Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:35:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716918.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_SRR9716918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716918.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:35:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	740,826
Mapped reads	601,201 / 81.15%
Unmapped reads	139,625 / 18.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,100 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	9,281 / 1.25%
Duplication rate	1.1%
Clipped reads	601,400 / 81.18%

2.2. ACGT Content

Number/percentage of A's	8,353,460 / 25.01%
Number/percentage of C's	6,469,674 / 19.37%
Number/percentage of T's	9,969,058 / 29.85%
Number/percentage of G's	8,601,457 / 25.76%
Number/percentage of N's	984 / 0%
GC Percentage	45.13%

2.3. Coverage

Mean	0.0108

Standard Deviation	0.1192

2.4. Mapping Quality

Mean Mapping Quality	40.42

2.5. Mismatches and indels

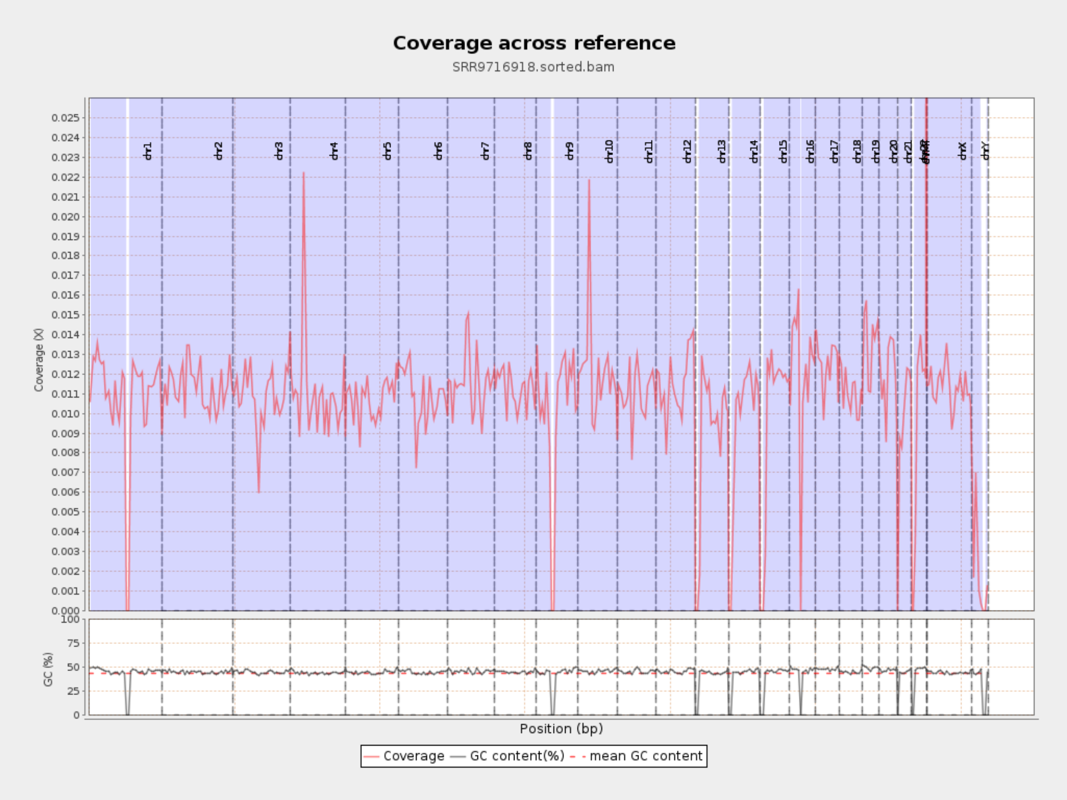
General error rate	0.56%
Mismatches	179,918
Insertions	3,101
Mapped reads with at least one insertion	0.51%
Deletions	5,798
Mapped reads with at least one deletion	0.95%
Homopolymer indels	34.42%

2.6. Chromosome stats

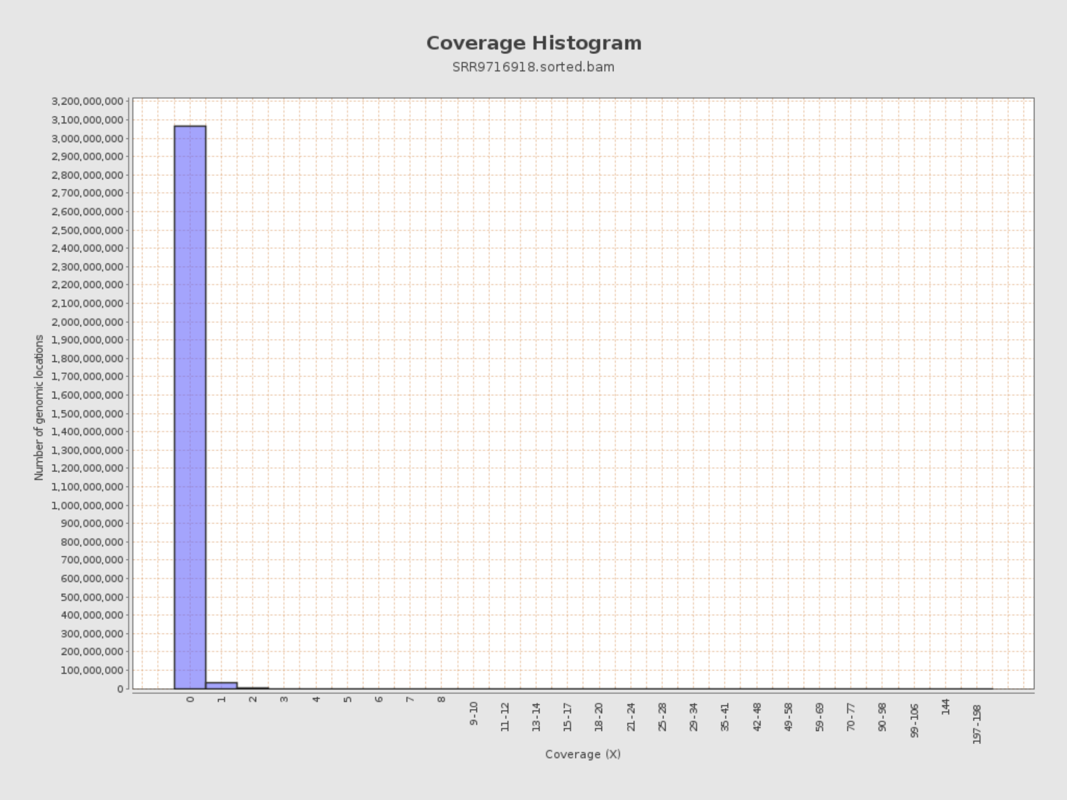
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2683664	0.0108	0.1228
chr2	243199373	2765884	0.0114	0.1467
chr3	198022430	2150693	0.0109	0.1108
chr4	191154276	2104074	0.011	0.1202
chr5	180915260	1945532	0.0108	0.1095
chr6	171115067	1872330	0.0109	0.1117
chr7	159138663	1838532	0.0116	0.1313

chr8	146364022	1649679	0.0113	0.1146
chr9	141213431	1401884	0.0099	0.1091
chr10	135534747	1654094	0.0122	0.1452
chr11	135006516	1488466	0.011	0.1206
chr12	133851895	1536829	0.0115	0.1128
chr13	115169878	1012392	0.0088	0.0988
chr14	107349540	1002404	0.0093	0.1029
chr15	102531392	995604	0.0097	0.1051
chr16	90354753	1086723	0.012	0.1209
chr17	81195210	1012451	0.0125	0.1205
chr18	78077248	864512	0.0111	0.1326
chr19	59128983	802898	0.0136	0.1342
chr20	63025520	751824	0.0119	0.118
chr21	48129895	456311	0.0095	0.1107
chr22	51304566	445042	0.0087	0.0998
chrMT	16571	2043	0.1233	0.3663
chrX	155270560	1763223	0.0114	0.1154
chrY	59373566	117527	0.002	0.066

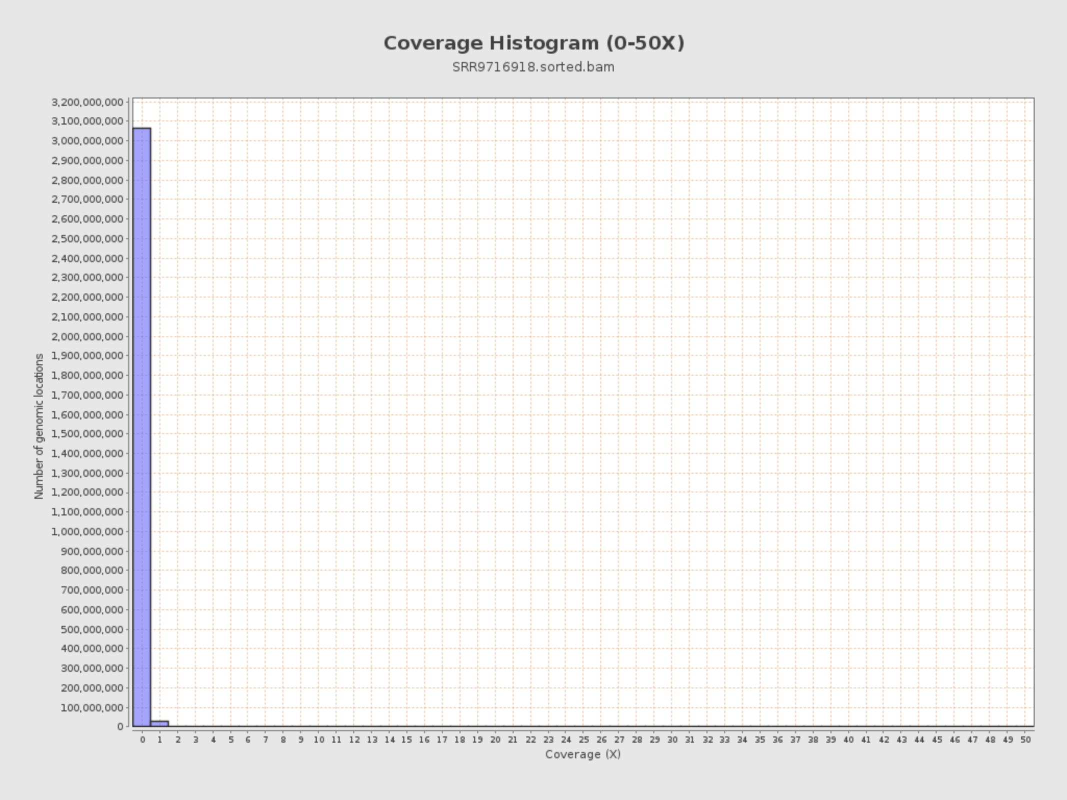
3. Results : Coverage across reference



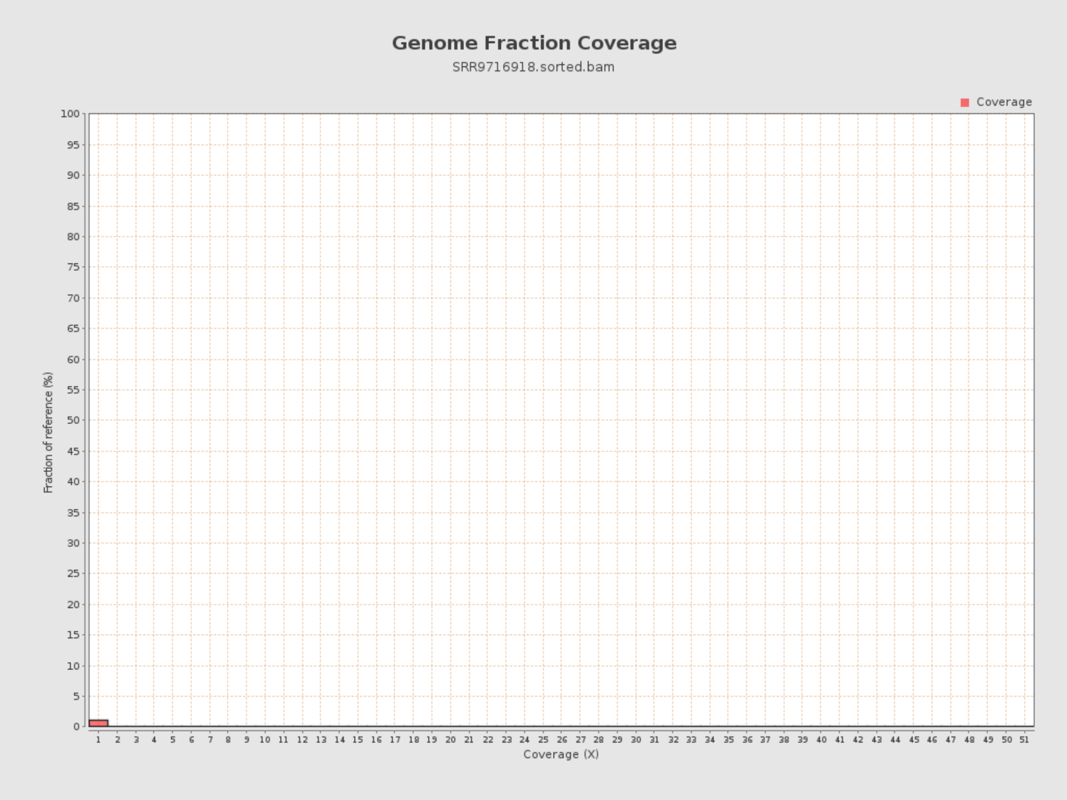
4. Results : Coverage Histogram



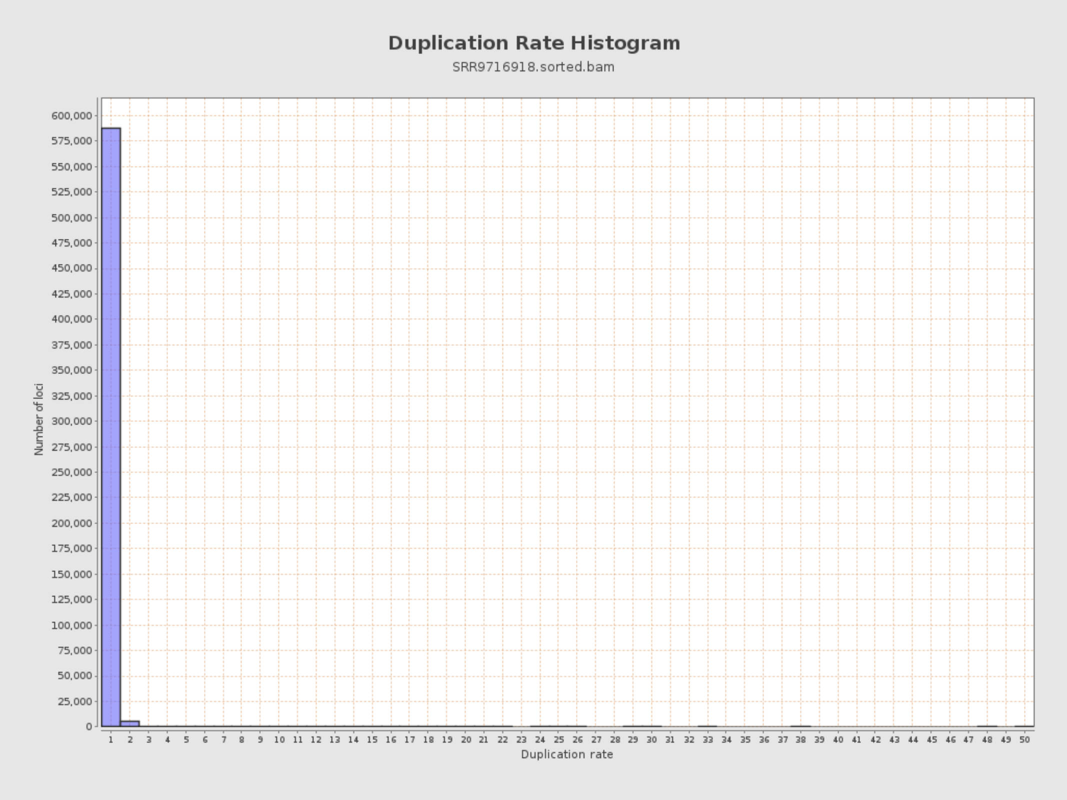
5. Results : Coverage Histogram (0-50X)



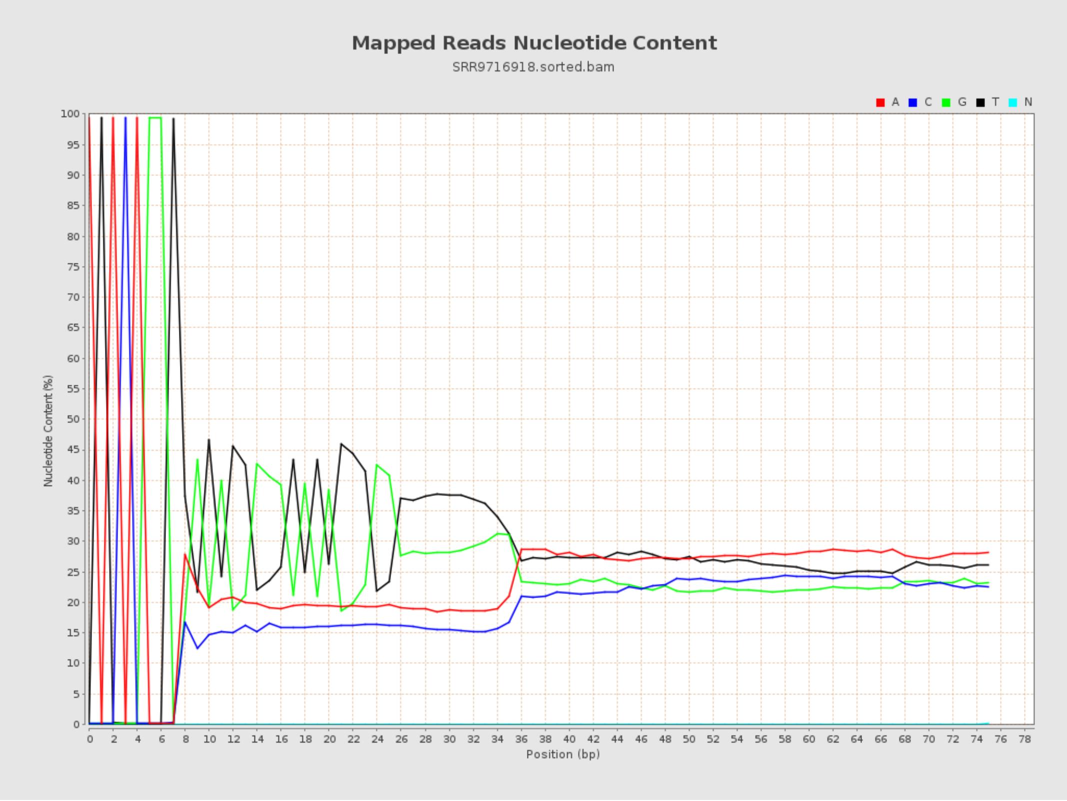
6. Results : Genome Fraction Coverage



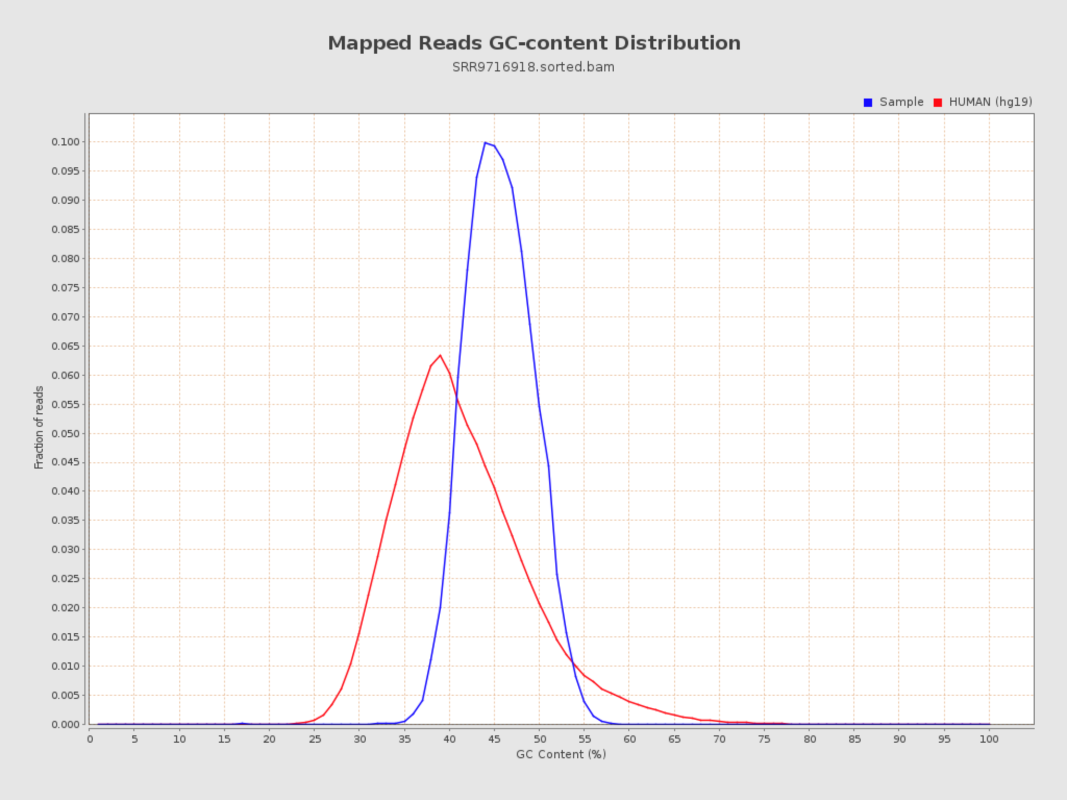
7. Results : Duplication Rate Histogram



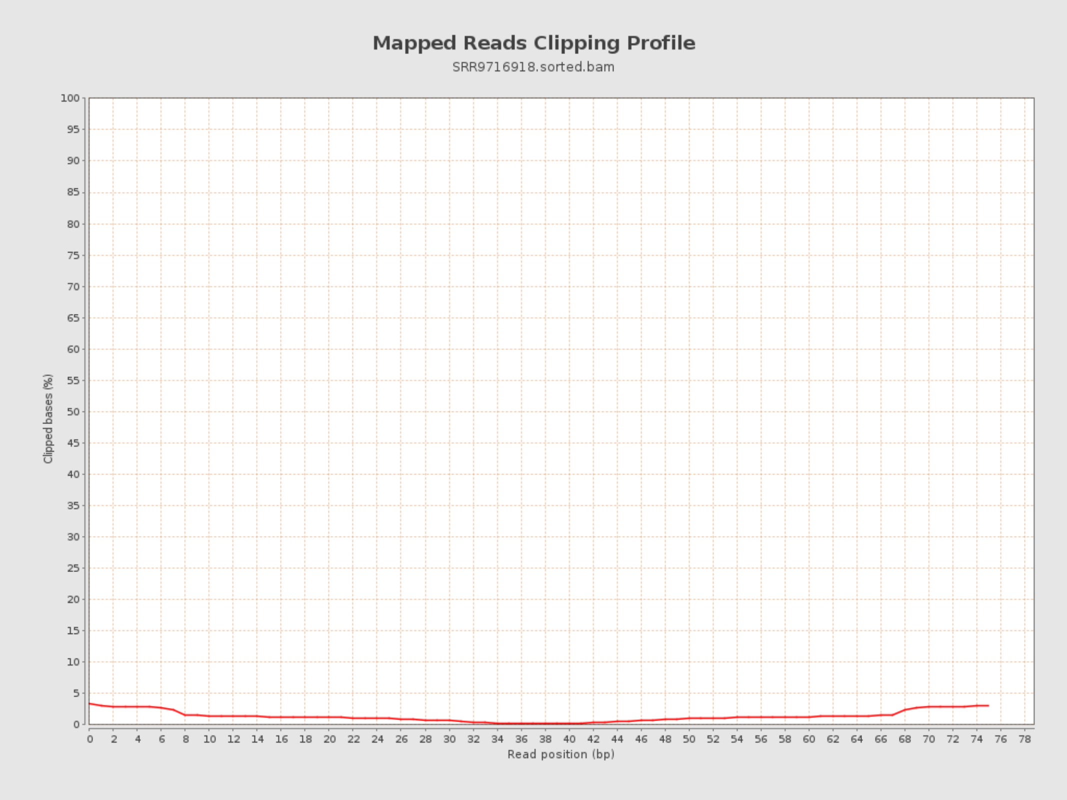
8. Results : Mapped Reads Nucleotide Content



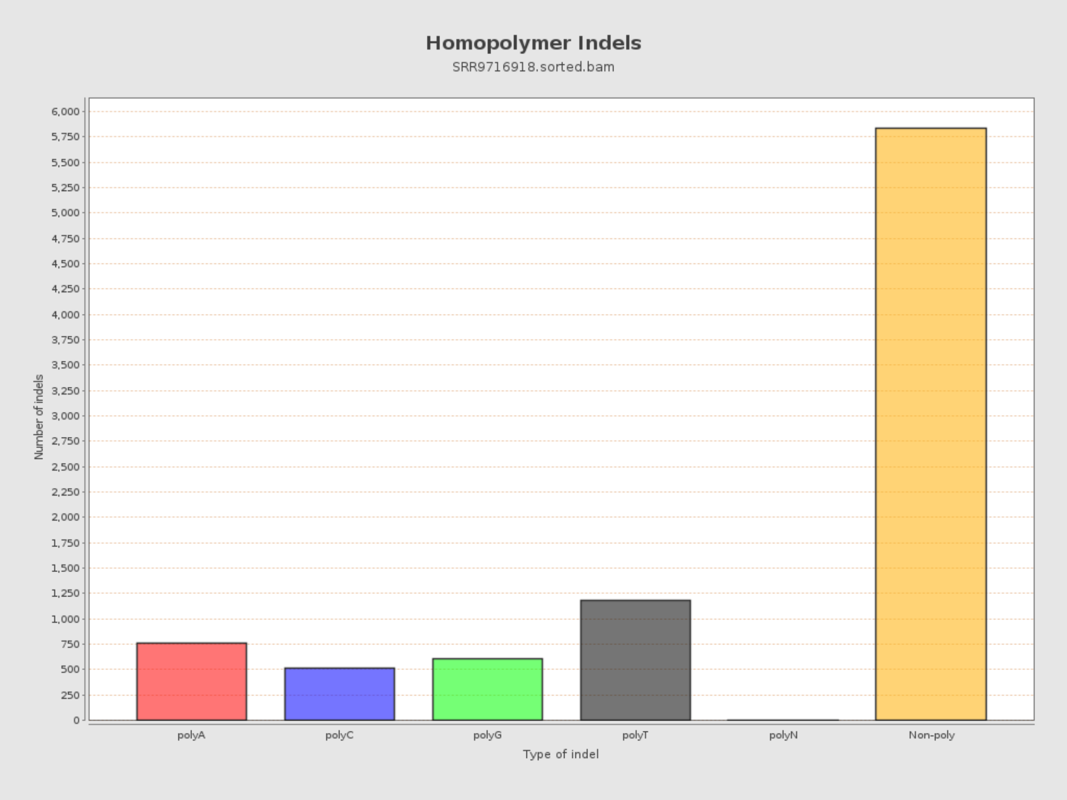
9. Results : Mapped Reads GC-content Distribution



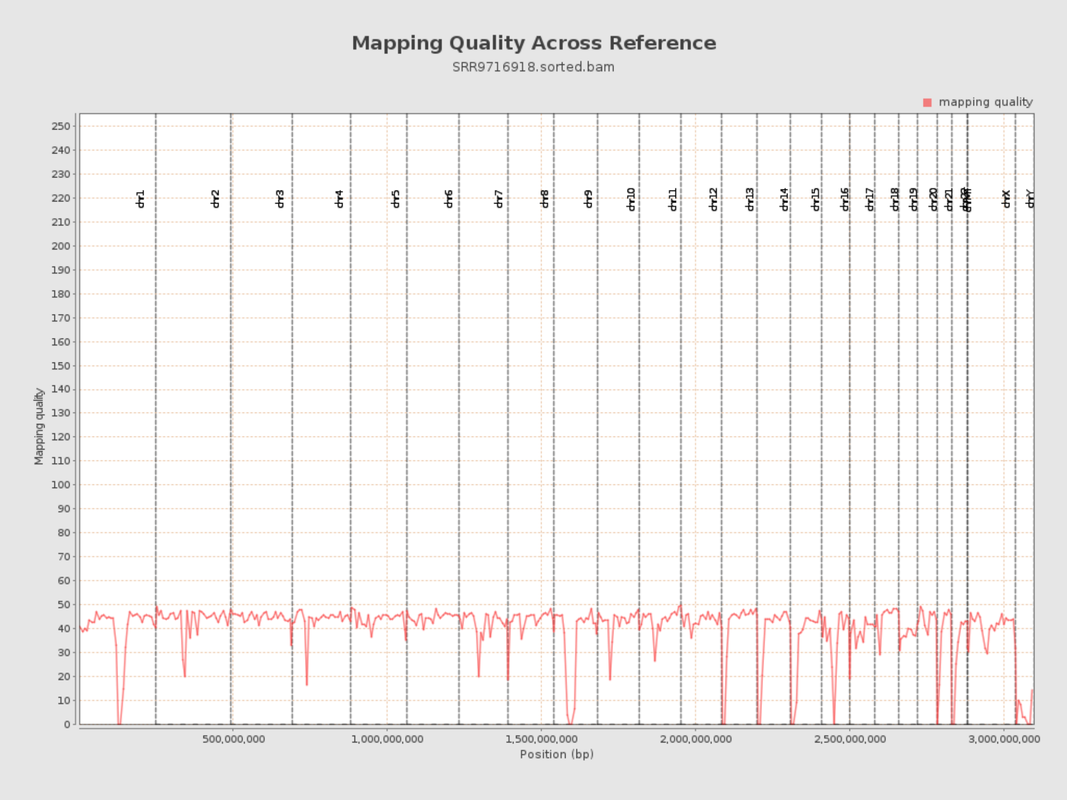
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram