Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:18:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716364.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_SRR9716364 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716364.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:18:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716364.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,302,060
Mapped reads	1,160,894 / 89.16%
Unmapped reads	141,166 / 10.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,282 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	36,621 / 2.81%
Duplication rate	2.21%
Clipped reads	1,165,612 / 89.52%

2.2. ACGT Content

Number/percentage of A's	17,212,949 / 25.94%
Number/percentage of C's	12,873,082 / 19.4%
Number/percentage of T's	20,636,341 / 31.1%
Number/percentage of G's	15,633,101 / 23.56%
Number/percentage of N's	1,053 / 0%
GC Percentage	42.96%

2.3. Coverage

Mean	0.0214

Standard Deviation	0.2309

2.4. Mapping Quality

Mean Mapping Quality	43.34

2.5. Mismatches and indels

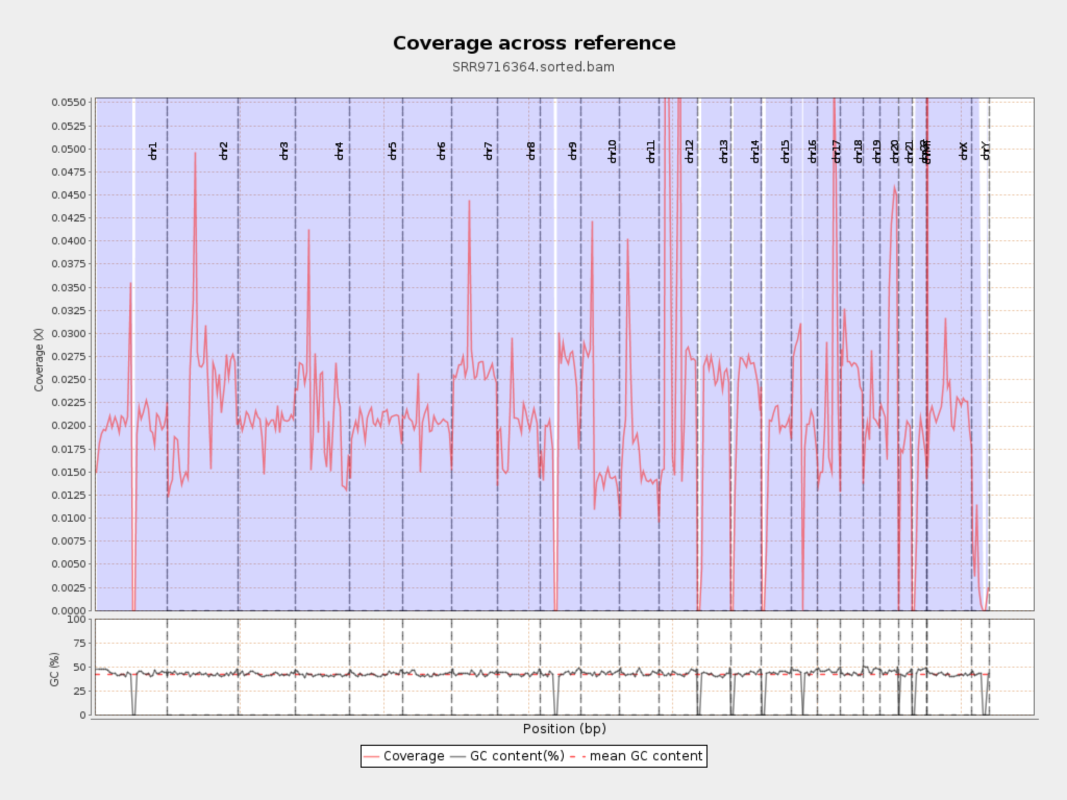
General error rate	0.57%
Mismatches	366,132
Insertions	4,722
Mapped reads with at least one insertion	0.4%
Deletions	11,820
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.61%

2.6. Chromosome stats

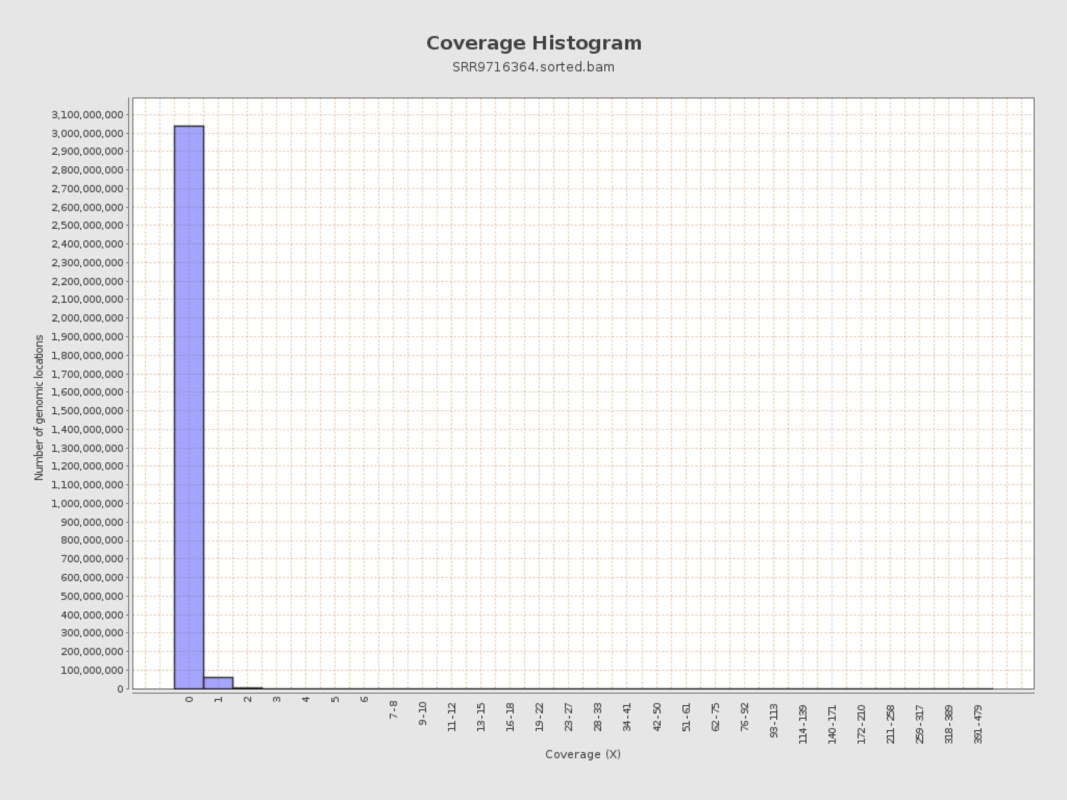
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4825360	0.0194	0.3929
chr2	243199373	5634686	0.0232	0.2633
chr3	198022430	4031028	0.0204	0.1511
chr4	191154276	4164951	0.0218	0.1736
chr5	180915260	3714702	0.0205	0.154
chr6	171115067	3491832	0.0204	0.1683
chr7	159138663	4264380	0.0268	0.306

chr8	146364022	2920226	0.02	0.2035
chr9	141213431	2927018	0.0207	0.2443
chr10	135534747	2618547	0.0193	0.2316
chr11	135006516	2409189	0.0178	0.1917
chr12	133851895	4548299	0.034	0.2085
chr13	115169878	2470980	0.0215	0.154
chr14	107349540	2337049	0.0218	0.1769
chr15	102531392	1708260	0.0167	0.1386
chr16	90354753	1914007	0.0212	0.1711
chr17	81195210	1985351	0.0245	0.1705
chr18	78077248	2100814	0.0269	0.4255
chr19	59128983	1222720	0.0207	0.3
chr20	63025520	1961522	0.0311	0.1939
chr21	48129895	800427	0.0166	0.154
chr22	51304566	662340	0.0129	0.1193
chrMT	16571	11834	0.7141	0.9045
chrX	155270560	3452187	0.0222	0.1879
chrY	59373566	198424	0.0033	0.0894

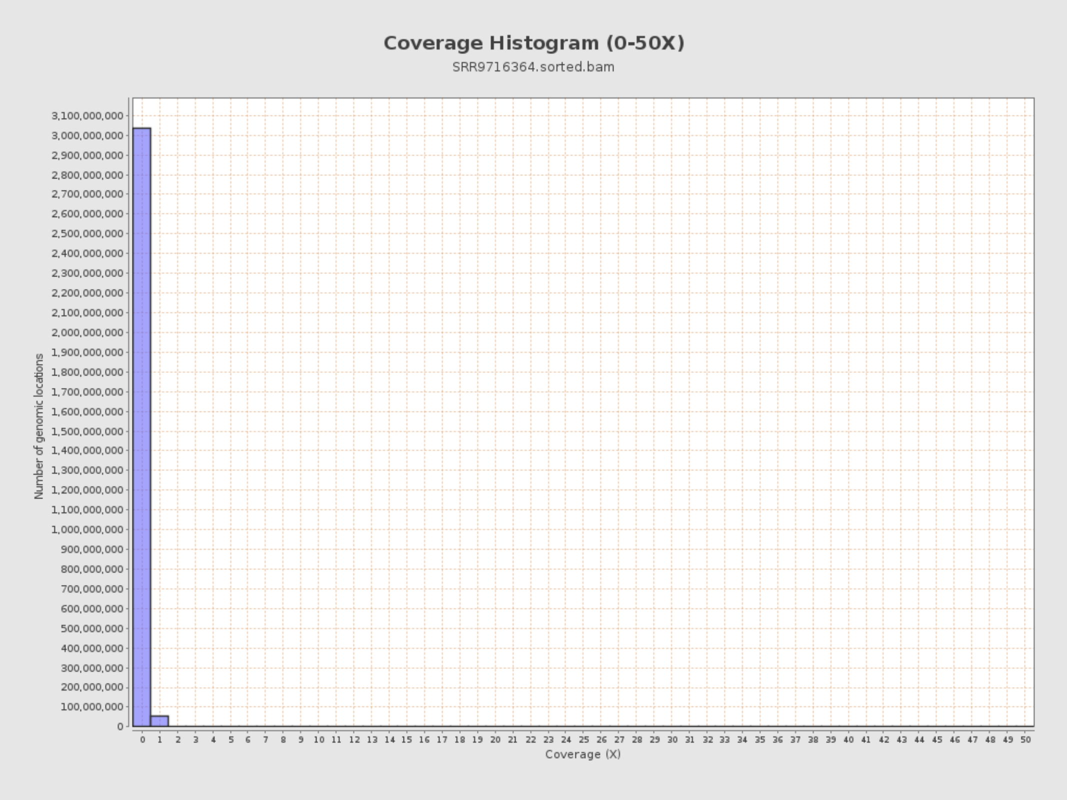
3. Results : Coverage across reference



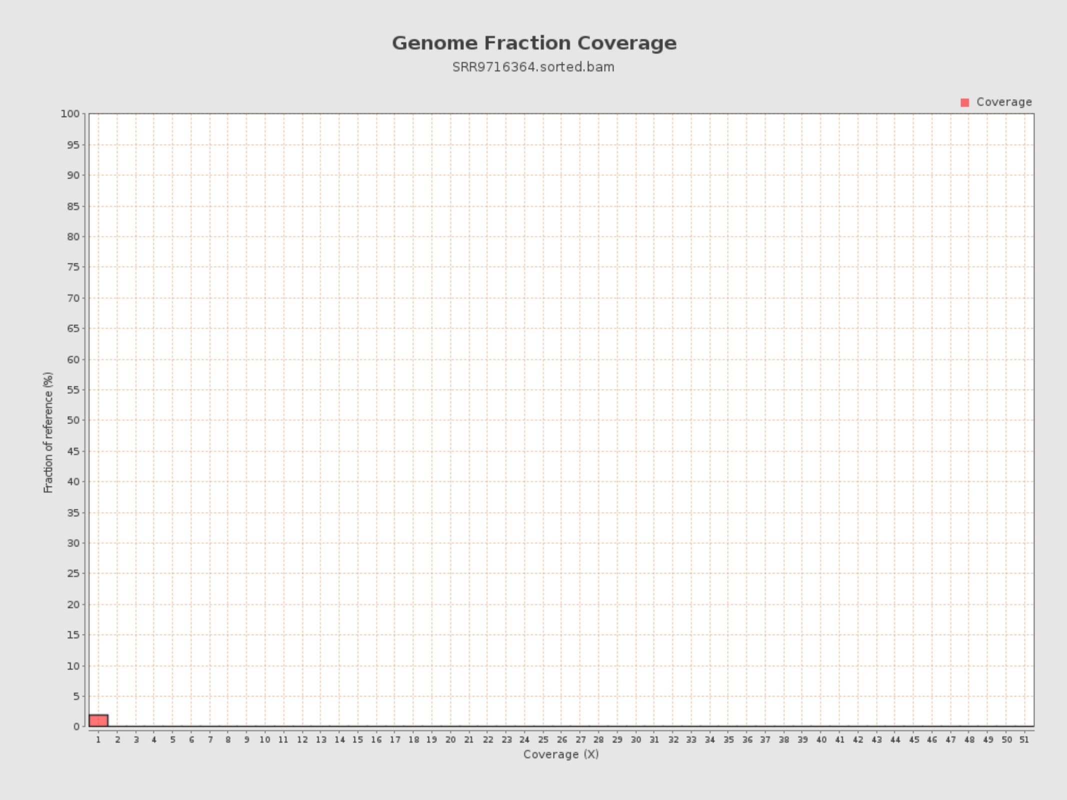
4. Results : Coverage Histogram



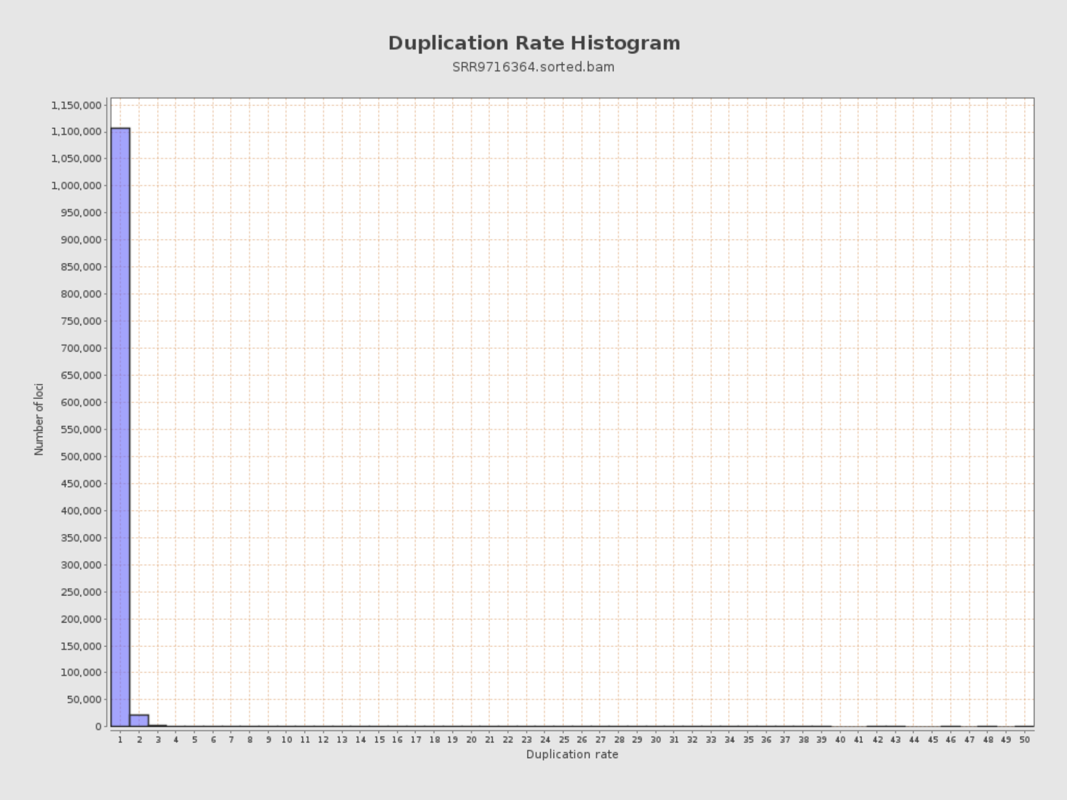
5. Results : Coverage Histogram (0-50X)



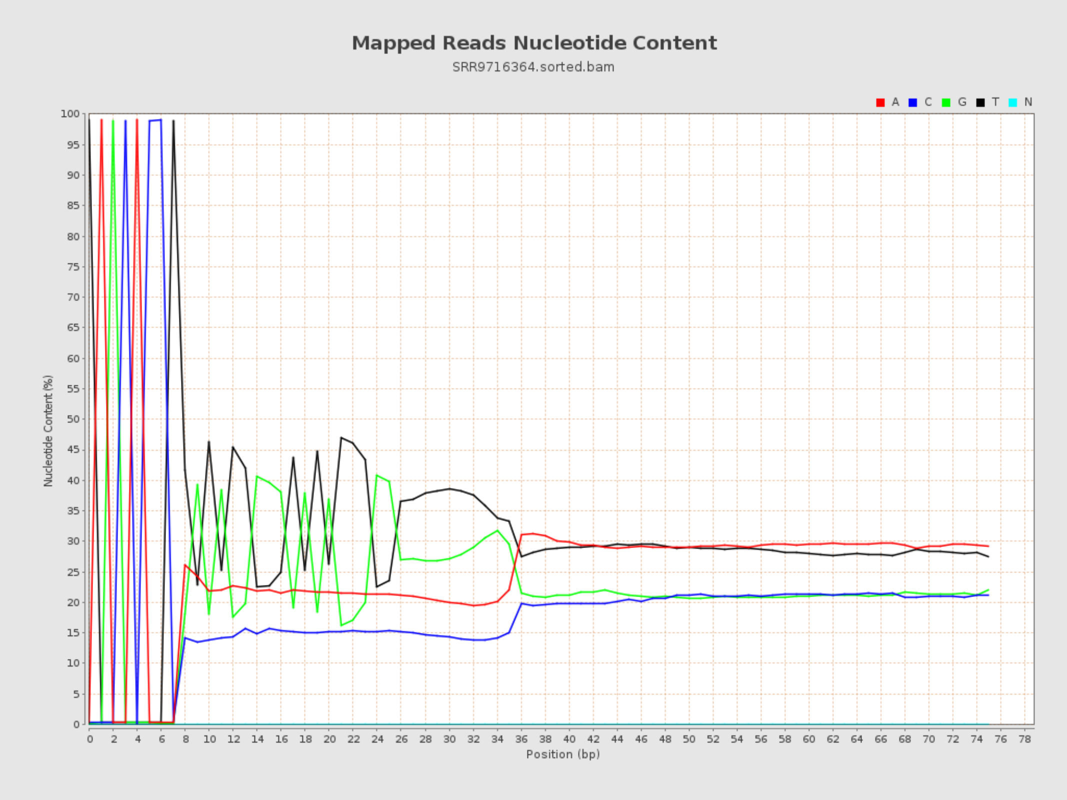
6. Results : Genome Fraction Coverage



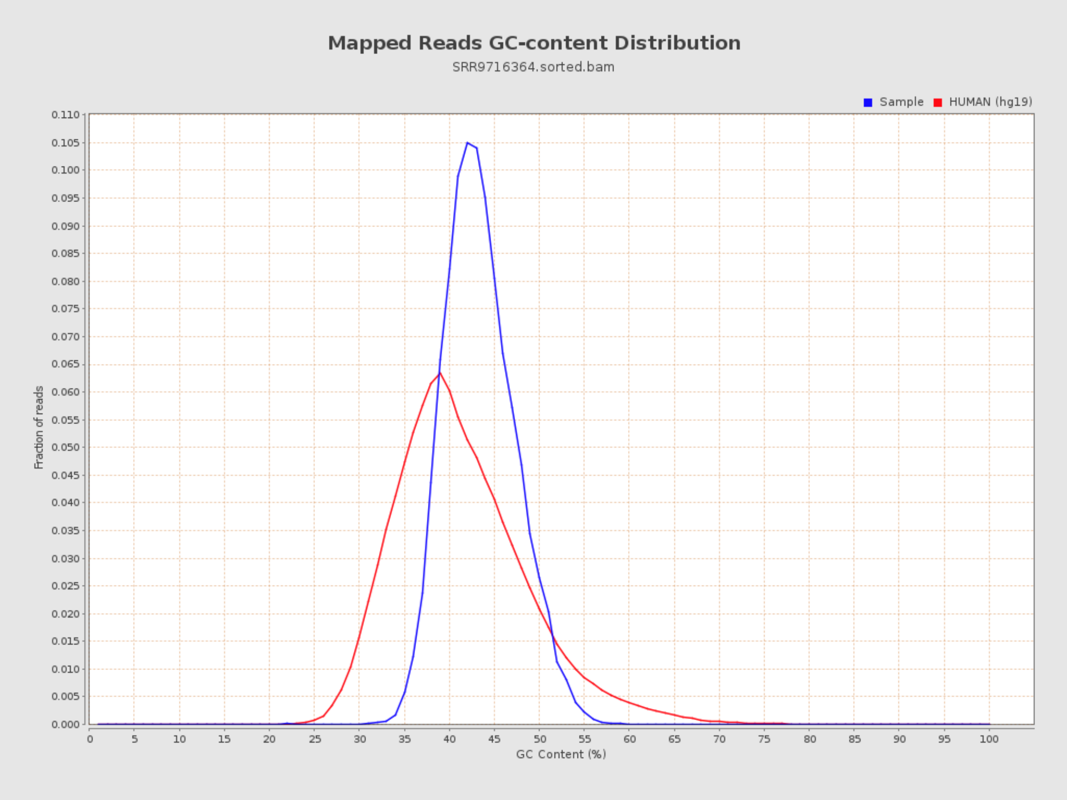
7. Results : Duplication Rate Histogram



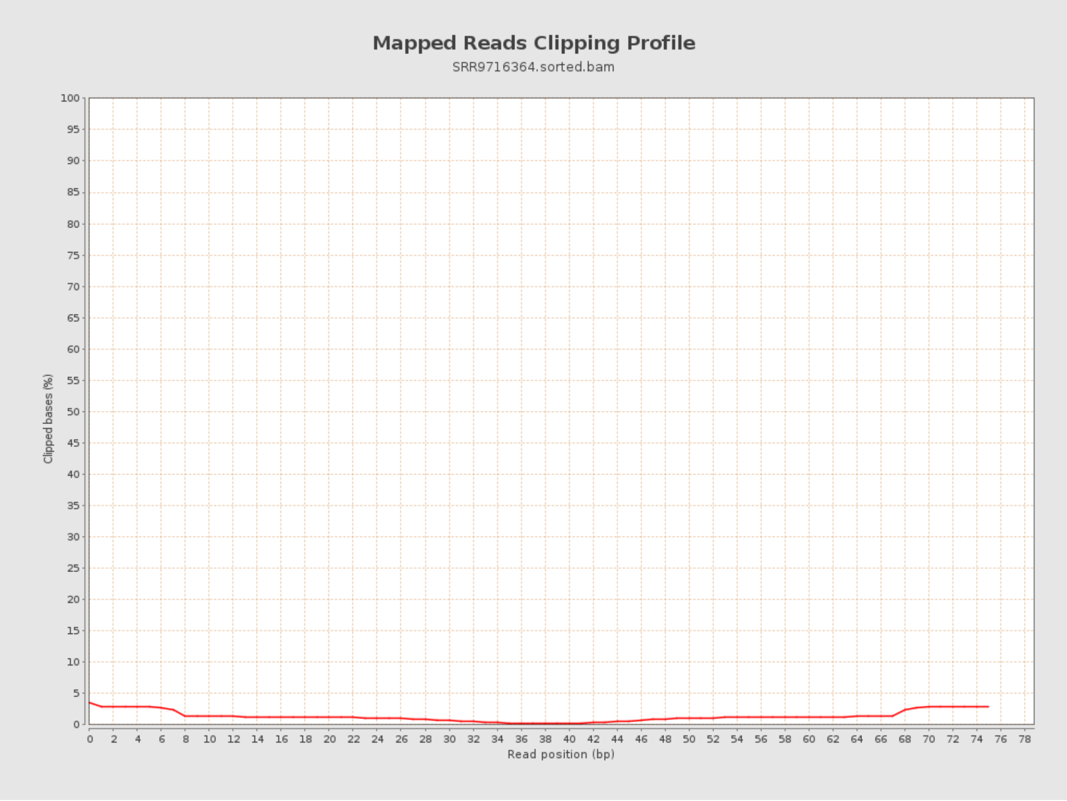
8. Results : Mapped Reads Nucleotide Content



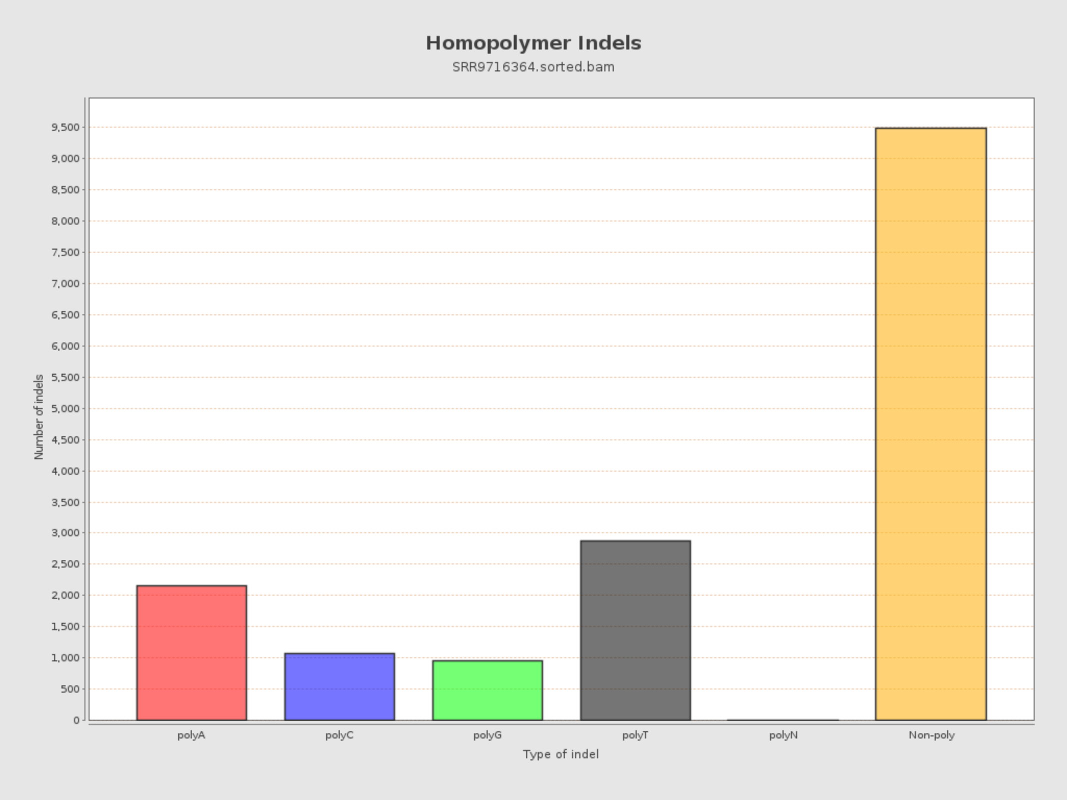
9. Results : Mapped Reads GC-content Distribution



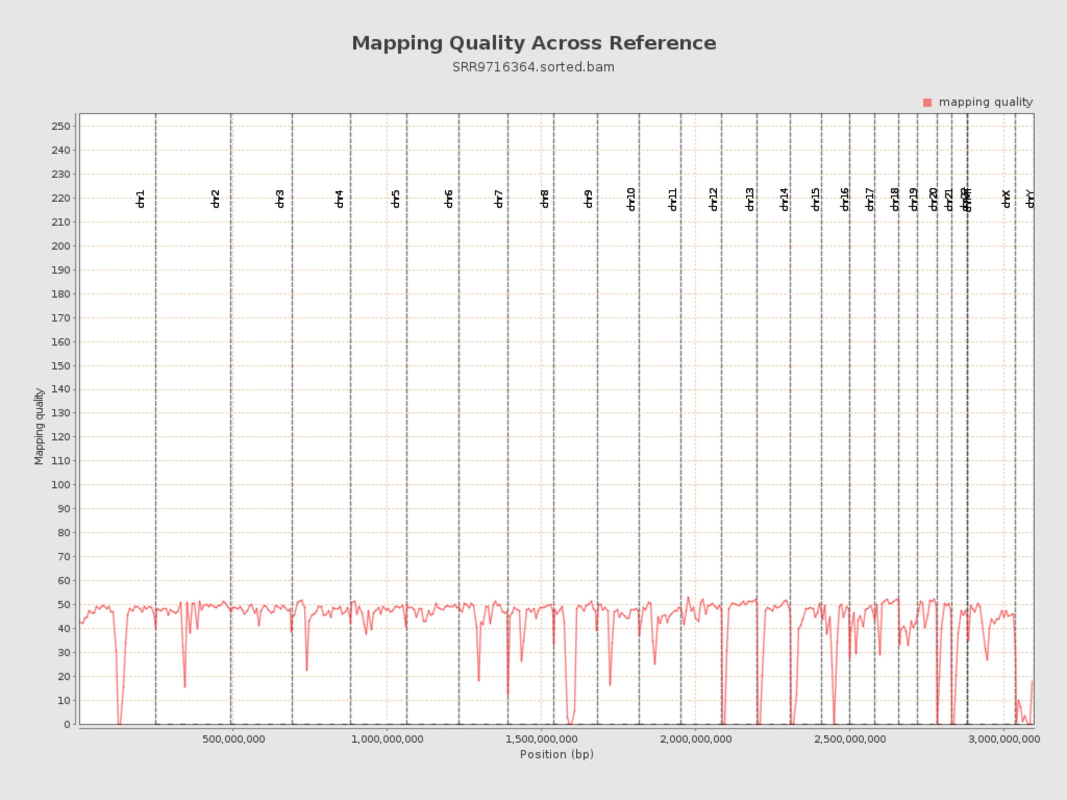
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram