Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:56:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716513.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_SRR9716513 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716513.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:56:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716513.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,573,791
Mapped reads	1,435,587 / 91.22%
Unmapped reads	138,204 / 8.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,292 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	46,609 / 2.96%
Duplication rate	2.36%
Clipped reads	1,439,529 / 91.47%

2.2. ACGT Content

Number/percentage of A's	21,232,952 / 25.61%
Number/percentage of C's	16,631,700 / 20.06%
Number/percentage of T's	25,421,612 / 30.66%
Number/percentage of G's	19,617,822 / 23.66%
Number/percentage of N's	975 / 0%
GC Percentage	43.72%

2.3. Coverage

Mean	0.0268

Standard Deviation	0.2558

2.4. Mapping Quality

Mean Mapping Quality	44.01

2.5. Mismatches and indels

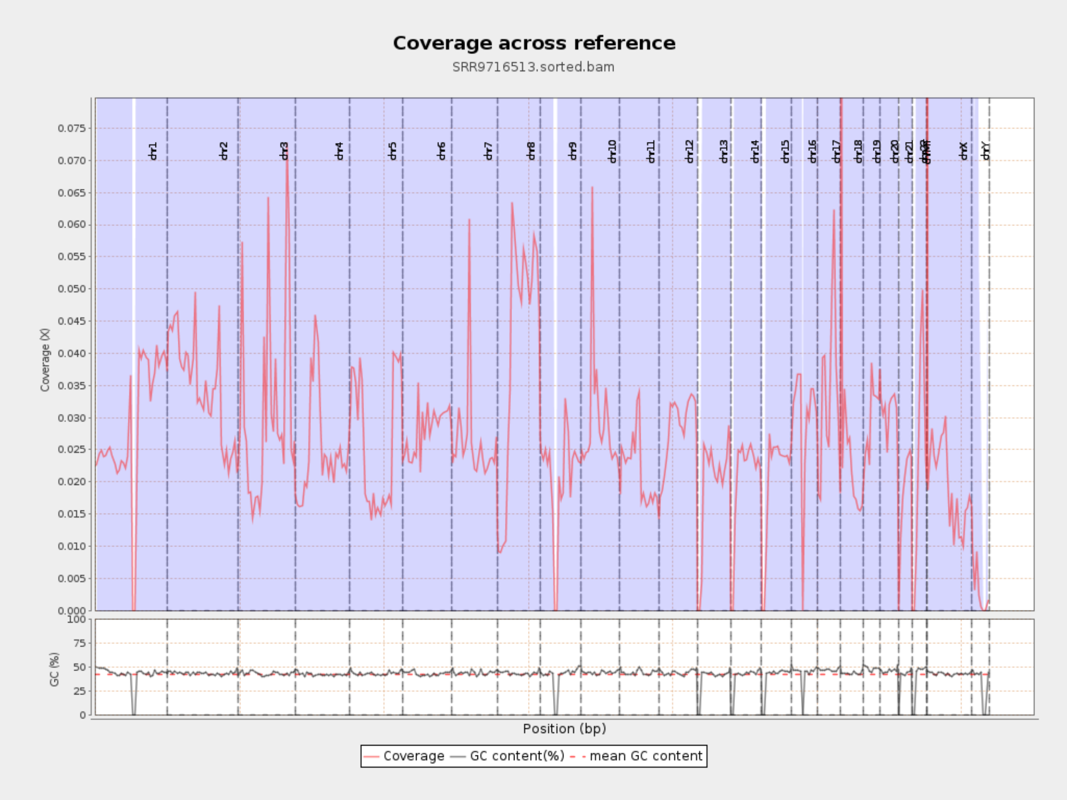
General error rate	0.5%
Mismatches	404,757
Insertions	6,623
Mapped reads with at least one insertion	0.46%
Deletions	13,874
Mapped reads with at least one deletion	0.96%
Homopolymer indels	40.03%

2.6. Chromosome stats

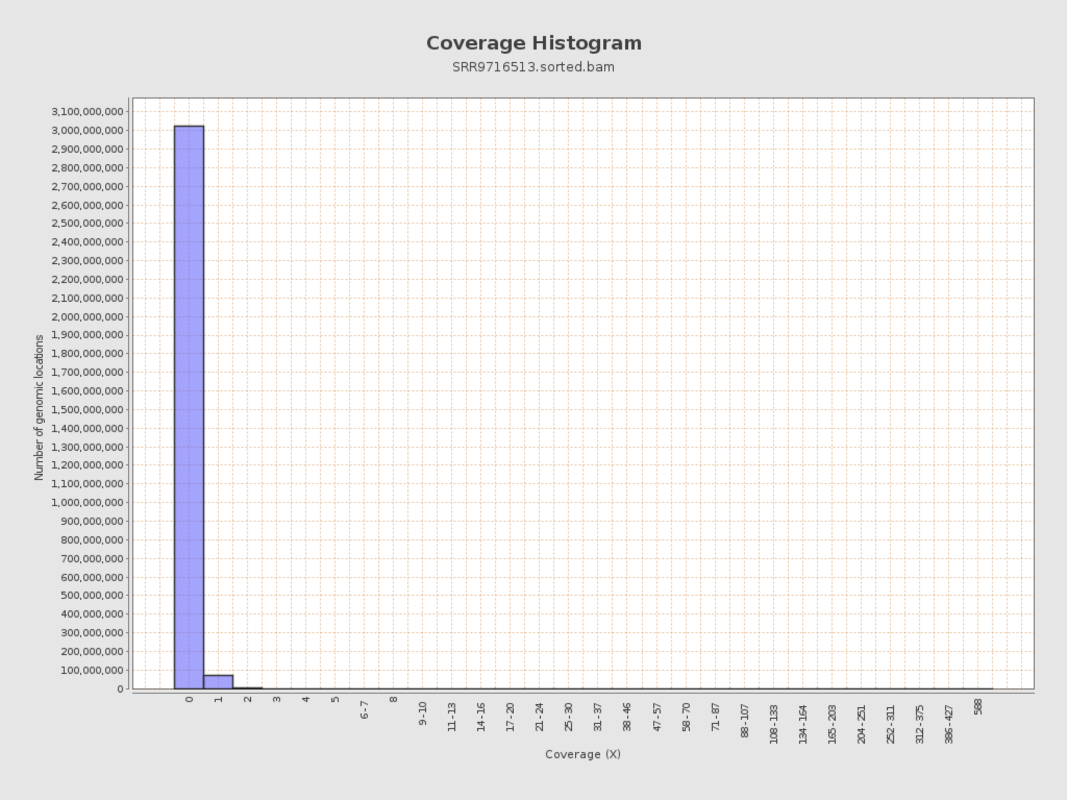
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7117283	0.0286	0.3638
chr2	243199373	8475975	0.0349	0.3216
chr3	198022430	6120875	0.0309	0.1985
chr4	191154276	4767479	0.0249	0.1802
chr5	180915260	4664813	0.0258	0.1742
chr6	171115067	4800996	0.0281	0.1963
chr7	159138663	4202551	0.0264	0.5008

chr8	146364022	6123637	0.0418	0.2848
chr9	141213431	2883887	0.0204	0.1797
chr10	135534747	3990087	0.0294	0.3134
chr11	135006516	2985343	0.0221	0.1917
chr12	133851895	3794223	0.0283	0.1938
chr13	115169878	2238789	0.0194	0.1523
chr14	107349540	2179446	0.0203	0.16
chr15	102531392	2059523	0.0201	0.1581
chr16	90354753	2644461	0.0293	0.1937
chr17	81195210	2759908	0.034	0.2037
chr18	78077248	2013567	0.0258	0.2876
chr19	59128983	1772267	0.03	0.3257
chr20	63025520	1943908	0.0308	0.1969
chr21	48129895	881421	0.0183	0.1508
chr22	51304566	1200472	0.0234	0.1668
chrMT	16571	116178	7.0109	4.5609
chrX	155270560	3010073	0.0194	0.1705
chrY	59373566	179563	0.003	0.0779

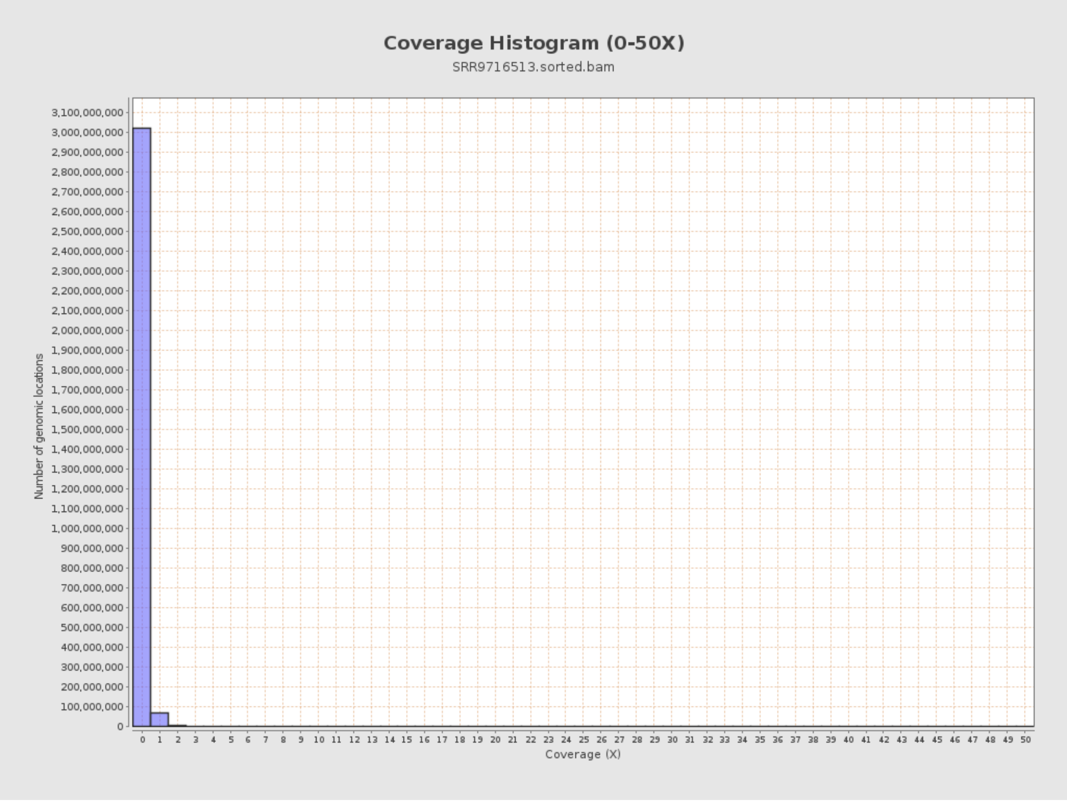
3. Results : Coverage across reference



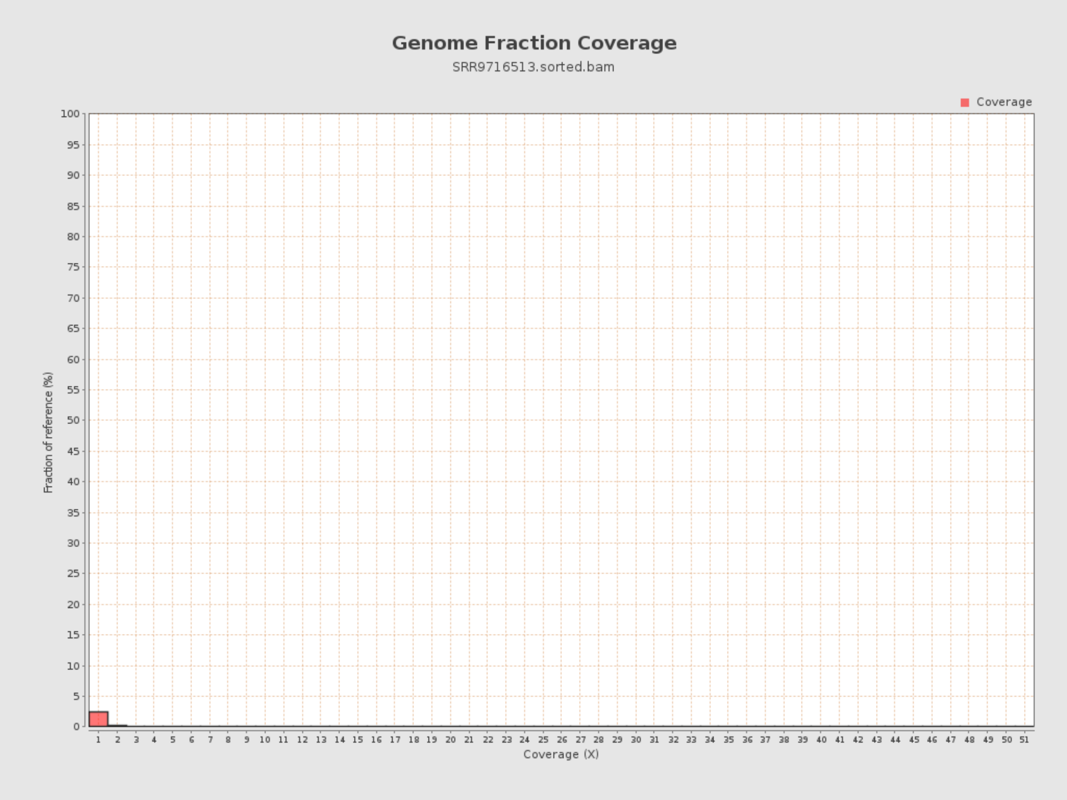
4. Results : Coverage Histogram



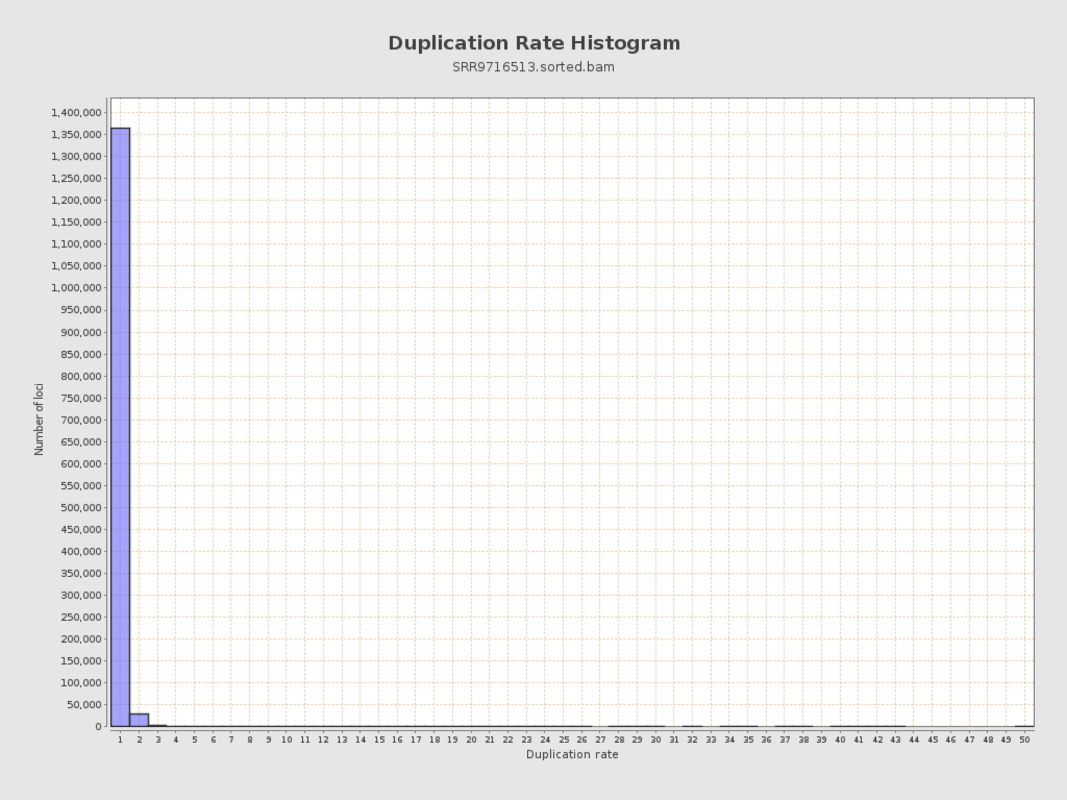
5. Results : Coverage Histogram (0-50X)



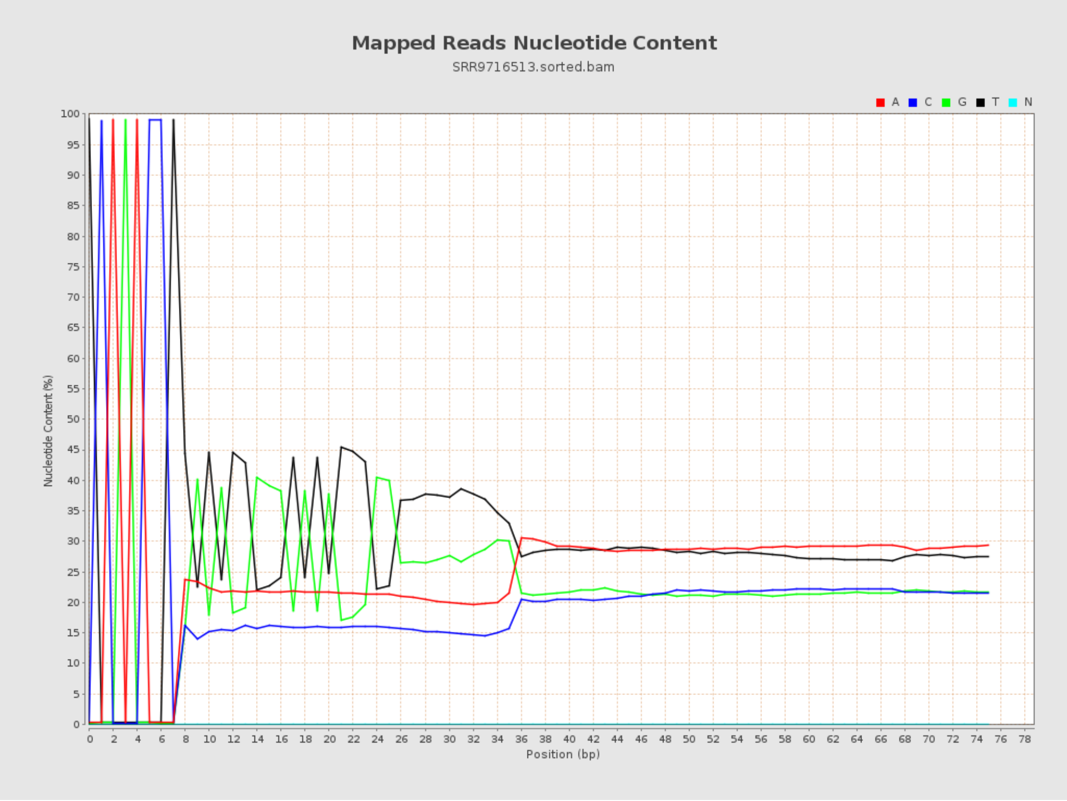
6. Results : Genome Fraction Coverage



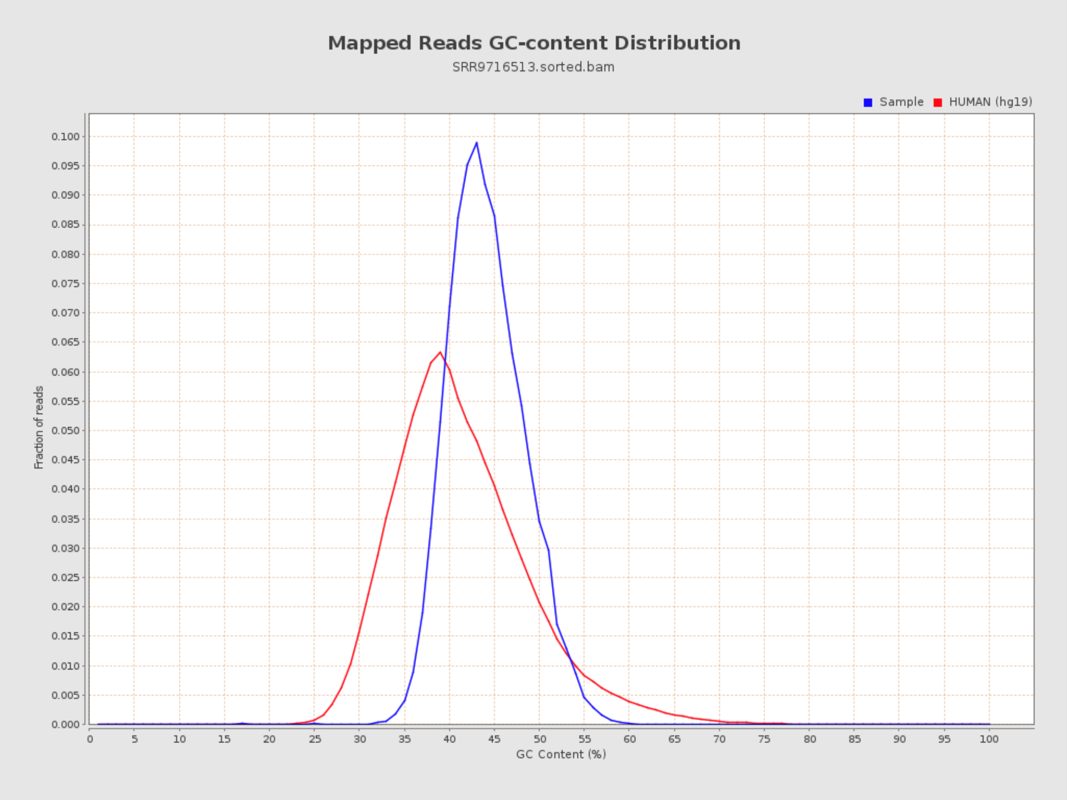
7. Results : Duplication Rate Histogram



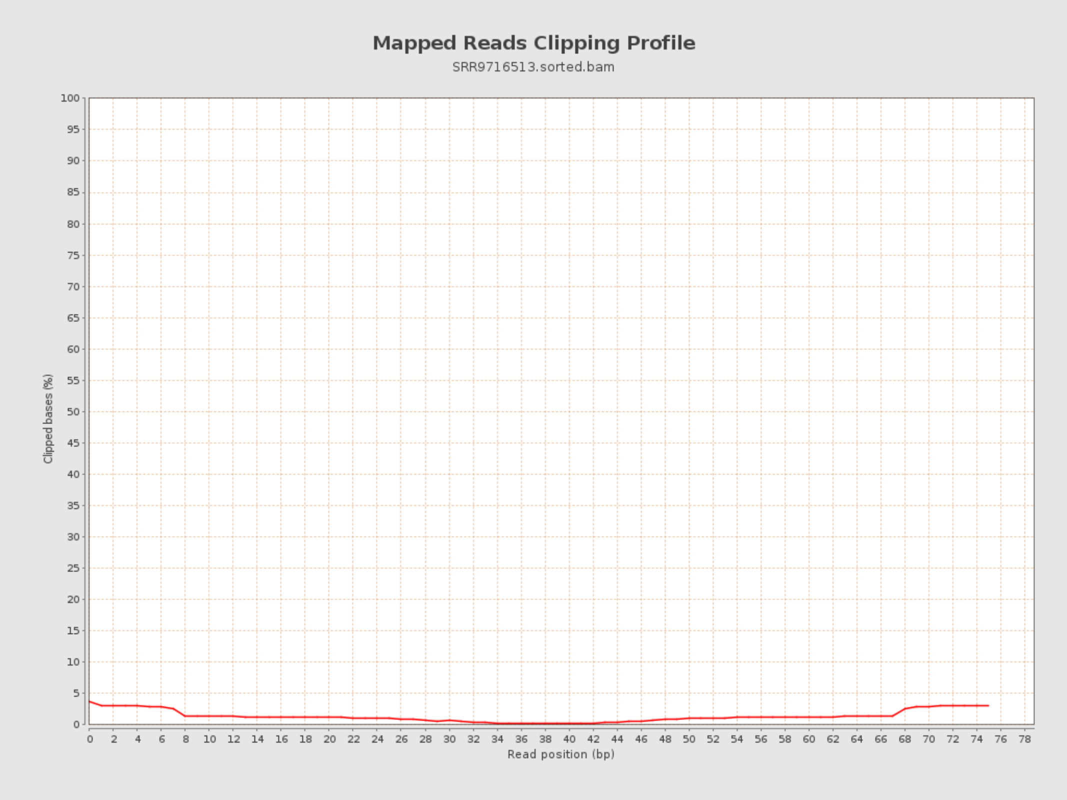
8. Results : Mapped Reads Nucleotide Content



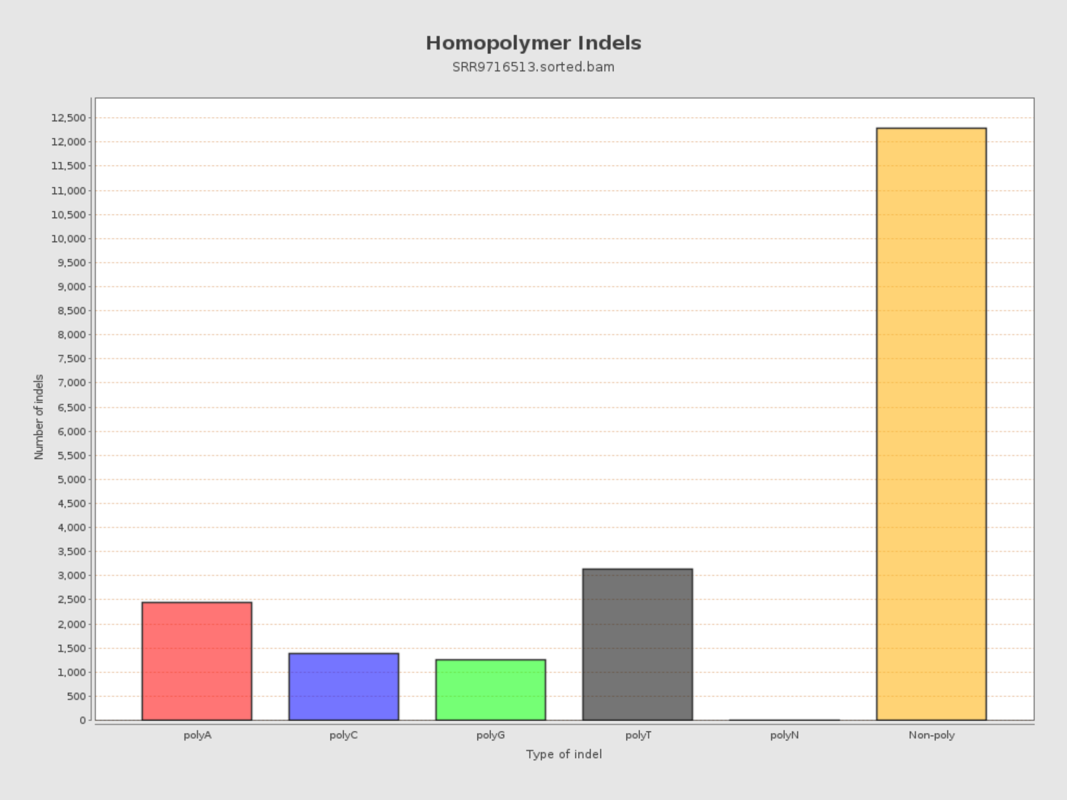
9. Results : Mapped Reads GC-content Distribution



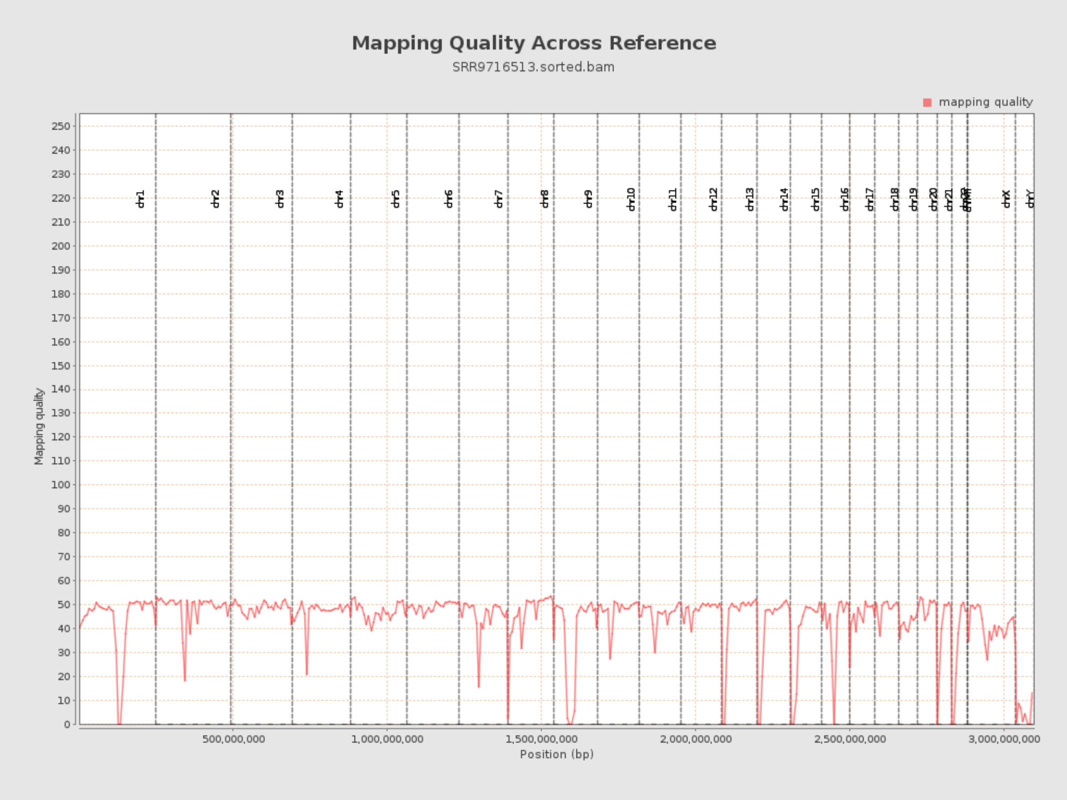
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram