Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:24:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716733.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_SRR9716733 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716733.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:24:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716733.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	753,786
Mapped reads	693,305 / 91.98%
Unmapped reads	60,481 / 8.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,776 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	12,635 / 1.68%
Duplication rate	1.28%
Clipped reads	696,104 / 92.35%

2.2. ACGT Content

Number/percentage of A's	10,489,236 / 25.53%
Number/percentage of C's	7,987,955 / 19.44%
Number/percentage of T's	12,195,901 / 29.68%
Number/percentage of G's	10,414,383 / 25.35%
Number/percentage of N's	406 / 0%
GC Percentage	44.79%

2.3. Coverage

Mean	0.0133

Standard Deviation	0.151

2.4. Mapping Quality

Mean Mapping Quality	45.07

2.5. Mismatches and indels

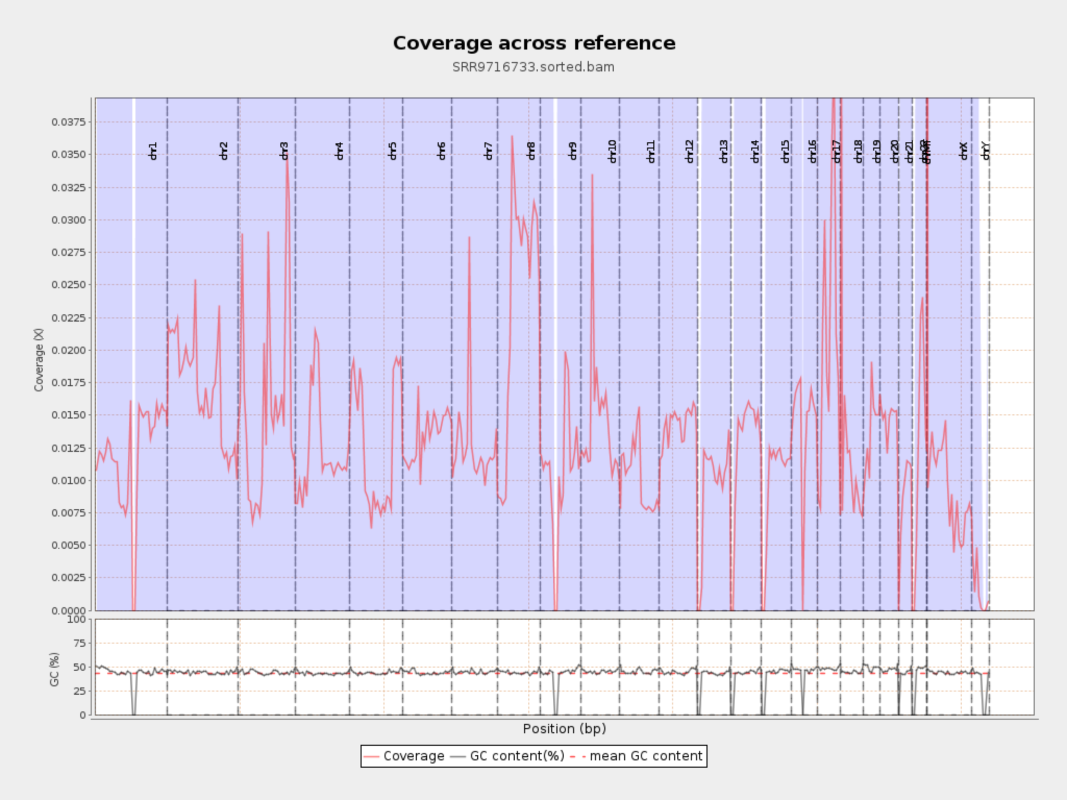
General error rate	0.51%
Mismatches	207,012
Insertions	2,290
Mapped reads with at least one insertion	0.33%
Deletions	7,684
Mapped reads with at least one deletion	1.1%
Homopolymer indels	44.12%

2.6. Chromosome stats

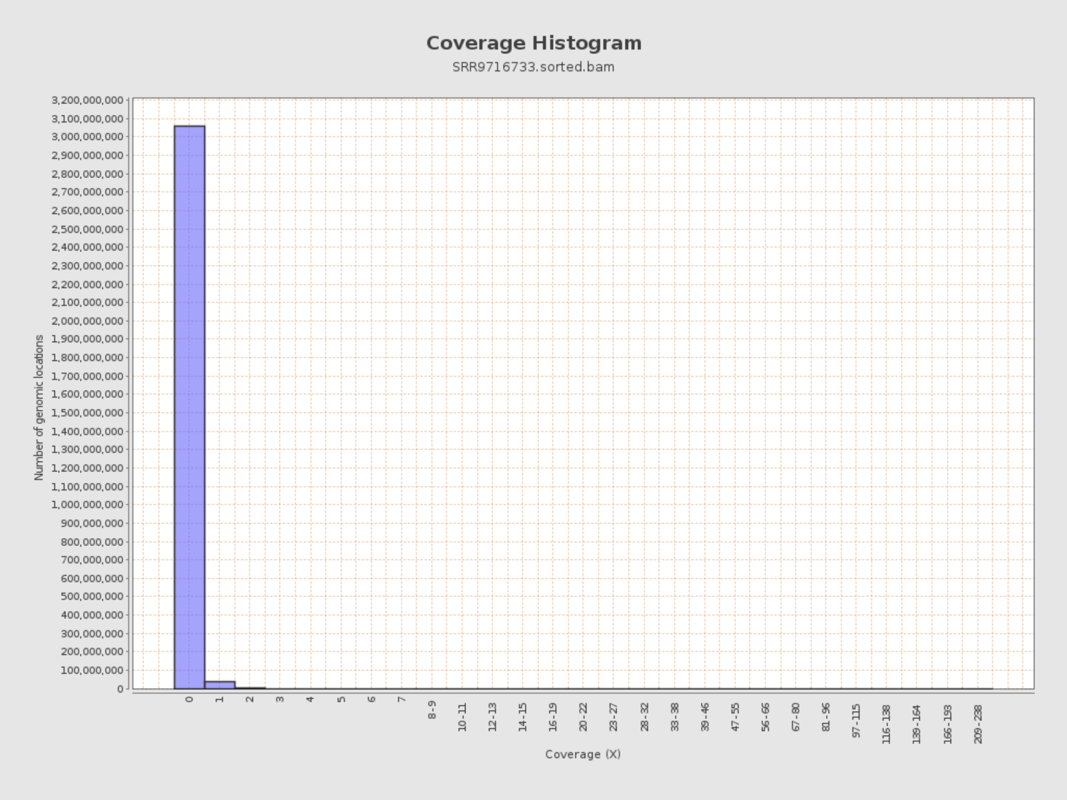
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2956922	0.0119	0.2073
chr2	243199373	4181062	0.0172	0.1743
chr3	198022430	3092451	0.0156	0.1309
chr4	191154276	2326101	0.0122	0.1177
chr5	180915260	2277453	0.0126	0.1163
chr6	171115067	2294424	0.0134	0.1248
chr7	159138663	2017389	0.0127	0.2472

chr8	146364022	3532360	0.0241	0.1943
chr9	141213431	1475914	0.0105	0.116
chr10	135534747	1980296	0.0146	0.1845
chr11	135006516	1387574	0.0103	0.1202
chr12	133851895	1909792	0.0143	0.1286
chr13	115169878	1077228	0.0094	0.0997
chr14	107349540	1341004	0.0125	0.1164
chr15	102531392	986453	0.0096	0.1013
chr16	90354753	1280058	0.0142	0.1265
chr17	81195210	1723400	0.0212	0.1535
chr18	78077248	922949	0.0118	0.1652
chr19	59128983	817786	0.0138	0.191
chr20	63025520	922755	0.0146	0.127
chr21	48129895	421144	0.0088	0.099
chr22	51304566	632449	0.0123	0.1152
chrMT	16571	9930	0.5992	0.8698
chrX	155270560	1446053	0.0093	0.1067
chrY	59373566	87159	0.0015	0.0504

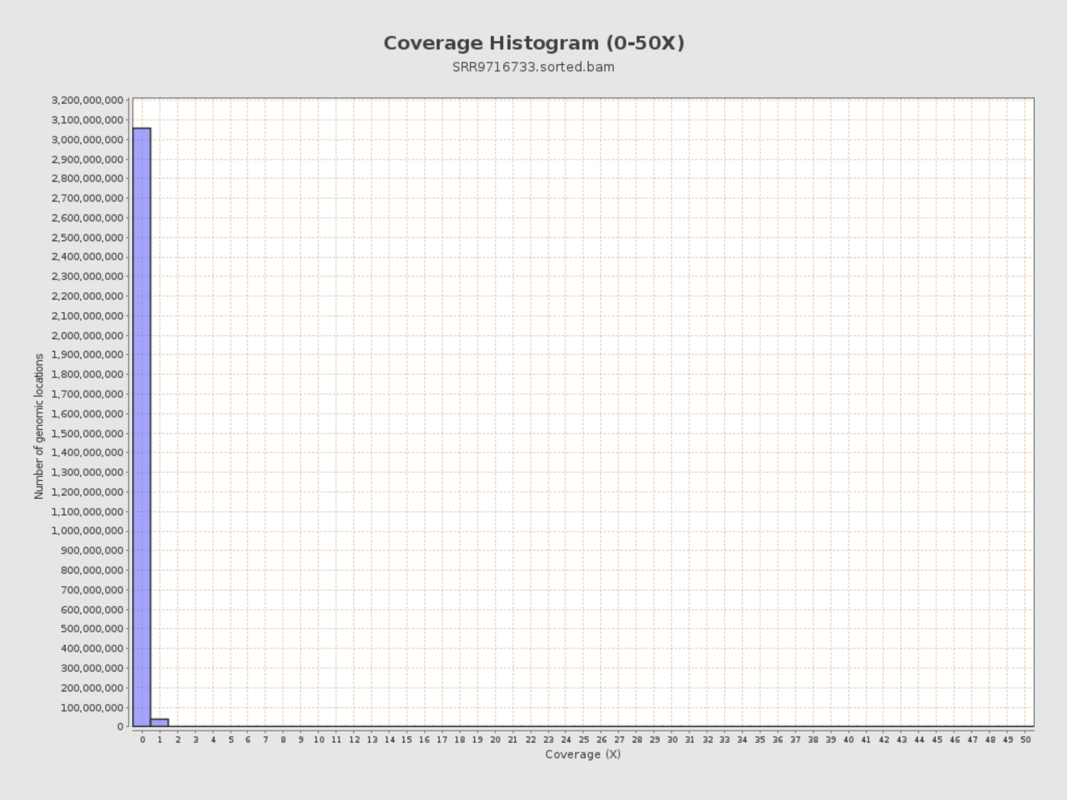
3. Results : Coverage across reference



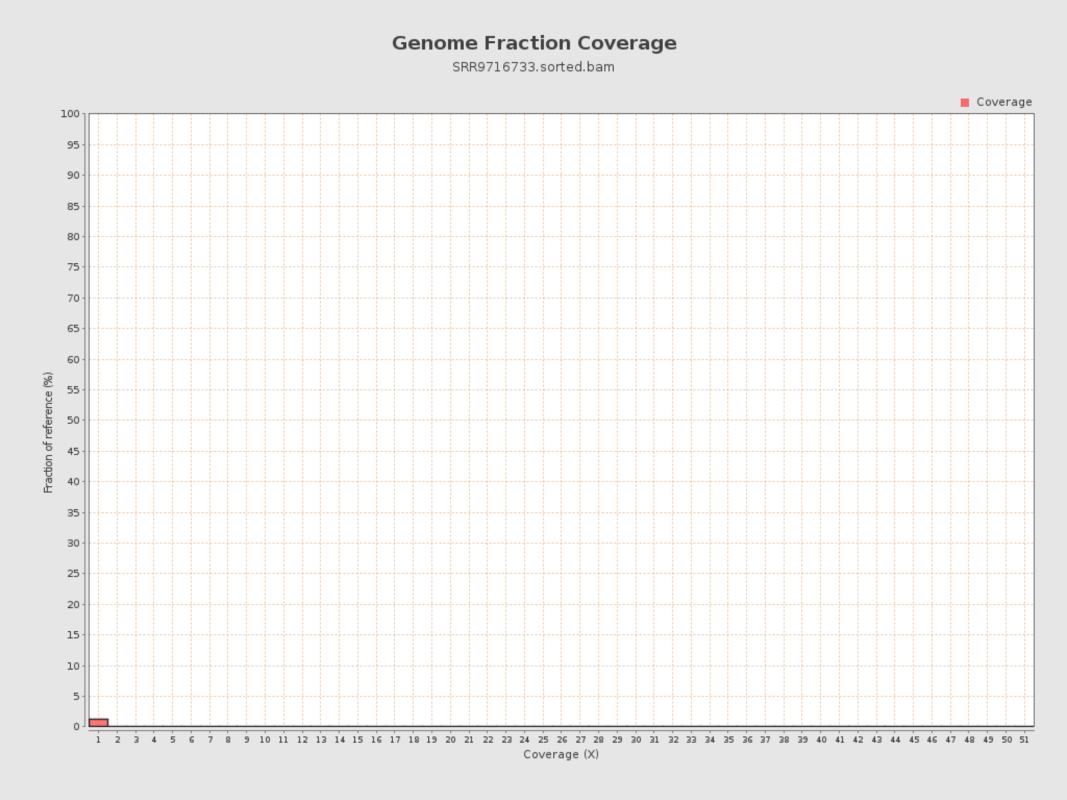
4. Results : Coverage Histogram



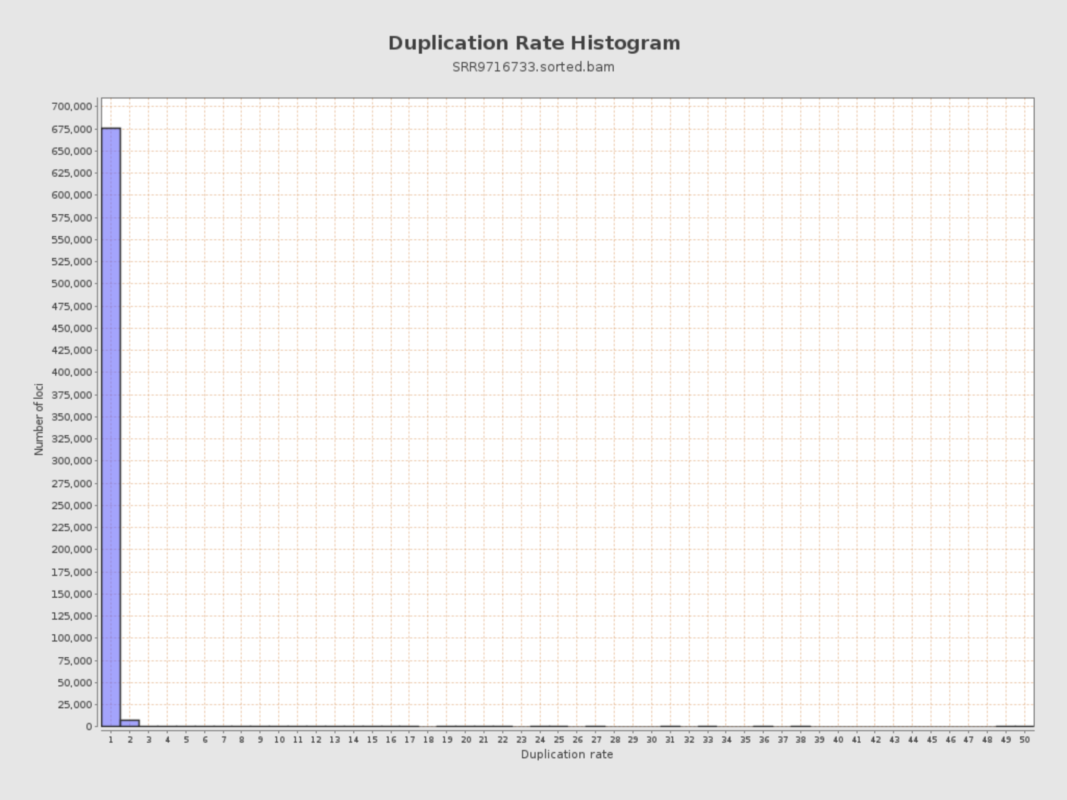
5. Results : Coverage Histogram (0-50X)



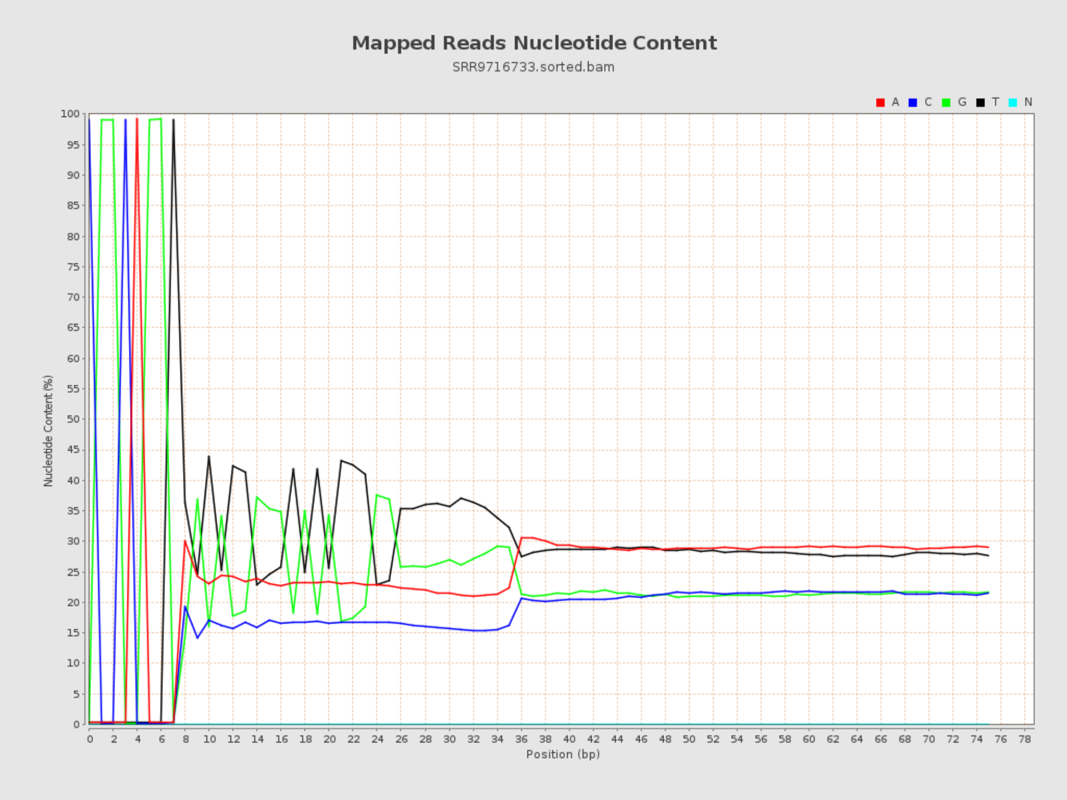
6. Results : Genome Fraction Coverage



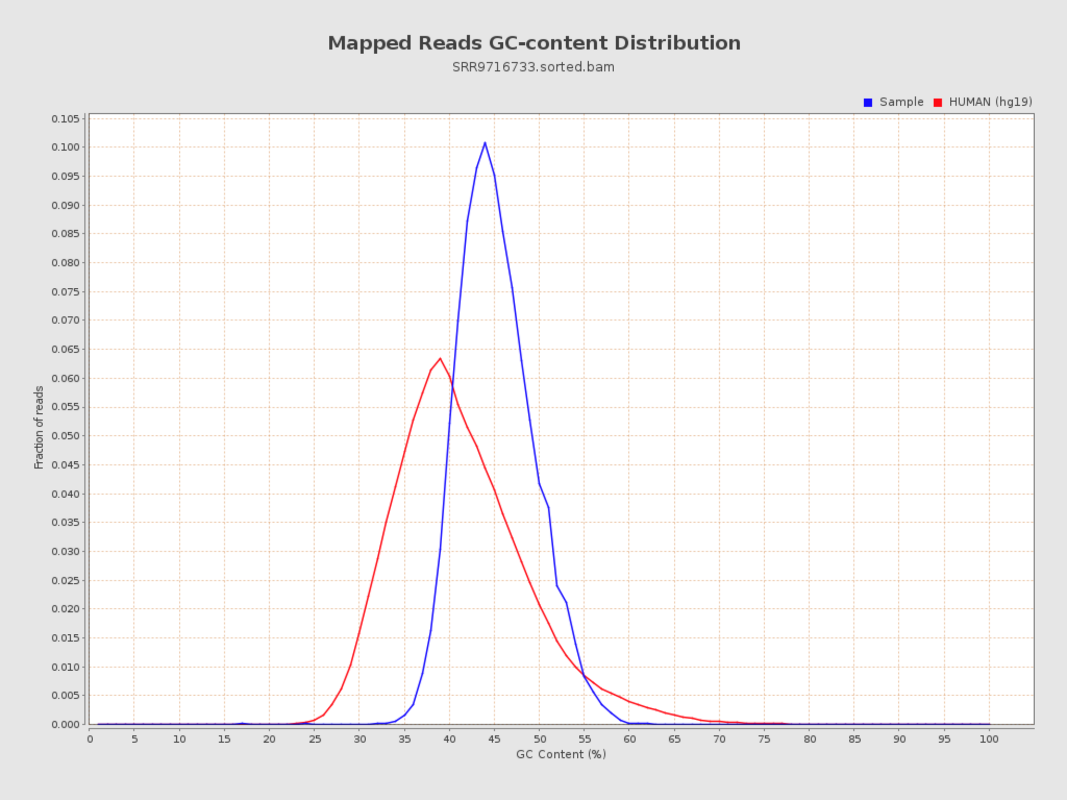
7. Results : Duplication Rate Histogram



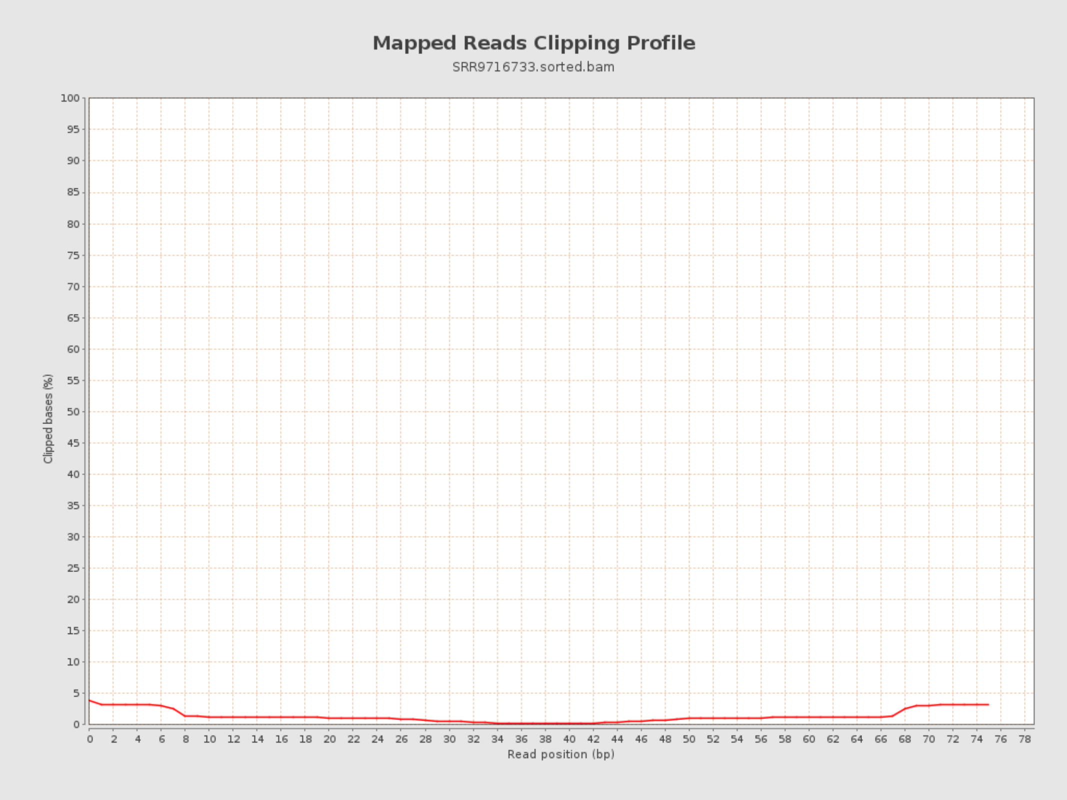
8. Results : Mapped Reads Nucleotide Content



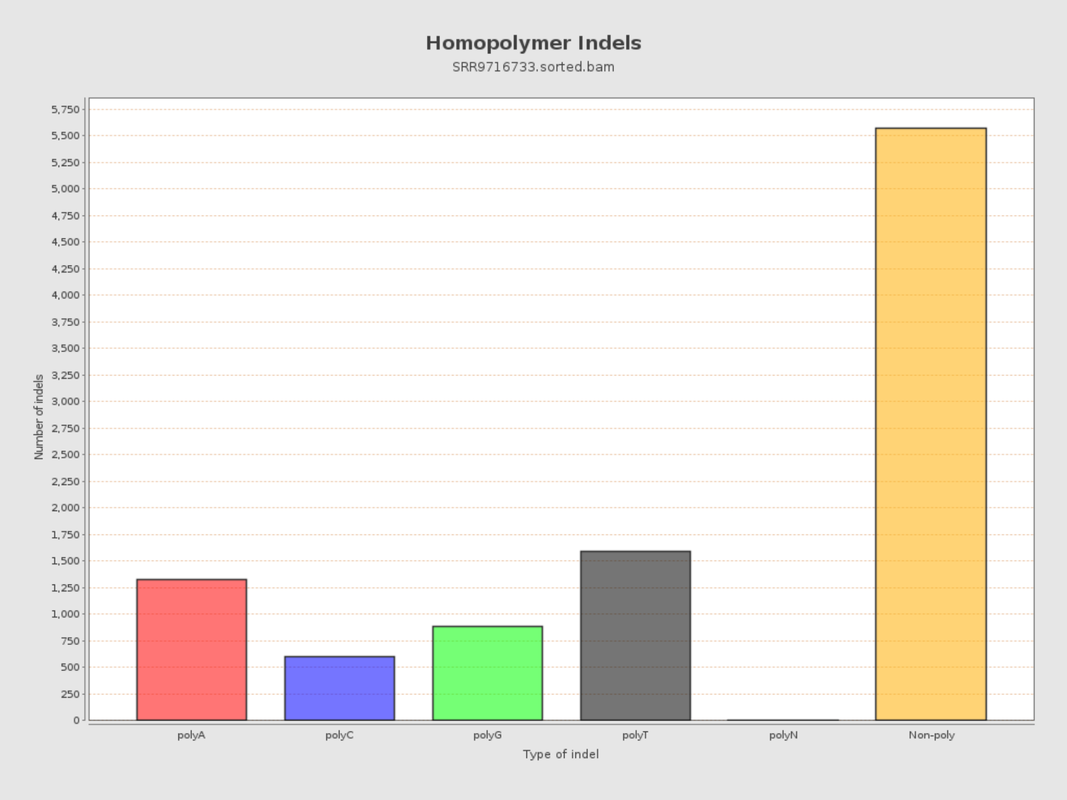
9. Results : Mapped Reads GC-content Distribution



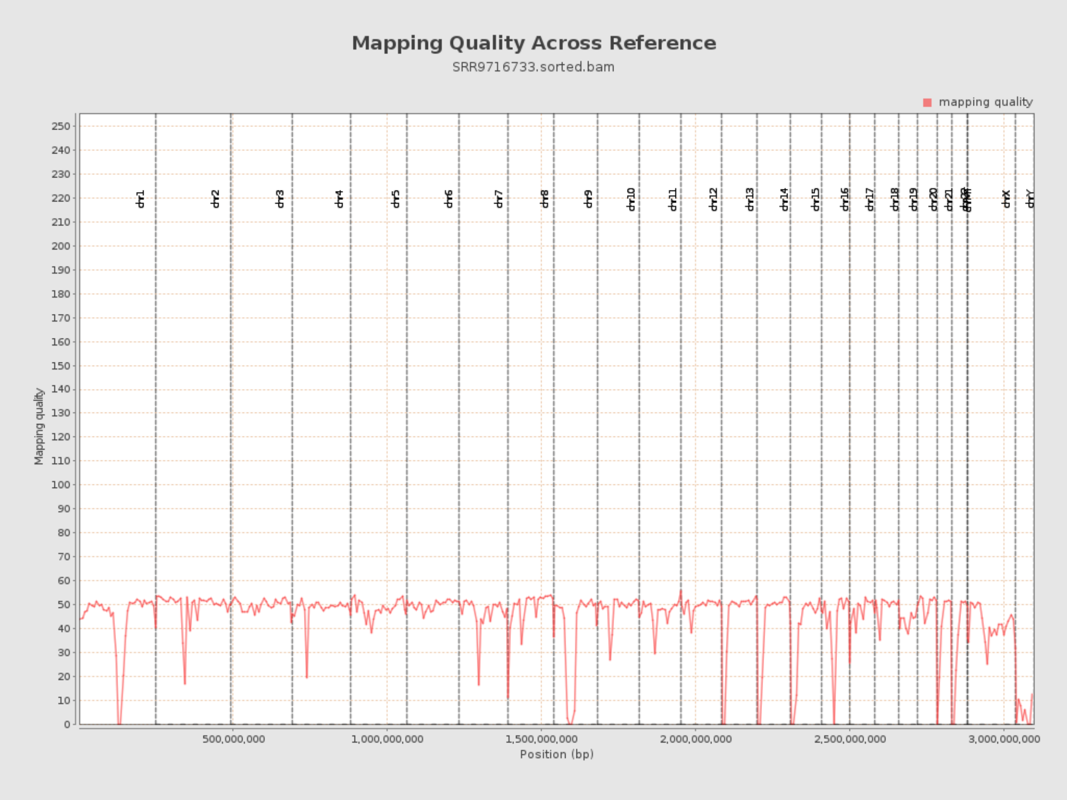
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram