Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 14:24:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716453.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_SRR9716453 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716453.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 14:24:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716453.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	464,103
Mapped reads	416,216 / 89.68%
Unmapped reads	47,887 / 10.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,433 / 1.39%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	10,776 / 2.32%
Duplication rate	1.54%
Clipped reads	422,261 / 90.98%

2.2. ACGT Content

Number/percentage of A's	8,221,988 / 24.82%
Number/percentage of C's	6,245,464 / 18.85%
Number/percentage of T's	10,105,298 / 30.5%
Number/percentage of G's	8,555,659 / 25.82%
Number/percentage of N's	2,127 / 0.01%
GC Percentage	44.68%

2.3. Coverage

Mean	0.0107

Standard Deviation	0.1597

2.4. Mapping Quality

Mean Mapping Quality	44.26

2.5. Mismatches and indels

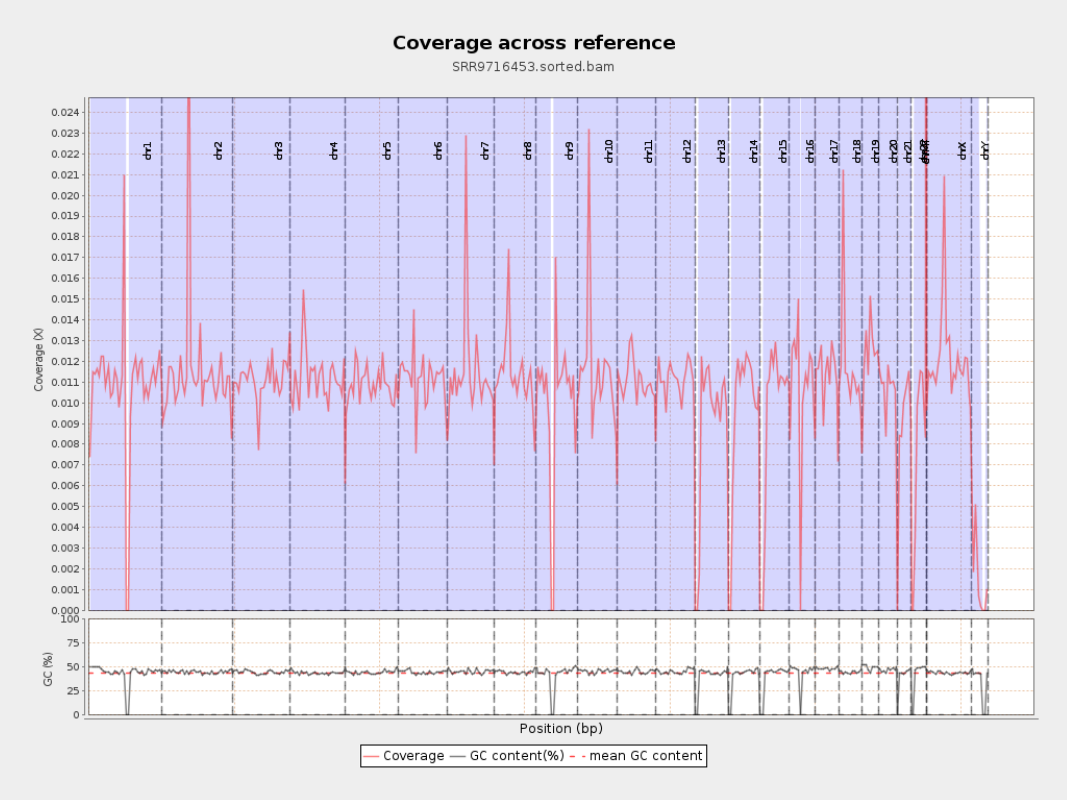
General error rate	0.85%
Mismatches	274,326
Insertions	2,916
Mapped reads with at least one insertion	0.69%
Deletions	8,519
Mapped reads with at least one deletion	2.01%
Homopolymer indels	43.78%

2.6. Chromosome stats

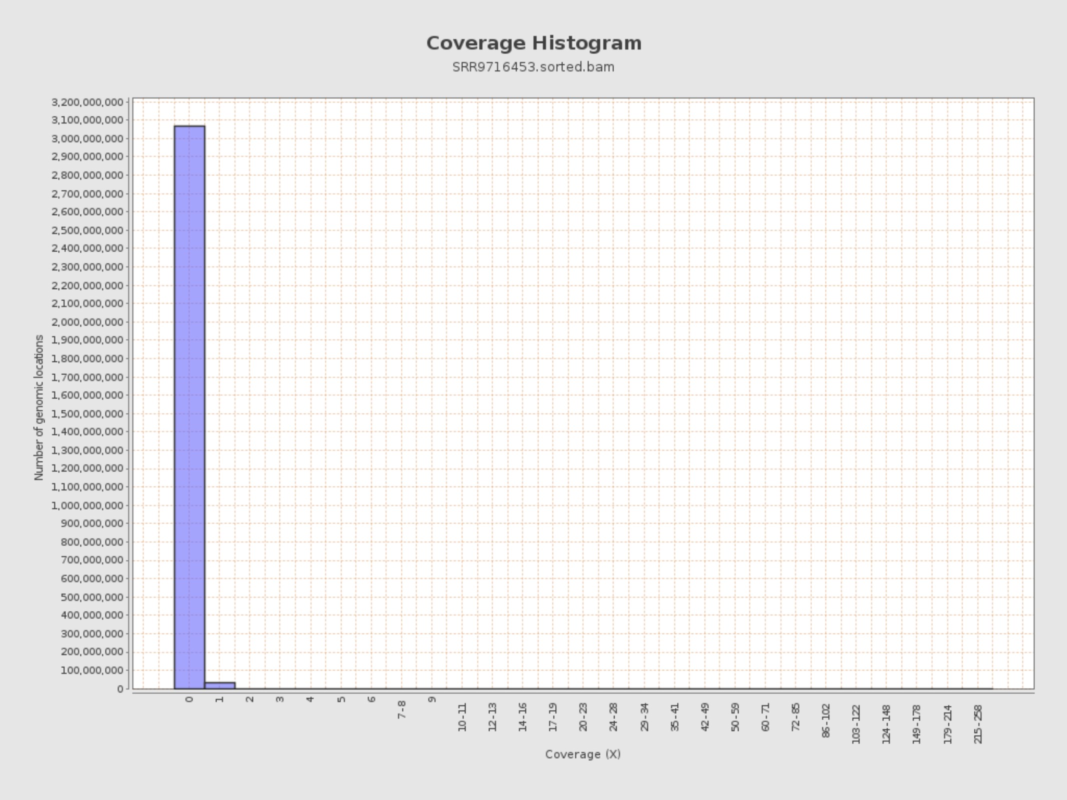
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2674455	0.0107	0.2377
chr2	243199373	2833932	0.0117	0.2131
chr3	198022430	2191297	0.0111	0.1102
chr4	191154276	2141981	0.0112	0.1149
chr5	180915260	1970136	0.0109	0.1099
chr6	171115067	1907828	0.0111	0.1223
chr7	159138663	1841633	0.0116	0.2034

chr8	146364022	1666764	0.0114	0.1939
chr9	141213431	1403652	0.0099	0.1616
chr10	135534747	1570104	0.0116	0.1555
chr11	135006516	1479894	0.011	0.156
chr12	133851895	1489573	0.0111	0.1123
chr13	115169878	1010472	0.0088	0.0969
chr14	107349540	1010513	0.0094	0.1178
chr15	102531392	947838	0.0092	0.1005
chr16	90354753	961907	0.0106	0.1166
chr17	81195210	917287	0.0113	0.1152
chr18	78077248	934763	0.012	0.3077
chr19	59128983	739646	0.0125	0.1913
chr20	63025520	665992	0.0106	0.1096
chr21	48129895	426051	0.0089	0.1015
chr22	51304566	368874	0.0072	0.088
chrMT	16571	3150	0.1901	0.4747
chrX	155270560	1896499	0.0122	0.1342
chrY	59373566	91077	0.0015	0.0554

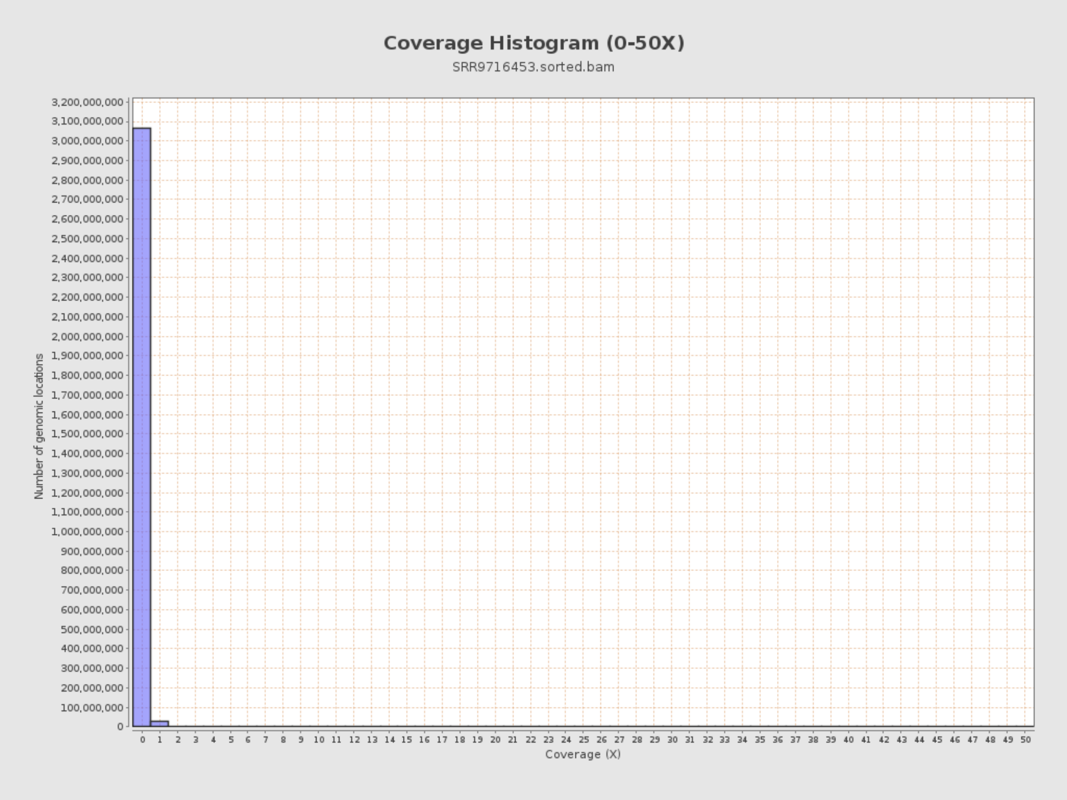
3. Results : Coverage across reference



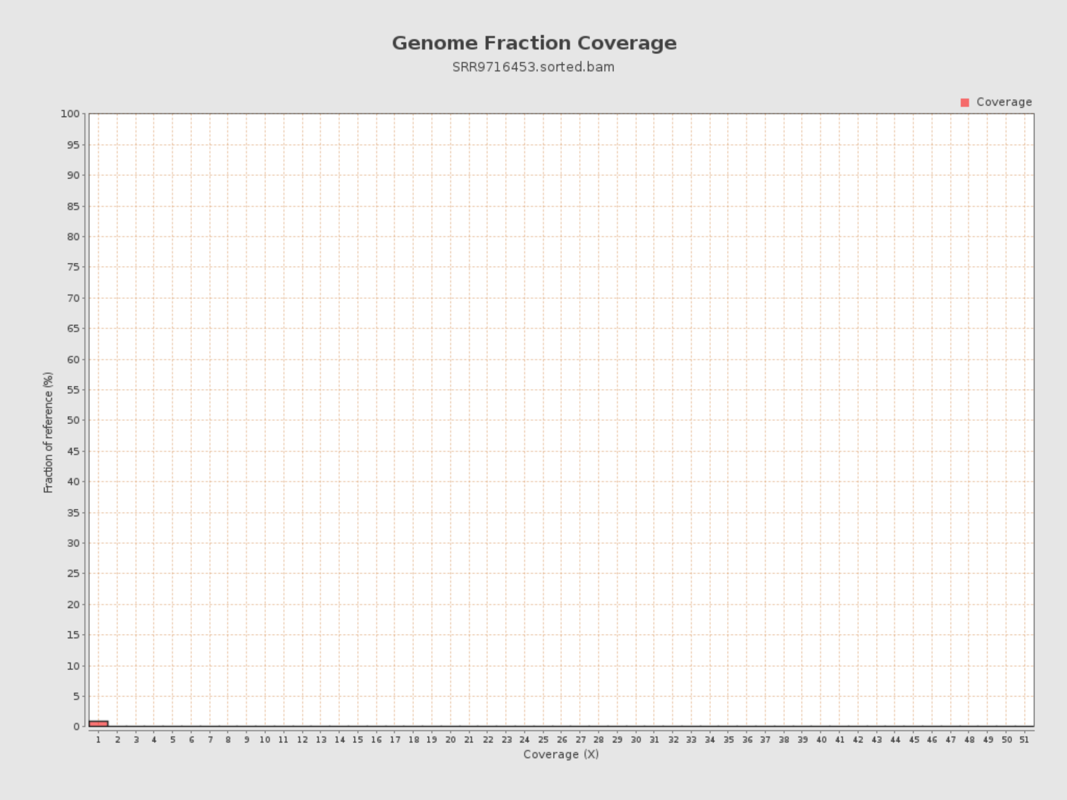
4. Results : Coverage Histogram



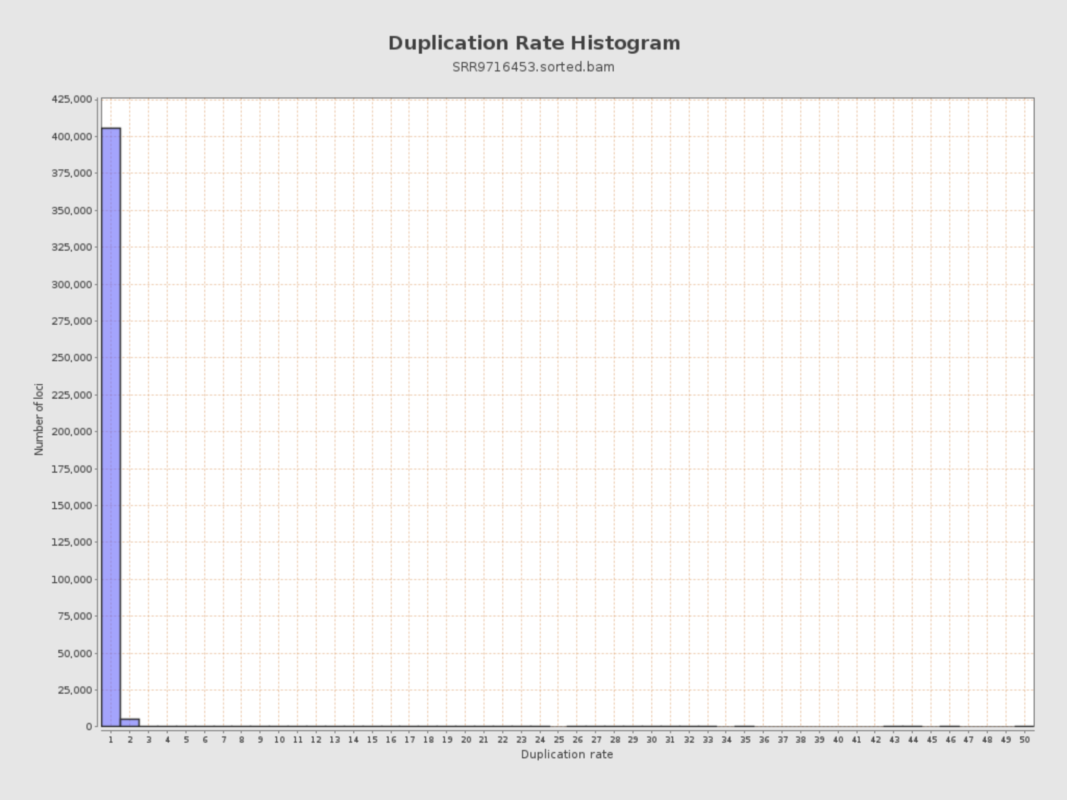
5. Results : Coverage Histogram (0-50X)



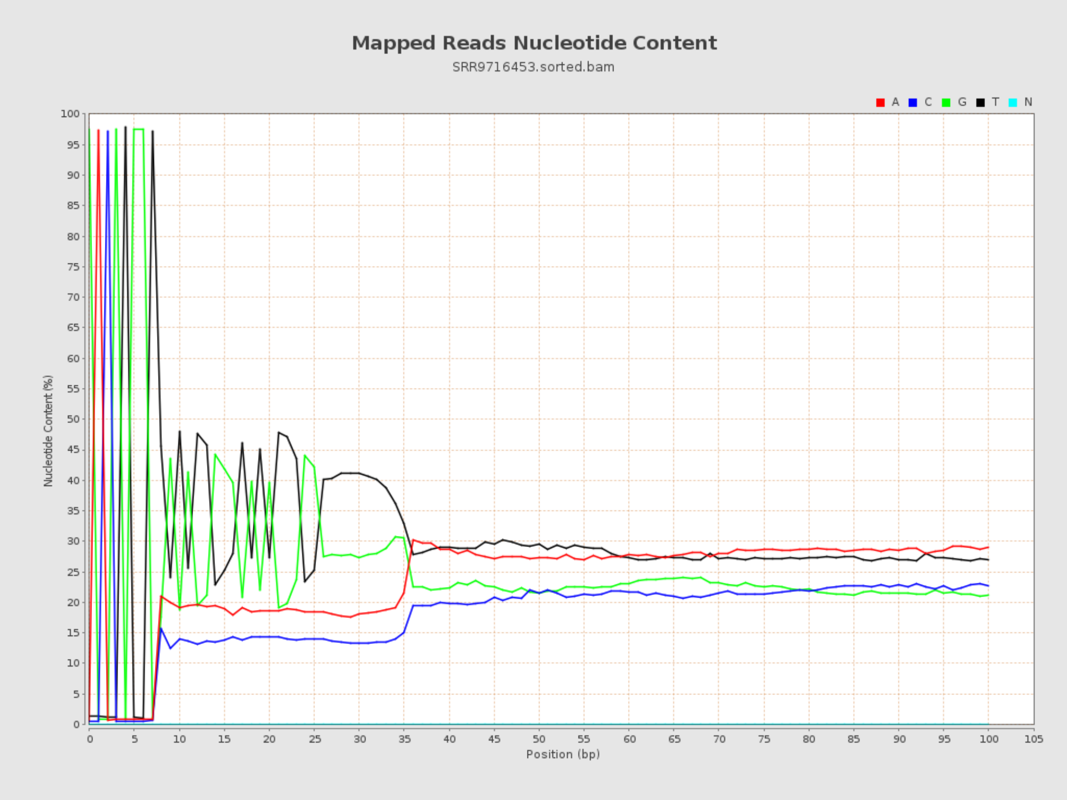
6. Results : Genome Fraction Coverage



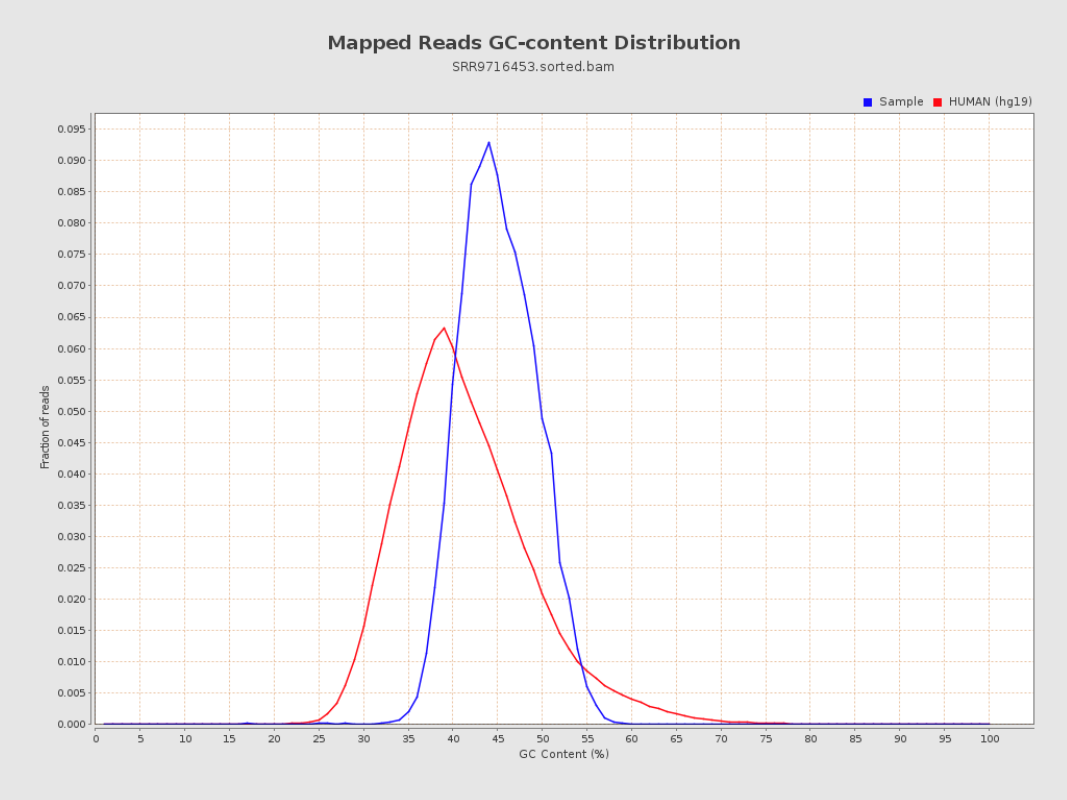
7. Results : Duplication Rate Histogram



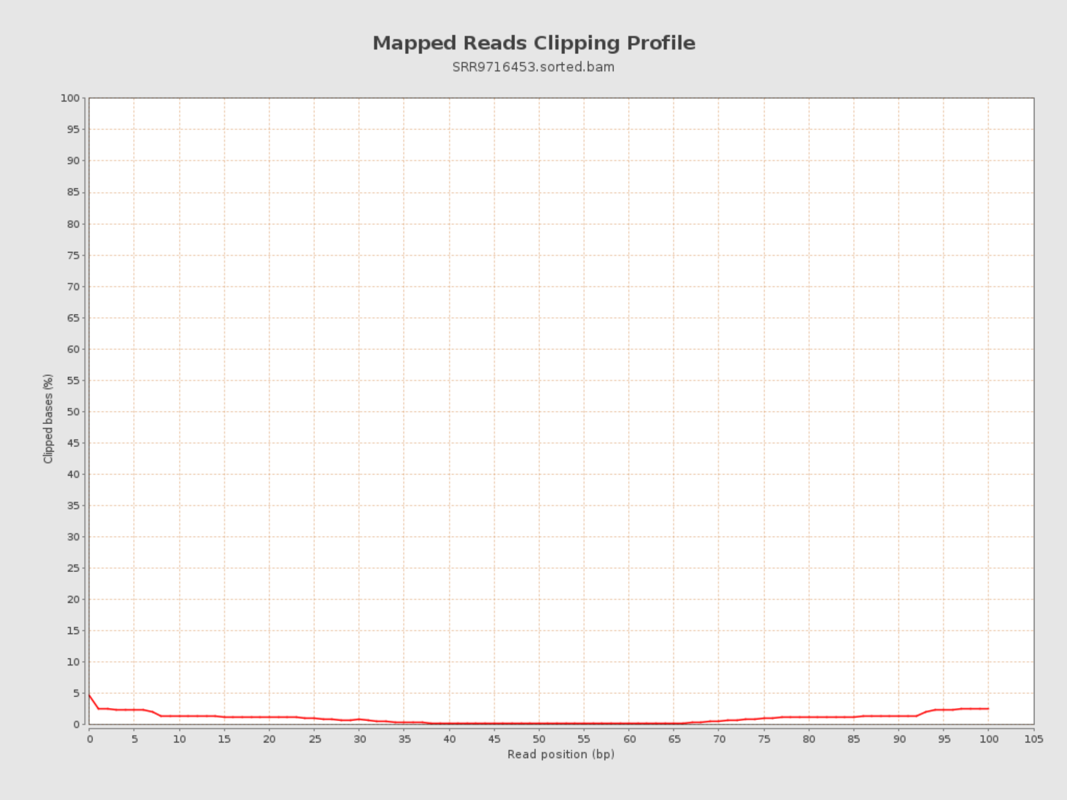
8. Results : Mapped Reads Nucleotide Content



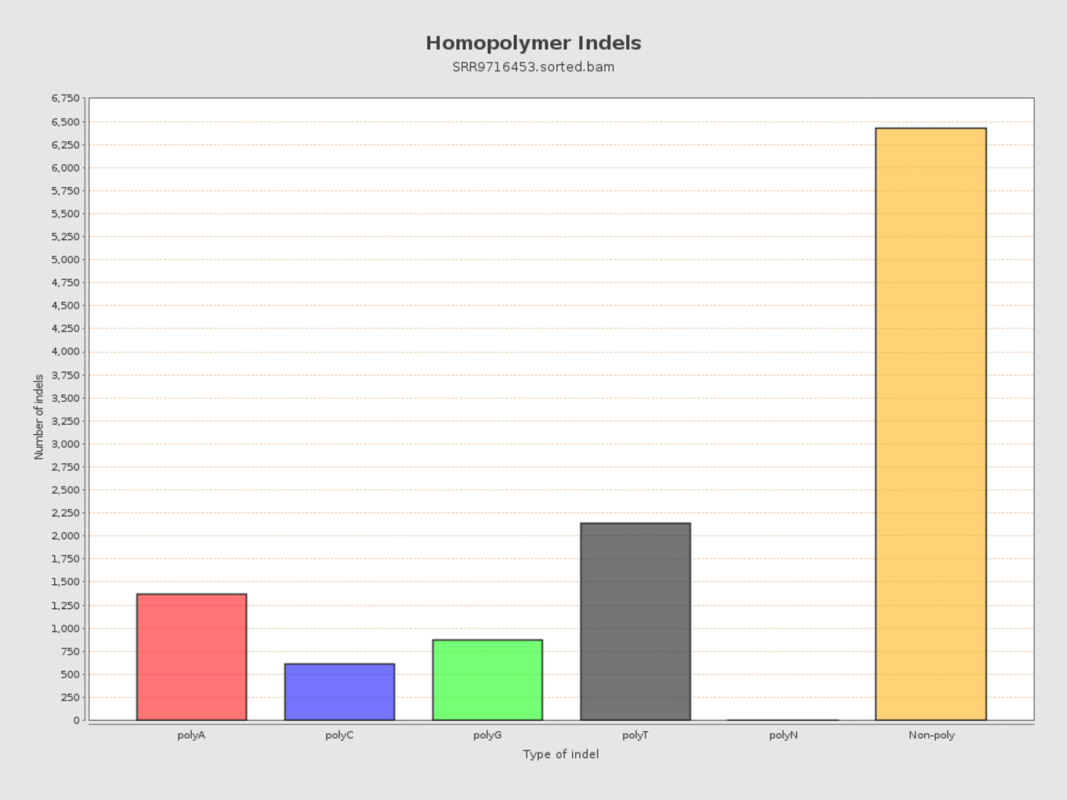
9. Results : Mapped Reads GC-content Distribution



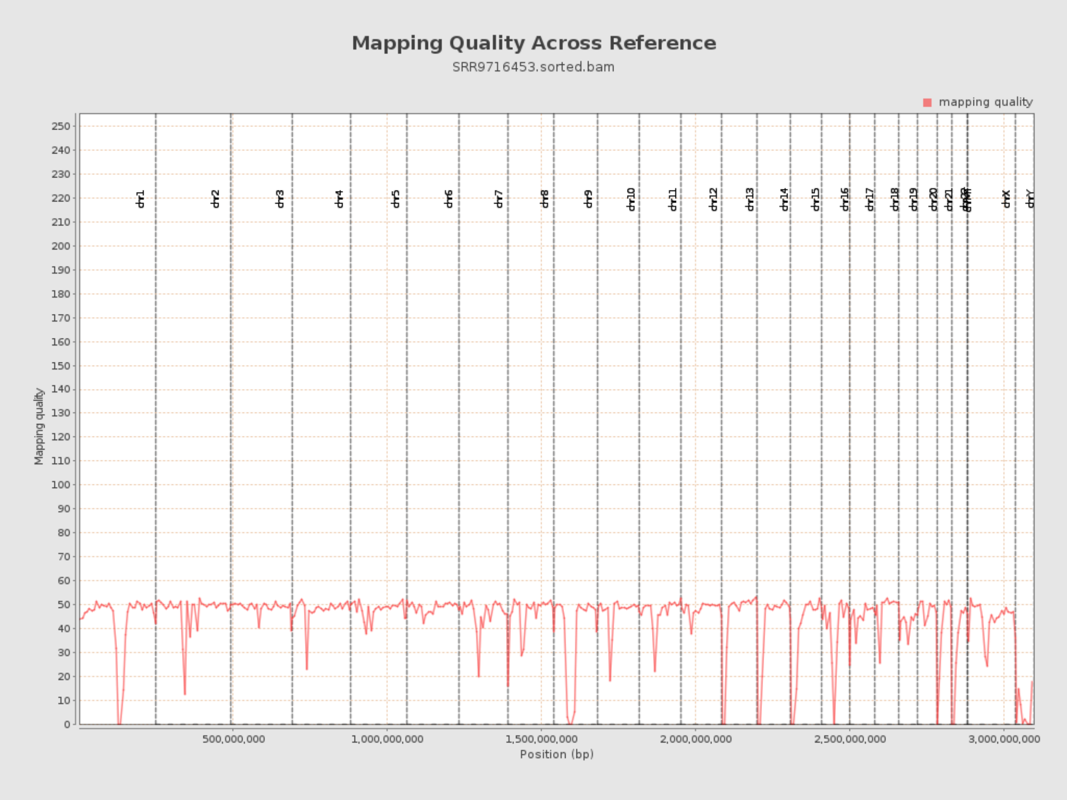
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram