Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:15:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716500.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_SRR9716500 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716500.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:15:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716500.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	702,035
Mapped reads	582,920 / 83.03%
Unmapped reads	119,115 / 16.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,392 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	8,941 / 1.27%
Duplication rate	1.02%
Clipped reads	586,153 / 83.49%

2.2. ACGT Content

Number/percentage of A's	7,843,234 / 23.85%
Number/percentage of C's	6,694,740 / 20.36%
Number/percentage of T's	9,999,513 / 30.41%
Number/percentage of G's	8,348,184 / 25.39%
Number/percentage of N's	465 / 0%
GC Percentage	45.74%

2.3. Coverage

Mean	0.0106

Standard Deviation	0.1288

2.4. Mapping Quality

Mean Mapping Quality	40.85

2.5. Mismatches and indels

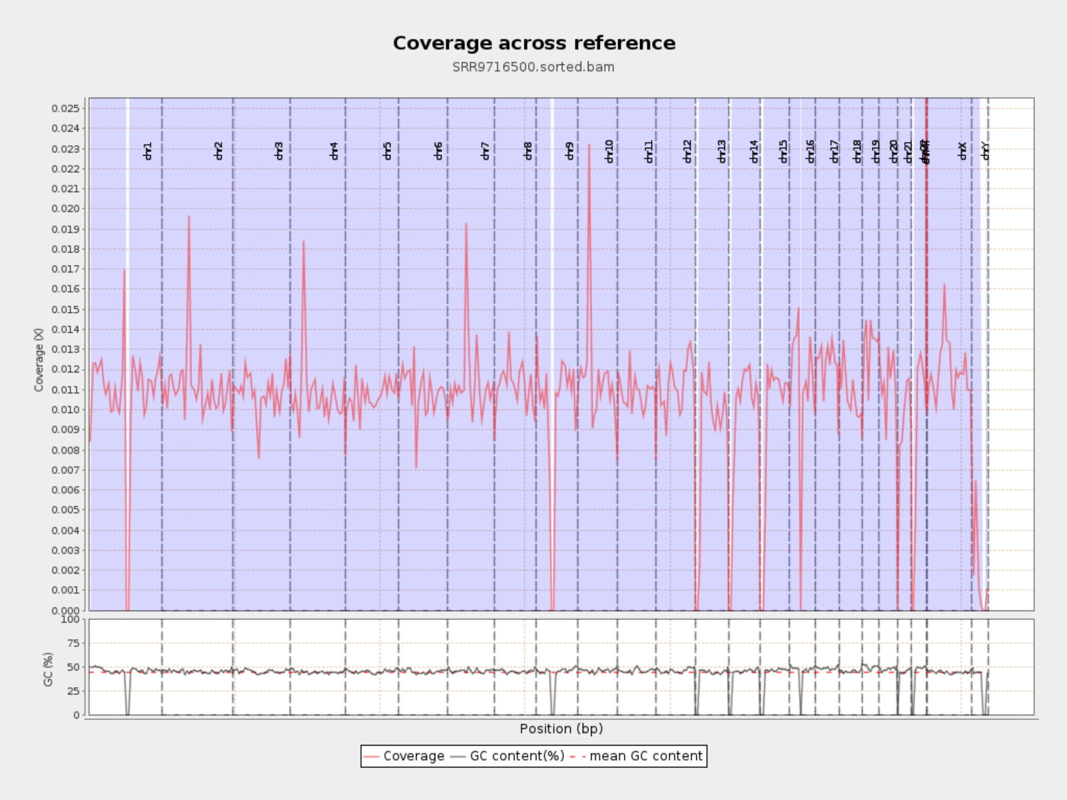
General error rate	0.53%
Mismatches	169,960
Insertions	2,012
Mapped reads with at least one insertion	0.34%
Deletions	5,547
Mapped reads with at least one deletion	0.94%
Homopolymer indels	39.08%

2.6. Chromosome stats

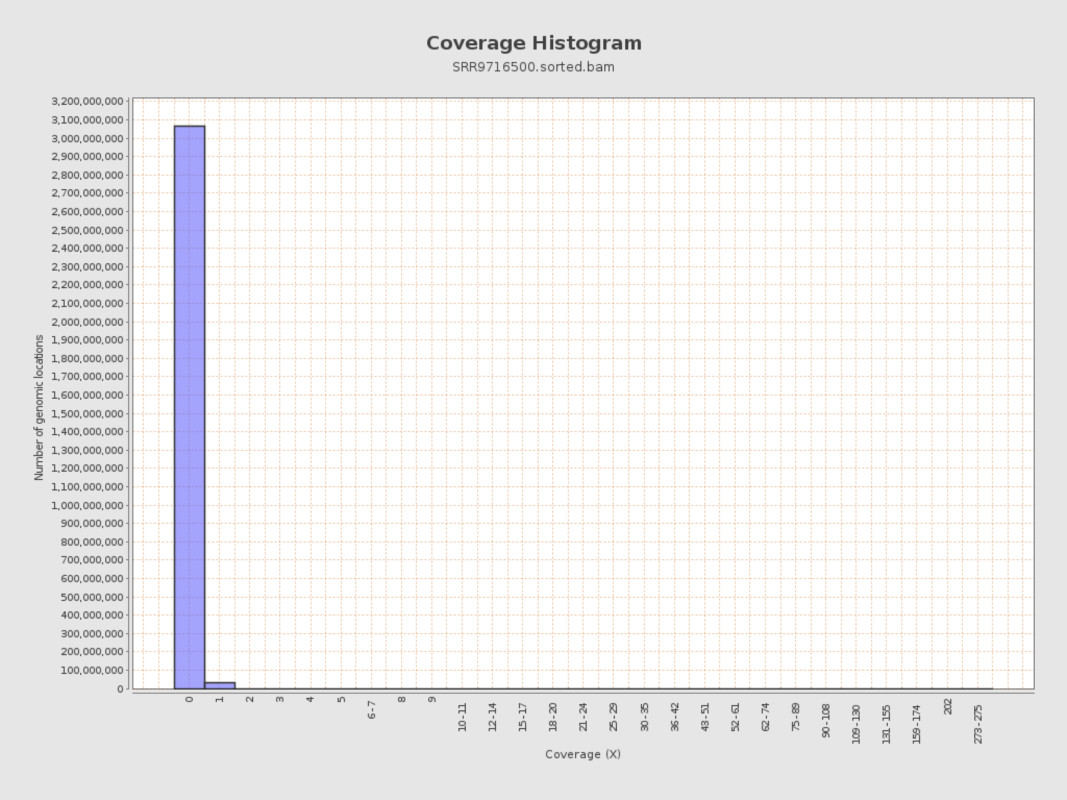
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2660012	0.0107	0.1737
chr2	243199373	2730601	0.0112	0.1676
chr3	198022430	2143460	0.0108	0.1068
chr4	191154276	2060362	0.0108	0.1118
chr5	180915260	1938911	0.0107	0.1059
chr6	171115067	1865642	0.0109	0.1127
chr7	159138663	1821656	0.0114	0.1646

chr8	146364022	1639355	0.0112	0.1256
chr9	141213431	1369942	0.0097	0.1149
chr10	135534747	1587373	0.0117	0.1432
chr11	135006516	1455109	0.0108	0.1195
chr12	133851895	1512757	0.0113	0.1096
chr13	115169878	993312	0.0086	0.095
chr14	107349540	1000444	0.0093	0.1017
chr15	102531392	949575	0.0093	0.0989
chr16	90354753	1013901	0.0112	0.1145
chr17	81195210	997483	0.0123	0.118
chr18	78077248	851476	0.0109	0.1702
chr19	59128983	775839	0.0131	0.1612
chr20	63025520	709855	0.0113	0.1094
chr21	48129895	428221	0.0089	0.1003
chr22	51304566	425981	0.0083	0.0938
chrMT	16571	6036	0.3643	0.6618
chrX	155270560	1848006	0.0119	0.1183
chrY	59373566	110077	0.0019	0.0603

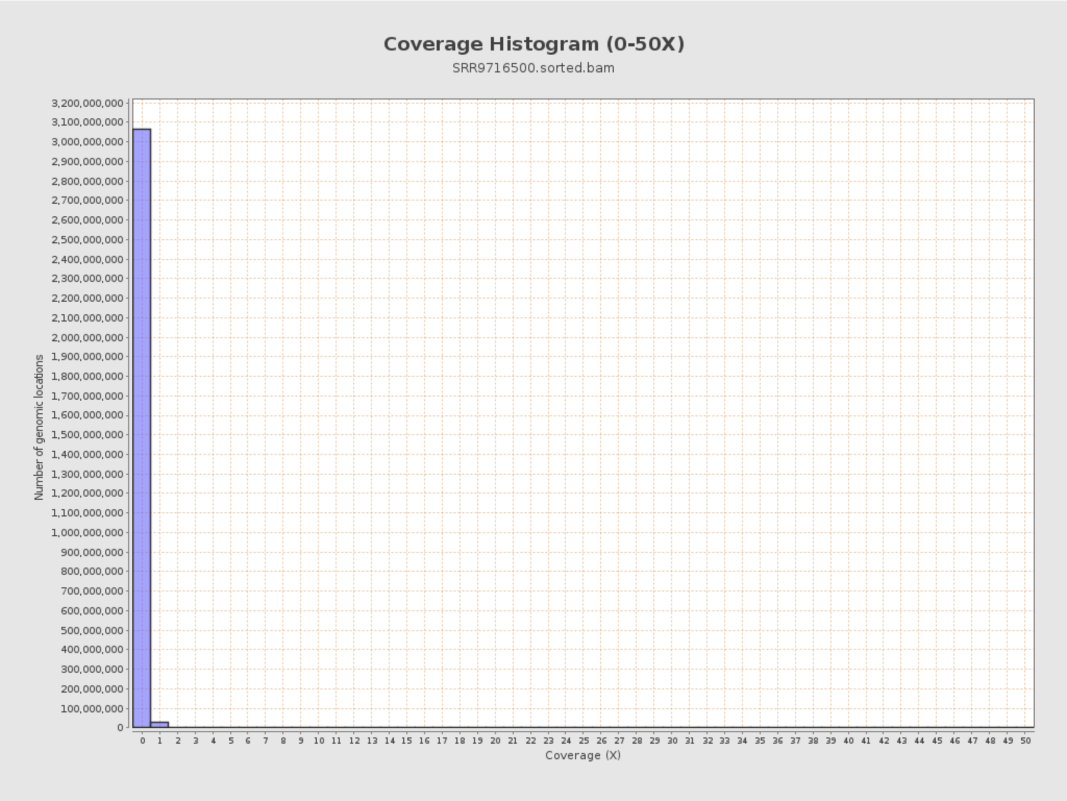
3. Results : Coverage across reference



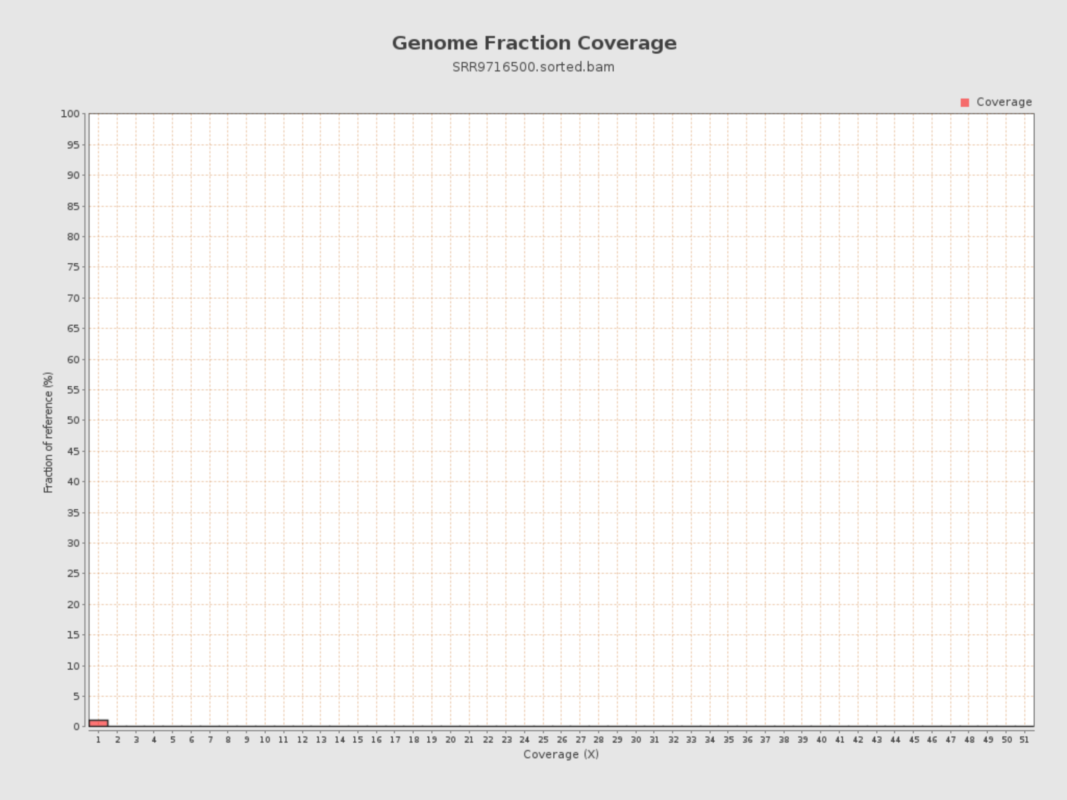
4. Results : Coverage Histogram



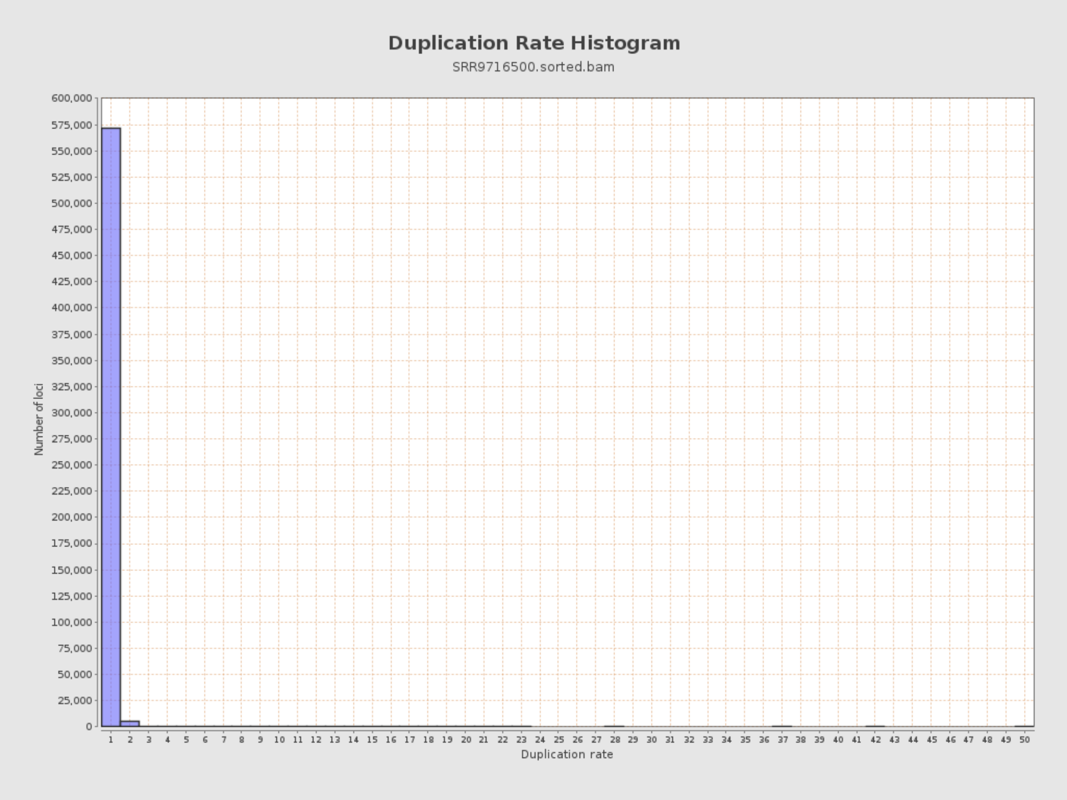
5. Results : Coverage Histogram (0-50X)



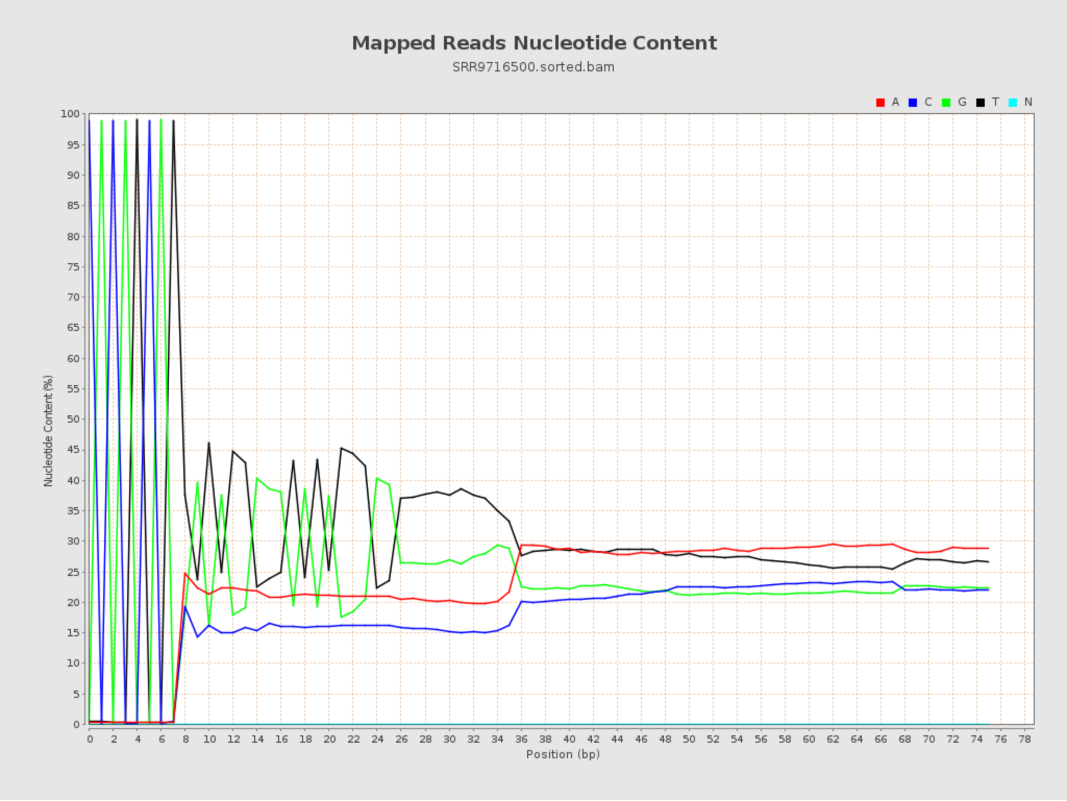
6. Results : Genome Fraction Coverage



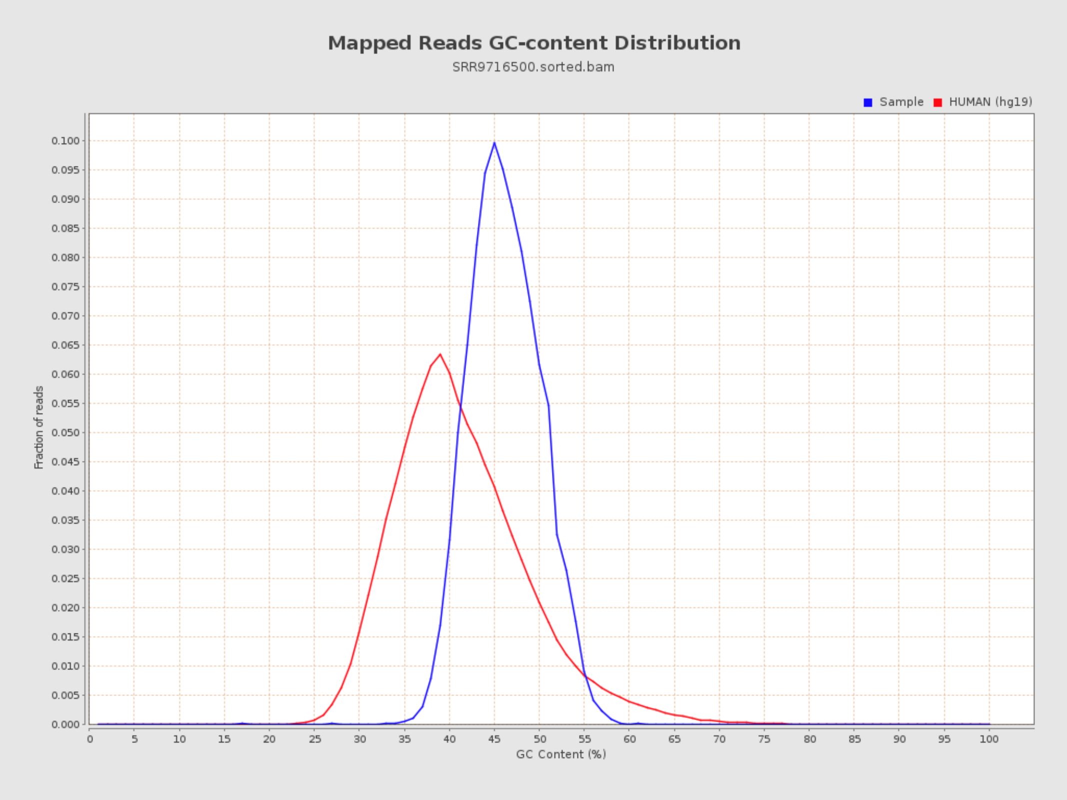
7. Results : Duplication Rate Histogram



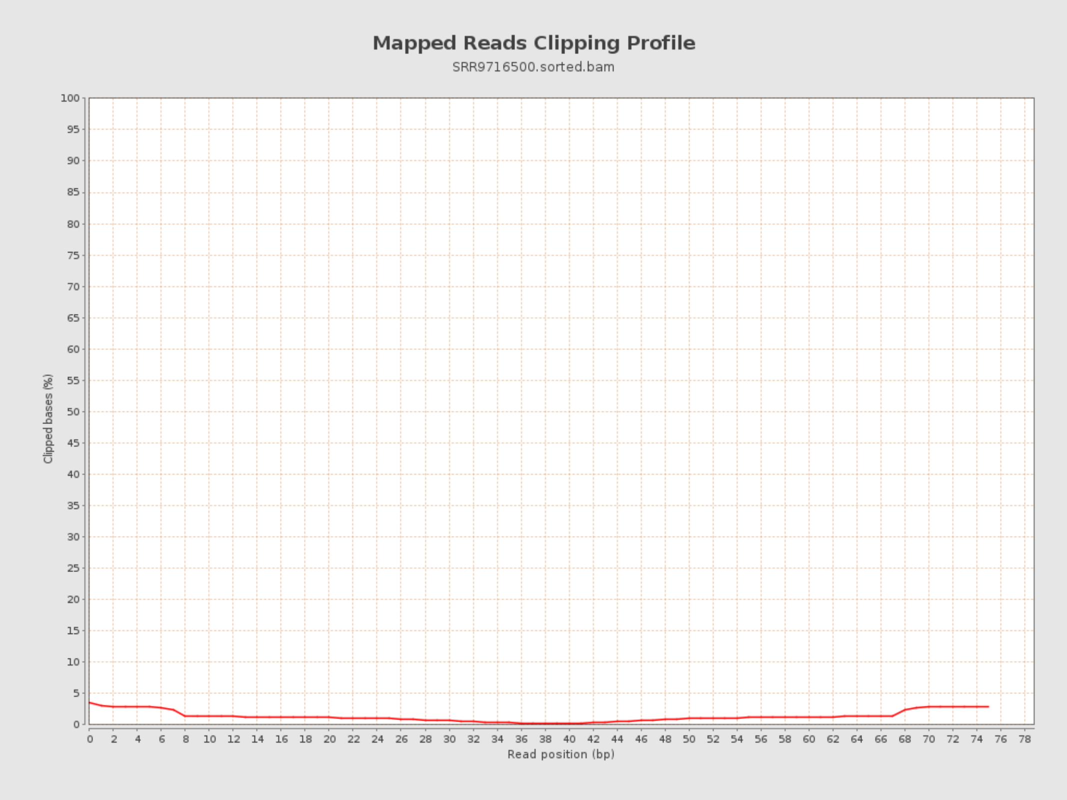
8. Results : Mapped Reads Nucleotide Content



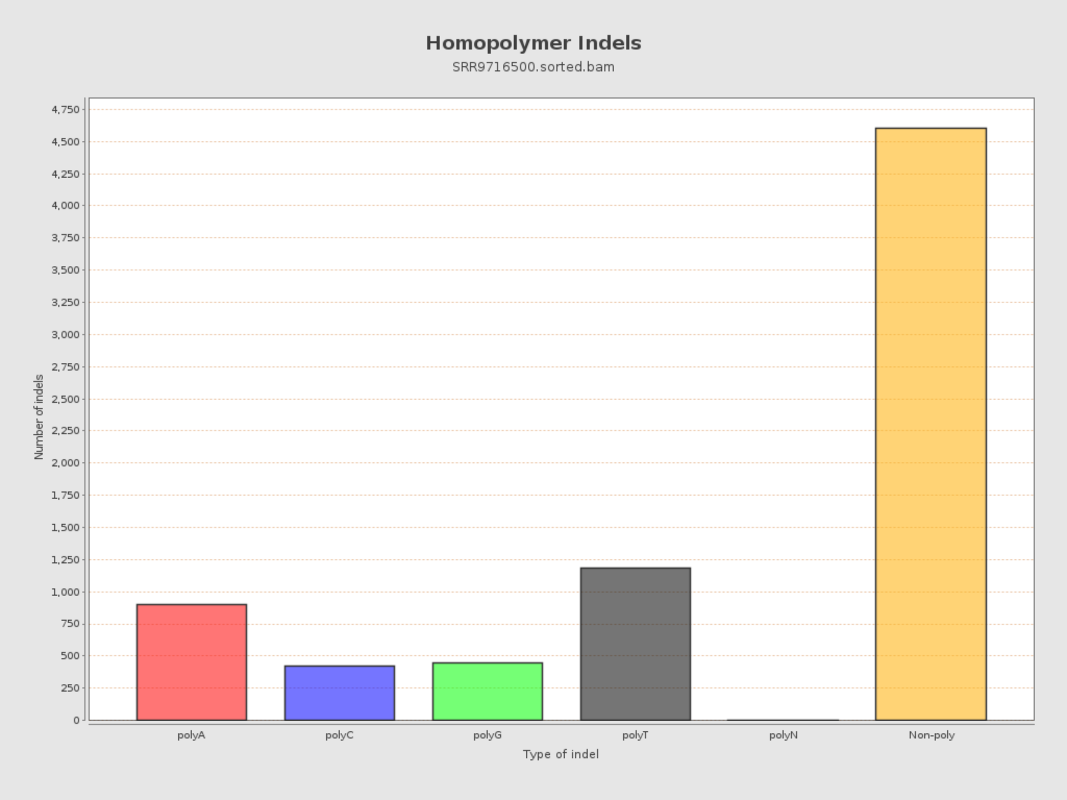
9. Results : Mapped Reads GC-content Distribution



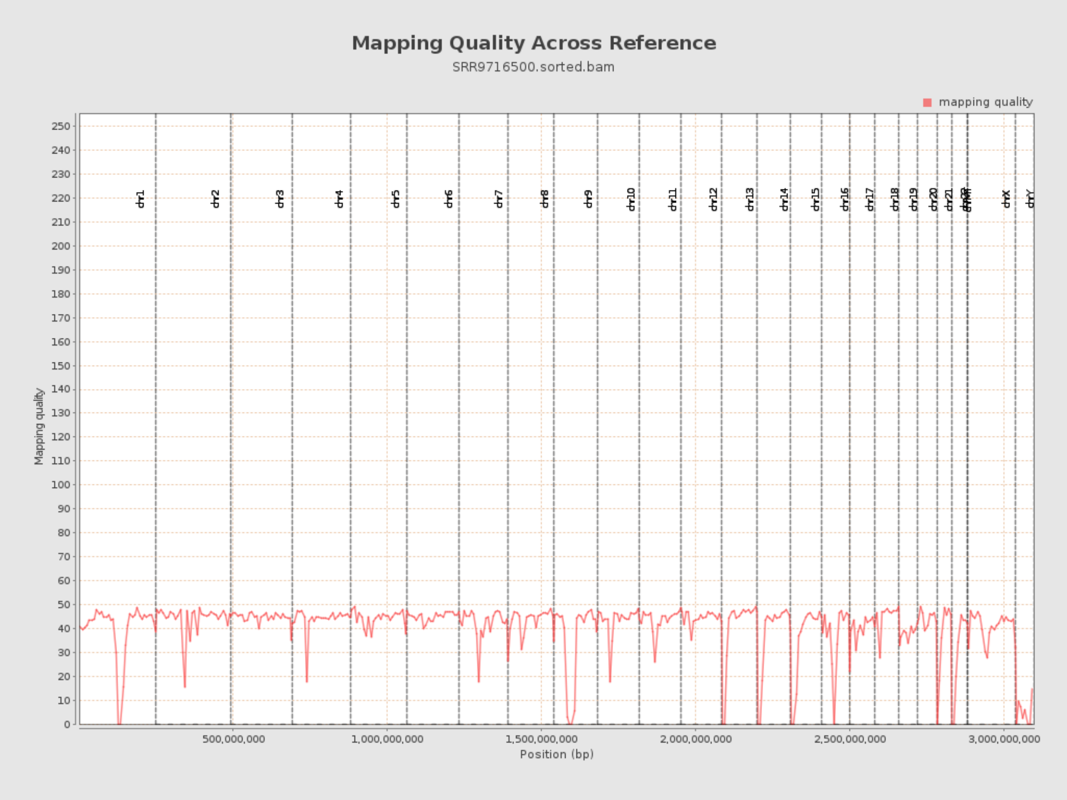
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram