Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:15:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716934.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_SRR9716934 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716934.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:15:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716934.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,312,369
Mapped reads	941,925 / 71.77%
Unmapped reads	370,444 / 28.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,092 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	66,359 / 5.06%
Duplication rate	6.02%
Clipped reads	941,332 / 71.73%

2.2. ACGT Content

Number/percentage of A's	11,015,257 / 22.07%
Number/percentage of C's	8,892,720 / 17.82%
Number/percentage of T's	16,492,762 / 33.05%
Number/percentage of G's	13,506,027 / 27.06%
Number/percentage of N's	915 / 0%
GC Percentage	44.88%

2.3. Coverage

Mean	0.0161

Standard Deviation	0.1695

2.4. Mapping Quality

Mean Mapping Quality	42.66

2.5. Mismatches and indels

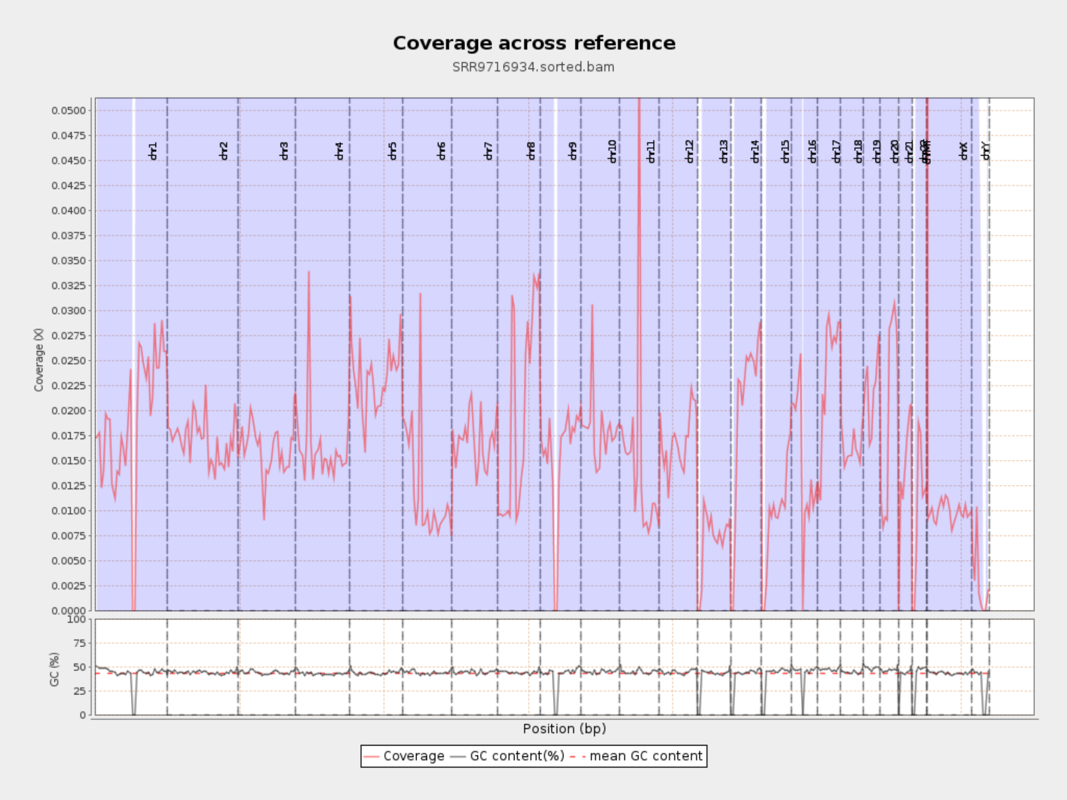
General error rate	0.72%
Mismatches	354,126
Insertions	3,028
Mapped reads with at least one insertion	0.32%
Deletions	8,003
Mapped reads with at least one deletion	0.85%
Homopolymer indels	39.01%

2.6. Chromosome stats

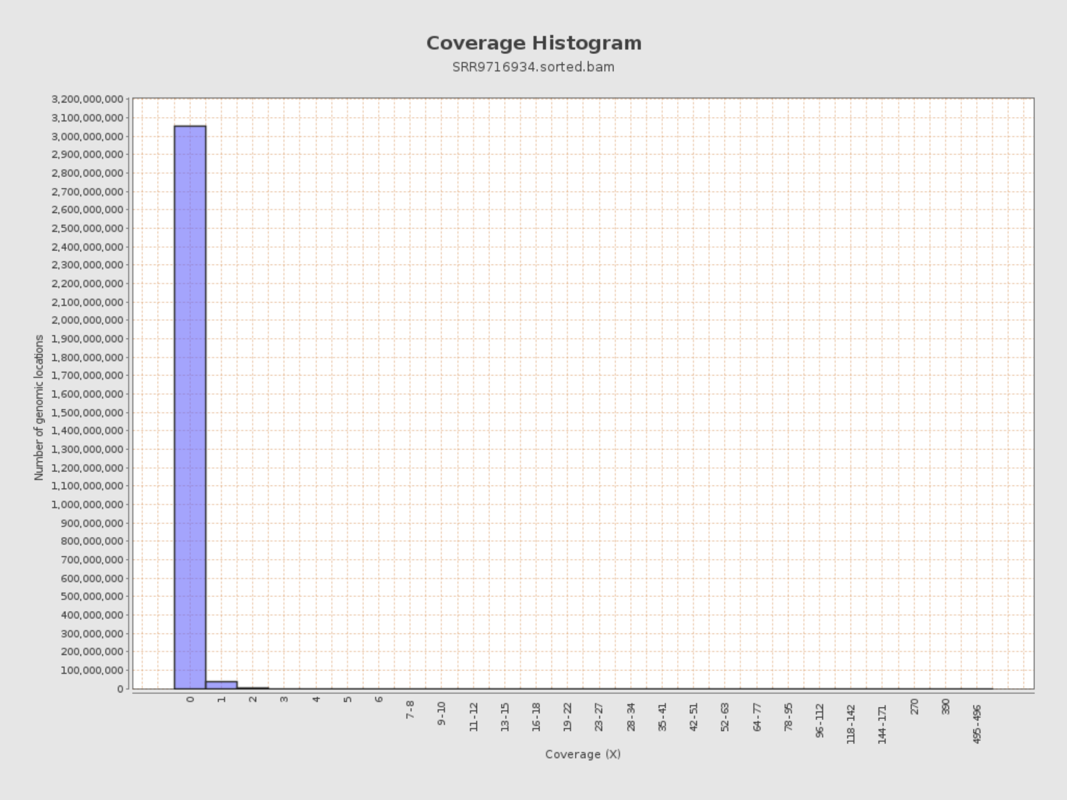
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4721845	0.0189	0.1928
chr2	243199373	4141977	0.017	0.2571
chr3	198022430	3182339	0.0161	0.1466
chr4	191154276	3133566	0.0164	0.1578
chr5	180915260	4216671	0.0233	0.1746
chr6	171115067	2084612	0.0122	0.1504
chr7	159138663	2702368	0.017	0.1707

chr8	146364022	2870517	0.0196	0.1656
chr9	141213431	2154766	0.0153	0.1516
chr10	135534747	2472239	0.0182	0.192
chr11	135006516	2081523	0.0154	0.1585
chr12	133851895	2261486	0.0169	0.1509
chr13	115169878	797927	0.0069	0.0972
chr14	107349540	2172825	0.0202	0.1665
chr15	102531392	950689	0.0093	0.1119
chr16	90354753	1293769	0.0143	0.1585
chr17	81195210	1911789	0.0235	0.1834
chr18	78077248	1263438	0.0162	0.1674
chr19	59128983	1291786	0.0218	0.2118
chr20	63025520	1244637	0.0197	0.1697
chr21	48129895	689253	0.0143	0.1512
chr22	51304566	532378	0.0104	0.122
chrMT	16571	51052	3.0808	2.8956
chrX	155270560	1531975	0.0099	0.1168
chrY	59373566	165999	0.0028	0.0917

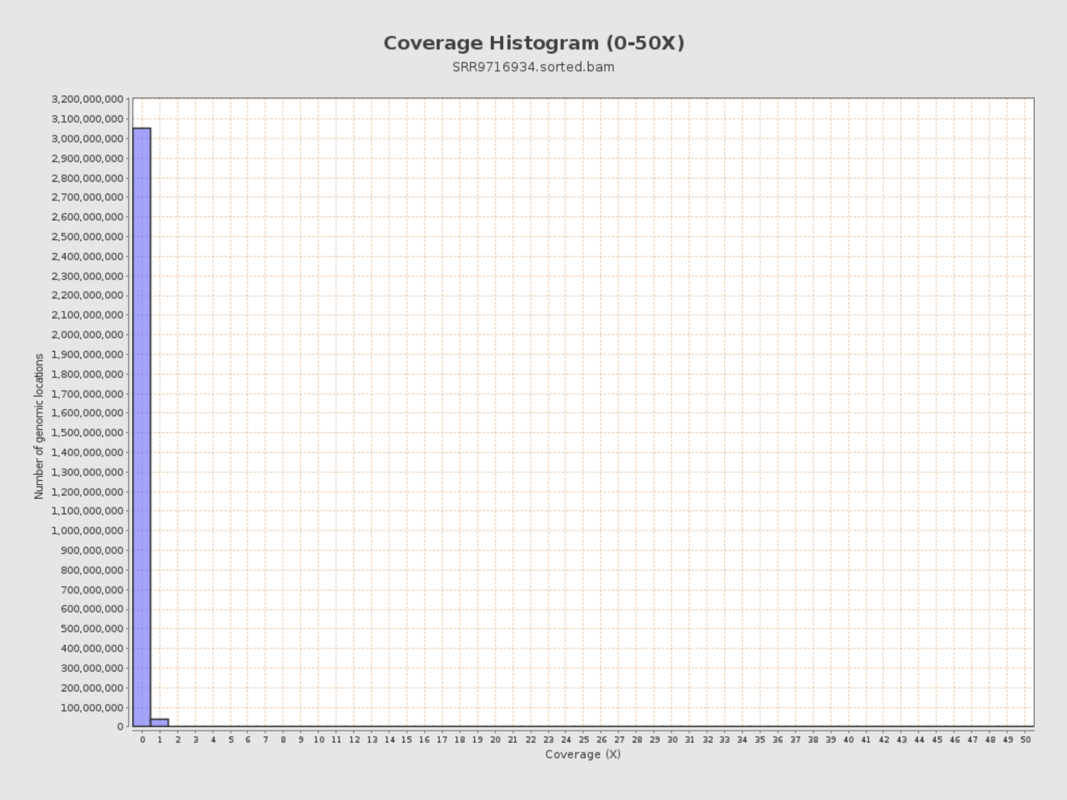
3. Results : Coverage across reference



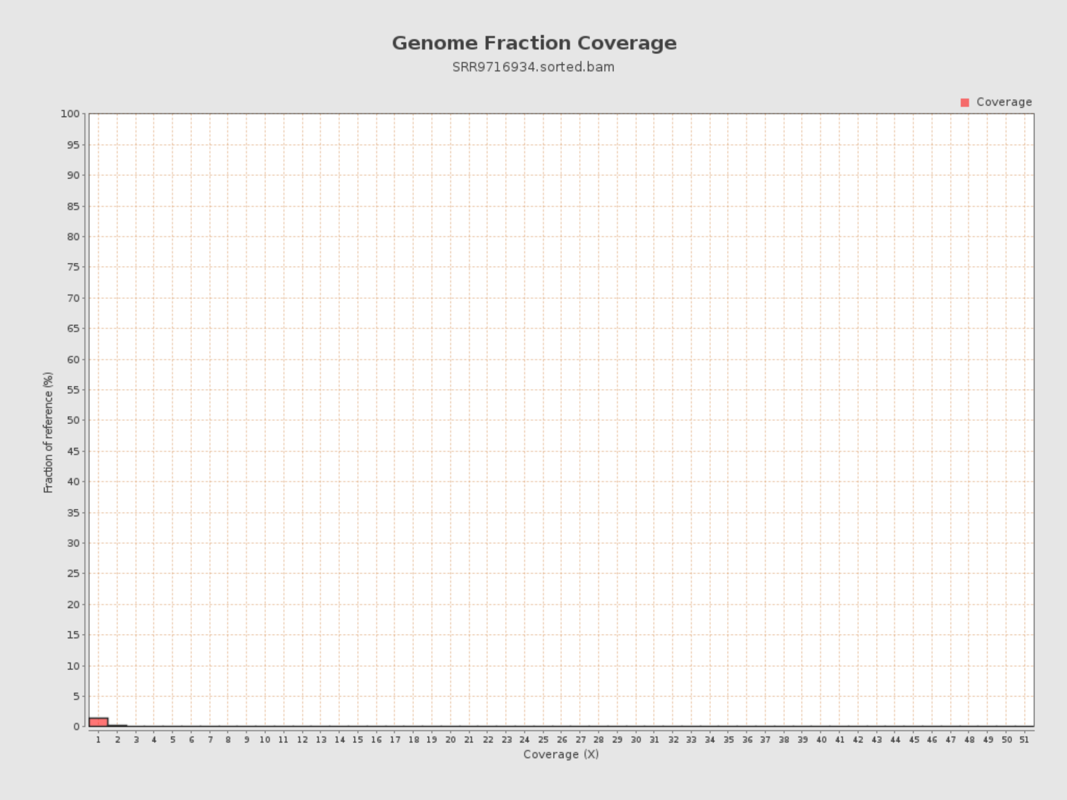
4. Results : Coverage Histogram



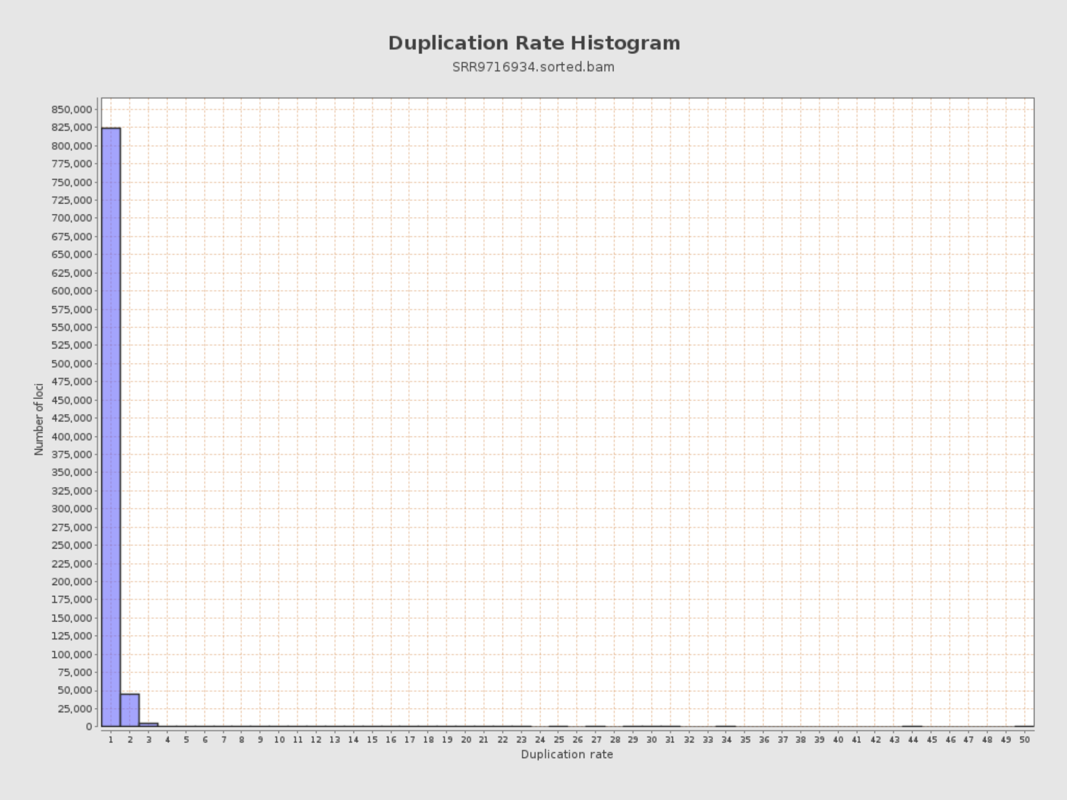
5. Results : Coverage Histogram (0-50X)



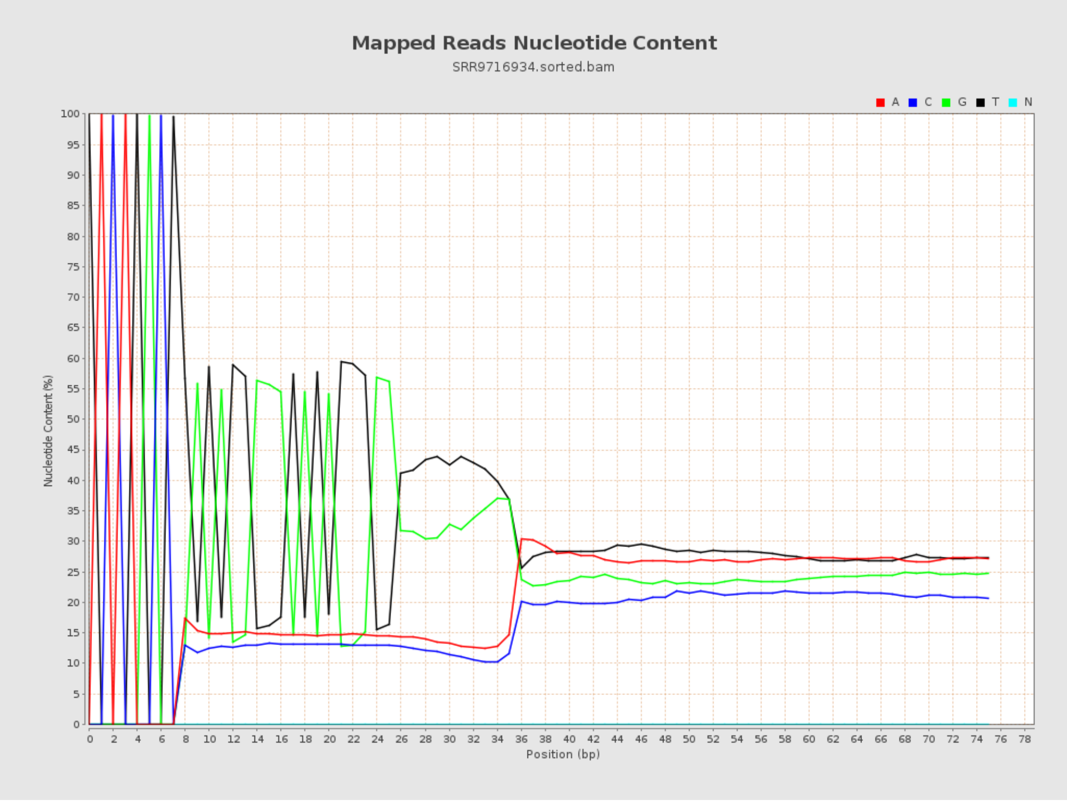
6. Results : Genome Fraction Coverage



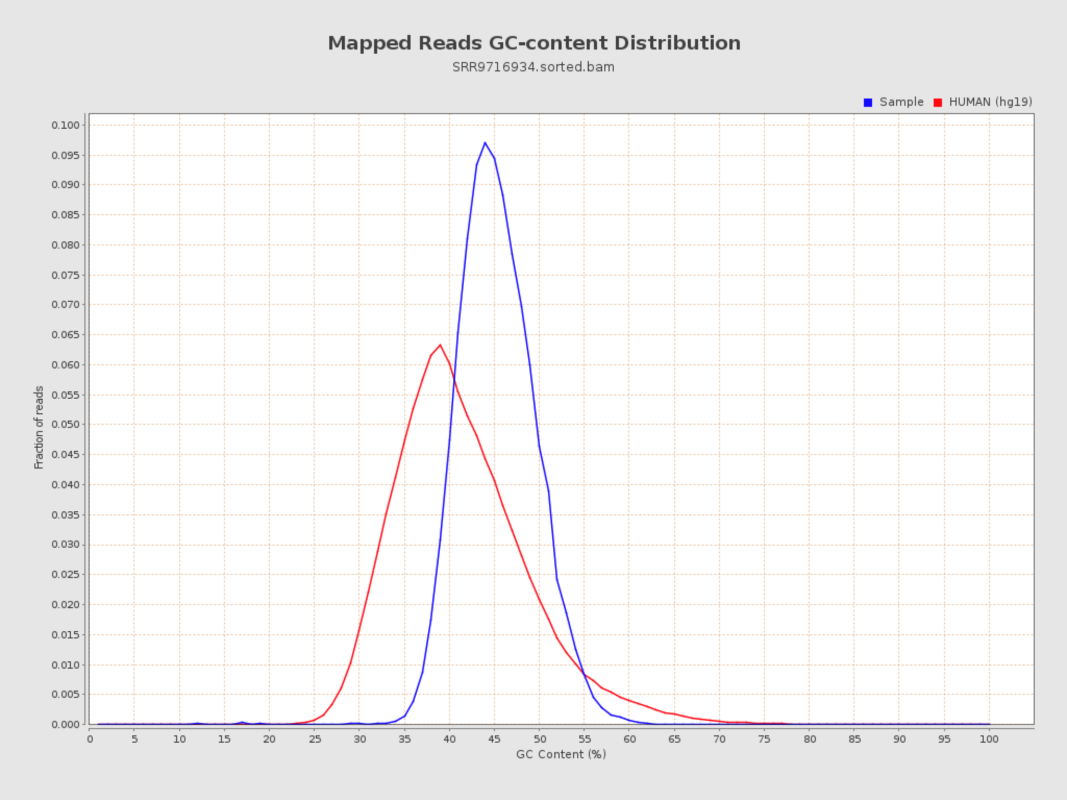
7. Results : Duplication Rate Histogram



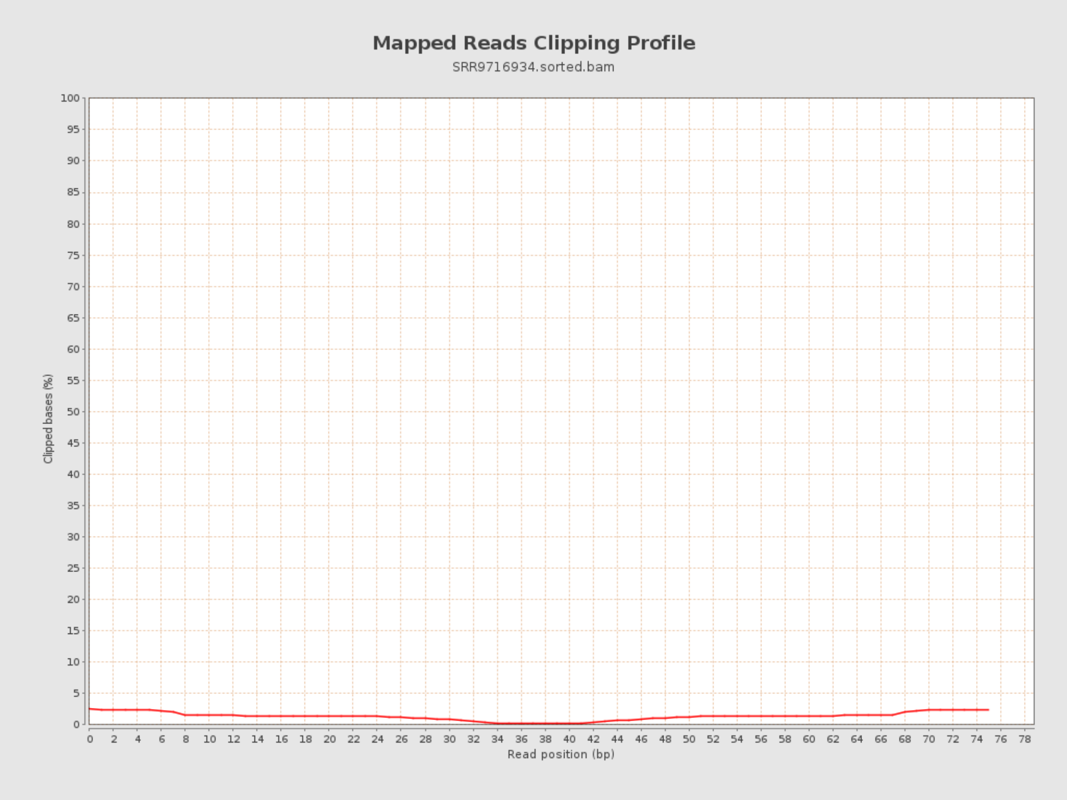
8. Results : Mapped Reads Nucleotide Content



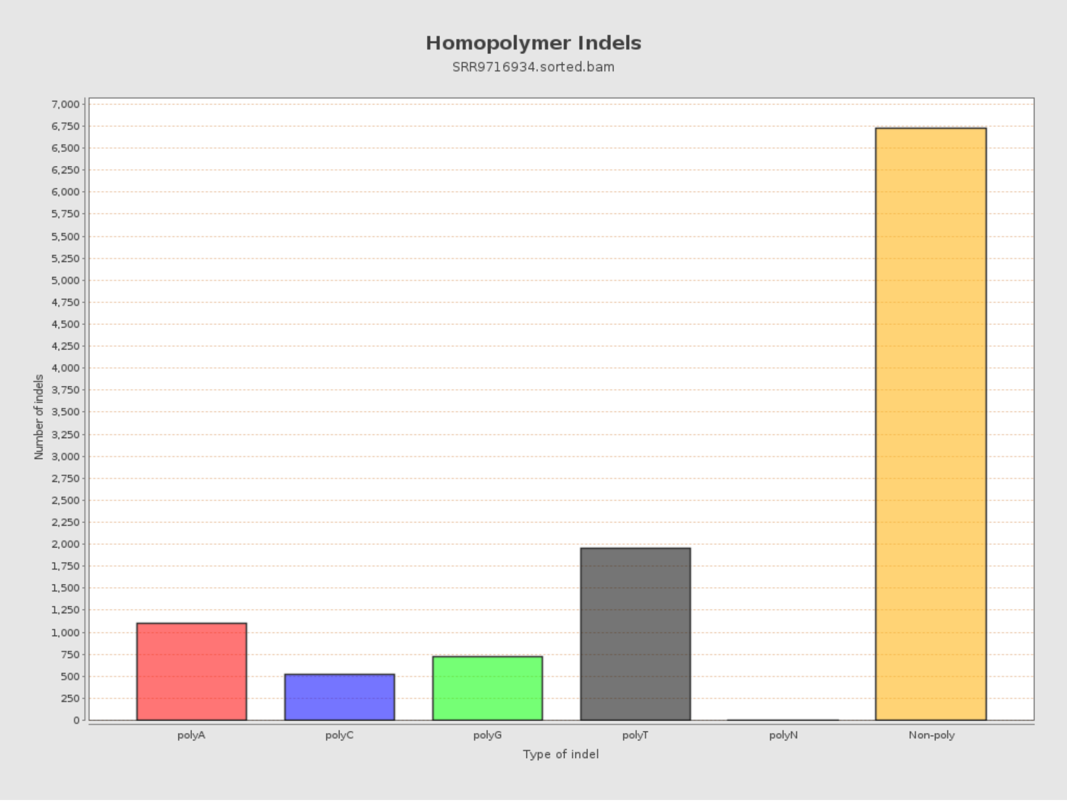
9. Results : Mapped Reads GC-content Distribution



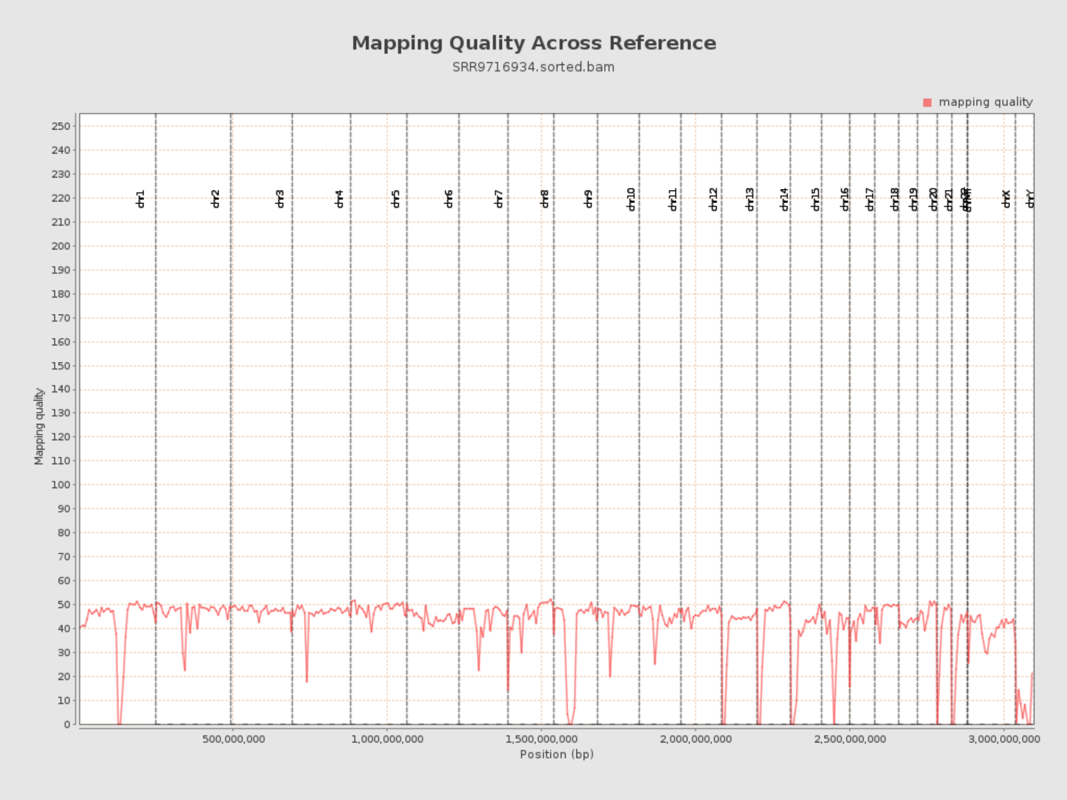
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram