Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:22:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716732.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_SRR9716732 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716732.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:22:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716732.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	537,161
Mapped reads	499,679 / 93.02%
Unmapped reads	37,482 / 6.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,708 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	7,630 / 1.42%
Duplication rate	1.11%
Clipped reads	501,845 / 93.43%

2.2. ACGT Content

Number/percentage of A's	7,871,882 / 26.34%
Number/percentage of C's	5,884,595 / 19.69%
Number/percentage of T's	8,741,715 / 29.25%
Number/percentage of G's	7,383,244 / 24.71%
Number/percentage of N's	375 / 0%
GC Percentage	44.4%

2.3. Coverage

Mean	0.0097

Standard Deviation	0.121

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

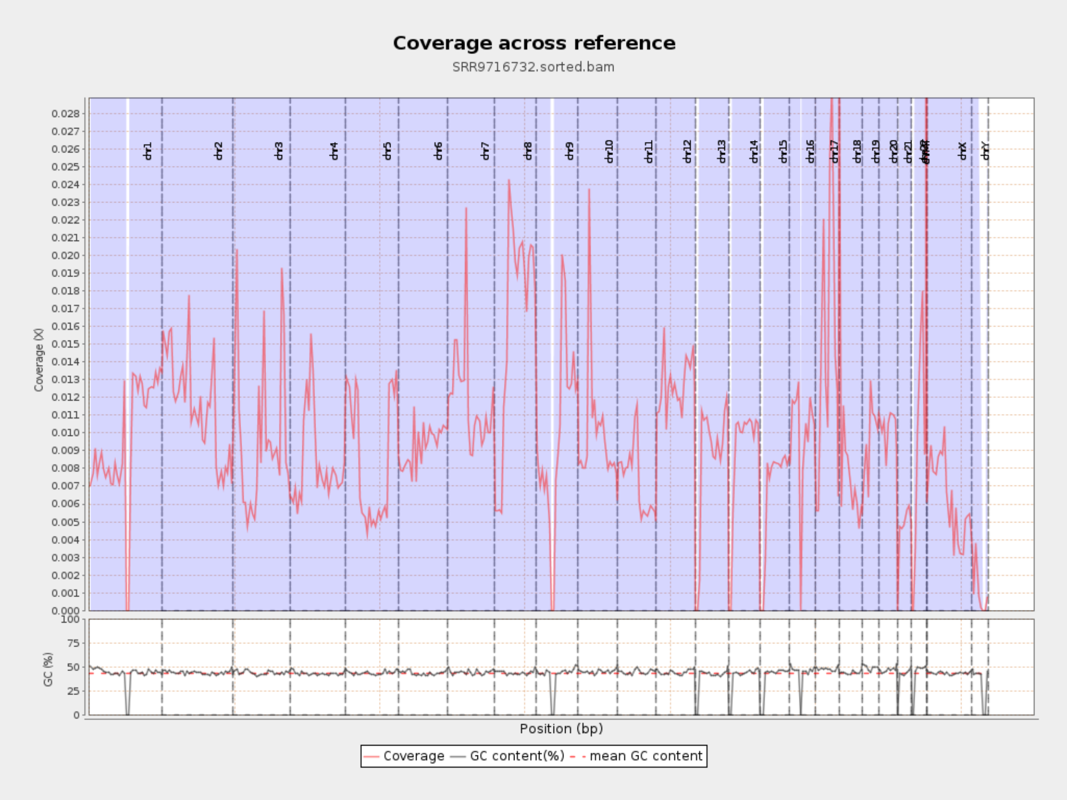
General error rate	0.49%
Mismatches	142,607
Insertions	1,809
Mapped reads with at least one insertion	0.36%
Deletions	5,600
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.21%

2.6. Chromosome stats

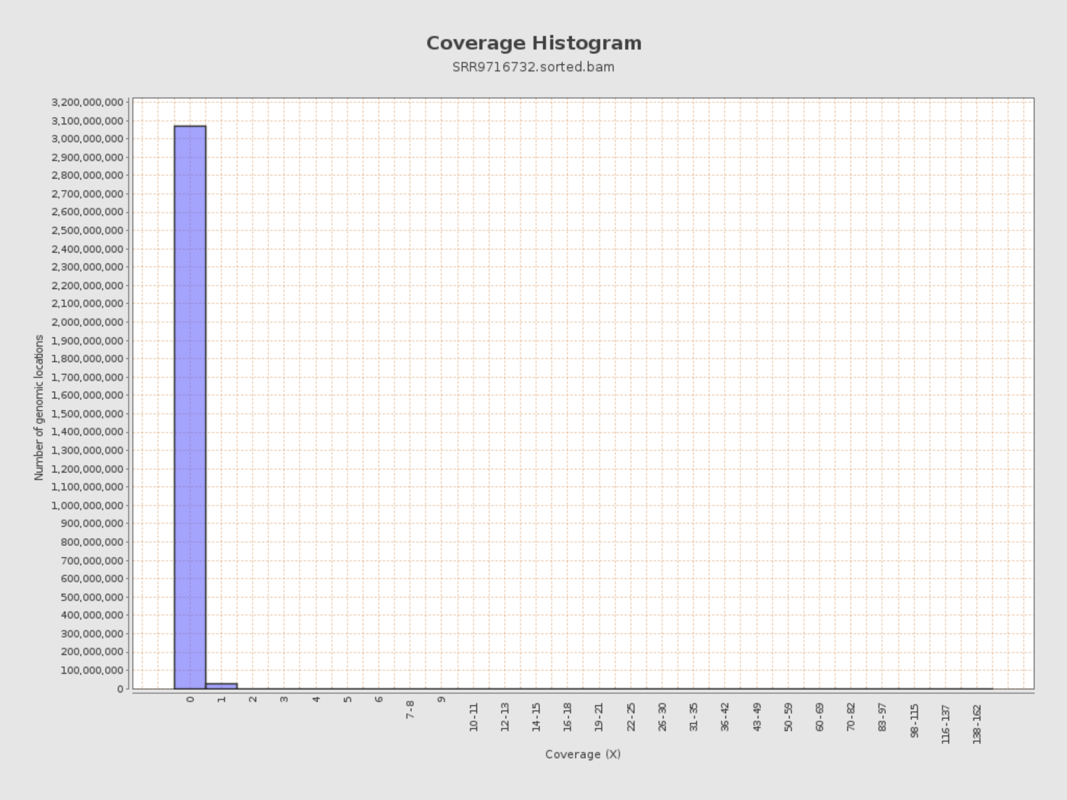
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2376530	0.0095	0.1607
chr2	243199373	2840775	0.0117	0.1354
chr3	198022430	1930857	0.0098	0.1019
chr4	191154276	1594152	0.0083	0.0977
chr5	180915260	1524829	0.0084	0.0944
chr6	171115067	1586428	0.0093	0.1022
chr7	159138663	1905686	0.012	0.1968

chr8	146364022	2395253	0.0164	0.1561
chr9	141213431	1356611	0.0096	0.1048
chr10	135534747	1362486	0.0101	0.137
chr11	135006516	987873	0.0073	0.0949
chr12	133851895	1700636	0.0127	0.1179
chr13	115169878	969851	0.0084	0.0946
chr14	107349540	940386	0.0088	0.0971
chr15	102531392	683866	0.0067	0.0841
chr16	90354753	894754	0.0099	0.1041
chr17	81195210	1221317	0.015	0.1281
chr18	78077248	647805	0.0083	0.1295
chr19	59128983	572233	0.0097	0.1391
chr20	63025520	650014	0.0103	0.1062
chr21	48129895	224075	0.0047	0.0733
chr22	51304566	450803	0.0088	0.0965
chrMT	16571	12330	0.7441	0.933
chrX	155270560	994880	0.0064	0.0855
chrY	59373566	66516	0.0011	0.0422

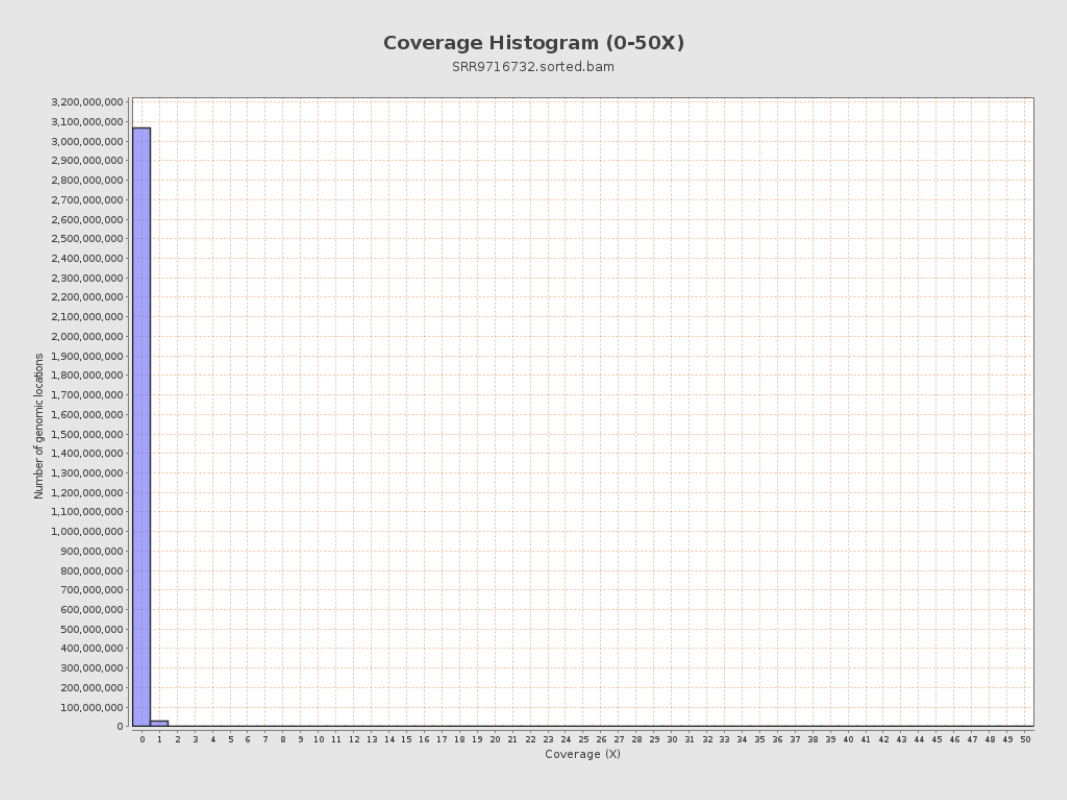
3. Results : Coverage across reference



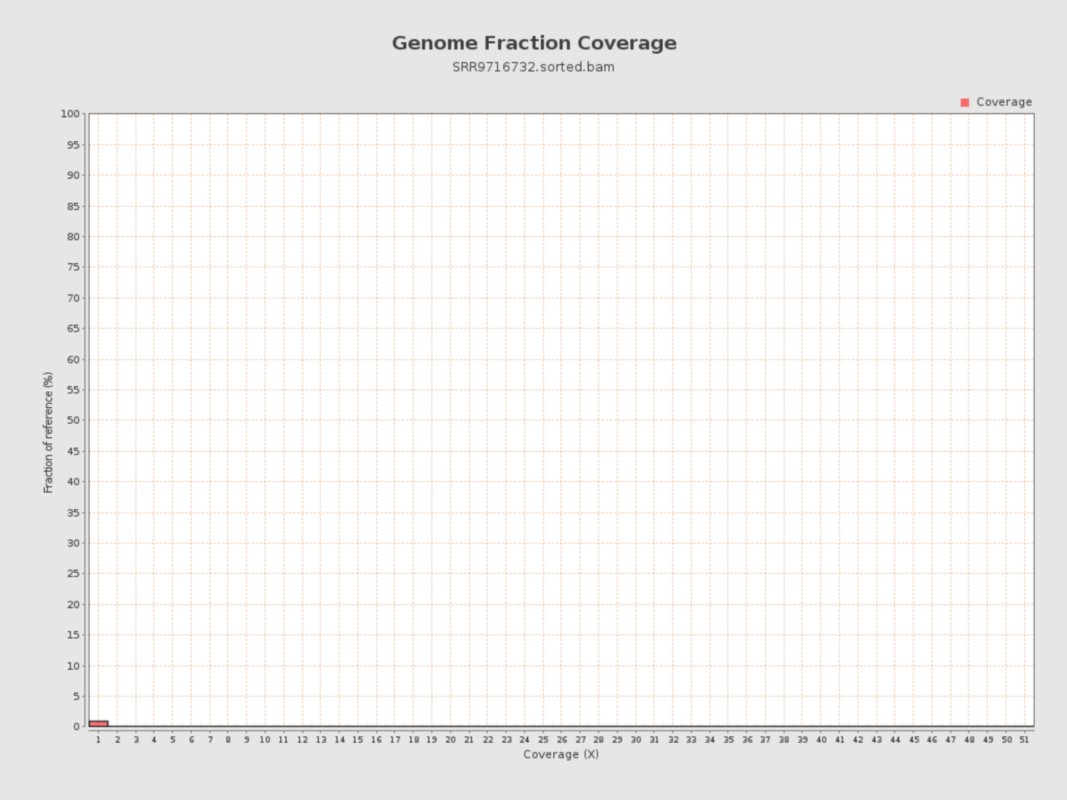
4. Results : Coverage Histogram



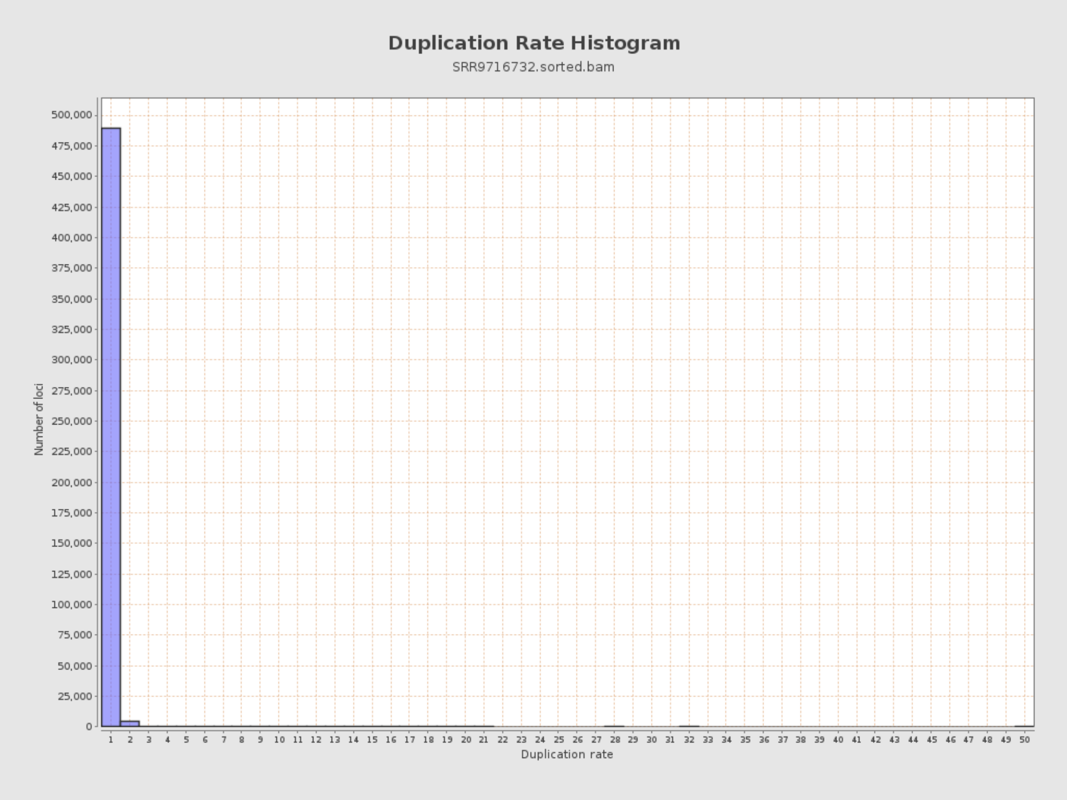
5. Results : Coverage Histogram (0-50X)



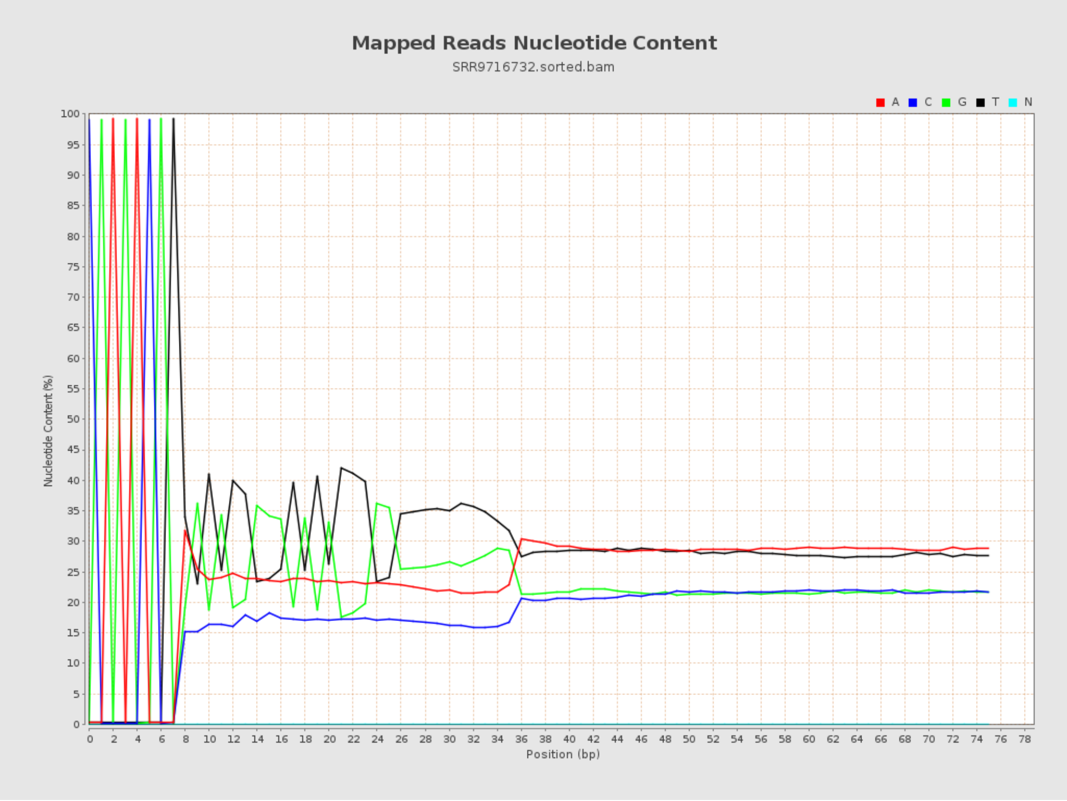
6. Results : Genome Fraction Coverage



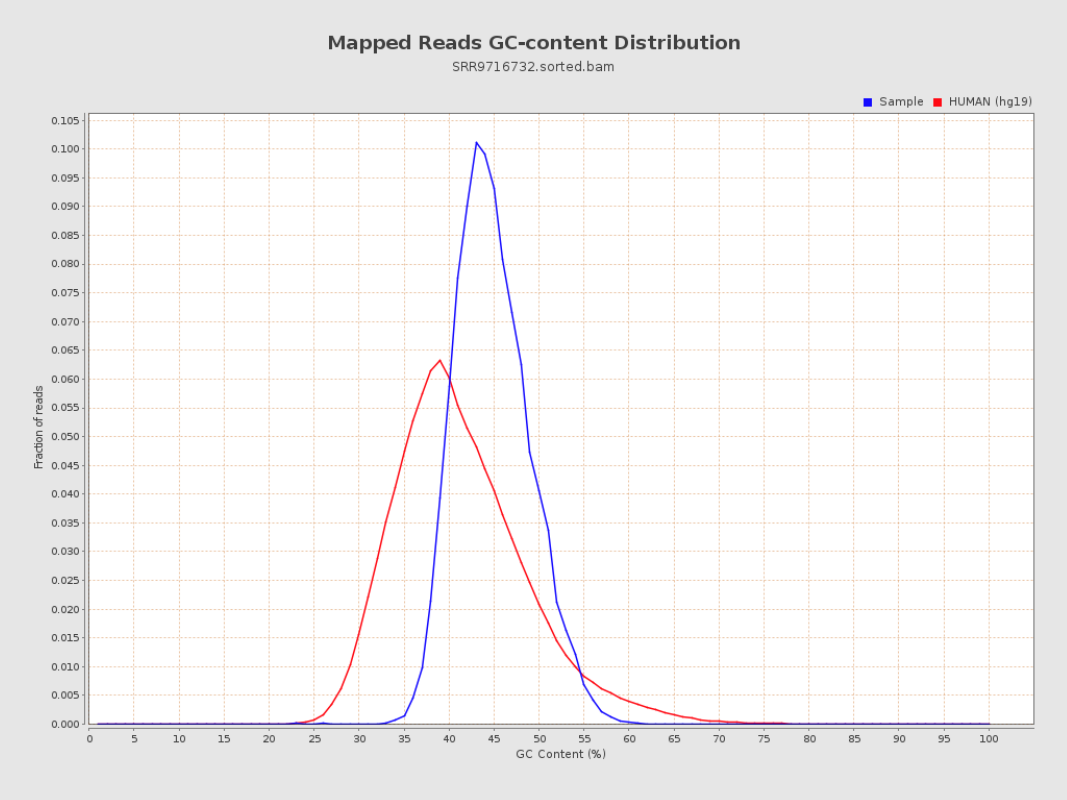
7. Results : Duplication Rate Histogram



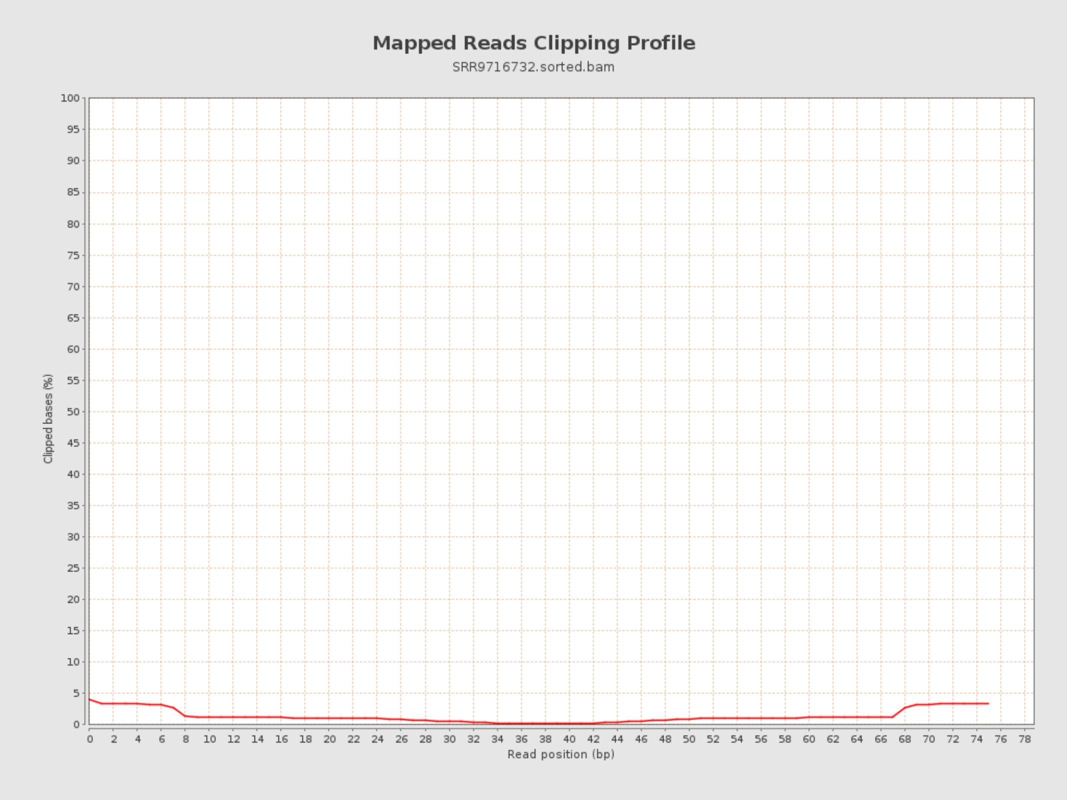
8. Results : Mapped Reads Nucleotide Content



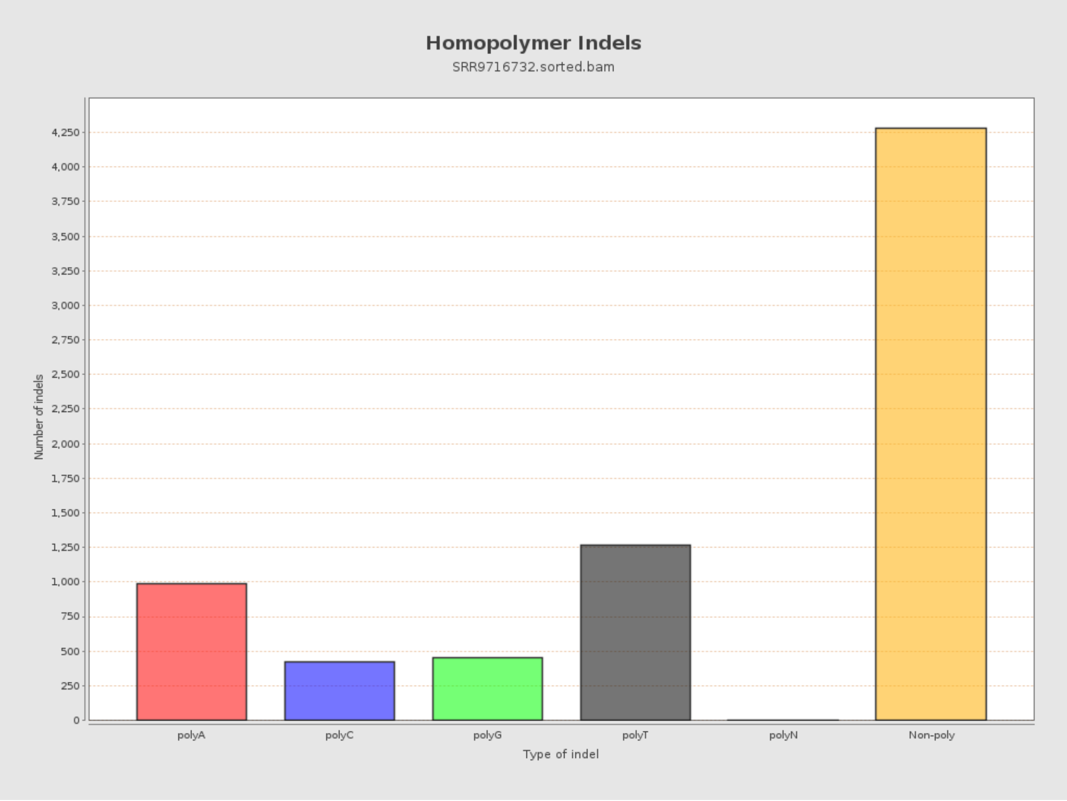
9. Results : Mapped Reads GC-content Distribution



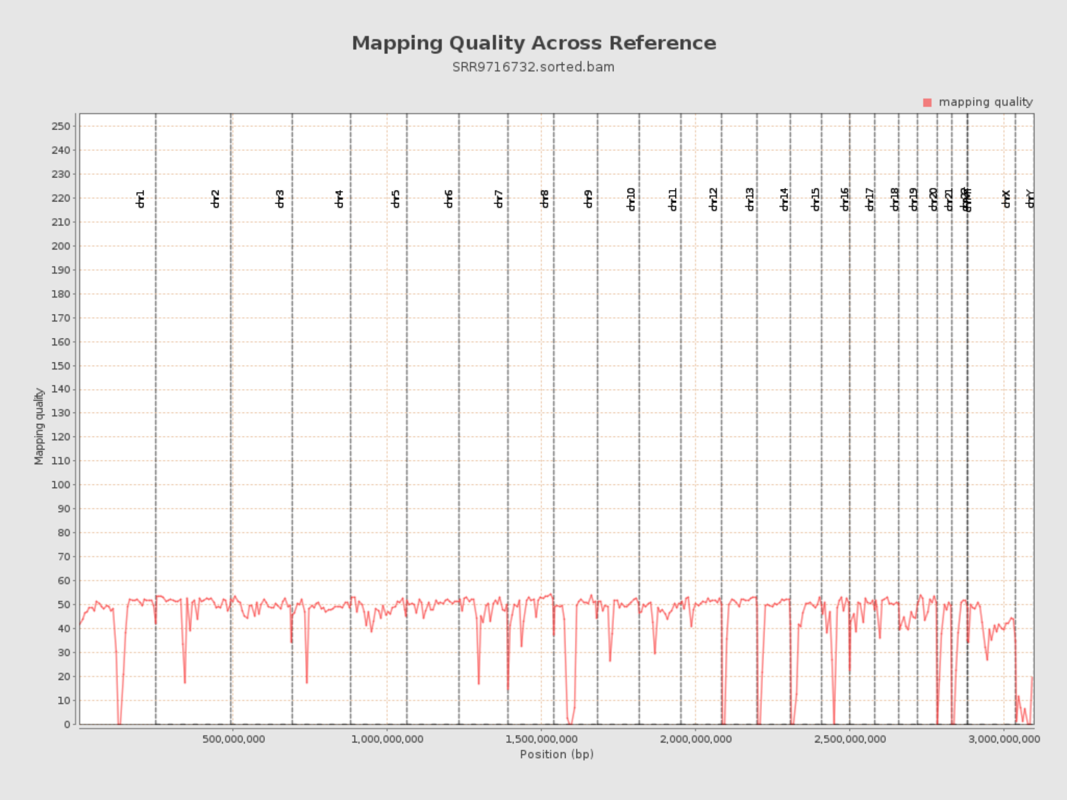
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram