Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:45:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716968.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_SRR9716968 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716968.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:45:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716968.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,019,244
Mapped reads	809,905 / 79.46%
Unmapped reads	209,339 / 20.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,470 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	13,497 / 1.32%
Duplication rate	1.26%
Clipped reads	810,637 / 79.53%

2.2. ACGT Content

Number/percentage of A's	10,079,744 / 22.7%
Number/percentage of C's	9,622,762 / 21.67%
Number/percentage of T's	13,006,806 / 29.3%
Number/percentage of G's	11,687,358 / 26.32%
Number/percentage of N's	1,255 / 0%
GC Percentage	48%

2.3. Coverage

Mean	0.0143

Standard Deviation	0.1399

2.4. Mapping Quality

Mean Mapping Quality	39.44

2.5. Mismatches and indels

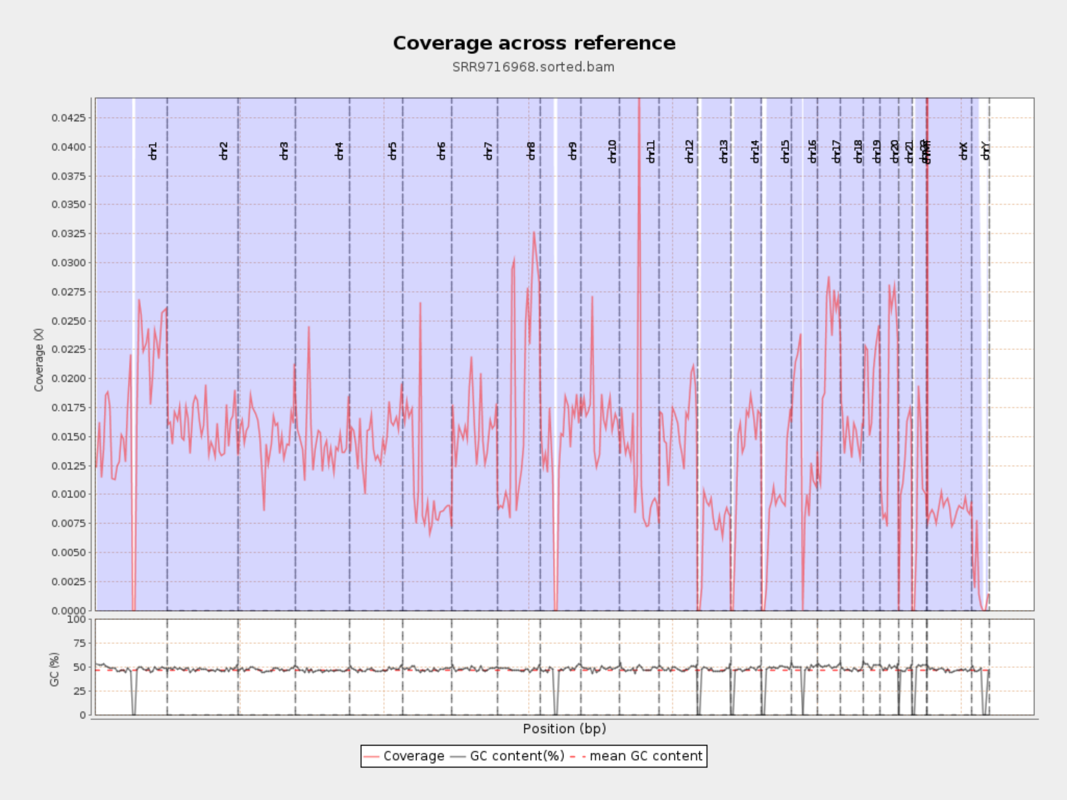
General error rate	0.53%
Mismatches	231,320
Insertions	3,216
Mapped reads with at least one insertion	0.39%
Deletions	6,992
Mapped reads with at least one deletion	0.86%
Homopolymer indels	33.74%

2.6. Chromosome stats

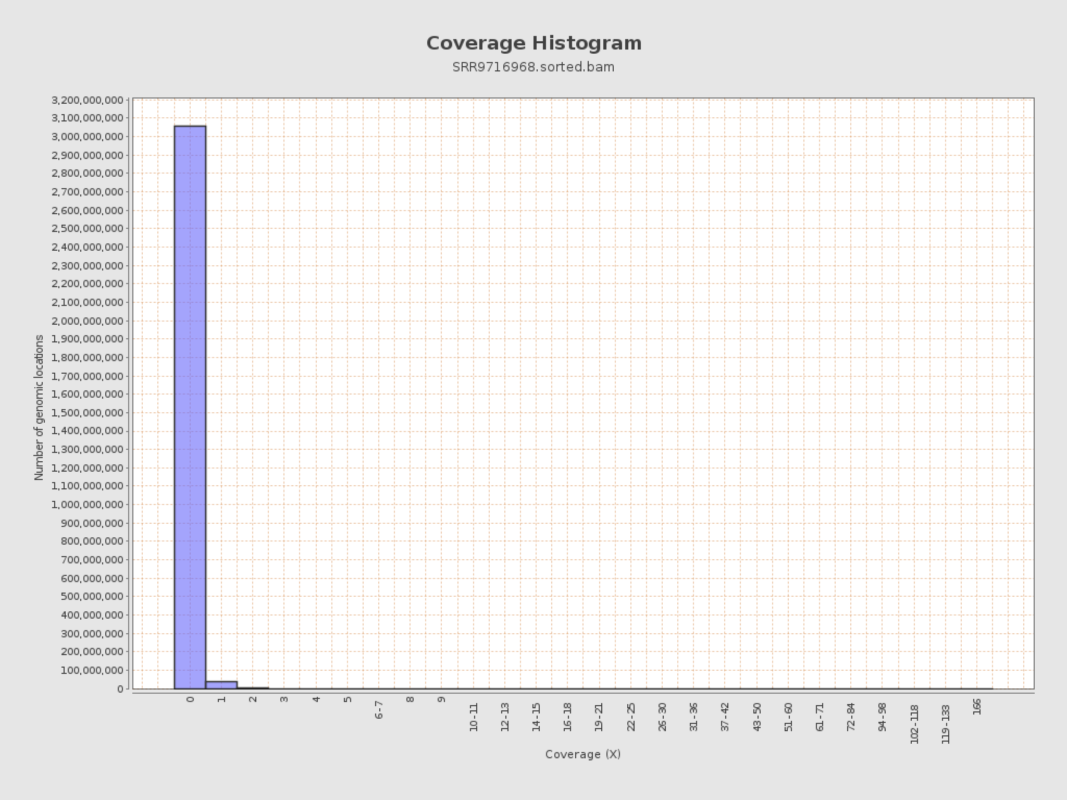
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4395440	0.0176	0.1687
chr2	243199373	3862324	0.0159	0.1606
chr3	198022430	2992366	0.0151	0.1327
chr4	191154276	2830516	0.0148	0.1385
chr5	180915260	2704278	0.0149	0.1304
chr6	171115067	1903036	0.0111	0.1147
chr7	159138663	2527801	0.0159	0.1552

chr8	146364022	2721542	0.0186	0.1516
chr9	141213431	1924589	0.0136	0.1306
chr10	135534747	2295480	0.0169	0.1776
chr11	135006516	1817083	0.0135	0.1399
chr12	133851895	2156819	0.0161	0.1363
chr13	115169878	807481	0.007	0.0917
chr14	107349540	1427714	0.0133	0.1251
chr15	102531392	897946	0.0088	0.101
chr16	90354753	1230251	0.0136	0.1323
chr17	81195210	1798758	0.0222	0.1651
chr18	78077248	1183084	0.0152	0.1526
chr19	59128983	1208077	0.0204	0.1656
chr20	63025520	1147091	0.0182	0.1514
chr21	48129895	603418	0.0125	0.127
chr22	51304566	492282	0.0096	0.1053
chrMT	16571	11618	0.7011	1.0508
chrX	155270560	1347535	0.0087	0.1048
chrY	59373566	123042	0.0021	0.0669

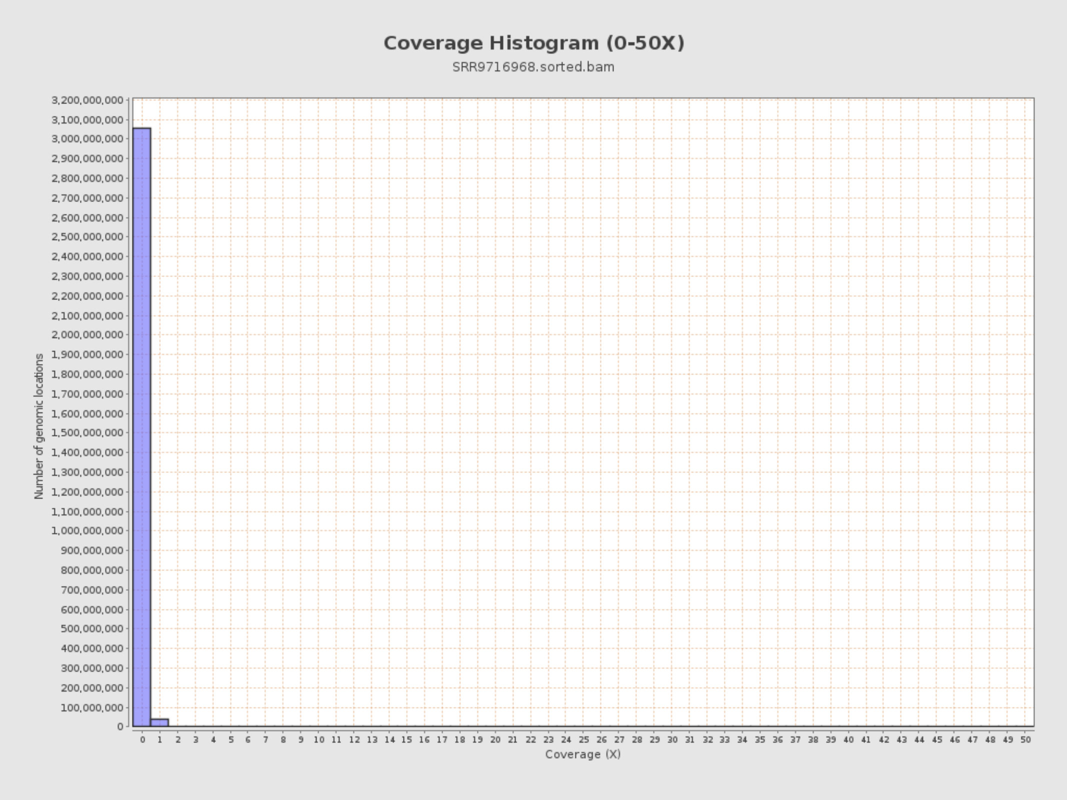
3. Results : Coverage across reference



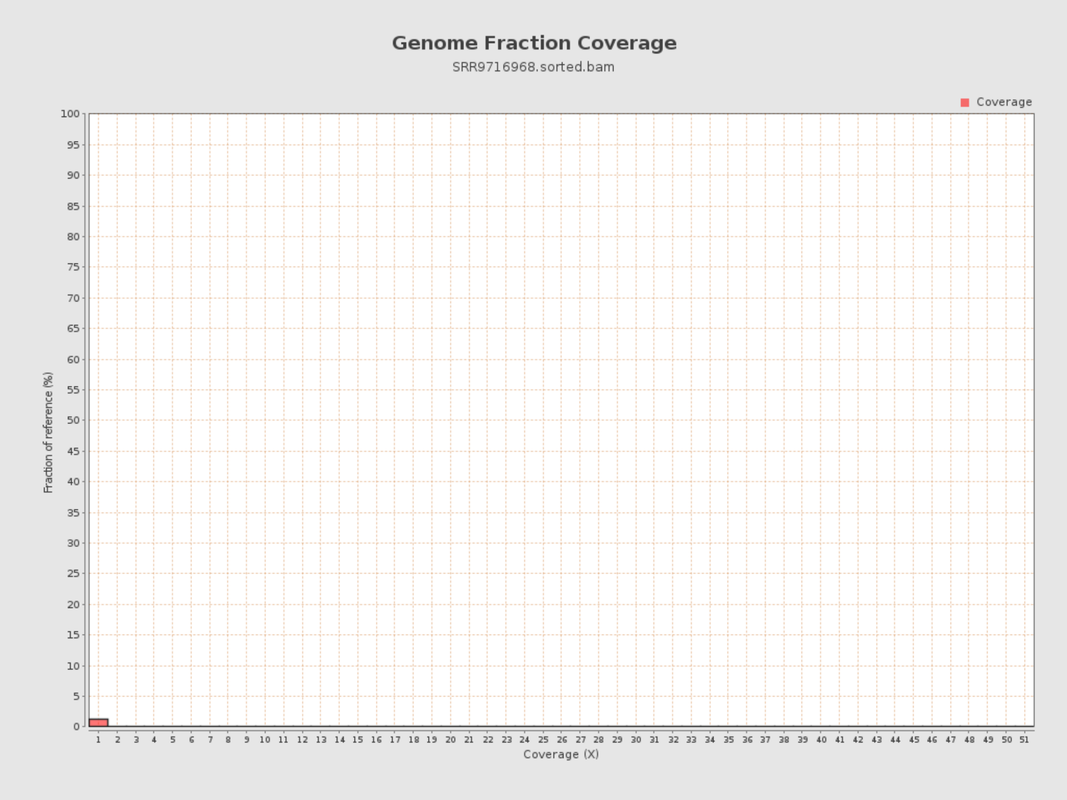
4. Results : Coverage Histogram



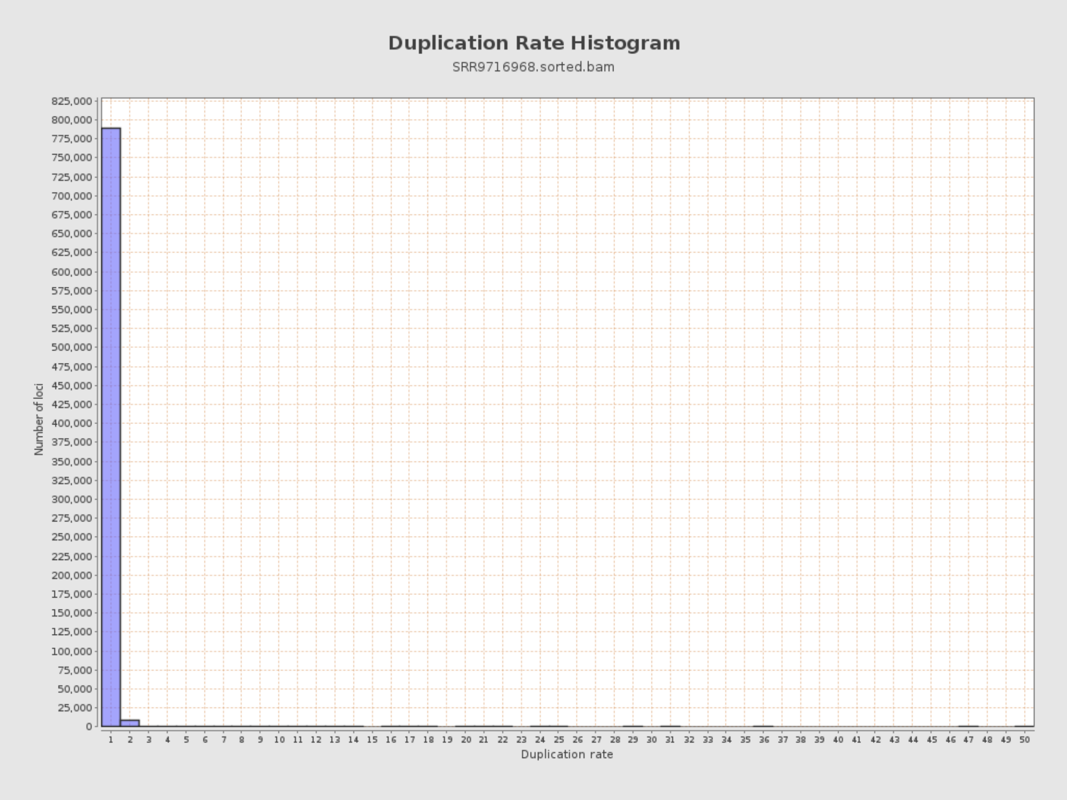
5. Results : Coverage Histogram (0-50X)



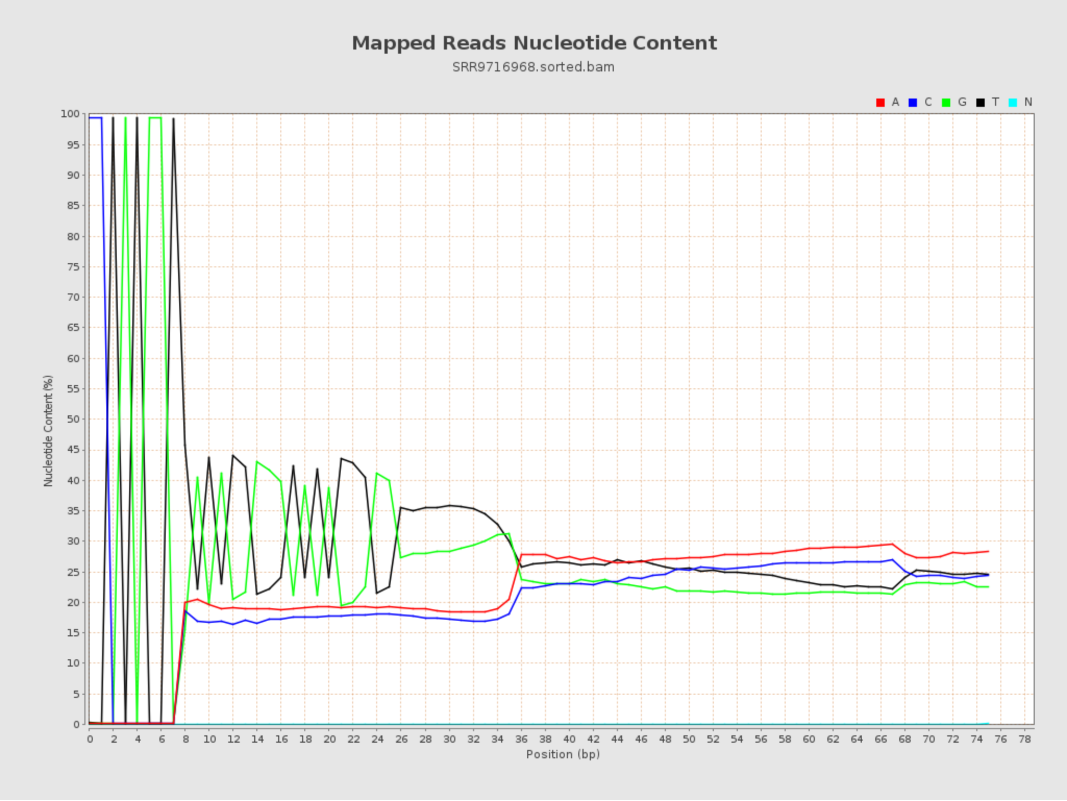
6. Results : Genome Fraction Coverage



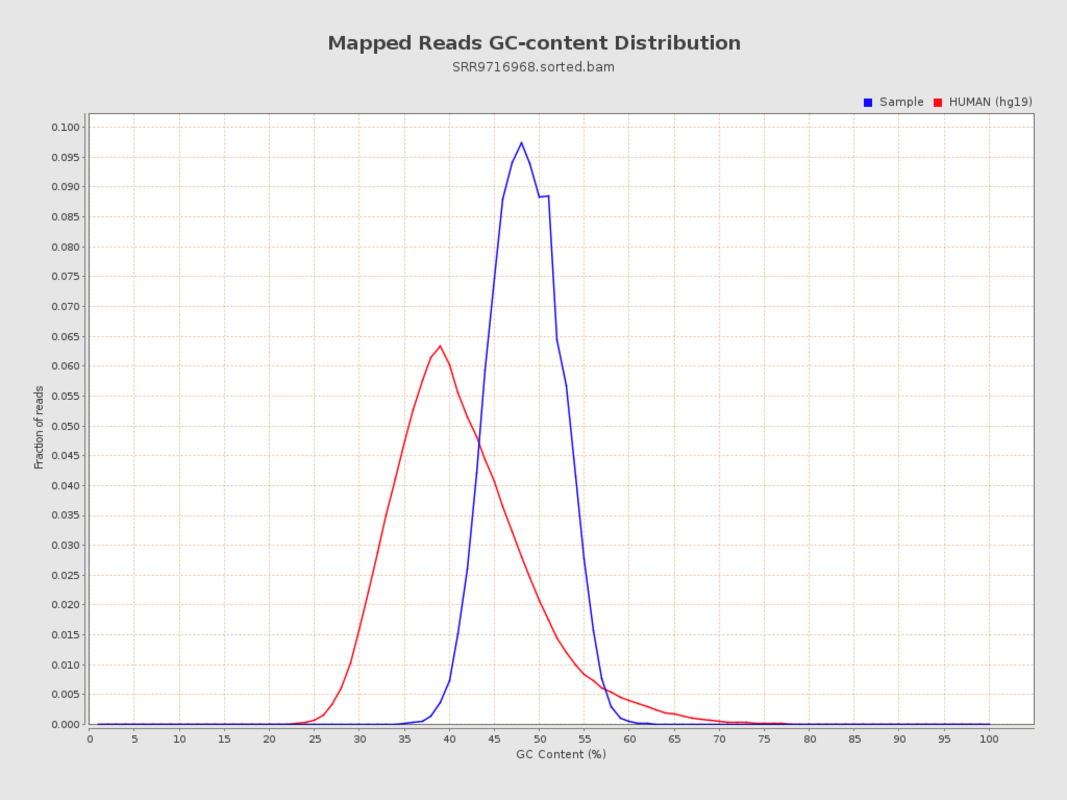
7. Results : Duplication Rate Histogram



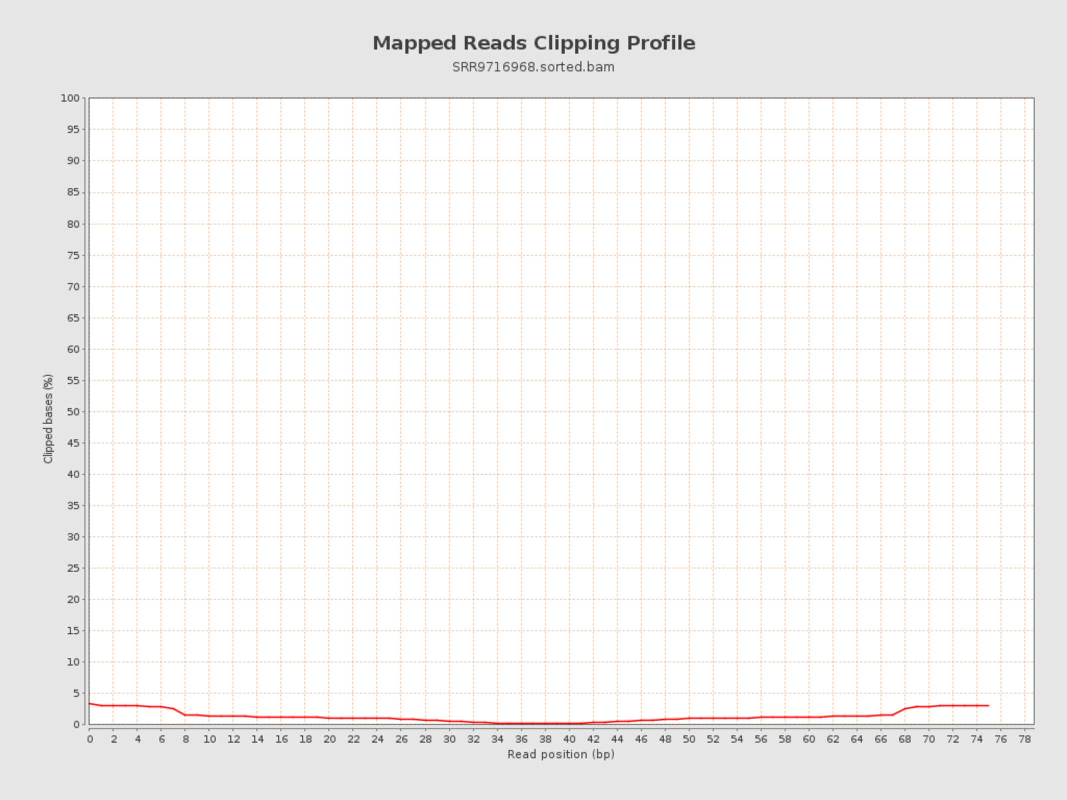
8. Results : Mapped Reads Nucleotide Content



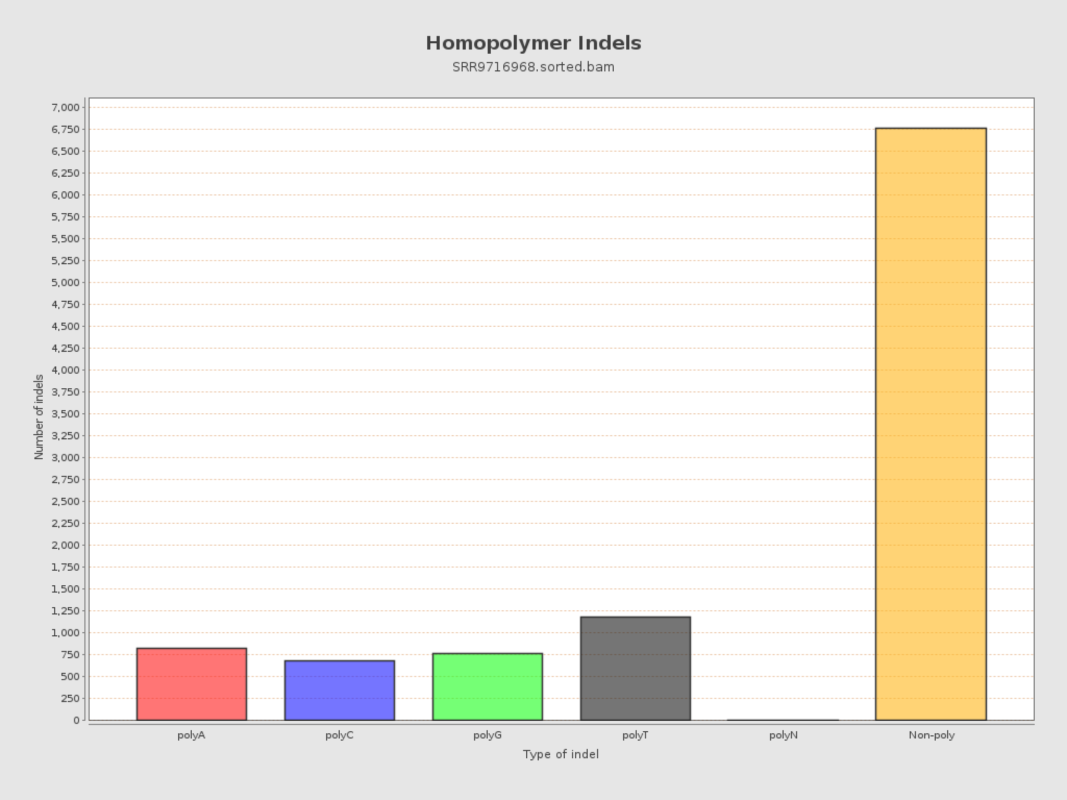
9. Results : Mapped Reads GC-content Distribution



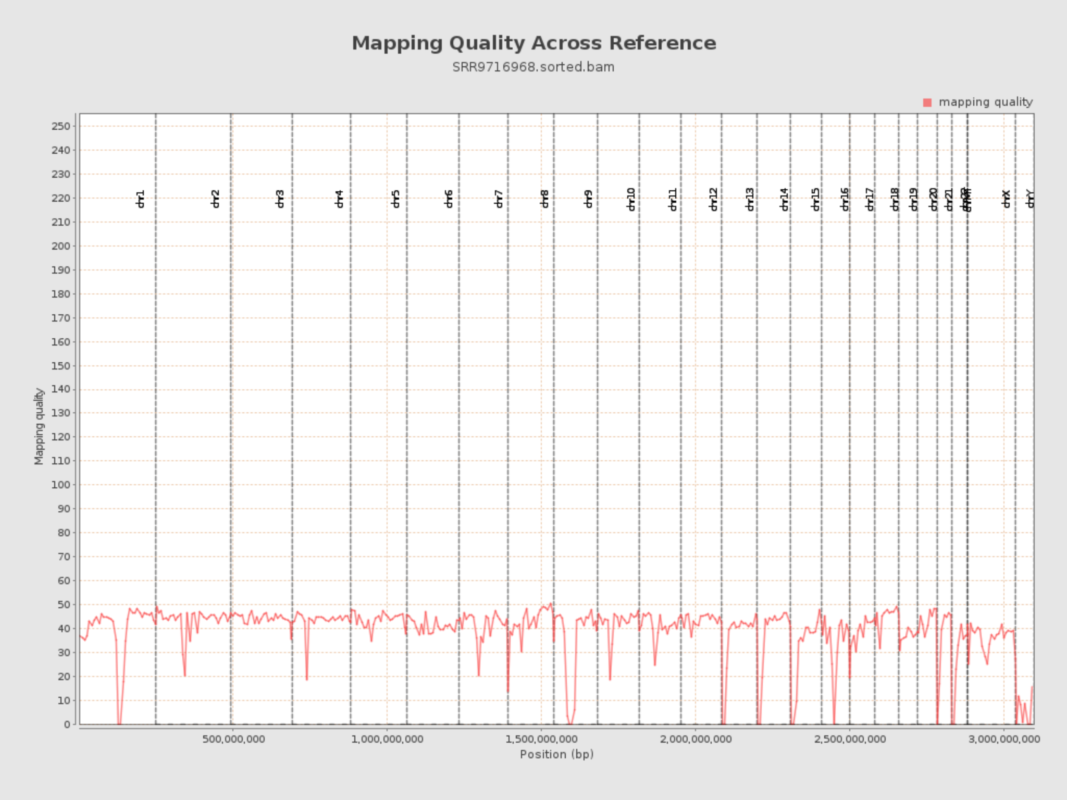
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram