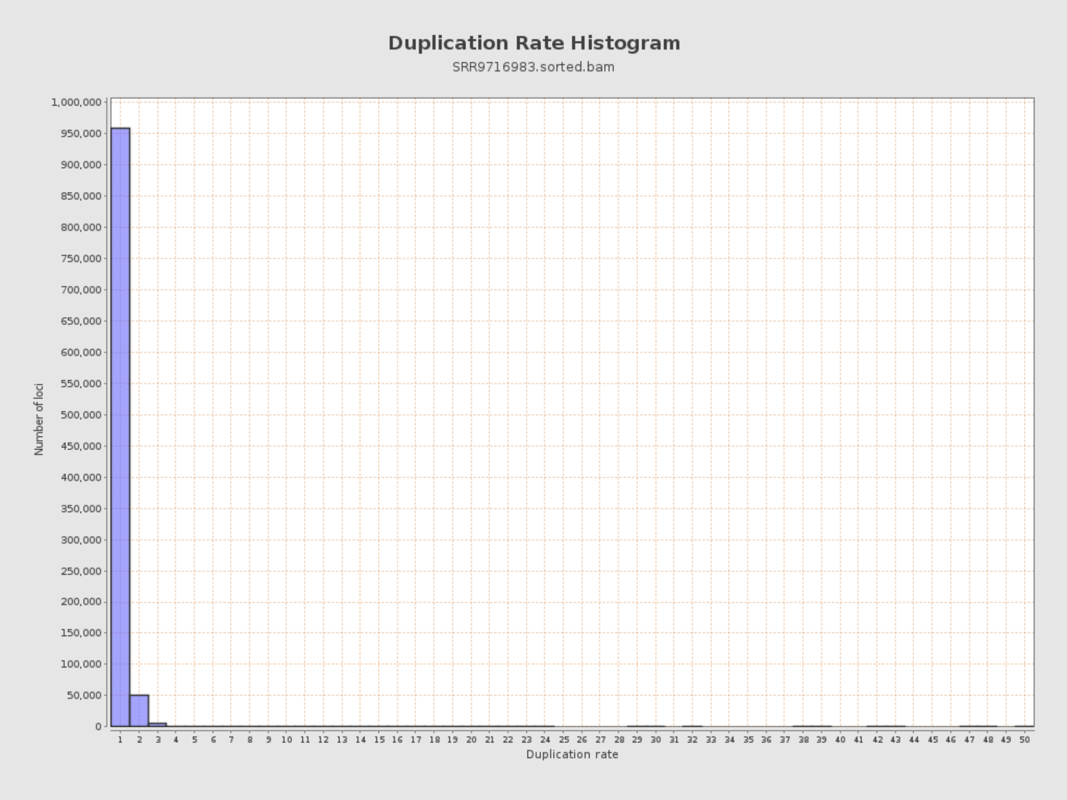
5. Results : Coverage Histogram (0-50X)



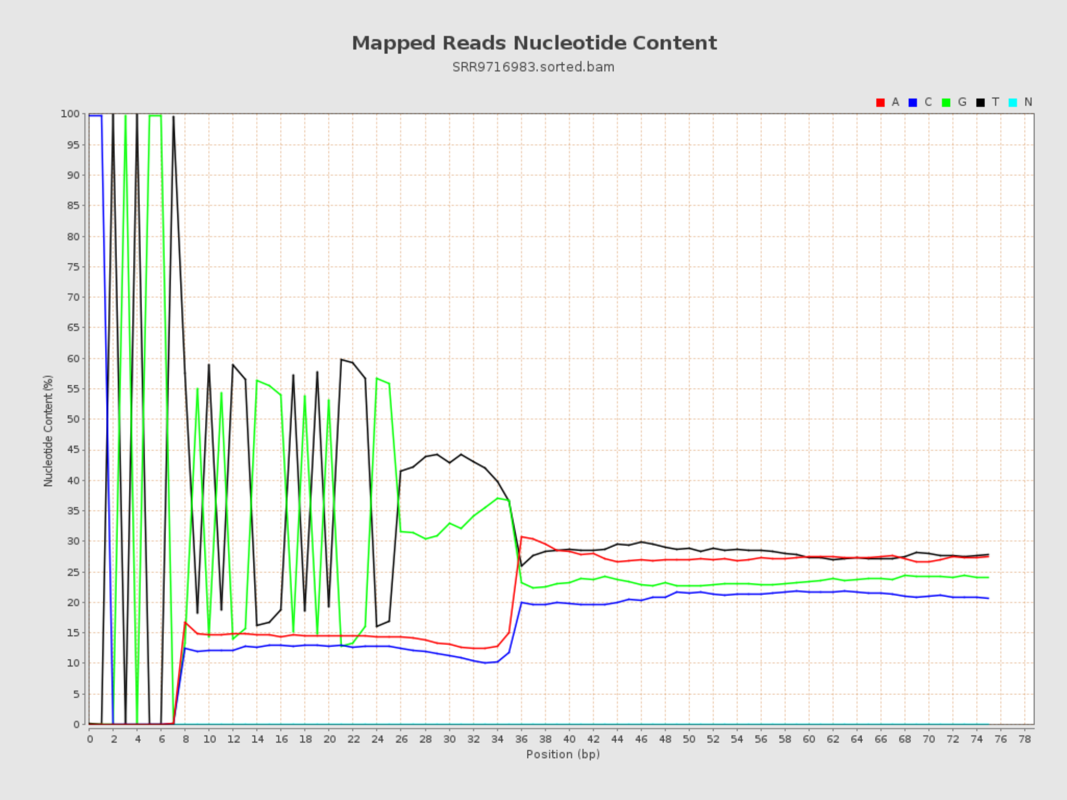
6. Results : Genome Fraction Coverage



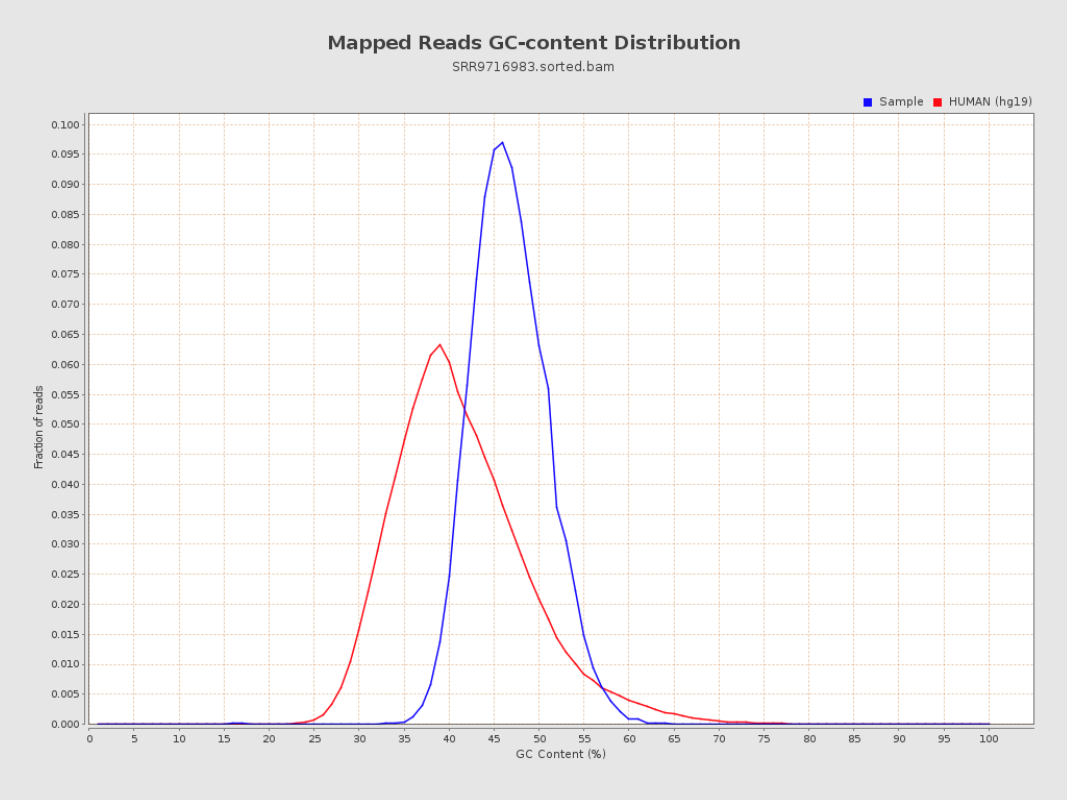
7. Results : Duplication Rate Histogram



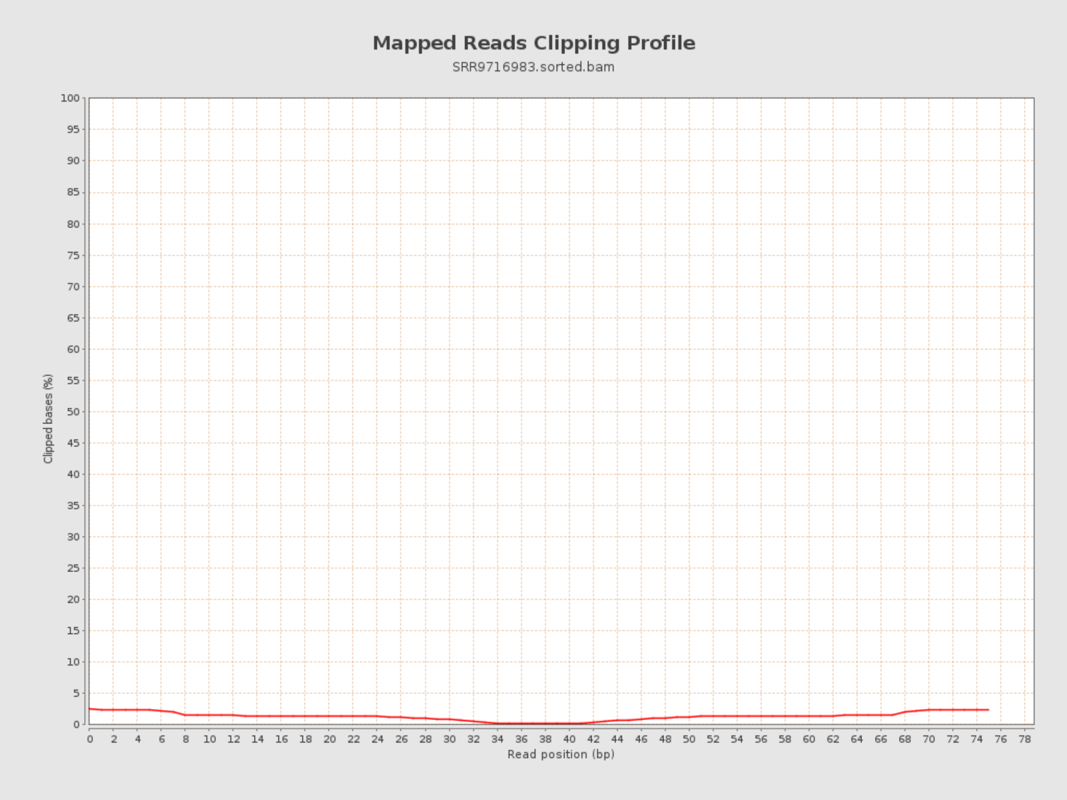
8. Results : Mapped Reads Nucleotide Content



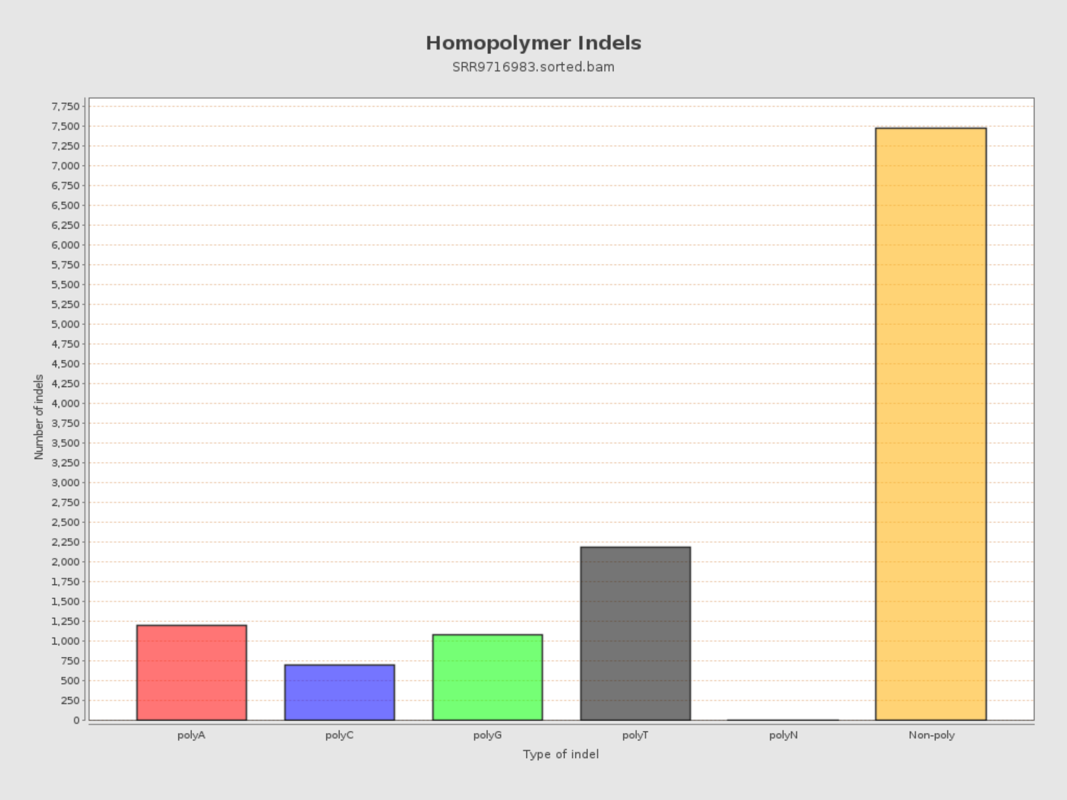
9. Results : Mapped Reads GC-content Distribution



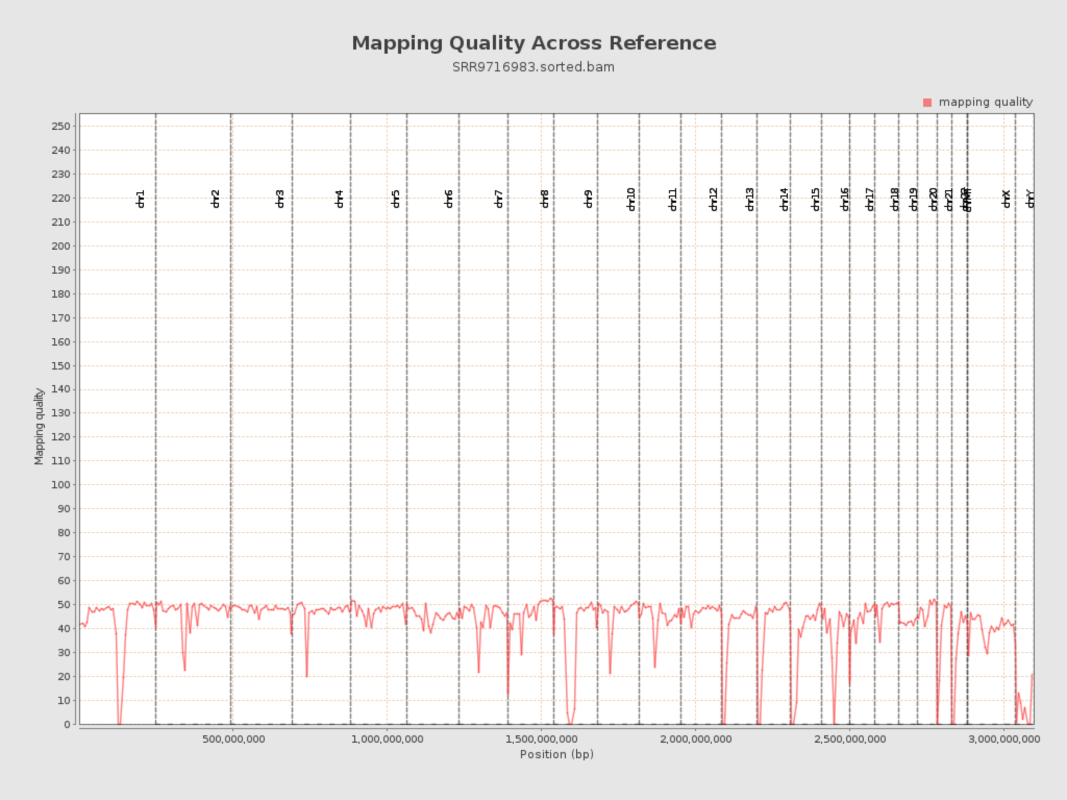
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram